Supplementary materials for the article:

Wang L. et al. Transcriptome Analysis of *Komagataeibacter europaeus* CGMCC 20445
Responses to Different Acidity Levels During Acetic Acid Fermentation
Pol J Microbiol. 2021, Vol. 70, No 3, 305–313.

Table SI
GO enrichment analysis of downregulated genes within the samples treated.

Time	GO accession		Corrected *p*-value
Biological process			
40h	GO:0006412	translation	0.00034176
	GO:0006518	peptide metabolic process	0.00034176
	GO:0043043	peptide biosynthetic process	0.00034176
	GO:0043604	amide biosynthetic process	0.0005494
	GO:0043603	cellular amide metabolic process	0.0010767
	GO:1901566	organonitrogen compound biosynthetic process	0.0027446
	GO:0006810	transport	0.0065878
	GO:0051234	establishment of localization	0.0067287
	GO:0051179	localization	0.0081136
	GO:0055085	transmembrane transport	0.017746
Cellular component			
40h	GO:0005840	ribosome	2.48E-06
	GO:1990904	ribonucleoprotein complex	4.98E-06
	GO:0005575	cellular_component	1.10E-05
	GO:0044444	cytoplasmic part	1.21E-05
	GO:0032991	protein-containing complex	0.00034176
	GO:0005737	cytoplasm	0.00034176
	GO:0043232	intracellular non-membrane-bounded organelle	0.00034176
	GO:0005623	cell	0.00039068
	GO:0044464	cell part	0.00039068
	GO:0043228	non-membrane-bounded organelle	0.00039068
	GO:0005622	intracellular	0.0034117
	GO:0016020	membrane	0.0055231
	GO:0044425	membrane part	0.0067287
	GO:0044424	intracellular part	0.0067423
	GO:0016021	integral component of membrane	0.0069379
	GO:0031224	intrinsic component of membrane	0.0081136
	GO:0043229	intracellular organelle	0.043902
Molecular function			
40h	GO:0003735	structural constituent of ribosome	2.48E-06
	GO:0005215	transporter activity	0.00034176
	GO:0005198	structural molecule activity	0.00039068
	GO:0022857	transmembrane transporter activity	0.0027446

Time	GO accession		Corrected *p*-value
	GO:0022804	active transmembrane transporter activity	0.0038552
	GO:0019843	rRNA binding	0.0044248
	GO:0015399	primary active transmembrane transporter activity	0.0069379
	GO:0015405	P-P-bond-hydrolysis-driven transmembrane transporter activity	0.0069379
	GO:0042626	ATPase activity, coupled to transmembrane movement of substances	0.026653
	GO:0043492	ATPase activity, coupled to movement of substances	0.026653
Biological process			
64h	GO:1901566	organonitrogen compound biosynthetic process	1.76E-05
	GO:0043043	peptide biosynthetic process	3.22E-05
	GO:0006518	peptide metabolic process	3.36E-05
	GO:0043604	amide biosynthetic process	3.49E-05
	GO:0006412	translation	3.82E-05
	GO:0043603	cellular amide metabolic process	8.31E-05
	GO:1901564	organonitrogen compound metabolic process	0.0013388
	GO:0044267	cellular protein metabolic process	0.012146
Cellular component			
64h	GO:0005840	ribosome	4.38E-06
	GO:1990904	ribonucleoprotein complex	1.14E-05
	GO:0005737	cytoplasm	8.31E-05
	GO:0044444	cytoplasmic part	0.00011873
	GO:0043228	non-membrane-bounded organelle	0.00062974
	GO:0043232	intracellular non-membrane-bounded organelle	0.0026467
	GO:0032991	protein-containing complex	0.0043888
	GO:0005623	cell	0.0046441
	GO:0044464	cell part	0.0046441
	GO:0005622	intracellular	0.012146
	GO:0044424	intracellular part	0.017737
	GO:0005575	cellular_component	0.018406
Molecular function			
64h	GO:0003735	structural constituent of ribosome	4.38E-06
	GO:0005198	structural molecule activity	0.0026467
	GO:0016638	oxidoreductase activity, acting on the CH-NH2 group of donors	0.043212
Biological process			
88h	GO:0043043	peptide biosynthetic process	1.03E-14
	GO:0043604	amide biosynthetic process	1.03E-14
	GO:0006412	translation	1.03E-14
	GO:0006518	peptide metabolic process	1.92E-14
	GO:0043603	cellular amide metabolic process	9.40E-14
	GO:1901566	organonitrogen compound biosynthetic process	5.14E-10
	GO:0044267	cellular protein metabolic process	4.29E-07

