The partitivirus HetPV13-an1 mediates severe growth debilitation and major alterations in the gene expression of a fungal forest pathogen

Eeva J. Vainio, Jaana Jurvansuu, Rafiqul Hyder, Muhammad Kashif, Tuula Piri, Tero Tuomivirta, Anna Poimala, Ping Xu, Salla Mäkelä, Dina Nitisa, Jarkko Hantula

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Table S1. Mapping statistics for the RNA-Seq data. *H. annosum* 94233 is infected with HetPV13-an1 and 94233/32D is an isogenic strain free of HetPV13-an1, and each strain was analyzed using three biological replicates.

Sample id	Number of reads	Number of reads mapped to reference genome	Percentage of mapped reads from all reads	Uniquely aligned reads	Reads mapped to more than one genome location	Reads not mapped to reference genome	Percentage of uniquely mapped reads
94233_1	19165920	13121029	68.46%	12778315	342714	6044891	97.4%
94233_2	19189260	13111270	68.33%	12785264	326006	6077990	97.5%
94233_3	19239707	12798798	66.52%	12449933	348865	6440909	97.3%
94233/32D_1	21666839	14917271	68.85%	14570928	346343	6749568	97.7%
94233/32D _2	18132529	12587443	69.42%	12301201	286242	5545086	97.7%
94233/32D _3	17921554	12437311	69.40%	12160000	277311	5484243	97.8%

Table S2. List of RNA-Seq fold changes (FC), reference gene names and probable functions for the downregulated (negative FC) and upregulated (positive FC) transcripts detected in this study. The gene names refer to the *H. annosum* v.2.0 genome sequence deposited at the JGI (http://genome.jgi.doe.gov/Hetan2/Hetan2.home.html).

No.	FC	Name	Protein	Function
1	-7.253	e_gw1.01.1262.1	-	
2	-32.406	e_gw1.01.2047.1	-	
3	-15.308	e_gw1.01.2531.1	fructosamine-3-kinase	Carbohydrate metabolism mannitol cycle?
4	-23.817	e_gw1.01.3559.1	Mitotic spindle checkpoint protein (mad2)	Cell cycle control /DNA damage
5	-18.976	e_gw1.01.3602.1	Ser-Thr-rich glycosyl-phosphatidyl-inositol-anchored membrane protein	Cell wall organisation /Fruiting body
6	-5.704	e_gw1.02.3514.1	Mannitol dehydrogenase	Carbohydrate metabolism mannitol cycle
7	9.137	e_gw1.03.1624.1		
8	-12.36	e_gw1.03.1854.1	-	
9	-4.151	e_gw1.03.2572.1	Ribonuclease?	
10	-104.712	e_gw1.03.373.1	-	
11	-19.299	e_gw1.03.569.1	-	
12	-13.829	e_gw1.04.1225.1	amidoligase	N-metabolism
13	-6.17	e_gw1.04.1596.1		
14	-6.116	e_gw1.04.2808.1	small heat-shock protein Hsp26/Hsp42	Chaperone
15	-23.478	e_gw1.05.105.1	Cytochrome P450	oxidative degradation
16	-4.041	e_gw1.05.1050.1	-	
17	-138.41	e_gw1.05.1364.1	-	
18	-5.778	e_gw1.05.468.1	RIO kinase	Cell cycle control
19	-24.721	e_gw1.06.288.1	Transposase family, tnp2	transposition
20	-4.226	e_gw1.06.444.1	-	
21	-174.28	e_gw1.06.934.1	-	
22	-6.352	e_gw1.07.1172.1	COG (conserved oligomeric Golgi) complex component, COG2	Golgi function
23	-15.93	e_gw1.07.1431.1	-	
24	-11.308	e_gw1.07.1957.1	glycoside hydrolase family 115 protein	Carbohydrate metabolism
25	-5.555	e_gw1.07.710.1	STE family Protein Kinases	Signal

				transduction
26	-8.174	e_gw1.08.2112.1	alpha-1,6-mannanase	Carbohydrate metabolism, (Yeast cell wall degradation)
27	-5.201	e_gw1.08.2119.1	-	
28	-171.572	e_gw1.09.1714.1	-	
29	-7.149	e_gw1.09.1784.1	Rad52/22	DNA damage
30	-10.684	e_gw1.09.399.1	-	
31	-4.468	e_gw1.09.916.1	-	
32	-4.669	e_gw1.10.340.1	-	
33	-9.325	e_gw1.10.538.1	-	
34	-8.894	e_gw1.11.905.1	HNH endonuclease	Transposition
35	-5.219	e_gw1.12.1238.1	Snurportin-1	Spliceosome function
36	-4.578	e_gw1.12.1332.1	Deoxycytidylate deaminase	Nucleotide metabolism, Thymidine synthesis (DNA damage)
37	-6.245	e_gw1.13.1133.1	betaine-aldehyde dehydrogenase	Energy production (mitochondria), Glycine, serine and threonine metabolism
38	-7.37	e_gw1.13.1363.1	CAMK/CAMKL/CHK1 protein kinase	Cell cycle control
39	-514.798	e_gw1.13.470.1	-	
40	-5.513	e_gw1.14.1005.1	-	
41	-6.464	e_gw1.14.70.1	-	
42	-23.035	estExt_fgenesh1_kg.C_020188	Protein Kinase	Signal transduction
43	-9.793	estExt_fgenesh1_kg.C_020422	S-adenosyl-L-methionine-dependent methyltransferase	Energy production, Biosynthesis of menaquinone and ubiqinone
44	-5.06	estExt_fgenesh1_kg.C_040370	-	
45	-4.131	estExt_fgenesh1_kg.C_050016	Fibritin	Chaperone
46	-33.937	estExt_fgenesh1_kg.C_050098	-	
47	-19.427	estExt_fgenesh1_kg.C_050342	-	
48	-17.421	estExt_fgenesh1_kg.C_050343	-	
49	-14.596	estExt_fgenesh1_kg.C_060355	-	
50	-4.444	estExt_fgenesh1_kg.C_060407	-	
51	-15.918	estExt_fgenesh1_kg.C_070076	-	
52	-4.458	estExt_fgenesh1_kg.C_070174	SUR7	Endocytosis, sporulation
53	-6.691	estExt_fgenesh1_kg.C_090182	Cwf15/Cwc15	Spliceosome function
54	-17.984	estExt_fgenesh1_kg.C_100045	linoleoyl phosphatidylcholine delta-12 acetylenase	Lipid metabolism
55	-6.241	estExt_fgenesh1_kg.C_100047	delta-12 fatty acid desaturase	Lipid metabolism
56	-8.342	estExt_fgenesh1_kg.C_120124	delta-12 fatty acid desaturase	Lipid metabolism, cell membrane fluidity
57	-4.36	estExt_fgenesh1_kg.C_120132	-	
58	-4.93	estExt_fgenesh1_kg.C_130076	-	

59	-4.022	estExt_fgenesh1_kg.C_130077	-	
60	-7.035	estExt_fgenesh1_kg.C_130079	Ankyrin repeat protein	Cell membrane
61	-4.861	estExt_fgenesh1_kg.C_130126	-	
62	-9.827	estExt_fgenesh1_pg.C_040006	-	
63	-64.969	estExt_fgenesh1_pg.C_050529	-	
64	-10.07	estExt_fgenesh1_pg.C_090253	-	
65	-4.213	estExt_fgenesh1_pg.C_110050	-	
66	-16.866	estExt_fgenesh1_pg.C_110256	-	
67	-7.698	estExt_fgenesh1_pg.C_140200	-	
68	-8.48	estExt_fgenesh1_pm.C_010707	polysaccharide lyase family 8	Carbohydrate metabolism
69	-4.982	estExt_fgenesh1_pm.C_020300	-	
70	-4.289	estExt_fgenesh1_pm.C_020325	-	
71	-15.52	estExt_fgenesh1_pm.C_040243	Protein Serine/Threonine Kinase	Signal transduction
72	-6.317	estExt_fgenesh1_pm.C_060082	phosphatidylinositol-specific phospholipas	Lipid membrane (carbon and phosphate metabolia, second messangers)
73	-52.2	estExt_fgenesh1_pm.C_060196	-	chaperone
74	-4.404	estExt_fgenesh1_pm.C_060628	-	
75	-9.603	estExt_fgenesh1_pm.C_140068	smc-domain containing protein	Cell division / Chromosome-associated
76	-5.176	estExt_Genemark.C_010128	importin 9	Nuclear transport
77	-32.819	estExt_Genemark.C_010152	-	
78	-7.017	estExt_Genemark.C_020627	-	
79	-5.217	estExt_Genemark.C_030505	Shwachman-Bodian-Diamond containing protein	Ribosome 60S maturation
80	-9.774	estExt_Genemark.C_030681	Cytochrome P450	Oxidative degradation
81	-15.79	estExt_Genemark.C_030874	-	
82	-64.62	estExt_Genemark.C_040367	-	
83	-12.886	estExt_Genemark.C_050519	serine- threonine-rich membrane-anchored protein	Cell wall organisation /fruiting body
84	-28.202	estExt_Genemark.C_050782	-	
85	-8.8	estExt_Genemark.C_060269	-	
86	-13.508	estExt_Genemark.C_080422	g2/mitotic-specific cyclin cdc13	Cell cycle control
87	-4.361	estExt_Genemark.C_090019	Flotillin	Cell membrane functions (membrane microdomains ie. scaffold)
88	-12.598	estExt_Genemark.C_090496	-	
89	-8.626	estExt_Genemark.C_090563	-	
90	-9.702	estExt_Genemark.C_100076	Esterase/lipase	Lipid metabolism
91	-5.731	estExt_Genemark.C_120151	NADP+-dependent D-mannitol dehydrogenase	Carbohydrate metabolism, mannitol cycle?
92	-76.159	estExt_Genemark.C_120348	galactose mutarotase	Carbohydrate metabolism, Leloir pathway?
93	-10.477	estExt_Genemark.C_120361	-	
94	-5.869	estExt_Genewise1.C_010098	Predicted flavoprotein involved in K+ transport	Inorganic ion transport
95	-7.556	estExt_Genewise1.C_010405	-	

