Supplementary Table 1. Primers designed in this study.

Panel	APEC O1 genomic island	APEC O1 gene locus	Product size (bp)		Sequence (5' to 3')
1	2	1716	533	F	CAGGGATTCGCTTGCCTCTTCTGTGTA
				R	CGACCGCCGGGATTTTAACCATAC
	2	1718	468	F	AGCGGTCACAGTGGCTTTCATAGGTG
				R	GCCCCGCTTTTCCAGGCACAC
	2	1712	392	F	TACCGGCGTGATGGCCACCTACA
				R	AAACAACGCCGGTTCTGCCTACCAG
	2	1713	366	F	CCGGCTCAGGAGAGTCTGTTAATACACT
				R	TGATAGCCCGCTCCAGATTTTCTTTAG
	2	1717	313	F	AAGCTATCCCGACTTGCTCTCGCTGTAA
				R	AAGGCGCTGGCACTGCAACAACTAC
	2	1724	266	F	TTGACCTGTACCCGCATAAACACTGGTT
				R	TGCGAGAGGTGCTTAACGCGATTTTC
	2	1721	215	F	GGTGGCGAGATAACCGACGTAGTGGT
				R	CCCCTGGCGAATGGAAAACAGAGAT

2	1	1770	573	F	GTCAGCCGCTGGACCCCCTATGAT
				R	TATCGCCGCTTCCCTCGCCTTATC
	1	1767	529	F	AGCGGCGTCCTGCTGCTTACTCTG
				R	CCGGCACCGGGGAGAAAATGA
	1	1756	446	F	CTGGCCCAACCCCACCGTTATCTT
				R	ATGGCCGGGTACGGGTGAAGTTTC
	1	1757		F	ATCGGCACCAGAAGTACCGGATTTGA
				R	GTCGGCAATATCTACGTGCAGGGACAC
	1	1753	358	F	CCCCACAGGCCGCTCCACAG
				R	TGCCCGATAGGCGAAGATGGGTTAT
	1	1761	310	F	GGAGGCGGCGGGTTTTGACAA
				R	GTATTCCGCCATCCGCCCATCC
	1	1772	250	F	CTGAGCCGTGCGCAGAATGTCAAC
				R	ACTCTTCCGCCTGCCCTGGACTGT
3	40	2277	681	F	TGAATGCCCGTATGACAAAGTAGGA
				R	GTTGCTTTGCGCTTGTCTTTTAGTCC
	40	2301	561	F	ATCAGCGCGGCGACTTTACGGTTAGT
				R	CCTGCGGCAGATTATCTCCCAGTGTG

	40	2271	501	F	TGGGCCCGGGCAACCACAA
				R	TGAGGGGGCTGCCAGTGAAAATGAC
	40	2291	456	F	CGCCGGTGCGCCCAACTG
				R	GCGATTTCCGCCGCCGTCTT
	40	2310	391	F	GTCACGGGAATGGCTTAATACACAGG
				R	GAGACCGCCTTTATTCCTTTCTGAGG
	40	2264	260	F	GCTACCGCGGAGATGGGGGATTAT
				R	CACGCGTTGCGGGTAGGTTTCA
	40	2314	164	F	GGCCCGCCGCAGACGCAGCATA
				R	ACCGGCACACCTCCCGCAGTGAACG
4	42	2103	404	F	CCTGGGGCAGTGCGAGCAACTTG
				R	CGGCGCACATAAATACCCTGGCTACAC
	42	2101	445	F	ATATGGGCGAATCGGAAGTGGCAGTT
				R	AGGCCGATGAATGCGCAAACCAAC
	42	2099	503	F	GGGAGCGCGTGCGGATGGTT
				R	ATTGCCGGCTCGTCCTTCCTTTTGA
	42	2095	338	F	GATTGCCGAATGTGCCGAGCGTAAA
				R	GTGCGCCGACGGCTAATTCTTCAATC

