

# **Metabolic difference analysis of *Clostridium cellulovorans* grown on glucose and cellulose**

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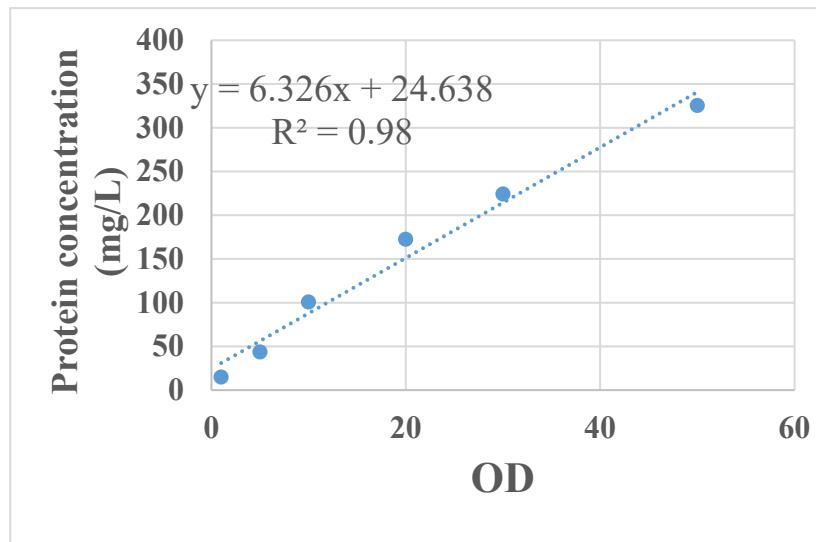


Figure S1. The standard curve of the corresponding relationship between absorbance ( $A_{600}$ ) and intracellular protein concentration

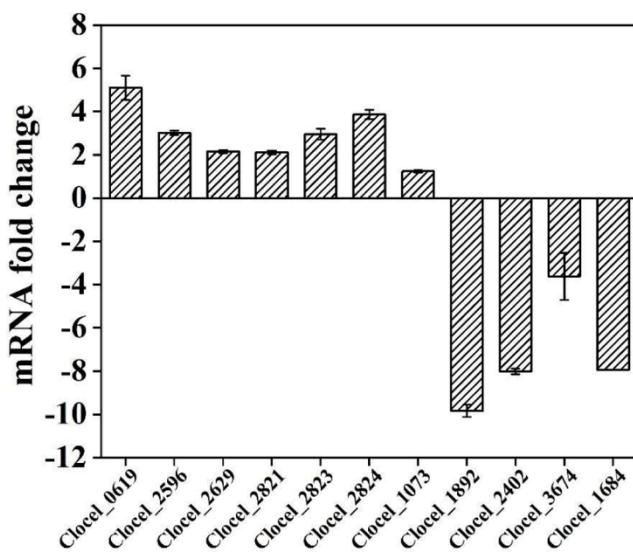


Figure S2. Expression profiles of selected genes using RT-PCR. Gene name: Genes are listed in the order of old ORF (open reading frame) numbers ([https://www.ncbi.nlm.nih.gov/nuccore/NC\\_014393.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_014393.1)).

Table S1 The primers used for RT-PCR in this study

Gene locus	Gene name	Primer	Sequence (5' to 3')
Clocel_0619	cellulase family glycosylhydrolase	0619-F	TGGCTAACTGGAGCTAAGTGG
		0619-R	TGGTGTGCCATTCAATCCAGC
Clocel_2596	sugar ABC transporter substrate-binding protein	2596-F	TTGGCAGGAGAAGAACTTGGTAA
		2596-R	TTAGCAGCATCACTGCCATA
Clocel_2629	3-hydroxyacyl-CoA dehydrogenase family protein	2629-F	AAGATAGGCAGTTGTGGGAGC
		2629-R	ACCTCTTCTGAAACGTCTACCA
Clocel_2821	glycoside hydrolase family 9 protein	2821-F	CTCCAGAACCAACAAACGCA
		2821-R	GCCAGTTCCCTGGAGTTGTGT
Clocel_2823	dockerin type I domain-containing protein	2823-F	AGACTGATCAACCAAGCGCAA
		2823-R	TCCTTACCTACAGCAGCACCA
Clocel_2824	cellulose-binding protein	2824-F	TGCAACAAATAGTGCAGTAACACC A
		2824-R	AGCTGTTGGAGCTACTGTTGAG
Clocel_1073	glycosidehydrolae	1073-F	GAAAGCATCACAGGCAAAG
		1073-R	ATAATCAGGGAGCCCATCT
Clocel_1684	pyruvate:ferredoxin (flavodoxin) oxidoreductase	1684-F	TGGCTACGTTATGTTGCAC
		1684-R	TCCGCTTCTACGGCTTT
Clocel_1892	acetate kinase	1892-F	CAGCAGTTGGACATAGAGT
		1892-R	CATAGGAACCTCTGGCATC
Clocel_2402	bifunctional acetaldehyde-CoA/alcohol dehydrogenase	2402-F	ATGGTTGTTGGGGATGGC
		2402-R	TCGCACCTTCCTCGCACT
Clocel_3674	butyrate kinase	3674-F	CTTACTGGAAAAGGTGGCT
		3674-R	CTTACCGTCAAGAACAGC
16s	internal standard	ly-16S-rF	CAGCMGCCGCGGTAAATWC
		ly-16S-rR	CCGTCAATTCTTTAGTTT

Table S2. The detailed products data in the end of fermentation of *C. cellulovorans*

	Glucose <sup>a</sup> (mM)	Lactate (mM)	Acetate <sup>b</sup> (mM)	Butyrate (mM)	Acids (mM)	H <sub>2</sub> (mM)	CO <sub>2</sub> (mM)
Glucose	268 ± 2	16.8 ± 5.8	42.3(20) ± 7.5	132.7 ± 5.5	<b>171.9</b>	<b>117.2 ± 14</b>	<b>36.8 ± 3</b>
Cellulose	204 ± 8	ND	31.5(20) ± 1.3	93.9 ± 4.4	<b>105.4</b>	<b>141.4 ± 12</b>	<b>66.2 ± 1</b>

<sup>a</sup>: Glucose consumption in the whole fermentation process during which the molecular weight of glucose in cellulose is 162; <sup>b</sup>: 20 mM acetate in the original fermentation medium; ND: not detected

Table S3. The detailed data of carbon source, redox balance analysis and stoichiometry in *C. cellulovorans* fermentation.

