Table S6: OTUs hierarchized according to their mean importance for the identification of a production line in the random forest production line model.

| Rank | OTUs | Bacterial Genus | Importance |
|---|---|---|---|
| 1 | Otu00045 | *Moraxella* | 0,00755239 |
| 2 | Otu00065 | *Neisseriaceae*_unclassified | 0,00715058 |
| 3 | Otu00019 | *Macrococcus* | 0,0070928 |
| 4 | Otu00006 | *Rothia(92)* | 0,00682821 |
| 5 | Otu00012 | *Psychrobacter* | 0,00629334 |
| 6 | Otu00022 | *Bacteroides* | 0,00586198 |
| 7 | Otu00033 | *Rhodopseudomonas* | 0,00524286 |
| 8 | Otu00034 | *Pasteurellaceae*_unclassified | 0,00496341 |
| 9 | Otu00002 | *Trueperella* | 0,00472953 |
| 10 | Otu00076 | *Anaerococcus* | 0,00413672 |
| 11 | Otu00122 | *Moraxellaceae*_unclassified | 0,00396747 |
| 12 | Otu00042 | *Chryseobacterium* | 0,00376229 |
| 13 | Otu00020 | *Acinetobacter* | 0,00349835 |
| 14 | Otu00059 | *Clostridium_sensu_stricto* | 0,0033976 |
| 15 | Otu00249 | *Gallicola* | 0,00333676 |
| 16 | Otu00109 | *Porphyromonas* | 0,00321097 |
| 17 | Otu00215 | *Clostridiales*_unclassified | 0,00312908 |
| 18 | Otu00005 | *Peptoniphilus* | 0,00301631 |
| 19 | Otu00014 | *Parvimonas* | 0,00288531 |
| 20 | Otu00242 | *Corynebacterium* | 0,00286469 |
| 21 | Otu00003 | *Pseudomonas* | 0,00281765 |
| 22 | Otu00208 | *Ezakiella* | 0,00269735 |
| 23 | Otu00082 | *Clostridiaceae_1*_unclassified | 0,00267705 |
| 24 | Otu00011 | *Acinetobacter* | 0,00267208 |
| 25 | Otu00120 | *Kurthia* | 0,00265106 |
| 26 | Otu00175 | *Dechloromonas* | 0,00259474 |
| 27 | Otu00008 | *Staphylococcus* | 0,00259435 |
| 28 | Otu00047 | *Psychrobacter* | 0,00256874 |
| 29 | Otu00055 | *Carnobacterium* | 0,00255095 |
| 30 | Otu00018 | *Peptostreptococcus* | 0,0025103 |
| 31 | Otu00232 | *Streptococcus* | 0,00250622 |
| 32 | Otu00281 | *Desulfovibrio* | 0,00239995 |
| 33 | Otu00063 | *Arthrobacter* | 0,00239343 |
| 34 | Otu00105 | *Peptoniphilus* | 0,00236185 |
| 35 | Otu00079 | *Porphyromonas* | 0,00233519 |
| 36 | Otu00141 | *Peptoniphilus* | 0,00232642 |
| 37 | Otu00258 | *Bacteroides* | 0,00225725 |
| 38 | Otu00112 | *Mycoplasma* | 0,00218713 |
| 39 | Otu00453 | *Bacteroidetes*_unclassified | 0,00217711 |

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|---|---|---|---|
| 40 | Otu00196 | *Soonwooa* | 0,00214222 |
| 41 | Otu00054 | *Stenotrophomonas* | 0,00213316 |
| 42 | Otu00010 | *Aerococcaceae*_unclassified | 0,00212038 |
| 43 | Otu00201 | *Flavobacteriaceae*_unclassified | 0,00205318 |
| 44 | Otu00023 | *Pseudomonas* | 0,00203361 |
| 45 | Otu00188 | *Bacteroidales*_unclassified | 0,00203197 |
