

Summarized results of predicted amplicon BLAST search against the RefSeq Genomes database (limited to Bacteria, taxid:2).

Summarized alignments of web-based BLAST search with the predicted PCR product of the primer pairs as query. The first line in the alignment represent the forward primer sequence (left) and the reverse-complement sequence of the reverse primer (right). The second line represents the predicted PCR product. Only one sequence per BLAST hit for a certain species is shown if the sequences were identical, the number of these redundant hits is given in the last row of the results table.

Ec faeca_acuI_1_P0

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Ecfaeca_acuI_P0      1 TCATTTCAAGCATTACGTTAAGAGA-----TCAACTGAAAACC
query_acuI_1        1 TCATTTCAAGCATTACGTTAAGAGAACAAGNTACATCTGTTATTGGTCAACTGAAAACC
BLASTHIT_1          1 TCATTTCAAGCATTACGTTAAGAGAACAAGATACATCTGTTATTGGTCAACTGAAAACC
BLASTHIT_2          1 TCATTTCAAGCATTACGTTAAGAGAACAAGATACATCTGTTATTGGTCAACTGAAAACC
BLASTHIT_3          1 TCATTTCAAGCATTACGTTAAGAGAACAAGATACATCTGTTATTGGTCAACTGAAAACC
BLASTHIT_4          1 TCATTTCAAGCATTACGTTAAGAGAACAAGATACATCTGTTATTGGTCAACTGAAAACC
BLASTHIT_5          1 TCATTTCAAGCATTACGTTAAGAGAACAAGATACATCTGTTATTGGTCAACTGAAAACC
BLASTHIT_6          1 TCATTTCAAGCATTACGTTAAGAGAACA-----TCAACTGAAAACC
BLASTHIT_7          1 -----TATTGGTCAAGTTGAGACC
BLASTHIT_8          1 -----GAAGAAGATTCACCTGTTATTGGTCAAGTGAACGCC
BLASTHIT_9          1 -----GAAGAAGATTCACCTGTTATTGGTCAAGTGAACGCC
BLASTHIT_10         1 -----TGGTCAACTGAAAACC
BLASTHIT_11         1 -----TACATCTGTTATTGGTCAACTGAAAACC
BLASTHIT_12         1 -----TGGTCAACTGAAAACC
BLASTHIT_13         1 -----ACAAGGAACATCTGTTATTGGTCAACTGAAAACC
BLASTHIT_14         1 -----AAAAGACAGGTTACTTTGTTATTGGTCAACTGAAAACC
BLASTHIT_15         1 --ATTCCAAGCATTACATTGAGAAGAGAACAAGGTAC
BLASTHIT_16         1 -----TTCTTGAATCAACTGAAAACC
BLASTHIT_17         1 -----CATCTGTTATTGGTCAACTGAAAACC
BLASTHIT_18         1 -----CAAGCATTACGTTAAGAGA-----TCAACTGAAAACC
BLASTHIT_19         1 -----TACGTTAAGAGAACAAGATACA-----TCAACTGAAAACC
BLASTHIT_20         1 -----TACGTTAAGAGAACAAGATACA-----TCAACTGAAAACC
...
N=96

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Ecfaeca_acuI_P0      40 ATTACTTTAGACG
query_acuI_1        61 ATTACTTTAGACG
BLASTHIT_1          61 ATTACTTTAGACG
BLASTHIT_2          61 ATTACTTTAGACG
BLASTHIT_3          61 ATTACTTTAGACG
BLASTHIT_4          61 ATTACTTTAGACG
BLASTHIT_5          61 ATTACTTTAGACG
BLASTHIT_6          1 -----
BLASTHIT_7          20 ATTACTTTAGA--
BLASTHIT_8          37 ATT-----
BLASTHIT_9          37 ATT-----
BLASTHIT_10         17 ATTACTTT-----
BLASTHIT_11         1 -----
BLASTHIT_12         18 ATTACTTTAGA--
BLASTHIT_13         1 -----
BLASTHIT_14         41 -----
BLASTHIT_15         1 -----
BLASTHIT_16         21 ATTACTTTAG-----
BLASTHIT_17         1 -----
BLASTHIT_18         1 -----
BLASTHIT_19         14 ATTACTTTAGAC--
BLASTHIT_20         1 -----
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N=96

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BLAST HIT	Species	Query coverage [%]	Identity [%]	Accession	redundant hits
1	Enterococcus faecalis	100	99	NC_004668.1	690 x
2	Enterococcus sp.	100	99	NZ_JWBQ01000067.1	3 x
3	Enterococcus faecalis	100	99	NZ_JUXC01000095.1	-
4	Enterococcus faecalis	100	97	NZ_PHLF01000001.1	-
5	Enterococcus faecalis	100	97	NZ_KZ845811.1	-
6	Staphylococcus aureus	40	100	NZ_LJOC01000115.1	1 x
7	Anaerorhabdus furcosa	41	90	NZ_FUWY01000002.1	-
8	Oceanihabitans sediminis	53	82	NZ_QPIG01000005.1	1 x
9	Flavobacteriaceae bacterium	53	82	NZ_MPGM01000017.1	-
10	Nitrosotalea sp.	33	96	NZ_FRFC01000001.1	-
11	Collimonas fungivorans	36	92	NZ_CP013232.1	-
12	Nostoc piscinale	38	89	NZ_CP012036.1	-
13	Ewingella americana	34	92	NZ_JMPJ01000065.1	-
14	Neisseriaceae bacterium	55	80	NZ_CP024847.1	-
15	Clostridium kluyveri	46	80	NZ_CP018335.1	-
16	Planktothrix agardhii	41	87	NZ_CM002803.1	-
17	Hungateiclostridium cellulolyticum	27	100	NZ_JH556653.1	-
18	Pseudoalteromonas atlantica	27	100	NC_008228.1	-
19	Bacillus simplex	34	92	NZ_NQLS01000166.1	2 x
20	Olleya namhaensis	30	95	NZ_FORM01000001.1	-

* anomalous sequences excluded from alignment

- gi|1423449487|ref|NZ_UEMU01000447.1|Escherichia coli strain KCRI-77E isolate RDK43_77E
- gi|1005608163|ref|NZ_FFHQ01000001.1|Listeria monocytogenes strain 2842STDY5753961
- gi|522836524|ref|NZ_KE352150.1|Enterococcus faecalis strain SB2C-2 Scaffold11
- gi|1120478950|ref|NZ_FQTZ01000002.1|Enterococcus faecium isolate Hp_76-17_S13_

