**Supplemental Data Table S1.** List of species identified using the MBTand VMS-P systems

|  |  |
| --- | --- |
|   | No. identifications |
| Species | MBT | VMS-P |
| *Achromobacter denitrificans* | - | 1 |
| *Acinetobacter baumannii* | 1 | 1 |
| *Acinetobacter dijkshoorniae* | 1 | - |
| *Acinetobacter pittii* | 1 | 2 |
| *Acinetobacter ursingii* | 1 | 1 |
| *Actinomyces funkei* | 1 | - |
| *Actinotignum schaalii* | 1 | 2 |
| *Aerococcus sanguinicola* | 2 | 2 |
| *Aerococcus urinae* | 3 | 3 |
| *Anaerococcus vaginalis* | 1 | 1 |
| *Bacillus cereus* | 2 | - |
| *Bacillus cereus* group | - | 2 |
| *Bacillus megaterium* | 1 | 2 |
| *Bacteroides dorei* | - | 1 |
| *Bacteroides fragilis* | 6 | 6 |
| *Bacteroides salyersiae* | 1 | - |
| *Bacteroides thetaiotaomicron* | 1 | 2 |
| *Bacteroides vulgatus* | 2 | 1 |
| *Bifidobacterium* spp. | - | 1 |
| *Brevibacterium casei* | 1 | 1 |
| *Brucella* spp*.* | - | 1 |
| *Candida albicans* | 131 | 129 |
| *Candida albicans\_(africana)* | 3 | - |
| *Candida dubliniensis* | 9 | 9 |
| *Candida glabrata* | 54 | 58 |
| *Candida inconspicua* | 1 | 1 |
| *Candida kefyr* | 9 | 8 |
| *Candida krusei* | 6 | 6 |
| *Candida lusitaniae* | 1 | 2 |
| *Candida nivariensis* | 3 | 3 |
| *Candida parapsilosis* | 4 | 4 |
| *Candida pararugosa* | 1 | 1 |
| *Candida pelliculosa* | - | 1 |
| *Candida tropicalis* | 22 | 23 |
| *Citrobacter amalonaticus* | 2 | 2 |
| *Citrobacter braakii* | - | 2 |
| *Citrobacter freundii* | 12 | 9 |
| *Citrobacter koseri* | 2 | 2 |
| *Clostridium perfringens* | 6 | 5 |
| *Clostridium tertium* | 4 | 3 |
| *Corynebacterium amycolatum* | - | 1 |
| *Corynebacterium durum* | - | 2 |
| *Corynebacterium simulans* | 1 | - |
| *Corynebacterium striatum* | 3 | 1 |
| *Corynebacterium tuberculostearicum* | - | 1 |
| *Corynebacterium urealyticum* | - | 1 |
| *Cutibacterium acnes* | 1 | 4 |
| *Cutibacterium avidum* | - | 1 |
| *Dialister pneumosintes* | - | 2 |
| *Enterobacter asburiae* | 2 | - |
| *Enterobacter bugandensis* | 1 | - |
| *Enterobacter cloacae* | 28 | 22 |
| *Enterobacter hormaechei* | 1 | 11 |
| *Enterobacter kobei* | 2 | 1 |
| *Enterobacter xiangfangensis* | 1 | - |
| *Enterococcus avium* | 2 | 3 |
| *Enterococcus faecalis* | 80 | 85 |
| *Enterococcus faecium* | 7 | 5 |
| *Enterococcus gallinarum* | 1 | 1 |
| *Enterococcus gilvus* | 2 | - |
| *Escherichia coli* | 134 | 139 |
| *Exophiala phaeomuriformis* complex | - | 1 |
| *Finegoldia magna* | 1 | 2 |
| *Fusobacterium gonidiaformans* | 2 | 1 |
| *Fusobacterium necrophorum* | - | 1 |
| *Fusobacterium nucleatum* | 1 | 1 |
| *Gardnerella vaginalis* | 7 | 7 |
| *Gemella morbillorum* | 1 | - |
| *Geotrichum candidum/klebahnii* | - | 9 |
| *Geotrichum silvicola* | 8 | - |
| *Granulicatella adiacens* | - | 1 |
| *Haemophilus influenzae* | 6 | 6 |
| *Haemophilus parainfluenzae* | 2 | 1 |
