Supplemental Information

Long-term strain improvements accumulate mutations in regulatory elements responsible for hyper-production of cellulolytic enzymes

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Table S1. Statistics of genome sequencing and assembly of *P. decumbens* JU-A10-T.

	JU-A10-T
454 single-end reads	1,096,639
454 reads total length (bp)	393,651,182
454 reads average length (bp)	359
Solexa mate-paired reads	9,031,102
Solexa paired-end reads	29,877,448
Assembly size (Mb)	30.68
Contig number	482
Scaffods number	24
Contig N50 (bp)	154,880
Scaffold N50 (bp)	2,808,009

Table S2. Statistics of predicted gene models in *P. decumbens* JU-A10-T.

	JU-A10-T
Nuclear genome	
Size of assembled genome (Mb)	30.7
GC content of assembled genome (%)	50.5
All protein-coding genes	10,464
Protein-coding genes (≥ 60 aa)	10,110
GC content of protein-coding region (%)	54.4
Average gene length (bp)	1,556
Average number of introns per gene	1.92
Genes with intron	7,986
Average intron size (bp)	115
Average exon size (bp)	456
Number of tRNA genes	169
Mitochondrial genome	
Size (bp)	26,536
GC content (%)	26.7
Protein-coding genes	9
Number of tRNA genes	29
454 transcriptome sequencing data support	
Coverage = 100%, Identity = 100%	3,913 (37.4%)
Coverage ≥ 95%, Identity ≥ 95%	4,719 (45.1%)
Coverage ≥ 70%, Identity ≥ 90%	5,759 (47.0%)
Intron-exon boundaries supported	13,887 (68.9%)
Function annotation	
NR (E-value ≤ 1e-5)	8,569
Swiss-Prot (E-value ≤ 1e-5)	6,318
KEGG (E-value ≤ 1e-5, Rank = 30)	3,902
String (E-value ≤ 1e-5, Rank = 5)	5,131

Table S3. Transcription factors with amino acid sequence variations between *P. decumbens* 114-2 and JU-A10-T.

Protein ID		**FTFD family name**	**Amino acid position**[a]	**Mutation**	**Affected domain**[b]
114-2	**JU-A10-T**				
Proteins with frameshift mutations					
PDE_03168	PDT_03340	C2H2 zinc finger	402	frameshift	
PDE_08589	PDT_08869	Zn2Cys6	317	frameshift	Fungal_trans
Proteins with nonsense mutations					
PDE_05870	PDT_06103	Zn2Cys6	263	W->*	
Proteins with amino acid substitutions and indels					
PDE_00052	PDT_00054	Zn2Cys6	162	G->V	
			870	K->E	
PDE_00115	PDT_00117	Tubby transcription factors	98	T->A	Tub_2
PDE_00222	PDT_00226	Zinc finger, CCHC-type	587	P->S	
PDE_00454	PDT_00468	C2H2 zinc finger;Homeobox;Homeodomain-like	22	I->V	
PDE_00496	PDT_00514	Zn2Cys6	96	K->R	
PDE_00521	PDT_00540	Zn2Cys6	242	P->S	
PDE_00531	PDT_00551	Zn2Cys6	242	P->S	
			367	N->D	
			504	S->C	
			656	F->I	
			769	S->L	
			820	N->D	
PDE_00548	PDT_00568	Zn2Cys6	586	I->L	Zip
			694	Q->H	
PDE_00588	PDT_00609	Zinc finger, NF-X1-type	798	P->S	
PDE_00841	PDT_00875	Winged helix repressor DNA-binding	315	N->S	AAA_16
PDE_00844	PDT_00878	Winged helix repressor DNA-binding	828	G->E	
PDE_00895	PDT_00931	C2H2 zinc finger	89	A->V	
			182	T->A	
			436	T->S	
PDE_00959	PDT_00998	Zn2Cys6	677	A->-	Fungal_trans
PDE_01231	PDT_01289	Zn2Cys6	182	P->S	
PDE_01258	PDT_01323	Zn2Cys6	91	T->S	Zn_clus
			111	V->A	
			121	P->S	
			155	I->L	

			323	P->L	Fungal_trans
			464	C->S	
			477	T->S	
			488	A->T	
			518	A->T	
			662	L->P	
PDE_01373	PDT_01450	Zn2Cys6	73	Q->R	
PDE_01570	PDT_01651	Zn2Cys6	438	E->K	
PDE_01749	PDT_01833	Zn2Cys6	686	D->N	
			731	N->S	
			732	Q->K	
			733	W->Q	
PDE_01792	PDT_01878	Zn2Cys6	611	P->H	
PDE_01813	PDT_01901	Myb;Homeodomain-like	575	S->P	
			581	N->S	
			642	L->P	
PDE_01919	PDT_02007	MADS-box	186	D->N	
PDE_01962	PDT_02050	Transcription factor jumonji	193	D->E	Cupin_8
PDE_02018	PDT_02107	C2H2 zinc finger;Zinc finger, Rad18-type putative	369	I->V	FYVE
PDE_02029	PDT_02120	GATA type zinc finger	105	N->-	
			343	R->G	
PDE_02064	PDT_02158	bZIP	80	F->I	ATG16
PDE_02646	PDT_02782	Zn2Cys6	73	K->Q	
			114	R->H	
			138	I->V	
			170	T->I	
			189	V->I	
			219	G->E	Fungal_trans
			329	G->S	Fungal_trans
			387	N->S	Fungal_trans
			524	K->R	
PDE_02772	PDT_02918	Zn2Cys6	615	Q->-	Peptidase_S49_N
			627-636	QQQQQQQQQQ->-	Peptidase_S49_N
PDE_02773	PDT_02919	Zn2Cys6	6	G->D	
PDE_02807	PDT_02955	Zn2Cys6	266	A->T	
PDE_02813	PDT_02961	C2H2 zinc finger;Zinc finger, BED-type predicted	319	M->T	
PDE_02852	PDT_03003	C2H2 zinc finger;Zn2Cys6	296	G->S	Fungal_trans
PDE_03008	PDT_03177	Myb;Homeodomain-like	172	Q->E	

			260	H->Y	
PDE_03129	PDT_03300	Zn2Cys6	99	+QQ	
PDE_03264	PDT_03443	bZIP	396	A->S	PAP1
PDE_03298	PDT_03479	Zn2Cys6	663	+QQQQ	Tim54
PDE_03324	PDT_03505	C2H2 zinc finger	400	T->I	
PDE_03334	PDT_03519	GATA type zinc finger	240	T->A	
PDE_03473[c]	PDT_03670	Centromere protein B, DNA-binding region;Homeodomain-like	424	H->Q	
			425	F->L	
			682	K->R	
PDE_03610	PDT_03815	Zn2Cys6	159	+N	
PDE_03741	PDT_03954	Zn2Cys6	50	V->A	
			61	V->A	
			77	G->D	
			78	A->T	
			315	S->L	Fungal_trans
			387	Q->K	Fungal_trans
			412	L->M	Fungal_trans
			443	E->D	
PDE_03754	PDT_03968	p53-like transcription factor	133	E->K	NDT80_PhoG
PDE_03970	PDT_04199	Homeobox;Homeodomain-like	107	T->A	
PDE_04009	PDT_04212	Zn2Cys6	240	F->L	
PDE_04056	PDT_04259	ssDNA-binding transcriptional regulator	32	T->K	PC4
PDE_04481	PDT_04680	Zn2Cys6	260	N->D	
PDE_04501	PDT_04701	bZIP	193	S->N	
PDE_04690	PDT_04908	Forkhead;Winged helix repressor DNA-binding	550	K->E	
			893	H->N	
			1002	P->S	
			1028	S->P	
			1108	M->I	
			1156	+Q	
PDE_04716	PDT_04939	CCR4-Not complex component, Not1	20	K->R	
			2184	T->A	Not1
PDE_04733	PDT_04958	Zn2Cys6	161	S->P	
			166	R->G	
			417	G->R	
PDE_04760	PDT_04986	Winged helix repressor	15	A->T	

		DNA-binding			
PDE_04763	PDT_04989	AT-rich interaction region	22	T->A	
			61	P->S	
			231	H->Q	
			298-299	QQ->-	
			419-420	HH->QQ	
			425	+QQQQP	
			444	+HQQQQ	
			475	S->P	
			514	P->L	
PDE_04782	PDT_05008	C2H2 zinc finger;Zn2Cys6	72	V->I	Zn_clus
			145	Q->R	
			150	D->N	
			193	T->A	
			229	N->S	
			234	F->L	
			243	V->A	
			306	T->I	
			460	N->D	
			525	T->A	
PDE_04896	PDT_05126	C2H2 zinc finger	691	G->V	
PDE_04903	PDT_05133	bZIP	9	I->N	
PDE_04931	PDT_05162	Homeobox;Homeodomain-like	544	I->K	
PDE_04957	PDT_05188	SGT1	318	S->G	SGT1
PDE_05021	PDT_05252	Zn2Cys6	364	L->P	Fungal_trans
PDE_05030	PDT_05261	Zinc finger, CCHC-type	548	P->S	
PDE_05166	PDT_05398	Zn2Cys6	798	E->D	
PDE_05378	PDT_05615	Zn2Cys6	35	+QQ	
			743	T->A	
PDE_05545	PDT_05779	bZIP	452	S->P	
PDE_05681	PDT_05916	Zn2Cys6	198	V->M	Fungal_trans
PDE_05810	PDT_06044	Zinc finger, CCHC-type	82	+AAEI	
PDE_05919	PDT_06150	Zn2Cys6	30	S->F	
PDE_05963	PDT_06195	Zn2Cys6	70	L->S	Zn_clus
			260	F->L	Fungal_trans
			266	I->T	Fungal_trans
			448	S->T	Fungal_trans
			511	S->P	
			795	L->P	
PDE_06057	PDT_06284	Zn2Cys6	142	E->G	
PDE_06088	PDT_06317	Zn2Cys6	420	R->C	Fungal_trans
PDE_06158	PDT_06390	Transcription factor	624	V->I	Cupin_8

		jumonji			
PDE_06213	PDT_06446	Zn2Cys6	434	M->T	
PDE_06331	PDT_06561	Winged helix repressor DNA-binding	490	Q->H	
PDE_06342	PDT_06572	Zn2Cys6	46	V->I	Zn_clus
PDE_06349	PDT_06579	Zinc finger, NF-X1-type	39	R->G	
			315	T->I	
			1213	Q->R	
PDE_06383	PDT_06614	Heteromeric CCAAT factors	231	E->K	Hus1
PDE_06407	PDT_06640	Zinc finger, DHHC-type	299	V->A	
			367	+Q	
PDE_06594	PDT_06830	Zinc finger, CCHC-type	61-88	VNAPWRNMDNPNGTAPNGWTTMYNNIIK->-	
			98	A->P	
			107	N->D	
			123	Q->K	
			124-132	SQFQSKPYG->-	
			141	V->A	
			151	G->E	
			153	Q->E	
			158	Y->-	
			161	T->A	
			169	S->D	
			172	D->E	
			174	Y->H	
			192	G->E	
			195	Q->H	
			202	V->F	
			215	R->G	
			219	D->N	
			220	A->T	
			223	A->P	
			225	K->T	
			226-227	GH->-	
			230	D->E	
			231	P->T	
			237	S->P	
			240	D->N	
			246	H->Y	
			257	A->T	
PDE_06660	PDT_06904	Zn2Cys6	607	Y->H	Fungal_trans_

					2
PDE_06698	PDT_06942	HMG	117	T->M	
			421	R->Q	
			425	D->N	
			614	T->I	
PDE_06695	PDT_06939	C2H2 zinc finger	55	L->M	
PDE_06696	PDT_06940	C2H2 zinc finger	21	H->L	zf-C2H2_jaz
			143	P->S	zf-C2H2
PDE_06747	PDT_06992	C2H2 zinc finger	20	V->I	
			51	L->S	
			137	L->W	
			424	T->A	
PDE_06784	PDT_07029	Zn2Cys6	83	N->S	
PDE_06843	PDT_07090	Zn2Cys6	39	V->A	
			172-173	QQ->-	Mitofilin
			190	H->L	Mitofilin
			422	S->N	
PDE_06846	PDT_07093	Zn2Cys6	124	T->I	Fungal_trans
PDE_06878	PDT_07123	Zn2Cys6	285	S->-	Fungal_trans
PDE_06888	PDT_07134	Zn2Cys6	543	Q->L	
PDE_06913	PDT_07161	Zn2Cys6	254	G->D	Fungal_trans
PDE_06927	PDT_07177	Myb;Homeodomain-like	511	A->T	Myb_Cef
			664	D->G	Myb_Cef
PDE_06945	PDT_07195	Winged helix repressor DNA-binding	934	S->P	
PDE_06963	PDT_07215	Winged helix repressor DNA-binding	766	P->S	Cullin
			861-868	AAAAAAAE->-	
			875	A->V	
PDE_07029	PDT_07284	Zn2Cys6	323	G->D	Fungal_trans_2
			357	S->T	Fungal_trans_2
			430	P->L	
PDE_07094	PDT_07349	C2H2 zinc finger	256	E->K	
PDE_07172	PDT_07427	Zn2Cys6	39	S->R	Zn_clus
PDE_07215	PDT_07471	Zn2Cys6	87	+AQ	
			308	V->F	Fungal_trans_2
PDE_07240	PDT_07496	Zn2Cys6	323	Y->D	Fungal_trans
			415	A->V	Fungal_trans
			587	R->K	
			684	P->Q	

PDE_07250	PDT_07507	Zn2Cys6	5	I->T	
			12	G->S	
			279	L->P	Fungal_trans_2
			473	S->L	
			477	H->R	
PDE_07338	PDT_07597	Zn2Cys6	29	T->A	
			63	K->E	Zn_clus
PDE_07343	PDT_07602	Zn2Cys6	112	A->T	
PDE_07392	PDT_07653	bZIP	1028	S->N	
PDE_07489	PDT_07751	C2H2 zinc finger;Zn2Cys6	10	G->D	
PDE_07546	PDT_07808	Myb;Homeodomain-like	99	T->P	
			482	+Q	
PDE_07554	PDT_07816	APSES	328	V->A	
PDE_07588	PDT_07851	GATA type zinc finger	82	A->T	
PDE_07596	PDT_07859	Zn2Cys6	110	H->R	
			604	G->V	Fungal_trans_2
			620	H->L	
			674	F->L	
PDE_07712	PDT_07980	Zn2Cys6	205	A->T	
			217	S->P	
			386	P->S	
			410	R->Q	
PDE_07750	PDT_08018	Zn2Cys6	503	Q->H	
PDE_07779	PDT_08048	Winged helix repressor DNA-binding	101	A->V	
			211	P->S	B-block_TFIIIC
			731	G->D	
			804	T->I	
			1847	S->L	
PDE_07781	PDT_08050	Zinc finger, DHHC-type	50	A->V	
PDE_07788	PDT_08057	Lambda repressor-like, DNA-binding	80	S->G	
PDE_07942	PDT_08210	Zn2Cys6	120	S->P	
PDE_08048	PDT_08312	Zn2Cys6	59	Q->L	
			623	C->Y	
PDE_08084	PDT_08349	Zn2Cys6	129	A->T	
			404	A->P	Fungal_trans_2
			469	H->Q	Fungal_trans_2

PDE_08088	PDT_08353	APSES	189	P->S	
			190	T->A	
			237	D->N	
PDE_08282	PDT_08550	C2H2 zinc finger	217	N->D	
PDE_08325	PDT_08594	Zinc finger, CCHC-type	504	S->P	
PDE_08568	PDT_08848	Zn2Cys6	274	V->L	Fungal_trans
PDE_08867	PDT_09158	Zn2Cys6	398	S->P	
PDE_08881	PDT_09174	Zinc finger, MIZ-type	106	N->H	
			162	E->D	
			298	S->F	
			479-481	EDE->-	
PDE_08894	PDT_09187	Zinc finger, DHHC-type	1338	A->S	
PDE_08983	PDT_09276	Zn2Cys6	617	T->A	
PDE_09026	PDT_09320	Zn2Cys6	723	N->T	
PDE_09032	PDT_09326	C2H2 zinc finger	4	T->A	
PDE_09037	PDT_09331	Zn2Cys6	370	G->T	Fungal_trans_2
PDE_09076	PDT_09375	Transcription factor jumonji	198	A->V	
PDE_09179	PDT_09479	Zn2Cys6	224	S->L	
PDE_09227	PDT_09528	Zn2Cys6	208	V->I	Fungal_trans
			451	H->D	
PDE_09243	PDT_09544	Zn2Cys6	142	D->N	AflR
PDE_09254	PDT_09557	Myb;Winged helix repressor DNA-binding;Homeodomain-like	24	A->V	
			265	A->T	
			273	T->A	
PDE_09356	PDT_09666	C2H2 zinc finger	132	P->L	
PDE_09385+PDE_09386[d]	PDT_09695	C2H2 zinc finger	243	G->A	
			408	A->T	Fungal_trans
			421	C->S	Fungal_trans
			592	T->N	Fungal_trans
			788	V->A	
PDE_09423	PDT_09734	C2H2 zinc finger;Zn2Cys6	122	D->-	
			251	D->E	Fungal_trans
			264	D->R	Fungal_trans
			360	P->A	
			365	S->P	
PDE_09437	PDT_09749	Zn2Cys6	151	T->S	

PDE_09498	PDT_09809	Transcription factor jumonji;AT-rich interaction region	595	V->I	
PDE_09536	PDT_09848	Zn2Cys6	11	Q->R	
			200	Y->N	
			517	Y->D	
PDE_09868	PDT_10182	Zn2Cys6	147	G->D	
			152	S->G	
PDE_09961	PDT_10277	Winged helix repressor DNA-binding	286	V->A	
PDE_09981[e]	PDT_10296	Myb;Homeodomain-like	324	+RD	
			1591	A->P	
			1949	I->M	
PDE_09985	PDT_10300	Zn2Cys6	285	V->L	Fungal_trans

[a] Amino acid positions refer to those in 114-2 proteins unless specially remarked.

[b] Affected domains are identified according to the envelope domain boundaries in Pfam prediction result.

[c] Amino acid position refers to that in JU-A10-T protein PDT_03670, and the mutation event means sequence change from JU-A10-T to 114-2.

[d] Amino acid position refers to that in JU-A10-T protein PDT_09695, and the mutation event means sequence change from JU-A10-T to 114-2.

[e] Amino acid position refers to that in JU-A10-T protein PDT_10296, and the mutation event means sequence change from JU-A10-T to 114-2.

Table S4. Genes in strain-specific genomic regions of *P. decumbens* 114-2 and JU-A10-T.

Gene ID	**Scaffold location**	**From..to**	**Protein length**	**Function prediction**	**Transcription level in CW medium (tags per million)**	
					114-2	**JU-A10-T**
114-2 specific						
PDE_00379	1	1028791..1030603	120	hypothetical protein	0	-
PDE_01250	2	6062..6787	223	hypothetical protein	9.86	-
PDE_01469	2	632794..633715	38	hypothetical protein	0	-
PDE_01473	2	684114..685242	107	hypothetical protein	0	-
PDE_01474	2	701962..703633	123	hypothetical protein	0	-
PDE_01475	2	709179..709559	126	transposase	0	-
PDE_01476	2	709811..710410	26	hypothetical protein	0	-
PDE_01477	2	732767..733337	33	hypothetical protein	1.02	-
PDE_01613	2	1136846..1137994	349	mating type protein MAT1-2-1	9.18	-
PDE_03980	4	2045687..2046594	196	hypothetical protein	0	-
PDE_03981	4	2046988..2048976	605	hypothetical protein	23.12	-
PDE_03982	4	2050786..2054302	1047	hypothetical protein	289	-
PDE_03983	4	2055554..2056159	201	hypothetical protein	0	-
PDE_03984	4	2057850..2061982	1344	NACHT and ankyrin domain protein	17.68	-
PDE_03985	4	2063106..2068201	1528	reverse transcriptase	30.6	-
PDE_03986	4	2068781..2072210	1044	ankyrin domain repeat protein	148.92	-
PDE_03987	4	2073680..2075914	596	NACHT domain protein	43.86	-
PDE_03988	4	2076407..2077357	316	hypothetical protein	0	-
PDE_03989	4	2078104..2079600	498	phosphotransferase enzyme family protein	52.36	-
PDE_03990	4	2080676..2080927	83	hypothetical protein	3512.54	-
PDE_03991	4	2083135..2083432	83	hypothetical protein	792.2	-
PDE_03992	4	2083462..2084600	362	hypothetical protein	9.52	-
PDE_03993	4	2085117..2086488	441	mitochondrial chaperone BCS1	7.48	-
PDE_03994	4	2087883..2090159	758	hypothetical protein	93.16	-
PDE_03995	4	2090842..2091289	91	hypothetical protein	0	-
PDE_03996	4	2093180..2093923	176	hypothetical protein	1.7	-
PDE_03997	4	2095163..2096141	233	hypothetical protein	2.72	-
PDE_03998	4	2097444..2099152	513	hypothetical protein	265.54	-
PDE_03999	4	2101489..2102364	291	zinc-finger double-stranded RNA-binding domain	14.96	-

				protein		
PDE_04000	4	2104010..2107179	921	NACHT domain protein	100.3	-
PDE_04001	4	2107889..2108644	214	hypothetical protein	1.7	-
PDE_04002	4	2110201..2111098	105	hypothetical protein	0	-
PDE_04003	4	2111365..2114252	826	Serine/threonine-protein kinase	96.9	-
PDE_04004	4	2116512..2119351	826	NACHT and WD domain protein	8.16	-
PDE_04005	4	2120517..2123023	781	hypothetical protein	62.56	-
PDE_04443	5	225..1684	450	hypothetical protein	1.7	-
PDE_04444	5	2485..3960	491	F-box domain protein	11.22	-
PDE_04445	5	6313..7551	412	hypothetical protein	0.68	-
PDE_04446	5	10344..10886	180	hypothetical protein	0	-
PDE_05450	5	2946199..2950094	1182	NACHT and ankyrin domain protein	135.66	-
PDE_05451	5	2951382..2953918	809	SAM and PH domain protein	45.22	-
PDE_05452	5	2954326..2955044	134	hypothetical protein	16.32	-
PDE_05453	5	2958976..2961145	682	C6 sexual development transcription factor NosA	112.88	-
PDE_05454	5	2963268..2963939	223	hypothetical protein	95.2	-
PDE_05455	5	2969385..2970576	377	hypothetical protein	41.14	-
PDE_06039	6	21223..22133	220	AAA family ATPase	0.68	-
PDE_06040	6	27590..28862	320	ankyrin domain repeat protein	0	-
PDE_06041	6	30097..30344	72	hypothetical protein	0	-
PDE_06244	6	672590..682299	7	hypothetical protein	0	-
PDE_06245	6	699794..700372	192	hypothetical protein	0	-
PDE_06246	6	705668..707086	472	kinesin light chain	15.64	-
PDE_06247	6	707304..708446	380	hypothetical protein	45.9	-
PDE_06248	6	708726..709763	324	hypothetical protein	152.66	-
PDE_06249	6	713046..714543	151	hypothetical protein	0	-
PDE_06250	6	714885..715259	124	hypothetical protein	0	-
PDE_06251	6	724162..725538	282	retrotransposon protein	0	-
PDE_06252	6	726346..729399	1017	retrotransposon protein	0	-
PDE_08027	7	4206361..4207261	253	trichodiene synthase	2.04	-
PDE_08028	7	4209008..4209125	26	hypothetical protein	0	-
PDE_08029	7	4213254..4213919	162	conidiation-specific protein 6	6.12	-
PDE_08030	8	1116..1774	118	hypothetical protein	8.16	-
PDE_08031	8	2504..3342	188	hypothetical protein	0	-
PDE_08032	8	10605..13316	903	nonribosomal peptide	78.2	-

				synthetase		
PDE_08033	8	14584..15525	280	oxidoreductase	120.02	-
PDE_08034	8	16805..18294	419	GDSL-like lipase/acylhydrolase	0	-
PDE_08035	8	18859..20614	530	lactose permease	42.16	-
PDE_08036	8	22922..24539	514	β-xylosidase/α-L-arabinofuranosidase	61.54	-
PDE_08037	8	25355..28220	900	β-xylosidase	1.36	-
PDE_08038	8	29770..31109	409	exo-α-L-1,5-arabinanase	8.5	-
PDE_08039	8	31746..32465	239	acetyltransferase	10.2	-
PDE_08040	8	33214..35085	571	phosphate transporter	1.02	-
PDE_08041	8	38615..39708	229	sugar transporter	0	-
PDE_09097	8	3228527..3229577	283	hypothetical protein	0	-
PDE_09250	8	3741965..3743764	599	hypothetical protein	171.36	-
PDE_09251	8	3745033..3746309	337	UDP-GlcNAc: N-acetylglucosaminyltransferase	357.68	-
PDE_09252	8	3747715..3748054	56	hypothetical protein	0	-
JU-A10-T specific						
PDT_00001	1	2554..6099	1181	hypothetical protein	-	0.55
PDT_00387	2	561..11989	459	Myb-like DNA-binding domain protein	-	11.83
PDT_01164	3	17582..18259	225	hypothetical protein	-	1035.34
PDT_01165	3	18299..23567	1738	retrotransposon protein	-	63.81
PDT_01307	5	1972..3888	574	cytochrome P450	-	26.68
PDT_01308	5	4095..6019	558	MFS-type transporter	-	5.5
PDT_01309	5	7217..8104	295	dehydrogenase/reductase	-	1.1
PDT_01310	5	8301..9400	290	hypothetical protein	-	4.4
PDT_01311	5	10783..10986	67	hypothetical protein	-	17.88
PDT_01312	5	13527..13805	92	hypothetical protein	-	0
PDT_01313	5	19053..19214	53	hypothetical protein	-	0
PDT_01548	5	660470..661472	312	hypothetical protein	-	12.38
PDT_01549	5	663017..664096	338	alcohol dehydrogenase	-	0
PDT_01550	5	665171..666339	345	aldo-keto reductase	-	0
PDT_01551	5	667398..668552	384	aryl-alcohol dehydrogenase	-	0
PDT_01552	5	669359..670474	371	aldo-keto reductase	-	0
PDT_01553	5	733415..734580	229	hypothetical protein	-	0
PDT_01696	5	1178667..1179638	305	mating type protein MAT1-1-1	-	0

