



Figure S1. Representative mass spectra of *E. coli* ATCC25922-R lipid A extracted by the method discussed above using Negative ion MALDI-TOF. Lipid A from colistin-resistant *E. coli* ATCC25922-R is modified by pETN and L-Ara4N which are detected as additional peaks at  $m/z$ 1914.5,  $m/z$  1934.4 and  $m/z$  2164.5.

**Supplementary Table S1. RT-PCR primers used in this study.**

<b>Primers</b>	<b>Sequences</b>	<b>Product</b>	<b>Source</b>
<i>pmrB</i> -F	CCTTTTGCCTGGAAGAGT	158 bp	Luo et al., 2019
<i>pmrB</i> -R	TCTTTGGGCGTCAGAATCAAC		
<i>relA</i> -F	ATGCCAACGTAGTCAGCGAA	166 bp	This study
<i>relA</i> -R	GCCAATAACATCCGGCGAAC		
<i>evgS</i> -F	TTAACACTCCGGGAATACGC	152 bp	This study
<i>evgS</i> -R	GCGCCGGAAAGGTAATTATC		
<i>evgA</i> -F	CTTGCTATCGCAGCAATTCGT	156 bp	This study
<i>evgA</i> -R	CTGGATACCGTTAACTCCGG		

Supplementary Table S2. The different expression of genes in sample B vs. sample A through transcriptome

GeneID	Annotation	length	B_25992-	B_25992-	B_25992-	A_25992	A_25992	A_25992	logCPM	log2Ratio(B/A)	Up-Down-Regulation	P-value	FDR
			_1_reads	_2_reads	_3_reads	_1_reads	_2_reads	_3_reads					
		Count	Count	Count	Count	Count	Count	Count					
D1792_03865	cold-shock protein CspB	216	0	0	0	16	11	6	0.1507137	-6.660978502	down	4.10E-07	6.02E-05
D1792_01810	regulatory protein AriR	267	0	0	0	10	4	13	0.0049062	-6.555259071	down	5.83E-06	0.000501
D1792_27505	hypothetical protein	324	0	1.33	0	14	29.67	21	1.030965	-5.685092327	down	3.66E-09	1.39E-06
D1792_27680	hypothetical protein	324	0	1.33	0	14	29.67	21	1.030965	-5.685080415	down	3.64E-09	1.39E-06
D1792_27330	hypothetical protein	324	0	1.33	0	14	29.67	21	1.030965	-5.685051395	down	3.58E-09	1.39E-06
D1792_03840	cold-shock protein CspI	213	0	1	0	5	10	11	-0.0130668	-4.720505765	down	4.20E-05	0.00222
D1792_00865	multiple stress resistance protein	258	14	10	18	166	256	258	4.4283933	-4.496639934	down	3.09E-15	7.03E-12
D1792_12355	protein GlcG	405	228	311	302	2062	5230	5486	8.7108938	-4.462864671	down	7.95E-15	1.21E-11
D1792_27500	hypothetical protein	246	1	3	0	23.5	17.5	23	1.0714848	-4.369175762	down	6.31E-08	1.10E-05
D1792_27685	hypothetical protein	246	1	3	0	23.5	17.5	23	1.0714848	-4.369155817	down	6.27E-08	1.10E-05
tnaA	tryptophanase	1416	19560	28861	35792	127180	334270	353336	14.746872	-3.78579198	down	5.93E-10	3.00E-07
D1792_15610	cold-shock protein	213	16	27	21	131	269	214	4.2992657	-3.734137124	down	5.81E-12	6.62E-09
D1792_11760	MarR family transcriptional regulator	552	16.64	238.9	22.06	454.64	962.5	916.54	6.2710756	-3.652801412	down	7.31E-06	0.000584
D1792_01505	hypothetical protein	558	16	81	1	246	317	244	4.6651663	-3.57355106	down	1.74E-05	0.001134
glcB	malate synthase	2172	4130	4225	3283	18542	35641	38394	11.609078	-3.556757764	down	1.26E-11	1.10E-08
D1792_24740	succinyl-CoA ligase subunit alpha	870	2769	4156	4552	13212	32551	35914	11.466511	-3.359325595	down	1.02E-08	2.72E-06
D1792_24735	succinyl-CoA ligase subunit beta	1167	3694	5687	5910	13651	44955	47922	11.860376	-3.341445638	down	5.95E-08	1.10E-05
D1792_00130	hypothetical protein	459	0.5	4.5	0	25	9	6.5	0.4929614	-3.274863744	down	0.0001556	0.005963
D1792_26560	hypothetical protein	459	0.5	4.5	0	25	9	6.5	0.4929614	-3.274862263	down	0.0001562	0.005963
D1792_12370	glycolate oxidase	1500	1991	2458	1577	8327	13632	14791	10.299841	-3.167017587	down	2.02E-10	1.15E-07
D1792_11780	fimbrial protein dihydrolypoyllysine-residue	528	22	38	3	66	129	146	3.5698931	-3.076139233	down	1.64E-05	0.00111
D1792_24730	succinyltransferase component of 2-oxoglutarate dehydrogenase complex	1218	5983	9904	10698	29290	60492	66030	12.413649	-3.061186287	down	6.00E-08	1.10E-05
D1792_05400	DNA polymerase III subunit theta	231	8	3	6	13	48	36	1.7530565	-2.990438963	down	2.39E-05	0.00138
D1792_16520	low affinity tryptophan permease	1248	2308	2534	2834	7402	17040	17674	10.531273	-2.984997077	down	3.13E-08	6.78E-06
D1792_13860	acetyl-CoA carboxylase	189	1	2	3	12	12	12	0.453314	-2.931250618	down	0.0001571	0.005963
D1792_06480	colibactin biosynthesis phosphopantetheinyl transferase ClbA	735	4	32	20	114	48	135	3.4043755	-2.930117724	down	9.89E-05	0.004288
D1792_03830	hypothetical protein	273	2	0	4	6	7	19	0.4014804	-2.918806684	down	0.0015672	0.0305
D1792_04090	multidrug transporter subunit MdtJ	366	101	124	167	275	948	860	6.1958035	-2.907345304	down	8.61E-08	1.45E-05
D1792_24720	succinate dehydrogenase iron-sulfur subunit	717	1990	2980	3147	7957	14962	15489	10.413148	-2.742794998	down	1.82E-07	2.86E-05
D1792_24245	cold-shock protein CspE	210	412	877	849	2576	3970	3754	8.4824279	-2.724251886	down	3.81E-08	7.88E-06
D1792_12360	glycolate oxidase iron-sulfur subunit	1224	1466	1821	1053	4361	6986	6956	9.3392855	-2.623629572	down	1.36E-08	3.26E-06
oppA	oligooetide transporter subunit	1632	6848	9643	12780	25089	47453	54447	12.176787	-2.61975629	down	2.50E-06	0.000271
D1792_11810	type 1 fimbrial protein	567	456	731	612	992	3420	3168	8.1036511	-2.607845007	down	1.32E-06	0.000162
D1792_24725	2-oxoglutarate dehydrogenase subunit E1	2802	9924	13856	15148	27990	62830	72249	12.552501	-2.60193248	down	3.26E-06	0.000319
D1792_11825	hypothetical protein	288	0	8	7	7	32	28	1.326238	-2.601475328	down	0.0022469	0.039205