Time	GO accession		Corrected *p*-value
	GO:1901564	organonitrogen compound metabolic process	4.89E-07
	GO:0019538	protein metabolic process	0.00044683
	GO:0006520	cellular amino acid metabolic process	0.038203
Cellular component			
88h	GO:0005840	ribosome	1.99E-14
	GO:1990904	ribonucleoprotein complex	5.21E-13
	GO:0043228	non-membrane-bounded organelle	1.58E-09
	GO:0044444	cytoplasmic part	3.58E-09
	GO:0032991	protein-containing complex	4.10E-09
	GO:0043232	intracellular non-membrane-bounded organelle	8.15E-09
	GO:0005737	cytoplasm	1.21E-08
	GO:0005623	cell	1.76E-06
	GO:0044464	cell part	1.76E-06
	GO:0005622	intracellular	2.39E-05
	GO:0043226	organelle	0.00089028
	GO:0043229	intracellular organelle	0.0027395
	GO:0005575	cellular_component	0.026913
Molecular function			
88h	GO:0003735	structural constituent of ribosome	1.99E-14
	GO:0005198	structural molecule activity	8.96E-08
	GO:0016638	oxidoreductase activity, acting on the CH-NH2 group of donors	0.016847
	GO:0019843	rRNA binding	0.03582

Table SII
KEGG PATHWAY enrichment result of differentially expressed genes

Time	KEGG PATHWAY	ID	Number of downregulated genes	Total number of genes	*p*-value
40h	Ribosome	gxl03010	35	64	9.03E-12
64h	Ribosome	gxl03010	36	64	7.44E-09
	Fatty acid biosynthesis	gxl00061	7	16	0.027938
	Citrate cycle (TCA cycle)	gxl00020	14	24	0.002379
	Oxidative phosphorylation	gxl00190	22	66	0.031898
	Butanoate metabolism	gxl00650	9	19	0.035021
88h	Ribosome	gxl03010	51	64	2.36E-10
	Citrate cycle (TCA cycle)	gxl00020	15	24	0.002936
	Butanoate metabolism	gxl00650	11	19	0.015426
	Pentose phosphate pathway	gxl00030	18	40	0.015563
	Oxidative phosphorylation	gxl00190	25	66	0.024263

Table SIII.1

Information about the gene expression level of KEGG PATHWAY in this study.

