

Supplemental Table 1. Microarray probes and primer sequences

gene	gi	source species	forward	length	position	reverse	length	position	product
agrB	2981293	<i>S. epidermidis</i>	CTTAGGGAAAAAGATGGGTAG	21	31	CGTAAAAATAACTTAGATCACATACAG	27	537	507
agrB2Stalugd	5802558	<i>S. lugdunensis</i>	TGCGAATTAAACAGTTAGGC	20	2	TTTTAGTTGCCGATGGTG	18	469	468
agrC	2981293	<i>S. epidermidis</i>	CCTCGCATATCAGTTTGTG	19	776	GATGATATTAATCTATTTCGTTTG	25	1287	512
agrC2Stalugd	5802558	<i>S. lugdunensis</i>	TTTAATGTTGTTATTGTTGCTAAA	25	42	AAATAGAGCATGATCAAAGATAAA	24	491	450
agrCStalugd	18251038	<i>S. lugdunensis</i>	TATCAATCTTTCAAGCAGTTATG	23	26	AAATAAAATATAGCGATGGTAAATG	25	491	466
alphSE1368	27466918	<i>S. epidermidis</i>	ATGAAGCACAAACCACATAC	20	703	GTATTATTTACGGTCTATTTAGCAAG	26	1236	534
ardeSE0106	27466918	<i>S. epidermidis</i>	CCACTTTTCTACTTCTAAACTTC	25	240	TATTTTCAAAGATGCAACACA	22	499	260
ardeSE0107	27466918	<i>S. epidermidis</i>	TTGATAACAAACAAATTCTGC	21	13	AACGTTTAAATCTTATCTTAACTG	24	434	422
aroiSE0105	27466918	<i>S. epidermidis</i>	TAACACTGAACCCCAATGA	19	562	ATCCGGTTTTATGGTATGA	20	883	322
atlE	2267238	<i>S. epidermidis</i>	CCTCAACAAGCAGAAAAAG	20	144	ACTAAATGGGGTGAATTGC	19	876	733
bsaE	21281729	<i>S. aureus</i>	CGGGATTCTCTGCATTATC	19	160	GTCCGCTGGTATTTCTTTG	19	695	536
bsaG	21281729	<i>S. aureus</i>	TTAATTGTTCTACCGCTCCA	20	8	CATTTGTACCCATTATTGTAACC	23	644	637
cap5h	1773339	<i>S. aureus</i>	AAAGATAATTGGTTTGCTGAA	21	18	TCAAATCGCTTCTTAATCACT	21	524	507
cap5i	1773339	<i>S. aureus</i>	CAAGGGTACTTAAACAAATAGAAAC	25	44	CTCGAATTATGAATGAAGGAG	21	682	639
cap5j	1773339	<i>S. aureus</i>	ACTTTGTGCAATTATCAGCA	20	15	ATGAAACAGAAAATATGAAAAATAC	25	394	380
cap5k	1773339	<i>S. aureus</i>	TTATGGATAGCGTAAAGACAATAA	24	20	TTCAGTGGTAATAAAACAACAA	23	519	500
cap8H	21203164	<i>S. aureus</i>	GATTCTTGGCGCTACTAACA	20	12	CCATCGGTACATTACTTTCTC	22	533	522
cap8I	21203164	<i>S. aureus</i>	TAATGTTTCCTTGCCTTATGT	21	44	TGATAACTTCTTCTTTCACCAA	22	698	655
cap8J	21203164	<i>S. aureus</i>	GTA AAAACATTTATGAAATCGAAA	24	7	TGTATGTTCCCCCAATTCTA	20	465	459
cap8K	21203164	<i>S. aureus</i>	AAGATACGATTGTGTGATTGTG	22	177	GGCCATACCATAAATACCC	19	738	562
cataSaur	7161886	<i>S. aureus</i>	TAAATTGTTTAGATTACAATCAGAGG	26	1293	TTCAAAGTTTTCGTATGTTTCA	22	1512	220
cataSaur	7161886	<i>S. aureus</i>	CGTGTGTTGGGTAAATTCC	19	628	ATAATGGTGTGTTCTCCAC	20	1170	543
clfA	397525	<i>S. aureus</i>	AAAAGAAAAACACGCAATTC	20	15	CATTCGTCAACTGATTCGTA	20	715	701
clfB	3393010	<i>S. aureus</i>	TAGCATAGCAACAAACAGTGA	21	465	GTTTTGACCTGAAGCTGTATC	21	1164	700
coa	216976	<i>S. aureus</i>	GCTGGTAAAGCTGAAGAAAC	20	1021	TACTGTGCCATCTTGATTG	20	1554	534
coa	216976	<i>S. aureus</i>	ACAAGAGAAGCAGTAGCAAAC	21	862	TTGTTTCAGTTGCTTGAGG	19	1366	505
coa	216976	<i>S. aureus</i>	AACAAAGCAGATGCGATAGT	20	64	GAAATACGATGCGGTTTATC	20	698	635
coa	216976	<i>S. aureus</i>	CTAGGCGCATTAGCAGTT	18	22	TAGCCTTCTCTTCCATTTC	20	553	532
EDIN	152997	<i>S. aureus</i>	AAAGATAGTTCTAAGATAAATGGTC	25	217	GGCCATTATTGGTCTGTTG	19	442	226
epiP-bsaP	21204850	<i>S. aureus</i>	CTTAGATGTCCCATGCTGAT	20	85	GTCAAACGAGTGCTAATGGT	20	797	713
eta	153005	<i>S. aureus</i>	GCTAGTGCATTTGTTATTCAAG	22	61	TTCATTCTGTGCATTTGG	19	636	576
etb	153011	<i>S. aureus</i>	TTTTAGCAGCGTCAATTTTT	20	29	CTGATCCAGAGTTTCTACCT	21	658	611
fblStalugd	15341502	<i>S. lugdunensis</i>	GAAGTGGAGCGTAATTTGTC	20	121	CTGCTTGACATCATCTGG	19	766	646
folQShaemolyt	1118000	<i>S. haemolyticus</i>	ATGAACATGAGCGACATCA	19	1	ATACGTTCTGCAAGATGTTCTA	22	245	245
gad	23451305	<i>S. epidermidis</i>	CTAAGCACAGAAGAGGCTCA	20	5	TCATCATCTATGAATTTACTACTATCC	27	290	286
gcaD	16024896	<i>S. epidermidis</i>	GCTTAACAACGTAAAACAAGC	21	108	TCTTTCTCTTCAACAATACGC	21	470	363
geh	153019	<i>S. aureus</i>	TTCAATAGGCGTGGTGTC	18	45	TTATCTGTGCGTTTCTCTGG	20	782	738
glucSE1191	27466918	<i>S. epidermidis</i>	ACGACGAATGATTCATAAGG	20	11	TTCTATCAATGCTGGATTCAC	21	391	381

gene	gi	source species	forward	length	position	reverse	length	position	product
gyrA	296393	<i>S. aureus</i>	AGGCTCGTATGATTGAAAAA	20	809	GGTTTTGAGCACGATATGTAG	21	1588	780
gyrB	296393	<i>S. aureus</i>	TTGGCACAACGTGATAAGACA	20	494	AAAAATCGTTCAAAGTGCTC	20	1115	622
hemB	2589180	<i>S. aureus</i>	ATCATCAGCGACAATGAGAG	20	30	TTTTTAACATCTCGAACTATATCTAA	26	785	756
hemC	2589180	<i>S. aureus</i>	GTGCCAATTGCAGGATATG	19	727	TAATGTTGTTTCATTTAAGCGTTTT	24	926	200
hemD	2589180	<i>S. aureus</i>	TTGATAACATTGCTGTGATAGG	22	194	TTCAATTAGTGATTTCGAGTGTT	22	645	452
hemN	14349226	<i>S. aureus</i>	TCTTCCATTCTCTCAGTCAAA	21	215	AGACCATGTATGTAGGTGGC	20	971	757
hglA	550421	<i>S. aureus</i>	AGAAAGAAAGTGATTTCTATGATT	24	19	TGGCCATATCATTCTTTTAAT	21	348	330
hglA	550421	<i>S. aureus</i>	TCGTTACACCGAATGGTC	18	611	AGGTGTGATGCTTTTAATTTTAC	24	960	350
hglB	550421	<i>S. aureus</i>	TTTAAGCGTACTATCACACAGAC	23	753	TATTGTTTTTCAGTTTCTTTTGATC	25	973	221
hglC	550421	<i>S. aureus</i>	TTGATAGCGATTTATTTGTAGG	22	611	CAATTCTGTCCTTTCACTTTG	21	947	337
hla	46763	<i>S. aureus</i>	GTCAGCTCAGTAACAACAACAC	22	16	GTAGCGAAGCTGGTGAAAA	20	767	752
hlb	619316	<i>S. aureus</i>	TGTTATCGACCGTTTTGTATC	21	158	TTTCATCTTTGGGGATATTTT	21	664	507
hld_orf5	2981293	<i>S. epidermidis</i>	AGCTCACGGCTTTAACTATG	20	440	TGTAGAACGTGGAAATGTTG	20	1219	780
hsdS	15922990	<i>S. aureus</i>	AGGGCAAATGCTTTCAGT	18	729	AAAAGGATTGTTTCTCTTTTCT	23	1192	464
hsdS	15922990	<i>S. aureus</i>	GTGCCAGAGTTGAGATTCC	19	25	ATTTGTCGGTTCGAGTTTG	18	557	533
hsp10	535340	<i>S. epidermidis</i>	TTAAACCATTAGGAAATCGTG	21	5	AATAGCTAATATATCTTCTTCATTT	25	276	272
icaA	23345084	<i>S. epidermidis</i>	TCAAGACACGCTTCTAGTG	20	186	ATCGAACCCTTTGTTC	18	799	614
icaB	23345084	<i>S. epidermidis</i>	GTTTTCTTATTACGAACCACATT	23	428	CTGAAGTGTAACCCATATTGA	22	756	329
icaC	23345084	<i>S. epidermidis</i>	GTATTTACGTGCGTTTATTTG	21	27	ATGAATTGATGAAAAGTGTC	20	527	501
icaD	23345084	<i>S. epidermidis</i>	GGTCAAGCCCAGACAGAG	18	3	ATGTCACGACCTTCTTATATTTT	24	302	300
icaR	23345084	<i>S. epidermidis</i>	CATTTAACAGTGAATATACTTGGTC	25	18	GAAATATATCGAAAAAGTGTTGAG	24	423	406
lip	393265	<i>S. aureus</i>	TGCATCTTCCATTTTAATAGC	21	48	GTCATTGTCCTTTGTGGTT	20	768	721
lipShaemolyt	6648931	<i>S. haemolyticus</i>	CCAAGATGCTAATGTGTCTTC	21	243	TTTGACCTGGAGTTAAATGG	20	877	635
lukF	551668	<i>S. aureus</i>	GGTGTCTATCTCGAAAACA	20	751	TTTTTCCTTAGATTGAGTATCTATT	25	963	213
lukS	551668	<i>S. aureus</i>	ATAAAGAAAGGAAATGATTTTATG	24	31	TATCTTTAACAAAATCAAAGTAA	24	250	220
lukS	551668	<i>S. aureus</i>	ATCATTAGGTAAAATGTCTGGA	22	630	AATTATGTCCTTTCACTTTAATTC	25	988	359
menC	1255258	<i>S. aureus</i>	TTGACAGCTTTGCATTTTAA	20	7	GGCTTTGTGTCTTTAATGA	20	422	416
msrw1Stwar	22218025	<i>S. warneri</i>	AAAAGATATGACATAATGTTACGAA	25	272	ATAGTATATGTAGCTGGCGGTTG	23	471	200
murC	2642658	<i>S. aureus</i>	GTATTATTGCTTGGGGTGAT	20	596	GGATATTTCTTTTCGTGCTGT	20	995	400
mvaCShaemolyticus	9937367	<i>S. haemolyticus</i>	TTGAATTGGGAACGACAG	18	80	ACTACTATTTGGGCGAACAC	20	642	563
mvaDShaemolyt	9937371	<i>S. haemolyticus</i>	AATGACGATGAAACTTCCTTT	21	469	ACCCATACGCTTGAATCT	19	699	231
mvaK1Shaemolyticus	9937371	<i>S. haemolyticus</i>	CATCAATTGTGTGATAATGATAAG	24	577	GCTGTTTGCAATTCTTTAGC	20	854	278
mvaSSepid	9937375	<i>S. epidermidis</i>	TTATTCTGCTATATGATATTCACG	24	1	AACATTAGTAGATGGATTCAAGG	23	220	220
mvaSShaemolyticus	9937367	<i>S. haemolyticus</i>	ACGTATATCGTCCTGAATATTTCTAA	27	22	CTACGCTAGTCGAAGGCTAT	20	221	200
NAG	2506026	<i>S. aureus</i>	AAGTTGCTCAAATACAAGCTG	21	760	TGATGTTAGCCCAATCTACA	20	1371	612
nitreSE1972	27466918	<i>S. epidermidis</i>	ACATTAAGTCAGCATTTGGAG	21	150	TAACCTTTAAGACGACTATCCATCA	24	359	210
nitreSE1974	27466918	<i>S. epidermidis</i>	ATTAGAGCCAAAGTACTCTCCAC	23	91	TAACAAACCAACCTTTCGATAC	22	290	200
nitreSE1975	27466918	<i>S. epidermidis</i>	TTTGATACCTGTAATTTGTTCTTG	24	2182	CACCAATTGATCCAATGTTAT	21	2465	284
nuc	46623	<i>S. aureus</i>	TGGCTATCAGTAATGTTTCG	20	74	GAATCAGCGTTGTCTTCG	18	686	613

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nukMStwar	9049353	<i>S. warneri</i>	CATCCAATTTACAGAACCATC	21	45	CGTCATCAGAAGTAGAAGTGAG	22	559	515
oiamtSE1209	27466918	<i>S. epidermidis</i>	AGCTTCTCGCACTACTTGAC	20	121	GAATGAGGCAGCTATCAAAC	20	841	721
ORF1Sepid	2267238	<i>S. epidermidis</i>	AAAGAAATTAAGTCTCTAGCCAAA	24	401	TTATTGTGCGTAAGGATAATTG	22	865	465
ORF3bSepid	2267238	<i>S. epidermidis</i>	AACCAACGATGCTAGATGA	20	19	AAGAATACTTTACCAAAAGGTGAG	24	380	362
pdhD	48871	<i>S. aureus</i>	ATGGTCAAGCTGCTGAAGT	19	1010	ATCATCTTCTTTAAGTGAATAAGTTT	27	1221	212
proDStwar	22218025	<i>S. warneri</i>	TGTATCAACTCCACTTTATTCATATT	26	2	TTTTTCGTATCTTATGGGTCTT	22	321	320
proMStwar	22218025	<i>S. warneri</i>	AGCAAGTTCTTTGTTAATTGC	21	21	TTCGTTTGATTGAACCTGAAC	21	291	271
psm_beta1and2	3212078	<i>S. epidermidis</i>	ATGTCAAAATTAGCAGAAGCTAT	23	1	TTAGAAACCGAAGATTTTACCT	22	325	325
purR	16024896	<i>S. epidermidis</i>	TGACACAATACCTCATGAACC	21	35	TCCTTTCTTATAACCACTACAGG	23	485	451
qacR	22476845	<i>S. epidermidis</i>	AGTTTTATAATATTCAGTGCAAAA	24	241	TGAAAGATAAAATACTAGGTGTCG	24	560	320
RNApolsigm	32396031	<i>S. haemolyticus</i>	AATCGTCCACTTGTCTTTTG	20	162	AATTTCACTAGGCGTATAATCAG	23	726	565
RNApolsigmSsapro	32396039	<i>S. saprophyticus</i>	AAGAGAACCAAAACCAATCG	19	49	TTCTTTCGGCTTAAAGTCAT	20	480	432
RNApolsigmSsapro	32396039	<i>S. saprophyticus</i>	GAAATAACCGCATTCCAAC	19	8	GATTTGTATATTTAGTGTTTCAGCA	25	507	500
rpoB	677848	<i>S. aureus</i>	TGGAAGACATCGTAAACGTA	20	24	TGGATCAAAGAAACGTGAAT	20	786	763
sak	47425	<i>S. aureus</i>	TGTTATTATTCTCATTTTCTTCAAT	25	38	ATGCTCTGATAAATCTGGGA	20	438	401
SAV0431	15922990	<i>S. aureus</i>	GGCAGTTGTACTCCCACA	18	1050	CTTTCACACCCCCAAGTTC	19	1549	500
SAV0439	15922990	<i>S. aureus</i>	TGAATAGAAATACTAGGACCACAA	24	2	TTAAGTTTAATCCATCTGAAAAAT	24	469	468
SAV0440	15922990	<i>S. aureus</i>	GGTGTATTAGATAATGAAGGTATGG	25	265	TCTTTATTTTTGGCAGGTTG	20	776	512
SAV0441	15922990	<i>S. aureus</i>	AACCAAAAGGCGAGAGTT	18	254	GCTGTCAACATAATAAATGCTTC	23	755	502
sea	153120	<i>S. aureus</i>	TTTTATTTCATTGCCCTAACG	20	26	TTTTCAGAGTTAATCGTTTTATTATC	26	740	715
seb	152999	<i>S. aureus</i>	CGTAGATGTGTTTGGAGCTA	20	324	CTTGAGCAGTCACCTTTTTTC	20	556	233
sec1	46566	<i>S. aureus</i>	AATTTTTGGCACATGATTTA	20	209	CTTTTATGTCTAGTTCTTGAGCTG	24	568	360
seg	19352023	<i>S. aureus</i>	CCACCTGTTGAAGGAAGAG	19	94	TTTAGGAAATAAGTCAAACCAAA	23	594	501
seh	19352025	<i>S. aureus</i>	GAAGATTACACGATAAAAGTGAG	24	1	AAATCATAAATGTCGAATGAGTAA	24	542	542
sel	14349227	<i>S. aureus</i>	AGTCTTATCTAACGGCGATG	20	63	AGTTGTAAGTGTGATGCTTG	22	405	343
set15	15922990	<i>S. aureus</i>	GGATATAAATACGGAATAAAAGTTACA	27	175	GAAGTCACAGAAGTAGTGTTG	23	446	272
set6	15922990	<i>S. aureus</i>	ATGAAATTTAAAGCGATAGCA	21	1	GTATAAACTACTTTGTGGTTCTTCTTT	27	450	450
set7	15922990	<i>S. aureus</i>	GTATTGAATATAAAATGTGACAGG	25	155	GACATTGATAACATCGGACA	20	654	500
set8	15922990	<i>S. aureus</i>	GCGCAATTACAGTAACGAC	19	56	TAGATTGCATTGGTTGTGG	19	439	384
sigB	1729791	<i>S. aureus</i>	GCGAAAGAGTCGAAATCAG	19	4	AAGGTGAACGCTCTAATTCA	20	403	400
sigrhoStwar	32396027	<i>S. warneri</i>	TATTGTCAAAGTCACAACAATTAGA	25	32	ACGTTGTATCGCATTGTAAA	20	531	500
sin	22476845	<i>S. epidermidis</i>	TTTAGAGAGACAGCTAGATAATTTGA	26	42	CAATCTTACTAATTGCTTGACCT	23	544	503
slamStalugd	5802563	<i>S. lugdunensis</i>	CAAAGGAGTGTGATTTTATGTC	22	273	TGGATTAGCTTTAGGACCAG	20	784	512
slushABCStalugd	1778750	<i>S. lugdunensis</i>	TGTCAGGTATCGTAGATGCAA	21	2	GGAATAATCCAATAATAAAGTCTACA	26	501	500
spa	21281729	<i>S. aureus</i>	CCGTTACGTTGTTCTTCAGT	20	587	GCAATGGTTTCATTCAAAGT	20	1115	529
spoVG	16024896	<i>S. epidermidis</i>	GTGACAGATGTAAGACTTAGAAAAATA	27	1	AGCTTCGCTGATTCTTCG	19	300	300
sprV8	46686	<i>S. aureus</i>	TTTAAAGTTAGTCTTTATTCTGTTG	26	15	ACTTGAATATAAGTTACGGGTGCAT	25	284	270
sstC	3724154	<i>S. aureus</i>	TGATATTGGAAGATATTAGCATAGA	25	44	TGACAATCGCTTTATTCATTT	21	571	528
tag	6434027	<i>S. aureus</i>	TTTTGATTTATCTTCTGACGG	21	48	CATTCATTTTATTCCCACCT	20	560	513