marB	hypothetical protein	219	1	3	3	11	16	7	0.3875292	-2.569349068	down	0.0008943	0.022013
D1792_27750	GNAT family N-acetyltransferase	1770	181	386	42.5	496	877.5	873.5	6.338345	-2.497253424	down	1.96E-05	0.001221
D1792_27435	hypothetical protein	1770	181	386	42.5	496	877.5	873.5	6.338345	-2.497253077	down	1.96E-05	0.001221
D1792_27745	class I SAM-dependent methyltransferase	804	19.5	92	33	112	249	211	4.347658	-2.495486177	down	5.34E-05	0.002641
D1792_27440	class I SAM-dependent methyltransferase	804	19.5	92	33	112	249	211	4.347658	-2.495485206	down	5.32E-05	0.002641
glcE	glycolate oxidase FAD binding	1053	1392	1565	850	3369	5223	5421	8.9861602	-2.444458201	down	9.04E-08	1.47E-05

D1792_26150	trifunctional transcriptional regulator/proline dehydrogenase/L-glutamate gamma-semialdehyde dehydrogenase	3963	7637	10585	8519	18732	39300	39400	11.80711	-2.39834326	down	2.79E-06	0.000295
D1792_01500	DUF1828 domain-containing protein	753	148	353	101	474	728	861	6.2588029	-2.369855743	down	1.89E-06	0.000221
D1792_25425	arginine/ornithine ABC transporter substrate-binding protein	732	434	352	341	1121	1604	1401	7.1927941	-2.365779225	down	1.45E-11	1.10E-08
D1792_02760	2-Cys peroxiredoxin	507	1521	2500	3145	6610	9261	10374	9.9149203	-2.342407206	down	6.56E-06	0.000537
D1792_06980	glycosyltransferase family 2 protein	861	27	131	16	131	229	226	4.4224023	-2.329794031	down	0.0006134	0.016629
D1792_24695	hypothetical protein	186	74	102	124	157	445	452	5.3071886	-2.325671303	down	1.84E-05	0.00118
D1792_25530	cold-shock protein CspD	225	49	123	71	92	326	373	4.9331076	-2.287849884	down	0.000191	0.006674
D1792_24715	succinate dehydrogenase flavoprotein subunit	1767	6107	9321	9591	16046	32892	34902	11.623824	-2.257847242	down	2.20E-05	0.001321
D1792_13770	DUF1471 domain-containing protein	264	23	29	20	64	107	77	3.1430304	-2.241377626	down	5.98E-06	0.000504
D1792_24700	hypothetical protein	240	22	53	34	79	144	140	3.7483694	-2.236830106	down	6.74E-05	0.003101
D1792_04160	fumarate hydratase class I%2C	1647	6501	9305	11458	14682	35232	38280	11.721019	-2.207856692	down	8.13E-05	0.003558
D1792_05890	multidrug SMR transporter	333	5	5	11	21	18	31	1.461303	-2.206525103	down	0.0013659	0.02802
D1792_24690	type II citrate synthase	1284	8301	12197	16011	21008	44259	51462	12.134408	-2.188320989	down	0.0001009	0.004335
D1792_20880	30S ribosomal protein S20	264	35	42	30	124	111	115	3.6583156	-2.183734471	down	2.34E-06	0.000259
D1792_25170	amino acid ABC transporter substrate-binding protein	747	2564	3574	3982	5897	13205	13173	10.25409	-2.177086629	down	3.59E-05	0.001993
phoH	conserved protein with nucleoside triphosphate hydrolase domain	924	2169	3701	3556	7232	11621	11354	10.133261	-2.158328413	down	1.24E-05	0.000885
D1792_05250	hypothetical protein	210	17	11	2	13	45	32	1.7683317	-2.149883129	down	0.0016607	0.031512
D1792_13760	malate dehydrogenase	939	6032	9749	10587	16003	32025	33777	11.607444	-2.134925344	down	6.55E-05	0.003045
D1792_06960	glycosyltransferase	1206	10	35	14	56	34	82	2.7587856	-2.129115557	down	0.0015125	0.02969
D1792_08745	DNA-binding response regulator	615	192	243	210	545	786	691	6.2083269	-2.12329026	down	1.87E-08	4.26E-06
D1792_05655	flagellar transcriptional activator FlhD	351	225	245	416	526	1134	1117	6.7202035	-2.11912139	down	1.23E-05	0.000885
D1792_23380	cytochrome bo(3) ubiquinol oxidase subunit 3	615	1257	1418	1745	2692	5151	5599	9.0078412	-2.118800412	down	2.29E-05	0.001352
ygeW	hypothetical protein	1191	2026	2042	2426	3777	7568	8045	9.5382307	-2.10260788	down	2.65E-05	0.001508
D1792_24375	glutamate/aspartate ABC transporter substrate-binding protein	909	2810	3811	4120	7819	11526	12749	10.25417	-2.077434952	down	2.34E-05	0.001367
D1792_25370	DUF1418 family protein	288	67	66	42	93	208	198	4.2467908	-2.071500663	down	5.13E-05	0.002597
D1792_23375	cytochrome o ubiquinol oxidase subunit IV	330	138	128	154	244	479	499	5.5508444	-2.062439449	down	9.28E-06	0.000716
D1792_00210	MarR family transcriptional regulator	552	9.36	67.1	13.94	64.36	98.5	97.46	3.2959959	-2.057698575	down	0.0029087	0.047608
D1792_01920	hypothetical protein	294	116	123	153	278	427	446	5.4499972	-2.044667827	down	4.95E-06	0.000433
D1792_21430	aconitate hydratase B	2598	18168	29484	32919	51244	86170	97536	13.148363	-2.04401684	down	0.0001096	0.004579
D1792_11815	major pilus subunit operon regulatory protein PapB	315	31	31	25	53	86	97	3.1971941	-1.982435091	down	0.000205	0.006914
D1792_20275	ClbS/DfsB family four-helix bundle protein	519	27	64.5	17.5	73.5	95	119	3.4835831	-1.97813678	down	0.0007278	0.019049
D1792_06840	hypothetical protein	519	27	64.5	17.5	73.5	95	119	3.4835831	-1.978130535	down	0.0007256	0.019049
D1792_25300	biofilm regulator BssR	384	176	232	127	293	542	578	5.7790295	-1.970758497	down	8.45E-06	0.000664
D1792_22835	transcriptional regulator	588	1708	2706	2609	4504	7282	7672	9.5514606	-1.968217991	down	5.54E-05	0.002686
D1792_12935	30S ribosomal protein S21	216	110	289	359	713	756	732	6.3599691	-1.931093588	down	4.85E-05	0.002482
D1792_15995	50S ribosomal protein L28	237	34	63	26	77	117	126	3.6329708	-1.928315502	down	0.0003336	0.010698
D1792_01470	lambda prophage-derived protein ea10	369	54	73	56	96	196	189	4.2225483	-1.916688922	down	0.0001637	0.006112
