**Supplementary files**

**Supplementary file 1**

**List of used real-time and conventional PCR methods previously developed.**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **PCR technologies** | **Methods** | **Targets** | **Oligonucleotides** | | **References** |
| **Names** | **Sequences** |
| Conventional PCR | KanR | *aadD* gene | aadD-F1 | GAATATTGGATAAATATGGGGATGA | Fraiture et al., 2020 kana |
| aadD-R1 | TATCCGTGTCGTTCTGTCCA |
| aadD-F2 | ATGGCTCTCTTGGTCGTCAG |
| aadD-R2 | CCTGAATCCCATTCCAGAAA |
| Real-time PCR | KanR | *aadD* gene | aadD-F | ATCAGATTGGCCGCTTACAC | Fraiture et al., 2020 kana |
| aadD-P | FAM-CGGTAGAAGCCCAAACGTTCCAC-TAMRA |
| aadD-R | ATAAGGGCACAAATCGCATC |
| Real-time PCR | pUB110 left part | pUB110 shuttle vector | pUB110\_Left-F | GCTCTGACCGTAAACATATTGAGA | Fraiture et al., 2020 dna walking |
| pUB110\_Left-P | FAM- AGATGAATGGACTGCTTATAGCGATAAAGTTAAATCAGA -TAMRA |
| pUB110\_Left-R | TGTGTCGTTTCGCTGGTACT |
| Real-time PCR | pUB110 right part | pUB110 shuttle vector | pUB110\_Right-F | TGAGCGAACACGTGAAAATT | Fraiture et al., 2020 dna walking |
| pUB110\_Right-P | FAM- CAACGAACGTGTCAAAGAAATTATTGAATCAC-TAMRA |
| pUB110\_Right-R | CAGCATCTTTCCTCGTTTTTC |

**Supplementary file 2**

***In silico* specificity assessment.** Amplicon generated by the developed real-time PCR method (Table 1) was blasted against the NCBI database (nr/nt) with default parameter. No hits of 100% in terms of identity and recovery was observed.

|  |  |  |  |
| --- | --- | --- | --- |
| **Description** | **Query Cover** | **Per. ident** | **Accession** |
| **Staphylococcus aureus plasmid pUB110** | **56%** | **98.73** | **M19465.1** |
| Staphylococcus aureus pUB110 low afinity penicillin binding protein (mecA) gene | 56% | 98.73 | AF181950.1 |
| Plasmid pUB110 (from S.aureus) kanamycin nucleotidyl transferase DNA | 56% | 98.73 | M37273.1 |
| Plasmid pUB110 fragment | 56% | 98.73 | K00564.1 |
| **Bacillus amyloliquefaciens alpha-amylase gene** | **48%** | **100.00** | **J01542.1** |
| Bacillus amyloliquefaciens strain RD7-7 | 48% | 98.51 | CP016913.1 |
| Bacillus velezensis strain SCDB 291 chromosome | 48% | 98.51 | CP022654.2 |
| Bacillus amyloliquefaciens strain MT45 | 48% | 98.51 | CP011252.1 |
| Bacillus amyloliquefaciens strain SRCM101267 | 48% | 100.00 | CP021505.1 |
| Bacillus amyloliquefaciens DSM7 complete genome | 48% | 100.00 | FN597644.1 |
| Staphylococcus hominis strain FDAARGOS\_661 plasmid unnamed2 | 56% | 98.73 | CP054551.1 |
| Enterococcus faecalis strain E211 plasmid pE211-2 | 56% | 98.73 | MK784777.1 |
| Staphylococcus warneri strain WB224 plasmid pWB224\_2 | 56% | 98.73 | CP053472.1 |
| Enterococcus faecalis strain E508 plasmid pE508-2 | 56% | 98.73 | MK784778.1 |
| Enterococcus faecium strain E211 plasmid pE211-2 | 56% | 98.73 | MK465704.1 |
| Enterococcus faecium strain E505 plasmid pE505-1 | 56% | 98.73 | MK465703.1 |
| Enterococcus faecalis strain E508 plasmid pE508-2 | 56% | 98.73 | MK465702.1 |
| Dolosigranulum pigrum strain KPL1934\_CDC4709-98 chromosome | 56% | 98.73 | CP040939.1 |
| Staphylococcus haemolyticus strain SCAID URN1-2019 chromosome | 56% | 98.73 | CP052055.1 |
| Enterococcus hirae strain fas4 plasmid pfas4-1 | 56% | 98.73 | MK798157.1 |
| Staphylococcus pseudintermedius strain VTH737 chromosome | 56% | 98.73 | CP039746.1 |
| Staphylococcus caprae strain SY333 plasmid pSY333-45 | 56% | 98.73 | CP051648.1 |
| Streptococcus gallolyticus strain FDAARGOS\_666 chromosome | 56% | 98.73 | CP050959.1 |
| Enterococcus hirae strain CQP3-9 plasmid pCQP3-9\_2 | 56% | 98.73 | CP037957.1 |
| Enterococcus faecalis strain ES-1 plasmid unnamed1 | 56% | 98.73 | CP049776.1 |
| Staphylococcus aureus strain SR153 chromosome | 56% | 98.73 | CP048643.1 |
| Enterococcus faecium strain M16/0594 plasmid pM16/0594 | 56% | 98.73 | MN831411.1 |
| Enterococcus faecium strain ME3 chromosome | 56% | 98.73 | CP043865.1 |
| Enterococcus faecium KUHS13 DNA | 56% | 98.73 | AP022341.1 |
| Staphylococcus aureus strain UP\_1442 chromosome | 56% | 98.73 | CP047802.1 |
| Staphylococcus aureus strain UP\_1106 chromosome | 56% | 98.73 | CP047863.1 |
| Staphylococcus aureus strain UP\_1322 chromosome | 56% | 98.73 | CP047861.1 |
| Staphylococcus aureus strain UP\_844 chromosome | 56% | 98.73 | CP047865.1 |
| Staphylococcus aureus strain UP\_774 chromosome | 56% | 98.73 | CP047804.1 |
| Staphylococcus aureus strain UP\_1435 chromosome | 56% | 98.73 | CP047856.1 |
| Staphylococcus aureus strain P2D1C1 chromosome | 56% | 98.73 | CP033987.1 |
| Staphylococcus aureus strain P2D8C1 chromosome | 56% | 98.73 | CP033982.1 |
| Staphylococcus aureus strain P2D15C1 chromosome | 56% | 98.73 | CP033977.1 |
| Enterococcus faecium strain VRE plasmid p5\_03A17012 | 56% | 98.73 | CP046076.1 |
| Staphylococcus epidermidis strain IRL01 chromosome | 56% | 98.73 | CP045648.1 |
| Enterococcus faecalis strain L15 plasmid pL15 | 56% | 98.73 | CP042214.1 |
| Enterococcus faecium strain LAC7.2 chromosome | 56% | 98.73 | CP045012.1 |
| Staphylococcus aureus strain ER05857.3 chromosome | 56% | 98.73 | CP030683.1 |
| Staphylococcus aureus strain ER02919.3 chromosome | 56% | 98.73 | CP030688.1 |
| Staphylococcus aureus strain ER01422.3 chromosome | 56% | 98.73 | CP030692.1 |
| Staphylococcus aureus strain ER01823.3 chromosome | 56% | 98.73 | CP030626.1 |
| Staphylococcus aureus strain ER03588.3 chromosome | 56% | 98.73 | CP030595.1 |
| Staphylococcus aureus strain ER04181.3 chromosome | 56% | 98.73 | CP030547.1 |
| Staphylococcus aureus strain ER00484.3 chromosome | 56% | 98.73 | CP030604.1 |
| Staphylococcus aureus strain ER01174.3 chromosome | 56% | 98.73 | CP030712.1 |
| Staphylococcus aureus strain ER02612.3 chromosome | 56% | 98.73 | CP030499.1 |
| Staphylococcus aureus strain ER03481.3 chromosome | 56% | 98.73 | CP030552.1 |
| Staphylococcus aureus strain ER01892.3 chromosome | 56% | 98.73 | CP030570.1 |
| Staphylococcus aureus strain ER01935.3 chromosome | 56% | 98.73 | CP030540.1 |
| Staphylococcus aureus strain ER04164.3 chromosome | 56% | 98.73 | CP030542.1 |
| Staphylococcus aureus strain ER01776.3 chromosome | 56% | 98.73 | CP030529.1 |
| Staphylococcus aureus strain ER04225.3 chromosome | 56% | 98.73 | CP030451.1 |