Gene ID	Gene name	z64h group FPKM	z88h group FPKM	z16h group FPKM	z40h group FPKM	padj (z40hvsz16h)	padj (z64hvsz16h)	padj (z88hvsz16h)	KEGG annotation
S101446_00972	*rpmG*	1661.841413	1124.223726	2389.92733	1330.819702	0.0016194	0.018565	1.65E-06	50S ribosomal protein L33
S101446_00998	*rpsB*	1937.0105	1675.481464	3916.202068	2256.673779	1.99E-08	1.35E-25	1.96E-27	30S ribosomal protein S2
S101446_01035	*rplT*	1728.823197	1465.65786	2236.223159	1274.095938	1.74E-07	0.053071	0.017147	50S ribosomal protein L20
S101446_01036	*rpmI*	3541.689443	3287.591847	5335.192022	4175.476865	0.045995	2.30E-07	2.01E-08	putative 50S ribosomal protein L35
S101446_01186	*rplU*	3781.508773	3226.499994	5653.262727	3657.926743	5.19E-06	7.17E-09	5.72E-11	50S ribosomal protein L21
S101446_01187	*rpmA*	1966.630147	1554.515148	2990.907825	1484.861282	2.64E-14	0.00017371	1.14E-08	50S ribosomal protein L27
S101446_01363	*rpmF*	4238.689497	3635.044696	5759.64167	3703.796484	5.96E-06	1.87E-05	2.69E-07	50S ribosomal protein L32
S101446_01377	*rplS*	1224.134562	1075.768823	1504.403386	1178.122867	0.15834	0.067451	0.0034333	50S ribosomal protein L19
S101446_01380	*rpsP*	1206.241555	1025.886903	1910.52373	1505.217534	0.063491	8.71E-08	4.08E-13	30S ribosomal protein S16
S101446_01456	*rplI*	1634.375537	1338.18861	3102.501837	1740.201278	1.00E-05	3.04E-14	5.74E-22	50S ribosomal protein L9
S101446_01457	*rpsR*	162.4023743	76.96134404	180.5635825	105.7754029	0.0049601	0.68458	1.53E-08	30S ribosomal protein S18
S101446_01458	*rpsF*	1458.382902	1093.154154	3344.000218	1858.815757	5.75E-11	4.02E-33	1.97E-47	30S ribosomal protein S6
S101446_01499	*rplQ*	1548.574532	1157.873585	1754.852397	1265.145674	0.0024796	0.24038	0.0061461	ribosomal protein L17
S101446_01501	*rpsK*	2956.516487	2319.870088	3457.84644	2966.975309	0.3909	0.088924	4.59E-06	30S ribosomal protein S11
S101446_01502	*rpsM*	6761.712257	5821.115432	8423.519115	6561.557174	0.02757	0.0076198	5.02E-05	30S ribosomal protein S13
S101446_01505	*rplO*	1376.658271	1184.864889	2027.630226	1190.84071	0.0095608	0.0022084	0.00020167	ribosomal protein L15
S101446_01507	*rpsE*	960.0058937	784.5559512	1515.17769	1196.194793	0.28442	0.0025933	1.36E-07	30S ribosomal protein S5
S101446_01508	*rplR*	426.3820936	330.0319915	576.8475784	440.3138323	0.19682	0.0020419	5.68E-06	50S ribosomal protein L18
S101446_01509	*rplF*	809.9604387	660.5364619	1124.138705	746.5768805	0.016188	4.68E-05	5.27E-05	50S ribosomal protein L6
S101446_01510	*rpsH*	570.3877142	422.2022793	956.5364069	591.8519602	1.35E-05	2.26E-10	9.45E-20	30S ribosomal protein S8
S101446_01511	*rpsN*	2690.586556	2296.531916	5214.599287	3178.905993	0.0007332	1.24E-10	8.63E-22	30S ribosomal protein S14
S101446_01512	*rplE*	1460.995998	1192.800195	2142.378922	1592.05385	0.063003	0.013266	2.55E-09	50S ribosomal protein L5
S101446_01513	*rplX*	498.3085845	378.3768599	685.208063	456.5360977	0.0061594	0.059781	4.56E-06	50S ribosomal protein L24
S101446_01514	*rplN*	1218.358296	942.9204324	1602.140528	1231.965913	0.031308	0.0023943	1.60E-09	ribosomal protein L14
S101446_01515	*rpsQ*	569.7675157	412.5138427	700.4804201	648.7616092	0.94931	0.37218	4.55E-07	30S ribosomal protein S17
S101446_01516	*rpmC*	940.9028605	664.9863288	1054.259232	1037.317831	0.78857	0.79778	0.029051	50S ribosomal protein L29
S101446_01517	*rplP*	1032.503525	780.5654312	1358.059281	1112.541221	0.17144	0.0064832	1.46E-10	50S ribosomal protein L16
S101446_01518	*rpsC*	923.9331141	728.0213303	1182.696248	894.5346604	0.2581	0.086134	0.0015402	30S ribosomal protein S3

