

## Supplemental Info S1: Commands

**Digital normalization** was done with the khmer package with the following steps and parameters:

1. `interleave-reads.py`
2. `normalize-by-median.py -C 20 -k 20 -N 4 -x 2.5e8`
3. `filter-abund.py clavariopsis.kh`
4. `normalize-by-median.py -C 5 -k 20 -N 4 -x 1e8`
5. `extract-paired-reads.py`

**Genome assembly** was done with velvet with the digitally normalized reads with the following commands:

1. `velveth -fastq.gz -shortPaired`
2. `velvetg -ins_length 900 -exp_cov 140 -cov_cutoff 50`

**De Novo transcriptome assembly** was done with Trinity with the following command:

`Trinity --seqType fq --max_memory 100G --single $INDATA --CPU 12 --trimmomatic --normalize_reads --SS_lib_type R`

**Genome guided transcriptome assembly** was done with Trinity with the following command:

`Trinity --genome_guided_bam $INDATA --genome_guided_max_intron 1000 --max_memory 30G --CPU 12`

The **PASA pipeline** was run with the following commands:

1. `cat Trinity.fasta Trinity-GG.fasta > ${TRANSCRIPTS}`
2. `accession_extractor.pl < Trinity.fasta > tdn.accs`
3. `Launch_PASA_pipeline.pl -c alignAssembly.conf -C -R -g ${GENOME} -t ${TRANSCRIPTS} --ALIGNERS blat,gmap --TDN tdn.accs --transcribed_is_aligned_orient --MAX_INTRON_LENGTH 3000`
4. `build_comprehensive_transcriptome.dbi -c alignAssembly.conf -t ${TRANSCRIPTS} --min_per_ID 95 --min_per_aligned 30`

## Supplemental Table S1

**Supplemental Table S1A: CAZy families predicted to be active by MGSA analysis. For comparison growth on straw compared to growth on malt extract**

condition	CAZy Family	activity	genes with this annotation in the genome	differentially expressed genes with this annotation	activation probability
straw-malt	AA9	AA9 (formerly GH61) proteins are copper-dependent lytic polysaccharide monooxygenases (LPMOs); cleavage of cellulose chains with oxidation of various carbons (C-1, C-4 and C-6) has been reported several times in the literature;	49	35	1
straw-malt	CE1	acetyl xylan esterase; cinnamoyl esterase; feruloyl esterase; carboxylesterase; S-formylglutathione hydrolase; diacylglycerol O-acyltransferase; trehalose 6-O-mycolyltransferase	10	9	0.9882
straw-malt	GH11	endo- $\beta$ -1,4-xylanase; endo- $\beta$ -1,3-xylanase	6	6	0.96
straw-malt	GH7	endo- $\beta$ -1,4-glucanase; reducing end-acting cellobiohydrolase; chitosanase; endo- $\beta$ -1,3-1,4-glucanase	7	6	0.877
straw-malt	GH10	endo-1,4- $\beta$ -xylanase; endo-1,3- $\beta$ -xylanase; tomatinase; xylan endotransglycosylase	4	4	0.7582
straw-malt	GH5_5	endo- $\beta$ -1,4-glucanase / cellulase; endo- $\beta$ -1,4-xylanase; $\beta$ -glucosidase; $\beta$ -mannosidase; $\beta$ -glucosylceramidase; glucan $\beta$ -1,3-glucosidase; licheninase; exo- $\beta$ -1,4-glucanase / cellodextrinase; glucan endo-1,6- $\beta$ -glucosidase; mannan endo- $\beta$ -1,4-mannosidase; cellulose $\beta$ -1,4-cellobiosidase; steryl $\beta$ -glucosidase; endoglycoceramidase; chitosanase; $\beta$ -primeverosidase; xyloglucan-specific endo- $\beta$ -1,4-glucanase; endo- $\beta$ -1,6-galactanase; hesperidin 6-O- $\alpha$ -L-rhamnosyl- $\beta$ -glucosidase; $\beta$ -1,3-mannanase; arabinoxylan-specific endo- $\beta$ -1,4-xylanase; mannan transglycosylase	5	5	0.6948

