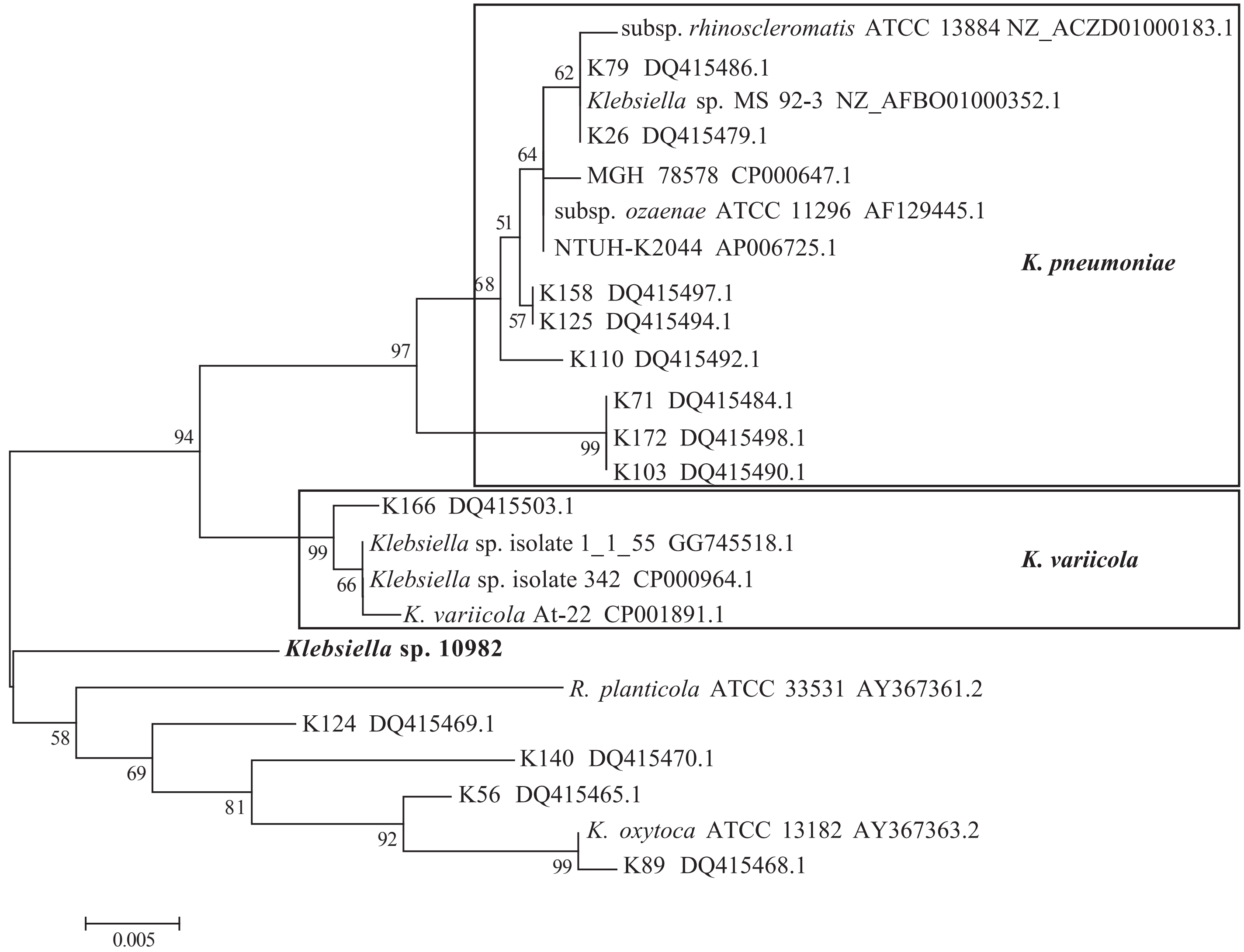
Supplemental Information

Supplemental Figure Legends

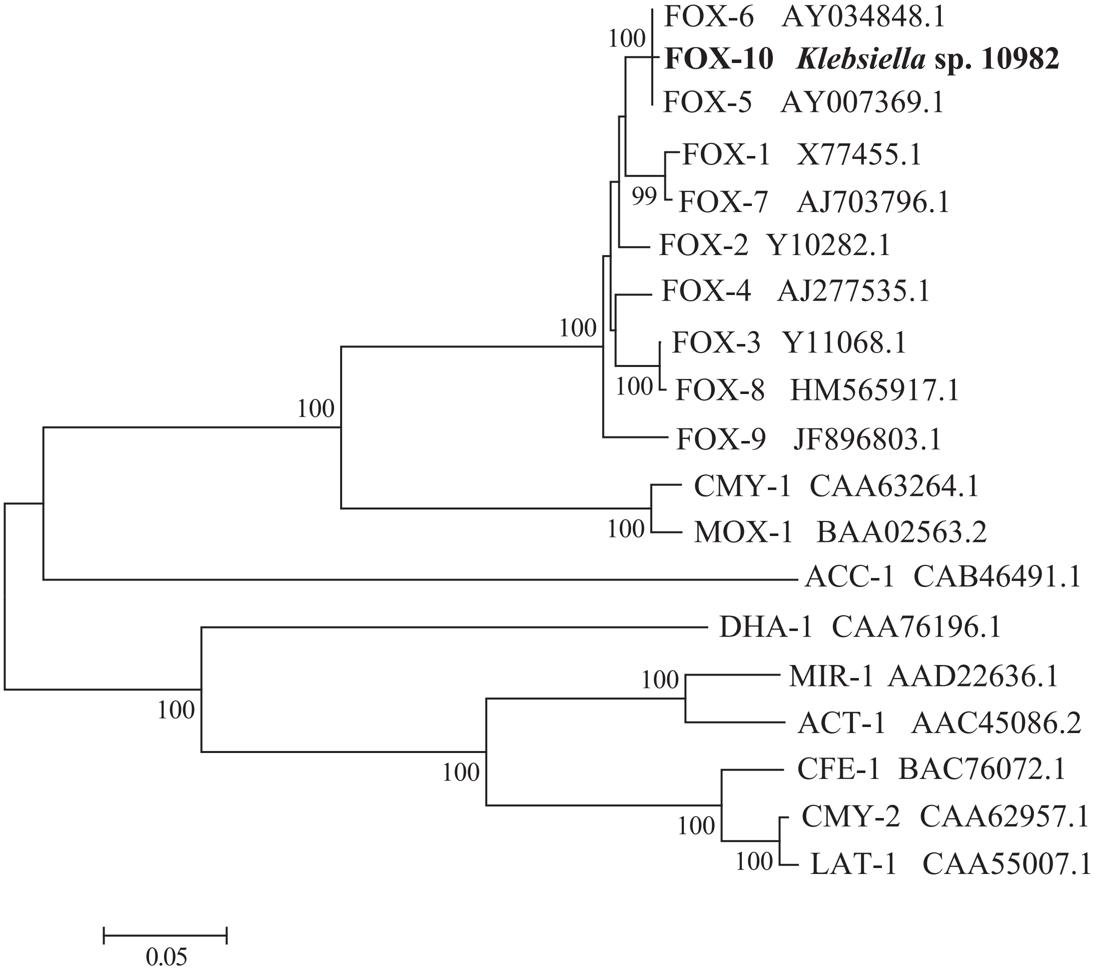
Supplemental Figure 1. Phylogenetic analysis of the partial *rpoB* nucleotide sequence (512 bp) constructed using the neighbor-joining method and Jukes-Cantor model with 1,000 bootstrap replications. The scale bar designates the evolutionary distance of 0.005 nucleotide substitutions per site. The accession numbers are indicated for sequences that were generated in a previous study (1) or were obtained from publicly available genomes that are listed in Supplemental Table 2.

Supplemental Figure 2. Phylogenetic analysis of the plasmid-encoded FOX-10 amino acid sequence from *Klebsiella* sp. 10982. The phylogeny was constructed with the neighbor-joining method and the p-distance model with 1,000 bootstrap replications. Only bootstrap values ≥50 are displayed. The scale bar designates the evolutionary distance of 0.05 amino acid substitutions per site. The FOX variants used in the phylogeny were those designated by the Lahey Clinic and are available on their website (http://www.lahey.org/Studies/). GenBank accession numbers are shown.

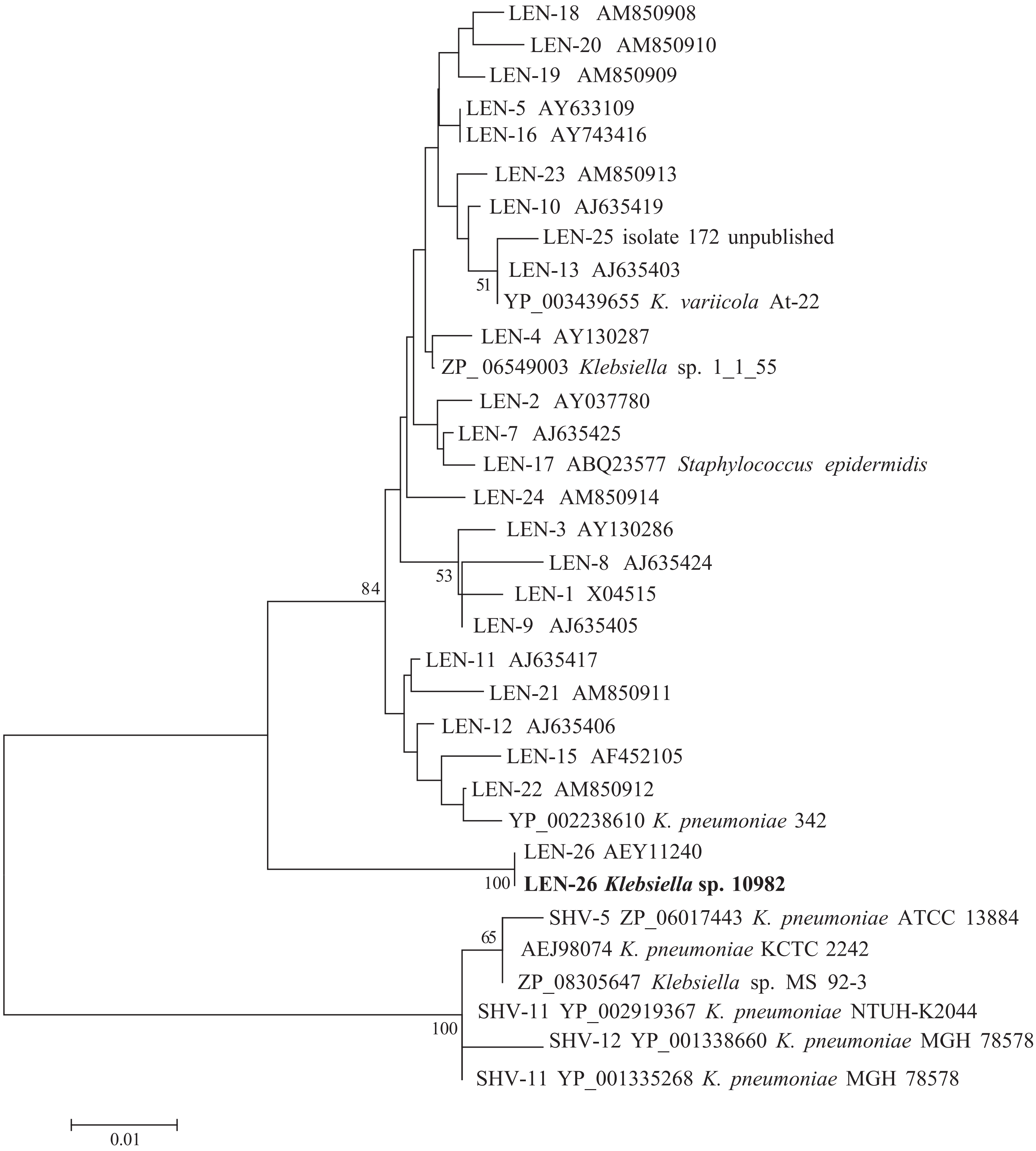
Supplemental Figure 3. Phylogenetic analysis of the LEN-26 amino acid sequence from *Klebsiella* sp. 10982. The phylogeny was constructed using MEGA5 (2) with the neighbor-joining method and the p-distance model with 1,000 bootstrap replications. Only bootstrap values ≥50 are shown. The scale bar designates the evolutionary distance of 0.01 amino acid substitutions per site. Accession numbers are shown for sequences from GenBank, while unpublished sequences that have been included in this phylogeny are available on the Institut Pasteur website (http://www.pasteur.fr/ip/easysite/pasteur/en/research/plates-formes-technologiques/pasteur-genopole-ile-de-france/genotyping-of-pathogens-and-public-health-pf8/beta-lactamase-enzyme-variants/beta-lactamase-enzyme-variants).



Supplemental Figure 1.



Supplemental Figure 2.



Supplemental Figure 3.

Supplemental Table 1. Primers used in this study

Primer	Sequence (5'-3')	Annealing Temperature	Amplicon size (bp)	Source
SHVS-F	GCCGGGTTATTCTTATTTGTCGC	58	992	(3)
SHVS-R	TCTTTCCGATGCCGCCGCCAGTCA			"
FOX_F	CAATTTCATTCACCACGAGAATA	52	1203	This study
FOX_R	AATGTGGACGCCTTGAACT			"
FOX5-A	ATGCAACAACGGCGTGCGTTC	56	1149	(4)
FOX5-B	TCACTCGGCCAACTGACTCAG			"
A/C FW	GAGAACCAAAGACAAAGACCTGGA	56	465	(5, 6)
A/C RV	ACGACAAACCTGAATTGCCTCCTT			"
allB_115F	GAGGCGAGGCAGGTCATGGA	58	1027	This study
allB_1142R	GCAATGCGGCCCTTATGCTTCAG			"
citC2_203F	AGGGAGAAGGGCTGAGCCTGA	58	743	"
citC2_946R	AGTTGCGCTGCCGGTAAAGCT			"
nifH_54F	CACCACCCAGAATCTCGTCGCG	58	674	"
nifH_728R	TGACGATATTCGTTGGCCTGCTGAC			"

The FOX and LEN genes of *Klebsiella* sp. 10982 were PCR amplified for sequencing using GoTaq polymerase (Promega) in a 50 µl reaction with the following concentrations of reagents: 1X Buffer, 2-2.5 mM $MgCl_2$, 0.2-0.4 µM of each primer, and 1U of Taq. The PCR for the allantoin and citrate synthesis gene were performed using AmpliTaq Gold 360 polymerase (Life Technologies). The PCR reaction was performed using the following final concentrations of reagents: 1X Buffer, 2 mM $MgCl_2$, 0.2 mM dNTPs, 0.2 µM of each primer, and 1.25 U of Taq, in a 15 µl final reaction volume. The PCR protocol included an initial denaturation at 95°C, followed by 30 cycles of 95˚C for 30s, 58˚C for 30s, and an elongation of 72˚C for 1m, and a final extension at 72˚C for 7m.

Supplemental Table 2. Genomes analyzed in this study

Organism	Strain Id	Isolate Source	Accession Number	Reference
K. pneumoniae	MGH 78578	human sputum	NC_009648.1	unpublished
K. pneumoniae	1162281	unknown	AFQL00000000.1	(7)
K. pneumoniae	NTUH-K2044	human blood	NC_012731.1	(8)
K. pneumoniae	JH1	unknown	AFQK00000000.1	(7)
K. pneumoniae	KCTC 2242	unknown	NC_017540.1	(9)
K. pneumoniae	1191100241	unknown	AFXH00000000.1	unpublished
K. pneumoniae	MS 92-3	unknown	AFBO00000000.1	unpublished
K. pneumoniae subsp. *rhinoscleromatis*	ATCC 13884	human airway sample	ACZD00000000.1	unpublished
Klebsiella sp.	10982	human perianal swab	AKYX00000000.1	This study
Klebsiella sp.	342	stem tissue of maize plant	NC_011283.1	(10)
Klebsiella sp.	1_1_55	human gastrointestinal tract	ACXA00000000.1	unpublished
K. variicola	At-22	*Atta cephalotes* fungus garden	CP001891.1	(11)
E. aerogenes	KCTC 2190	human specimen	NC_015663.1	(12)
E. lignolyticus	SCF1	rainforest soil	NC_014618.1	(13, 14)

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Supplemental Table 3. Predicted protein-encoding genes that are unique or shared for the genome of *Klebsiella* sp. 10982 compared to the *K. variicola* and *K. pneumoniae* genomes

