

Supplemental data

Peptide and amino acid metabolism is controlled by an OmpR-family response regulator in *Lactobacillus casei*

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Table S1. Primers used in this study.

Primer	Sequence (5'-3')	Observations
RR11up-f	TCCCCGGGCTGCAG TAATCGGCTTGAGAAAGCGC ^a	<i>prcR</i> deletion
RR11up-r	CGAATAAGTATAAGGAGACCATTGATGATTCCGAAGAAACAAACGCTTG	<i>prcR</i> deletion; complementary to RR11d-f
RR11d-f	CAAGCGTTTGTTTCTTCGGAATCATCAATGGTCTCCTTATACTTATTCG	<i>prcR</i> deletion
RR11d-r	CTTGATATCGAATTC AGCTGCAATATGGGGACTTG ^a	<i>prcR</i> deletion
RR11_LIC-F	<u>TACTTCCAATCCAT</u> GAGTAAAATCCTGATCATCGAGATGAAAAG ^b	Cloning of <i>prcR</i>
RR11_LIC-R	<u>TATCCACCTTTACT</u> GCTATTATCATTACGAACGCATAACATAGCC ^b	Cloning of <i>prcR</i>
RR11A-F:	TGCTTG CTTT GATGTTGCCAGAATTAACG ^c	Asp52->Ala replacement in <i>prcR</i>
RR11A-R:	ATCAA AG CAAGCAAGATGGCATCCCAGTCC ^c	Asp52->Ala replacement in <i>prcR</i>
q-1690-for	GTTAAGCCAACGAATAACGG	RT-qPCR <i>oppA</i> (LCABL_01690)
q-1690-rev	GAAGACGAAATCTTTGGCAG	RT-qPCR <i>oppA</i> (LCABL_01690)
q-2860-for	TCAATGGCAAAACATATGGC	RT-qPCR <i>bnA</i> G (LCABL_02860)
q-2860-rev	GCATATTTCAAGACCGCATC	RT-qPCR <i>bnA</i> G (LCABL_02860)
q-3060-for	TAAGCTTTTAGTCGCACAAC	RT-qPCR <i>pepT</i> -2 (LCABL_03060)
q-3060-rev	AAACTTTTTGTCGGCTTGTC	T-qPCR <i>pepT</i> -2 (LCABL_03060)
q-5350-for	TCCACCTTTAAGGATCAAGC	RT-qPCR <i>ylcA</i> (LCABL_05350)
q-5350-rev	ATGAACAACCCAATAGGTCC	RT-qPCR <i>ylcA</i> (LCABL_05350)
q-18970-for	ATGGGCTTTAACAGTAGGTG	RT-qPCR <i>prcK</i> (LCABL_18970)
q-18970-rev	GATTCATAAAATCTGCCGC	RT-qPCR <i>prcK</i> (LCABL_18970)
q-21470-for	TCTCAGGCCATGGACAATAC	RT-qPCR <i>oppA</i> (LCABL_21470)
q-21470-rev	TCCCACCATTGTTGCTTTG	RT-qPCR <i>oppA</i> (LCABL_21470)
q-22680-for	TCCTAGCTTGATTCTTGGTG	RT-qPCR LCABL_22680
q-22680-rev	ACGATGAAACTATAACCCAGC	RT-qPCR LCABL_22680
q-23270-for	ATTATGGGACTTTCCGGTTC	RT-qPCR <i>gbuA</i> (LCABL_23270)
q-23270-rev	CAATGTCATCACCGTCAATC	RT-qPCR <i>gbuA</i> (LCABL_23270)
q-prtP-for	CTTCTGAACGCTGGCATC	RT-qPCR <i>prtP</i> (LCABL_24520)
q-prtP-rev	GCCATTATCTGATGAACAGG	RT-qPCR <i>prtP</i> (LCABL_24520)
q-prsA-for	GCCCAAAGTGACTGTCCAGC	RT-qPCR <i>prsA</i> (LCABL_24530)
q-prsA-rev	TTCGCAAGCGTGGCAAATC	RT-qPCR <i>prsA</i> (LCABL_24530)
q-27210-for	GCAACATCTACAAGATGCAC	RT-qPCR <i>bcrA</i> (LCABL_27210)
q-27210-rev	GCAACATCTACAAGATGCAC	RT-qPCR <i>bcrA</i>

q-27240-for	ATTGTGGAAAAAGCGTTGAC	(LCABL_27210) RT-qPCR <i>gltA</i> (LCABL_27240)
q-27240-rev	CGGCATTGCCATTAAGATAC	RT-qPCR <i>gltA</i> (LCABL_27240)
q-30380-for	ATCCATCCAACAAGGATACC	RT-qPCR <i>rgg</i> (LCABL_30380)
q-30380-rev	AACCGATACTGTCGCTTAG	RT-qPCR <i>rgg</i> (LCABL_30380)
P-prt-F1	CTGAAATGCTTACAGTAAACG	Amplification of the <i>prtP-prsA</i> promoter region
P-prt-R1	TTCCAAAAGTTTCAGAACC	Amplification of the <i>prtP-prsA</i> promoter region
P-prt-F2	CATCTATAGTCTGTAAACGGC	
P-prt-F3	TAGGAAAATTAATAAAAAGATTAATAATTTTCG	
P-prt-R2	GATTATATACTCTCGAAGAACAG	
P-prt-R3	ATTAATTTTCTATCTGTAAATTAGC	
P-prt-R4	GCCGTTTACAGACTATAGATG	
P-prt-R5	CATTGAAATTCTCAATTGCCAAC	
M-prt-F4	TTGAATCTGTTCTTCGAGAG	
M-prt-R1	AATTGGATCCATAACCCGGTTCCAAAAGTTTCAGAACC	
P-prt-F3-M1	TAGGAC CG ATTAATAAAAAGATTAATAATTTTCGTTG ^c	Mutation of A tracks (fragment 2)
P-prt-F3-M2	TAGGAAAATTAATA CG AGATTAATAATTTTCGTTGAATCTG ^c	Mutation of A tracks (fragment 3)
P-prt-F3-M3	TAGGAAAATTAATAAAAAGATTAC CG ATTTTCGTTGAATCTGTTCTTC ^c	Mutation of A tracks (fragment 4)
P-prt-R6	GATGTTTTGAAATTTTGGC	
P-prt-R6-M1	GATGT CG TGAAATTTTGGCATTATTAGAAAATG ^c	Mutation of A tracks (fragment 6)
P-prt-R6-M2	GATGTTTTGAAATT CG TGGCATTATTAGAAAATGAG ^c	Mutation of A tracks (fragment 7)
P-prt-R7	GGCATTATTAGAAAATGAGTATTTG	
P-prt-R7-M1	GGCATTATTAGAC CG ATGAGTATTTGCATTGAAATTC ^c	Mutation of A tracks (fragment 9)
oppA-F	TTGTCTTTCAAACACTTCTG	Amplification of the putative LCABL_01690 promoter
oppA-R	CATTTACTCACCCCTCAAATG	
gltA-F	CCCCACCTTATTAGTTAACATC	Amplification of the putative LCABL_27240 promoter
gltA-R	ATCTTGCAACCGACCTTG	
pepT-F	TACCGAATAAAGTCAGCTTG	Amplification of the putative LCABL_03060/LCABL_0 3070 promoter region
pepT-R	AGTGGCAACATCAGTGTC	
gbuA-F	AAACGTTTGTTCATCGAATTG	Amplification of the putative LCABL_23270 promoter
gbuA-R	CCTTGACTTTCAGAGAAGC	
pepL-F	TCAATAGCTGGTTAGATGGTC	Amplification of the putative LCABL_21470 promoter
pepL-R	TATCGTATACTCCCTCCGC	
Rgg-F	ATTGAGTTTAGCGGAGTCAG	Amplification of the putative LCABL_30380 promoter
Rgg-R	CCCGACCCTTTTATGAGAAC	
22680-F	GTGCATGGTCTGAATGTGG	Amplification of the

22680-R	TCACATATGCTTTTAATAATTGCG	putative LCABL_22680 promoter
31170-F	CAGATACGATGATTCACTTGG	Amplification of the putative LCABL_31170 promoter
31170-R	CATCGACAAAACCTCTC	
bcaR-F	CGGTAATATCAGTCATGCAAC	Amplification of the putative LCABL_27210 promoter
bcaR-R	TTCGTTTTCTCCATCAAAC	
PrcR-F	ATGGTATACCGAAGCTTAATAAC	Amplification of the putative LCABL_18980 promoter
PrcR-R	ATCAATGGTCTCCTTATACTTATTC	
2860-F	TAGTCGCATGCTGAAAAGAG	Amplification of the putative LCABL_02860 promoter
2860-R	CCTTTTGTGGATGGTTTCTG	
ylcA-F	TGTTGGCCACGAAGATAAAG	Amplification of the putative LCABL_05350 promoter
ylcA-R	CTAAAAATCCCTCCAACAGC	

^a Tails for cloning with CloneEZ indicated in bold characters.

^b Tails for cloning in pNIC28-Bsa4 underlined.

^c Mutated positions are indicated in bold italics.

Table S2. Functional classification of genes differentially expressed in strain Δ RR11.

Upregulated genes								
Locus	Locus_tag	Product name	id	Mean BL23	Mean Δ RR11	foldChange	pval	padj
Biosynthesis of amino acids								
trpA	LCABL_00720	tryptophan synthase subunit alpha	CAQ65204	477.4715793	1328.099087	2.7815249	7.02E-14	3.05E-12
trpB	LCABL_00730	tryptophan synthase subunit beta	CAQ65205	387.567084	1126.128651	2.905635431	6.70E-15	3.08E-13
trpF	LCABL_00740	N-(5-phosphoribosyl)anthranilate isomerase (PRAI)	CAQ65206	48.39169593	193.5715274	4.000098027	1.28E-14	5.82E-13
trpC	LCABL_00750	indole-3-glycerol-phosphate synthase	CAQ65207	75.19947332	225.9612253	3.004824572	1.09E-10	3.84E-09
trpD	LCABL_00760	anthranilate phosphoribosyltransferase	CAQ65208	441.9133001	1309.289147	2.9627738	4.43E-08	1.11E-06
dapB	LCABL_00960	Dihydrodipicolinate reductase (DHPR)	CAQ65228	170.2362858	516.3088046	3.032895144	1.00E-13	4.22E-12
dapA	LCABL_00970	dihydrodipicolinate synthase	CAQ65229	73.98308785	198.3976504	2.681662204	8.51E-09	2.31E-07
dapE	LCABL_00980	Succinyl-diaminopimelate desuccinylase	CAQ65230	304.7492072	706.4137204	2.318016598	2.15E-09	6.23E-08
lysA	LCABL_01000	Diaminopimelate decarboxylase	CAQ65232	52.38057758	142.2767575	2.716212078	1.79E-07	4.22E-06
thrA	LCABL_01010	aspartate kinase	CAQ65233	302.2908832	972.6958128	3.217747761	1.10E-10	3.84E-09
dapF	LCABL_01020	diaminopimelate epimerase	CAQ65234	706.7782471	1644.79678	2.32717516	9.72E-09	2.61E-07
asd	LCABL_01030	Aspartate semialdehyde dehydrogenase	CAQ65235	1833.109994	3626.725455	1.978454903	1.27E-07	3.08E-06
cysK1	LCABL_05450	Cysteine synthase	CAQ65671	684.0603966	1054.970119	1.542217799	0.002155283	0.022203072
hisC	LCABL_16480	Histidinol-phosphate aminotransferase (Imidazole acetol-phosphate transaminase)	CAQ66729	467.9169044	2165.633538	4.628243857	3.42E-29	2.67E-27
hisE	LCABL_16490	phosphoribosyl-ATP pyrophosphatase	CAQ66730	75.32783229	416.6981683	5.531795562	2.44E-27	1.69E-25
hisI	LCABL_16500	Phosphoribosyl-AMP cyclohydrolase (PRA-CH)	CAQ66731	86.64457283	452.9272822	5.227416645	2.00E-25	1.29E-23
hisF	LCABL_16510	imidazole glycerol phosphate synthase subunit HisF	CAQ66732	206.6700907	1343.65547	6.501451011	1.44E-39	2.43E-37
hisA	LCABL_16520	1-(5-phosphoribosyl)-5-	CAQ66733	291.6296637	1454.284247	4.986750075	2.38E-30	2.07E-28
hisH	LCABL_16530	imidazole glycerol phosphate synthase subunit HisH	CAQ66734	333.4767769	1635.332413	4.903886946	2.17E-30	2.00E-28
hisB	LCABL_16540	imidazoleglycerol-phosphate dehydratase	CAQ66735	234.1550451	1506.195794	6.432472097	1.66E-39	2.66E-37
hisD	LCABL_16550	histidinol dehydrogenase	CAQ66736	433.2432902	2124.136665	4.902872618	2.28E-30	2.04E-28
hisG	LCABL_16560	ATP phosphoribosyltransferase catalytic subunit	CAQ66737	91.05388112	485.5814208	5.332901957	2.24E-26	1.51E-24
hisZ	LCABL_16570	ATP phosphoribosyltransferase regulatory subunit	CAQ66738	207.8739401	1273.379634	6.125730012	2.30E-36	3.04E-34
ilvE	LCABL_22070	branched-chain amino acid aminotransferase	CAQ67274	993.4071628	4318.625317	4.347286268	1.01E-27	7.29E-26
thrB	LCABL_23310	Homoserine kinase ThrB	CAQ67398	666.3739004	1217.151871	1.826529926	7.54E-06	0.000147848
thrC	LCABL_23320	threonine synthase	CAQ67399	1322.12388	2456.437602	1.85794814	2.47E-06	5.29E-05
thrA	LCABL_23330	Homoserine dehydrogenase	CAQ67400	338.2563351	1016.663585	3.005601016	5.43E-06	0.000110846
apk	LCABL_23340	aspartate kinase	CAQ67401	559.9623542	1581.922443	2.825051417	4.96E-11	1.79E-09
gltD	LCABL_27230	glutamate synthase subunit beta	CAQ67774	1046.304122	11571.45758	11.05936346	1.18E-43	2.57E-41
gltA	LCABL_27240	Glutamate synthase (Large subunit)	CAQ67775	2451.586514	34175.3973	13.94011474	1.05E-27	7.43E-26
Amino acid catabolism								
mmsB	LCABL_02430	3-hydroxyisobutyrate dehydrogenase	CAQ65375	441.9243543	1648.070176	3.729303805	3.88E-22	2.27E-20
AGR_pAT_610, Atu5418	LCABL_04530	Opine/octopine dehydrogenase (AGR_pAT_610p)	CAQ65579	66.12197076	222.035617	3.357970345	2.23E-12	8.80E-11
gdh	LCABL_06940	glutamate dehydrogenase	CAQ65819	162.2972797	272.1321057	1.676750875	0.000784394	0.009422033
cah	LCABL_07100	Carbonate dehydratase	CAQ65835	373.9460693	578.7050334	1.547562819	0.004087865	0.037645516

bkdC	LCABL_16660	Branched-chain alpha-keto acid, E2 component, dihydroliipoamide acetyltransferase	CAQ66747	118.8410842	211.6734218	1.781146843	0.000309479	0.004354197
bkdB	LCABL_16670	TPP-dependent branched-chain alpha-keto acid dehydrogenase, E1 beta subunit (Branched-chain alpha-keto acid dehydrogenase, E1 component, beta subunit)	CAQ66748	26.99176563	62.16025281	2.302933927	0.000419404	0.005715555
bkdA	LCABL_16680	Branched-chain alpha-keto acid dehydrogenase, E1 component, alpha subunit	CAQ66749	83.60443683	145.4588794	1.739846411	0.00157965	0.016844061
bkdD	LCABL_16690	Dihydroliipoyl dehydrogenase	CAQ66750	92.27161132	183.980896	1.993905746	5.15E-05	0.000884313
araT	LCABL_23390	Aromatic amino acid aminotransferase	CAQ67406	453.993275	1269.880326	2.797134662	7.67E-14	3.28E-12
-	LCABL_28150	HTH containing DNA-binding domain and MocR-like aminotransferase (<i>Asp aminotransferase</i>)	CAQ67865	68.51665258	336.0301319	4.904357106	2.72E-21	1.56E-19
Peptide and amino acid transport								
oppA	LCABL_01690	Oligopeptide ABC transporter, substrate-binding lipoprotein	CAQ65301	7144.517608	65874.70209	9.220314891	1.40E-58	3.54E-56
livA	LCABL_02650	Branched-chain amino acid ABC transporter, substrate binding protein	CAQ65391	679.0796949	3706.826166	5.458602568	1.12E-35	1.31E-33
livB	LCABL_02660	Branched-chain amino acid ABC transporter, permease protein	CAQ65392	950.8955652	4589.03584	4.826014557	9.05E-23	5.50E-21
livC	LCABL_02670	Branched-chain amino acid ABC transporter, permease protein	CAQ65393	401.7356275	2015.486148	5.016946495	2.82E-31	2.68E-29
livD	LCABL_02680	Branched-chain amino acid ABC transporter, ATP-binding protein	CAQ65394	734.6824706	3963.081147	5.394277536	1.55E-35	1.75E-33
livF	LCABL_02690	Putative branched chain amino acid ABC transporter, ATP-binding protein	CAQ65395	664.6265895	3856.276255	5.802169693	4.86E-38	7.04E-36
oppA	LCABL_03070	Oligopeptide ABC transporter substrate binding protein	CAQ65433	4241.66486	51878.45377	12.23068193	1.76E-31	1.73E-29
yxO	LCABL_04540	Probable amino-acid import ATP-binding protein yxO	CAQ65580	42.55949341	91.12903905	2.141215314	0.000212078	0.003151344
atmA	LCABL_04550	AtmA (Putative amino acid binding protein)	CAQ65581	54.16815505	156.4577813	2.888371982	6.69E-09	1.85E-07
tcyL	LCABL_04570	L-cystine transporter permease tcyL	CAQ65583	31.88386223	64.17280365	2.012704835	0.003334903	0.032072056
brnQ	LCABL_06660	Branched-chain amino acid transport system carrier protein	CAQ65791	713.5895734	1165.432998	1.633197907	0.000530699	0.006951693
sstT	LCABL_06910	Serine/threonine transporter SstT	CAQ65816	1038.647995	8966.209604	8.632577781	1.81E-41	3.45E-39
glnP2	LCABL_14900	Glutamine ABC transporter, permease protein	CAQ66571	675.495181	1082.495744	1.602521786	0.002776809	0.027487693
glnH2	LCABL_14920	Glutamine ABC transporter, substrate binding protein	CAQ66573	1060.002934	1652.223598	1.558697193	0.004849258	0.042849278
oppA	LCABL_18220	Oligopeptide ABC transporter substrate binding protein	CAQ66902	56281.28107	147322.276	2.617607012	1.34E-14	5.98E-13
oppC	LCABL_18230	Oligopeptide ABC transporter, permease component	CAQ66903	15612.31195	34188.44628	2.189838788	1.49E-09	4.50E-08
oppB	LCABL_18240	Oligopeptide ABC transporter, permease protein	CAQ66904	3456.459942	7831.629115	2.265794844	2.63E-10	8.42E-09
oppB	LCABL_18250	Oligopeptide ABC transporter, permease protein	CAQ66905	1519.02368	3421.56279	2.252474951	1.80E-09	5.32E-08
oppF	LCABL_18260	Oligopeptide ABC transporter (ATP-binding protein)	CAQ66906	11766.60614	27907.44491	2.371749728	2.25E-11	8.34E-10
oppD	LCABL_18270	Oligopeptide ABC transporter ATP-binding protein	CAQ66907	12270.66556	30143.2836	2.45653208	6.75E-09	1.85E-07
oppA	LCABL_21470	Oligopeptide ABC transporter, substrate binding protein	CAQ67214	2873.944219	27840.30068	9.687140236	7.86E-60	2.17E-57
glnP	LCABL_21860	Glutamine transport system permease protein	CAQ67253	3256.41577	5721.397875	1.756961727	6.63E-06	0.000131783
glnM	LCABL_21870	Glutamine ABC transporter permease	CAQ67254	3485.558646	6315.039654	1.811772601	5.00E-06	0.000103461