| *Hafnia alvei* | 3 | 3 |
| *Helicobacter pylori* | 1 | 2 |
| *Klebsiella aerogenes* | 10 | 10 |
| *Klebsiella oxytoca* | 9 | 9 |
| *Klebsiella pneumoniae* | 71 | 66 |
| *Klebsiella variicola* | 2 | 1 |
| *Kocuria palustris* | 1 | 1 |
| *Kocuria rhizophila* | - | 1 |
| *Lactobacillus casei/paracasei/rhamnosus* | - | 1 |
| *Lactobacillus crispatus* | 7 | 6 |
| *Lactobacillus delbrueckii* | 1 | 1 |
| *Lactobacillus gasseri* | 4 | - |
| *Lactobacillus acidophilus/gasseri* | - | 2 |
| *Lactobacillus iners* | 1 | 1 |
| *Lactobacillus jensenii* | 3 | 3 |
| *Lactobacillus mucosae* | 1 | - |
| *Lactobacillus oris* | 1 | - |
| *Lactobacillus plantarum* | 1 | - |
| *Lactobacillus pentosus/plantarum/paraplantarum* | - | 1 |
| *Lactobacillus rhamnosus* | 1 | - |
| *Micrococcus luteus* | 1 | 1 |
| *Moraxella catarrhalis* | 2 | 2 |
| *Moraxella osloensis* | - | 1 |
| *Morganella morganii* | 8 | 9 |
| *Myroides odoratimimus* | 2 | - |
| *Myroides* spp. | - | 2 |
| *Neisseria gonorrhoeae* | 3 | 3 |
| *Neisseria* spp. | 1 | - |
| *Neisseria subflava* | 3 | - |
| *Neisseria flava/perflava/subflava* | - | 1 |
| *Paeniclostridium sordellii* | 4 | 3 |
| *Pantoea agglomerans* | 2 | 3 |
| *Paracoccus yeei* | 2 | - |
| *Parvimonas micra* | 1 | 1 |
| *Peptoniphilus asaccharolyticus* | - | 2 |
| *Peptoniphilus indolicus* | 1 | - |
| *Plesiomonas shigelloides* | 1 | 1 |
| *Porphyromonas asaccharolytica* | 1 | 1 |
| *Prevotella bivia* | 1 | 1 |
| *Proteus hauseri* | 2 | - |
| *Proteus mirabilis* | 35 | 35 |
| *Proteus vulgaris* | 2 | 3 |
| *Pseudomonas aeruginosa* | 79 | 77 |
| *Pseudomonas mosselii* | - | 2 |
| *Pseudomonas monteilii* | 1 | - |
| *Rothia aeria* | 1 | 1 |
| *Rothia mucilaginosa* | 3 | 1 |
| *Saccharomyces cerevisiae* | 1 | 1 |
| *Salmonella* spp. | 6 | - |
| *Salmonella enterica* ssp*. enterica* | - | 6 |
| *Serratia marcescens* | 13 | 13 |
| *Slackia exigua* | 1 | - |
| *Staphylococcus aureus* | 91 | 97 |
| *Staphylococcus capitis* | 13 | 18 |
| *Staphylococcus caprae* | 3 | 3 |
| *Staphylococcus epidermidis* | 95 | 109 |
| *Staphylococcus haemolyticus* | 35 | 44 |
| *Staphylococcus hominis* | 15 | 19 |
| *Staphylococcus lugdunensis* | 4 | 5 |
| *Staphylococcus pettenkoferi* | 1 | - |
| *Staphylococcus saprophyticus* | 4 | 5 |
| *Staphylococcus simulans* | 1 | 1 |
| *Staphylococcus warneri* | 4 | 5 |
| *Stenotrophomonas maltophilia* | 6 | 5 |
| *Streptococcus agalactiae* | 5 | 8 |
| *Streptococcus anginosus* | 11 | 8 |
| *Streptococcus canis* | 1 | - |
| *Streptococcus gallolyticus* | 7 | - |
| *Streptococcus gallolyticus* ssp*. gallolyticus* | - | 12 |
| *Streptococcus gallolyticus* ssp*. pasteurianus* | - | 2 |
| *Streptococcus intermedius* | 2 | 2 |
| *Streptococcus mitis* | 5 | - |
| *Streptococcus oralis* | 6 | - |
| *Streptococcus mitis/Streptococcus oralis* |  | 9 |