<sup>a</sup>: Glucose consumption in the whole fermentation process during which the molecular weight of glucose in cellulose is 162;

	Glucose <sup>a</sup> (mM)	Glucose <sup>b</sup> (mM)	Ratio <sup>c</sup> (%)	H <sub>2</sub> <sup>d</sup> (mM)	H <sub>2</sub> <sup>e</sup> (mM)	Ratio <sup>f</sup> (%)	NADH <sup>g</sup> (mM)	NADH <sup>h</sup> (mM)	Ratio <sup>i</sup> (%)
Glucose	268 ± 2	152.3	57	420.4	117.2	28	536	414.9	77
Cellulose	204 ± 8	99.7	49	293.2	141.4	48	408	281.7	69

<sup>b</sup>: Glucose required for the acetate, lactate and butyrate synthesis; <sup>c</sup>: Ratio of glucose required for acids formation to total glucose consumption; <sup>d</sup>: Fd<sub>red</sub> formed during acetate and butyrate synthesis. These Fd<sub>red</sub> can theoretically convert to equimolar hydrogen; <sup>e</sup>: Hydrogen collected during the whole fermentation process; <sup>f</sup>: The ratio of hydrogen to hydrogen (e/d); <sup>g</sup>: NADH produced during glycolysis; <sup>h</sup>: NADH required for acids synthesis; <sup>i</sup>: The ratio of NADH to NADH (h/g).

Table S4. The expression profiles of the genes strongly induced during cellulose- and glucose-fermentation of *Clostridium cellulovorans*

Gene locus <sup>a</sup>	Product	RPKM <sup>b</sup>		Fold- change <sup>c</sup>
		Cellulose <i>t</i> =36 h	Glucose <i>t</i> =96 h	
Up-regulated genes in cellulose fermentation				
<i>Clocl_0148</i>	Leucine-rich repeat protein	3449	47	6.2
<i>Clocl_0272</i>	hypothetical protein	31820	409	6.3
<i>Clocl_1624</i>	glycoside hydrolase family 9 protein	4924	64	6.3
<i>Clocl_2816</i>	glycoside hydrolase family 9 protein	4855	70	6.1
<i>Clocl_4119</i>	dockerin type I domain-containing protein	8742	137	6.0
<i>Clocl_0149</i>	Ig-like domain-containing protein	4085	805	5.7
<i>Clocl_3111</i>	cellulase family glycosylhydrolase	2432	51	5.6
<i>Clocl_3176</i>	Ig-like domain-containing protein	7611	179	5.4
<i>Clocl_0140</i>	pre-peptidase C-terminal domain-containing protein	2937	75	5.3
<i>Clocl_3112</i>	hypothetical protein	1788	44	5.4
<i>Clocl_1134</i>	CIA30 family protein	3318	95	5.1
<i>Clocl_2295</i>	glycoside hydrolase family 11 protein	2600	66	5.3
<i>Clocl_2600</i>	discoidin domain-containing protein	4863	130	5.2
<i>Clocl_1182</i>	hypothetical protein	2123	60	5.1
<i>Clocl_2900</i>	endo-1,4-beta-xylanase	11548	332	5.1
<i>Clocl_1211</i>	Ig-like domain-containing protein	6824	239	4.8
<i>Clocl_3927</i>	methyl-accepting chemotaxis protein	1060	35	4.9
<i>Clocl_4053</i>	Ig-like domain-containing protein	2091	86	4.6
<i>Clocl_2626</i>	non-ribosomal peptide synthetase	1325	63	4.4
<i>Clocl_2576</i>	glycoside hydrolase family 9 protein	4415	197	4.5
<i>Clocl_2575</i>	dockerin type I domain-containing protein	2606	121	4.4
<i>Clocl_3077</i>	Ig-like domain-containing protein	1285	64	4.3
<i>Clocl_0619</i>	cellulase family glycosylhydrolase	9869	419	4.6
<i>Clocl_2741</i>	glycoside hydrolase family 9 protein	3589	159	4.5
<i>Clocl_2882</i>	glycoside hydrolase family 1 protein	3206	164	4.3
<i>Clocl_2821</i>	glycoside hydrolase family 9 protein	79338	4463	4.2
<i>Clocl_1184</i>	hypothetical protein	18372	1162	4.0
<i>Clocl_2880</i>	PTS transporter subunit EIIC	5185	255	4.3
<i>Clocl_2822</i>	glycoside hydrolase family 9 protein	25065	1549	4.0
<i>Clocl_1425</i>	leucine-rich repeat protein	451	30	3.9
<i>Clocl_2823</i>	dockerin type I domain-containing protein	79165	5029	4.0
<i>Clocl_2820</i>	cellulosome anchoring protein cohesin region	2351	170	3.8
<i>Clocl_2819</i>	glycoside hydrolase family 9 protein	7921	552	3.8
<i>Clocl_2824</i>	cellulose-binding protein	160115	10499	3.9
<i>Clocl_2850</i>	hemolysin-type calcium-binding protein	3004	226	3.7

Cloel_3181	M6 family metalloprotease domain-containing protein	804	61	3.7
Cloel_3197	glycosidase	463	40	3.5
Cloel_3905	ABC transporter ATP-binding protein/permease	832	66	3.7
Cloel_3555	DNA primase	601	56	3.4
Cloel_3583	helix-turn-helix domain-containing protein	408	32	3.7
Cloel_2849	calcium-binding protein	2894	275	3.4
<b>Cloel_0983</b>	<b>cellulase family glycosylhydrolase</b>	<b>58</b>	<b>50</b>	<b>3.6</b>
Cloel_0555	protein-tyrosine-phosphatase	463	49	3.2
Cloel_0276	phosphotransferase	422	44	3.3
Cloel_2826	RNA polymerase sigma-I factor	313	33	3.3
Cloel_0982	chitobiase/beta-hexosaminidase C-terminal domain-containing protein	1090	108	3.3
Cloel_3562	radical SAM protein	275	26	3.4
<b>Cloel_2818</b>	<b>dockerin type I domain-containing protein</b>	<b>7840</b>	<b>790</b>	<b>3.3</b>
<b>Cloel_1045</b>	<b>glycoside hydrolase family 3 C-terminal domain-containing protein</b>	<b>259</b>	<b>31</b>	<b>3.1</b>
<b>Cloel_3359</b>	<b>cellulase family glycosylhydrolase</b>	<b>14230</b>	<b>1425</b>	<b>3.3</b>
Cloel_4206	ribonuclease	849	81	3.4
<b>Cloel_0930</b>	<b>glycoside hydrolase family 9 protein</b>	<b>2074</b>	<b>244</b>	<b>3.1</b>
Cloel_3819	peptidoglycan-binding protein	826	81	3.4
Cloel_0557	LPS biosynthesis protein	359	40	3.2
Cloel_0556	CpsD/CapB family tyrosine-protein kinase	393	47	3.1
Cloel_0307	aldose 1-epimerase family protein	245	38	2.7
Cloel_3904	L-glyceraldehyde 3-phosphate reductase	776	82	3.2
<b>Cloel_3196</b>	<b>glycoside hydrolase family 130 protein</b>	<b>418</b>	<b>64</b>	<b>2.7</b>
<b>Cloel_1432</b>	<b>cellulase family glycosylhydrolase</b>	<b>209</b>	<b>30</b>	<b>2.8</b>
Cloel_3906	ABC transporter ATP-binding protein/permease	305	41	2.9
Cloel_0590	xylose isomerase	736	89	3.1
Cloel_2901	6-phosphofructokinase	734	110	2.7
Cloel_0886	methyl-accepting chemotaxis protein	490	64	2.9
Cloel_4109	Ig-like domain-containing protein	2841	375	2.9
Cloel_2827	hypothetical protein	193	27	2.8
Cloel_0302	hypothetical protein	318	56	2.5
Cloel_0040	carbohydrate ABC transporter permease	310	43	2.8
Cloel_0226	hypothetical protein	225	41	2.5
Cloel_3817	iron-containing alcohol dehydrogenase	1483	212	2.8
Cloel_3275	RICIN domain-containing protein	204	33	2.6
Cloel_0592	xylulokinase	795	146	2.4
Cloel_2567	dockerin type I domain-containing protein	243	34	2.8
Cloel_0519	glycogen/starch/alpha-glucan family phosphorylase	193	35	2.5
Cloel_0560	alpha-galactosidase	1171	216	2.4
<b>Cloel_3099</b>	<b>cellulase family glycosylhydrolase</b>	<b>168</b>	<b>29</b>	<b>2.5</b>
Cloel_1943	sporulation transcription factor Spo0A	553	106	2.4
Cloel_3596	DEAD/DEAH box helicase	467	98	2.3

