

Table of down- and up-regulated genes of strain Rut-C30 after 12h, 24h and 48h cultivation. The first value represents the regulation difference observed and the second value is the inverse value of expression in the replicate dye swap experiment. If more than two values appear, the others are replicates on the microarray slide. Down-regulated values are shown in green and up-regulated values in red. jgiTre2 = gene number from the second round sequencing of *T. reesei* genome.

jgi Tre2	Name of gene	12h	24h	48h
Cell growth, cell cycle, development and proliferation				
119989	Hydrophobin II		↓ (7.961, 0.502)	
123967	Partial match to Hydrophobin		↓ (4.682, 0.604)	
44230	Sexual development protein EsdC		↓ (12.882/ 0.559); ↓ (10.383/ 0.371)	
56448	Class V protein			↓ (0.421, 2.365)
121491	Trehalose synthase (clock-controlled gene-9 protein)		↓ (8.143, 0.659)	↓ (0.585, 8.352)
119989	Hydrophobin II			↑(0.627, 9.467)
123967	Partial match to Hydrophobin			↑(0.25, 15.623)
72379	Conidiospore surface protein			↑(0.537, 2.936)
61692	Nuclear condensin complex subunit		↑(0.623, 1.502)	
63747	Pwvp domain protein		↑(0.664, 1.625)	
64866	Dsba-like thioredoxin domain protein	↑(0.557, 1.651v)		
75444	Cop9 signalosome subunit 4		↑(0.639, 1.72)	
Transcription				
107564	Sin3 -associated polypeptide			↓ (0.607, 4.003)

jgi Tre2	Name of gene	12h	24h	48h
121670	Frequency clock protein			↓ (0.656, 2.405)
120117	GRE protein			↑(0.624, 1.727)
60810	Protein fun34		↑(0.621, 1.569)	
22115	Poly-ribose polymerase		↑(0.669, 1.562)	
32714	Duf726 domain protein		↑(0.642, 2.027)	
75965	Nuclear mrna splicing	↑(0.669, 1.576)		
Translation				
Ribosomal proteins and biosynthesis				
Metabolic pathway				
Amino acids				
82619	Argininosuccinate synthase			↓ (0.511, 2.256); ↓ (0.663, 1.671)
Fatty acids				
45250	Delta-12 fatty acid desaturase			↑(0.492, 4.425)
74228	Bifunctional D12/D15 fatty acid desaturase	↑(0.668, 2.194)		
Carbohydrate				
53872	Dihydroxy-acid dehydratase			↓ (0.667, 1.81)
58431	Isochorismatase family			↓ (0.603, 1.658)
123283	Alpha-N-arabinofuranosidase			↓ (0.633, 8.229)

jgi Tre2	Name of gene	12h	24h	48h
124016	Alpha galactosidase			↓ (0.389/ 5.217); ↓ (0.545/ 2.973)
22912	Glucose transporter (partial)		↓ (8.557, 0.326)	
23346	Beta-hexosaminidase beta chain precursor			↓ (0.659, 1.656)
80240	Beta galactosidase			↓ (0.581, 2.738)
121556	Hypothetical protein (Glyoxalase family protein)			↑(0.342, 9.497)
69465	Hypothetical protein (salicylate hydroxylase)			↑(0.213, 5.27)
120312	Endoglucanase III or II	↑(0.452, 4.033)		
123232	Endoglucanase 1 (endo-beta-1,4- glucanase)	↑(0.591, 1.737)		
123232	Endoglucanase 1 (endo-beta-1,4- glucanase)			↑(0.528/ 2.873); ↑(0.547/ 2.865)
Hydrolases				
72632	Alpha galactosidase			↓ (0.51, 4.199)
110894	Endo-beta-1,6-galactanase			↓ (0.657, 1.629)
71532	Alpha 1,3-glucanase		↓ (4.694, 0.411)	
106661	Aspergillo pepsin-2			↓ (0.438, 3.383)
76210	Abf2 (alpha-L-arabinofuranosidase)		↑(0.602, 2.045)	
71532	Alpha 1,3-glucanase			↑(0.374, 5.169)
104394	Alpha beta fold family protein	↑(0.567, 1.53)		
106636	Gtpase activating protein rga6	↑(0.66, 1.66)		

jgi Tre2	Name of gene	12h	24h	48h
71103	Dynamin family protein		↑(0.612, 1.505)	
25040	Rho gtpase activator		↑(0.54, 3.448)	
Dehydrogenases				
Oxidoreductases				
119933	Aldehyde hydrogenase		↑(0.588, 1.598)	
120911	Aldehyde reductase	↓ (2.507, 0.617)		
80659	Alcohol oxidase			↓ (0.289, 10.782)
36134	Protein kinase family protein			↓ (0.55, 2.629)
76155	Acid phosphatase			↓ (0.636, 1.754)
124282	Glyoxal oxidase			↑(0.457, 5.038)
58418	Beta-lactamase	↑(0.656, 1.676)		
64377	Cytochrome p450	↑(0.584, 1.55)		
70161	Cytochrome p450 alkane		↑(0.627, 1.52)	
Peptidases, proteases				
103049	Extracellular polygalacturonase			↓ (0.307, 6.985)
123354	Mitochondrial aaa		↓ (3.877, 0.653)	
120086	Peptidase m42 family protein			↓ (0.496, 1.735)
73897	Serine endopeptidase			↑(0.414, 4.361)

jgi Tre2	Name of gene	12h	24h	48h
Reductases				
22771	3-oxoacyl-(acyl-carrier-protein) reductase			↓ (0.664, 1.583)
Transferases				
31869	Nicotinamide mononucleotide adenylyl transferase			↓ (0.438, 1.768)
3362	Phosphatidylinositol 4-kinase	↓ (1.52, 0.636)		
70973	Gnat family protein			↓ (0.628, 2.17)
50607	Related to acyl-CoA sterol acyltransferase		↓ (1.945, 0.662)	
50616	Succinyl-CoA:3-ketoacid-coenzyme A transferase			↑ (0.513, 5.276)
104390	Glutathione-S-transferase		↑ (0.581, 2.093)	
77634	N-acetylglucosaminyl transferase component gpi1	↑ (0.665, 2.438)		
Protein folding / UPR				
80142	Heat shock protein 101			↓ (0.597, 5.411)
60378	mitochondrial chaperone bcs1	↑ (0.666, 1.616)		
Protein elimination / ERAD				
121138	Ubiquitin			↓ (0.405, 3.224)
21953	F-box protein			↓ (0.583, 2.025)
80400	26S proteasome-associated ubiquitin C-terminal	↑ (0.528, 1.656)	↑ (0.64, 1.538)	↓ (0.53, 1.969)
Trafficking				

jgi Tre2	Name of gene	12h	24h	48h
Transporters				
123473	Membrane transporter			↓ (0.518, 1.519)
123718	Amino acid transporter			↓ (0.651, 5.141)
21595	MFS multidrug			↓ (0.632, 1.707)
44956	MFS transporter			↓ (0.606, 3.004)
62380	MFS monosaccharide transporter		↓ (4.616, 0.37); ↓ (3.493, 0.472)	
62480	Mitochondrial tricarboxylate transporter			↓ (0.639, 1.633)
76682	ABC transporter (CDR4)			↓ (0.613, 2.33)
80187	Auxin efflux carrier superfamily	↓ (2.553, 0.661)		
51734	Coatomer subunit			↑ (0.64, 2.081)
69957	Hypothetical protein (maltose permease or MFS alpha-glucosidase transporter)		↑ (0.563, 4.015)	
81022	MFS allantate	↑ (0.608, 1.788)		
Unclassified				
73516	Glucose repressible protein Grg1			↓ (0.631, 4.396)
4876	Catechol dioxygenase			↓ (0.585, 3.308)
78274	1-phosphatidylinositol-3-phosphate 5-kinase Fab1			↓ (0.633, 1.817)
109117	Hypothetical protein			↓ (0.609, 1.655)
112105	Unnamed protein product (stress responsive A/B barrel domain protein)			↓ (0.65, 2.194)

jgi Tre2	Name of gene	12h	24h	48h
68618	Nacht and ankyrin domain protein			↓ (0.555, 1.659)
121416	Conserved hypothetical protein		↓ (12.365, 0.453)	
122095	Partial match to hypothetical protein			↓ (0.567, 2.151)
1818	Hypothetical protein			↓ (0.525, 4.036)
22000	Hypothetical protein		↓ (3.149, 0.53)	
3891	Hypothetical protein			↓ (0.524, 2.121)
43418	Hypothetical protein		↓ (3.254, 0.631)	
61593	Hypothetical protein		↓ (7.319, 0.623)	
78626	Hypothetical protein			↓ (0.611, 4.936)
111527	No real match			↓ (0.62, 6.314)
79238	No Match			↓ (0.544, 2.137)
102774	No match			↓ (0.592, 1.812)
102938	No match			↓ (0.626, 1.87)
104277	No match			↓ (0.636, 3.883)
111341	No match			↓ (0.61, 2.135)
103130	No match			↓ (0.508, 3.119)
74932	No match			↓ (0.548, 5.681)
74932	No match			↓ (0.577, 2.82)

jgi Tre2	Name of gene	12h	24h	48h
111591	No match	↑(0.597, 1.61)		
1857	No match	↑(0.577, 1.904)		
77836	No Match	↑(0.574, 1.672)		
110471	Low molecular weight glutenin		↑(0.591, 3.689)	
65595	DUF159 domain protein		↑(0.628, 2.04)	
21677	Hypothetical protein		↑(0.575, 1.917)	
109815	Hypothetical protein		↑(0.493, 1.579)	
111672	No match		↑(0.647, 2.004)	
111932	No match		↑(0.641, 1.514)	
57730	No match		↑(0.649, 1.902)	
72379	Conidiospore surface protein			↑(0.537, 2.936)
61995	Conserved hypothetical protein			↑(0.532, 2.757)
22386	Hypothetical protein			↑(0.53, 6.758)
43418	Hypothetical protein			↑(0.598, 1.802)
120823	No Match			↑(0.515, 4.258)
120823	No Match			↑(0.507, 3.535)

Table of down- and up-regulated genes of strains CVtΔ2 after 12h, 24h and 48h cultivation. The first value represents the regulation difference observed and the second value is the inverse value of expression in the replicate dye swap experiment. If more than two values appear, the others are replicates on the microarray slide. Down-regulated values are shown in green and up-regulated values in red. jgiTre2 = gene number from the second round sequencing of *T. reesei* genome.

jgi Tre2	Name of gene	12h	24h	48h
Cell growth, cell cycle, development and proliferation				
46382	GTP binding protein 1	↓ (5.022, 0.225)		
44230	Sexual development protein EsdC	↓ (8.576, 0.152)		
5084	Conidiation specific protein 10	↓ (2.509, 0.577)		
52463	Zinc metalloproteinase	↓ (2.473, 0.521)		
120830	Alpha tubulin	↓ (1.525, 0.642)		
122124	AAA family ATPase	↓ (2.033, 0.492)		
123992	Swollenin		↓ (14.773, 0.535)	
73173	Hydrophobin 1			↓ (2.799, 0.498)
62213	Hypothetical protein (Fasciclin domain family)	↑ (0.472, 2.233)		
119989	Hydrophobin II		↑ (0.538, 18.725)	
123967	Partial match to Hydrophobin		↑ (0.603, 21.017)	
106538	Hydrophobin		↑ (0.275, 29.251)	↑ (0.414, 15.485)
50323	Cellulose signalling related protein OOC1		↑ (0.353, 9.328)	↑ (0.287, 18.825) ↑ (0.568, 7.864)
Transcription				
67057	Sir2 family transcriptional regulator	↓ (1.564, 0.57)		
78695	Hypothetical protein (zinc finger protein zpr1)	↓ (9.45, 0.577)		
52924	NF-X1 finger transcription factor	↓ (1.872, 0.464) ↓ (2.856, 0.393)		
102581	Nucleotide excision repair RAD23	↓ (3.343, 0.513)		

jgi Tre2	Name of gene	12h	24h	48h
80200	Hypothetical protein (transcription factor Snd1/100)	↓ (2.127, 0.56)		
49197	Threonyl-tRNA synthetase/ligase	↓ (9.12, 0.612)		
77513	C6 transcription factor	↓ (2.204, 0.421) ↓ (9.142, 0.177)	↓ (5.303, 0.585)	
79686	Poly(A) RNA binding protein	↑ (0.52, 3.538)		
121785	Partially DNA damage responsive protein			↑ (0.656, 1.704)
104015	DNA directed RNA polymerase chain RPB8			↑ (0.651, 1.568)
78650	Hypothetical protein (Homeobox and C2H2 transcription factor)			↑ (0.535, 4.074)
Translation				
111131	Translation initiation factor eIF-2B alpha subunit	↓ (4.374, 0.523)		
121000	Tryptophanyl-tRNA synthetase	↓ (3.614, 0.664)		
123801	Aspartyl-tRNA synthetase	↓ (2.8, 0.561)		
21564	Eukaryotic translation initiation factor 3	↑ (0.626, 1.975)		
77456	Eukaryotic translation initiation factor Eif2a	↑ (0.652, 2.078)		
Ribosome structure and biosynthesis				
112384	ATP dependent RNA helicase dbp3	↑ (0.658, 2.374)		
81599	Protein SIK1 (pre-RNA processing nucleolar protein)	↑ (0.632, 2.883)		
22611	U3 small nucleolar ribonucleoprotein protein	↑ (0.581, 1.663)		
66436	Fibrillarin	↑ (0.665, 4.211)		
52976	Ribosome biogenesis protein Gar2	↑ (0.635, 1.875)		
3671	Hypothetical protein (H/ACA ribonucleoprotein complex subunit 1)	↑ (0.552, 2.257)		
69838	60S Ribosome subunit biogenesis protein	↑ (0.612, 1.947)		
80792	Hypothetical protein (ribosome biogenesis protein BRX1)	↑ (0.637, 2.813)		
76740	Zuotin (ribosome associated DNAJ chaperone Zuotin)	↑ (0.658, 3.254)		