	42	2093	556	F	GGGGGCGGATGAAGAAAATAAAAACTG
				R	TGCCCGTCCGCAAACCAACAG
	42	2080	250	F	AGGCCGATCTGGTGCGCAATTTTATTC
				R	AGCCGATCTACGCCTTTTTCAGCAACAC
	42	2078	595	F	GGGTGCAGCGGTGAGAGGAAAACTAACT
				R	GCGGGCTAAGGCGTTGTTGACCTG
	42	2071	298	F	TTGTCGCCCGCAAAACTAACGCTAAACC
				R	AATGCGGCGCTGGCCATGATTACC
	42	2068	211	F	AGCCGGGAAATTATCAGCCTGGCACTT
				R	CTTCGCCTTCGAGCACTTCCTGGATGT
6	3	1696	352	F	TAGCGGCCTACGCGTGCCTGAT
				R	GGGCGATTAAGCCGGGAACCACT
	30	3040	397	F	ATCGGGCCGACAAAATCAGTCCAC
				R	ATGGCCGACGGTTATTGCCTTAGC
	30	3030	515	F	CCGCGCTGAAATCATGGGTCGTAG
				R	TGGGGCGGATACTGACTGGAGCAC
	30	3032	298	F	CGCCAACGCCCGGTAATCCTC
				R	GCCGCCGGGACCGTTTGAGAT

	30	3034	269	F	CAAGCCCCTCTACCGAGCCATCTT
				R	TCATGCCGGAGTGGTTCGTATTGA
	30	3038	453	F	TCGCCCGCTGATCGCGTGTAAA
				R	CCGCCACCATTAGCCGTCTTTGTG
	3	1694	605	F	AAAAGCCGCTGGTGCTGTCTCTGC
				R	AAGCGGCCCGGCAACAAACTTC
	3	1698	234	F	GGTATTACGCGGGCCGCATTGTC
				R	CCTTGCTGCAACACGGGAGGAAT
7	8	4460	410	F	AGCCGGGCGGTCATGCTGAGTTATGGATTA
				R	CCAGCGAGGAACGGCAAGATGCTTACCAA
	8	4464	355	F	ATCGCCGCGCCTCGGAGTCCTGT
				R	CTCCACGCGCCAGCGCCTCAAG
	8	4467	463	F	CGAGGTCGGCGTGGCTGGCTTCCT
				R	TCCCGCCCGGTCTGGATTGGTTACGAC
	8	4468	277	F	ACCGCCCTGACCGAAAAGGTGAAATCCATT
				R	CTTTACTGCGGCGCTGCTGGGTCAGACTTT
	8	4472	317	F	GCCGCAAATCCGGGACTGGCTGAACT
				R	ATACCGCACACCGCAGGCAGTGACAGG

	8	4480	515	F	CGCGCAGTTTTGACGGGCGAATGAC
				R	GACCCGGCGACGCTTAAGCCCTCAAAC
	8	11	227	F	GGCCGCTGTGGGAATTAATACCCGCAATCT
				R	CCGCCGCCGCAATCCCCACAC
	8	12	159	F	TATGCGCCAGACGCTGCCACACCAGAC
				R	CCGCCGGTCAGTTCGGGATAAAGCACAC
8	13	516	404	F	TTTTTGCATTGGTGGCGGAGCGTGGTAT
				R	TATCGGCCAGGCGGGGAGTAAGTTTGTCAT
	13	517	308	F	GTCGCGTTATGGCGGCTGAAGTGCTCAAA
				R	GCCCGACGGCTCATAAACAGGCGTATCAA
	13	520	495	F	TATGAGGGGCAAGGTGCGACAGCTAACAGC
				R	ACGCCGGGCGGCAGCCTTATCCT
	13	522	437	F	ATCCGCCATATTATGCCCCGTCGAGTTGAA
				R	AGAAGTTTAGCGCCGGCATGACGCATCTG
	13	525	236	F	GTACCGGGGCCGTCAGCTCCGAATACC
				R	ACGGCGCGGGAAGCACCGAAATACA
	13	530	364	F	TGTCCCCGCAGGTTCTGGTTCAAAACTCAT
				R	GAGCCATCCGGGAGCCACCAATCTCATTAT

