Table S1. Gene Ontology (GO) enrichment analysis of differentially expressed genes in LB and M9 media

Category	GO ID	GO Term	Annotated[a]	LB		M9+ succinate	
				FE[b]	p-adj	FE	p-adj
CC	GO:0016021	integral component of membrane	58	1.25	0.55	0.79	1
BP	GO:0044238	primary metabolic process	57	1.23	0.85	0.86	1
BP	GO:0009987	cellular process	85	0.88	1	1.01	1
BP	GO:0008150	biological process	123	1.00	1	1.00	1
BP	GO:0008152	metabolic process	76	0.98	1	0.81	1
BP	GO:0071704	organic substance metabolic process	66	0.93	1	0.37	1
BP	GO:0044237	cellular metabolic process	54	0.73	1	0.68	1
CC	GO:0016020	membrane	92	1.02	1	0.99	1
CC	GO:0110165	cellular anatomical entity	98	1.00	1	1.00	1
CC	GO:0005575	cellular component	98	1.00	1	1.00	1
CC	GO:0031224	intrinsic component of membrane	58	1.25	1	0.79	1
MF	GO:0016491	oxidoreductase activity	123	1.17	1	0.93	1
MF	GO:0003677	DNA binding	78	1.02	1	0.98	1
MF	GO:0016787	hydrolase activity	65	1.06	1	0.98	1
MF	GO:0003676	nucleic acid binding	95	1.01	1	0.94	1
MF	GO:0003824	catalytic activity	341	1.04	1	0.75	1
MF	GO:0016740	transferase activity	83	1.09	1	0.31	1
MF	GO:0003674	molecular function	585	1.00	1	1.00	1
MF	GO:0005488	binding	236	0.92	1	1.40	1
MF	GO:0097159	organic cyclic compound binding	158	0.94	1	1.29	1
MF	GO:1901363	heterocyclic compound binding	158	0.94	1	1.29	1
MF	GO:0043167	ion binding	77	0.90	1	1.82	1
MF	GO:0036094	small molecule binding	64	0.83	1	1.99	1
MF	GO:1901265	nucleoside phosphate binding	61	0.87	1	1.88	1

MF	GO:0000166	nucleotide binding	61	0.87	1	1.88	1
MF	GO:0043168	anion binding	60	0.89	1	1.91	1
MF	GO:0097367	carbohydrate derivative binding	57	0.93	1	2.01	1
MF	GO:0032553	ribonucleotide binding	52	1.02	1	2.20	1

To facilitate comparison of broadly represented functional categories and reduce the influence of sparsely represented terms, only GO terms associated with more than 50 genes were displayed. Category indicates the GO domain. BP, biological process; CC, cellular component; MF, molecular function.

[a]Annotated indicates the number of genes assigned to each GO term within the reference gene set, which was identical for both media.

[b]FE refers to Fold Enrichment, the ratio of the observed to the expected number of significant genes annotated to a term.