Supplementary Table 1. Primers used for the amplification of genes/traits of interest

Gene/Trait	**Amplicon Size (bp)**	**Primer Seq. (5'-3')**	**Reference/Comments**
Plasmid PAI-Encoded Traits:			
cvaA	319	F ATCCGGGCGTTGTCTGACGGGAAAGTTG R ACCAGGGAACAGAGGCACCCGGCGTATT	Col V operon
cvaB3'	550	F GGCCCGTGCCGCCTCCTATTTTA R TCCCGCACCGGAAGCACCAGTTAT	Col V operon
cvaB5	247	F TGGCCACCCGGGCTCTTTCACTGGAGTT R ATGCGGGTCTGCAGGGTTTCCGACTGGA	Col V operon
*cvaC**	679	F CACACACAAACGGGAGCTGTT R CTTCCCGCAGCATAGTTCCAT	(3)
iroN†	667	F AAGTCAAAGCAGGGGTTGCCCG R GACGCCGACATTAAGACGCAG	(8)
iutA	302	F GGCTGGACATCATGGGAACTGG R CGTCGGGAACGGGTAGAATCG	(3)
sitA†	608	F AGGGGGCACAACTGATTCTCG R TACCGGGCCGTTTTCTGTGC	(9)
*traT**	290	F GGTGTGGTGCGATGAGCACAG R CACGGTTCAGCCATCCCTGAG	(3)
tsh‡	420	F GGGAAATGACCTGAATGCTGG R CCGCTCATCAGTCAGTACCAC	(7)
iss	323	F CAGCAACCCGAACCACTTGATG R AGCATTGCCAGAGCGGCAGAA	(6)
ompTp	496	F TCATCCCGGAAGCCTCCCTCACTACTAT R TAGCGTTTGCTGCACTGGCTTCTGATAC	Plasmid-encoded outer membrane protease
cbi	430	F ACAAGACAGCACCAGTTATGGGTATT R GTTGTTGGTTTTGTTGGCGTAGTTAT	Colicin B immunity
cma	498	F CAGCGCCATTACCCCATAAATAGTGA R GGTTCGTTCGCCGGTGTAAGCGTTAG	Colicin M activity
Chromosomally Encoded Traits: **Adhesins:**			
bmaE	507	F ATGGCGCTAACTTGCCATGCTG R AGGGGGACATATAGCCCCCTTC	(3)
fimH	508	F TCGAGAACGGATAAGCCGTGG R GCAGTCACCTGCCCTCCGGTA	(3)
focG	364	F CAGCACAGGCAGTGGATACGA R GAATGTCGCCTGCCCATTGCT	(3)

gafD	952	F TGTTGGACCGTCTCAGGGCTC	(3)
		R TCCCGGAACTCGCTGTTACT	
papA	717	F ATGGCAGTGGTGTTTTGGTG	(3)
		R CGTCCCACCATACGTGCTCTTC	
papC	205	F GTGGCAGTATGAGTAATGACCGTTA	(3)
		R ATATCCTTTCTGCAGGGATGCAATA	
papEF	326	F GCAACAGCAACGCTGGTTGCATCAT	(3)
		R AGAGAGAGCCACTCTTATACGGACA	
papG allele I§	461	F TCGTGCTCAGGTCCGGAATTT	(3)
		R TGGCATCCCCCAACATTATCG	
papG allele I'§	479	F CTACTATAGTTCATGCTCAGGTC	(3)
		R CCTGCATCCTCCACCATTATCGA	
papG allele II§	190	F GGGATGAGCGGGCCTTTGAT	(3)
		R CGGGCCCCCAAGTAACTCG	
papG allele III§	258	F GGCCTGCAATGGATTTACCTGG	(3)
		R CCACCAAATGACCATGCCAGAC	
*papG1**	1140	F CTGTAATTACGGAAGTGATTTCTG	
		R TTCCAGAAATAGCTCATGTAACCCG	
papG2/3	1070	R ACTATCCGGCTCCGGATAAACCAT	
sfaS	244	F GTGGATACGACGATTACTGTG	(3)
		R CCGCCAGCATTCCCTGTATTC	
sfa-foc	410	F CTCCGGAGAACTGGGTGCATCTTAC	(3)
		R CGGAGGAGTAATTACAAACCTGGCA	
adhC	411	F GTCGGCGAGGGCGTCACCAGCCTGAAGC	(4)
		R GGCCGCGCCCTGAATCACCGCCAGACC	
eaeH	605	F AAAAGCCGCTGGTGCTGTCTCTGC	EAE Locus
		R AAGCGGCCCGGCAACAAACTTC	
aufA	515	F CCGCGCTGAAATCATGGGTCGTAG	Auf fimbra
		R TGGGGCGGATACTGACTGGAGCAC	
aufC	298	F CGCCAACGCCCGGTAATCCTC	Auf fimbra
		R GCCGCCGGGACCGTTTGAGAT	
aufE	269	F CAAGCCCCTCTACCGAGCCATCTT	Auf fimbra
		R TCATGCCGGAGTGGTTCGTATTGA	
aufG	453	F TCGCCCGCTGATCGCGTGTAAA	Auf fimbra
		R CCGCCACCATTAGCCGTCTTTGTG	