| 46 | Otu00027 | *Janthinobacterium* | 0,00199127 |
| 47 | Otu00458 | *Mannheimia* | 0,00195721 |
| 48 | Otu00009 | *Bacteroides* | 0,00192371 |
| 49 | Otu00071 | *Enterococcus* | 0,00192169 |
| 50 | Otu00515 | *Lactobacillales*_unclassified | 0,00187147 |
| 51 | Otu00090 | *Atopobium* | 0,00182341 |
| 52 | Otu00016 | *Clostridium_sensu_stricto* | 0,00173585 |
| 53 | Otu00025 | *Chryseobacterium* | 0,00168543 |
| 54 | Otu00062 | *Aeromonas* | 0,00168175 |
| 55 | Otu00080 | *Helcococcus* | 0,0016784 |
| 56 | Otu00166 | *Paludibacter* | 0,00166812 |
| 57 | Otu00409 | *Leucobacter* | 0,00166659 |
| 58 | Otu00056 | *Phenylobacterium* | 0,00165141 |
| 59 | Otu00393 | *Acidaminococcus* | 0,00161787 |
| 60 | Otu00163 | *Finegoldia* | 0,00160598 |
| 61 | Otu00127 | *Exiguobacterium* | 0,00160188 |
| 62 | Otu00152 | *Porphyromonas* | 0,00158718 |
| 63 | Otu00161 | *Bacteroidales*_unclassified | 0,00158152 |
| 64 | Otu00490 | *Coriobacteriaceae*_unclassified | 0,00153199 |
| 65 | Otu00615 | *Desulfovibrio* | 0,00152779 |
| 66 | Otu00461 | *Deinococcus* | 0,00145036 |
| 67 | Otu00240 | *Prevotella* | 0,00143422 |
| 68 | Otu00081 | *Corynebacterium* | 0,00142584 |
| 69 | Otu00285 | *Rhodocyclaceae*_unclassified | 0,00140776 |
| 70 | Otu00140 | *Peptoniphilaceae*_unclassified | 0,00140308 |
| 71 | Otu00373 | *Propionivibrio* | 0,00140222 |
| 72 | Otu00477 | *Sulfurospirillum* | 0,00138963 |
| 73 | Otu00017 | *Bacteroides* | 0,00138454 |
| 74 | Otu00262 | *Lactococcus* | 0,0013752 |
| 75 | Otu00001 | *Fusobacterium* | 0,00135314 |
| 76 | Otu00157 | *Clostridiales_Incertae_Sedis_XI*_unclassified | 0,00134758 |
| 77 | Otu00041 | *Terrisporobacter* | 0,00131979 |
| 78 | Otu00375 | *Bacteroidales*_unclassified | 0,00131511 |
| 79 | Otu00199 | *Bacteroides* | 0,00129308 |
| 80 | Otu00044 | *Bradyrhizobium* | 0,00128157 |
| 81 | Otu00039 | *Yersinia* | 0,00126017 |
| 82 | Otu00028 | *Porphyromonas* | 0,00125809 |

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|---|---|---|---|
| 83 | Otu00251 | *Corynebacterium* | 0,001254 |
| 84 | Otu00052 | *Porphyromonas* | 0,00123527 |
| 85 | Otu00070 | *Sphingomonas* | 0,0012286 |
| 86 | Otu00099 | *Lactobacillus* | 0,00122703 |
| 87 | Otu00013 | *Porphyromonas* | 0,0012258 |
| 88 | Otu00316 | *Flavobacteriaceae*_unclassified | 0,00121006 |
| 89 | Otu00032 | *Porphyromonas* | 0,00120761 |
| 90 | Otu00206 | *Microvirgula* | 0,00118001 |
| 91 | Otu00155 | *Flavobacteriaceae*_unclassified | 0,00116817 |
| 92 | Otu00069 | *Lachnospiraceae*_unclassified | 0,00116382 |
| 93 | Otu00058 | *Turicibacter* | 0,00116148 |
| 94 | Otu00264 | *Bacteroides* | 0,0011565 |