glnH1	LCABL_21880	Glutamine ABC transporter, substrate binding protein	CAQ67255	4596.883592	7774.607252	1.691277818	6.74E-05	0.001143728
glnQ	LCABL_21890	Glutamine transport ATP-binding protein	CAQ67256	2029.566821	4155.595012	2.047528058	2.32E-08	6.02E-07
oppF	LCABL_22420	Oligopeptide ABC transporter, ATP-binding subunit	CAQ67309	3091.189883	19909.17979	6.440620131	1.54E-43	3.11E-41
oppD	LCABL_22430	Oligopeptide ABC transporter, ATP-binding subunit	CAQ67310	5012.041705	30595.9712	6.104492542	1.53E-36	2.12E-34
oppC	LCABL_22440	Oligopeptide ABC transporter, membrane-spanning subunit	CAQ67311	7155.92658	38031.92743	5.314745338	1.07E-35	1.31E-33
oppB	LCABL_22450	Oligopeptide ABC transporter, membrane-spanning subunit	CAQ67312	2883.159617	19040.45873	6.604025189	8.85E-23	5.49E-21
oppA	LCABL_22460	Oligopeptide ABC transporter, substrate-binding lipoprotein	CAQ67313	13643.56233	95624.81643	7.00878657	1.90E-09	5.56E-08
glnP	LCABL_30400	Amino acid ABC transporter, amino acid-binding protein/permease protein	CAQ68090	699.4159529	1735.693576	2.48163281	3.71748E-12	1.45E-10
-	LCABL_30410	ABC transporter related	CAQ68091	790.0150911	2080.864177	2.633954972	1.26E-13	5.26E-12
Proteolysis								
pepF1	LCABL_02440	Oligoendopeptidase F1	CAQ65376	2846.38097	9718.347338	3.414282009	9.49E-21	5.24E-19
pepT-2	LCABL_03060	Peptidase T	CAQ65432	1561.334803	24094.21129	15.43180313	8.23E-82	1.25E-78
pepN	LCABL_05340	Membrane alanine aminopeptidase	CAQ65660	10806.19581	15473.17986	1.431880389	0.004983448	0.04349017
pepX	LCABL_18670	x-prolyl-dipeptidyl aminopeptidase	CAQ66946	1769.844076	3990.127791	2.254508093	4.49E-10	1.42E-08
pepL	LCABL_21440	Prolyl aminopeptidase	CAQ67211	1922.976374	20300.18023	10.55664568	2.15E-22	1.28E-20
dppA	LCABL_21450	D-aminopeptidase	CAQ67212	983.9723731	13943.71606	14.17084102	2.41E-77	1.46E-74
ysdC	LCABL_21460	Peptidase M42 family	CAQ67213	788.5867369	11722.0524	14.86463296	2.77E-79	2.10E-76
pepR	LCABL_21620	Prolinase	CAQ67229	2311.027219	4131.353693	1.787669855	5.99E-06	0.000120518
prtP	LCABL_24520	PII-type proteinase precursor (Lactocepin) (Cell wall-associated serine proteinase) (LP151)	CAQ67518	2675.182788	77407.99017	28.93558919	1.52E-79	1.54E-76
prsA	LCABL_24530	peptidylprolyl isomerase	CAQ67519	396.3688197	1766.380947	4.456407415	1.69E-10	5.76E-09
pepC1	LCABL_25130	Cysteine aminopeptidase	CAQ67579	8687.113935	25263.2664	2.908131123	1.15E-16	5.65E-15
Sugar catabolism								
iolD	LCABL_02200	IolD	CAQ65352	103.0076968	168.3151823	1.63400588	0.003854685	0.035823812
pmi	LCABL_06290	Mannose-6-phosphate isomerase	CAQ65754	183.7975054	308.5677292	1.678846122	0.000824253	0.009823153
galK	LCABL_07300	Galactokinase (Galactose kinase)	CAQ65855	925.4329302	2736.596819	2.957099029	4.75E-16	2.29E-14
galE	LCABL_07310	UDP-glucose 4-epimerase (Galactowaldenase) (UDP-galactose 4-epimerase)	CAQ65856	1313.070192	2927.719053	2.229674445	1.56E-09	4.63E-08
galT	LCABL_07320	galactose-1-phosphate uridylyltransferase	CAQ65857	2984.300502	5715.797226	1.915288766	4.90E-07	1.11E-05
map2	LCABL_11440	maltose phosphorylase	CAQ66229	1331.814519	2407.275056	1.807515252	4.15E-06	8.77E-05
pgmA	LCABL_11450	Beta-phospho-glucomutase	CAQ66230	704.9764416	1096.317665	1.555112483	0.001174793	0.013125722
dexB	LCABL_11470	Glucan 1,6-alpha-glucosidase (Dextran glucosidase) (Exo-1,6-alpha-glucosidase) (Glucodextranase)	CAQ66232	1411.092632	2495.81744	1.768712687	8.61E-06	0.000167739
suhB	LCABL_15420	Myo-inositol-1(Or 4)-monophosphatase	CAQ66623	1273.390968	2444.741231	1.919866948	4.36E-07	9.96E-06
fruK	LCABL_15700	1-phosphofructokinase (Fructose-1-phosphate kinase)	CAQ66651	1542.404001	2507.393437	1.625639868	0.001304852	0.014264194
-	LCABL_16300	Galactose mutarotase related enzyme	CAQ66711	2224.514042	3343.8307	1.503173564	0.001492063	0.016079356
nagA	LCABL_20280	N-acetylglucosamine-6-phosphate deacetylase	CAQ67105	3639.205903	5066.411394	1.392174977	0.005831692	0.049229201
mocE	LCABL_22650	MocE	CAQ67332	443.1098957	2807.515655	6.335935357	1.35E-39	2.42E-37

xalA	LCABL_28750	XalA precursor	CAQ67925	1484.515807	2659.152843	1.791259366	6.58E-06	0.000131609
Organic acid metabolism								
pta	LCABL_11620	Phosphate acetyltransferase (Phosphotransacetylase)	CAQ66247	1798.445061	2658.480578	1.478210614	0.002239864	0.02291901
pdhB	LCABL_15370	Pyruvate dehydrogenase complex, E1 component, beta subunit	CAQ66618	3229.805099	5172.379254	1.601452439	0.000222648	0.003284602
pdhC	LCABL_15380	dihydrolipoamide acetyltransferase	CAQ66619	4303.025678	7010.460059	1.629193173	0.000147889	0.00230479
pdhD	LCABL_15390	dihydrolipoamide dehydrogenase	CAQ66620	9516.669916	14099.71906	1.481581182	0.003250533	0.031451475
ldh	LCABL_15400	L-lactate dehydrogenase (L-LDH)	CAQ66621	549.7585895	1440.299883	2.619876998	1.71E-12	6.84E-11
ldhA	LCABL_23380	D-lactate dehydrogenase	CAQ67405	316.8658029	814.0043414	2.568924554	1.24E-11	4.78E-10
Gluconeogenesis								
fbp	LCABL_22100	Fructose-1,6-bisphosphatase	CAQ67277	1158.646941	2004.272004	1.729838429	3.22E-05	0.000568709
ppdK	LCABL_25190	pyruvate phosphate dikinase	CAQ67585	607.6394838	1482.273415	2.439396146	2.04E-07	4.76E-06
Biosynthesis of polysaccharides								
glgD	LCABL_22040	Glucose-1-phosphate adenylyltransferase, subunit	CAQ67271	448.7973655	775.9634609	1.728983993	6.05E-05	0.00103299
glgC	LCABL_22050	glucose-1-phosphate adenylyltransferase	CAQ67272	160.2958572	315.5011309	1.968242575	9.13E-06	0.000176209
glgB	LCABL_22060	glycogen branching enzyme	CAQ67273	245.4637409	426.6196831	1.738015079	0.000342224	0.004727353
Sugar transport								
gntP	LCABL_02290	Gluconate:H(+) symporter	CAQ65361	326.1994845	554.9146445	1.7011512	0.000835233	0.00991513
levA	LCABL_04410	Fructose/mannose phosphotransferase system IIA component	CAQ65567	2585.666498	11342.03434	4.386503188	6.26079E-29	4.75664E-27
levB	LCABL_04420	Fructose/mannose phosphotransferase system IIB component	CAQ65568	3526.234616	14149.91805	4.012755698	2.72345E-26	1.79925E-24
levC	LCABL_04430	Fructose/mannose phosphotransferase system IIC component	CAQ65569	2921.188064	12582.92194	4.307467259	1.90466E-28	1.41177E-26
levD	LCABL_04440	LevD protein	CAQ65570	6158.868896	29292.70007	4.756181786	2.92115E-32	3.06116E-30
levX	LCABL_04450	LevX protein	CAQ65571	7987.177509	35704.48331	4.470225341	1.46918E-19	7.83305E-18
levC	LCABL_06310	Fructose/mannose phosphotransferase system IID component	CAQ65756	58.01382704	118.597253	2.044292871	0.000174923	0.002644736
msmK2	LCABL_11460	Multiple sugar ABC transporter, ATP-binding protein	CAQ66231	1442.228911	2793.768555	1.937118674	3.31E-07	7.61E-06
malE	LCABL_11480	Maltose ABC transporter substrate binding protein	CAQ66233	1250.453487	2173.640574	1.738281829	1.74E-05	0.000318594
malF	LCABL_11490	Maltose transport system permease protein malF	CAQ66234	926.0981694	1560.003793	1.684490742	4.86E-05	0.00084449
fruA	LCABL_15690	Fructose-specific phosphotransferase system, enzyme IIABC	CAQ66650	3366.184153	5081.142284	1.509466521	0.001066463	0.012184144
pfoSR	LCABL_23370	PTS system, fructose-specific IIBC component	CAQ67404	677.2636784	1504.165454	2.220945109	2.80E-09	8.02E-08
pts18CBA	LCABL_28880	N-acetylglucosamine and glucose PTS, EIICBA	CAQ67938	175.6948959	407.9677796	2.322024083	1.66E-05	0.000309665
sgaB	LCABL_29120	Phosphotransferase enzyme II, B compnent SgaB	CAQ67962	16.89802881	42.58526682	2.520132217	0.000686198	0.008454328
Ion transport								
-	LCABL_20450	hypothetical protein LCABL_20450	CAQ67121	69.20853372	128.7495811	1.860313667	0.001135329	0.012778759
Nitrogenous bases transport								
-	LCABL_22680	Permease for cytosine/purines, uracil, thiamine, allantoin	CAQ67335	1300.169959	16493.63204	12.68575075	3.26E-29	2.61E-27
Unsigned transporters								
-	LCABL_00870	hypothetical protein LCABL_00870 (<i>ABC permease</i>)	CAQ65219	98.43127245	172.6742177	1.754261765	0.004190438	0.038242466

upsA	LCABL_30350	UpsA	CAQ68085	49.16685381	283.415852	5.764368268	4.81E-15	2.25E-13
Metabolism of cofactors								
ppnK	LCABL_10160	inorganic polyphosphate/ATP-NAD kinase	CAQ66102	332.0107895	495.5197693	1.492480922	0.002285657	0.02323114
sufD	LCABL_14030	Conserved protein involved in Fe/S cluster assembly	CAQ66484	1514.000152	2199.361695	1.452682612	0.005730286	0.048609312
coaA	LCABL_21550	pantothenate kinase	CAQ67222	322.2945975	566.9313291	1.759046951	0.000105104	0.001735923
Lipoic acid metabolism								
lplA1	LCABL_16960	Lipoate-protein ligase	CAQ66777	6234.927839	10024.45527	1.607790102	0.000138638	0.002194386
Nitrogenous bases biosynthesis								
pyrB	LCABL_16780	aspartate carbamoyltransferase catalytic subunit	CAQ66759	633.9994247	967.7229764	1.526378319	0.001370671	0.014929998
DNA replication and repair								
dnaQ	LCABL_11660	DNA-directed DNA polymerase III, epsilon subunit	CAQ66251	549.4078376	802.5505752	1.4607556	0.004855091	0.042849278
recD	LCABL_22620	Putative exodeoxyribonuclease V	CAQ67329	1103.366986	2209.334964	2.002357322	1.36E-07	3.29E-06
hsdS	LCABL_22710	HsdS	CAQ67338	0.631948223	11.77561964	18.63383615	0.000630149	0.007880754
Transcriptional regulation								
lytR	LCABL_02460	Transcriptional regulator	CAQ65377	3065.228576	4607.088961	1.503016446	0.001140479	0.01278936
comX	LCABL_09250	Competence-specific sigma factor ComX	CAQ66019	714.3355695	1180.117836	1.652049662	0.000142589	0.002245223
-	LCABL_12470	hypothetical protein LCABL_12470	CAQ66331	624.4408845	1066.947658	1.70864478	0.002501586	0.025009274
fruR	LCABL_15710	Transcription regulator of fructose operon	CAQ66652	306.2072317	499.5726456	1.631485458	0.00530469	0.045539412
hpk5	LCABL_18970	Sensor protein (<i>HK11</i>)	CAQ66976	3569.320029	11183.73787	3.133296476	1.30E-18	6.84E-17
rex	LCABL_24270	redox-sensing transcriptional repressor Rex	CAQ67493	2248.082108	3504.764211	1.55900187	0.000582717	0.007440663
-	LCABL_27210	CBS domain containing protein	CAQ67772	4068.209318	12551.08723	3.085162598	5.46E-18	2.81E-16
yidA	LCABL_28870	Transcription regulator	CAQ67937	249.1280405	438.3266708	1.759443336	0.00093865	0.010887622
mutR	LCABL_30370	MutR	CAQ68087	158.795417	2110.86314	13.29297268	1.59E-67	6.05E-65
rgg	LCABL_30380	HTH-type transcriptional regulator rgg	CAQ68088	142.1422056	2150.067824	15.12617463	2.36E-73	1.02E-70
Cell envelope/secreted								
-	LCABL_03660	Beta-lactamase class A	CAQ65492	127.3583166	253.2209483	1.988256087	1.48E-05	0.000277782
pbpE	LCABL_05030	PbpE	CAQ65629	474.9324485	3260.177974	6.864508803	4.32E-30	3.65E-28
-	LCABL_06730	hypothetical protein LCABL_06730 (<i>signal peptide WxL domain</i>)	CAQ65798	9.105859204	49.46676539	5.432410526	2.13E-08	5.60E-07
-	LCABL_06750	hypothetical protein LCABL_06750 (<i>WxL domain</i>)	CAQ65800	29.2995438	71.99431721	2.45718219	6.82E-05	0.001151422
dltA	LCABL_08550	D-alanine--poly(phosphoribitol) ligase subunit 1 (D-alanine-activating enzyme) (DAE) (D-alanine-D-alanyl carrier protein ligase) (DCL)	CAQ65978	14173.99494	25200.92351	1.777968992	0.000145717	0.002282652
spl	LCABL_21960	Peptidoglycan lytic protein P45	CAQ67263	16381.65337	24498.0521	1.495456628	0.001208023	0.013416175
Stress response								
cspA	LCABL_06950	Cold shock protein A	CAQ65820	22157.8651	31896.27237	1.439501153	0.004278778	0.03870002
gst	LCABL_14360	Glutathione S-transferase	CAQ66517	141.5422821	223.0310433	1.575720273	0.00404607	0.037373876
mutT	LCABL_27440	Mutator mutT protein (7,8-dihydro-8-oxoguanine-triphosphatase)	CAQ67795	14.62317164	39.69084024	2.71424293	0.000767165	0.009251648
Prophage proteins								
54	LCABL_09800	Prophage LambdaBa04, Gp53	CAQ66066	77.34267829	173.7705795	2.246761857	0.000270666	0.003861757
54	LCABL_11060	Prophage LambdaBa04, Gp54	CAQ66191	144.8537578	292.1357567	2.016763397	0.002154889	0.022203072

