All Microarray Data Following Oxythioquinox Exposure

	1 DMSO - Average	1 DMSO - Stdev	1 15 - Average	1 15 - Stdev	1 60 - Average	1 60 - Stdev	1 120 - Average	1 120 - Stdev	2 dmso - Average	2 dmso - Stdev	2 15 - Average	2 15 - Stdev	2 60 - Average	2 60 - Stdev	2 120 - Average	2 120 - Stdev	3 dmso - Average
U43653_at	34.8	9.62	32.9	38.04	78.45	6.43	59.45	21.71	139.65	127.77	63.95	6.29	46.8	20.08	249.2	233.91	229.85
M55419_at	53.6	24.75	72.25	83.51	249.95	39.1	304.1	135.76	324.4	411.11	55.55	35.71	229.1	37.05	169.25	146.16	193.1
X13955_s_at	59.6	8.34	32.25	37.26	103.15	5.59	127.8	56	183.95	2.62	80.95	30.48	146.7	51.48	119.2	61.09	52.15
L76571_at	235.2	17.39	93.5	108.05	365.15	4.45	361.9	155	194.8	74.95	884.05	960.32	378.55	180.38	246.05	38.96	477.3
U03274_at	176.2	9.48	72.35	83.65	332.55	10.68	136.55	26.09	165.1	13.58	251.95	120.42	279.2	17.39	305.75	74.03	218.15
M19301_at	303.05	23.26	137.8	159.24	435.5	13.86	272.5	118.23	401.4	275.77	289.7	253.14	77.95	7.28	380.65	436.21	479.7
D14678_at	111.05	21.43	168.9	195.16	263.65	21.71	202.65	83.51	235.9	154.71	183.8	35.78	932.2	1167.29	137.35	58.34	222.85
U04840_at	269.95	81.81	270	311.98	689.75	99.49	642.85	648.2	363.15	216.87	510.05	319.82	106	100.69	370.85	384.31	447.85
AC002086_at	31.1	12.45	52.4	60.53	306.1	3.39	465.7	620.42	96.8	66.19	284.35	308.65	266.1	52.89	31.7	1.27	235.9
M83664_at	82.15	75.73	305.9	353.41	638.05	49	1000.7	853.2	404.8	307.31	519.7	594.54	636.55	166.24	401.15	217.72	400.55
HG4533-HT4	1342.6	28.43	403.7	466.41	1576.3	45.82	1332.55	281.64	1250.3	118.79	1528.6	720.54	1576.05	43.91	1266.5	438.55	1026
D63480_at	198.35	122.97	402.15	464.64	1063.9	136.05	1082.85	685.26	1258.55	87.04	1160.95	151.67	537.05	447.25	791.5	248.62	702.6
D50645_at	88.1	23.62	567.3	655.49	310.6	0.57	570.5	178.05	177.2	87.68	394.55	157.47	259.25	76.44	445.7	319.47	225.05
J00124_at	154774.5	3683.89	89160.95	103014.63	177933.66	3862.43	179068.44	35383.41	191494.3	29145.11	178102.84	29765.45	252400.2	15425.25	294318.25	136683.66	254747.09
L41919_rna1	289.8	20.51	108.4	125.3	609.95	50.13	949	1071.69	579.65	474.54	1178.2	397.68	280.4	9.62	1138.7	1412.66	712.25
S67156_at	42.65	21.14	355.25	410.48	269.2	6.08	464.75	393.36	29.6	10.18	286.2	352.99	200.95	102.32	179.7	214.39	120.55

J00220_cds4	858.95	183.35	423	488.75	2237.45	166.81	1063.5	157.12	908.4	539.52	1422.7	885.01	1232.1	211.99	1093.3	580.11	708.85
X98085_at	668.5	61.38	340.5	393.43	1030.75	51.69	545.2	568.09	969.85	513.01	702.95	522.34	1227.4	354.12	1137.2	1373.34	872.05
D86964_at	181.6	89.66	537.75	621.33	705.95	98.78	844.35	1043.05	557.4	566.11	820	923.2	1041.1	446.18	552.5	554.51	483.8
X89750_at	1902.95	110.52	2430.05	2807.57	3421.4	60.81	2542.45	1645.65	3485.4	570.07	4325.35	685.12	2465.2	1056.7	2686.7	1304.19	2415.8
D63482_at	162.95	44.48	377	435.58	654.85	61.59	194.55	161.43	835.75	635.34	459.45	203.58	835.4	722.24	123.1	51.05	698.2
D55654_at	5270.95	314.31	3139.55	3627.39	7176.4	168.86	5121.65	2298.73	8621.95	249.54	6001.25	769.97	7407.05	603.66	8896.45	1521.76	6299.8
K02766_at	58.85	23.12	132.45	153.09	184.75	17.75	393.6	525.1	125.6	5.8	106.95	31.18	445.45	178.69	423.35	21	295.85
U56814_at	486.75	53.95	140.85	162.71	1139.5	57.7	731.9	611.93	840.9	278.18	705.45	208.53	525.5	294.02	569.95	362.82	333.6
M14123_xpt4	97.5	5.66	348.75	402.98	160.6	4.67	651.8	773.72	715.25	858.64	177.95	66.82	162.4	47.09	554.9	546.88	94.5
U17418_at	223.15	6.58	109.1	126.01	306.25	0.21	160.25	10.39	459.75	214.18	206.5	27.58	242.95	67.39	339.4	37.62	188.05
L07868_at	92.95	30.62	51.55	59.61	267.5	25.46	253.1	101.68	154.55	58.19	49.85	37.12	90.85	2.47	571.75	163.7	101.55
X90824_s_at	1556.9	46.95	326	376.61	2299.85	61.02	1421.75	5.73	1960.05	364.37	1585.8	584.35	1258.35	199.47	976.1	309.43	1801.4
X63741_s_at	47.4	28	51.45	59.47	423.7	40.87	103.5	130.11	470.65	144.04	452.95	462.09	271.05	299.74	122.5	104.93	47.95
X14830_at	443.3	14.42	379.9	438.97	620.45	14.5	412.5	369.68	441	152.31	546.3	141.56	416.85	492.36	172.4	13.86	754.35
HG4058-HT4	131.65	34.86	236.35	273.01	329.85	24.82	914.3	502.33	267.6	85.28	644.6	650.96	335.1	198.98	502.95	453.89	155.45

U00944_at	301.05	29.34	284.9	329.23	582.8	48.37	65.7	15.98	329.15	279.66	675.6	566.11	337.55	266.51	399.85	376.68	175.8
HG3123-HT3	161.6	29.13	83.7	96.73	355.55	44.9	516.5	492.99	313.85	248.41	211.3	82.73	206.65	97.09	122.4	6.79	130.95
X64878_at	85.55	31.32	144.3	166.74	272.1	42.28	197.85	62.3	177.5	204.07	660.95	469.02	253.5	138.45	183.95	93.97	701.3
X78121_at	46	19.23	82.85	95.67	183.2	7.21	97.35	74.18	101.55	7.42	115.7	33.8	158.85	205.84	56.85	39.24	124.7
M83181_at	785.7	84.43	641.5	741.19	2023.1	129.82	1073.65	8.84	929.95	908.99	1564.7	613.06	1621.95	46.6	285.35	30.33	1469.4
X63468_at	179.5	19.8	251.95	291.12	500.1	3.25	98.55	57.63	299.8	330.64	517.55	147.71	685.4	372.5	139.7	102.25	504.2
L13258_at	168.8	16.4	100.45	116.04	242.6	16.12	158.4	75.94	276.05	162.42	161.4	66.04	221.4	32.67	242.1	182.43	133.6
U79302_at	335.3	74.1	244.15	282.06	912.65	85.63	273.85	77.29	293.8	22.63	456.85	267.92	340.65	86.62	484.9	220.19	349.4
X75315_at	506.4	259.65	1010.25	1167.22	2004.4	255.55	1263.7	1421.28	702.15	453.33	946.5	933.38	656.3	274.92	760.25	526.16	1023
AFFX-ThrX-M	53.35	15.77	61.15	70.64	257.5	6.65	190.4	8.49	150.3	8.77	84.85	59.47	63	9.62	80.5	67.6	56.15
AFFX-HUMG	146753.59	4673.27	86792.59	100278.34	213070.66	2427.85	180670.09	56681.25	154524.44	24978.34	158628.94	39753.05	210966.3	38336.21	203018.05	24352.4	184011.91
J05008_at	79.45	41.37	19.45	22.42	300.2	26.45	152.05	24.11	59.4	21.21	107.4	6.79	111.35	51.12	289.2	177.2	30.1
Z83745_at	116.45	16.05	55.15	63.71	264.65	21.57	404.75	266.37	305.8	376.18	206.9	87.12	290.45	277.54	36.45	1.48	220.15
X62822_at	167	17.54	53.3	61.52	405.3	28.85	190.3	106.49	170.1	49.21	177.75	46.17	201.95	76.86	141.55	17.61	122.5

S82185_at	106.8	5.09	65.9	76.08	243.15	12.94	39.1	23.76	275.7	35.07	129.2	15.13	59.6	18.38	275.1	266.3	111.75
J04040_at	47.2	14	521.4	602.45	216.45	18.6	191.2	137.18	366.75	132.16	363.8	298.26	226.25	106.56	410.65	38.25	89.4
U43586_at	249.95	37.26	111	128.27	432.2	35.36	503.9	270.96	310.8	37.9	503.1	169	1274.9	1190.48	480.05	190.99	434.4
X13451_s_at	128	40.87	74.1	85.56	660.5	29.84	149.45	135.27	308.9	286.38	163.45	109.25	422.05	408.21	161.5	34.22	281
U00951_at	513	91.5	390.05	450.64	1071.35	64.42	1160.05	1078.97	649.95	576.36	1399.7	33.94	561.6	287.51	1811.05	24.25	850.95
U34380_rna1	410.05	219.84	372.45	430.27	1488.75	112.5	1048.5	78.63	414.45	353.2	846.1	101.4	445.55	34.44	642.4	820.95	872.15
L34673_at	59.7	34.37	174.7	201.81	611.3	65.62	104	64.21	116.9	52.33	293.1	379.29	80.65	74.88	33.65	13.65	363.35
X59834_at	1127.2	5.94	548.15	633.36	1457.45	37.83	1307.45	646.22	1646.2	582.23	1537.05	332.69	2106.35	9.97	1541.4	181.87	3737.15
Y10512_at	90.45	24.25	58.65	67.81	347.05	1.77	149.35	50.98	125.95	75.17	182.2	72.69	151.1	14.28	161	158.82	123.25
L44140_cds4	508.6	25.31	740.2	855.17	1224.25	97.37	599.7	168.29	330.8	58.27	536.7	414.08	1037.9	922.92	1332.85	253.78	1582.35
U82613_at	531.8	84.43	790.65	913.51	1699.35	39.1	706.95	332.84	1317.8	661.14	1407.1	190.49	1338.35	446.11	1770.45	98.5	986.75
HG315-HT31	425.95	56.64	88.95	102.74	871.55	81.11	993.65	217.44	316.2	91.5	1179.55	802.35	634.1	558.19	361.55	166.52	314.45
X03484_at	570.8	17.39	1283.8	1483.23	869.55	7.14	442.75	248.97	511.85	326.75	1099	405.88	1138.4	607.55	908.1	295.15	1448.55
L32961_at	166.85	40.52	51.75	59.75	403.8	41.58	289.8	213.12	216.6	37.62	132.05	77.43	212.25	10.82	155.55	81.25	465.75

L18877_f_at	180.05	78.56	321.25	371.16	562.8	81.18	441.15	84.07	489.15	228.89	442.4	137.32	537.95	86.34	584.85	5.3	399.1
M55418_at	364.1	22.06	26.75	30.9	264.3	68.59	663.3	604.72	103.4	36.35	168.6	209.16	179.25	139.65	65.95	37.41	96.2
D85245_at	1074.65	179.53	119.4	137.89	616.25	69.08	948.1	113.28	663.65	325.76	1094.85	174.3	1548	1595.94	949.5	511.24	846.55
U17163_at	609.4	105.22	57.45	66.4	901.8	953.32	793.8	600.62	626.45	209.52	570.5	273.79	439.7	137.46	687.75	327.32	235.6
M96995_s_at	1827.75	187.6	148.95	172.04	1823.8	71.13	1927.15	939.96	1543.8	1047.37	1045.4	190.92	1545.65	426.03	1977.5	598.35	1653.4
L26336_at	418.05	86.05	50.8	58.69	295	214.82	245.2	220.19	616.2	223.59	351.75	76.44	485.1	190.92	263.05	243.17	673.45
X81889_at	543.15	14.5	53.05	61.31	436.25	260.57	271.85	17.61	796.4	149.91	561.8	318.91	606.4	64.21	465.2	148.35	499.45
S78873_s_at	1226.45	237.52	142	164.05	1160.65	1206.25	1191.2	592.98	182.6	21.07	1124.7	263.19	253.95	85.06	895.65	773.65	892.6
D84424_at	932.55	95.39	76.6	88.53	1452.45	670.97	387.3	64.06	337.95	93.27	1196.15	79.27	872.05	870.66	655.65	292.25	815.25
D87468_at	477.75	62.01	76.85	88.74	1032.7	840.33	789.9	320.6	762.9	468.67	742.05	183.07	1188.15	1183.77	688.65	364.23	345.4
M25756_at	269.05	47.87	31.45	36.27	678.75	806.03	233.15	136.12	159.7	36.91	199.55	30.19	125.6	78.49	296.8	148.21	557
Y09267_at	513.4	76.37	75	86.69	466.65	118.3	249.15	58.62	492.25	351.08	461.55	185.33	107.8	0.14	95.15	56.92	439.1
U49248_at	541.55	110.1	64.55	74.6	958.65	1233.83	570.2	682.36	355.25	247.28	506.15	435.65	671.7	89.52	637.45	134.7	120.75
HG3242-HT3	873.05	15.49	68.8	79.48	1333.35	258.45	1235.3	721.96	909.2	88.67	1157.9	410.4	1084.9	66.75	131.95	38.82	607.55
U61849_at	272.9	42.71	27.65	31.89	58.75	7.28	198.25	121.55	414.25	516.68	604.55	751.16	140.7	125.72	50.1	27.58	202.65
M36634_at	307.05	51.27	52.1	60.25	87.95	89.17	175.05	189.01	55.1	23.48	358	435.29	263.15	131.88	634.95	568.16	264.85

D49357_at	2454.5	192.05	228	263.47	2946.1	1357.65	1924.85	1940.8	795.95	244.16	951.25	454.46	2079.45	2326.45	1365.8	1328.65	2044.75
U37139_at	529.7	61.94	44.2	51.05	260.2	198.7	452.05	272.59	511.95	156.91	327.1	21.64	494.05	344.29	650.5	14.57	405.15
U96094_at	3692.55	500.28	352.2	406.87	2451.85	548.36	1992.6	127	2553.15	403.69	3305.8	923.34	3046.25	879.99	2685.35	848.88	2389
Y00097_s_at	1142.55	82.24	83.25	96.24	797.6	121.76	773.9	574.03	641.95	613.42	1051.95	289.7	1013.7	136.19	1079.3	307.45	1325.65
X99886_s_at	245.4	30.41	35.55	41.08	508.4	481.82	60.8	19.37	97.55	96.8	570.05	443.57	71.55	44.9	225.75	243.32	178.95
U87972_at	442.3	65.48	74.7	86.27	387.75	107.69	1146.05	1040.65	231.15	61.87	732.6	385.8	342.65	264.95	604.2	235.33	432.25
M85247_at	1815.35	10.68	121.7	140.57	1688.1	527.5	2440.95	1233.83	1659.25	253.22	1264.75	1416.12	2194.5	141.56	2281	263.04	1514.7
U70862_at	156	29.98	22.9	26.45	182.55	86.9	146.85	5.3	124.1	31.82	295.3	56.71	71.3	60.39	86.25	15.34	139.2
D14657_at	744.05	35.14	35.6	41.15	732.05	206.4	596.45	87.19	1392	154.71	928.4	351.01	1061.8	125.16	746.85	328.31	711.5
U05227_at	350.15	63.85	46.05	53.25	650.65	882.12	132.45	95.95	203.35	261.7	496.95	314.59	165.95	140.64	461.6	13.01	151.4
U58331_at	235.3	11.03	27	31.25	509.5	398.24	801.5	841.88	119.6	24.47	218.15	188.59	216.8	155.85	96.25	25.53	122
U50315_at	1252.25	67.39	156.75	181.09	1183.1	360.48	791.35	275.28	1282.4	421.86	565.25	273.44	1945.25	166.52	877	937.91	1581.8
M29273_at	1869.1	287.51	201.7	233.06	1586.45	651.46	2111.05	1748.89	1130	668.92	1931.75	684.83	2216.4	418.89	1619.05	304.27	1948.55
M33478_at	256.65	34.44	29.05	33.59	268.25	90.72	170.4	92.07	350.05	2.76	205.25	212.2	162.05	204.85	215.25	123.53	34.35

S82597_rna1	660.55	121.41	108.6	125.44	305.1	209.59	256.7	122.33	600.75	358.15	418.25	322.65	401.1	377.17	364.75	348.82	509
X92396_at	573.65	45.04	34.8	40.16	316.55	274	308.05	269.2	672	153.16	912.4	338.28	342.95	364.37	714.75	404.68	719.85
U67611_at	538.35	74.03	69.3	80.04	147.75	120.42	193.2	64.91	148.95	9.83	170	68.31	136.45	33.59	374.75	270.61	749.4
U11717_s_at	693.3	76.51	67.15	77.57	277.65	163.98	338.15	306.11	303.5	196.72	431.6	200.54	188.25	72.62	295.15	316.29	187.5
AB002318_at	2628.15	186.61	274.9	317.63	3716.7	2031.8	2965.35	1478.35	3395.75	1227.89	3729.3	1246.63	2430	230.23	3301.95	1205.26	1456.8
U17566_at	1465.35	230.3	186.4	215.38	1326.7	1222.02	685.7	585.34	1013.6	288.08	1033.75	798.54	536.05	195.09	1622.55	119.43	905.75
X05246_at	282.3	33.09	41.9	48.37	210.4	186.96	350.95	362.68	134.25	46.74	237.55	149.98	161.65	66.4	82.9	7.78	365.7
M57892_at	423.3	51.05	29.65	34.29	606	111.16	86.4	35.64	159.6	47.52	116.25	33.59	245.65	170.91	127.1	82.31	163.9
X79984_at	332.5	43.56	47.3	54.59	44.7	6.65	547.9	24.47	258	52.04	206.1	216.37	154.95	157.47	361.05	310.63	92.5
M33882_at	942.75	170.77	78.15	90.3	853.9	909.62	1446.55	246	415.8	323.85	535.75	437.49	231.5	4.67	111.05	25.81	614.2
U67932_s_at	316.7	62.79	48.25	55.79	553.15	7.85	127.55	68.24	226.3	156.84	257.7	154.29	353.4	467.54	326.8	418.18	485.1
X07730_at	3372.15	585.84	323.6	373.92	2898.5	237.73	3022	2398.65	2705.5	154.71	3499.6	629.61	4275.9	1889.11	2906.05	554.44	2861.25
L38935_at	1205.4	54.87	121.35	140.22	1488.35	397.75	1330.9	1078.05	1258.7	92.77	867.35	19.16	1132.65	81.11	294.45	214.47	681.35
U38545_at	737.45	143.19	109.45	126.5	650.2	680.38	393.35	319.54	563.55	431.69	756.85	387.14	1187.7	135.34	246.55	0.64	875.85

M62628_s_at	1821.75	310.21	207.8	240.13	1123.55	623.03	1304.4	127.28	642.15	208.53	1391.85	555.01	1375.15	994.83	1837	1603.86	862.05
AB003103_at	194.85	20.44	20.1	23.19	146.95	46.03	267.05	142.62	410.35	302.85	302.6	283.27	254.5	261.77	580.7	51.9	265.65
Y10141_s_at	1813.05	335.24	248.85	287.58	1517.4	1120.91	1532.05	906.44	557.45	143.33	730	296.56	1024.55	823.57	1417.45	1007.7	635.1
U33447_at	232.25	44.05	33.2	38.33	87.3	17.82	189.15	58.48	116.7	42.28	212	98.29	207.2	107.06	158.05	18.74	413.2
U57092_at	540.7	16.69	40.8	47.09	655.05	162.99	424.55	70.22	245.25	244.45	431.55	98.36	278.2	4.81	547.1	583.65	175.5
U60521_at	717.05	67.67	40.15	46.46	475.15	396.19	242.15	143.05	379.35	220.26	274.65	138.52	467.15	356.17	812.3	189.65	713.6
U08336_at	1333.45	164.54	197.4	228.11	1906.6	1350.72	1507.5	20.36	1057.9	894.49	398.9	102.39	946.15	781.42	471.85	135.69	1229.7
HG4258-HT4	344.25	49.85	31.15	35.99	696.05	409.49	556.75	651.46	453.85	415.57	1053.15	1290.12	511.55	61.16	243.35	92.98	346.3
U33921_at	508.45	30.33	62.7	72.41	363.4	389.19	386.2	163.2	169	16.83	608.15	748.05	286.8	151.32	306.2	216.09	526.35
Z96810_at	460.4	43.84	19.35	22.42	208.1	67.88	154.65	2.33	116.5	59.4	238.9	98.71	239.35	48.86	87.6	29.56	366.65
U56976_at	1004.55	135.55	145.65	168.22	848.1	767.21	653.4	105.5	521.15	306.67	507	131.52	1061.55	46.03	1095.95	502.97	483
X66610_at	199.8	35.07	32.4	37.48	111.75	31.32	115	69.72	112.75	19.87	232.25	98.78	115.2	3.11	86.75	48.72	231.1
X74331_at	277.6	34.08	41.2	47.66	216.9	128.27	183.85	23.55	592.9	461.32	309.65	338.35	418.9	96.59	242.05	50.56	236.4
D64015_at	438.85	43.2	55.65	64.28	226.45	218.71	54.05	23.26	202	216.8	92.2	40.31	237.95	229.6	285.25	363.67	171.25
HG4334-HT4	814.8	129.26	86.8	100.27	733.2	145.38	574.4	183	1011.8	344.22	895.25	29.77	804.55	393.65	668.15	644.95	712.1
M76231_at	861	137.74	78.1	90.23	706.85	300.73	602.4	329.65	346.75	116.6	410.4	14	1298.75	220.12	1077.4	592.13	270.2
X62048_at	281.8	32.67	16.15	18.6	271.9	329.79	247.1	6.65	342.5	350.72	408.2	172.53	241.3	230.52	85.75	27.65	385.05

U41344_at	1467.4	145.81	182.55	210.93	867.8	609.53	1633.2	450.57	2066.95	469.17	2012.95	150.12	1010.85	759.08	1251.75	1107.12	969.35
K03008_cds2	1103.4	77.64	109.45	126.5	884.7	145.38	543.1	23.33	598.7	452.83	1112.4	923.62	1136.8	626.5	1230.5	784.75	590.25
U15655_at	1711.25	177.7	203.45	235.11	1417.35	1362.52	752.25	495.61	853.6	517.46	2064.45	599.27	1788.75	7.71	1127.5	1074.38	2212.2
M59979_at	323.5	54.73	31.75	36.7	460.95	501.69	267.1	234.34	167.2	1.56	626.45	692.05	154.7	122.47	538.85	208.81	681.15
M31899_at	1110.5	89.1	121.95	140.93	417.8	16.97	266.25	122.4	394.15	120.42	590.4	303.07	302.9	85.56	779.5	864.23	387.35
X68836_at	1707.25	77.29	158.1	182.72	1308.55	247.84	993.05	1033.01	846.1	1119.07	989.2	452.69	821.85	395.34	1212.05	684.27	1830.15
X85781_s_at	940.4	93.48	73.6	84.99	562.95	221.54	734.3	233.49	295.35	64.56	1237.4	958.41	838.45	242.61	811	642.76	754.4
L13744_at	258.1	37.48	28.45	32.88	343.75	297.9	202	10.61	476.15	276.41	398.7	352.56	94.55	8.7	158.1	125.72	155.3
S81661_s_at	413.2	8.34	23	26.59	262.55	320.67	80.5	52.89	80.25	24.96	224.5	85.84	65.9	22.49	89.15	80.4	110.25
D84145_at	1354.85	141.49	116.55	134.7	1299.25	965.84	706.65	595.88	994.25	252.08	773.45	646.65	759.1	183.42	1307.2	164.61	701.7
M37763_at	611.2	122.61	96.4	111.44	764.35	857.93	355.95	220.55	667.05	259.01	360.75	160.87	422.3	349.31	756.1	45.25	615.1
X66922_at	490.55	74.46	53.25	61.59	197.25	210.08	542.05	7.99	435.05	87.19	372.05	313.6	287.45	282.77	194.1	106.35	604.75
U11872_at	1285.1	229.53	215.1	248.48	503.3	75.94	1788.55	334.53	1384.65	336.79	1853.8	77.22	1509.45	8.84	1800.35	441.16	1624.3
D16611_s_at	327.05	56.21	42.25	48.86	242.95	241.34	186.85	69.65	187.7	36.77	226.5	222.88	498.4	26.59	180.05	185.33	73.85

D49950_at	475.25	48.44	29.4	33.94	289.9	316.08	576.95	424.05	836.7	339.13	759.05	245.58	928.4	217.65	636.05	37.26	526.7
HG3897-HT4	124.45	15.34	19.9	23.05	193.1	211.99	162.05	152.95	84.05	6.01	124.05	37.69	96.55	63.43	87.15	25.24	145.4
M95678_at	4119.3	722.24	343.5	396.83	3374.05	1299.45	3003.8	951.77	3267.9	1135.75	2988.85	726.98	3908.4	373.49	2669.45	1018.16	3426.3
X07619_s_at	2247.45	189.29	234.05	270.47	2047.4	103.1	1457.8	473.34	1704.3	663.12	2090.1	177.06	2513.25	421.79	1781.35	1029.05	1154.9
X70940_s_at	2489.5	301.65	318.15	367.62	2610.05	68.8	3340.4	1898.72	2528.9	378.44	2504.95	1295.63	2259.75	537.05	2099.2	1227.4	2006.55
AD001527_c	1031.2	76.79	137.2	158.53	913.15	215.31	1240.7	836.08	850.4	103.8	1401.5	181.44	784.6	140.43	546.75	705.76	605.2
D50532_at	1145.4	196.01	192.65	222.53	367.85	111.09	829	331.49	323.05	28.64	1346.1	1215.09	582.65	119.57	990.9	85.84	461.2
M19650_s_a	1630.95	72.05	169	195.3	2158.7	821.23	1680.8	535.42	1631.15	395.77	1838.35	620.2	1915	540.09	1713.55	1217.14	1662.05
M83186_at	1258.55	143.33	149.65	172.89	639.1	651.39	864.3	366.71	772.5	569.5	923.45	784.25	1121.6	234.19	977.55	49.43	933.75
X67594_at	870.05	167.94	132.55	153.09	372.45	114.48	253.75	92.14	685.5	609.95	886.65	779.3	1483.4	53.32	309.55	108.12	668.25
M11717_rna1	5249.55	540.3	273.8	316.36	2480.05	1223.65	8134.5	6966.13	2581.25	154.22	1061.3	1358.78	2396.4	1147.21	4206.65	2534.34	2269.55
U93049_at	431.7	58.41	23.15	26.8	197.95	157.19	194.85	153.65	360.55	302.57	150.55	100.76	289.25	328.59	629.7	479.56	418.75
HG4417-HT4	911.3	123.6	124.25	143.61	1166.65	1369.17	1358	892.79	314	217.51	765.7	143.26	695.05	658.95	460.1	432.61	844.85
M35851_s_a	136.3	39.17	552.6	638.52	164.1	86.41	166.35	124.66	367.7	324.7	287.8	202.52	366.4	371.23	583.35	681.86	592.9
M64108_at	1134.4	377.45	663.35	766.43	1155.1	197.71	496.95	197.92	1548.35	31.18	1908.4	1342.65	886.65	334.53	1156.8	1406.72	602.2

X89109_s_at	214.65	92.84	136.7	157.97	289.85	95.39	475.9	528.63	218.9	104.23	238.6	55.3	343	62.23	325.4	159.52	477.35
X58377_at	632	309.85	115.7	133.64	732	374.34	512.3	549.28	363.9	355.82	835.1	678.68	139.9	1.56	341.9	305.61	344.7
U78722_at	217.1	46.67	229.15	264.81	262.1	145.95	92.6	85.14	186.95	201.17	143.85	3.32	107.55	55.51	248.45	265.52	216.65
D63998_at	529.9	173.1	280.25	323.78	918.55	435.08	424.85	329.44	294.2	270.4	442.05	403.26	377.75	441.31	264.85	296.21	489.6
M63175_at	1025.65	90.44	602.15	695.72	655.8	284.26	939.45	431.26	1337.1	138.59	1013.6	115.97	727.6	361.33	1257.05	355.89	1058.5
AFFX-LysX-M	92.15	73.04	39.95	46.17	118.7	81.88	101.85	15.34	234.5	265.45	374.4	147.93	118.65	22.27	91.75	7.42	259.6
M57609_at	1154.2	490.31	479.15	553.59	573.65	304.13	1332.55	508.06	1118.35	805.89	941.5	647.99	1479.9	963.22	665.4	435.44	1714.65
J04760_at	2564.35	813.24	1943.15	2245.13	2432.4	2918.51	1765.1	1639.92	337.35	245.3	3562.9	1698.19	2917.45	1828.79	1362.7	390.89	1192.1
M75099_at	5117.25	789.48	2589.6	2991.91	5157.45	22.7	4992.6	895.06	5290	71.42	4497.05	2549.05	5418.45	35.43	4684.95	61.45	4626.8
U76189_at	64.15	1.63	265.95	307.24	264.6	184.27	436.4	57.98	148.4	33.23	100.3	49.64	243.7	233.91	330.2	364.44	171.85
M31165_at	151.1	28.99	26	29.98	652.05	882.96	118.55	72.05	257.7	283.97	263.2	247.35	257.5	248.76	343.85	393.93	211.9
X56468_at	6029.55	2758.35	2482.8	2868.59	5953.1	1964.34	5892.1	1973.39	6714.4	610.8	4518.8	2539.64	5924.55	37.26	5871.9	332.76	7256.8
U56102_at	42.8	6.93	67.3	77.78	84	38.33	222.75	134.85	42.75	26.52	111.4	57.7	194.2	130.81	423.6	419.03	36.3
M31525_at	2518.05	38.96	1751.8	2024.02	3026.6	498.23	3321.1	830.14	3236.3	670.34	3780.45	87.04	3909.15	1.48	3076.5	129.12	3017.4

Y10659_at	628.9	126.57	205.45	237.38	640.7	57.98	377.5	256.82	630.65	440.6	789	100.55	325.8	264.46	513.9	112.85	651.25
L05500_at	389.4	285.53	143.5	165.75	249.35	173.03	145.5	45.11	222.3	173.81	300.9	232.36	294.9	142.84	183.45	94.26	220.6
Z22780_at	129.45	84.22	63.35	73.19	144.75	138.1	222.4	2.12	207.75	189.86	151.95	81.39	243.25	243.17	89.7	52.04	154.9
X96754_at	98.85	15.2	140.75	162.56	405.35	438.05	298.55	73.61	241.75	237.66	130.5	18.81	363.1	180.74	644.5	699.47	284.9
X63753_at	749.3	100.55	440.4	508.83	624.8	355.39	782.4	241.41	1133.35	330.71	1192.55	507.49	849.45	127.07	784.3	237.73	1150.85
U16660_at	3154.35	2320.94	1742.05	2012.78	4451.6	1909.47	4274.85	2778.15	2587.3	211.99	2975.25	1209.08	2292.05	1660.64	3767.75	2997.64	1924.45
U68536_at	97.05	39.1	130.5	150.76	490.65	382.05	403.1	292.6	560.4	243.1	224.65	28.64	501.8	118.23	611.65	149.13	119.85
U07358_at	695.35	105.01	554.45	640.57	368.95	108.26	511.9	399.23	1027.5	413.09	1177.8	257.39	822.8	25.46	1247.95	91.15	958.75
M91592_at	1803.5	7.64	742.45	857.79	1647.2	448.73	1419.1	10.04	973	957.42	1746.25	1228.17	1776.1	255.55	1177.8	112.85	1563.6
M11321_at	74.75	41.08	63.25	73.04	385.5	212.7	308.85	368.61	103.1	38.18	112.45	102.88	87.2	3.82	57.8	5.52	111.05
M16937_at	326.15	136.4	136.25	157.47	432.6	292.18	465.25	263.11	308.3	127.99	144.85	16.76	645.55	672.39	188.85	133.71	160.9
X00588_at	883.65	210.36	1432.8	1655.48	803.45	328.59	502.7	370.67	1168.65	327.04	661.05	786.37	905.8	158.82	592.9	648.28	1103.35
AB002332_at	776.7	161.5	317.4	366.71	927.4	132.65	459.5	119.5	452.5	173.67	813.4	423.98	552.75	209.94	819.9	304.34	784.6
HG2706-HT2	39.55	1.34	20.7	23.9	73	18.1	87.5	37.76	76.1	52.89	104.3	6.08	60.7	4.81	44.25	12.37	67
U64871_at	16.5	0.42	41.35	47.73	525.5	627.06	254.3	199.12	68.75	65.41	52.15	58.9	193.05	127.49	118.25	98.64	312.65
U41315_rna1	1037.1	373.64	485.1	560.45	849.1	535.28	508.3	272.24	645	345.21	792.9	138.88	701.05	594.04	730.75	147.57	1000.9

Y00433_at	37229	14742.19	26048.6	30096.02	45473.95	13392.25	43329.2	7111.09	34953.1	8221.53	37218.4	2394.69	33085.75	7541.93	36978.7	2499.06	32003.05
M17754_at	1578.3	207.04	1360.6	1572.04	1135.7	853.34	1145.35	679.74	1308	265.87	2389.4	1183.56	2175.95	655.56	1014.5	120.92	934
M24364_at	71.75	5.3	44.5	51.48	58	17.25	451.65	538.6	258.65	229.88	282.85	252.08	331.35	381.77	217.85	218.57	85.45
X72841_at	1393.85	314.17	802.25	926.95	935.9	17.39	565.85	459.69	1133.8	248.48	1270.95	216.3	1028.95	60.17	1461.9	253.85	1316.5
X17651_at	996.55	280.51	242.25	279.94	984.2	504.73	1268.05	1087.88	1081.85	1026.51	591.6	204.07	1864.15	1351.63	2041.55	279.8	977.25
HG2274-HT2	3398.1	954.17	639.45	738.86	3262.9	700.74	3842.6	2263.17	3935.4	211.14	3127.1	2332.32	2515.6	1568.93	2540.6	500.63	2215.85
X68242_at	388.65	153.37	246.75	285.03	240.3	148.07	83.75	66.68	92.45	58.34	105.15	97.51	87.6	21.07	600.65	325.06	196.05
M62324_at	1092.65	69.79	976.35	1128.05	905.85	589.8	1384.5	501.9	776.65	678.19	827.6	546.31	643.4	374.2	897.75	874.48	676.75
D87432_at	318.35	338.63	69.85	80.68	199.45	56.07	333.1	163.06	726.35	156.34	422.1	332.2	318.95	221.82	58.65	12.94	198.45
D87076_at	1018.3	808.08	1612.3	1862.8	1875.05	330.86	2376.05	1040.51	2353.75	308.51	2113.55	582.16	1384.7	115.97	1776.65	527.43	840.85
X72964_at	2770.3	150.33	1675.55	1935.85	2553.5	610.94	2862.65	839.83	3100.85	45.75	2731.5	130.67	3637.55	966.54	3420.55	603.37	2439.9
X98482_at	95.6	46.81	35.65	41.22	295.1	294.3	737.25	799.1	66.35	2.62	841.6	871.3	559.4	88.81	91.3	0.57	96.8
L21998_at	4273.2	488.19	1876.75	2168.34	4396.7	37.48	3490.1	106.77	3863.75	537.05	4401.75	1343.29	3968.75	1125.93	2802.05	476.52	3638.5
X65293_at	113.4	22.63	67.15	77.57	159.9	57.84	205.75	164.26	85.1	34.08	162.35	1.34	143.8	17.25	159.95	58.9	105.4
AFFX-PheX-3	210.8	55.44	141.45	163.41	245.45	103.17	1475	1820.38	244.8	27.29	1032.3	992.35	190.65	102.46	212.45	44.34	391.2
U79294_at	842.9	148.49	477.5	551.68	1386.95	169.92	1870.55	1119.99	1498.3	462.02	1807.3	297.27	1086.65	305.97	1163.95	245.01	1261.3

M65085_at	688.1	424.41	497.35	574.67	820.95	505.93	1033.65	88.46	822.4	194.88	1462.4	725.07	1067.35	505.79	882.1	432.75	798.7
S70348_at	406.1	389.9	244.95	283.05	546.3	359.21	427.35	336.23	461.1	54.02	346.65	432.25	637.25	416.56	617.5	458.21	153.25
M98776_rna1	838.1	220.05	673.55	778.17	608.4	87.26	1549.5	953.46	1157.85	793.02	1146.55	20.29	1647.45	340.9	1211.25	454.03	1498.5
D31765_at	1548.45	707.18	707.85	817.77	1482.15	43.63	1865.15	714.53	1553.3	449.44	1998.1	314.24	1851.45	109.39	2411.2	1077.63	1352.7
L25876_at	554.3	94.61	351.75	406.37	1317.1	903.97	943.55	233.27	941.3	14.57	835.9	273.23	1096.3	377.88	631.45	173.31	813.25
U61166_at	1006.25	261.56	375.55	433.95	707.15	661.07	584.45	602.38	1117.65	66.54	187.75	9.97	435.25	235.4	639.2	626.36	665.2
Z48314_s_at	264.1	57.56	78.05	90.16	489.05	401.57	693	767.49	377.7	180.6	349.25	147.86	344.25	82.1	359.65	42.36	197
D63391_at	2442.35	869.67	1411.2	1630.45	3888.5	26.87	2942.1	537.68	2447.85	748.19	3438	1491.71	2699.8	724.22	3412.4	348.6	2473.1
U75968_at	895.75	120	583.4	674.01	1337.1	137.46	919.75	149.69	1105.8	909.9	1043.15	972.2	1628.6	106.21	1290.85	346.69	596.7
U20759_s_at	102.7	11.17	54.55	63	85.9	42.57	128.05	115.61	100	53.6	103.75	87.04	64.9	15.27	129.25	3.61	91.3
HG998-HT99	901.2	238.15	516.8	597.08	898.15	251.66	619.6	347.76	598.95	253.64	672.05	291.54	800.3	219.63	406.75	444.98	533.55
M60974_s_at	2171.6	385.66	3458.8	3996.28	3079.2	647.71	1742.25	535.21	2528.1	453.11	2679	44.12	2238.7	456.79	2680.2	867.76	2016.7
S81003_at	3856.45	1957.2	1150.25	1329.01	2602.1	1371.36	3038.75	2037.67	3092.05	798.68	2115.95	824.42	1938.85	35.14	2933.85	393.65	3176.05
D00097_s_at	181.3	56.29	49.8	57.56	208.3	103.1	334.1	113.14	186.95	1.06	156.1	142.13	518.85	22.7	246.35	46.88	553
U39840_at	616	323.15	354.95	410.05	318.25	132.02	523.85	594.61	289.9	107.48	331.55	113.63	646.35	124.38	300.05	58.62	388.2

U19495_s_at	240.6	201.67	194.65	224.93	495.5	424.97	76	0.85	433.2	290.34	100.65	6.15	222.15	11.95	134.9	124.03	114.15
X87843_at	489.5	230.38	702.55	811.69	1329.6	1.41	624.05	517.25	1483.8	429.07	158.65	10.11	1288.45	284.47	517.8	27.44	647.1
M54992_at	220.95	160.02	278.6	321.88	429.9	185.69	268	6.08	138	115.68	412.15	83.51	139.75	159.59	469.15	414.86	594.8
X06268_at	671.85	261.84	312.55	361.12	544	241.97	483.15	391.81	913.35	6.29	444.1	519.72	480	501.48	918.45	39.24	73
U10886_at	232.8	224.15	279.1	322.44	222.85	211.07	90.2	17.68	265.2	259.93	717.35	400.72	286.3	258.94	107.55	13.08	310.3
M88108_at	1603.15	770.68	1227.9	1418.74	1409.85	509.75	1340.7	278.32	1697.25	555.72	1149.45	278.53	1849.05	219.56	2866.6	600.9	2005.65
M19267_s_at	1279.55	399.73	747.35	863.45	969.5	435.15	1361.4	250.6	1065.25	35.71	749.05	260	858.55	381.06	689.9	208.03	810.35
L05187_at	2353.7	507.84	1726.5	1994.75	1645.5	206.48	2363.35	34.86	2019.05	504.95	2099.65	459.83	2717.3	1379.99	3581	1201.09	3075.3
M34079_at	3667.9	1674.15	1698	1961.8	4187.05	1039.23	4329.6	1131.94	3642.4	549.99	3936.2	1052.32	3223.25	722.17	3493.75	538.18	3636.65
D87716_s_at	309	91.08	289.25	334.25	786.65	649.05	423.95	102.32	753.4	20.51	997.25	185.76	849.95	250.1	161.1	40.31	787.7
U28686_at	947.75	212.34	435.25	502.82	1285.25	890.32	829.6	760.42	948.15	406.23	905.7	161.5	675.9	216.09	916.05	162.99	844.35
X89267_at	3721.55	308.23	1551.3	1792.37	3774.35	194.38	3469.05	756.11	4168	294.58	3594.55	1280.36	4017.45	402.27	4353	206.19	3639.55
Z33905_at	316.1	59.96	122.2	141.14	463.5	131.95	276.25	173.31	241.95	91.29	348.7	88.95	623.45	545.82	464.3	433.03	460.65
X70340_at	484.1	446.18	534.5	617.59	406.05	92.56	620.2	392.87	760.2	326.54	707.5	81.74	312.85	188.3	144.55	133.01	809.45
M98447_rna1	1561.75	122.82	887.7	1025.59	621.4	348.46	1493.3	121.62	1316.3	1217.78	1087.35	1035.42	721.9	317.49	1656.85	1801.07	916

U82320_at	202.3	184.55	37.05	42.78	298.2	174.66	116.95	12.09	287.15	346.98	323.65	279.66	247.55	207.39	86.65	19.73	97.65
HG64-HT64_	911.45	109.11	678.65	784.11	991.25	434.38	1446.35	672.25	1194.15	112.92	1194.75	204.71	937.2	650.11	632.85	454.74	1142.4
M60459_at	278.35	119.71	327.85	378.8	434.65	153.23	447.2	197.85	808.35	333.83	817.75	349.66	1591.15	525.03	226.8	76.79	741.8
J00314_at	1272.85	174.87	541.9	626.07	1790.05	720.33	743.2	168.72	1485.8	186.25	607.65	57.63	1743.95	751.87	1266.4	1642.47	1894.8
X02404_at	151.4	13.01	383.6	443.21	578.15	708.03	427.9	317.77	532.65	190	389.5	25.88	404.75	66.4	512.4	98.85	153.2
X76104_at	772.1	84	686.15	792.74	1601.3	973.69	1365.8	435.01	745	226.98	663	394.57	1303.75	94.54	1029.05	102.32	953.35
Z34897_at	916.7	287.23	426.65	492.92	765.75	50.56	339.55	393.65	668.35	29.06	1296.7	757.74	120.35	17.04	541	325.83	681.45
M57423_f_at	139.45	37.69	118.1	136.47	114.55	43.63	434.85	440.88	159.2	15.27	111.7	39.32	963.35	1.06	66.5	33.94	211.75
U17969_at	2352.1	1.84	1228.8	1419.73	2761.35	733.76	1838.1	362.89	2657.35	1560.8	2282.35	472.84	1964.25	1005.01	2434.05	935.43	3647.1
M63138_at	12344.2	1951.47	6260.25	7232.92	14785.75	597.29	15342.65	2836.98	16117.35	7344.36	17030.35	141.07	17348.45	1430.27	16055.95	2355.02	14640.4
J05459_at	549.3	180.74	179.8	207.75	565.6	153.73	1014.25	3.75	589.4	304.48	390.6	218.92	989.35	109.39	551.55	237.52	565.6
HG3731-HT4	3139.8	1622.95	745.3	861.11	4295.15	222.24	3137.7	207.75	1751.8	2190.33	3892.35	1350.79	2853.2	436.43	1910.9	1231.07	3878.45
D85425_s_at	168.8	52.04	942.45	1088.87	195.6	28	274.35	84.78	308.45	181.51	260.9	123.6	227.6	96.45	259.65	87.89	529.8
S82471_s_at	331.45	271.46	723.8	836.22	617.2	57.42	135.85	112.22	775.25	274.99	336.2	213.97	303.6	252.72	957.65	104.58	838
U28833_at	390.7	12.59	464.3	536.41	724.35	370.88	227.65	117.17	621.35	472.28	557.3	315.23	391.6	102.25	295.8	121.06	125
D00749_s_at	1067	212.27	1095.85	1266.07	1284.55	330.43	789.35	775.63	1245.2	84.99	2446.5	85.14	1300.8	757.45	620.2	102.81	1558.4
U29195_at	564.5	120.21	204.25	235.96	700.5	381.98	723.15	148.28	356.35	340.61	381.85	395.63	62.25	23.12	360.8	289.07	178.5

AF002020_at	1639.25	338.63	1635.6	1889.67	1513.3	1020.21	1545.3	1038.17	2766.35	1414.99	1456	871.16	1621.9	607.83	1785.4	474.47	2018.4
M28213_s_at	1335.2	37.19	647.85	748.47	1464.75	315.02	1489.75	288.99	1310.45	209.52	992.1	57.7	945.55	167.94	882.9	457.64	1409.3
X66362_at	856.15	486.28	354.65	409.77	750.3	116.96	1412.5	1832.4	776.35	375.54	896.5	202.66	927.6	511.24	256.6	152.31	1069.75
U63743_at	892.85	825.55	1120.55	1294.64	859.65	712.83	1909	1493.41	1240.1	199.55	1816.7	407.15	1555.8	553.24	2863.5	1615.88	1397.1
X71428_at	8704.7	410.97	4943.45	5711.51	6645.45	1757.94	5968.6	14.42	8183.6	973.54	7578.15	1819.74	8665.95	1576.92	8452.4	1030.96	10836.25
M54951_at	113.55	93.55	78.05	90.16	206.25	147.15	389	319.19	296.8	315.09	237.25	199.33	207.6	194.74	592.9	272.52	238
X98482_r_at	36351.7	26846.16	22104.3	25538.86	19255.45	370.03	17761.55	854.26	36855.2	13397.41	13143.95	5753.23	40607.1	16379.28	34338.1	15012.02	21636.8
U37431_at	401.75	378.8	370.1	427.66	542.85	63.14	464.65	528.56	288.15	166.67	157	43.42	143.3	17.82	323.05	206.97	284.45
D82060_at	702.9	585.48	213	246.07	136.55	17.18	510	547.3	325.25	220.55	809.5	209.16	899.65	255.62	422.65	115.33	725.5
X57830_at	35.55	1.2	56.2	64.91	572.2	745.86	79.9	16.55	46.55	7.71	66.85	1.34	43.85	22.98	143.55	154.36	47.8
L19871_at	624.1	222.17	144.75	167.23	845.95	306.96	1324.35	640.99	979	347.05	1043.5	129.4	501.75	266.79	314.65	348.53	444.65
M34192_at	894.55	139.65	392.85	453.89	1217.3	297.13	862.3	683.35	767.65	515.83	1012.75	662.77	732.2	560.59	1008.6	563.56	609.8
L42542_at	1025.45	125.23	636.3	735.11	905.25	327.18	540.4	596.52	1465.4	385.66	1308	199.83	1239.65	186.04	1344.15	199.47	1337.25
U38864_at	732.1	435.72	911.4	1053.02	806.75	411.89	578.8	217.08	947.85	348.11	1627.35	457	860.55	682.43	740.1	747.98	1597.6

U39318_at	3746.75	884.94	2350.55	2715.78	3357.3	1533.01	3454.6	2425.94	2704.1	1227.25	3770.2	934.94	2536.75	702.65	3535.95	1600.54	3605
M30894_at	484.25	302.29	480.05	554.58	1090.5	188.66	754.35	75.59	885.35	260.14	679.35	134.28	591.85	184.2	651.65	240.49	398.1
X92972_at	1062.35	41.51	738.5	853.2	699.15	114.9	1264.8	782.77	501.95	405.67	1067.3	135.2	1360.8	158.53	901.55	628.41	852.7
D63481_at	5574.7	1196.42	3559.05	4112.04	4619.1	1068.16	4694.8	206.62	4603.9	1079.33	4883.5	115.26	5468.85	1889.88	5706.25	511.03	5641.65
U62317_rna7	1601.7	567.38	1045.9	1208.45	2016.4	1576.57	2648.15	1598.7	495.7	185.54	2018	7.35	1546.45	383.18	3130.4	671.75	2994.5
M97796_s_at	990.2	64.91	277.7	320.89	2378.55	1724.85	1049.9	681.37	2178.3	715.03	1312.8	696.22	1980.7	862.39	1954.95	302.57	1947.75
X00237_at	72.35	23.55	14.3	16.55	252.5	271.81	180.75	167.23	69	68.02	177.6	116.67	33.6	5.09	163.65	69.65	89.3
L42324_at	628.2	172.68	495.1	572.05	195.8	144.67	1077.45	879.99	409.3	14.42	703.15	236.81	1170.25	336.23	645.05	60.17	518

AC002115_c	6582.95	4104.83	3143.95	3632.48	9034.15	3038.79	9898.8	3637.07	12294.75	3226.32	7070.9	1458.48	7902	4495.64	9908.25	2079.95	8215.25
U82130_at	701.05	270.04	711.55	822.15	1301.6	643.47	1331.45	1249.95	1437	604.15	1039.55	480.62	696.6	181.44	1183.4	9.48	719.05
K03218_at	628.15	19.3	227.45	262.83	716.45	202.16	1094.3	1260.35	1398.05	146.02	1026.4	370.67	1325.75	952.83	920.4	615.47	1119.85
U03105_at	404.05	356.45	189.8	219.34	852.15	4.74	972.5	686.18	385	304.62	1180.6	886.99	555.5	253	489.55	25.95	637.65
X85785_rna1	3663.85	1907.28	1092.8	1262.61	3138.9	600.33	3160.45	1197.06	2046.75	663.62	3269.2	59.11	3403.9	385.23	2820.25	52.68	3089.05
X01677_f_at	154631.66	25905.92	118493.15	136904.44	207718.91	41658.49	213898.25	134541.13	162207.69	3426.5	180824.7	109644.12	253868.66	37934.79	248889.66	53069.7	199198.25
X98307_at	101.4	9.9	61.1	70.57	200.95	106.14	424.2	515.62	80.75	20.72	209.75	58.62	301.25	315.3	213.9	144.67	199.4
U62961_at	487.5	14.71	278.45	321.66	197.05	186.61	455.2	409.56	427.6	404.04	258.95	203.72	482.1	124.88	440.5	428.79	357.35
U59302_at	761.65	358.15	431.5	498.51	1116.65	1057.2	654.75	367.91	730.85	204.85	879.75	286.31	1374.3	31.96	1004.15	687.66	434.2
X82240_rna1	227.35	6.58	102.55	118.44	170.5	79.9	190.35	126.5	153.45	40.09	149.25	6.01	133.35	134.85	262	213.83	246.35

AB006781_s_	892.6	472.06	536	619.28	1267.5	991.08	1060.2	149.62	1393.9	27.58	1326.35	265.66	1210.95	955.8	697.4	742.46	763.15
HG4020-HT4	1972.3	1301.36	774.3	894.63	1606.1	1050.76	2882	1557.61	1750.3	189.36	1675.55	166.67	1287.1	380.42	1383.1	662.56	1808.9
M35128_at	3361.3	548.01	1970.3	2276.46	3050.1	925.6	3758.6	998.58	2848.2	155.85	2378.9	1529.9	3271.95	327.46	2756.8	945.54	3233.3
X69908_rna1	5410.3	1654.49	2332.8	2695.21	5069.65	4.6	5363.95	1655.97	3781.4	485.5	5024.25	944.91	4951.25	1717.21	5629.9	1403.18	4133.4
L41143_at	1489.45	651.88	431.95	499.01	2610	18.38	1979.95	1751.86	1478.55	1125.5	1907.9	1703.99	2497.15	1705.05	2245.15	811.69	3522.2
AF000562_at	3789.75	124.66	1421.35	1642.26	3205.35	148	3151.3	642.34	4571.2	2268.4	3651.7	1967.74	5098.9	1223.86	4133.15	3009.8	3984.5
HG3187-HT3	391.8	275.35	204.9	236.74	137.05	5.16	335.3	167.02	184.6	17.68	504.05	210.79	251.95	155.07	579.25	224.79	294.75
M12125_at	5737.2	1662.41	2189.9	2530.17	5469.5	1177.05	6903.85	1363.37	6010.3	1145.65	5125.55	978.28	6234.25	281.92	5896.05	2412.44	6073.05
U18088_s_at	165.65	74.03	98.2	113.42	217.6	190.35	218.35	237.23	84.7	21.07	106.2	13.86	132.6	6.36	96.15	18.17	114.2
Y07565_s_at	323.65	385.73	98.45	113.77	131.35	57.49	333.9	134.77	140.5	64.49	372.2	479.56	190.4	165.46	189	119.5	254.1
U05340_at	4374.5	104.93	3355.65	3877	3171.3	290.06	3590.85	1567.02	4877.25	1062	5251.05	173.45	6515.85	342.31	5090.95	839.83	6648.4
L22524_s_at	214.55	79.55	89.4	103.24	613.25	550.48	109.2	39.6	293.2	166.17	303.1	85.28	98.6	79.2	645.25	536.2	178.25
U65785_at	5743.1	143.4	3225.9	3727.16	4091	1027.71	4954.8	737.65	3964.9	1025.87	4376.2	1105.63	3917.4	18.67	4284.5	1040.01	5693.9
D12775_s_at	528.65	353.34	272.35	314.73	387.1	6.65	537.85	355.75	486.25	179.11	171.95	41.93	164.15	51.69	250.2	262.05	492
X51985_at	205.55	88.88	132.05	152.52	219.75	114.62	238.4	212.41	120.15	11.38	141.6	84.15	165.9	14.71	247.65	181.66	136.45

D87009_cds3	418	333.75	51.45	59.47	350.15	28.07	213.65	21.14	381	246.78	176.55	11.38	69.75	29.49	399.2	319.61	163.25
HG2261-HT2	734.6	56.57	359.55	415.43	625	190.35	605.2	81.03	751.2	22.77	1095.25	350.94	980.7	181.73	812.8	9.48	624.8
Z48051_rna1	109.5	33.66	94.2	108.89	197.2	126.01	469.7	373.21	428.55	116.18	208.55	190.71	393.4	433.32	75.5	43.42	290.25
U85946_at	360.2	30.97	428.2	494.69	352	108.05	324.65	40.8	433.25	173.03	659.45	318.98	450.05	247.28	207.65	111.37	397.5
L26339_at	347.05	173.74	137.7	159.1	522.8	52.89	436.8	51.9	454.15	154.22	310.75	29.06	372.3	86.83	441.35	40.09	450.5
D42039_at	407.65	195.8	144.15	166.52	595.85	164.26	360.05	114.06	217.25	28.78	581.65	221.4	701.15	557.98	915.05	335.66	199.25
X76534_at	190.15	187.03	221.25	255.62	489	71.42	638.3	709.79	616.85	72.9	567.9	92.35	380.65	193.39	451.45	8.41	380.95
X54993_s_at	1041.85	457.71	320.9	370.81	289.2	161.5	267.65	243.03	618.1	521.99	491.4	338.99	425.95	450.92	340.35	285.32	623.15
AB000449_at	1241.05	492.08	779.65	900.78	5415.25	6250.33	2753.5	2492.13	2387	755.9	1574.05	1208.09	2458.4	854.61	5611.85	6225.86	1756.9
U37547_at	245	152.74	730.35	843.79	293.65	27.08	84.6	30.97	533	101.96	307	308.44	633.6	223.59	519.05	592.63	375.15
X13255_at	1371.95	452.9	146.45	169.21	1132.8	168.43	257.4	24.75	573.55	280.23	1527.7	916.41	1096.55	1085.06	713.25	526.72	1078.95
D13644_at	49.2	13.72	67.2	77.64	293.45	364.94	280	151.18	644.3	133.22	334.3	5.09	375.2	270.68	199.4	151.6	84.1
U60269_cds2	739.25	386.29	284.85	329.16	540.25	150.4	1051.65	947.59	897.8	205.2	703.6	44.97	834.65	156.91	484.65	117.31	598.1
U27831_at	838.1	933.38	437.45	505.37	1078.25	0.49	1193.85	258.31	841.8	515.76	1153.7	126.57	1034.85	366.35	758.95	630.1	489.15

X16609_s_at	67.55	9.12	324.55	374.98	136.8	57.28	771.95	964.85	210.65	15.34	164.45	69.65	310.9	330.93	136.5	8.34	154.25
U83410_at	208.1	123.18	194.05	224.22	323.15	328.88	918.3	525.8	561.35	102.88	311.4	331.92	492.25	12.23	702.9	147.22	179.05
U85611_at	3876.35	1291.67	1457.05	1683.41	4188.25	2134.68	4142.55	182.79	3864.45	1012.36	3039.05	836.44	4370.35	608.04	4441.45	2594.3	4032.8
X00274_at	678.7	711.92	131.85	152.38	436.05	447.81	213.85	137.11	819.55	251.66	839.15	95.53	967.1	559.46	195.6	77.64	605.55
X56681_s_at	7679	1397.95	2982.5	3445.87	4476.25	2279.5	5270.35	504.1	5567.3	39.74	4900.25	1431.4	3936.45	818.19	3924.3	2157.52	6057.5
J03626_rna1_	231.65	288.43	463.1	535	702.7	835.94	180.95	172.75	410.65	394.35	612	385.66	411.25	413.45	231.9	146.23	264.5
U59919_at	788.7	141.28	280.6	324.14	888.55	69.93	1086.65	685.26	688.4	170.27	841.25	389.12	1022.55	73.89	546.55	167.65	593.1
D85131_s_at	1061.35	1208.52	75.9	87.68	194.1	5.52	376.4	365.86	189.65	120.84	390.75	292.11	476.35	451.63	293.15	201.6	206.35
L21934_at	75.75	79.27	39.2	45.25	197.2	126.01	291.15	373.42	224.5	2.12	62.35	32.88	258	150.76	268.15	346.41	131.35
L13210_at	4583.35	74.32	2289.65	2645.36	4379.85	302.43	3966.55	1222.52	3429.6	2287.21	4091.85	1653.43	3482.25	286.02	3268.65	787.93	4323.2
L14430_at	114.15	59.47	103.15	119.15	59.95	12.94	36.3	22.91	67.25	47.31	29.2	10.89	107	46.24	29.7	10.18	63.95
M33518_at	2794.1	1363.3	1559.9	1802.27	1939.2	1744.72	2509	30.26	2154.2	905.1	2763.85	1556.84	3809.65	480.76	3277.3	113.14	3259.85
U15128_at	572.9	10.89	365.55	422.35	749.8	525.66	265.05	199.76	293.45	129.61	771.35	507.21	148.65	113.63	640.55	137.82	522.2
AB003102_at	2061.4	746.85	1335.95	1543.54	2205.45	4.17	2388.15	866.14	2227.4	140.29	1712.9	14.28	1448.55	1804.18	2095.6	370.1	1738.2

J03260_s_at	138.7	36.2	194.85	225.07	345.35	291.82	332.7	163.77	161.4	14.71	341.7	203.08	122.1	40.59	148.35	84.5	181.3
L08835_rna2	1573	1051.33	796.55	920.3	649.95	543.55	684.9	406.44	1030.45	14.78	1875.55	1062.43	1312.25	798.82	1158.5	270.68	1395.55
X60489_at	13550.2	8437.9	6858.05	7923.63	15053.35	4298.71	14965.5	6857.95	14706.45	694.87	12821.55	2947.57	12193.75	4117.84	10927.8	2587.16	12231.25
L20814_at	138.85	38.25	278.1	321.31	237.35	163.41	217.45	118.02	104.8	53.6	597.45	591.64	135.35	62.15	92	5.8	307.1
M97675_at	492.4	303.49	48.45	55.93	666.45	9.4	210.85	64.42	368.95	231.58	913.15	114.2	876.2	102.39	725.25	469.45	497.8
M94065_at	655.95	322.94	200.95	232.14	342	195.87	299	304.9	411.55	443.99	920.55	440.32	829.55	655.42	665.95	81.81	469.05
AF000959_at	441.35	23.83	185.6	214.39	944.15	452.62	745.3	102.81	394.55	87.33	704.45	101.47	573.8	269.97	488.15	39.39	539.25
Y07512_at	291.45	20.44	56.2	64.91	96.6	71.28	118.7	24.89	490.6	181.3	144.95	81.81	389.85	181.94	159.15	97.23	335.15
U09550_at	689.95	619.35	266.1	307.45	347.35	76.72	282.2	17.39	239.5	113.7	320.6	152.31	229.3	47.94	378.65	104.44	283.1
X92493_s_at	50	16.26	19.1	22.06	721	533.16	100.6	20.93	460	234.9	196.2	42.28	455.55	74.74	231.7	257.39	328.55
U33839_at	303.6	42.85	163.15	188.44	889.45	697.56	175.35	121.69	170.1	162.78	456.6	263.33	583.45	30.62	548.3	408.99	224.4
X69090_at	170	18.53	116.6	134.77	316.55	174.02	244.7	118.37	182.4	94.47	234.15	38.54	187.35	55.65	486.05	493.07	115.05
U53446_at	915.15	62.72	431	497.94	730.75	175.15	741.65	213.33	1059.15	304.98	770.95	17.89	604.1	436.28	846	352.99	549.25
HG3597-HT3	4395.85	1188.43	2385.05	2755.67	4174.4	537.12	3841.5	24.32	4840.1	1407.99	3737.9	1005.93	4266.2	549.56	3361.3	630.6	5388.9
U23736_s_at	153.35	111.79	52.55	60.74	424.85	448.23	298.95	130.89	468.05	619.35	294.3	210.43	129.65	7.71	296.2	325.83	186.2
U76366_s_at	1383.25	420.09	1404.15	1622.32	537.15	217.44	913.05	248.83	1211.05	936	1583.7	564.84	1743	660.58	1333.4	1279.58	1828.45

L40399_at	370.4	216.52	171.9	198.56	254.25	82.1	460.05	351.5	316.8	1.27	175.45	124.1	546.85	163.55	393.35	9.26	280.2
D83017_s_at	680.2	816.99	436.4	504.17	677.65	841.67	231.45	16.9	274.5	124.59	862.75	268.49	1022.55	980.97	212.6	161.79	789.15
M94345_at	2978.3	22.63	1132.8	1308.85	2791.85	754.27	3451.5	627.63	5116.65	83.65	5326.75	861.75	4908.35	128.06	5770.6	1152.58	4996.25
L21954_at	12253.6	3233.74	6234.8	7203.58	14494	2378	15585.9	5513.17	15877.35	3947.56	14262.75	289.42	13644.85	1877.44	15751.95	2025.79	14216.3
U83192_at	564.7	173.24	85.55	98.78	270.75	131.31	316.1	151.18	593.65	240.06	487.05	43.77	223.2	90.65	231.6	8.34	302.9
Y11306_rna1	402.8	99.14	451.25	521.35	174.05	126.22	137.3	67.03	469.65	180.52	279.85	51.55	168.95	0.35	110.5	7.21	389
M55671_at	586.8	90.51	316.95	366.21	616.15	524.18	317.35	33.3	639.45	585.84	736.85	205.56	545.2	307.73	1231	267.14	647.25
S85655_at	3997.8	1514.06	1779.95	2056.48	4292.7	1685.74	4802.1	710.78	4081.9	1639.36	3929.35	639.15	4500.5	84.99	4865.9	782.91	4474.15
U31342_at	3554.5	60.39	1736.55	2006.42	2987.8	756.46	3064.85	641.28	3247.45	124.95	3349.35	101.89	4714.7	1627.05	4230.95	2452.74	3065.6
D10511_at	1559.2	475.18	1091.6	1261.2	1467.7	490.87	1556.9	158.67	1709.55	537.9	1427.3	1172.38	1066.9	154.15	1559.8	119.22	1889.7
HG3141-HT3	732.6	448.16	130.95	151.25	396.05	109.25	750.2	421.44	901.8	942.57	340.05	70.78	479	146.8	437.6	106.49	931.65
U31799_at	32.85	8.13	62.2	71.84	113.4	110.87	56.45	38.68	61.2	58.41	102.6	94.89	65.9	1.7	109.25	40.52	74.8
U49837_at	770.8	52.47	579.9	670.05	898.6	40.45	340.8	42	1531.1	553.52	470.8	200.25	1130.3	136.05	661.8	426.53	744.8
M31328_at	1523.5	108.19	906.2	1046.94	1952.45	1389.39	1872.15	294.65	1752.2	376.04	1452.05	1027.36	1637.25	246	2068.6	396.97	1451.9
U09848_at	315.5	181.16	277.55	320.67	668.3	263.47	210.2	80.33	264.75	44.48	813.35	223.23	656.25	17.47	392.6	32.39	595.15
D38251_s_at	7366.35	153.51	4001.85	4623.7	5739.45	938.54	6380.5	816.71	5733.95	2192.38	7343.9	1350.86	6060.7	935.5	5309.15	1252.07	7180.15
M74447_at	857.85	638.31	498.7	576.15	812.4	500.63	292.2	114.41	251.3	16.97	375.5	168.57	319.85	79.83	503.7	304.76	382.55

HG4321-HT4	867.65	369.46	56.2	64.91	400.6	500.49	170.85	105.57	364.15	236.67	386.1	316.64	654.25	751.02	82.45	41.08	385.4
U09953_at	28145.5	12157.85	15270.45	17643.09	37354	17735.65	41991.25	23891.8	46337.2	14674.16	34755	8005.58	33913.4	7563.21	31322.2	5043.51	31315.65
X90908_at	382.35	87.61	81.3	93.9	291.9	32.95	254.8	99.98	287.45	52.4	192.05	108.68	151.35	21.99	242.8	134.77	229.8
M74509_s_at	961.7	431.19	1779.75	2056.34	611.35	63.99	344.9	131.66	273.15	3.75	664.25	265.09	575.1	167.87	700.9	433.17	1090.15
M28130_rna1	413.65	330.29	555.85	642.27	1064.8	421.86	405.65	342.45	1244.05	131.45	733.45	129.61	253.6	10.04	559.2	175.93	991.9
L10386_at	1118	549.85	184.15	212.77	798.35	313.32	1650	853.48	866	777.11	1044.8	952.05	1393.9	288.36	1950.05	572.69	1482.5
U70439_s_at	6846.15	1506.49	6492	7500.71	5496.5	592.84	6654.25	1906.43	10770	2457.9	7126.8	670.62	7217.15	198.63	7074.65	1062.85	7078.8
D31884_at	3020.85	630.81	2347.4	2712.18	3105.4	206.19	4234.95	968.95	3178.8	732.28	3348.45	747.48	3666.45	459.97	3285.55	833.33	4026.25
M98399_s_at	493.4	300.24	350.6	405.03	131.8	139.58	187.05	93.55	170.75	0.49	178.35	41.79	239.75	182.65	521.15	145.03	296.6
U17714_at	315.2	53.03	141.85	163.84	433.55	155.92	316.25	431.83	475.3	472.91	653.45	164.97	174.4	118.37	287.05	205.13	255.95
M60752_at	80.15	9.97	65.9	76.08	85.95	22.27	73.95	1.77	65.8	11.6	89.95	42.78	140	21.35	218.95	223.94	142.85
X72304_at	375.35	188.3	72.65	83.93	656.7	616.31	244.45	228.04	224.8	37.34	266.35	6.58	114.1	76.23	150.9	95.46	198.65
X51466_at	38404.45	22832.27	16884.1	19507.52	41933.95	9034.92	38286.85	1500.27	35112.25	966.12	34248	6740.14	30526.1	2151.87	37241.9	9005.15	53838.9
U54999_at	355.45	276.55	680.75	786.51	331.8	232.36	407.5	133.5	249.7	259.93	447.85	462.52	1107.95	73.61	634.45	113.49	1443.2
M63582_at	327.75	53.25	174.15	201.17	1024.3	1036.62	269.15	52.96	507.9	291.47	1125.05	1092.83	352.45	163.7	315.85	186.61	493.5
S76942_s_at	3590.4	862.1	982.65	1135.4	1788.4	1729.3	2615.35	268.21	1861.65	1545.95	2376.3	22.49	3917.5	653.51	2738.9	157.4	2774.75
M21665_s_at	1301.75	5.73	167.5	193.46	1166.75	659.09	1256.05	470.44	999.25	101.75	1249.95	1033.58	860.55	644.95	251.6	45.68	1012.2

U67733_at	351.25	5.02	83.4	96.31	768.25	90.72	492.95	233.27	652.05	385.02	621.5	421.72	241.25	13.51	190.65	66.11	533.5
U35376_at	60.35	16.76	24.9	28.71	246.65	291.4	39.7	20.36	50.1	9.48	250.25	336.65	33.75	23.69	246.85	308.65	37.9
U91903_at	76.05	16.9	20.6	23.76	113.5	7.5	394.9	249.18	330.35	163.27	432.35	359.56	532.85	299.04	196.25	60.03	498.25
L76159_at	444.2	312.68	463.5	535.56	430.55	342.73	638.25	62.15	524.1	240.84	591.9	618.58	781.75	151.82	1127.45	303.56	918.2
X59131_at	334.4	242.54	89.85	103.87	202.85	168.22	609.2	723.51	243.3	143.4	432.15	291.96	187.25	43.35	101.1	73.54	137.75
U50553_at	890.35	88.32	501.9	579.83	583.4	14.14	940.6	626.07	596.75	181.09	334.95	360.13	503.05	139.09	574.8	726.91	700.95
D86957_at	385.1	395.41	92.75	107.13	767.85	191.13	818.15	248.27	549.6	498.09	472.65	247.84	574.65	208.1	808.1	873.98	630.9
U66615_at	1266.05	556.99	911.55	1053.24	1509.05	220.69	1436.45	944.91	1350.2	593.97	2078.9	70	1459.75	18.88	1383.75	248.83	1487.8
AF005775_at	890.35	97.51	425	491.01	1342.1	343.8	1151.8	529.91	1581.95	189.72	1621	297.27	1429.1	31.25	1744.45	618.79	941.65
U52155_at	57.15	27.22	28.3	32.67	138.5	127.56	161.5	117.95	110.55	49.57	160	70.43	84.7	30.26	85	4.53	119.2
X54162_at	69.5	33.38	95.6	110.45	112.25	29.34	56.1	22.49	118.8	117.52	182.15	182.5	102	78.63	129.85	107.27	64.55
D42084_at	1528.05	283.34	1109.25	1281.63	1936.95	1005.58	1980.55	83.65	2335.15	109.53	1325.95	621.48	2736	104.51	2162.55	247.56	2125.85
AB001106_at	1822.5	275.49	1398.4	1615.74	5584.2	3166	3404.25	2602.65	5231.7	3074.92	3351.7	1432.17	2114.95	286.45	3390.45	2339.75	1814.5
HG4178-HT4	1348.2	427.66	606.85	701.1	584.1	221.47	1057.1	169.71	974.45	9.83	897.15	116.6	1000.95	146.58	294.75	119.15	523.25
X76648_at	300.15	115.75	306.35	353.91	571.75	473.83	258.6	67.03	729.6	422.71	246.8	183.14	79	17.96	431.05	439.61	158.85
Y07759_at	237.45	208.81	174.75	201.88	511.7	121.48	794.5	573.18	541.95	270.33	240.35	191.84	372.2	346.77	105.95	105.43	138.45

X66839_at	1061	452.27	672.55	777.04	1506.95	743.52	1665.95	124.24	1150.5	24.89	1918.8	89.24	1742.45	39.39	1802.3	533.02	2236.25
U30313_at	1246.1	343.51	778.65	899.65	1007.2	544.9	1404.85	594.32	850.65	233.7	981.15	258.31	527.8	315.65	1195.95	562.5	2000.6
M55621_at	3756.45	72.05	1590.4	1837.49	1576.6	1134.48	4765.05	13.08	3524.6	1463.85	3741.7	585.34	5125.2	1346.33	3485.75	1441.44	4713.55
X89576_at	485.3	340.83	738.3	853.05	477.3	9.05	394.25	321.95	396.2	308.16	416.35	258.45	428.95	73.75	438.05	267.22	346.75
D21063_at	1845.1	1167.57	1060.05	1224.78	2494.95	902.48	1854.4	305.19	2944.75	1706.89	2557.05	12.66	1580.5	105.92	1777.55	968.67	2349.6
X15218_at	339.6	232.21	95.2	110.03	188.1	4.81	201.45	40.52	180.95	54.52	156.1	56.43	199.6	38.75	188.6	58.97	197.1
M28219_at	918.05	783.12	832.55	961.88	1844.5	706.54	1059.9	794.08	417.15	6.01	1198.9	997.73	1420.95	1017.31	364.55	22.98	1044.1
X68277_at	721.85	496.74	1269.7	1466.96	2463.7	39.17	3866.3	1290.75	726.65	281.5	2527.7	897.46	1352.05	1372	1634.6	1907.21	862.55
D63479_s_at	1280.75	658.67	867.6	1002.39	688.55	679.03	1296.9	563.99	900.9	666.8	1709.45	56.5	700.8	506.15	1251.75	257.32	1209.05
D82344_at	568.85	248.55	27.7	31.96	677.95	742.53	618.35	579.9	632.3	89.38	685.35	304.55	398.75	60.6	535.65	352.92	453.75
Z35102_at	804.8	531.46	456.45	527.43	595.1	133.5	757.1	896.33	212.35	130.89	353.95	337.22	417.55	481.33	480.05	457.99	442
S38742_s_at	550.8	204.21	138.65	160.16	828.25	301.86	1197.35	1067.09	816.95	49.43	812.2	109.46	339.8	334.32	190	161.93	582.8
X06614_at	2235.95	1573.81	457.5	528.63	1022.05	842.38	1628.65	747.34	1235.1	819.68	949.05	819.32	1971.3	1058.26	1793.7	340.4	1814.55
D17390_at	279.75	91.71	140	161.79	413	240.7	435.9	211.42	303.7	28.14	494.95	240.91	387.3	73.54	260.7	76.37	218.95
L38503_at	354.15	95.53	117.25	135.41	200.2	91.64	777.3	450	1243.8	106.07	723.9	332.34	1088.9	641.63	1483.3	53.17	1426.35
U39657_at	49.2	9.19	197.4	228.11	197	146.94	162	184.84	62.95	33.45	94.65	35.43	42.7	8.2	55.35	27.37	53.25

M62982_at	129.55	3.04	25.15	29.06	126.65	112.22	738.4	980.76	109.15	49.14	77.65	8.98	144.45	36.42	99.15	54.66	65.55
L47726_at	230.45	158.32	205.4	237.31	382.75	56.07	119.6	77.36	342.5	312.12	120.85	50.13	76.4	5.37	251.95	242.33	147.15
L15344_at	2448.1	110.87	2000.6	2311.39	1173.15	485	2161.45	490.8	2455.45	178.4	2242.55	1549.62	1684.4	473.34	976.05	181.66	2390.2
HG2797-HT2	7734.3	269.12	3573.85	4129.15	4718.35	2156.75	7822.35	3613.24	3108.5	973.97	4226.95	1199.75	4680.55	1285.59	6353	2391.58	7169.75
M69238_at	495.95	228.04	82.6	95.46	193.15	39.24	514.7	439.11	163.8	16.83	589.5	569.36	543.5	479.84	263.1	83.16	698.85
K03474_at	1296.8	853.62	177.9	205.49	897.8	67.74	825.5	266.58	1173.4	1060.52	973	703.15	1047.85	885.93	740.9	214.25	847.5
M18737_rna1	145.4	93.34	59.65	68.94	596.8	126.85	358.1	50.35	678.85	212.06	1016.45	671.26	729.2	171.83	802.75	45.04	679.5
S72487_at	1692.55	255.34	1118.45	1292.24	1063.9	588.17	1650.6	147.22	1709.55	911.39	1770.5	317.63	2476.85	611.01	1847.55	627.13	2596.9
M13955_at	29029.8	4421.82	11326.5	13086.43	20827.05	6366.29	22671.05	7923.77	31531.85	5090.39	26937.25	5557.08	27397.75	5828.47	26411.1	5614	36795.8
U63139_at	50.6	25.03	50.3	58.12	677.35	589.94	156.7	135.48	72.7	38.61	110.45	34.15	464.7	147.36	133.05	144.74	132.55
Z48520_at	58.3	10.61	13.9	16.12	79.2	25.88	133.65	122.54	63.75	30.9	82.65	56.07	270.6	327.81	248.7	300.1	38.25
U60415_at	63	16.69	25.5	29.42	49.4	21.64	212.35	17.32	185.85	64.13	265.15	171.33	59.95	9.55	100.3	13.15	120.4
U00954_at	83.95	16.76	39.8	45.96	247.7	162.21	106.65	73.61	80.05	37.55	82.25	38.96	117.85	99.49	89.1	60.25	109.85
X61615_at	503.7	585.34	257.25	297.2	422.55	21	953.95	369.89	588.85	210.36	598.4	40.73	554.6	502.05	870.55	101.47	425.15
L04282_at	387.35	152.24	597.3	690.14	629.05	372.86	449.6	141.99	396.45	414.15	681.65	21.57	494.6	99.56	638.15	241.05	655.05

X80507_at	706.55	138.38	293	338.56	773.15	98.92	484.25	426.46	382.15	343.44	398.95	355.89	592.15	398.17	674	27.44	785.95
U03270_at	873.95	308.23	344.9	398.53	865.1	304.48	329.75	317.42	813.45	315.72	1183.95	126.22	811.2	192.76	1191.8	510.96	1029.75
L34355_at	1285.7	526.94	213.45	246.57	601.95	1.34	631.55	103.31	521.35	84.5	865.7	671.19	536.9	64.06	230.75	36.42	1219.05
M26665_s_at	396.7	422.71	407.05	470.3	1182.65	1085.48	286.35	103.59	633.85	402.27	434.25	240.49	360.7	341.39	125.55	11.1	608.4
U14973_at	80403.4	46905.22	32172.2	37171.05	103632.95	11160.05	100145.15	50405.19	125770.2	24277.52	90212.85	27318.72	97701.95	57450.95	95146.95	19518.62	73276.75
U40705_at	80.85	58.48	255.6	295.29	395.1	402.63	112.25	23.12	133	44.97	282.9	41.15	326.45	276.97	267	183.85	171.25
D90064_at	62.3	52.33	12.6	14.57	100.5	67.6	122.25	106.42	377.95	386.01	69.85	26.09	94.9	2.69	262.6	19.66	89.45
X87344_cds1	957.55	310.07	89.75	103.73	208.4	80.47	225.3	102.11	523.3	200.39	347.1	6.51	694.95	300.03	268.05	88.46	266.5
HG3063-HT3	526.45	523.19	72.25	83.51	267.9	151.18	215.7	92.63	123.95	19.87	184	155.85	163.8	4.95	688.35	805.61	157.2
Z26491_s_at	1477.55	624.02	519.25	599.98	1928.8	31.82	1281.45	380.49	2262.2	8.63	1469.55	629.25	1366.95	150.4	1453.3	233.91	1577.55
U86214_at	198.85	33.16	204.75	236.53	219.15	40.09	332.15	244.87	525	599.77	107.4	4.1	313.35	225.92	446.35	361.97	104.6
J03040_at	4517.2	346.62	1552.95	1794.28	3823	2021.48	3460.75	166.67	4106.95	2166.36	3851.5	559.89	4306.1	2215.22	2903.45	570.14	4088
M37033_at	1060.15	639.58	731.55	845.2	1692.2	992.07	1301.55	594.75	1019.65	86.2	1676.8	579.4	1609.85	327.04	733.5	892.09	798.3
L19527_at	33173.5	17799.15	14489.35	16740.68	44077.95	1803.62	42014.05	16504.23	45674.5	12606.02	34334.5	7640.15	37011.9	12515.37	39465.1	5593.21	34579.5
U41635_at	4844.3	1004.52	2935.2	3391.28	3427.2	1172.24	4426.65	910.97	3857.25	489.25	5002.35	639.44	5180.35	1431.68	4598.35	1055.07	5494.85
U51678_at	1206.6	386.08	1112.2	1284.95	1842.3	146.23	1475.5	551.12	1933.9	31.11	1404.5	271.25	1136.3	4.53	1953.8	1240.12	1357.15

M80482_at	618.95	181.37	393.3	454.39	299.05	0.64	546.8	25.03	807.4	359.92	722.4	107.76	436.2	223.45	775.9	392.87	830.9
U09368_at	29.95	23.55	229.35	264.95	315.6	287.51	69.35	7.71	54.95	20.01	154.2	99.84	55.55	37.26	88.4	103.8	118.8
L04731_at	2243.65	1319.53	271.3	313.39	1609.1	1609.66	1481.45	286.73	1126.45	1154.63	2692.2	1162.91	1414.85	1031.32	1776.45	823.43	1852.95
M13686_s_at	642.3	523.4	182.55	210.93	347.55	203.72	674.8	360.34	277.85	65.12	348.7	143.68	537.9	304.06	712.2	419.6	870.65
X96586_at	610.4	51.62	370.95	428.58	1118.65	289.56	1102.25	205.56	931.15	178.69	707.95	100.2	781.35	239.07	408.7	329.94	592.1
X65965_s_at	2061.35	165.68	986.85	1140.21	2298.5	203.08	1833.95	117.87	1332.25	247.56	2184.75	569.43	1306.9	353.13	1330.35	447.67	990
D42038_at	170.75	49.99	18.75	21.71	283.05	201.17	955.35	953.82	559.2	37.76	293.05	298.33	119.35	52.68	702.95	880.28	280.5
J02883_at	522.9	84.71	299.8	346.34	1242.6	957.85	1143.35	337.64	668.9	695.79	604.9	430.77	1192.4	95.88	571.65	340.19	701.95
HG2463-HT2	743.5	556.21	376.15	434.66	771.6	757.59	580.7	381.13	351.05	51.12	563.8	8.2	705.55	595.88	997	1099.13	898.9
U64444_at	3961.9	875.26	1700.2	1964.34	4274.6	483.66	4605.6	1752.92	4992.65	217.44	4285.1	344.93	4388.95	41.22	4736.2	358.22	3993.15
M29971_at	1565.9	1039.59	809.6	935.36	1873.1	266.01	1843.15	541.01	1640	202.37	2166.05	633.36	1435.6	529.2	1169.15	371.02	1655.65
L14787_at	590	14.42	548.05	633.21	1268.6	86.97	556.2	392.59	1177.05	593.76	1212.05	363.95	1210.3	175.08	936.35	105.57	670
D23662_at	7638.1	1208.45	4174.15	4822.68	6525.1	1456.5	8253.9	2526.07	10136.95	1788.06	8838.4	2237.43	8779.4	1887.55	9178.95	1618.92	7215.65
L21715_at	170.7	81.18	69.8	80.61	145.85	1.34	76.05	2.19	105.75	15.49	126.6	0.85	192.4	50.35	206.85	154.79	151.05
U37518_at	50.25	31.04	27.95	32.31	214.25	66.96	467	613.49	56.75	11.67	644.8	574.17	240.6	290.34	156.3	79.2	122.45
U82319_at	111.8	49.5	173.2	200.11	766.95	120.84	932.75	686.95	496.1	147.93	290.6	128.27	396.05	7	179.35	208.81	368.55

L76465_at	211.55	233.98	276.55	319.54	489.15	667.44	535.9	702.72	113.5	64.06	333.4	456.93	303.8	374.63	366.9	333.9	229.45
X89960_at	469.9	65.76	561.05	648.2	1032.7	467.26	422.4	253.71	344.8	207.04	501.5	249.61	795	107.2	375.85	77.85	967.05
U65437_rna1	55.9	58.27	27.9	32.24	40.45	4.45	49.95	31.32	40	34.37	139.5	140.43	57	37.19	99.25	86.62	24.55
L32976_at	1241.8	433.46	292.9	338.42	956.55	526.72	1256.15	0.35	1162.95	110.8	965.2	544.47	1655.3	453.54	1061.95	686.25	1260.55
S75174_at	2393.6	170.98	937.6	1083.29	2308.75	181.8	2028.2	339.41	2042.65	660.65	2166.05	481.04	1396.2	477.16	1036.45	897.95	1726.65
X07696_at	6063.25	2537.31	2222.5	2567.79	5667.7	1474.46	6285.9	346.91	32712.1	21118.73	19358.7	190.64	30798.15	2108.24	28972.7	2283.39	18655.3
D86973_at	2497.8	291.33	1258.15	1453.6	3148.3	799.88	1229.15	1262.82	2914.35	297.34	2306.35	436.92	2461.3	633.85	3231.25	345.85	3479.35
D87957_at	492.05	152.66	320.3	370.1	593.15	428.72	712	284.26	332.9	222.03	579.05	147.15	129.35	65.27	438.55	447.39	317.1
S75256_s_at	2053.35	1496.31	1617.85	1869.24	1416.4	61.38	1894.85	733.91	2193.7	1021.34	1896.75	345	2765.15	482.74	2315.05	1097.64	2845.6
D79986_at	993	154.71	665.45	768.84	697.45	371.3	734.95	163.84	1448.3	3.39	695.8	461.03	1053.3	760.28	1114.25	128.91	994.85
D80001_at	190.15	1.06	362.2	418.47	213.65	222.24	291.5	267.14	508.45	240.06	655	512.37	276.1	303.91	56.8	15.13	322.35
HG2191-HT2	3003.35	382.33	938.45	1084.21	4231.45	5165.91	3245.4	3477.69	3203.9	1160.79	2464.3	2719.39	2741	2411.52	4290.5	3684.45	1212.5
U50531_at	509.55	16.48	358.75	414.44	284.45	157.76	200.05	110.1	251.5	129.12	735.6	929.99	87.65	35.85	567.75	112.92	213.5
M62400_at	185.3	170.7	40.2	46.39	286.05	310.77	675.55	783.12	98.5	69.44	408.35	404.25	392.3	141.42	182.05	90.16	223.1
X16665_at	2230	655.63	814.15	940.66	1832.95	30.76	1960.35	604.93	2073.05	611.58	2633.2	546.45	1691.4	57.28	2049.5	6.51	2059

U09813_at	10107.6	1125.29	6094.05	7040.87	9457.75	446.4	10655.95	5374.08	9544.65	517.81	6878.55	3981.93	7655.5	737.09	11140.2	4082.69	11000.4
M64231_rna1	2456.5	453.11	1320.6	1525.8	2216.85	558.4	2296.5	540.8	1042.75	1064.41	1936.15	8.98	2417.5	707.53	2268.25	362.82	2330.3
D55640_at	630.95	321.66	692.45	800.09	730.75	252.51	1405.7	371.51	293.25	92.7	1422.25	1587.1	1375.3	364.87	628.45	371.87	400.9
D13635_at	835.55	170.06	369.75	427.16	591	82.17	356.05	217.72	796.1	100.55	848.95	422.21	930.4	62.79	884.4	33.66	730.9
X80907_at	3689.3	1439.95	1188.05	1372.71	3359.4	614.76	3577.2	1989.94	2815.05	1094.67	4576.35	1579.04	4087	325.69	3074.6	319.75	3982.9
M11025_s_at	124.25	12.52	60.25	69.65	462.65	537.47	261.35	147.01	212.6	208.6	239.15	103.45	499.4	332.06	311.25	176.99	142.7
HG2379-HT3	248.2	103.94	72.7	84	978.55	1134.84	684.55	801.22	317.1	276.62	527.75	574.52	489.6	555.79	486.5	497.1	598.3
U92458_at	42.25	12.66	66.55	76.86	164.9	79.05	175.45	204	89.05	62.72	348.9	444.77	517.75	204.42	56.9	26.45	106.4
Y11681_at	6158.55	832.19	2855.05	3298.72	4754.7	1422.42	5723.75	2312.88	5258.5	1283.82	4916.9	484.93	5464.8	466.12	6835.95	1113.91	5400.4
M94880_f_at	10561.75	1963.57	8014.5	9259.85	8037.95	558.54	12065.3	3060.78	9947	1815.57	10270.35	724.29	11581.75	1162.41	11181.15	2324.33	10706.95
S74445_at	1228.35	239.64	730.65	844.21	332.55	31.18	1227.4	602.88	765.25	207.54	1281.4	1185.82	659.45	640.85	1349.9	78.77	559.6
Z30643_at	12351.4	2464.13	4954.1	5723.89	20980.65	4607.58	14844.65	4410.15	10337.95	2828.78	15284.85	2403.81	10436.1	676.98	14505.05	1628.96	10985.85
J00209_f_at	83.9	44.69	132.85	153.51	404.1	297.41	132	127.56	296.6	268.13	53	30.97	398.65	484.01	104.05	65.69	166.8
HG2290-HT2	266.25	34.15	689.4	796.49	816.75	777.04	819.5	609.24	592.05	355.6	1251.3	379.01	616.35	88.03	367.65	23.41	798.1
U57057_at	576.15	478.5	467.95	540.72	800.45	946.89	202.25	85.06	479.5	433.74	329.5	231.93	719.1	794.79	401.85	385.16	174
D64109_at	764.3	409.41	76.95	88.88	1433.3	415.5	613.25	267.78	1265.85	595.6	856.3	255.41	1618.3	372.22	338.5	120.21	831.6

X70083_at	460.85	133.71	960.55	1109.8	490.25	50.42	563.3	207.75	488.55	104.72	598.25	72.05	581.85	98.5	582.15	74.03	445.85
HG3996-HT4	124.9	56.85	84.3	97.44	143.45	100.76	131.55	57.49	101.45	19.73	107.45	65.83	89.05	15.06	145.55	9.4	136.9
U64998_at	133.95	58.34	56.4	65.2	70.1	11.74	152.5	47.94	126.9	3.68	287.25	292.81	159.9	45.96	167	35.78	89.4
HG2724-HT2	576.25	422.21	1937.3	2238.28	407.3	1.84	517.85	374.55	392.5	137.74	2122.7	1129.11	1221.6	1062.92	379.55	101.33	383.55
U19107_rna1	130.3	112.71	126.6	146.23	177.45	155.78	436	440.39	460.45	63.71	299.7	383.68	207	23.9	83.25	3.89	129.65
M20786_at	439.9	67.18	272.5	314.8	446.05	117.87	592.95	288.71	424.35	179.68	497.85	125.51	526.2	114.27	858.25	159.88	477.1
L03532_at	3164.35	556.99	2049.5	2367.96	2342.25	1248.54	2334.4	721.96	3870.9	2106.19	2945.55	4.45	3908.7	2514.19	4092.3	2217.49	4712.4
X75252_at	2549.45	696.43	1002.55	1158.31	1819.75	88.32	2071.35	146.16	3111.7	1039.73	2325.8	258.66	3339.4	398.1	3557.8	984.15	3290.4
D10326_s_at	226.5	13.86	262.3	303.07	356.55	63.43	373.3	171.54	367.45	92.42	381.8	153.16	337	187.95	324.3	66.19	254.35
HG3985-HT4	477.85	165.82	73.4	84.85	825.5	597.93	643.2	17.82	1269.4	252.86	394.4	213.4	330.45	85.49	230.6	165.18	415.2
L34059_at	1947.55	47.59	1196.65	1382.61	1548.85	1507.91	1701.5	251.02	1588.3	487.34	1921	1402.62	1195.45	350.65	1749.8	1695.08	1686.2
M64716_at	20585.5	7164.69	8419.05	9727.17	26047.25	2060.16	26676	5235.42	36435.75	18982.07	22814.4	785.74	25355.05	7741.05	27838.1	3687.56	21575
Z74792_s_at	1460.45	290.97	624.15	721.18	1456.1	243.95	1186.6	100.27	1353.8	338	1949.3	867.05	1253.75	872.22	496.4	490.45	1176.5
J03930_at	467.7	155.7	191.2	220.9	337.45	253.92	1042.1	1091.49	695.65	168.79	358.6	228.11	928.3	242.96	1036.8	914.85	729.9
X99141_at	1407.6	477.01	192.65	222.53	1102.15	39.24	1558.95	313.18	1353.8	332.91	1954.4	1310.27	1764.25	581.6	1205.45	1056.21	1031.1
L08246_at	3693.4	683.63	1937.9	2238.98	3306.2	1315.08	2232.45	387.42	6176.55	1682.14	3241.6	1663.26	4153.45	205.98	3000.05	794.72	4709.7
D87436_at	293.55	243.88	441.9	510.53	287.8	65.05	99.4	10.04	476.15	475.81	357.75	291.12	532.8	108.33	180.15	56.64	224.7
J03474_at	9375.05	2092.26	4302.75	4971.31	8042.85	1896.25	7670.4	2171.67	6345.25	651.88	5260.05	1760.63	4327.85	1222.23	4779.8	1579.11	3030.95
HG3137-HT3	52.3	14.99	31.55	36.42	168.7	128.13	96.75	83.23	255.95	243.6	209.8	112.71	99.65	8.13	534.75	216.45	42.4
L42572_at	1081.35	30.19	797.2	921.08	1318.6	272.38	1553.3	191.91	2253.35	95.11	1914	741.61	1843.25	74.18	1622.9	277.04	1211.7

X70683_at	1247.6	867.48	335.05	387.14	1575	773.15	1204.9	387.35	983.25	568.87	1118.75	303.99	956.3	140.86	719.5	597.22	1461.4
AFFX-HUMG	3060.95	176.42	1280.3	1479.27	3902.5	540.51	3224.35	1745.92	3042	998.29	2146	1048.22	3649.05	1313.45	4041.45	1288.14	4235.6
M13194_at	3640.45	616.24	1981	2288.76	3820.25	442.44	4067.9	312.82	3570.45	365.36	3355.1	608.39	3781.15	821.59	4374.4	437.84	3486.8
D87435_at	2363.1	51.62	917.85	1060.45	1826.65	213.9	2251.8	678.68	2036.4	39.88	2283.25	570.85	2739.95	255.19	2090.15	277.82	2296.6
U60800_at	204.45	25.24	124.9	144.25	433.9	270.26	399.15	128.06	290.35	66.4	250.6	56.57	493.3	46.67	208.7	8.2	223.15
U52111_rna3	248.75	43.77	82.4	95.18	642.35	745.93	331.05	308.79	232.55	93.27	173.8	49.21	213.4	7.07	218.55	57.91	196.3
U70663_at	199.7	30.97	73.45	84.92	164.8	76.23	337.55	215.88	422.2	280.86	236.6	69.72	270.3	149.91	272	111.3	278.8
M95178_at	13318.05	4366.6	6547.7	7565.05	7119.4	5497.33	7955.65	4167.19	8482.1	5347.85	6833.25	1390.95	10288.05	3742.36	11008.9	3602.99	10527.9
X16667_at	353.95	150.97	584.1	674.86	869.4	576.15	1057.15	1200.46	1344.05	480.05	855	471.5	1392.15	695.72	994.75	394.78	1049.8
U68233_at	315.1	262.05	54	62.37	316.65	192.97	157.9	83.44	465.25	24.4	330.65	114.2	466.35	181.51	618.95	637.32	276.35
L11373_at	2571.8	667.08	938.45	1084.21	2627.95	360.27	2733.1	535	2000.45	615.68	2562.1	1201.37	3779.9	132.23	3113.05	505.09	3166.6

U73167_cds5	4959.2	927.72	2238.45	2586.24	2660.85	2919.86	3488.6	3244.35	3241.35	849.16	3942.35	1613.97	3492.05	406.52	3593.25	783.26	4478.2
L05144_at	229.4	210.72	287.65	332.41	307.3	260.36	489.15	160.44	701.5	347.33	218.95	197.07	812.3	108.75	371.7	394.57	593.3
M62486_at	373.35	293.94	449.25	519.09	1052.25	1159.44	529.3	180.74	943.2	703.85	535	276.48	484.15	324.07	616.7	247.63	542.4
D38081_at	316	18.38	560.8	647.99	282.65	38.11	350.95	159.31	377.5	262.9	316.85	109.11	885.6	36.06	1091.05	1199.04	703.2
L19058_at	778.45	125.94	32.95	38.11	708.15	731.5	435.55	313.6	405.5	93.06	516.65	155.35	334.5	277.61	384.25	232.99	299.65
M26880_at	22155.95	3236.22	11767.15	13595.47	22342.25	97.51	43269.7	35790.92	22629.05	5072.29	28056.8	14935.08	24543.2	2666.22	19410.1	703.43	21110.35
K02405_f_at	3293.45	288.15	1630.1	1883.45	3353.5	43.7	2590.2	373.21	2669.95	82.66	2879.75	1507.2	3442.15	253.64	1991.1	212.13	2381.1
U33880_at	84.95	102.04	12.65	14.64	173.15	72.62	36.5	28.57	152	173.81	68.85	4.6	175.2	227.55	134.3	158.96	31.15
Y09943_s_at	1042.2	667.65	396.6	458.21	1743.9	1267.28	568.55	172.04	606.55	107.13	1040.5	76.23	857.55	424.48	1886.4	379.86	1028.65
M10943_at	469.85	232	56.2	64.91	262.2	19.23	300.75	24.54	601.4	598.5	1051.65	476.1	898.9	248.19	596.75	419.95	228.8
HG4462-HT4	45.55	34.58	14.65	16.9	46.25	36.13	46.5	36.49	65.65	31.18	178.15	46.88	51.9	26.16	31.85	14.92	42.5
D31886_at	790	0.14	79.7	92.07	228.95	85.35	461.1	115.12	954.5	223.73	1320.5	215.95	521.1	515.91	875.25	729.8	941
M74826_at	327.7	253	350.85	405.38	444.5	458.77	908.85	908.7	517.6	373.35	249.9	213.55	438.55	57.77	487	85.56	302.05
D89050_at	157.5	105.92	87.9	101.54	233.5	216.23	104.75	28.35	452.45	430.56	654.75	646.79	241.25	97.93	245.35	51.97	280.55

M26657_s_at	674.05	14.64	250.85	289.84	547.95	94.12	481.05	126.5	365.15	53.1	764.75	109.67	561.2	29.7	497.1	211.71	407.95
D80003_at	499	2.83	845.05	976.3	1107.1	534.57	421.9	162.78	747.55	509.47	816.9	236.6	694.45	419.53	827	358.93	411.8
M21121_at	489.6	465.28	43.25	49.99	451.9	431.9	211.9	86.13	129	18.81	305.3	15.98	141.25	44.76	372.25	297.34	792.65
J03909_at	1035.8	606.56	777.35	898.1	1403	381.98	1516.55	34.29	1611.35	668.99	1287.7	886.99	1279.7	301.37	1038.65	1163.26	951.8
M74524_at	1173.55	435.65	404.4	467.26	1188.65	1044.61	718.8	646.44	1196.55	526.44	803.55	522.34	906.05	326.05	336.4	152.03	732.25
Z18951_at	4671.5	1311.82	2077.1	2399.78	4011.75	1261.83	2611.05	362.67	4184.95	79.27	2968.75	637.88	5401.05	2428.28	3958.2	3235.86	5129.35
X63454_at	616.15	18.17	255.85	295.64	575.2	505.72	835.8	1032.09	515.75	588.95	419.2	363.31	707.7	321.03	633	298.68	168.15
U26266_s_at	1157.2	1068.44	661.3	764.1	773.15	303	2150.35	960.6	1201.3	1004.66	940.5	432.75	2135.55	1463.64	1597.9	368.12	2029.35
U18018_at	1590.2	631.45	1850.8	2138.43	2702.3	356.66	2931.15	283.48	1850.75	818.48	2962.25	542.42	3058.4	510.11	3573.5	791.82	4298.2
HG688-HT68	1896.6	728.89	426.75	493.07	2545.15	58.76	1619.15	363.38	2635.35	811.69	2216.95	2430.96	1639.35	1585.83	2159.35	823	2060.4
U07550_at	1431.7	375.33	339.9	392.73	764.3	13.44	610.65	532.8	1428.8	699.19	1004.6	371.09	918.5	161.08	1221.5	109.6	1139.55
X96506_s_at	8610.85	2933.57	6112.9	7062.72	5621.95	784.82	7914.1	1926.72	5820.85	1225.63	6197.45	543.41	7993	30.83	8058.95	846.48	8998
U22680_at	46	17.39	14.2	16.4	240	288.92	57.65	2.05	60.8	13.01	86.2	35.5	49.65	9.12	28.7	16.69	38.65
D86956_at	1327.6	179.75	753.3	870.31	700.55	696.85	490.95	422.07	1427.55	344.29	847.7	808.93	960.3	1180.16	1303.9	443.07	1116.3
M80397_s_at	3950.85	15.2	1609.75	1859.9	3902	1141.13	3006.5	1294.43	2397.55	1003.03	3652.85	1151.66	3193.4	1137.88	2162.85	717.5	3030.75

M16961_at	731.4	33.8	379.75	438.76	375.9	260.22	373.75	82.38	1122.85	98.22	692.9	404.75	535.2	213.83	312.5	264.74	301.55
Z80345_rna1	266.7	89.94	125.5	144.96	346.05	58.48	345.45	156.48	329.25	72.2	368.2	92.49	291.2	165.32	305.15	90.86	379.15
U67963_at	3120.05	645.09	1133.25	1309.35	2385.1	1351.99	2713.25	1192.39	2526.35	180.38	2766.1	619.85	2344.85	125.79	2639.8	363.17	2290
U44378_at	324.4	67.46	23.85	27.51	429.25	252.08	216.85	61.31	377.7	109.6	267.9	125.3	510	78.63	426.65	295.22	487.65
Z15108_at	581.2	83.58	1033.3	1193.88	1136.3	280.3	870.15	155.92	613.25	185.33	631.75	26.94	558.6	512.51	519.05	565.76	956.7
X62025_rna1	1148.55	594.32	959.5	1108.6	2138.1	484.93	1224.2	531.89	1223.2	1136.89	1420.1	5.37	1644.05	229.74	1870.9	866.21	1555.9
U43916_s_at	552.05	579.33	111.3	128.55	202.1	187.1	583.45	415	522.8	380.28	1060.5	137.74	1397.7	510.67	1401.05	1349.8	872.2
X13810_s_at	594.85	159.03	230.7	266.58	1805.6	378.02	927.95	673.8	995.2	804.26	453.6	55.58	678.7	165.04	775.35	580.04	457.5
HG3254-HT3	692.35	29.91	788.4	910.89	1186.3	857.58	954.5	372.5	633.65	75.59	1122	51.76	1001.3	356.1	947.05	215.6	1264.7
M16801_at	127.55	10.25	51.95	60.03	154.7	86.27	265.7	182.01	135.95	42.07	377.7	201.67	195.75	69.08	73.65	4.45	179.8
HG429-HT42	81.45	61.31	307	354.68	341.3	384.67	94.05	13.79	82.2	53.6	443.55	137.25	240.4	237.59	153.05	101.33	235.7
U09587_at	8613.25	1870.79	6434.35	7434.17	10219.5	1981.88	8868.1	2591.12	12247.5	2078.89	9328.9	849.94	8539.65	2148.83	7780.25	3405.92	8902.55
U39487_at	289.4	39.74	357.1	412.53	344.1	104.37	229.55	30.19	389.15	374.41	306.3	63.5	159.15	83.65	136.75	39.1	751.7
L36051_at	228.9	201.1	160.15	185.05	1035	1284.95	170.9	188.66	141.7	69.01	138.75	60.46	264.45	230.3	95.9	18.67	390.65
X14362_at	187.45	192.83	88.05	101.75	131.45	23.26	250.05	131.31	277.4	338	139.1	54.02	526.1	675.15	250.25	293.38	188.55
M59911_at	10517.5	882.61	6600.9	7626.57	8675.2	2684.18	9000.2	1005.65	8839.2	1850.78	8828.85	1756.1	8750	512.94	6204.3	1588.44	11134.8

X98225_at	171	149.48	504.5	582.94	169	123.89	282.7	216.09	192.75	44.05	840.25	437.77	183.4	39.6	113.05	37.12	136.5
Z54367_s_at	8757.05	6200.83	3591	4149.02	3127.95	1043.76	3357.35	1781.7	2444	2519.56	4216.6	876.81	6097.6	3720.51	5225.6	1383.81	9929.55
U51586_at	3375.55	55.37	1490.95	1722.58	3386.45	283.62	3547.6	455.8	3102.55	386.58	2721.75	1999.63	3416.9	239	2812.05	71.21	4376.6
U09303_at	2561.7	794.36	827.05	955.51	2987.9	1050.19	2842.65	1433.8	2462.65	181.37	2263.55	356.31	2954.65	163.7	3059.9	148.07	3160.2
L37868_s_at	451	424.69	93.5	108.05	277.6	247.91	192.7	131.1	239	163.62	359.5	328.52	204.25	29.91	347.45	197.35	596.85
L13939_s_at	6687.35	940.24	3005.1	3472.04	6107.65	72.9	6255.8	1444.34	5287.25	2355.44	6112.2	1654.63	6231.65	1329.71	4976.25	947.74	6683.8
HG3928-HT4	247	144.11	64.8	74.81	107.8	13.86	78.35	33.59	94	52.61	221.6	191.34	201.25	67.39	154.1	86.13	335.25
U34976_at	234.35	126.08	51.9	59.96	72.8	9.9	677.45	867.69	350.7	25.31	764.1	523.82	608.1	225	179.85	193.68	279.65
U29725_at	264.35	227.9	78.05	90.16	365.45	130.18	262	92.77	243	37.9	318.25	211.92	468.2	454.39	486.15	406.66	157.75
U71601_at	533.6	576.15	280.3	323.85	307.65	80.12	194.35	106.7	703.2	222.03	40.45	20.44	592.25	218.99	166.7	152.45	330.1
Y07829_xpt4	1043	115.4	379.3	438.26	2002.25	320.39	1977.9	468.25	873.85	739.28	1438.9	334.04	1705.25	44.76	1424.5	1634.55	1393.65
U33936_s_at	2858.95	390.54	2110.65	2438.6	2693.7	123.6	3065.35	438.9	3398.2	443.92	3192.95	1169.63	2720.15	996.38	3062.35	1047.3	2720.25
Z29481_at	1019.15	571.13	212.6	245.65	1620.65	1536.33	1729.3	1019.65	1249.9	233.06	790.1	654.64	976.95	448.52	745.65	564.34	619.9
D42041_at	2741.75	828.8	1813	2094.73	3287.6	38.47	2622.15	328.73	2926.65	683.7	3312.45	814.66	2408.9	125.72	2508.75	84.36	3482.85
HG4749-HT5	260.75	44.05	78.5	90.65	314.5	9.9	292.8	73.68	250.4	15.56	338.3	17.54	269.35	0.49	302.35	23.69	778.95
Z48570_at	321.55	271.32	137.55	158.89	329.1	222.17	136.75	19.87	506.85	323.93	205.05	127.92	171.4	94.47	702.55	504.1	308.05

M30185_at	2300.9	361.9	451.9	522.13	858.1	274.07	1153.75	376.11	1957.75	434.66	2203.3	121.76	2219.75	804.48	1271.2	902.27	2132.35
D88532_at	160.6	138.88	150.05	173.31	1369.75	506.22	125.55	36.56	336.35	57.2	196.6	27.58	126.4	34.37	379	293.03	394.4
U30521_at	195.8	116.53	33.4	38.61	185.3	13.15	366.55	63.57	141.4	87.12	483.1	530.33	425.9	24.47	307.4	300.24	96.5
L41147_at	804.9	55.58	129.4	149.48	731.55	479.35	394.4	220.76	898.95	425.89	1331.05	1394.06	936.45	177.84	658.5	35.5	435.5
X57766_at	1224.4	1077.07	2039	2355.8	1891.4	35.92	2713.9	2123.87	862.05	645.66	2195.35	1015.05	2149.35	546.52	2222.85	565.76	2291.85
M60094_rna1	318.9	352.99	212	244.94	774.95	419.53	128	1.56	425.15	151.96	580.05	681.44	253.25	216.02	740.65	104.02	381.9
Z50194_at	5144.75	2092.97	9783.35	11303.46	2668.7	3149.31	1471.7	1329.08	2857.3	2117.08	7092.3	2261.75	5408.5	2405.29	2186.3	1484.64	4661.05
M26167_rna1	29.35	14.07	312.7	361.33	35.75	5.44	121.9	2.97	188.35	120	298.4	140.43	27.75	16.9	267.1	46.53	46.9
HG3925-HT4	146.35	125.79	151.75	175.29	304.05	242.61	701.45	834.46	573.35	260.99	739.9	377.17	455.4	590.58	647.2	793.66	172.15
D78156_at	196.6	191.77	144.2	166.59	295.9	348.46	513.85	588.81	33.25	8.41	401.95	469.45	243.25	38.25	127.9	6.65	58.85
U38372_at	94	8.77	43.15	49.85	114.45	40.38	98.25	13.79	140.55	88.03	73.25	10.11	158.2	10.75	135	78.35	331.8
X84003_at	42.75	9.97	82	94.75	132.4	128.41	219.15	86.2	147.5	145.38	18.8	16.26	350.35	386.43	146.8	157.4	16.9
Z14982_rna1	707.7	216.52	925.4	1069.15	514.05	70.64	1075.2	706.26	325.1	45.25	860.25	722.59	690.9	400.51	436.15	233.98	629.2
U46023_at	542.2	404.18	181.2	209.3	344.55	236.24	503.3	237.45	230.7	89.52	939.25	86.2	664.55	574.95	528.75	521.63	691.35
M14636_at	474	70.85	237.35	274.29	1302.2	739.92	295.4	242.54	702	87.4	279.5	246.21	604.3	37.62	434.45	1.63	816.85

S83366_cds3	300.9	14.85	64.65	74.74	571.95	696.15	102.9	47.09	118.3	46.95	204.85	154.93	148.1	79.76	254.25	98.64	113.2
U52827_at	1040.1	272.94	87	100.55	1150.15	81.39	1411.05	861.33	1624.1	14.14	789.6	295.57	1489.05	152.24	955.5	544.47	723.7
U85943_at	954.55	990.87	112.05	129.47	228.6	92.77	488	72.27	623.5	697.91	405.15	356.31	435.8	139.02	275.6	111.72	165.05
D86976_at	1788.6	113.56	944	1090.64	1372.2	114.55	1113.9	62.79	1676.7	177.2	1437.3	124.59	1277.95	336.09	1841.45	720.05	1443.7
L38969_at	1212.05	68.52	912.55	1054.37	1035.35	635.19	791.7	322.44	671.25	366.49	910.25	702.23	1341.3	1161.64	361.35	15.77	1275.45
X15673_s_at	1000.7	456.79	757.7	875.4	989.35	226.63	758.6	285.11	1575.95	365.79	1554.1	666.38	910	860.69	486.25	441.73	1393.15
U68566_at	4667.65	1210.21	3146.95	3635.87	6474.9	325.27	6679.65	3468.15	5840.95	308.37	6475.85	3023.94	4425.65	739.42	4453.5	1311.12	5545.65
X72012_at	702.4	234.62	203.15	234.69	568.65	220.69	335.45	68.66	381.85	4.88	500.4	31.25	922.6	696.22	518.65	188.59	614.7
D86425_at	177.55	68.8	274.1	316.64	515.5	17.39	579.5	601.61	238.55	207.68	109.75	78.84	706.6	99.14	496.05	378.23	211.1
X72882_at	125.1	9.33	32.45	37.55	171.2	64.21	204.8	82.59	148.65	1.34	210.4	10.89	271.95	106.14	164.05	41.22	169.95
X12671_rna1	5835.6	134.21	6163.65	7121.34	5291.35	567.45	5620.35	3687.07	7522.5	3577.39	7248.9	1200.67	8045.85	1396.75	8454.7	916.83	9016.5
M24900_at	2343.8	226.84	741	856.16	1618.9	485.78	2207.95	1386	1434.75	1342.87	1885	525.52	1364.4	258.09	2006.6	1190.34	1372.85

Z15005_at	344.9	404.18	443.25	512.16	229.35	64.7	368.45	102.88	599.4	278.6	870.85	345.99	643.15	174.87	374.85	257.03	346.2
M77698_at	842.75	851.99	1419.15	1639.71	1485.6	67.88	902.1	207.47	1475.65	487.97	1190.6	118.94	1148.75	359.71	1226.45	69.23	1128.1
D83195_at	294.7	210.15	106.75	123.39	263	52.04	204.2	49.92	179.25	77.85	225.25	34.58	236.2	29.56	301.8	5.8	179.65
HG2686-HT2	139.55	101.47	154.75	178.83	545.2	662.56	128.05	81.81	171.8	81.18	143.95	3.61	130.15	46.74	112.3	10.75	343.65
U50383_at	293.05	53.53	163.3	188.66	525.35	371.73	594.2	455.52	224.75	36.7	437.9	250.6	275.15	146.87	266.25	37.12	375.65
M60746_at	410.95	153.94	82.15	94.96	755.65	36.56	771.15	406.09	768.4	755.76	610.65	473.27	610.85	341.89	992.85	169.92	694.1
U49928_at	539.6	316.93	201.4	232.64	330.8	96.87	488	200.25	465.95	345.85	395.6	81.88	862.35	467.04	438.2	68.59	452.9
L34587_at	5296	2903.52	2480.05	2865.41	5609.95	3018.29	5167.8	4361.15	7219.85	554.73	4913	2280.56	3855.5	1523.53	4801.15	1751.57	5002.3
U93205_at	12553.05	2463.06	8043.45	9293.29	9710.7	3970.12	12610.05	7530.19	11154.15	4060.99	9489.95	4285.14	11537.05	1349.23	12489.75	12.23	15247.3
X60486_at	152.05	20.44	287.7	332.34	943.4	570.35	153.35	68.09	623.3	227.83	597.8	367.55	331.8	158.11	947.25	758.09	240.2
L31801_at	1485.45	222.95	633.6	732	958.65	563.92	1147.2	563.28	963.65	944.2	1326.45	824.27	2158.35	269.9	1583.8	768.77	1074.4
Z46629_at	787.9	48.93	485.7	561.16	874.85	213.33	246.55	58.34	448.2	362.89	761.95	363.52	515.7	456.08	670.85	333.83	1355.1
U63542_at	71.35	59.61	280.8	324.42	765.05	522.06	271.45	28.21	97.6	45.4	85.2	80.61	94.85	14.78	162.75	68.52	88.15
U13219_at	203.75	258.02	14.85	17.18	170.7	196.29	111.4	130.39	47.75	30.05	85	41.3	51.85	15.91	71	43.98	152.9
D38548_at	2004.5	174.51	1308.35	1511.58	2215.9	600.33	3176.35	1154.63	2483.15	471.71	3037.8	643.75	3483.5	779.66	2695.65	780.72	2219.65
M63967_at	680.6	100.55	437.65	505.65	169.85	26.94	684.35	704.21	441.5	80.89	407.15	270.89	459.2	338.14	730.45	734.47	473.4

U13044_at	292.6	85.28	245.8	283.97	565.7	368.26	554.7	734.97	382.35	416.56	524.8	58.69	188	106.21	560.25	88.46	126.2
Z70276_s_at	137.95	42.64	83.15	96.1	259.4	60.95	167.05	108.82	133.95	149.41	608.25	219.84	70.4	50.77	90	32.67	113.7
U59748_at	390.7	212.84	127.3	147.08	771.8	192.19	675.2	276.05	682.2	560.59	608.85	424.19	404.05	342.73	215.2	23.62	465.8
K02215_at	125.35	97.65	225.45	260.43	427.05	505.93	73.5	19.52	387.05	356.88	129.15	86.05	219.75	162.99	89.15	0.78	46.55
U49250_at	370.4	48.93	284.15	328.31	285.75	137.39	304	279.73	536.15	472.14	609	293.73	140.4	35.92	702.3	597.65	541.1
S67798_at	187.25	236.53	244.7	282.7	564.95	53.25	578.1	292.18	552.9	233.06	324.45	380.07	303.05	327.46	320.75	298.33	266.05
J05243_at	2039.4	927.87	1021.1	1179.74	1413.65	403.12	1011	759.43	1459.85	393.65	1648	283.97	1190.05	305.68	1737.2	3.25	1849.75
D87969_at	269.15	106.56	463.15	535.07	371.6	68.45	695.3	890.11	514.3	159.66	539.9	549.56	346.15	371.44	188.35	191.41	149.55
HG1098-HT1	202.7	172.11	36.75	42.5	290.85	50.98	132.5	110.31	547.65	268.77	294.75	243.03	229.8	135.76	212.75	187.88	64.7
J04615_at	6220.9	709.94	2910	3362.15	6122.55	1287.99	5760.55	3029.03	4580.65	180.38	4130.8	94.33	4179.8	203.65	3797.5	359.92	3967.45
X66403_at	1004.65	7.28	777.45	898.24	407.4	245.37	606.65	210.51	373.55	368.61	1021.2	331.92	966.1	750.38	691.65	135.41	221.7
U35139_at	237.2	148.92	116.25	134.28	362.75	292.67	398.9	461.18	454.65	23.83	118.85	37.26	229.9	83.01	125.15	18.46	119.35
S68271_s_at	275.45	148.7	276.9	319.9	270.8	275.21	399.95	363.1	304.5	199.69	332.7	132.79	203.55	163.55	250.65	215.6	318.6
X90392_at	232.8	2.26	254.1	293.59	151.75	36.13	404	236.88	167.8	100.27	322.4	128.69	185	52.04	453.4	91.36	578.15
M81601_at	2621.6	679.67	2010.65	2323.06	2397.25	415.43	2032.7	714.74	2505.1	198.13	2594.45	1253.91	2137.4	53.46	2574.7	1732.27	1748.3
Y08976_at	2686.2	298.4	1148.35	1326.74	2438.45	854.54	1931.6	138.59	2120.6	107.62	2160.5	638.38	2300.7	210.44	2803.4	117.24	2173.35

M55150_at	2045.85	1496.17	1128.35	1303.69	3080.75	59.18	2407.6	1186.1	2437.8	922.92	2563.1	476.73	2236.3	256.68	2291.4	31.68	2064.1
X77094_at	447.55	362.11	220.7	254.98	110.9	20.93	353.55	260.29	576.65	663.76	598.85	99.35	85.3	11.31	540.4	461.46	325.5
AJ001487_at	208.6	178.9	74.35	85.91	426.35	482.32	685.8	746.28	195.7	37.19	135.3	12.59	164.1	73.54	140.75	5.44	107.25
U17886_at	2867.5	1009.47	1359.95	1571.26	2628.15	471.85	3488.95	384.74	2866.5	627.77	3157.5	242.82	2835.15	682.85	1929.15	345	2188.5
M91029_cds2	3722.55	732.63	2074.6	2396.95	3047.3	222.74	3507.95	76.44	3248.55	121.69	4021	192.33	3670.05	217.29	3953.2	665.53	3812.05
X61587_at	1611.3	196.86	1286.9	1486.9	754.45	563.07	934.75	971.64	1766.9	30.97	1095.15	210.65	1333.7	17.39	1610	132.65	2167.85
X12876_s_at	12681.05	2073.59	7578.2	8755.68	10697.2	4170.8	12969.15	5654.8	7357.75	315.3	7443.55	600.97	5185.15	1034.85	5949.7	873.7	4786.3
L20298_at	973.3	211.71	747.1	863.24	645.55	641.13	641.75	520.78	1638.1	396.69	1155.6	285.39	1398.55	48.72	1435.75	216.02	1373.8
X51435_s_at	487.55	213.05	339.65	392.37	539	250.74	610.9	422.71	754.9	97.86	320.9	121.76	476	635.97	633.4	30.12	537.95
D37931_at	370.9	64.91	486.35	561.94	135.2	17.82	508.9	46.39	369.3	28.85	497	547.16	502.65	649.48	428.35	338.77	518.9
U17743_s_at	749.15	160.87	290.1	335.17	451.35	393.65	188.1	133.64	722.4	78.49	733.55	339.91	560.05	23.83	192.15	169.92	330.6
X66363_at	4489.2	1036.05	1994.25	2304.11	2708.25	1720.6	3219.55	1449.36	2079.3	439.54	2274.45	1368.75	2909.9	789.56	2608	40.45	2986.4
M63959_at	5195.3	654.5	3050.55	3524.57	6334.4	112.43	7013.55	86.2	6294.65	897.11	4973.2	32.1	5078.4	288.64	4754.3	696.5	4648.75
L42379_at	3866.1	389.05	2170.8	2508.11	2795.7	1558.6	3025.5	1669.62	2682	69.72	3374.05	1408.06	1628.55	36.56	4697.35	1576.78	3355.2
U38276_at	2021.75	706.33	1533.5	1771.73	1755.75	250.53	1624.5	881.06	2243.55	1002.47	1874.85	89.73	2231.5	401.07	2710.7	567.52	3189.35
U13913_s_at	159.9	159.1	177.7	205.34	318.9	388.34	72.85	80.4	52.35	41.22	547.8	113	386.85	19.73	231.45	242.61	171.6

