

## Supplementary Information

The individual gene expression profiles of GSE14734, GSE14735, GSE27941, GSE52922, GSE54542 and GSE69008. Top 250 differentially expressed genes were obtained using the GEO2R analysis tool (based on GEOquery and limma) with Benjamini & Hochberg FDR (P-value correction) with supplier provided annotations and log transformation auto detected value options. This document covers the individual gene expression profiles, Box whisker plot and a table with differentially expressed gene profile list and heat maps of differentially expressed genes of different datasets.

### **Figure-S1: Profile graphs of individual genes differentially expressed by *P. chrysosporium* in cellulose and hemicellulose degradation**

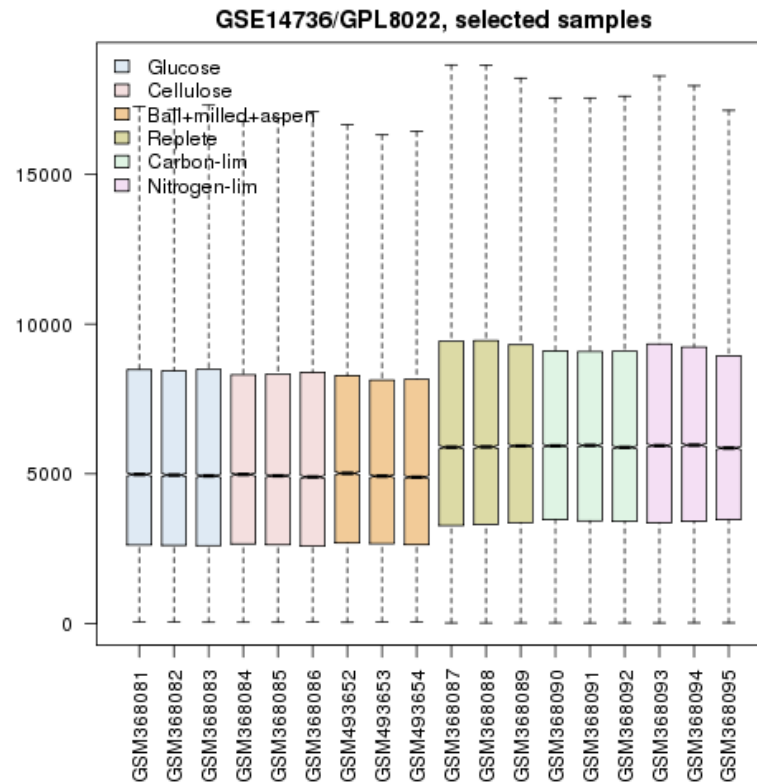
#### **GSE14736: (Super series consists of the following subseries)**

- **GSE14734: Cellulose induced regulation of *Phanerochaete chrysosporium* genes**

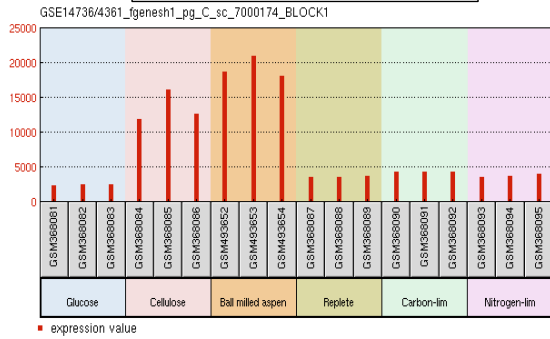
In order to study the extracellular proteins secreted by *P. chrysosporium* under standard cellulolytic conditions Wymelenberg et al (2009) have performed a whole transcriptome study. The gene expression studies have confirmed the significance of carbohydrate active enzymes and supported the function of many novel proteins involved in lignocellulose degradation.

- **GSE14735: Nutrient limitation-induced regulation of *Phanerochaete chrysosporium* genes**

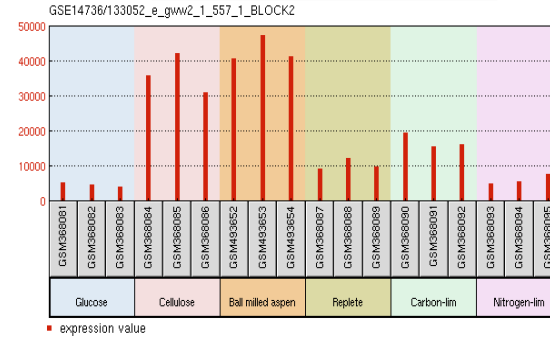
Wymelenberg et al (2009) have studied the extracellular protein products of *P. chrysosporium* grown under nutrient limited conditions. Studies have confirmed the expression of several lignocellulose degrading enzymes and also reinforced the role of novel proteins.



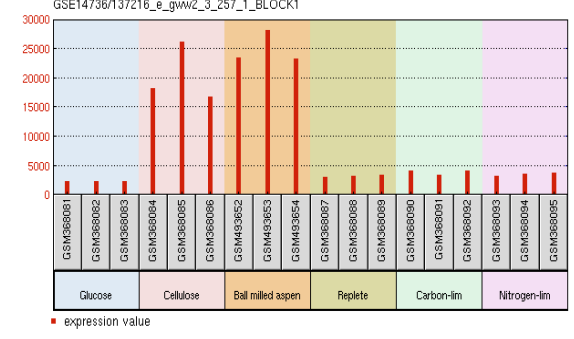
### Glycoside hydrolase 5



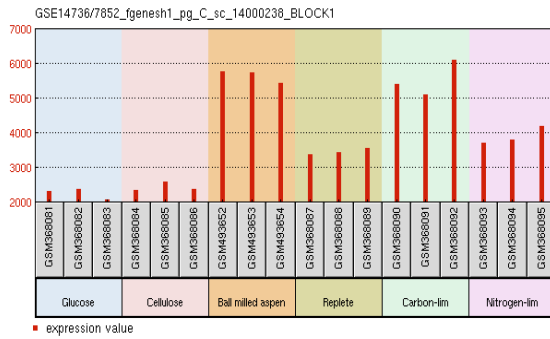
### Glycoside hydrolase 6



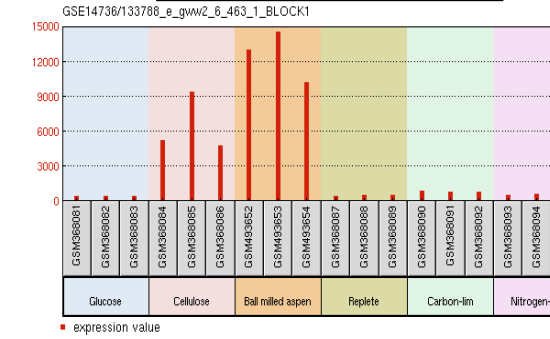
### Glycoside hydrolase 7



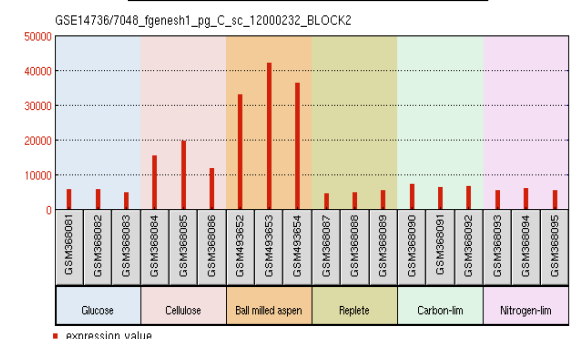
### Glycoside hydrolase 10



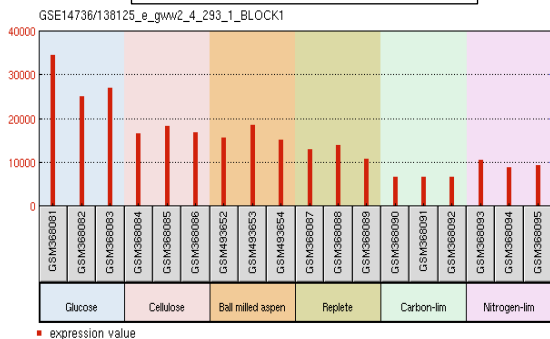
### Glycoside hydrolase 11



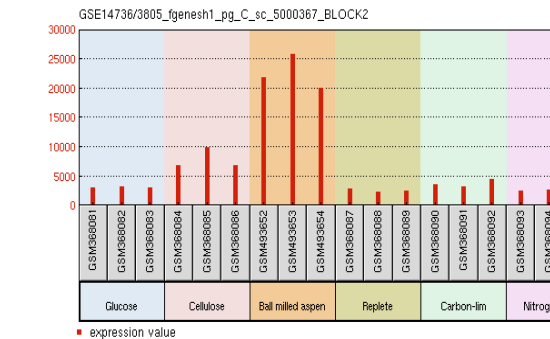
### Glycoside hydrolase 12



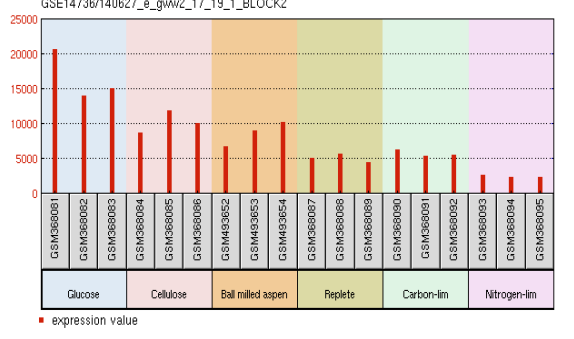
### Glycoside hydrolase 17



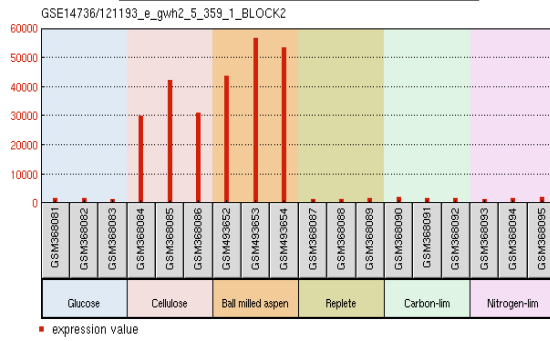
### Glycoside hydrolase 28



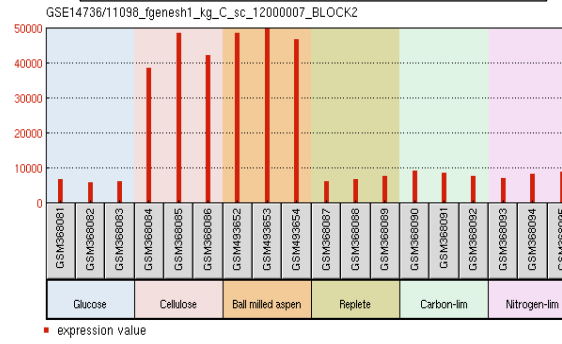
### Glycoside hydrolase 37



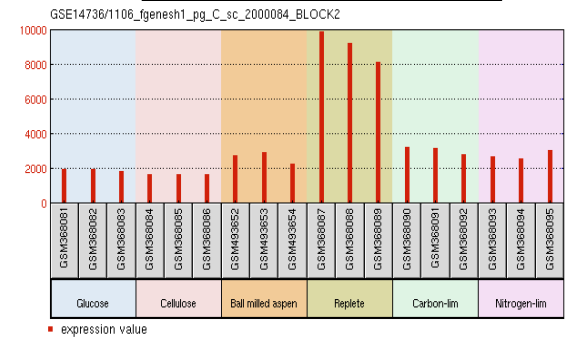
## Glycoside hydrolase 61



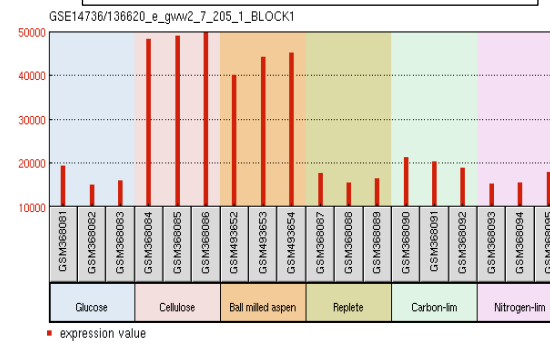
## Glycosyl hydrolase BNR repeat



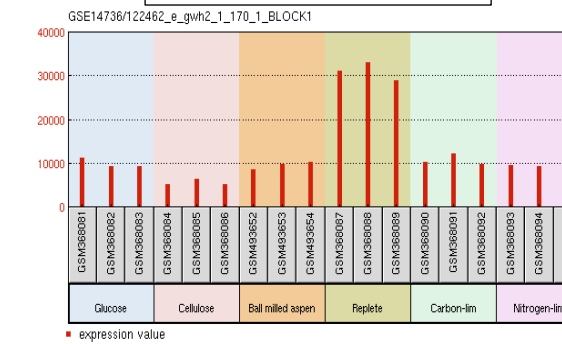
## Glycosyl hydrolase 88



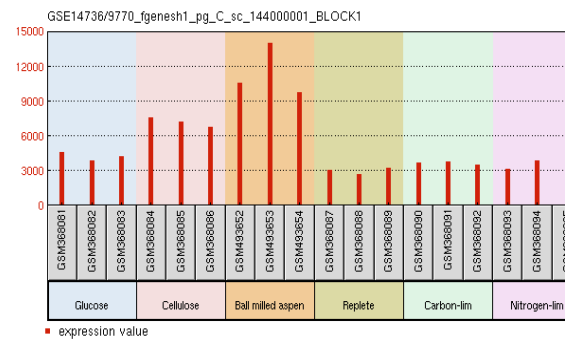
## Sugar Transporter superfamily



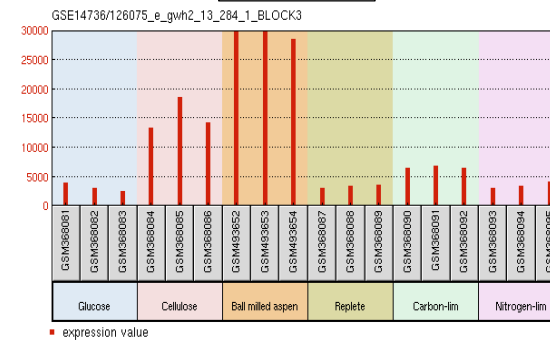
## Glycosyl transferase 1



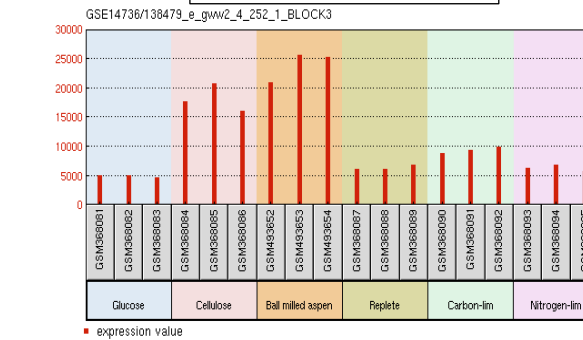
## GMC oxidoreductase



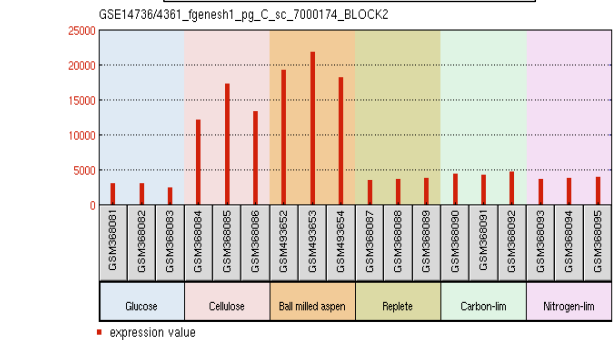
## Esterase



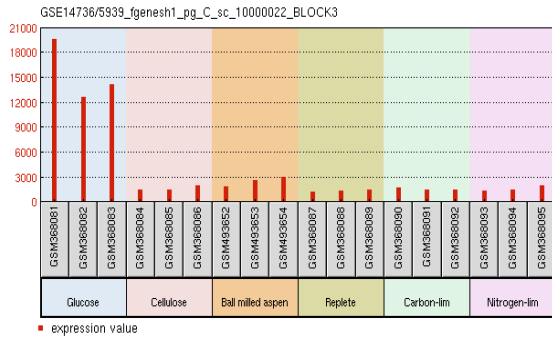
## Aldose-1-epimerase



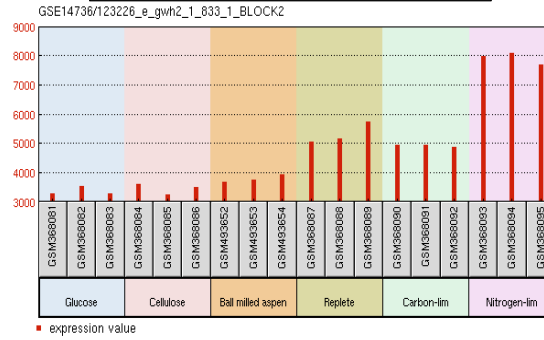
## Cellulose binding region



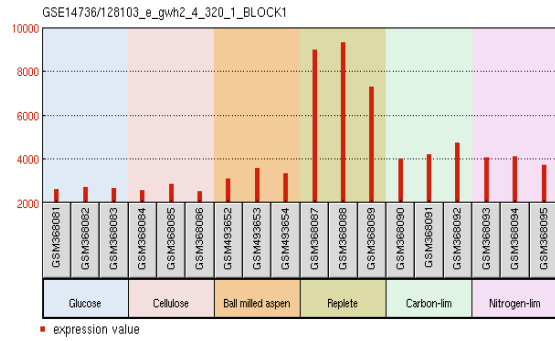
### Beta-ketoacyl synthase



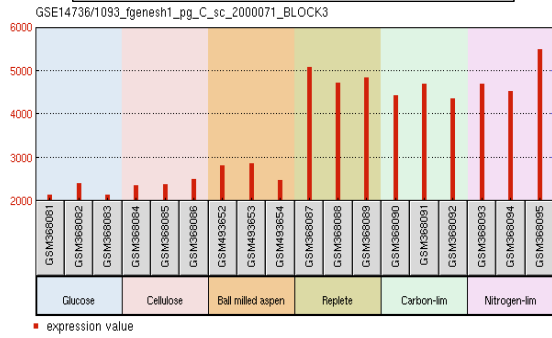
### Polysaccharide deacetylase



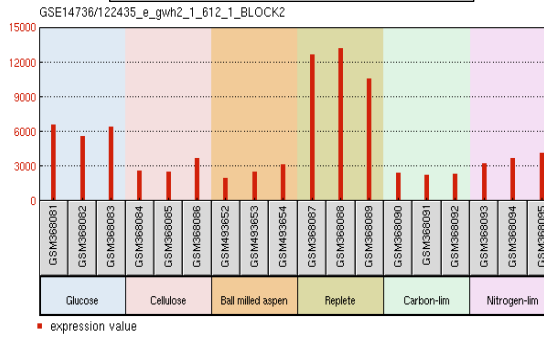
### Aldo/keto reductase



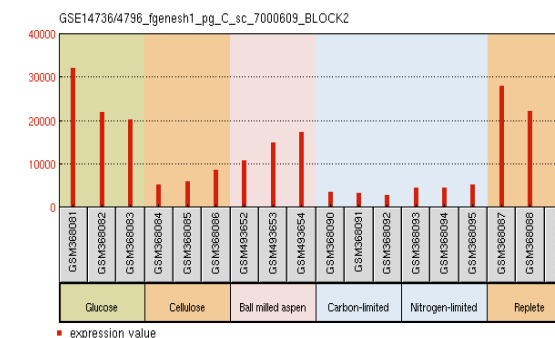
### Glucose ribitol dehydrogenase



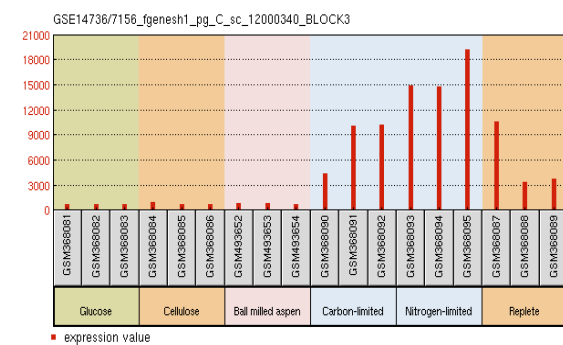
### Phosphoglycerate kinase



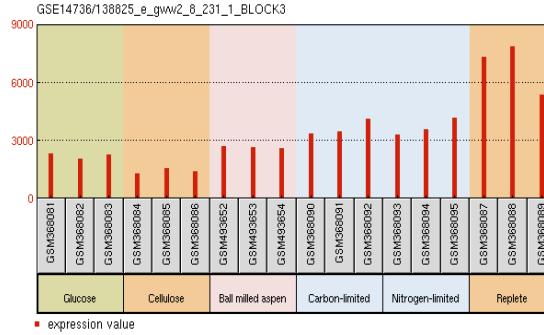
### Zn alcohol dehydrogenase



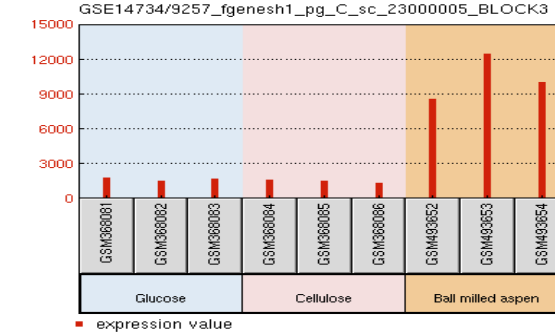
### Isocitrate lyase and phosphorymutase



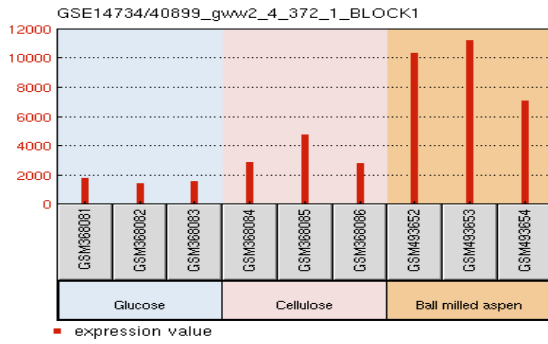
### Iron alcohol dehydrogenase



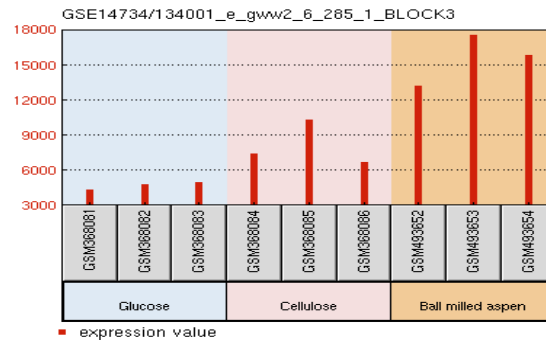
### Glycoside hydrolase 3



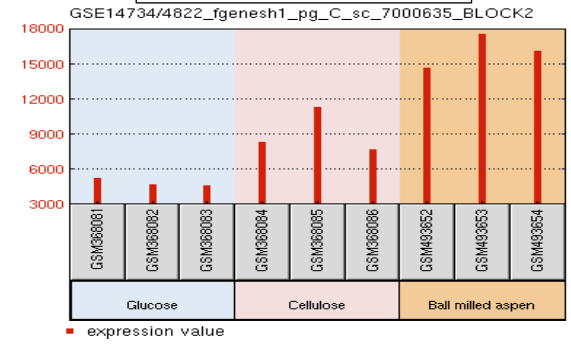
### Glycoside hydrolase 18



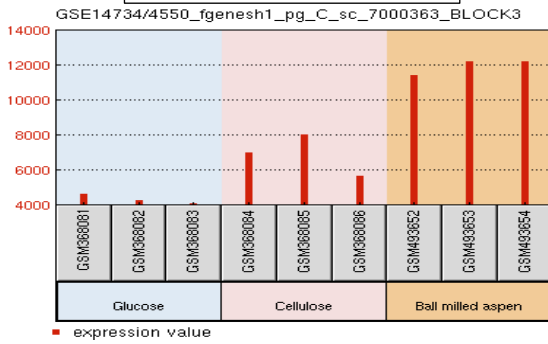
### Glycoside hydrolase 27



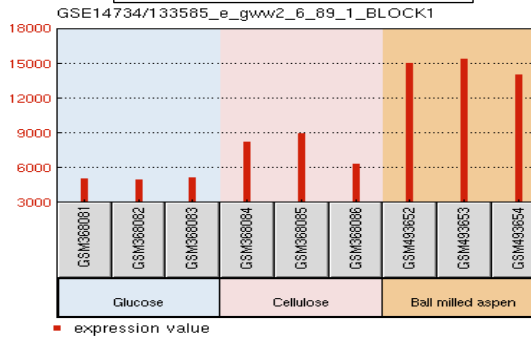
### Glycoside hydrolase 43



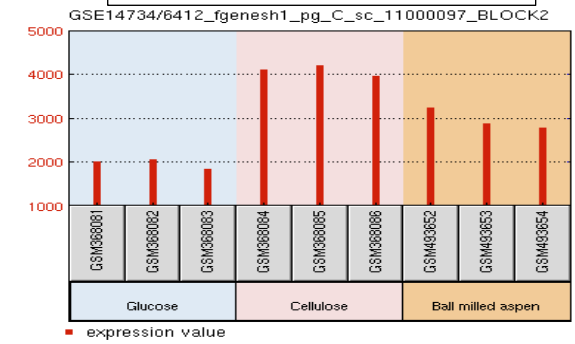
### Glycoside hydrolase 47



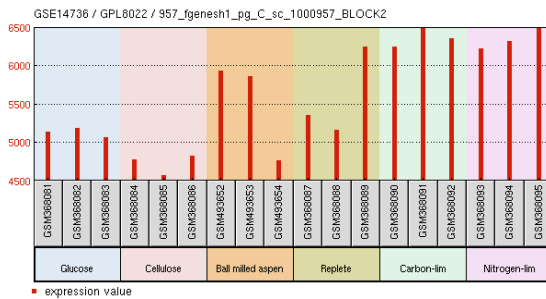
### Alpha-1,2-mannosidase



### Carbohydrate binding domain

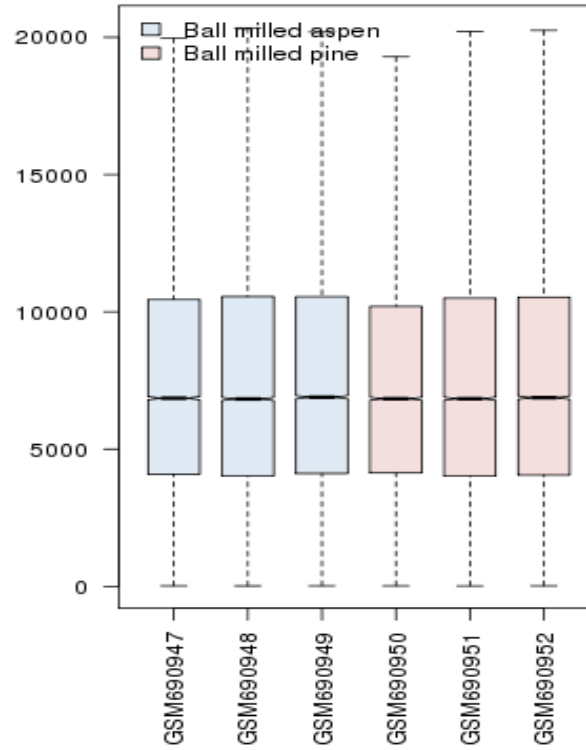


### Polysaccharide lyase 8

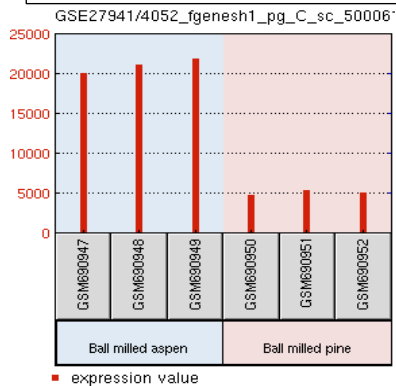


**GSE27941:** Wymelenberg et al (2011) have conducted transcriptome study to analyze the gene expression patterns of *Postia placenta* and *Phanerochaete chrysosporium* colonized on (aspen) *Populus grandidentata* and (pine) *Pinus strobus*. Results have showed that transcriptome of these fungi are significantly influenced by wood species, reflecting their basic wood decaying properties.

