

Supplementary Table 1

TRANSCRIPTOMICS

UP-regulated

Locus Tag	Gene Object ID	ID Description	EC Number	COG	Group	Functional Categories
ObacDRAFT_1002	641180481	ATP synthase F1, alpha subunit	3.6.3.14	0056	C	Energy production and conversion
ObacDRAFT_2008	641183125	NADH-ubiquinone/plastoquinone oxidoreductase	1.6.5.3	0839	C	Energy production and conversion
ObacDRAFT_4074	641180385	Quinone oxidoreductase putative PIG3	1.6.5.5	0604	CR	Energy production and conversion/General function prediction only
ObacDRAFT_3725	641183128	putative exopolysaccharide biosynthesis protein	N/A	0489	D	Cell cycle control, cell division, chromosome partitioning
ObacDRAFT_1474	641182918	ABC transporter related	N/A	0410	E	Amino acid transport and metabolism
ObacDRAFT_3647	641182410	D-isomer specific 2-hydroxyacid dehydrogenase	1.1.1.95	0111	E	Amino acid transport and metabolism
ObacDRAFT_1038	641183406	phosphofructokinase	2.7.1.11	0205	G	Carbohydrate transport and metabolism
ObacDRAFT_1367	641181180	Fructose-bisphosphate aldolase	4.1.2.13	0191	G	Carbohydrate transport and metabolism
ObacDRAFT_3927	641181225	Alpha/beta hydrolase fold-3 domain protein	3.7.1.-	0657	I	Lipid transport and metabolism
ObacDRAFT_2695	641182545	ribosomal protein L15	N/A	0200	J	Translation, ribosomal structure and biogenesis
ObacDRAFT_1498	641183640	lysyl-tRNA synthetase	6.1.1.6	1190	J	Translation, ribosomal structure and biogenesis
ObacDRAFT_3158	641182322	regulatory protein LacI	N/A	1609	K	Transcription
ObacDRAFT_1903	641180891	regulatory protein GntR HTH	N/A	1609	K	Transcription
ObacDRAFT_3386	641180148	helix-turn-helix- domain containing protein AraC	N/A	2207	K	Transcription
ObacDRAFT_3083	641183638	DNA-directed DNA polymerase	2.7.7.7	0389	L	Replication, recombination and repair
ObacDRAFT_1380	641183673	exodeoxyribonuclease VII, small subunit	3.1.11.6	1722	L	Replication, recombination and repair
ObacDRAFT_3711	641182838	integrase family protein	N/A	4974	L	Replication, recombination and repair
ObacDRAFT_3566	641180943	major facilitator superfamily MFS_1	N/A	2223	P	Inorganic ion transport and metabolism
ObacDRAFT_0993	641180470	Acetyl xylan esterase	N/A	3458	Q	Secondary metabolites biosynthesis, transport and catabolism
ObacDRAFT_0729	641183105	integral membrane sensor signal transduction	2.7.13.3	0642	T	Signal transduction mechanisms
ObacDRAFT_1492	641181088	type II and III secretion system protein	N/A	1450	U	Intracellular trafficking, secretion, and vesicular transport
ObacDRAFT_0510	641180714	type II secretion system protein	N/A	1459	U	Intracellular trafficking, secretion, and vesicular transport
ObacDRAFT_2682	641181536	export protein FliQ family 3	N/A	1987	U	Intracellular trafficking, secretion, and vesicular transport
ObacDRAFT_2604	641182131	WD40 domain protein beta Propeller	N/A	0823	U	Intracellular trafficking, secretion, and vesicular transport
ObacDRAFT_2168	641183701	TPR repeat-containing protein	N/A	N/A	N/A	
ObacDRAFT_1988	641181411	Inner membrane CreD family protein	N/A	4452	V	Defense mechanisms
ObacDRAFT_2832	641180795	ISRSO5-transposase protein	N/A	N/A		
ObacDRAFT_1479	641182388	regulatory protein LacI				
ObacDRAFT_2532	641181909	regulatory protein LacI				
ObacDRAFT_3485	641183617	helix-turn-helix- domain containing protein AraC				
ObacDRAFT_2379	641179917	hypothetical protein				
ObacDRAFT_3770	641180523	hypothetical protein				
ObacDRAFT_4115	641182554	hypothetical protein				
ObacDRAFT_2467	641180041	hypothetical protein				
ObacDRAFT_0304	641180335	protein of unknown function DUF147				
ObacDRAFT_0671	641182958	conserved hypothetical protein				
ObacDRAFT_0198	641179730	hypothetical protein				
ObacDRAFT_2291	641180546	hypothetical protein				
ObacDRAFT_2505	641181167	hypothetical protein				
ObacDRAFT_0172	641182653	hypothetical protein				
ObacDRAFT_0891	641181281	hypothetical protein				
ObacDRAFT_1818	641182755	hypothetical protein				
ObacDRAFT_2387	641179929	hypothetical protein				
ObacDRAFT_2703	641182547	hypothetical protein				
ObacDRAFT_2603	641182130	protein of unknown function DUF59				