int	LCABL_21530	Integrase	CAQ67220	212.9463251	477.1721997	2.240809742	4.96E-08	1.24E-06
Uncharacterized membrane proteins								
yveB	LCABL_01320	hypothetical protein LCABL_01320 (put. <i>memb. assoc. lipid phosphatase</i>)	CAQ65264	341.8810954	534.5252953	1.563483043	0.001612343	0.017132549
yhgE	LCABL_01640	hypothetical protein LCABL_01640 (<i>memb. Prot</i>)	CAQ65296	376.0925351	573.1987128	1.524089577	0.002351826	0.023823996
-	LCABL_03420	Putative uncharacterized protein (<i>memb.prot.</i>)	CAQ65468	4.476536193	16.38773874	3.660807828	0.005040373	0.04376484
-	LCABL_06720	hypothetical protein LCABL_06720 (<i>memb. Prot</i>)	CAQ65797	49.55678821	297.4610392	6.002427719	2.14E-08	5.60E-07
-	LCABL_17480	ABC-type transport system, permease component	CAQ66829	97.79233113	199.6959358	2.042040858	1.46E-05	0.000275461
ynaD	LCABL_18060	ABC transporter ABC binding and permease protein	CAQ66886	2020.665935	3216.564059	1.591833664	0.000359535	0.004944016
-	LCABL_19510	hypothetical protein LCABL_19510 (<i>memb. prot.</i>)	CAQ67029	82.50709387	568.6072955	6.891617058	9.12E-18	4.54E-16
yuaG	LCABL_23350	hypothetical protein LCABL_23350	CAQ67402	3281.850639	6970.653211	2.124000748	3.40E-09	9.67E-08
yheE	LCABL_23360	hypothetical protein LCABL_23360 (<i>memb. prot.</i>)	CAQ67403	534.1929243	951.121728	1.780483576	2.60E-05	0.000461829
Uncharacterized								
-	LCABL_02420	Diadenosine tetraphosphatase related serine/threonine protein phosphatase	CAQ65374	1189.394938	3759.625681	3.160956518	5.97E-18	3.02E-16
-	LCABL_04830	hypothetical protein LCABL_04830	CAQ65609	38.46140712	70.63975076	1.836639792	0.005080957	0.043866555
-	LCABL_04890	myosin-cross-reactive antigen	CAQ65615	7837.938021	13509.85433	1.723649038	1.67E-05	0.000309665
-	LCABL_05730	hypothetical protein LCABL_05730	CAQ65698	60.7743173	107.0854455	1.762018075	0.004322465	0.038979142
-	LCABL_06220	hypothetical protein LCABL_06220	CAQ65747	7780.386328	12036.54515	1.547036952	0.00058221	0.007440663
-	LCABL_06670	hypothetical protein LCABL_06670	CAQ65792	1134.776425	2856.139718	2.516918447	4.81E-09	1.35E-07
-	LCABL_11580	Acetyltransferase, GNAT family	CAQ66243	551.2066937	889.4026662	1.613555634	0.00063427	0.007899783
-	LCABL_13200	hypothetical protein LCABL_13200	CAQ66403	215.6500608	350.6643942	1.626080664	0.000765016	0.009251648
-	LCABL_14830	Predicted sugar phosphatase of HAD family	CAQ66564	621.8028954	908.6700268	1.461347372	0.004839111	0.042849278
-	LCABL_15410	hypothetical protein LCABL_15410	CAQ66622	88.79900158	218.6965483	2.462826658	3.97E-08	1.00E-06
-	LCABL_16160	hypothetical protein LCABL_16160	CAQ66697	133.5621955	233.7698825	1.75026984	0.000530612	0.006951693
-	LCABL_16170	hypothetical protein LCABL_16170	CAQ66698	424.3538188	688.6969485	1.622930955	0.000572542	0.007372696
-	LCABL_16460	GCN5-related N-acetyltransferase	CAQ66727	129.4042175	202.3817249	1.563949992	0.004439076	0.039794546
ydgl	LCABL_16470	Ydgl	CAQ66728	731.8820763	1232.519635	1.684041289	0.000117557	0.00188029
-	LCABL_19500	hypothetical protein LCABL_19500	CAQ67028	408.6581886	2495.665669	6.106975801	1.77E-39	2.70E-37
-	LCABL_20200	Putative uncharacterized protein	CAQ67097	409.6787178	616.1939242	1.504090639	0.004229742	0.038370708
-	LCABL_21630	hypothetical protein LCABL_21630	CAQ67230	426.875702	630.9173685	1.477988477	0.003694564	0.034760926
yrjD	LCABL_22500	hypothetical protein LCABL_22500	CAQ67317	745.0125829	1155.71526	1.551269451	0.001232178	0.013616683
yrjC	LCABL_22510	Iron-binding oxidase subunit	CAQ67318	1079.676442	1661.996073	1.539346426	0.001381591	0.014995195
yrjB	LCABL_22520	Oxidoreductase	CAQ67319	457.6778865	741.4420949	1.620008562	0.000744404	0.009074623
-	LCABL_22630	hypothetical protein LCABL_22630	CAQ67330	478.7294781	1120.944978	2.341499801	0.000588712	0.007485762
-	LCABL_22660	Hydantoinase/oxoprolinase	CAQ67333	3838.901071	50318.25699	13.10746384	4.45E-60	1.35E-57
-	LCABL_22670	hypothetical protein LCABL_22670	CAQ67334	1599.645034	21720.87778	13.57856107	5.21E-75	2.64E-72
-	LCABL_22700	hypothetical protein LCABL_22700	CAQ67337	634.8554812	997.6413789	1.571446429	0.000746514	0.009074623
-	LCABL_25690	hypothetical protein LCABL_25690	CAQ67635	15.12541616	42.87011546	2.834309813	0.000212578	0.003151344
-	LCABL_28480	Putative uncharacterized protein	CAQ67898	1986.251198	3012.272265	1.516561585	0.004724161	0.042225667
-	LCABL_29850	hypothetical protein LCABL_29850	CAQ68035	129.3013704	224.9949868	1.740081998	0.000902728	0.01051108
ypjH	LCABL_31170	Oxidoreductase	CAQ68166	2256.157386	38069.36865	16.87354299	7.44E-32	7.53E-30

Downregulated genes								
Biosynthesis of lipids								
fabG	LCABL_22380	3-ketoacyl-(acyl-carrier-protein) reductase	CAQ67305	254.0501816	153.3149759	0.60348304	0.009488402	0.009488402
accA	LCABL_22900	Acetyl-CoA carboxylase carboxyl transferase subunit alpha	CAQ67357	4781.68451	1888.409615	0.394925598	3.40E-06	3.40E-06
accD	LCABL_22910	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta	CAQ67358	6700.435828	2667.641108	0.398129491	4.60E-11	4.60E-11
accC	LCABL_22920	Biotin carboxylase	CAQ67359	6453.096305	2727.580561	0.422677802	7.01E-10	7.01E-10
fabZ	LCABL_22930	(3R)-hydroxymyristoyl-	CAQ67360	5639.090039	2017.490529	0.357768809	3.98E-08	3.98E-08
accB	LCABL_22940	Acetyl-CoA carboxylase, biotin carboxyl carrier protein	CAQ67361	10666.05741	3815.195173	0.357694978	9.53E-14	9.53E-14
fabF	LCABL_22950	3-oxoacyl-	CAQ67362	17487.28868	7130.413145	0.407748352	1.83E-09	1.83E-09
fabG	LCABL_22960	3-oxoacyl-	CAQ67363	6699.60255	3423.955849	0.511068503	4.22E-06	4.22E-06
fabD	LCABL_22970	Malonyl CoA-acyl carrier protein transacylase	CAQ67364	6352.357538	3503.454286	0.551520324	0.029886535	0.029886535
fabZ	LCABL_23020	(3R)-hydroxymyristoyl-	CAQ67369	8484.243028	5131.783568	0.60486051	0.006951693	0.006951693
Biosynthesis of nucleotides								
guaB	LCABL_02060	Inosine-5-monophosphate dehydrogenase	CAQ65338	4542.16279	589.7764015	0.12984484	5.07E-48	5.07E-48
-	LCABL_03800	Inosine/uridine-preferring nucleoside hydrolase	CAQ65506	219.3207916	54.72002651	0.24949767	3.70E-05	3.70E-05
guaC	LCABL_10240	guanosine 5'-monophosphate oxidoreductase	CAQ66110	2352.728337	393.6496687	0.167316244	5.67E-34	5.67E-34
purK2	LCABL_12790	Phospho ribosylaminoimidazole carboxylase (AIR carboxylase), ATPase subunit	CAQ66363	3499.383674	2447.130326	0.699303236	0.042849278	0.042849278
purB2	LCABL_12800	Adenylosuccinate lyase	CAQ66364	11581.7003	7975.8362	0.688658486	0.028921727	0.028921727
nrdE	LCABL_16920	ribonucleotide-diphosphate reductase subunit alpha	CAQ66773	8868.692799	5665.64569	0.638836615	0.002588452	0.002588452
apt	LCABL_17710	Adenine phosphoribosyltransferase	CAQ66851	2217.347598	1451.552788	0.654634749	0.010010706	0.010010706
purD	LCABL_19650	Phosphoribosylamine--glycine ligase (GARS) (Glycinamide ribonucleotide synthetase) (Phosphoribosylglycinamide synthetase)	CAQ67043	302.0507949	150.4331646	0.498039294	0.000195613	0.000195613
purH	LCABL_19660	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	CAQ67044	535.5891267	277.192669	0.51754723	0.001710971	0.001710971
purN	LCABL_19670	Phosphoribosylglycinamide formyltransferase	CAQ67045	105.5378131	56.76041789	0.537820675	0.013723375	0.013723375
purM	LCABL_19680	Phosphoribosylformylglycinamide cyclo-ligase (AIRS) (Phosphoribosyl-aminoimidazole synthetase) (AIR synthase)	CAQ67046	319.7998904	160.8163676	0.502865612	0.000176209	0.000176209
purF	LCABL_19690	Amidophosphoribosyltransferase	CAQ67047	239.8832435	144.0647554	0.600561979	0.010317677	0.010317677
purL	LCABL_19700	phosphoribosylformylglycinamide synthase II	CAQ67048	636.3273453	405.8859118	0.637857095	0.011854102	0.011854102
purC	LCABL_19730	phosphoribosylaminoimidazole-succinocarboxamide synthase	CAQ67051	113.8400024	63.07923133	0.554104269	0.011936866	0.011936866
purK1	LCABL_19740	phosphoribosylaminoimidazole carboxylase ATPase subunit	CAQ67052	116.1348373	57.00456965	0.490848147	0.001858955	0.001858955
Biosynthesis of oligosaccharides								
arbx	LCABL_11980	Glycosyl transferase	CAQ66283	1460.628367	914.8165504	0.626317119	0.006200242	0.006200242
Metabolism of cofactors								
-	LCABL_04330	hypothetical protein LCABL_04330 (S-adenosyl-L-methionine hydroxide adenosyltransferase)	CAQ65559	615.3637445	390.2851415	0.634234865	0.008744957	0.008744957

apbE	LCABL_06470	Thiamine biosynthesis lipoprotein	CAQ65772	694.2675963	402.7311484	0.580080578	0.001756268	0.001756268
Amino acid catabolism								
metC2	LCABL_04030	Cystathionine beta-lyase	CAQ65529	599.1549479	380.7845617	0.635536038	0.033363137	0.033363137
hutG	LCABL_17680	N-formylglutamate amidohydrolase	CAQ66848	141.9237645	55.81920197	0.393304125	0.031184903	0.031184903
asnA1	LCABL_24350	L-asparaginase	CAQ67501	831.6023086	452.1145439	0.543666773	0.000107699	0.000107699
Lipid catabolism								
-	LCABL_08780	Glycerophosphoryl diester phosphodiesterase (Fragment)	CAQ66001	572.5692304	372.3961073	0.6503949	0.019846551	0.019846551
Organic acid metabolism								
cidC	LCABL_05020	pyruvate oxidase	CAQ65628	341.1456503	99.63823571	0.292069489	1.52E-06	1.52E-06
adhE	LCABL_08380	bifunctional acetaldehyde-CoA/alcohol dehydrogenase	CAQ65961	307.1245564	191.9087356	0.624856371	0.02323114	0.02323114
ackA	LCABL_23490	acetate kinase	CAQ67416	290.8096937	155.610995	0.535095626	0.000884313	0.000884313
Sugar catabolism								
glcNAcase	LCABL_02860	Beta-N-acetylglucosaminidase precursor	CAQ65412	982.2058161	63.61596271	0.064768465	8.32E-63	8.32E-63
fbA	LCABL_05010	Fructose-bisphosphate aldolase	CAQ65627	21825.82709	8281.120502	0.379418405	1.82E-05	1.82E-05
treA	LCABL_06890	Alpha, alpha-phosphotrehalase	CAQ65814	222.4345536	60.58997515	0.272394618	0.000145807	0.000145807
pgk	LCABL_11310	phosphoglycerate kinase	CAQ66216	65991.29043	42325.58499	0.641381381	0.007507751	0.007507751
bglA	LCABL_19970	6-phospho-beta-glucosidase	CAQ67075	1321.608103	694.0033093	0.52512035	0.002588452	0.002588452
agl2	LCABL_28460	Alpha-glucosidase	CAQ67896	3630.599556	2277.147103	0.627209657	0.003329008	0.003329008
Sugar transport								
PST transporter	LCABL_00120	Polysaccharide transporter	CAQ65144	278.5200815	130.6285004	0.469009271	0.002798435	0.002798435
pts4ABC	LCABL_06900	Beta-glucosides PTS, EIIABC	CAQ65815	739.5139481	264.4848876	0.357646922	0.005888321	0.005888321
glpF	LCABL_08620	Glycerol uptake facilitator protein	CAQ65985	1723.877642	1209.644762	0.701699896	0.031451475	0.031451475
glcU	LCABL_12860	Probable glucose uptake protein glcU	CAQ66370	2337.69743	1319.001688	0.564231141	0.043866555	0.043866555
celD	LCABL_19980	cellobiose phosphotransferase system IIC component	CAQ67076	398.9696672	157.0700007	0.393689079	6.75E-05	6.75E-05
celC	LCABL_19990	Cellobiose phosphotransferase system IIA component	CAQ67077	189.7734802	73.55590402	0.387598435	1.00E-06	1.00E-06
pts20A	LCABL_20000	Cellobiose PTS, EIIA	CAQ67078	114.3079401	41.07813153	0.359363763	6.59E-06	6.59E-06
pts20B	LCABL_20010	Cellobiose PTS, EIIB	CAQ67079	260.0959683	95.69488675	0.367921454	2.55E-08	2.55E-08
manO	LCABL_30310	ManO	CAQ68081	6667.40688	4151.97245	0.622726725	0.003791907	0.003791907
Organic acid transport								
dcuC	LCABL_03810	C4-dicarboxylate transporter	CAQ65507	621.8908419	130.1737914	0.209319357	3.59E-23	3.59E-23
oxlT	LCABL_06870	Oxalate/Formate Antiporter	CAQ65812	184.0100374	97.11724317	0.527782313	0.004131544	0.004131544
Peptide and amino acid transport								
ylcA	LCABL_05350	Amino acid permease	CAQ65661	416.996112	49.44291086	0.118569237	1.09E-27	1.09E-27
-	LCABL_09260	Putative L-aspartate transport protein	CAQ66020	293.1925567	128.3065891	0.437618849	4.41E-05	4.41E-05
dtpT	LCABL_20340	Di-/tripeptide transporter	CAQ67110	996.4615408	614.2603983	0.616441652	0.003950291	0.003950291
lysP	LCABL_20620	Lysine:H(+) symporter	CAQ67129	1181.840792	563.5422727	0.476834339	7.64E-07	7.64E-07
gbuC	LCABL_23250	GbuC protein	CAQ67392	188.6320012	34.88173908	0.18491952	0.000271058	0.000271058
gbuB	LCABL_23260	Putative glycine betaine membrane transport protein GbuB (GbuB protein)	CAQ67393	449.2307037	60.81827304	0.135383162	1.47E-31	1.47E-31
gbuA	LCABL_23270	GbuA protein	CAQ67394	489.3875841	77.50557493	0.158372581	4.82E-18	4.82E-18
Nucleotide transport								
-	LCABL_01430	Xanthine/uracil/vitamin C permease	CAQ65275	1736.771059	668.4635585	0.384888702	2.98E-11	2.98E-11

pucK	LCABL_12780	Xanthine / uracil transport protein	CAQ66362	2013.314343	1400.976429	0.695855783	0.04223772	0.04223772
Ion transport								
-	LCABL_02410	ABC-type Mn2+/Zn2+ transport system, permease component	CAQ65373	5495.683346	2543.522534	0.462821887	0.002588452	0.002588452
pacL3	LCABL_07720	Cation transporting P-type ATPase	CAQ65897	689.1779325	383.1943109	0.556016513	0.004428844	0.004428844
phoU	LCABL_10550	Phosphate transport system protein	CAQ66141	7866.739911	5140.979586	0.65350827	0.010270566	0.010270566
mtsA	LCABL_25940	Putative ATP binding protein	CAQ67660	100.0764636	29.23823016	0.292158906	5.36E-07	5.36E-07
phnD	LCABL_26140	Phosphonate ABC transporter, substrate binding protein	CAQ67680	11839.54295	5081.483393	0.429195909	1.65E-09	1.65E-09
phnC	LCABL_26150	Phosphonates import ATP-binding protein phnC	CAQ67681	2010.071847	823.9612716	0.409916329	7.91E-10	7.91E-10
phnB	LCABL_26160	Phosphonate ABC transporter, permease protein	CAQ67682	1178.472	494.9635613	0.420004516	4.97E-09	4.97E-09
phnE	LCABL_26170	Phosphonate ABC transporter, permease protein	CAQ67683	1822.294533	671.4637431	0.368471579	2.19E-08	2.19E-08
czcD	LCABL_27560	Putative cation efflux system protein	CAQ67807	1817.059607	1088.868507	0.599247544	0.001261716	0.001261716
Unsigned transporters								
lmrB-2	LCABL_09460	Lincomycin resistance protein LmrB	CAQ66033	378.4628715	219.4550146	0.579858768	0.006131225	0.006131225
mdt(A)	LCABL_11340	Multidrug transporter	CAQ66219	363.8296654	206.5654763	0.567753254	0.002063483	0.002063483
lasY	LCABL_11640	Putative uncharacterized protein lasY	CAQ66249	3807.807847	2716.022869	0.713277292	0.048609312	0.048609312
tspO	LCABL_13600	Sensory protein	CAQ66442	148.555365	70.25232102	0.472903291	0.000452504	0.000452504
-	LCABL_14450	ABC-type multidrug transport system, permease component	CAQ66526	200.5111069	86.41248069	0.430961067	9.07E-05	9.07E-05
-	LCABL_14460	ABC transporter	CAQ66527	152.6572336	69.45390531	0.454966356	0.007318696	0.007318696
cps1C	LCABL_22280	Repeat unit transporter	CAQ67295	3024.955595	1784.062514	0.589781389	0.012191786	0.012191786
ccl	LCABL_22370	Citrulline cluster-linked	CAQ67304	7444.69417	3929.353789	0.527805938	0.003624235	0.003624235
ydeD	LCABL_23930	transporter	CAQ67460	1184.435388	828.278574	0.699302455	0.035266018	0.035266018
ORF00032	LCABL_25060	Potential ABC transporter	CAQ67572	123.3665902	64.050113	0.519185242	0.007781457	0.007781457
-	LCABL_27920	ABC-type antimicrobial peptide transport system, permease component	CAQ67843	394.8284654	191.8281222	0.485851804	2.26E-05	2.26E-05
macB	LCABL_27930	Macrolide transport protein (ABC superfamily, atp_bind (N-terminal), membrane (C-terminal))	CAQ67844	378.5283798	192.7396681	0.509181552	0.000103461	0.000103461
ydiA	LCABL_28000	Permease	CAQ67851	474.5747584	277.7459159	0.585252188	0.00185593	0.00185593
Protein secretion								
yajC	LCABL_08370	Protein translocase subunit	CAQ65960	1792.108697	1110.916793	0.619893645	0.031014612	0.031014612
secE	LCABL_24730	preprotein translocase subunit SecE	CAQ67539	856.7418299	572.3576233	0.668063124	0.033348733	0.033348733
Transcriptional regulation								
kdgR	LCABL_00540	GntR family transcription regulator	CAQ65186	280.5399404	161.7856608	0.576693859	0.006155007	0.006155007
rbsR	LCABL_03210	Rbs operon repressor RbsR	CAQ65447	110.447564	66.0563705	0.598079017	0.04349017	0.04349017
treR	LCABL_06880	Transcription regulator	CAQ65813	68.8540632	13.89404739	0.201789796	0.000664523	0.000664523
laaB	LCABL_08220	LaaB	CAQ65945	584.8926274	381.7822954	0.652739114	0.022272235	0.022272235
labQ	LCABL_09340	Putative transcriptional regulator	CAQ66028	466.7830871	312.1147451	0.668650501	0.047168873	0.047168873
cggR	LCABL_11290	Glycolytic genes regulator	CAQ66214	50587.3386	19318.036	0.381874922	1.42E-12	1.42E-12
spxA	LCABL_19550	Transcriptional regulator Spx	CAQ67033	973.9289191	657.5514357	0.675153415	0.037901533	0.037901533
yqzB	LCABL_25200	YqzB	CAQ67586	294.2027677	181.9043001	0.618295679	0.026348408	0.026348408
-	LCABL_26740	Predicted transcriptional regulator	CAQ67740	1895.725184	1038.513229	0.547818448	0.000112722	0.000112722