D1792_20075	DNA cytosine methyltransferase	1191	74	174	50	177	302	285	4.8742141	-1.910064524	down	0.0001832	0.006568
D1792_10280	mRNA interferase HigB	312	29	22	18	45	59	72	2.792575	-1.901461053	down	0.0004173	0.012475
D1792_05055	DUF1315 family protein	273	43	83	133	104	307	291	4.7912847	-1.893709145	down	0.0018933	0.034498
D1792_16695	asparagine synthetase A	993	2058	2667	1980	2983	6717	7163	9.3874794	-1.892677803	down	0.0001487	0.00589

acnA	aconitate hydratase	2676	3794	4084	3735	6621	11849	11561	10.185862	-1.890807231	down	5.67E-05	0.002707
D1792_12250	nucleotidyl transferase AbiEii/AbiGii	918	315	447	298	640	1067	1026	6.7197493	-1.887911603	down	1.46E-06	0.000175
D1792_23370	toxin family protein	891	1318	1636	1472	2340	4264	4639	8.7943252	-1.880717622	down	6.84E-05	0.003115
cedA	protoheme IX farnesyltransferase	264	29	51	62	70	150	153	3.8793971	-1.874321207	down	0.0013323	0.027704
nanR	cell division modulator	735	186	284	193	338	749	618	6.0330963	-1.86710845	down	1.16E-05	0.000851
D1792_23390	putative transcriptional regulator	948	5595	8202	10938	13658	22587	27147	11.308024	-1.856531297	down	0.0005408	0.015298
D1792_24705	cytochrome ubiquinol oxidase subunit II	390	344	453	550	800	1275	1374	7.0844059	-1.845539312	down	1.66E-05	0.00111
D1792_05720	succinate dehydrogenase cytochrome b556 subunit	498	707	1110	892	1664	2496	2659	8.0608928	-1.843766827	down	2.20E-05	0.001321
D1792_01365	non-heme ferritin	1251	15318	24545	29668	30843	68564	74348	12.769879	-1.825432901	down	0.0009596	0.022916
D1792_23385	NADP-dependent isocitrate dehydrogenase	1992	6929	9326	10835	13446	25837	27834	11.388118	-1.815973137	down	0.0004625	0.013415
D1792_01485	cytochrome ubiquinol oxidase subunit I	582	53	47	19	51	140	97	3.4639167	-1.815969986	down	0.0008479	0.021273
D1792_16660	superinfection exclusion protein B	240	33	67	75	108	192	157	4.1324277	-1.810564095	down	0.0006635	0.017878
D1792_10070	ATP synthase subunit C	1203	1345	1072	1046	3118	2623	2862	8.3537715	-1.79993163	down	3.29E-06	0.000319
D1792_01520	glycine betaine/L-proline ABC transporter ATP-binding protein	297	42	34	27	53	98	95	3.2798649	-1.794049151	down	0.0005339	0.015197
flhC	hypothetical protein	579	611	552	626	1038	1681	1645	7.4177953	-1.789913754	down	3.22E-06	0.000319
D1792_02800	DNA binding transcriptional dual regulator	258	160	336	292	483	715	740	6.2529831	-1.779667239	down	5.77E-05	0.002707
ihfB	DUF2534 family protein	285	57	63	31	77	149	130	3.797564	-1.778593713	down	0.0003992	0.012273
D1792_25680	integration host factor subunit beta	1674	6047	8361	10409	11270	22370	25698	11.236001	-1.771555787	down	0.0009611	0.022916
D1792_22825	30S ribosomal protein S1	1671	5097	6863	6793	9048	16982	17776	10.782125	-1.739564858	down	0.0004881	0.014068
proX	oxygen-dependent choline dehydrogenase	993	1339	1313	1171	2291	3113	3371	8.446002	-1.726040552	down	4.24E-05	0.00222
D1792_17945	glycine betaine transporter subunit Si-specific NAD(P)(+)	1401	5545	7925	8981	11898	19017	21310	11.042358	-1.717696682	down	0.0006723	0.018009
D1792_07715	transhydrogenase bifunctional murein DD-endopeptidase/murein LD-carboxypeptidase	567	383	286	375	839	862	800	6.5813092	-1.711510464	down	8.32E-07	0.000111
D1792_07350	type I fimbrial protein	543	204	377	164	297	591	719	6.0538762	-1.711448763	down	0.0004016	0.012273
D1792_26370	acyl carrier protein	252	24	14	6	45	45	19	2.006886	-1.707324863	down	0.0013604	0.02802
lpdA	dihydroliipoamide dehydrogenase	1424	11849	17211	18856	20885	42030	46344	12.124419	-1.705684176	down	0.0011878	0.025561
D1792_22830	betaine-aldehyde dehydrogenase	1473	5137	7699	7807	11044	17630	18662	10.894346	-1.693510271	down	0.0005757	0.015889
D1792_24115	carbon starvation protein	2106	4586	6610	6050	7592	15174	15681	10.610304	-1.677611811	down	0.0008324	0.021061
D1792_11105	PLP-dependent lyase/thiolase	1197	2092	2518	2316	3316	5784	6163	9.2759026	-1.667995938	down	0.0003708	0.011726
D1792_04085	spermidine export protein MdtI	330	87	77	43	108	141	183	4.1498695	-1.657873113	down	0.0008698	0.021528
msrB	methionine sulfoxide reductase B	414	423	475	497	559	1292	1220	6.9611645	-1.652665745	down	0.0001213	0.004978
dnaK	molecular chaperone	1917	7326	8960	9889	10220	23466	23449	11.193027	-1.641390567	down	0.0014521	0.029131
D1792_27430	LD-carboxypeptidase	1035	29	75	29	122	98	85	3.5389161	-1.63684962	down	0.0010592	0.024118
D1792_11110	YgeY family selenium metabolism-linked hydrolase	1212	2138	2010	2515	3511	5313	5687	9.2024552	-1.62658364	down	0.0004143	0.012475
D1792_09940	RnfH family protein	291	84	70	75	92	231	174	4.3074959	-1.606443275	down	0.0010392	0.023915
D1792_01975	alanine racemase catabolic	1071	1439	1928	1791	2508	4270	4271	8.8103943	-1.604168737	down	0.0004347	0.012853
D1792_01460	host cell division inhibitory peptide	270	50	77	43	78	136	140	3.8568872	-1.598621702	down	0.0017851	0.033453
D1792_09265	peroxiredoxin	471	390	423	491	940	917	1003	6.8297686	-1.596344203	down	1.15E-05	0.000851
ygfK	predicted oxidoreductase	3099	6158	6532	6225	9131	14753	15679	10.662168	-1.591299856	down	0.0006929	0.018454
D1792_01970	D-amino acid dehydrogenase small subunit	1299	2551	3625	3317	4077	8114	7780	9.6736663	-1.579038248	down	0.0010743	0.024142