Cloel_4023	hypothetical protein	331	62	2.4
Cloel_1263	DUF6514 family protein	532	68	3.0
Cloel_1703	flagellar assembly protein FliW	182	42	2.1
<a href="#">Cloel_1150</a>	<a href="#">cellulase family glycosylhydrolase</a>	<a href="#">170</a>	<a href="#">31</a>	<a href="#">2.5</a>
Cloel_0510	molecular chaperone HtpG	575	122	2.2
Cloel_0225	right-handed parallel beta-helix repeat-containing protein	345	86	2.0
Cloel_3874	DUF3369 domain-containing protein	232	48	2.3
Cloel_0039	ABC transporter permease subunit	263	54	2.3
Cloel_1148	alpha/beta hydrolase	145	32	2.2
Cloel_0038	ABC transporter substrate-binding protein	6512	1426	2.2
Cloel_4215	glutathione peroxidase	977	217	2.2
Cloel_0827	ATP-binding protein	220	53	2.1
<a href="#">Cloel_2607</a>	<a href="#">chitobiase/beta-hexosaminidase C-terminal domain-containing protein</a>	<a href="#">10260</a>	<a href="#">2296</a>	<a href="#">2.1</a>
Cloel_3650	dockerin type I domain-containing protein	204	45	2.1
Cloel_1977	single-stranded DNA-binding protein	153	37	2.1
<a href="#">Cloel_3662</a>	<a href="#">cellulase family glycosylhydrolase</a>	<a href="#">1334</a>	<a href="#">298</a>	<a href="#">2.1</a>
Cloel_0476	methyl-accepting chemotaxis protein	648	161	2.0
Cloel_4334	SEC-C domain-containing protein	235	82	1.9
Cloel_0516	4-alpha-glucanotransferase	214	57	1.9
Cloel_3103	glycosyltransferase family 39 protein	456	115	1.9
Cloel_4355	HD-GYP domain-containing protein	320	94	1.9
Cloel_3608	DNRLRE domain-containing protein	229	60	1.9
Cloel_4208	DMT family transporter	156	44	1.9
Cloel_3900	HD domain-containing protein	154	41	1.9
Cloel_0221	Hypothetical protein	321	103	1.9
Cloel_2074	Protein translocase subunit, SecF	631	169	1.9
<a href="#">Cloel_2593</a>	<a href="#">Galactose mutarotase</a>	<a href="#">215</a>	<a href="#">2</a>	<a href="#">7.0</a>
<a href="#">Cloel_2594</a>	<a href="#">Response regulator</a>	<a href="#">85</a>	<a href="#">0</a>	<a href="#">7.4</a>
<a href="#">Cloel_2595</a>	<a href="#">Sensor histidine kinase</a>	<a href="#">312</a>	<a href="#">7</a>	<a href="#">5.4</a>
<a href="#">Cloel_2596</a>	<a href="#">Extracellular solute-binding protein</a>	<a href="#">625</a>	<a href="#">12</a>	<a href="#">5.7</a>
<a href="#">Cloel_2597</a>	<a href="#">Glycoside hydrolase family 43 protein</a>	<a href="#">2528</a>	<a href="#">14</a>	<a href="#">7.5</a>
<a href="#">Cloel_2598</a>	<a href="#">Sugar ABC transporter substrate-binding protein</a>	<a href="#">1850</a>	<a href="#">5</a>	<a href="#">8.6</a>
<a href="#">Cloel_2599</a>	<a href="#">ABC transporter permease</a>	<a href="#">353</a>	<a href="#">0</a>	<a href="#">9.8</a>
<a href="#">Cloel_2600</a>	<a href="#">Sugar ABC transporter ATP-binding protein</a>	<a href="#">896</a>	<a href="#">2</a>	<a href="#">8.5</a>
<a href="#">Cloel_2621</a>	<a href="#">3-hydroxyacyl-CoA dehydrogenase family protein</a>	<a href="#">228</a>	<a href="#">3</a>	<a href="#">6.4</a>
Up-regulated genes in glucose fermentation				
<a href="#">Cloel_2402</a>	Bifunctional aldehyde/alcohol dehydrogenases	48	71	-0.7
Cloel_1931	Asp23/Gls24 family envelope stress response protein	172	511	-1.6
Cloel_3697	30S ribosomal protein S9	256	820	-1.7
Cloel_3097	hypothetical protein	57	198	-1.8
Cloel_3672	Phosphoglucomamine mutase	123	439	-1.8
Cloel_4332	Lactate utilization protein	56	188	-1.8
Cloel_3792	RNA-binding protein S1	111	399	-1.8

