Table S1. Genes required for growth in *G. mellonella* larvae

Annotation	Gene Name	Description	Read Ratio (Gm/LB)
Nutrient Acquisition/Metabolism			
		Micronutrient Acquitision	
ABUW_1173	*bauD*	ferric acinetobactin transport system permease	0.0119
ABUW_1174	*bauC*	ferric acinetobactin transport system permease	0.0976
ABUW_1176	*bauB*	ferric acinetobactin transport system periplasmic binding protein	0.0472
ABUW_1177	*bauA*	ferric acinetobactin receptor	0.0111
ABUW_1655	-	TonB-dependent siderophore receptor	0.0727
ABUW_1864	-	2Fe-2S iron-sulfur cluster binding domain protein	0.0783
ABUW_2232	-	biopolymer transport protein ExbD/TolR	0.0642
ABUW_2917	*yhgI*	IscR-regulated protein YhgI	0
ABUW_3740	*znuA*	high affinity Zn transport protein	0.0312
ABUW_3741	*zur*	transcriptional regulator, Fur family	0.0730
ABUW_3742	*znuC*	zinc import ATP-binding protein ZnuC	0.0685
ABUW_3743	*znuB*	high affinity Zn transport protein	0.0449
		Amino Acid Transport/Metabolism	
ABUW_1239	*alzC*	branched-chain amino acid permease	0.0985
ABUW_1240	*alzD*	branched chain amino acid transporter	0.0924
ABUW_1341	*hisM*	histidine transport system permease protein HisM	0.0947
ABUW_1726	-	D-amino acid dehydrogenase 3 small subunit	0.0741
ABUW_1816	*aro1*	3-deoxy-7-phosphoheptulonate synthase	0.0794
ABUW_1857	-	Glu-tRNA amidotransferase	0.0986
ABUW_2221	*gsiA*	glutathione import ATP-binding protein GsiA	0.0877
ABUW_2222	-	ABC-type dipeptide/oligopeptide/nickel transport system permease component	0.0748
ABUW_2330	*gltL*	glutamate/aspartate transport ATP-binding protein GltL	0.0931
ABUW_2332	*gltJ*	glutamate/aspartate transport system permease protein GltJ	0.0850
ABUW_2339	*metQ2*	D-methionine transport protein	0.0977
ABUW_2418	-	lysine exporter protein	0.0955
ABUW_2424	-	ABC-type amino acid transport system	0.0686
ABUW_2430	-	transporter, LysE family	0.0950
ABUW_2691	-	transporter LysE family	0.0585
ABUW_2798	-	D-serine/D-alanine/glycine transporter	0.0727
		Cysteine Metabolism/Sulfur Assimilation	
ABUW_0643	*cysI*	sulfite reductase	0.0217
ABUW_0722	*cysH*	phosphoadenosine phosphosulfate reductase	0
ABUW_0853	*cobA*	uroporphyrin-III C-methyltransferase	0
ABUW_1760	-	sulfate permease	0.0959
ABUW_1941	-	TauE-like transmembrane protein (probable	0

Table S1. Genes required for growth in *G. mellonella* larvae (continued)