D1792_08985	phosphocarrier protein HPr	258	53	89	76	97	189	176	4.235044	-1.574714424	down	0.0020419	0.036324

D1792_10985	RNA pyrophosphohydrolase	531	1067	1445	1327	1391	3270	3226	8.3540358	-1.564360911	down	0.0011899	0.025561
D1792_01490	antitermination protein N	273	40	51	54	83	115	112	3.6482105	-1.563806491	down	0.0016303	0.031193
D1792_24710	succinate dehydrogenase hydrophobic membrane anchor subunit	348	161	253	150	264	522	400	5.5590215	-1.563498471	down	0.0001885	0.006674
D1792_22555	sigma factor-binding protein Crl	402	1178	1815	1729	2204	3676	3892	8.6559976	-1.553481514	down	0.0009288	0.02262
D1792_00770	acyl carrier protein	237	155	362	313	359	727	665	6.1603176	-1.552759603	down	0.0009759	0.023027
D1792_00820	DUF1425 domain-containing protein	378	95	116	106	169	254	240	4.7445644	-1.551714405	down	0.0004191	0.012475
D1792_24550	transcriptional repressor	447	734	947	1074	1320	2092	2290	7.8824837	-1.549593824	down	0.0003463	0.01103
D1792_09435	nucleoside-diphosphate kinase	432	231	225	247	532	479	486	5.8867048	-1.542794618	down	1.74E-05	0.001134
D1792_05140	diguanylate cyclase	1026	988	829	824	1145	2149	2029	7.7691434	-1.537398178	down	0.0001034	0.0044
D1792_00765	beta-ketoacyl-ACP reductase	735	1511	1894	2103	2014	4538	4624	8.8679751	-1.536426861	down	0.00199	0.035679
D1792_21440	S-adenosylmethionine decarboxylase proenzyme	795	810	513	675	926	1367	1623	7.3588488	-1.519143886	down	0.000174	0.00634
D1792_20780	bifunctional aspartate kinase/homoserine dehydrogenase I	2463	5026	4527	4205	6058	10429	10668	10.134748	-1.519074967	down	0.0010002	0.023479
D1792_05430	DNA damage-inducible protein YebG	291	226	357	382	355	761	816	6.3485506	-1.512985645	down	0.0014243	0.028957
D1792_26770	type II toxin-antitoxin system RelE/ParE family toxin	348	210.5	186.5	251.5	230.5	548	522.5	5.7609491	-1.512575072	down	0.0011531	0.025239
D1792_27125	type II toxin-antitoxin system RelE/ParE family toxin	348	210.5	186.5	251.5	230.5	548	522.5	5.7609491	-1.512574969	down	0.0011525	0.025239
D1792_23875	peptidylprolyl isomerase B	495	589	635	634	861	1474	1391	7.2561286	-1.504121233	down	7.46E-05	0.003362
D1792_23685	transcriptional regulator	342	51	79	44	87	136	124	3.8225209	-1.503264308	down	0.0018469	0.034053
D1792_02365	YciI family protein	297	98	67	89	149	216	161	4.380025	-1.493490413	down	0.0005524	0.015471
oppC	oligopeptide transport subunit	909	948	724	721	1178	1825	1706	7.5869669	-1.492654298	down	3.98E-05	0.002159
D1792_19815	hypothetical protein	825	277	538	383	393	913	998	6.6172764	-1.492131678	down	0.0017605	0.033266
D1792_09845	bifunctional chorismate mutase/prephenate dehydratase	1161	2095	1629	1917	2508	4298	4242	8.8377697	-1.487701438	down	0.0008502	0.021273
D1792_01510	LexA family transcriptional regulator	696	622	725	689	815	1718	1488	7.3702562	-1.479407393	down	0.000192	0.006674
D1792_16655	ATP synthase subunit B	471	771	1101	1063	1084	2279	2331	7.9075768	-1.473384465	down	0.0011583	0.025239
D1792_12245	S-adenosylhomocysteine hydrolase	396	456	641	724	595	1621	1398	7.2332618	-1.472486288	down	0.0013092	0.027491
D1792_25585	leucine-responsive regulatory protein	495	594	600	735	880	1453	1464	7.3023889	-1.471847484	down	0.0002161	0.007235
D1792_02295	DNA-binding protein H-NS	414	2245	3850	4119	6065	6930	7474	9.7173047	-1.459639703	down	0.0019761	0.03557
yobA	hypothetical protein	375	363	612	620	587	1378	1188	7.0312901	-1.458012529	down	0.0010815	0.024142
D1792_04955	glutamate dehydrogenase	1344	1946	2582	2479	3591	5133	5032	9.1458177	-1.457136328	down	0.000975	0.023027
folE	GTP cyclohydrolase	669	939	1058	1350	1767	2552	2358	8.0936658	-1.45089441	down	0.0005537	0.015471
D1792_13405	tryptophan permease	1245	1692	1370	890	2200	2834	2476	8.2429672	-1.447144195	down	0.0001664	0.006163
D1792_02335	ABC transporter ATP-binding protein	1014	1297	1335	1244	1525	2914	2885	8.2643566	-1.447010339	down	0.0010801	0.024142
htpX	heat shock protein	882	1111	1315	1218	2343	2450	2343	8.172103	-1.430037501	down	0.0002002	0.006855
D1792_02810	transcriptional regulator FNR	753	1122	1375	1552	1974	2769	2989	8.3416697	-1.424065768	down	0.0013115	0.027491
D1792_25125	DUF1471 domain-containing protein	261	40	49	38	90	96	69	3.3346286	-1.422882248	down	0.0010398	0.023915
D1792_23280	HNH endonuclease	348	126	141	145	242	334	245	5.0324468	-1.421333022	down	0.0002751	0.008948
D1792_02340	oligopeptide transport ATP-binding protein OppF	1005	1595	1823	1984	2029	4034	4061	8.74536	-1.418899845	down	0.0025638	0.043244
D1792_14190	50S ribosomal protein L14	372	544	672	780	878	1299	1555	7.3188456	-1.415861892	down	0.0007685	0.019997
D1792_08380	NADH-quinone oxidoreductase subunit B	663	1064	1228	1643	1809	2744	2939	8.3047886	-1.411366257	down	0.0021515	0.037829
ihfA	integration host factor subunit alpha	300	344	748	782	762	1342	1452	7.2443111	-1.409373535	down	0.002709	0.045189
D1792_08465	dihydroneopterin triphosphate 2'-epimerase	363	50	85	59	118	136	118	3.9200436	-1.390107751	down	0.0020831	0.036913
D1792_01450	host-nuclease inhibitor protein Gam	297	74	78	69	106	179	133	4.0918782	-1.379519808	down	0.0018369	0.034006
D1792_17670	periplasmic protein CpxP	501	681	938	897	1920	1576	1424	7.6137726	-1.378869639	down	4.34E-05	0.002244