Predicted Protein[a]	Best KEGG match[b]	*K. variicola*	10982	*K. pneumoniae*
DNA-binding protein ; K07727 putative transcriptional regulator	kpe:KPK_2699	+	-	-
transcriptional regulator, LysR family	kpe:KPK_2822	+	-	-
protein UmuD homolog ; K03503 DNA polymerase V [EC:3.4.21.-]	kpe:KPK_3299	+	-	-
hypothetical protein	kpe:KPK_3528	+	-	-
hypothetical protein	kpu:KP1_2621	+	-	-
peptide ABC transporter, periplasmic peptide-binding protein ; K02035 peptide/nickel transport system substrate-binding protein	kpe:KPK_2655	+	-	-
hypothetical protein	kpe:KPK_1197	+	-	-
hypothetical protein	kpe:KPK_1526	+	-	-
hypothetical protein	ptm:GSPATT00024139001	+	-	-
hypothetical protein	kpu:KP1_2728	+	-	-
hypothetical protein	kpe:KPK_5546	+	-	-
hypothetical protein	kpe:KPK_4499	+	-	-
hypothetical protein	kpe:KPK_3790	+	-	-
hypothetical protein	tet:TTHERM_00777240	+	-	-
hypothetical protein	kpe:KPK_0105	+	-	-
hypothetical protein	kpe:KPK_1847	+	-	-
hypothetical protein	kpe:KPK_4415	+	-	-
hypothetical protein	kpu:KP1_3534	+	-	-
hypothetical protein	xom:XOO_1656	+	-	-
formate dehydrogenase, alpha subunit ; K00123 formate dehydrogenase, alpha subunit [EC:1.2.1.2]	dvm:DvMF_0643	+	-	-
hypothetical protein	kpe:KPK_2112	+	-	-
hypothetical protein	kpe:KPK_3796	+	-	-
hypothetical protein	kpe:KPK_2394	+	-	-
tufB; elongation factor Tu	kpu:KP1_5049	+	-	-
hypothetical protein	kpe:KPK_2487	+	-	-
hypothetical protein	kpe:KPK_3190	+	-	-
AraC family transcriptional regulator	reu:Reut_B4713	+	-	-
hypothetical protein	kpe:KPK_2923	+	-	-
putative DNA processing protein DprA ; K04096 DNA processing protein	cps:CPS_0022	+	-	-
hypothetical protein	kpe:KPK_3275	+	-	-
hypothetical protein	kpe:KPK_0821	+	-	-
GK16620 gene product from transcript GK16620-RA	dwi:Dwil_GK16620	+	-	-
MUT6; DEAH-box RNA helicase ; K12815 pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16 [EC:3.6.1.-]	cre:CHLREDRAFT_132956	+	-	-
putative sulfonate ABC transporter, permease protein ; K02050 sulfonate/nitrate/taurine transport system permease protein	kpe:KPK_3095	+	-	-
hypothetical protein	kpe:KPK_3742	+	-	-
hypothetical protein	tcr:507711.70	+	-	-
hypothetical protein	kpe:KPK_2526	+	-	-
hypothetical protein	pyo:PY02327	+	-	-
sec7 domain-containing protein (EC:3.2.1.52)	tgo:TGME49_028650	+	-	-
putative lipoprotein	kpe:KPK_3328	+	-	-
hypothetical protein	kpe:KPK_3631	+	-	-
type I secretion outer membrane protein, TolC	rpd:RPD_1907	+	-	-
hypothetical protein	kpe:KPK_0858	+	-	-
hypothetical protein	kpe:KPK_0875	+	-	-
(p)ppGpp synthetase I, SpoT/RelA (EC:2.7.6.5); K01139 guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase [EC:3.1.7.2]	oan:Oant_2636	+	-	-
hypothetical protein	kpe:KPK_5243	+	-	-
hypothetical protein	kpe:KPK_2377	+	-	-
S1 RNA binding domain protein ; K06959	kpe:KPK_0339	+	-	-
hypothetical protein	kpe:KPK_0913	+	-	-
3-beta hydroxysteroid dehydrogenase/isomerase family protein	kpe:KPK_3122	+	-	-
hypothetical protein	kpe:KPK_3298	+	-	-
DNAJB1; DnaJ (Hsp40) homolog, subfamily B, member 1; K09507 DnaJ homolog subfamily B member 1	bta:538426	+	-	-
hypothetical protein	cko:CKO_02430	+	-	-
hypothetical protein	kpe:KPK_2559	+	-	-
HdeB family protein	kpe:KPK_0636	+	-	-
hypothetical protein	kpe:KPK_2887	+	-	-
hypothetical protein	kpe:KPK_3333	+	-	-
hypothetical protein	kpe:KPK_2592	+	-	-
hypothetical protein	kpu:KP1_1301	+	-	-
hypothetical protein	kpe:KPK_0397	+	-	-
hypothetical protein	kpe:KPK_3789	+	-	-
hypothetical protein	kpe:KPK_0740	+	-	-
hypothetical protein	kpu:KP1_0696	+	-	-
conserved hypothetical protein	pfh:PFHG_02195	+	-	-
hypothetical protein	kpe:KPK_3282	+	-	-
putative methylmalonyl-CoA mutase ; K01847 methylmalonyl-CoA mutase [EC:5.4.99.2]	azc:AZC_1773	+	-	-
hypothetical protein	kpe:KPK_2517	+	-	-
drug resistance MFS transporter, drug:H+ antiporter-1 (DHA2) family ; K03446 MFS transporter, DHA2 family, multidrug resista	kpe:KPK_2659	+	-	-
tnnt3a; troponin T3a, skeletal, fast	dre:58084	+	-	-
hypothetical protein	kpe:KPK_2377	+	-	-
hypothetical protein	kpe:KPK_2692	+	-	-
hypothetical protein	kpe:KPK_3295	+	-	-
hypothetical protein	kpe:KPK_0619	+	-	-
hypothetical protein	pcb:PC000411.02.0	+	-	-
hypothetical protein	kpe:KPK_0822	+	-	-
sbcB; exonuclease I ; K01141 exodeoxyribonuclease I [EC:3.1.11.1]	kpn:KPN_02469	+	-	-
hypothetical protein	kpe:KPK_3070	+	-	-
hypothetical protein	kpe:KPK_2515	+	-	-
hypothetical protein	kpe:KPK_2814	+	-	-
hypothetical protein	kpe:KPK_4086	+	-	-
drug resistance MFS transporter, drug:H+ antiporter-1 (DHA2) family	kpe:KPK_3283	+	-	-
hypothetical protein	kpe:KPK_1674	+	-	-
hypothetical protein	kpe:KPK_4570	+	-	-
hypothetical protein	kpe:KPK_3304	+	-	-
DNA polymerase III, delta prime subunit (EC:2.7.7.7); K02341 DNA polymerase III subunit delta' [EC:2.7.7.7]	mmw:Mmwyl1_2266	+	-	-
hypothetical protein	kpe:KPK_2560	+	-	-
hypothetical protein	kpe:KPK_2112	+	-	-

hypothetical protein	kpe:KPK_4293	+	-	-
AMP-dependent synthetase and ligase ; K00666 fatty-acyl-CoA synthase [EC:6.2.1.-]	bph:Bphy_7172	+	-	-
hypothetical protein	kpe:KPK_1848	+	-	-
hypothetical protein	kpe:KPK_2190	+	-	-
putative ABC transporter, substrate binding protein; K02035 peptide/nickel transport system substrate-binding protein	bbt:BBta_4877	+	-	-
hypothetical protein	kpe:KPK_0640	+	-	-
hypothetical protein	kpe:KPK_0819	+	-	-
hypothetical protein	kpe:KPK_1468	+	-	-
hypothetical protein LOC100266372	vvi:100266372	+	-	-
hypothetical protein	kpe:KPK_1528	+	-	-
hypothetical protein	kpe:KPK_3581	+	-	-
hypothetical protein	kpe:KPK_3343	+	-	-
hypothetical protein	kpe:KPK_3816	+	-	-
hypothetical protein	kpe:KPK_0338	+	-	-
adhesin/hemagglutinin	pfl:PFL_0166	+	-	-
hypothetical protein	kpe:KPK_4262	+	-	-
amidase ; K01426 amidase [EC:3.5.1.4]	kpe:KPK_2671	+	-	-
hypothetical protein	kpe:KPK_3718	+	-	-
carbamoyl-phosphate synthase, small subunit	sde:Sde_2696	+	-	-
hypothetical protein	kpe:KPK_1860	+	-	-
hypothetical protein	kpe:KPK_2338	+	-	-
hypothetical protein	kpu:KP1_2471	+	-	-
hypothetical protein	kpe:KPK_1856	+	-	-
hypothetical protein	kpe:KPK_1554	+	-	-
hypothetical protein	kpe:KPK_2093	+	-	-
hypothetical protein	kpe:KPK_5469	+	-	-
putative histidine ammonia-lyase ; K01745 histidine ammonia-lyase [EC:4.3.1.3]	kpe:KPK_3142	+	-	-
cysteine desulfurase, SufS family ; K11717 cysteine desulfurase / selenocysteine lyase [EC:2.8.1.7 4.4.1.16]	kpe:KPK_1757	+	-	-
FAD-binding lipoprotein	kpe:KPK_2973	+	-	-
hypothetical protein	kpe:KPK_2678	+	-	-
drug resistance MFS transporter, drug:H+ antiporter-1 (DHA2) family	kpe:KPK_3283	+	-	-
MmgE/PrpD family protein	kpe:KPK_3102	+	-	-
adenylosuccinate lyase ; K01756 adenylosuccinate lyase [EC:4.3.2.2]	kpe:KPK_1826	+	-	-
mgtB; magnesium-translocating P-type ATPase (EC:3.6.3.2); K01531 Mg2+-importing ATPase [EC:3.6.3.2]	kpe:KPK_3276	+	-	-
MmgE/PrpD family protein	kpe:KPK_1822	+	-	-
putative symporter YagG	kpe:KPK_0600	+	-	-
sodium:citrate symporter family protein ; K11616 malate:Na+ symporter	kpe:KPK_1918	+	-	-
transporter, major facilitator family	kpe:KPK_1076	+	-	-
ntaA; nitrilotriacetate monooxygenase, component A (EC:1.14.13.-)	kpe:KPK_1828	+	-	-
transporter, major facilitator family	kpe:KPK_2037	+	-	-
putative transporter	kpe:KPK_5051	+	-	-
protein UmuC homolog ; K03502 DNA polymerase V	kpe:KPK_3300	+	-	-
putative sugar ABC transporter, periplasmic sugar-binding protein ; K02027 multiple sugar transport system substrate-binding prot	kpe:KPK_2004	+	-	-
aatB; aspartate transaminase (EC:2.6.1.1); K00812 aspartate aminotransferase [EC:2.6.1.1]	kpe:KPK_1829	+	-	-
ROK family protein	kpe:KPK_2005	+	-	-
aatA; aspartate transaminase (EC:2.6.1.1); K00812 aspartate aminotransferase [EC:2.6.1.1]	kpe:KPK_3294	+	-	-
acetyl-CoA acetyltransferase ; K00626 acetyl-CoA C-acetyltransferase [EC:2.3.1.9]	kpe:KPK_2972	+	-	-
sensor histidine kinase	kpe:KPK_2666	+	-	-
transporter, major facilitator family ; K08156 MFS transporter, DHA1 family, arabinose polymer transporter	kpe:KPK_2975	+	-	-
amidohydrolase family protein	kpe:KPK_1824	+	-	-
auxiliary transport protein, membrane fusion protein (MFP) family ; K03543 multidrug resistance protein A	kpe:KPK_2660	+	-	-
putative thiazole biosynthesis adenylyltransferase ThiF/rhodanese domain protein ; K03751 molybdopterin biosynthesis protein M	kpe:KPK_1755	+	-	-
peptidase, ArgE/DapE family (EC:3.4.-.-); K01438 acetylornithine deacetylase [EC:3.5.1.16]	kpe:KPK_3289	+	-	-
creatinase/peptidase, M24 family (EC:3.4.-.-); K01271 X-Pro dipeptidase [EC:3.4.13.9]	kpe:KPK_3291	+	-	-
SMP-30/gluconolactonase/LRE family protein	kpe:KPK_5219	+	-	-
efflux transporter, RND family, MFP subunit	kpe:KPK_2667	+	-	-
fimbrial usher protein	kpe:KPK_0826	+	-	-
putative tetracycline resistance protein	kpe:KPK_3280	+	-	-
monooxygenase, luciferase family ; K04091 alkanesulfonate monooxygenase [EC:1.14.14.5]	kpe:KPK_2268	+	-	-
oxidoreductase, FAD/FMN-binding ; K10680 N-ethylmaleimide reductase [EC:1.-.-.-]	kpe:KPK_3270	+	-	-
amidohydrolase family protein	kpe:KPK_4860	+	-	-
mandelate racemase/muconate lactonizing enzyme family protein (EC:5.1.1.-)	kpe:KPK_3290	+	-	-
CTP synthase family protein	kpe:KPK_3292	+	-	-
putative sugar ABC transporter, ATP-binding protein	kpe:KPK_2000	+	-	-
putative glycerol dehydrogenase ; K00005 glycerol dehydrogenase [EC:1.1.1.6]	kpe:KPK_1827	+	-	-
quiA_1; quinate/shikimate dehydrogenase (pyrroloquinoline-quinone) (EC:1.1.99.25); K05358 quinate dehydrogenase (pyrroloqui	kpe:KPK_2122	+	-	-
putative sulfonate ABC transporter, sulfonate-binding protein ; K02051 sulfonate/nitrate/taurine transport system substrate-binding	kpe:KPK_3097	+	-	-
oxidoreductase, aldo/keto reductase family	kpe:KPK_2974	+	-	-
ABC transporter, periplasmic substrate-binding protein ; K02051 sulfonate/nitrate/taurine transport system substrate-binding prote	kpe:KPK_2621	+	-	-
NAD-dependent epimerase/dehydratase family protein	kpe:KPK_3257	+	-	-
oxidoreductase, aldo/keto reductase family	kpe:KPK_3721	+	-	-
oxidoreductase, zinc-binding dehydrogenase family	kpe:KPK_2328	+	-	-
hypothetical protein	kpe:KPK_2983	+	-	-
putative transcriptional regulator, AraC family	kpe:KPK_3267	+	-	-
hypothetical protein	kpe:KPK_0827	+	-	-
peptide ABC transporter, permease protein ; K02033 peptide/nickel transport system permease protein	kpe:KPK_2656	+	-	-
oxidoreductase, zinc-binding dehydrogenase family	kpe:KPK_1819	+	-	-
transporter, auxin efflux carrier family ; K07088	kpe:KPK_1917	+	-	-
transcriptional regulator, LysR family	kpe:KPK_5218	+	-	-
D-isomer specific 2-hydroxyacid dehydrogenase family protein	kpe:KPK_2038	+	-	-
D-isomer specific 2-hydroxyacid dehydrogenase family protein	kpe:KPK_1079	+	-	-
transcriptional regulator, LysR family	kpe:KPK_3096	+	-	-
hypothetical protein	kpe:KPK_1756	+	-	-
amino acid ABC transporter, permease protein	kpe:KPK_1821	+	-	-
transcriptional regulator, LysR family	kpe:KPK_3269	+	-	-
transcriptional regulator, LysR family	kpe:KPK_2581	+	-	-
dihydrodipicolinate synthetase family protein	kpe:KPK_3293	+	-	-
transcriptional regulator, LysR family	kpe:KPK_3098	+	-	-
auxiliary transport protein, membrane fusion protein (MFP) family	kpe:KPK_3337	+	-	-

transcriptional regulator, LysR family	kpe:KPK_2824	+	-	-
dgoK; 2-dehydro-3-deoxygalactonokinase (EC:2.7.1.58); K00883 2-dehydro-3-deoxygalactonokinase [EC:2.7.1.58]	kpe:KPK_2034	+	-	-
putative cysteine synthase B ; K12339 cysteine synthase B [EC:2.5.1.47]	kpe:KPK_1752	+	-	-
transcriptional regulator, LysR family	kpe:KPK_4863	+	-	-
putative sugar ABC transporter, permease protein ; K02025 multiple sugar transport system permease protein	kpe:KPK_2003	+	-	-
transcriptional regulator, GntR family	kpe:KPK_3285	+	-	-
amino acid ABC transporter, periplasmic amino acid-binding protein	kpe:KPK_1820	+	-	-
QbdB protein	kpe:KPK_2669	+	-	-
transcriptional regulator, LysR family	kpe:KPK_2822	+	-	-
transcriptional regulator, LysR family	kpe:KPK_2816	+	-	-
hypothetical protein	kpe:KPK_1875	+	-	-
transcriptional regulator, LysR family	kpe:KPK_3256	+	-	-
diguanylate cyclase/cyclic diguanylate phosphodiesterase	kpe:KPK_2890	+	-	-
uca; UreA carboxylase (EC:6.3.4.6)	kpe:KPK_2626	+	-	-
transcriptional regulator, LysR family	kpe:KPK_2589	+	-	-
amino acid ABC transporter, periplasmic amino acid-binding protein	kpe:KPK_1532	+	-	-
transcriptional regulator, AraC family	kpe:KPK_0599	+	-	-
peptide ABC transporter, permease protein ; K02034 peptide/nickel transport system permease protein	kpe:KPK_2657	+	-	-
amino acid ABC transporter, periplasmic amino acid-binding protein ; K10018 octopine/nopaline transport system substrate-bindir	kpe:KPK_3146	+	-	-
metallo-beta-lactamase family protein ; K06897	kpe:KPK_0638	+	-	-
putative sugar ABC transporter, permease protein ; K02026 multiple sugar transport system permease protein	kpe:KPK_2002	+	-	-
short chain dehydrogenase	kpe:KPK_3268	+	-	-
ABC transporter, permease protein ; K02050 sulfonate/nitrate/taurine transport system permease protein	kpe:KPK_2622	+	-	-
amino acid ABC transporter, periplasmic amino acid-binding protein	kpe:KPK_3286	+	-	-
amino acid ABC transporter, ATP-binding protein ; K10021 octopine/nopaline transport system ATP-binding protein [EC:3.6.3.-]	kpe:KPK_3143	+	-	-
amino acid ABC transporter, ATP-binding protein	kpe:KPK_3100	+	-	-
amino acid ABC transporter, periplasmic amino acid-binding protein	kpe:KPK_3099	+	-	-
putative pyrroline-5-carboxylate reductase ; K00286 pyrroline-5-carboxylate reductase [EC:1.5.1.2]	kpe:KPK_1534	+	-	-
hypothetical protein	kpe:KPK_2971	+	-	-
MipA family protein	kpe:KPK_2664	+	-	-
oxidoreductase, short chain dehydrogenase/reductase family ; K00059 3-oxoacyl-[acyl-carrier protein] reductase [EC:1.1.1.100]	kpe:KPK_3284	+	-	-
amino acid ABC transporter, ATP-binding protein	kpe:KPK_1529	+	-	-
ABC transporter, ATP-binding protein ; K02049 sulfonate/nitrate/taurine transport system ATP-binding protein	kpe:KPK_2623	+	-	-
hypothetical protein	kpe:KPK_3297	+	-	-
amino acid ABC transporter, ATP-binding protein	kpe:KPK_1823	+	-	-
hypothetical protein	kpe:KPK_2676	+	-	-
amino acid ABC transporter, permease protein	kpe:KPK_1531	+	-	-
putative sulfonate ABC transporter, ATP-binding protein ; K02049 sulfonate/nitrate/taurine transport system ATP-binding protein	kpe:KPK_3094	+	-	-
acetyltransferase, GNAT family	kpe:KPK_2815	+	-	-
amino acid ABC transporter, ATP-binding protein ; K02028 polar amino acid transport system ATP-binding protein [EC:3.6.3.21]	kpe:KPK_3288	+	-	-
amino acid ABC transporter, permease protein ; K10019 octopine/nopaline transport system permease protein	kpe:KPK_3144	+	-	-
hypothetical protein ; K09967 hypothetical protein	kpe:KPK_2624	+	-	-
amino acid ABC transporter, permease protein ; K02029 polar amino acid transport system permease protein	kpe:KPK_3287	+	-	-
amino acid ABC transporter, permease protein ; K10020 octopine/nopaline transport system permease protein	kpe:KPK_3145	+	-	-
response regulator	kpe:KPK_1915	+	-	-
transcriptional regulator, IclR family	kpe:KPK_1077	+	-	-
hypothetical protein	kpe:KPK_2330	+	-	-
fusaric acid resistance domain protein	kpe:KPK_3334	+	-	-
amino acid ABC transporter, permease protein	kpe:KPK_1530	+	-	-
hypothetical protein	kpe:KPK_1078	+	-	-
DNA-binding response regulator	kpe:KPK_2665	+	-	-
transporter gate domain protein	kpe:KPK_4862	+	-	-
gram-negative pilus assembly chaperone	vap:KPK_0825	+	-	-
transcriptional regulator, LuxR family	kpe:KPK_2813	+	-	-
amino acid ABC transporter, permease protein	kpe:KPK_3101	+	-	-
HAD hydrolase, IB family, TIGR01490	kpe:KPK_2970	+	-	-
nthB; nitrile hydratase, beta subunit (EC:4.2.1.84); K01721 nitrile hydratase [EC:4.2.1.84]	kpe:KPK_2673	+	-	-
hypothetical protein	kpe:KPK_2628	+	-	-
hypothetical protein ; K09967 hypothetical protein	kpe:KPK_2625	+	-	-
glutathione S-transferase (EC:2.5.1.18); K00799 glutathione S-transferase [EC:2.5.1.18]	kpe:KPK_2590	+	-	-
transcriptional regulator, LuxR family	kpe:KPK_2808	+	-	-
nthA; nitrile hydratase, alpha subunit (EC:4.2.1.84); K01721 nitrile hydratase [EC:4.2.1.84]	kpe:KPK_2672	+	-	-
transcriptional regulator, TetR family	kpe:KPK_3296	+	-	-
hypothetical protein	kpe:KPK_3271	+	-	-
fimbrial protein ; K07345 major type 1 subunit fimbrin (pilin)	kpe:KPK_1142	+	-	-
tetR; tetracycline repressor protein class A from transposon 1721	kpe:KPK_3281	+	-	-
phosphoglycerate mutase family protein	kpe:KPK_2677	+	-	-
hypothetical protein	kpe:KPK_0641	+	-	-
translocator protein, LysE family	kpe:KPK_2817	+	-	-
isochorismatase hydrolase family protein (EC:3.-.-.-); K05993 isochorismatase [EC:3.3.2.1]	kpe:KPK_3346	+	-	-
fimbrial protein	kpe:KPK_0824	+	-	-
hypothetical protein	kpe:KPK_1533	+	-	-
acetyltransferase, GNAT family	kpe:KPK_1825	+	-	-
PilN family protein ; K12289 pilus assembly protein HofN	kpe:KPK_0351	+	-	-
hypothetical protein	kpe:KPK_2698	+	-	-
atzF; allophanate hydrolase (EC:3.5.1.54); K02433 aspartyl-tRNA(Asn)/glutamyl-tRNA (Gln) amidotransferase subunit A [EC:6.3	kpe:KPK_2627	+	-	-
hypothetical protein ; K09936 hypothetical protein	kpe:KPK_2583	+	-	-
transcriptional regulator, MarR family ; K03712 MarR family transcriptional regulator	kpe:KPK_2661	+	-	-
protozoan/cyanobacterial globin family protein ; K06886 hemoglobin	kpe:KPK_2670	+	-	-
hypothetical protein	kpe:KPK_3093	+	-	-
OsmC family protein	kpe:KPK_3347	+	-	-
hypothetical protein	kpe:KPK_4861	+	-	-
hypothetical protein	kpe:KPK_2674	+	-	-
glyoxalase family protein	kpe:KPK_2729	+	-	-
hypothetical protein ; K09936 hypothetical protein	kpe:KPK_2582	+	-	-
hypothetical protein ; K12290 pilus assembly protein HofO	kpe:KPK_0352	+	-	-
hypothetical protein	kpe:KPK_1753	+	-	-
glycerophosphoryl diester phosphodiesterase ; K01126 glycerophosphoryl diester phosphodiesterase [EC:3.1.4.46]	vap:Vapar_0332	+	-	-
hypothetical protein	kpe:KPK_4859	+	-	-