| *Streptococcus pneumoniae* | 8 | 7 |
| *Streptococcus pseudopneumoniae* | 2 | 1 |
| *Streptococcus pyogenes* | 4 | 3 |
| *Streptococcus vestibularis* | 2 | 2 |
| *Veillonella atypica* | 1 | 1 |
| *Vibrio fluvialis* | - | 3 |
| *Wickerhamomyces anomalus*  | 1 | - |
| *Yarrowia lipolytica* | 2 | 3 |

Abbreviations: VMS-P, VITEK MS PRIME system; MSP, MALDI Biotyper Microflex LT system

**Supplemental Data Table S2.** Discrepancies between the VMS-P and MBT systems

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Spot No.**  | **MBT** |  | **VMS-P** |  |  |
| **Identification** | **Score** | **Comment provided by software** |  | **Identification using VMS-P** | **Score VMS** | **Personal comment** | **Conclusion** |
| 2 | *Bacillus cereus* | 1.8 | *“Bacillus anthracis, cereus, mycoides, pseudomycoides, thuringiensis, and weihenstephanensis are similar and belong to the Bacillus cereus group”* |  | *Bacillus cereus* group | 99.9 |  | VMSD |
| 3 | 2.3 |  | 99.9 |  | VMSD |
| 4 | *Bacteroides vulgatus* | 2.4 | *“The species vulgatus/dorei from the Bacteroides genus display very similar profiles; it is difficult to distinguish these species. Bacteroides dorei is not included in the database MBT”* |  | *Bacteroides dorei/Bacteroides vulgatus* | 50/50 |  | VMSD |
| 6 | *Citrobacter freundii* | 2.3 | *“The profiles of species belonging to this genus are very similar. The differentiation of species is difficult”* |  | *Citrobacter freundii/Citrobacter braakii* | 50/50 |  | VMSD |
| 7 | 2.2 |  | 50/50 |  | VMSD |
| 8 | 2.3 |  | 50/50 |  | VMSD |
| 9 | 2.3 |  | 50/50 |  | VMSD |
| 10 | *Citrobacter freundii* | 2.4 | *“The profiles of species belonging to this genus are very similar. The differentiation of species is difficult”* |  | *Citrobacter freundii/Citrobacter werkmanii* | 50/50 |  | VMSD |
| 11 | *Citrobacter freundii* | 2.3 | *“The profiles of species belonging to this genus are very similar. The differentiation of species is difficult”* |  | *Citrobacter freundii/Citrobacter werkmanii* | 50/50 |  | VMSD |
| 16 | *Enterobacter asburiae* | 1.8 | *“Belong to the Enterobacter cloacae complex”* |  | *Enterobacter cloacae/Enterobacter asburiae* | 50/50 |  | VMSD |
| 17 | *Enterobacter cloacae* | 2.1 | *“Belong to the Enterobacter cloacae complex”* |  | *Enterobacter cloacae/Enterobacter asburiae* | 50/50 |  | VMSD |
| 18 | 2.3 |  | 50/50 |  | VMSD |
| 19 | 2.3 |  | 50/50 |  | VMSD |
| 20 | 2.3 |  | 50/50 |  | VMSD |
| 21 | 2.1 |  | 50/50 |  | VMSD |
| 22 | 2.3 |  | 50/50 |  | VMSD |
| 23 | 2.4 |  | 50/50 |  | VMSD |
| 24 | 2.2 |  | 50/50 |  | VMSD |
| 25 | 2.3 |  | 50/50 |  | VMSD |
| 26 | 2.2 |  | 50/50 |  | VMSD |
| 27 | 2.2 |  | 50/50 |  | VMSD |
| 28 | *Enterobacter cloacae* | 2.3 | *“Belong to the Enterobacter cloacae complex”* |  | *Enterobacter cloacae/Enterobacter asburiae/Enterobacter hormaechei* | 33/33/33 |  | VMSD |