**Supplemental Table S1B: KEGG pathways predicted to be active by MGSA analysis. For comparison growth on straw compared to growth**

**on malt extract, and growth on alder compared to malt extract**

condition	KEGG pathway ID	KEGG pathway name	genes with this annotation in the genome	differentially expressed genes with this annotation	activation probability
alder-malt	ko00040	Pentose and glucuronate interconversions	35	19	1
alder-malt	ko01120	Microbial metabolism in diverse environments	246	92	1
alder-malt	ko04146	Peroxisome	54	35	1
alder-malt	ko00280	Valine, leucine and isoleucine degradation	49	26	1
alder-malt	ko00640	Propanoate metabolism	28	12	0.9992
alder-malt	ko00460	Cyanoamino acid metabolism	26	13	0.9868
alder-malt	ko00906	Carotenoid biosynthesis	4	4	0.9804
alder-malt	ko04978	Mineral absorption	7	4	0.9438
alder-malt	ko00052	Galactose metabolism	30	12	0.7968
alder-malt	ko04920	Adipocytokine signaling pathway	9	4	0.6656
alder-malt	ko04260	Cardiac muscle contraction	12	4	0.6062
straw-malt	ko00500	Starch and sucrose metabolism	65	31	1
straw-malt	ko00040	Pentose and glucuronate interconversions	35	19	1
straw-malt	ko03008	Ribosome biogenesis in eukaryotes	64	23	1
straw-malt	ko00330	Arginine and proline metabolism	38	18	0.9978
straw-malt	ko00520	Amino sugar and nucleotide sugar metabolism	49	17	0.967
straw-malt	ko00980	Metabolism of xenobiotics by cytochrome P450	28	14	0.9512
straw-malt	ko00630	Glyoxylate and dicarboxylate metabolism	40	21	0.9136
straw-malt	ko00920	Sulfur metabolism	17	8	0.9056
straw-malt	ko00052	Galactose metabolism	30	15	0.897
straw-malt	ko00350	Tyrosine metabolism	50	20	0.838
straw-malt	ko00770	Pantothenate and CoA biosynthesis	23	11	0.7994
straw-malt	ko00910	Nitrogen metabolism	21	9	0.6518
straw-malt	ko01220	Degradation of aromatic compounds	32	17	0.6144

**Supplemental Table S1C: GO terms predicted to be active by MGSA analysis. For comparison growth on straw compared to growth on malt extract, and growth on alder compared to malt extract**

condition	GO ID	GO name	genes with this annotation in the genome	differentially expressed genes with this annotation	activation probability
alder-malt	GO:0016491	oxidoreductase activity	506	205	1
alder-malt	GO:0005975	carbohydrate metabolic process	226	72	1
alder-malt	GO:0071949	FAD binding	55	29	1
alder-malt	GO:0055085	transmembrane transport	513	165	1
alder-malt	GO:0055114	oxidation-reduction process	768	283	1
alder-malt	GO:0008152	metabolic process	387	158	1
alder-malt	GO:0008080	N-acetyltransferase activity	49	19	0.9998
alder-malt	GO:0006508	proteolysis	132	39	0.7976
straw-malt	GO:0008080	N-acetyltransferase activity	49	22	1
straw-malt	GO:0016491	oxidoreductase activity	506	192	1
straw-malt	GO:0005975	carbohydrate metabolic process	226	117	1
straw-malt	GO:0003824	catalytic activity	610	198	1
straw-malt	GO:0016787	hydrolase activity	165	54	1
straw-malt	GO:0071949	FAD binding	55	31	1
straw-malt	GO:0006508	proteolysis	132	53	1
straw-malt	GO:0055085	transmembrane transport	513	188	1
straw-malt	GO:0055114	oxidation-reduction process	768	279	1
straw-malt	GO:0000981	RNA polymerase II transcription factor activity, sequence-specific DNA binding	217	66	0.9982
straw-malt	GO:0042254	ribosome biogenesis	15	9	0.634