Annotation	Gene Name	Description	Read Ratio (Gm/LB)
		pseudogene)	
ABUW_2218	*cysQ*	3'(2'),5'-bisphosphate nucleotidase	0.0503
ABUW_2362	*cysE*	serine acetyltransferase	0.0361
ABUW_2895	*cysN*	sulfate adenylyltransferase subunit 1	0
ABUW_2896	*cysD*	sulfate adenylyltransferase subunit 2	0
		Aromatic Hydrocarbon Metabolism	
ABUW_1835	*pcaD*	3-oxoadipate enol-lactonase	0.0469
ABUW_1837	*pcaC*	4-carboxymuconolactone decarboxylase	0.0652
ABUW_1854	-	benzoate transport porin BenP	0.0305
ABUW_2090	-	4-hydroxybenzoate transporter	0.0909
ABUW_2349	-	4-oxalocrotonate tautomerase	0.0086
ABUW_2374	-	isochorismatase hydrolase	0.0631
ABUW_2523	*paaI1*	thioesterase domain protein	0.0069
ABUW_2524	*paaY*	phenylacetic acide degradation protein PaaY	0.0934
		Lipid Metabolism	
ABUW_0091	*pgpA*	phosphatidylglycerophosphatase A	0.0514
ABUW_0590	-	putative polysaccharide deacetylase	0
ABUW_0593	-	glycosyl hydrolase family 43 domain-containing protein	0.0287
ABUW_1438	-	acyltransferase 3 domain-containing protein	0.0588
ABUW_1509	*desC*	delta-9 acyl-lipid desaturase 1	0.0826
ABUW_1512	*cfa*	cyclopropane-fatty-acyl-phospholipid synthase	0.0761
ABUW_1636	-	short chain dehydrogenase	0.0770
ABUW_1637	-	oxidoreductase short-chain dehydrogenase/reductase family	0.0971
ABUW_2193	-	acyl-CoA dehydrogenase	0.0793
ABUW_2450	-	long-chain fatty-acid-CoA ligase	0.0933
ABUW_2454	*mgh*	3-methylglutaconyl-CoA hydratase	0.0810
ABUW_2461	-	thioesterase superfamily protein	0.0515
		Secondary Metabolite/Cofactor/Coenzyme Synthesis	
ABUW_0379	*dxs*	1-deoxy-D-xylulose-5-phosphate synthase	0.0992
ABUW_1228	*lipA1*	lipoic acid synthetase	0
ABUW_1710	-	thiamine S/molybdopterin converting factor subunit 1	0
ABUW_1711	*moaE*	molybdopterin converting factor, subunit 2	0.0092
ABUW_1713	-	molybdopterin biosynthesis protein	0.0857
ABUW_1904	-	antibiotic biosynthesis monooxygenase	0.0931
ABUW_2132	*lipA2*	lipoic acid synthetase	0.0288
ABUW_2171	*cobS*	cobalamin 5'-phosphate synthase	0.0804
ABUW_2226	-	heme-binding protein A	0.0656
ABUW_2395	*madL*	malonate transporter, MadL subunit	0.0103
ABUW_2449	-	putative SAM-dependent methyltransferase	0.0771

Table S1. Genes required for growth in *G. mellonella* larvae (continued)

Annotation	**Gene Name**	**Description**	**Read Ratio (Gm/LB)**
ABUW_3650	*ribE*	riboflavin synthase, alpha subunit	0
Cell Envelope/Membrane/Wall			
ABUW_2626	-	neuraminidase domain-containing protein	0.0511
ABUW_2679	-	hypothetical protein	0
ABUW_2692	-	hypothetical protein (probable pseudogene)	0.0476
ABUW_2898	-	hypothetical protein	0
ABUW_3360	*lptE*	lipopolysaccharide assembly lptE	0
ABUW_3447	*lpxL*	lipid A biosynthesis acyltransferase	0
ABUW_3448	*lptB*	glycosyl transferase, group 1	0.0248
ABUW_3638	*pbpG*	D-alanyl-D-alanine carboxypeptidase family protein	0
ABUW_3820	-	nucleotide sugar epimerase/dehydratase	0.0327
ABUW_3821	-	Spore coat polysaccharide biosynthesis protein spsC	0.0144
ABUW_3822	-	Bacterial transferase hexapeptide (three repeats) family protein	0
ABUW_3823	-	putative UDP-galactose phosphate transferase (WeeH)	0
ABUW_3824	-	family 1 glycosyl transferase	0.0056
ABUW_3825	-	hypothetical protein	0
ABUW_3826	-	family 1 glycosyl transferase	0.0869
ABUW_3828	-	UDP-glucose/GDP-mannose dehydrogenase family protein	0.0535
ABUW_3830	-	UDP-glucose/GDP-mannose dehydrogenase	0.0384
ABUW_3831	*wza*	polysaccharide export protein	0.0133
ABUW_3832	*ptp*	protein-tyrosine-phosphatase ptp	0
ABUW_3833	*ptk*	tyrosine-protein kinase ptk	0
Stress Response Genes			
ABUW_0655	*typA*	GTP-binding protein TypA/BipA	0.0223
ABUW_1447	-	M48 family peptidase	0.0042
ABUW_1501	*pqiA-2*	paraquat-inducible protein A	0.0768
ABUW_1595	*kef*	ion transport protein	0.0666
ABUW_1648	-	mechanosensitive ion channel family protein	0.0658
ABUW_1740	*rseP*	peptidase M50, putative membrane-associated zinc metallopeptidase	0.0279
ABUW_1763	-	UspA domain protein	0
ABUW_1804	*trkH*	K+ uptake system component	0.0639
ABUW_1805	*trkA*	K+ uptake system component	0.0822
ABUW_2237	-	monooxygenase, flavin-binding family	0.0838
ABUW_2371	*arsC*	arsenate reductase	0.0917
ABUW_2438	*cinA1*	competence/damage-inducible protein CinA	0
ABUW_2513	*csp2*	cold-shock DNA-binding domain protein	0.0095
ABUW_2521	-	UvrD/REP helicase	0.0460