zapA	protein localized to the cytokinetic	330	231	300	306	381	627	561	6.0291252	-1.377728132	down	0.0005708	0.015851

D1792_23185	pyrimidine/purine nucleoside phosphorylase	285	483	764	1007	1176	1557	1573	7.4922725	-1.374393326	down	0.0011817	0.025561
D1792_02325	peptide ABC transporter permease	921	792	473	673	627	1424	1395	7.2078841	-1.368338466	down	0.0015996	0.030736
purU	formyltetrahydrofolate deformylase	843	742	642	640	959	1398	1311	7.2583396	-1.359470913	down	0.0001069	0.004507
D1792_24060	LPS O-antigen length regulator	1134	590	357	506	658	985	975	6.7857211	-1.357233786	down	0.0004532	0.013314
D1792_11250	hemolysin III family protein	660	1532	1982	1811	2318	3596	3660	8.6666187	-1.351312589	down	0.0021134	0.037304
yhbY	predicted RNA-binding protein	294	83	127	121	220	236	182	4.6781766	-1.349001049	down	0.0010925	0.024174
evgS	hybrid sensory histidine kinase in two-component system	3594	875	729	646	1114	1482	1410	7.385065	-1.342919965	down	7.92E-05	0.0035
D1792_03645	diguanylate cyclase	891	359	280	302	669	598	494	6.1374097	-1.334711853	down	3.77E-05	0.002067
D1792_22100	hypothetical protein	810	138	71	69	141	237	133	4.3442086	-1.331504447	down	0.0018938	0.034498
D1792_02495	LysR family transcriptional regulator CysB	975	1064	1022	1075	1924	2039	1843	7.8926998	-1.329674928	down	0.0001177	0.004873
proQ	putative DNA competence effector	699	1113	1473	1412	1914	2527	2678	8.2408053	-1.325347787	down	0.0018332	0.034006
D1792_24400	endoribonuclease YbeY	468	631	616	665	746	1276	1314	7.1646919	-1.320205327	down	0.0007892	0.020304
D1792_03020	LysR family transcriptional regulator	924	1070	1079	1176	1471	2330	2128	7.9643831	-1.31815115	down	0.0007778	0.020125
D1792_23310	N utilization substance protein B	420	830	1341	1346	1516	2297	2426	8.0648647	-1.314720851	down	0.0031282	0.049957
D1792_08385	NADH-quinone oxidoreductase subunit A	444	382	509	392	537	786	873	6.5681693	-1.306170378	down	0.0008991	0.022013
D1792_18620	regulatory protein SoxS	324	161	177	135	301	320	242	5.1199568	-1.305042465	down	0.000266	0.008715
bamE	hypothetical protein	342	131	212	138	245	322	286	5.1519481	-1.304311681	down	0.001316	0.027491
D1792_16165	hypothetical protein	1827	296	567	179	519	576	647	6.2134284	-1.297650033	down	0.0022815	0.039357
D1792_14070	peptide deformylase	510	820	1077	997	1172	2035	1851	7.748581	-1.293945898	down	0.0010161	0.023608
D1792_18240	malate synthase A	1602	4109	5595	5350	9820	8204	8879	10.127503	-1.286929752	down	0.0028424	0.047071
D1792_07745	hypothetical protein	345	371	586	472	501	1050	919	6.7229885	-1.285400025	down	0.0019387	0.035175
D1792_13480	protein-export membrane protein	333	261	346	486	591	691	688	6.3772093	-1.279688056	down	0.0018097	0.033777
D1792_04850	nucleotide excision repair endonuclease	888	1011	894	864	1263	2015	1563	7.6513136	-1.278865014	down	0.0001963	0.006772
D1792_24320	ribosome silencing factor RsfS	318	86	109	110	147	279	142	4.504036	-1.275227255	down	0.0030429	0.049197
D1792_25955	BAX inhibitor protein	660	735	890	946	1740	1414	1453	7.5724869	-1.274181883	down	0.0002217	0.007368
D1792_24395	magnesium and cobalt efflux protein CorC	879	1158	1265	1220	1602	2351	2272	8.0542078	-1.268368597	down	0.0013548	0.02802
trpE	anthranilate synthase component I	1563	1434	1207	807	1802	2344	1774	7.9229834	-1.268108509	down	0.0001716	0.006302
D1792_25760	DUF882 domain-containing protein	549	453	398	342	569	781	687	6.4186319	-1.267413849	down	0.0002288	0.007551
D1792_18090	50S ribosomal protein L7/L12	366	677	938	1140	1149	1795	1806	7.6812571	-1.255884546	down	0.0027973	0.046492
D1792_16175	hypothetical protein	1101	353	654	486	591	1043	915	6.7656824	-1.254499061	down	0.0018826	0.034498
minC	septum formation inhibitor	696	902	1017	1159	1192	2131	1941	7.8202501	-1.254455993	down	0.0019694	0.035557
D1792_16650	ATP synthase subunit delta	534	713	902	589	937	1448	1299	7.2916529	-1.25162324	down	0.0004115	0.012475
yceD	hypothetical protein	522	522	562	643	709	1165	1067	6.9778773	-1.245266749	down	0.0010475	0.023972
D1792_11770	fimbrial protein	1011	266	167	130	225	353	324	5.2761145	-1.226295469	down	0.0028565	0.047132
D1792_13745	DUF1043 family protein	399	603	985	879	920	1604	1561	7.4761522	-1.220507277	down	0.0029167	0.047608
D1792_21710	ribosome-recycling factor	558	1120	1516	1499	2085	2428	2447	8.2178493	-1.217637934	down	0.0030464	0.049197
panD	aspartate 1-decarboxylase precursor	381	293	280	283	470	512	448	5.9096057	-1.192112976	down	0.0005161	0.014782
D1792_02380	intracellular septation protein A	540	366	245	273	356	524	515	5.9268977	-1.176037553	down	0.0022414	0.039205
D1792_14350	30S ribosomal protein S7	471	459	441	524	570	858	854	6.6440582	-1.171210776	down	0.0023365	0.039903
D1792_08055	DNA-binding response regulator	651	1059	1136	1310	1504	2185	2013	7.9466334	-1.170213383	down	0.0026545	0.044608
D1792_23625	adenylate kinase	645	894	1075	1120	1569	1666	1769	7.7590822	-1.166025388	down	0.001463	0.029169
D1792_26390	methyltransferase domain-containing protein	1059	794	471	573	639	1209	1030	6.9685391	-1.159997741	down	0.0022803	0.039357
ribA	GTP cyclohydrolase II protein	591	643	739	647	722	1370	1128	7.1254837	-1.154824033	down	0.0017737	0.033377
D1792_11150	molybdopterin-dependent oxidoreductase FAD-binding subunit	780	953	962	878	1100	1677	1587	7.5769445	-1.148684151	down	0.0014439	0.029095