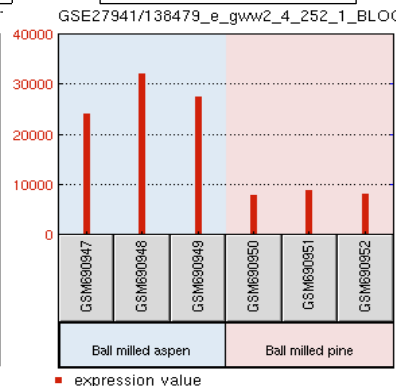
**GSE27941/GPL8022, selected samples:**



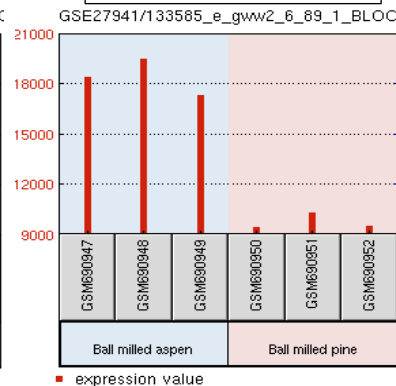
**Carbohydrate binding family V**



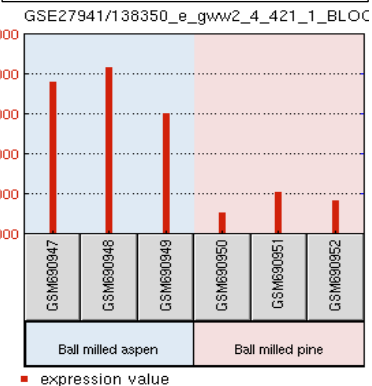
**Aldose 1-epimerase**



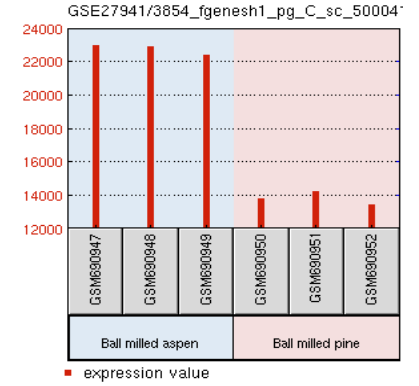
**Alpha-1,2-mannosidase**



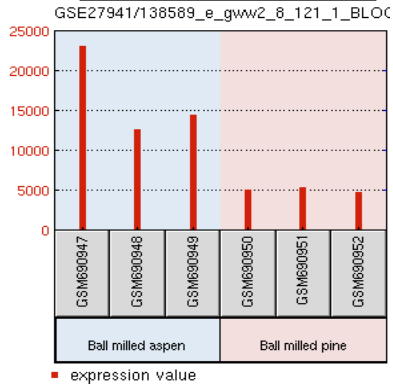
**Sugar transporter superfamily**



**Aldehyde dehydrogenase**



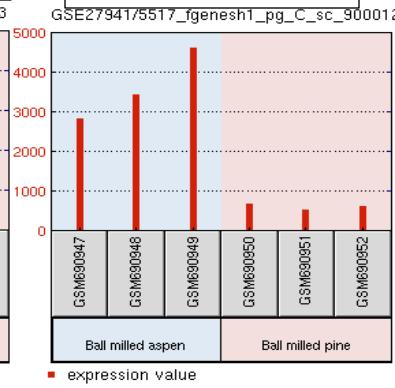
### Pyruvate decarboxylase



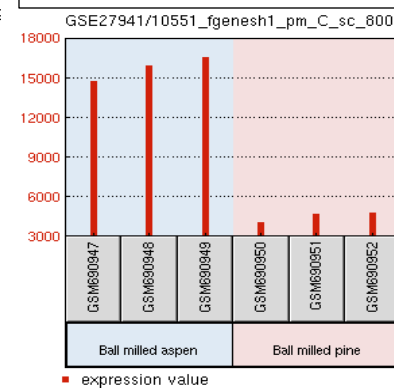
### Carbohydrate kinase, FGGY



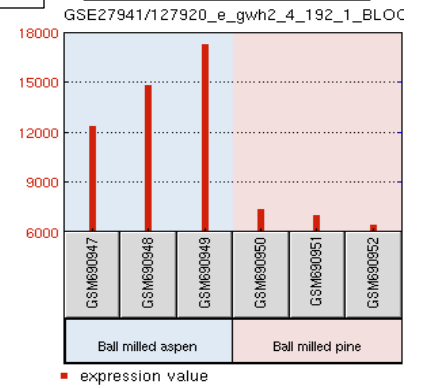
### Barwin endoglucanase



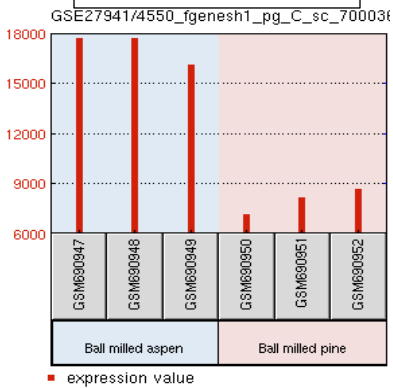
### Isocitrate lyase/ phosphorylmutase



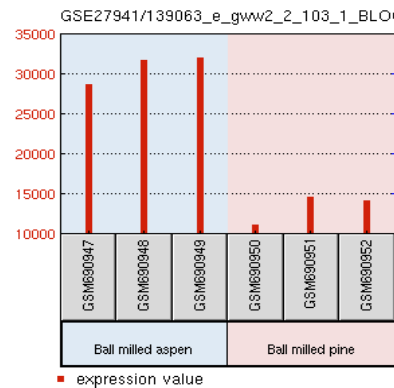
### Glycoside hydrolase 1



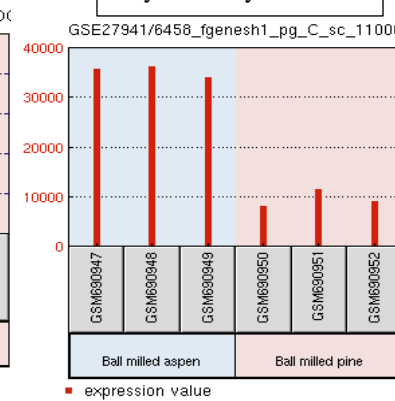
### Glycoside hydrolase 2



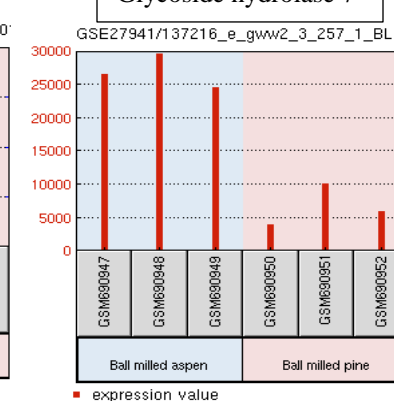
### Glycoside hydrolase 3



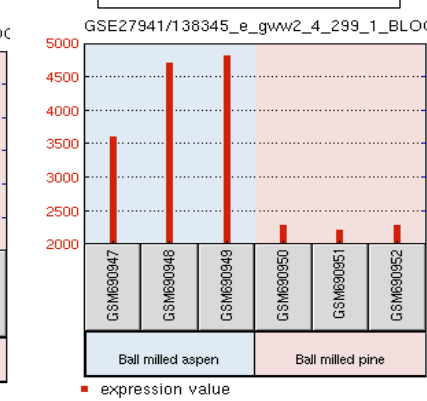
### Glycoside hydrolase 5



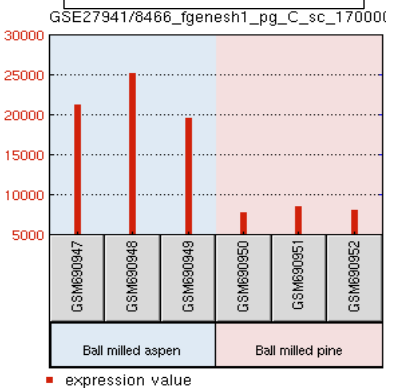
### Glycoside hydrolase 7



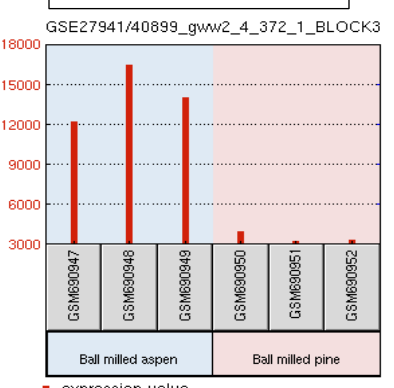
### Glycoside hydrolase 10



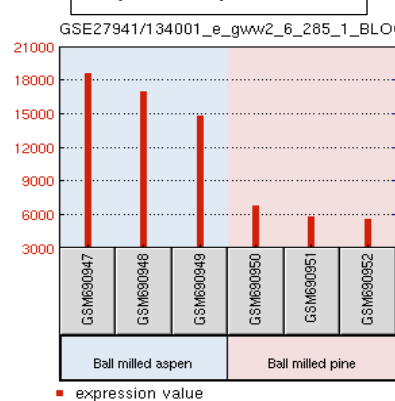
### Glycoside hydrolase 12



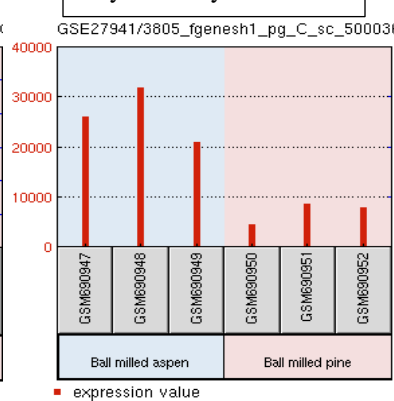
### Glycoside hydrolase 18



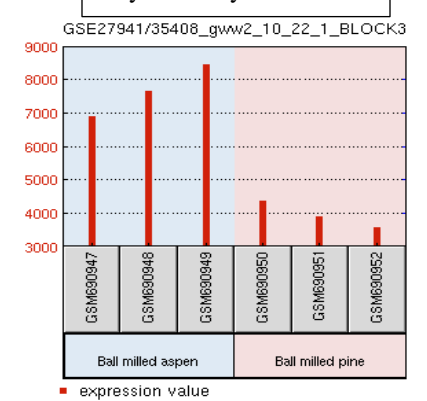
### Glycoside hydrolase 27

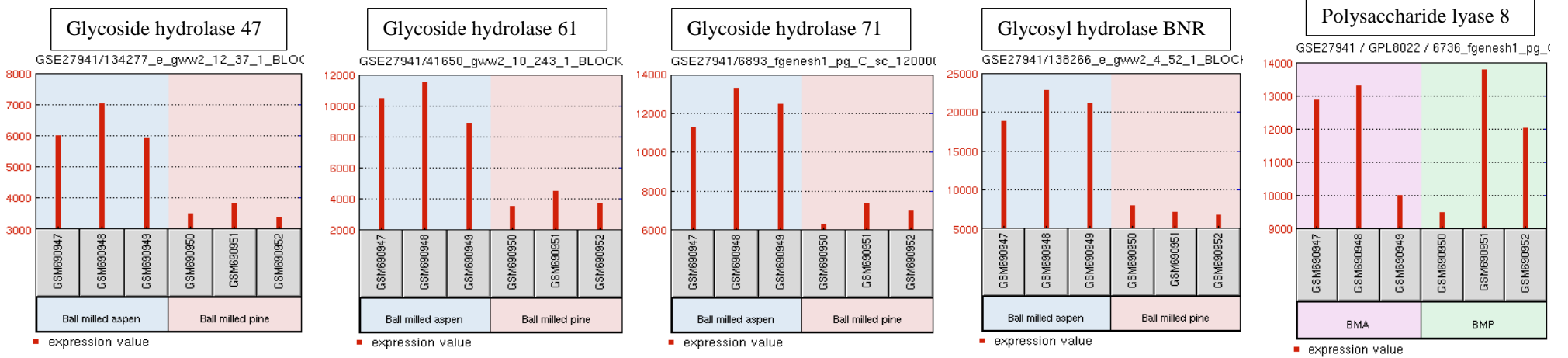


### Glycoside hydrolase 28

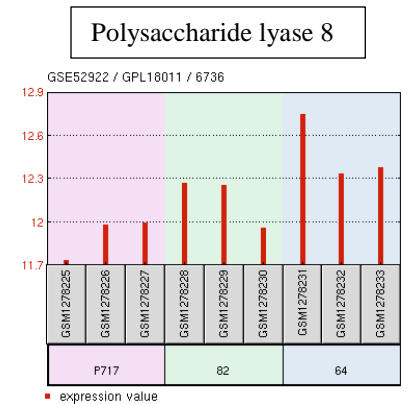
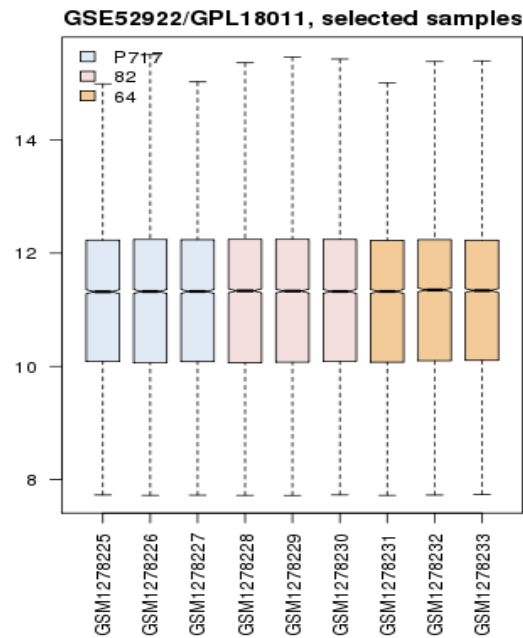


### Glycoside hydrolase 31



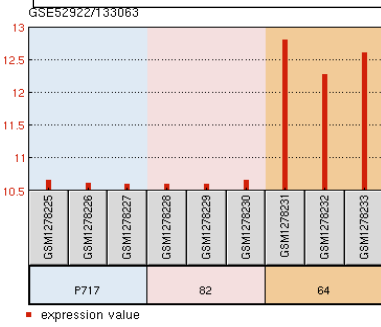


**GSE52922:** Gaskell, J et al (2014) have conducted this study to understand the gene expression patterns of *P. chrysosporium*, colonized on hybrid poplar (*Populus alba x tremula*) and two other syringyl rich transgenic derivatives. The microarray results have showed that gene expression patterns of *P. chrysosporium* are considerably influenced by lignin composition.

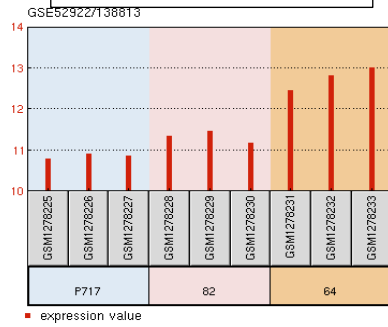




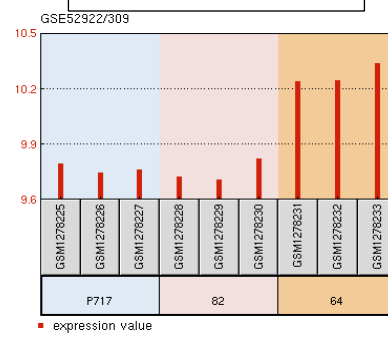
### Glutamate decarboxylase



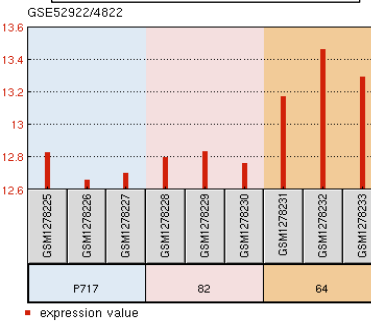
### Glycoside hydrolase 15



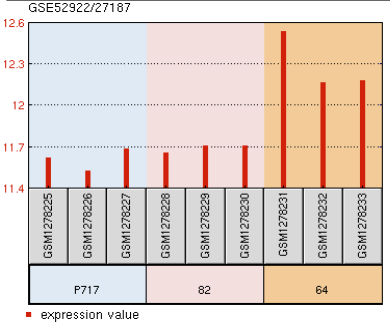
### Aldo/keto reductases



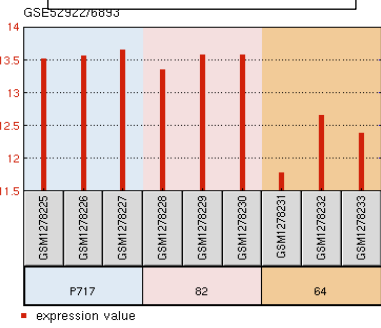
### Glycoside hydrolase 43



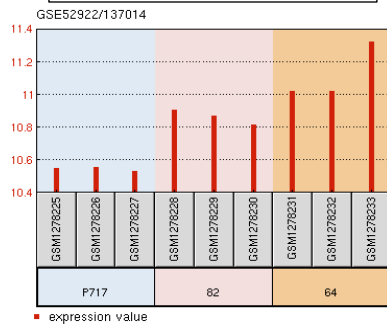
### Sugar transporter superfamily



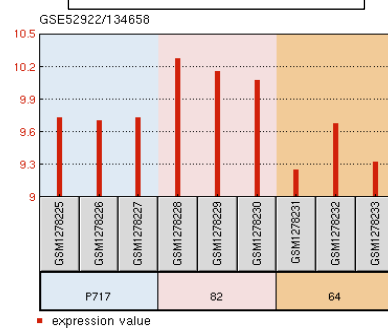
### Glycoside hydrolase 71



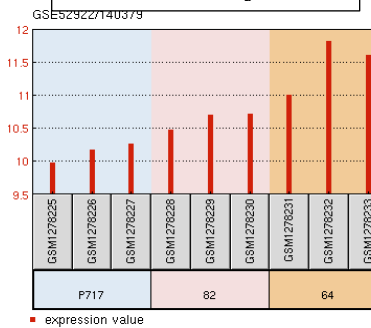
### Aldehyde dehydrogenases



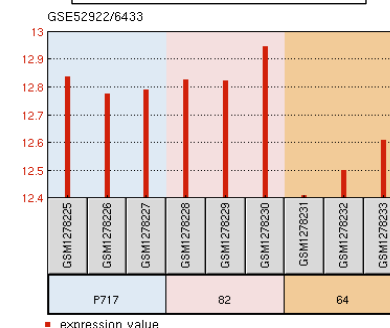
### Glycoside hydrolase 3



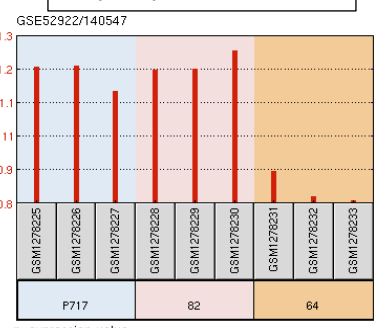
### Carbonic anhydrase



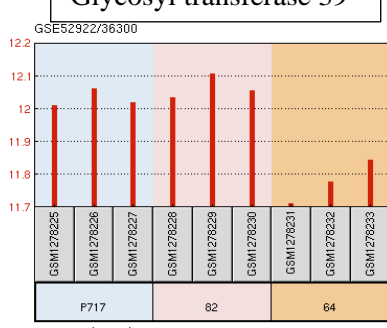
### Glycoside hydrolase 5



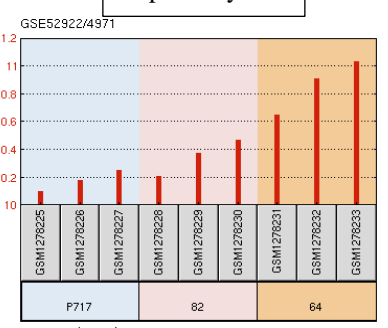
### Glycosyl transferase 2



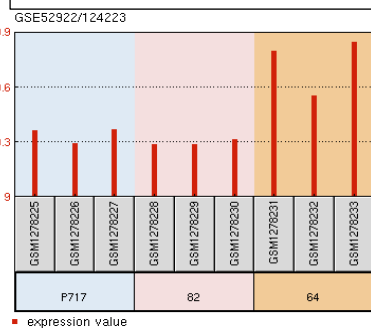
### Glycosyl transferase 39



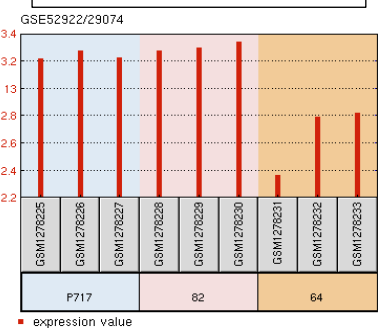
### Alpha amylase



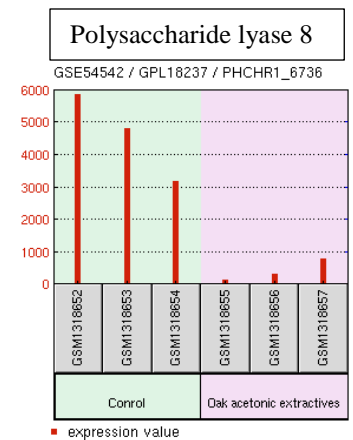
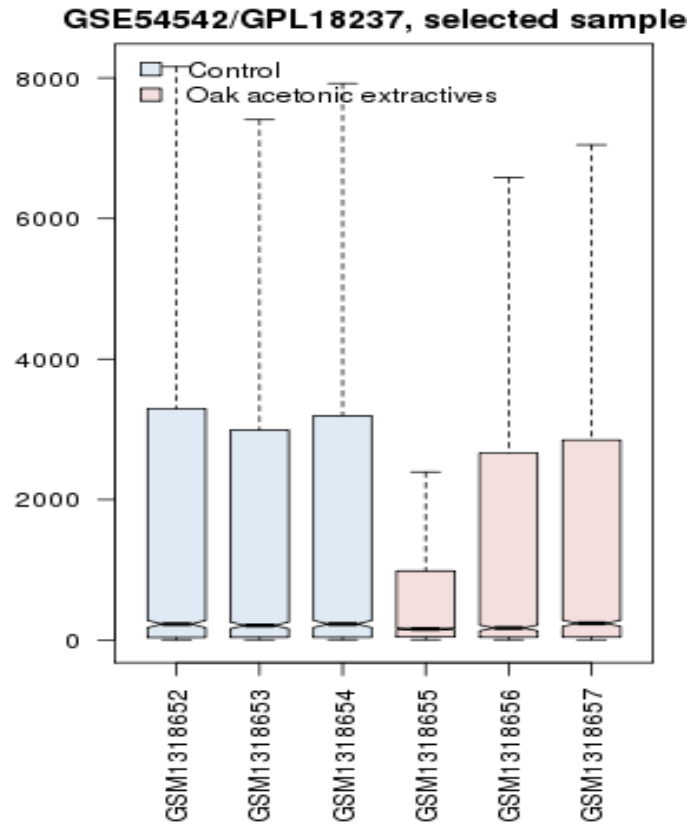
### Glucose/ribitol dehydrogenase



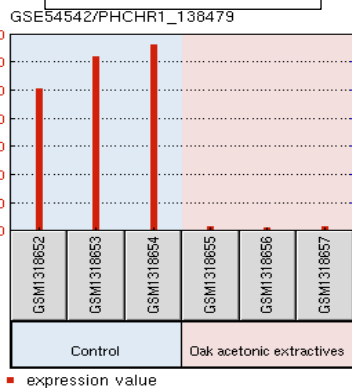
### Polysaccharide deacetylase



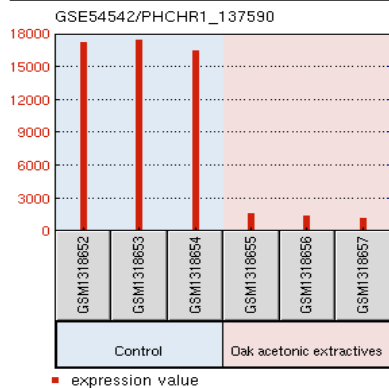
**GSE54542:** During wood degradation fungi comes across with several toxic compounds called extractives. Thuillier, Anne, et al (2014) have performed a transcriptome study of *Phanerochaete chrysosporium* cultured on oak acetonic extracts. Results have suggested that fungi employ intracellular antioxidative detoxification mechanisms along with extracellular enzymes for lignin degradation.



