

Transcriptome analysis of leaf tissue from Bermudagrass (*Cynodon dactylon*) using a normalised cDNA library

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Table S1

25 different protein motifs further annotated by InterProScan for 43 unigenes that were not significantly matched (No hits) in a BLASTX search (E-value <10⁻⁵; ^aInterProScan Identifiers; ^bNumber of protein motifs assigned)

IPR ID ^a	Motifs ^b	Functional description
IPR005819	9	Histone H5
IPR000347	4	Plant metallothionein, family 15
IPR007834	4	DSS1/SEM1
IPR007836	2	Ribosomal protein L41
IPR001813	2	Ribosomal protein 60S
IPR004184	2	Pyruvate formate-lyase, PFL
IPR010800	2	Glycine rich
IPR001878	1	Zinc finger, CCHC-type
IPR005124	1	Vacuolar (H ⁺)-ATPase G subunit
IPR001437	1	Transcription elongation factor, GreA/GreB region, prokaryotic
IPR005516	1	Remorin, C-terminal region
IPR007608	1	Protein of unknown function DUF584
IPR005174	1	Protein of unknown function DUF295
IPR012866	1	Protein of unknown function DUF1644
IPR009806	1	Photosystem II protein PsbW, class 2
IPR005770	1	Phosphonate-binding periplasmic protein
IPR002130	1	Peptidyl-prolyl cis-trans isomerase, cyclophilin-type
IPR012906	1	PaaX-like, N-terminal
IPR007513	1	Four F5 protein
IPR000259	1	Fimbrial protein
IPR000167	1	Dehydrin
IPR008276	1	Concentrative nucleoside transporter
IPR002543	1	Cell divisionFtsK/SpoIIIE
IPR000515	1	Binding-protein-dependent transport systems inner membrane component
IPR001188	1	Bacterial periplasmic spermidine/putrescine-binding protein
Total	43	

Table S2

Gene ontology (GO) mappings of 9414 unigenes using GOBlet's plants database. Note that individual GO categories can have multiple mappings

Categories and subcategories	GO ID	Representation		Percentage of total
(a) Molecular function	GO:0003674	4092		100
motor activity	GO:0003774	31		0.8
microtubule motor activity	GO:0003777	30		0.7
catalytic activity	GO:0003824	2300		56.2
glycogen debranching enzyme activity	GO:0004133	4		0.1
helicase activity	GO:0004386	75		1.8
transposase activity	GO:0004803	6		0.1
3,4-dihydroxy-2-butanone-4-phosphate synthase activity	GO:0008686	2		0.0
integrase activity	GO:0008907	2		0.0
oxidoreductase activity	GO:0016491	427		10.4
transferase activity	GO:0016740	861		21.0
hydrolase activity	GO:0016787	771		18.8
lyase activity	GO:0016829	133		3.3
isomerase activity	GO:0016853	105		2.6
ligase activity	GO:0016874	123		3.0
signal transducer activity	GO:0004871	135		3.3
two-component sensor molecule activity	GO:0001155	38		0.9
two-component response regulator activity	GO:0000156	19		0.5
receptor activity	GO:0004872	99		2.4
receptor signaling protein activity	GO:0005057	7		0.2
receptor binding	GO:0005102	5		0.1
structural molecule activity	GO:0005198	243		5.9
structural constituent of ribosome	GO:0003735	200		4.9
structural constituent of cell wall	GO:0005199	19		0.5
structural constituent of cytoskeleton	GO:0005200	21		0.5
transporter activity	GO:0005215	380		9.3
amine transporter activity	GO:0005275	8		0.2
lipid transporter activity	GO:0005319	2		0.0
organic acid transporter activity	GO:0005342	14		0.3
oxygen transporter activity	GO:0005344	3		0.1
carrier activity	GO:0005386	250		6.1
intracellular transporter activity	GO:0005478	5		0.1
electron transporter activity	GO:0005489	102		2.5
protein transporter activity	GO:0008565	30		0.7
ion transporter activity	GO:0015075	157		3.8
carbohydrate transporter activity	GO:0015144	21		0.5
drug transporter activity	GO:0015238	9		0.2
channel or pore class transporter activity	GO:0015267	24		0.6
ATPase activity, coupled to movement of substances	GO:0043492	58		1.4
binding	GO:0005488	2447		59.8
nucleotide binding	GO:0000166	886		21.7
pattern binding	GO:0001871	5		0.1
nucleic acid binding	GO:0003676	777		19.0
chromatin binding	GO:0003682	8		0.2
steroid binding	GO:0005496	1		<0.1
protein binding	GO:0005515	483		11.8
lipid binding	GO:0008289	39		1.0
selenium binding	GO:0008430	5		0.1
vitamin binding	GO:0019842	26		0.6
carbohydrate binding	GO:0030246	54		1.3
carboxylic acid binding	GO:0031406	9		0.2
peptide binding	GO:0042277	1		<0.1
ribonucleoprotein binding	GO:0043021	2		0.1
ion binding	GO:0043167	721		17.6
amine binding	GO:0043176	9		0.2
tetrapyrrole binding	GO:0046906	58		1.4
cofactor binding	GO:0048037	126		3.1
metal cluster binding	GO:0051540	7		0.2
antioxidant activity	GO:0016209	54		1.3
glutathione-disulfide reductase activity	GO:0004362	1		<0.1