D1792_12470	hydrogenase-2 assembly chaperone	489	480	660	555	647	1065	944	6.8587808	-1.132758611	down	0.0024685	0.04179

D1792_22805	LuxR family transcriptional regulator	795	727	461	353	786	936	677	6.6498518	-1.118719535	down	0.0004585	0.013384
D1792_09505	Fe-S cluster assembly transcriptional regulator IscR	489	374	432	381	660	589	595	6.3138507	-1.095394424	down	0.0012559	0.026725
D1792_24360	amino acid ABC transporter ATP-binding protein	726	717	915	605	880	1214	1197	7.1929389	-1.075098293	down	0.0024032	0.040837
D1792_05480	Mn2+/Zn2+ABC transporter ATP-binding protein	756	721	784	656	787	1415	1034	7.1380791	-1.051458093	down	0.0022568	0.039227
D1792_22790	autotransporter outer membrane beta-barrel domain-containing protein	1194	1269	782	691	1135	1682	1221	7.4421341	-1.048592542	down	0.0014138	0.028873
D1792_24365	glutamate ABC transporter permease	675	525	324	360	591	642	548	6.2720811	-1.030189397	down	0.0020303	0.036259
D1792_24560	flavodoxin-1	531	456	328	437	582	664	578	6.3155311	-1.028559581	down	0.003099	0.049869
D1792_27625	peptidyl-arginine deiminase	663	725	477	536	825.5	966.5	777.5	6.7975906	-1.025314918	down	0.0014732	0.029169
D1792_27380	peptidyl-arginine deiminase	663	725	477	536	825.5	966.5	777.5	6.7975906	-1.025314332	down	0.0014693	0.029169
D1792_18380	maltose ABC transporter permease	891	1329	1512	1046	797	584	183	6.9294023	1.02561122	up	0.0029554	0.048068
D1792_13290	PTS mannose/fructose/sorbose transporter family subunit IID	879	1087	1388	1136	599	481	288	6.8408316	1.043326934	up	0.0005865	0.016091
D1792_26270	putative C-S lyase	1164	1900	2362	2241	942	923	569	7.6978339	1.050935151	up	0.0008075	0.020659
D1792_19055	fliK flagellar hook-length control protein	1128	1518	1644	1510	857	708	263	7.205355	1.061522727	up	0.0008222	0.020918
D1792_18400	cadaverine/lysine antiporter	1335	1975	1657	1655	907	845	295	7.3716978	1.065779799	up	0.0006126	0.016629
D1792_00695	maltose/maltodextrin import ATP-binding protein MalK	1116	1504	1753	983	820	663	171	7.0246578	1.067991561	up	0.0031374	0.049957
D1792_17245	flagellar L-ring protein	699	694	873	694	442	278	143	6.1548022	1.071442033	up	0.0014959	0.02949
malF	2-dehydro-3-deoxy-6-phosphogalactonate aldolase	630	710	868	656	383	308	145	6.1268488	1.084805339	up	0.0007143	0.018911
prpR	maltose transporter subunit	1545	2602	2555	2154	1314	1078	364	7.8188344	1.113215466	up	0.0009559	0.022916
D1792_17255	DNA-binding transcriptional activator	1587	2526	2862	2383	1455	1068	384	7.9090798	1.13374691	up	0.0012987	0.027491
treC	IcIR family transcriptional regulator	768	1331	1611	1232	695	559	259	7.0101888	1.13474259	up	0.0001892	0.006674
D1792_18435	trehalose-6-P hydrolase	1656	4786	5321	5370	1822	2120	1291	8.9043678	1.183319282	up	0.0016371	0.031193
gadC	diacylglycerol kinase	369	268	254	216	98	82	61	4.5020941	1.203726438	up	0.0015585	0.030461
D1792_08540	predicted glutamate:gamma-aminobutyric acid antiporter	1536	1969	2393	2582	780	904	617	7.75543	1.205440281	up	0.0003195	0.010319
D1792_06940	aspartate-semialdehyde	1014	1960	2590	2406	922	856	546	7.7452249	1.215776393	up	0.0001564	0.005963
flgJ	UDP-glucose 6-dehydrogenase	1167	980	935	1143	470	364	208	6.5644419	1.225948993	up	0.0001509	0.005924
D1792_15895	flagellar biosynthesis protein	942	1484	1658	1402	753	609	193	7.0959356	1.268564091	up	0.0001605	0.006042
D1792_24585	divergent polysaccharide deacetylase family protein	960	1700	1928	1501	837	625	241	7.2578193	1.288457108	up	5.55E-05	0.002686
D1792_11500	putrescine-ornithine antiporter	1320	2534	2958	2740	1042	1038	526	7.9499131	1.316402932	up	5.75E-05	0.002707
D1792_13310	galactose-proton symporter	1395	2528	3080	2588	1237	954	418	7.9291981	1.343603565	up	7.56E-05	0.003376
flgI	tagatose-1%2C6-bisphosphate aldolase	861	1452	1816	1254	758	540	166	7.0548362	1.348821289	up	0.0001336	0.005382
malM	homolog of Salmonella P-ring of flagella basal body	1098	1439	1808	1489	798	555	179	7.1337601	1.363320317	up	0.0001273	0.005176
D1792_03400	maltose regulon periplasmic protein	921	1857	1882	1906	881	657	246	7.3870734	1.381061182	up	3.08E-05	0.00173
D1792_25325	glutamate decarboxylase beta	1401	3556.11	4942.6	4938.34	1340.09	1530.6	1057.43	8.655376	1.385848194	up	0.0003984	0.012273
D1792_17805	L-threonine/L-serine transporter	1332	5985	8267	9359	1732	2536	2037	9.4553339	1.47831657	up	0.0008661	0.021528
D1792_13285	undecaprenyl-diphosphate	597	723	962	895	362	255	122	6.2380087	1.503790163	up	1.35E-05	0.000947
D1792_00665	nucleoside-specific channel-forming protein Tsx	861	88	93	49	25	29	8	2.7522994	1.532165767	up	0.0014388	0.029095
D1792_05270	PTS mannose/fructose/sorbose/N-acetylgalactosamine transporter subunit IIC	780	1472	1915	1904	558	568	288	7.2587715	1.572418666	up	5.92E-07	8.17E-05
D1792_05270	flagellar biosynthesis protein FlgB	417	471	614	659	174	155	119	5.6702952	1.581644821	up	1.65E-05	0.00111
D1792_05270	PTS mannose transporter subunit IID	852	6844	9608	11298	1520	2610	2489	9.6623435	1.598645105	up	0.000949	0.022916



flgC	flagellar basal-body rod protein C	405	577	722	770	183	219	128	5.9066912	1.602388889 up	4.49E-06	0.000402
D1792_26285	SIS domain-containing protein	624	706	1024	952	309	292	105	6.2635452	1.645106734 up	3.70E-06	0.000351