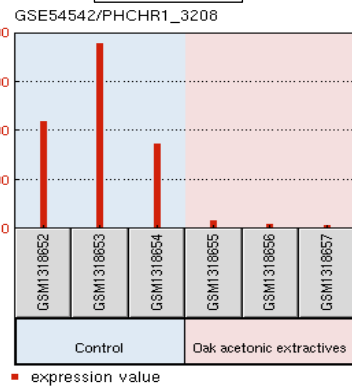
### Aldose-1-epimerase



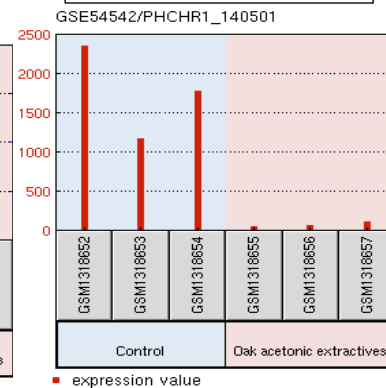
### Diacylglycerol acyl transferase



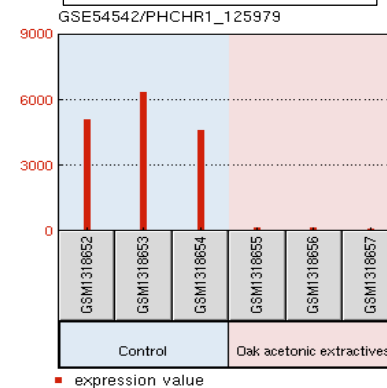
### Esterase



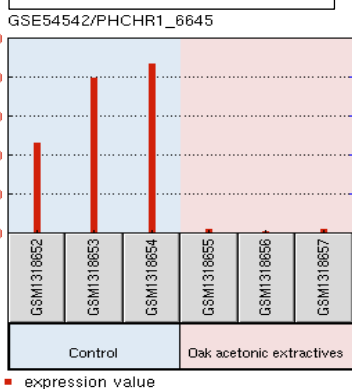
### Glycoside hydrolase 5



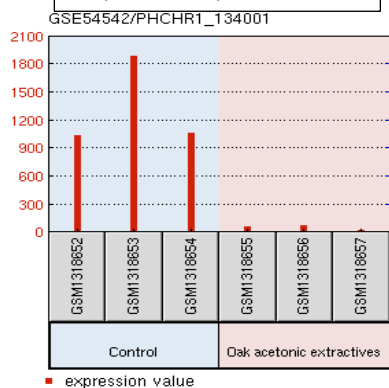
### Glycosyl transferase 8



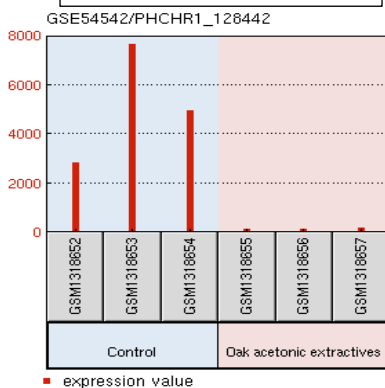
### G-protein beta WD-40



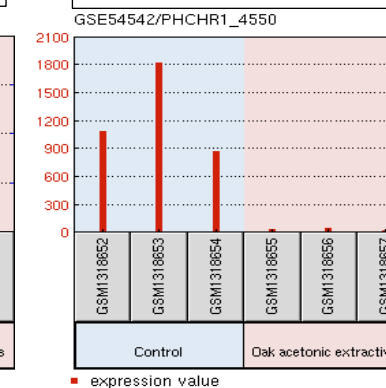
### Glycoside hydrolase 27



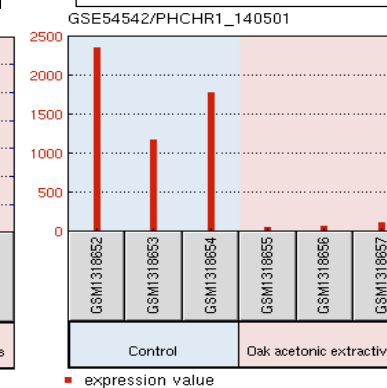
### Glycoside hydrolase, 3



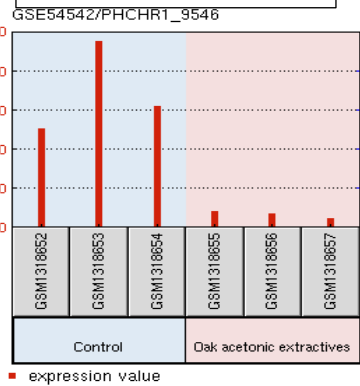
### Glycoside hydrolase 47



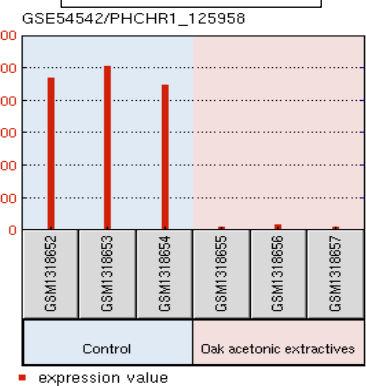
### Cellulose binding region



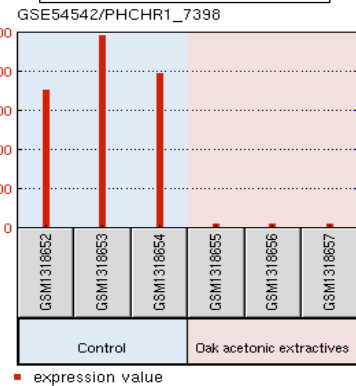
### Aldehyde dehydrogenase



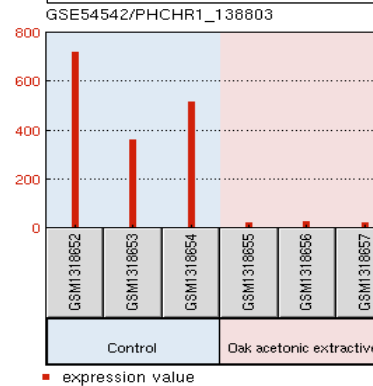
### Aldo/keto reductase



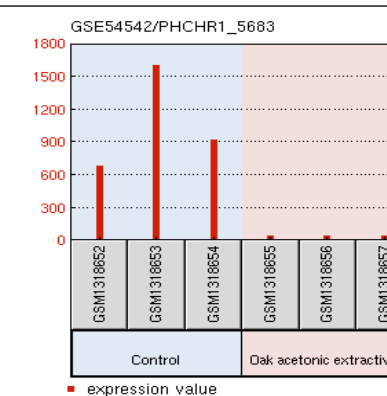
### Carboxylesterase, type B



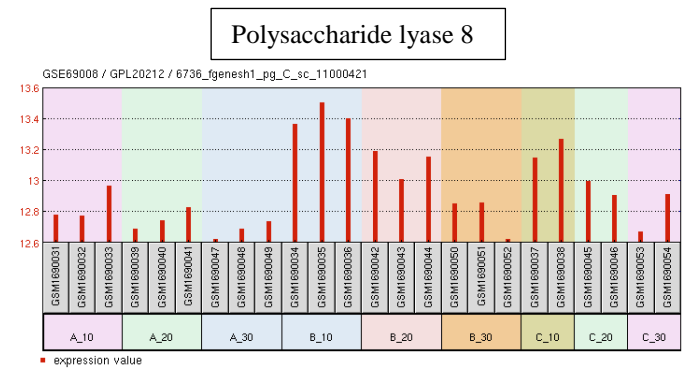
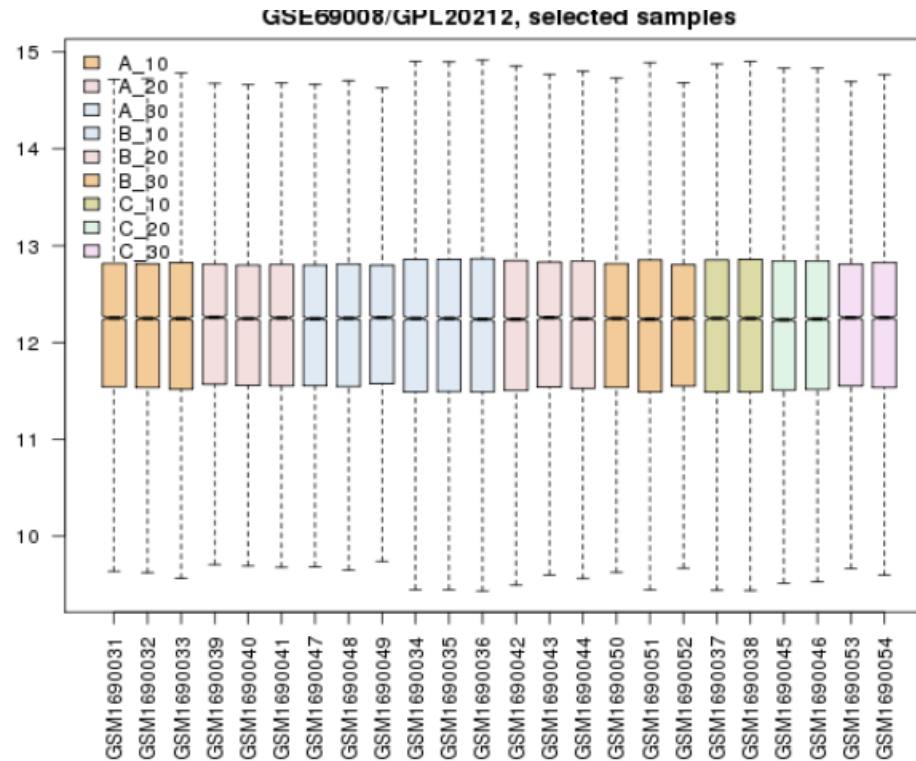
### Glucose/ribitol dehydrogenase



### Glyceraldehyde 3-phosphate dehydrogenase

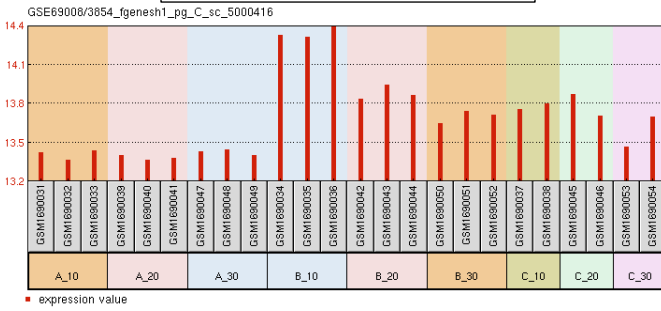


**GSE69008:** Mansfield S (2015), have performed a whole transcriptome study of *P. chrysosporium*. To understand the differential gene expression patterns of *P. chrysosporium* involved in cell wall degradation when cultured on three (poplar) *Populus trichocarpa* wood substrates with different chemical compositions.

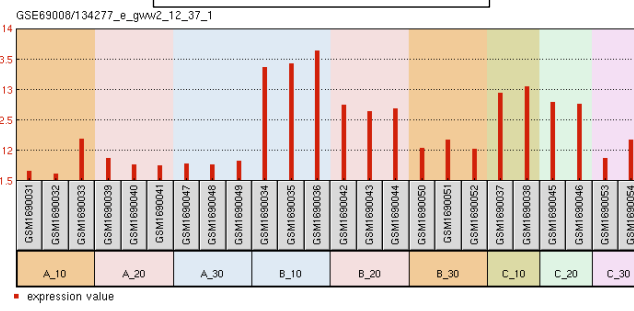




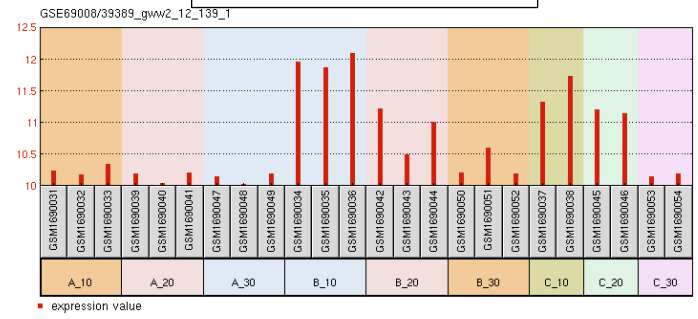
### Aldehyde dehydrogenase



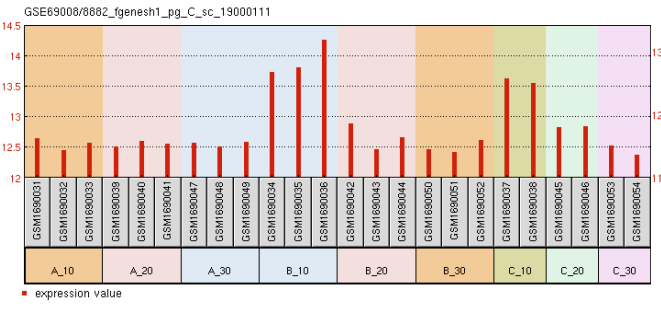
### Glycosyl transferase 2



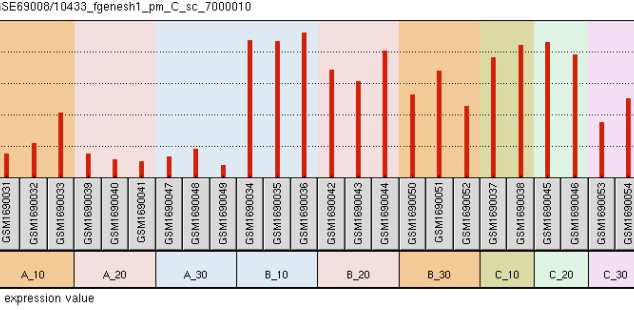
### Glycoside hydrolase 16



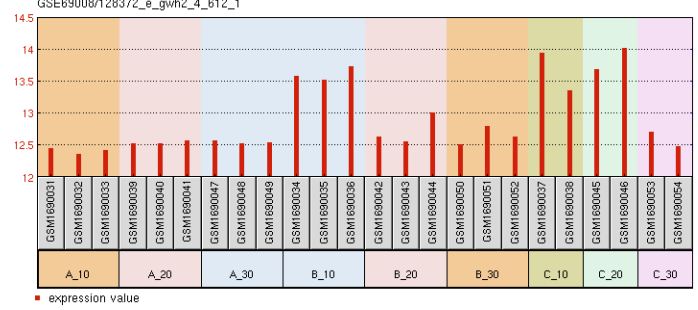
### Carbohydrate binding WSC



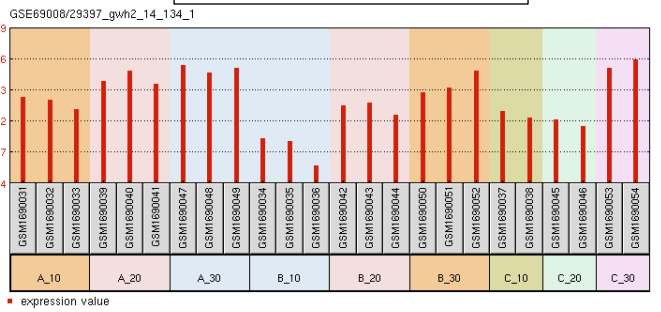
### Transketolase



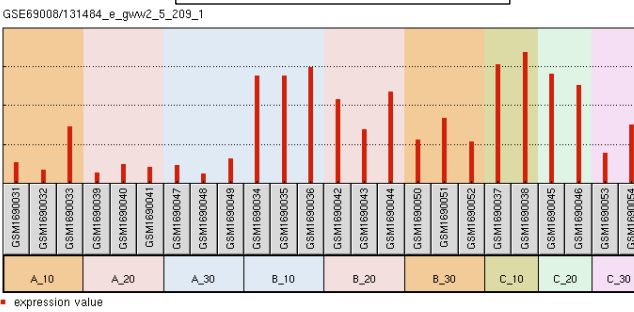
### Sugar transporter superfamily



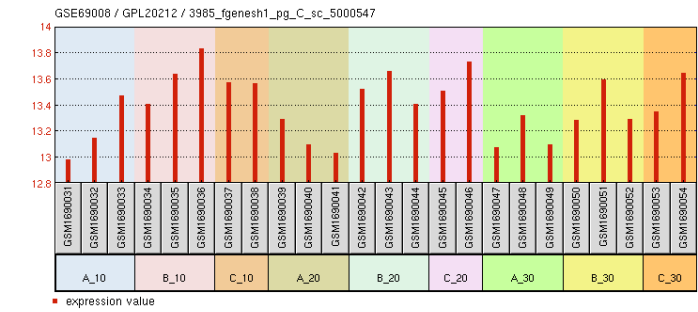
### Glycoside hydrolase 28



### Glycoside hydrolase 1



### Glycoside hydrolase 5

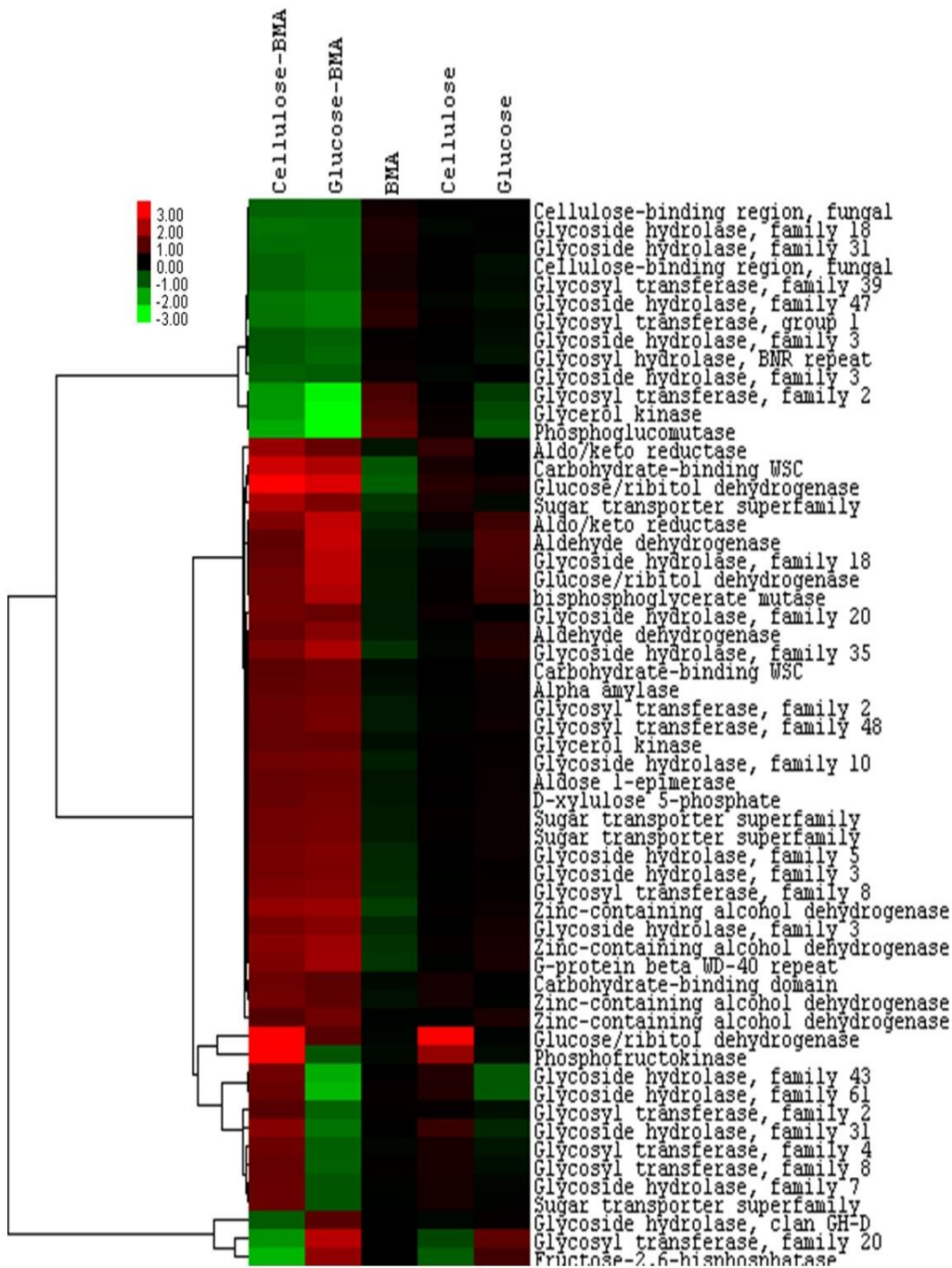


**Figure-S2:** Shows the hierarchical clusters of differentially expressed genes involved in cellulose and hemicellulose degradation, based on expression and fold change values.

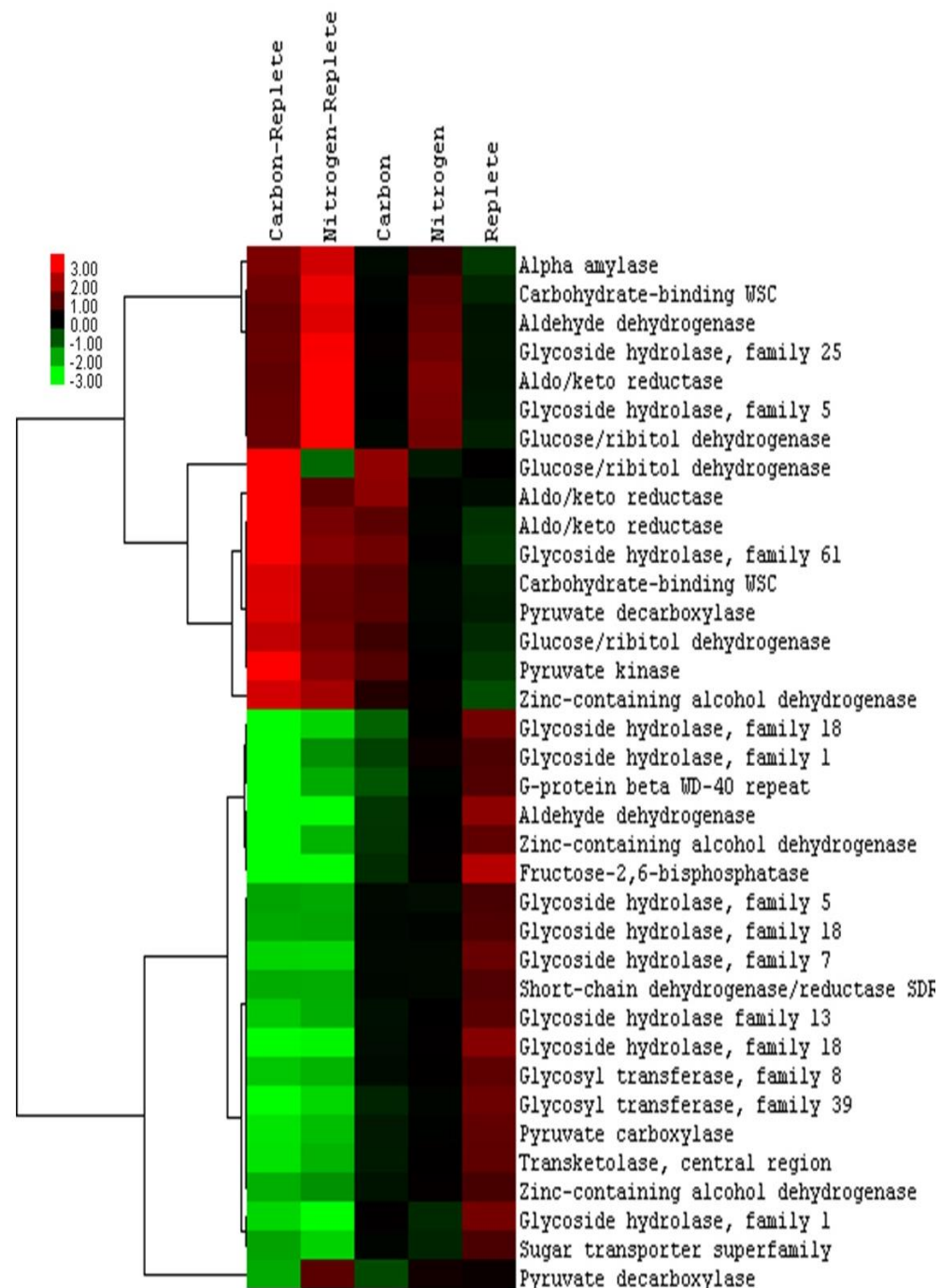
The following heat maps were generated using the Cluster 3.0 and Gene Treeview were used. The individual gene expression values from the NCBI GEO was obtained using the libraries GEOQuery and Biobase (Bioconductor packages) R software version 3.2.4. (ExpressionSet). The fold change values were calculated using the Microsoft Excel program and these values were used along with the individual expression values. Hierarchical clusters were developed using the clusters correlation centered for both the genes and arrays. The heat maps were generated for all the different datasets GSE14734, GSE14735, GSE27941, GSE52922, GSE54542, GSE69008, GSE69461 and GSE6649.