S101446_01519	*rplV*	844.2527469	645.5000698	973.2615852	876.0206921	0.81099	0.47648	0.0040284	50S ribosomal protein L22
S101446_01520	*rpsS*	393.0850355	274.7156306	562.2991492	510.4108945	0.84618	0.18411	1.66E-11	30S ribosomal protein S19
S101446_01521	*rplB*	1495.777525	1175.781856	2009.085632	1714.552694	0.60123	0.10668	0.00028883	50S ribosomal protein L2
S101446_01522	*rplW*	860.5123035	595.5734982	1103.796451	868.6775082	0.12001	0.21006	8.34E-07	Ribosomal protein L25/L23
S101446_01523	*rplD*	954.5503894	744.8065628	1328.417337	927.5103119	0.11766	0.0041008	0.00059055	50S ribosomal protein L4
S101446_01524	*rplC*	1874.326741	1496.695907	2800.831769	2017.337031	0.10478	0.019999	6.64E-07	50S ribosomal protein L3
S101446_01525	*rpsJ*	1678.921058	1191.012492	2186.223869	2101.633388	0.87573	0.31501	7.31E-12	30S ribosomal protein S10
S101446_01527	*rpsG*	2516.617462	1902.768676	3587.277413	2685.714639	0.0078727	1.68E-06	4.24E-12	30S ribosomal protein S7
S101446_01528	*rpsL*	10263.77658	8144.482448	14901.05735	11432.51782	0.024986	2.27E-07	4.00E-14	30S ribosomal protein S12
S101446_01531	*rplL*	5314.942176	4953.177542	13071.06692	6229.904873	0.00015688	3.60E-11	4.16E-14	50S ribosomal protein L7/L12
S101446_01532	*rplJ*	3757.485326	3193.256421	10367.75369	4803.567951	2.53E-07	3.46E-24	4.49E-50	50S ribosomal protein L10
S101446_01532	*rplJ*	3757.485326	3193.256421	10367.75369	4803.567951	2.53E-07	3.46E-24	4.49E-50	50S ribosomal protein L10
S101446_01533	*rplA*	1547.711464	1315.815871	2512.797277	1496.246384	0.0029372	4.39E-06	3.75E-08	50S ribosomal protein L1
S101446_01534	*rplK*	2400.909015	2057.872889	4244.749336	2947.927008	0.00021754	1.54E-13	9.11E-20	50S ribosomal protein L11
S101446_01566	*rpsA*	2168.262595	1927.221602	3221.15863	2221.607819	0.0009613	5.92E-07	6.74E-10	30S ribosomal protein S1
S101446_02424	*rpsO*	2088.354436	1514.943294	2645.25858	1754.551844	6.21E-05	0.0037249	6.05E-11	30S ribosomal protein S15
S101446_02568	*rpmJ*	1989.430116	1120.385701	2117.630841	1094.128109	0.001754	0.83083	0.0039503	LSU ribosomal protein L36P
S101446_02594	*rplM*	1113.403643	907.5727009	2948.482988	1358.421717	7.15E-10	4.45E-46	9.62E-50	50S ribosomal protein L13
S101446_02595	*rpsI*	618.619304	477.5385535	1432.387629	571.2980155	1.49E-21	2.89E-31	2.23E-40	30S ribosomal protein S9
S101446_02661	*rplY*	1125.394325	940.57225	3018.603553	1495.308528	1.50E-09	3.82E-48	8.37E-52	50S ribosomal protein L25
S101446_02874	*rpsD*	3266.383134	2642.761483	5860.140309	3658.975809	2.03E-07	3.81E-18	5.46E-24	30S ribosomal protein S4
S101446_03049	*rpmE*	2188.844528	1940.811324	3639.561755	2042.004075	2.67E-10	2.21E-13	1.51E-13	50S ribosomal protein L31
S101446_03187	*rpsT*	6480.742247	5514.460733	8502.48852	5430.048728	1.61E-06	0.0013826	1.36E-05	ribosomal protein S20

Table SIII.2

Information about the gene expression level of KEGG PATHWAY in this study.

Gene ID	Gene name	z64h group FPKM	z88h group FPKM	z16h group FPKM	z40h group FPKM	padj (z40hvsz16h)	padj (z64hvsz16h)	padj (z88hvsz16h)	KEGG annotation
S101446_02993	*adhA*	1910.243157	2579.038022	2497.630597	1587.396046	1.33E-06	0.08318	0.2101	alcohol dehydrogenase
S101446_02992	*adhB*	1404.012326	1831.969152	1642.425654	1114.620427	6.33E-05	0.12939	0.026032	alcohol dehydrogenase cytochrome c subunit
S101446_00495	*adhS*	24.06937708	32.58874231	14.75036339	19.18816003	0.63532	0.20389	0.0036559	alcohol dehydrogenase small subunit
S101446_00292	*aldh2*	39.35793825	39.45417366	73.89328909	51.28015606	0.019195	8.70E-05	1.06E-07	aldehyde dehydrogenase

Table SIII.3

Information about the gene expression level of KEGG PATHWAY in this study.

