Table S1: Relative content (%age) of cell wall polymers in all studied samples

Cell wall polymers	Lower wood (LW)	Upper wood (UW)	Normal wood (NW)
Lignin	21.79	23.50	23.46
Hemicellulose	29.59	27.47	26.77
Cellulose	48.62	49.03	49.77

Table S2 Quality evaluation of RNA seq Data

Sample	**Raw reads**	**Clean reads**	**Clean bases**	**Error rate**	**Q20**	**Q30**	**GC pct**
NW1	49523950	48448364	7.27G	0.03	97.48	92.99	43.45
NW2	44078816	43027212	6.45G	0.03	97.74	93.61	43.53
NW3	47313792	46323534	6.95G	0.03	97.67	93.41	43.36
LW1	52040510	51020920	7.65G	0.03	97.85	93.78	43.52
LW2	47437012	46470654	6.97G	0.02	98.04	94.27	43.56
LW3	45535078	44791128	6.72G	0.03	97.72	93.53	43.17
UW1	45997564	45103602	6.77G	0.03	97.71	93.56	42.92
UW2	47152244	46344026	6.95G	0.03	97.94	93.98	43.47
UW3	45644496	44509336	6.68G	0.02	98.07	94.21	42.8

Table S3 Alinement and statistics of clean reads on reference genome.

sample	total reads	total map	unique map	multimap	read1_map	read2_map
NW1	48448364	45924153(94.79%)	44548981(91.95%)	1375172(2.84%)	22392500(46.22%)	22156481(45.73%)
NW2	43027212	40924035(95.11%)	39706375(92.28%)	1217660(2.83%)	19899410(46.25%)	19806965(46.03%)
NW3	46323534	43912692(94.8%)	42575422(91.91%)	1337270(2.89%)	21363902(46.12%)	21211520(45.79%)
LW1	51020920	48266752(94.6%)	46752195(91.63%)	1514557(2.97%)	23454238(45.97%)	23297957(45.66%)
LW2	46470654	44280034(95.29%)	42779203(92.06%)	1500831(3.23%)	21432578(46.12%)	21346625(45.94%)
LW3	44791128	42445769(94.76%)	41155243(91.88%)	1290526(2.88%)	20643469(46.09%)	20511774(45.79%)
UW1	45103602	42427217(94.07%)	41049869(91.01%)	1377348(3.05%)	20573626(45.61%)	20476243(45.4%)
UW2	46344026	43822340(94.56%)	42391499(91.47%)	1430841(3.09%)	21268967(45.89%)	21122532(45.58%)
UW3	44509336	42132712(94.66%)	40758836(91.57%)	1373876(3.09%)	20427809(45.9%)	20331027(45.68%)