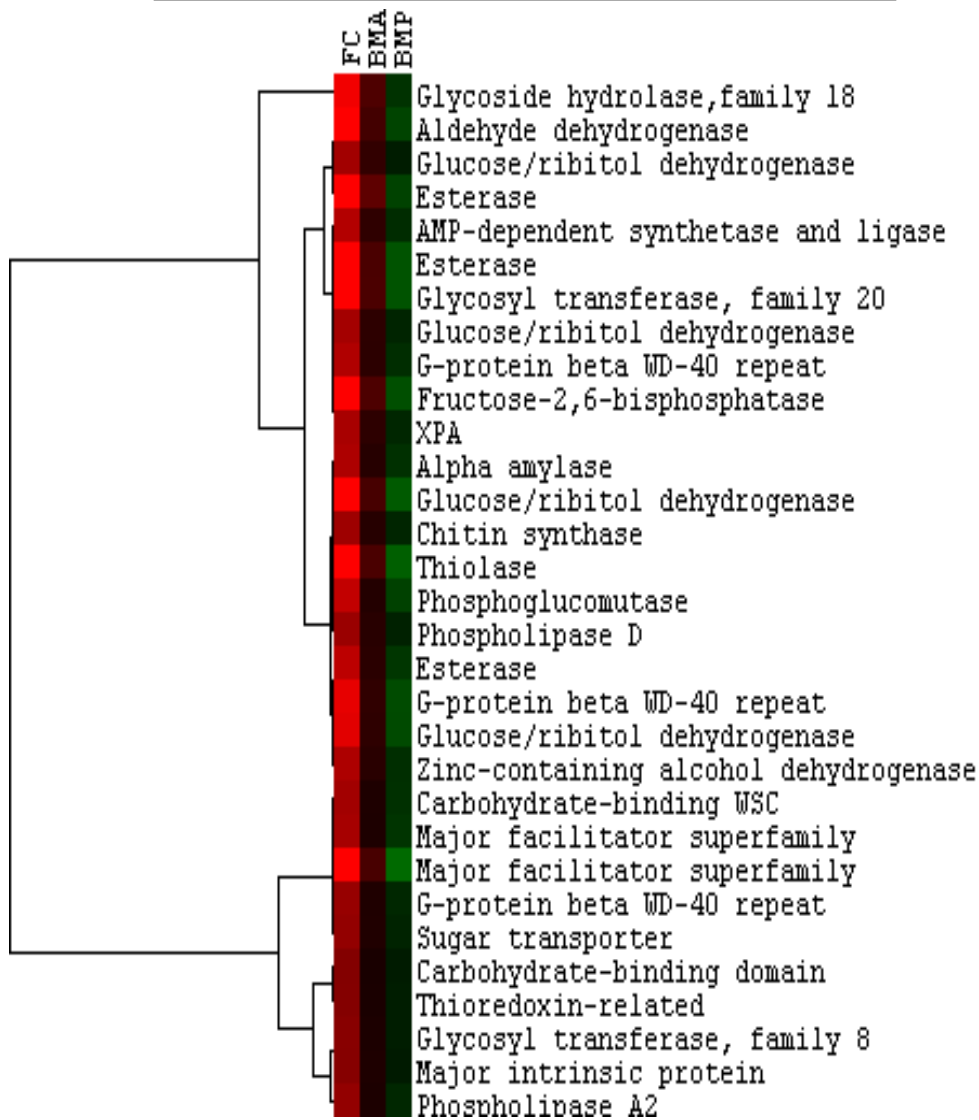
**GSE14734:** Genes involved in cellulose metabolism



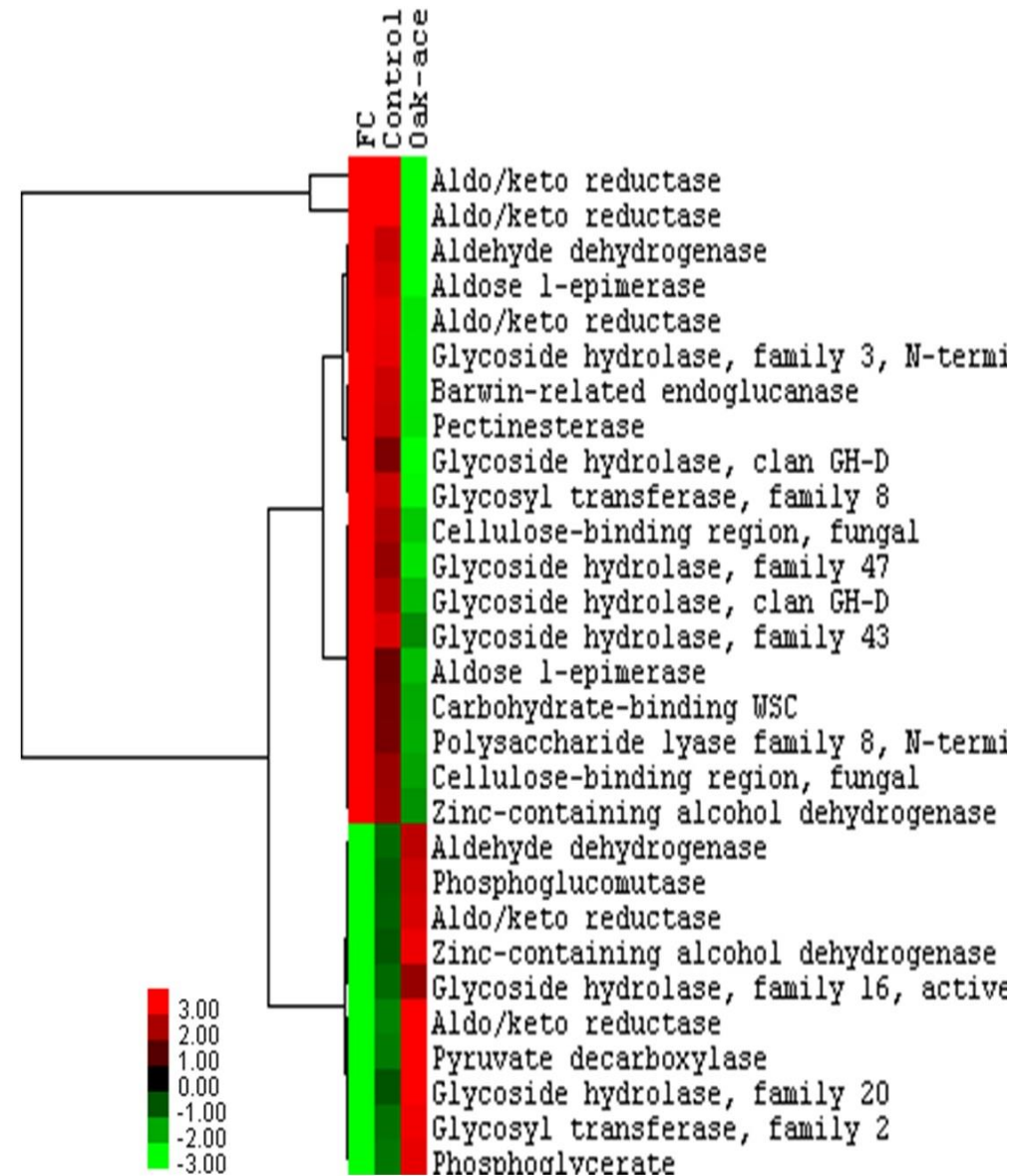
**GSE14735:** Genes involved in cellulose metabolism



**GSE27941:** Genes involved in cellulose metabolism

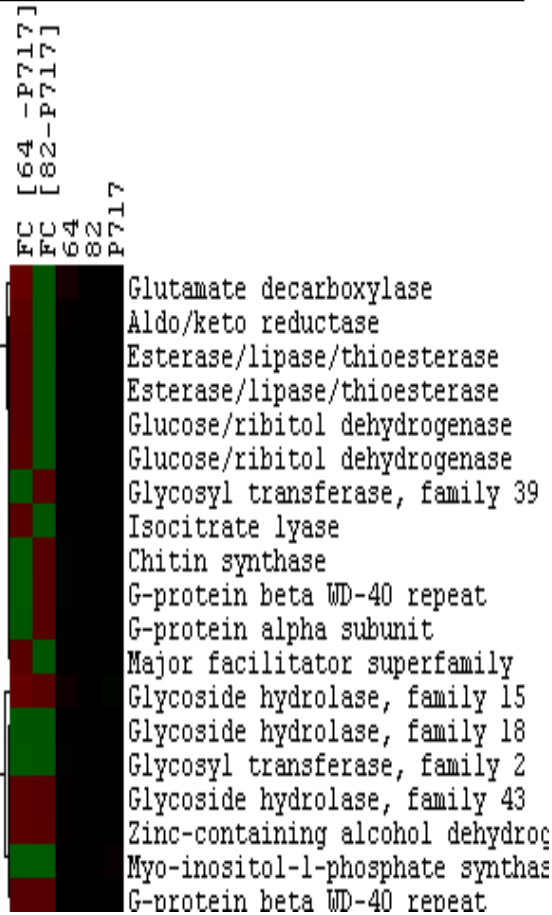


**GSE54542:** Genes involved in cellulose metabolism

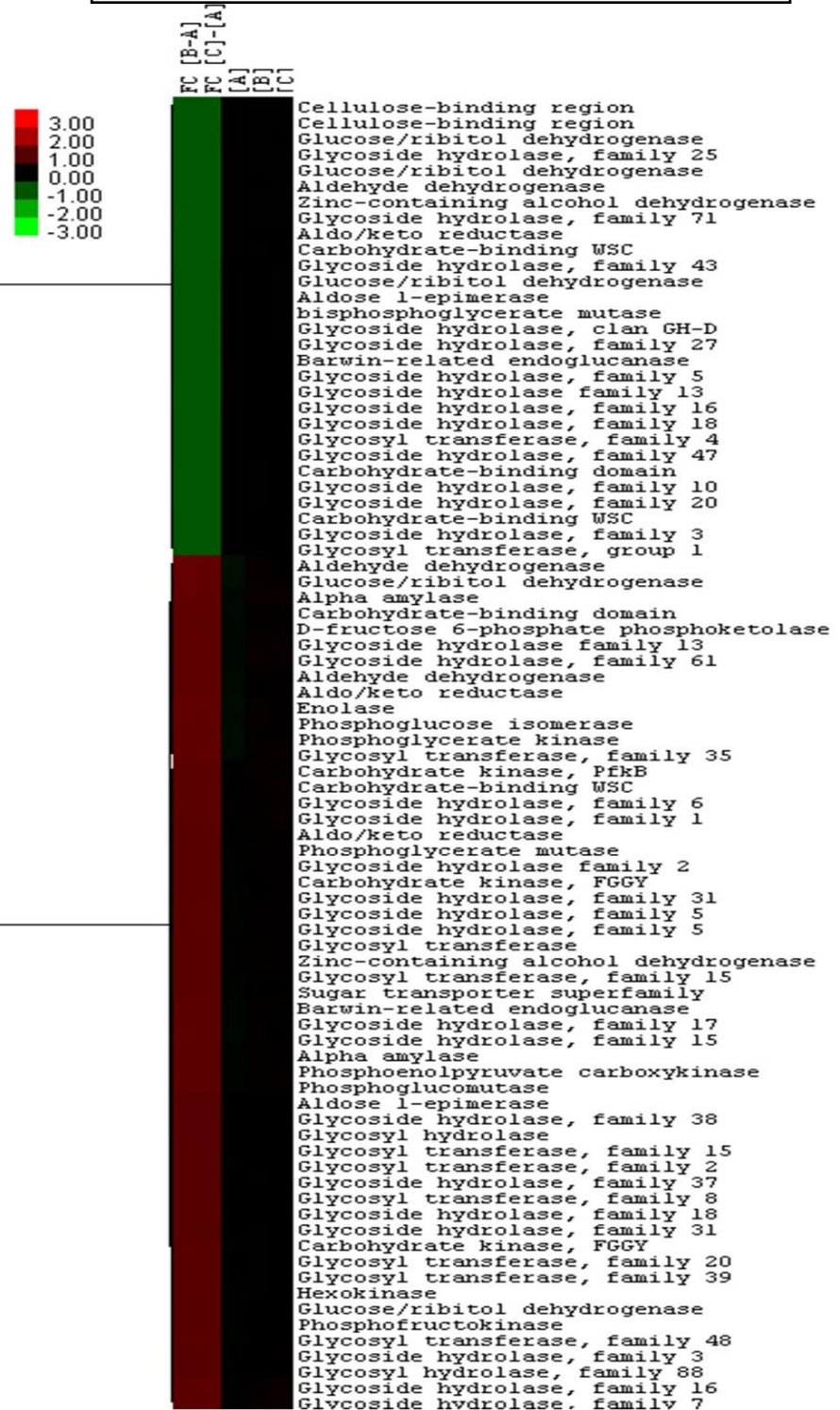




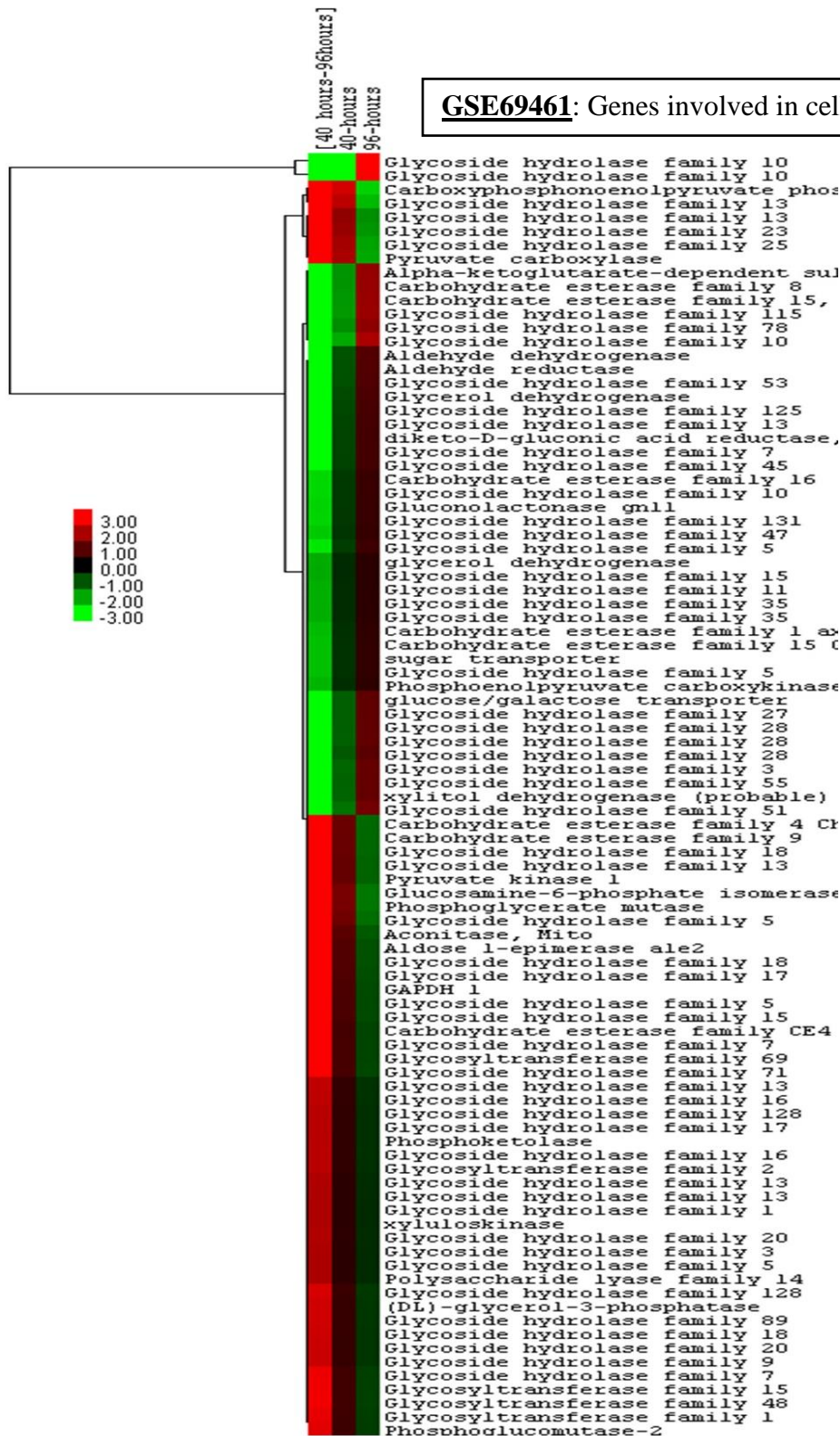
**GSE52922:** Genes involved in cellulose metabolism



**GSE69008:** Genes involved in cellulose metabolism

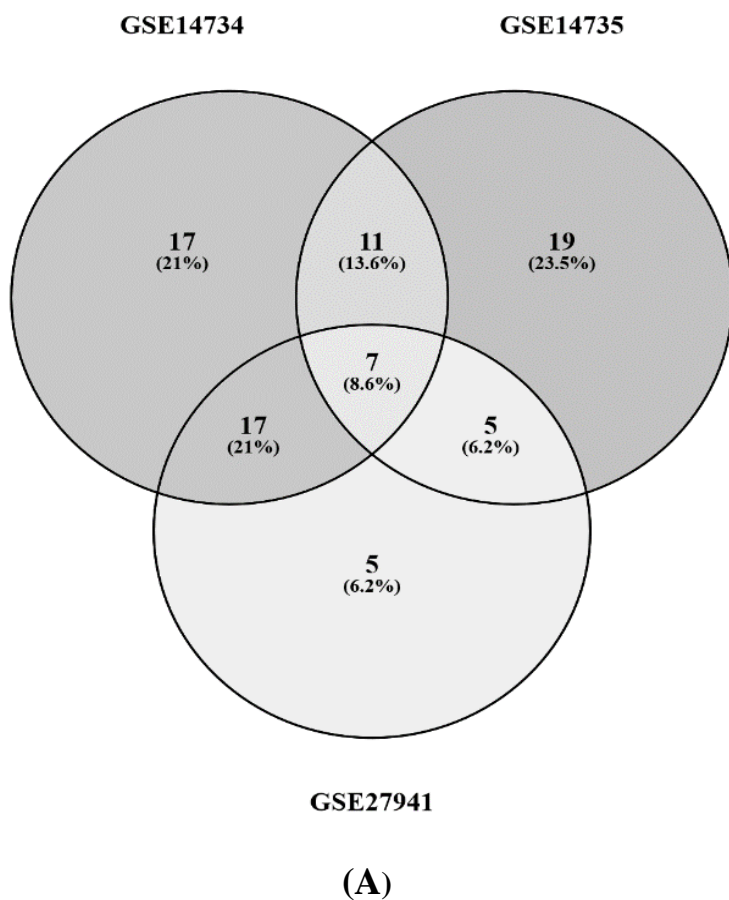


**GSE69461: Genes involved in cellulose metabolism**



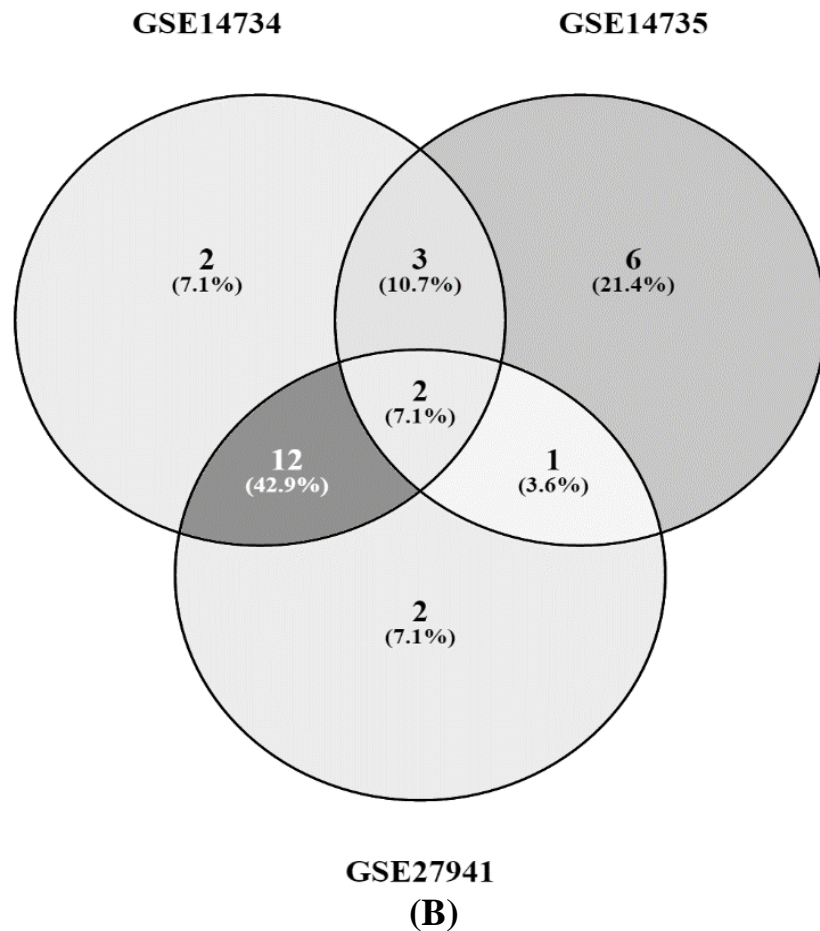
**Figure-S3:** Shows the three-way and four-way Venn diagrams showing the common differentially expressed gene lists obtained from different gene expression datasets:

**Figure-2:** Three way and four way Venn diagrams showing the common differentially expressed genes of *P. chrysosporium* when cultured in simple synthetic medium, cellulose and hemicellulose degrading genes (A), CAZymes (B) and complex natural plant biomass growth mediums, cellulose and hemicellulose degrading genes.



Three-way Venn diagram showing the common gene lists among the differentially expressed genes obtained from GSE14734, GSE14735 and GSE27941 datasets

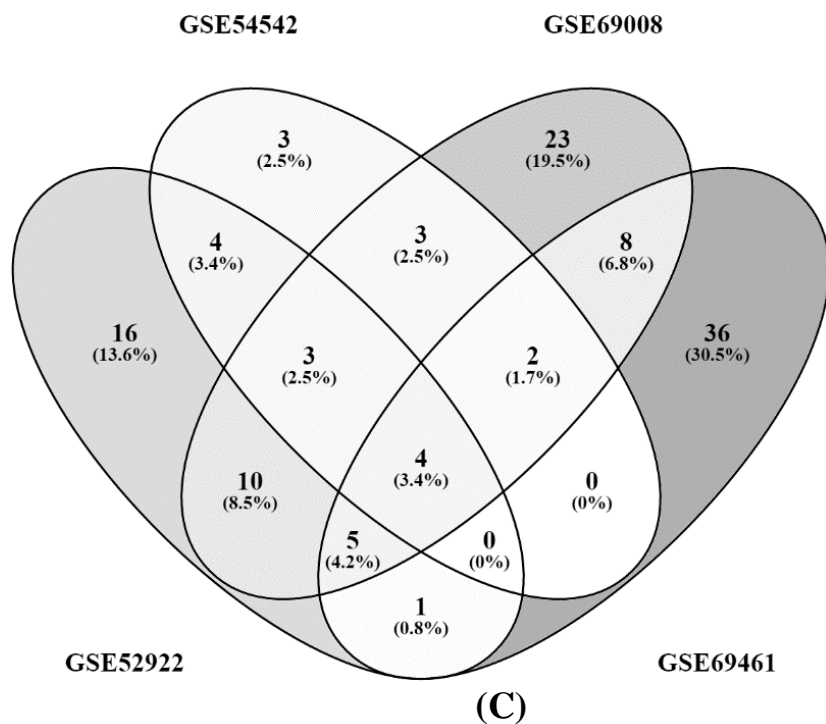
<b>GSE14734, GSE27941</b>	Aldose 1-epimerase Glycoside hydrolase, family 18 Cellulose-binding region, fungal Glycoside hydrolase, family 5 Glycoside hydrolase, family 1 Glycoside hydrolase, family 10 Glycoside hydrolase, family 28 Glycoside hydrolase, family 61 Glycoside hydrolase, family 7 Glycosyl hydrolase, BNR repeat Glycoside hydrolase, family 3 Iron-containing alcohol dehydrogenase Isocitrate lyase Lipase, class 3 Lipolytic enzyme, G-D-S-L Glycoside hydrolase, family 12 Glycoside hydrolase, family 27
<b>GSE14735, GSE27941</b>	Acetate and butyrate kinase Aldehyde dehydrogenase Pyruvate decarboxylase Barwin-related endoglucanase Carbohydrate-binding domain, family V/XII
<b>GSE14734, GSE14735</b>	Glycoside hydrolase, family 6 Enolase Fungal hydrophobin G-protein beta WD-40 repeat Aldo/keto reductase Alpha amylase Glycoside hydrolase, family 43 Glycosyl transferase, family 35 Glyceraldehyde 3-phosphate dehydrogenase Phosphoglycerate kinase Pyruvate kinase
<b>GSE14734, GSE14735, GSE27941</b>	Esterase Glucose-methanol-choline oxidoreductase Sugar transporter superfamily UTP--glucose-1-phosphate uridylyltransferase Zinc-containing alcohol dehydrogenase superfamily Glycoside hydrolase, family 31 Glycoside hydrolase, family 47



<b>GSE14734, GSE27941</b>	Glycoside hydrolase, family 18 Glycoside hydrolase, family 5 Glycoside hydrolase, family 1 Glycoside hydrolase, family 10 Glycoside hydrolase, family 28 Glycoside hydrolase, family 61 Glycoside hydrolase, family 7 Glycoside hydrolase, family 3 Glycoside hydrolase, family 12 Glycoside hydrolase, family 27 Glycoside hydrolase, BNR Repeat Cellulose binding region, fungal
<b>GSE14734, GSE14735, GSE27941</b>	Glycoside hydrolase, family 31 Glycoside hydrolase, family 47
<b>GSE14734, GSE14735</b>	Glycoside hydrolase, family 31 Glycoside hydrolase, family 31 Glycoside hydrolase, family 31
<b>GSE14735 GSE27941</b>	Carbohydrate-binding domain, family V/XII

Three-way Venn diagram showing the common gene lists among the differentially expressed genes encoding for CAZymes obtained from GSE14734, GSE14735 and GSE27941 datasets.

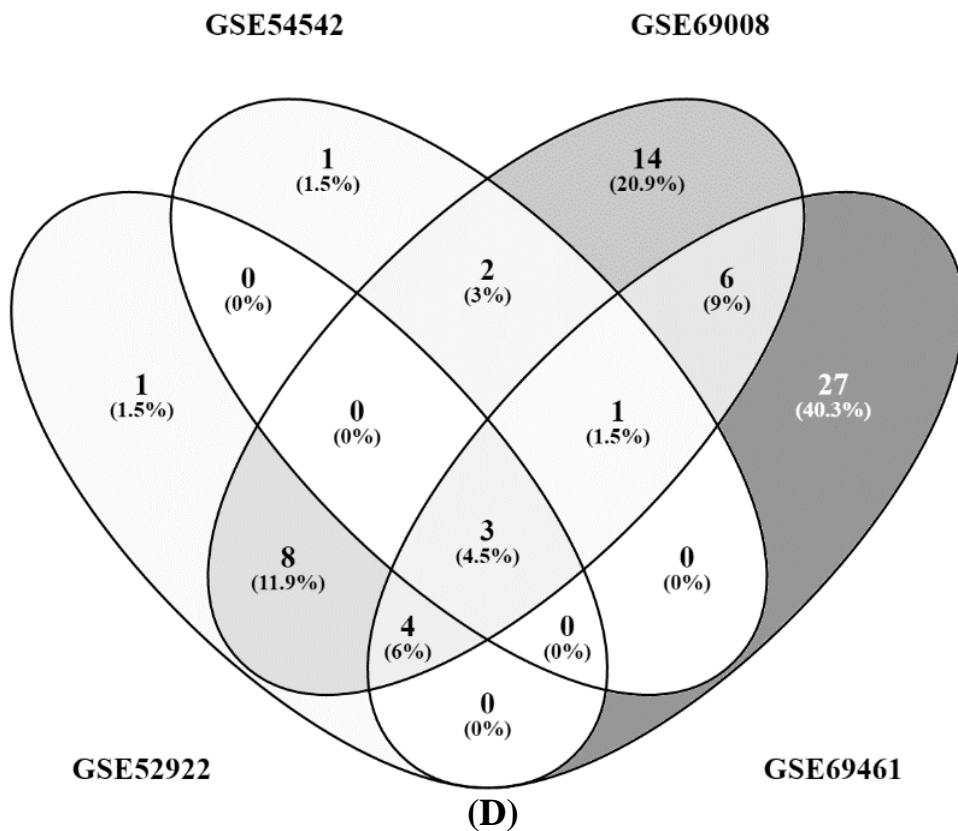




Four-way Venn diagram showing the common gene lists among the differentially expressed genes obtained from GSE54542, GSE69008, GSE52922 and GSE69461 datasets.

