

Supplemental materials

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**Space exposure enhanced pectin-degrading enzymes
expression and activity in *Aspergillus costaricaensis***

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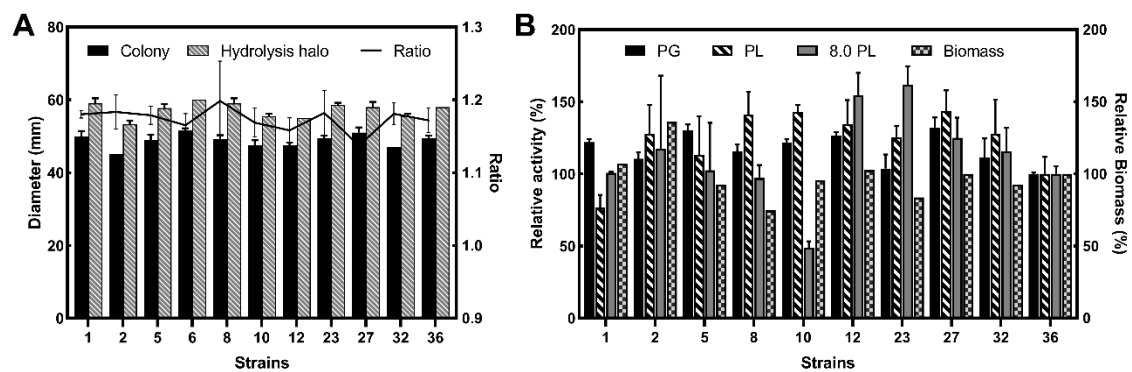


Fig.S1 Activity determination of 10 mutant strains in the preliminary screening stage. (A) Colony diameter, hydrolytic circle diameter, and relative ratio on the plate. (B) Determination of the activity of the mutant strain in liquid fermentation. The X-axis depicts the numeration of the strains, ranging from 1 to 32 for the space mutagenesis strains, and 36 for the ground control strains.

Table S1 Analysis of degradation products by negative ESI-MS.

	m/z	Proposed structure
DP1	193.037	GalA
DP2	369.0643	GalA2
	358.064	GalA2ox
DP3	545.0974	GalA3
	559.1094	GalA3Me
	575.1636	GalA3Meox
	603.0981	GalA3Acx
DP4	723.0564	GalA4
	731.1341	GalA4Me2-H2O
	735.1342	GalA4Me
	745.0353	GalA4Me3-H2O
	379.07	GalA4MeAc-H2O
	819.1156	GalA4MeAc2
DP5	897.2034	GalA5
	907.0776	GalA5Me2-H2O
	939.0617	GalA5Me3
	981.1627	GalA5Me3Ac
	995.2533	GalA5Me4Ac
DP6	1073.1295	GalA6
	537.1064	GalA6
	1111.1862	GalA6Me4-H2O
	555.1164	GalA6Me4-H2O
	1114.1929	GalA6Me3
	1139.2027	GalA6Me3Ac-H2O
	585.0876	GalA6MeAc2

Table S2 Summary of transcript reconstruction

Items	Statistics
Total Mapping Gene	10771
Known Gene	10732
Total Novel Transcript	1881
Coding Transcript	1881
Novel Isoform	1842
Novel Gene	39

Table S3 Differentially expressed genes (DEGs) Involved in carbohydrate-active enzymes(CAZyme) family classification.

Family	Known activities (GH, CE, PL, AA), binding specificities (CBM)	Number of DEGs	Relative abundance (%)
AA1	Laccase / p-diphenol:oxygen oxidoreductase / ferroxidase (EC 1.10.3.2); ; ferroxidase (EC 1.10.3.-); Laccase-like multicopper oxidase (EC 1.10.3.-)	2	1.05
AA3	cellobiose dehydrogenase (EC 1.1.99.18); glucose 1-oxidase (EC 1.1.3.4); aryl alcohol oxidase (EC 1.1.3.7); alcohol oxidase (EC 1.1.3.13); pyranose oxidase (EC 1.1.3.10)	8	4.21
AA4	vanillyl-alcohol oxidase (EC 1.1.3.38)	3	1.58
AA7	glucooligosaccharide oxidase (EC 1.1.3.-); chitooligosaccharide oxidase (EC 1.1.3.-)	11	5.79
AA9	lytic cellulose monooxygenase (C1-hydroxylating) (EC 1.14.99.54); lytic cellulose monooxygenase (C4-dehydrogenating) (EC 1.14.99.56)	1	0.53
5	Total AA	25	13.16
CE1	acetyl xylan esterase (EC 3.1.1.72); cinnamoyl esterase (EC 3.1.1.-); feruloyl esterase (EC 3.1.1.73); carboxylesterase (EC 3.1.1.1); S-formylglutathione hydrolase (EC 3.1.2.12); diacylglycerol O-acyltransferase (EC 2.3.1.20); trehalose 6-O-mycolyltransferase (EC 2.3.1.122)	1	0.53
CE2	acetyl xylan esterase (EC 3.1.1.72)	1	0.53
CE5	acetyl xylan esterase (EC 3.1.1.72); cutinase (EC 3.1.1.74)	3	1.58
CE8	pectin methylesterase (EC 3.1.1.11).	3	1.58
CE9	N-acetylglucosamine 6-phosphate deacetylase (EC 3.5.1.25); N-acetylglucosamine 6-phosphate deacetylase (EC 3.5.1.80)	1	0.53
CE12	pectin acetylesterase (EC 3.1.1.-); rhamnogalacturonan acetylesterase (EC 3.1.1.-); acetyl xylan esterase (EC 3.1.1.72)	2	1.05
CE16	acetylesterase (EC 3.1.1.6) active on various carbohydrate acetyl esters	2	1.05
CE18	N-acetylglactosamine deacetylase (EC 3.5.1.-)	1	0.53
8	Total CE	9	4.74
GH1	β -glucosidase (EC 3.2.1.21); β -galactosidase (EC 3.2.1.23); β -mannosidase (EC 3.2.1.25); β -glucuronidase (EC 3.2.1.31); β -xylosidase (EC 3.2.1.37); β -D-fucosidase (EC 3.2.1.38); phlorizin hydrolase (EC 3.2.1.62); exo- β -1,4-glucanase (EC 3.2.1.74); 6-phospho- β -galactosidase (EC 3.2.1.85); 6-phospho- β -glucosidase (EC 3.2.1.86); strictosidine β -glucosidase (EC 3.2.1.105); lactase (EC 3.2.1.108); amygdalin β -glucosidase (EC 3.2.1.117); prunasin β -glucosidase (EC 3.2.1.118); vicianin hydrolase (EC 3.2.1.119); raucaffricine β -glucosidase (EC 3.2.1.125); thioglucosidase (EC 3.2.1.147); β -primeverosidase (EC 3.2.1.149); isoflavonoid 7-O- β -apiosyl- β -glucosidase (EC 3.2.1.161); ABA-specific β -glucosidase (EC 3.2.1.175); DIMBOA β -glucosidase (EC 3.2.1.182); β -glycosidase (EC 3.2.1.-); hydroxyisourate hydrolase (EC 3.-.-)	2	1.05
GH2	β -galactosidase (EC 3.2.1.23) ; β -mannosidase (EC 3.2.1.25); β -glucuronidase (EC 3.2.1.31); α -L-arabinofuranosidase (EC 3.2.1.55); mannosylglycoprotein endo- β -mannosidase (EC 3.2.1.152); exo- β -glucosaminidase (EC 3.2.1.165)	3	1.58
GH3	β -glucosidase (EC 3.2.1.21); xylan 1,4- β -xylosidase (EC 3.2.1.37); β -glucosylceramidase (EC 3.2.1.45); β -N-acetylhexosaminidase (EC 3.2.1.52); α -L-arabinofuranosidase (EC 3.2.1.55); glucan 1,3- β -glucosidase (EC 3.2.1.58); glucan 1,4- β -glucosidase (EC 3.2.1.74); isoprimeverose-producing oligoxyloglucan hydrolase (EC 3.2.1.120); coniferin β -glucosidase (EC 3.2.1.126); exo-1,3-1,4-glucanase (EC 3.2.1.-)	7	3.68