Table S1. Genes required for growth in *G. mellonella* larvae (continued)

Annotation	Gene Name	Description	Read Ratio (Gm/LB)
ABUW_2590	*kefF*	NADPH oxidoreductase	0.0405
ABUW_3122	*otsB*	trehalose-phosphatase	0.0859
Antibiotic Resistance			
ABUW_0842	*adeK*	multidrug efflux protein AdeK	0
ABUW_0843	*adeJ*	multidrug efflux protein AdeJ	0.0157
ABUW_0844	*adeI*	multidrug efflux protein AdeI	0.0154
ABUW_1156	-	transporter, drug/metabolite exporter family	0.0442
ABUW_1499	-	EamA-like transporter family protein	0.0619
ABUW_1520	-	EamA-like transporter family protein	0.0635
ABUW_1673	-	bacterial transmembrane pair family protein	0.0458
ABUW_1851	-	aminoglycoside phosphotransferase	0.0912
ABUW_2123	-	metallo-beta-lactamase family protein	0.0828
ABUW_2550	-	EamA-like transporter family protein	0.0584
Transcriptional Regulation/Signal Transduction			
ABUW_1475	-	transcriptional regulator, AraC family	0.0757
ABUW_1515	-	two-component system response regulator protein	0.0909
ABUW_1571	-	transcriptional regulator, AraC family	0.0756
ABUW_1645	-	transcriptional regulator, TetR family	0.0437
ABUW_1672	-	transcriptional regulator, LysR family	0.0676
ABUW_1692	-	transcriptional regulator, TetR family	0.0493
ABUW_1755	*gigD*	transcriptional regulator, AsnC family	0
ABUW_1764	-	GGDEF family protein	0.0727
ABUW_1768	-	transcriptional regulator, MarR-family	0.0272
ABUW_1848	*pcaU*	pca operon regulatory protein	0.0852
ABUW_1849	-	transcriptional regulator, LysR family	0.0547
ABUW_1912	-	hypothetical protein	0.0114
ABUW_1966	-	transcriptional regulator, LysR family	0.0556
ABUW_2074	-	transcriptional regulator, fur family	0.0495
ABUW_2080	-	transcriptional regulator, ModE family	0.0785
ABUW_2196	*alkR*	transcriptional regulator, AraC family	0.0516
ABUW_2208	-	adenylate/guanylate cyclase	0.0296
ABUW_2236	-	transcriptional regulator, AraC family	0.0550
ABUW_2328	-	transcriptional regulator, AsnC family	0.0873
ABUW_2344	-	transcriptional regulator, Crp/Fnr family	0.0886
ABUW_2368	-	transcriptional regulator, LysR family	0.0817
ABUW_2370	*arsR*	transcriptional regulator, ArsR family	0
ABUW_2509	-	hypothetical protein (probable pseudogene)	0.0720
ABUW_2520	-	transcriptional regulator, TetR family	0.0666
ABUW_2544	-	transcriptional regulator, AraC family	0.0373
ABUW_2555	*soxR*	redox-sensitive transcriptional activator SoxR	0.0934

Table S1. Genes required for growth in *G. mellonella* larvae (continued)

Annotation	Gene Name	Description	Read Ratio (Gm/LB)
ABUW_2563	-	regulatory protein LysR:LysR, substrate-binding	0.0798
ABUW_2609	-	transcriptional regulator, LysR-type	0.0797
ABUW_2741	*vfr*	cyclic nucleotide-binding domain protein	0.0945
ABUW_3161	*gigC*	transcriptional regulator, LysR family	0.0007
ABUW_3180	*bfmS*	two-component system sensor kinase protein	0
ABUW_3260	*gigA*	putative two-component response regulator	0.0671
Hypothetical Proteins			
ABUW_0460	-	hypothetical protein	0
ABUW_0779	-	hypothetical protein	0.0705
ABUW_0933	-	hypothetical protein	0.0923
ABUW_0934	-	hypothetical protein	0.0733
ABUW_0935	-	hypothetical protein	0.0628
ABUW_0936	-	hypothetical protein	0
ABUW_1094	-	hypothetical protein	0.0249
ABUW_1095	-	hypothetical protein	0.0825
ABUW_1096	-	hypothetical protein	0.0576
ABUW_1121	-	hypothetical protein	0.0531
ABUW_1160	-	hypothetical protein	0
ABUW_1212	-	hypothetical protein	0.0900
ABUW_1284	-	hypothetical protein	0.0578
ABUW_1285	-	hypothetical protein	0.0457
ABUW_1287	-	hypothetical protein	0.0648
ABUW_1330	-	hypothetical protein	0.0691
ABUW_1388	-	hypothetical protein	0.0749
ABUW_1390	-	hypothetical protein	0.0558
ABUW_1396	-	hypothetical protein	0.0019
ABUW_1417	-	hypothetical protein	0.0850
ABUW_1439	-	hypothetical protein	0.0696
ABUW_1466	-	hypothetical protein	0.0545
ABUW_1516	-	hypothetical protein	0
ABUW_1587	-	hypothetical protein	0
ABUW_1594	-	hypothetical protein	0
ABUW_1628	-	hypothetical protein	0.0659
ABUW_1629	-	hypothetical protein	0.0988
ABUW_1643	-	hypothetical protein	0.0262
ABUW_1644	-	hypothetical protein	0.0617
ABUW_1651	-	hypothetical protein	0
ABUW_1652	-	hypothetical protein	0.0418
ABUW_1658	-	hypothetical protein	0
ABUW_1662	-	hypothetical protein	0