| 29 | 2.1 |  | 33/33/33 |  | VMSD |
| 30 | *Enterobacter cloacae* | 2.2 | *“Belong to the Enterobacter cloacae complex”* |  | *Enterobacter hormaechei* | 97.0 |  | VMSD |
| 31 | 2.2 |  | 97.0 |  | VMSD |
| 32 | 2.3 |  | 97.0 |  | VMSD |
| 33 | 2.3 |  | 99.9 |  | VMSD |
| 34 | 2.2 |  | 99.9 |  | VMSD |
| 35 | 2.3 |  | 99.9 |  | VMSD |
| 36 | 1.9 |  | 100.0 |  | VMSD |
| 37 | 2.3 |  | 99.9 |  | VMSD |
| 38 | *Enterobacter cloacae* | 2.4 | *“Belong to the Enterobacter cloacae complex”* |  | *Enterobacter hormaechei/Enterobacter asburiae/Enterobacter kobei* | 36/36/32 |  | VMSD |
| 39 | *Enterobacter cloacae* | 2.1 | *“Belong to the Enterobacter cloacae complex”* |  | *Enterobacter kobei* | 99.9 |  | VMSD |
| 40 | *Enterobacter hormaechei* | 2.0 | *“Belong to the Enterobacter cloacae complex”* |  | *Enterobacter cloacae/Enterobacter asburiae* | 50/50 |  | VMSD |
| 41 | *Enterobacter kobei* | 2.0 | *“Belong to the Enterobacter cloacae complex”* |  | *Enterobacter cloacae/Enterobacter asburiae* | 50/50 |  | VMSD |
| 42 | *Enterobacter xiangfangensis* | 2.4 | *“Belong to the Enterobacter cloacae complex”* |  | *Enterobacter cloacae/Enterobacter asburiae/Enterobacter hormaechei* | 32/34/34 |  | VMSD |
| 52 | *Hafnia alvei* | 2.4 |  |  | *Hafnia alvei/Obesumbacterium proteus* | 50/50 | Strong DNA homology between *Hafnia alvei* and *Obesumbacterium proteus* | VMSD |
| 53 | 2.4 |  |  | 50/50 | VMSD |
| 54 | 2.4 |  |  | 50/50 | VMSD |
| 61 | *Klebsiella variicola* | 2.5 | *“Similar to Klebsiella pneumoniae”* |  | *Klebsiella pneumoniae/Klebsiella variicola* | 50/50 |  | VMSD |
| 62 | *Lactobacillus gasseri* | 2.2 |  |  | *Lactobacillus acidophilus/gasseri* | 99.9 |  | VMSD |
| 63 | 1.9 |  |  | 99.9 |  | VMSD |
| 64 | *Lactobacillus plantarum* | 2.0 |  |  | *Lactobacillus pentosus/plantarum/paraplantarum* | 100.0 |  | VMSD |
| 65 | *Lactobacillus rhamnosus* | 1.9 |  |  | *Lactobacillus casei/paracasei/rhamnosus* | 99.9 |  | VMSD |
| 69 | *Neisseria subflava* | 2.1 |  |  | *Neisseria flava/perflava/subflava* | 99.9 |  | VMSD |
| 73 | *Porphyromonas asaccharolytica* | 2.3 |  |  | *Porphyromonas asaccharolytica/uenonis* | 99.9 |  | VMSD |
| 75 | *Proteus vulgaris* | 2.3 | *“Species hauseri/penneri/vulgaris from the Proteus genus display very similar profiles. It is difficult to distinguish these species”* |  | *Proteus vulgaris/Proteus penneri* | 50/50 |  | VMSD |
| 84 | *Streptococcus gallolyticus* | 2.1 | *“Species equinus/gallolyticus/infantarius/lutetiensis from the Streptococcus genus display very similar profiles. It is difficult to distinguish these species”* |  | *Streptococcus gallolyticus* ssp. *gallolyticus* | 99.9 |  | VMSD |
| 85 | 2.1 |  | 99.9 |  | VMSD |
| 86 | 2.0 |  | 99.9 |  | VMSD |
| 87 | 2.1 |  | 99.9 |  | VMSD |