gene	gi	source species	forward	length	position	reverse	length	position	product
tnpStwar	31074829	<i>S. warneri</i>	TCAGATATAAACAATTTAACAAGGA	25	11	GAAGGTGCCTGATCTGTAAT	20	410	400
tst	18266750	<i>S. aureus</i>	TTTTTATCGTAAGCCCTTTG	20	26	CAATAACCACCCGTTTTATC	20	581	556
tyrA	21204263	<i>S. aureus</i>	TGGATATAACAATCAAAATCACTC	24	5	TTTTAGAAATGATTCGACAGC	21	365	361
ureSE1861	27466918	<i>S. epidermidis</i>	TGAAAGAAGGGATAGTTTTGC	21	2	TTAAACGATTGGGTGATGG	19	321	320
ureSE1863	27466918	<i>S. epidermidis</i>	ATGCAAATTATGGAGATGAAG	21	110	GACAGCTTGACCTTTACCAG	20	612	503
ureSE1864	27466918	<i>S. epidermidis</i>	TGATTATAGAAGAAATTCAAGGAAA	25	2	TCAATCATGTGAATGTCCTA	20	453	452
ureSE1865	27466918	<i>S. epidermidis</i>	TTAACTTATTCAGATGGGATAGC	23	163	GAAATAAAGATTCGAACATGAAC	23	686	524
ureSE1867	27466918	<i>S. epidermidis</i>	TCGTATATGGAATTTGTAGCAG	22	313	TGTCGATGATAAATCGTTTG	20	812	500
yabJ	16024896	<i>S. epidermidis</i>	ATGAAAAATACTCAACTCAGATAAGG	25	1	TATAATTCCTTCACTTTACCTATCAA	26	380	380
ydhK	18148881	<i>S. hominis</i>	ATCGTGCTTTCAGTTTCATT	20	3	ATTATCAGCTTGCTCCAATAA	21	502	500
0487Straga	22533503	<i>S. agalactiae</i>	AGTAATGGCCAATTGTTGC	19	225	TGACTAATCCTACTTTCGGTGA	22	455	231
0488Straga	22533503	<i>S. agalactiae</i>	AATCCCTTTGGCTTGAGA	18	1915	AAAAGTACCCTAATAATCCAC	22	2154	240
0493Straga	22533503	<i>S. agalactiae</i>	CTATTATAAAGAACGAGGGCAAA	23	1290	AGTACTATTCAATTTAGCACGACA	24	1689	400
0495Straga	22533503	<i>S. agalactiae</i>	CCCTAAATCAAGCCATAAAG	20	45	TGCAATCATACCACACAAAG	20	672	628
0498Straga	22533503	<i>S. agalactiae</i>	AGTTTTATCTATTGACGATTTAAGC	25	477	CAACCGTAATCCCTCTATTATATC	24	864	388
0499Straga	22533503	<i>S. agalactiae</i>	GGAGCGCGTTTAGTTTACG	19	310	GCCACTACTTGTCCACCATC	20	539	230
0500Straga	22533503	<i>S. agalactiae</i>	TGTTCTTAACCATGCTGTTG	20	39	TCATTGATTGACGAATGTGA	20	448	410
0502Straga	22533503	<i>S. agalactiae</i>	TAATGAATGAAGGTGTGGAAC	21	230	ATTCTGACTTCTGGCGTACTT	21	469	240
0504Straga	22533503	<i>S. agalactiae</i>	AATGGGCATTCTCTTATTG	20	41	GTATAGAAGATGAAGCAGCATAAA	24	280	240
1760Strpneu	15459462	<i>S. pneumoniae</i>	TTGCTTGACTGGTTGTGTC	20	53	CTACTCCGTGAAGTGAAGG	20	598	546
573Stprmut	24376948	<i>S. mutans</i>	ACGTCCTCTTAACAGTCACAA	21	42	TGCGACTAGGATGGTTTC	18	561	520
580SStprmut	24376948	<i>S. mutans</i>	ATCAGGCTGTTATGCGTCT	19	836	TGCCCATCTTTCATTTCA	18	1298	463
581_582SStprmut	24376948	<i>S. mutans</i>	AATTGTGAACCAAGTTAGAAACC	22	51	TGCCACCTGATAGTGAGC	18	410	360
584SStprmut	24376948	<i>S. mutans</i>	GAAGAAACGTGAACGATTAGA	21	3	TTAATTGGCCATCCAAGA	18	465	463
acyPStrpneu	15459462	<i>S. pneumoniae</i>	TGCAAAAGGTTAGAATGATTG	21	2	AAGTCAGAGTAGGGAGGAAAG	21	263	262
CAMPfactor	840865	<i>S. agalactiae</i>	ACATATGATGTATCTATCTGGAATC	26	12	CTGTTAAGGCTTCTACACGAC	21	337	326
CAMPfactor	840865	<i>S. agalactiae</i>	TATACAAAATCAAACTTGATAAGGA	26	556	TTTTAATGCTGTTGAAGTGC	21	765	210
cap1EStrpneu	1944619	<i>S. pneumoniae</i>	ACTCTTGGCTTGATTTTGG	19	478	TTGAAGTCCCATCTCTTTTC	20	1050	573
cap1FStrpneu	1944619	<i>S. pneumoniae</i>	AAATATTGTTGGTTTACTTCGTG	23	18	TCATAATTTATCTCCCTTGA	21	552	535
cap1GStrpneu	1944619	<i>S. pneumoniae</i>	CTAAAGCATTGGAGAGATTG	21	95	TGGATTCTATTGCTACTCC	20	785	691
cap3AStrpneu	1658316	<i>S. pneumoniae</i>	TGTAGGAAGTATTGGATGA	21	477	CCATAACTCCCTTAACAGCA	20	985	509
cap3BStrpneu	1658316	<i>S. pneumoniae</i>	TTTCCAGACATAAACCATCC	20	227	GGCATTTCTAATCATCCAAG	20	921	695
celAStrpneu	3211752	<i>S. pneumoniae</i>	TCGTCATCTGTACTGGTCTG	20	41	CTCGTCTACTGACTTGAACCTG	22	582	542
celBStrpneu	3211752	<i>S. pneumoniae</i>	GTGGAATCTGCTGGTAAAG	20	147	GCTCATTCATCTCCTCAAAG	20	691	545
cglAStrpneu	3211747	<i>S. pneumoniae</i>	GATTATCGGAGAAATTCGTG	20	609	GATAGTCTCCACCAGATGAAA	21	1010	402
cglBStrpneu	3211747	<i>S. pneumoniae</i>	TGGACAAGCAGTGTGTGA	18	2	TAGGTCTGCACAAAGATTCC	20	464	463
cglCStrpneu	3211747	<i>S. pneumoniae</i>	AAAAATGATGACATTCTTGAAA	22	6	TTAATCATTGACTTTACGATTTG	23	327	322
cglDStrpneu	3211747	<i>S. pneumoniae</i>	ATGCTGGAAAGTCTCTTGG	19	19	TTTGTTCCTTAATGCGTTT	20	398	380
cinA	2398824	<i>S. pneumoniae</i>	GGCTGTAGGAGACAATGAAG	20	120	CTTTGTTGACAGACGTAGAGTG	22	666	547

gene	gi	source species	forward	length	position	reverse	length	position	product
cps14EStrpneum	2198539	<i>S. pneumoniae</i>	TTGTTAGAGAGACAGAACTTGAAC	24	80	AGATCGACAAACACCTCATC	20	599	520
cps14FStrpneum	2198539	<i>S. pneumoniae</i>	AATATTTTATCCATGTTATTATCCTAC	27	135	GTCGGAGCATCAATTCTATC	20	344	210
cps14GStrpneum	2198539	<i>S. pneumoniae</i>	TGAGGGATTATTTCAGGATG	20	75	TTAAAAAGGTTACTGATTTCAC	23	479	405
cps14HStrpneum	2198539	<i>S. pneumoniae</i>	TGCTTTAACTCTTTTACCAACC	22	102	TGGACAGAAAATTCCAATAAG	21	723	622
cps19aHStrpneum	3907597	<i>S. pneumoniae</i>	AAGGCAATTCCAATACAAAG	20	71	GATGGTGCAAGACCTTAATC	20	757	687
cps19aIStrpneum	3907597	<i>S. pneumoniae</i>	TTTCAATGCCTCTCTTGG	18	209	TCCCAGCTATCAAGCCTAC	19	742	534
cps19aKStrpneum	3907597	<i>S. pneumoniae</i>	TCCATTAGTCAATGAGTTGAAA	22	57	GTCACATAAACATTCTCTTACCTT	25	506	450
cps19fGStrpneum	1881538	<i>S. pneumoniae</i>	GAAGCATACGACAACTTCC	20	169	TCAGGTAGCGATCATACTCC	20	733	565
cps23fGStrpneum	3818479	<i>S. pneumoniae</i>	GTGATAGTGAACCTGGGATTG	21	73	AACGCCAGTAAAGAGATGAC	20	734	662
cpsA1Strgal	13022158	<i>S. agalactiae</i>	AAAGAAACACTCACATACACCTC	23	27	AAACCATAGCTTGACTATCACC	22	559	533
cpsB1Strgal	13022158	<i>S. agalactiae</i>	TAAACACGAAGCGGAAAA	18	186	TCAATAAAAAGTTGGTTAGCAC	22	695	510
cpsC1Strgal	13022158	<i>S. agalactiae</i>	TAATCACATTGTGGCCATT	20	77	CATCCAAAAATCCCATATAACT	23	610	534
cpsD1Strgal	13022158	<i>S. agalactiae</i>	CGTACAAACATACAGTTTAGTGG	23	73	TCCATAATCGCCGTAAGTAG	20	657	585
cpsE1Strgal	13022158	<i>S. agalactiae</i>	TTTGGAGTCGTGGCTATCT	19	143	GCTAAGTGCTCTACATTAACA	22	669	527
cpsG1Strgal	13022158	<i>S. agalactiae</i>	TGATCAAGAAGTGTTCATTCAA	22	87	TTATGACAAAACATATCATTATTTCC	26	446	360
cpsIStrgal	5823209	<i>S. agalactiae</i>	TGAGGTTTGATGAGAACTTAAAA	23	512	ATCCCTTTAATGATAAGTATTTGAC	25	895	384
cpsJStrgal	5823209	<i>S. agalactiae</i>	GGGTTGTCAGAAGCTAGAAA	20	220	TTATTCGCTCGTCTAATGCT	20	733	514
cpsKStrgal	5823209	<i>S. agalactiae</i>	TATTCTTGGGTGGTTCTGTC	20	368	AGTGGACGAATGTGTTATCC	20	891	524
cpsMStrgal	5823209	<i>S. agalactiae</i>	TACACTCGGGAATTTATTGG	20	39	AATCAAGGGAACAGACACAG	20	651	613
cpsYStrgal	5823209	<i>S. agalactiae</i>	TCAGGACTGTTATTTTTATGATT	24	1	CGACGATAATTCCTTAATTGC	21	451	451
cpsYStrgal	5823209	<i>S. agalactiae</i>	AAAGTTCGTATTGGGTCA	18	564	ATGAGAATTCAACAATTACAATA	23	924	361
cyclStrpyog	5851899	<i>S. pyogenes</i>	TAGCTCATATTGTGCGAAAG	20	23	TGATGGACCTCTGTTACCTC	20	533	511
cylBStraga	6007852	<i>S. agalactiae</i>	CGTTTCCTTAGGGACTGTT	19	4	TTGCCAATAAAAATAAGAATGAG	22	386	383
cylEStraga	6007852	<i>S. agalactiae</i>	TTACCTATGGTTGTTTAGATTGG	23	221	CGAACCCCTCTTACTTGTTT	20	755	535
cylFStraga	6007852	<i>S. agalactiae</i>	CTGGTGAAGAATGTGAAGAAG	21	74	AAATATCAGTAATGGGTTGTCC	22	592	519
cylHStraga	6007852	<i>S. agalactiae</i>	CGAGCATAAACAGCATCTC	19	57	CCAGAAGAATAGGGCTGAC	19	629	573
cylIStraga	6007852	<i>S. agalactiae</i>	TCTTATCATCTGCTGCTTCC	20	18	TGACGAGAGAGGACTTGTG	19	627	610
cylJStraga	6007852	<i>S. agalactiae</i>	AGCGATATGATGCTTTCTTT	20	194	GATAATGCCTTGGTAATGTCTT	22	799	606
cylKStraga	6007852	<i>S. agalactiae</i>	AAAAATAGGCAGTCTACATTGG	22	10	ATTCTTTTAAGTAAACCGCTTC	22	520	511
dexB	1658316	<i>S. pneumoniae</i>	AGAGCAAAAACGCTGGTT	18	315	TAGTAATTCCACACAGAAAGCA	22	694	380
dinF	2398824	<i>S. pneumoniae</i>	ACGAACAGTGGACCTGATAC	20	12	TAAACCTTGCGAAATAATGG	20	621	610
dltAStrmut	2952523	<i>S. mutans</i>	AGATATGATTGCAACAATTGAA	22	21	CGCATGATTGATTTGATAAG	20	432	412
dltBStrmut	2952523	<i>S. mutans</i>	GTGAAAAGTCGCATCAAATC	20	173	GCCATAAACATACATGACTCC	21	732	560
dltCppx1Strmut	2952523	<i>S. mutans</i>	CAGCTGTTGCAGAAGATTTAG	21	491	CCATTAGCTGCTTGTGATG	19	740	250
dltDStrmut	2952523	<i>S. mutans</i>	TTCTCTTAAATCAAACGGAAGT	23	470	ACCCATTTGGCATTAAACC	18	977	508
endAStrpneu	15459462	<i>S.pneumoniae</i>	GTTCCGTAATCCAGTTGAAG	20	26	TTAACAGACGCAGTCAAGAG	20	654	629
exoAStrpneu	153626	<i>S.pneumoniae</i>	CGTGGAATTTTAGAAGAACTC	22	168	CAAGGACTGGTTTTCTTTG	20	490	323
exp72	1208737	<i>S.pneumoniae</i>	AAAATTTGGGGGATTCACT	19	31	TCATAAGCAGCAGTAACCAA	20	236	206
fah_rph_hlo_Strpyog	15425741	<i>S. pyogenes</i>	TTAAATACGCTAAAGCCCTCT	21	247	AGGGTGCTTAATTTGACAAG	20	546	300