PDT_04089	7	1686022..1704576	24	hypothetical protein	-	0
PDT_04090	7	1712815..1716562	1172	NACHT domain protein	-	60.51
PDT_04091	7	1725011..1741734	32	hypothetical protein	-	0
PDT_05687	10	1779556..1783377	1175	NACHT and Ankyrin domain protein	-	91.87
PDT_05688	10	1784659..1787221	808	SAM and PH domain protein	-	56.94
PDT_05689	10	1790595..1792772	671	C6 sexual development transcription factor NosA	-	689.31
PDT_05690	10	1795282..1795908	208	hypothetical protein	-	1000.68
PDT_05691	10	1802057..1803261	382	hypothetical protein	-	410.39
PDT_06477	12	3032..3550	172	hypothetical protein	-	0
PDT_06478	12	4482..18995	30	hypothetical protein	-	0
PDT_06479	12	22169..22751	96	hypothetical protein	-	0
PDT_06848	12	1065024..1065239	71	hypothetical protein	-	2.75
PDT_06849	12	1065342..1065698	118	hypothetical protein	-	11.55
PDT_06850	12	1065791..1065937	48	hypothetical protein	-	0
PDT_08296	16	2647825..2657309	97	hypothetical protein	-	0
PDT_08297	16	2666090..2717900	15581	nonribosomal peptide synthase	-	1.93
PDT_08298	16	2719393..2720792	388	acetyl-CoA acetyltransferase	-	0.83
PDT_08299	16	2721475..2726739	1499	ABC multidrug transporter	-	34.66
PDT_08300	16	2727394..2728434	321	hypothetical protein	-	59.41
PDT_08301	16	2728861..2729490	145	hypothetical protein	-	237.38
PDT_08302	16	2730552..2731990	280	polyketide synthase	-	43.46
PDT_08303	16	2738361..2804589	21879	nonribosomal peptide synthase	-	40.98
PDT_08304	16	2805031..2805615	194	hypothetical protein	-	421.4
PDT_08305	16	2806711..2806902	63	hypothetical protein	-	0
PDT_09551	17	3689780..3690472	230	hypothetical protein	-	2.2
PDT_09552	17	3692008..3692931	307	NmrA-like family domain-containing protein	-	3.3
PDT_09553	17	3695558..3696608	306	alpha 1,2-galactosyltransferase	-	154.86
PDT_09554	17	3697918..3699041	333	glycophorin A domain protein	-	356.76
PDT_09555	17	3700812..3701781	279	hypothetical protein	-	8.25
PDT_09732	17	4205626..4206945	259	transferase family	-	0

				protein		
PDT_10330	18	2224..2469	43	hypothetical protein	-	1.65
PDT_10331	18	3811..4107	79	hypothetical protein	-	0
PDT_10332	18	5484..6268	240	hypothetical protein	-	0
PDT_10333	18	6625..8301	316	hypothetical protein	-	0
PDT_10334	18	8709..9393	111	hypothetical protein	-	0
PDT_10335	18	10429..11142	131	hypothetical protein	-	0
PDT_10336	18	11724..11902	36	hypothetical protein	-	0
PDT_10337	18	13383..14385	303	hypothetical protein	-	0
PDT_10339	18	17926..18312	128	hypothetical protein	-	1.38
PDT_10340	18	19525..19707	60	hypothetical protein	-	0
PDT_10341	18	24902..25490	45	hypothetical protein	-	0
PDT_10342	18	28658..38741	53	hypothetical protein	-	0
PDT_10343	18	48619..48855	59	chitinase	-	0
PDT_10344	18	59245..59798	54	hypothetical protein	-	0
PDT_10345	19	104..801	194	hypothetical protein	-	0
PDT_10346	19	4290..4705	106	hypothetical protein	-	12.65
PDT_10347	19	6226..6834	202	hypothetical protein	-	12.38
PDT_10348	19	7161..8336	298	hypothetical protein	-	18.98
PDT_10349	19	9709..11284	428	chitinase	-	2.75
PDT_10351	19	13712..14119	135	hypothetical protein	-	0
PDT_10352	19	17871..20685	706	translation elongation factor EF-2 subunit	-	0.83
PDT_10353	19	24943..25272	61	hypothetical protein	-	0
PDT_10354	19	46841..47534	146	hypothetical protein	-	0
PDT_10355	19	53604..54506	220	hypothetical protein	-	0
PDT_10356	19	59826..60166	40	hypothetical protein	-	0
PDT_10358	20	1983..2767	240	hypothetical protein	-	0
PDT_10359	20	4044..4340	79	hypothetical protein	-	0
PDT_10361	20	8357..9196	66	hypothetical protein	-	0
PDT_10362	20	10823..11012	44	hypothetical protein	-	0
PDT_10363	20	13988..14479	163	alpha/beta hydrolase fold domain protein	-	0
PDT_10364	20	17745..17965	23	hypothetical protein	-	0
PDT_10365	20	20651..23016	368	hypothetical protein	-	0
PDT_10366	20	24619..25290	223	hypothetical protein	-	0
PDT_10367	20	27055..27656	110	hypothetical protein	-	0
PDT_10368	20	28234..33079	981	exo-β-1,3-glucanase	-	0
PDT_10369	20	34044..41393	1455	chitinase	-	1.1
PDT_10371	20	44405..44698	97	hypothetical protein	-	0
PDT_10374	20	53066..54248	278	cyclin-dependent protein kinase	-	6.88
PDT_10375	20	55228..56414	375	hypothetical protein	-	0.83

PDT_10376	20	57567..59162	531	hypothetical protein	-	0
PDT_10377	20	59771..60448	191	hypothetical protein	-	51.71
PDT_10379	20	61373..63388	640	hypothetical protein	-	11.83
PDT_10380	20	66416..67650	372	hypothetical protein	-	46.21
PDT_10381	20	69834..70013	59	hypothetical protein	-	0.83
PDT_10382	20	70464..70679	71	hypothetical protein	-	2.75
PDT_10383	20	73045..74717	522	hypothetical protein	-	3.58
PDT_10384	20	77832..81558	988	NACHT domain protein	-	8.53
PDT_10385	20	82038..83021	327	hypothetical protein	-	16.5
PDT_10386	20	83200..84549	449	hypothetical protein	-	5.78
PDT_10387	20	87507..88271	254	allergen Asp F4-like	-	0.83
PDT_10388	20	89882..90460	192	hypothetical protein	-	2.48
PDT_10389	20	91845..93019	372	NACHT domain protein	-	3.58
PDT_10390	20	93173..93481	102	hypothetical protein	-	1.38
PDT_10391	20	93525..95117	310	WD40 domain protein	-	0.83
PDT_10392	20	98139..99530	463	hypothetical protein	-	4.95
PDT_10393	20	101678..103730	439	serine/threonine-protein kinase	-	0
PDT_10394	20	104316..106047	465	patatin-like phospholipase	-	0.55
PDT_10395	20	107504..108040	178	hypothetical protein	-	1.38
PDT_10396	20	111460..112652	363	hypothetical protein	-	0
PDT_10397	20	113928..114365	145	ankyrin repeat protein	-	20.08
PDT_10398	20	118064..118914	262	ferric-chelate reductase	-	0
PDT_10399	20	121259..123025	224	hypothetical protein	-	1.93
PDT_10400	20	128378..128803	119	hypothetical protein	-	0
PDT_10401	20	137550..138365	252	hypothetical protein	-	15.95
PDT_10402	20	141254..141744	125	hypothetical protein	-	0
PDT_10403	20	142859..143395	159	hypothetical protein	-	5.23
PDT_10404	20	144494..146549	552	hypothetical protein	-	37.96
PDT_10406	20	151121..151866	235	hypothetical protein	-	23.93
PDT_10407	20	152653..153192	179	hypothetical protein	-	0
PDT_10408	20	156814..157666	248	hypothetical protein	-	7.43
PDT_10409	20	158669..159863	312	hypothetical protein	-	56.39
PDT_10410	20	160755..161132	125	hypothetical protein	-	0.55
PDT_10411	20	163003..164498	197	hypothetical protein	-	0.55
PDT_10412	20	164921..167278	320	hypothetical protein	-	0
PDT_10413	20	168336..168943	179	hypothetical protein	-	1.38
PDT_10414	20	172715..172810	31	hypothetical protein	-	2.48
PDT_10416	20	176870..178414	361	hypothetical protein	-	1.38
PDT_10417	20	181018..182121	367	hypothetical protein	-	77.02
PDT_10418	20	183069..185903	802	NACHT domain protein	-	15.68
PDT_10419	20	188014..188478	154	hypothetical protein	-	0

PDT_10420	20	195141..195293	50	hypothetical protein	-	0
PDT_10421	20	196046..198636	216	hypothetical protein	-	0
PDT_10422	20	199676..200225	134	hypothetical protein	-	0.55
PDT_10423	20	203538..204380	280	hypothetical protein	-	17.33
PDT_10424	20	204740..206333	514	phosphotransferase enzyme family protein	-	35.48
PDT_10425	20	208160..208796	171	hypothetical protein	-	257.18
PDT_10426	20	209013..209972	319	hypothetical protein	-	47.04
PDT_10427	20	210358..210854	149	hypothetical protein	-	0
PDT_10428	20	211089..211388	99	hypothetical protein	-	0
PDT_10429	20	213697..215361	462	hypothetical protein	-	0.55
PDT_10430	20	216826..217480	178	ribonuclease	-	0
PDT_10431	20	219505..220938	372	ferric-chelate reductase	-	1.65
PDT_10432	20	223288..223821	177	hypothetical protein	-	0.83
PDT_10433	20	225273..225671	132	hypothetical protein	-	0
PDT_10434	21	172..804	210	hypothetical protein	-	0
PDT_10435	21	1123..1685	171	hypothetical protein	-	3.3
PDT_10436	21	2509..2895	128	hypothetical protein	-	1.1
PDT_10437	21	3450..4273	237	hypothetical protein	-	9.35
PDT_10438	21	6659..7496	259	hypothetical protein	-	15.4
PDT_10439	21	9113..9800	190	hypothetical protein	-	1.65
PDT_10440	21	14853..14927	24	hypothetical protein	-	0
PDT_10441	21	15579..16277	151	hypothetical protein	-	51.99
PDT_10442	21	17084..17509	119	hypothetical protein	-	0
PDT_10443	21	21246..21370	17	hypothetical protein	-	0.83
PDT_10445	21	28078..28791	237	hypothetical protein	-	6.33
PDT_10446	21	29160..29477	64	hypothetical protein	-	0
PDT_10447	21	32232..33244	300	hypothetical protein	-	10.73
PDT_10448	21	33810..36119	720	hypothetical protein	-	0.83
PDT_10449	21	37640..38620	326	hypothetical protein	-	27.23
PDT_10450	21	39693..42156	655	NACHT domain protein	-	1.38
PDT_10451	21	42752..44137	461	hypothetical protein	-	71.24
PDT_10452	21	44610..45311	217	hypothetical protein	-	0.83
PDT_10453	21	46861..48117	382	hypothetical protein	-	1.65
PDT_10455	22	3258..3620	120	hypothetical protein	-	0
PDT_10456	22	4187..4915	160	hypothetical protein	-	0
PDT_10457	22	5087..5786	90	hypothetical protein	-	0
PDT_10458	22	11927..12472	142	hypothetical protein	-	0
PDT_10459	22	13743..14127	111	hypothetical protein	-	16.23
PDT_10460	22	15163..15954	224	hypothetical protein	-	2.75
PDT_10461	22	16581..19726	963	patatin-like phospholipase	-	48.69
PDT_10462	22	19897..20067	56	hypothetical protein	-	3.3

PDT_10463	22	20944..23614	789	retroelement reverse transcriptase	-	0

Table S5. Cellulases and hemicellulases with amino acid sequence variations between *P. decumbens* 114-2 and JU-A10-T.

Protein ID		**Function prediction**	**CAZy family**	**Amino acid position**[a]	**Mutation**	**Affected PFAM domain**[b]	**Detected in secretome**	**Notes**[c]
114-2	**JU-A10-T**							
Cellulases								
PDE_07945	PDT_08213	cellobiohydrolase	GH7	489	T->-		Yes	nonconserved aa, linker region
PDE_07929	PDT_08197	endo-beta-1,4-glucanase	GH7	411	+T		Yes	nonconserved aa, linker region
PDE_00698	PDT_00728	endo-beta-1,4-glucanase	GH61	299	+SSSGSSSSGS			nonconserved aa, linker region
PDE_01261	PDT_01326	endo-beta-1,4-glucanase	GH61	264	G->V			nonconserved aa, linker region
				268	A->T			nonconserved aa, linker region
				280	L->S			nonconserved aa, linker region
				300	T->A			nonconserved aa, linker region
				308	+GSGSGP			nonconserved aa, linker region
				355	S->T			nonconserved aa
PDE_03711	PDT_03921	endo-beta-1,4-glucanase	GH5	364	T->-			nonconserved aa, linker region
PDE_09226	PDT_09527	endo-beta-1,4-glucanase	GH5	352	+TTTKAPV		Yes	nonconserved aa, linker region
PDE_09969	PDT_10285	endo-beta-1,4-glucanase	GH5	602	V->G		Yes	nonconserved aa
Hemicellulases								
PDE_06067	PDT_06294	alpha-L-arabinofuranosidase	GH43	130	S->P	Glyco_hydro_43	Yes	nonconserved aa
PDE_06665	PDT_06909	alpha-L-arabinofuranosidase	GH43	216	Q->R	Glyco_hydro_43		nonconserved aa
PDE_07334	PDT_07593	beta-xylosidase/alpha-L-arabinofuranosidase	GH43	260	R->S	Glyco_hydro_43	Yes	nonconserved aa
				373	F->S			nonconserved aa
				412	L->I			nonconserved aa
PDE_02583	PDT_02715	endo-beta-1,4-galactanase	GH53	307	A->T	Glyco_hydro_53	Yes	nonconserved aa
PDE_03401	PDT_03594	alpha-galactosidase	GH27	4	V->I			nonconserved aa

PDE_05594	PDT_05828	alpha-galactosidase	GH36	321	E->D			nonconserved aa
PDE_03572	PDT_03773	alpha-glucuronidase	GH67	238	Q->K	Glyco_hydro_67M		nonconserved aa
PDE_07013	PDT_07267	alpha-glucuronidase and N-acetyl beta-glucosaminidase	GH67 and GH84	13	G->V			nonconserved aa
				80	A->V	Glyco_hydro_67N		nonconserved aa
				418	R->C	NAGidase		nonconserved aa
				629	R->K			nonconserved aa
PDE_08238	PDT_08506	feruloyl esterase	CE1	298	P->A			nonconserved aa

[a] Amino acid positions refer to those in 114-2 proteins.

[b] Affected domains were identified according to the envelope domain boundaries in Pfam prediction result.

[c] Conservation of amino acid residues was analyzed using BLASTp search against the NCBI nonredundant database.

Table S6. Secreted proteins identified by LC-MS/MS and 2DE-MS/MS in *P. decumbens*.

Protein ID		Name	Function prediction	CAZy family	Secretion prediction	Analyzing methods	Protein ratios[a]		Transcription levels in CW medium (tags per million)	
114-2	**JU-A10-T**						**114-2**	**JU-A10-T**	**114-2**	**JU-A10-T**
Cellulases										
PDE_05445	PDT_05682	Cel7A-1	cellobiohydrolase	GH7	Yes	LC-MS/MS	0.09%	3.46%	18.7	657.4
PDE_07945	PDT_08213	Cel7A-2	cellobiohydrolase	GH7	Yes	Both	9.59%	19.92%	1192.38	6732.45
PDE_07124	PDT_07378	Cel6A	cellobiohydrolase	GH6	Yes	Both	1.50%	7.38%	1271.26	17660.16
PDE_00507	PDT_00525	Cel5A	endo-beta-1,4-glucanase	GH5		LC-MS/MS	0.22%	1.53%	472.6	7469.89
PDE_09226	PDT_09527	Cel5B	endo-beta-1,4-glucanase	GH5	Yes	Both	2.46%	5.39%	564.4	5622.84
PDE_09969	PDT_10285	Cel5C	endo-beta-1,4-glucanase	GH5	Yes	2DE-MS/MS	-	-	248.2	2162.82
PDE_05193	PDT_05427	Cel5D	endo-beta-1,4-glucanase	GH5	Yes	LC-MS/MS	-	-	10.2	40.98
PDE_05633	PDT_05867	Cel61A	endo-beta-1,4-glucanase	GH61		Both	5.58%	14.59%	2422.5	3991.44
PDE_06439	PDT_06673	Cel12A	endo-beta-1,4-glucanase	GH12	Yes	2DE-MS/MS	-	-	21.42	698.11
PDE_07929	PDT_08197	Cel7B	endo-beta-1,4-glucanase	GH7	Yes	LC-MS/MS	1.85%	4.65%	246.16	357.86
PDE_02102	PDT_02199	SWO	swollenin	-	Yes	LC-MS/MS	0.26%	1.36%	1170.96	10282.14
Hemicellulases										
PDE_01302	PDT_01369	Axe2A	acetyl xylan esterase	CE2	Yes	LC-MS/MS	-	-	49.64	133.13
PDE_04182	PDT_04384	Axe5A	acetyl xylan esterase	CE5	Yes	2DE-MS/MS	-	-	42.16	306.15
PDE_09278	PDT_09582	Axe1A	acetyl xylan esterase	CE1	Yes	Both	0.48%	0.74%	196.18	495.66
PDE_02583	PDT_02715	Gal53A	endo-beta-1,4-galactanase	GH53	Yes	2DE-MS/MS	-	-	65.28	211.8
PDE_08094	PDT_08360	Xyn10A	endo-beta-1,4-xylanase	GH10	Yes	Both	3.25%	15.21%	388.96	4945.91
PDE_02418	PDT_02533	Xyn10B	endo-beta-1,4-xylanase	GH10	Yes	Both	0.13%	1.48%	125.46	575.98
PDE_00752	PDT_00783	Xyn10C	endo-beta-1,4-xylanase	GH10	Yes	LC-MS/MS	-	-	11.22	71.24

PDE_02101	PDT_02197	Xyn11A	endo-beta-1,4-xylanase	GH11	Yes	Both	0.04%	0.28%	366.18	4728.06
PDE_02682	PDT_02819	Xyn11B	endo-beta-1,4-xylanase	GH11	Yes	2DE-MS/MS	-	-	60.86	3927.63
PDE_04478	PDT_04677	Xyn11C	endo-beta-1,4-xylanase	GH11	Yes	2DE-MS/MS	-	-	205.36	1122.53
PDE_03573	PDT_03774	Xyn30A	endo-beta-1,4-xylanase	GH30	Yes	2DE-MS/MS	-	-	18.02	131.21
PDE_00014	PDT_00016	Xyn30B	endo-beta-1,4-xylanase	GH30	Yes	LC-MS/MS	-	-	2.04	5396.74
PDE_02514	PDT_02635	Aga27A	alpha-galactosidase	GH27	Yes	Both	0.31%	1.02%	100.64	635.95
PDE_06067	PDT_06294	Abf43A	alpha-L-arabinofuranosidase	GH43	Yes	LC-MS/MS	0.00%	0.40%	18.36	77.57
PDE_00015	PDT_00017	Abf43B	alpha-L-arabinofuranosidase	GH43	Yes	LC-MS/MS	-	-	28.9	532.25
PDE_07585	PDT_07848	Abf43C	alpha-L-arabinofuranosidase	GH43	Yes	LC-MS/MS	-	-	758.88	28.88
PDE_07334	PDT_07593	Abf43D	beta-xylosidase/ alpha-L-arabinofuranosidase	GH43	Yes	LC-MS/MS	-	-	14.96	14.3
PDE_00016	PDT_00018	Abf62A	alpha-L-arabinofuranosidase	GH62	Yes	Both	0.35%	0.85%	54.74	920.09
PDE_07897	PDT_08165	Abf62B	alpha-L-arabinofuranosidase	GH62	Yes	Both	0.00%	0.28%	41.14	328.7
PDE_09988	PDT_10303	Abf54A	alpha-L-arabinofuranosidase	GH54	Yes	2DE-MS/MS	-	-	87.04	1171.22
PDE_06023	PDT_06254	Man5A	beta-1,4-mannanase	GH5	Yes	LC-MS/MS	0.09%	0.62%	125.8	8659.54
PDE_00049	PDT_00051	Xyl3A	beta-xylosidase	GH3	Yes	LC-MS/MS	-	-	29.58	58.31
PDE_06649	PDT_06892	Fae1A	feruloyl esterase	CE1	Yes	2DE-MS/MS	-	-	304.64	145.23
Amylases										
PDE_09417	PDT_09727	Amy15A	glucoamylase	GH15	Yes	Both	28.85%	4.60%	4429.53	41.81
PDE_05527	PDT_05762	Amy15B	glucoamylase	GH15	Yes	LC-MS/MS	-	-	194.82	23.11
PDE_01201	PDT_01258	Amy13A	alpha-amylase	GH13	Yes	Both	10.95%	0.51%	7288.59	65.74
PDE_01021	PDT_01062	Amy13B	alpha-amylase	GH13		LC-MS/MS	-	-	32.64	14.58
PDE_03966	PDT_04195	Agl31A	alpha-glucosidase	GH31	Yes	LC-MS/MS	0.88%	0.00%	587.86	1.65
Proteases										
PDE_07927	PDT_08195	PepB	aspartic protease	-	Yes	Both	6.16%	0.17%	10281.61	245.08

			penicillopepsin							
PDE_07344	PDT_07603	PepC	aspartic protease penicillopepsin	-	Yes	LC-MS/MS	0.88%	0.00%	633.08	260.48
PDE_07933	PDT_08201	PepD	glutamic peptidase	-	Yes	LC-MS/MS	-	-	223.04	460.18
PDE_01200	PDT_01257	PepE	serine peptidase	-	Yes	LC-MS/MS	-	-	416.84	183.47
PDE_01282	PDT_01349	PepF	serine peptidase	-	Yes	LC-MS/MS	-	-	43.18	3.3
PDE_01353	PDT_01430	PepG	serine peptidase	-	Yes	LC-MS/MS	-	-	48.28	15.4
PDE_06031	PDT_06262	PepH	serine peptidase	-	Yes	LC-MS/MS	-	-	182.24	26.41
PDE_08082	PDT_08347	PepI	serine peptidase	-	Yes	LC-MS/MS	-	-	42.5	61.61
Other proteins										
PDE_02736	PDT_02878	BGLI	beta-glucosidase	GH3	Yes	Both	3.39%	1.19%	559.64	581.21
PDE_04162	PDT_04363	Pga28A	endopolygalacturonase	GH28	Yes	LC-MS/MS	-	-	173.06	435.98
PDE_01385	PDT_01462	Rgl4A	rhamnogalacturonan lyase	PL4	Yes	LC-MS/MS	0.00%	0.62%	11.9	157.06
PDE_08122	PDT_08390	Chi18A	chitinase	GH18	Yes	Both	4.93%	2.44%	5407.03	318.8
PDE_01779	PDT_01865	Chi18B	chitinase	GH18	Yes	2DE-MS/MS	-	-	258.4	0
PDE_00333	PDT_00341	Man47A	alpha-mannosidase	GH47	Yes	LC-MS/MS	0.48%	0.17%	556.58	92.15
PDE_08139	PDT_08407	Bgn55A	exo-beta-1,3-glucanase	GH55	Yes	LC-MS/MS	0.92%	0.11%	696.32	11.83
PDE_02004	PDT_02092	Bgn30A	beta-1,6-glucanase	GH30	Yes	LC-MS/MS	0.48%	0.11%	59.16	20.35
PDE_06138	PDT_06369	Ecm33	GPI-anchored cell wall organization protein Ecm33	-		LC-MS/MS	0.26%	0.91%	470.22	520.42
PDE_03296	PDT_03477	Mur25A	lysozyme/muramidase	GH25	Yes	Both	1.76%	0.34%	1000.28	39.61
PDE_04519	PDT_04720	EBP1	IgE-binding protein	-	Yes	LC-MS/MS	0.48%	0.00%	811.24	105.62
PDE_05097	PDT_05330	AEP1	aldose 1-epimerase	-	Yes	2DE-MS/MS	-	-	43.18	253.88
PDE_03255	PDT_03434	ACP1	allergenic cerato-platanin	-	Yes	2DE-MS/MS	-	-	1734.68	5.5
PDE_01335	PDT_01406	PGAM1	phosphoglycerate mutase	-	Yes	Both	0.84%	0.00%	2162.4	124.05

PDE_05941	PDT_06172	Nuc1	nuclease	-	Yes	2DE-MS/MS	-	-	184.96	40.43
PDE_01330	PDT_01400	RNase1	guanyl-specific ribonuclease	-	Yes	LC-MS/MS	0.35%	0.00%	2.72	1.65
PDE_02801	PDT_02948	Gus2A	beta-glucuronidase	GH2	Yes	LC-MS/MS	0.00%	0.57%	357.34	44.56
PDE_03474	PDT_03671	DO1	dioxygenase	-	Yes	LC-MS/MS	0.00%	0.57%	0	4.95
PDE_07803	PDT_08072	HP1	hypothetical protein containing six-hairpin glycosidase domain DUF1237	-	Yes	LC-MS/MS	1.28%	0.00%	311.78	4.95
PDE_00503	PDT_00521	HP2	hypothetical protein	-	Yes	2DE-MS/MS	-	-	263.16	55.01
PDE_06089	PDT_06318	HP3	hypothetical protein	-	Yes	2DE-MS/MS	-	-	3065.44	240.13
PDE_00401	PDT_00409		chitin glucanosyltransferase	GH16		LC-MS/MS	-	-	31.96	7.98
PDE_05263	PDT_05498		chitin glucanosyltransferase	GH16		LC-MS/MS	-	-	352.92	151.83
PDE_07531	PDT_07793		chitin glucanosyltransferase	GH16		LC-MS/MS	-	-	1.02	18.98
PDE_03112	PDT_03282		exo-beta-1,3-glucanase	GH17		LC-MS/MS	-	-	210.12	58.04
PDE_01280	PDT_01346		exo-beta-glucosaminidase	GH2	Yes	LC-MS/MS	-	-	158.1	4.95
PDE_06511	PDT_06746		beta-1,6-N-acetylglucosaminidase	GH20	Yes	LC-MS/MS	-	-	55.08	17.6
PDE_06400	PDT_06632		beta-N-acetylhexosaminidase	GH3	Yes	LC-MS/MS	-	-	265.2	70.14
PDE_00282	PDT_00289		beta-galactosidase	GH35	Yes	LC-MS/MS	-	-	99.28	68.22
PDE_05515	PDT_05750		beta-1,3-glucanase	GH64		LC-MS/MS	-	-	285.26	28.61
PDE_03452	PDT_03648		beta-1,3-glucanosyltransglycosylase	GH72		LC-MS/MS	-	-	56.78	232.43
PDE_04618	PDT_04823		beta-1,3-glucanosyltransglycosylase	GH72		LC-MS/MS	-	-	534.14	147.16
PDE_08733	PDT_09023		chitosanase	GH75	Yes	LC-MS/MS	-	-	20.06	0.83
PDE_01949	PDT_02037		beta-glucuronidase	GH79	Yes	LC-MS/MS	-	-	31.28	1.1

