Whole genome analysis of halotolerant and alkalotolerant plant growth-promoting rhizobacterium Klebsiella sp. D5A

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Table S1 Genes related to PGP traits

	Gene ID	COG ID	Gene annotation	KO/Gene_ID	KEGG_GENE_NAME
	ORF				
Indole-3-acetic acid (IAA) biosynthesis	orf03176_1		nitrile hydratase, alpha subunit	K01721	nthA
	orf03175_1		nitrile hydratase, beta subunit	K01721	nthB
	orf03759_1	COG3961	indole-3-pyruvate decarboxylase	K04103	ipdC
	orf03177_1	COG0154	amidase	K01426	amiE
	orf00635_1	COG1012	aldehyde dehydrogenase	K00128	E1.2.1.3
Phosphate solubilization	orf03914_1	_	coenzyme PQQ synthesis protein D	K06138	pqqD
	orf03915_1	COG1235	pyrroloquinoline quinone biosynthesis protein PqqB	K06136	pqqB
	orf03916_1	COG0535	pyrroloquinoline quinone biosynthesis protein PqqE	K06139	pqqE
	orf03917_1	COG1025	coenzyme PQQ biosynthesis protein PqqF	_	pqqF
	orf03918_1	COG5424	pyrroloquinoline quinone biosynthesis protein PqqC	K06137	pqqC
	orf01964_1	COG4993	quinoprotein glucose dehydrogenase	K00117	gcd
Phosphate uptake	orf04595_1	COG0226	phosphate ABC transporter periplasmic substrate-binding protein PstS	K02040	pstS
	orf04594_1	COG0573	phosphate transporter permease subunit PstC	K02037	pstC
	orf04593_1	COG0581	phosphate transporter permease subunit PtsA	K02038	pstA
	orf04592_1	COG1117	phosphate transporter subunit	K02036	pstB
	orf01743_1	COG0306	low-affinity inorganic phosphate transporter	K16322	pit
	orf04108_1	COG3638	phosphonate ABC transporter, ATP-binding protein	K02042	phnC
	orf04109_1	COG3221	phosphonate ABC transporter, periplasmic phosphonate-binding protein	K05781	phnD
	orf04111_1	COG3639	phosphonate ABC transporter, permease protein	K06163	phnE1
	orf04110_1	COG3639	phosphonate ABC transporter, permease protein	K06166	phnE2

Siderophore production	orf00726_1	COG1028	2,3-dihydroxybenzoate-2,3-dehydrogenase	K00216	entA
	orf00725_1	COG3433;COG1535	2,3-dihydro-2,3-dihydroxybenzoate synthetase, isochroismatase	K01252	entB, dhbB, vibB, mxcF
	orf00724_1	COG1021	enterobactin synthase subunit E	K02363	entE, dhbE, vibE, mxcE
	orf00723_1	COG1169	isochorismate synthase EntC	K02361	entC
	orf00721_1	COG0477	enterobactin exporter EntS	K08225	entS
	orf00717_1	COG1020;COG3319	enterobactin synthase subunit F	K02364	entF
	orf00713_1	COG2977	4'-phosphopantetheinyl transferase EntD	K02362	entD
Fe uptake	orf01388_1	COG4771	colicin I receptor FepA	K16089	TC.FEV.OM2, fepA, iroN, cirA, pfeA, cfrA, hmuR
	orf00714_1	COG4771	outer membrane receptor/ferric enterobactin receptor FepA	K16089	TC.FEV.OM2, fepA, iroN, cirA, pfeA, cfrA, hmuR
	orf02458_1	COG4771	outer membrane receptor/ferric enterobactin receptor FepA	K16089	TC.FEV.OM2, fepA, iroN, cirA, pfeA, cfrA, hmuR
	orf04037_1	COG4774	catecholate siderophore receptor fiu	K16090	fiu
	orf00543_1	COG1629	TonB-dependent receptor		TC.FEV.OM3, tbpA, hemR, lbpA, hpuB, bhuR, hugA, hmbR
	orf00577_1	_	hypothetical protein(TonB-dependent siderophore receptor)		TC.FEV.OM
	orf02635_1	COG1629	TonB-dependent siderophore receptor		tonB
	orf02824_1	COG1629	TonB-dependent receptor		ABC.FEV.P
	orf03828_1	COG1629	TonB-dependent receptor		TC.FEV.OM
	orf04232_1	COG1629	ferric aerobactin receptor	K02014	TC.FEV.OM
	orf03486_1	COG1629	ferrioxamine receptor foxA	K02014	TC.FEV.OM
	orf01930_1	COG1629	ferrichrome outer membrane receptor	K02014	TC.FEV.OM
	orf00816_1	COG0735	ferric uptake regulator		fur

Fe transport	orf01825_1	COG1918	ferrous iron transport protein A	K04758	feoA
	orf01824_1	COG0370	ferrous iron transport protein B	K04759	feoB
	orf01823_1	_	hypothetical protein; May function as a transcriptional regulator that controls feoABC	K07490	feoC
	orf00551_1	COG1121	iron transporter: fur regulated	K11607	sitB
	orf00550_1	COG1108	iron ABC transporter, permease protein AfeC	K11605	sitC
	orf00552_1	COG0803	iron transport system periplasmic binding component	K11604	sitA
	orf00549_1	COG1108	iron ABC transporter, permease protein AfeD	K11606	sitD
	orf03856_1	COG1178	ABC transporter, permease protein; Part of a binding-protein-dependent transport system.		afuB, fbpB
	orf02844_1	COG1120	ABC transporter, iron chelate uptake transporter (FeCT) family, ATP-binding protein	K02013	ABC.FEV.A
	orf02844_1	COG1120	ABC transporter, iron chelate uptake transporter (FeCT) family, ATP-binding protein	K02013	ABC.FEV.A
	orf02843_1	COG0609	iron-siderophore ABC transporter permease		TC.FEV.OM
	orf02843_1	COG0609	ABC transporter, iron chelate uptake transporter (FeCT) family, permease protein	K02015	ABC.FEV.P
	orf02842_1	COG0614	ABC transporter, iron chelate uptake transporter (FeCT) family		ABC.FEV.S
	orf02842_1	COG0614	ABC transporter, iron chelate uptake transporter (FeCT) family	K02016	ABC.FEV.S
	orf02717_1	COG0810	transport protein TonB	K03832	TC.FEV.OM
	orf02681_1	COG1120	iron ABC transporter, ATP-binding protein	K02013	ABC.FEV.A
	orf02680_1	COG0609	iron ABC transporter, permease protein	K02015	ABC.FEV.P
	orf02679_1	COG0614	iron ABC transporter, periplasmic iron-binding protein	K02016	ABC.FEV.S
	orf02656_1	COG1120	iron chelate ABC transporter, ATP-binding protein	K02013	ABC.FEV.A
	orf02655_1	COG0609	iron chelate ABC transporter, permease protein	K02015	ABC.FEV.P