gene	gi	source species	forward	length	position	reverse	length	position	product
fasCAXStrdysg	21629521	<i>S. dysgalactiae</i>	GACATTGAGATTGGTGATGAG	21	178	TTAAGCGTGAGACCATACAG	20	700	523
fnlAStrpneu	33113982	<i>S. pneumoniae</i>	CCTCTAAGGCTATGATGGAA	20	425	CTATTAAGGGATTGCGTTTG	20	934	510
fnlBStrpneu	33113982	<i>S. pneumoniae</i>	TGAAAGATGGACGAGATAGG	20	74	GATGGGCTAGGTAAGATTTG	20	662	589
fnlCStrpneu	33113982	<i>S. pneumoniae</i>	TACATGGATGCTGTTGGAG	19	223	GATCTAGGATGGCAAGAATATAAG	24	767	545
folDStraga	22533503	<i>S. agalactiae</i>	TCGAAACCTTTCTGAGGTAA	20	576	GAACAGGTGTTATCATACTAGCAA	24	775	200
gct18Strpneum	13377447	<i>S. pneumoniae</i>	CATATGGTACATTTGATTTATTGC	24	17	GTGTCAATATGGTAGTCTTTAACATC	26	266	250
hexB1	4495245	<i>S. pneumoniae</i>	CTCCTAGTGCCCTATATCTTTG	22	4	TACGATGATTGGCCTTGA	18	286	283
hftsHstrpneu	5739310	<i>S. pneumoniae</i>	CTTGGTGACAGAGTCCT	18	68	TTTTCGTCATTCATTTTTGA	20	351	284
hlyXStrmut	2952523	<i>S. mutans</i>	GTGATATTATCCAAACCATTCTC	23	707	TTAAAGCGGTCAAAGGTC	19	919	213
hylStragal	22536185	<i>S. agalactiae</i>	CTAGGGAATGGTCTGCTTG	19	368	GAGACGGATTGGTTAGAGTG	20	889	522
igaStrmitis	1870144	<i>S. mitis</i>	ATTGGACTTGTGTGAGCTTC	20	55	CCTTTGTCTACCTTCATTGG	20	669	615
igaStrpneu	1460093	<i>S. pneumoniae</i>	GTGGATGCTCAAGAACTG	19	118	CTTATGTTGCGCTAATTGTTC	21	840	723
igaStrsanguis	2288954	<i>S. sanguinis</i>	GAAGGCAATGAGGAGACTTAC	21	223	CTACTCGGCCAGACAAGAC	19	763	541
immunofrag1Strpneu	33077817	<i>S. pneumoniae</i>	AAGTAGGCGATGGTTATGTC	20	1157	TATTTCTGAATCCTGATGG	20	1783	627
immunofrag2Strpneu	33077816	<i>S. pneumoniae</i>	GCATCTCTCGTTATGTCTTTG	21	1238	TTTGAGCTTTGTATGTGTG	20	2021	784
immunofrag3Strpneu	33077815	<i>S. pneumoniae</i>	GACCATTACCACTTTATTCCTTAC	24	931	TTTGCTCTTCTGTCAAGTCC	20	1432	502
int	1877426	<i>S. pyogenes</i>	CCGGTTATGTTAATGGAAAG	20	62	TCAAATCATCCCAAGTTAGTG	21	640	579
int315.5	28876381	<i>S. pyogenes</i>	GCTATTTGGCCCTGTGTAG	19	131	CAAACGTAGATCAATGCAAG	20	637	507
kdtBStrpneu	15459462	<i>S. pneumoniae</i>	TTTCATTTCTTATTTCTCTCCA	21	12	GCTTATTCACAGGCTCATTT	20	473	462
lichStrbov	2231061	<i>S. bovis</i>	AATTGTTCTCTTATTGGCTTTC	22	24	CCTGGATTTTTAATAGGTTTCA	22	323	300
lipStragal	22536185	<i>S. agalactiae</i>	TCCCACTTAACATATGTTGCTC	21	137	CTTGCTGACTATTTGATGAC	21	722	586
lysAStrpneu	15459462	<i>S. pneumoniae</i>	GATTTCTGTATGAGGCAGTTC	21	184	CTTCCTAGCGTCCAATACC	19	691	508
lytA	4495247	<i>S. pneumoniae</i>	ATTATCACTGGCGGAAAGA	19	3	GATAAGAGCCGTCTGAATGT	20	467	465
lytRStrpmut	24376948	<i>S. mutans</i>	GTCTTGGCGCGAGTTTAA	18	167	TTGAAGCCTTTTGAGCAG	18	432	266
lytSStrpmut	24376948	<i>S. mutans</i>	CATTGGTTCGATCAGTCAG	19	966	GCTTTGGTAGGATATATTAGTGG	23	1365	400
murEStrpyog	13621628	<i>S. pyogenes</i>	GCTCACGGTCACTAATAATCTC	22	147	CTGACAACCAGATCACCAC	19	647	501
nanA	1163109	<i>S. pneumoniae</i>	AATGGAATGAACGGAAGTG	19	10	TGTTCTCTCTTTTCCCTAGC	21	461	452
nanBStrpneu	1163109	<i>S. pneumoniae</i>	GGTCAACTGTCCATATCTCC	20	115	GACTGATTTCAACAATACTTCC	22	640	526
neuA1Strgal	13022158	<i>S. agalactiae</i>	TGAATCTGGAATGTTTGATAAG	22	114	GACCGATGACGTGGATAA	18	658	545
neuB1Strgal	13022158	<i>S. agalactiae</i>	TTATTCTTTTCGACGGGTATG	20	410	ATCATCTTGCCTTCTTG	18	966	557
neuC1Strgal	13022158	<i>S. agalactiae</i>	GCTGAATACGGAATAATGAAG	21	34	TGGTTAGAGGAGGAATTGATAG	22	565	532
neuD1Strgal	13022158	<i>S. agalactiae</i>	AGTCATGCTGATGCGATT	18	34	CGATGAAATATCCAAGGTTT	20	540	507
oppA	1420857	<i>S. pyogenes</i>	CCCAGTTCAATTAGATTACCC	21	1296	TTGACTTAGCCTTTGCTTTC	20	1927	632
oppCStrpyog	1420857	<i>S. pyogenes</i>	TTTGATGGTGTGGGTATG	19	298	AAAGAGGTAGGCATTTGTTG	20	831	534
oppD	1420857	<i>S. pyogenes</i>	TCGAAGAGATTTTCTATGATCC	22	731	CAGACATTTCTTCCTCCT	19	1070	340
pcpBStrpneu	1914873	<i>S. pneumoniae</i>	GGCTGTTAGTCCAAGTCAAG	20	246	GCTACCTGTAACCATTGCTC	20	897	652
pcpCStrpneu	1914873	<i>S. pneumoniae</i>	AGTCGCACTAGCCACATT	18	27	GAGAATCAAAGCCACCATC	19	532	506
pepQStrmut	2323340	<i>S. mutans</i>	TGATTAAAGGAGTTAAGTTGGTG	23	699	TGTCAAAATTAGCACAGATTG	21	1079	381
perMStrmut	2952523	<i>S. mutans</i>	TTTTATTGGGAGGTTTTCTTT	21	134	AACAAATATGAAGGCAGCA	19	696	563

gene	gi	source species	forward	length	position	reverse	length	position	product
pflCStrmut	2952523	<i>S. mutans</i>	AGAAAAAGTTGACTACGAAAAAG	23	6	AGATAAATAACGCGCACAAG	20	510	505
pflCStrpneu	15459462	<i>S. pneumoniae</i>	CTTGTGCTGTTCTTCGTTG	19	337	CTTGCGCTACCGTGGTTT	18	586	250
plpA	1658316	<i>S. pneumoniae</i>	TTGATATCCAACAACACAAAAA	23	524	AGCTTTTTGGTATTCATCTACAG	23	1023	500
ply	47403	<i>S. pneumoniae</i>	ATTTCGAGTGTTGCTTATGG	20	709	GTAAAGTGAGCCGTCAAATC	20	1226	518
prtA1Strpneu	9943836	<i>S. pneumoniae</i>	AGGAAACAGAAAATAAAGAGAAAC	24	143	CAAACGGAGCATTGATAGAC	20	667	525
prtAStrpneu	13345020	<i>S. pneumoniae</i>	GGGTAACATATGCGACTTCTG	20	1134	AGCTTTACACCATCATCTCC	20	1667	534
pspA	153840	<i>S. pneumoniae</i>	GATCAACAAGCTGAAGAAGAC	21	1179	CATCTTTACCCAACCTG	18	1782	604
pspC1Strpneu	6469846	<i>S. pneumoniae</i>	CATTGAAACCAGGAGAAAAGG	21	401	TTTTTACTCTCAACTTCTCTTTTGC	26	650	250
pspC2	6469844	<i>S. pneumoniae</i>	AAAAGCGAAAGTTAAGAGTGAA	22	600	GGATGGGCTTGGAAAGAGT	18	879	280
purRStrpneu	15459462	<i>S. pneumoniae</i>	AAGATATTGCCAACCTCAAC	20	17	GGTTATGACCGTAGCAACTAA	21	430	414
pyrDAStrpneum	5578890	<i>S. pneumoniae</i>	GCTTGTATGACGATAGAGGAG	21	70	TAGCTCAGTCAGACCACGA	19	381	312
recNStrpmut	24376948	<i>S. mutans</i>	TGATGCTGAGTACAAGGATTT	21	780	CTTTAAATCAGCCTTATCCA	21	1186	407
recNStraga	22533503	<i>S. agalactiae</i>	GCATGACCAAGAGGAACTAA	20	390	TGTAGTAAACCAGCGTCAAA	20	899	510
sloStrep	13699903	<i>S. dysgalactiae</i>	TGTTAATAGTAAATCTTAGATGG	24	813	CCGCTTCAACATCATTAC	18	1099	287
SP0828Strpneu	14972300	<i>S. pneumoniae</i>	TTGTAGGGCTAGGAACAGG	19	62	AATCTGAAGTCCATCTCGTC	20	660	599
SP0830Strpneu	14972300	<i>S. pneumoniae</i>	ATGACGCGCTATGCTTTG	18	1	ATAGGCAGTCTTAGAATAGGATTCTTC	27	450	450
SP0833Strpneu	14972300	<i>S. pneumoniae</i>	AACCATGTATTGAGGAAAGTG	21	85	TGGAAGTTTGTATGAGTGACAG	22	611	527
SP0834Strpneu	14972300	<i>S. pneumoniae</i>	TGTTCCGATTGAGCTAGAAG	20	42	TAATTTTACGGTGGGGTTG	19	460	419
SP0834Strpneu	14972300	<i>S. pneumoniae</i>	GTGTCAGCACAAATTACGATT	21	1	TCGTCACTCACCTTGGA	18	500	500
SP0837_38Strpneu	14972300	<i>S. pneumoniae</i>	GGACTTCCTTTTCTTATCCAG	21	13	CAGTCCATAGAGGCTGTTTT	20	573	561
SP0839Strpneu	14972300	<i>S. pneumoniae</i>	TTTGCAGATTGTGAGATTG	20	90	TACGTTTACAGATGCTACGG	20	592	503
sphtraStrpneu	2109442	<i>S. pneumoniae</i>	ATCTGTAGAAGTCTTGTTTC	22	789	ATTCTAAATCACCTGAAGTCTTG	23	1189	401
SPy0382Strpyog	13621628	<i>S. pyogenes</i>	CACCAGACAACCTTTCTTTC	20	30	CAAGTGTAACCAGAGCTTCC	20	571	542
SPy0390Strpyog	13621628	<i>S. pyogenes</i>	TTAATTGCAGTAGCAGCATC	20	916	AGCCACCAATAATGAGGAG	19	1531	616
SpyM3_1351	28876381	<i>S. pyogenes</i>	AGCAGTAATCTTTGGTACTGTTT	23	170	TGGTGAAGATAGATGAGATACTTAAT	26	377	208
ugdStrpneu	33113982	<i>S. pneumoniae</i>	AATAGCAGTAGCAGGGACAG	20	6	TGCTCCGTATCTCTCAAATC	20	506	501
uncC	18653430	<i>S. pneumoniae</i>	ATGAATTTAACATTTTTAGGCTTAT	25	1	TATTTGATAATAAATGAGAAGACAAGA	27	200	200
vicXStrepneu	6689277	<i>S. pneumoniae</i>	ATGAGTGAAATAGGCTTTAAATACA	25	1	CACCTTGCCAAGATATTTACTATT	24	300	300
vicXStrpyog	6689351	<i>S. pyogenes</i>	TTATCTGATTTAGGACATTTATC	23	580	ATATCAGTTAATGGACAAGCAG	22	809	230
wchA6bStrpneum	13377419	<i>S. pneumoniae</i>	TTGCACTTTATATCCTCCATT	21	116	GTTACATCAATCCCATCGT	20	665	550
wci4Strpneum	13377403	<i>S. pneumoniae</i>	AAGTAGGGGCTTTCTTGC	18	290	AACTTTCTTTCTTACCACTACCC	23	634	345
wciJStrpneu	33113982	<i>S. pneumoniae</i>	ATTGTGAGGATCTTGTGAG	21	58	GGTATTCTTCTCTATCAAAGTGG	23	747	690
wciK4Strpneum	13377403	<i>S. pneumoniae</i>	TAACGAGATTATTACAAAACAAAC	25	120	TCTTTAGGCTGGAATGTGTC	20	719	600
wciL4Strpneum	13377403	<i>S. pneumoniae</i>	GAAAGAAATGGGTGCAAAAG	19	150	TCATCCTCACCATTACCAAC	20	710	561
wciN6bStrpneum	13377419	<i>S. pneumoniae</i>	GCTTCCATCAAATCACTTTAC	21	49	GTGCAACATTACTGCCTTC	19	784	736
wciO6bStrpneum	13377419	<i>S. pneumoniae</i>	TGGAAGACCTTTATCCTGTC	20	96	AAAATAGTTAATAGCAGTAAACCTG	26	620	525
wciP6bStrpneum	13377419	<i>S. pneumoniae</i>	CTATAATGGTGAGCGATATTTG	22	33	AGAACAACACCTTCCCATAC	20	628	596
wciY18Strpneum	13377447	<i>S. pneumoniae</i>	CGTATCAAGTCGGCATTT	18	528	GCAATTTATCAAAGTTATCATCC	23	1057	530
wzdbStrpneum	13377419	<i>S. pneumoniae</i>	GGATATGCCAGCAAAAAC	18	306	TGTCAAAATCTGGAACGAG	19	685	380