<b>GSE52922 GSE69088 GSE69461</b>	Glycoside hydrolase, family 10 Glycoside hydrolase, family 15 Sugar transporter superfamily Glycoside hydrolase, family 18 Glycoside hydrolase, family 71
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<b>GSE52922, GSE54542</b>	Esterase Major facilitator superfamily Pectinesterase Protein kinase
<b>GSE54542, GSE69088</b>	Barwin-related endoglucanase Glycoside hydrolase, clan GH-D Glycosyl transferase, family 8
<b>GSE52922, GSE54542, GSE69008</b>	Aldo/keto reductase Glucose/ribitol dehydrogenase Zinc-containing alcohol dehydrogenase
<b>GSE52922, GSE69008</b>	Carbohydrate kinase, PfkB Glycoside hydrolase, family 31 Glycoside hydrolase, family 37 Glycoside hydrolase, family 61 Glycosyl transferase, group 1 Glycosyl transferase Alpha amylase Glycosyl transferase, family 2 Glycoside hydrolase, family 43 Glycosyl transferase, family 39
<b>GSE69088, GSE69461</b>	Phosphoglycerate mutase Glycoside hydrolase, family 1 Glycoside hydrolase, family 16 Glycoside hydrolase, family 17 Glycoside hydrolase, family 20 Glycoside hydrolase, family 25 Glycoside hydrolase, family 7 Phosphoenolpyruvate carboxykinase
<b>GSE54542, GSE69088, GSE69461</b>	Aldose 1-epimerase Glycoside hydrolase, family 47
<b>GSE52922, GSE69461</b>	Pyruvate carboxylase
<b>GSE52922, GSE54542, GSE69088 GSE69461</b>	Aldehyde dehydrogenase Glycoside hydrolase, family 27 Glycoside hydrolase, family 3 Glycoside hydrolase, family 5



Four-way Venn diagram showing the common gene lists among the differentially expressed genes encoding for CAZymes obtained from GSE54542, GSE69008, GSE52922 and GSE69461 datasets

<b>GSE54542, GSE69008</b>	Glycoside hydrolase, clan GH-D Glycosyl transferase, family 8
<b>GSE69008, GSE69461</b>	Glycoside hydrolase, family 1 Glycoside hydrolase, family 16 Glycoside hydrolase, family 17 Glycoside hydrolase, family 20 Glycoside hydrolase, family 25 Glycoside hydrolase, family 7
<b>GSE54542, GSE69008, GSE69461,</b>	Glycoside hydrolase, family 47
<b>GSE52922, GSE54542, GSE69008, GSE69461</b>	Glycoside hydrolase, family 27 Glycoside hydrolase, family 3 Glycoside hydrolase, family 5
<b>GSE52922, GSE69008, GSE69461</b>	Glycoside hydrolase, family 10 Glycoside hydrolase, family 15 Glycoside hydrolase, family 18 Glycoside hydrolase, family 71
<b>GSE52922, GSE69008</b>	Glycoside hydrolase, family 31 Glycoside hydrolase, family 37 Glycoside hydrolase, family 61 Glycosyl transferase, group 1 Glycosyl transferase Glycosyl transferase, family 2 Glycoside hydrolase, family 43 Glycosyl transferase, family 39

**Table-S1: Illustrates the protein ID, genome position and gene length of common differentially expressed CAZymes involved in cellulose degradation, obtained from DOE-JGI databases:**

<b>Protein ID</b>	<b>Genome Position</b>	<b>Gene Length</b>	<b>CAZy Class Annotation</b>
Phchr2-2902324	scaffold_4:1889642-1892512	2870	GH1 Glycoside Hydrolase Family 1
Phchr2- 2903670	scaffold_5:878708-880945	2237	GH1 Glycoside Hydrolase Family 1
Phchr2 139304	scaffold_2:140355-144133	3778	GH2 Glycoside Hydrolase Family 2
Phchr2 2919132	scaffold_21:214533-217991	3458	GH2 Glycoside Hydrolase Family 2
Phchr2 2898439	scaffold_2:1647844-1650103	2259	GH3 Glycoside Hydrolase Family 3
Phchr2 2908992	scaffold_8:134342-137404	3062	GH3 Glycoside Hydrolase Family 3
Phchr2 2912549	scaffold_11:90797-94850	4053	CBM1 Carbohydrate-Binding Module Family 1
			GH3 Glycoside Hydrolase Family 3
Phchr2 2919526	scaffold_23:59945-62395	2450	GH3 Glycoside Hydrolase Family 3
Phchr2 2945552	scaffold_2:290868-294793	3925	GH3 Glycoside Hydrolase Family 3
Phchr2 2974470	scaffold_1:2367076-2371207	4131	GH3 Glycoside Hydrolase Family 3
Phchr2 3002242	scaffold_2:1681000-1684486	3486	GH3 Glycoside Hydrolase Family 3
Phchr2 3003144	scaffold_4:823431-826864	3433	GH3 Glycoside Hydrolase Family 3
Phchr2 3024052	scaffold_2:2979183-2982380	3197	GH3 Glycoside Hydrolase Family 3
Phchr2 3028741	scaffold_9:765392-767456	2064	GH3 Glycoside Hydrolase Family 3
Phchr2 140501	scaffold_18:190811-192684	1873	CBM1 Carbohydrate-Binding Module Family 1
			GH5_7 Glycoside Hydrolase Family 5
Phchr2 2895579	scaffold_1:1210045-1212391	2346	GH5_9 Glycoside Hydrolase Family 5
Phchr2 2902609	scaffold_4:1182779-1185339	2560	GH5_9 Glycoside Hydrolase Family 5
Phchr2 2915237	scaffold_13:292079-293833	1754	GH5_9 Glycoside Hydrolase Family 5
Phchr2 2932560	scaffold_7:1291315-1293834	2519	GH5_50 Glycoside Hydrolase Family 5
Phchr2 2943450	scaffold_1:834515-836736	2221	GH5_50 Glycoside Hydrolase Family 5
Phchr2 2950731	scaffold_4:2247390-2250801	3411	GH5_12 Glycoside Hydrolase Family 5
Phchr2 2955500	scaffold_8:945247-947330	2083	CBM1 Carbohydrate-Binding Module Family 1
			GH5_7 Glycoside Hydrolase Family 5
Phchr2 2971505	scaffold_14:90062-91558	1496	GH5_31 Glycoside Hydrolase Family 5
Phchr2 2976412	scaffold_2:2535612-2538947	3335	GH5_9 Glycoside Hydrolase Family 5
Phchr2 2979836	scaffold_5:1157933-1160343	2410	GH5_9 Glycoside Hydrolase Family 5
Phchr2 2981757	scaffold_7:489140-491192	2052	CBM1 Carbohydrate-Binding Module Family 1
			GH5_5 Glycoside Hydrolase Family 5
Phchr2 2985730	scaffold_11:427396-429760	2364	CBM1 Carbohydrate-Binding Module Family 1
			GH5_5 Glycoside Hydrolase Family 5
Phchr2 2988862	scaffold_16:419672-421769	2097	GH5_9 Glycoside Hydrolase Family 5

Phchr2 2989703	scaffold_19:32534-34797	2263	GH5_22 Glycoside Hydrolase Family 5
Phchr2 3007303	scaffold_19:30579-32234	1655	GH5_22 Glycoside Hydrolase Family 5
Phchr2 3014854	scaffold_1:3073371-3076973	3602	GH5_12 Glycoside Hydrolase Family 5
Phchr2 3024315	scaffold_3:704555-706748	2193	GH5_15 Glycoside Hydrolase Family 5
Phchr2 3029839	scaffold_11:759163-761548	2385	GH5_7 Glycoside Hydrolase Family 5
Phchr2 2965119	scaffold_1:1540917-1542621	1704	CBM1 Carbohydrate-Binding Module Family 1
			GH6 Glycoside Hydrolase Family 6
Phchr2 137042	scaffold_14:522860-524539	1679	GH7 Glycoside Hydrolase Family 7
			CBM1 Carbohydrate-Binding Module Family 1
Phchr2 137372	scaffold_3:948653-950362	1709	GH7 Glycoside Hydrolase Family 7
			CBM1 Carbohydrate-Binding Module Family 1
Phchr2 2971598	scaffold_14:525250-526833	1583	GH7 Glycoside Hydrolase Family 7
Phchr2 2971601	scaffold_14:540055-541711	1656	GH7 Glycoside Hydrolase Family 7
			CBM1 Carbohydrate-Binding Module Family 1
Phchr2 2976245	scaffold_2:2207605-2209644	2039	GH7 Glycoside Hydrolase Family 7
			CBM1 Carbohydrate-Binding Module Family 1
Phchr2 2976248	scaffold_2:2215861-2217914	2053	GH7 Glycoside Hydrolase Family 7
			CBM1 Carbohydrate-Binding Module Family 1
Phchr2 3007720	scaffold_85:734-1148	414	GH7 Glycoside Hydrolase Family 7 (fragment) old model (1761)
Phchr2 3024803	scaffold_3:2068409-2070058	1649	GH7 Glycoside Hydrolase Family 7
			CBM1 Carbohydrate-Binding Module Family 1
Phchr2 2975231	scaffold_2:442144-444641	2497	GH9 Glycoside Hydrolase Family 9
Phchr2 1416762	scaffold_12:718019-719304	1285	GH12 Glycoside Hydrolase Family 12
Phchr2 3007125	scaffold_17:105891-107013	1122	GH12 Glycoside Hydrolase Family 12
Phchr2 133070	scaffold_1:3126077-3127288	1211	GH43 Glycoside Hydrolase Family 43
Phchr2 2896433	scaffold_1:1018027-1020296	2269	GH43 Glycoside Hydrolase Family 43
Phchr2 2933015	scaffold_7:2032452-2035039	2587	GH43 Glycoside Hydrolase Family 43
Phchr2 2973689	scaffold_1:904294-906716	2422	GH43 Glycoside Hydrolase Family 43
			CBM35 Carbohydrate-Binding Module Family 35
Phchr2 2980868	scaffold_6:905347-906396	1049	GH45 Glycoside Hydrolase Family 45
Phchr2 3004240	scaffold_6:1797623-1798341	718	GH45 Glycoside Hydrolase Family 45
Phchr2 2954077	scaffold_7:806466-808421	1955	GH51 Glycoside Hydrolase Family 51
Phchr2 3037385	scaffold_5:705192-708287	3095	GH51 Glycoside Hydrolase Family 51
Phchr2 138739	scaffold_8:465492-466728	1236	GH131 Glycoside Hydrolase Family 131 (fragment)
			CBM1 Carbohydrate-Binding Module Family 1 (fragment)
Phchr2 1521209	scaffold_13:1196824-1198084	1260	GH131 Glycoside Hydrolase Family 131 (fragment)



Phchr2 3031966	scaffold_17:239882-241057	1175	GH131 Glycoside Hydrolase Family 131
Phchr2 2912797	scaffold_11:1249935-1253189	3254	GH74 Glycoside Hydrolase Family 74
			CBM1 Carbohydrate-Binding Module Family 1
Phchr2 2927412	scaffold_4:181827-185150	3323	GH74 Glycoside Hydrolase Family 74
Phchr2 3043746	scaffold_144:15-1370	1355	GH74 Glycoside Hydrolase Family 74 (fragment)
Phchr2 3091442	scaffold_53:2-2722	2720	GH74 Glycoside Hydrolase Family 74 (fragment)
Phchr2 129693	scaffold_2:1499366-1501724	2358	CBM48 Carbohydrate-Binding Module Family 48
			GH13_8 Glycoside Hydrolase Family 13
Phchr2 2661256	scaffold_8:503537-505912	2375	GH13_40 Glycoside Hydrolase Family 13
Phchr2 2911333	scaffold_10:1089577-1091652	2075	GH13_40 Glycoside Hydrolase Family 13
Phchr2 2917244	scaffold_16:234315-236855	2540	GH13_5 Glycoside Hydrolase Family 13
Phchr2 2973784	scaffold_1:1066532-1074544	8012	GH13_22 Glycoside Hydrolase Family 13
			GT5 Glycosyl Transferase Family 5
Phchr2 2983917	scaffold_9:309142-311442	2300	GH13_1 Glycoside Hydrolase Family 13 (fragment) old model (PC.88.23.1) was better
Phchr2 3001496	scaffold_1:2048283-2050415	2132	GH13_1 Glycoside Hydrolase Family 13
Phchr2 3024363	scaffold_3:847098-852572	5474	GH13_25 Glycoside Hydrolase Family 13
			GH133 Glycoside Hydrolase Family 133
Phchr2 7087	scaffold_12:835019-837355	2336	GH13_32 Glycoside Hydrolase Family 13
			CBM20 Carbohydrate-Binding Module Family 20
Phchr2 1216344	scaffold_10:488243-489330	1087	AA9 Auxiliary Activity Family 9 (fragment)
Phchr2 2908293	scaffold_7:1591640-1592893	1253	AA9 Auxiliary Activity Family 9
Phchr2 2934397	scaffold_9:311898-314146	2248	AA9 Auxiliary Activity Family 9 too long at N-term;
Phchr2 2975821	scaffold_2:1458446-1459587	1141	AA9 Auxiliary Activity Family 9
Phchr2 2976448	scaffold_2:2698849-2700557	1708	AA9 Auxiliary Activity Family 9
			CBM1 Carbohydrate-Binding Module Family 1
Phchr2 2980158	scaffold_5:1726957-1728554	1597	AA9 Auxiliary Activity Family 9
			CBM1 Carbohydrate-Binding Module Family 1
Phchr2 2982319	scaffold_7:1589252-1590681	1429	AA9 Auxiliary Activity Family 9
Phchr2 2982894	scaffold_8:492080-493688	1608	AA9 Auxiliary Activity Family 9
Phchr2 3003776	scaffold_5:1643104-1644697	1593	AA9 Auxiliary Activity Family 9
			CBM1 Carbohydrate-Binding Module Family 1
Phchr2 3004691	scaffold_7:1587181-1588300	1119	AA9 Auxiliary Activity Family 9
Phchr2 3005492	scaffold_10:527184-528465	1281	AA9 Auxiliary Activity Family 9
			CBM1 Carbohydrate-Binding Module Family 1
Phchr2 3026777	scaffold_6:1059298-1060697	1399	AA9 Auxiliary Activity Family 9
Phchr2 3027731	scaffold_7:1715400-1716790	1390	AA9 Auxiliary Activity Family 9

			CBM1 Carbohydrate-Binding Module Family 1
Phchr2 3029242	scaffold_10:522449-523796	1347	AA9 Auxiliary Activity Family 9
			CBM1 Carbohydrate-Binding Module Family 1
Phchr2 3040475	scaffold_10:1235253-1237125	1872	AA9 Auxiliary Activity Family 9 (fragment) splicing problem; ; old model (42504) was better
Phchr2 42616	scaffold_10:536193-536923	730	AA9 Auxiliary Activity Family 9 fragment C-term;
Phchr2 2904202	scaffold_5:1181565-1183330	1765	GH28 Glycoside Hydrolase Family 28
Phchr2 2916357	scaffold_14:755385-757424	2039	GH28 Glycoside Hydrolase Family 28
			CBM1 Carbohydrate-Binding Module Family 1
Phchr2 2979830	scaffold_5:1154388-1156534	2146	GH28 Glycoside Hydrolase Family 28
Phchr2 2989563	scaffold_18:317922-320381	2459	GH28 Glycoside Hydrolase Family 28
Phchr2 3027410	scaffold_7:801878-803817	1939	GH28 Glycoside Hydrolase Family 28
Phchr2 2920193	scaffold_32:444-2369	1925	GH35 Glycoside Hydrolase Family 35 (fragment)
Phchr2 2986919	scaffold_12:1229817-1234610	4793	GH35 Glycoside Hydrolase Family 35
Phchr2 2990791	scaffold_27:43732-47821	4089	GH35 Glycoside Hydrolase Family 35

**Table-S2: Illustrates the protein ID, genome position and gene length of common differentially expressed CAZymes involved in hemicellulose degradation, obtained from DOE-JGI databases:**

Protein ID	Genome Position	Gene Length	CAZy Class Annotation
Phchr2 2902324	scaffold_4:1889642-1892512	2870	GH1 Glycoside Hydrolase Family 1
Phchr2 2903670	scaffold_5:878708-880945	2237	GH1 Glycoside Hydrolase Family 1
Phchr2 2903539	scaffold_4:581445-582946	1501	CBM1 Carbohydrate-Binding Module Family 1
			GH10 Glycoside Hydrolase Family 10
Phchr2 2935636	scaffold_10:688713-690445	1732	GH10 Glycoside Hydrolase Family 10
Phchr2 2983729	scaffold_8:1830584-1832199	1615	CBM1 Carbohydrate-Binding Module Family 1
			GH10 Glycoside Hydrolase Family 10
Phchr2 3024004	scaffold_2:2818411-2819918	1507	CBM1 Carbohydrate-Binding Module Family 1
			GH10 Glycoside Hydrolase Family 10
Phchr2 3030351	scaffold_12:704574-706322	1748	CBM1 Carbohydrate-Binding Module Family 1
			GH10 Glycoside Hydrolase Family 10
Phchr2 3042040	scaffold_14:792639-794113	1474	GH10 Glycoside Hydrolase Family 10
Phchr2 2905606	scaffold_6:584800-585734	934	GH11 Glycoside Hydrolase Family 11
			CBM1 Carbohydrate-Binding Module Family 1
Phchr2 1416762	scaffold_12:718019-719304	1285	GH12 Glycoside Hydrolase Family 12

Phchr2 3007125	scaffold_17:105891-107013	1122	GH12 Glycoside Hydrolase Family 12
Phchr2 2917733	scaffold_17:354020-356241	2221	GH20 Glycoside Hydrolase Family 20
Phchr2 2972234	scaffold_17:362940-364937	1997	GH20 Glycoside Hydrolase Family 20
Phchr2 2973374	scaffold_1:215681-218071	2390	GH20 Glycoside Hydrolase Family 20
Phchr2 2985725	scaffold_11:408066-410486	2420	GH20 Glycoside Hydrolase Family 20 (fragment)
Phchr2 2981806	scaffold_7:701386-704283	2897	GH27 Glycoside Hydrolase Family 27
Phchr2 3005667	scaffold_11:117750-119732	1982	GH27 Glycoside Hydrolase Family 27
Phchr2 3010808	scaffold_6:1771747-1773902	2155	CBM1 Carbohydrate-Binding Module Family 1
			GH27 Glycoside Hydrolase Family 27
Phchr2 2904202	scaffold_5:1181565-1183330	1765	GH28 Glycoside Hydrolase Family 28
Phchr2 2916357	scaffold_14:755385-757424	2039	GH28 Glycoside Hydrolase Family 28
			CBM1 Carbohydrate-Binding Module Family 1
Phchr2 2979830	scaffold_5:1154388-1156534	2146	GH28 Glycoside Hydrolase Family 28
Phchr2 2989563	scaffold_18:317922-320381	2459	GH28 Glycoside Hydrolase Family 28
Phchr2 3027410	scaffold_7:801878-803817	1939	GH28 Glycoside Hydrolase Family 28
Phchr2 2984123	scaffold_9:745108-747010	1902	GH30 Glycoside Hydrolase Family 30
Phchr2 2990154	scaffold_20:351890-355188	3298	GH30_3 Glycoside Hydrolase Family 30
Phchr2 135833	scaffold_10:1362850-1366208	3358	GH31 Glycoside Hydrolase Family 31
Phchr2 2895063	scaffold_1:3095813-3099113	3300	GH31 Glycoside Hydrolase Family 31
Phchr2 2950055	scaffold_4:1269311-1272582	3271	GH31 Glycoside Hydrolase Family 31
Phchr2 3022485	scaffold_1:1910371-1913265	2894	GH31 Glycoside Hydrolase Family 31
Phchr2 3029505	scaffold_10:1346654-1350263	3609	GH31 Glycoside Hydrolase Family 31
Phchr2 3029525	scaffold_10:1411204-1414713	3509	GH31 Glycoside Hydrolase Family 31
Phchr2 133070	scaffold_1:3126077-3127288	1211	GH43 Glycoside Hydrolase Family 43
Phchr2 2896433	scaffold_1:1018027-1020296	2269	GH43 Glycoside Hydrolase Family 43
Phchr2 2933015	scaffold_7:2032452-2035039	2587	GH43 Glycoside Hydrolase Family 43
Phchr2 2973689	scaffold_1:904294-906716	2422	GH43 Glycoside Hydrolase Family 43
			CBM35 Carbohydrate-Binding Module Family 35
Phchr2 2579514	scaffold_7:1095087-1098003	2916	GH47 Glycoside Hydrolase Family 47
Phchr2 2894724	scaffold_1:351116-353143	2027	GH47 Glycoside Hydrolase Family 47
Phchr2 2924247	scaffold_2:1013743-1017191	3448	GH47 Glycoside Hydrolase Family 47
Phchr2 3024192	scaffold_3:351877-354057	2180	GH47 Glycoside Hydrolase Family 47
Phchr2 3032176	scaffold_18:232262-234795	2533	GH47 Glycoside Hydrolase Family 47
Phchr2 126075	scaffold_13:54883-56123	1240	CBM1 Carbohydrate-Binding Module Family 1 old model (7224) was better

			CE1 Carbohydrate Esterase Family 1 old model (7224) was better
Phchr2 135348	scaffold_21:91249-92052	803	CE1 Carbohydrate Esterase Family 1 (fragment)
Phchr2 2966850	scaffold_3:1945735-1947475	1740	CE1 Carbohydrate Esterase Family 1 (fragment)
Phchr2 2983171	scaffold_8:931586-933309	1723	CBM1 Carbohydrate-Binding Module Family 1 (fragment)
			CE1 Carbohydrate Esterase Family 1 (fragment)
Phchr2 2899912	scaffold_2:2291467-2293106	1639	CE4 Carbohydrate Esterase Family 4
Phchr2 2936309	scaffold_11:331549-333315	1766	CE4 Carbohydrate Esterase Family 4
Phchr2 3028265	scaffold_8:1208558-1210261	1703	CE4 Carbohydrate Esterase Family 4
Phchr2 3082211	scaffold_3:2106877-2108940	2063	CE4 Carbohydrate Esterase Family 4
Phchr2 2934294	scaffold_9:118655-120533	1878	CE8 Carbohydrate Esterase Family 8
Phchr2 2989297	scaffold_17:457343-459493	2150	CE8 Carbohydrate Esterase Family 8
Phchr2 2902077	scaffold_4:1326983-1328875	1892	CE9 Carbohydrate Esterase Family 9
Phchr2 2912243	scaffold_11:520070-521401	1331	CE15 Carbohydrate Esterase Family 15
Phchr2 2918304	scaffold_18:295842-297362	1520	CBM1 Carbohydrate-Binding Module Family 1
			CE15 Carbohydrate Esterase Family 15
Phchr2 2944067	scaffold_1:1496455-1497614	1159	CE16 Carbohydrate Esterase Family 16
Phchr2 2945410	scaffold_2:126272-127923	1651	CE16 Carbohydrate Esterase Family 16
Phchr2 2967260	scaffold_4:1165153-1166770	1617	CBM1 Carbohydrate-Binding Module Family 1
			CE16 Carbohydrate Esterase Family 16
Phchr2 2974034	scaffold_1:1495224-1496493	1269	CE16 Carbohydrate Esterase Family 16
Phchr2 2974203	scaffold_1:1785224-1786802	1578	CE16 Carbohydrate Esterase Family 16
Phchr2 3004047	scaffold_6:944120-945299	1179	CE16 Carbohydrate Esterase Family 16
Phchr2 3038104	scaffold_6:947551-948836	1285	CE16 Carbohydrate Esterase Family 16
Phchr2 3030006	scaffold_11:1190477-1193363	2886	PL8_4 Polysaccharide Lyase Family 8
Phchr2 1196899	scaffold_1:3047062-3049612	2550	PL14 Polysaccharide Lyase Family 14
Phchr2 2881328	scaffold_2:2401579-2402447	868	PL14_4 Polysaccharide Lyase Family 14 (fragment) old model (1817) was better
Phchr2 2906498	scaffold_6:1088603-1089858	1255	PL14_5 Polysaccharide Lyase Family 14 (2906498)
Phchr2 2988953	scaffold_16:593308-594564	1256	PL14_4 Polysaccharide Lyase Family 14 (fragment)
Phchr2 964	scaffold_1:3084684-3085714	1030	PL14_4 Polysaccharide Lyase Family 14

**Table-S3:** Lists the differentially expressed cellulolytic and hemicellulolytic enzymes and CAZymes of GSE69461 dataset obtained after the Limma analysis.