## Supplemental Table S2

condition	CAZy Family	activity	genes with this annotation in the genome	differentially expressed genes with this annotation	activation probability
alder-straw	AA9	AA9 (formerly GH61) proteins are copper-dependent lytic polysaccharide monooxygenases (LPMOs); cleavage of cellulose chains with oxidation of various carbons (C-1, C-4 and C-6) has been reported several times in the literature;	49	35	1
alder-straw	CE1	acetyl xylan esterase; cinnamoyl esterase; feruloyl esterase; carboxylesterase; S-formylglutathione hydrolase; diacylglycerol O-acyltransferase; trehalose 6-O-mycolyltransferase	10	9	0.9826
alder-straw	GH11	endo- $\beta$ -1,4-xylanase; endo- $\beta$ -1,3-xylanase	6	6	0.935
alder-straw	GH7	endo- $\beta$ -1,4-glucanase; reducing end-acting cellobiohydrolase; chitosanase; endo- $\beta$ -1,3-1,4-glucanase	7	6	0.8518
alder-straw	GH131	broad specificity exo- $\beta$ -1,3/1,6-glucanase with endo- $\beta$ -1,4-glucanase activity;	4	4	0.7446
alder-straw	GH10	endo-1,4- $\beta$ -xylanase; endo-1,3- $\beta$ -xylanase; tomatinase; xylan endotransglycosylase	4	4	0.7428
alder-straw	GH5_5	endo- $\beta$ -1,4-glucanase / cellulase; endo- $\beta$ -1,4-xylanase; $\beta$ -glucosidase; $\beta$ -mannosidase; $\beta$ -glucosylceramidase; glucan $\beta$ -1,3-glucosidase; licheninase; exo- $\beta$ -1,4-glucanase / cellodextrinase; glucan endo-1,6- $\beta$ -glucosidase; mannan endo- $\beta$ -1,4-mannosidase; cellulose $\beta$ -1,4-cellobiosidase; steryl $\beta$ -glucosidase; endoglycoceramidase; chitosanase; $\beta$ -primeverosidase; xyloglucan-specific endo- $\beta$ -1,4-glucanase; endo- $\beta$ -1,6-galactanase; hesperidin 6-O- $\alpha$ -L-rhamnosyl- $\beta$ -glucosidase; $\beta$ -1,3-mannanase; arabinoxylan-specific endo- $\beta$ -1,4-xylanase; mannan	5	5	0.6984

		transglycosylase			
solid-liquidExp	GH7	endo- $\beta$ -1,4-glucanase; reducing end-acting cellobiohydrolase; chitosanase; endo- $\beta$ -1,3-1,4-glucanase	7	7	0.937
solid-liquidExp	AA9	AA9 (formerly GH61) proteins are copper-dependent lytic polysaccharide monooxygenases (LPMOs); cleavage of cellulose chains with oxidation of various carbons (C-1, C-4 and C-6) has been reported several times in the literature;	49	26	0.813
solid-liquidExp	GH72	$\beta$ -1,3-glucanosyltransglycosylase	7	6	0.7628
solid-liquidExp	AA7	glucooligosaccharide oxidase; chitoooligosaccharide oxidase	25	14	0.6684
solid-liquidExp	GH3	$\beta$ -glucosidase; xylan 1,4- $\beta$ -xylosidase; $\beta$ -glucosylceramidase; $\beta$ -N-acetylhexosaminidase; $\alpha$ -L-arabinofuranosidase; glucan 1,3- $\beta$ -glucosidase; glucan 1,4- $\beta$ -glucosidase; isoprimeverose-producing oligoxyloglucan hydrolase; coniferin $\beta$ -glucosidase; exo-1,3-1,4-glucanase; $\beta$ -N-acetylglucosaminide phosphorylases	19	11	0.6038
solid-liquidSta	AA9	AA9 (formerly GH61) proteins are copper-dependent lytic polysaccharide monooxygenases (LPMOs); cleavage of cellulose chains with oxidation of various carbons (C-1, C-4 and C-6) has been reported several times in the literature;	49	33	1
solid-liquidSta	GH7	endo- $\beta$ -1,4-glucanase; reducing end-acting cellobiohydrolase; chitosanase; endo- $\beta$ -1,3-1,4-glucanase	7	7	0.9634
solid-liquidSta	CE16	acetyl esterase active on various carbohydrate acetyl esters	5	5	0.847
solid-liquidSta	AA12	The pyrroloquinoline quinone-dependent oxidoreductase activity was demonstrated for the	6	5	0.745