gene	gi	source species	forward	length	position	reverse	length	position	product
wze6bStrpneum	13377419	<i>S. pneumoniae</i>	ATCAACGACTTCCACCAA	18	147	AATATTTACGCAAGGTTTCAAG	22	436	290
wziyStrpneu	33113982	<i>S. pneumoniae</i>	CAACTTCTGATTATGCCTTTG	21	130	TCCTAATGTCCGTCCAATC	19	717	588
wzxStrpneu	33113982	<i>S. pneumoniae</i>	AGTGGAACTATGTGTTTAATCTTG	24	29	GATGTCAGCAACCATCCTAC	20	767	739
wzy18Strpneum	13377447	<i>S. pneumoniae</i>	AGATTACACTTTTACAGCTATCTCC	25	279	TCAACTCCCTTCCATAAATC	20	785	507
wzy4Strpneum	13377403	<i>S. pneumoniae</i>	TCTGGACTCTCGATAATTGG	20	71	AGGAGAACACACCAGGAAG	19	628	558
wzy6bStrpneum	13377419	<i>S. pneumoniae</i>	ACATTTGTTATAGTTTCCTTGTTG	24	202	TTTGGTAAGTTGAGATTTAGGAC	23	717	516
xpt	4495149	<i>S. pneumoniae</i>	TTTTAACCCACCAAGTTGAC	20	2	GATACCGATAGCTTGGACTG	20	384	383
ytqBStrmut	2952523	<i>S. mutans</i>	CGGCAGACAAGTCAGTCA	18	2	TATAATTTCTCTATCATCACCAAAA	25	251	250
ABC-eltA	15418957	<i>E. faecalis</i>	CATGTATTGGTTGTTAGATAGGG	23	204	GAGGATAAGGCCATGACTG	19	740	537
ace	10863251	<i>E. faecalis</i>	TAGTTGGAATGACCGAGAAC	20	128	AGTGTAACGGACGATAAAGG	20	717	590
agrBfs	6492218	<i>E. faecalis</i>	GATCAGGAAGATCAATCAGG	20	40	CTTAGTTCACACCATCAC	20	645	606
agrCfs	6492218	<i>E. faecalis</i>	GTTGGGCTACTCTTGGTTG	19	153	GTGTTGATACGTTGTTCTTCC	21	659	507
arcA	14349113	<i>E. faecalis</i>	ATATCGAAGTGGTCTATTTAGAGG	24	188	TTGATTCTGAACGATCATAGACT	23	637	450
arcC	14349113	<i>E. faecalis</i>	AATTAACAAAGCAGGAATCA	21	300	CCACCACATGAAATGGTAA	19	579	280
asa1	47047	<i>E. faecalis</i>	CAGGAGGAACATTGGTTGT	19	1007	CGTCATACCCTGGATTGTT	19	1591	585
asp1	43323	<i>E. faecalis</i>	CGACAGAACTTGCTAAAGTAGA	22	1859	GTGATTCCGCCATAGTTG	18	2402	544
bglB	4704705	<i>E. faecium</i>	TCTTCATTTGTTGAATATGCTG	22	213	TGGAATCGAACCTGTTTATC	20	712	500
bglR	4704705	<i>E. faecium</i>	ATTATTGTCGCCTCTTTCC	19	7	GCTATTTGTTATCGCATTCTG	21	671	665
bglS	4704705	<i>E. faecium</i>	CTCCTGATCCTCTTCTGTG	20	502	ATGTTATACTCTGCTCTTCAACC	23	1005	504
bkdA	5901691	<i>E. faecalis</i>	AGTTGCACAAGTAGCGATG	19	156	TGAGAAGTCAAGCGAGAAAC	20	755	600
cad	19481589	<i>E. faecalis</i>	CGCAGACAAGAAAGACAAC	19	72	GTGTGGTAGCCGTTTGAG	18	599	528
camE1	20522053	<i>E. faecalis</i>	TTTTCACTTTTAGGAGCTATTTTT	24	28	CTTTTTCATCTGCCGTAGTC	20	478	451
cgh	30058650	<i>E. faecalis</i>	CTTCTTTCGTGCTTTCAAC	19	507	AAATTTAGATCATCATTTTGC	21	847	341
csrA	5457307	<i>E. faecalis</i>	CAAAACCAACAGAAGAAGATTA	23	5	CGAACTTCTACTCGGTGCAT	20	278	274
cylA	30058650	<i>E. faecalis</i>	AAACCTGGATGATAGTGATAGG	22	201	GACTCATTTCTGCTGATG	19	794	594
cylB	30058650	<i>E. faecalis</i>	CAAGGAGAGCATAGTGAATGT	21	25	TGCAATAGGAATTAAGAGTAATAAAA	26	528	504
cylI	30058650	<i>E. faecalis</i>	GTTAGGGCACTTAGCTTTTG	20	120	TGGGTATATTAGTTTTAATTTCTATT	27	681	562
cylL_cylS	30058650	<i>E. faecalis</i>	TGGAATAATTAAGTGTAGTTCCT	23	2	CTACTCCTAAGCCTATGGTAAAC	24	403	402
cylM	30058650	<i>E. faecalis</i>	AGCAAAGTGGTAACGAGAAG	20	56	ATACGCATCAACTCAGGATAG	21	617	562
dacA	12188895	<i>E. faecalis</i>	GGCTTAGTTGTCAGTTGTGG	20	61	AATTCCTTGCAATTTGATACAG	21	624	564
dfr	4103866	<i>E. faecalis</i>	GTTTGATTGTTGCGAGGT	18	8	AATCTACTCAATTCATTTTTCCTT	24	485	478
dhoD1a	30025891	<i>E. faecalis</i>	TTTTACTAAACCATTAGGTGTAAAT	26	501	CAAAACTTGTTGGACCTTCT	20	880	380
dnaE	21314373	<i>E. faecalis</i>	TTACGTTAGAAGAAGCATACCA	22	1349	AGGACGATACAGGGCATT	18	1848	500
ebsA	388106	<i>E. faecalis</i>	TTTATGAAGGCCCAAAGA	18	31	AGCCAGAATTAGCATCAACA	20	437	407
ebsB	388106	<i>E. faecalis</i>	TTTACCTCACCGACCAATC	19	65	TGGCTGAAGAAGCTCAAC	18	671	607
eep	5714509	<i>E. faecalis</i>	TCTGTTTACGTTAGCGGTCT	20	564	TCCCTAAGTTTCATTGACAACA	21	1084	521
ef00108	21693259	<i>E. faecalis</i>	TCAACGTCACAAACAAGAAC	20	33	CCTAAGAGACTTCCTTCATCC	21	680	648
ef00109	21693259	<i>E. faecalis</i>	TCGGAAGTATTGCGTTTG	18	98	TTATCGACATTCTCTGTTTCC	21	617	520
ef0011	21693259	<i>E. faecalis</i>	TTGTCTTTGGGCTTCTCTC	19	17	TTTCTGTATTGCTTCTTGGTC	21	684	668

gene	gi	source species	forward	length	position	reverse	length	position	product
ef00113	21693259	<i>E. faecalis</i>	CTATAGATTCCTATCTTGTTGG	23	69	ATATTTACCGCAATGAAACAC	21	585	517
ef0012	21693259	<i>E. faecalis</i>	ATGTATGTATCTTTTGTCTAAGTTGT	27	1	AAATCCCAATCGTCTAAGTG	20	380	380
ef0022	21693259	<i>E. faecalis</i>	AAAGTACTACCTTTTATTGCCTTAGT	26	7	TGTTTTATAAGTGTTCTTTGTTTTTC	26	326	320
ef0031	21693259	<i>E. faecalis</i>	TGAACAAAAAGCACAGGATAG	21	78	TACTAAACCCCCGTTGTG	18	580	503
ef0032	21693259	<i>E. faecalis</i>	TGATGAAAATTTAAAAGAAGAAGC	24	39	TAAATCCTCCATTAAATCCTCCA	23	258	220
ef0040	21693259	<i>E. faecalis</i>	TCAAATACACGTAAGCCTTCT	21	491	AAGTTTTCATTTGAGAAGTTG	22	870	380
ef0058	21693259	<i>E. faecalis</i>	CATTATTTTCATTAGGGGATATTAG	25	146	AGATTCCTTACTTTAGCTTTTCC	23	656	511
efaR	15425977	<i>E. faecalis</i>	GGCGACGAAGTTAAAGTG	18	49	AATGGTGATCGGTCCTTC	18	579	531
efmA	3790617	<i>E. faecium</i>	CGGATGAAGGAAGTAAAGAA	20	83	CATATGCTCGTAAATACTTGAAA	23	637	555
efmB	3790617	<i>E. faecium</i>	AAAGCGATTTGTTGCTGA	18	398	GAAAATTAATTAGCAAGGATAAAA	25	798	401
efmC	3790617	<i>E. faecium</i>	AGCCGGTAAACTCAGTCC	18	197	CACCATAAGGCAATTGAAG	19	703	507
enIA	11078548	<i>E. faecalis</i>	TTGCGATTTCTGTTGTAGG	19	18	AACCAAAGTCAAACCCATC	19	543	526
entA_entI	7271910	<i>E. faecium</i>	TCTATTAACAGACACAACCTTATCTAT	27	22	CCGGGATCTAATTCATATTT	20	342	321
entD	4760901	<i>E. faecium</i>	TTCATAAGGACGATGTGTTG	20	242	TGTTCTAGCTCTTGCTTTCC	20	854	613
entR	4760901	<i>E. faecium</i>	ATTATGTGAAGATCAAATTATACA	24	18	TTTTGTGTCATCTATCCTTTC	21	417	400
esa	493016	<i>E. faecalis</i>	AATCAAGCCGCTGAAAAG	18	64	CAAATTTAGCTTTGGCTTCC	20	568	505
esp	30058650	<i>E. faecalis</i>	AAATGGGTGAAGGAAGATTAG	21	149	ACCAGTGCTTTCTATTCCAG	20	705	557
gelE	1339878	<i>E. faecalis</i>	AGGTACAGGCATCTTTGTTG	20	30	TTCCATAATTGTTCCATCTGT	21	552	523
gls24_glsB	2274939	<i>E. faecalis</i>	GATACGAAGAAGATAGCGAAA	21	404	ACAATAGCCATCCCAGCTA	19	745	342
gph	9187965	<i>E. faecalis</i>	AAGATGGTACGTGTATTCGTTT	22	29	AATTACTTCTGTGCGCTTCA	20	540	512
groEL	15625348	<i>E. faecalis</i>	CTGGTTCAAAAGAAGCCATT	20	1001	TTTAGTTGTCAACAATCACTG	22	1400	400
groES	15625348	<i>E. faecalis</i>	GATCGCGTCGTAATTAGAGT	20	19	TTCAACAGTGGCAATAATGT	20	282	264
gyrAEf	15982566	<i>E. faecalis</i>	TTATTTCTGTTGAGGGCAAA	20	1802	TCTTCTCCACTTCTTCTGG	20	2444	643
H+ATPase	15667455	<i>E. faecium</i>	TTGGCAATGCGATGTTAG	18	29	CGCGATTTGAAGAGAGAG	18	429	401
metEf	2353762	<i>E. faecalis</i>	TTGATCGTTTTGACGTAATG	20	26	TAATCGTTTCTTTCTTTTGG	21	427	402
mntHCb2	29134879	<i>E. faecalis</i>	AGCGACTAGAGAGCATACAAG	21	309	TCAGAGCATCAAATAAATCAAC	22	916	608
mob2	4127803	<i>E. faecalis</i>	AAATTGTTGCACGTATGGA	19	8	TTTGCCGACTAAACACCT	18	457	450
mreC	9246947	<i>E. faecium</i>	ATTACTCGTTTCCCCTGAC	19	6	ACAATCGTCACAACTGACAC	20	461	456
mreD	9367034	<i>E. faecium</i>	ATGTTGAAGAAAGAAACAATGA	22	1	CTGAATAATTTCTTAAAGGGAAAA	24	500	500
mvaD	9937385	<i>E. faecalis</i>	CAATGGAACAAAGGCCACT	19	451	TGCTTGGCGAACTAAAGC	18	810	360
mvaDEfaecium	9937392	<i>E. faecium</i>	TCAGTCAGTTTCTTGACCTTT	21	215	TTAGTCCGTTTCTTTCCATC	20	721	507
mvaE	9937382	<i>E. faecalis</i>	CTGCGGTAAAGTCGTTG	18	261	AATCACGTAGCCTTACATCC	20	786	526
mvaEEfaecium	9937389	<i>E. faecium</i>	CCAATTAGGTGAAGCAGAAC	20	306	TTTGATGGTTGCTAAATAAGG	21	813	508
mvaK1Efaecium	9937392	<i>E. faecium</i>	GATTGCCTTTCTTTCTATG	20	81	ACATCTTTGACGGCTTCTC	19	581	501
mvaK2Efaecium	9937392	<i>E. faecium</i>	CAAGAACAAGAACTCAGCA	20	550	CATGTAACGGCAGTGGAG	18	1054	505
mvaSEfaecium	9937389	<i>E. faecium</i>	AAATTCACCTACTGCACCAGA	21	214	ATGGCGAAAGAATATGTCAA	20	798	585
oep	9246947	<i>E. faecium</i>	ATCTTGATCTTGCCATTCC	19	775	TGCTTTCTCAATCTTCGTTT	20	1307	533
orf3_4Efaeciumb	4704705	<i>E. faecium</i>	GCATATTTGCTTGATATATAGGT	24	243	TTATTCATGCTGGATTATTCG	21	542	300
orf6_7Efaecium	3342117	<i>E. faecium</i>	ATATTTCATCCCCAGCTCTT	20	19	AAGTATGAAAGAGATAAAACAAACAT	26	291	273

gene	gi	source species	forward	length	position	reverse	length	position	product
orf7_8Efaecium	4704705	<i>E. faecium</i>	AGCAGTTCGGTATCTCTTT	20	53	TGAAGAAAGGGTAATGTTTTG	21	678	626
orf9_10Efaecium	4704705	<i>E. faecium</i>	TGAAGTCCTTTGTCTTTGTTG	21	7	CAATACACACCGATTTAGAGG	21	514	508
parC	15982569	<i>E. faecalis</i>	ATCCGACTATGCGTTTACTG	20	1236	TATGTTTCGCCAATTTCTTTC	20	1747	512
pcfG	30841312	<i>E. faecalis</i>	AGGATCAATCGTAAATGGTG	20	87	TTCGCTGCAATCTTATCC	18	690	604
phoZ	5020413	<i>E. faecalis</i>	AAGATGGTGAAACATTGGTG	20	947	TCTTTAATCTCAGCTTTTTGC	21	1397	451
polC	21314371	<i>E. faecalis</i>	GTTTCCGTTCAAATAACCAC	20	193	CAATTCACGCACTTCTTTATC	21	735	543
ptb	5901691	<i>E. faecalis</i>	AATTGCAGGAGGTTCAACA	18	15	CTTCAGAGGTGCGTAAATCA	20	592	578
recS1	30058650	<i>E. faecalis</i>	AATGCGTGATCAGGGTGTAT	20	20	TGTAATTATGAGTCGAACATTTTTATT	27	339	320
rpoN	12003288	<i>E. faecalis</i>	CTCAACAGCTTCAACAATCC	20	59	CCACTATTGCATCTTCCTTG	20	751	693
rt1	27262899	<i>E. faecalis</i>	ATCTCGCGGAACAATTAGA	19	41	AATAAGCCAATCCACATATCA	21	545	505
sagA	9367034	<i>E. faecium</i>	TGAATCTTCAGCAACAGA	18	1017	TTTGGTTGTTCAAGTGTT	18	1187	171
sala	14906073	<i>E. faecalis</i>	TCGGCTCTAATGGTATGTTT	20	19	GTTGACGTGCTTGTCTTC	19	706	688
salb	14906081	<i>E. faecalis</i>	GCTTCATTAGCATTAGAACAATC	23	601	AAACCTGCATCCCATACTAC	20	1100	500
sea1	49019	<i>E. faecalis</i>	TTAACTGAACAAGAAAAGCAAG	22	964	TTAAATCTCCTGAAATAGAACTG	24	1492	529
sep1	1272652	<i>E. faecalis</i>	ACAACCAACAGTGAAAGCTAC	21	126	TTGTTAGCCAATTCTGCTTC	20	683	558
tms	4103864	<i>E. faecalis</i>	AGGTTTAGAAGTGGGGGAGT	20	245	ATCGGCGCTTTAATCGTT	18	454	210
tyrDC	21309881	<i>E. faecalis</i>	AACGCACATCTGAAAGCTAC	20	173	TACCTGAACGAGCTGAATG	19	676	504
tyrS	21309881	<i>E. faecalis</i>	ATGGAGGGTGATAACATGAA	20	1	AAGATAGTTCTGATAACCAATCG	23	400	400
vicK	6687468	<i>E. faecalis</i>	CATTGGTGGCTATTTCATTC	20	93	CTTTCTGCTTCCATTGTTTC	20	779	687
yycH	6687468	<i>E. faecalis</i>	TATCTTAGCTTCGCAACCAG	20	231	ATTGTCTGCCACGTATAACC	20	764	534
yycI	6687468	<i>E. faecalis</i>	GAGCAACGTCTCTTCTTCC	19	156	GAGCGTGTCTATCGCATC	18	702	547
yycJ	6687468	<i>E. faecalis</i>	TTCATCGCAATAATCGTTC	19	410	TAACACATCCGCCATCAC	18	633	224
b1169	16127994	<i>E. coli</i>	GTTTGGGACTTATTGCTCTG	20	29	CATCAGCCACAGTTTCAAG	19	775	747
b1202	16127994	<i>E. coli</i>	GAATACCAAAGCAGATCGTC	20	24	CCGAGATCGACAACAGAG	18	758	735
eae	145852	<i>E. coli</i>	CTAACTATTGTGGTGGAGC	20	28	CTTGTCATCGGTATGTTG	19	536	509
eltB	145830	<i>E. coli</i>	GGCGTTACTATCCTCTCTATG	21	33	TTTCCATACTGATTGCCG	18	370	338
envZ	453286	<i>E. coli</i>	AGCCTGGTGACGACTTATC	19	76	ATCCGCCAGTTGCTTAAC	18	696	621
escR	2897961	<i>E. coli</i>	TTTGTTGTTATTGGTACTTCATTC	24	79	ATCGAAATTGTTACTGGCG	19	578	500
escT	2897961	<i>E. coli</i>	TTACGCTTCCGATCATAGTAG	21	137	GAATACGTTTAGTTGAGGCG	20	639	503
escU	2897961	<i>E. coli</i>	AAGTGAAGAGGTAATGGCTG	20	72	TACCATCAGTATCCTTGGC	19	688	617
espB	1657262	<i>E. coli</i>	GATGGTGACTCTATTGCAGG	20	174	CCATACGATTCTGGACCTC	19	913	740
fes	145916	<i>E. coli</i>	TGTTTGAGGTCACTTTCTGG	20	2	CAATAGCTTTCACCAGGG	18	718	717
fes	145916	<i>E. coli</i>	TGTTTCTGCACTCGAAATG	19	342	GGCAATAGCTTTCACCAG	18	720	379
fliCb	8071787	<i>E. coli</i>	ACCACGACAGGTCTTTATG	19	598	AGAGAGGCACCGTCACTAC	19	1046	449
fteA	1621225	<i>E. coli</i>	TATGCTGCTCCAACATTCC	20	25	ATTATCTCCATCTTTCAGGG	20	426	402
hlyA	525328	<i>E. coli</i>	CTTGGAATGTTGGTAAAGC	20	77	TAAACTCCTTCGGTTGAGC	19	800	724
hlyB	1247757	<i>E. coli</i>	TCAATGCTGAAACTATAAGGC	21	74	ACTTAGCACCCAGTTCGAC	19	691	618
iucA	474189	<i>E. coli</i>	CATCAGGCAGTTATCCTGTC	20	215	AGTCGTCTCCTGCATTAC	19	982	768
iucB	474189	<i>E. coli</i>	TTCACAGCGGATATGGAC	18	20	CACTTTGCTCCCAGAAATAC	20	520	501