Transcription								
greA	LCABL_18860	Transcription elongation factor GreA (Transcriptcleavage factor GreA)	CAQ66965	5450.680525	3780.186979	0.693525691	0.04349017	0.04349017
DNA replication and repair								
ssb	LCABL_00080	Single-stranded DNA-binding protein	CAQ65140	28.03564735	8.321803746	0.296829377	0.009997292	0.009997292
-	LCABL_07190	DNA mismatch repair protein MutS-like hypothetical protein LCABL_07200 (<i>uracil-DNA glycosylase</i>)	CAQ65844	254.1823228	131.7767366	0.518433915	0.000609695	0.000609695
ysiD	LCABL_07200		CAQ65845	64.83473048	33.8127401	0.521522028	3.36E-02	3.36E-02
ruvB	LCABL_08340	Holliday junction DNA helicase RuvB	CAQ65957	4702.805045	3034.256411	0.645201403	0.018902297	0.018902297
scpB	LCABL_15910	Segregation and condensation protein B	CAQ66672	2375.744366	1482.484987	0.62400863	0.011552671	0.011552671
rep	LCABL_27980	ATP-dependent DNA helicase	CAQ67849	4069.394778	2632.409326	0.646879811	0.007318696	0.007318696
tRNA modification								
queA	LCABL_08350	S-adenosylmethionine tRNA ribosyltransferase-isomerase	CAQ65958	13805.66488	9866.256477	0.714652758	0.048350863	0.048350863
tgt	LCABL_08360	Queuine tRNA-ribosyltransferase (tRNA-guanine transglycosylase) (Guanine insertion enzyme)	CAQ65959	2915.630679	1988.454355	0.681998021	0.03505754	0.03505754
gid	LCABL_16260	tRNA (uracil-5-)-methyltransferase Gid	CAQ66707	832.5428218	548.0365519	0.658268305	0.026984263	0.026984263
spoU	LCABL_18940	23S rRNA methyltransferase	CAQ66973	1476.424549	1014.300187	0.686997645	0.037933034	0.037933034
gidA	LCABL_31220	tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA	CAQ68171	8084.559698	5397.873829	0.667676909	0.014143818	0.014143818
Ribosomal proteins								
rimL	LCABL_21070	Ribosomal-protein-serine acetyltransferase	CAQ67174	36526.65287	25820.63211	0.70689839	0.047177462	0.047177462
Protein folding								
trxA	LCABL_02620	Thioredoxin (Trx)	CAQ65388	226.9160384	140.0408503	0.617148313	0.039794546	0.039794546
Cell envelope/secreted								
uppP	LCABL_10200	undecaprenyl pyrophosphate phosphatase	CAQ66106	2975.186816	2010.67996	0.675816372	0.020108705	0.020108705
-	LCABL_12590	Predicted Zn-dependent protease	CAQ66343	64.97876345	32.96475718	0.507315859	0.025009274	0.025009274
-	LCABL_12830	Phosphoglycerol transferase related protein, alkaline phosphatase superfamily	CAQ66367	1282.008449	763.7183892	0.595720246	0.002307199	0.002307199
pbp2A	LCABL_19450	Bifunctional glycosyltransferase/transpeptidase penicillin binding protein 2A	CAQ67024	2478.575898	1522.890978	0.614421765	0.002589674	0.002589674
-	LCABL_21220	hypothetical protein LCABL_21220 (<i>signal pept</i>)	CAQ67189	383.0548557	229.1374128	0.598184331	0.00468185	0.00468185
zmp3	LCABL_21230	Extracellular zinc metalloproteinase (Putative)	CAQ67190	1323.325472	683.8271034	0.516748992	0.024910225	0.024910225
-	LCABL_26070	Possible cell surface protein	CAQ67673	169.8350547	85.28903018	0.502187433	0.000461829	0.000461829
-	LCABL_27060	hypothetical protein LCABL_27060 (<i>WxL, lectin domain</i>)	CAQ67757	360.8453552	187.6723579	0.520090823	0.000387852	0.000387852
-	LCABL_30010	Putative uncharacterized protein (<i>signal pept</i>)	CAQ68051	2426.51986	1501.120021	0.618630841	0.005922204	0.005922204
Uncharacterized membrane proteins								
-	LCABL_00420	hypothetical protein LCABL_00420 (<i>memb prot</i>)	CAQ65174	189.2758412	106.7477625	0.56397986	0.006498106	0.006498106
ywjH	LCABL_01790	hypothetical protein LCABL_01790 (<i>memb prot</i>)	CAQ65311	559.6305696	301.9885832	0.539621314	0.003329008	0.003329008
pip	LCABL_04840	Phage infection protein	CAQ65610	1304.208689	789.069078	0.605017498	0.001423715	0.001423715
-	LCABL_08640	hypothetical protein LCABL_08640 (<i>memb prot</i>)	CAQ65987	3628.715122	2048.260558	0.564458903	0.00031787	0.00031787
-	LCABL_11350	hypothetical protein LCABL_11350 (<i>memb prot</i>)	CAQ66220	62.3663079	27.9953562	0.448885899	0.007318696	0.007318696
-	LCABL_13630	Predicted integral membrane protein	CAQ66445	167.7370049	55.37501338	0.330129976	4.17E-08	4.17E-08

ypaA	LCABL_15930	hypothetical protein LCABL_15930 (<i>memb prot</i>)	CAQ66674	237.9930061	146.3584671	0.614969614	0.017260381	0.017260381
hly	LCABL_16090	Hemolysin III	CAQ66690	549.4417683	98.35283531	0.179005021	1.22E-05	1.22E-05
-	LCABL_17090	hypothetical protein LCABL_17090	CAQ66790	1907.135208	1318.381179	0.691288784	0.033569352	0.033569352
ygcC	LCABL_18880	hypothetical protein LCABL_18880	CAQ66967	27883.08607	18527.54824	0.664472655	0.012208848	0.012208848
-	LCABL_21760	hypothetical protein LCABL_21760	CAQ67243	1115.903277	698.5871101	0.62602837	0.017796042	0.017796042
-	LCABL_23590	Predicted membrane protein	CAQ67426	42.18074161	18.76856963	0.444955895	0.018032426	0.018032426
-	LCABL_24470	hypothetical protein LCABL_24470	CAQ67513	2332.647136	1452.086215	0.622505733	0.024098345	0.024098345
cad	LCABL_24770	Sex pheromone cAD1	CAQ67543	3157.127667	2147.231527	0.680121856	0.028736084	0.028736084
-	LCABL_25080	Integral membrane protein, PIN and TRAM domains	CAQ67574	6194.392566	4374.54517	0.706210516	0.04349017	0.04349017
mtsB	LCABL_25930	Hydrophobic membrane protein	CAQ67659	45.40973209	20.77785328	0.457563882	0.031337605	0.031337605
-	LCABL_27470	Predicted membrane protein	CAQ67798	97.02753254	54.26019215	0.559224694	0.035722606	0.035722606
-	LCABL_27490	Putative uncharacterized protein	CAQ67800	101.2748199	51.60761001	0.509579874	0.038370708	0.038370708
Uncharacterized cytoplasmic proteins								
cydA	LCABL_00140	Cytochrome bd-I ubiquinol oxidase subunit I	CAQ65146	50.47826123	21.748976	0.430858264	0.008356189	0.008356189
FNV1622	LCABL_00200	CAAX amino terminal protease family (<i>self-immunity?</i>)	CAQ65152	46.01021818	17.42685953	0.378760637	0.00468185	0.00468185
-	LCABL_01460	hypothetical protein LCABL_01460 (<i>memb prot</i>)	CAQ65278	566.6765729	331.9803953	0.585837515	0.002881767	0.002881767
-	LCABL_01820	hypothetical protein LCABL_01820	CAQ65314	311.1987774	179.5739105	0.577039254	0.003691353	0.003691353
-	LCABL_02850	hypothetical protein LCABL_02850	CAQ65411	3699.852016	1927.099671	0.520858581	1.75E-05	1.75E-05
wecD	LCABL_03080	Acetyltransferase	CAQ65434	675.5038408	215.891634	0.319600898	0.001778091	0.001778091
wecD	LCABL_03820	Acetyltransferase	CAQ65508	553.6974996	133.3103034	0.240763781	2.05E-19	2.05E-19
-	LCABL_13490	hypothetical protein LCABL_13490	CAQ66432	1574.414242	1052.723156	0.66864433	0.016404249	0.016404249
-	LCABL_14630	hypothetical protein LCABL_14630 (<i>helicase? Truncated</i>)	CAQ66544	225.9222928	127.9270698	0.566243677	0.033140188	0.033140188
-	LCABL_15630	MazG nucleotide pyrophosphohydrolase	CAQ66644	1913.428869	1167.424385	0.610121654	0.015471069	0.015471069
-	LCABL_16240	hypothetical protein LCABL_16240	CAQ66705	565.431895	316.5310874	0.55980409	0.000351108	0.000351108
-	LCABL_17290	hypothetical protein LCABL_17290	CAQ66810	162.4593512	76.95667741	0.473698047	0.043892652	0.043892652
-	LCABL_18470	hypothetical protein LCABL_18470	CAQ66927	384.5532333	177.2411762	0.460901537	0.005486631	0.005486631
-	LCABL_18480	hypothetical protein LCABL_18480	CAQ66928	112.3431479	41.99384286	0.37379977	1.68E-05	1.68E-05
FNV1452	LCABL_19180	hypothetical protein LCABL_19180	CAQ66997	691.814358	441.8215148	0.638641725	0.013416175	0.013416175
yjjH	LCABL_20330	hypothetical protein LCABL_20330 (<i>phosphoesterase?</i>)	CAQ67109	2019.485145	928.6547988	0.459847304	1.38E-07	1.38E-07
eps3O	LCABL_22150	Eps3O	CAQ67282	1529.005196	964.0166526	0.630486185	0.012642487	0.012642487
wcxM	LCABL_22290	Putative acetyl transferase	CAQ67296	2067.937008	1346.595179	0.651178045	0.017495193	0.017495193
-	LCABL_23060	hypothetical protein LCABL_23060	CAQ67373	229.196837	150.5833975	0.657004693	0.036009193	0.036009193
-	LCABL_24330	hypothetical protein LCABL_24330	CAQ67499	92.0301601	43.4070879	0.471661549	0.001858955	0.001858955
-	LCABL_24340	hypothetical protein LCABL_24340	CAQ67500	1786.189621	893.0992205	0.500002469	2.59E-06	2.59E-06
-	LCABL_25820	Putative uncharacterized protein	CAQ67648	250.8574553	141.0317843	0.562198896	0.003476159	0.003476159
yabO	LCABL_27120	YabO	CAQ67763	574.7269611	352.8562723	0.613954619	0.008454328	0.008454328
-	LCABL_28090	hypothetical protein LCABL_28090	CAQ67859	52.56344062	23.81552922	0.453081627	0.033363137	0.033363137
tnp6	LCABL_29980	Transposase	CAQ68048	105.8618643	58.44984934	0.552133195	0.016770585	0.016770585

Table S3. Genes differentially expressed in Δ RR12 ordered according to their genomic location^a.

Operon ^b	Locus	Locus_tag	id	Mean BL23	Mean Δ RR12	Fold change	pval	padj
	ssb	LCABL_00080	CAQ65140	28.03564735	8.321803746	0.296829377	0.000845444	0.009997292
	PST transporter	LCABL_00120	CAQ65144	278.5200815	130.6285004	0.469009271	0.00018601	0.002798435
1	cydA	LCABL_00140	CAQ65146	50.47826123	21.748976	0.430858264	0.000673664	0.008356189
1	cydB	LCABL_00150	CAQ65147	39.69574877	30.23107956	0.761569702	0.346244755	0.67342476
	FNV1622	LCABL_00200	CAQ65152	46.01021818	17.42685953	0.378760637	0.000337389	0.00468185
	-	LCABL_00420	CAQ65174	189.2758412	106.7477625	0.56397986	0.000489657	0.006498106
	kdgR	LCABL_00540	CAQ65186	280.5399404	161.7856608	0.576693859	0.000459752	0.006155007
2	trpA	LCABL_00720	CAQ65204	477.4715793	1328.099087	2.7815249	7.02E-14	3.05E-12
2	trpB	LCABL_00730	CAQ65205	387.567084	1126.128651	2.905635431	6.70E-15	3.08E-13
2	trpF	LCABL_00740	CAQ65206	48.39169593	193.5715274	4.000098027	1.28E-14	5.82E-13
2	trpC	LCABL_00750	CAQ65207	75.19947332	225.9612253	3.004824572	1.09E-10	3.84E-09
2	trpD	LCABL_00760	CAQ65208	441.9133001	1309.289147	2.9627738	4.43E-08	1.11E-06
3	-	LCABL_00870	CAQ65219	98.43127245	172.6742177	1.754261765	0.004190438	0.038242466
3	-	LCABL_00880	CAQ65220	68.81377425	87.3625626	1.269550516	0.431853013	0.733185088
3	stpC	LCABL_00890	CAQ65221	28.72049421	43.70641001	1.521784747	0.072035301	0.270265777
4	dapB	LCABL_00960	CAQ65228	170.2362858	516.3088046	3.032895144	1.00E-13	4.22E-12
4	dapA	LCABL_00970	CAQ65229	73.98308785	198.3976504	2.681662204	8.51E-09	2.31E-07
4	dapE	LCABL_00980	CAQ65230	304.7492072	706.4137204	2.318016598	2.15E-09	6.23E-08
4	dapD	LCABL_00990	CAQ65231	108.4352197	227.7664574	2.100484125	0.012308224	0.085398842
4	lysA	LCABL_01000	CAQ65232	52.38057758	142.2767575	2.716212078	1.79E-07	4.22E-06
5	thrA	LCABL_01010	CAQ65233	302.2908832	972.6958128	3.217747761	1.10E-10	3.84E-09
5	dapF	LCABL_01020	CAQ65234	706.7782471	1644.79678	2.32717516	9.72E-09	2.61E-07
5	asd	LCABL_01030	CAQ65235	1833.109994	3626.725455	1.978454903	1.27E-07	3.08E-06
	yveB	LCABL_01320	CAQ65264	341.8810954	534.5252953	1.563483043	0.001612343	0.017132549
	-	LCABL_01430	CAQ65275	1736.771059	668.4635585	0.384888702	7.26E-13	2.98E-11
	-	LCABL_01460	CAQ65278	566.6765729	331.9803953	0.585837515	0.000192497	0.002881767
6	yhgE	LCABL_01640	CAQ65296	376.0925351	573.1987128	1.524089577	0.002351826	0.023823996
6	tetR	LCABL_01650	CAQ65297	59.99661654	80.46311528	1.341127549	0.148147935	0.418033032
	oppA	LCABL_01690	CAQ65301	7144.517608	65874.70209	9.220314891	1.40E-58	3.54E-56
7	yxaA	LCABL_01780	CAQ65310	615.054461	484.3431901	0.787480168	0.08675647	0.306227376
7	ywjH	LCABL_01790	CAQ65311	559.6305696	301.9885832	0.539621314	0.000226783	0.003329008
	-	LCABL_01820	CAQ65314	311.1987774	179.5739105	0.577039254	0.000256293	0.003691353
	guaB	LCABL_02060	CAQ65338	4542.16279	589.7764015	0.12984484	2.17E-50	5.07E-48
8	iolT	LCABL_02160	CAQ65348	29.70526633	37.44600549	1.260584742	0.393838892	0.711166378
8	iolA	LCABL_02170	CAQ65349	80.56508295	94.80204145	1.176713757	0.337554788	0.663537517
8	iolB	LCABL_02180	CAQ65350	70.93498012	71.28889344	1.004989264	0.93702317	0.994625712
8	iolC	LCABL_02190	CAQ65351	41.71063595	46.5823771	1.116798535	0.571822883	0.810905152