ObacDRAFT_3299	641183335 hypothetical protein
ObacDRAFT_0149	641180431 hypothetical protein
ObacDRAFT_2383	641179922 hypothetical protein
ObacDRAFT_1681	641182784 Uncharacterized protein-like protein

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ObacDRAFT_3488	641183430 Beta-glucosidase	3.2.1.21	2723	G	Carbohydrate transport and metabolism
ObacDRAFT_2780	641182885 acetylglutamate kinase	2.7.2.8	0548	E	Amino acid transport and metabolism
ObacDRAFT_1952	641183714 Pyrroline-5-carboxylate reductase	1.5.1.2	0345	E	Amino acid transport and metabolism
ObacDRAFT_1865	641180361 Ribulose-phosphate 3-epimerase	5.1.3.1	0036	G	Carbohydrate transport and metabolism
ObacDRAFT_3182	641183345 sugar-phosphate isomerase, RpiB/LacA/LacB	5.3.1.6	0698	G	Carbohydrate transport and metabolism
ObacDRAFT_3215	641183152 2-amino-4-hydroxy-6-hydroxymethylidihydropteridine pyrop	2.7.6.3	0801	H	Coenzyme transport and metabolism
ObacDRAFT_3157	641182327 biotin--acetyl-CoA-carboxylase ligase	6.3.4.15	0340	H	Coenzyme transport and metabolism
ObacDRAFT_2424	641182974 GCN5-related N-acetyltransferase	N/A	1670	J	Translation, ribosomal structure and biogenesis
ObacDRAFT_1590	641182699 translation elongation factor Ts	N/A	0264	J	Translation, ribosomal structure and biogenesis
ObacDRAFT_0988	641181375 helix-turn-helix- domain containing protein AraC	N/A	2207	K	Transcription
ObacDRAFT_2322	641183407 transcriptional regulator, LysR family	N/A	0583	K	Transcription
ObacDRAFT_0045	641182511 DNA-directed DNA polymerase	2.7.7.7	0847	K	
ObacDRAFT_1223	641181018 Methyltransferase type 12	N/A	N/A		
ObacDRAFT_3212	641183546 hypothetical protein				
ObacDRAFT_2769	641181319 hypothetical protein				
ObacDRAFT_2328	641182819 hypothetical protein				
ObacDRAFT_2044	641179849 hypothetical protein				
ObacDRAFT_0797	641181333 hypothetical protein				
ObacDRAFT_0711	641181999 conserved hypothetical protein				
ObacDRAFT_3441	641181152 hypothetical protein				
ObacDRAFT_2130	641180866 hypothetical protein				
ObacDRAFT_0819	641179783 conserved hypothetical protein				
ObacDRAFT_2414	641181788 hypothetical protein				
ObacDRAFT_0265	641180554 hypothetical protein				
ObacDRAFT_4102	641180409 hypothetical protein				
ObacDRAFT_0241	641179761 hypothetical protein				