	13	532	532	F	TGGCTGCGGCGCTAAGAAATCTTGAACAAC
				R	GCCGGGCCAATCCCACCGAACATA
9	17	1177	197	F	CGCCGTCGCTGCGGGTGATGGTAA
				R	GTCACTGGCCGGAATTAAAATCCCGCACAT
	17	1179	242	F	CTGCCGTGCCTTTTCAAGTGCATGACCAGT
				R	CCGGCGAAGCGGAAACACGAATGAGTAA
	17	1180	322	F	CGCGCCCTGAAAACCGGCCATAACC
				R	GCGCCAGTGTGGACGGGGTGGAGA
	17	1181	443	F	AGCGCCCTTAACTCTGCCTGGCTGAATGAG
				R	AGCCAGCCGTTTATTTCCCGAATCCTGTCC
	17	1184	285	F	CGCCGCGAGGCAATTTGCGTAGTTCAC
				R	ATGCGCTCAAAGAGGATGGCGACGAAAGAG
	17	1185	495	F	AGGAAACACAACGCGTGGCTGACGGGTAAG
				R	TCGCGGGGAGGTGCTTTGATGTCCTGTT
10	20	4059	268	F	AAATTACCGCCCCAGCCAAAGCCCCTAAAG
				R	GCCCCCACTCTGCTGGCTCGTTCTGTAAA
	20	4055	377	F	GCGGTGGGCGTTCTGCGGATTCC
				R	GGCGCGGGCAGAGTATAGACGCATTGGTT

	20	4053	443	F	CCGCGAGAGTTAATAAATCTGCCGACACCA
				R	GCTGCGGCGGTAACTTCTCTACAGGGTTTT
	20	4051	408	F	TCCCTGCGTCGAAATCCCTCTGCTCTGAAC
				R	GCGGCGGCCACTATGGGGGCTACC
	20	4041	512	F	CCGCCATCCCCATCGCCATCATTTGT
				R	GCGGCAGACCATCAACAGCGCCTACTTC
	20	4038	322	F	TAGTCCGGCGAATGCCTCAGTGTTGTGCTC
				R	TCCAGAGACGCGCTATCAGCCGCTTATGCT
	20	4030	214	F	CTGTGTCCGGAGGCGTACTCATGGGTTCTG
				R	AGATTCCCGTGGCGGCATCCGGTTATGTA
	20	4022	584	F	AGGATCGCGGTTCGCAGGGACCAATGTA
				R	GGCGGGCGAACAGTTCAATGCGAGAAAC
11	4	1684	379	F	CATTTCCCGCGGTGGTATGTTTCTGTTT
				R	GATATCAGCGGTAAAGCGAGCGGTGACT
	4	1683	422	F	CCGGGAAGCGTTCTGACATGACGATTGT
				R	ACCAGCGCAGTTCGCAGCTCTATCAACC
	4	1682	340	F	CACCGCATCCCGTATAGAGCAGCCTGAA
				R	TGCCTGACCGGTGACTCCGACTGGTT

	4	1681	227	F	CACCCCTTTAAAACGAGCAGCATTACTG
				R	AACGCCGCCCTATCAGCAGACAACATTT
	5	1665	489	F	AATCCCCCGGTCAGCCAAGTGCTAACTG
				R	CGACGGCCGCGAGTGCGTAACC
	5	1664	273	F	GCGGGATCTGCGTGGTCTTCGTCAGT
				R	CGCCCGCTTCCACCCGCAAGTTA
	5	1663	158	F	GCGGGCGGCATCGGCATTTTACT
				R	CACGGCGGAAAGTCGTACAGCCACAC
	5	1662	527	F	GTGATGGCGTGGGTGGCGACTCAGTATC
				R	GCCGCGAGGATTGACACCAGCAAGTAAG
12	13_14	542	552	F	CTTCGCCACCGGGAAAGAATGTAG
				R	TTGCCGCTCTGACAGGTGGACTTA
	13_14	545	512	F	CAGGGCGTTGTTGGGTCGTATTTG
				R	AGTTGCCCGCTTTCTTCAGACAGA
	13_14	544	465	F	TGCGGTAAATCAACGAGGGCTTCT
				R	AGTAATCCCGGCGACACCGTATCA
	13_14	523	429	F	GCTGGGGGATACCAATGAGCAGAT
				R	CCGGCCACCACGCCATCC

	13_14	543	390	F	TGATTTTGCCGGGTATTTCTTTTG
				R	TCGGACGCGATGCCACTGT
	13_14	518	335	F	TCGGGTGGATCGCAACTATGACCA
				R	CGCCGCTGTTTTTCTGCGTCTGT

Supplementary Table 2. Prevalence of APEC O1 genomic island (GI)-associated genes among various *Escherichia coli* groups. Cells are colored based upon prevalence (blue = 0-25%, green = 25-50%, orange = 50-75%, red = 75-100%). Statistical comparisons between groups are presented to the right, with cells with P < 0.05 (by Fisher's exact test) shaded yellow.

