Appendix 3c External Validation; Medical Record Selection

Using the blood culture line listing you request from each selected facility, you will select all reported CLABSIs (or up to 20, by random sample), and unreported candidate CLABSIs (up to 40, stratified by adult/pediatric ICUs (75%) vs. NICU (25%, if available), and prioritizing targeted pathogens where reporting errors are considered likely), from the past year of surveillance. Fixing surveillance to a calendar year is helpful for tracking which data are validated, but not essential to the process of quality improvement.

In reality, many hospitals will have far fewer events to sample than the prescribed goals here, but the goal numbers will establish a cap on medical record reviews for larger facilities. Roughly half of the unreported candidate CLABSIs will be eliminated during screening for a central line, and half should have a central line, in which case they may be fully reviewed.

Targeted pathogens include:

- *Candida spp.*, *Torulopsis* spp.
- *Enterococcus spp*.
- *Staphylococcus aureus*, including MSSA and MRSA
- Coagulase-negative staphylococcus
- Common gram-negative organisms (limited to *Klebsiella spp.*, *E. coli spp.*, or *Pseudomonas spp*.)

Following are the steps to be taken when selecting the medical record sample.

1. Assign a random number to each positive blood culture on the line listing. Sort line listing by Medical record number (and admission date if available) to generate recognizable patients and records.
2. Assure line listing is complete (contains all positive blood cultures from all ICU locations throughout the year, including reported CLABSIs)
    a. If some ICUs are not represented on the blood culture line listing, verify with IP that list is complete and there were no positive blood cultures from that location
    b. Identify reported CLABSIs on the positive blood culture line listing, and select all (up to maximum 20 by random number) for review. All positive blood cultures assigned to these records will be considered part of stratum 1 (reported CLABSI), whether or not they are part of the actual CLABSI event.
3. Next, limit the list to non-stratum 1 blood cultures. Sort the list by pathogen (Org 1) and identify all "targeted pathogens" listed above and assign these blood cultures to stratum 2. The remaining blood cultures are stratum 3.
4. Sort stratum 2 and 3 blood cultures by facility location and identify two ICU strata (NICU and non-NICU)
5. Select the NICU screening sample, where NICU= Yes and stratum=2 (targeted pathogens); sort by random number and MRN (and admission date if available). Select the first 10 random numbers that identify unique patients/records. If additional NICU records are needed, select NICU records from stratum 3. (Skip this step if there is no NICU, and add the 10 random numbers to the sample below for a total of 40 records).
6. Select the non-NICU screening sample, where NICU = No and stratum = 2 (targeted pathogens); sort by random number and MRN (and admission date if available). Select the first 30 random numbers that identify unique patients/records. If additional records are needed, select non-NICU records from stratum 3.

Your screening sample should include

- All (or up to 20) records with reported CLABSIs
- All (or up to 10) NICU records with unreported candidate CLABSIs in facilities with NICUs
- All (or up to 30) non-NICU ICU records with unreported candidate CLABSIs in facilities with NICUs
- All (or up to 40) non-NICU ICU records with unreported candidate CLABSIs in facilities without NICUs.