		CC1G_09525 protein of Coprinopsis cinerea.			
solid-liquidSta	GH55	exo- $\beta$ -1,3-glucanase; endo- $\beta$ -1,3-glucanase	4	4	0.7364
solid-liquidSta	GH11	endo- $\beta$ -1,4-xylanase; endo- $\beta$ -1,3-xylanase	6	5	0.7024
stat-exp	CE8	pectin methylesterase	6	5	0.6276
straw-malt	AA9	AA9 (formerly GH61) proteins are copper-dependent lytic polysaccharide monooxygenases (LPMOs); cleavage of cellulose chains with oxidation of various carbons (C-1, C-4 and C-6) has been reported several times in the literature;	49	35	1
straw-malt	CE1	acetyl xylan esterase; cinnamoyl esterase; feruloyl esterase; carboxylesterase; S-formylglutathione hydrolase; diacylglycerol O-acyltransferase; trehalose 6-O-mycolyltransferase	10	9	0.9882
straw-malt	GH11	endo- $\beta$ -1,4-xylanase; endo- $\beta$ -1,3-xylanase	6	6	0.96
straw-malt	GH7	endo- $\beta$ -1,4-glucanase; reducing end-acting cellobiohydrolase; chitosanase; endo- $\beta$ -1,3-1,4-glucanase	7	6	0.877
straw-malt	GH10	endo-1,4- $\beta$ -xylanase; endo-1,3- $\beta$ -xylanase; tomatinase; xylan endotransglycosylase	4	4	0.7582
straw-malt	GH5_5	endo- $\beta$ -1,4-glucanase / cellulase; endo- $\beta$ -1,4-xylanase; $\beta$ -glucosidase; $\beta$ -mannosidase; $\beta$ -glucosylceramidase; glucan $\beta$ -1,3-glucosidase; licheninase; exo- $\beta$ -1,4-glucanase / cellodextrinase; glucan endo-1,6- $\beta$ -glucosidase; mannan endo- $\beta$ -1,4-mannosidase; cellulose $\beta$ -1,4-cellobiosidase; steryl $\beta$ -glucosidase; endoglycoceramidase; chitosanase; $\beta$ -primeverosidase; xyloglucan-specific endo- $\beta$ -1,4-glucanase; endo- $\beta$ -1,6-galactanase; hesperidin 6-O- $\alpha$ -L-rhamnosyl- $\beta$ -glucosidase; $\beta$ -1,3-mannanase; arabinoxylan-specific endo- $\beta$ -1,4-xylanase; mannan	5	5	0.6948

		transglycosylase			
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## Supplemental Table S3

condition	KEGG pathway ID	KEGG pathway name	genes with this annotation in the genome	differentially expressed genes with this annotation	activation probability
alder-malt	ko00040	Pentose and glucuronate interconversions	35	19	1
alder-malt	ko01120	Microbial metabolism in diverse environments	246	92	1
alder-malt	ko04146	Peroxisome	54	35	1
alder-malt	ko00280	Valine, leucine and isoleucine degradation	49	26	1
alder-malt	ko00640	Propanoate metabolism	28	12	0.9992
alder-malt	ko00460	Cyanoamino acid metabolism	26	13	0.9868
alder-malt	ko00906	Carotenoid biosynthesis	4	4	0.9804
alder-malt	ko04978	Mineral absorption	7	4	0.9438
alder-malt	ko00052	Galactose metabolism	30	12	0.7968
alder-malt	ko04920	Adipocytokine signaling pathway	9	4	0.6656
alder-malt	ko04260	Cardiac muscle contraction	12	4	0.6062
alder-straw	ko00500	Starch and sucrose metabolism	65	32	1
alder-straw	ko01120	Microbial metabolism in diverse environments	246	96	1
alder-straw	ko04146	Peroxisome	54	33	1
alder-straw	ko00040	Pentose and glucuronate interconversions	35	16	0.9972