| Staphylococcus aureus strain ER00767.3 chromosome | 56% | 98.73 | CP030474.1 |
| Staphylococcus aureus strain ER04261.3 chromosome | 56% | 98.73 | CP030464.1 |
| Staphylococcus aureus strain ER04385.3 chromosome | 56% | 98.73 | CP030441.1 |
| Staphylococcus aureus strain ER01518.3 chromosome | 56% | 98.73 | CP030496.1 |
| Staphylococcus aureus strain ER00695.3 chromosome | 56% | 98.73 | CP030462.1 |
| Staphylococcus aureus strain ER02836.3 chromosome | 56% | 98.73 | CP030432.1 |
| Staphylococcus aureus strain ER01121.3 chromosome | 56% | 98.73 | CP030471.1 |
| Staphylococcus aureus strain ER02972.3 chromosome | 56% | 98.73 | CP030422.1 |
| Staphylococcus aureus strain ER04142.3 chromosome | 56% | 98.73 | CP030391.1 |
| Staphylococcus aureus strain ER03321.3 chromosome | 56% | 98.73 | CP030702.1 |
| Staphylococcus pseudintermedius strain D20 pRE25-like element genomic sequence | 56% | 98.73 | MK775653.1 |
| Staphylococcus aureus strain GD1706 chromosome | 56% | 98.73 | CP040232.1 |
| Enterococcus faecium strain 27 plasmid pC27-2 | 56% | 98.73 | MH784602.1 |
| Enterococcus faecium strain 25 plasmid pC25-1 | 56% | 98.73 | MH784601.1 |
| Staphylococcus aureus strain 16439 chromosome | 56% | 98.73 | CP043300.1 |
| Enterococcus faecalis S7316 plasmid pS7316optrA DNA | 56% | 98.73 | LC499744.1 |
| Staphylococcus aureus KUN1163 DNA | 56% | 98.73 | AP020324.1 |
| Enterococcus durans strain VREdu plasmid pSULI | 56% | 98.73 | CP043327.1 |
| Enterococcus durans strain VREdu chromosome | 56% | 98.73 | CP042598.1 |
| Staphylococcus aureus strain X22 plasmid unnamed | 56% | 98.73 | CP042651.1 |
| Enterococcus durans strain VREdu chromosome | 56% | 98.73 | CP042597.1 |
| Staphylococcus pseudintermedius strain VB88 chromosome | 56% | 98.73 | CP030715.1 |
| Staphylococcus pseudintermedius strain AH18 chromosome | 56% | 98.73 | CP030374.1 |
| Enterococcus faecium strain HB2-2 plasmid pHB2-2 | 56% | 98.73 | CP038165.1 |
| Enterococcus faecium strain HN11 plasmid pHN11 | 56% | 98.73 | CP038176.1 |
| Enterococcus faecium strain SCBC1 plasmid pSCBC1 | 56% | 98.73 | CP038169.1 |
| Enterococcus faecium strain SDGJP3 plasmid pSDGJP3 | 56% | 98.73 | CP038171.1 |
| Enterococcus faecium strain YN2-1 plasmid pYN2-1 | 56% | 98.73 | CP038173.1 |
| Staphylococcus warneri strain 16A plasmid unnamed2 | 56% | 98.73 | CP031268.1 |
| Enterococcus faecalis EnGen0107 strain B594 plasmid p2 | 56% | 98.73 | CP041740.1 |
| Dolosigranulum pigrum strain 83VPs-KB5 chromosome | 56% | 98.73 | CP041626.1 |
| Staphylococcus aureus JRA307 plasmid: pJRA307-1 DNA | 56% | 98.73 | AP019752.1 |
| Staphylococcus aureus strain FDAARGOS\_766 chromosome | 56% | 98.73 | CP041010.1 |
| Staphylococcus aureus strain GD1696 chromosome | 56% | 98.73 | CP040233.2 |
| Staphylococcus aureus strain D592 chromosome | 56% | 98.73 | CP040665.1 |
| Enterococcus faecium strain HOU503 chromosome | 56% | 98.73 | CP040706.1 |
| Staphylococcus aureus strain D592-HR chromosome | 56% | 98.73 | CP040623.1 |
| Enterococcus faecium strain UAMSEF\_01 chromosome | 56% | 98.73 | CP035648.1 |
| Enterococcus faecium strain UAMSEF\_08 chromosome | 56% | 98.73 | CP035654.1 |
| Enterococcus faecium strain UAMSEF\_09 chromosome | 56% | 98.73 | CP035660.1 |
| Enterococcus faecium strain UAMSEF\_20 chromosome | 56% | 98.73 | CP035666.1 |
| Staphylococcus aureus strain R46 chromosome | 56% | 98.73 | CP039164.1 |
| Staphylococcus haemolyticus strain PK-01 chromosome | 56% | 98.73 | CP035541.1 |
| Enterococcus faecium strain VB3240 chromosome | 56% | 98.73 | CP040368.1 |
| Enterococcus faecalis strain FC plasmid unnamed1 | 56% | 98.73 | CP028836.1 |
| Staphylococcus aureus strain pa3 plasmid pPA3 | 56% | 98.73 | MH785229.1 |
| Streptococcus pasteurianus strain WUSP067 chromosome | 56% | 98.73 | CP039457.1 |
| Staphylococcus aureus subsp. aureus strain WCUH29 chromosome | 56% | 98.73 | CP039156.1 |
| Staphylococcus aureus KG-22 DNA | 56% | 98.73 | AP019545.1 |
| Staphylococcus aureus KG-18 DNA | 56% | 98.73 | AP019543.1 |
| Staphylococcus aureus KG-03 DNA | 56% | 98.73 | AP019542.1 |
| Enterococcus faecium isolate E8481 genome assembly | 56% | 98.73 | LR536672.1 |
| Enterococcus faecium isolate E8407 genome assembly | 56% | 98.73 | LR536658.1 |
| Enterococcus faecium strain 37BA plasmid pEf37BA | 56% | 98.73 | MG957432.1 |
| Enterococcus faecium isolate E1334 genome assembly | 56% | 98.73 | LR134097.1 |
| Staphylococcus epidermidis strain 107.2 plasmid pAQZ1 | 56% | 98.73 | MK046687.1 |
| Staphylococcus warneri strain SWO plasmid unnamed2 | 56% | 98.73 | CP033100.1 |
| Staphylococcus aureus strain WG1647 plasmid pWBG615 | 56% | 98.73 | MH587578.1 |
| Staphylococcus aureus strain NX-T55 chromosome | 56% | 98.73 | CP031839.1 |
| Staphylococcus aureus strain QD-CD9 chromosome | 56% | 98.73 | CP031838.1 |
| Staphylococcus aureus strain CFBR-105 chromosome | 56% | 98.73 | CP031779.1 |
| Staphylococcus aureus strain 592 chromosome | 56% | 98.73 | CP035791.1 |
| Staphylococcus aureus isolate BPH3244 genome assembly | 56% | 98.73 | LR027877.1 |
| Staphylococcus aureus strain JKD6009 genome assembly | 56% | 98.73 | LR027876.1 |
| Staphylococcus aureus strain BPH2019 genome assembly | 56% | 98.73 | LR027870.1 |
| Staphylococcus aureus isolate BPH2869 genome assembly | 56% | 98.73 | LR027869.1 |
| Staphylococcus aureus strain S57 chromosome | 56% | 98.73 | CP030136.1 |
| Staphylococcus aureus SI1 DNA | 56% | 98.73 | LC425379.1 |
| Staphylococcus aureus NN3 DNA | 56% | 98.73 | LC425378.1 |
| Staphylococcus schleiferi strain OT1-1 chromosome | 56% | 98.73 | CP035007.1 |
| Staphylococcus aureus strain USA 100 isolate 30-47 chromosome | 56% | 98.73 | CP029474.1 |
| Enterococcus faecium isolate E8172 genome assembly | 56% | 98.73 | LR135372.1 |
| Enterococcus faecium isolate E7948 genome assembly | 56% | 98.73 | LR135357.1 |
| Enterococcus faecium isolate E7654 genome assembly | 56% | 98.73 | LR135327.1 |
| Enterococcus faecium isolate E7663 genome assembly | 56% | 98.73 | LR135320.1 |
| Enterococcus faecium isolate E7240 genome assembly | 56% | 98.73 | LR135307.1 |
| Enterococcus faecium isolate E7098 genome assembly | 56% | 98.73 | LR135256.1 |
| Enterococcus faecium isolate E7025 genome assembly | 56% | 98.73 | LR135226.1 |