Ec_faeca_g3060_1_P0

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Ecfaeca_g3060_P 1 CCCTCTTTAACATTAATTGGACTTGC-----AGCCAAGCCTAT
query_g3060_1 1 CCCTCTTTAACATTAATTGGACTTGCNCAGCAATTATTTATTAGTAAAGCCAAGCCTAT
BLASTHIT_1 1 CCCTCTTTAACATTAATTGGACTTGCNCAGCAATTATTTATTAGTAAAGCCAAGCCTAT
BLASTHIT_2 1 CCCTCTTTAACATTAATTGGACTTGCNCAGCAATTATTTATTAGTAAAGCCAAGCCTAT
BLASTHIT_3 1 CCCTCTTTAACATTAATTGGACTTGCNCAGCAATTATTTATTAGTAAAGCCAAGCCTAT
BLASTHIT_4 1 ---TCCTTAAACATTAATTGGACTTGCNCAGCAATTATTTATTAGTAAAGCCAAGCCTAT
BLASTHIT_5 1 -----GCAAGTATTT-TTAGTAAAGCCAAGCCTAT
BLASTHIT_6 1 -----AATTATTTATTAGTAAAGCCAAGCCTAT
BLASTHIT_7 1 -----AGTAAAGCCAAGCCTAT
BLASTHIT_8 1 -----
BLASTHIT_9 1 -----
BLASTHIT_10 1 -----
BLASTHIT_11 1 -----TTGTTTATTAGTAAAGCCAAGCCTAT
BLASTHIT_12 1 -----AGCGATTATTTTATTAGTAAAGCCAAGCCTAT
BLASTHIT_13 1 -----TATTAGTAAAGCCAAGCCTAT
BLASTHIT_14 1 -----TTACTTATTAGTAAAGCCAAGCCTAT
BLASTHIT_15 1 -----ATTAGTAAAGCCAAGCCTAT
BLASTHIT_16 1 -----TTGTTTATTAGTAAAGCCAAGCCTAT
BLASTHIT_17 1 -----AATGATTTATTAGTAAAGCCAAGCCTAT
BLASTHIT_18 1 -----ATTAGTAAAGCCAAGCCTAT
BLASTHIT_19 1 -----GGACTTGCAGCAATTATTTATTAGTAAAGCCAAGCCTAT
BLASTHIT_20 1 -----ATTATTTATTAGTAAAGCCAAGCCTAT
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N=206

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Ecfaeca_g3060_P 39 AAATTAAGAAATCA
query_g3060_1 61 AAATTAAGAAATCA
BLASTHIT_1 61 AAATTAAGAAATCA
BLASTHIT_2 61 AAATTAAGAAATCA
BLASTHIT_3 61 AAATTAAGAAATCA
BLASTHIT_4 58 AAATTAAGAAATCA
BLASTHIT_5 30 AAATTA
BLASTHIT_6 29 AAATTA
BLASTHIT_7 19 AAATTAAGAAATCA
BLASTHIT_8 -----
BLASTHIT_9 -----
BLASTHIT_10 -----
BLASTHIT_11 28 GAATTAAGAAAT
BLASTHIT_12 -----
BLASTHIT_13 23 AAATTAAGAAAT
BLASTHIT_14 28 AAATTA
BLASTHIT_15 22 AAATTA
BLASTHIT_16 28 GAATTAAGAAAT
BLASTHIT_17 -----
BLASTHIT_18 22 -----
BLASTHIT_19 40 AA
BLASTHIT_20 -----
...
N=206

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BLAST HIT	Species	Query coverage [%]	Identity [%]	Accession	redundant hits
1	Enterococcus faecalis	100	99	NC_004668.1	687 x
2	Enterococcus sp.	100	99	NZ_JWBQ01000066.1	2 x
3	Enterococcus faecalis	100	99	NZ_GL454749.1	-
4	Enterococcus faecalis	96	99	NZ_PTYL01000009.1	-
5	Flavobacterium sp.	48	87	NZ_CP031557.1	-
6	Buchnera aphidicola	42	90	NC_004061.1	1 x
7	Acinetobacter johnsonii	43	88	NZ_FUUY01000018.1	-
8	Pasteurella multocida subsp. septica	39	90	NZ_UGSW01000001.1	1 x
9	Pasteurella multocida	39	90	NZ_PSQH01000001.1	4 x
10	Pasteurella multocida	39	90	NZ_CP023972.1	-
11	Enterococcus thailandicus	53	82	NZ_LWMN01000016.1	2 x
12	Algoriphagus halophilus	39	90	NZ_FSRC01000001.1	-
13	Candidatus Borrelia	41	89	NZ_CP025785.1	-
14	Elizabethkingia ursingii	43	89	NZ_MBDS01000002.1	-
15	Clostridiales bacterium	32	96	NZ_JQKL01000001.1	-
16	Enterococcus sp.	53	82	NZ_NGMR01000001.1	-
17	Flavobacterium beibuense	35	92	NZ_JRLV01000001.1	-
18	Aliterella atlantica	28	100	NZ_JYON01000010.1	-
19	Herpetosiphon geysericola	56	79	NZ_LGKP01000017.1	-
20	Corynebacterium kutscheri	28	100	NZ_CP011312.1	-

* anomalous sequences excluded from alignment
 gi|1005608163|ref|NZ_FFHQ01000001.1|Listeria monocytogenes strain 2842STDY5753961
 gi|522836690|ref|NZ_KE352316.1|Enterococcus faecalis strain SB2C-2 Scaffold89
 gi|1120479204|ref|NZ_FQZT01000012.1|Enterococcus faecium isolate Hp_76-17_S13
 gi|1129541613|ref|NZ_CWML01000029.1|Listeria monocytogenes isolate LM52