peroxidase activity	GO:0004601	52	1.3
thioredoxin-disulfide reductase activity	GO:0004791	1	<0.1
enzyme regulator activity	GO:0030234	36	0.9
enzyme inhibitor activity	GO:0004857	16	0.4
enzyme activator activity	GO:0008047	4	0.1
kinase regulator activity	GO:0019207	5	0.1
phosphatase regulator activity	GO:0019208	7	0.2
GTPase regulator activity	GO:0030695	8	0.2
transcription regulator activity	GO:0030528	184	4.5
two-component response regulator activity	GO:0000156	19	0.5
transcription factor activity	GO:0003700	281	6.9
RNA polymerase II transcription factor activity	GO:0003702	4	0.1
transcriptional elongation regulator activity	GO:0003711	6	0.1
transcription cofactor activity	GO:0003712	31	0.8
transcription termination factor activity	GO:0003715	1	0.0
transcriptional activator activity	GO:0016563	8	0.2
transcriptional repressor activity	GO:0016564	14	0.3
transcription initiation factor activity	GO:0016986	7	0.2
translation regulator activity	GO:0045182	60	1.5
translation factor activity, nucleic acid binding	GO:0008135	108	2.6
nutrient reservoir activity	GO:0045735	11	0.3
(b) Cellular component	GO:0005575	1882	100
extracellular region	GO:0005576	34	1.8
apoplast	GO:0048046	20	1.1
cell	GO:0005623	1832	97.3
cell fraction	GO:0000267	1	0.1
intracellular	GO:0005622	1510	80.2
cell surface	GO:0009986	3	0.2
membrane	GO:0016020	668	35.5
external encapsulating structure	GO:0030312	32	1.7
periplasmic space	GO:0042597	5	0.3
cell projection	GO:0042995	7	0.4
virion	GO:0019012	9	0.5
viral capsid	GO:0019028	7	0.4
viral envelope	GO:0019031	2	0.1
membrane-enclosed lumen	GO:0031974	15	0.8
organelle lumen	GO:0043233	15	0.8
envelope	GO:0031975	177	9.4
cell envelope	GO:0030313	2	0.1
organelle envelope	GO:0031967	175	9.3
organelle	GO:0043226	1181	62.8
vesicle	GO:0031982	36	1.9
membrane-bound organelle	GO:0043227	928	49.3
non-membrane-bound organelle	GO:0043228	333	17.7
intracellular organelle	GO:0043229	1167	62.0
organelle lumen	GO:0043233	15	0.8
protein complex	GO:0043234	548	29.1
phosphopyruvate hydratase complex	GO:0000015	31	1.6
exocyst	GO:0000145	17	0.9
1,3-beta-glucan synthase complex	GO:0000148	17	0.9
ubiquitin ligase complex	GO:0000151	11	0.6
exosome (RNase complex)	GO:0000178	1	0.1
proteasome complex (sensu Eukaryota)	GO:0000502	32	1.7
nucleosome	GO:0000786	44	2.3
nuclear pore	GO:0005643	95	5.0
transcription factor complex	GO:0005667	44	2.3
signal peptidase complex	GO:0005787	8	0.4
heterotrimeric G-protein complex	GO:0005834	1	0.1
fatty acid synthase complex	GO:0005835	3	0.2
proteasome regulatory particle (sensu Eukaryota)	GO:0005838	8	0.4
eukaryotic translation initiation factor 3 complex	GO:0005852	2	0.1
eukaryotic translation elongation factor 1 complex	GO:0005853	3	0.2
microtubule associated complex	GO:0005875	35	1.9
unlocalized protein complex	GO:0005941	26	1.4