| Enterococcus faecium isolate E7040 genome assembly | 56% | 98.73 | LR135221.1 |
| Enterococcus faecium isolate E7171 genome assembly | 56% | 98.73 | LR135203.1 |
| Enterococcus faecium isolate E6055 genome assembly | 56% | 98.73 | LR135197.1 |
| Enterococcus faecium isolate E4456 genome assembly | 56% | 98.73 | LR135484.1 |
| Enterococcus faecium isolate E8423 genome assembly | 56% | 98.73 | LR135475.1 |
| Enterococcus faecium isolate E8927 genome assembly | 56% | 98.73 | LR135428.1 |
| Enterococcus faecium isolate E1774 genome assembly | 56% | 98.73 | LR135183.1 |
| Enterococcus faecium strain RBWH1 chromosome | 56% | 98.73 | CP033206.1 |
| Staphylococcus aureus strain WCH-SK2 chromosome | 56% | 98.73 | CP031537.1 |
| Staphylococcus aureus strain F17SA003 chromosome | 56% | 98.73 | CP031130.1 |
| Staphylococcus aureus strain E16SA093 chromosome | 56% | 98.73 | CP031131.1 |
| Staphylococcus lentus strain Sle-341Lar plasmid pSle-341Lar | 56% | 98.73 | MH423314.1 |
| Staphylococcus aureus strain NCTC13277 genome assembly | 56% | 98.73 | LS483484.1 |
| Staphylococcus aureus strain AR\_0220 chromosome | 56% | 98.73 | CP029673.1 |
| Staphylococcus aureus strain AR\_0228 chromosome | 56% | 98.73 | CP029663.1 |
| Staphylococcus aureus strain AR\_0228 plasmid unnamed1 | 56% | 98.73 | CP029661.1 |
| Staphylococcus aureus strain AR\_0468 chromosome | 56% | 98.73 | CP029657.1 |
| Staphylococcus aureus strain AR\_0215 chromosome | 56% | 98.73 | CP029680.1 |
| Staphylococcus aureus strain AR\_0469 chromosome | 56% | 98.73 | CP029655.1 |
| Staphylococcus aureus strain AR\_0467 chromosome | 56% | 98.73 | CP029658.1 |
| Staphylococcus aureus strain AR\_0219 chromosome | 56% | 98.73 | CP029675.1 |
| Staphylococcus aureus strain AR\_0470 chromosome | 56% | 98.73 | CP029653.1 |
| Staphylococcus aureus strain AR461 chromosome | 56% | 98.73 | CP029087.1 |
| Staphylococcus aureus strain AR465 chromosome | 56% | 98.73 | CP029082.1 |
| Staphylococcus aureus strain CR14-035 chromosome | 56% | 98.73 | CP020544.1 |
| Staphylococcus aureus strain SA112 chromosome | 56% | 98.73 | CP020553.1 |
| Enterococcus faecium strain 13-022 chromosome | 56% | 98.73 | CP025392.1 |
| Enterococcus faecium strain 13-009 chromosome | 56% | 98.73 | CP025389.1 |
| Staphylococcus aureus strain FDAARGOS\_6 plasmid unnamed1 | 56% | 98.73 | CP026963.1 |
| Staphylococcus aureus strain FDAARGOS\_40 chromosome | 56% | 98.73 | CP026958.1 |
| Staphylococcus aureus strain HPV107 chromosome | 56% | 98.73 | CP026074.1 |
| Staphylococcus aureus strain NRS70 chromosome | 56% | 98.73 | CP026079.1 |
| Staphylococcus aureus strain NRS120 chromosome | 56% | 98.73 | CP026072.1 |
| Staphylococcus aureus strain NRS1 chromosome | 56% | 98.73 | CP026069.1 |
| Enterococcus faecium strain AALTL chromosome | 56% | 98.73 | CP025754.1 |
| Enterococcus faecium strain Efaecium\_ER04526.3A chromosome | 56% | 98.73 | CP023808.1 |
| Enterococcus faecium strain Efaecium\_ER04619.3A isolate isolate chromosome | 56% | 98.73 | CP023804.1 |
| Enterococcus faecium strain Efaecium\_ER04526.5A chromosome | 56% | 98.73 | CP023799.1 |
| Enterococcus faecium strain Efaecium\_ER04484.3A chromosome | 56% | 98.73 | CP023794.1 |
| Enterococcus faecium strain Efaecium\_ER04462.3A chromosome | 56% | 98.73 | CP023789.1 |
| Enterococcus faecium strain Efaecium\_ER04120.3A chromosome | 56% | 98.73 | CP023784.1 |
| Enterococcus faecium strain Efaecium\_ER03933.3A isolate isolate chromosome | 56% | 98.73 | CP023780.1 |
| Enterococcus faecalis strain Transconjugant T4 plasmid pJH-T4 | 56% | 98.73 | KY290886.1 |
| Enterococcus faecalis strain Transconjugant T4 plasmid pLAG | 56% | 98.73 | KY264168.1 |
| Enterococcus faecalis ARO1/DG plasmid pARO1.1 | 56% | 98.73 | CP022484.1 |
| Enterococcus faecium strain E232 chromosome | 56% | 98.73 | CP017787.1 |
| Enterococcus faecium strain E243 chromosome | 56% | 98.73 | CP017797.1 |
| Enterococcus faecium strain E240 chromosome | 56% | 98.73 | CP017792.1 |
| Enterococcus faecium strain 16-346 chromosome | 56% | 98.73 | CP021849.1 |
| Enterococcus faecium strain K60-39 plasmid pTT39\_p3 | 56% | 98.73 | CP023426.1 |
| Staphylococcus arlettae strain SA-01 plasmid pSA-01 | 56% | 98.73 | KX274135.1 |
| Staphylococcus aureus strain FORC\_040 | 56% | 98.73 | CP016398.1 |
| Uncultured bacterium clone fosmid PCA-60D/21 genomic sequence | 56% | 98.73 | KY686304.1 |
| Uncultured bacterium clone fosmid MRS-60D/3 genomic sequence | 56% | 98.73 | KY686302.1 |
| Ureibacillus thermosphaericus DNA | 56% | 98.73 | AP018335.1 |
| Ligilactobacillus salivarius strain ZLS006 plasmid unnamed2 | 56% | 98.73 | CP020860.1 |
| Staphylococcus aureus strain BA01611 plasmid pBA01611 | 56% | 98.73 | KY662247.1 |
| Enterococcus faecalis strain 6742 plasmid p6742\_2 | 56% | 98.73 | KY513281.1 |
| Staphylococcus sciuri strain P723 plasmid pSSC723 | 56% | 98.73 | KY389065.1 |
| Staphylococcus aureus strain SR434 | 56% | 98.73 | CP019563.1 |
| Staphylococcus capitis DNA | 56% | 98.73 | AP014956.1 |
| Streptococcus pasteurianus strain AL101002 plasmid pAL101002 | 56% | 98.73 | KU511280.1 |
| Staphylococcus aureus subsp. aureus strain UCI 28 | 56% | 98.73 | CP018768.1 |
| Enterococcus faecium strain ISMMS\_VRE\_9 | 56% | 98.73 | CP018830.1 |
| Enterococcus faecium strain ISMMS\_VRE\_12 | 56% | 98.73 | CP018828.1 |
| Uncultured bacterium clone Control\_TwinB\_Time1\_TE\_3 genomic sequence | 56% | 98.73 | KX128514.1 |
| Uncultured bacterium clone AmoxDisc\_TwinB\_Time2\_CH\_11 genomic sequence | 56% | 98.73 | KX127030.1 |
| Enterococcus faecium strain VRE001 plasmid unnamed2 | 56% | 98.73 | CP018072.1 |
| Staphylococcus aureus strain ST93 SCCmec-IVn genomic island | 56% | 98.73 | KX385846.1 |
| Enterococcus faecalis strain EF123 plasmid pEF123 | 56% | 98.73 | KX579977.1 |
| Enterococcus faecium strain ISMMS\_VRE\_10 genome | 56% | 98.73 | CP012471.1 |
| Enterococcus faecium strain ISMMS\_VRE\_7 | 56% | 98.73 | CP012460.1 |
| Enterococcus faecium strain ISMMS\_VRE\_5 | 56% | 98.73 | CP012454.1 |
| Enterococcus faecium strain ISMMS\_VRE\_3 genome | 56% | 98.73 | CP012440.1 |
| Enterococcus faecium strain ISMMS\_VRE\_2 | 56% | 98.73 | CP012436.1 |
| Enterococcus faecium strain ISMMS\_VRE\_1 | 56% | 98.73 | CP012430.1 |