PROTEOMICS

UP-regulated

Locus Tag	Gene Object ID	ID Description	EC Number	COG	Group	Functional Categories
ObacDRAFT_3061	641182673	aldo/keto reductase	N/A	0667	C	Energy production and conversion
ObacDRAFT_1943	641182117	D-lactate dehydrogenase (cytochrome)	1.1.3.15	0277	C	Energy production and conversion
ObacDRAFT_2903	641182424	FGGY-family pentulose kinase	2.7.1.16	1069	C	Energy production and conversion
ObacDRAFT_1327	641181096	Phosphoenolpyruvate carboxykinase (GTP)	4.1.1.32	1274	C	Energy production and conversion
ObacDRAFT_2731	641180635	succinate dehydrogenase and fumarate reductase iron-sul	1.3.99.1	0479	C	Energy production and conversion
ObacDRAFT_2730	641180634	succinate dehydrogenase or fumarate reductase, flavoprot	1.3.5.4	1053	C	Energy production and conversion
ObacDRAFT_2013	641181659	ferredoxin	1.6.5.3	1143	C	Energy production and conversion
ObacDRAFT_2017	641181663	NADH dehydrogenase (ubiquinone) 30 kDa subunit	1.6.5.3	0852	C	Energy production and conversion
ObacDRAFT_2887	641182650	Alanine--glyoxylate transaminase	2.6.1.-	0075	E	Amino acid transport and metabolism
ObacDRAFT_0053	641181674	Glutamate dehydrogenase (NADP(+))	1.4.1.4	0334	E	Amino acid transport and metabolism
ObacDRAFT_1864	641180360	lipolytic protein G-D-S-L family		2755	E	Amino acid transport and metabolism

ObacDRAFT_0053	641181674	glutamate synthase, NADH/NADPH, small subunit	1.4.1.13	0493	E	Amino acid transport and metabolism
ObacDRAFT_0782	641181325	ROK family protein	2.7.1.63	1940	G	Carbohydrate transport and metabolism
ObacDRAFT_1414	641181838	glyceraldehyde-3-phosphate dehydrogenase, type I	1.2.1.12	0057	G	Carbohydrate transport and metabolism
ObacDRAFT_1969	641182248	glycogen/starch synthase, ADP-glucose type	2.4.1.21	0297	G	Carbohydrate transport and metabolism
ObacDRAFT_2426	641181843	glycoside hydrolase family 2 TIM barrel	3.2.1.23	3250	G	Carbohydrate transport and metabolism
ObacDRAFT_3988	641181601	phosphofructokinase	2.7.1.11	0205	G	Carbohydrate transport and metabolism
ObacDRAFT_0714	641182004	pyruvate, phosphate dikinase	2.7.9.1	0574	G	Carbohydrate transport and metabolism
ObacDRAFT_1412	641181836	Triose-phosphate isomerase	5.3.1.1	149	G	Carbohydrate transport and metabolism
ObacDRAFT_3012	641180254	Xylose isomerase domain protein TIM barrel	5.3.1.5	1082	G	Carbohydrate transport and metabolism
ObacDRAFT_1973	641182252	Xylose isomerase domain protein TIM barrel				
ObacDRAFT_0419	641182902	Xylose isomerase domain protein TIM barrel				
ObacDRAFT_2850	641182487	TonB-dependent receptor plug	N/A	4206	H	Coenzyme transport and metabolism
ObacDRAFT_3600	641182497	biotin/lipoyl attachment domain-containing protein	N/A	0511	I	Lipid transport and metabolism
ObacDRAFT_2918	641181729	glutaminyl-tRNA synthetase	6.1.1.18	0008	J	Translation, ribosomal structure and biogenesis
ObacDRAFT_2699	641182550	ribosomal protein S11	N/A	0100	J	Translation, ribosomal structure and biogenesis
ObacDRAFT_1703	641181809	translation elongation factor G	3.6.5.3	0480	J	Translation, ribosomal structure and biogenesis
ObacDRAFT_2586	641183246	tryptophanyl-tRNA synthetase	6.1.1.2	0180	J	Translation, ribosomal structure and biogenesis
ObacDRAFT_3342	641180098	two component transcriptional regulator, LuxR family	N/A	2197	K	
ObacDRAFT_3586	641182162	DNA mismatch repair protein MutS domain protein	N/A	0249	L	Replication, recombination and repair
ObacDRAFT_0959	641182396	twitching motility protein	N/A	2805	N	Cell motility
ObacDRAFT_1758	641181629	ATPase AAA-2 domain protein	N/A	0542	O	Posttranslational modification, protein turnover, chaperones
ObacDRAFT_1710	641182761	ferric uptake regulator, Fur family	N/A	0735	P	Inorganic ion transport and metabolism
ObacDRAFT_1220	641181014	phosphopantetheine-binding	N/A	0236	Q	Secondary metabolites biosynthesis, transport and catabolism
ObacDRAFT_1706	641181812	2,5-didehydrogluconate reductase	N/A	0656	R	General function prediction only
ObacDRAFT_0445	641181248	band 7 protein	N/A	2268	S	Function unknown
ObacDRAFT_0605	641181912	putative CRISPR-associated protein, APE2256 family		4006	S	Function unknown
ObacDRAFT_1966	641183420	SecA Wing and Scaffold	N/A	0653	U	Intracellular trafficking, secretion, and vesicular transport
ObacDRAFT_3531	641180213	Tetratricopeptide TPR_2 repeat protein		5010	U	Intracellular trafficking, secretion, and vesicular transport
ObacDRAFT_2613	641183326	TPR repeat-containing protein				
ObacDRAFT_1558	641181288	Nucleotidyl transferase	2.7.7.8	N/A		
ObacDRAFT_3338	641180094	hypothetical protein ObacDRAFT_3338				
ObacDRAFT_2602	641182983	conserved hypothetical protein				
ObacDRAFT_3954	641181565	conserved hypothetical protein				
ObacDRAFT_1126	641180760	hypothetical protein ObacDRAFT_1126				
ObacDRAFT_0266	641180556	hypothetical protein ObacDRAFT_0266				
ObacDRAFT_4041	641183491	hypothetical protein ObacDRAFT_4041				
ObacDRAFT_3315	641181266	conserved hypothetical protein				
ObacDRAFT_1965	641183567	conserved hypothetical protein-signal peptide and transmembrane prediction				
ObacDRAFT_3500	641182172	protein of unknown function DUF303 acylesterase putative				
ObacDRAFT_1489	641181085	hypothetical protein ObacDRAFT_1489				
ObacDRAFT_3940	641181463	hypothetical protein ObacDRAFT_3940				
ObacDRAFT_1245	641182420	conserved hypothetical protein				
ObacDRAFT_1015	641183098	protein of unknown function DUF303 acylesterase putative				
ObacDRAFT_1491	641181087	hypothetical protein ObacDRAFT_1491				