Gene ID	Gene name	z64h group FPKM	z88h group FPKM	z16h group FPKM	z40h group FPKM	padj (z40hvsz16h)	padj (z64hvsz16h)	padj (z88hvsz16h)	KEGG annotation
S101446_00032	*sucD*	253.2083096	218.2176624	326.1007797	283.9024106	0.69935	0.12496	0.011911	succinyl-CoA synthetase, alpha subunit
S101446_00033	*sucC*	391.5250092	312.06091	529.3621182	400.0612432	0.020154	0.0012095	7.06E-09	succinyl-CoA synthetase, beta subunit
S101446_00552	*acs*	2763.385161	4147.914772	268.841917	2064.672787	2.25E-35	6.74E-42	3.89E-279	acetyl-CoA synthetase
S101446_01070	*aarC*	274.6407469	717.0522485	203.5226264	224.343083	0.2114	0.0010244	7.47E-07	succinate CoA transferase
S101446_01074	*gltA*	622.2040831	2487.337072	478.6381798	508.2303513	0.61282	0.038007	4.32E-07	citrate synthase
S101446_02160	*fumC*	342.6635027	613.2454959	241.5623338	262.3414194	0.51812	0.015375	0.0001528	fumarate hydratase
S101446_02246	*ackA*	257.5709815	294.5604405	124.8188273	267.9701898	0.0007431	0.0003025	0.0011781	acetate kinase
S101446_02247	*ackA*	1281.557269	1834.233115	774.4060887	1091.350902	3.71E-07	3.20E-15	5.53E-38	acetate kinase
S101446_02412	*acnA*	1614.372304	2737.375483	1050.468934	1394.306878	0.012944	8.71E-05	1.43E-07	aconitate hydratase
S101446_02449	*sdhB*	539.7234434	1577.150724	374.9698041	448.0140392	0.23746	0.00038937	5.24E-16	succinate dehydrogenase iron-sulfur subunit
S101446_02450	*sdhA*	437.4417077	1013.953271	285.1012813	373.8879044	0.037193	3.79E-05	2.84E-07	succinate dehydrogenase flavoprotein subunit
S101446_02451	*frdC*	288.1566842	751.4381937	157.0580998	206.745873	0.010188	1.11E-10	2.69E-08	succinate dehydrogenase, hydrophobic membrane anchor protein
S101446_02452	*frdC*	1025.318457	3062.602894	694.8895511	803.1042412	0.29532	0.00086136	3.28E-14	putative Succinate dehydrogenase cytochrome b556 subunit
S101446_02460	*ogdH*	1155.383686	1761.772779	630.5259073	1060.320796	0.00074443	2.01E-23	1.20E-12	2-oxoglutarate dehydrogenase, E1 subunit
S101446_02461	*sucB*	843.2844945	1289.941845	455.0848881	778.9768523	0.0024796	4.55E-22	6.58E-16	2-oxoglutarate dehydrogenase E2 component
S101446_02462	*pdhD*	904.0383987	1580.705212	461.9693394	847.1052419	0.00040195	2.04E-21	8.80E-19	dihydrolipoamide dehydrogenase
S101446_02527	*fumA*	430.8045058	517.4999325	307.8863629	398.7252586	0.0011202	2.59E-07	3.52E-14	fumarate hydratase class
S101446_02900	*pta*	64.14981411	107.5350053	62.84021394	44.56897841	0.093631	0.85207	2.44E-08	phosphate acetyltransferase
S101446_02901	*mqo*	307.3063242	664.3077049	251.4025364	254.0264141	0.70972	0.054225	2.65E-05	malate:quinone oxidoreductase
S101446_03035	*idh3*	1134.090199	3494.165329	850.5709711	941.7637057	0.30502	0.0051462	2.11E-08	Isocitrate dehydrogenase (NAD(+))

Table SIII.4

Information about the gene expression level of KEGG PATHWAY in this study.

Gene ID	Gene name	z64h group FPKM	z88h group FPKM	z16h group FPKM	z40h group FPKM	padj (z40hvsz16h)	padj (z64hvsz16h)	padj (z88hvsz16h)	KEGG annotation
S101446_00353	*gabD*	94.65772593	83.38338314	66.95410834	99.25485137	5.44E-05	0.00016201	0.0087064	succinic semialdehyde dehydrogenase
S101446_00354	*gabT*	75.38999211	53.08855143	39.26497368	91.30339294	4.70E-14	2.36E-10	0.0049313	transcriptional regulator MocR family
S101446_00474	*gabD_1*	129.682377	141.0488195	93.99050145	140.3831213	9.01E-06	5.40E-05	0.00027001	aldehyde dehydrogenase

Table SIII.5

Information about the gene expression level of KEGG PATHWAY in this study.