jgi Tre2	Name of gene	12h	24h	48h
Metabolic pathway				
21746	Unnamed protein product (4-carboxymuconolactone decarboxylase)	↓ (4.253, 0.378)		
22004	D-galacturonic acid reductase	↓ (6.999, 0.556)		
123827	Bifunctional catalase-peroxidase Cat2	↓ (1.651, 0.61)		
55421	Hypothetical protein (DUF775 domain)	↓ (5.073, 0.599)		
79037	Asparagine synthetase	↓ (3.787, 0.659)		
121556	Hypothetical protein (Glyoxalase family protein)			↓ (5.45, 0.638)
68608	Thiazole biosynthetic enzyme (stress inducible enzyme?)			↓ (12.748, 0.365)
47221	Nucleoside diphosphate kinase			↓ (7.065, 0.529)
57947	5-aminolevulinate synthase	↑ (0.511, 3.381)		
69863	Amidase family protein	↑ (0.588, 2.037)		
59791	Chitinase 18-15 (37kDa chitinase)			↑ (0.619, 1.585)
108781	Dibenzothiophene desulfurization enzyme A/ xenobiotic compound monooxygenase			↑ (0.664, 2.168)
Metabolic pathway, amino acids				
65882	Dihydrodipicolinate synthetase family protein	↓ (1.716, 0.332)		
82516	Pentafunctional polypeptide (AROM)	↓ (3.061, 0.667) ↓ (4.537, 0.633)		
81188	Imidazole glycerol phosphate synthase	↓ (1.613, 0.498)		
119788	Saccharopine dehydrogenase	↓ (10.274, 0.547)		
67003	Trifunctional tryptophan biosynthesis enzyme	↓ (2.878, 0.644)		
123771	Glutaryl-coA dehydrogenase, mitochondrial	↓ (1.516, 0.636)		
23298	Chorismate mutase	↓ (1.544, 0.527)		
3641	Cystathionine gamma synthase	↓ (4.777, 0.543)		
42825	Hypothetical protein (Cytidine deaminase)	↓ (1.883, 0.45)		

jgi Tre2	Name of gene	12h	24h	48h
120219	Chorismate mutase	↓ (2.558, 0.654)		
4152	GMP synthase	↑(0.63, 2.525)		
81339	Glycine dehydrogenase	↑(0.569, 6.6)		
65921	Methylcrotonoyl-CoA carboxylase alpha chain	↑(0.59, 2.888)		
45138	Sulfite reductase beta subunit	↑(0.409, 5.253)		
Metabolic pathway, fatty acid, lipids				
122091	Hypothetical protein (Patatin family phospholipase)	↓ (5.33, 0.383)		
61442	Enoyl CoA hydratase (mitochondrial methylglutaconyl-CoA hydratase)	↑(0.496, 2.414)		
69465	Hypothetical protein (salicylate hydroxylase)		↑(0.453, 4.529)	
Metabolic pathway, carbohydrate				
120198	Glycogen phosphorylase			↓(2.41, 0.492)
44529	Glycogen (starch) synthase	↓ (2.401, 0.481)		
49976	Endoglucanase V		↓(15.537, 0.494)	
58356	Glycerol kinase	↓ (5.076, 0.308)		
73638	Cip1		↓(7.616, 0.445)	
111849	Cellulose Hydrolase	↓ (4.895, 0.244)	↓3.562, (0.612)	
112392	Endo-1,4-beta xylanase 1			↓(2.436, 0.456)
122081	Endoglucanase I		↓(11.143, 0.506)	
107776	NAD(P)H dependant D-xylose reductase	↓ (5.862, 0.228)		
120312	Endoglucanase III or II	↓ (1.529, 0.473)		
82227	Cel3c (beta glucosidase)	↓ (4.796, 0.2)		
120749	Beta-glucosidase 2	↓ (25.049, 0.067)		
73643	Endoglucanase 4	↓ (7.165, 0.166)		
121127	Beta-xylosidase		↓(6.148, 0.663)	

jgi Tre2	Name of gene	12h	24h	48h
104072	Putative xylose permease		↓(2.641, 0.62)	
121294	Endo-1,3(4)-beta-glucanase			↓(2.222, 0.578)
74194	L-xylulose reductase	↓ (2.283, 0.59) ↓ (3.7, 0.517)	↓(1.709, 0.47)	↓(6.791, 0.388)
123232	Endoglucanase 1 (endo-beta-1,4-glucanase)		↓(8.503, 0.514)	↑(0.649, 7.062)
123989	Cellobiohydrolase 1 / Exoglucanase 1	↓ (20.87, 0.116)		↑(0.493, 9.432)
77284	Hypothetical protein (endoglucanase)	↑(0.5, 3.462)		
121746	Glucan 1,3-beta glucosidase		↑(0.6, 1.937)	
64827	Raffinose synthase protein Sip1		↑(0.633, 1.698)	
124115	Phosphoenolpyruvate carboxykinase		↑(0.594, 1.549)	
120229	Xylanase III			↑(0.574, 5.819) ↑(0.461, 4.462)
123726	Endo glucosidase (endo-1,3(4)-beta-glucanase)			↑(0.569, 2.844)
123940	Cip2			↑(0.518, 4.045)
79677	Hexokinase			↑(0.609, 2.01)
120873	Alpha-1,3-glucanase (mutanase)			↑(0.52, 3.395)
76672	Beta-D-glucosidase glucohydrolase			↑(0.413, 8.283)
Metabolic pathway, hydrolases				
72567	Exoglucanase II (CBHII)	↓ (6.323, 0.165)		
107263	Patatin-like serine hydrolase / patatin-like phospholipase domain protein	↓ (4.18, 0.461)		
107263	Patatin-like serine hydrolase / patatin-like phospholipase domain protein	↓ (3.647, 0.586)		
51365	Serin endopeptidase	↓ (15.355, 0.168) ↓ (24.028, 0.098)		
73643	Endoglucanase 4	↓ (7.165, 0.166)		
121418	Acetyl esterase		↓(2.53, 0.602)	

jgi Tre2	Name of gene	12h	24h	48h
21668	Dipeptidyl peptidase			↓(1.83, 0.464)
Metabolic pathway, dehydrogenases				
22271	Alcohol dehydrogenase	↓ (1.637, 0.534)		
30759	Alcohol dehydrogenase	↓ (2.119, 0.63)		
108732	Isovaleryl-coA dehydrogenase	↑(0.512, 3.655)		
111912	Carbonic anhydrase	↑(0.332, 11.255)		
80019	Short chain dehydrogenase / reductase family		↑(0.659, 2.513)	
22633	Glutathione-dependant formaldehyde dehydrogenase			↑(0.637, 2.439)
Metabolic pathway, oxidoreductases				
77806	Hyp protein (oxidoreductase, zinc binding)	↓ (2.148, 0.457)		
123577	Oxidoreductin	↓ (5.357, 0.283)		
22426	Hypothetical protein (oxidoreductase)	↓ (1.829, 0.62)		
54086	Sorbose reductase SOU1	↓ (2.222, 0.404)		
45445	Tyrosinase 2	↓ (5.145, 0.564)		
56840	NAD-binding Rossmann fold oxidoreductase		↓(5.907, 0.388) ↓(11.181, 0.483)	
74278	Hypothetical protein (Thioredoxin reductase, pyridine nucleotide-disulphide oxidoreductase)			↓(3.153, 0.556)
66345	Superoxide dismutase			↓(10.102, 0.294)
78223	Cytochrome P450 monooxygenase			↓(0.591, 0.35)
46936	2-deoxy-D-gluconate 3-dehydrogenase			↓(1.886, 0.597)
103012	Alpha-ketoglutarate-dependent taurine dioxygenase	↑(0.567, 4.253)		
123979	Alpha-ketoglutarate-dependent taurine dioxygenase	↑(0.443, 7.956)		
52375	Hypothetical protein (betaine aldehyde dehydrogenase)	↑(0.652, 4.134)		
112567	TfdA family taurine dioxygenase	↑(0.466, 3.71)		

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71094	Extracellular dioxygenase	↑(0.441, 1.529)		
121856	4-hydroxyphenylpyruvate dioxygenase	↑(0.41, 3.677)		
22110	Hypothetical protein (Flavin containing monooxygenase)	↑(0.405, 2.281)		
76215	Pyridine nucleotide-disulphide oxidoreductase	↑(0.544, 4.152)		↑(0.656, 1.691)
106686	TfdA family oxidoreductase/ Taurine catabolism dioxygenase	↑(0.32, 6.536)		↑(0.418, 3.15)
51893	Fatty acid oxygenase PpoC		↑(0.39, 6.947)	
Metabolic pathway, peptidases, proteases				
73897	Subtilisin-like protease	↓ (14.531, 0.466) ↓ (10.774, 0.409)		
119876	Aspartic endopeptidase	↓ (2.332, 0.567)		
63381	Conserved hypothetical protein (cupin domain)		↓(1.546, 0.636)	
109234	Peptidase family T4 (D-aminopeptidase)	↓ (17.459, 0.116)	↓(3.23, 0.478)	
123244	Serine carboxypeptidase			↓(4.639, 0.443)
82141	Serine endopeptidase			↓(7.348, 0.231)
74030	Protein phosphatase 2c			↑(0.66, 2.021)
Metabolic pathway, reductases				
56432	Mitochondrial cytochrome b2	↓ (2.47, 0.513)		
Metabolic pathway, transferases				
122240	Carnitine acetyl transferase	↓ (5.631, 0.376) ↓ (9.72, 0.178)		
21406	Phosphoglycerate kinase			↓(8.636, 0.527)
4484	Hypothetical protein (N-acetyltransferase GNAT family)	↓ (4.022, 0.457)		
108637	Hypothetical protein (partially match to acetyltransferase GNAT family protein)	↓ (3.949, 0.609)		
70201	GNAT family acetyltransferase	↓ (1.712, 0.569)		

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68022	Geranylgeranyl pyrophosphate synthase	↓ (3.984, 0.509)		
74725	Aspartate aminotransferase	↓ (6.966, 0.464)		
74913	Histidinol-phosphate aminotransferase	↓ (2.31, 0.616)		
121345	Phosphoserine aminotransferase	↓ (7.554, 0.482)		
104121	Alpha-1,3-mannosyltransferase	↓ (2.008, 0.588)		
119823	ubiE/COG5 methyltransferase	↓ (9.286, 0.359)		
120290	Hypothetical protein (Thiamin pyrophosphokinase-related protein)	↓ (2.413, 0.63)		
68036	Cystathionine gamma synthase			↓ (2.665, 0.487)
50616	Succinyl-CoA:3-ketoacid-coenzyme A transferase			↓ (4.394, 0.356)
111082	UbiE/COQ5 family methyltransferase			↓ (4.039, 0.647) ↓ (5.033, 0.402)
54865	Putative methionine permease	↑ (0.426, 5.467)		
121405	4-aminobutyrate aminotransferase GatA	↑ (0.528, 5.489)		
Protein folding / UPR				
46902	Transcriptional activator HAC1	↓ (3.303, 0.591) ↓ (3.397, 0.619) ↓ (2.946, 0.645) ↓ (2.811, 0.572) ↓ (2.695, 0.652)		
122920	78kDa glucose-regulated protein (BIP)	↓ (3.669, 0.543) ↓ (3.565, 0.509) ↓ (4.4, 0.505) ↓ (3.968, 0.46)		
22064	Hypothetical protein (DNAJ heat shock family protein)	↓ (5.204, 0.623)		
46285	Small heat shock protein	↓ (10.276, 0.451)		