orf02654_1	COG0614	iron chelate ABC transporter, periplasmic iron chelate-binding protein	K02016	ABC.FEV.S
orf02634_1	COG1120	iron ABC transporter, ATP-binding protein	K02013	ABC.FEV.A
orf02633_1	COG0609	iron ABC transporter, permease protein	K02015	ABC.FEV.P
orf02632_1	COG0609	iron ABC transporter, permease protein	K02015	ABC.FEV.P
orf02631_1	COG0614	iron ABC transporter, periplasmic iron-binding protein	K02016	ABC.FEV.S
orf02617_1	_	_	K02013	ABC.FEV.A
orf02616_1	_	_	K02015	ABC.FEV.P
orf02615_1	_	_	K02016	ABC.FEV.S
orf02127_1	COG4114	ferric iron reductase involved in ferric hydroximate transport	K13255	fhuF
orf01929_1	COG1120	iron-hydroxamate transporter ATP-binding subunit	K02013	ABC.FEV.A
orf01928_1	COG0614	iron-hydroxamate transporter substrate-binding subunit	K02016	ABC.FEV.S
orf01927_1	COG0609	iron-hydroxamate transporter permease subunit	K02015	ABC.FEV.P
orf01099_1	COG1178	iron(III) ABC transporter, permease protein;		afuB, fbpB
orf01098_1	COG1840	iron(III) ABC transporter, periplasmic iron(III)-binding protein		afuA, fbpA
orf00722_1	COG4592	iron-enterobactin transporter periplasmic binding protein	K02016	ABC.FEV.S
orf00720_1	COG0609	ferric enterobactin (enterochelin) transport		ABC.FEV.P
orf00720_1	COG0609	ferric enterobactin (enterochelin) transport	K02015	ABC.FEV.P
orf00719_1	COG4779	iron-enterobactin transporter permease	K02015	ABC.FEV.P
orf00718_1	COG1120	iron-enterobactin transporter ATP-binding protein	K02013	ABC.FEV.A
orf00541_1	COG4558	hemin ABC transporter, periplasmic hemin-binding protein	K02016	ABC.FEV.S
orf00540_1	COG0609	hemin ABC transporter, permease protein	K02015	ABC.FEV.P
orf00539_1	COG4559	hemin importer ATP-binding subunit	K02013	ABC.FEV.A
orf00231_1	COG0848	biopolymer transport protein ExbD	K03559	exbD
orf00230_1	COG0811	biopolymer transport protein ExbB	K03561	exbB

Acetoin and 2, 3-butanediol synthesis	orf04628_1	COG3978	acetolactate synthase 2 regulatory subunit	K11258	ilvM
	orf02240_1	COG3962	putative acetolactate synthase large subunit	K03336	iolD
	orf02015_1	COG0440	acetolactate synthase 3 regulatory subunit	K01653	E2.2.1.6S, ilvH, ilvN
	orf04551_1	COG0440	acetolactate synthase 1 regulatory subunit	K01653	E2.2.1.6S, ilvH, ilvN
	orf02016_1	COG0028	acetolactate synthase 3 catalytic subunit	K01652	E2.2.1.6L, ilvB, ilvG, ilvI
	orf02580_1	COG0028	acetolactate synthase	K01652	E2.2.1.6L, ilvB, ilvG, ilvI
	orf00545_1	COG0028	acetolactate synthase catalytic subunit	K01652	E2.2.1.6L, ilvB, ilvG, ilvI
	orf03057_1	COG0028	acetolactate synthase large subunit	K01576	mdlC
	orf02581_1	COG1028	acetoin reductase	K03366	butA, budC
	orf02579_1	COG3527	alpha-acetolactate decarboxylase	K01575	E4.1.1.5, alsD
Antimicrobial compounds					
Phenazine production	orf03100_1	COG0384	phenazine biosynthesis protein PhzF family		
4-hydroxybenzoate production	orf02481_1	COG3161	chorismate pyruvate lyase		ubiC
Chitinase production	orf04356_1	COG3325	putative chitinase II	K01183	E3.2.1.14
γ-aminobutyric acid (GABA)	orf01112_1	COG1012	putative succinate-semialdehyde dehydrogenase (NAD(P)(+))	K00135	gabD
	orf04143_1	COG1012	succinate-semialdehyde dehydrogenase I	K00135	gabD
	orf02181_1	COG1012	aldehyde dehydrogenase (NAD) family protein	K00135	gabD
	orf04144_1	COG0160	4-aminobutyrate aminotransferase	K07250	gabT
	orf04145_1	COG1113	gamma-aminobutyrate transporter	K11735	gabP
Other PGPR fitness conferring genes					
	orf00281_1	COG1166	arginine decarboxylase	K01585	E4.1.1.19S, speA
	orf00282_1	COG0010	agmatinase; Catalyzes the formation of putrescine from agmatine (By similarity)	K01480	E3.5.3.11, speB
	orf01969_1	COG0421	spermidine synthase	K00797	speE, SRM