Gene ID	Gene name	z64h group FPKM	z88h group FPKM	z16h group FPKM	z40h group FPKM	padj (z40hvsz16h)	padj (z64hvsz16h)	padj (z88hvsz16h)	KEGG annotation
S101446_01315	*nuoN*	76.14518797	356.7513325	32.37877388	57.44747966	0.0041754	1.04E-17	2.53E-27	proton-translocating NADH-quinone oxidoreductase, chain N
S101446_01316	*nuoL*	104.6757579	430.6039697	46.34189951	65.42921076	0.039965	1.56E-22	2.39E-50	proton-translocating NADH-quinone oxidoreductase, chain L
S101446_01317	*nuoK*	17.62778654	75.59864178	7.688521019	9.278104381	0.7657	0.035404	5.21E-13	NADH-ubiquinone oxidoreductase chain 4L
S101446_01318	*nuoJ*	86.59508009	437.7263516	37.52840024	62.65432129	0.021426	1.27E-12	1.23E-48	NADH-ubiquinone/plastoquinone oxidoreductase chain 6
S101446_01319	*nuoI*	63.31411671	350.9944696	20.70378124	48.05656369	0.079614	2.00E-10	3.44E-32	NADH dehydrogenase subunit I
S101446_01320	*nuoH*	64.0654754	353.3570273	20.66016261	34.05364894	0.064756	6.61E-11	3.50E-57	NADH dehydrogenase (quinone)
S101446_01321	*nuoG*	130.0382914	756.5382323	52.03879006	77.13692773	0.24459	2.24E-14	8.18E-31	NADH dehydrogenase subunit G
S101446_01322	*nuoF*	76.87778243	527.8668492	34.34679394	45.87844464	0.37542	1.78E-10	2.22E-42	NADH dehydrogenase I subunit F
S101446_01323	*nuoE*	119.1673059	618.9834945	49.25663606	66.35395961	0.31148	1.46E-14	6.70E-27	NADH-quinone oxidoreductase, E subunit
S101446_01324	*nuoD*	142.9347946	801.2277021	69.3981837	80.56625545	0.59761	1.43E-07	1.99E-33	NADH dehydrogenase subunit D
S101446_01325	*nuoC*	125.654849	678.430817	69.78823854	77.69879228	0.52418	1.62E-07	1.57E-17	NADH (or F420H2) dehydrogenase, subunit C
S101446_01326	*nuoB*	204.7422368	1140.932039	136.6581808	119.761473	0.91832	0.0064231	2.33E-14	NADH dehydrogenase subunit B
S101446_01806	*nuoM*	245.0612039	906.6721988	176.2780981	159.2998772	0.96833	0.011607	1.83E-18	proton-translocating NADH-quinone oxidoreductase, chain M
S101446_02944	*atuG*	119.0953189	111.7384076	63.15856653	90.46087314	0.0022131	3.69E-10	9.11E-09	NADH dehydrogenase (ubiquinone)

Table SIII.6

Information about the gene expression level of KEGG PATHWAY in this study.

Gene ID	Gene name	z64h group FPKM	z88h group FPKM	z16h group FPKM	z40h group FPKM	padj (z40hvsz16h)	padj (z64hvsz16h)	padj (z88hvsz16h)	KEGG annotation
S101446_00744	*tal-pgi*	27.28614903	901.3415845	13.64251006	13.98903008	0.70551	1.54E-07	3.42E-22	binoteal transaldolase/phosoglucose isomerase
S101446_00377	*glpX-SEBP*	328.2826436	358.648152	277.5577528	364.0730994	0.0003501	0.22987	0.00024839	fructose-1,6-bisphosphatase class II
S101446_00378	*fbaA*	205.9135533	216.1860175	172.6769418	205.9464877	0.052813	0.015415	0.004149	fructose-bisphosphate aldolase
S101446_02245	*xfp*	1669.42916	1940.222678	1306.770275	1510.13033	0.008969	4.86E-05	1.01E-10	putative phosphoketolase
S101446_00743	*tktA*	40.82823802	1812.962755	15.94441044	14.83875229	0.99082	8.78E-18	2.42E-31	transketolase

Table SIII.7

Information about the gene expression level of KEGG PATHWAY in this study.

Gene ID	Gene name	z64h group FPKM	z88h group FPKM	z16h group FPKM	z40h group FPKM	padj (z40hvsz16h)	padj (z64hvsz16h)	padj (z88hvsz16h)	KEGG annotation
S101446_00039	*fabD*	122.6451609	103.9894811	213.2679055	129.0108506	3.65E-05	1.38E-07	4.30E-13	malonyl CoA-acyl carrier protein transacylase
S101446_00040	*fabG*	161.091261	132.8006576	295.7098065	174.895623	1.35E-05	6.04E-06	9.36E-16	3-oxoacyl-[acyl-carrier-protein] reductase
S101446_01361	*fabH*	309.9766363	268.0052371	515.6493433	330.4094529	2.12E-05	1.54E-11	9.10E-14	3-oxoacyl-(acyl carrier protein) synthase III
S101446_02351	*accD*	256.6159982	223.6266288	378.2538723	346.2365114	0.87025	6.82E-06	1.36E-07	acetyl-CoA carboxylase, carboxyl transferase, beta subunit
S101446_02403	*accC*	400.0980664	328.5556426	493.765217	395.9066606	0.1009	0.017541	2.85E-05	acetyl-CoA carboxylase biotin carboxylase subunit
S101446_02404	*accB*	303.4601731	247.9847544	426.8970294	272.555885	0.00043358	0.0030473	0.00024329	acetyl-CoA carboxylase, biotin carboxyl carrier protein
S101446_02889	*accA*	674.954545	596.4566791	922.6780326	645.521789	0.00053137	2.78E-05	1.67E-06	acetyl-CoA carboxylase carboxyltransferase subunit alpha