hypothetical protein	kpe:KPK_3279	+	-	-
malate dehydrogenase ; K00027 malate dehydrogenase (oxaloacetate-decarboxylating) [EC:1.1.1.38]	kpe:KPK_1916	+	-	-
pemK; protein PemK ; K07171	kpe:KPK_1741	+	-	-
pemI; protein PemI ; K07172	kpe:KPK_1740	+	-	-
hypothetical protein	kpe:KPK_2591	+	-	-
hypothetical protein	kpe:KPK_3295	+	-	-
peptide ABC transporter, ATP binding protein ; K02031 peptide/nickel transport system ATP-binding protein; K02032 peptide/nick	kpe:KPK_2658	+	-	-
ThiS family protein	kpe:KPK_1754	+	-	-
hypothetical protein	kpe:KPK_4896	+	-	-
putative Na/Pi-cotransporter ; K03324 phosphate:Na+ symporter, PNaS family	kpe:KPK_3278	+	-	-
hypothetical protein	kpe:KPK_2430	+	-	-
hypothetical protein	kpe:KPK_1952	+	-	-
pmrD; polymyxin B resistance protein PmrD	kpe:KPK_1746	+	-	-
hypothetical protein	kpe:KPK_3274	+	-	-
putative xylan 1,4-beta-xylosidase	kpe:KPK_0598	+	-	-
hypothetical protein	kpe:KPK_0639	+	-	-
RND transporter, hydrophobe/amphiphile efflux-1 (HAE1) family	kpe:KPK_2668	+	-	-
hypothetical protein	kpe:KPK_2950	+	-	-
hypothetical protein	kpe:KPK_3277	+	-	-
hypothetical protein	kpe:KPK_3335	+	-	-
hypothetical protein	kpe:KPK_2675	+	-	-
hypothetical protein	pat:Patl_0188	+	-	-
hypothetical protein	kpe:KPK_1951	+	-	-
nifJ; pyruvate-flavodoxin oxidoreductase (EC:1.2.7.1); K03737 putative pyruvate-flavodoxin oxidoreductase [EC:1.2.7.-]	kpe:KPK_1715	+	+	-
peptidyl-prolyl cis-trans isomerase, FKBP-type domain	kpe:KPK_4610	+	+	-
porin, LamB family	kpe:KPK_1432	+	+	-
aldH; aldehyde dehydrogenase (NADP(+)) (EC:1.2.1.4)	kpe:KPK_4822	+	+	-
amino acid permease family protein	kpe:KPK_4821	+	+	-
nifA; Nif-specific regulatory protein ; K02584 Nif-specific regulatory protein	kpe:KPK_1698	+	+	-
nifK; nitrogenase molybdenum-iron protein beta chain (EC:1.18.6.1); K02591 nitrogenase molybdenum-iron protein beta chain [E	kpe:KPK_1712	+	+	-
nifL; nitrogen fixation negative regulator NifL	kpe:KPK_1699	+	+	-
nifD; nitrogenase molybdenum-iron protein alpha chain (EC:1.18.6.1); K02586 nitrogenase molybdenum-iron protein alpha chain	kpe:KPK_1713	+	+	-
nifB; nitrogenase cofactor biosynthesis protein NifB ; K02585 nitrogen fixation protein NifB	kpe:KPK_1697	+	+	-
cobZ; tricarballylate dehydrogenase	kpe:KPK_3866	+	+	-
nifN; nitrogenase molybdenum-iron cofactor biosynthesis protein NifN ; K02592 nitrogenase molybdenum-iron protein NifN	kpe:KPK_1708	+	+	-
nifE; nitrogenase MoFe cofactor biosynthesis protein NifE ; K02587 nitrogenase molybdenum-cofactor synthesis protein NifE	kpe:KPK_1709	+	+	-
PTS system, lactose/cellobiose family IIC component (EC:2.7.1.69); K02761 PTS system, cellobiose-specific IIC component	kpe:KPK_1430	+	+	-
monooxygenase, luciferase family	kpe:KPK_2008	+	+	-
hypothetical protein ; K00837 [EC:2.6.1.-]	kpe:KPK_3265	+	+	-
transporter, major facilitator family ; K03535 MFS transporter, ACS family, glucarate transporter	kpe:KPK_2459	+	+	-
transporter, major facilitator family	kpe:KPK_4700	+	+	-
citrate:proton symporter	kpe:KPK_3868	+	+	-
pyridine nucleotide-disulfide oxidoreductase	kpe:KPK_4828	+	+	-
acyl-CoA dehydrogenase, C-terminal domain protein	kpe:KPK_2322	+	+	-
nifS; cysteine desulfurase NifS (EC:2.8.1.7); K04487 cysteine desulfurase [EC:2.8.1.7]	kpe:KPK_1705	+	+	-
mandelate racemase/muconate lactonizing enzyme family protein ; K01781 mandelate racemase [EC:5.1.2.2]	kpe:KPK_2460	+	+	-
nifV; homocitrate synthase (EC:2.3.3.14); K01655 homocitrate synthase [EC:2.3.3.14]; K02594 homocitrate synthase NifV	kpe:KPK_1704	+	+	-
citB; citrate utilization protein B	kpe:KPK_3867	+	+	-
auxiliary transport protein, membrane fusion protein (MFP) family	kpe:KPK_1564	+	+	-
FAD-dependent oxidoreductase	kpe:KPK_4826	+	+	-
hypothetical protein	kpe:KPK_4500	+	+	-
quaternary amine uptake ABC transporter (QAT) family, ATP-binding protein ; K05847 osmoprotectant transport system ATP-bind	kpe:KPK_2012	+	+	-
transcriptional regulator, LuxR family	kpe:KPK_2311	+	+	-
hypothetical protein	kpe:KPK_3698	+	+	-
ABC transporter, ATP-binding protein ; K02071 D-methionine transport system ATP-binding protein	kpe:KPK_2319	+	+	-
acyl-coenzyme A:6-aminopenicillanic acid acyl-transferase	kpe:KPK_3259	+	+	-
sugar binding transcriptional regulator, LacI family ; K02529 LacI family transcriptional regulator	kpe:KPK_5053	+	+	-
sugar binding transcriptional regulator, LacI family ; K06145 LacI family transcriptional regulator, gluconate utilization system Gr	kpe:KPK_2461	+	+	-
transcriptional regulator, LysR family	kpe:KPK_1561	+	+	-
transcriptional regulator, LysR family	kpe:KPK_1561	+	+	-
sugar binding transcriptional regulator, LacI family	kpe:KPK_4702	+	+	-
sugar binding transcriptional regulator, LacI family ; K02529 LacI family transcriptional regulator	kpe:KPK_5053	+	+	-
D-isomer specific 2-hydroxyacid dehydrogenase family protein ; K00050 hydroxypyruvate reductase [EC:1.1.1.81]	kpe:KPK_4701	+	+	-
proline racemase family protein ; K12658 4-hydroxyproline epimerase [EC:5.1.1.8]	kpe:KPK_4825	+	+	-
putative lipoprotein	kpe:KPK_2561	+	+	-
dihydrodipicolinate synthetase family protein ; K01714 dihydrodipicolinate synthase [EC:4.2.1.52]	kpe:KPK_5052	+	+	-
transcriptional regulator, LysR family	kpe:KPK_3865	+	+	-
paeX; acetylesterase (EC:3.1.1.6)	kpe:KPK_1995	+	+	-
putative dihydrodipicolinate synthase ; K01714 dihydrodipicolinate synthase [EC:4.2.1.52]	kpe:KPK_4823	+	+	-
quaternary amine uptake ABC transporter (QAT) family, periplasmic amine-binding protein ; K05845 osmoprotectant transport sys	kpe:KPK_2009	+	+	-
nifH; nitrogenase iron protein (EC:1.18.6.1); K02588 nitrogenase iron protein NifH [EC:1.18.6.1]	kpe:KPK_1714	+	+	-
hypothetical protein	kpe:KPK_3698	+	+	-
putative diaminopimelate epimerase ; K01778 diaminopimelate epimerase [EC:5.1.1.7]	kpe:KPK_2448	+	+	-
transcriptional regulator, RpiR family	kpe:KPK_3266	+	+	-
hypothetical protein	kpe:KPK_1991	+	+	-
nifU; Fe-S cluster assembly protein NifU ; K04488 nitrogen fixation protein NifU and related proteins; K07400 Fe/S biogenesis pr	kpe:KPK_1706	+	+	-
metallo-beta-lactamase domain protein	kpe:KPK_2333	+	+	-
transcriptional regulator, AraC family	kpe:KPK_4824	+	+	-
hypothetical protein	kpe:KPK_1990	+	+	-
nifM; nitrogen fixation protein NifM	kpe:KPK_1701	+	+	-
ABC transporter, periplasmic substrate-binding protein ; K02073 D-methionine transport system substrate-binding protein	kpe:KPK_2320	+	+	-
hypothetical protein	kpe:KPK_2983	+	+	-
idnO; gluconate 5-dehydrogenase (EC:1.1.1.69); K00046 gluconate 5-dehydrogenase [EC:1.1.1.69]	kpe:KPK_4703	+	+	-
oligogalacturonate-specific porin protein (KdgM)	kpe:KPK_5054	+	+	-
oligogalacturonate-specific porin protein (KdgM)	kpe:KPK_5054	+	+	-
transcriptional regulator, GntR family ; K03482 GntR family transcriptional regulator, glv operon transcriptional regulator	kpe:KPK_1428	+	+	-
glnQ; glutamine ABC transporter ATP-binding protein ; K10038 glutamine transport system ATP-binding protein [EC:3.6.3.-]	kpe:KPK_3261	+	+	-
thiopurine S-methyltransferase family protein	kpe:KPK_2449	+	+	-
ABC transporter, permease protein ; K02072 D-methionine transport system permease protein	kpe:KPK_2321	+	+	-

hypothetical protein	kpe:KPK_5050	+	+	-
hypothetical protein	kpe:KPK_5050	+	+	-
quaternary amine uptake ABC transporter (QAT) family, permease protein ; K05846 osmoprotectant transport system permease pr	kpe:KPK_2010	+	+	-
NifY protein	kpe:KPK_1710	+	+	-
O-methyltransferase family protein	kpe:KPK_2982	+	+	-
quaternary amine uptake ABC transporter (QAT) family, permease protein ; K05846 osmoprotectant transport system permease pr	kpe:KPK_2011	+	+	-
neutral amino-acid efflux protein ; K11249 cysteine/O-acetylserine efflux protein	kpe:KPK_4501	+	+	-
neutral amino-acid efflux protein ; K11249 cysteine/O-acetylserine efflux protein	kpe:KPK_4501	+	+	-
putative lipoprotein	kpe:KPK_4061	+	+	-
pseudogene	kpe:KPK_1582	+	+	-
idnK; thermosensitive gluconokinase (EC:2.7.1.12); K00851 gluconokinase [EC:2.7.1.12]	kpe:KPK_4704	+	+	-
nifF; flavodoxin FldA ; K03839 flavodoxin I	kpe:KPK_1700	+	+	-
pseudogene	kpe:KPK_1582	+	+	-
nifQ; nitrogen fixation protein NifQ	kpe:KPK_1696	+	+	-
acetyltransferase, GNAT family	kpe:KPK_5257	+	+	-
acetyltransferase, GNAT family	kpe:KPK_5257	+	+	-
hypothetical protein	kpe:KPK_2523	+	+	-
nifX; NifX protein ; K02596 nitrogen fixation protein NifX	kpe:KPK_1707	+	+	-
hypothetical protein	kpe:KPK_4705	+	+	-
putative anti-sigma B factor ; K04757 anti-sigma B factor [EC:2.7.11.1]	kpe:KPK_3075	+	+	-
putative transporter	kpe:KPK_5051	+	+	-
DNA-binding protein	kpe:KPK_1581	+	+	-
putative NifZ protein ; K02597 nitrogen fixation protein NifZ	kpe:KPK_1702	+	+	-
pseudogene	kpe:KPK_4089	+	+	-
hypothetical protein	kpe:KPK_3326	+	+	-
hypothetical protein	kpe:KPK_5263	+	+	-
hypothetical protein	kpe:KPK_1563	+	+	-
hypothetical protein	kpe:KPK_1563	+	+	-
hypothetical protein	kpe:KPK_5262	+	+	-
hypothetical protein	kpe:KPK_2986	+	+	-
PTS system, lactose/cellobiose specific IIB subunit ; K02760 PTS system, cellobiose-specific IIB component [EC:2.7.1.69]	kpe:KPK_1429	+	+	-
PTS system, lactose/cellobiose specific IIA subunit ; K02759 PTS system, cellobiose-specific IIA component [EC:2.7.1.69]	kpe:KPK_1431	+	+	-
PTS system, lactose/cellobiose specific IIA subunit ; K02759 PTS system, cellobiose-specific IIA component [EC:2.7.1.69]	kpe:KPK_1431	+	+	-
hypothetical protein	kpe:KPK_3664	+	+	-
DNA-binding protein	kpe:KPK_2987	+	+	-
PTS system, lactose/cellobiose specific IIB subunit ; K02760 PTS system, cellobiose-specific IIB component [EC:2.7.1.69]	kpe:KPK_1429	+	+	-
2Fe-2S iron-sulfur cluster binding domain protein	kpe:KPK_4827	+	+	-
putative NifW protein	kpe:KPK_1703	+	+	-
hypothetical protein	kpe:KPK_0823	+	+	-
nifT; probable nitrogen fixation protein FixT ; K02593 nitrogen fixation protein NifT	kpe:KPK_1711	+	+	-
hypothetical protein ; K07090	kpe:KPK_2573	+	+	-
hypothetical protein	kpe:KPK_3933	+	+	-
hypothetical protein	kpu:KP1_2471	+	+	-
hypothetical protein	cel:F35A5.1	+	+	-
pseudogene	kpe:KPK_1743	+	+	-
hypothetical protein	kpe:KPK_2219	+	+	-
protein translocase subunit SecA ; K03070 preprotein translocase subunit SecA	lhk:LHK_03041	+	+	-
hypothetical protein	kpu:KP1_3126	+	+	-
hypothetical protein	kpu:KP1_4310	+	+	-
fslC; G-protein-coupled receptor (GPCR) family protein	ddi:DDB_0231833	+	+	-
hypothetical protein	kpe:KPK_2689	+	+	-
hypothetical protein	kpu:KP1_2726	+	+	-
putative heat shock protein ; K04046 hypothetical chaperone protein	smd:Smed_0648	+	+	-
hypothetical protein	kpe:KPK_3119	+	+	-
hypothetical protein	kpe:KPK_0541	+	+	-
hypothetical protein	kpu:KP1_2017	+	+	-
hypothetical protein	kpe:KPK_1143	+	+	-
hypothetical protein	kpu:KP1_2017	+	+	-
hypothetical protein	kpu:KP1_3986	+	+	-
hypothetical protein	kpe:KPK_2812	+	+	-
hypothetical protein	kpe:KPK_5443	+	+	-
hypothetical protein	kpe:KPK_5243	+	+	-
LipA and NB-ARC domain protein	afm:AFUA_3G14650	+	+	-
hydroxypyruvate reductase (EC:1.1.1.81); K00050 hydroxypyruvate reductase [EC:1.1.1.81]	lch:Lcho_3177	+	+	-
hypothetical protein	kpe:KPK_1223	+	+	-
hypothetical protein	tgo:TGME49_020200	+	+	-
hypothetical protein	kpe:KPK_1141	+	+	-
hypothetical protein	kpu:KP1_2732	+	+	-
YALI0F07018p	yli:YALI0F07018g	+	+	-
hypothetical protein	kpe:KPK_3446	+	+	-
putative phosphatase/sulfatase	kpu:KP1_4085	-	+	+
phnW; 2-aminoethylphosphonate--pyruvate transaminase ; K03430 2-aminoethylphosphonate-pyruvate transaminase [EC:2.6.1.37	kpu:KP1_5436	-	+	+
putative arylsulfatase ; K01130 arylsulfatase [EC:3.1.6.1]	kpu:KP1_1453	-	+	+
hypothetical protein ; K07047	kpn:KPN_01910	-	+	+
bifunctional putative acetyl-CoA:acetoacetyl-CoA transferase: alpha subunit/beta subunit	kpu:KP1_2747	-	+	+
putative 5'-nucleotidase/2',3'-cyclic phosphodiesterase	kpu:KP1_0099	-	+	+
putative metal-dependent phosphohydrolase with HD subdomain ; K06885	kpu:KP1_2389	-	+	+
hypothetical protein	kpu:KP1_0751	-	+	+
putative general substrate transporter	kpu:KP1_4124	-	+	+
codB; probable transporter ; K03457 nucleobase:cation symporter-1, NCS1 family	kpu:KP1_2330	-	+	+
hypothetical protein ; K11911 type VI secretion system protein VasL	kpu:KP1_3364	-	+	+
major facilitator family transporter	kpn:KPN_01692	-	+	+
putative alpha-galactosidases/6-phospho-beta-glucosidases ; K01222 6-phospho-beta-glucosidase [EC:3.2.1.86]	kpu:KP1_2349	-	+	+
putative Na+ dependent nucleoside transporter ; K03317 concentrative nucleoside transporter, CNT family	kpu:KP1_0794	-	+	+
hypothetical protein	kpu:KP1_0750	-	+	+
putative acetyl-CoA acetyltransferase ; K00626 acetyl-CoA C-acetyltransferase [EC:2.3.1.9]	kpu:KP1_2745	-	+	+
putative iron-sulfur modifier protein ; K06871	kpn:KPN_00528	-	+	+
putative arylsulfatase regulator ; K06871	kpu:KP1_4084	-	+	+
glycerate kinase I	kpn:KPN_01689	-	+	+