Resistance to oxidative stress					
Peroxidase	orf03876_1	COG2128;COG4950	putative peroxidase	None	_
	orf01147_1	COG2837	deferrochelatase/peroxidase EfeB	K16301	efeB
	orf03730_1	COG2837	dyp-type peroxidase family protein	K07223	K07223
	orf04367_1	COG0386	glutathione peroxidase family protein	K00432	E1.11.1.9
	orf03910_1	COG0376	catalase/peroxidase HPI	K03782	katG
	orf02698_1	COG0386	putative glutathione peroxidase	K00432	E1.11.1.9
	orf03689_1	COG1225	thioredoxin-dependent thiol peroxidase	K03564	BCP, PRXQ, DOT5
	orf03969_1	COG2077	thiol peroxidase	K11065	tpx
Catalase	orf04050_1	COG0753	hydroperoxidase II;	K03781	katE, CAT, catB, srpA
	orf03910_1	COG0376	catalase/peroxidase HPI	K03782	katG
	orf04443_1	COG3546	putative manganese containing catalase	K07217	K07217
Superoxide dismutase	orf04808_1	COG0605	superoxide dismutase	K04564	SOD2
	orf04489_1	COG0605	superoxide dismutase	K04564	SOD2
	orf04818_1	COG2032	superoxide dismutase	K04565	SOD1
	orf00329_1	_	putative superoxide dismutase, iron	_	_
Glutathione S-transferase	orf02200_1	COG0346	glutathione transferase, FosA		_
	orf03847_1	COG0625	glutathione S-transferase domain protein	K11208	yncG
	orf03255_1	COG0625	glutathione S-transferase	K00799	GST, gst
	orf04138_1	COG0625	glutathione S-transferase family protein	K00799	GST, gst
	orf00702_1	COG0625	putative S-transferase	_	_
	orf02440_1	COG0625	putative glutathione S-transferase	K00799	GST, gst
	orf01661_1	COG0625	putative glutathione S-transferase	_	_
	orf00235_1	COG0625	putative glutathione S-transferase YghU	K11209	yghU
	orf01497_1	COG0625	putative glutathione S-transferase	_	_

	orf00973_1	COG0625	glutathione S-transferase family protein	_	_
	orf01734_1	COG0625	glutathione S-transferase domain protein	K00799	GST, gst
	orf01496_1	COG0625	glutathione S-transferase domain protein	_	_
Hydroperoxide	orf03015_1	COG0450	putative thiol - alkyl hydroperoxide reductase	K03386	E1.11.1.15, PRDX, ahpC
	orf00764_1	COG3634	alkyl hydroperoxide reductase subunit F	K03387	ahpF
	orf00763_1	COG0450	alkyl hydroperoxide reductase subunit C	K03386	E1.11.1.15, PRDX, ahpC
Heat shock	orf00667_1	COG0576	heat shock protein GrpE;	K03687	GRPE
	orf01089_1	COG3785	heat shock protein HspQ;	K11940	hspQ
	orf01317_1	COG0443	DnaK domain protein	K04046	yegD
	orf01832_1	COG1188	ribosome-associated heat shock protein HSP15	K04762	hslR
	orf02078_1	COG0484	chaperone protein DnaJ; Participates actively in the response to hyperosmotic	K03686	dnaJ
	orf02079_1	COG0443	molecular chaperone DnaK; Acts as a chaperone	K04043	dnaK
	orf02376_1	COG0459	chaperonin GroEL;	K04077	groEL, HSPD1
	orf02377_1	COG0234	co-chaperonin GroES	K04078	groES, HSPE1
	orf02914_1	COG0326	heat shock protein 90	K04079	htpG, HSP90A
	orf03065_1	COG0071	Heat shock protein20/alpha crystallin family protein	K04080	ibpA
	orf03423_1	COG3187	heat shock protein HslJ	K03668	hslJ
	orf03528_1	COG0501	heat shock protein HtpX	K03799	htpX
	orf03650_1	COG0443	chaperone protein HscA	K04044	hscA
	orf04566_1	COG0071	heat shock chaperone IbpB	K04081	ibpB
	orf04567_1	COG0071	heat shock protein IbpA	K04080	ibpA
Cold shock	orf01682_1	COG1278	major cold shock protein	K03704	cspA
	orf00770_1	COG1278	cold shock protein CspE	K03704	cspA
	orf04877_1	COG1278	'cold-shock' DNA-binding domain protein	K03704	cspA

	orf01018_1	COG1278	DNA replication inhibitor	K03704	cspA
Rhodanese: catalysis of the detoxification of cyanide	orf02644_1	COG0607	rhodanese-like protein sulfurtransferase	None	_
	orf00629_1	COG0607	rhodanese domain protein	None	_
	orf01204_1	COG0476;COG0607	putative thiazole biosynthesis adenylyltransferase ThiF/rhodanese domain protein	K11996	MOCS3, UBA4, moeB
	orf04193_1	COG1054	sulfurtransferase rhodanese	K07146	K07146
	orf03085_1	COG0607	rhodanese	None	_
	orf01645_1	COG0607	rhodanese domain protein	None	_

Table S2 General genome features of the five studied *Klebsiella* genomes

Klebsiella sp.	D5A	*variicola* At22	*variicola* DX120	*variicola* 342	*pneumoniae*78578
Genome size (bp)	5540009	5458505	5718430	5920260	5694890
G+C content (%)	57.2	57.6	57.1	56.9	57.2
Protein-coding genes	4999	5113	5342	5554	5652
No. of protein-coding genes with COGs	4684	4979	5195	5369	5453
rRNA genes	4	25	25	25	25
tRNA genes	73	85	87	88	86
Other RNA genes	_	2	1	1	1
Plasmid	_	_	2	2	5
Accession number	LOAR00000000	NC_013850.1	NZ_CP009274.1	NC_011283.1	NC_009648.1