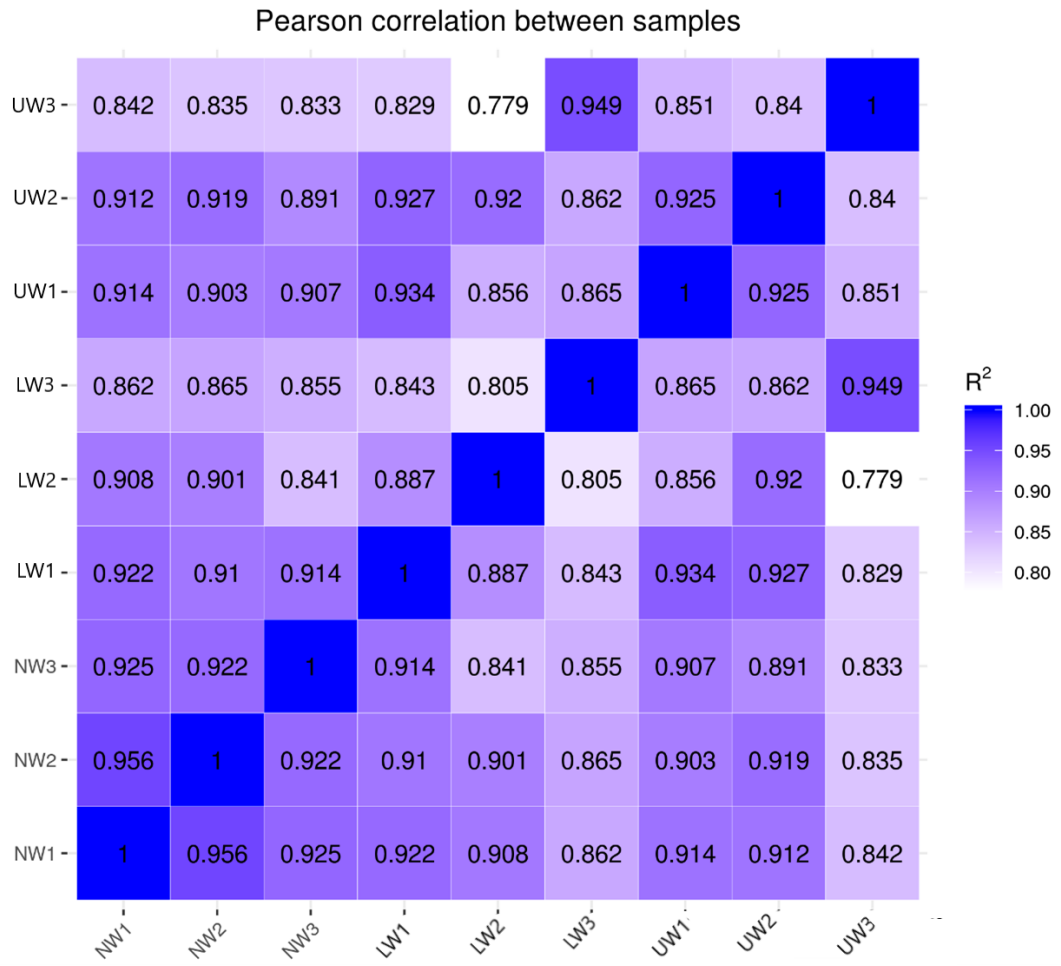


Figure S1: Pearson correlation coefficient among all three biological replicates from each samples

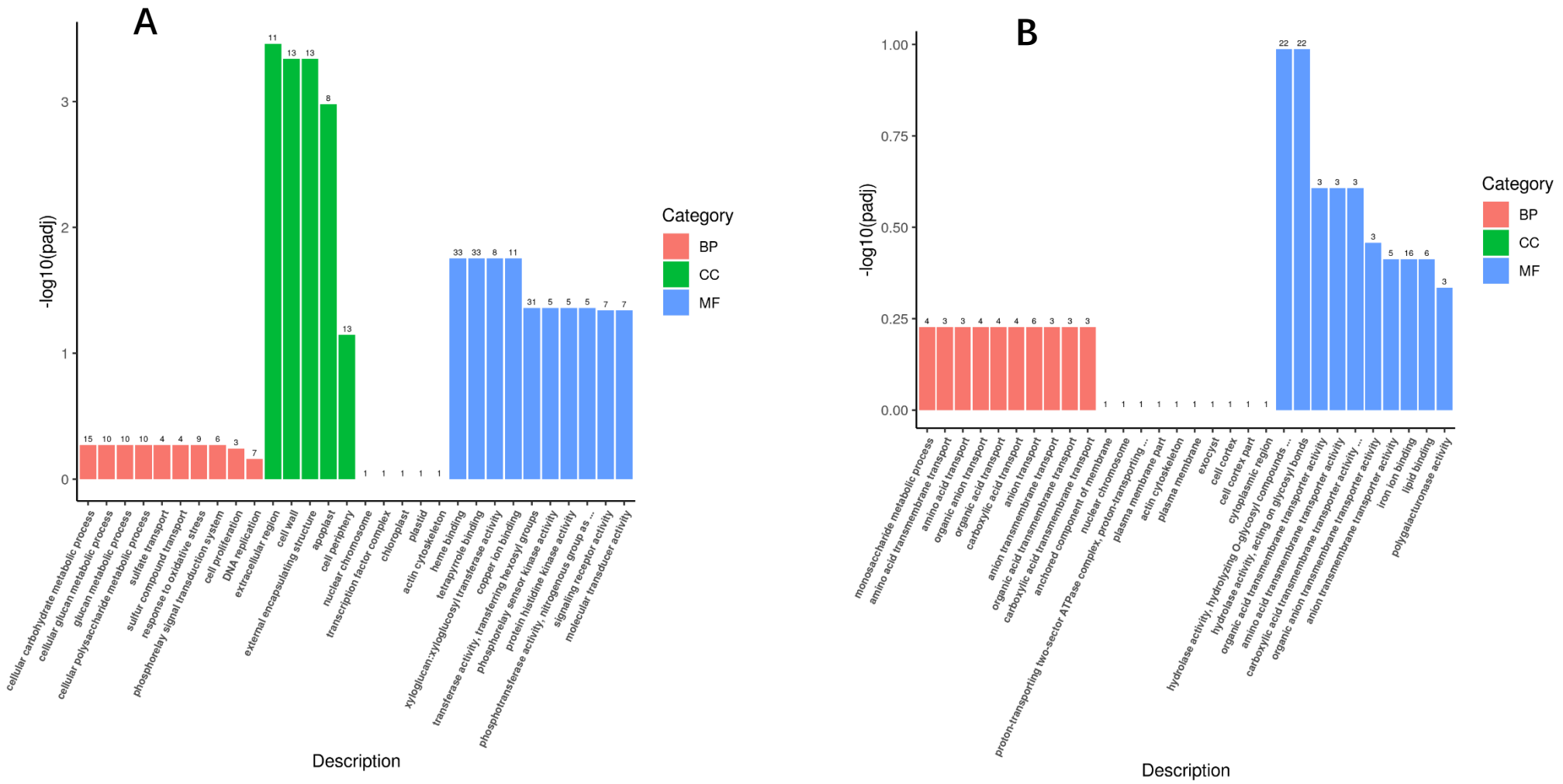


Figure S2: Go terms LWvsNW. A) Go terms for upregulated genes B) Go terms for downregulated genes