| Lactobacillus johnsonii strain BS15 | 56% | 98.73 | CP016400.1 |
| Staphylococcus aureus strain SA7112 plasmid pSA7112-2 sequence | 56% | 98.73 | KX011077.1 |
| Staphylococcus epidermidis isolate BPH0662 genome assembly | 56% | 98.73 | LT571449.1 |
| Staphylococcus aureus strain NCCP14562 | 56% | 98.73 | CP013955.1 |
| Staphylococcus aureus strain NCCP14558 | 56% | 98.73 | CP013953.1 |
| Staphylococcus aureus strain ZJ5499 | 56% | 98.73 | CP011685.1 |
| Enterococcus faecium strain E39 | 56% | 98.73 | CP011281.1 |
| Staphylococcus aureus subsp. aureus RN4220 plasmid pRM27 | 56% | 98.73 | KT780704.1 |
| Enterococcus faecium strain UW8175 plasmid unnamed2 | 56% | 98.73 | CP011830.1 |
| Uncultured bacterium clone TE\_040204\_Contig\_4 genomic sequence | 56% | 98.73 | KU548974.1 |
| Uncultured bacterium clone TE\_11F\_Contig\_21 genomic sequence | 56% | 98.73 | KU547946.1 |
| Uncultured bacterium clone TE\_01J\_010\_Contig\_8 genomic sequence | 56% | 98.73 | KU545620.1 |
| Uncultured bacterium clone TE\_01J\_000\_Contig\_13 genomic sequence | 56% | 98.73 | KU545550.1 |
| Uncultured bacterium clone TE\_01G\_000\_Contig\_1 genomic sequence | 56% | 98.73 | KU545396.1 |
| Uncultured bacterium clone TE\_01C\_014\_Contig\_12 genomic sequence | 56% | 98.73 | KU545105.1 |
| Uncultured bacterium clone TE\_060101\_060102\_Contig\_51 genomic sequence | 56% | 98.73 | KU543789.1 |
| Staphylococcus aureus strain FORC\_012 | 56% | 98.73 | CP010998.1 |
| Uncultured bacterium clone 4-D5\_TE\_Contig\_9 genomic sequence | 56% | 98.73 | KU608064.1 |
| Uncultured bacterium clone 4-B7\_CZ\_Contig\_6 genomic sequence | 56% | 98.73 | KU607794.1 |
| Uncultured bacterium clone 5-B1\_TE\_Contig\_22 genomic sequence | 56% | 98.73 | KU605947.1 |
| Staphylococcus aureus DNA | 56% | 98.73 | LC068960.1 |
| Staphylococcus aureus DNA | 56% | 98.73 | LC068959.1 |
| Staphylococcus aureus DNA | 56% | 98.73 | AP017320.1 |
| Staphylococcus aureus subsp. aureus strain JS395 | 56% | 98.73 | CP012756.1 |
| Enterococcus faecium strain E506 transposon Tn6248 | 56% | 98.73 | KP834592.1 |
| Staphylococcus schleiferi strain 2317-03 | 56% | 98.73 | CP010309.1 |
| Staphylococcus aureus subsp. aureus DNA | 56% | 98.73 | AP014653.1 |
| Staphylococcus aureus subsp. aureus DNA | 56% | 98.73 | AP014652.1 |
| Staphylococcus aureus plasmid pN315G DNA | 56% | 98.73 | AP012550.1 |
| Staphylococcus aureus plasmid pV7037 | 56% | 98.73 | HF586889.1 |
| Staphylococcus aureus subsp. aureus CN1 | 56% | 98.73 | CP003979.1 |
| Staphylococcus aureus CA-347 | 56% | 98.73 | CP006044.1 |
| Staphylococcus aureus subsp. aureus SCCmec staphylococcal cassette region | 56% | 98.73 | HF569114.1 |
| Staphylococcus aureus subsp. aureus SCCmec staphylococcal cassette region | 56% | 98.73 | HF569111.1 |
| Staphylococcus aureus subsp. aureus SCCmec staphylococcal cassette region | 56% | 98.73 | HF569110.1 |
| Staphylococcus aureus subsp. aureus SCCmec staphylococcal cassette region | 56% | 98.73 | HF569106.1 |
| Staphylococcus aureus subsp. aureus SCCmec staphylococcal cassette region | 56% | 98.73 | HF569101.1 |
| Staphylococcus aureus subsp. aureus SCCmec staphylococcal cassette region | 56% | 98.73 | HF569100.1 |
| Staphylococcus aureus subsp. aureus SCCmec staphylococcal cassette region | 56% | 98.73 | HF569095.1 |
| Staphylococcus aureus subsp. aureus SCCmec staphylococcal cassette region | 56% | 98.73 | HF569094.1 |
| Enterococcus faecium DO plasmid 1 | 56% | 98.73 | CP003584.1 |
| Staphylococcus aureus DNA | 56% | 98.73 | AB665981.1 |
| Staphylococcus aureus strain Sa0059 ACME-SCCmec region genomic sequence | 56% | 98.73 | JQ412578.1 |
| Enterococcus faecium strain VB3338 chromosome | 56% | 98.73 | CP062265.1 |
| Enterococcus faecalis strain EGM183 plasmid pEGM183 | 56% | 98.73 | CP050492.1 |
| Staphylococcus aureus strain pt217 chromosome | 56% | 98.73 | CP049510.1 |
| Staphylococcus aureus strain ER06977.3 chromosome | 56% | 98.73 | CP052006.1 |
| Staphylococcus aureus strain ER09001.3 chromosome | 56% | 98.73 | CP051990.1 |
| Staphylococcus aureus strain ER09113.3 chromosome | 56% | 98.73 | CP051989.1 |
| Staphylococcus aureus strain ER09164.3 chromosome | 56% | 98.73 | CP051984.1 |
| Staphylococcus aureus strain ER09245.3 chromosome | 56% | 98.73 | CP051982.1 |
| Staphylococcus aureus strain ER09494.3 chromosome | 56% | 98.73 | CP051972.1 |
| Staphylococcus aureus strain ER09690.3 chromosome | 56% | 98.73 | CP051963.1 |
| Staphylococcus aureus strain ER10617.3 chromosome | 56% | 98.73 | CP051933.1 |
| Staphylococcus aureus strain ER10741.3 chromosome | 56% | 98.73 | CP051921.1 |
| Staphylococcus aureus strain ER10823.3 chromosome | 56% | 98.73 | CP051919.1 |
| Staphylococcus aureus strain ER10920.3 chromosome | 56% | 98.73 | CP051917.1 |
| Staphylococcus aureus strain ER11011.3 chromosome | 56% | 98.73 | CP051915.1 |
| Staphylococcus aureus strain pt172 chromosome | 56% | 98.73 | CP049581.1 |
| Staphylococcus aureus strain pt173 chromosome | 56% | 98.73 | CP049580.1 |
| Staphylococcus aureus strain pt209 chromosome | 56% | 98.73 | CP049526.1 |
| Staphylococcus aureus strain pt226 chromosome | 56% | 98.73 | CP049490.1 |
| Staphylococcus aureus strain pt230 chromosome | 56% | 98.73 | CP049482.1 |
| Staphylococcus aureus strain pt233 chromosome | 56% | 98.73 | CP049478.1 |
| Staphylococcus aureus strain pt235 chromosome | 56% | 98.73 | CP049474.1 |
| Staphylococcus aureus strain pt239 chromosome | 56% | 98.73 | CP049467.1 |
| Staphylococcus aureus strain pt252 chromosome | 56% | 98.73 | CP049441.1 |
| Staphylococcus aureus strain pt255 chromosome | 56% | 98.73 | CP049435.1 |
| Staphylococcus aureus strain pt263 chromosome | 56% | 98.73 | CP049421.1 |
| Staphylococcus aureus strain pt279 chromosome | 56% | 98.73 | CP049400.1 |
| Staphylococcus aureus strain pt280 chromosome | 56% | 98.73 | CP049399.1 |
| Staphylococcus aureus strain pt290 chromosome | 56% | 98.73 | CP049384.1 |
| Staphylococcus aureus strain pt300 chromosome | 56% | 98.73 | CP049371.1 |
| Staphylococcus aureus strain pt301 chromosome | 56% | 98.73 | CP049369.1 |
| Staphylococcus warneri strain WS479 plasmid pWS-31 | 56% | 98.73 | CP061042.1 |
| Staphylococcus pseudintermedius strain Z0118SP0108 chromosome | 56% | 98.73 | CP061030.1 |
