Table S1: Monomicrobial identification performance (pre-discrepancy testing) for the 253 analyzable runs

Species	True Positive	True Negative	False Positive	False Negative	Indeterminate	Sensitivity	Specificity	PPV	NPV
CNS	66	165	9	1	12	98.5%	94.8%	88.0%	99.4%
EFS	8	243	0	0	2	100%	100%	100%	100%
EFM	3	248	2	0	0	100%	99.2%	60.0%	100%
SAU	29	198	11	1	14	96.7%	94.7%	72.5%	99.5%
SLU	0	251	0	0	2	N/A	100%	N/A	100%
STR	12	234	7	0	0	100%	97.1%	63.2%	100%
ABA	1	252	0	0	0	100%	100%	100%	100%
CIT	3	250	0	0	0	100%	100%	100%	100%
ENT	1	249	0	0	3	100%	100%	100%	100%
ECO	44	208	1	0	0	100%	99.5%	97.8%	100%
KLE	16	234	0	0	3	100%	100%	100%	100%
PRO	5	247	1	0	0	100%	99.6%	83.3%	100%
PAE	10	242	0	1	0	90.9%	100%	100%	99.6%
SMA	6	247	0	0	0	100%	100%	100%	100%
CAL	3	249	1	0	0	100%	99.6%	75.0%	100%
CGL	2	243	8	0	0	100%	96.8%	20.0%	100%
Gram-Positive Organisms	118	1339	29	2	30	98.3%	97.9%	80.3%	99.9%
Gram-Negative Organisms	86	1929	2	1	6	98.9%	99.9%	97.7%	100%
All Yeast	5	492	9	0	0	100%	98.2%	35.7%	100%
All Organisms	209	3760	40	3	36	98.6%	99.0%	83.9%	99.9%

PPV: Positive predictive value, NPV: Negative predictive value, CNS: Coagulase Negative *Staphylococcus* spp., EFS: *Enterococcus faecalis*, EFM: *Enterococcus faecium*, SAU: *Staphylococcus aureus*, SLU: *Staphylococcus lugdunensis*, STR: *Streptococcus* spp., ABA: *Acinetobacter baumannii*, CIT: *Citrobacter* spp., ENT: *Enterobacter* spp., ECO: *Escherichia coli*, KLE: *Klebsiella* spp., PRO: *Proteus* spp., PAE: *Pseudomonas aeruginosa*, SMA: *Serratia marcescens*, CAL: *Candida albicans*, CGL: *Candida glabrata*