X60957_at	600.2	139.72	495.55	572.54	993	787.72	1073.7	266.01	1075.55	108.54	1040.3	599.91	745.5	584.35	1745.85	1150.67	1882.4
U45328_s_at	7476.7	1291.6	2776.05	3207.37	5665	2601.16	6802	971.42	6276.65	2942.2	6457.25	2005.14	5290.15	1024.24	3210.8	570.07	4789.45
AB000466_at	517.75	182.08	556.15	642.55	3434.6	4022.59	4813.95	6272.67	1509	38.33	2413.75	2952.67	1846.7	2085.12	5391.5	6938.27	1427.6
X52773_at	596.95	359.71	211.55	244.45	883.8	273.79	1166.75	1264.66	270.1	18.24	1243.5	1447.73	400.6	317.35	842.15	17.32	1014.5
L38517_at	261.95	4.88	183.8	212.41	755.8	482.67	420.75	291.26	628	274.78	362.9	1.84	428.7	86.69	478.65	300.03	352
U40282_at	2708.1	1194.44	1845	2131.64	2527	786.02	3350	177.63	2329.45	618.08	2616.05	217.29	2382.65	564.06	2439.2	745.86	2698.6
HG2492-HT2	326.65	92.84	101.8	117.66	322.35	167.8	494.2	434.87	318.8	18.38	243.85	164.12	321.8	35.78	323.15	58.05	501.15
X17360_rna1	941.15	313.32	440.45	508.9	476.05	119.71	1051.35	606.49	466.7	526.94	929.25	112.64	1078.15	108.82	582.3	481.96	646.8
U48296_at	2045.1	286.8	1794.1	2072.81	1366.05	109.11	1560.95	211.5	1938.45	224.79	1928.35	60.46	1279.25	19.73	2290.75	1654.42	1854.15
X86809_at	6852.65	1898.23	4751.15	5489.34	5211.15	2223.64	6848.7	1834.94	7759	1461.73	7556.9	922.77	8081.4	1868.32	5468.2	480.27	6855
M76180_at	609	258.52	56.35	65.12	288.85	254.35	127.35	50.98	247.65	100.2	187.6	83.58	311.45	126.5	409.45	309.92	290.05
U00947_s_at	5561.85	754.41	3348	3868.16	3826.05	1543.26	4322.05	2967.8	7660.55	267.5	5514.55	2641.26	6865.3	3471.89	6808.7	708.24	5865.05
U31215_s_at	71.5	38.75	23.5	27.15	123.15	53.1	213.05	154.08	67.3	10.04	182	121.06	123.7	25.46	127.7	65.2	72.25
X78687_at	1937.05	517.39	517.3	597.65	1074.1	176.92	1824.4	192.05	955.05	564.91	1716.85	339.2	1395.9	120.35	2078	366.28	1629.05
S83364_at	2133.7	233.77	632.3	730.58	2130	599.34	2985.4	792.53	1934.05	171.76	1671.5	372.36	1620.85	574.67	1466.7	220.9	1950.55
U90908_at	1347.35	79.41	773.8	894.07	1489.8	629.89	1350.8	227.83	1218.4	130.67	882.85	633.21	966.15	198.2	984.9	42.85	1176.8

U04270_at	398.05	23.26	96.85	111.93	333.45	34.58	394.4	141.7	341.5	51.05	528.35	319.4	733.05	217.58	319.35	28.78	378.25
X60592_at	1188.35	91.85	431.4	498.37	1275.15	755.26	1176.05	705.2	1481.25	235.82	1996.3	751.37	1603.15	284.75	2205.75	426.6	1845.55
X72475_at	620.7	546.17	179.35	207.25	721	132.79	629.55	383.18	440.3	296.14	1379.7	274.22	603.1	555.79	440.1	357.94	1346.9
U59736_at	518.5	500.21	86.9	100.41	1534.25	325.06	568.8	55.86	768.2	22.77	595.55	409.63	855.7	424.69	808.65	10.11	578.25
M64595_at	1315.2	72.69	196.7	227.26	1340.85	9.69	550.45	237.94	1012.15	1129.18	591.2	391.45	527.4	523.97	1428.15	134.99	1302.6
U66559_at	325.05	26.52	164.1	189.65	320	46.39	786.35	569.86	211.2	60.39	729	562.01	264.7	26.16	364.15	124.52	271.7
U22398_at	249.7	238.58	46.05	53.25	127.6	27.72	316.9	326.68	257.8	15.84	522.85	539.31	437.65	417.26	142	46.67	95.8
U73330_at	29.5	13.29	94.6	109.32	22.2	17.68	25.5	18.24	39.85	44.19	47.95	54.52	24.6	17.82	60.2	32.1	97.45
M68519_rna1	322.05	20.44	161.6	186.68	659.25	461.67	396.75	64.13	1051.55	1065.54	267.55	112.78	547.4	222.03	645.65	267.36	371.15
U96781_cds1	1025.4	43.84	138.05	159.45	1461.35	1150.67	1145.55	507.35	1020.2	404.75	1072.8	530.61	745.65	839.27	589.8	471.92	1197.15
D87449_at	613.6	33.09	550.15	635.62	580.65	201.6	996.5	482.81	419	200.39	584.45	263.96	468	11.46	601.65	300.03	759.95
HG4052-HT4	279.7	134.63	416.4	481.12	252.65	90.44	201.35	0.92	443.3	296.42	507.15	308.51	634.25	728.39	642.75	727.68	552.45
M62397_at	534.3	4.38	354.7	409.84	807.2	435.15	658.95	417.26	506.75	256.04	623.95	45.04	167.85	180.52	630.55	18.17	450.25
M68891_at	1650.65	304.55	906.3	1047.08	1912	123.74	1986.5	764.24	2419	222.46	1370.35	1042.49	2248.65	575.23	2379.5	621.12	2792.7

X71129_at	3099.35	565.33	1404.6	1622.81	3418.7	769.9	3524.9	938.76	3930	48.79	2580.8	580.39	3314.9	1186.95	2890.8	208.46	3614.1
M99436_at	251.05	117.73	83	95.88	263.1	82.17	148.15	44.05	178	29.56	154.55	117.31	92.85	31.04	152.5	43.7	157.65
M24398_at	7856.65	4951.94	1045.1	1207.46	3104.9	280.58	4176.2	187.52	1992.85	962.02	7445.4	1064.05	5202.65	660.93	5137.8	4026.12	4335.2
D45132_at	128.35	10.25	189.6	219.06	531.8	519.86	206.35	131.31	271.3	258.8	163.75	102.46	458.55	175.43	234.55	108.97	496.6
U65402_at	3682.15	172.04	1650.5	1906.93	4006.65	550.06	3542.9	409.84	4509	283.55	3514.55	96.94	3132.9	284.54	3044.35	544.12	3945.05
HG3248-HT3	372.3	79.9	180.55	208.67	537.8	686.46	736.5	482.39	807.25	32.88	371.95	426.03	296.7	46.81	540.75	549.21	587
U13022_at	650	20.22	564.2	651.81	1053.95	538.04	295.4	294.3	245.65	251.24	959.6	408.42	843.95	341.04	356.8	221.32	402.65
Y12393_s_at	248.8	128.69	246.3	284.54	241.25	213.19	236.4	180.03	421.1	261.21	303.7	170.13	151.45	166.95	357.05	398.88	416.45
U95006_at	351.75	325.48	244.1	281.99	864.9	41.01	844.6	397.39	1726.5	538.67	780.7	201.81	615.1	307.59	856	844.14	1066.65
L22009_at	1107.15	195.52	781.45	902.9	1051.35	109.81	956.45	5.44	1602.5	720.26	949.45	329.44	929.7	274.5	843.8	64.49	1133.05
U40152_s_at	448.6	215.24	454.1	524.67	1007.45	374.7	1264.1	686.03	1287.95	169.63	759.8	278.88	517.9	412.38	563	298.54	707.25
M17885_at	133746.06	38102.95	94285.16	108935.11	196164.44	11054.41	161898.66	8916.41	171593.7	44368.12	148798	11594.01	150941.59	36571.99	174434.84	14460.12	147523.75
X65463_at	2876.5	390.75	1560.15	1802.63	3172.4	1558.46	2183.4	1185.11	1792.8	527.93	2287.15	155.21	2518.5	682.5	2244.3	1301.36	2137.9
X94754_at	5905.2	1682.91	5143.55	5942.74	5879.95	2299.16	6698.55	2855.09	5570.8	233.35	6021.65	568.44	4151.4	2412.79	4324.6	3113.82	5453.65
D83777_at	304.25	290.41	333.7	385.51	995.75	1270.32	259.1	163.48	687.3	752.79	861.4	838.35	205.65	180.52	519.1	590.01	783.65
HG896-HT89	779.75	172.89	141	162.92	673.6	83.3	543.75	346.55	176.25	3.46	452.2	246.92	390.05	44.05	958.3	382.69	322.85

U14417_at	1023.5	228.54	255.3	295	1032.95	702.65	868.3	12.3	552	43.7	404	255.97	1061.1	571.06	630.4	585.77	574.3
L22075_at	105.85	12.66	50.95	58.9	92.4	35.07	125.35	114.9	404.25	0.21	471.45	166.67	143.3	60.39	244.15	147.71	363.65
M28882_s_at	1588.1	62.37	546.75	631.66	2167.6	672.74	2124.95	1167.65	1793.35	355.32	2092.65	534.5	1819.4	298.12	1380.05	473.13	1618.95
U41745_at	947.55	386.58	503.35	581.6	374.9	273.79	371.75	317.14	668.9	106.21	966.15	310.21	713.1	233.2	495.8	512.09	1118.15
AFFX-PheX-M	109.55	53.1	59.4	68.59	817.15	1054.23	60.1	48.65	53.65	4.6	151.25	160.58	46.9	15.84	122.05	128.06	85.35
J04152_rna1_	3593.75	31.47	1262.8	1459.04	3038.6	620.84	3847.3	191.06	10259.1	2294.99	3842.75	566.89	5188.2	1564.26	5503.05	1727.53	4278.9
J05070_at	682.8	618.58	275.15	317.84	455.25	100.06	188.2	54.59	657.35	181.23	625.1	519.02	574.7	333.75	681.4	565.4	985.35
M14158_cds4	304.15	163.7	115.05	132.87	464.3	594.82	251.65	68.09	389.85	428.86	244.3	26.02	370.4	240.56	441.6	413.52	160.65
X98266_cds2	64.05	14.78	74.1	85.56	376.95	428.01	167.9	153.16	195.8	183	51.85	24.25	365.2	127.7	136.1	60.67	198.15
U14969_at	111530.45	54325.53	59488.05	68731.27	166913.84	6204.78	133143.7	7891.31	134489.66	18115.16	127579.8	6893.73	143004.5	76020.91	133106.16	27697.73	107994.35
L78833_cds4	1032.3	134.77	389.9	450.43	444.05	550.48	358.85	364.8	366.4	267.14	351.4	309.29	804.4	215.95	400.15	371.73	493.8

HG2442-HT2	863.6	188.09	540	623.95	1105.9	187.24	1041.6	133.22	762.8	250.74	738.4	696.92	1304.35	281.36	796.35	184.77	571.1
HG537-HT53	412.25	39.67	319.15	368.76	358.3	26.87	586.3	273.65	525.45	233.27	498.35	41.65	562.8	28.14	376.95	289.7	404.4
HG3236-HT3	26121.7	9458.4	16387.1	18933.35	21375.4	3847.37	22330.15	10581.92	19842.3	13190.23	24921.35	11500.6	28068.75	803.63	24969.4	2093.46	25071.05
HG3491-HT3	133.15	122.82	103.95	120.14	214.85	40.94	193.4	118.37	170.2	48.65	211.85	76.58	497.75	421.65	80.15	31.32	189.5
HG4593-HT4	835.5	185.97	598.4	691.41	931.4	852.49	573.4	134.92	830.35	548.36	1107.7	481.4	554	270.26	545.5	362.89	770.95
D13645_at	311.8	208.46	633.9	732.42	632.1	361.33	390.8	341.53	570.25	187.6	403.25	321.52	555.1	239.85	295.4	58.12	462.3
D50857_at	1268.35	200.89	1055.25	1219.26	1489.05	633.5	1014.25	414.58	1563.3	327.96	1752.05	205.41	1396.95	329.72	1224.7	43.98	1285.4
S81957_at	170.4	145.66	50.1	57.84	437.65	370.31	126.95	120.84	486.95	252.08	223.3	182.15	369.5	154.15	386.05	327.89	233.25
M34181_at	253.9	184.55	342.95	396.19	294.45	120	124	30.83	288.1	136.61	302.55	283.62	216.95	136.54	724.6	206.9	339.95
U19906_at	258.35	80.96	238.2	275.21	463.25	345	261.2	340.68	85.2	13.44	382.9	498.51	381.2	256.4	413.3	535.7	131.05
D64142_at	4483.15	787.22	2103.45	2430.26	3336.5	499.22	3851.4	1807.36	4006.2	69.3	4872	1259.36	3044.4	89.8	3081.85	652.45	3218.2
X59871_at	84.2	44.26	179.3	207.18	101.55	12.94	156.95	49	315.1	420.02	298.3	320.74	53.65	27.93	189.9	214.82	19.65
U01212_at	3141.8	418.18	1282.4	1481.67	4008.15	1.77	3459.6	1163.19	1468.9	677.97	2963.15	500.28	3123.7	1544.89	2328.35	244.02	2874.7
AB002533_at	44631.6	17811.31	23484	27132.96	61902	4196.25	69720.41	15725.77	50397.35	21760.15	48244.65	2854.66	42165.95	5792.12	55055.1	963.79	47336.2
X70297_at	252.6	118.65	573.7	662.84	648.25	694.03	270.1	50.77	412	15.7	362.15	421.51	599.65	199.19	112.95	53.53	603.6
Z29074_at	293.65	122.12	117.95	136.26	749.2	703.01	248	25.31	293.8	45.96	550.05	266.93	305.1	56.57	320.8	10.32	794.95
U20647_at	1002.45	233.27	859.95	993.56	2306.85	1322.5	1556.35	1155.48	887.15	813.24	1127.4	333.75	1044.15	565.61	845.3	644.6	1546.65
L37936_at	1796.75	54.38	914	1055.99	1342.95	553.45	1395.45	688.09	1568.35	186.75	1498.65	327.89	1765.85	412.31	1379.3	441.38	1531.95

M68907_s_at	205.4	136.75	95.85	110.8	119.05	73.33	147.75	51.55	251.7	87.26	123.3	24.61	98.6	69.86	321.95	305.54	87.8
D10923_at	199.2	18.24	309.1	357.09	274.3	3.96	408.65	415.99	539.45	531.53	212.75	21.99	346.7	325.69	422.55	495.33	186.75
L36529_at	73.5	37.76	150.25	173.59	202.65	143.05	178.7	129.97	510.65	342.59	751.65	714.39	355.25	371.3	242.7	191.06	296.3
U25034_s_at	1548.1	672.03	861.1	994.9	1216.9	1214.39	844	108.47	1213.75	601.96	822.35	247.28	1176.65	10.39	1404.9	816.28	991.25
U01923_at	51.25	55.51	169.8	196.15	49.3	22.34	133.5	18.38	253.55	279.1	826.4	798.32	324.9	48.79	296.45	58.34	220
U55206_at	636.25	272.17	471.65	544.97	294.5	243.24	262.85	14.07	625.35	86.76	171.5	21.5	431.5	178.62	222.15	101.89	488.6
L36847_at	567.15	573.25	461.3	533.02	254.3	40.59	436.75	303.99	724.45	399.02	593.45	345.28	91.8	15.56	636.65	515.83	159.85
U20938_at	84.7	41.15	14.15	16.33	632.45	209.66	65.25	3.46	177.1	25.03	129.3	82.45	394.75	288.43	237.7	174.23	296.95
S73840_at	221.55	61.73	285.45	329.87	82.1	14.85	199.2	145.81	306.75	160.58	114.95	14.64	163.6	8.06	284.4	43.27	143.6
M16474_s_at	80.45	85.77	27.25	31.47	231.3	128.69	355.35	491.79	52.9	9.62	152.35	140.36	63.95	36.42	182	198.84	324.35
J02960_cds1	1550	167.16	805.05	930.2	1510.75	977.43	696.3	236.32	435.25	150.97	687.1	346.48	711.65	590.22	1524.55	730.79	1144.6
M32313_at	1413.2	340.26	481.5	556.35	1435.6	539.66	1877.6	1026.58	1225.3	518.17	1302.25	48.44	1552.5	127.14	1702.6	463.44	1309.3
X14885_rna1	82.65	56.07	26.25	30.33	226.05	122.26	71.2	55.15	553.5	170.27	61	4.53	86.25	68.66	95.75	53.53	52.75
X97324_at	63.1	0.42	63.5	73.4	178.2	60.39	133.85	36.56	98.85	13.36	131.1	100.97	82.2	10.61	69.8	2.69	188.4

D43951_at	576.45	119.01	667	770.6	939.25	99.49	363.85	74.46	1046.9	201.81	804.55	184.91	679.15	422.64	660.15	173.17	744
M59964_at	179.05	111.37	34.8	40.16	100.7	76.23	88.75	46.32	31.2	9.19	399.75	415.99	58.05	29.77	63.95	29.34	94.1
M17446_s_at	170.4	16.26	60.8	70.29	142	53.46	109.05	68.24	171.05	16.62	215.65	142.06	151.85	21.99	175.95	60.6	106.5
U79252_at	1055.55	83.23	1061.5	1226.41	926.1	406.87	1017.2	131.95	1174.15	154.79	926.6	318.48	1265.75	325.48	910.8	147.22	1087.3
J02963_at	322.45	298.89	37.7	43.56	457.35	433.81	307.8	28.57	794	435.86	295.25	207.68	575.55	190.42	387.65	397.89	441.55
M94630_at	2408.1	312.82	1245.25	1438.75	1537.6	1197.27	1985.25	432.82	3617	514.63	3251.95	279.8	1798.65	302.57	3328.25	457.71	2642.8
L07949_at	80.05	67.25	103.4	119.5	53.7	10.89	79.35	14.78	209.3	33.94	57.65	24.11	28.9	14.71	155	169.28	126.05
X02750_at	400.55	113.49	109.25	126.22	613.25	257.32	240.9	30.83	1165.8	530.9	306.75	55.37	598.75	134.99	461.2	22.34	341.65
U13737_at	580.55	295.36	719.4	831.13	1167.5	419.17	367.8	261.63	500.3	174.23	942.5	539.38	593.8	154.15	769	157.54	635.35
HG3033-HT3	10380	3955.7	1954.25	2257.86	5246.25	237.52	3589.85	1132.29	5512.5	3460.58	10261.2	1219.76	7336.15	4938.79	7618.95	2342.29	4020
X82835_at	101.8	98.85	30.45	35.14	192.9	243.24	556.55	740.13	179.25	218.57	62.7	35.21	21.25	1.48	76	63.22	35.25
J03925_at	75.05	0.21	82.9	95.74	155.65	19.45	302.2	202.8	85.9	82.45	161.1	60.95	156.55	124.95	78.2	30.83	113
M61832_s_at	7191.45	1449.5	3042.2	3514.89	5821.6	1899.71	5132.2	2635.39	6240.45	1902.33	6602.4	446.75	7472.35	20.72	6471.2	1638.65	7519.15
M95623_cds:	1850.45	438.05	831.75	961.03	1995.3	56.85	1981.75	424.33	1593.35	906.02	1553.35	62.72	1511.35	200.18	1608.05	140.22	1541.85
HG1019-HT1	319.3	189.08	883.45	1020.71	991.65	729.8	1265.95	1382.46	374.5	0.57	954.4	661.85	548.35	149.55	1120.7	55.3	1752.15
M27891_at	11085.3	340.83	5821.15	6725.65	10007.15	2194.36	11303.15	3993.67	10221.3	156.41	9679.7	2451.26	11385.25	254.77	9312	1320.88	11874.45
U42408_at	5017.65	1307.94	1938.65	2239.9	3089.35	2148.97	3682.65	1960.74	4622.45	3365.33	4745.25	1455.44	6532.15	360.13	5913.75	55.08	7548.4

U43965_at	547.25	434.23	69.3	80.04	407.6	18.67	417.15	80.26	709	182.01	588.6	98.29	154.85	154.64	588	217.08	702.25
M24351_cds3	1413.3	377.31	706.55	816.35	1024.05	710.15	638.05	786.94	1438.05	454.46	951.4	556.21	701.9	345.78	494.65	340.9	1594.95
M37075_at	1577.75	509.89	597.9	690.84	920.9	410.69	1236	680.94	1430.2	26.73	1288	234.62	2056.4	450.57	1623.3	98.99	1595.95
HG658-HT65	8522.15	13.08	5237.15	6050.92	7105.15	3916.74	6979.9	1284.67	6651.95	597.29	6441.9	343.37	7474.75	865.71	6732.55	626.57	5866.65
HG3510-HT3	74.75	17.89	179.3	207.18	188.4	88.67	171.8	4.38	56.5	20.51	361.1	373.35	321.25	297.2	85.1	0	72.7
M58459_at	298.1	341.25	285.85	330.29	268.65	214.04	412.95	481.04	420.95	444.7	321.9	29.84	171.1	22.77	434.45	425.32	110.15
Y11215_at	954.05	41.08	462.2	534.01	335.9	223.59	492.6	455.94	925.55	484.58	997.65	238.65	805.2	507.84	551.2	597.65	465.9
U04209_at	1388.55	129.19	460	531.46	1259.65	763.89	784.7	376.75	1179.05	29.34	1009.55	435.51	1112.1	26.59	1173.9	9.33	1155.5
X59244_f_at	577.55	212.49	451.8	521.99	422.55	485.85	737	700.18	390.15	82.8	631.9	633.85	384.65	25.53	86.55	70.92	414.9
L46353_at	106.35	107.27	42.1	48.65	224.3	147.22	420.4	324.42	303.9	54.73	614.75	571.13	682.4	820.24	294.35	268.63	185.65
L31881_at	1294.85	1010.81	580.8	671.04	2940.4	303.91	1849.55	1419.8	1680	590.58	1735.15	2075.99	1286.9	1228.81	1826.35	920.02	1356.4
X82153_at	456.95	220.12	52.5	60.67	332.75	100.2	577.1	704.84	496.05	2.19	583.05	360.7	122.55	77.29	374.9	186.39	453.9
X89067_at	180.65	158.75	26.75	30.9	84.1	42.99	95.15	72.34	368.7	417.62	90.5	14.71	307.45	117.17	358.05	326.75	95.65
M13994_s_at	217.45	61.16	62.95	72.76	440.6	425.25	287.6	124.88	164.95	54.52	181.9	123.6	301.75	128.76	850.75	965.55	307.5

S45630_at	1720.8	344.93	890.45	1028.77	2003.4	368.97	2003.65	236.24	1763.85	457.29	2029.2	411.96	1889.15	536.76	1018.9	171.4	1579.1
U43923_at	2398.7	391.03	689.6	796.77	2421.4	301.23	2470.6	284.12	1543.9	275.91	1709.35	122.12	1916	63.92	2122.6	955.73	1909.15
M85165_at	115.9	119.78	59.95	69.23	109.1	73.82	121.75	90.58	213.95	220.12	115.8	16.4	209.85	257.88	113.9	107.2	147.6
L78440_at	605.5	267.43	444.85	514	422.5	349.17	675.15	335.66	506.95	37.55	890.25	287.01	1165.45	137.39	926.2	415.5	625.9
U07563_cds1	647.2	416.49	875.85	1011.94	425.85	11.95	1297.2	137.04	662.55	558.54	1310.15	91.57	1605.35	419.39	347.55	369.04	471.65
U33920_at	191	28.14	373.4	431.48	364.05	57.49	140.95	60.03	295.05	137.39	432.35	384.17	635.9	524.39	200.45	27.93	175.75
U73960_at	800.85	97.51	622.95	719.76	815.9	70.15	1048.7	266.86	1344	257.95	1232.35	401.57	567.25	437.77	692.5	242.4	1015.2
AF009426_at	25	5.37	17.6	20.36	38.7	33.66	48.05	47.45	48	1.27	41.4	27.01	49.15	33.3	123	103.52	20.7
S81578_at	610.05	344.43	238.65	275.7	550.2	376.61	433.05	86.76	455.3	405.31	832.2	548.29	445.85	275.56	551.8	435.44	411.8
U75370_at	1608.05	88.18	1191.8	1377.02	1746.25	1063.84	1103.6	822.51	1530.55	1336.93	2012.7	242.11	1873.6	256.26	1408.45	687.66	1753.65
M83651_at	268.9	17.96	100.85	116.46	341.75	229.74	195.05	125.09	374.95	195.94	261.3	86.13	272.8	135.06	203.4	135.48	252.25
U56085_at	337.65	341.18	267.5	309.01	654.65	121.69	295.2	40.73	173.7	109.32	550.3	159.81	350.7	76.93	369.85	86.34	1015.25
X00129_at	214.45	147.29	141	162.92	223.8	142.41	189.1	82.59	374.75	154.36	94.2	49.36	158	153.73	206.15	259.58	122.35
L41870_at	197.6	137.32	397.2	458.91	321.3	87.54	107.45	28.21	271.65	71.91	533.4	244.38	147.55	140.08	762.55	257.46	101.5

U87460_at	60.8	12.45	35.3	40.73	847.05	454.32	301.4	40.59	227.25	252.51	107.65	68.38	39.3	4.67	231.95	266.23	97.05
M13934_cds:	101.2	0.71	50.3	58.12	176.3	42.14	136.8	57.42	102.7	23.76	102.9	1.41	119.85	61.87	109.05	81.25	91.4
M12959_s_at	1449.45	582.44	1138.15	1315.01	720.55	125.79	736.95	3.61	1130.55	155.07	616	172.25	1387.8	281.57	1288.05	995.54	1094.7
HG884-HT88	539	212.27	700.5	809.35	73.55	4.17	461.9	18.67	207.35	229.03	314.95	164.12	500	112.15	444.6	474.89	469.7
U73477_s_at	1237.9	17.96	687.8	794.65	1386	224.29	1986.4	1943.41	1551.9	390.04	1452.25	598.28	575.1	431.9	810.85	691.62	1136.55
HG721-HT48	385.95	45.75	478.85	553.31	274.75	60.03	470.4	277.75	593	177.77	1006.05	783.83	688.85	296.63	490.4	118.37	477.7
D42085_at	1407.65	227.48	1899.3	2194.44	1290.3	152.31	1552.8	421.72	2269.5	1267.28	541.9	35.92	689.75	516.97	1400.5	1139.71	2291.8
U51004_at	7686.75	3023.38	4408.2	5093.15	8980.3	1971.27	10491	4626.32	9339.1	1815.14	8294.9	1047.37	6488.05	1426.45	7037.1	90.79	6264.45
X16260_s_at	269.95	50.84	208.65	241.05	534.35	442.3	265.6	192.05	948.7	698.48	459.65	34.86	858.35	536.34	297.95	65.97	252.2
M96980_at	374.65	53.81	790.65	913.51	1195.95	421.36	1356	535.14	585.4	101.12	742.15	337.08	740.05	566.46	232	36.91	363.1
U79259_at	1602.7	740.06	580.4	670.62	1232.95	834.03	892.95	360.55	1463.2	675.85	2393.05	1565.18	2749.75	1056.63	1570.35	25.81	1893.8
X06948_at	228.2	182.29	23.6	27.29	51.8	1.84	125.45	69.08	395.05	175.15	145.2	7.92	376.55	219.84	185.3	38.18	423.7
HG4535-HT4	2756.45	941.8	1469.7	1698.05	3049.6	272.38	2539.5	808.36	2060.25	290.27	2364.2	559.89	2488.55	284.75	2503.45	446.11	1779.9
K02268_at	116.35	28.21	123.15	142.34	367.75	312.47	545.3	596.23	122.2	31.4	312.25	140.08	260.55	133.01	88.4	34.65	257.2
HG4074-HT4	898.1	39.6	416.1	480.69	1369.75	475.81	1300.6	291.89	2065.95	122.54	783.65	785.81	877.85	661.5	2005.2	332.34	1583.75
L13972_at	149.7	35.5	69.2	79.9	484.3	239.85	288.5	191.91	206.75	10.82	211.85	5.44	694.55	160.3	294	101.26	510.85

X91249_at	426.1	160.94	311.05	359.42	500.15	421.51	511.85	551.05	381.1	333.19	403.1	316.78	386.95	27.51	360.9	388.34	425
Z11793_at	60.25	56.5	67.05	77.43	79	94.61	390.8	528.21	195.9	228.82	149.65	40.38	157.8	184.98	224	235.61	124.05
U38810_at	33.6	31.4	10.85	12.52	384.5	201.81	100.75	76.01	67.8	23.9	103.7	65.05	198.8	98.15	187.25	212.34	278.35
M94055_at	496.9	185.26	125.05	144.46	121.75	50.7	355.05	411.75	466.25	486.14	105.4	42.14	379.3	405.31	152.7	162.35	395.55
U92436_at	162.45	186.46	192.8	222.74	254.45	43.35	98.85	54.94	288.15	332.27	638.95	866.14	406.5	510.25	233	210.58	62.25
J03161_at	3199.45	191.98	2301.45	2659.08	3630.55	719.06	3424.75	502.4	3420.85	23.41	4204.65	989.31	3458.05	108.68	3635.45	1175.85	3284.8
X58521_at	1066	63.64	645.15	745.36	1273.6	731.71	400.6	252.01	1346.75	28.92	946.8	518.17	1315.45	8.41	1137	1159.66	1363.55
L09235_at	258.5	129.97	155.85	180.1	809.2	299.39	344.1	8.49	626.15	255.62	172.4	152.59	457.95	74.6	546.85	192.55	532.3
L26584_s_at	173.1	30.97	73.8	85.28	276.45	221.11	132.1	119.22	394.6	297.97	695.8	884.87	162.6	2.83	889.3	1035.49	211.65
U38227_s_at	185.9	118.79	40.45	46.74	41.55	1.34	65.45	33.87	40.5	5.8	52.55	44.76	221.95	231.01	82.45	44.76	88.05
X57579_s_at	2198.75	685.4	1680.65	1941.79	2498.1	65.76	1675.85	890.32	1873.9	1159.8	1355.25	840.54	1922.25	327.32	1013.5	231.22	642.5
Z25521_s_at	1281.75	317.84	417.1	481.96	1701.1	46.24	1773.75	523.75	1667.95	103.31	832.85	790.47	1151.95	96.1	759.9	363.03	1602.05
D80008_at	708.25	242.04	247.55	286.02	388.6	396.55	326.1	311.41	777.15	152.24	326.35	244.73	652.45	201.74	757.25	222.39	136.7
U10439_at	1479.9	303.63	1105.95	1277.81	886.75	181.23	2015	519.3	1495.05	248.97	1672.8	81.74	1498.35	122.82	1570.7	1831.83	2462.7
U52513_at	555.6	280.01	132.15	152.66	744.15	488.26	1344.15	712.83	561.65	218.43	611.4	222.17	710.2	535.28	842.8	286.38	485.05

Y10210_at	34.25	4.74	69.95	80.82	51.35	10.25	63.25	30.48	59.2	1.13	54.3	24.89	116	91.08	79.65	40.94	92.9
M19720_rna1	915.45	210.36	88.8	102.53	770	122.33	563.3	11.46	1301.6	294.3	647.85	428.58	743.55	811.55	928	223.87	832.05
AFFX-HUMTI	244.25	187.03	478.1	552.39	355.7	144.53	519.05	228.61	485.7	492	365.7	290.2	420.7	441.52	650.35	249.11	461.65
X17254_at	856.25	398.45	261.7	302.36	1349.75	467.89	686.7	550.55	649.45	342.88	1782.55	99.21	1008.45	755.26	351.35	11.38	1200.7
U39817_at	166.05	65.27	415.9	480.55	226.4	73.11	201.2	60.1	178.65	50.42	214.65	35.99	462.2	451.7	265.05	36.56	340.35
HG3264-HT3	737.25	695.72	143.35	165.68	178.85	30.9	224.1	156.98	293.95	112.78	265.7	13.44	199.8	49.21	529.4	476.73	209.6
U68133_at	173.45	144.32	230.05	265.8	173.85	54.09	97.85	34.44	442.8	541.5	83.55	35.57	85.9	29.13	97.75	103.03	322.05
M93107_at	750.05	500.14	407.1	470.37	449.35	237.94	838.75	198.63	1150.2	218.5	972.95	361.12	1309.55	635.05	700.6	562.43	776.7
AD000684_c	3015.9	23.48	1514	1749.24	1674.7	783.47	1552	1561.01	2221.5	174.66	2132.5	2409.25	2843.75	858.5	2604.9	67.6	2216.35
X67698_at	9847.6	2463.42	4339.15	5013.32	8931.3	4907.18	7459.5	2572.74	10205.8	1486.2	8759.05	1510.59	11230	1152.87	10708.2	2925.87	9514
HG944-HT94	564.75	8.13	232.95	269.2	718.8	217.36	453.1	53.32	564	18.1	554.15	365.08	600.2	20.51	579.65	73.61	513.6
U70064_s_at	881.1	139.87	393.95	455.16	1058.1	7.64	869.5	467.68	912.65	87.47	1264.9	696.08	1077.45	162.85	510.45	321.95	434
S78203_at	121.55	0.49	140.35	162.14	396.35	341.46	156.95	29.91	366.6	58.97	228.6	162.07	234.35	94.68	377.4	297.13	365.75

U27193_at	234.05	187.17	25.15	29.06	350.15	402.13	114.8	16.97	97.85	16.76	218.55	213.48	200.9	68.17	372.45	453.47	113.55
U58522_at	262.3	48.79	268.2	309.85	59.9	28.71	488.85	535.92	251.45	321.38	519	592.84	75.65	72.05	298.45	390.96	242.1
HG3514-HT3	10232.05	2375.95	7291.6	8424.61	9403.55	2844.76	11190.9	6936.58	13745.6	302.92	8971.8	4674.12	10240.65	889.33	9982.1	660.16	10213.2
J05016_rna1_	606.2	94.89	428.85	495.47	767.2	339.84	190.8	16.69	183.9	64.91	739.15	343.44	302	198.27	716.95	105.43	662.85
U48436_s_at	193.95	249.54	16.6	19.23	495.85	288.71	460.3	515.34	620.4	151.6	361.45	483.59	400.7	72.41	205.3	107.48	115.5
U90546_at	122.55	9.97	36.8	42.57	340.85	205.41	66.6	56.14	67.4	16.55	69.9	63.07	111.55	5.16	90.5	37.19	73.15
AB000409_at	1617.55	375.69	391.35	452.19	12810.15	14202.45	3333.25	2479.61	4062.65	1795.98	3048.35	1867.96	3713.1	2197.41	8823.15	7433.6	2120.3
M31642_at	1163.5	338	647.75	748.33	889.75	297.62	631.6	693.81	1261.5	28.71	1180.15	525.31	1105.6	279.31	1650.9	116.67	1263.3
X99975_at	583.35	296.91	491.7	568.09	1359.2	1164.46	242.3	137.18	436	465.7	366.35	407.93	358.1	358.5	305.1	194.31	407.15
U20979_at	485	120.07	170.7	197.28	473	104.23	587.25	570.85	1471.75	668	967.35	856.8	941.3	864.23	1536.55	775.06	1162.45
M25079_s_at	4363.15	1418.95	1328.35	1534.78	4227.55	850.15	2255	1628.47	2984.75	1209.08	3965.25	908.42	3691.4	1388.33	1967	1276.89	2106.9
U81006_at	280.1	278.46	50.85	58.76	202.5	69.01	539.45	265.09	905.5	294.02	664.35	307.66	286.35	307.66	339	362.89	652
U79716_at	261.25	61.59	317.6	366.99	253.85	213.76	823.35	993.56	250.5	87.82	562.4	18.95	647.1	179.32	266.4	282.84	423.1
L20010_at	1270.1	1092.9	1026.9	1186.53	1213.2	331.35	1677.25	404.54	1484.45	769.54	1062.95	161.15	1160.05	986.91	1451.5	292.74	1772.75
HG3707-HT3	233.45	30.9	92	106.35	309.7	127.84	209.45	140.78	210.35	10.96	386.7	52.33	183.05	27.93	140.35	53.25	207.4
M22638_at	185.9	24.47	38.3	44.26	161.6	10.47	165	86.83	124	53.32	125.95	55.79	127.9	12.02	128.65	12.52	124.6
D59253_at	939.3	2.69	689	796.06	964.4	212.41	607.8	571.63	1028.75	182.93	918.2	495.54	1595.9	231.79	975.7	322.86	908.25

U43142_at	114.95	16.76	78	90.09	205.7	51.76	202.75	55.08	137.65	6.58	215.3	41.01	142.9	2.55	180.95	81.67	134.9
D31897_at	1357.05	883.53	254.45	293.94	1566.15	1044.61	1905.4	2444.75	1048.95	805.75	883.05	67.95	958.15	104.02	1340.1	1156.54	830.1
U19251_s_at	437	365.29	348.35	402.41	298.85	298.19	1049.65	884.94	440.15	360.13	403.9	9.05	315.7	7.21	443.35	146.58	575.15
X95325_s_at	10670.1	4196.4	5138.55	5936.94	10915.75	4159.7	12305.5	1635.96	10149.35	1872.35	8974.1	1093.19	8096.2	1688.43	10791.5	1955.72	10617.05
M16505_at	65.7	0.99	214.55	247.84	874.9	657.04	149.4	22.91	360.5	294.16	312	230.66	101.8	21.35	307	307.73	312.6
L29306_s_at	139.7	106.07	42.55	49.14	75.65	46.17	43.15	26.23	378.9	312.82	237.9	32.39	63.4	32.67	370.7	403.05	57.05
X13238_at	3725.65	597.15	1947.7	2250.3	3291.1	163.06	2002.75	535.07	3917.5	1065.19	2700.6	177.34	2642.95	806.88	3681.1	148.92	3172.35
J03824_at	1548.45	393.36	1160.65	1341.03	2063.3	245.37	1597.55	783.4	2982.65	296.35	1556.55	1396.75	2412	52.47	2161.55	216.73	1394.15
X87852_at	149.6	114.69	82.85	95.67	199.6	188.94	82.6	40.73	115.3	42.28	136.75	47.73	162	62.08	160.15	92.56	134.85
X74801_at	7420.65	297.9	3191.25	3687.07	6095.3	2126.84	6616.3	3172.36	5550.35	321.1	6228.3	972.27	5892.35	489.67	7323.5	34.51	7606.75
M24736_s_at	207.95	245.15	195.9	226.27	251.85	174.87	166.95	155.63	346.45	430.7	510.95	475.53	302.95	34.86	523.35	229.74	242.3
D28473_s_at	3373.8	1305.04	2715.1	3137.01	4261.65	1263.95	2846.35	928.5	3727.65	105.43	2749.4	1069.71	2346.85	322.79	2382.35	1487.96	3470.95
M64554_rna1	32.6	6.22	9.45	10.96	128.65	112.64	44.2	37.9	38.6	16.4	53.6	48.08	49.8	39.03	40.75	10.82	48.2
M28827_at	482.25	185.76	311.8	360.2	411.8	50.49	322.5	18.1	273.55	68.94	1201.65	1135.26	833.7	721.53	255.4	16.26	738.9
X97261_r_at	88	106.63	30.4	35.07	51.15	24.25	23.2	24.47	321.9	368.83	55.9	65.76	18.3	5.52	242.4	312.54	11.3

X95826_at	75.4	7.07	426.8	493.14	177.35	82.24	117.75	82.52	81.65	39.39	161.9	183.28	221.3	97.44	100.35	67.53	240.65
M37755_f_at	460.8	429.07	508.55	587.54	711.5	500.49	801.2	518.03	1014.85	865.15	1126.25	651.6	961.2	299.25	341.55	152.1	299.1
L37792_at	2601.6	212.56	1666.45	1925.38	2498.7	669.35	3240.8	1551.39	1712.25	63.29	2241.7	983.59	3330.05	187.45	2588.75	33.87	2088.8
M62424_at	93.2	117.1	336.1	388.34	68.55	4.88	366.15	355.32	164.65	205.7	49.45	28.5	84.6	99.98	195.7	221.75	94.95
D14446_at	232.4	132.79	377.1	435.72	1033.4	759.15	251.35	22.13	633.1	303.63	653.25	236.39	831.8	211.71	882.5	361.47	313.85
U71203_s_at	404.15	146.58	375.4	433.74	241.3	180.03	168.35	51.69	639.25	150.83	370.5	215.95	161.65	63	326.7	320.6	91.95
X78710_at	98.25	50.7	54.25	62.72	55.4	13.01	312.7	97.16	148.45	53.81	420.15	510.46	95.85	61.87	91.25	23.69	75.55
Z22951_rna1	1478.2	403.76	964.8	1114.68	1895.45	745.79	1718.35	853.55	1105.25	419.1	1448.65	176.85	1702.25	7	1186.9	319.19	1357.6
M65290_at	304.95	12.52	228.3	263.75	443.85	152.66	133.45	4.03	392.9	226.98	544.55	359.85	121.3	102.11	204.2	155.99	79.6
K01900_at	682.3	151.04	322.7	372.79	469.3	338.42	936	826.75	563.25	629.11	357.85	222.81	989.35	17.04	1099.2	506.15	383.55
U89995_at	201.65	111.79	128.5	148.49	427.55	426.74	107.9	77.07	555.1	49.78	506	372.5	233.55	29.34	496.55	222.39	125.85
U58682_at	59655.45	27923.01	23692.75	27374.15	93873.7	15216.8	89904.66	33634.88	82747.05	35870.89	60055.05	6357.38	61923.4	20944.5	78914.85	10929.96	63200.95
D29675_s_at	2862.6	82.59	1385.5	1600.75	1167.7	1069.29	1308.9	1158.95	2471.65	642.69	2562.2	1705.97	2667.45	625.15	2102.75	51.55	1853
L14076_at	1406.35	561.94	820.55	948.02	1070.4	531.74	1251.95	167.65	1705.9	459.2	980.1	231.08	1370.1	497.94	1382.05	539.88	1130.45

J05257_at	419.5	76.51	259.35	299.6	687.65	446.68	1050.2	10.61	880.95	525.31	782.3	14.14	1175.05	779.73	462.9	13.58	594.45
X98172_at	389.8	398.38	46.55	53.81	824.35	449.79	254.55	26.66	255.2	130.25	411.8	208.17	417.05	175.57	322.35	372.29	225.05
HG2325-HT2	2031.5	29.84	725.4	838.06	3201.35	1452.47	2653.35	1579.46	2274.15	570.71	2582.75	585.56	2363.8	627.49	2233.9	103.24	1613.7
U48250_at	67.75	17.75	26.05	30.05	161.4	182.86	148.8	179.18	240.55	171.19	221.25	85.06	56.85	16.05	193.2	142.98	37.15
D17400_at	3206.55	239.21	1505.25	1739.13	3225.85	79.27	2477.1	1316.63	1714.75	857.51	2539.65	377.95	2263.15	382.33	1880.7	226.84	3975.65
M17236_at	56.25	56.36	26.6	30.69	33.7	35.5	76.05	93.27	53.7	54.59	77.6	101.12	64.05	62.44	70.7	28.28	920.45
X81636_at	259.6	73.4	342.95	396.19	187.3	10.75	289.45	171.47	267.6	41.58	380.5	252.58	643.05	573.96	665.6	660.01	677.15
X63546_at	58.1	15.41	18.9	21.78	776.3	886.71	149.75	32.74	138.75	7.85	516.6	278.88	313.55	397.32	465.15	300.73	193.35
Z49148_s_at	43274.05	30542.84	20878.85	24123.02	42633.8	17739.04	55853.85	15034.72	49763	20800.68	47737.75	5871.32	60838.45	26420.55	54778.7	15954.88	48623.8
X51688_at	181.15	98.92	65.7	75.94	104.95	10.54	84.1	46.95	671.4	106.63	516.5	132.23	731.85	362.39	370.2	214.25	566.65
D63879_at	1063.8	60.95	564.55	652.31	1063.05	244.45	446.65	396.62	1109.5	206.9	980.55	597.86	1547.4	436.28	1228.35	887.49	773.85
U61232_at	274.2	199.12	74.4	85.98	301.8	341.53	359.45	157.19	581.45	54.24	424.5	282.28	112.7	6.93	454.55	155.07	535.05
X15357_at	757.5	727.75	640.45	739.99	392.35	247.56	862.9	321.03	954.9	298.26	1182.3	682.64	825.7	633	1206.05	492.36	467.6
D31888_at	659	255.83	1147.75	1326.04	933.55	802.21	459.5	94.47	750.2	192.62	587.05	5.3	417.45	66.82	543.65	234.55	768.3
Y10615_at	687.6	201.38	25.35	29.34	849.9	56.85	362.8	424.69	602.05	296.07	601.45	708.45	119.15	46.03	450.7	401.21	439.35
U29607_at	203.95	148.56	425.85	492.08	754.35	172.89	460.8	165.18	681.9	223.45	806.85	270.89	226.75	99.07	440.8	535.42	311.8
M27783_s_at	338.2	110.03	203.45	235.11	833.3	671.61	285	230.52	306.65	103.59	397.15	220.55	269.85	24.54	374.95	106	530.5
HG2915-HT3	4236.3	590.15	3213.4	3712.74	3127.25	411.61	3925	783.76	3951.1	1285.52	4145	758.58	4991.95	170.77	3858.4	719.27	5052.85

D85429_at	9398.55	953.82	2723.2	3146.34	8924.5	1258.65	13672.25	570	11512.9	124.45	9663.65	926.24	7784.65	484.3	8785.35	548.93	8422.4
X95190_at	257.6	65.05	103.2	119.22	169.2	9.05	256.85	124.24	186.85	5.16	352.05	182.79	307.9	31.4	245.5	104.09	223.4
HG273-HT27	2224.55	255.19	602.85	696.57	1298.7	691.41	1857.35	1050.69	868.4	244.09	1962.25	522.34	1496.45	437.77	1399.5	74.1	1677.35
U92314_s_at	285.3	187.95	100.95	116.6	313.95	51.55	331.1	195.44	183.2	54.02	245.45	39.39	438	23.19	273.4	225.85	285.35
M34376_s_at	141.65	78.56	50.35	58.19	225.35	239.36	121.5	26.59	407.5	466.27	282.7	371.8	273.9	314.24	301.1	178.62	59.05
Z26317_at	1060.55	790.76	536.4	619.71	932.5	863.09	324.6	125.44	842.65	414.58	1133.85	23.55	1384.5	706.68	1362.85	724.01	937.5
X01038_rna1	388.3	119.22	573.5	662.56	274.5	165.6	207.1	56.85	628.25	450.07	256.2	148.78	437.2	184.41	363	74.95	588.25
X91992_at	102.4	56.57	153.8	177.77	446.1	455.66	145.95	93.55	242.7	118.94	111.7	102.11	282.55	250.1	71.85	22.27	328.35
AFFX-TrpnX-	40.2	16.12	20.05	23.12	96.25	77.29	62.65	31.18	60.8	21.21	69.35	44.05	57.2	17.25	68.35	19.45	52.65
M86852_at	368.3	14.14	246.85	285.18	320.4	285.11	181.65	127.92	348.95	417.12	426.6	8.77	529.4	384.24	421.5	89.24	253.05
M23575_f_at	499.4	471.78	96.2	111.16	503.3	399.8	644.8	649.83	217.95	145.45	508.05	234.69	652.35	290.27	724.25	68.09	619.2
X04898_rna1	605.8	335.73	579.8	669.91	778.9	80.47	569.45	448.66	369.2	374.06	676.25	537.9	656.85	759.79	283.25	99.91	1029.05
U61145_at	241.7	235.75	247.4	285.81	87.75	39.1	87.9	23.33	288.8	239.43	375.3	180.88	270.1	236.74	145.65	33.59	627.3
U18914_at	118.2	118.51	115.5	133.5	308.75	319.82	295.75	196.36	595.75	91.15	213.05	254.63	384.4	270.4	282.2	335.73	419.3
U31216_s_at	409.8	139.3	117.5	135.76	169.05	20.15	299.15	123.11	663.45	566.6	804.1	700.04	490.25	157.76	568.7	422.85	196
U57094_at	725.95	59.47	742.7	858.14	1154.85	658.53	775.35	168.5	830.9	159.38	480.9	380.56	651.75	398.03	722.75	32.88	798.4

M22877_at	1234.05	330.01	672	776.4	1954.8	870.73	897.1	613.77	1509.2	323.01	1447.65	83.23	1383.85	190	1136.8	128.13	951.7
D87447_at	838.45	428.29	759.25	877.17	1560.3	79.2	1093.55	69.08	1311.2	35.78	798.1	761.98	1153.9	535	1414.05	140.78	1142.35
M10050_at	55.6	36.2	56.65	65.41	71.45	2.62	37.95	34.29	75.4	22.06	98.1	92.35	137.55	27.93	143.2	137.04	33.3
D90224_at	69.15	6.29	56.75	65.55	111.05	92.14	98.95	35.85	180.4	11.17	205.65	180.81	126.55	16.33	68.1	13.58	78
M59815_at	2314.05	207.25	691.35	798.82	2777.95	292.25	2128.9	354.83	1444	891.8	2950.8	462.31	1948.2	1123.31	2965.35	32.31	2611.9
L29217_at	450.9	64.49	276.35	319.26	1039.6	364.87	889.65	520.64	377.9	21.21	530.15	192.97	506.4	105.5	501.55	105.01	881.9
S76756_s_at	509.55	481.61	486.35	561.94	544.4	489.6	485.8	499.08	493.05	105.85	145.1	32.1	529.95	323.64	471.7	366.71	546.3
D25218_at	1389.15	211.21	1183.85	1367.76	1243.1	308.58	1377.6	802.71	1849.5	164.47	1465.15	397.89	1857.7	867.48	1246.35	363.52	1662.65
X82324_at	365.65	429.99	162.95	188.3	327.75	212.63	1104.25	1142.61	61.35	59.61	603.9	550.98	94.15	59.04	99.2	11.88	311.3
U86602_at	2665.85	671.26	2061.05	2381.32	2458.8	949.93	3300.1	237.87	2799.6	13.72	2618.35	389.97	2317.9	658.6	2470.8	29.42	2329.25
Y00339_s_at	524.8	107.34	229.35	264.95	977	166.31	774.6	446.33	1273.9	371.23	784.2	7.5	749.2	40.59	903.6	74.81	398.65
D43947_at	1621.95	378.51	761.05	879.29	1487.7	805.96	1132.8	603.16	622.45	7.42	1414.65	224.37	1035.05	286.02	1748.4	279.45	2039.3
U83463_at	483.55	120.56	344.45	398.03	412.25	266.08	368.35	101.33	767.95	345.28	647.4	305.61	388.25	69.65	431.15	201.31	565.35
X15573_at	2179.3	1054.44	696.85	805.18	1107.5	54.59	1686.9	779.37	771.7	86.55	1209.85	348.25	1881.45	984.93	3173.45	388.7	1892.2
X97064_at	335.55	114.62	46	53.17	150.45	124.95	83.65	0.64	105.95	49.99	162.45	80.54	112.9	103.38	78.55	57.91	291.4
X14975_at	256.45	220.97	102.85	118.86	310.15	30.33	537.15	587.68	201.7	160.8	383.15	333.4	216.9	61.94	116.7	16.69	475.65
D83174_s_at	5356.85	312.75	1926.35	2225.62	4208.1	972.7	4117.5	248.05	5933.05	1649.47	6068.4	1467.53	6462.2	9.05	4949.2	756.18	4927.35

M16707_rna1	1076.65	742.82	257.15	297.06	1647.6	1623.66	406.85	15.91	970.1	716.58	2533.4	2257.65	502.5	117.8	2294.9	1249.17	357.25
M11973_cds:	137.9	87.54	23.95	27.65	95.65	22.27	86	79.76	139.95	63.43	91.95	81.39	193.05	187.88	46.35	4.45	134.1
AFFX-DapX-5	72.75	47.16	22.95	26.52	175.3	211.57	349.6	435.86	85.7	10.89	135.35	40.38	106.8	8.06	109.7	75.24	153.5
D43636_at	55.1	7.78	37.3	43.13	48.8	25.46	45.95	24.68	55.35	36.13	271.95	324.49	139.05	34.86	60.3	27.72	69.7
HG491-HT49	145.85	27.65	101.5	117.24	109.25	16.62	413.8	456.65	163.9	34.22	210	137.6	524	82.59	421.05	396.33	279.4
M20471_at	7742.9	2711.47	3294.25	3806.14	8477.25	2347.38	8454.45	5349.05	8986.4	932.96	6561.75	437.63	5476.3	1562.42	7013.1	581.95	6509.85
HG2358-HT4	199.9	50.2	44.4	51.34	112.25	21.85	125.35	66.96	201.2	36.06	598.4	419.03	686	52.47	151.05	9.26	164.05
L17418_cds2	45.05	21.28	62.35	72.05	128.3	101.26	60.7	9.33	497	301.09	96.75	73.47	189.8	231.93	71.2	8.06	154.5
M13149_at	373.1	352.99	232.1	268.13	436.95	32.74	314.75	291.96	287.25	136.54	67.2	12.87	145.85	82.24	360.5	13.72	438.75
U11701_at	70.9	3.82	451.4	521.56	106.55	35.99	77.25	13.08	290	184.7	212.2	94.61	339.7	290.48	111.25	65.12	452.55
U40380_at	650.15	204.57	310.35	358.57	1926.75	1988.74	611.5	74.67	524.5	51.34	676.1	55.58	585.45	45.18	475.7	78.06	567.1
L20815_at	1566.55	93.13	1451.4	1676.97	2121.4	536.27	2288.75	1668.42	918.9	320.18	2033.2	773.86	1638.35	63.71	1560.15	1194.52	970.15
HG4069-HT4	812.2	51.05	355.6	410.83	828.8	89.1	890.75	348.11	926.05	141.77	1043.95	385.73	477.15	99.07	844.85	47.45	824.75
M80254_at	1607.15	131.17	1320.7	1525.94	899.4	377.31	1830.75	1039.8	1212.2	499.78	1356.5	189.5	1152.05	269.2	1017	47.52	1949
X83368_at	339.9	88.25	118.95	137.39	209.75	223.94	209.1	193.61	244.95	76.3	407.8	238.58	221.25	57.77	377.6	424.26	387.15

U40369_rna1	1386.7	295.15	999.3	1154.56	1413.35	0.21	1533.8	175.65	1374.55	196.08	1523.8	280.44	1344.45	11.24	1081.8	211.71	1008.6
U85430_at	259.4	9.19	89.3	103.24	261.65	219.84	443.45	407.36	459.5	220.9	228.65	122.68	541.85	290.13	241.5	223.16	179.4
M63483_at	1800.9	400.51	1560.5	1802.98	2173.85	242.75	971.5	682.08	1876.8	782.48	2351.3	178.76	2737.4	871.44	2577.05	45.89	2065.6
U21689_at	927.95	202.16	203.3	234.9	833.15	354.05	577	120.35	683.7	115.4	571.95	81.25	983.8	46.1	735.1	32.67	656.8
L48211_at	298.25	43.2	124.8	144.25	145.2	32.24	1089.9	1307.3	494	438.41	262.15	102.88	459	325.98	177.3	43.42	457.35
U73304_rna1	135.45	148.42	83.05	95.95	106.9	87.68	177.2	210.58	351.85	70.07	110.95	81.39	119.5	150.47	127.45	114.34	337.5
S73885_s_at	1981.45	525.73	1585.4	1831.69	1692.95	557.27	1183.25	617.66	2577.9	999.71	2235.8	179.04	2358.2	25.31	2281.5	659.45	2544.2
S57212_s_at	618.75	168.93	511.85	591.35	1289.1	976.09	580.75	64.98	735.45	190.28	1089.75	324.35	867.05	107.98	695.6	178.62	1123.8
L41690_at	2399.35	35.28	710.35	820.74	2338.85	689.64	1544.7	237.87	2084.85	1859.05	2952.35	526.44	2517.1	635.55	2029.9	239.85	2057.6
AF006084_at	7202.05	1415.56	3334.15	3852.25	7067.45	1940.09	8260.1	1178.89	6164.05	777.04	5981.65	670.41	7349.35	1813.09	6477.6	2279.01	7499.1
X74570_at	2790.95	651.6	862.2	996.17	1834.4	769.33	2365.9	1784.45	2758.65	852.56	2401.1	363.31	2031.7	278.46	1755.8	100.83	1443.2
M31606_at	1024.1	1058.4	249.7	288.5	487.4	46.53	478.8	35.78	508.9	84.57	518.9	127	682.25	230.02	384.6	20.93	241.3
D00591_at	1985.85	681.58	283.4	327.39	1036.95	104.58	1634.8	118.65	1371.85	1433.8	1452.65	706.61	3104.5	1297.82	2947	3205.74	2349.75

U95626_rna1	171.3	128.41	112.75	130.32	799.5	899.86	570.6	54.02	564.15	69.23	1244.35	550.48	483.7	225.28	436	538.67	470.8
U52373_s_at	35.55	10.96	19.6	22.63	484.8	627.35	545.1	674.58	66.5	21.64	444.9	557.91	261.1	10.75	43.3	2.26	64.8
AFFX-TrpnX-	28.85	10.82	13.45	15.49	53.9	32.81	51.85	33.3	38.5	5.94	63.7	58.55	52.3	23.9	99.1	0.71	35.85
D43948_at	908.5	69.44	852.75	985.21	1360.9	201.67	932.4	9.62	1736	28	1616.9	24.04	1388.55	244.73	1804.85	553.03	1219.2
D80010_at	196.8	146.8	101.75	117.59	107.15	28.92	117.7	57.98	218.7	184.27	62.65	47.73	471.75	492.5	139.6	82.02	365.55
L34820_at	973.1	239.85	284.25	328.45	760.5	283.97	713.4	100.41	816.2	96.87	837.55	298.89	929.85	634.91	381.7	15.7	900.3
U31382_at	728.6	490.59	244.9	282.98	869.5	332.34	510.9	395.13	372.55	227.62	673.3	0.28	647.5	686.88	458.4	445.9	505.65
M28249_at	442	66.89	518	598.5	459.2	504.45	529.55	291.4	897.2	116.25	1024.4	144.25	843.25	95.53	862.55	259.44	500.55
M30496_at	991.25	372.01	609.6	704.28	1480.55	78.28	583.3	633.43	1611.55	1086.33	1146.9	346.77	983.05	188.02	1155.85	202.02	1207.25
J02902_at	5953.1	1542.77	2324.9	2686.16	6112.85	1528.27	6869.85	1695.15	4422.65	1660.78	5534.25	1497.3	6326.95	533.09	5924.1	931.26	7971
Y10205_at	44.75	23.55	222.35	256.89	123.2	19.52	86.75	57.91	380.75	481.04	176.8	21.92	557.85	277.12	170.25	163.41	80.9
U60060_at	6184.5	1660.99	3406.3	3935.61	6563.15	412.46	4982.35	2118.85	4048	622.25	4158.8	1281.7	3234.25	20.29	3318.1	643.04	4090.95
U66468_at	473.85	486.7	80.3	92.77	779.95	311.9	325.4	302.22	721.35	6.01	526.75	299.88	242.3	47.94	255.9	40.59	837.35

HG1140-HT4	2294.15	149.69	1106.2	1278.02	2489.7	1176.34	989.15	609.03	1738	1794.78	1776.6	112.43	2083.5	438.26	2398.25	1043.62	1623.55
U16120_s_at	53.45	4.45	15.3	17.68	415.3	489.04	444.9	607.55	277.1	328.95	616.1	716.44	289.35	190.71	184.75	80.4	284.4
X97748_s_at	1199	508.83	937.05	1082.65	983.6	507.99	764.3	591	1103.75	203.29	1782.75	266.23	1667.85	778.74	1310.85	46.32	1121.5
L24559_at	1820.35	1121.83	1070.35	1236.66	1243.05	360.13	1990.45	1719.61	3078.1	646.72	1693.75	805.89	1931.15	1065.54	3634.75	581.17	1893.45
X66087_at	222.75	177.27	406.25	469.31	193.7	15.98	191.55	55.08	454.75	134.7	292.45	173.03	216.65	192.83	370.6	31.54	65.95
Y13247_at	1823.75	1361.25	1262.7	1458.9	1871.65	939.82	1749.65	296.91	1088.65	720.05	995.4	565.97	942.2	693.81	579.85	532.8	2341.5
U68142_at	758.35	437.77	630.7	728.74	547.85	534.64	1848.1	785.74	808.95	299.18	1165.65	262.69	528.3	279.31	1434.8	601.32	1334.75
U07919_at	2570.3	1408.98	1815.25	2097.35	1356.4	147.08	1487.65	81.81	5920.25	1137.1	4292.4	740.48	5016.9	978.35	4395.8	232.07	2393.35
L10102_rna1	136.1	51.62	277.75	320.96	247.45	203.86	173	47.52	583.55	424.9	78.7	75.24	247.4	185.69	158.5	44.41	80.2
M55998_s_at	310.35	321.66	327.5	378.44	874.7	386.36	534.85	464.5	663.55	81.67	746.45	526.16	374.75	126.22	718.25	88.03	578.5
X16546_at	740.65	844.07	451.05	521.07	744	883.6	403.9	436.71	912.95	119.43	391.9	264.74	594.55	308.65	466.9	422.85	959.4
Z74616_s_at	270.55	227.05	51.7	59.68	87.85	54.52	111.8	0.42	62.3	20.93	168.25	166.81	116.9	3.82	106.55	12.94	92.25
M55172_at	222.35	61.45	104.5	120.77	1030.5	895.06	599.65	103.73	211.2	99.7	282.6	84.29	448	405.6	233.1	16.97	237.9
J00212_f_at	757.9	47.94	368.7	425.96	1014.35	104.3	417.4	73.4	970.7	229.95	1192.45	234.12	889.2	183.42	677.05	205.41	915.35
S83513_s_at	1710.1	862.39	1043.1	1205.19	1608.55	30.05	1305.5	218.92	1592.95	238.79	1809.55	532.24	2720.7	943.14	1618.35	74.03	1515.45
U16296_at	829.6	1.56	100.1	115.68	797.65	409.2	1106.15	608.04	514.05	573.96	163.75	4.03	532.7	96.73	293.45	315.58	281.2
U14970_at	53812.2	44517.46	28428.15	32845.32	77210.45	9131.5	89279	41033.12	64334.95	3532.35	68263.5	19155.52	64533	32431.17	70614.2	20964.58	59248.1

U19517_at	118.5	98.85	70	80.89	222.55	117.59	146.4	141.56	138.55	19.45	281.5	32.39	119.7	44.26	158.15	106.14	208.35
V00599_s_at	28808.65	1322.78	13146.15	15188.72	25053	5109.55	20320.95	1962.15	27732.25	11773.96	23847.75	3050.25	35723.3	21911.96	31892.9	9159.29	42396.4
D28383_at	1062.4	1133.35	145.65	168.22	1628.3	137.6	2431.2	303.35	1868	1512.78	1770	446.04	1318.25	258.16	1107.95	917.47	1509.6
X66417_at	275.55	189.58	252.4	291.61	193.5	137.6	1167.1	1069	828.35	611.44	961.9	337.86	600.05	468.32	695.95	153.09	672.9
D85423_at	63.5	27.29	141.45	163.41	192.3	85.98	237.9	143.4	221.25	1.2	125.5	48.22	193.3	104.65	131.95	18.03	85.75
HG2167-HT2	557.45	267.92	251.55	290.69	603.9	100.41	721.1	100.41	1176.2	402.63	1264.95	796.13	551.85	99.63	746	8.2	776
X57303_at	1637.15	556.56	888.6	1026.72	992	183.85	562.25	413.45	770.75	115.19	707.65	804.33	1018.35	106.84	875.65	903.61	1629.25
V00551_f_at	113.15	93.69	108.3	125.16	60.85	17.47	97.3	97.72	52.5	36.06	355.3	310	54.65	45.33	324.8	429.07	148.15
X06318_at	162.55	44.19	53.3	61.52	157.65	127.35	116.05	63	114.95	55.08	409.85	285.88	291.4	146.51	137.65	79.13	142.1
U20285_at	7599.95	131.03	3339.35	3858.19	8564.6	2504.57	7630.7	482.53	6538.95	380.07	6854.7	929.28	6225.5	162.07	7127.25	1967.67	7552.95
X86681_at	706.6	483.1	134.55	155.49	266.4	92.91	686.8	483.24	331.6	27.44	766.05	57.2	421.25	73.61	998.75	169.35	429
U96114_at	877	367.7	547.9	633	1119.25	441.87	184.85	34.01	650.45	451.06	567.9	85.14	1114.7	179.18	865.55	213.19	853.5
U55766_at	37.3	36.91	67.2	77.64	218.2	223.59	206.95	31.32	209.1	30.41	92.35	28.21	301.05	190.57	24.2	1.7	231.35
X51954_at	193.85	20.01	76.95	88.88	1006.5	936.49	293.05	188.02	174.6	91.92	1342.7	1191.62	461.7	472.06	677.55	159.59	800.2
M14539_at	195.7	28.14	172.95	199.76	574.1	498.79	283.4	199.26	562.65	526.44	290.9	175.93	376.35	273.3	102.2	10.47	101.85
M15059_at	1348.1	238.01	541.6	625.79	1121.7	197.99	819.35	565.33	1883.7	855.03	1126.15	759.22	2017.35	1570.84	1937.4	378.3	1013.4

X57809_at	350.55	390.39	245.15	283.2	141.15	100.62	78.25	73.75	224.2	73.4	437.1	542.49	117.35	94.96	473.5	625.08	616.3
Z34822_f_at	107.05	45.18	92.4	106.77	335.95	78.42	180.1	163.62	251.4	96.45	160.35	14.5	338.95	226.06	144.8	44.69	215.95
D00761_at	7395.45	2647.05	3348	3868.16	6352.6	2283.95	6989.75	2273.28	6740.9	6.79	4995.45	1064.41	6488.5	578.84	6514.2	1378.58	5524.05
D87074_at	352.55	361.12	372.2	430.06	799.05	442.3	1040.15	232.99	535.95	357.87	930.65	481.19	546.9	551.68	1638.95	353.91	602.5
M86808_at	297.5	355.39	62.3	71.98	315.15	324.77	238.3	38.18	155.2	96.17	406.95	542.99	115.7	73.68	360.25	100.76	182.9
M24069_at	2284.75	737.58	1519.95	1756.1	1509.2	832.26	2000.45	1220.54	1733.7	334.32	1394.7	321.45	1336.05	167.51	1606.8	423.13	1705.15
U40462_at	824.05	273.44	70.8	81.74	173.65	23.55	731.2	793.66	382.4	190.07	717.75	871.23	492.05	229.31	413	385.8	355.55
Y10204_at	229.7	93.9	179.25	207.11	322.1	202.66	120	129.4	194.4	187.1	81.75	49.29	216.3	243.53	238	61.09	156.6
U82108_s_at	326.95	147.57	519.15	599.84	141.7	73.82	576.85	519.79	222.95	99.63	243.5	14.57	274	71.56	383.7	133.93	569.7
U75272_s_at	1449.85	534.36	190.55	220.12	1438.65	504.38	1595.55	1202.29	1826.45	505.37	971.6	879.36	1190.25	594.89	1987.8	319.47	1826
U56833_at	1043	145.66	581.95	672.39	899	233.2	614.6	73.82	1286.85	266.08	1200.05	324.77	1003.2	509.97	929.35	55.93	986.25
HG4390-HT4	76.5	80.89	307.6	355.39	694.25	843.65	257.25	264.53	179.2	121.76	103.25	10.96	345.1	64.63	270.25	349.52	257.6
X89416_at	4531.8	2405.86	2044.1	2361.74	806.2	100.97	1794.95	367.77	965.6	19.23	3883.35	4066.36	2012.45	1055.07	3141	2707.23	2775
X54150_at	62.75	17.47	45	52.04	185.55	58.48	74.45	41.08	75	21.5	79.1	22.49	420.75	172.32	91.85	80.68	27.2
X55666_at	722.4	695.93	1271.4	1468.94	980.15	240.06	1450.4	1378.86	1082.4	802.85	1305.1	642.05	1389.5	406.02	593.2	284.4	653.55
D42073_at	739.2	12.45	1041.8	1203.64	639.9	145.24	1164.3	158.67	705.8	211	1535	172.53	814	510.11	1011.65	130.6	665.6
L10373_at	170	87.12	426.05	492.22	219.9	6.51	287.25	255.19	174.4	47.8	123.9	49.21	243.3	125.3	363.45	265.8	406.9

X89066_at	321.25	54.8	418.5	483.52	544.25	255.62	185.45	113.35	585.7	92.49	329.05	84.78	486.25	571.27	449.35	119.43	542.95
U09860_at	106.25	118.72	138.55	160.02	115.15	118.02	233	300.24	383.75	456.01	175.2	37.62	267.8	296.42	569.85	585.98	121.5
X71874_cds1	551.1	427.94	496	573.04	1648.35	225.35	650.9	289.35	635.55	116.32	1122.85	446.82	1361.85	665.74	772.5	740.62	325.9
U51561_at	195.55	33.16	331.8	383.39	258.4	236.46	75.45	74.32	152.25	39.95	218.65	256.75	103.3	15.84	227.15	191.27	202.25
U72514_at	1129	216.52	962.5	1112	984.2	454.81	1201.7	1077.77	1002.7	234.76	1678.55	42.36	1048.2	311.27	1127.45	464.22	1153.65
U03100_at	1671.55	111.51	901.1	1041.14	1362.6	450.57	2189.25	306.39	2036.25	369.46	1933.65	419.67	1789.9	415.35	1957.6	321.73	1349.5
X16983_at	102.8	23.9	120.05	138.66	650.85	300.31	134.3	161.08	199	259.65	191.9	160.09	359.75	406.37	114.5	97.72	193.7
X66364_at	3486	120.63	1823.1	2106.33	3546.7	9.76	3610.6	1112.42	3212.7	959.97	3349.95	129.75	3275.6	231.51	3515.05	291.82	3648.25
S68874_s_at	56.65	35.99	291.8	337.15	161.5	43.56	592.6	415.5	635.3	5.66	266.85	213.76	800.8	111.3	127.3	106.63	416.05
D78261_at	128.6	124.73	43.85	50.7	269.2	280.72	328.95	401.42	576.35	496.18	316.25	254.35	68.3	16.97	73.95	10.96	130.5
M73746_s_at	85.3	49.78	260.8	301.37	151.95	105.15	125.5	135.62	70.45	22.56	199.85	219.98	74.7	4.38	217.95	264.81	142.4
Z34974_s_at	805.85	121.55	791.65	914.64	377.9	19.52	595.35	65.97	799.45	633.5	620.65	12.37	1605.25	1021.7	694.9	487.76	1572.3
D50692_at	112.2	32.81	202.95	234.55	393.5	158.11	853.95	500.7	223.2	55.3	455.55	371.16	1140.55	846.19	434	343.23	540.5
U43527_at	1889.05	492.08	705.55	815.22	1846.2	337.71	2214.9	381.55	1724.4	4.81	2378.5	500.35	2391.2	466.41	2613.9	1488.32	2152.55
U32114_at	1940.8	111.58	1302.5	1504.86	2075.5	191.77	1461.7	1068.16	2649.25	101.05	1717.85	888.9	1982.35	499.85	1890.35	549.07	2014.55

U87593_f_at	93.05	14.07	45.45	52.54	209.3	204.92	75	17.11	94.05	12.52	90.2	63.78	141	89.24	123.85	128.48	144.2
U01062_at	3164.7	103.38	1752.6	2024.87	2897.3	320.46	3449.3	154.43	3242.35	124.66	3550.1	147.22	4061.95	436.64	3677.45	928.5	3289.85
X07384_at	346.75	4.31	418.2	483.24	556.4	48.08	484.9	57.28	443.4	52.75	198	149.62	140.45	45.61	349.7	165.6	207.05
L35854_at	257.1	18.53	513	592.7	477.75	294.37	836.05	1017.46	748.8	82.02	716	376.61	938	233.91	985.15	148.42	496.35
X83301_s_at	30.9	9.62	17.55	20.29	51.75	8.27	58.4	9.48	70.45	46.03	64.45	36.7	85.2	6.79	57.3	47.66	46.1
D31840_s_at	720.8	587.75	380.85	440.03	459.65	494.34	293.05	302.43	244	246.21	94.05	33.87	494.3	375.47	951.1	657.47	481.1
HG3088-HT3	177.55	50.98	53.9	62.23	88.55	27.65	189.85	37.69	108.1	12.87	397.6	519.3	307.3	299.81	200.75	215.31	146
M34677_at	1414.5	752.64	239.55	276.83	765.35	78.98	737.5	430.35	409.95	2.05	787.6	456.51	1357	836.37	438.05	77.29	345.75
U79282_at	186.8	93.76	320.25	370.03	439.45	112.5	247	69.44	299.85	109.81	480	196.29	87.8	20.93	347.9	107.76	226.55
D45917_s_at	1673.25	294.09	1055.2	1219.19	1099.35	309.08	1284.85	96.94	1212.75	18.88	1003.55	388.13	793.65	126.22	890.25	900.64	1236.4
M21389_at	129460.6	13373.23	57627	66581.03	119530.45	11701.98	114120.3	9783.25	134000.95	4225.74	100434.05	2698.53	141140.75	5967.76	160473.41	51442.58	125954.16
S73149_at	5715.25	1220.68	3694.05	4268.03	4941.4	118.65	7325.05	684.13	5032.85	324.49	6663.5	557.48	8367.4	3051.45	7657.2	2430.61	7417.65
D82343_at	52.35	8.41	19.05	21.99	411.75	506.64	62.15	25.24	84.85	71.77	57.9	3.11	61.6	7.92	68.15	64.98	116.3
X12794_at	3992.95	143.33	2225.05	2570.83	3697.1	451.98	2723.25	12.52	3451.2	68.45	3159.6	420.45	3782.65	608.47	3682.6	131.8	4349.1
Z70723_at	279.45	285.6	14.25	16.48	585.45	768.27	302.05	374.84	118.5	71.42	154.8	118.09	82.25	73.33	160.85	154.79	237.15
M57703_s_at	273.9	202.23	215.4	248.9	376.7	164.33	634.75	603.8	234	245.51	319.25	207.96	264.2	232.5	406.55	59.33	382.55

U22377_at	863.2	244.23	85.35	98.64	411.75	165.39	420.8	60.39	254.75	255.48	1009.65	604.51	751.4	323.15	289.5	142.13	534.35
D21255_at	47.65	34.58	242.55	280.23	238.55	96.1	31.7	24.89	25.7	8.34	217.7	247.2	150.3	173.81	107.3	126.57	93.65
U05255_s_at	10217.4	2822.77	3103.6	3585.88	6517.3	83.44	5948.95	694.59	5551.25	1651.87	5109.15	1073.88	6439.15	1155.62	5813.4	247.2	6695.4
HG3921-HT4	1657.35	710.43	160.75	185.76	966	863.24	1672.85	915.35	581.25	323.64	1438.15	593.47	1409.65	154.22	708.7	612.35	1403
S79048_at	176.35	142.91	152.85	176.56	495.35	523.19	596.15	542.7	292.5	227.69	895	733.27	211.6	95.6	501.2	587.04	200.9
U01922_at	126	25.46	95.6	110.45	208.6	129.26	84.55	14.07	180.1	177.91	370.15	334.25	159.2	57.13	106.8	8.2	144.3
S66541_s_at	259.05	96.38	113.75	131.45	261.9	25.31	148.3	83.16	252.1	4.81	242.75	49	213.05	6.15	841.5	574.59	262.25
D17532_at	148.75	16.76	146.05	168.79	507.9	464.99	526.65	329.58	215	67.03	450.75	265.66	147.15	53.95	612.5	706.54	708.35
HG3636-HT3	2473.35	1524.31	1625.95	1878.57	1969.7	1515.05	2233.35	1981.81	1493.6	271.25	1573.05	337.5	1453.1	599.91	1764.95	1119.56	1686
X07290_at	173.05	3.32	681.5	787.43	691.2	67.18	160.4	154.43	282.95	64.56	187.8	120.49	771.85	751.44	209.4	69.16	296.05
X63597_at	174.45	150.54	129.3	149.34	41.25	34.58	163.9	193.46	24.6	0.42	326.8	384.24	43.25	19.87	291	384.52	225.7
U52152_at	123.8	32.67	144.1	166.45	196.3	39.03	246.4	217.65	170.75	13.08	181.85	43.63	190.35	74.88	156.2	6.51	136.5
U83908_at	409.25	76.58	23.15	26.8	495.75	142.62	631.85	371.3	369.6	32.81	248.65	215.6	344.25	385.16	399.85	421.36	469.65
M87499_at	301.2	91.5	131.25	151.67	282.1	88.67	186.05	39.39	170.05	55.79	226.4	71.28	188.95	51.41	301.05	33.87	246.8
X78565_at	1204.85	309.64	910.05	1051.4	1246.3	86.13	610.3	633.71	964.95	271.03	943.5	18.1	620.2	4.38	661	115.4	881.4
D63487_at	4274.4	32.95	2351.4	2716.7	2959.1	1746.41	4744.85	1037.54	4913.2	976.23	3842.2	151.89	4431.25	2286.85	5054.05	53.81	3794.1
M97925_rna1	1366.75	580.18	721.3	833.4	1485.2	145.66	673.95	136.4	1535.8	8.63	1865.55	123.96	1552	409.13	1482.55	545.96	1786.95
U85267_at	929.7	406.87	480.5	555.22	1002	36.06	761.5	318.48	781.7	622.25	1161.3	502.89	846.95	516.82	931.5	1029.69	766.15

M95167_at	132.5	26.59	105.35	121.69	193.95	51.97	305	40.59	173.25	13.93	474.5	189.22	239.35	22.7	434.2	159.95	210.05
Z83802_at	249.8	134.21	256.35	296.21	272.3	272.94	551.9	356.38	599.75	574.95	201.45	177.27	245.65	291.26	136.9	153.87	348.15
HG2510-HT2	95.5	21.92	38.7	44.69	183.45	162.71	78.1	47.38	67.45	25.81	86.55	85.49	124.8	73.96	75.7	79.2	34.1
L06175_at	562.35	310.77	82.45	95.25	419.25	194.81	288.05	91	253.35	103.87	573.85	363.52	636.1	216.94	225.65	103.73	512.15
U60873_at	85.15	11.67	92.5	106.91	166.7	47.38	168.15	100.06	114.7	52.33	103.85	8.13	107.4	10.04	137.8	41.58	823.45
X58399_at	185.5	199.83	103.8	119.93	85.1	38.47	106.5	77.64	140.55	83.51	187.7	140.86	372.55	358.15	149.65	96.8	96.15
U47105_at	2481.7	194.74	939	1084.84	2330.75	232	2655.3	597.93	2888.7	6.51	1819.7	553.38	2578.2	60.95	4225.4	1719.68	3214.35
Z80780_f_at	482.45	232.85	192.8	222.74	490.8	305.05	445.45	147.29	490.1	433.32	760.2	413.09	302.5	42	290.15	189.29	269.4
HG3231-HT3	420.35	348.39	254.2	293.73	470.2	321.31	305.7	126.01	605.7	608.54	1118.55	271.18	1110.55	504.24	1030.6	1112.42	585.7
HG880-HT88	370.1	309.43	71.4	82.45	143.9	57.13	105.7	8.91	212.35	87.33	95.1	23.9	98.55	77.29	138.3	16.69	81.9
HG4660-HT5	1319.35	375.83	815.9	942.71	1802.9	641.35	1357.2	946.53	1392.35	292.67	1613.75	196.93	652.55	176.71	874.4	688.44	570.5
U17034_at	113.25	124.95	139.15	160.73	501.85	418.11	36.7	18.38	137.8	44.69	114.3	51.05	133.8	146.09	333.4	309.71	141.25
M64929_at	2091.85	115.33	1681.25	1942.49	1120.2	1235.6	1299.85	1525.02	1852.45	177.55	2273.15	101.19	1950.1	592.7	2001.75	246.14	2098.8
X75042_at	188.3	189.36	22	25.46	324.35	264.39	180.1	36.2	105.3	61.24	27.75	6.29	444.55	344.71	31.45	6.43	33.65
M94250_at	2344.8	1050.19	1623.8	1876.1	2693.55	466.76	2761.85	209.94	1523.25	710.15	2861.55	53.53	3174.75	383.32	1919.2	805.11	2761.6
L25444_at	1848.25	193.68	1178.45	1361.53	1726.65	792.45	1533	293.17	459.7	240.7	1137.95	70.92	1742.45	337.5	1433.95	883.25	2436.05
U11862_s_at	1179.7	0.99	161.75	186.89	764.7	307.73	1091.3	1189.64	272.2	36.06	319.55	40.66	382.45	7.42	409.8	49.36	313.95

M14123_xpt2	681.55	821.87	172	198.7	282.8	131.8	394.55	78.84	325.4	360.77	375.05	279.8	145.75	81.95	850.25	473.13	401.3
X82494_at	1412.4	241.41	662.2	765.09	2193.55	873.77	910.65	328.59	1356.8	740.77	1550.4	325.83	1315.6	259.37	1447.6	225.71	2004
D29954_at	1399.6	656.76	964.5	1114.4	1160.75	679.03	675.35	266.08	1585.6	530.19	1953.5	1354.25	2342.7	380.71	1892.65	759.08	1589.05
D63475_at	11967.65	2967.23	5997.9	6929.79	10526.8	2268.26	12191.05	5016.99	9666.2	3474.72	8798.6	2453.94	9309.3	676.84	9291.95	773.93	12525.3
M60527_at	140.85	52.54	48.3	55.86	582	627.35	66.95	74.46	192.05	51.27	88.85	82.24	242.45	273.44	245.05	8.27	101.8
D28791_at	183.35	55.65	8.75	10.11	100.75	58.34	57.05	64.42	346.2	51.19	475.95	601.82	301.5	343.09	118.85	52.82	416.95
U01828_at	219.45	221.4	310.85	359.14	275.8	35.92	603	549.7	680.7	253.99	93.35	26.23	412.65	390.54	199.7	218.07	158.95
AF000177_at	1650.65	681.3	584.2	675	1820.25	547.8	2015.95	426.74	1861.95	59.47	1874.65	958.06	1782	253.29	2106.4	17.68	2426.3
U63824_at	306.7	315.09	488.1	563.99	550.45	395.06	1415.1	866.49	751.6	12.59	1001.45	19.73	271.9	310.99	624.65	681.3	810.4
S79219_s_at	348.5	142.84	566.15	654.14	909.55	457.57	818.15	582.87	731.85	21.71	575.85	119.71	353.85	214.04	741.1	133.08	465.5
U21858_at	823.75	74.32	692.2	799.74	1000.25	117.17	1066.95	280.79	1141.85	181.23	515.05	648.49	723.15	858.36	1065.75	527.29	846.4
AB002382_at	1861.35	552.18	1121.9	1296.27	1573.15	120.84	991.45	123.96	1661	601.61	1297.6	116.96	1521.15	72.34	1273.6	811.19	1520.85
HG172-HT39	326.85	239.07	84.45	97.51	861.4	530.9	819.2	366.99	218.85	104.16	347.15	310.77	557.45	301.16	168.8	46.53	174.85
M65131_rna1	356.7	84.57	181.75	209.94	229.8	26.02	322.5	48.22	939.8	320.04	330.95	362.39	606.05	262.12	578.7	71.98	691.4
HG2059-HT2	1481.15	396.33	970.5	1121.33	1681.25	211.92	1578.85	756.82	1349.95	638.02	979	698.9	1448.85	385.44	1656.05	186.61	1203.5

L42176_at	2799.9	363.59	1638.35	1892.85	1949.55	141.77	2003.6	1278.87	2830.45	34.72	1911.1	804.83	2779.45	96.52	2669.3	405.6	2754.15
S82362_s_at	418.65	288.43	408.6	472.06	999.65	152.38	706.05	858.22	603.55	181.37	747.45	360.7	545.25	410.33	240.6	104.93	326.95
Z69720_at	1070.2	266.44	657.3	759.43	1339.75	442.01	1817	95.88	1187.25	200.61	1652.35	214.04	855.9	720.82	1811.7	303.49	1246.5
L39211_at	492.3	427.94	221.1	255.41	355.05	135.55	287.05	234.83	338.65	233.13	309.25	162.71	338.1	257.25	517.25	181.66	143
U79298_at	1063.75	230.16	320.35	370.17	326.2	297.97	128.05	38.4	207.8	111.3	319.2	164.05	899.8	68.31	456	91.5	284.05
L33075_at	3380.15	1341.45	2050.1	2368.67	1759.55	803.63	1428.5	619.28	3633.6	1023.47	2636.45	498.44	3479.45	792.45	2881.5	542.35	3446.8
Z70222_at	877.35	160.02	560.7	647.85	979.1	458.91	427.45	374.98	285.9	107.62	636.65	168.08	606.55	578.91	560.45	234.97	340.15
S72370_at	511.35	381.91	737.45	851.99	227.25	118.16	503.75	355.04	444.15	244.73	324.5	231.08	959.45	386.01	827.6	507.42	771.65
Z22865_at	264.5	165.04	368.4	425.68	774.9	278.88	264.1	149.77	369.4	372.65	266.7	236.74	816.6	953.6	988	500.35	418.55
AFFX-BioDn-	174241.69	44798.19	76483.91	88367.84	593690.31	556481.44	630069.81	710849.38	345507.06	234358.02	454386.59	489250.16	204711.41	155050.84	286009.84	57797.85	203701
Y09443_at	747.45	54.24	411.35	475.25	930	378.02	666.65	211.5	852.75	286.17	429.7	332.91	856.2	102.53	1249.75	393.93	513.05
L13391_at	473.65	256.04	523.55	604.93	400.3	160.09	350.7	19.94	809.85	260	875.6	422.71	384.5	25.88	593.8	785.03	1447.75

U33632_at	580.3	293.03	447.35	516.82	322.25	31.75	173.3	78.49	668.4	415.07	589.35	338.92	487.35	251.09	350.15	68.09	384.45
M55542_at	179.3	180.74	171.35	197.92	341.25	148.14	342.9	287.23	87.95	43.35	148.5	135.76	33.75	22.13	50.3	12.3	32.85
L00634_s_at	981.95	129.33	496.75	573.96	1152.3	0.99	615.85	702.37	843.45	211.5	1084.9	197.28	522.75	147.43	714.85	122.54	1063.8
D87684_at	556.8	8.34	478.1	552.39	435.6	443.78	658.15	171.47	666.35	7.14	424.2	452.83	271.3	234.76	1009.45	263.68	555.2
AD000092_c	1927.95	716.79	1062	1226.97	2416.2	1975.09	1529.55	688.51	2501.05	242.89	3238.45	2128.46	2871.75	27.51	1168.75	445.97	2010.35
U73682_at	341.6	225.57	382.3	441.66	536.25	376.25	811.45	883.39	452.65	355.18	203.2	34.08	179.05	64.13	236.7	88.67	341.65
X98834_rna1	581.7	179.89	502.45	580.46	830.05	432.82	333.35	29.34	1139.2	229.67	707.5	823.5	662.1	113	440.4	443.78	784.3
U66036_at	157.6	196.72	13.15	15.2	59.8	32.39	193.3	54.31	227.4	160.8	271.85	154.08	293.95	314.45	177.25	116.46	70.4
X05997_at	417.7	132.51	106.35	122.82	353.25	165.39	262.8	300.52	249.9	216.52	546.45	692.61	170.3	185.26	419.1	68.31	197.65
HG3238-HT4	142.4	97.16	64.45	74.46	373.3	411.54	433	554.37	30.3	2.26	381.65	405.81	64.95	5.16	154	4.81	50.25

Z29077_xpt1_	188.45	162.71	143.1	165.32	1052.35	770.68	554.6	557.48	505.45	602.81	232.2	21.64	169.95	48.44	160.8	143.26	279.5
M31520_rna1	703.75	499.71	106.9	123.46	1003.25	1002.47	234.6	76.65	887.6	784.04	88.9	90.37	284.9	191.48	197.1	119.5	39.75
L40400_at	955	446.33	139.45	161.15	575.75	559.67	496.2	143.4	818.8	265.02	1268.25	875.19	1216.25	5.73	678.1	307.31	821.2
U03891_at	837.4	117.66	335.35	387.42	938.95	259.15	756	438.12	1242.6	44.69	1276.15	161.15	1010.85	190.42	1894.8	528.35	1074.6
X76040_at	1525.85	190.14	1083.5	1251.86	1238.75	131.59	1592.35	771.1	1340.85	439.61	1361.7	722.1	1393.2	138.88	830	138.03	1212.7
U28386_at	1006.25	77.43	509.95	589.23	1207.2	290.2	1096.9	75.52	1034.05	245.15	1022.8	380	1293	103.24	1629.95	915.63	1582.85
U69127_at	146.85	75.02	205.35	237.23	297.75	153.8	250.4	245.65	619.7	128.98	403.35	446.68	235.7	60.81	375.35	437.77	185.75
U07681_at	822.9	128.69	363.9	420.45	1159.55	536.06	688.2	274.92	917.4	372.08	841.85	653.72	954.45	216.59	1069.5	141.7	532.35
X07876_at	68.45	31.18	99.65	115.19	209.75	110.95	594.55	600.4	100.7	62.79	190.1	226.84	103.55	24.68	56.5	27.44	120.7
X15940_at	45643.3	19536.23	22907.7	26467.01	64138.7	11019.41	53153.65	25674.83	68084.95	21871.17	45991.85	20164.78	53791.6	24798.52	56575.5	5403.85	42455.7
D38163_s_at	365.45	123.96	159.5	184.27	368.25	233.98	243.8	174.37	209.8	33.94	268.2	4.67	236.05	56.07	224.25	112.22	216.85
D49824_at	75.55	7.71	44.15	50.98	206.55	179.68	88.5	47.38	81.9	6.36	104.1	6.22	84.05	3.46	97.8	18.95	78.75
D49728_at	1229.95	513.29	400.85	463.08	1102.95	911.11	881.4	430.2	836.05	271.46	658.95	19.02	2308.95	1405.52	1228.65	614.69	940.5
U48861_at	355.95	34.72	109.6	126.57	393.95	200.18	312.15	56.36	236.65	135.27	406.8	60.53	537.85	195.37	345.2	115.26	396
L76380_at	96.85	64.13	240.9	278.32	260.4	38.61	171.45	10.68	160.55	115.89	318.25	219.84	572.15	342.17	283.05	352.92	528.35
D63880_at	954.75	336.79	634.2	732.7	1356.85	655.56	1198.75	89.31	1233.8	546.73	743.45	502.97	1692.15	359.71	1829.85	764.45	1046.75

M14200_rna1	3303.6	175.22	2449.7	2830.27	3358	20.51	2284.05	1678.88	3661.2	520.71	2299.7	1040.01	4166.95	1012.51	4393.6	3344.9	2845.7
D16688_s_at	306	191.48	109.35	126.36	305.85	290.27	103.65	29.91	116.4	71.56	108.3	40.31	97.4	12.45	95.5	19.09	117.25
S74221_at	715.2	65.34	639.35	738.71	680.55	183.78	368.85	211.21	1141.25	171.9	834.3	207.47	1178.35	303.56	319.15	43.63	757.45
D21337_at	563.35	629.4	435.3	502.89	490.75	288.57	607.65	697.84	324.35	250.53	606.35	571.7	740.5	802.71	677.3	120.35	799
M86934_at	729.7	117.38	557.35	643.96	1354.45	761.62	802.4	208.03	976.7	165.32	1014.3	125.58	1093.45	148.14	680.55	301.3	889.85
U51166_at	286.35	262.55	393.75	454.88	306.95	190.71	900.25	1077.42	257.2	18.24	614.75	735.32	783	223.73	379.55	413.16	561.4
Z47553_at	359.15	202.44	8.35	9.69	496.95	681.72	342.9	234.34	470.65	205.41	304.35	403.26	391.3	149.91	316	44.26	221.25
U37689_at	4991.4	788.99	3028.45	3498.98	4859.2	697.35	5607.3	244.23	4968.4	17.82	4875.8	68.31	4388.9	660.58	4610.3	139.02	3929.05
X15722_at	68.35	45.61	41.7	48.22	120.1	11.03	116.25	120.7	263.25	161.72	67.8	33.23	47.9	3.82	69.35	22.7	132.25
U15932_at	2134.8	599.91	2197.2	2538.65	2659.35	975.31	2265.2	69.58	1970.4	142.69	2616.55	579.76	1679.45	166.24	1696.45	946.04	2106.15

AC002115_rr	2253.65	93.55	1203.7	1390.74	1948.3	669.49	2340.7	463.15	1992.1	815.15	2467	434.31	1459.1	1731.42	1615.85	1256.32	2406.75
Z83741_at	112.55	35.99	311.85	360.27	153.05	52.11	160.75	132.3	67.95	15.77	260.4	83.16	93	12.16	119.15	74.88	126.85
X83416_s_at	1749.75	841.53	2383.2	2753.47	1253.4	230.8	1911.25	229.17	3086	1047.93	2281.25	964.99	2302.6	1110.02	2522	602.45	2558.35
AF012024_s_	267.4	89.38	64.7	74.81	329.05	7.42	180.9	52.33	365.3	414.51	187.15	101.05	331.85	93.41	600.35	346.55	371.55
U57592_at	316.6	149.91	744.35	860.05	471	28.28	662.65	313.6	182.4	80.04	609.95	371.58	425	441.23	807.7	215.1	555.75
L42451_at	2718.25	198.77	728.9	842.16	3260.85	833.89	3004.75	481.75	2268.85	108.68	2925.7	986.13	3036.35	747.77	2069.9	563.14	2222.85
L26494_at	331.15	110.8	202.95	234.55	413.1	389.05	492.3	1.98	322.35	197.78	564.2	368.26	972.9	388.2	430.25	265.94	565.35
D42046_at	573.45	376.25	385.9	445.9	1325.5	647.57	1003.6	533.02	1226	272.8	1069.5	581.1	1003.4	218.5	692.2	386.36	1022.35
X15949_at	212.25	131.73	304.15	351.36	875.65	789.91	184.65	159.03	237.5	211.14	286.65	291.12	71.95	41.08	397.75	425.32	476.25
L27476_at	1063.15	232.14	490.5	566.68	547.15	231.44	847.6	193.04	1166.8	361.05	839.05	81.39	1252.75	452.05	1168.9	56.29	1222.65
M73047_at	42.75	16.19	261.1	301.65	56	14.99	326.65	56.5	46.2	0.57	393.7	399.52	209.15	260.85	119.35	95.95	151.1
HG174-HT17	4523.35	582.59	3097.5	3578.81	2736	1835.08	2695.2	1392.29	3795.6	2448.71	3926.35	2094.8	3906.25	2252.35	4763.1	1988.95	5540.35

M13452_s_at	5765.2	1009.61	2733.15	3157.87	4726	931.12	5641.8	2404.45	4676.2	140.15	5096	352	5101.55	1127.62	4679.75	273.86	6199.95
Y07827_s_at	251	163.34	92.3	106.63	54.5	23.48	76.4	61.09	307.1	350.87	307.6	196.29	92.25	20.01	542.2	525.38	231.35
HG3288-HT3	471.15	156.34	47.4	54.73	387	363.31	363.55	290.27	217.2	135.91	428.6	18.38	213	3.82	332.95	29.49	406.65
U11690_at	555.75	75.87	545.1	629.75	442.45	19.02	216.4	101.96	405.6	291.33	264.55	48.72	613.8	598.35	489.65	431.41	956.25
D90097_at	48.65	0.64	50.45	58.34	64.4	66.89	418.8	563	55.6	39.88	95.95	80.68	150.05	146.87	53.95	37.97	36.25
X68314_at	1927.45	438.76	715.7	826.89	1443.45	198.77	2402.95	491.09	1447.15	228.18	1081.75	216.73	1359.9	872.57	1775.35	1717.77	2578.45
V00533_rna1	122.65	64.98	69.45	80.26	278.7	315.94	81.1	59.4	104.4	77.36	97.15	38.96	172.85	131.73	112.7	28.28	210.8
X82850_s_at	1954.2	323.57	1696.35	1959.89	1274.45	181.94	1861.55	541.71	1215.95	812.96	1239.1	587.18	1275.4	769.76	1748.05	2243.15	893.75
U42412_at	3375.35	1037.68	1366.1	1578.4	3134.25	568.58	2751.4	1071.55	3349.4	148.78	2733.9	255.69	4017.45	912.52	3087.9	1312.11	2556.35
X97544_at	1526.9	510.67	497.8	575.16	950.8	598.07	574	195.16	1486.35	502.12	986.95	36.42	1151.4	395.7	526.35	618.08	1227.9
U82256_at	340.7	381.7	314.15	362.96	103	43.7	191.35	36.84	427.2	140.71	121.25	74.32	504.1	616.17	77.75	14.35	448.6
U90904_at	1341.05	133.43	1018.1	1176.34	445.45	287.01	733.2	530.75	1169.8	85.84	1597.9	114.83	1014.55	645.66	1132.6	483.1	1381.7
U70671_at	3485.65	645.38	2212.15	2555.84	2824.55	184.91	4547.2	1709.5	2857.45	709.3	4838	2850.35	3010	122.05	2793.15	1308.36	3382.35
Y10807_s_at	15107.9	2685.17	7266.1	8395.05	13271.9	4247.59	11770.9	4397.78	11235.4	3355.36	11695.6	1516.46	11182.45	1654.98	10882.5	1740.61	11692.4
U29171_at	5150.5	349.31	2831.3	3271.22	4291.6	800.16	4616.2	382.97	4340.1	2347.88	5950.85	933.73	4953.15	179.39	5526.7	1613.48	5571.8
U20648_at	197.55	165.39	24.15	27.93	154.9	78.21	411.65	481.61	46.95	32.88	69.25	71.77	44.15	13.22	67.9	25.46	33.15
X64364_at	11964	2976.64	4964.4	5735.77	7892.7	3050.88	4801.6	414.65	4512.95	4154.75	5947.55	3670.66	6154.6	241.12	4456.75	423.34	5774.3
HG4662-HT5	507.05	4.6	198.25	229.03	541.05	40.52	570.9	483.66	351	296.14	453.1	45.68	567.4	43.13	500.75	219.7	592

M33374_at	1290.7	1042.56	626.85	724.29	1530.8	64.63	1441.6	522.83	1138.05	743.52	910.65	523.47	977.7	921.36	1362.45	215.88	1592.65
U15555_at	191.3	104.93	50.15	57.91	165.65	145.73	353.45	400.43	155	35.78	92.25	29.63	504.15	451.49	79.3	4.24	242.1
S77094_at	82.65	3.32	24.35	28.07	740.25	237.23	88.15	20.58	218.35	77	284.65	142.76	96.5	5.8	180.95	121.83	145.8
U95019_s_at	81.8	26.73	52.15	60.32	115.5	21.5	185.2	145.66	134	55.01	108.7	61.38	463.2	503.6	340.75	236.67	925.75
U22963_at	664.05	620.49	479.4	553.95	674.1	489.32	1376	957	830.3	676.56	1451.05	133.01	1054.6	120.35	1054.4	1106.06	888
X99688_at	5808.5	2462	3237.5	3740.59	5453.8	1298.53	5761.55	1843.07	4938.6	1629.17	6700.8	1519.71	5241.35	228.47	5030.65	708.17	6106.2
AF002700_at	469.45	152.38	154.65	178.69	257.45	140.22	319.1	184.7	722.8	460.89	424.6	136.19	406.95	130.6	310.9	47.09	194.4
X51823_at	35.4	15.41	49	56.57	910.1	233.91	66	56.29	371.8	488.05	63.15	57.91	793.4	291.47	98.4	34.79	48.25
Z83804_at	317.85	81.67	326.8	377.6	778.25	245.15	79.25	25.24	385.4	288.08	185.95	152.52	710.65	290.41	264.55	282.91	278.55
M11749_at	1029.4	338.14	392.65	453.61	1035.55	11.67	987.25	565.9	926.75	154.22	1556.85	268.63	1098.8	914.29	1700.3	76.37	1340.4
U79734_at	163.9	117.8	61.4	70.99	207.55	30.19	118.75	28.5	102.9	6.93	174.05	28.78	151.95	94.26	144.15	37.12	140
X96584_at	52.55	7.71	65.8	76.08	426.4	436.28	288.95	109.67	160.4	90.09	133.15	101.89	104.2	96.87	90.75	13.93	82.85
X77567_s_at	1459.8	286.1	723.95	836.44	768.1	865.64	1057.5	587.04	677.7	141.14	1518.8	1039.02	668.25	290.69	293.6	24.61	1264.75

X06256_at	2540.75	532.1	1303.65	1506.21	1721.55	1973.32	2914.6	1059.67	1890.95	68.94	1014.65	525.88	886.35	250.1	1488.85	1044.89	1984.2
S74017_at	789.5	84.29	591	682.78	1314.45	130.89	402.05	365.93	1870.3	37.76	1465.8	814.16	1199.05	17.32	1220.65	555.57	828.55
Y00318_at	390.05	268.35	129.3	149.34	322.95	197.92	79.3	22.49	443.6	146.94	316.95	296.63	172.65	164.12	190.7	182.72	356.5
M30818_at	492.55	125.23	499.85	577.49	1890.15	2028.05	1186.55	915.07	388.55	272.31	1304.6	901.7	842.8	49.36	741	5.52	908.35
D80012_at	997.2	189.5	475.5	549.42	1206.9	157.68	525.9	442.08	1676.55	303.99	1432.85	622.18	1070.95	274.71	849.45	59.18	1634.3
D38583_at	53916.8	5304.57	19996.85	23103.94	49574.25	5001.58	51630.8	18291.58	57235.7	4389.29	48795.8	13751.39	60386.3	1388.19	55482.9	12289.66	55246.95
U07969_s_at	501.3	164.33	142.55	164.69	584.4	169.14	281.35	251.8	1044.1	309.15	327.1	35.36	205.5	11.46	193.5	42	905
U50079_s_at	2638.2	378.73	916.1	1058.4	2567.35	159.59	2352.6	352.7	2571.75	20.44	1789.65	1020.57	2669.35	59.47	2728.45	784.68	2564.75
U18549_at	167.15	169.49	291.7	337.01	602.5	199.26	189.35	97.65	531.65	549.92	187.9	62.23	616	228.68	137.25	19.73	242.55
M36341_at	7579.15	2778.29	2994.4	3459.73	6046.35	2623.44	5441.15	3783.52	8902.85	467.19	6729.15	3773.76	5724.15	663.05	5536.9	2655.75	6716.55
L32866_at	598.9	187.1	475.5	549.42	463.1	174.94	486.65	125.09	796.65	206.12	671.35	188.59	1203.6	428.08	341.65	33.59	818.8
U06681_at	781.8	214.68	77.7	89.8	664.3	276.9	663.9	91.64	537.1	476.73	482.4	478.29	507.95	408.07	1194.1	847.26	510.8
U00943_at	747.55	86.76	464.5	536.69	987	506.29	584	307.45	921	470.23	693.6	57.28	1249	36.2	805.85	465.21	367.15
U50535_at	814.4	262.2	504.7	583.08	1073.3	402.77	999.5	839.34	902.5	121.2	1011.6	272.94	1039.8	161.5	460.3	504.59	1164.1
L40396_at	189.85	43.77	382.65	442.15	116.9	135.06	535.7	730.02	243.35	283.76	386.1	522.41	45.3	12.16	476.55	203.43	154.8

M74558_at	40.85	14.92	62.7	72.41	245.25	235.11	90.05	48.86	113.2	114.98	453.8	171.83	286.65	290.97	51.1	25.74	293.45
X74987_s_at	598.85	329.72	576.55	666.17	629.3	329.94	156.75	148.28	180	197.99	279.5	172.53	681.3	609.67	267.1	326.54	321.1
U83843_at	4169.3	502.89	2383.1	2753.33	3472.15	127.07	4878.8	108.47	3156.6	1299.1	3294.85	925.96	3249.95	207.54	3583.2	422.43	4165.85
U32315_at	379.6	124.31	297.75	344.01	151.2	163.2	358.2	255.41	333.8	296.28	464.1	235.89	123.6	29.42	496.05	116.04	655.4
U83115_at	2111.9	164.61	1941.75	2243.44	2428.4	1203.92	2163.85	460.96	2884.1	193.89	3363.6	1158.67	4254.8	815.72	3410.5	280.44	4159
X61755_rna1	1743.1	51.34	1045.55	1207.95	1769.65	1848.17	1424.15	467.89	506.8	188.23	1344.15	185.05	1812.55	651.46	1861.8	1737.5	1830.05
U66669_at	306.6	112.43	30.05	34.72	226	237.31	117.45	93.83	200	106.07	538.2	249.75	449.95	389.83	201.35	258.31	257.4
M93311_at	78.9	9.33	288.05	332.84	525.65	621.48	73.2	27.01	318.55	95.39	520.5	643.33	127.3	44.69	603.85	106.28	468.5
U49278_at	5867.2	1347.89	2676.55	3092.39	6619.9	905.38	5794	1434.15	5526.5	326.12	5575.35	991.01	5183.7	243.95	5141.5	99.42	6699.35
M85164_at	558.85	112.36	423.65	489.53	196.95	89.87	290.7	159.38	477.3	165.04	325.45	199.19	509.75	238.22	322.55	363.24	356.85
L17128_at	816.55	174.44	763.5	882.19	996.3	296.28	1104.65	363.52	1096.45	144.74	1162.75	8.84	867.55	166.67	1278.8	460.89	928.75
Y10256_at	277.7	144.82	353	407.86	440.3	209.16	252.25	96.8	218.95	93.83	336.4	165.18	201.1	15.13	217.65	20.72	228.5
L20773_at	1428.9	185.97	467.15	539.73	1464.55	6.43	1874	961.1	1542.15	13.79	1671.25	868.82	1716.15	111.94	1622.7	754.91	1132.15
X80497_at	917.2	113.99	498.35	575.8	1038.2	106.77	1196.25	583.15	835.05	149.55	1446.7	583.65	762.15	331.85	755.65	68.24	864.6
Z49155_at	1262.35	144.89	1140.1	1317.2	1636.35	751.16	1344.5	110.03	1117.1	326.68	2110.1	1035.91	1617.65	725.42	1568.7	135.06	1796.6
D30715_xpt5	721.65	129.75	165.75	191.56	763.6	230.38	679.7	744.87	264.65	41.08	862.85	893.29	1118.5	303.21	264.95	221.11	696

D50582_at	173.45	29.63	316.45	365.64	165.8	98.43	497.4	369.39	645.85	516.97	809.05	461.95	568.35	228.89	234.15	53.81	664.3
U40490_at	164.85	118.72	31.15	35.99	286.5	334.32	255.55	97.23	128.8	57.98	285.75	124.38	167.75	20.58	290.45	226.06	383.4
M31210_at	28.4	16.97	203.75	235.4	334.95	301.72	209.65	285.46	320.45	434.8	77.55	66.96	154.65	126.08	263.4	301.79	23.9
HG4185-HT4	433.65	220.97	428.6	495.26	364.35	266.37	452.65	114.34	417.45	267.92	747	53.74	508.5	374.06	461.7	180.6	539.9
M34455_at	1555.3	86.13	624.95	722.03	1828	281.43	2831.15	1219.41	2185.35	862.46	1329.25	762.19	2218.8	80.33	1589.4	69.3	1210.5
HG3565-HT3	562.65	142.2	67.75	78.28	521.8	96.45	507.65	8.84	319.35	204.28	635.2	40.45	686.45	665.6	369.7	88.25	443.35
M97676_at	1578.05	675.92	1146.9	1325.12	1524.15	187.88	1302.6	875.4	1183.85	390.39	1436.1	972.7	1475.9	990.66	1111.15	602.53	1184.55
L77571_at	539.7	9.9	776.2	896.75	1037	923.48	523.55	203.72	1198.95	708.17	1053.05	841.24	921.35	341.32	1698.35	119.71	649.55
M27878_at	488.2	133.78	289.75	334.82	337.2	424.26	344	294.58	652.15	14.78	290.6	113.14	96.25	27.93	400.95	290.69	358.75
X71973_at	9406.1	5073.63	4466.1	5160.04	12995.15	2299.02	10624.05	896.68	9399.25	1343.01	12770.85	683.14	9701.05	3120.82	9041.35	2856.36	7588.1
D31764_at	6844.6	3583.48	3813.3	4405.84	6653.45	623.46	7270.8	1386.07	4292.95	2643.24	8467.8	1301.08	6235.8	2295.41	7395.2	398.38	6204.7
M55409_s_at	48322.45	21322.45	25100.1	29000.15	52114.25	7664.97	54854.75	17223.78	44488.45	3095.64	42186.45	248.69	47896.35	5610.25	54090.95	8815.99	47339.35
M69225_at	1258.8	195.73	1145.2	1323.14	1253.25	226.77	698.75	818.9	1851.15	0.07	1339	153.72	1793.3	361.05	1699.55	1306.95	1026.6
U29091_at	765.65	175.15	251.2	290.2	589.9	165.32	577.95	248.83	360.45	111.65	965.05	907.85	503.55	278.53	367	102.81	537.6
U05589_at	36.3	0	31	35.78	83.65	56.78	47.2	25.46	74.05	32.74	59	18.53	40.45	26.09	44.6	9.48	51.25
U70136_at	231.1	218.21	375.25	433.53	162	129.12	165.05	120.7	159.3	137.74	263.35	286.87	80.5	21.92	154.6	171.97	131.65
HG4332-HT4	543.75	32.6	282.25	326.05	276.1	211.71	313	134.21	936.9	162.63	618.35	834.17	795.1	305.89	878.15	8.98	860.3

X76105_at	2396.05	664.61	1854.55	2142.75	1213.75	368.61	2009.65	1966.53	2059.4	832.55	2558.45	407.65	2626.15	495.33	2371.55	288.29	2777.7
M96843_at	175	132.79	18.5	21.35	641.45	836.58	125.8	11.88	86.7	78.49	137.75	13.79	510.55	402.98	538.8	398.67	114.45
U82275_at	174.6	106.49	58.65	67.81	530.45	675.5	628.4	770.18	930.6	572.19	418.4	453.68	271.75	105.15	264.2	39.6	397.55
J05633_at	1979.45	104.3	2092.85	2418.09	1796.6	4.24	1477.2	483.1	2659.9	548.15	1547.85	1394.2	2403.05	687.38	2156	108.89	2647.4
U63090_at	1963.15	136.97	451.9	522.13	2118.25	303	1756.9	736.52	1591.15	340.9	2463.1	2000.26	1419.95	378.51	956.5	150.33	1713.1
U62531_at	1683.1	138.17	833.15	962.58	947	225.57	1280.35	71.49	2760.85	682	2569.15	2475.09	795.6	147.08	1317.2	398.38	832.15
U59309_at	1107.25	424.48	965.8	1115.81	1694.55	2.05	1500.45	636.61	1622.25	660.65	1649.75	17.47	1734.4	52.18	1946.3	1002.54	2100.5
L00972_at	1112.85	629.4	606.65	700.96	1135.25	345.99	1370.4	93.48	807	267.99	1519.85	1044.04	1942.35	177.27	1305.4	235.33	1549.05
U80017_rna2	120.9	125.16	296.5	342.52	98.3	12.59	123.1	83.01	259.2	318.2	419	479.56	84.55	21.99	37.9	6.93	209.5
U87964_at	1532.85	336.37	1266.1	1462.86	1097.8	788.71	321.75	191.98	1494	826.89	969	472.91	885.55	415.99	1331.35	427.16	1946.1
X61079_at	66.65	26.8	16.4	18.95	457.7	203.93	295.65	352.07	86.35	39.95	231	141.7	126.1	40.87	493.85	588.95	46
HG4297-HT4	1738.65	80.54	927.1	1071.13	2025	717.57	1446.95	252.65	2645.7	467.26	2561.25	52.82	2253.25	258.02	2699.1	179.32	1995.3

U05572_s_at	257	5.66	202.35	233.84	253.5	53.6	335.95	92.42	133.6	44.41	244.65	43.63	240.6	74.67	161.25	49.57	264.5
HG1496-HT1	360.1	100.55	78.8	91.08	179.7	87.54	233.15	52.26	456.15	379.5	311.3	65.34	468.05	538.04	122.4	38.75	181.8
X52979_rna1	10083	1467.25	6538.6	7554.59	9708.7	993.06	10492.6	1906.64	10971.4	107.62	9468.45	458.28	7619.8	1636.25	9089.25	1267.63	9253.45
Y00705_at	41.1	4.38	23.05	26.66	145.55	94.54	207.2	251.73	67.95	2.19	90.9	86.27	77.5	27.86	51.15	1.77	53.55
X90858_at	35375.65	5428.81	35923.4	41505.19	35897	12909.08	36454.55	18589.48	33446.9	6956.8	44143.7	3330.61	25998.7	16254.26	23389.45	18594.29	31715.3
U12779_at	10270.25	480.2	3771.55	4357.55	9350.5	1499.07	9905.8	830.43	8057.2	2069.7	10602.15	1584.7	9378.8	1467.11	8064.05	123.11	9090.7
J03258_at	792.8	380.42	355.8	411.11	333.9	57.84	701.35	474.54	1151.55	621.76	509.35	319.26	788.5	87.68	756.65	131.31	917.85
L02426_at	3494.4	388.34	2420.3	2796.32	3666.45	920.16	3865.85	1131.3	4002.8	513.36	4277.35	838.7	3911.15	282.21	4140.55	265.94	3597.9
AFFX-ThrX-3	62.7	41.86	32.4	37.48	261.15	50.7	128.55	51.27	125.2	38.61	53.85	10.11	190.95	152.81	189.85	180.67	73.6
U37426_at	91.2	13.29	173.35	200.32	102.8	100.27	135.3	147.93	217	94.89	151.75	53.95	121.7	38.18	119.2	78.91	418.65
S42303_at	122.85	115.33	21.1	24.32	164.6	6.22	78.9	2.97	75.9	55.58	120.2	134.63	77.75	59.47	63.15	50.98	102.95
U59632_s_at	245.4	7.78	131.05	151.39	269.75	22.13	250.95	121.27	301.25	144.74	321.5	208.74	281.7	38.33	267.05	125.37	329.35
U74612_at	230.7	60.1	242.95	280.65	408.95	336.37	217.55	141.21	674.85	583.86	261.95	139.94	472.4	253.71	954.65	403.4	1248.65
U50733_at	3756.8	746.14	2276	2629.59	3917.4	912.59	4082.6	924.33	3726.05	420.09	3494.65	799.81	3518.15	539.03	3878.2	811.76	3317.75

D13969_at	147.25	31.47	524.05	605.5	197.75	12.09	320.25	234.41	524.65	478.64	207	35.78	235.55	28.07	204.25	9.97	175.45
X83973_at	871.75	121.98	560.85	648.06	998.55	249.96	714.2	669.21	703.65	130.46	1356.65	242.47	472.9	547.44	955.2	55.3	1224.6
L02320_at	199.3	181.73	122.85	141.92	146.95	120.99	859.25	584.14	543.7	544.05	500.25	602.38	370.35	53.81	298.9	360.91	74.15
U34252_at	937.85	259.72	1011.95	1169.2	735	536.98	717.1	548.01	1099.45	840.4	978.95	26.09	740	114.13	901.8	746	830.35
U40223_at	3062.7	952.05	1824.4	2107.89	3628.85	911.25	2432.5	879.36	3225.5	2010.45	3897	171.69	3245.75	967.11	3220.2	667.93	3155.2
L38486_at	415.45	390.82	304.75	352.07	487.35	235.11	1005.35	66.54	912.1	45.11	1164.25	466.76	811.95	194.95	938.25	260.14	376.85
U72936_s_at	175.1	182.15	263.3	304.2	117.3	41.86	238.7	143.12	449.3	117.8	128.45	125.79	88.15	12.52	352.3	86.83	291.9
U72649_at	2082.55	513.57	2240.65	2588.79	1295.75	904.6	1840.2	133.5	2709.2	219.63	2615.4	977.22	2460.6	740.76	2430.8	978.64	1686.25
U00001_s_at	385.05	67.25	15.05	17.32	727.55	904.88	848.2	744.87	608.4	46.95	238.15	290.83	96.95	87.89	497.75	241.05	347.6
U91316_at	3508.2	1949.92	1929.9	2229.79	3376.4	856.02	3225.65	2061.43	3846.4	1146.64	3264.2	1050.48	3073.5	529.06	3415.05	317.84	6030.35
U22322_s_at	519.6	369.53	35.3	40.73	262.2	48.93	34.95	11.81	136.1	56.29	78.9	60.1	51.4	23.33	190.35	87.47	81.65
M17236_s_at	1426.75	340.75	1748.25	2019.85	776	483.24	532.95	425.61	902.95	660.37	199.05	76.44	1418.75	1435.07	1515.9	67.18	1992.8
L40027_at	3590.85	307.24	2169.75	2506.91	3700.5	430.35	3949.4	1168	4296.45	271.6	3441.75	693.32	4704.75	1542.69	3562.4	371.37	4450.65
M55131_at	432.9	171.97	47.2	54.59	949.6	1159.94	184.6	18.1	335.95	345.14	207.55	169.35	534.5	65.48	358.1	423.98	420.1

D87461_at	389	103.66	304.35	351.64	932.5	969.44	254.6	151.04	687.05	11.53	791.35	438.34	811.9	104.65	326.6	287.65	349.85
X98178_s_at	195.15	167.09	72.6	83.86	241.3	292.88	213.85	232.71	82	31.68	123.9	56.71	61.35	6.43	179.6	23.62	362.95
L37042_at	4194.1	289.91	2178.65	2517.23	4110.45	1138.37	2673.8	752.08	3209	382.12	3294.25	1713.25	3626.15	1327.88	3010.1	1038.6	3843.9
L11702_at	246.7	96.45	57.15	65.97	870.25	331.85	854.65	601.96	597.9	427.8	627.85	74.46	352.35	154.93	418.05	89.59	703.95
L20688_at	1172.05	399.59	318.45	367.91	1494.8	260.64	1041.9	447.6	1793.35	13.22	1848.7	1515.47	1662	518.17	966.9	252.3	1464.05
X66534_at	40.4	8.06	46.85	54.09	257.5	104.51	516.75	659.94	172.4	162.49	149.3	87.4	353.75	324.07	343.15	284.75	161.25
U15177_at	2165.95	206.55	1004.7	1160.79	2287.9	1034.36	1412.1	28.99	2050.3	13.58	1701.4	412.67	2132.65	60.32	2280.5	365.29	1290.8
L41816_at	189.9	25.03	58.05	67.1	165.45	48.44	241.75	148	195.25	2.76	269.05	85.91	243	133.36	202.05	21.99	168.85
M11119_at	2629.95	877.17	1526.7	1763.95	2467.05	1558.11	3053.65	679.18	3083.1	11.6	3504.05	66.26	3373.05	220.26	3120.45	278.39	2973.55
X58822_rna1	229.4	207.32	310.8	359.07	131.15	69.08	549.55	203.72	344.3	243.24	600.75	159.45	112.35	39.24	330.15	319.97	96.3
L36069_at	234	13.15	462.15	533.94	287.8	5.66	191.95	54.8	313.1	80.33	249.55	36.13	250.25	13.65	266.7	133.78	221
U14971_at	23561.35	11943.1	19041.85	22000.57	34808.35	4812.64	41456.65	5381.44	33963.4	1974.53	33391.45	3937.52	36803.3	13326.7	43357.5	106.49	34614
D85815_at	19704.75	1294.93	9591.9	11082.34	19872.2	1199.68	17424.75	211.21	15579.8	1343.93	16038.05	624.59	16092.15	97.93	15783.25	1451.76	17453.1
M27543_at	305.1	97.02	42.45	49	259.45	183.07	115.85	100.34	913.15	697.7	569.8	442.93	330.15	323.64	236.75	254.35	59.15
U82010_rna1	1302.35	349.24	1049.7	1212.83	1737.45	980.55	1431.7	187.24	1177.7	222.17	1533.25	360.13	1546.55	127.92	1443.65	10.82	1289.5