Cloel_3479	NUDIX hydrolase	57	197	-1.8
Cloel_1351	DEAD/DEAH box helicase	207	810	-1.9
Cloel_2694	Hypothetical protein	39	148	-1.9
Cloel_0718	Cro/CI family transcriptional regulator	424	1578	-1.9
Cloel_1663	Membrane protein	72	261	-1.9
Cloel_1368	Triple tyrosine motif-containing protein	86	346	-2.0
Cloel_3752	23S rRNA (guanosine(2251)-2'-O)-methyltransferase RlmB	29	119	-2.0
Cloel_0105	Energy-coupled thiamine transporter ThiT	53	212	-2.0
Cloel_1557	Dihydroorotate dehydrogenase	63	273	-2.1
Cloel_2206	Uroporphyrinogen-III C-methyltransferase	80	355	-2.1
Cloel_3950	Recombinase family protein	31	134	-2.1
tRNA (N(6)-L-threonylcarbamoyladenosine(37)-C(2))				
Cloel_1441	-methylthiotransferase	57	255	-2.2
Cloel_2011	RNA methyltransferase	46	214	-2.2
Cloel_1418	50S ribosomal protein L11 methyltransferase	51	226	-2.2
Cloel_0382	Peptidoglycan glycosyltransferase	94	439	-2.2
Cloel_2770	Maf-like protein	31	141	-2.2
Cloel_4111	S8 family peptidase	90	402	-2.2
Cloel_1020	Glycoside hydrolase family 1 protein	51	235	-2.2
Cloel_1814	Replication-associated recombination protein A	109	552	-2.3
Cloel_2101	GTPase HflX	64	323	-2.3
Cloel_0524	ABC transporter ATP-binding protein	104	526	-2.3
Cloel_3433	[FeFe] hydrogenase H-cluster radical SAM maturase HydG	145	694	-2.3
Cloel_3067	Peptide chain release factor 1	157	758	-2.3
Cloel_1552	Trypsin-like peptidase domain-containing protein	283	1399	-2.3
<b>Cloel_0521</b>	<b>Sulfate ABC transporter substrate-binding protein</b>	<b>70</b>	<b>377</b>	<b>-2.4</b>
Cloel_4149	Metallophosphoesterase	111	598	-2.4
Cloel_1464	KUP/HAK/KT family potassium transporter	60	323	-2.4
Cloel_2149	Homoserine O-succinyltransferase	40	206	-2.4
Cloel_3026	Glycosyltransferase family 2 protein	75	403	-2.4
Cloel_1990	Glycerol dehydrogenase	44	241	-2.4
Cloel_2532	Cysteine synthase	74	3894	-2.4
Cloel_0629	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase	716	3856	-2.4
Cloel_1272	Permease-like cell division protein FtsX	145	804	-2.5
Cloel_1558	Orotate phosphoribosyltransferase	56	323	-2.5
Cloel_2403	Glutamine--fructose-6-phosphate transaminase (isomerizing)	148	861	-2.5
Cloel_2983	Right-handed parallel beta-helix repeat-containing protein	67	383	-2.5
<b>Cloel_4152</b>	<b>PhnD/SsuA/transferrin family substrate-binding protein</b>	<b>301</b>	<b>1666</b>	<b>-2.5</b>
Cloel_1540	Glycosyltransferase family 39 protein	36	206	-2.5
Cloel_1556	Dihydroorotate dehydrogenase electron transfer subunit	36	197	-2.5
Cloel_0605	MATE family efflux transporter	380	2211	-2.5
<b>Cloel_1183</b>	<b>Fibronectin</b>	<b>93</b>	<b>545</b>	<b>-2.6</b>
Cloel_0683	Sulfur carrier protein ThiS adenylyltransferase ThiF	48	316	-2.7
Cloel_1329	Serine O-acetyltransferase	42	266	-2.7

Cloel_1542	Glycosyltransferase family 2 protein	37	258	-2.8
Cloel_0528	GTP-binding protein	323	2254	-2.8
Cloel_0525	Adenylyl-sulfate reductase subunit alpha	169	1173	-2.8
Cloel_1576	Transcriptional repressor	161	1129	-2.8
Cloel_4150	ABC transporter ATP-binding protein	50	367	-2.9
Cloel_1032	Cadmium-translocating P-type ATPase	78	583	-2.9
Cloel_0527	Sulfate adenyltransferase subunit 2	119	864	-2.9
Cloel_0684	2-iminoacetate synthase ThiH	185	1449	-3.0
Cloel_0682	Thiamine phosphate synthase	107	911	-3.1
Cloel_1306	Hypothetical protein	132	1105	-3.1
Cloel_1991	Dihydroxyacetone kinase subunit DhaK	73	604	-3.1
Cloel_1271	Cell division ATP-binding protein FtsE	61	531	-3.1
Cloel_2018	Phosphoglycerate dehydrogenase	979	8207	-3.1
Cloel_0685	Thiazole synthase	90	770	-3.1
Cloel_3475	Cysteine synthase A	124	1058	-3.1
Cloel_0056	ABC transporter ATP-binding protein	29	263	-3.2
Cloel_1533	L-lactate dehydrogenase	152	1461	-3.3
Cloel_2017	DUF1015 family protein	410	4237	-3.4
Cloel_1597	Vitamin B12-dependent ribonucleotide reductase	486	5587	-3.5
Cloel_1773	GTP-sensing pleiotropic transcriptional regulator CodY	84	965	-3.5
Cloel_2842	M42 family metallopeptidase	129	1437	-3.5
Cloel_2384	Flagellin	88	1006	-3.5
Cloel_2675	MetQ/NlpA family ABC transporter substrate-binding protein	134	1932	-3.8
Cloel_2844	GTP cyclohydrolase II	43	668	-4.0
Cloel_1827	Fe-S cluster assembly scaffold protein NifU	105	1836	-4.1
Cloel_2812	Phosphomethylpyrimidine synthase ThiC	150	2680	-4.2
Cloel_0022	Cadherin-like beta sandwich domain-containing protein	121	2420	-4.3
Cloel_2677	Methionine ABC transporter ATP-binding protein	36	697	-4.3
Cloel_1826	Cysteine desulfurase NifS	128	2673	-4.4
Cloel_0511	EAL domain-containing protein	57	1336	-4.6

<sup>a</sup>: Genes are listed in the order of old ORF (Open reading frame) numbers;

<sup>b</sup>: RPKM is the abbreviation of Reads Per Kilobase per Million mapped reads.

<sup>c</sup>: Data represent the log<sub>2</sub> values change folds of PRKM.

Table S5. The expression profiles of the important genes during cellulose- and glucose-fermentation of *C. cellulovorans*.

