

**Supplementary Table 4.2.** Comparison between the transcription levels of genes commonly expressed by the pathogenic and non-pathogenic homologous *L. intracellularis* isolate PHE/MN1-00.

Locus	Gene product	Passage 60	Passage 10	Fold change	p_value*
		Log <sub>2</sub> (RPKM)	Log <sub>2</sub> (RPKM)		
LI0003	hypothetical protein LI0003	15.2	15.2	0.05	1.011
LI0005	superoxide dismutase precursor (Cu-Zn)	14.8	15.5	0.69	0.637
LI0007	nucleotide transport protein	12.6	12.6	-0.01	1.009
LI0018	proton/sodium-glutamate symport protein	12.9	13.2	0.27	1.032
LI0022	tyrosyl-tRNA synthetase	12.2	11.6	-0.67	1.029
LI0024	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	13.5	13.6	0.08	1.041
LI0025	phosphoenolpyruvate synthase/pyruvate phosphate	12.4	12.5	0.13	1.054
LI0027	flagellar motor switch protein	12.6	11.7	-0.88	0.914
LI0041	hypothetical protein LI0041	12.0	11.6	-0.47	1.016
LI0042	hypothetical protein LI0042	12.7	12.2	-0.47	1.032
LI0043	hypothetical protein LI0043	12.4	12.1	-0.32	1.031
LI0045	hypothetical protein LI0045	12.9	12.7	-0.22	1.034
LI0060	transcriptional regulators of sugar metabolism	12.8	11.8	-0.99	0.898
LI0063	hypothetical protein LI0063	12.5	12.4	-0.09	1.039
LI0064	transcriptional regulator	13.6	13.3	-0.33	1.033
LI0069	hypothetical protein LI0069	12.3	11.7	-0.58	0.923
LI0070	hypothetical protein LI0070	12.7	12.5	-0.24	1.059
LI0071	hypothetical protein LI0071	12.3	12.2	-0.08	1.031
LI0072	hypothetical protein LI0072	13.5	13.2	-0.30	1.102
LI0075	phosphodiesterase	12.7	12.4	-0.29	1.055
LI0076	sugar ABC transporter, ATP-binding protein	12.0	11.9	-0.11	1.027
LI0077	extracellular solute-binding protein	11.7	11.8	0.13	1.040
LI0082	hypothetical protein LI0082	11.5	11.1	-0.39	1.065
LI0091	phosphopyruvate hydratase	12.3	12.0	-0.25	1.110
LI0093	hypothetical protein LI0093	12.3	12.2	-0.10	1.034
LI0098	hypothetical protein LI0098	16.1	15.4	-0.75	1.021
LI0112	hypothetical protein LI0112	11.9	11.8	-0.17	1.056

LI0126	ATPases with chaperone activity, ATP-binding subunit	12.9	12.2	-0.73	1.021
LI0143	hypothetical protein LI0143	12.9	12.4	-0.51	1.026
LI0145	GTP-binding protein LepA	11.9	11.9	0.00	1.010
LI0148	ATP-dependent protease	11.7	11.8	0.10	1.053
LI0149	DNA repair proteins	12.1	12.0	-0.13	1.062
LI0155	GTP cyclohydrolase II, partial	12.8	12.9	0.10	1.026
LI0160	3-oxoacyl-ACP synthase	12.2	12.2	0.08	1.045
LI0161	3-oxoacyl-ACP reductase	13.1	13.2	0.16	1.066
LI0168	SNF2 family DNA/RNA helicase	11.2	11.1	-0.11	1.048
LI0188	ATP-dependent Zn proteases	12.0	12.1	0.17	1.061
LI0203	tRNA methyltransferase	13.3	13.7	0.32	1.053
LI0204	Fe-S oxidoreductases	12.8	12.9	0.16	1.053
LI0205	delta-aminolevulinic acid dehydratase	13.0	13.5	0.51	1.051
LI0206	Fe-S oxidoreductases	11.9	12.0	0.16	1.057
LI0207	transcriptional regulators	12.1	12.4	0.31	1.076