8	iolD	LCABL_02200	CAQ65352	103.0076968	168.3151823	1.63400588	0.003854685	0.035823812
8	iolG1	LCABL_02210	CAQ65353	40.83977939	56.07531178	1.373056187	0.151679588	0.422893823
8	iolG2	LCABL_02220	CAQ65354	42.32342984	58.23599629	1.375975352	0.214581392	0.513474685
8	iolE	LCABL_02230	CAQ65355	77.88196036	101.1531306	1.29880052	0.14433365	0.410955566
8	iolJ	LCABL_02240	CAQ65356	107.3840841	131.1133572	1.220975699	0.214949707	0.513951344
9	fecE	LCABL_02400	CAQ65372	8570.858992	4900.704568	0.571786862	0.052458861	0.223397526
9	-	LCABL_02410	CAQ65373	5495.683346	2543.522534	0.462821887	0.000167803	0.002588452
10	-	LCABL_02420	CAQ65374	1189.394938	3759.625681	3.160956518	5.97E-18	3.02E-16
10	mmsB	LCABL_02430	CAQ65375	441.9243543	1648.070176	3.729303805	3.88E-22	2.27E-20
10	pepF1	LCABL_02440	CAQ65376	2846.38097	9718.347338	3.414282009	9.49E-21	5.24E-19
	lytR	LCABL_02460	CAQ65377	3065.228576	4607.088961	1.503016446	0.001140479	0.01278936
11	trxA	LCABL_02620	CAQ65388	226.9160384	140.0408503	0.617148313	0.004429263	0.039794546
11	labL	LCABL_02630	CAQ65389	641.7254997	386.8729737	0.602863645	0.056746338	0.235409265
11	-	LCABL_02640	CAQ65390	228.7512409	150.4156035	0.657550984	0.181485068	0.470247754
12	livA	LCABL_02650	CAQ65391	679.0796949	3706.826166	5.458602568	1.12E-35	1.31E-33
12	livB	LCABL_02660	CAQ65392	950.8955652	4589.03584	4.826014557	9.05E-23	5.50E-21
12	livC	LCABL_02670	CAQ65393	401.7356275	2015.486148	5.016946495	2.82E-31	2.68E-29
12	livD	LCABL_02680	CAQ65394	734.6824706	3963.081147	5.394277536	1.55E-35	1.75E-33
12	livF	LCABL_02690	CAQ65395	664.6265895	3856.276255	5.802169693	4.86E-38	7.04E-36
	-	LCABL_02850	CAQ65411	3699.852016	1927.099671	0.520858581	7.87E-07	1.75E-05
	glcNAcase	LCABL_02860	CAQ65412	982.2058161	63.61596271	0.064768465	2.46E-65	8.32E-63
	pepT-2	LCABL_03060	CAQ65432	1561.334803	24094.21129	15.43180313	8.23E-82	1.25E-78
	oppA	LCABL_03070	CAQ65433	4241.66486	51878.45377	12.23068193	1.76E-31	1.73E-29
	wecD	LCABL_03080	CAQ65434	675.5038408	215.891634	0.319600898	0.000108827	0.001778091
	rbsR	LCABL_03210	CAQ65447	110.447564	66.0563705	0.598079017	0.004994429	0.04349017
	-	LCABL_03420	CAQ65468	4.476536193	16.38773874	3.660807828	0.005040373	0.04376484
	-	LCABL_03660	CAQ65492	127.3583166	253.2209483	1.988256087	1.48E-05	0.000277782
13	-	LCABL_03800	CAQ65506	219.3207916	54.72002651	0.24949767	1.71E-06	3.70E-05
13	dcuC	LCABL_03810	CAQ65507	621.8908419	130.1737914	0.209319357	5.68E-25	3.59E-23
13	wecD	LCABL_03820	CAQ65508	553.6974996	133.3103034	0.240763781	3.64E-21	2.05E-19
13	crgR	LCABL_03830	CAQ65509	1015.565868	715.057623	0.704097731	0.01898381	0.112679293
14	metC2	LCABL_04030	CAQ65529	599.1549479	380.7845617	0.635536038	0.003513065	0.033363137
14	frvR	LCABL_04040	CAQ65530	352.8011462	283.4850223	0.803526364	0.158653639	0.433238476
	-	LCABL_04330	CAQ65559	615.3637445	390.2851415	0.634234865	0.000713639	0.008744957
15	levA	LCABL_04410	CAQ65567	2585.666498	11342.03434	4.386503188	6.26E-29	4.76E-27
15	levB	LCABL_04420	CAQ65568	3526.234616	14149.91805	4.012755698	2.72E-26	1.80E-24
15	levC	LCABL_04430	CAQ65569	2921.188064	12582.92194	4.307467259	1.90E-28	1.41E-26
15	levD	LCABL_04440	CAQ65570	6158.868896	29292.70007	4.756181786	2.92E-32	3.06E-30
15	levX	LCABL_04450	CAQ65571	7987.177509	35704.48331	4.470225341	1.47E-19	7.83E-18
16	AGR_pat_610,	LCABL_04530	CAQ65579	66.12197076	222.035617	3.357970345	2.23E-12	8.80E-11

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16	yxwO	LCABL_04540	CAQ65580	42.55949341	91.12903905	2.141215314	0.000212078	0.003151344
16	atmA	LCABL_04550	CAQ65581	54.16815505	156.4577813	2.888371982	6.69E-09	1.85E-07
16	CAC0878	LCABL_04560	CAQ65582	28.12146698	51.99947492	1.849102501	0.009501728	0.070773898
16	tcyL	LCABL_04570	CAQ65583	31.88386223	64.17280365	2.012704835	0.003334903	0.032072056
17			CAQ65608	22.23217632	52.43946939	2.358719571	0.000618015	0.007781457
17	-	LCABL_04830	CAQ65609	38.46140712	70.63975076	1.836639792	0.005080957	0.043866555
	pip	LCABL_04840	CAQ65610	1304.208689	789.069078	0.605017498	8.53E-05	0.001423715
	-	LCABL_04890	CAQ65615	7837.938021	13509.85433	1.723649038	1.67E-05	0.000309665
	fba	LCABL_05010	CAQ65627	21825.82709	8281.120502	0.379418405	8.25E-07	1.82E-05
	cidC	LCABL_05020	CAQ65628	341.1456503	99.63823571	0.292069489	6.16E-08	1.52E-06
	pbpE	LCABL_05030	CAQ65629	474.9324485	3260.177974	6.864508803	4.32E-30	3.65E-28
	pepN	LCABL_05340	CAQ65660	10806.19581	15473.17986	1.431880389	0.004983448	0.04349017
	ylcA	LCABL_05350	CAQ65661	416.996112	49.44291086	0.118569237	1.32E-29	1.09E-27
18	metA	LCABL_05440	CAQ65670	230.9970972	324.9076124	1.406544136	0.030444062	0.153981861
18	cysK1	LCABL_05450	CAQ65671	684.0603966	1054.970119	1.542217799	0.002155283	0.022203072
	-	LCABL_06220	CAQ65747	7780.386328	12036.54515	1.547036952	0.00058221	0.007440663
19	pml	LCABL_06290	CAQ65754	183.7975054	308.5677292	1.678846122	0.000824253	0.009823153
19	fosD	LCABL_06300	CAQ65755	76.00833432	116.3370135	1.530582331	0.030576925	0.154357599
19	levC	LCABL_06310	CAQ65756	58.01382704	118.597253	2.044292871	0.000174923	0.002644736
19	levB	LCABL_06320	CAQ65757	54.81413065	71.33162798	1.301336483	0.191492651	0.484257058
19	manX	LCABL_06330	CAQ65758	28.44421466	35.62716952	1.252527797	0.366954854	0.690953005
	apbE	LCABL_06470	CAQ65772	694.2675963	402.7311484	0.580080578	0.000106913	0.001756268
	brnQ	LCABL_06660	CAQ65791	713.5895734	1165.432998	1.633197907	0.000530699	0.006951693
	-	LCABL_06670	CAQ65792	1134.776425	2856.139718	2.516918447	4.81E-09	1.35E-07
	-	LCABL_06720	CAQ65797	49.55678821	297.4610392	6.002427719	2.14E-08	5.60E-07
20	-	LCABL_06730	CAQ65798	9.105859204	49.46676539	5.432410526	2.13E-08	5.60E-07
20	-	LCABL_06740	CAQ65799	11.78643891	25.64725015	2.175996528	0.017874221	0.108639515
20	-	LCABL_06750	CAQ65800	29.2995438	71.99431721	2.45718219	6.82E-05	0.001151422
20	-	LCABL_06760	CAQ65801	37.56492455	69.73407774	1.856361448	0.014972908	0.098704268
	oxlT	LCABL_06870	CAQ65812	184.0100374	97.11724317	0.527782313	0.000292294	0.004131544
	treR	LCABL_06880	CAQ65813	68.8540632	13.89404739	0.201789796	3.80E-05	0.000664523
21	treA	LCABL_06890	CAQ65814	222.4345536	60.58997515	0.272394618	7.39E-06	0.000145807
21	pts4ABC	LCABL_06900	CAQ65815	739.5139481	264.4848876	0.357646922	0.000434019	0.005888321
	sstT	LCABL_06910	CAQ65816	1038.647995	8966.209604	8.632577781	1.81E-41	3.45E-39
	gdh	LCABL_06940	CAQ65819	162.2972797	272.1321057	1.676750875	0.000784394	0.009422033
	cspA	LCABL_06950	CAQ65820	22157.8651	31896.27237	1.439501153	0.004278778	0.03870002
22	-	LCABL_07090	CAQ65834	472.6798923	646.6313955	1.368011219	0.035151272	0.168759425
22	cah	LCABL_07100	CAQ65835	373.9460693	578.7050334	1.547562819	0.004087865	0.037645516
23	-	LCABL_07190	CAQ65844	254.1823228	131.7767366	0.518433915	3.47E-05	0.000609695

23	ysiD	LCABL_07200	CAQ65845	64.83473048	33.8127401	0.521522028	0.003556871	0.033569352
24	galK	LCABL_07300	CAQ65855	925.4329302	2736.596819	2.957099029	4.75E-16	2.29E-14
24	galE	LCABL_07310	CAQ65856	1313.070192	2927.719053	2.229674445	1.56E-09	4.63E-08
24	galT	LCABL_07320	CAQ65857	2984.300502	5715.797226	1.915288766	4.90E-07	1.11E-05
24	galR	LCABL_07330	CAQ65858	3275.024885	4246.11058	1.296512463	0.042700699	0.192819353
24	galM	LCABL_07340	CAQ65859	3181.04835	4267.21399	1.341448956	0.03157836	0.157582953
	pacL3	LCABL_07720	CAQ65897	689.1779325	383.1943109	0.556016513	0.000316242	0.004428844
	laaB	LCABL_08220	CAQ65945	584.8926274	381.7822954	0.652739114	0.002169326	0.022272235
	ruvB	LCABL_08340	CAQ65957	4702.805045	3034.256411	0.645201403	0.001809993	0.018902297
	queA	LCABL_08350	CAQ65958	13805.66488	9866.256477	0.714652758	0.005679914	0.048350863
25	tgt	LCABL_08360	CAQ65959	2915.630679	1988.454355	0.681998021	0.003737625	0.03505754
25	yajC	LCABL_08370	CAQ65960	1792.108697	1110.916793	0.619893645	0.00317392	0.031014612
	adhE	LCABL_08380	CAQ65961	307.1245564	191.9087356	0.624856371	0.002284026	0.02323114
	dltA	LCABL_08550	CAQ65978	14173.99494	25200.92351	1.777968992	0.000145717	0.002282652
	glpF	LCABL_08620	CAQ65985	1723.877642	1209.644762	0.701699896	0.003260025	0.031451475
26	-	LCABL_08640	CAQ65987	3628.715122	2048.260558	0.564458903	1.72585E-05	0.00031787
26	-	LCABL_08650	CAQ65988	865.9873354	632.5781556	0.730470447	0.015536633	0.100459211
	-	LCABL_08780	CAQ66001	572.5692304	372.3961073	0.6503949	0.001906941	0.019846551
	comX	LCABL_09250	CAQ66019	714.3355695	1180.117836	1.652049662	0.000142589	0.002245223
	-	LCABL_09260	CAQ66020	293.1925567	128.3065891	0.437618849	2.04E-06	4.41E-05
	labQ	LCABL_09340	CAQ66028	466.7830871	312.1147451	0.668650501	0.00551002	0.047168873
27	lmrB-2	LCABL_09460	CAQ66033	378.4628715	219.4550146	0.579858768	0.000455958	0.006131225
27	yjdF	LCABL_09470	CAQ66034	230.3393034	170.7681768	0.741376631	0.059081848	0.241006356
		54 LCABL_09800	CAQ66066	77.34267829	173.7705795	2.246761857	0.000270666	0.003861757
	ppnK	LCABL_10160	CAQ66102	332.0107895	495.5197693	1.492480922	0.002285657	0.02323114
	uppP	LCABL_10200	CAQ66106	2975.186816	2010.67996	0.675816372	0.001938746	0.020108705
	guaC	LCABL_10240	CAQ66110	2352.728337	393.6496687	0.167316244	4.48E-36	5.67E-34
	phoU	LCABL_10550	CAQ66141	7866.739911	5140.979586	0.65350827	0.000875313	0.010270566
		54 LCABL_11060	CAQ66191	144.8537578	292.1357567	2.016763397	0.002154889	0.022203072
28	cggR	LCABL_11290	CAQ66214	50587.3386	19318.036	0.381874922	3.23E-14	1.42E-12
28	gap-1	LCABL_11300	CAQ66215	135985.1898	108038.8754	0.794490014	0.268736914	0.590069338
28	pgk	LCABL_11310	CAQ66216	65991.29043	42325.58499	0.641381381	0.000592912	0.007507751
28	tpiA	LCABL_11320	CAQ66217	17376.23295	11096.44483	0.638598991	0.044438569	0.197890953
28	eno	LCABL_11330	CAQ66218	105390.3245	71645.71667	0.679813038	0.013833725	0.093423756
29	mdt(A)	LCABL_11340	CAQ66219	363.8296654	206.5654763	0.567753254	0.000129689	0.002063483
29	-	LCABL_11350	CAQ66220	62.3663079	27.9953562	0.448885899	0.000565129	0.007318696
30	map2	LCABL_11440	CAQ66229	1331.814519	2407.275056	1.807515252	4.15E-06	8.77E-05
30	pgmA	LCABL_11450	CAQ66230	704.9764416	1096.317665	1.555112483	0.001174793	0.013125722
30	msmK2	LCABL_11460	CAQ66231	1442.228911	2793.768555	1.937118674	3.31E-07	7.61E-06
30	dexB	LCABL_11470	CAQ66232	1411.092632	2495.81744	1.768712687	8.61E-06	0.000167739

30	malE	LCABL_11480	CAQ66233	1250.453487	2173.640574	1.738281829	1.74E-05	0.000318594
30	malF	LCABL_11490	CAQ66234	926.0981694	1560.003793	1.684490742	4.86E-05	0.00084449
30	malG	LCABL_11500	CAQ66235	430.5689302	607.6307703	1.411227629	0.018028612	0.108708238
-	-	LCABL_11580	CAQ66243	551.2066937	889.4026662	1.613555634	0.00063427	0.007899783
31	pta	LCABL_11620	CAQ66247	1798.445061	2658.480578	1.478210614	0.002239864	0.02291901
31	ydiB	LCABL_11630	CAQ66248	1273.307736	1619.341534	1.271759754	0.057330087	0.236468135
32	lasY	LCABL_11640	CAQ66249	3807.807847	2716.022869	0.713277292	0.005742265	0.048609312
32	ysdA	LCABL_11650	CAQ66250	3599.239242	2791.917432	0.775696542	0.046629885	0.204758344
	dnaQ	LCABL_11660	CAQ66251	549.4078376	802.5505752	1.4607556	0.004855091	0.042849278
33	-	LCABL_11970	CAQ66282	1131.78134	737.7447229	0.651843865	0.042451185	0.191977902
33	arbx	LCABL_11980	CAQ66283	1460.628367	914.8165504	0.626317119	0.000465171	0.006200242
33	wbbM	LCABL_11990	CAQ66284	679.9530619	538.3969585	0.791814889	0.140418127	0.402576122
33	arbZ	LCABL_12000	CAQ66285	981.5294381	688.1073177	0.70105622	0.012702818	0.087537107
34	-	LCABL_12590	CAQ66343	64.97876345	32.96475718	0.507315859	0.00250175	0.025009274
34	-	LCABL_12600	CAQ66344	58.89400005	34.54947969	0.586638361	0.043947218	0.196408815
35	xpt	LCABL_12770	CAQ66361	834.5771146	677.4345127	0.811709908	0.076603626	0.282865638
35	pucK	LCABL_12780	CAQ66362	2013.314343	1400.976429	0.695855783	0.004739409	0.04223772
35	purK2	LCABL_12790	CAQ66363	3499.383674	2447.130326	0.699303236	0.004864429	0.042849278
35	purB2	LCABL_12800	CAQ66364	11581.7003	7975.8362	0.688658486	0.002940709	0.028921727
-	-	LCABL_12830	CAQ66367	1282.008449	763.7183892	0.595720246	0.000148803	0.002307199
	glcU	LCABL_12860	CAQ66370	2337.69743	1319.001688	0.564231141	0.005069517	0.043866555
-	-	LCABL_13200	CAQ66403	215.6500608	350.6643942	1.626080664	0.000765016	0.009251648
-	-	LCABL_13490	CAQ66432	1574.414242	1052.723156	0.66864433	0.001527609	0.016404249
	tspO	LCABL_13600	CAQ66442	148.555365	70.25232102	0.472903291	2.52E-05	0.000452504
-	-	LCABL_13630	CAQ66445	167.7370049	55.37501338	0.330129976	1.37E-09	4.17E-08
36	ysfB	LCABL_14020	CAQ66483	1029.576297	1371.930292	1.332519306	0.038010429	0.178813769
36	sufD	LCABL_14030	CAQ66484	1514.000152	2199.361695	1.452682612	0.005730286	0.048609312
36	csd1	LCABL_14040	CAQ66485	1404.847402	1897.385425	1.350598949	0.026640481	0.1415392
36	iscU	LCABL_14050	CAQ66486	1189.28563	1630.651945	1.37111885	0.013876549	0.093505173
36	sufB	LCABL_14060	CAQ66487	2736.623401	3232.92857	1.181356766	0.182649277	0.470798263
	gst	LCABL_14360	CAQ66517	141.5422821	223.0310433	1.575720273	0.00404607	0.037373876
37	-	LCABL_14450	CAQ66526	200.5111069	86.41248069	0.430961067	4.33E-06	9.07E-05
37	-	LCABL_14460	CAQ66527	152.6572336	69.45390531	0.454966356	0.000565697	0.007318696
	traISLpl1	LCABL_14580	CAQ66539	225.3437647	551.3459548	2.44668831	1.82E-10	5.90E-09
-	-	LCABL_14630	CAQ66544	225.9222928	127.9270698	0.566243677	0.003456874	0.033140188
-	-	LCABL_14830	CAQ66564	621.8028954	908.6700268	1.461347372	0.004839111	0.042849278
38	glnP2	LCABL_14900	CAQ66571	675.495181	1082.495744	1.602521786	0.002776809	0.027487693
38	glnQ4	LCABL_14910	CAQ66572	886.4909478	1140.36498	1.286380851	0.036019317	0.17184098
38	glnH2	LCABL_14920	CAQ66573	1060.002934	1652.223598	1.558697193	0.004849258	0.042849278
39	pdhA	LCABL_15360	CAQ66617	6208.475683	8543.335968	1.376076255	0.010655002	0.076369227