Family	Known activities (GH, CE, PL, AA), binding specificities (CBM)	Number of DEGs	Relative abundance (%)
GH5	chitosanase (EC 3.2.1.132); β -mannosidase (EC 3.2.1.25); endo- β -1,4-glucanase / cellulase (EC 3.2.1.4); glucan β -1,3-glucosidase (EC 3.2.1.58); licheninase (EC 3.2.1.73); glucan endo-1,6- β -glucosidase (EC 3.2.1.75); mannan endo- β -1,4-mannosidase (EC 3.2.1.78); endo- β -1,4-xylanase (EC 3.2.1.8); cellulose β -1,4-cellobiosidase (EC 3.2.1.91); β -1,3-mannanase (EC 3.2.1.-); xyloglucan-specific endo- β -1,4-glucanase (EC 3.2.1.151); mannan transglycosylase (EC 2.4.1.-); endo- β -1,6-galactanase (EC 3.2.1.164); endoglycoceramidase (EC 3.2.1.123); β -primeverosidase (EC 3.2.1.149); β -glucosylceramidase (EC 3.2.1.45); hesperidin 6-O- α -L-rhamnosyl- β -glucosidase (EC 3.2.1.168); exo- β -1,4-glucanase / cellodextrinase (EC 3.2.1.74); β -glucosidase (EC 3.2.1.21); arabinoxylan-specific endo- β -1,4-xylanase (EC 3.2.1.-)	2	1.05
GH7	endo- β -1,4-glucanase (EC 3.2.1.4); reducing end-acting cellobiohydrolase (EC 3.2.1.176); chitosanase (EC 3.2.1.132); endo- β -1,3-1,4-glucanase (EC 3.2.1.73)	1	0.53
GH11	endo- β -1,4-xylanase (EC 3.2.1.8); endo- β -1,3-xylanase (EC 3.2.1.32)	2	1.05
GH12	endoglucanase (EC 3.2.1.4); xyloglucan hydrolase (EC 3.2.1.151); β -1,3-1,4-glucanase (EC 3.2.1.73); xyloglucan endotransglycosylase (EC 2.4.1.207)	3	1.58
GH13	α -amylase (EC 3.2.1.1); pullulanase (EC 3.2.1.41); cyclomaltodextrin glucanotransferase (EC 2.4.1.19); cyclomaltodextrinase (EC 3.2.1.54); trehalose-6-phosphate hydrolase (EC 3.2.1.93); oligo- α -glucosidase (EC 3.2.1.10); maltogenic amylase (EC 3.2.1.133); neopullulanase (EC 3.2.1.135); α -glucosidase (EC 3.2.1.20); maltotetraose-forming α -amylase (EC 3.2.1.60); isoamylase (EC 3.2.1.68); glucodextranase (EC 3.2.1.70); maltohexaose-forming α -amylase (EC 3.2.1.98); maltotriose-forming α -amylase (EC 3.2.1.116); branching enzyme (EC 2.4.1.18); trehalose synthase (EC 5.4.99.16); 4- α -glucanotransferase (EC 2.4.1.25); maltopentaose-forming α -amylase (EC 3.2.1.-); amylosucrase (EC 2.4.1.4); sucrose phosphorylase (EC 2.4.1.7); malto-oligosyltrehalose trehalohydrolase (EC 3.2.1.141); isomaltulose synthase (EC 5.4.99.11); malto-oligosyltrehalose synthase (EC 5.4.99.15); amylo- α -1,6-glucosidase (EC 3.2.1.33); α -1,4-glucan: phosphate α -maltosyltransferase (EC 2.4.99.16); 6'-P-sucrose phosphorylase (EC 2.4.1.-); amino acid transporter	6	3.16
GH15	glucoamylase (EC 3.2.1.3); glucodextranase (EC 3.2.1.70); α , α -trehalase (EC 3.2.1.28)	2	1.05
GH16	xyloglucan:xyloglucosyltransferase (EC 2.4.1.207); keratan-sulfate endo-1,4- β -galactosidase (EC 3.2.1.103); endo-1,3- β -glucanase (EC 3.2.1.39); endo-1,3(4)- β -glucanase (EC 3.2.1.6); licheninase (EC 3.2.1.73); β -agarase (EC 3.2.1.81); κ -carrageenase (EC 3.2.1.83); xyloglucanase (EC 3.2.1.151); endo- β -1,3-galactanase (EC 3.2.1.181); β -porphyranase (EC 3.2.1.178); hyaluronidase (EC 3.2.1.35); endo- β -1,4-galactosidase (EC 3.2.1.-); chitin β -1,6-glucanosyltransferase (EC 2.4.1.-); endo- β -1,4-galactosidase (EC 3.2.1.-)	3	1.58
GH17	glucan endo-1,3- β -glucosidase (EC 3.2.1.39); licheninase (EC 3.2.1.73); ABA-specific β -glucosidase (EC 3.2.1.175); β -1,3-glucanosyltransglycosylase (EC 2.4.1.-); β -1,3-glucosidase (EC 3.2.1.-)	1	0.53
GH20	β -hexosaminidase (EC 3.2.1.52); lacto-N-biosidase (EC 3.2.1.140); β -1,6-N-acetylglucosaminidase (EC 3.2.1.-); β -6-SO ₃ -N-acetylglucosaminidase (EC 3.2.1.-)	1	0.53
GH27	α -galactosidase (EC 3.2.1.22); α -N-acetylgalactosaminidase (EC 3.2.1.49); isomalto-dextranase (EC 3.2.1.94); β -L-arabinopyranosidase (EC 3.2.1.88); galactan:galactan galactosyltransferase (EC 2.4.1.-)	2	1.05