L11672_r_at	218.3	80.04	265.05	306.25	17.35	6.86	1258.25	1517.8	411.3	516.61	804.7	1013.99	483.8	372.79	387.4	136.75	327.1
J04794_at	5311.8	301.23	3327.05	3844.04	5012.9	1121.33	6002.05	687.94	5008.15	1006.71	5595.5	1921.21	5406.85	1721.03	4683.3	444.35	4612.05
X95808_s_at	1075.95	89.02	699.15	807.73	832.05	331.42	728.3	181.3	1045.3	645.59	1220.85	601.39	634.1	588.31	1043.2	258.52	913.3
U03397_s_at	386.6	214.82	243.75	281.64	736.8	73.26	338.4	390.61	423.75	44.19	587.8	527.08	342.4	233.35	470.6	265.02	85.35
L11669_at	6801.3	2999.55	3976.15	4594	6103.75	1147.85	6502.5	267.99	5158.35	636.04	5161.95	1761.19	5455.55	711.99	5199.05	2133.69	6504.05
U31449_at	71.85	59.61	65.45	75.59	53.7	34.65	133.95	150.12	86.95	61.31	60.65	12.37	55.6	20.08	65.05	10.11	115.6
U40372_at	149.45	39.95	115.95	134	162.55	13.22	168.15	65.12	328.5	66.61	220.75	23.41	138.55	30.9	121.6	5.66	232.15
U20530_at	516.5	285.53	58.9	68.02	508.15	96.38	503.8	239.71	552.75	57.06	328.9	234.9	123.05	9.4	112.55	36.84	519.7
M61855_at	220.35	86.05	286.4	330.93	370.05	331.14	478.05	527.86	183.1	11.03	322.25	71.49	67.15	22.7	232.95	179.11	489.05
X97267_rna1	733.1	33.66	507.1	585.91	1046.75	273.86	708.7	159.95	803.85	130.46	1208	605.85	1874.55	1375.53	1625.5	1200.81	716.35
Y10375_s_at	3723.85	2305.1	1746.95	2018.44	2246.75	575.37	3456.6	1604.57	1840.3	674.3	3410.7	937.62	3112.9	87.68	3897.4	568.23	3415.1
L07758_at	1929.65	421.22	743.75	859.35	1122.6	234.76	1794.85	1021.84	1518.35	78.7	1951.15	261.42	1742.45	52.68	2118.1	764.52	1723.1
Z48501_s_at	32024.25	587.53	19293.75	22291.61	24519.05	16903.6	19239.25	12875.78	20351.35	8852.48	20187.2	3703.83	26757.9	1804.54	19518.4	4776.37	22857.15
D14520_at	486.3	37.9	290.25	335.38	490.5	88.39	316.7	90.79	607.05	7.42	1135.95	199.19	248.45	293.38	990.05	591.78	652
M59830_at	766.95	187.45	323.7	374.06	337.6	149.48	532.8	179.46	1036.95	234.41	599.25	328.03	793.85	616.67	997.2	507	826.55

M61764_at	2487.6	94.75	1753.7	2026.14	1994.9	1441.08	2956.75	924.82	3223.45	1088.17	2941.3	63.92	3642.85	393.22	2857.85	996.24	3438.15
X89211_at	549.95	462.52	208.4	240.84	833.95	615.4	302.05	324.92	723.2	418.04	723.65	481.61	553.7	101.68	929.3	592.98	534.45
U47011_cds1	604.4	507.14	171.3	197.85	990.85	74.74	640.9	271.39	210.3	75.66	1562.75	742.11	177.1	77.07	361.4	253.71	591.45
Z29066_s_at	42.25	10.54	289	333.9	220.35	103.73	248.75	314.73	157.2	59.82	287.1	318.34	439.9	209.73	245.7	244.23	310.85
L22005_at	3344.65	940.66	935.45	1080.81	3109.75	188.16	3660.55	711.99	2146.9	937.91	2802.4	1.98	1848.5	1065.75	1822.2	172.96	3243.25
U65406_rna4	472.2	181.3	406.05	469.17	1219	1386.07	536.35	477.08	319.85	5.59	250.55	225.64	559.05	248.97	407.3	505.02	361.6
HG1996-HT2	347.1	298.96	79.1	91.36	570.65	431.97	822.95	69.08	267.3	120.35	629.9	736.1	112.75	16.9	119.8	8.49	360.8
U60206_s_at	63.9	14.42	19	21.92	124.8	118.94	96.1	72.83	69.9	20.08	135.2	95.74	75.65	27.22	61.55	27.22	200.05
D87448_at	38.2	15.56	42.25	48.86	71.85	9.55	56.7	23.19	194.2	246.92	64.1	6.22	302.9	339.55	41.85	17.75	223.5
U05237_at	83.55	91	38.1	43.98	232.15	78.7	124.7	7.92	130.5	55.3	64.85	37.97	167	130.96	91.15	10.11	54.1
J04182_at	7640.35	861.89	5279.1	6099.36	4458.75	2266.21	5648.95	1640.84	6862.6	327.96	4285.3	2255.81	4758.8	646.86	4672.6	143.97	6408.6
X04729_s_at	2666.2	398.38	719.05	830.78	1581.65	498.72	1708.25	1224.78	2710.1	1642.18	1726.45	402.41	1951.5	1316.21	1687.95	518.24	3955.6
L40904_at	675.15	334.67	44.1	50.91	514.35	196.65	1119.6	1228.39	256.7	141.56	710.05	159.74	178.05	40.94	358.8	247.06	297.9
HG1686-HT4	175.5	168.01	155.8	180.03	327.15	104.16	494.9	40.45	402.35	299.88	258.5	147.93	239.9	157.97	691.6	167.3	455.75
HG2936-HT3	361.25	54.24	220.35	254.63	598.5	484.37	435.25	406.94	330.2	192.05	447.65	198.77	251.2	176.21	218.3	209.3	45.1

X91141_at	260.65	295.5	44.4	51.34	312.35	393.08	93.05	59.18	155.9	172.25	129.2	13.72	78.55	17.32	110.7	106.35	78.35
M24283_at	731.75	20.86	305.75	353.2	719.7	667.37	538.3	36.91	1015.95	116.18	926.85	1124.94	966.25	458.56	815.3	61.52	779.9
U16861_at	346.05	76.44	542.6	626.92	168.5	172.39	568.55	246.57	515.7	102.11	419.35	72.62	265.25	189.01	979.55	738.71	344.95
L39060_at	51.3	45.68	42.45	49	116.15	77.57	112.95	101.75	594.3	74.81	226.35	194.95	140.45	102.46	84.2	2.26	57.6
U05259_rna1	1396.8	441.52	531.2	613.77	845.2	127.56	1510.65	1509.89	548	158.25	1343.35	1310.34	833.55	29.49	531.6	99.28	1034.25
Z47043_at	180.85	52.26	99.05	114.48	165.65	24.82	163.2	110.03	159.7	111.02	102.7	26.3	149.85	4.74	138.85	14.35	184.4
Z49107_s_at	2815.1	514.35	1404	1622.1	3078.55	785.52	2811.85	668.71	2730.7	653.65	2175.6	283.27	3034.9	204.07	1655.9	1356.37	2434.2
U91930_at	3089.95	122.4	2844	3285.93	2040.75	1104.29	1817.05	110.38	2362.8	1343.64	2311.75	421.22	2225.8	48.37	2973.8	1561.01	3315.4
J02888_at	1471.45	158.89	839.2	969.58	1880.6	354.54	2272.75	83.37	2861.55	710.01	3031.7	24.61	2712.15	622.04	2562.35	470.58	2466.4
U49436_at	552.9	105.78	692.05	799.53	560.1	165.18	368.55	16.48	658	53.74	340.55	283.48	361.95	370.17	669.25	35.28	744.15
X07979_at	19742	3217.2	14386.45	16621.75	15896.25	6208.04	8607.6	6194.25	20289.15	4347.36	12294.15	9045.38	18596.05	7618.3	18241.25	3226.74	18774.15
X75861_at	8191.7	2764.79	4144.65	4788.6	4482.3	347.9	3207.6	140.57	6200.95	1042.63	4214.05	1539.3	5170.8	2126.41	6347.7	231.51	7069.35
U50360_s_at	448.4	419.74	240.9	278.32	156.3	2.4	155.5	94.19	211	129.4	873.2	1110.44	198.1	50.63	122.45	63.43	189.1
AF005361_at	125.15	141.07	13.5	15.56	876.35	1153.36	454.9	583.65	578.6	247.77	92.9	39.6	245.5	141.7	103.25	69.51	293.5
U11037_at	324.05	77.85	164.7	190.35	385.8	241.41	486.05	562.5	601.15	784.82	147.05	15.63	436.5	264.18	742.65	239.5	568.5

U59058_s_at	748.35	115.05	751.9	868.75	981.8	9.9	460.9	443.36	1343.7	401.21	579.95	245.58	733.7	81.18	967	602.17	634.45
X62055_at	664.35	49.29	737	851.5	903.8	199.69	1067.8	683.91	849.65	1.77	869.55	199.19	706.2	305.89	915.7	0.71	633.4
M19311_at	27	2.83	64.55	74.6	253.45	171.05	190.55	185.62	192.6	227.83	24.55	6.72	19.9	6.65	205.9	92.35	287.35
X79781_at	1365.6	140.57	604.65	698.55	1357.15	286.73	1208.75	736.45	1105.2	281.43	1355.7	27.86	1704.2	86.83	673.9	678.12	1184.7
L13852_at	2008	1149.33	1312.8	1516.74	2091.25	530.68	1751.75	249.4	1618.75	1182.35	2873	1108.46	1871.65	1831.76	2080.75	1475.38	1614.75
X99076_rna1	241.55	155.63	104.75	120.99	236.15	75.73	225.5	40.45	182.8	40.59	284.05	169.78	206.6	18.24	329.85	105.01	194.35
U41068_cds2	4199.15	1727.82	1982.85	2290.96	1561.9	948.65	2417.25	834.17	2104.45	68.09	2739.05	207.96	3211.1	782.48	2683.35	287.3	2888.3
U16129_at	392.2	225.43	639.05	738.29	201.3	154.01	525.15	632.08	232.95	253.64	384.3	161.93	404.5	109.46	823.75	86.48	195.55
X03363_s_at	1931.65	127.92	1162.25	1342.87	1895.95	675.22	1403.6	362.75	1722.1	19.09	2223.9	64.49	1738.35	25.1	1517.25	43.2	2427.15
L40371_at	458	29.56	243.2	281	897.5	592.13	483.95	197.64	756.9	368.26	395.1	151.75	570.05	409.77	171.25	160.73	662.25
U68485_at	834	720.68	239.8	277.04	1015.1	520.43	501.35	439.18	421.55	183.35	713.5	330.08	945.15	796.84	1328.85	70.78	1449.7
X04201_at	1420.6	191.48	654.65	756.39	1283.9	176.92	917.3	99.42	1575.95	369.18	1934.05	440.17	2299	313.67	1609.35	476.8	1423.7
U03886_at	263.1	54.87	208.75	241.19	407.75	350.65	470.1	298.54	488	85.98	174.1	136.19	143.15	150.97	263.45	186.32	169.9
L10838_at	7337.6	2066.87	3513.3	4059.22	6745.65	862.74	7837.45	1789.47	7391.8	956.72	6486.05	157.05	5682.45	99.21	6707.15	2087.45	5311.8
X83572_at	1418.7	70.43	838.05	968.24	1552.05	52.68	996.25	808.15	1383.5	740.2	820.4	423.98	767.15	725.28	1426.1	171.12	988.45
U26914_at	521.35	166.81	488.1	563.99	528	146.65	331.4	93.48	944.7	139.02	581.7	446.89	750.15	329.16	1117.85	862.32	553.75

L76927_rna1_	307.6	1.98	210.8	243.53	1362.7	1410.4	356.8	158.39	327.85	280.79	337.4	84.85	376.9	135.76	323.75	189.43	269.2
U27185_at	57.85	8.84	15.65	18.03	477	632.86	61.65	34.29	215.6	116.53	495.85	372.29	263.95	114.48	29.75	0.49	161.55
U15590_at	67.7	3.54	83.75	96.8	175.8	137.74	117.6	30.83	90	20.22	164.25	0.64	90.4	68.02	110.8	15.98	68.3
AB000895_at	705.3	88.53	266.8	308.3	3904.55	2168.06	2694.8	2375.74	4235.75	1157.32	2088.05	1271.73	688.95	128.62	1585.4	1626.49	493.4
U79267_at	578.8	181.3	1057.95	1222.38	1055.9	653.37	463.2	302.78	1167.25	828.09	1231.45	353.34	1126.65	652.16	697.1	266.3	1378.2
Z48482_at	243.15	0.92	153.4	177.2	319.6	211.85	314.5	78.91	182.7	115.12	207.45	39.39	224.5	6.79	190.25	39.53	301.1
HG3395-HT3	3381	522.27	1340.45	1548.78	2143.9	873.98	1965.5	752.36	2151.3	212.13	2986.6	786.87	2777.95	151.53	2073.85	18.03	2127.25
D50912_at	1334	202.09	1179.45	1362.67	1585.75	136.97	1365.9	280.72	1134.8	611.79	1731.85	25.24	1504.7	149.34	1308.8	553.52	1641.1
M93221_at	71.5	57.98	209.25	241.76	285.15	368.19	97.2	14.28	257.6	171.97	41.4	19.52	116.8	112.85	192.75	76.3	27.55
M77142_at	175.2	88.81	194.85	225.07	75.05	15.91	155.25	150.68	346.2	224.15	214.4	28	65.2	4.81	275.95	332.55	508.2
M16652_s_at	76.15	75.59	35.95	41.51	114.5	40.59	302.15	359.99	141.75	80.68	625.7	843.86	89.25	43.06	298.45	345.28	90.5
Y08999_at	3838.15	87.19	2278.25	2632.21	3464.05	639.44	4915.25	765.73	4578.2	23.19	3755.3	644.46	3835	380.57	4458.85	700.67	4416.05
D16294_at	1741.55	1021.27	895.95	1035.13	2446	0.57	1891.8	314.95	2214.3	256.54	2162.2	264.46	1636.65	256.04	1498.2	99.7	2054.35

AD000092_c	2487.4	474.33	1389.75	1605.63	1462.15	1322.64	2699	10.04	1579.3	648.13	3790.45	465.35	2082.35	782.84	1486.5	1011.02	918.7
L12060_s_at	535	436.99	452.5	522.83	266.6	19.8	707.8	14.28	331.7	72.12	599.25	386.58	665.35	254.35	267.1	48.93	276.55
U78556_at	803.55	40.09	432.75	500	1579.75	823.57	925.05	92.28	1142.3	427.52	853.95	458.98	1281.8	179.32	1190.95	129.05	698.1
Z73903_at	213.1	53.17	195.95	226.34	388.6	117.1	362.45	319.97	460.7	241.97	874.05	1042.77	278.05	31.47	293.25	98.64	130.5
M37457_s_at	261.3	11.03	62.65	72.34	310.45	161.01	258.45	61.59	316.45	77.71	280.6	14.99	319.4	168.01	323.2	72.41	553.25
L00352_at	8295.45	239.07	6029.4	6966.27	6494.25	786.8	8584.75	3626.4	12827.25	4241.86	7766.3	1148.06	9522.1	943.28	9246	1832.96	9831.7
U72648_s_at	643.25	427.3	212.7	245.79	1723.45	1996.52	946.5	261.63	814.3	543.91	403.55	31.47	946.1	105.36	1113.5	153.58	705.65
L49209_s_at	236	112.57	223.65	258.45	62.1	26.87	528.25	398.74	294.8	357.09	87.9	74.81	84.65	26.94	39.3	26.3	407.65
X95654_at	51.65	34.58	36.8	42.57	99.45	35.43	53.2	30.41	87.85	13.65	171.05	52.4	68.5	43.56	117.35	37.83	71.3

L13761_rna1_	568.2	61.66	676.35	781.42	804.7	121.06	759.8	349.03	897.7	290.62	519.1	632.44	678.9	76.37	586.5	113.7	714.55
X58255_at	3003.2	658.17	897.2	1036.62	2498.65	340.05	3029.25	218.71	2948.65	1013.21	3195.25	1379.78	2444.6	380.85	1633.6	568.8	2021.6
U81556_at	2733.4	1178.61	1821.65	2104.7	3200.4	339.41	2999.4	248.05	2625.7	336.3	2873.25	149.98	2824.35	12.94	2737.75	775.77	2700.9
X98411_at	959.8	653.65	1525.85	1762.89	483.75	405.24	1436.85	568.44	274.6	233.77	1102.1	299.95	1442.85	224.65	1630.95	892.72	1017.5
L76569_at	154.4	147.64	278.25	321.52	288.25	371.3	169.15	159.74	390.6	381.13	143.45	16.9	287.8	101.68	195.45	221.82	157.95
L12350_at	213.3	183.56	79	91.22	344.15	183.64	808.35	838.28	767.45	272.73	547.85	285.6	546.8	397.82	518.05	579.62	587.75
L19437_at	2348.35	203.58	1748.5	2020.2	3387	911.18	4209.05	619.92	2936.75	1466.47	2913.2	193.89	2716.6	121.62	3644.15	386.72	2760.35
Z75190_s_at	124.65	68.38	61.3	70.85	131.6	11.46	127.2	3.54	274.7	186.53	139.5	21.5	192.8	81.18	427.25	188.73	138.65
L34060_at	494.3	164.05	170.6	197.14	1037.4	947.38	774.8	851.5	591.5	291.61	919.25	585.56	795.9	98.71	565.25	98.92	562.55
X05610_at	4205.7	1171.11	2868.35	3314	3679.1	261.21	3248.1	321.73	3141.25	89.02	2911.4	147.5	2553.6	384.24	1654.85	5.59	3531.1
U03187_at	503.65	78.7	172.9	199.83	638.25	231.15	690.05	423.34	3615.7	4641.73	675.55	331.7	523.75	112.78	586	116.53	415.35
X68486_at	1095.05	283.34	558.05	644.81	1757.8	1383.67	1076.1	399.37	732.35	810.98	462.45	321.24	848.75	713.82	281.55	122.12	764.35
K02100_at	342.55	202.02	211.05	243.88	78.45	57.35	161.4	6.36	82.35	77.71	537.4	608.11	116.2	82.59	149.35	110.8	86.45
U80034_at	325.9	70.57	170.05	196.5	168.75	19.3	138.35	84.78	307.45	147.15	188.45	66.26	168.1	6.65	684.5	12.87	297.1
U60519_at	162.8	39.17	175.05	202.3	192.5	46.95	478.95	554.44	245.65	29.06	190.05	19.59	230.2	244.23	576.65	107.13	162

X70811_at	333.35	127.35	254.85	294.51	487.7	65.62	670.3	664.96	305.85	93.41	251.35	81.67	541.45	693.46	708.85	309.22	323.2
U09413_at	31.55	5.3	37.15	42.92	83.2	12.02	88.7	89.24	216.55	65.12	110.95	126.22	34.8	15.56	359.1	117.8	66.25
S77582_at	66.05	4.74	539.15	622.89	383.6	412.1	527.75	129.61	315.85	232.43	154.05	149.13	231	33.8	395.3	19.52	459.45
Z19585_at	186.35	6.72	77.9	89.94	187.1	50.49	712.25	786.09	256	153.16	210.1	35.5	231.2	78.06	242.35	224.65	141.45
D11139_at	479.85	390.54	470.05	543.13	961.75	365.64	2032.25	1718.2	1368.55	845.35	1035.2	230.94	525.7	532.73	324.35	121.98	676.05
X64877_at	749.25	223.23	10.55	12.23	831.05	359.71	291.7	341.39	661.65	95.81	342.85	214.61	21.95	1.06	312.15	335.8	874
D50477_s_at	320.8	173.52	97.75	112.92	565.9	258.8	381.6	331.07	796.25	1007.13	124.65	88.18	189.55	44.62	88.1	44.26	340.1
M89796_rna1	38.5	1.56	26.05	30.05	60.95	26.09	72.35	31.04	347.4	144.96	115.3	71.28	336.7	39.17	260.1	305.47	53.15
D87119_at	462.6	219.49	81.8	94.47	326.5	45.11	186.65	162.28	381.25	388.27	886.1	274.78	349.15	21.85	820.55	106.84	458.1
HG846-HT84	357.25	238.93	144.8	167.3	944.55	647.07	720.75	573.11	779.45	53.53	692.8	744.16	846.65	125.94	372.45	385.02	293.2
M16336_s_at	1187.55	655.84	636.85	735.74	639.75	305.54	1309.35	783.12	659.15	474.12	1346.7	831.84	1455.95	118.44	739.55	244.16	1062.2
X70218_at	3019.8	818.41	2317.85	2678.03	3360.9	716.86	3250.15	58.48	2911.5	1401.06	3738.9	442.51	3455	496.95	2899.05	928.08	3871.75
Z35085_s_at	449.55	103.17	298.1	344.36	481.7	79.2	409.1	284.4	400.45	72.9	742.5	761.41	218.35	256.33	433.45	507.49	542.2
L20348_at	355.6	316.64	324.2	374.63	796.75	1022.26	111.65	29.49	840.4	512.79	574.6	268.84	741.85	162.85	403.9	247.49	302.3
D14134_at	174.05	149.84	44.5	51.48	554.2	700.46	604.75	607.9	118.75	66.4	62.1	47.66	169.6	107.2	104.7	19.23	48.9
L08424_at	233.25	272.45	93.5	108.05	187.3	172.96	136.35	92.42	145	7.5	105.45	0.35	55.2	35.92	126.3	55.01	59.65

X87160_at	816.3	390.04	264.8	305.89	690.7	17.39	438.15	65.69	1041.7	55.86	989.5	721.39	1123.65	161.29	942.15	194.1	1182.5
D50926_at	331.3	72.12	102.55	118.44	262.8	238.44	336.7	42.14	715.45	69.51	284.6	205.63	639.95	11.24	672.35	253.92	624.9
L77730_at	841.25	112.5	633.5	732	727.85	190.42	898.7	244.09	298.15	363.52	762.9	202.09	708.25	326.9	341.85	22.42	588.75
Z23090_at	82703.34	51680.95	22626.1	26141.74	111758.15	32173.99	103210.2	5295.52	106746.1	44929.71	100679.7	13629.34	105615.84	64818.71	101463.85	30430.84	47009.85
U73167_cds3	141.05	13.65	49.6	57.28	114.55	12.09	201.3	10.75	174	92.77	185.85	8.13	158.65	60.03	206.35	96.8	164.25
U05321_at	610.8	364.73	246.9	285.25	394.5	337.01	308.95	21	97.45	46.46	234.15	142.76	65.85	56.07	203.85	194.24	168.3
U01147_at	1306.1	175.65	1285.3	1485.07	1562.8	76.37	1098.2	150.19	1613.45	357.58	1855.9	549.42	1660.4	97.02	1996	380.85	1264.45
U51096_at	177.1	14.28	100.5	116.11	146.8	43.98	849.95	712.13	165.95	71.77	410.7	210.01	203.2	2.26	297.55	196.5	374.85
J05556_at	143.85	135.98	303.65	350.8	340.5	413.37	62.85	51.41	169.8	190.49	720.5	518.31	560.2	262.48	334.85	19.45	213.05
M77836_at	5240.65	1115.74	3021.95	3491.48	4669.6	363.31	5535.2	150.19	3191.25	720.19	4587.2	283.41	4011.45	462.09	2966.15	1587.53	4247.3
D00596_at	1734.85	159.45	1412.4	1631.86	1571.85	301.58	1422.4	222.46	2008.6	495.82	1657.25	107.55	1951.3	373.07	2245.15	265.38	2236.05
U11313_at	36.1	10.04	103.25	119.29	424.8	573.04	32.15	14.92	303.2	71.84	419.7	132.65	49.9	15.27	160.7	156.69	267.3
U61167_at	50.2	18.1	34.45	39.81	123.05	93.69	67.15	33.45	52.05	0.64	91.9	36.2	66.5	5.52	126.7	38.04	57.8
U51269_at	2989	1367.4	1458.45	1685.11	1386.6	703.29	1558.3	707.25	1112.5	251.45	2742	2854.59	845.5	88.95	2486.75	2450.34	2184.9

U89896_at	2150.75	764.45	1184.95	1369.03	1015.7	123.89	1272.9	390.46	1484.6	148.63	2488.45	1081.94	1805.35	765.87	2499.95	233.7	2072.1
U94585_at	2808.5	277.47	1781.4	2058.25	3417.8	1323.85	2456.15	82.8	2565.25	242.04	3033.95	479.49	3559	538.67	2939.9	719.83	2403.6
U22233_at	244.75	104.72	195.8	226.27	87.3	51.34	602.8	389.19	419.45	402.7	625	322.44	64.85	6.29	212.7	185.83	404.45
U33818_at	5312.7	2501.89	2708.55	3129.44	4448.85	1258.44	4499.55	973.76	4538.05	439.47	4104.85	509.61	5227.8	697.91	3705.8	689.43	6690.65
AFFX-HUMG	126228.3	25928.47	79454.7	91800.28	204406.25	59214.05	181070.36	120766	130354.8	32208.43	156731.09	82546.23	237881.05	80189.51	222825.25	20643.05	177885.2
L02648_at	1363.15	774.21	204.35	236.1	650.55	260	776.45	352.49	594.85	1.06	851.75	533.79	1536.8	110.59	963.45	599.98	775.2
D13413_rna1	37124.45	34399.4	17856.35	20630.9	44861.65	16334.24	49746.65	12245.89	81027.25	36954.75	43305.95	13.36	42879.65	22164.76	58481.15	3752.55	34021.5
X75208_at	1964.95	630.81	931.5	1076.22	1614.55	802.92	2788.8	915	1580.6	529.48	2345	780.65	2389.65	69.79	2677.3	762.12	2072.4
U27655_at	1372.8	46.67	819.2	946.53	1484.15	623.17	1243.3	90.37	1420.25	63.71	1187.45	668.15	1097.95	1151.66	2116.3	647.99	2536.2
U73167_cds2	1603.35	1169.77	345.4	399.09	2072.75	717.08	913.4	94.19	443.4	99.7	1428.65	1297.05	1389.15	1033.44	574.55	5.16	720.75
X16560_at	8514.85	3785.5	3761.2	4345.6	10480.6	2366.12	8224.05	3736.14	11392.8	1762.53	6434	2074.09	8138.95	1724.56	8024.85	505.23	6112.1
U78525_at	6347.5	1466.96	4478.5	5174.32	5341.6	2065.32	6741.95	3004.57	6167	297.98	5502.35	118.16	6373.8	789.56	7675.6	1651.38	8020

L40992_at	338.1	10.75	305.3	352.7	351.5	306.6	213.3	112.15	306.5	56.14	733.85	658.67	197.6	91.78	685.8	417.33	389.6
X66113_s_at	693.1	195.59	609.75	704.49	407.35	367.34	618.35	488.26	1273.35	81.95	989.5	256.82	650.15	85.91	986.85	45.47	788.05
D14878_at	1652.95	247.42	830.7	959.83	1685.85	253.5	1438.95	494.62	2028.25	245.44	1748.4	296.14	1733.85	151.25	1361.2	205.2	1676.05
L10338_s_at	2571.6	129.4	1228.05	1418.81	2111.15	878.44	2236.95	305.54	1933.05	208.53	2287.8	617.3	2666.5	692.54	2207.95	508.9	2249.65
Y09022_at	2842.9	174.94	1771.65	2046.86	3035	452.27	3361.35	488.96	2917.55	1374.12	3424.35	1181.22	1188.45	991.86	3755.3	2092.61	3270.6
D14694_at	6001.85	379.5	3108.95	3592.03	6491.75	739.14	8705.9	993.06	6914.75	1745.78	5385.5	75.66	6153.9	150.61	6774	251.31	6800.7
D13540_at	514.4	274.22	328.25	379.22	466	19.8	108.25	58.19	410	109.32	450.8	212.13	146.6	98.43	511.55	162.85	451.2
M22538_at	4773.6	1592.26	3181.4	3675.68	5329.3	1045.95	5452.5	3532.71	5472.6	192.9	4545.65	1278.24	4875.3	1437.55	5170.75	877.45	5153.5
Y13620_at	308.45	113.49	260.05	300.45	463.1	298.96	455.8	390.32	313.55	11.53	294.65	128.06	574.85	235.25	453.5	147.36	514.05
D13636_at	1372.95	719.06	918.05	1060.73	1284.75	19.45	1889.05	633.21	1164.35	1282.62	1912.65	286.59	1002.45	971.78	1030.45	1163.54	1822.75
X52479_at	788.95	132.02	360.2	416.2	917.1	428.22	1282.2	974.25	883.9	341.25	505.6	284.26	622.15	97.37	1035.8	43.56	911.8
S77583_at	129.55	85.63	488.95	564.91	346	16.83	162.95	102.32	74.15	14.64	509	190.35	389.95	50.42	366.85	377.24	177.15
U68111_at	289.85	80.96	61.65	71.21	240.8	279.73	464.25	282.35	335.6	218.07	350.55	127.77	106.5	117.38	117.35	85.35	169.25
L19314_at	2121.1	528.77	912.35	1054.08	1742.4	925.74	1420.6	544.47	1730.7	404.18	1683.45	190.42	1852.45	723.02	626.4	367.27	675.95
L23852_at	505.05	63.14	88.15	101.89	516.95	164.12	543.85	169.92	519.3	332.76	1134.7	1049.63	499.35	399.3	148.1	76.65	686.7

U29700_at	435.45	261.7	61.6	71.13	687.3	599.63	1054.9	716.86	633.4	569.79	667.6	690.98	727.1	188.09	126.55	11.95	509.5
X96783_rna1	1214.05	720.9	377.25	435.93	609.1	528.49	498.4	91.22	487.25	227.62	1327.45	0.92	960.15	200.18	1134	1052.74	781.6
U48263_at	579.25	60.74	544	628.48	1302.5	975.67	1269.25	956.08	1080.35	569.57	2251.5	1284.39	1891.35	553.31	1275.1	143.4	1326
X51630_at	220.65	43.63	180.15	208.1	79	30.26	217.45	32.46	405.05	230.87	160.75	111.93	124.6	53.32	257.7	306.32	295.1
L21936_at	2435.3	456.23	1802.8	2082.85	2292.2	236.03	2050.6	924.9	2222.2	108.75	2453.3	416.34	1925.35	551.61	2983.05	1319.11	2403.25
X62573_at	315.5	37.34	564.75	652.45	504.8	120.49	564.2	396.97	378.25	55.23	380.15	182.36	326.05	21.85	896.85	111.79	390.6
HG2714-HT2	134.8	7.64	148.3	171.4	224.05	91.99	195.55	128.91	165.75	7.28	117.55	73.04	146.2	13.01	126.55	12.94	116.7
HG2846-HT2	527.65	175.72	417.3	482.11	893.35	687.52	301.3	39.6	852.55	231.72	445.8	111.58	370.85	346.98	727	190.07	555.35
U02566_s_at	368.5	105.08	205.75	237.66	405.15	167.8	1369.65	1673.79	547.85	14.64	348.35	118.86	394.95	119.43	438.55	20.29	1061.35
X65614_at	935.7	16.4	636.6	735.53	902.3	310	1076.1	43.56	791.7	827.31	1153.4	108.61	720.05	787.79	1369.7	289.91	624.6
U89606_at	2166.75	139.65	1245.5	1438.96	2289.6	409.7	3016.65	1500.98	1577.55	258.02	1616.1	553.24	921.3	193.75	1334.1	165.04	2265.35
U10099_s_at	689.15	183.21	472.9	546.31	631.85	187.03	569.05	153.65	766.7	740.06	668.3	394.57	1355	48.22	645.9	674.72	545.95
L17075_s_at	554.55	275.84	55.6	64.21	813.2	574.31	292.9	39.88	312.7	1.27	279.55	55.51	229.35	80.12	371.2	292.18	402.45
X74328_rna1	156.25	42.78	150.15	173.45	307.3	127.84	301.3	213.69	172.95	20.86	526.25	497.73	264.15	86.48	824.45	648.49	196.95
X94612_at	256.45	217.58	238.9	276.05	497.3	264.74	965	883.88	375.4	219.2	106.35	37.12	212.95	143.47	217.55	246.43	287.3
X74819_at	306.15	281.07	488.9	564.84	803.85	715.1	410.5	293.59	321.05	68.38	1027	971.71	584.95	179.53	786	321.17	612.3

M60314_at	251	31.54	114.9	132.79	644.95	682.85	438.4	215.53	248.95	86.2	401.6	438.69	598.9	387.35	800.8	207.89	284.15
X71125_at	338.15	69.51	136.8	158.11	171.65	211.92	204.65	134.42	100.3	20.65	177.85	195.52	73.2	33.66	223.2	230.09	363.95
D31890_at	4811.05	866.7	2896.75	3346.81	5657.8	880.63	5861.25	1901.76	5069.85	413.16	5035.65	1538.88	4873.4	870.45	4986.15	388.84	5535
U29680_at	147.1	145.24	53.75	62.15	549.85	36.13	100.85	49.85	224.45	232.85	545.5	40.02	230.15	246.14	247.9	30.12	465.2
X80822_at	55321.1	37147.29	31824.4	36769.27	96188.3	11753.39	74952.55	10240.25	60256.7	12918.56	78334.9	8652.01	69977.35	30182.21	81537.2	9494.32	64897.9
X59711_at	106.2	78.35	159.15	183.92	717.75	478.92	153.55	59.47	752.45	995.54	546.4	233.77	535.4	32.81	190.3	165.89	74.75
J04469_at	1592.8	157.83	581.95	672.39	908.7	71.56	1166.45	334.82	2022.1	222.03	783.9	819.25	2034.6	139.44	2332.7	709.79	1906.65
Z11502_at	150.25	73.75	44.05	50.84	247.15	170.06	119.5	32.81	98.9	22.49	214.5	7.07	195.8	90.51	201.45	32.88	132.9
HG907-HT90	724.5	150.05	756.5	873.98	970.45	519.65	1170.45	1096.23	727.5	368.4	785.95	129.75	819.3	170.13	560.95	251.66	886.25
U18934_at	700.15	61.59	348	402.06	494.5	113.28	547.5	411.68	200.15	43.35	563.05	210.79	605.7	237.45	495.35	29.34	696.65
U50078_at	189.2	43.84	349.15	403.4	74.8	15.27	370.95	450.07	374.1	352.14	142.3	35.21	218.6	149.06	282.4	240.84	316.05
U70735_at	4767.45	675.78	2408.6	2782.89	4883.95	828.09	5526.05	1097.22	4185.95	272.02	4827.05	411.47	4976.65	766.01	5436.85	846.76	5000.05
M15395_at	194.1	65.48	311.55	359.99	184.35	73.75	561.3	590.15	58.05	18.31	136.7	77.5	97.75	64.13	100.3	70.85	236.4
S77356_at	2428.4	898.73	1099.65	1270.46	1874.85	297.76	2190.55	332.69	2344.15	912.95	2671.05	347.68	3457.15	410.9	2510.4	215.1	2286.1
M29960_at	627.8	331.21	120.15	138.81	354.75	272.87	197.05	138.1	389.65	407.22	922.25	768.84	76.95	41.08	432.4	28.28	335.55

U93553_at	200	94.05	361.85	418.11	750.35	503.95	557.75	371.02	441.9	432.47	782.85	608.32	185.6	7.78	205.55	109.39	175.35
L49229_f_at	276	92.35	39.15	45.18	46.2	12.02	130.85	68.52	58.75	32.74	508.85	411.47	459.35	169.78	135.5	4.38	182.25
X86163_at	395.7	449.58	110.7	127.84	240.15	234.83	733.5	528.21	329.7	276.34	678.35	126.36	618.4	266.15	75.8	22.77	314.6
U66406_at	1566.1	410.69	571.85	660.65	1866.6	510.67	718	511.66	1080.55	550.34	1507.7	367.55	1550.55	123.25	1375.4	291.33	1444
X16662_at	10136.15	218.14	3932.75	4543.8	10718.3	1870.16	8842.85	3161.69	8929.1	1924.89	6824.55	701.66	7807.3	669.35	8661.8	803.41	7908.7
L43338_at	263	320.18	69.45	80.26	153.55	10.68	160.35	174.58	127	5.66	315.35	307.52	310.75	247.98	624.6	411.96	236.85
M64099_at	886.15	169.21	948.45	1095.8	856.05	706.89	1447.8	1183.84	738.95	403.12	907.8	970.15	697.4	426.24	1677.35	539.73	818.7
M16652_at	31613.4	2186.66	11261.95	13011.83	30394.2	3131.49	27065.1	7877.59	23231.45	8344.21	27453.1	10166.21	28409.4	6297.07	26422.2	4001.23	25735.05
M76125_s_at	673.95	492.78	53.5	61.8	288.45	177.55	321.05	178.97	649.35	133.57	186.35	107.83	169.65	54.52	335.05	268.06	155.95
D87685_at	42.3	25.31	166.55	192.4	164.3	101.68	361.85	475.95	118.7	85.7	170.55	160.3	449.75	115.89	450.1	17.25	36.15
AB002559_at	1975.8	130.96	1070.45	1236.8	2442.2	1040.44	1902.5	229.39	1418.3	687.17	1931.15	874.76	1115.05	1068.23	2306.35	259.72	2361.4
D50312_at	61.85	40.66	49.3	56.99	231.95	226.2	530.85	655.98	193.85	162.56	437.55	465.77	252.6	245.08	76.95	47.59	46.75
M58286_s_at	3956.3	207.18	2359.85	2726.53	3141.15	645.66	3577.25	868.26	4013.05	294.65	3356.7	1436.28	4234.9	39.17	3267.15	577.78	4524.6
U88629_at	1707.35	18.88	1020.25	1178.82	1962.75	1249.81	1761.55	209.94	1690.95	628.97	2125.3	669.35	1282	393.01	1229.85	148	974.2
HG363-HT36	2251.7	1000.41	916.45	1058.89	826.55	775.63	951.85	767.14	2090.65	482.74	3282.15	2374.96	1689.2	271.25	1801.9	309.57	1793

U80457_at	522.9	227.41	577.55	667.3	309.7	81.46	344.95	154.79	741	722.95	1000.45	37.97	1333.7	866.91	531.95	520.93	593.5
M58525_s_at	8259.75	952.69	4100.4	4737.47	8165.1	814.16	8035	1003.1	8393.05	4998.18	9140.05	33.16	8479.55	1651.16	9528.6	2036.75	10204.05
D86959_at	641.3	162.35	611.25	706.19	575.7	51.05	730.65	560.52	865.1	107.9	463.65	29.06	738.15	336.23	743.3	185.26	560.05
X14894_at	174.6	110.73	101.25	117.03	546.3	559.75	72.3	31.11	212.85	246.43	573.1	668.92	75.15	43.2	217.9	231.65	111.3
U08377_at	638.6	447.6	623.55	720.47	418.6	15.56	616.75	273.16	676.5	201.24	365.35	42.78	1016.65	785.81	826.75	703.92	1011.2
U30828_at	981.4	92.21	669.55	773.65	690.75	232.57	625.8	421.01	234.4	241.69	138.9	86.27	159.95	57.35	272.85	255.19	992
L49169_at	3014.95	255.76	1626.7	1879.49	3476.45	347.54	4600.5	619	2222.3	828.59	2316.8	2117.36	3442.7	1351.85	2710.3	1361.32	2850.5
S69115_at	648.45	211.07	762.1	880.49	525.7	118.65	1155.1	1098.28	1674.15	894	706.55	195.94	1035.2	806.67	451.9	64.91	1078.25
HG1980-HT2	21612.35	462.09	5177.55	5982.05	13441.8	4663.09	15171.65	1120.13	21829.8	3817.53	11974.1	1292.03	23703.25	9066.03	28623.4	16112.98	32536.1
Y11416_at	261.3	40.16	183.5	211.99	206.1	73.4	263.35	77.71	203.35	66.26	269.3	98.15	139.85	3.89	186.65	80.4	319.55
X96698_at	1465.95	337.22	939.95	1086.05	1827.45	388.7	1793.85	746.21	2143.4	385.37	1414.7	62.51	1556.55	570.99	723.75	321.52	1569.85
HG2441-HT2	244.55	234.41	114.35	132.16	278.2	298.82	884.65	916.76	481.1	212.98	518.3	19.66	198.45	87.75	196.45	44.62	296.65
S66431_at	87.9	4.95	48.7	56.29	142.95	61.45	79.55	20.86	56.1	13.15	103.6	73.26	61.8	16.55	101.65	23.26	72.75
L29376_at	245.65	94.12	153.75	177.7	337.75	222.24	274.9	206.62	157.65	55.23	467.7	88.39	318.5	106.21	616.95	567.74	221.05
Z18956_at	229.3	29.42	200.75	232	844.75	381.2	993.35	927.37	462.5	44.26	164.25	128.62	458.05	186.75	635.7	130.81	455.05
U78107_at	361.45	411.32	294.35	340.05	945.6	301.23	157.7	55.15	416.8	410.97	284	192.33	704.8	222.88	477.45	462.8	379.95
U50743_at	1747.1	170.55	650.15	751.16	1148.75	231.15	1067	227.26	1593.85	44.34	1313.3	989.24	996.05	585.41	1957.1	40.73	1774.4

U67615_at	50.65	8.41	19	21.92	90.2	44.26	79.85	45.75	273.2	280.3	103.2	100.97	48.45	15.91	375.6	407.72	109.1
X79510_at	804.9	615.18	978.75	1130.88	1112.6	583.36	542.05	376.39	1015.1	391.6	1250.05	861.04	893.55	755.97	665.8	703.15	755.5
U90543_at	221.25	54.52	365.2	422	547.4	310.99	682.95	466.9	843.05	833.18	1089.35	1334.38	161.8	15.7	823.15	609.88	275.6
U29589_at	48.35	9.26	29.55	34.15	187.75	117.17	101.95	40.09	71.35	18.6	112.9	46.95	195.9	160.8	61.15	30.9	69.55
U57911_at	81.25	56.36	34.5	39.88	85.1	62.37	73.1	12.45	163.4	199.69	43.1	34.65	32.5	13.86	51.85	12.8	34.7
X94333_at	107.65	8.13	37.8	43.7	118.35	17.32	149.15	137.96	89.3	16.97	183.05	90.16	114.7	31.82	85.1	10.04	94.35
S74683_at	219.35	16.48	163.35	188.73	150.25	108.82	535.6	181.73	446.8	458.49	709.5	767.64	407.75	391.67	515.85	350.37	449.8
U13680_at	240.05	36.7	305.5	352.99	119.05	32.74	755.65	498.16	401.35	199.19	581.9	738.22	266.55	214.32	394.25	329.16	240.4
HG3790-HT4	70.55	50.28	34.75	40.09	142.3	39.03	229.8	253.14	125.95	12.23	116.4	117.38	204.2	85.7	252.45	235.68	70.2
U33761_at	100.6	22.34	36.45	42.07	95.1	37.05	155.8	157.4	377.35	316.15	191.3	140.71	275.2	319.75	154.45	139.94	153.55
U72509_s_at	875.95	702.65	794.35	917.75	507.65	338.21	478.65	13.36	859.8	110.59	985	1045.67	607.75	391.24	668.25	28.78	1049.2
K03021_at	3419.3	289.77	1807.1	2087.94	3094.45	271.88	2996.25	505.65	827.45	602.24	811.2	198.27	1356.4	242.54	167.2	95.6	2513.2
HG4245-HT4	62.9	24.75	110.55	127.77	59.65	47.02	207.55	161.72	77.5	35.92	332.75	404.96	186.55	55.23	335.95	416.98	86.45
HG2730-HT2	279.9	192.19	369.2	426.53	275.15	146.44	309.55	78.42	432.7	361.61	456.95	16.48	521.55	351.64	682.9	112.15	1095.2
U47050_at	332.7	317.92	278.8	322.16	471.95	12.94	299.4	194.03	172.75	27.65	385.15	263.54	126.1	92.49	360.55	71.49	524.25
U72508_at	2306.8	535.56	836.85	966.83	1433.9	613.91	2745.65	1310.91	1390.9	646.01	1970.15	164.12	1819.2	1035.91	1566.4	202.94	2132.15

X99101_at	1556.15	80.54	529.7	612.07	1443.5	204.07	1392.75	367.2	1665.15	219.13	1455.2	22.63	1275.25	821.3	735.8	550.69	1206.7
M29064_at	4966.65	1504.65	3282.2	3792.21	3730.65	793.44	3466.5	1841.31	5441.5	1348.45	4028.95	2111.07	6328.85	3171.87	5989.25	3185.45	5912.25
U37251_at	305.65	28.21	309.65	357.73	763.6	225.14	178.25	193.96	554.55	389.55	659.5	357.94	720.4	16.55	743.7	181.59	323.25
J05073_at	139.45	44.62	55.85	64.56	177.4	154.86	152.15	78.56	163.55	58.19	90.6	1.56	209.05	27.65	213.55	48.3	97.3
L15296_s_at	1246.3	83.86	975.7	1127.27	1046.75	806.17	301.65	103.73	732.5	346.34	1528	663.27	666	222.6	707.05	837.14	277.8
M75106_at	306.25	313.18	215.2	248.62	419.5	481.96	744.05	801.08	494.95	390.96	229.55	168.79	134.3	11.74	349	331.77	64.45
D78514_at	732	170.13	476.4	550.41	623.65	745.36	980.6	361.05	1152.7	503.32	521.8	538.82	255.6	209.87	396.8	231.08	746.3
X52943_at	288.55	62.3	89.45	103.31	355.75	144.32	221.45	92.84	312	121.2	978	965.48	585.15	574.67	819.8	722.38	226.05
Z22535_at	201	16.26	170.65	197.21	113.25	72.62	170.5	213.26	194.65	8.56	45.8	4.95	135.85	119.85	379.7	222.17	395.5
HG3993-HT4	140.45	36.7	46.6	53.88	155.7	47.94	177.1	116.25	107.95	17.18	111.25	55.65	106.7	47.52	76.45	28.21	80.25
L20320_at	1343.5	863.94	693.4	801.15	1625.35	165.11	1031.35	115.61	1791	84.99	1876.2	240.7	1496.55	378.8	1361.75	369.6	1019.4
U69126_s_at	2544.65	1848.45	1330.45	1537.18	1602.4	249.04	1053.55	605.07	1908.75	98.08	1668.15	301.44	2149.95	942.64	1964.45	409.06	2762.15
D13370_at	4339	1920.36	1906.3	2202.5	5438.15	1156.76	4567.9	1224.85	4098.1	1685.46	4179.65	1363.94	4540.15	548.5	3882.5	81.6	4790.8
J03473_at	1913.85	409.34	1034.85	1195.65	1605.75	276.97	1271.8	564.7	2109.65	390.82	2172.1	240.98	1328.6	32.24	1602.9	443.21	1667
U66083_at	115.45	24.11	78.25	90.44	426.9	135.34	185.95	166.38	202.95	54.66	183.45	114.34	147.75	38.25	189.9	92.91	293.95

AFFX-M2783	15957.95	9987.95	5152.55	5953.2	28473.25	5269.57	22551.85	16673.93	22354.6	10663.45	17563.2	7859.92	21476.5	349.74	23970.55	3864.55	17206.15
L77213_at	2513.5	811.48	978.75	1130.88	2169.75	268.63	1926.55	341.6	2251.15	186.75	2910.45	443.71	2473	300.1	2235.65	174.44	2772.75
L18960_at	1945.75	780.58	1419.45	1639.99	2761.65	69.08	1736.65	107.55	2374.3	654.36	2750.35	1318.82	2046.85	226.06	2273.95	1813.09	1654.15
M26061_at	937	29.42	514.7	594.68	894.4	221.75	450.8	240.13	1304.45	431.55	1266	105.22	443.85	260.14	1187.95	190.99	624.55
HG4606-HT5	3434.55	586.83	1320.4	1525.51	3806.05	504.95	2234.55	290.13	2510.35	2902.74	3210	765.94	3233.25	932.04	2866.3	177.2	3804.15
Z79581_at	251.8	255.27	27.55	31.89	218.8	188.8	58.8	36.77	255.6	243.39	151.7	120.21	265.25	156.2	276.55	136.83	187.9
X98261_at	4007.35	928.22	1578.1	1823.35	3596.35	848.6	3617.95	1170.05	2468.2	296.7	3245.55	22.84	3532.05	1340.32	2448.6	23.76	2824.45
L13923_at	241.1	138.17	386.2	446.18	855.25	558.83	745.2	293.73	318.45	39.39	791.45	313.46	942.2	784.18	86.65	13.51	516.9
M62831_at	3116.7	161.5	2610.15	3015.74	4165.1	706.12	3425.1	45.25	4246.95	592.48	6002.65	379.08	3510.9	1385.08	3184.85	1285.03	2631.55
L14595_at	284.75	102.6	605.7	699.75	1408.45	560.52	452.05	330.43	359.55	37.55	646.2	500.77	429.45	155.07	387.1	178.76	401.55
X59372_at	291.25	93.41	108.4	125.3	242.4	122.47	213.15	110.1	562.55	598.57	350.3	82.73	167.7	14.14	179.15	103.59	288.35
L33243_at	3865.35	333.26	2519.6	2911.16	3942.65	13.36	3542.9	356.66	3722.15	1514.27	3346.05	1235.24	2998.15	896.96	4155.75	426.6	2644.75
AF000231_at	97.95	42.5	104.3	120.49	774.45	554.87	568.2	262.76	274.15	140.93	662.65	68.94	518.5	492.85	672.7	365.29	251.3
K02574_at	3458	185.4	1488.35	1719.61	3759.1	514.35	3871.45	1308.36	3693.5	1236.02	2879.9	150.19	3670.7	621.97	4483.7	2225.69	4725.35
S73591_at	2952.8	489.18	9671.2	11173.84	3926.2	507.99	2946.2	90.09	3105.75	134.7	11005.8	2870.15	4137.65	3127.18	2159.85	1014.34	3430.35

L38696_at	4832.25	194.95	1927.85	2227.46	3381	331.63	5393.45	160.73	3563.75	182.93	3895.7	1262.61	3412.35	397.61	4017.65	210.36	4367.45
U29175_at	1874.8	248.05	397.35	459.12	949.4	1137.31	1200.65	354.05	1060.05	562.22	701.6	901.7	1419.6	72.55	514.55	594.89	946.2
HG4411-HT4	181.5	10.89	253.4	292.74	723.35	731.22	511.25	274.29	209.1	41.72	265.65	134.42	398	396.97	315.6	53.6	191.6
M90366_at	1513.45	309.36	563.3	650.82	1234.65	167.09	1221.25	415	1071.6	80.89	2030	605.14	1414.9	53.03	1105.9	766.5	1389.65
M73489_at	431.2	196.58	191.65	221.4	509.95	73.61	603.45	221.25	137.5	56.99	430.1	48.37	304.05	339.76	158.3	51.62	281.95
Y07828_at	421.35	401	183.55	212.06	353.75	282.63	214.6	207.89	555.85	54.52	284.7	131.8	560.25	467.33	615.4	675.15	217.6
M81829_at	1152.25	366.92	506.25	584.85	871.85	37.12	1539.2	710.08	874.35	350.94	1566.35	775.34	948.1	348.46	806	789.13	667.8
S46622_at	140.9	102.81	419.45	484.58	125.95	3.61	391.85	289.14	124.8	81.03	440.25	264.53	336.5	229.81	514.3	20.65	241.75
AFFX-BioC-3	42134.35	2165.37	16416.05	18966.79	168136.3	157777.72	182127.5	202004.42	84815.8	57599.93	127515.55	144395.23	65210.8	62692.08	67094.5	8443.56	54841.1
HG2339-HT2	296.95	73.47	113.7	131.38	872.8	963.79	480.45	108.12	218.35	53.81	347.9	85.98	500.1	318.48	747.2	841.17	216.85
U86358_at	425.9	244.09	85.8	99.14	701.65	21.99	1141.6	661.29	132	22.91	879.3	919.8	659.95	462.8	304.7	55.15	213.85
U37219_at	1011.65	750.74	586.1	677.13	1210.55	1397.6	1288.7	644.6	904.6	822.22	1237.3	1249.74	1039.5	411.96	1489.2	240.7	790.95
M18391_s_at	1941.25	542	866.15	1000.77	1352.7	82.87	1229.2	386.79	1638.2	120.63	1231.2	68.87	1469.6	66.19	1914.65	760.07	1748.25
U08023_at	657.9	703.71	346.5	400.36	778.2	572.05	807.15	975.17	573.5	479.84	735.6	719.83	529.1	341.25	568.9	456.08	526.75
M81778_s_at	173.5	160.37	18.7	21.64	74.2	49.64	490.55	433.53	236.1	114.55	359.9	468.25	108.5	110.17	324.65	367.34	63.75

V00571_rna1	177.55	218.57	125.9	145.52	238.35	0.92	44.2	27.58	79.7	10.04	143	64.06	68.25	41.51	98.95	60.03	170.9
D78334_at	278.7	272.24	21.55	24.96	203.65	13.51	182.75	195.37	335.15	194.95	248.95	263.11	64.8	1.13	315.5	66.61	472.65
U79258_at	150.6	77.64	222	256.54	308.1	250.32	316.45	126.64	127.7	55.3	559.55	558.97	301.7	276.9	472.4	404.04	700.4
X65962_s_at	1611.05	1048.57	474.9	548.71	426.7	273.08	705.55	435.79	848.8	625.22	1118.1	91.36	733.3	20.08	897.25	446.68	703.35
L08187_at	2916.7	79.76	782.35	903.89	2804.45	576.79	2765.65	803.77	2240.3	1401.06	2804.6	959.4	1845.15	417.41	2933.8	201.53	2405.1
M19481_at	1063.4	410.55	1139.8	1316.92	939.55	105.15	1438.3	153.73	1073.1	314.38	1450.3	412.67	1423.1	282.98	1522.3	692.54	1262.3
D10523_at	1782.1	90.09	644.85	745.08	1219	1267.7	1176.5	378.02	2112.6	112.43	2489.25	252.51	2058.2	461.6	1946.95	375.26	2309.9
HG4322-HT4	2420.4	387.21	532.1	614.76	2097.55	532.95	2128.25	962.44	3013.05	131.88	1468.65	617.09	2784.9	180.17	2243.6	324	2267.1
X15880_at	3299.15	406.37	2231.05	2577.76	3373.8	886	2968.85	715.38	3030.7	932.67	3413.3	193.89	2845.1	2283.67	2720.75	126.78	3156.1
U70732_rna1	3035.35	1111.5	698.3	806.81	1733.15	1112.92	2241.1	255.41	1238.4	579.26	1403.4	1067.87	2592.3	410.69	2703.65	156.34	3145.25
D82326_at	183.2	0.71	197.05	227.62	497.95	213.9	915.75	828.09	778.45	17.18	409.1	168.86	496.95	538.32	161.15	103.45	296.35
Z69030_s_at	762.6	165.32	602.3	695.93	463.5	297.97	268.85	62.58	1149.7	422.99	1331.15	270.33	687.85	251.52	987.2	177.2	1095.35
M63379_at	2658.4	1134.06	1649.55	1905.86	2650.6	1422.13	2752.35	290.13	3288.85	1131.58	3152	536.98	3619.65	598.85	3732.2	532.59	2966.25
X55954_at	25309	13238.59	9929.95	11472.88	26617.3	4795.31	25072.75	12873.52	35123.6	243.24	25285.1	6169.08	24697.05	5345.94	28883.65	3754.24	26167.3
Z34918_at	504.65	216.45	196.25	226.77	397	262.05	418.25	2.33	876.4	539.95	951.05	373.99	455.25	21.85	590.2	81.32	628.5
X99459_at	1898.1	337.29	1692.3	1955.29	2339.2	393.86	1848.8	191.63	426.35	106.56	1454.1	902.27	2014.95	570.14	1873.05	362.96	1862.4
U44429_at	50.8	5.52	34.75	40.09	131.25	51.55	115.15	42.07	222	119.93	34.75	9.26	106.45	56.92	144.3	148.63	163.3

M64590_at	418.9	274.78	152.45	176.14	714.4	489.18	437.55	391.38	353.85	249.54	259.65	144.46	271.5	14.14	168.8	66.19	263.9
J02645_at	2932.9	410.26	1902.4	2197.97	3433.05	219.7	3113.35	2125.21	3957	1558.04	3197.85	299.18	2924.1	1426.52	2609.5	98.15	3417.85
M20030_f_at	2741.7	652.94	1007.6	1164.18	2447.85	192.69	728.55	311.48	1062.8	683.77	1187.85	895.83	2096.05	760.49	1521.45	757.1	1054.4
S76475_at	376.4	236.03	57.3	66.19	457.8	463.15	760.9	856.16	601.85	595.88	473.85	315.44	173.75	8.84	132.75	61.16	232.2
U14394_at	3947.55	995.11	1712.1	1978.06	4050.6	1175.07	3341.5	1113.27	4110.95	1011.09	2894.65	534.36	3086.15	983.51	3055.9	1577.41	2867.75
X66114_rna1	2053.4	488.19	1277.3	1475.73	1254.75	791.75	2206.25	807.45	1094.55	705.76	449.75	28.5	2047.55	192.12	868.2	31.54	1568.4
U59286_at	166.8	76.65	464.25	536.34	675.2	347.47	920.25	1112.07	414.85	480.62	532.3	312.54	299.55	301.58	79.6	41.01	174.55
D86331_s_at	928.55	753	162.5	187.81	335.8	15.7	563	399.8	481.6	47.94	422.9	182.43	253.85	80.54	352.6	172.53	722.6
M29994_s_at	218.25	241.34	364.2	420.73	888.15	15.2	130.65	32.17	184.05	8.98	1247.85	1132.86	451.4	277.47	315.6	332.91	397.15
L09209_s_at	6480.8	2497.64	4577.15	5288.38	3944.6	1125.15	4322.25	2498.14	5995.9	1222.73	5751	3156.52	6507.65	1165.95	5519.5	298.12	7056.2
D85181_at	809.3	716.44	237.35	274.29	614.9	46.53	359.9	250.46	788.15	59.89	183.35	197.49	1008.1	753.49	1062.9	434.73	488.05
U04810_at	144.9	7.5	66	76.23	362.2	193.32	153.25	21.85	147.7	19.09	179.35	25.39	349.8	85.14	825.95	837.99	484.7
M27533_s_at	136.3	107.2	477.75	552.04	182.1	77.5	646.25	748.19	131.25	2.76	333.6	213.55	175.4	36.2	262.25	84.22	317.15
HG2614-HT2	1187.5	637.1	823.9	951.91	612.2	57.42	586.2	85.56	608.25	238.93	860.7	47.66	487.3	198.56	1202.1	395.56	1547.85
S82592_at	55.2	14.42	176.85	204.28	153.85	156.77	577.3	770.18	145.75	112.64	46.9	13.58	107.1	87.96	166.3	110.73	297.6
L37347_at	103.85	65.55	66.85	77.29	250.7	31.68	188.2	50.35	103.65	28.35	141.1	6.36	191.65	146.58	145.9	4.95	92.25

U09770_at	2282.95	601.11	1209.15	1397.03	1775.55	85.35	1430.55	989.74	1818.8	484.23	2555.7	171.54	2681.5	769.9	2915.9	851.64	1960.6
U89505_at	3176.7	494.55	1651.55	1908.13	3227.35	343.87	3653.2	832.12	3626.25	422.5	3378.2	285.11	3235.85	486.14	2889.2	1337	2727.25
U31099_at	84.6	19.52	272.2	314.52	885.35	411.89	505.6	518.87	390.45	1.2	1029.9	686.88	645.35	353.91	1083.6	514.63	87.8
HG4169-HT4	189.2	195.02	64.8	74.81	169.85	134.99	120.65	38.54	94.95	88.74	187.3	154.01	86.55	26.52	132.1	98.29	120.15
HG2987-HT3	215.75	123.67	172.3	199.12	597.6	485.78	713.1	678.68	274.6	234.76	65.85	6.01	690.7	318.06	400.4	27.01	301.6
X83535_s_at	4213.1	5519.96	773.55	893.71	214.4	24.32	594.7	400.36	286.2	65.62	474.75	123.67	1479.6	1244.93	307.15	211.21	767.85
M33653_at	138.45	54.8	128.05	148	145.3	99.56	112.55	35.43	65.6	1.7	172.05	70.78	121.9	70.14	146.1	47.94	115.65
L29008_at	658.75	263.4	666	769.47	1157.65	482.03	554.4	119.64	839.7	322.02	706.05	293.1	1319.9	527.78	841.95	824.7	885.15
U01877_at	534.1	527.22	569.3	657.75	453.75	338.21	175.75	41.65	624.35	216.3	111.1	16.97	316.95	263.54	377	270.82	213.7
Z69923_at	516.75	168.5	422.9	488.61	326.9	144.39	519.1	61.09	290.4	14.71	417.45	169.21	789.65	703.36	1887	305.05	954.55
L01406_at	613.1	272.38	186.05	214.89	294.2	57.56	319.6	85.28	650.4	285.81	463.35	116.46	456.45	164.4	982.6	846.27	362.75
U81262_at	512.4	143.4	181.75	209.94	482.35	580.75	409.65	177.7	575.45	255.62	185.2	47.66	264.5	266.86	323.6	374.2	332.9
U75308_at	276.15	313.46	28.05	32.46	78.85	46.46	222.1	4.1	352.1	415.5	338.95	324.21	86.2	38.04	260.55	326.9	268.6
Z38133_s_at	696.5	271.53	68.95	79.69	149.85	46.88	414.5	465.13	378.1	366.71	460.8	192.76	279.15	187.45	121.6	25.46	290.5
D78134_at	3491.1	490.73	2524.65	2916.89	3581.7	171.83	4121.65	1425.74	4296.3	1455.08	3750.85	1621.61	3925.6	182.01	4781.05	260	3693.3
U43328_at	91.1	3.25	136.45	157.61	298.05	336.79	75.95	43.91	40.65	43.06	40.05	14.92	165	178.62	391.1	188.09	194

U37055_rna1	279.4	138.31	194.55	224.79	287.3	60.1	148.35	35.71	276	159.66	191.75	52.11	242.05	38.25	806.45	927.65	173.4
L07765_at	1594.1	131.66	384.05	443.71	1432.5	506.85	1053.3	38.75	1270.55	907.01	821.65	648.2	1194.85	444.98	1016.55	189.43	1173.7
X79066_at	284	27.72	123.45	142.62	302.4	169.42	188.25	155.07	97.6	62.93	110.9	12.02	69.7	33.8	378.1	447.74	119.2
M55683_at	265	39.74	162.1	187.24	212.9	148.92	273.85	129.19	195.1	89.1	380.55	278.81	231.05	32.74	304.05	86.48	126.45
U44772_at	923.95	268.49	510.65	589.94	1339.75	383.61	761.35	410.05	937.2	215.81	854.9	200.96	1169.2	227.97	1041.15	320.53	1259.3
Z46967_at	409.95	150.12	237.7	274.64	1011.05	953.67	1086.1	507.7	842.9	431.62	290.15	118.58	950.4	987.12	890.8	865.22	436.3
X54870_at	363	65.2	200.4	231.51	477.5	282.42	356.6	340.83	681.9	0.99	191.8	4.24	278.85	186.04	321.8	172.11	290.7
U70451_at	1337.85	202.59	856.7	989.81	536.65	629.82	1410.3	549.7	1176.6	568.09	1759.55	755.54	1142	186.53	1099.55	742.25	1331.9
V00565_s_at	1028.5	548.57	337.65	390.11	702.05	27.51	1038.35	861.19	866.15	751.3	811.55	151.67	1300.75	236.53	717.45	355.18	1227.9
U05040_at	1778.5	44.55	2101.65	2428.13	1997.35	120.99	1597.5	1127.55	1704.45	513.85	2213.95	716.23	2046	276.2	2825.85	1031.46	2307.25
U30894_at	934.1	80.04	300.2	346.91	1356.4	965.91	790.9	375.62	1177.05	382.76	1250.4	831.7	705.1	66.19	1003.5	678.12	1067.45
X90568_at	217.5	218.64	10.3	11.88	73.45	3.75	65.55	73.47	242.15	263.68	55.15	17.75	66.25	11.95	228.25	258.45	55.1
L36922_at	2953.5	1153.43	1184.1	1368.11	2210.6	175.65	3070.55	1311.75	1922.55	328.17	2555.75	321.52	3162.75	767.42	2395.3	579.97	2387.45
U00968_at	6447.95	128.62	3560.85	4114.16	5367.15	1651.45	6677.75	281.5	6990.5	394.14	7180.95	1803.62	6269.65	990.44	6224.9	17.68	7810.4
U00952_at	1208.55	632.51	412.45	476.52	696.25	252.37	571.15	623.6	1020.55	245.44	1144.35	162.85	875.35	826.25	368.6	234.62	900.1
HG167-HT16	130.6	28.14	47.35	54.66	183.2	17.39	300.45	258.02	159.7	2.26	198.35	166.67	114.2	15.13	126.95	76.3	124.75

Z47727_at	1487.8	182.72	858.2	991.51	1522.3	210.43	1194.8	91.78	1569.45	37.41	1035.35	288.29	1485.65	202.59	1721.7	235.47	1171.8
J02906_at	2040.95	459.97	1051.2	1214.53	2411.4	1356.94	2607.55	2338.76	1902.25	506.64	1874.75	148.42	3345	241.69	2373.05	1277.81	1818.8
U78180_at	133.25	14.35	72.75	84.07	87.35	2.62	160.3	164.76	167.85	2.05	105.2	27.01	136.1	80.04	73.8	16.97	98.95
D00632_at	542.5	169.99	225.65	260.71	807.55	549.35	620.95	185.33	930.1	619	1298.3	583.5	1101.85	168.5	1140.25	16.48	457.1
U15009_at	1208	573.04	1047.05	1209.79	1633.95	85.21	1418.95	419.95	1304.75	54.24	1398.7	24.04	1275.25	237.66	1419.35	605.21	1233.8
X99050_rna1	172.6	167.3	324.6	375.05	455.1	390.32	323	141.42	320.45	277.26	691	902.83	726.45	328.45	520.5	393.01	575.45
M18728_at	50.9	26.73	260.2	300.66	309.55	378.66	164.4	121.48	104.95	1.48	347.35	373.71	174.6	88.25	83.55	55.93	60.05
L11701_s_at	692.35	250.25	236.4	273.08	552.65	611.29	498.65	133.57	357.65	146.72	362.05	446.96	208.1	53.6	581.6	525.95	374.5
AFFX-CreX-5	3059.2	230.66	1764.35	2038.52	9259.95	9073.1	10746.1	11444.66	6275.6	3794.76	7242.4	6890.61	4271.1	2471.76	5809.65	1135.12	3579
L07540_at	129.55	18.74	91.85	106.14	88.25	8.98	199.5	123.18	114.3	67.18	115.35	7.85	113.4	12.16	99.6	3.96	132.45
D87078_at	1289.7	206.76	814.15	940.66	1376.8	576.86	688.5	549.56	853.55	546.1	873.15	478.92	502.9	273.51	938.6	674.44	1053.25
D87434_at	823.6	119.22	839.1	969.44	1262.9	371.37	1313.35	503.25	1194.9	256.4	1147.2	124.17	1097.9	310.84	997.6	472.06	1006.35
X59543_at	873.3	24.89	1087.35	1256.32	427.25	515.55	785.9	359.78	1226.9	473.05	1448.75	188.02	1208.35	136.26	1523.65	585.41	1283.85
U19142_at	234.9	176.64	56.1	64.77	534.3	62.51	311.85	54.38	551.95	22.42	168.65	67.39	462	309.57	206.35	154.22	387.5
X91648_at	86	14.42	55.5	64.06	313.1	207.89	134.5	83.44	96.7	79.2	59.6	32.67	493.55	109.11	90.5	81.03	327.2

X55777_cds2	222.15	111.37	36.55	42.21	329.2	81.18	384.45	482.03	123.95	68.24	259.05	266.08	155.05	28.92	134.05	72.05	249.05
S81243_s_at	464.75	34.86	94.2	108.89	781.65	834.46	596.75	689.92	1307.65	991.15	394.1	281.15	147.2	21.07	399.25	381.34	618.4
D00760_at	1748.65	640.99	707.25	817.2	2527.85	459.55	2313.85	754.84	2471.5	385.09	2262.8	608.39	1644.25	418.82	1813.7	385.51	2192.35
U43148_at	1527.4	46.39	876.35	1012.51	1505.6	1033.08	1268.65	248.12	1231.6	241.26	1579.85	1241.75	1756.8	836.93	1329.6	785.6	1876.8
X83928_at	631.15	327.04	307.85	355.75	465.4	230.94	359.4	259.08	381.15	204.57	590.9	341.39	419.1	318.48	673.2	186.82	664.5
U06631_at	325.55	372.01	265	306.18	658	616.6	244.75	257.6	929.25	187.17	354.6	171.12	294.05	121.13	950.95	392.8	664
M16750_s_at	1800.6	139.02	1285.05	1484.71	1575.7	1072.4	2894.1	459.05	2274.15	950.42	1342.9	703.85	2287.45	573.53	2841.3	912.03	892.85
U01038_at	2422.55	651.32	1336.25	1543.83	2157.45	466.62	2252.45	410.33	3245.2	659.87	3443	255.41	3421.4	345.49	2513.3	68.02	2608.25
M28825_at	316.65	167.23	104.1	120.21	215.05	81.67	288.7	167.58	242.45	39.39	338.3	141.7	608.65	530.26	251.85	119.43	202.15
S90469_at	1872.6	102.39	620.05	716.37	1057.9	800.02	1251.25	1168.49	1602	186.39	1819.4	926.03	1034.7	936.92	1787.55	318.55	2365.2
L10035_at	479	502.19	488.8	564.7	473.6	277.33	914.2	136.61	622.3	134.92	628.6	19.66	629.15	186.18	178.1	9.05	477.6
U85265_at	627.85	128.91	177.55	205.13	605.3	247.2	634.25	85.77	566.8	237.73	503.9	286.38	653.1	357.8	697.7	337.43	464.35
U84569_at	4477.65	1293.23	1611.4	1861.81	5060.05	234.69	4489.15	1106.41	4064.6	1394.13	4277.7	91.36	4374	403.48	4535.9	952.61	3469.1
X00371_rna1	727.35	155.63	532.5	615.18	265	102.67	858.25	360.27	813.95	529.55	297.35	55.93	605.85	490.1	640.75	744.51	485.95
L38608_at	440.15	275.7	256.75	296.63	623.4	85.28	820.55	615.25	548.85	89.73	273.65	9.26	607.7	749.39	83.25	8.41	442.2
U44060_at	62.35	47.16	35.4	40.87	150.4	148.78	62.9	48.51	110.5	99.7	171.85	27.08	54.9	46.24	43.65	16.76	383.55
M59465_at	1197.4	152.74	1230.1	1421.28	2092.15	275.14	1132.95	247.98	1566.6	1067.73	1672.55	52.54	945.75	234.26	783.25	375.12	653.25

X78933_at	65.7	70.29	41	47.38	60.95	16.33	225.65	297.2	50.85	15.77	106.7	120.63	35.5	16.69	64.65	37.69	148.7
Z80783_at	485.55	238.65	648.05	748.76	1007.25	303.7	820.4	805.96	963.6	505.72	417.7	76.65	513	440.53	818.95	31.89	409.5
X91103_at	408.45	138.52	28.25	32.6	239.45	183.21	554.35	371.3	190.95	96.24	224.25	51.41	341.7	122.05	260.25	214.32	187
X04011_at	449.9	120.49	59.4	68.59	509.25	598.42	614.2	645.45	403.3	534.86	451.75	294.09	76.15	64.56	500.75	151.25	244.2
D42087_at	830.4	104.51	370.95	428.58	782	120.21	465.85	175.57	1077.45	306.39	1356.45	531.82	708.3	162.35	858.3	145.66	800.85
Z11695_at	1291.9	337.71	662.25	765.16	613.5	203.79	676.7	48.51	603.5	442.51	792.35	931.33	1157.7	225.28	915.6	25.03	998.6
U66580_at	88.1	14.57	41.35	47.73	153.2	102.39	180.15	113.21	381.35	447.1	275.65	24.25	119.4	57.56	135.85	111.51	151.95
U77396_at	3397.95	809.71	1638.55	1893.14	2722.6	225.43	2713.95	2977.98	2389.65	1158.03	2269	1017.67	2629.55	259.86	2520.85	170.62	2718.45
Z11518_s_at	900.1	93.9	328.75	379.79	817.95	166.52	727.85	434.66	1148.95	29.49	583.8	256.82	680.25	233.27	1178.1	24.18	633.85
Z28339_at	219.1	267.57	371.7	429.5	535.7	483.24	486.65	667.3	52.75	8.7	266.75	231.01	268.1	238.86	223.9	251.87	230.9
D86977_at	1729	417.05	1317.7	1522.4	2169.45	647.64	1846.1	1098.56	1893.95	1141.34	1523.2	253.57	1143.1	504.73	829.35	869.1	2015.25
HG2981-HT3	4247.35	675.22	3126.3	3612.04	3036.6	924.47	2580.75	19.73	2807.85	2105.83	2287.7	1153.72	2813	677.41	2664.3	87.68	5687.55
HG2175-HT2	476.6	484.09	132.55	153.09	366.2	185.69	113.4	69.01	629.8	427.94	439.8	200.39	504.15	183.49	529.55	568.73	208.45
L77701_at	1043.45	531.67	406.45	469.59	721.6	39.17	1168.45	974.32	1148.4	961.38	550.1	33.66	590.45	60.88	791.35	227.9	1067.4
HG3107-HT3	1138.35	104.44	349.85	404.25	1482.25	798.68	653.95	263.82	537.75	66.4	489.85	426.46	621.95	623.6	1144.7	770.89	1156.1
X83218_at	4675.15	1779.86	1886.25	2179.37	4661.15	2368.45	4950.25	2173.43	4426.9	1274.77	3733.8	807.09	4042.95	818.19	3646.65	4.6	3552.95

U80017_rna1	200.75	14.64	155.4	179.61	395.5	251.31	637.65	526.02	372.65	351.5	264.55	263.54	152.7	121.91	429.6	95.18	248.5
U82759_at	1442.45	358.86	897.25	1036.69	1404.1	1576.57	1797.65	46.46	1583.85	381.34	1343.25	169.21	1525.45	625.72	2199.65	198.63	1202.3
U29953_rna1	1079.5	339.41	410.8	474.61	1816.4	477.16	1631.55	421.22	689.75	42.78	961.85	871.08	1197.2	190.49	265.35	19.02	1157.15
M21302_at	3272.6	930.55	1886.2	2179.3	1787.75	1258.16	2762.6	63.36	1496.15	755.12	2404.95	502.26	1890.45	637.32	3723.75	260.71	3314.05
U55209_at	715.05	397.32	631.7	729.88	623.15	344.57	1007.25	771.52	1078.65	236.24	1089.1	264.88	936.05	681.44	1398.55	413.3	998.85
M30135_at	68.05	23.97	26.45	30.62	94.65	8.84	62.7	45.54	44.7	6.08	48.05	16.9	53.85	16.9	53.65	7.71	58.2
U52696_s_at	10648.55	2782.68	4610.75	5327.13	8265.7	348.18	6027.1	490.45	9223.95	694.17	10535	4180.98	9766	86.55	8176.1	423.13	8324.35
HG25930-HT	318.8	5.23	220.6	254.84	713.7	346.2	259.85	85.91	557.45	235.25	1551.1	479.56	813.8	645.87	942.1	829.72	776.5
X95152_rna1	79.25	62.58	215.75	249.26	402.7	530.19	674.7	574.31	171.55	106.42	448.4	273.37	117.1	86.83	112.65	24.25	32.85
U32324_at	354.3	20.93	62.15	71.77	1038.7	293.17	1104.8	1413.08	428.45	49.43	357.95	331.56	171.25	29.06	510.6	92.21	194.3
U65002_at	39.3	29.7	17.15	19.87	115.45	133.71	253.75	282.21	48.35	44.76	149.95	151.82	97.2	106.63	20.15	1.06	21.55

D88152_at	101.9	6.79	22.95	26.52	320.05	208.1	458.35	633.78	306.85	201.03	157.85	3.32	340.45	144.04	27.35	14.78	296.9
X04706_s_at	102.65	52.68	16.4	18.95	74	25.6	90.7	59.96	101.45	67.53	127.1	80.19	95.3	43.84	51.4	7.5	58.4
L12760_s_at	100.55	3.32	29.6	34.22	302.55	293.8	217.9	74.95	71.8	15.98	115	40.31	495.7	9.05	153.2	96.03	84.95
HG2239-HT2	6149.85	462.8	2702.2	3122.02	5699.2	512.37	5573.3	367.13	4413.3	835.52	5658.15	1918.17	6498.05	1076.57	6061.05	1.91	6221.65
D83785_at	1005.6	725.07	983.45	1136.25	630.85	58.76	698.1	22.91	1403.25	14.5	649.75	583.01	961.6	1130.38	867.3	518.45	1144.85
V00594_at	146436.66	50180.61	60774	70216.98	130093.15	5937.5	107106.5	4602.14	164806.75	17836.55	95947.59	24996.65	201874.69	3570.75	213767.94	156467.52	160928.25
D28137_at	627.8	203.08	505.1	583.65	889.9	21.35	1137.7	503.6	1483.8	115.26	1428.75	499.01	1151.75	371.3	1340.9	512.79	1010.95
L19872_at	408.85	224.65	465.4	537.68	458.6	244.8	625.8	483.66	268.15	217.86	552.15	171.05	135	78.77	325.45	270.04	268.7
U49114_at	307.45	81.81	28.1	32.53	339.8	395.84	654.15	445.41	105.15	105.01	122.75	0.64	299.55	273.01	288	353.27	123.5
HG2825-HT2	1598.7	98.85	992.3	1146.5	941.15	878.58	1515.9	452.55	1425.35	139.51	2375.5	435.58	1662.2	890.67	2326	347.9	1379.05
HG3513-HT3	165.45	167.09	148.95	172.04	433.35	272.02	347.25	439.18	73.95	36.13	238.75	119.29	151.45	132.72	652.2	84.71	103.8
X58431_rna2	1067.45	140.08	694.6	802.57	628.25	633.78	835.45	167.51	603.55	441.16	852.2	598.21	755.2	370.81	871.9	713.33	766.55
L36531_at	1078.15	509.47	526.05	607.76	1181.25	334.82	1206.95	243.03	1941.85	64.7	1235.9	226.7	1013.7	816.99	916.05	168.5	633.6
D25547_at	1519.7	455.52	991.75	1145.87	1868.7	165.46	2111.25	492.5	2389.3	915	1919.5	531.6	2373.2	435.15	1922.8	162.92	1473.65
U40572_at	544.3	370.95	432.1	499.22	903.35	65.97	794.9	879.92	1340.35	131.59	1041.6	111.86	963.6	337.29	639.15	61.73	400.75
L36983_at	706.1	185.12	208.85	241.34	485.05	28.5	579.15	165.68	483.1	46.95	429.55	26.52	615.9	396.55	466.1	193.18	1216.6
U30255_at	3853.85	656.83	1771.65	2046.86	2049.65	2007.26	4242.9	199.69	3202.4	884.87	3010.9	930.69	4637.95	539.45	5897.55	2414.7	4268.6

X01715_at	161.7	108.05	281.4	325.13	112.45	13.51	295.95	19.02	447.05	111.65	282.95	1.91	203.25	142.91	812	800.3	345.1
AB000114_at	1541.55	690.35	1732.65	2001.89	2854.6	3249.16	2244.2	2026.43	2567.95	1691.19	2148.2	1685.6	1645.35	476.1	2291.25	920.58	1593.7
K03183_f_at	7943.85	2551.88	2723.85	3147.12	3644.8	3572.02	3057.45	1564.9	3056.3	1884.3	3973.15	671.54	5622.85	1506.35	4827.3	1087.11	5099.15
M21624_at	117.3	73.68	123.7	142.98	530.45	462.38	602.45	170.34	205.85	147.29	263.35	271.74	351.45	14.92	73.25	46.88	289.55
Z70220_at	652.6	435.58	112.4	129.82	501.05	323.36	771.4	495.26	490.3	282.98	612.65	553.45	488.15	260.57	413.1	239.57	519.9
U96769_rna1	96.8	14	73.15	84.5	312.3	316.64	307.8	289.21	149.5	35.92	273.1	210.86	152.75	93.83	134.05	71.63	164.1
X05309_at	409.55	468.74	180.4	208.46	96.55	19.87	543.3	410.97	289.25	97.37	204.4	107.9	119.95	37.83	338.4	307.31	243.95
U41804_at	1019.75	537.47	1008.9	1165.59	1241.4	1159.94	816.5	367.98	1262.85	212.34	596.25	248.41	929.7	258.24	1117.45	318.13	462.25
D26350_at	65.95	34.01	43.95	50.84	92.95	65.55	360.4	456.08	52.35	31.89	121.8	127	73.75	37.26	83.25	19.02	139.5
U63842_at	1639.85	547.65	370.05	427.59	2407.5	1404.74	2038.95	464.92	1328.85	632.37	2623.65	582.73	1609.95	250.39	1471.25	237.52	1672.8
L24774_s_at	6217.2	1191.47	3736.05	4316.53	7560.15	926.1	7427.5	1147.21	6170.15	881.83	5895.45	496.46	4613.6	1890.52	4280.4	2327.23	3879.9
U32680_at	640.15	32.88	253.35	292.67	345.35	67.53	1350.85	1218.98	697	234.62	681.75	395.63	1203.65	945.47	1233.5	601.61	478.05
D50922_at	665.25	449.51	600.8	694.1	807.65	762.33	1137.5	127.7	1843.45	574.38	914.75	389.83	1086.75	34.86	1381.45	194.67	973.25
L09749_at	46.35	14.92	98.5	113.84	429.1	548.86	329.4	415.64	62.85	4.6	161.4	41.01	109.05	13.36	153.1	64.35	114.2
M74099_at	440.65	230.3	251.65	290.69	531.85	298.05	549.4	603.87	376.8	321.73	287.1	130.81	215.65	233.42	347.35	254.06	334.5

X63629_at	18965	1589.44	10532	12168.46	15403.25	4390.78	18053.8	2022.75	20149.1	309.29	20863.35	1050.83	16741.05	603.23	18612.9	4836.04	23353.4
U58970_at	2111.7	487.06	1749.85	2021.69	2118.4	638.09	2180.4	481.68	1695.65	871.37	2436.6	151.89	1732.65	145.03	1688.45	372.01	2211.2
M27288_at	813.2	446.33	227.8	263.19	716.65	421.65	779.55	569.43	1362.25	537.19	665.75	349.1	827	646.86	706.35	66.96	421.6
HG2564-HT2	200.25	213.05	13.3	15.41	83.05	31.61	111.45	2.76	49.55	51.41	446.35	434.52	46.7	43.42	480.9	35.64	54.25
X98253_at	571.35	492.64	745.15	860.9	668.75	243.46	1367.85	1121.54	1068.6	428.37	918.95	287.3	913.35	286.73	1052.15	648.49	1129.65
D63506_at	438.35	140.64	613.6	708.95	558.7	36.77	718.25	503.39	797.75	90.86	313.95	362.68	606.4	112.71	798.2	163.62	870.1
M28170_at	361.5	173.52	37.8	43.7	90.3	62.65	179.05	28.78	126.7	18.81	106.4	63.36	259.7	227.69	101.65	4.88	68.75
U90552_s_at	137.4	114.13	73.45	84.92	843.6	1122.6	824.5	1040.72	58.3	36.91	158.85	17.18	167.1	21.64	1487.6	62.08	149.5
HG3454-HT3	741.4	172.82	133.2	153.87	490.5	206.05	718.35	6.29	1163.7	70.29	1073.35	197.07	970.85	545.25	884.05	369.75	620.95
U79718_at	523.15	489.25	459.6	531.04	721.95	515.55	581.75	442.01	161.55	26.66	1552.75	1484.99	482.35	224.65	353.95	91.57	669.7
X64044_at	1195.25	650.61	659.3	761.7	666.9	467.26	469.9	426.95	858	374.34	241.25	63.43	1050.55	138.38	778.6	254.42	1275.15
X76013_at	3307.5	1414.78	1423.8	1645.01	4423.75	386.01	3761.6	140.86	3363.9	664.11	2954.15	534.78	4034.55	274.85	3611.2	214.25	3690.5
M83712_s_at	284.65	209.23	486.9	562.57	302.9	189.5	450.95	37.97	482.4	343.23	267.25	74.32	601.15	370.17	268.95	331.42	359
Z14978_at	8413.05	4450.18	3734.15	4314.41	6362.5	395.56	4762.15	936.7	4982.85	160.02	6692.25	2362.37	6387.25	1409.33	6356.4	425.54	6038.2
X16707_at	1262.6	1119.07	1410.7	1629.88	589.3	291.05	423.45	51.27	533.85	543.41	1687.2	1374.05	1797.75	1646.64	752.55	453.75	509.9
HG3703-HT3	143.8	98.43	120.7	139.44	106.65	79.55	124.5	72.97	76.8	49.21	90.65	39.24	115.6	45.96	80.9	40.45	93
M84605_at	147.45	121.13	70.1	81.03	178.8	106.91	335	232.92	304	292.6	275.6	137.89	47.35	32.88	196.95	256.33	92.3

M26958_s_at	1399.85	283.76	399.2	461.18	1901.15	459.41	1816.9	1201.09	1189.4	1025.59	1259.55	873.49	1277.2	577.14	641.3	477.72	1515.25
HG821-HT82	43966.9	23516.25	18296.85	21139.73	56807.7	1246.2	51662.75	19189.82	55788.8	2563.12	42957.3	7411.89	39527.2	6841.82	42746.55	7639.79	41189.5
HG4557-HT4	93.65	124.24	5.6	6.51	62.75	16.62	14.05	16.48	15.85	14.35	89.55	98.64	38.7	49.92	28.8	1.7	16.4
U82818_at	1049.35	61.73	211.65	244.59	1591.85	499.57	1494.95	716.65	1177.2	207.18	1141.5	384.95	1048.05	371.58	755.3	464	954.65
D14662_at	4518.95	1173.44	2912.1	3364.56	4773.5	616.88	4599.25	1236.94	5664.6	880.07	4795.65	986.34	4657.2	1221.46	4632.2	258.52	5000
S83309_s_at	500.9	459.2	339.8	392.59	1202.65	816.78	634.7	614.19	447.55	514	506.9	74.67	748.05	147.71	448.65	44.9	483.9
L41390_at	410.9	25.17	57	65.9	704.5	759.57	403.05	198.91	374.45	374.84	278.3	138.03	739.7	502.89	527	645.31	230.75
D16480_at	4771.9	1001.97	2866.55	3312.02	3936.35	723.87	3890.35	2829.35	3524.8	1031.95	3659.2	1730.43	5196.8	860.97	4586.55	252.08	4677.75
HG3364-HT3	71933.25	55358.89	26173.2	30239.99	99752	5070.24	83865	22458.71	103020.95	5006.81	81447.2	14102.68	80049.7	26547.9	76078.66	11808.61	67657.3
D86640_at	364.5	53.6	316.9	366.14	414.75	67.53	951.4	522.69	408.75	533.94	967.65	305.4	215.25	64.7	783.1	181.44	494.45
M62800_at	221.35	131.88	61.85	71.49	249.05	65.83	161.35	95.67	212.55	83.37	129.3	26.3	175	38.47	125.75	39.53	192.5
D45906_at	3070	178.9	1891.85	2185.74	2753.45	1032.45	2576.4	591.99	3724.3	193.32	3271.8	171.69	2577.75	284.89	2991.35	15.77	2975.8
S57887_at	180.1	122.05	117.45	135.69	274.15	133.01	369.9	231.51	488.8	315.23	229.05	53.39	190.25	62.58	214.2	126.15	284.15
U78027_rna3	21471.95	9551.1	8744.15	10102.79	25650.2	3816.96	20740.6	8733.19	32379.2	4379.68	23284.65	7064.21	20119.1	4899.83	22074.45	3872.61	21501.5
HG2663-HT2	185.6	6.79	367.25	424.33	477.15	160.58	233.5	27.15	249.5	88.67	348.55	278.39	506.85	385.44	663.65	353.91	193.2

X69150_at	94528.25	76156.6	52624.5	60801.29	149241.8	10838.53	145349.84	29414.16	149096.44	717.92	121885.05	2920.84	124627.25	51332.48	121447.55	28400.73	99587.95
L16862_at	4731.3	525.66	1799.05	2078.54	4494.6	1032.09	4385.15	582.02	3899.05	370.88	4508.45	195.52	4370.65	856.09	3975.6	1723.78	4883
M37400_at	2227.95	47.73	1493.25	1725.27	1744.9	535.56	1595.1	1675.42	2558.1	330.78	1915.2	1265.44	1513.95	384.03	2212.25	387.99	1604.15
D79205_at	35243.7	26881.65	12418.8	14348.47	54542.1	5357.18	50684.25	26548.68	91978.84	941.09	84818.34	8139.43	65614.2	35164.43	72709.55	24122.74	58177.05
K03207_f_at	445.75	447.81	228.35	263.82	1295.7	1701.72	412.25	169.35	275.95	64.56	386.55	264.53	296.95	12.66	162.3	15.98	243.55
L38025_at	308.9	142.98	278.4	321.59	1214.15	1023.68	419.7	396.69	266.2	275.77	1040.75	249.54	1222.75	103.59	1405.3	299.53	673.45
HG668-HT47	128.5	12.02	295.8	341.82	124.35	26.8	129.4	113.56	162.55	14.21	405.15	319.26	494.3	511.95	57.15	9.26	374.15
M20218_at	157.3	76.79	37.55	43.35	798.05	438.62	229.75	41.37	984.35	993.56	340.5	270.11	398.5	48.65	636.7	715.59	226.95
M83363_at	310.05	132.02	112.9	130.39	176.15	53.1	350.8	173.24	849.25	346.41	353.75	86.62	351.9	349.88	395.45	496.32	727.55
U79274_at	470	152.59	570.55	659.24	881.4	218.78	944.1	248.34	1184.75	707.6	1296.35	409.06	1051.6	446.89	953.95	183.92	1066.2
M31682_at	128.65	22.98	105.25	121.55	206.5	9.19	658.2	685.19	139	2.97	235.05	134.7	158.6	33.8	207.3	4.81	201.35
L24203_at	6221.2	427.52	2782	3214.22	5299.55	1660.78	6139.15	1565.32	4348.8	1788.84	4716.7	3015.81	5464.75	225.21	4992.35	1475.1	6276.1
X75342_at	578.75	185.05	77.65	89.73	946.65	550.34	1074.35	972.77	708.8	762.4	537.85	440.74	903.65	254.77	814.35	864.72	1206.9
M69013_at	2202.35	393.22	849.05	980.97	1909.75	760.63	1867.95	457.85	1690.65	447.81	1305.35	96.52	2047.35	602.38	2198.3	632.01	3034.2
M94046_at	5815.55	148.56	2128.6	2459.32	4249.8	915.56	4958.95	405.67	4684.75	979.84	4286.05	688.37	4927.9	266.86	4872.85	1942.21	5024.65
J04611_at	4591.1	2306.3	2236.65	2584.12	7234.1	491.72	6398	1431.47	7074.65	1952.11	6875.4	1720.53	6686.55	183.78	8137.3	2054.43	9520.1

Z27113_at	6727.15	553.88	4038.85	4666.41	7063.1	392.02	7926.7	1958.4	8781.6	2138.43	5758.1	491.58	7516.7	493.42	6556.65	267.64	8401.75
M63904_at	3814.1	440.81	1762	2035.76	3262.75	1276.12	3008.45	1630.38	4994.7	140.86	4993.35	1966.68	5496.95	659.09	5099.7	472.49	5833.4
M10901_at	626.15	215.03	384.4	444.06	530.6	224.01	648.6	702.3	183.45	113.63	458.4	219.2	478.4	262.9	106.2	53.88	592.1
U90549_at	1051.2	166.31	612.5	707.67	546.25	411.61	640.1	347.19	1542.3	759.86	1376.35	118.72	933.35	577.49	1003.4	31.68	623
Z81326_at	123.1	133.78	61.05	70.5	222.05	214.47	92.8	93.06	254.7	287.79	62.45	27.37	86.6	8.63	82.05	10.68	21
X13930_f_at	2489.85	565.05	1247.55	1441.44	1977.05	756.82	1450.25	315.44	1585.7	261.06	2029.45	1027.78	2214.35	473.69	1743	286.24	1006.95
X87342_at	281.25	11.24	186.15	215.03	374.85	119.01	239.95	178.12	221	68.02	282.4	135.48	283.55	12.37	248.15	8.41	238.8
X91788_at	1134.8	617.45	654.05	755.69	1074.7	570.07	825.65	877.31	1768.3	457.5	1535.3	183.14	1155.55	214.61	1175.1	394.14	1866.8
M93718_at	1181.15	1209.51	844.7	975.95	1791.8	907.08	986.5	758.3	407.1	49.07	2107.1	623.95	1437.05	475.39	1510.7	1457.63	455.55
D14812_at	4237.5	220.05	2674.4	3089.92	4604.1	776.12	5513.7	602.6	5534.2	556.35	3658.3	1376.74	5980.8	712.34	5690.4	331.77	4771.85
U34683_at	1906.95	659.66	1838.8	2124.57	2689	764.81	2942.55	2007.69	2453.25	420.94	2659.2	599.2	1357.2	614.05	2026.3	290.06	2316.2
U62325_at	463.3	103.94	618.35	714.39	354.6	363.59	657	55.3	249.75	218.85	840.95	69.23	324.1	261.35	670.65	35.43	538.1
X97303_at	110.45	27.37	65.65	75.87	156.8	123.74	304	337.71	235.65	78.28	132.35	13.51	250.05	272.17	87.55	26.38	64.8
X58298_s_at	931.95	607.76	161.95	187.17	519.3	375.62	658.4	149.77	840.6	735.67	660.35	238.08	804.7	206.9	1294.6	622.96	939.35
U59057_at	649	294.72	73.85	85.35	244.85	0.07	454.9	174.66	296.65	2.76	178	81.32	148.5	1.7	307.5	84.99	333.35
D49738_at	2927.7	480.41	1355.4	1565.96	3612.8	489.18	2942.95	1722.58	4318.15	449.79	3485.4	420.02	3723.85	671.54	3399.3	464.29	2572.95

U52521_at	516.75	202.59	271.2	313.39	282.2	278.32	888.4	600.48	260.45	128.48	887.1	430.91	802.3	646.58	886.4	680.24	654.9
U20325_at	301.5	326.26	75.6	87.4	475.4	79.34	1052.85	1139.36	654.5	418.18	1091.25	1013.21	477.75	49.99	781.9	154.86	23.3
HG919-HT91	2185.95	445.12	854.65	987.47	2422.2	228.82	2481.85	916.62	2385.6	290.9	2569.25	76.72	2711.7	511.1	1926.25	272.31	1452.05
Y00503_at	93.75	53.81	21.95	25.39	105.5	37.05	87.2	91.92	204.25	101.05	242.45	1.91	135.8	114.98	36.5	2.4	42.55
X73079_at	831.2	480.55	641.95	741.68	881.3	149.06	1970.45	903.05	1368.6	442.51	1579.25	53.95	1664.55	345.99	788	712.06	845.35
AFFX-HUMG	4675.75	562.93	2725.75	3149.24	4680.85	28.07	4875.45	1624.15	3457.3	294.44	3139.8	566.68	5966.85	185.76	6110.7	1741.32	4858.45
U58087_at	1691.6	112.01	1087.7	1256.67	1310.6	241.55	773.55	727.68	2018.65	116.74	1693.75	600.69	1681.95	206.26	1936.35	81.11	1216.2
M21494_at	1199.55	382.9	880.1	1016.82	1155.8	43.84	1004.3	328.66	1466.15	792.17	1719.8	334.74	1665.65	263.11	1754.85	511.87	1896.05
U52153_at	300.75	137.39	55.05	63.57	864.2	914.71	758.35	812.82	117.1	74.67	403.05	338.92	355.35	173.59	456.5	597.08	271.3
U25182_at	2138.95	300.73	1231.85	1423.19	1957	935.93	2873.75	172.46	1994.4	79.76	1688.8	119.64	1342.2	92.77	1452.3	207.32	1685.95
U72671_at	216.65	186.32	59.85	69.08	70.9	45.96	270.75	310.63	179.85	178.83	307.3	42.57	274.75	321.8	414.45	376.96	77.65
X57348_s_at	44216.55	9123.02	20622.6	23826.95	29823.5	11020.68	36870.45	14479.64	36541.25	15115.89	30731.6	8326.75	44425.55	1542.13	31971.85	9419.3	39624.8
M90299_at	2278.45	771.38	1324.2	1529.9	2329.9	725.92	3051.25	792.88	3178.35	9.12	3320.2	645.31	2721.2	1150.46	2832.6	1059.39	1214.75
X14968_at	227.55	147.15	47.5	54.87	546.6	320.89	211.9	190.78	169.6	52.89	342.35	146.58	141.85	34.15	147.7	92.77	340.9
X03066_at	938.9	332.76	324.8	375.33	1144.6	372.79	546.4	198.27	451.5	10.47	756.05	362.39	988.7	299.53	649.8	106.91	861.05
J05068_at	445	322.44	55.65	64.28	94.65	16.76	254.2	82.45	431.7	296.98	207.1	82.59	239.7	185.12	147.4	127.28	163.05
X89984_at	445.45	211.64	456.6	527.5	271.3	217.65	304.95	289.14	558.55	704.63	169	76.08	440.5	129.82	307	299.25	489.3

M64676_at	757.3	772.58	173.15	200.04	409.4	381.84	396.75	71.21	737.3	161.79	460.4	151.46	1052.25	417.55	981.55	36.84	344.4
S57235_at	347.65	56.64	179.15	206.97	453.1	10.75	473.45	140.78	627.9	178.9	598.75	189.86	457.5	160.65	241	41.58	406.3
HG1067-HT1	834.25	371.87	235.25	271.74	1073.15	749.89	256.25	6.72	343.1	74.25	442.2	234.9	1025.95	730.37	448.35	158.6	435.4
U25849_at	745.2	470.08	451.4	521.56	974	247.35	465.1	386.08	919.7	425.25	674.2	12.45	1021.55	180.52	390.2	95.04	837.25
Y00978_at	176.2	147.08	385.8	445.76	406.2	541.93	183	123.74	146.05	105.43	120.25	68.38	343.3	362.32	158.65	146.87	622.35
M19878_s_at	178.05	162.28	395.2	456.65	806.45	658.67	365.95	200.75	174.55	150.4	261	92.77	425.65	200.89	231.05	208.53	356.7
U57721_at	217.85	25.39	317.95	367.34	904.1	726.34	294.35	160.44	380.45	77.43	447.95	200.75	630.2	135.91	268.3	60.81	459.95
D63485_at	2656.15	231.44	1363.65	1575.5	2352.45	299.46	2285.35	26.8	2136.05	163.84	1912.5	923.76	2655.8	384.52	2157.25	299.46	2354.25
X82629_at	22.5	15.98	11.05	12.8	142.2	131.52	44.15	17.75	42.25	17.89	61.75	49.29	48.9	51.62	308.15	382.76	108.7
L22342_at	1557.3	5.94	886.15	1023.82	2213.35	483.02	1205.95	663.76	1495.2	357.94	2128.8	381.41	1821.35	313.04	1709.35	248.69	1423.4
M74096_at	193.25	122.97	393.5	454.67	912.3	646.72	332.25	291.96	366.55	213.19	684.4	109.6	522.45	73.19	222.3	204.78	315.45
AB000816_s_	85.85	60.03	365.35	422.07	174.25	174.58	106.15	89.31	160.4	69.01	339.2	276.76	281.6	313.25	50.35	16.05	72.55
J02982_f_at	633.65	526.16	370.7	428.37	478.45	45.04	433.1	221.61	202.8	75.52	415.3	217.65	828.35	50.98	279.25	124.1	687.55
U62293_rna1	1200	86.41	326.2	376.89	1646.6	438.83	1812.1	689	1421.05	630.53	817.45	272.31	1077.35	288.99	1386.65	343.3	912.4
U79667_s_at	359.85	48.3	197.4	228.11	567.45	98.36	406.45	69.79	302.4	24.32	446.7	160.23	238.05	48.72	224.25	126.93	617.5

D13315_at	3459.9	522.27	1743.35	2014.19	3998.7	840.47	2515.4	1209.44	6176.45	568.44	3471.95	3.89	4733.75	79.55	5534.5	187.95	3914.45
M24400_at	659.15	21.71	193.65	223.8	826.75	728.67	508.55	44.34	297.45	39.95	727.35	338.77	677.1	210.01	372.35	259.58	582.55
HG2702-HT2	1250.7	358.08	507	585.77	1175.05	4.6	1302.4	470.08	927.55	160.44	1489.15	747.48	1341.95	285.32	784.75	19.73	919.45
U48408_at	8104.35	1657.25	2139.1	2471.48	6436.85	643.11	8904.2	1995.88	5989.45	1541.71	9056.3	2687.29	6735.45	1496.59	6466.25	2026.36	6780.85
HG4318-HT4	1005.25	854.96	138.8	160.37	1310.1	1449.43	267.65	24.96	370.1	14.28	436.7	40.87	395.15	53.1	204.45	137.53	365.85
X91653_s_at	183.4	183.71	98.7	113.99	139.6	118.51	334.95	420.52	637.65	791.46	773.9	459.9	142.35	132.16	207.35	226.2	270.95
X81372_at	277.45	194.1	62.05	71.63	193.1	141.28	105.45	92.14	1228.4	1535.69	178.7	88.67	131.1	24.89	255.35	16.19	371.45
L02840_at	91.7	11.17	348.65	402.84	192.15	123.11	455.15	505.37	99.05	33.16	671	704	642.6	58.27	376.35	405.38	88.15
U12465_at	39142.35	30426.59	14754.95	17047.57	63582.7	4526.76	55879.55	19541.95	68130.7	8805.6	46209.7	4777.35	51058.95	32589.77	58641.2	7372.29	45238.15
L37882_at	626.15	557.7	804.75	929.77	790	5.09	361.05	114.9	630.1	479.98	817	751.09	1854.8	699.33	1162.1	773.57	358.85
U65928_at	535.35	256.33	375.95	434.38	910.8	560.74	575.8	679.11	617.1	79.9	788.45	548.36	684.6	167.87	450.95	8.98	647.6
M92303_at	1046.8	316.22	666.6	770.18	1118.7	48.93	1046	349.74	1358.35	416.42	1062.9	203.51	1570.6	466.27	1337.4	236.17	1422.45
AB002380_at	377.25	220.55	110.35	127.49	544.15	532.52	678.25	888.2	375.55	19.16	540.25	188.44	280.2	147.08	743.9	635.41	515.9
X83127_at	612.4	560.59	354.95	410.05	299.4	25.74	654.85	273.3	837.8	644.46	844.9	687.31	532.25	412.74	392.8	133.93	522.25
X92762_at	1364.4	737.09	1704.25	1969.08	1115.75	101.47	1487.5	109.32	1524.8	544.61	1519.45	180.52	1148.85	612.85	1521.05	881.83	592.9
M87339_at	614.9	206.62	605.2	699.19	560.45	96.1	431.6	117.8	988.5	598.64	367.75	132.87	876.55	534.64	789.85	374.55	717.55

M19684_at	212.6	59.68	41.6	48.08	223.65	31.61	327.65	233.98	699	373.07	188.9	83.01	276.85	65.83	155.15	76.16	178.25
X51801_at	425.7	318.34	445.3	514.49	297.5	233.2	397.6	414.93	167.35	9.12	317.95	94.54	691	678.82	723.1	738.22	667.75
U65932_at	388.45	424.33	287.65	332.41	295.15	14.92	1029.95	1146.43	563.45	397.32	565.65	96.1	261.45	210.51	703.3	300.66	692.55
M74715_s_at	1607.9	25.74	189.55	218.99	1216.5	1083	2344.6	1343.08	1328.45	644.81	990.15	280.08	1256.65	754.27	1068.8	132.23	1163.9
U24704_at	2270.95	1169.06	1589.8	1836.78	3738.45	478.92	2595	516.05	3414.7	78.49	2860.75	313.04	2313.8	913.44	2403.8	1488.04	2940.4
M86737_at	3128.9	181.59	1843.1	2129.52	2177.05	944.48	2808.95	538.6	2337.9	922.77	3178.7	518.03	2389.6	152.31	3433.75	1822.99	3287.75
HG3578-HT3	156.1	10.89	220.95	255.34	341.7	315.65	862.15	774.92	127.95	11.38	233.55	240.35	499.2	528.92	98.85	37.83	599.35
HG3255-HT3	693.65	216.3	366.5	423.42	1188.6	370.1	1290.75	621.76	1568.15	861.61	522.65	286.31	1292.45	558.69	1388.2	16.26	434
D00762_at	3158.65	541.43	1836.8	2122.17	2668.65	442.3	1657.6	722.24	2893.15	846.34	2488	1494.26	2646.1	633.43	2764.7	126.85	2236.5
U89916_at	221.9	4.24	248.45	287.01	168.05	105.01	190.75	90.72	438.45	552.6	762.55	730.37	194.25	114.34	259.55	238.22	209.85

U89336_cds6	657.15	53.95	563.65	651.17	845.05	1030.89	895.45	646.65	648.75	46.17	950.65	57.49	697.05	32.74	1200.9	990.66	480.5
M15182_at	1029.65	304.98	731	844.57	1632.8	246.5	1733.65	712.55	991.55	165.25	1699	377.45	1117.75	579.76	1531.35	269.2	1111.55
Y08564_at	77.25	5.3	59.3	68.45	83.95	26.52	125.35	120.14	55.8	37.9	158.15	82.66	106.45	15.49	239.4	275.49	120.4
X07834_at	361.3	142.41	41.6	48.08	49	30.69	234.85	45.18	369.6	402.77	182.85	132.16	168.3	159.66	81.95	79.41	75.7
X55733_at	3654.85	596.44	1804.5	2084.83	3820.05	1.91	3558.2	125.72	3592.8	608.68	4785.5	889.54	4037.05	188.3	4177.3	1151.17	5157.8
AF008937_at	330.35	56.64	479.5	553.95	136.55	16.48	342.5	4.24	464.55	448.23	434.2	474.19	699.35	345.85	515	177.63	532.75
X67155_at	185.1	105.92	285.65	330.01	218.25	222.81	278.7	187.67	565.55	214.89	163.6	147.64	465.35	241.76	313.65	71.77	226.8
X17620_at	3393	1696.63	2203.35	2545.66	4596.45	733.76	4938.45	2268.61	4353.7	595.1	3684.1	110.45	3893.1	329.23	4991.25	92.42	4289.1

M23254_at	10571.6	268.7	6182.75	7143.41	7451.35	3095.36	7498.6	3297.8	12234.85	660.51	8998	4650.64	9373	3321.99	10285.3	604.86	12557
HG2271-HT2	107.1	21.64	140.2	161.93	669.9	757.59	327.3	288.64	140.75	16.9	226.15	11.81	259.75	101.61	203.4	72.12	190.6
M18000_at	86067.65	43424.49	50315.35	58133.3	107082.91	12081.91	112395.05	34716.61	112563.45	24001.11	93159.8	23827.52	99866	40200.02	115928.75	4392.61	78318.55
M58285_at	1739.8	283.69	908.55	1049.7	2185.5	157.83	2441.4	1273.5	1667.85	294.51	1747.5	402.2	1644	577.85	2526.8	282.98	2367.25
U47414_at	356.35	103.87	318.55	368.05	721.3	249.33	260.7	96.73	504.8	68.02	825.8	155.99	428.55	93.83	811.35	656.97	324.2
D86550_at	64.35	60.88	552.85	638.73	64.5	5.94	761.3	655.77	435.05	541.01	688.6	164.05	70.1	14.14	954.6	287.93	600.9
U52700_at	177.95	46.88	29.3	33.8	1199.55	1166.37	322.4	20.79	460.05	235.82	510.95	484.16	1200.75	32.6	91.45	11.81	236.15
S52028_s_at	240.55	18.17	223.4	258.09	440.85	532.1	55.65	41.08	147.1	112.57	171.8	156.84	286.9	333.9	336.45	234.12	376.1
J03764_at	17388.7	6390.12	4412.2	5097.82	8301.45	2357.28	8575.15	2739.4	11271.5	1076.64	8146.9	3184.95	11982.25	6679.4	8904.65	2706.59	22733.45
M33764_at	22025.6	4659.41	17551.25	20278.34	12357.15	4869.21	19876.85	7649.13	19452.8	2539.64	19708.2	8124.37	25766.4	5106.3	18746.15	1203.85	22009.6
X91911_s_at	1888.05	117.45	1175.6	1358.21	1621.95	662.21	1321.55	668.15	1288.35	118.58	742.85	345	881.2	394.28	705.25	53.67	494.9
D90359_at	220.5	173.1	163	188.37	1016.85	1130.88	299.55	152.38	200	32.39	948.05	908.42	281.4	21.5	173.4	61.09	387.8
U67122_s_at	910.25	133.71	444.95	514.14	650.75	429.71	584	377.45	1210.25	324.49	1246.7	75.66	1379.45	81.53	1827.65	223.52	908.35
U20158_at	62.3	11.74	244.35	282.35	445.2	189.79	65.25	16.33	189.25	155.78	662.05	788.64	160.95	173.45	64.85	37.97	77.75

S77812_at	872.5	239.99	509.85	589.09	1236.15	378.51	664.85	614.55	768.4	72.97	1193.45	140.93	1040.7	141.85	590.75	266.79	904.95
S81294_at	37.05	10.11	66.6	76.93	327.8	174.66	99.3	80.75	315.65	393.22	142.75	138.38	151.55	97.51	205.1	86.69	48.55
U33838_s_at	1211.25	69.08	956.85	1105.56	913.4	216.37	585.75	60.32	365.55	160.87	1434.05	171.19	812.15	297.06	670.1	144.11	942.05
L47345_at	2644.65	762.76	512.25	591.78	1799.6	778.95	2025.3	1006.35	1905.9	855.74	2482.1	1154.99	2537.15	861.89	1708.15	329.44	2732.15
X97301_at	238.45	23.97	117.15	135.41	670.45	142.34	171.5	136.9	654.95	127.49	172.45	102.04	105.5	1.56	152.9	3.25	331
HG3431-HT3	49.75	33.45	55.25	63.85	175.75	46.6	294.1	392.02	102.9	44.41	86	8.2	79.85	33.16	271.45	292.25	194.05
U51241_at	851.35	429.28	374.6	432.75	402.7	372.22	515.7	325.55	374.75	237.52	638.8	98.85	587.45	35.28	466.6	192.19	637.35
X64643_at	146.25	55.79	214.35	247.7	639.2	520.15	98.95	47.45	153.45	25.81	258.65	51.41	131.7	6.36	200	197.42	238.9
X04366_at	4990.05	125.09	2526.05	2918.58	3805.55	1094.25	4921.6	435.58	4776.5	1239.84	3233.7	927.16	5295.85	206.26	3194.65	79.27	6187.45
U78313_at	1727.35	357.3	759.5	877.52	1101.35	269.9	661.65	205.98	1519.3	571.48	902.5	400.93	1356.75	769.4	1299.15	22.13	1743.1
U72661_at	1609.15	708.31	979.9	1132.22	2643.15	184.91	2737.65	105.71	1711.4	439.25	2017.75	449.65	1401	1611.5	1609	484.65	1801.05
S75463_at	9239.7	5512.6	3908	4515.16	10597.75	4646.89	9256.6	1994.61	9786.75	4076.82	9341.15	55.51	8550.3	466.69	8704.55	1594.03	8571.25
D16815_at	310.2	364.02	131.8	152.31	150.6	170.27	104.9	30.55	262.05	280.23	199.15	69.51	76.65	58.76	174.35	95.67	148.1
L08096_s_at	1176.65	908.7	870.25	1005.44	1143.95	549.78	1024.55	259.44	850.05	818.19	864.45	233.42	1206	196.43	848.3	499.36	1263.65

D15049_at	325.7	19.09	152.85	176.56	474.55	110.24	1490.45	1643.1	1035	677.13	1814.3	1989.23	1026.3	208.88	865.8	162.63	655.7
U22815_at	100.4	1.84	55.75	64.42	392.25	435.22	105.45	96.66	392.45	139.23	190.45	53.39	342.1	302.64	425.1	424.97	80
X52889_at	2197.7	52.75	1214.6	1403.32	2594.95	1147.28	1769.55	745.93	1711.6	520.15	2752.35	495.61	1926.25	1205.83	1187.5	970.86	2556.1
U30827_s_at	1137.55	555.86	626.9	724.36	1011.15	295.92	817.45	429.85	947.8	29.98	643.55	58.62	1003.65	3.04	919.15	199.19	1027.7
HG4109-HT4	539.1	494.55	324.2	374.63	862.4	632.72	192.1	60.39	843.8	317.49	727.65	175.57	650.75	558.97	521	438.55	1127.25
U34343_at	2490.25	50.7	1604.55	1853.82	2862.05	604.93	3441.7	445.48	1962.65	844.36	3343.7	542.07	2458.35	115.47	2456.25	315.44	2111.95
M10277_s_at	161252.45	42251.4	69023.7	79748.49	133027.55	46215.44	115891	5430.44	144166.2	511.66	105156.1	5554.32	130589.1	17772.14	119140.95	41477.12	159520.75
M94077_at	138.2	0.57	98.4	113.7	205.3	188.8	286.5	120.49	146.85	27.51	207.95	118.02	252.05	61.45	185	40.45	167.5
HG4340-HT4	31.95	8.7	123.45	142.62	405.05	91	233.85	302.43	60.45	10.54	448.15	153.09	153.55	136.12	312.55	401.57	32
J05500_at	1537.75	704.07	1044.5	1206.75	1935.55	334.25	1692.85	897.95	1360.3	254.7	1357.15	519.09	1920.1	25.6	1358.15	101.75	903.3
U01691_s_at	4066.7	1121.05	1588.45	1835.3	2686.55	2747.89	3416.6	91.64	2818.9	1428.78	3065.95	147.71	3295.75	540.58	2956.3	877.94	3780.05
U52100_at	558.85	278.11	262.1	302.78	659.6	67.32	254.75	228.18	561.6	18.53	157	72.97	811.25	76.86	634.35	669.7	674.95
D55643_s_at	272.45	49.14	54.25	62.72	609.45	820.17	429.1	491.58	189.05	111.23	257.8	137.46	81	66.75	314	247.49	403.8
U50062_at	693.4	105.08	656.3	758.3	607.4	76.23	540.8	191.48	936.95	621.19	436.7	412.81	553.85	224.36	940.35	61.45	1005.4
U90313_at	7866.75	2059.87	3657.8	4226.09	8457.95	1216.86	7809.65	1871.22	7632.45	1193.81	5897	389.19	5588.2	1251.86	5820.05	66.54	6789.95
M58378_cds:	2952.35	69.08	1415.25	1635.18	2301.8	460.89	2630.1	258.38	2571.4	285.25	3875.45	372.72	3768.8	972.41	2112.1	2006.2	2330.75
HG4116-HT4	469.55	423.2	78.85	91.15	219.1	65.9	352	166.17	241.85	42.64	307.8	114.98	291.1	14.28	485.2	482.67	446.45
U16282_at	1363.9	471.64	288.15	332.98	2660.85	2275.68	2261.75	1394.63	1578.45	459.12	1181.2	1179.6	2712.65	213.33	2154.9	407.43	2340.4

Y11180_at	312.25	247.84	74.3	85.84	264.5	63.07	605.5	585.06	191.4	138.17	62.7	6.65	445.75	425.47	406.95	225.64	167.95
L27080_at	531.85	12.09	270.05	312.05	620.85	204.99	517.55	65.12	403.65	101.47	624.65	72.48	535	11.74	528.15	100.2	469.35
HG4704-HT5	1566.05	693.88	1415.2	1635.11	1122.3	442.79	1682.05	344.29	1487.4	70.71	1412.1	705.83	803.65	44.05	1153.3	53.32	1116.45
L05148_at	244.45	64.7	499.25	576.79	994.2	773.57	232.3	84.57	675.85	741.97	370	117.38	384.55	13.08	877.6	809.07	345.95
M65214_s_at	1947.9	122.61	688.25	795.14	2213.65	714.25	1902.8	481.68	1790.1	1150.75	1469.75	404.68	1772.55	93.13	1882.15	82.8	2160.3
U50939_at	989.4	208.46	848.1	979.91	1018.65	249.96	747.75	163.98	1371.75	243.17	1397.75	20.72	1273.3	142.69	946.1	182.86	921.85
X87344_cds1	5661.25	230.16	870.1	1005.36	2368.15	772.37	3352.85	2053.79	1926.8	1430.62	3080.05	1668.14	3020.5	2570.9	5719.5	1789.12	1049.05
U65581_at	714.2	462.87	153.55	177.41	1472.8	596.09	1655.4	1222.02	279.95	88.32	1057.7	1353.12	960	866.91	1382.3	497.8	1680.5
U79273_at	264.75	201.03	163.85	189.29	322.9	220.33	604.55	679.88	225.65	38.96	196.8	48.08	152.1	35.21	120.5	71.42	198.8
D83646_at	638.65	317.84	670.05	774.21	541.7	155.7	338.65	206.83	366.6	295.71	1466.5	411.25	242.85	271.18	1534.2	188.09	693
HG2229-HT2	67.45	16.62	27	31.25	98.65	9.55	109.75	50.42	104.85	42.5	110.9	27.44	82.15	20.29	65.6	4.81	49.95
Y09305_at	1042.25	232.57	503.8	582.09	1303.05	133.15	1307.5	351.15	1059.8	436.14	901.5	79.2	1508.2	464	1134.5	1327.66	761.25
X66276_s_at	170.45	10.82	367.8	424.97	617.1	387.92	408.6	233.49	568.25	274.99	330.3	203.36	185.75	138.52	302.6	228.96	148.95
U40992_at	242.8	197.99	67.85	78.42	270.5	137.89	129	128.98	482.2	160.94	217.65	230.73	312	60.53	355.95	289.14	565.05
HG2873-HT3	64189.95	33752.82	30875.9	35673.4	89221.34	4955.33	87871.05	29754.7	85140.95	20764.83	71047.05	15175.29	66733.9	20108.56	74097.05	2807.99	58790
S62907_s_at	222.7	301.23	15.15	17.47	81.05	70.78	57.55	47.31	62.25	62.86	37.1	23.48	79.4	42.85	282.45	332.69	96.55
HG3405-HT3	611.2	234.05	281.45	325.2	560.1	137.32	148.4	46.1	101.9	16.26	780.85	727.83	210.3	200.25	210.85	88.88	181.55