LI0212	threonyl-tRNA synthetase	11.8	11.8	0.05	1.018
LI0213	translation initiation factor IF-3	13.3	13.4	0.15	1.055
LI0214	50S ribosomal protein L20	13.2	13.6	0.45	1.017
LI0216	phenylalanyl-tRNA synthetase subunit beta	12.3	11.8	-0.46	1.056
LI0219	transketolase	11.5	10.9	-0.61	1.034
LI0220	tRNA-(guanine-N1)-methyltransferase	12.5	12.2	-0.31	1.042
LI0221	50S ribosomal protein L19	13.0	13.6	0.63	1.000
LI0226	ABC transporter ATP-binding protein	12.0	11.9	-0.04	1.011
LI0228	fructose 1,6-bisphosphatase II	11.1	11.2	0.15	1.044
LI0245	hydrogenase accessory protein HypB	12.0	12.1	0.13	1.062
LI0248	hypothetical protein LI0248	11.7	11.6	-0.11	1.039
LI0254	hypothetical protein LI0254	12.1	10.5	-1.57	0.608
LI0257	DNA polymerase III, alpha subunit	11.3	11.2	-0.13	1.048
LI0258	FOF1-type ATP synthase, subunit c	12.8	11.9	-0.86	0.914
LI0261	glutamate decarboxylase isozyme	12.8	13.1	0.32	1.018
LI0264	transcription termination factor Rho	12.6	12.6	0.00	1.001
LI0265	cysteine sulfinate desulfurase/cysteine desulfurase	13.5	14.3	0.83	0.443
LI0266	NifU homolog involved in Fe-S cluster formation, partial	13.7	14.6	0.83	0.375
LI0267	hypothetical protein LI0267	14.0	14.1	0.11	1.056

LI0269	hypothetical protein LI0269	11.3	10.9	-0.40	1.066
LI0273	desulfoferrodoxin	15.1	15.6	0.51	0.789
LI0274	uncharacterized flavoproteins	11.9	12.6	0.65	0.956
LI0275	cytochrome bd-type quinol oxidase, subunit 1	12.9	12.8	-0.11	1.037
LI0276	cytochrome bd-type quinol oxidase, subunit 2	13.2	12.9	-0.31	1.080
LI0278	ferredoxin oxidoreductase, gamma subunit	14.6	14.5	-0.04	1.034
LI0288	PAP2 superfamily protein	11.8	11.6	-0.18	1.059
LI0293	fumarate hydratase	12.3	11.3	-0.98	0.782
LI0294	fumarate hydratase	12.1	12.1	0.00	1.004
LI0299	glycyl-tRNA synthetase, beta subunit	11.1	10.8	-0.25	1.061
LI0300	glycyl-tRNA synthetase subunit alpha	11.9	11.8	-0.11	1.035
LI0302	hypothetical protein LI0302	11.7	12.0	0.25	1.063
LI0303	parvulin-like peptidyl-prolyl isomerase	12.5	12.5	0.01	1.009
LI0304	parvulin-like peptidyl-prolyl isomerase	13.1	12.2	-0.94	0.899
LI0329	Glyen debranching enzyme	11.2	10.4	-0.81	0.843
LI0331	alpha-amylase	11.9	10.8	-1.12	0.850
LI0332	carbohydrate phosphorylase family protein	11.6	11.1	-0.46	1.067
LI0346	trypsin domain/PDZ domain-containing protein	12.4	12.5	0.08	1.016
LI0354	replicative DNA helicase	11.6	11.5	-0.17	1.048
LI0360	nicotinate-nucleotide pyrophosphorylase	11.3	11.5	0.23	1.074
LI0366	thioredoxin reductase	12.5	12.3	-0.21	1.072
LI0367	Thiol-disulfide isomerase and thioredoxins	15.1	15.2	0.08	1.021
LI0369	fructose-1,6-bisphosphatase	11.6	11.5	-0.10	1.054
LI0370	hypothetical protein LI0370	12.2	12.4	0.22	1.061
LI0371	hypothetical protein LI0371	12.3	12.6	0.33	1.099
LI0377	30S ribosomal protein S2	12.6	12.9	0.31	1.053
LI0378	elongation factor Ts	12.4	12.1	-0.30	1.033