Gene locus <sup>a</sup>	Product	RPKM <sup>b</sup>		Fold-change <sup>c</sup>
		Cellulose <i>t</i> =96 h	Glucose <i>t</i> =36 h	
<b>Cellulase</b>				
Clocl_0031	Glycoside hydrolase family 3 C-terminal domain-containing protein	193	69	2.8
Clocl_0035	Glycoside hydrolase family 3 C-terminal domain-containing protein	31	18	1.7
Clocl_0589	Glycoside hydrolase family 95 protein	151	23	6.5
Clocl_0619	Cellulase family glycosylhydrolase	9869	419	23.6
Clocl_0905	Cellulase family glycosyl hydrolase	1359	20	66.4
Clocl_0930	Glycoside hydrolase family 9 protein	2074	244	8.5
Clocl_0983	Cellulase family glycosylhydrolase, Exoglucanase	584	49	11.8
Clocl_1045	Glycoside hydrolase family 3 C-terminal domain-containing protein	259	31	8.4
Clocl_1073	Glycoside hydrolase	134	79	17
Clocl_1134	CIA30 family protein, mannanase	3318	95	35
Clocl_1150	Cellulase family glycosylhydrolase, Endoglucanase	170	31	5.5
Clocl_1420	Glycoside hydrolase family 9 protein	493	7.4	66.3
Clocl_1432	Cellulase family glycosylhydrolase	209	30	6.9
Clocl_1476	Glycoside hydrolase family 9 protein	335	5	66
Clocl_1477	Glycoside hydrolase family 9 protein	81	4	20.8
Clocl_1478	Glycoside hydrolase family 9 protein	1944	23	84.6
Clocl_1543	Glycoside hydrolase family 25 protein	32	11	2.8
Clocl_1624	Glycoside hydrolase family 9 protein, Endoglucanase	4924	64	77.1
Clocl_2256	Glycoside hydrolase family 88 protein	195	14	13.6
Clocl_2295	Glycoside hydrolase family 11 protein	2599	66	39.3
Clocl_2575	Dockerin type I domain-containing protein, mannanase	2606	121	21.5
Clocl_2576	Glycoside hydrolase family 9 protein, Endoglucanase	4415	197	22.4
Clocl_2595	Glycoside hydrolase family 43 protein	2304	15	154.3
Clocl_2600	Discoidin domain-containing protein, Endoglucanase	4863	130	37.4
Clocl_2606	Cellulase family glycosylhydrolase, Endoglucanase	609	185	3.3
Clocl_2607	Chitobiase/beta-hexosaminidase, mannanase	10260	2296	4.5
Clocl_2741	Glycoside hydrolase family 9 protein, Endoglucanase	3589	159	22.5
Clocl_2816	Glycoside hydrolase family 9 protein	4854	70	69
Clocl_2818	Dockerin type I domain-containing protein, Cellulosose-binding protein A	7840	790	9.9
Clocl_2819	Glycoside hydrolase family 9 protein	7921	552	14.4
Clocl_2820	Cellulosome anchoring protein cohesin region	2350	170	13.8
Clocl_2821	Glycoside hydrolase family 9 protein, Exoglucanase	79338	4463	17.78
Clocl_2822	Glycoside hydrolase family 9 protein, Endoglucanase	25065	1549	16.2

<b>Cloel_2824</b>	<b>Cellulose-binding protein</b>	<b>160115</b>	<b>10498</b>	<b>15.3</b>
Cloel_2882	Glycoside hydrolase family 1 protein	3206	164	19.5
Cloel_2900	Endo-beta-xylanase	11548	332	34.7
Cloel_3099	Cellulase family glycosylhydrolase	168	29	5.8
Cloel_3111	Cellulase family glycosylhydrolase, Exoglucanase	2432	51	47.4
Cloel_3196	Glycoside hydrolase family 130 protein	418	64	6.5
Cloel_3205	Glycoside hydrolase family 2 protein	156	51	3.1
Cloel_3242	Cellulase family glycosylhydrolase	367	193	1.9
Cloel_3359	Cellulase family glycosylhydrolase, Exoglucanase	14230	1425	10.0
Cloel_3657	Glycoside hydrolase family 43 protein	210	89	2.4
Cloel_3662	Cellulase family glycosylhydrolase	1334	298	4.5
Cloel_4063	Glycoside hydrolase family 1 protein	103	66	1.6
Cloel_4119	Dockerin type I domain-containing protein, mannanase	8742	137	63.7
<b>Central metabolic pathway</b>				
Cloel_2901	ATP-dependent 6-phosphofructokinases	734	110	6.7
Cloel_0388	ATP-dependent 6-phosphofructokinases	75	173	0.4
Cloel_1603	Pyrophosphate (PPi)-fructose 6-phosphate 1-phosphotransferase	50	82	0.6
Cloel_0719	Glyceraldehyde-3-phosphate dehydrogenase	14356	20741	0.7
Cloel_0720	Phosphoglycerate kinase	3371	5369	0.6
Cloel_0721	Triosephosphate isomerase	1455	1949	0.8
Cloel_1364	Glucose-6-phosphate isomerase	754	985	0.8
Cloel_1533	Lactate dehydrogenase, <i>ldh</i>	152	1461	0.1
Cloel_2700	Lactate dehydrogenase, <i>ldh</i>	23	59	0.4
Cloel_4097	Fe-only hydrogenase, <i>hyd</i>	528	1097	0.5
<a href="#">Cloel_1684</a>	Pyravate ferredoxin oxidoreductase, <i>pfor</i>	<a href="#">13316</a>	<a href="#">20539</a>	<a href="#">0.7</a>
Cloel_1811	Pyravate formate lyase, <i>pfl</i>	10220	22995	0.4
Cloel_1812	Pyravate-formate lyase activating enzyme, <i>pflAE</i>	864	2428	0.4
Cloel_1891	Phosphate acetyltransferase, <i>pta</i>	189	384	0.5
<a href="#">Cloel_1892</a>	Acetate kinase, <i>ack</i>	<a href="#">200</a>	<a href="#">485</a>	<a href="#">0.4</a>
Cloel_3058	Acetyl-CoA acetyltransferase, <i>thl</i>	4904	10026	0.5
Cloel_2972	3-hydroxybutyryl-CoA dehydrogenase, <i>hbd</i>	4085	6539	0.6
Cloel_2973	Electron transfer flavoprotein subunit alpha	3676	7508	0.5
Cloel_2974	Electron transfer flavoprotein subunit beta	1645	3752	0.4
Cloel_2975	Acyl-CoA dehydrogenase, <i>bcd</i>	4100	6284	0.7
Cloel_2976	Short-chain-enoyl-CoA hydratase, <i>ech</i>	1268	1970	0.6
<a href="#">Cloel_3674</a>	Butyrate kinase, <i>buk</i>	<a href="#">982</a>	<a href="#">1894</a>	<a href="#">0.5</a>
Cloel_3675	Phosphate butyryltransferase, <i>ptb</i>	471	879	0.5
Cloel_1405	Hydratase, aconitase	275	647	0.4
Cloel_3688	Citrate/2-methylcitrate synthase, citrate synthase	275	350	0.8
Cloel_2469	Isocitrate/isopropylmalate dehydrogenase family protein	318	840	0.4
Cloel_0392	Class II fumarate hydratase, <i>fumC</i>	1284	103	1.2
Cloel_1284	NADP-specific glutamate dehydrogenase, <i>gdhA</i>	2400	1264	1.9
Cloel_2665	Glutamate synthase large subunit, <i>gltB</i>	1099	2011	0.6
Cloel_2992	NADPH-dependent glutamate synthase, <i>gltA</i>	167	446	0.4

Possible genes involved in sutoysis				
Clocl_1077	C45 family autoproteolytic acyltransferase/hydrolase	189	77	2.4
Clocl_3136	C45 family autoproteolytic acyltransferase/hydrolase	67	5	13.2
RT-PCR				
Clocl_2596	sugar ABC transporter substrate-binding protein	1800	4	506.8
Clocl_2629	3-hydroxyacyl-CoA dehydrogenase family protein	191	3	74.5
Clocl_2823	dockerin type I domain-containing protein	79165	5029	15.7
Clocl_2402	bifunctional acetaldehyde-CoA/alcohol dehydrogenase	360.05	81	1.2