39	pdhB	LCABL_15370	CAQ66618	3229.805099	5172.379254	1.601452439	0.000222648	0.003284602
39	pdhC	LCABL_15380	CAQ66619	4303.025678	7010.460059	1.629193173	0.000147889	0.00230479
39	pdhD	LCABL_15390	CAQ66620	9516.669916	14099.71906	1.481581182	0.003250533	0.031451475
40	ldh	LCABL_15400	CAQ66621	549.7585895	1440.299883	2.619876998	1.71E-12	6.84E-11
40	-	LCABL_15410	CAQ66622	88.79900158	218.6965483	2.462826658	3.97E-08	1.00E-06
40	suhB	LCABL_15420	CAQ66623	1273.390968	2444.741231	1.919866948	4.36E-07	9.96E-06
41	engB	LCABL_15620	CAQ66643	1120.486831	999.1691917	0.891727742	0.380695922	0.70044507
41	-	LCABL_15630	CAQ66644	1913.428869	1167.424385	0.610121654	0.001430527	0.015471069
42	fruA	LCABL_15690	CAQ66650	3366.184153	5081.142284	1.509466521	0.001066463	0.012184144
42	fruK	LCABL_15700	CAQ66651	1542.404001	2507.393437	1.625639868	0.001304852	0.014264194
42	fruR	LCABL_15710	CAQ66652	306.2072317	499.5726456	1.631485458	0.00530469	0.045539412
43	scpA	LCABL_15900	CAQ66671	2278.474002	1703.967924	0.74785489	0.026929829	0.142330002
43	scpB	LCABL_15910	CAQ66672	2375.744366	1482.484987	0.62400863	0.000999787	0.011552671
	ypaA	LCABL_15930	CAQ66674	237.9930061	146.3584671	0.614969614	0.001630052	0.017260381
	hly	LCABL_16090	CAQ66690	549.4417683	98.35283531	0.179005021	5.41E-07	1.22E-05
	-	LCABL_16160	CAQ66697	133.5621955	233.7698825	1.75026984	0.000530612	0.006951693
	-	LCABL_16170	CAQ66698	424.3538188	688.6969485	1.622930955	0.000572542	0.007372696
	-	LCABL_16240	CAQ66705	565.431895	316.5310874	0.55980409	1.93E-05	0.000351108
	gid	LCABL_16260	CAQ66707	832.5428218	548.0365519	0.658268305	0.002717073	0.026984263
44	hslV	LCABL_16280	CAQ66709	2754.134467	3307.24063	1.200827581	0.284868643	0.606243562
44	hslU	LCABL_16290	CAQ66710	2732.578179	3826.16172	1.400202106	0.009242089	0.069867431
44	-	LCABL_16300	CAQ66711	2224.514042	3343.8307	1.503173564	0.001492063	0.016079356
45	-	LCABL_16450	CAQ66726	103.2592878	153.4245406	1.485818311	0.020844324	0.118847846
45	-	LCABL_16460	CAQ66727	129.4042175	202.3817249	1.563949992	0.004439076	0.039794546
	ydgl	LCABL_16470	CAQ66728	731.8820763	1232.519635	1.684041289	0.000117557	0.00188029
46	hisC	LCABL_16480	CAQ66729	467.9169044	2165.633538	4.628243857	3.42E-29	2.67E-27
46	hisE	LCABL_16490	CAQ66730	75.32783229	416.6981683	5.531795562	2.44E-27	1.69E-25
46	hisI	LCABL_16500	CAQ66731	86.64457283	452.9272822	5.227416645	2.00E-25	1.29E-23
46	hisF	LCABL_16510	CAQ66732	206.6700907	1343.65547	6.501451011	1.44E-39	2.43E-37
46	hisA	LCABL_16520	CAQ66733	291.6296637	1454.284247	4.986750075	2.38E-30	2.07E-28
46	hisH	LCABL_16530	CAQ66734	333.4767769	1635.332413	4.903886946	2.17E-30	2.00E-28
46	hisB	LCABL_16540	CAQ66735	234.1550451	1506.195794	6.432472097	1.66E-39	2.66E-37
46	hisD	LCABL_16550	CAQ66736	433.2432902	2124.136665	4.902872618	2.28E-30	2.04E-28
46	hisG	LCABL_16560	CAQ66737	91.05388112	485.5814208	5.332901957	2.24E-26	1.51E-24
46	hisZ	LCABL_16570	CAQ66738	207.8739401	1273.379634	6.125730012	2.30E-36	3.04E-34
47	bkdC	LCABL_16660	CAQ66747	118.8410842	211.6734218	1.781146843	0.000309479	0.004354197
47	bkdB	LCABL_16670	CAQ66748	26.99176563	62.16025281	2.302933927	0.000419404	0.005715555
47	bkdA	LCABL_16680	CAQ66749	83.60443683	145.4588794	1.739846411	0.00157965	0.016844061
47	bkdD	LCABL_16690	CAQ66750	92.27161132	183.980896	1.993905746	5.15E-05	0.000884313
47	buk	LCABL_16700	CAQ66751	35.99799736	65.95007306	1.832048389	0.010376288	0.075587021

47	ptb	LCABL_16710	CAQ66752	49.02674964	73.26686126	1.494426243	0.048577693	0.210730808
	pyrB	LCABL_16780	CAQ66759	633.9994247	967.7229764	1.526378319	0.001370671	0.014929998
48	nrdH	LCABL_16910	CAQ66772	614.4212828	415.6960368	0.676565165	0.016689393	0.104854858
48	nrdE	LCABL_16920	CAQ66773	8868.692799	5665.64569	0.638836615	0.000169497	0.002588452
48	nrdF	LCABL_16930	CAQ66774	3616.113971	2593.711156	0.71726477	0.02582906	0.139669953
	lplA1	LCABL_16960	CAQ66777	6234.927839	10024.45527	1.607790102	0.000138638	0.002194386
	-	LCABL_17090	CAQ66790	1907.135208	1318.381179	0.691288784	0.003551716	0.033569352
49	-	LCABL_17480	CAQ66829	97.79233113	199.6959358	2.042040858	1.46E-05	0.000275461
49	mppX	LCABL_17490	CAQ66830	78.78992742	115.1801194	1.461863504	0.045530413	0.201470411
	hutG	LCABL_17680	CAQ66848	141.9237645	55.81920197	0.393304125	0.003201609	0.031184903
50	apt	LCABL_17710	CAQ66851	2217.347598	1451.552788	0.654634749	0.000849872	0.010010706
50	recJ	LCABL_17720	CAQ66852	3214.328655	2546.124797	0.792117132	0.052873574	0.224239099
51	mdlB	LCABL_18050	CAQ66885	3142.032647	3823.15405	1.216777316	0.123987363	0.370863776
51	ynaD	LCABL_18060	CAQ66886	2020.665935	3216.564059	1.591833664	0.000359535	0.004944016
	oppA	LCABL_18220	CAQ66902	56281.28107	147322.276	2.617607012	1.34E-14	5.98E-13
52	oppC	LCABL_18230	CAQ66903	15612.31195	34188.44628	2.189838788	1.49E-09	4.50E-08
52	oppB	LCABL_18240	CAQ66904	3456.459942	7831.629115	2.265794844	2.63E-10	8.42E-09
52	oppB	LCABL_18250	CAQ66905	1519.02368	3421.56279	2.252474951	1.80E-09	5.32E-08
52	oppF	LCABL_18260	CAQ66906	11766.60614	27907.44491	2.371749728	2.25E-11	8.34E-10
52	oppD	LCABL_18270	CAQ66907	12270.66556	30143.2836	2.45653208	6.75E-09	1.85E-07
53	-	LCABL_18470	CAQ66927	384.5532333	177.2411762	0.460901537	0.0004008	0.005486631
53	-	LCABL_18480	CAQ66928	112.3431479	41.99384286	0.37379977	7.54E-07	1.68E-05
	pepX	LCABL_18670	CAQ66946	1769.844076	3990.127791	2.254508093	4.49E-10	1.42E-08
54	greA	LCABL_18860	CAQ66965	5450.680525	3780.186979	0.693525691	0.004989843	0.04349017
54	udk	LCABL_18870	CAQ66966	4971.835155	3696.99013	0.743586626	0.030923391	0.155589712
	ygcC	LCABL_18880	CAQ66967	27883.08607	18527.54824	0.664472655	0.001076661	0.012208848
	spoU	LCABL_18940	CAQ66973	1476.424549	1014.300187	0.686997645	0.00414405	0.037933034
55	hpk5	LCABL_18970	CAQ66976	3569.320029	11183.73787	3.133296476	1.30E-18	6.84E-17
55	rrp5	LCABL_18980	CAQ66977	1032.793656	1.545704322	0.001496625	2.29E-140	6.95E-137
56	FNV1452	LCABL_19180	CAQ66997	691.814358	441.8215148	0.638641725	0.001209619	0.013416175
56	-	LCABL_19190	CAQ66998	127.593255	87.49949	0.685768931	0.034152094	0.16500511
	pbp2A	LCABL_19450	CAQ67024	2478.575898	1522.890978	0.614421765	0.000170429	0.002589674
57	-	LCABL_19500	CAQ67028	408.6581886	2495.665669	6.106975801	1.77E-39	2.70E-37
57	-	LCABL_19510	CAQ67029	82.50709387	568.6072955	6.891617058	9.12E-18	4.54E-16
	spxA	LCABL_19550	CAQ67033	973.9289191	657.5514357	0.675153415	0.004128137	0.037901533
58	purD	LCABL_19650	CAQ67043	302.0507949	150.4331646	0.498039294	1.02E-05	0.000195613
58	purH	LCABL_19660	CAQ67044	535.5891267	277.192669	0.51754723	0.00010303	0.001710971
58	purN	LCABL_19670	CAQ67045	105.5378131	56.76041789	0.537820675	0.001246348	0.013723375
58	purM	LCABL_19680	CAQ67046	319.7998904	160.8163676	0.502865612	9.16E-06	0.000176209
58	purF	LCABL_19690	CAQ67047	239.8832435	144.0647554	0.600561979	0.000882723	0.010317677

58	purL	LCABL_19700	CAQ67048	636.3273453	405.8859118	0.637857095	0.001029774	0.011854102
58	purQ	LCABL_19710	CAQ67049	170.737707	117.3396645	0.687251027	0.018967273	0.112679293
58	purS	LCABL_19720	CAQ67050	77.47313234	50.06376386	0.646208077	0.029322841	0.150527217
58	purC	LCABL_19730	CAQ67051	113.8400024	63.07923133	0.554104269	0.001040892	0.011936866
58	purK1	LCABL_19740	CAQ67052	116.1348373	57.00456965	0.490848147	0.000115204	0.001858955
58	purE	LCABL_19750	CAQ67053	31.23193637	17.36329662	0.555946849	0.067858099	0.260379752
59	bglA	LCABL_19970	CAQ67075	1321.608103	694.0033093	0.52512035	0.000169008	0.002588452
59	celD	LCABL_19980	CAQ67076	398.9696672	157.0700007	0.393689079	3.18E-06	6.75E-05
59	celC	LCABL_19990	CAQ67077	189.7734802	73.55590402	0.387598435	3.92E-08	1.00E-06
59	pts20A	LCABL_20000	CAQ67078	114.3079401	41.07813153	0.359363763	2.84E-07	6.59E-06
59	pts20B	LCABL_20010	CAQ67079	260.0959683	95.69488675	0.367921454	8.23E-10	2.55E-08
-	-	LCABL_20200	CAQ67097	409.6787178	616.1939242	1.504090639	0.004229742	0.038370708
60	gntR	LCABL_20270	CAQ67104	2306.019579	2994.113348	1.298390255	0.029830905	0.152363228
60	nagA	LCABL_20280	CAQ67105	3639.205903	5066.411394	1.392174977	0.005831692	0.049229201
61	yjjH	LCABL_20330	CAQ67109	2019.485145	928.6547988	0.459847304	4.94E-09	1.38E-07
61	dtpT	LCABL_20340	CAQ67110	996.4615408	614.2603983	0.616441652	0.000278171	0.003950291
62	feoA	LCABL_20440	CAQ67120	189.9365945	318.7899465	1.678401928	0.017432486	0.10696616
62	-	LCABL_20450	CAQ67121	69.20853372	128.7495811	1.860313667	0.001135329	0.012778759
	lysP	LCABL_20620	CAQ67129	1181.840792	563.5422727	0.476834339	2.97E-08	7.64E-07
	rimL	LCABL_21070	CAQ67174	36526.65287	25820.63211	0.70689839	0.005526547	0.047177462
-	-	LCABL_21220	CAQ67189	383.0548557	229.1374128	0.598184331	0.000337282	0.00468185
	zmp3	LCABL_21230	CAQ67190	1323.325472	683.8271034	0.516748992	0.002475448	0.024910225
	traISLpl1	LCABL_21240	CAQ67191	225.3437647	551.6223823	2.447915003	1.78E-10	5.80E-09
	traISLpl1	LCABL_21430	CAQ67210	226.4644515	554.1333651	2.446888956	1.72E-10	5.77E-09
63	pepL	LCABL_21440	CAQ67211	1922.976374	20300.18023	10.55664568	2.15E-22	1.28E-20
63	dppA	LCABL_21450	CAQ67212	983.9723731	13943.71606	14.17084102	2.41E-77	1.46E-74
63	ysdC	LCABL_21460	CAQ67213	788.5867369	11722.0524	14.86463296	2.77E-79	2.10E-76
63	oppA	LCABL_21470	CAQ67214	2873.944219	27840.30068	9.687140236	7.86E-60	2.17E-57
	int	LCABL_21530	CAQ67220	212.9463251	477.1721997	2.240809742	4.96E-08	1.24E-06
	coaA	LCABL_21550	CAQ67222	322.2945975	566.9313291	1.759046951	0.000105104	0.001735923
64	pepR	LCABL_21620	CAQ67229	2311.027219	4131.353693	1.787669855	5.99E-06	0.000120518
64	-	LCABL_21630	CAQ67230	426.875702	630.9173685	1.477988477	0.003694564	0.034760926
65	-	LCABL_21760	CAQ67243	1115.903277	698.5871101	0.62602837	0.001692351	0.017796042
65	-	LCABL_21770	CAQ67244	456.8315489	387.7098725	0.848693295	0.278868587	0.601477384
66	glnP	LCABL_21860	CAQ67253	3256.41577	5721.397875	1.756961727	6.63E-06	0.000131783
66	glnM	LCABL_21870	CAQ67254	3485.558646	6315.039654	1.811772601	5.00E-06	0.000103461
66	glnH1	LCABL_21880	CAQ67255	4596.883592	7774.607252	1.691277818	6.74E-05	0.001143728
66	glnQ	LCABL_21890	CAQ67256	2029.566821	4155.595012	2.047528058	2.32E-08	6.02E-07
67	glgD	LCABL_22040	CAQ67271	448.7973655	775.9634609	1.728983993	6.05E-05	0.00103299
67	glgC	LCABL_22050	CAQ67272	160.2958572	315.5011309	1.968242575	9.13E-06	0.000176209

67	glgB	LCABL_22060	CAQ67273	245.4637409	426.6196831	1.738015079	0.000342224	0.004727353
	ilvE	LCABL_22070	CAQ67274	993.4071628	4318.625317	4.347286268	1.01E-27	7.29E-26
	eps3O	LCABL_22150	CAQ67282	1529.005196	964.0166526	0.630486185	0.001119062	0.012642487
68	wbaq	LCABL_22270	CAQ67294	3204.33997	2020.221837	0.630464263	0.008472077	0.065310835
68	cps1C	LCABL_22280	CAQ67295	3024.955595	1784.062514	0.589781389	0.001071144	0.012191786
	wcxM	LCABL_22290	CAQ67296	2067.937008	1346.595179	0.651178045	0.001657985	0.017495193
	ccl	LCABL_22370	CAQ67304	7444.69417	3929.353789	0.527805938	0.000250441	0.003624235
69	fabG	LCABL_22380	CAQ67305	254.0501816	153.3149759	0.60348304	0.000793042	0.009488402
69	-	LCABL_22390	CAQ67306	65.44251157	42.73037435	0.652945208	0.046145355	0.203240193
70	oppF	LCABL_22420	CAQ67309	3091.189883	19909.17979	6.440620131	1.54E-43	3.11E-41
70	oppD	LCABL_22430	CAQ67310	5012.041705	30595.9712	6.104492542	1.53E-36	2.12E-34
70	oppC	LCABL_22440	CAQ67311	7155.92658	38031.92743	5.314745338	1.07E-35	1.31E-33
70	oppB	LCABL_22450	CAQ67312	2883.159617	19040.45873	6.604025189	8.85E-23	5.49E-21
70	oppA	LCABL_22460	CAQ67313	13643.56233	95624.81643	7.00878657	1.90E-09	5.56E-08
71	yrjD	LCABL_22500	CAQ67317	745.0125829	1155.71526	1.551269451	0.001232178	0.013616683
71	yrjC	LCABL_22510	CAQ67318	1079.676442	1661.996073	1.539346426	0.001381591	0.014995195
71	yrjB	LCABL_22520	CAQ67319	457.6778865	741.4420949	1.620008562	0.000744404	0.009074623
72	recD	LCABL_22620	CAQ67329	1103.366986	2209.334964	2.002357322	1.36E-07	3.29E-06
72	-	LCABL_22630	CAQ67330	478.7294781	1120.944978	2.341499801	0.000588712	0.007485762
	mocE	LCABL_22650	CAQ67332	443.1098957	2807.515655	6.335935357	1.35E-39	2.42E-37
73	-	LCABL_22660	CAQ67333	3838.901071	50318.25699	13.10746384	4.45E-60	1.35E-57
73	-	LCABL_22670	CAQ67334	1599.645034	21720.87778	13.57856107	5.21E-75	2.64E-72
73	-	LCABL_22680	CAQ67335	1300.169959	16493.63204	12.68575075	3.26E-29	2.61E-27
74	-	LCABL_22690	CAQ67336	399.719574	586.0554967	1.46616662	0.06889051	0.263675391
74	-	LCABL_22700	CAQ67337	634.8554812	997.6413789	1.571446429	0.000746514	0.009074623
	hsdS	LCABL_22710	CAQ67338	0.631948223	11.77561964	18.63383615	0.000630149	0.007880754
75	accA	LCABL_22900	CAQ67357	4781.68451	1888.409615	0.394925598	1.42E-07	3.40E-06
75	accD	LCABL_22910	CAQ67358	6700.435828	2667.641108	0.398129491	1.14E-12	4.60E-11
75	accC	LCABL_22920	CAQ67359	6453.096305	2727.580561	0.422677802	1.85E-11	7.01E-10
75	fabZ	LCABL_22930	CAQ67360	5639.090039	2017.490529	0.357768809	1.30E-09	3.98E-08
75	accB	LCABL_22940	CAQ67361	10666.05741	3815.195173	0.357694978	2.01E-15	9.53E-14
75	fabF	LCABL_22950	CAQ67362	17487.28868	7130.413145	0.407748352	5.11E-11	1.83E-09
75	fabG	LCABL_22960	CAQ67363	6699.60255	3423.955849	0.511068503	1.79E-07	4.22E-06
75	fabD	LCABL_22970	CAQ67364	6352.357538	3503.454286	0.551520324	0.003048643	0.029886535
75	fabK	LCABL_22980	CAQ67365	97562.60839	67792.12623	0.694857665	0.116611221	0.357475207
75	acpP	LCABL_22990	CAQ67366	11929.14769	7083.821362	0.593824601	0.135644091	0.393341977
75	fabH	LCABL_23000	CAQ67367	25595.23162	18771.18087	0.733385857	0.100204182	0.325342425
75	marR	LCABL_23010	CAQ67368	7618.746251	5101.499119	0.669598245	0.018615045	0.111360474
75	fabZ	LCABL_23020	CAQ67369	8484.243028	5131.783568	0.60486051	0.000526293	0.006951693
	-	LCABL_23060	CAQ67373	229.196837	150.5833975	0.657004693	0.003886481	0.036009193