alder-straw	ko00190	Oxidative phosphorylation	73	25	0.9796
alder-straw	ko00520	Amino sugar and nucleotide sugar metabolism	49	18	0.974
alder-straw	ko00770	Pantothenate and CoA biosynthesis	23	10	0.9574
alder-straw	ko04142	Lysosome	40	13	0.955
alder-straw	ko00330	Arginine and proline metabolism	38	17	0.9466
alder-straw	ko00906	Carotenoid biosynthesis	4	4	0.9202
alder-straw	ko00600	Sphingolipid metabolism	21	11	0.8762
alder-straw	ko00910	Nitrogen metabolism	21	6	0.8466
alder-straw	ko00780	Biotin metabolism	9	5	0.7978
alder-straw	ko00740	Riboflavin metabolism	11	5	0.7602
alder-straw	ko04978	Mineral absorption	7	4	0.727
alder-straw	ko00380	Tryptophan metabolism	40	21	0.702
alder-straw	ko05130	Pathogenic Escherichia coli infection	13	5	0.6742
alder-straw	ko00640	Propanoate metabolism	28	13	0.6634
solid-liquidExp	ko00970	Aminoacyl-tRNA biosynthesis	40	28	0.9998
solid-liquidExp	ko01230	Biosynthesis of amino acids	116	58	0.9152
solid-liquidExp	ko00520	Amino sugar and nucleotide sugar metabolism	49	28	0.8352
solid-	ko03030	DNA replication	32	27	0.7924

liquidExp					
solid-liquidExp	ko03008	Ribosome biogenesis in eukaryotes	64	31	0.7612
solid-liquidExp	ko00280	Valine, leucine and isoleucine degradation	49	26	0.7048
solid-liquidExp	ko04111	Cell cycle - yeast	75	43	0.6586
solid-liquidExp	ko01524	Platinum drug resistance	29	18	0.6358
solid-liquidExp	ko03050	Proteasome	35	18	0.6236
solid-liquidSta	ko03008	Ribosome biogenesis in eukaryotes	64	38	1
solid-liquidSta	ko00500	Starch and sucrose metabolism	65	38	0.997
solid-liquidSta	ko00040	Pentose and glucuronate interconversions	35	25	0.9964
solid-liquidSta	ko03030	DNA replication	32	22	0.983
solid-liquidSta	ko00970	Aminoacyl-tRNA biosynthesis	40	22	0.9042
solid-liquidSta	ko00052	Galactose metabolism	30	20	0.882
solid-liquidSta	ko00564	Glycerophospholipid metabolism	39	22	0.8494
solid-	ko00770	Pantothenate and CoA biosynthesis	23	15	0.7834

liquidSta					
solid-liquidSta	ko00965	Betalain biosynthesis	17	12	0.6102
stat-exp	ko00040	Pentose and glucuronate interconversions	35	21	1
stat-exp	ko03010	Ribosome	99	29	1
stat-exp	ko01120	Microbial metabolism in diverse environments	246	60	0.9772
stat-exp	ko00280	Valine, leucine and isoleucine degradation	49	17	0.9676
stat-exp	ko00520	Amino sugar and nucleotide sugar metabolism	49	12	0.8906
stat-exp	ko00620	Pyruvate metabolism	41	11	0.8554
stat-exp	ko00260	Glycine, serine and threonine metabolism	47	11	0.845
stat-exp	ko00250	Alanine, aspartate and glutamate metabolism	31	9	0.7604
stat-exp	ko01110	Biosynthesis of secondary metabolites	355	94	0.7382
straw-malt	ko00500	Starch and sucrose metabolism	65	31	1
straw-malt	ko00040	Pentose and glucuronate interconversions	35	19	1
straw-malt	ko03008	Ribosome biogenesis in eukaryotes	64	23	1
straw-malt	ko00330	Arginine and proline metabolism	38	18	0.9978
straw-malt	ko00520	Amino sugar and nucleotide sugar metabolism	49	17	0.967
straw-malt	ko00980	Metabolism of xenobiotics by cytochrome P450	28	14	0.9512
straw-malt	ko00630	Glyoxylate and dicarboxylate metabolism	40	21	0.9136
straw-malt	ko00920	Sulfur metabolism	17	8	0.9056

straw-malt	ko00052	Galactose metabolism	30	15	0.897
straw-malt	ko00350	Tyrosine metabolism	50	20	0.838
straw-malt	ko00770	Pantothenate and CoA biosynthesis	23	11	0.7994
straw-malt	ko00910	Nitrogen metabolism	21	9	0.6518
straw-malt	ko01220	Degradation of aromatic compounds	32	17	0.6144