X79440_at	104.75	51.12	88.15	101.89	161.7	96.03	109.15	97.09	75.3	18.67	404.85	386.01	51.15	45.04	200.15	154.08	76.95
M14745_at	327.3	107.62	273.35	315.86	593.35	619.64	454.45	440.88	379.05	21.28	782.65	500.14	437.35	45.75	202.3	38.18	288.6
L08069_at	2778.35	137.67	847.4	979.06	1689.15	739.85	1975.5	1172.38	2728.25	552.04	1963.45	257.46	2378.1	730.72	3033.8	699.33	2399.2
J04111_at	338.8	94.47	163.15	188.44	522.15	76.86	702	620.27	689.35	40.66	525.2	204.07	462.5	160.8	267.9	325.41	568.5
Z31560_s_at	1816.05	370.59	554.6	640.78	1930.6	49.5	1497.15	646.79	1527.85	253.5	1589.45	13.08	1961.5	440.1	1433.05	331.56	1314.1
U12535_at	206	171.4	270.7	312.82	216.6	149.48	63.55	8.13	180.1	162.07	161.55	174.58	379.6	371.94	510.25	39.81	95.75
M29335_at	5680.1	2308.42	2049.1	2367.53	2739.45	1514.98	4714.95	2980.95	4260.2	458.35	3391.2	583.36	4813.25	101.75	3898.15	2304.39	4228.7
D76435_at	114.4	18.95	22.5	26.02	216.35	119.85	175.25	194.38	313.75	57.63	523.45	292.53	300	345.07	98.1	78.21	223.75
D84110_at	1698.1	14	805.25	930.34	1873.7	573.32	1861.2	581.81	1644.05	27.37	1770.05	541.43	2040	526.79	1562.95	434.23	2099.6
X91504_at	6300.85	547.23	4617.55	5335.05	7055.55	639.72	6802.55	2138.5	6882.4	71.42	8819.05	1570.27	6738.95	399.59	6359.5	1385.65	6551.95
U43901_rna1	71673.45	26253.67	45376.45	52426.95	90895.55	12944.22	104462.6	15630.74	68809.25	15523.89	73355.15	1376.24	68928.4	13320.62	77097.3	3546.85	72083.75
HG1116-HT1	4327.35	650.89	2763.15	3192.52	3915.8	770.32	4052.1	317.07	4181.25	528.85	3884.55	82.24	4235.8	125.16	4360.6	469.94	3791.55
M94893_at	388.35	20.15	114.9	132.79	282.55	168.36	215.5	137.89	368.05	105.71	270.6	235.04	678.25	470.3	418.15	371.87	718.9
S69265_s_at	1024.2	410.69	481.55	556.42	1616.35	1451.05	1372.1	764.81	1027.25	247.56	511.15	109.81	1445.95	546.81	856.4	514.92	362.8
U62136_at	539.4	334.6	781.4	902.83	510.2	13.58	608.65	26.94	771.95	199.62	1003.3	566.39	876.2	172.39	1272.1	50.2	860.65

U16812_s_at	1315.45	265.24	751.2	867.9	1520.25	481.75	1906.9	1419.16	1430.4	621.26	1408.1	248.48	1100	336.58	1303.9	722.52	1733.6
M31951_at	402.95	1.77	138.05	159.45	377.6	203.36	238.1	35.78	220.4	103.94	477.9	97.72	451.4	81.46	218.5	97.16	229.15
Z70759_at	51511.3	20074.34	16631.3	19215.48	86544.5	23752.42	63381.2	46736.93	59615.05	21491.45	84848.2	42847.14	55570.05	37900.71	63127.85	52716.15	73677.35
X57351_at	12067.6	2091.34	5559	6422.79	8606.4	918.53	9964.65	2343.85	10292.3	1866.2	11741.5	3833.23	10062.85	465.21	6973.25	3569.12	10044.3
U56244_at	319.05	1.06	232.15	268.21	409.4	277.61	1220.7	1548.28	121.4	81.88	775.35	623.6	530.9	221.75	800.15	68.38	215.45
X01388_at	2821.7	731.01	1964.05	2269.18	4454.65	502.54	3781.25	1137.81	2730.95	47.16	4047.3	474.04	3819.7	611.79	3131.2	526.37	3481.35
Y10202_at	140	136.75	26.4	30.55	145.4	161.93	41	15.27	63.9	59.54	173.3	217.51	235.95	169.21	282.1	313.96	66.15
J04027_at	515.45	256.04	751.8	868.61	359.05	203.72	232.65	207.11	577.6	680.24	1124.2	70	740.95	358.29	560.8	19.94	567.4
S79854_at	256.5	15.84	67.15	77.57	219.45	8.27	258.85	222.24	176.5	81.74	192.4	1.7	185.7	0.14	273.4	88.39	196.15
L24564_at	104.8	24.89	77.9	89.94	137.75	23.97	130.9	24.32	144.95	64.13	186.3	175.22	162.3	18.53	177.6	108.05	119.3
L27559_s_at	49.35	24.82	133.15	153.8	182.75	125.37	125.8	133.08	166.25	154.22	60.75	23.55	60.65	16.33	234	278.46	100.2
U34605_at	728.15	443.29	474.9	548.71	1089.05	497.59	842.4	301.79	1037.6	467.96	683.85	323.36	728.55	333.4	469.15	69.79	854.6
L27841_at	1308.9	388.06	821.6	949.22	1308.65	72.34	1125.2	266.58	966.8	370.24	776.1	686.18	792.6	178.19	350.8	4.53	1110.85
U77827_at	1934.75	244.73	1046.85	1209.51	1302.1	61.94	1684.9	560.03	1079.9	204.64	1405.9	159.95	1650.15	50.42	2045.6	163.06	1790.15
X78712_at	116.65	87.47	62.4	72.12	399.45	436.07	126.5	69.86	59.3	17.68	73	4.1	117.75	8.56	58.45	24.4	228.2

X07173_at	456.8	400.93	229.3	264.88	314.85	94.12	514.35	109.25	247.35	67.81	323.75	372.57	601.25	178.69	242.55	212.77	544.25
X86371_s_at	1593.55	642.27	1028.2	1187.94	1178.45	486.84	1208.45	306.81	1112.1	87.54	1447.45	304.41	1572.85	509.33	1691.55	141.07	1451.6
U27330_at	1074.45	71.35	396.2	457.78	1199.4	1145.09	737.55	163.7	1219.7	707.53	1030.25	664.33	1701.9	238.58	2045.9	1470.64	1133.4
Y08765_s_at	2411.6	1898.3	416.1	480.69	705.4	154.71	1338.1	581.52	658.15	202.02	436.5	200.68	1073	394.28	862.8	136.05	1156.55
M29277_at	1406.25	658.25	57.2	66.04	3299.9	3294.83	2324.5	626.07	4041.45	90.3	4601.95	5231.53	1416.15	554.58	1178.7	1132.36	1434.75
D13748_at	30625.35	5144.56	16633.85	19218.38	29810.4	9084.06	32548.45	9895.89	30976.55	5597.39	27110.4	5331.44	34794.2	4683.17	36425.95	6858.16	33974.3
L07515_at	383.15	439.33	80.9	93.48	93.05	80.96	116.15	1.91	74.55	5.87	123.8	30.26	464.1	41.72	508.7	309.01	380.9
U73328_at	213.9	78.63	612.4	707.53	440.4	471.64	150.55	158.89	745.6	764.1	492.2	254.84	440.65	332.13	519.15	560.66	619.3
L14848_s_at	2581.25	576.08	2063.35	2384.01	1050.2	704.7	2628.15	263.54	1509.8	977.79	1914.45	240.77	2624.65	1036.69	3346.65	740.98	3022.65
U47742_at	1253.2	269.97	719.05	830.78	960.5	153.87	933.35	538.89	572.45	456.72	1617.7	63.5	1072.7	225.43	540.25	445.27	1484.05
Z83735_at	142.25	115.05	279.9	323.43	46	7.92	58.4	4.1	212.5	254.13	160.55	15.49	303.4	79.05	66.4	40.73	77.75
X85134_rna1	132.25	159.45	80.75	93.27	334.45	243.17	114.55	83.51	148	117.95	168.35	119.29	332.2	347.9	159.35	188.02	350.3
U34038_at	3859.5	638.94	2017.05	2330.41	2531.9	214.54	5038.9	1172.1	2434.85	370.45	3798.2	905.8	3592.6	210.86	4279.8	139.87	4037.75
X67734_at	1647.85	592.06	400.45	462.66	2659	952.19	1611.25	219.84	1602.15	815.36	1737.2	1325.83	1713.45	881.97	2650.2	2380.12	2010.9

S77576_at	873.45	432.54	418.3	483.24	790.1	371.94	746.2	297.55	285	123.6	623.2	646.86	858.8	52.61	383.95	159.59	434.95
D49493_at	73.5	11.31	75.6	87.4	135.45	125.94	50.15	25.67	269.35	266.08	66.9	39.74	44.65	4.45	55.6	17.68	79.5
L02785_at	34.85	21.99	29.65	34.29	280.45	353.06	95.3	4.1	71.65	59.75	125	16.12	375.25	474.68	334.45	371.02	110.5
HG2809-HT2	2600.35	662.91	1479.25	1709.15	2396.45	1088.03	2125.35	649.48	2217.35	421.36	2684	685.75	2297.25	467.61	1852.4	1250.02	2446.6
U09367_at	139.8	98.71	59	68.17	462.05	507.77	185.7	51.19	250.05	56.64	106.35	15.77	207.45	23.83	200.05	11.24	158.6
X85786_at	1342.4	395.13	1124.4	1299.1	1069.4	465.7	1263.6	116.81	1581.85	261.28	1467.45	33.87	1016.95	255.9	1792.75	807.3	1428.35
D87446_at	735.1	96.59	899.55	1039.38	596.5	178.9	441	515.48	1671.05	159.31	1281.1	552.53	967.05	559.96	1566.2	195.73	1564.95
U57629_at	234.35	265.66	245.45	283.62	200.55	227.48	129.1	145.1	164.8	116.39	585.55	176	161.3	62.51	29.45	1.06	66
X66365_at	736.65	526.3	65.7	75.94	648.8	155.14	1289.3	345.21	147.35	54.52	442.75	260.85	394	185.26	1510.3	1907.63	1175.35
U07132_at	2964.85	737.87	1155.75	1335.37	2501.75	1185.18	2559.7	707.25	2251.8	910.19	3476.55	182.08	2620.35	6.01	2609.8	100.55	2950.1
U63295_at	188.35	148.99	43.75	50.56	249.35	28.64	268.8	136.33	537.9	9.05	1118.5	645.16	331.45	380.35	495.25	625.01	70.65
X77197_at	307.65	145.03	9.9	11.46	394.55	470.58	509.2	559.46	279.4	238.15	217.1	64.77	254.85	194.24	322.3	361.33	225.45
J04982_at	318.8	162.35	254.25	293.8	724.5	941.58	182.2	154.57	100.75	16.9	154.5	101.68	457.45	554.87	432.75	572.83	378.4
D31889_at	398.9	148.92	433.9	501.34	193.85	154.93	149.1	90.23	258.9	86.97	500.55	78.42	136.8	29.27	578.9	605.42	294.05
Z68274_at	1065.85	4.6	280.7	324.28	260.8	92.35	1177.6	635.83	507.15	314.31	453.9	80.75	485.45	4.17	687.5	329.51	957
HG1112-HT1	11413.75	1025.94	8326.2	9619.9	11242.85	700.67	13661.55	8177.05	11458.05	1449.22	11517.65	2503.94	10932.9	452.83	11332.55	1769.82	9446.85

Y10515_at	51.85	56.07	32.65	37.69	126.75	96.24	118.5	117.38	264.85	337.08	164.75	150.54	222.05	61.73	211.8	271.81	70.85
L34219_at	215.4	164.05	403.15	465.77	362.15	203.29	501	490.17	370.7	364.87	493.45	204.28	244.95	81.53	202.9	3.11	309.75
U90306_at	1265.05	202.87	381.75	441.02	1699.35	771.81	484.6	38.61	997.4	1198.69	812.05	83.37	1290.1	199.97	764.2	753.78	1479.8
U49395_at	1776.9	375.05	576.75	666.31	1341.35	1288.84	1357.75	98.5	1419.4	488.47	1826.35	1168.92	1463.95	744.51	727.2	313.39	2130.95
AFFX-ThrX-5	73	1.7	45	52.04	181.95	120	68.2	0.99	444.5	442.79	289.45	30.19	121.35	57.49	216.95	190.99	102.05
X06290_at	142.9	71.56	189.5	218.92	391.5	476.17	641.95	604.93	165	86.83	349	392.02	221.25	36.84	148.3	133.64	49.25
U46569_at	2021.3	364.87	647.7	748.4	2033.35	491.09	1393.3	550.84	1588.3	810.63	2448.5	601.04	2241.95	281.36	2137.05	271.74	2012.25
HG4518-HT4	1214.65	700.67	232.9	269.12	597.85	516.82	975.4	211.71	697.1	191.06	822.6	105.64	739.35	859.06	960.7	136.05	1152.9
L33404_at	1252.6	375.62	598.65	691.62	508.15	320.81	1270.05	443	2251.65	728.81	1622.35	27.22	2721.35	452.62	2560.55	901.35	1776.6
U83239_s_at	4004.65	972.06	1687.9	1950.2	4790.4	100.41	4609	314.66	4798.7	1236.02	5325.55	1118.71	4445.85	1203.28	4923.6	240.27	4775.35
U62389_at	934.85	154.5	469.3	542.21	712.95	743.38	1787.75	500.28	1517.85	245.3	1364.05	118.02	1340.55	149.84	1370.8	384.52	1288.75
U49188_at	2224.15	727.83	151.25	174.73	2600.9	749.25	1785.25	1226.76	1729.45	105.57	2410.45	167.66	1885.05	1351.92	1575.7	827.46	2139.65
AFFX-HUMIS	670.2	203.36	293.4	338.99	392.4	231.22	340.5	372.36	508.4	331.77	667.2	349.17	612.9	229.67	454.75	279.1	189.25
HG3175-HT3	984.3	395.13	429.95	496.74	1961.75	1101.46	1604.4	644.46	1361.75	510.6	1807.9	1040.72	1658.1	7.35	860.4	498.51	1230.1

M69203_s_at	92.15	2.47	69.1	79.9	119.45	55.37	336.25	350.8	123.45	80.4	170.4	151.46	114.95	7.57	102.4	8.49	128.55
L03785_at	1362.25	40.09	584.65	675.5	1247.15	94.4	1256.25	242.75	905.05	519.94	1387.05	316.57	1205.3	167.16	1348.25	251.09	732.55
L07592_at	958.05	966.4	384.25	443.99	540.9	340.68	965.2	871.3	1430.15	15.77	743.45	53.67	923.5	454.25	757.45	809.71	1497.95
X52003_at	207.55	50.84	89.6	103.52	158.45	26.38	295.95	122.68	207.95	77.29	268.25	103.45	507.45	563.35	139.85	42.92	559.7
X65727_cds2	231.45	143.9	111.6	128.98	113.75	74.18	195	32.95	211.95	25.67	351.85	59.04	129.95	66.11	445.95	329.58	319
Y00796_at	1946.8	421.86	1809.85	2091.13	1288.35	106.28	2180.7	1072.96	648.05	223.23	971.5	230.23	1711.3	497.94	2020.7	551.97	1552.1
M24122_s_at	990.35	67.67	587.1	678.26	881.5	151.18	742.8	74.95	1291.7	1573.17	388.55	162.42	1393.35	1464.49	420.9	70	819.4
L33262_s_at	333.6	143.4	20.35	23.55	169.8	134.21	710.35	873.63	90.55	9.12	147.9	79.05	60.25	12.66	129.7	90.37	76.3
X52142_at	811.15	188.87	765.45	884.38	828.55	13.51	1177.05	822.15	924.7	2.4	450.3	504.45	506.95	546.1	1167.75	216.87	1491.1

3 dmso - Stdev	3 15 - Average	3 15 - Stdev	3 60 - Average	3 60 - Stdev	3 120 - Average	3 120 - Stdev	4 dmso - Average	4 dmso - Stdev	4 15 - Average	4 15 - Stdev	4 60 - Average	4 60 - Stdev	4 120 - Average	4 120 - Stdev
219.13	35.2	22.91	49.1	3.25	173.55	217.01	161.8	183.99	48.4	10.75	484.8	634.84	309.8	69.86
158.39	116.35	128.34	120.8	122.05	472.65	633.92	241.7	82.17	579.6	376.04	269	44.41	152.35	65.97
1.06	52.1	26.59	78.75	11.1	82.45	55.65	161.9	61.09	94.7	53.03	164.55	90.86	113.65	66.11
335.88	266.4	146.8	294.3	186.25	333.1	20.79	911.7	640.5	361.2	9.62	446.9	284.82	446.45	79.97
119.71	225.4	94.89	218.85	104.16	322	227.26	261.35	43.35	206.65	96.38	227.4	165.04	318.05	50.84
53.46	331.05	27.93	337.05	19.45	512.15	448.94	284.45	129.19	472.75	364.51	437.15	149.27	632.2	764.24
14.21	243.9	194.74	253.55	181.09	320.1	308.72	287.95	19.59	230.15	107.69	378.2	347.61	406.8	203.79
135.84	162.65	84.78	132.65	42.36	725.45	780.43	1119	1082.44	555.3	303.77	273.4	27.29	136.2	94.05
50.06	133	9.19	132.45	8.41	157.85	155.35	842.95	1112.21	614.65	819.32	299.45	148.14	645.9	309.57
319.4	188.6	67.03	299.55	223.94	625.05	385.44	848.7	553.52	371.95	401	976.7	781.78	325.95	352.63
418.32	1641.95	802.35	1702.3	717.01	1250.95	10.54	1862.75	911.25	1006.75	457.85	1401.55	702.79	1749.8	20.36
79.05	727.85	197.92	659.7	101.54	294.7	213.97	389.45	400.15	616.55	212.49	450.8	136.05	428.4	106.91
22.42	183.4	17.82	249.2	75.24	961.45	712.13	610.95	205.84	226.65	66.26	232.1	176.49	286	35.36
73538.13	154775	123306.41	184190.84	81706.12	146094.55	86852.73	150623.16	127296.27	182591.69	16994.75	174275.69	9199.6	144228.7	33831.11
647.64	346.95	142.06	355.7	129.68	1473.55	1344.99	895.35	538.89	519	129.12	1345.75	1589.36	606	521.28
7.42	51.3	5.66	46.5	1.13	111.85	146.58	173.1	183.56	155.65	33.45	674.75	885.09	184.9	182.43

403.69	559.1	415.64	849.1	5.52	1105.15	1019.44	1791	1512.93	1506.9	522.83	464.55	95.11	1754.75	168.64
97.65	622.8	168.86	658.35	118.58	1250.3	806.24	591.4	216.37	1409.35	986.34	443.75	318.83	1002.05	81.11
384.67	880.4	955.3	943.75	865.71	1356	1583.78	303.65	215.6	245.15	34.44	516.15	412.74	219.4	38.89
87.26	4054.8	892.65	4039.75	871.37	2980.8	184.41	2098.2	14.99	3500.9	737.23	2631	571.77	1755.45	390.11
119.36	445.45	191.27	555.6	347.05	347.8	147.5	1380.55	275.84	855.4	28	737.7	491.58	634.45	186.61
2688.28	5543.1	751.37	6635.75	2296.61	4426.9	2674.42	5705.45	2543.96	3241.5	1819.24	5161.75	1750.44	4663.95	228.18
97.23	190.55	60.88	134.25	140.5	94.45	110.8	264.55	93.83	241.9	228.11	893.85	1126.49	129.35	58.62
273.37	419.15	148.99	289.75	331.99	388.35	137.96	1970.05	2352.19	886.1	81.6	477.15	517.67	655.55	22.84
68.87	476.05	340.75	477.4	338.85	290.8	334.74	698.6	529.2	449	434.3	1035.1	1285.52	1122.75	1310.62
58.48	384.05	292.81	438.65	215.6	223.1	81.03	467.6	445.9	396.25	191.56	253.05	11.53	452.55	9.97
36.27	664	863.09	665.55	860.9	303.3	296.56	614.55	655.13	238.1	2.4	165.95	161.43	96.4	40.16
1424.82	3070	349.03	3185.3	185.97	1932.1	269.12	2042.2	135.76	2429.75	228.61	2249.55	1543.97	2417.7	679.25
1.48	86.3	93.06	109.95	59.61	87.05	47.16	132.7	31.25	119.65	4.31	207.3	90.65	151.1	131.24
494.06	869.65	886.64	862.7	896.47	279.1	219.77	353.6	58.69	902.6	425.4	630	544.05	1242.05	50.28
17.61	405.95	92.28	286.95	260.57	212.45	139.51	1469.95	1654.28	211.4	11.31	1635.15	1175.85	542.05	550.48

8.77	297.85	273.16	400.4	128.13	54	3.54	1100	905.24	503.9	28	847.3	17.11	513.05	323.36
53.53	411.3	316.22	551.75	117.59	196.9	88.81	186.05	14.21	395.15	59.47	304.95	192.4	753.9	743.73
52.61	800.75	253.5	566.7	584.49	339.75	130.46	713	556.63	647	578.55	618.85	196.65	761.4	629.61
48.22	72.05	28.35	36.4	22.06	99	26.02	412.05	461.25	492.4	611.93	141.8	63.78	378.65	160.87
107.9	1430.2	207.89	1245.75	468.74	1024.2	986.56	1111.6	68.02	917.95	537.47	2037.8	626.21	1417	801.01
68.45	493.15	369.6	608.05	207.11	275.8	61.94	291.6	103.94	51.65	27.08	990.9	1031.81	214.75	40.66
25.03	155.65	80.68	175.4	52.75	193.3	78.77	286.1	95.6	203.3	19.94	299.55	151.53	531.35	441.73
42.85	231.8	52.89	231.15	53.81	754.4	804.4	481.05	35.85	469.25	49.43	930.7	726.48	706.5	461.03
968.03	449.55	110.38	781.85	359.56	784.5	487.48	902.85	776.62	1841.25	1075.58	1256.65	1035.98	1170.2	1108.74
30.33	81.9	30.97	50.45	13.51	128.55	30.05	131	136.05	113.35	111.65	443	525.24	401.05	485.43
19358.74	133551.3	91811.45	160783.84	53298.81	111493	45852.2	129276.5	63819.35	196448.2	74986.27	146853.95	98927	197103.56	40944.1
13.86	351.6	419.03	348.7	423.13	491.25	656.97	264	254.84	64.8	15.98	637.05	763.32	98.2	14.57
224.93	199.1	47.52	125.4	151.75	148.15	80.12	415.95	34.72	92.25	38.54	734.2	525.66	473	439.82
36.63	359.95	339.48	371.8	322.72	623.55	271.32	199.95	116.6	167.5	0.42	174.8	38.47	244.1	25.03

96.24	99.7	17.82	64.8	31.54	108.4	102.11	189.35	158.32	96.5	62.51	109.5	86.13	297.1	217.22
20.36	698.9	293.31	471.45	614.97	245.05	25.39	217.5	147.5	1667.55	2194.22	653.35	599.27	262.45	115.61
78.35	208	67.46	327.4	101.4	399.45	123.25	1493.4	1597.35	484.8	122.33	1598.25	1656.54	443.2	290.2
208.6	118.65	72.9	114.1	79.34	225.05	159.31	397.35	402.98	183.45	49.43	205.05	165.82	99.25	44.19
305.97	1106.95	958.2	1110.2	953.6	452.35	412.46	789.95	795.99	952.95	52.4	611.9	293.87	380.55	301.58
143.47	836.9	542.63	992.4	322.72	650.2	65.9	1131.35	1317.55	1395.35	29.77	1771.7	1140.85	375.95	40.38
72.76	40.65	8.84	59.5	17.82	181.6	52.47	293.35	91.57	54.7	15.84	178.35	10.25	213.85	119.57
712.83	2651.75	2015.75	2551.75	1874.33	2569.95	1358.85	1001.75	241.19	1528.65	181.94	1584.35	249.96	1334.25	454.74
83.51	189.6	117.24	162.8	155.14	239.05	111.79	164.4	112.01	701.5	689.29	544.15	31.89	467.3	599.91
290.41	1769.9	15.41	1502.65	362.53	973.55	596.59	1215.05	644.39	1298.3	1119.21	1101.75	525.17	946	739.49
806.17	1446.05	695.3	1315.2	880.35	969.2	618.72	660.9	499.78	2104.4	72.69	815.35	508.62	759.6	549.99
131.45	953.1	601.47	583.55	78.84	927	669.77	1326.3	1626.2	1300.35	879	1046.35	385.73	993.15	528.42
405.24	942.3	267.14	944.55	270.33	791.75	799.67	475.55	496.74	680.6	485.36	792.45	606.91	898.5	982.31
188.59	186.15	156.77	176.65	170.2	188.2	202.94	463.2	67.6	147.95	114.2	596.25	567.17	590.85	568.73

415.64	461.65	63.71	388	167.87	1128.05	867.13	316.9	148.35	968.4	120.92	302.35	254.06	393.6	89.24
52.75	458.75	243.32	330.55	424.62	116.4	7.64	330.3	270.96	423.95	425.61	391.1	470.23	261.7	157.54
758.23	499.75	99.07	720.05	212.49	697.45	663.76	1132.05	1353.61	2296.35	2380.76	592.45	401.28	869.05	724.71
206.9	485.3	162.78	557.2	61.09	1004.75	936.14	765.6	486.35	247.1	229.95	400.75	300.31	746.25	82.52
42.99	2121.55	735.46	2060.25	822.15	1547	363.88	1381.3	502.61	1297.15	414.58	2118	1280	1289.55	288
182.65	430.85	227.19	307.5	52.75	165.45	135.27	788.5	941.72	263.05	169.63	481.8	136.05	695	155.99
14.64	670.25	403.4	712.5	343.65	242.25	104.58	138.5	15.27	499.25	87.19	688.15	283.2	588.5	66.89
13.15	1140.95	193.82	731.7	772.58	908	74.39	1667.8	1429.49	638.2	285.67	1580.95	857.93	1016.15	175.15
305.54	775.8	371.66	540.75	39.24	1455.55	544.97	1113.25	740.84	771.05	830.5	766.5	549.56	424.2	113.84
118.37	444.2	118.23	353.3	10.32	748.75	505.65	1804.1	1423.69	325.5	170.27	433.95	358.43	1027.7	985.28
146.23	192.45	25.81	119.15	77.85	337.65	71.49	314.25	288.43	147	112.29	224.1	129.68	369.55	298.19
73.54	163.05	84.64	176.05	66.26	655.35	448.66	311.9	158.11	1102.9	874.41	641.65	572.69	1110.45	626.99
5.59	160.7	103.8	227.2	197.85	327.9	150.76	920.9	1129.53	614.45	462.09	976.7	718.42	442.4	291.61
287.01	700.3	396.12	899.05	115.05	564.4	525.24	1081.3	616.03	1424.2	168.86	706.9	811.05	889.8	167.3
190	282.15	63	194.25	187.31	199.95	61.87	243.05	174.3	110.55	43.63	132.7	53.46	315.25	323.93
260.57	131.7	89.94	49.7	26.02	128.95	73.04	408.7	263.47	128.05	20.44	455.45	282.21	209.35	129.47

914.5	881.75	309.08	798.9	426.24	1017.9	724.93	4147.55	984.51	2782.4	3015.53	834.15	138.81	734.8	2.55
82.94	746.75	204.14	529.35	103.31	341.2	330.78	338.65	88.6	379.3	241.69	1042.1	635.41	412.7	384.81
703.71	1883.05	78.98	2245.05	432.96	1998.85	101.47	2607.35	583.15	990.4	703.01	1697.95	1419.52	2929.6	1876.8
12.23	775.35	229.6	855.3	116.53	477	325.41	770.6	519.72	1374.6	305.47	1612.6	959.26	1446.05	824.98
89.02	334.2	292.88	275	376.61	78.25	59.61	479.25	372.01	301.5	256.54	350.25	278.39	314.1	315.51
327.32	1151.15	998.36	1261.95	841.67	555.7	293.31	330.65	32.46	69.5	25.46	349.9	214.54	186.15	134.42
243.95	2118.6	948.94	2187.45	851.57	1976.15	757.1	2599.3	1102.38	2107.15	747.62	2651.3	732	1374.15	1291.11
163.34	302.55	198.63	267.95	247.56	171.65	170.2	106.7	1.27	65.15	14.64	140.55	115.05	382.5	253
50.35	862.75	265.09	698.5	32.81	579.6	55.72	252.15	118.16	367.3	291.61	269.8	107.06	353	272.66
133.5	363.9	169.42	343.75	197.92	379.3	497.52	413.7	86.27	258.2	103.24	828.1	414.36	331.9	229.53
23.76	210.1	53.88	125.1	66.33	520.9	632.72	610.2	775.84	232.1	127.7	661.8	280.58	258.3	142.69
57.13	1603	1260.49	1390.15	1561.5	620.45	253.78	361.6	68.73	1081.75	324.21	869.8	507.7	2092.65	846.34
803.2	822.5	226.7	1306.85	911.67	1365.05	39.67	3502.55	1481.18	2002.05	530.26	1094.6	274.64	1564.75	6.29
18.6	92	69.3	32.85	14.35	622.4	811.76	794.75	771.81	95.2	36.77	203.45	169.35	175.05	9.97

47.38	653.9	20.22	704.8	92.21	1078.15	373.85	1316.35	1558.82	414.95	400.43	785.3	892.09	307.5	126.85
174.16	401.9	133.78	424.25	165.39	501.6	207.89	397.7	389.76	406.9	333.33	203.65	172.32	454.35	8.84
11.88	226.75	181.37	111.65	18.6	199.25	42.36	159.65	15.77	439.9	491.58	735.9	936.07	112.1	15.84
18.53	267.7	144.53	277.2	131.1	337.4	260.36	560.4	641.2	1015.25	746.92	361.95	235.11	564.15	147.01
425.82	2739.25	967.53	2948.9	671.04	1601.25	1532.65	2838.75	1059.32	2005.2	759.72	4859.7	2238.98	3453.05	63.71
880.28	418.4	7.35	677.45	359	1067.9	673.31	838.6	115.82	1222.6	18.24	684.25	273.72	400.45	166.38
365.01	154.8	107.9	136.75	82.38	539.75	474.26	221	110.45	224.55	62.01	160.65	121.98	224.45	202.73
121.06	206.8	202.66	185.1	171.97	310.35	49.99	925.65	1071.05	677.9	211.57	337.7	43.27	142.4	64.63
9.33	346.35	70.92	242	218.5	241.1	173.95	225.95	236.1	340.65	97.93	227.9	147.93	281.15	191.13
638.23	1589.25	200.89	1628.7	256.68	586.8	64.35	966	373.21	648.15	599.41	824.3	406.87	1191	408
278.88	508.4	303.77	472.85	354.05	100.35	73.47	256.3	47.38	244.45	277.82	334.05	447.53	278.25	326.9
538.32	2445.4	826.47	1783.85	1762.04	2758.5	1006.78	1657.25	515.55	2529.95	1348.24	1478.35	1364.36	3462.8	1527.21
333.12	878.65	167.51	814.55	258.16	1304.45	790.19	1515.2	1245.64	1749.65	1380.48	1161.25	421.51	874.15	77.57
71.35	549	123.74	643.65	257.6	918.05	354.19	331.7	251.59	1004	124.31	1947.15	1818.61	742	184.41

664.89	939.7	358.93	906.55	312.05	1217	231.65	2336.7	2375.03	1002.55	587.11	893.55	388.13	763.25	315.16
277.12	228.55	47.16	534.25	479.49	348.15	271.6	183.15	118.16	117.9	27.15	345.2	77.22	374.95	307.66
71.98	507.85	91.99	988.65	587.96	1351.5	986.27	1071.5	669.21	1294.2	653.37	627.4	526.09	748.3	174.94
283.41	156.2	73.82	149.05	83.93	218.3	165.89	242.05	136.97	170.95	49.57	110.3	10.89	230.2	143.54
30.41	240.45	44.9	299.8	39.03	309.2	281.43	487.6	104.93	474.65	218.99	482.15	403.97	223.4	59.54
492.15	171.9	33.66	148.9	66.19	656.25	553.03	887.85	595.6	781.55	795.99	1250.15	630.67	292.35	11.95
226.98	1035.4	253.43	1189.8	35.07	1433.55	1090.85	760.95	641.7	824	528.63	342.45	3.46	1761.2	416.06
155.56	257.35	185.05	548.45	226.63	224.15	157.9	742.65	689.22	808.9	418.04	280.7	44.69	757.85	551.9
32.74	186.95	249.26	39.45	40.66	266	39.46	1249.8	1534.56	314.55	319.26	304.75	85.35	177.8	76.79
120.99	274.25	260.99	295.3	231.22	751.3	964.64	565.75	704.77	172.3	25.74	282.65	202.16	151.55	83.79
347.61	939.6	692.12	875.4	782.91	1195.9	873.84	1025.3	1141.98	1395.55	592.06	241.8	149.34	1604.7	615.75
171.4	330.35	373.42	330.15	373.71	117.3	132.94	203	148.35	145.45	81.95	380.15	246.29	114.7	20.79
99.98	431.15	49.14	409.6	79.62	527.4	282.42	511.9	279.87	583.4	259.37	149.05	102.32	265.65	196.5
49.57	164.5	80.47	302.6	114.83	181.05	49.71	124.3	133.64	45.95	18.17	173.05	69.65	101.55	20.72
8.63	699.05	166.1	465	164.9	913.7	365.86	403.3	21.78	459.5	344.22	483.4	442.51	617.65	189.29
38.89	610.3	518.59	823.35	217.29	243.1	146.09	256.45	80.12	854.9	1028.56	280.25	55.37	220.45	71.49
68.09	226.6	196.86	248.4	227.69	173.4	147.93	506.85	363.95	247.45	141.49	754.05	374.27	276.8	266.58

714.53	1215.85	429.57	1143.45	531.96	398.45	196.65	563.45	14.5	1627.8	159.1	761.1	331.49	469.35	373
269.48	930.95	331	868.2	419.74	1257.8	461.32	248.45	18.31	582.6	239.71	706.15	582.59	613.7	497.94
378.73	1603.65	778.31	1788.6	1039.87	2434.35	422.78	825.9	596.09	1280.8	338.56	1775.6	1708.51	847.2	176.78
73.47	582.9	12.16	463.7	180.74	468.95	424.19	347.6	32.1	129.2	31.4	344.7	185.54	192.75	121.98
276.69	817	841.6	1220.55	270.89	430.15	248.41	253.85	48.86	379.8	49.78	606.85	507.91	207.75	54.94
357.87	1759.2	799.03	2048.7	389.62	1667.35	407.22	1177.9	417.48	578.4	446.47	771	707.25	1248.05	547.65
135.06	407.5	144.11	743.7	331.35	443.1	212.27	837.9	414.36	2110.05	1223.51	395.9	159.66	1210.65	477.23
43.84	429.85	479.63	524.5	345.78	197.95	1.63	643.5	685.19	566.7	76.93	716.6	396.26	305.75	261.7
25.1	47.05	17.75	45.25	20.29	324.25	170.77	627.35	766.15	196.6	142.69	200.35	15.91	300.1	207.75
374.91	730.4	724.5	308.65	128.06	782.75	809.14	664.3	360.77	863.7	861.96	213.1	125.44	574.9	452.83
8.63	923.55	644.1	891.25	689.78	259.1	8.06	165.4	67.03	364.3	21.35	519.25	188.87	927.5	201.67
124.24	306.05	220.26	319.4	239.14	604.65	235.96	618.2	249.47	414.85	398.88	1392	1130.52	209.8	140.71
410.55	1478.15	112.5	1711.25	442.15	1229.85	115.89	489.7	437.84	1519.8	421.72	1777.3	1200.53	990.5	730.87
30.05	174.4	195.3	281.65	43.63	146.4	9.19	113.3	127.99	348.45	69.23	299.8	18.53	372.45	411.89

60.25	552.15	285.03	515.2	232.78	902.75	371.02	1108.75	491.51	1142.9	286.38	1113.75	40.94	1073.35	328.03
42.71	108.05	67.67	120.5	50.06	138.45	124.66	166.15	51.27	109	26.3	317.3	398.24	168.75	46.88
528.35	4615.3	1512.5	4132.65	2195.07	3185.05	132.87	2998.75	508.2	2584.3	1255.26	3160.65	1385.58	3061.1	506.57
950.78	1516.55	684.27	2227.55	321.24	956.45	646.79	1622.4	714.04	2419.5	778.67	2621.55	1666.72	1492	534.01
745.22	2661.45	1324.48	2561.15	1466.33	1672.7	0.28	1925.2	600.48	3168.25	1391.94	1624.25	823.28	3281.85	865.29
466.83	1275.2	468.25	1167.4	620.7	1055	422.14	769.7	517.89	1613.8	474.47	1463.05	112.5	1266.65	75.31
223.87	550.15	18.88	915.35	535.35	418.35	151.67	692.8	100.69	437.45	42.36	769.65	392.23	455.4	36.06
556.99	1921.25	567.45	1882.45	622.32	868	408.71	2212.6	1785.16	1939.45	553.59	1059.8	286.66	1411.25	175.72
8.84	1035.45	282.63	1135.1	141.7	690.95	568.58	609.05	204.42	724.25	687.38	784.8	658.17	1019.75	66.11
25.24	393.55	210.51	327.15	116.6	469.7	380.56	232.25	32.6	396.4	26.02	362.6	84.71	378.4	68.17
1239.91	1813.25	614.41	3590.2	1898.58	6562.65	4911.35	3917.45	2834.86	2144.9	1443.2	3145.9	1562.99	6946.6	4938.43
101.19	518.1	285.53	418.25	426.74	117.4	70.57	270.75	238.08	176.9	39.32	492.5	8.49	775.6	356.95
360.84	661	97.3	390.25	285.6	556.8	110.59	2042	2541.2	1028.7	866.77	337.4	224.86	580.55	59.33
664.82	145.8	114.69	62.2	3.54	271.6	140.71	161.05	66.96	279.75	171.47	159.45	50.84	259.15	38.68
574.88	609.3	692.54	520.8	567.38	1368.75	34.15	1322.9	1506.28	863.85	792.17	687.55	433.67	1307.75	300.45

50.13	267.85	27.22	230.5	25.6	157.4	74.1	217.45	78.7	389.55	207.68	165.55	33.59	320	175.79
337.43	761.35	790.05	727.7	837.64	338.5	143.54	619	683.21	592.9	73.26	135.4	58.83	795	452.41
214.32	119.15	131.03	85.15	82.94	195.05	184.06	743.4	235.18	169.2	126.01	620.05	467.61	338.7	233.06
427.52	1180.95	739.14	1153.55	777.89	792.55	598	549.15	620.49	330.65	31.89	590.25	292.53	672.65	709.3
294.02	1537.25	168.5	1684.05	39.1	1105.5	165.18	1048.3	807.23	764.45	83.51	890.6	755.05	1648.8	74.25
257.95	128.05	71.06	126.6	73.11	204.35	137.82	235.65	247.7	217.1	197.57	147.05	127.92	136.6	0.28
1564.05	1366.5	721.96	1552.35	459.12	1726.75	755.26	1086	95.04	1771.85	1431.82	1648.9	892.93	1547.25	247.42
323.57	1086.65	807.87	1469.45	266.51	1846.9	1833.25	2146.95	1953.52	1920.45	1758.79	2734.2	49.36	1275.2	620.42
1373.77	4186.1	2095.16	4231.95	2160	5263.6	750.38	8085.6	2288.2	5491.05	1269.75	5063.9	832.41	5562.5	588.45
186.89	139.35	122.54	104.3	72.97	105.3	30.97	99.05	23.55	68.2	53.03	739.9	981.18	122.4	85.14
10.18	97.3	47.66	128.9	92.35	513.05	681.16	618.6	791.68	90.4	55.86	1482.35	2015.75	112.15	79.41
412.1	6919.8	2507.82	7874.55	3858.04	7646.35	5019.12	4722.3	1270.39	5385.35	3594.72	5573.2	1278.59	5556.05	1623.73
24.47	98.95	31.32	58.55	25.81	63.5	60.95	155.2	153.3	396.05	451.91	44.8	39.03	137.5	59.68
208.03	3546.9	567.81	3788.85	225.64	2848.75	52.26	5153.35	2182.91	3467.6	155.99	3847.95	1175.99	3905.55	1406.08

38.25	892.55	163.55	786.1	314.1	1399.6	870.31	934.1	470.79	254.35	188.44	950.8	435.72	690.5	407.15
115.12	322.55	124.24	282.5	180.88	315.35	158.04	448.2	123.32	242.5	4.1	302.6	58.69	335.15	75.02
49.36	100.2	43.42	100.2	43.42	286.95	165.25	585.65	776.33	182.1	163.77	367.6	148.63	692.9	225.71
201.95	163.35	61.73	237.1	42.57	430.85	15.63	295.25	199.47	587.65	505.65	457.5	321.88	273.6	82.59
402.27	640.3	508.98	427.35	207.82	885.95	289.14	417.2	437.7	890.6	327.39	811.9	166.88	1075.2	32.95
2370.15	1881.05	1328.02	2059.75	1580.74	2339.15	1629.95	2537.7	3212.1	3194.05	235.54	1629.1	1142.97	2138.55	170.06
108.97	170.7	5.8	187.7	18.24	416.6	311.13	623.6	497.8	133.45	84.22	209.15	149.84	442.25	72.48
289.7	759.9	348.04	879.55	178.83	610.8	180.17	410.6	287.37	686.2	316.22	1065.95	841.95	1506.15	334.96
189.65	1286.4	569.22	987.7	146.8	1488.9	464	2427.05	681.44	2153.05	635.62	2580.8	1986.55	523.3	92.77
25.24	90.15	82.24	95.4	74.81	441.9	531.46	113.6	45.96	79	37.48	138.3	35.78	145.05	74.32
6.51	303.9	196.86	482.1	55.15	845.05	1060.59	381.1	92.49	381.3	297.69	393.3	121.2	336.9	53.88
67.25	774.6	718.42	500.85	331.28	946.9	672.46	454.35	115.05	516.6	498.79	1076.75	1071.34	867.55	413.45
144.82	502.05	43.77	508.8	34.22	1219.9	859.13	245.1	169.71	533.3	137.46	319	52.75	703.6	477.58
41.01	496.25	567.45	473.5	599.63	78.6	21.64	263.7	239.71	192.25	66.54	209.15	190.85	174.35	148
49.57	56.9	38.75	146.3	87.68	242.7	321.31	64	4.38	405.35	479.63	83.25	41.79	101.7	63.64
255.41	861.75	241.62	423	378.87	698.15	445.97	509.55	386.86	813.25	493.77	676.6	294.44	1154.6	100.55

3750.85	33464.25	377.39	33590.8	198.42	33262.9	5625.74	19819.7	8770.67	27743.85	11327.07	18166.3	8950.27	30337.55	4573.07
774.14	1609.65	8.13	1314.65	425.32	665.25	539.45	937.45	517.81	1448.95	124.52	613.3	114.69	802.75	441.73
12.09	203.05	186.18	58.85	17.75	294	226.42	745	994.19	1404.95	1061.86	1013.65	1218.7	117.1	40.45
427.09	1596.85	190.85	1469.7	370.67	1929.6	727.19	1687.1	428.65	1059.45	522.48	409.1	416.2	585.05	163.55
447.53	618	258.52	1060.8	367.7	532.7	207.89	268.6	61.38	1134.35	345.99	966.4	664.54	1371.55	622.47
944.06	3469.5	433.88	3622.65	650.47	2945.45	712.69	2033.6	1960.24	2679.5	2213.24	2884.65	385.73	3204.95	345.85
238.37	303.3	287.93	273.2	330.5	105.45	111.09	433.6	354.54	269.25	291.4	82.15	79.55	106.35	17.75
105.43	1236.55	496.88	1232.1	503.18	407.4	232.78	1892.2	1346.47	1276.15	56.5	1299.85	1100.33	677.4	427.52
120	425.55	136.12	232.45	136.97	416.3	434.16	260.45	204.28	116.7	79.48	324.9	7.07	602.05	695.58
90.3	942.15	549.63	1165.05	864.86	2184.8	650.26	2375.85	741.12	1501.8	166.59	1321.05	838.7	1173	691.13
669.35	2731.75	86.2	2801.65	185.05	2887	204.92	1766.3	561.02	2458.25	134.56	2619.3	1200.67	3354.9	241.69
59.96	126.9	75.8	211.4	43.7	249.6	151.32	558.35	711.99	209.15	165.39	404.5	331.77	489	447.17
296.56	3533.85	143.61	3870.45	332.41	4604.85	941.65	4451.1	2364.99	5070.3	1036.48	3323.1	1956.42	3874.4	578.84
24.04	134.5	106.21	165.75	62.01	487.5	519.86	106.5	89.24	140.65	90.86	241.2	202.23	380.2	337.29
82.45	329.7	127.14	252.5	17.96	316.35	129.9	613.4	208.17	690.7	628.48	1320.35	1296.9	675.2	428.93
144.53	1142.7	36.2	1126	59.82	2207.55	1820.02	1310.1	1430.05	2111.7	874.69	1669.75	1209.79	1588.5	595.24

228.11	455.05	214.32	527.75	317.14	483.05	151.11	469.35	523.05	997.5	195.44	1092.55	389.55	1115.65	136.68
91.57	234.7	173.67	150.6	54.73	805.8	207.89	1852.8	1708.79	240	103.1	714.35	829.22	685.7	348.04
344.08	1111.45	263.82	1006.95	411.61	1321	1095.73	1747.1	934.94	1549.45	233.56	2306.35	1455.72	1546.05	663.05
196.15	1669.95	592.06	1977.85	156.62	1676.05	458.56	2193.15	1348.24	1218	68.45	2521.8	1247.62	1652.15	430.42
271.18	589.9	64.49	492.35	73.47	939.9	357.65	894.55	1169.48	116	55.3	667.6	250.03	795.1	496.81
281.29	274.2	174.94	269.35	181.8	665.2	713.05	652.6	651.39	219.15	58.62	257.35	121.27	598.45	97.37
95.46	187.8	8.34	215.9	48.08	478.95	259.15	2598.4	3316.9	410.6	199.69	394.25	176.85	502.2	217.51
269.83	2300.15	4.45	2737.8	623.39	2542.25	344.29	1917.85	444.98	2333.05	526.72	2732	199.69	1512.05	136.54
248.34	1571.95	627.7	1803	300.94	1285.05	17.89	805.95	527.01	870.65	163.84	1446.95	1082.51	1521.15	136.4
1.98	61.8	33.66	93.5	11.17	316.1	325.98	158.35	127.63	157.25	117.73	139	6.51	177.05	29.77
624.02	633.3	315.09	513.55	484.44	982.5	657.33	587.35	356.17	504.5	34.22	215.85	34.58	582.25	310.07
916.83	3344.75	262.12	3279.6	354.26	2397.2	31.82	1995.1	553.1	1847.15	268.63	1487.95	1797.96	2522.15	182.79
869.39	3422.1	1109.87	2721.3	118.79	2729.35	3168.33	1569.25	736.45	1962.1	216.09	2449.9	227.97	1569.35	901.91
394	129.45	79.97	126.1	84.71	620.4	696.78	269.85	121.13	233.8	142.84	789.35	927.65	251.8	236.74
113.7	548.3	229.95	516.5	274.92	187.15	61.87	596.95	623.17	634.05	658.53	142.05	56.36	961.8	384.24

44.48	118.05	53.1	91.3	90.93	199.7	6.65	410.7	130.53	566.05	628.41	112.05	19.73	140.8	151.32
673.45	802.55	816.64	332.8	152.31	503.85	255.48	379.35	247.7	1166.05	1268.62	606.55	709.02	975	364.73
281.29	232.55	155.35	96.1	37.62	392.3	366	335.8	127.99	535.1	682.92	376.55	357.3	85.45	17.61
1.13	314.75	167.51	452.7	362.6	441.85	388.98	285	83.72	621.55	426.03	723.65	260.71	276.15	133.01
10.32	312.15	135.69	137.3	111.58	242.55	231.86	288.3	184.84	306.95	240.49	252.35	122.82	269.15	235.11
655.28	1619	195.3	1549.6	293.45	1663.7	296.14	870.25	704.49	827.35	384.17	804.65	663.05	1485.5	669.21
155.07	785.25	610.16	786.15	608.89	1126.6	1067.59	511.15	196.22	528.7	639.22	704.5	215.1	1180.9	564.98
1165.74	2161.8	46.67	2363.8	239	3479.2	1585.76	2607.8	324.56	2177.95	576.08	2901.75	1538.45	3695	215.95
537.61	3478.3	642.34	3266.2	342.38	3518.8	829.44	1993.3	1063.06	2722.05	1608.17	2174.25	1026.51	2586.4	354.83
539.81	603.25	26.94	453.55	238.65	335	123.04	666.15	757.38	218.55	37.26	689.05	390.82	371.3	388.2
14.64	600.2	14	697.2	151.18	701.6	27.15	285.3	211.71	981.8	315.51	378.25	361.26	201.25	62.15
415.99	3191.1	323.01	3659.6	339.55	3829.45	756.68	4747.2	112.43	5026.15	1227.18	4052.35	2313.02	4354.35	664.04
138.66	334.15	94.26	296	148.21	255.55	18.17	203.2	191.34	276.15	43.2	426.9	168.86	424.6	61.24
304.41	675.75	11.67	651.65	45.75	779.2	350.72	464.6	408.28	503.4	303.91	577.95	133.43	547	724.5
592.41	2047	792.24	1882.85	1024.39	1724.2	1387.63	2222.8	477.44	1877.7	375.9	1961.1	1038.17	1207.65	823.85

94.26	112.25	46.88	115	42.99	104.7	21.64	160.05	60.74	368.6	384.52	310.15	314.17	151.6	121.91
311.69	969.5	84.57	1057.2	208.6	1058.8	446.61	1112.4	896.75	1291.4	351.57	791.55	274.85	1231.4	574.03
704	782.4	675.43	356.95	73.75	466.5	165.18	276.5	197.85	591.3	490.45	468.9	393.29	1572.45	108.97
817.98	786.2	49.36	792.1	57.7	436.8	346.48	515.4	484.23	1021.95	772.94	1353.4	878.23	1386.65	250.95
176.35	354.05	122.82	302.25	196.08	500.6	470.79	600.75	303.84	437.55	472.14	538.4	360.34	472.05	154.22
409.2	542.2	153.44	746	134.77	1048.65	559.53	1132.2	8.77	1759.55	794.72	1331.75	893.43	1208.55	320.53
31.75	757.85	78.84	601.9	141.7	1207	1005.51	864.95	708.03	893.3	22.63	821.75	403.69	882.4	638.8
63.43	141	58.41	70.95	40.66	460.6	98.71	598	605.85	482.05	168.22	132.6	11.74	134.2	59.4
373.49	2514.25	472.98	2552.45	418.96	2998.6	929.85	6323.5	6454.33	2618.25	1008.83	2055.15	851.85	2440.3	487.62
624.52	18707.6	4526.47	21074.85	1178.68	14799.25	4604.89	13815.35	7302.93	17670.2	7861.61	20541	8626.7	13337.5	3998.83
369.53	765.35	323.08	733.6	367.98	483.35	109.67	449.2	175.65	760.1	144.39	1280.3	373.21	1421.7	530.47
3118.55	2938.65	752.15	3268.15	286.17	1558.2	70.99	1040.5	1095.73	3237.4	841.03	2136	584.35	1444.2	436.71
356.52	452.9	376.89	152.65	47.73	629.35	690.77	392.55	74.03	122.95	30.9	607.6	712.2	722.7	230.09
57.84	565.8	25.03	355.35	322.65	697	205.91	578.45	385.16	1438.9	203.08	930.6	402.77	643.7	460.04
84.57	584.85	342.31	584.05	343.44	633.6	529.48	620.05	22.84	489.95	451.2	298.35	194.24	719.05	307.1
262.76	1694.3	364.02	1555.95	559.67	1943.55	1050.55	1714.5	179.18	2011.1	279.87	695.35	682.43	2101.85	139.51
86.69	236.6	246.5	268.6	201.24	156.05	46.88	539	110.87	97.3	11.31	310.8	17.25	676.3	536.84

305.33	1945.55	268.91	1669.9	120.92	1987.55	266.08	1646.3	1131.37	1849.2	149.62	1931.45	129.61	2155.2	349.73
280.58	1277.35	278.81	1316.55	334.25	1010.5	907.22	1033.25	313.18	941.1	179.61	1277.45	258.16	1691.05	363.81
853.55	405.95	43.49	412.15	52.26	275.55	53.81	691.85	682.43	1096	398.53	664.35	807.3	907.6	762.83
1298.11	1812.85	847.04	1993.5	591.57	2284.3	1610.93	2758.25	2966.52	1592.95	545.67	790.7	761.41	1567.1	673.59
1525.44	6473.4	263.89	7297.35	1429.13	5711.85	2559.8	3397.55	1550.05	3710.15	28.21	3276.25	1647.21	4923.2	494.41
183.28	581.8	643.75	609.65	604.36	643.35	830.78	292.4	67.32	291.4	154.29	380.7	55.86	448.9	162.78
9007.13	19378	1597.92	23030.95	3568.13	31738.8	4537.65	12796.55	1543.4	32193.4	3532.7	16278.8	19315.47	26659.15	7856.45
310.35	980.6	463.72	752.65	786.09	577.8	649.97	592.9	252.58	551.2	507.14	445.65	36.56	248.65	174.3
167.73	355.05	285.18	175.3	30.97	1054.5	282.98	397.15	87.75	662.65	579.33	1128.05	242.18	430.25	279.66
12.45	75.8	69.72	80.5	63.07	81.75	49.71	89.65	44.19	264.25	266.37	590.4	767.64	71.95	50.56
129.9	1126.55	176.14	943.25	435.37	711.25	350.37	409.45	354.47	575.75	287.16	537.3	183.42	727.65	60.32
492.99	633.5	82.17	479.4	135.76	574.5	108.89	583.9	154.43	1362.4	653.51	633.55	639.44	1031.45	659.66
136.83	1375.1	697.63	1232.7	496.25	1393.4	121.91	1141.45	921.86	698.3	640.78	803.15	338.35	1031.15	40.8
970.29	1263.2	706.82	1540.25	315.02	1140.5	133.08	1273.15	630.81	1575.55	708.87	1667.55	1810.69	1784.25	953.82

849.66	4789.25	1767.27	3910.8	524.96	4082.5	4069.26	4307.75	655.13	2468.55	1092.13	2832	311.41	3946.55	936.85
425.4	654.85	35.71	641.5	16.83	955.4	311.83	1662.1	490.31	353.95	217.44	782.6	449.86	1021.4	333.9
664.11	1456.1	450.57	1345.85	606.49	915.25	474.82	916	314.8	1440.95	741.97	2486.6	2052.87	643.6	537.12
855.25	5424.45	926.95	5554.25	743.38	4317.65	766.29	4539.7	876.11	4136.35	482.6	3307.85	918.6	4677.2	475.88
1477.71	1025.8	16.69	1576.75	795.85	2089.9	125.02	955.4	198.13	1599.8	1123.03	688.85	62.86	835.9	324.28
762.33	1731.8	1908.34	2376.8	996.17	1382.35	368.61	858.1	191.48	2531.4	2267.13	1627.1	822.08	1710.65	1414.28
65.2	355.15	259.15	289.7	351.71	440.4	555.08	204.65	166.81	238.7	272.38	101.85	71.21	198.6	198.98
66.04	378.05	124.24	531	340.54	280.45	218.14	581.25	118.16	545.75	262.27	568.55	409.2	444.9	460.04

2295.34	8330.95	426.31	10426.9	3390.44	8428	941.16	14266	12161.25	10407.05	2030.32	12607.25	1119	13981.6	5175.03
27.79	1048.45	395.48	627.95	199.19	532.35	473.83	502.3	581.81	218.5	198.56	427.3	358.93	1112.8	605
481.04	1089.65	283.2	908.4	539.52	778.55	419.39	1643.95	65.12	1465.75	89.02	967.6	1091.77	471.2	300.52
117.03	640.3	197.14	654.2	177.48	229.6	179.89	633.3	322.3	626.35	130.46	525.2	234.9	603.15	413.73
101.89	2784.45	988.89	3324.1	225.71	3295.5	1733.68	1732.6	1264.87	4060.3	317.63	1920.65	1744.79	3435.2	631.3
24862.65	146594.05	126492.98	171109.09	91823.47	119054.8	80388.71	133907.25	93248.79	195514.8	24099.61	126800.75	94906.81	259753.41	8152.1
211.14	191.1	62.51	104.55	59.89	327.05	98.64	462.35	161.72	152.8	79.76	141.3	124.17	308.55	211.78
234.55	428.55	35.71	263.45	269.2	995.1	783.33	579.85	530.54	215.8	32.67	639.5	30.69	351.35	187.74
350.44	662.75	64.42	823	162.21	376.55	82.52	694.3	83.16	1098.85	569.29	1632.3	1161.49	552.9	612.35
125.65	207.3	58.69	139.2	37.62	818.55	913.51	191.6	56.99	133.8	25.88	291	114.98	223.6	1.7

227.19	1049.95	604.93	1163.75	443.99	2215	2013.27	1806.1	1159.23	1276.8	370.67	597.75	301.3	565.2	305.47
202.23	1830.3	597.65	1794.2	648.7	1808.25	319.12	1911.85	1796.69	1333.7	913.3	1766.05	37.97	1197.35	265.09
357.09	2671.1	163.48	2574.15	300.59	2757.15	85.63	2903.55	11.81	3072.6	298.26	3665.6	655.63	4782.9	797.33
1013.28	5294.4	1253.7	4923.25	728.82	5484.05	955.8	8206.8	2149.32	4846.75	775.2	6039.45	2077.13	5171.75	1252.78
1873.27	2158.8	817.98	1362	308.86	1035.85	175.43	1279.5	250.46	1883.65	1268.34	2036.5	422.85	2474.75	1887.2
578.13	3623.75	939.82	3971.35	448.23	4142.5	936.21	4895.75	4124.34	4247.55	1090.85	3964.5	2888.53	3560	3475.85
250.53	411.7	89.94	343.65	186.18	706	363.17	407.6	0.42	655.05	166.95	522.55	94.96	269.4	229.67
1933.87	5280.25	451.77	5691.95	130.46	4337.95	177.98	1717.45	1375.25	3278.55	473.27	2785.85	900.36	2048.4	212.7
7.07	98.55	44.34	113.25	23.55	209.2	206.76	128.95	49.43	182.55	128.34	237.6	172.11	75.9	2.69
276.2	221.2	152.03	175.4	216.8	429.7	304.06	127.45	16.05	168	117.1	121.15	39.39	630.2	494.83
2274.2	5392.6	98.71	4841.2	878.51	2660.25	677.34	406.45	17.47	2571.45	934.02	2709.15	489.39	1029.95	498.72
130.18	325.85	67.25	307.1	93.76	137.25	75.31	545.7	579.69	499.55	356.88	592.5	421.44	982.5	569.65
742.04	5595.05	1483.44	3919.4	886.29	6253.45	1863.58	5209.6	1984.14	4884	356.24	4556.75	166.24	6844.45	1082.09
290.2	169.15	22.7	385.35	283.05	313	80.75	252.4	216.23	1128.55	517.25	200.7	182.43	759.75	928.93
104.02	136.3	58.12	131.6	64.77	168.55	124.38	315.6	266.44	193.7	95.04	420.4	120.77	192.8	47.09

51.41	547.1	619.57	524.35	651.74	1478.8	1989.66	205.35	276.69	77.9	14.85	200.95	18.6	97.45	16.05
65.05	562.4	191.48	557.05	183.92	695.5	40.45	1184.2	499.5	854.95	107.69	1078.9	232.78	991.75	285.6
117.31	90	38.61	46.25	23.26	170.6	80.33	941.2	1253.28	290.25	77.57	736.35	607.62	133.4	87.96
296.14	255.15	43.49	289	4.38	556.9	358.08	207.9	170.84	446.75	278.67	509.65	43.91	662.6	125.72
95.04	507.9	42	364.3	245.08	293.15	34.15	489.85	230.16	276.35	11.1	267.6	140.29	482.2	66.61
18.6	1073.85	1063.56	603.2	397.96	482.1	455.94	342.25	95.53	817.45	86.34	629.15	563.21	467.3	211.14
197.64	735.2	421.15	1149.2	164.33	267	155.99	324.3	306.04	680.5	323.85	450.05	139.37	631.85	165.82
387.85	588.1	334.32	457.85	518.52	867.8	321.59	550.75	425.75	320.5	226.27	1082.65	1263.81	148.3	37.05
1146.93	1957.8	1290.05	1887.5	1389.46	3022.6	3147.61	7323.4	7619.36	2415.45	1856.08	20979.95	10751.49	4435.8	1068.86
228.04	655.45	538.04	567.8	661.99	527.5	19.66	322.35	106.42	91.3	23.62	317.35	87.33	64.65	49
122.97	1494.35	816.78	1634	619.28	1277.25	65.27	354.65	281.64	1871.55	722.31	822.65	170.2	917.85	588.95
12.3	146.15	105.29	142.75	110.1	410	269.55	862.25	1064.69	279.05	178.26	467.65	273.44	314.9	226.98
135.2	913	421.01	836.3	529.48	373.1	106.21	1003.2	521.28	724.4	58.12	1370.7	678.68	1400.6	255.12
388.41	1141.6	356.95	854.9	48.51	606.15	306.39	1031.8	309.71	737.75	717.36	1436.95	408.92	829.85	887.91

81.11	143.6	103.24	142.2	105.22	152.55	113.91	972.35	841.67	241.3	263.19	137.8	43.84	218.45	71.35
147.15	319.3	330.36	265.3	253.99	205.9	46.67	2031.9	1987.82	378.9	147.36	514.25	643.4	193.35	53.25
286.24	4197.2	243.24	3313.65	1492.77	2763.95	507.77	3452.65	1516.96	3475.5	976.51	2795.95	1620.19	3777.35	100.2
136.26	595.65	382.19	486.95	535.92	1218.9	1092.48	1084.25	1060.73	697.3	676.28	1126.4	778.81	877.5	1096.3
1172.38	3492.3	2058.95	3288.9	1771.3	5399.6	1169.13	4297.4	414.65	4991.85	2425.45	2695.25	1663.75	3648.65	396.19
218.21	311.1	275.35	91.8	34.79	915.5	1092.34	227.05	195.37	126.3	57.13	309.75	73.75	299.9	292.18
100.41	437.9	118.65	433.7	112.71	783.45	227.05	1563.8	736.81	371.1	119.22	866.9	176.78	700.55	298.75
28.35	708.85	857.23	708.2	858.14	785.35	470.86	1459.85	1909.12	800.4	195.73	1381.75	160.58	681.9	723.65
143.9	226.3	124.45	163.8	212.84	325.1	342.66	114.85	37.55	43.5	6.79	179.5	137.32	171.25	185.33
33.38	5349.7	352.28	6207.6	860.97	4401	100.83	2364.45	1701.23	2829.65	2666.15	3351.6	2932.94	2607.45	1694.16
62.44	39	21.78	46.25	11.53	43	29.84	148.25	181.23	56.25	33.87	555.9	516.61	183.95	100.34
548.64	2191	1833.53	2105.15	1712.12	1948.2	1246.49	2051.7	316.08	3155.35	223.52	3581	432.33	2386.85	889.33
160.65	362.3	312.54	257.1	163.77	741.5	159.66	200.55	157.19	354	265.17	567.35	127.77	1009.9	405.6
112.29	2138.1	1090.08	1566.35	281.5	1835.7	891.1	1790.9	152.88	1130.9	588.74	3022.1	1864.22	1159.35	397.75

67.88	209.45	32.74	183.55	69.37	753.7	928.01	514.05	510.18	197.75	46.74	177.4	125.72	1090.35	1413.29
1442.71	1459.8	300.52	1672.55	0.35	1177.35	123.39	491.15	167.66	1218.3	675	649.55	80.54	804.75	355.04
6052.91	14527.3	6219.15	13572.95	4869.49	15424.45	7836.37	12023.15	5783.64	12651.2	4171.79	10368.95	4946.57	14005.25	3988.29
138.31	593.1	543.2	567.75	579.05	676.05	651.88	759.15	582.3	64.05	30.9	231.6	176.35	91.45	51.69
293.17	238.9	194.74	324.4	315.65	812.4	60.53	1743.9	2004.65	704.45	279.38	1019.55	441.73	455.4	1.7
77.15	963.75	517.81	909.05	595.17	966	254.13	1274.85	1200.46	970.55	566.6	459.15	292.25	836.55	710.15
177.55	477.75	174.58	505	136.05	559.7	162.35	645.65	153.65	506.4	149.62	2322.6	2911.02	473.2	123.46
57.06	138.8	117.66	70.75	21.43	457.15	467.61	299.85	311.34	73.25	4.45	315.25	127.49	370.85	10.39
73.26	214.6	49.21	205.95	61.45	394.85	274.29	423	374.06	420.85	227.76	321.35	169.49	261.65	23.97
32.03	209.95	76.72	149.2	9.19	271.75	24.96	200.25	63.85	127.3	110.87	464.35	20.15	224.8	176.35
169.85	851.3	631.59	706.1	836.93	332.85	2.9	241.95	49.71	410.2	276.34	1341.45	489.39	961.8	1147.92
27.93	207.8	140.43	223.7	117.95	202.8	97.02	326.3	147.64	287.85	129.05	423.6	93.76	186.75	72.76
296.21	1358.95	476.94	960.45	86.62	1430.7	787.43	1369.3	269.69	1215	179.46	605.55	601.25	1012.75	313.6
2273.35	4324.7	104.79	4250.7	209.44	4479.1	541.08	4557.95	1731.07	4253.3	653.08	3623.1	1365.14	5745.2	706.82
71.7	151.95	55.08	66.8	65.34	232.7	200.96	121.8	73.54	142.3	0.14	352.15	41.37	395.85	293.1
174.44	2033.25	231.58	1712.85	221.54	1216.85	963.57	2378	1961.23	1191.7	612.64	1544.75	990.73	1021.95	698.41

58.83	324.3	240.7	356.7	194.88	288.35	4.17	1188.05	1156.76	348.35	139.23	279.95	33.87	417.9	121.48
116.74	318.6	147.36	231.35	270.75	775.1	591.14	1379.3	764.95	447.1	398.53	977.05	1150.11	771.35	572.54
130.74	5336.95	1673.23	5546.95	1376.24	4847.3	765.66	7345.4	1289.9	6323.9	938.05	6234.65	848.03	7697.85	461.95
1279.44	15269.85	622.33	16222.75	725.28	14932.1	1122.6	13948.85	9399.5	16598.2	520.85	15678.45	1022.12	16008.6	1226.83
61.09	265	18.53	282.15	5.73	661.55	393.36	703.95	760.78	1066	969.58	786.15	946.46	810.55	95.11
285.11	200.35	16.05	204.6	22.06	760.25	764.45	506.5	471.64	614.95	461.81	298.85	256.18	597.65	171.19
479.21	836.25	832.34	1016.7	577.14	635.4	493.14	465.75	302.71	1580	642.19	1299	503.74	1364.2	1048.22
1348.52	4302.6	14.42	4694.15	568.16	4003.05	352.35	3084.2	2336.71	2195.7	1770.17	2004.8	2348.87	3570	314.24
888.97	3792.5	1374.76	4245	734.83	1997.45	1355.17	4239.9	648.28	5356.15	1894.83	4619.55	309.5	3676.8	685.33
325.55	2455.05	111.09	2339.65	52.11	1920.15	76.01	433.05	175.72	757.5	486.21	1705.45	890.46	454.7	463.3
847.75	527.7	142.55	942.45	443.99	1243.15	1202.86	1157.2	1012.72	590.75	65.27	2032.1	2242.24	532.45	259.58
7.78	81.65	72.2	77.05	78.7	141.25	159.74	150.95	37.41	320.95	379.22	75.8	32.53	65.95	2.33
62.65	974.45	306.25	951.5	338.7	607.15	420.52	2350.75	2353.75	1142.7	469.52	1197.9	358.22	595.15	181.8
505.02	1207.35	371.44	931.75	18.31	1144.75	394.78	2980.8	1666.08	1597.2	305.75	825.85	545.96	2261.85	1036.41
258.87	814.75	99.91	573.3	441.38	346.55	254.77	610.7	39.32	503.95	115.33	777.9	358.36	530	668.22
1803.05	6353.55	641.98	6293.2	727.33	5975.8	409.27	3065.6	3276.73	4081.25	2473.53	4835.95	2265.64	5460.25	572.97
313.6	319.9	211.28	315.75	217.15	677.15	705.34	252	179.61	573.7	320.04	248.3	98.71	169	21.35

22.2	508.5	90.79	405	55.58	607.1	130.39	437	347.05	588.8	430.49	771.05	1009.96	911.05	218.99
8806.38	36938.4	6420.81	38662.45	8858.99	42202.4	1549.41	39026.45	25051.45	31675.2	9708.15	29537.25	12080.14	49447.6	4240.66
64.21	135.35	58.76	159.7	24.32	122.05	40.23	811.5	1023.47	569.4	679.39	566.15	433.95	299.3	0.85
1036.97	357	49.64	330.95	86.48	638.7	384.24	1911.35	1335.09	1391.1	889.68	779.8	566.11	879.4	491.01
233.49	604.6	21.92	435.05	261.7	972.2	229.67	1620.25	2026.21	465.85	382.19	428.35	465.49	995.25	821.3
549.56	533.4	124.73	489.4	186.96	1221.8	1360.76	1121.15	164.4	1891.85	5.16	759	18.24	956.6	667.37
1577.7	7303.35	3767.25	6164.95	2157.31	8810.1	1508.12	5651.4	3464.4	4927.65	245.15	3873.25	138.24	4864.05	422.64
980.12	3821.35	225.78	3361.7	424.26	3612.6	543.77	3420.2	2234.17	3507.5	681.09	4164.25	1530.53	4800.2	937.2
62.79	93.85	8.41	71.9	22.63	464.1	394.99	101.55	43.35	192.8	140.86	479.6	517.32	126.05	62.15
132.72	458.35	172.89	493.3	123.46	471.7	329.65	522.65	619.35	274.95	229.03	209.7	16.83	342.55	40.66
5.59	89.05	77.29	187.6	62.08	108.8	10.89	425.85	465.35	260.25	205.41	162.95	56.92	81.9	9.9
37.41	123.4	48.37	153.9	91.5	87.3	25.17	146.25	32.46	156.35	93.41	286.9	39.03	233.4	183
34882.99	42501	47.38	49804.7	10376.37	39076.3	11634.59	40787.05	35523.98	49524.35	21237.18	31261.5	12736.41	46445.5	7966.41
256.96	983.4	415.35	684.1	838.63	767.05	51.69	653.05	458.98	220.5	48.93	492.8	497.66	1014.75	817.91
133.78	534.2	424.55	576.25	365.08	666.2	573.04	1791.6	1732.55	455.3	146.65	905.15	1066.39	619.55	80.54
374.7	2475.75	1140.49	2985.05	420.23	2246.25	791.04	1951.9	948.51	2386.7	2156.25	2842.95	470.86	843.6	123.6
289.35	1817.7	1298.11	1677.2	1496.8	738.2	63.36	1041.7	550.98	1612.05	530.68	411.65	404.54	1466.4	332.06

352	558.45	446.11	847.7	37.05	567.35	102.46	968.2	26.02	1038.35	877.02	1081.9	333.75	953.05	1034.85
21.21	45.25	53.67	50.4	46.39	182.45	242.89	658	902.83	71.75	48.58	64.55	55.08	162.95	151.25
84.92	111.45	63	78.85	16.9	104.9	52.75	145.65	3.89	708.95	697.28	310.35	170.91	501.15	591.78
132.09	508.6	407.72	406.95	263.96	705.6	20.79	536.45	545.82	309.85	315.02	262.8	235.75	837.65	59.75
49.43	326.05	273.72	270.8	195.59	151.75	150.12	354.4	108.33	178.75	89.87	114.55	19.87	457.7	404.04
191.56	547.1	156.84	768.2	155.85	849.7	27.86	266.25	193.68	893.95	61.87	965.25	63.14	779.1	46.53
314.24	988.2	150.33	793.2	426.1	537.7	324.7	674.25	432.68	584.7	482.11	1298.1	229.39	502.25	341.04
49.92	1682.1	761.98	1858.55	512.44	1647.4	693.67	2253.15	27.36	1806.95	1228.03	2434.25	1568.86	1701.35	827.81
299.04	1908.75	235.96	1557.75	732.35	1393.8	860.69	2640.2	1815.99	738.05	903.75	1328.4	39.6	1692.8	111.58
16.4	97.7	90.79	57.4	33.8	178.95	209.66	203.95	47.87	166.3	171.12	287.05	173.45	127.1	7.5
7.71	129.15	102.32	128.4	103.38	116	64.77	303.35	210.08	73.65	8.41	433.7	444.91	107.5	65.48
45.33	1976.05	573.82	2029.4	649.27	2087.05	96.38	1362.9	1484.08	535.2	588.74	663.6	550.55	1761.6	316.22
603.02	2948.7	36.35	2735.75	337.5	4123.5	2792.51	8208.8	8559.95	3838.15	2248.25	5639.7	1526.93	7387.3	5499.03
132.72	1045.1	42.99	794.5	311.41	923.2	741.19	1155.3	1342.51	1368.45	309.36	1757.15	353.62	878.6	278.6
10.54	119.1	108.89	89.65	67.25	496.45	488.96	693.3	692.68	265.4	83.86	1435.95	1732.34	362.5	339.55
99.21	104.85	44.62	184.5	157.26	495.2	222.88	98.4	57.42	430.35	223.94	210.8	226.27	289.4	239.14

2.19	1697.35	859.21	1919.65	544.83	2008.9	953.6	2544.25	2186.44	2150.1	98.29	2292.3	1232.49	1286	447.74
325.83	1830.5	608.82	1872.3	549.7	865.2	259.51	1281.15	790.62	1486.8	329.94	2653.65	754.84	2011.15	368.76
335.8	4368.35	549.92	4281.5	672.74	4232.5	161.64	2034.5	2333.45	3199.45	1486.41	3255.55	510.46	3464.45	95.39
2.47	750.75	445.41	407	40.73	696	458.06	338.4	44.69	1148.55	1096.51	565.85	332.84	548.05	224.65
602.88	2284.8	189.5	2459.8	57.98	1971.55	568.87	1693.45	720.05	1279.95	426.88	2106.75	1531.1	1691.4	1017.1
61.8	176.5	27.72	163.9	45.54	158.55	99.21	109.6	75.38	248.15	101.33	304.65	72.34	195.35	43.91
148.07	1221	1237.72	1192.55	1277.95	397.05	61.31	300.8	51.76	460.75	112.92	1460.95	358.29	463.55	145.88
881.41	2064.05	192.12	2207.4	394.85	999.15	473.97	1172.55	163.55	1388.1	57.98	1029.6	188.09	1163.8	309.29
746.78	1200.35	343.87	1089.85	500.14	1003.9	698.06	1842.25	339.76	1103.45	358.86	1518.65	644.39	1068.2	318.06
31.04	414.3	91.92	500.4	29.84	925.45	734.33	141.65	127.63	494.85	434.09	317.25	292.53	602.55	184.63
303.63	774.25	131.59	378.9	427.52	742.95	100.06	932.85	534.64	251.6	16.4	363.05	273.86	485.95	373.99
27.72	778.9	101.12	434.75	385.59	551.5	565.83	479.15	211.35	376.2	346.91	887	927.02	173.9	115.68
507.91	1398.25	364.37	1717.65	87.33	2269.95	1115.32	657.6	178.76	2506.45	1193.53	2030.15	1323.77	834.65	97.09
6.58	226.05	55.51	269.3	5.66	271.6	93.2	456.05	121.13	334.55	11.81	700.2	541.5	347.9	114.13
271.03	1152.25	189.29	1105.15	255.9	1321.85	560.24	1689.55	1093.4	1115.3	168.72	849.15	556.56	605.2	352.85
35	98.85	15.77	74.25	50.56	103.45	63.57	282.25	90.16	390.65	424.33	148.05	115.61	220.25	130.32

18.6	73.85	7.99	58.9	29.13	107.55	77.71	103.45	66.68	180.85	48.44	78.6	17.82	227.85	143.47
20.72	247.15	44.48	151.35	91	212.75	94.68	507.75	504.52	350.5	327.67	256.15	46.74	123.8	65.9
130.53	1807.3	512.09	1657.65	300.45	2059.05	575.09	1999.2	739.49	1619.05	1141.34	495.4	82.31	1769.25	899.37
1769.53	4712.2	1516.18	4014.15	528.99	5743.85	1722.02	2692.45	2958.89	3551.05	60.03	2362.5	1847.1	1817.9	257.53
475.11	600.8	480.97	281.5	29.42	577.2	258.24	737.25	501.83	419.8	20.65	1354.35	1649.33	675.65	762.9
717.29	925.4	260.07	698.65	60.6	471.7	47.23	817.2	171.83	971.3	264.74	1099.5	738.79	1164.8	663.97
269.97	701.7	453.68	661.8	510.11	548.8	37.76	1063.8	285.81	575.2	368.4	1568.25	1161.99	968.3	82.17
545.6	2549.5	1014.98	2687.5	819.82	1760.4	417.76	1246.5	706.26	2343.85	326.33	2075.15	697.28	2748.2	148.07
5081.41	33555.45	8279.87	29905.65	3118.27	23507.1	9096.22	19820.2	10344.97	25701.85	12373.59	32583.6	24105.83	25629.7	11338.46
92.42	186.8	143.97	124	55.15	255.65	0.07	121.1	121.48	353.65	391.1	116.95	7	109.8	90.79
12.8	248.25	293.66	234.55	313.04	47.2	36.63	87.85	70.5	99.35	66.26	276.2	291.05	109.05	48.15
65.48	182.25	13.08	106.45	94.12	565.55	446.11	196.25	111.37	622.5	435.58	281.25	347.4	248.65	63.14
120.7	105.55	74.6	88.2	99.14	96.45	66.96	357.25	359.56	100.6	11.74	98.55	9.55	115.8	77.92
398.74	731.85	147.57	748.5	124.03	489.3	8.63	394.95	431.83	660.1	198.56	498.5	375.62	537.2	118.79
359.71	457.55	245.15	648.55	24.96	420.05	335.24	1961.6	1274.07	526.1	605	554.75	352.35	746.4	919.52

163.7	552.25	592.2	537.6	571.48	489.15	333.54	231.15	130.18	819.6	266.44	711.05	104.58	702.3	163.48
114.06	821.1	213.26	756.25	304.98	1149.5	713.75	1354.95	991.29	1697.85	1174.15	1855.1	1432.6	1026.1	54.45
761.34	454.2	120.77	457.4	125.3	450	219.49	372.3	64.21	740.8	59.11	373.25	325.91	495.7	159.66
33.09	302.15	21.28	191.1	178.33	432.15	225.92	142.4	56.71	448.3	240.42	90.4	46.39	450.55	43.2
11224.54	74669.15	9783.74	93695.8	36691.49	82983.75	13323.52	110772.95	131886.38	123754.05	21797.77	123698.55	1025.23	154028.75	20990.53
112.5	93.95	61.02	80.2	41.58	139.65	8.13	170.25	148.85	186.95	47.73	202.2	84.99	449.5	465.98
104.16	37.15	0.35	55.6	25.74	536.35	454.74	111.4	1.98	206.05	176.56	751.8	885.16	110.05	100.48
221.32	461.75	194.24	400.75	280.51	1631.2	2063.2	258.8	217.08	378.7	70.14	204.2	2.12	325.35	122.12
6.65	246.5	215.1	265.5	188.23	143.9	61.38	171.65	104.16	81.55	6.58	216.4	86.69	169.7	42.85
582.87	2011.35	2252.63	1361.25	1333.25	3424.55	1023.4	705.9	873.28	1443.4	126.85	807.65	596.02	1291.15	225.92
8.91	171.3	132.09	256.7	11.31	367.7	104.23	965.5	290.34	1141.5	793.23	1090.25	537.47	734.5	635.41
774.71	3308.2	110.59	4076.9	1197.7	3003.05	220.12	2136.05	704.77	2991.75	1310.48	4183.85	1910.25	1879.25	1321.79
13.44	1204.35	292.95	1318.75	131.17	1279.35	455.87	1357.3	503.04	850.8	61.38	1276.65	53.25	1135.95	133.29
6680.89	34803.25	8632.71	40806.75	17122.95	43448.55	2225.34	52508.95	38085.97	50525.1	1817.41	58849.6	11173.84	49397.85	12363.83
459.12	4544.5	338.28	4817.2	47.38	3798.85	1041.5	5150.25	318.83	4081.05	393.08	5183.75	1240.34	6020.5	2516.03
38.11	1642.7	320.46	1464.95	69.08	1919.1	506.57	1142.35	535.92	519.05	110.66	1889.75	1531.24	914.8	24.18

192.19	1059.1	412.24	1051.1	423.56	692.75	263.54	396.95	337.5	353.85	79.13	671.8	607.97	669.9	540.65
110.73	257	111.44	176.05	225.92	108.7	108.47	420.4	527.78	273.4	293.03	219	275.35	66.8	50.06
331.56	2947.05	2125.35	2747.45	2407.63	2165.5	225.71	2669.15	195.52	2447.3	1177.19	4327.3	1874.26	3358.3	674.16
97.23	210.3	41.01	222.15	24.25	224.8	49.92	183.5	83.16	978.65	1059.74	657.1	548.57	370.35	110.38
287.51	792.15	142.91	676.65	20.44	1311.75	376.25	878	588.74	826.55	217.86	418.7	200.82	825.45	139.23
9.33	1627.95	593.62	2083.25	50.28	1146.15	387.85	904.45	674.79	1460.5	426.95	1399.05	148.85	1257.9	566.11
312.12	1023.75	896.26	980.25	957.78	178.65	160.87	204.7	235.33	412.8	412.67	745.3	674.58	128.55	66.96
65.41	921.15	363.52	941.95	334.11	494.6	506.29	1086.5	35.5	751.65	334.39	1061.05	406.23	1626.35	1125.22
761.13	1399.9	450.85	1395.1	444.06	1128	114.27	2525.8	1291.32	671.75	186.18	282.65	138.38	356.45	242.75
8.56	3430.35	203.01	3721.75	209.09	3341.6	711.77	3170.65	420.52	3975.2	176.21	3336.75	15.06	3572.8	215.24
358.72	2143.45	43.77	1999.25	247.7	1049.95	866.98	936.95	799.67	1081.05	1060.87	1072.3	1168.56	1282.85	30.05
108.61	891.05	409.77	1001.5	253.57	1372.35	656.12	586.95	452.76	1068.7	675.99	691.2	674.01	918.1	855.74
861.61	8185.8	1420.15	8308.5	1593.68	8067.9	2618.84	8274.45	3983.77	6245.4	2470.91	8164.1	1645.01	9081.1	1933.37
60.32	154.05	88.32	159.1	81.18	178.5	152.03	165.75	143.05	108	10.32	148	73.96	150.2	22.34
14.21	393.15	300.45	330.75	388.7	139.6	53.32	278.4	330.93	243.2	11.74	400.15	6.86	79.15	28.92
9.83	387.25	15.49	410.85	48.86	378.95	321.24	1331.4	917.97	787	186.39	933.95	151.39	720.9	58.83

89.45	137.9	171.97	158.35	143.05	369.65	368.9	345.2	207.18	245.7	172.25	130.5	5.66	447.15	159.59
499.71	452.75	350.94	246.75	59.61	279.05	174.16	696.9	613.2	919.35	611.29	395.2	74.95	292.1	234.48
0.07	132.45	121.83	30.6	22.2	40.7	37.05	113.8	65.34	92.75	62.58	87.4	97.72	47.25	7.14
520.78	1111.35	403.4	1371.85	35	617.45	278.39	1309.45	1445.11	1217.05	368.9	2029.55	1365.35	1264.65	637.32
440.6	1529.85	417.12	1503.15	379.36	1779.4	481.54	2763.4	1311.82	1615.7	920.09	1481.6	759.57	442.9	96.03
3944.95	15873.7	1678.81	22442	7610.17	12374.65	2185.46	38591.5	34243.48	26971.2	11201.7	24939.2	12125.18	35990.5	6173.04
1200.88	2393.95	850.3	2714.4	397.11	1739.5	8.2	1046.7	793.94	2378.65	549.78	2799.05	1839.68	2070.1	482.67
299.67	313.8	94.61	311.65	91.57	409	5.23	389	268.7	269.25	120	249	131.8	400.45	364.65
559.6	2089	802	2206.95	635.19	1211.8	353.69	2233.7	57.98	3289.9	210.86	2018.15	331.42	2289.95	641.84
444.42	785.55	239.21	1354.35	565.19	844.8	124.88	219.9	112.29	599.6	717.15	317.35	368.76	934.95	458.28
388.27	436.4	291.05	381.5	213.4	291.65	31.61	851.2	656.34	185.65	65.27	77.35	56.36	192.75	19.59
796.63	1264	1279.86	2173.95	7	3110.5	3774.54	2993.95	3112.19	3126.35	3589.63	1914.3	1637.94	674.1	58.55
170.7	497.6	484.23	249.95	134	706.65	812.82	224.1	36.2	213.6	144.53	262.1	171.54	667.4	777.96
279.87	408.85	46.74	229.15	300.87	679.25	763.32	379.65	341.6	102.55	6.29	1408.2	1031.53	302.1	99.14
185.69	2269.8	221.89	2201.9	317.92	1473.05	140.36	1506.85	10.82	1903.7	45.68	1624.95	393.22	1818.5	626.92

5302.17	8691.05	501.83	9877.3	2179.44	8429.1	3465.67	6538.25	7223.31	5695.9	2038.31	6837.75	686.25	7255	2019.07
665.67	1813.3	585.63	1856.9	523.97	1948.3	352.14	2186.15	614.55	2771.3	1070.28	1541.9	0.57	2507.7	103.66
150.9	745.45	653.15	797.95	578.91	1360.4	1354.53	1326	1439.25	562.75	319.82	1049.85	445.27	426.1	3.82
94.75	870.9	83.86	833.2	30.55	741.6	252.15	1289.9	1540.5	842.95	325.76	933.55	540.58	704.8	87.26
240.7	3782.3	1943.13	4016.35	1612.13	3757.85	754.7	3497.5	654.78	4934.55	1252.92	3227	20.22	4698.25	179.11
27.01	160.45	49.99	177.3	26.16	160.4	19.8	882	1092.2	276.55	232	402.75	396.05	220.25	151.25
637.81	297.6	200.39	260.8	148.35	375.8	451.7	260.4	47.94	178.1	111.44	188.8	124.45	148.05	52.82
53.88	61.45	60.17	67.45	51.69	85.4	100.69	143.9	124.88	251.9	311.13	320.25	373.99	74.8	50.91
578.84	5427.3	341.25	5756.55	124.38	5532.95	181.23	4220.65	2759.77	4175.45	654.99	3485.6	2881.04	5295.55	983.51
972.77	9969.4	328.52	9318.5	1249.03	8578.05	2312.31	9062.25	5804.29	11127.55	1536.19	9806.45	2550.46	18544.5	5406.11
334.6	868.6	683.91	1249.05	145.88	344.25	77.85	1559.95	1851.56	1621.8	553.81	585.65	530.68	852.15	568.02
2923.82	13197.2	1284.11	12137.55	214.47	13207.55	2977.56	8856.3	5620.79	13838.65	3203.41	9734.65	11295.25	15065.6	1627.05
169.71	68.65	22.84	45.3	10.18	139.4	26.45	164.2	56.14	661.95	488.82	178.75	220.26	571.35	714.11
42.99	173.3	52.89	180.65	42.5	340.6	327.53	541.75	302.29	504.9	446.33	1779.4	933.1	1265.65	63.71
74.95	379.1	112.57	389.2	126.85	704.05	398.03	1505.7	1733.97	416	293.87	1179.25	823.85	376.95	241.76
771.03	1902.25	683.98	1795.3	835.23	1913	1448.44	1227	1307.72	1393.5	260.07	1210.35	648.91	2114.85	95.25

36.98	873.3	839.48	885.15	822.72	457.3	34.93	610.55	135.98	846.1	408.85	646.2	277.47	628.1	159.81
83.58	156.1	153.3	156.25	153.09	187.15	161.01	134.75	84.36	150.7	91.64	234.55	198.63	148.5	83.16
3.96	118.7	21.78	98.3	7.07	1032.95	1350.79	567.85	575.51	534.5	612.5	244.65	174.02	209.55	29.91
24.96	720.35	497.31	387.95	27.22	336.85	75.31	473.85	55.08	641.9	477.72	1154.45	1170.33	446.7	374.63
12.8	319.9	254.28	282.75	306.81	54.5	12.73	205.45	82.52	533.65	710.01	838.85	1033.01	649.15	123.39
6.22	398.8	235.89	456.05	154.93	479.1	99.14	416.75	8.84	361	46.53	676.2	362.32	477.3	128.41
3037.31	2541.3	248.05	3049.7	470.93	2348	295.99	1913.15	630.81	1553.25	25.24	1348.35	490.52	1723.5	562.72
759.43	2351.3	73.4	2909.7	716.3	1600.65	624.73	1966.2	443.21	2496.45	1316.56	3478.65	526.3	1870.25	462.24
183.64	336.25	222.81	357.15	193.25	239.85	90.58	305.95	232.14	657.55	300.17	319.9	78.21	280.25	102.6
307.87	937.85	255.9	648.55	665.03	1089.25	1186.31	1056.9	835.8	319.3	88.39	237.35	48.3	287.3	40.02
65.34	2042.75	542.85	1767.45	932.18	1427.95	325.62	1797.25	523.61	2080.75	633.07	1353.15	1111.93	1581.8	619.28
2844.97	19382.3	10807.7	23859.65	17139.63	23920.35	2280.21	40101.4	9481.45	38460.95	13077.45	47540.4	23321.23	36988.2	2184.39
40.87	1635.3	430.91	1395.35	770.25	1047.15	862.88	237.55	111.23	793.75	196.08	498.15	535.63	1430.6	1006.35
690.14	749.15	472.84	398.1	23.62	1040.5	1060.24	234.05	84.22	673.85	455.02	1784.25	1179.67	317.05	18.31
463.01	2044	1009.89	1973.65	1109.38	1708.05	506.78	1702.6	838.06	1042.9	42.29	1894.85	753.42	803.9	757.45
1017.81	5022.65	331.85	4982	274.36	4012.45	631.52	3686.7	1958.83	2307.6	735.96	4314.3	963.36	4265.5	1404.46
107.62	318.7	223.3	381.55	312.19	267.15	219.98	993.8	1071.69	143.45	30.9	507.05	140.22	194.1	37.19
895.41	4857.4	1783.89	6217.95	140.22	1573.8	1304.89	5195.65	4249.36	4591.65	98.08	5059.05	83.65	3476.8	923.76
5.52	133.15	131.45	145.25	114.34	118.25	23.69	371.4	81.18	75.75	22.98	152.25	21.57	317.55	206.55
113.84	1403.6	599.2	1149.3	239.57	1369.85	61.02	1987.15	1154.21	1016.15	559.25	832.4	292.04	1502.5	74.81

478.71	2408.25	1123.24	2976.4	319.75	1356.15	668.85	1718.85	843.51	1632.9	106.35	2491	165.6	1995.2	646.72
317.49	3157	1345.77	2803.05	1846.33	3769.85	2795.12	8097.5	7234.83	10143.7	10056.33	12784.85	11699.01	2819.75	1518.09
415.21	4778.25	366.49	4543.1	33.94	4255.65	1077.56	2955.6	3558.16	4899.25	782.98	5159.05	1107.12	4648	207.18
391.03	2625.6	834.24	2839.45	531.82	1309.3	811.62	1467.4	508.41	1984.5	259.37	2200.15	189.86	1478.75	1505.22
100.06	249.9	187.81	329.15	75.73	472.95	351.79	495.5	157.54	299.75	162.42	447.3	263.04	285.1	186.96
127.99	174.5	76.37	201.7	37.9	260.9	208.31	351.85	311.34	322.2	61.09	230.8	40.31	248.8	92.49
34.65	212.15	75.73	228.3	98.57	221.8	18.1	326.4	244.38	184.2	9.19	238.05	66.96	262.05	4.03
5364.11	5364.75	2949.41	5368.9	2955.28	5522.7	4118.76	5044.95	965.7	6295.6	1672.87	6750.4	2837.9	4853.5	3189.48
246.78	198.95	91.57	631.6	520.29	1457.8	1192.89	1873.85	2285.3	1008.75	770.82	701.75	378.37	1052.35	193.39
243.6	665.35	686.25	638.25	724.57	377.9	223.59	1477.55	985.64	83.05	44.62	1404.3	1334.88	804.25	331.56
869.18	2767.4	677.55	3138.85	152.24	3178.45	1423.76	2840.4	632.72	3770.7	270.26	4038.75	232	3490.7	1098

1573.17	4128	1693.24	3407.1	673.73	5179.35	1194.52	1569.55	1131.16	1968.25	2250.51	1605.8	1602.45	2043.25	1378.93
22.91	581.55	194.38	607.05	158.32	907.3	423.7	279.95	277.12	574.1	401.21	486.95	280.65	720.4	318.48
607.4	558	279.45	696.05	84.22	1179.9	1169.27	522.35	283.76	233.75	234.41	1713.55	1641.41	609.2	123.04
117.95	388.75	181.09	500.95	22.42	1273.95	1385.72	899	654.5	452.1	130.67	441.15	119.85	287.5	198.56
239.36	177.1	138.59	296.9	30.83	168.85	90.16	1067.25	1246.98	258.5	267.99	592.35	725.42	470.25	505.51
6005.95	22252.65	4751.97	27559.2	12256.56	24702.85	13640.16	22016.05	7114.84	16251	140.57	13509.8	276.62	22506.35	11738.89
113.28	2379.8	375.19	2290.65	501.27	2565.1	1447.87	2777.9	835.8	2520.55	485	1799.05	1202.86	2958.75	201.6
15.63	46.3	19.09	19.4	18.95	88.25	103.45	139.55	134	62.55	54.38	75.55	81.25	397.85	458.84
634.35	797.3	401.07	962.4	167.58	497.35	123.39	853.45	199.9	1650.4	854.33	1376.75	913.37	737.7	108.61
65.62	309.75	214.89	305.3	221.18	716	674.01	429.15	258.16	212.2	114.55	884.3	859.42	265.35	16.05
5.09	187.2	242.68	196.2	229.95	52.8	53.32	262.05	273.01	139.95	97.93	63.95	30.9	101.85	93.69
30.26	762.5	851.64	574.4	585.63	863.1	683.77	2016.9	1265.3	373.05	256.89	268.1	71.98	214.95	32.88
24.68	330.85	198.63	359.1	158.67	654.75	591.07	131	104.65	747.8	1004.8	220.75	195.23	165.75	57.35
23.12	131.55	49.71	126.1	57.42	201.5	140.29	729.35	716.09	65.1	70.71	362.35	136.68	201.8	154.86

55.51	640.9	410.83	655.6	390.04	486.05	125.65	721.8	386.08	543.55	167.51	298.5	83.16	390.9	64.06
363.59	560.35	72.05	460.6	69.01	600.95	407.79	1060.05	51.97	489.8	341.25	548.8	380.85	977	493.84
10.82	540.05	222.67	500.5	166.74	425.3	149.48	362.6	86.13	573.7	105.36	1148.15	1087.46	257.5	65.9
189.5	1428.3	132.51	1642.45	170.34	1049.4	168.43	1858.5	1998.28	1743.45	345.28	1191	984.15	1374.4	343.65
22.42	657	590.15	536.35	419.53	1180.95	94.68	679.6	465.13	816.4	179.75	460.45	493.21	655.9	226.98
1669.41	6293.9	2688.99	7551.85	909.98	4980.45	1617.08	1791.85	288.15	1472.45	1444.27	2203.4	1970.28	4108.8	2785.29
20.58	354.6	97.58	452.9	236.6	589.45	709.3	305.85	298.19	498.45	462.09	357.3	310.84	242.6	74.39
553.45	1177.1	837.07	1097.4	724.36	923.5	851.64	1518.3	791.96	1923.15	1193.95	2029.35	517.96	576.55	170.77
1117.23	3121.65	1013.92	2568.75	232	3778.85	749.75	1426.85	1168.78	4226.75	566.46	2141.3	497.38	2598.75	967.82
15.27	1478.7	1120.48	1479.15	1121.12	2355.7	1398.23	1194.15	847.61	3119	23.05	2668.95	1092.27	2601.15	739.99
349.24	677.85	621.62	704.55	659.38	692.55	799.81	467.55	533.23	691.35	175.72	1267.65	831.35	526.1	431.62
471.22	6786.2	332.76	6618.6	569.79	6124.3	4062.61	7248.15	2549.47	10730.05	50.28	10105.55	1496.03	9446.05	1913.78
4.6	78.65	80.12	84.7	71.56	121.6	90.09	109.3	5.94	56.25	4.45	41	27.44	96.15	38.25
1232.06	406.3	297.41	694.45	704.91	882.55	718.49	705.65	779.02	138.95	36.42	187.4	35.36	1007.95	907.71
302.43	3361.75	764.03	3476.2	602.17	2388.75	1947.16	3205.65	1456.43	2827.2	1332.47	2328.45	311.34	3007.95	1577.63

255.48	1016.55	554.3	910.85	703.78	747.3	412.53	310.75	40.52	364.25	73.75	564.8	462.31	481.95	427.3
48.3	311.65	53.81	227.05	65.83	562.85	337.36	406.5	378.44	377.55	247.28	250.9	71.42	470.35	50.7
474.47	2818.5	727.05	2737.7	841.32	2253.3	60.53	1480	1325.54	2249	775.41	2655.35	557.55	2721	35.64
113.77	371.6	83.01	249	90.37	362.75	150.83	469.6	447.88	175.25	91.43	527.3	410.4	383.65	157.9
59.54	883.6	418.18	1126.45	74.74	1028.95	559.11	1118.8	1131.8	698.55	793.73	964.1	443.5	1331.85	1068.08
350.02	1857.15	1260.14	2395.35	499.01	2377.75	1314.44	1051.2	697.91	965.7	737.51	828.4	762.69	1466.9	346.34
445.19	857.25	311.9	844.1	330.5	856.15	526.3	723.7	294.3	1449.6	749.67	1111.25	809.57	487.55	329.58
127.28	623.75	398.88	705.95	282.63	1599.65	1810.97	662.5	571.48	1705.7	1644.31	1567.65	1569	584.85	34.58
79.34	498.35	179.53	480.9	154.86	1185.05	518.1	994.25	75.02	495.95	501.69	961.3	667.08	1706.35	1173.73
128.41	556.2	253.85	386.2	494.27	389.35	134.14	118	15.13	359.55	267.07	350.3	383.39	358.35	343.02
212.98	272.85	293.94	315.7	233.35	297.3	233.06	325	18.81	676.45	766.01	748.75	993.84	692.9	163.2
4504.48	9422.15	6848.97	7054	3499.9	10618.55	3632.48	6753.1	2814.99	9677.2	4201.49	5106.1	6842.96	8944.1	1232.49
682.64	840.35	86.34	1017.85	337.36	385.8	27.58	250.2	98.85	484.65	406.66	647.45	79.13	372.75	333.83
202.87	165.15	165.82	200.85	115.33	274.4	217.79	510	9.33	208.15	76.01	348.6	214.11	233.85	89.45
204.14	67.45	37.97	63.6	43.42	184.6	116.96	80.8	13.44	166.4	69.72	1035.2	965.34	136.95	20.44
2642.88	10472.2	2234.74	9012.6	170.55	9062.05	3401.54	8208.4	5102.91	10790.2	1315.08	7546.8	1582.65	9317.45	65.27

41.44	254.9	25.17	212.65	84.92	318.4	215.53	460.3	195.73	1154.55	814.66	154.5	31.54	499.8	160.37
4747.87	4421.35	3781.68	4109.85	3341.15	4972.75	1634.62	2118.05	186.61	5963.5	277.75	5182	5064.58	3714.85	385.44
886.71	2918.35	80.82	3590.9	1031.95	3100.5	2167.71	2090	1942.99	2444.85	965.7	3732.3	1198.83	2602.45	286.59
50.06	3406.1	1527.21	3611.5	1236.73	2285.65	94.12	3309.45	2067.37	2871.55	396.62	3388.65	76.44	2499.3	566.25
233.13	401	162.35	399.2	164.9	160.6	143.68	585.4	489.6	365	285.11	505.95	55.93	233.25	171.19
34.08	5762.2	1344.21	6107.15	856.38	5897.35	1426.73	5569.3	3773.97	4698.7	1172.81	3263.85	3079.52	6184.3	377.03
372.72	131.95	39.24	119.6	56.71	145.45	63.71	113.6	12.3	130	18.67	170.8	18.1	176.1	33.09
158.04	301.5	396.12	298.5	400.36	237.7	34.65	698.1	267.85	591.2	722.66	249	302.22	250.8	232.78
123.39	497.5	8.77	714.4	315.51	195	118.65	175.6	17.11	508.95	424.19	230.25	26.38	565.1	323.85
190.07	535.65	352.07	504.3	396.4	672.6	302.08	462.7	70.71	398.3	76.37	472.3	5.66	248.1	285.39
1536.9	1732.4	484.93	1759.7	446.33	627.5	433.46	2400.95	915.07	1908.9	474.47	2186.8	865.22	1751.1	160.09
602.95	3201.5	1238.29	2335.45	13.51	3271.2	2278.86	1277.9	824.35	2299.5	74.39	1597	204.35	2373.55	1042.63
191.06	413.3	198.27	907.95	501.27	905.35	799.95	1332.35	445.41	1700.1	185.4	1104.25	1157.04	411.7	14.99
695.58	3803.7	528.49	3849.2	464.14	3188.6	285.25	1904.05	783.83	3081.65	484.01	1433.55	1021.13	2127.6	526.51
263.82	686.55	704.91	734.35	637.32	1203.75	728.96	764.75	571.55	367.05	137.67	288.95	326.47	258.15	76.86
375.4	303.15	116.74	329.2	79.9	209.45	139.37	312.75	61.73	257.55	196.65	832.55	937.13	46.05	12.94

664.04	2040.3	775.55	2109.65	677.48	1355.55	499.15	933.55	261.56	2015.6	101.26	1621.75	1212.48	824.65	29.2
15.7	508.95	163.98	397.35	321.8	497.65	406.66	391.55	441.87	1066.95	410.62	809.45	914.93	481.9	475.6
25.74	135.05	85.63	273.9	110.73	151.3	115.97	284.35	54.38	484.25	491.23	138.5	87.82	593.6	181.16
276.34	285.65	99.77	311.3	63.5	845.65	417.55	1318.7	1518.44	650.65	317.14	1658.1	667.08	736.25	416.98
367.06	1531.15	202.59	1287.6	547.02	3155.7	1586.32	1771.1	110.45	1178.6	998.86	2718.2	1974.67	814.3	406.44
149.06	197	34.37	123.35	69.79	227.2	117.66	363.4	287.51	457.25	116.46	603.4	47.09	806.3	256.4
1307.37	8011.75	5327.84	5312.4	1510.38	4116.15	2009.81	3440.95	867.55	7375.65	2862.3	4367.25	3448.06	3457.25	1639.99
17.68	169.55	167.94	37.25	19.16	363.3	378.16	282.35	326.9	37.2	33.94	75.15	66.96	360.3	473.34
120.56	148.65	83.79	342.45	357.87	1276.1	1748.53	112.1	127.99	538.05	625.86	54.55	36.13	62.5	17.11
6.01	374.1	243.39	313.15	329.58	157.6	50.49	473.25	306.53	258.25	87.61	1137.75	1432.67	321.3	113.7
294.86	100.05	42.64	95.4	49.21	91.1	8.77	499.05	557.41	132.45	21.43	331.15	254.77	180.1	66.89
7.07	88.95	111.65	13.95	5.59	522.1	700.88	73.8	26.87	214.2	211.85	57.1	4.95	381.95	131.88
315.09	1005.3	657.47	565.9	36.06	715.05	552.18	194.7	33.8	938.6	638.52	225.1	9.48	447.4	44.41
234.12	889.4	135.06	819.65	36.42	516.9	53.17	737.7	273.51	874.35	850.3	277.6	166.45	936.3	936.07
106.14	1168.25	117.59	1090.3	227.83	676.7	162.35	277.45	125.65	988.15	592.63	564.55	382.33	935.2	39.46

78.06	133.25	17.61	296.25	248.12	548.95	393.93	2873.8	3803.53	207.4	222.31	863.2	954.45	168.05	122.4
459.05	1107.35	429.43	750.8	933.66	1285.15	812.25	1464.05	1324.2	1042.5	387.35	853.4	76.65	1145.2	569.22
96.8	225.4	186.39	261.95	134.7	266.6	93.06	1536.8	820.95	1027	1299.8	261.2	231.93	377.5	59.54
242.4	1911.1	742.18	1958.5	675.15	1133.15	413.45	1741.55	325.2	1499.1	908.35	1772.45	150.12	1855.85	1101.04
2.33	1740.2	831.13	1865.35	654.14	814.35	536.34	498.7	157.54	1110.4	679.25	1015.2	60.39	1307.85	671.68
267.78	1095.55	117.87	1080.3	139.44	978	18.38	2462.75	2346.11	1356.6	158.39	1364.35	692.33	1489.2	1147.07
2450.2	5692.65	229.6	4846.7	966.76	6605.6	202.23	4884.3	1576.71	7797.35	3276.8	4191.75	986.48	4615.15	137.82
67.74	868.5	665.25	945.5	556.35	413.25	9.83	579.55	360.27	758.4	160.94	501.35	96.1	501.85	83.65
70.29	609.2	375.19	555.4	451.28	397.45	151.67	278.35	33.16	89.25	42.92	307.05	160.87	148	146.94
55.08	168.4	113.56	178.9	98.71	232.1	16.12	373.5	155.14	800.2	31.4	167.15	124.1	289.75	65.97
1298.96	7867.55	2367.46	8777.7	3654.61	7748.15	1346.97	5984.85	4165.07	3460.9	2093.04	5813.7	1780.64	7394.5	99.28
190.71	1381.25	119.29	1760.3	416.77	700.55	475.81	1522.6	179.89	1910.1	478.57	727.25	219.7	2008.75	656.55

77.64	276.85	78.7	199.65	30.48	535.5	593.26	220	124.31	182.45	166.38	241.75	193.39	161.9	98
239.28	1111.6	1168.28	795.3	720.97	1422.4	1000.84	1652.5	900.29	794.55	831.2	1948.05	657.26	860	478.43
43.91	241.9	133.36	244.15	130.18	228.15	84.36	372.5	126.15	182.4	36.49	363.65	146.87	331.1	47.38
393.5	189.85	11.24	133.8	68.02	419.1	436.43	408.2	482.95	122.15	75.59	249.15	31.89	266.35	270.04
21.85	448.45	121.98	558.2	33.23	260.55	3.18	1458.45	690.77	199.55	69.79	697.05	90.44	352.25	6.72
69.58	202.15	145.31	124.75	35.85	548.65	227.76	701.7	795.5	611.65	476.66	509.1	3.11	780.85	386.58
26.73	396.1	161.08	639.75	183.49	224.95	47.87	857.05	214.75	512	348.6	954.95	86.9	507.95	196.22
1261.9	5729.1	3987.37	4746.3	2597.49	6110	4106.73	2554.55	3181.34	2151.05	1343.01	2387.9	1571.19	3854.6	53.74
2413.78	13256.5	7673.24	12297.05	6316.37	12305.3	7958.06	8100.55	7533.44	11639.8	6170.64	11116.9	6640.02	10807.75	4125.47
90.51	716.55	60.74	543.5	183.99	550.2	349.74	1168.05	1536.05	252.55	74.18	420.9	331.35	638.9	238.29
131.1	1759.15	151.82	2208.3	787.01	3051.6	381.41	1694.4	670.48	499.55	365.22	1421.6	410.69	1318.9	309.57
128.13	601.15	289.42	815.8	592.98	1373.95	606.77	1669.2	199.69	277.05	279.38	685.05	402.84	978.15	334.53
20.01	166.2	48.22	151.85	68.52	145	133.36	462	531.89	189.85	147.01	72.65	22.13	179.75	25.67
89.52	172.4	218.35	175.75	213.62	107.55	129.75	205.45	190.85	125.1	74.1	120.85	100.76	72.8	16.83
201.45	2825.8	1068.3	3033.85	774.07	2748.7	1284.81	3216.3	180.88	2291.3	429.07	3427.55	1960.88	3136.15	730.37
263.89	515.85	514.7	152.2	0.42	761.5	558.76	1518.1	1095.45	249.35	104.86	302.25	167.09	430.95	181.8

30.12	375.4	67.46	398.95	100.76	239.1	4.53	1315.5	1165.88	537.25	411.18	555.9	491.01	537.35	525.31
39.17	305.85	198.06	237.8	294.3	237.4	308.16	1148.15	1378.79	219.6	251.87	578.45	353.91	286.95	232.85
446.04	301.4	206.33	174.9	27.44	658.75	245.58	370.3	0.71	731.25	200.18	426.4	102.67	741.65	196.36
18.6	114.5	69.3	98.6	91.78	92.4	89.66	181.65	118.86	370.25	141.07	554.4	552.11	214.65	142.34
389.05	322.45	223.8	235.15	100.34	908.45	1020.99	723.15	882.68	345.2	231.79	775.65	115.75	894.15	10.54
343.58	338.1	49.78	183.2	169.28	406.05	413.16	1220.95	1151.81	280.05	130.46	933.25	672.81	920.7	333.05
297.2	1440.15	275.84	1514.35	380.78	862.05	926.8	1587.05	509.75	1378.5	459.34	1941.05	246.14	959.4	809.5
86.76	483.2	244.66	516.8	197.14	965.05	1107.12	159.05	39.95	553.4	563.71	727.2	692.4	628.05	4.17
10.18	101.15	42.07	103.4	38.89	353.7	416.49	178.35	3.61	446	473.62	235.6	148.21	244.8	245.51
370.88	5255.25	1273.99	5261.3	1282.55	5107.45	1522.61	3211.2	2896.88	4734.8	2799.15	4937.25	2398.01	4181	1213.11
48.51	1227.95	694.87	1266.25	640.71	723.85	194.1	925.45	431.55	794.4	158.96	1420.6	831.42	1134.4	525.66
21.85	317	252.86	296.7	281.57	176.55	80.82	266.7	228.54	82.65	13.22	255.35	237.09	249.85	132.3
377.88	574.1	395.27	602.95	354.47	411.75	34.72	649.5	658.74	809.05	901.21	463.3	218.78	218.45	243.88
605.64	959.6	30.55	949.75	44.48	613	237.73	588.05	204.14	1172.05	281.22	550.15	193.25	1085	563.56
327.39	2933.8	881.2	2495	260.64	4010.15	2264.23	1341.6	760	1566.9	736.24	1869.15	759.22	2615	1126.7
787.36	2455.3	1661.84	3391.05	338.49	2705.5	1428.21	2232.85	1144.88	3184.35	179.68	1910.7	986.13	2747.2	314.38

530.33	2630.9	518.31	2687.45	438.34	2533.55	887.91	2392.25	286.73	2859.4	114.55	2314.8	555.36	2213.8	567.52
342.95	350.3	95.32	249.3	238.15	215.15	110.66	1166.2	714.04	529.2	25.6	412.7	101.26	565.2	592.56
3.61	128.35	5.44	117.95	20.15	159.35	143.61	155.35	125.65	125.3	42	162.1	4.53	130	35.92
863.94	2413.2	1245.92	1988.25	644.95	3139.1	490.73	2017.85	310.77	1786.25	980.69	1388.5	1207.6	2258.3	748.54
159.74	3136.7	562.15	3392.45	200.46	3657.15	1585.69	3342.4	72.83	4521	1255.82	4384.55	1973.18	3993.7	479.56
55.93	2046.6	187.38	1917.5	369.96	1485.3	30.55	2151.8	301.51	2341.55	230.59	1354.55	779.87	1416.45	70.64
1376.6	4712.95	1106.83	3530.2	565.83	5281.5	1491.71	5808.75	2750.86	5989.6	303.77	3321.1	2069.28	6685.85	569.86
72.83	1232.55	977.58	1478.45	1325.33	1932.1	553.95	254.9	106.77	493	432.61	815.1	887.42	1305.15	319.68
261.98	784	686.18	710.9	789.56	829.6	699.05	1422.55	1350.22	891.3	461.6	944.95	1233.12	119.4	85.98
249.75	799.8	531.89	788.6	547.72	722.45	203.29	133.35	127.21	315.85	189.86	1138.55	1146.72	133.75	79.27
141.7	497.15	235.54	388.2	389.62	437.7	122.19	236.05	203.86	737.8	250.03	666.8	8.2	712.85	175.57
978.35	2981.25	1335.8	2690.8	925.04	3249.1	1514.2	1836.55	735.46	3254.55	1587.38	2707.05	2085.33	3075.5	183.28
370.03	5291.95	201.88	5374.65	84.92	4078.2	867.62	4100.85	2932.3	4691.9	382.12	4973.5	1132.79	4537.75	803.2
286.24	3534.35	509.47	3813.4	904.11	3926.45	143.9	1869.35	1339.33	4179	488.61	4407.35	237.38	3924.1	1481.81
61.45	3045.65	1506.21	3167.15	1334.38	2940.3	1462.44	1228.3	1071.27	2955.15	991.86	1597.9	904.25	2074.9	1231.36
179.89	124.6	43.56	51.3	60.1	227.85	293.1	1530.2	2074.79	108	130.25	184.1	210.72	62.95	37.26

1102.95	577.4	472.35	217.75	36.27	1739.05	1154.07	1138.3	998.72	1174.1	40.16	1890.3	1215.23	1191.9	268.56
2335.79	6685.3	2709.49	6442.8	2366.55	7927.6	1945.25	6965.15	519.79	6364.85	904.32	5470.5	2980.6	6406.05	56.78
1166.16	1945.25	2062.98	1929.55	2085.19	6003.4	8068.8	5422.45	7141	1751.5	1913.01	4924.6	4005.05	2733.35	106.14
32.53	861.95	344.29	639.3	29.42	609.6	80.19	331.2	101.82	583.5	352.56	1681.65	1316.14	1192.5	740.48
142.98	481.2	8.77	402.95	101.89	360	21.5	1285.05	1344.56	290.6	9.9	420.3	10.32	365.1	43.42
479.42	2096.55	736.73	2034.7	649.27	2200.85	22.13	2431.9	1372.78	2101.95	31.18	1115.25	995.11	2793.05	308.09
220.26	341.85	293.94	443.4	150.33	532.2	472.77	1764.45	1938.11	418.15	176.14	712.4	478.71	337.05	114.34
450.57	494.15	284.89	463.6	241.69	578.35	173.88	391.5	235.04	877.6	247.35	584.45	489.67	903.05	585.7
623.88	1921.15	1012.79	1272.3	95.18	2473.95	296.21	1349.8	154.86	1259.9	586.9	1534.5	22.63	1105.5	439.11
418.32	6556.45	1340.6	6474.85	1225.2	6573.6	1847.1	2669.9	1206.18	4326.55	2959.17	2699.05	647.92	5009.9	58.69
294.65	668.85	459.97	559	615.32	521.3	169	142.55	100.2	298.4	196.72	163.1	135.76	168.5	22.63
1901.06	6689.25	3249.51	7611.05	4553.13	5843.75	3162.54	4196.5	2243.51	3559.1	1075.37	4116.9	2369.8	4831.65	466.05
51.41	61.7	22.91	59.55	25.95	112.5	65.05	331.35	299.88	144.8	20.22	194	75.38	54.7	20.51
43.77	641	171.4	828.5	436.57	1703.15	419.95	936.7	648.28	2080.4	185.26	880.75	731.78	1322.85	1267.77
276.83	1881.15	264.67	1632.85	86.48	1779.25	393.65	2625.4	1051.61	1374.05	57.49	1664.3	503.88	1673.85	336.94
8.06	957.25	593.62	1158.6	308.86	845.9	758.02	989.6	123.04	2613.45	313.32	940.2	321.03	848.4	430.35

130.74	577.95	93.97	455.85	266.65	1084.6	1290.61	402.65	22.7	368.35	177.27	339.8	41.01	313.1	0
557.55	2154.3	1317.91	2355.25	1033.72	1546.15	738.86	1404.85	359.28	1938.25	151.25	1029.05	925.81	1355.1	408
90.65	1151.45	905.59	1196.75	841.53	344.25	83.23	893.55	1032.73	837.45	671.82	850.45	884.66	1021.2	654.22
606.91	401.45	250.53	376.4	215.1	1301.85	749.6	592.15	320.11	1509.6	749.39	871.7	907.22	1402.9	454.39
1322.01	1775.75	421.65	1858.25	538.32	1795	263.61	1190.35	817.06	1518.3	466.55	1454.25	1180.23	2330.4	864.93
28.28	227.55	15.34	176.35	57.06	423.6	311.13	260.95	7	435.25	295.22	860.35	843.79	418.05	27.51
84	102	52.75	123.8	21.92	221.25	205.13	318.95	124.52	144	112.85	210.5	183.28	94.6	17.25
62.15	19.1	10.04	16.2	14.14	367.6	501.34	57.05	61.87	29.25	13.65	541.25	728.39	629.3	504.45
7.71	298.3	12.59	327.45	28.64	231.55	20.58	548.25	354.05	409.2	50.77	503.65	348.67	779.05	302.15
428.86	1072.75	177.13	1136.65	86.76	703.65	56.64	935.7	28.14	1397.1	909.48	1213.4	604.58	1543.45	186.89
869.67	500.95	346.84	601.6	204.5	461	9.05	504.75	147.01	901	547.87	661	206.76	695.9	545.18
457.29	329.4	58.41	197.35	128.34	763	640.92	1501.6	553.66	706.15	313.88	953.3	914.43	611.1	217.22
94.68	577.7	153.44	593.25	131.45	732.95	590.93	889.85	663.34	355.75	197.92	218.45	104.44	789.05	362.96
573.04	2875.3	491.72	3071.05	214.89	1059.85	863.45	1094.7	801.15	2536.95	261.28	1993.85	1169.34	2814.3	1294.01

1089.51	3638.5	793.23	3347.35	1204.98	2926.7	1452.96	1875.2	2217.35	2748.05	652.45	2543.8	735.67	3556.65	1318.68
47.59	207.3	206.33	242.9	155.99	191.45	104.16	620.45	701.66	307.55	216.45	242.9	65.34	183.05	34.44
349.17	3327	2314.78	4454.4	3909.17	4806.65	1381.47	3274.3	2160.92	3739.35	915.07	5656.85	1262.4	1424.3	792.95
210.15	151	120.49	264.75	40.38	194	157.68	463.65	545.96	313.9	181.02	244.8	214.54	300.15	153.94
663.62	4471.65	982.38	4132.65	1461.8	3326.9	935.22	4183.65	2126.62	3945.95	348.25	2980.5	2208.44	3757.65	352.63
250.6	175.4	100.27	109	6.36	386.05	51.55	513.4	532.03	212.6	193.04	316.75	378.51	193.6	86.13
305.4	698.15	25.24	539.95	198.48	1323.1	1426.8	1206.8	1020.5	1038.9	933.38	1360.85	1205.69	285.9	96.31
24.68	278.35	281.5	76.15	4.45	523.6	2.12	171.15	17.75	109.3	72.12	402.25	260.99	150.9	68.59
172.6	836.25	268.77	940.1	121.91	587.25	212.2	262.15	66.96	328.3	136.75	663.45	166.95	467.25	176
700.81	1081.5	171.54	917.8	59.96	1212.1	73.96	363.2	27.58	473.65	92.42	1078.85	557.98	715.8	230.38
714.96	419.5	269.97	194.65	48.01	741.7	225	220.85	162	648.1	502.47	1315.6	97.02	1102.75	856.66
4399.97	123939.05	64577.87	152487.84	24203.77	127357	51694.04	190996.2	172069.63	155098	28259.81	151629.95	15634.48	214879.8	10767.54
21.21	2808.25	798.96	2910.75	654	2174.25	5.44	1760.9	63.92	1141.75	949.29	1008.45	965.41	563.55	180.81
4231.68	5814.7	3873.25	3829.4	1065.61	6548.45	3074.71	3230.75	574.95	5208.35	526.16	1886.8	1014.56	2887.35	272.17
936.14	1698.9	1398.23	1264.5	783.9	1471	18.95	1202.75	336.94	371.6	171.54	1240.1	553.95	1142.9	383.68
181.37	521.95	382.62	475.5	316.93	489.4	114.98	916.4	509.54	504.85	573.25	203.85	54.52	650	645.73