| Staphylococcus pseudintermedius strain cdc 18-1182 chromosome | 56% | 98.73 | CP060700.1 |
| Enterococcus faecium strain 15-307-1 plasmid p15-307-1\_03 | 56% | 98.73 | CP044319.1 |
| Enterococcus hirae strain HDC14-2 plasmid pHDC14-2.133K | 56% | 98.73 | CP042290.1 |
| Enterococcus faecium strain BP3378 chromosome | 56% | 98.73 | CP059793.1 |
| Enterococcus faecium strain A11051 plasmid pA11051\_P1 | 56% | 98.73 | CP059765.1 |
| Enterococcus faecium strain A10290 plasmid pA10290\_P1 | 56% | 98.73 | CP059756.1 |
| Staphylococcus aureus strain 07-059 chromosome | 56% | 98.73 | CP045439.1 |
| Staphylococcus aureus strain 08-028 chromosome | 56% | 98.73 | CP045435.1 |
| Staphylococcus hyicus strain 9811071-1 plasmid p9811071-1 | 56% | 98.73 | JF968540.1 |
| Enterococcus faecium plasmid pM7M2 | 56% | 98.73 | JF800907.1 |
| Streptococcus pasteurianus ATCC 43144 DNA | 56% | 98.73 | AP012054.1 |
| Staphylococcus aureus subsp. aureus ECT-R 2 complete genome | 56% | 98.73 | FR714927.1 |
| Staphylococcus aureus 04-02981 | 56% | 98.73 | CP001844.2 |
| Staphylococcus aureus subsp. aureus str. JKD6008 | 56% | 98.73 | CP002120.1 |
| Uncultured bacterium MID12 genomic sequence | 56% | 98.73 | GU951538.1 |
| Staphylococcus aureus subsp. aureus ST398 plasmid pKKS627 | 56% | 98.73 | FN390948.1 |
| Streptococcus gallolyticus UCN34 complete genome | 56% | 98.73 | FN597254.1 |
| Staphylococcus epidermidis plasmid SAP016A | 56% | 98.73 | GQ900381.1 |
| Staphylococcus aureus plasmid SAP014A | 56% | 98.73 | GQ900379.1 |
| Streptococcus suis BM407 complet genome | 56% | 98.73 | FM252032.1 |
| Staphylococcus aureus partial plasmid pKKS2187 | 56% | 98.73 | FM207105.1 |
| Staphylococcus aureus pGO1 plasmid | 56% | 98.73 | FM207042.1 |
| Staphylococcus aureus strain cm11 SCCmec type IVA element | 56% | 98.73 | EU437549.2 |
| Staphylococcus aureus complete SCCmec IV element | 56% | 98.73 | AM943017.1 |
| Staphylococcus aureus subsp. aureus Mu3 DNA | 56% | 98.73 | AP009324.1 |
| Bursa aurealis delivery vector pBursa | 56% | 98.73 | AY672109.3 |
| Staphylococcus aureus plasmid pSK41 | 56% | 98.73 | AF051917.1 |
| Staphylococcus aureus subsp. aureus Mu50 DNA | 56% | 98.73 | BA000017.4 |
| Shuttle expression-secretion vector pP43NMK | 56% | 98.73 | DQ264732.1 |
| Enterococcus faecalis plasmid pAMalpha1 | 56% | 98.73 | AF503772.1 |
| Staphylococcus aureus subsp. aureus N315 DNA | 56% | 98.73 | BA000018.3 |
| Bacillus stearothermophilus plasmid pTB19 tetracycline resistance protein (tetL) | 56% | 98.73 | M63891.1 |
| Bacillus subtilis (plasmid pGR71) K1 delta 1 gene | 56% | 98.73 | X15503.1 |
| Staphylococcus aureus subsp. aureus strain MRSA252 | 56% | 98.73 | BX571856.1 |
| Staphylococcus aureus DNA | 56% | 98.73 | AB037420.1 |
| Staphylococcus aureus DNA | 56% | 98.73 | AB037419.1 |
| Staphylococcus aureus DNA | 56% | 98.73 | D86934.2 |
| Staphylococcus cohnii plasmid pIP1714 streptogramin B lactonase (vgbB) | 56% | 98.73 | AF015628.1 |
| Bacillus cereus plasmid pBC16 | 56% | 98.73 | U32369.1 |
| Bacillus sp. plasmid pTB53 preT gene for plasmid recombination enzyme | 56% | 98.73 | D14852.1 |
| Cloning vector pSCCmec | 55% | 98.72 | KY701739.1 |
| Cloning vector pSCCcat | 55% | 98.72 | KY701738.1 |
| Cloning vector pUCTV2 tet gene | 55% | 98.72 | AJ810977.1 |
| B.polymyxa (ATCC 8523) DNA insert for beta-amylase precursor fragment in a plasmid of B. subtilis | 55% | 98.72 | Y00150.1 |
| Cloning vector pLR16-pheS\* | 55% | 98.72 | KY286114.1 |
| Shuttle vector pMK3 | 55% | 98.72 | EU549779.1 |
| Staphylococcus warneri strain WB224 plasmid pWB224\_2 | 56% | 98.73 | CP053472.1 |
| Cloning vector pME10 | 54% | 98.70 | KT350984.1 |
| Expression vector pME9 | 54% | 98.70 | KC679683.1 |
| Shuttle vector pME8 | 54% | 98.70 | KC679682.1 |
| Expression vector pME10 | 54% | 98.70 | KC679681.1 |
| Artificial cloning vector plasmid BD64 | 56% | 97.50 | X51450.1 |
| Enterococcus faecium isolate E4456 genome assembly | 55% | 97.47 | LR135483.1 |
| Staphylococcus aureus subsp. aureus VC40 | 55% | 97.47 | CP003033.1 |
| Promoter screenings vector pMM225 | 55% | 97.47 | AF076213.1 |
| Promoter screenings vector pMM223 | 55% | 97.47 | AF076212.1 |
| Bacillus amyloliquefaciens strain 205 chromosome | 48% | 100.00 | CP054415.1 |
| Bacillus amyloliquefaciens strain HK1 chromosome | 48% | 100.00 | CP018902.1 |
| B.stearothermophilus maltogenic alpha-amylase (amyM) gene | 50% | 98.59 | M36539.1 |
| Staphylococcus aureus plasmid pAFS11 apramycin resistance gene region | 56% | 94.94 | FN806789.3 |
| Staphylococcus aureus strain RIVM4256 plasmid pRIVM4256 | 56% | 94.94 | CP013629.1 |
| Staphylococcus epidermidis plasmid pSWS47 | 56% | 94.94 | HG380319.1 |
| S.aureus neomycin resistance gene | 56% | 94.94 | M20270.1 |
| Bacillus amyloliquefaciens strain H chromosome | 48% | 98.51 | CP041693.1 |
| Bacillus amyloliquefaciens strain YP6 chromosome | 48% | 98.51 | CP032146.1 |
| Bacillus velezensis strain SCGB 1 chromosome | 48% | 98.51 | CP023320.1 |
| Bacillus subtilis strain ATCC 13952 | 48% | 98.51 | CP009748.1 |
| Bacillus amyloliquefaciens isolate PP19 chromosome | 48% | 98.51 | CP062984.1 |
| Bacillus velezensis strain Y4\_39 chromosome | 48% | 98.51 | CP061704.1 |
| Bacillus amyloliquefaciens XH7 | 48% | 98.51 | CP002927.1 |
| Bacillus amyloliquefaciens LL3 | 48% | 98.51 | CP002634.1 |
| Bacillus amyloliquefaciens TA208 | 48% | 98.51 | CP002627.1 |
| Bacillus velezensis strain SRCM100072 | 48% | 97.01 | CP021888.1 |
| Bacillus velezensis strain JSRB 08 chromosome | 48% | 97.01 | CP059497.1 |
| Bacillus velezensis strain DKU\_NT\_04 chromosome | 46% | 96.88 | CP026533.1 |
| Bacillus siamensis strain SCSIO 05746 chromosome | 43% | 96.67 | CP025001.1 |
| Bacillus sp. SDLI1 | 43% | 96.67 | CP013950.1 |
| Bacillus velezensis strain WLYS23 chromosome | 46% | 92.19 | CP055160.1 |
| Bacillus amyloliquefaciens strain R8-25 chromosome | 48% | 91.04 | CP054479.1 |
| Bacillus velezensis strain B268 chromosome | 46% | 92.19 | CP053764.1 |
| Bacillus velezensis strain A2 chromosome | 48% | 91.04 | CP053717.1 |
| Bacillus velezensis strain EN01 chromosome | 46% | 92.19 | CP053377.1 |
| Bacillus amyloliquefaciens strain WF02 chromosome | 46% | 92.19 | CP053376.1 |