6-phosphofructokinase complex	GO:0005945	20	1.1
protein kinase CK2 complex	GO:0005956	5	0.3
glycine cleavage complex	GO:0005960	8	0.4
glycine dehydrogenase complex (decarboxylating)	GO:0005961	3	0.2
voltage-gated potassium channel complex	GO:0008076	9	0.5
signalosome complex	GO:0008180	19	1.0
F-actin capping protein complex	GO:0008290	2	0.1
cytochrome b6f complex	GO:0009512	1	0.1
photosystem I	GO:0009522	26	1.4
photosystem II	GO:0009523	20	1.1
oxygen evolving complex	GO:0009654	20	1.1
prefoldin complex	GO:0016272	8	0.4
eukaryotic 43S preinitiation complex	GO:0016282	2	0.1
myosin	GO:0016459	17	0.9
proton-transporting two-sector ATPase complex	GO:0016469	107	5.7
hydrogen-translocating V-type ATPase complex	GO:0016471	2	0.1
chromatin remodeling complex	GO:0016585	17	0.9
DNA-directed RNA polymerase II, holoenzyme	GO:0016591	3	0.2
light-harvesting complex	GO:0030076	1	0.1
ribonucleoprotein complex	GO:0030529	252	13.4
Mre11 complex	GO:0030870	12	0.6
RNA polymerase complex	GO:0030880	2	0.1
NADH dehydrogenase complex (quinone)	GO:0030964	6	0.3
mitochondrial intermembrane space protein transporter complex	GO:0042719	6	0.3
GPI-anchor transamidase complex	GO:0042765	9	0.5
receptor complex	GO:0043235	1	0.1
oxoglutarate dehydrogenase complex	GO:0045252	4	0.2
pyruvate dehydrogenase complex	GO:0045254	6	0.3
proton-transporting ATP synthase complex	GO:0045259	9	0.5
proton-transporting ATP synthase complex, catalytic core	GO:0045261	9	0.5
proton-transporting ATP synthase complex, coupling factor	GO:0045263	1	0.1
respiratory chain complex I	GO:0045271	4	0.2
respiratory chain complex III	GO:0045275	5	0.3
ubiquinol-cytochrome-c reductase complex	GO:0045285	5	0.3
ribulose biphosphate carboxylase complex	GO:0048492	11	0.6
(c) Biological process	GO:0008150	3195	100
reproduction	GO:0000003	8	0.3
sexual reproduction	GO:0019953	8	0.3
development	GO:0007275	40	1.3
pattern specification	GO:0007389	1	<0.1
aging	GO:0007568	2	0.1
morphogenesis	GO:0009653	1	<0.1
post-embryonic development	GO:0009791	5	0.2
cell differentiation	GO:0030154	9	0.3
regulation of gene expression, epigenetic	GO:0040029	14	0.4
root development	GO:0048364	2	0.1
meristem development	GO:0048507	1	<0.1
organ development	GO:0048513	2	0.1
regulation of development	GO:0050793	1	<0.1
physiological process	GO:0007582	3073	96.2
metabolism	GO:0008152	2603	81.5
photosynthesis	GO:0015979	63	2.0
death	GO:0016265	57	1.8
homeostasis	GO:0042592	18	0.6
regulation of physiological process	GO:0050791	359	11.2
coagulation	GO:0050817	1	0.03
organismal physiological process	GO:0050874	6	0.2
cellular physiological process	GO:0050875	2801	87.7
localization	GO:0051179	626	19.6
cellular process	GO:0009987	2853	89.3
cell communication	GO:0007154	137	4.3
cell adhesion	GO:0007155	7	0.2
cell differentiation	GO:0030154	9	0.3

regulation of cellular process	GO:0050794	353	11.0
cellular physiological process	GO:0050875	2801	87.7
growth	GO:0040007	1	0.03
cell growth	GO:0016049	1	0.03
regulation of biological process	GO:0050789	388	12.1
regulation of gene expression, epigenetic	GO:0040029	14	0.4
positive regulation of biological process	GO:0048518	8	0.3
negative regulation of biological process	GO:0048519	26	0.8
regulation of enzyme activity	GO:0050790	23	0.7
regulation of physiological process	GO:0050791	359	11.2
regulation of development	GO:0050793	1	0.03
regulation of cellular process	GO:0050794	353	11.0
response to stimulus	GO:0050896	267	8.4
response to stress	GO:0006950	220	6.9
response to external stimulus	GO:0009605	32	1.0
response to biotic stimulus	GO:0009607	96	3.0
response to abiotic stimulus	GO:0009628	119	3.7
response to endogenous stimulus	GO:0009719	78	2.4
detection of stimulus	GO:0051606	3	0.1
interaction between organisms	GO:0051704	4	0.1
interspecies interaction between organisms	GO:0044419	4	0.1
physiological interaction between organisms	GO:0051706	1	<0.1

(a) 4092 clusters generated 13 301 multiple mappings. Percentage representation is based on 4092.

(b) 1882 clusters generated 9732 multiple mappings. Percentage representation is based on 1882.

(c) 3195 clusters generated 17 859 multiple mappings. Percentage representation is based on 3195.