78.77	962.65	153.94	1112.6	58.12	816.8	3.82	312.1	243.67	923.1	83.44	1398.9	852.63	336.55	211.92
22.56	446.35	260.71	411.55	309.92	352.6	354.68	537.4	331.49	308.35	318.13	590.7	385.23	607.85	150.54
15.77	2340.25	974.18	1772.25	1777.45	803.2	751.94	1040.75	1101.04	1266.65	186.89	1001.3	266.58	1002.65	83.09
236.53	689.3	366.28	472.05	59.04	453.55	151.82	526.5	489.18	526.9	253.71	178.05	21.85	412.15	108.26
56.36	110.55	26.66	61.15	43.2	63.5	75.38	580.7	707.67	93.35	40.94	407.1	103.1	299.7	341.82
1760.55	3696.55	2447.37	4895	752.5	3085.8	516.9	5777.9	1511.51	3365.95	151.11	3541.5	851.07	4891.6	1084.56
25.95	259.15	106.84	241.8	131.38	577.3	324.42	797.85	639.86	680.9	526.79	705.15	104.3	1264.9	44.55
54.38	256.75	257.03	48.7	37.19	645.2	597.93	574.35	377.1	632.65	696.43	1229.55	1516.96	845.45	227.62
190.28	219.35	97.09	159.9	181.16	485.3	528.07	950.3	764.67	684.7	684.34	475.8	323.43	276.1	12.45
23899	107947.45	56072.79	143092.84	6369.7	101551	51082.81	188331.16	164305.38	166564.25	46048.56	178269.8	17862.64	264279.19	4557.87
23.9	688.7	79.48	735.15	145.17	441.65	266.65	188.2	126.29	952	569.08	470.8	567.52	444.5	526.37

265.17	987.05	49.29	925.6	37.62	801.3	37.76	1664.05	1960.17	507.4	373.07	718.85	534.36	597.65	32.03
18.95	297.7	31.11	256.15	27.65	453	55.01	722.8	142.55	318.45	164.12	501.6	297.69	552.45	277.12
4636.85	18490.85	2216.71	19996.05	88.03	27545.9	13307.61	35108.15	13814.11	39131.45	26608.5	41093.3	21900.65	23789.75	5636.42
56.57	486.1	626.64	478.95	636.75	118.15	71.49	1427.1	1933.37	109	3.68	285.15	204.28	891.8	779.51
98.08	856.5	483.24	859.55	478.92	887.4	702.86	339.3	144.53	1114.4	111.72	974.1	362.89	908.25	426.74
520.85	740.15	326.61	658.05	210.51	518.35	553.03	1122.55	114.48	262.45	213.19	230.8	220.05	104.1	12.87
535.99	858	508.98	1130.45	894.28	2147.3	570.07	3468.8	4026.97	812.65	788.78	1593.05	579.05	1334.9	481.54
182.93	307.55	375.12	428.9	203.51	115.45	42.5	485.1	502.47	513.75	477.51	340.35	91.99	734.75	141.92
151.11	476.8	268.28	502.5	231.93	350.15	12.66	359.55	89.59	504.75	319.68	434.65	343.87	252.6	288.64
58.76	397.3	268.98	434.1	216.94	386	462.45	116.2	119.93	60.7	46.24	158.35	38.11	265.85	128.06
617.87	3763.4	1766.49	3528.15	1433.8	2344.15	2068.5	2199.55	2371	3932.6	1103.23	6228.7	598.78	3249.75	101.19
1.2	122	138.73	118.6	143.54	331.35	449.65	154.5	164.47	52.7	10.61	636.55	631.8	56	30.12
527.36	3459.85	735.18	3467.8	723.94	2804.15	331.7	2819.05	741.54	3805.4	243.81	4331.15	1256.88	3544.8	685.19
7722.31	49347.8	9657.52	54402.55	2509.03	50944.9	6585.43	71098.5	29697.36	58387.25	13612.16	68576.84	9057.26	74911.8	5817.65
57.7	123.1	32.81	121.3	35.36	876.7	1137.17	282.25	81.67	645.6	774.56	578.95	73.19	384.45	158.32
562.36	272.3	24.32	264.55	35.28	351.1	148.63	296.6	2.26	535.9	452.27	305.65	75.45	363.9	107.62
163.55	1601.85	151.96	1669.5	56.29	2390.5	2041.98	774.15	246.14	355.45	23.26	638.9	231.79	922.25	919.59
137.82	1649.05	148.14	1540.9	301.09	1434.8	278.18	2094.55	180.52	1864.1	85.84	3863.25	2434.22	1173.85	140.78

21.5	71.9	14.42	125.25	61.02	218.65	240.06	1484.3	1940.87	294.85	349.81	196.65	130.46	178.45	40.8
19.02	543.95	196.5	646.15	51.97	229.15	105.57	3013.65	336.37	592.85	522.34	273	176.64	227.3	63.22
274.78	275.5	260.5	348.85	156.77	707.05	594.75	112.15	31.04	560.4	703.01	633.2	486.21	138.3	116.25
462.94	636.95	764.74	819.7	506.29	438.6	128.41	2157	1379.42	1725.05	1495.6	1399.15	986.06	1362.95	483.31
39.88	332.35	337.36	331.5	338.56	580.75	650.18	823.8	876.25	804.2	741.61	132.2	154.86	251.15	4.6
433.88	431.75	153.65	323.7	0.85	523.2	126.71	528.45	262.97	444.05	374.84	372.15	136.97	685.3	744.16
37.55	430.05	3.89	432.25	7	247.95	192.12	560.5	260.78	409.2	409.98	310.75	113.07	691.1	657.75
90.01	203.45	22.13	220.5	46.24	385.85	300.31	755	32.81	677.45	917.9	719.1	783.19	481.45	557.84
13.58	159.5	0.71	172	16.97	641.3	704	423.05	360.98	440.5	382.12	813.1	227.97	286.75	160.44
147.71	27.4	5.66	24.5	1.56	321.1	388.34	991.85	1297.19	249.95	316.15	97.7	89.94	275.6	300.38
166.31	601.75	252.08	310.7	159.52	489.25	28.5	684.9	270.11	1078.7	899.58	656.75	358.43	832.25	135.84
244.52	1795.25	71.49	1909.25	232.71	1422	358.64	919.35	901.77	1758.4	352.14	1744.9	348.04	1007.9	481.96
36.27	43.2	5.52	46.7	0.57	179.1	100.83	153.6	9.48	166.85	153.23	305.6	63.36	449.6	235.33
52.75	126.7	104.51	138.2	88.25	984.95	1302.7	240.35	167.37	124.25	65.69	152.6	69.86	124.25	78.56

64.21	878.3	219.91	779.55	80.26	566.55	547.23	873.4	107.2	507.2	400.51	492.5	250.88	743.35	439.18
63.78	53.25	12.37	60.85	1.63	82.2	49.64	577.6	767.07	81.4	18.38	207.1	215.1	182.4	79.9
18.24	180.45	145.59	194.1	126.29	226.05	170.77	328.65	198.34	242.25	48.72	198.85	60.03	169.45	58.9
355.67	887.85	894.28	442.65	264.67	1087.35	451.91	618.55	461.25	519.35	105.15	631.3	405.17	1260.35	83.23
101.89	267.15	189.43	217.8	119.64	524.15	313.88	496.55	157.19	251.95	2.62	1025.3	1125.29	1027.85	144.04
636.4	3267.35	733.62	2631.9	165.04	1667.85	1884.65	855.05	377.38	1447.45	587.54	1492.35	861.75	2314.35	647.92
47.59	105.2	21.21	108.4	16.69	134.3	161.36	460.15	603.37	193.85	204.71	160.4	173.67	242.4	199.12
25.81	939.7	23.76	719.5	335.17	1100.2	1221.03	848.15	660.93	1204.25	1273.43	455.85	129.47	467.85	310.63
685.82	921.3	6.65	907.75	12.52	584.25	176.14	162.8	156.98	564.7	557.2	382.25	140.36	493.45	552.46
957	7694.8	1976.79	8296.15	1126.35	4652.1	2014.26	7690.65	5108.35	3085.95	2288.13	5594.75	3688.48	4793	1406.72
22.56	57.15	19.16	43	39.17	36.9	22.63	222.1	248.9	328.95	423.06	84.2	32.67	42.8	17.68
9.19	65.85	2.47	56.3	11.03	675.7	885.58	535.55	355.18	295.8	198.13	362.8	422.71	154.5	50.06
1386.57	7138.85	270.19	7614.4	402.34	6186.3	2441.22	4082.7	1119.92	5697.9	1652.79	4991.65	3556.11	6629.3	24.89
977.43	1200.65	884.38	1143.45	803.49	1913.25	83.51	1697.85	1286.58	937.1	597.65	788.25	95.39	581.7	358.79
151.39	684.65	586.55	367.35	137.82	1268.1	183.28	1281.3	1430.9	926.2	818.69	1158.85	795.14	708.55	422.35
2911.65	13169.2	148.92	13384.35	453.18	9227.3	2394.97	9103.65	4961.7	10690.2	2783.6	12220.9	862.81	9735.4	2313.94
839.05	6129.2	3963.76	5397.8	2929.4	6173.65	2897.51	3898.7	4079.02	5628.2	3563.68	4419.8	5206.43	4836.25	1904.31

79.27	377.4	260.07	251.25	81.67	967.85	633.64	1583.05	2202.71	858.45	561.23	656.75	250.25	325.55	77.99
965.84	801.4	134.92	1023.8	449.44	1218.55	256.89	1427.3	238.15	810.9	97.02	2263.8	1301.08	1443.4	142.55
253.36	1856.55	851.85	1338.45	1584.56	1807.2	1048.07	1114.4	398.38	2139.65	1058.19	1217.1	1100.68	1083.5	809.21
237.66	7459.45	1258.72	7139.4	806.1	5655.5	2089.92	5741.05	1407.5	9419.55	3995.51	4721.3	6224.52	7893.45	989.31
54.16	63.6	28	81.9	2.12	96.8	33.94	423.75	528.42	693	876.95	156.8	70.99	384.65	290.27
4.17	159.15	148.28	190.85	103.45	302.9	49.78	277.4	94.33	223.35	133.86	141.25	7.28	529.2	298.26
405.88	557.15	171.05	788.15	155.63	996.35	817.77	543.3	246.5	648.55	642.12	899.4	1017.24	303.65	157.19
386.93	750.85	584.42	590.3	357.37	563.95	379.65	892.8	321.31	1291.6	694.94	1660.1	1257.24	1259.4	29.27
61.94	540.25	206.69	365.5	453.82	1025.3	666.24	1207.6	845.98	1584.9	1255.82	1121.2	1202.08	466.4	569.36
71.35	220.3	228.11	209.4	243.53	139.05	64.28	587.9	337.86	279.75	159.59	461.15	110.24	498.5	7.21
90.65	1808.15	613.13	2219.05	32.03	626.35	352.49	2290.15	862.18	1452.15	82.52	573.55	108.68	977.75	281.64
18.38	624.25	542.85	623.3	544.19	1074.45	1244.44	997.95	617.52	936.15	722.73	997.2	1243.24	99.05	37.12
7.28	67.4	15.41	53.25	35.43	119.45	115.05	212.55	223.66	94.15	17.75	991.35	1285.31	104.45	33.87
64.06	218.55	185.9	204.65	205.56	1440.95	1196.07	225.7	170.84	477.85	125.09	1683.45	2173.86	355.45	30.33

95.18	1957.6	761.13	2248.75	349.38	2138.25	581.6	3514.85	1285.87	1802.6	359.92	3273.5	677.27	2689.85	392.09
326.9	2220.3	387.35	2282.85	298.89	2769.25	1250.52	1348.15	270.75	2793.35	446.82	1455.45	320.11	1778.95	8.56
111.16	134.7	107.06	184.35	177.27	190.5	81.18	126	61.24	329.75	342.59	665.55	850.72	190.75	156.62
74.67	308.55	206.97	328.65	235.4	725.05	307.95	648.8	347.05	729.5	20.93	1653.6	1825.89	836.4	201.1
259.01	1269.75	817.06	490.5	284.96	1767.1	753.78	577.05	168.93	1110.3	707.67	928.8	637.95	1141.2	1156.12
67.53	213.7	179.46	252.7	124.31	274.55	178.54	458.75	166.95	208.1	43.56	359.15	26.52	320.4	183.85
3.82	1105	1038.74	975.25	855.25	1429.3	169.14	892.95	748.9	937.95	27.65	1586	616.74	528.25	325.62
1.7	31.2	30.83	43.05	14.07	51.5	54.02	98.35	93.97	82.85	76.01	85.5	10.32	231.95	247.7
243.67	1251.4	817.13	1194.35	897.81	964.65	779.3	1824.2	1727.89	980.75	121.27	249.6	65.34	820.55	440.74
485	1970.25	493.49	2061.1	621.97	2145.15	424.48	1170.5	1297.68	1722.75	893.57	1142.8	563.28	2534.25	869.95
2.19	225.85	9.97	180.05	74.74	706.85	760.21	727.45	651.46	460.3	210.29	470.85	61.73	312.35	13.79
497.73	461.6	436.43	494.15	482.46	430.15	235.82	627.05	121.13	223.7	35.92	228.25	41.08	157.05	29.49
8.56	273.1	185.4	230.4	245.79	524.45	372.72	398.65	218.14	882.4	687.31	186.05	32.31	122.75	76.86
93.34	184.05	191.84	179.7	185.69	218.25	97.23	327.8	124.17	294.75	297.2	373.7	151.89	104.2	36.06

61.31	175.65	112.64	139.7	163.48	258.1	322.72	1195.15	1077.28	504.3	589.16	644.45	282.91	129.55	6.43
32.67	70.85	30.33	84.95	10.39	249.35	203.43	117.25	35.28	174.6	127.42	99.3	31.11	112.3	17.54
75.38	1356.15	743.38	1101.2	1103.94	624.1	286.66	170.4	7.5	969.9	153.72	1512.1	489.32	1253.55	464.64
267.99	490.55	28.07	287.85	314.73	194.65	79.13	1443.4	1477.29	105	41.44	248.2	65.48	117.4	27.86
16.05	1336.55	502.82	1451.75	339.91	972.55	560.95	460.55	310.49	222.2	211.14	703.4	474.61	1490.5	1251.01
66.47	268.4	158.25	93	89.8	304.05	1.77	287.1	45.25	1079.75	821.02	932.9	648.28	1064.95	122.68
284.26	1652.45	739.28	1781.7	556.49	1040.85	137.39	3057.5	999.14	630	68.59	255.45	52.68	1424.4	1044.4
786.66	8332.65	3432.37	6968.3	1502.88	9086	3301.06	4868.6	4187.63	6334.05	3037.24	5717.95	3339.17	9202.55	1284.6
33.23	309.25	36.7	282.6	74.39	1351.4	1584.2	414.5	191.91	350.05	8.27	859.6	786.73	427.9	54.73
84.71	680.15	319.4	670.85	306.25	535.05	138.24	447.05	188.02	822.6	629.47	1939.15	479.35	465.15	174.16
255.12	1072.55	571.27	1002.1	471.64	2364.85	753.56	1841.15	1318.26	2074.9	165.04	981.8	819.82	1469.65	1322.08
199.26	431	360.77	525.1	227.69	455.7	390.75	613.6	599.06	546.65	128.62	191.65	23.55	549.95	308.51
259.93	2625.35	1007.13	2623.4	1009.89	1438.2	674.3	3780.75	2681.7	3420.75	132.02	2225.95	358.57	2352.3	1646.57
138.59	234.7	158.25	289.55	80.68	208.25	75.31	444	386.93	244.35	70.07	431.3	303.07	116.25	2.05
891.03	1631.55	1017.6	1983.15	520.36	746	144.39	809.8	428.79	1770.8	1693.66	965.15	342.73	1368.1	260.36
500.14	232.25	124.38	221.5	139.58	192.9	49.78	297.55	38.25	205.3	65.34	179.5	17.96	207.75	18.17

51.19	791.15	417.12	650.2	616.46	728.25	463.79	684.45	661.5	921.65	184.2	871.45	478.92	820.35	39.53
107.69	280.55	316.85	255.55	352.21	471.8	583.22	571.5	701.45	268.9	42.85	639.05	874.34	48.55	18.6
73.04	224	164.05	188.2	214.68	172.6	227.26	77.25	60.46	138.25	1.06	94.75	63.29	162.7	17.11
282.21	252.35	277.54	146.5	127.84	380.7	399.52	257.25	128.62	146.1	12.87	711.95	581.31	190.05	36.27
48.01	177.75	136.4	195.2	161.08	98.65	58.34	243.95	268.35	333	264.88	229.4	205.06	363.1	191.34
772.3	3464.85	1397.46	3922.75	749.89	3456.25	77.85	3689.75	909.55	1996.55	438.62	3310.65	777.18	3730.05	528
1113.06	1086.8	621.12	1192.45	471.71	642.05	706.33	3102.8	1833.25	1256.45	212.34	1248.3	302.64	469.75	213.76
510.11	250.85	234.97	521.2	617.3	563.55	94.26	370.7	96.87	94.65	2.19	858.9	126.85	184.55	156.06
78.84	135.7	29.56	287.5	185.12	363.2	367.84	808.95	901.91	872.8	883.88	277.4	159.38	287.3	36.63
4.45	42.1	11.31	41.4	12.3	65.75	25.53	89.95	43.2	309.95	376.39	200.8	214.96	86.4	21.92
373.64	524.35	171.61	743.2	481.12	530.95	375.54	1524.65	592.06	1823.8	133.64	1935.7	249.33	1915.55	259.58
91	1261.25	476.24	1049.75	177.13	1350.9	441.23	778.35	69.08	1502.4	1247.62	1055.4	607.97	1194.85	163.13
116.67	320.95	204.28	364.45	265.8	726.95	585.56	466.3	330.22	267.05	277.12	334.6	138.88	138.5	11.17
1032.52	1818.85	1029.48	1089.05	2.62	2055.25	398.88	868.1	726.76	954.15	855.67	962.4	502.05	1034.55	434.23
480.34	1004.55	74.74	1082	34.79	635.35	246.99	541.55	189.72	1550.1	1730.86	2407.35	1479.62	1091.65	1102.87

7.64	69.5	69.01	67.95	71.21	211.05	261.7	119.5	68.87	179.35	173.03	75.95	33.73	128.2	81.18
200.32	1359.9	9.9	1074.55	393.65	1319.3	916.98	1286.45	674.37	1039	954.03	1501.9	587.18	1247.45	91.71
210.65	269	139.16	254.55	118.72	233.25	87.04	611.8	78.35	231.7	152.03	986.6	947.81	328.7	292.6
34.79	948.9	210.86	1105.6	10.75	1208.6	67.18	1469.3	875.82	1100.95	683.98	1967.85	1730.36	2262.15	856.38
224.79	155.15	139.94	333.4	392.02	527.2	512.51	318.75	100.06	951.45	834.32	299.1	220.76	260	107.48
28.28	212.8	43.7	233.2	72.55	235.05	155.49	475.4	209.16	329.95	17.18	520.45	130.74	193.95	44.34
69.65	135.55	3.89	69.7	89.24	145.6	53.17	249.85	307.24	164.7	81.46	393.25	493.63	160.2	29.7
851.78	680.35	312.33	501.75	59.75	947.9	392.44	2200.5	1084.56	1604.1	85.42	1764.3	1111.01	804.05	363.38
752.86	2011.3	582.51	2732.95	1603.08	2146.55	1073.74	1499.4	1598.77	2492.3	1141.98	2394	2649.39	2069.4	79.2
1416.33	11789.1	359.49	13407.7	2648.54	8301.75	1758.93	7866.35	5780.39	11972.5	6421.38	13599.2	10179.37	14195.35	1403.68
17.68	517	124.45	509.35	113.63	402.6	1.13	315.15	88.88	648.3	300.8	1088.5	863.52	683.55	169.35
42.57	698.6	227.55	663.8	276.76	1098.75	842.8	2111.55	2250.23	1138.95	559.39	1472.2	718.28	1165	41.86
88.88	168.65	69.23	96.9	32.24	95.35	47.31	256.8	123.74	126.2	57.13	1527.3	1507.41	546.7	351.29

93.83	210.05	124.1	187.65	155.78	114.55	87.75	110.25	58.76	126.3	30.97	403.1	55.01	329	337.57
302.92	275.4	29.27	254.25	59.18	652	877.38	331.05	131.45	162.2	102.39	1365.85	1372.99	154.4	117.52
229.95	11196.2	2447.44	11059.95	2254.75	12066.2	6154.23	7411.3	6124.39	7334.7	2897.58	6147.85	1911.95	9105.05	1555.85
511.73	632.65	302.71	601.75	346.41	546.55	98.5	753.75	591.64	555.2	380.56	174.7	109.04	685.4	306.18
69.58	65.55	36.84	56.85	49.14	714.2	975.81	95.45	50.42	236.1	185.26	630.85	722.45	172.65	71.35
4.6	68.55	22.56	51.5	46.67	141.25	179.82	360.8	318.91	218.4	182.15	48.35	17.61	85.4	49.5
1.27	3426.85	1444.41	2862.05	2243.16	4939.55	4747.73	8256.45	6889.98	5356.75	3519.62	20370	11004.42	6248.3	1341.95
220.48	1217.8	1394.56	869.85	902.48	1532.75	671.82	845.55	447.81	582.05	18.31	1254.15	738.29	711.8	55.58
306.25	207.35	125.79	192.1	104.23	160.5	56.99	487.1	172.25	156.65	133.01	505	577.42	186.05	53.1
1261.12	978.45	435.37	1043.65	343.16	785.7	201.53	301.3	9.19	704.25	658.67	1135.45	1328.72	319.45	24.25
1782.47	3507.1	1702.29	4243.15	661.36	1039.6	313.67	5521.7	1653.5	1487.65	304.83	3529	2854.59	1349.4	195.3
20.93	560.1	52.75	556.85	48.15	437.3	546.17	285.9	168.29	553.75	364.51	853.4	152.31	228.45	276.55
220.19	451.5	441.66	401.95	511.73	211.45	93.41	772.45	360.55	551.5	705.27	657.15	789.63	881.1	108.33
753	1089.75	760.35	923.55	525.31	1055.3	744.87	922	917.26	1179.45	90.44	614.4	622.96	583.35	408.64
47.23	235.7	146.65	244	134.92	220.2	118.09	247.8	7.07	220.55	85.63	183.55	67.95	324.3	87.26
51.48	132.6	119.22	166.35	71.49	137.6	109.18	168.9	20.79	337.85	162.85	223.9	106.91	150.45	47.59
64.98	1449.9	354.12	1453.35	349.24	1270.9	7.78	1318.9	1024.6	633.7	445.62	1486.1	510.25	1230.55	199.9

59.11	459.95	424.05	456.05	429.57	95.75	26.8	560.75	465.77	113.25	13.08	207.3	129.12	117.65	72.48
170.84	1447.05	1543.83	1498.6	1470.92	670.05	20.01	1171.15	480.62	1220.2	385.66	2289.95	2130.72	1940.2	411.68
81.81	604.85	141.21	617.45	123.39	306.45	87.47	402.75	266.93	697.6	119.78	629.65	447.53	708.1	217.22
1085.2	9269.85	1238.22	10354.35	2771.93	10669.85	3913.2	7127.35	5676.72	10772.8	564.13	8377.65	1512.15	7458.35	1064.12
370.38	421.1	414.51	402.45	440.88	387.45	500.14	894.2	1202.36	579.5	84.43	1019.3	845.7	52	11.6
21.14	337.75	179.96	258.3	292.32	69.5	73.11	123.95	145.88	90.2	20.36	145.35	152.1	111.25	122.82
1446.39	2504	1185.39	2441	1096.3	2590.25	2315.14	2249.7	1311.68	2487.05	943.78	2834.95	113.77	2394.2	97.16
182.08	2454.85	642.69	2329.2	820.39	2647.55	501.27	2140.7	1.56	1478.55	452.19	1299.6	875.54	1547.7	39.17
39.53	135.75	96.38	132.8	100.55	112.2	68.45	156.55	44.9	275.65	260.71	183.15	93.27	196.25	134
1007.13	5803.4	1494.54	5679.9	1319.89	6181.55	2191.96	4092.15	1877.3	3635.45	1446.67	4913.95	431.69	4862.35	401.14
248.62	290.25	278.11	331.75	219.42	126.9	4.95	1114.8	1511.51	70.75	32.31	368.9	283.13	456.55	465.06
1465.05	3427.15	1688.22	2649.3	588.17	4666.2	747.27	1871.9	2043.96	2387.05	76.58	1392.05	727.97	2436.25	233.7
39.03	31.6	24.04	44.9	5.23	26.35	11.53	420.25	533.51	155.5	15.56	190.85	216.59	44.25	3.32
703.15	430.35	172.6	424.55	164.4	387.05	141.49	477.8	270.4	1278.6	379.15	360.9	90.93	766.3	116.53
1.98	20	23.48	27.15	13.36	839.55	1177.97	370.05	267.92	38.7	23.62	54.45	42.07	51.65	36.98

149.13	93.45	38.96	78.65	59.89	94.5	39.6	189.05	200.75	76.5	18.38	1161.4	1537.82	113.45	15.34
233.49	922.9	587.61	723.15	870.09	1774.35	1822.14	491.4	376.75	753.75	0.35	950.3	257.25	713.8	471.07
761.98	2577.2	477.44	2367.8	773.57	2383.8	1347.6	1857.9	2076.63	3339.45	122.82	3381.35	96.66	3279.45	125.65
119.01	222.65	108.26	269.4	42.14	81.75	8.27	112.65	39.81	106.3	18.24	80.05	59.61	68.05	63.57
120.28	209.15	67.53	199.15	53.39	1024.5	737.09	901.1	48.79	447.45	247.7	191.7	143.83	207.85	98.78
80.54	580.9	143.12	352.95	465.49	760	576.29	413.65	350.23	550.9	243.39	175.05	134.85	568.15	16.9
4.03	155	114.13	139.5	136.05	228.1	219.06	108.5	92.35	160.9	2.12	663.95	384.17	93.4	81.74
154.15	1958.7	1196.14	2032.4	1091.91	1343.2	246.07	712.85	687.94	1839.05	185.9	2237.1	975.1	1872.65	266.79
43.42	189.85	170.06	87.8	25.74	157.15	94.12	295.85	29.63	239.9	294.58	332.6	274.78	342.7	274.07
418.68	527.2	185.69	474.15	260.71	366.6	321.73	638.05	69.65	834.85	209.37	1017.35	190.85	879.65	157.76
133.01	626.05	608.47	630.15	602.67	308.75	343.87	198.95	126.5	571.35	159.31	736.2	442.93	180.8	99.28
11931.37	59249.45	32605.05	78776.35	4989.84	72344.95	22944.56	98419.59	73251.59	97951.4	3389.02	86606.7	11091.11	102968.15	4395.59
1197.7	2480.3	1120.62	2791.4	680.66	2550.3	390.32	2415.2	1617.01	2045.85	1541.42	1754.1	1653.78	2466.7	75.24
255.76	1186.25	1329.15	999.5	1065.04	1692.4	17.82	2444.15	1070.91	1052.9	390.89	1081.2	847.11	2009.9	298.54

179.82	544.55	102.88	986	521.42	735.95	140.93	369.05	142.91	618.4	169.14	1030	1168.85	600	245.93
92.56	309.45	147.15	289.2	118.51	250.6	126.43	458	151.89	212.6	177.63	401.05	61.02	520.3	200.11
10.61	2724.85	984.08	2658.2	1078.34	2530.05	812.68	3420.45	1430.55	1617.6	1209.86	1941.2	334.6	2816.25	2.62
26.52	116.9	27.72	70.65	37.69	86.85	34.29	323.3	83.72	86.3	33.38	174	178.05	80	58.55
765.58	3526.85	1168.07	3589.75	1257.02	3936.1	2063.2	1358.7	1354.53	1095.4	924.75	1407.1	780.5	1052.65	1091.84
1259	30.9	28.99	29.4	31.11	47.15	49.99	1894.65	2642.25	122.15	67.53	203.8	259.51	363.75	462.52
359.71	439.8	79.34	381.15	162.28	628.35	298.75	877.9	863.52	326.1	1.84	206.5	43.84	867.7	499.36
170.48	245.9	32.53	146.6	172.96	388.1	464.57	117.1	87.26	509.55	487.27	204.15	55.51	214.6	82.45
18313.5	51091.35	756.96	58344	11013.75	46617.35	7770.61	58485.85	43429.86	74408.41	14752.79	64556.05	26703.25	79294.3	13346.07
90.86	248.85	177.27	268.55	205.13	207.1	84.71	493.15	542.7	238.95	70.36	119.75	28.21	114.35	54.52
37.83	563.35	343.02	648.85	463.93	1064.1	708.1	472.9	225.99	1010.3	585.63	1333.55	1061.16	1009.6	132.79
366.35	215.05	200.04	357.1	0.85	307.2	176.78	513.1	307.73	443.5	363.31	313.25	111.09	835.25	693.04
552.82	787.35	527.71	548	189.22	204.05	86.05	337.95	169.92	399.85	183.92	296.3	210.86	800	67.74
213.69	367	386.93	325.8	328.66	691.6	110.17	1493.8	1322.01	817.6	383.82	771.95	854.82	1100.95	137.53
21.43	333.1	299.95	98.75	31.47	299.15	34.58	130.25	107.27	501.25	251.24	166.6	98.57	776.05	772.51
309.71	415.3	124.17	313.1	268.7	498.75	439.75	296.9	61.94	682.5	422	271.3	210.58	440.6	172.25
252.58	303.6	290.76	401.5	152.31	605.1	590.72	2457.4	2913.42	384.25	125.51	779.45	718.49	842.05	952.83
872.22	4898.5	595.95	4548.1	100.41	5118.55	1642.96	3823.8	2918.65	6502.8	1046.66	6845.05	2862.01	4391.1	173.38

122.75	8703.45	532.24	10517.35	3097.48	13819.9	735.25	18232.6	11819.01	8977.65	2161.7	12014.2	1296.69	19453.85	6650.69
1.13	185.55	33.59	237.05	39.24	159.3	67.03	313.8	118.37	380.2	28.71	268.8	36.63	170.8	9.48
248.41	1862.15	291.82	1751	449.01	1818.65	341.04	701.2	431.48	2229.15	93.55	1084.25	262.97	1661.8	836.51
8.13	350.7	22.91	227.75	196.79	303.65	232.85	432.2	41.44	345.85	50.13	507.05	466.62	470.6	189.65
25.39	233.75	124.66	224.1	138.31	333.75	353.77	106.95	55.51	598.05	591.21	930.85	417.69	166.15	125.79
41.86	663.45	571.13	493.45	330.71	582.45	388.98	382.25	255.48	1416.2	218.35	1347.6	413.52	526.5	357.23
254.63	212.7	165.18	307.75	30.76	1634.7	1932.95	558.85	444.13	1927.3	2029.26	443.75	267.78	536.1	77.64
414.29	113.2	42.28	60.4	32.39	598.85	712.83	97.8	83.44	164.95	76.3	1090.05	1375.39	183.55	116.32
10.82	46	32.24	51.6	24.32	79.95	76.01	133.2	77.22	74.7	24.89	129	41.72	96.6	9.33
214.75	756.6	245.08	891.05	54.94	351.8	391.6	577.45	350.8	781.35	304.98	685.5	111.72	508.1	275.21
641.06	626.6	736.24	735.05	582.87	172	53.03	131.8	84.85	656.3	758.73	680.2	321.31	686.15	196.22
307.66	700.4	320.74	532.8	557.77	946.65	672.39	1196.75	1285.45	1076.35	236.95	242.9	87.68	509.7	216.66
165.46	157.95	2.9	218.6	88.67	313.2	168.15	554.8	266.3	61.75	30.33	208.2	231.37	61.85	16.19
135.62	228.6	144.25	154.25	39.1	661.3	622.68	155.35	123.39	529.95	189.01	713.3	887.84	98.15	30.76
32.81	334.2	150.05	276.2	232.07	444	94.05	1023.25	483.17	1303.1	1450.98	433.7	288.64	306.8	85.28
100.83	266.35	257.03	278.2	273.79	902.8	9.62	419.2	235.75	1258.8	829.29	854.2	53.88	1100.25	391.95

150.9	1551.55	164.69	1133.45	755.97	1377.45	415.43	486.1	564.41	681.15	79.27	832.15	5.87	606.25	401.14
302.57	1599.7	409.56	1400.45	691.34	1199.85	24.68	1170.5	87.12	1021.6	438.97	991.55	137.67	1283.1	550.27
3.54	64.05	43.06	60.9	47.52	53.9	24.32	109.75	86.05	72.8	33.8	91.2	57.98	78.75	13.51
24.04	120.9	53.17	102.2	26.73	165.5	192.62	373.5	464.57	412.1	297.97	1078.75	1360.4	89.35	23.55
248.48	2069.15	378.51	2439.65	145.45	2461.05	185.62	2905.8	1040.72	2405.6	637.1	2850.8	459.34	1596.05	162.42
652.66	414.35	25.67	931.75	757.38	490	159.81	667.4	367.98	677.45	173.74	526.4	51.76	529.65	53.1
225	770.7	890.53	817	825.05	1028.1	1163.76	721.05	254.63	858.25	106.42	849.9	368.12	529.5	229.39
31.47	1470.75	103.45	1486.2	125.3	2083	300.52	1235.6	1.98	807.45	837.14	2590.85	1899.36	1005.25	784.53
304.48	401.15	315.3	417.85	291.68	386.6	55.86	246.05	137.67	349.7	316.36	787.55	963.15	184.5	118.09
651.46	2487.6	1399.65	1585.45	123.81	3157.9	426.1	1553.2	1511.94	1781.15	220.97	1222.95	339.06	1746.4	201.81
390.68	535.1	245.79	481.5	321.59	427.9	32.95	753.95	731.93	346.55	174.73	1640.9	554.23	505.9	33.52
970.72	1336.8	124.03	1184.05	340.05	1360.55	381.06	1250.4	385.94	818.55	546.52	850.2	614.62	834.25	1057.76
244.02	453.95	122.54	460.95	112.64	431.3	242.96	466.9	189.36	538.05	433.39	286.75	197.78	467.4	215.95
331.07	2065.5	796.06	1410.6	130.11	1952.4	1082.72	924.6	198.7	1326.85	349.95	1451.8	380.28	1356.2	51.76
151.46	59.55	8.13	56.2	12.87	128.85	100.62	423.15	281.64	105.6	34.08	99.7	42.28	106.7	79.62
146.3	402.55	69.65	288.55	91.57	623.25	308.65	331.95	264.25	922.7	783.62	986.95	798.54	601.95	654.57
694.03	6152.8	1151.88	6135.8	1175.92	5467.35	1477.22	1571.9	1147.63	4288.3	331.92	3212.65	1925.95	4075.1	530.61

69.08	409.8	121.48	423.25	102.46	3264.2	4080.15	1350.7	1254.27	590.65	24.25	1563.95	1833.88	557.45	112.22
90.51	93.4	112.29	95.4	109.46	755.4	1019.37	87.05	34.44	115.75	113.91	179.2	190.07	91.65	30.9
169.56	171.35	132.87	140.9	175.93	249.05	124.38	424.05	526.16	86.3	60.53	108.6	74.81	79.6	19.66
26.59	180.8	157.12	57.55	17.18	630.75	655.56	150.25	66.4	89.15	10.39	371.5	468.67	99.3	72.27
101.82	175.55	174.44	207.15	129.75	580.35	669.98	960.4	1224.57	666.7	6.79	80.95	17.04	428.35	418.4
1203.28	7113.9	2926.15	6053.25	1426.16	6482.8	2636.94	7568.15	975.31	5213.5	2068.15	5713.35	3788.32	6067.2	1836.36
42.64	173.05	8.98	145.65	29.77	245.4	58.41	293.3	135.06	211.9	27.72	213.45	17.61	272.8	106.07
132.37	70.4	31.96	54.2	54.87	72.9	57.13	1262.95	1594.31	134.5	68.45	136.95	135.27	229.05	186.89
135.84	366.4	19.23	273.8	111.72	207.45	116.46	973.1	827.88	310.35	336.09	702.65	906.3	486.95	416.27
482.32	89.6	57.28	103.85	37.12	132.15	92.14	193.25	150.97	148	95.6	134.9	100.13	127.85	71.21
155.7	459.1	45.4	408.7	116.67	480.15	87.04	679.6	86.13	706.8	318.76	746.05	36.27	677.3	210.15
603.23	982.15	29.06	905.8	137.04	1901.65	104.44	1980.35	1142.47	2345.75	182.08	1633.8	282.14	1720.85	49.14
110.52	623.2	335.17	433.5	66.89	666.2	65.2	1139.1	1006.21	1343	391.74	701.05	762.47	1324.1	811.48
4.38	1303.2	513.22	1348.6	449.01	1374.55	798.11	1746.75	654.99	898.6	946.67	1934.55	1284.32	1412.35	183.21
18.31	344.8	212.98	269.55	319.4	102.65	63.43	117.5	0.57	267.6	300.94	286	131.66	297.6	295

103.94	836.15	317.28	1024.35	583.43	1973.05	870.94	1535.45	147.29	1629.55	511.87	1524.85	493.77	1396.95	94.12
109.6	202.2	22.49	131	123.18	271.45	94.68	102.75	16.33	776.7	875.54	292.25	337.5	204.6	153.87
773.01	2383.7	320.46	2519.65	128.2	1357.7	409.7	1188.7	874.13	2073.15	67.53	2301.3	544.05	1999.3	446.33
43.98	476.55	50.84	600.05	225.5	863.85	389.69	941.75	519.94	901.35	390.11	379	352	412	125.87
421.08	164.3	133.08	204.75	75.87	154.55	33.16	241.65	44.76	125.25	60.88	243.45	154.08	255.3	196.15
93.2	50.55	20.44	143	110.31	309.75	252.08	84.65	51.83	165.1	142.27	102.75	76.86	157.3	71.42
9.62	1949.05	58.19	1442.05	775.2	1305.3	940.03	910.65	656.41	2953.1	814.45	1686.3	435.58	2478.85	388.41
60.53	829.7	342.1	938.25	188.59	1406.7	1010.74	668.6	262.05	1480.95	703.08	815.45	50.7	1269.15	463.65
98.85	2193.3	198.84	2402.95	495.33	2104.45	68.09	3088	795.5	2049.75	941.51	1592.5	937.62	1990.4	244.52
315.09	7053.95	520.5	7267.15	822.01	6595.5	2318.04	8240.75	72.62	6586.75	2567.43	7219.35	2707.02	7549.8	4508.8
444.77	1375.7	196.86	1590.15	106.42	1697.25	100.76	2532.4	1792.8	1718.45	776.9	1214.4	752.79	872.35	305.4
47.09	419.95	102.46	356.8	13.15	348.15	28.78	451.1	115.4	297.25	44.05	588	315.23	395.15	165.82
237.23	2015.5	49.64	2533.05	781.57	1514.55	745.79	2276.3	807.66	2083.1	167.58	1798.1	1231.5	1548.05	1148.7

135.76	306.6	287.37	126.9	33.23	284.1	76.08	185.3	118.23	537.45	657.26	743.55	360.13	393.05	103.73
38.47	66.8	55.15	66	56.29	142.5	103.52	303.4	88.53	436.6	560.74	91.2	70.57	414.05	441.31
10.11	45.7	41.15	50.2	34.79	156.65	196.79	86.85	40.52	48.35	26.94	314.6	372.5	132.2	111.3
373.35	1822.25	262.12	1756.2	355.53	1315.4	97.72	577.7	531.74	1053.2	175.79	1476.4	952.19	1078.95	236.1
130.04	359.7	29.56	222.5	223.59	183.55	58.62	97.6	8.34	202.65	168.36	73.8	39.32	126.95	69.93
307.17	471.7	139.02	612.7	60.39	959.4	750.1	782.05	352.92	974.4	267.57	1972.7	1351.99	665.3	303.21
30.9	788.75	666.73	851.75	577.64	911.7	800.87	180.3	60.53	487.2	49.5	1325.4	1289.48	281.1	229.53
41.93	364.1	371.37	557.05	644.24	803.6	32.53	1045.4	927.58	502.7	33.8	1617.9	115.68	1121.15	589.37
397.61	1065.85	184.77	1051.7	164.76	850.85	800.8	545.05	606.63	140.85	100.48	479.2	548.01	1140.9	102.67
664.11	7902.95	542	8048.6	336.02	6832.7	0.99	5475.15	3882.94	6869	1305.46	7330.8	546.73	7383.65	2790.88
60.53	61.1	29.42	38.15	3.04	179.45	70.36	159.8	188.94	38.45	11.67	879.85	748.47	327.35	119.29
815.93	3575.75	1499.56	2933.6	591.42	4124.25	1620.05	1864.85	718.07	3380.95	726.84	3201.9	1348.31	2791	216.66
171.47	711.35	76.58	661.85	6.58	305.65	265.94	1741.6	718	511.45	12.8	1014.25	707.74	187.95	12.37

275.42	1416.2	452.55	1349.85	358.72	1422.45	242.18	2995.65	1421.78	2126.4	307.45	3087.65	1397.31	1811.8	544.76
82.02	302.55	401.57	336.2	353.98	91.1	84.15	399.55	251.94	495.55	582.87	943.65	1259.99	280.8	310.99
207.61	988.75	152.52	1097.05	305.68	955.4	910.05	752.7	442.08	1233.7	1141.98	1884.7	478.99	949.2	770.32
1159.3	1749.7	524.11	2456.2	1523.25	2421.85	1388.97	956.8	20.22	1480.5	903.54	1395.95	548.79	1629.2	1478.7
18.46	300.95	325.48	288.65	342.88	811.55	838.13	802.3	668.92	387.65	252.65	968.9	976.23	643.1	787.86
21.92	1622.35	569.86	2145.45	169.92	1739.75	267.5	3197.85	3439.3	1545.6	761.41	1883.5	486.77	1680.6	1701.58
19.45	1247.85	507.91	1096.8	721.53	536.5	547.02	1418.95	289.56	1907.3	231.08	2606.8	1613.19	1617.25	424.62
342.03	2766.15	1307.65	2432.35	835.59	2444.15	772.23	4338.75	360.98	3397.2	67.6	4324.35	632.51	3744.45	557.84
10.75	142.2	38.47	67.65	66.96	361.85	377.67	556.25	73.61	514.1	151.75	224.65	12.8	319.6	153.58
247.49	552.55	181.37	498.8	257.39	976.6	793.37	881.25	23.26	807	173.52	2273.15	2529.67	656	159.52
462.02	596.95	580.32	761.65	347.4	611.9	144.82	1124.9	924.33	1270.45	638.73	326.45	246.29	1027.3	570.78
14.35	139.95	26.38	81.95	55.65	107.95	102.6	640.2	791.39	136.5	35.64	178.25	205.84	541.4	618.29
12.02	185.1	115.12	182.2	119.22	217.45	227.62	1785.7	1554.79	385.2	257.39	648.15	568.73	510.7	124.03
534.93	971.15	115.75	726.75	461.39	980.1	259.65	1531.15	1169.2	1112.2	70.43	406.5	416.06	1579.1	35.5
23.69	1311.65	425.32	1331.35	397.46	1250.2	239.57	869.15	761.91	2125.5	1154.85	2292.25	73.75	2151.5	189.93
22.49	700.2	453.82	596.95	599.84	547	434.45	1178	258.24	1136.85	511.45	507.6	88.11	703.75	494.06
28262.35	69712.5	8680.3	76241.1	17913.14	72270.05	13010.13	73615.05	69015.96	76512.5	14143.55	73255.2	6621.49	98510.55	557.13

45.04	196.7	71.84	154.05	132.16	243.55	247.7	208.5	79.05	176.95	119.71	428.5	526.51	236.6	33.52
19082.13	29567.55	4404.5	33567.75	1252.64	21888.75	1769.53	14619.2	7269.76	25451.45	7623.53	24356.95	11700.99	21762.5	1155.98
405.03	1648	1513.21	1535.15	1353.61	1601.2	647.29	844.65	272.45	552.55	284.04	765.05	664.19	1001.1	965.34
433.74	678.4	830.28	865.55	565.61	259.1	226.56	1747.5	1247.62	614.7	291.75	1754.8	787.86	781.65	294.93
66.68	169.95	32.74	125.45	30.19	137.4	70.85	1196.6	1582.36	456.85	565.47	1053.65	1249.25	130.45	101.61
605.28	1323.75	638.02	1489.45	403.69	1729.55	1280.36	1304	1241.82	780.4	628.34	898.55	55.37	1456.2	110.73
532.1	1346.45	283.76	1147.55	565.05	962.25	609.03	648.85	752.43	1055	388.77	1283.35	916.91	1095.15	1017.46
6.43	172.2	18.67	84.7	105.08	159.4	170.84	155.25	11.81	95.6	71.98	177.5	35.21	97.65	1.2
171.4	157.1	80.04	119.3	133.5	752.8	776.97	144.8	72.41	191.05	121.98	268.05	346.69	54.45	68.09
777.46	6696.75	385.16	6681.8	406.3	6615.85	1130.03	7396.25	1791.74	6576.95	729.95	5891.1	204.07	7243.4	850.23
165.04	328.1	115.82	336.8	103.52	542.3	99.84	2339.45	2498.99	879	914.43	457.4	328.8	861.4	183.14
240.98	439.75	215.17	404.7	165.6	1099.65	728.96	820.4	294.44	607.7	515.2	1286.65	570.14	1107.1	984.01
42.36	216.6	256.26	214.45	259.3	586.8	687.73	87.25	21.71	167.85	204.14	148.35	151.96	144.75	146.72
936.63	240.3	2.97	255.1	17.96	725.55	880.14	331.85	179.25	659.5	341.25	883.3	115.68	521.15	438.19
12.09	295.25	27.79	280.1	49.21	184.95	45.18	230.45	164.4	280.95	309.78	272.4	90.93	366.55	109.25
286.38	919.7	513.5	1197.85	906.86	1627.25	68.66	1246.45	984.08	2181.6	1058.68	1753.55	98.08	2411.85	404.82

228.25	181.4	154.57	268.5	277.75	755.15	615.54	2409.3	3288.9	167.4	87.26	300.85	211.78	1425.85	971.92
62.44	126.8	71.42	161.05	22.98	235.9	75.8	265.4	216.37	285.75	174.02	169.85	9.4	287.35	7.57
1407.92	5577.85	604.65	5693.6	768.34	5552	1358.21	5215.55	1772.93	3644.75	2071.89	2979.3	2349.57	4477.65	518.95
9.33	824.65	289.84	928	143.68	733.85	515.41	961.95	829.22	908.5	481.68	1508.45	1322.93	1371.15	725.28
171.69	215.75	277.54	336.05	107.41	320.6	307.73	96.5	62.51	566.7	191.2	341.45	403.55	227.3	163.62
779.3	2073.35	1884.09	1606.1	1223.29	2462.2	1578.12	956.4	1115.53	1758.8	316.93	1132.3	269.55	1125.15	359.56
246	440.75	248.69	503.6	159.81	241.95	128.91	289.3	207.04	399.6	434.16	269.45	140.78	255	160.23
156.27	73.3	82.45	77.1	77.07	88.3	34.37	252.95	138.24	524.55	434.52	1070.8	1476.72	259.6	114.41
138.88	525.55	126.22	307	182.86	378.35	229.6	2163.4	1825.04	1305.1	1225.84	429.45	104.86	372.35	114.34
449.58	1145.05	136.26	1385.05	203.15	938.55	245.01	933.5	711.21	2698.25	422.21	1731.2	73.68	1866.35	1.2
436.36	889.1	322.44	745.15	118.86	720.4	770.75	196.75	6.01	697.65	488.96	381.75	377.24	1071.1	700.88
192.05	287.7	311.69	261.55	348.67	78.25	59.33	231.35	205.84	121.25	96.66	124.6	3.54	171.6	6.79
3002.8	1772.7	946.53	1027.05	107.98	2831.6	1133.21	1898.15	1351.35	1810.75	985.49	2012.95	864.72	1688.2	463.86
2.69	107.1	20.22	68.35	75.02	223	131.8	401.3	527.22	523.4	486.63	77.45	53.67	299.75	260.43
460.82	1396.3	1011.87	1416.2	983.73	486.1	429.07	1274.9	662.84	1810.85	555.29	1413.05	295.5	1550.45	30.05
672.6	592.25	444.7	602.15	458.7	670.15	718.92	632.65	285.03	552.75	483.17	1239.55	785.1	1172.9	221.47
132.79	343.95	406.94	376.15	361.4	145.5	111.44	1046.35	861.75	368.45	428.15	266.3	126.57	357.45	387.71

334.67	377.35	229.46	422.95	164.97	203.55	164.69	1253.85	1071.2	392.05	359.71	383.9	63.07	394.05	318.27
33.94	80.15	71.35	175.3	63.22	56.95	13.93	126.75	116.6	197.05	256.33	240.25	256.33	266.35	313.04
75.38	990.1	893.36	453.4	134.35	796.6	320.04	272.6	21.21	1035.45	1001.48	351.45	347.97	696.55	260.99
28.78	148.1	29.84	80.65	65.55	260.5	80.75	700.35	833.18	49.85	14.5	186.5	174.51	573.2	260.07
149.41	978.3	637.24	806.5	394.28	1944.5	720.12	885.1	755.9	475.6	470.23	2054.95	980.55	1483.35	77.43
19.66	2565.8	458.35	2370.6	734.4	2550.7	411.25	1008.55	573.68	969.25	538.46	769.15	904.18	1083.15	324.63
211.99	46.45	22.98	62.9	0.28	56.7	10.04	194.65	149.55	158.25	3.61	167.4	149.34	365.05	212.77
876.88	3802.95	914.22	3914.95	755.83	3560.1	928.43	3202.7	1731.85	3811.3	349.74	3060.45	782.84	3337.25	1131.3
240.49	551.1	367.13	516.8	415.64	309.25	24.11	428.9	4.67	374.7	42.99	1073.75	392.09	491.3	167.87
160.94	606.1	530.9	527	642.76	67.7	63.64	577.4	673.87	529.85	684.83	247.1	78.77	313.6	23.76
116.11	114.2	52.47	58.95	25.67	208.5	225	177.05	158.04	272.35	340.9	429.4	276.62	344.3	175.5
150.9	1224.6	200.54	1097.4	20.65	1036.7	619.85	642.65	281.5	658.9	564.84	581.1	185.12	1719.7	120.35
541.08	183.75	38.54	239.05	39.67	405.65	168.64	1046	1199.11	445.45	88.03	193.85	85.91	181.6	45.25
324.63	2245.45	646.22	2419	400.79	989.35	437.49	2967.2	271.53	1989.55	358.01	2181.8	159.95	1737.95	1751.01
112.92	2275.4	1171.11	2203.2	1069	2021.5	1822.36	1593.8	553.81	1209.3	102.81	649.4	701.45	1217.25	284.61

7.78	73.5	34.37	178.45	114.06	265.8	102.95	217.95	138.52	150.2	96.03	117.4	4.38	195.35	130.6
917.75	3377.4	413.09	3578.4	128.83	2856.6	1426.52	3729.8	2768.18	3890.4	13.29	3656.6	1473.19	4187.05	792.88
56.5	281.55	44.62	368.8	168.01	348.15	199.76	698.15	837.99	1346.95	441.31	438.4	154.01	796.45	376.68
295.64	399.6	149.06	244.7	70	412	172.82	532.8	123.04	1152.15	1281.49	965.9	479.42	481.3	254.42
18.67	44.9	43.84	43.8	45.4	53.2	41.72	381.55	489.95	187.15	130.46	113.35	119.71	220.25	96.66
125.72	240.55	160.87	98.9	39.46	413.45	264.25	226.45	85.06	391.05	253.78	2037.5	1668.63	624.85	619.64
145.95	304.65	366.07	38.4	10.47	477.85	198.63	78.55	14.5	36.7	5.09	339	218.64	86.7	52.04
1.77	480.9	421.72	908.95	183.64	1106.05	877.17	1273.9	814.16	253	7.92	469.7	189.22	821.1	538.11
172.32	512.7	495.26	575.6	406.3	208.85	148.14	559.45	747.2	264.1	247.06	131.85	150.4	135.2	142.27
329.23	1091.2	155.85	1155.55	246.85	1462.15	504.24	875.5	781.92	1470.45	810.42	1888.25	1493.34	2119.5	572.19
25722.5	90832.16	30009.68	110149.85	2690.33	78892.7	10760.33	54657.5	47486.75	93732.2	7936.14	91515.3	32413.21	50381.45	28263.98
2667.28	6005.95	2183.05	6253.15	1833.46	5108.7	245.37	6039.7	917.54	8383.45	2733.6	9124.05	3074.57	6534.85	1778.87
10.04	89.3	6.22	76	12.59	35.75	18.46	96.45	37.97	315.5	346.62	380.95	456.58	374.4	416.91
1274.77	4933.75	1951.83	4917.05	1975.44	3041.35	717.36	3744.85	97.37	3809.5	782.91	4886.35	1494.75	4728.65	590.22
299.32	418.55	532.8	508.25	405.95	129.1	152.74	66.5	41.86	261.9	116.67	1224.7	1197.7	174.05	53.95
241.76	171.35	153.09	56.3	9.62	924.35	1063.56	211.95	138.95	496.35	513.85	450.45	361.69	154.7	85.84

195.23	243.95	124.52	456.95	176.71	960.5	725.49	1202	1451.55	926.7	1038.32	618.8	427.8	416.75	313.88
102.74	132.7	123.6	27.25	25.53	47.25	32.17	565.2	709.65	80.55	79.97	58.7	39.17	154.6	191.06
1598.63	5688.3	379.86	6065.85	913.79	4309.8	1640.63	1882.75	1695.85	7087.35	3704.04	3526.4	4626.18	6590.65	653.44
971.42	893.7	551.83	752.15	351.64	1605.95	975.45	970.85	933.45	1613.7	56.85	2142.5	387.64	2494.7	548.01
150.76	145.75	63	138.9	72.69	152.3	114.27	315.85	252.93	355.05	22.84	1041.85	827.53	416.65	407.65
96.73	105.95	18.31	99.7	27.15	299.3	289.77	265.2	215.1	135.25	18.31	124.3	56.99	296.45	198.77
218.43	141.15	75.87	163.75	43.91	107.9	11.31	185.25	118.3	322.95	58.48	122.15	6.43	319.65	3.61
220.69	432.45	281.64	490	363.03	792.45	908.14	434.5	252.86	868.1	947.24	569.75	405.38	329.2	273.37
19.66	807.5	271.95	1048.8	613.2	1965.9	883.88	2358.05	1415.56	2318.65	1388.97	2026.2	69.86	1305.3	362.32
69.79	553.05	563.49	552.85	563.78	751	963.93	358.75	189.72	920.25	892.3	1484.05	926.52	487.45	274.99
249.61	84.8	11.46	82.3	7.92	341.6	455.66	885	1067.17	202.15	176.56	301.15	382.76	319.35	260.57
27.01	129.25	33.02	147.15	7.71	130.25	14.78	204.75	135.69	233.75	95.11	317.5	108.75	268.7	25.6
161.01	626.55	315.58	679.8	240.27	366.45	155.92	302.9	264.88	390.9	49.36	129.35	74.18	60.65	13.36
22.34	223.7	116.11	235.95	98.78	430.2	130.67	277.7	88.95	218.35	89.73	924.85	995.82	265.85	65.97
313.25	758.8	118.51	546.35	418.96	1220.6	718.99	803.05	741.97	1145.2	246.07	866.45	425.47	1172.8	88.95
2611.2	4384.4	324.42	4817.3	936.63	3144.25	1348.81	4018.95	2763.44	2729.45	819.18	5423.8	2465.4	4498.7	1375.18
304.69	1554.1	331.77	1409.45	536.34	747.55	590.08	1142.5	49.21	2249.4	319.9	1991.3	745.71	1425.4	60.1
106.7	721.7	567.95	290.75	41.51	990.7	575.02	600	566.96	690	345.21	1684.2	1851.06	870.15	671.26

42.92	137.7	2.83	148.5	12.45	195.65	53.67	100.15	32.46	995	130.67	1110.7	1295	151.25	45.18
43.2	247.6	252.01	168.8	140.57	537.2	305.61	794.05	1022.55	505.1	187.81	1495.25	1958.61	522.5	36.49
9.9	221.05	64.7	223.5	61.24	188.3	55.86	103.3	106.63	61.2	53.6	58.05	49	41.9	20.51
388.84	402.5	267.85	240.35	38.54	1173.7	1495.96	277.6	56.43	351.35	214.18	1510.5	612.35	212.25	76.72
1011.09	108.65	50.13	106.05	53.81	72.75	20.29	214.05	114.48	154.75	92.42	336.6	178.62	99.6	43.84
15.77	124.7	126.57	127.05	123.25	103.75	3.75	216.05	195.23	241.1	98.71	572.3	773.43	613.55	623.46
1052.1	2367.4	136.9	2683	309.43	2891.25	905.45	2939.9	577.28	2054.7	430.06	1638.75	1110.65	3164.9	718
100.13	460.5	62.23	968.5	656.2	614.5	323.01	221	40.31	389.65	46.17	987.35	187.45	293.25	71.21
369.39	1199.85	851.29	1247.95	783.26	1043.9	1130.1	903.4	1121.33	1303.8	1550.54	1151.25	1427.3	1329.15	885.51
12.59	117.3	19.8	125.3	8.49	210.45	53.67	193.55	104.02	236	78.06	1225.15	1469.86	125.85	19.73
208.46	1494.45	238.08	1528.7	189.65	1938.95	450.07	861.95	698.41	830.75	426.88	1487.7	230.38	1370.9	740.34
144.74	352.95	466.62	441.4	341.53	130.75	86.76	560.85	767.71	93.65	37.55	492.05	622.18	92.35	33.02
313.96	2400.3	1610.93	1643.25	540.3	3144.15	217.86	1250.75	1178.68	1380.45	142.76	1599.4	145.1	1330.25	166.1
12.52	58.6	10.32	34.15	24.25	159.85	19.45	193.25	167.51	466.75	585.27	597.45	762.76	310.5	91.5
253.57	2162.85	31.47	2573.45	549.21	3287.3	2051.46	1129.4	1046.52	2169.2	293.02	1921.05	1132.15	2186.6	541.22
232.99	1962.6	446.33	1965.35	450.21	1350.4	601.32	1136.75	981.82	853.95	674.08	1001.8	235.33	387.3	29.7
39.24	1158.6	310.84	794.3	826.04	441.05	226.63	452.85	166.38	421	74.1	684.35	228.47	1817	1372.07

416.77	739.2	616.74	643.3	752.36	1504.55	2076.56	2163.3	834.53	530.3	517.74	1324.9	1347.75	236.85	66.82
62.37	1166.45	137.53	1374	155.99	1410.95	926.24	2050.65	1470.29	2192.15	1616.8	1357.15	128.91	2908.1	1166.02
472.98	1624.35	900.22	1386.5	1236.59	793.35	375.54	1957.75	2345.26	1848.35	518.66	3100.05	1777.45	2452.45	39.39
1712.61	10113.8	2013.56	10074.1	1957.41	10300.35	4401.39	7022.7	4681.19	7069.4	4826.85	6194.45	3941.91	8540.3	1301.36
94.89	220.95	43.2	190	86.97	512.3	703.85	65	40.87	170.8	222.31	135.95	139.37	381.7	404.89
23.12	391.35	366.63	382.85	378.66	527.95	571.98	770.65	1006	62.95	26.52	272.4	357.51	323.65	267.22
166.81	1036.75	973.47	891	1179.6	510.75	538.32	948.4	1272.79	292.2	213.55	129.9	56.43	824.15	325.91
487.76	1911.2	656.2	1947.8	707.96	2204.6	317.49	1241.55	645.09	1216.85	196.22	1565.45	24.96	1415.9	1072.82
6.79	852.55	51.12	663.4	318.62	678.95	813.81	1233.95	1570.41	117.85	2.05	333.1	335.17	567.85	39.67
64.21	563.95	237.52	537.1	275.49	896.95	712.98	1276.6	1568.36	665.05	481.19	345.4	233.91	517.9	593.26
137.46	1111.65	385.16	751.4	124.31	1268.8	185.54	663.05	49.71	560.55	118.72	1799.65	1334.81	795.65	386.86
148.99	2099.05	749.04	1668.85	140.64	2288.25	205.13	1407.65	1277.53	1348.4	619.71	1778.1	839.05	1356.8	601.32
174.87	258.95	60.46	196.8	27.44	318.45	313.88	480.3	398.53	253.55	195.09	455.05	388.41	385.85	278.11
80.33	587.2	58.69	623.3	109.74	460.05	389.69	533.7	169.42	255.9	178.05	1472.95	1109.66	475.3	80.61
710.64	1498.4	189.22	1663.2	43.84	959.95	616.53	1602.25	1018.45	1838.95	180.95	3348.2	2178.03	2169.2	105.78

577.78	2341.05	1280.78	2419.1	1391.16	2709.6	1779.22	2181.05	2611.56	2007.45	250.81	2030.6	24.61	1871	182.86
107.13	337.25	30.33	224.45	129.19	996	1090.22	1000.2	895.62	830.7	824.06	1172.85	872.92	236.45	152.66
216.8	1497.65	648.35	1631.8	458.63	1805.7	1010.88	771.75	640.43	1052.4	945.4	905.2	541.93	1512.7	439.54
40.73	276.95	149.84	150.3	29.27	138.35	111.51	323.6	326.54	233.6	3.54	1314.05	1321.94	155.5	61.52
240.63	557.9	327.25	469.85	202.73	360.05	391.53	476.2	47.66	1478.15	1310.34	271.35	26.23	626.35	6.58
964.78	3299.35	692.05	3207.85	562.64	2959.1	1377.59	1312.55	460.82	1818.45	81.53	1950	1123.88	2038.15	853.97
258.45	505.2	275.06	546.85	333.97	606.2	446.04	386.95	167.94	1113.1	805.82	1168.05	1147.14	1151.35	285.74
418.96	684.15	219.98	810.7	398.95	1126.25	85.91	165.8	21.92	230.4	93.2	1262.3	1290.05	245.65	50.7
190	520.45	87.89	531.95	71.63	751.95	180.38	314.05	263.68	384.7	239.28	310.85	233.7	750.75	328.31
21659.68	220136.89	227388.27	243707.94	194053.78	631784.88	790119.88	1007248.5	673319.56	497006.03	393974.22	847241.56	945567	300476.75	69238.13
79.97	589.75	567.31	453.05	373.99	423.15	430.7	270.6	168.43	789.95	431.12	1356.9	782.63	267.85	141.49
4.03	1378.55	1507.76	966.05	924.4	1290.7	22.63	664.6	664.11	545.35	590.08	1231.45	123.25	501	489.88

39.1	739	16.55	546.3	255.97	965.35	670.97	606.1	104.51	860.05	654.57	650.95	301.02	632.05	48.15
5.73	70.1	55.86	98.05	16.33	160.3	11.88	51.8	26.59	160.95	187.74	658.3	891.52	343.3	464.14
247.2	1080.75	783.12	575.35	68.38	921.25	477.08	370.85	187.74	452.6	461.6	546.3	599.49	464.1	45.4
461.18	435.95	551.61	299.55	358.72	420.5	512.65	280.4	265.59	656.75	18.88	244.7	259.51	223.2	122.75
64.13	1943.45	1179.52	2367.1	580.39	1461.55	353.2	2531	720.54	2013.5	771.74	2464.5	1130.66	2266.6	32.95
311.34	195.4	91.5	246.55	163.84	341.6	202.52	1474.55	1234.54	285.9	86.83	199.5	64.77	433.35	502.4
501.48	714.4	292.88	638.95	399.59	758.4	754.62	1309.8	1577.27	1223.75	873.35	388.25	280.79	558.75	9.4
32.24	75.65	56.36	64.4	72.27	449.35	376.82	1607.35	2181.78	102.2	23.33	179.55	135.13	439.95	544.12
168.93	240.25	133.15	187.1	208.31	434.15	342.73	1407.15	1283.19	176.45	182.22	382.95	202.59	387.45	188.16
27.08	74.4	57.84	75.15	56.78	156.5	126.43	102.95	43.35	74.25	12.66	79.25	78.56	72.45	11.67

68.17	512.15	523.05	485.95	560.1	563	717.29	1059.1	1429.06	1106.15	1474.25	693.05	174.58	668.2	530.75
43.49	400.45	170.2	152.85	179.96	1098.2	1503.17	956.25	374.84	241.6	276.48	188.9	188.51	1327.65	367.34
69.16	568.4	21.35	397.75	262.69	471.55	310.49	1160	116.96	854.5	360.91	1425.25	294.51	960	1099.13
338.14	626.2	574.45	715.15	700.25	914.6	759.15	317.7	114.41	596.7	561.16	1297.65	525.03	1106.95	216.16
135.48	1157.15	16.9	1064.9	147.36	1223.7	44.69	1054.3	422.85	629.75	361.97	718.95	102.18	1154	92.49
699.54	1230.3	238.58	1442.95	62.15	1594.3	1032.38	581.9	451.42	579.05	195.94	793.45	701.52	804.2	433.74
190.85	303.9	12.87	272.9	56.71	179.1	118.23	678.2	826.47	685.25	354.05	652.15	713.54	618.15	128.2
48.58	1138.55	506.78	1256.65	339.76	859.3	409.27	1085.75	1041.5	868.25	372.57	1916.4	967.89	585.65	327.46
147.93	184.75	176.85	49.6	14.28	568	600.05	218.35	38.82	157.05	114.2	710.55	782.84	179.1	84.99
1421.14	44947.2	10518.35	51732.85	20114.71	47576.4	7677.34	59735.9	43074.26	53130.7	3773.26	51427.75	5027.18	70457.15	3738.83
1.34	166.3	47.09	188.45	15.77	328.75	125.23	280.6	129.97	941.05	832.76	860.05	882.12	269.8	54.45
2.19	72.5	37.05	94.25	6.29	89.3	54.59	157.7	108.75	95.7	26.59	93.25	56.07	104.9	28.71
786.59	1272.6	915.99	1155.65	1081.38	1501.95	977.29	1020.5	650.4	966.9	189.08	1009.55	456.44	2238.7	488.47
30.26	180.75	44.19	273.4	86.83	467.45	363.24	390.85	153.23	365.45	92.84	1078.65	1132.43	356.3	36.63
254.06	359.75	274.15	433.75	169.49	154.4	153.02	818.3	861.4	243.8	155.85	782.55	911.11	549.7	530.61
315.44	1146.35	181.8	1339.8	91.78	871.25	121.55	607.85	293.1	387.05	437.2	576.25	273.3	1044.45	364.94

1945.68	2604.15	188.16	2499.5	336.16	2162.25	132.44	1690	594.82	1608.9	306.18	1462.8	351.57	1835.9	314.95
85.91	230.75	135.13	112.55	32.03	307.2	5.09	295.9	274.22	86.2	14.28	87.1	51.9	267.6	261.06
281.64	438.3	358.08	573.35	549.07	343.2	234.48	407.1	295.43	234.05	223.94	768.3	822.37	1363.95	632.08
198.13	426.4	455.24	376.4	384.52	457	238.01	1407.1	1620.41	507.05	430.84	700.05	133.01	617.8	286.8
143.47	1044.35	136.4	844.45	419.1	1996.6	1495.39	2340.95	1560.37	861.9	446.75	474.2	406.59	915.85	187.31
681.51	262.55	298.19	288.1	334.32	448.35	169.21	345.85	59.47	273.05	265.94	277.7	212.7	198.85	49.85
68.09	195.8	162.63	185.1	177.77	687.65	644.24	589.9	70.85	340.85	23.55	549.2	542.21	190.95	70.36
30.33	2607.4	1879.77	2383.65	1563.34	3999.7	977.5	2820.4	2502.59	5241.5	2143.52	4218.7	438.26	5639.35	465.35
22.7	102	86.97	108.15	78.28	83.15	12.52	166.85	152.24	75.2	47.8	227.1	89.66	87.1	33.09
61.59	4072.55	1531.52	3230.6	340.83	2137.3	445.34	996.55	282.35	2654.95	361.54	2008.2	406.87	1467.75	843.22

446.96	1624.05	758.09	1982.55	1265.08	1241.9	1092.2	1488.75	1212.62	1301.2	1309	2763.65	794.01	1900.9	312.54
53.95	130.9	106.21	148.95	80.68	137.4	7.35	492.65	207.96	117.9	71.7	140.2	114.55	201.35	198.63
233.13	2472.5	1068.86	2029.8	442.79	3183.5	1601.46	949.45	969.23	2255	2003.23	1568.45	384.6	1511.9	336.72
122.68	297.1	15.84	170.3	195.16	507.1	638.09	376.15	125.94	192.35	54.09	586.1	580.96	314.5	31.54
514.42	1070.8	803.56	860.55	1100.89	437.7	471.36	450.7	292.88	300.35	17.75	1650.9	1451.97	650.05	306.39
290.41	2439.25	757.66	2863.8	157.26	2384.15	1296.34	3717.55	528.85	3605.15	946.89	2832.45	1915.48	2762	414.36
397.89	501.95	193.25	406.75	327.89	143.1	28.43	684.55	673.8	319	87.54	316.6	115.26	335.4	37.62
341.89	1058.35	270.61	982.7	377.59	1435.8	959.54	1707.05	1158.03	1072.7	508.41	1416.2	706.26	1268.15	328.59
157.19	706.2	519.16	701.55	525.73	116.05	35.28	114	84.57	765.95	562.93	853.5	615.32	892.55	122.26
301.58	1266.6	459.2	1347.75	344.43	592	627.35	1502.35	735.6	708.2	492.15	2135.15	1494.19	1031.45	284.19
162.78	72.85	63.57	107.85	14.07	58.8	9.9	106.4	108.61	272.2	338.28	328	382.12	80	6.36
847.89	5247.6	63.92	5711.95	720.61	4044.6	4837.46	1514.65	1644.66	2135.45	910.26	3343.45	1043.48	3296	339.69

241.9	6121.15	1088.45	6448.95	624.87	4379.05	2529.53	3211.35	1422.77	5457.4	1010.31	6495.65	1072.04	6416.65	929.49
207.68	70.1	53.32	75.3	45.96	147	139.3	124	57.7	148.75	114.9	300.1	65.34	125.8	15.84
170.34	233.7	82.17	139.8	50.63	849.35	578.34	480.75	279.66	378.2	335.31	138	33.09	784.35	553.17
131.45	594.5	112.43	562.75	67.53	403	321.03	1017.45	161.86	888.3	376.75	551.65	126.08	194.55	56.64
9.26	128.6	79.34	103.6	114.69	151.85	157.05	283.45	288.57	46.75	12.37	76.75	36.56	323.7	372.22
829.37	1555.05	189.72	1711.9	32.1	1358.4	237.87	2867.8	901.42	1118.9	1114.54	1440.55	640.29	1308.95	130.74
100.41	62.35	14.35	61.45	15.63	224.85	2.05	1347.75	1846.89	100.45	70.64	250.15	190.28	97.05	25.81
692.61	1247.25	1235.81	1578.7	767.07	2100.05	961.31	848.25	189.29	2643.85	271.74	1038.7	765.94	1882.5	126.01
417.97	3424.6	369.53	2894.3	380.42	2941.85	294.23	1863.8	799.6	2886.65	798.25	2637.75	1107.97	3473.25	401.14
284.26	1040.65	200.04	898.25	1.34	1924.5	915.42	729.6	284.54	1169.25	7.71	995.1	113.84	1501.5	98.85
356.1	553.9	225.14	419.85	414.72	187.1	39.32	188.25	6.72	100.15	7.71	197.5	79.76	697.35	374.55
1038.03	974.25	37.41	1066.2	92.63	1275.25	737.16	783.2	136.33	737	331.63	1466.1	1075.37	1132.7	214.54
1034.85	3282.8	331.35	3317.45	282.35	3077.75	529.69	2390.15	2373.97	3555.5	412.95	3355.2	1015.97	2646.15	1071.05
4185.22	11469.55	2503.37	10502.1	1135.19	12248.8	3697.32	7592.95	1460.11	8935.1	2737.35	5050.75	5263.63	10132.45	94.26
1779.79	5342.4	643.75	5728.2	1189.35	4788.5	1103.94	6063.9	3523.37	5823.55	2243.86	6388.25	823.43	5775.85	1616.09
18.46	276.65	373.42	291.3	352.7	120.2	69.72	185.35	135.27	75.5	73.68	727.25	561.65	71.85	39.81
279.73	5198.6	2542.05	5068.75	2358.41	6939.7	2707.23	2457.25	2736.57	7576.8	3556.04	7380.9	5391.26	4217.6	1329.36
410.4	626.3	241.69	592	290.2	698.25	345	461	189.5	519	20.51	543.4	39.88	510.9	202.66

180.52	1341.6	445.9	1716.85	84.78	1221.2	471.5	1248.3	1268.83	579	327.81	609.05	1.48	1279.2	1146.36
209.73	150.25	132.02	186.5	80.75	319.05	68.52	230.15	64.98	332.45	274.29	107	6.22	180.55	101.33
56.43	222.7	172.68	222.45	173.03	313.35	218.99	164.3	165.89	203.35	198.34	947.4	1197.13	172.15	82.52
1194.09	128.9	97.86	135.75	88.18	399.9	508.83	110.4	74.39	478.25	611.01	110.7	61.52	205.7	77.78
153.3	1425.3	339.69	1496.7	238.72	1429.05	468.74	995.8	351.57	1256.55	131.45	996.8	382.54	797.8	785.74
1616.73	4399.05	1752.85	5279.45	507.77	5478.45	2113.05	6760.3	483.1	8077.4	1883.45	4845.25	874.62	6661.65	3375.8
27.15	649.85	643.96	615.9	691.97	1005.8	1219.33	414.3	479.14	429.1	99.7	160.4	97.3	303.5	287.93
38.11	69.1	34.08	65.5	39.17	40.55	27.65	228.2	246.78	82.45	54.66	367.4	404.32	224.65	276.41
183.49	528	252.86	384.35	456.01	668.4	573.32	905.45	653.86	402.4	346.91	293.45	139.37	366.1	199.69
199.12	1636.2	431.05	1754.65	263.54	1480.65	898.66	2115.5	1570.48	1005.4	768.77	2297.85	793.44	759.6	625.79
88.39	100.6	42.85	88.85	59.47	506.9	408.99	179.2	19.94	221.5	84.29	223.75	120.14	551.7	501.2
2.19	67.3	35.64	65.7	37.9	269.9	289.21	206.65	217.15	177.3	88.25	391.9	421.29	289.95	270.75
707.04	663.35	288	954.8	700.18	681.45	385.87	837.9	416.91	1135.45	298.89	1008.15	706.75	947.4	546.59

690.7	2251.95	402.27	2135.85	566.46	1248.5	1105.49	1977.5	2087.1	3306.55	1056.77	1503.25	1283.89	2873	38.47
379.93	1717.1	138.88	1483.85	468.74	1038	609.95	1055.45	39.1	517.45	154.08	1109.15	495.61	603.5	126.57
427.23	214.2	6.22	231.8	18.67	297.45	73.33	1159.35	1163.54	554.75	316.15	909.75	984.79	515.05	484.44
116.04	583.35	110.1	614.5	66.04	1225.7	961.1	1044.9	1148.91	597.55	352.07	773.4	312.12	479.8	244.23
819.54	1861.9	160.94	1711.65	51.55	1560.75	501.69	2760.9	2012.14	866.5	901.84	1246.05	368.33	1374.7	249.89
4943.74	55805.15	2403.95	61775.85	6039.9	49455.85	19085.59	73861.9	75602.59	74038.66	30347.68	89496.45	26920.19	74184.5	27658.06
863.94	668.75	101.89	438	224.44	812.95	380.49	384.55	318.41	369.75	201.45	249.2	41.3	512.65	581.17
1209.08	2857.05	467.19	2632.2	785.17	2740.9	1158.24	2924.45	1206.54	2972.4	629.75	3097.75	1608.46	3284.45	1008.83
266.93	269.25	31.04	251.05	56.78	710.75	726.98	283	235.89	64.9	37.05	566.55	231.72	403.9	325.41
3288.97	7998.6	5247.3	6510.85	3143.3	8244.9	4730.69	4384.35	2527.84	4215.2	2235.45	4568.7	3167.98	5320.95	1366.63
147.5	824.25	722.03	790.3	674.01	1286.75	538.46	1596.2	1256.95	292.4	112.71	412.5	407.72	547	525.24
578.41	1229	666.24	1156.6	768.63	374.65	205.56	263.55	173.59	1206.1	774.85	1050.45	446.68	762.4	1.56
294.09	664.55	467.75	744.05	355.32	508.9	169.71	1289.1	529.34	1049.05	525.17	295.6	123.46	1446.6	719.13
324.84	1029.65	867.69	1127.6	729.17	447.65	287.16	2218.25	1791.17	453.85	402.41	664.2	614.19	1277.15	331.56
176.49	51.25	29.34	153.7	115.54	528.15	670.69	206.65	140.22	72.95	34.44	240.65	11.38	138.15	74.88

60.74	450.65	341.89	509.65	258.45	448.2	222.31	181.25	77.43	710.65	539.31	681.6	852.06	572.75	240.91
254.56	226.75	197.07	57.85	41.79	440.9	126.71	416.85	76.3	148.35	104.72	567.85	719.48	190.1	67.46
505.09	3782.5	221.47	3679.7	76.08	4101.45	1111.5	2338.6	573.46	3320.55	78.14	1868.3	0.71	2535.85	64.13
532.31	694.8	253.57	546	464	945.6	454.1	837.5	395.27	1228.95	827.81	68.7	18.1	295.4	275.35
1729.44	3651	609.1	3613.3	555.79	3916.3	1510.95	1086.65	1308.78	1220.2	707.81	1155.25	1269.04	2217.75	1103.44
152.24	699.1	31.68	997.75	390.68	2631.15	3195.2	1086.8	6.22	1847.35	23.12	838.35	230.16	1698.3	1061.65
276.48	301.55	319.97	285.8	342.24	91.1	86.13	250.45	220.83	548.1	549	609.05	789.2	496.2	414.08
276.2	142.65	56.36	133.45	69.37	90.75	61.31	206.1	174.94	467.8	553.81	125.35	39.1	167.1	76.23
2186.16	6905.9	159.81	6827.2	48.51	5742.65	1814.65	4435.75	1353.19	5105.85	1723.43	4461.1	481.26	5065.55	139.51
108.54	744.9	292.6	611.7	480.97	145.9	96.31	789.15	647.07	449.75	290.13	639.15	306.53	601.85	481.89
148.85	1032.95	269.2	1076.5	330.78	1633.3	668.5	2448.65	1949.56	1226.3	503.74	1418.5	350.58	1162	606.84
1.41	305	187.52	285.9	214.54	538.95	510.32	460.35	244.73	869.3	949.93	232.95	17.61	422.7	87.4
43.35	1590.8	264.74	1470.3	435.15	1676.65	428.86	1367.95	455.87	1379.1	33.23	1875.35	333.4	1752	848.39
78.06	1095.2	197.99	1103.85	185.76	592.95	279.66	1650.1	1207.03	985.8	253.29	1002.5	128.55	1437.75	113.91
437.27	1737.2	754.06	1940.25	466.9	836.35	596.87	808.75	280.93	690.65	859.21	1835.85	963.72	1539.8	346.06
575.44	474.3	435.58	482.3	424.26	615	552.67	1651.6	1576	463.9	243.95	274.9	164.76	464.3	296.14

739.92	883.35	753.71	900.3	729.73	1106.7	880.91	270.25	36.98	801.15	669.98	415.2	85.7	172	66.47
72.41	694.75	786.94	715.1	758.16	144.25	53.1	1133	1231.07	199.4	112.85	282.55	113.49	76.05	0.92
10.75	76.55	12.66	55.7	42.14	69.85	71.63	474	651.81	28.35	3.61	171.95	222.39	60.3	61.94
1.98	692.3	141.56	634.3	223.59	801.45	432.11	1027.1	483.8	627.8	1.98	397	4.24	775	37.9
259.08	1377.15	360.98	1957.8	460.19	1777.85	746.07	2863.7	1461.87	1752.85	626.71	1475.05	518.66	2276	529.91
177.41	493	121.91	412.1	236.32	399	307.59	439.3	380.14	294.05	50.13	472.9	314.95	306.75	203.29
470.58	963.2	38.18	1060.75	176.14	611.15	466.2	1114.8	364.02	1306.55	43.35	457.75	229.88	1012.5	942.01
564.34	684.75	434.66	743.5	351.57	731.95	369.89	2868.6	1151.88	2388.65	318.98	1348.35	439.04	1402.35	311.34
428.29	491.6	249.89	447.8	311.83	143.25	142.62	229.35	213.9	99.6	53.74	860.2	751.8	340.15	101.75
3064.18	12335.05	641.13	13047.35	366.21	9338.4	2058.53	12145	1179.74	13023.45	4754.23	12670.1	6401.44	15867.1	1081.31
690.14	6816.6	606.41	4232.4	3048.2	6419.8	3706.09	2867.9	2407.13	3785.4	3747.1	2645.65	1860.19	3098.9	2037.74
6792.96	46774.3	5218.45	50368.4	10301.27	38005.25	13687.68	38341.2	29673.45	49283.5	10102.29	32031.65	26710.89	59501.65	986.77
507.14	586.1	240.13	1427.7	950.07	592.3	589.16	1020.1	83.44	759.8	488.47	1053.7	40.59	726.4	501.2
356.1	1353.4	958.84	1240.5	1118.5	345.35	108.4	349.75	131.31	863.7	733.84	940.3	818.97	1952.8	243.53
21.99	64.85	54.09	68.2	49.36	298.95	380.07	99.2	100.69	48.55	28.64	88.75	92.28	51.1	11.88
86.34	371.1	361.33	354.3	385.09	762.25	834.32	396.85	518.24	126.35	89.87	262.4	84.57	205.45	174.58
523.82	885.5	697.77	745.45	895.83	889.5	806.67	343.15	221.54	1363.65	631.94	1110	1400.92	885.5	831.7

68.87	1731.6	1162.06	1360.15	636.75	1765.9	891.94	1420.25	1737.71	946.4	770.46	865.6	590.43	1718.05	1384.73
83.51	482.85	302.85	383.85	442.86	449.05	463.65	372.25	340.47	179.8	105.36	726.5	911.74	338.35	74.74
393.93	182.05	106.14	180.75	107.98	585.75	620.06	1623.2	2013.27	561.55	702.79	468.6	155.85	529.7	533.16
85.42	2442.15	1034.99	2406.8	985	2549.05	231.15	1068.2	666.24	2061.95	663.76	916.2	1220.18	2219.9	282.84
1179.45	1992.9	1095.45	1812.75	1350.22	2128.75	1302.14	1760.2	1279.86	2642.55	239.64	1039.85	725.85	1781.6	155.42
224.51	2899.4	292.32	2558.25	190.14	3029.5	1105.21	1131.4	19.94	852.5	10.75	2186.4	768.06	1888	900.57
579.4	1469.7	282.7	1483.25	301.86	1543.65	273.44	1020.5	665.39	1325.75	174.16	675.85	713.4	448.05	397.04
985.21	1852.6	399.66	1246.1	458.06	1834.25	484.01	1693.4	632.86	949.05	198.91	2057.55	1715.37	925.15	525.03
90.79	138.95	23.97	73.75	68.24	454.85	232.43	697.8	743.17	81.1	34.51	696.15	741.12	444.2	33.23
183.56	2073.1	401.35	2138.8	308.44	1790.3	666.94	1863.95	474.26	2610.45	143.75	1987.6	1365.71	1435.95	201.45
23.33	305.6	294.72	283.55	325.91	499.7	340.54	776.45	481.89	272.25	165.53	860.6	1104.93	162.4	127.7
1135.75	1546.3	578.98	1530.65	556.85	2151.5	699.05	1046.65	385.16	658.7	498.93	1880.9	231.65	1896.05	324.21

43.56	281.7	41.86	213	55.3	191.9	52.61	322.6	156.55	215.9	79.76	201.5	42.71	240	34.79
58.83	235.3	75.8	136.3	64.21	224.4	156.98	1256.75	1610.44	256.8	21.07	159.3	96.73	311.3	57.7
941.23	8327.25	181.37	7912.35	768.13	7893.05	299.18	4416.55	3463.48	6810.15	259.44	3822.2	2915.26	5364.5	240.42
4.03	72.35	30.62	64.85	41.22	71	50.35	103.7	54.73	121.7	78.91	133.8	69.01	94.6	79.76
29049.64	37025.25	23926.16	20554.15	632.51	40480.35	13627.57	16910.35	5052.63	52920.05	14081.4	22705.8	14746	36415.85	826.96
2856	10986.7	1682.07	11014.65	1642.54	6503.05	870.94	9113.65	4228.29	10552.95	1291.25	8543.05	964.56	5479.1	444.77
361.4	608.75	420.23	512.25	283.76	458.85	212.49	1922.65	1731.78	828.7	297.55	1260.1	820.1	537.85	317.42
404.32	3336.7	48.65	3453.4	116.39	2812.05	2698.11	4030.1	1167.29	2096.95	1032.59	2605.05	663.9	3235	234.19
42	79.65	2.19	53.75	34.44	96.5	63.78	295.85	97.23	107.6	62.65	528.9	623.24	134.2	115.54
508.62	114.9	36.35	103.75	52.11	76.4	5.09	376.55	437.49	100.8	54.02	214.1	167.02	74.05	21
80.68	17.8	7.5	20.3	3.96	83.55	59.47	198.55	40.8	154.1	161.08	494.2	650.54	25.65	9.97
168.22	306.9	151.32	327.05	122.82	211.8	22.2	440.9	252.01	992.1	785.03	294.15	171.19	207.45	36.84
778.6	966.5	356.52	890.55	463.93	449.2	475.18	112	67.46	306.25	253.21	723.5	893.36	122.1	48.37
606.2	4113.2	680.94	3910.65	394.49	3565.6	1063.35	3189.5	1908.76	4203.4	287.23	3139.1	1239.98	3076.7	58.97

57.35	385.1	55.86	288.4	80.89	189.7	137.74	357.45	253.36	287.75	225.07	437.65	129.47	197.45	29.2
785.88	999.65	602.1	1146.55	394.35	1298.25	515.55	459.9	178.76	912.5	1003.81	1648.95	512.3	1374.5	411.82
19.87	473.3	200.68	404.45	298.05	58.15	29.2	368.6	424.97	201.15	78.7	212.8	242.68	118.3	110.59
31.32	1023.05	646.51	965.5	565.12	1244	145.81	1097.1	327.67	625.9	551.12	507.15	290.41	1467	629.75
163.48	2544.8	60.53	2839.9	477.86	1568.2	1096.72	2646.15	7.99	3863.55	833.89	3381.2	1657.32	4022.4	2157.38
320.39	822.4	402.06	834.15	385.44	342.4	89.8	713.45	287.72	575.9	243.67	1387.3	885.16	915.55	276.27
35.07	276.9	5.52	156.3	165.04	497.4	638.38	749.45	365.22	395.75	504.66	242.55	28.5	433.4	538.67
164.97	2851.85	836.01	2225.5	49.78	1620.1	77.78	1460.35	1367.9	1473.25	1004.16	2493.65	371.02	1723.7	311.13
405.17	218.85	38.54	170.9	29.27	237.6	208.31	510	623.24	585.6	257.81	383.05	236.1	852.65	216.87
1299.87	5043.15	2063.13	4145.7	793.94	4907.7	3194.99	1901.85	2237.22	2911	1724.77	2774.9	1783.89	3103.25	567.17
95.67	311.25	389.97	395.6	270.68	55.05	37.41	182	159.38	296.8	374.06	86.8	96.17	68.1	5.09
679.53	1172.15	261.42	841.2	729.45	1429.9	244.38	2524.15	442.58	1003.05	1063.42	687.25	410.05	574.8	89.38
522.06	4057.05	731.64	3827.65	407.22	3562.6	0.42	2991.15	1971.48	3684.7	170.55	3614.1	18.53	3840.65	27.65
247.06	121.85	111.09	297	136.61	1016.3	1010.31	680.25	96.52	234.65	226.06	604.65	687.38	345.15	299.04

78.56	607.5	143.68	517.05	15.77	311.55	269.34	1203.1	1005.79	505.35	124.1	128.85	30.62	700.45	378.37
289.7	184.2	176.92	171.8	194.45	75.45	26.8	772.15	954.95	60.15	9.26	823.9	1030.54	243	69.72
1102.8	5743.5	3591.25	3848.95	911.96	5213.25	3850.55	1513.05	1575.65	2751.9	1275.62	2477.55	1763.74	3013.15	202.16
95.53	588.75	171.19	662.6	66.75	803.75	164.4	564.1	648.56	711.45	349.52	408.7	419.88	991.1	362.75
491.37	1075.3	109.46	1049.6	73.11	1748.2	1237.3	1689.7	400.93	1418.4	992.92	1399.45	569.43	1021.85	386.43
202.02	100.15	14.64	96.3	9.19	172.85	130.18	638.25	727.12	131.55	83.51	90.25	84.22	274.3	296.56
720.4	1759.85	38.25	1620.85	158.32	1815.85	371.58	2713.9	1626.63	1844.3	148.49	2190.05	634.49	1618.2	433.88
26.94	212.05	110.1	241.8	68.02	206.45	71.91	439.4	150.19	228.55	0.92	340.05	250.25	210.05	51.12
655.56	2510.1	618.01	3057.7	1392.43	3995.95	2403.95	4170.4	2542.05	2887.2	276.62	2246.1	1487.89	3370.95	537.19
14	167.7	180.45	175.5	169.42	447.3	308.86	195.95	167.51	507.45	620.77	146.5	57.98	306.3	131.52
105.64	324.2	172.39	327.15	168.22	240.05	22.7	405.25	196.93	277.65	145.59	686.4	331.35	440	45.96
5589.25	41580.3	676.13	42295.45	335.24	37742.5	2130.66	41318.55	31912.37	39296.1	1309.14	37391.45	6306.9	48113.15	9219.33
787.72	16809.3	267.99	16584.15	50.42	18805.9	58.27	12146.7	1537.53	11812.1	2212.25	12797.6	2240.11	13354.05	751.3
3.18	169.35	31.32	97.85	69.79	517.65	355.32	657.4	114.27	277.95	128.34	189.95	157.76	508.9	605.85
130.67	1480.45	155.35	1476.5	149.77	1443.35	206.4	1252.6	1240.69	2360.95	1475.66	1964.65	1175.56	1464	33.8

264.88	125	104.23	131.2	113	1492.45	1574.94	1056.9	83.3	1019.2	89.24	379.95	276.13	176.35	140.64
118.86	4738.65	853.27	5160.8	1450.28	3653.4	1527.35	5585.9	4784.85	3338.95	3098.05	3507.6	1522.54	6284.6	277.75
225.28	804.75	18.03	883.5	93.34	1110.95	261.98	501.2	265.87	1366.2	1352.7	1180.8	352.28	1077.65	242.33
8.13	279.75	122.4	246.85	75.87	186.5	62.51	460.7	551.68	688.2	836.79	391.35	48.44	879.95	126.93
1723.15	5152.9	941.58	5224.45	840.4	4999.15	982.1	7281.35	3030.02	5901.15	433.53	5872.3	111.58	5707.6	272.8
72.97	41.5	22.06	41.3	22.34	59.15	47.16	77.7	54.02	203.95	212.77	273.2	330.78	56.5	6.51
91.15	162.2	1.7	143.95	27.51	208.9	84.99	481.5	254.56	195.05	34.15	358.1	114.41	308.1	57.98
169.56	974.55	561.37	899.1	668.07	1004.6	736.95	259.95	141.21	1109.2	1057.55	755.35	578.2	601.25	74.32
123.25	538.7	449.72	575.05	398.31	115.3	60.67	105.95	16.76	388.3	121.76	270.8	5.23	113.3	2.12
67.67	626	246.64	1350.95	778.6	633.6	86.41	890.25	333.4	1410.3	490.02	677.8	478	1673.45	1113.2
1453.25	2787.4	1169.41	3458.2	220.76	1855.45	1189.57	653.6	242.4	3540.6	1756.31	1627.1	1291.6	2287.75	1845.76
32.1	2345.5	1625.92	1667	666.38	1877.25	860.62	1256.35	1556.84	641.5	446.75	1987.6	242.82	1016.6	63.64
5056.59	23087.05	11271.64	19138.65	5687.75	22731.3	18024.72	14432.9	12508.01	22871.9	4001.38	16172.4	16107.19	21008.5	3702.13
99.84	1639.3	60.25	1144.2	639.93	555.2	141.14	985.3	283.97	338.65	230.59	174.15	34.86	949.35	589.23
73.61	662.75	238.93	927.05	134.85	1697.85	182.79	840.6	634.98	931.75	265.09	1328.4	843.01	1447.15	100.48

616.1	2473.25	123.39	2600.95	303.99	1773.05	160.44	993	1131.94	1711.2	506.43	1441.85	1101.32	951	717.43
227.48	843	389.47	681.75	617.52	376.1	297.27	457.6	525.95	762.2	416.2	898.55	441.59	918.9	134.92
342.17	284.2	77.64	306.7	45.82	454.65	80.68	469.25	420.8	311.45	96.94	523.6	127.28	425.95	139.79
114.06	506.7	372.79	466.05	430.27	596.95	635.9	319	218.07	228.5	126.43	290.45	335.52	142.2	107.76
140.08	2837	391.88	2739.2	253.57	3064.95	383.18	1543.65	1028.77	2340.75	1065.26	2955.9	755.61	3155.05	890.18
415.64	305.6	103.38	131.2	143.26	127	25.17	773.2	211.14	395.75	489.81	242.65	101.89	537.75	228.04
47.38	344.75	268.49	578.4	61.94	490.1	33.38	355.25	121.69	253.45	83.65	182.55	76.58	759.2	59.11
211.64	320.35	269.48	268.85	342.31	60.35	18.03	51.85	48.3	90.5	48.08	84.95	57.91	286.15	352.63
286.1	56.4	30.41	56.25	30.62	46.1	41.86	74.4	34.22	83.85	40.09	80.05	57.35	94.9	86.41
8.91	542.85	147.43	349.85	420.37	297.85	135.98	205.9	49.92	233.2	263.61	396.7	75.52	244.5	267.99
1096.72	6790.5	760	6195.95	80.82	5954.7	2220.74	3220.95	509.75	5057.45	2017.16	2708.7	2479.82	4698.55	339.62
251.16	2254.8	376.75	2246.4	388.63	2001.25	1086.61	1925.05	343.58	3480.5	517.18	3547.2	499.92	2864.65	1023.68
255.27	534.6	294.58	480.05	371.73	970.15	916.62	1350.1	1358.92	987.4	37.62	1185.25	756.96	438.2	94.47
117.17	233.3	64.77	238.7	57.13	401.85	63	609.25	460.11	1071	1341.66	265.55	24.4	316.9	81.46
16.26	628.05	707.6	643.25	686.11	546.3	329.94	207.15	43.35	426.25	255.05	810.7	795.64	756.65	280.37

55.65	83.15	98.08	86.1	93.9	75.55	15.49	1060.15	1340.32	423.25	519.09	1195.05	1524.73	64.5	19.8
442.93	336.8	314.95	392.1	236.74	214.3	97.02	2051.6	1606.26	675.8	503.04	899.45	423.06	1043.6	335.88
40.8	151.55	52.11	143.4	40.59	791.15	671.82	803.85	282.49	1475.5	744.3	166.65	54.38	280.05	203.72
13.72	156	187.81	155.55	188.44	94.7	97.72	81.7	16.97	86.5	5.52	167.35	172.6	81.8	77.78
852.56	1251.2	362.32	1700.1	272.52	427.35	179.53	1692.2	376.75	1035.35	928.78	2000.1	424.26	1806.15	814.52
52.33	103	18.38	119.35	4.74	153.05	83.65	576	700.18	437.5	83.86	277	117.8	453.5	463.15
273.51	1892.75	21.85	2177.8	424.97	2872.9	2049.2	3493.25	3476.35	4158.75	1078.55	1689.1	1427.65	1787.2	1412.09
612.92	2071	429.78	2157.35	307.66	2345.4	899.16	2626.4	2000.69	2073.95	712.55	949.7	186.25	2568.55	60.88
453.96	2761.85	687.52	3011	335.17	2219	101.26	2727.6	381.98	2094.1	87.4	2675.55	230.02	2578.45	544.68
300.31	462.7	277.04	559.4	140.29	297.6	43.27	486.1	29.13	194.25	198.77	827.2	865.07	472.2	323.57
6866.93	20896	9113.62	20379.15	8382.68	19648.45	11941.83	5411.1	3139.13	7593.5	4925.99	10162.3	8469.02	11744.2	606.27
1439.74	5209.95	855.25	4882.35	391.95	5264.75	1017.03	3247.5	2997.14	4156.25	1427.86	4761.25	1667.71	4185.35	52.68
162.92	194.85	65.41	156.9	119.08	176.85	166.24	959.65	1185.61	149.05	28.92	183.45	13.36	93.9	26.16
277.75	207.3	269.12	238.35	225.21	665.45	724.57	1625	2237	339.15	350.51	647.45	612.85	304	332.2
185.83	194.35	96.52	316.15	75.73	978.75	286.59	681.75	74.46	226.1	225.28	555.85	319.97	141.65	82.8

297.76	1519.95	1557.97	1521.25	1556.13	1631.15	1297.47	928.1	482.95	1302	166.31	1907.2	810.2	1254.75	544.26
216.8	766.3	256.26	817.45	183.92	466.5	330.08	604.2	709.23	787.25	255.05	475.75	479.21	429.65	80.82
384.6	107.85	114.48	20.65	8.84	57.55	22.98	121.05	53.67	40.9	15.56	373.15	410.33	120.45	96.38
204.64	859.5	64.91	1118.7	301.65	1070.8	98.57	2155.45	2040.22	1385.6	387.07	1908.55	1378.79	1320	374.63
1175.99	1818.95	66.82	1936.7	99.7	1608.8	170.13	1687.4	564.84	2774.55	1220.54	2697.4	2151.3	1429.9	1073.39
0.78	213.55	18.03	233.9	46.81	209.85	38.11	182.2	13.01	187.55	49.29	178.9	80.61	301.75	88.74
385.94	1937.5	1074.38	1871.4	980.9	1467.55	939.82	1673.65	740.84	3445.05	297.48	1224.05	731.64	2358.95	289.14
110.8	100.7	9.05	99.4	10.89	218.65	99.63	618.65	383.75	626.65	747.77	864.55	650.18	401.3	48.51
201.17	2022.25	102.6	1753.3	482.95	2838.55	1283.05	1887.9	580.25	1850	385.37	1797.55	563.35	1743.9	542.35
773.93	485.15	451.63	260.35	133.71	381	298.54	1449.25	1736.3	653.05	758.09	751.8	7.07	488.1	324.14
222.17	656.5	402.06	544.35	243.46	718.5	70	468.75	176.71	392.2	176.49	693.75	2.47	313	155.14
8.91	1297.3	209.59	1364.5	114.55	1406.7	257.25	815.15	638.16	1384.85	359.99	797.45	755.83	1242.6	240.98
171.83	265.7	212.56	280.25	191.98	536.25	462.66	417.9	123.74	208.85	70.36	1400.1	1313.95	534.6	201.24
32.53	7490.35	2206.81	8037.15	1433.52	6094.05	2460.52	3601.8	63.07	3081.1	896.33	1919.95	2103.15	4642.95	629.82
968.95	1380.9	144.11	867.7	869.88	1197.95	443.99	1236.1	1410.4	1638.5	5.09	656.05	150.97	781.95	934.3
355.18	1076.2	310.99	796.85	706.05	392.8	80.33	1039.95	589.37	642.45	19.87	494.95	392.8	293.9	8.2

29.84	242.2	170.27	274.15	125.09	199.1	90.79	322.95	266.79	530.8	176.64	356.15	355.32	508.95	31.18
193.39	195.55	97.93	148.95	163.84	627.3	855.6	107.95	1.34	336.9	431.9	1049.05	1369.6	44.4	22.63
51.34	111.15	61.59	123.65	43.91	108.25	120.56	128.95	123.53	119.15	29.2	213.55	27.08	134.55	25.81
19.52	2540.45	589.66	2417	764.24	4369.8	4441.05	16392	20554.32	2856.55	2931.45	4778.95	9.26	3607.65	2219.96
586.33	1016.9	455.09	652.55	60.17	766.2	631.45	1578.5	299.67	455.65	303.99	523.15	535.35	724.15	211.5
16.97	320.2	235.18	292.15	274.85	203.95	17.04	304.2	24.89	359.25	314.17	300.5	91.5	253.3	50.49
340.75	3471.8	169.56	2854.2	1042.98	1401.9	1262.33	1645.6	16.97	3453.4	373.35	2016	717.43	2011.65	279.52
101.12	1704.15	109.53	1628.35	216.73	1087.5	807.8	815.3	634.7	1318.1	1203.78	1700.7	702.58	1143.75	255.48
1.06	92.55	96.94	117.3	61.94	682.85	893.71	65.75	34.29	489.6	559.32	145.35	120.99	152.8	172.96
61.94	93.5	81.32	180.05	41.08	123.2	137.6	112.3	99.56	122.85	41.65	75	10.75	172.4	14.71
3.11	44.4	9.62	27.35	14.5	632	867.9	183	158.82	85.9	83.44	75.35	63.71	104.85	60.46
12.23	3525.75	48.72	3811.65	453.04	3107.5	1660	4379.5	2277.45	4312.2	1125.71	4464.1	422.14	4522.05	1026.79
417.41	1906.5	458.77	1800.2	308.44	1609.95	843.08	703.6	267.43	953.7	897.46	624.85	712.27	1046	472.06

538.53	2529.15	242.04	2178.35	254.06	2546.7	689.71	2189.9	259.37	3315.7	218.5	2232.7	1011.87	2515.4	864.93
26.94	414.35	189.86	370.6	127.99	567.35	467.04	231.6	14.42	412.3	210.58	488.55	344.15	213.75	68.24
858.14	1815.6	0	1562.65	357.73	1017.65	470.44	1742.25	951.84	1550	314.95	837.95	226.63	815.65	315.44
87.54	178.95	121.27	267.9	4.53	474.25	488.26	168.7	70.57	249.95	69.08	258.2	111.3	343.4	170.7
600.26	172.35	16.48	190.25	8.84	255.25	28.35	318.15	134.14	634.45	544.54	215.05	7.57	317.2	0.99
6389.98	7350.4	1963.78	8690.75	68.24	7582.1	1342.94	5874.45	3047.42	3667.65	997.8	4392.9	593.26	5827	570.92
83.93	1119	922.07	1666.2	148.21	689.5	41.58	1525.35	555.86	1371.2	855.17	1239.55	284.19	2949.65	2966.1
78.84	410.15	345.56	403.25	355.32	111.6	47.52	94.6	93.62	43.8	1.13	205.75	91.99	38.35	20.01
3.25	213.3	33.8	107.35	116.04	128.8	85.84	985.1	906.51	77.6	69.3	98.95	69.79	121.25	18.03

114.06	525.8	79.62	702.7	329.79	972.25	197.07	606.3	418.32	389	52.33	658.45	368.47	675.85	382.76
1950.77	1903.3	167.87	2075.95	412.03	1497.35	620.2	5035.3	3750.92	3348.55	1030.18	3553.45	1552.74	2208.45	808.44
1484.78	3862.85	283.76	2993.2	946.11	2512.4	872.43	1421.55	739.56	3041.1	1557.33	1718.25	2021.41	2766.45	514.28
439.82	916.8	161.36	749.25	398.31	887.9	261.91	1079.5	465.13	966.3	521	718.7	141.99	1330.8	339.69
139.65	45.2	8.77	34.25	24.25	653	892.93	181.55	29.2	253.65	284.47	89	18.95	286.45	309.64
166.38	601.55	136.4	568.95	90.3	1234.25	947.31	102	16.83	72.3	17.39	654.1	408.42	405.1	41.01
503.95	2515.45	107.13	2314.5	177.06	2047.5	670.62	2749.5	1854.32	2877.5	569.79	3247.3	531.6	3702.4	1301.92
61.73	405.4	356.38	512.95	204.28	239.1	245.93	295.6	289.77	264.95	150.12	877.25	912.66	298.5	113.99
144.89	603.75	343.72	586.5	368.12	678.15	414.86	1276.4	1087.11	747	173.38	1391.05	398.31	524.3	199.69
47.94	2902.25	532.38	2697.8	243.24	2112.2	1350.57	1243.15	760.21	1697.65	960.6	1254.6	289.21	1384.1	577.28
48.3	575.25	378.09	650	272.38	1741.6	1987.82	693.85	438.34	745.85	209.8	501.35	79.69	563.8	2.83
401.14	452.55	39.95	333.7	128.13	601.2	511.95	1091.3	640.92	990.1	296.98	1667.75	649.9	865.15	432.96
46.46	232	146.65	174.45	65.27	121.35	85.63	513.35	559.82	500.35	550.34	275.85	200.32	154.1	3.11
192.9	511.85	498.44	332.7	245.08	428.15	457.99	644.15	718.49	651.5	596.94	147.55	87.89	202	147.5
10.75	188.75	140.08	259.45	40.09	298.65	281.5	403.1	71.84	361.4	130.96	389	199.4	582.05	619.78

118.09	498.75	266.93	440.35	349.52	354	154.29	1066.2	887.7	369.9	51.62	261.4	31.96	346.95	239.92
19.59	260.2	47.23	229.35	3.61	185.1	76.65	123.2	3.54	47.15	22.42	719.75	912.52	188.45	209.66
76.86	368.75	46.74	268.5	188.51	140.1	130.53	513.4	419.17	787.05	894	1069.9	893.92	413.3	367.7
29.91	198.4	100.55	235.35	48.3	189.65	6.43	246	109.32	454.55	277.54	111.7	23.62	171.15	110.8
77	584.85	110.95	812.3	432.61	1069.5	268.28	2070.25	1531.81	1866.15	781.28	2138.05	497.45	1228.25	94.4
557.2	546.05	108.54	457.65	233.56	446.7	44.97	1002.85	609.6	330.85	61.73	80.95	11.67	1272.75	441.73
358.79	128.3	44.41	151.3	11.88	179.7	150.61	251.2	183.71	684.95	910.97	390.2	250.03	582.45	346.69
23.12	414.05	272.73	374.75	328.31	282.85	363.52	316.85	319.26	77.45	57.2	721.95	976.87	59.55	3.04
357.94	390.35	104.72	266.6	70.29	662.45	297.34	678.35	365.36	247.95	124.8	361.15	193.25	476.2	408.14
197	685.2	755.33	690.2	748.26	720.85	877.31	924.6	300.24	794.35	503.67	734.6	17.96	450.45	66.82
180.88	1071.3	493.98	1083.2	477.16	1260.85	1021.27	1342.05	249.26	744.55	354.19	919.2	692.54	558.2	110.17
927.94	3027.35	2068.08	2551.4	1394.98	3338.6	1675.84	2165.4	2711.19	3419.9	673.02	3265.15	824.84	3039.3	612.21
141.7	243.5	163.34	255.05	179.68	745.65	690.91	337.85	159.17	293.6	334.04	209.1	137.74	705.55	380.21
244.66	309.35	121.13	236.3	17.82	311.8	309.71	459.2	479.56	633.7	636.82	277.25	140.08	579.8	155.14
31.96	83.1	55.72	266.1	203.08	58.7	1.41	194.55	127.49	163.35	164.26	139.3	88.95	160	56.57
32.6	164.35	91.43	168.35	85.77	202.4	0.42	102.95	27.65	129.6	38.61	530.15	141.21	482.85	534.93

382.4	569.1	378.02	700.6	563.99	643	488.33	985.1	544.33	1785.15	87.04	1139.75	637.46	320.55	217.44
111.86	308.15	346.84	372.85	438.34	253.35	97.79	422.95	364.51	363.6	125.3	344.45	259.86	322.65	267.78
45.18	634.4	98.29	635.3	97.02	1275.7	891.1	822.8	62.65	816.5	33.09	1017.3	1274.35	402.2	341.25
2425.16	68185.05	34126.46	90877.1	2035.05	49911.85	5132.53	88587.9	56313.98	84053.55	18492.89	69392.05	22700.46	82523.55	5236.62
10.11	102.95	10.11	155.6	64.35	178.1	140.57	453.8	326.97	289.4	160.09	578.5	617.02	124.1	4.1
122.33	547.7	530.75	525.2	562.57	254.65	100.06	957.1	922.63	89.8	33.66	836.3	718.14	128	24.32
438.62	1849.55	642.97	1705.05	847.33	1349.2	556.63	3069.95	1558.39	1866.3	238.29	2182.8	250.17	2412.6	65.34
358.72	276.4	103.38	226.8	33.23	234.2	206.76	1050.7	38.89	521.5	279.45	604.5	750.24	356.85	294.79
227.48	368.4	134.21	387.75	106.84	449.1	469.24	288.25	268.49	367.9	19.37	1132.9	1088.24	1618.05	1760.48
1679.66	4485.85	1712.82	3599.6	459.48	4940.5	820.24	4643.85	1289.83	3974.7	176.64	4893.7	1775.4	4423.2	912.45
71.21	2080	536.55	2042.4	589.73	2342.9	759.29	1534.7	1169.41	1215.3	134.92	1034.8	204.64	1172.65	184.06
343.37	155.7	69.3	159.8	75.09	130.35	126.22	138	66.61	122.05	63.71	87.85	97.51	49.3	1.27
29.42	70.85	73.19	93	41.86	77.95	74.03	174.8	101.26	88.75	46.32	228.5	202.66	76.15	44.9
796.49	1681.8	1271.1	2022.4	789.41	2578.95	2892.14	2930.5	2517.58	1395.4	1186.38	1673.55	905.03	1565.9	688.72

405.6	1595.9	70	1877.9	468.81	961.75	869.95	603.85	179.39	1395.3	1596.22	1821.85	369.18	1453.65	215.17
280.72	3362	837.5	2654.7	162.78	3840.5	2210.56	1940.65	75.45	3679.9	408.57	2199.05	266.93	2605.5	73.4
57.63	346.5	97.72	320.15	134.99	208.65	71.21	929.4	1014.27	403.3	259.51	1087.05	889.33	151.75	143.61
2926.5	6570.6	1590.57	7453.4	2839.03	6520.45	4678.01	4945.7	3230.06	6226.25	2090.56	5255.8	2652.64	5671.65	1498.85
7061.88	147464.34	96730.73	148483.55	95289.35	133957.2	60362.17	150237.45	85104.62	184602.91	29586.05	175724.16	106201.44	228848.94	39231.91
644.88	925.7	417.76	922.5	413.23	501.05	166.52	1171.45	835.73	817.95	309.5	1568.6	670.9	965.4	685.19
6751.74	46288.7	5349.12	52514.15	3454.99	56768.2	16316.91	74739.25	51272.1	42416.4	2545.87	37872.15	20998.17	85277.55	9470.21
1576.57	2407.2	1150.75	2670.5	778.38	2221.6	304.62	2480.4	275.91	2391.6	479.56	1375.35	265.8	2313	871.01
1007.77	1429.15	102.32	1579.4	110.17	1289.4	131.24	871.3	579.83	910.8	695.09	897.25	831.2	1075.95	136.4
408.21	332.65	145.31	836.45	857.79	342.8	171.54	613.25	160.87	1363.45	393.22	1379.9	794.93	727.4	33.38
86.69	7524.05	1623.73	7360.7	1392.72	7899.5	986.13	8759.5	5839.85	9414.05	1804.61	5906.15	1857.78	8553.55	3835.28
306.32	6215.3	219.49	6065.3	7.35	5139.6	1909.33	2175.25	1146.01	3529.3	1415.06	2144.25	2314.71	3946.85	806.6

356.24	366.75	62.72	245.1	109.32	342.05	17.47	1000.55	1183.91	343.85	130.6	930.85	993.56	141.5	58.55
94.54	880.25	108.82	852.8	70	718.2	203.93	473.9	92.07	685.5	102.39	510.75	37.83	974.35	107.98
391.24	1975.55	608.61	1757.7	300.52	1881.05	19.87	1487	301.65	774.35	11.38	1218.9	28	1798.8	576.86
581.45	2121.05	832.19	2703.75	8.13	2392.3	891.1	3047.35	512.44	3060.35	364.65	2813.9	1013.85	2789	361.05
200.11	3473.85	339.06	3234.1	0	3321.85	1082.23	2434.85	312.61	2571.65	248.27	2034	1020.21	2142.55	391.1
1224.28	6560.5	280.16	6125.65	334.82	5641.1	1168	5639.7	4005.62	4154.55	1580.88	5396.75	170.2	4853.75	446.54
98.43	222.3	146.09	323.3	288.92	688.7	233.2	197.05	241.9	724.75	154.5	610.5	355.25	509.25	26.52
156.84	5024.7	806.24	4904.1	635.69	4610.2	2235.73	4528.5	2678.1	2434.2	824.2	3553.9	289.91	3692.25	943.63
58.9	285.5	70.99	319.2	23.33	377.15	128.48	325.45	218.99	404.15	169.35	250.1	143.83	504.4	304.62
479.35	2237.9	79.9	1912.5	540.09	902.35	698.69	1360.5	290.62	1968.15	461.53	1908.55	1015.9	812	700.32
23.19	384.85	224.22	455.25	323.78	421.4	252.72	4498.15	5402.08	1308.05	663.2	2440.75	1659.23	900.05	71.49
136.97	153.3	20.79	192.55	76.3	104.1	14.14	235.55	71.49	824.5	929.85	509.05	367.91	521.05	426.03
184.91	135.7	41.3	68.2	54.16	167.05	97.51	748.95	317.7	53.7	23.05	170.1	52.33	345.7	432.89
457.43	1404.35	959.19	1494.9	831.13	1913	1170.97	228.6	149.2	1139.45	1101.88	1351.6	1600.04	1587.15	1763.88
303.21	884.7	515.76	692.35	787.79	877.35	1098.91	490.6	175.93	849.5	211.42	382.25	350.8	230.75	87.33

544.05	512	7.64	287.55	325.06	337.9	168.72	488	197.71	489.15	300.45	647.4	29.42	213.35	126.93
608.54	748.1	72.27	841.55	59.89	711.9	208.17	478.75	375.54	768.15	259.86	688.65	726.27	543.2	181.3
145.38	1122.25	546.38	1273.25	332.84	1948.9	1717.85	2096.05	1087.04	1457.1	38.75	1178	194.74	1249.1	50.77
66.19	148.6	112.43	141.45	122.54	816.9	902.98	273.2	313.25	853.4	986.7	145.15	82.94	94.8	1.84
23.83	2583.5	305.61	2543.15	248.55	2628.15	360.41	1678.7	1528.62	2371.65	319.97	1776.1	1153.43	2453.1	370.52
222.46	545.6	140.57	732	404.18	352.9	168.57	1121.35	1137.81	319.95	24.82	341.1	240.13	974.35	68.38
30.69	155.7	76.08	251.2	58.97	1072.25	1314.16	682.3	770.04	206.25	174.58	148.75	84.22	418.85	24.25
141.92	652.8	382.83	692.9	326.12	323.6	126.01	682.6	165.6	794.8	387.35	903	720.68	400.05	399.73
782.98	836.85	678.89	974.6	484.09	402.75	126.36	623.3	177.2	924.9	468.81	1023.05	774.35	594.95	200.61
549.7	1236.45	662.91	1106.85	846.19	605.75	85.77	1008.15	647.21	1811.95	108.12	1173.25	113.21	1948.45	715.38
1274.84	2298.2	689.43	2054.15	344.29	2270.35	349.24	1442.45	1311.47	1557.2	1247.62	1830.3	1152.73	1666.05	1055.78
146.87	847.95	224.93	921.45	328.88	964.75	814.23	615.75	238.79	591.9	85.98	438.35	250.25	544.05	254.06
147.43	584.35	514.84	550.45	562.79	254.95	36.13	210.55	51.69	1085.85	1051.26	426	94.47	588.4	554.37
112.5	355.7	265.73	416.25	180.1	233.05	113.35	366.7	319.47	303.45	89.45	1001.35	992.71	308.45	80.96
88.11	566.2	459.62	512.15	536.06	90.2	5.37	537.05	266.37	350.7	62.51	455.45	162.14	442.2	262.62
182.86	504.7	114.55	394	271.1	298.55	138.38	1960.75	1302.42	685.2	645.73	1122.5	959.97	912.95	559.96

204.71	376.45	98.64	418.35	157.9	330.85	101.75	1078.8	1196.71	244.7	136.47	109.2	38.47	500.05	447.53
111.37	23.3	3.25	21.45	0.64	247	91.36	670.1	830.99	164.65	18.74	183.2	139.87	543.2	248.34
1028.84	5506.35	2008.4	5105.35	1441.3	6198	3130.22	3794.15	2403.53	3596.1	1196.28	4828.45	302.15	4731.15	716.51
33.8	278	172.11	243.1	122.75	837.4	879.08	953	687.73	440.6	416.06	378.25	79.83	632.45	789.48
34219.3	57374.65	14959.62	73028.05	7177.63	66222.2	23377.09	110367.8	76812.88	103795.85	4609.98	81373.75	5440.98	124195.45	3467.87
6.15	483.25	293.52	530	227.41	409.7	298.54	300.9	133.08	172.05	76.72	413.95	7.71	409.05	277.68
657.4	1558.6	341.96	1537.85	312.61	2120.2	11.17	1141.45	920.87	1080.9	872.99	2309.25	1015.05	1367.2	96.03
29.42	130.1	15.13	112.35	9.97	233.65	11.38	376.9	299.11	204.4	107.48	136.8	28.14	365.75	323.93
273.16	1005.2	199.83	918	76.51	1328.7	1042.7	694.5	179.18	748.65	86.48	931.45	55.93	807.85	125.51
385.59	633.6	299.39	753.15	130.32	1061.6	765.8	314.05	19.45	740	542.21	481.45	448.38	166.15	89.02
125.65	74.7	13.44	64.35	1.2	180.5	29.27	445.7	52.47	175.4	108.61	81.4	59.96	209.95	57.35
1106.41	4386.85	612.43	4539.2	827.88	4085.9	2484.63	3122.95	1555	3781.9	1401.2	5850.45	216.16	4820.2	12.02
171.26	118.05	16.9	76.5	75.66	632.75	755.97	143.15	152.1	185.8	28.28	371.25	230.02	127.95	58.34
800.16	3372.4	29.7	3126.65	317.84	2265.05	939.39	2733.5	1213.96	4517.8	605.85	5878.95	72.34	2766.35	1702.93
278.25	384.7	216.09	485.4	73.68	326.1	21.21	377.85	412.03	496.7	119.22	461.2	312.97	114	23.62

68.52	409.35	500.28	443.55	451.91	353.1	70.57	346.5	374.91	236.95	33.02	337.7	27.44	184.1	91.78
44.76	235.3	121.91	115.15	48.01	538.25	355.18	390.75	483.45	149.35	143.19	642.15	563.78	75.7	56.57
8.63	552.45	646.79	665.9	486.35	164.65	80.68	807.8	860.41	143.7	38.75	205.35	167.94	398.7	187.1
36.2	750.6	573.46	1103.8	1072.96	1775.9	578.84	1525.95	535.77	1276	233.63	1451.5	376.32	935.45	434.94
315.65	7838.4	794.36	8523.9	175.08	6650.2	2422.55	5861.25	3340.87	7693.15	2498.84	6625.25	1159.44	9051.8	597.36
188.44	239.85	271.18	260.85	241.48	127.25	121.98	817.85	305.68	741	201.1	602.95	682	699.05	834.03
450.85	633.45	331.42	412.9	19.52	328.45	192.55	1124.65	1159.73	750.3	791.39	847.35	938.4	610.3	300.52
3077.82	23411.45	10474.73	27680.1	4437.94	25593.15	7317.78	22162.35	4656.65	28163.85	3891.7	20088.3	13239.3	29499.4	2682.06
35.71	356.25	103.03	385.85	61.16	800.25	529.69	427.55	135.98	616.15	394.78	219	50.63	123.35	60.6
14.92	138.1	4.95	145.05	14.78	829.85	993.56	679.1	861.96	233.45	279.1	167.95	91.29	129.1	30.41
365.01	2845.45	877.02	2770.85	982.52	1826.15	710.85	2168	1349.16	2693.5	1335.02	4258	1578.26	1775.65	400.29
9.97	49.55	6.01	151.15	149.69	476.15	360.98	605.9	652.24	67.85	31.32	126.5	4.24	356.65	374.13
1065.89	4006.8	1198.97	3977.15	1157.04	3067.8	1898.86	1428.1	810.49	4754.75	1021.13	3532.85	1475.8	4472.4	32.53
1231.36	1820.2	300.94	1437.6	240.13	1637.25	1020.14	565.95	662.21	849.9	903.12	1234.9	806.24	1106.7	129.12
416.63	2878.85	1359.13	2722.15	1580.74	2383.4	1644.31	2792.35	2712.11	2024.5	951.2	3323.25	1239.77	2024.2	28