LI0392	rod shape-determining protein MreB	12.4	12.3	-0.12	1.056
LI0401	F0F1 ATP synthase subunit alpha	11.9	11.8	-0.05	1.006
LI0434	glycosyltransferase	13.2	13.1	-0.09	1.037
LI0439	hydrogenase-1 small subunit	13.0	13.1	0.11	1.057
LI0440	hydrogenase-1 large subunit	13.1	13.2	0.15	1.060
LI0441	Ni/Fe-hydrogenase 1 B-type cytochrome subunit	12.5	12.5	0.06	1.007
LI0447	hypothetical protein LI0447	17.6	18.5	0.89	0.230

LI0448	hypothetical protein LI0448	12.4	12.8	0.42	0.985
LI0450	phosphoribosylformylglycinamide synthase	12.9	12.4	-0.50	1.052
LI0451	CTP synthetase	11.7	11.6	-0.08	1.028
LI0461	hypothetical protein LI0461	15.9	16.0	0.10	1.050
LI0473	DNA methylase	13.3	13.6	0.28	1.096
LI0476	ribonucleotide-diphosphate reductase subunit alpha	11.7	11.8	0.08	1.045
LI0482	flagellar motor protein MotA	13.2	12.0	-1.10	0.798
LI0488	biotin carboxylase	11.8	10.3	-1.44	0.730
LI0489	Acetyl-CoA carboxylase alpha subunit	11.7	11.9	0.16	1.051
LI0492	single-stranded DNA-binding protein	12.8	12.7	-0.05	1.010
LI0493	glutaminyl-tRNA synthetase	11.5	10.6	-0.91	0.822
LI0496	branched chain amino acid ABC transporter	13.1	12.4	-0.71	0.893
LI0500	branched chain amino acid ABC transporter, ATP-binding	12.0	11.6	-0.40	1.056
LI0501	membrane-bound proton-translocating pyrophosphatase	12.8	13.0	0.21	1.026
LI0507	hypothetical protein LI0507	11.6	11.2	-0.42	1.046
LI0509	carbon starvation protein, membrane protein	12.5	11.8	-0.73	1.028
LI0517	DNA-directed RNA polymerase (sigma70/sigma32)	11.1	10.9	-0.24	1.060
LI0518	DNA primase	12.5	10.9	-1.63	0.612
LI0520	hypothetical protein LI0520	14.5	14.8	0.35	1.016
LI0534	transcription elongation factor NusA	12.2	12.4	0.19	1.106
LI0535	translation initiation factor 2 (IF-2; GTPase)	12.0	12.0	-0.01	1.011
LI0553	diaminopimelate decarboxylase	11.8	12.4	0.59	0.910
LI0559	50S ribosomal protein L13	13.7	14.6	0.88	0.647
LI0560	30S ribosomal protein S9	13.2	13.3	0.16	1.053
LI0573	RimM protein, required for 16S rRNA processing	14.4	14.5	0.03	1.013
LI0574	RNA-binding protein	15.2	15.5	0.24	1.067
LI0575	Signal renition particle GTPase	11.8	11.9	0.06	1.013
LI0587	hypothetical protein LI0587	12.6	12.4	-0.22	1.054
LI0590	GMP synthase	11.5	11.4	-0.09	1.030
LI0591	IMP dehydrogenase/GMP reductase	11.8	11.8	-0.07	1.041
LI0596	peroxiredoxin	13.6	14.0	0.42	0.927
LI0606	transcriptional regulator	13.7	14.0	0.30	1.008
LI0612	TPR repeat-containing protein	11.9	11.4	-0.50	1.009
LI0613	DNA-directed RNA polymerase (sigma70/sigma32)	12.2	12.0	-0.20	1.068

LI0624	co-chaperonin GroES	15.7	16.1	0.47	0.847
LI0625	chaperonin GroEL	15.6	16.1	0.44	0.205
LI0627	UDP-3-O	12.1	12.5	0.32	1.094
LI0629	hypothetical protein LI0629	13.1	12.1	-0.96	0.930
LI0630	preprotein translocase subunit SecA	16.0	14.3	-1.74	0.641
LI0631	hydrogenase maturation factor	12.4	11.7	-0.75	0.814