Table S3 Genes involved in the N cycle

	Gene ID	COG ID	Gene annotation	KO/Gene_ID	KEGG_GENE_NAME
	ORF				
Nitrogenase complex	orf01255_1	COG0674;COG1014;COG1013	pyruvate-flavodoxin oxidoreductase	K03737	nifJ
	orf01256_1	COG1348	nitrogenase iron protein	K02588	nifH
	orf01257_1	COG2710	nitrogenase molybdenum-iron protein alpha chain	K02586	nifD
	orf01258_1	COG2710	nitrogenase molybdenum-iron protein beta chain	K02591	nifK
	orf01259_1	_	probable nitrogen fixation protein FixT	K02593	nifT
	orf01260_1	_	NifY protein	None	nifY
	orf01261_1	COG2710	nitrogenase MoFe cofactor biosynthesis protein NifE	K02587	nifE
	orf01262_1	COG2710	nitrogenase molybdenum-cofactor biosynthesis protein NifN	K02592	nifN
	orf01263_1	_	NifX protein	K02596	nifX
	orf01265_1	COG1104	cysteine desulfurase NifS	K04487	nifS
	orf01266_1	COG0119	homocitrate synthase	K02594	nifV
	orf01267_1	_	putative NifW protein	K02595	nifW
	orf01268_1	_	putative NifZ protein	K02597	nifZ
	orf01269_1	COG0760	nitrogen fixation protein NifM	K03769	nifM
	orf01270_1	COG0716	flavodoxin FldA	K03839	nifF
	orf01271_1	COG2202	nitrogen fixation negative regulator NifL	None	nifL
	orf01272_1	COG3604	Nif-specific regulatory protein	K02584	nifA
	orf01273_1	COG0535	nitrogenase cofactor biosynthesis protein NifB	K02585	nifB
	orf01274_1	_	nitrogen fixation protein NifQ	K15790	nifQ
	orf03425_1	COG0674;COG1014;COG1013	putative pyruvate:ferredoxin (flavodoxin) oxidoreductase	K03737	nifJ
	orf03647_1	COG0822	scaffold protein	K04488	iscU, nifU

Nitrogenase transport	orf03772_1	COG4657	Na(+)-translocating NADH-quinone reductase subunit E	K03617	rnfA
	orf03771_1	COG2878	electron transport complex protein RnfB; Required for nitrogen fixation.	K03616	rnfB
	orf04836_1	_	electron transport complex protein rnfC	K03615	rnfC
	orf04835_1	COG4658	electron transport complex protein RnfD; Required for nitrogen fixation.	K03614	rnfD
	orf04833_1	COG4660	NADH-ubiquinone oxidoreductase	K03613	rnfE
	orf04834_1	COG4659	electron transport complex protein RnfG	K03612	rnfG

Table S4 Genes involved in TCS

orf	COG ID	Gene annotation	KO/Gene_ID	KEGG_GENE_NAME	Func Name
orf00171_1					two-component system NarL family, sensor histidine kinase
orf00823_1	COG0745	KDP operon transcriptional regulatory protein KdpE	K07667	kdpE	two-component system, OmpR family, KDP operon response regulator KdpE
orf00824_1	COG2205	sensor protein KdpD	K07646	kdpD	two-component system, OmpR family, sensor histidine kinase KdpD
orf00995_1	COG2205;COG0642	sensor histidine kinase	_	_	
orf01318_1	COG2205	sensor histidine kinase	_	_	
orf01356_1	COG3275	putative two-compoent regulatory system sensor kinase	K02478	K02478	two-component system, LytT family, sensor kinase
orf01443_1	COG0642;COG2198	phosphotransfer intermediate protein in two-component regulatory system with RcsBC	K07676	rcsD	two-component system, NarL family, sensor histidine kinase RcsD
orf01828_1	COG0745	osmolarity response regulator	K07659	ompR	two-component system, OmpR family, phosphate regulon response regulator OmpR
orf01829_1	COG0642	osmolarity sensor protein	K07638	envZ	two-component system, OmpR family, osmolarity sensor histidine kinase EnvZ
orf02044_1	COG3290	sensor histidine kinase	K07700	dpiB, citA	two-component system, CitB family, cit operon sensor histidine kinase CitA
orf02097_1	COG0745	DNA-binding response regulator CreB	K07663	creB	two-component system, OmpR family, catabolic regulation response regulator CreB
orf02415_1	COG0642;COG0784	sensor histidine	_	_	

		kinase/response regulator			
orf02584_1	COG0642	sensor histidine protein kinase (RstA regulator)	_	_	
orf02748_1	COG3850	nitrate/nitrite sensor protein NarX	K07673	narX	two-component system, NarL family, nitrate/nitrite sensor histidine kinase NarX
orf02749_1	COG2197	transcriptional regulator NarL	K07684	narL	two-component system, NarL family, nitrate/nitrite response regulator NarL
orf03182_1	COG0642	sensor histidine kinase	_	_	
orf03306_1	COG3290	sensory histidine kinase DcuS	K07701	dcuS	two-component system, CitB family, sensor histidine kinase DcuS
orf03631_1	COG0642	putative 2-component sensor protein	K07711	glrK, qseE	two-component system, NtrC family, sensor histidine kinase GlrK
orf03763_1	COG3275	sensor histidine kinase	K02478	K02478	two-component system, LytT family, sensor kinase
orf03902_1	COG3662	hypothetical protein/ histidine kinase	_	_	_
orf03922_1	COG0642	sensor histidine kinase	_	_	_
orf04277_1	COG2200;COG2203	histidine kinase/ cyclic diguanylate phosphodiesterase (EAL) domain protein	_	_	_
orf04487_1	COG0642	two-component sensor protein	K07640	cpxA	two-component system, OmpR family, sensor histidine kinase CpxA
orf04549_1	COG3851	sensory histidine kinase UhpB	K07675	uhpB	two-component system, NarL family, sensor histidine kinase UhpB