BP=Biological process CC=Cellular component and MF=Molecular function

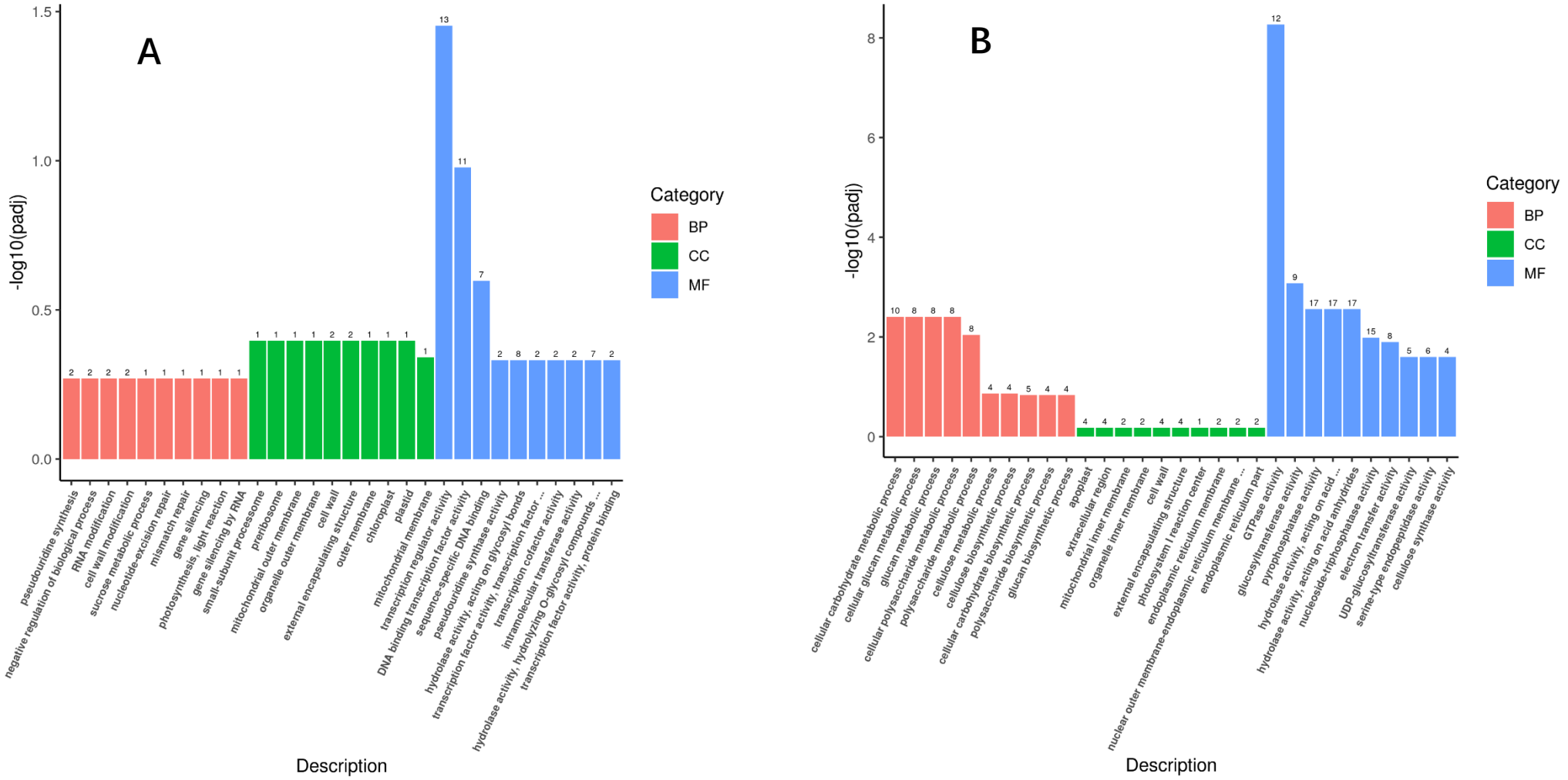


Figure S3: Go terms UWvsLW. A) Go terms for upregulated genes B) Go terms for downregulated genes

