

Supplementary Table S1. ORFs between the *pgsA* and *flhD* genes in the P12b genome

Locus tag	Gene name	Position of gene	G+C content (%)	Similar protein(s), strain(s) (Genbank accession No.)	% Identical /% similar (No. of aa overlap)	Putative function of protein
c1152	<i>pgsA</i>	1249581..1250129	52.8	phosphatidylglycerophosphate synthetase, <i>E. coli</i> O157:H7EDL933 (NP_288373)	100/100(182)	phosphatidylglycerophosphate synthetase
c1153	<i>sdaB</i>	complement (1251173..1252540)	57.4	L-serine ammonia-lyase 2, <i>E. coli</i> B171 (ZP_03059033)	91/96(455)	L-serine ammonia-lyase
c1154	<i>sdaC</i>	complement (1252601..1253890)	52.8	serine transporter, <i>Klebsiella pneumoniae</i> 342(YP_002236852)	92/95(429)	serine transporter
c1155		1254144..1254542	52.4	transposase, <i>Shewanella putrefaciens</i> CN-32(YP_001184434)	73/83(100)	transposase
c1156	<i>insH</i>	complement (1254581..1255561)	55.6	putative transposase, <i>E. coli</i> APEC O1(YP_001481374)	99/99(326)	transposase
c1157	<i>int1157</i>	1255726..1256928	48.4	phage integrase family protein, <i>Actinobacillus minor</i> NM305 (ZP_04752588)	50/70(406)	integrase
c1158		complement (1256950..1257453)	54.8	IS1 transposase orfB, <i>E. coli</i> SMS-3-5 (NP_569348)	99/99(167)	transposase
c1159		complement (1257372..1257599)	52.6	IS1 repressor protein InsA, <i>E. coli</i> ED1a (YP_002397850)	100/100(75)	IS1 repressor protein

c1160		complement (1257840..1258763)	46.4	DNA-directed DNA polymerase, <i>A. minor</i> NM305(ZP_04752587)	34/54(321)	unknown
c1161		1259222..1259725	55.0	IS1 transposase orfB, <i>E. coli</i> SMS-3-5 (NP_569348)	99/99(167)	transposase
c1162	<i>flnA</i>	1259891..1261414	47.6	FlnA, <i>E. coli</i> P12b (ACN58226)	99/99(477)	flagellin
c1163		1261626..1262639	40.5	IS605 family transposase orfB, <i>E. coli</i> SMS-3-5 (YP_001742549)	44/60(375)	transposase
c1164		complement (1262730..1263233)	54.8	IS1 transposase orfB, <i>E. coli</i> SMS-3-5 (YP_001739974)	98/98(167)	transposase
c1165		complement (1263152..1263379)	53.5	IS1 repressor protein InsA, <i>E. coli</i> ED1a (YP_002397850)	100/100(75)	IS1 repressor protein
c1166		1263514..1263975	44.8	hypothetical protein, <i>Shewanella</i> sp. MR-7(YP_739732)	52/67(138)	hypothetical protein
c1167		1264005..1264922	56.9	putative transposase, <i>K. pneumoniae</i> (ACJ76652)	89/95(278)	transposase
c1168		1264958..1266313	45.7	hypothetical protein, <i>Shewanella</i> sp. MR-7(YP_739732)	72/85(444)	hypothetical protein
c1169		1266350..1266673	53.7	putative IS629 transposase OrfA, <i>E. coli</i> O103:H2 (YP_003225086)	76/84(108)	transposase
c1170		1266939..1267151	56.8	IS629, transposase orfB	80/81(70)	transposase
c1171		complement (1267100..1267450)	54.7	hypothetical protein, <i>E. coli</i> B171 (NP_053119)	100/100(86)	hypothetical protein
c1172		1267759..1269267	53.6	Group II intron-encoded reverse transcriptase/maturase,	99/100(502)	reverse transcriptase/maturase