Iron-Related:			
feoB	470	F AATTGGCGTGCATGAAGATAACTG R AGCTGGCGACCTGATAGAACAATG	(9)
fyuA	787	F TGATTAACCCCGCGACGGGAA R CGCAGTAGGCACGATGTTGTA	(3)
fyuA1	390	F AACCCCGCCGTCACCCTGTATGTC R GTCCGGCGCCAGACGCAGTTT	
ireA	254	F GATGACTCAGCCACGGGTAA R CCAGGACTCACCTCACGAAT	(8)
irp-2	287	F AAGGATTCGCTGTTACCGGAC R TCGTCGGGCAGCGTTTCTTCT	(1)
Protectins:			
kpsMT K1	153	F TAGCAAACGTTCTATTGGTGC R CATCCAGACGATAAGCATGAGCA	(3)
kpsMT II	272	F GCGCATTTGCTGATACTGTTG R CATCCAGACGATAAGCATGAGCA	(3)
kpsMT III	392	F TCCTCTTGCTACTATTCCCCCT R AGGCGTATCCATCCCTCCTAAC	(3)
Toxins:			
cdtB	430	F GAAAATAAATGGAACACACATGTCCG F’ GAAAGTAAATGGAATATAAATGTCCG R AAATCTCCTGCAATCATCCAGTTA R’ AAATCACCAAGAATCATCCAGTTA	(3)
cnf-1	1105	F ATCTTATACTGGATGGGATCATCTTGG R GCAGAACGACGTTCTTCATAAGTATC	(3)
hlyD	904	F CTCCGGTACGTGAAAAGGAC R GCCCTGATTACTGAAGCCTG	(8)
hlyF	599	F GGCGATTTAGGCATTCCGATACTC R ACGGGGTCGCTAGTTAAGGAG	Hemolysin F
Miscellaneous:			
fliC (H7)	547	F ACGATGCAGGCAACTTGACG R GGGTTGGTCGTTGCAGAACC	(8)
ibeA	171	F AGGCAGGTGTGCGCCGCGTAC R TGGTGCTCCGGCAAACCATGC	(3)
ompT	559	F ATCTAGCCGAAGAAGGAGGC R CCCGGGTCATAGTGTTCATC	(8)
maIX PAI	925	F GGACATCCTGTTACAGCGCGCA R TCGCCACCAATCACAGCCGAAC	(3)