PDE_07606	PDT_07871		6-hydroxy-D-nicotine oxidase	-	Yes	LC-MS/MS	-	-	23.46	15.13
PDE_08180	PDT_08448		6-hydroxy-D-nicotine oxidase	-	Yes	LC-MS/MS	-	-	4.08	1.1
PDE_01372	PDT_01449		acid phosphatase	-	Yes	LC-MS/MS	-	-	188.7	13.2
PDE_01404	PDT_01481		catalase	-	Yes	LC-MS/MS	-	-	4.42	19.53
PDE_02596	PDT_02731		elongation factor EF-1 alpha subunit	-		LC-MS/MS	-	-	1088.68	1539.53
PDE_01798	PDT_01885		glutaminase	-	Yes	LC-MS/MS	-	-	321.64	8.53
PDE_02379	PDT_02490		heat shock protein 70	-		LC-MS/MS	-	-	1965.88	274.79
PDE_05537	PDT_05771		lysophospholipase	-		LC-MS/MS	-	-	668.44	178.24
PDE_00500	PDT_00518		non-hemolytic phospholipase C precursor	-	Yes	LC-MS/MS	-	-	346.12	22.56
PDE_04950	PDT_05181		prenylcysteine oxidase	-	Yes	LC-MS/MS	-	-	27.54	34.38
PDE_04101	PDT_04304		related to blastomyces yeast phase-specific protein 1	-		LC-MS/MS	-	-	2964.46	16.78
PDE_00092	PDT_00094		ribonuclease T2	-	Yes	LC-MS/MS	-	-	200.94	65.74
PDE_05044	PDT_05276		serine/threonine-protein kinase	-		LC-MS/MS	-	-	10.88	14.3
PDE_04579	PDT_04781		tubulin alpha	-		LC-MS/MS	-	-	347.82	196.67
PDE_01168	PDT_01220		hypothetical protein	-	Yes	LC-MS/MS	-	-	214.54	14.3
PDE_01346	PDT_01419		hypothetical protein	-	Yes	LC-MS/MS	-	-	59.84	8.25
PDE_02536	PDT_02658		hypothetical protein	-		LC-MS/MS	-	-	92.82	77.57
PDE_02854	PDT_03005		hypothetical protein	-	Yes	LC-MS/MS	-	-	350.2	1.38
PDE_03340	PDT_03525		hypothetical protein	-		LC-MS/MS	-	-	124.1	147.16
PDE_04403	PDT_04605		hypothetical protein	-		LC-MS/MS	-	-	73.44	2.75
PDE_04506	PDT_04706		hypothetical protein	-	Yes	LC-MS/MS	-	-	50.66	20.35
PDE_07106	PDT_07361		hypothetical protein	-	Yes	LC-MS/MS	-	-	9511.85	400.49

PDE_07911	PDT_08179		hypothetical protein	-		LC-MS/MS	-	-	476	1736.2
PDE_09289	PDT_09594		hypothetical protein	-	Yes	LC-MS/MS	-	-	265.54	24.21

[a] Protein ratios were calculated using peptide counts of corresponding protein groups obtained in LC-MS/MS.

Table S7. Statistics of digital gene expression profiling in *P. decumbens* 114-2 and JU-A10-T.

	114-2	**JU-A10-T**
Raw data processing		
Total number of raw tags	3,137,364	3,741,500
Distinct number of raw tags	215,965	168,718
Total number of clean tags	2,941,173	3,635,528
Distinct number of clean tags	76,923	67,784
Mapping Tags to genes		
Total number of tags mapped to genes	1,967,160 (66.88%)	2,091,900 (57.54%)
Distinct number of tags mapped to genes	23,370 (30.38%)	16,669 (24.59%)
Number of tag-mapped genes	8,456 (84.38%)	8,213 (78.42%)

Table S8. Manually checked sequence variations in cellulase gene promoters between 114-2 and JU-A10-T.

Gene ID	Function prediction	CAZy family	Nucleotide position[a]	Mutation	Affected transcription factor binding motifs
PDE_05445	cellobiohydrolase	GH7	-143	G->T	
			-258	G->C	
			-478	G->A	
			-526	A->G	
			-714	C->T	
			-752	G->A	CreA (adjacent 5'-SYGGRG-3' motifs)
			-891	G->A	
			-1067	C->T	
			-1069	C->T	
			-1251	A->G	
			-1333	T->A	
PDE_07945	cellobiohydrolase	GH7	-491	G->T	
			(-1066)-(-1064)	AAG->-	
			-1142	G->-	
			-1438	C->G	
PDE_00507	endo-beta-1,4-glucanase	GH5	-19	C->T	
			-25	A->G	
			-201	T->C	
			-284	+AGA	
			-752	+T	
			-794	G->A	
			-1156	T->C	
			-1303	+AGAGA	
			-1353	C->T	
PDE_09969	endo-beta-1,4-glucanase	GH5	-975	G->-	
PDE_03711	endo-beta-1,4-glucanase	GH5	(-153)-(-152)	CT->-	
PDE_09267	endo-beta-1,4-glucanase	GH5	-13	C->T	
PDE_06439	endo-beta-1,4-glucanase	GH12	-688	G->A	
			-1004	T->C	
PDE_07928	endo-beta-1,4-glucanase	GH45	-547	T->C	
PDE_00698	endo-beta-1,4-glucanase	GH61	-420	T->A	
			-1174	T->G	
			-1207	C->T	
PDE_01261	endo-beta-1,4-glucanase	GH61	-2	C->G	
			-10	A->C	
			-48	G->A	
			-52	A->G	

			-69	C->T	
			-93	G->T	
			-113	G->A	
			-184	C->T	
			-231	A->C	
			-275	A->G	
			-297	G->-	
			-402	A->T	
			-426	T->C	
			-459	C->T	
			-481	T->G	
			-510	C->T	
			-513	G->T	
			(-524)-(-522)	TAA->AGC	
			-541	A->G	
			-545	A->G	
			-547	C->T	
			-573	A->G	
			-581	C->T	
			-602	T->C	
			-623	T->C	
			(-626)-(-625)	CG->TA	
			-632	C->T	
			-634	A->G	
			-637	A->G	
			-652	A->C	
			-655	+C	
			-681	T->C	
			-743	A->G	
			-791	G->A	
			-800	G->A	
			-811	G->A	
			-843	T->C	
			-913	T->A	
			-942	G->A	
			-983	G->A	
			(-1046)-(-1045)	AA->GG	
			-1052	C->T	
			-1063	A->G	
			-1065	G->A	
			-1071	T->C	
			-1122	A->G	

			-1125	A->C	
			-1239	T->A	
			-1258	C->A	
			-1267	G->T	
			-1289	C->T	
			-1305	A->G	
			(-1317)-(-1316)	GT->AG	
			-1358	A->G	
			-1361	G->A	
			(-1366)-(-1365)	GG->T	
			-1485	A->G	
PDE_06768	endo-beta-1,4-glucanase	GH61	-97	A->G	
			-100	T->C	
			(-240)-(-236)	AAT->-	
			-267	C->T	
			(-299)-(-298)	AG->GA	
			(-328)-(-327)	TC->GG	
			-532	T->C	
			-545	A->G	
			-598	C->T	
			-642	C->G	
			-685	T->C	
			-977	T->C	
			-1033	T->A	
			-1047	C->T	
			-1369	C->G	
			-1454	T->C	

[a] Nucleotides are numbered relative to the start codon in 114-2.

Table S9. Gene ontology (GO) enrichment analysis of genes of significantly differential expression between *P. decumbens* 114-2 and JU-A10-T. GO categories with false discovery rate (FDR) ≤ 0.05 are shown.

GO ID	**Description**	**Category**	**Number of genes**		**FDR**	**Gene IDs**
			Tested	**Reference**		
Up-regulated in JU-A10-T relative to 114-2						
GO:0005576	extracellular region	C	44	94	8.12E-22	PDE_05931, PDE_05193, PDE_04478, PDE_08094, PDE_07259, PDE_03698, PDE_05998, PDE_08709, PDE_06441, PDE_06439, PDE_02101, PDE_02102, PDE_04162, PDE_04182, PDE_00507, PDE_05210, PDE_02886, PDE_09226, PDE_09278, PDE_03399, PDE_05445, PDE_01261, PDE_03287, PDE_02682, PDE_06023, PDE_00014, PDE_00015, PDE_00016, PDE_07124, PDE_01983, PDE_02583, PDE_07938, PDE_07945, PDE_04768, PDE_06067, PDE_02514, PDE_07928, PDE_07911, PDE_09988, PDE_09969, PDE_01302, PDE_02418, PDE_07897, PDE_03572
GO:0004553	hydrolase activity, hydrolyzing O-glycosyl compounds	F	56	177	1.42E-18	PDE_05931, PDE_05193, PDE_04478, PDE_08094, PDE_01690, PDE_05998, PDE_09710, PDE_06441, PDE_06439, PDE_02101, PDE_02102, PDE_07531, PDE_04151, PDE_04152, PDE_06306, PDE_04162, PDE_04182, PDE_00507, PDE_00579, PDE_03010, PDE_05210, PDE_02886, PDE_01750, PDE_09226, PDE_09278, PDE_09279, PDE_09267, PDE_05445, PDE_00615, PDE_01256, PDE_01261, PDE_00752, PDE_02682, PDE_04859, PDE_06023, PDE_00014, PDE_00015, PDE_00016, PDE_07124, PDE_03573, PDE_02583, PDE_07938, PDE_07945, PDE_06067, PDE_02514, PDE_07928, PDE_06944, PDE_07013, PDE_09988, PDE_09969, PDE_01302, PDE_03542, PDE_02418, PDE_07897, PDE_03572, PDE_00076
GO:0005975	carbohydrate metabolic process	P	80	342	2.13E-18	PDE_05931, PDE_05193, PDE_04478, PDE_08094, PDE_01690, PDE_07330, PDE_07259, PDE_00398, PDE_01584, PDE_05998, PDE_01540, PDE_05097, PDE_09710, PDE_08709, PDE_06441, PDE_03147, PDE_06439, PDE_01008, PDE_02101, PDE_02102, PDE_02929, PDE_07531, PDE_01899, PDE_04151, PDE_06306, PDE_04162, PDE_03036, PDE_04182, PDE_00507, PDE_00579, PDE_03010, PDE_05210, PDE_09532, PDE_02886, PDE_01750, PDE_09226, PDE_09278, PDE_09279, PDE_09267, PDE_05445, PDE_00615, PDE_01256, PDE_01261, PDE_09398, PDE_00752, PDE_02682, PDE_07688, PDE_07674, PDE_04859, PDE_06023, PDE_00014, PDE_00015, PDE_00016, PDE_07124, PDE_03573, PDE_01924, PDE_02583, PDE_07938, PDE_07945, PDE_06067, PDE_02514, PDE_01468, PDE_09135, PDE_07928, PDE_06944, PDE_04588, PDE_07918, PDE_06951, PDE_07013, PDE_09988, PDE_03452, PDE_09969,

						PDE_01302, PDE_03542, PDE_02418, PDE_07897, PDE_03572, PDE_01385, PDE_00076, PDE_00917
GO:0030248	cellulose binding	F	23	29	2.48E-18	PDE_08094, PDE_08709, PDE_02101, PDE_02102, PDE_04182, PDE_00507, PDE_05210, PDE_09226, PDE_09278, PDE_05445, PDE_01261, PDE_02682, PDE_06023, PDE_00014, PDE_00015, PDE_00016, PDE_07124, PDE_07945, PDE_06067, PDE_02514, PDE_07928, PDE_09969, PDE_01302
GO:0016798	hydrolase activity, acting on glycosyl bonds	F	59	206	1.14E-17	PDE_05931, PDE_05193, PDE_04478, PDE_08094, PDE_01690, PDE_00347, PDE_05998, PDE_09710, PDE_06441, PDE_06439, PDE_02101, PDE_02102, PDE_07531, PDE_04151, PDE_04152, PDE_06306, PDE_04162, PDE_04182, PDE_00507, PDE_00579, PDE_03010, PDE_05210, PDE_09532, PDE_02886, PDE_01750, PDE_09218, PDE_09226, PDE_09278, PDE_09279, PDE_09267, PDE_05445, PDE_00615, PDE_01256, PDE_01261, PDE_00752, PDE_02682, PDE_04859, PDE_06023, PDE_00014, PDE_00015, PDE_00016, PDE_07124, PDE_03573, PDE_02583, PDE_07938, PDE_07945, PDE_06067, PDE_02514, PDE_07928, PDE_06944, PDE_07013, PDE_09988, PDE_09969, PDE_01302, PDE_03542, PDE_02418, PDE_07897, PDE_03572, PDE_00076
GO:0001871	pattern binding	F	24	39	2.84E-15	PDE_08094, PDE_08709, PDE_02101, PDE_02102, PDE_04182, PDE_00507, PDE_05210, PDE_09226, PDE_09278, PDE_05445, PDE_01261, PDE_02682, PDE_06023, PDE_00014, PDE_00015, PDE_00016, PDE_07124, PDE_07945, PDE_06067, PDE_02514, PDE_07928, PDE_09969, PDE_01302, PDE_07897
GO:0030247	polysaccharide binding	F	24	39	2.84E-15	PDE_08094, PDE_08709, PDE_02101, PDE_02102, PDE_04182, PDE_00507, PDE_05210, PDE_09226, PDE_09278, PDE_05445, PDE_01261, PDE_02682, PDE_06023, PDE_00014, PDE_00015, PDE_00016, PDE_07124, PDE_07945, PDE_06067, PDE_02514, PDE_07928, PDE_09969, PDE_01302, PDE_07897
GO:0030246	carbohydrate binding	F	31	68	4.26E-15	PDE_08094, PDE_01540, PDE_05097, PDE_08709, PDE_02101, PDE_02102, PDE_08629, PDE_04182, PDE_00507, PDE_03010, PDE_05210, PDE_09226, PDE_09278, PDE_09279, PDE_05445, PDE_01261, PDE_02682, PDE_06023, PDE_00014, PDE_00015, PDE_00016, PDE_07124, PDE_07945, PDE_06067, PDE_02514, PDE_07928, PDE_06944, PDE_09969, PDE_01302, PDE_07897, PDE_01385
GO:0000272	polysaccharide catabolic process	P	31	73	4.68E-14	PDE_05931, PDE_05193, PDE_04478, PDE_08094, PDE_07259, PDE_05998, PDE_08709, PDE_06441, PDE_06439, PDE_02101, PDE_06306, PDE_04162, PDE_04182, PDE_05210, PDE_02886, PDE_09278, PDE_05445, PDE_00752, PDE_02682, PDE_07674, PDE_07124, PDE_02583, PDE_07938, PDE_07945, PDE_06067, PDE_07928, PDE_07013, PDE_09988, PDE_02418, PDE_07897, PDE_03572
GO:0016052	carbohydrate catabolic	P	39	122	4.45E-13	PDE_05931, PDE_05193, PDE_04478, PDE_08094, PDE_07330, PDE_07259, PDE_05998, PDE_08709, PDE_06441,

	process					PDE_06439, PDE_01008, PDE_02101, PDE_06306, PDE_04162, PDE_03036, PDE_04182, PDE_05210, PDE_02886, PDE_09278, PDE_05445, PDE_01256, PDE_09398, PDE_00752, PDE_02682, PDE_07688, PDE_07674, PDE_07124, PDE_02583, PDE_07938, PDE_07945, PDE_06067, PDE_07928, PDE_04588, PDE_07918, PDE_07013, PDE_09988, PDE_02418, PDE_07897, PDE_03572
GO:0005976	polysaccharide metabolic process	P	31	88	1.89E-11	PDE_05931, PDE_05193, PDE_04478, PDE_08094, PDE_07259, PDE_05998, PDE_08709, PDE_06441, PDE_06439, PDE_02101, PDE_06306, PDE_04162, PDE_04182, PDE_05210, PDE_02886, PDE_09278, PDE_05445, PDE_00752, PDE_02682, PDE_07674, PDE_07124, PDE_02583, PDE_07938, PDE_07945, PDE_06067, PDE_07928, PDE_07013, PDE_09988, PDE_02418, PDE_07897, PDE_03572
GO:0045493	xylan catabolic process	P	15	20	3.50E-11	PDE_04478, PDE_08094, PDE_08709, PDE_02101, PDE_06306, PDE_05210, PDE_00752, PDE_02682, PDE_07674, PDE_06067, PDE_07013, PDE_09988, PDE_02418, PDE_07897, PDE_03572
GO:0045491	xylan metabolic process	P	15	20	3.50E-11	PDE_04478, PDE_08094, PDE_08709, PDE_02101, PDE_06306, PDE_05210, PDE_00752, PDE_02682, PDE_07674, PDE_06067, PDE_07013, PDE_09988, PDE_02418, PDE_07897, PDE_03572
GO:0010383	cell wall polysaccharide metabolic process	P	15	21	9.89E-11	PDE_04478, PDE_08094, PDE_08709, PDE_02101, PDE_06306, PDE_05210, PDE_00752, PDE_02682, PDE_07674, PDE_06067, PDE_07013, PDE_09988, PDE_02418, PDE_07897, PDE_03572
GO:0010410	hemicellulose metabolic process	P	15	21	9.89E-11	PDE_04478, PDE_08094, PDE_08709, PDE_02101, PDE_06306, PDE_05210, PDE_00752, PDE_02682, PDE_07674, PDE_06067, PDE_07013, PDE_09988, PDE_02418, PDE_07897, PDE_03572
GO:0009057	macromolecule catabolic process	P	33	137	2.32E-07	PDE_05931, PDE_05193, PDE_04478, PDE_08094, PDE_07259, PDE_05998, PDE_08709, PDE_06441, PDE_06439, PDE_02101, PDE_06306, PDE_04162, PDE_04182, PDE_00506, PDE_05210, PDE_02886, PDE_09278, PDE_05445, PDE_00752, PDE_02682, PDE_07674, PDE_07124, PDE_02492, PDE_02583, PDE_07938, PDE_07945, PDE_06067, PDE_07928, PDE_07013, PDE_09988, PDE_02418, PDE_07897, PDE_03572
GO:0071554	cell wall organization or biogenesis	P	22	67	2.87E-07	PDE_05931, PDE_04478, PDE_08094, PDE_07259, PDE_01529, PDE_08709, PDE_02101, PDE_06306, PDE_04162, PDE_05210, PDE_02886, PDE_00752, PDE_02682, PDE_07674, PDE_02583, PDE_07938, PDE_06067, PDE_07013, PDE_09988, PDE_02418, PDE_07897, PDE_03572
GO:0044036	cell wall macromolecule metabolic process	P	15	34	1.12E-06	PDE_04478, PDE_08094, PDE_08709, PDE_02101, PDE_06306, PDE_05210, PDE_00752, PDE_02682, PDE_07674, PDE_06067, PDE_07013, PDE_09988, PDE_02418, PDE_07897, PDE_03572
GO:0030245	cellulose catabolic process	P	9	12	2.35E-06	PDE_05193, PDE_08709, PDE_06441, PDE_06439, PDE_04182, PDE_09278, PDE_05445, PDE_07124, PDE_07945

GO:0030243	cellulose metabolic process	P	9	12	2.35E-06	PDE_05193, PDE_08709, PDE_06441, PDE_06439, PDE_04182, PDE_09278, PDE_05445, PDE_07124, PDE_07945
GO:0009251	glucan catabolic process	P	9	13	6.80E-06	PDE_05193, PDE_08709, PDE_06441, PDE_06439, PDE_04182, PDE_09278, PDE_05445, PDE_07124, PDE_07945
GO:0008810	cellulase activity	F	9	15	3.90E-05	PDE_05193, PDE_06439, PDE_00507, PDE_02886, PDE_09226, PDE_01261, PDE_07124, PDE_07928, PDE_09969
GO:0009056	catabolic process	P	58	391	3.90E-05	PDE_05931, PDE_05193, PDE_04478, PDE_08094, PDE_07342, PDE_07330, PDE_05063, PDE_07259, PDE_03738, PDE_09720, PDE_09719, PDE_05998, PDE_07217, PDE_09704, PDE_08709, PDE_06441, PDE_06439, PDE_01008, PDE_02101, PDE_02947, PDE_01899, PDE_06306, PDE_04162, PDE_03036, PDE_04182, PDE_00506, PDE_05210, PDE_02886, PDE_09278, PDE_08414, PDE_05427, PDE_05445, PDE_01256, PDE_09398, PDE_00752, PDE_02682, PDE_07688, PDE_07674, PDE_07124, PDE_02492, PDE_02583, PDE_02592, PDE_07938, PDE_07945, PDE_06067, PDE_09135, PDE_07928, PDE_04588, PDE_07918, PDE_07013, PDE_09988, PDE_03486, PDE_05806, PDE_08948, PDE_02418, PDE_07897, PDE_08183, PDE_03572
GO:0005198	structural molecule activity	F	30	149	6.78E-05	PDE_03807, PDE_03827, PDE_05983, PDE_05108, PDE_01695, PDE_05026, PDE_04327, PDE_03780, PDE_08757, PDE_01824, PDE_00406, PDE_01817, PDE_05316, PDE_02916, PDE_03178, PDE_05253, PDE_05203, PDE_00629, PDE_04939, PDE_02793, PDE_02754, PDE_07774, PDE_06150, PDE_02649, PDE_00734, PDE_04897, PDE_03668, PDE_02599, PDE_05652, PDE_00162
GO:0044042	glucan metabolic process	P	9	16	7.31E-05	PDE_05193, PDE_08709, PDE_06441, PDE_06439, PDE_04182, PDE_09278, PDE_05445, PDE_07124, PDE_07945
GO:0005840	ribosome	C	31	158	7.31E-05	PDE_03807, PDE_05983, PDE_05108, PDE_01695, PDE_05026, PDE_04327, PDE_03780, PDE_08758, PDE_08757, PDE_02153, PDE_01824, PDE_00406, PDE_01817, PDE_05316, PDE_02916, PDE_03178, PDE_05253, PDE_05203, PDE_00629, PDE_04939, PDE_02793, PDE_02754, PDE_07774, PDE_02649, PDE_00734, PDE_04897, PDE_03668, PDE_02599, PDE_00825, PDE_00106, PDE_08174
GO:0044238	primary metabolic process	P	215	2211	1.25E-04	PDE_05175, PDE_03807, PDE_05931, PDE_05194, PDE_05193, PDE_05983, PDE_06679, PDE_05103, PDE_05108, PDE_04478, PDE_00285, PDE_00223, PDE_00222, PDE_08094, PDE_01690, PDE_01695, PDE_02298, PDE_09601, PDE_08070, PDE_02244, PDE_07342, PDE_07330, PDE_08857, PDE_05063, PDE_05070, PDE_05026, PDE_07259, PDE_07279, PDE_04360, PDE_03752, PDE_00398, PDE_03738, PDE_04327, PDE_03780, PDE_01576, PDE_01584, PDE_09720, PDE_09719, PDE_08758, PDE_08757, PDE_07236, PDE_05998, PDE_07217, PDE_01540, PDE_09704, PDE_05097, PDE_09710, PDE_08709, PDE_01824, PDE_06441, PDE_03147, PDE_05389, PDE_00406, PDE_01817, PDE_06439, PDE_01008, PDE_00473, PDE_04220, PDE_05316, PDE_02101, PDE_02102, PDE_09467, PDE_02916,