Family	Known activities (GH, CE, PL, AA), binding specificities (CBM)	Number of DEGs	Relative abundance (%)
GH28	polygalacturonase (EC 3.2.1.15); exo-polygalacturonase (EC 3.2.1.67); exo-polygalacturonosidase (EC 3.2.1.82); rhamnogalacturonase (EC 3.2.1.171); rhamnogalacturonan α -1,2-galacturonohydrolase (EC 3.2.1.173); rhamnogalacturonan α -L-rhamnopyranohydrolase (EC 3.2.1.174); endo-xylogalacturonan hydrolase (EC 3.2.1.-)	12	6.32
GH31	α -glucosidases, α -xylosidases, isomaltosyltransferases, maltase/glucoamylases	6	3.16
GH32	invertase (EC 3.2.1.26); endo-inulinase (EC 3.2.1.7); β -2,6-fructan 6-levanbiohydrolase (EC 3.2.1.64); endo-levanase (EC 3.2.1.65); exo-inulinase (EC 3.2.1.80); fructan β -(2,1)-fructosidase/1-exohydrolase (EC 3.2.1.153); fructan β -(2,6)-fructosidase/6-exohydrolase (EC 3.2.1.154); sucrose:sucrose 1-fructosyltransferase (EC 2.4.1.99); fructan:fructan 1-fructosyltransferase (EC 2.4.1.100); sucrose:fructan 6-fructosyltransferase (EC 2.4.1.10); fructan:fructan 6G-fructosyltransferase (EC 2.4.1.243); levan fructosyltransferase (EC 2.4.1.-); [retaining] sucrose:sucrose 6-fructosyltransferase (6-SST) (EC 2.4.1.-); cycloinulo-oligosaccharide fructanotransferase (EC 2.4.1.-)	2	1.05
GH35	β -galactosidase (EC 3.2.1.23); exo- β -glucosaminidase (EC 3.2.1.165); exo- β -1,4-galactanase (EC 3.2.1.-); β -1,3-galactosidase (EC 3.2.1.-)	4	2.11
GH36	α -galactosidase (EC 3.2.1.22); α -N-acetylgalactosaminidase (EC 3.2.1.49); stachyose synthase (EC 2.4.1.67); raffinose synthase (EC 2.4.1.82)	1	0.53
GH38	α -mannosidase (EC 3.2.1.24); mannosyl-oligosaccharide α -1,2-mannosidase (EC 3.2.1.113); mannosyl-oligosaccharide α -1,3-1,6-mannosidase (EC 3.2.1.114); α -2-O-mannosylglycerate hydrolase (EC 3.2.1.170); mannosyl-oligosaccharide α -1,3-mannosidase (EC 3.2.1.-)	1	0.53
GH43	β -xylosidase (EC 3.2.1.37); α -L-arabinofuranosidase (EC 3.2.1.55); arabinanase (EC 3.2.1.99); xylanase (EC 3.2.1.8); galactan 1,3- β -galactosidase (EC 3.2.1.145); α -1,2-L-arabinofuranosidase (EC 3.2.1.-); exo- α -1,5-L-arabinofuranosidase (EC 3.2.1.-); [inverting] exo- α -1,5-L-arabinanase (EC 3.2.1.-); β -1,3-xylosidase (EC 3.2.1.-)	9	4.74
GH47	α -mannosidase (EC 3.2.1.113)	3	1.58
GH51	endoglucanase (EC 3.2.1.4); endo- β -1,4-xylanase (EC 3.2.1.8); β -xylosidase (EC 3.2.1.37); α -L-arabinofuranosidase (EC 3.2.1.55)	4	2.11
GH53	endo- β -1,4-galactanase (EC 3.2.1.89)	1	0.53
GH54	α -L-arabinofuranosidase (EC 3.2.1.55); β -xylosidase (EC 3.2.1.37)	1	0.53
GH55	exo- β -1,3-glucanase (EC 3.2.1.58); endo- β -1,3-glucanase (EC 3.2.1.39)	3	1.58
GH62	α -L-arabinofuranosidase (EC 3.2.1.55)	1	0.53
GH63	processing α -glucosidase (EC 3.2.1.106); α -1,3-glucosidase (EC 3.2.1.84); α -glucosidase (EC 3.2.1.20); mannosylglycerate α -mannosidase / mannosylglycerate hydrolase (EC 3.2.1.170)	1	0.53
GH67	α -glucuronidase (EC 3.2.1.139); xylan α -1,2-glucuronidase (EC 3.2.1.131)	1	0.53
GH71	α -1,3-glucanase (EC 3.2.1.59).	1	0.53
GH72	β -1,3-glucanosyltransglycosylase (EC 2.4.1.-)	2	1.05
GH75	chitosanase (EC 3.2.1.132)	1	0.53
GH76	α -1,6-mannanase (EC 3.2.1.101)	4	2.11
GH78	α -L-rhamnosidase (EC 3.2.1.40)	3	1.58