| Bacillus velezensis strain UCMB5140 chromosome | 46% | 92.19 | CP051463.1 |
| Bacillus sp. HNA3 chromosome | 46% | 92.19 | CP040881.1 |
| Bacillus velezensis strain Htq6 chromosome | 46% | 92.19 | CP050462.1 |
| Bacillus velezensis strain S4 chromosome | 46% | 92.19 | CP050424.1 |
| Bacillus velezensis strain BIM B-1312D chromosome | 46% | 92.19 | CP050448.1 |
| Bacillus velezensis strain UB2017 chromosome | 46% | 92.19 | CP049741.1 |
| Bacillus velezensis strain LPL061 chromosome | 46% | 92.19 | CP042271.1 |
| Bacillus sp. LUNF1 chromosome | 46% | 92.19 | CP048876.1 |
| Bacillus velezensis strain CACC 316 chromosome | 46% | 92.19 | CP048002.1 |
| Bacillus velezensis strain SRCM102755 chromosome | 46% | 92.19 | CP028204.1 |
| Bacillus sp. AM1(2019) chromosome | 46% | 92.19 | CP047644.1 |
| Bacillus velezensis strain DH8043 chromosome | 46% | 92.19 | CP047268.1 |
| Bacillus velezensis strain FJAT-45028 chromosome | 46% | 92.19 | CP047157.1 |
| Bacillus velezensis strain BA-26 chromosome | 46% | 92.19 | CP046918.1 |
| Bacillus velezensis strain HN-Q-8 chromosome | 46% | 92.19 | CP045711.1 |
| Bacillus velezensis strain BvL03 chromosome | 46% | 92.19 | CP041192.1 |
| Bacillus velezensis strain AL7 chromosome | 46% | 92.19 | CP045926.1 |
| Bacillus velezensis strain FJAT-52631 chromosome | 46% | 92.19 | CP045186.1 |
| Bacillus amyloliquefaciens strain KC41 chromosome | 46% | 92.19 | CP044444.1 |
| Bacillus velezensis strain LC1 chromosome | 46% | 92.19 | CP044349.1 |
| Bacillus velezensis strain FJAT-46737 chromosome | 46% | 92.19 | CP044133.1 |
| Bacillus amyloliquefaciens strain DH8030 chromosome | 46% | 92.19 | CP041770.1 |
| Bacillus velezensis strain ZeaDK315Endobac16 chromosome | 46% | 92.19 | CP043809.1 |
| Bacillus amyloliquefaciens strain ARP23 chromosome | 48% | 91.04 | CP035899.1 |
| Bacillus velezensis strain ONU 553 chromosome | 46% | 92.19 | CP043416.1 |
| Bacillus amyloliquefaciens strain X030 chromosome | 46% | 92.19 | CP040672.1 |
| Bacillus amyloliquefaciens strain ZJU1 chromosome | 46% | 92.19 | CP041691.1 |
| Bacillus velezensis strain LG37 chromosome | 48% | 91.04 | CP023341.1 |
| Bacillus velezensis strain WRN014 chromosome | 46% | 92.19 | CP041361.1 |
| Bacillus velezensis strain At1 chromosome | 46% | 92.19 | CP041145.1 |
| Bacillus velezensis strain UCMB5007 chromosome | 46% | 92.19 | CP041143.1 |
| Bacillus velezensis strain UCMB5044 chromosome | 46% | 92.19 | CP041144.1 |
| Bacillus velezensis strain P34 chromosome | 46% | 92.19 | CP040378.1 |
| Bacillus velezensis strain LPL-K103 chromosome | 46% | 92.19 | CP039380.1 |
| Bacillus velezensis isolate UFLA258 chromosome | 46% | 92.19 | CP039297.1 |
| Bacillus amyloliquefaciens strain FS1092 chromosome | 48% | 91.04 | CP038028.1 |
| Bacillus velezensis strain LB002 chromosome | 46% | 92.19 | CP037417.1 |
| Bacillus velezensis strain UTB96 chromosome | 46% | 92.19 | CP036527.1 |
| Bacillus velezensis strain ANSB01E chromosome | 48% | 91.04 | CP036518.1 |
| Bacillus velezensis strain BCSo1 chromosome | 46% | 92.19 | CP034037.1 |
| Bacillus velezensis strain 1B-23 chromosome | 48% | 91.04 | CP033967.1 |
| Bacillus velezensis strain NY12-2 chromosome | 46% | 92.19 | CP033576.1 |
| Bacillus velezensis strain Bac57 chromosome | 46% | 92.19 | CP033054.1 |
| Bacillus velezensis strain JT3-1 chromosome | 46% | 92.19 | CP032506.1 |
| Bacillus velezensis strain Hx05 chromosome | 48% | 91.04 | CP029473.2 |
| Bacillus velezensis strain ZF2 chromosome | 46% | 92.19 | CP032154.1 |
| Bacillus velezensis strain BIM B-439D chromosome | 46% | 92.19 | CP032144.1 |
| Bacillus velezensis strain OSY-GA1 chromosome | 46% | 92.19 | CP031880.1 |
| Bacillus velezensis strain K26 chromosome | 46% | 92.19 | CP023075.1 |
| Bacillus velezensis strain 83 chromosome | 46% | 92.19 | CP034203.1 |
| Bacillus velezensis strain B-4 chromosome | 46% | 92.19 | CP031424.1 |
| Bacillus amyloliquefaciens strain SH-B74 chromosome | 46% | 92.19 | CP030097.1 |
| Bacillus velezensis strain DSYZ chromosome | 46% | 92.19 | CP030150.1 |
| Bacillus velezensis strain W1 chromosome | 46% | 92.19 | CP028375.1 |
| Bacillus velezensis strain SGAir0473 chromosome | 46% | 92.19 | CP027868.1 |
| Bacillus amyloliquefaciens strain ALB79 chromosome | 46% | 92.19 | CP029071.1 |
| Bacillus amyloliquefaciens strain ALB69 chromosome | 46% | 92.19 | CP029070.1 |
| Bacillus amyloliquefaciens strain ALB65 chromosome | 46% | 92.19 | CP029069.1 |
| Bacillus velezensis strain KD1 chromosome | 46% | 92.19 | CP014990.2 |
| Bacillus velezensis strain BS-37 chromosome | 48% | 91.04 | CP023414.1 |
| Bacillus velezensis strain LDO2 chromosome | 48% | 91.04 | CP029034.1 |
| Bacillus velezensis strain QST713 chromosome | 46% | 92.19 | CP025079.1 |
| Bacillus velezensis strain GYL4 chromosome | 48% | 91.04 | CP020874.1 |
| Bacillus velezensis strain 8-2 chromosome | 48% | 91.04 | CP028439.1 |
| Bacillus velezensis strain 131-4 chromosome | 46% | 92.19 | CP028441.1 |
| Bacillus velezensis strain J7-1 chromosome | 48% | 91.04 | CP028440.1 |
| Bacillus velezensis strain DR-08 chromosome | 46% | 92.19 | CP028437.1 |
| Bacillus velezensis strain VCC-2003 chromosome | 48% | 91.04 | CP027429.1 |
| Bacillus velezensis strain CGMCC 11640 chromosome | 46% | 92.19 | CP026610.1 |
| Bacillus velezensis strain 10075 chromosome | 48% | 91.04 | CP025939.1 |
| Bacillus velezensis strain GFP-2 chromosome | 46% | 92.19 | CP021011.1 |
| Bacillus velezensis strain CMT-6 chromosome | 46% | 92.19 | CP025341.1 |
| Bacillus velezensis strain Lzh-a42 chromosome | 46% | 92.19 | CP025308.1 |
| Bacillus sp. SJ-10 chromosome | 48% | 91.04 | CP025258.1 |
| Bacillus velezensis strain CN026 chromosome | 46% | 92.19 | CP024897.1 |
| Bacillus velezensis strain AGVL-005 chromosome | 46% | 92.19 | CP024922.1 |
| Bacillus sp. Lzh-5 chromosome | 46% | 92.19 | CP024647.1 |
| Bacillus velezensis strain OSY-S3 chromosome | 46% | 92.19 | CP024706.1 |
| Bacillus velezensis strain ATR2 chromosome | 46% | 92.19 | CP018133.1 |
| Bacillus velezensis strain NKG-1 chromosome | 46% | 92.19 | CP024203.1 |
| Bacillus velezensis S141 DNA | 46% | 92.19 | AP018402.1 |
| Bacillus velezensis strain LABIM40 chromosome | 46% | 92.19 | CP023748.1 |