Ec_faeci_cysS_3_P1

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Ecfaeci_cysS_P1 1 GCAGCCACCAATTTACAACGA-----
query_cysS_3 1 GCAGCCACCAATTTACAACGANTGAAGAATACGTTTGACAATTTGAAATTCGGCCAAGAA
BLASTHIT_1 1 GCAGCCACCAATTTACAACGACTGAAGAATACGTTTGACAATTTGAAATTCGGCCAAGAA
BLASTHIT_2 1 GCAGCCACCAATTTACAACGACTGAAGAATACGTTTGACAATTTGAAATTCGGCCAAGAA
BLASTHIT_3 1 GCAGCCACCAATTTACAACGACTGAAGAATACGTTTGACAATTTGAAATTCGGCCAAGAA
BLASTHIT_4 1 GCAGCCACCAATTTACAACGACTGAAGAATACGTTTGACAATTTGAAATTCGGCCAAGAA
BLASTHIT_5 1 GCAGCCACCAATTTACAACGACTGAAGAATACGTTTGACAATTTGAAATTCGGCCAAGAA
BLASTHIT_6 1 GCAGCCACCAATTTACAACGACTGAAGAATACGTTTGACAATTTGAAATTCGGCCAAGAA
BLASTHIT_7 1 GCAGCCACCAATTTACAACGACTGAAGAATACGTTTGACAATTTGAAATTCGGCCAAGAA
BLASTHIT_8 1 GCAGCCACCAATTTACAACGACTGAAGAATACGTTTGACAATTTGAAATTCGGCCAAGAA
BLASTHIT_9 1 GCAGCCACCAATTTACAACGACTGAAGAATACGTTTGACAATTTGAAATTCGGCCAAGAA
BLASTHIT_10 1 GCAGCCACCAATTTACAACGACTGAAGAATACGTTTGACAATTTGAAATTCGGCCAAGAA
BLASTHIT_11 1 GCAGCCACCAATTTACAACGACTGAAGAATACGTTTGACAATTTGAAATTCGGCCAAGAA
BLASTHIT_12 1 GCAGCCACCAATTTACAACGACTGAAGAATACGTTTGACAATTTGAAATTCGGCCAAGAA
BLASTHIT_13 1 GCAGCCACCAATTTACAACGACTGAAGAATACGTTTGACAATTTGAAATTCGGCCAAGAA
BLASTHIT_14 1 GCAGCCACCAATTTACAACGACTGAAGAATACGTTTGACAATTTGAAATTCGGCCAAGAA
BLASTHIT_15 1 GCAGCCACCAATTTACAACGACTGAAGAATACGTTTGACAATTTGAAATTCGGCCAAGAA
BLASTHIT_16 1 GCAGCCACCAATTTACAACGACTGAAGAATACGTTTGACAATTTGAAATTCGGCCAAGAA
BLASTHIT_17 1 -----CCAATTTCAACGTTTGAAGAATACG-----AAGAA
BLASTHIT_18 1 -----TGAAGAATACGTTTGACAATTTCAAATTC-----A
BLASTHIT_19 1 -----
BLASTHIT_20 1 -----
...
...
N=44

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Ecfaeci_cysS_P1 22 ----CCTCAGAGAATTTGGCAGATGA
query_cysS_3 61 ACTGCCTCAGAGAATTTGGCAGATGA
BLASTHIT_1 61 ACTGCCTCAGAGAATTTGGCAGATGA
BLASTHIT_2 61 ACTGCCTCAGAGAATTTGGCAGATGA
BLASTHIT_3 61 ACTGCCTCAGAGAATTTGGCAGATGA
BLASTHIT_4 61 ACTGCCTCAGAGAATTTGGCAGATGA
BLASTHIT_5 61 ACTGCCTCAGAGAATTTGGCAGATGA
BLASTHIT_6 61 ACTGCCTCAGAGAATTTGGCAGATGA
BLASTHIT_7 61 ACTGCCTCAGAGAATTTGGCAGATGA
BLASTHIT_8 61 ATTGCCTCAGAGAATTTGGCAGATGA
BLASTHIT_9 61 ACTGCCTCAGAGAATTTGGCAGATGA
BLASTHIT_10 -----
BLASTHIT_11 -----
BLASTHIT_12 -----
BLASTHIT_13 -----
BLASTHIT_14 -----
BLASTHIT_15 -----
BLASTHIT_16 -----
BLASTHIT_17 -----
BLASTHIT_18 6 ACTGCCTCAGAGAATTTGGCAGATGA
BLASTHIT_19 2 ACTGCCTCAGAGAATTTGGCAGATGA
...
...
N=44

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BLAST HIT	Species	Query coverage [%]	Identity [%]	Accession	redundant hits
1	Enterococcus faecium	100	98	NC_017960.1	1051 x
2	Enterococcus sp.	100	98	NZ_AJRB03000003.1	37 x
3	Enterococcus faecium	100	98	NZ_PTV01000111.1	-
4	Enterococcus faecium	100	98	NZ_KB029683.1	-
5	Enterococcus sp.	100	97	NZ_KV829502.1	-
6	Enterococcus faecium	100	97	NZ_PUAH01000015.1	-
7	Enterococcus faecium	100	97	NZ_PUBG01000061.1	-
8	Enterococcus faecium	100	97	NZ_PTTS01000223.1	-
9	Enterococcus faecium	100	97	NZ_MJDZ01000007.1	-
10	Enterococcus mundtii	62	83	NZ_PTUS01000014.1	17 x
11	Enterococcus mundtii	62	83	NZ_PYGS01000082.1	-
12	Enterococcus mundtii	62	81	NC_022878.1	-
13	Enterococcus mundtii	62	81	NZ_AFWZ01000346.1	-
14	Enterococcus pernyi	62	81	NZ_KV388085.1	-
15	Enterococcus ratti	62	79	NZ_JXLB01000002.1	-
16	Enterococcus villorum	62	77	NZ_MJEB01000016.1	1 x
17	Bacillus okhensis	30	92	NZ_JRJU01000050.1	-
18	Anaplasma phagocytophilum	28	96	NZ_LANV01000001.1	17 x
19	Chitinophaga terrae	34	89	NZ_FNRL01000002.1	-
20	Amycolatopsis sacchari	24	100	NZ_FORP01000012.1	-