76	gbuC	LCABL_23250	CAQ67392	188.6320012	34.88173908	0.18491952	1.43E-05	0.000271058
76	gbuB	LCABL_23260	CAQ67393	449.2307037	60.81827304	0.135383162	1.35E-33	1.47E-31
76	gbuA	LCABL_23270	CAQ67394	489.3875841	77.50557493	0.158372581	8.87E-20	4.82E-18
77	thrB	LCABL_23310	CAQ67398	666.3739004	1217.151871	1.826529926	7.54E-06	0.000147848
77	thrC	LCABL_23320	CAQ67399	1322.12388	2456.437602	1.85794814	2.47E-06	5.29E-05
78	thrA	LCABL_23330	CAQ67400	338.2563351	1016.663585	3.005601016	5.43E-06	0.000110846
78	apk	LCABL_23340	CAQ67401	559.9623542	1581.922443	2.825051417	4.96E-11	1.79E-09
79	yuaG	LCABL_23350	CAQ67402	3281.850639	6970.653211	2.124000748	3.40E-09	9.67E-08
79	yheE	LCABL_23360	CAQ67403	534.1929243	951.121728	1.780483576	2.60E-05	0.000461829
80	pfoSR	LCABL_23370	CAQ67404	677.2636784	1504.165454	2.220945109	2.80E-09	8.02E-08
80	ldhA	LCABL_23380	CAQ67405	316.8658029	814.0043414	2.568924554	1.24E-11	4.78E-10
80	araT	LCABL_23390	CAQ67406	453.993275	1269.880326	2.797134662	7.67E-14	3.28E-12
81	-	LCABL_23580	CAQ67425	101.2230053	48.40990393	0.478250016	0.02890799	0.149917031
81	-	LCABL_23590	CAQ67426	42.18074161	18.76856963	0.444955895	0.001720765	0.018032426
81	-	LCABL_23600	CAQ67427	25.19891463	9.535938878	0.378426572	0.009395815	0.070329754
-	-	LCABL_24330	CAQ67499	92.0301601	43.4070879	0.471661549	0.000115611	0.001858955
-	-	LCABL_24340	CAQ67500	1786.189621	893.0992205	0.500002469	1.06E-07	2.59E-06
asnA1	-	LCABL_24350	CAQ67501	831.6023086	452.1145439	0.543666773	5.24E-06	0.000107699
-	-	LCABL_24470	CAQ67513	2332.647136	1452.086215	0.622505733	0.002386838	0.024098345
prtP	-	LCABL_24520	CAQ67518	2675.182788	77407.99017	28.93558919	1.52E-79	1.54E-76
prsA	-	LCABL_24530	CAQ67519	396.3688197	1766.380947	4.456407415	1.69E-10	5.76E-09
secE	-	LCABL_24730	CAQ67539	856.7418299	572.3576233	0.668063124	0.003489601	0.033348733
cad	-	LCABL_24770	CAQ67543	3157.127667	2147.231527	0.680121856	0.002912377	0.028736084
82	ORF00031	LCABL_25050	CAQ67571	75.86883393	59.7959946	0.788149646	0.302088332	0.623175836
82	ORF00032	LCABL_25060	CAQ67572	123.3665902	64.050113	0.519185242	0.000619649	0.007781457
-	-	LCABL_25080	CAQ67574	6194.392566	4374.54517	0.706210516	0.004960545	0.04349017
pepC1	-	LCABL_25130	CAQ67579	8687.113935	25263.2664	2.908131123	1.15E-16	5.65E-15
ppdK	-	LCABL_25190	CAQ67585	607.6394838	1482.273415	2.439396146	2.04E-07	4.76E-06
yqzB	-	LCABL_25200	CAQ67586	294.2027677	181.9043001	0.618295679	0.002644378	0.026348408
-	-	LCABL_25690	CAQ67635	15.12541616	42.87011546	2.834309813	0.000212578	0.003151344
-	-	LCABL_25820	CAQ67648	250.8574553	141.0317843	0.562198896	0.000239065	0.003476159
83	mtsC	LCABL_25920	CAQ67658	64.15242651	43.04396183	0.670963893	0.071112682	0.267707952
83	mtsB	LCABL_25930	CAQ67659	45.40973209	20.77785328	0.457563882	0.003227598	0.031337605
83	mtsA	LCABL_25940	CAQ67660	100.0764636	29.23823016	0.292158906	2.01E-08	5.36E-07
traISLp1	-	LCABL_25970	CAQ67663	225.3437647	551.6223823	2.447915003	1.78E-10	5.80E-09
-	-	LCABL_26070	CAQ67673	169.8350547	85.28903018	0.502187433	2.59E-05	0.000461829
84	phnD	LCABL_26140	CAQ67680	11839.54295	5081.483393	0.429195909	4.49E-11	1.65E-09
84	phnC	LCABL_26150	CAQ67681	2010.071847	823.9612716	0.409916329	2.11E-11	7.91E-10
84	phnB	LCABL_26160	CAQ67682	1178.472	494.9635613	0.420004516	1.44E-10	4.97E-09
84	phnE	LCABL_26170	CAQ67683	1822.294533	671.4637431	0.368471579	6.98E-10	2.19E-08

	traISlp1	LCABL_26180	CAQ67684	225.3437647	551.9943787	2.449565798	1.73E-10	5.77E-09
	-	LCABL_27060	CAQ67757	360.8453552	187.6723579	0.520090823	2.14E-05	0.000387852
85	divIC	LCABL_27110	CAQ67762	2339.802551	1656.150852	0.7078165	0.056307758	0.234409968
85	yabO	LCABL_27120	CAQ67763	574.7269611	352.8562723	0.613954619	0.00068714	0.008454328
85	ltrB	LCABL_27130	CAQ67764	1957.500842	1423.256161	0.727078186	0.01411575	0.094897104
	-	LCABL_27210	CAQ67772	4068.209318	12551.08723	3.085162598	5.46E-18	2.81E-16
	yciB	LCABL_27220	CAQ67773	173.655924	226.0593998	1.301766128	0.229771612	0.532628473
86	gltD	LCABL_27230	CAQ67774	1046.304122	11571.45758	11.05936346	1.18E-43	2.57E-41
86	gltA	LCABL_27240	CAQ67775	2451.586514	34175.3973	13.94011474	1.05E-27	7.43E-26
	mutT	LCABL_27440	CAQ67795	14.62317164	39.69084024	2.71424293	0.000767165	0.009251648
	-	LCABL_27470	CAQ67798	97.02753254	54.26019215	0.559224694	0.00383204	0.035722606
87	nudA	LCABL_27480	CAQ67799	64.59975094	41.22557501	0.638169256	0.083823301	0.300045951
87	-	LCABL_27490	CAQ67800	101.2748199	51.60761001	0.509579874	0.004220976	0.038370708
88	czcD	LCABL_27560	CAQ67807	1817.059607	1088.868507	0.599247544	7.51E-05	0.001261716
88	ipk	LCABL_27570	CAQ67808	1548.456721	1218.866051	0.78714893	0.065601045	0.255919865
89	-	LCABL_27920	CAQ67843	394.8284654	191.8281222	0.485851804	1.03E-06	2.26E-05
89	macB	LCABL_27930	CAQ67844	378.5283798	192.7396681	0.509181552	4.98E-06	0.000103461
	rep	LCABL_27980	CAQ67849	4069.394778	2632.409326	0.646879811	0.000565941	0.007318696
	ydiA	LCABL_28000	CAQ67851	474.5747584	277.7459159	0.585252188	0.000114202	0.00185593
	-	LCABL_28150	CAQ67865	68.51665258	336.0301319	4.904357106	2.72E-21	1.56E-19
	agl2	LCABL_28460	CAQ67896	3630.599556	2277.147103	0.627209657	0.000227849	0.003329008
	-	LCABL_28470	CAQ67897	1.396705627	0.965278534	0.691110937	0.987305415	1
	-	LCABL_28480	CAQ67898	1986.251198	3012.272265	1.516561585	0.004724161	0.042225667
	xalA	LCABL_28750	CAQ67925	1484.515807	2659.152843	1.791259366	6.58E-06	0.000131609
90	yidA	LCABL_28870	CAQ67937	249.1280405	438.3266708	1.759443336	0.00093865	0.010887622
90	pts18CBA	LCABL_28880	CAQ67938	175.6948959	407.9677796	2.322024083	1.66E-05	0.000309665
	sgaB	LCABL_29120	CAQ67962	16.89802881	42.58526682	2.520132217	0.000686198	0.008454328
91	-	LCABL_29840	CAQ68034	44.55073487	68.22619502	1.531426928	0.050658035	0.21805916
91	-	LCABL_29850	CAQ68035	129.3013704	224.9949868	1.740081998	0.000902728	0.01051108
	tnp6	LCABL_29980	CAQ68048	105.8618643	58.44984934	0.552133195	0.001567241	0.016770585
	-	LCABL_30010	CAQ68051	2426.51986	1501.120021	0.618630841	0.000438465	0.005922204
	manO	LCABL_30310	CAQ68081	6667.40688	4151.97245	0.622726725	0.000264523	0.003791907
	upsA	LCABL_30350	CAQ68085	49.16685381	283.415852	5.764368268	4.81E-15	2.25E-13
92	mutR	LCABL_30370	CAQ68087	158.795417	2110.86314	13.29297268	1.59E-67	6.05E-65
92	rgg	LCABL_30380	CAQ68088	142.1422056	2150.067824	15.12617463	2.36E-73	1.02E-70
93	glnP	LCABL_30400	CAQ68090	699.4159529	1735.693576	2.48163281	3.72E-12	1.45E-10
93	-	LCABL_30410	CAQ68091	790.0150911	2080.864177	2.633954972	1.26E-13	5.26E-12
	ypjH	LCABL_31170	CAQ68166	2256.157386	38069.36865	16.87354299	7.44E-32	7.53E-30
94	gidA	LCABL_31220	CAQ68171	8084.559698	5397.873829	0.667676909	0.001289186	0.014143818
94	trmE	LCABL_31230	CAQ68172	3048.491809	2267.269362	0.743734772	0.025686564	0.139166949

^a Genes putatively belonging to transcriptional units where at least one of the members is significantly differentially expressed have been included

^b Numbers have been arbitrarily assigned to indicate genes belonging to the same putative transcriptional units.

Table S4. Genes putatively involved in amino acid biosynthesis

Locus_tag	Locus	Mean BL23	Mean Δ RR11	Fold change	padj
Arginine					
LCABL_30160	argG	149.4706271	150.8392949	1.009156768	0.968190071
LCABL_30170	argH	325.4572476	329.7844376	1.013295725	0.980459135
LCABL_18700	speF	308.0303554	292.6905314	0.950200285	0.937319843
LCABL_04530	Atu5418	66.12197076	222.035617	3.357970345	8.7954E-11
Histidine					
LCABL_14250	hisK	182.2834127	132.1964421	0.725224748	0.254116148
LCABL_16480	hisC	467.9169044	2165.633538	4.628243857	2.67E-27
LCABL_16490	hisE	75.32783229	416.6981683	5.531795562	1.69E-25
LCABL_16500	hisI	86.64457283	452.9272822	5.227416645	1.29E-23
LCABL_16510	hisF	206.6700907	1343.65547	6.501451011	2.43E-37
LCABL_16520	hisA	291.6296637	1454.284247	4.986750075	2.07E-28
LCABL_16530	hisH	333.4767769	1635.332413	4.903886946	2.00E-28
LCABL_16540	hisB	234.1550451	1506.195794	6.432472097	2.66E-37
LCABL_16550	hisD	433.2432902	2124.136665	4.902872618	2.04E-28
LCABL_16560	hisG	91.05388112	485.5814208	5.332901957	1.51E-24
LCABL_16570	hisZ	207.8739401	1273.379634	6.125730012	3.04E-34
Ala,Asn,Asp,Gln,Glu					
LCABL_24350	asnA1	831.6023086	452.1145439	0.543666773	0.000107699
LCABL_23430	asnH	13316.91718	10876.11165	0.816713921	0.359815804
LCABL_29320	asdA	130.2141625	130.1731341	0.999684916	0.991371933
LCABL_23560	ald1	25.18877487	12.17006154	0.483154167	0.182991753
LCABL_30650	aspA	292.0767916	256.620819	0.878607361	0.73383851
LCABL_06940	gdh	162.2972797	272.1321057	1.676750875	0.009422033
LCABL_27230	gltD	1046.304122	11571.45758	11.05936346	2.57037E-41
LCABL_27240	gltA	2451.586514	34175.3973	13.94011474	7.43024E-26
LCABL_05060	glnA	491.1513612	525.595168	1.070128701	0.87158495
LCABL_18680	glnA	21248.7594	22564.38792	1.061915545	0.935342811
Gly,Lys,Ser,Thr					
LCABL_14180	sdhB-2	1216.402782	946.9664457	0.778497435	0.238641775
LCABL_14190	sdhA-2	1476.621205	1412.226126	0.956390252	0.906207341
LCABL_13800	glyA	1390.095506	1512.966659	1.08839044	0.793761148
LCABL_23570	tdcB	24.18174293	11.1849145	0.462535498	0.108708238
LCABL_01010	thrA	302.2908832	972.6958128	3.217747761	3.84139E-09
LCABL_01030	asd	1833.109994	3626.725455	1.978454903	3.08E-06
LCABL_23330	thrA	338.2563351	1016.663585	3.005601016	0.000110846
LCABL_23310	thrB	666.3739004	1217.151871	1.826529926	0.000147848
LCABL_23320	thrC	1322.12388	2456.437602	1.85794814	5.29219E-05
LCABL_00970	dapA	73.98308785	198.3976504	2.681662204	2.30821E-07

LCABL_00960	dapB	170.2362858	516.3088046	3.032895144	4.22251E-12
LCABL_00990	dapD	108.4352197	227.7664574	2.100484125	0.085398842
LCABL_23390	araT	453.993275	1269.880326	2.797134662	3.28107E-12
LCABL_09310	araT1	1531.970959	1474.700515	0.962616495	0.87158495
LCABL_00980	dapE	304.7492072	706.4137204	2.318016598	6.23145E-08
LCABL_01020	dapF	706.7782471	1644.79678	2.32717516	2.61348E-07
LCABL_01000	lysA	52.38057758	142.2767575	2.716212078	4.2237E-06
Cys, Met					
LCABL_05440	metA	230.9970972	324.9076124	1.406544136	0.153981861
LCABL_05450	cysK1	684.0603966	1054.970119	1.542217799	0.022203072
LCABL_02990	patB	36.74307901	33.23674947	0.675013813	0.870329647
LCABL_04030	metC2	599.1549479	380.7845617	0.635536038	0.033363137
LCABL_06620	metB	264.9061329	205.115582	0.774295331	0.244092469
LCABL_10070	malY	7254.112948	5111.528669	0.704638693	0.249550412
LCABL_06830	metE	2642.097295	2264.831769	0.857209829	0.604228584
LCABL_06820	metF	872.8226822	870.3945222	0.997218037	0.969650937
LCABL_09430	metK	7020.262474	7733.791612	1.101638527	0.717074327
LCABL_15190	pfs	2203.272176	1730.618872	0.785476661	0.256683872
LCABL_08310	luxS	299.1705854	307.7055425	1.028528731	0.958181533
Ile, Leu, Val					
LCABL_23570	tdcB	24.18174293	11.1849145	0.462535498	0.108708238
LCABL_20650	als	1248.263681	1223.507697	0.980167664	0.929151839
LCABL_22070	ilvE	993.4071628	4318.625317	4.347286268	7.29326E-26
Proline					
LCABL_25350	proA	1620.874469	1953.641171	1.205300724	0.498026101
LCABL_25360	proB	885.3102925	728.9795439	0.823416999	0.322538606
LCABL_20290	proC	1156.563531	1634.98706	1.413659533	0.055934663
LCABL_03540	-	173.8583162	179.1489288	1.030430598	0.982331716
Phe, Trp, Tyr					
LCABL_00720	trpA	477.4715793	1328.099087	2.7815249	3.04934E-12
LCABL_00730	trpB	387.567084	1126.128651	2.905635431	3.0829E-13
LCABL_00740	trpF	48.39169593	193.5715274	4.000098027	5.82048E-13
LCABL_00750	trpC	75.19947332	225.9612253	3.004824572	3.84139E-09
LCABL_00760	trpD	441.9133001	1309.289147	2.9627738	1.11235E-06
LCABL_12100	pheB	122.44616	90.39628548	0.738253331	0.256614453
LCABL_05430	aroE	7.316113692	5.325964039	0.727977211	0.956105786
Unassigned					
LCABL_17080	aspB	8483.898827	8284.96029	0.976551048	0.940590651
LCABL_28150	-	68.51665258	336.0301319	4.904357106	1.5617E-19
LCABL_16580	hisC	279.4936941	347.4881495	1.243277243	0.470798263

Table S5. Composition of the chemically defined medium used in this study^a.

Glucose	10 g
Ammonium chloride	3 g
FeSO ₄ 7H ₂ O	10 mg
KH ₂ PO ₄	2 g
K ₂ HPO ₄	2 g
MgSO ₄ 7H ₂ O	0.2 g
MnSO ₄ H ₂ O	50 mg
Sodium acetate (trihydrate)	6 g
NaCl	50 mg
Adenine	5 mg
Guanine HCl	5 mg
Uracil	5 mg
Xanthine	5 mg
Ascorbic acid	0.25 g
Biotin	20 µg
Folic acid	0.1 mg
Nicotinic acid	1 mg
p-aminobenzoic acid	0.2 mg
Calcium pantothenate	1 mg
Pyridoxal	0.1 mg
Riboflavin	1 mg
Thiamine HCl	0.2 mg
Tween 80	1 ml
Glutathione reduced	0.25 g
L-Arg	0.5 g
L-Asn	0.25 g
L-Asp	0.25 g
L-Cys	0.25 g
L-Gln	0.25 g
L-Glu	0.25 g
L-Gly	0.25 g
L-Ile	0.5 g
L-Leu	0.12 g
L-Met	0.25 g
L-Phe	0.12 g
L-Ser	0.25 g
L-Trp	0.5 g
L-Tyr	0.5 g
L-Val	0.5 g

^a Composition per liter of medium. The medium pH was adjusted to 6.8 with NaOH.