jgi Tre2	Name of gene	12h	24h	48h
62100	Small heat shock protein	↓ (7.857, 0.371)		
122363	Small Heat Shock protein 30kD	↓ (10.777, 0.297)		
78626	Hypothetical protein (ThiJ/Pfp1 superfamily protein)	↓ (6.015, 0.588)		
122415	Protein disulfide isomerase	↓ (5.237, 0.395)		
28928	PDI related protein, PrpA	↓ (1.634, 0.497)		
123922	Peptidyl-prolyl cis-trans isomerase B	↓ (3.878, 0.495) ↓ (6.904, 0.451)		
52050	40kDa peptidyl-prolyl cis-trans isomerase	↓ (0.683, 0.644) ↓ (1.594, 0.603)		
2687	Heat Shock protein 78	↓ (4.73, 0.646)		
80142	Heat shock protein 101	↓ (6.813, 0.471)		
119924	HSP70 nucleotide exchange factor Fes1	↓ (9.127, 0.604)		
3678	Calnexin	↓ (2.022, 0.619) ↓ (1.603, 0.631) ↓ (2.066, 0.669) ↓ (1.704, 0.644)		
Protein elimination / ERAD				
121397	SEC61 alpha subunit	↓ (3.315, 0.506) ↓ (3.52, 0.571) ↓ (3.792, 0.533)		
35465	Heat shock protein 70-like protein, Lhs1		↓ (1.545, 0.638)	
104211	FK506-binding protein 1 (peptidyl-prolyl-isomerase)	↑ (0.152, 29.127)		
120571	Hyp protein (RNA-binding protein Pno1p)	↑ (0.653, 2.848)		
Trafficking				
119551	Mitochondrial carrier protein	↑ (0.648, 1.946)		

jgi Tre2	Name of gene	12h	24h	48h
Transporters				
44956	MFS transporter	↓ (1.674, 0.65)		
47897	ABC transporter CDR4	↓ (4.865, 0.591)		
49970	Sodium/nucleoside cotransporter 1	↓ (2.658, 0.554)		
56176	Hypothetical protein (ABC bile acid transporter)	↓ (2.356, 0.431)		
62711	Amino acid transporter	↓ (2.233, 0.512)		
79169	K ⁺ channel protein subunit	↓ (6.33, 0.464)		
79202	MFS transporter	↓ (8.023, 0.235)		
79510	Hypothetical protein (ABC bile acid transporter)	↓ (2.55, 0.636)		
47987	ZIP metal ion transporter	↓ (2.102, 0.55) ↓ (2.244, 0.569)		
75204	AN1 zinc finger protein	↓ (3.677, 0.401)		
3405	Sugar transporter	↓ (18.375, 0.09)		
54632	MFS transporter	↓ (2.957, 0.299)		
60945	Putative sugar transporter	↓ (4.182, 0.478)		
62171	MFS multidrug transporter	↓ (1.858, 0.587)		
51110	Amino acid permease IND1		↓ (0.603, 2.738)	
50894	MFS sugar transporter		↓ (0.507, 6.671) ↓ (0.223, 4.406)	
67562	Zinc regulated transporter 1			↓ (14.273, 0.188)
44175	Hypothetical protein (sugar transporter family protein)	↓ (2.385, 0.397)		↓ (2.531, 0.567)
56911	Sodium/proline symporter (urea transport protein)	↑ (0.539, 2.164)		
54365	Amino acid transporter	↑ (0.139, 20.428)		
79741	Sulfate transport, sulfate permease	↑ (0.445, 3.18)		

jgi Tre2	Name of gene	12h	24h	48h
65583	Hypothetical protein (MFS transporter)	↑(0.665, 1.765)		
62380	MFS monosaccharide transporter	↑(0.288, 12.394) ↑(0.351, 6.166)		
Unclassified				
119816	Hypothetical protein (DUF221 domain)	↓ (2.788, 0.521)		
22739	Hypothetical protein (integral membrane protein)	↓ (3.382, 0.555)		
46002	Hypothetical protein (partial)	↓ (13.919, 0.249)		
121870	Hypothetical protein (partially arrestin, N-terminal domain)	↓ (6.986, 0.474)		
57936	Hypothetical protein (partially IFRD domain protein)	↓ (6.488, 0.557)		
124097	Hypothetical protein (phenazine biosynthesis like protein PhzC/PhzF)	↓ (3.592, 0.31)		
121445	Hypothetical protein (SGT1 and CS domain containing protein)	↓ (1.703, 0.627)		
23458	Conserved hypothetical protein	↓ (3.423, 0.649)		
61995	Conserved hypothetical protein	↓ (5.312, 0.566)		
124249	Partial match to hypothetical protein	↓ (1.959, 0.431)		
21412	Partial match to predicted protein	↓ (9.003, 0.294)		
20228	Poor match to conserved hypothetical protein	↓ (2.07, 0.595)		
105381	Poor match to hypothetical protein	↓ (4.177, 0.443)		
120120	predicted protein (poor match)	↓ (10.961, 0.13)		
108583	Unnamed protein product	↓ (1.74, 0.403)		
105444	Hypothetical protein	↓ (2.533, 0.504)		
44178	Hypothetical protein	↓ (2.003, 0.632)		
44967	Hypothetical protein	↓ (7.786, 0.451) ↓ (8.344, 0.446)		
121717	Hypothetical protein	↓ (25.993, 0.119)		

jgi Tre2	Name of gene	12h	24h	48h
53893	Hypothetical protein	↓ (8.087, 0.663)		
54052	Hypothetical protein	↓ (4.508, 0.422)		
55443	Hypothetical protein	↓ (2.085, 0.627)		
61593	Hypothetical protein	↓ (3.498, 0.493) ↓ (5.411, 0.463)		
73708	Hypothetical protein	↓ (3.735, 0.649)		
75394	Hypothetical protein	↓ (1.517, 0.552)		
77706	Hypothetical protein	↓ (10.166, 0.329)		
78956	Hypothetical protein	↓ (5.581, 0.478)		
79448	Hypothetical protein	↓ (6.894, 0.472)		
105406	No match	↓ (5.081, 0.594)		
120030	No Match	↓ (3.285, 0.25)		
120311	No match	↓ (3.624, 0.244) ↓ (1.582, 0.526)		
123396	No match	↓ (5.85, 0.335)		
123686	No Match	↓ (10.646, 0.365)		
48280	No match	↓ (3.965, 0.37)		
108806	No real match	↓ (1.605, 0.465)		
111527	No real match	↓ (5.101, 0.532)		
112477	No real match	↓ (2.755, 0.519)		
124059	No real match	↓ (7.205, 0.272)		
111778	Poor match to a predicted protein		↓ (1.816, 0.638)	
119806	Poor partial match to hypothetical protein		↓ (2.051, 0.594)	
120504	Hypothetical protein		↓ (1.579, 0.625)	

jgi Tre2	Name of gene	12h	24h	48h
22000	Hypothetical protein		↓(4.101, 0.473)	
104401	Hypothetical protein (poor match CFEM domain protein)		↓(1.555, 0.47)	
33482	Hypothetical protein		↓(1.69, 0.591)	
104227	No match		↓(7.567, 0.448)	
121416	Conserved hypothetical protein		↓(25.208, 0.596)	↓(16.92, 0.445)
102966	Hypothetical protein	↓ (9.693, 0.163)	↓(1.752, 0.556)	
122108	Partial match to hypothetical protein	↓ (10.473, 0.141) ↓ (5.115, 0.237)	↓(8.371, 0.625)	
71851	Hypothetical protein (cyanovirin-N-like protein)	↓ (4.321, 0.635) ↓ (3.101, 0.59)		↓(6.502, 0.473) ↓(3.088, 0.636)
123914	No match	↓ (11.021, 0.182) ↓ (7.117, 0.138)		↓(11.65, 0.304) ↓(7.904, 0.234)
121126	Integral membrane protein			↓(3.148, 0.668)
122569	partial match to Hypothetical protein			↓(6.874, 0.397) ↓(5.462, 0.406)
22386	Hypothetical protein			↓(1.65, 0.557)
49649	Hypothetical protein			↓(1.932, 0.376)
81329	Hypothetical protein			↓(2.001, 0.655)
105311	No Match			↓(3.737, 0.524)
119902	No real match			↓(2.625, 0.353)
54790	No real match			↓(2.612, 0.344)
123475	No Match	↑(0.643, 1.82)		↓(11.631, 0.358)
82374	Hypothetical protein	↑(0.441, 1.64)		
58077	Hypothetical protein	↑(0.647, 2.351)		
112034	DUF895 domain containing protein	↑(0.349, 3.07)		

jgi Tre2	Name of gene	12h	24h	48h
76256	Conserved hypothetical protein	↑(0.578, 2.059)		
111088	Hypothetical protein	↑(0.629, 1.629)		
124296	Hypothetical protein	↑(0.503, 4.474)		
31075	Hypothetical protein	↑(0.325, 2.778)		
43418	Hypothetical protein	↑(0.31, 8.559)		
47049	Hypothetical protein		↑(0.591, 4.396)	
120823	No Match		↑(0.437, 14.26) ↑(0.279, 11.49)	
106879	No Match		↑(0.561, 1.648)	
124277	No real match		↑(0.482, 1.542)	
123236	No Match		↑(0.509, 11.848)	↑(0.357, 7.428)
108457	No Match		↑(0.648, 2.214)	↑(0.55, 1.541)
52476	Hypothetical protein		↑(0.352, 9.683)	↑(0.317, 8.758)
123955	Eliciting plant response-like protein Epl1		↑(0.632, 6.944)	↑(0.648, 3.169)
72379	Conidiospore surface protein		↑(0.374, 13.62) ↑(0.497, 17.334)	↑(0.399, 6.332) ↑(0.431, 8.414)
119552	Poor match to Sed1p		↑(0.45, 9.491)	↑(0.397, 10.641)
110261	No match			↑(0.582, 2.32)
123199	No real match			↑(0.62, 1.51)
124198	No real match			↑(0.568, 5.841)
120877	Metallo-beta-lactamase domain protein	↑(0.333, 4.031)		↑(0.585, 3.654) ↑(0.575, 4.853)

Table of down- and up-regulated genes of strains CVtΔ4 after 12h, 24h and 48h cultivation. The first value represents the regulation difference observed and the second value is the inverse value of expression in the replicate dye swap experiment. If more than two values appear, the others are replicates on the microarray slide. Down-regulated values are shown in green and up-regulated values in red. jgiTre2 = gene number from the second round sequencing of *T. reesei* genome.

jgiTre2	Name of gene	12h	24h	48h
Cell growth, cell cycle, development and proliferation				
122124	AAA family ATPase	↓(1.981, 0.639)		
52463	Zinc metalloproteinase	↓(2.958, 0.613)		
50947	Cell cycle control protein CDC123	↓(2.182, 0.612)		
121350	CipC1 or phosphoglycerate mutase family protein			↓(9.734, 0.666)
5898	Hypothetical protein (metaphase/anaphase transition protein Mlo2)			↓(1.505, 0.481)
50323	Cellulose signalling related protein OOC1		↓(2.426, 0.479)	↑(0.337, 17.739)
74215	Hypothetical protein (RTM1-like protein)	↑(0.533, 2.109)		
74622	Hypothetical protein (DEAD box family helicase)	↑(0.67, 1.851)		
4514	Hypothetical protein (tetraspanin)	↑(0.568, 1.574)		
Transcription				
122529	Probable nuclease S1	↓(2.651, 0.488)		
3803	mRNA 3'-end-processing protein RNA14	↓(1.847, 0.603)		
77513	C6 transcription factor	↓(1.913, 0.521)		
77513	C6 transcription factor	↓(9.606, 0.403)		
52924	NF-X1 finger transcription factor	↓(3.227, 0.634)		
78445	Transcription factor ACEII	↓(1.692, 0.597)		
120805	Unnamed protein product (CCR4-NOT transcriptional complex subunit CAF120)	↓(1.949, 0.528)		
22925	Hypothetical protein (C6 transcription factor RosA-like)	↓(1.632, 0.539)		
76374	Hypothetical protein (Lys R family regulatory protein)	↓(2.2, 0.654)		

igiTre2	Name of gene	12h	24h	48h
55272	Hypothetical protein (C6 transcription factor)		↓(1.578, 0.571)	
123220	DNA directed RNA polymerase I 135kDa polypeptide	↑(0.642, 2.257)		
64752	DNA directed RNA polymerases I/II/III subunit 10	↑(0.635, 1.993)		
66436	Fibrillarin, snRNP	↑(0.596, 5.735)		
79686	Poly(A) RNA binding protein	↑(0.63, 3.257)		
78650	Hypothetical protein (Homeobox and C2H2 transcription factor)			↑(0.628, 1.548)
75418	Zinc finger transcription factor ace1			↑(0.639, 7.223)
Translation				
74233	Decapping enzyme Dcp2			↓(1.854, 0.625)
109443	Hypothetical protein (Puf family RNA binding protein)	↑(0.644, 1.95)		
5227	Isoleucyl-tRNA synthetase			↑(0.656, 1.685)
Ribosome structure and biosynthesis				
81599	Protein SIK1 (pre-RNA processing nucleolar protein)	↑(0.657, 2.297)		
81599	Protein SIK1 (pre-RNA processing nucleolar protein)	↑(0.652, 3.057)		
5324	50S ribosomal protein L14	↑(0.6, 1.531)		
52976	Ribosome biogenesis protein Gar2	↑(0.505, 2.128)		
3671	Hypothetical protein (H/ACA ribonucleoprotein complex subunit 1)	↑(0.631, 2.644)		
47766	Exosome complex exonuclease Rrp 6	↑(0.629, 1.871)		
48301	Ribosome biogenesis protein Nop4	↑(0.644, 2.139)		
69838	60S Ribosome subunit biogenesis protein	↑(0.565, 1.805)		
58299	Ribosome biogenesis protein (Rrb1)	↑(0.639, 2.476)		
80792	Hypothetical protein (ribosome biogenesis protein BRX1)	↑(0.645, 2.679)		
Metabolic pathway				
60018	Hypothetical protein (phosphoribulokinase/uridine kinase)	↓(2.617, 0.593)		