				Pathotype				**P value**			
GI	**ORF**[A]	**Predicted protein**	**Gene**	**APEC**[B]	**AFEC**[B]	**UPEC**[B]	**NMEC**[B]	**APEC vs. AFEC**	**APEC vs. UPEC**	**APEC vs. NMEC**	**UPEC vs. NMEC**
1	1753	putative endopeptidase		7.5	1.9	39.5	74.3	0.029	0.000	0.000	0.000
	1756	type VI secretion system protein		10.0	0.9	60.0	71.4	0.001	0.000	0.000	0.113
	1757	hemolysin co-regulated protein; type VI secretion system protein	*hcp*	15.9	12.3	55.5	77.1	0.452	0.000	0.000	0.002
	1761	type VI secretion system protein		9.7	2.8	44.0	77.1	0.019	0.000	0.000	0.000
	1767	type VI secretion system ATPase		10.4	0.9	49.0	71.4	0.001	0.000	0.000	0.001
	1770	type VI secretion system protein, associated with macrophage killing		9.5	2.8	49.0	71.4	0.029	0.000	0.000	0.001
	1772	type VI secretion system effector protein		11.1	6.6	45.5	77.1	0.213	0.000	0.000	0.000
2	1712	vacuolating autotransporter	*vat*	71.9	13.2	64.5	82.9	0.000	0.065	0.059	0.004

	1713	putative transcriptional regulator		31.0	4.7	63.5	78.6	0.000	0.000	0.000	0.026
	1716	conserved hypothetical protein		9.1	8.5	1.5	7.1	1.000	0.000	0.820	0.030
	1717	conserved hypothetical protein		12.6	10.4	2.0	8.6	0.622	0.000	0.431	0.021
	1718	conserved hypothetical protein		2.4	1.9	0.0	1.4	1.000	0.022	1.000	0.259
	1721	conserved hypothetical protein		11.9	6.6	2.5	5.7	0.122	0.000	0.153	0.244
	1724	conserved hypothetical protein		8.4	3.8	0.0	2.9	0.150	0.000	0.145	0.067
3	1694	putative attaching and effacing protein	*eaeH*	92.4	50.9	95.5	97.1	0.667	0.000	0.000	0.734
	1696	putative aldo/keto reductase		41.8	16.0	81.5	88.6	0.231	0.000	0.000	0.196
	1698	putative LysR-like transcriptional regulator		28.7	17.9	79.0	88.6	0.459	0.000	0.000	0.106
4	1681	putative site-specific recombinase		46.7	16.3	72.0	84.3	0.000	0.000	0.000	0.053
	1682	putative LuxR-like transcriptional regulator		46.7	16.3	71.0	84.3	0.000	0.000	0.000	0.038
	1683	conserved hypothetical protein		46.7	12.5	69.0	84.3	0.000	0.001	0.000	0.013
	1684	putative autotransporter		46.7	13.8	71.0	84.3	0.000	0.000	0.000	0.038
5	1662	sugar ABC transporter, permease component		45.3	42.5	32.0	78.6	0.748	0.048	0.000	0.000
	1663	sugar ABC transporter, transmembrane component		46.7	45.0	37.5	84.3	0.873	0.170	0.000	0.000
	1664	sugar ABC transporter, ATP-binding		46.7	45.0	38.0	84.3	0.873	0.215	0.000	0.000

		component									
	1665	sugar ABC transporter, periplasmic-binding component		45.3	45.0	35.5	84.3	1.000	0.163	0.000	0.000
8	4460	phage-associated protein	*cox*	5.3	1.3	4.5	15.7	0.198	0.755	0.055	0.006
	4464	putative phage replication initiation protein		50.7	22.5	24.5	42.9	0.000	0.000	0.406	0.006
	4467	putative phage terminase		48.0	27.5	29.5	48.6	0.012	0.007	1.000	0.005
	4468	putative phage capsid scaffolding protein		48.0	21.3	29.5	50.0	0.001	0.007	0.869	0.003
	4472	putative phage lysis holin		46.7	21.3	30.5	50.0	0.001	0.016	0.741	0.006
	4480	putative phage baseplate assembly protein		42.7	22.5	29.0	40.0	0.010	0.043	0.866	0.102
	11	putative phage tail protein		50.7	21.3	25.5	48.6	0.000	0.000	0.869	0.001
	12	putative phage tail protein		53.3	22.5	30.0	50.0	0.000	0.000	0.741	0.004
13-14	516	phage-associated protein	*trkG*	32.0	58.8	5.0	11.4	0.001	0.000	0.005	0.091
	517	putative transcriptional regulator		29.3	58.8	5.0	11.4	0.000	0.000	0.013	0.091
	518	phage-associated protein		35.0	49.1	14.0	14.3	0.008	0.000	0.001	1.000
	520	putative phage terminase		26.7	38.8	4.5	10.0	0.126	0.000	0.011	0.137
	522	conserved hypothetical protein		26.7	33.8	4.5	10.0	0.384	0.000	0.011	0.137
	523	putative phage morphogenesis protein		25.4	20.8	10.0	11.4	0.380	0.000	0.010	0.820