96	-7.607	estExt_Genewise1.C_022666	-	
97	-9.123	estExt_Genewise1.C_032716	-	
98	-57.427	estExt_Genewise1.C_032736	-	
99	-7.366	estExt_Genewise1.C_040784	Cyanase	N-metabolism
100	-14.339	estExt_Genewise1.C_041543	Tyrosine protein kinase	Signal transduction
101	-4.046	estExt_Genewise1.C_050271	maintenance of ploidy protein, mob2	Cell cycle control
102	-4.136	estExt_Genewise1.C_051727	dephospho-CoA kinase	Energy production, Lipid metabolism, Citric acid cycle
103	-4.631	estExt_Genewise1.C_090061	-	
104	-12.161	estExt_Genewise1.C_090192	-	
105	-10.424	estExt_Genewise1.C_090718	Pyridine nucleotide-disulphide oxidoreductase	Oxidation-reduction process
106	-12.775	estExt_Genewise1.C_111398	RNA polymerase III	Non-translated RNA synthesis
107	-27.82	estExt_Genewise1.C_120772	-	
108	-16.021	estExt_Genewise1Plus.C_011290	-	
109	-17.214	estExt_Genewise1Plus.C_020036	Protein kinase	Signal transduction
110	-6.195	estExt_Genewise1Plus.C_032683	-	
111	-8.842	estExt_Genewise1Plus.C_042002		
112	-31.486	estExt_Genewise1Plus.C_050332		
113	-7.175	estExt_Genewise1Plus.C_051139	Old yellow enzyme	Oxidation-reduction process, oxidative stress
114	-10.579	estExt_Genewise1Plus.C_070930	-	
115	-9.955	estExt_Genewise1Plus.C_071477	-	
116	-6.078	estExt_Genewise1Plus.C_080388	-	
117	-5.248	estExt_Genewise1Plus.C_090364	-	
118	-13.191	estExt_Genewise1Plus.C_091304	-	RNA binding
119	-18.594	estExt_Genewise1Plus.C_110726	-	
120	-27.866	estExt_Genewise1Plus.C_130454	-	
121	-6.191	estExt_Genewise1Plus.C_130816	-	
122	-5.682	fgenesh1_kg.01_#_141_#_1529_1_CCOZ_CCPA_CCPB_CCPC_EXTA	-	
123	-20.446	fgenesh1_kg.01_#_29_#_4383_0_CCOZ3613.b1_CCOZ_CCPA_CCPB_CCPC_EXTA	-	
124	-5.249	fgenesh1_kg.01_#_430_#_1038_1_CCOZ_CCPA_CCPB_CCPC_EXTA	expansin family protein	Cell wall organisation or pathogenesis?
125	-6.115	fgenesh1_kg.01_#_554_#_0_0_A710D1_CCOZ_CCPA_CCPB_CCPC_EXTA	-	
126	-5.77	fgenesh1_kg.02_#_13_#_3656_0_CCOZ3079.b1_CCOZ_CCPA_CCPB_CCPC_EXTA	-	
127	-8.63	fgenesh1_kg.02_#_41_#_2763_1_CCOZ_CCPA_CCPB_CCPC_EXTA	-	
128	-10.179	fgenesh1_kg.03_#_323_#_776_1_CCOZ_CCPA_CCPB_CCPC_EXTA	-	
128	-34.857	fgenesh1_kg.05_#_100_#_4987_0_CCPB659.g1_CCOZ_CCPA_CCPB_CCPC_EXTA	-	
130	-6.497	fgenesh1_kg.05_#_517_#_0_0_CCPB3358.b1_CCOZ_CCPA_CCPB_CCPC_EXTA	GCN5-related N-acetyltransferase	Acetyl Coenzyme acetyltransferase
131	-16.388	fgenesh1_kg.06_#_248_#_1288_1_CCOZ_CCPA_CCPB_CCPC_EXTA	Haloacid dehalogenase-like hydrolases	Phosphoryl transfer reaction

132	-5.72	fgenesh1_kg.09_#_300_#_144896	Cytochrome P450 monooxygenase 97	Oxidative degradation
133	-7.319	fgenesh1_kg.11_#_193_#_1582_1_CCOZ_CCPA_CCPB_CCPC_EXTA	-	
134	-11.838	fgenesh1_kg.11_#_89_#_1931_1_CCOZ_CCPA_CCPB_CCPC_EXTA	serine- threonine-rich membrane-anchored protein	Cell wall organisation
135	-7.101	fgenesh1_kg.12_#_200_#_214_0_CCPC7322.g1_CCOZ_CCPA_CCPB_CCPC_EXTA	-	
136	-191.707	fgenesh1_pg.01_#_57	N-acetylmuramoyl-L-alanine amidase	Cell wall organisation
137	-25.44	fgenesh1_pg.02_#_128	-	
138	-25.635	fgenesh1_pg.02_#_49	-	
139	-5.967	fgenesh1_pg.03_#_407	PaaI_thioesterase-like protein	Aromatic compounds catabolism
140	-9.357	fgenesh1_pg.03_#_710	-	
141	-4.415	fgenesh1_pg.04_#_163	-	
142	-4.492	fgenesh1_pg.04_#_178	Protein Serine/Threonine Kinase	Signal transduction
143	-4.327	fgenesh1_pg.04_#_396	Vta1 like	Endosome function
144	-110.09	fgenesh1_pg.05_#_548	-	
145	-17.798	fgenesh1_pg.06_#_23	-	
146	-138.59	fgenesh1_pg.07_#_77	-	
147	-8.374	fgenesh1_pg.08_#_277	-	
148	-6.048	fgenesh1_pg.11_#_150	NEK protein kinase	Cell cycle control
149	-4.951	fgenesh1_pg.12_#_109	-	
150	-6.344	fgenesh1_pg.12_#_119	E3 ubiquitin ligase	Protein degration
151	-42.204	fgenesh1_pg.12_#_301	Vta1 like	Endosome function
152	-5.692	fgenesh1_pg.13_#_75	E3 ubiquitin ligase	Protein degration
153	-4.467	fgenesh1_pg.14_#_41	-	
154	-4.023	fgenesh1_pm.01_#_143	-	
155	-4.364	fgenesh1_pm.01_#_270	Ngg1-interacting factor 3 protein NIF3L1	Transcription
156	-4.174	fgenesh1_pm.02_#_1070	Proteophosphoglycan	Cell wall organisation
157	-24.589	fgenesh1_pm.02_#_71	Transposase family tnp2	Transposition
158	-4.009	fgenesh1_pm.03_#_698	-	
159	-9.78	fgenesh1_pm.04_#_264	Lipase/esterase	Lipid metabolism
160	-10.146	fgenesh1_pm.05_#_54	-	
161	-26.834	fgenesh1_pm.05_#_593	G protein-coupled glucose receptor regulating Gpa2 ;Git3	Carbohydrate metabolism, adenylate cyclase activation
162	-7.844	fgenesh1_pm.06_#_17	-	
163	-5.89	fgenesh1_pm.06_#_393	Osmotically inducible protein C (OsmC)	Oxidative stress
164	-7.359	fgenesh1_pm.08_#_105	Serine/threonine protein kinase	Signal transduction
165	-13.959	fgenesh1_pm.08_#_201	-	
166	-6.715	fgenesh1_pm.08_#_409	Major royal jelly protein/ apalbumin	-
167	-4.386	fgenesh1_pm.08_#_597	-	
168	-21.932	fgenesh1_pm.09_#_234	Cupredoxin-like	Electron transfer
169	-4.285	fgenesh1_pm.09_#_449	Cytochrome P450	Oxidative degradation

170	-4.906	fgenesh1_pm.10_#_428	-	
171	-10.862	Genemark.1061_g	-	
172	-4.288	Genemark.1110_g	Inner centromere protein (INCENP)	Cell cycle control
173	-4.988	Genemark.1341_g	P-loop containing nucleoside triphosphate hydrolase protein	Energy production Protein conformation
174	-19.139	Genemark.1879_g	-	
175	-4.364	Genemark.2438_g	Fumarylacetoacetate (FAA) hydrolase	Energy production, Citric acid cycle, Tyrosine catabolic pathway
176	-21.935	Genemark.2646_g	-	
177	-257.534	Genemark.2840_g	-	
178	-41.703	Genemark.306_g	Double-stranded RNA binding motif protein	Unspecific dsRNA binding
179	-57.071	Genemark.3463_g	protein kinase	Signal transduction
180	-15.319	Genemark.3618_g	-	
181	-14.239	Genemark.4960_g	-	
182	-7.817	Genemark.5694_g	ribosomal-protein-alanine acetyltransferase	Translation
183	-11.55	Genemark.5920_g	Peptidase separin	Protein degration Cell cycle control
184	-36.6	Genemark.7118_g	-	
185	-4.526	Genemark.7491_g	Protein Kinase	Signal transduction
186	-5.226	gw1.01.2714.1	Protein Serine/Threonine Kinase cell division-related protein kinase 2	Signal transduction, Cell cycle control
187	-5.912	gw1.01.3727.1	Protein Kinase	Signal transduction
188	-4.797	gw1.02.2324.1	set and mynd domain-containing protein 3	Transcription
189	-6.462	gw1.02.3427.1	Thioesterase/thiol ester dehydrase-isomerase	Lipid metabolism
190	-12.268	gw1.08.1240.1	-	
191	-50.572	gw1.09.775.1	-	DNA binding, Transcription
192	-8.278	gw1.12.1443.1	HSP20-like chaperone	chaperon
193	-5.907	gw1.13.549.1	-	
194	-5.619	gw1.14.1148.1	-	
195	-113.379	gw1.14.918.1	-	
196	-16.428	Hetan1.e_gw1.1.404.1	E3 ubiquitin ligase	Protein degradation
197	-7.036	Hetan1.e_gw1.14.656.1	Sirtuin 5	Transciprion
198	-6.042	Hetan1.e_gw1.18.41.1	Clavaminate synthase-like protein	Citric acid cycle
199	-4.338	Hetan1.e_gw1.2.201.1	serine protease S53	Protein degradation