gene	gi	source species	forward	length	position	reverse	length	position	product
iucC	474189	<i>E. coli</i>	AGACTGGGATTTGGTCAAC	19	12	AGACACCATCCTGCCTTC	18	732	721
nfrB	16127994	<i>E. coli</i>	ATGGAATTGCGTCTGTTC	18	529	AAGTTTAGCCACAGCAGG	18	1232	704
nlpA	146648	<i>E. coli</i>	ATAATCCTCGTCATTGTCAG	20	518	GACTTCGGGTGATTGATAAG	20	768	251
papG	42307	<i>E. coli</i>	GGAGTATATTGCGTGGGTAG	20	234	AAGATTCACCATAGAGGCG	19	952	719
pilAe	147269	<i>E. coli</i>	CTCTGTCCCTCAGTTCTACG	20	38	TGGTATTGGTTCCGTATTTC	20	460	423
rfbE	1911762	<i>E. coli</i>	AAATGAATGTCTGGACTCAAC	21	57	TGTAAACAACGGTCATAAAGTG	22	617	561
shuA	21954703	<i>E. coli</i>	AGCAGCATCAGGTTCTTG	18	23	CAGTTGTTCAAACGCGAG	18	779	750
SLTII	304950	<i>E. coli</i>	TTCTTCGGTATCCTATTCCC	20	48	TGTGAGGTCCACTTCTTCC	19	663	616
toxA-LTPA	148027	<i>E. coli</i>	AAATGGCGACAAATTATACC	20	54	CTGGGTCTCCTCATTACAAG	20	666	613
VT2vaB	148261	<i>E. coli</i>	AAGAAGATGTTTATGGCGG	19	4	GATTCACAGGTACTGGATTTG	21	230	227
yacH	16127994	<i>E. coli</i>	GACTCGGTACAGCGATTG	18	517	CTGACGTTGGGTATCTCG	18	1284	768
yagX	16127994	<i>E. coli</i>	CTTTACGACGGTCTCCCC	18	5	AATCTTCCTGCTGAAATG	19	792	788
ycdS	16127994	<i>E. coli</i>	TTGAAACTTCTTACTGCCG	19	46	AATTTCTAATGCAGCGTATTG	21	795	750
yciQ	16127994	<i>E. coli</i>	ATAGCAGGGCTGTTGTATC	20	34	GACACGGAACCAAATTAAC	20	766	733
ymcA	16127994	<i>E. coli</i>	TATTGTCATCGCGCAGAG	18	541	TGTTGGGTGAAAGAGTAGC	20	1296	756
acoA	501025	<i>K. pneumoniae</i>	TAACGGCAAAGACGCTAA	18	380	TGACCAGGGCTTCTACTTC	19	880	501
acoB	501025	<i>K. pneumoniae</i>	CCTATAATATCTTTGCCACCA	21	440	CCAGGGATCCAGAGTTTT	18	974	535
acoC	501025	<i>K. pneumoniae</i>	GCTTGAAATGCCAAAGTG	18	18	CAGATCAGAAACAGAGATACGA	22	560	543
ahlK	31540968	<i>K. pneumoniae</i>	CAGTCAGGAACACAGCATT	19	31	TCTAAGGTATAAGCCGCATC	20	626	596
aldA	29243337	<i>K. pneumoniae</i>	GGGGAGAATATCCTTGCTT	20	397	GCAGCGGCCATAATTTTT	18	722	326
aldA	29243337	<i>K. pneumoniae</i>	GACTCGCGGGTGATTAAC	18	823	CAGTCCCTTAATCGCTTTC	19	1287	465
atsA	7963895	<i>K. pneumoniae</i>	AGGATCATTTGTCTCCTACG	20	1080	ATGGTGCCTTAGCAAAT	18	1598	519
atsB	7963895	<i>K. pneumoniae</i>	CTGATCAACGACGCATGG	18	361	GCGCTGAGCTGGTATCCT	18	680	320
budC	3907615	<i>K. pneumoniae</i>	CCGATCGAGTCCATTACC	18	280	GCGTACGGCGAATTTACT	18	480	201
cim	6176537	<i>K. pneumoniae</i>	AATTTAACCTGGTTTGATAAGAA	23	16	CAAAATATGAACTATCAGAAAGATTG	26	226	211
citA	924990	<i>K. pneumoniae</i>	GCCTGCTTCGTTGATAGATT	20	1261	ATACTGCCGCCTGCTTGT	18	1565	305
citW	18140905	<i>K. pneumoniae</i>	GCCACCTTTATTCTTCC	18	289	AGCATCCCCATCATATACAG	20	896	608
citX	18140905	<i>K. pneumoniae</i>	GTCAGCATCGAGGCATTG	18	31	CGTCAATCATCTGCTCAAC	19	520	490
cymA	854227	<i>K. oxytoca</i>	CTCTGCCTCTATTGCTCTTG	20	18	GCACTATATCCCTGCTCTTG	20	602	585
cymD	854227	<i>K. oxytoca</i>	TATCGATGCGGATGAAAAT	19	512	TTAATATAACCTTCAAGCAACACT	24	851	340
cymE	854227	<i>K. oxytoca</i>	ATCCAATGACCAGAAATGAG	20	210	AGATATGCGTAATCCACAGG	20	817	608
cymH	854227	<i>K. oxytoca</i>	CGTAAATATGGGACAAAGGT	20	1132	TAGATTTGCGACAGTCAAAG	20	1720	589
cymI	854227	<i>K. oxytoca</i>	GCAAGGGTAGAGGTGTATTG	20	8	TGGCTGTGAACTTTGTGTAG	20	535	528
cymJ	854227	<i>K. oxytoca</i>	ATAAGCCATGTGTTTCTTCC	20	174	CACGTTCTAGCGTCTACTCA	20	683	510
dalD	2905644	<i>K. pneumoniae</i>	GTTGTTCTCCACTACCCACT	20	637	AGATCACCTCAATCCAGAAA	20	1145	509
dalK	2905644	<i>K. pneumoniae</i>	GACTTCCGGTTTTTCACAC	19	106	CGGTACATGCGTTTTGTGTC	18	638	533
dalT	2905644	<i>K. pneumoniae</i>	CCAGCTCGGAAAATTCT	18	636	GGCGATTGTCCATAACGTC	19	895	260
ddrA	3115375	<i>K. oxytoca</i>	GCCGGTAATCTTGAGCTG	18	781	CCGATCTGCACGTCGATA	18	1163	383
fdt-1	1304134	<i>K. oxytoca</i>	CCTGCTCTATTCCGTCAG	18	5	GATTTCTGTACCCGGATG	19	404	400

gene	gi	source species	forward	length	position	reverse	length	position	product
fdt-2	1304134	<i>K. oxytoca</i>	GGCTGTCTGCTATGGATTT	19	85	GGTCGATCATCAGATTGG	18	619	535
fdt-3	1304134	<i>K. oxytoca</i>	TGGCGTTTATTTTCTGGA	18	2	GTAGCGTTGCATGGGATA	18	401	400
fimK	349480	<i>K. pneumoniae</i>	CCGTTACCGATGTTGATT	18	52	GAGTGAGGAGGGTATGTTGA	20	744	693
gatY	18139839	<i>K. oxytoca</i>	CGTTCTCCCCTGATTCTT	18	124	TCATAGCGGTGGCTCAGT	18	383	260
glfKPN2	765057	<i>K. pneumoniae</i>	CCGATCATGAGAACATCAG	19	617	GGCATCTCTTCCTGGTTAG	19	1130	514
hemly	24305989	<i>K. pneumoniae</i>	ATGAAACGACCTGATTGC	18	1	GTGTGGACCGAAGAATTG	18	465	465
hydH	12584123	<i>K. oxytoca</i>	CGGCGCATTAAAAATATC	18	908	CATTAACCGGCAAATAGAAC	20	1363	456
liac	19568920	<i>K. pneumoniae</i>	CCTGCTGCTATTGCTGTC	18	39	GTATGGTGCCAGATGCTC	18	728	690
ltrA	924990	<i>K. pneumoniae</i>	AGAGATGGGCTGCAAAC	18	132	CGATCCCTAAATGCTGTCT	19	715	584
masA	392019	<i>K. oxytoca</i>	TATTGAAGGCACCACCAG	18	24	GATGAATATCGGACAGGAAC	20	559	536
mdcC	2240010	<i>K. pneumoniae</i>	ACAGATTACATTGTCTTTCCTG	23	6	CCTCCTCAAAAACCTGTTC	19	286	281
mdcF	2240010	<i>K. pneumoniae</i>	ATGGATTTTGCTTACCC	18	121	CCAAGTAACATCACCAGACC	20	776	656
mdcH	2240010	<i>K. pneumoniae</i>	TATTTACCTTTCCCGGTCA	19	11	CAATCACGAACTGCGTTT	18	466	456
mrkA	149187	<i>K. pneumoniae</i>	TGCTGCTGATACCAATGTAG	20	63	GTAATTCGTAAGTCGCGTAG	21	599	537
mtrK	21264676	<i>K. pneumoniae</i>	CGCAATACCATACCTTCAC	19	5	CTCGTGATCTGATACGG	18	558	554
nasA	4755081	<i>K. oxytoca</i>	CCTGGAGTGTGCATAAGG	18	1610	CAGCGAAAGATGGATAATG	19	2166	557
nasE	2642135	<i>K. oxytoca</i>	ACACGCATATAAACCGCAAC	20	6	GAATCCAGCGTGGAGAGC	18	236	231
nasF	2642135	<i>K. oxytoca</i>	GCGATAAGTTTTCGATTTC	20	5	GCTGACCGATCCGTTTTT	18	463	459
nifF	43820	<i>K. pneumoniae</i>	GTGCGTTTAATCTCCTCAAG	20	11	GCTATCCGGACAACCTCG	18	230	220
nifK	43820	<i>K. pneumoniae</i>	AAATTGCCGAAGCTCAAT	18	649	CTGACGGTCATCAGCAGT	18	989	341
nifN	43820	<i>K. pneumoniae</i>	AGAGAGCGTCATTGAGCA	18	450	AATTTTCGCCAGTTGATG	18	849	400
pehX	17978816	<i>K. oxytoca</i>	ATGTCATGGTTCGATACTG	20	134	CTTTATCAAGCGGATACTGG	20	727	594
pelX	17981479	<i>K. oxytoca</i>	AAGCTGGAACGTACTAACGA	20	670	TAATCACTGCGGCTAATACA	20	1294	625
pSL017	7328180	<i>K. pneumoniae</i>	TTGCGTATATAGAAGTCATACCA	23	10	GCGTGAGCTGTCTACCAG	18	279	270
pSL020	7328182	<i>K. pneumoniae</i>	GATTCTGCTCTGACAACC	19	6	GCCTTGAATACTGGAAGAAAG	21	411	406
rcsA	24459262	<i>K. pneumoniae</i>	ATTGACGGGATATCTGACC	19	45	ACATTTGCGAGCATATTTGATT	21	445	401
rmlC	22759339	<i>K. pneumoniae</i>	CAGCAGCAAGGTGTTTAATG	20	90	GCAGTGCCAGAGTATGT	18	539	450
rmlD	22759339	<i>K. pneumoniae</i>	GGGGAGAAAGAGACCCTCA	19	511	TATTTGCCCAGGACTTCTGTT	21	890	380
tagH	18139839	<i>K. oxytoca</i>	ACAGGATAGCGAACACCTC	19	300	AAAGCCAGCTCCGTTTAG	18	802	503
tagK	18139839	<i>K. oxytoca</i>	ATCCATACCCTGACACTCAA	20	4	GATCAACAAAGGCCGTAA	18	537	534
tagT	18139839	<i>K. oxytoca</i>	GCTTCAGGTGTTGAAAATG	19	124	AGCAGCAGCATAAAATAACC	20	722	599
tyrP	6942303	<i>K. pneumoniae</i>	ACAGGGTTGATCCTCGTC	18	115	GTTAATGAAACGGCGAAAC	19	650	536
ureA	149330	<i>K. pneumoniae</i>	AAAAGACAAGCTGTTGCTG	19	21	CAGATAATCGGGTTGTGAA	19	302	282
waaG	5006979	<i>K. pneumoniae</i>	AGTAAATTCAGGCTGGCTCT	20	4	TTTACGTGGGTTACAGATATGG	22	183	180
wbbD	6137211	<i>K. pneumoniae</i>	TCATTGAAGAACGACACAG	20	22	GTCAGGCCATATTGTTGG	18	710	689
wbbM	765057	<i>K. pneumoniae</i>	TGCCTCTATTATCCAACCTC	20	54	GACGATCCAGAATGCTAAAC	20	634	581
wbbN	765057	<i>K. pneumoniae</i>	GGTTTAAGGCAGGTAGTCAG	20	203	CCACGATACATGAAACACAG	20	851	649
wbbO	765057	<i>K. pneumoniae</i>	ATTCATAAACTCGGATTGG	20	17	GGCAAACAGCACTACAGG	18	603	587
wbdA	6137211	<i>K. pneumoniae</i>	GTGGCATTGGTCGTTATAGT	20	50	CAAGGACGGACTCTTTCTC	19	655	606

gene	gi	source species	forward	length	position	reverse	length	position	product
wbdC	6137211	<i>K. pneumoniae</i>	TGACCTATCACTCGGATATTG	21	47	AGAGCTGGAAGAGAATGTATTT	22	496	450
wza	4808912	<i>K. pneumoniae</i>	AGGTTCAGGTAGCTGGAAAA	20	235	ATGATTCTGGGTTAGATCTCC	21	554	320
wzb	4808912	<i>K. pneumoniae</i>	TGATTCAATTTTAGTGATCTGC	22	6	AGGTGCTATCCGGCTAAT	18	285	280
wzmKPN2	765057	<i>K. pneumoniae</i>	ACATGATCCCGGAGAAAT	18	581	TTACAAAATCTCTGCAAATCG	21	780	200
wztKpn	3142231	<i>K. pneumoniae</i>	TTCAGGCGAAATGCTATG	18	536	TGGTTCCGTAGAGGAATAAG	20	1042	507
wztKPN2	765057	<i>K. pneumoniae</i>	TGGAACCACTGATCAATTTTC	20	2	GCTGCTGAACTTCCTTCC	18	388	387
yibD	5006979	<i>K. pneumoniae</i>	GCTATGAACTGATCCTGGTG	20	101	CGATATGGCGTACTTTATCC	20	778	678
yojH	2240010	<i>K. pneumoniae</i>	GGTGTCATCCCAAACCTG	18	124	GGTACCGAAGTGGTGGTC	18	348	225
aad	1015425	<i>P. mirabilis</i>	CGCTATTAACCTTGCTGAAC	20	207	CCTTTCTCACTACCACATC	20	734	528
atfA	1504104	<i>P. mirabilis</i>	TGAAAAAGTTATTATTATCTGCAA	24	2	ATCAGTGGAATAAGAGAAGC	21	501	500
atfB	1504104	<i>P. mirabilis</i>	AGATGAAAAGCTTGCTAATGA	21	333	TTAATGAACGATTCTTTTT	20	678	346
atfC	1504104	<i>P. mirabilis</i>	TGGCTGACTCTCCTGATG	18	119	TTGCAGATAGGTATTGATATGG	22	681	563
ccmPrmi1	3395515	<i>P. mirabilis</i>	ATGGATAATAAGCGAACACAG	21	1	GACATACTGCCACAACGAC	19	527	527
cyaPrmi	726356	<i>P. mirabilis</i>	TTATATTGAAACACTGAAGCAAC	23	9	CTCCTGCCCATTTGTTCTA	18	439	431
end	2673847	<i>P. vulgaris</i>	GTTCATAGGCTTCACGTAGTTC	22	1	GTCAAATCCATTACTTAGCACA	22	260	260
envZPrvu	2623217	<i>P. vulgaris</i>	CATCTTATTGTGGGTCCAAG	20	106	AAGAGCGAATACCTGATGAC	20	688	583
flaA	6959881	<i>P. mirabilis</i>	ATCACTTCTATCCAAACGAA	21	325	AAGTTGCTAAAGCGTCATCT	20	844	520
flaD	6959881	<i>P. mirabilis</i>	CAACAGTGATTTCCATTTGAG	21	18	ACGCCTTGAACCTTtagac	19	532	515
flfB	1857436	<i>P. mirabilis</i>	TTGTTGCAATACAGCCATC	19	7	CGATAAATTACAAAATACGTTTCA	24	415	409
flfD	1857436	<i>P. mirabilis</i>	AACTTTAGCCCCACTACTATCA	22	16	AATACCATTATCGGGGAAG	19	528	513
flfN	1857436	<i>P. mirabilis</i>	ACTCCGCCAGACCTTAGA	18	12	ATATTGAACGCTGTGCTTGT	20	415	404
flhD	2384645	<i>P. mirabilis</i>	GCGATTCTATGGCTGATG	18	116	TTATGCCCGTTTCTTTGTAG	20	351	236
fliA	6959881	<i>P. mirabilis</i>	ACACAATCCATTcatcagttag	22	301	TTTCGGGAAGCAATTCTAT	19	574	274
floA	1857436	<i>P. mirabilis</i>	TCTAATCTTAATTCCTCTGTTCT	24	62	TGATATAGACTTGATTAAGGTGATT	26	694	633
frdC	45917	<i>P. vulgaris</i>	CGTAAGCCTTATGTTCTGTG	19	13	TAAACAATTAGCGCCACTG	19	395	383
frdD	45917	<i>P. vulgaris</i>	AATCAGAATCAACTTCCTAAGC	22	4	AACACCAATAATTGCGATAAC	21	348	345
ftsK	1922904	<i>P. mirabilis</i>	TCTTTACTGAGCTTCCATCC	20	118	CATCACTATCTGGCTCTATTTG	22	745	628
gstB	1053074	<i>P. mirabilis</i>	TATTGAGCGCATTGATTTAC	20	78	CTATGCACATTAGGACGTTG	20	578	501
hemCPrmi	726356	<i>P. mirabilis</i>	TCATATCGCTGTATTACCTTGA	22	1	CTTATTAGCCGCCCTTAAC	19	301	301
hemDPrmi	726356	<i>P. mirabilis</i>	AGCGCAAACCTTCAGATAC	20	86	TTTAATCACTCGTCCTAGCC	20	592	507
hev	2394311	<i>P. mirabilis</i>	AATATTGGTCAAGCTGCAA	19	4	ATGTTCTGTCCCTGTTTGG	19	405	402
hpmA	150888	<i>P. mirabilis</i>	GACTTAATTGCTCCTCGTATTG	22	583	CGCGTCTAAGGTAACATCTC	20	1239	657
hpmB	150888	<i>P. mirabilis</i>	ATTAAGCGCAAATGAAACAG	20	54	GATATTGAGATGCCAAGGTG	20	675	622
infBPrvu	3850829	<i>P. vulgaris</i>	GCGAAGTAGAAGAGAAAGCA	20	359	TTTCAGAGTGGCGGTATT	19	892	534
katA	8347010	<i>P. mirabilis</i>	AAATAGTGGTGGTGTTCC	20	1152	TTAGCGTCTTCCCTTCTAAC	21	1451	300
lad	7007411	<i>P. vulgaris</i>	AGCTGATGTTGTTGTTGTTG	20	162	TTGATTGCACCTTTCTCTG	19	743	582
lpp1	150895	<i>P. mirabilis</i>	ATGAAAGCAAAAATTGTACTAGG	23	1	TTACTTGGTTATCTAGACGCTGA	23	220	220
lpsPrmi	14624978	<i>P. mirabilis</i>	AAAAATGTAGTGTTCAGATTTTAG	25	23	TCATAGCGATACTTTATTATGTTTT	25	472	450
menE	8347010	<i>P. mirabilis</i>	TGCACTTGTTTACGAGAGATT	21	32	GAAATGGCCTCTACTGTTTG	20	552	521