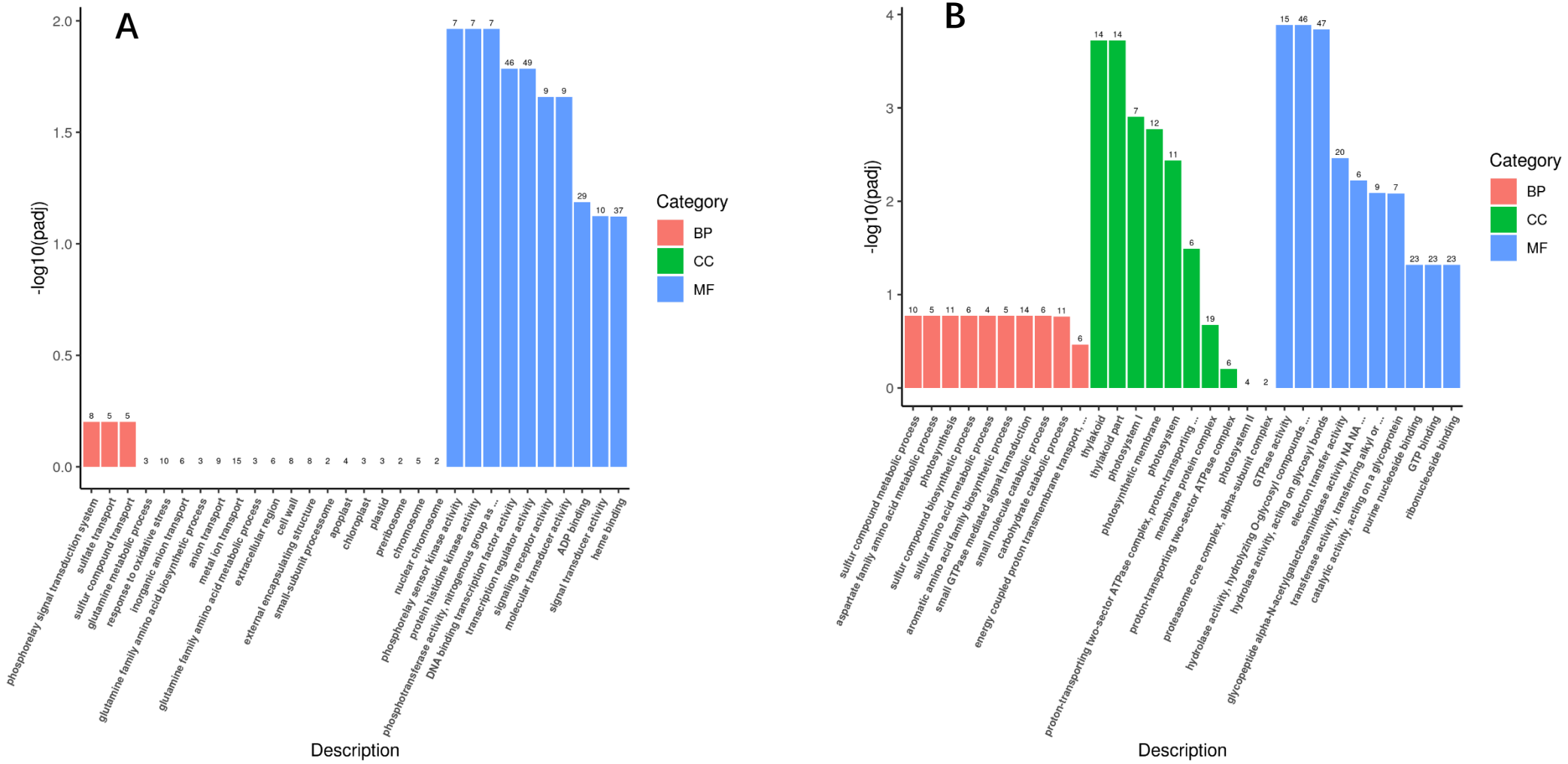
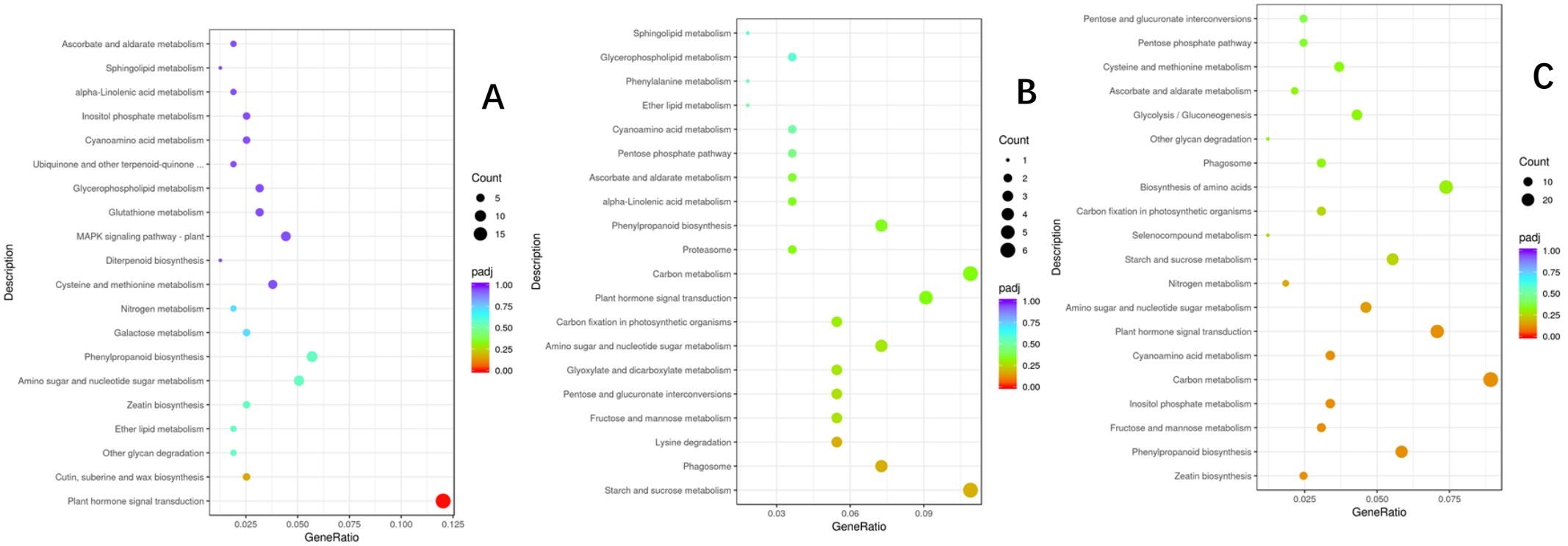