Table S6. The expression profiles of the protein induced during cellulose- and glucose-fermentation of *Clostridium cellulovorans*

Gene locus <sup>a</sup>	Products	Spectral Counts		Fold- change <sup>b</sup>	Signal peptide <sup>c</sup>
		Glucose <i>t</i> =36 h	Cellulose <i>t</i> =96 h		
<b>Glucose fermentation (Spectral Counts≥1.00E+10)</b>					
<i>Clocel_2823</i>	Dockerin type I domain-containing protein	4.72E+10	1.97E+11	-2.1	Y
<i>Clocel_2050</i>	Hypothetical protein	1.03E+11	3.34E+11	-1.7	
<i>Clocel_2974</i>	Electron transfer flavoprotein subunit beta/FixA family protein	6.78E+10	1.19E+10	2.5	
<i>Clocel_2018</i>	Phosphoglycerate dehydrogenase	6.45E+10	8.94E+09	2.9	
<i>Clocel_2973</i>	Electron transfer flavoprotein subunit alpha/FixB family protein	6.21E+10	1.63E+10	1.9	
<i>Clocel_0111</i>	Trypsin-like peptidase domain-containing protein	5.89E+10	1.01E+10	2.5	
<i>Clocel_3736</i>	Elongation factor G	4.98E+10	2.44E+10	1.0	
<i>Clocel_0553</i>	Class II fructose-1,6-bisphosphate aldolase	4.96E+10	8.25E+09	2.6	
<i>Clocel_0528</i>	GTP-binding protein	4.75E+10	8.27E+09	2.5	
<i>Clocel_1775</i>	Translation elongation factor Ts	2.95E+10	1.36E+10	1.1	
<i>Clocel_1454</i>	Pyruvate, phosphate dikinase	2.70E+10	1.61E+11	-2.6	
<i>Clocel_3735</i>	Elongation factor Tu	2.60E+10	6.94E+09	1.9	
<i>Clocel_2849</i>	Calcium-binding protein	2.37E+10	7.39E+10	-1.6	
<i>Clocel_2359</i>	Calcium-binding protein	2.23E+10	7.81E+09	1.5	
<i>Clocel_1684</i>	Pyruvate:ferredoxin (flavodoxin) oxidoreductase	2.21E+10	3.05E+09	2.9	
<i>Clocel_1674</i>	Aminopeptidase	2.08E+10	5.42E+09	1.9	
<i>Clocel_2086</i>	Hypothetical protein	2.00E+10	6.08E+09	1.7	
<i>Clocel_3111</i>	Cellulase family glycosylhydrolase	1.96E+10	8.24E+10	-2.1	
<i>Clocel_0510</i>	Molecular chaperone HtpG	1.96E+10	3.77E+09	2.4	
<i>Clocel_3686</i>	Phosphoenolpyruvate--protein phosphotransferase	1.86E+10	7.87E+09	1.2	
<i>Clocel_0730</i>	Phosphopyruvate hydratase	1.77E+10	7.94E+09	1.2	
<i>Clocel_2975</i>	Acyl-CoA dehydrogenase	1.74E+10	4.74E+09	1.9	
<i>Clocel_3475</i>	Cysteine synthase A	1.67E+10	2.23E+09	2.9	
<i>Clocel_1811</i>	Formate C-acetyltransferase	1.59E+10	7.38E+09	1.1	
<i>Clocel_0379</i>	NADH peroxidase	1.59E+10	9.88E+10	-2.6	
<i>Clocel_1516</i>	Anaerobic carbon-monoxide dehydrogenase catalytic subunit	1.56E+10	3.70E+10	-1.3	
<i>Clocel_2885</i>	Cold-shock protein	1.53E+10	1.55E+09	3.3	
<i>Clocel_1773</i>	GTP-sensing pleiotropic transcriptional regulator CodY	1.51E+10	3.38E+10	-1.2	
<i>Clocel_0272</i>	Hypothetical protein	1.49E+10	3.37E+10	-1.2	
<i>Clocel_2665</i>	Glutamate synthase large subunit	1.45E+10	2.94E+10	-1.0	
<i>Clocel_2402</i>	Bifunctional acetaldehyde-CoA/alcohol dehydrogenase	1.37E+10	6.28E+09	1.1	
<i>Clocel_4154</i>	Desulfoferrodoxin	1.37E+10	3.18E+10	-1.2	
<i>Clocel_4136</i>	Acetyl-CoA carboxylase biotin carboxylase subunit	1.35E+10	4.72E+09	1.5	
<i>Clocel_0192</i>	Acetyl-CoA C-acetyltransferase	1.25E+10	3.58E+09	1.8	