jgiTre2	Name of gene	12h	24h	48h
108781	Dibenzothiophene desulfurization enzyme A/ xenobiotic compound monooxygenase	↑(0.623, 12.222)		
22826	Ribose phosphate pyrophosphokinase 2	↑(0.605, 2.936)		
103039	cyanophycinase	↑(0.45, 2.374)		
57947	5-aminolevulinate synthase	↑(0.329, 7.138)		
56236	Sterol 24-C methyltransferase	↑(0.197, 12.925)		
75468	Cytochrome P450 51 (eburicol 14-alpha demethylase)	↑(0.526, 2.819)		
60847	ATP synthase protein 9		↑(0.62, 21.282)	
80523	pH response regulator protein			↑(0.542, 5.194)
108781	Dibenzothiophene desulfurization enzyme A/ xenobiotic compound monooxygenase			↑(0.529, 3.269)
123029	Cu/Zn superoxide dismutase			↑(0.523, 2.767) ↑(0.411, 7.949)
Metabolic pathway, amino acid				
65290	Cross pathway control protein 1			↑(0.5, 8.547)
65882	Dihydrodipicolinate sythetase family protein	↓(1.997, 0.527)		
81188	Imidazole glycerol phosphate synthase	↓(2.149, 0.646)		
42825	Hypothetical protein (Cytidine deaminase)	↓(1.797, 0.633)		
77647	Threonine aldolase	↑(0.566, 2.256)		
45138	Sulfite reductase beta subunit	↑(0.479, 7.638)		
Metabolic pathway, lipid				
122091	Hypothetical protein (Patatin family phospholipase)	↓(5.801, 0.526)		
64397	Unnamed protein product (neutral/alkaline nonlysosomal ceramidase)	↓(1.811, 0.415)		
69465	Hypothetical protein (salicylate hydroxylase)		↓(1.597, 0.532)	
74228	Bifunctional D12/D15 fatty acid desaturase	↑(0.602, 1.928)		
Metabolic pathway, carbohydrate				

jgiTre2	Name of gene	12h	24h	48h
58356	Glycerol kinase	↓(4.968, 0.488)		
123989	Cellobiohydrolase 1 / Exoglucanase 1	↓(23.621, 0.235)		
111849	Cellulose Hydrolase	↓(4.241, 0.283)		
82227	Cel3c (beta glucosidase)	↓(4.686, 0.275)		
60033	Sorbitol utilisation protein SOU2 / L-xylulose reductase	↓(1.7, 0.64)		
120749	Beta-glucosidase 2	↓(24.845, 0.144)		
74194	L-xylulose reductase	↓(5.005, 0.622)		
123538	1,3-beta-glucanosyltransferase Gel1		↓(1.622, 0.576)	
74223	Endo-1,4-beta xylanase 1			↓(3.988, 0.409)
112392	Endo-1,4-beta xylanase 1			↓(2.137, 0.473)
77284	Hypothetical protein (endoglucanase)	↑(0.529, 3.792)		
73516	Glucose repressible protein Grg1			↑(0.412, 13.954)
73638	Cip1			↑(0.423, 5.559)
120961	Cel61b (endoglucanase 4)			↑(0.656, 19.296)
120229	Xylanase III			↑(0.65, 7.929)
120229	Xylanase III			↑(0.622, 4.141)
60089	Hypothetical protien (succinate dehydrogenase)			↑(0.518 2.21)
76672	Beta-D-glucosidase glucohydrolase			↑(0.568, 4.011)
73643	Endoglucanase 4			↑(0.437, 6.125)
Metabolic pathway, hydrolases				
107263	Patatin-like serine hydrolase / patatin-like phospholipase domain protein	↓(4.824, 0.542)		
107263	Patatin-like serine hydrolase / patatin-like phospholipase domain protein	↓(4.803, 0.67)		
51365	Serin endopeptidase	↓(12.78, 0.298) ↓(19.41, 0.28)		

jgiTre2	Name of gene	12h	24h	48h
73632	Acetylxylylase			↑(0.533, 5.114) ↑(0.322, 14.344)
Metabolic pathway, dehydrogenases				
104606	Fe(iron) containing alcohol dehydrogenase	↓(1.812, 0.519)		
123946	NADP(+) dependent dehydrogenase			↓(1.745, 0.657)
111912	Carbonic anhydrase	↑(0.185, 16.569)		
110455	Short chain dehydrogenase , oxidoreductase	↑(0.31, 8.628)		
122556	Short chain dehydrogenase, reductase	↑(0.273, 9.697)		
Metabolic pathway, oxidoreductases				
77806	Hyp protein (oxidoreductase, zinc binding)	↓(2.031, 0.603)		
123577	Oxidoreductin	↓(5.273, 0.583)		
5345	Hypothetical protein (berberine bridge enzyme, glucooligosaccharide oxidase)	↓(1.531, 0.407)		
54086	Sorbose reductase SOU1	↓(2.333, 0.502)		
53567	Glutathione-disulfide reductase	↑(0.606, 3.151)		
103012	Alpha-ketoglutarate-dependent taurine dioxygenase	↑(0.206, 26.391)		
123979	Alpha-ketoglutarate-dependent taurine dioxygenase	↑(0.245, 20.498)		
76215	Pyridine nucleotide-disulphide oxidoreductase	↑(0.629, 7.243)		
79738	Zinc-binding oxidoreductase	↑(0.546, 2.671)		
112567	TfdA family taurine dioxygenase	↑(0.164, 19.405)		
55351	Peroxisomal protein (Allergen Asp f 3)	↑(0.651, 6.453)		
55351	Peroxisomal protein (Allergen Asp f 3)	↑(0.388, 12.526)		
58689	Cytochrome P450	↑(0.528, 3.874)		
22110	Hypothetical protein (Flavin containing monooxygenase)	↑(0.311, 7.371)		
106686	TfdA family oxidoreductase/ Taurine catabolism dioxygenase	↑(0.259, 6.338)	↓(2.447, 0.372)	↑(0.566, 2.065)

jgiTre2	Name of gene	12h	24h	48h
53673	NADP:D-xylose dehydrogenase			↑(0.526, 3.868)
52267	Mannitol-1-phosphate 5-dehydrogenase			↑(0.654, 4.26)
Metabolic pathway, peptidases				
109234	Peptidase family T4 (D-aminopeptidase)	↓(12.814, 0.312)		
112519	Endopolyphosphate	↓(1.545, 0.511)		
63381	Conserved hypothetical protein (cupin domain)			↓(1.516, 0.648)
82623	Tripeptidyl peptidase A. tppA			↓(2.757, 0.548)
109234	Peptidase family T4 (D-aminopeptidase)			↑(0.275, 11.903)
Metabolic pathway, reductases				
102766	Keto reductase	↑(0.324, 3.795)		
62335	Methionine aminopeptidase	↑(0.642, 2.001)		
105282	Aldo/keto reductase	↑(0.448, 3.367)		
Metabolic pathway, transferases				
122240	Carnitine acetyl transferase	↓(6.72, 0.506)		
108637	Hypothetical protein (partially match to acetyltransferase GNAT family protein)	↓(4.176, 0.515)		
120290	Hypothetical protein (Thiamin pyrophosphokinase-related protein)	↓(1.541, 0.635)		
82662	Epl1 (snodprot1)			↓(1.551, 0.611)
68036	Cystathionine gamma synthase			↓(1.927, 0.667)
64959	CDP-alcohol phosphatidyltransferase/ synthase	↑(0.335, 7.198)		
82085	Glutaredoxin-1	↑(0.573, 19.363)		
2591	Methyltransferase BUD23	↑(0.588, 1.651)		
54865	Putative methionine permease	↑(0.322, 14.822)		
23240	Hypothetical protein (methyltransferase)	↑(0.209, 11.929)		
121405	4-aminobutyrate aminotransferase GatA	↑(0.472, 10.808)		

jgiTre2	Name of gene	12h	24h	48h
104222	Hypothetical protein (poor match GNAT family acetyltransferase)			↑(0.55, 6.544)
Protein folding / UPR				
52050	40kDa peptidyl-prolyl cis-trans isomerase	↓(1.775, 0.635)		
122920	78kDa glucose-regulated protein (BIP)	↓(3.667, 0.644) ↓(4.54, 0.621) ↓(4.257, 0.664)		↑(0.451, 12.325) ↑(0.368, 7.251) ↑(0.386, 9.595) ↑(0.407, 8.18)
121948	Hypothetical protein (microsomal signal peptidase Spc12)	↓(1.779, 0.651)		
2687	Heat Shock protein 78	↓(3.056, 0.569)		
122363	Small Heat Shock protein 30kD	↓(13.544, 0.65)		
28928	PDI related protein, PrpA	↓(1.764, 0.642) ↓(2.301, 0.62)	↓(1.956, 0.635)	
21246	Ubiquitin fusion degradation protein	↓(1.768, 0.6)		
56434	FK506-binding protein 4 (Peptidyl-prolyl cis-trans isomerase)	↑(0.64, 2.846)		
104211	FK506-binding protein 1 (peptidyl-prolyl-isomerase)	↑(0.189, 28.062)		↑(0.641, 13.655)
22164	DnaJ-class molecular chaperone with C-terminal Zinc finger domain			↑(0.591, 7.843)
119890	Protein disulfide isomerase TigA			↑(0.614, 7.382)
122415	Protein disulfide isomerase			↑(0.427, 26.836)
35465	Heat shock protein 70-like protein, Lhs1		↓(2.053, 0.659)	↑(0.655, 1.814) ↑(0.609, 2.544)
80142	Heat shock protein 101			↑(0.652, 3.124)
73678	Calnexin			↑(0.65, 7.332)
Protein elimination / ERAD				
82512	26S proteasome regulatory subunit-like protein, Rpn4	↓(11.622, 0.445)		
49149	Translocation protein (Sec66)		↓(1.5, 0.568)	

jgiTre2	Name of gene	12h	24h	48h
80843	26S proteasome regulatory subunit rpn8			↓(1.816, 0.665)
120571	Hyp protein (RNA-binding protein Pno1p)	↑(0.492, 3.449)		
27384	Ubiquitin ligase complex F-box protein GRR1		↑(0.647, 1.894)	
72606	Ubiquitin activating enzyme E1			↑(0.577, 2.689)
119903	Hypothetical protein, Der1 homology			↑(0.619, 2.347)
121397	SEC61 alpha subunit			↑(0.612, 5.107) ↑(0.651, 4.992) ↑(0.628, 4.888)
Trafficking				
119551	Mitochondrial carrier protein	↑(0.652, 1.846)		
23316	Protein Yop1 (membrane biogenesis protein)			↑(0.653, 2.358)
22531	Vacuolar protein sorting 29			↑(0.644, 3.644)
Transporters				
56176	Hypothetical protein (ABC bile acid transporter)	↓(2.608, 0.455)		
79202	MFS transporter	↓(7.418, 0.387)		
79510	Hypothetical protein (ABC bile acid transporter)	↓(2.126, 0.665)		
47987	ZIP metal ion transporter	↓(2.67, 0.661)		
44175	Hypothetical protein (sugar transporter family protein)	↓(2.311, 0.42)		
50894	MFS sugar transporter	↓(1.552, 0.569)		
62711	Amino acid transporter	↓(2.797, 0.563)		
82095	Ammonium permease (transporter)	↓(2.084, 0.631)		
75204	AN1 zinc finger protein	↓(3.409, 0.433)		
3405	Sugar transporter	↓(15.08, 0.154)		
54632	MFS transporter	↓(3.427, 0.411)		
60945	Putative sugar transporter	↓(4.673, 0.527)		