LI0633	hypothetical protein LI0633	14.2	13.0	-1.25	0.785
LI0634	hypothetical protein LI0634	15.3	15.4	0.16	1.057
LI0635	coenzyme F390 synthetase	11.6	11.4	-0.27	1.062
LI0638	hypothetical protein LI0638	14.6	14.6	0.00	1.003
LI0641	flagellar motor switch/type III secretory pathway protein	14.1	12.7	-1.35	0.649
LI0649	hypothetical protein LI0649	12.5	13.0	0.51	0.768
LI0650	Zn-dependent peptidases, insulinase-like	12.7	13.0	0.26	1.060
LI0653	Zn-dependent protease with chaperone function	11.7	11.5	-0.21	1.053
LI0656	argininosuccinate synthase	11.3	11.4	0.03	1.007
LI0657	argininosuccinate lyase	12.2	12.2	-0.05	1.020
LI0658	tRNA(5-methylaminomethyl-2-thiouridylate) methyltransferase	12.5	11.7	-0.84	0.792
LI0660	bacterioferritin (cytochrome b1)	12.4	12.1	-0.31	1.062
LI0661	glucosamine 6-phosphate synthetase	11.8	11.5	-0.27	1.065
LI0665	hypothetical protein LI0665	12.6	11.8	-0.84	0.768
LI0670	S-adenosyl-L-homocysteine hydrolase	13.5	13.1	-0.40	1.049
LI0671	phosphoglycerate dehydrogenase	12.9	12.2	-0.68	1.022
LI0674	hypothetical protein LI0674	12.5	10.9	-1.58	0.621
LI0675	membrane protease subunits, stomatin/prohibitin	12.5	12.8	0.27	1.023
LI0676	membrane protease subunits, stomatin/prohibitin	12.5	12.0	-0.45	1.024
LI0677	hypothetical protein LI0677	13.5	13.4	-0.06	1.015
LI0685	chaperone protein DnaJ	12.2	12.1	-0.02	1.009
LI0686	leucyl aminopeptidase	11.7	11.8	0.13	1.067
LI0690	hypothetical protein LI0690	12.6	13.2	0.59	0.873
LI0691	Outer membrane protein	14.4	14.4	0.02	1.008
LI0692	periplasmic component of the Tol biopolymer	13.5	12.6	-0.92	0.798
LI0693	colicin uptake membrane protein	11.8	11.1	-0.67	1.026
LI0694	biopolymer transport protein	12.4	12.0	-0.35	1.101

LI0695	biopolymer transport proteins	12.7	12.4	-0.27	1.069
LI0696	rubrerythrin	14.6	15.3	0.71	0.584
LI0697	rubredoxin 2 (Rd-2)	16.6	17.3	0.71	0.794
LI0700	TPR repeat-containing protein	13.9	13.1	-0.81	0.643
LI0701	nuclease subunit of the excinuclease complex	11.8	10.8	-1.02	0.829
LI0706	hypothetical protein LI0706	12.2	11.4	-0.83	0.852
LI0710	flagellin-like protein	11.9	11.7	-0.14	1.049
LI0712	dihydroorotate dehydrogenase	12.2	11.8	-0.46	1.061
LI0726	S-adenosylmethionine synthetase	12.0	12.2	0.15	1.059
LI0728	ribosomal protein S1	12.6	12.2	-0.32	1.016
LI0729	chemotaxis signal transduction protein	14.9	15.0	0.10	1.024
LI0740	flagellar basal body rod protein	12.0	11.8	-0.21	1.087
LI0755	30S ribosomal protein S1	12.0	12.1	0.04	1.028
LI0761	HD-superfamily hydrolase	12.3	12.1	-0.26	1.101
LI0763	fructose/tagatose bisphosphate aldolase	13.3	12.3	-0.99	0.696
LI0764	glyceraldehyde-3-phosphate dehydrogenase	11.5	11.4	-0.16	1.069
LI0773	Kef-type K <sup>+</sup> transport systems, membrane components	11.7	11.8	0.14	1.052
LI0783	hypothetical protein LI0783	12.9	12.9	-0.08	1.019
LI0784	Type IIA topoisomerase, A subunit	12.6	12.4	-0.23	1.074
