

Supplementary data for article:

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Table S4. Gene ontology (GO) cellular component analyses revealed that TOT, SPP a

Table S4. was generated by QuickGO (<http://www.ebi.ac.uk/QuickGO>). Software was "fed" by protein group (defined 99 GO terms-identifiers) was used, thus containing all relevant terms for 3 aspects: cellular local

Green cell colour marks lyase activity and its annotation percentage by protein.

TOT annotations (by protein)				SPP annotations (by protein)			
Code	Name	Percentage	Count	Code	Name	Percentage	Count
GO:004310	ion binding	57.14	36	GO:0043167	ion binding	57.14	36
GO:000010	nucleotide binding	33.33	21	GO:0009056	catabolic process	33.33	21
GO:000180	nucleoside binding	28.57	18	GO:0008152	metabolic process	28.57	18
GO:000810	metabolic process	26.98	17	GO:0016829	lyase activity	26.98	17
GO:000900	catabolic process	25.40	16	GO:0000166	nucleotide binding	25.40	16
GO:000910	nucleotide metabolic process	20.63	13	GO:0005976	polysaccharide metabolic process	20.63	13
GO:000910	nucleoside metabolic process	20.63	13	GO:0016491	oxidoreductase activity	20.63	13
GO:001680	lyase activity	19.05	12	GO:0009117	nucleotide metabolic process	19.05	12
GO:000590	carbohydrate metabolic process	17.46	11	GO:0009116	nucleoside metabolic process	17.46	11
GO:001670	hydrolase activity	14.29	9	GO:0001882	nucleoside binding	14.29	9
GO:001640	oxidoreductase activity	14.29	9	GO:0009058	biosynthetic process	14.29	9
GO:000900	biosynthetic process	14.29	9	GO:0016740	transferase activity	14.29	9
GO:000670	phosphorus metabolic process	12.70	8	GO:0006082	organic acid metabolic process	12.70	8
GO:000590	polysaccharide metabolic process	12.70	8	GO:0005975	carbohydrate metabolic process	12.70	8
GO:005110	cofactor metabolic process	11.11	7	GO:0051186	cofactor metabolic process	11.11	7
GO:001630	kinase activity	11.11	7	GO:0016787	hydrolase activity	11.11	7
GO:000990	cellular process	11.11	7	GO:0016301	kinase activity	11.11	7
GO:000600	generation of precursor metabolite	11.11	7	GO:0016020	membrane	11.11	7
GO:000600	organic acid metabolic process	11.11	7	GO:0009536	plastid	11.11	7
GO:001670	transferase activity	9.52	6	GO:0006793	phosphorus metabolic process	9.52	6
GO:000580	cytoskeleton	9.52	6	GO:0005515	protein binding	9.52	6
GO:000570	cytoplasm	9.52	6	GO:0006950	response to stress	9.52	6
GO:001680	isomerase activity	7.94	5	GO:0006091	generation of precursor metabolite	7.94	5
GO:000550	protein binding	7.94	5	GO:0065007	biological regulation	7.94	5
GO:001600	membrane	6.35	4	GO:0048037	cofactor binding	6.35	4
GO:000690	response to stress	6.35	4	GO:0009055	electron carrier activity	6.35	4
GO:000380	catalytic activity	6.35	4	GO:0006810	transport	6.35	4
GO:001640	proton-transporting two-sector ATPase	4.76	3	GO:0005856	cytoskeleton	4.76	3
GO:000950	plastid	4.76	3	GO:0005739	mitochondrion	4.76	3
GO:000680	hydrogen transport	4.76	3	GO:0005737	cytoplasm	4.76	3
GO:000680	ion transport	4.76	3	GO:0046906	tetrapyrrole binding	4.76	3
GO:000680	transport	4.76	3	GO:0044255	cellular lipid metabolic process	4.76	3
GO:000560	intracellular	4.76	3	GO:0030234	enzyme regulator activity	4.76	3
GO:000520	transporter activity	4.76	3	GO:0016853	isomerase activity	4.76	3
GO:006500	biological regulation	3.17	2	GO:0009987	cellular process	3.17	2
GO:004800	cofactor binding	3.17	2	GO:0008233	peptidase activity	3.17	2
GO:004690	tetrapyrrole binding	3.17	2	GO:0006508	proteolysis	3.17	2
GO:004420	cellular metabolic process	3.17	2	GO:0006457	protein folding	3.17	2
GO:001620	antioxidant activity	3.17	2	GO:0003824	catalytic activity	3.17	2