jgiTre2	Name of gene	12h	24h	48h
123718	Amino acid transporter			↓(1.949, 0.601)
119710	MFS multidrug transporter	↑(0.61, 1.507)		
56911	Sodium/proline symporter (urea transport protein)	↑(0.357, 6.079) ↑(0.32, 4.799)		
60144	High affinity methionine permease	↑(0.267, 5.178) ↑(0.2.73, 7.59)		
65583	Hypothetical protein (MFS transporter)	↑(0.586, 1.961)		
79741	Sulfate transporte, sulfate permease	↑(0.461, 1.967)		
120150	Ras-like protein	↑(0.64, 4.488)		
121486	Amino acid transporter	↑(0.543, 1.794)		
54365	Amino acid transporter	↑(0.148, 24.347)		
57015	Amino acid transporter	↑(0.597, 1.721)		
81125	Amino acid permease (transporter)	↑(0.628, 1.945)		
54461	MFS transporter	↑(0.397, 2.136)		
62380	MFS monosaccharide transporter	↑(0.408, 4.177)		
59333	MFS transporter	↑(0.503, 2.196)		
6005	MFS transporter	↑(0.391, 4.207)		
51110	Amino acid permease IND1		↑(0.607, 2.8)	
23221	Cation-transporting ATPase4, ER membrane P-type ATPase			↑(0.667, 1.89)
82150	Inorganic phosphate transporter PHO88			↑(0.652, 1.958)
Unclassified				
46002	Hypothetical protein (partial)	↓(16.663, 0.382)		
109560	Partial match to hypothetical protein	↓(1.689, 0.44)		
119956	Partial match to hypothetical protein	↓(1.513, 0.569)		

jgiTre2	Name of gene	12h	24h	48h
122108	Partial match to hypothetical protein	↓(12.459, 0.237) ↓(5.062, 0.264)		
124249	Partial match to hypothetical protein	↓(2.109, 0.64)		
120120	predicted protein (poor match)	↓(14.314, 0.183)		
108583	Unnamed protein product	↓(1.526, 0.571)		
102966	Hypothetical protein	↓(1.752, 0.556)		
105408	Hypothetical protein	↓(2.368, 0.475)		
105444	Hypothetical protein	↓(2.405, 0.592)		
106155	Hypothetical protein	↓(1.586, 0.612)		
110692	Hypothetical protein	↓(2.747, 0.463)		
119690	Hypothetical protein	↓(1.648, 0.542)		
121717	Hypothetical protein	↓(32.116, 0.21)		
123881	Hypothetical protein	↓(2.264, 0.444)		
27992	Hypothetical protein	↓(1.588, 0.597)		
40290	Hypothetical protein	↓(1.542, 0.574)		
44178	Hypothetical protein	↓(2.463, 0.623)		
44967	Hypothetical protein	↓(10.738, 0.549)		
55443	Hypothetical protein	↓(2.259, 0.595)		
58475	Hypothetical protein	↓(1.638, 0.591)		
77706	Hypothetical protein	↓(9.742, 0.629)		
123686	No Match	↓(17.716, 0.491) ↓(8.156, 0.6)		
108806	No real match	↓(2.097, 0.651)		
120311	No match	↓(3.831, 0.328)		
72379	Conidiospore surface protein		↓(3.883, 0.539)	

jgiTre2	Name of gene	12h	24h	48h
106251	No match		↓(1.572, 0.528)	
119902	No real match			↓(2.265, 0.584)
54790	No real match			↓(2.071, 0.441)
63914	Hypothetical protein (integral membrane protein)			↓(2.009, 0.636)
77758	Cytochrome c heme lyase	↑(0.647, 1.507)		
123475	No Match	↑(0.594, 6.176)		
120160	No match	↑(0.609, 2.129)		
112034	DUF895 domain containing protein	↑(0.261, 5.48)		
64049	Hypothetical protein (DUF895 domain membrane protein)	↑(0.47, 2.68)		
124296	Hypothetical protein	↑(0.311, 7.786)		
31075	Hypothetical protein	↑(0.394, 2.134)		
55252	Hypothetical protein	↑(0.564, 1.818)		
82374	Hypothetical protein	↑(0.619, 2.303)		
43418	Hypothetical protein	↑(0.261, 13.499)		↑(0.631, 6.992)
40775	RTA1 domain protein		↑(0.609, 3.673)	
121416	Conserved hypothetical protein		↑(0.626, 12.03) ↑(0.572, 10.3)	
21677	Hypothetical protein	↓(2.314, 0.416)	↑(0.648, 1.507)	
22000	Hypothetical protein		↑(0.497, 3.483)	
123236	No Match		↓(2.958, 0.506)	↑(0.3, 8.534)
123236	No Match		↓(1.615, 0.506)	↑(0.321, 4.979)
52476	Hypothetical protein		↓(3.144), 0.503)	↑(0.362, 4.819)
123914	No match	↓(7.867, 0.316)	↑(0.645, 7.771)	↓(8.958, 0.652)
69013	Hypothetical protein		↑(0.654, 2.672)	↓(2.863, 0.485)

jgiTre2	Name of gene	12h	24h	48h
69468	Hypothetical protein		↑(0.626, 1.877)	
72379	Conidiospore surface protein			↑(0.557, 15.596)
22560	Hypothetical protein (SLS1?)			↑(0.578, 4.436)
120189	Poor match to GPI anchored protein			↑(0.658, 5.184)
119552	Poor match to Sed1p			↑(0.409, 10.891)
23458	Conserved hypothetical protein			↑(0.585, 2.233)
69288	Hypothetical protein			↑(0.577, 2.975)
55375	Hypothetical protein			↑(0.659, 3.269)
54858	Hypothetical protein			↑(0.665, 2.664)
107349	No real match			↑(0.57, 4.245)
112281	No match			↑(0.598, 15.723)
120030	No Match			↑(0.404, 6.206) ↑(0.219, 10.879)

Table of down- and up-regulated genes of strains CVtΔ5 after 12h, 24h and 48h cultivation. The first value represents the regulation difference observed and the second value is the inverse value of expression in the replicate dye swap experiment. If more than two values appear, the others are replicates on the microarray slide. Down-regulated values are shown in green and up-regulated values in red. jgiTre2 = gene number from the second round sequencing of *T. reesei* genome.

jgiTre2	Name of gene	12h	24h	48h
Cell growth, cell cycle and development				
46382	GTP binding protein 1	↓(1.596, 0.39)		
44230	Sexual development protein EsdC	↓(1.866, 0.246)		
64300	Hypothetical protien (cell polarity protein Tea1)		↓(1.631, 0.576)	
70266	Cell division control protein 2		↓(1.819, 0.604) ↓(1.577, 0.636)	
73173	Hydrophobin 1			↓(3.192, 0.625) ↓(8.905, 0.344)
22201	Hypothetical protein (copper resistance protein Crd2)	↑(0.54, 2.198)		
50429	Partial match to hypothetical protein (cytochrome c oxidase assembly protein PET191)	↑(0.514, 2.911)		
107325	Hypothetical protein (partially DUF543 domain protein)	↑(0.627, 3.051)		
120313	Hypothetical protein (cytoskeleton organisation protein Dec1)	↑(0.586, 2.141)		
58188	Chitin synthase 4	↑(0.608, 1.509)		
62663	Chitin synthase regulator 3	↑(0.604, 1.509)		
65625	Hypothetical protein (mitochondrial genome maintenance protein mgr2)	↑(0.607, 3.571) ↑(0.472, 1.94)		
76029	GTP binding protein (Bud4)	↑(0.65, 1.552)		
123213	Partial match to hypothetical protein (partially cell surface flocculin)	↑(0.464, 1.624)		
121276	Cytoskeleton assembly control protein Sla2	↑(0.643, 1.559)		

jgiTre2	Name of gene	12h	24h	48h
22381	Calcium/calmodulin dependent protein kinase (serine/threonine protein kinase)	↑(0.469, 1.51)		
105351	Hypothetical protein (cell cycle control protein Cwf8 / Ubiquitin protein ligase E4)		↑(0.631, 2.091)	
120969	NADPH oxidase regulator NoxR		↑(0.662, 1.613)	
119989	Hydrophobin II		↑(0.464, 35.588) ↑(0.344, 42.234)	
123967	partial match to Hydrophobin		↑(0.454, 43.941)	
106538	Hydrophobin			↑(0.514, 18.892)
50323	Cellulose signalling related protein OOC1		↑(0.647, 3.665)	↑(0.435, 21.809) ↑(0.473, 7.487)
58366	Hypothetical protein (Stage V sporulation protein K / AAA family ATPase)			↑(0.646, 1.856)
27719	Glucan synthesis regulatory protein (1,3-beta glucan synthesis protein)			↑(0.626, 2.133)
44704	GTPase activating protein (Evi5)			↑(0.649, 4.88)
54089	Predicted protein			↑(0.608, 3.921)
121539	Mitogen-activated protein kinase			↑(0.668, 1.528)
71078	Calcium/calmodulin-dependent protein kinase			↑(0.653, 3.489)
Transcription				
77513	C6 transcription factor	↓(3.494, 0.319)		
78695	Hypothetical protein (zinc finger protein zpr1)	↓(10.381, 0.469)		
52924	NF-X1 finger transcription factor	↓(1.658, 0.633)		
69933	Hypothetical protien (DNA repair protein)		↓(1.684, 0.41)	
111126	DNA repair protein Rad5		↓(1.698, 0.624)	
104104	Hypothetical protein (poor match to fungal specific transcription factor)		↓(1.779, 0.489)	
104104	Hypothetical protein (poor match to fungal specific transcription factor)		↓(2.037, 0.49)	

jgiTre2	Name of gene	12h	24h	48h
54567	Hypothetical protein (C6 transcription factor)		↓(1.523, 0.584)	
77713	Mitochondrial genome maintenance protein MGM101	↑(0.641, 2.177)		
103291	U6 SNRNA-associated SM-like protein LSM5	↑(0.627, 1.896)		
21250	RuvB-like helicase 2 (AAA family ATPase)	↑(0.505, 2.528)		
54256	Splicing factor 3b subunit 4	↑(0.442, 2.009)		
74682	Hypothetical protein (Not2 family protein)	↑(0.574, 1.776)		
78765	Mitochondrial DNA replication protein (Yhm2)	↑(0.644, 8.351)		
66436	Fibrillarin, snRNP	↑(0.558, 3.047)		
55125	DNA topoisomerase 2		↑(0.649, 2.372)	
108211	Hypothetical protein (partially mitochondrion organization and biogenesis protein)		↑(0.667, 1.677)	
75032	Hypothetical protein (PHD finger domain protein)		↑(0.665, 1.596)	
57720	SWR1-complex protein 5			↑(0.644, 1.898)
63442	SWR1-complex protein 4			↑(0.663, 2.151)
67907	Mannosylphosphorylation protein Mnn4			↑(0.538, 2.086)
57049	Hypothetical protein (mRNA binding post-transcriptional regulator Cxs1)			↑(0.648, 3.094)
78543	RNA-binding La domain protein	↑(0.462, 2.006)		↑(0.63, 3.232)
Translation				
75687	Eukaryotic translation initiation factor 3 subunit EifCj	↑(0.62, 2.94)		
77613	Eukaryotic translation initiation factor 3 subunit 6	↑(0.556, 2.456)		
33359	Translation machinery associated protein 22	↑(0.537, 1.719)		
61804	Hypothetical protein	↑(0.522, 2.022)		
109722	Mitochondrial import inner membrane translocation subunit TIM23	↑(0.513, 1.718)		
121569	Translation initiation factor eIF-2b epsilon			↑(0.647, 2.91)

jgiTre2	Name of gene	12h	24h	48h
62345	Translation initiation factor 4e			↑(0.617, 3.499) ↑(0.617, 3.499)
Ribosome protein and synthesis				
67325	U3 small nucleolar ribonucleoprotein protein Mpp10		↓(1.561, 0.509)	
123900	37S ribosomal protein s9		↓(1.502, 0.532)	
74442	Microtubule associated protein (Ytm1)	↑(0.638, 1.704)		
122210	30S ribosomal subunit S4 (mitochondrial)	↑(0.642, 3.708)		
123145	60S ribosomal protein L17	↑(0.57, 2.925)		
124206	30S Ribosomal protein S10	↑(0.585, 2.041)		
22332	Small nuclear ribonucleoprotein SmE	↑(0.523, 2.782)		
22821	Hypothetical protein (mitochondrial large ribosomal subunit)	↑(0.449, 4.275)		
3909	Hypothetical protein (mitochondrial ribosomal protein L43)	↑(0.62, 3.218)		
49909	Hypothetical protein (partial match to 30S ribosomal protein s7)	↑(0.656, 3.466)		
65808	Hypothetical protein (mitochondrial ribosomal protein L31)	↑(0.461, 4.676)		
121801	Nucleolar protein NOP58-like protein	↑(0.65, 3.373)		
23327	AdoMet-dependent rRNA methyltransferase spb1	↑(0.669, 1.809)		
3671	Hypothetical protein (H/ACA ribonucleoprotein complex subunit 1)	↑(0.648, 1.971)		
54349	Small nuclear ribonucleoprotein SmF	↑(0.575, 1.854)		
58299	Ribosome biogenesis protein (Rrb1)	↑(0.601, 2.172)		
58427	ATP dependent RNA helicase dbp2	↑(0.54, 2.604)		
76073	U6 snRNA-associated Sm-like protein LSm6)	↑(0.544, 3.082)		
70017	Mitochondrial ribosomal protein s19	↑(0.653, 4.727)		
105647	Partial match to a rRNA processing protein Cgr1		↑(0.614, 1.727)	