Table S5 Genes involved in salt tolerance

	Gene ID	COG ID	Gene annotation	KO/Gene_ID	KEGG_GENE_NAME
	ORF				
Glycine-betaine synthesis	orf00698_1	COG1292	choline transport protein BetT	K02168	betT, betS
	orf00696_1	COG1012	betaine aldehyde dehydrogenase	K00130	betB, gbsA
	orf00695_1	COG2303	choline dehydrogenase	K00108	betA, CHDH
	orf00697_1	COG1309	transcriptional regulator BetI	K02167	betI
	orf02401_1	COG0477	proline/glycine betaine transporter	K03762	proP
	orf00615_1	COG4176	glycine betaine transporter membrane protein	K02001	proW
	orf00616_1	COG4175	glycine betaine/L-proline ABC transporter, ATP-binding protein	K02000	proV
	orf00614_1	COG2113	glycine betaine transporter periplasmic subunit	K02002	proX
	orf01141_1	COG0591	sodium/proline symporter	K11928	putP
	orf01114_1	COG1292	putative transporter	K03451	TC.BCT
Trehalose metabolism	orf03896_1	COG0366	putative trehalose synthase	K05343	treS
	orf01732_1	COG1626	trehalase	K01194	treA, treF
	orf03581_1	COG0380	trehalose-6-phosphate synthase	K00697	otsA
	orf03582_1	COG1877	trehalose-6-phosphate phosphatase	K01087	otsB
	orf02262_1	COG1609	trehalose repressor	K03485	treR1, treR
Genes involved in Na$^+$ and K$^+$ transport	orf00035_1	COG0471	transporter, divalent anion:Na+ symporter (DASS) family	None	_
	orf00070_1	COG0530	putative calcium/sodium:proton antiporter	K07301	yrbG
	orf01209_1	COG0025	Na+/H+ antiporter	K03316	TC.CPA1
	orf01488_1	COG0471	transporter, divalent anion:Na+ symporter (DASS) family	None	_
	orf02077_1	COG3004	pH dependent Na+/H antiporter	K03313	nhaA
	orf02438_1	COG0025	Na+/H+ antiporter	K03316	TC.CPA1
	orf02493_1	COG0385	Na+ symporter, BASS family	K03453	TC.BASS
	orf03496_1	COG3067	Sodium/proton antiporter; Na (+)/H (+) antiporter t	K03314	nhaB

	orf04048_1	COG1823	transporter, dicarboxylate/amino acid:cation (Na+ or H+) symporter (DAACS) family	K06956	K06956
	orf00827_1	COG2060	potassium-transporting ATPase subunit A	K01546	kdpA
	orf00826_1	COG2216	potassium-transporting ATPase subunit B	K01547	kdpB
	orf00825_1		potassium-transporting ATPase subunit C	K01548	kdpC
	orf02076_1	COG0583	transcriptional activator NhaR	K03717	nhaR
	orf02724_1	COG1226	transporter, cation channel family	K10716	kch, trkA, mthK, pch
	orf02910_1	COG1226;COG4651	putative cation:proton antiport protein	K03455	TC.KEF
	orf02923_1	COG3264	potassium efflux protein KefA	K05802	kefA, bspA, aefA
	orf03491_1	COG3263	potassium/proton antiporter	K11105	cvrA, nhaP2
	orf03883_1	COG0221	inorganic diphosphatase /potassium-transporting ATPase subunit C	K01507	ppa
	orf04615_1	COG3158	potassium transport protein Kup	K03549	kup
	orf04699_1	COG0168	potassium transporter	K03498	trkH
	orf04935_1	COG0569	potassium transporter peripheral membrane component	K03499	trkA

Table S6 Genes involved in pH wide adaptation

	Gene ID	COG ID	Gene annotation	KO/Gene_ID	KEGG_GENE_NAME
	ORF				
Acid expressed	orf00827_1	COG2060	potassium-transporting ATPase subunit A	K01546	kdpA
	orf00826_1	COG2216	potassium-transporting ATPase subunit B	K01547	kdpB
	orf00825_1	COG2156	potassium-transporting ATPase subunit C	K01548	kdpC
	orf00824_1	COG2205	sensor protein KdpD	K07646	kdpD
	orf00823_1	COG0745	KDP operon transcriptional regulatory protein KdpE	K07667	kdpE
	orf04595_1	COG0226	phosphate ABC transporter periplasmic substrate-binding protein PstS	K02040	pstS
	orf04594_1	COG0573	phosphate transporter permease subunit PstC	K02037	pstC
	orf04593_1	COG0581	phosphate transporter permease subunit PtsA	K02038	pstA
	orf04592_1	COG1117	phosphate transporter subunit	K02036	pstB
	orf02866_1	COG1982	lysine decarboxylase 1	K01582	ldcC, cadA
	orf01895_1	COG1982	lysine decarboxylase 2, constitutive	K01582	ldcC, cadA
	orf02966_1	COG0776	transcriptional regulator HU subunit beta	K03530	hupB
	orf04859_1	COG0776	transcriptional regulator HU subunit alpha	K05787	hupA
	orf00942_1	COG0783	DNA starvation/stationary phase protection protein Dps	K04047	dps
	orf01957_1	COG0853	aspartate alpha-decarboxylase	K01579	panD
	orf02969_1	COG1219	ATP-dependent protease ATP-binding subunit ClpX	K03544	clpX, CLPX
	orf02970_1	COG0740	ATP-dependent Clp protease proteolytic subunit	K01358	clpP, CLPP
	orf02477_1	COG1974	LexA repressor; Represses a number of genes involved in the response to DNA damage	K01356	lexA
	orf00190_1	COG0804	urease subunit alpha	K01428	ureC
	orf00191_1	COG0832	urease subunit beta	K01429	ureB
	orf00192_1	COG0831	urease subunit gamma	K01430	ureA