	525	phage-associated protein		32.0	31.3	5.0	10.0	1.000	0.000	0.002	0.156
	530	conserved hypothetical protein		26.7	27.5	5.0	10.0	1.000	0.000	0.011	0.156
	532	putative phage tail protein	*ynaA*	28.0	27.5	5.0	8.6	1.000	0.000	0.003	0.376
	542	cytolethal distending toxin type IV subunit A	*cdtA*	0.4	0.0	0.5	0.0	1.000	1.000	1.000	1.000
	543	cytolethal distending toxin type IV subunit B	*cdtB*	0.4	0.0	2.5	1.4	1.000	0.031	0.351	1.000
	544	cytolethal distending toxin type IV subunit C	*cdtC*	0.7	0.0	2.0	1.4	1.000	0.210	0.439	1.000
	545	putative protease/hydrolase		14.2	8.5	15.5	65.7	0.149	0.718	0.000	0.000
17	1177	putative phage tail protein		56.0	26.3	28.0	55.7	0.000	0.001	1.000	0.001
	1179	putative phage tail protein		52.0	21.3	24.0	51.4	0.000	0.001	1.000	0.001
	1180	phage-associated protein		50.7	22.5	28.0	54.3	0.000	0.007	0.740	0.001
	1181	phage-associated protein		54.7	22.5	24.0	48.6	0.000	0.000	0.508	0.003
	1184	phage-associated protein		53.3	22.5	28.0	55.7	0.000	0.003	0.868	0.001
	1185	conserved hypothetical protein		52.0	22.5	26.7	37.1	0.000	0.002	0.095	0.212
20	4022	putative adenine methylase		5.3	18.8	12.0	31.4	0.014	0.245	0.000	0.005
	4030	phage-associated protein		17.3	18.8	13.3	38.6	0.838	0.651	0.005	0.001
	4038	putative phage terminase		17.3	18.8	13.3	37.1	0.838	0.651	0.009	0.001
	4041	putative phage tail protein		6.7	0.0	0.0	0.0	0.025	0.058	0.059	1.000
	4051	phage-associated protein		2.7	11.3	4.0	4.3	0.058	1.000	0.673	1.000

	4053	phage-associated protein		4.0	12.5	6.7	2.9	0.081	0.719	1.000	0.444
	4055	phage-associated protein		1.3	0.0	0.0	1.4	0.484	1.000	1.000	0.483
	4059	phage-associated protein		14.7	1.3	4.0	34.3	0.002	0.046	0.007	0.000
30	3030	Auf fimbriae major subunit precursor	*aufA*	27.8	7.5	59.0	78.6	0.057	0.000	0.000	0.004
	3032	Auf fimbriae outer membrane usher protein	*aufC*	27.8	7.5	59.0	81.4	0.057	0.000	0.000	0.001
	3034	Auf fimbriae minor subunit precursor	*aufE*	27.8	7.5	59.0	81.4	0.057	0.000	0.000	0.001
	3038	Auf fimbrial protein	*aufG*	63.3	53.8	64.5	67.1	0.000	0.000	0.000	0.771
	3040	conserved hypothetical protein		84.8	59.4	80.0	88.6	0.007	0.000	0.000	0.145
40	2264	putative Orn/Lys/Arg decarboxylase		2.0	4.7	19.5	14.3	0.157	0.000	0.000	0.373
	2271	conserved hypothetical protein		3.3	3.8	17.0	11.4	0.769	0.000	0.007	0.339
	2277	conserved hypothetical protein		2.4	2.8	16.5	12.9	0.736	0.000	0.000	0.567
	2291	ethanolamine utilization protein	*eutE*	1.3	0.0	17.0	14.3	0.601	0.000	0.000	0.708
	2301	response regulator of two-component signal transduction system		22.8	11.3	40.0	31.4	0.008	0.000	0.132	0.252
	2310	conserved hypothetical protein		23.2	11.3	44.5	31.4	0.005	0.000	0.137	0.067
	2314	conserved hypothetical protein		60.0	58.5	77.0	61.4	0.826	0.000	0.896	0.018
42	2068	putative Na(+)/H(+) exchanger	*yjcE*	16.4	21.7	48.5	80.0	0.201	0.000	0.000	0.000
	2071	C4-dicarboxylate transport system		16.4	21.7	51.0	81.4	0.201	0.000	0.000	0.000