200	-4.467	Hetan1.e_gw1.4.1655.1	mitochondrial carrier protein	Energy production
201	-4.417	Hetan1.e_gw1.4.286.1	Six-hairpin glycosidase-like	Carbohydrate metabolism
202	-5.558	Hetan1.e_gw1.4.316.1	tartrate transporter	Carbohydrate metabolism
203	-5.804	Hetan1.e_gw1.5.100.1	glucose-methanol-choline oxidoreductase family. GMC oxidoreductase 7	Reduction process, Glycine, serine and threonine metabolism
204	-5.434	Hetan1.e_gw1.5.75.1	mfs monosaccharide	Carbohydrate metabolism
205	-18.244	Hetan1.e_gw1.6.1498.1	-	
206	-6.194	Hetan1.e_gw1.7.180.1	lycoside Hydrolase Family 79 protein b-glucuronidase	Carbohydrate metabolism
207	-6.696	Hetan1.e_gw1.7.656.1	C6 zinc binuclear cluster DNA-binding domain protein	Transcription
208	-38.103	Hetan1.e_gw1.8.123.1	beta-glucosidase	Carbohydrate metabolism, Cellulose degradation
209	-9.965	Hetan1.e_gw1.8.20.1	vegetative incompatibility protein HET-E-1	Vegetative incompatibility
210	-9.991	Hetan1.e_gw1.9.122.1	murein transglycosylase	Cell wall organisation
211	-11.06	Hetan1.e_gw1.9.93.1	tartrate transporter	Carbohydrate metabolism
212	-13.518	Hetan1.estExt_fgenesh2_pg.C_100028	Choline dehydrogenase 3	Reduction process, Glycine, serine and threonine metabolism
213	-19.212	Hetan1.estExt_fgenesh2_pg.C_170070	mannan endo-1,4-beta-mannosidase	Carbohydrate metabolism, mannitol cycle?
214	-5.448	Hetan1.estExt_fgenesh2_pm.C_100163	MFS general substrate transporter	Cell transport
215	-155.097	Hetan1.estExt_fgenesh2_pm.C_10627	Oligoxyloglucan reducing end-specific cellobiohydrolase	Carbohydrate metabolism, Cellulose degradation
216	-4.227	Hetan1.estExt_fgenesh2_pm.C_110093	Transketolase	Energy production, Carbohydrate metabolism, Glycolysis, Pentose phosphate pathway
217	-4.18	Hetan1.estExt_fgenesh2_pm.C_140112	-	
218	-6.798	Hetan1.estExt_fgenesh2_pm.C_30354	amidohydrolase	Metal-dependent hydrolase
219	-7.557	Hetan1.estExt_fgenesh2_pm.C_60162	mitochondrial chaperone bcs1	Chaperone, Energy production
220	-5.934	Hetan1.estExt_fgenesh2_pm.C_80170	Serine/threonine protein kinase	Signal transduction

221	-19.187	Hetan1.estExt_fgenesh2_pm.C_90173	Piwi-like protein	RNA related
222	-8.118	Hetan1.estExt_fgenesh2_pm.C_90257		
223	-53.985	Hetan1.estExt_fgenesh3_kg.C_110095	Aegerolysin-like protein	Fruiting body
224	-7.218	Hetan1.estExt_fgenesh3_kg.C_130051	Monocarboxylate transporter	Carbohydrate metabolism
225	-4.296	Hetan1.estExt_fgenesh3_kg.C_130113	-	
226	-238.507	Hetan1.estExt_fgenesh3_kg.C_140135	prolyl aminopeptidase	Protein degradation, citric acid cycle?
227	-4.687	Hetan1.estExt_fgenesh3_kg.C_30057	1,3(4)-beta-D-glucanases	Carbohydrate metabolism
228	-4.004	Hetan1.estExt_fgenesh3_kg.C_40133	]. 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	Amino acid metabolism, Methionin synthesis
229	-53.453	Hetan1.estExt_fgenesh3_kg.C_90130	hydrophobin 2 HAH	Cell wall organisation, conidia
230	-612.846	Hetan1.estExt_Genewise1.C_110899	[reducing end-acting] cellobiohydrolase	Carbohydrate metabolism, cellulose degradation, Pathogenesis
231	-67.691	Hetan1.estExt_Genewise1.C_140270	OAH1, oxaloacetate acetylhydrolase	Pathogenesis?
232	-10	Hetan1.estExt_Genewise1.C_41982	MFS monocarboxylate transporter Fucose or D-galactonate?	carbohydrate metabolism
233	-4.914	Hetan1.estExt_Genewise1.C_70859	-	
234	-7.318	Hetan1.estExt_Genewise1.C_80386	clp1	Transcription, Sex
235	-7.123	Hetan1.estExt_Genewise1Plus.C_120793	serine protease S53 Grifolisin	Fruiting bodies
236	-11.438	Hetan1.estExt_Genewise1Plus.C_130206	aryl-alcohol oxidase 11, aao11 (GMC oxidoreductase family)	Aromatic compounds catabolism
237	-4.064	Hetan1.estExt_Genewise1Plus.C_140577	cysteine desulfurase Molybdenum cofactor sulfurase	Nitrogen fixation
238	-239.723	Hetan1.estExt_Genewise1Plus.C_20287	cellulase CEL6B	Carbohydrate metabolism, cellulose degradation Pathogenesis
239	-4.126	Hetan1.estExt_Genewise1Plus.C_20298	Carboxylesterase	Lipid metabolism, Aromatic compounds catabolism
240	-5.102	Hetan1.estExt_Genewise1Plus.C_20997	-	transcription
241	-11.565	Hetan1.estExt_Genewise1Plus.C_21347	beta-glucosidase from glycoside hydrolase family GH3	Carbohydrate metabolism, cellulose degradation, Pathogenesis
242	-16.917	Hetan1.estExt_Genewise1Plus.C_30014	-	
243	-516.44	Hetan1.estExt_Genewise1Plus.C_30112	carotenoid ester lipase	Lipid

			precursor	metabolism, Aromatic compounds catabolism
244	-117.021	Hetan1.estExt_Genewise1Plus.C_31603	CEL4b mannanase	Carbohydrate metabolism, mannitol cycle?
245	-13.215	Hetan1.estExt_Genewise1Plus.C_41986	Choline dehydrogenase 6, chd6	Reduction process Glycine, serine and threonine metabolism
246	-7.121	Hetan1.estExt_Genewise1Plus.C_50658	glucan endo-1,3-beta-D-glucosidase	Cell wall organisation, carbohydrate metabolism
247	-7.965	Hetan1.estExt_Genewise1Plus.C_70854	cytochrome P450 monooxygenase 12, cyp12	Oxidative degradation
248	-538.916	Hetan1.estExt_Genewise1Plus.C_70955	cytochrome P450 monooxygenase 8 cyp8	Oxidative degradation
249	-21.521	Hetan1.estExt_Genewise1Plus.C_90100	Alpha-amylase	Carbohydrate metabolism, Starch, glycogen
250	-8.27	Hetan1.estExt_Genewise1Plus.C_90792	aryl-alcohol oxidase-like protein	Aromatic compounds catabolism
251	-14.617	Hetan1.EuGene10000524	high affinity methionine permease	Amino acid metabolism
252	-650.372	Hetan1.EuGene1000637	B2 mating type protein	Sex, pathogenesis
253	-10.818	Hetan1.EuGene1001300	-	
254	-4.454	Hetan1.EuGene12000113	Lipid-translocating Exporter	Lipid metabolism
255	-5.805	Hetan1.EuGene12000379	-	
256	-140.42	Hetan1.EuGene14000316	expansin-like protein	Cell wall organisation or pathogenesis?
257	-21.51	Hetan1.EuGene3000933	-	
258	-8.892	Hetan1.EuGene4000483	Cytochrome P450 monooxygenase 86, cpm86	
259	-13.264	Hetan1.EuGene4000639	zfp5	Transcription
260	-5.014	Hetan1.EuGene4000651	-	
261	-5.195	Hetan1.EuGene4000673	-	
262	-6.978	Hetan1.EuGene4001280	-	
263	-11.868	Hetan1.EuGene5000221	Heterokaryon incompatibility protein	Sex
264	-28.08	Hetan1.EuGene5000627	cytochrome P450 monooxygenase 33, cyp33	
265	-11.32	Hetan1.EuGene7000238	DNA repair metallo-beta-lactamase	DNA damage
266	-22.495	Hetan1.EuGene7000331	MFS sugar transporter	Carbohydrate metabolism
267	-5.095	Hetan1.EuGene8000624	-	