gene	gi	source species	forward	length	position	reverse	length	position	product
mfd	3360265	<i>P. mirabilis</i>	CAGACAATGCGTTTATTTTG	20	6	TACGTAATGCGGCGATTTC	18	278	273
mrpA	6453631	<i>P. mirabilis</i>	TAAATTAGCTTTAGTTCCTGGTTTAG	26	12	GTTTTGAGCAGCACTTGG	18	411	400
mrpB	6453631	<i>P. mirabilis</i>	TGGCACCACCTATTGCTATG	19	14	TTTTGGCGTATCGTTATTTT	20	513	500
mrpC	6453631	<i>P. mirabilis</i>	GATGGTAATGCTGATAATAACAAA	24	1504	ACTAACGCGGTGTAATGCT	19	2049	546
mrpD	6453631	<i>P. mirabilis</i>	CAATCTATGCCTCGCAA	18	431	AGCTGCCGTTTCTGTTACT	19	750	320
mrpE	6453631	<i>P. mirabilis</i>	AACAGTGGTTTAGCCCAAG	19	11	TGGCAACAAAATCTCCAC	18	517	507
mrpF	6453631	<i>P. mirabilis</i>	TTACTAAATTCTACAGCAGTAATGG	25	34	ATTGGTATTCTGCTAATAAGGTG	23	484	451
mrpG	6453631	<i>P. mirabilis</i>	CCGGTTCATATTGGGTCT	18	24	TCAGTCATAATTCAAATAGAAGGT	24	549	526
mrpH	6453631	<i>P. mirabilis</i>	CCTTCTAACGCCACTTACAC	20	109	ATGCGATAACCAACACTTTC	20	613	505
mrpI	6453631	<i>P. mirabilis</i>	AACATATGAGGGTGTGGACT	20	158	GAAGCAACGTAAATTTCTTACAC	23	565	408
mrpJ	6453631	<i>P. mirabilis</i>	TTGATTTTGCGAATATAGATGT	22	14	CAATAATGAAAAGCATCAGGT	21	323	310
nrpA	4097157	<i>P. mirabilis</i>	AAACAATAGATACTTTGCCACTT	23	8	TTCGCTGTTAATATCCCACT	20	776	769
nrpB	4097157	<i>P. mirabilis</i>	CTTGCCGTAGTTGAAGGTC	19	76	TACATTGGCATTAGCATCAG	20	591	516
nrpG	4097157	<i>P. mirabilis</i>	TTAAGTAAAGCTAAATCCAGAATG	24	73	ATAAATGATGTGGCAGGTTG	20	745	673
nrpS	4097157	<i>P. mirabilis</i>	ATTATTCTCGCCAGTGTTTC	20	1049	CGATACGTTTAGCACCTTG	19	1730	682
nrpT	4097157	<i>P. mirabilis</i>	AATGTAAATAAAGACAATGCTAACC	25	46	ATCTTGCCATGCTTCAAC	18	654	609
nrpU	4097157	<i>P. mirabilis</i>	TAAAGCATTCGGTATTCCAC	20	138	AGCGCATTATTCCATTCTAC	20	746	609
pat	3395515	<i>P. mirabilis</i>	AATTGGCTACTCCTCGATTAC	21	5	TGTTGTGCTAAAGGGTGTG	19	506	502
patA	14624978	<i>P. mirabilis</i>	TGGAGTATCAGAGCTATTTGT	23	34	AGTCAGCCATAATTTATCTAGTTTT	25	543	510
pmfA	515900	<i>P. mirabilis</i>	TGCGGCTTAGTATTTGG	18	27	GAAGTTGATAACGGCTTGG	19	537	511
pmfC	515900	<i>P. mirabilis</i>	TTTCTCACAAGCAGAGCAG	19	72	TCATCGCTTTGTAAATTGG	19	797	726
pmfE	515900	<i>P. mirabilis</i>	ATGCCGTATTAGATCACACC	20	137	TTTCCACATTACCAAAGTC	20	704	568
ppaA	2624374	<i>P. mirabilis</i>	AACAGGCACATTAACAGAGG	20	1146	TTTATCTTCAGGGAGCAATC	20	1689	544
pqrA	506865	<i>P. vulgaris</i>	TGGCTGAAAATGTCGTTAAT	20	2	AATGATTTAGCCGCTTCT	18	200	199
putA	6959881	<i>P. mirabilis</i>	CTATCAGCCACCTCTTCTTG	20	1172	CTAATGAGCATCGTTTAGCC	20	2105	934
rsbA	3320463	<i>P. mirabilis</i>	GCACACTGACCCAATTAAG	20	5	ATTAAACATGGTGCGATAGG	20	645	641
rsbC	3320463	<i>P. mirabilis</i>	TGGCTTGGAACACAATC	18	31	AATTCGAGTGATGGACAAAC	20	729	699
speB	31616612	<i>P. mirabilis</i>	CGAGCATGACACTAATAATGG	21	606	CCGCTTGCGAGATATAGCAT	19	946	341
stmA	3769579	<i>P. mirabilis</i>	TACGTACATCGCCACCAG	18	157	AAAGGAACAGGACTACTTTGAG	22	479	323
stmB	3769579	<i>P. mirabilis</i>	GAAATACGCATTAGGCTCTG	20	3	GCGTTATAGCAGTTTAATCCA	21	362	360
terA	5702376	<i>P. mirabilis</i>	CAAGGTTTCGCTAACTAAAGAG	22	540	ACTTTGATTGATCCGTTTTTC	20	1055	516
terD	5702376	<i>P. mirabilis</i>	TTCTAAAGGTGGTAATGTTTCTT	23	15	GCATATCCTTGGCCTACA	18	530	516
tna2	150910	<i>P. vulgaris</i>	CTAAATATGGCGCAGGAAC	19	197	ATAGTGCCAATCATCCAAAG	20	749	553
uca	881951	<i>P. mirabilis</i>	GCACTAGCTACTATTCTTCTGCT	24	19	AACGGTTGCTTTTACATCC	19	519	501
umoA	3360256	<i>P. mirabilis</i>	GAGCCTTGTTTATCCCTCTT	20	11	TCTATCCCAGCGGTTAAAA	19	510	500
umoB	3360259	<i>P. mirabilis</i>	GCTCATATCATCTTCCATCC	20	92	CCTAAGCAAATTAACGAACC	20	641	550
umoC	3360262	<i>P. mirabilis</i>	AAGATAGGTACGCTTTTAATTCT	24	4	AGTAATAATTTAGTCGCCATT	22	404	401
ureDPmi	150914	<i>P. mirabilis</i>	GAGGTACTGCATCGCAA	18	275	TACCTTCTCTAAATGGTGTGA	22	657	383
ureEPmi	150914	<i>P. mirabilis</i>	GCGCTTGAACCTCTAC	20	37	GGATGACCCACCATAAGC	18	450	414

gene	gi	source species	forward	length	position	reverse	length	position	product
ureFPrmi	150914	<i>P. mirabilis</i>	GCTCAGCAGAAACCTTGTC	19	110	CTGGCGTAAACTGCCAATA	19	609	500
ureR	45657	<i>P. mirabilis</i>	TCACAGTCACCACTAATCTCAC	22	122	ACGAAACGCCCTCTTTAC	18	634	513
urg	45933	<i>P. vulgaris</i>	GAAAGGACTTAAACTTAACTATCCAG	26	75	AGGGTCGTGAATAGAAACAAG	21	294	220
xerC	2645801	<i>P. mirabilis</i>	ACGTCCCTGAAACACTCTC	19	17	AACCAATGCTGTAACCACTC	20	599	583
ygbA	3395515	<i>P. mirabilis</i>	CAGGAACGGGTTTCTTATC	19	33	GCTTATAAAAGACTAGATAAATGTCG	26	225	193
zapA	3493594	<i>P. mirabilis</i>	GGGATCTTCTATAACTATTCAACC	24	67	TAACCTGGAACATTCTGACC	20	626	560
zapB	3493594	<i>P. mirabilis</i>	TTTCTTTGATCTACCTTGGTTC	22	408	TGTAGGCTGCTTTACTACTATCC	23	916	509
zapD	3493594	<i>P. mirabilis</i>	AAGAACAAGTAGCAGGTAAAGAG	23	128	CAGTTAGCTTTGCGATGTG	19	703	576
zapE	3493594	<i>P. mirabilis</i>	CCAATTACTTCTATCTACCTGATG	25	28	GTTCCAGAGTATTGGTATTGTTC	23	653	626
algB	150990	<i>P. aeruginosa</i>	CACTTTCCGTTATTGCCTC	19	66	GAGGATGAGGATGTTGGC	18	522	457
algN	150999	<i>P. aeruginosa</i>	GACTGGCTGAATCGTCTC	18	76	GCAGGTCGTACCAGGAAG	18	364	289
algR	151003	<i>P. aeruginosa</i>	ATTGTCGATGACGAACCTC	19	13	TTCAGGTAGAGCTGGAATG	20	671	659
aprA	45279	<i>P. aeruginosa</i>	CATTGAAAGGTCGTAGCG	18	20	CGACGAAGTGGATATTGG	18	364	345
aprE	45279	<i>P. aeruginosa</i>	GGTCAAGCACATCCTAGTG	19	186	ACTTCCTTGCGGTACTCC	18	761	576
ctx	45312	<i>P. aeruginosa</i>	CCGAAGGACTTGGTTACT	19	148	CTATGGAAGGTGCCTGTG	18	728	581
ExoS	13892017	<i>P. aeruginosa</i>	CGTTTGGGACAGATTGAG	18	67	GATACTCTGCTGACCTCGC	19	695	629
fpvA	1633044	<i>P. aeruginosa</i>	AATGCGATAACCATCAGC	18	331	CCGTCGTACTGGAAGTTG	18	662	332
glpR	1399486	<i>P. aeruginosa</i>	CAAGCACAACAAGAAATACG	20	9	TAGACCTCCGAAGAGTTGC	19	683	675
lasRa	309873	<i>P. aeruginosa</i>	CTGGGACGTTAGTGTCATC	19	96	GTCTTGGCATTGAGTTCG	18	551	456
lasRb	151325	<i>P. aeruginosa</i>	GAGCGACCTTGATTCTC	18	81	ATAAGACCCAAATTAACGGC	20	710	630
lipA	45340	<i>P. aeruginosa</i>	AAGAAGTCTCTGCTCCCC	18	7	ACGATTTCTCCACCTGT	18	281	275
lipH	483463	<i>P. aeruginosa</i>	ATGGCAGTTTCAGTGTCG	18	53	CGAAATAGTCGTCCAGCC	18	700	648
Orf159	4545246	<i>P. aeruginosa</i>	AATGTCGGCATCATTCTC	18	28	GTAGACCTCGCGTTGAA	18	432	405
Orf252	4545242	<i>P. aeruginosa</i>	GACCTGCTGTTCCAGTTG	18	172	AATTCACGGGTTTTCTCG	18	713	542
OrfX	1399486	<i>P. aeruginosa</i>	ATGGATGCTCGGGTACTG	18	97	CTCAGCTACAGCCACGAC	18	420	324
pa0260	15595198	<i>P. aeruginosa</i>	GATCGTCTCTGCCAGTC	18	27	ACATTGATGGTGTCGTCC	18	695	669
pa0572	15595198	<i>P. aeruginosa</i>	AGGAGAGAACATGAGTCGC	19	36	TCCTTGTCCCAGTAGTTACC	20	845	810
pa0625	15595198	<i>P. aeruginosa</i>	AGGAGCAACTGAAGCGAC	18	236	TCTGCCTTTACCCAGGAC	18	759	524
pa0636	15595198	<i>P. aeruginosa</i>	AAGGTTGGCAGGATCAAC	18	76	CTAGTGGCGAAATTGAACAG	20	779	704
pa1046	15595198	<i>P. aeruginosa</i>	AGGCATCCATCGAGCTAC	18	386	AACGTCCGAGCAGGATAC	18	619	234
pa1069	15595198	<i>P. aeruginosa</i>	GCGAGGAGGTATTCGACA	18	539	CCCTTCTGCGAGTAGTGTT	19	887	349
pa1846	15595198	<i>P. aeruginosa</i>	AAGGACTTCTGGTCGGTG	18	286	CAGGAACAGGTGCTCGTAG	19	687	402
pa3866	15595198	<i>P. aeruginosa</i>	TTCCCTAACGAATGCTGTC	19	1365	CGTTGCTCCCTCATACAC	18	1878	514
pa4082	15595198	<i>P. aeruginosa</i>	CGAGCACCAATATCGAAC	18	1148	GAGCCGTAGGTGTTATCG	18	1751	604
pchG	4325021	<i>P. aeruginosa</i>	CCTGCTCAACACCTTCTATC	20	354	GTCGAACAACGCGAACAG	18	780	427
PhzA	5616088	<i>P. aeruginosa</i>	GTTGAAAGGGTTTACCGAC	19	18	AATTTCTGCATCGGGTTC	18	434	417
PhzB	5616088	<i>P. aeruginosa</i>	ATGCTCGATAATGCTATTCC	20	1	TTCTCGTAGTAACCCTCGG	19	356	356
pilAp	18535593	<i>P. aeruginosa</i>	GCTTTACCTTGATCGAACTG	20	17	TCAATAGAGCCAGTCACACC	20	428	412
PilAp2	21629637	<i>P. aeruginosa</i>	TGCCGTGAGTGAAATCAG	18	123	CGTAGTTGGCTTTCCAGTT	19	442	320