		permease									
	2078	EcoKI restriction-modification system protein	*hsdS*	6.0	6.6	5.0	42.9	0.822	0.716	0.000	0.000
	2080	conserved hypothetical protein		14.4	20.8	36.5	55.7	0.136	0.000	0.000	0.007
	2093	invasion protein	*ibeA*	11.7	6.6	17.5	72.9	0.162	0.062	0.000	0.000
	2095	glyoxylate carboligase	*gclA*	11.9	6.6	18.5	72.9	0.122	0.037	0.000	0.000
	2099	putative carnitine transporter	*cniT*	8.6	6.6	11.5	48.6	0.563	0.250	0.000	0.000
	2101	putative major facilitator familytefflux protein		11.7	6.6	18.0	72.9	0.162	0.036	0.000	0.000
	2103	dihydroxyacetone kinase	*dhaK*	11.9	6.6	18.0	72.9	0.122	0.048	0.000	0.000

[A] ORF = open reading frame locus from APEC O1 annotation.

[B] APEC = avian pathogenic *E. coli*; AFEC = avian fecal *E. coli*; UPEC = uropathogenic *E. coli*; NMEC = neonatal meningitis-associated *E. coli*.

Supplementary Table 3. Prevalence of APEC O1 genomic island (GI)-associated genes according to serogroup and phylogenetic group. Cells are colored based upon prevalence (blue = 0-25%, green = 25-50%, orange = 50-75%, red = 75-100%).

				Serogroup					Phylogenetic group			
GI	**ORF[A]**	**Predicted protein**	**Gene**	**O1**	**O2**	**O6**	**O18**	**O78**	**A**	**B1**	**B2**	**D**
1	1753	putative endopeptidase		74.3	31.5	45.2	85.0	0.9	2.9	0.9	54.0	4.4
	1756	type VI secretion system protein		74.3	44.9	88.1	85.0	0.9	3.7	1.7	69.3	9.3
	1757	hemolysin co-regulated protein; type VI secretion system protein	*hcp*	82.9	39.3	50.0	85.0	7.3	13.2	14.5	62.8	18.1
	1761	type VI secretion system protein		85.7	39.3	47.6	85.0	0.9	4.1	1.7	62.2	4.9
	1767	type VI secretion system ATPase		82.9	38.2	45.2	85.0	0.9	4.5	1.7	59.7	14.2
	1770	type VI secretion system protein, associated with macrophage killing		80.0	34.8	45.2	85.0	1.8	4.1	1.7	58.8	15.2
	1772	type VI secretion system effector protein		88.6	39.3	47.6	85.0	1.8	4.1	4.3	63.1	8.3
2	1712	vacuolating autotransporter / temperature-sensitive hemaggutinin	*vat/tsh*	91.4	74.2	95.2	87.5	66.7	49.0	45.3	84.9	58.3
	1713	putative transcriptional regulator		88.6	66.3	95.2	85.0	0.9	5.8	6.8	79.5	43.6
	1716	conserved hypothetical protein		14.3	2.2	0.0	2.5	12.6	8.6	12.8	3.1	6.9
	1717	conserved hypothetical protein		20.0	4.5	0.0	5.0	13.5	9.1	19.7	6.0	8.3