putative sugar diacid utilization regulator	kpn:KPN_01688	-	+	+
hypothetical protein	kpu:KP1_0097	-	+	+
putative arylsulfatase regulator ; K06871	kpn:KPN_02831	-	+	+
phnS; 2-aminoethylphosphonate transporter, periplasmic-binding component ; K11081 2-aminoethylphosphonate transport system	kpn:KPN_04061	-	+	+
transcriptional regulator	kpn:KPN_04798	-	+	+
putative LysR-family bacterial regulatory protein	kpu:KP1_2348	-	+	+
hypothetical protein	kpu:KP1_0103	-	+	+
phnU; 2-aminoethylphosphonate transporter, membrane component ; K11083 2-aminoethylphosphonate transport system permeas	kpn:KPN_04059	-	+	+
hypothetical protein	kpn:KPN_02871	-	+	+
phnV; 2-aminoethylphosphonate transport system memrane component ; K11082 2-aminoethylphosphonate transport system perm	kpu:KP1_5429	-	+	+
phnR; 2-aminoethylphosphonate transporter repressor	kpu:KP1_5434	-	+	+
hypothetical protein	kpu:KP1_3088	-	+	+
hypothetical protein	kpu:KP1_3088	-	+	+
LuxR transcriptional regulator	kpn:KPN_01599	-	+	+
keto-hydroxyglutarate-aldolase/keto-deoxy- phosphogluconate aldolase ; K01631 2-dehydro-3-deoxyphosphogalactonate aldolase	kpu:KP1_0755	-	+	+
putative fimbrial-like protein ; K07345 major type 1 subunit fimbrin (pilin)	kpu:KP1_4251	-	+	+
hypothetical protein	kpu:KP1_3023	-	+	+
hypothetical protein	kpu:KP1_0752	-	+	+
hypothetical protein	kpu:KP1_0752	-	+	+
hypothetical protein	spq:SPAB_05210	-	+	+
hypothetical protein	kpu:KP1_0715	-	+	+
hypothetical protein	kpu:KP1_0715	-	+	+
bioA; adenosylmethionine--8-amino-7-oxononanoate transaminase ; K00833 adenosylmethionine-8-amino-7-oxononanoate amino	kpu:KP1_1749	-	+	+
hypothetical protein	ecm:EcSMS35_2443	-	+	+
hypothetical protein	spq:SPAB_04790	-	+	+
hypothetical protein	kpu:KP1_4791	-	+	+
hypothetical protein	mlo:mll1989	-	+	+
hypothetical protein	kpe:KPK_0327	-	+	+
hypothetical protein	kpe:KPK_0821	-	+	+
hypothetical protein	kpu:KP1_0751	-	+	+
aminopeptidase B ; K07751 PepB aminopeptidase [EC:3.4.11.23]	amc:MADE_03542	-	+	+
putative NAD(P)-binding and starvation-sensing dehydrogenase ; K08322 starvation sensing protein RspB [EC:1.1.1.-]	kpu:KP1_4933	-	+	+
hypothetical protein	kpu:KP1_2893	-	+	+
hypothetical protein	kpu:KP1_3434	-	+	+
hypothetical protein	kpu:KP1_2893	-	+	+
hypothetical protein	kpu:KP1_1301	-	+	+
hypothetical protein	kpu:KP1_2726	-	+	+
hypothetical protein LOC100121689	nvi:100121689	-	+	+
hypothetical protein	kpu:KP1_1780	-	+	+
putative IS1 encoded protein	sfv:SFV_3919	-	+	+
hypothetical protein	kpu:KP1_2508	-	+	+
EGF-like domain containing protein	bmy:Bm1_48015	-	+	+
cyclopropane fatty acyl phospholipid synthase ; K00574 cyclopropane-fatty-acyl-phospholipid synthase [EC:2.1.1.79]	esa:ESA_02022	-	+	+
putative ATPase	hpb:HELPY_0949	-	+	+
hypothetical protein	kpu:KP1_4570	-	+	+
hypothetical protein	lel:LELG_04836	-	+	+
yddG; hypothetical protein	kpn:KPN_01868	-	+	+
hypothetical protein	kpu:KP1_0744	-	+	+
umuC; DNA polymerase V subunit C ; K03502 DNA polymerase V	kpu:KP1_2206	-	+	+
major facilitator superfamily transporter	pna:Pnap_3821	-	+	+
hypothetical LOC585699	spu:585699	-	+	+
hypothetical protein	cko:CKO_03197	-	+	+
putative transmembrane protein	kpu:KP1_0378	-	+	+
putative sensor-regulator protein (EC:2.7.13.1)	rhi:NGR_b14580	-	+	+
hypothetical protein	kpu:KP1_2211	-	+	+
hypothetical protein	vsa:VSAL_I2407	-	+	+
hypothetical protein	kpu:KP1_1780	-	+	+
helicase domain protein	oca:OCAR_7659	-	+	+
hypothetical protein	kpu:KP1_3326	-	+	+
murC; UDP-N-acetylmuramate--L-alanine ligase ; K01924 UDP-N-acetylmuramate--alanine ligase [EC:6.3.2.8]	kpu:KP1_0913	-	+	+
hypothetical protein	aeh:Mlg_0667	-	+	+
hypothetical protein ; K09904 hypothetical protein	kpe:KPK_1537	-	+	+
hypothetical protein	ure:UREG_00538	-	+	+
ribulokinase	kpu:KP1_3764	-	-	+
putative phosphotransferase protein ; K02761 PTS system, cellobiose-specific IIC component	kpn:KPN_04650	-	-	+
dgoT; D-galactonate transport ; K08194 MFS transporter, ACS family, D-galactonate transporter	kpn:KPN_04094	-	-	+
putative transmembrane amino acid transporter protein ; K03837 serine transporter	kpn:KPN_00964	-	-	+
hypothetical protein	kpu:KP1_0271	-	-	+
putative peptidase ; K06016 N-carbamoyl-L-amino-acid hydrolase [EC:3.5.1.87]	kpu:KP1_1935	-	-	+
yjiO; putative sugar transport protein	kpu:KP1_3182	-	-	+
putative peptidase ; K01451 hippurate hydrolase [EC:3.5.1.32]	kpn:KPN_00966	-	-	+
diaminopropionate ammonia-lyase ; K01751 diaminopropionate ammonia-lyase [EC:4.3.1.15]	kpn:KPN_00963	-	-	+
regulator of gluconate (gnt) operon	kpu:KP1_3762	-	-	+
protein of unknown function DUF979	kpu:KP1_1679	-	-	+
dgoK; 2-oxo-3-deoxygalactonate kinase ; K00883 2-dehydro-3-deoxygalactonokinase [EC:2.7.1.58]	kpn:KPN_04097	-	-	+
putative ribitol dehydrogenase	kpn:KPN_02546	-	-	+
hypothetical protein	kpn:KPN_04647	-	-	+
ygaZ; putative amino acid transport protein	kpu:KP1_0270	-	-	+
protein of unknown function DUF969	kpu:KP1_1678	-	-	+
lasT; putative RNA methyltransferase ; K02533 tRNA/rRNA methyltransferase [EC:2.1.1.-]	kpn:KPN_04857	-	-	+
putative Mg(2+) transport ATPase ; K07507 putative Mg2+ transporter-C (MgtC) family protein	kpu:KP1_2873	-	-	+
putative O-methyltransferase	kpu:KP1_2488	-	-	+
putative 2-component transcriptional regulator	kpu:KP1_2619	-	-	+
putative regulator with helix-turn-helix motif	kpu:KP1_4811	-	-	+
putative transport protein ; K11249 cysteine/O-acetylserine efflux protein	kpu:KP1_1076	-	-	+
putative fimbrial-like protein ; K07345 major type 1 subunit fimbrin (pilin)	kpu:KP1_4251	-	-	+
hypothetical protein	kpu:KP1_1473	-	-	+
hypothetical protein	kpn:KPN_03433	-	-	+
regulator for leucine (or lrp) regulon and high-affinity branched-chain amino acid transport system	kpn:KPN_00962	-	-	+

hypothetical protein	kpn:KPN_01552	-	-	+
hypothetical protein	kpu:KP1_0748	-	-	+
major facilitator superfamily transporter	kpu:KP1_4083	-	-	+
ansP; L-asparagine permease	kpn:KPN_04417	-	-	+
hypothetical protein	kpe:KPK_1129	-	-	+
hypothetical protein	kpn:KPN_01317	-	-	+
relE; putative inner membrane protein ; K06218 RelE protein	kpu:KP1_0521	-	-	+
yedR; putative outer membrane protein N precursor	kpu:KP1_3562	-	-	+
putative phosphotransferase protein ; K02760 PTS system, cellobiose-specific IIB component [EC:2.7.1.69]	kpn:KPN_04648	-	-	+
yjjA; putative outer membrane protein	kpn:KPN_04810	-	-	+
hypothetical protein	kpu:KP1_3043	-	-	+
hypothetical protein	kpu:KP1_2485	-	-	+
hypothetical protein	kpe:KPK_1506	-	-	+
relB; putative helix-turn-helix protein	kpu:KP1_0520	-	-	+
putative permease of the Na+:galactoside symporter family	kpu:KP1_0936	-	-	+
citrate transporter	msl:Msil_0517	-	-	+
hypothetical protein	esa:ESA_01079	-	-	+
2-oxoacid ferredoxin oxidoreductase, beta subunit (EC:1.2.7.-); K00175 2-oxoglutarate ferredoxin oxidoreductase subunit beta [E	sat:SYN_03163	-	-	+
SORBIDRAFT_02g006142; hypothetical protein	sbi:SORBI_02g006142	-	-	+
hypothetical protein	kpn:KPN_01828	-	-	+
sdaC; putative L-serine dehydratase; K01752 L-serine dehydratase [EC:4.3.1.17]	stt:t0659	-	-	+
ybiL; catecholate siderophore receptor Fiu ; K02014 iron complex outermembrane recepter protein	kpn:KPN_01250	-	-	+
hypothetical protein	kpe:KPK_1129	-	-	+
PTS family enzyme IIBC component, cellobiose/salicin/arbutin-specific	kpn:KPN_01839	-	-	+
hypothetical protein	tva:TVAG_373470	-	-	+
hypothetical protein	kpu:KP1_0774	-	-	+
hypothetical protein	kpu:KP1_3043	-	-	+
DNA mismatch repair protein mutS ; K08741 DNA mismatch repair protein MSH5	edi:EDI_290570	-	-	+
UreA amidolyase related protein (EC:6.3.4.6); K01941 urea carboxylase [EC:6.3.4.6]	vei:Veis_4581	-	-	+
conserved hypothetical protein	pfh:PFHG_02069	-	-	+
hypothetical protein	kpe:KPK_2416	-	-	+
putative transposase B	cro:ROD_19661	-	-	+
dgoD; putative mandelate racemase/muconate lactonizing enzyme ; K01684 galactonate dehydratase [EC:4.2.1.6]	kpu:KP1_5473	-	-	+
hypothetical protein	kpu:KP1_5509	-	-	+
hypothetical protein	kpu:KP1_5510	-	-	+
hypothetical protein	kpu:KP1_2547	-	-	+
togT; putative oligogalacturonide transporter	kpu:KP1_3530	-	-	+
hypothetical protein	kpu:KP1_2728	-	-	+
hypothetical protein ; K12290 pilus assembly protein HofO	kpu:KP1_5094	-	-	+
hypothetical protein	kpu:KP1_4836	-	-	+
purL; phosphoribosylformylglycinamidine synthase (EC:6.3.5.3); K01952 phosphoribosylformylglycinamidine synthase [EC:6.3.	ftn:FTN_1699	-	-	+
yhjX; putative oxalate:formate antiporter ; K08177 MFS transporter, OFA family, oxalate/formate antiporter	kpu:KP1_5250	-	-	+
transcriptional regulator, LysR family	kpe:KPK_5218	-	-	+
hypothetical protein	kpu:KP1_0285	-	-	+
hypothetical protein	kpe:KPK_3816	-	-	+
hypothetical protein	kpe:KPK_3631	-	-	+
FOG EAL domain-containing protein	vvu:VV1_3056	-	-	+
hypothetical protein	kpu:KP1_4470	-	-	+
exonuclease ; K10746 exonuclease 1 [EC:3.1.-.-]	aag:AaeL_AAEL006209	-	-	+
hypothetical protein	kpu:KP1_2587	-	-	+
hypothetical protein	kpu:KP1_4511	-	-	+
hypothetical protein	sed:SeD_A0834	-	-	+
hypothetical protein	tva:TVAG_344220	-	-	+
hypothetical protein	pbe:PB001147.02.0	-	-	+
hypothetical protein	kpe:KPK_2950	-	-	+
cnrP; importin 9	ddi:DDB_0229883	-	-	+
yjeA; lysyl-tRNA synthetase ; K04568 lysyl-tRNA synthetase, class II [EC:6.1.1.6]	kpu:KP1_0426	-	-	+
hypothetical protein similar to ferrochelatase; K01772 ferrochelatase [EC:4.99.1.1]	pfh:PFHG_03543	-	-	+
hypothetical protein	kpe:KPK_2524	-	-	+
hypothetical protein	pan:PODANSg5803	-	-	+
hypothetical protein	ptm:GSPATT00028622001	-	-	+
ybjZ; ABC-type macrolide transport system efflux carrier ; K05685 macrolide transport system permease protein; K05686 macroli	kpu:KP1_1880	-	-	+
hypothetical protein	kpu:KP1_5277	-	-	+
hypothetical protein	kpu:KP1_3296	-	-	+
hypothetical protein	kpu:KP1_1447	-	-	+
peptidase S41	swp:swp_1400	-	-	+
hypothetical protein	kpu:KP1_0313	-	-	+
hypothetical protein	cko:CKO_04875	-	-	+
negative transcriptional regulator of cel operon	kpu:KP1_0722	-	-	+
hypothetical protein LOC100273691	zma:100273691	-	-	+
CaJ7_0141; hypothetical protein	cal:CaO19_6907	-	-	+
hypothetical protein	kpu:KP1_2620	-	-	+
tolA; TolA protein	ccs:CCNA_03339	-	-	+
fabF; 3-oxoacyl-[acyl-carrier-protein] synthase II ; K09458 3-oxoacyl-[acyl-carrier-protein] synthase II [EC:2.3.1.179]	dma:DMR_39980	-	-	+
hypothetical protein	kpu:KP1_2564	-	-	+
hypothetical protein	kpu:KP1_3299	-	-	+
hypothetical protein	kpu:KP1_2660	-	-	+
hypothetical protein	kpe:KPK_1141	-	-	+
hypothetical protein	gur:Gura_2475	-	-	+
hypothetical protein	kpu:KP1_2286	-	-	+
yfeU; hypothetical protein	kpn:KPN_00289	-	-	+
hypothetical protein	kpn:KPN_03988	-	-	+
hypothetical protein	kpu:KP1_3995	-	-	+
Clan ME, family M16, insulinase-like metallopeptidase ; K06972	tva:TVAG_371040	-	-	+
putative AraC-type regulatory protein	kpu:KP1_2616	-	-	+
hypothetical protein	kpu:KP1_0526	-	-	+
ptsP; phosphoenolpyruvate-protein phosphotransferase (EC:2.7.3.9); K08484 phosphotransferase system, enzyme I, PtsP [EC:2.7.	bra:BRADO0573	-	-	+
ygdL; putative enzyme	kpn:KPN_04165	-	-	+
hypothetical protein	kpu:KP1_2660	-	-	+

hypothetical protein	kpu:KP1_2618	-	-	+
hypothetical protein	bra:BRADO6983	-	-	+
hypothetical protein	kpu:KP1_4510	-	-	+
membrane anchored protein	reh:H16_A0029	-	-	+
aliphatic sulfonate ABC transporter periplasmic ligand-binding protein ; K02051 sulfonate/nitrate/taurine transport system substrat	bid:Bind_3087	-	-	+
dppA; periplasmic dipeptide transport protein (EC:3.1.3.26)	ctu:Ctu_20820	-	-	+
hypothetical protein	scl:sce1811	-	-	+
hypothetical protein	kpu:KP1_2188	-	-	+
hypothetical protein	cvi:CV_3738	-	-	+
putative AraC-type regulatory protein	kpn:KPN_01600	-	-	+
pyrG; CTP synthetase (EC:6.3.4.2); K01937 CTP synthase [EC:6.3.4.2]	swd:Swoo_3351	-	-	+
oxidoreductase, zinc-binding dehydrogenase family	kpe:KPK_2328	-	-	+
dcuS; two-component system sensor kinase for C4-dicarboxylate regulation of anaerobic fumurate respiratory system ; K07701 tw	kpu:KP1_2568	-	-	+
putative peptidase ; K06016 N-carbamoyl-L-amino-acid hydrolase [EC:3.5.1.87]	kpu:KP1_1935	-	-	+
putative 2-component transcriptional regulator	kpu:KP1_2619	-	-	+
hypothetical protein	ddi:DDBDRAFT_0190955	-	-	+
hypothetical protein	kpu:KP1_0271	-	-	+
hypothetical protein	kpu:KP1_4970	-	-	+
hypothetical protein	kpu:KP1_0323	-	-	+
hypothetical protein	kpu:KP1_2995	-	-	+
hypothetical protein	kpu:KP1_3926	-	-	+
beta-adaptin (clathrin assembly protein complex 2 large beta chain), putative	cdu:CD36_13020	-	-	+
hypothetical protein	ptm:GSPATT00005598001	-	-	+
hypothetical protein	kpe:KPK_3074	-	-	+
ygfF; putative oxidoreductase	kpu:KP1_4624	-	-	+
hypothetical protein	tet:TTHERM_00784720	-	-	+
similar to HrES-AP	hmg:100213700	-	-	+
hypothetical protein	kpu:KP1_5248	-	-	+
hypothetical protein	kpu:KP1_2615	-	-	+
hypothetical protein	tet:TTHERM_00370670	-	-	+
hypothetical protein	kpu:KP1_1831	-	-	+
hypothetical protein	spq:SPAB_04017	-	-	+
hypothetical protein ; K09780 hypothetical protein	kpu:KP1_3294	-	-	+
yncA; hypothetical acetyltransferase ; K03823 phosphinothricin acetyltransferase [EC:2.3.1.183]	kpu:KP1_2978	-	-	+
hypothetical protein	kpu:KP1_2471	-	-	+
hypothetical protein	pyo:PY04365	-	-	+
histidine kinase	ank:AnaeK_2081	-	-	+
putative transmembrane protein	kpn:KPN_04510	-	-	+
adenylylsulfate kinase ; K00860 adenylylsulfate kinase [EC:2.7.1.25]	dvm:DvMF_0018	-	-	+
nucleoid protein H-NS ; K03746 DNA-binding protein H-NS	bvi:Bcep1808_7011	-	-	+
pstA; putative Na+-dependent transporter ; K03453 bile acid:Na+ symporter, BASS family	kpu:KP1_0262	-	-	+
hemagglutination activity domain protein	ttu:TERTU_1697	-	-	+
transcriptional regulator, Sir2 family protein	tva:TVAG_362260	-	-	+
hypothetical protein	kpu:KP1_3228	-	-	+
glycosyl transferase, family 3-like protein	ddc:Dd586_2440	-	-	+

[a] Features were detected in all three *K. variicola* genomes and all eight of the *K. pneumoniae* genomes to be counted as present (+) for that species.