340.68	645.3	426.95	945.2	2.83	451.5	159.66	515.05	306.25	248.6	7.92	743.4	501.9	1058.6	780.93
3053.36	9377	2665.65	9120.7	2303.19	9251.1	3317.46	7298.2	202.52	8685.2	2047.5	6976.05	3416.81	7492.05	93.97
217.86	341.95	366.49	308.6	319.33	264.3	166.59	294.85	127.35	242.55	171.9	699.5	852.49	811.15	315.58
57.84	109.25	0.35	75.1	47.94	336.4	430.49	710.5	985.57	293.05	318.13	1101.95	978.42	145	98.71
171.97	568.3	245.22	629	331.07	411.2	187.1	411.55	171.61	465.05	96.66	557.6	267.43	394.55	42.21
489.88	465.55	200.32	481.65	177.55	163.95	98.5	262.8	194.31	898.05	778.17	463.35	474.26	140.35	11.24
5.09	3385.5	313.67	3595.05	17.32	2405.35	96.1	3967.95	590.36	3364.2	294.72	1817.35	2057.47	3023.05	46.46
819.18	733.2	481.4	740.2	471.5	752.3	584.92	1322.5	349.17	931.2	395.98	1415.9	424.26	860.15	166.67
15636.11	16555.15	2300.15	20422.3	3168.83	18039.4	2162.62	11599.75	9870.01	8676.35	3016.31	9470.4	1023.61	17275	4840
30.33	289	219.06	351.45	130.74	176.8	74.1	330.3	148.21	292.75	214.75	368.35	143.05	481.25	258.73
577.92	1005.3	0.14	1205	282.56	1836.55	595.88	948.2	856.31	1436.4	326.26	1280.85	272.02	1821.95	409.77
92.42	521.25	210.79	461.9	294.72	362.8	134.63	1094.45	417.41	267.2	14.28	212.95	2.19	493.55	531.82
33.02	124.25	31.89	105	59.11	154.95	102.46	350.25	336.79	111	73.4	153.35	25.1	121.55	21.57
34.86	265.25	154.22	293.8	113.84	213.45	170.48	401.65	26.23	772.2	560.45	1568.6	1729.44	326.8	20.79
110.66	941.35	784.25	844	921.93	662.6	396.4	357.85	41.37	718.85	429.71	1136.6	570.35	516.8	26.59
68.24	251.2	74.53	336.45	195.09	172	53.46	478.9	628.76	316.95	313.46	553.15	89.87	1012	469.38
854.75	1773.4	356.1	1233.25	1119.99	392.9	18.38	1629.55	123.53	1487.5	877.8	616.75	15.49	833.55	226.91

2.12	91.35	64.56	164.5	38.89	78.9	36.77	206.4	227.83	51.6	5.37	227.35	89.17	59.45	31.32
122.75	691.6	160.37	631.2	245.79	532.6	293.59	1816.7	1095.31	712.95	573.11	1339.95	1696.7	630.35	514.56
28.14	131.05	56.21	157.15	19.3	394.35	374.55	2204.9	2737.21	199.6	65.62	382.8	327.81	195.95	50.98
54.66	104.6	78.77	105.45	77.57	57.75	22.13	584.85	765.44	70.75	7.57	314.9	387.07	48.95	13.36
22.77	86.2	94.75	118.15	49.57	159.7	91.92	769.7	972.98	136.35	108.97	523.45	724.57	88.25	51.97
11.38	181.35	157.61	181.8	156.98	83.65	6.86	133.9	20.93	239.25	88.32	249.45	240.63	184.65	2.33
28.57	200.35	125.51	196.75	130.6	473.15	479.06	1128	988.82	181.55	11.24	770.5	822.08	1284.6	542.63
44.83	541.3	618.58	609.8	521.7	271.5	139.87	948.8	629.18	671.75	194.95	955.5	759.15	552.65	32.6
14.85	309.8	381.55	318.75	368.9	78.65	28.07	102	13.29	116.1	73.54	263.5	154.86	150	116.11
156.91	277.25	126.5	245.8	170.98	90.1	28.57	185.7	54.87	295.8	306.88	418.9	489.32	527.25	31.04
307.73	498.1	340.12	508.2	354.4	1454.4	1421.99	1502.45	791.46	1666.6	1510.24	816.15	174.3	1781.3	797.76
894.77	2330.1	90.51	2808.8	767.49	1818.8	307.31	463.55	30.9	697.75	485.29	575.95	437.06	356.25	15.2
25.67	800.15	510.32	591.45	805.47	493.45	623.74	144.15	116.04	379.6	286.1	282.3	30.83	240.05	260.14
179.89	226.75	95.53	240.05	76.72	520.25	19.73	626.55	239.92	890.95	680.59	459.5	313.96	1053.25	807.16
504.1	127	16.69	231.4	130.96	364.95	131.03	793.7	25.17	884.45	851.57	420.75	284.75	508.3	447.74
392.51	2006.45	583.29	2181.15	336.23	2723.85	2134.4	2128	569.36	2604.55	860.48	2061.9	394.71	2986.55	105.71

816.85	1535.6	93.62	1342.25	179.82	1993	744.44	1758.6	1931.67	2564	918.25	1543.5	1020.07	1157.4	112.01
4909.94	3483.75	1661.49	3718.85	1993.97	4660.45	1912.65	1839.6	198.56	1008.35	740.98	996.7	822.37	2007.6	801.58
81.25	248.75	163.98	134.3	2.12	832.35	1062.29	579	203.93	547.9	405.31	332.65	79.27	636.8	213.69
33.66	279.85	17.61	175	165.89	119.6	50.49	169.6	148.49	214.15	76.72	216.8	72.27	243	31.54
35.64	1037.55	624.87	789.85	975.17	1788.95	1567.02	653	560.17	1041.7	150.76	3145.7	1158.52	1643.9	59.68
16.05	306.25	12.52	209.95	123.67	564.85	342.59	838.05	1083.78	289.9	310.42	142.65	142.62	319.15	387.57
218.21	946.3	158.96	836.5	3.68	1170.25	181.51	1422.4	1278.02	1266.9	692.82	1438	1015.83	1104.85	333.12
44.34	461.35	289.56	261.45	6.86	296.85	90.72	507.15	516.54	795.15	638.59	406.4	53.74	648.7	668.07
341.82	131.5	122.75	48.8	5.8	580.05	473.83	648.45	835.59	95.95	105.29	65	37.19	147.15	159.74
29.34	142.45	56.64	85.05	24.54	151.25	137.11	184.85	138.1	117.8	31.4	143.7	44.12	134.15	34.72
12.87	1770.1	504.59	1551.1	194.88	1692.35	45.61	845.25	654	1665.65	605.92	1308.45	958.34	1164	334.89
774.78	1336.05	1204.84	1027.25	768.13	1668.25	1280.22	2807.65	1151.1	3388.1	550.27	2212.5	675.85	2431.65	782.13
835.94	5633.6	282.42	6067.6	896.19	3878.05	2143.03	4309.25	3052.79	3304.05	442.01	5173	2036.04	5708.6	1783.75
630.88	1683.25	248.83	1635.35	316.57	862.4	1001.97	498.3	568.66	1053	83.01	1706.25	721.18	1231.7	620.13
283.76	444.3	180.6	405.7	235.18	622.2	668.36	410.7	163.77	407.3	310.14	534.05	221.68	253.4	100.55

8955.01	21783.85	10142.39	24879.8	5764.05	24953.95	19705.16	79335	60691.12	42891.1	20276.71	45195.45	30577.49	28403.1	324.28
18.31	2041.9	116.11	2135.5	16.26	1257.25	1297.47	1121.85	944.91	2404.65	5.02	2360.4	399.09	1718.75	370.74
145.45	2852.45	1725.84	2441.8	1145.09	2931.4	1983.86	914.4	858	849.05	380.78	1264.15	288.99	1557.4	718.56
98.08	1192.45	604.36	1265.2	501.48	1068.7	42	1219.35	1572.39	1675.45	849.87	648.7	619	1171.2	198.56
738.86	2544.65	893.85	2823.55	1288.28	3260.15	133.71	1502.9	1644.02	2098.2	638.09	3171.85	1354.75	1425.35	1187.16
87.4	110.25	97.93	29.95	15.63	160.6	69.01	174.1	40.87	106.55	39.53	789.2	1005.08	476.3	422.71
104.58	3069.25	353.34	2747.05	102.32	2914.3	126.29	2259.85	523.19	3380.25	162	2635.35	452.19	3264.35	1427.3
112.71	777.85	261.98	693.1	381.84	610.9	168.01	842.95	338.92	346.7	236.32	965.65	1266.78	671.8	604.29
126.36	4719.6	2038.59	4265.35	1396.18	2469.45	145.03	3183.55	782.27	4538	846.83	6265.75	1160.15	2972.4	1336.01
310.63	558.6	291.47	548.3	276.9	351.3	143.68	262.2	54.16	512.7	160.94	702.9	32.67	305.7	57.84
43.06	772	846.69	823.6	773.72	187.3	16.55	637.6	603.59	301.1	65.76	151.9	0.99	397.55	59.33
440.46	1913.25	1429.7	2191.25	1822.85	2577.5	534.71	5721.1	2114.96	3873.55	446.26	5505.4	3376.58	2839.65	2264.09
286.24	233.2	189.93	363.85	374.7	487.4	522.69	216.9	93.62	269.95	102.04	937.3	271.53	392.85	178.12
124.66	3245.9	663.83	4211.8	702.16	4210.8	106.35	4110.2	1540.79	3377.75	265.24	3970.85	357.3	4119.9	3353.67
475.39	6778.45	5010.49	2910.1	460.19	1443.55	814.37	1829.15	2182.48	8533.35	154.22	1264.55	457.14	1175.95	620.49

161.15	3861.9	10.32	3836	26.3	3664.7	559.89	1956.3	1569.92	3319.4	258.38	2140.55	2082.78	1777	686.74
716.86	1307.55	1017.46	1250.9	937.34	1023.25	1243.16	267.9	75.94	795.8	37.34	583.8	746.28	251.3	70.99
0.14	242.2	103.52	261.6	76.08	139.55	9.69	707.35	297.06	224.35	138.95	323.5	59.82	270.7	66.04
39.81	1060.05	19.45	1051.85	31.04	1603.4	946.53	2280.7	1264.87	1176.45	12.23	1344.15	233.42	1537.1	625.22
170.34	282.95	254.06	383.85	396.76	283.35	110.8	1208.6	708.8	1090.65	315.58	1475.25	1920.15	397.15	401.85
103.38	250.05	69.93	229.75	41.22	197.35	132.72	267.35	284.04	299.8	148.63	333.25	280.79	480.95	496.04
43.56	1439.05	944.34	1430.15	956.93	607.5	413.09	2599.25	1599.55	891.95	908.56	1267.95	761.48	1095.6	73.82
192.97	549.8	210.86	552.6	206.9	216.15	36.42	386.4	128.98	136.95	55.08	160.95	106.99	677.1	595.67

3772.7	67654.05	66370.24	70261.35	62682.96	150169.5	181905.48	452245.16	431449.91	99534.16	61922.12	173326	163414.94	75453.15	11068.55
8.7	419.6	92.77	350.45	190.57	332.3	162.49	393.2	141.99	316.3	91.78	309.95	22.84	309.4	88.25
56.92	266.1	124.73	259.2	134.49	287	111.58	850.45	760.78	241.2	61.52	1375.5	1634.69	360.05	58.9
268.35	851.45	680.31	1404.25	101.47	1751.95	2101.31	1226.25	1142.76	873.05	596.59	1629.85	268.49	517.7	317.77
544.26	1343.35	553.03	967.85	1084.07	1729.4	521.99	1168.25	826.25	2077.45	177.98	1791.35	316.85	1732.7	621.97
147.86	770.25	124.66	930.05	101.33	1409.6	1342.51	574.9	362.18	418.75	58.62	513.75	325.34	672.2	597.22
24.25	202.95	158.6	160.55	218.57	323.35	417.55	607.95	797.12	71.7	64.77	615.35	834.6	540.3	671.61

205.91	121.9	102.39	37	17.68	176.6	57.84	252.4	295.99	147.25	37.26	138.15	71.06	141.35	2.05
204	520.9	425.4	611.15	297.76	283.3	328.66	223.05	137.67	140.4	12.73	315.2	326.68	597.4	186.25
0.42	498.2	99.7	333.9	332.06	459.75	254.49	1079.25	1371.58	671.3	237.02	345.85	109.11	328.55	320.25
321.24	597.4	493.42	670	596.09	840.55	802.35	876.25	301.44	778.6	702.02	712.7	72.97	939.05	85.21
292.04	3076.25	198.49	3047.9	158.39	3947.1	1728.88	3432.4	827.6	2680.6	349.31	3100.9	1644.16	2986.6	707.81
290.62	1073.2	185.4	1186.7	24.89	1123.4	298.68	237.65	109.25	619.55	505.51	597.75	421.79	733.15	641.98
419.03	2090.45	499.57	2175.9	620.42	2842.9	451.7	1815.9	356.52	2401.45	136.83	2458.95	1472.27	2511.55	375.97
8.91	1491.3	413.8	2078.1	416.06	1801.55	145.59	1478.75	1238.5	2177.15	660.23	1490.9	1887.83	2754.9	356.38
703.57	2730.4	1368.96	2695.25	1418.67	1106.65	983.23	2043.3	374.48	3522.15	470.16	2250.9	499.92	2847.9	1184.55
707.18	2013.85	1032.31	2896.9	216.52	1852.6	298.26	1008.15	504.1	1391.35	135.55	2961.4	66.47	1387.8	903.26
280.79	495.3	112.29	327	350.3	152.25	98.08	759.95	225.64	503.6	490.17	712.55	765.16	517.95	323.64
856.8	976.2	276.76	1016.85	219.27	1150.55	312.05	626.1	196.29	606.7	671.47	225.8	114.83	739.25	870.66
892.44	2765.65	749.46	2763.95	747.06	2846.85	738.01	1728.65	1578.62	3628.7	96.17	1842.6	1131.37	2247.65	169.35
5765.89	27832.9	12934.96	31816.5	18568.62	31487.4	10622.72	39481.5	7777.75	49429.45	17056.76	40527.65	8621.97	39501	5957.52
62.51	568.2	46.24	614.75	112.08	398.6	268.98	786.75	171.33	466.45	11.95	1358.85	663.9	967.3	98
835.66	2096.2	498.79	1732.05	16.19	1127.35	1039.09	1540.1	387.64	1661.7	814.3	1215.2	454.81	1431.35	547.94
174.66	121.15	76.86	99.55	107.41	57.65	35.43	603.25	278.81	353.3	339.69	230.1	137.46	44.05	3.61

218.07	678.3	297.55	631.85	363.24	507.3	87.82	277.75	9.55	638.9	363.17	391.5	68.59	328.6	291.33
1048.99	3564	1487.75	3247.9	1040.72	4169.65	2364.49	1139.75	1203.71	1920.95	156.77	2216.8	233.91	2553.5	424.12
968.45	1903.1	205.49	1549.2	295.01	2883.15	1200.74	952.5	554.94	1863.35	46.88	1910.05	1217.14	2320.15	1631.37
207.18	150.9	37.34	82.35	59.61	595.6	530.9	199.75	41.37	884.85	375.97	1016.15	580.32	297.3	300.52
1012.93	3243.8	364.3	3333.65	237.23	3081.2	27.29	3164.05	1673.09	3242.25	275.28	2870.4	733.55	3417.8	281.57
444.91	1933.7	564.98	1994.1	479.56	1716.55	100.06	2406.75	3040.35	2167.55	504.24	918.4	557.91	1304.1	1041.43
94.82	255.3	33.38	168.55	89.31	253.85	103.17	766.55	394.21	337.55	336.51	290.1	263.33	204.9	164.76
601.32	426.3	133.93	608.35	123.53	522.2	23.19	736.5	396.26	1635.3	1801	908.25	729.38	378.55	52.82
449.37	231.9	52.89	221.95	66.96	330.5	412.53	1258.85	884.8	837.55	0.07	292.75	103.87	756.95	365.93
938.47	6905.3	2057.68	6429.75	1385.15	6100.85	3567.99	3806.4	2296.68	5831.75	1669.27	4947.6	2329.35	6979.5	1441.08
611.29	633.05	458.84	738.05	310.35	388	72.55	213.75	84.5	758.5	895.06	311.25	233.42	316	305.47
449.01	196.1	8.06	177.4	34.51	178.8	74.67	445.75	525.88	373.1	12.45	711.75	650.47	212.45	172.75
110.8	343.85	171.19	204.3	26.16	340.35	47.02	755.8	392.44	739.9	605.28	1169.75	1285.59	521.4	474.04
233.27	1786.95	211.78	1711.4	104.93	1378.6	185.54	461.05	278.53	1152.15	701.38	1617.7	1473.47	375.35	36.56
6.08	509.2	74.81	279.35	250.25	224.05	259.3	221.85	224.79	202.5	183.14	335.75	384.03	143.4	33.38
67.95	293.2	149.91	132.8	76.93	374.1	370.95	360	213.4	188.2	94.89	151.45	121.13	351.35	230.3

639.93	2214.8	499.92	2459.6	153.73	2097.8	28.57	1737.15	605.35	2287.3	270.11	1507.55	672.67	1373.7	784.75
797.69	3297.2	711.21	3227.55	809.71	1961.6	1842.58	2424.3	1284.11	2755.9	1300.94	2387.25	95.67	2934.3	6.51
22.91	393.95	310.49	362.1	355.53	532.3	210.15	472.5	42.71	284.3	328.38	245.25	10.54	538.95	373.99
42.36	92.15	67.1	85.2	76.93	86.8	69.3	251.9	161.22	111.95	35.85	687.95	879.71	86.8	5.37
280.58	369.75	445.55	370.5	444.49	1006.6	1245.92	804	322.86	194	31.4	509	630.88	443.5	529.48
221.96	610.5	142.55	1096.15	544.26	592.65	349.24	575.55	252.51	776.55	394.92	2706.1	579.83	671.05	204.42
8.98	220.3	131.95	93.75	47.02	125.3	79.62	1086.6	1464.42	380.4	203.65	196.65	109.67	205.7	35.5
359.85	491.35	384.74	880.2	934.65	529.45	389.97	209.6	154.01	812.2	17.25	631.5	704	434.75	319.4
164.76	570.35	159.74	389.55	415.43	453.95	349.52	971.15	1074.17	193.5	203.93	341.25	128.06	114.15	33.16
955.23	725.2	336.72	953	14.57	846.9	893.78	438.85	137.25	584.55	570.99	645.55	507.49	508.8	115.26
67.53	311.15	260.85	382.7	159.66	1405.05	1581.73	248.1	30.69	449.55	147.71	554.95	361.4	549.2	34.79
310.14	324.6	67.88	300.1	102.53	662.85	541.43	303.2	53.6	90.75	25.81	625.65	92.56	885.15	487.97
258.52	131.15	53.39	62.05	44.34	145.05	29.34	76.55	20.01	147.7	68.17	94.75	18.74	118.7	60.81
156.27	85.2	5.52	297.4	305.61	131.1	32.53	197.85	36.84	723.75	376.68	398.7	529.91	835.9	380.71
606.56	3892.95	294.65	3775.45	128.48	3069.4	1619.7	2702.55	3000.75	3644.8	469.24	3603.3	749.96	4134.65	480.48
222.31	137.4	92.91	109.65	53.67	377.45	326.47	496.8	527.36	177.95	93.41	65.15	16.05	344.5	323.01

96.73	245.8	165.89	265.25	138.38	245.8	161.36	328.65	60.74	424.5	312.26	347.9	208.17	289.55	203.72
406.3	1369.8	162.63	967.15	732.07	1125.25	433.53	810.65	492.92	1037.8	84	2200.95	1330.14	1599.65	24.25
58.97	136.15	155.78	158.55	124.1	129	92.35	200.5	231.51	187.05	115.89	116.55	59.47	107.2	17.54
34.58	205.75	114.62	260.3	37.48	674.8	670.9	481.8	344.22	318.25	238.79	375.25	216.87	162.7	25.6
347.47	1428.9	125.72	1371.25	207.25	1238.05	537.61	681.2	105.92	843.85	19.87	703.85	234.26	838.05	577.35
283.41	845.55	524.18	844.35	525.88	1323.8	1211.42	1071.3	992.64	1310.9	383.53	1059.6	567.95	918.65	806.31
190.92	600.75	340.19	485.5	503.18	361.55	109.81	702.4	367.27	237.35	108.26	141.7	2.12	1110.25	527.86
82.59	1450.2	350.02	1579.65	166.95	1296.8	238.01	1497.2	261.49	1192	31.11	1600	485.92	1662.8	996.74
1170.54	1011.55	402.84	1093.6	286.8	1620.55	1370.44	3209.4	2038.45	844.45	279.1	1070.1	387.21	938.2	534.71
625.44	1481.55	1330.28	1765.75	1732.2	1514.45	1844.77	1897.35	1847.32	869.6	589.59	2539.55	556	2008.5	579.4
610.3	647.05	266.65	673.3	303.77	1484.7	759.86	1136.8	318.76	1731.8	927.16	596.8	565.26	749.35	79.97
27.58	240	147.5	87.35	68.38	182.2	65.34	135.5	102.25	95.25	39.24	141.7	101.96	510.4	580.39
86.2	3289.85	1470	2924.45	1986.76	2732.05	1649.04	924.95	18.74	3101.7	3.39	2113	480.55	2788	225.71
2948.21	7820.7	3126.54	8284.3	2470.91	5486.4	733.98	6077.85	2502.38	6335.3	1362.45	5339.65	153.09	5217.65	368.05
406.59	977.65	146.72	860.85	311.9	1364.6	710.64	819.7	220.05	781.4	738.36	964.2	142.13	1193.85	435.51
37.83	129.2	63.5	115.05	43.49	167.45	116.6	257.9	164.47	159.85	54.09	150.9	41.86	229.55	140.64

179.18	1144.9	604.29	1003.55	404.39	1511.3	170.41	545.75	568.73	1130.85	282.91	1764.05	644.1	1050.65	365.93
363.17	939.95	615.54	990.3	686.74	988.5	142.27	3151.1	159.24	2416.95	82.52	2647.75	714.39	1802.5	383.82
13.93	222.45	171.9	218.65	177.27	112.65	1.48	209.25	34.15	415.4	191.77	358.35	319.26	394.7	468.25
334.32	1352.6	559.18	1455	414.36	695.9	105.36	719.2	861.4	582.4	206.62	1922.35	635.62	988.9	270.4
416.06	1496.05	110.95	1632.1	303.35	821.8	825.62	1232.6	428.65	756.85	647.36	1161.95	72.48	496.85	464.07
149.13	506.75	178.69	431.15	285.6	207.6	79.76	498.1	67.03	726.3	393.01	747.15	509.75	382.05	462.24
42.78	145.05	103.87	126.75	129.75	143.1	91.22	724.35	409.49	263.55	242.18	682	802.85	834.05	1058.33
241.69	186.6	96.59	163.6	129.12	280.3	158.25	1020.45	630.95	630.1	372.36	274.55	64.56	192.6	30.55
709.65	4042.75	2659.64	4034.8	2670.88	9089.65	10962.77	24829.75	25866.75	6536.2	4890.63	10345.15	8758.44	4813.15	834.03
56.92	160.9	118.37	182	88.53	118.85	58.48	370.55	373.42	161.15	7.14	301.45	260.14	247.55	194.38
287.58	1395.65	498.72	1782	47.66	979.25	325.91	2081.6	1427.22	1289.3	355.96	282.1	88.67	624.55	199.62
24.4	1942.35	392.94	1695.25	742.39	383.9	185.26	1668.7	1872.56	1004.45	41.08	645.05	674.37	1056.1	747.41
1263.1	938.85	414.58	806.8	227.83	1268.65	213.62	391	348.46	682.25	204.57	114.75	11.95	229	62.23
116.53	357.1	60.95	353.3	66.33	555.65	483.17	416.25	30.05	148.6	36.49	288.65	92.42	393.7	345.49
388.2	264.6	1.84	144.75	171.33	201.9	22.06	83.05	73.04	231	152.03	175.55	99.07	53.75	17.61

201.74	140.55	127.35	148.25	116.46	437.9	478	202.85	97.23	605.05	690.63	200.9	12.02	231.45	71.63
690.98	805.45	490.24	631.55	736.17	335.7	143.68	274.05	228.18	1236.55	395.91	645.25	459.12	759.75	861.04
277.54	2799.65	862.46	2892.55	993.84	2136.6	2376.16	2141.4	236.6	1567.35	72.05	2052	440.1	1733.85	585.13
63.22	1962.95	492.64	1591.9	1017.39	2087.9	1430.9	1516	935.79	1621.2	104.51	1453.35	6.01	2263.9	430.06
158.82	647.5	18.53	735.05	105.29	469	258.38	1858.35	1539.02	353.4	23.19	468.95	329.02	1167	894.21
473.2	485.45	477.37	470.6	498.37	428.6	437.56	704.5	736.66	386.4	441.66	469.5	548.01	421.85	188.16
694.45	1893	411.39	1760.3	599.06	1541.2	268.98	1032.1	1117.09	1558.35	1738.28	957.5	946.82	681.8	465.13
499.15	3522.85	538.32	3416.3	689	2184.75	433.39	2504.3	1655.62	2603.15	842.38	1711.95	124.24	2028.5	504.17
26.09	240.85	135.13	245.7	128.27	273.45	154.22	482.9	363.88	323.8	46.95	1054	1211.42	526.1	456.08
93.2	1762.05	210.36	1870.55	56.92	1283.4	629.33	3032.25	491.23	2058.45	1301.15	1136.95	276.13	1633.25	732.92
273.79	546.65	5.44	505.4	52.89	404.75	193.96	409.05	357.02	138.65	48.44	191.2	119.78	225.5	156.98
215.31	790.4	919.52	973.6	660.44	959.9	602.31	377.2	126.15	277.85	179.68	750.4	114.98	579.1	559.32
428.22	3882.1	594.96	4481.45	252.65	3021.65	437.2	5991.55	1772.93	5110.15	589.09	4086.5	867.34	4281.75	321.24
317	712	374.63	788.55	266.37	522.6	573.32	946.6	718.99	537.15	42.36	1654.4	1496.24	600.05	298.05
15.7	254.05	52.96	308.2	129.54	797.7	574.88	822.7	847.54	190.45	71.35	669.55	519.09	749.95	240.91
53.67	159.8	196.15	32.9	16.69	168.05	155.07	709.4	971	141.35	132.72	210.25	232.14	207.25	155.35
123.11	982.15	95.53	1108.3	273.93	991.45	67.67	1241.75	322.37	1531.8	656.62	2607.2	317.35	637.1	111.44

132.94	83.95	99.07	88.8	92.21	74	42.57	72.95	51.41	101.25	64.98	110	36.91	136.8	97.44
134.07	646.4	398.24	694.1	330.78	1551.15	1846.04	1264.85	566.18	1143.1	1440.09	400.4	78.21	1622.1	536.27
34.51	363.5	263.04	338.25	298.75	184.85	39.81	1446.6	1510.24	371.25	456.86	450.55	237.52	100.05	15.06
133.22	319.65	89.59	355.5	38.89	463.45	238.79	167.35	60.6	297.15	55.23	327.5	253.14	717.7	298.4
90.16	799.6	85.98	748.65	13.93	882.65	159.88	634.9	585.34	345.6	229.95	1547.45	1006.85	998.4	118.79
88.67	481.25	589.94	682.4	874.41	817	726.2	266.55	15.91	596	489.18	716.3	604.72	403.1	352.85
40.66	69.95	17.61	84	37.48	332.9	417.19	215.95	230.3	559.6	732.99	214.55	97.79	538.8	293.03
369.89	2676.85	1363.51	2328.4	870.73	3601.6	1420.15	1306.1	327.25	1387.85	1611.85	1499	1483.65	1921.1	295.85
84.92	923.3	491.44	891.95	535.77	927.6	247.77	605.7	71.28	821.15	88.03	879.75	743.81	763.5	560.31
270.4	413.05	232.43	343.65	330.57	265.4	166.03	432.1	371.37	186.45	164.69	360.05	4.45	76.1	29.84
102.04	2204.8	629.61	2225	601.04	2153.9	499.36	2856.95	1570.55	942.85	690.63	1621.8	308.44	1962.2	144.39
625.29	6230.75	2992.26	5327.6	1715.02	5568.5	4698.87	2582.9	263.19	4016.35	2393.49	2411.85	3122.94	2510.35	568.73
82.52	460.3	52.75	378.05	63.57	560.65	367.48	907.15	155.78	628.25	414.01	1174.5	1015.83	254.45	12.37
420.02	633.9	6.65	535.65	132.3	859.2	490.17	735.2	142.84	501.4	222.17	670.9	66.19	849.8	24.89
92.21	550.5	40.16	998	592.7	1254.8	620.84	382.9	54.73	1626.7	646.44	1126.85	238.51	756.85	401.71
77	4002.9	1589.72	3748.55	1230.01	4064.25	1467.88	1663.2	2069.42	3362.5	1527.92	3257.7	1353.69	2924.7	739.07

122.05	160.4	73.82	139.45	103.45	144.75	20.15	113.6	0.99	124.05	87.33	258.15	183.78	226.05	228.47
83.01	975.6	795.5	709.45	419.1	850.95	667.86	1923.8	179.32	1297.55	1322.08	806.25	752.57	1624.8	894.21
82.24	676.1	564.98	481.1	289.21	874.65	769.26	1380.65	893.15	845.95	926.24	916.85	780.58	283.55	38.4
775.06	1212.85	778.17	1617.7	1350.72	1523.9	902.41	695.5	448.02	4575.7	503.04	1749.75	682.15	2753.05	223.09
180.52	848.05	894.28	955.6	742.18	455.5	115.97	493.1	319.9	1016.35	331.56	625.65	501.83	1108.15	430.13
1.98	61.6	45.96	65.55	40.38	93.15	72.05	230.7	27.01	137.9	50.2	77.75	84.5	42.95	2.47
887.07	6732	277.04	7549.55	1433.23	7412.3	197.42	7001	2512.63	14393.25	3375.52	6151.95	3443.68	9806.25	2057.89
3.25	472.7	282.56	674.35	2.62	1819.95	2009.1	578.3	423.56	648.15	5.73	1021.75	1273.57	345.7	246.36
8.84	217.7	30.12	138.65	141.92	313.45	404.11	205.7	94.05	330.7	236.46	120.55	42.92	90.6	30.26
72.12	302.2	283.69	234	187.24	435.15	357.02	675.3	768.06	210.95	84.5	818.1	737.51	728.75	201.03
12.66	150.8	99.14	120.05	142.62	360.8	493.7	183	221.89	427	574.17	82.4	79.2	163.95	203.01

142.41	110.35	96.94	113.5	101.4	237.35	39.67	479.75	341.04	48.75	35.43	89.65	86.2	79.75	1.06
0.57	71.05	30.33	33.45	22.84	133.7	122.33	878.6	1125.15	65.8	19.23	196.8	218.5	76.35	21.43
22.84	348.75	269.48	282.7	362.89	60.35	13.36	164	62.93	574.2	187.52	176.55	92.98	543.5	629.33
667.86	6994.15	3540.84	7491.25	2837.83	4693.8	1476.44	4596.15	447.53	5430.05	2030.32	5221.7	1119.07	7241.35	1055.92
78.56	932.55	814.66	836	678.12	974.6	392.16	609.25	485.71	266.05	61.02	1702.65	316.71	692.15	510.6
108383.7	130575.95	102722.6	150380.25	74715.09	118341.5	77987.8	175079.41	28465.85	154917.45	13350.24	161316.34	40692.23	195929.06	20359.52
129.05	1668.65	717.36	1901.55	387.99	427.9	56	1244.8	461.03	698.85	326.05	1556	729.17	967.95	767.42
350.58	476.75	267.5	391.15	146.44	321.1	183.28	168.8	120.63	77.45	38.68	406.25	296.35	332.85	61.45
133.64	136.9	59.68	157.15	31.04	113.65	4.45	176.75	78.84	127.4	34.08	544.7	728.04	80.7	72.83
65.12	1520.1	665.53	1412.55	513.43	1355.2	27.44	1419.1	578.55	1932.15	405.81	2704	219.77	1894.2	589.59
26.45	426.35	371.02	448.9	339.13	761.6	852.21	997.3	1303.34	732.9	268.84	493.25	121.55	829.75	199.47
268.91	635.1	103.38	340.9	312.68	827.45	743.95	1067.8	254.7	983.95	861.89	638.9	91.22	221.8	32.39
38.75	1278.4	524.67	1373.2	390.61	1092.75	417.97	1451	1060.94	1160.9	327.25	1001.5	367.13	794.75	629.11
234.41	2180.25	886.36	2019.25	658.67	2029.8	677.83	1185.1	1018.94	1339.2	146.8	1110.85	606.06	1432.75	833.04
242.18	632.7	581.52	588.9	519.58	971.2	38.18	243.8	118.65	1010.25	314.31	655.1	239.71	292.15	70.78
624.09	649.25	5.87	712.45	95.25	534	59.82	605.05	194.53	459.8	52.04	451.9	140.29	434.2	130.11
3838.74	2798.45	641.56	3125.45	179.11	2652.3	690.42	4377	824.91	3377.2	704	3431.65	1047.15	5115.3	1034.78

347.9	301.85	30.9	180.75	140.36	253.8	280.86	364.95	197.64	389.35	66.11	344.7	206.19	620.75	501.13
374.2	1618.6	1493.69	1566.75	1567.02	4196.15	5172.56	5471.8	4001.38	22002.95	29620.07	21714.65	18306.92	6839.15	1628.11
1040.37	4135.55	442.86	3842.05	27.79	3539.65	2823.27	2326.05	841.81	5058.5	1323.14	3224.35	4328.13	5066.55	818.33
273.58	460.1	42.43	315.2	247.35	275.3	146.51	1062.05	1165.1	285.6	15.84	355.95	174.58	462.7	142.69
425.11	167.65	62.72	168	62.23	1012	1220.89	1677.8	2012.14	345.3	221.18	450.2	270.54	215.25	54.94
25.17	171.1	143.26	267.8	6.51	166.2	138.59	491.25	382.62	270.25	192.4	575.3	588.74	291	15.98
253.78	409.4	435.72	413.6	429.78	125.65	16.33	458.8	579.12	559.15	437.35	841.8	411.96	453.6	80.89
170.91	503.8	173.95	643.65	23.83	1170	623.39	2191.7	2044.25	1620.95	838.7	2219.7	702.3	1204.9	463.15
89.94	56.05	14.21	53.4	10.47	127.45	74.74	858	1025.87	122.6	96.59	278.8	214.25	78.35	53.25
26.59	1451.05	181.94	1489.3	236.03	1052.3	739.49	3416.75	2065.53	1132.7	919.52	2524.4	1682.49	556.4	36.2
1787.71	4212.95	1231.43	3556.7	303.35	5204.55	1659.93	3092.4	642.34	6447.35	448.8	2265.1	1501.05	4968.2	112.29
125.79	482.9	183	490.35	172.46	368.6	26.45	686.5	31.4	286.1	154.01	657.3	468.67	583.15	63.57
1023.25	1762.15	354.61	2152.2	197	875.65	357.58	1235.45	1091.84	677.6	619.57	759.25	479.21	1090.65	849.31
76.51	49.75	24.54	27.2	7.35	138.25	148.56	181.2	36.35	128.35	70.22	190.65	180.38	146.75	93.27
86.55	300.6	135.06	290	120.07	179	108.19	283.9	296.14	188.5	86.97	397.5	207.04	294.1	124.03

5604.53	22188.95	1545.24	21711.15	2220.95	17048.4	3262.31	13335	7091.71	18999.35	1998.92	18183.85	4214	19522.15	1810.12
657.61	1763.1	42.99	1931.75	281.5	2613.85	28.35	2150.45	1132.86	1862.3	654.5	2307.7	455.52	2318.3	817.42
19.52	449	173.24	809.7	336.87	790.05	783.97	1741.6	1989.37	2640.65	759.08	1674.65	750.03	1558.65	1584.41
4.45	391.9	386.5	351.7	443.36	40.6	32.53	705	335.03	402.45	486.84	291.25	303.42	519.55	292.67
222.95	1179.55	444.13	1086.75	575.37	1801.45	1723.43	1662.55	1219.69	1908.15	860.48	974.9	121.34	1533.45	1170.33
526.23	393.3	196.72	386.55	187.17	859.85	450.21	785.2	63.92	367.95	155.92	955.05	1279.65	911	348.32
45.47	84.8	12.16	66.2	38.47	228.3	174.37	120.25	56.21	164.8	130.96	67.85	18.31	67.3	19.09
146.23	93.85	23.69	256	253	620.9	370.38	808.35	584.57	1137.3	855.03	731.5	571.77	252.25	259.3
170.34	866.55	157.05	910.1	95.46	785.4	31.25	1110.6	179.04	1258.7	149.77	588.4	697.49	1468.7	111.3
638.52	456.5	92.49	453.5	88.25	1008.85	1075.16	404.1	208.6	580	397.68	483.65	52.82	620.55	512.58
105.15	883.5	553.52	1074.85	282.91	659.2	450	1242.35	1628.4	754.95	234.26	1016.35	186.75	742.15	11.1
302.92	3862.25	662.77	4437.1	150.19	2986.7	407.15	4138.35	755.54	4475.35	395.63	3016.45	50.98	4498.35	616.24
400.79	420.3	199.26	453.45	152.38	288.85	124.66	163.4	19.37	193.7	183.85	1104.5	1386.35	238	142.55
1410.82	4672.65	16.33	5415.15	1066.39	6282.3	1931.53	4063	2549.54	7510	2787.13	4340.65	2156.89	4222.85	1490.23
127.14	2136.2	2385.64	1167.6	1015.83	1060.8	1032.94	388.75	95.81	1789.3	1645.72	1708.25	2046.86	534.95	7.85
10.61	65.7	0.99	64.75	2.33	150.25	107.98	968.05	1253.06	223.3	263.33	129.55	73.47	129.55	23.41
61.8	506.1	361.47	464.3	420.59	329.6	120.35	1064.5	1321.3	519.35	719.06	92.9	0.99	79.95	12.09

208.67	1321.55	696.15	1404.4	578.98	1333.65	65.12	799.2	307.73	979.1	82.45	1537.05	140.36	1783	25.46
9493.33	47810.95	6063.51	50413.9	9744.64	51655.4	11520.04	43147.8	34237.97	48908	21470.59	48972.1	24940.08	57535.65	15906.15
7.35	56.35	23.12	23.7	23.05	31.1	36.49	48.15	51.97	68.25	59.04	24.15	25.53	21.5	13.01
1.06	969.7	467.4	1133.8	235.33	1447.4	1464.98	498.5	192.33	734.25	679.6	876.15	581.74	1074.7	741.47
2081.72	4459.2	953.6	4625.85	1189.28	4978	1814.15	3323.55	1291.95	3351.35	1708.72	2791.8	3342.07	3872	1065.47
154.15	804.8	571.34	679.75	748.19	1645.25	1717.21	471.15	24.54	1164.1	464.71	369.95	322.09	926.75	925.39
158.89	64.6	2.12	133.1	98.99	309.25	219.56	480.3	637.24	64.95	17.47	239.1	88.53	339.65	200.89
144.18	4209	1347.04	4267.6	1429.91	3216.7	2052.87	2146.55	1693.31	2089.9	2307.15	2996.7	1837.49	3544.3	238.01
22720.47	73966.55	12173.06	84611.8	27227.71	84137.8	99.13	107613.45	84350.55	90168.95	26501.58	91787.8	25764.99	98293.5	30219.48
660.08	478.7	482.95	238.9	143.83	805.45	277.82	984.95	1168.92	184.4	82.17	551	196.43	223.85	127.77
75.38	210.65	74.18	199.4	90.09	143.85	68.24	413.85	343.44	133.15	2.47	327.8	234.19	197.95	56.36
109.74	2904.1	233.91	3244.55	715.38	3009.55	329.3	3713.15	1110.65	1685.5	1794.5	1647.8	1758.01	2200.6	547.16
228.04	579.4	283.41	480.15	423.77	118.65	44.19	677.1	915.14	894.75	593.76	281.9	26.73	138.15	15.63
2439.38	25006.45	7731.29	26248.6	9487.96	24551.5	8774.63	21177	13112.45	21123.6	7199.62	20362.65	5271.41	25247.3	1329.78
55.44	621	577	188.1	35.21	413.65	51.12	203.5	89.94	319.65	50.98	332.05	230.59	877.45	798.54

46000.48	101271.84	24898.01	125303.2	9087.46	109134.45	17929.62	144578.25	61649.6	158720.25	19857.33	117201.4	49766.32	157313.8	20440.05
279.02	3899.65	648.91	3976	756.89	3598.3	931.83	3364.8	2061.07	4028.35	1258.86	4168.65	1683.13	4471.05	584
298.05	2327.5	1390.03	1434.6	127.28	2329.85	1437.76	1250.4	1379	1430.35	978.71	459.4	16.12	904.9	741.33
24275.05	80360.85	16971.77	85698.15	24519.84	78564.34	18536.03	117650.5	117469.53	92781.25	36949.93	103256.2	49309.95	118209.75	37860.4
99.07	239.85	84.5	251.85	67.53	633.9	275.91	4008.45	5474.07	792.55	474.26	979	1013.28	835.9	686.18
589.09	745.1	290.2	613.75	475.95	1170.65	1369.88	3345.15	2790.6	1193.55	338.77	823.5	571.91	971.45	51.27
119.85	120	0.28	121.65	2.05	221.35	195.37	874.95	976.87	277.55	184.2	846.45	201.6	201.35	94.96
179.96	388.6	78.06	229.6	146.8	550.15	387	841.75	894.84	473.85	97.37	1093.45	487.41	927.7	422.14
4.45	359.95	361.69	306.95	286.73	667.2	440.81	1044.9	524.67	540.75	101.47	518.2	19.52	468.55	322.94
156.13	1024.1	63.36	829.3	338.85	898.1	153.3	1082.2	565.54	621.05	321.24	510.2	43.56	966.65	111.09
7.71	242.6	189.08	274.4	144.11	245.05	150.26	177.85	62.58	179.25	4.74	243.75	123.39	177.2	94.33
2261.61	6965.6	931.12	7432.5	1591.41	6544.85	2294.77	5933.6	1394.7	4850.4	3625.9	6700.05	1116.88	4548.45	132.3
225.71	848.35	767.28	784.95	677.62	698.25	464.92	561.55	193.82	1053.25	555.29	1096.95	100.76	833.05	12.8
990.94	1203.35	217.29	1323.9	387.78	1829.05	151.82	1060.5	887.42	1794.4	734.26	900.65	368.19	1092	258.09
559.82	4578.4	559.6	4246.05	89.59	5119.35	428.58	5430.2	1633.42	5480.9	1111.01	5290.8	1110.58	4900.35	1479.34
444.35	7004.8	107.62	8140.55	1713.81	4151.65	3917.58	2947.35	3358.97	4633.75	2875.73	3637.45	3997.35	4173.9	50.06

537.61	5904.2	264.18	6723.45	894.42	8139.55	883.81	8267.45	1073.18	5947.25	81.95	4599.55	951.69	7764.95	50.42
1392.01	3990.75	920.02	4288.4	1340.96	4205.1	158.67	4696.75	5418.21	4384.7	1535.69	2542.2	2589	4998	323.29
58.97	489.1	110.87	479.1	96.73	1034.3	958.98	375.75	36.84	473.65	307.1	1069.35	1114.61	485.25	576.65
59.82	676.15	51.69	907.3	275.21	1072.85	166.81	536.55	378.51	761.55	676.21	697.8	637.39	1418.55	152.24
4.53	97.95	67.39	104.05	58.76	151.2	174.37	587.7	792.24	172.65	23.55	116.15	78.98	111	37.76
442.58	1747.3	665.1	1691.3	744.3	2046.95	738.71	2084.55	1426.02	1876.75	1185.75	1721.8	748.26	1710.9	237.87
113.84	259.05	215.31	267.95	202.73	245.05	60.32	610.85	346.69	304.95	27.65	231.3	45.82	178.4	55.01
41.72	1548.9	537.97	1377.35	295.36	2162.5	210.29	1845.3	780.65	1226.35	18.88	825.75	906.58	1738.45	150.68
53.95	1314.45	1301.85	1568.55	942.5	806.5	662.84	1703.85	489.67	2162.85	1630.8	1605.65	1701.23	1534.8	955.58
2493.47	5280.05	1453.6	4893.1	906.37	5238.1	784.32	4386.75	768.98	2992.55	609.6	4445.3	401.92	4016.5	130.96
1645.15	2084.9	1078.62	1672.25	495.05	2852.5	1118.64	1740.75	169.49	1725.85	37.69	1797.5	688.44	1452.55	345.85
149.48	644.4	195.73	551.2	327.53	331.55	139.65	385.85	430.7	266.6	154.86	233	49.07	517.75	134.85
11.6	143.55	15.34	199.7	64.06	184.4	53.74	166.35	80.12	267.95	163.98	278.35	99.21	93.65	33.3
133.43	613.5	600.76	881.75	221.4	674.35	207.54	1035.8	166.17	978.35	249.4	448.45	272.59	625.25	456.86
31.61	143.1	88.67	167.5	54.16	369.1	61.09	417.6	146.37	307.3	273.65	595.8	523.4	380.3	290.34
327.04	3098.4	502.75	2875.15	187.03	3522.4	442.93	3958.25	1299.87	2405.95	893.29	3094.15	832.62	3099.6	677.83

136.75	436.9	242.11	443.1	250.88	417.3	28	462.15	89.73	545.4	641.77	1839.65	1570.13	1126.6	690.42
5.23	516.2	370.95	608.35	240.63	774.4	428.51	675.5	512.23	933.6	366.14	355.15	5.87	960.05	33.02
55.37	2382.25	72.34	2008.95	600.26	2529.85	1077.56	3365.35	2239.62	2029.6	732.85	1812.1	655.91	1561.65	77.29
1.06	71.4	49.36	78.25	39.67	195.9	241.69	1353.85	1812.39	92.5	52.47	622.15	549.49	94.3	39.46
170.48	510.15	107.55	798.05	514.7	1298.25	578.48	432.95	280.79	841.2	325.69	837.8	609.1	842.1	385.23
219.98	4996.85	3389.09	5287.25	2978.4	4031.4	2724.2	8859.3	7096.81	9804.25	8970.43	13935.3	12245.53	2125.4	1501.05
588.45	1380.6	122.61	1185.5	398.53	1463.65	240.91	523.15	123.67	304.75	99.07	1946.2	1179.03	845.45	689.78
319.68	878.95	621.62	806.9	519.72	1494.85	177.7	2052.4	1742.45	904.25	887.91	1958.3	1014.42	1459.15	500.7
82.45	83	17.39	136.35	58.05	420.7	361.9	150.4	114.98	500.05	139.8	412.1	335.59	92.15	5.02
301.44	1933.8	469.24	1992.65	552.46	2335.55	367.2	2012.55	21.14	1037.45	1084.77	1213.75	1027.78	1571.35	489.11
55.23	143	16.4	91.2	56.85	95.2	7.78	210.65	95.53	124.9	14.28	194.7	26.02	943.45	738.01
3817.1	34099.9	2268.82	37010.2	6384.61	33708.85	11903.93	21372.3	3221.72	31690.1	9196.49	25307.65	22954.31	30900.1	1077.35
1077.7	2979.4	320.46	2475.4	392.3	2517.5	482.67	1344.95	1450.91	3143.2	683.21	2396.5	14.14	2309.75	245.01
212.7	187.25	58.34	161	95.46	551.15	677.2	295.35	196.5	683.6	618.01	315.35	192.97	635.6	718.14
318.98	710.65	251.66	786.45	144.46	565.3	132.79	1081	202.66	1217.35	927.65	1350.5	1247.34	1383.85	10.54
86.34	679.25	833.33	682.6	828.59	182.55	0.92	375.5	433.6	452.1	443.64	330.85	245.15	332.9	150.33
399.94	256.8	88.67	297.7	146.51	349.4	140.15	783.4	295.99	446.95	87.04	390.2	212.56	692.7	656.76

103.66	463.5	404.18	574.8	246.78	394.2	144.82	416.55	166.1	801.7	867.48	260.55	61.45	336.9	16.12
152.59	347.4	154.43	421.65	49.43	362.3	124.73	943.95	627.27	549.1	102.81	413.55	11.53	583.45	261.28
40.16	405.45	66.26	434.55	107.41	645.4	217.93	558	605.71	445.55	91.85	187.95	135.98	862.45	516.12
129.19	714.5	42.57	750.55	8.41	907.65	123.67	922.2	1085.27	335.2	268.98	399.7	92.77	756.45	257.74
105.15	312.75	224.79	258.8	301.09	450.65	510.88	619.45	408.64	132.45	96.1	1329.45	1825.96	109.75	80.12
285.67	210.85	155.21	233.2	123.6	202	225.85	413.45	375.97	694.15	99.63	325.95	100.06	469.85	101.33
216.59	356.85	358.29	407.2	287.09	597.15	618.36	651.25	416.7	540.1	455.38	385.1	248.19	457.95	207.54
314.59	2465.85	335.95	2551.35	456.86	1934.15	904.6	2715.1	1817.12	3441.95	687.94	2073.85	1256.18	2305.15	398.88
131.8	65.6	13.44	45.4	42	98.55	129.47	104.4	111.02	90.6	88.53	121.3	151.18	293.35	282.63
45.82	2062.95	251.94	2203.4	450.57	1765.05	368.76	1407.05	78.98	1426.6	910.75	1061.6	736.81	1648.1	1670.47
264.67	509.4	324.28	542.75	277.12	556.65	580.32	210.9	224.29	482.1	539.24	283.1	113.28	498.75	675.36
7.28	375.5	75.24	222.55	291.54	99.35	57.63	758.95	910.82	95.75	62.15	222	57.13	241.5	167.02
86.05	563.4	415.07	458.1	563.99	372.05	73.75	1637.55	1294.36	807.7	853.9	190	42.71	1274.2	612.07
340.12	1246	334.6	1232	354.4	822.35	190.57	605.85	395.77	1364.35	628.26	2266.45	1402.55	1479.25	308.09
493.28	493.45	12.66	400.5	118.79	217.2	28	433.6	393.72	376.15	106.84	266.7	0.71	407.4	104.93

1412.3	4975.9	104.37	5735.85	970.36	4061.65	1416.69	1403.6	1387.34	1278.1	331.63	1794.3	829.15	2650.75	377.1
94.4	571.75	97.93	683.4	59.96	527.65	197.07	749.6	491.72	1140.85	716.94	692.65	547.65	669.3	192.47
41.37	1059.3	141.14	1179.75	29.2	1282	146.23	1690.6	1549.41	1248.85	228.89	597.95	619.78	1158.25	53.67
548.64	6702.65	1035.84	7545	155.42	5469.55	1929.62	5088.7	824.91	6036.75	1845.2	5761.5	3380.54	5742.6	534.29
166.81	518.9	128.27	432.85	249.96	977.4	899.16	527.9	325.27	339.25	82.24	374	11.03	461.35	72.9
176	187.15	107.27	144.4	167.73	186.8	128.55	270.2	146.37	115.15	17.47	756.25	694.31	259.2	50.77
367.48	66	24.61	44.9	5.23	242.8	56.29	195.1	197.71	202.7	44.12	52.55	29.34	244.6	198.27
77.71	138.75	32.6	241.65	178.12	286.15	122.82	1284.45	195.52	308.5	291.61	503.2	593.97	333	265.59
19456.68	55295	12180.9	61765.15	3030.73	49563.25	2672.08	50062.6	31840.31	63653.8	12459.08	49563.95	5378.04	69684.3	26567.84
206.26	1200.75	430.42	1462.3	60.53	534.45	324.63	826.45	415.85	1760.45	1344.56	444.15	54.38	1354.25	450.36
95.32	703.6	263.04	646.05	181.66	507.85	642.27	389.95	330.57	403.4	411.96	687.05	195.8	1246.75	231.86
398.17	1458.45	84.5	1174.05	486.7	901.5	290.34	1935.8	894.63	1492.9	659.73	2661.1	22.34	2107.9	323.71
23.19	367.05	263.96	279.1	139.58	299.1	103.94	191.7	46.24	175.6	180.31	695.2	64.35	355.1	204.35
21	958.05	82.66	575.35	458.56	791.25	212.91	651.9	262.34	451.85	348.67	579.45	106.84	554.6	508.83
119.22	783.45	12.52	1351.15	815.36	2220.25	1481.6	577.35	524.18	1867.95	827.1	624.1	62.79	1514.15	1625
501.55	768.75	119.71	645.4	294.16	306.55	88.6	926.35	140.36	535.1	244.8	904.65	1247.97	488.1	218.07

23.83	280.1	220.33	326.55	154.64	195.7	146.09	816.6	78.77	263.5	76.93	307.7	184.7	305.4	22.63
191.27	286.6	51.19	163.4	123.04	339.55	252.93	302.95	111.51	359	280.3	125	4.81	259.5	122.75
335.52	263.65	239.92	379.2	403.33	490.9	39.74	534.45	622.47	1035.55	489.53	2000.25	1169.63	660.7	490.87
572.47	1135	144.82	1252.1	20.79	1224.05	285.03	379.2	159.38	1873.9	179.46	1695.95	731.78	1828.1	1010.74
894.77	2057.65	399.16	2084.3	436.85	3096.4	751.94	2766.85	1373.13	1775.6	916.83	2676.9	887.98	1128.3	511.8
1155.62	3061.15	573.53	2672.05	1123.8	2818.85	67.81	1626.15	1142.61	2049.75	981.96	2503.2	1195.72	1757.3	390.32
277.12	846.5	576.86	676	817.98	377.55	399.44	520.25	369.46	347.95	156.06	275.8	256.54	95.7	54.16
42.85	1078.45	452.62	1179.4	309.85	591.55	78.7	3056.8	1828.44	1509.8	911.46	1318.8	564.41	1848.05	1075.72
465.28	2008.05	991.15	1865.25	789.2	2580.15	1292.94	1404	515.2	1300.85	427.02	891.3	818.41	1580.05	42.07
158.18	69.85	29.34	69.95	29.49	208.35	186.61	373.3	372.22	383.9	49.07	103.85	97.79	134.55	2.05

214.54	521.5	3.11	311.75	299.74	412	41.58	68.55	44.05	1122.1	682.36	1231.3	720.54	932.35	617.66
91.29	938.8	57.84	996.25	139.09	1102.9	111.16	863.6	618.86	701.5	50.63	1728.65	1066.25	953.65	366.35
49.36	79	31.4	79.7	30.41	71.9	69.72	281.55	301.16	703.5	819.11	190.9	193.46	385.35	316.85
56.99	367	10.04	346.25	39.39	506.2	471.07	198.25	104.86	152.15	15.06	318.5	234.05	432.95	210.36
2993.47	5341.05	2523.59	4996.35	2036.11	5391.1	254.42	6815.5	4110.55	4209.6	601.75	5221.15	1992.7	6121.1	332.06
450.5	488.5	99.7	535.8	166.59	341.7	318.06	314.7	184.7	427.55	432.68	95.3	21.35	482.25	587.68
294.72	110.4	61.38	92.35	35.85	458.95	312.89	312.8	228.11	185.7	39.88	1044.3	1006.35	448.1	91.22
660.86	3549.65	191.13	4173.6	1073.53	4422.5	20.65	2039.8	1240.27	2380.3	654.64	2873.45	726.98	2505.3	332.76

1579.96	12158.95	3193.51	11372.8	2081.72	10117.2	5310.66	6336.25	5970.88	8484.95	3514.96	7772.1	5112.95	8708.25	3123.22
57.7	130.55	13.65	126.3	7.64	182.85	38.4	171.45	147.86	227.8	2.12	1320.95	1536.76	351.7	2.69
5085.16	93730.1	20015.51	113662.05	8172.52	83979.95	10276.31	111533.91	99513.97	101541.75	28842.11	98256.6	20305.42	147473.84	16987.46
276.55	2055.1	575.44	2069	555.79	3030.8	1336.15	2445.75	1163.83	2337.95	761.91	2862.7	659.31	2268.4	624.52
304.62	747.15	36.42	529	344.93	329.05	263.54	851.75	737.44	1088.3	221.47	612.95	443.71	154.8	129.54
154.86	599.8	9.76	334.65	384.74	622.45	435.51	695.55	647.36	78.1	50.91	137.1	3.96	188.65	36.13
54.38	245.1	95.6	193.25	168.93	273.35	117.03	724.45	569.57	332.9	155.14	1155.9	1177.62	187.15	28.64
281.57	213.45	215.6	45.05	22.56	387.15	39.81	866.9	763.68	140.15	62.72	545.45	459.12	204.2	171.4
11732.39	10490.25	1336.08	11726.65	3084.61	7892.75	852.7	11791.6	8205.97	10979.5	4241.65	9594.05	3681.13	12473	2291.73
2484.91	15887.85	5263.63	13153.65	1396.89	17907.95	8371.51	8201.7	4330.89	13928.6	3032.36	7326	4830.81	9416.7	948.51
581.38	888.2	202.52	743.05	407.79	1168.55	162.42	406	315.65	741.8	168.43	371.45	56.92	154.9	62.93
261.91	1266.35	520.93	921.8	1008.19	247.1	16.26	361.4	267.43	1271.3	1024.17	510.95	267.92	226.8	98.99
455.31	879.5	177.06	913.3	224.86	781.7	761.55	578.7	481.68	162.85	76.44	710.2	76.65	521.55	274.15
59.75	165.85	160.87	75.95	33.73	826.95	813.67	1274.1	1184.69	159.9	48.79	174.4	0.71	375.85	94.82

367.91	1082.5	388.2	1147.55	296.21	1472.55	688.37	532.35	317.28	1010.8	254.13	2176.45	1023.25	1274.4	1.98
23.26	86.55	58.76	92.15	50.84	584	758.02	434.85	442.86	68.7	0.57	212	267.57	531.15	623.74
963.01	884.15	659.24	718.45	424.9	1511.3	641.91	1906.7	928.86	1469.25	690.91	2412.5	1547.43	621.3	85.7
216.87	2581.1	583.36	2283.6	162.63	1711.45	1602.66	1348.05	1044.61	2179.05	233.98	1474.35	1157.32	1471.25	1614.96
238.15	103.15	36.13	153.85	35.57	682.2	868.61	578.45	349.95	178.25	29.06	591.45	500.28	285.55	31.75
53.1	48.6	10.47	34.5	30.41	140.4	154.57	202.95	166.24	122.85	107.83	180.6	226.42	445.15	152.1
140.36	952.05	751.87	945.05	761.77	242.85	126.22	1526.35	1943.34	423.75	140.36	984.4	540.37	543.65	383.75
6.65	101.85	37.41	107.9	45.96	330.1	282.7	239.4	92.49	135.25	82.8	338.3	12.02	268.05	20.86
1458.69	5596.35	952.97	5811.75	648.35	4097.65	231.01	2407.9	1033.93	5192.75	1112.49	4027.6	3749.79	3760.4	1006.92
209.44	1503.45	827.39	1335.2	589.44	1397.5	36.49	1440.8	159.52	1895.25	39.81	1204.4	446.18	932.35	1057.62
521.63	1253.95	395.34	1109.25	190.71	1016.6	1179.88	1321.3	383.96	1634.55	305.82	633.85	388.27	663.6	120.21
3550.74	9350.5	3208	8772.65	2390.8	9049.45	3277.65	4045.65	4951.8	9166.85	3836.97	5568.7	2416.04	6576.35	145.73
77.78	352.55	225.21	347.95	231.72	246.6	285.67	196.4	79.9	56.05	13.51	404.05	428.58	559.9	735.25
216.3	608.85	103.45	1144.65	654.29	924.8	491.01	2556.65	1127.76	2287.25	1154.07	516.55	275.84	465.5	91.5

554.23	1050.3	724.5	812.5	388.2	847.35	325.34	1266.7	1060.09	1281.45	82.8	960.95	226.06	1041.55	353.77
37.9	106.1	89.94	121.05	68.8	274.2	306.18	315.15	71.77	537.65	646.93	76.95	27.79	111.4	26.59
822.93	1179.7	175.22	1111.4	78.63	1653.05	596.02	1223.5	1190.06	1471.35	644.67	2090.6	6.08	3172.1	1288.91
650.4	698.25	215.31	761.05	126.5	975.6	227.12	2110.9	1676.83	599.9	78.06	1020.3	641.91	641.15	371.58
479.35	798.55	330.86	696.8	474.75	393.05	39.39	1444.7	1117.37	333.95	50.28	814.85	315.3	121.45	33.87
50.28	2588.75	473.41	2760.95	229.88	3263.4	826.61	2444.55	936.99	2562.75	543.69	2155.4	228.82	2591.35	1495.46
2396.87	88314.45	75536.62	122259.5	27531.06	60394.85	15438.19	88609.8	38286.58	139406.75	17433.36	80183.4	67891.87	90652.6	4298.36
37.9	121.4	28.43	87.7	19.23	251.3	210.29	240	23.33	244.65	37.83	511.65	490.66	280.2	195.16
14.85	481.05	640.29	472.8	651.95	30	29.84	1267	570.64	682.55	691.34	12	4.53	60.95	33.59
36.06	1343.65	115.75	1160.45	374.84	1435.85	880.14	685.75	263.96	1555.5	883.03	2413	868.89	2591.7	713.61
1022.97	3637.5	229.39	4030.25	784.82	3532.1	1463.71	3339.25	646.08	3091.65	2522.04	3224.9	1021.49	3111.35	1557.26
220.26	511.3	312.4	669.85	88.18	612.6	245.51	309.75	35.14	410.9	321.31	293.3	192.76	486.7	107.06
3.82	373.8	312.54	368.35	320.25	803.8	819.68	934.9	1117.94	590.4	159.52	937.85	770.39	290.45	350.23
376.75	703.1	151.89	716.7	132.65	424.85	3.32	1143.75	847.04	583.75	432.54	1794.95	1207.95	824.8	314.95
904.04	7641.05	763.32	6831.7	381.27	6129.8	2520.69	7533	3058.8	7950.45	2440.01	7268.25	3843.34	9518	3694.21
592.2	3425.05	489.39	3066.35	17.89	3631.7	739.07	2100.35	1673.37	4808.35	2162.54	3035.3	150.05	1948.1	847.11
309.22	185.4	35.5	165.1	64.21	331.55	57.49	1007.15	1192.96	711.35	786.23	837.4	590.29	932.3	999.42
233.06	1119.95	767.42	959.3	540.23	2150.1	1382.39	3009.35	1444.27	1453.35	1166.23	3805.25	2868.8	2546.95	361.69

175.72	201.55	117.45	68.5	70.71	656.1	869.32	1094.95	1231.43	160.8	80.33	653.25	720.75	211.8	148.78
112.78	483.7	89.24	529.25	24.82	460.2	37.34	790.75	209.09	568.7	108.61	507.15	24.25	456.2	306.46
593.05	1853.95	596.87	1195.1	334.89	868.05	1034.29	1295.3	1494.26	357.7	0.71	479.55	482.46	889.95	892.16
19.73	203.7	124.59	236	78.91	431.2	172.53	679.6	358.64	376.2	370.1	1032.7	113.84	536.25	288.99
1001.55	1384.15	1368.32	1356.85	1329.71	3381.9	1000.27	1539.85	241.19	1675.25	1302.56	2079.75	648.35	2461.65	9.69
172.32	801.05	413.73	727.5	309.71	1237.65	439.75	1162.9	423.84	729.05	91.99	549.25	79.13	847.4	399.94
125.65	1159.9	306.18	2417.4	2084.55	1198.9	213.97	1545.65	813.53	4296.85	4398.27	2408.35	570.28	3197.35	1193.81
235.18	928.8	294.72	874.45	217.86	276.45	190.57	1759.5	399.37	1829.95	745.36	960.1	230.52	1508.95	179.82
128.69	701.15	380.07	744.05	319.4	353.15	142.48	211.15	34.29	204.9	105.78	241.15	144.32	328.3	249.61
106.35	356.9	114.98	393.55	166.81	1043.85	534.93	403.85	340.9	1042.65	1088.59	1374.7	601.18	1002.75	198.2
7	90.85	31.18	90.6	31.54	72.7	39.32	124.35	101.75	71.7	20.93	95.85	37.97	101	14.85
692.19	1030.6	673.73	911.45	505.23	965.7	1135.33	2189.45	722.31	931.85	572.4	914.65	747.2	1192.6	422.14
15.77	240.45	243.17	318.15	133.29	649.4	491.44	266.65	260.99	587.9	679.25	985.5	1196.14	256.85	8.13
313.04	538.55	273.86	537.9	274.78	276.35	8.56	172.75	50.56	394.95	391.53	814.45	897.67	239.4	195.02
10414.13	67846.05	6401.79	76187.2	18197.96	77327.16	6030.99	102780.95	97895.6	75651	21598.43	74561.7	16456.36	102565.7	11370.14
113.21	31.75	36.27	49.3	11.46	469.45	649.34	195.9	98.57	221.15	257.17	115	100.41	340.6	447.74
25.1	212.5	63.92	313.3	78.63	760.45	961.59	768.95	820.31	831.65	979.13	387.9	36.49	676.95	888.2

28.64	66.85	7	71	1.13	113.6	56.85	145.95	58.05	164.5	56	234.15	251.38	319.1	333.9
250.74	397.3	61.09	458.5	25.46	222.7	214.54	687.6	56.43	719.3	16.55	389.25	315.44	950.85	308.93
934.65	1766.4	151.32	2297	901.7	2988.8	624.66	1448.35	1766.14	1678.65	542.42	2847.15	692.75	2686.6	345.49
292.74	82.65	18.03	269.95	246.85	519.9	249.33	103.6	40.87	216.15	68.8	736.1	907.36	350.7	380.99
220.9	1339.65	181.8	1358.55	155.07	1572.05	309.22	1771.15	443.14	2030.35	103.31	924.2	268.13	1203.75	458.98
30.33	832.05	621.9	802.6	663.55	305.15	65.83	828.7	414.93	352.95	395.34	359.75	357.3	437.85	503.96
118.09	3529.15	141.92	4237.75	1144.03	4833.45	949.01	1912.6	2073.52	5766.35	1498.43	2030.85	2275.82	5642.2	2348.02
130.74	236.75	134.99	97.8	61.52	150.45	75.17	520.95	652.87	190.65	115.61	1187.45	879.99	658.3	698.2
675.43	2393	192.76	1933.65	456.86	1961.5	622.82	1924.3	226.27	1821.35	377.52	1171.15	1470.29	1847.3	204.21
1582.86	6920.6	2715.86	7715.6	1591.56	5615.65	244.87	8666.65	3627.1	9745.8	809.64	5980.2	247.77	6831.8	431.05
8969.58	70866	8422.63	73864.85	4181.62	76246.65	5602.9	68704.8	35938.7	69412.45	1146.29	54929.85	11277.71	104437.09	17934.07
894	4086	852.91	3356.8	178.33	3479.1	166.74	3476.3	2274.06	2596.25	210.51	4383	668.78	5271.6	630.17
339.98	302.2	16.12	265.45	68.09	543.9	330.5	1112.35	752.57	886.15	40.66	1565.1	1616.45	768.95	542.14
98.57	225.75	83.65	342.3	81.18	1691.2	1027.28	644.45	439.75	1672.75	342.59	1726.25	1718.62	1178.4	1307.72
57.77	247.5	142.41	358.6	299.53	889.35	396.9	392.4	472.06	773.65	305.4	511.8	37.34	686.9	214.54

199.83	1640.3	484.65	1790.55	272.17	1677.2	102.25	741.85	27.79	1672.35	142.34	1084.2	656.62	1433.05	12.23
27.93	817.65	699.82	855.4	646.44	407.5	240.84	282.8	1.41	321.25	58.34	371.35	112.36	441.6	64.91
56018.48	57549.65	13206.42	79276	17519.28	91269.95	52029.13	151571.16	99614.16	129518.75	46206.38	95582.5	13255.28	113679.75	122.12
1006.35	11060.2	4932.07	11935.3	3694.49	11267.2	4400.18	16566.7	3239.54	16331.9	3621.38	11884.15	1956.49	15360.15	1086.04
38.4	194.25	43.2	205.85	59.61	388.9	47.66	718.55	432.68	849.65	186.32	991.5	836.93	632.95	662.21
274	3827.7	1211.42	4483.5	283.97	4594.55	453.75	3704.6	42.14	3809.4	1141.84	4987	989.24	3444.05	221.25
7.85	141.85	149.13	33.6	3.96	797.55	1015.19	248.85	248.55	1077.05	763.75	70.75	44.05	201.1	56.57
623.24	576.3	548.43	470.2	398.38	813.45	658.53	591.95	492.08	182.35	130.04	620.9	5.66	622.8	393.58
34.01	180.05	13.79	139.75	70.78	194.8	119.22	271	65.9	255.05	89.31	200.05	31.75	129.2	41.72
14.28	76.55	26.66	87	11.88	88.6	25.74	202.4	106.77	169.7	70.43	411.85	233.7	142.7	14.57
25.17	209.15	167.23	170.25	112.22	82.65	62.44	725.65	891.31	118	98.71	398.65	298.61	377.2	488.05
39.74	797.95	322.51	944.3	115.54	905.95	343.58	1740.95	833.18	263	22.77	880.95	433.53	972.05	937.98
566.32	714.95	59.33	944.35	383.75	1290.4	342.81	1450.8	951.34	478.6	356.52	346.2	110.31	309.9	17.96
398.17	1816.4	633.57	1721.65	767.56	1914.95	394.64	1445.1	1231.64	2134.55	765.58	2447.95	827.95	1998.75	13.08
188.37	60.35	26.94	69.25	14.35	232.7	240.13	98.45	97.09	128.15	68.24	175.75	43.91	355.9	284.96

115.19	682.4	489.04	583.05	629.54	112.15	80.68	416.9	433.32	840.85	1101.6	243.55	12.23	268.65	107.27
324.28	1781.85	929.77	1969.4	664.54	1399.1	180.17	1904.1	782.2	743.6	690.56	586.35	342.73	1915.25	187.88
113.99	1468.75	228.61	1337.1	414.79	1381.55	452.48	3210.9	2173.79	1950.35	228.47	1445.1	152.31	1405.1	248.76
141.35	834.85	36.27	776.95	45.61	489.15	306.96	1767.2	1575.72	430.5	166.74	764.9	272.09	824.3	494.83
1919.3	3205.2	263.04	2508.65	722.03	3582.75	1363.23	2663.05	1445.26	2071.65	1085.34	1951	2038.31	1507.3	451.84
1711.48	28849.05	8512.65	30305.85	10572.87	31428.2	2400.49	27754.5	24133.41	22666.65	8346.62	25633.5	7960.61	27610.25	13379.1
281	687.8	471.92	565.45	644.95	483.85	375.12	398.95	19.45	133.5	45.11	215.1	125.72	154.9	115.82
294.86	155.4	66.89	253.15	71.35	269.2	230.09	132.45	26.94	327.35	27.79	699.7	42.85	686.8	809.07
991.72	2208	407.15	2122.4	528.21	2113.5	583.93	2307.65	1060.59	2279	137.46	1266.9	967.89	3012.75	310.91
168.93	1145	103.66	1072.1	0.57	790.7	460.47	1919.05	2010.09	763.05	336.51	1810.55	1309.35	1651.95	447.1
67.25	600.1	774.56	584.6	796.49	519.85	683.98	515.05	694.03	135.5	35.64	97.6	64.35	170.5	173.1
114.27	553.85	321.38	426.2	501.9	373.6	151.89	427.1	338.28	370.3	130.25	143.05	110.95	172.35	124.95
249.11	3496.75	292.11	3090.1	282.98	4579.5	768.34	2494.35	2554.85	4281.55	17.89	5312.85	626	5923.1	911.32
1007.49	1401.4	162.07	1089.7	278.74	2517.65	1455.01	4280.4	2589.85	2203.05	1544.96	544.4	12.02	2007.45	840.26

344.71	421.55	98.92	421.75	98.64	585.1	162.92	351.55	108.54	395.9	289.49	812.45	602.81	786	27.29
52.61	85	75.8	110.9	39.17	113.9	104.79	192.1	33.94	207.05	89.45	116.65	89.73	158.6	90.79
101.12	48.6	36.77	60.55	19.87	193.1	253.57	1181.2	1585.19	70.4	33.8	745.9	808.08	225.6	202.66
230.09	1899.6	610.8	1970.85	510.04	1752.7	741.19	1417.35	1315.71	2105.5	279.59	1544.5	335.88	2568	723.94
129.12	128.55	68.8	153.8	33.09	135.55	25.53	548.05	60.32	527.95	178.83	249.5	154.71	279.85	145.03
259.58	1361.4	28.99	1426.25	120.7	1505.25	903.61	1779.2	61.8	1411.4	554.23	2572.4	1691.4	1355.4	261.77
635.05	1139.65	82.24	1110.1	40.45	1008.1	326.4	622.45	718.63	631.9	315.37	971.8	1030.11	1258.6	563.85
41.44	55.35	29.06	81.05	7.28	148.55	88.74	216.65	22.56	454.6	525.66	325.5	361.61	91.45	81.67
1205.26	529.55	490.66	306.25	174.87	920.95	200.75	846.95	349.52	3195.55	3838.25	1482	258.66	231.25	12.8
674.01	2670.9	125.72	2786.05	288.57	2132.4	169.99	1411.55	1591.77	3647.5	447.74	2633.7	1006.5	2593	511.38
31.75	360.65	102.88	273.65	225.92	319.3	59.4	612.85	642.41	335.3	66.89	376.9	306.18	581.6	653.51
125.94	459.1	407.29	389.05	506.36	321.65	307.66	196.95	226.06	666.45	412.17	112.8	94.05	415.75	18.17
83.58	488.2	207.32	339.05	418.25	314.55	159.03	151.85	23.26	137.15	70.22	618.25	655.98	305.25	355.18
257.6	229.3	215.81	247.9	189.5	327.6	165.32	173	11.17	137.55	2.76	212.2	125.44	275.1	283.27
674.3	597.1	481.96	761.8	249.04	156.2	9.76	1678.6	1753.91	1413.15	1177.69	599.8	401.64	1305.3	829.86
1310.62	14559.15	1423.9	12554.6	1410.96	13673.45	6719.28	8384.35	6446.76	11174.95	2434.64	8148.7	2648.11	10571.25	2181.64

50.42	468.95	365.93	438.75	408.64	352.7	259.08	1295.2	1534.7	657.8	470.51	64.95	15.49	342.1	146.94
92.7	542.65	332.41	446.2	468.81	253.6	13.44	719.25	749.18	541.4	35.78	340.6	271.25	420.35	275.7
496.53	990.1	352.99	1150.15	126.64	1018.9	369.39	307.6	264.74	1389.95	89.17	1354.25	301.58	623.1	336.02
797.26	2376.85	243.88	2070.85	676.63	2012.45	240.2	1780.7	224.72	2931.25	710.57	1754.9	802.14	1736.35	1814.22
11.53	111.35	5.59	281.95	235.68	642.35	790.47	410.45	112.64	94.95	7.71	105.65	100.06	91.5	16.69
4.74	290.35	372.29	317.05	334.53	92.75	75.87	1254.3	1043.41	305.45	186.89	492.4	600.48	497.75	64.98
430.84	2021.7	294.16	1960.35	380.92	1786.95	367.48	2433.15	1315.15	2524	582.51	959.8	1021.63	2491.4	880.35
196.29	369.35	289.42	560.7	560.03	151.4	71.13	1395.3	423.98	515.3	592.56	470.25	645.52	936	402.49
276.05	2081.3	75.94	2175	56.57	1331.7	268.42	2634.35	2868.24	3023.85	380.64	2569.6	2372.63	3609.35	454.17
1275.69	4787.9	896.19	5631.15	296.35	3306.55	1259.85	5099.85	3749.15	4958.2	211.71	3504.35	1317.13	4510.85	732.63
111.51	1236.7	350.16	1287.85	277.82	710.65	769.69	639.85	424.05	1066.6	632.29	1432.75	833.04	1399.95	321.52
1153.93	2334.85	232.99	2326.8	221.61	2893.7	450.71	1418.45	1570.55	1725.95	630.1	2384.7	323.01	2853.9	466.69
60.03	1203.1	274.5	1266.9	184.27	600.15	78.56	1660.3	1837.35	832.6	93.48	314.7	289.77	529.75	461.39
381.98	993.85	494.62	893.55	352.78	941.1	35.5	2564.05	1812.39	1279.5	916.13	2343.95	729.1	1931.65	799.24

121.13	440.6	528.35	443.6	524.11	66.95	15.77	131.35	12.37	137.45	22.84	138.9	90.79	230	109.46
33.87	1093.6	37.19	1206.2	122.05	1730.2	728.89	1726.05	828.8	1261.25	127.63	988.25	776.62	1357.3	320.74
481.04	537.95	260.71	554.7	284.4	1479.6	958.98	1387.75	1447.94	943.25	540.02	2194.75	283.76	1727.9	200.39
556.07	225.4	92.63	212.1	111.44	298.9	161.36	293.05	242.61	193.35	122.97	1140.7	302.08	223.05	153.23
364.73	190.55	57.49	164.1	94.89	173.5	119.78	298.75	215.74	361.55	303	377.8	364.02	176.9	139.72
563.28	1241.85	45.61	1738.65	656.97	1982.6	1092.2	759.1	385.51	2345.8	1614.32	742.75	391.52	2131	44.26
162.07	786.4	281.29	579.8	573.46	642.6	400.65	925.5	771.59	920.85	524.46	849.35	348.25	580.35	34.44
2.4	131.1	88.11	143.6	70.43	304.4	181.87	270.85	315.44	107.65	30.48	91.05	67.81	155.75	14.5
446.33	1043.4	112.15	833.65	184.48	767.25	249.68	610.65	675.07	561.85	521.35	285.15	257.03	122.6	15.98

Description

U43653, class A, 20 probes, 20 in U43653 2816-3155, Human obese protein (ob) mRNA, complete cds

M55419, class C, 20 probes, 20 in all_M55419 2275-2470, Human amelogenin (AMELY) gene, 3 end of cds

X13955, class C, 20 probes, 20 in all_X13955 675-827, Human mRNA for myosin alkali light chain

L76571, class B, 20 probes, 10 in L76571cds 440-734: 10 in reverseSequence, 1070-1310, Homo sapiens nuclear hormone receptor (shp) gene, 3 end of cds

U03274, class A, 20 probes, 20 in U03274 1497-1941, Human biotinidase mRNA, complete cds

M19301, class A, 20 probes, 20 in M19301mRNA 944-1448, Human branched-chain alpha-keto acid dehydrogenase (E2) mRNA, complete cds

D14678, class A, 20 probes, 20 in D14678 1244-1748, Human mRNA for kinesin-related protein, partial cds

U04840, class A, 20 probes, 20 in U04840 3088-3646, Human onconeural ventral antigen-1 (Nova-1) mRNA, complete cds

AC002086, class A, 20 probes, 19 in AC002086cds 1686-1974: 1 in reverseSequence, 98485, Human PAC clone DJ525N14 from Xq23

M83664, class A, 20 probes, 20 in M83664 1098-1416, Human MHC class II lymphocyte antigen (HLA-DP) beta chain mRNA, complete cds

Kallistatin, Protease Inhibitor 4

D63480, class A, 20 probes, 20 in D63480 2623-3187, Human mRNA for KIAA0146 gene, partial cds

D50645, class A, 20 probes, 20 in D50645 502-1006, Human mRNA for SDF2, complete cds

J00124, class A, 20 probes, 17 in J00124exon#8 14-227: 3 not in GB record, Homo sapiens 50 kDa type I epidermal keratin gene, complete cds

L41919, class A, 20 probes, 20 in L41919mRNA 1877-2450, Homo sapiens HIC-1 gene fragment

S67156, class A, 20 probes, 20 in S67156 876-1368, ASP=aspartoacylase [human, kidney, mRNA, 1435 nt]

J00220, class C, 20 probes, 20 not in GB record, Human Ig germline H-chain G-E-A region A: gamma-3 5 flank, Human Ig germline H-chain G-E-A region A: gamma-3 5 flank

X98085, class C, 20 probes, 20 in all_X98085 4149-4642, H.sapiens mRNA for tenascin-R

D86964, class A, 20 probes, 20 in D86964 5449-5995, Human mRNA for KIAA0209 gene, partial cds

X89750, class C, 20 probes, 20 in all_X89750 1061-1512, H.sapiens mRNA for TGIF protein

D63482, class A, 20 probes, 20 in D63482 1722-2226, Human mRNA for KIAA0148 gene, complete cds

D55654, class A, 20 probes, 20 in D55654 786-1224, Human mRNA for cytosolic malate dehydrogenase, complete cds

K02766, class A, 20 probes, 20 in K02766 2028-2436, Human complement component C9 mRNA, complete cds

U56814, class A, 20 probes, 20 in U56814 495-957, Human DNAse I homologous protein (DHP2) mRNA, complete cds

M14123, class A, 20 probes, 20 in M14123cds#3 13-175, pol from Human endogenous retrovirus HERV-K10. /gb=M14123 /ntype=DNA /annot=CDS, pol from Human endogenous retrovirus HERV-K10. /gb=M14123 /ntype=DNA /annot=CDS, pol from Human endogenous retrovirus HERV-K10. /gb=M14123 /ntype=DNA /annot=CDS, pol from Human endogenous retrovirus HERV-K10. /gb=M14123 /ntype=DNA /annot=CDS

U17418, class A, 20 probes, 20 in U17418 1591-2071, Human parathyroid hormone/parathyroid hormone-related peptide receptor mRNA, complete cds

L07868, class A, 20 probes, 20 in L07868 4919-5429, Homo sapiens receptor tyrosine kinase (ERBB4) gene, complete cds

X90824, class C, 19 probes, 19 in all_X90824 828-1337, H.sapiens mRNA for USF2a & USF2b, clone P9DH

X63741, class C, 19 probes, 19 in all_X63741 3695-4230, H.sapiens pilot mRNA

X14830, class A, 20 probes, 18 in X14830cds 1033-1423: 2 in reverseSequence, 1547-1571, Human mRNA for muscle acetylcholine receptor beta-subunit

Oncogene Aml1-Evi-1, Fusion Activated

U00944, class A, 20 probes, 20 in U00944 1121-1619, Human clone A9A2BRB6 (CAC)n/(GTG)n repeat-containing mRNA

Homeotic Protein Gbx2

X64878, class C, 20 probes, 20 in all_X64878 3508-3965, H.sapiens mRNA for oxytocin receptor

X78121, class B, 20 probes, 13 in X78121mRNA 1730-1940: 7 in reverseSequence, 1970-2036, H.sapiens mRNA for choroideremia

M83181, class B, 20 probes, 10 in M83181cds 918-1206: 10 in reverseSequence, 1639-1867, Human serotonin receptor gene, complete cds

X63468, class C, 20 probes, 20 in all_X63468 2398-2915, H.sapiens mRNA for transcription factor TFIIE alpha

L13258, class A, 20 probes, 20 in L13258 2109-2463, Homo sapiens renal Na/Pi-cotransporter mRNA, complete cds

U79302, class A, 20 probes, 20 in U79302 1414-1906, Human clone 23855 mRNA, partial cds.

X75315, class C, 20 probes, 20 in all_X75315 849-1348, H.sapiens seb4B mRNA

B. subtilis /GEN=thrC, thrB /DB_XREF=gb:X04603.1 /NOTE=SIF corresponding to nucleotides 995-1562 of gb:X04603.1, not 100% identical /DEF=B. subtilis thrB and thrC genes for homoserine kinase and threonine synthase EC 2.7.1.39 and EC 4.2.99.2, respectively).

Homo sapiens /REF=M33197 /DEF=Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) mRNA, complete cds /LEN=1268 (_5, _M, _3 represent transcript regions 5 prime, Middle, and 3 prime respectively)

J05008, class A, 20 probes, 20 in J05008exon#5 637-1183, Homo sapiens endothelin-1 (EDN1) gene, complete cds

Z83745, class A, 20 probes, 20 in Z83745exon 49-367, Human DNA sequence from PAC 453A3 contains EST and STS.

X62822, class C, 20 probes, 20 in all_X62822 2104-2645, H.sapiens gene encoding beta-galactoside alpha-2,6-sialyltransferase

S82185, class A, 20 probes, 20 in S82185 419-905, BRAG-1=brain-related apoptosis gene/Bcl-2 homolog [human, MG-107 glioma, mRNA Partial, 960 nt]. /gb=S82185 /ntype=RNA

J04040, class A, 20 probes, 20 in J04040mRNA 563-1016, Human glucagon mRNA, complete cds

U43586, class A, 20 probes, 20 in U43586 1531-2101, Human kinase suppressor of ras-1 (KSR1) mRNA, partial cds

X13451, class C, 20 probes, 20 in all_X13451 84-268, Human mRNA for lymphocyte lineage-restricted mb-1 membrane glycoprotein C-term. (m-mb-1 homolog.).

U00951, class A, 20 probes, 20 in U00951 1325-1691, Human clone A9A2BR11 (CAC)n/(GTG)n repeat-containing mRNA

U34380, class C, 20 probes, 20 not in GB record, TEC gene extracted from Human protein tyrosine kinase TEC (tec) gene, partial cds, and tyrosine kinase TXK (txk) gene

L34673, class A, 20 probes, 20 in L34673mRNA 2853-3381, Human ATPase, DNA-binding protein (HIP116) mRNA, 3 end

X59834, class A, 20 probes, 20 in X59834mRNA 2120-2690, Human rearranged mRNA for glutamine synthase

Y10512, class A, 20 probes, 20 in Y10512mRNA 14-452, H.sapiens mRNA for CD282 protein. /gb=Y10512 /ntype=RNA

L44140, class A, 20 probes, 19 in L44140exon#61-62 44-221: 1 not in GB record, DNL1L gene extracted from Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds

U82613, class A, 20 probes, 20 in U82613 163-685, Human DNA-binding protein ABP/ZF mRNA, complete cds

Beta-1-Glycoprotein 11, Pregnancy-Specific

X03484, class C, 20 probes, 20 in all_X03484 2418-2947, Human mRNA for raf oncogene

L32961, class A, 20 probes, 20 in L32961 1584-1679, Human 4-aminobutyrate aminotransferase (GABAT) mRNA, complete cds

L18877, class A, 20 probes, 20 in L18877exon#2 980-1530, Human MAGE-12 protein gene, complete cds

M55418, class C, 20 probes, 20 in all_M55418 2452-2650, Human amelogenin (AMELX) gene, 3 end of cds

D85245, class A, 20 probes, 20 in D85245 1248-1806, Human mRNA for TR3beta, complete cds

U17163, class A, 20 probes, 20 in U17163 1086-1644, Human transcription factor ETV1 mRNA, complete cds

M96995, class A, 20 probes, 20 in M96995 497-1025, Homo sapiens epidermal growth factor receptor-binding protein GRB2 (EGFRBP-GRB2) mRNA sequence

L26336, class C, 20 probes, 20 in all_L26336 2691-3220, Human heat shock protein HSPA2 gene, complete cds

X81889, class A, 20 probes, 18 in X81889cds 3255-3561: 2 in reverseSequence, 3774-3786, H.sapiens mRNA for p0071 protein

S78873, class A, 20 probes, 20 in S78873 291-835, mss4=Zn2+ binding protein/guanine nucleotide exchange factor [human, brain, mRNA Partial, 922 nt]

D84424, class A, 20 probes, 20 in D84424 1603-2053, Human fetal brain mRNA for hyaluronan synthase, complete cds

D87468, class A, 20 probes, 20 in D87468 2496-2886, Human mRNA for KIAA0278 gene, partial cds

M25756, class A, 20 probes, 20 in M25756 1777-2287, Human secretogranin II gene, complete cds

Y09267, class A, 20 probes, 20 in Y09267 1148-1664, H.sapiens mRNA for flavin-containing monooxygenase 2 /gb=Y09267 /ntype=RNA

U49248, class A, 20 probes, 20 in U49248 4807-5251, Human canalicular multispecific organic anion transporter (cMOAT), gene, complete cds

Calcium Channel, Voltage-Gated, Alpha 1e Subunit, Alt. Splice 2 - Also Represents: L27745

U61849, class A, 20 probes, 20 in U61849 4650-5040, Human neuronal pentraxin 1 (NPTX1) mRNA, complete cds

M36634, class A, 20 probes, 20 in M36634 1340-1450, Human vasoactive intestinal peptide (VIP) mRNA, complete cds

D49357, class A, 20 probes, 20 in D49357 958-1438, Human mRNA for S-adenosylmethionine synthetase, complete cds

U37139, class A, 20 probes, 20 in U37139mRNA#1 596-998, Human beta 3-endonexin mRNA, long form and short form, complete cds

U96094, class A, 20 probes, 20 in U96094 193-667, Human sarcolipin (SLN) mRNA, complete cds.

Y00097, class B, 20 probes, 13 in Y00097cds 1757-1982: 7 in reverseSequence, 2114-2324, Human mRNA for protein p68

X99886, class C, 19 probes, 17 in all_X99886 601-2202: 2 in X99886cds 96-127, H.sapiens MCP-2 gene

U87972, class A, 20 probes, 20 in U87972 91-373, Human NAD+-isocitrate dehydrogenase mRNA, partial cds. /gb=U87972 /ntype=RNA

M85247, class A, 20 probes, 20 in M85247mRNA 141-597, H.sapiens dopamine D1A receptor gene, complete exon 1, and exon 2, 5 end. /gb=M85247 /ntype=DNA /annot=mRNA

U70862, class A, 20 probes, 20 in U70862 1029-1248, Human nuclear factor I B3 mRNA, complete cds

D14657, class A, 20 probes, 20 in D14657 355-775, Human mRNA for KIAA0101 gene, complete cds

U05227, class A, 20 probes, 20 in U05227 1078-1564, Human Rar protein mRNA, complete cds

U58331, class A, 20 probes, 20 in U58331 762-1041, Human placental delta sarcoglycan mRNA, complete cds

U50315, class A, 20 probes, 20 in U50315 2179-2551, Human enhancer of zeste homolog 1 (EZH1) mRNA, complete cds

M29273, class A, 20 probes, 20 in M29273 1749-2307, Human myelin-associated glycoprotein (MAG) mRNA, complete cds

M33478, class A, 20 probes, 20 in M33478mRNA 653-1049, Human 33-kDa phototransducing protein mRNA, complete cds

S82597, class A, 20 probes, 20 in S82597mRNA 9-507, Description: UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase gene extracted from UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase/GalNAc-transferase {3 region, exon 11} [human, placenta, Genomic, 1902 nt]

X92396, class C, 20 probes, 20 in all_X92396 1999-2480, H.sapiens mRNA for novel gene in Xq28 region

U67611, class A, 20 probes, 18 in U67611 788-1130: 2 not in GB record, Mouse transaldolase gene mRNA, complete cds. /gb=U67611 /ntype=RNA

U11717, class A, 20 probes, 20 in U11717 3500-3743, Human calcium activated potassium channel (hslo) mRNA, complete cds

AB002318, class A, 20 probes, 20 in AB002318 6384-6786, Human mRNA for KIAA0320 gene, partial cds. /gb=AB002318 /ntype=RNA

U17566, class A, 20 probes, 20 in U17566 2214-2754, Human 65 kDa hydrophobic protein mRNA, complete cds

X05246, class C, 20 probes, 20 in all_X05246 1045-1556, Human testis-specific PGK-2 gene for phosphoglycerate kinase (ATP:3-phospho-D-glycerate 1-phosphotransferase, EC 2.7.2.3)

M57892, class A, 20 probes, 20 in M57892mRNA 775-1267, Human carbonic anhydrase isozyme VI (CA6) mRNA, complete cds

X79984, class C, 20 probes, 20 in all_X79984 16-269, H.sapiens AA1 mRNA. /gb=X79984 /ntype=RNA

M33882, class A, 20 probes, 20 in M33882 2348-2762, Human p78 protein mRNA, complete cds

U67932, class A, 20 probes, 20 in U67932mRNA 1128-1700, Human cAMP phosphodiesterase (Pde7A2) mRNA, complete cds. /gb=U67932 /ntype=RNA

X07730, class C, 20 probes, 20 in all_X07730 1535-1680, Human mRNA for prostate specific antigen

L38935, class A, 20 probes, 20 in L38935mRNA 564-1026, Homo sapiens GT212 mRNA

U38545, class A, 20 probes, 20 in U38545 3056-3578, Human ARF-activated phosphatidylcholine-specific phospholipase D1a (hPLD1) mRNA, complete cds

M62628, class C, 20 probes, 20 in all_M62628 1743-2182, Human alpha-1 Ig germline C-region membrane-coding region, 3 end

AB003103, class A, 20 probes, 20 in AB003103 2965-3463, Human mRNA for proteasome subunit p55, complete cds

Y10141, class A, 20 probes, 20 in Y10141cds 56-286, H.sapiens DAT1 gene, partial, VNTR. /gb=Y10141 /ntype=DNA /annot=CDS

U33447, class C, 20 probes, 20 in all_U33447 1311-1888, Human putative G-protein-coupled receptor (GPR17) gene, complete cds

U57092, class A, 20 probes, 20 in U57092 317-779, Human small GTP-binding protein rab30

U60521, class A, 20 probes, 20 in U60521 1398-1860, Human protease proMch6 (Mch6) mRNA, complete cds

U08336, class A, 20 probes, 20 in U08336 368-872, Human basic helix-loop-helix transcription factor mRNA, complete cds

Kinase Inhibitor P27kip1, Cyclin-Dependent

U33921, class A, 20 probes, 20 in U33921 578-1046, HSU33921 Homo sapiens cDNA

Z96810, class A, 20 probes, 20 in Z96810cds 482-968, Human DNA sequence from PAC 452H17 on chromosome X contains sodium-and chloride-dependent glycine transporter 1 (GLYT-1) like, ESTs.

U56976, class A, 20 probes, 20 in U56976 1664-2240, Human calmodulin dependent phosphodiesterase PDE1B1 mRNA, complete cds

X66610, class C, 20 probes, 20 in all_X66610 1372-1697, H.sapiens mRNA for enolase

X74331, class C, 20 probes, 20 in all_X74331 1801-2288, H.sapiens mRNA for DNA primase (subunit p58)

D64015, class A, 20 probes, 20 in D64015 1126-1222, Homo sapiens mRNA for T-cluster binding protein, complete cds. /gb=D64015 /ntype=RNA

Glycogenin - Also Represents: U31525

M76231, class A, 20 probes, 20 in M76231 292-790, Human sepiapterin reductase mRNA, complete cds

X62048, class C, 20 probes, 20 in all_X62048 1820-2343, H.sapiens Wee1 hu gene

U41344, class A, 20 probes, 20 in U41344mRNA 1478-1988, Human prolargin (PRELP) gene, 5 flanking sequence and

K03008, class C, 20 probes, 2 in K03008cds 90-118: 18 not in GB record, gamma-G2-psi gene extracted from Human gamma-C-crystallin (gamma-3) gene, gamma-G2-psi gene extracted from Human gamma-C-crystallin (gamma-3) gene

U15655, class A, 20 probes, 20 in U15655 2102-2576, Human ets domain protein ERF mRNA, complete cds

M59979, class A, 20 probes, 20 in M59979 2109-2511, Human prostaglandin endoperoxide synthase mRNA, complete cds

M31899, class A, 20 probes, 20 in M31899 2318-2708, Human DNA repair helicase (ERCC3) mRNA, complete cds

X68836, class A, 20 probes, 20 in X68836cds 653-1139, H.sapiens mRNA for S-adenosylmethionine synthetase

X85781, class A, 19 probes, 19 in X85781exon 2-551, H.sapiens NOS2 gene, exon 27 /gb=X85781 /ntype=DNA /annot=exon

L13744, class A, 20 probes, 20 in L13744 2775-3345, Human AF-9 mRNA, complete cds

S81661, class A, 20 probes, 20 in S81661 588-1164, Keratinocyte growth factor [human, mRNA, 1200 nt]

D84145, class A, 20 probes, 20 in D84145 458-980, Human WS-3 mRNA, complete cds

M37763, class A, 20 probes, 18 in M37763cds 350-740: 2 in reverseSequence, 965-989, Human neurotrophin-3 (NT-3) gene, complete cds

X66922, class A, 20 probes, 18 in X66922cds 362-728: 2 in reverseSequence, 848-872, H.sapiens mRNA for myo-insositol monophosphatase

U11872, class A, 20 probes, 20 in U11872 36-72, Human interleukin-8 receptor type B (IL8RB) mRNA, splice variant IL8RB1, partial cds. /gb=U11872 /ntype=RNA

D16611, class A, 20 probes, 20 in D16611 1726-2299, Human mRNA for coproporphyrinogen oxidase, complete cds

D49950, class A, 20 probes, 20 in D49950 495-918, Human Liver mRNA for interferon-gamma inducing factor(IGIF), complete cds
Sodium Channel, Type Iii, Alpha Subunit, Brain

M95678, class A, 20 probes, 20 in M95678 3990-4494, Homo sapiens phospholipase C-beta-2 mRNA, complete cds
X07619, class C, 20 probes, 20 in all_X07619 658-1162, Human mRNA for cytochrome P450 db1 variant b
X70940, class B, 20 probes, 10 in X70940cds 1130-1298: 10 in reverseSequence, 1591-1722, H.sapiens mRNA for elongation factor 1 alpha-2

AD001527, class A, 20 probes, 17 in AD001527cds#1 317-575: 3 in reverseSequence, 3640-3802, comment for location 3447-3655: BLASTX gi|103290|pir||S16356 ovo protein - fruit fly (Drosophila melanogaster), PVal= 3.80E-47 gene extracted from Homo sapiens DNA from chromosome 19-cosmid f24590 containing CAPNS and POL2RI, genomic sequence
D50532, class A, 20 probes, 20 in D50532 839-1283, Human mRNA for macrophage lectin 2, complete cds
M19650, class A, 20 probes, 20 in M19650 1446-1700, Human 2 ,3 -cyclic nucleotide 3 -phosphodiesterase mRNA, complete cds
M83186, class A, 20 probes, 20 in M83186 103-316, Human cytochrome c oxidase subunit VIIa (COX7A) muscle isoform mRNA, complete cds
X67594, class A, 20 probes, 16 in X67594cds 507-909: 4 in reverseSequence, 1119-1221, H.sapiens mRNA for MSH receptor

M11717, class A, 20 probes, 20 in M11717mRNA 2135-2393, Human heat shock protein (hsp 70) gene, complete cds
U93049, class A, 20 probes, 20 in U93049 1841-2375, Human SLP-76 associated protein mRNA, complete cds.
Homeotic Protein Hpx-2

M35851, class A, 20 probes, 18 in M35851cds 2287-2708: 2 in reverseSequence, 200-266, Human androgen receptor gene
M64108, class A, 20 probes, 20 in M64108 2031-2571, Human udulin 1 mRNA, 3 end

X89109, class A, 20 probes, 17 in X89109cds 860-1326: 3 in reverseSequence, 1457-1488, H.sapiens mRNA for coronin

X58377, class A, 20 probes, 20 in X58377mRNA 1716-2232, Human mRNa for adipogenesis inhibitory factor

U78722, class A, 20 probes, 20 in U78722 1523-1965, Homo sapiens zinc finger protein 165 (Zpf165) mRNA, complete cds.

D63998, class A, 20 probes, 20 in D63998 3542-4046, Human mRNA for golgi alpha-mannosidaseII, complete cds

M63175, class A, 20 probes, 20 in M63175 1221-1689, Human autocrine motility factor receptor mRNA

B. subtilis /GEN=lys /DB_XREF=gb:X17013.1 /NOTE=SIF corresponding to nucleotides 720-990 of gb:X17013.1, not 100% identical /DEF=B subtilis lys gene for diaminopimelate decarboxylase (EC 4.1.1.20).

M57609, class A, 20 probes, 20 in M57609mRNA 4490-5012, Human DNA-binding protein (GLI3) mRNA, complete cds

J04760, class A, 20 probes, 20 in J04760mRNA 233-791, Human slow-twitch skeletal troponin I (TNN1) mRNA, complete cds

M75099, class A, 20 probes, 20 in M75099 25-493, Human rapamycin- and FK506-binding protein, complete cds

U76189, class A, 20 probes, 20 in U76189 49-355, Human EXTL3 mRNA, partial cds. /gb=U76189 /ntype=RNA

M31165, class A, 20 probes, 20 in M31165mRNA 843-1353, Human tumor necrosis factor-inducible (TSG-6) mRNA fragment, adhesion receptor CD44 putative CDS

X56468, class A, 20 probes, 20 in X56468mRNA 1303-1789, Human mRNA for 14.3.3 protein, a protein kinase regulator

U56102, class A, 20 probes, 20 in U56102 1973-2537, Human adhesion molecule DNAM-1 mRNA, complete cds

M31525, class A, 20 probes, 20 in M31525mRNA 517-1081, Human MHC class II lymphocyte antigen (HLA-DNA) gene, complete cds

Y10659, class B, 20 probes, 13 in Y10659cds 1011-1239: 7 in reverseSequence, 1342-1552, H.sapiens IL-13Ra mRNA

L05500, class A, 20 probes, 20 in L05500 2226-2688, Human fetal brain adenylyl cyclase mRNA, 3 end

Z22780, class B, 20 probes, 10 in Z22780cds 1528-1774: 10 in reverseSequence, 1780-1870, H.sapiens cylicin mRNA

X96754, class C, 20 probes, 20 in all_X96754 846-1051, H.sapiens gene encoding kappa light chain constant region.

X63753, class C, 20 probes, 20 in all_X63753 5116-5621, H.sapiens son-a mRNA

U16660, class A, 20 probes, 20 in U16660 685-1153, Human peroxisomal enoyl-CoA hydratase-like protein (HPXEL) mRNA, complete cds

U68536, class A, 20 probes, 20 in U68536 1918-2410, Human zinc finger protein mRNA, complete cds

U07358, class A, 20 probes, 20 in U07358 2794-3310, Human protein kinase (zpk) mRNA, complete cds

M91592, class A, 20 probes, 20 in M91592 1971-2325, Human zinc-finger protein (ZNF76) gene, partial cds

M11321, class A, 20 probes, 20 in M11321mRNA 1193-1703, Human group-specific component vitamin D-binding protein mRNA, complete cds

M16937, class A, 20 probes, 20 in M16937 806-1310, Human homeo box c1 protein, mRNA, complete cds

X00588, class C, 20 probes, 20 in all_X00588 5021-5514, Human mRNA for precursor of epidermal growth factor receptor

AB002332, class A, 20 probes, 20 in AB002332 5132-5666, Human mRNA for KIAA0334 gene, complete cds. /gb=AB002332 /ntype=RNA

Serine/Threonine Kinase (Gb:Z25428)

U64871, class A, 20 probes, 17 in U64871cds 870-1212: 3 in reverseSequence, 1665-1773, Human putative G protein-coupled receptor (GPR19) gene, complete cds

U41315, class A, 20 probes, 20 in U41315mRNA#1 3083-3653, Human ring zinc-finger protein (ZNF127-Xp) gene and 5 flanking sequence

Y00433, class B, 20 probes, 13 in Y00433cds 233-581: 7 in reverseSequence, 905-1109, Human mRNA for glutathione peroxidase (EC 1.11.1.9.)

M17754, class A, 20 probes, 20 in M17754 1298-1838, Human BN51 mRNA, complete cds

M24364, class C, 20 probes, 20 in all_M24364 1059-1435, Human MHC class II lymphocyte antigen DQB mRNA, complete cds, haplotype DR7, DQw9

X72841, class C, 20 probes, 20 in all_X72841 1378-1937, H.sapiens IEF 7442 mRNA

X17651, class C, 20 probes, 20 in all_X17651 829-1412, Human Myf-4 mRNA for myogenic determination factor

Rna Polymerase Ii, 14.5 Kda Subunit

X68242, class C, 20 probes, 20 in all_X68242 408-889, H.sapiens mRNA for Hin-1

M62324, class A, 20 probes, 20 in M62324 1584-2052, Human modulator recognition factor I (MRF-1) mRNA, 3 end

D87432, class A, 20 probes, 20 in D87432 5731-6253, Human mRNA for KIAA0245 gene, complete cds

D87076, class A, 20 probes, 20 in D87076 5065-5581, Human mRNA for KIAA0239 gene, partial cds

X72964, class C, 20 probes, 20 in all_X72964 606-1027, H.sapiens mRNA for caltractin

X98482, class B, 14 probes, 14 in X98482mRNA 2-46, H.sapiens TNNT2 gene exon 11 /gb=X98482 /ntype=DNA /annot=mRNA, H.sapiens TNNT2 gene exon 11 /gb=X98482 /ntype=DNA /annot=mRNA

L21998, class A, 20 probes, 20 in L21998 15275-15677, Human intestinal mucin (MUC2) mRNA, complete cds

X65293, class A, 20 probes, 20 in X65293cds 1670-2180, H.sapiens mRNA for protein kinase C-Epsilon

B. subtilis /GEN=pheB /DB_XREF=gb:M24537.1 /NOTE=SIF corresponding to nucleotides 2885-3326 of gb:M24537.1, not 100% identical /DEF=Bacillus subtillis sporulation protein (spoOB), GTP-binding protein (obg), phenylalanine biosynthesis associated protein (pheB), and monofunctional prephenate dehydratase (pheA) genes, complete cds.

U79294, class A, 20 probes, 20 in U79294 831-1371, Human clone 23748 mRNA, complete cds.

M65085, class A, 20 probes, 20 in M65085 1792-2302, Human follicle stimulating hormone receptor mRNA, complete cds

S70348, class A, 20 probes, 20 in S70348 55-367, integrin beta 3 {alternatively spliced, clone beta 3C} [human, erythroleukemia cell HEL, mRNA Partial, 409 nt]

M98776, class A, 20 probes, 20 in M98776mRNA 1864-2266, Human keratin 1 gene, complete cds

D31765, class A, 20 probes, 20 in D31765 3735-4191, Human mRNA for KIAA0061 gene, partial cds

L25876, class A, 20 probes, 20 in L25876 359-785, Homo sapiens protein tyrosine phosphatase (CIP2)mRNA, complete cds

U61166, class A, 20 probes, 20 in U61166 2652-3150, Human SH3 domain-containing protein SH3P17 mRNA, complete cds

Z48314, class B, 20 probes, 13 in Z48314cds 2683-3086: 7 in reverseSequence, 3110-3249, H.sapiens mRNA for apomucin

D63391, class A, 20 probes, 20 in D63391 341-773, Human mRNA for platelet activating factor acetylhydrolase IB gamma-subunit, complete cds

U75968, class A, 20 probes, 20 in U75968 3641-4139, Human clone C3 CHL1 protein (CHLR1) mRNA, alternatively spliced, complete cds

U20759, class A, 20 probes, 20 in U20759 3683-3758, Human parathyroid cell calcium-sensing receptor mRNA, complete cds

Sulfotransferase, Phenol-Preferring - Also Represents: U20499

M60974, class A, 20 probes, 20 in M60974 731-1304, Human growth arrest and DNA-damage-inducible protein (gadd45) mRNA, complete cds

S81003, class A, 20 probes, 20 in S81003 130-640, L-UBC=ubiquitin conjugating enzyme [human, odontogenic keratocysts, mRNA Partial, 683 nt]

D00097, class A, 20 probes, 20 in D00097exon#2 152-710, Human serum amyloid P component (SAP) gene with upstream promoter

U39840, class A, 20 probes, 20 in U39840 2313-2823, Human hepatocyte nuclear factor-3 alpha (HNF-3 alpha) mRNA, complete cds

U19495, class A, 20 probes, 20 in U19495 1634-2204, Human intercrine-alpha (hIRH) mRNA, complete cds

X87843, class B, 20 probes, 15 in X87843cds 690-894: 5 in reverseSequence, 1045-1201, H.sapiens mRNA for cyclin H assembly factor

M54992, class A, 20 probes, 20 in M54992 924-1494, Human B cell differentiation antigen mRNA, complete cds

X06268, class C, 20 probes, 20 in all_X06268 1159-1337, Human mRNA for pro-alpha 1 (II) collagen 3 end C-term. triple helical and C-terminal non-helical domain

U10886, class A, 20 probes, 20 in U10886 4762-5068, Human density enhanced phosphatase-1 mRNA, complete cds

M88108, class A, 20 probes, 20 in M88108 2156-2636, Human p62 mRNA, complete cds

M19267, class A, 19 probes, 19 in M19267 1476-1600, Human tropomyosin mRNA, complete cds

L05187, class C, 20 probes, 20 in all_L05187 2284-2339, Homo sapiens small proline-rich protein 1 (SPRR1A) gene, complete cds

M34079, class A, 20 probes, 20 in M34079 830-1298, Human immunodeficiency virus tat transactivator binding protein-1 (tbp-1) mRNA, complete cds

D87716, class A, 20 probes, 20 in D87716 2447-2942, Human mRNA for KIAA0007 gene, partial cds

U28686, class A, 20 probes, 20 in U28686 973-1486, Human putative RNA binding protein RNPL mRNA, complete cds

X89267, class A, 20 probes, 20 in X89267exon#10 225-312, H.sapiens DNA for uroporphyrinogen decarboxylase gene. /gb=X89267 /ntype=DNA /annot=exon

Z33905, class A, 20 probes, 20 in Z33905mRNA 1190-1598, H.sapiens gene for 43kD acetylcholine receptor-associated protein (Rapsyn)

X70340, class C, 20 probes, 20 in all_X70340 3545-4062, H.sapiens mRNA for transforming growth factor alpha

M98447, class A, 20 probes, 20 in M98447mRNA 2256-2670, H.sapiens keratinocyte transglutaminase gene, complete cds

U82320, class A, 20 probes, 20 in U82320 546-1050, Human unknown protein mRNA, partial cds. /gb=U82320 /ntype=RNA

M60459, class A, 20 probes, 20 in M60459 1277-1745, Human erythropoietin receptor mRNA, complete cds

J00314, class A, 20 probes, 20 in J00314mRNA#1 4079-4173, Human beta-tubulin gene, clone m40

X02404, class C, 20 probes, 20 in all_X02404 227-750, Human mRNA fragment for second calcitonin gene related peptide (CGRP) from medullary thyroid carcinoma (MTC)

X76104, class B, 20 probes, 12 in X76104cds 4113-4257: 8 in reverseSequence, 4629-4827, H.sapiens DAP-kinase mRNA

Z34897, class A, 20 probes, 20 in Z34897 1138-1654, H.sapiens mRNA for H1 histamine receptor

M57423, class A, 20 probes, 20 in M57423 485-1016, Homo sapiens phosphoribosylpyrophosphate synthetase subunit III mRNA, 3 end.

U17969, class A, 20 probes, 20 in U17969exon#6 165-663, Human initiation factor eIF-5A gene, complete cds

M63138, class A, 20 probes, 20 in M63138mRNA 1545-2007, Human cathepsin D (catD) gene

J05459, class A, 20 probes, 20 in J05459mRNA 695-1187, Human glutathione transferase M3 (GSTM3) mRNA, complete cds

Immunoglobulin Heavy Chain, Vdjrc Regions (Gb:L23566)

D85425, class A, 20 probes, 20 in D85425 758-1328, Human mRNA for transactivator HSM-1, complete cds

S82471, class A, 20 probes, 20 in S82471 77-298, SSX3=Kruppel-associated box containing SSX gene [human, testis, mRNA Partial, 675 nt]. /gb=S82471 /ntype=RNA

U28833, class A, 20 probes, 20 in U28833 1571-2075, Human Down syndrome critical region protein (DSCR1) mRNA, complete cds

D00749, class A, 19 probes, 19 in D00749exon 346-525, Human T cell surface antigen CD7 gene

U29195, class A, 20 probes, 20 in U29195exon 927-1443, Human neuronal pentraxin II (NPTX2) gene

AF002020, class A, 20 probes, 20 in AF002020 4090-4600, Homo sapiens Niemann-Pick C disease protein (NPC1) mRNA, complete cds. /gb=AF002020 /ntype=RNA

M28213, class A, 20 probes, 20 in M28213 94-627, Homo sapiens GTP-binding protein (RAB2) mRNA, complete cds

X66362, class B, 20 probes, 14 in X66362cds 743-1097: 6 in reverseSequence, 1121-1217, H.sapiens mRNA PCTAIRE-3 for serine/threonine protein kinase

U63743, class A, 20 probes, 20 in U63743 2187-2715, Human mitotic centromere-associated kinesin mRNA, complete cds.

X71428, class A, 20 probes, 20 in X71428mRNA 1284-1788, H.sapiens fus mRNA

M54951, class A, 20 probes, 20 in M54951mRNA 438-852, Human atrial natriuretic factor gene

X98482, class C, 3 probes, 3 in all_X98482 45-72, H.sapiens TNNT2 gene exon 11 /gb=X98482 /ntype=DNA /annot=mRNA, H.sapiens TNNT2 gene exon 11 /gb=X98482 /ntype=DNA /annot=mRNA

U37431, class A, 20 probes, 20 in U37431mRNA#1 2114-2540, Human HOXA1 mRNA, long transcript and alternatively spliced forms, complete cds

D82060, class A, 20 probes, 20 in D82060 1801-2215, Human kidney mRNA for putative membrane protein with histidine rich charge clusters, complete cds

X57830, class C, 20 probes, 20 in all_X57830 2409-3016, H.sapiens serotonin 5-HT2 receptor mRNA

L19871, class A, 20 probes, 20 in L19871 1361-1793, Human activating transcription factor 3 (ATF3) mRNA, complete cds

M34192, class A, 20 probes, 20 in M34192mRNA 1406-1826, Human isovaleryl-coA dehydrogenase (IVD) mRNA, complete cds

L42542, class A, 20 probes, 20 in L42542mRNA 3353-3803, Human RLIP76 protein mRNA, complete cds

U38864, class A, 20 probes, 20 in U38864 1766-2186, Human zinc-finger protein C2H2-150 mRNA, complete cds

U39318, class A, 20 probes, 20 in U39318 159-675, Human E2 ubiquitin conjugating enzyme UbcH5C (UBCH5C) mRNA, complete cds

M30894, class A, 20 probes, 20 in M30894 1015-1513, Human T-cell receptor Ti rearranged gamma-chain mRNA V-J-C region, complete cds

X92972, class B, 20 probes, 14 in X92972cds 585-885: 6 in reverseSequence, 968-1148, H.sapiens mRNA for protein phosphatase 6

D63481, class A, 20 probes, 20 in D63481 4350-4890, Human mRNA for KIAA0147 gene, partial cds

U62317, class A, 20 probes, 20 in U62317mRNA#7 2016-2532, hypothetical protein 384D8_2 gene extracted from Chromosome 22q13 BAC Clone CIT987SK-384D8 complete sequence., hypothetical protein 384D8_2 gene extracted from Chromosome 22q13 BAC Clone CIT987SK-384D8 complete sequence., hypothetical protein 384D8_2 gene extracted from Chromosome 22q13 BAC Clone CIT987SK-384D8 complete sequence.

M97796, class A, 19 probes, 19 in M97796 88-595, Human helix-loop-helix protein (Id-2) mRNA, complete cds

X00237, class C, 20 probes, 20 in all_X00237 613-824, Human F variable segment 5 to antithrombin III gene (AT III)

L42324, class A, 20 probes, 20 in L42324cds 530-944, Homo sapiens (clone GPCR W) G protein-linked receptor gene (GPCR) gene, 5 end of cds. /gb=L42324 /ntype=DNA /annot=CDS

AC002115, class A, 20 probes, 16 in AC002115mRNA#2 3349-7559: 4 not in GB record, COX6B gene (COXG) extracted from Human DNA from overlapping chromosome 19 cosmids R31396, F25451, and R31076 containing COX6B and UPKA, genomic sequence, COX6B gene (COXG) extracted from Human DNA from overlapping chromosome 19 cosmids R31396, F25451, and R31076 containing COX6B and UPKA, genomic sequence, COX6B gene (COXG) extracted from Human DNA from overlapping chromosome 19 cosmids R31396, F25451, and R31076 containing COX6B and UPKA, genomic sequence, COX6B gene (COXG) extracted from Human DNA from overlapping chromosome 19 cosmids R31396, F25451, and R31076 containing COX6B and UPKA, genomic sequence

U82130, class A, 20 probes, 20 in U82130 1151-1451, Human tumor susceptiblity protein (TSG101) mRNA, complete cds

K03218, class B, 20 probes, 12 in K03218cds 1068-1587: 8 in reverseSequence, 197-230, Human c-src-1 proto-oncogene

U03105, class A, 20 probes, 20 in U03105 1538-1916, Human B4-2 protein mRNA, complete cds

X85785, class A, 20 probes, 20 in X85785mRNA 1060-1498, H.sapiens DARC gene

X01677, class B, 20 probes, 15 in X01677cds 629-983: 5 in reverseSequence, 1109-1229, Human liver mRNA for glyceraldehyde-3-phosphate dehydrogenase (G3PD, EC 1.2.1.12)

X98307, class A, 20 probes, 20 in X98307mRNA 13-355, H.sapiens mRNA for UV-B repressed sequence, HUR 7

U62961, class A, 20 probes, 20 in U62961 2749-3241, Human succinyl CoA:3-oxoacid CoA transferase precursor (OXCT) mRNA, complete cds

U59302, class A, 20 probes, 20 in U59302 4047-4617, Human steroid receptor coactivator-1 F-SRC-1 mRNA, complete cds

X82240, class A, 20 probes, 20 in X82240mRNA 723-1251, TCL1 gene (T cell leukemia) extracted from H.sapiens mRNA for Tcell leukemia/lymphoma 1

AB006781, class A, 20 probes, 20 in AB006781 528-1007, Homo sapiens mRNA for galectin-4, complete cds. /gb=AB006781 /ntype=RNA

Transglutaminase - Also Represents: U31905

M35128, class B, 20 probes, 11 in M35128cds 1044-1320: 9 in reverseSequence, 1936-2038, Human muscarinic acetylcholine receptor gene, complete cds

X69908, class A, 20 probes, 20 in X69908mRNA 151-721, P2 gene for c subunit of mitochondrial ATP synthase gene extracted from H.sapiens gene for mitochondrial ATP synthase c subunit (P2 form)

L41143, class A, 20 probes, 20 in L41143 1635-2085, Homo sapiens expressed pseudo TCTA mRNA at t(1;3) translocation site, complete cds.