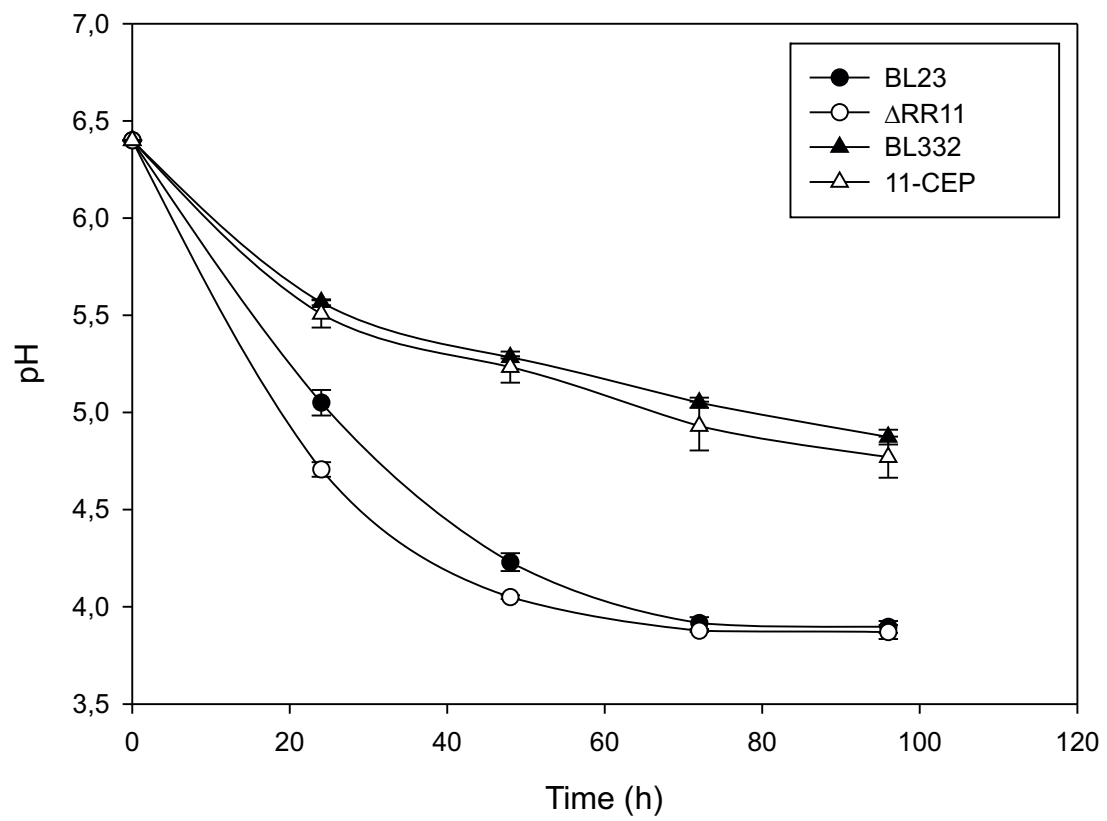


Figure S1. Variation of pH during growth in skim milk of *L. casei* BL23 and derivative strains. Error bars indicate SD (four replicates).

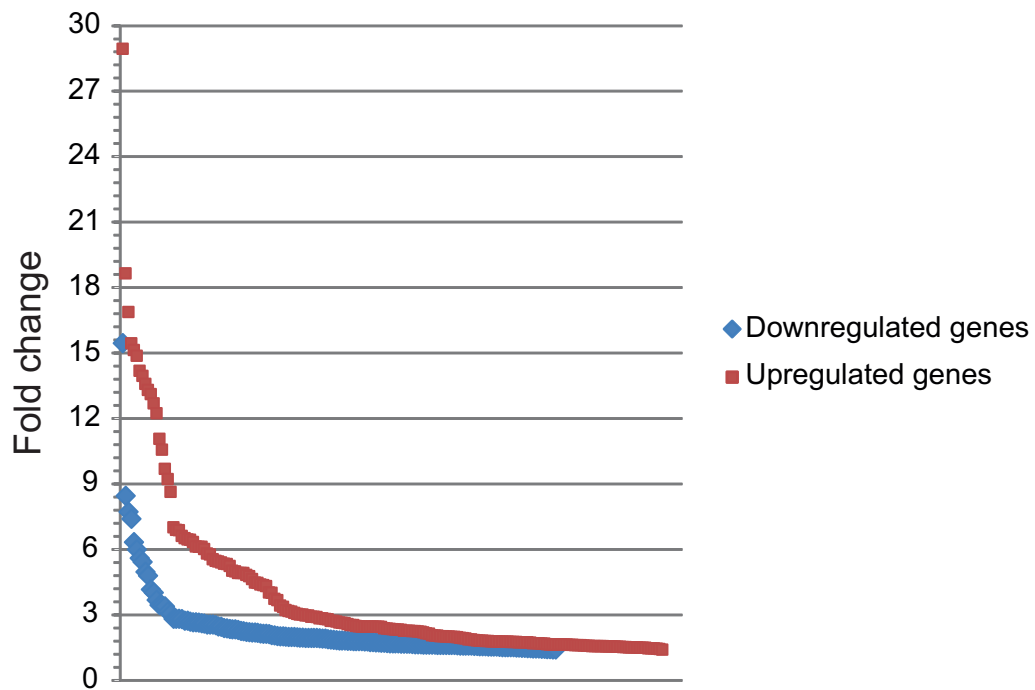


Fig. S2. Graphical representation of the fold change values of significantly differentially expressed genes of *L. casei* Δ RR11 compared to the wild-type strain BL23.

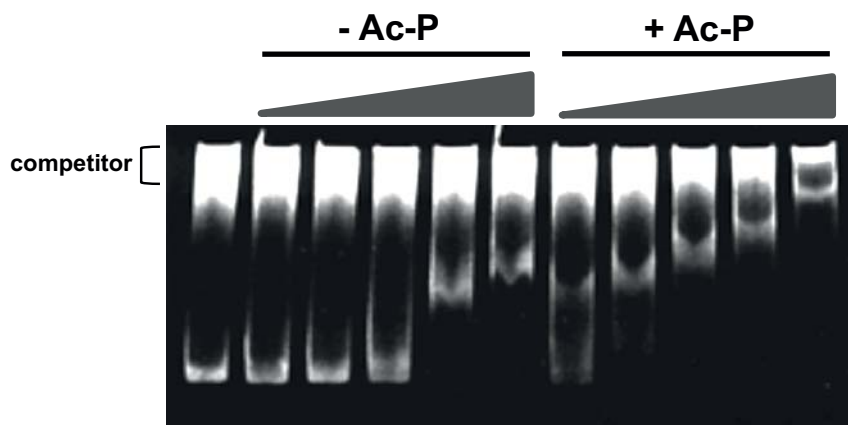


Fig. S3. Titration of PrcR binding to the *prtP/prsA* promoter regions. Reactions contained 100 ng of target DNA and increasing amounts of PrcR (indicated by the grey triangles; 0.079, 0.158, 0.317, 0.635 and 1.27 μ M). Binding was performed in the absence (-) or presence (+) of 10 mM acetyl phosphate (Ac-P). Competitor indicates the band corresponding to salmon sperm DNA added to the binding reactions.

Fig. S5. Intergenic regions recognized by PrcR. A tracts, RBS and translational start sites are indicated. In the prtP/prsA intergenic region, only A tracts shown to be involved in PrcR binding (see Fig. 6) are indicated.

oppA (LCABL_01690) 172032-172276

CTTCAGTTGTCTTTCAAACACTTCTGCTTGCAGGGGTGTTTTTTTTGTGCCGACTAGCAAGTTGGCGATGGCGCG
 GCGATTCACGAAATTCACATATTTAAAAAGTGGGACGTGAGACTTTGATGAGTAACTTCTGCTGGTAAAAAGGCCACG
AAAACAAGTAATATCTGCAAATTTTTCTTTACTTTCTTCATACTCTAATGTATTCTCAACGTAATATCATTTTGAGG
 GTGAGTAAATG->*oppA*

bnag (LCABL_02860) 288592-288854

GCTGCTAGTTCGCATGCTGAAAAGAGTCATTCCATTTGGGATGGCTCTTTTTACATACCAACAAGACCATCTAGATCCC
 TTAAAGCGAGGGGTAACCATTTAAAAGCAAACATACGATGAATAATATTAACGAAATATGAGAATAACGTGTGAGAT
 ATGAAAATCATTTTGAATTGAAAGCGATTCCAGCATATTCTTAAGTTGTTGGTGAATAGCCAATCTTGTGCAGAA
 ACCATCCACAAAAGGAGGTTGAAGTTTTG

pepT/oppA (LCABL_03060/LCABL_03070) 312552-312672

pepT<-CAATGAAATCCCTGCCTTTTCGATGAGAAAAAATATTAATATTGCATTGCAATAAGTTTGGATCTGGCTTAGTA
TTTTGTCAATAGTTGATTGTTACCGCGATTTTGGAGGGAATACATATG->*oppA*

ylcA (LCABL_05350) 547603-547813

TTTTCTGCGATTGTTGGCCACGAAGATAAAGCCCAAGGCTCATTTTCACATTTTTTCATAACTTATAATGGTTAATTCA
 CAACGTTAATTTAAGAAAAATCTAATCCTCATCTACACAATTTACGCGGAAAGAAAACGGGTTAAACCGGTACTACTGA
AAAATGAGTCGCTGTTGATTGATGGACAGGCGGCTGTTTTGGAGGATTTTTAGTG

prcR (LCABL_18980) 1840504-1840778

TAATAACTTCATATTTTATAAAAATGAAGACCAATCTCACAAACATATTTATTGTTTGAAGGATGGTCTTTTTATGAG
 AATTTACCAGTTTTGAAAAATGAGAAAGTCTCCGAACAAAGATTTCTTGTGTTTGTGCGAGCCCCATCGTTGCCGGCT
 GATAGTCAAAATGAGAAAACTGTGCTAACTGTCGTAGCATATGTTTTTATGAGAAAAAACAAATGGATTCACTCTGT
 GAGTGCCTCAGAGACGAATAAGTATAAAGGAGACCATTGATG->*prcR*

oppA (LCABL_21470) 2073990-2073717

CCTTCAACATAGGATCAATAGCTGGTTAGATGGTCATCTCTCACACTGTTTGCACCAGATCCCATTACATAAAAGGAT
 TTTATTGTGAGTTTTCAAGCATTCTCATCTTTATATTGAGCTTATAAAAGGCCAAGCTTCCAGTGGCGAAAGATTAA
AAAGATTGTATTAAAATTATAATTGACTTAGCTAAGAATGAGACTTAATGTGTTTCTTATAAGAGACGCACCTTGTCC
 TTTACCTAATACTAATTTGCGGAAGGAGTATACGATATG->*oppA*

LCABL_22680 2212677-2212309

AAGCGCGTGCATGGTCTGAATGTGGCGGCGGCTTCAACGTCGCGTATGTTTATGAAGAGACTGATACAGCGCTTAAACG
 CTACAAGCACAATGGCATTTAGCCCCTTAATTTTGATATTTTAAAAAGTGACGACTCATTTCGATTGACTGCTTCACT
 CGGTCATCGGCATGAGTCGCTTTTTTTAAATTTGAAAATAAACGCGACAATTTTCCGGAATACATTTTAAAAATT
 TGGATGAACATGTTGACACATAATCTCATAAACTTATAATCAAGCTATTACATTTCAACTGGCAATCGATTTCAGCT
 TAAATATTAGTCGAAATGTACGCAATTATTAAGCATATGTGAGGTAGCCGATATG->LCABL_22680

prtP/prsA (LCABL_24520-LCABL_24530) 2411330-2411621

prtP<-CATCCAATACCCCTCCACTTCCCAAAAGTTTCAGAACCAATCAAATCCACGCTTGATGTAGTTAAGATTATA

TACTCTCGAAGAACAGATTCAACGAAAATTTTAATCTTTTATTAATTTTCCTATCTGTAAATTAGCTTTTAGTGTTAT
TATTTAGCCGTTTACAGACTATAGATGTTTTGAAATTTTTGGCATTATTAGAAAATGAGTATTTGCATTGAAATTC
AATTGCCAACGCTAGAATAAATACACAACGTTTACTGTAAGCATTTTCAGAGGGAGACCGAGTCGATG->prsa

bcaR (LCABL_27210) 2672860-2673030

AAACAATTGTTTCTGAATAGCATTGTGCAACAGATATAACATTACCTCTGAAAGTGATCTTCAGCATGAACAGTCCAG
AAAACGTTACACCGCCAGTGATCTATGGTATCATAAAGCAAGATTAGAATATTTAATAAAGTGATACCTGTTTGAT
GGAGGAAAAACGAATG->bcaR

gltA (LCABL_27240) 2681100-2680826

TGGCAGTTATCTTAAACAACCTAAAAAATAAAAAAGATCTTGCAACCGACCTTGACTACCAGTGCACCAGTCTGATTT
CTATTAATCAGTCTGATGCACTGTTTTTATTGTTGACCAGATGGCGGATTCTGCAAGCTTTGATAGACTTCGGAGCC
AAATGTGAAACGGCAGACAAAGAAAAAAGCATTGTAATCTTGTCAATTATTAGAATACTATGAGACCAATATCTTTAGG
CTCAAGACATTGATGTTAACTAATAAGGTGGGGATTTCATG->gltA

rgg (LCABL_30380) 2994477-2994030

CGCAACCTCTATTTCTTGGTGGTGTATTTAAATGTCAAAATTGAGTTTAGCGGAGTCAGGGATGGATGTCAATTTATA
ATGGCAGAGCGTGAGCAAGTGCAGTTTCTAGGTCTGCTCACACGTTTTAGATGGCACAGTAGAAGGATTCGCTCTTCT
GATGCTTGTGAGCAGGCTTCGATAGTCTGAGCTGGTTTTTGTAAAATTCCGGAGTAGCGACCGCCAAGGCTAAGGCGC
TGGTATGGCCGCTCCATTGAATTTTCGTTACTGCCTGATGTCTATCAGAAAAAATGCGTAAAAAATTCTTGGGACTAG
CACCCATGTTTAGGCAGCGTTTAAAAACAAAAATATTCAAATTTGAGGTGCAATAAGTAGTAAGATATTTTGAAAAAA
TGGCAAAACGTGTTAAGTTTGTCTAATAAAGTTCTCATAAAGGGTCGGGTGCTGATG->rgg

ypjH (LCABL_31170) 3067154-3067797

GATCCTCCTACAGCCATGTTAATAGCGATTCCCGTCACGACGCTTAACGAACCATCTCAGATACGATGATTCACTTGG
AAACAGTAAGCGGTGTAGAATCTGTTTTTTCATTATATAACTGATTTTATTAAAAACGGAAAAATTTGTATCCAATTT
TCAGAAAATAATTTTATAAATATTGCGATAGAACCAGTCTGAAACCGGCATTAACCTCAAGTGCTTGTTTTTAAATGTA
TCGCCGATCCTCTGTTGTTTCTGCAAATCAGCTACATCTTCGATCACAATAAAAAACACGATGTTGGTCAACGATCC
ATCGTGTTTTTTGACAAGTATCTTTTTAGAGCAGACCCACTTACCAATTTTGGCGAGCTGCTTCTTTAATCGTGC
CGGACTCATCAGCAACTTGCTTAAGTTGAGCTTCTGACCACACTTATCTTCAAAGCTTTTCATCATTCTATCAGTATA
TTTTTAATTAAGATTCGTTTGTGTTGCAATCTAAACAAATGGCAAGCATTGTTGTTGTAATCGTAACAACAAGGCTTTGC
AGATTGTTTTTCAATTTCTAGTTGACTTCATACAGAATCGCGTATGTTAAAAATTATCACATAAGATGAGATTTACA
TGAGAGGAGTTTTGTCGATG->ypjH

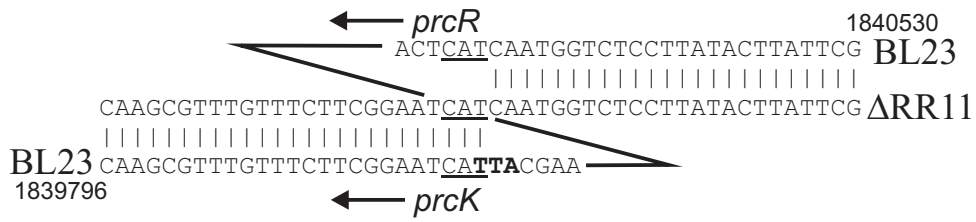


Fig. S6. Sequence comparison of the Δ RR11 derivative strain with the parental strain BL23. Translational start codons are underlined. Translational stop codons are indicated in bold characters. The zigzagged lines represent intervening sequence. The coordinates correspond to the *L. casei* BL23 genomic sequence (Acc N° FM177140).

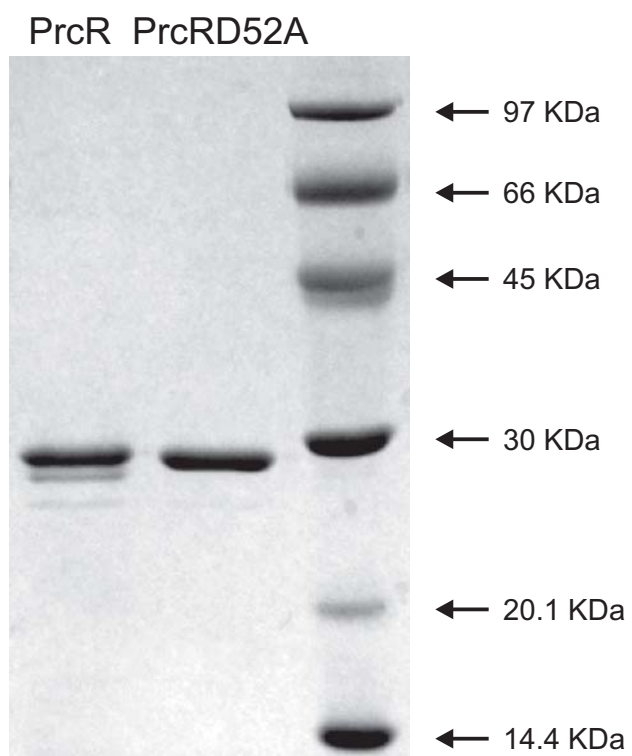


Fig. S7. SDS-PAGE of purified fractions of PrcR and PrcRD52A proteins (0.5 μ g of protein loaded).