Figure S4: Go terms UWvsNW. A) Go terms for upregulated genes B) Go terms for down regulated genes



Figurer S5: KEGG pathway enrichment analysis a) LWvsNW b) UWvsLW c) UWvsNW

Table S4: Expression of gene related to sugar synthesis, transport and metabolism during bending stress in *N. cadamba*

***N.cadamba* gene_id**	**NW1**	**NW2**	**NW3**	**LW1**	**LW2**	**LW3**	**UW1**	**UW2**	**UW3**	**Associated gene**
evm.TU.Contig96.44	19.08	10.14	25.94	31.06	25.20	46.43	41.97	18.10	35.28	Thermospermine synthase
evm.TU.Contig421.510	27.25	50.96	72.86	39.74	14.35	64.77	111.01	79.38	71.19	Beta-glucosidase 1
evm.TU.Contig341.557	6.73	8.53	9.35	8.57	5.42	8.26	14.43	13.81	20.35	Beta-glucosidase 11
evm.TU.Contig421.509	16.11	12.76	15.68	24.40	35.84	21.71	26.78	27.37	23.45	Beta-glucosidase 11
evm.TU.Contig421.511	18.76	39.28	53.86	35.59	9.83	35.88	68.07	56.76	51.30	Beta-glucosidase 11
evm.TU.Contig66.81	62.13	51.50	54.82	47.61	58.10	38.76	45.55	45.98	39.62	Beta-glucosidase 12
evm.TU.Contig184.901	114.13	79.08	88.94	404.67	90.64	194.79	216.18	183.28	275.67	Beta-glucosidase 17
evm.TU.Contig81.360	163.86	155.16	138.82	104.54	134.69	203.77	96.34	119.86	131.61	Chorismate synthase 1, chloroplastic
evm.TU.Contig256.101	304.37	413.25	300.87	265.52	264.82	297.48	217.66	254.60	182.62	3-phosphoshikimate 1-carboxyvinyltransferase
evm.TU.Contig797.212	85.70	83.19	71.86	63.50	70.95	75.56	58.74	62.83	56.70	P23981.1 3-phosphoshikimate 1-carboxyvinyltransferase 1
evm.TU.Contig14.86	188.79	174.62	151.67	111.02	115.70	150.98	115.01	83.96	86.45	Probable galacturonosyltransferase-like 1
novel.906	249.14	257.63	220.90	155.75	217.35	263.07	171.00	173.23	188.58	Probable galacturonosyltransferase 12
evm.TU.Contig421.306	20.36	24.16	27.35	18.19	17.53	45.09	42.97	27.17	40.72	Probable galacturonosyltransferase 6
evm.TU.Contig3.73	218.47	226.21	210.02	95.41	101.08	169.32	96.70	62.25	133.40	UDP-glucuronatexylan alpha-glucuronosyltransferase 1
evm.TU.Contig555.387	127.24	165.92	127.64	128.74	98.02	118.93	122.71	70.47	86.35	UDP-glucuronatexylan alpha-glucuronosyltransferase 2
evm.TU.Contig16.459	156.21	147.90	124.66	110.77	95.91	115.58	100.40	68.95	76.55	Probable polygalacturonase
evm.TU.Contig477.134	51.80	66.49	87.05	23.98	17.70	47.08	18.55	16.06	37.87	Probable polygalacturonase
evm.TU.Contig600.201	71.30	78.69	61.16	58.78	45.65	84.93	54.62	38.70	45.06	Probable polygalacturonase
evm.TU.Contig22.204	7.77	9.62	8.33	10.47	13.37	12.27	15.65	13.86	14.56	UDP-glucose iridoid glucosyltransferase