268	-85.737	Hetan1.EuGene9000498	Peptidase separin	Protein degradation, cell cycle control
269	-24.008	Hetan1.EuGene9000612	GMC oxidoreductase 11, gor11	Reduction process
270	-4.819	Hetan1.fgenesh2_pg.C_scaffold_10000052	-	
271	-36.422	Hetan1.fgenesh2_pg.C_scaffold_1000073	-	
272	-4.401	Hetan1.fgenesh2_pg.C_scaffold_1000112	-	
273	-5.118	Hetan1.fgenesh2_pg.C_scaffold_1000570	-	
274	-4.077	Hetan1.fgenesh2_pg.C_scaffold_13000220	d-4,5 unsaturated-glucuronyl hydrolase-like protein	Carbohydrate metabolism, pectin degradation
275	-6.442	Hetan1.fgenesh2_pg.C_scaffold_14000198	-	
276	-4.12	Hetan1.fgenesh2_pg.C_scaffold_15000146	Mitogen-activated protein kinase kinase kinase kinase (MAP4K)	Signal transduction
277	-9.345	Hetan1.fgenesh2_pg.C_scaffold_16000041	-	
278	-8.847	Hetan1.fgenesh2_pg.C_scaffold_18000039	-	Transcription
279	-8.585	Hetan1.fgenesh2_pg.C_scaffold_2000301	Carbohydrate Esterase Family 16 protein	Lipid matabolism
280	-62.583	Hetan1.fgenesh2_pg.C_scaffold_3000085	mediator of replication checkpoint protein 1	Cell cycle control
281	-9.807	Hetan1.fgenesh2_pg.C_scaffold_4000481	-	
282	-12.484	Hetan1.fgenesh2_pg.C_scaffold_7000396	-	
283	-4.696	Hetan1.fgenesh2_pm.C_scaffold_12000112	N-acetylglucosaminyl phosphatidylinositol de-N-acetylase	Cell membrane, Cell wall
284	-32.664	Hetan1.fgenesh2_pm.C_scaffold_12000213	hexose transporter	Carbohydrate metabolism
285	-6.244	Hetan1.fgenesh2_pm.C_scaffold_13000200	cation binding protein	
286	-4.759	Hetan1.fgenesh2_pm.C_scaffold_4000072	b-glucosidase, Glycoside Hydrolase Family 3 protein	Carbohydrate metabolism, cellulose degradation
287	-31.182	Hetan1.fgenesh2_pm.C_scaffold_4000773	cep3 - cellulose expressed protein 3, cep3	Carbohydrate metabolism, cellulose degradation
288	-35.332	Hetan1.fgenesh2_pm.C_scaffold_5000208	Cytochrome P450 CYP2 subfamily cyp61	
289	-5.046	Hetan1.fgenesh2_pm.C_scaffold_8000058	Sirtuin 5	Transciprion, sex
290	-4.28	Hetan1.fgenesh3_kg.2_#_382_#_4800_1_CCOZ_CCPA_CCPB_CCPC_EXTA	-	
291	-11.868	Hetan1.Genemark.10294_g	beta-mannosidase	Carbohydrate metabolism, hemicelluloses/galactomannan degradation mannitol cycle
292	-6.118	Hetan1.Genemark.10427_g	-	
293	-5.199	Hetan1.Genemark.1565_g	-	
294	-6.802	Hetan1.Genemark.1909_g	-	
295	-11.457	Hetan1.Genemark.2406_g	-	

296	-9.16	Hetan1.Genemark.2891_g	-	
297	-5.013	Hetan1.Genemark.3213_g	-	
298	-5.416	Hetan1.Genemark.4326_g	MFS monocarboxylate transporter	Carbohydrate metabolism
299	-11.21	Hetan1.Genemark.4817_g	beta-Keto acyl carrier protein reductase	Lipid metabolism, Fatty acid, Acetyl-CoA
300	-96.542	Hetan1.Genemark.4989_g	SMK1	Signal transduction, Transcription, DNA damage
301	-8.412	Hetan1.Genemark.5376_g	Peptidase M50B	Protein degradation
302	-47.953	Hetan1.Genemark.5475_g	-	
303	-4.951	Hetan1.Genemark.5539_g	-	
304	-5.027	Hetan1.Genemark.5746_g	nitrite reductase	N-metabolism ammonium
305	-6.445	Hetan1.Genemark.6435_g	protein-tyrosine phosphatase	Signal transduction, Cell cycle control
306	-28.659	Hetan1.Genemark.6603_g	-	
307	-11.186	Hetan1.Genemark.6966_g	lep7, lignin medium expressed protein 7	Transcription carbohydrate metabolism lignin
308	-8.906	Hetan1.Genemark.7973_g	-	
309	-9.483	Hetan1.Genemark.9238_g	lep4, lignin medium expressed protein 4	Carbohydrate metabolism, lignin
310	-4.003	Hetan1.Genemark.9640_g	-	
311	-163.391	Hetan1.gw1.1.1854.1	pectin methylesterase	Carbohydrate metabolism pectin
312	-8.003	Hetan1.gw1.12.56.1	N-acylaminoacyl-peptide hydrolase	Protein degradation
313	-13.733	Hetan1.gw1.9.332.1	-	
314	-14.952	Hetan1.Genemark.9236_g	-	-
315	-7.65	e_gw1.01.1649.1	six-hairpin glycosidase-like protein	Carbohydrate metabolism
316	-16.369	e_gw1.02.189.1	P-loop containing nucleoside triphosphate hydrolase protein	Nucleotide metabolism
317	-7.408	e_gw1.03.1713.1	-	-
318	-7.082	e_gw1.05.2398.1	-	-
319	-308.451	e_gw1.05.2603.1	DNA polymerase IV	DNA damage

320	-4.061	e_gw1.08.1769.1	archaerhodopsin-2	Ion channel / proton pump
321	-9.475	e_gw1.09.438.1	-	
322	-11.315	e_gw1.12.629.1	dephospho-CoA kinase	Lipid metabolism Mitochondria energy production
323	-36.813	e_gw1.13.1294.1	Peptidoglycan-binding LysM	Cell wall / membrane
324	-27.522	estExt_fgenesh1_kg.C_040359	Tyrosine protein kinase	Kinases (signal transduction)
325	-26.015	estExt_fgenesh1_kg.C_060034	-	
326	-16.993	estExt_fgenesh1_kg.C_110167	-	
327	-12.556	estExt_fgenesh1_kg.C_140228	rRNA 2'-O-methyltransferase Fibrillarin	Translation, Ribosomes RNA related
328	-26.629	estExt_fgenesh1_pg.C_020126	dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit-like	Post-translational protein modification, Protein glycosylation
329	-12.791	estExt_fgenesh1_pg.C_020714	RNA-directed RNA polymerase QDE-1	RNAi, RNA related
330	-9.236	estExt_fgenesh1_pg.C_090017	-	
331	-24.976	estExt_fgenesh1_pm.C_100390	-	
332	-17.445	estExt_fgenesh1_pm.C_120211	-	
333	-17.799	estExt_Genemark.C_070135	peptidase	Protein degradation
334	-10.187	estExt_Genemark.C_120379	FAD-binding monooxygenase	Redox
335	-14.345	estExt_Genewise1.C_020032	-	Cell wall / membrane
336	-26.139	estExt_Genewise1.C_091331	U1-like zinc finger	RNA related
337	-9.799	estExt_Genewise1.C_120256	rna helicase	RNA related
338	-8.428	estExt_Genewise1Plus.C_020116	-	-
339	-49.743	estExt_Genewise1Plus.C_051707	transporter	Unspecific cell transport
340	-6.258	estExt_Genewise1Plus.C_120696	Transaldolase	Pentose phosphate pathway à

				NADPH glycolysis, Carbohydrate metabolism, Nucleotide metabolism, Lipid metabolism, Amino acid metabolism
341	-15.522	fgenesh1_kg.01_#_66_#_1583_1_CCOZ_CCPA_CCPB_CCPC_EXTA	-	
342	-4.248	fgenesh1_kg.01_#_67_#_1583_0_CCPB920.b1_CCOZ_CCPA_CCPB_CCPC_EXTA	-	
343	-53.312	fgenesh1_kg.03_#_767_#_4245_1_CCOZ_CCPA_CCPB_CCPC_EXTA	-	
344	-57.23	fgenesh1_kg.05_#_424_#_0_0_CCOZ4875.b1_CCOZ_CCPA_CCPB_CCPC_EXTA	-	
345	-4.104	fgenesh1_kg.06_#_109_#_5379_1_CCOZ_CCPA_CCPB_CCPC_EXTA	chaperon	Chaperons
346	-15.86	fgenesh1_kg.10_#_5_#_4549_1_CCOZ_CCPA_CCPB_CCPC_EXTA	-	
347	-380.579	fgenesh1_pg.06_#_536	-	
348	-15.668	fgenesh1_pg.13_#_262	-	
349	-12.494	fgenesh1_pg.14_#_240	-	
350	-22.61	fgenesh1_pm.03_#_82	AAA+ ATPase	-
351	-593.949	fgenesh1_pm.04_#_184	STE20-like serine/threonine kinase	Cell cycle control, Kinases (signal transduction)
352	-7.949	fgenesh1_pm.07_#_191	RIO1 atypical serine kinase	Cell cycle control, Kinases (signal transduction)
353	-11.16	fgenesh1_pm.08_#_371	peptidase	Protein degradation
354	-7.698	fgenesh1_pm.11_#_121	-	-
355	-9.647	fgenesh1_pm.12_#_40	histone-lysine n-methyltransferase ezh1-like	Transcription repression
356	-15.778	fgenesh1_pm.14_#_95	-	
357	-28.614	Genemark.1248_g	-	
358	-49.041	Genemark.2041_g	-	
359	-481.12	Genemark.2126_g	peptidase	Signal transduction, Protein degradation Increases aa uptake
360	-10.781	Genemark.33_g	-	
361	-9.005	Genemark.3357_g	-	
362	-7.329	Genemark.442_g	vacuolar protein sorting-associated protein VTA1	endosomal function