Annotation	Gene Name	Description	Read Ratio (Gm/LB)
ABUW_1681	-	hypothetical protein	0
ABUW_1691	-	PepSY-associated TM helix domain- containing protein	0.0937
ABUW_1724	-	hypothetical protein	0
ABUW_1727	-	hypothetical protein	0.0945
ABUW_1753	-	hypothetical protein	0.0733
ABUW_1774	-	hypothetical protein	0.0440
ABUW_1788	-	hypothetical protein	0.0598
ABUW_1828	-	hypothetical protein	0.0546
ABUW_1860	-	hypothetical protein	0.0761
ABUW_1879	-	hypothetical protein	0.0903
ABUW_1901	-	hypothetical protein	0.0458
ABUW_1915	-	hypothetical protein	0.0541
ABUW_1918	-	hypothetical protein	0.0670
ABUW_1960	-	hypothetical protein	0.0662
ABUW_2061	-	hypothetical protein	0.0661
ABUW_2064	-	hypothetical protein	0.0555
ABUW_2065	-	hypothetical protein	0.0688
ABUW_2094	-	hypothetical protein	0.0255
ABUW_2103	-	hypothetical protein	0.0882
ABUW_2107	-	hypothetical protein	0.0721
ABUW_2145	-	hypothetical protein	0.0160
ABUW_2149	-	hypothetical protein	0.0904
ABUW_2156	-	hypothetical protein	0.0784
ABUW_2167	*puiB*	hypothetical protein	0.0753
ABUW_2179	-	hypothetical protein	0.0959
ABUW_2181	-	hypothetical protein	0.0762
ABUW_2219	-	hypothetical protein	0.0692
ABUW_2238	-	hypothetical protein	0.0937
ABUW_2291	-	hypothetical protein	0
ABUW_2298	-	hypothetical protein	0.0030
ABUW_2308	-	hypothetical protein	0
ABUW_2309	-	hypothetical protein	0.0441
ABUW_2314	-	hypothetical protein	0
ABUW_2345	-	hypothetical protein	0.0641
ABUW_2363	-	hypothetical protein	0.0184
ABUW_2372	-	hypothetical protein	0.0637
ABUW_2416	-	hypothetical protein	0.0971
ABUW_2434	-	hypothetical protein	0
ABUW_2439	-	hypothetical protein	0.0588
ABUW_2441	-	hypothetical protein	0.0530

Table S1. Genes required for growth in *G. mellonella* larvae (continued)