Ec_faeci_purD_2_P0

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Ecfaeci_purD_P0 1 GGAATGAAAGAAGCTAGGACGCT-----ATTGCTACG
query_purD_2 1 GGAATGAAAGAAGCTAGGACGCTCTTTCACGGGTGTTTTATATGCGGGTTTNAATTGCTACG
BLASTHIT_1 1 GGAATGAAAGAAGCTAGGACGCTCTTTCACGGGTGTTTTATATGCGGGTTTNAATTGCTACG
BLASTHIT_2 1 GGAATGAAAGAAGCTAGGACGCTCTTTCACGGGTGTTTTATATGCGGGTTTNAATTGCTACG
BLASTHIT_3 1 GGAATGAAAGAAGCTAGGACGCTCTTTCACGGGTGTTTTATATGCGGGTTTNAATTGCTACG
BLASTHIT_4 1 GGAATGAAAGAAGCTAGGACGCTCTTTCACGGGTGTTTTATATGCGGGTTTNAATTGCTACG
BLASTHIT_5 1 GGAATGAAAGAAGCTAGGACGCTCTTTCACGGGTGTTTTATATGCGGGTTTNAATTGCTACG
BLASTHIT_6 1 -----GGGCGCTCTTTCACGGGTGTTTTATATGCGGGTTTNAATTGCTACG
BLASTHIT_7 1 GGAATGAAAGAACTAGGACGCTCCGTTTACTGGTATTTTATATGCGGGTTTNAATTGCTACG
BLASTHIT_8 1 GGAATGAAAGAACTAGGACGCTCCATTACTGGTATTTTATATGCGGGTTTNAATTGCTACG
BLASTHIT_9 1 GGAATGAAAGAAGCTAGGACGCTCCATTACTGGTATTTTATATGCGGGTTTNAATTGCTACG
BLASTHIT_10 1 -----GGGCGCTCTTTCACGGGTGTTTTATATGCGGGTTTNAATTGCTACG
BLASTHIT_11 1 -----GGGCGCTCTTTCACGGGTGTTTTATATGCGGGTTTNAATTGCTACG
BLASTHIT_12 1 -----GGGCGCTCTTTCACGGGTGTTTTATATGCGGGTTTNAATTGCTACG
BLASTHIT_13 1 GGAATGAAAGAAGCTAGGACGCTCCATTACTGGTATTTTATATGCGGGTTTNAATTGCTACG
BLASTHIT_14 1 GGAATGAAAGAAGCTAGGACGCTCCATTACTGGTATTTTATATGCGGGTTTNAATTGCTACG
BLASTHIT_15 1 -----AGGTGCTTTCGTTTACTGGTATTTTATATGCGGGTTTNAATTGCTACG
BLASTHIT_16 1 GGAATGAAAGAACTAGGACGCTCCGTTTACTGGTATTTTATATGCGGGTTTNAATTGCTACG
BLASTHIT_17 1 -----ATGGAAGAAGAGGCGCATCCTTCACTGGAGTTTTATATGCGGGTTTNAATTGCTACG
BLASTHIT_18 1 GGAATGAAAGAAGCTAGGACGCTCCATTACTGGTATTTTATATGCGGGTTTNAATTGCTACG
BLASTHIT_19 1 GGAATGAAAGAAGCTAGGACGCTCCATTACTGGTATTTTATATGCGGGTTTNAATTGCTACG
BLASTHIT_20 1 -----AATGGAAGAAGAGGCGCTCTTTCACGGGTGTTTTATATGCGGGTTTNAATTGCTACG
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N=67

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Ecfaeci_purD_P0 32 AAGGAAGGACC-
query_purD_2 61 AAGGAAGGACC-
BLASTHIT_1 61 AAGGAAGGACC-
BLASTHIT_2 61 AAGGAAGGACC-
BLASTHIT_3 61 AAGGAAGGACC-
BLASTHIT_4 61 AAGGAAGGACC-
BLASTHIT_5 61 AAGGAAGGACC-
BLASTHIT_6 46 AATTAAGGA-
BLASTHIT_7 61 GCAGGAAGGACC-
BLASTHIT_8 61 GCAGGAAGGACC-
BLASTHIT_9 61 GCAGGAAGGACC-
BLASTHIT_10 46 AATTAAGGA-
BLASTHIT_11 46 AATTAAGGA-
BLASTHIT_12 46 AA-----
BLASTHIT_13 -----
BLASTHIT_14 61 GCAGGAAGGACC-
BLASTHIT_15 47 AA-----
BLASTHIT_16 60 AGTTGAAAGGACC-
BLASTHIT_17 57 GAAAGAAAGGACC-
BLASTHIT_18 -----
BLASTHIT_19 -----
BLASTHIT_20 59 AAGGAAGGACC-
...
N=67

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BLAST HIT	Species	Query coverage [%]	Identity [%]	Accession	redundant hits
1	Enterococcus faecium	100	99	NC_017960.1	1080 x
2	Enterococcus sp.	100	99	NZ_AJRB03000044.1	37 x
3	Enterococcus sp.	100	99	NZ_NGMF01000001.1	-
4	Enterococcus faecium	100	99	NZ_JH804745.1	-
5	Enterococcus faecium	100	97	NZ_JWEB01000121.1	-
6	Bacillus cihuenis	75	87	NZ_AYSD01000010.1	-
7	Enterococcus mundtii	100	79	NZ_PYGS01000033.1	5 x
8	Enterococcus mundtii	100	79	NZ_FOUC01000005.1	-
9	Enterococcus mundtii	100	79	NZ_NGMS01000001.1	-
10	Paenibacillus sp.	76	83	NZ_LMVB01000002.1	-
11	Bacillus sp.	76	83	NZ_LMXG01000002.1	-
12	Bacillus loiseleuriae	66	85	NZ_LFWZ01000001.1	-
13	Enterococcus pernyi	83	80	NZ_KV388085.1	-
14	Enterococcus mundtii	100	76	NZ_PTUS01000023.1	-
15	Enterococcus faecalis	68	83	NZ_KE351686.1	-
16	Enterococcus gallinarum	99	76	NZ_BCQE01000018.1	9 x
17	Ureibacillus thermosphaericus	95	76	NZ_AJIK01000018.1	1 x
18	Enterococcus mundtii	83	78	NZ_AFWZ01000136.1	-
19	Enterococcus mundtii	83	78	NZ_PYGU01000006.1	-
20	Lysinibacillus sp.	97	75	NZ_LT985980.1	-

* anomalous sequences excluded from alignment
 gi|1129541523|ref|NZ_CWML01000013.1|Listeria monocytogenes isolate LM52