						PDE_03178, PDE_06473, PDE_05349, PDE_03192, PDE_02929, PDE_02947, PDE_08629, PDE_07531, PDE_01899, PDE_07580, PDE_01858, PDE_04151, PDE_04152, PDE_06306, PDE_06309, PDE_03014, PDE_04162, PDE_06322, PDE_03036, PDE_04182, PDE_05253, PDE_00506, PDE_00507, PDE_00579, PDE_03916, PDE_03010, PDE_00542, PDE_06359, PDE_05203, PDE_05210, PDE_09532, PDE_02817, PDE_02857, PDE_07448, PDE_02886, PDE_01750, PDE_01714, PDE_09226, PDE_01190, PDE_09278, PDE_09279, PDE_09267, PDE_09260, PDE_00629, PDE_03392, PDE_08437, PDE_03408, PDE_04939, PDE_05427, PDE_07782, PDE_02774, PDE_05445, PDE_07794, PDE_02793, PDE_02754, PDE_00615, PDE_07774, PDE_01256, PDE_07722, PDE_01261, PDE_06117, PDE_06100, PDE_04799, PDE_06146, PDE_09398, PDE_00752, PDE_03241, PDE_03287, PDE_08360, PDE_02682, PDE_07688, PDE_03308, PDE_05565, PDE_07674, PDE_07667, PDE_07668, PDE_02649, PDE_00734, PDE_06179, PDE_04890, PDE_04897, PDE_04828, PDE_04859, PDE_06023, PDE_00014, PDE_00015, PDE_00016, PDE_06805, PDE_07124, PDE_02492, PDE_05727, PDE_08219, PDE_01983, PDE_03573, PDE_03672, PDE_05687, PDE_05694, PDE_01924, PDE_03668, PDE_02549, PDE_08270, PDE_03644, PDE_03617, PDE_02599, PDE_05652, PDE_02583, PDE_02593, PDE_07938, PDE_07933, PDE_07944, PDE_07945, PDE_00816, PDE_04768, PDE_06067, PDE_06771, PDE_02514, PDE_01468, PDE_02509, PDE_09135, PDE_06907, PDE_09131, PDE_06918, PDE_04574, PDE_00987, PDE_09141, PDE_06948, PDE_07928, PDE_06944, PDE_04588, PDE_07918, PDE_06951, PDE_07013, PDE_09988, PDE_03452, PDE_09961, PDE_03486, PDE_09969, PDE_05806, PDE_01302, PDE_03542, PDE_08948, PDE_02418, PDE_07897, PDE_03572, PDE_08111, PDE_03511, PDE_08919, PDE_01385, PDE_00076, PDE_00917, PDE_04626, PDE_07895
GO:0031176	endo-1,4-beta-xylanase activity	F	6	7	1.50E-04	PDE_04478, PDE_02101, PDE_05210, PDE_00752, PDE_02682, PDE_02418
GO:0003735	structural constituent of ribosome	F	26	128	2.80E-04	PDE_03807, PDE_05983, PDE_05108, PDE_01695, PDE_05026, PDE_04327, PDE_03780, PDE_08757, PDE_01824, PDE_00406, PDE_01817, PDE_05316, PDE_02916, PDE_03178, PDE_05253, PDE_05203, PDE_00629, PDE_04939, PDE_02793, PDE_02754, PDE_07774, PDE_02649, PDE_00734, PDE_04897, PDE_03668, PDE_02599
GO:0016787	hydrolase activity	F	131	1219	3.92E-04	PDE_05931, PDE_05194, PDE_05193, PDE_06697, PDE_09688, PDE_05103, PDE_04478, PDE_00285, PDE_00222, PDE_02317, PDE_08094, PDE_01690, PDE_09608, PDE_04504, PDE_08857, PDE_05026, PDE_05002, PDE_07279, PDE_00347, PDE_09720, PDE_04410, PDE_08758, PDE_05998, PDE_07214, PDE_08722, PDE_09704, PDE_09710, PDE_01529, PDE_08709, PDE_06441, PDE_05390, PDE_06439, PDE_03108, PDE_09487, PDE_05316, PDE_02101,

						PDE_02102, PDE_09467, PDE_06473, PDE_03192, PDE_02033, PDE_02947, PDE_02974, PDE_07531, PDE_08616, PDE_01830, PDE_01858, PDE_04151, PDE_04152, PDE_06306, PDE_06309, PDE_03014, PDE_04162, PDE_06322, PDE_03036, PDE_04182, PDE_00506, PDE_00507, PDE_00579, PDE_03010, PDE_05210, PDE_09532, PDE_02817, PDE_02857, PDE_02886, PDE_01750, PDE_09218, PDE_09226, PDE_09278, PDE_09279, PDE_09267, PDE_09260, PDE_03399, PDE_03408, PDE_05427, PDE_04907, PDE_07782, PDE_05445, PDE_02789, PDE_02756, PDE_00615, PDE_01256, PDE_01261, PDE_00752, PDE_03287, PDE_02682, PDE_02635, PDE_06179, PDE_04859, PDE_06023, PDE_00014, PDE_00015, PDE_00016, PDE_09821, PDE_07124, PDE_05727, PDE_08215, PDE_01983, PDE_03573, PDE_03672, PDE_02549, PDE_03617, PDE_02583, PDE_07938, PDE_07933, PDE_07944, PDE_07945, PDE_04768, PDE_06067, PDE_02514, PDE_02504, PDE_02509, PDE_09131, PDE_07928, PDE_06944, PDE_01285, PDE_07013, PDE_09173, PDE_09988, PDE_03486, PDE_09964, PDE_09969, PDE_05806, PDE_01300, PDE_01302, PDE_03542, PDE_02418, PDE_07897, PDE_03572, PDE_00076, PDE_04624
GO:0009067	aspartate family amino acid biosynthetic process	P	9	19	3.94E-04	PDE_05175, PDE_01576, PDE_07236, PDE_03916, PDE_08437, PDE_04799, PDE_06146, PDE_03308, PDE_05687
GO:0044262	cellular carbohydrate metabolic process	P	25	131	1.28E-03	PDE_05931, PDE_07330, PDE_07259, PDE_01584, PDE_01540, PDE_05097, PDE_08709, PDE_03147, PDE_01008, PDE_02929, PDE_01899, PDE_04162, PDE_03036, PDE_09398, PDE_07688, PDE_00016, PDE_01924, PDE_02583, PDE_07938, PDE_09135, PDE_04588, PDE_07918, PDE_09988, PDE_07897, PDE_00917
GO:0044444	cytoplasmic part	C	70	564	1.30E-03	PDE_06615, PDE_03807, PDE_03827, PDE_03828, PDE_05983, PDE_05108, PDE_01695, PDE_09601, PDE_01610, PDE_05026, PDE_04327, PDE_03780, PDE_09720, PDE_08758, PDE_08757, PDE_02153, PDE_07214, PDE_08717, PDE_01824, PDE_00406, PDE_01817, PDE_05316, PDE_09467, PDE_02916, PDE_03178, PDE_04229, PDE_06473, PDE_05349, PDE_08629, PDE_01899, PDE_03014, PDE_05253, PDE_05248, PDE_03916, PDE_03004, PDE_05203, PDE_07448, PDE_06215, PDE_09260, PDE_00629, PDE_08412, PDE_04939, PDE_02793, PDE_02754, PDE_07774, PDE_03251, PDE_02649, PDE_04875, PDE_00734, PDE_04897, PDE_00014, PDE_09059, PDE_03573, PDE_05694, PDE_03668, PDE_02599, PDE_05652, PDE_00825, PDE_04768, PDE_09135, PDE_00132, PDE_00106, PDE_04588, PDE_01285, PDE_00162, PDE_08976, PDE_08980, PDE_08174, PDE_03511, PDE_05751
GO:0044106	cellular amine metabolic process	P	35	218	0.001322	PDE_05175, PDE_06679, PDE_00223, PDE_09601, PDE_03738, PDE_01576, PDE_07236, PDE_07217, PDE_05389, PDE_04220, PDE_03916, PDE_00542, PDE_06359, PDE_01714, PDE_03392, PDE_08437, PDE_06117, PDE_06100,

						PDE_04799, PDE_06146, PDE_03241, PDE_08360, PDE_03308, PDE_04890, PDE_04828, PDE_06805, PDE_08219, PDE_05687, PDE_03644, PDE_02593, PDE_00816, PDE_06771, PDE_06907, PDE_09141, PDE_08111
GO:0009066	aspartate family amino acid metabolic process	P	9	22	0.001531	PDE_05175, PDE_01576, PDE_07236, PDE_03916, PDE_08437, PDE_04799, PDE_06146, PDE_03308, PDE_05687
GO:0006520	cellular amino acid metabolic process	P	34	211	0.001539	PDE_05175, PDE_06679, PDE_00223, PDE_09601, PDE_03738, PDE_01576, PDE_07236, PDE_07217, PDE_05389, PDE_04220, PDE_03916, PDE_00542, PDE_06359, PDE_01714, PDE_03392, PDE_08437, PDE_06117, PDE_06100, PDE_04799, PDE_06146, PDE_03241, PDE_08360, PDE_03308, PDE_04890, PDE_04828, PDE_06805, PDE_08219, PDE_05687, PDE_03644, PDE_02593, PDE_00816, PDE_06907, PDE_09141, PDE_08111
GO:0015935	small ribosomal subunit	C	7	14	0.002771	PDE_05983, PDE_05108, PDE_01695, PDE_03780, PDE_00406, PDE_02754, PDE_02649
GO:0042180	cellular ketone metabolic process	P	40	277	0.003734	PDE_05175, PDE_06679, PDE_00223, PDE_09601, PDE_07330, PDE_03738, PDE_01576, PDE_02153, PDE_07236, PDE_07217, PDE_05389, PDE_01008, PDE_04220, PDE_01899, PDE_03916, PDE_00542, PDE_06359, PDE_01714, PDE_08414, PDE_03392, PDE_08437, PDE_06117, PDE_06100, PDE_04799, PDE_06146, PDE_03241, PDE_08360, PDE_03308, PDE_04890, PDE_04828, PDE_06805, PDE_08219, PDE_05687, PDE_03644, PDE_02593, PDE_00816, PDE_06907, PDE_09141, PDE_03486, PDE_08111
GO:0044275	cellular carbohydrate catabolic process	P	13	49	0.004184	PDE_05931, PDE_07330, PDE_07259, PDE_08709, PDE_01008, PDE_04162, PDE_03036, PDE_09398, PDE_07688, PDE_02583, PDE_07938, PDE_04588, PDE_07918
GO:0043436	oxoacid metabolic process	P	39	271	0.004686	PDE_05175, PDE_06679, PDE_00223, PDE_09601, PDE_07330, PDE_03738, PDE_01576, PDE_02153, PDE_07236, PDE_07217, PDE_05389, PDE_01008, PDE_04220, PDE_01899, PDE_03916, PDE_00542, PDE_06359, PDE_01714, PDE_03392, PDE_08437, PDE_06117, PDE_06100, PDE_04799, PDE_06146, PDE_03241, PDE_08360, PDE_03308, PDE_04890, PDE_04828, PDE_06805, PDE_08219, PDE_05687, PDE_03644, PDE_02593, PDE_00816, PDE_06907, PDE_09141, PDE_03486, PDE_08111
GO:0019752	carboxylic acid metabolic process	P	39	271	0.004686	PDE_05175, PDE_06679, PDE_00223, PDE_09601, PDE_07330, PDE_03738, PDE_01576, PDE_02153, PDE_07236, PDE_07217, PDE_05389, PDE_01008, PDE_04220, PDE_01899, PDE_03916, PDE_00542, PDE_06359, PDE_01714, PDE_03392, PDE_08437, PDE_06117, PDE_06100, PDE_04799, PDE_06146, PDE_03241, PDE_08360, PDE_03308, PDE_04890, PDE_04828, PDE_06805, PDE_08219, PDE_05687, PDE_03644, PDE_02593, PDE_00816, PDE_06907, PDE_09141, PDE_03486, PDE_08111

GO:0006082	organic acid metabolic process	P	39	273	0.0054	PDE_05175, PDE_06679, PDE_00223, PDE_09601, PDE_07330, PDE_03738, PDE_01576, PDE_02153, PDE_07236, PDE_07217, PDE_05389, PDE_01008, PDE_04220, PDE_01899, PDE_03916, PDE_00542, PDE_06359, PDE_01714, PDE_03392, PDE_08437, PDE_06117, PDE_06100, PDE_04799, PDE_06146, PDE_03241, PDE_08360, PDE_03308, PDE_04890, PDE_04828, PDE_06805, PDE_08219, PDE_05687, PDE_03644, PDE_02593, PDE_00816, PDE_06907, PDE_09141, PDE_03486, PDE_08111
GO:0003824	catalytic activity	F	294	3382	0.005922	PDE_06615, PDE_05175, PDE_06626, PDE_05183, PDE_05931, PDE_05194, PDE_05193, PDE_05198, PDE_03828, PDE_05121, PDE_05953, PDE_05146, PDE_06679, PDE_05156, PDE_04490, PDE_03857, PDE_06697, PDE_09688, PDE_05103, PDE_04478, PDE_00285, PDE_00223, PDE_00222, PDE_02317, PDE_00251, PDE_08094, PDE_04540, PDE_01690, PDE_02298, PDE_09601, PDE_09604, PDE_08070, PDE_09608, PDE_04504, PDE_00192, PDE_02244, PDE_01610, PDE_07330, PDE_01651, PDE_08857, PDE_05046, PDE_05026, PDE_07259, PDE_05002, PDE_07279, PDE_00398, PDE_03738, PDE_00347, PDE_01576, PDE_01584, PDE_09720, PDE_04410, PDE_08758, PDE_02189, PDE_09735, PDE_09757, PDE_02152, PDE_02153, PDE_07236, PDE_05998, PDE_07217, PDE_07214, PDE_08722, PDE_01540, PDE_09704, PDE_09701, PDE_05097, PDE_09710, PDE_01529, PDE_08709, PDE_06421, PDE_04270, PDE_04273, PDE_06441, PDE_05390, PDE_03147, PDE_05389, PDE_06439, PDE_01008, PDE_03114, PDE_03108, PDE_00449, PDE_00473, PDE_04220, PDE_09487, PDE_05316, PDE_02101, PDE_02102, PDE_09467, PDE_06473, PDE_05349, PDE_03192, PDE_08681, PDE_02929, PDE_02033, PDE_02947, PDE_02010, PDE_08639, PDE_02974, PDE_07531, PDE_02992, PDE_01899, PDE_08616, PDE_01830, PDE_07593, PDE_01858, PDE_04151, PDE_04152, PDE_06306, PDE_06309, PDE_03014, PDE_04162, PDE_06322, PDE_03036, PDE_04168, PDE_04182, PDE_00502, PDE_00506, PDE_05248, PDE_00507, PDE_04193, PDE_03926, PDE_00579, PDE_03910, PDE_03916, PDE_03010, PDE_00542, PDE_06359, PDE_08594, PDE_09593, PDE_03978, PDE_05210, PDE_02828, PDE_09532, PDE_08560, PDE_02817, PDE_02857, PDE_02886, PDE_01750, PDE_06215, PDE_09218, PDE_09223, PDE_09226, PDE_09207, PDE_06231, PDE_09278, PDE_09279, PDE_09267, PDE_09260, PDE_08412, PDE_08414, PDE_03360, PDE_09295, PDE_03399, PDE_08465, PDE_03392, PDE_05506, PDE_08437, PDE_03408, PDE_08484, PDE_05427, PDE_04907, PDE_08476, PDE_07782, PDE_02774, PDE_03437, PDE_03439, PDE_05445, PDE_07794, PDE_03444, PDE_02760, PDE_02789, PDE_02756, PDE_00615, PDE_01256, PDE_06985, PDE_01261, PDE_06117, PDE_06100, PDE_09353, PDE_01044, PDE_04799, PDE_06146, PDE_09398, PDE_00752, PDE_03241, PDE_08313, PDE_03287, PDE_08366,

						PDE_08360, PDE_04805, PDE_02682, PDE_07688, PDE_03308, PDE_03312, PDE_07667, PDE_07668, PDE_01109, PDE_02635, PDE_06179, PDE_04061, PDE_04890, PDE_04894, PDE_04828, PDE_04085, PDE_04859, PDE_06023, PDE_00864, PDE_09810, PDE_00013, PDE_00014, PDE_00015, PDE_00016, PDE_09821, PDE_07118, PDE_06805, PDE_07124, PDE_07136, PDE_05727, PDE_08215, PDE_08219, PDE_05737, PDE_09083, PDE_09082, PDE_01983, PDE_03573, PDE_03672, PDE_05687, PDE_05694, PDE_01924, PDE_02549, PDE_08270, PDE_03644, PDE_03617, PDE_02583, PDE_02592, PDE_02593, PDE_07938, PDE_07933, PDE_07944, PDE_07945, PDE_04703, PDE_06751, PDE_04712, PDE_00816, PDE_04768, PDE_06770, PDE_06067, PDE_06771, PDE_02514, PDE_01467, PDE_02504, PDE_02509, PDE_09135, PDE_06907, PDE_09131, PDE_04574, PDE_00987, PDE_09141, PDE_07928, PDE_06944, PDE_04588, PDE_07918, PDE_06951, PDE_01285, PDE_07013, PDE_09984, PDE_09173, PDE_09988, PDE_03452, PDE_03486, PDE_09964, PDE_09969, PDE_05806, PDE_01300, PDE_01302, PDE_03542, PDE_08980, PDE_02418, PDE_07897, PDE_02414, PDE_08183, PDE_03572, PDE_08111, PDE_02452, PDE_08919, PDE_01385, PDE_01380, PDE_00935, PDE_00076, PDE_00917, PDE_04624, PDE_07895, PDE_01324
GO:0006412	translation	P	38	266	0.006415	PDE_03807, PDE_05983, PDE_06679, PDE_05108, PDE_01695, PDE_05026, PDE_04360, PDE_03752, PDE_04327, PDE_03780, PDE_09720, PDE_08757, PDE_01824, PDE_05389, PDE_00406, PDE_01817, PDE_05316, PDE_02916, PDE_03178, PDE_05253, PDE_05203, PDE_00629, PDE_04939, PDE_02793, PDE_02754, PDE_07774, PDE_08360, PDE_02649, PDE_00734, PDE_04897, PDE_04828, PDE_06805, PDE_08219, PDE_03668, PDE_02599, PDE_06907, PDE_00987, PDE_03486
GO:0008152	metabolic process	P	300	3475	0.007788	PDE_06615, PDE_05175, PDE_06626, PDE_03807, PDE_05183, PDE_05931, PDE_05194, PDE_05193, PDE_05198, PDE_03828, PDE_05121, PDE_05953, PDE_05983, PDE_05146, PDE_06679, PDE_05156, PDE_03857, PDE_09688, PDE_05103, PDE_05108, PDE_04478, PDE_00285, PDE_00223, PDE_00222, PDE_00251, PDE_08094, PDE_04540, PDE_01690, PDE_01695, PDE_02298, PDE_09601, PDE_08070, PDE_04504, PDE_02244, PDE_07342, PDE_01610, PDE_07330, PDE_08857, PDE_05063, PDE_05070, PDE_05046, PDE_05026, PDE_07259, PDE_07279, PDE_04360, PDE_03752, PDE_00398, PDE_03738, PDE_04327, PDE_03780, PDE_00347, PDE_01576, PDE_01584, PDE_09720, PDE_09719, PDE_08758, PDE_08757, PDE_02189, PDE_09735, PDE_09757, PDE_02152, PDE_02153, PDE_07236, PDE_05998, PDE_07217, PDE_01540, PDE_09704, PDE_09701, PDE_05097, PDE_09710, PDE_08709, PDE_04270, PDE_04273, PDE_00412, PDE_01824, PDE_06441, PDE_05390, PDE_03147, PDE_05389, PDE_00406, PDE_01817,

						PDE_06439, PDE_01008, PDE_03114, PDE_00449, PDE_00473, PDE_04220, PDE_05316, PDE_02101, PDE_02102, PDE_09467, PDE_02916, PDE_03178, PDE_06473, PDE_05349, PDE_03192, PDE_08681, PDE_02929, PDE_02947, PDE_08639, PDE_08629, PDE_02974, PDE_07531, PDE_01899, PDE_08616, PDE_07593, PDE_07580, PDE_01858, PDE_04151, PDE_04152, PDE_06306, PDE_06309, PDE_03014, PDE_04162, PDE_06322, PDE_03036, PDE_04182, PDE_05253, PDE_00502, PDE_00506, PDE_05248, PDE_00507, PDE_04193, PDE_03926, PDE_00579, PDE_03916, PDE_03010, PDE_00542, PDE_06359, PDE_08594, PDE_09593, PDE_05203, PDE_03978, PDE_05210, PDE_02828, PDE_09532, PDE_08560, PDE_02817, PDE_02857, PDE_07448, PDE_02886, PDE_01750, PDE_01714, PDE_06215, PDE_09218, PDE_09223, PDE_09226, PDE_09207, PDE_01190, PDE_09278, PDE_09279, PDE_09267, PDE_09260, PDE_00629, PDE_08412, PDE_08414, PDE_03360, PDE_09295, PDE_08465, PDE_03392, PDE_08437, PDE_03408, PDE_04939, PDE_08484, PDE_05427, PDE_08476, PDE_07782, PDE_02774, PDE_03439, PDE_05445, PDE_07794, PDE_03444, PDE_02793, PDE_02754, PDE_00615, PDE_07774, PDE_01256, PDE_07722, PDE_01261, PDE_06117, PDE_06100, PDE_01044, PDE_04799, PDE_06146, PDE_09398, PDE_00752, PDE_03241, PDE_08313, PDE_03287, PDE_08366, PDE_08360, PDE_04805, PDE_02682, PDE_07688, PDE_03308, PDE_05565, PDE_03312, PDE_07674, PDE_07667, PDE_07668, PDE_02649, PDE_01109, PDE_00734, PDE_06179, PDE_04061, PDE_04890, PDE_04894, PDE_04897, PDE_04828, PDE_04085, PDE_04859, PDE_06023, PDE_09810, PDE_00013, PDE_00014, PDE_00015, PDE_00016, PDE_06805, PDE_07124, PDE_07136, PDE_02492, PDE_05727, PDE_08215, PDE_08219, PDE_05737, PDE_09083, PDE_09082, PDE_01983, PDE_03573, PDE_03672, PDE_05687, PDE_05694, PDE_01924, PDE_03668, PDE_02549, PDE_08270, PDE_03644, PDE_03617, PDE_02599, PDE_05652, PDE_02583, PDE_02592, PDE_02593, PDE_07938, PDE_07933, PDE_07944, PDE_07945, PDE_04703, PDE_06751, PDE_04712, PDE_00816, PDE_04768, PDE_06770, PDE_06067, PDE_06771, PDE_02514, PDE_01468, PDE_02504, PDE_02509, PDE_09135, PDE_06907, PDE_09131, PDE_06918, PDE_04574, PDE_00987, PDE_09141, PDE_06948, PDE_07928, PDE_06944, PDE_04588, PDE_07918, PDE_06951, PDE_07013, PDE_09984, PDE_09988, PDE_03452, PDE_09961, PDE_03486, PDE_09969, PDE_05806, PDE_01302, PDE_03542, PDE_08980, PDE_08948, PDE_02418, PDE_07897, PDE_08183, PDE_03572, PDE_08111, PDE_02452, PDE_03511, PDE_08919, PDE_01385, PDE_01380, PDE_00933, PDE_00076, PDE_00917, PDE_04626, PDE_07895, PDE_01324
GO:0045490	pectin catabolic process	P	6	12	0.0085	PDE_05931, PDE_07259, PDE_08709, PDE_04162, PDE_02583, PDE_07938

GO:0045488	pectin metabolic process	P	6	12	0.0085	PDE_05931, PDE_07259, PDE_08709, PDE_04162, PDE_02583, PDE_07938
GO:0030529	ribonucleoprotein complex	C	35	242	0.00881	PDE_03807, PDE_05983, PDE_05108, PDE_01695, PDE_02298, PDE_08855, PDE_05026, PDE_04327, PDE_03780, PDE_08758, PDE_08757, PDE_02153, PDE_01824, PDE_00406, PDE_01817, PDE_05316, PDE_02916, PDE_03178, PDE_05253, PDE_05203, PDE_09553, PDE_00629, PDE_03408, PDE_04939, PDE_02793, PDE_02754, PDE_07774, PDE_02649, PDE_00734, PDE_04897, PDE_03668, PDE_02599, PDE_00825, PDE_00106, PDE_08174
GO:0009308	amine metabolic process	P	35	243	0.009292	PDE_05175, PDE_06679, PDE_00223, PDE_09601, PDE_03738, PDE_01576, PDE_07236, PDE_07217, PDE_05389, PDE_04220, PDE_03916, PDE_00542, PDE_06359, PDE_01714, PDE_03392, PDE_08437, PDE_06117, PDE_06100, PDE_04799, PDE_06146, PDE_03241, PDE_08360, PDE_03308, PDE_04890, PDE_04828, PDE_06805, PDE_08219, PDE_05687, PDE_03644, PDE_02593, PDE_00816, PDE_06771, PDE_06907, PDE_09141, PDE_08111
GO:0071840	cellular component organization or biogenesis	P	39	282	0.009292	PDE_05931, PDE_05147, PDE_04478, PDE_00222, PDE_02317, PDE_08094, PDE_02298, PDE_07259, PDE_00362, PDE_09704, PDE_01529, PDE_08709, PDE_02101, PDE_06306, PDE_04162, PDE_05210, PDE_02886, PDE_00752, PDE_02682, PDE_07674, PDE_00898, PDE_00014, PDE_03573, PDE_02583, PDE_07938, PDE_06067, PDE_02509, PDE_00132, PDE_07013, PDE_09988, PDE_03486, PDE_09966, PDE_02418, PDE_07897, PDE_03572, PDE_08174, PDE_08919, PDE_07819, PDE_07895
GO:0005996	monosaccharide metabolic process	P	15	69	0.010271	PDE_07330, PDE_01540, PDE_05097, PDE_03147, PDE_01008, PDE_02929, PDE_03036, PDE_09398, PDE_07688, PDE_00016, PDE_01924, PDE_04588, PDE_07918, PDE_09988, PDE_07897
GO:0016837	carbon-oxygen lyase activity, acting on polysaccharides	F	4	5	0.010396	PDE_05931, PDE_07259, PDE_01467, PDE_01385
GO:0044247	cellular polysaccharide catabolic process	P	6	13	0.013113	PDE_05931, PDE_07259, PDE_08709, PDE_04162, PDE_02583, PDE_07938
GO:0000097	sulfur amino acid biosynthetic process	P	7	18	0.013486	PDE_05175, PDE_01576, PDE_07236, PDE_04220, PDE_01714, PDE_04799, PDE_05687
GO:0016162	cellulose 1,4-beta-cellobiosidase activity	F	3	3	0.027912	PDE_05445, PDE_07124, PDE_07945
GO:0043228	non-membrane-bounded	C	40	310	0.02951	PDE_03807, PDE_05983, PDE_05147, PDE_05108, PDE_02317, PDE_01695, PDE_02298, PDE_05026, PDE_04327,

	organelle					PDE_03780, PDE_08758, PDE_08757, PDE_02153, PDE_09704, PDE_01824, PDE_00406, PDE_01817, PDE_05316, PDE_02916, PDE_03178, PDE_05253, PDE_05203, PDE_00629, PDE_04939, PDE_02793, PDE_02754, PDE_07774, PDE_02649, PDE_00734, PDE_04897, PDE_03668, PDE_02599, PDE_00825, PDE_02509, PDE_00132, PDE_00106, PDE_03486, PDE_09966, PDE_08174, PDE_07819
GO:0043232	intracellular non-membrane-bounded organelle	C	40	310	0.02951	PDE_03807, PDE_05983, PDE_05147, PDE_05108, PDE_02317, PDE_01695, PDE_02298, PDE_05026, PDE_04327, PDE_03780, PDE_08758, PDE_08757, PDE_02153, PDE_09704, PDE_01824, PDE_00406, PDE_01817, PDE_05316, PDE_02916, PDE_03178, PDE_05253, PDE_05203, PDE_00629, PDE_04939, PDE_02793, PDE_02754, PDE_07774, PDE_02649, PDE_00734, PDE_04897, PDE_03668, PDE_02599, PDE_00825, PDE_02509, PDE_00132, PDE_00106, PDE_03486, PDE_09966, PDE_08174, PDE_07819
GO:0044281	small molecule metabolic process	P	75	692	0.033602	PDE_05175, PDE_06626, PDE_05146, PDE_06679, PDE_03857, PDE_00223, PDE_09601, PDE_07330, PDE_05063, PDE_07279, PDE_03738, PDE_01576, PDE_09720, PDE_09719, PDE_02153, PDE_07236, PDE_07217, PDE_01540, PDE_09704, PDE_09701, PDE_05097, PDE_04270, PDE_03147, PDE_05389, PDE_01008, PDE_00473, PDE_04220, PDE_02929, PDE_01899, PDE_03014, PDE_03036, PDE_03916, PDE_00542, PDE_06359, PDE_09593, PDE_01714, PDE_06215, PDE_09207, PDE_08414, PDE_03392, PDE_08437, PDE_05427, PDE_06117, PDE_06100, PDE_04799, PDE_06146, PDE_09398, PDE_03241, PDE_08360, PDE_07688, PDE_03308, PDE_04890, PDE_04828, PDE_00016, PDE_06805, PDE_08219, PDE_05687, PDE_01924, PDE_03644, PDE_02593, PDE_07944, PDE_00816, PDE_06771, PDE_06907, PDE_09141, PDE_04588, PDE_07918, PDE_09988, PDE_03486, PDE_05806, PDE_08948, PDE_07897, PDE_08111, PDE_03511, PDE_07895
GO:0008652	cellular amino acid biosynthetic process	P	18	103	0.036263	PDE_05175, PDE_00223, PDE_09601, PDE_01576, PDE_07236, PDE_04220, PDE_03916, PDE_00542, PDE_01714, PDE_08437, PDE_06100, PDE_04799, PDE_06146, PDE_03308, PDE_04890, PDE_05687, PDE_03644, PDE_00816
GO:0005737	cytoplasm	C	91	882	0.041863	PDE_06615, PDE_03807, PDE_03827, PDE_03828, PDE_05983, PDE_06679, PDE_05108, PDE_00223, PDE_01695, PDE_09601, PDE_01610, PDE_05070, PDE_05026, PDE_03752, PDE_04327, PDE_03780, PDE_01576, PDE_09720, PDE_08758, PDE_08757, PDE_02153, PDE_07217, PDE_07214, PDE_08717, PDE_01824, PDE_05389, PDE_00406, PDE_01817, PDE_00473, PDE_05316, PDE_09467, PDE_02916, PDE_03178, PDE_04229, PDE_06473, PDE_05349, PDE_08629, PDE_01899, PDE_01858, PDE_03014, PDE_05253, PDE_05248, PDE_03916, PDE_03004, PDE_00542, PDE_05203, PDE_02857, PDE_07448, PDE_06215, PDE_09260, PDE_00629, PDE_08412, PDE_04939, PDE_02793,