[b] Predicted protein function of the top BLASTN hit of each feature to the KEGG database irrespective of the alignment length and e-value.

Supplemental Table 4. Features of *Klebsiella* sp. 10982 that were not identified in the genomes of the endosymbiont *Klebsiella* spp. or in the *K. pneumoniae* lineage

Predicted protein[a]	Best KEGG match[b]	Best match length	% Identities	e-value	Alignment length
hypothetical protein	eck:EC55989_2911	3852	93	0	1295
hypothetical protein ; K01307 gamma-glutamyl hydrolase [EC:3.4.19.9]	tet:TTHERM_00130000	1698	100	3.1	21
LysR-family transcriptional regulator	bav:BAV2502	909	100	0.012	25
hypothetical protein	pag:PLES_15871	3381	90	1.00E-05	50
lambda family phage tail tape measure protein	ecm:EcSMS35_1198	3228	81	2.00E-19	225
putative kinase	kpn:KPN_01432	3087	90	3.00E-12	69
pseudogene	smd:Smed_6169	532	100	0.58	22
hypothetical protein	sme:SM_b21069	1419	100	0.036	24
putative tail length tape measure protein	eoh:ECO103_2072	2562	83	4.00E-14	136
hypothetical protein LOC100251846	vvi:100251846	6282	100	0.56	22
fdhA; formate dehydrogenase, alpha subunit ; K00123 formate dehydrogenase, alpha subunit [EC:1.2.1.2]	avi:Avi_4097	2880	100	0.52	22
beta-N-acetylhexosaminidase (EC:3.2.1.52); K12373 beta-hexosaminidase [EC:3.2.1.52]	ent:Ent638_0442	2385	82	8.00E-71	485
thiol-disulfide isomerase and thioredoxin	xau:Xaut_3943	273	100	0.49	22
hypothetical protein	pfh:PFHG_02360	8682	100	0.03	24
GI15923 gene product from transcript GI15923-RA ; K00911 1D-myo-inositol-triphosphate 3-kinase [EC:2.7.1.127]	dmo:Dmoj_GI15923	1977	100	0.03	24
non-specific protein-tyrosine kinase (EC:2.7.10.2); K00903 protein-tyrosine kinase [EC:2.7.10.-]	spe:Spro_1585	2175	86	3.00E-14	104
ATPase	ppf:Pput_4620	2589	94	0.007	33
AsmA family protein; K07290 hypothetical protein	mei:Msip34_1055	2064	100	1.8	21
hypothetical protein; K07459 putative ATP-dependent endonuclease of the OLD family	aav:Aave_0676	2139	94	0.028	32
hypothetical protein	vvy:VVA1175	3654	100	1.8	21
hypothetical protein	see:SNSL254_A1133	2265	81	7.00E-43	380
hypothetical protein	sgl:SG1233	1368	82	4.00E-20	182
hypothetical protein ; K03497 chromosome partitioning protein, ParB family	kpn:KPN_pKPN4p07111	2010	81	1.00E-53	494
pdxA; 4-hydroxythreonine-4-phosphate dehydrogenase ; K00097 4-hydroxythreonine-4-phosphate dehydrogenase [EC:1.1.1.262]	ses:SARI_02913	990	100	0.41	22
putative glycosyl transferase	stm:STM0726	1896	78	1.00E-22	434
putative protease/scaffold protein	eci:UTI89_C5120	2124	81	1.00E-50	417
phage terminase large subunit (GpA)	ecx:EcHS_A2094	2127	84	1.00E-147	731
transglycosylase SLT domain protein	kpe:KPK_4128	1926	94	0	549
RNA polymerase, sigma-24 subunit, ECF subfamily; K03088 RNA polymerase sigma-70 factor, ECF subfamily	hna:Hneap_1204	405	100	3.00E-11	39
hypothetical protein	spq:SPAB_02223	2082	84	5.00E-25	182
hypothetical protein	sgl:SG0823	1770	97	2.00E-06	35
hypothetical protein	kpe:KPK_A0083	1863	84	7.00E-89	449
uvrD; DNA helicase II (EC:3.6.1.-); K03657 DNA helicase II / ATP-dependent DNA helicase PcrA [EC:3.6.1.-]	cvi:CV_0205	2142	92	0.002	38
arsA; arsenical pump-driving ATPase (EC:3.6.3.16); K01551 arsenite-transporting ATPase [EC:3.6.3.16]	kpe:KPK_A0054	1752	87	3.00E-29	145
mqo; malate:quinone oxidoreductase (EC:1.1.99.16); K00116 malate dehydrogenase (acceptor) [EC:1.1.99.16]	abu:Abu_0518	1359	100	1.4	21
sodium/hydrogen exchanger ; K03455 monovalent cation:H+ antiporter-2, CPA2 family	rpf:Rpic12D_0617	1716	92	0	1415
hypothetical protein	bbr:BB3632	1683	82	9.00E-05	104
RSp1343; hypothetical protein	rso:RS04767	1167	96	0.35	26
FlrB; two-component sensor kinase ; K10942 two-component system, sensor histidine kinase FlrB [EC:2.7.13.3]	vfm:VFMJ11_1987	1062	100	1.4	21
similar to uncharacterized conserved nucleotide binding protein found outside of yeast	cal:CaO19.2043	903	100	0.34	22
lambda family phage portal protein	ecx:EcHS_A2092	1575	83	1.00E-107	639
IS66 family element, transposase	sbc:SbBS512_A0193	1539	93	0	1539
hypothetical protein	ecv:APECO1_O1CoBM79	1566	93	0	1566
hypothetical protein	ecc:c3645	1539	89	0	1540
recombinase	rsh:Rsph17029_3501	1572	88	0.08	43
ADP-L-glycero-D-mannoheptose-6-epimerase (EC:5.1.3.20); K03274 ADP-L-glycero-D-manno-heptose 6-epimerase [EC:5.1.3.20]	nis:NIS_1449	996	100	0.32	22
hypothetical protein	sdy:SDY_1922	663	86	1.00E-12	93
pseudogene	cro:ROD_05881	1518	79	5.00E-31	452
gp29; hypothetical protein	bpt:Bpet4408	1476	83	5.00E-06	98
putative phage tail sheath protein	cro:ROD_25901	1503	82	4.00E-25	226
putative portal protein (head-tail preconnector protein) from putative prophage	eck:EC55989_1707	1581	83	2.00E-33	232
ygcE; putative kinase	eum:ECUMN_3103	1479	82	0	1257
hypothetical protein	net:Neut_2620	1593	100	4.8	20
hypothetical protein LOC100280317	zma:100280317	1260	100	0.31	22
hypothetical protein	ses:SARI_00371	2472	81	1.00E-169	1191
hypothetical protein	cko:CKO_04128	1455	85	0	1241
hypothetical protein ; K02433 aspartyl-tRNA(Asn)/glutamyl-tRNA (Gln) amidotransferase subunit A [EC:6.3.5.6 6.3.5.7]	rlt:Rleg2_5792	1371	84	0.005	73
polysaccharide biosynthesis protein	kpn:KPN_02500	1503	94	0.019	32
ATP-dependent DNA helicase Rep (EC:3.6.1.-); K03656 ATP-dependent DNA helicase Rep [EC:3.6.1.-]	dar:Daro_3879	1992	100	0.074	23
hypothetical protein	ecx:EcHS_A2088	387	85	3.00E-10	93
putative sugar transport-related, membrane protein	pfs:PFLU1074	1341	84	2.00E-17	137
NADH dehydrogenase subunit G (EC:1.6.5.3); K00336 NADH dehydrogenase I subunit G [EC:1.6.5.3]	rpb:RPB_1352	2619	100	1.1	21
tyrosine phenol-lyase ; K01668 tyrosine phenol-lyase [EC:4.1.99.2]	cko:CKO_03467	1398	85	0	1367
hypothetical protein ; K08195 MFS transporter, AAHS family, 4-hydroxybenzoate transporter	cko:CKO_00650	1428	83	2.00E-85	515
nrdR; transcriptional regulator NrdR; K07738 transcriptional repressor NrdR	asa:ASA_0978	450	100	0.28	22
pseudogene	ecm:EcSMS35_1112	644	88	4.00E-28	131
tolA; cell envelope integrity inner membrane protein TolA ; K03646 colicin import membrane protein	kpe:KPK_3827	1338	98	0	609
argO; arginine exporter	cro:ROD_50761	636	100	0.28	22
protein HipA ; K07154	sea:SeAg_B4814	1329	83	3.00E-38	260
ygcS; putative transporter	ecq:ECED1_3220	1338	81	4.00E-74	596
HK97 family phage portal protein	ppu:PP_1565	1296	84	0.069	63
hypothetical protein	app:CAP2UW1_3394	1131	96	0.068	27
hypothetical protein	cko:CKO_04131	1299	84	0	1205
hypothetical protein ; K00313 electron transfer flavoprotein-quinone oxidoreductase [EC:1.5.5.-]	cko:CKO_04121	1272	82	2.00E-30	239
hypothetical protein	ecv:APECO1_1183	1284	80	2.00E-60	629
hypothetical protein	ptm:GSPATT00023598001	2052	96	0.26	26
hypothetical protein	cko:CKO_03466	1263	83	1.00E-95	544
glutamine amidotransferase class-II	mei:Msip34_2423	897	100	4.1	20
int; bacteriophage integrase	stt:t4371	1260	94	0	1250
hypothetical protein	etr:ETAE_1077	348	100	0.26	22
hypothetical protein	pna:Pnap_4211	882	100	1	21
tnpA; IS256 family transposase	asa:ASA_P5G090	1215	94	0	1215
similar to conserved hypothetical protein	api:100165219	1212	96	0.064	27
hypothetical protein	tps:THAPSDRAFT_1280	2829	100	0.99	21
major head protein	pag:PLES_25421	1188	81	2.00E-05	113
gpf; F protein (gpF) (protein GP30)	bpt:Bpet4409	795	87	0.016	52
Os01g0148000; hypothetical protein	osa:4325212	5943	96	0.25	26
transposase mutator type	dda:Dd703_3078	1203	88	0	1203
peptidase S8 and S53, subtilisin, kexin, sedolisin	shn:Shewana3_2745	1566	100	0.063	23
hypothetical protein	ptm:GSPATT00030850001	4875	100	0.001	26
putative N-hydroxybenzoate hydroxylase	cro:ROD_22631	1194	84	0	1116
hypothetical protein ; K02055 putative spermidine/putrescine transport system substrate-binding protein	pfl:PFL_1368	1209	90	1.00E-18	83
putative transmembrane transport protein	stt:t0584	1191	83	7.00E-48	308
dynein heavy chain	pkn:PKH_070250	17334	100	0.96	21
putative outer membrane protein	sml:Smlt0614	876	100	0.016	24
multidrug efflux system protein MdtL; K08163 MFS transporter, DHA1 family, multidrug resistance protein	asa:ASA_1192	1173	89	0	1156
putative prophage DNA-binding protein	cro:ROD_09401	1158	84	1.00E-110	601
hypothetical protein	sdl:Sdel_1779	870	96	0.061	27
yjfC; hypothetical protein	set:SEN4142	1164	81	3.00E-81	714

hypothetical protein	spq:SPAB_02226	1152	82	6.00E-45	331
putative trypsin-like serine protease	bmj:BMULJ_00932	1152	92	0	946
putative baseplate J protein	ecx:EcHS_A2084	1149	95	0	878
iron-containing alcohol dehydrogenase	dze:Dd1591_2599	1149	89	4.00E-06	54
hypothetical protein	rpf:Rpic12D_0619	1146	98	0	1146
filamentation induced by cAMP protein Fic	pwa:Pecwa_0711	1143	88	0	1143
bacteriophage lambda NinG family protein	ent:Ent638_1024	621	100	0.92	21
hypothetical protein	isc:IscW_ISCW023246	3612	96	0.23	26
glycogen/starch synthase, ADP-glucose type (EC:2.4.1.21); K00703 starch synthase [EC:2.4.1.21]	gem:GM21_3463	1461	100	0.9	21
hypothetical protein	ecg:E2348C_2761	423	86	6.00E-39	193
two-component hybrid sensor and regulator	dma:DMR_36660	3036	100	0.88	21
bacteriophage Mu P protein	ecx:EcHS_A2087	1086	83	4.00E-43	284
ampC; beta-lactamase (EC:3.5.2.6); K01467 beta-lactamase [EC:3.5.2.6]	asa:ASA_1191	1233	88	0	796
hypothetical protein	ptm:GSPATT00027860001	3759	94	0.004	33
phospholipase/carboxylesterase	hap:HAPS_1871	1347	100	0.22	22
SF4520	sfl:SF4520	359926	98	3.00E-16	51
hypothetical protein	ecg:E2348C_2761	423	84	9.00E-41	244
putative phage capsid protein	cro:ROD_25951	1050	84	1.00E-70	398
hypothetical protein	eci:UTI89_C5110	1053	79	1.00E-21	420
SLC7A3; solute carrier family 7 (cationic amino acid transporter, y+ system), member 3	gga:422213	1893	100	0.055	23
hypothetical protein; K09778 hypothetical protein	rak:A1C_00645	657	100	3.4	20
cell division protease FtsH-like protein	abb:ABBFA_002565	942	92	9.00E-04	38
putative gentisate 1,2-dioxygenase	cro:ROD_22661	1038	85	0	827
yhjK; putative phosphodiesterase	eta:ETA_33870	1995	100	0.84	21
hypothetical protein	sme:SMa1162	678	100	0.83	21
hypothetical protein	eic:NT01EI_2733	1095	85	0	971
putative transposase, IS110 family	efe:EFER_2149	1026	95	0	1018
CobW/P47K family protein	kpe:KPK_1556	978	97	0.003	29
putative bacteriophage protein	sec:SC2593	1032	91	3.00E-25	94
hypothetical protein	cko:CKO_04246	1428	91	0	943
hypothetical protein	ent:Ent638_4311	1020	82	1.00E-21	196
GntR family transcriptional regulator	psp:PSPPH_3936	1002	82	0.003	89
putative tail protein	ppg:PputGB1_1748	1695	96	0.052	27
binding-protein-dependent transport systems inner membrane component ; K10228 sorbitol/mannitol transport system permease protein	rlg:Rleg_3751	882	100	0.81	21
pseudogene	ecz:ECS88_2766	333	88	1.00E-27	126
hypothetical protein	ecv:APECO1_1182	1050	86	2.00E-16	107
yihM; hypothetical protein	sfv:SFV_3627	981	86	1.00E-05	65
SORBIDRAFT_03g010040; hypothetical protein ; K12619 5'-3' exoribonuclease 2 [EC:3.1.13.-]	sbi:SORBI_03g010040	3201	100	0.2	22
sodium/hydrogen exchanger ; K03316 monovalent cation:H+ antiporter, CPA1 family	shl:Shal_1106	1287	96	0.013	28
putative fimbrial adhesin precursor	kpu:KP1_0601	954	83	3.00E-06	90
ksgA; dimethyladenosine transferase (EC:2.1.1.-); K02528 dimethyladenosine transferase [EC:2.1.1.-]	las:CLIBASIA_01415	855	96	0.2	26
LysR family transcriptional regulator	asa:ASA_1193	963	90	0	959
serA2; D-3-phosphoglycerate dehydrogenase (EC:1.1.1.95)	bpt:Bpet0409	924	90	0.003	41
putative transmembrane protein	bgl:bglu_2g11640	1371	100	0.78	21
cation diffusion facilitator family transporter ; K03295 cation efflux system protein, CDF family	sfr:Sfri_3473	960	99	0	960
transcriptional regulator, LysR family	ddc:Dd586_2850	963	81	2.00E-04	119
hypothetical protein	kpu:KP1_2402	1923	86	1.00E-134	556
hypothetical protein	kpe:KPK_4115	2532	87	1.00E-11	83
Pc06g01390	pcs:Pc06g01390	1206	100	0.19	22
hypothetical protein	cvi:CV_2155	993	93	6.00E-20	73
PfkB	pol:Bpro_5091	930	93	5.00E-05	40
probable ring-cleaving dioxygenase PA0817; K06991	atc:AGR_pAT_700	414	100	0.012	24
hypothetical protein	cvi:CV_2155	993	85	2.00E-16	115
hypothetical protein	ecc:c5175	132	96	3.00E-12	48
similar to CG8597-PA, isoform A; K13187 RNA-binding protein 4	tca:659335	1077	100	0.75	21
hypothetical protein	ses:SARI_02599	2298	85	1.00E-61	307
glycosyl transferase, group 2 family protein; K12992 rhamnosyltransferase [EC:2.4.1.-]	ecx:EcHS_A2189	912	79	2.00E-07	224
IS4 orf	ssn:SSON_4044	1347	89	0	891
hypothetical protein	rpf:Rpic12D_0622	915	97	0	915
membrane protein-like protein	ajs:Ajs_1869	600	100	0.74	21
hypothetical protein	ecy:ECSE_1688	1221	81	3.00E-25	282
putative transcriptional regulator	cro:ROD_22681	909	81	1.00E-103	769
hypothetical protein	pcb:PC000059.03.0	2331	96	0.73	25
transcription regulator protein	rso:RSc0144	966	82	1.00E-11	135
cyclic nucleotide-binding domain containing protein	tet:TTHERM_00686210	3255	100	2.9	20
intA; integrase	eck:EC55989_2909	1242	94	0	897
ParB family protein; K03497 chromosome partitioning protein, ParB family	ypi:YpsIP31758_0771	891	89	7.00E-04	46
putative DNA binding protein	cro:ROD_20691	888	90	0	888
hypothetical protein	mfa:Mfla_1164	888	96	0	888
ZNF275; zinc finger protein 275; K09228 KRAB domain-containing zinc finger protein	mcc:695012	1035	100	0.18	22
putative integrase ; K07497 putative transposase	stm:STM0947	684	92	0	672
polysaccharide deacetylase family protein	pfl:PFL_1362	882	84	3.00E-77	437
hypothetical protein	ses:SARI_00611	879	83	3.00E-09	107
protein with unknown function	rcu:RCOM_0118640	2226	100	0.71	21
hypothetical protein	kpu:KP1_4467	912	93	0	659
S49 family peptidase	ecx:EcHS_A2091	867	91	9.00E-56	177
hypothetical protein	ddi:DDBDRAFT_0167273	1182	100	0.045	23
GK12957 gene product from transcript GK12957-RA	dwi:Dwil_GK12957	1551	100	0.7	21
hypothetical protein	cko:CKO_04125	855	82	9.00E-25	217
5-carboxymethyl-2-hydroxymuconate delta-isomerase (EC:5.3.3.10)	dze:Dd1591_2323	885	92	2.00E-19	76
phage lysis protein, endopeptidase	hde:HDEF_1455	498	100	0.68	21
hypothetical protein, probable fragment	eta:ETA_18660	261	88	4.00E-05	56
hypothetical protein ; K07088	dde:Dde_0880	954	96	0.66	25
microcystin LR degradation protein MlrC-like protein	met:M446_0874	1464	100	0.17	22
hypothetical protein	las:CLIBASIA_05532	1026	100	0.66	21
hypothetical protein	hpg:HPG27_669	627	100	0.042	23
GE16755 gene product from transcript GE16755-RA	dya:Dyak_GE16755	9507	96	0.17	26
deoxyguanosinetriphosphate triphosphohydrolase, putative (EC:3.1.5.1); K01129 dGTPase [EC:3.1.5.1]	eic:NT01EI_3100	1530	96	0.16	26
yihN; putative resistance protein	sfv:SFV_3626	1059	81	5.00E-51	437
short chain dehydrogenase/reductase family oxidoreductase	kpu:KP1_1537	798	86	2.00E-34	173
hypothetical protein	cko:CKO_04130	786	84	1.00E-159	786
hypothetical protein	cko:CKO_04126	783	83	8.00E-19	155
GP23	sew:SeSA_A0683	804	84	2.00E-13	122
rplI; ribosomal protein L9; K02939 large subunit ribosomal protein L9	asa:ASA_0709	447	100	0.63	21
fabG; short chain dehydrogenase/reductase family oxidoreductase ; K00059 3-oxoacyl-[acyl-carrier protein] reductase [EC:1.1.1.100]	pfl:PFL_1364	762	80	3.00E-15	213
putative bacteriophage protein	ent:Ent638_0818	681	92	0.003	37
RNA polymerase, sigma 70 subunit, RpoD ; K03086 RNA polymerase primary sigma factor	vap:Vapar_1762	2265	100	2.5	20
dam; putative prophage DNA adenine methylase	cro:ROD_09331	771	82	3.00E-52	399
hypothetical protein	kpe:KPK_4162	933	93	5.00E-29	92
putative ABC transporter	dma:DMR_44170	2541	100	0.039	23
Ead domain protein	kpe:KPK_4165	666	96	3.00E-95	215
triphosphoribosyl-dephospho-CoA synthase CitG (EC:2.7.8.25); K05966 triphosphoribosyl-dephospho-CoA synthase [EC:2.7.8.25]	dze:Dd1591_2317	909	89	4.00E-08	61