Pd_acidi_asnS_2_P0

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Pdacidi_asnS_P0 1  GCCATCCACGAATTCCTCCA-----ACT
query_asnS_2 1  GCCATCCACGAATTCCTCCA-----ACT
BLASTHIT_1 1  GCCATCCACGAATTCCTCCA-----ACT
BLASTHIT_2 1  GCCATCCACGAATTCCTCCA-----ACT
BLASTHIT_3 1  GCCATCCACGAATTCCTCCA-----ACT
BLASTHIT_4 1  -----CAGGAATTCCTCAACACAATGACTTTGTTACGTTAACACCCCAATCATCACA
BLASTHIT_5 1  -----AATTCCTCAACACAATGACTTTGTTACGTTAACACCCCAATCATCACA
BLASTHIT_6 1  -----AATTCCTCAACACAATGACTTTGTTACGTTAACACCCCAATCATCACA
BLASTHIT_7 1  -----AATTCCTCAACACAATGACTTTGTTACGTTAACACCCCAATCATCACA
BLASTHIT_8 1  -----AATTCCTCAACACAATGACTTTGTTACGTTAACACCCCAATCATCACA
BLASTHIT_9 1  -----CAGGAATTCCTCAACACAATGACTTTGTTACGTTAACACCCCAATCATCACA
BLASTHIT_10 1  -----CAGGAATTCCTCAACACAATGACTTTGTTACGTTAACACCCCAATCATCACA
BLASTHIT_11 1  -----CAGGAATTCCTCAACACAATGACTTTGTTACGTTAACACCCCAATCATCACA
BLASTHIT_12 1  -----CAGGAATTCCTCAACACAATGACTTTGTTACGTTAACACCCCAATCATCACA
BLASTHIT_13 1  -----CAGGAATTCCTCAACACAATGACTTTGTTACGTTAACACCCCAATCATCACA
BLASTHIT_14 1  -----CAGGAATTCCTCAACACAATGACTTTGTTACGTTAACACCCCAATCATCACA
BLASTHIT_15 1  -----CAGGAATTCCTCAACACAATGACTTTGTTACGTTAACACCCCAATCATCACA
BLASTHIT_16 1  -----CAGGAATTCCTCAACACAATGACTTTGTTACGTTAACACCCCAATCATCACA
BLASTHIT_17 1  -----CAGGAATTCCTCAACACAATGACTTTGTTACGTTAACACCCCAATCATCACA
BLASTHIT_18 1  -----CAGGAATTCCTCAACACAATGACTTTGTTACGTTAACACCCCAATCATCACA
BLASTHIT_19 1  -----CAGGAATTCCTCAACACAATGACTTTGTTACGTTAACACCCCAATCATCACA
BLASTHIT_20 1  -----CAGGAATTCCTCAACACAATGACTTTGTTACGTTAACACCCCAATCATCACA
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N=128

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Pdacidi_asnS_P0 24 TCTAGTGATACGGAAGGTGC
query_asnS_2 61 TCTAGTGATACGGAAGGTGC
BLASTHIT_1 61 TCTAGTGATACGGAAGGTGC
BLASTHIT_2 61 TCTAGTGATACGGAAGGTGC
BLASTHIT_3 61 TCTAGTGATACGGAAGGTGC
BLASTHIT_4 55 AGTACTGATACGAAGGTGC
BLASTHIT_5 51 AGCAGTGATACGAAGGTGC
BLASTHIT_6 51 AGCAGTGATACGAAGGTGC
BLASTHIT_7 51 AGCAGTGATACGAAGGTGC
BLASTHIT_8 51 AGCAGTGATACGAAGGTGC
BLASTHIT_9 55 AGTACTGATACGAAGGTGC
BLASTHIT_10 55 AGTACTGATACGAAGGTGC
BLASTHIT_11 55 AGTACTGATACGAAGGTGC
BLASTHIT_12 55 AGTACTGATACGAAGGTGC
BLASTHIT_13 61 GGAAGTGATACGAAGGTGC
BLASTHIT_14 61 GGAAGTGATACGAAGGTGC
BLASTHIT_15 61 GGAAGTGATACGAAGGTGC
BLASTHIT_16 55 AGTACTGATACGAAGGTGC
BLASTHIT_17 61 GGAAGTGATACGAAGGTGC
BLASTHIT_18 55 AGTACTGATACGAAGGTGC
BLASTHIT_19 55 AGTACTGATACGAAGGTGC
BLASTHIT_20 55 AGTACTGATACGAAGGTGC
...
...
N=128

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BLAST HIT	Species	Query coverage [%]	Identity [%]	Accession	redundant hits
1	Pediococcus acidilactici	100.0	98.0	NZ_CP015206.1	16 x
2	Pediococcus acidilactici	100.0	98.0	NZ_QYRQ01000020.1	-
3	Pediococcus acidilactici	100.0	98.0	NZ_JQCC01000002.1	-
4	Lactobacillus kunkeei	92.0	78.0	NZ_CP012920.1	11 x
5	Pediococcus pentosaceus	88.0	79.0	NC_008525.1	11 x
6	Pediococcus pentosaceus	88.0	79.0	NZ_JD VW01000006.1	-
7	Pediococcus pentosaceus	88.0	79.0	NZ_JQBF01000008.1	-
8	Pediococcus pentosaceus	88.0	79.0	NC_022780.1	-
9	Lactobacillus kunkeei	92.0	77.0	NZ_JXCZ01000012.1	-
10	Lactobacillus kunkeei	92.0	77.0	NZ_JXDA01000004.1	-
11	Lactobacillus kunkeei	92.0	77.0	NZ_BDDX01000015.1	-
12	Lactobacillus kunkeei	92.0	77.0	NZ_JXDD01000007.1	-
13	Ruminiclostridium cellobioparum subsp. termitidis	100.0	74.0	NZ_AORV01000003.1	-
14	Lactobacillus sp.	100.0	74.0	NZ_CP031933.1	-
15	Leptotrichia sp.	100.0	74.0	NZ_CP016753.1	-
16	Lactobacillus kunkeei	92.0	74.0	NZ_JXDC01000005.1	-
17	Ruminiclostridium cellobioparum	100.0	72.0	NZ_JHYD01000026.1	-
18	Faecalibacterium prausnitzii	74.0	76.0	NZ_QVFB01000007.1	9 x
19	Lactobacillus sp.	92.0	73.0	NZ_CP032626.1	-
20	Faecalibacterium prausnitzii	74.0	76.0	NZ_NMTZ01000018.1	-