DOWN-regulated

ObacDRAFT_3556	641183484	6-phosphogluconate dehydrogenase NAD-binding	1.1.1.44	2084	I	Lipid transport and metabolism
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ObacDRAFT_0038	641183259	uridylylate kinase	2.7.4.22	0528	F	Nucleotide transport and metabolism
ObacDRAFT_1019	641181412	Adenosylhomocysteinase	4.4.1.21	0499	H	Coenzyme transport and metabolism
ObacDRAFT_1018	641183101	Methionine adenosyltransferase	2.5.1.6	0192	H	Coenzyme transport and metabolism
ObacDRAFT_2307	641183495	acetate--CoA ligase	6.2.1.1	0365	I	Lipid transport and metabolism
ObacDRAFT_4010	641180594	FeS assembly protein SufB	N/A	0719	O	Posttranslational modification, protein turnover, chaperones
ObacDRAFT_2287	641180534	Hpt protein	N/A	2198	T	Signal transduction mechanisms
ObacDRAFT_1073	641181950	cell surface receptor IPT/TIG domain protein	N/A	N/A		
ObacDRAFT_2744	641182035	Uncharacterized protein-like protein				
ObacDRAFT_1288	641183076	conserved repeat domain				
ObacDRAFT_1612	641180499	hypothetical protein ObacDRAFT_1612				
ObacDRAFT_3883	641181926	protein of unknown function DUF306 Meta and HslJ				
ObacDRAFT_4012	641180596	protein of unknown function DUF59				