LI0785	Type IIA topoisomerase, B subunit	12.4	11.7	-0.76	0.978
LI0786	DNA polymerase sliding clamp subunit (PCNA homolog)	11.5	11.4	-0.10	1.040
LI0790	2-ketoisovalerate ferredoxin reductase	12.4	12.2	-0.23	1.076
LI0791	ferredoxin oxidoreductases, beta subunit	13.9	13.9	0.06	1.016
LI0792	ferredoxin oxidoreductases, gamma subunit	12.5	11.8	-0.70	1.001
LI0793	FKBP-type peptidyl-prolyl cis-trans isomerase	11.7	11.6	-0.10	1.050
LI0795	ATP-dependent protease ATP-binding subunit ClpX	12.7	12.7	0.08	1.059
LI0796	ATP-dependent protease	12.0	11.9	-0.15	1.071
LI0798	hypothetical protein LI0798	13.4	12.7	-0.66	1.029
LI0800	hypothetical protein LI0800	12.8	11.7	-1.09	0.753
LI0807	naphthoate synthase	12.3	12.3	-0.01	1.006
LI0808	hydrolase, haloacid dehalogenase-like hydrolase	13.7	12.8	-0.92	0.804
LI0809	hypothetical protein LI0809	13.2	14.0	0.85	0.761
LI0810	integral membrane protein, interacts with FtsH	13.1	13.7	0.62	0.793
LI0814	chromosome partitioning ATPase	13.2	12.2	-1.01	0.845

LI0815	transcriptional regulator	11.6	11.7	0.09	1.035
LI0838	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	11.5	10.8	-0.72	1.042
LI0841	invasin	15.2	14.9	-0.31	0.999
LI0845	hypothetical protein LI0845	12.1	11.4	-0.72	0.811
LI0846	lipopolysaccharide core biosynthesis protein RfaG	11.5	11.8	0.27	1.087
LI0857	flagellar biosynthesis/type III secretory pathway lipoprotein	12.6	11.3	-1.24	0.840
LI0859	flagellar basal body rod protein	12.5	11.9	-0.62	1.023
LI0860	flagellar basal body rod protein FlgB	13.2	12.6	-0.57	0.987
LI0879	glucose-6-phosphate isomerase	11.8	12.3	0.42	1.041
LI0887	hypothetical protein LI0887	12.7	11.8	-0.87	0.951
LI0894	nucleoid DNA-binding protein	13.4	13.8	0.46	1.057
LI0896	dihydrodipicolinate synthase	12.7	12.0	-0.76	0.845
LI0902	outer membrane protein	14.4	14.4	0.01	1.008
LI0904	DNA-directed RNA polymerase, beta subunit	13.2	13.3	0.07	1.056
LI0905	DNA-directed RNA polymerase subunit beta	14.2	14.4	0.22	0.908
LI0906	glutamate-1-semialdehyde aminotransferase	12.7	11.9	-0.81	1.013
LI0907	transcriptional regulators	12.2	12.2	0.02	1.007
LI0912	molecular chaperone DnaK	12.8	13.4	0.55	0.803
LI0914	D-alanyl-D-alanine carboxypeptidase	11.8	10.8	-0.95	0.848
LI0920	membrane proteins related to metalloendopeptidases	12.9	13.5	0.57	0.858
LI0921	phosphoribosylamine--glycine ligase	12.4	11.0	-1.39	0.791
LI0930	50S ribosomal protein L7/L12	14.2	14.3	0.11	1.047
LI0931	50S ribosomal protein L10	13.3	13.2	-0.11	1.060
LI0932	50S ribosomal protein L1	12.5	13.2	0.71	0.789
LI0933	50S ribosomal protein L11	13.6	13.1	-0.52	0.934
LI0934	transcription antiterminator	13.8	13.7	-0.06	1.033
LI0935	elongation factor Tu	14.4	14.5	0.14	1.089
LI0936	Zn-dependent peptidase	13.2	12.8	-0.36	1.061
LI0937	thiamine biosynthesis protein ThiC	12.2	12.2	-0.05	1.012