			homolog	
363	-5.739	Genemark.5072_g	-	
364	-4.623	Genemark.5850_g	-	
365	-7.158	Genemark.6565_g	12-oxophytodienoate reductase	Redox
366	-37.981	Genemark.7258_g	protein kinase	Kinases (signal transduction)
367	-202.249	Genemark.7960_g	-	
368	-6.115	Genemark.8378_g	-	RNA related
367	-8.914	Genemark.9061_g	-	
370	-10.368	gw1.03.1690.1	Protein kinase	Kinases (signal transduction)
371	-15.071	gw1.04.2473.1	Transcription factor of the Forkhead/HNF3 family	transcription
372	-9.523	gw1.08.1665.1	Cell division control protein 7-like Protein Serine/Threonine Kinase	Cell cycle control
373	-8.648	gw1.12.1340.1	alpha-dehydro-beta-deoxy-D-glucarate aldolase	Mitochondria energy production, Pyruvate is product
374	-4.974	Hetan1.e_gw1.10.91.1	Sugar/inositol transporter	Carbohydrate metabolism
375	-5.532	Hetan1.e_gw1.5.283.1	putative L-fuculose-phosphate aldolase (fucA)	Carbohydrate metabolism, Fructose and mannose metabolism
376	-33.381	Hetan1.e_gw1.7.418.1	kinase	Molecular kinase (not protein kinase)
377	-22.281	Hetan1.estExt_fgenesh2_pg.C_100320	phenol 2-monooxygenase	Detoxification, Aromatic compound metabolism
378	-6.481	Hetan1.estExt_fgenesh2_pm.C_100194	-	
379	-17.843	Hetan1.estExt_fgenesh3_kg.C_10018	-	
380	-7.659	Hetan1.estExt_fgenesh3_kg.C_100192	MFS glucose transporter	Carbohydrate metabolism, Glucose
381	-11.814	Hetan1.estExt_fgenesh3_kg.C_110064	MFS glucose transporter	Carbohydrate metabolism, Glucose
382	-14.828	Hetan1.estExt_fgenesh3_kg.C_110205	lignin medium expressed protein 12, lep12	Carbohydrate metabolism, lignin
384	-4.547	Hetan1.estExt_fgenesh3_kg.C_60112	-	
385	-47.113	Hetan1.estExt_Genewise1Plus.C_100341	alpha/beta hydrolase fold	Redox
386	-19.347	Hetan1.estExt_Genewise1Plus.C_100682	MFS glucose transporter	Carbohydrate metabolism, Glucose
387	-1388.277	Hetan1.EuGene1000636	HD1 homeodomain transcription factor, mating type protein	Sex, Transcription
388	-6.796	Hetan1.EuGene13000249	-	

389	-5.576	Hetan1.EuGene5000616	cytochrome P450 monooxygenase 23, cyp23	Detoxification Redox
390	-23.692	Hetan1.EuGene8000195	-	
391	-17.958	Hetan1.EuGene9000385	Piwi-domain-containing protein	RNA related
392	-11.565	Hetan1.fgenesh2_pg.C_scaffold_13000145	Formin homology protein	Cell cycle control
393	-12.73	Hetan1.fgenesh2_pg.C_scaffold_8000178	-	
394	-8.111	Hetan1.fgenesh2_pm.C_scaffold_16000017	2OG-Fe(II) oxygenase family protein	Redox
395	-73.271	Hetan1.fgenesh3_kg.4_#_519_#_4514_0_CCOZ805.b1_CCOZ_CCPA_CCPB_CCPC_EXTA	-	
396	-16.313	Hetan1.Genemark.1190_g	Cytochrome P450 monooxygenase 115	Detoxification Redox
397	-37.315	Hetan1.Genemark.1932_g		
398	-15.081	Hetan1.Genemark.2637_g	-	
399	-5.735	Hetan1.Genemark.293_g	-	
400	-16.625	Hetan1.Genemark.48_g	-	
401	-41.979	Hetan1.Genemark.4888_g	cytochrome P450 monooxygenase 1, cyp1	Detoxification Redox
402	-5.798	Hetan1.Genemark.6765_g	NTPase-like protein	-
403	-7.02	Hetan1.Genemark.6963_g	lignin expressed protein - lep1	Carbohydrate metabolism, lignin
404	-7.357	Hetan1.Genemark.7152_g	-	
405	-7.212	Hetan1.Genemark.7431_g	-	
406	-21.091	Hetan1.Genemark.8356_g	Aldo/keto reductase	Redox
407	-11.005	Hetan1.Genemark.8846_g	beta-xylosidase	Carbohydrate metabolism, Hemicellulose
408	-23.658	Hetan1.gw1.11.527.1	HMG-box transcription factor SOX5	Transcription
409	-11.802	Hetan1.gw1.11.531.1		
410	4.697	e_gw1.01.2177.1	terpenoid synthase	Lipid metabolism, Sterol synthesis, Cell membrane
411	9.203	e_gw1.01.2627.1	hydrolase	-
412	4.781	e_gw1.01.2919.1		
413	4.806	e_gw1.02.2634.1	Chorismase synthase	Amino acid metabolism, Aromatic compounds synthesis, Shikimate acid pathway
414	8.413	e_gw1.02.3296.1	cytochrome c oxidase copper chaperone	Chaperone, Mitochondria, Energy production
415	5.813	e_gw1.02.3483.1	Adenylate kinase	Energy production, AMP amount
416	4.212	e_gw1.04.1139.1	Receptor Protein Tyrosine Kinase	Signal transduction
417	5.479	e_gw1.04.2235.1	delta7-sterol-C-5-desaturase	Lipid metabolism, Ergosterol biosynthesis, Cell membrane
418	16.619	e_gw1.04.2611.1	Taurine catabolism	Sulphite

			dioxygenase TauD	metabolia, Indicative of absence of sulfate
419	7.699	e_gw1.05.1967.1	3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase	Lipid metabolism, Shikimate pathway
420	9.6	e_gw1.05.2261.1	-	
421	4.269	e_gw1.06.1825.1	Histone deacetylase	Transcription, Cell cycle control
422	14.457	e_gw1.06.412.1	phenol 2-monooxygenase	aromatic compounds catabolism
423	6.482	e_gw1.06.495.1	-	
424	7.637	e_gw1.08.1568.1	squalene epoxidase	Sterol synthesis
425	19.405	e_gw1.09.1227.1	alpha/beta-hydrolase	-
426	14.231	e_gw1.10.853.1	small heat-shock protein Hsp26/Hsp42	Chaperone
427	140.549	e_gw1.11.1529.1	-	
428	73.167	e_gw1.11.1662.1	-	
429	4.012	e_gw1.11.404.1	Glycosyl hydrolase family 43	Carbohydrate metabolism
430	8.468	e_gw1.13.1032.1	Pentafunctional AroM protein	Amino acid metabolism, Aromatic compounds synthesis, Shikimate acid pathway
431	13.576	e_gw1.13.1308.1	-	
432	6.156	e_gw1.13.638.1	-	
433	6.891	e_gw1.14.1091.1	-	Oxidation-reduction process
434	11.456	e_gw1.14.1135.1	-	
435	8.46	estExt_fgenesh1_kg.C_010315	Protoglobin	Oxygen sensor?
436	132.879	estExt_fgenesh1_kg.C_010505	short-chain alcohol dehydrogenase	Oxidation-reduction process
437	4.116	estExt_fgenesh1_kg.C_030424	fatty acid elongase 3-ketoacyl-CoA synthase 1 domain protein	Lipid metabolism
438	10.44	estExt_fgenesh1_kg.C_030713	D-lactaldehyde dehydrogenase	Fermentation, Pyruvate metabolism
439	5.982	estExt_fgenesh1_kg.C_040495	Galactokinase	Carbohydrate metabolism, Leloir pathway
440	5.292	estExt_fgenesh1_kg.C_080387	-	
441	41.545	estExt_fgenesh1_kg.C_080388	-	
442	30.521	estExt_fgenesh1_kg.C_100061	short-chain alcohol dehydrogenases	Oxidation-reduction process
443	17.521	estExt_fgenesh1_kg.C_110012	-	
444	7.536	estExt_fgenesh1_kg.C_130044	-	
445	5.89	estExt_fgenesh1_pg.C_030798	-	
446	16.528	estExt_fgenesh1_pg.C_040344	IucA/IucC Siderophore synthetase component	Metal metabolism
447	4.95	estExt_fgenesh1_pg.C_090021	metacaspase	Programmed cell death
448	5.554	estExt_fgenesh1_pg.C_110327	Homeodomain-containing transcription factor	Transcription

449	6.214	estExt_fgenesh1_pg.C_140172	DNA polymerase IV (family X)	DNA damage
450	4.042	estExt_fgenesh1_pm.C_011095	golgin	Golgi function
451	9.856	estExt_fgenesh1_pm.C_030160	homoserine o-acetyltransferase	Amino acid metabolism, Methionin synthesis
452	4.935	estExt_fgenesh1_pm.C_030891	cytochrome b2	Energy prodution
453	7.824	estExt_fgenesh1_pm.C_040709	-	
454	7.309	estExt_fgenesh1_pm.C_080008	-	
455	11.036	estExt_fgenesh1_pm.C_080652	-	
456	22.542	estExt_fgenesh1_pm.C_090057	Aldo-keto reductases	oxidation-reduction process
457	4.209	estExt_fgenesh1_pm.C_090444	Hydroxymethylglutaryl-CoA synthase	Lipid metabolism, Sterol synthesis, Mevalonate pathway, terpenoid synthesis
458	17.498	estExt_fgenesh1_pm.C_110048	2-cysteine peroxiredoxin	Oxidative stress
459	29.034	estExt_Genemark.C_020382	-	
460	4.454	estExt_Genemark.C_040233	Separins?	Cell cycle control
461	12.314	estExt_Genemark.C_060605	major facilitator superfamily transporters	
462	4.4	estExt_Genemark.C_060709	-	
463	9.653	estExt_Genemark.C_080024	transcription factor	Transcription
464	4.491	estExt_Genemark.C_080155	methyltransferase	-
465	4.304	estExt_Genemark.C_080215	septation ring formation regulator EzrA -like	Cell cycle regulation, Negative regulation of septation
466	4.897	estExt_Genemark.C_110407	phospholipase D	Lipid metabolism, Cell membrane, Signal transduction, Endosome function
467	6.348	estExt_Genemark.C_120043	-	
468	5.156	estExt_Genemark.C_120355	cytochrome b2	Energy prodution
469	4.163	estExt_Genewise1.C_031030	Glutamine synthetase	Amino acid metabolism
470	4.111	estExt_Genewise1.C_080549	receptor-activated Ca2+-permeable cation channel	Ion metabolism
471	4.223	estExt_Genewise1.C_081179	sterol o-acyltransferase	Lipid metabolism, Cell cycle control, Sporulation, Sex, Sterol metabolism
472	9.502	estExt_Genewise1.C_140929	-	
473	14.848	estExt_Genewise1Plus.C_010240	UDP-glucose 4-epimerase	Carbohydrate metabolism Leloir pathway
474	6.91	estExt_Genewise1Plus.C_010621	-	
475	8.165	estExt_Genewise1Plus.C_012733	alpha-ketoglutarate-dependent sulfonate dioxygenase	Sulphite metabolia
476	10.039	estExt_Genewise1Plus.C_012758	Carbonic anhydrases	Carbon fixation