N.cadamba gene_id	NW1	NW2	NW3	LW1	LW2	LW3	UW1	UW2	UW3	Associated gene
evm.TU.Contig477.772	32.54	24.96	20.14	20.44	32.93	7.50	12.21	23.08	12.21	Probable xyloglucan endotransglucosylase/hydrolase protein 10
evm.TU.Contig63.448	69.68	31.26	42.70	36.65	66.12	13.65	18.44	27.36	11.83	Probable xyloglucan endotransglucosylase/hydrolase protein 32
evm.TU.Contig138.26	99.74	114.20	77.93	133.98	236.46	179.85	99.79	148.06	113.20	Xyloglucan endotransglucosylase/hydrolase protein 9
evm.TU.Contig12.412	78.13	134.28	144.50	38.13	37.32	70.29	26.64	23.63	56.05	Anti-sigma-I factor RsgI6
evm.TU.Contig131.49	31.49	29.67	29.53	22.43	29.67	26.37	20.12	20.94	20.78	Phosphoserine phosphatase
evm.TU.Contig14.221	356.96	306.10	232.70	217.38	238.55	334.66	175.03	179.91	204.26	Endoglucanase 10
evm.TU.Contig16.723	19.58	25.95	69.96	22.01	12.21	17.54	14.37	12.42	19.91	Inactive beta-amylase 9
evm.TU.Contig16.766	24.53	29.50	22.51	26.27	27.29	184.07	39.05	28.90	150.47	Glutamine synthetase leaf isozyme, chloroplastic
evm.TU.Contig184.275	26.39	27.22	31.43	28.48	36.67	16.42	21.52	21.50	12.82	Spermidine synthase
evm.TU.Contig184.626	5.53	9.88	13.78	13.52	10.78	22.77	17.74	15.00	27.37	UDP-glycosyltransferase 73E1
evm.TU.Contig21.419	419.31	395.45	418.18	353.72	441.57	364.80	308.65	328.10	348.26	Glutamine synthetase nodule isozyme
evm.TU.Contig214.15	77.87	66.04	65.57	54.72	85.90	47.23	48.27	56.66	33.40	Serine hydroxymethyltransferase 4
evm.TU.Contig245.66	39.23	32.42	20.06	40.08	42.96	37.80	53.91	57.88	59.70	Beta-hexosaminidase 3
evm.TU.Contig33.24	10.23	11.31	6.09	25.30	63.64	13.32	24.77	20.28	13.24	Beta-galactosidase 10
evm.TU.Contig33.52	59.16	61.04	54.60	52.84	63.58	44.26	40.12	49.26	32.09	Fructose-bisphosphate aldolase 3, chloroplastic
evm.TU.Contig331.24	53.50	44.82	28.33	33.63	84.21	16.32	13.36	34.66	18.42	Endoglucanase 8
evm.TU.Contig341.556	14.76	14.42	19.18	15.72	9.06	13.95	23.64	25.99	42.95	Cyanidin 3-O-glucoside 5-O-glucosyltransferase (acyl-glucose)
evm.TU.Contig341.628	200.50	180.48	142.89	178.52	364.42	54.07	148.43	93.90	53.54	Probable beta-D-xylosidase 2
evm.TU.Contig387.25	886.65	570.40	602.37	505.27	600.95	688.63	231.31	350.00	324.86	Serine hydroxymethyltransferase 4
evm.TU.Contig387.26	1661.42	1530.26	1395.51	902.05	1153.84	1611.05	639.64	737.83	958.06	Serine hydroxymethyltransferase 4
evm.TU.Contig39.23_evm.TU.Contig39.24	50.37	42.10	41.87	98.86	264.26	21.56	58.07	61.86	17.76	Lysosomal beta glucosidase