c1173		1269432..1269806	58.4	<i>E. coli</i> IAI39 (YP_002406484) integrase catalytic region,	98/98(124)	remnant of integrase
c1175		complement (1272784..1273764)	55.7	<i>E. coli</i> ATCC 8739(YP_001726350) putative transposase,	99/99(325)	transposase
c1176		complement (1273810..1274904)	43.7	<i>E. coli</i> APEC O1 (YP_001481374) hypothetical protein,	42/61(361)	hypothetical protein
c1177		complement (1275069..1275455)	55.8	<i>Shewanella</i> sp. MR-7(YP_739732) IS629 orfB,	83/92(128)	transposase
c1178		complement (1275632..1277140)	53.6	<i>Shigella flexneri</i> 2a2457T(NP_836758) Group II intron-encoded reverse transcriptase/maturase,	99/100(502)	reverse transcriptase/maturase
c1179		complement (1277748..1278173)	55.6	<i>E. coli</i> IAI39 (YP_002406484) integrase catalytic region,	97/98(120)	remnant of integrase
c1180	<i>yecA</i>	1279073..1279738	52.9	<i>E. coli</i> ATCC 8739(YP_001726350) conserved protein,	100/100(221)	metal-binding protein
c1181	<i>tyrP</i>	complement (1279800..1280951)	51.2	<i>E. coli</i> K12 (NP_416421) tyrosine-specific transport protein,	99/99(383)	tyrosine-specific permease
c1182	<i>fnA</i>	complement (1281478..1281975)	43.0	<i>E. coli</i> E24377A (YP_001463213) ferritin-1,	100/100(165)	iron-storage ferritin
c1183		complement (1282122..1282625)	52.6	<i>E. coli</i> IHE3034 (CP001969) IS1 transposase orfB,	99/99(167)	transposase
c1184		complement (1282544..1282771)	52.6	<i>E. coli</i> SMS-3-5 (YP_001739974) IS1 repressor protein Insa,	100/100(75)	IS1 repressor protein
c1185		complement (1283686..1284066)	48.3	<i>E. coli</i> SMS-3-5 (YP_002397850) conserved hypothetical protein,	90/92(126)	hypothetical protein
				<i>S. flexneri</i> 2a 301(AAN43500)		

c1186	<i>yecI</i>	complement (1284041..1284544)	47.8	ferritin-like protein, <i>E. coli</i> O157:H7 EDL933 (NP_288337)	100/100(167)	ferritin
c1187	<i>araF</i>	1285341..1286330	51.4	L-arabinose-binding periplasmic protein precursor, <i>E. coli</i> UTI89 (YP_541108)	99/100(329)	L-arabinose-binding periplasmic protein precursor
c1188	<i>araG</i>	1286400..1287914	52.2	L-arabinose transporter ATP-binding protein, <i>E. coli</i> E24377A (YP_001463204)	99/99(504)	L-arabinose transporter ATP-binding protein
c1189	<i>araH</i>	1288007..1288915	50.5	L-arabinose transporter permease protein, <i>E. coli</i> 83972 (ZP_04003480)	100/100(302)	L-arabinose transporter permease protein
c1190	<i>otsB</i>	1289271..1289882	50.5	trehalose-6-phosphate phosphatase, <i>E. coli</i> CFT073 (NP_754203)	99/100(203)	trehalose-6-phosphate phosphatase
c1191	<i>otsA</i>	1289857..1291281	49.3	trehalose-6-phosphate synthase, <i>E. coli</i> K12 (NP_416410)	100/100(474)	trehalose-6-phosphate synthase
c1192	<i>yecG</i>	complement (1291288..1291716)	45.2	universal stress protein, <i>E. coli</i> 55989 (YP_002403126)	99/99(142)	universal stress protein
c1193	<i>flhD</i>	1292497..1292847	46.7	transcriptional activator FlhD, <i>E. coli</i> CFT073 (NP_754200)	99/99(116)	transcriptional activator