jgiTre2	Name of gene	12h	24h	48h
120779	40S ribosomal protein s8			↑(0.611, 3.61)
Metabolic pathway				
79059	Myo-inositol-phosphate synthase	↓(2.261, 0.548)		
77739	Homogentisate 1,2-dioxygenase		↓(1.574, 0.527)	
106258	Partially match to DUF636 domain protein		↓(1.77, 0.626)	
112525	Hypothetical protein (partially class II aldolase)		↓(1.783, 0.467)	
51806	Phosphatide cytidyltransferase		↓(1.592, 0.616)	
74379	C-8 sterol isomerase		↓(1.686, 0.515)	
124282	Glyoxal oxidase			↓(1.593, 0.561)
109282	NAD dependent epimerase/dehydratase family protein	↑(0.587, 2.242)		
81930	Inosine triphosphate pyrophosphatase	↑(0.524, 1.653)		
60346	Hypothetical protein (para-aminobenzoate synthase)	↑(0.582, 1.533)		
66524	Hypothetical protein (iron-sulfur cluster biosynthesis protein)	↑(0.538, 3.066)		
72612	Vacuolar carboxypeptidase Cps1	↑(0.644, 5.211)		
110890	Porphobilinogen deaminase Hem3	↑(0.576, 1.755)		
75468	Cytochrome P450 51 (eburicol 14-alpha demethylase)	↑(0.447, 2.038)		
124117	Casein kinase II beta subunit	↑(0.479, 2.514)		
123738	Arginase		↑(0.663, 2.379)	
5107	1-aminocyclopropane-1-carboxylate deaminase			↑(0.655, 2.693)
Metabolic pathway, amino acids				
56350	OK match to cysteine synthase		↓(1.53, 0.613)	
120884	Phosphoribosylglycinamide formyltransferase	↑(0.625, 1.966)		
65921	Methylcrotonoyl-CoA carboxylase alpha chain	↑(0.459, 3.315)		
80872	Bifunctional purine biosynthetic protein Ade1	↑(0.532, 2.936)		

jgiTre2	Name of gene	12h	24h	48h
81339	Glycine dehydrogenase	↑(0.487, 9.811)		
82451	ARD/ARD family protein	↑(0.44, 2.377)		
45138	Sulfite reductase beta subunit	↑(0.528, 4.485)		
75514	Mitochondrial ornithine carrier protein (amino acid transporter Arg13)	↑(0.662, 2.014)		
123655	Arginine metabolism regulation protein iii			↑(0.667, 4.066)
23298	Chorismate mutase			↑(0.648, 2.775)
3600	Hypothetical protein (protein kinase)			↑(0.631, 2.167)
3717	Dihydrodipicolinate synthase			↑(0.618, 4.726)
40199	Hypothetical protein (acetylornithine deacetylase)			↑(0.642, 2.753)

Metabolic pathway, fatty acids, lipids

122091	Hypothetical protein (Patatin family phospholipase)	↓(2.683, 0.497)		
4860	Glycerophosphoryl diester phosphodiesterase family protein		↓(1.549, 0.51)	
61442	Enoyl CoA hydratase (mitochondrial methylglutaconyl-CoA hydratase)	↑(0.526, 3.018)		

Metabolic pathway, carbohydrate

49976	Endoglucanase V	↓(1.764, 0.483)		
58356	Glycerol kinase	↓(2.821, 0.437)		
82227	Cel3c (beta glucosidase)	↓(3.727, 0.23)		
120749	Beta-glucosidase 2	↓(14.717, 0.099)		
107776	NAD(P)H dependant D-xylose reductase	↓(4.415, 0.354)		
73643	Endoglucanase 4	↓(4.576, 0.229)		
73248	Exo-beta-1,3-glucanase		↓(1.562, 0.501)	
108714	Hypothetical protein (ok match to phosphoglycerate mutase)		↓(1.657, 0.653)	

jgiTre2	Name of gene	12h	24h	48h
120784	Hypothetical protein (partial match to aldolase 1-epimerase)		↓(1.887, 0.613)	
74223	Endo-1,4-beta xylanase 1			↓(3.015, 0.404)
73638	Cip1		↓(1.629, 0.614)	↑(0.42, 13.193)
123989	Cellobiohydrolase 1 / Exoglucanase 1	↓(5.464, 0.652)		↑(0.412, 12.697)
121019	Succinate dehydrogenase	↑(0.631, 2.108)		
75890	C1-tetrahydrofolate synthase	↑(0.554, 1.824)		
120229	Xylanase III			↑(0.586, 7.451) ↑(0.569, 3.472)
123726	Endo glucosidase (endo-1,3(4)-beta-glucanase)			↑(0.47, 4.277)
76672	Beta-D-glucosidase glucohydrolase			↑(0.428, 10.445)
123232	Endoglucanase 1 (endo-beta-1,4-glucanase)			↑(0.489, 12.062)
73643	Endoglucanase 4			↑(0.507, 8.575)

Metabolic, hydrolases

107263	Patatin-like serine hydrolase / patatin-like phospholipase domain protein	↓(2.395, 0.559)		
51365	Serin endopeptidase	↓(13.531, 0.236) ↓(24.763, 0.234)		
72685	6-phosphogluconate dehydrogenase	↑(0.457, 2.084)		
75769	Glucose-6-phosphate 1-dehydrogenase	↑(0.654, 2.353)		
70021	Esterase	↑(0.561, 1.672)		
57975	Hypothetical protein (Phosphatidylinositol phospholipase C)	↑(0.623, 1.822)		
69557	beta-N-acetylglucosaminidase		↑(0.601, 1.541)	
71532	Alpha 1,3-glucanase		↑(0.641, 22.177)	
60163	Hypothetical protein (alpha/beta hydrolase)			↑(0.581, 1.819)
73632	Acetylxytan esterase			↑(0.66, 4.526)

jgiTre2	Name of gene	12h	24h	48h
Metabolic, dehydrogenases				
58815	Hypothetical protein (alternative NADH-dehydrogenase)	↑(0.6, 1.603)		
108732	Isovaleryl-coA dehydrogenase	↑(0.448, 6.412)		
79395	D-lactate dehydrogenase	↑(0.49, 1.788)	↑(0.644, 1.878)	
44965	S-(hydroxymethyl)glutathione dehydrogenase / alcohol dehydrogenase			↑(0.535, 4.499)
Metabolic, oxidoreductases				
54086	Sorbose reductase SOU1	↓(2.117, 0.461)		
78496	Hypothetical protein (flavin-binding monooxygenase)	↓(3.619, 0.339)		
66753	Phytanoyl-CoA dioxygenase		↓(1.58, 0.457)	
68585	Ribose 5-phosphate isomerase		↓(1.598, 0.508)	
66345	Superoxide dismutase			↓(7.783, 0.62)
78223	Cytochrome P450 monooxygenase			↓(1.823, 0.622)
123979	Alpha-ketoglutarate-dependent taurine dioxygenase	↑(0.319, 7.151)		
123265	Short chain dehydrogenase / reductase	↑(0.619, 1.693)		
53567	Glutathione-disulfide reductase	↑(0.619, 1.849)		
5849	Hypothetical protein (partially DUF967 domain protein)	↑(0.557, 4.655)		
55351	Peroxisomal protein (Allergen Asp f 3)	↑(0.497, 4.718)		
61212	Hypothetical protein (Cytochrome P450 monooxygenase)	↑(0.42, 1.95)		
23368	L-ornithine 5-monooxygenase	↑(0.46, 2.74)		
55351	Peroxisomal protein (Allergen Asp f 3)	↑(0.513, 2.495)		↑(0.657, 2.155)
56897	Oxidoreductase CipA		↑(0.636, 2.266)	
104418	Hypothetical protein (salicylate hydroxylase)		↑(0.652, 2.425)	
54086	Sorbose reductase SOU1			↑(0.647, 2.416)

jgiTre2	Name of gene	12h	24h	48h
120154	Cytochrome P450 oxidoreductase			↑(0.663, 2.16)
4682	Hypothetical protein (oxidoreductase / short chain dehydrogenase)			↑(0.568, 3.31)
79769	Hypothetical protein (cytochrome C1 heme lyase)			↑(0.603, 2.463)

Metabolic, proteases, peptidases

109234	Peptidase family T4 (D-aminopeptidase)	↓(6.486, 0.198)		
73897	Serine endopeptidase			↓(2.847, 0.486)
63398	Mitochondrial metalloproteinase Oma1	↑(0.663, 1.555)		
119887	Rhomboid family membrane protein (protease)	↑(0.544, 1.657)		
81362	Lipoic acid synthetase		↑(0.66, 1.889)	
j74884	Serine/threonine-protein phosphatase PP2A			↑(0.627, 1.768)
123561	Kexin-like protease			↑(0.606, 2.577)
4982	ATP-dependent Clp protease proteolytic subunit 1			↑(0.64, 1.905)

Metabolic, reductases

63354	Hypothetical protein (FAD synthetase)		↓(1.561, 0.57)	
62335	Methionine aminopeptidase	↑(0.502, 1.588)		
62335	Methionine aminopeptidase	↑(0.599, 2.841)		
78264	Peptide methionine sulfoxide reductase	↑(0.639, 3.713)		
122505	Aryl alcohol dehydrogenase AAD	↑(0.437, 3.135)		
105282	Aldo/keto reductase	↑(0.401, 1.548)		

Metabolic, transferases

122240	Carnitine acetyl transferase	↓(3.49, 0.413) ↓(5.904, 0.282)		
4484	Hypothetical protein (N-acetyltransferase GNAT family)	↓(3.915, 0.644)		

jgiTre2	Name of gene	12h	24h	48h
119823	ubiE/COG5 methyltransferase	↓(5.182, 0.612)		
70035	Mannosyltransferase Alg2		↓(1.629, 0.477)	
77602	Trehalose-6-phosphate synthase		↓(1.674, 0.434)	
22093	Geranylgeranyltransferase / farnesyltransferase type I alpha subunit (RAM2)	↑(0.585, 1.81)		
58055	Para-hydroxybenzoate-polyprenyltransferase	↑(0.657, 1.833)		
66844	Phosphoethanolamine N-methyltransferase	↑(0.612, 1.613)		
78306	Thiosulfate sulfurtransferase	↑(0.537, 2.011)		
53956	Hypothetical protein (partial match to MT-A70 family)	↑(0.629, 1.622)		
121405	4-aminobutyrate aminotransferase GatA	↑(0.506, 9.029)		
80732	Histone H3 lysine 36 (K36) methyltransferase (Set2)	↑(0.655, 3.055)		↑(0.65, 7.87)
69868	Alpha-1,2-mannosyltransferase			↑(0.653, 2.844)
75294	Branched chain amino acid aminotransferase			↑(0.664, 2.316)
104359	Unnamed protein product (NACHT and WD domain protein / beta transducin-like protein)			↑(0.634, 1.798)
122131	Protein-beta-aspartate methyltransferase			↑(0.646, 1.804)
Protein folding /UPR				
122920	78kDa glucose-regulated protein (BIP)	↓(4.462, 0.596) ↓(2.931, 0.652) ↓(2.302, 0.613) ↓(2.814, 0.574)		
46285	Small heat shock protein	↓(7.071, 0.41)		
62100	Small heat shock protein	↓(3.65, 0.346)		
122363	Small Heat Shock protein 30kD	↓(9.528, 0.339)		
78626	Hypothetical protein (ThiJ/Pfp1 superfamily protein)	↓(2.017, 0.637)		
2687	Heat Shock protein 78	↓(3.881, 0.595)		

jgiTre2	Name of gene	12h	24h	48h
80142	Heat shock protein 101	↓(3.414, 0.514)		
73678	Calnexin	↓(1.998, 0.612)		
81984	Palmitoyl-protein thioesterase		↓(1.53, 0.581)	
33960	Prefoldin subunit 6	↑(0.572, 2.874)		
33960	Prefoldin subunit 6	↑(0.658, 3.615)		
104211	FK506-binding protein 1 (peptidyl-prolyl-isomerase)	↑(0.14, 26.671)		
65774	Hypothetical protein (HSP70 family protein)	↑(0.538, 2.378)		
42462	Hypothetical protein (HSP90 binding co- chaperone Sba1)	↑(0.506, 3.06)		
120394	T complex protein 1 subunit alpha	↑(0.56, 1.531)		
120994	T complex protein 1 subunit gamma	↑(0.668, 1.853)		
122857	Prohibitin 2	↑(0.602, 2.143)		
23420	Prohibitin PHB1	↑(0.6, 1.596)		
22994	Cell division control protein CDC48			↑(0.592, 4.836)
22994	Cell division control protein CDC48			↑(0.638, 4.995)
102794	Cyclophilin / peptidyl prolyl cis-trans isomerase E			↑(0.646, 1.958)
73678	Calnexin			↑(0.541, 3.923)
79797	Protein OS-9 homolog			↑(0.665, 2.277)
Protein elimination / ERAD				
82512	26S proteasome regulatory subunit-like protein, Rpn4	↓(6.388, 0.359)		
122048	Good partial match to hypothetical protein (Sec61 beta)	↑(0.664, 1.904)		
120571	Hyp protein (RNA-binding protein Pno1p)	↑(0.526, 2.52)		
76010	Proteasome component Pre6 (20S alpha 7)	↑(0.602, 2.412)		
76010	Proteasome component Pre6 (20S alpha 7)	↑(0.619, 2.232)		
68304	26S proteasome regulatory subunit rpn5/RpnE/RPN5	↑(0.655, 2.512)		