| Bacillus velezensis strain SCGB 574 chromosome | 46% | 92.19 | CP023431.1 |
| Bacillus velezensis strain J01 chromosome | 46% | 92.19 | CP023133.1 |
| Bacillus velezensis strain NJAU-Z9 | 48% | 91.04 | CP022556.1 |
| Bacillus velezensis strain 157 | 46% | 92.19 | CP022341.1 |
| Bacillus velezensis strain T20E-257 | 46% | 92.19 | CP021976.1 |
| Bacillus velezensis strain GQJK49 | 46% | 92.19 | CP021495.1 |
| Bacillus velezensis strain ZL918 | 46% | 92.19 | CP021338.1 |
| Bacillus velezensis strain CBMB205 chromosome | 48% | 91.04 | CP011937.1 |
| Bacillus vallismortis strain NBIF-001 | 46% | 92.19 | CP020893.1 |
| Bacillus velezensis strain JTYP2 | 46% | 92.19 | CP020375.1 |
| Bacillus velezensis strain sx01604 | 48% | 91.04 | CP018007.1 |
| Bacillus velezensis strain GH1-13 | 46% | 92.19 | CP019040.1 |
| Bacillus sp. 275 | 48% | 91.04 | CP019626.1 |
| Bacillus amyloliquefaciens strain WS-8 | 48% | 91.04 | CP018200.1 |
| Bacillus amyloliquefaciens strain LM2303 | 48% | 91.04 | CP018152.1 |
| Bacillus subtilis strain J-5 | 46% | 92.19 | CP018295.1 |
| Bacillus amyloliquefaciens strain Y14 | 46% | 92.19 | CP017953.1 |
| Bacillus velezensis strain 9912D | 46% | 92.19 | CP017775.1 |
| Bacillus velezensis strain SYBC H47 | 48% | 91.04 | CP017747.1 |
| Bacillus velezensis strain LS69 chromosome | 46% | 92.19 | CP015911.1 |
| Bacillus velezensis strain S3-1 | 46% | 92.19 | CP016371.1 |
| Bacillus velezensis strain CBMB205 | 46% | 92.19 | CP014838.1 |
| Bacillus velezensis strain SB1216 | 46% | 92.19 | CP015417.1 |
| Bacillus velezensis strain CC09 | 48% | 91.04 | CP015443.1 |
| Bacillus amyloliquefaciens strain B15 | 46% | 92.19 | CP014783.1 |
| Bacillus amyloliquefaciens UMAF6614 | 46% | 92.19 | CP006960.1 |
| Bacillus amyloliquefaciens UMAF6639 | 46% | 92.19 | CP006058.1 |
| Bacillus amyloliquefaciens strain MBE1283 | 46% | 92.19 | CP013727.1 |
| Bacillus velezensis strain G341 chromosome | 46% | 92.19 | CP011686.1 |
| Bacillus velezensis strain YJ11-1-4 chromosome | 48% | 91.04 | CP011347.1 |
| Bacillus velezensis strain JJ-D34 chromosome | 46% | 92.19 | CP011346.1 |
| Bacillus velezensis NJN-6 | 46% | 92.19 | CP007165.1 |
| Bacillus amyloliquefaciens strain HM618 chromosome | 46% | 92.19 | CP029466.1 |
| Bacillus velezensis strain BSC16a chromosome | 46% | 92.19 | CP062074.1 |
| Bacillus amyloliquefaciens strain MOH1-5b chromosome | 46% | 92.19 | CP061853.1 |
| Bacillus amyloliquefaciens strain INH2-4b chromosome | 46% | 92.19 | CP061852.1 |
| Bacillus velezensis strain AK-0 chromosome | 46% | 92.19 | CP047119.1 |
| Bacillus velezensis strain ZF145 chromosome | 46% | 92.19 | CP061176.1 |
| Bacillus amyloliquefaciens strain T-5 chromosome | 46% | 92.19 | CP061168.1 |
| Bacillus velezensis strain CLA178 chromosome | 46% | 92.19 | CP061087.1 |
| Bacillus velezensis strain YB-130 chromosome | 46% | 92.19 | CP054562.1 |
| Bacillus velezensis strain HAB-2 chromosome | 48% | 91.04 | CP060085.1 |
| Bacillus velezensis strain Pm9 chromosome | 48% | 91.04 | CP059855.1 |
| Bacillus velezensis strain JSRB 166 chromosome | 46% | 92.19 | CP059495.1 |
| Bacillus velezensis strain MV2 chromosome | 46% | 92.19 | CP059405.1 |
| Bacillus velezensis strain K01 chromosome | 48% | 91.04 | CP059344.1 |
| Bacillus velezensis strain BIOMA BV10 chromosome | 46% | 92.19 | CP059318.1 |
| Bacillus velezensis strain LABIM22 chromosome | 46% | 92.19 | CP045993.1 |

**Supplementary file 3**

**Sequence identity verification of the amplicon generated by the developed real-time PCR method applied on the Dextzyme HT matrix (sample n°1) as well as on other food enzyme products (samples n°2-7).** The generated amplicon was aligned against the reference targeted sequence (Table 1).

|  |
| --- |
| Targeted Sequence GAAAAACGAGGAAAGATGCTGTTCTTGTAAATGAGTTGCTAGTACATCTGACCGAGATTT  Sample n°1 GAAAAACGAGGAAAGATGCTGTTCTTGTAAATGAGTTGCTAGTACATCTGACCGAGATTT  Sample n°2 GAAAAACGAGGAAAGATGCTGTTCTTGTAAATGAGTTGCTAGTACATCTGACCGAGATTT  Sample n°3 GAAAAACGAGGAAAGATGCTGTTCTTGTAAATGAGTTGCTAGTACATCTGACCGAGATTT  Sample n°4 GAAAAACGAGGAAAGATGCTGTTCTTGTAAATGAGTTGCTAGTACATCTGACCGAGATTT  Sample n°5 GAAAAACGAGGAAAGATGCTGTTCTTGTAAATGAGTTGCTAGTACATCTGACCGAGATTT  Sample n°6 GAAAAACGAGGAAAGATGCTGTTCTTGTAAATGAGTTGCTAGTACATCTGACCGAGATTT  Sample n°7 GAAAAACGAGGAAAGATGCTGTTCTTGTAAATGAGTTGCTAGTACATCTGACCGAGATTT  \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*  Targeted Sequence TTTTGAGCAACTGGATCCCACGTTGTGATTAAAAGCAGCGATCCCGATGAACAATCCATA  Sample n°1 TTTTGAGCAACTGGATCCCACGTTGTGATTAAAAGCAGCGATCCCGATGAACAATCCATA  Sample n°2 TTTTGAGCAACTGGATCCCACGTTGTGATTAAAAGCAGCGATCCCGATGAACAATCCATA  Sample n°3 TTTTGAGCAACTGGATCCCACGTTGTGATTAAAAGCAGCGATCCCGATGAACAATCCATA  Sample n°4 TTTTGAGCAACTGGATCCCACGTTGTGATTAAAAGCAGCGATCCCGATGAACAATCCATA  Sample n°5 TTTTGAGCAACTGGATCCCACGTTGTGATTAAAAGCAGCGATCCCGATGAACAATCCATA  Sample n°6 TTTTGAGCAACTGGATCCCACGTTGTGATTAAAAGCAGCGATCCCGATGAACAATCCATA  Sample n°7 TTTTGAGCAACTGGATCCCACGTTGTGATTAAAAGCAGCGATCCCGATGAACAATCCATA  \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*  Targeted Sequence TTGGAAGCAGCTACGATCG  Sample n°1 TTGGAAGCAGCTACGATCG  Sample n°2 TTGGAAGCAGCTACGATCG  Sample n°3 TTGGAAGCAGCTACGATCG  Sample n°4 TTGGAAGCAGCTACGATCG  Sample n°5 TTGGAAGCAGCTACGATCG  Sample n°6 TTGGAAGCAGCTACGATCG  Sample n°7 TTGGAAGCAGCTACGATCG  \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* |

**Supplementary file 4**

**Calculation of LOD95% based on the POD curve for the sensitivity (A) and transferability (B) assessments of the developed real-time PCR method.** To this end, based on Table 3, the “Validation of qualitative PCR methods within a single laboratory” web-tool was used as previously described (Uhlig et al. 2015; Grohmann et al., 2016).

|  |
| --- |
| 1. **Sensitivity assessment** |
|  |
| 1. **Transferability assessment** |
|  |

**Supplementary file 5**

**Evaluation for the presence of the full-length *aadD* gene in commercialized food enzyme products (sample n°1-7).** (A) PCR amplification visualisation. The molecular-weight size marker is going from 25 to 1,500 bp. As positive control (PC), DNA from the GMM *B. subtilis* RASFF2014.1249 strain was used. (B) Generated sequences aligned against the reference *aadD* gene sequence (GenBank: M19465.1).