Family	Known activities (GH, CE, PL, AA), binding specificities (CBM)	Number of DEGs	Relative abundance (%)
GH79	β -glucuronidase (EC 3.2.1.31); hyaluronoglucuronidase (EC 3.2.1.36); heparanase (EC 3.2.1.166); baicalin β -glucuronidase (EC 3.2.1.167); β -4-O-methyl-glucuronidase (EC 3.2.1.-)	2	1.05
GH81	endo- β -1,3-glucanase (EC 3.2.1.39)	1	0.53
GH88	d-4,5-unsaturated β -glucuronyl hydrolase (EC 3.2.1.-)	1	0.53
GH92	mannosyl-oligosaccharide α -1,2-mannosidase (EC 3.2.1.113); mannosyl-oligosaccharide α -1,3-mannosidase (EC 3.2.1.-); mannosyl-oligosaccharide α -1,6-mannosidase (EC 3.2.1.-); α -mannosidase (EC 3.2.1.24); α -1,2-mannosidase (EC 3.2.1.-); α -1,3-mannosidase (EC 3.2.1.-); α -1,4-mannosidase (EC 3.2.1.-); mannosyl-1-phosphodiester α -1,P-mannosidase (EC 3.2.1.-)	1	0.53
GH93	exo- α -L-1,5-arabinanase (EC 3.2.1.-)	1	0.53
GH95	α -1,2-L-fucosidase (EC 3.2.1.63); α -L-fucosidase (EC 3.2.1.51)	1	0.53
GH105	unsaturated rhamnogalacturonyl hydrolase (EC 3.2.1.172); d-4,5-unsaturated β -glucuronyl hydrolase (EC 3.2.1.-)	1	0.53
GH109	α -N-acetylgalactosaminidase	2	1.05
GH125	exo- α -1,6-mannosidase (EC 3.2.1.-)	1	0.53
GH142	β -L-arabinofuranosidase (EC 3.2.1.185)	1	0.53
43	Total GH	103	54.21
PL1	pectate lyase (EC 4.2.2.2); exo-pectate lyase (EC 4.2.2.9); pectin lyase (EC 4.2.2.10).	5	2.63
PL4	rhamnogalacturonan lyase (EC 4.2.2.-).	1	0.53
PL42	L-rhamnose- α -1,4-D-glucuronate lyase (EC 4.2.2.-); L-Rha- α -1,4-GlcA α -L-rhamnhydrolase (EC 3.2.1.-)	1	0.53
3	Total PL	7	3.68
CBM20	starch, cyclodextrins	1	0.53
CBM21	starch	1	0.53
CBM42	arabinofuranose	1	0.53
CBM43	β -1,3-glucan	2	1.05
CBM67	L-rhamnose	1	0.53
CBM87	cellulose galactosaminogalactan	1	0.53
CBM91	xylans	2	1.05
7	Total CBM	9	3.93
GT1	UDP-glucuronosyltransferase (EC 2.4.1.17); zeatin O- β -xylosyltransferase (EC 2.4.2.40); 2-hydroxyacylsphingosine 1- β -galactosyltransferase (EC 2.4.1.45); N-acylsphingosine galactosyltransferase (EC 2.4.1.47); flavonol 3-O-glucosyltransferase (EC 2.4.1.91);	3	1.58
GT2	cellulose synthase (EC 2.4.1.12); chitin synthase (EC 2.4.1.16); dolichyl-phosphate β -D-mannosyltransferase (EC 2.4.1.83); dolichyl-phosphate β -glucosyltransferase (EC 2.4.1.117); N-acetylglucosaminyltransferase (EC 2.4.1.-); N-acetylgalactosaminyltransferase (EC 2.4.1.-); hyaluronan synthase (EC 2.4.1.212); chitin oligosaccharide synthase (EC 2.4.1.-);	4	2.11
GT20	α , α -trehalose-phosphate synthase [UDP-forming] (EC 2.4.1.15); Glucosylglycerol-phosphate synthase (EC 2.4.1.213); trehalose-6-P phosphatase (EC 3.1.3.12); [retaining] GDP-valeniol: validamine 7-phosphate valeniolyltransferase (EC 2.-.-.-)	3	1.58

Family	Known activities (GH, CE, PL, AA), binding specificities (CBM)	Number of DEGs	Relative abundance (%)
GT22	Dol-P-Man: Man6GlcNAc2-PP-Dol α -1,2-mannosyltransferase (EC 2.4.1.259); Dol-P-Man: Man8GlcNAc2-PP-Dol α -1,2-mannosyltransferase (EC 2.4.1.261);	2	1.05
GT24	UDP-Glc: glycoprotein α -glucosyltransferase (EC 2.4.1.-).	1	0.53
GT25	lipopolysaccharide β -1,4-galactosyltransferase (EC 2.4.1.-); β -1,3-glucosyltransferase (EC 2.4.1.-); β -1,2-glucosyltransferase (EC 2.4.1.-); β -1,2-galactosyltransferase (EC 2.4.1.-); LPS β -1,4-galactosyltransferase (EC 2.4.1.-); occidiofungin β -xylosyltransferase (EC 2.4.2.-); UDP-Gal:procollagen β -galactosyltransferase (EC 2.4.1.50)	4	2.11
GT32	α -1,6-mannosyltransferase (EC 2.4.1.-); α -1,4-N-acetylglucosaminyltransferase (EC 2.4.1.-); α -1,4-N-acetylgalactosaminyltransferase (EC 2.4.1.-); GDP-Man: inositol-phosphorylceramide transferase (EC 2.4.1.-); UDP-Gal: β -galactoside α -1,4-galactosyltransferase (EC 2.4.1.-)	2	1.05
GT35	glycogen or starch phosphorylase (EC 2.4.1.1).	1	0.53
GT4	sucrose synthase (EC 2.4.1.13); sucrose-phosphate synthase (EC 2.4.1.14); α -glucosyltransferase (EC 2.4.1.52); lipopolysaccharide N-acetylglucosaminyltransferase (EC 2.4.1.56); phosphatidylinositol α -mannosyltransferase (EC 2.4.1.57);	3	1.58
GT66	dolichyl-diphosphooligosaccharide - protein glycotransferase (EC 2.4.99.18); undecaprenyl-diphosphooligosaccharide - protein glycotransferase (EC 2.4.99.19)	1	0.53
GT71	α -mannosyltransferase (EC 2.4.1.-)	1	0.53
GT90	UDP-Xyl: (mannosyl) glucuronoxylomannan/galactoxylomannan β -1,2-xylosyltransferase (EC 2.4.2.-); UDP-Glc: protein O- β -glucosyltransferase (EC 2.4.1.-); UDP-Xyl: protein O- β -xylosyltransferase (EC 2.4.2.-)	1	0.53
GT109	UDP-GalNAc: β -1,4-N-acetylgalactosaminyltransferase (EC 2.4.1.-)	1	0.53
13	Total GT	26	13.68

Table S4 The details of Differentially expressed genes involved in carbohydrate-active enzymes (DEG-CAZymes).