477	44.682	estExt_Genewise1Plus.C_021169		
478	4.843	estExt_Genewise1Plus.C_021367	Galactose-1-phosphate uridylyltransferase	Carbohydrate metabolism, Leloir pathway
479	4.835	estExt_Genewise1Plus.C_022322	cupredoxin	Electron transfer
480	4.797	estExt_Genewise1Plus.C_030660	-	
481	5.29	estExt_Genewise1Plus.C_031102	-	
482	4.313	estExt_Genewise1Plus.C_040229	cep5 cellulose medium expressed protein 5 Aminoglycoside 3'-phosphotransferase	Carbohydrate metabolism Small molecule inactivation
483	16.885	estExt_Genewise1Plus.C_040941	NAD dependent epimerase/dehydratase 1 Nucleoside-diphosphate-sugar epimerase	Carbohydrate metabolism
484	5.13	estExt_Genewise1Plus.C_060199	phenol 2-monooxygenase	Aromatic compounds catabolism
485	6.679	estExt_Genewise1Plus.C_061412	Shikimate 5-dehydrogenase	Carbohydrate metabolism shikimate acid pathway
486	4.359	estExt_Genewise1Plus.C_071035	Regulatory protein MLP and related LIM proteins	Signal transduction
487	4.597	estExt_Genewise1Plus.C_071244	Subunit 21 of Mediator complex	Transcription
488	9.118	estExt_Genewise1Plus.C_080415	-	
489	4.985	estExt_Genewise1Plus.C_080577	ubiquinone biosynthesis hydroxylase family protein	Energy production, Electron transfer, Mitochondria, Mevalonate pathway
490	4.42	estExt_Genewise1Plus.C_081191	DOPA 4,5-dioxygenase	oxidative stress? Carbohydrate metabolism?
491	4.7	estExt_Genewise1Plus.C_110025		
492	162.423	estExt_Genewise1Plus.C_110307	pentachlorophenol 4-monooxygenase	aromatic compounds catabolism Small molecule inactivation
493	5.697	estExt_Genewise1Plus.C_110862	glucooligosaccharide oxidase	Carbohydrate metabolism
494	9.297	estExt_Genewise1Plus.C_110926	Aldo/keto reductase	Oxidation-reduction process
495	27.853	estExt_Genewise1Plus.C_120304	3-oxoacyl-[acyl-carrier-protein] reductase	Lipid metabolism Fatty acid synthesis
496	5.708	fgenesh1_kg.01_#_263_#_897_1_CCOZ_CCPA_CCPB_CCPC_EXTA	-	
497	4.109	fgenesh1_kg.01_#_652_#_3189_1_CCOZ_CCPA_CCPB_CCPC_EXTA	-	
498	4.245	fgenesh1_kg.02_#_311_#_1194_1_CCOZ_CCPA_CCPB_CCPC_EXTA	tetraspanin	Cell membrane processes
499	23.436	fgenesh1_kg.02_#_603_#_5185_0_CCPC4567.g1_CCOZ_CCPA_CCPB_CCPC_EXTA	-	
500	17.396	fgenesh1_kg.05_#_437_#_1624_1_CCOZ_	anthranilate	Amino acid

		CCPA_CCPB_CCPC_EXTA	phosphoribosyltransferase	metabolism
501	5.91	fgenesh1_kg.06_#_190_#_5273_0_CCPC6878.g1_CCOZ_CCPA_CCPB_CCPC_EXTA	-	
502	5.749	fgenesh1_kg.06_#_340_#_4618_1_CCOZ_CCPA_CCPB_CCPC_EXTA	Trypsin-like cysteine/serine peptidase	Protein degradation
503	7.662	fgenesh1_kg.07_#_79_#_165_1_CCOZ_CCPA_CCPB_CCPC_EXTA	Aldo-keto reductases	Oxidation-reduction process
504	7.596	fgenesh1_kg.08_#_143_#_1871_1_CCOZ_CCPA_CCPB_CCPC_EXTA	-	
505	5.319	fgenesh1_kg.09_#_240_#_4283_1_CCOZ_CCPA_CCPB_CCPC_EXTA	alpha/beta-hydrolase	Oxidation-reduction process
506	33.827	fgenesh1_kg.09_#_97_#_266_1_CCOZ_CCPA_CCPB_CCPC_EXTA	Aldo/keto reductase	Oxidation-reduction process
507	8.114	fgenesh1_kg.13_#_101_#_165_1_CCOZ_CCPA_CCPB_CCPC_EXTA	Aldo/keto reductase	oxidation-reduction process
508	17.846	fgenesh1_pg.04_#_127	proton-transporting two-sector ATPase complex	Ion metabolism
509	4.205	fgenesh1_pg.04_#_342	Cation transport ATPase	Ion metabolism
510	56.723	fgenesh1_pg.05_#_630	NADH flavin oxidoreductase/NADH oxidase	Oxidation-reduction process
511	4.843	fgenesh1_pg.05_#_631	NADH flavin oxidoreductase/NADH oxidase	Oxidation-reduction process
512	22.604	fgenesh1_pg.06_#_13	G protein-coupled glucose receptor regulating Gpa2 ;Git3	Carbohydrate metabolism, Glucose detection via activation of adenylate cyclase
513	30.298	fgenesh1_pg.09_#_296	Dehydrogenase	
514	8.354	fgenesh1_pg.10_#_103	-	
515	7.113	fgenesh1_pg.11_#_188	O-acetylhomoserine aminocarboxypropyltransferase	Amino acid methabolism Cysteine and methionine
516	4.203	fgenesh1_pm.02_#_1189	Dehydrogenases	Oxidation-reduction process
517	4.879	fgenesh1_pm.02_#_779	Fructose-1,6-bisphosphatase	Carbohydrate metabolism, Gluconeogenesis pathway
518	6.664	fgenesh1_pm.02_#_982	LigT-like protein	Translation, tRNA
519	5.193	fgenesh1_pm.03_#_546	-	
520	4.745	fgenesh1_pm.03_#_933	-	
521	6.269	fgenesh1_pm.04_#_837	Indoleamine 2,3-dioxygenase	Amino acid metabolism, Tryptophan catabolism, Kynurenine pathway/NAD+ production/redox
522	21.063	fgenesh1_pm.08_#_137	cytochrome P450 monooxygenase 45	Oxidative degradation
523	4.286	fgenesh1_pm.10_#_534	isoamyl alcohol oxidase	Amino acid metabolism?
524	11.468	fgenesh1_pm.11_#_431	-	
525	58.735	fgenesh1_pm.12_#_243	delta9-fatty acid desaturase	Lipid metabolism

526	13.811	fgenesh1_pm.12_#_439	Isoprenylcysteine carboxyl methyltransferase	Cell membrane
527	4.677	Genemark.2177_g	Pyridine nucleotide-disulphide oxidoreductase	Oxidation-reduction process
528	5.74	Genemark.2322_g	-	
529	5.056	Genemark.298_g	-	
530	7.847	Genemark.3471_g	Citrate synthase	Energy production citric acid cycle
531	5.231	Genemark.3759_g	.	
532	13.604	Genemark.4614_g	alcohol dehydrogenase	Fermentation? detocification
533	4.944	Genemark.6168_g	trypsin-like serine and cysteine peptidase	Protein degradation
534	4.83	Genemark.6589_g	-	Transcription
535	8.508	Genemark.7893_g	Pyridine nucleotide-disulphide oxidoreductase	Oxidation-reduction process
536	5.583	Genemark.8651_g	-	
537	6.086	Genemark.9054_g	-	
538	23.224	gw1.01.3206.1	transcription factor	Transcription
539	5.963	gw1.02.2781.1	YeeE/YedE family protein	Sulphite metabolia Sulphur transport
540	4.162	gw1.02.3193.1	Cytochrome c oxidase subunit IV	Energy production mitochondria
541	4.003	gw1.03.3642.1	-	
542	10.6	gw1.04.2350.1	Alpha-beta-hydrolase	Oxidation-reduction process
543	5.072	gw1.06.2171.1	Transcription factor	Transcription
544	14.048	gw1.07.2121.1	-	
545	12.989	gw1.08.1470.1	-	
546	17.969	gw1.09.1495.1	-	
547	5.419	gw1.09.1578.1	-	
548	4.308	Hetan1.e_gw1.1.474.1	secreted ribonuclease T2	Detoxification defence
549	5.141	Hetan1.e_gw1.11.388.1	-	
550	4.295	Hetan1.e_gw1.13.668.1		Carbohydrate metabolism pentose phosphate pathway
551	11.484	Hetan1.e_gw1.14.153.1	lipase 2	Lipid metabolism
552	5.425	Hetan1.e_gw1.14.57.1	phospholipid/diacylglycerol acyltransferase	Lipid metabolism Sterol synthesis
553	8.365	Hetan1.e_gw1.2.1473.1	quinone oxidoreductase 6, qor6	Oxidation-reduction process, Aromatic compounds catabolism
554	4.239	Hetan1.e_gw1.4.254.1	pantothenate transporter, putative	Citric acid cycle, Coenzyme-A synthesis, Lipid metabolism
555	8.546	Hetan1.e_gw1.4.255.1	Amino acid transporter	Amino acid metabolism
556	4.203	Hetan1.e_gw1.4.367.1	Permease of the major facilitator superfamily	Cell transport
557	5.755	Hetan1.e_gw1.4.803.1	-	
558	5.114	Hetan1.e_gw1.7.75.1	4-hydroxybenzoate	Cell transport,