	1718	conserved hypothetical protein		8.6	1.1	0.0	0.0	0.9	0.8	3.4	1.4	1.5
	1721	conserved hypothetical protein		22.9	4.5	0.0	5.0	12.6	9.5	15.4	5.4	7.4
	1724	conserved hypothetical protein		20.0	4.5	0.0	0.0	1.8	4.5	6.8	5.1	5.4
3	1694	putative attaching and effacing protein	*eaeH*	94.3	91.7	100.0	100.0	89.3	73.5	79.8	96.3	90.3
	1696	putative aldo/keto reductase		94.3	77.8	97.6	86.2	1.8	12.3	13.1	92.2	67.2
	1698	putative LysR-like transcriptional regulator		91.4	58.3	95.2	86.2	1.8	11.7	11.9	91.0	45.5
4	1681	putative site-specific recombinase		100.0	88.0	97.1	88.5	0.0	16.9	18.2	89.5	41.8
	1682	putative LuxR-like transcriptional regulator		100.0	88.0	97.1	88.5	0.0	16.9	18.2	89.0	40.5
	1683	conserved hypothetical protein		100.0	88.0	97.1	88.5	0.0	15.7	6.8	89.5	38.0
	1684	putative autotransporter		100.0	88.0	94.1	88.5	0.0	16.9	18.2	88.1	40.5
5	1662	sugar ABC transporter, permease component		82.4	48.0	5.9	92.3	0.0	15.7	70.5	42.0	64.6
	1663	sugar ABC transporter, transmembrane component		82.4	48.0	5.9	92.3	0.0	15.7	86.4	45.7	68.4
	1664	sugar ABC transporter, ATP-binding component		82.4	48.0	5.9	92.3	0.0	15.7	86.4	46.1	68.4
	1665	sugar ABC transporter, periplasmic-binding component		82.4	48.0	5.9	92.3	0.0	15.7	79.5	45.7	65.8
8	4460	phage-associated protein	*cox*	3.4	0.0	0.0	23.3	5.9	4.4	4.5	7.0	1.1
	4464	putative phage replication initiation protein		6.9	25.7	14.3	40.0	41.2	25.6	31.8	26.9	34.7

	4467	putative phage terminase		10.3	25.7	16.7	46.7	29.4	25.6	34.1	31.5	37.9
	4468	putative phage capsid scaffolding protein		6.9	28.6	16.7	46.7	11.8	22.2	36.4	30.1	38.9
	4472	putative phage lysis holin		6.9	28.6	16.7	46.7	5.9	21.1	38.6	30.1	40.0
	4480	putative phage baseplate assembly protein		6.9	28.6	16.7	33.3	17.6	21.1	36.4	27.6	35.8
	11	putative phage tail protein		6.9	22.9	14.3	40.0	29.4	25.6	36.4	25.9	37.9
	12	putative phage tail protein		6.9	28.6	16.7	46.7	29.4	26.7	40.9	30.1	38.9
13-14	516	phage-associated protein	*trkG*	6.9	14.3	0.0	6.7	23.5	28.9	45.5	7.0	30.5
	517	putative transcriptional regulator		6.9	14.3	0.0	6.7	23.5	32.2	45.5	5.9	28.4
	518	phage-associated protein		6.7	0.0	5.9	12.5	100.0	27.6	33.3	8.6	23.8
	520	putative phage terminase		6.9	14.3	0.0	6.7	23.5	18.9	36.4	5.6	25.3
	522	conserved hypothetical protein		6.9	14.3	0.0	6.7	23.5	17.8	36.4	4.5	25.3
	523	putative phage morphogenesis protein		0.0	0.0	5.9	12.5	100.0	17.2	25.0	7.5	14.3
	525	phage-associated protein		6.9	14.3	0.0	6.7	23.5	17.8	36.4	4.9	27.4
	530	conserved hypothetical protein		6.9	14.3	0.0	6.7	23.5	15.6	34.1	4.2	24.2
	532	putative phage tail protein	*ynaA*	6.9	14.3	0.0	6.7	23.5	14.4	34.1	4.2	26.3
	542	cytolethal distending toxin type IV subunit A	*cdtA*	6.7	0.0	0.0	0.0	0.0	0.0	0.0	0.5	0.0
	543	cytolethal distending toxin type IV subunit B	*cdtB*	6.7	0.0	2.9	0.0	0.0	3.4	0.0	2.7	0.0