|  |
| --- |
| A |
|  |
| **B** |
| M19465.1 ACTGATGGGCCCTATTCGGATATTGAGATGATGTGTGTCATGTCAACAGAGGAAGCAGAG  1 ACTGATGGGCCCTATTCGGATATTGAGATGATGTGTGTCATGTCAACAGAGGAAGCAGAG  2 ACTGATGGGCCCTATTCGGATATTGAGATGATGTGTGTCATGTCAACAGAGGAAGCAGAG  3 ACTGATGGGCCCTATTCGGATATTGAGATGATGTGTGTCATGTCAACAGAGGAAGCAGAG  4 ACTGATGGGCCCTATTCGGATATTGAGATGATGTGTGTCATGTCAACAGAGGAAGCAGAG  5 ACTGATGGGCCCTATTCGGATATTGAGATGATGTGTGTCATGTCAACAGAGGAAGCAGAG  6 ACTGATGGGCCCTATTCGGATATTGAGATGATGTGTGTCATGTCAACAGAGGAAGCAGAG  7 ACTGATGGGCCCTATTCGGATATTGAGATGATGTGTGTCATGTCAACAGAGGAAGCAGAG  \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*  M19465.1 TTCAGCCATGAATGGACAACCGGTGAGTGGAAGGTGGAAGTGAATTTTGATAGCGAAGAG  1 TTCAGCCATGAATGGACAACCGGTGAGTGGAAGGTGGAAGTGAATTTTGATAGCGAAGAG  2 TTCAGCCATGAATGGACAACCGGTGAGTGGAAGGTGGAAGTGAATTTTGATAGCGAAGAG  3 TTCAGCCATGAATGGACAACCGGTGAGTGGAAGGTGGAAGTGAATTTTGATAGCGAAGAG  4 TTCAGCCATGAATGGACAACCGGTGAGTGGAAGGTGGAAGTGAATTTTGATAGCGAAGAG  5 TTCAGCCATGAATGGACAACCGGTGAGTGGAAGGTGGAAGTGAATTTTGATAGCGAAGAG  6 TTCAGCCATGAATGGACAACCGGTGAGTGGAAGGTGGAAGTGAATTTTGATAGCGAAGAG  7 TTCAGCCATGAATGGACAACCGGTGAGTGGAAGGTGGAAGTGAATTTTGATAGCGAAGAG  \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*  M19465.1 ATTCTACTAGATTATGCATCTCAGGTGGAATCAGATTGGCCGCTTACACATGGTCAATTT  1 ATTCTACTAGATTATGCATCTCAGGTGGAATCAGATTGGCCGCTTACACATGGTCAATTT  2 ATTCTACTAGATTATGCATCTCAGGTGGAATCAGATTGGCCGCTTACACATGGTCAATTT  3 ATTCTACTAGATTATGCATCTCAGGTGGAATCAGATTGGCCGCTTACACATGGTCAATTT  4 ATTCTACTAGATTATGCATCTCAGGTGGAATCAGATTGGCCGCTTACACATGGTCAATTT  5 ATTCTACTAGATTATGCATCTCAGGTGGAATCAGATTGGCCGCTTACACATGGTCAATTT  6 ATTCTACTAGATTATGCATCTCAGGTGGAATCAGATTGGCCGCTTACACATGGTCAATTT  7 ATTCTACTAGATTATGCATCTCAGGTGGAATCAGATTGGCCGCTTACACATGGTCAATTT  \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*  M19465.1 TTCTCTATTTTGCCGATTTATGATTCAGGTGGATACTTAGAGAAAGTGTATCAAACTGCT  1 TTCTCTATTTTGCCGATTTATGATTCAGGTGGATACTTAGAGAAAGTGTATCAAACTGCT  2 TTCTCTATTTTGCCGATTTATGATTCAGGTGGATACTTAGAGAAAGTGTATCAAACTGCT  3 TTCTCTATTTTGCCGATTTATGATTCAGGTGGATACTTAGAGAAAGTGTATCAAACTGCT  4 TTCTCTATTTTGCCGATTTATGATTCAGGTGGATACTTAGAGAAAGTGTATCAAACTGCT  5 TTCTCTATTTTGCCGATTTATGATTCAGGTGGATACTTAGAGAAAGTGTATCAAACTGCT  6 TTCTCTATTTTGCCGATTTATGATTCAGGTGGATACTTAGAGAAAGTGTATCAAACTGCT  7 TTCTCTATTTTGCCGATTTATGATTCAGGTGGATACTTAGAGAAAGTGTATCAAACTGCT  \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*  M19465.1 AAATCGGTAGAAGCCCAAACGTTCCACGATGCGATTTGTGCCCTTATCGTAGAAGAGCTG  1 AAATCGGTAGAAGCCCAAACGTTCCACGATGCGATTTGTGCCCTTATCGTAGAAGAGCTG  2 AAATCGGTAGAAGCCCAAACGTTCCACGATGCGATTTGTGCCCTTATCGTAGAAGAGCTG  3 AAATCGGTAGAAGCCCAAACGTTCCACGATGCGATTTGTGCCCTTATCGTAGAAGAGCTG  4 AAATCGGTAGAAGCCCAAACGTTCCACGATGCGATTTGTGCCCTTATCGTAGAAGAGCTG  5 AAATCGGTAGAAGCCCAAACGTTCCACGATGCGATTTGTGCCCTTATCGTAGAAGAGCTG  6 AAATCGGTAGAAGCCCAAACGTTCCACGATGCGATTTGTGCCCTTATCGTAGAAGAGCTG  7 AAATCGGTAGAAGCCCAAACGTTCCACGATGCGATTTGTGCCCTTATCGTAGAAGAGCTG  \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*  M19465.1 TTTGAATATGCAGGCAAATGGCGTAATATTCGTGTGCAAGGACCGACAACATTTCTACCA  1 TTTGAATATGCAGGCAAATGGCGTAATATTCGTGTGCAAGGACCGACAACATTTCTACCA  2 TTTGAATATGCAGGCAAATGGCGTAATATTCGTGTGCAAGGACCGACAACATTTCTACCA  3 TTTGAATATGCAGGCAAATGGCGTAATATTCGTGTGCAAGGACCGACAACATTTCTACCA  4 TTTGAATATGCAGGCAAATGGCGTAATATTCGTGTGCAAGGACCGACAACATTTCTACCA  5 TTTGAATATGCAGGCAAATGGCGTAATATTCGTGTGCAAGGACCGACAACATTTCTACCA  6 TTTGAATATGCAGGCAAATGGCGTAATATTCGTGTGCAAGGACCGACAACATTTCTACCA  7 TTTGAATATGCAGGCAAATGGCGTAATATTCGTGTGCAAGGACCGACAACATTTCTACCA  \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*  M19465.1 TCCTTGACTGTACAGGTAGCAATGGCAGGTGCCATGTTGATTGGTCTGCATCATCGCATC  1 TCCTTGACTGTACAGGTAGCAATGGCAGGTGCCATGTTGATTGGTCTGCATCATCGCATC  2 TCCTTGACTGTACAGGTAGCAATGGCAGGTGCCATGTTGATTGGTCTGCATCATCGCATC  3 TCCTTGACTGTACAGGTAGCAATGGCAGGTGCCATGTTGATTGGTCTGCATCATCGCATC  4 TCCTTGACTGTACAGGTAGCAATGGCAGGTGCCATGTTGATTGGTCTGCATCATCGCATC  5 TCCTTGACTGTACAGGTAGCAATGGCAGGTGCCATGTTGATTGGTCTGCATCATCGCATC  6 TCCTTGACTGTACAGGTAGCAATGGCAGGTGCCATGTTGATTGGTCTGCATCATCGCATC  7 TCCTTGACTGTACAGGTAGCAATGGCAGGTGCCATGTTGATTGGTCTGCATCATCGCATC  \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*  M19465.1 TGTTATACGACGAGCGCTTCGGTCTTAACTGAAGCAGTTAAGCAATCAGATCTTCCTTCA  1 TGTTATACGACGAGCGCTTCGGTCTTAACTGAAGCAGTTAAGCAATCAGATCTTCCTTCA  2 TGTTATACGACGAGCGCTTCGGTCTTAACTGAAGCAGTTAAGCAATCAGATCTTCCTTCA  3 TGTTATACGACGAGCGCTTCGGTCTTAACTGAAGCAGTTAAGCAATCAGATCTTCCTTCA  4 TGTTATACGACGAGCGCTTCGGTCTTAACTGAAGCAGTTAAGCAATCAGATCTTCCTTCA  5 TGTTATACGACGAGCGCTTCGGTCTTAACTGAAGCAGTTAAGCAATCAGATCTTCCTTCA  6 TGTTATACGACGAGCGCTTCGGTCTTAACTGAAGCAGTTAAGCAATCAGATCTTCCTTCA  7 TGTTATACGACGAGCGCTTCGGTCTTAACTGAAGCAGTTAAGCAATCAGATCTTCCTTCA  \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*  M19465.1 GGTTATGACCATCTGTGCCAGTTCGTAATGTCTGGTCAACTTTCCGACTCTGAGAAACTT  1 GGTTATGACCATCTGTGCCAGTTCGTAATGTCTGGTCAACTTTCCGACTCTGAGAAACTT  2 GGTTATGACCATCTGTGCCAGTTCGTAATGTCTGGTCAACTTTCCGACTCTGAGAAACTT  3 GGTTATGACCATCTGTGCCAGTTCGTAATGTCTGGTCAACTTTCCGACTCTGAGAAACTT  4 GGTTATGACCATCTGTGCCAGTTCGTAATGTCTGGTCAACTTTCCGACTCTGAGAAACTT  5 GGTTATGACCATCTGTGCCAGTTCGTAATGTCTGGTCAACTTTCCGACTCTGAGAAACTT  6 GGTTATGACCATCTGTGCCAGTTCGTAATGTCTGGTCAACTTTCCGACTCTGAGAAACTT  7 GGTTATGACCATCTGTGCCAGTTCGTAATGTCTGGTCAACTTTCCGACTCTGAGAAACTT  \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*  M19465.1 CTGGAATCGCTAGAGAA  1 CTGGAATCGCTAGAGAA  2 CTGGAATCGCTAGAGAA  3 CTGGAATCGCTAGAGAA  4 CTGGAATCGCTAGAGAA  5 CTGGAATCGCTAGAGAA  6 CTGGAATCGCTAGAGAA  7 CTGGAATCGCTAGAGAA  \*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* |