gene	gi	source species	forward	length	position	reverse	length	position	product
pilC	18535591	<i>P. aeruginosa</i>	GGTATCAACCCACTAAAGGTC	21	127	GTCCAGAGCTTCTACCAGAG	20	864	738
PLC	151492	<i>P. aeruginosa</i>	GACTTCGCTGTTCGACTTC	19	1356	TCGGTTCGAGTTCATAGC	18	2026	671
plcN	151497	<i>P. aeruginosa</i>	GTGTTCCAGGTGTTTCGAC	18	1570	GATAGACGTTGTCCTTGACC	20	1873	304
plcR	151499	<i>P. aeruginosa</i>	ACAACCTGGAACAGCAACT	19	23	CGACTCTTGCGCGTATTC	18	324	302
PstP	4545246	<i>P. aeruginosa</i>	GAAGTGAAGTCCGCCAAG	18	31	TCGAGCATCATCAGGTAGAC	20	770	740
purK	1621599	<i>P. aeruginosa</i>	TCGAGAAGTCGATGTTCAAG	20	299	CTTGCCGTAGTGATGCAG	18	978	680
pvdD	1633044	<i>P. aeruginosa</i>	GTCAAGGGTGTTGTCTGC	18	6665	CTCTGCACAAACTCAGGG	18	7386	722
pvdF	1633044	<i>P. aeruginosa</i>	AAGTCGGTACTGGAGTCCTT	20	100	TCAGCACATCATGGAACA	18	715	616
pyocinS1	286179	<i>P. aeruginosa</i>	CTTCAGTTCCGAGATGCC	18	241	GTAACGAACGCTATCGGG	18	981	741
pyocinS1im	286179	<i>P. aeruginosa</i>	ATATACGGAAAAAGAGTTTCTTGAG	25	21	AGCACGCCATTCTTTAACTTC	21	231	211
pyocinS2	286182	<i>P. aeruginosa</i>	TATACGGCTTCAGACTTTCC	20	382	TGGCATAAGTATTGGCAG	18	970	589
pys2	15595198	<i>P. aeruginosa</i>	TCGCCAATAAGAAGAAATTG	20	758	AGTGGTACTCGAAGGGTTCT	20	1509	710
pys2	15595198	<i>P. aeruginosa</i>	ATCCAGTATATTCTGCTCG	20	70	TGCAATTTCTTCTTATTGGC	20	779	752
rbf303	836903	<i>P. aeruginosa</i>	ATCGTTCTGGTCTTCTTG	19	157	ACCAAAGAGTGTTGATAGCC	20	895	739
rhlA	452502	<i>P. aeruginosa</i>	AGTCTGTTGGTATCGGTTTG	20	13	CTCCAGGTCGAGGAAATG	18	768	756
rhlB	452502	<i>P. aeruginosa</i>	AACGCTTTCTCGATCAGG	18	731	GATACTGTGCGGTTGTGA	18	1203	473
rhlR	1117916	<i>P. aeruginosa</i>	TTCGATTACTACGCCTATGG	20	118	GGTCCATTGCAGGATCTC	18	576	459
TnAP41	216903	<i>P. aeruginosa</i>	CCCCTATTCCATACCTTACC	20	86	TATTGAGGACGCTGATTTTC	20	604	519
toxA	15595198	<i>P. aeruginosa</i>	GTGCGCTACAGCTACACG	18	328	CTTGCCTTCCCAGGTATC	18	744	417
uvrDII	3249556	<i>P. aeruginosa</i>	AGACCTACAACAAGGTTTCG	20	281	TGAGGATAGTCCCTTCGC	18	490	210
vsmI	695153	<i>P. aeruginosa</i>	ATTCTCTCTGAATCGCTG	19	9	AATATCTTCATCGCCAGTTG	20	359	351
vsmR	695153	<i>P. aeruginosa</i>	AGGAATGACGGAGGCTTT	18	4	GGGTTGGACATCAGCATC	18	533	530
xcpX	45433	<i>P. aeruginosa</i>	TTCAACCTCAACGGACTG	18	328	TGCAAGGTACTCACCAGC	18	896	569
5triphosphatase	3786332	<i>C. albicans</i>	GACACTCCGTCAGATTCAAC	20	148	ATTCCCCTCATCAACATTAG	20	684	537
AAF1	1177214	<i>C. albicans</i>	ACATAGTCAGCCACAACCAC	20	564	GCACTCGAATTGTTATTTCC	20	1124	561
ADH1	608689	<i>C. albicans</i>	TCAAGAAAGCTACTGATGGTG	21	701	ATTTACTGGTGTCCAAGACG	20	1051	351
ALS1	704426	<i>C. albicans</i>	CTCAGTCCTTTGCTACAACC	20	1334	AACGGTATCAGTTTCACCAG	20	2040	707
ALS7	9754770	<i>C. albicans</i>	AACGGTCATATCCAAAGAAG	20	42	ACCCATGAAACAAGGTGTAG	20	627	586
ARG56	1770097	<i>C. albicans</i>	AAACGCATTGTTAAGAGACC	20	1068	ACCTCTAGCACCAATCAAAG	20	1629	562
ASL43f	3598683	<i>C. albicans</i>	CAGGTAAGTCAAAGTCTGGTG	21	476	ATTGCCACCTTGTATATTGG	20	999	524
BGL2	532775	<i>C. albicans</i>	GATTAATGACATCAAGGGTTAGT	24	402	GCAAAGCTTGCATAACATC	19	631	230
CACHS3	218361	<i>C. albicans</i>	TCTGGTGAAGGTTTAGGAAG	20	61	ACCACTTGACTCGAACAAAC	20	692	632
CCN1	510578	<i>C. albicans</i>	TCGACCATACCATCCAATAC	20	69	TTCACAAAGAAACCTAGCAAC	21	681	613
CCT8	3419680	<i>C. albicans</i>	CACCAAACTCAGGCTTATTC	20	23	AGACCATACCTTGACCAC	19	655	633
CDC28	520627	<i>C. albicans</i>	AGAAATTTGGCCTGATGTTA	20	690	GGTGTTTGTCAATCCCAATA	20	940	251
CDC37	18029900	<i>C. albicans</i>	GAATGCAAAGAAACATTGAAA	21	125	CCGTATGCAAAATCATCACT	19	589	465
CEF3	2497	<i>C. albicans</i>	TGTCTGCTGCTAGTGAATCC	20	2	AAGCAATTTGAGCTTTAGCA	20	505	504
CHS1	2501	<i>C. albicans</i>	TGACAGGTTCAATTGGTGTC	19	1412	ACAGCCTCAAATTCCTCAC	19	1937	526
CHS2	170844	<i>C. albicans</i>	TCAGATGGTGATGAACTGTC	20	76	GACTTCTTGTTGTGGAGGAG	20	696	621

gene	gi	source species	forward	length	position	reverse	length	position	product
CHS4	2073104	<i>C. albicans</i>	AACTAGGGCTGCTAATGTTG	20	1434	TTGAGCAAGAGATCCTGAA	19	2040	607
CHS5	3551164	<i>C. albicans</i>	AGTCAGAGCAGGGTCAATC	19	108	ATGTCGGGTAAGACACAATC	20	800	693
CHT1	15530177	<i>C. albicans</i>	GTCAACAACAAGGCAAGAC	19	260	CTAGCCACGACTCTTTGAAC	20	770	511
CHT2	571426	<i>C. albicans</i>	CTGTCAAGAACTGACGTTG	20	129	TTGTTGTAGAATTGGATGAATG	22	638	510
CHT4	11496138	<i>C. albicans</i>	TTGGCTCGATTAAGAAATAAA	21	496	CTGAAACATCACCAGCAGA	19	1072	577
CLN2	510580	<i>C. albicans</i>	AACAGCAACCAGAAATCAAG	20	191	TTAAATCAACAGGAATCTTCAAC	23	754	564
CPH1	558949	<i>C. albicans</i>	GCTACCACTTTAACCGACAC	20	643	CTTCTCCACCATTAGCACTC	20	1222	580
CSA1	3406797	<i>C. albicans</i>	GCTCCATCTAGCAACTCATC	20	2695	GAGACCAACAAACACGAAAC	20	3603	909
CYB1	1103927	<i>C. albicans</i>	TTTCATCACCACTCAAGTC	20	140	ATTTCAACAAGCCAATCAAC	20	743	604
EDT1	25989656	<i>C. albicans</i>	AACATTAGAAACGGAACAGG	20	28	CTCAGTTCTGCATTGGTTC	20	719	692
EFG1	6468469	<i>C. albicans</i>	CCAGCAAACAATTCTTAATC	20	342	TTCCCATTAACCGCTAGAAC	19	1076	735
ELF	2707896	<i>C. albicans</i>	CAAAGTTCACCATTTC AAC	20	292	ATTGATCCTAATGCTTCCAC	20	797	506
ESS1	12655855	<i>C. albicans</i>	ATCGACATCAACAGGCTTAC	20	6	TCTTTGGAGGATATGGACAC	20	525	520
FAL1	6468269	<i>C. albicans</i>	CAATAGCACAGGCACAATC	19	197	AAATCTCATCCCTCTTACC	20	703	507
GAP1	18568389	<i>C. albicans</i>	TTCATTCAAACAGCCTTAC	20	102	TTCACCATACCATCTTACACC	21	636	535
GNA1	4115734	<i>C. albicans</i>	CACAAGTTATACATTAGAAAAC	24	11	CTACATACCATTCAACACCAC	22	443	433
GSC1	2274846	<i>C. albicans</i>	AAACCATAAATCAACAACCAC	21	1448	CACCAACACATCTCATTGTC	20	1987	540
GSL1	2274848	<i>C. albicans</i>	TATTATGGCGATTCCACAG	19	724	CAGCCCCAATTCTTGTTTC	18	1297	574
HIS1	4033356	<i>C. albicans</i>	CGTTTGTTATTTGCTGTTCC	20	28	GCTGCTTTCATAGTTTCACC	20	533	506
HTS1	21724236	<i>C. albicans</i>	AGCTAAATCCAAAGACGATG	20	249	CCTTGATTATGCGAGAAATG	20	787	539
HWP1	4028879	<i>C. albicans</i>	GCTACCACTCCAACACTTC	20	709	AGACGACAGCACTAGATTCC	20	1738	1030
HYR1	11121427	<i>C. albicans</i>	TTGGTGGGTTAGAAGTTGAG	20	176	TTGAAACAGCATGAACAATC	20	703	528
INT1a	1144530	<i>C. albicans</i>	CAAGAGAAAGGGAAAGAAGAG	21	184	AGGTTTCGTCGTATGAAGTG	20	711	528
KRE15f	170875	<i>C. albicans</i>	CGTTAACTCAGTCATATACTACATTTT	27	6	GCAATAAAAGAAACCCCAAT	20	365	360
KRE6	1944423	<i>C. albicans</i>	GATCCAGATGCTGTAACCAC	20	1171	CATCGTAAATAACCCGTTTC	20	1871	701
KRE9	3435197	<i>C. albicans</i>	TAATTTCCCTTGTTGTTTCC	20	23	TCAATCCAACCATCTTCTTC	20	816	794
MIG1	4688626	<i>C. albicans</i>	ACATTCATTGGGTTTCATCTC	20	903	ATTGGTGGTAATTGTGTTCC	20	1556	654
MLS1	6980008	<i>C. albicans</i>	TGTCCAGAAAGTGCTAAAC	20	60	AATACCACCGGAAACTGG	18	588	529
MNT1	1480085	<i>C. albicans</i>	GCTCGTTTGATTAGATTGG	20	22	TGTTACGGACTAAAGCAG	19	584	563
MP65	12057030	<i>C. albicans</i>	TTAGTCATCAACATCATCAAC	22	58	GCTTTAATTGACTTGGAGTG	21	704	647
NDE1	7270979	<i>C. albicans</i>	ACTGTCGTTTCTGGTCATTC	20	574	ACGAGTGAAATCTCTTGGTG	20	1209	636
PFK2	4490768	<i>C. albicans</i>	GGTACGAACAGACAACACC	20	1921	AACAGCTCTAATGGCAATC	20	2586	666
PHR1	8132881	<i>C. albicans</i>	TTAGCCAAGTTTGAATCGTC	20	55	AATTTCTTCGTCATCATTGG	20	642	588
PHR2	2293529	<i>C. albicans</i>	TCAATCTTGGCTGCTACTTC	20	25	GGCTAATGAACTCTGATGG	20	633	609
PHR3	6911252	<i>C. albicans</i>	ATTGGGTATCAACACCATTTC	20	114	CCATAGTTGTTTGGTTCCTG	20	797	684
PRA1	1916851	<i>C. albicans</i>	ATTAGCTGAACATGCCAGAG	20	192	ATCTCCATTGCACCCTTC	18	723	532
PRS1	1276446	<i>C. albicans</i>	GATTTACACGCCTCACAAA	19	391	GCAATAACAGCAGAAATATCAA	22	896	506
RBF1	1378025	<i>C. albicans</i>	AACAGCAAGCTGCTCAGT	18	1082	TTACAAAAACCCACTTCTTTTC	22	1584	503
RBF1	1378025	<i>C. albicans</i>	CCCAACTAATTCAGCATCAC	20	36	GTACCAATTCGGCTTACTG	20	589	554

gene	gi	source species	forward	length	position	reverse	length	position	product
RBT1	9963981	<i>C. albicans</i>	TACCACGATAGCTCCATTTTC	20	136	ACCCAAAGTTCTCTTGCTG	19	741	606
RBT4	9963985	<i>C. albicans</i>	GTGGTGTACTGTTGGTGAA	20	83	GTAGCATCCCAAGTCAAATC	20	707	625
RHO1	2766184	<i>C. albicans</i>	AAGAGATGATCCTCATACTATTGAA	25	375	CAAGACAACACATTCTTCTTC	22	594	220
RIM101	5802567	<i>C. albicans</i>	GTCCTTTCAAGTGTGTGG	20	443	TATTGTGTGTGGGTGTTG	20	1166	724
RIM8	5802569	<i>C. albicans</i>	ATAACCCACATAAGGTCTGG	20	119	AGCTAGTTCGTGGATCTTTG	20	661	543
RNR1	7271005	<i>C. albicans</i>	TAAGAGAGATGGCCGTAAAG	20	12	TTACCGTGAATACCGACAG	19	542	531
RPB7	12655857	<i>C. albicans</i>	TTTTGGACCTCAAATGGAC	19	51	AAATAGTCTTCTTTATGCTTCCT	24	503	453
RPL13	4115901	<i>C. albicans</i>	CCAAGAACTTACCATTATTGAAC	23	11	TTTCGTTTCTAGCCAATCTC	20	535	525
RVS167	7271023	<i>C. albicans</i>	TTAAAGGATTCAAAAAGGGTGT	22	8	AATAATTCTTGTGCTGGTTCA	21	407	400
SEC14	897694	<i>C. albicans</i>	TGACTACGATGACTACTGAAGAA	23	2	TTTTAGCAACAATGGGTTTT	20	316	315
SEC4	2642181	<i>C. albicans</i>	ATTGGTTTCAAACAGTTACTCA	22	320	ATTCTCTTCAACATGCTTCTCT	22	549	230
SHA3	7271025	<i>C. albicans</i>	CATGGCACCAGAAAGAAC	18	123	AATTGTTGGTTTGCAGTAGG	20	644	522
SKN1	1944425	<i>C. albicans</i>	TATAATGCCCCGAAAATAAA	20	19	TTAAGCGGATATCTATCGTACC	22	518	500
SRB1	3777502	<i>C. albicans</i>	TGGAACCTGTTGTACTTGAC	21	684	CTAGCCCACTTTCCAATTC	19	962	279
TCA1	2852981	<i>C. albicans</i>	GATTTCTAGCCGGAATG	18	21	ATTATGTAACCTTAGTCGTAATTGTC	26	617	597
TRP1	3419680	<i>C. albicans</i>	AAGACGACTGAGCGTGTC	18	3	TGGACTGGAAGATAAGCTAGAG	22	352	350
TUP1	2245633	<i>C. albicans</i>	AAAGAGCTAACCACGTCAAG	20	443	GATCGACAAAGTCAAGGAAC	20	1017	575
YAE1	7271003	<i>C. albicans</i>	ACATGTCAAGAGGATTGTTC	21	4	TTTACATTGATTGATTAATTTGC	24	333	330
YPT1	15077427	<i>C. albicans</i>	AGGTGGTGTCATGAAATTATTAG	23	333	ACAGGAATTCGATTGGTTAG	20	618	286
YRB1	13518294	<i>C. albicans</i>	GCCGAAGATACTAAACAAA	20	7	TCAGAAACATCAGCAGTAACA	21	530	524
YST1exon2	7270972	<i>C. albicans</i>	TCTGATGTTGCTGTTTGTTTC	20	121	ATCTTCAGTTTCACCAGTCC	20	633	513
ZNF1CZF1	170941	<i>C. albicans</i>	TTGCCAATCAGCATTAC	18	448	ACACCTTGGTCTTGTTTCAC	20	1005	558
abcXStrpmut	2952523	<i>S. mutans</i>	GAAATGATATTGACGGGACT	20	41	TCAACACAAGGACAGGTTG	19	621	581
acrA	17973457	<i>P. mirabilis</i>	CTGGCTCTGTAGTGCTTTC	20	28	CTGTTACCGTTGATTACCTG	21	571	544
acrB	17973457	<i>P. mirabilis</i>	CCTTTGAAGCTGGTACTGAC	20	278	CTGTGAACCGTCTTGATTG	19	777	500
acrR	17973457	<i>P. mirabilis</i>	TGTCATCATAGCTCTTAACATAATC	25	130	CTAAACGCCAAGCACAAAG	18	632	503
albA	22135424	<i>K. oxytoca</i>	TGAGCAGCGTAACCAGAC	18	60	AGTCATCCACGTTCTTTTC	19	591	532
arr2	12024948	<i>E. coli</i>	GCAAGGACCGTTCTATCA	18	48	CTTCAATGACGTGTAAACCA	20	448	401
cadBStalugd	1658278	<i>S. lugdunensis</i>	GAGGTGTAATTATGATTCAGACTATT	26	3	TCGTACCAACTAATTTAGACAATC	24	346	344
elkT-abcA	1841513	<i>S. aureus</i>	ATTAGAAATTGCGACTGGTG	20	786	AGCGTGTCATATCCTTCATC	20	1394	609
emeA	22775586	<i>E. faecalis</i>	GACCAGGAGTTGGTGGTT	18	464	AACAGCTGACAAATCAACG	19	806	343
mexA	5616092	<i>P. aeruginosa</i>	CTCGACCCGATCTACGTC	18	34	GTCTTCACCTCGACACCC	18	536	503
mexB	5616092	<i>P. aeruginosa</i>	TGTCGAAGTTTTTCATTGATAG	22	2	AAGGTCACGGTGATGGTC	18	281	280
mexR	886021	<i>P. aeruginosa</i>	GAAC TACCCCGTGAATCC	18	3	CACTGGTCGAGGAGATGC	18	413	411
mreA	7548683	<i>S. aureus</i>	TACGATGACACCACTCTTTG	20	15	ATCGACAAAACGTACAGGAT	20	756	742
msrCb	6687492	<i>E. faecium</i>	AGAACATATCCGCAAACAAG	20	30	TGATGTAACAAAATCGTTCC	21	399	370
norA23	4115706	<i>S. aureus</i>	GGT TACTGTTGCTGCTTTT	20	122	CGTAATCGCAATCGAATA	19	735	614
nov	558416	<i>E. coli</i>	AACCGTTTATACGTTGGTGAG	21	6	GATTAACGCCTGCATCAC	18	405	400
qacEdelta1	12024948	<i>E. coli</i>	AAGGCTGGCTTTTTCTTG	18	5	AATTATGAGCCCCATACCTAC	21	285	281