	544	cytolethal distending toxin type IV subunit C	*cdtC*	6.7	0.0	2.9	0.0	0.0	3.4	0.0	2.1	0.0
	545	putative protease/hydrolase		0.0	25.0	2.9	58.3	100.0	31.0	8.3	29.9	26.2
17	1177	putative phage tail protein		14.3	37.0	5.9	50.0	29.4	31.5	40.0	34.5	37.8
	1179	putative phage tail protein		14.3	29.6	5.9	40.9	29.4	27.4	34.3	30.1	36.5
	1180	phage-associated protein		14.3	37.0	5.9	50.0	11.8	23.3	37.1	34.5	36.5
	1181	phage-associated protein		14.3	37.0	5.9	45.5	41.2	28.8	37.1	28.6	35.1
	1184	phage-associated protein		14.3	33.3	5.9	50.0	29.4	28.8	37.1	34.0	36.5
	1185	conserved hypothetical protein		14.3	37.0	5.9	36.4	23.5	24.7	37.1	28.2	35.1
20	4022	putative adenine methylase		9.5	7.4	11.8	40.9	0.0	21.9	2.9	20.9	2.7
	4030	phage-associated protein		14.3	14.8	11.8	45.5	5.9	23.3	2.9	20.9	13.5
	4038	putative phage terminase		14.3	14.8	11.8	45.5	5.9	23.3	2.9	23.8	13.5
	4041	putative phage tail protein		4.8	7.4	0.0	0.0	0.0	0.0	0.0	1.5	2.7
	4051	phage-associated protein		4.8	3.7	5.9	0.0	0.0	13.7	0.0	4.4	0.0
	4053	phage-associated protein		4.8	3.7	5.9	9.1	0.0	17.8	0.0	5.3	2.7
	4055	phage-associated protein		4.8	0.0	0.0	9.1	0.0	0.0	0.0	2.9	0.0
	4059	phage-associated protein		9.5	11.1	0.0	45.5	5.9	2.7	0.0	19.4	9.5
30	3030	Auf fimbriae major subunit precursor	*aufA*	77.1	65.3	95.2	86.2	1.8	6.2	6.0	74.8	33.6
	3032	Auf fimbriae outer membrane usher protein	*aufC*	77.1	65.3	95.2	86.2	1.8	6.8	6.0	75.1	33.6

	3034	Auf fimbriae minor subunit precursor	*aufE*	77.1	65.3	95.2	86.2	1.8	6.8	6.0	75.1	33.6
	3038	Auf fimbrial protein	*aufG*	80.0	56.9	95.2	100.0	96.4	63.6	79.8	68.5	34.3
	3040	conserved hypothetical protein		91.4	81.9	100.0	100.0	98.2	67.9	86.9	93.5	59.0
40	2264	putative Orn/Lys/Arg decarboxylase		77.1	16.9	0.0	5.0	0.9	4.1	1.7	18.5	3.9
	2271	conserved hypothetical protein		71.4	16.9	0.0	2.5	3.6	4.5	0.9	18.5	2.5
	2277	conserved hypothetical protein		80.0	18.0	0.0	2.5	0.0	1.2	0.9	18.5	5.4
	2291	ethanolamine utilization protein	*eutE*	80.0	15.7	0.0	2.5	0.0	1.2	0.9	18.2	2.0
	2301	response regulator of two-component signal transduction system		82.9	47.2	50.0	32.5	1.8	7.8	7.7	39.8	42.6
	2310	conserved hypothetical protein		71.4	49.4	59.5	35.0	1.8	7.4	7.7	42.9	42.2
	2314	conserved hypothetical protein		80.0	80.9	88.1	52.5	31.5	52.7	59.8	69.6	71.6
42	2068	putative Na(+)/H(+) exchanger	*yjcE*	48.6	34.8	71.4	85.0	2.7	8.8	6.0	69.0	13.2
	2071	C4-dicarboxylate transport system permease		48.6	34.8	71.4	85.0	2.7	9.2	6.0	70.5	13.2
	2078	EcoKI restriction-modification system protein	*hsdS*	20.0	14.6	0.0	77.5	0.0	4.2	0.0	19.3	2.5
	2080	conserved hypothetical protein		25.7	29.2	66.7	87.5	3.6	9.2	13.7	42.0	19.1
	2093	invasion protein	*ibeA*	22.9	18.0	4.8	82.5	0.0	3.8	0.0	42.9	6.9
	2095	glyoxylate carboligase	*gclA*	22.9	18.0	4.8	82.5	0.0	3.8	0.0	43.2	7.8
	2099	putative carnitine transporter	*cniT*	20.0	16.9	2.4	82.5	0.0	1.7	0.0	31.0	5.9

	2101	putative major facilitator familytefflux protein		22.9	18.0	4.8	82.5	0.0	3.8	0.0	42.9	7.4
	2103	dihydroxyacetone kinase	*dhaK*	22.9	18.0	4.8	82.5	0.0	3.8	0.0	43.2	7.4

[A] ORF = open reading frame locus from APEC O1 annotation.