GO:00090: electron carrier activity	3.17	2	GO:0045333 cellular respiration
GO:00082: peptidase activity	3.17	2	GO:0044237 cellular metabolic process
GO:00081: translation factor activity, RNA bi	3.17	2	GO:0043234 protein complex
GO:00065: proteolysis	3.17	2	GO:0043021 ribonucleoprotein complex bindi
GO:00064: translation	3.17	2	GO:0016874 ligase activity
GO:00057: mitochondrion	3.17	2	GO:0016469 proton-transporting two-sector /
GO:00051: structural molecule activity	3.17	2	GO:0016209 antioxidant activity
GO:00508: response to stimulus	1.59	1	GO:0015979 photosynthesis
GO:00442: cellular lipid metabolic process	1.59	1	GO:0009719 response to endogenous stimulu
GO:00432: protein complex	1.59	1	GO:0009317 acetyl-CoA carboxylase complex
GO:00430: ribonucleoprotein complex bindi	1.59	1	GO:0008289 lipid binding
GO:00302: enzyme regulator activity	1.59	1	GO:0008135 translation factor activity, RNA bi
GO:00159: photosynthesis	1.59	1	GO:0007165 signal transduction
GO:00096: response to abiotic stimulus	1.59	1	GO:0006869 lipid transport
GO:00095: thylakoid	1.59	1	GO:0006818 hydrogen transport
GO:00093: amine metabolic process	1.59	1	GO:0006811 ion transport
GO:00082: lipid binding	1.59	1	GO:0006730 one-carbon metabolic process
GO:00068: lipid transport	1.59	1	GO:0006629 lipid metabolic process
GO:00066: lipid metabolic process	1.59	1	GO:0006464 cellular protein modification pro
GO:00064: cellular protein modification pro	1.59	1	GO:0006412 translation
GO:00064: protein folding	1.59	1	GO:0006396 RNA processing
GO:00060: cellular aldehyde metabolic proc	1.59	1	GO:0006119 oxidative phosphorylation
GO:00060: alcohol metabolic process	1.59	1	GO:0006081 cellular aldehyde metabolic proc
GO:00058: cytosol	1.59	1	GO:0005829 cytosol
GO:00056: nucleus	1.59	1	GO:0005783 endoplasmic reticulum
GO:00037: RNA binding	1.59	1	GO:0005634 nucleus
GO:00036: nucleic acid binding	1.59	1	GO:0005622 intracellular
TOTAL OF 66 GO identifiers			GO:0005576 extracellular region
			GO:0005215 transporter activity
			GO:0003723 RNA binding
			TOTAL OF 69 GO identifiers

and APE have different number of GO identifiers.

entries from Tables S1-3, Plant GO Slim (a selection of pre-
 zylation, molecular functions and biological processes.

APE annotations (by protein)					
Percentage	Count	Code	Name	Percentage	Count
55.17	32	GO:004316	ion binding	55.56	25
24.14	14	GO:000901	catabolic process	22.22	10
24.14	14	GO:000815	metabolic process	22.22	10
22.41	13	GO:000181	nucleoside binding	22.22	10
18.97	11	GO:000016	nucleotide binding	22.22	10
17.24	10	GO:001687	lyase activity	15.56	7
15.52	9	GO:001648	oxidoreductase activity	15.56	7
15.52	9	GO:000597	polysaccharide metabolic process	15.56	7
15.52	9	GO:000691	response to stress	13.33	6
15.52	9	GO:000597	carbohydrate metabolic process	11.11	5
12.07	7	GO:000557	protein binding	11.11	5
10.34	6	GO:001674	hydrolase activity	8.89	4
10.34	6	GO:000917	nucleotide metabolic process	8.89	4
10.34	6	GO:000917	nucleoside metabolic process	8.89	4
8.62	5	GO:000607	organic acid metabolic process	8.89	4
8.62	5	GO:005111	cofactor metabolic process	6.67	3
8.62	5	GO:001687	isomerase activity	6.67	3
8.62	5	GO:001674	transferase activity	6.67	3
8.62	5	GO:001631	kinase activity	6.67	3
8.62	5	GO:000901	biosynthetic process	6.67	3
8.62	5	GO:000671	phosphorus metabolic process	6.67	3
6.90	4	GO:000607	generation of precursor metabolites	6.67	3
6.90	4	GO:000581	cytoskeleton	6.67	3
5.17	3	GO:000577	cytoplasm	6.67	3
5.17	3	GO:006501	biological regulation	4.44	2
5.17	3	GO:004691	tetrapyrrole binding	4.44	2
5.17	3	GO:003021	enzyme regulator activity	4.44	2
5.17	3	GO:001621	antioxidant activity	4.44	2
5.17	3	GO:000901	electron carrier activity	4.44	2
5.17	3	GO:000641	protein folding	4.44	2
3.45	2	GO:000381	catalytic activity	4.44	2
3.45	2	GO:005081	response to stimulus	2.22	1
3.45	2	GO:004421	cellular lipid metabolic process	2.22	1
3.45	2	GO:004421	cellular metabolic process	2.22	1
3.45	2	GO:001601	membrane	2.22	1
3.45	2	GO:000991	cellular process	2.22	1
3.45	2	GO:000951	plastid	2.22	1
3.45	2	GO:000821	lipid binding	2.22	1
3.45	2	GO:000821	peptidase activity	2.22	1