						PDE_02754, PDE_07774, PDE_09398, PDE_03251, PDE_08360, PDE_02649, PDE_04875, PDE_00734, PDE_04897, PDE_04828, PDE_09810, PDE_00014, PDE_06805, PDE_02492, PDE_08219, PDE_09059, PDE_03573, PDE_05694, PDE_03668, PDE_02599, PDE_05652, PDE_00816, PDE_00825, PDE_04768, PDE_09135, PDE_06907, PDE_00132, PDE_00106, PDE_04588, PDE_01285, PDE_00162, PDE_08976, PDE_08980, PDE_08174, PDE_03511, PDE_05751, PDE_04624
GO:0019321	pentose metabolic process	P	5	11	0.043663	PDE_02929, PDE_00016, PDE_07918, PDE_09988, PDE_07897
GO:0009086	methionine biosynthetic process	P	5	11	0.043663	PDE_05175, PDE_01576, PDE_07236, PDE_04799, PDE_05687
GO:0015926	glucosidase activity	F	8	28	0.045247	PDE_09710, PDE_06441, PDE_04151, PDE_04152, PDE_00579, PDE_03010, PDE_02583, PDE_03542
GO:0000096	sulfur amino acid metabolic process	P	7	22	0.046771	PDE_05175, PDE_01576, PDE_07236, PDE_04220, PDE_01714, PDE_04799, PDE_05687
Down-regulated in JU-A10-T relative to 114-2						
GO:0005506	iron ion binding	F	56	166	2.01E-05	PDE_05132, PDE_00298, PDE_05907, PDE_04530, PDE_08098, PDE_04527, PDE_01689, PDE_08009, PDE_05886, PDE_05885, PDE_08821, PDE_06706, PDE_02205, PDE_00370, PDE_03787, PDE_09748, PDE_02139, PDE_09762, PDE_07206, PDE_07207, PDE_01023, PDE_04265, PDE_04228, PDE_02071, PDE_08660, PDE_03956, PDE_00525, PDE_05239, PDE_06327, PDE_02802, PDE_07439, PDE_10010, PDE_10004, PDE_10003, PDE_10008, PDE_09230, PDE_04936, PDE_06295, PDE_01216, PDE_06972, PDE_01064, PDE_01070, PDE_05566, PDE_04016, PDE_04015, PDE_04025, PDE_01395, PDE_05708, PDE_01418, PDE_00811, PDE_02386, PDE_03490, PDE_08962, PDE_02454, PDE_02461, PDE_04632
GO:0020037	heme binding	F	43	115	2.01E-05	PDE_05907, PDE_04530, PDE_08098, PDE_01689, PDE_08009, PDE_05886, PDE_05885, PDE_08821, PDE_06706, PDE_02205, PDE_00370, PDE_09748, PDE_09762, PDE_07206, PDE_07207, PDE_04228, PDE_02071, PDE_08660, PDE_03956, PDE_00525, PDE_06327, PDE_02802, PDE_10010, PDE_10004, PDE_10003, PDE_10008, PDE_09230, PDE_04936, PDE_01216, PDE_06972, PDE_01064, PDE_01070, PDE_05566, PDE_04016, PDE_04015, PDE_04025, PDE_01395, PDE_05708, PDE_01418, PDE_00811, PDE_08962, PDE_02454, PDE_02461
GO:0046906	tetrapyrrole binding	F	43	116	2.01E-05	PDE_05907, PDE_04530, PDE_08098, PDE_01689, PDE_08009, PDE_05886, PDE_05885, PDE_08821, PDE_06706, PDE_02205, PDE_00370, PDE_09748, PDE_09762, PDE_07206, PDE_07207, PDE_04228, PDE_02071, PDE_08660,

						PDE_03956, PDE_00525, PDE_06327, PDE_02802, PDE_10010, PDE_10004, PDE_10003, PDE_10008, PDE_09230, PDE_04936, PDE_01216, PDE_06972, PDE_01064, PDE_01070, PDE_05566, PDE_04016, PDE_04015, PDE_04025, PDE_01395, PDE_05708, PDE_01418, PDE_00811, PDE_08962, PDE_02454, PDE_02461
GO:0055114	oxidation reduction	P	166	767	0.003193	PDE_05158, PDE_05132, PDE_05973, PDE_04495, PDE_02350, PDE_09681, PDE_00298, PDE_09693, PDE_03899, PDE_05907, PDE_00249, PDE_04530, PDE_08885, PDE_08098, PDE_04527, PDE_01689, PDE_09616, PDE_08009, PDE_05886, PDE_08814, PDE_08806, PDE_08821, PDE_08859, PDE_08042, PDE_06706, PDE_08847, PDE_08849, PDE_07286, PDE_07272, PDE_07278, PDE_02205, PDE_04366, PDE_06586, PDE_04376, PDE_00370, PDE_03787, PDE_02172, PDE_09748, PDE_09770, PDE_02139, PDE_09761, PDE_02128, PDE_09762, PDE_07232, PDE_07234, PDE_07226, PDE_07206, PDE_07208, PDE_07207, PDE_05363, PDE_01023, PDE_06414, PDE_03105, PDE_04218, PDE_04216, PDE_09498, PDE_09492, PDE_04265, PDE_04264, PDE_04228, PDE_06474, PDE_09453, PDE_02071, PDE_08630, PDE_08660, PDE_03956, PDE_00525, PDE_05239, PDE_03901, PDE_06396, PDE_03064, PDE_03073, PDE_06327, PDE_03974, PDE_03975, PDE_07439, PDE_01780, PDE_02881, PDE_10010, PDE_10004, PDE_10003, PDE_10008, PDE_09229, PDE_09230, PDE_01188, PDE_09239, PDE_00643, PDE_00646, PDE_08495, PDE_04936, PDE_06295, PDE_01220, PDE_01216, PDE_01217, PDE_06972, PDE_01238, PDE_01064, PDE_01070, PDE_01068, PDE_09342, PDE_00787, PDE_09367, PDE_01080, PDE_09380, PDE_03254, PDE_03282, PDE_05550, PDE_05548, PDE_07692, PDE_04020, PDE_05566, PDE_04016, PDE_04015, PDE_03316, PDE_04028, PDE_04025, PDE_02605, PDE_06017, PDE_09027, PDE_01395, PDE_06831, PDE_09047, PDE_09870, PDE_05708, PDE_01406, PDE_05675, PDE_08297, PDE_01413, PDE_01418, PDE_01482, PDE_00809, PDE_07956, PDE_07957, PDE_07139, PDE_06745, PDE_00811, PDE_06052, PDE_01451, PDE_09933, PDE_06915, PDE_00170, PDE_06955, PDE_01278, PDE_06939, PDE_02393, PDE_02386, PDE_02372, PDE_02368, PDE_02379, PDE_03468, PDE_03483, PDE_08966, PDE_08156, PDE_08906, PDE_08904, PDE_02461, PDE_00923, PDE_01384, PDE_01374, PDE_04605, PDE_00966, PDE_04629, PDE_04628, PDE_00968, PDE_04632, PDE_07852
GO:0016491	oxidoreductase activity	F	173	816	0.005864	PDE_05158, PDE_05943, PDE_05132, PDE_05973, PDE_04495, PDE_02350, PDE_09681, PDE_00298, PDE_09691, PDE_09693, PDE_03899, PDE_05907, PDE_00249, PDE_04530, PDE_08098, PDE_04527, PDE_01689, PDE_09616, PDE_08009, PDE_05886, PDE_05885, PDE_08814, PDE_08806, PDE_08821, PDE_08859, PDE_08042, PDE_06706, PDE_08847, PDE_08849, PDE_07286, PDE_07272, PDE_02205, PDE_04366, PDE_06586, PDE_04376, PDE_00370,

						PDE_03787, PDE_09714, PDE_02172, PDE_09748, PDE_09770, PDE_02139, PDE_09761, PDE_02128, PDE_09762, PDE_09758, PDE_07246, PDE_07232, PDE_07226, PDE_07206, PDE_07208, PDE_07207, PDE_01808, PDE_05363, PDE_01023, PDE_06412, PDE_04277, PDE_03105, PDE_04218, PDE_04216, PDE_09492, PDE_04265, PDE_04264, PDE_04228, PDE_06474, PDE_09453, PDE_02071, PDE_08630, PDE_08660, PDE_01701, PDE_03956, PDE_00525, PDE_05239, PDE_03901, PDE_06396, PDE_03064, PDE_03073, PDE_06327, PDE_03975, PDE_07439, PDE_01780, PDE_10004, PDE_10003, PDE_10002, PDE_10008, PDE_09229, PDE_09230, PDE_01188, PDE_09239, PDE_00643, PDE_00646, PDE_05500, PDE_08495, PDE_04936, PDE_06295, PDE_01220, PDE_01216, PDE_01217, PDE_06972, PDE_01238, PDE_01064, PDE_01070, PDE_01068, PDE_00799, PDE_09342, PDE_00787, PDE_09367, PDE_01080, PDE_09380, PDE_03254, PDE_03282, PDE_05550, PDE_05548, PDE_07692, PDE_04020, PDE_05566, PDE_04016, PDE_03316, PDE_04028, PDE_04025, PDE_00709, PDE_02605, PDE_06017, PDE_09027, PDE_06042, PDE_01395, PDE_06831, PDE_09047, PDE_09870, PDE_05708, PDE_01406, PDE_05675, PDE_01413, PDE_01418, PDE_01482, PDE_00809, PDE_07956, PDE_07957, PDE_07139, PDE_06745, PDE_01451, PDE_09933, PDE_06915, PDE_00111, PDE_00170, PDE_06955, PDE_01278, PDE_06939, PDE_02393, PDE_02386, PDE_09999, PDE_02372, PDE_02368, PDE_02379, PDE_03468, PDE_09194, PDE_08966, PDE_08156, PDE_02419, PDE_02454, PDE_08904, PDE_02461, PDE_01390, PDE_00923, PDE_01384, PDE_01374, PDE_04605, PDE_00966, PDE_04629, PDE_04628, PDE_00968, PDE_04632, PDE_07852
GO:0009055	electron carrier activity	F	37	126	0.049181	PDE_05132, PDE_00298, PDE_04530, PDE_01689, PDE_05886, PDE_08821, PDE_06706, PDE_08847, PDE_09714, PDE_09748, PDE_07206, PDE_07207, PDE_01808, PDE_04228, PDE_08660, PDE_03956, PDE_06327, PDE_09546, PDE_10010, PDE_10004, PDE_10003, PDE_10008, PDE_09230, PDE_04936, PDE_01216, PDE_06972, PDE_01064, PDE_01070, PDE_01068, PDE_04016, PDE_04015, PDE_04025, PDE_01395, PDE_01418, PDE_00811, PDE_02461, PDE_04632

Table S10. Transcription levels of genes involved in pentose metabolism, central metabolism and intracellular cellodextrin metabolism.

Gene ID		Function prediction	Transcription level (tags per million)		Change^a
114-2	JU-A10-T		114-2	JU-A10-T	
D-xylose metabolism					
PDE_02929	PDT_03086	aldose reductase	29.24	94.9	Up
PDE_05826	PDT_06059	xylitol dehydrogenase	68.68	134.23	
PDE_09158	PDT_09456	D-xylulose kinase	15.98	36.03	
L-arabinose metabolism					
PDE_00398	PDT_00406	L-arabinitol 4-dehydrogenase	52.7	161.19	Up
PDE_07136	PDT_07390	L-xylulose reductase	36.38	73.99	Up
Pentose phosphate pathway					
PDE_01924	PDT_02012	glucose-6-phosphate 1-dehydrogenase	25.16	224.18	Up
PDE_03036	PDT_03206	6-phosphogluconolactonase	84.32	207.67	Up
PDE_08859	PDT_09150	6-phosphogluconate dehydrogenase	484.84	118.55	Down
PDE_08816	PDT_09107	6-phosphogluconate dehydrogenase	16.32	0.55	
PDE_06557	PDT_06792	ribulose-phosphate 3-epimerase	73.1	69.04	
PDE_07918	PDT_08186	ribose 5-phosphate isomerase A	39.1	94.07	Up
PDE_03075	PDT_03245	ribose 5-phosphate isomerase B	0	0.83	
PDE_00194	PDT_00198	transketolase	127.84	236.55	
PDE_04193	PDT_04395	transketolase	130.9	287.17	Up
PDE_09398	PDT_09708	transaldolase	140.76	426.35	Up
Glycolysis					
PDE_03370	PDT_03559	glucokinase	13.26	9.08	
PDE_03592	PDT_03793	hexokinase	58.82	50.89	
PDE_00878	PDT_00914	hexokinase	13.94	1.65	
PDE_03526	PDT_03726	hexokinase	1.7	0	
PDE_09139	PDT_09437	glucokinase	3.06	2.75	
PDE_03736	PDT_03949	glucose-6-phosphate isomerase	22.78	14.85	
PDE_01271	PDT_01337	6-phosphofructokinase	35.02	45.94	
PDE_08481	PDT_08759	fructose-1,6-bisphosphatase	56.1	49.24	
PDE_04802	PDT_05028	fructose-bisphosphate aldolase	1046.18	920.64	
PDE_07330	PDT_07588	triosephosphate isomerase	137.02	335.03	Up
PDE_03074	PDT_03244	triosephosphate isomerase	16.66	14.03	
PDE_09952	PDT_10268	glyceraldehyde 3-phosphate dehydrogenase	1295.4	1998.06	
PDE_04588	PDT_04791	glyceraldehyde 3-phosphate dehydrogenase	0.68	29.98	Up
PDE_07158	PDT_07413	phosphoglycerate kinase	25.16	5.5	
PDE_04961	PDT_05192	phosphoglycerate mutase	122.74	177.42	
PDE_07305	PDT_07562	phosphoglycerate mutase	29.58	42.63	

PDE_03403	PDT_03596	phosphoglycerate mutase	27.54	38.51	
PDE_08991	PDT_09284	phosphoglycerate mutase	5.1	3.3	
PDE_02546	PDT_02669	enolase	239.36	128.73	
PDE_05188	PDT_05422	pyruvate kinase	87.04	106.45	
Citrate cycle					
PDE_02440	PDT_02555	pyruvate dehydrogenase E1 component subunit alpha	76.16	91.32	
PDE_01446	PDT_01525	pyruvate dehydrogenase E1 component subunit beta	22.78	19.8	
PDE_02153	PDT_02249	pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase)	189.04	624.39	Up
PDE_01946	PDT_02034	pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase)	67.32	68.22	
PDE_01700	PDT_01785	dihydrolipoamide dehydrogenase	113.22	156.51	
PDE_09135	PDT_09433	citrate synthase	375.7	814.46	Up
PDE_03487	PDT_03685	citrate synthase	80.92	68.77	
PDE_07922	PDT_08190	ATP-citrate synthase subunit 1	21.42	11.55	
PDE_07924	PDT_08192	ATP-citrate synthase subunit 2	51.34	12.65	Down
PDE_08183	PDT_08451	aconitate hydratase	7.48	118.83	Up
PDE_02592	PDT_02726	aconitate hydratase	53.38	262.69	Up
PDE_01899	PDT_01987	isocitrate dehydrogenase	132.26	495.66	Up
PDE_08580	PDT_08860	2-oxoglutarate dehydrogenase E1 component	83.3	69.32	
PDE_01492	PDT_01571	2-oxoglutarate dehydrogenase E2 component (dihydrolipoamide succinyltransferase)	209.78	147.71	
PDE_00668	PDT_00697	succinyl-CoA synthetase alpha subunit	6.46	21.45	
PDE_09282	PDT_09586	succinyl-CoA synthetase alpha subunit	127.5	142.21	
PDE_05762	PDT_05996	succinyl-CoA synthetase beta subunit	76.16	57.49	
PDE_01111	PDT_01156	succinyl-CoA synthetase beta subunit	1.7	0	
PDE_01985	PDT_02073	succinate dehydrogenase (ubiquinone) flavoprotein subunit	104.38	90.5	
PDE_01648	PDT_01732	succinate dehydrogenase (ubiquinone) flavoprotein subunit	257.72	358.41	
PDE_07264	PDT_07521	succinate dehydrogenase (ubiquinone) iron-sulfur protein	226.78	279.74	
PDE_00477	PDT_00494	succinate dehydrogenase (ubiquinone) membrane anchor subunit	73.78	41.53	

PDE_09828	PDT_10141	succinate dehydrogenase (ubiquinone) cytochrome b subunit	168.3	329.8	
PDE_03394	PDT_03587	fumarate hydratase	75.82	101.5	
PDE_02150	PDT_02246	malate dehydrogenase	879.58	1543.93	
PDE_01008	PDT_01049	malate dehydrogenase	2.72	318.25	Up
Intracellular cellodextrin metabolism					
PDE_00607	PDT_00629	cellodextrin/lactose transporter[b]	159.8	1531.83	Up
PDE_07257	PDT_07514	cellodextrin/lactose transporter	7.82	43.46	Up
PDE_00753	PDT_00784	cellodextrin/lactose transporter	366.52	1236.16	Up
PDE_02109	PDT_02206	cellodextrin/lactose transporter	4.42	1.41	
PDE_02900	PDT_03055	cellodextrin/lactose transporter	4.08	3.11	
PDE_04820	PDT_05046	cellodextrin/lactose transporter	7.48	0	
PDE_04857	PDT_05087	cellodextrin/lactose transporter	22.44	92.97	Up
PDE_08035	Not present	cellodextrin/lactose transporter	30.99	-	
PDE_09011	PDT_09305	cellodextrin/lactose transporter	11.9	0	
PDE_09395	PDT_09705	cellodextrin/lactose transporter	9.52	4.8	
PDE_09534	PDT_09846	cellodextrin/lactose transporter	1.02	0	
PDE_00579	PDT_00600	intracellular beta-glucosidase	892.84	9123.3	Up
PDE_09535	PDT_09847	intracellular beta-glucosidase	4.42	3.03	
PDE_04859	PDT_05089	intracellular beta-glucosidase	38.08	108.37	Up
PDE_02108	PDT_02205	intracellular beta-glucosidase	19.04	34.11	
PDE_03485	PDT_03683	intracellular beta-glucosidase	19.72	20.63	
PDE_04251	PDT_04455	intracellular beta-glucosidase	98.26	117.45	

[a] Significantly differential expression in JU-A10-T relative to 114-2 (FDR lower than 0.001).

[b] Cellodextrin transporter in fungi may also transport lactose and *vice versa*.

Table S11. KEGG annotation of amino acids biosynthesis-involved enzymes significantly up-regulated in JU-A10-T.

Gene ID		KEGG Orthology	KEGG Pathway	Transcription level (tags per million)	
114-2	**JU-A10-T**			**114-2**	**JU-A10-T**
PDE_00223	PDT_00227	K13830,pentafunctional AROM polypeptide [EC:4.2.3.4 4.2.1.10 1.1.1.25 2.7.1.71 2.5.1.19]	Phenylalanine, tyrosine and tryptophan biosynthesis	103.02	320.45
PDE_00542	PDT_00562	K00052,3-isopropylmalate dehydrogenase [EC:1.1.1.85]	Valine, leucine and isoleucine biosynthesis	31.28	95.72
PDE_00816	PDT_00849	K00765,ATP phosphoribosyltransferase [EC:2.4.2.17]	Histidine metabolism	20.74	50.89
PDE_01576	PDT_01657	K00958,sulfate adenylyltransferase [EC:2.7.7.4]	Sulfur metabolism;Purine metabolism;Selenocompound metabolism	42.84	316.6
PDE_03644	PDT_03852	K01653,acetolactate synthase I/III small subunit [EC:2.2.1.6]	Valine, leucine and isoleucine biosynthesis;Pantothenate and CoA biosynthesis;Butanoate metabolism;C5-Branched dibasic acid metabolism	92.82	237.38
PDE_03916	PDT_04140	K01655,homocitrate synthase [EC:2.3.3.14]	Lysine biosynthesis;Pyruvate metabolism	70.72	149.91
PDE_04061	PDT_04264	K00147,glutamate-5-semialdehyde dehydrogenase [EC:1.2.1.41]	Arginine and proline metabolism	21.76	155.14
PDE_04220	PDT_04423	K01738,cysteine synthase A [EC:2.5.1.47]	Sulfur metabolism;Cysteine and methionine metabolism	83.98	241.78
PDE_04799	PDT_05025	K00003,homoserine dehydrogenase [EC:1.1.1.3]	Lysine biosynthesis;Cysteine and methionine metabolism;Glycine, serine and threonine metabolism	9.18	63.81
PDE_04890	PDT_05120	K01694,tryptophan synthase [EC:4.2.1.20]	Glycine, serine and threonine metabolism;Phenylalanine, tyrosine and tryptophan biosynthesis	39.1	240.96
PDE_05175	PDT_05409	K00549,5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase [EC:2.1.1.14]	Cysteine and methionine metabolism;Selenocompound metabolism	3.74	25.86
PDE_05687	PDT_05921	K01760,cystathionine beta-lyase [EC:4.4.1.8]	Sulfur metabolism;Cysteine and methionine metabolism;Selenocompound metabolism	36.04	74.27

PDE_06100	PDT_06329	K03785,3-dehydroquinate dehydratase I [EC:4.2.1.10]	Phenylalanine, tyrosine and tryptophan biosynthesis	60.86	144.96
PDE_06146	PDT_06378	K01953,asparagine synthase (glutamine-hydrolysing) [EC:6.3.5.4]	Alanine, aspartate and glutamate metabolism;Nitrogen metabolism	35.36	322.37
PDE_07236	PDT_07492	K00860,adenylylsulfate kinase [EC:2.7.1.25]	Sulfur metabolism;Purine metabolism	14.28	147.16
PDE_08437	PDT_08712	K00143,L-aminoadipate-semialdehyde dehydrogenase [EC:1.2.1.31]	Lysine biosynthesis;Lysine degradation	39.78	273.41
PDE_09601	PDT_09914	K00620,glutamate N-acetyltransferase / amino-acid N-acetyltransferase [EC:2.3.1.35 2.3.1.1]	Arginine and proline metabolism	53.04	112.23

Table S12. Transcription levels of genes involved in protein folding in *P. decumbens* 114-2 and JU-A10-T.