	orf00189_1	COG2371	urease accessory protein UreE	K03187	ureE
	orf00188_1	COG0830	urease accessory protein UreF	K03188	ureF
	orf00187_1	COG0378	urease accessory protein UreG	K03189	ureG
	orf00193_1	COG0829	urease accessory protein UreD	K03190	ureD, ureH
	orf02079_1	COG0443	molecular chaperone DnaK; Acts as a chaperone (By similarity)	K04043	dnaK
	orf02376_1	COG0459	chaperonin GroEL	K04077	groEL, HSPD1
	orf00173_1		HdeB family protein		
Alkaline expressed	orf03496_1	COG3067	sodium/proton antiporter; Na(+)/H(+) antiporter	K03314	nhaB
	orf03491_1	COG3263	potassium/proton antiporter; Participates in control of cell volume in low-osmolarity condition	K11105	cvrA, nhaP2
	orf02910_1	COG1226;COG4651	putative cation:proton antiport protein	K03455	TC.KEF
	orf02761_1	COG0387	calcium/sodium:proton antiporter	K07300	chaA, CAX
	orf02438_1	COG0025	Na+/H+ antiporter	K03316	TC.CPA1
	orf02077_1	COG3004	pH dependent Na+/H antiporter	K03313	nhaA
	orf02076_1	COG0583	transcriptional activator NhaR	K03717	nhaR
	orf01209_1	COG0025	Na+/H+ antiporter	K03316	TC.CPA1
	orf00977_1	COG0477	multidrug translocase MdfA	K08160	cmr, mdfA
	orf04606_1	COG0356	ATP synthase subunit A; Key component of the proton channel;	K02108	ATPF0A, atpB
	orf04604_1	COG0711	F0F1 ATP synthase subunit B	K02109	ATPF0B, atpF
	orf04605_1	COG0636	F0F1 ATP synthase subunit C	K02110	ATPF0C, atpE
	orf04602_1	COG0056	F0F1 ATP synthase subunit alpha	K02111	ATPF1A, atpA
	orf04600_1	COG0055	F0F1 ATP synthase subunit beta	K02112	ATPF1B, atpD
	orf04603_1	COG0712	F0F1 ATP synthase subunit delta	K02113	ATPF1D, atpH
	orf04599_1	COG0355	F0F1 ATP synthase subunit epsilon	K02114	ATPF1E, atpC
	orf04601_1	COG0224	F0F1 ATP synthase subunit gamma	K02115	ATPF1G, atpG

	orf04607_1	COG3312	F0F1 ATP synthase subunit I	K02116	atpI
	orf02722_1	COG1502	cardiolipin synthetase	K06131	cls
	orf02485_1	COG2182	maltose ABC transporter periplasmic protein	K10108	malE
	orf03436_1	COG2885	OmpA domain protein	None	_
	orf04704_1	COG2885	OmpA domain protein	None	_
	orf00944_1	COG3637	outer membrane protein X	K11934	ompX
	orf03514_1	COG1760	L-serine deaminase	K01752	sdaA
	orf00491_1	COG1760	L-serine ammonia-lyase 2	K01752	sdaA

Table S7 Genes involved in degradation of aromatic compounds

Gene ID ORF	COG ID	Gene annotation	KO/Gene_ID	KEGG_GENE_NAME
orf02133_1	COG0654	4-hydroxybenzoate 3-monooxygenase	K00481	pobA
orf02132_1	COG2207	transcriptional regulator PobR	None	_
orf03864_1	COG4638	2-chlorobenzoate 1,2-dioxygenase, alpha subunit	K05549	benA-xylX
orf03865_1	COG5517	3-phenylpropionate dioxygenase beta subunit	K05550	benB-xylY
orf03800_1	COG3135	benzoate transporter family protein	K05782	benE
orf03867_1	COG1028	1,6-dihydroxycyclohexa-2,4-diene-1-carboxylate dehydrogenase	K05783	benD-xylL
orf03866_1	COG0543	2-chlorobenzoate 1,2-dioxygenase, electron transfer subunit	K05784	benC-xylZ
orf03863_1	COG3485	catechol 1,2-dioxygenase	K03381	catA
orf03861_1	COG4948	muconate cycloisomerase	K01856	catB
orf03862_1	COG4829	muconolactone delta-isomerase	K03464	catC
orf03315_1	COG0015	3-carboxy-cis,cis-muconate cycloisomerase	K01857	pcaB
orf00326_1	COG0599	carboxymuconolactone decarboxylase family protein	K01607	pcaC
orf03120_1	COG0599	carboxymuconolactone decarboxylase family protein	K01607	pcaC
orf03313_1	COG0599	4-carboxymuconolactone decarboxylase	K01607	pcaC
orf04377_1	_	hypothetical protein	K01607	pcaC
orf04471_1	COG0599	carboxymuconolactone decarboxylase family protein	K01607	pcaC
orf03314_1	COG0596	3-oxoadipate enol-lactonase	K01055	pcaD
orf03787_1	COG3485	protocatechuate 3,4-dioxygenase, alpha subunit	K00448	pcaG
orf03788_1	COG3485	protocatechuate 3,4-dioxygenase, beta subunit	K00449	pcaH
orf03318_1	COG1788	3-oxoadipate CoA-transferase, subunit A	K01031	pcaI
orf03317_1	COG2057	3-oxoadipate CoA-transferase, subunit B	K01032	pcaJ
orf01684_1	COG0477	4-hydroxybenzoate transporter	K08195	pcaK
orf02987_1	COG0477	4-hydroxybenzoate transporter	K08195	pcaK

orf02981_1	COG1414	transcriptional regulator, IclR family	K02624	pcaR
orf03319_1	COG1414	Pca regulon regulatory protein	K02624	pcaR
orf03860_1	COG1414	transcriptional regulator, IclR family	K02624	pcaR
orf02646_1	COG0477	putative 3-hydroxyphenylpropionic transporter MhpT	K05819	mhpT
orf02653_1	COG1414	DNA-binding transcriptional activator MhpR	K05818	mhpR
orf02650_1	COG0596	2-hydroxy-6-ketonona-2,4-dienedioic acid hydrolase	K05714	mhpC
orf02651_1	_	3-(2,3-dihydroxyphenyl)propionate dioxygenase	K05713	mhpB
orf02652_1	COG0654	3-(3-hydroxyphenyl)propionate hydroxylase	K05712	mhpA
orf02648_1	COG4569	acetaldehyde dehydrogenase; Catalyzes the conversion of acetaldehyde to acetyl-CoA	K04073	mhpF
orf02649_1	COG3971	2-keto-4-pentenoate hydratase	K02554	mhpD
orf02647_1	COG0119	4-hydroxy-2-oxovalerate aldolase	K01666	mhpE