			transporter	Aromatic compounds catabolism
559	7.124	Hetan1.e_gw1.8.125.1	Cytochrome P450, cpm82	oxidative degradation
560	6.533	Hetan1.e_gw1.8.675.1	vacuolar DHA amino acid exporter	Amino acid metabolism, Amino acid storage
561	88.307	Hetan1.e_gw1.8.682.1	cytochrome P450 monooxygenase 4, cyp4	Oxidative degradation
562	8.794	Hetan1.e_gw1.9.799.1		
563	18.878	Hetan1.e_gw1.9.87.1	MFS monosaccharide transporter	Carbohydrate metabolism
564	72.483	Hetan1.estExt_fgenesh2_pm.C_10179	ABC transporter: heme ABC exporter	Metal metabolism
565	10.877	Hetan1.estExt_fgenesh2_pm.C_130083	quinone oxidoreductase 18, qor18	Oxidation-reduction process, Aromatic compounds catabolism
566	9.276	Hetan1.estExt_fgenesh2_pm.C_180013	oligopeptide transporter protein	Amino acid metabolism
567	7.882	Hetan1.estExt_fgenesh2_pm.C_30038	-	
568	11.212	Hetan1.estExt_fgenesh2_pm.C_30280	bifunctional sulfate adenylyltransferase subunit 1/adenylylsulfate kinase protein	Sulphite metabolia
569	4.592	Hetan1.estExt_fgenesh2_pm.C_40252	Alpha-amylase	Carbohydrate metabolism, Starch, glycogen
570	16.526	Hetan1.estExt_fgenesh2_pm.C_60042	Choline dehydrogenase 4, chd4	Reduction process, Glycine, serine and threonine metabolism
571	12.899	Hetan1.estExt_fgenesh2_pm.C_70066	fruit-body specific gene C	Sex, Fruiting body
572	11.21	Hetan1.estExt_fgenesh2_pm.C_70087	aryl-alcohol oxidase 12, aao12	Aromatic compounds catabolism
573	48.804	Hetan1.estExt_fgenesh2_pm.C_70196	methyltransferase	-
574	33.302	Hetan1.estExt_fgenesh2_pm.C_90223	-	
575	8.91	Hetan1.estExt_fgenesh3_kg.C_100170	Major facilitator superfamily	-
576	8.103	Hetan1.estExt_fgenesh3_kg.C_130022	-	
577	6.824	Hetan1.estExt_fgenesh3_kg.C_20469	epsin-like protein ent1 2	Cell membrane, Endocytosis
578	10.319	Hetan1.estExt_fgenesh3_kg.C_30165	MFS nicotinic acid transporter Tna1	Oxidation-reduction process, Energy production
579	5.923	Hetan1.estExt_fgenesh3_kg.C_30237	glyoxal oxidase 2, glox2	Oxidation-reduction process, Oxidative degradation, Lignin degradation
580	17.079	Hetan1.estExt_fgenesh3_kg.C_30410	quinone oxidoreductase 16, qor16	Oxidation-reduction process,

				Aromatic compounds catabolism
581	6.252	Hetan1.estExt_fgenesh3_kg.C_40221	Chloroperoxidase 2, cpx2	Oxidation-reduction process, Chlorination, Oxidative degradation
582	22.855	Hetan1.estExt_fgenesh3_kg.C_40528	cytochrome P450 monooxygenase 36, cyp36	Oxidative degradation
583	6.649	Hetan1.estExt_fgenesh3_kg.C_60126	-	
584	16.185	Hetan1.estExt_fgenesh3_kg.C_70052	highly expressed on lignin media	Carbohydrate metabolism, Lignin degradation
585	9.988	Hetan1.estExt_fgenesh3_kg.C_80054	Cytochrome P450 monooxygenase 100, cpm100	
586	13.308	Hetan1.estExt_fgenesh3_kg.C_80070	-	
587	4.209	Hetan1.estExt_fgenesh3_kg.C_80090	Ferric reductase	Ion metabolism, Metal metabolism, Oxidation-reduction process
588	11.799	Hetan1.estExt_fgenesh3_kg.C_90003	Glutathione S-transferase, GST1	detoxification
588	78.124	Hetan1.estExt_Genewise1.C_100265	hydrolase	-
590	86.362	Hetan1.estExt_Genewise1.C_120774	ferric reductase	Ion metabolism metal metabolism oxidation-reduction process
591	17.936	Hetan1.estExt_Genewise1.C_130249	sugar:H+ symporter	Carbohydrate metabolism
592	23.73	Hetan1.estExt_Genewise1.C_130445	aryl-alcohol oxidase 6, aao6	Aromatic compounds catabolism
593	35.495	Hetan1.estExt_Genewise1.C_21412	high affinity sulphate transporter 1	Sulphite metabolia
594	8.117	Hetan1.estExt_Genewise1.C_41556	Cytochrome oxidase assembly factor COX15	Energy production, mitochondria
595	16.066	Hetan1.estExt_Genewise1.C_60107	Secreted Lipase, class 3	Lipid metabolism
596	74.799	Hetan1.estExt_Genewise1.C_80752	aryl-alcohol oxidase 3, aao3	Aromatic compounds catabolism
597	14.879	Hetan1.estExt_Genewise1Plus.C_10610	phthalate transporter	Aromatic compounds catabolism
598	4.039	Hetan1.estExt_Genewise1Plus.C_130082	MFS polyamine transporter	N-metabolism
599	6.809	Hetan1.estExt_Genewise1Plus.C_160207	GMC oxidoreductase 8, gor8	Oxidation-reduction process Aromatic compounds catabolism
600	19.921	Hetan1.estExt_Genewise1Plus.C_170060	MFS quinate transporter, qui	Carbohydrate metabolism, Aromatic compounds catabolism

601	4.243	Hetan1.estExt_Genewise1Plus.C_21883	a-glucosidase, Glycoside Hydrolase Family 31 protein	Carbohydrate metabolism, Strach degradation
602	4.536	Hetan1.estExt_Genewise1Plus.C_21961	MFS polyamine transporter	N-metabolism
603	6.66	Hetan1.estExt_Genewise1Plus.C_30278	quinone oxidoreductase 5, qor5	Oxidation-reduction process, Aromatic compounds catabolism
604	7.61	Hetan1.estExt_Genewise1Plus.C_31727	endochitinase	Cell wall
605	4.789	Hetan1.estExt_Genewise1Plus.C_40163	Secreted serine protease S53	Protein degradation
606	10.045	Hetan1.estExt_Genewise1Plus.C_41737	MFS drug/polyamine transporter	N-metabolism
607	6.435	Hetan1.estExt_Genewise1Plus.C_60912	Mitochondrial carrier protein MRS3/4	Energy production, Mitochondria, Metal metabolism, Iron transfer
608	35.318	Hetan1.estExt_Genewise1Plus.C_61257	Catalase	Oxidative stress, Detoxification: H2O2
609	5.715	Hetan1.estExt_Genewise1Plus.C_70313	carboxylic acid transporter protein	Amino acid metabolism lipid metabolism
610	4.683	Hetan1.estExt_Genewise1Plus.C_70834	NADPH cytochrome P450 reductase (CYPOR1)	Oxidation-reduction process
611	5.365	Hetan1.estExt_Genewise1Plus.C_90814	ABC-transporter protein	Transport
612	8.597	Hetan1.EuGene10000525		
613	10.512	Hetan1.EuGene10000605	-	
614	5.54	Hetan1.EuGene1000294	-	
615	6.332	Hetan1.EuGene1000624	-	
616	6.859	Hetan1.EuGene1000671	alpha/beta-hydrolase	Oxidation-reduction process
617	4.498	Hetan1.EuGene1001337	-	
618	6.948	Hetan1.EuGene1001353	Beta-lactamase	Detoxification, Defence
619	4.232	Hetan1.EuGene14000174	N-acetyl-glucosamine-6-phosphate deacetylase	Carbohydrate metabolism, Cell wall
620	13.6	Hetan1.EuGene2000701	-	
621	4.569	Hetan1.EuGene2001183	Expansin	Cell wall
622	4.887	Hetan1.EuGene4000482	cytochrome P450 monooxygenase 88, cyp88	Oxidative degradation
623	5.638	Hetan1.EuGene8000110	long-chain fatty acid CoA synthetases	Lipid metabolism
624	4.438	Hetan1.EuGene8000406	Cytochrome P450 monooxygenase 92, cpm92	Oxidative degradation
625	5.129	Hetan1.fgenesh2_pg.C_scaffold_15000038	-	
626	7.028	Hetan1.fgenesh2_pg.C_scaffold_5000228	oxidoreductases	Oxidation-reduction process
627	11.312	Hetan1.fgenesh2_pg.C_scaffold_5000293	-	
628	4.778	Hetan1.fgenesh2_pg.C_scaffold_7000321	-	
629	7.076	Hetan1.fgenesh2_pm.C_scaffold_12000183	uridine permease Fui1	Nucleotide metabolism
630	13.003	Hetan1.fgenesh2_pm.C_scaffold_2000190	MFS amino acid permease	Amino acid