Pd_acidi_g1164_1_P0

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Pdacidi_g1164_P 1 TTTAGGAGCAATCATCGCAATC-----GGTAG
query_g1164_1 1 TTTAGGAGCAATCATCGCAATGTTTTCGGCATTATCTGGGTCACGNTGGCTTGGTAG
BLASTHIT_1 1 TTTAGGAGCAATCATCGCAATGTTTTCGGCATTATCTGGGTCACGATTGGCTTGGTAG
BLASTHIT_2 1 -----CAATCATCGCAATGTTTTGGGTTTATCTG-----
BLASTHIT_3 1 TTTAGGAGCAATCATCGCAATCTTTTCGGCATTATCTGGGTCACGATTGGCTTGGTAG
BLASTHIT_4 1 -----GCGAGGATTTCGGCATCATCTGGGGCAC-----
BLASTHIT_5 1 -----CAATCATCGCACGATTATCGGGATTATC-----
BLASTHIT_6 1 -----CAATCATCGCACGATTATCGGGATTATC-----
BLASTHIT_7 1 TTTAGGAGCAATCATCGCAATGAT-----
BLASTHIT_8 1 -----ATCATCGCAATTTTTCTGTATTTCTGGGTCACG-----
BLASTHIT_9 1 -----GCGAGGATTTCGGCATCATCTGGGGCACG-----
BLASTHIT_10 1 TTTAGGAGCAATCATCGCAATGATT-----
BLASTHIT_11 1 TTTAGGAGCAATCATCGCAATGATT-----
BLASTHIT_12 1 TTTAGGAGCAATCATCGCAATGATT-----
BLASTHIT_13 1 TTTAGGAGCAATCATCGCAATGATT-----
BLASTHIT_14 1 TTTAGGAGCAATCATCGCAATGATT-----
BLASTHIT_15 1 -----ATCATCGCACGATTATTTAGTCAATTATCTGGG-----
BLASTHIT_16 1 TTTAGGAGCAATCATCGCAATGATT-----
BLASTHIT_17 1 -----ATCGCAATGTTTTCGGCATT-----
BLASTHIT_18 1 -----GCAATCATCGCAATTTTT-----
BLASTHIT_19 1 -----TTTTCGGCATTATCTGGGTCAC-----
BLASTHIT_20 1 -----CATCGAATGATTTTTCGGCATTATCT-----
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Pdacidi_g1164_P 28 CGCGGTATTAGTTGG
query_g1164_1 61 CGCGGTATTAGTTGG
BLASTHIT_1 61 CGCGGTATTAGTTGG
BLASTHIT_2 -----
BLASTHIT_3 -----
BLASTHIT_4 -----
BLASTHIT_5 -----
BLASTHIT_6 -----
BLASTHIT_7 -----
BLASTHIT_8 -----
BLASTHIT_9 -----
BLASTHIT_10 -----
BLASTHIT_11 -----
BLASTHIT_12 -----
BLASTHIT_13 -----
BLASTHIT_14 -----
BLASTHIT_15 -----
BLASTHIT_16 -----
BLASTHIT_17 -----
BLASTHIT_18 -----
BLASTHIT_19 -----
BLASTHIT_20 -----
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N=207

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BLAST HIT	Species	Query coverage [%]	Identity [%]	Accession	redundant hits
1	<i>Pediococcus acidilactici</i>	100.0	97.0	NZ_CP015206.1	22 x
2	<i>Helicobacter</i> sp.	41.0	90.0	NZ_MLAM01000013.1	-
3	<i>Gallibacterium</i> genomosp.	47.0	86.0	NZ_JTJS01000032.1	-
4	<i>Erwinia iniecta</i>	39.0	90.0	NZ_JRXE01000016.1	1 x
5	<i>Yersinia kristensenii</i>	39.0	90.0	NZ_CWJK01000005.1	4 x
6	<i>Yersinia frederiksenii</i>	39.0	90.0	NZ_CP009364.1	1 x
7	<i>Bacillus vietnamensis</i>	32.0	96.0	NZ_LIXZ01000003.1	-
8	<i>Catelicoccus marimammalium</i>	48.0	83.0	NZ_AMYT01000022.1	-
9	<i>Erwinia persicina</i>	41.0	87.0	NZ_BCTN01000009.1	1 x
10	<i>Megamonas rupellensis</i>	35.0	92.0	NZ_KB899597.1	3 x
11	<i>Acinetobacter kyonggiensis</i>	35.0	92.0	NZ_FNPK01000003.1	-
12	<i>Megamonas</i> sp.	35.0	92.0	NZ_FOCY01000013.1	-
13	<i>Macrocococcus epidermidis</i>	36.0	92.0	NZ_PZJH01000003.1	-
14	<i>Macrocococcus goetzii</i>	36.0	92.0	NZ_MJBI02000002.1	-
15	<i>Sphingobacterium faecium</i>	41.0	87.0	NZ_QBKH01000003.1	-
16	<i>Acinetobacter</i> sp.	35.0	92.0	NZ_NEGM01000001.1	1 x
17	<i>Bacillus</i> sp.	28.0	100.0	NZ_LMTJ01000002.1	9 x
18	<i>Pseudomonas batumici</i>	28.0	100.0	NZ_XJDG01000015.1	-
19	<i>Rhodovulum</i> sp.	28.0	100.0	NZ_QPLK01000071.1	-
20	<i>Roseovarius</i> sp.	35.0	92.0	NZ_OUMZ01000007.1	-

* anomalous sequences excluded from alignment
 gj|522836680|ref|NZ_KE352306.1|Enterococcus faecalis strain SB2C-2 Scaffold825