## Supplemental Table S4

condition	GO ID	GO name	genes with this annotation in the genome	differentially expressed genes with this annotation	activation probability
alder-malt	GO:0016491	oxidoreductase activity	506	205	1
alder-malt	GO:0005975	carbohydrate metabolic process	226	72	1
alder-malt	GO:0071949	FAD binding	55	29	1
alder-malt	GO:0055085	transmembrane transport	513	165	1
alder-malt	GO:0055114	oxidation-reduction process	768	283	1
alder-malt	GO:0008152	metabolic process	387	158	1
alder-malt	GO:0008080	N-acetyltransferase activity	49	19	0.9998
alder-malt	GO:0006508	proteolysis	132	39	0.7976
alder-straw	GO:0016491	oxidoreductase activity	506	211	1
alder-straw	GO:0003824	catalytic activity	610	212	1
alder-straw	GO:0016787	hydrolase activity	165	57	1

alder-straw	GO:0071949	FAD binding	55	28	1
alder-straw	GO:0006508	proteolysis	132	53	1
alder-straw	GO:0055114	oxidation-reduction process	768	301	1
alder-straw	GO:0055085	transmembrane transport	513	176	0.9952
alder-straw	GO:0005975	carbohydrate metabolic process	226	110	0.988
solid-liquidExp	GO:0005524	ATP binding	497	231	1
solid-liquidExp	GO:0005515	protein binding	749	314	1
solid-liquidExp	GO:0003824	catalytic activity	610	256	1
solid-liquidExp	GO:0055085	transmembrane transport	513	230	1
solid-liquidExp	GO:0055114	oxidation-reduction process	768	341	0.9992
solid-liquidExp	GO:0006508	proteolysis	132	68	0.9848
solid-liquidExp	GO:0005975	carbohydrate metabolic process	226	115	0.9762
solid-liquidExp	GO:0005634	nucleus	389	180	0.9716
solid-liquidExp	GO:0016787	hydrolase activity	165	77	0.913
solid-liquidExp	GO:0016491	oxidoreductase activity	506	231	0.8836

solid-liquidExp	GO:0003676	nucleic acid binding	294	130	0.6472
solid-liquidSta	GO:0003824	catalytic activity	610	283	1
solid-liquidSta	GO:0005975	carbohydrate metabolic process	226	125	0.9898
solid-liquidSta	GO:0055114	oxidation-reduction process	768	335	0.9868
solid-liquidSta	GO:0008152	metabolic process	387	180	0.9798
solid-liquidSta	GO:0055085	transmembrane transport	513	264	0.975
solid-liquidSta	GO:0006508	proteolysis	132	66	0.8306
stat-exp	GO:0003824	catalytic activity	610	164	1
stat-exp	GO:0055114	oxidation-reduction process	768	232	1
stat-exp	GO:0016491	oxidoreductase activity	506	153	0.9988
stat-exp	GO:0071949	FAD binding	55	21	0.9874
stat-exp	GO:0005975	carbohydrate metabolic process	226	67	0.9518
stat-exp	GO:0055085	transmembrane transport	513	113	0.8948
straw-malt	GO:0008080	N-acetyltransferase activity	49	22	1
straw-malt	GO:0016491	oxidoreductase activity	506	192	1
straw-malt	GO:0005975	carbohydrate metabolic process	226	117	1

straw-malt	GO:0003824	catalytic activity	610	198	1
straw-malt	GO:0016787	hydrolase activity	165	54	1
straw-malt	GO:0071949	FAD binding	55	31	1
straw-malt	GO:0006508	proteolysis	132	53	1
straw-malt	GO:0055085	transmembrane transport	513	188	1
straw-malt	GO:0055114	oxidation-reduction process	768	279	1
straw-malt	GO:0000981	RNA polymerase II transcription factor activity, sequence-specific DNA binding	217	66	0.9982
straw-malt	GO:0042254	ribosome biogenesis	15	9	0.634