Annotation	Gene Name	Description	Read Ratio (Gm/LB)
ABUW_2442	-	hypothetical protein	0
ABUW_2443	-	hypothetical protein	0.0762
ABUW_2444	-	hypothetical protein	0
ABUW_2463	-	hypothetical protein	0.0845
ABUW_2510	-	hypothetical protein	0
ABUW_2511	-	hypothetical protein	0
ABUW_2512	-	hypothetical protein	0
ABUW_2556	-	hypothetical protein	0
ABUW_2559	-	hypothetical protein	0.0822
ABUW_2597	-	hypothetical protein (probable pseudogene)	0.0914
ABUW_2598	-	hypothetical protein	0.0702
ABUW_2600	-	hypothetical protein	0.0351
ABUW_2611	-	hypothetical protein	0.0945
ABUW_2612	-	hypothetical protein	0.0839
ABUW_2624	-	hypothetical protein	0.0477
ABUW_2652	-	hypothetical protein	0.0845
ABUW_2657	-	hypothetical protein (probable pseudogene)	0.0836
ABUW_2658	-	hypothetical protein	0.0823
ABUW_2674	-	hypothetical protein	0.0788
ABUW_2684	-	phage putative head morphogenesis protein	0.0449
ABUW_2685	-	hypothetical protein	0.0044
ABUW_2744	-	putative membrane protein	0.0185
ABUW_2756	-	hypothetical protein	0.0366
ABUW_2795	-	hypothetical protein	0.0152
ABUW_2796	-	hypothetical protein	0.0430
ABUW_2797	-	hypothetical protein	0.0411
ABUW_2811	-	hypothetical protein	0.0407
ABUW_2815	-	hypothetical protein	0.0887
ABUW_2819	-	hypothetical protein	0.0987
ABUW_2833	-	hypothetical protein	0.0987
ABUW_2846	-	hypothetical protein	0.0410
ABUW_2860	-	hypothetical protein	0.0980
ABUW_3003	-	hypothetical protein	0.0558
ABUW_3192	-	hypothetical protein	0
ABUW_4005	-	hypothetical protein	0
ABUW_4025	-	hypothetical protein	0.0179
ABUW_4077	-	hypothetical protein	0
ABUW_4091	-	hypothetical protein	0.0695
Miscellaneous Proteins			
ABUW_0719	*cafA*	ribonuclease G	0

Table S1. Genes required for growth in *G. mellonella* larvae (continued)

Annotation	**Gene Name**	**Description**	**Read Ratio (Gm/LB)**
ABUW_1497	-	ADP-ribose pyrophosphatase (probable pseudogene)	0.0703
ABUW_1504	*uraH2*	transthyretin	0.0615
ABUW_1537	*gidA*	glucose inhibited division protein A	0.0357
ABUW_1603	-	putative acetyltransferase	0.0819
ABUW_1625	-	putative helicase	0.0743
ABUW_1632	-	PapD-like P pilus assembly protein	0.0530
ABUW_1654	-	acetyltransferase, gnat family	0.0479
ABUW_1684	-	iron-containing alcohol dehydrogenase	0.0866
ABUW_1734	-	TRAM domain-containing protein	0.0901
ABUW_1747	*recX*	regulatory protein RecX	0.0922
ABUW_1750	-	HAD-superfamily hydrolase	0.0969
ABUW_1758	-	alpha/beta hydrolase fold-3	0.0912
ABUW_1962	-	acetyltransferase (probable pseudogene)	0
ABUW_2066	*acdP*	dipeptidase	0.0681
ABUW_2177	-	HAD-superfamily hydrolase	0.0959
ABUW_2214	*rraA*	regulator of ribonuclease activity A	0.0956
ABUW_2217	-	phosphoglycerate mutase	0.0739
ABUW_2233	-	acetyltransferase, gnat family	0
ABUW_2235	-	AFG1-family ATPase	0.0602
ABUW_2252	*gspG*	general secretion pathway protein G	0.0683
ABUW_2262	*spoOJ*	chromosome partitioning protein ParB	0.0535
ABUW_2268	*surA*	PpiC-type peptidyl-prolyl cis-trans isomerase	0.0405
ABUW_2304	*ruvC*	crossover junction endodeoxyribonuclease RuvC	0.0930
ABUW_2311	-	pili assembly chaperone	0.0403
ABUW_2313	-	fimbrial protein	0.0907
ABUW_2322	-	phage integrase	0.0798
ABUW_2342	*ychF*	GTP-binding protein YchF	0.0085
ABUW_2408	-	LrgA family protein	0.0849
ABUW_2558	-	acetyltransferase, gnat family	0.0881
ABUW_2592	-	urea carboxylase-associated protein 1	0.0927
ABUW_2593	-	urea carboxylase-associated protein 2	0.0777
ABUW_2613	-	RHS family protein	0.0765
ABUW_2640	-	acetyltransferase	0.0316
ABUW_2678	-	17 kDa surface antigen	0.0675
ABUW_2826	*rnt*	ribonuclease T	0.0132
ABUW_3083	*smpB*	SsrA-binding protein	0
ABUW_3385	*prc*	carboxy-protease	0.0774
ABUW_3589	*rpoC*	DNA-directed RNA polymerase, beta' subunit	0.0315
ABUW_3710	-	putative acetyltransferase	0.0946
ABUW_3846	*dsbA*	thiol:disulfide interchange protein DsbA	0.0764

Table S1. Genes required for growth in *G. mellonella* larvae (continued)

Annotation	Gene Name	Description	Read Ratio (Gm/LB)
ABUW_4023	-	Protein incC	0