Protein_ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	iprDesc
3001496	2.17E+03	1.22E+03	2.04E+02	1.45E-29	1.98E-25	49.02403	Glycosyl hydrolase, family 13,
3010472	2.76E+02	3.05E+02	8.63E+01	2.15E-23	2.01E-20	42.07078	Glycoside hydrolase, family 18,
3038646	3.44E+03	2.06E+03	7.69E+01	1.47E-22	6.88E-20	40.66031	Glycoside hydrolase, family 25
2912549	-2.07E+02	3.36E+02	-6.91E+01	8.51E-22	3.05E-19	39.28522	Glycoside hydrolase, family 3,
3010808	-2.54E+01	1.76E+01	-6.85E+01	9.68E-22	3.21E-19	39.18158	Cellulose-binding region, fungal
2915237	4.34E+02	3.03E+02	6.39E+01	3.08E-21	6.88E-19	38.23167	Glycoside hydrolase, family 5
2938536	-2.24E+02	1.30E+02	-5.94E+01	1.03E-20	1.94E-18	37.21624	Carboxylesterase, type B
2902469	2.58E+02	2.72E+02	5.45E+01	4.25E-20	5.84E-18	35.97712	Glycoside hydrolase, family 17
2985730	-7.99E+02	1.02E+03	-4.42E+01	1.30E-18	9.91E-17	32.85653	Glycoside hydrolase, family 5
3004615	-7.29E+01	9.73E+01	-3.99E+01	6.94E-18	3.93E-16	31.27354	Carboxylesterase, type B
3005443	-3.38E+02	2.90E+02	-3.87E+01	1.17E-17	5.98E-16	30.7696	Carboxylesterase, type B
7087	7.18E+01	4.65E+01	3.67E+01	2.80E-17	1.22E-15	29.92791	Glycosyl hydrolase, family 13,
2661256	-3.20E+02	2.64E+02	-3.67E+01	2.82E-17	1.22E-15	29.91963	Glycosyl hydrolase, family 13,
1479415	-1.28E+02	1.06E+02	-3.65E+01	3.03E-17	1.28E-15	29.85275	Carboxylesterase, type B
2894724	-1.67E+01	1.84E+01	-3.43E+01	8.24E-17	3.10E-15	28.8736	Glycoside hydrolase, family 47
2983917	7.31E+01	6.24E+01	3.31E+01	1.52E-16	5.13E-15	28.27234	Glycosyl hydrolase, family 13,
2914306	6.79E+01	7.88E+01	3.27E+01	1.86E-16	5.97E-15	28.07493	Glycoside hydrolase, family 16
3029839	-2.57E+02	2.28E+02	-3.15E+01	3.32E-16	9.75E-15	27.49845	Glycoside hydrolase, family 5
133070	1.41E+02	8.33E+01	3.07E+01	5.24E-16	1.44E-14	27.04477	Glycoside hydrolase, family 43
2981829	3.63E+01	2.99E+01	2.95E+01	9.83E-16	2.46E-14	26.41697	Glycoside hydrolase, family 16
3032176	-5.75E+01	1.05E+02	-2.77E+01	2.69E-15	5.90E-14	25.40605	Glycoside hydrolase, family 47
1563091	-5.68E+00	9.84E+00	-2.68E+01	4.57E-15	9.23E-14	24.87296	Glycosyl transferase, group 1
3004591	-1.11E+03	6.47E+02	-2.64E+01	6.03E-15	1.17E-13	24.5928	Carboxylesterase, type B
2988504	7.18E+01	5.75E+01	2.63E+01	6.35E-15	1.22E-13	24.53963	Glycosyl transferase, family 15
1807461	1.37E+02	1.31E+02	2.62E+01	6.65E-15	1.27E-13	24.49389	Glycoside hydrolase, family 5
123179	6.86E+01	7.10E+01	2.62E+01	6.84E-15	1.30E-13	24.46501	Glycosyl transferase, family 48
2975231	5.71E+00	9.74E+00	2.53E+01	1.17E-14	2.08E-13	23.92448	Glycoside hydrolase, family 9
2972234	7.15E+01	6.66E+01	2.47E+01	1.75E-14	2.95E-13	23.51071	Glycoside hydrolase, family 20,
3024192	-5.21E+01	8.94E+01	-2.32E+01	4.78E-14	6.92E-13	22.48873	Glycoside hydrolase, family 47
3029505	-2.20E+01	2.24E+01	-2.27E+01	6.92E-14	9.46E-13	22.11061	Glycoside hydrolase, family 31
2971505	1.64E+01	1.85E+01	2.23E+01	8.79E-14	1.16E-12	21.86535	Glycoside hydrolase, family 5
140501	-4.60E+02	4.64E+02	-2.23E+01	9.19E-14	1.21E-12	21.82028	Glycoside hydrolase, family 5
3006243	2.07E+03	1.24E+03	2.09E+01	2.48E-13	2.91E-12	20.80204	Glycoside hydrolase, family 18,
2983171	-7.70E+02	8.69E+02	-2.04E+01	3.59E-13	4.01E-12	20.42252	Cellulose-binding region, fungal
2933600	-7.94E+00	1.81E+01	-2.04E+01	3.72E-13	4.14E-12	20.38574	Glycosyl transferase, family 4

2976248	-3.01E+03	3.45E+03	-2.04E+01	3.73E-13	4.14E-12	20.38366	Glycoside hydrolase, family 7
2989206	-9.68E+00	2.29E+01	-2.03E+01	4.12E-13	4.53E-12	20.28125	Glycosyl transferase, group 1
1511835	2.68E+01	6.58E+01	1.96E+01	7.26E-13	7.44E-12	19.69638	Glycosyl transferase, family 8
2986919	-2.85E+01	3.12E+01	-1.94E+01	7.96E-13	8.08E-12	19.60178	Glycoside hydrolase, family 35
2947739	1.01E+01	1.27E+01	1.93E+01	9.35E-13	9.32E-12	19.43641	Glycoside hydrolase, family 16
2899470	-7.09E+00	1.95E+01	-1.84E+01	1.84E-12	1.72E-11	18.73766	ALG6, ALG8 glycosyltransferase
2579514	-9.44E+01	9.44E+01	-1.84E+01	1.88E-12	1.75E-11	18.71296	Glycoside hydrolase, family 47
3026777	1.76E+01	1.69E+01	1.80E+01	2.66E-12	2.37E-11	18.35559	Glycoside hydrolase, family 61
2985660	8.99E+02	5.03E+02	1.76E+01	3.76E-12	3.21E-11	17.99981	Glycoside hydrolase, family 18,
2903539	-5.04E+01	1.27E+02	-1.73E+01	4.96E-12	4.10E-11	17.71082	Glycoside hydrolase, family 10
2967175	1.54E+03	9.31E+02	1.73E+01	5.29E-12	4.33E-11	17.64457	Glycoside hydrolase, family 18,
2983729	-6.82E+02	3.44E+02	-1.72E+01	5.68E-12	4.59E-11	17.57116	Glycoside hydrolase, family 10
1405090	-2.38E+01	3.39E+01	-1.70E+01	6.45E-12	5.16E-11	17.43966	Glycoside hydrolase, family 71
2890266	-2.34E+01	6.35E+01	-1.59E+01	1.88E-11	1.33E-10	16.32827	Glycosyl hydrolase, family 88
3030418	-1.23E+02	1.37E+02	-1.57E+01	2.37E-11	1.63E-10	16.09132	Glycoside hydrolase 15-related
2967260	-3.47E+02	3.51E+02	-1.57E+01	2.42E-11	1.66E-10	16.06765	Cellulose-binding region, fungal
2905526	9.41E+00	2.45E+01	1.55E+01	2.69E-11	1.83E-10	15.95779	Glycoside hydrolase, family 18,
3003144	5.34E+01	1.23E+02	1.54E+01	3.23E-11	2.17E-10	15.76937	Glycoside hydrolase, family 3,
3042040	-3.17E+02	1.73E+02	-1.52E+01	4.01E-11	2.63E-10	15.54471	Glycoside hydrolase, family 10
2982319	-2.58E+03	3.01E+03	-1.51E+01	4.43E-11	2.87E-10	15.43901	Glycoside hydrolase, family 61
2934397	-2.71E+02	1.63E+02	-1.48E+01	5.64E-11	3.56E-10	15.18929	Glycoside hydrolase, family 61
2928769	-9.89E+00	2.39E+01	-1.48E+01	5.86E-11	3.68E-10	15.14936	Alg9-like mannosyltransferase
3027731	-1.21E+03	1.41E+03	-1.44E+01	8.86E-11	5.34E-10	14.71912	Cellulose-binding region, fungal
137042	-3.69E+00	4.22E+00	-1.44E+01	9.01E-11	5.43E-10	14.70176	Glycoside hydrolase, family 7
2905250	7.25E+01	1.62E+02	1.40E+01	1.35E-10	7.77E-10	14.28085	Glycosyl transferase, family 2
3030749	-3.60E+00	9.92E+00	-1.40E+01	1.40E-10	8.04E-10	14.23934	Carboxylesterase, type B
3029242	-1.22E+03	1.48E+03	-1.38E+01	1.62E-10	9.13E-10	14.09137	Glycoside hydrolase, family 61
3034582	-2.20E+02	3.83E+02	-1.38E+01	1.64E-10	9.22E-10	14.08085	Glycosyl transferase, group 1
2924247	-1.31E+01	3.52E+01	-1.35E+01	2.25E-10	1.24E-09	13.74845	Glycoside hydrolase, family 47
2981757	-1.13E+03	2.73E+03	-1.35E+01	2.50E-10	1.35E-09	13.641	Glycoside hydrolase, family 5
3027410	-2.58E+02	1.77E+02	-1.33E+01	2.99E-10	1.59E-09	13.45437	Glycoside hydrolase, family 28
2905144	-1.85E+02	1.35E+02	-1.33E+01	3.04E-10	1.62E-09	13.43672	Carboxylesterase, type B
2903670	5.27E+01	1.66E+02	1.31E+01	3.60E-10	1.89E-09	13.25829	Glycoside hydrolase, family 1
2896433	-1.07E+02	7.11E+01	-1.31E+01	3.68E-10	1.92E-09	13.23761	Glycoside hydrolase, family 43
2908961	9.93E+00	2.35E+01	1.29E+01	4.51E-10	2.31E-09	13.02374	Glycosyl transferase, family 28
2950055	-2.51E+01	9.84E+01	-1.29E+01	4.89E-10	2.48E-09	12.94031	Glycoside hydrolase, family 31



3003440	-5.18E+01	5.08E+01	-1.28E+01	5.11E-10	2.58E-09	12.89393	Glycosyl hydrolase 92
2903808	-2.97E+01	1.25E+02	-1.25E+01	7.85E-10	3.81E-09	12.44675	Carboxylesterase, type B
2917733	4.63E+01	4.70E+01	1.24E+01	8.80E-10	4.23E-09	12.32761	Glycoside hydrolase, family 20,
2982894	-4.66E+01	6.77E+01	-1.23E+01	9.11E-10	4.36E-09	12.29218	Glycoside hydrolase, family 61
2959592	-4.76E+01	1.73E+02	-1.23E+01	1.01E-09	4.82E-09	12.17918	Glycosyl transferase, family 2
2913826	2.48E+01	2.90E+01	1.22E+01	1.08E-09	5.10E-09	12.11236	Glycoside hydrolase, family 71
3007303	-2.62E+01	3.13E+01	-1.20E+01	1.38E-09	6.36E-09	11.85545	Glycoside hydrolase, family 5
2981885	-2.30E+01	4.59E+01	-1.19E+01	1.51E-09	6.86E-09	11.76658	Carboxylesterase, type B
2917244	4.15E+00	7.79E+00	1.17E+01	2.09E-09	9.25E-09	11.4242	Glycosyl hydrolase, family 13,
2974311	-8.53E+00	5.07E+01	-1.16E+01	2.23E-09	9.79E-09	11.35905	Glycoside hydrolase, family 63
2977447	-3.40E+01	1.56E+02	-1.15E+01	2.75E-09	1.18E-08	11.14117	Glycosyl transferase, family 39
3025644	4.31E+01	8.78E+01	1.14E+01	2.93E-09	1.26E-08	11.07159	Glycosyl transferase, family 48
3040475	-1.13E+01	1.57E+01	-1.14E+01	2.99E-09	1.28E-08	11.05343	Glycoside hydrolase, family 61
2989563	-8.26E+01	5.55E+01	-1.12E+01	3.65E-09	1.53E-08	10.84461	Glycoside hydrolase, family 28
2965119	-2.64E+03	3.38E+03	-1.10E+01	4.85E-09	2.00E-08	10.54661	Glycoside hydrolase, family 6
131440	-5.17E+02	9.86E+02	-1.10E+01	4.92E-09	2.02E-08	10.53197	Cellulose-binding region, fungal
2971598	-5.11E+00	1.44E+01	-1.09E+01	5.42E-09	2.21E-08	10.43146	Glycoside hydrolase, family 7
2981883	9.40E+00	2.87E+01	1.08E+01	6.40E-09	2.58E-08	10.25821	Glycosyltransferase sugar-binding DXD motif
3024004	-1.41E+02	1.16E+02	-1.03E+01	1.31E-08	5.00E-08	9.507578	Glycoside hydrolase, family 10
2983356	-8.97E+01	6.75E+01	-1.03E+01	1.33E-08	5.06E-08	9.495527	Glycosyl hydrolase 53
2897258	2.42E+01	1.10E+02	1.03E+01	1.36E-08	5.18E-08	9.469373	Carboxylesterase, type B
2909460	3.60E+01	4.17E+01	1.00E+01	1.91E-08	7.08E-08	9.114959	Glycoside hydrolase 15
2989061	7.34E+00	4.12E+01	9.91E+00	2.28E-08	8.33E-08	8.932117	Glycosyl transferase, family 3
2979830	-9.85E+01	6.70E+01	-9.88E+00	2.40E-08	8.71E-08	8.881416	Glycoside hydrolase, family 28
2971601	6.97E+02	9.66E+02	9.87E+00	2.43E-08	8.82E-08	8.866168	Glycoside hydrolase, family 7
2985725	1.33E+01	2.94E+01	9.77E+00	2.79E-08	1.00E-07	8.721979	Glycoside hydrolase, family 20,
121734	1.26E+02	1.49E+02	9.59E+00	3.63E-08	1.27E-07	8.447777	Glycoside hydrolase, family 16
2980975	-2.04E+02	2.88E+02	-9.59E+00	3.66E-08	1.28E-07	8.439314	Cellulose-binding region, fungal
1504690	-3.95E+00	2.43E+01	-9.37E+00	5.05E-08	1.72E-07	8.103113	Alg9-like mannosyltransferase
2899497	-1.40E+00	5.63E+00	-9.21E+00	6.43E-08	2.14E-07	7.851858	Glycoside hydrolase, family 85
2935636	-1.12E+03	5.68E+02	-9.13E+00	7.32E-08	2.41E-07	7.715938	Glycoside hydrolase, family 10
2988862	-6.92E+00	1.83E+01	-9.12E+00	7.37E-08	2.42E-07	7.709227	Glycoside hydrolase, family 5
2973689	-1.43E+02	1.69E+02	-9.04E+00	8.36E-08	2.72E-07	7.578477	Glycoside hydrolase, family 43
2919526	-2.40E+02	1.61E+02	-9.03E+00	8.47E-08	2.76E-07	7.564335	Glycoside hydrolase, family 3,
2990791	-1.07E+02	1.15E+02	-8.89E+00	1.05E-07	3.36E-07	7.338116	Glycoside hydrolase, family 35
2902099	6.29E+00	6.37E+01	8.83E+00	1.16E-07	3.68E-07	7.237384	Glycoside hydrolase, family 37

2973784	6.73E+01	1.54E+02	8.83E+00	1.16E-07	3.68E-07	7.236039	Glycosyl hydrolase, family 13,
2902324	5.26E+02	9.39E+02	8.79E+00	1.24E-07	3.91E-07	7.168921	Glycoside hydrolase, family 1
3717	-1.54E+01	3.89E+01	-8.52E+00	1.90E-07	5.80E-07	6.723535	Cellulose-binding region, fungal
3007125	-2.38E+02	4.44E+02	-8.33E+00	2.58E-07	7.71E-07	6.404551	Glycoside hydrolase, family 12
2933015	-1.22E+02	1.06E+02	-8.28E+00	2.79E-07	8.31E-07	6.321449	Glycoside hydrolase, family 43
2943421	6.40E+00	2.49E+01	8.20E+00	3.15E-07	9.30E-07	6.195198	ALG3
3002242	1.29E+00	3.69E+00	8.17E+00	3.33E-07	9.77E-07	6.13916	Glycoside hydrolase, family 3
2945552	-2.84E+01	6.60E+01	-7.93E+00	4.94E-07	1.41E-06	5.727434	Glycoside hydrolase, family 3
2990154	5.45E+01	7.51E+01	7.92E+00	5.09E-07	1.44E-06	5.697055	Glycoside hydrolase, family 30
2979836	-2.05E+01	1.90E+01	-7.78E+00	6.37E-07	1.78E-06	5.463926	Glycoside hydrolase, family 5
135833	6.08E+01	2.57E+02	7.69E+00	7.50E-07	2.07E-06	5.293528	Glycoside hydrolase, family 31
2907097	7.57E-01	1.43E+00	7.64E+00	8.05E-07	2.21E-06	5.220277	Glycosyl hydrolase, family 88
1610537	-2.18E+01	5.33E+01	-7.64E+00	8.17E-07	2.23E-06	5.204858	Cellulose-binding region, fungal
2963771	9.32E+00	4.28E+01	7.61E+00	8.61E-07	2.34E-06	5.150077	ALG6, ALG8 glycosyltransferase
2978123	4.25E+02	7.12E+02	7.60E+00	8.64E-07	2.35E-06	5.146207	Glycoside hydrolase, family 18
2906548	-8.30E+00	3.02E+01	-7.50E+00	1.03E-06	2.78E-06	4.960657	Glycoside hydrolase, family 16
2908992	-5.60E+01	1.76E+02	-7.47E+00	1.09E-06	2.91E-06	4.908084	Glycoside hydrolase, family 3
2904202	-9.35E+02	6.62E+02	-7.45E+00	1.13E-06	3.01E-06	4.871072	Glycoside hydrolase, family 28
2955500	-5.40E+01	1.45E+02	-7.43E+00	1.17E-06	3.11E-06	4.835653	Glycoside hydrolase, family 5
2988656	1.05E+02	3.21E+02	7.33E+00	1.39E-06	3.66E-06	4.650823	Glycosyl transferase, family 20
5751	-2.12E+02	3.11E+02	-7.14E+00	1.96E-06	5.02E-06	4.296787	Glycosyl transferase, family 35
3030351	-1.72E+03	1.79E+03	-7.06E+00	2.22E-06	5.65E-06	4.164529	Glycoside hydrolase, family 10
42616	1.10E+02	3.82E+02	7.06E+00	2.23E-06	5.65E-06	4.163082	Glycoside hydrolase, family 61
2895063	-2.60E+01	4.17E+01	-6.97E+00	2.61E-06	6.56E-06	3.998935	Glycoside hydrolase, family 31
2917930	-1.21E+01	1.43E+01	-6.72E+00	4.17E-06	1.02E-05	3.513041	Glycoside hydrolase, family 37
2989703	-1.14E+02	4.30E+02	-6.66E+00	4.65E-06	1.13E-05	3.398492	Glycoside hydrolase, family 5
1416762	-1.02E+03	1.13E+03	-6.34E+00	8.42E-06	1.98E-05	2.784984	Glycoside hydrolase, family 12
2973374	-1.28E+01	2.84E+01	-6.22E+00	1.06E-05	2.45E-05	2.548046	Glycoside hydrolase, family 20
3022485	-2.07E+01	1.50E+02	-6.15E+00	1.20E-05	2.77E-05	2.415614	Glycoside hydrolase, family 31
2918304	-6.49E+02	6.44E+02	-6.13E+00	1.26E-05	2.88E-05	2.36963	Cellulose-binding region, fungal
2911333	-2.32E+00	7.78E+00	-6.09E+00	1.36E-05	3.10E-05	2.290349	Glycosyl hydrolase, family 13
2101068	-8.19E-01	1.53E+00	-6.08E+00	1.37E-05	3.12E-05	2.279915	Glycosyl transferase, family 8
2932560	-3.54E+00	2.03E+01	-5.91E+00	1.90E-05	4.26E-05	1.942111	Glycoside hydrolase, family 5
2898439	-2.13E-01	2.28E-01	-5.83E+00	2.23E-05	4.94E-05	1.777804	Glycoside hydrolase, family 3
139304	-9.14E+00	1.09E+02	-5.74E+00	2.70E-05	5.90E-05	1.582265	Glycoside hydrolase family 2
2905606	-1.51E+03	1.56E+03	-5.35E+00	5.83E-05	1.21E-04	0.79043	Glycoside hydrolase, family 11



2974351	2.97E+00	2.46E+01	5.32E+00	6.13E-05	1.27E-04	0.738372	Glycosyl hydrolase, family 88
2976448	-7.24E+02	3.65E+03	-5.22E+00	7.58E-05	1.54E-04	0.520875	Glycoside hydrolase, family 61
2898059	-2.53E+00	1.26E+01	-5.05E+00	1.08E-04	2.16E-04	0.158278	Glycosyl hydrolase 92
137372	-1.86E+03	1.48E+03	-5.00E+00	1.19E-04	2.37E-04	0.055068	Glycoside hydrolase, family 7
1405277	1.16E+00	3.09E+00	4.99E+00	1.22E-04	2.42E-04	0.030007	Glycoside hydrolase, family 71
125979	-3.59E+00	2.59E+01	-4.70E+00	2.21E-04	4.23E-04	-0.57489	Glycosyl transferase, family 8
2978860	-2.11E+01	9.35E+01	-4.65E+00	2.44E-04	4.62E-04	-0.67268	Glycoside hydrolase, family 18,
2895067	-3.82E+01	9.67E+01	-4.45E+00	3.71E-04	6.89E-04	-1.10016	Cellulose-binding region, fungal
2960840	-2.46E+00	1.53E+01	-4.42E+00	4.02E-04	7.42E-04	-1.18028	Alg9-like mannosyltransferase
2953310	-2.30E+01	9.78E+01	-4.26E+00	5.61E-04	1.02E-03	-1.51873	Glycosyl hydrolase 92
2980158	-2.93E+01	4.11E+01	-4.19E+00	6.51E-04	1.17E-03	-1.6689	Glycoside hydrolase, family 61
2910409	1.46E+01	9.37E+01	4.10E+00	7.79E-04	1.39E-03	-1.85039	Glycosyl transferase, family 20
2943450	1.13E+00	6.89E+00	4.00E+00	9.80E-04	1.72E-03	-2.08262	Glycoside hydrolase, family 5
3031980	3.40E-01	1.19E+00	3.94E+00	1.10E-03	1.92E-03	-2.20149	Carboxylesterase, type B
3005667	-4.46E+00	1.46E+01	-3.87E+00	1.30E-03	2.24E-03	-2.36453	Glycoside hydrolase, clan GH-D
3005755	-2.74E+00	3.31E+01	-3.73E+00	1.73E-03	2.94E-03	-2.65461	Glycosyl transferase, family 2
3002489	-1.45E+01	5.65E+01	-3.73E+00	1.74E-03	2.96E-03	-2.66087	Glycosyl hydrolase 92
2897299	-1.04E+01	1.31E+02	-3.61E+00	2.27E-03	3.79E-03	-2.92236	Glycosyl transferase, family 39
3022184	-7.17E+00	5.47E+01	-3.58E+00	2.42E-03	4.03E-03	-2.98609	Glycosyl transferase, family 28,
3024704	3.66E-01	1.12E+00	3.55E+00	2.56E-03	4.24E-03	-3.04126	Carboxylesterase, type B
2975821	-1.61E+03	3.13E+03	-3.46E+00	3.08E-03	5.06E-03	-3.22843	Glycoside hydrolase, family 61
3003776	-6.89E+01	7.55E+02	-3.40E+00	3.52E-03	5.74E-03	-3.3599	Glycoside hydrolase, family 61
2908293	6.15E+01	1.57E+02	3.25E+00	4.89E-03	7.80E-03	-3.68365	Glycoside hydrolase, family 61
2919440	4.79E-01	2.25E+00	2.99E+00	8.38E-03	1.30E-02	-4.21149	Glycoside hydrolase, family 18,
3039695	-4.79E+00	5.90E+01	-2.88E+00	1.05E-02	1.61E-02	-4.43399	Glycoside hydrolase, family 38
2562	-3.91E-01	1.08E+00	-2.81E+00	1.23E-02	1.86E-02	-4.58348	Glycosyl transferase, family 8
1216344	2.01E+01	9.04E+01	2.81E+00	1.24E-02	1.87E-02	-4.58789	Glycoside hydrolase, family 61
2908361	4.71E+01	3.35E+02	2.64E+00	1.76E-02	2.60E-02	-4.92582	Glycosyl transferase, family 20
3024052	1.38E+01	1.64E+02	2.60E+00	1.92E-02	2.82E-02	-5.00842	Glycoside hydrolase, family 3,
2973415	-4.04E+00	7.08E+01	-2.54E+00	2.17E-02	3.17E-02	-5.12474	Glycosyl transferase, family 39
3028741	1.80E+00	3.34E+01	2.19E+00	4.32E-02	6.03E-02	-5.77018	Glycoside hydrolase, family 3,
3007720	-1.10E+01	8.01E+00	-2.15E+00	4.69E-02	6.51E-02	-5.84619	Glycoside hydrolase, family 7
3008474	-1.68E+00	2.70E+01	-2.12E+00	4.99E-02	6.89E-02	-5.9026	Glycosyl transferase, group 1
30940	-1.47E+01	1.63E+02	-2.02E+00	6.01E-02	8.20E-02	-6.07255	Glycosyltransferase sugar-binding DXD motif
3024803	3.08E-01	2.49E+00	1.94E+00	6.95E-02	9.37E-02	-6.20258	Glycoside hydrolase, family 7
2973764	3.94E+00	8.05E+01	1.80E+00	9.01E-02	1.19E-01	-6.43289	Glycosyl transferase, family 15