AF000562, class A, 20 probes, 20 in AF000562 43-427, Homo sapiens uroplakin II mRNA, partial cds

Tyrosine Phosphatase 1, Non-Receptor, Alt. Splice 3 - Also Represents: HG3187-HT3365, U12128, HG3187-HT3364

M12125, class A, 20 probes, 20 in M12125mRNA 671-1013, Human fibroblast muscle-type tropomyosin mRNA, complete cds

U18088, class A, 18 probes, 18 in U18088 1188-1742, Human 3 ,5 -cyclic AMP phosphodiesterase inactive splice variant HSPDE4A8A mRNA, complete cds

Y07565, class B, 20 probes, 13 in Y07565cds 307-614: 7 in reverseSequence, 833-1024, H.sapiens mRNA for RIN protein

U05340, class A, 20 probes, 20 in U05340 1103-1571, Human p55CDC mRNA, complete cds

L22524, class B, 18 probes, 15 in L22524cds 462-734: 3 in reverseSequence, 46-197, Human matrilysin gene

U65785, class A, 20 probes, 20 in U65785 4028-4442, Human 150 kDa oxygen-regulated protein ORP150 mRNA, complete cds

D12775, class A, 20 probes, 20 in D12775 3124-3662, Human mRNA for erythrocyte-specific AMP deaminase, complete cds

X51985, class B, 20 probes, 15 in X51985cds 1083-1479: 5 in reverseSequence, 1787-1829, Human LAG-3 mRNA for CD4-related protein involved in lymphocyte activation

D87009, class B, 20 probes, 14 in D87009cds#5 1325-1565: 6 in fullSequence, 35519-35735, 5 OY11.1 gene extracted from Human (lambda) DNA for immunogloblin light chain

Antigen, Prostate Specific, Alt. Splice Form 3

Z48051, class A, 20 probes, 20 in Z48051mRNA 1733-2303, H.sapiens gene for myelin oligodendrocyte glycoprotein (MOG)

U85946, class A, 20 probes, 20 in U85946 2030-2288, Human brain secretory protein hSec10p (HSEC10) mRNA, complete cds

L26339, class A, 20 probes, 20 in L26339 4094-4580, Human autoantigen mRNA, complete cds

D42039, class A, 20 probes, 20 in D42039 3568-4074, Human mRNA for KIAA0081 gene, partial cds

X76534, class C, 20 probes, 20 in all_X76534 2145-2614, H.sapiens NMB mRNA

X54993, class C, 20 probes, 20 in all_X54993 1096-1685, H.sapiens TFIID mRNA

AB000449, class A, 20 probes, 20 in AB000449 1091-1607, Human mRNA for VRK1, complete cds

U37547, class A, 20 probes, 20 in U37547 2931-3477, Human IAP homolog B (MIHB) mRNA, complete cds

X13255, class C, 20 probes, 20 in all_X13255 2280-2725, Human mRNA for dopamine beta-hydroxylase type a (EC 1.14.17.1)

D13644, class A, 20 probes, 20 in D13644 4013-4523, Human mRNA for KIAA0019 gene, complete cds

U60269, class A, 20 probes, 20 in U60269cds#2 171-429, Human endogenous retrovirus HERV-K(HML6) proviral clone HML6.17 putative polymerase and envelope genes, partial cds, and 3LTR., Human endogenous retrovirus HERV-K(HML6) proviral clone HML6.17 putative polymerase and envelope genes, partial cds, and 3LTR., Human endogenous retrovirus HERV-K(HML6) proviral clone HML6.17 putative polymerase and envelope genes, partial cds, and 3LTR.

U27831, class B, 20 probes, 14 in U27831cds 1110-1578: 6 in reverseSequence, 1602-1680, Human striatum-enriched phosphatase (STEP) mRNA, partial cds

X16609, class C, 20 probes, 20 in all_X16609 6641-7241, Human mRNA for ankyrin (variant 2.1)

U83410, class A, 20 probes, 20 in U83410 2256-2772, Human CUL-2 (cul-2) mRNA, complete cds.

U85611, class A, 20 probes, 20 in U85611 385-919, Human DNA-PK interaction protein (KIP) mRNA, complete cds

X00274, class A, 20 probes, 16 in X00274exon#5 1-337: 4 not in GB record, Human gene for HLA-DR alpha heavy chain a class II antigen (immune response gene) of the major histocompatibility complex (MHC)

X56681, class A, 20 probes, 20 in X56681mRNA 1311-1835, Human junD mRNA

J03626, class A, 19 probes, 19 in J03626mRNA#1 1151-1653, UMPS gene extracted from Human UMP synthase mRNA, complete cds

U59919, class A, 20 probes, 20 in U59919 2047-2575, Human Smg GDS-associated protein SMAP mRNA, complete cds

D85131, class A, 20 probes, 20 in D85131 1126-1679, Human mRNA for Myc-associated zinc-finger protein of human islet, complete cds

L21934, class A, 20 probes, 20 in L21934 3401-3905, Human acyl coenzyme A:cholesterol acyltransferase mRNA, complete cds

L13210, class A, 20 probes, 20 in L13210 1668-2214, Human Mac-2 binding protein mRNA, complete cds

L14430, class C, 20 probes, 20 not in GB record, Human UDP-glucose pyrophosphorylase mRNA, complete cds and flanking regions

M33518, class A, 20 probes, 17 in M33518exon 5570-5900: 3 in reverseSequence, 6168-6198, Human HLA-B-associated transcript 2 (BAT2) gene, 5 flank

U15128, class B, 20 probes, 14 in U15128cds 1011-1299: 6 in reverseSequence, 2065-2233, Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds

AB003102, class A, 20 probes, 20 in AB003102 956-1442, Human mRNA for proteasome subunit p44.5, complete cds

J03260, class A, 20 probes, 20 in J03260mRNA 2076-2576, Human transducin alpha-subunit (GNAZ) mRNA, complete cds

L08835, class A, 20 probes, 20 in L08835mRNA#1 3166-3367, DM kinase gene (myotonic dystrophy kinase) extracted from Human myotonic dystrophy kinase (DM kinase) gene, complete cds

X60489, class A, 20 probes, 20 in X60489mRNA 381-915, Human mRNA for elongation factor-1-beta

L20814, class A, 20 probes, 20 in L20814 2826-3306, Human glutamate receptor 2 (HBGR2) mRNA, complete cds

M97675, class A, 20 probes, 20 in M97675 2799-3309, Human transmembrane receptor (ror1) mRNA, complete cds

M94065, class A, 20 probes, 20 in M94065 1051-1417, Human dihydroorotate dehydrogenase mRNA, 3 end

AF000959, class A, 20 probes, 20 in AF000959 759-1269, Homo sapiens transmembrane protein mRNA, complete cds.

Y07512, class A, 20 probes, 20 in Y07512 3211-3715, Human mRNA for type I beta cGMP-dependent protein kinase (EC 2.7.1.37)

U09550, class A, 20 probes, 20 in U09550 1597-2149, Human oviductal glycoprotein mRNA, complete cds

X92493, class A, 20 probes, 20 in X92493mRNA 2160-2672, H.sapiens mRNA for STM-7 protein

U33839, class C, 20 probes, 20 not in GB record, Human potassium channel mRNA, complete cds. /gb=U33839 /ntype=RNA

X69090, class A, 20 probes, 20 in X69090 4322-4880, H.sapiens mRNA for skeletal muscle 190kD protein

U53446, class A, 20 probes, 20 in U53446 2680-3220, Human mitogen-responsive phosphoprotein DOC-2 mRNA, complete cds

Major Histocompatibility Complex, Class I (Gb:X12432)

U23736, class A, 20 probes, 20 in U23736 779-1348, Human GATA-3 binding protein G3B mRNA, partial cds.

U76366, class A, 20 probes, 20 in U76366 4225-4720, Human Treacher Collins syndrome (TCOF1) mRNA, complete cds

L40399, class A, 20 probes, 20 in L40399mRNA 993-1467, Homo sapiens (clone S240ii117/zap112) mRNA, complete cds

D83017, class A, 20 probes, 20 in D83017 2365-2810, Human mRNA for nel-related protein, complete cds

M94345, class A, 20 probes, 20 in M94345 752-1160, Homo sapiens macrophage capping protein mRNA, complete cds

L21954, class A, 20 probes, 16 in L21954exon 36-384: 4 not in GB record, Human peripheral benzodiazepine receptor gene

U83192, class A, 20 probes, 20 in U83192 3401-3905, Human post-synaptic density protein 95 (PSD95) mRNA, complete cds

Y11306, class A, 20 probes, 20 in Y11306mRNA 1993-2395, hTcf-4 gene extracted from H.sapiens mRNA for beta catenin/TCF-4

M55671, class A, 20 probes, 20 in M55671mRNA 968-1448, Human protein Z (plus 66 bp insertion) mRNA, complete cds

S85655, class A, 20 probes, 20 in S85655 435-969, prohibitin [human, mRNA, 1043 nt]

U31342, class A, 20 probes, 20 in U31342mRNA 1173-1629, Human nucleobindin gene

D10511, class B, 20 probes, 15 in D10511cds 860-1256: 5 in reverseSequence, 165-243, Human gene for mitochondrial acetoacetyl-CoA thiolase

Nadh-Ubiquinone Oxidoreductase, 39 Kda Subunit

U31799, class C, 20 probes, 18 in all_U31799 528-683: 2 in U31799cds 1746-1777, Human melanocyte protein Pmel 17 gene

U49837, class A, 20 probes, 20 in U49837 684-1218, Human LIM protein MLP mRNA, complete cds

M31328, class A, 20 probes, 20 in M31328mRNA 1054-1480, Human guanine nucleotide-binding protein beta-3 subunit mRNA, complete cds

U09848, class A, 20 probes, 20 in U09848 2904-3474, Human zinc finger protein (ZNF139) mRNA, partial cds

D38251, class A, 20 probes, 20 in D38251 642-1149, Human mRNA for RPB5 (XAP4), complete cds

M74447, class A, 20 probes, 20 in M74447mRNA 2012-2510, Human PSF-2 mRNA, complete cds

Ahnak-Related Sequence
U09953, class A, 20 probes, 20 in U09953 153-621, Human ribosomal protein L9 mRNA, complete cds
X90908, class A, 20 probes, 20 in X90908cds 11-353, H.sapiens mRNA for I-15P (I-BABP) protein

M74509, class A, 20 probes, 20 in M74509 7730-8246, Human endogenous retrovirus type C oncovirus sequence.
M28130, class A, 20 probes, 20 in M28130mRNA 654-1002, Human interleukin 8 (IL8) gene, complete cds

L10386, class A, 20 probes, 20 in L10386 2036-2498, Homo sapiens transglutaminase E3 (TGASE3) mRNA, complete cds

U70439, class A, 20 probes, 20 in U70439 956-1407, Human silver-stainable protein SSP29 mRNA, complete cds
D31884, class A, 20 probes, 20 in D31884 2579-3023, Human mRNA for KIAA0063 gene, complete cds
M98399, class A, 18 probes, 18 in M98399 1688-2165, Human antigen CD36 (clone 21) mRNA, complete cds
U17714, class B, 20 probes, 13 in U17714 2774-3068: 7 not in GB record, Human putative tumor suppressor (SNC6) mRNA, complete cds
M60752, class C, 20 probes, 20 in all_M60752 611-863, Human histone H2A.1 (H2A) gene, complete cds

X72304, class C, 20 probes, 20 in all_X72304 1456-1688, H.sapiens mRNA for corticotrophin releasing factor receptor
X51466, class C, 20 probes, 20 in all_X51466 2702-3057, Human mRNA for elongation factor 2
U54999, class A, 20 probes, 20 in U54999 1795-2287, Human LGN protein mRNA, complete cds
M63582, class A, 20 probes, 20 in M63582mRNA 1062-1518, Human preprothyrotropin-releasing hormone gene
S76942, class A, 19 probes, 19 in S76942 5-311, dopamine D4 receptor {exon 1} [human, brain tumor tissue, mRNA Partial Mutant, 386 nt].
M21665, class A, 20 probes, 20 in M21665mRNA 1535-1621, Human beta-myosin heavy chain mRNA, 3 end

U67733, class A, 20 probes, 20 in U67733 3650-4178, Human cGMP-stimulated 3 ,5 -cyclic nucleotide phosphodiesterase PDE2A3 (PDE2A) mRNA, complete cds

U35376, class A, 20 probes, 20 in U35376 2006-2254, Human repressor transcriptional factor (ZNF85) mRNA, complete cds

U91903, class A, 20 probes, 20 in U91903 1323-1815, Human Fritz mRNA, complete cds

L76159, class A, 20 probes, 20 in L76159mRNA 471-957, Homo sapiens FRG1 mRNA, complete cds

X59131, class A, 20 probes, 17 in X59131 2735-3119: 3 not in GB record, H.sapiens D13S106 mRNA for a highly charged amino acid sequene

U50553, class A, 20 probes, 20 in U50553 2647-3079, Human helicase like protein 2 mRNA, complete cds

D86957, class A, 20 probes, 20 in D86957 3869-4265, Human mRNA for KIAA0202 gene, partial cds

U66615, class A, 20 probes, 20 in U66615 4601-5165, Human SWI/SNF complex 155 KDa subunit (BAF155) mRNA, complete cds

AF005775, class A, 20 probes, 20 in AF005775 275-755, Homo sapiens caspase-like apoptosis regulatory protein 2 (clarp) mRNA, alternatively spliced, complete cds. /gb=AF005775 /ntype=RNA

U52155, class A, 20 probes, 20 in U52155 1646-2168, Human ATP-dependent inwardly rectifying potassium channel Kir4.1 mRNA, complete cds

X54162, class A, 20 probes, 20 in X54162mRNA 3362-3818, Human mRNA for a 64 Kd autoantigen expressed in thyroid and extra-ocular muscle

D42084, class A, 20 probes, 20 in D42084 2112-2610, Human mRNA for KIAA0094 gene, partial cds

AB001106, class A, 20 probes, 20 in AB001106 3542-4088, Human mRNA for glia maturation factor, complete cds

Af-17

X76648, class C, 20 probes, 20 in all_X76648 338-777, H.sapiens mRNA for glutaredoxin

Y07759, class C, 20 probes, 20 in all_Y07759 5956-6377, H.sapiens mRNA for myosin heavy chain 12

X66839, class B, 20 probes, 15 in X66839cds 909-1335: 5 in reverseSequence, 1407-1491, H.sapiens MaTu MN mRNA for p54/58N protein

U30313, class A, 20 probes, 20 in U30313 372-756, Human diadenosine tetraphosphatase mRNA, complete cds. /gb=U30313 /ntype=RNA

M55621, class A, 20 probes, 20 in M55621 2074-2452, Human N-acetylglucosaminyltransferase I (GlcNAc-TI) mRNA, complete cds

X89576, class A, 20 probes, 20 in X89576 1772-2255, H.sapiens mRNA for putative MT4-MMP protein

D21063, class A, 20 probes, 20 in D21063 2853-3303, Human mRNA for KIAA0030 gene, partial cds

X15218, class C, 20 probes, 20 in all_X15218 3012-3511, Human ski oncogene mRNA

M28219, class A, 20 probes, 20 in M28219 7-253, Homo sapiens low density lipoprotein receptor (FH 10 mutant causing familial hypercholesterolemia) mRNA, 3 end.

X68277, class C, 20 probes, 20 in all_X68277 1459-1952, H.sapiens CL 100 mRNA for protein tyrosine phosphatase

D63479, class A, 20 probes, 20 in D63479 5529-6079, Human mRNA for KIAA0145 gene, complete cds

D82344, class A, 20 probes, 20 in D82344 2434-2986, Human mRNA for NBPhox, complete cds

Z35102, class C, 20 probes, 20 in all_Z35102 2543-3018, H.sapiens mRNA for Ndr protein kinase

S38742, class A, 20 probes, 20 in S38742 1370-1835, HOX11=HOX11 homeodomain {homeobox} [human, mRNA, 1988 nt]

X06614, class C, 20 probes, 20 in all_X06614 2300-2889, Human mRNA for receptor of retinoic acid

D17390, class A, 20 probes, 20 in D17390 2313-2829, Human mRNA for MDC protein

L38503, class A, 20 probes, 20 in L38503 531-993, Homo sapiens glutathione S-transferase theta 2 (GSTT2) mRNA, complete cds

U39657, class A, 20 probes, 20 in U39657 2341-2863, Human MAP kinase kinase 6 (MKK6) mRNA, complete cds

M62982, class A, 20 probes, 20 in M62982 1795-2299, Human arachidonate 12-lipoxygenase mRNA, complete cds

L47726, class A, 20 probes, 20 in L47726 2090-2552, Homo sapiens phenylalanine hydroxylase (PAH) mutant Q20stop mRNA

L15344, class A, 20 probes, 20 in L15344 1360-1768, Human high molecular weight B cell growth factor mRNA sequence

Clathrin, Light Polypeptide B, Alt. Splice 2 - Also Represents: X81637, HG2797-HT2905

M69238, class A, 20 probes, 20 in M69238 2033-2579, Human aryl hydrocarbon receptor nuclear translocator (ARNT) mRNA, complete cds

K03474, class B, 20 probes, 15 in K03474exon#5 562-829: 5 in reverseSequence, 2817-2919, Human Mullerian inhibiting substance gene, complete cds

M18737, class A, 20 probes, 20 in M18737mRNA 269-815, GJA1P1 gene extracted from Human Hanukah factor serine protease (HuHF) mRNA, complete cds

S72487, class A, 20 probes, 20 in S72487 1134-1582, orf1 5 to PD-ECGF/TP...orf2 5 to PD-ECGF/TP [human, epidermoid carcinoma cell line A431, mRNA, 3 genes, 1718 nt]

M13955, class A, 20 probes, 20 in M13955mRNA 904-1450, Human mesothelial keratin K7 (type II) mRNA, 3 end

U63139, class A, 20 probes, 20 in U63139 5305-5779, Human Rad50 (Rad50) mRNA, complete cds

Z48520, class A, 20 probes, 18 in Z48520exon#5 1-98: 2 in reverseSequence, 154-163, H.sapiens XG mRNA (clone RACE6). /gb=Z48520 /ntype=RNA

U60415, class A, 20 probes, 20 in U60415 2126-2570, Human bHLH-PAS protein JAP3 mRNA, complete cds.

U00954, class A, 20 probes, 20 in U00954 738-1224, Human clone CE29 7.2 (CAC)n/(GTG)n repeat-containing mRNA

X61615, class B, 20 probes, 13 in X61615cds 2830-3160: 7 in reverseSequence, 3482-3548, H.sapiens mRNA for leukemia inhibitory factor (LIF) receptor

L04282, class A, 20 probes, 20 in L04282 1873-2329, Human CACCC box-binding protein mRNA, complete cds

X80507, class B, 20 probes, 10 in X80507cds 1020-1314: 10 in reverseSequence, 1624-1828, H.sapiens YAP65 mRNA

U03270, class A, 20 probes, 20 in U03270 626-1136, Human centrin mRNA, complete cds

L34355, class A, 20 probes, 20 in L34355 827-961, Homo sapiens (clone p4) 50 kD dystrophin-associated glycoprotein mRNA, complete cds

M26665, class B, 14 probes, 14 in M26665 267-484, Human histatin 2 (HIS2) mRNA, complete cds, Human histatin 2 (HIS2) mRNA, complete cds

U14973, class A, 20 probes, 20 in U14973 13-235, Human ribosomal protein S29 mRNA, complete cds

U40705, class A, 20 probes, 20 in U40705 2127-2625, Homo sapiens telomeric repeat binding factor (TRF1) mRNA, complete cds

D90064, class A, 20 probes, 20 in D90064 1806-2184, Human CGM6 mRNA for CD66b (NCA-95)

X87344, class B, 15 probes, 15 in X87344mRNA#26 769-945, H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes., H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes. Major Histocompatibility Complex, Class I (Gb:L19693)

Z26491, class A, 20 probes, 20 in Z26491exon#5 388-430, H.sapiens gene for catechol O-methyltransferase

U86214, class A, 20 probes, 20 in U86214 1736-2000, Human Fas-associated death domain protein interleukin-1b-converting enzyme 2 mRNA, complete cds.

J03040, class A, 20 probes, 20 in J03040 1508-2000, Human SPARC/osteonectin mRNA, complete cds

M37033, class A, 20 probes, 20 in M37033 915-1395, Human CD53 glycoprotein mRNA, complete cds

L19527, class A, 20 probes, 20 in L19527 31-415, Homo sapiens ribosomal protein L27 (RPL27) mRNA, complete cds

U41635, class A, 20 probes, 20 in U41635 2207-2651, Human OS-9 precurosor mRNA, complete cds

U51678, class A, 20 probes, 20 in U51678 276-756, Human small acidic protein mRNA, complete cds

M80482, class A, 20 probes, 20 in M80482 3922-4324, Human subtilisin-like protein (PACE4) mRNA, complete cds

U09368, class A, 20 probes, 20 in U09368 1908-2298, Human zinc finger protein ZNF140

L04731, class A, 20 probes, 20 in L04731 13654-14152, Homo sapiens translocation T(4:11) of ALL-1 gene to chromosome 4

M13686, class A, 20 probes, 20 in M13686 388-897, Human pulmonary surfactant-associated protein mRNA, complete cds, clone MPSAP-6A

X96586, class C, 20 probes, 20 in all_X96586 2898-3343, H.sapiens mRNA for FAN protein

X65965, class A, 18 probes, 18 in X65965exon#1-2 32-94, H.sapiens SOD-2 gene for manganese superoxide dismutase. /gb=X65965 /ntype=DNA /annot=exon

D42038, class A, 20 probes, 20 in D42038 3730-4216, Human mRNA for KIAA0087 gene, complete cds

J02883, class A, 20 probes, 20 in J02883mRNA 55-493, Human colipase mRNA, complete cds

Guanine Nucleotide-Binding Protein G25k

U64444, class A, 20 probes, 20 in U64444 633-1113, Human ubiquitin fusion-degradation protein (UFD1L) mRNA, complete cds

M29971, class A, 20 probes, 20 in M29971 282-750, Human 6-O-methylguanine-DNA methyltransferase (MGMT) mRNA, complete cds

L14787, class A, 20 probes, 20 in L14787 1203-1641, Human DNA-binding protein mRNA, 3 end

D23662, class A, 20 probes, 20 in D23662 61-565, Human mRNA for ubiquitin-like protein, complete cds

L21715, class A, 20 probes, 20 in L21715 127-631, Homo sapiens troponin I fast-twitch isoform mRNA, complete cds

U37518, class A, 20 probes, 20 in U37518 1162-1390, Human TNF-related apoptosis inducing ligand TRAIL mRNA, complete cds

U82319, class A, 20 probes, 20 in U82319 470-980, Human clone YDD19 mRNA sequence

L76465, class A, 20 probes, 20 in L76465 1929-2493, Homo sapiens NAD+-dependent 15 hydroxyprostaglandin dehydrogenase (PGDH) mRNA, complete cds

X89960, class B, 20 probes, 10 in X89960cds 21-327: 10 in reverseSequence, 458-698, H.sapiens mRNA for mitochondrial capsule selenoprotein

U65437, class A, 20 probes, 20 in U65437mRNA 7-307, Human homeodomain-containing protein (HANF) gene, partial cds

L32976, class A, 20 probes, 20 in L32976 2969-3533, Human protein kinase (MLK-3) mRNA, complete cds

S75174, class A, 20 probes, 20 in S75174 1316-1511, E2F-4=transcription factor [human, Nalm6 and HeLa cells, mRNA, 1539 nt]

X07696, class C, 20 probes, 20 in all_X07696 1300-1685, Human mRNA for cytokeratin 15

D86973, class A, 20 probes, 20 in D86973 7230-7716, Human mRNA for KIAA0219 gene, partial cds

D87957, class A, 20 probes, 16 in D87957cds 549-825: 4 in reverseSequence, 1148-1256, Human male foreskin fibroblast DNA for protein involved in sexual development, complete cds

S75256, class A, 20 probes, 20 in S75256 32-446, HNL=neutrophil lipocalin [human, ovarian cancer cell line OC6, mRNA Partial, 534 nt]. /gb=S75256 /ntype=RNA

D79986, class A, 20 probes, 20 in D79986 4973-5513, Human mRNA for KIAA0164 gene, complete cds

D80001, class A, 20 probes, 20 in D80001 4465-4939, Human mRNA for KIAA0179 gene, partial cds

Crystallin, Beta B3 (Gb:X15145)

U50531, class A, 20 probes, 20 in U50531 4295-4847, Human BRCA2 region, mRNA sequence CG030

M62400, class A, 20 probes, 20 in M62400 1400-1928, Human gamma-aminobutyric acid receptor type A rho-1 subunit (GABA-A rho-1) mRNA, complete cds

X16665, class B, 20 probes, 13 in X16665cds 871-1039: 7 in reverseSequence, 1135-1369, Human HOX2H mRNA from the Hox2 locus

U09813, class A, 20 probes, 20 in U09813mRNA 225-765, Human mitochondrial ATP synthase subunit 9, P3 gene copy, mRNA, nuclear gene encoding mitochondrial protein, complete cds

M64231, class A, 20 probes, 20 in M64231mRNA 1264-1624, Human spermidine synthase gene, complete cds

D55640, class A, 20 probes, 20 in D55640 110-635, Human monocyte PABL (pseudoautosomal boundary-like sequence) mRNA, clone Mo2. /gb=D55640 /ntype=RNA

D13635, class A, 20 probes, 20 in D13635 4583-5117, Human mRNA for KIAA0010 gene, complete cds

X80907, class A, 20 probes, 20 in X80907 2095-2557, H.sapiens mRNA for p85 beta subunit of phosphatidyl-inositol-3-kinase

M11025, class A, 20 probes, 20 in M11025mRNA 783-1263, Human asialoglycoprotein receptor H2 mRNA, complete cds

Serine Hydroxymethyltransferase, Cytosolic, Alt. Splice 3 - Also Represents: L11931

U92458, class A, 20 probes, 20 in U92458 3747-4269, Human metabotropic glutamate receptor 7 mRNA, complete cds

Y11681, class C, 20 probes, 20 in all_Y11681 529-1040, Homo sapiens mRNA for mitochondrial ribosomal protein S12. /gb=Y11681 /ntype=RNA

M94880, class A, 40 probes, 40 in M94880 515-1055, Human MHC class I (HLA-A*8001) mRNA

S74445, class A, 20 probes, 20 in S74445 152-662, cellular retinoic acid-binding protein [human, skin, mRNA, 735 nt]

Z30643, class A, 20 probes, 20 in Z30643cds 1860-1921, H.sapiens mRNA for chloride channel (putative) 2139bp

J00209, class A, 20 probes, 20 in J00209mRNA 366-878, Human leukocyte interferon (ifn-alpha) alpha-c mRNA,complete cds

Calcitonin

U57057, class B, 20 probes, 14 in U57057cds 1239-1515: 6 in reverseSequence, 1871-2069, Human WD protein IR10 mRNA, complete cds

D64109, class A, 20 probes, 20 in D64109 642-1152, Human mRNA for tob family, complete cds

X70083, class A, 20 probes, 20 in X70083mRNA 166-460, H.sapiens ABP-280-like mRNA for filamin (695 bps). /gb=X70083 /ntype=RNA

Cpg-Enriched Dna, Clone S21

U64998, class A, 20 probes, 20 in U64998cds 61-361, Human ribonuclease k6 precursor gene, complete cds. /gb=U64998 /ntype=DNA /annot=CDS

Oncogene Tls/Chop, Fusion Activated

U19107, class C, 20 probes, 20 in all_U19107 3423-3658, Human ZNF127 (ZNF127) gene, complete cds

M20786, class A, 20 probes, 20 in M20786exon 630-1146, Human alpha-2-plasmin inhibitor gene

L03532, class A, 20 probes, 20 in L03532 1898-2372, Human M4 protein mRNA, complete cds

X75252, class C, 20 probes, 20 in all_X75252 1083-1408, H.sapiens phosphatidylethanolamine binding protein mRNA

D10326, class A, 20 probes, 20 in D10326 1427-1981, Human mRNA for pyruvate kinase

Cpg-Enriched Dna, Clone E04

L34059, class A, 20 probes, 20 in L34059 2447-3017, Homo sapiens cadherin-4 mRNA, complete cds

M64716, class A, 20 probes, 20 in M64716mRNA 31-451, Human ribosomal protein S25 mRNA, complete cds

Z74792, class A, 20 probes, 20 in Z74792mRNA 1470-1917, H.sapiens mRNA for CCAAT transcription binding factor subunit gamma.

J03930, class A, 20 probes, 20 in J03930exon#11 638-1118, Human intestinal alkaline phosphatase (ALPI) gene, complete cds

X99141, class C, 20 probes, 20 in all_X99141 1411-1715, H.sapiens mRNA for hair keratin, hHb3

L08246, class A, 20 probes, 20 in L08246 3333-3819, Human myeloid cell differentiation protein (MCL1) mRNA

D87436, class A, 20 probes, 20 in D87436 5660-6116, Human mRNA for KIAA0249 gene, complete cds

J03474, class A, 20 probes, 20 in J03474cds 3-255, Human serum amyloid A gene, complete cds

Zinc Finger Protein Znf81 (Gb:X0729)

L42572, class A, 20 probes, 20 in L42572mRNA 2192-2648, Homo sapiens p87/89 gene, complete cds

X70683, class C, 20 probes, 20 in all_X70683 2322-2752, H.sapiens mRNA for SOX-4 protein

M13194, class A, 20 probes, 20 in M13194mRNA 586-1006, Human excision repair protein (ERCC1) mRNA, complete cds, clone pcDE

D87435, class A, 20 probes, 20 in D87435 5153-5591, Human mRNA for KIAA0248 gene, partial cds

U60800, class A, 20 probes, 20 in U60800 3638-4010, Human semaphorin (CD100) mRNA, complete cds

U52111, class A, 20 probes, 20 in U52111mRNA#3 2176-2659, Homo sapiens Xq28 genomic DNA in the region of the ALD locus containing the genes for creatine transporter (SLC6A8), CDM, adrenoleukodystrophy (ALD), Na+-isocitrate dehydrogenase gamma subunit (IDH), and translocon-associated protein delta (TRAP) genes, complete cds, plexin related protein (PLEXR) and serine kinase (SK) genes, partial cds, Xq28lu1 gene and cytochrome C (CCp) pseudogene., Homo sapiens Xq28 genomic DNA in the region of the ALD locus containing the genes for creatine transporter (SLC6A8), CDM, adrenoleukodystrophy (ALD), Na+-isocitrate dehydrogenase gamma subunit (IDH), and translocon-associated protein delta (TRAP) genes, complete cds, plexin related protein (PLEXR) and serine kinase (SK) genes, partial cds, Xq28lu1 gene and cytochrome C (CCp) pseudogene.

U70663, class A, 20 probes, 20 in U70663 1532-1928, Human zinc finger transcription factor hEZF (EZF) mRNA, complete cds

M95178, class A, 20 probes, 20 in M95178 2567-2996, Human non-muscle alpha-actinin mRNA, complete cds

X16667, class C, 20 probes, 20 in all_X16667 1634-1917, Human HOX2G mRNA from the Hox2 locus

U68233, class A, 20 probes, 20 in U68233 1565-2063, Human farnesol receptor HRR-1 (HRR-1) mRNA, complete cds

L11373, class A, 20 probes, 20 in L11373 4183-4609, Human protocadherin 43 mRNA, complete cds for abbreviated PC43

U73167, class B, 20 probes, 14 in U73167cds#4 1050-1254: 5 in reverseSequence, 13521-13767: 1 not in GB record, H_LUCA14.2a gene extracted from Human cosmid LUCA14, H_LUCA14.2a gene extracted from Human cosmid LUCA14, H_LUCA14.2a gene extracted from Human cosmid LUCA14, H_LUCA14.2a gene extracted from Human cosmid LUCA14, H_LUCA14.2a gene extracted from Human cosmid LUCA14

L05144, class A, 20 probes, 20 in L05144 2488-2598, Homo sapiens (clone lamda-hPEC-3) phosphoenolpyruvate carboxykinase (PCK1) mRNA, complete cds

M62486, class B, 20 probes, 15 in M62486exon 17-359: 5 not in GB record, Human C4b-binding protein gene

D38081, class A, 20 probes, 20 in D38081 2769-2853, Human mRNA for thromboxane A2 receptor, complete cds

L19058, class A, 20 probes, 20 in L19058 2599-3163, Human glutamate receptor (GLUR5) mRNA, complete cds

M26880, class A, 20 probes, 20 in M26880 2206-2246, Human ubiquitin mRNA, complete cds

K02405, class C, 20 probes, 19 in all_K02405 5550-7761: 1 in K02405cds 778, Human MHC class II HLA-DC-3-beta gene (DR3,3)

U33880, class A, 16 probes, 16 in U33880mRNA 189-240, Human beta 1 integrin isoform D (ITGB1) gene, partial cds. /gb=U33880 /ntype=DNA /annot=exon

Y09943, class A, 20 probes, 17 in Y09943cds 117-452: 3 in reverseSequence, 561-602, H.sapiens mRNA for NGF-inducible PC3 anti-proliferative protein

M10943, class C, 20 probes, 20 in all_M10943 444-1929, Human metallothionein-If gene (hMT-If)

Immunoglobulin Heavy Chain, Vdjc Regions (Gb:L23565)

D31886, class A, 20 probes, 20 in D31886 3076-3592, Human mRNA for KIAA0066 gene, partial cds

M74826, class A, 20 probes, 20 in M74826 1928-2396, Human glutamate decarboxylase (GAD-2) mRNA, complete cds

D89050, class A, 20 probes, 20 in D89050 691-1219, Human mRNA for lectin-like oxidized LDL receptor, complete cds

M26657, class A, 20 probes, 20 in M26657 1861-2430, Human testicular angiotensin converting enzyme mRNA, complete cds

D80003, class A, 20 probes, 20 in D80003 6029-6395, Human mRNA for KIAA0181 gene, partial cds

M21121, class A, 20 probes, 20 in M21121 958-1129, Human T cell-specific protein (RANTES) mRNA, complete cds

J03909, class A, 20 probes, 20 in J03909 461-995, Human gamma-interferon-inducible protein (IP-30) mRNA, complete cds

M74524, class A, 20 probes, 20 in M74524 1190-1658, Human HHR6A (yeast RAD 6 homologue) mRNA, complete cds

Z18951, class A, 20 probes, 16 in Z18951cds 311-509: 4 in reverseSequence, 627-813, H.sapiens mRNA for caveolin

X63454, class B, 20 probes, 15 in X63454cds 327-567: 5 in reverseSequence, 659-719, H.sapiens hst-2 (FGF-6) mRNA

U26266, class A, 19 probes, 19 in U26266 490-1046, Human deoxyhypusine synthase mRNA, complete cds. /gb=U26266 /ntype=RNA

U18018, class A, 20 probes, 20 in U18018 1732-2290, Human E1A enhancer binding protein (E1A-F) mRNA, partial cds

Major Histocompatibility Complex, Class Ii, Dr Beta 2 (Gb:X65561)

U07550, class A, 20 probes, 20 in U07550 139-493, Human chaperonin 10 mRNA, complete cds

X96506, class A, 20 probes, 18 in X96506cds 96-441: 2 in reverseSequence, 600-631, H.sapiens mRNA for NC2 alpha subunit

U22680, class A, 20 probes, 20 in U22680 6048-6558, Human X2 box repressor mRNA, complete cds

D86956, class A, 20 probes, 20 in D86956 3139-3589, Human mRNA for KIAA0201 gene, complete cds

M80397, class A, 20 probes, 20 in M80397 2847-3368, Human DNA polymerase delta catalytic subunit mRNA, complete cds

M16961, class A, 20 probes, 20 in M16961 937-1477, Human alpha-2-HS-glycoprotein alpha and beta chain mRNA, complete cds

Z80345, class A, 20 probes, 20 in Z80345mRNA 4931-5457, H.sapiens SCAD gene, 5 UTR exon 1 and 2 (and joined CDS).

U67963, class A, 20 probes, 20 in U67963 590-1148, Human lysophospholipase homolog (HU-K5) mRNA, complete cds

U44378, class A, 20 probes, 20 in U44378 2091-2655, Human homozygous deletion target in pancreatic carcinoma (DPC4) mRNA, complete cds

Z15108, class C, 20 probes, 20 in all_Z15108 1535-2130, H.sapiens mRNA for protein kinase C zeta

X62025, class A, 20 probes, 20 in X62025mRNA 877-1180, H.sapiens rod cG-PDE G gene for 3 , 5 -cyclic nucleotide phosphodiesterase

U43916, class A, 20 probes, 20 in U43916 147-698, Human tumor-associated membrane protein homolog (TMP) mRNA, complete cds

X13810, class C, 20 probes, 20 in all_X13810 1940-1986, Human OTF-2 mRNA for lymphoid-specific transcription factor

Phosphatidylinositol 3-Kinase P110, Beta Isoform

M16801, class A, 20 probes, 20 in M16801mRNA 5250-5724, Human mineralocorticoid receptor mRNA (hMR), complete cds

B-Cell Growth Factor 1

U09587, class A, 20 probes, 20 in U09587 2261-2330, Human glycyl-tRNA synthetase mRNA, complete cds.

U39487, class A, 20 probes, 20 in U39487 3877-4339, Human xanthine dehydrogenase/oxidase mRNA, complete cds

L36051, class A, 20 probes, 20 in L36051exon#6 678-1086, Human thrombopoietin gene, complete cds

X14362, class C, 20 probes, 20 in all_X14362 1961-2370, Human CR1 mRNA for C3b/C4b receptor secreted form

M59911, class A, 20 probes, 20 in M59911 4048-4612, Human integrin alpha-3 chain mRNA, complete cds

X98225, class A, 20 probes, 20 in X98225cds 31-331, H.sapiens mRNA for gastrin-binding protein. /gb=X98225 /ntype=RNA

Z54367, class A, 20 probes, 19 in Z54367cds 13580-14031: 1 in reverseSequence, 14140, H.sapiens gene for plectin

U51586, class A, 20 probes, 20 in U51586 1262-1676, Human siah binding protein 1 (SiahBP1) mRNA, partial cds.

U09303, class A, 20 probes, 20 in U09303 2354-2870, Human T cell leukemia LERK-2 (EPLG2) mRNA, complete cds

L37868, class C, 20 probes, 20 in all_L37868 3521-4088, Homo sapiens POU-domain transcription factor (N-Oct-3), complete cds

L13939, class A, 20 probes, 20 in L13939 3297-3791, Human beta adaptin protein mRNA, complete cds

Surfacant Protein Sp-A1 Delta - Also Represents: M30838

U34976, class A, 20 probes, 20 in U34976 1059-1575, Human gamma-sarcoglycan mRNA, complete cds

U29725, class A, 20 probes, 20 in U29725 2517-2937, Human BMK1 alpha kinase mRNA, complete cds

U71601, class A, 20 probes, 20 in U71601 960-1422, Human zinc finger protein zfp47 (zf47) mRNA, partial cds

Y07829, class A, 20 probes, 20 in Y07829exon#2 13-364, exon from H.sapiens gene encoding RING finger protein. /gb=Y07829 /ntype=DNA /annot=exon, exon from H.sapiens gene encoding RING finger protein. /gb=Y07829 /ntype=DNA /annot=exon

U33936, class A, 20 probes, 20 in U33936 578-1050, Human adenosine kinase mRNA, complete cds. /gb=U33936 /ntype=RNA

Z29481, class B, 20 probes, 10 in Z29481cds 624-792: 10 in reverseSequence, 898-1186, H.sapiens mRNA for 3-hydroxyanthranilic acid dioxygenase

D42041, class A, 20 probes, 20 in D42041 3435-3771, Human mRNA for KIAA0088 gene, partial cds

Calmitine Calcium-Binding Protein, Mitochondrial

Z48570, class C, 20 probes, 20 in all_Z48570 1408-1991, H.sapiens Sp17 gene

M30185, class A, 20 probes, 20 in M30185mRNA 1234-1666, Human cholesteryl ester transfer protein mRNA, complete cds

D88532, class A, 20 probes, 20 in D88532 3016-3328, Human mRNA for p55pik, complete cds

U30521, class A, 20 probes, 20 in U30521 1621-1951, Human P311 HUM -3.1 mRNA, complete cds

L41147, class A, 20 probes, 20 in L41147mRNA 1383-1959, Homo sapiens 5-HT6 serotonin receptor mRNA, complete cds

X57766, class A, 20 probes, 20 in X57766mRNA 1658-2168, Human stromelysin-3 mRNA

M60094, class A, 20 probes, 20 in M60094mRNA 196-640, Human testicular H1 histone (H1) gene, complete cds

Z50194, class B, 20 probes, 15 in Z50194cds 664-856: 5 in reverseSequence, 1345-1372, H.sapiens mRNA for PQ-rich protein

M26167, class A, 20 probes, 20 in M26167mRNA 385-730, Human platelet factor 4 varation 1 (PF4var1) gene, complete cds

Surfacant Protein Sp-A2 Delta - Also Represents: M30838, M68519_rna1, HG3928-HT4198, M13686

D78156, class B, 20 probes, 12 in D78156cds 888-1140: 8 in reverseSequence, 2058-2292, Human mRNA for rasGTPase activating protein, partial cds

U38372, class A, 20 probes, 20 in U38372 13-331, Human huntingtin associated protein (hHAP1) mRNA, partial cds.

X84003, class A, 20 probes, 17 in X84003cds 140-305: 3 in reverseSequence, 373-379, H.sapiens TAFII18 mRNA for transcription factor TFIID

Z14982, class A, 20 probes, 20 in Z14982mRNA#1 616-1150, MHC-encoded proteasome subunit gene LAMP7-E1 gene (proteasome subunit LMP7) extracted from H.sapiens gene for major histocompatibility complex encoded proteasome subunit LMP7

U46023, class A, 20 probes, 20 in U46023 4040-4544, Human Xq28 mRNA, complete cds

M14636, class A, 20 probes, 20 in M14636 2317-2665, Human liver glycogen phosphorylase mRNA, complete cds

S83366, class C, 20 probes, 20 in all_S83366 910-2840, region centromeric to t(12;17) brakepoint: orf1/unknown 43 amino acid transcript...orf3/unknown 50 amino acid transcript [human, testis, acampomelic campomelic dysplasia and sex reversal patient, Genomic, 3 genes, 3414 nt]., region centromeric to t(12;17) brakepoint: orf1/unknown 43 amino acid transcript...orf3/unknown 50 amino acid transcript [human, testis, acampomelic campomelic dysplasia and sex reversal patient, Genomic, 3 genes, 3414 nt].

U52827, class A, 20 probes, 20 in U52827 1022-1508, Human Cri-du-chat region mRNA, clone NIBB11

U85943, class A, 20 probes, 20 in U85943 1527-1680, Human mRNA-associated protein mrnp41 mRNA, complete cds. /gb=U85943 /ntype=RNA

D86976, class A, 20 probes, 20 in D86976 3592-4060, Human mRNA for KIAA0223 gene, partial cds

L38969, class A, 20 probes, 17 in L38969cds 2517-2835: 3 in reverseSequence, 2946-2964, Homo sapiens thrombospondin 3 (THBS3) gene, complete cds

X15673, class A, 20 probes, 20 in X15673mRNA 623-1121, Human pTR2 mRNA for repetitive sequence. /gb=X15673 /ntype=RNA

U68566, class A, 20 probes, 20 in U68566 638-1124, Human HS1 binding protein HAX-1 mRNA, nuclear gene encoding mitochondrial protein, complete cds

X72012, class C, 20 probes, 20 in all_X72012 2495-3060, H.sapiens end mRNA for endoglin

D86425, class A, 20 probes, 20 in D86425 4224-4776, Human osteoblast mRNA for osteonidogen, complete cds

X72882, class B, 20 probes, 14 in X72882cds 19-103: 6 in reverseSequence, 144-186, H.sapiens 14A6CK DNA sequence

X12671, class A, 20 probes, 20 in X12671mRNA 1450-1726, hnrnp a1 protein gene extracted from Human gene for heterogeneous nuclear ribonucleoprotein (hnRNP) core protein A1

M24900, class C, 20 probes, 20 in all_M24900 1501-2054, Human triiodothyronine recptor (THRA1, ear1), and ear2 genes, last 2 exons each

Z15005, class B, 20 probes, 11 in Z15005cds 7614-7968: 9 in reverseSequence, 8076-8184, H.sapiens CENP-E mRNA

M77698, class A, 20 probes, 20 in M77698 1764-2310, Homo sapiens GLI-Krupple related protein (YY1) mRNA, complete cds

D83195, class A, 20 probes, 18 in D83195cds 448-802: 2 in reverseSequence, 3957-3963, Human DNASE1 gene for deoxyribonuclease I, complete cds

Ryanodine Receptor 3

U50383, class A, 20 probes, 20 in U50383 2015-2441, Human retinoic acid-responsive protein (NN8-4AG) mRNA, complete cds

M60746, class C, 20 probes, 20 in all_M60746 531-844, Human histone H3.1 (H1F3) gene, complete cds

U49928, class A, 20 probes, 20 in U49928 2513-3035, Human TAK1 binding protein 1 (TAB1) mRNA, complete cds

L34587, class A, 20 probes, 20 in L34587 109-403, Homo sapiens RNA polymerase II elongation factor SIII, p15 subunit mRNA, complete cds

U93205, class A, 20 probes, 20 in U93205 588-1020, Human nuclear chloride ion channel protein (NCC27) mRNA, complete cds

X60486, class C, 20 probes, 20 in all_X60486 394-737, H.sapiens H4/g gene for H4 histone

L31801, class A, 20 probes, 20 in L31801 2229-2535, Homo sapiens monocarboxylate transporter 1 (SLC16A1) mRNA, complete cds

Z46629, class A, 20 probes, 20 in Z46629mRNA 3352-3730, Homo sapiens SOX9 mRNA

U63542, class A, 20 probes, 20 in U63542 303-750, Human putative FAP protein mRNA, partial cds

U13219, class A, 20 probes, 20 in U13219 1945-2473, Human forkhead protein FREAC-1 mRNA, complete cds

D38548, class A, 20 probes, 20 in D38548 4682-5210, Human mRNA for KIAA0076 gene, complete cds

M63967, class A, 20 probes, 20 in M63967exon#2 1319-1625, Human mitochondrial aldehyde dehydrogenase x gene, complete cds

U13044, class A, 20 probes, 20 in U13044 1429-1945, Human nuclear respiratory factor-2 subunit alpha mRNA, complete cds

Z70276, class A, 20 probes, 20 in Z70276cds 2-294, H.sapiens mRNA for fibroblast growth factor 12 (partial).

U59748, class A, 20 probes, 20 in U59748 28-187, Human desert hedgehog (hDHH) mRNA, partial cds. /gb=U59748 /ntype=RNA

K02215, class A, 20 probes, 20 in K02215mRNA#2 1510-2026, Human angiotensinogen mRNA, complete CDS

U49250, class A, 20 probes, 20 in U49250 2323-2851, Human putative cerebral cortex transcriptional regulator T-Brain-1 (Tbr-1) mRNA, complete cds

S67798, class A, 20 probes, 20 in S67798 1420-1930, PH-20 [human, testis, mRNA, 1973 nt]

J05243, class A, 20 probes, 20 in J05243 7216-7732, Human nonerythroid alpha-spectrin (SPTAN1) mRNA, complete cds

D87969, class A, 20 probes, 20 in D87969 1206-1686, Human mRNA for CMP-sialic acid transporter, complete cds

Cystatin D

J04615, class A, 20 probes, 20 in J04615mRNA 833-1265, Human lupus autoantigen (small nuclear ribonuclepoprotein, snRNP, SM-D) mRNA, complete cds

X66403, class C, 20 probes, 20 in all_X66403 1856-2301, H.sapiens mRNA for acetylcholine receptor (epsilon subunit)

U35139, class A, 20 probes, 20 in U35139 1111-1507, Human NECDIN related protein mRNA, complete cds

S68271, class A, 20 probes, 20 in S68271 891-1191, CREM=cyclic AMP-responsive element modulator [human, mRNA, 1431 nt]

X90392, class C, 20 probes, 20 in all_X90392 2058-2545, H.sapiens mRNA for DNase X gene

M81601, class A, 20 probes, 20 in M81601 2039-2483, Human transcription elongation factor (SII) mRNA, complete cds

Y08976, class C, 20 probes, 20 in all_Y08976 956-1548, H.sapiens mRNA for FEV protein

M55150, class A, 20 probes, 20 in M55150mRNA 978-1422, Human fumarylacetoacetate hydrolase mRNA, complete cds

X77094, class B, 20 probes, 14 in X77094cds 634-994: 6 in reverseSequence, 1136-1214, H.sapiens mRNA for p40phox

AJ001487, class A, 20 probes, 20 in AJ001487 25-265, Homo sapiens mRNA for transformation-sensitive protein, 3 UTR. /gb=AJ001487 /ntype=RNA

U17886, class A, 20 probes, 20 in U17886mRNA 507-981, Human succinate dehydrogenase iron-protein subunit (sdhB) gene

M91029, class A, 20 probes, 20 in M91029exon#3 2581-2977, Human AMP deaminase (AMPD2) mRNA

X61587, class A, 20 probes, 20 in X61587mRNA 701-1259, H.sapiens rhoG mRNA for GTPase

X12876, class A, 20 probes, 20 in X12876mRNA 144-670, Human mRNA fragment for cytokeratin 18.

L20298, class A, 20 probes, 20 in L20298 2250-2790, Homo sapiens transcription factor (CBFB) mRNA, 3 end

X51435, class C, 20 probes, 20 in all_X51435 8408-8982, Human PRDII-BF1 gene for a DNA-binding protein

D37931, class A, 20 probes, 20 in D37931 395-911, Human mRNA for RNase 4, complete cds

U17743, class A, 20 probes, 20 in U17743 699-1221, Human JNK activating kinase (JNKK1) mRNA, complete cds

X66363, class B, 20 probes, 13 in X66363cds 1279-1459: 7 in reverseSequence, 1594-1702, H.sapiens mRNA PCTAIRE-1 for serine/threonine protein kinase

M63959, class A, 20 probes, 20 in M63959 1030-1444, Human alpha-2-macroglobulin receptor-associated protein mRNA, complete cds

L42379, class A, 20 probes, 20 in L42379mRNA 2645-3155, Homo sapiens bone-derived growth factor (BPGF-1) mRNA, complete cds

U38276, class A, 20 probes, 20 in U38276 2969-3509, Human semaphorin III family homolog mRNA, complete cds

U13913, class A, 20 probes, 20 in U13913 3871-4120, Human large-conductance calcium-activated potassium channel (hSlo) mRNA, complete cds

X60957, class B, 20 probes, 10 in X60957cds 3066-3378: 10 in reverseSequence, 3432-3678, Human tie mRNA for putative receptor tyrosine kinase

U45328, class A, 20 probes, 20 in U45328 591-1079, Human ubiquitin-conjugating enzyme (UBE2I) mRNA, complete cds

AB000466, class A, 20 probes, 20 in AB000466 2465-2963, Human mRNA, clone RES4-24C, exon 1, 2, 3

X52773, class C, 20 probes, 20 in all_X52773 1343-1866, Human mRNA for retinoic acid receptor-like protein

L38517, class A, 20 probes, 20 in L38517mRNA 766-1228, Homo sapiens indian hedgehog protein (IHH) mRNA, 5 end

U40282, class A, 20 probes, 20 in U40282 1205-1706, Human integrin-linked kinase (ILK) mRNA, complete cds

Glutamate Receptor Subunit

X17360, class A, 20 probes, 20 in X17360mRNA 4536-5034, Human HOX 5.1 gene for HOX 5.1 protein

U48296, class A, 20 probes, 20 in U48296 1629-2175, Human protein tyrosine phosphatase PTPCAAX1 (hPTPCAAX1) mRNA, complete cds

X86809, class C, 20 probes, 20 in all_X86809 1916-2367, H.sapiens mRNA for major astrocytic phosphoprotein PEA-15

M76180, class A, 20 probes, 20 in M76180 1461-1887, Human aromatic amino acid decarboxylase (ddc) mRNA, complete cds

U00947, class A, 20 probes, 20 in U00947 1301-1347, Human clone C4E 3.2 (CAC)n/(GTG)n repeat-containing mRNA

U31215, class A, 20 probes, 20 in U31215 3797-4037, Human metabotropic glutamate receptor 1 alpha (mGluR1alpha) mRNA, complete cds

X78687, class A, 20 probes, 20 in X78687exon#6 172-670, H.sapiens G9 gene encoding sialidase

S83364, class A, 20 probes, 20 in S83364 19-325, putative Rab5-interacting protein {clone L1-57} [human, HeLa cells, mRNA Partial, 366 nt]. /gb=S83364 /ntype=RNA

U90908, class A, 20 probes, 20 in U90908 1268-1784, Human clones 23549 and 23762 mRNA, complete cds

U04270, class A, 20 probes, 20 in U04270 3505-3973, Human putative potassium channel subunit (h-erg) mRNA, complete cds

X60592, class A, 20 probes, 20 in X60592mRNA 415-973, Human CDw40 mRNA for nerve growth factor receptor-related B-lymphocyte activation molecule

X72475, class A, 20 probes, 20 in X72475cds 111-343, H.sapiens mRNA for rearranged Ig kappa light chain variable region (I.114)

U59736, class A, 20 probes, 20 in U59736 2496-2772, Human transcription factor (NFATc.b) mRNA, complete cds

M64595, class A, 20 probes, 20 in M64595mRNA 216-648, Human small G protein (Gx) mRNA, 3 end

U66559, class A, 20 probes, 20 in U66559 4812-5244, Human anaplastic lymphoma kinase receptor mRNA, complete cds

U22398, class A, 20 probes, 20 in U22398 1030-1468, Human Cdk-inhibitor p57KIP2 (KIP2) mRNA, complete cds

U73330, class A, 20 probes, 20 in U73330exon 13-77, Human PAC 85D2, complete sequence. /gb=U73330 /ntype=DNA /annot=exon

M68519, class A, 20 probes, 20 in M68519mRNA 1542-1916, Human pulmonary surfactant-associated protein SP-A (SFTP1) gene, complete cds

U96781, class A, 20 probes, 20 in U96781mRNA#1 2433-2961, ATP2A1 gene (Ca2+ ATPase of fast-twitch skeletal muscle sacroplasmic reticulum, neonatal isoform) extracted from Human Ca2+ ATPase of fast-twitch skeletal muscle sarcoplasmic reticulum adult and neonatal isoforms (ATP2A1) gene

D87449, class A, 20 probes, 20 in D87449 5359-5785, Human mRNA for KIAA0260 gene, partial cds

Glutamate Ionotropic Receptor 1

M62397, class A, 20 probes, 20 in M62397 3586-4126, Human colorectal mutant cancer protein mRNA, complete cds

M68891, class A, 20 probes, 20 in M68891 2398-2686, Human GATA-binding protein (GATA2) mRNA, complete cds

X71129, class A, 20 probes, 20 in X71129cds 213-705, H.sapiens mRNA for electron transfer flavoprotein beta subunit

M99436, class A, 20 probes, 20 in M99436 1808-2246, Human transducin-like enhancer protein (TLE2) mRNA, complete cds

M24398, class A, 20 probes, 20 in M24398mRNA 522-970, Human parathymosin mRNA, complete cds

D45132, class A, 20 probes, 20 in D45132 5577-6099, Human kidney mRNA for zinc-finger DNA-binding protein, complete cds

U65402, class B, 20 probes, 14 in U65402cds 651-915: 6 in reverseSequence, 1437-1647, Human seven transmembrane G-coupled receptor (GPR31) gene, complete cds.

Fibroblast Growth Factor, Antisense Mrna

U13022, class A, 20 probes, 20 in U13022 1572-2124, Human negative regulator of programmed cell death ICH-1S (Ich-1) mRNA, complete cds

Y12393, class A, 20 probes, 20 in Y12393 346-819, H.sapiens mRNA for SRP1-like protein, partial

U95006, class A, 20 probes, 20 in U95006 114-654, Human D9 splice variant A mRNA, complete cds.

L22009, class A, 20 probes, 20 in L22009 1642-2056, Human hnRNP H mRNA, complete cds

U40152, class A, 20 probes, 20 in U40152 2541-3103, Human origin recognition complex 1 (HsORC1) mRNA, complete cds

M17885, class A, 20 probes, 20 in M17885mRNA 532-946, Human acidic ribosomal phosphoprotein P0 mRNA, complete cds

X65463, class C, 20 probes, 20 in all_X65463 1187-1734, H.sapiens mRNA for MHC class I promoter binding protein

X94754, class A, 20 probes, 18 in X94754cds 2213-2645: 2 in reverseSequence, 2712-2730, H.sapiens mRNA for yeast methionyl-tRNA synthetase homologue

D83777, class A, 20 probes, 20 in D83777 4475-5003, Human mRNA for KIAA0193 gene, complete cds

Thrombospondin 2 (Gb:L07803)

U14417, class A, 20 probes, 20 in U14417 567-1017, Human Ral guanine nucleotide dissociation stimulator mRNA, partial cds

L22075, class A, 20 probes, 20 in L22075 795-1377, Human guanine nucleotide regulatory protein (G13) mRNA, complete cds

M28882, class A, 17 probes, 17 in M28882 2907-3186, Human MUC18 glycoprotein mRNA, complete cds

U41745, class A, 20 probes, 20 in U41745 296-794, Human PDGF associated protein mRNA, complete cds

B. subtilis /GEN=pheA /DB_XREF=gb:M24537.1 /NOTE=SIF corresponding to nucleotides 2437-2828 of gb:M24537.1 /DEF=Bacillus subtillis sporulation protein (spoOB), GTP-binding protein (obg), phenylalanine biosynthesis associated protein (pheB), and monofunctional prephenate dehydratase (pheA) genes, complete cds.

J04152, class A, 20 probes, 20 in J04152mRNA 1181-1648, M1S1 gene extracted from Human gastrointestinal tumor-associated antigen GA733-1 protein gene, complete cds, clone 5516

J05070, class A, 20 probes, 20 in J05070 1805-2303, Human type IV collagenase mRNA, complete cds

M14158, class C, 20 probes, 20 in all_M14158 1529-1794, T-cell receptor beta-chain J1.3 gene extracted from Human T-cell receptor germline beta-chain D1.1 and J1.1 to J1.6 genes

X98266, class B, 20 probes, 14 in X98266cds#2 1028-1340: 6 in reverseSequence, 2103-2223, ligase-like protein gene extracted from H.sapiens mRNA for ligase like protein, X-1

U14969, class A, 20 probes, 20 in U14969 43-451, Human ribosomal protein L28 mRNA, complete cds

L78833, class C, 20 probes, 20 in reverse_L78833 2267-2337, BRCA1 gene extracted from Human BRCA1, Rho7 and vatI genes, complete cds, and ipf35 gene, partial cds, BRCA1 gene extracted from Human BRCA1, Rho7 and vatI genes, complete cds, and ipf35 gene, partial cds, BRCA1 gene extracted from Human BRCA1, Rho7 and vatI genes, complete cds, and ipf35 gene, partial cds

Tropomyosin, Alpha, Muscle, Alt. Splice 2, Skeletal Muscle (Fibroblast)
Collagen, Type Viii, Alpha 2
Neurofibromatosis 2 Tumor Suppressor (Gb:L27065)
Zinc Finger Protein Zfp-36
Sodium Channel 1
D13645, class A, 20 probes, 20 in D13645 1517-2027, Human mRNA for KIAA0020 gene, complete cds
D50857, class A, 20 probes, 20 in D50857 5954-6440, Human DOCK180 protein mRNA, complete cds

S81957, class A, 20 probes, 20 in S81957mRNA#1 40-112, BMP-5=bone morphogenic protein-5 {promoter} [human, Genomic, 1116 nt]. /gb=S81957 /ntype=DNA /annot=mRNA
M34181, class A, 20 probes, 20 in M34181 2356-2872, Human testis-specific cAMP-dependent protein kinase catalytic subunit (C-beta isoform) mRNA, complete cds
U19906, class C, 20 probes, 20 in all_U19906 5284-5711, Human arginine vasopressin receptor 1 (AVPR1) gene, complete cds
D64142, class A, 20 probes, 20 in D64142mRNA 625-1177, Human mRNA for histone H1x, complete cds

X59871, class A, 20 probes, 20 in X59871mRNA 2672-2836, Human TCF-1 mRNA for T cell factor 1 (splice form C)
U01212, class B, 20 probes, 12 in U01212cds 153-411: 8 in reverseSequence, 1715-1943, Human olfactory marker protein (OMP) gene, complete cds
AB002533, class A, 20 probes, 20 in AB002533 1726-2128, Human mRNA for Qip1, complete cds
X70297, class C, 20 probes, 20 in all_X70297 1563-2020, H.sapiens mRNA for neuronal nicotinic acetylcholine receptor alpha-7 subunit
Z29074, class C, 20 probes, 20 in all_Z29074 1968-2269, H.sapiens mRNA for cytokeratin 9
U20647, class A, 20 probes, 20 in U20647 232-736, Human zinc finger protein (ZNF151) mRNA, partial cds
L37936, class A, 20 probes, 20 in L37936 439-961, Human nuclear-encoded mitochondrial elongation factor Ts (EF-Ts) mRNA, 3 end of cds

M68907, class A, 19 probes, 19 in M68907 2-187, Human tachykinin-A (gamma-PPT-A) gene, partial cds. /gb=M68907 /ntype=RNA

D10923, class A, 20 probes, 20 in D10923 1452-1962, Human mRNA for HM74

L36529, class A, 20 probes, 20 in L36529mRNA 1491-2043, Human (clone N5-4) protein p84 mRNA, complete cds

U25034, class A, 20 probes, 20 in U25034 588-1127, Human neuronatin beta mRNA, complete cds

U01923, class A, 20 probes, 20 in U01923 1649-2090, Human BTK region clone ftp-3 mRNA

U55206, class A, 20 probes, 18 in U55206 790-1222: 2 not in GB record, Human gamma-glutamyl hydrolase (hGH) mRNA, complete cds

L36847, class A, 20 probes, 20 in L36847cds 1044-1578, Human (clone p17/90) rearranged iduronate-2-sulphatase homologue gene. /gb=L36847 /ntype=DNA /annot=CDS

U20938, class A, 20 probes, 20 in U20938 3946-4348, Human lymphocyte dihydropyrimidine dehydrogenase mRNA, complete cds.

S73840, class A, 20 probes, 20 in S73840 408-784, type IIx myosin heavy chain {3 region} [human, skeletal muscle, mRNA Partial, 827 nt]

M16474, class A, 20 probes, 20 in M16474mRNA 1788-2223, Human fetal butyrylcholinesterase mRNA, complete cds

J02960, class B, 20 probes, 10 in J02960cds#1 394-729: 10 in reverseSequence, 1015-1252, unknown protein gene extracted from Human beta-2-adrenergic receptor gene, complete cds

M32313, class A, 20 probes, 20 in M32313mRNA 1537-2047, Human steroid 5-alpha-reductase mRNA, complete cds

X14885, class A, 19 probes, 19 in X14885mRNA 2506-2558, H.sapiens gene for transforming growth factor-beta 3 (TGF-beta 3) exon 1 (and joined CDS)

X97324, class A, 20 probes, 20 in X97324cds 749-1277, H.sapiens mRNA for adipophilin. /gb=X97324 /ntype=RNA

D43951, class A, 20 probes, 20 in D43951 4874-5264, Human mRNA for KIAA0099 gene, complete cds

M59964, class A, 20 probes, 20 in M59964 816-1380, Human stem cell factor mRNA, complete cds

M17446, class A, 20 probes, 20 in M17446mRNA 648-1186, Human Kaposi sarcoma oncogene fibroblast growth factor mRNA, complete cds

U79252, class A, 20 probes, 20 in U79252 1026-1530, Human clone 23679 mRNA, complete cds.

J02963, class A, 20 probes, 20 in J02963 641-1049, Human platelet glycoprotein IIb mRNA, 3 end

M94630, class A, 20 probes, 20 in M94630 832-1027, Homo sapiens hnRNP-C like protein mRNA, complete cds

L07949, class A, 20 probes, 20 in L07949 1619-2075, Homo sapiens GnRH receptor mRNA, complete cds

X02750, class C, 20 probes, 20 in all_X02750 1332-1729, Human liver mRNA for protein C

U13737, class A, 20 probes, 20 in U13737 2046-2556, Human cysteine protease CPP32 isoform alpha mRNA, complete cds
Spliceosomal Protein Sap 62

X82835, class C, 20 probes, 20 in all_X82835 5995-6350, H.sapiens mRNA for voltage-activated sodium channel

J03925, class A, 20 probes, 20 in J03925 4110-4656, Human Mac-1 gene encoding complement receptor type 3, CD11b, complete cds

M61832, class A, 20 probes, 20 in M61832 1472-2002, Human S-adenosylhomocysteine hydrolase (AHCY) mRNA, complete cds

M95623, class A, 20 probes, 19 in M95623exon#14-15 2-383: 1 not in GB record, PBGD gene (hydroxymethylbilane synthase) extracted from Homo sapiens hydroxymethylbilane synthase gene, complete cds
Serine Kinase Psk-H1

M27891, class B, 20 probes, 10 in M27891exon 13-58: 7 in reverseSequence, 145-370: 3 not in GB record, Human cystatin C (CST3) gene

U42408, class A, 20 probes, 20 in U42408 1997-2393, Human ladinin (LAD) mRNA, complete cds

U43965, class A, 20 probes, 20 in U43965 3313-3389, Human ankyrin G119 (ANK3) mRNA, complete cds

M24351, class A, 20 probes, 20 in M24351exon 248-404, PTHLH gene (parathyroid hormone-like protein A) extracted from Human parathyroid hormone-like protein (PLP) gene, PTHLH gene (parathyroid hormone-like protein A) extracted from Human parathyroid hormone-like protein (PLP) gene

M37075, class C, 20 probes, 20 not in GB record, Human embryonic/atrial myosin light chain (MLC-1-emb/A isoform) gene

Major Histocompatibility Complex, Class I, C (Gb:X58536) - Also Similar To: L42345, HG2920-HT3064, Z22651, HG2904-HT3048, HG658-HT658

V-Erba Related Ear-3 Protein

M58459, class A, 20 probes, 20 in M58459 295-829, Human ribosomal protein (RPS4Y) isoform mRNA, complete cds

Y11215, class C, 20 probes, 20 in all_Y11215 971-1446, Homo sapiens mRNA for SKAP55 protein. /gb=Y11215 /ntype=RNA

U04209, class A, 20 probes, 20 in U04209 1396-1834, Human associated microfibrillar protein mRNA, complete cds

X59244, class A, 20 probes, 20 in X59244mRNA 2391-2967, Human ZNF43 mRNA

L46353, class A, 20 probes, 20 in L46353mRNA 6579-7077, Homo sapiens high-mobility group phosphoprotein (HMGI-C) gene, exons 3-Jan

L31881, class A, 20 probes, 20 in L31881 929-1385, Human nuclear factor I-X mRNA, complete cds

X82153, class C, 20 probes, 20 in all_X82153 1128-1615, H.sapiens mRNA for cathepsin O

X89067, class C, 20 probes, 20 in all_X89067 751-1136, H.sapiens mRNA for trpc2 transcript (possible pseudogene)

M13994, class A, 20 probes, 20 in M13994mRNA 4482-5005, Human B-cell leukemia/lymphoma 2 (bcl-2) proto-oncogene mRNA encoding bcl-2-alpha protein, complete cds

S45630, class A, 20 probes, 20 in S45630 108-612, alpha B-crystallin=Rosenthal fiber component [human, glioma cell line, mRNA, 691 nt]

U43923, class A, 20 probes, 20 in U43923 888-1410, Human transcription factor SUPT4H mRNA, complete cds

M85165, class A, 20 probes, 20 in M85165 1311-1809, Homo sapiens SRF accessory protein 1A (SAP-1) mRNA, complete cds

L78440, class A, 20 probes, 20 in L78440mRNA 2089-2509, Homo sapiens STAT4 mRNA, complete cds

U07563, class C, 20 probes, 20 not in GB record, Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene

U33920, class A, 20 probes, 20 in U33920 2564-2644, Human clone lambda 5 semaphorin mRNA, complete cds

U73960, class A, 20 probes, 20 in U73960 566-1022, Human ADP-ribosylation factor-like protein 4 mRNA, complete cds

AF009426, class A, 20 probes, 20 in AF009426 7540-8044, Homo sapiens clone 22 mRNA, alternative splice variant beta-1, complete cds. /gb=AF009426 /ntype=RNA

S81578, class A, 20 probes, 20 in S81578 13-271, dioxin-responsive gene {putative polyadenylation signal region} [human, hepatoma G2 cell line, mRNA Partial, 302 nt]. /gb=S81578 /ntype=RNA

U75370, class A, 20 probes, 20 in U75370 3396-3732, Human mitochondrial RNA polymerase mRNA, nuclear gene encoding mitochondrial protein, complete cds

M83651, class A, 20 probes, 20 in M83651 1947-2451, Human beta-1,4 N-acetylgalactosaminyltransferase mRNA, complete cds

U56085, class A, 20 probes, 20 in U56085 2568-3048, Human periodic tryptophan protein 2 (PWP2) mRNA, complete cds

X00129, class B, 20 probes, 11 in X00129cds 332-566: 9 in reverseSequence, 671-851, Human mRNA for retinol binding protein (RBP)

L41870, class A, 20 probes, 20 in L41870 4412-4814, Homo sapiens retinoblastoma susceptibility protein (RB1) mRNA and mutations

U87460, class A, 20 probes, 20 in U87460 3537-4113, Human putative endothelin receptor type B-like protein mRNA, complete cds

M13934, class C, 20 probes, 20 in all_M13934 834-1309, RPS14 gene (unknown protein) extracted from Human ribosomal protein S14 gene, complete cds, RPS14 gene (unknown protein) extracted from Human ribosomal protein S14 gene, complete cds

M12959, class A, 17 probes, 17 in M12959 1035-1486, Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds

Oncogene E6-Ap, Papillomavirus - Also Represents: U84404

U73477, class A, 18 probes, 18 in U73477 440-885, Human acidic nuclear phosphoprotein pp32 mRNA, complete cds

Placental Protein 14, Endometrial Alpha 2 Globulin, Alt. Splice 2 - Also Represents: M34046

D42085, class A, 20 probes, 20 in D42085 2200-2572, Human mRNA for KIAA0095 gene, complete cds

U51004, class A, 20 probes, 20 in U51004 166-508, Human putative protein kinase C inhibitor (PKCI-1) mRNA, complete cds

X16260, class B, 20 probes, 13 in X16260cds 2053-2485: 7 in reverseSequence, 2508-2631, Human mRNA for inter-alpha-trypsin inhibitor subunit 3

M96980, class A, 20 probes, 20 in M96980 2034-2598, Homo sapiens myelin transcription factor 1 (MTF1) mRNA, 3 end

U79259, class A, 20 probes, 20 in U79259 1214-1610, Human clone 23945 mRNA, complete cds.

X06948, class B, 20 probes, 12 in X06948cds 482-680: 8 in reverseSequence, 918-1146, Human mRNA for high affinity IgE receptor alpha-subunit (FcERI)

Dematin - Also Represents: U28389

K02268, class A, 20 probes, 20 in K02268mRNA 3155-3677, Human enkephalin B (enkB) gene, 5 flank and

Rad2

L13972, class A, 20 probes, 20 in L13972 1930-2224, Homo sapiens beta-galactoside alpha-2,3-sialyltransferase (SIAT4A) mRNA, complete cds

X91249, class C, 20 probes, 20 in all_X91249 2428-2855, H.sapiens mRNA for white gene protein

Z11793, class C, 20 probes, 20 in all_Z11793 1553-2001, H.sapiens mRNA for selenoprotein P

U38810, class A, 20 probes, 20 in U38810 2191-2659, Human mab-21 cell fate-determining protein homolog (CAGR1) mRNA, complete cds

M94055, class A, 20 probes, 20 in M94055 5925-6285, Human voltage-gated sodium channel mRNA, complete cds

U92436, class A, 20 probes, 20 in U92436 2591-3077, Human mutated in multiple advanced cancers protein (MMAC1) mRNA, complete cds.

J03161, class A, 20 probes, 20 in J03161mRNA 3636-4122, Human serum response factor (SRF) mRNA, complete cds

X58521, class B, 20 probes, 13 in X58521cds 1250-1544: 7 in reverseSequence, 1701-1785, Human mRNA for p62 nucleoporin

L09235, class A, 20 probes, 20 in L09235 1323-1845, Human vacuolar ATPase (isoform VA68) mRNA, complete cds

L26584, class A, 20 probes, 20 in L26584 3368-3933, Human (CDC25) mRNA, complete cds

U38227, class A, 19 probes, 19 in U38227 3-411, Human testis-specific hexokinase 1 (hHK1-tb) mRNA, partial cds. /gb=U38227 /ntype=RNA

X57579, class A, 20 probes, 18 in X57579exon 545-840: 2 in reverseSequence, 1392-1555, H.sapiens activin beta-A subunit (exon 2)

Z25521, class A, 20 probes, 17 in Z25521cds 526-884: 3 in reverseSequence, 1068-1179, H.sapiens integrin associated protein mRNA, complete CDS,.

D80008, class A, 20 probes, 20 in D80008 2695-3205, Human mRNA for KIAA0186 gene, complete cds

U10439, class A, 20 probes, 20 in U10439 5983-6529, Human double-stranded RNA adenosine deaminase mRNA, complete cds

U52513, class A, 20 probes, 20 in U52513 1318-1642, Human RIG-G mRNA, complete cds

Y10210, class A, 20 probes, 20 in Y10210mRNA 55-433, H.sapiens mRNA for CD22 protein. /gb=Y10210 /ntype=RNA

M19720, class C, 20 probes, 20 in all_M19720 2034-2557, L-myc gene (L-myc protein) extracted from Human L-myc protein gene, complete cds, L-myc gene (L-myc protein) extracted from Human L-myc protein gene, complete cds

Homo sapiens /REF=M11507 /DEF=Human transferrin receptor mRNA, complete cds /LEN=2826 (_5, _M, _3 represent transcript regions 5 prime, Middle, and 3 prime respectively)

X17254, class B, 20 probes, 13 in X17254cds 911-1211: 7 in reverseSequence, 1335-1449, Human mRNA for the transcription factor Eryf1

U39817, class A, 20 probes, 20 in U39817 3917-4373, Human Bloom syndrome protein (BLM) mRNA, complete cds
Af-6 (Gb:U02478)

U68133, class A, 20 probes, 20 in U68133 4-133, Human SCC-S4 mRNA expressed in primary and relatively radiosensitive squamous cell carcinoma, partial 3 sequence. /gb=U68133 /ntype=RNA

M93107, class A, 20 probes, 20 in M93107 978-1278, Homo sapiens heart (R)-3-hydroxybutyrate dehydrogenase mRNA, 3 end

AD000684, class B, 20 probes, 11 in AD000684cds#1 934-1252: 9 in reverseSequence, 16809-17037, LISCH7 gene (liver-specific bHLH-Zip transcription factor) extracted from Homo sapiens DNA from chromosome 19-cosmid R30879 containing USF2, genomic sequence

X67698, class C, 20 probes, 20 in all_X67698 228-709, H.sapiens tissue specific mRNA
Dopamine Receptor D4 - Also Represents: L12398

U70064, class A, 20 probes, 20 in U70064 6458-7030, Human lysosomal trafficking regulator (LYST) mRNA, partial cds

S78203, class A, 20 probes, 20 in S78203 2096-2660, PEPT 2=H+/peptide cotransporter [human, kidney, mRNA Partial, 2685 nt]

U27193, class A, 20 probes, 20 in U27193 1872-2346, Human protein-tyrosine phosphatase mRNA, complete cds

U58522, class A, 20 probes, 20 in U58522 1608-2124, Human huntingtin interacting protein (HIP2) mRNA, complete cds

Tropomyosin Tm30nm, Cytoskeletal

J05016, class A, 20 probes, 20 in J05016mRNA 2252-2824, Human (clone pA3) protein disulfide isomerase related protein (ERp72) mRNA, complete cds

U48436, class A, 20 probes, 20 in U48436 5739-6290, Human fragile X mental retardation protein FMR2p (FMR2) mRNA, complete cds

U90546, class B, 12 probes, 12 in U90546 1301-1344, Human butyrophilin (BTF4) mRNA, complete cds, Human butyrophilin (BTF4) mRNA, complete cds

AB000409, class A, 20 probes, 20 in AB000409 2046-2538, Human mRNA for MNK1, complete cds

M31642, class A, 20 probes, 20 in M31642mRNA 802-1288, Human hypoxanthine phosphoribosyltransferase (HPRT) mRNA, complete cds

X99975, class C, 20 probes, 20 in all_X99975 3672-4243, H.sapiens mRNA for hRTR/hGCNF protein

U20979, class A, 20 probes, 20 in U20979 2612-3068, Human chromatin assembly factor-I p150 subunit mRNA, complete cds

M25079, class A, 20 probes, 20 in M25079 163-230, Human sickle cell beta-globin mRNA, complete cds

U81006, class A, 20 probes, 20 in U81006 1886-2348, Human p76 mRNA, complete cds

U79716, class A, 20 probes, 20 in U79716 11015-11537, Human reelin (RELN) mRNA, complete cds

L20010, class A, 20 probes, 20 in L20010 7717-8185, Human HCF1 gene related mRNA sequence

Guanine Nucleotide-Binding Protein, Alpha Inhibiting Activity Polypeptide 2

M22638, class A, 20 probes, 20 in M22638exon#4 154-682, Human LYL-1 protein gene, complete cds

D59253, class A, 20 probes, 20 in D59253 306-618, Human mRNA for NCBP interacting protein 1, complete cds

U43142, class A, 20 probes, 20 in U43142 1456-1972, Human vascular endothelial growth factor related protein VRP mRNA, complete cds

D31897, class A, 20 probes, 20 in D31897 1050-1548, Human mRNA for Doc2 (Double C2), complete cds

U19251, class C, 20 probes, 20 not in GB record, Homo sapiens neuronal apoptosis inhibitory protein mRNA, complete cds.

X95325, class A, 20 probes, 20 in X95325mRNA 783-1250, H.sapiens mRNA for DNA binding protein A variant

M16505, class C, 20 probes, 20 in all_M16505 6015-6520, Human steroid sulfatase (STS) mRNA, complete cds

L29306, class A, 17 probes, 17 in L29306 723-1116, Homo sapiens tryptophan hydroxylase (Tph) mRNA, complete cds. /gb=L29306 /ntype=RNA

X13238, class B, 20 probes, 13 in X13238cds 19-199: 7 in reverseSequence, 272-386, Human mRNA for cytochrome c oxidase subunit VIc

J03824, class A, 20 probes, 20 in J03824 756-1230, Human uroporphyrinogen III synthase mRNA, complete cds

X87852, class A, 20 probes, 16 in X87852cds 5374-5560: 4 in reverseSequence, 5780-5966, H.sapiens mRNA for SEX gene

X74801, class B, 20 probes, 12 in X74801cds 1282-1552: 8 in reverseSequence, 1636-1837, H.sapiens Cctg mRNA for chaperonin

M24736, class A, 20 probes, 20 in M24736 3222-3785, Human endothelial leukocyte adhesion molecule 1 (ELAM-1) mRNA, complete cds

D28473, class A, 20 probes, 20 in D28473 3882-4418, Human T-lymphocyte mRNA for isoleucyl-tRNA synthetase, complete cds

M64554, class A, 20 probes, 20 in M64554mRNA 1602-1962, F13A1 gene (coagulation factor XIIIb) extracted from Human factor XIII b subunit gene, complete cds

M28827, class A, 20 probes, 20 in M28827 620-1112, Human thymocyte antigen CD1c mRNA, complete cds

X97261, class C, 2 probes, 2 in all_X97261 25-333, H.sapiens mRNA for metallothionein isoform 1R, H.sapiens mRNA for metallothionein isoform 1R

X95826, class A, 20 probes, 20 in X95826cds 203-773, H.sapiens ART4 gene. /gb=X95826 /ntype=DNA /annot=CDS

M37755, class B, 20 probes, 11 in M37755exon 15-256: 6 in reverseSequence, 280-453: 3 not in GB record, Human pregnancy-specific beta-1-glycoprotein gene PSGGA

L37792, class A, 20 probes, 20 in L37792mRNA 1565-2015, Human syntaxin 1A mRNA, complete cds

M62424, class A, 20 probes, 20 in M62424 2868-3117, Human thrombin receptor mRNA, complete cds

D14446, class A, 20 probes, 20 in D14446 794-1166, Human HFREP-1 mRNA for unknown protein, complete cds

U71203, class A, 20 probes, 20 in U71203 339-753, Human rit mRNA, complete cds.

X78710, class A, 20 probes, 20 in X78710mRNA 2773-3247, H.sapiens MTF-1 mRNA for metal-regulatory transcription factor

Z22951, class A, 20 probes, 20 in Z22951mRNA 717-1231, Homo sapiens of p65 gene encoding p65 subunit of transcription factor NF-kappaB

M65290, class A, 20 probes, 20 in M65290 1957-2215, Human natural killer cell stimulatory factor (NKSF) mRNA, complete cds, clone p40

K01900, class A, 20 probes, 20 in K01900mRNA 655-1213, Human lymphocyte interferon alpha type 201 mRNA, complete cds

U89995, class A, 20 probes, 20 in U89995 3040-3460, Human DNA binding protein FKHL15 (FKHL15) mRNA, complete cds

U58682, class A, 20 probes, 20 in U58682 31-313, Human ribosomal protein S28 mRNA, complete cds

D29675, class A, 16 probes, 16 in D29675exon 2-136, Human inducible nitric oxide synthase gene, promoter and exon 1 /gb=D29675 /ntype=DNA /annot=exon, Human inducible nitric oxide synthase gene, promoter and exon 1 /gb=D29675 /ntype=DNA /annot=exon

L14076, class A, 20 probes, 20 in L14076 1469-2051, Human pre-mRNA splicing factor SRp75 mRNA, complete cds

J05257, class A, 20 probes, 20 in J05257 1239-1713, Homo sapiens (clones MDP4, MDP7) microsomal dipeptidase (MDP) mRNA, complete cds

X98172, class C, 20 probes, 20 in all_X98172 2240-2754, H.sapiens mRNA for MACH-alpha-1 protein

Retinoic Acid Receptor, Gamma 2

U48250, class A, 20 probes, 20 in U48250 1490-2030, Human protein kinase C-binding protein RACK17 mRNA, partial cds

D17400, class A, 20 probes, 20 in D17400 196-622, Human mRNA for 6-pyruvoyl-tetrahydropterin synthase, complete cds

M17236, class C, 5 probes, 5 in all_M17236 1896-2224, Human MHC class II HLA-DQ-alpha gene (DR4,w6), Human MHC class II HLA-DQ-alpha gene (DR4,w6)

X81636, class C, 20 probes, 20 in all_X81636 2127-2329, H.sapiens clathrin light chain a gene

X63546, class C, 20 probes, 20 in all_X63546 7261-7856, H.sapiens mRNA for tre oncogene (clone 210)

Z49148, class A, 20 probes, 16 in Z49148cds 2-418: 4 in reverseSequence, 18-589, H.sapiens mRNA for ribosomal protein L29

X51688, class A, 20 probes, 20 in X51688mRNA 1054-1438, Human mRNA for cyclin A

D63879, class A, 20 probes, 20 in D63879 3065-3599, Human mRNA for KIAA0156 gene, complete cds

U61232, class A, 20 probes, 20 in U61232 1407-1869, Human tubulin-folding cofactor E mRNA, complete cds

X15357, class B, 20 probes, 10 in X15357cds 2853-3135: 10 in reverseSequence, 3262-3454, Human mRNA for natriuretic peptide receptor (ANP-A receptor)

D31888, class A, 20 probes, 20 in D31888 4700-5186, Human mRNA for KIAA0071 gene, partial cds

Y10615, class A, 20 probes, 20 in Y10615cds 115-535, H.sapiens CYRN2 gene. /gb=Y10615 /ntype=DNA /annot=CDS

U29607, class A, 20 probes, 20 in U29607 1974-2148, Human methionine aminopeptidase mRNA, complete cds

M27783, class A, 20 probes, 20 in M27783 2-433, Human neutrophil elastase mRNA, 3 end.

Major Histocompatibility Complex, Class I, E (Gb:M20022)

D85429, class A, 20 probes, 20 in D85429exon#3 813-1347, Human DNA for heat shock protein 40, complete cds

X95190, class A, 20 probes, 19 in X95190cds 1574-1958: 1 in reverseSequence, 2170, H.sapiens mRNA for Branched chain Acyl-CoA Oxidase

Lymphocyte Antigen Hla-G3 - Also Represents: J03027

U92314, class A, 20 probes, 20 in U92314 840-1415, Homo sapiens hydroxysteroid sulfotransferase SULT2B1a (HSST2) mRNA, complete cds.

M34376, class A, 20 probes, 20 in M34376mRNA 2-238, Homo sapiens (clone lambda MSP131) beta-microseminoprotein (MSP) gene

Z26317, class A, 20 probes, 17 in Z26317cds 2904-3324: 3 in reverseSequence, 3443-3491, H.sapiens mRNA for desmoglein 2

X01038, class A, 20 probes, 20 in X01038mRNA 285-824, Human fetal gene for apolipoprotein AI precursor

X91992, class C, 20 probes, 20 in all_X91992 1340-1929, H.sapiens mRNA for alkB protein homolog

B. subtilis /GEN=trpD, trpC /DB_XREF=gb:K01391.1 /NOTE=SIF corresponding to nucleotides 2880-3359 of gb:K01391.1, not 100% identical /DEF=B.subtilis tryptophan (trp) operon, complete cds.

M86852, class A, 20 probes, 20 in M86852 1041-1557, H.sapiens peroxisome assembly factor-1 mRNA, complete cds

M23575, class A, 20 probes, 20 in M23575 1395-1933, Human pregnancy-specific beta-1 glycoprotein mRNA, complete cds

X04898, class A, 20 probes, 20 in X04898mRNA 49-445, Human gene for apolipoprotein AII

U61145, class A, 20 probes, 20 in U61145 2035-2509, Human enhancer of zeste homolog 2 (EZH2) mRNA, complete cds

U18914, class C, 20 probes, 20 in all_U18914 2694-3199, Human 19.8 kDa protein mRNA, complete cds

U31216, class A, 20 probes, 20 in U31216 3168-3641, Human metabotropic glutamate receptor 1 beta (mGluR1beta) mRNA, complete cds

U57094, class A, 20 probes, 20 in U57094 502-1018, Human small GTP-binding protein mRNA, complete cds

M22877, class C, 20 probes, 20 in all_M22877 1917-2434, Human somatic cytochrome c (HCS) gene, complete cds

D87447, class A, 20 probes, 20 in D87447 5712-6258, Human mRNA for KIAA0258 gene, complete cds

M10050, class A, 20 probes, 20 in M10050mRNA 25-424, Human liver fatty acid binding protein (FABP) mRNA, complete cds

D90224, class A, 20 probes, 20 in D90224 2791-3319, Human mRNA for glycoprotein 34 (gp34)

M59815, class A, 20 probes, 20 in M59815mRNA 5022-5424, Human complement component C4A gene

L29217, class A, 20 probes, 20 in L29217mRNA 1299-1683, Homo sapiens clk3 mRNA, complete cds

S76756, class A, 19 probes, 19 in S76756 510-954, 4R-MAP2=microtubule-associated protein 2 4R isoform [human, brain, mRNA Partial, 1012 nt]. /gb=S76756 /ntype=RNA

D25218, class A, 20 probes, 20 in D25218 1125-1575, Human mRNA for KIAA0112 gene, partial cds

X82324, class B, 20 probes, 12 in X82324cds 866-1055: 8 in reverseSequence, 1096-1450, H.sapiens Brain 4 mRNA

U86602, class A, 20 probes, 20 in U86602 772-1240, Human nucleolar protein p40 mRNA, complete cds

Y00339, class C, 20 probes, 20 in all_Y00339 913-1465, Human mRNA for carbonic anhydrase II (EC 4.2.1.1)

D43947, class A, 20 probes, 20 in D43947 6379-6901, Human mRNA for KIAA0100 gene, complete cds

U83463, class A, 20 probes, 20 in U83463 1406-1862, Human scaffold protein Pbp1 mRNA, complete cds.

X15573, class C, 20 probes, 20 in all_X15573 2313-2800, Human liver-type 1-phosphofructokinase (PFKL) mRNA, complete cds

X97064, class B, 20 probes, 10 in X97064cds 1988-2210: 10 in reverseSequence, 2435-2678, H.sapiens mRNA for Sec23A isoform, 2748bp

X14975, class C, 20 probes, 20 in all_X14975 7566-8337, Human CD1 R2 gene for MHC-related antigen

D83174, class A, 20 probes, 20 in D83174 1524-1896, Human mRNA for collagen binding protein 2, complete cds

M16707, class C, 7 probes, 7 in all_M16707 590-631, Human histone H4 gene, complete cds, clone FO108, Human histone H4 gene, complete cds, clone FO108

M11973, class C, 20 probes, 20 not in GB record, Human gamma-B-crystallin gene (gamma 1-2)

B. subtilis /GEN=dapB /DB_XREF=gb:L38424.1 /NOTE=SIF corresponding to nucleotides 1428-1926 of gb:L38424.1 /DEF=Bacillus subtilis dihydropicolinate reductase (jojE) gene, complete cds; poly(A) polymerase (jojI) gene, complete cds; biotin acetyl-CoA-carboxylase ligase (birA) gene, complete cds; jojC, jojD, jojF, jojG, jojH genes, complete cds s.

D43636, class A, 20 probes, 20 in D43636 3576-4080, Human mRNA for KIAA0096 gene, partial cds

Fc Receptor Iib3 For Igg, Low Affinity

M20471, class A, 20 probes, 20 in M20471 512-1066, Human brain-type clathrin light-chain a mRNA, complete cds

Proto-Oncogene Ets-1, Alt. Splice 2 - Also Represents: J04101

L17418, class B, 20 probes, 10 in L17418exon 3-229: 10 not in GB record, complement receptor 1 gene extracted from Human complement receptor type 1 (alleles S and F) gene, enhancer and

M13149, class A, 20 probes, 20 in M13149 1540-2008, Human histidine-rich glycoprotein mRNA, complete cds

U11701, class A, 20 probes, 20 in U11701 1316-1862, Human LIM-homeobox domain protein (hLH-2) mRNA, complete cds

U40380, class A, 20 probes, 20 in U40380 961-1027, Human presenilin I-374 (AD3-212) mRNA, complete cds

L20815, class A, 20 probes, 20 in L20815 2031-2445, Human S protein mRNA, complete cds

Monocyte Chemotactic Protein 1 - Also Represents: HG2254-HT2341, M26683

M80254, class A, 20 probes, 20 in M80254 492-840, H.sapiens cyclophilin isoform (hCyP3) mRNA, complete cds

X83368, class C, 20 probes, 20 in all_X83368 4789-5345, H.sapiens mRNA for phosphatidylinositol 3 kinase gamma

U40369, class A, 20 probes, 20 in U40369mRNA 851-995, Human spermidine/spermine N1-acetyltransferase (SSAT) gene, complete cds

U85430, class A, 20 probes, 20 in U85430 3114-3279, Human transcription factor NFATx4 mRNA, complete cds.

M63483, class A, 20 probes, 20 in M63483 757-1255, Human major nuclear matrix protein mRNA

U21689, class C, 20 probes, 20 in all_U21689 2955-3116, Human glutathione S-transferase-P1c gene, complete cds

L48211, class B, 20 probes, 14 in L48211cds 31-151: 6 in reverseSequence, 1691-1775, Homo Sapiens angiotensin II receptor gene, complete cds

U73304, class A, 20 probes, 20 in U73304mRNA 4973-5447, Human CB1 cannabinoid receptor (CNR1) gene, complete cds.

S73885, class A, 20 probes, 20 in S73885 1537-2082, AP-4=basic helix-loop-helix DNA-binding protein [human, cervical carcinoma, HeLa cells, mRNA, 2149 nt]

S57212, class A, 20 probes, 20 in S57212 1561-2027, hMEF2C=myocyte enhancer-binding factor 2 [human, skeletal muscles, mRNA, 2161 nt]

L41690, class A, 20 probes, 20 in L41690 906-1332, Homo sapiens TNF receptor-1 associated protein (TRADD) mRNA, 3 end of cds

AF006084, class A, 20 probes, 20 in AF006084 935-1277, Homo sapiens Arp2/3 protein complex subunit p41-Arc (ARC41) mRNA, complete cds. /gb=AF006084 /ntype=RNA

X74570, class C, 20 probes, 20 in all_X74570 1140-1711, H.sapiens mRNA for Gal-beta(1-3/1-4)GlcNAc alpha-2.3-sialyltransferase

M31606, class A, 20 probes, 20 in M31606mRNA 1102-1528, Human phosphorylase kinase (PSK-C3) mRNA, complete cds

D00591, class A, 20 probes, 20 in D00591exon#14 597-1041, Human RCC1 gene, complete cds

U95626, class A, 20 probes, 20 in U95626mRNA#2 1641-2133, ccr2 gene (ccr2a) extracted from Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence., ccr2 gene (ccr2a) extracted from Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.

U52373, class A, 20 probes, 20 in U52373 1810-2355, Human serine/threonine kinase MNB (mnb) mRNA, complete cds

B. subtilis /GEN=trpC, trpF /DB_XREF=gb:K01391.1 /NOTE=SIF corresponding to nucleotides 3790-4368 of gb:K01391.1, not 100% identical /DEF=B.subtilis tryptophan (trp) operon, complete cds.

D43948, class A, 20 probes, 20 in D43948 6033-6549, Human mRNA for KIAA0097 gene, complete cds

D80010, class A, 20 probes, 20 in D80010 4778-5198, Human mRNA for KIAA0188 gene, partial cds

L34820, class A, 20 probes, 20 in L34820 566-938, Human NAD+-dependent succinate-semialdehyde dehydrogenase (SSADH) mRNA, 3 end

U31382, class A, 20 probes, 20 in U31382 69-621, Human G protein gamma-4 subunit mRNA, complete cds

M28249, class A, 20 probes, 20 in M28249 4850-5306, Human very late antigen-2 (VLA-2)/collagen receptor alpha-2 subunit mRNA, complete cds

M30496, class A, 20 probes, 20 in M30496 321-759, Human ubiquitin carboxyl-terminal hydrolase (PGP 9.5, UCH-L3) isozyme L3 mRNA, complete cds

J02902, class A, 20 probes, 20 in J02902mRNA 1694-2156, Human protein phosphatase 2A regulatory subunit alpha-isotype (alpha-PR65) mRNA, complete cds

Y10205, class A, 20 probes, 20 in Y10205mRNA 146-548, H.sapiens mRNA for CD88 protein. /gb=Y10205 /ntype=RNA

U60060, class A, 20 probes, 20 in U60060 1090-1540, Human FEZ1 mRNA, complete cds

U66468, class A, 20 probes, 20 in U66468 586-1126, Human cell growth regulator CGR11 mRNA, complete cds

Collagen, Type Vi, Alpha 2, Alt. Splice 2 - Also Represents: M34570

U16120, class A, 20 probes, 20 in U16120 2267-2833, Human placental taurine transporter mRNA, complete cds

X97748, class A, 20 probes, 20 in X97748mRNA 59-189, H.sapiens PTX3 gene promotor region. /gb=X97748 /ntype=DNA /annot=mRNA

L24559, class A, 20 probes, 20 in L24559 1634-2078, Homo sapiens DNA polymerase alpha mRNA, complete cds

X66087, class C, 20 probes, 20 in all_X66087 3046-3563, H.sapiens a-myb mRNA

Y13247, class A, 20 probes, 20 in Y13247 3077-3581, Homo sapiens fb19 mRNA

U68142, class A, 20 probes, 20 in U68142 1372-1900, Human RalGDS-like 2 (RGL2) mRNA, partial cds

U07919, class A, 20 probes, 20 in U07919 2973-3399, Human aldehyde dehydrogenase 6 mRNA, complete cds

L10102, class A, 20 probes, 20 in L10102mRNA#1 392-794, Homo sapiens sex-determining region Y (SRY) gene, complete cds

M55998, class C, 20 probes, 20 in all_M55998 2-265, Human alpha-1 collagen type I gene, 3 end

X16546, class C, 20 probes, 20 in all_X16546 724-1319, Human DNA for eosinophil derived neurotoxin

Z74616, class C, 20 probes, 20 in all_Z74616 4470-4992, H.sapiens mRNA for prepro-alpha2(I) collagen.

M55172, class A, 20 probes, 20 in M55172 6712-7102, Human large aggregating cartilage proteoglycan core protein mRNA, complete cds

J00212, class A, 20 probes, 20 in J00212mRNA 393-761, Human leukocyte interferon (ifn-alpha) alpha-f mRNA, complete cds

S83513, class A, 20 probes, 20 in S83513 1328-1840, pituitary adenylate cyclase activating polypeptide [human, mRNA, 1940 nt]

U16296, class A, 20 probes, 20 in U16296 4938-5478, Human T-lymphoma invasion and metastasis inducing TIAM1 protein (TIAM1) mRNA, complete cds

U14970, class A, 20 probes, 20 in U14970 122-656, Human ribosomal protein S5 mRNA, complete cds

U19517, class A, 20 probes, 20 in U19517 1692-2010, Human (apoargC) long mRNA, complete cds

V00599, class A, 20 probes, 20 in V00599mRNA 903-1380, Human mRNA fragment encoding beta-tubulin. (from clone D-beta-1)

D28383, class A, 20 probes, 20 in D28383 4-37, Human mRNA for ATP synthase B chain, 5 UTR (sequence from the 5 cap to the start codon). /gb=D28383 /ntype=RNA

X66417, class B, 20 probes, 13 in X66417cds 230-524: 7 in reverseSequence, 658-766, H.sapiens casK mRNA for kappa-casein

D85423, class A, 20 probes, 20 in D85423 133-439, Human mRNA for Cdc5, partial cds. /gb=D85423 /ntype=RNA

Protein Kinase Ht31, Camp-Dependent

X57303, class A, 20 probes, 18 in X57303cds 1488-1866: 2 in reverseSequence, 2022-2028, H.sapiens REC1L mRNA

V00551, class A, 20 probes, 20 in V00551mRNA 366-878, Messenger RNA for human leukocyte (alpha) interferon

X06318, class C, 20 probes, 20 in all_X06318 2381-2541, Human mRNA for protein kinase C (PKC) type beta I

U20285, class A, 20 probes, 20 in U20285 1283-1811, Human Gps1 (GPS1) mRNA, complete cds

X86681, class C, 20 probes, 20 in all_X86681 1848-2257, H.sapiens mRNA for nucleolar protein, HNP36

U96114, class A, 20 probes, 20 in U96114 2964-3390, Homo sapiens Nedd-4-like ubiquitin-protein ligase WWP2 mRNA, complete cds.

U55766, class A, 20 probes, 20 in U55766 535-1081, Human Rev interacting protein Rip-1 mRNA, complete cds

X51954, class A, 20 probes, 20 in X51954exon 10-148, Human UCP gene for uncoupling protein exon 5 /gb=X51954 /ntype=DNA /annot=exon

M14539, class A, 20 probes, 20 in M14539 3238-3730, Human factor XIII subunit a mRNA, 3 end

M15059, class A, 20 probes, 20 in M15059mRNA 1025-1487, Human Fc-epsilon receptor (IgE receptor) mRNA, complete cds (H107 epitope)

X57809, class C, 8 probes, 8 in all_X57809 309-474, Human rearranged immunoglobulin lambda light chain mRNA, Human rearranged immunoglobulin lambda light chain mRNA

Z34822, class A, 40 probes, 40 in Z34822 6145-6595, H.sapiens (HLCC85) mRNA for voltage-dependent L-type Ca channel alpha 1 subunit (splice variant)

D00761, class A, 20 probes, 20 in D00761 252-750, Human mRNA for proteasome subunit HC5

D87074, class A, 20 probes, 20 in D87074 6650-7184, Human mRNA for KIAA0237 gene, complete cds

M86808, class C, 20 probes, 20 in all_M86808 2578-2977, Human pyruvate dehydrogenase complex (PDHA2) gene, complete cds

M24069, class A, 20 probes, 20 in M24069mRNA 1401-1543, Human DNA-binding protein A (dbpA) gene, 3 end

U40462, class A, 20 probes, 20 in U40462 3034-3574, Human Ikaros/LyF-1 homolog (hIk-1) mRNA, complete cds

Y10204, class A, 20 probes, 20 in Y10204mRNA 49-505, H.sapiens mRNA for CD77 protein. /gb=Y10204 /ntype=RNA

U82108, class A, 20 probes, 20 in U82108 987-1464, Human SIP-1 mRNA, complete cds

U75272, class A, 20 probes, 20 in U75272 743-1283, Human gastricsin mRNA, complete cds

U56833, class A, 20 probes, 20 in U56833 940-1468, Human VHL binding protein-1 (VBP-1) mRNA, partial cds

Ribosomal Protein L18a Homolog

X89416, class B, 20 probes, 10 in X89416cds 1386-1440: 10 in reverseSequence, 1533-1932, H.sapiens mRNA for protein phosphatase 5

X54150, class A, 20 probes, 20 in X54150mRNA 978-1530, Human mRNA for Fc receptor

X55666, class C, 20 probes, 20 in all_X55666 1222-1613, Human usf mRNA for late upstream transcription factor

D42073, class A, 20 probes, 20 in D42073 1551-2049, Human mRNA for reticulocalbin, complete cds

L10373, class A, 20 probes, 20 in L10373 1311-1713, Human (clone CCG-B7) mRNA sequence

X89066, class C, 20 probes, 20 in all_X89066 3817-4019, H.sapiens mRNA for TRPC1 protein

U09860, class A, 20 probes, 20 in U09860 3095-3653, Human enterokinase mRNA, complete cds

X71874, class A, 20 probes, 18 in X71874cds#1 268-739: 2 in reverseSequence, 4531-4534, proteasome-like subunit MECL-1 gene extracted from H.sapiens genes for proteasome-like subunit (MECL-1), chymotrypsin-like protease (CTRL-1) and protein serine kinase (PSK-H1) last exon

U51561, class C, 20 probes, 19 in all_U51561 10617-28244: 1 in U51561cds 50, Human cosmid N79E2, complete sequence.

U72514, class A, 20 probes, 20 in U72514 405-837, Human C2f mRNA, complete cds

U03100, class A, 20 probes, 20 in U03100 2985-3501, Human alpha2(E)-catenin mRNA, complete cds

X16983, class C, 20 probes, 20 in all_X16983 3252-3787, Human mRNA for integrin alpha-4 subunit

X66364, class A, 20 probes, 19 in X66364cds 454-814: 1 in reverseSequence, 922, H.sapiens mRNA PSSALRE for serine/threonine protein kinase

S68874, class A, 20 probes, 20 in S68874 113-469, EP3 prostanoid receptor EP3-I {3 region, alternatively spliced} [human, mRNA Partial, 598 nt]

D78261, class A, 20 probes, 20 in D78261 1293-1433, Human ICSAT transcription factor mRNA, partial cds, similar to mouse Pip/LSIRF (IRF-4) sequence

M73746, class A, 20 probes, 20 in M73746 2409-2894, Homo sapiens lutropin/choriogonadotropin receptor (LHCGR) mRNA, complete cds

Z34974, class A, 20 probes, 17 in Z34974cds 1816-2144: 3 in reverseSequence, 2439-2515, H.sapiens mRNA for plakophilin (partial)

D50692, class A, 20 probes, 20 in D50692 31-469, Human mRNA for c-myc binding protein, complete cds

U43527, class A, 20 probes, 18 in U43527 180-728: 2 not in GB record, Human malignant melanoma metastasis-suppressor (KiSS-1) gene, mRNA, complete cds

U32114, class A, 20 probes, 20 in U32114 756-1278, Human caveolin-2 mRNA, complete cds

U87593, class A, 40 probes, 40 in U87593 31-568, Human endogenous retrovirus clone P1.8 polymerase mRNA, partial cds. /gb=U87593 /ntype=RNA

U01062, class A, 20 probes, 20 in U01062mRNA 8334-8778, Human type 3 inositol 1,4,5-trisphosphate receptor (ITPR3) mRNA, complete cds

X07384, class B, 20 probes, 15 in X07384cds 2933-3269: 5 in reverseSequence, 3377-3527, Human mRNA for GLI protein

L35854, class A, 20 probes, 20 in L35854mRNA 3-75, Human dystrophin (dp140) mRNA, 5 end. /gb=L35854 /ntype=RNA

X83301, class C, 20 probes, 20 in all_X83301 1254-1471, H.sapiens SMA5 mRNA.

D31840, class A, 20 probes, 20 in D31840 3679-4148, Human DRPLA mRNA for ORF, complete cds

Splicing Factor Sc35, Alt Splice Form 3

M34677, class C, 20 probes, 20 in all_M34677 1486-1913, Human nested gene protein gene, complete cds

U79282, class A, 20 probes, 20 in U79282 1087-1651, Human clone 23801 mRNA sequence

D45917, class A, 20 probes, 20 in D45917 634-1120, Human mRNA for TIMP-3, partial cds (C-terminus region)

M21389, class A, 20 probes, 20 in M21389mRNA 1754-2192, Human keratin type II (58 kD) mRNA, complete cds

S73149, class A, 20 probes, 20 in S73149mRNA 293-827, insulin-like growth factor II {intron 7} [human, Genomic, 1702 nt]. /gb=S73149 /ntype=DNA /annot=mRNA

D82343, class A, 20 probes, 20 in D82343 474-960, Human mRNA for AMY, complete cds

X12794, class B, 20 probes, 10 in X12794cds 864-1176: 10 in reverseSequence, 1905-2139, Human v-erbA related ear-2 gene

Z70723, class C, 20 probes, 20 in all_Z70723 1812-2239, H.sapiens mRNA for serum aryldiakylphosphatase.

M57703, class A, 19 probes, 19 in M57703 129-629, Human melanin concentrating hormone (MCH) mRNA, complete cds

U22377, class A, 20 probes, 20 in U22377 5634-6168, Human Zn-15 related zinc finger protein (rlf) mRNA, complete cds

D21255, class A, 20 probes, 20 in D21255 3362-3812, Human mRNA for OB-cadherin-2, complete cds

U05255, class A, 16 probes, 16 in U05255 159-261, Human glycophorin HeP2 mRNA, partial cds, Human glycophorin HeP2 mRNA, partial cds

Homeotic Protein C6, Class I

S79048, class A, 20 probes, 20 in S79048 61-421, LPRP=pHL E1F1 [human, lacrimal gland, mRNA Partial, 507 nt]

U01922, class A, 20 probes, 20 in U01922 405-921, Human BTK region clone fci-12 mRNA

S66541, class B, 20 probes, 11 in S66541cds 375-687: 9 in reverseSequence, 99-314, B-50=neural phosphoprotein [human, Genomic, 1845 nt 3 segments]

D17532, class A, 20 probes, 20 in D17532 3624-4104, Human mRNA for RCK, complete cds

Myosin, Heavy Polypeptide 9, Non-Muscle

X07290, class C, 20 probes, 20 in all_X07290 1212-1723, Human HF.12 gene mRNA

X63597, class C, 20 probes, 20 in all_X63597 5486-5979, H.sapiens si mRNA for sucrase-isomaltase

U52152, class A, 20 probes, 20 in U52152 2642-3020, Human inwardly rectifying potassium channel Kir3.3 mRNA, complete cds

U83908, class B, 20 probes, 15 in U83908cds 941-1295: 5 in reverseSequence, 1589-1649, Human nuclear antigen H731 mRNA, complete cds

M87499, class B, 20 probes, 14 in M87499cds 586-880: 6 in reverseSequence, 2927-3041, Human uracil-DNA glycosylase (UNG) gene, complete cds

X78565, class C, 20 probes, 20 in all_X78565 6971-7512, H.sapiens mRNA for tenascin-C, 7560bp

D63487, class A, 20 probes, 20 in D63487 2889-3369, Human mRNA for KIAA0153 gene, partial cds

M97925, class A, 20 probes, 20 in M97925mRNA 121-409, H.sapiens defensin 5 gene, complete cds

U85267, class A, 20 probes, 20 in U85267 7-145, Human down syndrome critical region 1 (DSCR1) gene, alternative exon 1, partial cds. /gb=U85267 /ntype=RNA

M95167, class A, 20 probes, 20 in M95167mRNA 3333-3897, Homo sapiens dopamine transporter (SLC6A3) mRNA, complete cds

Z83802, class A, 20 probes, 20 in Z83802 133-511, H.sapiens mRNA for axonemal dynein heavy chain (partial, ID hdhc3).

Ras-Specific Guanine Nucleotide-Releasing Factor

L06175, class A, 20 probes, 20 in L06175 1924-2482, Homo Sapiens P5-1 mRNA, complete cds

U60873, class A, 20 probes, 20 in U60873 115-439, Human clone 137308 mRNA, partial cds

X58399, class A, 20 probes, 20 in X58399mRNA 491-903, Human L2-9 transcript of unrearranged immunoglobulin V(H)5 pseudogene.

U47105, class A, 20 probes, 20 in U47105 616-1174, Human H105e3 mRNA, complete cds

Z80780, class A, 20 probes, 20 in Z80780cds 2-339, H.sapiens H2B/h gene.

Protease Receptor-1, Effector Cell

Mucin 6, Gastric (Gb:L07517) - Also Represents: HG881-HT881

Microtubule-Associated Protein 1b

U17034, class A, 20 probes, 20 in U17034 4182-4584, Human soluble PLA2 receptor mRNA, complete cds

M64929, class A, 20 probes, 20 in M64929 1572-2100, Human protein phosphatase 2A alpha subunit mRNA, complete cds

X75042, class B, 20 probes, 13 in X75042cds 1607-1817: 7 in reverseSequence, 2024-2252, H.sapiens rel proto-oncogene mRNA

M94250, class A, 20 probes, 18 in M94250exon#4-5 43-301: 2 not in GB record, Human retinoic acid inducible factor (MK) gene exons 1-5, complete cds

L25444, class A, 20 probes, 20 in L25444 2124-2694, Homo sapiens (TAFII70-alpha) mRNA, complete cds

U11862, class A, 20 probes, 20 in U11862 1844-2402, Human clone HP-DAO1 diamine oxidase, copper/topa quinone-containing mRNA, complete cds

M14123, class A, 20 probes, 20 in M14123cds#1 263-665, pol from Human endogenous retrovirus HERV-K10. /gb=M14123 /ntype=DNA /annot=CDS, pol from Human endogenous retrovirus HERV-K10. /gb=M14123 /ntype=DNA /annot=CDS, pol from Human endogenous retrovirus HERV-K10. /gb=M14123 /ntype=DNA /annot=CDS, pol from Human endogenous retrovirus HERV-K10. /gb=M14123 /ntype=DNA /annot=CDS

X82494, class A, 20 probes, 20 in X82494mRNA 3527-3965, H.sapiens mRNA for fibulin-2

D29954, class A, 20 probes, 20 in D29954 4458-4920, Human mRNA for KIAA0056 gene, partial cds

D63475, class A, 20 probes, 20 in D63475 1309-1819, Human mRNA for KIAA0109 gene, complete cds

M60527, class A, 20 probes, 20 in M60527mRNA 1877-2369, Human deoxycytidine kinase mRNA, complete cds

D28791, class A, 20 probes, 20 in D28791exon 1763-2267, Human PIG-A gene, 5 flanking region and

U01828, class A, 20 probes, 20 in U01828 5837-5942, Human microtubule-associated protein 2 (MAP2) mRNA, complete cds

AF000177, class A, 20 probes, 20 in AF000177 293-851, Homo sapiens Sm-like protein CaSm (CaSm) mRNA, complete cds. /gb=AF000177 /ntype=RNA

U63824, class A, 20 probes, 20 in U63824 1129-1645, Human transcription factor RTEF-1 (RTEF1) mRNA, complete cds

S79219, class A, 20 probes, 20 in S79219 344-902, metastasis-associated gene [human, highly metastatic lung cell subline Anip[937], mRNA Partial, 978 nt]

U21858, class A, 20 probes, 20 in U21858 704-1064, Human transcriptional activation factor TAFII32 mRNA, complete cds

AB002382, class A, 20 probes, 20 in AB002382 4858-5320, Human mRNA for KIAA0384 gene, complete cds. /gb=AB002382 /ntype=RNA

Spermidine/Spermine N1-Acetyltransferase, Alt. Splice 2

M65131, class A, 20 probes, 20 in M65131mRNA 2187-2709, Human methylmalonyl-CoA mutase (MCM) mRNA, complete cds

Arrestin, Beta 2

L42176, class A, 20 probes, 20 in L42176 844-1384, Homo sapiens (clone 35.3) DRAL mRNA, complete cds

S82362, class A, 20 probes, 20 in S82362 1119-1690, hRAR-beta 2=retinoic-acid-receptor beta/suspected tumor suppressor {5 region, transcription control region} [human, mRNA Partial, 1730 nt]. /gb=S82362 /ntype=RNA

Z69720, class C, 20 probes, 20 in all_Z69720 14484-15067, Human DNA sequence from cosmid RA36 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains 3-methyl-adenine DNA glycosylase, ESTs and CpG island.

L39211, class A, 20 probes, 20 in L39211 1877-2399, Homo sapiens mitochondrial carnitine palmitoyltransferase I mRNA, complete cds

U79298, class A, 20 probes, 20 in U79298 928-1312, Human clone 23803 mRNA, partial cds.

L33075, class A, 20 probes, 20 in L33075 6978-7530, Homo sapiens ras GTPase-activating-like protein (IQGAP1) mRNA, complete cds

Z70222, class A, 20 probes, 17 in Z70222cds 3-213: 3 in reverseSequence, 25-37, H.sapiens mRNA for ORF (clone ICRFp507G2490).

S72370, class A, 20 probes, 20 in S72370 3422-3962, pyruvate carboxylase [human, kidney, mRNA, 4017 nt]

Z22865, class A, 20 probes, 19 in Z22865cds 164-578: 1 in reverseSequence, 620, H.sapiens dermatopontin mRNA, complete CDS

E. coli /GEN=bioD /DB_XREF=gb:J04423.1 /NOTE=SIF corresponding to nucleotides 5286-5570 of gb:J04423.1, not 100% identical /DEF=E.coli 7,8-diamino-pelargonic acid (bioA), biotin synthetase (bioB), 7-keto-8-amino-pelargonic acid synthetase (bioF), bioC protein, and dethiobiotin synthetase (bioD), complete cds.

Y09443, class A, 20 probes, 20 in Y09443 1545-1935, H.sapiens mRNA for alkyl-dihydroxyacetonephosphate synthase precursor

L13391, class A, 20 probes, 20 in L13391exon#5 265-808, Human helix-loop-helix basic phosphoprotein (G0S8) gene, complete cds

U33632, class A, 20 probes, 20 in U33632 1401-1839, Human two P-domain K+ channel TWIK-1 mRNA, complete cds

M55542, class A, 20 probes, 20 in M55542mRNA 2310-2802, Human guanylate binding protein isoform I (GBP-2) mRNA, complete cds

L00634, class A, 19 probes, 19 in L00634 734-1246, Human farnesyl-protein transferase alpha-subunit mRNA, complete cds

D87684, class A, 20 probes, 20 in D87684 3222-3696, Human mRNA for KIAA0242 gene, partial cds

AD000092, class C, 20 probes, 11 in AD000092 21426-21637: 7 in AD000092cds#1 3369-3688: 2 in all_AD000092 21396-21427, hypothetical human serine-threonine protein kinase R31240_1 gene extracted from Homo sapiens DNA from chromosome 19p13.2 cosmids R31240, R30272 and R28549 containing the EKLF, GCDH, CRTC, and RAD23A genes, genomic sequence, hypothetical human serine-threonine protein kinase R31240_1 gene extracted from Homo sapiens DNA from chromosome 19p13.2 cosmids R31240, R30272 and R28549 containing the EKLF, GCDH, CRTC, and RAD23A genes, genomic sequence, hypothetical human serine-threonine protein kinase R31240_1 gene extracted from Homo sapiens DNA from chromosome 19p13.2 cosmids R31240, R30272 and R28549 containing the EKLF, GCDH, CRTC, and RAD23A genes, genomic sequence

U73682, class A, 20 probes, 20 in U73682 2255-2651, Human meningioma-expressed antigen 11 (MEA11) mRNA, partial cds

X98834, class A, 20 probes, 20 in X98834mRNA 4116-4620, zinc finger protein Hsal2 gene extracted from H.sapiens mRNA for zinc finger protein, Hsal2

U66036, class A, 20 probes, 20 in U66036 732-1236, Human sulfotransferase mRNA, complete cds

X05997, class B, 20 probes, 15 in X05997cds#1 726-1158: 5 in reverseSequence, 1280-1316, Human mRNA for gastric lipase

Prostaglandin Ep3 Receptor, Alt. Splice 8 - Also Represents: D86096_cds6

Z29077, class A, 20 probes, 20 in Z29077mRNA#1 3-55, un-named-transcript-1 from H.sapiens cdc25 gene promoter region. /gb=Z29077 /ntype=DNA /annot=mRNA

M31520, class C, 4 probes, 4 in M31520mRNA 2-131, Human ribosomal protein S24 mRNA, Human ribosomal protein S24 mRNA, Human ribosomal protein S24 mRNA

L40400, class A, 20 probes, 20 in L40400mRNA 2014-2542, Homo sapiens (clone zap113) mRNA, 3 end of cds

U03891, class A, 20 probes, 20 in U03891 90-576, Human phorbolin I mRNA, partial cds

X76040, class C, 20 probes, 20 in all_X76040 2954-3309, H.sapiens mRNA for Lon protease-like protein

U28386, class A, 20 probes, 20 in U28386 1405-1933, Human nuclear localization sequence receptor hSRP1alpha mRNA, complete cds

U69127, class A, 20 probes, 20 in U69127 2758-3106, Human FUSE binding protein 3 (FBP3) mRNA, partial cds

U07681, class A, 20 probes, 20 in U07681 2075-2585, Human NAD(H)-specific isocitrate dehydrogenase alpha subunit precursor mRNA, complete cds

X07876, class C, 20 probes, 20 in all_X07876 1706-2205, Human mRNA for irp protein (int-1 related protein)

X15940, class A, 20 probes, 18 in X15940cds 66-348: 2 in reverseSequence, 379-385, Human mRNA for ribosomal protein L31

D38163, class A, 20 probes, 20 in D38163 3117-3661, Human mRNA for a1(XIX) collagen chain, complete cds

D49824, class B, 13 probes, 13 in D49824 945-1110, Human HLA-B null allele mRNA, Human HLA-B null allele mRNA

D49728, class A, 20 probes, 20 in D49728 2002-2330, Human NAK1 mRNA for DNA binding protein, complete cds

U48861, class A, 20 probes, 20 in U48861 1914-2430, Human beta 4 nicotinic acetylcholine receptor subunit mRNA, complete cds

L76380, class A, 20 probes, 20 in L76380mRNA 2459-2969, Homo sapiens (clone HSNME29) CGRP type 1 receptor mRNA, complete cds

D63880, class A, 20 probes, 20 in D63880 4952-5504, Human mRNA for KIAA0159 gene, complete cds

M14200, class A, 20 probes, 20 in M14200mRNA 139-469, Human diazepam binding inhibitor (DBI) mRNA, complete cds

D16688, class A, 20 probes, 20 in D16688 876-1448, Human LTG9/MLLT3 mRNA, C-terminal

S74221, class A, 20 probes, 20 in S74221 317-695, IK=IK factor [human, leukemic cells K562, chronic myeloid leukemia patient, mRNA, 756 nt]

D21337, class A, 20 probes, 20 in D21337 5825-6353, Human mRNA for collagen

M86934, class A, 20 probes, 20 in M86934 1529-1973, Human GS1 (protein of unknown function) mRNA, complete cds

U51166, class A, 20 probes, 20 in U51166 2941-3361, Human G/T mismatch-specific thymine DNA glycosylase mRNA, complete cds

Z47553, class A, 20 probes, 20 in Z47553mRNA 1761-2247, H.sapiens mRNA for flavin-containing monooxygenase 5 (FMO5)

U37689, class A, 20 probes, 20 in U37689 344-752, Human RNA polymerase II subunit (hsRPB8) mRNA, complete cds

X15722, class A, 20 probes, 18 in X15722cds 931-1411: 2 in reverseSequence, 1569-1575, Human mRNA for glutathione reductase (EC 1.6.4.2)

U15932, class A, 20 probes, 20 in U15932 1928-2294, Human dual-specificity protein phosphatase mRNA, complete cds

AC002115, class A, 20 probes, 20 in AC002115mRNA#1 932-1448, COX6B gene (COXG) extracted from Human DNA from overlapping chromosome 19 cosmids R31396, F25451, and R31076 containing COX6B and UPKA, genomic sequence, COX6B gene (COXG) extracted from Human DNA from overlapping chromosome 19 cosmids R31396, F25451, and R31076 containing COX6B and UPKA, genomic sequence, COX6B gene (COXG) extracted from Human DNA from overlapping chromosome 19 cosmids R31396, F25451, and R31076 containing COX6B and UPKA, genomic sequence, COX6B gene (COXG) extracted from Human DNA from overlapping chromosome 19 cosmids R31396, F25451, and R31076 containing COX6B and UPKA, genomic sequence

Z83741, class C, 20 probes, 20 in all_Z83741 654-1183, H.sapiens hH2A/m gene.