LI0939	carbamoylphosphate synthase large subunit	11.2	10.9	-0.30	1.060
LI0941	Mg <sup>2+</sup> /Co <sup>2+</sup> transporter	13.3	13.3	-0.07	1.034
LI0942	30S ribosomal protein S12	13.6	13.5	-0.10	1.050
LI0943	30S ribosomal protein S7	12.6	12.3	-0.32	1.063
LI0944	elongation factor G	12.9	12.9	-0.01	1.006

LI0945	dienelactone hydrolase	13.2	13.0	-0.22	1.050
LI0948	glycosyltransferase	16.4	15.6	-0.76	1.005
LI0949	hypothetical protein LI0949	13.2	13.4	0.19	1.056
LI0959	30S ribosomal protein S10	14.1	14.1	0.02	1.006
LI0960	50S ribosomal protein L3	12.7	12.8	0.07	1.033
LI0961	50S ribosomal protein L4	14.1	14.8	0.74	0.999
LI0963	50S ribosomal protein L2	13.2	13.1	-0.12	1.063
LI0965	50S ribosomal protein L22	13.6	13.6	0.00	0.998
LI0966	30S ribosomal protein S3	12.4	13.2	0.74	0.688
LI0967	50S ribosomal protein L16	14.3	14.1	-0.24	1.051
LI0969	50S ribosomal protein L14	13.9	14.0	0.06	1.037
LI0970	50S ribosomal protein L24	14.3	13.5	-0.78	0.754
LI0971	50S ribosomal protein L5	12.4	13.0	0.57	0.984
LI0972	30S ribosomal protein S8	13.5	13.7	0.24	1.111
LI0973	50S ribosomal protein L6	12.8	13.0	0.19	1.083
LI0975	30S ribosomal protein S5	13.7	13.6	-0.17	1.059
LI0976	50S ribosomal protein L15	13.1	12.7	-0.48	1.060
LI0977	preprotein translocase subunit SecY	12.5	12.6	0.12	1.045
LI0978	methionine aminopeptidase	13.0	13.1	0.11	1.050
LI0979	30S ribosomal protein S13	14.2	13.8	-0.35	1.021
LI0980	30S ribosomal protein S11	14.0	14.6	0.64	0.792
LI0981	30S ribosomal protein S4	13.5	13.5	-0.06	1.036
LI0982	DNA-directed RNA polymerase subunit alpha	13.0	13.0	0.05	1.027
LI0983	ribosomal protein L17	14.1	14.2	0.09	1.047
LI0985	Na <sup>+</sup> /H <sup>+</sup> antiporter	11.9	11.9	0.02	1.006
LI0987	aspartyl-tRNA synthetase	11.7	11.4	-0.26	1.057
LI0994	acriflavin resistance protein D	11.7	10.8	-0.86	0.968
LI0998	orotate phosphoribosyltransferase	12.6	12.0	-0.63	1.024
LI0999	hypothetical protein LI0999	13.0	13.0	-0.03	1.003
LI1000	hypothetical protein LI1000	12.8	12.4	-0.43	1.023
LI1002	chain A, cytochrome C nitrite reductase	12.5	11.0	-1.54	0.201
LI1005	pseudouridine synthase	12.9	13.5	0.52	0.802
LI1006	polynucleotide phosphorylase	11.7	11.8	0.11	1.041
LI1013	major facilitator superfamily permease	14.3	12.3	-1.94	0.307



LI1015	phosphoglyceromutase	12.2	12.3	0.08	1.023
LI1016	hypothetical protein LI1016	13.9	13.2	-0.75	0.837
LI1017	hypothetical protein LI1017	13.8	12.8	-0.99	0.619
LI1019	UDP-N-acetylglucosamine acyltransferase	12.1	12.0	-0.13	1.054
LI1021	UDP-3-O	12.1	11.7	-0.48	1.007
LI1022	Outer membrane protein	12.8	12.9	0.15	1.068
LI1024	Outer membrane protein/protective antigen OMA87	11.8	11.8	0.02	1.006
LI1027	lysyl-tRNA synthetase (class II)	12.0	11.0	-1.05	0.779
LI1032	hypothetical protein LI1032	13.5	13.7	0.20	1.092
LI1034	hypothetical protein LI1034	12.1	11.2	-0.96	0.588