gimB	619	F AAAAGCCGCCCAGGAATCAGAAGAACAA R TTACCCACAAAAGGCCGGGGAGTGATAA	ExPEC Gim B island
O2ColV39	437	F TACTGCCCGGTGTGATATTTCCAACAAA R TAAGATTGACAATTGCAGGACCGTAACC	ColV hypothetical gene
vat	370	F GAGGCCGGCGACCAGTGGTTCTCCATTA R TGAACCGGCACCCTGCGTGACAGAGTTT	Vacuolating autotransporter
1024UI	598	F GGCTTTCCCGCCTTCTTTTACCACTACG R GGACGGCGACGTTGTGTTATTCGGTAAT	Inc FIB recombinase/integrase
1051UI	664	F CACGCCGTTACTGGTCGCGGAAAAAT R AACCCACGGCCTCTATTGGCGAAGAACT	ColV gene
parB	534	F TCGTGGCCGAGTTCTTGGCAACAGC R GCGGCCTGAAACGCACGAGTCACTTT	Inc FIB Plasmid partitioning
umuC	474	F CCGCCGTACGGAAAAACTGCTGTCACTG R ACGGCAGCGGCAATGATGTCCTGTGTAT	UV protection gene
rfc	788	F ATCCATCAGGAGGGGACTGGA R AACCATACCAACCAATGCGAG	O antigen polymerase
iha	829	F CTGGCGGAGGCTCTGAGATCA R TCCTTAAGCTCCCGCGGCTGA	UPEC Island
afa	594	F GGCAGAGGGCCGGCAACAGGC R CCCGTAACGCGCCAGCATCTC	Afimbrial adhesin Afa
etsA	450	F CAACTGGGCGGGAACGAAATCAGGA R TCAGTTCCGCGCTGGCAACAACCTAC	*E. coli* transport system
etsB	537	F CAGCAGCGCTTCGGACAAAATCTCCT R TTCCCCACCACTCTCCGTTCTCAAAC	*E. coli* transport system
eitA	284	F ACGCCGGGTTAATAGTTGGGAGATAG R ATCGATAGCGTCAGCCCGGAAGTTAG	*E. coli* iron transport
eitB	380	F TGATGCCCCGCCAAACTCAAGA R ATGCGCCGGCCTGACATAAGTGCTAA	*E. coli* iron transport
blaTEM	558	F ATGTGCGCGGAACCCCTATTTGTTTA R AAAAAGCGGTTAGCTCCTTCGGTCCT	Ampicillin resistance
aac3 VIa	502	F GGCACCCGCGACGCCCTGGTCCAAAAG R GGGCCCGGCGCCGATCGACAGGATTT	Gentamicin resistance
aac3 VIb	302	F GGGCAAGCGCCGCGTCACTTATT R CGCGGCGTTGTTTCGGCTTCA	Gentamicin resistance
tetA	372	F CGGGGCGACTGGGGCGGTAGC R CAAAGCGCGGCCGGCACCTGT	Tetracycline resistance
tetB	446	F AACGCGTGAAGTGGTTCGGTTGGT R TTCGCCCCATTTAGTGGCTATTCTTC	Tetracycline resistance

groEL	318	F CGCCGGCATGAACCCGATGGACCTCA R TCGGCCTGCATCGACTGCGGGTTGTTG	Chaperone
aph3IA	378	F TCGGGCAATCAGGTGCGACAATCTA R TGCCAGCGCATCAACAATATTTTCACC	Gentamicin resistance
terD	231	F CCACTGCGCGGAATTTCCACTCACCAT R ACGCCGTCCCGTCTGATGTTGACAAG	Tellurite resistance
terF	428	F CCGACAAACTTCCAGAAGATGGGGTAGT R GAGGCAGCGGTTGCATTTGTACTTGACG	Tellurite resistance
terX	576	F ATGCGCCGCCTGCCTGTTTACCTTGTTA R CGCGCTTGTGCTGCCGGAAGACA	Tellurite resistance
terY3	302	F CCTGGGGCCGTCAGCGGACCTG R TCCTTGCTGGTGGCCGTTCATACTTCAT	Tellurite resistance
pcoA	507	F ATCCGGAAGGTCAGCACCGTCCATAGAC R GACCTCGCGGATGTCAGTGGCTACACCT	Copper resistance
pcoD	502	F GGCGCCCAGAATGATAATCGCAACA R GGGCGTGGCGCTGGCTACACTT	Copper resistance
pcoE	385	F GTGGGGCAGCTTTTGCTCAGTCCAGTGA R CGAAGCTTTCTTGCCTGCGTCTGATGTG	Copper resistance
dfr1	328	F ATCGGGAATGGCCCTGATA R CTTCCGGCTCGATGTCTATTGTAG	Trimethoprim resistance
dfr7	214	F TCTTTAAAGCGCTCACATATAATCAGTG R ATTTGACCGCCACCAGAGACA	Trimethoprim resistance
dfr17	243	F ATATCCCGTGGTCAGTAAAAGGTG R GACCCCCGCCAGAGACATA	Trimethoprim resistance
arsC	153	F CCAGCCTGCGGCACCTCGCGTAATAC R ACGCAGCAGCGCTCGTACTGAAATACCC	Arsenic resistance
silE	364	F TCGGCCTGGGCCACTGAAACCGTGAATA R GGCGGTGCGCTTCGGCCATAGCCTGATG	Silver resistance
silP	603	F ACACCCCGGCCTGGGCTCCTT R TGCGGGCACGGGAACAAACCTC	Silver resistance
sul1	462	F CGCCGCTCTTAGACGCCCTGTCC R CAACGGTGGCGCCCAAGAAGGAT	Sulfa resistance
merA	250	F GATCCGCGCCGCCCATATCGCCCATCTG R CACGCGCTCGCCGCCGTCGTTGAGTTG	Mercury resistance
intI1	545	F CACTCCGGCACCGCCAACTTTC R GAACGGGCATGCGGATCAGTGAG	Integrase
iseC12	404	F CGCGGCCACGTAAACCGAAAGATAAA R GCGCGGGTGCACAGCAACCTC	Transposase