X83416, class A, 20 probes, 20 in X83416exon 1688-2160, H.sapiens PrP gene, exon 2

AF012024, class A, 20 probes, 20 in AF012024 658-1175, Homo sapiens integrin cytoplasmic domain associated protein (Icap-1b) mRNA, complete cds. /gb=AF012024 /ntype=RNA

U57592, class A, 20 probes, 20 in U57592 3563-4043, Human jumonji putative protein (jumonji) mRNA, complete cds

L42451, class A, 20 probes, 20 in L42451mRNA 947-1397, Homo sapiens pyruvate dehydrogenase kinase isoenzyme 2 (PDK2) mRNA, complete cds

L26494, class A, 20 probes, 20 in L26494 1598-2084, Homo sapiens (oct-6) mRNA, complete cds

D42046, class A, 20 probes, 20 in D42046 3648-4077, Human mRNA for KIAA0083 gene, partial cds

X15949, class C, 20 probes, 20 in all_X15949 1543-2144, Human mRNA for interferon regulatory factor-2 (IRF-2)

L27476, class A, 20 probes, 20 in L27476 3901-4429, Human X104 mRNA, complete cds

M73047, class A, 20 probes, 20 in M73047 4025-4565, Homo sapiens tripeptidyl peptidase II mRNA, complete cds

Desmoplakin I

M13452, class A, 20 probes, 20 in M13452 1927-2435, Human lamin A mRNA, 3 end

Y07827, class A, 20 probes, 20 in Y07827cds 785-972, H.sapiens mRNA for put. B7,3 molecule of CD80-CD60 protein family

Xanthine Dehydrogenase (Gb:U06117)

U11690, class A, 20 probes, 20 in U11690 3665-4241, Human faciogenital dysplasia (FGD1) mRNA, complete cds

D90097, class A, 20 probes, 20 in D90097cds 983-1499, Human AMY2B gene for alpha-amylase

X68314, class C, 20 probes, 20 in all_X68314 466-923, H.sapiens mRNA for glutathione peroxidase-GI

V00533, class A, 20 probes, 20 in V00533mRNA 391-915, IFNA gene (interferon alpha-h2) extracted from Human gene for leukocyte (alpha) interferon H

X82850, class B, 20 probes, 14 in X82850cds 722-1090: 6 in reverseSequence, 1108-1238, H.sapiens mRNA for thyroid transcript factor 1

U42412, class A, 20 probes, 20 in U42412 977-1535, Human 5 -AMP-activated protein kinase, gamma-1 subunit mRNA, complete cds

X97544, class B, 20 probes, 15 in X97544cds 291-453: 5 in reverseSequence, 508-724, H.sapiens mRNA for TIM17 preprotein translocase

U82256, class A, 20 probes, 20 in U82256 1325-1823, Human arginase type II mRNA, complete cds

U90904, class A, 20 probes, 20 in U90904 1102-1342, Human clone 23773 mRNA sequence

U70671, class A, 20 probes, 20 in U70671 695-1115, Human ataxin-2 related protein mRNA, partial cds

Y10807, class A, 20 probes, 20 in Y10807 650-1227, H.sapiens mRNA for arginine methyltransferase, splice variant, 1262 bp

U29171, class A, 20 probes, 20 in U29171 1340-1742, Human casein kinase I delta mRNA, complete cds

U20648, class A, 20 probes, 20 in U20648 316-766, Human zinc finger protein (ZNF154) mRNA, partial cds

X64364, class C, 20 probes, 20 in all_X64364 1014-1561, H.sapiens mRNA for M6 antigen

Omega Light Chain, Immunoglobulin Lambda Light Chain Related

M33374, class A, 20 probes, 20 in M33374mRNA 19-427, Human cell adhesion protein (SQM1) mRNA, complete cds

U15555, class A, 20 probes, 20 in U15555 1003-1489, Human serine palmitoyltransferase (LCB2) mRNA, partial cds

S77094, class A, 20 probes, 20 in S77094 1075-1621, nicotinic acetylcholine receptor alpha subunit|AChR alpha subunit [human, thymic carcinoma, myasthenia gravis-associated thymoma patient 1494/88, mRNA Partial, 1676 nt]

U95019, class A, 20 probes, 20 in U95019 2358-2862, Human voltage-dependent calcium channel beta-2c subunit mRNA, complete cds.

U22963, class A, 20 probes, 20 in U22963 752-1238, Human class I histocompatibility antigen-like protein mRNA, complete cds.

X99688, class A, 20 probes, 20 in X99688 3790-4270, H.sapiens mRNA from TYL gene

AF002700, class A, 20 probes, 20 in AF002700 931-1471, Homo sapiens TGF-beta related neurotrophic factor receptor 2 (TRNR2) mRNA, complete cds.

X51823, class C, 6 probes, 6 in all_X51823 2-51, Human mRNA for B-subunit of coagulation factor XIII (FXIIIB) (partial). /gb=X51823 /ntype=RNA, Human mRNA for B-subunit of coagulation factor XIII (FXIIIB) (partial). /gb=X51823 /ntype=RNA

Z83804, class A, 20 probes, 20 in Z83804 29-261, H.sapiens mRNA for axonemal dynein heavy chain (partial, ID hdhc7).

M11749, class B, 20 probes, 12 in M11749cds 141-405: 8 in reverseSequence, 1501-1747, Human Thy-1 glycoprotein gene, complete cds

U79734, class A, 20 probes, 20 in U79734 4119-4683, Human huntingtin interacting protein (HIP1) mRNA, complete cds.

X96584, class C, 20 probes, 20 in all_X96584 1444-1961, H.sapiens mRNA for NOV protein

X77567, class B, 20 probes, 15 in X77567cds 853-1215: 5 in reverseSequence, 1354-1518, H.sapiens mRNA for InsP3 5-phosphatase

X06256, class C, 20 probes, 20 in all_X06256 3681-4180, Human mRNA for fibronectin receptor alpha subunit

S74017, class A, 20 probes, 20 in S74017 1721-2213, Nrf2=NF-E2-like basic leucine zipper transcriptional activator [human, hemin-induced K562 cells, mRNA, 2304 nt]

Y00318, class B, 20 probes, 15 in Y00318cds#1 1317-1653: 5 in reverseSequence, 1814-1916, Human mRNA for complement control protein factor I

M30818, class A, 20 probes, 20 in M30818mRNA 2384-2888, Human interferon-induced cellular resistance mediator protein (MxB) mRNA, complete cds

D80012, class A, 20 probes, 20 in D80012 2697-3237, Human mRNA for KIAA0190 gene, partial cds

D38583, class A, 20 probes, 20 in D38583 109-475, Human mRNA for calgizzarin, complete cds

U07969, class A, 20 probes, 20 in U07969 2956-3259, Human intestinal peptide-associated transporter HPT-1 mRNA, complete cds

U50079, class A, 20 probes, 20 in U50079 1013-1569, Human histone deacetylase HD1 mRNA, complete cds

U18549, class A, 20 probes, 20 in U18549exon#2 1091-1571, Human GPR6 G protein-coupled receptor gene, complete cds

M36341, class A, 20 probes, 20 in M36341 912-1458, Human ADP-ribosylation factor 4 (ARF4) mRNA, complete cds

L32866, class C, 20 probes, 20 in all_L32866 67-452, Human effector cell protease receptor-1 (EPR-1) gene, partial cds

U06681, class A, 20 probes, 20 in U06681 1348-1774, Human clone CCA12 mRNA containing CCA trinucleotide repeat

U00943, class A, 20 probes, 20 in U00943 1017-1203, Human clone A9A2BRB2 (CAC)n/(GTG)n repeat-containing mRNA

U50535, class A, 20 probes, 20 in U50535 1856-2270, Human BRCA2 region, mRNA sequence CG006

L40396, class A, 20 probes, 20 in L40396mRNA 1542-2028, Homo sapiens (clone s22i71) mRNA fragment

M74558, class A, 20 probes, 20 in M74558 4849-5170, Human SIL mRNA, complete cds

X74987, class C, 20 probes, 20 in all_X74987 2208-2684, H.sapiens mRNA for 2 -5 oligoadenylate binding protein

U83843, class A, 20 probes, 20 in U83843 725-1145, Human HIV-1 Nef interacting protein (Nip7-1) mRNA, partial cds. /gb=U83843 /ntype=RNA

U32315, class A, 20 probes, 20 in U32315 1374-1842, Human syntaxin 3 mRNA, complete cds

U83115, class A, 20 probes, 20 in U83115 6327-6753, Human non-lens beta gamma-crystallin like protein (AIM1) mRNA, partial cds

X61755, class A, 20 probes, 20 in X61755mRNA 1020-1562, Human HOX3D gene for homeoprotein HOX3D

U66669, class A, 20 probes, 16 in U66669 785-1240: 4 not in GB record, Human 3-hydroxyisobutyryl-coenzyme A hydrolase mRNA, complete cds

M93311, class C, 20 probes, 20 in all_M93311 1950-2085, Human metallothionein-III gene, complete cds

U49278, class A, 20 probes, 20 in U49278 2752-3262, Human putative DNA-binding protein mRNA, partial cds

M85164, class A, 20 probes, 20 in M85164 1354-1852, Homo sapiens SRF accessory protein 1B (SAP-1) mRNA, complete cds

L17128, class A, 20 probes, 20 in L17128 1940-2480, Homo sapiens (clone H4/H16) gamma-glutamic carboxylase mRNA, complete cds

Y10256, class A, 20 probes, 20 in Y10256 2797-3247, H.sapiens mRNA for serine/threonine protein kinase, NIK

L20773, class A, 20 probes, 20 in L20773 1025-1517, Homo sapiens mRNA in the region near the btk gene involved in a-gamma-globulinemia

X80497, class C, 20 probes, 20 in all_X80497 3995-4428, H.sapiens PHKLA mRNA

Z49155, class C, 20 probes, 20 in reverse_Z49155 27087-27346, Human DNA from cosmid L83d3, Huntingtons Disease Region, chromosome 4p16.3

D30715, class A, 20 probes, 20 in D30715mRNA#3 3-198, alternative splicing; type-2 mRNA from Human PAP (pancreatitis-associated protein) gene, 5 -flanking region. /gb=D30715 /ntype=DNA /annot=mRNA

D50582, class B, 20 probes, 10 in D50582cds 954-1128: 10 in reverseSequence, 1367-1535, Human gene for inward rectifier K channel, complete cds

U40490, class A, 20 probes, 20 in U40490 3673-4177, Human nicotinamide nucleotide transhydrogenase mRNA, nuclear gene encoding mitochondrial protein, complete cds

M31210, class A, 20 probes, 20 in M31210 2258-2708, Human endothelial differentiation protein (edg-1) gene mRNA, complete cds

Estrogen Sulfotransferase, Ste

M34455, class A, 20 probes, 20 in M34455 1427-1889, Human interferon-gamma-inducible indoleamine 2,3-dioxygenase (IDO) mRNA, complete cds

Zinc Finger Protein (Gb:M88357)

M97676, class A, 20 probes, 20 in M97676 1406-1646, Homo sapiens (region 7) homeobox protein (HOX7) mRNA, complete cds

L77571, class A, 20 probes, 20 in L77571mRNA 1738-2218, Homo sapiens DGS-A mRNA, 3 end

M27878, class A, 20 probes, 20 in M27878 2656-3172, Human DNA binding protein (HPF2) mRNA, complete cds

X71973, class B, 20 probes, 14 in X71973cds 200-530: 6 in reverseSequence, 658-808, H.sapiens GPx-4 mRNA for phospholipid hydroperoxide glutathione peroxidase

D31764, class A, 20 probes, 20 in D31764 1478-1982, Human mRNA for KIAA0064 gene, complete cds

M55409, class A, 20 probes, 20 in M55409 556-1069, Human pancreatic tumor-related protein mRNA, 3 end

M69225, class A, 20 probes, 20 in M69225mRNA 8371-8845, Human bullous pemphigoid antigen (BPAG1) mRNA, complete cds

U29091, class A, 20 probes, 20 in U29091 960-1368, Human selenium-binding protein (hSBP) mRNA, complete cds. /gb=U29091 /ntype=RNA

U05589, class A, 20 probes, 20 in U05589 877-1453, Human ribosomal protein S1 homolog mRNA, partial cds

U70136, class A, 20 probes, 20 in U70136 4546-4957, Human megakaryocyte stimulating factor mRNA, complete cds

Zinc Finger Protein Znfpt1

X76105, class C, 20 probes, 20 in all_X76105 1661-2208, H.sapiens DAP-1 mRNA

M96843, class A, 20 probes, 20 in M96843 668-1112, Human striated muscle contraction regulatory protein (Id2B) mRNA, complete cds

U82275, class A, 20 probes, 20 in U82275 1335-1647, Human immunoglobulin-like transcript 1 mRNA, complete cds

J05633, class A, 20 probes, 20 in J05633 2714-3008, Human integrin beta-5 subunit mRNA, complete cds

U63090, class A, 20 probes, 20 in U63090 1303-1813, Human Gal beta-1,3 GalNAc alpha-2,3 sialyltransferase (ST3Gal II) mRNA, complete cds

U62531, class A, 20 probes, 20 in U62531 3465-4029, Human AE2 anion exchanger (SLC4A2) mRNA, complete cds

U59309, class A, 20 probes, 20 in U59309 1200-1710, Human fumarase precursor (FH) mRNA, nuclear gene encoding mitochondrial protein, complete cds

L00972, class A, 20 probes, 20 in L00972 2064-2202, Human cystathionine-beta-synthase (CBS) mRNA

U80017, class A, 20 probes, 20 in U80017mRNA#2 5760-6039, btf2p44 gene (basic transcription factor 2 p44) extracted from Human basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds, btf2p44 gene (basic transcription factor 2 p44) extracted from Human basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds, btf2p44 gene (basic transcription factor 2 p44) extracted from Human basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds

U87964, class A, 20 probes, 20 in U87964 1515-2094, Human putative G-protein (GP-1) mRNA, complete cds.

X61079, class A, 20 probes, 20 in X61079mRNA 10-211, Human mRNA for T cell receptor, clone IGRA24.

Transcriptional Coactivator Pc4

U05572, class A, 20 probes, 20 in U05572 2563-3028, Human lysosomal alpha-mannosidase (MANB) mRNA, complete cds
Adrenal-Specific Protein Pg2 - Also Represents: U15979

X52979, class C, 20 probes, 18 in all_X52979 759-895: 2 not in GB record, SmB protein gene extracted from Human gene for small nuclear ribonucleoproteins SmB and SmB

Y00705, class C, 20 probes, 20 in all_Y00705 5-356, Homo sapiens pstI mRNA for pancreatic secretory inhibitor (expressed in neoplastic tissue).

X90858, class A, 20 probes, 17 in X90858cds#2 396-888: 3 in reverseSequence, 1270-1306, H.sapiens mRNA for uridine phosphorylase

U12779, class A, 20 probes, 20 in U12779 1685-1959, Human MAP kinase activated protein kinase 2 mRNA, complete cds

J03258, class A, 20 probes, 20 in J03258mRNA 4003-4561, Human vitamin D receptor mRNA, complete cds

L02426, class A, 20 probes, 20 in L02426 1040-1556, Human 26S protease (S4) regulatory subunit mRNA, complete cds

B. subtilis /GEN=thrB /DB_XREF=gb:X04603.1 /NOTE=SIF corresponding to nucleotides 1689-2151 of gb:X04603.1 /DEF=B. subtilis thrB and thrC genes for homoserine kinase and threonine synthase EC 2.7.1.39 and EC 4.2.99.2, respectively).

U37426, class A, 20 probes, 20 in U37426 4269-4815, Human kinesin-like spindle protein HKSP (HKSP) mRNA, complete cds

S42303, class A, 20 probes, 20 in S42303 3537-4029, N-cadherin [human, umbilical vein endothelial cells, mRNA, 4132 nt]

U59632, class A, 20 probes, 20 in U59632 2578-3138, Human H5 mRNA, partial cds, and platelet glycoprotein Ib beta chain mRNA, complete cds

U74612, class A, 20 probes, 20 in U74612 2915-3425, Human hepatocyte nuclear factor-3/fork head homolog 11A (HFH-11A) mRNA complete cds.

U50733, class A, 20 probes, 20 in U50733 1132-1642, Human dynamitin mRNA, complete cds

D13969, class A, 20 probes, 20 in D13969 1638-2148, Human mRNA for Mel-18 protein, complete cds

X83973, class B, 20 probes, 13 in X83973cds 2262-2538: 7 in reverseSequence, 2738-2822, H.sapiens mRNA for TTF-I

L02320, class A, 20 probes, 20 in L02320 1463-1997, Human radixin mRNA, complete cds

U34252, class A, 20 probes, 20 in U34252 2177-2579, Human gamma-aminobutyraldehyde dehydrogenase mRNA, complete cds

U40223, class A, 20 probes, 19 in U40223cds 660-1068: 1 in reverseSequence, 1548, Human uridine nucleotide receptor (UNR) gene, complete cds

L38486, class A, 20 probes, 20 in L38486mRNA 1162-1720, Human microfibril-associated glycoprotein 4 (MFAP4) mRNA, 3 end of cds

U72936, class A, 20 probes, 20 in U72936 9836-10377, Human putative DNA dependent ATPase and helicase (ATRX) mRNA, alternatively spliced product 1, complete cds

U72649, class A, 20 probes, 20 in U72649 2206-2584, Human BTG2 (BTG2) mRNA, complete cds

U00001, class A, 20 probes, 20 in U00001 2019-2547, Human homologue of S. pombe nuc2+ and A. nidulans bimA

U91316, class A, 20 probes, 20 in U91316 891-1461, Human acyl-CoA thioester hydrolase mRNA, complete cds

U22322, class A, 20 probes, 20 in U22322 2205-2587, Human nuclear tyrosine protein kinase Rak mRNA, complete cds

M17236, class C, 15 probes, 15 in all_M17236 1896-2224, Human MHC class II HLA-DQ-alpha gene (DR4,w6), Human MHC class II HLA-DQ-alpha gene (DR4,w6)

L40027, class A, 20 probes, 20 in L40027mRNA 1586-2132, Homo sapiens glycogen synthase kinase 3 mRNA, complete cds

M55131, class A, 20 probes, 20 in M55131mRNA 5636-6134, Human cystic fibrosis transmembrane conductance regulator (CFTR) gene

D87461, class A, 20 probes, 20 in D87461 2959-3517, Human mRNA for KIAA0271 gene, complete cds

X98178, class A, 20 probes, 20 in X98178cds 567-607, H.sapiens mRNA for MACH-beta-4 protein. /gb=X98178 /ntype=RNA

L37042, class A, 20 probes, 20 in L37042mRNA 960-1314, Homo sapiens casein kinase I alpha isoform (CSNK1A1) mRNA, complete cds

L11702, class A, 20 probes, 20 in L11702 2837-3335, Human phospholipase D mRNA, complete cds

L20688, class A, 20 probes, 20 in L20688 864-1188, Human GDP-dissociation inhibitor protein (Ly-GDI) mRNA, complete cds

X66534, class C, 20 probes, 20 in all_X66534 2622-2953, H.sapiens soluble guanylate cyclase large subunit mRNA

U15177, class C, 20 probes, 20 in all_U15177 2291-2724, Human cosmid CRI-JC2015 at D10S289 in 10sp13

L41816, class A, 20 probes, 20 in L41816mRNA 891-1389, Homo sapiens cam kinase I mRNA, complete cds

M11119, class A, 20 probes, 20 in M11119mRNA 722-1011, Human endogenous retrovirus envelope region mRNA (PL1)

X58822, class A, 20 probes, 20 in X58822mRNA 905-1422, Human IFN-omega 1 gene for interferon-omega 1

L36069, class A, 20 probes, 20 in L36069 1283-1709, Human high conductance inward rectifier potassium channel alpha subunit mRNA, complete cds

U14971, class A, 20 probes, 20 in U14971 91-661, Human ribosomal protein S9 mRNA, complete cds

D85815, class B, 20 probes, 12 in D85815cds 282-564: 8 in reverseSequence, 753-879, Human DNA for rhoHP1, complete cds

M27543, class A, 20 probes, 20 in M27543mRNA 2548-3070, Human guanine nucleotide-binding protein (Gi) alpha subunit mRNA, complete cds

U82010, class A, 20 probes, 20 in U82010mRNA 2432-2930, Homo sapiens Human heme A: farnesyltransferase (COX10) gene promoter region and

L11672, class C, 3 probes, 3 in all_L11672 3552-3579, Human Kruppel related zinc finger protein (HTF10) mRNA, complete cds, Human Kruppel related zinc finger protein (HTF10) mRNA, complete cds

J04794, class A, 20 probes, 20 in J04794mRNA 567-1071, Human aldehyde reductase mRNA, complete cds

X95808, class A, 20 probes, 20 in X95808mRNA 5503-6037, H.sapiens mRNA for protein encoded by a candidate gene, DXS6673E, for mental retardation

U03397, class A, 20 probes, 20 in U03397 787-1358, Human receptor protein 4-1BB mRNA, complete cds

L11669, class A, 20 probes, 20 in L11669 1355-1715, Human tetracycline transporter-like protein mRNA, complete cds

U31449, class A, 20 probes, 20 in U31449 773-1337, Human intestinal and liver tetraspan membrane protein (il-TMP) mRNA, complete cds

U40372, class A, 20 probes, 20 in U40372 1565-2021, Human 3 ,5 cyclic nucleotide phosphodiesterase (HSPDE1C3A) mRNA, partial cds

U20530, class A, 20 probes, 20 in U20530 47-593, Human bone phosphoprotein spp-24 precursor mRNA, complete cds. /gb=U20530 /ntype=RNA

M61855, class C, 20 probes, 20 in all_M61855 1535-1714, Human cytochrome P4502C9 (CYP2C9) mRNA, clone 25

X97267, class A, 20 probes, 20 in X97267mRNA 321-861, H.sapiens LPAP gene

Y10375, class C, 20 probes, 20 in all_Y10375 1179-1706, H.sapiens mRNA for SIRP-alpha1

L07758, class A, 20 probes, 20 in L07758 1288-1762, Human IEF SSP 9502 mRNA, complete cds

Z48501, class A, 19 probes, 19 in Z48501cds 957-1429, H.sapiens mRNA for polyadenylate binding protein II. /gb=Z48501 /ntype=RNA

D14520, class A, 20 probes, 20 in D14520 718-1258, Human mRNA for GC-Box binding protein BTEB2, complete cds

M59830, class C, 20 probes, 20 in all_M59830 2432-2661, Human MHC class III HSP70-2 gene (HLA), complete cds

M61764, class A, 20 probes, 20 in M61764mRNA 1015-1495, Human gamma-tubulin mRNA, complete cds

X89211, class A, 20 probes, 20 in X89211cds 1571-2129, H.sapiens DNA for endogenous retroviral like element. /gb=X89211 /ntype=DNA /annot=CDS

U47011, class B, 20 probes, 12 in U47011mRNA#1 581-791: 8 in reverseSequence, 751-961, FGF8 gene (fibroblast growth factor 8 precursor) extracted from Human fibroblast growth factor 8 (FGF8) gene

Z29066, class C, 20 probes, 20 in all_Z29066 1451-2035, H.sapiens nek2 mRNA for protein kinase

L22005, class A, 20 probes, 20 in L22005 797-1349, Human ubiquitin conjugating enzyme mRNA, partial cds

U65406, class A, 20 probes, 20 in U65406mRNA#1 1860-2370, KCNJ1 gene (potassium channel ROM-K3) extracted from Human alternatively spliced potassium channels ROM-K1, ROM-K2, ROM-K3, ROM-K4, ROM-K5, and ROM-K6 (KCNJ1) gene, complete cds

Guanine Nucleotide-Binding Protein Rap2, Ras-Oncogene Related

U60206, class A, 20 probes, 20 in U60206 1537-2003, Human stress responsive serine/threonine protein kinase Krs-1 mRNA, complete cds

D87448, class A, 20 probes, 20 in D87448 4763-5183, Human mRNA for KIAA0259 gene, partial cds

U05237, class A, 20 probes, 20 in U05237 2192-2570, Human fetal Alz-50-reactive clone 1 (FAC1) mRNA, complete cds

J04182, class A, 20 probes, 20 in J04182 1914-2394, Homo sapiens lysosomal membrane glycoprotein-1 (LAMP1) mRNA, complete cds

X04729, class C, 19 probes, 19 in all_X04729 2-263, Human mRNA for plasminogen activator inhibitor type 1 N-terminus. /gb=X04729 /ntype=RNA

L40904, class A, 20 probes, 20 in L40904mRNA 1228-1656, H. sapiens peroxisome proliferator activated receptor gamma, complete cds

Transcription Factor E4tf1, Respiratory, Gamma 2 Subunit, Alt. Splice 4 - Also Represents: U13047, D13316

Immunoglobulin Heavy Chain, Enhancer Element

X91141, class A, 20 probes, 20 in X91141mRNA 2412-2904, H.sapiens mRNA for RABAPTIN-5 protein

M24283, class A, 20 probes, 20 in M24283mRNA 2420-2954, Human major group rhinovirus receptor (HRV) mRNA, complete cds

U16861, class A, 20 probes, 20 in U16861 1076-1610, Human inward rectifying potassium channel mRNA, complete cds

L39060, class A, 20 probes, 20 in L39060mRNA 1037-1547, Homo sapiens transcription factor SL1 mRNA, complete cds

U05259, class C, 20 probes, 17 in all_U05259 4343-4740: 3 not in GB record, Human MB-1 gene, complete cds

Z47043, class A, 20 probes, 20 in Z47043cds 540-1080, Human partial cDNA sequence, clone x529, unknown open reading frame;. /gb=Z47043 /ntype=DNA /annot=CDS

Z49107, class B, 20 probes, 13 in Z49107cds 619-947: 7 in reverseSequence, 1046-1259, H.sapiens mRNA for galectin

U91930, class A, 20 probes, 20 in U91930 4196-4682, Human AP-3 complex delta subunit mRNA, complete cds

J02888, class A, 20 probes, 20 in J02888 453-915, Human quinone oxidoreductase (NQO2) mRNA, complete cds

U49436, class A, 20 probes, 20 in U49436 1303-1783, Human translation initiation factor 5 (eIF5) mRNA, complete cds

X07979, class C, 20 probes, 20 in all_X07979 3223-3596, Human mRNA for fibronectin receptor beta subunit

X75861, class C, 20 probes, 20 in all_X75861 1977-2566, H.sapiens TEGT gene

U50360, class A, 20 probes, 20 in U50360 81-385, Human calcium, calmodulin-dependent protein kinase II gamma mRNA, partial cds. /gb=U50360 /ntype=RNA

AF005361, class A, 20 probes, 20 in AF005361 1159-1663, Homo sapiens importin alpha 6 mRNA, complete cds. /gb=AF005361 /ntype=RNA

U11037, class A, 20 probes, 20 in U11037 19-499, Human Sel-1 like mRNA, complete cds

U59058, class A, 20 probes, 20 in U59058 8-508, Human beta-A3/A1 crystallin (CYRBA3/A1) mRNA, partial cds

X62055, class B, 20 probes, 10 in X62055cds 1413-1767: 10 in reverseSequence, 2028-2232, H.sapiens PTP1C mRNA for protein-tyrosine phosphatase 1C

M19311, class C, 4 probes, 4 in all_M19311 876-1059, Human calmodulin mRNA, complete cds, Human calmodulin mRNA, complete cds

X79781, class A, 20 probes, 18 in X79781cds 276-546: 2 in reverseSequence, 675-681, H.sapiens ray mRNA

L13852, class A, 20 probes, 20 in L13852 2790-3270, Homo sapiens ubiquitin-activating enzyme E1 related protein mRNA, complete cds

X99076, class A, 20 probes, 20 in X99076mRNA 736-1234, H.sapiens NRGN gene, exons 2,3 & 4 (joined CDS)

U41068, class B, 20 probes, 14 in U41068cds 2-268: 6 in reverseSequence, 944-1155, Human retinoid X receptor beta (RXRbeta) gene, partial 3 transcript, and collagen alpha2(XI) (COL11A2) gene

U16129, class A, 20 probes, 20 in U16129 2108-2684, Human glutamate receptor (GluR4) mRNA, complete cds.

X03363, class C, 20 probes, 20 in all_X03363 3873-4408, Human c-erb-B-2 mRNA

L40371, class A, 20 probes, 20 in L40371mRNA 661-1075, Homo sapiens thyroid receptor interactor (TRIP4) mRNA, 3 end of cds

U68485, class A, 20 probes, 19 in U68485 1356-1788: 1 not in GB record, Human Box-dependent MYC-interacting protein-1 (BIN1) mRNA, complete cds

X04201, class C, 20 probes, 20 in all_X04201 619-1073, Human skeletal muscle 1.3 kb mRNA for tropomyosin

U03886, class A, 20 probes, 20 in U03886 2214-2730, Human GS2 mRNA, complete cds

L10838, class A, 20 probes, 20 in L10838 79-499, Homo sapiens SR protein family, pre-mRNA splicing factor (SRp20) mRNA, complete cds

X83572, class A, 20 probes, 20 in X83572 1392-1920, H.sapiens ARSD mRNA

U26914, class A, 20 probes, 20 in U26914 3113-3533, Human ras-responsive element binding protein (RREB-1) mRNA, complete cds

L76927, class A, 20 probes, 20 in L76927mRNA 760-1330, Human galactokinase (GALK1) gene, complete cds

U27185, class A, 20 probes, 20 in U27185 263-791, Human RAR-responsive (TIG1) mRNA, complete cds

U15590, class A, 20 probes, 20 in U15590 306-840, Human heat shock protein 27 (HSP27) mRNA, complete cds

AB000895, class A, 20 probes, 20 in AB000895 25-385, Homo sapiens mRNA for cadherin FIB1, partial cds. /gb=AB000895 /ntype=RNA

U79267, class A, 20 probes, 20 in U79267 987-1437, Human clone 23840 mRNA, partial cds.

Z48482, class C, 20 probes, 20 in all_Z48482 2998-3401, H.sapiens mRNA for membrane-type matrix metalloproteinase 2

Dnaj Homolog (Gb:X63368), Alt. Splice Form 2 - Also Represents: X63368

D50912, class A, 20 probes, 20 in D50912 2685-3183, Human mRNA for KIAA0122 gene, partial cds

M93221, class A, 20 probes, 20 in M93221mRNA 4618-5110, Human macrophage mannose receptor (MRC1) gene

M77142, class A, 20 probes, 20 in M77142 1629-2193, Human polyadenylate binding protein (TIA-1) mRNA, complete cds

M16652, class A, 16 probes, 16 in M16652mRNA 324-858, Human pancreatic elastase IIA mRNA, complete cds, Human pancreatic elastase IIA mRNA, complete cds

Y08999, class A, 20 probes, 19 in Y08999cds 583-1045: 1 in reverseSequence, 1132, H.sapiens mRNA for Sop2p-like protein

D16294, class A, 20 probes, 20 in D16294 1019-1523, Human mRNA for mitochondrial 3-oxoacyl-CoA thiolase, complete cds

AD000092, class B, 20 probes, 15 in AD000092cds#2 714-1008: 5 in fullSequence, 87557-87797, hypothetical human serine-threonine protein kinase R31240_1 gene extracted from Homo sapiens DNA from chromosome 19p13.2 cosmids R31240, R30272 and R28549 containing the EKLF, GCDH, CRTC, and RAD23A genes, genomic sequence, hypothetical human serine-threonine protein kinase R31240_1 gene extracted from Homo sapiens DNA from chromosome 19p13.2 cosmids R31240, R30272 and R28549 containing the EKLF, GCDH, CRTC, and RAD23A genes, genomic sequence, hypothetical human serine-threonine protein kinase R31240_1 gene extracted from Homo sapiens DNA from chromosome 19p13.2 cosmids R31240, R30272 and R28549 containing the EKLF, GCDH, CRTC, and RAD23A genes, genomic sequence

L12060, class A, 20 probes, 20 in L12060mRNA 1032-1411, Homo sapiens retinoic acid receptor (gamma-7) mRNA

U78556, class A, 20 probes, 20 in U78556 2774-3248, Human cisplatin resistance associated alpha protein (hCRA alpha) mRNA, complete cds

Z73903, class C, 20 probes, 20 in all_Z73903 5001-5554, H.sapiens mRNA for TRPC1A.

M37457, class A, 16 probes, 16 in M37457cds 2823-2990, Human Na+,K+ #NAME? catalytic subunit alpha-III isoform gene, Human Na+,K+ #NAME? catalytic subunit alpha-III isoform gene

L00352, class A, 20 probes, 20 in L00352exon 1952-2492, Human low density lipoprotein receptor gene

U72648, class B, 17 probes, 10 in U72648cds 1037-1354: 7 in reverseSequence, 4177-4210, Human alpha2-C4-adrenergic receptor gene, complete cds

L49209, class A, 20 probes, 20 in L49209exon 25-92, Homo sapiens retinoblastoma susceptibility protein (RB1) I66D 4 bp deletion mutant (resulting in premature stop at amino acid 134) gene, exon 4 (L11910 bases 41867-42075).

X95654, class B, 20 probes, 11 in X95654cds 2682-2862: 9 in reverseSequence, 3022-3202, H.sapiens mRNA for SCP1 protein

L13761, class A, 20 probes, 20 in L13761mRNA 3838-4270, Human dihydrolipoamide dehydrogenase gene, exon 14

X58255, class A, 20 probes, 20 in X58255mRNA 2472-2862, Human Flg-2 gene for fibroblast growth factor receptor

U81556, class A, 20 probes, 20 in U81556 1541-1925, Human hypothetical protein A4 mRNA, complete cds

X98411, class B, 20 probes, 11 in X98411cds 2016-2256: 9 in reverseSequence, 2340-2490, H.sapiens mRNA for myosin-IE

L76569, class A, 20 probes, 20 in L76569mRNA 6762-7284, Homo sapiens (clones cYG3, B5P6C4) fragile X E mental retardation syndrome protein (FMR2) mRNA, complete cds

L12350, class A, 20 probes, 20 in L12350mRNA 5247-5721, Human thrombospondin 2 (THBS2) mRNA, complete cds

L19437, class A, 20 probes, 20 in L19437 857-1211, Human transaldolase mRNA containing transposable element, complete cds

Z75190, class B, 18 probes, 13 in Z75190cds 1747-2070: 5 in reverseSequence, 2087-2276, H.sapiens mRNA for apolipoprotein E receptor 2.

L34060, class A, 20 probes, 20 in L34060 2124-2502, Homo sapiens cadherin-8 mRNA, complete cds

X05610, class C, 20 probes, 20 in all_X05610 1701-2098, Human mRNA for type IV collagen alpha -2 chain

U03187, class A, 20 probes, 20 in U03187 1505-2015, Human IL12 receptor component mRNA, complete cds

X68486, class C, 20 probes, 20 in all_X68486 2465-2934, H.sapiens mRNA for A2a adenosine receptor

K02100, class A, 20 probes, 20 in K02100mRNA 983-1421, Human ornithine transcarbamylase (OTC) mRNA, complete coding sequence

U80034, class A, 20 probes, 20 in U80034 1785-2283, Human mitochondrial intermediate peptidase precursor (MIPEP) mRNA, mitochondrial gene encoding mitochondrial protein, complete cds.

U60519, class A, 20 probes, 20 in U60519 2965-3499, Human apoptotic cysteine protease Mch4 (Mch4) mRNA, complete cds

X70811, class C, 20 probes, 20 in all_X70811 2067-2566, H.sapiens mRNA for beta 3 adrenergic receptor

U09413, class A, 20 probes, 20 in U09413 1957-2389, Human zinc finger protein ZNF135 mRNA, complete cds

S77582, class A, 19 probes, 19 in S77582 2-55, HERVK10/HUMMTV reverse transcriptase homolog {clone RT240} [human, multiple sclerosis, brain plaques, mRNA Partial, 89 nt]. /gb=S77582 /ntype=RNA

Z19585, class A, 20 probes, 16 in Z19585cds 2522-2858: 4 in reverseSequence, 2909-2939, H.sapiens mRNA for thrombospondin-4

D11139, class C, 20 probes, 20 in all_D11139 1902-2407, Human gene for tissue inhibitor of metalloproteinases, partial sequence

X64877, class C, 4 probes, 4 in all_X64877 494-529, H.sapiens mRNA for serum protein, H.sapiens mRNA for serum protein

D50477, class A, 20 probes, 20 in D50477 1507-2066, Human mRNA for membrane-type matrix metalloproteinase 3, complete cds

M89796, class A, 20 probes, 20 in M89796mRNA 3128-3671, Human high affinity IgE receptor beta chain gene, complete cds

D87119, class A, 20 probes, 20 in D87119 3614-4160, Human cancellous bone osteoblast mRNA for GS3955, complete cds

Cyclophilin-Related Protein

M16336, class A, 20 probes, 20 in M16336mRNA 923-1463, Human T-cell surface antigen CD2 (T11) mRNA, complete cds, clone PB1

X70218, class A, 20 probes, 20 in X70218 771-1203, H. sapiens mRNA for protein phosphatase X

Z35085, class C, 19 probes, 19 in all_Z35085 1960-2506, H.sapiens mRNA for unknown antigen

L20348, class B, 20 probes, 11 in L20348exon 15-219: 9 not in GB record, Homo sapiens oncomodulin gene

D14134, class A, 20 probes, 20 in D14134 1646-2192, Human mRNA for RAD51, complete cds

L08424, class A, 20 probes, 20 in L08424 1124-1586, Homo sapiens achaete scute homologous protein (ASH1) mRNA, complete cds

X87160, class C, 20 probes, 20 in all_X87160 2768-3339, H.sapiens mRNA for gamma subunit of epithelial amiloride-sensitive sodium channel

D50926, class A, 20 probes, 20 in D50926 3626-4124, Human mRNA for KIAA0136 gene, partial cds

L77730, class A, 20 probes, 20 in L77730exon 529-1009, Homo sapiens A3 adenosine receptor (ADORA3) gene

Z23090, class A, 20 probes, 17 in Z23090cds 277-589: 3 in reverseSequence, 1086-1098, H.sapiens mRNA for 28 kDa heat shock protein

U73167, class C, 20 probes, 20 in all_U73167 4971-35099, H_LUCA14.2a gene extracted from Human cosmid LUCA14, H_LUCA14.2a gene extracted from Human cosmid LUCA14, H_LUCA14.2a gene extracted from Human cosmid LUCA14, H_LUCA14.2a gene extracted from Human cosmid LUCA14, H_LUCA14.2a gene extracted from Human cosmid LUCA14

U05321, class A, 20 probes, 20 in U05321mRNA 3734-4220, Human X-linked PEST-containing transporter (XPCT) gene, promoter and

U01147, class A, 20 probes, 20 in U01147mRNA 4659-5211, Human guanine nucleotide regulatory protein (ABR) mRNA, complete cds

U51096, class A, 20 probes, 20 in U51096 1240-1720, Human homeobox protein Cdx2 mRNA, complete cds

J05556, class A, 20 probes, 20 in J05556mRNA 1640-2198, Homo sapiens collagenase mRNA, complete cds

M77836, class A, 20 probes, 20 in M77836 1239-1749, Human pyrroline 5-carboxylate reductase mRNA, complete cds

D00596, class C, 20 probes, 20 in all_D00596 15645-16192, Human thymidylate syntase (EC 2.1.1.45) gene, complete cds

U11313, class A, 20 probes, 20 in U11313mRNA 2104-2587, Human sterol carrier protein-X/sterol carrier protein-2 (SCP-X/SCP-2) gene, promoter and

U61167, class A, 20 probes, 20 in U61167 3488-4028, Human SH3 domain-containing protein SH3P18 mRNA, complete cds

U51269, class A, 20 probes, 20 in U51269 3408-3900, Human armadillo repeat protein mRNA, complete cds

U89896, class A, 20 probes, 20 in U89896 1184-1688, Human casein kinase I gamma 2 mRNA, complete cds

U94585, class A, 20 probes, 20 in U94585 1810-2308, Homo sapiens requiem homolog (hsReq) mRNA, complete cds.

U22233, class A, 20 probes, 20 in U22233 1659-2166, Human methylthioadenosine phosphorylase (MTAP) mRNA, complete cds

U33818, class A, 20 probes, 20 in U33818 1889-2351, Human inducible poly(A)-binding protein mRNA, complete cds

Homo sapiens /REF=M33197 /DEF=Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) mRNA, complete cds /LEN=1268 (_5, _M, _3 represent transcript regions 5 prime, Middle, and 3 prime respectively)

L02648, class A, 20 probes, 20 in L02648 1312-1852, Homo sapiens (clone V6) transcobalamin II (TCN2) mRNA, complete cds

D13413, class A, 18 probes, 18 in D13413mRNA 578-617, Human mRNA for tumor-associated 120 kDa nuclear protein p120, partial cds(carboxyl terminus)

X75208, class C, 20 probes, 20 in all_X75208 3276-3781, H.sapiens HEK2 mRNA for protein tyrosine kinase receptor

U27655, class A, 20 probes, 20 in U27655 2169-2577, Human RGP3 mRNA, complete cds

U73167, class A, 20 probes, 20 in U73167cds#2 79-834, H_LUCA14.2a gene extracted from Human cosmid LUCA14, H_LUCA14.2a gene extracted from Human cosmid LUCA14, H_LUCA14.2a gene extracted from Human cosmid LUCA14, H_LUCA14.2a gene extracted from Human cosmid LUCA14, H_LUCA14.2a gene extracted from Human cosmid LUCA14

X16560, class B, 20 probes, 11 in X16560cds 1-163: 9 in reverseSequence, 13-295, Human COX VIIc gene for subunit VIIc of cytochrome c oxidase (EC 1.9.3.1)

U78525, class A, 20 probes, 20 in U78525 2480-2942, Human eukaryotic translation initiation factor (eIF3) mRNA, complete cds

L40992, class A, 20 probes, 20 in L40992mRNA 906-1368, Homo sapiens (clone PEBP2aA1) core-binding factor, runt domain, alpha subunit 1 (CBFA1) mRNA, 3 end of cds.

X66113, class B, 19 probes, 15 in X66113cds 2199-2633: 4 in reverseSequence, 2682-2729, H.sapiens mRNA for PM/Scl 100kD nucleolar protein

D14878, class A, 20 probes, 20 in D14878 1001-1499, Human mRNA for protein D123, complete cds

L10338, class A, 20 probes, 20 in L10338 953-1360, Human sodium channel beta-1 subunit (SCN1B) mRNA, complete cds

Y09022, class A, 20 probes, 16 in Y09022cds 805-1291: 4 in reverseSequence, 1328-1406, H.sapiens mRNA for Not56-like protein

D14694, class A, 20 probes, 20 in D14694 2143-2455, Human mRNA for KIAA0024 gene, complete cds

D13540, class A, 20 probes, 20 in D13540 1948-2500, Human mRNA for protein-tyrosine phosphatase

M22538, class A, 20 probes, 20 in M22538 286-778, Human nuclear-encoded mitochondrial NADH-ubiquinone reductase 24Kd subunit mRNA, complete cds

Y13620, class A, 20 probes, 20 in Y13620 5732-6182, Homo sapiens mRNA for BCL9 gene. /gb=Y13620 /ntype=RNA

D13636, class A, 20 probes, 20 in D13636 3011-3539, Human mRNA for KIAA0011 gene, complete cds

X52479, class B, 20 probes, 13 in X52479cds 1689-1995: 7 in reverseSequence, 2040-2202, Human PKC alpha mRNA for protein kinase C alpha

S77583, class A, 20 probes, 20 in S77583 4-66, HERVK10/HUMMTV reverse transcriptase homolog {clone RT244} [human, multiple sclerosis, brain plaques, mRNA Partial, 90 nt]. /gb=S77583 /ntype=RNA

U68111, class A, 20 probes, 20 in U68111mRNA 858-1374, Human protein phosphatase inhibitor 2 (PPP1R2) gene

L19314, class C, 20 probes, 20 in all_L19314 3362-3789, Human HRY gene, complete cds

L23852, class A, 20 probes, 20 in L23852mRNA 1122-1674, Homo sapiens (clone Z146) retinal mRNA, 3 end and repeat region

U29700, class A, 20 probes, 16 in U29700cds 1308-1644: 4 in reverseSequence, 8352-8382, Human anti-mullerian hormone type II receptor precursor gene, complete cds

X96783, class A, 20 probes, 20 in X96783mRNA 1442-2015, H.sapiens Syt V gene (genomic and cDNA sequence)

U48263, class A, 20 probes, 20 in U48263 627-1173, Human pre-pro-orphanin FQ (OFQ) mRNA, complete cds

X51630, class A, 20 probes, 17 in X51630mRNA 2403-2955: 3 in reverseSequence, 2961-2979, Human Wilms tumor WT1 mRNA for zinc finger protein, Krueppel-like

L21936, class A, 20 probes, 20 in L21936 1796-2222, Human succinate dehydrogenase flavoprotein subunit (SDH) mRNA, complete cds

X62573, class C, 20 probes, 20 in all_X62573 1608-2161, H.sapiens RNA for Fc receptor, TC9

Tyrosine Kinase (Gb:Z25436)

Dihydrofolate Reductase, Alt. Splice 6

U02566, class A, 20 probes, 20 in U02566 2456-2990, Human receptor tyrosine kinase tif mRNA, partial cds

X65614, class B, 20 probes, 10 in X65614cds 10-262: 10 in reverseSequence, 19-391, H.sapiens mRNA for calcium-binding protein S100P

U89606, class A, 20 probes, 20 in U89606 521-917, Human pyridoxal kinase mRNA, complete cds.

U10099, class A, 19 probes, 19 in U10099 938-1435, Human POM-ZP3 mRNA, complete cds

L17075, class A, 20 probes, 20 in L17075 1130-1607, Human TGF-b superfamily receptor type I mRNA, complete cds.

X74328, class A, 20 probes, 20 in X74328mRNA 1175-1745, CB2 (peripheral) cannabinoid receptor gene extracted from H.sapiens mRNA for CB2 (peripheral) cannabinoid receptor

X94612, class C, 20 probes, 20 in all_X94612 2745-3328, H.sapiens mRNA for type II cGMP-dependent protein kinase

X74819, class A, 20 probes, 16 in X74819cds 509-809: 4 in reverseSequence, 913-1015, H.sapiens mRNA for cardiac troponin T

M60314, class A, 20 probes, 20 in M60314 1582-2044, Human transforming growth factor-beta (tgf-beta) mRNA, complete cds

X71125, class B, 20 probes, 15 in X71125UTR#1 20-398: 5 in reverseSequence, 985-1093, H.sapiens mRNA for glutamine cyclotransferase

D31890, class A, 20 probes, 20 in D31890 1375-1909, Human mRNA for KIAA0070 gene, partial cds

U29680, class A, 20 probes, 20 in U29680 251-659, Human A1 protein mRNA, complete cds

X80822, class B, 20 probes, 13 in X80822cds 13-331: 7 in reverseSequence, 56-578, H.sapiens mRNA for ORF

X59711, class A, 20 probes, 16 in X59711cds 626-998: 4 in reverseSequence, 1244-1280, H.sapiens mRNA for CAAT-box DNA binding protein subunit A

J04469, class B, 20 probes, 11 in J04469exon#9 11-173: 9 not in GB record, Human mitochondrial creatine kinase (CKMT) gene, complete cds

Z11502, class C, 20 probes, 20 in all_Z11502 886-1451, H.sapiens mRNA for intestine-specific annexin

Mg44

U18934, class A, 20 probes, 20 in U18934 4229-4311, Human receptor tyrosine kinase (DTK) mRNA, complete cds

U50078, class A, 20 probes, 20 in U50078 14603-15101, Human guanine nucleotide exchange factor p532 mRNA, complete cds

U70735, class A, 20 probes, 20 in U70735 507-1005, Human 34 kDa mov34 isologue mRNA, complete cds. /gb=U70735 /ntype=RNA

M15395, class A, 20 probes, 20 in M15395 2621-2736, Human leukocyte adhesion protein (LFA-1/Mac-1/p150,95 family) beta subunit mRNA

S77356, class A, 20 probes, 20 in S77356 3-41, transcript ch21=oligomycin sensitivity conferral protein oscp homolog [human, RF1,RF48 stomach cancer cell lines, mRNA, 262 nt]. /gb=S77356 /ntype=RNA

M29960, class A, 20 probes, 20 in M29960mRNA 1721-2141, Human steroid receptor (TR2-11) mRNA, complete cds

U93553, class A, 20 probes, 20 in U93553 1729-2251, Human alpha1-fetoprotein transcription factor (hFTF) mRNA, complete cds.

L49229, class A, 20 probes, 20 in L49229cds 2-87, Homo sapiens retinoblastoma susceptibility protein (RB1) gene, with a 3 bp deletion in exon 22 (L11910 bases 161855-162161). /gb=L49229 /ntype=DNA /annot=CDS

X86163, class C, 20 probes, 20 in all_X86163 2233-2564, H.sapiens mRNA for B2-bradykinin receptor, 3

U66406, class A, 20 probes, 20 in U66406 2835-3255, Human putative EPH-related PTK receptor ligand LERK-8 (Eplg8) mRNA, complete cds

X16662, class C, 20 probes, 20 in all_X16662 1399-1916, Human mRNA for vascular anticoagulant-beta (VAC-beta)

L43338, class A, 20 probes, 20 in L43338mRNA 25-151, Homo sapiens (clone JJ1a) cadherin mRNA fragment. /gb=L43338 /ntype=RNA

M64099, class A, 20 probes, 20 in M64099 1873-2371, Human gamma-glutmyl transpeptidase-related protein (GGT-Rel) mRNA, complete cds

M16652, class C, 4 probes, 4 in all_M16652 714-760, Human pancreatic elastase IIA mRNA, complete cds, Human pancreatic elastase IIA mRNA, complete cds

M76125, class A, 20 probes, 20 in M76125 2612-3170, Human tyrosine kinase receptor (axl) mRNA, complete cds

D87685, class A, 20 probes, 20 in D87685 5584-5920, Human mRNA for KIAA0244 gene, partial cds

AB002559, class A, 20 probes, 20 in AB002559 1302-1746, Human mRNA for hunc18b2, complete cds

D50312, class A, 20 probes, 20 in D50312 1206-1668, Human mRNA for uKATP-1, complete cds

M58286, class A, 20 probes, 20 in M58286 1533-2054, Homo sapiens tumor necrosis factor receptor mRNA, complete cds

U88629, class A, 20 probes, 20 in U88629cds 1508-1898, Human RNA polymerase II elongation factor ELL2, complete cds. /gb=U88629 /ntype=DNA /annot=CDS

Epidermal Growth Factor Receptor-Related Protein

U80457, class A, 20 probes, 20 in U80457 2243-2645, Human transcription factor SIM2 short form mRNA, complete cds

M58525, class A, 20 probes, 20 in M58525 603-933, Homo sapiens catechol-O-methyltransferase (COMT) mRNA, complete cds

D86959, class A, 20 probes, 20 in D86959 5435-5867, Human mRNA for KIAA0204 gene, complete cds

X14894, class C, 20 probes, 20 in all_X14894 826-1385, Human mRNA for myogenic factor Myf-5

U08377, class A, 20 probes, 20 in U08377 2654-3134, Human homolog of Drosophila splicing regulator suppressor-of-white-apricot mRNA, complete cds

U30828, class A, 20 probes, 20 in U30828 1078-1630, Human splicing factor SRp55-2 (SRp55) mRNA, complete cds

L49169, class A, 20 probes, 20 in L49169mRNA 3270-3612, Human G0S3 mRNA, complete cds

S69115, class A, 20 probes, 20 in S69115 250-808, granulocyte colony-stimulating factor induced gene [human, CML patient, bone marrow mononuclear cells, mRNA, 833 nt]

Tubulin, Beta 2

Y11416, class A, 20 probes, 20 in Y11416mRNA 1639-2209, H.sapiens mRNA for P73.

X96698, class C, 20 probes, 20 in all_X96698 662-1245, H.sapiens mRNA for D1075-like gene

Retinoblastoma Protein, Mutated - Also Represents: L41870

S66431, class A, 20 probes, 20 in S66431 5869-6361, RBP2=retinoblastoma binding protein 2 [human, Nalm-6 pre-B cell leukemia, mRNA, 6455 nt]

L29376, class A, 20 probes, 20 in L29376 616-1126, Homo sapiens (clone 3.8-1) MHC class I mRNA fragment

Z18956, class C, 20 probes, 20 in all_Z18956 3398-3951, H.sapiens mRNA for taurine transporter

U78107, class A, 20 probes, 20 in U78107 667-1105, Human gamma SNAP mRNA, complete cds.

U50743, class A, 20 probes, 20 in U50743 13-439, Human Na,K-ATPase gamma subunit mRNA, complete cds

U67615, class A, 20 probes, 20 in U67615 12883-13381, Human beige protein homolog (chs) mRNA, complete cds

X79510, class B, 20 probes, 12 in X79510cds 3165-3459: 8 in reverseSequence, 3839-3971, H.sapiens mRNA for protein-tyrosine-phosphatase D1

U90543, class C, 8 probes, 8 in all_U90543 2501-2545, Human butyrophilin (BTF1) mRNA, complete cds, Human butyrophilin (BTF1) mRNA, complete cds

U29589, class A, 20 probes, 20 in U29589exon 2948-3488, Human m3 muscarinic acetylcholine receptor (CHRM3) gene, complete cds

U57911, class A, 20 probes, 20 in U57911 1693-2203, Human fetal brain (239FB) mRNA, from the WAGR region, complete cds

X94333, class A, 20 probes, 20 in X94333 1617-2157, H.sapiens mRNA for TGN46 protein

S74683, class A, 20 probes, 20 in S74683 848-1268, ADP-ribosyltransferase [human, skeletal muscle, mRNA, 1334 nt]

U13680, class A, 20 probes, 20 in U13680 767-1160, Human lactate dehydrogenase-C (LDH-C) mRNA, complete cds

Immunoglobulin Heavy Chain, Fd Fragment

U33761, class A, 20 probes, 20 in U33761 1017-1557, Human cyclin A/CDK2-associated p45 (Skp2) mRNA, complete cds

U72509, class A, 19 probes, 19 in U72509mRNA 2-255, Human alternatively spliced B8 (B7) mRNA, partial sequence. /gb=U72509 /ntype=RNA

K03021, class A, 20 probes, 20 in K03021exon#14 343-853, Human tissue plasminogen activator (PLAT) gene, complete cds

Forkhead Family Afx1

Fibrinogen, A Alpha Polypeptide, Alt. Splice 2, E - Also Represents: HG2730-HT2829, HG2730-HT2828, M58569

U47050, class A, 20 probes, 20 in U47050 2888-3296, Human putative calcium influx channel (htrp3) mRNA, complete cds

U72508, class A, 20 probes, 20 in U72508 757-1105, Human B7 mRNA, complete cds

X99101, class B, 20 probes, 12 in X99101cds 1121-1409: 8 in reverseSequence, 1439-1535, H.sapiens mRNA for estrogen receptor.

M29064, class A, 20 probes, 20 in M29064 1225-1657, Human hnRNP B1 protein mRNA

U37251, class A, 20 probes, 20 in U37251 1908-2328, Human KRAB zinc finger protein (ZNF177) mRNA, splicing variant, complete cds

J05073, class A, 20 probes, 20 in J05073cds 239-641, Human phosphoglycerate mutase (PGAM-M) gene, complete cds

L15296, class C, 20 probes, 20 in all_L15296 3031-3082, Homo sapiens clone hRCNC2b retinal rod cyclic nucleotide-gated cation channel gene, complete cds

M75106, class A, 20 probes, 20 in M75106 1138-1618, Human prepro-plasma carboxypeptidase B mRNA, complete cds

D78514, class A, 20 probes, 16 in D78514cds 73-409: 4 in reverseSequence, 511-565, Human mRNA for ubiquitin-conjugating enzyme, complete cds

X52943, class C, 20 probes, 20 in all_X52943 2163-2728, Human mRNA for ATF-a transcription factor

Z22535, class C, 20 probes, 20 in all_Z22535 2433-2932, H.sapiens ALK-3 mRNA

Cpg-Enriched Dna, Clone S12

L20320, class A, 20 probes, 19 in L20320cds 605-953: 1 in reverseSequence, 1218, Human protein serine/threonine kinase stk1 mRNA, complete cds

U69126, class A, 20 probes, 20 in U69126 1831-2345, Human FUSE binding protein 2 (FBP2) mRNA, partial cds

D13370, class A, 20 probes, 20 in D13370exon#5 193-637, Human APX gene encoding APEX nuclease, complete cds

J03473, class A, 20 probes, 20 in J03473mRNA 3212-3752, Human poly(ADP-ribose) synthetase mRNA, complete cds

U66083, class C, 20 probes, 20 in all_U66083 2217-2758, Human contig of two cosmids from LLNL X chromosome library (U83F1, U109H10), including MAGE-9 antigen (MAGE9) gene, complete cds, and three genes of unknown function

Homo sapiens /REF=M27830 /DEF=Human 28S ribosomal RNA gene, complete cds /LEN=1955 (_5, _M, _3 represent transcript regions 5 prime, Middle, and 3 prime respectively)

L77213, class A, 20 probes, 20 in L77213mRNA 479-959, Homo sapiens phosphomevalonate kinase mRNA, complete cds

L18960, class A, 20 probes, 20 in L18960 679-1177, Human protein synthesis factor (eIF-4C) mRNA, complete cds

M26061, class A, 20 probes, 19 in M26061mRNA 2449-2890: 1 not in GB record, Human cGMP phosphodiesterase alpha subunit (CGPR-A) mRNA, complete cds

Centractin, Alpha

Z79581, class A, 20 probes, 20 in Z79581exon 19-226, H.sapiens LAZ3/BCL6 gene, first non coding exon.

X98261, class B, 20 probes, 12 in X98261cds 121-352: 8 in reverseSequence, 388-583, H.sapiens mRNA for M-phase phosphoprotein, mpp5

L13923, class A, 20 probes, 20 in L13923 9109-9601, Homo sapiens fibrillin mRNA, complete cds

M62831, class A, 20 probes, 20 in M62831mRNA 1210-1750, Human transcription factor ETR101 mRNA, complete cds

L14595, class A, 20 probes, 20 in L14595 1801-2077, Human alanine/serine/cysteine/threonine transporter (ASCT1) mRNA, complete cds

X59372, class A, 20 probes, 20 in X59372mRNA 610-1090, Human HOX4C mRNA for a homeobox protein

L33243, class A, 20 probes, 20 in L33243mRNA 13655-14051, Homo sapiens polycystic kidney disease 1 protein (PKD1) mRNA, complete cds

AF000231, class A, 20 probes, 20 in AF000231 1768-2308, Homo sapiens rab11a GTPase mRNA, complete cds.

K02574, class A, 20 probes, 20 in K02574mRNA 817-1363, Human purine nucleoside phosphorylase (PNP) mRNA, complete cds

S73591, class A, 20 probes, 20 in S73591 2169-2649, brain-expressed HHCPA78 homolog [human, HL-60 acute promyelocytic leukemia cells, mRNA, 2704 nt]

L38696, class A, 20 probes, 20 in L38696 961-1375, Homo sapiens autoantigen p542 mRNA, 3 end of cds

U29175, class A, 20 probes, 20 in U29175 5199-5223, Human transcriptional activator (BRG1) mRNA, complete cds.
Mucin, Gastric

M90366, class A, 20 probes, 20 in M90366 1683-2175, Human zona pellucida glycoprotein 2 (ZP2) mRNA, complete cds

M73489, class A, 20 probes, 20 in M73489 3312-3660, Human heat-stable enterotoxin receptor mRNA, complete cds

Y07828, class B, 20 probes, 14 in Y07828cds 345-675: 6 in reverseSequence, 844-994, H.sapiens mRNA for RING protein

M81829, class B, 20 probes, 14 in M81829cds 915-1137: 6 in reverseSequence, 1260-1476, Human somatostatin receptor isoform 1 gene, complete cds

S46622, class A, 20 probes, 20 in S46622 1569-2055, calcineurin A catalytic subunit [human, testis, mRNA, 2134 nt]

E. coli /GEN=bioC /DB_XREF=gb:J04423.1 /NOTE=SIF corresponding to nucleotides 4626-4878 of gb:J04423.1 /DEF=E.coli 7,8-diamino-pelargonic acid (bioA), biotin synthetase (bioB), 7-keto-8-amino-pelargonic acid synthetase (bioF), bioC protein, and dethiobiotin synthetase (bioD), complete cds.
Nuclear Factor 1, Variant Hepatic

U86358, class A, 20 probes, 20 in U86358 296-818, Human chemokine (TECK) mRNA, complete cds. /gb=U86358 /ntype=RNA

U37219, class C, 20 probes, 20 in all_U37219 2132-2583, Human cyclophilin-like protein CyP-60 mRNA, complete cds

M18391, class A, 20 probes, 20 in M18391 2780-3147, Human tyrosine kinase receptor (eph) mRNA, complete cds

U08023, class A, 20 probes, 20 in U08023 3037-3529, Human cellular proto-oncogene (c-mer) mRNA, complete cds

M81778, class A, 20 probes, 20 in M81778 2123-2689, Human serotonin 5-HT1C receptor mRNA, complete cds

V00571, class A, 20 probes, 20 in V00571mRNA 714-1218, Human gene encoding prepro form of corticotropin releasing factor

D78334, class A, 20 probes, 20 in D78334 496-1018, Human mRNA for ankyrin motif, complete cds

U79258, class A, 20 probes, 20 in U79258 861-1407, Human clone 23732 mRNA, partial cds.

X65962, class C, 20 probes, 20 in all_X65962 1115-1174, H.sapiens mRNA for cytochrome P-450

L08187, class A, 20 probes, 20 in L08187 551-1079, Human cytokine receptor (EBI3) mRNA, complete cds

M19481, class C, 20 probes, 14 in all_M19481 278-651: 6 in M19481cds 818-921, Human follistatin gene

D10523, class A, 20 probes, 20 in D10523 3533-4079, Human mRNA for 2-oxoglutarate dehydrogenase, complete cds

Tubulin, Beta

X15880, class C, 20 probes, 20 in all_X15880 1690-2273, Human mRNA for collagen VI alpha-1 C-terminal globular domain

U70732, class A, 20 probes, 20 in U70732mRNA 1335-1899, Human glutamate pyruvate transaminase (GPT) gene, complete cds

D82326, class A, 20 probes, 20 in D82326 2784-3312, Human mRNA for Na+-independent neutral and basic amino acid transporter, complete cds

Z69030, class A, 18 probes, 18 in Z69030cds 838-1186, H.sapiens mRNA for gamma 1 isoform of 61kDa regulatory subunit of PP2A.

M63379, class A, 20 probes, 20 in M63379mRNA 1190-1646, Human TRPM-2 protein gene

X55954, class A, 20 probes, 18 in X55954cds 19-385: 2 in reverseSequence, 427-433, Human mRNA for HL23 ribosomal protein homologue

Z34918, class A, 20 probes, 20 in Z34918cds 1559-2051, H.sapiens mRNA for translation initiation factor eIF-4gamma (partial)

X99459, class C, 20 probes, 20 in all_X99459 1516-1799, H.sapiens mRNA for sigma 3B protein

U44429, class C, 20 probes, 20 in all_U44429 1151-1626, Human D53 (hD53) mRNA, partial cds

M64590, class A, 20 probes, 20 in M64590 3317-3737, Human glycine decarboxylase mRNA, complete cds

J02645, class A, 20 probes, 20 in J02645mRNA 882-1314, Human translational initiation factor (eIF-2), alpha subunit mRNA, complete cds

M20030, class A, 20 probes, 20 in M20030 68-612, Human small proline rich protein (sprII) mRNA, clone 930

S76475, class A, 20 probes, 20 in S76475 2144-2659, trkC [human, brain, mRNA, 2715 nt]

U14394, class C, 20 probes, 20 in all_U14394 4004-4533, Human tissue inhibitor of metalloproteinases-3 mRNA, complete cds

X66114, class A, 20 probes, 20 in X66114mRNA 564-1074, H.sapiens gene for 2-oxoglutarate carrier protein

U59286, class A, 20 probes, 20 in U59286 49-439, Human beta-R1 mRNA, partial cds. /gb=U59286 /ntype=RNA

D86331, class A, 20 probes, 20 in D86331 1281-1777, Human MT2-MMP gene for matrix metalloprotein, complete cds

M29994, class A, 18 probes, 18 in M29994exon#1 2-80, Human alpha-I spectrin gene, exon 12 /gb=M29994 /ntype=DNA /annot=exon

L09209, class A, 20 probes, 20 in L09209 3114-3666, Homo sapiens amyloid protein homologue mRNA, complete cds

D85181, class A, 20 probes, 20 in D85181 1502-2018, Human mRNA for fungal sterol-C5-desaturase homolog, complete cds

U04810, class A, 20 probes, 20 in U04810 2050-2536, Human tastin mRNA, complete cds

M27533, class A, 20 probes, 20 in M27533 883-1451, Human Ig rearranged B7 protein mRNA VC1-region, complete cds. Collagen, Type Viii, Alpha 1

S82592, class A, 20 probes, 20 in S82592 357-861, Evi-1=Evi-1 protein {3 region, deletion region} [human, megakaryoblastoid cell line MOLM-1, chronic myelocytic leukemia patient, mRNA Partial Mutant, 916 nt]

L37347, class A, 20 probes, 20 in L37347 1301-1835, Human integral membrane protein (Nramp2) mRNA, partial

U09770, class A, 20 probes, 20 in U09770 61-391, Human cysteine-rich heart protein (hCRHP) mRNA, complete cds

U89505, class A, 20 probes, 20 in U89505 1087-1537, Human Hlark mRNA, complete cds.

U31099, class A, 20 probes, 20 in U31099 13-469, Human DP prostanoid receptor (PTGDR) mRNA, partial cds.

Syntaxin 1b - Also Represents: D37933

Vasoactive Intestinal Peptide - Also Represents: M36634

X83535, class C, 18 probes, 18 in all_X83535 1791-2208, H.sapiens mRNA for membrane-type matrix metalloproteinase

M33653, class A, 20 probes, 20 in M33653 467-965, Human (clones HT-[125,133]) alpha-2 type IV collagen (COL4A2) mRNA, complete cds

L29008, class A, 20 probes, 20 in L29008 2014-2464, Human L-iditol-2 dehydrogenase mRNA, complete cds

U01877, class A, 20 probes, 20 in U01877 8517-8997, Human p300 protein mRNA, complete cds

Z69923, class B, 20 probes, 10 in Z69923cds 1572-1818: 10 in reverseSequence, 6905-7019, Human DNA sequence from cosmid L219F9, Huntingtons Disease Region, chromosome 4p16.3 contains hepatocyte growth factor (HGF) precursor, ESTs, STSs and a CpG island.

L01406, class A, 20 probes, 20 in L01406 1010-1562, Human growth hormone-releasing hormone receptor mRNA, complete cds

U81262, class A, 20 probes, 20 in U81262 2433-2877, Human lerk-5 (Lerk-5) mRNA, complete cds.

U75308, class A, 20 probes, 20 in U75308 3654-4092, Human TBP-associated factor (hTAFII130) mRNA, partial cds

Z38133, class C, 20 probes, 20 in all_Z38133 5578-5993, H.sapiens mRNA for myosin

D78134, class A, 20 probes, 20 in D78134 727-1261, Human mRNA for glycine-rich RNA binding protein CIRP, complete cds

U43328, class A, 20 probes, 20 in U43328 1158-1698, Human link protein mRNA, complete cds

U37055, class A, 20 probes, 20 in U37055mRNA 1680-2195, Human hepatocyte growth factor-like protein gene, complete cds

L07765, class A, 20 probes, 20 in L07765 1443-1923, Human carboxylesterase mRNA, complete cds

X79066, class C, 20 probes, 20 in all_X79066 390-973, H. sapiens ERF-1 mRNA 5 end.

M55683, class A, 20 probes, 20 in M55683 2732-3242, Human cartilage matrix protein (CMP) mRNA, exons 8-Mar

U44772, class A, 20 probes, 20 in U44772 1738-2176, Human palmitoyl protein thioesterase mRNA, complete cds

Z46967, class A, 20 probes, 20 in Z46967cds 1216-1714, H.sapiens mRNA for calicin (partial)

X54870, class A, 20 probes, 20 in X54870mRNA 1162-1702, Human mRNA for NKG2-D gene

U70451, class A, 20 probes, 20 in U70451 2097-2607, Human myleoid differentiation primary response protein MyD88 mRNA, complete cds.

V00565, class C, 20 probes, 20 in all_V00565 2218-2422, Human gene for preproinsulin, from chromosome 11 Includes a highly polymorphic region upstream from the insulin gene containing tandemly repeated sequences

U05040, class A, 20 probes, 20 in U05040 1814-2282, Human FUSE binding protein mRNA, complete cds

U30894, class A, 20 probes, 20 in U30894 2068-2626, Human N-sulphoglucosamine sulphohydrolase mRNA, complete cds

X90568, class C, 20 probes, 20 in all_X90568 81371-81864, H.sapiens mRNA for titin protein (clone hh1-hh54)

L36922, class C, 20 probes, 20 in all_L36922 938-1125, Homo sapiens Met-ase gene, exon 1

U00968, class A, 20 probes, 20 in U00968 3595-4069, Human SREBP-1 mRNA, complete cds

U00952, class A, 20 probes, 20 in U00952 488-998, Human clone A9A2BRB7 (CAC)n/(GTG)n repeat-containing mRNA

H. Sapiens Hypothetical Protein Npiiy20 (Gb:M76676) - Also Represents: M76676

Z47727, class B, 20 probes, 10 in Z47727cds 6-150: 10 in reverseSequence, 28-313, H.sapiens mRNA for RNA polymerase II subunit

J02906, class A, 20 probes, 20 in J02906mRNA 1254-1782, Human cytochrome P450IIF1 protein (CYP2F) mRNA, complete cds

U78180, class A, 20 probes, 20 in U78180 3340-3880, Human sodium channel 2 (hBNaC2) mRNA, alternatively spliced, complete cds

D00632, class A, 20 probes, 20 in D00632 1032-1470, Human plasma (extracellular) mRNA for glutathione peroxidase, complete cds

U15009, class A, 20 probes, 20 in U15009 25-541, Human SnRNP core protein Sm D3 mRNA, complete cds

X99050, class A, 20 probes, 20 in X99050mRNA 3041-3461, orf gene extracted from H.sapiens mRNA for 63 kDa protein

M18728, class A, 20 probes, 20 in M18728mRNA 1932-2460, Human nonspecific crossreacting antigen mRNA, complete cds

L11701, class A, 17 probes, 17 in L11701 2320-2609, Human phospholipase D mRNA, complete cds

X03453 Bacteriophage P1 cre recombinase protein (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)

L07540, class A, 20 probes, 20 in L07540 721-1159, Human replication factor C, 36-kDa subunit mRNA, complete cds

D87078, class A, 20 probes, 20 in D87078 4798-5296, Human mRNA for KIAA0235 gene, partial cds

D87434, class A, 20 probes, 20 in D87434 4737-5295, Human mRNA for KIAA0247 gene, complete cds

X59543, class A, 20 probes, 20 in X59543mRNA 2500-3016, Human mRNA for M1 subunit of ribonucleotide reductase

U19142, class A, 20 probes, 20 in U19142 69-510, Human GAGE-1 protein mRNA, complete cds

X91648, class C, 20 probes, 20 in all_X91648 1082-1611, H.sapiens mRNA for pur alpha extended 3 untranslated region

X55777, class C, 20 probes, 20 in all_X55777 1833-2326, put. ORF gene extracted from H.sapiens Mahlavu hepatocellular carcinoma hhc(M) DNA

S81243, class A, 20 probes, 20 in S81243 2102-2660, CHN=steroid/thyroid orphan receptor homolog gene [human, fetal brain, mRNA Partial, 2714 nt]

D00760, class A, 20 probes, 20 in D00760 277-781, Human mRNA for proteasome subunit HC3

U43148, class A, 20 probes, 20 in U43148 6015-6483, Human patched homolog (PTC) mRNA, complete cds

X83928, class C, 20 probes, 20 in all_X83928 456-919, H.sapiens mRNA for transcription factor TFIID subunit TAFII28

U06631, class A, 20 probes, 20 in U06631 3269-3779, Human (H326) mRNA, complete cds

M16750, class A, 20 probes, 20 in M16750 1699-2210, Human pim-1 oncogene mRNA, complete cds

U01038, class A, 20 probes, 20 in U01038 1649-2123, Human pLK mRNA, complete cds

M28825, class A, 20 probes, 20 in M28825 1513-2047, Human thymocyte antigen CD1a mRNA, complete cds

S90469, class A, 20 probes, 20 in S90469 1802-2300, cytochrome P450 reductase [human, placenta, mRNA Partial, 2403 nt]

L10035, class A, 20 probes, 18 in L10035 162-666: 2 in reverseSequence, 684-690, Human crystallin beta-B2 mRNA, complete cds

U85265, class A, 20 probes, 20 in U85265 7-63, Human down syndrome critical region 1 (DSCR1) gene, alternative exon 1 /gb=U85265 /ntype=RNA

U84569, class A, 20 probes, 20 in U84569 647-1217, Human YF5 mRNA, complete cds

X00371, class A, 20 probes, 20 in X00371mRNA 495-1011, Human myoglobin gene (exon 1) (and joined CDS)

L38608, class A, 20 probes, 20 in L38608 1950-2478, Homo sapiens CD6 ligand (ALCAM) mRNA, complete cds

U44060, class A, 20 probes, 20 in U44060 2395-2845, Human homeodomain protein (Prox 1) mRNA, complete cds

M59465, class A, 20 probes, 20 in M59465 3867-4341, Human tumor necrosis factor alpha inducible protein A20 mRNA, complete cds

X78933, class C, 20 probes, 20 in all_X78933 1420-1970, H.sapiens HZF10 mRNA for zinc finger protein

Z80783, class C, 20 probes, 20 in all_Z80783 510-565, H.sapiens H2B/l gene.

X91103, class A, 20 probes, 18 in X91103cds 587-965: 2 in reverseSequence, 1055-1097, H.sapiens mRNA for Hr44 protein. /gb=X91103 /ntype=RNA

X04011, class C, 20 probes, 20 in all_X04011 3678-4255, Human mRNA of X-CGD gene involved in chronic granulomatous disease located on chromosome X

D42087, class A, 20 probes, 20 in D42087 1034-1388, Human mRNA for KIAA0118 gene, partial cds

Z11695, class C, 20 probes, 20 in all_Z11695 2189-2736, H.sapiens 40 kDa protein kinase related to rat ERK2

U66580, class A, 20 probes, 17 in U66580cds 510-1026: 3 in reverseSequence, 1075-1081, Human putative G protein-coupled receptor (GPR21) gene, complete cds

U77396, class C, 20 probes, 20 not in GB record, Human TNF-alpha inducible responsive element mRNA, complete cds

Z11518, class A, 20 probes, 20 in Z11518mRNA 1546-2066, H.sapiens mRNA for histidyl-tRNA synthetase

Z28339, class C, 20 probes, 20 in all_Z28339 2084-2649, H.sapiens mRNA for delta 4-3-oxosteroid 5 beta-reductase

D86977, class A, 20 probes, 20 in D86977 3721-4141, Human mRNA for KIAA0224 gene, complete cds

Epican, Alt. Splice 12 - Also Represents: HG2981-HT3126, HG2981-HT3127, HG2981-HT3931, HG2981-HT3125, HG2981-HT3932, L05424_cds2

Myosin, Heavy Polypeptide 10, Non-Muscle - Also Represents: M69181

L77701, class A, 20 probes, 20 in L77701mRNA 43-337, Homo sapiens COX17 mRNA, complete cds

Plasma Membrane Calcium Pump Hpmca2a - Also Represents: U15688

X83218, class A, 20 probes, 20 in X83218cds 215-539, H.sapiens mRNA for ATP synthase

U80017, class A, 20 probes, 20 in U80017mRNA#1 412-673, btf2p44 gene (basic transcription factor 2 p44) extracted from Human basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds, btf2p44 gene (basic transcription factor 2 p44) extracted from Human basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds, btf2p44 gene (basic transcription factor 2 p44) extracted from Human basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds

U82759, class A, 20 probes, 20 in U82759 406-571, Human homeodomain protein HoxA9 mRNA, complete cds.

U29953, class A, 20 probes, 20 in U29953mRNA 1150-1468, Human pigment epithelium-derived factor gene, complete cds

M21302, class A, 20 probes, 20 in M21302 402-514, Human small proline rich protein (sprII) mRNA, clone 174N

U55209, class A, 20 probes, 20 in U55209 3812-3977, Human myosin VIIa transcript 2 mRNA, complete cds

M30135, class A, 20 probes, 16 in M30135cds 139-361: 4 in reverseSequence, 4255-4303, Human P40 T-cell and mast cell growth factor (hP40) gene, complete cds

U52696, class A, 20 probes, 20 in U52696 703-742, Human adrenal Creb-rp homolog (Creb-rp), complete cds, and tenascin-X (XB), partial cds, mRNA. /gb=U52696 /ntype=RNA

X95152, class A, 20 probes, 20 in X95152mRNA 10974-11274, H.sapiens brca2 gene exon 2 (and joined coding region)

U32324, class A, 20 probes, 20 in U32324 1353-1671, Human interleukin-11 receptor alpha chain mRNA, complete cds

U65002, class A, 20 probes, 20 in U65002 6724-7240, Human zinc finger protein PLAG1 mRNA, complete cds.

D88152, class A, 20 probes, 20 in D88152 2081-2639, Human mRNA for acetyl-coenzyme A transporter, complete cds

X04706, class C, 20 probes, 20 in all_X04706 1122-1295, Human homeobox gene (clone HHO.c13)

L12760, class A, 19 probes, 19 in L12760exon#9 396-721, Human phosphoenolpyruvate carboxykinase (PCK1) gene, complete cds with repeats

Potassium Channel Protein (Gb:Z11585)

D83785, class A, 20 probes, 20 in D83785 5214-5634, Human mRNA for KIAA0200 gene, complete cds

V00594, class C, 8 probes, 8 in all_V00594 15-75, Human mRNA for metallothionein from cadmium-treated cells, Human mRNA for metallothionein from cadmium-treated cells

D28137, class A, 20 probes, 20 in D28137 395-743, Human mRNA for BST-2, complete cds

L19872, class A, 20 probes, 20 in L19872 4756-5059, Human AH-receptor mRNA, complete cds

U49114, class A, 20 probes, 20 in U49114 2196-2700, Human prohormone convertase 5 precursor (PC5) mRNA, partial cds

Ret Transforming Gene

Myosin, Heavy Polypeptide, Light Meromyosin

X58431, class A, 20 probes, 20 in X58431mRNA#1 1781-2299, HOX 2.2 gene extracted from Human Hox2.2 gene for a homeobox protein

L36531, class A, 20 probes, 20 in L36531mRNA 2573-3059, Homo sapiens integrin alpha 8 subunit mRNA, 3 end

D25547, class A, 20 probes, 20 in D25547 779-864, Human mRNA for PIMT isozyme I, complete cds

U40572, class A, 20 probes, 20 in U40572 1105-1627, Human beta2-syntrophin (SNT B2) mRNA, complete cds

L36983, class A, 20 probes, 20 in L36983mRNA 3012-3546, Homo sapiens dynamin (DNM) mRNA, complete cds

U30255, class A, 20 probes, 20 in U30255 977-1493, Human phosphogluconate dehydrogenase (hPGDH) gene, complete cds

X01715, class C, 20 probes, 9 in X01715cds 1338-1537: 11 not in GB record, H.sapiens gene fragment for the acetylcholine receptor gamma subunit precursor (exons 1 and 2)

AB000114, class A, 20 probes, 20 in AB000114 1818-2208, Human mRNA for osteomodulin, complete cds

K03183, class A, 20 probes, 20 in K03183cds 2-326, Human chorionic gonadotropin beta subunit gene

M21624, class A, 20 probes, 20 in M21624mRNA 603-1149, Human T-cell receptor delta chain mRNA (VJC-region), complete cds

Z70220, class C, 20 probes, 20 in all_Z70220 31-266, H.sapiens mRNA for 5UTR for unknown protein (clone ICRFp507O0882).

U96769, class A, 20 probes, 20 in U96769mRNA 1266-1746, Homo sapiens chondroadherin gene, 5 flanking region and

X05309, class C, 20 probes, 20 in all_X05309 4846-5240, Human mRNA for C3b/C4b receptor (CR1) F allotype.

U41804, class A, 20 probes, 20 in U41804 882-1254, Human putative T1/ST2 receptor binding protein precursor mRNA, complete cds

D26350, class A, 20 probes, 20 in D26350 10043-10481, Human mRNA for type 2 inositol 1,4,5-trisphosphate receptor, complete cds

U63842, class C, 20 probes, 20 in all_U63842 423-1018, Human neurogenic basic-helix-loop-helix protein (neuroD3) gene, complete cds

L24774, class A, 20 probes, 20 in L24774 272-757, Homo sapiens delta3, delta2-CoA-isomerase mRNA, 3 end

U32680, class A, 20 probes, 20 in U32680 1088-1664, Human CLN3 mRNA, complete cds

D50922, class A, 20 probes, 20 in D50922 1972-2452, Human mRNA for KIAA0132 gene, complete cds

L09749, class A, 20 probes, 20 in L09749 1019-1463, Homo sapiens (clone F4) transmembrane protein mRNA sequence

M74099, class A, 20 probes, 20 in M74099 4835-5327, Human displacement protein (CCAAT) mRNA

X63629, class C, 20 probes, 20 in all_X63629 2582-3126, H.sapiens mRNA for p cadherin

U58970, class A, 20 probes, 20 in U58970 1284-1824, Human putative outer mitochondrial membrane 34 kDa translocase hTOM34 mRNA, complete cds

M27288, class B, 20 probes, 11 in M27288exon 225-555: 9 in reverseSequence, 567-768, Human oncostatin M gene

Gamma-Aminobutyric Acid (Gaba) A Receptor, Alpha Subunit - Also Represents: X14766

X98253, class C, 20 probes, 20 in all_X98253 1221-1334, H.sapiens ZNF183 gene. /gb=X98253 /ntype=RNA

D63506, class A, 20 probes, 20 in D63506 1940-2435, Human mRNA for unc-18homologue, complete cds

M28170, class A, 20 probes, 20 in M28170 1894-1987, Human cell surface protein CD19 (CD19) gene, complete cds

U90552, class B, 12 probes, 12 in U90552 2814-3377, Human butyrophilin (BTF5) mRNA, complete cds, Human butyrophilin (BTF5) mRNA, complete cds

Zinc Finger Protein 20

U79718, class A, 20 probes, 20 in U79718 532-1012, Human endonuclease III homolog 1 (OCTS3) mRNA, complete cds.

X64044, class A, 20 probes, 18 in X64044cds 1066-1402: 2 in reverseSequence, 1538-1592, H.sapiens mmRNA for large subunit of splicing factor U2AF

X76013, class A, 20 probes, 17 in X76013cds 1933-2257: 3 in reverseSequence, 2328-2394, H.sapiens QRSHs mRNA for glutaminyl-tRNA synthetase

M83712, class A, 20 probes, 20 in M83712 1078-1646, H.sapiens nicotinic receptor alpha 5 subunit mRNA, complete cds.

Z14978, class C, 20 probes, 20 in all_Z14978 1422-1673, H.sapiens mRNA for actin-related protein

X16707, class A, 20 probes, 16 in X16707cds 379-733: 4 in reverseSequence, 869-923, Human fra-1 mRNA

Udp-Glucuronosyltransferase 1 Family, Polypeptide 1, Alt. Splice 1 - Also Represents: HG3703-HT3916

M84605, class A, 20 probes, 20 in M84605 4280-4766, Human putative opioid receptor mRNA, complete cds

M26958, class A, 18 probes, 18 in M26958 46-235, Human parathyroid hormone-related protein (PTHrP) mRNA, 5 flank, clone pBRF52. /gb=M26958 /ntype=RNA

Ribosomal Protein S13

Small Nuclear Ribonucleoprotein U1, 1snrp

U82818, class A, 20 probes, 20 in U82818 1005-1058, Homo sapiens UCP3S mRNA, complete cds. /gb=U82818 /ntype=RNA

D14662, class A, 20 probes, 20 in D14662 1082-1592, Human mRNA for KIAA0106 gene, complete cds

S83309, class A, 20 probes, 20 in S83309 1291-1856, germ cell nuclear factor [human, embryonal carcinoma NT2/D1, mRNA, 1916 nt]

L41390, class A, 20 probes, 20 in L41390exon#1 244-395, Homo sapiens core 2 beta-1,6-N-acetylglucosaminyltransferase (core 2 GnT) gene, exon 1 /gb=L41390 /ntype=DNA /annot=exon

D16480, class A, 20 probes, 20 in D16480 2089-2641, Human mRNA for mitochobdrial enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenese alpha-subunit of trifunctional protein, complete cds

Ribosomal Protein L37

D86640, class A, 20 probes, 20 in D86640 2374-2902, Human mRNA for stac, complete cds

M62800, class A, 20 probes, 20 in M62800mRNA 1350-1827, Human 52-kD SS-A/Ro autoantigen mRNA, complete cds

D45906, class A, 20 probes, 20 in D45906 3097-3613, Human mRNA for LIMK-2, complete cds

S57887, class C, 20 probes, 20 in all_S57887 739-980, (T1)=elastin translocation allele {exon 28, translocation} [human, Genomic Mutant, 1300 nt]

U78027, class A, 20 probes, 20 in U78027mRNA#3 3-350, L44L gene (L44-like ribosomal protein) extracted from Human Bruton tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds, L44L gene (L44-like ribosomal protein) extracted from Human Bruton tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds

Homeotic Protein Emx2

X69150, class A, 20 probes, 20 in X69150mRNA 25-403, L06432 H.sapiens mRNA for ribosomal protein S18.

L16862, class A, 20 probes, 20 in L16862 2289-2763, Homo sapiens G protein-coupled receptor kinase (GRK6) mRNA, complete cds

M37400, class A, 20 probes, 20 in M37400mRNA 1352-1886, Human cytosolic aspartate aminotransferase mRNA, complete cds

D79205, class A, 20 probes, 18 in D79205 5-319: 2 in reverseSequence, 323-325, Human mRNA for ribosomal protein L39, complete cds

K03207, class B, 20 probes, 14 in K03207mRNA 286-748: 6 in reverseSequence, 772-848, Human PRB4 locus salivary proline-rich protein mRNA, complete cds

L38025, class A, 20 probes, 16 in L38025exon#1-3 30-106: 4 not in GB record, Homo sapiens ciliary neurotrophic factor alpha receptor gene

T-Cell Factor 1, A/B/C, Alt. Splice 1, A

M20218, class B, 20 probes, 12 in M20218exon 15-249: 8 not in GB record, Human coagulation factor XI gene

M83363, class A, 20 probes, 20 in M83363 4104-4614, Human plasma membrane calcium-pumping ATPase (PMCA4) mRNA, complete cds

U79274, class A, 20 probes, 20 in U79274 883-1381, Human clone 23733 mRNA, complete cds.

M31682, class A, 20 probes, 20 in M31682mRNA 2130-2526, Human testicular inhibin beta-B-subunit mRNA, 3 end

L24203, class A, 20 probes, 20 in L24203 2423-2891, Homo sapiens ataxia-telangiectasia group D-associated protein mRNA, complete cds

X75342, class B, 20 probes, 12 in X75342cds 1407-1767: 8 in reverseSequence, 2095-2239, H.sapiens SHB mRNA

M69013, class A, 20 probes, 20 in M69013 1053-1515, Human guanine nucleotide-binding regulatory protein (G-y-alpha) mRNA, complete cds

M94046, class A, 20 probes, 20 in M94046 1788-2346, Human zinc finger protein (MAZ) mRNA

J04611, class A, 20 probes, 20 in J04611 1533-2061, Human lupus p70 (Ku) autoantigen protein mRNA, complete cds

Z27113, class A, 20 probes, 17 in Z27113cds 73-325: 3 in reverseSequence, 439-463, H.Sapiens gene for RNA polymerase II subunit 14.4 kD

M63904, class A, 20 probes, 20 in M63904mRNA 1519-2029, Human G-alpha 16 protein mRNA, complete cds

M10901, class A, 20 probes, 20 in M10901mRNA 4325-4655, Human glucocorticoid receptor alpha mRNA, complete cds

U90549, class A, 20 probes, 20 in U90549 1452-1932, Human non-histone chromosomal protein (NHC) mRNA, complete cds

Z81326, class A, 20 probes, 17 in Z81326cds 913-1189: 3 in reverseSequence, 1348-1486, H.sapiens mRNA for protease inhibitor 12 (PI12; neuroserpin).

X13930, class A, 20 probes, 17 in X13930cds 1147-1454: 3 in reverseSequence, 1650-1695, Human CYP2A4 mRNA for P-450 IIA4 protein

X87342, class C, 20 probes, 20 in all_X87342 2921-3456, H.sapiens mRNA for human giant larvae homolog

X91788, class C, 20 probes, 20 in all_X91788 857-1284, H.sapiens mRNA for Icln protein

M93718, class A, 20 probes, 20 in M93718 3536-4034, Human nitric oxide synthase mRNA, complete cds

D14812, class A, 20 probes, 20 in D14812 1345-1747, Human mRNA for KIAA0026 gene, complete cds

U34683, class A, 20 probes, 20 in U34683 1261-1735, Human glutathione synthetase mRNA, complete cds

U62325, class A, 20 probes, 20 in U62325 2343-2805, Human FE65-like protein (hFE65L) mRNA, partial cds

X97303, class A, 20 probes, 20 in X97303mRNA 11-93, H.sapiens mRNA for Ptg-12 protein. /gb=X97303 /ntype=RNA

X58298, class A, 20 probes, 19 in X58298cds 824-1371: 1 in reverseSequence, 1441, Human mRNA for interleukin-6-receptor

U59057, class A, 20 probes, 20 in U59057 226-754, Human beta-A4 crystallin (CRYBA4) mRNA, complete cds

D49738, class A, 20 probes, 20 in D49738 456-990, Human cytoskeleton associated protein (CG22) mRNA, complete cds

U52521, class A, 20 probes, 20 in U52521 753-1131, Human arfaptin 1, putative target protein of ADP-ribosylation factor, mRNA, complete cds

U20325, class A, 20 probes, 20 in U20325exon#3 57-477, Human cocaine and amphetamine regulated transcript CART (hCART) gene, complete cds

Dna Polymerase, Epsilon, Catalytic Subunit

Y00503, class A, 20 probes, 18 in Y00503cds 799-1165: 2 in reverseSequence, 1221-1227, Human mRNA for keratin 19

X73079, class C, 20 probes, 20 in all_X73079 2348-2919, Homo sapiens encoding Polymeric immunoglobulin receptor

U58087, class A, 20 probes, 20 in U58087 2096-2462, Human Hs-cul-1 mRNA, complete cds

M21494, class C, 20 probes, 18 in all_M21494 152-645: 2 in M21494cds 888-967, Human muscle creatine kinase gene (CKMM), 5 flank

U52153, class A, 20 probes, 20 in U52153 2069-2513, Human inwardly rectifying potassium channel Kir3.2 mRNA, complete cds

U25182, class A, 20 probes, 20 in U25182 350-860, Human antioxidant enzyme AOE37-2 mRNA, complete cds

U72671, class A, 20 probes, 20 in U72671 2390-2930, Human telencephalin precursor mRNA, complete cds

X57348, class C, 19 probes, 19 in all_X57348 844-1377, H.sapiens mRNA (clone 9112)

M90299, class A, 20 probes, 20 in M90299mRNA 2142-2628, Human glucokinase (GCK) mRNA, complete cds

X14968, class C, 20 probes, 20 in all_X14968 1221-1636, Human testis mRNA for the RII-alpha subunit of cAMP dependent protein kinase

X03066, class C, 20 probes, 20 in all_X03066 787-1268, Human mRNA for HLA-D class II antigen DO beta chain

J05068, class A, 20 probes, 20 in J05068 984-1494, human transcobalamin I mRNA, complete cds

X89984, class B, 20 probes, 11 in X89984cds 465-573: 9 in reverseSequence, 1646-1820, H.sapiens mRNA for BCL7A protein

M64676, class A, 20 probes, 20 in M64676mRNA 1619-1892, Human K+ channel subunit gene, complete cds

S57235, class A, 20 probes, 20 in S57235 1085-1664, CD68=110kda transmembrane glycoprotein [human, promonocyte cell line U937, mRNA, 1722 nt]
Mucin (Gb:M22406)

U25849, class A, 20 probes, 20 in U25849mRNA 1717-2137, Human red cell-type low molecular weight acid phosphatase (ACP1) gene, 5 flanking region and

Y00978, class C, 20 probes, 20 in all_Y00978 2012-2535, Human mRNA for dihydrolipoamide acetyltransferase (PDC-E2) (EC 2.3.1.12)

M19878, class B, 15 probes, 14 in M19878cds 3-125: 1 in reverseSequence, 1964, Homo sapiens calbindin 27 gene, exons 1 and 2, and Alu repeat. /gb=M19878 /ntype=DNA /annot=exon, Homo sapiens calbindin 27 gene, exons 1 and 2, and Alu repeat. /gb=M19878 /ntype=DNA /annot=exon

U57721, class A, 20 probes, 20 in U57721 1126-1588, Human L-kynurenine hydrolase mRNA, complete cds

D63485, class A, 20 probes, 20 in D63485 2710-3196, Human mRNA for KIAA0151 gene, complete cds

X82629, class C, 20 probes, 20 in all_X82629 1744-2297, H.sapiens mRNA for Mox-2

L22342, class A, 20 probes, 20 in L22342 672-810, Human nuclear phosphoprotein mRNA, complete cds

M74096, class A, 20 probes, 20 in M74096 1694-2096, Human long chain acyl-CoA dehydrogenase (ACADL) mRNA, complete cds

AB000816, class A, 20 probes, 20 in AB000816 783-1357, Human mRNA for BMAL1d, partial cds. /gb=AB000816 /ntype=RNA

J02982, class A, 20 probes, 20 in J02982 23-439, Human glycophorin B mRNA, complete cds

U62293, class A, 20 probes, 20 in U62293mRNA 2576-3152, LIMK1 gene (LIM-kinase1) extracted from Human LIM-kinase1 and alternatively spliced LIM-kinase1 (LIMK1) gene, complete cds

U79667, class A, 20 probes, 20 in U79667 3199-3522, Human alpha1A-voltage-dependent calcium channel mRNA, splice form BI-1-V2-GGCAG, partial cds

D13315, class C, 20 probes, 20 in all_D13315 1488-1975, Human mRNA for lactoyl glutathione lyase

M24400, class A, 20 probes, 20 in M24400mRNA 282-840, Human chymotrypsinogen mRNA, complete cds

Serine/Threonine Kinase (Gb:Z25424)

U48408, class A, 20 probes, 20 in U48408 752-1322, Human kidney water channel (hKID) mRNA, complete cds

Lim-Domain Transcription Factor Lim-1 - Also Represents: U14755

X91653, class A, 20 probes, 20 in X91653exon 5-125, H.sapiens DNA for exon encoding for N-acetylglucosaminyltransferase V (340 bp). /gb=X91653 /ntype=DNA /annot=exon

X81372, class B, 20 probes, 10 in X81372cds 701-791: 10 in reverseSequence, 1027-1195, H.sapiens mRNA for biphenyl hydrolase-related protein

L02840, class A, 20 probes, 16 in L02840mRNA 3224-3602: 4 in reverseSequence, 3674-3710, Homo sapiens potassium channel Kv2.1 mRNA, complete cds

U12465, class A, 20 probes, 20 in U12465 19-367, Human ribosomal protein L35 mRNA, complete cds

L37882, class A, 20 probes, 20 in L37882 1340-1814, Human frizzled gene product mRNA, complete cds

U65928, class A, 20 probes, 20 in U65928 711-1125, Human Jun activation domain binding protein mRNA, complete cds

M92303, class A, 20 probes, 20 in M92303 3057-3633, Human voltage-dependent calcium channel beta-1 subunit mRNA, complete cds

AB002380, class A, 20 probes, 20 in AB002380 5644-6142, Human mRNA for KIAA0382 gene, partial cds. /gb=AB002380 /ntype=RNA

X83127, class C, 20 probes, 20 in all_X83127 1494-1624, H.sapiens mRNA for voltage gated potassium channels, beta subunit

X92762, class C, 20 probes, 20 in all_X92762 1360-1883, H.sapiens mRNA for tafazzins protein

M87339, class A, 20 probes, 20 in M87339 875-1361, Human replication factor C, 37-kDa subunit mRNA, complete cds

M19684, class B, 20 probes, 12 in M19684cds 912-1212: 8 in reverseSequence, 3443-3539, Human alpha-1-antitrypsin-related protein gene

X51801, class C, 20 probes, 20 in all_X51801 1415-1824, Human OP-1 mRNA for osteogenic protein

U65932, class A, 20 probes, 20 in U65932 1244-1634, Human extracellular matrix protein 1 (ECM1) mRNA, complete cds

M74715, class A, 20 probes, 20 in M74715 1574-2080, Human alpha-L-iduronidas (IDUA) mRNA, complete cds

U24704, class A, 20 probes, 20 in U24704 790-1264, Human antisecretory factor-1 mRNA, complete cds

M86737, class A, 20 probes, 20 in M86737 2236-2776, Human high mobility group box (SSRP1) mRNA, complete cds

Autoimmune Antigen, Thyroid Disease-Related Antigen

Gamma-Aminobutyric Acid (Gaba) A Receptor Beta 2 Subunit

D00762, class A, 20 probes, 20 in D00762 237-777, Human mRNA for proteasome subunit HC8

U89916, class A, 20 probes, 20 in U89916 375-879, Homo sapiens putative OSP like protein mRNA, partial cds.

U89336, class A, 20 probes, 19 in U89336exon#46-49 2-143: 1 in fullSequence, 26932:, unknown gene extracted from Human HLA class III region containing NOTCH4 gene, partial sequence, homeobox PBX2 (HPBX) gene, receptor for advanced glycosylation end products (RAGE) gene, complete cds, and 6 unidentified cds, complete sequence., unknown gene extracted from Human HLA class III region containing NOTCH4 gene, partial sequence, homeobox PBX2 (HPBX) gene, receptor for advanced glycosylation end products (RAGE) gene, complete cds, and 6 unidentified cds, complete sequence., unknown gene extracted from Human HLA class III region containing NOTCH4 gene, partial sequence, homeobox PBX2 (HPBX) gene, receptor for advanced glycosylation end products (RAGE) gene, complete cds, and 6 unidentified cds, complete sequence., unknown gene extracted from Human HLA class III region containing NOTCH4 gene, partial sequence, homeobox PBX2 (HPBX) gene, receptor for advanced glycosylation end products (RAGE) gene, complete cds, and 6 unidentified cds, complete sequence., unknown gene extracted from Human HLA class III region containing NO

M15182, class A, 20 probes, 20 in M15182mRNA 1686-2106, Human beta-glucuronidase mRNA, complete cds

Y08564, class A, 20 probes, 20 in Y08564cds 1238-1688, H.sapiens GalNAc-T4 gene. /gb=Y08564 /ntype=DNA /annot=CDS

X07834, class C, 20 probes, 20 in all_X07834 515-1026, Human mRNA for manganese superoxide dismutase (EC 1.15.1.1)

X55733, class B, 20 probes, 10 in X55733cds 1611-1773: 10 in reverseSequence, 1840-2056, H.sapiens initiation factor 4B cDNA

AF008937, class A, 20 probes, 20 in AF008937 508-916, Homo sapiens syntaxin-16C mRNA, complete cds. /gb=AF008937 /ntype=RNA

X67155, class C, 20 probes, 20 in all_X67155 2735-3228, H.sapiens mRNA for mitotic kinesin-like protein-1

X17620, class A, 20 probes, 20 in X17620mRNA 257-677, Human mRNA for Nm23 protein, involved in developmental regulation (homolog. to Drosophila Awd protein)

M23254, class A, 20 probes, 20 in M23254 2672-3164, Human Ca2-activated neutral protease large subunit (CANP) mRNA, complete cds

Profilaggrin - Also Represents: M60503, HG1077-HT1077

M18000, class A, 20 probes, 20 in M18000cds 78-360, Human ribosomal protein S17 gene, complete cds

M58285, class A, 20 probes, 20 in M58285 3356-3788, Human membrane-associated protein (HEM-1) mRNA, complete cds

U47414, class A, 20 probes, 20 in U47414 1449-1959, Human cyclin G2 mRNA, complete cds

D86550, class A, 20 probes, 20 in D86550 5888-6338, Human mRNA for serine/threonine protein kinase, complete cds

U52700, class A, 20 probes, 20 in U52700 70-328, Human tenascin-X (XB) mRNA, RACE clone N1, partial cds. /gb=U52700 /ntype=RNA

S52028, class A, 20 probes, 20 in S52028 582-1141, cystathionine gamma-lyase {clone HCL-1} [human, liver, mRNA, 1194 nt]

J03764, class C, 20 probes, 20 in all_J03764 14604-15049, Human, plasminogen activator inhibitor-1 gene, exons 2 to 9

M33764, class B, 20 probes, 12 in M33764cds 1158-1350: 8 in reverseSequence, 7989-8235, Human ornithine decarboxylase gene, complete cds

X91911, class A, 20 probes, 18 in X91911cds 321-711: 2 in reverseSequence, 912-950, H.sapiens mRNA for RTVP-1 protein

D90359, class A, 20 probes, 20 in D90359 5384-5912, Human CCG1 mRNA

U67122, class A, 20 probes, 20 in U67122 469-728, Human ubiquitin-related protein SUMO-1 mRNA, complete cds.

U20158, class A, 20 probes, 20 in U20158 1551-1911, Human 76 kDa tyrosine phosphoprotein SLP-76 mRNA, complete cds

S77812, class A, 20 probes, 20 in S77812 148-211, flt=vascular endothelial growth factor receptor/VEGF receptor/cell surface tyrosine kinase {clone FLT14} [human, ovarian carcinoma ascitic cells, mRNA Partial Mutant, 338 nt]

S81294, class A, 20 probes, 20 in S81294 4-160, DCC=deleted in colorectal cancer {alternatively spliced, exon 1A} [human, brain tumor, tumor no. 245, mRNA Partial, 216 nt]. /gb=S81294 /ntype=RNA

U33838, class A, 16 probes, 16 in U33838 2-188, Human NF-kappa-B p65delta3 mRNA, spliced transcript lacking exons 6 and 7, partial cds. /gb=U33838 /ntype=RNA, Human NF-kappa-B p65delta3 mRNA, spliced transcript lacking exons 6 and 7, partial cds. /gb=U33838 /ntype=RNA

L47345, class A, 20 probes, 20 in L47345 2141-2609, Homo sapiens elongin A mRNA, complete cds

X97301, class A, 20 probes, 20 in X97301mRNA 13-148, H.sapiens mRNA for Ptg-11 protein. /gb=X97301 /ntype=RNA

Decorin, Alt. Splice 1 - Also Represents: HG3431-HT3617

U51241, class B, 20 probes, 12 in U51241cds 717-1029: 8 in reverseSequence, 1257-1497, Human eosinophil eotaxin receptor (CMKBR3) gene, complete cds

X64643, class C, 20 probes, 20 in all_X64643 1944-2407, H.sapiens c6.1A mRNA

X04366, class C, 20 probes, 20 in all_X04366 2448-2986, Human mRNA for calcium activated neutral protease large subunit (muCANP, calpain, EC 3.4.22.17)

U78313, class A, 20 probes, 20 in U78313 963-1515, Human myogenic repressor I-mf (MDFI) mRNA, complete cds

U72661, class A, 20 probes, 20 in U72661 650-1196, Human ninjurin1 mRNA, complete cds.

S75463, class A, 20 probes, 20 in S75463 1145-1565, P43=mitochondrial elongation factor homolog [human, liver, mRNA, 1644 nt]

D16815, class A, 20 probes, 20 in D16815 1642-2086, Human mRNA for EAR-1r, complete cds

L08096, class A, 20 probes, 20 in L08096 314-794, Human CD27 ligand mRNA, complete cds.

D15049, class A, 20 probes, 20 in D15049 3317-3845, Human mRNA for protein tyrosine phosphatase

U22815, class A, 20 probes, 20 in U22815 3771-3923, Human LAR-interacting protein 1a mRNA, complete cds

X52889, class C, 20 probes, 20 in all_X52889 24339-24440, Human gene for cardiac beta myosin heavy chain

U30827, class A, 20 probes, 20 in U30827 1253-1817, Human splicing factor SRp40-3 (SRp40) mRNA, complete cds

Olfactory Receptor Or17-30

U34343, class A, 20 probes, 20 in U34343 110-560, Human 13kD differentiation-associated protein mRNA, partial cds. /gb=U34343 /ntype=RNA

M10277, class C, 20 probes, 20 in all_M10277 3236-3578, Human cytoplasmic beta-actin gene, complete cds

M94077, class A, 20 probes, 20 in M94077exon#2 657-1125, Human loricrin gene exons 1 and 2, complete cds

Soxa

J05500, class A, 20 probes, 20 in J05500mRNA#1 6200-6740, Human beta-spectrin (SPTB) mRNA, complete cds

U01691, class A, 20 probes, 20 in U01691mRNA 1257-1743, Human annexin V (ANX5) gene, 5 -untranslated region

U52100, class A, 20 probes, 20 in U52100 167-605, Human XMP mRNA, complete cds

D55643, class A, 20 probes, 20 in D55643 443-1019, Human spleen PABL (pseudoautosomal boundary-like sequence) mRNA, clone Sp2. /gb=D55643 /ntype=RNA

U50062, class A, 20 probes, 20 in U50062 1713-2181, Human RIP protein kinase gene, complete cds

U90313, class A, 20 probes, 20 in U90313 212-758, Human glutathione-S-transferase homolog mRNA, complete cds.

M58378, class C, 20 probes, 17 in all_M58378 75-406: 2 in M58378cds#1 1893-1930: 1 in M58378cds#2 2002, SYN1 gene (synapsin I) extracted from Human synapsin I (SYN1) gene

Olfactory Receptor Or17-219 - Also Represents: HG4108-HT4378

U16282, class A, 20 probes, 20 in U16282 2336-2744, Human ELL mRNA, complete cds

Y11180, class A, 20 probes, 20 in Y11180mRNA 31-247, H.sapiens mRNA for twist protein, partial. /gb=Y11180 /ntype=RNA

L27080, class B, 20 probes, 15 in L27080cds 538-946: 5 in reverseSequence, 1159-1207, Human melanocortin 5 receptor (MC5R) gene, complete cds

Glial Growth Factor 2

L05148, class A, 20 probes, 20 in L05148 1890-2388, Human protein tyrosine kinase related mRNA sequence

M65214, class A, 20 probes, 20 in M65214 492-997, Human (HeLa) helix-loop-helix protein HE47 (E2A) mRNA, 3 end

U50939, class A, 20 probes, 20 in U50939 1224-1662, Human amyloid precursor protein-binding protein 1 mRNA, complete cds

X87344, class B, 13 probes, 13 in X87344mRNA#26 769-945, H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes., H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes.

U65581, class A, 20 probes, 20 in U65581 958-1420, Human ribosomal protein L3-like mRNA, complete cds.

U79273, class A, 20 probes, 20 in U79273 851-1127, Human clone 23933 mRNA sequence

D83646, class A, 20 probes, 20 in D83646 1984-2452, Human mRNA for metalloproteinase, complete cds

Paired Box Hup1 (Gb:X15250)

Y09305, class B, 20 probes, 15 in Y09305cds 267-675: 5 in reverseSequence, 711-771, H.sapiens mRNA for protein kinase, Dyrk4, partial

X66276, class C, 20 probes, 20 in all_X66276 3221-3734, H.sapiens mRNA for skeletal muscle C-protein

U40992, class A, 20 probes, 20 in U40992 839-1175, Human heat shock protein hsp40 homolog mRNA, complete cds

Ribosomal Protein L30 Homolog

S62907, class A, 20 probes, 20 in S62907 1577-2136, gamma-aminobutyric acidA receptor alpha 2 subunit [human, fetal brain, mRNA, 2189 nt]

Zinc Finger Protein Hzf3 (Gb:X60153)

X79440, class A, 20 probes, 16 in X79440cds 1303-1759: 4 in reverseSequence, 1827-1851, H.sapiens mRNA for NADP+-dependent malic enzyme

M14745, class A, 20 probes, 20 in M14745 5435-5981, Human bcl-2 mRNA

L08069, class A, 20 probes, 20 in L08069 909-1347, Human heat shock protein, E. coli DnaJ homologue mRNA, complete cds

J04111, class A, 20 probes, 20 in J04111exon#1 2735-3251, Human c-jun proto oncogene (JUN), complete cds, clone hCJ-1

Z31560, class A, 20 probes, 19 in Z31560cds 475-923: 1 in reverseSequence, 953, H.sapiens sox-2 mRNA (partial)

U12535, class A, 20 probes, 20 in U12535 3273-3783, Human epidermal growth factor receptor kinase substrate (Eps8) mRNA, complete cds

M29335, class C, 5 probes, 5 in all_M29335 62-94, Human MHC class II DO-alpha mRNA, partial cds, Human MHC class II DO-alpha mRNA, partial cds

D76435, class A, 20 probes, 20 in D76435 2639-3065, Human mRNA for Zic protein, complete cds

D84110, class A, 20 probes, 20 in D84110 1113-1515, Human mRNA for Werner syndrome-1/type 4, complete cds

X91504, class C, 20 probes, 20 in all_X91504 970-1523, H.sapiens mRNA for ARP1 protein

U43901, class A, 20 probes, 20 in U43901mRNA#1 429-557, Human 37 kD laminin receptor precursor/p40 ribosome associated protein gene, complete cds
Proliferating-Cell Nucleolar Antigen, 120 Kda

M94893, class A, 20 probes, 20 in M94893 989-1499, Human testis-specific protein (TSPY) mRNA, 3 end, clone pJA923

S69265, class A, 19 probes, 19 in S69265 1402-1943, neuron-specific RNA recognition motifs (RRMs)-containing protein [human, hippocampus, mRNA, 1992 nt]

U62136, class A, 20 probes, 20 in U62136 660-1050, Human putative enterocyte differentiation promoting factor mRNA, partial cds

U16812, class B, 20 probes, 14 in U16812cds 274-601: 6 in reverseSequence, 3897-4028, Human Bak-2 gene, complete cds

M31951, class A, 20 probes, 19 in M31951exon#2 671-1061: 1 in reverseSequence, 6169, Human perforin (PRF1) gene, complete cds

Z70759, class C, 20 probes, 20 in all_Z70759 4-251, H.sapiens mitochondrial 16S rRNA gene (partial).

X57351, class C, 8 probes, 8 in all_X57351 294-891, Human 1-8D gene from interferon-inducible gene family, Human 1-8D gene from interferon-inducible gene family

U56244, class C, 20 probes, 20 not in GB record, Human HIG-1 mRNA, complete cds

X01388, class B, 20 probes, 12 in X01388cds 14-272: 8 in reverseSequence, 349-529, Human mRNA for pre-apolipoprotein CIII

Y10202, class A, 20 probes, 20 in Y10202mRNA 169-529, H.sapiens mRNA for CD207 protein. /gb=Y10202 /ntype=RNA

J04027, class A, 20 probes, 20 in J04027 4061-4343, Human plasma membrane Ca2+ pumping ATPase mRNA, complete cds

S79854, class A, 20 probes, 20 in S79854 1585-1963, type 3 iodothyronine deiodinase=selenoenzyme [human, placenta, mRNA, 2066 nt]

L24564, class A, 20 probes, 20 in L24564 854-1400, Human Rad mRNA, complete cds

L27559, class A, 20 probes, 20 in L27559UTR#1 111-166, Human insulin-like growth factor binding protein 5 (IGFBP5) gene

U34605, class A, 20 probes, 20 in U34605 3365-3851, Human retinoic acid- and interferon-inducible 58K protein RI58 mRNA, complete cds

L27841, class A, 20 probes, 20 in L27841 6012-6498, Human autoantigen pericentriol material 1 (PCM-1) mRNA, complete cds

U77827, class C, 20 probes, 20 in all_U77827 1053-1630, Human orphan G protein-coupled receptor (CEPR) gene, complete cds.

X78712, class B, 20 probes, 11 in X78712cds 1319-1637: 9 in reverseSequence, 1691-1823, H.sapiens mRNA for glycerol kinase testis specific 2

X07173, class A, 20 probes, 18 in X07173cds 2503-2803: 2 in reverseSequence, 2956-3028, Human mRNA for second protein of inter-alpha-trypsin inhibitor complex

X86371, class A, 19 probes, 19 in X86371cds 2629-3129, H.sapiens mRNA for tumour suppressor protein, HUGL

U27330, class A, 20 probes, 20 in U27330 1474-1933, Human alpha (1,3) fucosyltransferase (FUT5) mRNA, minor transcript II, complete cds

Y08765, class C, 20 probes, 20 in all_Y08765 1854-2207, H.sapiens mRNA for splicing factor, SF1-HL1 isoform

M29277, class C, 6 probes, 6 in all_M29277 2842-2926, Human isolate JuSo MUC18 glycoprotein mRNA (3 variant), complete cds, Human isolate JuSo MUC18 glycoprotein mRNA (3 variant), complete cds

D13748, class A, 20 probes, 20 in D13748 812-1352, Human mRNA for eukaryotic initiation factor 4AI

L07515, class A, 20 probes, 20 in L07515 253-790, Human heterochromatin protein homologue (HP1) mRNA, complete cds

U73328, class A, 20 probes, 20 in U73328 918-1314, Human DLX7 (Dlx7) mRNA, complete cds

L14848, class A, 20 probes, 20 in L14848 802-1181, Human MHC class I-related protein mRNA, complete cds

U47742, class A, 20 probes, 20 in U47742 7360-7810, Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds

Z83735, class C, 20 probes, 20 in all_Z83735 344-817, H.sapiens hH3/k gene.

X85134, class A, 20 probes, 20 in X85134mRNA 2737-3007, H.sapiens RBQ-3 mRNA

U34038, class A, 20 probes, 20 in U34038 880-1390, Human proteinase-activated receptor-2 mRNA, complete cds

X67734, class C, 20 probes, 20 in all_X67734 4037-4470, H.sapiens mRNA for transient axonal glycoprotein (tag-1)

S77576, class A, 20 probes, 20 in S77576 3-60, ERV9 reverse transcriptase homolog {clone RT18} [human, multiple sclerosis, brain plaques, mRNA Partial, 84 nt]. /gb=S77576 /ntype=RNA

D49493, class A, 20 probes, 20 in D49493exon#3 403-811, Human gene for human bone morphogenetic protein-3b

L02785, class A, 20 probes, 20 in L02785 2412-2790, Homo sapiens colon mucosa-associated (DRA) mRNA, complete cds

Lung Surfactant Protein D - Also Represents: L05485

U09367, class A, 20 probes, 20 in U09367 1942-2449, Human zinc finger protein ZNF136

X85786, class C, 20 probes, 20 in all_X85786 1751-2262, H.sapiens mRNA for DNA binding regulatory factor

D87446, class A, 20 probes, 20 in D87446 5583-6135, Human mRNA for KIAA0257 gene, partial cds

U57629, class A, 20 probes, 20 in U57629 2195-2735, Human retinitis pigmentosa GTPase regulator (RPGR) mRNA, complete cds

X66365, class B, 20 probes, 11 in X66365cds 543-957: 9 in reverseSequence, 1080-1206, H.sapiens mRNA PLSTIRE for serine/threonine protein kinase

U07132, class A, 20 probes, 20 in U07132 1415-1961, Human steroid hormone receptor Ner-I mRNA, complete cds

U63295, class A, 20 probes, 20 in U63295 1285-1795, Human seven in absentia homolog mRNA, complete cds

X77197, class C, 20 probes, 20 in all_X77197 2631-3166, H.sapiens mRNA for chloride channel

J04982, class C, 20 probes, 20 in all_J04982 4001-5444, Human heart/skeletal muscle ATP/ADP translocator (ANT1) gene, complete cds

D31889, class A, 20 probes, 20 in D31889 2835-3279, Human mRNA for KIAA0072 gene, partial cds

Z68274, class A, 20 probes, 20 in Z68274cds 182-632, Human DNA sequence from cosmid L129H7, Huntington Disease Region, chromosome 4p16.3 contains Pseudogene and CpG island. /gb=Z68274 /ntype=DNA /annot=CDS

Ras-Like Protein Tc4

Y10515, class A, 20 probes, 20 in Y10515mRNA 79-307, H.sapiens mRNA for CD58 T7 protein. /gb=Y10515 /ntype=RNA

L34219, class A, 20 probes, 18 in L34219exon#7 26-452: 2 not in GB record, Homo sapiens retinaldehyde-binding protein (CRALBP) gene, complete cds

U90306, class A, 20 probes, 20 in U90306 13-175, Human iroquois-class homeodomain protein IRX-4 mRNA, partial cds. /gb=U90306 /ntype=RNA

U49395, class A, 20 probes, 20 in U49395 1361-1907, Human ionotropic ATP receptor P2X5a mRNA, complete cds

B. subtilis /GEN=thrC /DB_XREF=gb:X04603.1 /NOTE=SIF corresponding to nucleotides 288-932 of gb:X04603.1 /DEF=B. subtilis thrB and thrC genes for homoserine kinase and threonine synthase EC 2.7.1.39 and EC 4.2.99.2, respectively).

X06290, class B, 20 probes, 10 in X06290cds 13307-13442: 10 in reverseSequence, 13709-13913, Human mRNA for apolipoprotein(a)

U46569, class B, 20 probes, 11 in U46569mRNA 1025-1241: 9 in reverseSequence, 300-498, Human aquaporin-5 (AQP5) gene

Transcription Factor Btf3 Homolog (Gb:M90355)

L33404, class A, 20 probes, 20 in L33404 464-890, Human stratum corneum chymotryptic enzyme mRNA, complete cds

U83239, class A, 20 probes, 20 in U83239 323-877, Human CC chemokine STCP-1 mRNA, complete cds

U62389, class A, 20 probes, 20 in U62389 31-409, Human putative cytosolic NADP-dependent isocitrate dehydrogenase mRNA, partial cds. /gb=U62389 /ntype=RNA

U49188, class A, 20 probes, 20 in U49188 1187-1685, Human placenta (Diff33) mRNA, complete cds

Homo sapiens /REF=M97935 /DEF=transcription factor ISGF-3 mRNA, complete cds /LEN=3970 (_5, _MA, MB, _3 represent transcript regions 5 prime, MiddleA, MiddleB, and 3 prime respectively)

Carcinoembryonic Antigen

M69203, class A, 20 probes, 16 in M69203cds 4-254: 4 in reverseSequence, 122-144, Human cytokine (SCYA2) gene

L03785, class A, 20 probes, 20 in L03785 72-582, Human regulatory myosin light chain (MYL5) mRNA, complete cds

L07592, class A, 20 probes, 20 in L07592 2760-3228, Human peroxisome proliferator activated receptor mRNA, complete cds

X52003, class B, 20 probes, 10 in X52003cds 63-213: 10 in reverseSequence, 289-445, H.sapiens pS2 protein gene

X65727, class A, 20 probes, 20 in X65727cds#1 199-591, GSTalpha locus gene (glutathione S-transferase) extracted from H.sapiens GSTalpha gene for glutathione S-tranferase exon 2

Y00796, class C, 20 probes, 20 in all_Y00796 4559-5109, Human mRNA for leukocyte-associated molecule-1 alpha subunit (LFA-1 alpha subunit)

M24122, class A, 17 probes, 17 in M24122mRNA 309-774, Human myosin alkali light chain (ventricular) mRNA, complete cds

L33262, class A, 19 probes, 19 in L33262 1751-2273, Homo sapiens DNA repair and recombination homologue (RAD52) gene, complete cds

X52142, class C, 20 probes, 20 in all_X52142 2163-2734, Human mRNA for CTP synthetase (EC 6.3.4.2)