Table SIII.8

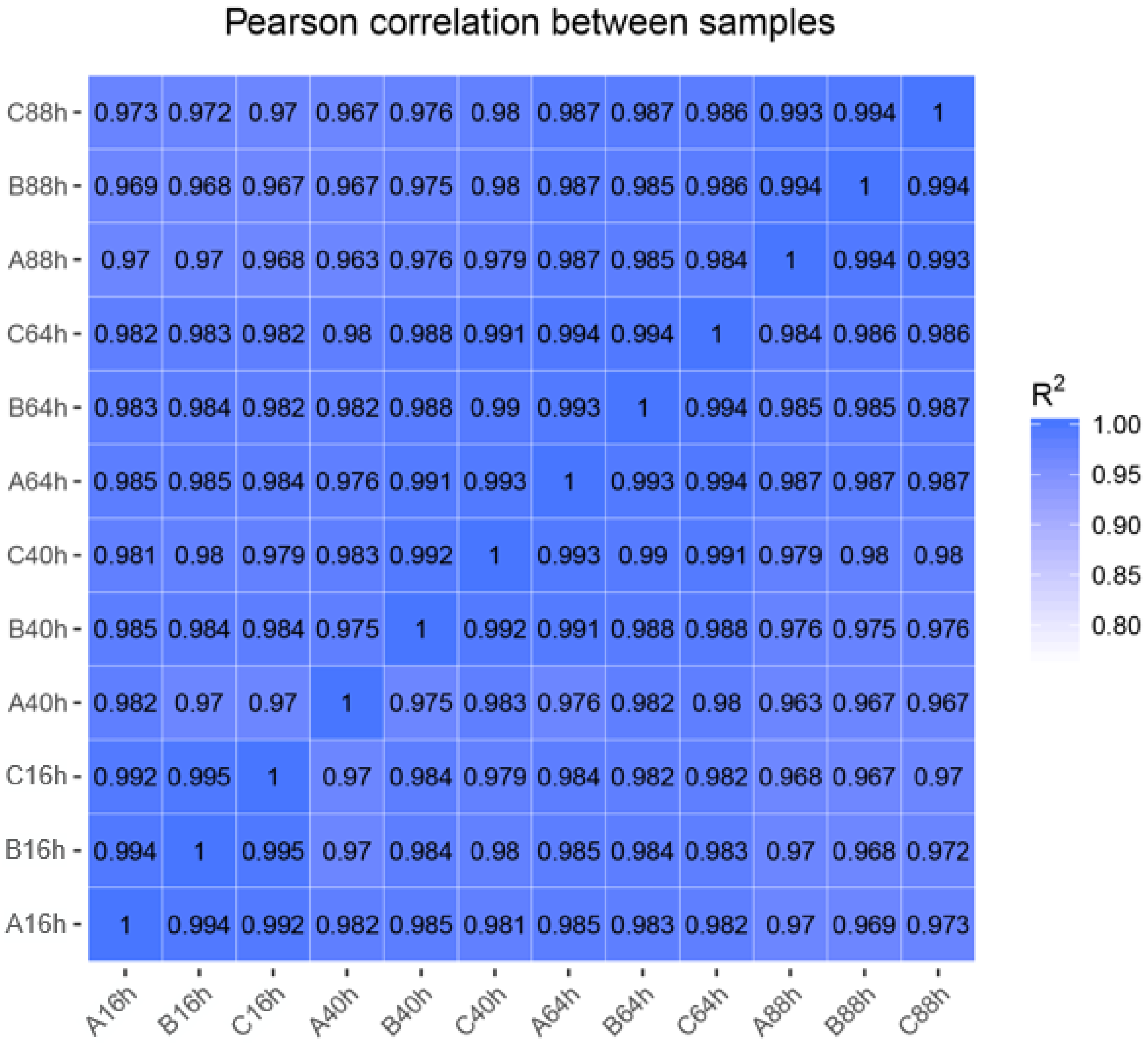
Information about the gene expression level of KEGG PATHWAY in this study.