Table S8 Genes involved in the sulfur cycle

	Gene ID	COG ID	Gene annotation	KO/Gene_ID	KEGG_GENE_NAME
	ORF				
Thiosulfate or sulfate transporter and convert-related genes	orf00517_1	COG0583	transcriptional regulator CysB	K13634	cysB
	orf01167_1	COG0031	putative cysteine synthase B	K12339	cysM
	orf03744_1	COG0031	cysteine synthase B	K12339	cysM
	orf01649_1	COG0765	amino acid ABC transporter, permease protein	K10009	ABC.CYST.P
	orf03733_1	COG2981	putative sulfate transport protein CysZ	K06203	cysZ
	orf00512_1	COG4150	thiosulfate transporter subunit	K02048	cysP, sbp
	orf02887_1	COG1613	sulfate transporter subunit	K02048	cysP, sbp
	orf00513_1	COG4208	sulfate/thiosulfate transporter permease subunit	K02047	cysW
	orf01168_1	COG0555	sulfate/thiosulfate transporter subunit	K02046	cysU
	orf00514_1	COG1118	sulfate/thiosulfate transporter subunit	K02045	cysA
	orf02959_1	COG0031	cysteine synthase A	K01738	cysK
	orf04011_1	COG0031	pyridoxal-phosphate dependent enzyme	K01738	cysK
	orf03731_1	COG0175	sulfate adenylyltransferase subunit 2	K00957	cysD
	orf01591_1	COG2895	sulfate adenylyltransferase subunit 1	K00956	cysN
	orf03734_1	COG0529	adenylylsulfate kinase	K00860	cysC
	orf02306_1	COG0175	phosphoadenosine phosphosulfate reductase	K00390	cysH
	orf03735_1	COG0155	sulfite reductase subunit beta	K00381	cysI
	orf01207_1	COG0369	sulfite reductase subunit alpha	K00380	cysJ
Sulfonate or alkanesulfonate related genes	orf01069_1	COG1116	aliphatic sulfonates transport ATP-binding subunit	K15555	ssuB
	orf01066_1	COG1116	putative sulfonate ABC transporter, ATP-binding protein	K15555	ssuB
	orf03957_1	COG0600	alkanesulfonate transporter permease subunit	K15554	ssuC
	orf02641_1	COG0600	putative sulfonate ABC transporter, permease protein	K15554	ssuC
	orf03958_1	COG0715	putative ABC-type transport protein	K15553	ssuA

	orf02639_1	COG0715	aliphatic sulfonates ABC transporter family, periplasmic substrate-binding protein	K15553	ssuA
	orf01068_1	COG0715	aliphatic sulfonates ABC transporter, periplasmic sulfonate-binding protein	K15553	ssuA
	orf01067_1	COG0715	putative sulfonate ABC transporter, sulfonate-binding protein	K15553	ssuA
	orf01065_1	COG2141	alkanesulfonate monooxygenase	K04091	ssuD
	orf03959_1	COG0431	NAD(P)H-dependent FMN reductase	K00299	ssuE
Taurine transporter	orf03341_1	COG4521	taurine ABC transporter, periplasmic taurine-binding protein	K15551	tauA
	orf04083_1	COG0600	taurine transporter subunit; Part of a binding-protein-dependent transport system	K15552	tauC
	orf04084_1	COG4525	taurine transporter ATP-binding subunit	K10831	tauB
	orf04085_1	COG2175	taurine dioxygenase	K03119	tauD

Table S9 Genes involved in secretion systems

	Gene ID ORF	COG ID	Gene annotation	KO/Gene_ID	KEGG_GENE_NAME
tat	orf00773_1	COG1826	twin arginine translocase protein E	K03425	tatE
	orf02114_1	COG0084	hydrolase, TatD family	K03424	tatD
	orf04222_1	COG0084	putative metallodependent hydrolase	K03424	tatD
	orf04688_1	COG1826	twin arginine translocase protein A	K03116	tatA
	orf04690_1	COG0805	twin-arginine protein translocation system subunit TatC	K03118	tatC
	orf04689_1	COG1826	sec-independent translocase	K03117	tatB
	orf04691_1	COG0084	DNase TatD	K03424	tatD
sec	orf04837_1	COG0690	preprotein translocase subunit SecE	K03073	secE
	orf00091_1	COG1314	preprotein translocase subunit SecG	K03075	secG
	orf04927_1	COG0201	preprotein translocase subunit SecY; Involved in protein export (By similarity)	K03076	secY
	orf03010_1	COG0342	preprotein translocase subunit SecD	K03072	secD
	orf03617_1	COG3086	SoxR reducing system protein RseC	K03803	rseC
	orf00217_1	COG0642	sensor protein QseC	K07645	qseC
	orf03009_1	COG0341	preprotein translocase subunit SecF	K03074	secF
	orf01996_1	_	SecA regulator SecM	K13301	secM
	orf01647_1	COG1952	preprotein translocase subunit SecB	K03071	secB
	orf01995_1	COG0653	preprotein translocase subunit SecA	K03070	secA
	orf02973_1	COG3056	hypothetical protein	K07286	yajG
	orf03011_1	COG1862	preprotein translocase subunit YajC	K03210	yajC
	orf03167_1	COG2188	putative transcriptional regulator	K03482	yidP
	orf04561_1	COG2149	hypothetical protein	K00389	yidH
	orf04579_1	COG0706	putative inner membrane protein translocase component YidC	K03217	yidC, spoIIIJ, OXA1
	orf04564_1	COG2188	transcriptional regulator, GntR family	K03482	yidP