| 88 | 2.0 |  | 99.9 |  | VMSD |
| 89 | *Streptococcus gallolyticus* | 1.9 | *“Species equinus/gallolyticus/infantarius/lutetiensis from the Streptococcus genus display very similar profiles. It is difficult to distinguish these species”* |  | *Streptococcus gallolyticus* ssp. *gallolyticus/Streptococcus gallolyticus* ssp. *pasteurianus* | 50/50 |  | VMSD |
| 90 | *Streptococcus gallolyticus* | 2.2 | *“Species equinus/gallolyticus/infantarius/lutetiensis from the Streptococcus genus display very similar profiles. It is difficult to distinguish these species”* |  | *Streptococcus gallolyticus* ssp. *pasteurianus* | 99.9 |  | VMSD |
| 91 | *Streptococcus mitis* | 2.2 | *“Streptococcus mitis/oralis/peroris/pneumoniae/pseudopneumoniae are similar. The result has to be confirmed through complementary analysis (optochin, bile)”* |  | *Streptococcus mitis/Streptococcus oralis* | 99.9 |  | VMSD |
| 92 | 2.2 |  | 99.8 |  | VMSD |
| 93 | 2.5 |  | 82.0 |  | VMSD |
| 94 | 2.1 |  | 99.9 |  | VMSD |
| 95 | *Streptococcus oralis* | 2.2 | *“Streptococcus mitis/oralis/peroris/pneumoniae/pseudopneumoniae are similar. The result has to be confirmed through complementary analysis (optochin, bile)”* |  | *Streptococcus mitis/Streptococcus oralis* | 99.9 |  | VMSD |
| 96 | 2.1 |  | 99.9 |  | VMSD |
| 97 | 2.0 |  | 99.9 |  | VMSD |
| 100 | *Streptococcus vestibularis* | 1.8 |  |  | *Streptococcus vestibularis/Streptococcus salivarius* ssp. *thermophilus/Streptococcus salivarius* ssp. *salivarius* | 33/33/33 |  | VMSD |
| 101 | 1.8 |  |  | 33/33/33 |  | VMSD |
| 103 | *Candida albicans\_(africana)* | 2.1 |  |  | *Candida albicans* | 99.9 |  | VMSD |
| 104 | 2.1 |  |  | 99.9 |  | VMSD |
| 105 | 2.1 |  |  | 99.9 |  | VMSD |
| 116 | *Yarrowia lipolytica* | 2.1 |  |  | *Candida lipolytica* | 100.0 | Taxonomic synonym | VMSD |
| 117 | 2.2 |  |  | 100.0 | VMSD |
| 115 | *Wickerhamomyces anomalus* | 1.8 |  |  | *Candida pelliculosa* | 99.9 | Taxonomic synonym | VMSD |
| 107 | *Geotrichum silvicola* | 1.9 | *“Species candidum/silvicola from the Geotrichum genus display very similar profiles. It is difficult to distinguish these species”* |  | *Geotrichum candidum/klebahnii* | 99.9 |  | Same genus |
| 108 | 2.0 |  | 99.9 |  | Same genus |
| 109 | 2.0 |  | 99.9 |  | Same genus |
| 110 | 2.0 |  | 99.9 |  | Same genus |
| 111 | 2.0 |  | 100.0 |  | Same genus |
| 112 | 2.0 |  | 100.0 |  | Same genus |
| 113 | 2.0 |  | 100.0 |  | Same genus |
| 114 | 2.1 |  | 100.0 |  | Same genus |
| 1 | *Acinetobacter dijkshoorniae* | 2.2 | *“Species belonging to Acinetobacter baumannii/calcoaceticus complex. An extraction has to be performed”* |  | *Acinetobacter pittii* | 100.0 |  | Same genus |
| 5 | *Citrobacter freundii* | 2.2 | *“The profiles of species belonging to this genus are very similar. The differentiation of species is difficult”* |  | *Citrobacter braakii* | 99.8 |  | Same genus |