oxidoreductase, short chain dehydrogenase/reductase family	pst:PSPTO_4200	750	83	3.00E-12	128
hypothetical protein	nve:NEMVE_v1g61906	810	100	0.59	21
plasmid SOS inhibition protein A	kpn:KPN_pKPN4p07114	723	89	5.00E-23	106
hypothetical protein	ecg:E2348C_2638	711	87	6.00E-07	67
putative transport periplasmic protein ; K02035 peptide/nickel transport system substrate-binding protein	sdy:SDY_1409	1635	100	0.58	21
yihL; putative DNA-binding transcriptional regulator	eoh:ECO103_4299	711	82	3.00E-21	191
c2; P22 repressor protein C2	seh:SeHA_C0382	651	94	2.00E-04	35
bepA; hypothetical protein	btr:Btr_1700	1635	100	2.3	20
glutamine amidotransferase ; K01951 GMP synthase (glutamine-hydrolysing) [EC:6.3.5.2]	cko:CKO_00370	717	91	6.00E-07	47
head maturation protease, putative ; K06904	ppu:PP_1566	702	84	1.00E-05	77
putative tail component of cryptic prophage CP-933P	etw:ECSP_2099	717	94	4.00E-11	50
hypothetical protein	cko:CKO_00652	702	88	1.00E-120	413
yjfJ; putative phage shock protein A	stm:STM4371	699	91	7.00E-13	65
putative phage repressor protein CI	eoj:ECO26_3204	651	97	0.002	29
peptidase M48 Ste24p ; K03799 heat shock protein HtpX [EC:3.4.24.-]	rpf:Rpic12D_0615	966	95	0	696
hypothetical protein ; K00782 hypothetical protein	cko:CKO_04247	696	88	0	697
FtsH-2 peptidase (EC:3.6.4.6); K03798 cell division protease FtsH [EC:3.4.24.-]	dde:Dde_3415	1884	86	1.00E-161	622
Ig domain protein, group 2 domain protein	vfm:VFMJ11_A0011	3585	100	0.55	21
FAD linked oxidase domain protein ; K06911	geo:Geob_0863	2913	100	0.14	22
similar to ubiquitin-conjugating enzyme UbcM3; K06689 ubiquitin-conjugating enzyme E2 D/E [EC:6.3.2.19]	cin:100185453	756	100	0.14	22
CI; bacteriophage 186 repressor protein CI	eta:ETA_05540	579	82	2.00E-06	102
GSVIVT00003057001; hypothetical protein LOC100259015	vvi:100259015	450	100	0.54	21
LppC family lipoprotein ; K07121	swd:Swoo_0352	1905	100	0.53	21
yjfK; hypothetical protein	sbo:SBO_4272	660	83	2.00E-10	117
hypothetical protein	ptm:GSPATT00016606001	1392	100	0.53	21
putative bacteriophage protein	stt:t1873	756	83	3.00E-36	260
RND efflux transporter	mpt:Mpe_B0595	2421	100	0.53	21
3-ketoacyl-CoA thiolase (EC:2.3.1.16 2.3.1.9)	vex:VEA_001989	1176	100	0.13	22
GntR-family transcriptional regulator	pmr:PMI0404	651	82	1.00E-35	275
putative inner membrane protein	sea:SeAg_B4652	639	81	6.00E-07	135
glutathione-S-transferase-family protein	stt:t0679	645	84	2.00E-62	372
hypothetical protein	bmj:BMULJ_00938	612	99	0	597
hypothetical protein	ecx:EcHS_A2097	525	95	0	419
fumarate/tartrate hydratase, alpha subunit ; K01677 fumarate hydratase subunit alpha [EC:4.2.1.2]	sun:SUN_0573	852	100	2	20
hypothetical protein	kpe:KPK_4144	486	97	9.00E-46	108
BcepMu22; putative soluble lytic murein transglycosylase	bcj:BCAS0533	612	97	5.00E-07	35
transcriptional regulator, LuxR family	kpe:KPK_2813	630	86	8.00E-37	189
cobyrinic acid a,c-diamide synthase ; K03496 chromosome partitioning protein	ent:Ent638_4322	642	79	3.00E-36	548
helicase C2	ajs:Ajs_2428	2568	100	0.13	22
rap, ninG; structure-specific endonuclease	ecd:ECDH10B_1336	642	86	1.00E-66	291
DNA polymerase III subunits gamma and tau (EC:2.7.7.7); K02343 DNA polymerase III subunit gamma/tau [EC:2.7.7.7]	bur:Bcep18194_A5128	2376	100	0.5	21
hypothetical protein	cro:ROD_09421	612	85	1.00E-94	446
hypothetical protein	msu:MS0416	744	100	0.031	23
resolvase	eta:ETA_pET460080	606	99	0	606
hypothetical protein	ncr:NCU00739	372	100	0.48	21
Ead domain protein	kpe:KPK_4165	666	91	7.00E-31	111
lacA; galactoside O-acetyltransferase ; K00633 galactoside O-acetyltransferase [EC:2.3.1.18]	ses:SARI_02830	606	97	0.002	29
putative lipoprotein	kpe:KPK_3060	528	96	1.00E-120	266
bacteriophage Mu GP45 protein	ecx:EcHS_A2086	582	87	5.00E-07	67
hypothetical protein	kpn:KPN_pKPN5p08207	582	91	0.03	35
similar to zinc finger protein 544	dre:798256	903	100	0.47	21
hypothetical protein	ecx:EcHS_A2090	591	86	8.00E-49	237
hypothetical protein ; K02443 glycerol uptake operon antiterminator	cko:CKO_04123	576	85	1.00E-81	404
hypothetical protein	kpu:KP1_3654	576	86	6.00E-25	137
hypothetical protein	ptm:GSPATT00017241001	3924	100	0.12	22
exonuclease (EC:3.1.11.-); K03546 exonuclease SbcC	sat:SYN_00200	3672	100	0.46	21
rrmJ; ribosomal RNA large subunit methyltransferase J ; K02427 ribosomal RNA large subunit methyltransferase E [EC:2.1.1.-]	bmr:BMI_II681	648	100	0.12	22
groEL; chaperonin GroEL ; K04077 chaperonin GroEL	slo:Shew_0472	1650	100	0.11	22
GK25249 gene product from transcript GK25249-RA	dwi:Dwil_GK25249	3474	100	0.45	21
putative glycosyl hydrolase, BNR repeat (EC:3.2.1.21)	cti:RALTA_B2028	1158	100	0.45	21
3'-5' exoribonuclease ; K12573 ribonuclease R [EC:3.1.-.-]	azc:AZC_1859	2445	96	0.45	25
hypothetical protein	esa:ESA_00997	741	95	2.00E-06	38
cyclic beta-1,2-glucan synthase	asa:ASA_3213	8511	100	0.11	22
GGDEF domain	oca:OCAR_4736	2292	96	0.028	27
hypothetical protein	lbc:LACBIDRAFT_298451	2841	91	0.44	33
hypothetical protein	cro:ROD_25921	546	80	1.00E-07	168
thiS; thiamine biosynthesis protein ThiS ; K03154 thiamine biosynthesis ThiS	cjr:CJE1191	192	100	0.44	21
protein tyrosine phosphatase ; K03741 arsenate reductase [EC:1.20.4.1]	rfr:Rfer_3666	483	94	5.00E-13	53
rpsB; 30S ribosomal protein S2 ; K02967 small subunit ribosomal protein S2	cjd:JJD26997_0547	792	100	0.43	21
capsule polysaccharide export protein KpsC	fph:Fphi_1180	975	100	1.7	20
Na(+)-translocating NADH-quinone reductase subunit A ; K00346 Na+-transporting NADH:ubiquinone oxidoreductase subunit A [EC:1.6.5.-	sdn:Sden_0982	1335	96	1.7	24
yrfC; hypothetical protein ; K12289 pilus assembly protein HofN	kpn:KPN_03765	534	89	1.00E-108	353
hypothetical protein	ent:Ent638_0796	546	87	1.00E-13	90
sodium:dicarboxylate symporter	dar:Daro_0480	1302	100	1.7	20
cytochrome-c peroxidase (EC:1.11.1.5); K00428 cytochrome c peroxidase [EC:1.11.1.5]	msl:Msil_3903	930	94	0.002	33
hypothetical protein	eck:EC55989_2618	480	93	2.00E-71	195
putative prophage DNA-binding protein	cro:ROD_26201	558	83	4.00E-26	191
hypothetical protein	pyo:PY01292	7761	100	0.1	22
fimbrial protein ; K07345 major type 1 subunit fimbrin (pilin)	kpu:KP1_0597	513	81	8.00E-21	230
alpha-hemolysin translocation ATP-binding protein HlyB; K11004 ATP-binding cassette, subfamily B, bacterial HlyB/CyaB	ecp:ECP_4554	2124	100	1.6	20
hypothetical protein	spq:SPAB_05418	495	90	7.00E-06	49
hypothetical protein	nve:NEMVE_v1g173914	3165	93	0.4	29
U3 snoRNP-associated protein Utp16 (predicted)	spo:SPBP8B7.10c	1041	100	0.4	21
GD12212 gene product from transcript GD12212-RA	dsi:Dsim_GD12212	1260	96	0.4	25
hypothetical protein	pan:PODANSg8044	1542	96	0.1	26
hypothetical protein	ecx:EcHS_A2095	564	89	1.00E-53	193
similar to ankyrin repeat domain 5	tgu:100219020	2394	100	0.1	22
Na(+)-translocating NADH-quinone reductase subunit A ; K00346 Na+-transporting NADH:ubiquinone oxidoreductase subunit A [EC:1.6.5.-	dps:DP1802	1338	96	0.1	26
yhhY; putative acyltransferase ; K03825 putative acetyltransferase [EC:2.3.1.-]	kpu:KP1_5140	489	87	2.00E-46	201
hypothetical protein	cgr:CAGL0A00913g	4281	96	0.025	27
hypothetical protein	ecw:EcE24377A_1452	540	92	0.002	37
putative tail component of prophage CP-933K	sfx:S0748	741	90	0.025	39
magnesium transporter ; K06213 magnesium transporter	dol:Dole_0412	1386	100	0.38	21
recB; exodeoxyribonuclease V, beta subunit (EC:3.1.11.5); K03582 exodeoxyribonuclease V beta subunit [EC:3.1.11.5]	mca:MCA0691	3603	100	0.38	21
NUDIX hydrolase ; K08311 putative (di)nucleoside polyphosphate hydrolase [EC:3.6.1.-]	tau:Tola_2963	525	100	1.5	20
DNA helicase/exodeoxyribonuclease V, beta subunit (EC:3.1.11.5); K03582 exodeoxyribonuclease V beta subunit [EC:3.1.11.5]	gme:Gmet_1893	3603	100	1.4	20
conserved hypothetical protein; putative exported protein	ecz:ECS88_2910	513	86	6.00E-09	74
heat shock protein HSP20	rpf:Rpic12D_0623	459	97	0	459
putative bacteriophage protein	ent:Ent638_0805	531	82	0.001	89
phage protein GP46	ecx:EcHS_A2085	450	89	1.00E-22	105
gguA; sugar uptake ABC transporter ATP-binding protein ; K10548 putative multiple sugar transport system ATP-binding protein	sme:SM_b20894	1521	96	0.36	25
repressor protein for FtsI ; K04753 suppressor of ftsI	spe:Spro_4257	1416	100	0.023	23