| 95 | Otu00150 | *Ezakiella* | 0,00114923 |
| 96 | Otu00078 | *Polaromonas* | 0,00111556 |
| 97 | Otu00391 | *Vitreoscilla* | 0,00110177 |
| 98 | Otu00102 | *Fusobacterium* | 0,00108047 |
| 99 | Otu00097 | *Eubacterium* | 0,00107498 |
| 100 | Otu00576 | *Petrimonas* | 0,00107408 |
| 101 | Otu00406 | *Actinomycetaceae*_unclassified | 0,00106972 |
| 102 | Otu00172 | *Cloacibacterium* | 0,00104756 |
| 103 | Otu00259 | *Moraxella* | 0,00103668 |
| 104 | Otu00447 | *Bacteria_unclassified* | 0,00103381 |
| 105 | Otu00154 | *Ruminococcaceae*_unclassified | 0,00103342 |
| 106 | Otu00664 | *Synergistaceae*_unclassified | 0,00103071 |
| 107 | Otu00317 | *Catenibacterium* | 0,0010273 |
| 108 | Otu00136 | *Clostridium_sensu_stricto* | 0,00102662 |
| 109 | Otu00237 | *Streptococcus* | 0,00101221 |
| 110 | Otu00606 | *Synergistaceae*_unclassified | 0,00098553 |
| 111 | Otu00298 | *Clostridiales*_unclassified | 0,00097175 |
| 112 | Otu00049 | *Prevotella* | 0,00095805 |
| 113 | Otu00197 | *Campylobacter* | 0,00095794 |
| 114 | Otu00537 | *Brachymonas* | 0,00095132 |
| 115 | Otu00015 | *Aerococcaceae*_unclassified | 0,00095121 |
| 116 | Otu00110 | *Coriobacteriaceae*_unclassified | 0,00095112 |
| 117 | Otu00454 | *Porphyromonas* | 0,00094579 |
| 118 | Otu00106 | *Duganella* | 0,00094553 |
| 119 | Otu00203 | *Clostridium_sensu_stricto* | 0,00093991 |
| 120 | Otu00359 | *Bacteroidetes*_unclassified | 0,00092562 |
| 121 | Otu00035 | *Fusobacterium* | 0,00090469 |
| 122 | Otu00104 | *Helcococcus* | 0,00090286 |
| 123 | Otu00186 | *Peptostreptococcus* | 0,00089187 |
| 124 | Otu00193 | *Porphyromonas* | 0,00088142 |
| 125 | Otu00211 | *Phascolarctobacterium* | 0,00087206 |

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|---|---|---|---|
| 126 | Otu00130 | *Facklamia* | 0,00086857 |
| 127 | Otu00526 | *Lachnospiraceae*_unclassified | 0,00086839 |
| 128 | Otu00089 | *Porphyromonadaceae*_unclassified | 0,0008669 |
| 129 | Otu00075 | *Romboutsia* | 0,00084347 |
| 130 | Otu00480 | *Flavobacterium* | 0,00084301 |
| 131 | Otu00225 | *Fastidiosipila* | 0,00083872 |
| 132 | Otu00510 | *Telmatospirillum* | 0,00081654 |
| 133 | Otu00253 | *Lachnospiraceae*_unclassified | 0,00081054 |
| 134 | Otu00138 | *Flavobacterium* | 0,00081005 |
| 135 | Otu00142 | *Brevibacterium* | 0,00080723 |
| 136 | Otu00207 | *Micrococcaceae*_unclassified | 0,00080632 |
| 137 | Otu00624 | *Synergistaceae*_unclassified | 0,00079537 |
| 138 | Otu00107 | *Clostridiales*_unclassified | 0,00078719 |
| 139 | Otu00093 | *Psychrobacter* | 0,00078295 |
| 140 | Otu00159 | *Prevotella* | 0,0007544 |
| 141 | Otu00085 | *Bacteria*_unclassified | 0,00075285 |