jgiTre2	Name of gene	12h	24h	48h
68304	26S proteasome regulatory subunit rpn5/RpnE/RPN5	↑(0.667, 2.081)		
80843	26S proteasome regulatory subunit rpn8	↑(0.606, 2.393)		
48366	Proteasome regulatory particle Rpn12	↑(0.569, 1.876)		
103625	Hypothetical protein (20S proteasome maturation protein Ump1)			↑(0.668, 5.015)
66707	Proteasome component PRE3 Beta 6)			↑(0.578, 1.539)
Trafficking				
121033	Partially COPII vesicles protein Yip3		↓(1.533, 0.583)	
5912	Autophagy protein Atg13		↓(1.536, 0.543)	
65821	Autophagy related protein 18		↓(1.675, 0.514)	
122546	Vacuolar protein sorting-associated protein 27		↓(2.355, 0.484)	↑(0.617, 6.557)
109722	Mitochondrial import inner membrane translocation subunit TIM23	↑(0.513, 1.718)		
21773	Mitochondrial import inner membrane translocase subunit TIM14	↑(0.549, 3.267)		
75859	Arsenical pump-driving ATPase ArsA	↑(0.669, 1.558)		
79104	Coatomer subunit epsilon	↑(0.659, 1.594)		
120661	AP-2 complex subunit sigma	↑(0.652, 1.725)		
74054	Related to protein transport protein SEC6			↑(0.638, 1.64)
5979	Integral membrane protein Ptm1			↑(0.579, 2.311)
Transporters				
56176	Hypothetical protein (ABC bile acid transporter)	↓(2.721, 0.552)		
79202	MFS transporter	↓(9.176, 0.332)		
51110	Amino acid permease IND1	↓(3.049, 0.191)		
82095	Ammonium permease (transporter)	↓(1.751, 0.518)		
3405	Sugar transporter	↓(4.172, 0.133)		
121743	succinate/fumarate transporter	↓(1.921, 0.327)		

jgiTre2	Name of gene	12h	24h	48h
54632	MFS transporter	↓(4.056, 0.366)		
58296	Hypothetical protein (MFS transporter)		↓(1.771, 0.462)	
62362	P-type calcium ATPase		↓(1.613, 0.618)	
59364	Hypothetical protein (oligopeptide transporter 4)		↓(1.571, 0.475)	
75128	Hypothetical protein (DEAD/DEAH box helicase)		↓(1.502, 0.494)	
104320	Hypothetical protein (poor match MFS transporter)		↓(1.502, 0.453)	
66611	Amino acid permease inda1		↓(1.573, 0.628)	
67562	Zinc regulated transporter 1			↓(2.094, 0.352)
44956	MFS transporter	↓(1.823, 0.657)		↑(0.63, 4.094)
4901	Cytochrome c-oxidase-assembly factor COX16	↑(0.591, 1.548)		
56911	Sodium/proline symporter (urea transport protein)	↑(0.366, 2.834)		
60815	Hypothetical protein (CRAL/TRIO domain)	↑(0.544, 2.138)		
53818	ABC transporter	↑(0.632, 1.967)		
50542	ATP-binding cassette sub-family F member 2 (ABC transporter)	↑(0.642, 2.955)		
45868	MFS phosphate transporter	↑(0.664, 2.016)		
54005	MFS quinate transporter		↓(1.56, 0.55)	
121482	D-xylose-proton symporter (MFS sugar transporter)			↑(0.642, 1.775)
2845	G protein alpha subunit			↑(0.607, 2.281)
121608	MFS transporter			↑(0.626, 1.646)
Unclassified				
119816	Hypothetical protein (DUF221 domain)	↓(2.5, 0.664)		
46002	Hypothetical protein (partial)	↓(2.019, 0.357)		
121870	Hypothetical protein (partially arrestin, N-terminal domain)	↓(2.474, 0.639)		
57936	Hypothetical protein (partially IFRD domain protein)	↓(4.715, 0.637)		

jgiTre2	Name of gene	12h	24h	48h
122108	Partial match to hypothetical protein	↓(5.381, 0.191) ↓(5.537, 0.188)		
21412	Partial match to predicted protein	↓(3.896, 0.599)		
120120	predicted protein (poor match)	↓(6.786, 0.167)		
102966	Hypothetical protein	↓(3.822, 0.183)		
105444	Hypothetical protein	↓(1.934, 0.458)		
44967	Hypothetical protein	↓(4.613, 0.601) ↓(3.829, 0.561)		
53893	Hypothetical protein	↓(4.189, 0.662)		
54052	Hypothetical protein	↓(4.046, 0.655)		
77706	Hypothetical protein	↓(5.068, 0.302)		
82049	Hypothetical protein	↓(2.357, 0.622)		
124059	No real match	↓(5.871, 0.342)		
120030	No Match	↓(2.514, 0.554) ↓(2.51, 0.429)		
120311	No match	↓(1.713, 0.392)		
123686	No Match	↓(10.972, 0.566)		
123914	No match			
123396	No match	↓(3.275, 0.46)		
111527	No real match	↓(6.731, 0.549)		
123914	No match	↓(2.759, 0.286) ↓(1.701, 0.165)		↓(3.028, 0.458)
70608	Hemerythrin HHE cation binding domain protein		↓(1.559, 0.606)	
106697	Alpha/beta hydrolase		↓(1.606, 0.427)	
74771	Hypothetical protein (DUF221 domain protein)		↓(1.512, 0.571)	
34277	Hypothetical protein (DUF427 domain)		↓(1.552, 0.591)	

jgiTre2	Name of gene	12h	24h	48h
111186	Hypothetical protein (partially match DNA repair protein Rad1)		↓(1.521, 0.637)	
57140	Hypothetical protein (RNP domain protein)		↓(1.666, 0.539)	
105466	Predicted protein		↓(1.529, 0.505)	
56546	Predicted protein		↓(1.501, 0.628)	
112094	Unnamed protein product		↓(1.517, 0.656)	
112193	Unnamed protein product		↓(1.72, 0.629)	
109716	Hypothetical protein		↓(1.619, 0.606)	
53824	Hypothetical protein		↓(1.671, 0.613)	
55876	Hypothetical protein		↓(1.847, 0.511)	
73708	Hypothetical protein		↓(1.585, 0.585)	
102377	No match		↓(1.581, 0.581)	
103801	No match		↓(1.516, 0.459)	
107338	No match		↓(1.531, 0.564)	
108996	No match		↓(1.543, 0.455)	
110862	No match		↓(1.839, 0.449)	
112427	No match		↓(1.682, 0.588)	
112540	No match		↓(1.75, 0.415)	
121350	CipC1 or phosphoglycerate mutase family protein			↓(9.412, 0.318)
61593	Hypothetical protein			↓(2.126, 0.401)
34079	Small nuclear ribonucleoprotein Sm D3	↑(0.597, 1.988)		
64685	Hypothetical protein (Mitochondrial hypoxia responsive domain)	↑(0.617, 1.576)		
61122	Hypothetical protein (mitochondrial protein Fmp26?)	↑(0.607, 1.508)		
47829	Hypothetical protein (regulatory protein)	↑(0.535, 2.166)		
123690	Mago nashi domain protein	↑(0.573, 1.891)		

jgiTre2	Name of gene	12h	24h	48h
111027	No real match (partially mitochondrial F1F0 ATP synthetase)	↑(0.565, 2.312)		
103167	Potential hypothetical protein (4F5 protein/ small EDRK rich factor 2) poor scores	↑(0.495, 2.857)		
108778	Hypothetical protein	↑(0.615, 2.795)		
122095	Partial match to hypothetical protein	↑(0.626, 1.551)		
120407	Hypothetical protein	↑(0.582, 1.634)		
121660	Hypothetical protein	↑(0.478, 1.507)		
43418	Hypothetical protein	↑(0.22, 9.866)		
53431	Hypothetical protein	↑(0.519, 1.94)		
53701	Hypothetical protein	↑(0.568, 2.676)		
55205	Hypothetical protein	↑(0.55, 1.785)		
63151	Hypothetical protein	↑(0.652, 1.956)		
65209	Hypothetical protein	↑(0.55, 1.566)		
58077	Hypothetical protein	↑(0.571, 3.813)		
66269	Hypothetical protein	↑(0.56, 3.738)		
75447	Hypothetical protein	↑(0.644, 1.671)		
111237	No match	↑(0.441, 2.99)		
120160	No match	↑(0.431, 2.055)		
123475	No Match	↑(0.431, 2.512)		
107577	No real match	↑(0.518, 4.761)		
111035	No real match	↑(0.591, 4.686)		
123282	No real match	↑(0.536, 1.982)		↑(0.663, 2.222)
122422	Poor match to a Hypothetical protein		↑(0.668, 1.759)	
110651	Predicted protein		↑(0.665, 1.515)	

jgiTre2	Name of gene	12h	24h	48h
106575	Unnamed protein product		↑(0.638, 1.502)	
106131	Hypothetical protein		↑(0.654, 1.589)	
106248	Hypothetical protein		↑(0.589, 3.801)	
111915	Hypothetical protein		↑(0.566, 8.984)	
105157	Hypothetical protein		↑(0.607, 1.549)	
60300	Hypothetical protein		↑(0.642, 2.182)	
111429	No match		↑(0.626, 1.784)	
120823	No Match		↑(0.539, 16.224)	
107436	No real match		↑(0.662, 1.667)	
120877	Metallo-beta-lactamase domain protein			↑(0.571, 10.428)
123226	Trehalase			↑(0.648, 1.919)
112105	Unnamed protein product (stress responsive A/B barrel domain protein)			↑(0.667, 1.506)
47127	Hypothetical protein (vascular aspartyl aminopeptidase Lap4)			↑(0.595, 1.589)
72379	Conidiospore surface protein		↑(0.25, 28.063)	↑(0.526, 11.957)
65437	Hypothetical protein (DUF572 domain protein)			↑(0.653, 3.804)
57474	Hypothetical protein (DUF726 domain)			↑(0.667, 3.234)
75975	Hypothetical protein (LMBR1 domain)			↑(0.648, 2.161)
110691	No match (partially protein tyrosine phosphatase)			↑(0.664, 2.068)
111272	No real match(partially D-aminopeptidase)			↑(0.656, 2.118)
120189	Poor match to GPI anchored protein			↑(0.561, 5.209)
119552	Poor match to Sed1p			↑(0.459, 18.242)
61618	Conserved hypothetical protein			↑(0.626, 1.688)
102773	Partial match to a hypothetical protein			↑(0.643, 4.128)
76539	Partial match to a hypothetical protein			↑(0.611, 1.775)

jgiTre2	Name of gene	12h	24h	48h
107853	Partial match to an unnamed protein product			↑(0.48, 5.986)
108906	Hypothetical protein			↑(0.583, 2.334)
1737	Hypothetical protein			↑(0.649, 2.239)
21152	Hypothetical protein			↑(0.6, 1.677)
2250	Hypothetical protein			↑(0.657, 3.267)
40943	Hypothetical protein			↑(0.603, 1.763)
4154	Hypothetical protein			↑(0.651, 3.166)
59078	Hypothetical protein			↑(0.601, 1.977)
65315	Hypothetical protein			↑(0.58, 1.679)
66786	Hypothetical protein			↑(0.549, 2.125)
70838	Hypothetical protein			↑(0.668, 2.974)
80007	Hypothetical protein			↑(0.648, 10.658)
81183	Hypothetical protein			↑(0.659, 2.132)
103002	No match			↑(0.632, 1.695)
103174	No match			↑(0.661, 1.769)
104715	No match			↑(0.651, 1.961)
105206	No match			↑(0.649, 1.765)
106554	No match			↑(0.662, 2.09)
108573	No match			↑(0.669, 2.33)
109972	No match			↑(0.659, 1.719)
111593	No match			↑(0.55, 1.853)
112689	No match			↑(0.629, 2.172)
102627	No real match			↑(0.62, 1.575)
108806	No real match			↑(0.622, 1.987)

jgiTre2	Name of gene	12h	24h	48h
110096	No real match			↑(0.668, 1.873)
120697	No real match			↑(0.593, 3.373)
124198	No real match			↑(0.588, 4.143)
70223	No real match			↑(0.651, 1.562)

Table of down- and up-regulated genes of strains Rut-C30, CVt and CVtΔ4 at 48h growth under proteasome inhibition conditions. The first value represents the regulation difference observed and the second value is the inverse value of expression in the replicate dye swap experiment. If more than two values appear, the others are replicates on the microarray slide. Down-regulated values are shown in green and up-regulated values in red. jgiTre2 = gene number from the second round sequencing of *T. reesei* genome.