aadA	365	F TAACGGCGCAGTGGCGGTTTTCA R AAGCTCGCCGCGTTGTTTCATCAAG	Aminoglycoside resistance
qacE delta	250	F TCGGCCTCCGCAGCGACTTCC F CTTGCCCCTTCCGCCGTTGTCTAAT	Quaternary ammonium compounds
qnr	440	F TCGCCGCTGCCGCTTTTATCAGT R GCCAACAGTCGCGGGAGAAGGTG	qnr plasmid fluoroquinolone resistance
Plasmid-Replicon Types:			
B/O	159	F GCGGTCCGGAAAGCCAGAAAAC R TCTGCGTTCCGCCAAGTTCGA	(5)
FIC	262	F GTGAACTGGCAGATGAGGAAGG R TTCTCCTCGTCGCCAAACTAGAT	(5)
A/C	465	F GAGAACCAAAGACAAAGACCTGGA R ACGACAAACCTGAATTGCCTCCTT	(5)
P	534	F CTATGGCCCTGCAAACGCGCCAGAAA R TCACGCGCCAGGGCGCAGCC	(5)
T	750	F TTGGCCTGTTTGTGCCTAAACCAT R CGTTGATTACACTTAGCTTTGGAC	(5)
K/B	160	F GCGGTCCGGAAAGCCAGAAAAC R TCTTTCACGAGCCCGCCAAA	(5)
W	242	F CCTAAGAACAACAAAGCCCCCG R GGTGCGCGGCATAGAACCGT	(5)
FIIA	270	F CTGTCGTAAGCTGATGGC R CTCTGCCACAAACTTCAGC	(5)
FIA	462	F CCATGCTGGTTCTAGAGAAGGTG R GTATATCCTTACTGGCTTCCGCAG	(5)
FIB	702	F GGAGTTCTGACACACGATTTTCTG R CTCCCGTCGCTTCAGGGCATT	(5)
Y	765	F AATTCAAACAACACTGTGCAGCCTG R GCGAGAATGGACGATTACAAAACTTT	(5)
I1	139	F CGAAAGCCGGACGGCAGAA R TCGTCGTTCCGCCAAGTTCGT	(5)
X	376	F AACCTTAGAGGCTATTTAAGTTGCTGAT R TGAGAGTCAATTTTTATCTCATGTTTTAGC	(5)
HI1	471	F GGAGCGATGGATTACTTCAGTAC R TGCCGTTTCACCTCGTGAGTA	(5)
N	559	F GTCTAACGAGCTTACCGAAG R GTTTCAACTCTGCCAAGTTC	(5)

HIII	644	F TTTCTCCTGAGTCACCTGTTAACAC R GGCTCACTACCGTTGTCATCCT	(5)
L/M	785	F GGATGAAAACTATCAGCATCTGAAG R CTGCAGGGGCGATTCTTTAGG	(5)

APEC O1 Genomic Islands of Unknown Function:

1712	392	F TACCGGCGTGATGGCCACCTACA R AAACAACGCCGGTTCTGCCTACCAG	APEC O1 genomic island
1717	313	F AAGCTATCCCGACTTGCTCTCGCTGTAA R AAGGCGCTGGCACTGCAACAACTAC	APEC O1 genomic island
1718	468	F AGCGGTCACAGTGGCTTTCATAGGTG R GCCCCGCTTTTCCAGGCACAC	APEC O1 genomic island
1716	533	F CAGGGATTCGCTTGCCTCTTCTGTGTA R CGACCGCCGGGATTTTAACCATAC	APEC O1 genomic island
1721	215	F GGTGGCGAGATAACCGACGTAGTGGT R CCCCTGGCGAATGGAAAACAGAGAT	APEC O1 genomic island
1713	366	F CCGGCTCAGGAGAGTCTGTTAATACACT R TGATAGCCCGCTCCAGATTTTCTTTAG	APEC O1 genomic island
1724	266	F TTGACCTGTACCCGCATAAACACTGGTT R TGCGAGAGGTGCTTAACGCGATTTTC	APEC O1 genomic island
1753	358	F CCCCACAGGCCGCTCCACAG R TGCCCGATAGGCGAAGATGGGTTAT	APEC O1 genomic island
1756	446	F CTGGCCCAACCCCACCGTTATCTT R ATGGCCGGGTACGGGTGAAGTTTC	APEC O1 genomic island
1757		F ATCGGCACCAGAAGTACCGGATTTGA R GTCGGCAATATCTACGTGCAGGGACAC	APEC O1 genomic island
1761	310	F GGAGGCGGCGGGTTTTGACAA R GTATTCCGCCATCCGCCCATCC	APEC O1 genomic island
1767	529	F AGCGGCGTCCTGCTGCTTACTCTG R CCGGCACCGGGGAGAAAATGA	APEC O1 genomic island
1770	573	F GTCAGCCGCTGGACCCCCTATGAT R TATCGCCGCTTCCCTCGCCTTATC	APEC O1 genomic island
1771	250	F CTGAGCCGTGCGCAGAATGTCAAC R ACTCTTCCGCCTGCCCTGGACTGT	APEC O1 genomic island
4460	410	F AGCCGGGCGGTCATGCTGAGTTATGGATTA R CCAGCGAGGAACGGCAAGATGCTTACCAA	APEC O1 genomic island
4464	355	F ATCGCCGCGCCTCGGAGTCCTGT R CTCCACGCGCCAGCGCCTCAAG	APEC O1 genomic island

4467	463	F CGAGGTCGGCGTGGCTGGCTTCCT R TCCCGCCCGGTCTGGATTGGTTACGAC	APEC O1 genomic island
4468	277	F ACCGCCCTGACCGAAAAGGTGAAATCCATT R CTTTACTGCGGCGCTGCTGGGTCAGACTTT	APEC O1 genomic island
4472	317	F GCCGCAAATCCGGGACTGGCTGAACT R ATACCGCACACCGCAGGCAGTGACAGG	APEC O1 genomic island
4480	515	F CGCGCAGTTTTGACGGGCGAATGAC R GACCCGGCGACGCTTAAGCCCTCAAAC	APEC O1 genomic island
11	227	F GGCCGCTGTGGGAATTAATACCCGCAATCT R CCGCCGCCGCAATCCCCACAC	APEC O1 genomic island
12	159	F TATGCGCCAGACGCTGCCACACCAGAC R CCGCCGGTCAGTTCGGGATAAAGCACAC	APEC O1 genomic island
516	404	F TTTTTGCATTGGTGGCGGAGCGTGGTAT R TATCGGCCAGGCGGGGAGTAAGTTTGTCAT	APEC O1 genomic island
517	308	F GTCGCGTTATGGCGGCTGAAGTGCTCAAA R GCCCGACGGCTCATAAACAGGCGTATCAA	APEC O1 genomic island
520	495	F TATGAGGGGCAAGGTGCGACAGCTAACAGC R ACGCCGGGCGGCAGCCTTATCCT	APEC O1 genomic island
522	437	F ATCCGCCATATTATGCCCCGTCGAGTTGAA R AGAAGTTTAGCGCCGGCATGACGCATCTG	APEC O1 genomic island
525	236	F GTACCGGGGCCGTCAGCTCCGAATACC R ACGGCGCGGGAAGCACCGAAATACA	APEC O1 genomic island
530	364	F TGTCCCCGCAGGTTCTGGTTCAAAACTCAT R GAGCCATCCGGGAGCCACCAATCTCATTAT	APEC O1 genomic island
532	532	F TGGCTGCGGCGCTAAGAAATCTTGAACAAC R GCCGGGCCAATCCCACCGAACATA	APEC O1 genomic island
1177	197	F CGCCGTCGCTGCGGGTGATGGTAA R GTCACTGGCCGGAATTAAAATCCCGCACAT	APEC O1 genomic island
1179	242	F CTGCCGTGCCTTTTCAAGTGCATGACCAGT R CCGGCGAAGCGGAAACACGAATGAGTAA	APEC O1 genomic island
No locus 17-3	418	F TGCGCGGGTGCACAGCAACCTC R CTGCGCGGCCACGTAAACCGAAAAGATAAA	APEC O1 genomic island
No locus 17-4	370	F AGTTCGCCACCGCAATGAGTACGCCTTCA R GGATTATTTCCCGGCCTCGGCCATTCATTT	APEC O1 genomic island
1180	322	F CGCGCCCTGAAAACCGGCCATAACC R GCGCCAGTGTGGACGGGGTGGAGA	APEC O1 genomic island
1181	443	F AGCGCCCTTAACTCTGCCTGGCTGAATGAG R AGCCAGCCGTTTATTTCCCGAATCCTGTCC	APEC O1 genomic island