2966954	-6.46E+00	5.14E+01	-1.69E+00	1.09E-01	1.43E-01	-6.59879	Glycosyl transferase, family 2
3005492	1.79E+00	1.40E+01	1.55E+00	1.39E-01	1.79E-01	-6.8068	Glycoside hydrolase, family 61
2920193	-6.10E-02	1.30E-01	-1.37E+00	1.90E-01	2.39E-01	-7.06397	Glycoside hydrolase, family 35
3003319	-8.59E-02	5.24E-01	-1.35E+00	1.95E-01	2.44E-01	-7.08477	Glycoside hydrolase, family 18
4464	1.72E-01	1.05E+00	1.16E+00	2.62E-01	3.20E-01	-7.31447	Glycosyltransferase sugar-binding DXD motif
2965653	-1.50E+00	3.99E+01	-9.59E-01	3.51E-01	4.18E-01	-7.52582	Glycosyl hydrolase, family 88
840	-3.71E+00	6.38E+01	-9.10E-01	3.76E-01	4.45E-01	-7.57256	Glycosyl hydrolase, family 88
3004691	1.03E+02	2.72E+03	8.53E-01	4.06E-01	4.77E-01	-7.62326	Glycoside hydrolase, family 61
1854721	6.58E-02	4.57E-01	8.22E-01	4.23E-01	4.94E-01	-7.6495	Glycoside hydrolase, family 3,
3002377	2.14E-02	5.88E-02	7.09E-01	4.88E-01	5.63E-01	-7.73766	Glycoside hydrolase, family 18,
3029525	-5.84E+00	8.36E+01	-6.79E-01	5.07E-01	5.82E-01	-7.75954	Glycoside hydrolase, family 31
2981806	-3.36E-01	2.29E+01	-6.54E-01	5.22E-01	5.97E-01	-7.77671	Glycoside hydrolase, clan GH-D
3005328	-2.62E-01	5.29E+00	-6.43E-01	5.29E-01	6.04E-01	-7.78408	Glycosyl transferase, family 17
3007725	9.48E-02	3.75E-01	6.32E-01	5.36E-01	6.11E-01	-7.79138	Glycosyl transferase, family 2
2974470	1.21E+00	4.72E+01	5.64E-01	5.80E-01	6.55E-01	-7.83339	Glycoside hydrolase, family 3
2921170	2.78E-01	1.89E+01	5.28E-01	6.05E-01	6.80E-01	-7.85399	Alg9-like mannosyltransferase
2904243	2.01E-01	4.38E+00	3.50E-01	7.31E-01	8.03E-01	-7.93558	Glycosyl transferase, family 8
2913220	2.69E-01	1.62E+01	3.13E-01	7.58E-01	8.29E-01	-7.94847	Glycosyl transferase, family 28
2898363	5.22E-02	3.93E+00	2.98E-01	7.70E-01	8.40E-01	-7.95334	Glycosyl transferase, family 8
2916357	-6.84E+00	3.22E+02	-2.15E-01	8.32E-01	8.97E-01	-7.97562	Cellulose-binding region, fungal
2901646	-1.46E-02	1.46E+00	-9.25E-02	9.27E-01	9.85E-01	-7.99564	Glycosyl transferase, family 8
2976245	-2.04E-19	2.00E-03	-8.52E-18	1.00E+00	1.00E+00	-8.00017	Glycoside hydrolase, family 7
3025918	-1.55E+03	8.20E+02	-1.22E+02	7.37E-26	2.00E-22	45.59945	Major facilitator superfamily MFS-1
11055	-6.28E+02	3.77E+02	-8.90E+01	1.30E-23	1.61E-20	42.42022	Aldo/keto reductase
3082211	1.75E+02	1.40E+02	7.80E+01	1.15E-22	5.58E-20	40.84563	Polysaccharide deacetylase
3082211	1.75E+02	1.40E+02	7.80E+01	1.15E-22	5.58E-20	40.84563	Polysaccharide deacetylase
1475950	-2.47E+02	1.73E+02	-6.93E+01	8.04E-22	2.96E-19	39.33018	Aldo/keto reductase
2990225	-3.26E+01	4.68E+01	-6.94E+01	7.93E-22	2.96E-19	39.34133	Major facilitator superfamily MFS-1
3030673	-7.97E+01	5.03E+01	-6.36E+01	3.35E-21	7.34E-19	38.16366	Alcohol dehydrogenase, zinc-binding
2979948	-2.66E+02	1.82E+02	-5.87E+01	1.25E-20	2.20E-18	37.04779	Aldehyde dehydrogenase
2989142	-2.25E+02	1.14E+02	-5.40E+01	4.87E-20	6.43E-18	35.85708	Major facilitator superfamily MFS-1
3100406	-2.45E+02	2.17E+02	-5.21E+01	8.84E-20	1.03E-17	35.32535	Major facilitator superfamily MFS-1
2906938	2.08E+01	1.36E+01	5.15E+01	1.09E-19	1.21E-17	35.1399	Major facilitator superfamily MFS-1
3025694	-5.36E+02	2.74E+02	-5.05E+01	1.47E-19	1.53E-17	34.87047	Major facilitator superfamily MFS-1
3028589	-4.55E+02	3.88E+02	-4.90E+01	2.45E-19	2.38E-17	34.40353	Aldo/keto reductase

3028265	2.53E+02	3.12E+02	4.72E+01	4.55E-19	4.02E-17	33.83495	Polysaccharide deacetylase
3028265	2.53E+02	3.12E+02	4.72E+01	4.55E-19	4.02E-17	33.83495	Polysaccharide deacetylase
3046761	-4.92E+01	4.72E+01	-4.27E+01	2.33E-18	1.65E-16	32.30904	Major facilitator superfamily MFS-1
2966854	-2.71E+02	2.36E+02	-4.25E+01	2.54E-18	1.74E-16	32.22996	Major facilitator superfamily MFS-1
2965601	9.49E+00	1.25E+01	4.19E+01	3.15E-18	2.13E-16	32.02559	Alcohol dehydrogenase, zinc-binding
3028048	-1.16E+02	8.52E+01	-4.16E+01	3.55E-18	2.33E-16	31.91219	Aldo/keto reductase
2986615	-6.84E+02	8.53E+02	-4.14E+01	3.84E-18	2.46E-16	31.83697	Transaldolase
2986615	-6.84E+02	8.53E+02	-4.14E+01	3.84E-18	2.46E-16	31.83697	Transaldolase
3028998	-2.26E+01	1.55E+01	-3.83E+01	1.37E-17	6.80E-16	30.62036	Major facilitator superfamily MFS-1
3021882	-3.81E+01	5.14E+01	-3.74E+01	2.02E-17	9.31E-16	30.24467	Pyruvate carboxyltransferase
3021882	-3.81E+01	5.14E+01	-3.74E+01	2.02E-17	9.31E-16	30.24467	Pyruvate carboxyltransferase
3002295	7.24E+01	7.86E+01	3.63E+01	3.31E-17	1.38E-15	29.76632	Isocitrate/isopropylmalate dehydrogenase
2981181	2.04E+02	1.36E+02	3.51E+01	5.87E-17	2.27E-15	29.20706	Aldehyde dehydrogenase
3030674	-8.34E+01	1.04E+02	-3.42E+01	8.84E-17	3.30E-15	28.80531	Alcohol dehydrogenase, zinc-binding
3027892	1.37E+01	2.06E+01	3.38E+01	1.07E-16	3.81E-15	28.62026	Major facilitator superfamily MFS-1
1677212	-1.13E+02	5.98E+01	-3.32E+01	1.40E-16	4.82E-15	28.35178	Aldo/keto reductase
3006287	1.42E+04	7.70E+03	3.32E+01	1.42E-16	4.87E-15	28.33838	Isocitrate lyase and phosphorylmutase
2897929	1.65E+01	1.42E+01	3.32E+01	1.45E-16	4.96E-15	28.31627	Alcohol dehydrogenase, zinc-binding
3027616	1.24E+02	6.84E+01	3.20E+01	2.54E-16	7.75E-15	27.76549	Carbohydrate-binding WSC
2947158	-3.22E+01	6.24E+01	-3.20E+01	2.62E-16	7.95E-15	27.73435	Major facilitator superfamily MFS-1
2975107	1.34E+02	1.42E+02	3.13E+01	3.74E-16	1.08E-14	27.37901	Isocitrate/isopropylmalate dehydrogenase
2908453	-5.45E+01	7.31E+01	-3.13E+01	3.81E-16	1.09E-14	27.36192	Major facilitator superfamily MFS-1
2979276	2.58E+02	3.53E+02	3.09E+01	4.59E-16	1.29E-14	27.17712	Alcohol dehydrogenase, zinc-binding
2985848	7.83E+01	6.02E+01	3.03E+01	6.23E-16	1.64E-14	26.87227	Major facilitator superfamily MFS-1
3091373	1.82E+01	4.17E+01	2.94E+01	1.05E-15	2.61E-14	26.35052	Major facilitator superfamily MFS-1
3030607	-1.03E+02	1.11E+02	-2.91E+01	1.25E-15	3.01E-14	26.17883	Carbohydrate/purine kinase
2594256	7.28E+01	8.42E+01	2.86E+01	1.59E-15	3.76E-14	25.93214	Carbohydrate-binding WSC
2895206	-3.91E+01	9.94E+01	-2.85E+01	1.73E-15	4.03E-14	25.84761	Major facilitator superfamily MFS-1
3023018	-1.58E+02	1.29E+02	-2.83E+01	1.86E-15	4.25E-14	25.7768	Major facilitator superfamily MFS-1
3059317	-2.24E+02	2.56E+02	-2.66E+01	5.08E-15	1.01E-13	24.76576	Aldo/keto reductase
2895329	-8.33E+00	7.77E+00	-2.63E+01	6.15E-15	1.19E-13	24.57167	Major facilitator superfamily MFS-1
2990177	6.24E+01	1.32E+02	2.59E+01	8.05E-15	1.50E-13	24.29932	Aldose 1-epimerase
3936	6.33E+00	9.87E+00	2.52E+01	1.26E-14	2.22E-13	23.84333	Major facilitator superfamily MFS-1
7127	4.61E+01	6.76E+01	2.49E+01	1.55E-14	2.66E-13	23.63773	Carbonic anhydrase
3026723	-2.75E+02	1.90E+02	-2.43E+01	2.28E-14	3.69E-13	23.24196	Major facilitator superfamily MFS-1

1675787	-1.47E+01	2.64E+01	-2.33E+01	4.31E-14	6.33E-13	22.59389	Major facilitator superfamily MFS-1
1303762	5.74E+02	4.90E+02	2.26E+01	7.37E-14	9.99E-13	22.04552	Pyruvate kinase, barrel
1303762	5.74E+02	4.90E+02	2.26E+01	7.37E-14	9.99E-13	22.04552	Pyruvate kinase, barrel
3011118	-1.19E+02	1.68E+02	-2.17E+01	1.37E-13	1.72E-12	21.41428	Pyruvate carboxyltransferase
3011118	-1.19E+02	1.68E+02	-2.17E+01	1.37E-13	1.72E-12	21.41428	Pyruvate carboxyltransferase
2976077	-1.30E+02	8.63E+01	-2.15E+01	1.60E-13	1.99E-12	21.25332	Major facilitator superfamily MFS-1
2960185	3.59E+01	5.94E+01	2.10E+01	2.29E-13	2.72E-12	20.88333	Aldehyde dehydrogenase
2941093	-8.36E+00	9.42E+00	-2.09E+01	2.52E-13	2.95E-12	20.78442	Aldo/keto reductase
2979145	-1.32E+02	3.13E+02	-2.09E+01	2.53E-13	2.95E-12	20.78302	Isocitrate/isopropylmalate dehydrogenase
137014	-1.36E+03	1.01E+03	-2.07E+01	2.95E-13	3.37E-12	20.62414	Aldehyde dehydrogenase
3024173	5.87E+01	4.31E+01	2.07E+01	2.97E-13	3.39E-12	20.61756	Aldo/keto reductase
3082965	-1.94E+02	1.10E+02	-2.07E+01	3.00E-13	3.42E-12	20.60526	Major facilitator superfamily MFS-1
3023016	3.80E+00	3.46E+00	2.04E+01	3.85E-13	4.26E-12	20.35141	Major facilitator superfamily MFS-1
2907283	-3.36E+01	2.26E+01	-2.01E+01	4.53E-13	4.92E-12	20.18264	Major facilitator superfamily MFS-1
2909931	-5.36E+01	4.47E+01	-2.01E+01	4.85E-13	5.23E-12	20.11203	Major facilitator superfamily MFS-1
2924239	-1.23E+02	8.14E+01	-1.98E+01	5.83E-13	6.17E-12	19.92341	Major facilitator superfamily MFS-1
3021841	4.03E+01	6.97E+01	1.98E+01	6.17E-13	6.47E-12	19.86547	Major facilitator superfamily MFS-1
2968678	-3.29E+02	3.96E+02	-1.96E+01	7.19E-13	7.38E-12	19.707	Transketolase, N-terminal
2968678	-3.29E+02	3.96E+02	-1.96E+01	7.19E-13	7.38E-12	19.707	Transketolase, N-terminal
2973429	-3.47E+01	2.91E+01	-1.94E+01	8.02E-13	8.13E-12	19.59501	Aldo/keto reductase
3007552	-1.98E+01	2.79E+01	-1.93E+01	9.28E-13	9.27E-12	19.44414	Aldo/keto reductase
2966550	1.75E+02	3.93E+02	1.90E+01	1.11E-12	1.09E-11	19.2561	Carbohydrate kinase, FGGY
3023711	-3.15E+02	1.65E+02	-1.86E+01	1.58E-12	1.50E-11	18.89378	Major facilitator superfamily MFS-1
2986743	-9.38E+01	1.27E+02	-1.86E+01	1.63E-12	1.54E-11	18.86336	Aldo/keto reductase
2899470	-7.09E+00	1.95E+01	-1.84E+01	1.84E-12	1.72E-11	18.73766	ALG6, ALG8 glycosyltransferase
3030006	-1.04E+02	8.83E+01	-1.83E+01	2.05E-12	1.89E-11	18.62441	Polysaccharide lyase family 8, central
3030006	-1.04E+02	8.83E+01	-1.83E+01	2.05E-12	1.89E-11	18.62441	Polysaccharide lyase family 8, central
2897399	1.10E+02	1.89E+02	1.81E+01	2.58E-12	2.31E-11	18.38923	Major facilitator superfamily MFS-1
2901678	-9.28E+00	1.28E+01	-1.77E+01	3.53E-12	3.05E-11	18.0652	Major facilitator superfamily MFS-1
140379	-2.61E+01	2.90E+01	-1.76E+01	3.92E-12	3.33E-11	17.95638	Carbonic anhydrase
2118989	-5.53E+00	1.28E+01	-1.76E+01	3.95E-12	3.35E-11	17.94819	Carbohydrate-binding WSC
2981948	2.20E+01	3.43E+01	1.72E+01	5.55E-12	4.51E-11	17.59456	Major facilitator superfamily MFS-1
1222106	-1.84E+01	2.26E+01	-1.71E+01	5.90E-12	4.75E-11	17.53259	Major facilitator superfamily MFS-1
3019522	-1.20E+02	1.34E+02	-1.71E+01	6.23E-12	5.00E-11	17.47527	Aldehyde dehydrogenase
2874053	-3.16E+01	7.94E+01	-1.68E+01	8.25E-12	6.41E-11	17.18435	Major facilitator superfamily MFS-1
2905638	8.29E+01	1.18E+02	1.67E+01	8.72E-12	6.71E-11	17.12763	Alcohol dehydrogenase, zinc-binding

2918146	1.97E+01	1.22E+01	1.65E+01	1.11E-11	8.30E-11	16.87472	Major facilitator superfamily MFS-1
2985035	-2.74E+01	1.76E+01	-1.63E+01	1.33E-11	9.67E-11	16.69273	Major facilitator superfamily MFS-1
2983158	9.07E+00	9.13E+00	1.61E+01	1.50E-11	1.08E-10	16.56212	Major facilitator superfamily MFS-1
2988496	1.99E+01	7.42E+01	1.58E+01	2.01E-11	1.41E-10	16.26028	Carbohydrate kinase, FGGY
1171533	-3.13E+00	6.05E+00	-1.57E+01	2.34E-11	1.61E-10	16.10369	Major facilitator superfamily MFS-1
2953754	1.35E+01	1.52E+01	1.55E+01	2.83E-11	1.92E-10	15.90703	Major facilitator superfamily MFS-1
2348115	2.40E+00	2.98E+00	1.52E+01	3.79E-11	2.50E-10	15.60301	Major facilitator superfamily MFS-1
2898751	1.83E+01	6.10E+01	1.51E+01	4.32E-11	2.80E-10	15.46726	Carbohydrate kinase, FGGY
2899026	-1.45E+01	1.71E+01	-1.50E+01	4.86E-11	3.12E-10	15.34332	Aldo/keto reductase
2936309	-4.05E+01	1.43E+02	-1.49E+01	5.19E-11	3.30E-10	15.27534	Polysaccharide deacetylase
2936309	-4.05E+01	1.43E+02	-1.49E+01	5.19E-11	3.30E-10	15.27534	Polysaccharide deacetylase
3013791	-4.64E+00	1.13E+01	-1.49E+01	5.21E-11	3.31E-10	15.2712	Major facilitator superfamily MFS-1
2928769	-9.89E+00	2.39E+01	-1.48E+01	5.86E-11	3.68E-10	15.14936	Alg9-like mannosyltransferase
3004959	2.04E+03	1.78E+03	1.48E+01	6.02E-11	3.76E-10	15.12025	Isocitrate lyase and phosphorylmutase
3029387	-5.19E+00	1.36E+01	-1.47E+01	6.31E-11	3.92E-10	15.07252	Major facilitator superfamily MFS-1
2967033	8.65E+00	7.22E+00	1.47E+01	6.34E-11	3.94E-10	15.06716	Alcohol dehydrogenase, zinc-binding
2898456	-2.12E+01	3.58E+01	-1.46E+01	7.18E-11	4.41E-10	14.93783	Carboxyl transferase
2912533	-3.86E+01	1.38E+02	-1.46E+01	7.32E-11	4.49E-10	14.9172	Aldose 1-epimerase
2985089	-1.93E+01	3.60E+01	-1.42E+01	1.06E-10	6.27E-10	14.53295	Major facilitator superfamily MFS-1
3057388	9.40E+00	2.38E+01	1.40E+01	1.32E-10	7.63E-10	14.30448	Phosphoglycerate mutase
3057388	9.40E+00	2.38E+01	1.40E+01	1.32E-10	7.63E-10	14.30448	Phosphoglycerate mutase
3002629	-1.18E+01	1.57E+01	-1.40E+01	1.34E-10	7.71E-10	14.28963	Major facilitator superfamily MFS-1
2902784	-1.09E+02	6.79E+01	-1.38E+01	1.77E-10	9.92E-10	13.9962	Major facilitator superfamily MFS-1
2973416	1.90E+01	5.93E+01	1.37E+01	1.96E-10	1.09E-09	13.89373	Major facilitator superfamily MFS-1
1472281	-5.69E+00	8.39E+00	-1.35E+01	2.35E-10	1.29E-09	13.70271	Alcohol dehydrogenase, zinc-binding
3001158	-4.20E+01	9.67E+01	-1.35E+01	2.39E-10	1.30E-09	13.686	Aldo/keto reductase
3002302	9.73E+01	2.27E+02	1.34E+01	2.56E-10	1.38E-09	13.61593	Transketolase, central region
3002302	9.73E+01	2.27E+02	1.34E+01	2.56E-10	1.38E-09	13.61593	Transketolase, central region
3031560	2.52E+00	2.55E+00	1.34E+01	2.78E-10	1.49E-09	13.52889	Aldose 1-epimerase
2960428	1.24E+00	8.16E-01	1.33E+01	2.96E-10	1.58E-09	13.46465	Isocitrate lyase and phosphorylmutase
3021888	5.38E+01	1.10E+02	1.32E+01	3.36E-10	1.77E-09	13.33198	Alcohol dehydrogenase, zinc-binding
2972289	-3.22E+01	4.20E+01	-1.31E+01	3.70E-10	1.93E-09	13.23205	Aldo/keto reductase
2934371	-1.26E+01	3.38E+01	-1.31E+01	3.74E-10	1.95E-09	13.21932	Aldo/keto reductase
2990363	-7.34E+01	1.48E+02	-1.30E+01	4.24E-10	2.18E-09	13.08904	Aldehyde dehydrogenase
3028636	-4.18E+00	1.59E+01	-1.28E+01	5.27E-10	2.65E-09	12.86212	Mannose-6-phosphate isomerase, type I
3028636	-4.18E+00	1.59E+01	-1.28E+01	5.27E-10	2.65E-09	12.86212	Mannose-6-phosphate isomerase, type I

2967674	-9.09E+01	2.46E+02	-1.28E+01	5.46E-10	2.74E-09	12.82496	Phosphoglucose isomerase (PGI)
2967674	-9.09E+01	2.46E+02	-1.28E+01	5.46E-10	2.74E-09	12.82496	Phosphoglucose isomerase (PGI)
2914255	3.14E+00	4.78E+00	1.28E+01	5.47E-10	2.74E-09	12.82247	Alcohol dehydrogenase, zinc-binding
2916926	-2.00E+00	3.88E+00	-1.26E+01	6.57E-10	3.23E-09	12.63182	Major facilitator superfamily MFS-1
2230206	-4.09E+00	6.93E+00	-1.23E+01	9.18E-10	4.39E-09	12.28367	Major facilitator superfamily MFS-1
2895840	-3.60E+01	3.19E+01	-1.22E+01	1.06E-09	5.00E-09	12.13625	Aldehyde dehydrogenase
2895856	2.50E+00	2.33E+00	1.22E+01	1.08E-09	5.07E-09	12.11816	Aldehyde dehydrogenase
3005716	-2.77E+00	5.59E+00	-1.21E+01	1.22E-09	5.66E-09	11.99052	Major facilitator superfamily MFS-1
2989332	-2.73E+01	5.26E+01	-1.20E+01	1.40E-09	6.41E-09	11.84645	Alcohol dehydrogenase, zinc-binding
3033703	6.63E+01	1.29E+02	1.20E+01	1.47E-09	6.73E-09	11.7896	Major facilitator superfamily MFS-1
2990461	-3.92E+00	1.12E+01	-1.17E+01	1.98E-09	8.80E-09	11.48097	Alcohol dehydrogenase, zinc-binding
2983908	2.00E+01	3.51E+01	1.17E+01	2.10E-09	9.26E-09	11.42287	Aldo/keto reductase
3042361	5.16E+00	4.35E+00	1.16E+01	2.26E-09	9.92E-09	11.34454	Aldehyde dehydrogenase
1350	1.67E+02	3.96E+02	1.16E+01	2.28E-09	9.98E-09	11.33697	Aldehyde dehydrogenase
2974106	-2.38E+01	3.73E+01	-1.14E+01	3.12E-09	1.33E-08	11.00841	Transketolase, central region
2974106	-2.38E+01	3.73E+01	-1.14E+01	3.12E-09	1.33E-08	11.00841	Transketolase, central region
2947905	-3.81E+01	4.86E+01	-1.13E+01	3.45E-09	1.46E-08	10.9033	Carbohydrate kinase, FGGY
2901862	2.38E+01	3.55E+01	1.11E+01	4.58E-09	1.90E-08	10.60727	Major facilitator superfamily MFS-1
3025148	-3.91E+02	5.20E+02	-1.11E+01	4.68E-09	1.93E-08	10.58493	Aldose 1-epimerase
2954171	9.04E+00	4.04E+01	1.09E+01	5.94E-09	2.41E-08	10.33664	Major facilitator superfamily MFS-1
2973432	6.15E+00	2.24E+01	1.07E+01	7.16E-09	2.86E-08	10.14158	Major facilitator superfamily MFS-1
2984077	1.74E+00	2.75E+00	1.07E+01	7.35E-09	2.93E-08	10.11332	Carbohydrate/purine kinase
336	1.68E+02	1.26E+02	1.06E+01	8.66E-09	3.40E-08	9.942939	Aldo/keto reductase
3099150	6.02E+00	1.09E+01	1.06E+01	9.11E-09	3.56E-08	9.88942	Aldo/keto reductase
3035175	-1.62E+00	3.86E+00	-1.06E+01	9.29E-09	3.63E-08	9.869166	Major facilitator superfamily MFS-1
1018805	-7.93E+00	1.30E+01	-1.03E+01	1.27E-08	4.86E-08	9.54055	Major facilitator superfamily MFS-1
140008	-6.21E+00	1.41E+01	-1.03E+01	1.36E-08	5.19E-08	9.4682	Major facilitator superfamily MFS-1
2918287	1.72E+00	2.48E+00	1.02E+01	1.45E-08	5.50E-08	9.402062	Major facilitator superfamily MFS-1
3001516	2.72E+00	6.81E+00	9.90E+00	2.32E-08	8.47E-08	8.913208	Major facilitator superfamily MFS-1
2985524	-1.67E+01	6.52E+01	-9.79E+00	2.73E-08	9.82E-08	8.743331	Carbonic anhydrase
3023609	3.41E+01	7.29E+01	9.78E+00	2.78E-08	9.98E-08	8.725575	Aldehyde dehydrogenase
2969986	-7.79E+01	1.37E+02	-9.77E+00	2.78E-08	9.99E-08	8.724319	Alcohol dehydrogenase, zinc-binding
2917607	-3.87E+00	7.71E+00	-9.75E+00	2.87E-08	1.02E-07	8.694462	Major facilitator superfamily MFS-1
2915194	-4.99E+01	7.41E+01	-9.71E+00	3.04E-08	1.08E-07	8.631942	Alcohol dehydrogenase, zinc-binding
3039746	-1.58E+00	2.07E+00	-9.65E+00	3.33E-08	1.18E-07	8.539062	Aldo/keto reductase
2666328	7.48E+00	8.86E+00	9.41E+00	4.75E-08	1.63E-07	8.167406	Phosphoglycerate mutase

2666328	7.48E+00	8.86E+00	9.41E+00	4.75E-08	1.63E-07	8.167406	Phosphoglycerate mutase
3022385	4.83E+00	9.19E+00	9.40E+00	4.81E-08	1.65E-07	8.153385	Phosphoglycerate mutase
3022385	4.83E+00	9.19E+00	9.40E+00	4.81E-08	1.65E-07	8.153385	Phosphoglycerate mutase
1504690	-3.95E+00	2.43E+01	-9.37E+00	5.05E-08	1.72E-07	8.103113	Alg9-like mannosyltransferase
2971004	-1.07E+01	5.64E+01	-9.18E+00	6.77E-08	2.25E-07	7.798455	Mannose-6-phosphate isomerase, type I
2971004	-1.07E+01	5.64E+01	-9.18E+00	6.77E-08	2.25E-07	7.798455	Mannose-6-phosphate isomerase, type I
3004870	-7.38E+00	2.66E+01	-8.88E+00	1.08E-07	3.44E-07	7.314095	Phosphoglycerate mutase
3004870	-7.38E+00	2.66E+01	-8.88E+00	1.08E-07	3.44E-07	7.314095	Phosphoglycerate mutase
3085082	-2.44E+02	3.81E+02	-8.74E+00	1.34E-07	4.19E-07	7.088523	Aldo/keto reductase
2990963	1.03E+01	6.20E+01	8.65E+00	1.54E-07	4.78E-07	6.941098	Aldehyde dehydrogenase
2917695	-1.33E+01	5.71E+01	-8.60E+00	1.66E-07	5.12E-07	6.863281	Aldo/keto reductase
2266583	-7.00E+00	5.73E+00	-8.59E+00	1.68E-07	5.19E-07	6.84967	Major facilitator superfamily MFS-1
3028067	1.86E+00	6.23E+00	8.47E+00	2.05E-07	6.24E-07	6.642013	Major facilitator superfamily MFS-1
3005400	-6.80E+01	9.76E+01	-8.46E+00	2.07E-07	6.29E-07	6.632988	Major facilitator superfamily MFS-1
3025513	-7.81E+01	2.72E+02	-8.35E+00	2.47E-07	7.41E-07	6.450104	Aldo/keto reductase
2988909	-8.02E+00	9.59E+00	-8.28E+00	2.79E-07	8.30E-07	6.323725	Major facilitator superfamily MFS-1
2943421	6.40E+00	2.49E+01	8.20E+00	3.15E-07	9.30E-07	6.195198	ALG3
3007415	1.37E+00	2.61E+00	8.09E+00	3.83E-07	1.11E-06	5.993613	Major facilitator superfamily MFS-1
2989759	-4.81E+01	3.56E+01	-8.01E+00	4.32E-07	1.24E-06	5.866571	Transketolase, central region
2989759	-4.81E+01	3.56E+01	-8.01E+00	4.32E-07	1.24E-06	5.866571	Transketolase, central region
2638087	-8.34E+00	1.46E+01	-7.92E+00	5.03E-07	1.43E-06	5.708413	Major facilitator superfamily MFS-1
2977687	4.15E+00	2.12E+01	7.90E+00	5.19E-07	1.47E-06	5.676763	Carbohydrate kinase
8339	-6.81E-01	2.17E+00	-7.80E+00	6.13E-07	1.72E-06	5.504051	Major facilitator superfamily MFS-1
2946412	3.77E+00	2.16E+01	7.78E+00	6.36E-07	1.77E-06	5.464824	Carbohydrate/purine kinase
1501854	-9.20E-01	1.10E+00	-7.78E+00	6.37E-07	1.78E-06	5.464047	Major facilitator superfamily MFS-1
2980826	3.89E+00	1.19E+01	7.75E+00	6.74E-07	1.87E-06	5.404004	Major facilitator superfamily MFS-1
2974223	8.08E+00	9.72E+00	7.70E+00	7.31E-07	2.02E-06	5.319782	Alcohol dehydrogenase, zinc-binding
3035159	8.11E-01	1.84E+00	7.61E+00	8.57E-07	2.34E-06	5.154359	Major facilitator superfamily MFS-1
2963771	9.32E+00	4.28E+01	7.61E+00	8.61E-07	2.34E-06	5.150077	ALG6, ALG8 glycosyltransferase
3003710	2.30E+01	3.33E+01	7.53E+00	9.76E-07	2.64E-06	5.019481	Aldehyde dehydrogenase
2908242	-7.18E+01	5.00E+01	-7.34E+00	1.36E-06	3.57E-06	4.677972	Major facilitator superfamily MFS-1
3021248	1.70E+00	9.44E+00	7.33E+00	1.39E-06	3.65E-06	4.654485	Major facilitator superfamily MFS-1
3028066	-6.37E-01	1.53E+00	-7.16E+00	1.87E-06	4.79E-06	4.346334	Major facilitator superfamily MFS-1
1542	-1.56E+01	4.73E+01	-7.15E+00	1.90E-06	4.88E-06	4.325697	Isocitrate/isopropylmalate dehydrogenase
3031021	-2.04E+00	5.45E+00	-7.09E+00	2.12E-06	5.40E-06	4.214785	Major facilitator superfamily MFS-1
1393200	-5.21E+00	1.83E+01	-7.06E+00	2.24E-06	5.69E-06	4.155566	Aldo/keto reductase