D1792_08765	oxalyl-CoA decarboxylase	1695	2475	2477	2543	1030	809	172	7.7210159	1.67228722 up	4.08E-05	0.002188
D1792_08775	hypothetical protein	633	579	631	561	210	201	45	5.6323991	1.700175619 up	2.01E-05	0.001238
D1792_01585	porin	1083	19031	31179	33076	3188	7011	7276	11.21081	1.746628635 up	0.001073	0.024142
D1792_13195	propionate kinase	1209	6806	8935	10971	1469	2313	1981	9.5664482	1.772473671 up	0.0001371	0.005475
D1792_06760	hypothetical protein	411	239	403	402	52	68	93	4.8986312	1.780987291 up	0.000385	0.012093
flgD	flagellar basal body rod modification protein D	696	1849	2563	2944	530	641	444	7.6964674	1.807965774 up	5.27E-07	7.50E-05
ompA	outer membrane protein A	1053	63663	106299	134546	11418	23789	25922	13.082842	1.822886898 up	0.0010081	0.023544
D1792_00685	flagellar basal body rod protein FlgF	756	2048	2606	2521	640	598	351	7.6343014	1.823713816 up	1.20E-08	3.04E-06
D1792_13275	tagatose-1%2C6-bisphosphate aldolase	1281	2953	4122	3576	1179	886	362	8.1928995	1.849016469 up	2.26E-06	0.000257
D1792_13280	PTS N-acetylgalactosamine transporter subunit IIB	474	563	895	879	204	213	102	6.0292397	1.855336137 up	2.86E-07	4.34E-05
D1792_03445	putative oxidoreductase	2280	3528	4205	4033	1373	1050	287	8.3298526	1.877637517 up	1.08E-05	0.000819
ydeO	predicted DNA-binding transcriptional activator	762	57	86	72	29	20	1	2.6357343	1.892272274 up	0.0023395	0.039903
D1792_13305	AgaS family sugar isomerase	1155	2951	4322	3890	1233	941	305	8.2520897	1.919270667 up	4.50E-06	0.000402
hdeA	acid-resistance protein, possible chaperone	333	2002	3477	4031	275	726	736	8.0493117	1.953710894 up	0.0002039	0.006914
D1792_00680	flagellar hook protein FlgE	1206	5924	6969	8777	1239	1498	1153	9.1968515	2.076963699 up	1.29E-06	0.000162
D1792_08770	formyl-CoA--oxalate CoA-transferase	1251	1756	1947	2142	566	438	142	7.2866341	2.097031842 up	5.87E-09	1.91E-06
D1792_20000	autotransporter adhesin Ag43	2847	18424	27946	31682	3971	5321	4288	11.043999	2.108915213 up	6.61E-06	0.000537
D1792_15315	acid stress chaperone HdeB	327	951	1723	1521	124	278	264	6.8074066	2.158152301 up	2.90E-06	0.000301
D1792_18170	zinc resistance-associated protein	420	1864	3477	3859	393	597	518	7.9574603	2.180403782 up	1.17E-06	0.000152
D1792_00690	flagellar basal body rod protein FlgG	783	2315	3348	3908	535	618	417	7.9943835	2.241352705 up	8.22E-09	2.34E-06
D1792_13205	serine/threonine dehydratase	990	7943	12868	14628	1208	2190	1857	9.8736969	2.309255845 up	3.81E-06	0.000354
malE	maltose ABC transporter periplasmic protein	1191	4258	5329	6000	956	860	616	8.6721451	2.312920991 up	7.85E-09	2.34E-06
D1792_19050	lysine decarboxylase CadA	2148	9399	12890	14551	1611	1994	1249	9.8801463	2.557858102 up	5.85E-09	1.91E-06
D1792_18405	maltoporin	1341	5359	7014	7377	1082	884	366	8.9377813	2.804430146 up	4.09E-11	2.66E-08
D1792_15350	hypothetical protein	282	14	12	9	3	0	0	0.1935973	3.043871527 up	0.0003994	0.012273
D1792_15900	glycosyltransferase	1035	5244	6903	9216	566	492	213	8.9825114	3.806677264 up	3.77E-16	1.72E-12
D1792_01180	phage terminase large subunit family protein	207	12	9	2	0	0	0	-0.328688	5.727408491 up	0.000183	0.006568

Supplementary Table S3. The different expression of genes in sample C vs. sample B through transcriptome

GeneID	Annotation	length	C_25992-1- 2_1_reads Count	C_25992-1- 2_2_reads Count	C_25992-1- 2_3_reads Count	B_25992- 1_1_reads Count	B_25992- 1_2_reads Count	B_25992- 1_3_reads Count	logCPM	log2Ratio(C/B)	Up-Down- Regulation(C _25992_1_2/B _25992_1)	P-value	FDR
D1792_06205	Hypothetical protein	291	0	11	19	0	0	0	0.01622666	6.288436231	up	6.30E-05	0.007189449
D1792_08715	MULTISPECIES: DNA recombinase	570	7	4	12	0	0	0	-0.2119809	6.043570473	up	2.37E-05	0.003098102
D1792_01810	MULTISPECIES: regulatory protein AriR	267	8	5	9	0	0	0	-0.2446939	6.009644888	up	2.87E-05	0.003450484
D1792_27685	hypothetical protein	246	54.5	62.5	59.5	1	3	0	2.30853533	5.544173049	up	5.99E-15	9.11E-12
D1792_27500	hypothetical protein	246	54.5	62.5	59.5	1	3	0	2.30853533	5.544162769	up	5.91E-15	9.11E-12
D1792_06175	MULTISPECIES: hypothetical protein	732	63	39	27	4	0	1	1.9637408	4.889511268	up	1.45E-09	6.20E-07
D1792_27505	hypothetical protein	324	12.67	13.33	11.33	0	1.33	0	0.34423453	4.659172696	up	1.44E-06	0.0002708
D1792_27680	hypothetical protein	324	12.67	13.33	11.33	0	1.33	0	0.34423453	4.659136475	up	1.42E-06	0.0002708
D1792_27330	hypothetical protein	324	12.67	13.33	11.33	0	1.33	0	0.34423453	4.659128905	up	1.42E-06	0.0002708
D1792_06480	MULTISPECIES: 4&apos;- phosphopantetheinyl transferase	735	396	519	307	4	32	20	5.10703175	4.64150324	up	2.72E-14	2.48E-11
D1792_22260	MULTISPECIES: hypothetical protein	966	51	69	85	5	4	0	2.51038597	4.637217589	up	1.23E-13	9.33E-11
tdcR	threonine dehydratase operon activator protein	345	13	11	21	0	2	0	0.55016779	4.417657715	up	1.48E-06	0.0002708
D1792_06120	TcpC	864	117	127	62	0	5	11	3.16664833	4.398511508	up	9.91E-09	3.23E-06
D1792_06170	rep protein	582	59	32	93	4	4	2	2.3868218	4.333893462	up	1.12E-10	5.68E-08
D1792_12305	glycerol-3-phosphate cytidyltransferase	396	26	19	35	0	0	4	1.28097825	4.326454374	up	8.73E-08	2.49E-05
D1792_06960	Glycosyl transferase group 1	1206	281	356	264	10	35	14	4.67860708	4.146446684	up	1.01E-14	1.15E-11