| 15 | *Corynebacterium striatum* | 1.9 |  |  | *Corynebacterium durum* | 99.9 |  | Same genus |
| 45 | *Enterococcus faecium* | 2.0 |  |  | *Enterococcus avium* | 99.9 | Several species isolated from abdominal specimens without *Enterococcus avium* | Same genus |
| 46 | 2.0 |  |  | 99.9 | Same genus |
| 50 | *Fusobacterium gonidiaformans* | 2.2 | *“Species gonidiaformans/necrophorum belonging to the Fusobacterium genus display very similar profiles. Species are difficult to distinguish”* |  | *Fusobacterium necrophorum* | 99.9 |  | Same genus |
| 60 | *Klebsiella variicola* | 2.4 | *“Similar to Klebsiella pneumoniae”* |  | *Klebsiella pneumoniae* | 99.6 |  | Same genus |
| 66 | *Myroides odoratimimus* | 2.3 |  |  | *Myroides* spp. | 99.9 |  | Same genus |
| 67 | 2.2 |  |  | 99.9 |  | Same genus |
| 72 | *Peptoniphilus indolicus* | 2.1 | *“Species harei/indolicus from the Peptoniphilus genus display very similar profiles. It is difficult to distinguish these species”* |  | *Peptoniphilus asaccharolyticus* | 99.9 |  | Same genus |
| 74 | *Proteus hauseri* | 2.4 | *“Species hauseri/penneri/vulgaris from the Proteus genus display very similar profiles. It is difficult to distinguish these species”* |  | *Proteus vulgaris* | 99.9 |  | Same genus |
| 77 | *Pseudomonas monteilii* | 1.9 | *“Belong to the Pseudomonas putida group”* |  | *Pseudomonas mosselii* | 99.9 |  | Same genus |
| 98 | *Streptococcus pneumoniae* | 1.9 | *“Streptococcus mitis/oralis/peroris/pneumoniae/pseudopneumoniae are similar. The result has to be confirmed through complementary analysis (optochin, bile)”* |  | *Streptococcus mitis/Streptococcus oralis* | 99.9 |  | Same genus |
| 99 | *Streptococcus pseudopneumoniae* | 2.3 | *“Streptococcus mitis/oralis/peroris/pneumoniae/pseudopneumoniae are similar. The result has to be confirmed through complementary analysis (optochin, bile)”* |  | *Streptococcus mitis/Streptococcus oralis* | 99.9 |  | Same genus |
| 12 | *Clostridium perfringens* | 2.4 |  |  | *Clostridium perfringens/Proteus mirabilis* | 50/50 | *Proteus mirabilis* and *Clostridium perfringens* present in the specimen | Cont. |
| 14 | *Clostridium perfringens* | 2.0 |  |  | *Proteus mirabilis* | 99.9 | *Proteus mirabilis* and *Clostridium perfringens* present in the specimen | Cont. |
| 43 | *Enterococcus faecalis* | 1.8 |  |  | *Escherichia coli* | 100.0 | *Enterococcus faecalis* and *Escherichia coli* present in the specimen | Cont. |
| 44 | *Enterococcus faecalis* | 2.2 |  |  | *Staphylococcus haemolyticus* | 99.9 | *Enterococcus faecalis* and *Staphylococcus haemolyticus* associated from genital flora | Cont. |
| 47 | *Enterococcus faecium* | 2.4 |  |  | *Enterococcus faecium/Corynebacterium durum* | 50/50 | Polymicrobial drainage fluid | Cont. |