N.cadamba gene_id	NW1	NW2	NW3	LW1	LW2	LW3	UW1	UW2	UW3	Associated gene
evm.TU.Contig394.291	58.76	58.41	40.93	50.83	141.04	20.73	22.09	46.98	28.83	Beta-galactosidase 3
evm.TU.Contig401.2	15.85	17.04	13.30	20.58	27.42	26.88	22.17	28.92	34.03	Beta-hexosaminidase 3
evm.TU.Contig447.325	62.16	64.77	57.94	52.11	60.67	54.30	43.57	52.29	43.06	Pyruvate kinase isozyme A
evm.TU.Contig462.308	148.62	220.12	249.38	66.23	58.36	155.00	44.62	34.72	99.85	Mannan endo-1,4-beta-mannosidase 6
evm.TU.Contig471.211	10.58	10.33	11.87	14.77	26.38	12.16	11.65	12.12	13.83	Plastidial pyruvate kinase 2
evm.TU.Contig471.249	49.67	43.62	41.81	37.88	38.29	41.55	35.01	30.07	34.99	Spermine synthase
evm.TU.Contig477.309	19.03	18.89	19.14	21.16	22.43	18.51	26.28	23.28	23.57	Probable galacturonosyltransferase 3
evm.TU.Contig477.391	46.24	41.12	29.93	20.91	18.27	22.07	31.41	32.10	42.10	Probable endo-1,4-beta-xylanase C
evm.TU.Contig480.237	83.89	58.48	75.50	88.16	251.73	68.15	52.19	69.79	57.86	Probable glucan endo-1,3-beta-glucosidase A6
evm.TU.Contig481.85	96.12	107.45	89.11	117.57	169.72	181.15	123.32	156.85	117.83	Fructose-bisphosphate aldolase 3
evm.TU.Contig555.158	29.67	28.32	26.92	26.99	35.95	21.03	23.26	20.50	20.97	Hexokinase-2
evm.TU.Contig585.15	716.17	593.11	521.76	562.16	734.40	365.20	363.25	416.42	317.12	Fructokinase-2
evm.TU.Contig63.482	26.94	27.79	24.64	25.13	29.15	18.35	20.66	19.57	18.92	Isocitrate dehydrogenase [NAD] catalytic subunit 5, mitochondrial
evm.TU.Contig66.167	6.06	7.33	5.99	7.14	8.63	9.99	8.00	9.65	9.00	Isocitrate dehydrogenase [NADP], chloroplastic/mitochondrial
evm.TU.Contig66.950	94.29	95.85	80.35	78.21	49.88	51.75	68.22	28.56	37.66	Serine hydroxymethyltransferase, mitochondrial
evm.TU.Contig69.10	33.09	27.10	47.80	31.42	27.19	10.18	22.37	15.65	11.08	Beta-amylase 1
evm.TU.Contig69.9	23.70	19.47	28.30	22.55	19.09	8.03	11.66	9.29	8.03	Beta-amylase 1
evm.TU.Contig7.272	420.50	424.99	347.56	401.67	598.54	478.86	300.32	391.25	314.98	Fructose-bisphosphate aldolase 6
evm.TU.Contig906.31	158.40	184.51	124.81	113.46	204.42	124.29	76.05	121.51	52.73	Fructose-bisphosphate aldolase 6
evm.TU.Contig985.20	112.63	142.13	145.06	50.69	57.24	81.66	43.95	26.92	80.73	Beta-L-arabinofuranosidase
novel.32	221.78	251.07	356.82	212.09	76.90	180.12	213.96	141.33	101.89	UDP-glucoronosyl and UDP-glucosyl transferase
novel.36	12.83	10.96	7.11	14.11	24.38	14.69	12.48	26.50	26.23	UDP-glycosyltransferase 74E2

Table S5: Expression of cell wall esterases and signalling molecules expressed during bending stress in *N. cadamba*

Gene id	NW1	NW2	NW3	LW1	LW2	LW3	UW1	UW2	UW3	Gene name	GH Family	Gene description
evm.TU.Contig138.26	99.74	114.20	77.93	133.98	236.46	179.85	99.79	148.06	113.20	XTH9	GH16	Xyloglucan endotransglucosylase/hydrolase protein 9
evm.TU.Contig14.119	5.86	7.41	5.17	11.22	18.74	8.84	8.57	12.57	8.97	NA	GH17	Glucan endo-1,3-beta-glucosidase 7
evm.TU.Contig14.221	356.96	306.10	232.70	217.38	238.55	334.66	175.03	179.91	204.26	At1g75680	GH9	Endoglucanase 10
evm.TU.Contig16.459	156.21	147.90	124.66	110.77	95.91	115.58	100.40	68.95	76.55	NA	GH28	Probable polygalacturonase
evm.TU.Contig16.723	19.58	25.95	69.96	22.01	12.21	17.54	14.37	12.42	19.91	BAM1	GH14	Inactive beta-amylase 9
evm.TU.Contig184.901	114.13	79.08	88.94	404.67	90.64	194.79	216.18	183.28	275.67	AA5GT	GH1	Beta-glucosidase 17
evm.TU.Contig207.323	27.42	25.66	8.33	37.09	51.52	36.14	18.18	43.28	29.61	LAC2	Laccase	Laccase-2
evm.TU.Contig245.66	39.23	32.42	20.06	40.08	42.96	37.80	53.91	57.88	59.70	HEXO3	GH20	Beta-hexosaminidase 3
evm.TU.Contig278.41	50.01	95.59	79.05	43.15	33.68	38.72	41.21	41.22	26.33	BGAL9	GH35	Beta-galactosidase 9
evm.TU.Contig296.267	110.00	116.91	66.23	139.91	169.02	141.50	94.04	193.19	90.00	LAC2	Laccase	Laccase-2
evm.TU.Contig296.367	78.79	226.99	154.59	121.32	555.98	352.42	110.06	509.78	138.95	LAC17	Laccase	Laccase-17
evm.TU.Contig33.24	10.23	11.31	6.09	25.30	63.64	13.32	24.77	20.28	13.24	BGAL10	GH35	Beta-galactosidase 10
evm.TU.Contig331.24	53.50	44.82	28.33	33.63	84.21	16.32	13.36	34.66	18.42	CEL1	GH9	Endoglucanase 8