Gene ID		**Function prediction**[a]	**Transcription level (tags per million)**		**Change**[b]
114-2	**JU-A10-T**		**114-2**	**JU-A10-T**	
PDE_06215	PDT_06448	protein disulfide-isomerase A1 (PdiA)	537.2	3204.21	Up
PDE_07464	PDT_07726	protein disulfide-isomerase A6	0	0	
PDE_02993	PDT_03160	protein disulfide-isomerase A6	242.76	390.86	
PDE_03829	PDT_04047	protein disulfide-isomerase	76.5	106.45	
PDE_06501	PDT_06735	endoplasmic oxidoreductin-1	40.12	43.74	
PDE_07994	PDT_08262	FAD synthetase	11.9	7.7	
PDE_00166	PDT_00169	GTP cyclohydrolase II	40.8	15.68	
PDE_04627	PDT_04834	uracil-regulated protein 1	145.18	100.95	
PDE_03322	PDT_03503	FAD-containing monooxygenase EthA	100.3	80.87	
PDE_02526	PDT_02648	uncharacterized J domain-containing protein	41.82	57.21	
PDE_04145	PDT_04346	DnaJ-related protein SCJ1	124.1	16.23	Down
PDE_08629	PDT_08911	calnexin	71.74	479.16	Up
PDE_03689	PDT_03898	peptidyl-prolyl cis-trans isomerase B (cyclophilin B)	717.74	41.81	
PDE_05349	PDT_05586	FK506-binding protein 2	39.1	190.34	Up
PDE_08980	PDT_09273	molecular chaperone BipA	863.94	2352.89	
PDE_00412	PDT_00420	Hsp70 family chaperone Lhs1/Orp150	42.16	126.25	Up

[a] Proteins are annotated according to the results in *Aspergillus niger* CBS 513.88 [1].

[b] Significantly differential expression in JU-A10-T relative to 114-2 (FDR lower than 0.001).

Reference

1. Pel HJ, de Winde JH, Archer DB, Dyer PS, Hofmann G, et al. (2007) Genome sequencing and analysis of the versatile cell factory *Aspergillus niger* CBS 513.88. Nat Biotechnol 25: 221-231.

Table S13. KEGG annotation of oxidoreductases significantly down-regulated in JU-A10-T.

Gene ID		**KEGG annotation**		**Transcription level (tags per million)**		**Amino acid metabolism involved**
114-2	**JU-A10-T**	**Orthology**	**Pathway**	**114-2**	**JU-A10-T**	
PDE_00111	PDT_00113	K00100,E1.1.1.-	Fructose and mannose metabolism;Bisphenol degradation;Linoleic acid metabolism;Chloroalkane and chloroalkene degradation;Butanoate metabolism	54.4	10.45	
PDE_00170	PDT_00173	K00540,E1.-.-.-	-	60.86	6.88	
PDE_00249	PDT_00254	-	-	113.56	36.58	
PDE_00298	PDT_00305	K05920,E1.16.1.-	-	40.12	4.95	
PDE_00370	PDT_00378	K00362,nitrite reductase (NAD(P)H) large subunit [EC:1.7.1.4]	Nitrogen metabolism	92.14	4.4	
PDE_00525	PDT_00544	K00517,E1.14.-.-	Bisphenol degradation;Polycyclic aromatic hydrocarbon degradation;Aminobenzoate degradation;Limonene and pinene degradation;Stilbenoid, diarylheptanoid and gingerol biosynthesis	343.06	36.31	
PDE_00643	PDT_00671	K10256,omega-6 fatty acid desaturase (delta-12 desaturase) [EC:1.14.19.-]	Biosynthesis of unsaturated fatty acids	44.2	7.7	
PDE_00646	PDT_00674	K00276,primary-amine oxidase [EC:1.4.3.21]	Glycine, serine and threonine metabolism;Tyrosine metabolism;Phenylalanine metabolism;beta-Alanine metabolism;Isoquinoline alkaloid biosynthesis;Tropane, piperidine and pyridine alkaloid biosynthesis	23.46	1.65	Yes
PDE_00709	PDT_00739	-	-	58.82	17.6	
PDE_00787	PDT_00820	K07119,K07119	-	116.96	31.91	
PDE_00799	PDT_00832	K00059,3-oxoacyl-[acyl-carrier	Fatty acid biosynthesis;Biosynthesis of unsaturated fatty acids	103.36	7.43	

		protein] reductase [EC:1.1.1.100]				
PDE_00809	PDT_00842	K00540,E1.-.-.-	-	18.7	0	
PDE_00923	PDT_00960	K03843,alpha-1,3/alpha-1,6-mannosyltransferase [EC:2.4.1.132 2.4.1.-]	-	121.04	1.65	
PDE_00966	PDT_01005	K00108,choline dehydrogenase [EC:1.1.99.1]	Glycine, serine and threonine metabolism	136.34	51.16	Yes
PDE_00968	PDT_01007	K00130,betaine-aldehyde dehydrogenase [EC:1.2.1.8]	Glycine, serine and threonine metabolism	45.56	9.08	Yes
PDE_01023	PDT_01064	K00227,lathosterol oxidase [EC:1.14.21.6]	Steroid biosynthesis	165.58	36.86	
PDE_01064	PDT_01106	K00517,E1.14.-.-	Bisphenol degradation;Polycyclic aromatic hydrocarbon degradation;Aminobenzoate degradation;Limonene and pinene degradation;Stilbenoid, diarylheptanoid and gingerol biosynthesis	27.54	0	
PDE_01068	PDT_01110	K00492,E1.14.13.-	Histidine metabolism;Chlorocyclohexane and chlorobenzene degradation;Bisphenol degradation;Toluene degradation;Polycyclic aromatic hydrocarbon degradation;Naphthalene degradation;Aminobenzoate degradation;Limonene and pinene degradation	129.54	3.3	Yes
PDE_01070	PDT_01112	K00517,E1.14.-.-	Bisphenol degradation;Polycyclic aromatic hydrocarbon degradation;Aminobenzoate degradation;Limonene and pinene degradation;Stilbenoid, diarylheptanoid and gingerol biosynthesis	34.68	0	
PDE_01080	PDT_01123	K00122,formate dehydrogenase [EC:1.2.1.2]	Glyoxylate and dicarboxylate metabolism;Methane metabolism	1574.88	116.35	
PDE_01188	PDT_01245	-	-	761.94	10.45	
PDE_01216	PDT_01274	K00517,E1.14.-.-	Bisphenol degradation;Polycyclic aromatic hydrocarbon degradation;Aminobenzoate degradation;Limonene and pinene degradation;Stilbenoid, diarylheptanoid and gingerol biosynthesis	127.84	0.55	

PDE_01217	PDT_01275	K00667,fatty acid synthase subunit alpha, fungi type [EC:2.3.1.86]	Fatty acid biosynthesis	608.6	0	
PDE_01220	PDT_01278	K00668,fatty acid synthase subunit beta, fungi type [EC:2.3.1.86]	Fatty acid biosynthesis	550.8	146.06	
PDE_01238	PDT_01296	-	-	21.76	2.2	
PDE_01278	PDT_01344	K13953,alcohol dehydrogenase, propanol-preferring [EC:1.1.1.1]	Glycolysis / Gluconeogenesis;Fatty acid metabolism;Tyrosine metabolism;Chloroalkane and chloroalkene degradation;Naphthalene degradation;Retinol metabolism;Metabolism of xenobiotics by cytochrome P450;Drug metabolism - cytochrome P450	56.1	0	Yes
PDE_01374	PDT_01451	K00155,E1.2.1.-	Geraniol degradation;Naphthalene degradation;Limonene and pinene degradation	95.54	29.16	
PDE_01384	PDT_01461	K00281,glycine dehydrogenase [EC:1.4.4.2]	Glycine, serine and threonine metabolism	92.48	23.66	Yes
PDE_01390	PDT_01467	K00540,E1.-.-.-	-	52.02	1.1	
PDE_01395	PDT_01472	K00517,E1.14.-.-	Bisphenol degradation;Polycyclic aromatic hydrocarbon degradation;Aminobenzoate degradation;Limonene and pinene degradation;Stilbenoid, diarylheptanoid and gingerol biosynthesis	90.1	33.01	
PDE_01406	PDT_01483	-	-	37.06	0	
PDE_01413	PDT_01490	K00108,choline dehydrogenase [EC:1.1.99.1]	Glycine, serine and threonine metabolism	38.08	0	Yes
PDE_01418	PDT_01496	K00517,E1.14.-.-	Bisphenol degradation;Polycyclic aromatic hydrocarbon degradation;Aminobenzoate degradation;Limonene and pinene degradation;Stilbenoid, diarylheptanoid and gingerol biosynthesis	44.54	3.85	
PDE_01451	PDT_01530	K00667,fatty acid synthase subunit alpha, fungi type [EC:2.3.1.86]	Fatty acid biosynthesis	95.2	26.96	
PDE_01482	PDT_01561	K00016,L-lactate dehydrogenase	Glycolysis / Gluconeogenesis;Cysteine and methionine	17	0	Yes

		[EC:1.1.1.27]	metabolism;Pyruvate metabolism;Propanoate metabolism			
PDE_01689	PDT_01773	K14338,cytochrome P450 / NADPH-cytochrome P450 reductase [EC:1.14.14.1 1.6.2.4]	Fatty acid metabolism;Tryptophan metabolism;Aminobenzoate degradation	23.46	2.75	Yes
PDE_01701	PDT_01786	K07078,unclassified	-	19.38	0.83	
PDE_01780	PDT_01866	K00135,succinate-semialdehyde dehydrogenase (NADP+) [EC:1.2.1.16]	Alanine, aspartate and glutamate metabolism;Tyrosine metabolism;Butanoate metabolism	275.74	16.78	Yes
PDE_01808	PDT_01896	K03671,thioredoxin 1	-	439.96	29.98	
PDE_02071	PDT_02166	K00463,indoleamine 2,3-dioxygenase [EC:1.13.11.52]	Tryptophan metabolism;African trypanosomiasis	107.1	11.28	Yes
PDE_02128	PDT_02224	-	-	78.2	4.4	
PDE_02139	PDT_02235	K00540,E1.-.-.-	-	18.36	0	
PDE_02172	PDT_02269	K00012,UDPglucose 6-dehydrogenase [EC:1.1.1.22]	Pentose and glucuronate interconversions;Ascorbate and aldarate metabolism;Starch and sucrose metabolism;Amino sugar and nucleotide sugar metabolism	34.68	7.7	
PDE_02205	PDT_02303	K00507,stearoyl-CoA desaturase (delta-9 desaturase) [EC:1.14.19.1]	Biosynthesis of unsaturated fatty acids;PPAR signaling pathway	187	23.93	
PDE_02350	PDT_02460	K00100,E1.1.1.-	Fructose and mannose metabolism;Bisphenol degradation;Linoleic acid metabolism;Chloroalkane and chloroalkene degradation;Butanoate metabolism	85.34	12.93	
PDE_02368	PDT_02478	K00540,E1.-.-.-	-	102.34	15.13	
PDE_02372	PDT_02483	K00228,coproporphyrinogen III oxidase [EC:1.3.3.3]	Porphyrin and chlorophyll metabolism	320.62	47.59	
PDE_02379	PDT_02490	K03283,heat shock 70kDa protein 1/8	Spliceosome;MAPK signaling pathway;Protein processing in endoplasmic reticulum;Endocytosis;Antigen processing and presentation;Legionellosis;Toxoplasmosis;Measles;Influenza	1965.88	274.79	

			A;Epstein-Barr virus infection			
PDE_02386	PDT_02500	K00264,glutamate synthase (NADPH/NADH) [EC:1.4.1.13 1.4.1.14]	Alanine, aspartate and glutamate metabolism;Nitrogen metabolism	69.7	17.88	Yes
PDE_02393	PDT_02507	K00309,E1.5.3.-	-	145.52	11.28	
PDE_02419	PDT_02534	K00540,E1.-.-.-	-	37.4	7.43	
PDE_02454	PDT_02570	K00463,indoleamine 2,3-dioxygenase [EC:1.13.11.52]	Tryptophan metabolism;African trypanosomiasis	115.6	1.65	Yes
PDE_02461	PDT_02579	K00360,nitrate reductase (NADH) [EC:1.7.1.1]	Nitrogen metabolism	75.14	5.23	
PDE_02605	PDT_02741	-	-	78.54	8.25	
PDE_03064	PDT_03234	K00121,S-(hydroxymethyl)glutathione dehydrogenase / alcohol dehydrogenase [EC:1.1.1.284 1.1.1.1]	Glycolysis / Gluconeogenesis;Fatty acid metabolism;Tyrosine metabolism;Chloroalkane and chloroalkene degradation;Naphthalene degradation;Methane metabolism;Retinol metabolism;Metabolism of xenobiotics by cytochrome P450;Drug metabolism - cytochrome P450	396.78	122.13	Yes
PDE_03073	PDT_03243	K00226,dihydroorotate oxidase [EC:1.3.3.1]	Pyrimidine metabolism	34	2.48	
PDE_03105	PDT_03275	K00297,methylenetetrahydrofolate reductase (NADPH) [EC:1.5.1.20]	One carbon pool by folate;Methane metabolism;Carbon fixation pathways in prokaryotes	62.56	2.2	
PDE_03254	PDT_03433	K00528,ferredoxin--NADP+ reductase [EC:1.18.1.2]	-	85.34	38.23	
PDE_03282	PDT_03462	K00018,glycerate dehydrogenase [EC:1.1.1.29]	Glycine, serine and threonine metabolism;Glyoxylate and dicarboxylate metabolism;Methane metabolism	133.28	9.08	Yes
PDE_03316	PDT_03497	K14171,alkyl hydroperoxide reductase 1 [EC:1.11.1.15]	Sulfur relay system	167.28	53.91	
PDE_03468	PDT_03664	K03379,cyclohexanone	Caprolactam degradation	24.48	2.48	

		monooxygenase [EC:1.14.13.22]				
PDE_03787	PDT_04005	K00469,inositol oxygenase [EC:1.13.99.1]	Ascorbate and aldarate metabolism;Inositol phosphate metabolism	189.38	48.14	
PDE_03899	PDT_04123	K00129,aldehyde dehydrogenase (NAD(P)+) [EC:1.2.1.5]	Glycolysis / Gluconeogenesis;Histidine metabolism;Tyrosine metabolism;Phenylalanine metabolism;beta-Alanine metabolism;Metabolism of xenobiotics by cytochrome P450;Drug metabolism - cytochrome P450	41.48	4.4	Yes
PDE_03901	PDT_04125	K00276,primary-amine oxidase [EC:1.4.3.21]	Glycine, serine and threonine metabolism;Tyrosine metabolism;Phenylalanine metabolism;beta-Alanine metabolism;Isoquinoline alkaloid biosynthesis;Tropane, piperidine and pyridine alkaloid biosynthesis	75.82	15.13	Yes
PDE_03956	PDT_04184	K07824,benzoate 4-monooxygenase [EC:1.14.13.12]	Benzoate degradation;Aminobenzoate degradation	39.44	0	
PDE_03975	PDT_04204	K00327,NADPH-ferrihemoprotein reductase [EC:1.6.2.4]	-	50.32	14.85	
PDE_04016	PDT_04219	K00517,E1.14.-.-	Bisphenol degradation;Polycyclic aromatic hydrocarbon degradation;Aminobenzoate degradation;Limonene and pinene degradation;Stilbenoid, diarylheptanoid and gingerol biosynthesis	127.84	0	
PDE_04020	PDT_04223	K00359,NADH oxidase [EC:1.6.-.-]	-	101.32	17.05	
PDE_04025	PDT_04228	-	-	20.4	0	
PDE_04028	PDT_04231	-	-	110.84	0	
PDE_04216	PDT_04418	-	-	65.96	6.05	
PDE_04218	PDT_04420	K00120,E1.1.-.-	Bisphenol degradation;Polycyclic aromatic hydrocarbon degradation;Chloroalkane and chloroalkene degradation;Naphthalene degradation;Aminobenzoate degradation;Limonene and pinene degradation	141.78	30.81	
PDE_04228	PDT_04431	K10438,3-hydroxyphenylacetate	Styrene degradation	288.66	19.8	

		6-hydroxylase [EC:1.14.13.63]				
PDE_04264	PDT_04467	-	-	135.66	34.93	
PDE_04265	PDT_04469	K00517,E1.14.-.-	Bisphenol degradation;Polycyclic aromatic hydrocarbon degradation;Aminobenzoate degradation;Limonene and pinene degradation;Stilbenoid, diarylheptanoid and gingerol biosynthesis	284.58	60.79	
PDE_04277	PDT_04482	K00100,E1.1.1.-	Fructose and mannose metabolism;Bisphenol degradation;Linoleic acid metabolism;Chloroalkane and chloroalkene degradation;Butanoate metabolism	109.14	2.48	
PDE_04366	PDT_04569	-	-	119.34	19.53	
PDE_04376	PDT_04579	-	-	108.8	18.43	
PDE_04495	PDT_04694	K00059,3-oxoacyl-[acyl-carrier protein] reductase [EC:1.1.1.100]	Fatty acid biosynthesis;Biosynthesis of unsaturated fatty acids	352.24	0.83	
PDE_04527	PDT_04728	K00456,cysteine dioxygenase [EC:1.13.11.20]	Cysteine and methionine metabolism;Taurine and hypotaurine metabolism	78.88	1.38	Yes
PDE_04530	PDT_04731	K00413,ubiquinol-cytochrome c reductase cytochrome c1 subunit [EC:1.10.2.2]	Oxidative phosphorylation;Nitrogen metabolism;Two-component system;Cardiac muscle contraction;Alzheimer's disease;Parkinson's disease;Huntington's disease	403.58	61.61	
PDE_04605	PDT_04810	K00480,salicylate hydroxylase [EC:1.14.13.1]	Dioxin degradation;Polycyclic aromatic hydrocarbon degradation;Naphthalene degradation	60.52	13.48	
PDE_04628	PDT_04835	-	-	50.66	2.75	
PDE_04629	PDT_04836	-	-	177.82	6.88	
PDE_04632	PDT_04839	K05920,E1.16.1.-	-	26.86	2.75	
PDE_04936	PDT_05167	K11987,prostaglandin-endoperoxide synthase 2 [EC:1.14.99.1]	Arachidonic acid metabolism;VEGF signaling pathway;Retrograde endocannabinoid signaling;Serotonergic synapse;Leishmaniasis;Pathways in cancer;Small cell lung cancer	39.78	1.93	
PDE_05132	PDT_05365	K05920,E1.16.1.-	-	113.22	14.85	

PDE_05158	PDT_05392	K00540,E1.-.-.-	-	56.1	15.4	
PDE_05239	PDT_05474	K03381,catechol 1,2-dioxygenase [EC:1.13.11.1]	Chlorocyclohexane and chlorobenzene degradation;Benzoate degradation;Fluorobenzoate degradation;Toluene degradation	167.62	7.7	
PDE_05363	PDT_05600	-	-	48.28	12.38	
PDE_05500	PDT_05736	K01552,E3.6.3.-	-	262.48	42.36	
PDE_05548	PDT_05782	K00129,aldehyde dehydrogenase (NAD(P)+) [EC:1.2.1.5]	Glycolysis / Gluconeogenesis;Histidine metabolism;Tyrosine metabolism;Phenylalanine metabolism;beta-Alanine metabolism;Metabolism of xenobiotics by cytochrome P450;Drug metabolism - cytochrome P450	109.48	33.01	Yes
PDE_05550	PDT_05784	K03386,peroxiredoxin (alkyl hydroperoxide reductase subunit C) [EC:1.11.1.15]	-	168.3	43.46	
PDE_05566	PDT_05800	K00257,E1.3.99.-	Geraniol degradation	593.3	199.42	
PDE_05675	PDT_05910	K14729,multifunctional beta-oxidation protein [EC:4.2.1.- 1.1.1.-]	-	448.12	119.93	
PDE_05708	PDT_05942	K03781,catalase [EC:1.11.1.6]	Tryptophan metabolism;Glyoxylate and dicarboxylate metabolism;Methane metabolism;Peroxisome;Amyotrophic lateral sclerosis (ALS)	94.86	1.38	Yes
PDE_05885	PDT_06117	K00463,indoleamine 2,3-dioxygenase [EC:1.13.11.52]	Tryptophan metabolism;African trypanosomiasis	55.42	0	Yes
PDE_05886	PDT_06118	-	-	466.82	7.43	
PDE_05907	PDT_06138	K00463,indoleamine 2,3-dioxygenase [EC:1.13.11.52]	Tryptophan metabolism;African trypanosomiasis	967.64	190.07	Yes
PDE_05943	PDT_06174	K00480,salicylate hydroxylase [EC:1.14.13.1]	Dioxin degradation;Polycyclic aromatic hydrocarbon degradation;Naphthalene degradation	34	1.65	
PDE_05973	PDT_06205	K00309,E1.5.3.-	-	47.6	14.58	

PDE_06017	PDT_06248	-	-	196.52	5.78	
PDE_06042	PDT_06267	K00435,peroxiredoxin [EC:1.11.1.-]	-	15.98	0	
PDE_06295	PDT_06525	K00452,3-hydroxyanthranilate 3,4-dioxygenase [EC:1.13.11.6]	Tryptophan metabolism	112.2	50.34	Yes
PDE_06327	PDT_06557	K00517,E1.14.-.-	Bisphenol degradation;Polycyclic aromatic hydrocarbon degradation;Aminobenzoate degradation;Limonene and pinene degradation;Stilbenoid, diarylheptanoid and gingerol biosynthesis	581.74	26.41	
PDE_06396	PDT_06628	-	-	26.86	2.2	
PDE_06412	PDT_06645	-	-	28.9	4.4	
PDE_06474	PDT_06708	K00295,methylenetetrahydrofolate dehydrogenase (NAD+) [EC:1.5.1.15]	One carbon pool by folate	78.2	11.55	
PDE_06586	PDT_06822	K00540,E1.-.-.-	-	487.22	89.67	
PDE_06706	PDT_06950	K00540,E1.-.-.-	-	175.1	0.83	
PDE_06745	PDT_06990	K00120,E1.1.-.-	Bisphenol degradation;Polycyclic aromatic hydrocarbon degradation;Chloroalkane and chloroalkene degradation;Naphthalene degradation;Aminobenzoate degradation;Limonene and pinene degradation	144.16	3.85	
PDE_06831	PDT_07078	K00111,glycerol-3-phosphate dehydrogenase [EC:1.1.5.3]	Glycerophospholipid metabolism	45.22	10.73	
PDE_06915	PDT_07163	K00002,alcohol dehydrogenase (NADP+) [EC:1.1.1.2]	Glycolysis / Gluconeogenesis;Glycerolipid metabolism;Caprolactam degradation	35.36	9.35	
PDE_06939	PDT_07189	K03885,NADH dehydrogenase [EC:1.6.99.3]	Oxidative phosphorylation	64.26	17.05	
PDE_06955	PDT_07207	-	-	198.56	0.55	
PDE_06972	PDT_07226	K00517,E1.14.-.-	Bisphenol degradation;Polycyclic aromatic hydrocarbon degradation;Aminobenzoate degradation;Limonene and pinene degradation;Stilbenoid, diarylheptanoid and gingerol biosynthesis	110.84	28.33	

PDE_07139	PDT_07394	K00517,E1.14.-.-	Bisphenol degradation;Polycyclic aromatic hydrocarbon degradation;Aminobenzoate degradation;Limonene and pinene degradation;Stilbenoid, diarylheptanoid and gingerol biosynthesis	231.2	42.08	
PDE_07206	PDT_07462	K00517,E1.14.-.-	Bisphenol degradation;Polycyclic aromatic hydrocarbon degradation;Aminobenzoate degradation;Limonene and pinene degradation;Stilbenoid, diarylheptanoid and gingerol biosynthesis	399.5	1.93	
PDE_07207	PDT_07463	K00517,E1.14.-.-	Bisphenol degradation;Polycyclic aromatic hydrocarbon degradation;Aminobenzoate degradation;Limonene and pinene degradation;Stilbenoid, diarylheptanoid and gingerol biosynthesis	60.86	10.45	
PDE_07208	PDT_07464	K00540,E1.-.-.-	-	53.04	9.35	
PDE_07226	PDT_07482	K03379,cyclohexanone monooxygenase [EC:1.14.13.22]	Caprolactam degradation	35.02	1.65	
PDE_07232	PDT_07488	K00108,choline dehydrogenase [EC:1.1.99.1]	Glycine, serine and threonine metabolism	53.38	9.08	Yes
PDE_07246	PDT_07502	K00457,4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27]	Ubiquinone and other terpenoid-quinone biosynthesis;Tyrosine metabolism;Phenylalanine metabolism	13.6	0	Yes
PDE_07272	PDT_07529	K00100,E1.1.1.-	Fructose and mannose metabolism;Bisphenol degradation;Linoleic acid metabolism;Chloroalkane and chloroalkene degradation;Butanoate metabolism	45.9	7.15	
PDE_07286	PDT_07543	K00411,ubiquinol-cytochrome c reductase iron-sulfur subunit [EC:1.10.2.2]	Oxidative phosphorylation;Nitrogen metabolism;Two-component system;Cardiac muscle contraction;Alzheimer's disease;Parkinson's disease;Huntington's disease	231.54	99.02	
PDE_07439	PDT_07701	K06892,unclassified	-	32.64	7.98	
PDE_07692	PDT_07959	K00100,E1.1.1.-	Fructose and mannose metabolism;Bisphenol degradation;Linoleic acid metabolism;Chloroalkane and chloroalkene degradation;Butanoate metabolism	53.72	3.03	