1184	285	F CGCCGCGAGGCAATTTGCGTAGTTCAC R ATGCGCTCAAAGAGGATGGCGACGAAAGAG	APEC O1 genomic island
1185	495	F AGGAAACACAACGCGTGGCTGACGGGTAAG R TCGCGGGGAGGTGCTTTGATGTCCTGTT	APEC O1 genomic island
2314	164	F GGCCCGCCGCAGACGCAGCATA R ACCGGCACACCTCCCGCAGTGAACG	APEC O1 genomic island
18-2	207	F GGGGGATAGCACGAAAACAAACCTCA R ATCGGGCAAGATTCAGTAGCGGAAGC	APEC O1 genomic island
2310	391	F GTCACGGGAATGGCTTAATACACAGG R GAGACCGCCTTTATTCCTTTCTGAGG	APEC O1 genomic island
2301	561	F ATCAGCGCGGCGACTTTACGGTTAGT R CCTGCGGCAGATTATCTCCCAGTGTG	APEC O1 genomic island
2291	335	F TTCCGCCACGCACGGCAGGTTGTT R CACATCCGCGCTCGCGCAAAGTGTC	APEC O1 genomic island
2277	681	F TGAATGCCCGTATGACAAAGTAGGA R GTTGCTTTGCGCTTGTCTTTTAGTCC	APEC O1 genomic island
2291	456	F CGCCGGTGCGCCCAACTG R GCGATTTCCGCCGCCGTCTT	APEC O1 genomic island
2271	501	F TGGGCCCGGGCAACCACAA R TGAGGGGGCTGCCAGTGAAAATGAC	APEC O1 genomic island
2264	260	F GCTACCGCGGAGATGGGGGATTAT R CACGCGTTGCGGGTAGGTTTCA	APEC O1 genomic island
2103	404	F CCTGGGGCAGTGCGAGCAACTTG R CGGCGCACATAAATACCCTGGCTACAC	APEC O1 genomic island
2101	445	F ATATGGGCGAATCGGAAGTGGCAGTT R AGGCCGATGAATGCGCAAACCAAC	APEC O1 genomic island
2099	503	F GGGAGCGCGTGCGGATGGTT R ATTGCCGGCTCGTCCTTCCTTTTGA	APEC O1 genomic island
2095	338	F GATTGCCGAATGTGCCGAGCGTAAA R GTGCGCCGACGGCTAATTCTTCAATC	APEC O1 genomic island
2093	556	F GGGGGCGGATGAAGAAAATAAAAACTG R TGCCCGTCCGCAAACCAACAG	APEC O1 genomic island
2080	250	F AGGCCGATCTGGTGCGCAATTTTATTC R AGCCGATCTACGCCTTTTTCAGCAACAC	APEC O1 genomic island
2078	595	F GGGTGCAGCGGTGAGAGGAAAACTAACT R GCGGGCTAAGGCGTTGTTGACCTG	APEC O1 genomic island
2071	298	F TTGTCGCCCGCAAAACTAACGCTAAACC R AATGCGGCGCTGGCCATGATTACC	APEC O1 genomic island