Pd_pento_nagK_1_P0

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query_nagK_1         1 GGGTGTCACTAACGGAGCAAACNATCGCCCTTGATGATGGTGAAGTTCTGGCTTAGTTTT
BLASTHIT_1           1 GGGTGTCACTAACGGAGCAAACCATCGCCCTTGATGATGGTGAAGTTCTGGCTTAGTTTT
BLASTHIT_2           1 -----GGCGTAAGTTCAGGAATTGTTTT
BLASTHIT_3           1 -----TCTCGCTTAGTTTT
BLASTHIT_4           1 -----AAGTTATGGCTTAGTTTT
BLASTHIT_5           1 -----
BLASTHIT_6           1 -----TTCTTGTTTACTTTTT
BLASTHIT_7           1 -----TTATTTTT
BLASTHIT_8           1 -----TTCTTGTTTACTTTTT
BLASTHIT_9           1 -----ATCTCCCTCGATGATGGTGAAGTTTGGGCTT
BLASTHIT_10          1 -----ATCGCCCTTGATTATGATTTAAGTTATGG--AGTTTT
BLASTHIT_11          1 -----TTCTGGCTTAGTTTT
BLASTHIT_12          1 -----ATCGCCCTTGATTATGATTTAAGTTATGG--AGTTTT
BLASTHIT_13          1 -----CTGGCTTAGTTTT
BLASTHIT_14          1 -----CTGGCTTAGTTTT
BLASTHIT_15          1 -----
BLASTHIT_16          1 -----CTGGTTAGTTAT
BLASTHIT_17          1 -----TGATGATGGTGAATTTCTGGATT-GTCTT
BLASTHIT_18          1 -----TTAGTTTT
BLASTHIT_19          1 -----TTAT
BLASTHIT_20          1 -----TGATGATGTTGTAGTTCCTGGCTTAG
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Fdpento_nagK_P0      21 -----CTTACAAGCGGGCGGAATTG
query_nagK_1         61 AAATCACCAGATTTTTCTGGTCCCACTTACAAGCGGGCGGAATTG
BLASTHIT_1           61 AAATCACCAGATTTTTCTGGTCCCACTTACAAGCGGGCGGAATTG
BLASTHIT_2           24 AAACAACAAAATCTTATCAGGCTCTCACTTACAAGCGGGCGGAATTG
BLASTHIT_3           15 AAATAGCCCGATTTTTTCT
BLASTHIT_4           19 AAATAA--AGATTTTT
BLASTHIT_5           1 -----CAGATTTTTTGGTCCCACTTACAAGCGGGCGGAATTG
BLASTHIT_6           16 AAATCACCAGATTTATT
BLASTHIT_7           9 AAATCATCAGATTTTTCT
BLASTHIT_8           16 AAATCACCAGATTTATT
BLASTHIT_9           -----
BLASTHIT_10          36 AA-----
BLASTHIT_11          16 CAATAACTCCAGATTTTTT
BLASTHIT_12          36 AA-----
BLASTHIT_13          14 AAATCACCAGA-----
BLASTHIT_14          14 AAATCACCAGA-----
BLASTHIT_15          1 -----TTTTTCTGGTCCCACTTACAAGCGGGCGGAATTG
BLASTHIT_16          14 TAACAACAAAATTTTTCTGGTT
BLASTHIT_17          30 AAA-----
BLASTHIT_18          9 ATTAATTACCAGATTTTTCTGACTTCGACTT
BLASTHIT_19          5 AAATCACCAGATTTTTCTGTTGCCA-----
BLASTHIT_20          -----
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N=114

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BLAST HIT	Species	Query coverage [%]	Identity [%]	Accession	redundant hits
1	<i>Pediococcus pentosaceus</i>	100.0	99.0	NC_008525.1	14 x
2	<i>Pediococcus stilesii</i>	65.0	74.0	NZ_JQBX01000011.1	-
3	<i>Zhouia amylolytica</i>	31.0	88.0	NZ_FPAG01000004.1	-
4	<i>Clostridium perfringens</i>	30.0	86.0	NZ_CYYX01000001.1	4 x
5	<i>Flavobacterium haoranii</i>	25.0	93.0	NZ_FQZH01000005.1	-
6	<i>Acinetobacter bereziniae</i>	30.0	88.0	NZ_QWV01000007.1	3 x
7	<i>Mycoplasma auris</i>	25.0	93.0	NZ_QKUB01000015.1	-
8	<i>Acinetobacter</i> sp.	30.0	88.0	NZ_AMFQ01000033.1	4 x
9	<i>Thiomonas intermedia</i>	30.0	88.0	NC_014153.1	-
10	<i>Leptospira meyeri</i>	34.0	80.0	NZ_AKXE01000002.1	1 x
11	<i>Chryseobacterium scophthalmum</i>	30.0	83.0	NZ_FSRQ01000001.1	-
12	<i>Leptospira</i> sp.	34.0	80.0	NZ_NPEB01000007.1	2 x
13	<i>Acinetobacter brisouii</i>	22.0	96.0	NZ_JZRE01000019.1	-
14	<i>Acinetobacter</i> sp.	22.0	96.0	NZ_KB851219.1	-
15	<i>Clostridium pasteurianum</i>	24.0	92.0	NC_021182.1	-
16	<i>Mycoplasma pullorum</i>	34.0	83.0	NZ_CP017813.1	1 x
17	<i>Lutibacter profundus</i>	30.0	87.0	NZ_CP013355.1	-
18	' <i>Nostoc azollae</i> '	35.0	80.0	NC_014248.1	-
19	<i>Elizabethkingia meningoseptica</i>	29.0	87.0	NZ_BARD01000013.1	19 x
20	<i>Sporomusa silvacetica</i>	24.0	92.0	NZ_LSLK01000054.1	-

Pd_pento_g4364_1_P0

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query_g4364_1 1 TGCTTACCACCAACCTGCTTATAACCAAGCTNGTCAAAAGATAACGGTTAAATTTAACGG
BLASTHIT_1 1 TGCTTACCACCAACCTGCTTATAACCAAGCTAGTCAAAAGATAACGGTTAAATTTAACGG
BLASTHIT_2 1 TGCTTACCACCAACCTGCTTATAACCAAGCTGGTCAAAAGATAACGGTTAAATTTAACGG
BLASTHIT_3 1 -----AAAAAGATAACGGTTAAATTTAAC
BLASTHIT_4 1 -----CAGCAACCRGCTCATAACCAAGCT-----
BLASTHIT_5 1 TGCTTGTGACCAACCTGCTTATAACCAAG-----
BLASTHIT_6 1 -----CAACCCTGCTCATAACCAAGCTCGTCA-----
BLASTHIT_7 1 -----GTCTGAAAAGAA--ACGGTTAAATTTAACGG
BLASTHIT_8 1 -----GTTAAATCTAACGG
BLASTHIT_9 1 -----AAGATGGTCAAAAGATAACGGTTAA-----
BLASTHIT_10 1 -----AACGGTTAAATTTAACAG
BLASTHIT_11 1 -----AAAAAGATAACGGTTCAATTTAACGG
BLASTHIT_12 1 TGCTTACCACCAACCTGCTTATCAGCAA-----
BLASTHIT_13 1 -----TAAACGGTTAAATTTAACGG
BLASTHIT_14 1 -----AAAAATAACGGATAAATTTAACGA
BLASTHIT_15 1 -----GTCAAAAGATTACGGTTAAA--TTGACGG
BLASTHIT_16 1 -----ACCAACCTGCTTCTAACCAAGCT-----
BLASTHIT_17 1 -----GGTTAAATTTAACCG
BLASTHIT_18 1 -----CTTAACATCAAGCTATTTAAAGAAAAGCGGTTAAATTTTCATG
BLASTHIT_19 1 -----GTCAAAAGATTACGGTTAAA--TTGACGG
BLASTHIT_20 1 -----TAAACGGTTAAATTTAACGG
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Fdpento_g4364_P 25 AAACCTAGAACGTCCA
query_g4364_1 61 AAACCTAGAACGTCCA
BLASTHIT_1 61 AAACCTAGAACGTCCA
BLASTHIT_2 61 AAACCTAGAACGTCCA
BLASTHIT_3 26 GGAAC
BLASTHIT_4 -----
BLASTHIT_5 -----
BLASTHIT_6 -----
BLASTHIT_7 27 AA-----
BLASTHIT_8 15 AAACCTAGA-----
BLASTHIT_9 -----
BLASTHIT_10 19 AACTACCGAGAACG--
BLASTHIT_11 26 AAA-----
BLASTHIT_12 -----
BLASTHIT_13 20 AAAC-----
BLASTHIT_14 25 AAAGCCAGA-----
BLASTHIT_15 28 AA-----
BLASTHIT_16 -----
BLASTHIT_17 16 AAACCTAG-----
BLASTHIT_18 44 GAAA-----
BLASTHIT_19 28 AA-----
BLASTHIT_20 20 AAAC-----
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N=37