Cloel_2824	Cellulose-binding protein	1.23E+10	2.70E+10	-1.1	Y
Cloel_0337	3-deoxy-7-phosphoheptulonate synthase	1.22E+10	3.34E+09	1.9	
Cloel_1957	Valine-tRNA ligase	1.20E+10	4.74E+09	1.3	
<b>Cloel_3196</b>	<b>Glycoside hydrolase family 130 protein</b>	<b>1.17E+10</b>	<b>2.89E+10</b>	<b>-1.3</b>	
Cloel_2840	Pyruvate:ferredoxin (flavodoxin) oxidoreductase	1.15E+10	2.36E+09	2.3	
<b>Cloel_2900</b>	<b>Endo-1,4-beta-xylanase</b>	<b>1.13E+10</b>	<b>6.58E+10</b>	<b>-2.5</b>	Y
Cloel_4114	O-acetylhomoserine aminocarboxypropyltransferase/cysteine synthase	1.09E+10	5.14E+09	1.1	
Cloel_3781	Transcription elongation factor GreA	1.07E+10	2.21E+09	2.3	
Cloel_1805	Serine hydroxymethyltransferase	1.07E+10	3.53E+09	1.6	
Cloel_3180	Leucyl aminopeptidase	1.05E+10	2.65E+09	2.0	
<b>Cloel_0521</b>	<b>Sulfate ABC transporter substrate-binding protein</b>	<b>3.10E+09</b>	<b>4.29E+08</b>	<b>2.9</b>	Y
<b>Cloel_4152</b>	<b>PhnD/SsuA/transferrin family substrate-binding protein</b>	<b>2.96E+08</b>	<b>5.05E+08</b>	<b>0.6</b>	Y
<b>Cloel_1183</b>	<b>Fibronectin</b>	<b>1.65E+10</b>	<b>1.57E+10</b>	<b>1.05</b>	Y
<b>Cloel_2675</b>	<b>MetQ family ABC transporter substrate-binding protein</b>	<b>1.11E+09</b>	<b>1.20E+09</b>	<b>0.92</b>	Y
<b>Cellulose fermentation (Spectral Counts≥1.00E+10)</b>					
<b>Cloel_2050</b>	<b>Hypothetical protein</b>	<b>1.03E+11</b>	<b>3.34E+11</b>	<b>-1.7</b>	
<b>Cloel_2823</b>	<b>Dockerin type I domain-containing protein</b>	<b>4.72E+10</b>	<b>1.97E+11</b>	<b>-2.1</b>	Y
Cloel_1454	Pyruvate, phosphate dikinase	2.70E+10	1.61E+11	-2.6	
Cloel_0379	NADH peroxidase	1.59E+10	9.88E+10	-2.6	
<b>Cloel_3111</b>	<b>Cellulase family glycosylhydrolase</b>	<b>1.96E+10</b>	<b>8.24E+10</b>	<b>-2.1</b>	
<b>Cloel_2849</b>	<b>Calcium-binding protein</b>	<b>2.37E+10</b>	<b>7.39E+10</b>	<b>-1.6</b>	
<b>Cloel_2900</b>	<b>Endo-1,4-beta-xylanase</b>	<b>1.13E+10</b>	<b>6.58E+10</b>	<b>-2.5</b>	Y
Cloel_2596	Sugar ABC transporter substrate-binding protein	6.13E+09	4.92E+10	-3.0	
<b>Cloel_1684</b>	<b>Pyruvate:ferredoxin (flavodoxin) oxidoreductase</b>	<b>1.80E+11</b>	<b>4.77E+10</b>	<b>1.9</b>	
<b>Cloel_1516</b>	<b>Anaerobic carbon-monoxide dehydrogenase catalytic subunit</b>	<b>1.56E+10</b>	<b>3.70E+10</b>	<b>-1.3</b>	
Cloel_4153	Rubrerythrin family protein	9.44E+09	3.38E+10	-1.8	
<b>Cloel_1773</b>	<b>GTP-sensing pleiotropic transcriptional regulator CodY</b>	<b>1.51E+10</b>	<b>3.38E+10</b>	<b>-1.2</b>	
<b>Cloel_0272</b>	<b>Hypothetical protein</b>	<b>1.49E+10</b>	<b>3.37E+10</b>	<b>-1.2</b>	
<b>Cloel_4154</b>	<b>Desulfoferrodoxin</b>	<b>1.37E+10</b>	<b>3.18E+10</b>	<b>-1.2</b>	
<b>Cloel_2607</b>	<b>Chitobiase/beta-hexosaminidase C-terminal domain-containing protein</b>	<b>4.41E+09</b>	<b>3.12E+10</b>	<b>-2.8</b>	Y
<b>Cloel_2402</b>	<b>Bifunctional acetaldehyde-CoA/alcohol dehydrogenase</b>	<b>4.94E+09</b>	<b>3.03E+10</b>	<b>-2.6</b>	
Cloel_3817	Iron-containing alcohol dehydrogenase	9.78E+09	3.00E+10	-1.6	
<b>Cloel_2665</b>	<b>Glutamate synthase large subunit</b>	<b>1.45E+10</b>	<b>2.94E+10</b>	<b>-1.0</b>	
<b>Cloel_3196</b>	<b>Glycoside hydrolase family 130 protein</b>	<b>1.17E+10</b>	<b>2.89E+10</b>	<b>-1.3</b>	
Cloel_0391	N,N'-diacetylchitobiose phosphorylase	7.49E+09	2.85E+10	-1.9	
Cloel_2006	Translation initiation factor IF-3	3.26E+09	2.82E+10	-3.1	
Cloel_0038	ABC transporter substrate-binding protein	9.70E+09	2.74E+10	-1.5	
<b>Cloel_3736</b>	<b>Elongation factor G</b>	<b>4.98E+10</b>	<b>2.44E+10</b>	<b>1.0</b>	
Cloel_0148	Leucine-rich repeat protein	3.85E+09	2.31E+10	-2.6	
Cloel_0590	Xylose isomerase	4.09E+09	2.23E+10	-2.4	
<b>Cloel_2818</b>	<b>Dockerin type I domain-containing protein</b>	<b>2.55E+09</b>	<b>2.19E+10</b>	<b>-3.1</b>	Y
Cloel_4143	Acyl carrier protein	7.87E+09	2.08E+10	-1.4	
Cloel_2744	RidA family protein	8.57E+09	2.06E+10	-1.3	
<b>Cloel_2741</b>	<b>Glycoside hydrolase family 9 protein</b>	<b>9.22E+09</b>	<b>1.93E+10</b>	<b>-1.1</b>	Y

Cloel_0146	Protease inhibitor I42 family protein	1.60E+09	1.84E+10	-3.5	Y
Cloel_4206	Ribonuclease	5.44E+09	1.73E+10	-1.7	
Cloel_3727	30S ribosomal protein S3	1.85E+09	1.71E+10	-3.2	
Cloel_1417	Molecular chaperone DnaJ	7.17E+09	1.70E+10	-1.2	
Cloel_3802	SurA N-terminal domain-containing protein	7.28E+09	1.68E+10	-1.2	Y
<b>Cloel_2973</b>	<b>Electron transfer flavoprotein subunit alpha</b>	<b>6.21E+10</b>	<b>1.63E+10</b>	<b>1.9</b>	
Cloel_3754	Proline--tRNA ligase	3.39E+09	1.54E+10	-2.2	
Cloel_3800	Stage V sporulation protein T	5.10E+09	1.50E+10	-1.6	
Cloel_1364	Glucose-6-phosphate isomerase	1.55E+09	1.47E+10	-3.3	
Cloel_0022	Cadherin-like beta sandwich domain-containing protein	4.46E+09	1.41E+10	-1.7	Y
Cloel_3201	Extracellular solute-binding protein	5.41E+09	1.38E+10	-1.3	Y
<b>Cloel_1775</b>	<b>Translation elongation factor Ts</b>	<b>2.95E+10</b>	<b>1.36E+10</b>	<b>1.1</b>	
Cloel_2237	L-fucose/L-arabinose isomerase family protein	5.87E+09	1.35E+10	-1.2	
Cloel_0664	Sugar-phosphatase	1.05E+09	1.33E+10	-3.7	
Cloel_1606	Diaminopimelate epimerase	2.87E+09	1.31E+10	-2.2	
Cloel_1384	Hypothetical protein	3.60E+09	1.20E+10	-1.7	Y
Cloel_1601	SPFH/Band 7/PHB domain protein	4.30E+09	1.19E+10	-1.5	
<b>Cloel_2974</b>	<b>Electron transfer flavoprotein subunit beta</b>	<b>6.78E+10</b>	<b>1.19E+10</b>	<b>2.5</b>	
Cloel_2025	Cell division protein ZapA	1.30E+09	1.18E+10	-3.2	
Cloel_3081	Polysaccharide deacetylase family protein	3.64E+09	1.12E+10	-1.6	Y
Cloel_1739	Flagellar basal body rod protein FlgG	4.01E+09	1.10E+10	-1.5	
Cloel_1693	Chemotaxis protein CheA	3.13E+09	1.06E+10	-1.8	
Cloel_2375	DJ-1/PfpI family protein	2.93E+09	1.04E+10	-1.8	
Cloel_0307	Aldose 1-epimerase family protein	4.24E+09	1.03E+10	-1.3	
<b>Cloel_0111</b>	<b>Trypsin-like peptidase domain-containing protein</b>	<b>5.89E+10</b>	<b>1.01E+10</b>	<b>2.5</b>	
Cloel_1284	NADP-specific glutamate dehydrogenase	4.22E+09	1.01E+10	-1.3	