D1792_16330	hypothetical membrane protein	861	31	39	26	0	1	5	1.5498873	4.072081398	up	8.09E-08	2.46E-05
D1792_06970	MULTISPECIES: glycosyl transferase family 1	1146	242	194	135	11	13	16	4.08706355	4.065975882	up	1.79E-12	1.17E-09
D1792_27430	microcin C7 self-immunity protein MccF	1035	544	483	443	29	75	29	5.43441973	3.720189347	up	4.69E-15	9.11E-12
D1792_12290	XcbB	1029	410	470	273	16	59	40	5.10287748	3.542659501	up	5.73E-11	3.27E-08
D1792_03245	MULTISPECIES: hypothetical protein	822	9	8	6	0	2	0	-0.116389	3.513761368	up	0.00056744	0.044384306
D1792_27640	DNA distortion polypeptide 3	357	40.5	51	85	2	15.5	1.5	2.36416934	3.367558042	up	9.10E-07	0.000197934
D1792_27365	DNA distortion polypeptide 3	357	40.5	51	85	2	15.5	1.5	2.36416934	3.367552172	up	9.07E-07	0.000197934
D1792_06495	unnamed protein product	399	18	13	33	1	6	0	1.03832797	3.308615944	up	1.58E-05	0.002115996
D1792_15330	Uncharacterised protein (plasmid)	528	112	97	73	11	24	1	3.12123816	3.282149398	up	2.22E-06	0.000364953
D1792_27650	RepB family plasmid replication initiator protein	843	92.5	89	122	6	30.5	2.5	3.17587264	3.195580663	up	2.53E-06	0.000384653
D1792_27355	RepB family plasmid replication initiator protein	843	92.5	89	122	6	30.5	2.5	3.17587264	3.195569478	up	2.51E-06	0.000384653
D1792_22925	UPF0379 protein yahO	276	10	19	4	1	3	0	0.29447078	3.168230321	up	0.00031787	0.027384609
D1792_11760	PapX protein	552	722.86	512.96	411.04	16.64	238.9	22.06	5.71270204	2.923119297	up	0.00015177	0.014436766
D1792_01505	Uncharacterised protein (plasmid)	558	195	203	201	16	81	1	4.19409136	2.913521857	up	0.0004875	0.039748567
D1792_06980	Glycosyl transferase	861	338	384	329	27	131	16	5.00698395	2.871169202	up	3.46E-06	0.000509648
D1792_27740	mccC, MFS transporter	1215	146.5	178	139.5	26.5	36.5	16	3.84620268	2.780431375	up	7.47E-09	2.62E-06
D1792_27445	MFS transporter	1215	146.5	178	139.5	26.5	36.5	16	3.84620268	2.780427108	up	7.40E-09	2.62E-06

D1792_26225	membrane protein	1818	7560	5629	5033	615	2634	371	9.19629061	2.665390215	up	1.77E-06	0.000310432
D1792_17080	Protein of uncharacterised function (DUF3289)	849	41	54	74	12	19	0	2.39354	2.65538073	up	8.50E-05	0.00902242
D1792_27745	mccD	804	233.5	256	205.5	19.5	92	33	4.47292916	2.502625697	up	7.10E-06	0.000982409
D1792_27440	mccD	804	233.5	256	205.5	19.5	92	33	4.47292916	2.502625427	up	7.09E-06	0.000982409
D1792_12300	licD family protein	1236	218	129	132	32	76	14	4.02576852	2.307508877	up	0.00014531	0.014117086
D1792_11780	fimbrial protein papE	528	83	57	99	22	38	3	2.99097139	2.194339385	up	0.00057682	0.044384306
D1792_06975	Glycosyl transferase	1032	364	330	308	77	169	26	5.06210184	2.179787654	up	4.86E-05	0.005694612
D1792_16165	conserved phage-associated protein	1827	1456	1152	1160	296	567	179	6.98766577	2.139374953	up	1.49E-09	6.20E-07
D1792_27735	bacteriocin biosynthesis cyclodehydratase, SagC family	1128	283.5	266	262	53	92.5	68.5	4.75919818	2.13133662	up	8.68E-07	0.000197934
D1792_27450	bacteriocin biosynthesis cyclodehydratase, SagC family	1128	283.5	266	262	53	92.5	68.5	4.75919818	2.131335506	up	8.47E-07	0.000197934
D1792_06095	MULTISPECIES: hypothetical protein	1821	352	360	239	68	121	107	5.05462342	1.901212972	up	2.53E-05	0.003207756
D1792_20075	DNA cytosine methyltransferase	1191	318	311	250	74	174	50	4.9459949	1.835751732	up	0.00012886	0.012791241
D1792_22095	MULTISPECIES: hypothetical protein	738	159	218	119	34	81	52	4.12715191	1.781759919	up	0.00038753	0.032171669
D1792_27415	ATP-dependent endonuclease	1902	938.5	830.5	673	183.5	567.5	140	6.44782992	1.750117683	up	7.10E-05	0.007713556
D1792_27590	ATP-dependent endonuclease	1902	938.5	830.5	673	183.5	567.5	140	6.44782992	1.750117267	up	7.08E-05	0.007713556
D1792_01500	MULTISPECIES: hypothetical protein	753	592	488	443	148	353	101	5.79597619	1.628789173	up	0.00023536	0.021932102
D1792_07350	fimbrial protein	543	725	416	486	204	377	164	5.96941545	1.423215592	up	0.00058324	0.044384306
D1792_06955	Mannose-1-phosphate guanylyltransferase	1440	1637	1298	1205	412	1048	514	7.31937692	1.328780361	up	0.00010818	0.010977042
D1792_24740	MULTISPECIES: succinyl-CoA ligase subunit alpha	870	10046	7375	7034	2769	4156	4552	9.89439479	1.310354602	up	0.00034885	0.029497094
D1792_24735	MULTISPECIES: succinyl-CoA ligase subunit beta	1167	12880	10225	9430	3694	5687	5910	10.3003364	1.304355254	up	0.00026608	0.023822054
D1792_16520	MULTISPECIES: low affinity tryptophan permease	1248	5921	4578	4090	2308	2534	2834	9.1947696	1.154190664	up	0.00056215	0.044384306
D1792_08765	MULTISPECIES: oxalyl-CoA decarboxylase	1695	711	1482	1101	2475	2477	2543	8.02890327	-1.051846518	down	2.77E-05	0.003413998
D1792_03445	MULTISPECIES: oxidoreductase	2280	1158	1748	1566	3528	4205	4033	8.62060955	-1.243881867	down	2.24E-06	0.000364953
D1792_19050	MULTISPECIES: lysine decarboxylase CadA	2148	4748	4142	4009	9399	12890	14551	10.2635355	-1.319515702	down	9.92E-05	0.010291452
D1792_08770	formyl-CoA--oxalate CoA-transferase	1251	504	959	523	1756	1947	2142	7.57633686	-1.400970212	down	5.73E-07	0.000153867
D1792_25640	MULTISPECIES: formate acetyltransferase 1	2283	32644	23674	20925	55710	85267	101691	12.9602827	-1.432041675	down	0.00028197	0.024759418