hypothetical protein	gem:GM21_0957	756	100	1.4	20
hypothetical protein	tet:TTHERM_00279700	2556	100	1.4	20
hypothetical protein	pcs:Pc13g06980	954	96	0.088	26
GF13640 gene product from transcript GF13640-RA	dan:Dana_GF13640	2646	100	0.35	21
gntP; fructuronate transporter; K03299 gluconate:H+ symporter, GntP family	ecz:ECS88_4939	1344	87	1.00E-93	372
Ead domain protein	kpe:KPK_4165	666	92	9.00E-82	224
putative prophage regulatory protein	cro:ROD_09451	426	88	0.022	43
PMT family 4-amino-4-deoxy-L-arabinose transferase/glycosyltransferase	reu:Reut_B3508	1614	100	1.3	20
insertion element protein	ecl:EcolC_3185	699	100	1.00E-131	239
rpsB; 30S ribosomal protein S2 ; K02967 small subunit ribosomal protein S2	rpb:RPB_2828	996	100	0.34	21
hypothetical protein ; K12290 pilus assembly protein HofO	kpe:KPK_0352	429	86	5.00E-65	280
fumarate hydratase, class II	ddc:Dd586_2084	1398	100	0.33	21
hypothetical protein	kpu:KP1_2161	603	93	1.00E-127	313
hypothetical protein	kpe:KPK_4168	534	100	4.00E-13	41
Hypothetical 71.7 kDa protein F52H3.2 in chromosome II, putative; K03495 glucose inhibited division protein A	bmy:Bm1_42115	1917	100	0.084	22
Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; YBL107C is not an essential	sce:YBL107C	591	100	0.082	22
hypothetical protein	ecx:EcHS_A2089	510	82	5.00E-06	101
putative cytoplasmic protein	stm:STM0948	402	92	1.00E-159	402
hypothetical protein	see:SNSL254_p_0052	636	100	1.00E-179	319
yjfL; putative inner membrane protein ; K08989 putative membrane protein	sec:SC4249	399	82	2.00E-42	330
type I secretion outer membrane protein, TolC family	pwa:Pecwa_3318	1413	100	0.079	22
hypothetical protein	cqu:CpipJ_CPIJ008196	1077	100	0.005	24
hypothetical protein	bbt:BBta_4140	1326	100	0.079	22
rpsC; 30S ribosomal protein S3 ; K02982 small subunit ribosomal protein S3	cco:CCC13826_1771	699	100	0.079	22
traM; conjugal transfer protein TraM	kpn:KPN_pKPN4p07124	399	83	0.02	75
transposase IS4 family protein	ppw:PputW619_3354	981	91	1.00E-133	390
hypothetical protein	cbr:CBG09837	1113	100	0.02	23
hypothetical protein	dvu:DVU2023	540	100	0.019	23
yfeK; hypothetical protein	set:SEN2419	384	78	2.00E-05	228
adenylosuccinate synthetase (EC:6.3.4.4); K01939 adenylosuccinate synthase [EC:6.3.4.4]	ppd:Ppro_0518	1293	100	0.29	21
hypothetical protein	cro:ROD_25891	372	88	2.00E-14	83
chromosome segregation protein SMC ; K03529 chromosome segregation protein	msl:Msil_3824	3456	100	0.29	21
hypothetical protein	spq:SPAB_03662	144	98	1.00E-12	44
crossover junction endodeoxyribonuclease RusA family protein	kpe:KPK_2853	357	94	2.00E-36	104
hypothetical protein	pan:PODANSg4614	2148	100	1.1	20
4-aminobutyrate aminotransferase (EC:2.6.1.19)	aav:Aave_4333	1374	100	1.1	20
hypothetical protein	pst:PSPTO_3423	285	100	0.072	22
similar to ATP-binding cassette, sub-family A (ABC1), member 10; K05652 ATP-binding cassette, subfamily A (ABC1), member 10	tgu:100223114	4989	100	0.072	22
hypothetical protein	kpu:KP1_0406	369	88	0.28	41
Os03g0372500; hypothetical protein	osa:4332941	2934	100	0.071	22
hypothetical protein	ang:An18g04810	1272	100	0.28	21
low complexity, questionable orf	cal:CaO19.6878	573	93	0.27	29
IS911 transposase orfB	ecm:EcSMS35_1101	747	93	1.00E-132	328
DNA polymerase II (EC:2.7.7.7); K02336 DNA polymerase II [EC:2.7.7.7]	vex:VEA_003097	2364	100	1.1	20
murD; UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase (EC:6.3.2.9); K01925 UDP-N-acetylmuramoylalanine--D-glutamate ligase	las:CLIBASIA_05005	1407	100	4.2	19
hypothetical protein	ecx:EcHS_A2080	1995	85	9.00E-26	150
probable two-component response regulator protein	rhi:NGR_c18600	1248	100	1.1	20
hypothetical protein	kpn:KPN_01381	210	100	3.00E-10	36
hypothetical protein	swd:Swoo_1506	252	100	1	20
ATP-binding region, ATPase-like domain-containing protein	ath:AT4G36280	1881	96	1	24
yihN; putative transporter	eoj:ECO26_4716	1266	84	1.00E-21	155
gifsy-2 prophage; putative RecA/RadA recombinase	sbp:Sbal223_0784	324	93	0.064	30
hypothetical protein	eic:NT01EI_3129	318	87	6.00E-76	314
transposase	ebr:ECB_03524	348	95	1.00E-135	309
hypothetical protein	kpe:KPK_0888	321	95	2.00E-17	60
putative transposase ; K07497 putative transposase	set:SEN2616	1113	93	7.00E-82	228
algI; alginate O-acetylation protein AlgI	abo:ABO_0389	1419	100	0.97	20
peptidase M1, membrane alanine aminopeptidase	ade:Adeh_0324	2625	100	0.061	22
thioredoxin ; K03672 thioredoxin 2 [EC:1.8.1.8]	rpf:Rpic12D_0618	441	92	1.00E-106	288
yjfI; putative cytoplasmic protein ; K09980 hypothetical protein	stm:STM4370	405	89	0.004	44
anti-anti-sigma regulatory factor	vvy:VVA0580	921	100	0.24	21
putative sugar ABC transporter ATP-binding protein ; K02056 simple sugar transport system ATP-binding protein [EC:3.6.3.17]	sme:SM_b20485	1530	96	0.059	26
similar to predicted protein	hmg:100207382	708	100	0.059	22
gidA; tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA ; K03495 glucose inhibited division protein A	abu:Abu_2210	1878	100	0.92	20
folD; bifunctional: 5,10-methylene-tetrahydrofolate dehydrogenase; 5,10-methylene-tetrahydrofolate cyclohydrolase (EC:1.5.1.5 3.5.4.9); K0	cti:RALTA_A1289	852	100	0.23	21
hypothetical protein	esa:ESA_01037	396	89	0.058	38
proS; prolyl-tRNA synthetase (EC:6.1.1.15); K01881 prolyl-tRNA synthetase [EC:6.1.1.15]	lpc:LPC_2600	1710	100	0.91	20
GK15020 gene product from transcript GK15020-RA	dwi:Dwil_GK15020	2517	100	0.91	20
GI16257 gene product from transcript GI16257-RA	dmo:Dmoj_GI16257	6162	100	0.23	21
apg3; autophagy associated protein Apg3 (predicted); K08343 autophagy-related protein 3	spo:SPBC3B9.06c	828	100	0.058	22
GH24537 gene product from transcript GH24537-RA	dgr:Dgri_GH24537	1311	100	0.22	21
poly(A) polymerase	tbr:Tb11.01.7300	1002	93	0.85	28
hypothetical protein	scl:sce5761	1791	100	0.85	20
hypothetical protein	cro:ROD_25881	279	85	2.00E-07	75
hypothetical protein	dma:DMR_40370	633	100	0.21	21
SORBIDRAFT_09g030110; hypothetical protein	sbi:SORBI_09g030110	1506	100	0.84	20
response regulator receiver modulated diguanylate cyclase/phosphodiesterase	pat:Patl_3545	1710	100	0.83	20
hypothetical protein	ptm:GSPATT00024006001	1752	93	0.21	29
glutamate receptor kainate	smm:Smp_153780	2799	100	0.82	20
fhaS; adhesin	bpe:BP2667	7662	100	0.8	20
hypothetical protein	kpe:KPK_3735	261	93	2.00E-63	169
hypothetical protein	cko:CKO_04122	261	86	1.00E-08	77
acetyl-CoA carboxylase, biotin carboxylase ; K01946 biotin carboxylase [EC:6.3.4.14]; K01961 acetyl-CoA carboxylase, biotin carboxylase s	mno:Mnod_6042	1356	93	0.2	29
Mlh2-like protein	gla:GL50803_33083	4425	93	0.2	29
curved-DNA-binding protein; K05516 curved DNA-binding protein	psp:PSPPH_4482	960	100	0.2	21
hypothetical protein	tet:TTHERM_01123880	3870	94	0.012	31
hypothetical protein; K02684 DNA primase small subunit [EC:2.7.7.-]	mgl:MGL_2934	1416	100	0.049	22
hypothetical protein	kpu:KP1_2987	252	85	6.00E-51	252
hypothetical protein	eoj:ECO26_1176	261	96	0.012	27
hypothetical protein	hpj:jhp0052	984	100	0.19	21
hypothetical protein	tet:TTHERM_00459220	2253	96	0.74	24
amino acid ABC transporter permease	cju:C8J_0857	753	96	0.18	25
hypothetical protein	nve:NEMVE_v1g213276	2295	100	0.72	20
pmrD; polymyxin B resistance protein	kpu:KP1_3573	246	87	2.00E-47	202
transposase B ; K07497 putative transposase	eic:NT01EI_0924	549	91	7.00E-78	233
hypothetical protein	lbc:LACBIDRAFT_297118	3294	96	0.7	24
hypothetical protein	tad:TRIADDRAFT_50243	1014	100	0.045	22
O-antigen polymerase	nmu:Nmul_A1429	1218	100	0.68	20
peptidase M48 Ste24p ; K03799 heat shock protein HtpX [EC:3.4.24.-]	rpf:Rpic12D_0615	966	99	1.00E-115	224
cell surface antigen Sca2	ccs:CCNA_03609	1350	100	0.67	20
oac-26; O-ACyltransferase homolog	cel:F41D3.2	2049	100	0.67	20
chain length determinant family protein	dde:Dde_0831	1509	100	0.17	21

hypothetical protein	rcu:RCOM_0297000	150	100	0.65	20
bacteriophage lysis protein	sbc:SbBS512_E1451	300	100	0.17	21
hypothetical protein	kpu:KP1_0389	105	100	4.00E-08	32
hypothetical protein	kpe:KPK_B0060	126	88	2.00E-25	128
rpsN; 30S ribosomal protein S14 ; K02954 small subunit ribosomal protein S14	wpi:WPa_1179	309	100	0.16	21
hypothetical protein	eoi:ECO111_3368	237	87	7.00E-07	62
similar to hCG2037011	ssc:100156026	507	100	0.63	20
UspA domain-containing protein	ppw:PputW619_3029	927	100	0.62	20
transcriptional regulator, LysR family	kpe:KPK_1300	885	95	2.00E-07	39
putative fimbrial protein	kpu:KP1_4578	1242	92	1.00E-45	143
PAS/PAC sensor hybrid histidine kinase	dal:Dalk_2075	2241	96	2.5	23
putative invertase	kpn:KPN_01436	279	93	5.00E-54	149
rplJ; 50S ribosomal protein L10 ; K02864 large subunit ribosomal protein L10	net:Neut_1797	516	100	0.01	23
putative IS602 transposase OrfB	eoi:ECO111_3779	747	95	1.00E-88	207
PDZ/DHR/GLGF domain-containing protein	bid:Bind_0797	981	96	0.002	28
cytochrome c oxidase, cbb3-type, subunit I; K00404 cb-type cytochrome c oxidase subunit I [EC:1.9.3.1]	sit:TM1040_2545	1605	100	2.4	19
importin-like protein	tan:TA11715	3846	100	0.15	21
epimerase, PhzC/PhzF-like protein (EC:5.1.-.-); K06998	reh:H16_A2781	861	100	0.002	24
hypothetical protein	cqu:CpipJ_CPIJ007470	1467	100	0.6	20
minD; septum site-determining protein; K03609 septum site-determining protein MinD	lpc:LPC_1164	831	100	0.59	20
hypothetical protein	kpu:KP1_3253	126	96	3.00E-18	57
glgS; glycogen synthesis protein	kpu:KP1_4739	204	91	2.00E-13	65
arsR; arsenical resistance operon repressor	ctu:Ctu_1p00510	378	91	1.00E-08	53
hypothetical protein	kpu:KP1_2686	195	95	2.00E-84	195
GE24339 gene product from transcript GE24339-RA	dya:Dyak_GE24339	4656	100	0.15	21
GH23138 gene product from transcript GH23138-RA	dgr:Dgri_GH23138	5919	100	0.037	22
hypothetical protein	nmi:NMO_1071	624	96	0.57	24
transcriptional regulator, LysR family	kpe:KPK_2589	876	80	6.00E-07	148
yadF; putative carbonic anhdrase ; K01673 carbonic anhydrase [EC:4.2.1.1]	kpu:KP1_0572	681	99	2.00E-40	90
Gm8286, EG666784; predicted gene 8286	mmu:666784	1764	100	0.57	20
hypothetical protein	kpu:KP1_1144	111	91	4.00E-05	43
hypothetical protein	tva:TVAG_432880	1239	100	2.2	19
hypothetical protein	eca:ECA0366	312	83	3.00E-21	162
hypothetical protein	kpe:KPK_3871	192	91	7.00E-59	193
hypothetical protein	mlo:mlr8225	483	100	0.009	23
similar to KIAA1432	ecb:100059612	4032	96	0.55	24
hypothetical protein	bra:BRADO4654	261	100	2.2	19
hypothetical protein	pcb:PC000816.04.0	921	100	0.036	22
hypothetical protein; K02210 minichromosome maintenance protein 7 (cell division control protein 47)	ang:An16g04890	2424	100	0.54	20
hypothetical protein	kpu:KP1_0696	234	93	6.00E-41	123
hypothetical protein	dat:HRM2_17910	1302	100	0.54	20
putative metal-dependent phosphohydrolase with HD subdomain ; K06885	kpu:KP1_2389	1533	98	1.00E-57	123
hypothetical protein ; K11985 TRAF-interacting protein	aag:AaeL_AAEL003787	1281	100	0.53	20
waaL; O-antigen ligase	kpu:KP1_5317	1083	100	0.53	20
hypothetical protein	sil:SPO1682	123	100	0.53	20
lacA; thiogalactoside acetyltransferase	eoh:ECO103_0324	612	97	4.00E-60	135
yeiE; putative transcriptional regulator (LysR family)	kpn:KPN_00284	171	95	3.00E-18	61
hypothetical protein	sfr:Sfri_3475	306	99	4.00E-45	98
hypothetical protein LOC100240780	vvi:100240780	2202	100	0.13	21
hypothetical protein	kpe:KPK_0338	114	91	7.00E-25	92
GJ17609 gene product from transcript GJ17609-RA	dvi:Dvir_GJ17609	1365	100	0.009	23
DNA polymerase I (EC:2.7.7.7); K02335 DNA polymerase I [EC:2.7.7.7]	spc:Sputcn32_3906	2769	100	0.52	20
hypothetical protein	kpe:KPK_2112	123	100	4.00E-11	37
nitrate ABC transporter, inner membrane subunit ; K02050 sulfonate/nitrate/taurine transport system permease protein	rpi:Rpic_0236	852	96	0.033	26
PIK3AP1; phosphoinositide-3-kinase adaptor protein 1; K12230 phosphoinositide 3-kinase adapter protein 1	mcc:705017	2418	96	2	23
hypothetical protein	kpu:KP1_2355	117	93	6.00E-44	117
miaA; tRNA delta(2)-isopentenylpyrophosphate transferase (EC:2.5.1.8); K00791 tRNA delta(2)-isopentenylpyrophosphate transferase [EC:2	nis:NIS_0303	900	96	0.13	25
hypothetical protein	ecc:c5175	132	96	6.00E-13	48
hypothetical protein	dar:Daro_0095	822	100	0.13	21
hypothetical protein	kpu:KP1_3534	336	100	0.13	21
hypothetical protein	kpe:KPK_1494	123	87	4.00E-17	95
hypothetical protein	ecq:ECED1_2586	183	93	2.00E-06	45
putative transporter	acn:ACIS_00875	1329	100	7.7	18
hypothetical protein	kpu:KP1_1220	117	100	6.00E-59	117
hypothetical protein	kpu:KP1_4770	366	95	1.00E-16	58
hypothetical protein	dol:Dole_1861	996	100	0.03	22
acyl-CoA dehydrogenase domain protein	geo:Geob_2422	1233	100	0.12	21
similar to CG3164-PB, isoform B	ame:414051	2112	100	0.03	22
grpE; heat shock protein HSP70 cofactor (EC:5.1.3.1); K03687 molecular chaperone GrpE	efe:EFER_0459	1053	92	3.00E-42	117
transposase IS3/IS911 family protein	dda:Dd703_2340	279	87	7.00E-31	150
ascG; ascBF operon repressor ; K03487 LacI family transcriptional regulator, asc operon repressor	kpu:KP1_4316	1056	100	3.00E-14	42
c3-1; complement component C3	cin:445694	5322	100	1.8	19
YD repeat-containing protein	ypb:YPTS_3419	4485	100	0.12	21
hypothetical protein	tcr:503823.150	1599	96	0.45	24
hypothetical protein	pfh:PFHG_02388	1060	96	0.11	25
putative adenylate cyclase	cja:CJA_3519	2214	100	0.45	20
hypothetical protein	kpe:KPK_0972	117	100	1.00E-22	56
DNA-directed polymerase kappa (EC:6.3.5.5); K03511 DNA polymerase kappa subunit [EC:2.7.7.7]	afm:AFUA_7G01270	1845	100	0.029	22
b2688, gsh-I, gshA; glutamate--cysteine ligase (EC:6.3.2.2); K01919 glutamate--cysteine ligase [EC:6.3.2.2]	yen:YE0838	1560	100	1.8	19
hypothetical protein	kpe:KPK_2923	159	86	1.00E-19	119
isocitrate dehydrogenase, NADP-dependent ; K00031 isocitrate dehydrogenase [EC:1.1.1.42]	nmu:Nmul_A2245	1254	100	0.11	21
hypothetical protein	kpu:KP1_2660	129	93	2.00E-09	46
slc22a5; solute carrier family 22 (organic cation transporter), member 5; K08202 MFS transporter, OCT family, solute carrier family 22 (orga	xla:380592	1647	100	0.11	21
phage minor tail protein L	mno:Mnod_5753	732	100	1.7	19
hypothetical protein	dha:DEHA0B06732g	3480	100	0.43	20
integral membrane sensor signal transduction histidine kinase	ddc:Dd586_1341	1071	96	0.43	24
hypothetical protein	ecw:EcE24377A_B0002	150	97	4.00E-69	150
similar to acrosomal matrix component AM67	ecb:100056262	2409	100	0.43	20
hypothetical protein	tet:TTHERM_00864920	606	93	0.027	30
sucB; dihydrolipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex (EC:2.3.1.61); K00658 2-oxoglutarate deh	bab:bbp281	1233	96	0.11	25
IS5 transposase	vcj:VCD_000992	981	83	1.00E-04	86
hypothetical protein	kpe:KPK_3962	120	92	0.007	39
hypothetical protein	kpe:KPK_1141	117	92	2.00E-24	87
hypothetical protein	kpu:KP1_1985	171	90	4.00E-35	129
putative cytoplasmic protein	rrj:RrIowa_0840	324	100	1.6	19
Cytochrome P450 family protein (EC:1.14.14.1); K00493 unspecific monooxygenase [EC:1.14.14.1]	tet:TTHERM_00200550	1551	100	0.42	20
hypothetical protein	scl:sce2396	285	93	0.027	30
cytochrome c family protein	ank:AnaeK_3174	3990	100	0.1	21
hypothetical protein	kpu:KP1_2587	186	85	5.00E-22	143
hypothetical protein LOC432253	xla:432253	1839	100	0.41	20
hypothetical protein	zro:ZYRO0D13398g	1917	100	0.41	20
rprA; regulatory RNA	stm:STM1363	107	100	0.026	22