evm.TU.Contig341.556	14.76	14.42	19.18	15.72	9.06	13.95	23.64	25.99	42.95	AA5GT	GH1	Cyanidin 3-O-glucoside 5-O-glucosyltransferase (acyl-glucose)
evm.TU.Contig341.557	6.73	8.53	9.35	8.57	5.42	8.26	14.43	13.81	20.35	BGLU11	GH1	Beta-glucosidase 11
evm.TU.Contig394.291	58.76	58.41	40.93	50.83	141.04	20.73	22.09	46.98	28.83	BGAL3	GH35	Beta-galactosidase 3
evm.TU.Contig401.2	15.85	17.04	13.30	20.58	27.42	26.88	22.17	28.92	34.03	HEXO3	GH20	Beta-hexosaminidase 3
evm.TU.Contig421.509	16.11	12.76	15.68	24.40	35.84	21.71	26.78	27.37	23.45	BGLU11	GH1	Beta-glucosidase 11
evm.TU.Contig421.510	27.25	50.96	72.86	39.74	14.35	64.77	111.01	79.38	71.19	BGLU1	GH1	Beta-glucosidase 1
evm.TU.Contig421.511	18.76	39.28	53.86	35.59	9.83	35.88	68.07	56.76	51.30	BGLU11	GH1	Beta-glucosidase 11
evm.TU.Contig462.160	491.41	378.37	382.31	361.90	370.84	368.85	352.37	266.51	299.55	LAC10	Laccase	Laccase-10
evm.TU.Contig462.308	148.62	220.12	249.38	66.23	58.36	155.00	44.62	34.72	99.85	MAN6	GH5	Mannan endo-1,4-beta-mannosidase 6
evm.TU.Contig462.71	238.29	130.22	124.27	140.89	196.41	97.88	117.58	79.71	59.58	LAC17	Laccase	Laccase-17
evm.TU.Contig464.29	14.03	15.43	9.21	12.83	16.49	70.68	13.47	18.33	97.86	At5g56590	GH28	Aspartic proteinase-like protein 1
evm.TU.Contig477.134	51.80	66.49	87.05	23.98	17.70	47.08	18.55	16.06	37.87	NA	GH10	Probable polygalacturonase
evm.TU.Contig477.391	46.24	41.12	29.93	20.91	18.27	22.07	31.41	32.10	42.10	xlnC	GH16	A1CHQ0.1 Probable endo-1,4-beta-xylanase C
evm.TU.Contig477.772	32.54	24.96	20.14	20.44	32.93	7.50	12.21	23.08	12.21	XTH10	GH17	Probable xyloglucan endotransglucosylase/hydrolase protein 10
evm.TU.Contig480.236	191.19	120.65	184.74	171.85	509.68	124.67	117.98	128.80	81.50	At1g11820	GH17	Glucan endo-1,3-beta-glucosidase 1
evm.TU.Contig480.237	83.89	58.48	75.50	88.16	251.73	68.15	52.19	69.79	57.86	A6	GH28	Probable glucan endo-1,3-beta-glucosidase A6
evm.TU.Contig600.201	71.30	78.69	61.16	58.78	45.65	84.93	54.62	38.70	45.06	NA	GH16	Probable polygalacturonase
evm.TU.Contig63.448	69.68	31.26	42.70	36.65	66.12	13.65	18.44	27.36	11.83	XTH32	GH1	Probable xyloglucan endotransglucosylase/hydrolase protein 32
evm.TU.Contig66.1552	39.89	38.47	35.72	34.23	32.10	29.61	25.43	22.49	19.52	CXE11	GH14	Probable carboxylesterase 11
evm.TU.Contig66.1553	33.43	32.76	25.92	26.32	26.66	27.46	20.50	19.71	19.85	CXE11	GH14	Probable carboxylesterase 11

evm.TU.Contig66.81	62.13	51.50	54.82	47.61	58.10	38.76	45.55	45.98	39.62	BGLU12	Laccase	Beta-glucosidase 12
evm.TU.Contig69.10	33.09	27.10	47.80	31.42	27.19	10.18	22.37	15.65	11.08	NA	GH127	Beta-amylase 1; chloroplastic
evm.TU.Contig69.9	23.70	19.47	28.30	22.55	19.09	8.03	11.66	9.29	8.03	BAM1		Beta-amylase 1; chloroplastic
evm.TU.Contig96.209	258.15	394.02	307.81	252.84	209.50	280.12	220.29	173.91	186.54	LAC22		Laccase-22
evm.TU.Contig985.20	112.63	142.13	145.06	50.69	57.24	81.66	43.95	26.92	80.73	NA	GH127	Beta-L-arabinofuranosidase,