Gene ID	id	Log2(FC)	HMMER	Annotation	Ground-FPKM			Space-FPKM		
					G-A	G-B	G-C	S-A	S-B	S-C
1422755544	37190947	1.29	AA1(42-575)	L-ascorbate oxidase	0.71	0.61	0.66	2.52	2	1.95
1422764071	37188075	-1.15	AA1(51-580)	laccase TilA	8	6.97	8.97	4.95	3.99	5.32
1422790977	37192950	3.32	AA3(217-740)	hypothetical protein ASPFODRAFT_27949	8.59	7.22	9.09	133.21	108.31	92.3
1422736992	37184839	-1.60	AA3_2(14-531)	glucose-methanol-choline oxidoreductase	8.61	5.62	7.08	2.26	4.54	2.29
1422715969	37183185	2.91	AA3_2(39-609)	GMC oxidoreductase	8.5	9.17	10.59	100.63	104.36	79.16
1422728517	37188520	5.91	AA3_2(5-567)	GMC oxidoreductase	0.41	0.45	0.46	37.19	38.33	33.59
1422739040	37192471	2.50	AA3_2(5-596)	oxidoreductase	1.05	1.12	0.99	9.95	7.65	6.41
1422753717	37192614	3.73	AA3_2(7-561)	oxidoreductase	2.75	3.16	2.96	44.75	45.71	69.55
1422766027	37185314	-3.17	AA3_2(9-575)	oxidoreductase	2104.8	2377.8	2342.3	186.24	284.83	501.41
1422713582	37189188	3.42	AA3_3(12-598)	alcohol oxidase	0.36	0.17	0.42	5.15	5.35	3.59
1422723806	37183316	1.73	AA4(104-342)	oxidoreductase, FAD-binding protein	11.14	13.02	12.42	50.11	54.01	57.86
1422781583	37184087	-1.35	AA4(110-307)	hypothetical protein BDQ94DRAFT_149863	89.41	91.1	91.76	39.14	43.12	59.28
1422750005	37183641	2.63	AA4(111-337)	D-lactate dehydrogenase	3.14	2.68	4.46	31.35	26.35	29.74
1422765628	37188857	-1.24	AA7(125-545)	FAD/FMN-containing isoamyl alcohol oxidase MreA	17.9	14.46	15.28	7.3	8.85	10.51
1422775556	37191411	-1.86	AA7(129-314)	isoamyl alcohol oxidase	4.72	5.34	4.02	0.74	1.8	2.22
1422714073	37187203	2.32	AA7(131-327)	FAD-binding domain-containing protein	0.16	0.25	0.27	1.62	1.33	1.73
1422751236	37185047	3.74	AA7(185-393)	FAD-binding domain-containing protein	1.27	1.2	1.43	20.84	20.95	28.7
1422754464	37183689	1.74	AA7(20-433)	FAD binding domain protein	1.04	1.87	1.71	6.78	6.48	7.58
1422755353	37186568	-1.39	AA7(28-223)	L-galactono-gamma-lactone oxidase	41.08	36.96	37.18	16.41	15.78	25.67
1422782730	37182868	1.25	AA7(35-269)	FAD binding domain-containing protein	0.61	0.38	0.56	2.56	1.15	1.3
1422791878	37185769	-1.97	AA7(37-465)	FAD binding oxidoreductase	3.58	4.1	6.62	1.4	1.92	1.39
1422763759	37186678	2.77	AA7(56-267)	hypothetical protein ASPTUDRAFT_117656	1.37	0.76	0.9	10.05	9.68	8.36
1422732521	37192010	3.66	AA7(63-519)	FAD-binding domain-containing protein	0.2	0.1	0.23	6.45	2.73	1.23
1422718773	37183238	1.52	AA7(89-270)	FAD binding domain protein	0.75	0.55	0.55	2.05	2.24	2.87
1422780976	37184079	1.29	AA9(10-235)	endo-1,4-beta-glucanase	0.65	0.95	0.86	2.72	3.07	2.34
1422720298	37193266	-2.72	CBM21(321-429)	hypothetical protein BO79DRAFT_43738	4.26	5.01	3.49	0.49	0.79	1.21
1422756812	37185155	1.37	CBM67(128-313) +GH78(336-864)	alfa-L-rhamnosidase	0.7	0.87	1.05	1.84	2.69	4.73
1422789981	37187055	-1.14	CBM87(149-366) +CE18(367-734)	extracellular serine-rich protein	69.68	29	28.25	14.71	31.33	28.71
1422746280	37183598	-1.70	CE1(25-283)	esterase	318.86	303.88	360.5	107.99	132.68	158.4

1422741029	37189383	9.29	CE12(19-232)	rhamnogalacturonan acetyl esterase RgaeA	0.09	0.05	0.05	69.28	95.62	88.96
1422756653	37188769	6.61	CE12(31-226)	esterase	0.06	0.05	0.06	5.22	10.09	28.19
1422758691	37188028	7.54	CE16(33-340)	GDSL lipase/acylhydrolase family protein	1.74	3.02	3.16	507.41	642.25	1027.6
1422720777	37184533	6.05	CE16(37-332)	lysophospholipase A	10.07	9.22	12.61	816.56	985.32	1093.5
1422776438	37192820	1.19	CE2(162-367)	acetylxyloxy esterase	4.78	4.05	4.92	10.77	15.41	14.11
1422775702	37185505	3.51	CE5(123-285)	carbohydrate esterase family 5 protein	9.12	10	10.86	219.05	150.51	101.39
1422772426	37182749	4.48	CE5(36-212)	sugar transporter	1.95	1.67	2.04	81.57	75.65	26.54
1422776248	37193289	4.92	CE5(47-223)	cutinase-domain-containing protein	11.2	13.84	13.53	498.76	696.83	410.27
1422765588	37191218	5.56	CE8(28-307)	pectinesterase	18.87	17.14	18.81	867.17	1244.2	1437.6
1422756434	37190971	5.87	CE8(41-304)	pectinesterase family protein	1.09	1.42	1.67	74.52	93.05	199.31
1422767328	37191256	6.53	CE8(60-373)	hypothetical protein ASPTUDRAFT_200738	21.47	21.4	38.73	3397	3647.8	3584.8
1422736985	37186339	2.67	CE9(15-416)	n-acetylglucosamine-6-phosphate deacetylase	4.16	4.84	6.76	57.44	68.48	16.85
1422769943	37185395	4.53	GH1(150-595)	beta-glucosidase	0.23	0.21	0.45	10.65	12.86	6.57
1422755537	37185136	1.39	GH1(7-477)	beta-glucosidase 1B	3.36	2.89	3.73	9.39	11.33	14.51
1422753739	37188743	4.88	GH105(42-362)	glycosyl hydrolase	4.13	5.05	5.5	113.36	179.78	334.22
1422766287	37182682	6.20	GH109(3-159)	NAD binding Rossmann fold oxidoreductase	0.16	0.06	0.2	13.59	14.74	19.33
1422793699	37184253	-2.19	GH109(7-156)	NAD binding Rossmann fold oxidoreductase	430.11	429.66	511.62	174.02	134.65	77.56
1422751135	37190848	9.73	GH11(33-208)	endo-1,4-beta-xylanase 3	0.07	0.15	0.68	339.72	390.64	696.22
1422715591	37190863	1.81	GH11(47-223)	xylanase precursor	0.73	1.03	1	3.73	3.23	6.44
1422766201	37183850	1.03	GH12(111-256)	concanavalin A-like lectin/glucanase	1.25	0.75	0.72	2.97	1.72	2.86
1422753888	37190908	-1.52	GH12(87-238)	endoglucanase A	3.2	3.32	4.66	1.52	1.68	1.88
1422719898	37187688	3.59	GH12(93-240)	xyloglucan-specific endo-beta-1,4-glucanase A	14.21	16.66	15.01	174.88	195.73	407.19
1422756988	37189499	1.47	GH125(83-516)	DUF1237 domain protein	25.52	22.17	25.26	102.48	80.61	85.97
1422738365	37186352	-1.11	GH13_1(8-217)	hypothetical protein ASPTUDRAFT_61158	14.94	12	9.96	8.89	8.37	4.91
1422738378	37189368	-1.58	GH13_22(100-497) +GH13_22(1166-1633)	alpha-1,3-glucan synthase Ags1	2.35	1.73	1.26	0.66	0.98	0.69
1422767707	37191269	2.20	GH13_40(35-391)	oligo-1,6-glucosidase	1.78	1.46	2.14	7.26	11.84	14.6
1422754637	37183691	-1.36	GH13_40(42-405)	alpha-glucosidase, partial	1.61	1.22	1.54	0.5	0.98	0.74
1422753037	37185083	1.35	GH13_8(239-532)	1,4-alpha-glucan-branching enzyme	8.48	12.14	14.34	42.07	35.85	41.02
1422783189	37185644	5.40	GH142(30-511)	six-hairpin glycosidase	9.71	10.24	16.88	644.64	825.76	697.59
1422737879	37192462	-2.49	GH15(279-671)	glycosyl hydrolase	5.37	6.82	11.71	1.83	1.87	1.76
1422765400	37189579	1.82	GH15(43-448) +CBM20(538-627)	histidine-tagged glucoamylase	12.43	12.04	14.82	64.55	58.88	60.73
1422799929	37193799	1.51	GH16_1(68-264)	endo-1,3(4)-beta-glucanase	0.48	0.45	0.49	1.91	1.62	1.97
1422731145	37192389	1.25	GH16_18(67-223)	cell wall glucanase	15.93	10.98	12.22	39	43.83	41.33