2068	211	F AGCCGGGAAATTATCAGCCTGGCACTT R CTTCGCCTTCGAGCACTTCCTGGATGT	APEC O1 genomic island
ace37	420	F CGCTGTCATGGTTTTGGCAAAGAAATC R AATCGCGGGTGTTACTTCCGGATACATC	APEC BEN2908 EPI-I
ace41	365	F CACCGTGGTCAATGACTTCCTGGACTG R AGGTGCGCCATTTAATGTTGCGATAGGT	APEC BEN2908 EPI-I
ace43	496	F GAGCTGGCCCTGGGCATCTGC R CGGCGGTAACTATCGGGGTAATGATTTC	APEC BEN2908 EPI-I
ace46	299	F TTAATCGGGCCAGGAGGCAGAAGAAGA R CGGCCCGGCTTATCTGCTTTTTAGTTAT	APEC BEN2908 EPI-I
ace58	558	F CCGGCGGTGAAAACGTTCGAAGAGTAT R TGCTATAACCCCGGCCTTTCGTTTCTGT	APEC BEN2908 EPI-I
ace63	459	F ATTCTCCGCGGCACTCCTCAATGA R CAACCACGCAGGGGAAACGCTTTAT	APEC BEN2908 EPI-I
ace68	246	F AATTGCCGGAGCGCTGGTTGAAGA R ACGGGGCGTTGCCTGATGATACTGAC	APEC BEN2908 EPI-I
ace71	209	F ACCGGGGAAATGTGGTGGACAGAGTC R CCGGCGTCGTGGCGTCAGAAT	APEC BEN2908 EPI-I
ace35	155	F AAGGGCACAGTAACGCAACCGAACCT R GAATGGCATCCGGCCGTATGTTGTT	APEC BEN2908 EPI-I
1696	352	F TAGCGGCCTACGCGTGCCTGAT R GGGCGATTAAGCCGGGAACCACT	APEC O1 genomic island
3040	397	F ATCGGGCCGACAAAATCAGTCCAC R ATGGCCGACGGTTATTGCCTTAGC	APEC O1 genomic island
1698	234	F GGTATTACGCGGGCCGCATTGTC R CCTTGCTGCAACACGGGAGGAAT	APEC O1 genomic island
4059	268	F AAATTACCGCCCCAGCCAAAGCCCCTAAAG R GCCCCCACTCTGCTGGCTCGTTCTGTAAA	APEC O1 genomic island
4055	377	F GCGGTGGGCGTTCTGCGGATTCC R GGCGCGGGCAGAGTATAGACGCATTGGTT	APEC O1 genomic island
4053	443	F CCGCGAGAGTTAATAAATCTGCCGACACCA R GCTGCGGCGGTAACTTCTCTACAGGGTTTT	APEC O1 genomic island
4051	408	F TCCCTGCGTCGAAATCCCTCTGCTCTGAAC R GCGGCGGCCACTATGGGGGCTACC	APEC O1 genomic island
4041	512	F CCGCCATCCCCATCGCCATCATTTGT R GCGGCAGACCATCAACAGCGCCTACTTC	APEC O1 genomic island
4038	322	F TAGTCCGGCGAATGCCTCAGTGTTGTGCTC R TCCAGAGACGCGCTATCAGCCGCTTATGCT	APEC O1 genomic island

4030	214	F CTGTGTCCGGAGGCGTACTCATGGGTTCTG R AGATTCCCGTGGCGGCATCCGGTTATGTA	APEC O1 genomic island
4022	584	F AGGATCGCGGTTCGCAGGGACCAATGTA R GGCGGGCGAACAGTTCAATGCGAGAAAC	APEC O1 genomic island
1684	379	F CATTTCCCGCGGTGGTATGTTTCTGTTT R GATATCAGCGGTAAAGCGAGCGGTGACT	APEC O1 genomic island
1683	422	F CCGGGAAGCGTTCTGACATGACGATTGT R ACCAGCGCAGTTCGCAGCTCTATCAACC	APEC O1 genomic island
1682	340	F CACCGCATCCCGTATAGAGCAGCCTGAA R TGCCTGACCGGTGACTCCGACTGGTT	APEC O1 genomic island
1681	227	F CACCCCTTTAAAACGAGCAGCATTACTG R AACGCCGCCCTATCAGCAGACAACATTT	APEC O1 genomic island
1665	489	F AATCCCCCGGTCAGCCAAGTGCTAACTG R CGACGGCCGCGAGTGCGTAACC	APEC O1 genomic island
1664	273	F GCGGGATCTGCGTGGTCTTCGTCAGT R CGCCCGCTTCCACCCGCAAGTTA	APEC O1 genomic island
1663	158	F GCGGGCGGCATCGGCATTTTACT R CACGGCGGAAAGTCGTACAGCCACAC	APEC O1 genomic island
1662	527	F GTGATGGCGTGGGTGGCGACTCAGTATC R GCCGCGAGGATTGACACCAGCAAGTAAG	APEC O1 genomic island

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§ = *pap*G genotypes were assessed using an allele-specific assay developed by Johnson and Brown (2).

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