gene	gi	source species	forward	length	position	reverse	length	position	product
rtn	558808	<i>P. vulgaris</i>	CCTGAAATCCACTACTGACC	20	180	CCAACGACAGTTCCACTC	18	752	573
sul	17129524	<i>E. coli</i>	CATCGTCAACATAACCTCG	19	27	AATTCTTGCGGTTTCTTTC	19	810	784
sull	12024948	<i>E. coli</i>	CTCTTAGACGCCCTGTCC	18	202	GTTTCCGAGAAGGTGATTG	19	785	584
uvrA	2696019	<i>E. faecalis</i>	GCGTAGAACGTGGACTTG	18	86	TCATAAATGGACCGAATACC	20	668	583
wbbl	22759339	<i>K. pneumoniae</i>	ATAAAGCAATGAAGCCTAAAGT	22	8	TTTACGATCAAGGAACCATC	20	777	770
wzm	22759339	<i>K. pneumoniae</i>	ATGAAAAACCCTCATCAAAA	20	1	GGGAAAAAGACCAAAGGTAA	20	500	500
wzt	22759339	<i>K. pneumoniae</i>	ATGTTCTCGTGCAGTTC	18	722	ACCAAACTTTATTTTCATCATC	23	1261	540
aacA_aphDStwar	31074829	<i>S. warneri</i>	AGTTGAAAATGAAATATGTATAAGAAC	27	9	AACTGCATTAGCATTTCCTTC	21	399	391
aacA4	14276839	<i>P. aeruginosa</i>	TGCGATGCTCTATGAGTG	18	18	GTACCTTGCCCTCTCAAACC	19	440	423
aacA4	14276839	<i>P. aeruginosa</i>	GCTAAATCGATCTCATATCGTC	22	36	GGCGTGTTTGAACCATGTA	19	487	452
aacA-aphD	3676412	<i>S. aureus</i>	AGATTTGCCAGAACATGAAT	20	473	TGTTGCATTTAGTCTTTCCA	20	1085	613
aacC1	13094933	<i>P. aeruginosa</i>	CCTGACCAAGTCCAATCC	18	31	TAGATCAGTAAGCACCAAG	20	359	329
aacC1	13094933	<i>P. aeruginosa</i>	TCATTGCGACATGTAGGC	18	8	GGGATCGTCACCGTAATC	18	387	380
aacC2	45769	<i>E. coli</i>	GACCGATCACCTACGAG	18	184	CGAAATGCTTCTCAAGATAGG	21	799	616
aadA	3540256	<i>E. faecalis</i>	GCCGAAGTATCGACTCAAC	19	19	AGCACTACATTTGCTCATC	20	563	545
aadB	623029	<i>E. coli</i>	GCAGGTCACATTGATACACA	20	60	CATATCGCGACCTGAAAG	18	574	515
aadD	21623792	<i>S. aureus</i>	GCTATTGGTGTTTATGGCTC	20	97	CTGATTGCTTAAGTCTTCA	20	598	502
aphA3	3138990	synthetic construct	AAGATACGGAAGGAATGTCTC	21	124	ACAAAGATGTTGCTGTCTCC	20	655	532
aph-A3	1272325	<i>S. aureus</i>	GAGAATATCACCGGAATTGA	20	12	GCTCGACATACTGTTCTTCC	20	718	707
strA	17222205	<i>E. coli</i>	CTCATTTGGCTCAAAGGTC	19	163	TGAATAGGACAGCGAAGG	18	727	565
strB	17129524	<i>E. coli</i>	AAGTTTCATTGCCAGACG	18	86	TAGACTGCGTTGCTCCTC	18	792	707
ampC	28864526	<i>K. oxytoca</i>	TTATCTGCAACACTGATTTCC	21	13	TTTCCGGCACAGTAATAAAG	20	637	625
bla_FOX-3	1841437	<i>K. oxytoca</i>	CTTACTATCGGAGCTGGTCA	20	461	AGGGCATCTCCCTGATAC	18	800	340
blaA	522103	<i>P. vulgaris</i>	TCACTCATTAACCATTGCTG	20	26	GTATGCTACTCAAGGTGCTG	20	793	768
blaB	522103	<i>P. vulgaris</i>	ACACTGGCTGAATTAAGTGC	20	367	AACCCGCTTTAATACTGTTATC	22	688	322
bla-CTX-M-22	19526203	<i>K. pneumoniae</i>	TCACGCTGTTGTTAGGAAG	19	50	AGGCTGGGTGAAGTAAGTG	19	807	758
blaIMP-7	13094933	<i>P. aeruginosa</i>	ACTGACGCTTATTTGATTGAC	21	178	GTACGTTTCAAGAGTGATGC	20	680	503
blaIMP-7	13094933	<i>P. aeruginosa</i>	TTGACGAAGGCGTTTATG	18	89	TGTGACTTGAACAACCAG	19	646	558
blaShaemolyt	8574410	<i>S. haemolyticus</i>	GCCAATAAGCAAGTTGAAATA	21	4	ATTTAAATGTCTCGCAATTCT	22	363	360
blaOXA-1	152062	Plasmid RGN238	TTTGAAGGAAGTGAAGGTTG	20	109	TTCTATTTGCTGTGAATCCTG	21	673	565
blaOXA-10	12024948	<i>P. aeruginosa</i>	TAGCTCGTGCATCAAAGG	18	167	AACCTCTGTCTCCTTCTCAAC	21	696	530
blaOXA-2	47874	<i>S. typhimurium</i>	CACGATAGTTGTGGCAGAC	19	126	ACTCAACCCATCCTACCC	18	676	551
blaOXA-32	14276839	<i>P. aeruginosa</i>	ACGTTCTGACTGGAGGAAG	19	81	TTCAATAGAGCGAAGGATTG	20	783	703
blaOXY	18844705	<i>K. oxytoca</i>	GACAATACCGCATGAATA	19	400	CCGGTGGTATTGCCTTTTA	19	659	260
blaOXY-KLOX	32130556	<i>K. oxytoca</i>	TGTGCAGTACCAGTAAGGTG	20	385	CTCCGGTTGGGTAAAGTAG	19	980	595
blaPER-1	396144	<i>P. aeruginosa</i>	CCATCAGGCAACAGAATG	18	137	TGACGATCTGGAACCTTTAC	20	769	633
blaPrmi	7672820	<i>P. mirabilis</i>	GCGGTAAGATCCTTGAGAG	19	152	AGTGGTCTGCAACTTTATC	20	653	502
blaRShaemolyt	8574410	<i>S. haemolyticus</i>	AGCTTTTGTTTTATATTTCTATTGG	25	31	TTTAGCTTTTGTCAATTACACTTTT	26	587	557
blaSHV-1	4337047	<i>K. pneumoniae</i>	CGTAGGCATGATAGAAATGG	20	117	GTATCCCGCAGATAAATCAC	20	785	669

gene	gi	source species	forward	length	position	reverse	length	position	product
blaTEM-106	21464484	<i>E. coli</i>	ACATCGAACTGGATCTCAAC	20	131	TCTCAGCGATCTGTCTATTTCT	21	832	702
blavim	5420397	<i>P. aeruginosa</i>	CATGCGTGTAATCATCGT	19	72	CCCTTGAGCGGAAGTATC	18	371	300
blaZ	1575124	<i>S. aureus</i>	TGCTTTAGTTTTAAGTGCATGT	22	30	TCCTTCATTACACTCTTGGC	20	839	810
cumA	511055	<i>P. vulgaris</i>	ACAACATTTTCGCCAAACA	18	16	TTGAGCTAAAGACATTCCTGT	21	378	363
dacCStrpyog	1420857	<i>S. pyogenes</i>	AATCATCCTCGTGGCTTT	18	150	GCTAAATTGGGATAGTCTCG	20	754	605
femA	4929298	<i>S. aureus</i>	TACAGTCATTTACGCCAAAC	20	58	TCACGCTCTTCATTTAGTTCT	21	770	713
femBShaemolyt	4539615	<i>S. haemolyticus</i>	AATGATGGCTTTGAAGTAGTG	21	106	CCTGTTCTTGCTTCTGTTTC	20	650	545
fmhA	4574232	<i>S. aureus</i>	TGACTTCGGATGAGTTCAAT	20	17	GCTGTTAATTGTTGTTGCTTT	21	779	763
fmhB	4574234	<i>S. aureus</i>	CTCACCCAAATGGAGATTTA	20	50	CTTGCTTTTCAGATGTTTCC	20	799	750
fox-6	14626421	<i>K. pneumoniae</i>	GGCTTACGGGATCAAGAC	18	723	ATTGGCCTGGAAGCTCAC	18	948	226
ftsWEF	4633279	<i>E. faecium</i>	ACAGTGCCAGTTCTTATCGT	20	35	GAAGCCAACCTTTATTTCT	20	592	558
mecA	13785452	<i>S. aureus</i>	AGTTGTAGTTGTCGGGTTTG	20	36	TGAAGTCGCTTTTCCTAGAG	20	750	715
mecISepid	46995	<i>S. epidermidis</i>	ATGGATAATAAACGTATGAA	21	1	CAATTCTTCTATTTTCATCTGTG	23	348	348
mecR1Sepid	46995	<i>S. epidermidis</i>	AAGTATAATCAGTTCATTGCTCAC	24	24	GTTTCGACTACGACAGTTGG	20	575	552
pbp1a	23451740	<i>S. pneumoniae</i>	CTTGTTAGCGATTCAAGTAG	21	248	CAATTCATCGTCTGGATAGG	20	777	530
pbp2aStrpneu	6165959	<i>S. pneumoniae</i>	CGGAACTGTATAATCCCTTG	20	740	AGTGGAACAGCAGGTAG	18	1419	680
pbp2b	49391	<i>S. pneumoniae</i>	TGAGGAAGGTAGTAAGGGAAA	21	38	CAAACATATTGGGTTGATAGG	21	537	500
pbp2primeSepid	46993	<i>S. epidermidis</i>	TAGCAATACAATCGCACATAC	21	915	TGGTATATCTTCACCAACACC	21	1479	565
pbp2x	886954	<i>S. pneumoniae</i>	TGAAGATGGCAGCAAGAG	18	368	TCAAACCCTCATTAACATCC	20	891	524
pbp3Saureuc	6912038	<i>S. aureus</i>	AGAGATGAATGCAGGAACAG	20	558	ACCACCTTGGAATGTAATG	20	1272	715
pbp4	7688169	<i>E. faecalis</i>	CAAACAAGAATTAGCCGAAG	20	120	CAGAAGCAACTGTGATTGG	19	742	623
pbp5Efaecium	13786076	<i>E. faecium</i>	TACAGATGCAGACGGTGTAG	20	963	CCCTGTCCATATCCAGTATC	20	1622	660
pbpC	2149899	<i>E. faecalis</i>	GCCGGTGTATCACTAAAGG	19	160	CTGTTCTAGTCCCATTGCTC	20	681	522
psrb	790434	<i>E. faecium</i>	TTATCTGTTTGTACTGCTTACAC	25	25	TTCTAATCCTCCCAAAGTCC	20	592	568
cat	46651	<i>S. aureus</i>	AGAAAATTGGGATAGAAAAGAA	22	88	CTGCAAGGCAACTGGTAT	18	622	535
catEfaecium	7595743	<i>E. faecium</i>	GATAACCATCACAAACAGAATG	22	69	TTATTTGAACCAACAAACGAC	21	598	530
cmlA5	12024948	<i>E. coli</i>	TGGAATGGGTAGCTTCTTC	19	672	GGGAAACACAGACAGACC	19	1177	506
ble	1567207	<i>S. aureus</i>	TACAGTCTATCCGGGCATT	19	5	TGTTGTCGGGATCAATTACT	20	364	360
ddl	460079	<i>E. faecalis</i>	GAAGATGGAACAATTCAAGG	20	307	TTTCCCACAGTAAAGGATACA	21	979	673
vanA	43335	<i>E. faecium</i>	GTGCGGTATTGGGAAACA	18	650	CGGCCGTTATCTTGTAAG	18	899	250
vanB	148323	<i>E. faecalis</i>	TTGTCTGGTATCCCCTATGT	20	11	AAAAGATCAACACGAGCAAG	20	552	542
vanC-2	1857221	<i>E. flavescens</i>	AAGCTGCCTTATGTAGGTTG	20	5	AGCACCGACAGTCAAAGA	18	364	360
vanH(tn)	155036	<i>E. faecium</i>	TCTTATGGCAGTACGCAAC	19	345	CCAGTTTCCCGTTTCTAAT	20	748	404
vanHB2	11878534	<i>E. faecium</i>	AAGTGTGGGCATTACTGTTT	20	9	CCTTGCTTCATCTCTCCA	18	671	663
vanR	148331	<i>E. faecium</i>	ACGAGAATTATACGTTTTTCA	21	71	ATCAATGGTGTCTGTTCAATT	20	642	572
vanRB2	11878534	<i>E. faecium</i>	GAATTCTACTGTGCGAGGATG	21	11	TCTGCCTCTGCATCAAAC	18	290	280
vanS(tn)	155036	<i>E. faecium</i>	AATGATCCGAGGGAAACT	18	117	TTTGTTAGCGTTATCGTTTGT	21	680	564
vanSB2	11878534	<i>E. faecium</i>	ACATGAGTTGGAGGAAACAC	20	651	TACGATGGCAAGTCCTAAAC	20	1245	595
vanWB2	11878534	<i>E. faecium</i>	GGCAGCAAAGACCTTAAAC	19	231	TCATTGGTTCTCCTCTCTG	18	828	598

gene	gi	source species	forward	length	position	reverse	length	position	product
vanX(tn)	155036	<i>E. faecium</i>	GACATACGAGTTGGCTGAA	19	126	CTATTGGGGTATGGTTCGT	19	584	459
vanXB2	11878534	<i>E. faecium</i>	TGGGATAACTTCACAGGAAA	20	70	GGTATGGCTCATCAATCAA	19	577	508
vanY(tn)	155036	<i>E. faecium</i>	ATACTTAGGTTATGACTACGTTAATGA	27	42	AAATGAACCCGTATTTCCA	19	592	551
vanYB2	11878534	<i>E. faecium</i>	GTGCGTTCATTATTTTCGTTT	20	83	GCCATCTATAAACCTCGTTG	20	634	552
vanZ(tn)	155036	<i>E. faecium</i>	AGGATTGCTAGCTTTATATTTAGTG	25	21	ATTTATTCTTAAATGGGTACGG	22	477	457
ermA	13785452	<i>S. aureus</i>	CCAGAAAAACCCTAAAGACA	20	6	AAAGAACACGATATTCACGG	20	619	614
ermB	6273677	<i>S. aureus</i>	CATTTAACGACGAAACTGG	19	124	AATTGTTTACTTTGGCGTGT	20	667	544
ermC	4138444	<i>S. aureus</i>	ACACAGTCAAACTTTATTACTTCA	25	21	CAACAAGTTTATTTTCTGTAGTTT	24	220	200
linB	4633124	<i>E. faecium</i>	CGTTTACCAAAGGAGAAGGT	20	86	TGTTTAGCCAATTATCAGCA	20	595	510
mdrSA	3892641	<i>S. aureus</i>	GACAGATTTTCGATCCCTTA	20	45	CCTTTTTGTTTTGATGCACT	20	752	708
mefA	18478326	<i>S. pyogenes</i>	GGTCTTGCTATGGCTTCAC	20	132	CATTCTTCTTGCAATTTCTC	20	636	505
mphBM	3892641	<i>S. aureus</i>	GCATATAAATATCAAAACCATACAAG	26	429	TTTCAATGCCATCGTTTC	18	879	451
mrx	807701	<i>E. coli</i>	GTTGAGAATGGGAGAGACTG	20	259	AACGTCGCGATTCTAGGT	18	798	540
msrA	15077570	<i>S. aureus</i>	CATTAGCAGGAGGATGTTTC	20	20	TGAACCACGTTGATATTGG	19	486	467
satA	433714	<i>E. faecium</i>	GTCCGAATCCTATGAAAATG	20	23	GCAGCTGATTTATTGTATCTTG	22	547	525
satSA	1272325	<i>S. aureus</i>	GTGATTACAGAAATGAAAGCAG	22	1	AGATATATTACCTTATCAGTATTGTCA	27	227	227
tetAJ	4104704	<i>P. mirabilis</i>	TTAGCACTCTATGCGACGA	19	139	AATACACCAAGAAATGCAAGA	21	770	632
tetL	1041816	<i>E. faecalis</i>	CACCTGCGAGTACAAACTG	19	140	CCCACAAAGAACTCCAATC	19	795	656
tetM	1065723	<i>E. faecalis</i>	GACAAAGGTACAACGAGGAC	20	109	GCACTTCCATGATAAAGAGG	20	662	554
dfrA	3676404	<i>S. aureus</i>	CAATTACCTTGGCACTTACC	20	58	CCCTTTTCTACGCACTAAAT	20	480	423
dfrStrpneu	3513549	<i>S. pneumoniae</i>	ACTAAGAAAATCGTAGCTATTTGG	24	4	ACTTCCTTTCTCTTGCGATA	20	503	500