| 142 | Otu00337 | *Morganella* | 0,00074823 |
| 143 | Otu00118 | *Bacteria*_unclassified | 0,00073945 |
| 144 | Otu00518 | *Alphaproteobacteria*_unclassified | 0,00073545 |
| 145 | Otu00260 | *Bacteria*_unclassified | 0,00072761 |
| 146 | Otu00216 | *Anaerococcus* | 0,00070862 |
| 147 | Otu00116 | *Mycobacterium* | 0,00070682 |
| 148 | Otu00202 | *Anaerococcus* | 0,000704 |
| 149 | Otu00482 | *Bacteroidales*_unclassified | 0,00070046 |
| 150 | Otu00115 | *Mycoplasma* | 0,00069574 |
| 151 | Otu00179 | *Pseudomonas* | 0,00068442 |
| 152 | Otu00322 | *Azonexus* | 0,00068263 |
| 153 | Otu00486 | *Flavobacterium* | 0,00068001 |
| 154 | Otu00231 | *Sphingopyxis* | 0,00067664 |
| 155 | Otu00088 | *Streptococcus* | 0,00067636 |
| 156 | Otu00029 | *Streptococcus* | 0,00067517 |
| 157 | Otu00250 | *Clostridiales_Incertae_Sedis_XI*_unclassified | 0,00067288 |
| 158 | Otu00468 | *Pseudomonas* | 0,00066168 |
| 159 | Otu00351 | *Ruminococcaceae*_unclassified | 0,00064984 |
| 160 | Otu00516 | *Macellibacteroides* | 0,00064831 |
| 161 | Otu00046 | *Escherichia/Shigella* | 0,00063966 |
| 162 | Otu00217 | *Propionispira* | 0,00063472 |
| 163 | Otu00347 | *Prevotella* | 0,00062642 |
| 164 | Otu00031 | *Epilithonimonas* | 0,00060814 |
| 165 | Otu00131 | *Clostridiales*_unclassified | 0,00060486 |
| 166 | Otu00703 | *Lachnospiraceae*_unclassified | 0,00059495 |
| 167 | Otu00400 | *Clostridiales*_unclassified | 0,00059451 |
| 168 | Otu00068 | *Actinomyces* | 0,00057723 |

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|---|---|---|---|
| 169 | Otu00363 | *Dysgonomonas* | 0,000569 |
| 170 | Otu00503 | *Proteiniclasticum* | 0,00056821 |
| 171 | Otu00134 | *Gemella* | 0,00056605 |
| 172 | Otu00030 | *Bacteroides* | 0,0005535 |
| 173 | Otu00313 | *Lactobacillus* | 0,0005428 |
| 174 | Otu00026 | *Salmonella* | 0,00053659 |
| 175 | Otu00132 | *Lactococcus* | 0,00051584 |
| 176 | Otu00611 | *Bacteroidales*_unclassified | 0,00050892 |
| 177 | Otu00233 | *Campylobacter* | 0,0005029 |
| 178 | Otu00164 | *Actinomycetaceae*_unclassified | 0,00049325 |
| 179 | Otu00153 | *Ruminococcaceae*_unclassified | 0,00048525 |
| 180 | Otu00603 | *Cellulomonas* | 0,00048046 |
| 181 | Otu00223 | *Porphyromonas* | 0,00043022 |
| 182 | Otu00581 | *Veillonellaceae*_unclassified | 0,00040995 |

Column: 1 – Rank of importance of the OTU in the prediction of a sample belonging to a particular production line; 2- OTU number; 3- Bacterial genus; 4- median of the decrease in accuracy (mean decrease in Gini coefficient) when an OTU is removed from the model among the 100 replications of random forest.