| 51 | *Gardnerella vaginalis* | 2.0 |  |  | *Gardnerella vaginalis/Cutibacterium avidum/Streptomyces griseus/Brevibacillus* spp. | 26/26/26/22 | Non-isolated microcolonies from female urine | Cont. |
| 55 | *Klebsiella pneumoniae* | 2.4 | *“Similar to Klebsiella variicola”* |  | *Escherichia coli/Klebsiella pneumoniae* | 50/50 | *Escherichia coli* and *Klebsiella pneumoniae* present in the specimen | Cont. |
| 56 | 2.4 |  | 48/52 | Cont. |
| 57 | 2.4 |  | 50/50 | Cont. |
| 58 | 2.4 |  | 48/52 | Cont. |
| 71 | *Paeniclostridium sordellii* | 2.3 |  |  | *Paeniclostridium sordellii/Proteus mirabilis* | 50/50 | *Paeniclostridium sordellii* and *Proteus mirabilis* present in the specimen | Cont. |
| 13 | *Clostridium perfringens* | 2.0 |  |  | *Peptoniphilus asaccharolyticus* | 99.9 | Anaerobic flora from a biopsy | WCP |
| 48 | *Escherichia coli* | 2.2 | *“Escherichia coli is similar to Shigella and Escherichia fergusonii. It cannot be clearly distinguished”* |  | *Enterococcus faecalis* | 100.0 | No explanation | WCP |
| 49 | *Escherichia coli* | 2.2 |  |  | *Staphylococcus haemolyticus* | 100.0 | No explanation | WCP |
| 59 | *Klebsiella pneumoniae* | 2.4 | *“Similar to Klebsiella variicola”* |  | *Staphylococcus epidermidis* | 99.9 | No explanation | WCP |
| 68 | *Neisseria sp* | 2.0 |  |  | *Haemophilus influenzae* | 99.9 | Oropharyngeal flora | WCP |
| 70 | *Paeniclostridium sordellii* | 2.1 |  |  | *Clostridium perfringens* | 99.9 | Anaerobic flora from a biopsy | WCP |
| 76 | *Pseudomonas aeruginosa* | 2.1 |  |  | *Enterococcus faecalis* | 100.0 | *Pseudomonas aeruginosa* and *Enterococcus faecalis* present in the specimen | WCP |
| 78 | *Staphylococcus epidermidis* | 1.8 |  |  | *Morganella morganii* | 99.9 | No explanation | WCP |
| 79 | *Staphylococcus epidermidis* | 1.8 |  |  | *Staphylococcus hominis* | 99.9 | Blood culture with several *Staphylococcus* strains | WCP |
| 80 | *Staphylococcus saprophyticus* | 2.1 |  |  | *Klebsiella pneumoniae* | 99.9 | No explanation | WCP |
| 81 | *Streptococcus agalactiae* | 1.8 |  |  | *Enterococcus faecalis* | 99.9 | Polymicrobial urinary specimen | WCP |
| 82 | *Streptococcus anginosus* | 2.0 |  |  | *Aerococcus urinae* | 99.9 | Polymicrobial urinary specimen | WCP |
| 83 | *Streptococcus anginosus* | 2.4 |  |  | *Lactobacillus jensenii* | 99.9 | Polymicrobial urinary specimen | WCP |
| 102 | *Candida albicans* | 2.1 |  |  | *Candida dubliniensis* | 99.9 | Several yeast species identified in the sputum | WCP |
| 106 | *Candida dubliniensis* | 1.7 |  |  | *Candida glabrata* | 100.0 | Several yeast species identified in the sputum | WCP |

Abbreviations: Cont., contamination; MSP, MALDI Biotyper Microflex LT; VMS, VITEKMS; VMSD, very minor species discrepancy; VMS-P, VITEK MS PRIME; WCP, wrong colony picked