#### Glucose vs Cellulose (LogFC≥2)

Cloel_0975	Hypothetical protein	2.39E+09	4.81E+07	5.6
Cloel_2774	Cytidine/deoxycytidylate deaminase family protein	1.21E+08	2.86E+06	5.4
Cloel_3410	FAD-dependent oxidoreductase	1.35E+09	4.98E+07	4.8
Cloel_3735	Elongation factor Tu	3.15E+09	1.58E+08	4.3
Cloel_1944	PH domain-containing protein	8.75E+09	4.78E+08	4.2
Cloel_0375	RNase adapter RapZ	3.10E+09	1.80E+08	4.1
Cloel_3723	50S ribosomal protein L14	3.71E+09	2.48E+08	3.9
Cloel_0528	GTP-binding protein	2.91E+09	1.99E+08	3.9
Cloel_4030	Methyl-accepting chemotaxis protein	1.28E+09	9.73E+07	3.7
Cloel_2843	6,7-dimethyl-8-ribityllumazine synthase	2.14E+09	1.74E+08	3.6
Cloel_0550	Blp family class II bacteriocin	7.11E+08	5.82E+07	3.6
Cloel_1907	50S ribosomal protein L19	7.17E+09	6.05E+08	3.6
Cloel_1789	30S ribosome-binding factor RbfA	1.79E+09	1.62E+08	3.5
Cloel_2885	Cold-shock protein	1.53E+10	1.55E+09	3.3
Cloel_3714	50S ribosomal protein L15	4.83E+08	5.00E+07	3.3
Cloel_2750	50S ribosomal protein L27	3.23E+09	3.61E+08	3.2
Cloel_2863	Methylglyoxal synthase	1.04E+09	1.18E+08	3.1

Cloel_3871	Peptidylprolyl isomerase	1.61E+09	1.83E+08	3.1	
Cloel_3025	Glucose-1-phosphate thymidylyltransferase RfbA	7.53E+08	8.72E+07	3.1	
Cloel_1883	Asp23/Gls24 family envelope stress response protein	1.28E+09	1.58E+08	3.0	
Cloel_3290	NAD(P)H-dependent oxidoreductase	8.14E+09	1.02E+09	3.0	
Cloel_2782	Gfo/Idh/MocA family oxidoreductase	1.24E+09	1.62E+08	2.9	
Cloel_1892	Acetate kinase	9.95E+09	1.32E+09	2.9	
Cloel_3475	Cysteine synthase A	1.67E+10	2.23E+09	2.9	
Cloel_3051	F0F1 ATP synthase subunit alpha	7.81E+08	1.96E+08	2.0	
<b>Glucose vs Cellulose (LogFC≤-3)</b>					
Cloel_2734	Pyrroline-5-carboxylate reductase	3.60E+07	6.07E+09	-7.4	
Cloel_0667	CBS domain-containing protein	3.43E+07	1.29E+09	-5.2	
Cloel_1021	Cold-shock protein	5.97E+07	2.15E+09	-5.2	
Cloel_2070	D-tyrosyl-tRNA(Tyr) deacylase	6.61E+07	2.28E+09	-5.1	
Cloel_0553	Class II fructose-1,6-bisphosphate aldolase	5.35E+06	1.75E+08	-5.0	
Cloel_3784	Formate--tetrahydrofolate ligase	7.13E+06	1.82E+08	-4.7	
Cloel_4328	MBL fold metallo-hydrolase	3.67E+08	8.68E+09	-4.6	
Cloel_1747	Redox-regulated ATPase YchF	4.01E+07	8.62E+08	-4.4	
Cloel_0730	Phosphopyruvate hydratase	1.16E+08	2.42E+09	-4.4	
Cloel_3754	Proline--tRNA ligase	5.07E+08	9.97E+09	-4.3	
Cloel_2101	GTPase HflX	3.81E+08	7.46E+09	-4.3	
Cloel_1897	Ribonuclease III	1.97E+08	3.74E+09	-4.2	
Cloel_2402	Bifunctional acetaldehyde-CoA/alcohol dehydrogenase	6.50E+06	1.22E+08	-4.2	
Cloel_2882	Glycoside hydrolase family 1 protein	3.99E+07	7.08E+08	-4.2	
Cloel_2630	Acyl carrier protein	1.27E+08	2.08E+09	-4.0	
Cloel_1581	Hypothetical protein	3.61E+07	5.72E+08	-4.0	
Cloel_1811	Formate C-acetyltransferase	3.44E+08	5.31E+09	-3.9	
Cloel_4153	Rubrerythrin family protein	6.02E+07	9.24E+08	-3.9	
Cloel_1412	Translation elongation factor 4	6.55E+08	8.98E+09	-3.8	
Cloel_1255	L-ribulose-5-phosphate 4-epimerase	1.80E+07	2.46E+08	-3.8	
Cloel_3188	J domain-containing protein	5.42E+08	7.32E+09	-3.8	
Cloel_1358	Peptide ABC transporter substrate-binding protein	7.48E+08	8.70E+09	-3.5	
Cloel_2752	50S ribosomal protein L21	6.74E+07	6.92E+08	-3.4	
Cloel_0037	Response regulator transcription factor	7.97E+08	8.12E+09	-3.3	
Cloel_3800	Stage V sporulation protein T	1.01E+08	1.02E+09	-3.3	
Cloel_2148	DUF1540 domain-containing protein	1.14E+07	1.10E+08	-3.3	
Cloel_0164	DUF3997 domain-containing protein	2.85E+07	2.62E+08	-3.2	
Cloel_1267	Type II toxin-antitoxin system PemK/MazF family toxin	1.43E+08	1.28E+09	-3.2	
Cloel_2472	DUF402 domain-containing protein	5.01E+07	4.40E+08	-3.1	
Cloel_2824	Cellulose-binding protein	4.85E+10	4.19E+11	-3.1	
Cloel_2818	Dockerin type I domain-containing protein	2.55E+09	2.19E+10	-3.1	
Cloel_0675	Hypothetical protein	9.43E+08	7.89E+09	-3.1	

<sup>a</sup>: Genes are listed in the order of old ORF (Open reading frame) numbers;

<sup>b</sup>: Data represent the log<sub>2</sub> values change folds of spectral counts;

<sup>c</sup>: Y indicates that this protein has signal peptide.