jgiTre2	Name of gene	Rut-C30 +/- MG132	CVt +/- MG132	CVtΔ4 +/- MG132
Cell growth, cell cycle and development				
121491	Trehalose synthase (clock-controlled gene-9 protein)	↓ (0.17, 11.215), ↓ (0.415, 3.788)		
30214	Hypothetical protein (capsule polysaccharide biosynthesis protein)		↓ (0.502, 2.111)	
51407	Hypothetical protein (Kelch repeat protein)	↓ (0.564, 1.582)		
62213	Hypothetical protein (Fasciclin domain family)			↑ (3.616, 0.67)
73173	Hydrophobin 1	↓ (0.183, 9.795)		
Transcription / translation				
68608	Thiazole biosynthetic enzyme (stress inducible enzyme)	↓ (0.178, 10.546)		
75418	Zinc finger transcription factor ace1	↓ (0.593, 3.306)		
Ribosome structure and biogenesis				
58428	Hypothetical protein (ribosome biogenesis protein Rrs1)	↑ (1.683, 0.508)	↓ (0.666, 3.326)	
Metabolic pathways				
120635	Transketolase	↓ (0.466, 3.945)		
121620	Thiamine biosynthesis protein Nmt1	↓ (0.082, 21.724)		
122811	Glutamine synthetase	↓ (0.474, 6.078)		
63813	Cytochrome b5	↓ (0.669, 1.74)		
77764	Phytochrome-like histidine kinase	↓ (0.59, 2.317)		
121534	Pyruvate decarboxylase	↓ (0.308, 8.484)		↑ (4.755, 0.63)
64397	Unnamed protein product (neutral/alkaline nonlysosomal ceramidase)	↑ (1.613, 0.642)		
76155	Acid phosphatase	↑ (1.596, 0.572)		
73621	Citrinin polyketide synthase		↑ (0.575, 1.423)	
121534	Pyruvate decarboxylase			↑ (3.361, 0.515)

jgiTre2	Name of gene	Rut-C30 +/- MG132	CVt +/- MG132	CVtΔ4 +/- MG132
120568	Enolase			↑(3.857, 0.666)
j66345	Superoxide dismutase			↑(5.159, 0.395)
Fatty acid, lipids				
45250	Delta-12 fatty acid desaturase	↓ (0.655, 3.923)		
48788	Fatty acid synthase alpha subunit	↓ (0.565, 2.796)		
48788	Fatty acid synthase alpha subunit	↓ (0.653, 1.995)		
78611	Phospholipase PldA	↓ (0.66, 1.592)		
Carbohydrate metabolism				
77284	Hypothetical protein (endoglucanase)	↓ (0.597, 2.156)		
50215	Glucan 1,3-beta-glucosidase	↓ (0.64, 1.547)		
55999	Alpha-galactosidase	↓ (0.476, 2.072)		
111849	Cellulose Hydrolase			↓ (0.64, 2.491)
120312	Endoglucanase III or II			↓ (0.546, 3.814)
73638	Cip1			↓ (0.642, 4.351)
120961	Cel61b (endoglucanase 4)	↑(8.141, 0.564)		↓ (0.283, 8.286)
120229	Xylanase III	↑(1.507, 0.633)		
123232	Endoglucanase 1 (endo-beta-1,4-glucanase)	↑(2.072, 0.66); ↑(4.138, 0.497)		
123818	Endoxylanase II	↑(10.029, 0.295)		
Hydrolases				
76210	Abf2 (alpha-L-arabinofuranosidase)	↓ (0.648, 3.43)		
123283	Alpha-N-arabinofuranosidase			↓ (0.394, 4.195)
Dehydrogenases				
119735	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)			↑(6.166, 0.626)
119735	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)			↑(6.794, 0.626)
123729	Malate dehydrogenase	↓ (0.589, 3.159)		
Oxidoreductases				
81102	Flavin-binding monooxygenase-like protein	↓ (0.336, 4.323)		
81525	Oxidoreductase CipA-like (NmrA-like family)	↓ (0.425, 2.875)		

jgiTre2	Name of gene	Rut-C30 +/- MG132	CVt +/- MG132	CVtΔ4 +/- MG132
120357	Hypothetical protein (zinc-binding oxidoreductase)	↓ (0.44, 5.525)		
121230	Squalene epoxidase	↓ (0.635, 2.999)		
121275	Cytochrome c oxidase	↓ (0.6, 4.341)		
123251	Flavohemoglobin	↓ (0.639, 3.423)		
1751	Hypothetical protein (FAD monooxygenase)	↓ (0.661, 2.861)		
50786	ERV2-like protein (FAD dependent sulfhydryl oxidase)		↑ (0.665, 1.335)	
Peptidases, proteases				
73897	Serine endopeptidase	↑ (7.562, 0.34)		
120998	Carboxypeptidase Y			↑ (3.821, 0.643)
21659	Dipeptidyl peptidase			↑ (1.675, 0.495)
77579	Vacuolar protease A			↑ (1.9, 0.658)
Reductases				
74194	L-xylulose reductase	↓ (0.665, 3.724)		
Transferases				
119616	Serine/threonine protein kinase psk1	↓ (0.665, 1.544)		
121824	ATP citrate synthase subunit 1	↓ (0.584, 2.314)		
121826	ATP citrate lyase subunit 2	↓ (0.53, 3.047)		
81260	Adenylate kinase 2	↓ (0.425, 2.969)		
107206	Hypothetical protein (bis(5'-nucleosyl)-tetrphosphatase)		↓ (0.588, 1.682)	
31869	Nicotinamide mononucleotide adenylyl transferase		↓ (0.643, 1.74)	
21406	Phosphoglycerate kinase	↓ (0.635, 3.074)		↑ (4.339, 0.574)
21716	Acetate kinase			↑ (1.793, 0.614)
58356	Glycerol kinase	↑ (2.076, 0.549)		
Stress response/ UPR				
121839	Hypothetical protein (related to HSP70)	↓ (0.493, 3.774)		
Protein elimination / ERAD				
121343	Proteasome component PRE5 (20S alpha 1)	↑ (1.525, 0.569)		↑ (3.109, 0.653) ↑ (3.27, 0.65)

jgiTre2	Name of gene	Rut-C30 +/- MG132	CVt +/- MG132	CVtΔ4 +/- MG132
73564	Proteasome subunit alpha 3	↑(2.102, 0.611)		↑(2.332, 0.537), ↑(2.508, 0.605), ↑(2.68, 0.577), ↑(3.166, 0.582)
55644	Proteasome alpha subunit PUP2 (alpha5)	↑(2.489, 0.544), ↑(2.185, 0.499)		↑(1.919, 0.604), ↑(2.098, 0.613)
120650	Proteasome subunit alpha 6			↑(4.146, 0.662), ↑(2.888, 0.646), ↑(3.339, 0.642)
76010	Proteasome component Pre6 (20S alpha 7)	↑(2.491, 0.492), ↑(2.116, 0.523), ↑(2.447, 0.61)		↑(2.055, 0.541)
78882	Proteasome component C5 (Beta 1)	↑(1.684, 0.57)		
53554	Proteasome subunit beta 2	↑(2.31, 0.577), ↑(2.483, 0.636)		
58125	Proteasome subunit beta type 3	↑(2.008, 0.653)		↑(4.739, 0.538), ↑(4.509, 0.649), ↑(4.282, 0.546), ↑(3.447, 0.608), ↑(3.573, 0.646), ↑(3.562, 0.569), ↑(3.668, 0.614)
78925	Proteasome beta Pre4 (20S beta 4)			↑(3.064, 0.534), ↑(1.836, 0.602), ↑(2.323, 0.57), ↑(2.201, 0.629)
121009	Proteasome component Pre2 (20S beta 5)	↑(1.79, 0.665)		↑(1.838, 0.609)
73574	26S proteasome regulatory subunit 7 (19S RPT1)	↑(2.126, 0.656)		↑(2.895, 0.606), ↑(2.388, 0.661), ↑(2.814, 0.529)

jgiTre2	Name of gene	Rut-C30 +/- MG132	CVt +/- MG132	CVtΔ4 +/- MG132
77591	Proteasome regulatory particle RpnC/3	↑(2.069, 0.573)		
77330	Proteasome regulatory particle RpnI/9	↑(1.605, 0.624), ↑(1.592, 0.665)		
80843	26S proteasome regulatory subunit rpn8			↑(1.654, 0.614), ↑(1.556, 0.641), ↑(1.846, 0.578), ↑(1.877, 0.618)
Transporters				
123718	Amino acid transporter	↓ (0.669, 3.849)		
22912	Glucose transporter (partial)	↓ (0.441, 4.545)		
123702	Hypothetical protein (sugar transporter)	↑(1.539, 0.647)		
67562	Zinc regulated transporter 1			↑(3.635, 0.576)
Unclassified				
108449	Hypothetical protein	↓ (0.337, 3.299)		
111527	No real match	↓ (0.655, 2.673)		
119690	Hypothetical protein	↓ (0.513, 1.527)		
119902	No real match	↓ (0.625, 1.562)		
120120	predicted protein (poor match)	↓ (0.533, 2.689)		
119902	No real match	↓ (0.625, 1.562)		
120503	No match	↓ (0.509, 1.662)		
121126	Hypothetical protein (integral membrane protein)	↓ (0.425, 5.785), ↓ (0.642, 6.333)		
122065	Hypothetical protein	↓ (0.634, 1.962)		
122569	partial match to Hypothetical protein	↓ (0.429, 5.812), ↓ (0.341, 6.174)		
123502	Hypothetical protein (protein phosphatase regulatory subunit Gac1)	↓ (0.654, 1.591)		
2698	Hypothetical protein (translocator protein)	↓ (0.664, 2.376)		
61227	Hypothetical protein (CobW domain / cobalamin synthesis protein)	↓ (0.644, 2.73)		

jgiTre2	Name of gene	Rut-C30 +/- MG132	CVt +/- MG132	CVtΔ4 +/- MG132
73516	Glucose repressible protein Grg1	↓ (0.238, 7.105)		
74060	Hypothetical protein (allergen Asp f 4)	↓ (0.561, 5.764)		
66776	Unnamed protein product	↓ (0.611, 1.802)		
72859	Hypothetical protein	↓ (0.55, 5.746)		
75383	Hypothetical protein	↓ (0.445, 2.391)		
33827	Hypothetical protein	↓ (0.627, 4.726)		
21135	Hypothetical protein	↓ (0.613, 1.846)		
79972	Hypothetical protein	↓ (0.637, 3.298)		
80441	Hypothetical protein	↓ (0.504, 2.678)		
41895	Hypothetical protein	↓ (0.389, 3.921)		
43430	Hypothetical protein	↓ (0.542, 1.567)		
61078	Hypothetical protein	↓ (0.552, 2.607)		
123476	No real match	↓ (0.65, 2.057)		
123650	No Match	↓ (0.544, 3.997)		
123686	No Match	↓ (0.515, 4.853)		
123475	No Match	↓ (0.229, 14.912)		
56593	poor match to a hypothetical		↓ (0.472, 2.727)	
61995	Conserved hypothetical protein		↓ (0.25, 6.541)	
70488	Hypothetical protein (merozoite capping protein 1 / disrupter of telomere silencing protein)		↓ (0.633, 1.581)	
121111	Hypothetical protein		↓ (0.631, 1.946)	
61593	Hypothetical protein		↓ (0.248, 8.417)	
3891	Hypothetical protein		↓ (0.669, 1.818)	
41794	Hypothetical protein			↓ (0.658, 1.69)
121350	CipC1 or phosphoglycerate mutase family protein	↓ (0.563, 9.71)		↑ (9.62, 0.332)
121416	Conserved hypothetical protein	↓ (0.226, 13.96), ↓ (0.568, 5.185)		↑ (4.284, 0.46)
44967	Hypothetical protein	↓ (0.34, 9.821), ↓ (0.505, 8.152)		↑ (6.621, 0.502), ↑ (5.608, 0.558)
48280	No match	↑ (1.561, 0.599)	↓ (0.236, 6.434)	

jgiTre2	Name of gene	Rut-C30 +/- MG132	CVt +/- MG132	CVtΔ4 +/- MG132
61593	Hypothetical protein	↑(2.099, 0.448)	↓ (0.359, 5.261)	
54052	Hypothetical protein		↓ (0.177, 11.519)	↑(1.685, 0.477)
78695	Hypothetical protein (zinc finger protein zpr1)	↑(2.222, 0.493)		
102966	Hypothetical protein	↑(1.927, 0.444)		
105860	Hypothetical protein	↑(1.999, 0.584)		
22386	Hypothetical protein	↑(3.374, 0.332), ↑(2.09, 0.394)		
69468	Hypothetical protein		↑(0.613, 1.314)	
75794	ZZ type zinc finger domain protein			↑(5.648, 0.572), ↑(5.76, 0.601)
108543	Hypothetical protein			↑(2.204, 0.577)
119805	No real match			↑(3.342, 0.604)
121605	No match			↑(6.706, 0.518)
76098	Hypothetical protein	↑(2.169, 0.621)		↑(1.723, 0.66)