	orf01521_1	COG2188	transcriptional regulator, GntR family	K03482	yidP
	orf00087_1	COG0293	23S rRNA methyltransferase J	K02427	rlmE, rrmJ, ftsJ
	orf02010_1	COG0768	peptidoglycan synthetase FtsI	K03587	ftsI
	orf02001_1	COG1589	cell division protein FtsQ	K03589	ftsQ
	orf01774_1	COG2884	cell division protein FtsE	K09812	ftsE
	orf03523_1	COG0768	putative peptidoglycan synthetase FtsI	K03587	ftsI
	orf01775_1	COG2177	cell division protein FtsX	K09811	ftsX
	orf00521_1	COG2919	cell division protein FtsB; Required for the cell division process (By similarity)	K05589	ftsB
	orf02005_1	COG0772	cell division protein FtsW	K03588	ftsW, spoVE
	orf01773_1	COG0552	cell division protein FtsY	K03110	ftsY
	orf01999_1	COG0206	cell division protein FtsZ;	K03531	ftsZ
	orf00088_1	COG0465	ATP-dependent metalloprotease	K03798	ftsH, hflB
	orf02000_1	COG0849	cell division protein FtsA	K03590	ftsA
	orf01027_1	COG1674	cell division protein	K03466	ftsK, spoIIIE
	orf02011_1	COG3116	cell division protein FtsL	K03586	ftsL
	orf04478_1	COG3087	cell division protein FtsN	K03591	ftsN
	orf00670_1	COG0541	signal recognition particle protein	K03106	SRP54, ffh
	orf03619_1	COG0681	signal peptidase I	K03100	lepB
	orf02072_1	COG0597	lipoprotein signal peptidase	K03101	lspA
Type I	orf00209_1	COG1538	outer membrane channel protein	K12340	tolC
	orf00413_1	_	hypothetical protein	None	_
	orf01558_1	COG1538	putative outer membrane efflux protein	None	_
	orf00339_1	COG1538	putative outer membrane efflux protein MdtP	K15550	mdtP
Type II	orf01935_1	COG3031	pullulanase secretion envelope protein PulC	K02452	gspC
	orf01940_1	_	pullulanase secretion protein PulH	K02457	gspH
	orf01941_1	COG2165	pullulanase secretion protein PulI	K02458	gspI

	orf01936_1	COG1450	pullulanase secretion envelope protein PulD;	K02453	gspD
	orf01942_1	COG4795	pullulanase secretion protein PulJ	K02459	gspJ
	orf01938_1	COG1459	pullulanase secretion protein PulF	K02455	gspF
	orf01939_1	COG2165	pullulanase G protein;	K02456	gspG
	orf01947_1	COG1989	pullulanase secretion protein PulO;	K02464	gspO
	orf01943_1	COG3156	pullulanase secretion protein PulK	K02460	gspK
	orf01933_1	_	pullulanase-specific type II secretion system component B	K02451	gspB
	orf01932_1	_	pullulanase secretion protein PulS	K02465	gspS
	orf00238_1	COG0754	bifunctional glutathionylspermidine amidase/glutathionylspermidine synthetase	K01460	gsp
	orf01945_1	COG3149	pullulanase secretion protein PulM	K02462	gspM
	orf01937_1	COG2804	pullulanase secretion protein PulE	K02454	gspE
	orf01946_1	_	pullulanase secretion protein PulN	K02463	gspN
	orf01944_1	COG3297	pullulanase secretion protein PulL	K02461	gspL
Type III	orf03073_1	COG3395	YgbK domain protein	None	_
	orf03105_1	COG3395	hypothetical protein	None	_
	orf04783_1	_	type III restriction enzyme, res subunit	None	_
	orf01416_1	COG1061	putative helicase	K17677	IRC3
Type V	orf03618_1	COG0481	GTP-binding protein LepA	K03596	lepA
	orf03619_1	COG0681	signal peptidase I	K03100	lepB
Type VI	orf04715_1	COG3521	hypothetical protein	K11906	vasD, lip
	orf01541_1	COG3521	hypothetical protein	K11906	vasD, lip
	orf04706_1	COG0542	type VI secretion ATPase, ClpV1 family	K11907	vasG, clpV
	orf03437_1	COG3455	type IV/VI secretion system protein, DotU family	K11892	impK, ompA, vasF, dotU
	orf04712_1	COG3515	ImpA domain-containing protein	K11910	vasJ
	orf02779_1	COG3518	type VI secretion system lysozyme-related protein	K11905	K11905
	orf04714_1	COG3520	hypothetical protein	K11895	impH, vasB

	orf04705_1	COG3157	hypothetical protein	K11903	K11903, hcp
	orf02781_1	COG3520	type VI secretion protein, VC_A0111 family	K11895	impH, vasB
	orf04713_1	COG3519	hypothetical protein	K11896	impG, vasA
	orf04703_1	COG3455	type IV/VI secretion system protein, DotU family	K11892	impK, ompA, vasF, dotU
	orf04979_1	_	_	K11906	vasD, lip
	orf04702_1	COG3522	hypothetical protein	K11893	impJ, vasE
	orf02780_1	COG3521	type VI secretion lipoprotein, VC_A0113 family	K11906	vasD, lip
	orf02778_1	COG3515	ImpA domain protein	K11911	vasL
	orf04990_1	COG3522	hypothetical protein	K11893	impJ, vasE
	orf04711_1	COG3523	hypothetical protein	K11891	impL, vasK, icmF
	orf02783_1	COG3523	ImcF-related family protein	K11891	impL, vasK, icmF
	orf04989_1	COG3455	hypothetical protein	K11892	impK, ompA, vasF, dotU