1422721491	37189849	-1.53	GH16_2(267-590)	beta-1,6 glucan synthetase	4.19	4.49	6.14	2.08	1.94	2.71
1422799078	37193747	1.89	GH17(394-666)	endo-1,3-beta-glucanase BtgC	5.71	5.5	5.13	27.51	26.92	26.11
1422751221	37189468	4.30	GH2(15-502)	glycoside hydrolase family 2 protein	0.07	0.26	0.21	3.63	5.65	6.34
1422743038	37183561	2.99	GH2(43-765)	glycoside hydrolase	1.92	1.72	1.61	15.92	17.92	22.21
1422738855	37184860	2.42	GH2(8-671)	beta-mannosidase	2.44	1.84	2.12	17.86	11.83	16.39
1422750609	37186499	2.75	GH20(177-546)	beta-hexosaminidase precursor	11.96	11.95	15.64	161.23	104.58	93.96
1422789850	37184185	3.25	GH27(124-417)	glycoside hydrolase	0.46	0.38	0.39	4.98	4.37	6.08
1422776585	37185519	6.41	GH27(132-379)	putative alpha-galactosidase D	0.48	0.6	0.53	78.15	54.04	59.4
1422709321	37190450	1.17	GH28(166-486)	endo-polygalacturonase D	0.75	0.7	1.14	2.99	2.48	2.33
1422722009	37184561	1.03	GH28(38-360)	endopolygalacturonase	41.34	47.02	46.79	87.73	148.3	134.6
1422789354	37191737	3.48	GH28(40-356)	putative endopolygalacturonase II	0.69	1.19	0.74	12.19	12.46	15.66
1422780025	37185587	4.48	GH28(48-368)	polygalacturonase (Pgal)	4.18	4.62	5.73	60.12	106.32	338.33
1422756426	37190970	4.71	GH28(56-392)	endo-xylogalacturonan hydrolase A	0.68	0.64	0.48	16.66	15.76	36.22
1422767286	37191255	7.15	GH28(57-420)	exo-polygalacturonase	1.82	1.85	3.14	308.28	469.04	638.32
1422760227	37182624	4.66	GH28(58-374)	polygalacturonase E precursor pgaE	1.1	1.17	1.82	48.81	42.08	50.96
1422751207	37187962	6.10	GH28(60-382)	pectinase 3	0.04	0.07	0.11	4.49	8.24	16.72
1422753030	37185082	-1.16	GH28(64-375)	pectin lyase-like protein	6.42	7.53	9.67	3.52	3.15	4.87
1422750255	37189461	7.90	GH28(70-424)	Exopolygalacturonase X	6.14	7.69	15.13	3176.1	3268.7	3815.5
BGI_novel_G000025	-	7.82	GH28(7-198)	galacturan 1,4-alpha-galacturonidase	0.35	0.97	0.42	135.17	210.5	279.11
1422765263	37188078	9.83	GH28(77-424)	CobW domain protein	0.36	0.38	1.02	642.74	824.16	1145.7
1422790767	37192947	5.17	GH3(101-348)	beta-xylosidase	3.61	4.03	8.76	248.97	246.17	361.53
1422793648	37191844	4.88	GH3(113-338)	hypothetical protein ASPTUDRAFT_120885	2.38	2.27	2.3	71.46	85.43	125.02
1422793521	37189098	2.41	GH3(31-245)	beta-glucosidase J	0.84	0.76	0.64	4.73	5.56	5.68
1422737030	37184840	1.55	GH3(78-303)	beta-N-acetylglucosaminidase	3.7	3.34	3.73	17.46	12.45	11.97
1422773448	37189639	1.54	GH3(79-300)	beta-glucosidase	207.78	265.71	518.43	1475.7	1190.3	1239
1422772344	37185442	6.14	GH3(87-306)	beta-glucosidase	0.25	0.2	0.29	40.73	27.05	13.07
1422743206	37188645	5.73	GH3(91-303)	beta glucosidase	0.32	0.19	0.27	30.32	19.73	11.15
1422734525	37184783	6.09	GH31(209-654)	hypothetical protein BO79DRAFT_190787	0.36	0.3	0.61	25.66	41.03	62.07
1422759356	37185197	4.13	GH31(232-717)	neutral alpha-glucosidase	0.15	0.09	0.19	5.26	3	2.68
1422771050	37183943	3.86	GH31(241-766)	alpha-glucosidase	1.6	1.97	2.98	46.11	54.99	31.03
1422709353	37183088	2.81	GH31(245-723)	alpha-xylosidase	7.65	7.45	9.73	52.45	79.74	105.79
1422754265	37190909	4.58	GH31(267-710)	putative glycoside hydrolase family 31 protein	0.12	0.26	0.22	3.74	6.79	11.02
1422711003	37192182	1.65	GH31(368-815)	glucosidase II alpha subunit	55.29	43.47	49.59	173.94	212.58	235.97
1422715258	37190562	1.63	GH32(19-363)	glycosyl hydrolase family protein	1	1.07	1.19	5.43	3.79	4.26
1422749016	37185025	2.58	GH32(54-401)	hypothetical protein ASPBRDRAFT_199799	12.42	13.1	12.85	66.78	109.68	136.13