Gene ID	Gene name	z64h group FPKM	z88h group FPKM	z16h group FPKM	z40h group FPKM	padj (z40hvsz16h)	padj (z64hvsz16h)	padj (z88hvsz16h)	KEGG annotation
S101446_01800	*ompA*	1893.381944	1921.323115	1790.518697	2075.231806	0.0088638	0.28862	0.088175	OmpA/MotB domain protein
S101446_02503	*ompH*	955.0399537	827.9648425	1189.984997	1019.001726	0.37841	0.0085478	0.00020355	outer membrane chaperone Skp (OmpH)
S101446_00385	*metQ*	87.32797955	88.95176414	139.0705154	118.0697794	0.68692	0.008657	0.0076632	D-methionine transporter substrate-binding periplasmic protein
S101446_02321	*ompW*	3513.746634	3526.141802	2935.074177	2857.997039	0.75336	0.0027772	0.00073066	outer membrane protein

Table SIII.9

Information about the gene expression level of KEGG PATHWAY in this study.

Gene ID	Gene name	z64h group FPKM	z88h group FPKM	z16h group FPKM	z40h group FPKM	padj (z40hvsz16h)	padj (z64hvsz16h)	padj (z88hvsz16h)	KEGG annotation
S101446_02206	*clpB*	4556.237742	5376.66432	4230.62276	3998.282262	0.93062	0.15707	2.31E-05	ATP-dependent chaperone ClpB
S101446_02333	*dnaK*	9181.177583	9085.76905	9163.592566	8335.19882	0.84626	0.72935	0.54192	molecular chaperone DnaK
S101446_02334	*dnaJ*	877.9212614	879.6189261	870.7978995	959.7687914	0.29226	0.78936	0.49809	chaperone protein DnaJ
S101446_02833	*rpoH*	2414.590396	3231.453225	1665.159651	2010.546546	0.0016352	1.40E-09	3.07E-25	RNA polymerase factor sigma-32
S101446_02983	*groES*	19140.84813	14208.36207	28073.13339	21913.53556	0.37134	0.014142	3.44E-05	heat shock protein GroES
S101446_02984	*groEL*	8197.536376	5749.865079	11360.58291	9404.504011	0.6492	0.086429	0.00087063	chaperonin GroEL
S101446_01213	*recN*	215.9321191	186.6560893	254.4322446	209.2100065	0.20239	0.071908	0.0051511	DNA repair protein RecN
S101446_02079	*uvrA*	113.9007156	125.6256338	97.09095044	111.1025171	0.040508	0.024313	0.00015871	excinuclease ABC subunit A
S101446_02949	*uvrB*	404.5321004	360.0335329	407.0540774	456.9114258	0.038277	0.94446	0.6747	excinuclease ABC subunit B
S101446_01086	*uvrC*	270.6436581	244.1334194	274.2095921	312.2490324	0.040608	0.91382	0.63533	excinuclease ABC subunit C
S101446_01902	*dinB*	139.2659949	140.725345	113.9106998	134.4027303	0.045995	0.027963	0.0048179	DNA-directed DNA polymerase



	A16h	B16h	C16h	A40h	B40h	C40h	A64h	B64h	C64h	A88h	B88h	C88h
C88h	0.973	0.972	0.97	0.967	0.976	0.98	0.987	0.987	0.986	0.993	0.994	1
B88h	0.969	0.968	0.967	0.967	0.975	0.98	0.987	0.985	0.986	0.994	1	0.994
A88h	0.97	0.97	0.968	0.963	0.976	0.979	0.987	0.985	0.984	1	0.994	0.993
C64h	0.982	0.983	0.982	0.98	0.988	0.991	0.994	0.994	1	0.984	0.986	0.986
B64h	0.983	0.984	0.982	0.982	0.988	0.99	0.993	1	0.994	0.985	0.985	0.987
A64h	0.985	0.985	0.984	0.976	0.991	0.993	1	0.993	0.994	0.987	0.987	0.987
C40h	0.981	0.98	0.979	0.983	0.992	1	0.993	0.99	0.991	0.979	0.98	0.98
B40h	0.985	0.984	0.984	0.975	1	0.992	0.991	0.988	0.988	0.976	0.975	0.976
A40h	0.982	0.97	0.97	1	0.975	0.983	0.976	0.982	0.98	0.963	0.967	0.967
C16h	0.992	0.995	1	0.97	0.984	0.979	0.984	0.982	0.982	0.968	0.967	0.97
B16h	0.994	1	0.995	0.97	0.984	0.98	0.985	0.984	0.983	0.97	0.968	0.972
A16h	1	0.994	0.992	0.982	0.985	0.981	0.985	0.983	0.982	0.97	0.969	0.973

Fig. S1. Pearson correlation coefficient value of gene expression between samples of this study. The number in each blue grid represents the value of the square of the Pearson correlation coefficient between pair of samples. The more the two samples are similar to each other, the closer the value of the square of the Pearson correlation coefficient is to 1.