				metabolism
631	4.399	Hetan1.fgenesh2_pm.C_scaffold_3000337	Inosine-uridine nucleoside N-ribohydrolase	Nucleotide metabolism
632	10.409	Hetan1.fgenesh2_pm.C_scaffold_4000008	siderochrome-iron transporter Sit1	Metal metabolism
633	4.549	Hetan1.fgenesh2_pm.C_scaffold_4000675	-	
634	12.179	Hetan1.fgenesh2_pm.C_scaffold_9000210	3-ketoacyl-acyl carrier protein reductase	Lipid metabolism
635	23.235	Hetan1.fgenesh3_kg.13_#_160_#_3340_1_CCOZ_CCPA_CCPB_CCPC_EXTA	Glycoside Hydrolase Family 12 protein candidate endo-b-1,4-glucanase or xyloglucanase, gh12.3	Carbohydrate metabolism, Cellulose or hemicellulose degradation
636	6.732	Hetan1.fgenesh3_kg.8_#_108_#_5336_1_CCOZ_CCPA_CCPB_CCPC_EXTA	dehydrogenase	Oxidation-reduction process
637	4.849	Hetan1.fgenesh3_kg.8_#_121_#_2183_1_CCOZ_CCPA_CCPB_CCPC_EXTA	molybdopterin-biosynthesis enzyme	Oxidation-reduction process
638	6.592	Hetan1.Genemark.4297_g	Cytochrome P450 monooxygenase 76, cpm76	oxidative degradation
639	20.242	Hetan1.Genemark.4417_g	dioxygenases	Oxidation-reduction process
640	32.202	Hetan1.Genemark.4807_g	Choline dehydrogenase 7, chd7	Oxidation-reduction process
641	4.553	Hetan1.Genemark.696_g	Alpha/beta hydrolase	oxidation-reduction process
642	12.311	Hetan1.Genemark.73_g	The Major Facilitator Superfamily	Transport
643	5.283	Hetan1.Genemark.9730_g	dimethylaniline monooxygenase	Oxidation-reduction process, Aromatic compounds catabolism
644	52.332	Hetan1.gw1.14.303.1	-	
645	4.339	Hetan1.gw1.6.412.1	-	
646	7.195	Hetan1.YAI_gw1.12.856.1	quinone oxidoreductase 2, qor2	
647	158.37	estExt_Genemark.C_120425	Cytochrome P450 CYP4/CYP19/CYP26 subfamilies	Detoxification, Redox
648	8.148	estExt_Genewise1.C_012332	glutathione transferase	Detoxification
649	9.321	Hetan1.estExt_fgenesh2_pm.C_20683	quinone oxidoreductase 11, qor11	Redox
650	12.606	Hetan1.estExt_Genewise1.C_80167	ABC transporter	-
651	19.659	e_gw1.01.2810.1	nucleoporin-interacting protein NIC96	Nuclear transport
652	6.641	e_gw1.07.1277.1	-	
653	8.974	e_gw1.07.1789.1	Uroporphyrinogen III synthase UROS/HEM4	Inorganics metabolism, Haem synthesis
654	6.904	e_gw1.09.761.1	-	
655	7.237	e_gw1.09.92.1	-	
656	225.423	e_gw1.12.503.1	sorbitol dehydrogenase	Carbohydrate metabolism, Glucose to sorbitol to fructose
657	5.611	estExt_fgenesh1_kg.C_080207	-	
658	56.045	estExt_fgenesh1_pg.C_080141	-	

659	66.523	estExt_fgenesh1_pg.C_130285	-	
660	7.925	estExt_Genewise1.C_060510	cysteine synthase	Amino acid metabolism, Cysteine biosynthesis
661	871.124	estExt_Genewise1Plus.C_080637	-	DNA damage
662	5.954	fgenesh1_kg.07_#_10_#_4808_0_CCPB2375.b1_CCOZ_CCPA_CCPB_CCPC_EXTA	-	
663	65.946	fgenesh1_kg.07_#_94_#_0_0_A95E1_CCOZ_CCPA_CCPB_CCPC_EXTA	-	
664	18.614	fgenesh1_pg.06_#_410	-	
665	78.988	fgenesh1_pm.02_#_834	carbohydrate-binding module family 19	Carbohydrate metabolism, Chitin Cell wall / membrane
666	44.843	fgenesh1_pm.07_#_10	-	
667	10.95	fgenesh1_pm.12_#_318	short-chain dehydrogenase	Redox
668	61.373	fgenesh1_pm.12_#_408	-	
669	17.83	Genemark.1079_g	-	
670	5.643	gw1.07.642.1	-	
671	13.797	gw1.13.1244.1	tetraspanin family protein	Cell wall / membrane
672	4.708	Hetan1.estExt_Genewise1.C_60500	MFS glucose transporter	Carbohydrate metabolism, Glucose
673	20.138	Hetan1.estExt_Genewise1Plus.C_130459	aryl-alcohol oxidase 9, aao9	Redox Carbohydrate metabolism: production of hydrogen peroxidise to degrade lignin
674	13.514	Hetan1.estExt_Genewise1Plus.C_40642	RTA1-domain-containing protein	Detoxification
675	4.213	Hetan1.estExt_Genewise1Plus.C_60438	Dihydroorotate dehydrogenase 1, dhod1	Nucleotide metabolism
676	202.242	Hetan1.EuGene10000523	cytochrome P450 monooxygenase 20, cpm20	Detoxification, Redox
677	7.905	Hetan1.EuGene6000302	Thioesterase/thiol ester dehydrase-isomerase	Lipid metabolism
678	6.179	Hetan1.EuGene6000314	Lipase, class 3	Lipid metabolism
679	11.312	Hetan1.fgenesh2_pg.C_scaffold_5000293	-	
680	4.234	Hetan1.fgenesh2_pg.C_scaffold_5000294	-	
681	5.163	Hetan1.fgenesh2_pm.C_scaffold_5000139	mitochondrial tricarboxylate transporter	Mitochondria energy production
682	5.111	Hetan1.Genemark.5207_g	-	
683	10.105	Hetan1.Genemark.7627_g	-	

Table S3. Statististical data from the RNA-Seq and RT-qPCR analyses.

TG	Gene ID in *H. annosum* genome v.2.0 at JGI	RNA-Seq for *H. annosum*		RT-qPCR for *H. annosum* (94233 vs 94233/32D)		RT-qPCR for *H. parviporum* (RK15A* vs RK15A)	
		Standard deviation[1]		Relative expression level	Standard error[2]	Relative expression level	Standard error[2]
		94233	94233/32D				
1	fgenesh1_pm.02_#_834	802.453	6.129	30.743	2.599	30.910	20.910
2	Hetan1.estExt_Genewise1Plus.C_40642	12.025	0.751	7.345	1.074	3.342	0.623
3	gw1.13.1244.1	56.787	3.553	11.886	2.279	1.900	1.034
4	Hetan1.estExt_Genewise1Plus.C_130459	57.032	0.981	16.994	3.693	5.080	0.829
5	estExt_Genemark.C_120425	90.256	1.815	9.366	5.823	ND	ND
6	Hetan1.fgenesh2_pm.C_scaffold_2000190	12.242	0.615	9.410	1.472	3.480	0.685
7	e_gw1.13.1032.1	23.748	1.200	4.988	1.294	6.300	2.043
8	estExt_Genewise1Plus.C_010240	583.099	2.971	10.526	3.181	0.680	0.439
9	Genemark.3471_g	137.134	14.954	17.683	11.969	5.210	1.376
10	estExt_fgenesh1_pg.C_040344	9.521	0.22	21.899	6.577	ND	ND
11	Hetan1.estExt_Genewise1Plus.C_61257	165.231	1.308	22.783	4.451	4.500	1.275
12	Hetan1.estExt_fgenesh2_pm.C_70066	31.225	0.441	10.754	4.923	1.140	0.539
13	Hetan1.estExt_Genewise1Plus.C_100682	0.154	6.377	0.074	0.01	2.810	0.856
14	Hetan1.Genemark.6963_g	0.515	0.552	0.325	0.079	2.160	0.486
15	Hetan1.Genemark.8846_g	0.289	3.876	0.178	0.008	1.980	1.153
16	gw1.08.1665.1	0.240	0.176	1	0.512	9.990	3.150
17	fgenesh1_pm.04_#_184	0.020	1.915	-	-	0.924	0.153
18	estExt_fgenesh1_pg.C_020714	0.179	5.631	0.117	0.017	0.957	0.193
19	Hetan1.fgenesh2_pg.C_scaffold_13000145	1.047	5.356	0.053	0.005	ND	ND
20	Hetan1.EuGene9000385	0.692	2.505	0.003	0	0.356	0.055
21	Hetan1.EuGene1000636	0	1.300	-	-	ND	ND
22	gw1.04.2473.1	0.775	1.800	0.146	0.070	3.170	2.236
23	Hetan1.estExt_Genewise1.C_110899	1.813	832.734	0.005	0.001	231.00	86.476
24	e_gw1.01.3559.1	4.425	26.332	0.601	0.204	0.739	0.148
25	Hetan1.estExt_fgenesh3_kg.C_90130	100.488	1656.718	0.075	0.025	2.740	0.389
26	Hetan1.estExt_Genewise1Plus.C_70955	0.028	2.794	0.195	0.122	0.263	0.050
27	Hetan1.estExt_fgenesh2_pm.C_90173	0.419	4.721	0.092	0.021	0.249	0.052
28	Hetan1.EuGene4000639	2.037	3.562	0.202	0.075	0.541	0.093

[1] Standard deviations for the mean expression values reported in Table 1

[2] Standard errors were determined using REST version 2009 (Qiagen)