PDE_07852	PDT_08119	-	-	81.94	14.85	
PDE_07956	PDT_08224	K00480,salicylate hydroxylase [EC:1.14.13.1]	Dioxin degradation;Polycyclic aromatic hydrocarbon degradation;Naphthalene degradation	144.16	0	
PDE_07957	PDT_08225	K00128,aldehyde dehydrogenase (NAD+) [EC:1.2.1.3]	Glycolysis / Gluconeogenesis;Pentose and glucuronate interconversions;Ascorbate and aldarate metabolism;Fatty acid metabolism;Valine, leucine and isoleucine degradation;Lysine degradation;Arginine and proline metabolism;Histidine metabolism;Tryptophan metabolism;beta-Alanine metabolism;Glycerolipid metabolism;Pyruvate metabolism;Chloroalkane and chloroalkene degradation;Propanoate metabolism;Limonene and pinene degradation	571.2	252.78	Yes
PDE_08009	PDT_08278	K00257,E1.3.99.-	Geraniol degradation	183.6	49.51	
PDE_08042	PDT_08306	-	-	137.7	10.73	
PDE_08098	PDT_08364	K00435,peroxiredoxin [EC:1.11.1.-]	-	15.3	0	
PDE_08156	PDT_08424	-	-	559.3	153.21	
PDE_08495	PDT_08774	K00321,E1.5.99.-	-	190.06	38.23	
PDE_08630	PDT_08912	K00140,methylmalonate-semialdehyde dehydrogenase [EC:1.2.1.27]	Valine, leucine and isoleucine degradation;beta-Alanine metabolism;Inositol phosphate metabolism;Propanoate metabolism	341.36	41.26	Yes
PDE_08660	PDT_08945	K00517,E1.14.-.-	Bisphenol degradation;Polycyclic aromatic hydrocarbon degradation;Aminobenzoate degradation;Limonene and pinene degradation;Stilbenoid, diarylheptanoid and gingerol biosynthesis	148.92	35.21	
PDE_08806	PDT_09097	K00166,2-oxoisovalerate dehydrogenase E1 component, alpha subunit [EC:1.2.4.4]	Valine, leucine and isoleucine degradation	110.16	14.85	Yes
PDE_08814	PDT_09105	K00294,1-pyrroline-5-carboxylate dehydrogenase [EC:1.5.1.12]	Alanine, aspartate and glutamate metabolism;Arginine and proline metabolism	96.22	26.41	Yes
PDE_08821	PDT_09112	K00517,E1.14.-.-	Bisphenol degradation;Polycyclic aromatic hydrocarbon	94.18	39.88	

			degradation;Aminobenzoate degradation;Limonene and pinene degradation;Stilbenoid, diarylheptanoid and gingerol biosynthesis			
PDE_08847	PDT_09138	K00387,sulfite oxidase [EC:1.8.3.1]	Sulfur metabolism	20.06	0	
PDE_08849	PDT_09140	K00540,E1.-.-.-	-	913.58	58.04	
PDE_08859	PDT_09150	K00033,6-phosphogluconate dehydrogenase [EC:1.1.1.44]	Pentose phosphate pathway;Glutathione metabolism	484.84	118.55	
PDE_08904	PDT_09197	K00457,4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27]	Ubiquinone and other terpenoid-quinone biosynthesis;Tyrosine metabolism;Phenylalanine metabolism	149.26	60.51	Yes
PDE_08966	PDT_09259	-	-	120.02	52.26	
PDE_09027	PDT_09321	K03379,cyclohexanone monooxygenase [EC:1.14.13.22]	Caprolactam degradation	332.18	21.73	
PDE_09047	PDT_09341	K00167,2-oxoisovalerate dehydrogenase E1 component, beta subunit [EC:1.2.4.4]	Valine, leucine and isoleucine degradation	73.1	12.93	Yes
PDE_09194	PDT_09494	-	-	48.62	12.93	
PDE_09229	PDT_09530	K00480,salicylate hydroxylase [EC:1.14.13.1]	Dioxin degradation;Polycyclic aromatic hydrocarbon degradation;Naphthalene degradation	29.92	0.55	
PDE_09230	PDT_09531	K05917,cytochrome P450, family 51 (sterol 14-demethylase) [EC:1.14.13.70]	Steroid biosynthesis	24.82	3.58	
PDE_09239	PDT_09540	K00059,3-oxoacyl-[acyl-carrier protein] reductase [EC:1.1.1.100]	Fatty acid biosynthesis;Biosynthesis of unsaturated fatty acids	36.04	1.38	
PDE_09342	PDT_09650	K00249,acyl-CoA dehydrogenase [EC:1.3.99.3]	Fatty acid metabolism;Valine, leucine and isoleucine degradation;beta-Alanine metabolism;Propanoate metabolism;PPAR signaling pathway	250.92	16.23	Yes
PDE_09367	PDT_09677	K00329,NADH dehydrogenase	Oxidative phosphorylation	114.24	0	

		[EC:1.6.5.3]				
PDE_09380	PDT_09690	-	-	81.6	4.95	
PDE_09453	PDT_09764	K05909,E1.10.3.2	-	83.98	4.4	
PDE_09492	PDT_09803	K05909,E1.10.3.2	-	122.4	0.83	
PDE_09616	PDT_09929	K00120,E1.1.-.-	Bisphenol degradation;Polycyclic aromatic hydrocarbon degradation;Chloroalkane and chloroalkene degradation;Naphthalene degradation;Aminobenzoate degradation;Limonene and pinene degradation	106.76	0.55	
PDE_09681	PDT_09993	K13237,peroxisomal 2,4-dienoyl-CoA reductase [EC:1.3.1.34]	Peroxisome	87.04	2.48	
PDE_09691	PDT_10003	K03959,NADH dehydrogenase (ubiquinone) 1 beta subcomplex 3 [EC:1.6.5.3 1.6.99.3]	Oxidative phosphorylation;Alzheimer's disease;Parkinson's disease;Huntington's disease	42.16	8.8	
PDE_09693	PDT_10005	K00276,primary-amine oxidase [EC:1.4.3.21]	Glycine, serine and threonine metabolism;Tyrosine metabolism;Phenylalanine metabolism;beta-Alanine metabolism;Isoquinoline alkaloid biosynthesis;Tropane, piperidine and pyridine alkaloid biosynthesis	148.24	7.15	Yes
PDE_09714	PDT_10027	K03671,thioredoxin 1	-	122.74	8.25	
PDE_09748	PDT_10060	-	-	210.46	1.1	
PDE_09758	PDT_10070	K00492,E1.14.13.-	Histidine metabolism;Chlorocyclohexane and chlorobenzene degradation;Bisphenol degradation;Toluene degradation;Polycyclic aromatic hydrocarbon degradation;Naphthalene degradation;Aminobenzoate degradation;Limonene and pinene degradation	526.32	29.98	Yes
PDE_09761	PDT_10073	K00457,4-hydroxyphenylpyruvate dioxygenase [EC:1.13.11.27]	Ubiquinone and other terpenoid-quinone biosynthesis;Tyrosine metabolism;Phenylalanine metabolism	2216.12	36.31	Yes
PDE_09762	PDT_10074	K00101,L-lactate dehydrogenase (cytochrome) [EC:1.1.2.3]	Pyruvate metabolism	370.94	97.92	

PDE_09770	PDT_10082	-	-	83.64	33.01	
PDE_09870	PDT_10184	K00323,NAD(P) transhydrogenase [EC:1.6.1.2]	Nicotinate and nicotinamide metabolism	375.36	182.37	
PDE_09933	PDT_10248	-	-	16.66	0.55	
PDE_09999	PDT_10315	K00480,salicylate hydroxylase [EC:1.14.13.1]	Dioxin degradation;Polycyclic aromatic hydrocarbon degradation;Naphthalene degradation	109.14	0	
PDE_10002	PDT_10318	K00019,3-hydroxybutyrate dehydrogenase [EC:1.1.1.30]	Synthesis and degradation of ketone bodies;Butanoate metabolism	54.06	0	
PDE_10003	PDT_10319	K00517,E1.14.-.-	Bisphenol degradation;Polycyclic aromatic hydrocarbon degradation;Aminobenzoate degradation;Limonene and pinene degradation;Stilbenoid, diarylheptanoid and gingerol biosynthesis	24.82	0	
PDE_10004	PDT_10320	-	-	62.22	1.1	
PDE_10008	PDT_10324	-	-	13.6	0	

Table S14. Transcription levels of secondary metabolism gene clusters in *P. decumbens* 114-2 and JU-A10-T.

NRPS, Nonribosomal peptide synthetases; DMAT, Demethylallyl tryptophan synthase; PKS, Polyketide synthases.

Gene ID		**SMURF "backbone gene" prediction**	**Transcription level (tags per million, TPM)**		**Change[a]**
114-2	**JU-A10-T**		**114-2**	**JU-A10-T**	
Cluster_1					
PDE_00814	PDT_00847		3.06	9.9	
PDE_00813	PDT_00846		1.36	4.95	
PDE_00812	PDT_00845		0.68	0	
PDE_00811	PDT_00844		41.82	0.55	Down
PDE_00810	PDT_00843	NRPS	6.46	0.83	
PDE_00809	PDT_00842		18.7	0	Down
PDE_00808	PDT_00841		10.2	0	
PDE_00807	PDT_00840	DMAT	47.94	0	Down
PDE_00806	PDT_00839		55.76	0.55	Down
PDE_00805	PDT_00838		28.56	0	Down
PDE_00804	PDT_00837		58.82	0	Down
PDE_00803	PDT_00836		35.02	0	Down
PDE_00802	PDT_00835		7.14	0	
PDE_00801	PDT_00834		68.34	0	Down
PDE_00800	PDT_00833		11.22	0	
PDE_00799	PDT_00832		103.36	7.43	Down
PDE_00798	PDT_00831		113.9	1.38	Down
PDE_00797	PDT_00830	DMAT	361.42	0.55	Down
PDE_00796	PDT_00829		30.94	0	Down
PDE_00795	PDT_00828		22.78	0	Down
PDE_00794	PDT_00827		148.58	0	Down
PDE_00793	PDT_00826	NRPS	4.42	2.75	
PDE_00792	PDT_00825		51	0	Down
PDE_00791	PDT_00824		19.04	0	Down
PDE_00790	PDT_00823		56.44	2.75	Down
PDE_00789	PDT_00822	NRPS	4.08	0	
PDE_00788	PDT_00821		22.78	0	Down
PDE_00787	PDT_00820		116.96	31.91	Down
Cluster_2					
PDE_01077	PDT_01119	NRPS	0	0	
PDE_01076	PDT_01118		0	0	
PDE_01075	PDT_01117		0	0	

PDE_01074	PDT_01116		0.68	0	
PDE_01073	PDT_01115		3.4	0	
PDE_01072	PDT_01114		0	0	
PDE_01071	PDT_01113	NRPS	24.48	0.55	Down
PDE_01070	PDT_01112		34.68	0	Down
PDE_01069	PDT_01111		62.56	0	Down
PDE_01068	PDT_01110		129.54	3.3	Down
PDE_01067	PDT_01109		93.16	1.1	Down
PDE_01066	PDT_01108	DMAT	60.18	0.83	Down
PDE_01065	PDT_01107		161.84	0.83	Down
PDE_01064	PDT_01106		27.54	0	Down
Cluster_3					
PDE_01177	PDT_01230		4.42	2.75	
PDE_01176	PDT_01229		0.68	18.15	Up
PDE_01175	PDT_01227		79.56	67.67	
PDE_01174	PDT_01226		11.9	8.53	
PDE_01173	PDT_01225	PKS-Like	11.9	16.5	
PDE_01172	PDT_01224		0	0	
PDE_01171	PDT_01223		10.88	22.56	
PDE_01170	PDT_01222		13.94	19.25	
PDE_01169	PDT_01221		0	0	
PDE_01168	PDT_01220		214.54	14.3	Down
PDE_01167	PDT_01219		12.58	13.75	
PDE_01166	PDT_01218		74.46	102.05	
Cluster_4					
PDE_01198	PDT_01255		24.48	44.84	
PDE_01197	PDT_01254		0	0	
PDE_01196	PDT_01253		60.86	7.43	Down
PDE_01195	PDT_01252		229.5	1.38	Down
PDE_01194	PDT_01251		915.96	81.69	Down
PDE_01193	PDT_01250		6.46	0	
PDE_01192	PDT_01249		161.84	0	Down
PDE_01191	PDT_01248		231.88	437.9	
PDE_01190	PDT_01247		89.08	187.32	Up
PDE_01189	PDT_01246		114.24	3.03	Down
PDE_01188	PDT_01245		761.94	10.45	Down
PDE_01187	PDT_01244		286.62	15.68	Down
PDE_01186	PDT_01243		9.86	9.9	
PDE_01185	PDT_01242	NRPS-Like	5.1	0	
Cluster_5					

PDE_01218	PDT_01276		290.36	10.18	Down
PDE_01217	PDT_01275		608.6	0	Down
PDE_01216	PDT_01274		127.84	0.55	Down
PDE_01215	PDT_01273		632.74	6.88	Down
PDE_01214	PDT_01272		179.86	3.3	Down
PDE_01213	PDT_01271		49.64	0	Down
PDE_01212	PDT_01270	NRPS	172.72	10.45	Down
PDE_01211	PDT_01269		50.32	32.73	
PDE_01210	PDT_01268		0	0	
PDE_01209	PDT_01267		0	4.68	
PDE_01208	PDT_01266		1.36	1.65	
PDE_01207	PDT_01265		18.36	40.98	
PDE_01206	PDT_01264		66.3	314.4	Up
PDE_01205	PDT_01263		0	0	
PDE_01204	PDT_01262		0	0	
PDE_01203	PDT_01261		0	0	
PDE_01202	PDT_01260		10.2	7.7	
Cluster_6					
PDE_01242	PDT_01300		0	0	
PDE_01241	PDT_01299		2.72	1.65	
PDE_01240	PDT_01298		27.88	7.98	
PDE_01239	PDT_01297		4.42	3.85	
PDE_01238	PDT_01296		21.76	2.2	Down
PDE_01237	PDT_01295		5.78	0.55	
PDE_01236	PDT_01294		1.02	13.75	
PDE_01235	PDT_01293	PKS	13.6	2.2	
PDE_01234	PDT_01292		38.76	5.5	Down
PDE_01233	PDT_01291		0.68	1.38	
PDE_01232	PDT_01290		38.08	32.73	
PDE_01231	PDT_01289		55.08	4.4	Down
PDE_01230	PDT_01288		20.4	10.45	
Cluster_7					
PDE_01433	PDT_01511		3.4	0	
PDE_01432	PDT_01510	NRPS	0	0.55	
PDE_01431	PDT_01509		1.7	1.1	
PDE_01430	PDT_01508		0	0	
PDE_01429	PDT_01507		0.68	0	
PDE_01428	PDT_01506		0	5.78	
PDE_01427	PDT_01505		0	0	
PDE_01426	PDT_01504		2.72	1.1	
PDE_01425	PDT_01503		6.12	0.83	

PDE_01424	PDT_01502		132.94	5.5	Down
PDE_01423	PDT_01501		0	0	
PDE_01422	PDT_01500		2.04	17.33	
PDE_01421	PDT_01499		2.38	4.13	
PDE_01420	PDT_01498		17	16.23	
PDE_01419	PDT_01497		8.84	4.13	
PDE_01418	PDT_01496		44.54	3.85	Down
Cluster_8					
PDE_02141	PDT_02237	PKS	12.92	1.38	
PDE_02140	PDT_02236		19.04	0	Down
PDE_02139	PDT_02235		18.36	0	Down
PDE_02138	PDT_02234		5.1	0	
PDE_02137	PDT_02233		5.44	0.55	
PDE_02136	PDT_02232		9.52	0.55	
PDE_02135	PDT_02231		4.42	0.83	
PDE_02134	PDT_02230		2.04	3.3	
PDE_02133	PDT_02229		57.46	57.49	
PDE_02132	PDT_02228		2.04	0.83	
PDE_02131	PDT_02227	NRPS	7.82	3.85	
PDE_02130	PDT_02226		0.68	0	
Cluster_9					
PDE_02204	PDT_02302		3.74	0	
PDE_02203	PDT_02301	NRPS-Like	1.36	0	
Cluster_10					
PDE_02610	PDT_02746	NRPS	4.42	18.15	
PDE_02609	PDT_02745		11.9	6.88	
PDE_02608	PDT_02744		0	0	
PDE_02607	PDT_02743		20.4	3.58	
PDE_02606	PDT_02742		15.98	11.28	
PDE_02605	PDT_02741		78.54	8.25	Down
PDE_02604	PDT_02740		8.5	7.43	
PDE_02603	PDT_02739		76.5	44.56	
PDE_02602	PDT_02738		39.78	25.58	
PDE_02601	PDT_02737		78.2	31.91	Down
PDE_02600	PDT_02736		78.88	75.09	
Cluster_11					
PDE_03304	PDT_03485	NRPS-Like	1.7	3.3	
PDE_03303	PDT_03484		0	0	
PDE_03302	PDT_03483		36.38	40.43	
PDE_03301	PDT_03482		28.56	32.73	

PDE_03300	PDT_03481		1.7	3.03	
PDE_03299	PDT_03480		129.88	48.41	Down
PDE_03298	PDT_03479		145.18	13.48	Down
Cluster_12					
PDE_03416	PDT_03609	NRPS	0	0.55	
PDE_03415	PDT_03608		0	0.55	
Cluster_13					
PDE_03455	PDT_03651	PKS	17.68	7.7	
PDE_03454	PDT_03650		34	4.4	Down
PDE_03453	PDT_03649		63.24	1.1	Down
Cluster_14					
PDE_03929	PDT_04154		1.02	6.88	
PDE_03928	PDT_04153		33.32	821.89	Up
PDE_03927	PDT_04152		45.56	157.61	Up
PDE_03926	PDT_04151	PKS	12.92	359.51	Up
PDE_03925	PDT_04150		25.5	23.38	
PDE_03924	PDT_04149		11.9	0	
PDE_03923	PDT_04148		0	0	
PDE_03922	PDT_04147		1.7	0	
PDE_03921	PDT_04146		59.5	57.49	
PDE_03920	PDT_04145		211.14	228.85	
Cluster_15					
PDE_04025	PDT_04228		20.4	0	Down
PDE_04024	PDT_04227		79.9	1.1	Down
PDE_04023	PDT_04226		166.26	14.03	Down
PDE_04022	PDT_04225		13.6	11.83	
PDE_04021	PDT_04224		354.62	255.81	
PDE_04020	PDT_04223		101.32	17.05	Down
PDE_04019	PDT_04222		9.52	0	
PDE_04018	PDT_04221	PKS	40.12	13.2	
PDE_04017	PDT_04220	HYBRID	257.72	2.48	Down
PDE_04016	PDT_04219		127.84	0	Down
PDE_04015	PDT_04218		82.28	0.55	Down
PDE_04014	PDT_04217		6.46	6.33	
PDE_04013	PDT_04216		10.2	2.48	
PDE_04012	PDT_04215		43.18	35.48	
PDE_04011	PDT_04214		0	0	
PDE_04010	PDT_04213		0	0	
PDE_04009	PDT_04212		991.44	7.15	Down
PDE_04008	PDT_04211		209.44	0.83	Down

Cluster_16					
PDE_04267	PDT_04471		138.72	97.1	
PDE_04266	PDT_04470		163.2	22.01	Down
PDE_04265	PDT_04469		284.58	60.79	Down
PDE_04264	PDT_04467		135.66	34.93	Down
PDE_04263	PDT_04466		67.32	32.73	
PDE_04262	PDT_04465		0.68	0	
PDE_04261	PDT_04464		0	0	
PDE_04260	PDT_04463		113.56	1.38	Down
PDE_04259	PDT_04462		2.38	0	
PDE_04258	PDT_04461		7.14	2.48	
PDE_04257	PDT_04460		0	0	
PDE_04256	PDT_04459		0	0	
PDE_04255	PDT_04458		1.36	0	
PDE_04254	PDT_04457		32.3	-	
PDE_04253	PDT_04457		10.88	-	
PDE_04252	PDT_04456	HYBRID	10.88	2.2	
Cluster_17					
PDE_04545	PDT_04746		1.7	0	
PDE_04544	PDT_04745		2.04	1.38	
PDE_04543	PDT_04744	NRPS	0	0	
PDE_04542	PDT_04743		19.04	20.63	
PDE_04541	PDT_04742		37.06	56.66	
PDE_04540	PDT_04741		7.48	27.51	Up
Cluster_18					
PDE_05569	PDT_05803		73.78	31.91	Down
PDE_05568	PDT_05802		122.4	101.5	
PDE_05567	PDT_05801		0.68	0	
PDE_05566	PDT_05800		593.3	199.42	
PDE_05565	PDT_05799		37.74	94.07	Up
PDE_05564	PDT_05798	NRPS-Like	9.18	16.23	
PDE_05563	PDT_05797		9.86	5.23	
PDE_05562	PDT_05796		0	0	
PDE_05561	PDT_05795		22.44	39.06	
PDE_05560	PDT_05794		12.58	3.03	
PDE_05559	PDT_05793		5.78	7.43	
PDE_05558	PDT_05792		54.74	63.81	
PDE_05557	PDT_05791		0	0	
PDE_05556	PDT_05790		8.84	1.93	Down
Cluster_19					

PDE_06213	PDT_06446		81.6	7.98	Down
PDE_06212	PDT_06445		0	0	
PDE_06211	PDT_06444		0	110.03	Up
PDE_06210	PDT_06443		4.08	0	
PDE_06209	PDT_06442		253.98	0.55	Down
PDE_06208	PDT_06441		1.36	0	
PDE_06207	PDT_06440		0	0	
PDE_06206	PDT_06439	NRPS-Like	2.04	2.75	
PDE_06205	PDT_06438		0	0	
PDE_06204	PDT_06437		0	0	
PDE_06203	PDT_06436		1.36	0	
PDE_06202	PDT_06435		0.68	0	
Cluster_20					
PDE_06630	PDT_06873	NRPS-Like	0	0	
PDE_06629	PDT_06872		0	0	
PDE_06628	PDT_06871		7.14	1.1	
PDE_06627	PDT_06870		1.02	2.75	
PDE_06626	PDT_06869		68.34	165.59	Up
PDE_06625	PDT_06868		0	0	
PDE_06624	PDT_06867		36.72	53.09	
PDE_06623	PDT_06866		10.2	7.7	
Cluster_21					
PDE_07006	PDT_07260		25.84	9.08	
PDE_07005	PDT_07259	NRPS	12.58	1.38	
PDE_07004	PDT_07258		10.88	1.1	
PDE_07003	PDT_07257		6.12	0.55	
PDE_07002	PDT_07256		5.44	0	
PDE_07001	PDT_07255		35.7	9.08	Down
Cluster_22					
PDE_07172	PDT_07427		11.22	33.01	
PDE_07171	PDT_07426		4.08	20.9	
PDE_07170	PDT_07425		54.4	28.33	
PDE_07169	PDT_07424		0.68	0.55	
PDE_07168	PDT_07423		35.36	42.91	
PDE_07167	PDT_07422		14.62	4.95	
PDE_07166	PDT_07421		2.72	3.58	
PDE_07165	PDT_07420		7.48	1.1	
PDE_07164	PDT_07419		1.7	0	
PDE_07163	PDT_07418	NRPS	132.94	11.83	Down
PDE_07162	PDT_07417		6.12	89.95	Up

Cluster_23					
PDE_07378	PDT_07638		37.74	49.51	
PDE_07377	PDT_07637		4.42	12.1	
PDE_07376	PDT_07636		0	0.83	
PDE_07375	PDT_07635		11.22	9.35	
PDE_07374	-		0	-	
PDE_07373	PDT_07633	NRPS-Like	58.48	59.14	
Cluster_24					
PDE_08155	PDT_08423	NRPS-Like	284.58	51.99	Down
PDE_08154	PDT_08422		45.22	3.03	Down
Cluster_25					
PDE_09202	PDT_09503		0.68	0.55	
PDE_09201	PDT_09502		1.02	0	
PDE_09200	PDT_09501		5.1	6.6	
PDE_09199	PDT_09500		5.1	0.55	
PDE_09198	PDT_09499	HYBRID	0	0	
PDE_09197	PDT_09497		0.68	0	
PDE_09196	PDT_09496		0.68	0	
PDE_09195	PDT_09495		460.36	414.25	
PDE_09194	PDT_09494		48.62	12.93	Down
PDE_09193	PDT_09493		1.02	0.83	
PDE_09192	PDT_09492		0	0.55	
PDE_09191	PDT_09491		0	0	
PDE_09190	PDT_09490		1.02	0.55	
PDE_09189	PDT_09489		0	0	
PDE_09188	PDT_09488		0	0	
Cluster_26					
PDE_09243	PDT_09544		1.02	0.83	
PDE_09242	PDT_09543		96.56	0	Down
PDE_09241	PDT_09542		30.26	0	Down
PDE_09240	PDT_09541		94.18	0	Down
PDE_09239	PDT_09540		36.04	1.38	Down
PDE_09238	PDT_09539		25.16	0	Down
PDE_09237	PDT_09538	PKS	38.08	0	Down
PDE_09236	PDT_09537		123.08	0	Down
PDE_09235	PDT_09536		16.66	0	Down
PDE_09234	PDT_09535		51	0.83	Down
PDE_09233	PDT_09534		44.2	0	Down
PDE_09232	PDT_09533		26.52	0	Down
PDE_09231	PDT_09532		11.9	0.55	

PDE_09230	PDT_09531		24.82	3.58	Down
PDE_09229	PDT_09530		29.92	0.55	Down
PDE_09228	PDT_09529		146.2	3.03	Down
PDE_09227	PDT_09528		96.56	17.05	Down
Cluster_27					
PDE_09496	PDT_09807		1.7	1.38	
PDE_09495	PDT_09806		9.86	6.33	
PDE_09494	PDT_09805		20.06	2.48	Down
PDE_09493	PDT_09804		0	0	
PDE_09492	PDT_09803		122.4	0.83	Down
PDE_09491	PDT_09802	PKS	147.56	1.65	Down
Cluster_28					
PDE_10009	PDT_10325		43.86	0.83	Down
PDE_10008	PDT_10324		13.6	0	Down
PDE_10007	PDT_10323		18.36	3.85	
PDE_10006	PDT_10322	PKS	6.46	0.55	
PDE_10005	PDT_10321		155.72	0.55	Down
PDE_10004	PDT_10320		62.22	1.1	Down
PDE_10003	PDT_10319		24.82	0	Down
PDE_10002	PDT_10318		54.06	0	Down
PDE_10001	PDT_10317		11.56	0	
PDE_10000	PDT_10316		20.4	0	Down
PDE_09999	PDT_10315		109.14	0	Down
PDE_09998	PDT_10314		0	0	
PDE_09997	PDT_10313		0	0	
PDE_09996	PDT_10312		0.68	0	
PDE_09995	PDT_10311		27.2	12.1	
PDE_09994	PDT_10310		299.88	55.56	Down

[a] Significantly differential expression in JU-A10-T relative to 114-2 (FDR lower than 0.001).