ATP-dependent metalloprotease FtsH (EC:3.6.4.3); K03798 cell division protease FtsH [EC:3.4.24.-]	rpf:Rpic12D_0624	1818	100	4.00E-75	144
similar to CG9092-PA	tca:655997	1968	100	1.6	19
intA; integrase	eck:EC55989_2909	1242	94	9.00E-27	83
ribosomal rna methyltransferase ; K02427 ribosomal RNA large subunit methyltransferase E [EC:2.1.1.-]	pkn:PKH_070600	1605	96	0.025	26
adenylate/guanylate cyclase with CHASE sensor	geo:Geob_0882	2106	97	0.1	29
hypothetical protein	kpu:KP1_3926	135	100	5.00E-13	40
queF; 7-cyano-7-deazaguanine reductase	vei:Veis_4790	846	96	0.1	25
similar to myosin, heavy chain 1, skeletal muscle, adult; K10352 myosin heavy chain	tgu:100225611	5835	96	0.4	24
hypothetical protein	kpe:KPK_2377	141	90	7.00E-12	62
hypothetical protein	kpu:KP1_5510	138	96	1.00E-35	94
similar to IkappaB kinase gamma	hmg:100213125	3147	100	0.1	21
hypothetical protein	ptm:GSPATT00037997001	609	100	0.4	20
hypothetical protein	ses:SARI_02634	477	92	5.00E-13	64
hypothetical protein; K02462 general secretion pathway protein M	aav:Aave_0919	654	96	0.098	25
Os01g0362100; hypothetical protein	osa:4325812	2097	96	0.39	24
transcriptional regulator, LuxR family	kpe:KPK_4797	723	87	5.00E-28	137
transporter AcrB/D/F family	vex:VEA_000655	3063	100	1.5	19
phosphoenolpyruvate-dependent PTS family enzyme IIA component	kpu:KP1_2729	450	92	2.00E-27	92
putative bacteriophage protein (gene 65)	ecz:ECS88_2522	153	94	1.00E-04	34
hypothetical protein	kpe:KPK_0397	108	92	3.00E-08	48
hypothetical protein	tad:TRIADDRAFT_53596	8205	100	0.095	21
pepN; aminopeptidase N (EC:3.4.11.2); K01256 aminopeptidase N [EC:3.4.11.2]	abb:ABBFA_001374	2607	100	1.5	19
hypothetical protein	ptm:GSPATT00008844001	510	100	0.38	20
hypothetical protein	kpn:KPN_02457	183	83	1.00E-07	95
hypothetical protein; K03126 transcription initiation factor TFIID subunit D10	ctp:CTRG_00709	2412	100	0.37	20
hypothetical protein	scl:sce1912	1494	96	0.37	24
hypothetical protein	hac:Hac_1450	921	100	0.006	23
response regulator	pfl:PFL_1972	1185	100	0.093	21
Cob(I)yrinic acid a,c-diamide adenosyltransferase (EC:2.5.1.17); K00798 cob(I)alamin adenosyltransferase [EC:2.5.1.17]	pen:PSEEN4473	567	100	0.093	21
hypothetical protein	cak:Caul_1641	816	100	0.36	20
ygdL; putative enzyme	kpn:KPN_04165	168	97	2.00E-05	31
trwL6; TrwL6 protein	bhe:BH15620	315	100	1.4	19
hypothetical protein	pbe:PB000253.03.0	3096	100	0.36	20
GH24601 gene product from transcript GH24601-RA	dgr:Dgri_GH24601	1263	100	0.36	20
integrase catalytic subunit ; K07497 putative transposase	ent:Ent638_0741	813	92	4.00E-04	37
multidrug resistance pump, putative	rcu:RCOM_0845260	1467	100	0.023	22
guaB; inosine-5'-monophosphate dehydrogenase (EC:1.1.1.205); K00088 IMP dehydrogenase [EC:1.1.1.205]	ttu:TERTU_2616	1476	100	0.36	20
GD23395 gene product from transcript GD23395-RA	dsi:Dsim_GD23395	2469	96	0.36	24
hypothetical protein	pan:PODANSg8758	5076	100	0.023	22
carB; carbamoylphosphate synthase large subunit (split gene in MJ) ; K01955 carbamoyl-phosphate synthase large subunit [EC:6.3.5.5]	lip:LI0939	3231	100	0.091	21
hypothetical protein	kpu:KP1_1844	288	89	0.001	44
IclR regulatory protein	bgl:bglu_1g24760	810	100	5.6	18
hypothetical protein	ppp:PHYPADRAFT_75061	378	100	0.091	21
GE15592 gene product from transcript GE15592-RA	dya:Dyak_GE15592	1617	100	0.088	21
thrombospondin type 3 repeat family	cja:CJA_2517	5805	100	0.088	21
rsmC; 16S ribosomal RNA m2G1207 methyltransferase ; K00564 ribosomal RNA small subunit methyltransferase C [EC:2.1.1.52]	sbo:SBO_4432	1032	100	1.4	19
thiamineS protein	bac:BamMC406_5087	270	100	1.4	19
hypothetical protein	ppp:PHYPADRAFT_68797	1482	100	0.35	20
similar to predicted protein	cin:100183007	864	100	0.35	20
hypothetical protein	ddi:DDBDRAFT_0188581	1821	100	1.4	19
hypothetical protein	stt:t4368	213	98	7.00E-18	56
hypothetical protein	fgr:FG00401.1	243	100	0.34	20
hypothetical protein	ctp:CTRG_04705	1602	100	0.086	21
TetR family transcriptional regulator	bxe:Bxe_B0084	618	100	1.3	19
glycosyl transferase group 1	gbm:Gbem_0853	1182	96	1.3	23
LolC/E family lipoprotein releasing system, transmembrane protein ; K09808 lipoprotein-releasing system permease protein	reu:Reut_A1076	1251	100	0.34	20
hypothetical protein	ecm:EcSMS35_4832	651	96	1.3	23
methyl-accepting chemotaxis protein ; K03406 methyl-accepting chemotaxis protein	abu:Abu_0528	1902	100	0.022	22
glucose dehydrogenase ; K00117 quinoprotein glucose dehydrogenase [EC:1.1.5.2]	pin:Ping_3086	2328	100	0.34	20
histidine kinase	azc:AZC_4066	1779	100	5.3	18
hypothetical protein	sew:SeSA_A2675	126	88	1.00E-06	57
fibronectin, type III domain-containing protein	gur:Gura_0068	5088	100	0.086	21
hypothetical protein	kpe:KPK_2190	120	97	1.00E-06	33
hypothetical protein	kpu:KP1_2621	198	90	4.00E-22	91
hypothetical protein	nve:NEMVE_v1g202346	1653	100	0.33	20
UDP-glucose 6-dehydrogenase (EC:1.1.1.22); K00012 UDPglucose 6-dehydrogenase [EC:1.1.1.22]	xau:Xaut_3551	1317	100	0.083	21
glutaredoxin	sdn:Sden_1584	444	100	5.1	18
ATP-binding cassette (ABC) superfamily protein ; K02471 putative ATP-binding cassette transporter	fph:Fphi_0895	1671	100	0.33	20
hypothetical protein	kpe:KPK_5243	144	92	5.00E-28	97
long-chain acyl-CoA synthetase	vvy:VV2667	1686	93	0.33	28
oligopeptide/dipeptide ABC transporter, ATPase subunit ; K02032 peptide/nickel transport system ATP-binding protein	mes:Meso_3136	966	96	0.005	27
isftu1; transposase	ftf:FTF1780	786	100	7.00E-61	120
hypothetical protein	tva:TVAG_127280	1188	100	1.3	19
putative sugar ABC transporter, periplasmic protein; K10439 ribose transport system substrate-binding protein	yen:YE0818	975	93	2.00E-05	43
aroB; 3-dehydroquinate synthase (EC:4.2.3.4); K01735 3-dehydroquinate synthase [EC:4.2.3.4]	abu:Abu_1125	1035	100	0.081	21
pseudogene	ypg:YpAngola_0019	560	100	0.001	24
Os06g0148900; hypothetical protein	osa:4340134	1107	100	0.32	20
hypothetical protein	ddi:DDBDRAFT_0189420	2901	100	0.02	22
hypothetical protein	kpu:KP1_5277	249	100	3.00E-23	57
conserved hypothetical protein	pfh:PFHG_02801	2224	96	0.02	26
hypothetical protein	spq:SPAB_05502	111	100	9.00E-08	31
conserved hypothetical protein	pfh:PFHG_01746	1632	93	0.081	29
hypothetical protein	kpe:KPK_4286	129	100	2.00E-18	49
hypothetical protein	kpu:KP1_2016	117	98	2.00E-21	58
Atm; ataxia telangiectasia mutated homolog (human) (EC:2.7.11.1); K04728 ataxia telangectasia mutated family protein [EC:2.7.11.1]	mmu:11920	9201	91	0.32	32
Tubb2c; tubulin, beta 2C; K07375 tubulin beta	mmu:227613	1338	100	0.081	21
hypothetical protein	pyo:PY06423	4384	100	0.32	20
hypothetical protein	dvl:Dvul_2206	267	100	0.31	20
major facilitator transporter	bam:Bamb_3946	1287	100	0.31	20
FAD-dependent pyridine nucleotide-disulphide oxidoreductase ; K00384 thioredoxin reductase (NADPH) [EC:1.8.1.9]	bph:Bphy_3740	1056	100	1.2	19
yeeO; putative MATE family transport protein	kpu:KP1_3579	1470	96	0.001	28
subunit of the histone acetyltransferase SAGA complex, putative	cdu:CD36_35060	3849	100	0.31	20
ApbE family lipoprotein ; K03734 thiamine biosynthesis lipoprotein	mch:Mchl_1534	981	100	0.078	21
amiB; N-acetylmuramoyl-L-alanine amidase (EC:3.5.1.28); K01448 N-acetylmuramoyl-L-alanine amidase [EC:3.5.1.28]	cps:CPS_0322	1332	100	1.2	19
hypothetical protein	kpe:KPK_2338	114	85	4.00E-16	113
hypothetical protein	acb:A1S_0060	768	100	0.078	21
hypothetical protein	sea:SeAg_B2544	123	89	0.078	37
hypothetical protein	kpu:KP1_3837	114	83	1.00E-09	87
alkanesulfonate transporter substrate-binding subunit ; K02051 sulfonate/nitrate/taurine transport system substrate-binding protein	spe:Spro_1738	966	100	1.2	19
hutC; histidine utilization repressor C ; K05836 GntR family transcriptional regulator, histidine utilization repressor	kpu:KP1_1744	726	91	5.00E-06	44
multidrug efflux system outer membrane protein	bav:BAV1655	1464	96	0.078	25
cytochrome-c oxidase (EC:1.9.3.1); K02274 cytochrome c oxidase subunit I [EC:1.9.3.1]	bxe:Bxe_A2184	2040	100	1.2	19

idhA; inositol 2-dehydrogenase (EC:1.1.1.18); K00010 myo-inositol 2-dehydrogenase [EC:1.1.1.18]	kpe:KPK_4081	1008	97	1.00E-28	74
hypothetical protein	ppp:PHYPADRAFT_45234	684	100	0.31	20

[a] Predicted protein function of the top BLASTN hit of each unique 10982 feature to the KEGG database irrespective of the alignment length and e-value.

[b] The gene id of the top BLAST hit

Supplemental Table 5. BSR analysis using TBLASTN of the amino acid sequences of putative virulence genes, nitrogen-fixation genes, allantoin metabolism genes, and citrate fermentation genes.

		K. variicola genomes			*Klebsiella* sp.	*K. pneumoniae* genomes							
Gene[a]	Accession Number[b]	At-22	342	1_1_55	10982	MGH 78578	1162281	JH1	KMS_92_3	1191100241	ATCC 13884	KCTC 2242	NTUH-K2044
Virulence-associated													
magA	BAC76772.1	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05	1.00
allS	BAD14988.1	0.27	0.27	0.27	0.95	0.27	0.27	0.27	0.27	0.27	0.27	0.27	0.95
rmpA	YP_001687850.1	0.09	0.09	0.09	0.07	0.07	0.09	0.08	0.07	0.07	1.00	1.00	1.00
kfu	BAH62695.1	0.93	0.93	0.93	0.96	0.99	0.99	0.99	0.99	0.99	0.99	0.99	1.00
uge/wcaG	AAP68521.1	0.97	0.98	0.98	0.98	0.97	0.98	0.98	0.98	0.98	0.97	0.98	0.98
wabG	AAX20104.1	0.97	0.97	0.97	0.97	0.99	0.98	0.99	0.99	0.98	0.98	0.99	0.99
ureA	ABR78861.1	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
fimH	AAA25091.1	0.93	0.93	0.93	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Nitrogen-fixation													
hypothetical	YP_002237546.1	0.9419	1	0.8564	0.99	0.90	0.66	0.49	0.81	0.88	0.66	0.71	0.88
nifQ	YP_002237547.1	1.00	1.00	1.00	0.99	0.08	0.08	0.08	0.08	0.08	0.08	0.08	0.08
nifB	YP_002237548.1	1.00	1.00	1.00	1.00	0.05	0.05	0.05	0.05	0.05	0.05	0.05	0.05
nifA	YP_002237549.1	1.00	1.00	1.00	1.00	0.27	0.27	0.27	0.27	0.27	0.27	0.27	0.27
nifL	YP_002237550.1	1.00	1.00	1.00	1.00	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04
nifF	YP_002237551.1	0.99	1.00	1.00	1.00	0.42	0.42	0.42	0.42	0.42	0.42	0.42	0.42
nifM	YP_002237552.1	0.99	1.00	0.99	1.00	0.11	0.11	0.11	0.11	0.11	0.11	0.11	0.11
nifZ	YP_002237553.1	1.00	1.00	0.99	1.00	0.10	0.10	0.10	0.10	0.09	0.10	0.10	0.10
nifW	YP_002237554.1	1.00	1.00	1.00	1.00	0.17	0.17	0.17	0.16	0.17	0.17	0.16	0.17
nifV	YP_002237555.1	1.00	1.00	1.00	1.00	0.23	0.23	0.23	0.23	0.23	0.23	0.23	0.23
nifS	YP_002237556.1	1.00	1.00	0.99	1.00	0.40	0.40	0.40	0.40	0.40	0.40	0.40	0.40
nifU	YP_002237557.1	1.00	1.00	1.00	1.00	0.22	0.22	0.22	0.22	0.22	0.22	0.22	0.22
nifX	YP_002237558.1	1.00	1.00	1.00	1.00	0.09	0.09	0.09	0.09	0.09	0.09	0.09	0.09
nifN	YP_002237559.1	0.98	1.00	1.00	0.99	0.03	0.03	0.03	0.03	0.03	0.03	0.03	0.03
nifE	YP_002237560.1	1.00	1.00	1.00	1.00	0.03	0.03	0.03	0.03	0.03	0.03	0.03	0.03
nifY	YP_002237561.1	0.99	1.00	0.98	0.98	0.07	0.07	0.07	0.08	0.07	0.07	0.07	0.07
nifT	YP_002237562.1	0.99	1.00	1.00	1.00	0.19	0.19	0.19	0.19	0.19	0.19	0.19	0.19
nifK	YP_002237563.1	1.00	1.00	1.00	1.00	0.03	0.03	0.03	0.03	0.03	0.03	0.03	0.03
nifD	YP_002237564.1	1.00	1.00	1.00	1.00	0.03	0.03	0.03	0.03	0.03	0.03	0.03	0.03
nifH	YP_002237565.1	0.98	1.00	0.98	0.98	0.07	0.07	0.07	0.07	0.07	0.06	0.06	0.08
nifJ	YP_002237566.1	1.00	1.00	1.00	1.00	0.47	0.47	0.47	0.47	0.47	0.47	0.47	0.47
hypothetical	YP_002237567.1	1.00	1.00	1.00	1.00	0.97	0.97	0.97	0.96	0.97	0.97	0.97	0.97
Allantoin metabolism													
ybbB	YP_002918198.1	0.96	0.96	0.97	0.97	0.98	0.98	0.98	0.96	0.98	0.97	0.98	1.00
allS	YP_002918199.1	0.25	0.25	0.25	0.99	0.25	0.25	0.25	0.25	0.25	0.25	0.25	1.00
allA	YP_002918200.1	0.08	0.08	0.08	1.00	0.09	0.08	0.08	0.08	0.09	0.08	0.08	1.00
allR	YP_002918201.1	0.37	0.37	0.37	1.00	0.37	0.37	0.37	0.37	0.37	0.37	0.37	1.00
gcl	YP_002918202.1	0.27	0.27	0.27	1.00	0.27	0.27	0.27	0.27	0.27	0.27	0.27	1.00
hyi	YP_002918203.1	0.43	0.40	0.40	0.84	0.42	0.41	0.42	0.42	0.42	0.42	0.41	1.00
glxR	YP_002918204.1	0.40	0.40	0.40	0.99	0.39	0.39	0.35	0.39	0.39	0.39	0.39	1.00
hypothetical	YP_002918205.1	0.12	0.12	0.12	0.98	0.11	0.11	0.11	0.11	0.11	0.11	0.11	1.00
ybbW	YP_002918206.1	0.27	0.27	0.27	0.99	0.27	0.27	0.27	0.27	0.27	0.05	0.27	1.00
allB	YP_002918207.1	0.05	0.05	0.05	1.00	0.05	0.05	0.05	0.05	0.05	0.18	0.18	1.00
ybbY	YP_002918208.1	0.06	0.06	0.06	0.99	0.06	0.06	0.06	0.06	0.06	0.05	0.07	1.00
glxK	YP_002918209.1	0.59	0.60	0.59	1.00	0.62	0.62	0.61	0.61	0.61	0.61	0.61	1.00
hypothetical	YP_002918210.1	0.05	0.05	0.05	0.97	0.05	0.05	0.05	0.05	0.05	0.05	0.05	1.00
allC	YP_002918211.1	0.23	0.23	0.23	0.99	0.23	0.23	0.23	0.21	0.23	0.22	0.23	1.00
ylbC	YP_002918212.1	0.18	0.18	0.18	1.00	0.18	0.18	0.18	0.18	0.18	0.18	0.18	1.00
fdrA	YP_002918213.1	0.05	0.05	0.05	1.00	0.05	0.05	0.05	0.05	0.05	0.05	0.05	1.00
ylbE	YP_002918214.1	0.04	0.04	0.04	1.00	0.04	0.04	0.04	0.04	0.04	0.04	0.04	1.00
ylbF	YP_002918215.1	0.05	0.05	0.05	1.00	0.05	0.05	0.05	0.05	0.05	0.06	0.06	1.00
arcC	YP_002918216.1	0.05	0.05	0.05	1.00	0.05	0.05	0.05	0.05	0.05	0.05	0.05	1.00
purK	YP_002918217.1	0.98	0.98	0.98	0.96	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Citrate synthesis													
lysR	YP_001333717.1	0.96	0.95	0.96	0.95	1.00	0.99	0.99	1.00	0.99	0.99	1.00	1.00
citB	YP_001333718.1	0.98	0.98	0.37	0.96	1.00	0.38	0.37	0.38	1.00	0.38	1.00	0.38
citA	YP_001333719.1	0.98	0.98	0.40	0.96	1.00	0.42	0.42	0.42	1.00	0.42	1.00	0.42
oadB	YP_001333720.1	1.00	1.00	1.00	0.35	1.00	0.04	0.04	1.00	0.84	0.04	0.99	1.00
oadA	YP_001333721.1	0.98	0.98	0.88	0.43	1.00	0.04	0.05	0.99	0.52	0.04	0.99	0.98
oadG	YP_001333722.1	0.95	0.95	0.96	0.95	1.00	0.26	0.27	0.54	0.94	0.26	0.94	0.94
citS	YP_001333723.1	0.99	0.99	0.22	0.98	1.00	0.23	0.23	0.23	1.00	0.22	1.01	0.23
citC2	YP_001333724.1	0.96	0.97	0.04	0.93	1.00	0.04	0.04	0.04	1.00	0.04	1.00	0.04
citD2	YP_001333725.1	0.92	0.92	0.19	0.98	1.00	0.19	0.19	0.19	1.00	0.19	1.00	0.19
citE2	YP_001333726.1	1.00	0.99	0.06	0.98	1.00	0.05	0.05	0.06	1.00	0.05	1.00	0.05
citF2	YP_001333727.1	0.98	0.99	0.03	0.99	1.00	0.03	0.03	0.03	1.00	0.03	1.00	0.03
citG2	YP_001333728.1	0.98	0.98	0.23	0.92	1.00	0.23	0.22	0.23	1.00	0.23	1.00	0.23
dapB	YP_001333729.1	0.99	0.99	0.99	0.98	1.00	0.99	1.00	0.81	0.85	0.99	1.00	1.00

[a] The BSR values were generated by TBLASTN with the amino acid sequences encoded by each gene compared to the publicly available genomes examined in this study. Ratios that were >1 due to differences in contig length are displayed as 1.

[b] The Accession Numbers of the amino acid sequences used are indicated.

[c] BSR values ≥0.8 are highlighted in yellow, while values between 0.4 and 0.8 are highlighted in green.

[d] Reference sequences for virulence-associated genes are those specified in Brisse et al. 2009