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BLAST HIT	Species	Query coverage [%]	Identity [%]	Accession	redundant hits
1	Pediococcus pentosaceus	100.0	99.0	NC_008525.1	13 x
2	Pediococcus pentosaceus	100.0	99.0	NZ_JDVW01000004.1	-
3	Firmicutes bacterium	39.0	88.0	NZ_QUDS01000002.1	-
4	Pseudovibrio hongkongensis	32.0	96.0	NZ_LLWC01000022.1	-
5	Luteibacter rhizovicinus	38.0	90.0	NZ_JPLB01000036.1	1 x
6	Burkholderia multivorans	34.0	92.0	NZ_PVGD01000058.1	-
7	Streptococcus gallolyticus	37.0	88.0	NZ_FNFJ01000002.1	1 x
8	Unicellular cyanobacterium	30.0	96.0	NZ_NETF01000197.1	-
9	Staphylococcus gallinarum	33.0	92.0	NZ_JXCF01000010.1	1 x
10	Pyrenomonas methylaliphatogenes	40.0	86.0	NZ_CBXV010000006.1	-
11	Maribacter sedimenticola	37.0	89.0	NZ_FZNV01000002.1	-
12	Mannheimia haemolytica	37.0	89.0	NC_021082.1	66 x
13	Hungateiclostridium thermocellum	30.0	96.0	NC_009012.1	6 x
14	Virgibacillus siamensis	43.0	85.0	NZ_FUIH01000007.1	-
15	Streptococcus sanguinis	38.0	89.0	NZ_GL890988.1	-
16	Bacillus sp.	30.0	96.0	NZ_QPJG01000005.1	-
17	Bacillus taeanensis	30.0	96.0	NZ_QOCW01000025.1	-
18	Actinobacillus minor	61.0	78.0	NZ_ACQL01000172.1	-
19	Streptococcus sp.	38.0	89.0	NZ_LSJN01000035.1	-
20	Ruminiclostridium thermocellum	30.0	96.0	NZ_CP016502.1	1 x

*Anomalous sequences excluded from alignment

<p>gi 522836524 ref NZ_KE352150.1 Enterococcus faecalis strain SB2C-2 Scaffold11 gi 522836690 ref NZ_KE352316.1 Enterococcus faecalis strain SB2C-2 Scaffold89 gi 522836680 ref NZ_KE352306.1 Enterococcus faecalis strain SB2C-2 Scaffold825</p> <p>Excluded because we suspected a wrong taxonomic classification.</p> <p>The classification was corrected on 2018-10-26. Enterococcus faecium SB2C-2 before 2018-10-26 (see Taxonomic-Update-Statistics)</p>
<p>gi 1120478950 ref NZ_FQZT01000002.1 Enterococcus faecium isolate Hp_76-17_S13_ gi 1120479204 ref NZ_FQZT01000012.1 Enterococcus faecium isolate Hp_76-17_S13_</p> <p>Excluded because we suspect a wrong taxonomic classification.</p> <p>Taxonomy report of BLAST search (using default values, Nucleotide collection) of this sequence (NZ_FQZT01000002.1) shows best hits for Enterococcus faecalis and no hits for Enterococcus faecium.</p> <p>BLAST search (using default values, Nucleotide collection) of this sequence (NZ_FQZT01000012.1) shows best hits for Enterococcus faecalis and less similarity for Enterococcus faecium genome assemblies.</p>
<p>gi 1423449487 ref NZ_UEMU01000447.1 Escherichia coli strain KCRI-77E isolate RDK43_77E</p> <p>Excluded because we suspect a contamination.</p> <p>Taxonomy report of BLAST search (using default values, Nucleotide collection) of this sequence (NZ_UEMU01000447.1) shows only results for Enterococcus faecalis.</p>
<p>gi 1129541523 ref NZ_CWML01000013.1 Listeria monocytogenes isolate LM52 gi 1129541613 ref NZ_CWML01000029.1 Listeria monocytogenes isolate LM52</p> <p>Excluded because we suspect a wrong taxonomic classification.</p> <p>The corresponding assembly (GCA_001495195.1) shows only 79.251 % gapped identity to the closest related Listeria monocytogenes assembly.</p> <p>BLAST search (using default values, Nucleotide collection) of these sequences (NZ_CWML01000013.1, NZ_CWML01000029.1) shows high similarity with Enterococcus thailandicus and some similarity to other Enterococcus species but no hits for Listeria species.</p>
<p>gi 1005608163 ref NZ_FFHQ01000001.1 Listeria monocytogenes strain 2842STDY5753961</p> <p>Excluded because we suspect a wrong taxonomic classification.</p> <p>The corresponding assembly (GCA_900017475.1) shows only 87.1677 % gapped identity to the closest related Listeria monocytogenes assembly.</p> <p>Taxonomy report of BLAST search (using default values, Nucleotide collection) of the first 100000 bases of this sequence (NZ_FFHQ01000001.1) shows best hits for Enterococcus faecalis and no hits for Listeria species.</p>