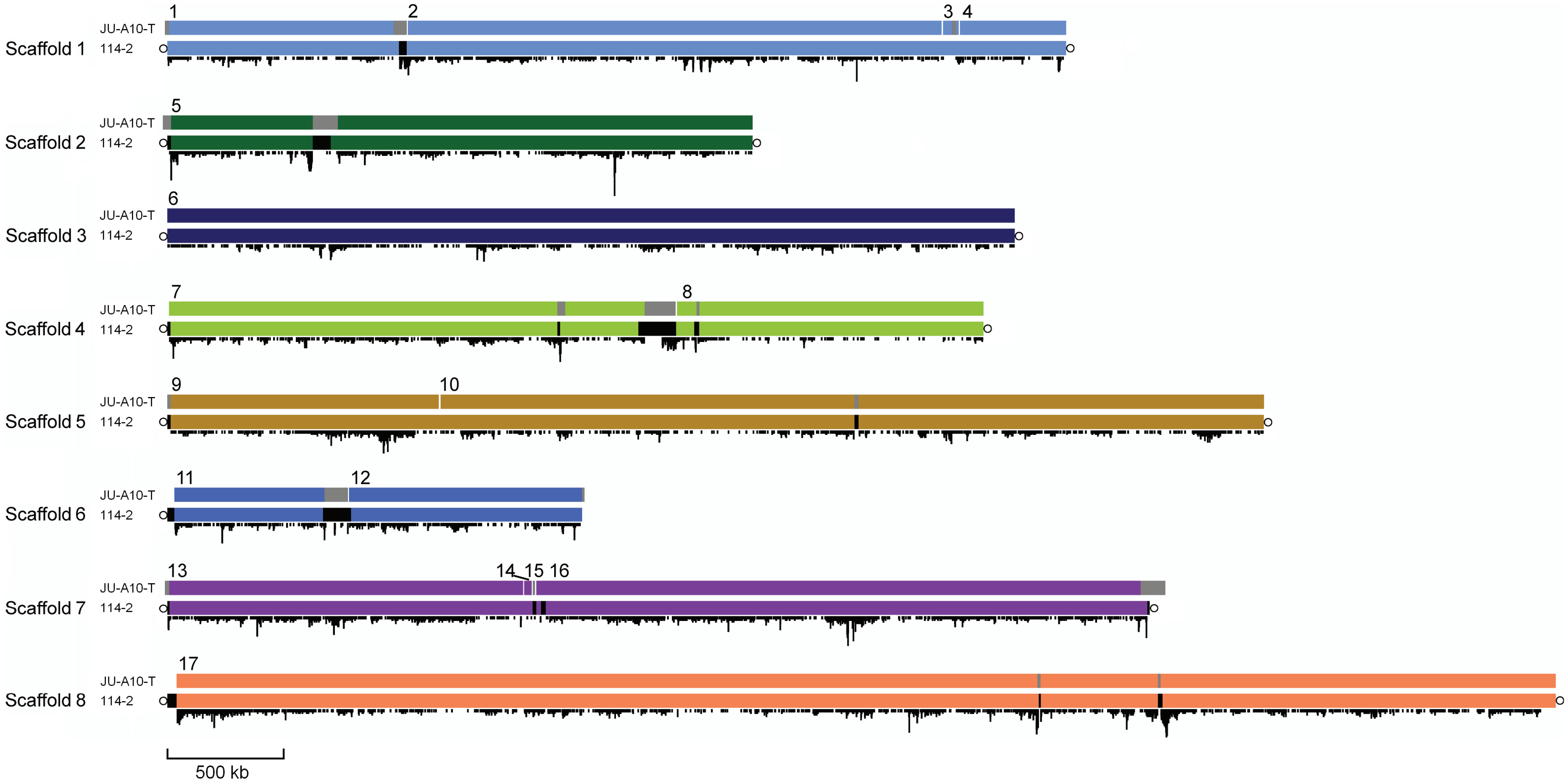

Figure S1. Schematic diagram of scaffold mapping.

Single nucleotide variation (SNV) density (black histograms) was calculated using a 100-bp window. Blocks in black and gray indicate strain-specific regions in

114-2 and JU-A10-T, respectively. Scaffold ends with telomeric repeats in 114-2 are indicated by hollow black circles. Five small scaffolds (Scaffold 18 to 22) in JU-A10-T could not be mapped to the 114-2 genome and are not shown here. Scaffold 23 (1,222-bp long) of JU-A10-T was mapped to Scaffold 2 (1514726–1515948) of 114-2, while a gap existed in the corresponding region of JU-A10-T Scaffold 5.

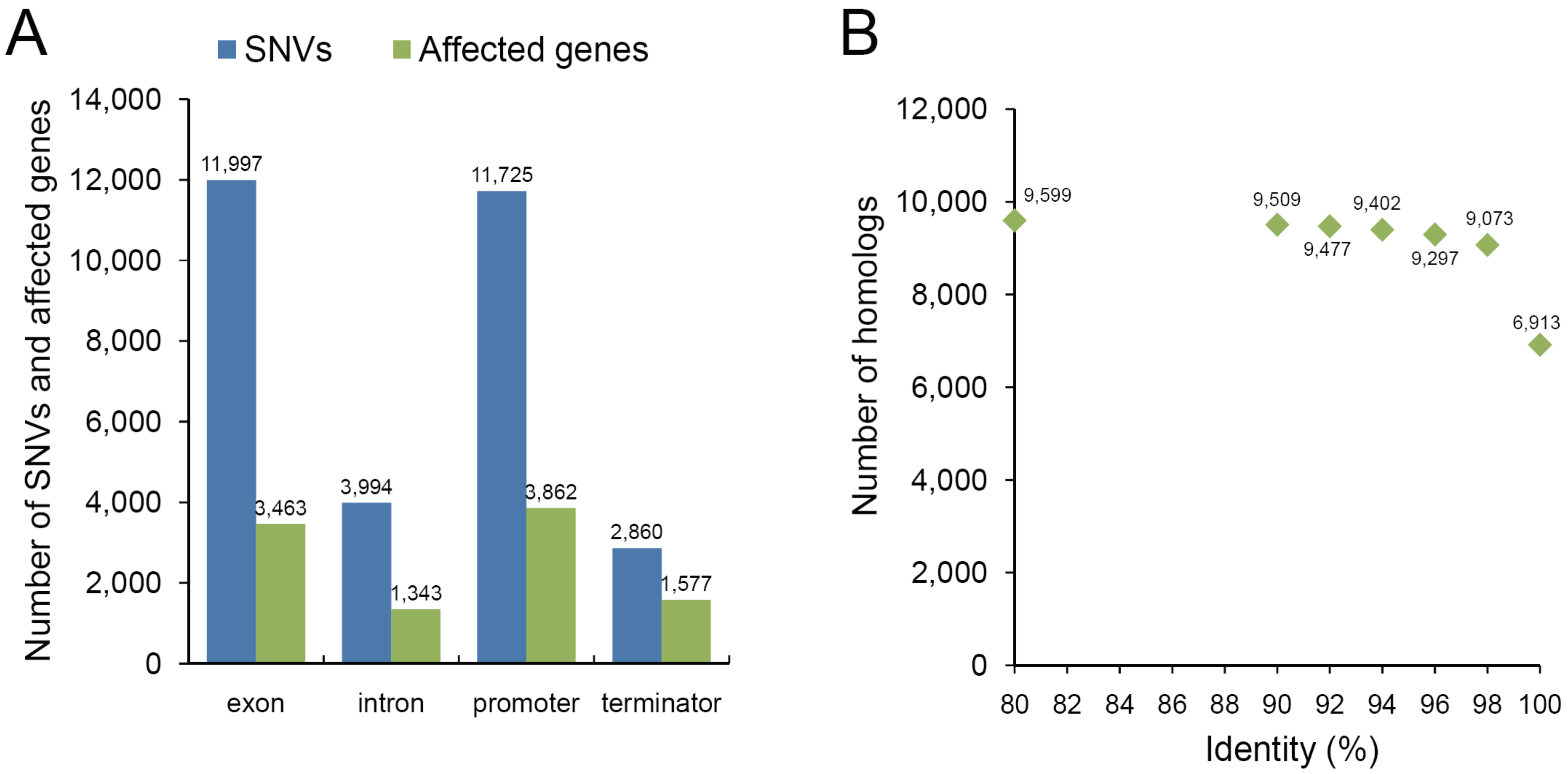

Figure S2. Genetic variations between strains 114-2 and JU-A10-T.

(**A**) Single nucleotide variations (SNVs) and affected genes between 114-2 and JU-A10-T. SNVs in exons, introns, 1,000 bp-long upstream promoters or 200 bp-long downstream terminators were all analyzed. Note that one SNV may affect more than one gene, and one gene may contain SNVs at different regions (e.g. both exons and introns). (**B**) Numbers of proteins of different sequence identities between 114-2 and JU-A10-T (alignment coverage ≥ 80%).

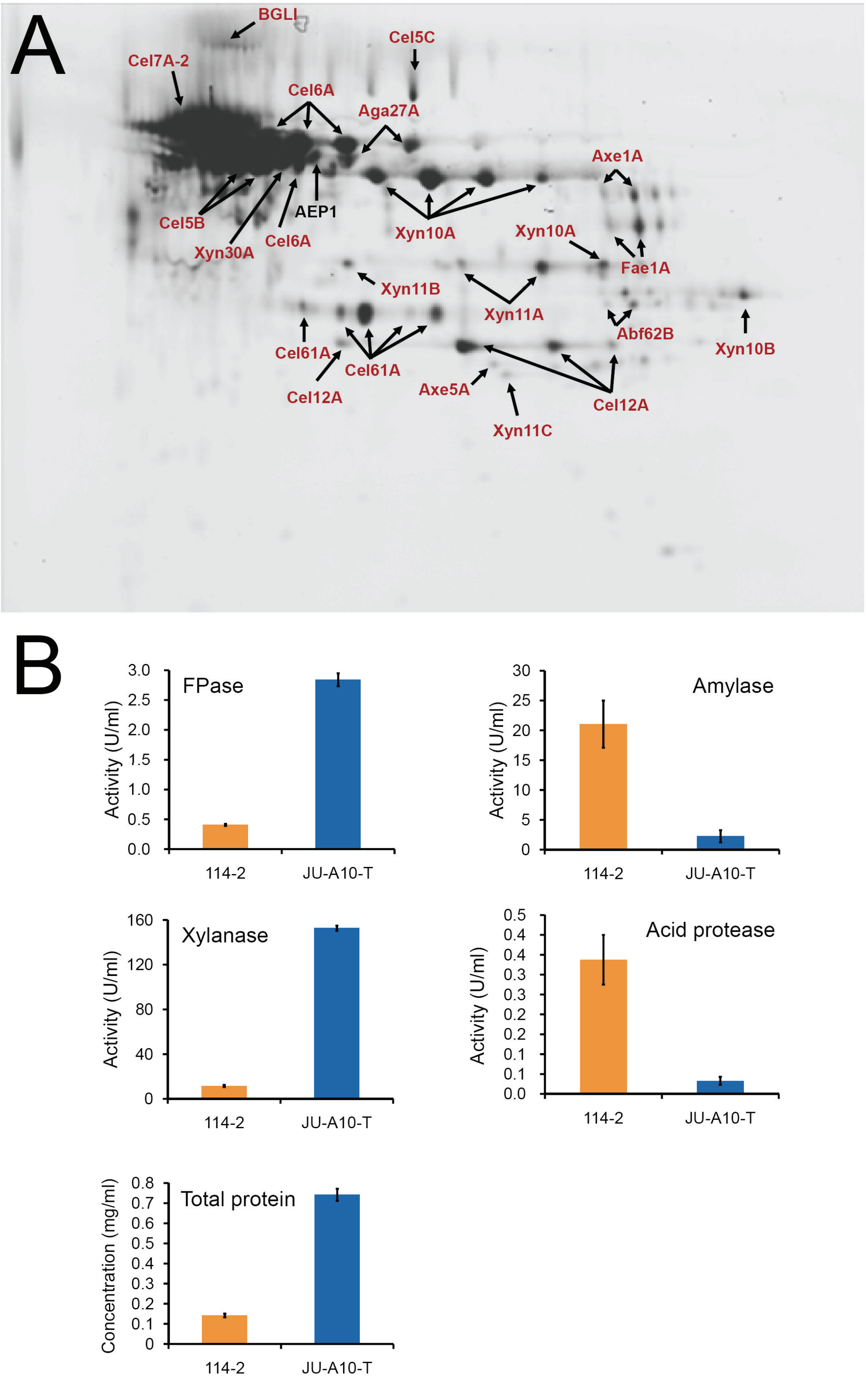

Figure S3. Characters of the secretome of *P. decumbens* JU-A10-T grown in cellulose-wheat bran medium for 48 h.

(**A**) Two-dimensional electrophoresis map of the JU-A10-T secretome. Lignocellulolytic enzymes are indicated in red color. (**B**) Extracellular hydrolase activities of JU-A10-T in comparison with those in 114-2. Error bars represent standard deviations of triplicate independent cultures.

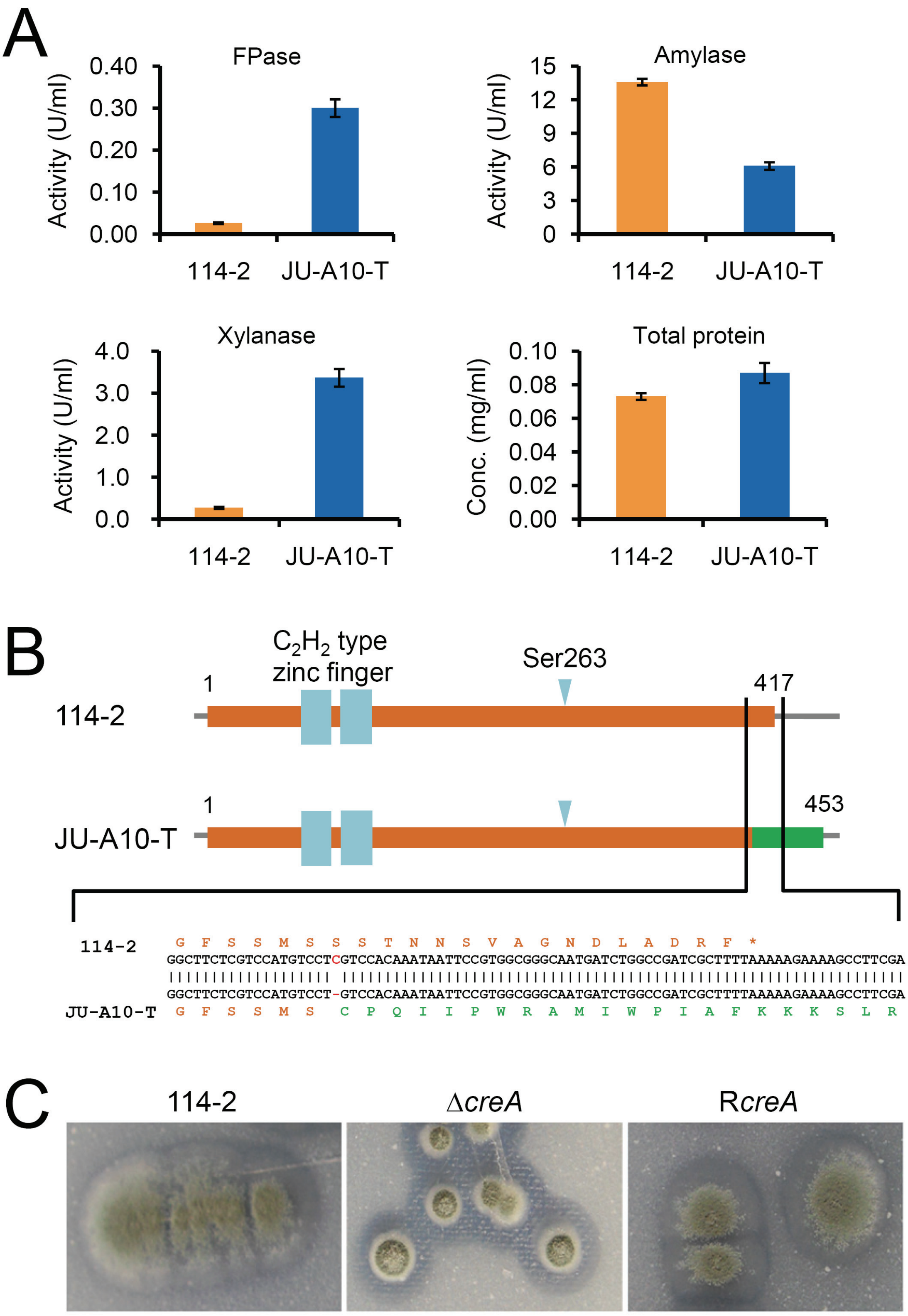

Figure S4. Carbon catabolite repression-resistant expression of lignocellulolytic enzymes in *P. decumbens*.

(A) Extracellular hydrolase activities of 114-2 and JU-A10-T grown in glucose medium for 48 h.

(**B**) Schematic diagram of the sequence variation in *creA*. The frameshift mutation is shown in red.

C_2H_2 zinc finger DNA-binding domain and the predicted phosphorylation site Ser263 are indicated in the figure. (**C**) Effect of *creA* upon cellulase production in the presence of glucose. Strain Δ*creA* was generated by deleting *creA* in 114-2, and R*creA* was obtained by retransformation of *creA* expression cassette into Δ*creA* via homologous recombination. Strains were grown on medium containing 0.5% (w/v) glucose and 0.5% (w/v) ball-milled cellulose. Note that the ratio of hydrolytic halo diameter to colony diameter of Δ*creA* is higher than those of 114-2 and R*creA*.

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114-2     -1500 AAGCTCATCCTGAGGTGGTGACAGTAAAGATGAAGTTGATCATTACCGCCTTGTAGTAATTCTTCCTTGTATATGCAAGTGACAGAAGGCGTTATAATCA -1401
JU-A10-T  -1500 .................................................................................................... -1401

114-2     -1400 CAGGGTGTCTCCCCGCAATTGCGATCGACAGTCGCCAAGATGAAGAGGCCTGTACGTCCCCTCTTCGTCTTCCGACCCCATCACTTTTGACCGTGGCCGA -1301
JU-A10-T  -1400 ...................................................................A................................ -1301

114-2     -1300 TTGAGTTTAACGGCATCTTGAAGAGCACTCACCTAGTGATAATTGACTAAGATGGTCTTCTGATCTGTGTGATGAATCTTTCTACAAAATTTCCGTTGCG -1201
JU-A10-T  -1300 .................................................G.................................................. -1201

114-2     -1200 GGAAAAGGCTCACCATTAGACAGGGCAGTGTACAATGTTCGTCCTGCTTTGCTTTCCCCCTCATCAGAAACTAGGAGGCAAATGAATCCAGGACATCGCC -1101
JU-A10-T  -1200 .................................................................................................... -1101

114-2     -1100 GCTCATGTAAGATAAGCGATCGATGTAATTGCTCCATTAACTTCTTCATTTCACCCAGCGGCTATAGTCCAGTCGGAACGGTAGGGTGATTCATGTTGTT -1001
JU-A10-T  -1100 ...............................T.T.................................................................. -1001

114-2     -1000 TCAGTGGGATGTGTGAGGAAGGGATTCGGTTTCGAGTAGAAATAATGGAGCAGACACCATGACAAGATTCGGCCAAGATCGCCAGGGAAAATCACGGGGT -901
JU-A10-T  -1000 .................................................................................................... -901

114-2      -900 ATAGTCAGCGCTAAGCTCTCATTGAAGGATATTTTGCGCTTTCATCCCGTCAGACCTGGGGAAATTTCCGGATATGTGGGATACAGCGCCGATCTGAAAC -801
JU-A10-T   -900 .........A.......................................................................................... -801

114-2      -800 GCTCTATGCCCAAAACAGCATGCAGAATGCCCCGGACAATTCGACGCCGCGGAGCGCGGTGTAGGTCCCTGCAGAGTGGGATGCTGCTCATGTATTGATG -701
JU-A10-T   -800 ................................................A.....................................T............. -701

114-2      -700 CGGGCGCTTTCCAGAAGCAAAACGCCCAACGCTTTACCGACCGTATGTGGCACGATCATGGCGCCAGGTGGCGGCGCCAGCGGATTTAACCTATAGCTCT -601
JU-A10-T   -700 .................................................................................................... -601

114-2      -600 AATGAGCTCTGCAGCTGTCGTAGGGTCTTTCACCATCTACATCGTACTAGATCTCTTGATATTTGAGTCTCCGCAAGAAGTCTGGCAAGTGAAATAGTAT -501
JU-A10-T   -600 ..........................................................................G......................... -501

114-2      -500 AGATTTGCATTTTCTTTTCAGCGCAGATCTCCGATGGTGATGCCATTTCAAGCTCGGAGATGGGCCCGTCTAGCGAGGACCAAAATCGCTAGTCACTAGA -401
JU-A10-T   -500 ......................A............................................................................. -401

114-2      -400 CGATAGCTCATGACTCCAGCAACGAATCTTGCACGTCGTTGGTCGAGATCAACTTTCTTGGACGATCTTTCCTCGCTTGGCAGTGAAACTCGATCCACCT -301
JU-A10-T   -400 .................................................................................................... -301

114-2      -300 TCATTTTGATGCAGAACGTGGGCCATGATTCTCCTTGCAATGGCCCTGGTCGGAGACCGGTCTCTTGTCTTGGCTGAGTTGAACACTCCATCTAGTTTCT -201
JU-A10-T   -300 ..........................................C......................................................... -201

114-2      -200 GAACAATATGGCTCGCAGGAGCCACGACAGTCTGTGTCAATCTTGGCAAAACTCGATGAGAGATCTATATAAAGACCTCGGTGCTGCTCCCTCATCTCAA -101
JU-A10-T   -200 .........................................................T.......................................... -101

114-2      -100 GAATCATCAACTGCAGGCCAGTGAGACAATCCTACTACGCTTCCCTCCCTCATATACAAACTTTCATACGTCAGGTCCATTCCTTTCATTGATCTCCATT -1
JU-A10-T   -100 .................................................................................................... -1
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Figure S5. Sequence variations in the promoter region of *cel7A-1*.

Nucleotides are numbered relative to the start codon, and variations between the two strains are shown in red. Single motifs of putative CreA binding sites (5'-SYGGRG-3') are underlined.

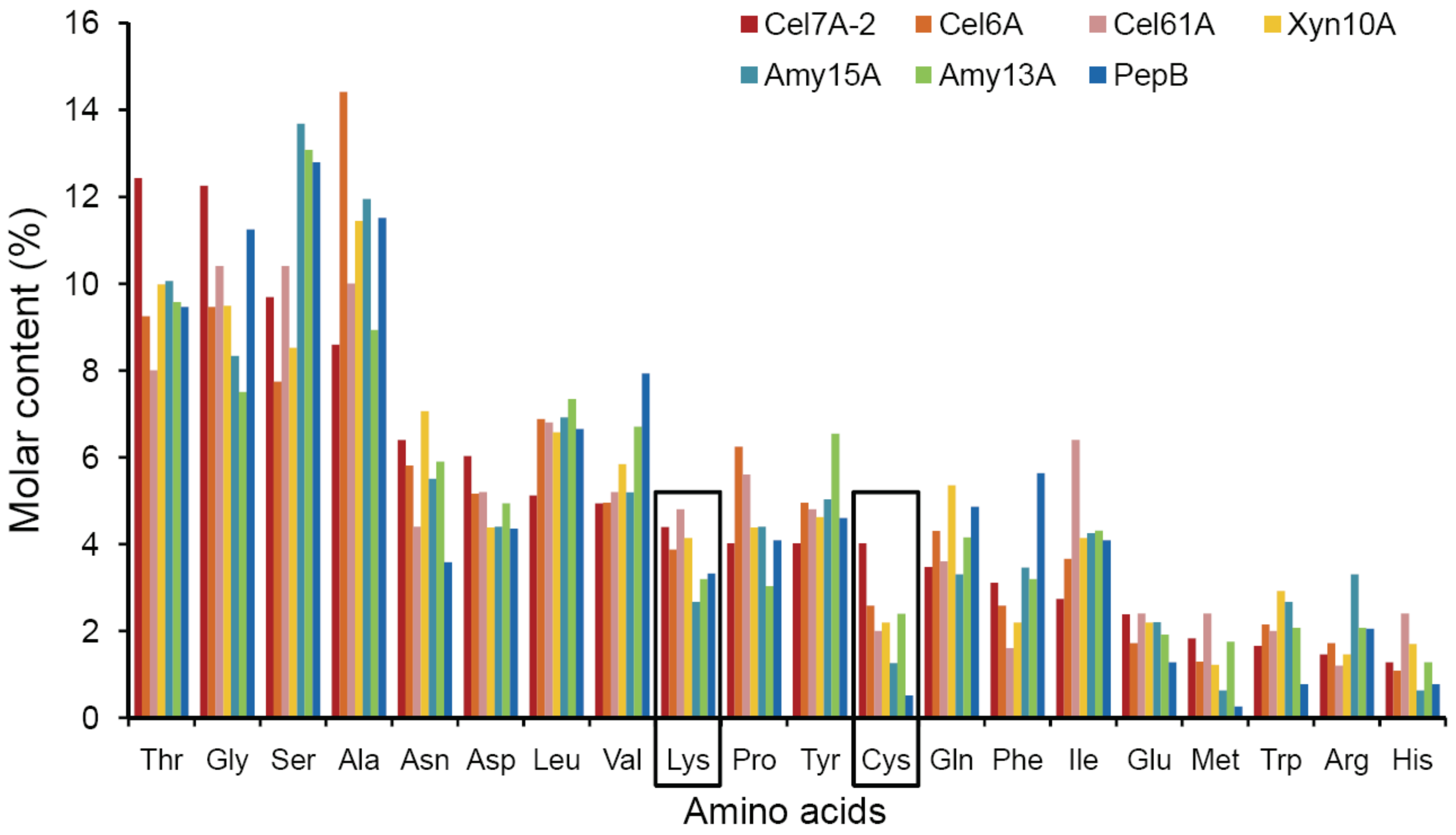

Figure S6. Amino acid composition of seven major components of the secretomes of strains 114-2 and JU-A10-T.

Differences in the contents of lysine and cysteine among the proteins are boxed.