1422748918	37190773	5.97	GH35(35-370)	beta-galactosidase	0.8	1.14	1.74	85.95	109.07	133.49
1422722955	37184574	3.70	GH35(48-393)	putative beta-galactosidase B	53.64	48.03	74.58	1036	1096.5	970.45
1422752254	37190874	3.10	GH35(49-397)	beta-galactosidase	0.12	0.15	0.25	1.63	1.57	3.08
1422779497	37188992	7.79	GH35(53-385)	beta-galactosidase	2.65	3.34	7.69	1489.9	1574.5	1557.2
1422740320	37184878	1.99	GH36(41-730)	alpha-galactosidase C, partial	25.27	26.48	27.07	117.79	134.19	167.09
1422766879	37192728	1.84	GH38(284-542)	alpha-mannosidase	4.11	5.55	7.41	35.62	20.09	26.82
1422775392	37192811	6.12	GH43_13(2-301) +CBM91(327-526)	glycosyl hydrolase	0.56	0.43	0.85	50.51	62.37	65.84
1422716510	37191073	3.24	GH43_14(26-311) +CBM91(343-556)	hypothetical protein BO79DRAFT_267588	0.27	0.2	0.25	2.16	3.12	4.6
1422747228	37181966	4.64	GH43_24(44-276)	glycosyl hydrolase family 43 protein	1.49	1.57	1.98	37.22	77.24	62.24
1422799944	37193040	1.17	GH43_30(112-391)	glycosyl hydrolase family 43 protein	0.81	0.77	0.55	1.76	1.68	3.05
1422712728	37183134	5.64	GH43_30(40-317)	endo-arabinase	0.08	0.12	0.12	15.83	10.37	3.5
1422778552	37182819	2.43	GH43_34(25-310)	xylanase D	0.74	0.73	0.57	5.8	4.85	4.3
1422781632	37189687	3.62	GH43_6(26-315)	glycosyl hydrolase family 43 protein	0.45	0.38	0.71	16.05	8.33	3.87
1422740878	37183542	10.60	GH43_6(30-319)	arabinan endo-1,5-alpha-L-arabinosidase A	0.2	0.19	0.48	777.37	730.94	614.36
1422776020	37185508	1.22	GH43_6(97-441)	endo-1,5-alpha-L-arabinanase B	2.23	2.09	1.58	6.8	6.47	5.36
1422757797	37188782	1.84	GH47(103-573)	class I alpha-mannosidase	3.57	2.35	2.61	13.43	11.06	16.62
1422796888	37190425	1.75	GH47(153-702)	mannosyl-oligosaccharide alpha-1,2-mannosidase	20.49	16.21	14.99	66.2	88.8	77.47
1422764924	37188850	1.63	GH47(49-509)	mannosyl-oligosaccharide alpha-1,2-mannosidase 1B	13.7	14.82	18.93	89.19	66.01	41.7
1422782739	37187529	7.84	GH5_16(33-367)	cellulase family protein	0.6	0.93	1.58	525.87	330.07	246.25
1422737660	37183514	-2.76	GH5_7(72-346)	glycoside hydrolase	2.93	7.11	7.06	1	0.94	1.25
1422716396	37184446	7.71	GH51(14-502)	alpha-L-arabinofuranosidase	11.69	11.88	19.27	4766.6	3833	4078.5
1422790403	37191758	4.41	GH51(214-451) +GH51(433-626)	alpha-L-arabinofuranosidase a precursor abfA	3.53	4.34	9.55	234.62	165.74	134.37
1422793833	37191845	3.61	GH51(421-625)	glycoside hydrolase	1.97	1.51	4.34	57.52	47.29	31.39
1422759572	37185209	4.83	GH53(24-351)	arabinogalactan endo-1,4-beta-galactosidase A	4.65	4.76	5.47	156.37	206.02	212.61
1422713503	37190540	5.99	GH54(20-334) +CBM42(352-492)	alpha-N-arabinofuranosidase B	60.38	58.97	154.38	9728.5	9138.4	6949.9
1422779215	37193331	1.17	GH55(40-442) +GH55(528-947)	exo-beta-1,3-glucanase	23.5	18.92	21.38	58.32	64.02	68.5
1422767660	37185339	2.17	GH55(6-706)	pectin lyase-like protein	0.33	0.4	0.43	1.98	2.4	2.29
1422782699	37186971	5.04	GH62(28-302)	beta-D-arabinoxylan arabinofuranohydrolase	0.55	0.51	1.14	28.82	32.26	41.23
1422714523	37183165	1.20	GH63(595-806)	mannosyl-oligosaccharide glucosidase	30.09	26.06	29.41	60.49	97.63	104.77
1422752262	37190875	4.50	GH67(22-691)	hypothetical protein ASPTUDRAFT_194940	0.48	0.35	0.29	9.35	8.9	17.84