3004611	1.36E+01	1.77E+01	7.04E+00	2.34E-06	5.92E-06	4.1117	Aldo/keto reductase
2509638	1.94E+00	1.65E+01	6.89E+00	3.04E-06	7.56E-06	3.840975	Major facilitator superfamily MFS-1
3086257	-3.29E+01	5.31E+01	-6.79E+00	3.63E-06	8.94E-06	3.657288	Aldehyde dehydrogenase
2899158	-2.57E+01	8.20E+01	-6.66E+00	4.64E-06	1.13E-05	3.401836	Major facilitator superfamily MFS-1
2956261	2.13E+00	2.17E+00	6.63E+00	4.86E-06	1.18E-05	3.353944	Aldo/keto reductase
3021902	-1.50E+01	1.74E+01	-6.61E+00	5.03E-06	1.22E-05	3.318087	Aldo/keto reductase
2968494	8.34E-01	1.91E+00	6.59E+00	5.29E-06	1.28E-05	3.265156	Aldehyde dehydrogenase
2909520	1.27E+00	2.37E+00	6.58E+00	5.40E-06	1.30E-05	3.24381	Major facilitator superfamily MFS-1
2979208	-1.51E+01	9.98E+01	-6.58E+00	5.41E-06	1.30E-05	3.242978	Hexokinase
3022822	-1.65E+01	5.34E+01	-6.51E+00	6.16E-06	1.47E-05	3.10774	Polysaccharide deacetylase
3022822	-1.65E+01	5.34E+01	-6.51E+00	6.16E-06	1.47E-05	3.10774	Polysaccharide deacetylase
3024530	-8.03E+00	3.17E+01	-6.50E+00	6.20E-06	1.48E-05	3.102152	Major facilitator superfamily MFS-1
2976973	-4.89E+00	8.82E+00	-6.45E+00	6.89E-06	1.64E-05	2.992251	Major facilitator superfamily MFS-1
1211460	-7.76E-01	1.59E+00	-6.37E+00	7.98E-06	1.88E-05	2.840709	Major facilitator superfamily MFS-1
2910031	-6.47E+01	5.17E+01	-6.37E+00	7.99E-06	1.88E-05	2.838884	Major facilitator superfamily MFS-1
2932727	4.26E+00	1.44E+01	6.33E+00	8.51E-06	2.00E-05	2.774473	Major facilitator superfamily MFS-1
3011677	-6.91E+00	9.08E+00	-6.32E+00	8.80E-06	2.06E-05	2.739762	Major facilitator superfamily MFS-1
2973772	1.84E+01	1.54E+01	6.22E+00	1.06E-05	2.45E-05	2.550133	Aldo/keto reductase
2988797	4.97E+01	9.90E+01	6.04E+00	1.49E-05	3.37E-05	2.197429	Alcohol dehydrogenase, zinc-binding
2919836	-2.56E+00	1.18E+01	-6.00E+00	1.62E-05	3.65E-05	2.11042	Major facilitator superfamily MFS-1
2899971	-1.21E+02	1.31E+02	-5.95E+00	1.79E-05	4.01E-05	2.006539	Major facilitator superfamily MFS-1
3032059	1.18E+00	4.20E+00	5.91E+00	1.91E-05	4.26E-05	1.940495	Major facilitator superfamily MFS-1
3047884	1.02E+01	1.08E+01	5.84E+00	2.20E-05	4.88E-05	1.792747	Major facilitator superfamily MFS-1
2959786	9.53E+00	1.25E+01	5.81E+00	2.33E-05	5.13E-05	1.734956	Alcohol dehydrogenase, zinc-binding
3006107	-5.12E+01	2.79E+02	-5.62E+00	3.37E-05	7.26E-05	1.354363	Aldo/keto reductase
2982681	1.19E+01	4.81E+01	5.62E+00	3.40E-05	7.33E-05	1.343433	Major facilitator superfamily MFS-1
1245014	-9.70E-01	3.03E+00	-5.60E+00	3.54E-05	7.61E-05	1.303652	Aldo/keto reductase
2927749	-1.31E+00	4.15E+00	-5.55E+00	3.90E-05	8.32E-05	1.203271	Major facilitator superfamily MFS-1
2902564	5.09E-01	6.57E-01	5.55E+00	3.92E-05	8.36E-05	1.197689	Alcohol dehydrogenase, zinc-binding
2926409	1.87E+00	9.78E+00	5.50E+00	4.33E-05	9.16E-05	1.094972	Alcohol dehydrogenase, zinc-binding
2906171	-2.20E+00	5.31E+00	-5.47E+00	4.58E-05	9.65E-05	1.037168	Aldo/keto reductase
2980794	-6.01E+00	3.42E+01	-5.36E+00	5.67E-05	1.18E-04	0.819265	Alcohol dehydrogenase, zinc-binding
2915260	1.08E+01	6.10E+01	5.34E+00	5.97E-05	1.23E-04	0.766152	Major facilitator superfamily MFS-1
2988388	1.29E+01	2.70E+01	4.96E+00	1.29E-04	2.55E-04	-0.02612	Aldo/keto reductase
1803168	2.01E+00	8.86E+00	4.93E+00	1.37E-04	2.69E-04	-0.08254	Major facilitator superfamily MFS-1
3023346	4.58E+00	1.48E+01	4.93E+00	1.38E-04	2.72E-04	-0.09604	Aldo/keto reductase



2903059	-7.93E+00	2.23E+01	-4.83E+00	1.70E-04	3.31E-04	-0.30833	Aldo/keto reductase
2908845	8.80E-01	6.51E+00	4.67E+00	2.34E-04	4.46E-04	-0.63269	Major facilitator superfamily MFS-1
2935101	-4.12E+00	8.57E+00	-4.67E+00	2.36E-04	4.49E-04	-0.64151	Major facilitator superfamily MFS-1
2988567	1.40E+00	4.87E+00	4.67E+00	2.37E-04	4.50E-04	-0.64252	Aldehyde dehydrogenase
3026678	4.20E+01	1.70E+02	4.54E+00	3.08E-04	5.78E-04	-0.9123	Carbohydrate-binding family V/XII
3028291	5.44E-01	1.58E+00	4.53E+00	3.15E-04	5.89E-04	-0.93294	Aldo/keto reductase
133152	-5.02E-01	2.07E+00	-4.53E+00	3.19E-04	5.96E-04	-0.94544	Major facilitator superfamily MFS-1
2906377	1.07E+00	8.25E+00	4.52E+00	3.26E-04	6.09E-04	-0.96798	Major facilitator superfamily MFS-1
2971649	-1.50E+00	7.72E+00	-4.42E+00	3.98E-04	7.36E-04	-1.1716	Alcohol dehydrogenase, zinc-binding
2960840	-2.46E+00	1.53E+01	-4.42E+00	4.02E-04	7.42E-04	-1.18028	Alg9-like mannosyltransferase
3022489	3.56E+01	2.60E+02	4.41E+00	4.10E-04	7.56E-04	-1.20102	Transketolase, N-terminal
3022489	3.56E+01	2.60E+02	4.41E+00	4.10E-04	7.56E-04	-1.20102	Transketolase, N-terminal
1471773	2.02E+00	1.50E+01	4.34E+00	4.72E-04	8.65E-04	-1.34394	Alcohol dehydrogenase, zinc-binding
2910700	-4.65E+00	1.43E+01	-4.31E+00	5.04E-04	9.20E-04	-1.41094	Major facilitator superfamily MFS-1
2917441	-6.61E-01	3.64E+00	-4.16E+00	6.89E-04	1.24E-03	-1.72623	Major facilitator superfamily MFS-1
2899912	1.36E+01	5.15E+01	4.12E+00	7.57E-04	1.35E-03	-1.82154	Polysaccharide deacetylase
2899912	1.36E+01	5.15E+01	4.12E+00	7.57E-04	1.35E-03	-1.82154	Polysaccharide deacetylase
2895118	3.41E+00	1.05E+01	4.07E+00	8.39E-04	1.49E-03	-1.92527	Major facilitator superfamily MFS-1
3028591	5.69E+00	3.29E+01	4.02E+00	9.38E-04	1.65E-03	-2.03817	Aldo/keto reductase
2917112	1.77E+00	6.12E+00	3.95E+00	1.08E-03	1.89E-03	-2.18319	Major facilitator superfamily MFS-1
3009191	6.49E+00	4.03E+01	3.80E+00	1.48E-03	2.54E-03	-2.49811	Major facilitator superfamily MFS-1
2895437	3.46E+01	1.75E+02	3.72E+00	1.78E-03	3.01E-03	-2.67866	Phosphoglycerate kinase
2895437	3.46E+01	1.75E+02	3.72E+00	1.78E-03	3.01E-03	-2.67866	Phosphoglycerate kinase
1501819	1.11E+00	1.94E+00	3.64E+00	2.13E-03	3.57E-03	-2.85784	Major facilitator superfamily MFS-1
3022907	-2.34E+00	3.56E+01	-3.50E+00	2.85E-03	4.71E-03	-3.15034	Major facilitator superfamily MFS-1
1713852	2.57E-01	1.41E+00	3.49E+00	2.93E-03	4.83E-03	-3.17707	Major facilitator superfamily MFS-1
3102073	5.81E-01	2.22E+00	3.38E+00	3.69E-03	5.99E-03	-3.40479	Aldo/keto reductase
2898591	3.57E+00	3.32E+01	3.37E+00	3.76E-03	6.11E-03	-3.42575	Phosphoglycerate mutase
2898591	3.57E+00	3.32E+01	3.37E+00	3.76E-03	6.11E-03	-3.42575	Phosphoglycerate mutase
2904627	-5.45E+00	1.73E+01	-3.36E+00	3.86E-03	6.26E-03	-3.45113	Pyruvate carboxyltransferase
2904627	-5.45E+00	1.73E+01	-3.36E+00	3.86E-03	6.26E-03	-3.45113	Pyruvate carboxyltransferase
2985939	-7.76E+00	6.43E+01	-3.22E+00	5.16E-03	8.21E-03	-3.73705	Phosphoglycerate mutase
2985939	-7.76E+00	6.43E+01	-3.22E+00	5.16E-03	8.21E-03	-3.73705	Phosphoglycerate mutase
2989343	6.76E-01	4.85E+00	3.17E+00	5.73E-03	9.06E-03	-3.84005	Aldo/keto reductase
2908585	6.49E-01	2.11E+00	3.12E+00	6.38E-03	1.00E-02	-3.94461	Aldehyde dehydrogenase
3007486	1.64E+00	1.16E+01	3.11E+00	6.56E-03	1.03E-02	-3.9727	Major facilitator superfamily MFS-1

2917077	5.62E-01	2.98E+00	3.11E+00	6.60E-03	1.04E-02	-3.97744	Major facilitator superfamily MFS-1
3027813	2.01E-01	5.35E-01	3.09E+00	6.81E-03	1.07E-02	-4.00846	Major facilitator superfamily MFS-1
2909996	-5.25E-01	3.38E+00	-3.03E+00	7.77E-03	1.21E-02	-4.13709	Major facilitator superfamily MFS-1
2982212	2.69E+01	2.77E+02	2.99E+00	8.36E-03	1.29E-02	-4.20877	Aldo/keto reductase
3006747	-1.80E+01	3.62E+02	-2.85E+00	1.12E-02	1.71E-02	-4.49285	Aldo/keto reductase
2917113	-1.29E+00	1.28E+01	-2.81E+00	1.24E-02	1.88E-02	-4.59174	Major facilitator superfamily MFS-1
2916462	7.11E-01	8.07E-01	2.80E+00	1.25E-02	1.89E-02	-4.6016	Aldehyde dehydrogenase
3007633	-4.85E-01	2.86E+00	-2.70E+00	1.53E-02	2.29E-02	-4.79606	Major facilitator superfamily MFS-1
132181	5.29E-01	6.23E+00	2.62E+00	1.80E-02	2.67E-02	-4.95084	Major facilitator superfamily MFS-1
2536767	1.68E+01	1.14E+02	2.53E+00	2.18E-02	3.18E-02	-5.13011	Major facilitator superfamily MFS-1
3018100	5.18E+01	2.74E+02	2.51E+00	2.26E-02	3.29E-02	-5.16441	Aldo/keto reductase
3003053	5.77E-01	4.76E+00	2.49E+00	2.39E-02	3.46E-02	-5.21639	Alcohol dehydrogenase, zinc-binding
140069	-4.60E+00	3.40E+01	-2.45E+00	2.56E-02	3.70E-02	-5.28286	Major facilitator superfamily MFS-1
3005826	6.55E+00	3.31E+01	2.45E+00	2.58E-02	3.72E-02	-5.28875	Major facilitator superfamily MFS-1
1211351	-3.69E+00	5.37E+01	-2.43E+00	2.69E-02	3.88E-02	-5.32874	Major facilitator superfamily MFS-1
2975289	-1.85E+00	3.88E+01	-2.41E+00	2.80E-02	4.03E-02	-5.36687	Isocitrate/isopropylmalate dehydrogenase
122125	-7.21E-01	2.99E+00	-2.40E+00	2.85E-02	4.09E-02	-5.3825	Major facilitator superfamily MFS-1
1677900	3.57E-01	2.98E+00	2.32E+00	3.31E-02	4.71E-02	-5.52452	Aldo/keto reductase
138233	-4.44E-01	4.16E+00	-2.29E+00	3.55E-02	5.01E-02	-5.58838	Major facilitator superfamily MFS-1
2912489	6.57E-01	4.72E+00	2.28E+00	3.65E-02	5.15E-02	-5.61374	Aldehyde dehydrogenase
2982230	5.33E+00	7.52E+01	2.09E+00	5.20E-02	7.16E-02	-5.94106	Aldehyde dehydrogenase
3011859	-1.95E+00	8.74E+00	-2.09E+00	5.24E-02	7.20E-02	-5.9467	Alcohol dehydrogenase, zinc-binding
2908930	-2.94E-01	2.42E+00	-1.99E+00	6.32E-02	8.58E-02	-6.11675	Carbohydrate-binding WSC
3007036	2.87E+01	2.56E+02	1.97E+00	6.63E-02	8.97E-02	-6.16036	Major facilitator superfamily MFS-1
2975087	-8.57E+00	9.34E+01	-1.90E+00	7.50E-02	1.01E-01	-6.27022	Aldehyde dehydrogenase
3036980	1.02E-01	5.43E-01	1.89E+00	7.71E-02	1.03E-01	-6.29494	Major facilitator superfamily MFS-1
2917023	2.08E+00	1.07E+01	1.85E+00	8.20E-02	1.09E-01	-6.35017	Aldo/keto reductase
3020994	-1.64E-01	1.91E+00	-1.73E+00	1.01E-01	1.33E-01	-6.53608	Major facilitator superfamily MFS-1
2909030	2.48E-01	1.11E+00	1.72E+00	1.04E-01	1.37E-01	-6.55853	Carbohydrate-binding WSC
138784	-5.25E+00	2.24E+01	-1.71E+00	1.06E-01	1.40E-01	-6.57759	Major facilitator superfamily MFS-1
2987480	-1.83E-01	2.08E+00	-1.69E+00	1.10E-01	1.44E-01	-6.60487	Major facilitator superfamily MFS-1
3003016	-2.90E-01	2.24E+00	-1.55E+00	1.40E-01	1.81E-01	-6.81438	Major facilitator superfamily MFS-1
2903308	-2.87E-01	4.96E+00	-1.49E+00	1.56E-01	1.99E-01	-6.90151	Major facilitator superfamily MFS-1
3029003	-2.21E+00	2.22E+01	-1.43E+00	1.73E-01	2.18E-01	-6.98508	Major facilitator superfamily MFS-1
2900190	5.02E-01	9.02E+00	1.40E+00	1.79E-01	2.26E-01	-7.01516	Major facilitator superfamily MFS-1
3023015	-9.99E-01	3.00E+01	-1.40E+00	1.80E-01	2.27E-01	-7.02005	Major facilitator superfamily MFS-1

3033111	-2.53E-01	3.45E+00	-1.36E+00	1.91E-01	2.40E-01	-7.06802	Major facilitator superfamily MFS-1
2964731	2.28E+00	9.09E+01	1.36E+00	1.92E-01	2.41E-01	-7.07312	Major facilitator superfamily MFS-1
2974222	2.31E+00	3.41E+01	1.34E+00	1.99E-01	2.49E-01	-7.10038	Alcohol dehydrogenase, zinc-binding
2934359	1.29E+00	2.46E+01	1.31E+00	2.07E-01	2.57E-01	-7.12957	Aldo/keto reductase
2899370	-4.24E-01	5.94E+00	-1.25E+00	2.29E-01	2.83E-01	-7.21058	Aldo/keto reductase
2914482	7.34E-01	2.27E+01	1.24E+00	2.33E-01	2.87E-01	-7.22264	Phosphoglycerate mutase
2914482	7.34E-01	2.27E+01	1.24E+00	2.33E-01	2.87E-01	-7.22264	Phosphoglycerate mutase
3023394	-4.32E-01	1.45E+01	-1.17E+00	2.60E-01	3.18E-01	-7.30767	Major facilitator superfamily MFS-1
2919341	1.06E+00	1.60E+01	1.16E+00	2.64E-01	3.22E-01	-7.31959	Major facilitator superfamily MFS-1
3008745	-6.31E+00	1.35E+02	-1.13E+00	2.73E-01	3.32E-01	-7.34489	Hexokinase
2908759	-2.48E-01	3.56E+00	-1.04E+00	3.13E-01	3.77E-01	-7.44567	Carbohydrate-binding WSC
2981910	1.33E+00	1.91E+01	9.59E-01	3.51E-01	4.19E-01	-7.52614	Major facilitator superfamily MFS-1
2968290	4.33E-01	7.26E+00	8.72E-01	3.96E-01	4.66E-01	-7.60639	Aldo/keto reductase
2910954	-1.96E-01	3.37E+00	-8.68E-01	3.98E-01	4.68E-01	-7.60999	Major facilitator superfamily MFS-1
3005222	1.35E-01	1.90E+00	8.60E-01	4.02E-01	4.72E-01	-7.61674	Aldo/keto reductase
2990693	2.57E-01	5.32E+00	8.47E-01	4.09E-01	4.80E-01	-7.62826	Carbonic anhydrase
3012827	2.22E-01	4.41E+00	7.97E-01	4.37E-01	5.09E-01	-7.66987	Aldo/keto reductase
2903003	1.39E-01	3.07E+00	7.89E-01	4.42E-01	5.14E-01	-7.67684	Major facilitator superfamily MFS-1
3030826	-8.54E-01	3.58E+01	-7.28E-01	4.77E-01	5.51E-01	-7.72358	Isocitrate lyase and phosphorylmutase
3006065	1.43E-01	4.62E+00	6.99E-01	4.94E-01	5.69E-01	-7.74527	Major facilitator superfamily MFS-1
2981596	8.96E-01	4.48E+01	6.61E-01	5.18E-01	5.92E-01	-7.77182	Aldo/keto reductase
3022934	7.32E-02	1.45E+00	6.58E-01	5.20E-01	5.94E-01	-7.77373	Major facilitator superfamily MFS-1
136001	-3.83E+00	1.17E+02	-6.33E-01	5.36E-01	6.11E-01	-7.79079	Aldo/keto reductase
3028350	-3.88E-01	1.85E+01	-5.95E-01	5.60E-01	6.35E-01	-7.81481	Carbohydrate-binding WSC
3028025	-3.59E-01	2.14E+01	-5.84E-01	5.67E-01	6.42E-01	-7.82149	Major facilitator superfamily MFS-1
2980635	4.48E-01	1.94E+01	5.83E-01	5.68E-01	6.43E-01	-7.82223	Aldo/keto reductase
2894506	7.22E+00	1.25E+02	5.81E-01	5.69E-01	6.43E-01	-7.82311	Polysaccharide deacetylase
2894506	7.22E+00	1.25E+02	5.81E-01	5.69E-01	6.43E-01	-7.82311	Polysaccharide deacetylase
2896237	2.23E-01	1.44E+01	5.80E-01	5.70E-01	6.44E-01	-7.82407	Mannosyltransferase, DXD
2896237	2.23E-01	1.44E+01	5.80E-01	5.70E-01	6.44E-01	-7.82407	Mannosyltransferase, DXD
3029431	1.01E-01	2.91E+00	5.68E-01	5.77E-01	6.52E-01	-7.83067	Aldo/keto reductase
3003368	1.32E-01	1.78E+00	5.47E-01	5.92E-01	6.67E-01	-7.84336	Alcohol dehydrogenase, zinc-binding
2921170	2.78E-01	1.89E+01	5.28E-01	6.05E-01	6.80E-01	-7.85399	Alg9-like mannosyltransferase
3023124	9.38E-01	4.56E+01	5.22E-01	6.08E-01	6.83E-01	-7.85693	Major facilitator superfamily MFS-1
2908745	-2.39E+00	1.43E+02	-4.92E-01	6.29E-01	7.04E-01	-7.87271	Transketolase, central region
2908745	-2.39E+00	1.43E+02	-4.92E-01	6.29E-01	7.04E-01	-7.87271	Transketolase, central region

131090	4.99E-01	2.82E+01	4.76E-01	6.40E-01	7.15E-01	-7.88093	Major facilitator superfamily MFS-1
2933584	-4.73E-02	2.39E+00	-3.21E-01	7.52E-01	8.23E-01	-7.94562	Major facilitator superfamily MFS-1
3017078	-5.01E-02	2.51E+00	-2.85E-01	7.79E-01	8.49E-01	-7.95735	Aldo/keto reductase
2896242	-7.15E-01	7.62E+01	-2.26E-01	8.24E-01	8.90E-01	-7.97322	Major facilitator superfamily MFS-1
3027403	-9.49E-02	1.80E+01	-1.91E-01	8.51E-01	9.15E-01	-7.9809	Major facilitator superfamily MFS-1
3030943	-4.48E+00	2.12E+03	-1.88E-01	8.53E-01	9.17E-01	-7.98143	Aldo/keto reductase
3027909	-1.41E-02	5.06E-01	-1.56E-01	8.78E-01	9.40E-01	-7.98725	Alcohol dehydrogenase, zinc-binding
3006884	-4.19E-02	5.27E+00	-1.20E-01	9.06E-01	9.65E-01	-7.99255	Aldo/keto reductase
1805361	1.06E+00	6.73E+01	1.04E-01	9.18E-01	9.77E-01	-7.99444	Major facilitator superfamily MFS-1
1805361	1.06E+00	6.73E+01	1.04E-01	9.18E-01	9.77E-01	-7.99444	Major facilitator superfamily MFS-1
2918429	3.37E-02	1.13E+01	8.72E-02	9.32E-01	9.89E-01	-7.99614	Major facilitator superfamily MFS-1
2918429	3.37E-02	1.13E+01	8.72E-02	9.32E-01	9.89E-01	-7.99614	Major facilitator superfamily MFS-1
3311	-1.22E-03	6.35E-01	-1.16E-02	9.91E-01	1.00E+00	-8.0001	Alcohol dehydrogenase, zinc-binding
3031490	-2.04E-19	2.00E-03	-8.52E-18	1.00E+00	1.00E+00	-8.00017	Aldo/keto reductase
3033333	-2.04E-19	2.00E-03	-8.52E-18	1.00E+00	1.00E+00	-8.00017	Aldo/keto reductase
2974276	3.50E-02	2.34E+01	3.97E-02	9.69E-01	1.00E+00	-7.99933	Major facilitator superfamily MFS-1
3032078	1.01E-02	2.86E+00	3.91E-02	9.69E-01	1.00E+00	-7.99936	Major facilitator superfamily MFS-1
2973373	-2.44E-03	1.21E+00	-2.62E-02	9.79E-01	1.00E+00	-7.9998	Major facilitator superfamily MFS-1
3006874	1.00E-02	4.13E+00	4.35E-02	9.66E-01	1.00E+00	-7.99917	Mannosyltransferase, PIG-V
2974276	3.50E-02	2.34E+01	3.97E-02	9.69E-01	1.00E+00	-7.99933	Major facilitator superfamily MFS-1
3032078	1.01E-02	2.86E+00	3.91E-02	9.69E-01	1.00E+00	-7.99936	Major facilitator superfamily MFS-1
2973373	-2.44E-03	1.21E+00	-2.62E-02	9.79E-01	1.00E+00	-7.9998	Major facilitator superfamily MFS-1
3006874	1.00E-02	4.13E+00	4.35E-02	9.66E-01	1.00E+00	-7.99917	Mannosyltransferase, PIG-V

**Figure-S4:** Shows the volcano plot showing the differentially expressed significant genes obtained from the statistical analysis