LI1043	lactate dehydrogenase and related dehydrogenases	13.1	13.0	-0.09	1.046
LI1053	hypothetical protein LI1053	12.4	12.4	0.00	1.006
LI1057	F0F1-type ATP synthase, subunit a	11.8	11.7	-0.05	1.014
LI1058	F0F1-type ATP synthase, subunit c	16.2	14.7	-1.50	0.614
LI1059	redox-sensing transcriptional repressor Rex	12.4	12.7	0.26	1.059
LI1060	flagellar biosynthesis chaperone	12.3	11.9	-0.41	1.074
LI1064	Fe-S-cluster-containing hydrogenase components 1	12.4	13.5	1.13	0.700
LI1070	preprotein translocase subunit YidC	11.3	11.9	0.61	1.038
LI1073	ribonuclease D	13.7	11.9	-1.83	0.626
LI1075	dioxygenases related to 2-nitropropane dioxygenase	13.3	13.7	0.45	0.851
LI1080	hypothetical protein LI1080	12.8	12.9	0.05	1.009
LI1082	Fe <sup>2+</sup> transport system protein A	14.4	14.4	0.05	1.029
LI1083	Fe <sup>2+</sup> transport system protein B	11.9	12.2	0.28	1.064
LI1092	response regulator	12.7	11.5	-1.18	0.760
LI1095	pyruvate kinase	11.9	12.0	0.10	1.051
LI1108	cell division protein FtsA	12.2	12.4	0.20	1.083
LI1109	cell division protein FtsZ	12.7	12.9	0.15	1.058
LI1114	parvulin-like peptidyl-prolyl isomerase	11.7	11.6	-0.16	1.063
LI1116	hydroxylamine reductase	12.9	12.9	0.00	1.008
LI1117	chemotaxis signal transduction protein	11.6	10.7	-0.85	0.994
LI1119	glyceraldehyde-3-phosphate dehydrogenase	13.5	13.2	-0.34	1.028
LI1121	nucleoside-diphosphate kinase	13.1	12.9	-0.21	1.053
LI1123	periplasmic protease	12.5	12.1	-0.44	1.011
LI1155	hypothetical protein LI1155	12.4	12.5	0.10	1.039

LI1156	hypothetical protein LI1156	13.2	12.4	-0.72	0.836
LI1157	regulatory protein PcrH	13.6	12.8	-0.83	0.735
LI1158	hypothetical protein LI1158	13.5	12.3	-1.23	0.788
LI1159	hypothetical protein LI1159	14.3	13.7	-0.62	0.808
LI1161	hypothetical protein LI1161	12.6	11.8	-0.81	1.014
LI1166	translocation protein in type III secretion	11.3	10.9	-0.16	1.065
LI1170	chemotaxis signal transduction protein	13.1	12.8	-0.28	1.054
LI1171	5'-nucleotidase	13.4	13.5	0.12	1.047
LI1182	recombinase A	11.5	12.0	0.48	1.022
LIB001	hypothetical protein LIB001	15.3	15.2	-0.04	1.009
LIB004	Asn/Thr/Ser/Val rich protein	11.7	11.5	-0.22	1.057
LIC004	dTDP-6-deoxy-D-glucose-3,5-epimerase	12.4	11.6	-0.76	0.918
LIC014	UDP-glucose 6-dehydrogenase	12.4	11.5	-0.97	0.834
LIC041	hypothetical protein LIC040	13.0	12.4	-0.60	1.028
LIC053	hypothetical protein LIC053	12.0	11.3	-0.75	0.835
LIC059	hypothetical protein LIC059	11.3	11.6	0.24	1.071
LIC060	hypothetical protein LIC060	12.2	11.8	-0.39	1.048
LIC097	WblB protein	13.2	12.4	-0.83	0.980
LIC099	hypothetical protein LIC099	12.3	11.7	-0.57	1.041
LIC102	putative cytochrome C peroxidase	12.7	11.7	-1.01	0.763
LIC103	methyl-accepting chemotaxis protein	12.0	11.5	-0.56	0.826

\* Adjusted *p*-value for multiple comparisons using false discovery rate (FDR) - Benjamini-Hochberg correction