1422726818	37183374	3.34	GH7(19-448)	exoglucanase I	0.23	0.13	0.29	4.75	2.11	2.62
1422727232	37191808	1.27	GH71(43-432)	alpha-1,3-glucanase/mutanase	1.71	1.18	1.81	6.66	4.13	4.41
1422735471	37182275	-1.65	GH72(19-311) +CBM43(363-452)	1,3-beta-glucanosyltransferase	3.97	2.52	1.6	1.52	0.59	1.06
1422765691	37182680	1.16	GH72(19-318) +CBM43(372-457)	1,3-beta-glucanosyltransferase	7.2	7.87	7.88	14.08	20.43	34.86
1422766271	37191239	1.65	GH75(46-242)	Chitosanase-domain-containing protein	0.47	0.39	0.36	1.86	1.64	1.77
1422748852	37192564	1.59	GH76(29-399)	glycosyl hydrolase family 76 protein	17.37	16.87	16.55	78.8	56.73	68.47
1422720812	37184535	1.16	GH76(30-397)	glycosyl hydrolase	23.25	18.54	17.3	56.39	56.9	61.73
1422771829	37189627	2.39	GH76(30-415)	hypothetical protein BO79DRAFT_246974	0.55	0.72	0.49	5.86	4.26	2.52
1422733641	37183461	2.30	GH76(32-395)	glycosyl hydrolase	0.46	0.49	0.62	3.81	3.41	3.27
1422758391	37188789	6.36	GH78(108-661)	bacterial alpha-L-rhamnosidase domain protein	1.04	1.1	1.33	86.25	135.87	187.78
1422750879	37190839	3.04	GH78(424-835)	Six-hairpin glycosidase	0.41	0.42	0.52	1.54	4.14	11.28
1422776661	37191485	7.52	GH79(46-416)	hypothetical protein BO79DRAFT_272930	1.38	1.87	2.27	444.61	457.99	497.78
1422766956	37191253	3.74	GH79(53-534)	beta-glucuronidase	0.74	0.81	0.87	11.86	14.79	17.31
1422719760	37187226	2.21	GH81(242-932)	endo-1,3-beta-glucanase Eng1	2.59	2.51	2.09	12.17	14.19	18.48
1422718715	37187221	4.13	GH88(72-460)	Six-hairpin glycosidase	0.17	0.25	0.03	5.55	3.55	2.89
1422717128	37189209	2.21	GH92(263-772)	hypothetical protein BO79DRAFT_242254	0.71	0.72	0.82	5.97	3.99	3.65
1422753853	37186545	-1.16	GH93(58-321)	BNR/Asp-box repeat protein	159.92	205.76	234.39	124.72	136.94	91.71
1422731081	37188543	2.16	GH95(499-1209)	FAD/NAD(P)-binding domain-containing protein	5.02	4.79	4.19	32.38	18.94	33.03
1422772106	37191337	1.26	GT1(134-514)	UDP-glucose,sterol transferase	1.42	1.54	1.49	5.74	3.77	4.65
1422757235	37190989	3.56	GT1(175-479)	diacylglycerol acyltransferase family	3.75	3.55	5.97	96.21	73.29	47.45
1422728300	37187254	1.17	GT1(868-1281)	sterol 3-beta-glucosyltransferase	7.88	7.33	8.2	26.46	22.02	21.1
1422753602	37192612	1.92	GT109(25-426)	integral membrane protein	0.9	0.69	0.73	3.98	4.18	3.67
1422765985	37183849	-1.28	GT2(105-335)	glycosyl transferase	89.56	82.34	74.27	39.63	40.82	53.19
1422755889	37183709	2.08	GT2(106-331)	dolichyl-phosphate beta-glucosyltransferase	18.19	15.07	16.77	92.85	115.22	74.82
1422708624	37193625	1.18	GT2(227-395) +GT2(372-575)	chitin synthase G	45.68	32.54	29.71	121.26	105.5	98.88
1422724622	37186135	-1.21	GT20(117-658)	hypothetical protein BO79DRAFT_207152	59.74	66.25	60.62	24.93	36.31	45.37
1422761115	37185236	-1.73	GT20(181-632)	alpha,alpha-trehalose phosphate synthase subunit Tps	17.07	28.45	27.54	7.27	9.2	12.42
1422776384	37184016	-1.34	GT20(4-465)	alpha,alpha-trehalose-phosphate synthase subunit	1.91	5.79	8.65	3.04	3.13	2.09
1422732615	37192012	1.63	GT22(10-416)	alpha-1,6-mannosyltransferase subunit	6.34	6.02	5.01	20.29	33.07	18.76
1422770681	37187483	1.03	GT22(86-544)	mannosyltransferase	8.44	8.57	8.45	24.31	22.22	22.25
1422728433	37184665	1.01	GT24(1188-1435)	UDP-glucose:glyco protein glucosyltransferase	12.53	10.45	10.89	23.62	33.89	33.57
1422741717	37188630	5.29	GT25(323-538)	LPS glycosyltransferase	2.3	2.73	2.75	216.41	158.96	84.02

1422779180	37184058	1.03	GT25(59-258)	LPS glycosyltransferase	5.89	4.29	4.3	12.62	13.53	13.2
1422718506	37184487	2.40	GT25(70-271)	hypothetical protein BO79DRAFT_186497	1.11	1.53	1.13	9.19	8.01	9.71
1422786718	37192911	3.27	GT25(75-286)	LPS glycosyltransferase	0.83	0.85	0.58	16.41	10.46	4.39
1422715078	37182003	1.40	GT32(75-155)	hypothetical protein BO79DRAFT_133413	22.53	13.96	14.13	57.92	65.87	51.54
1422751574	37186510	2.79	GT32(94-180)	glycosyl transferase	49.48	35.07	41.09	443.48	423.95	298.01
1422799037	37183074	-1.07	GT35(160-875)	glycogen phosphorylase GlpV/Gph1	19.87	21.13	24.6	15.69	12.21	13.07
1422752198	37185063	1.45	GT4(234-400)	alpha-1,2-mannosyltransferase	7.79	8.27	8.06	22.93	41.34	24.07
1422759551	37185208	1.86	GT4(346-507)	alpha-1,2-mannosyltransferase	24.07	26.44	25.38	122.22	161.03	86.79
1422784462	37186993	-2.37	GT4(452-622)	trehalose synthase (Ccg-9)	34.18	37.57	39.97	8.18	9.9	10.38
1422736672	37183502	1.55	GT66(23-663)	oligosaccharyl transferase subunit	77.82	64.08	68.89	203.04	331.73	294.56
1422711722	37185929	-1.26	GT71(161-416)	hypothetical protein BO85DRAFT_448534	19.5	24.38	18.44	8.42	14.54	11.14
1422781925	37184091	1.14	GT90(193-423)	endoplasmic reticulum-resident kdel protein	2.06	2.46	2.19	8.74	6.25	4.69
1422754392	37190915	5.68	PL1_4(112-297)	pectin lyase pelD	0.04	0.11	0.27	8.87	9.32	16.24
1422797650	37193013	-2.34	PL1_4(114-298)	pectin lyase pelB	4.54	6.33	6.38	1.08	1.64	1.71
1422752958	37188739	6.68	PL1_4(114-298)	pectin Lyase A	22.81	19.02	23.92	2215.2	2816.9	4577
1422777663	37182813	1.40	PL1_4(115-298)	pectin lyase	1.31	1.19	1.93	5.01	6.23	4.4
1422758827	37185190	3.02	PL1_7(79-260)	pectin lyase-like protein	0.62	0.44	0.71	4.55	4.85	11.45
1422772297	37188923	2.80	PL4_3(19-648)	rhamnogalacturonate lyase B	0.75	0.75	0.96	2.87	3.64	24.34
1422776668	37185522	6.13	PL42(19-339)	dockerin type 1	1.58	1.45	1.78	148.46	155.18	153.34