

Table S1. Identified proteins in roots of *Musa acuminata* cv. Berangan

Spot	Identification	Taxonomy	Accession number	Database	Mascot scores	Matched peptide	Protein sequence coverage (%)	Theoretical		Experimental	
								Mass (kDa)	pI	Mass (kDa)	pI
Carbohydrate and energy metabolism											
180	Malate dehydrogenase	Nicotiana tabacum	MDH_TOB AC	SwissProt	291	15	21	36	5.9	43	6.8
47	Glutathione S-transferase	Silene vulgaris	GSTF_SILV U	SwissProt	34	1	3	25	5.9	27	6.1
Defense and stress response											
78	Germin-like protein 5-1	Oryza sativa subsp. japonica	GL52_ORY SJ	SwissProt	125	10	13	23	8.4	32	8.5
171	Isoflavone reductase homolog A622	Nicotiana tabacum	IFRH_TOB AC	LudwigNR	44	1	3	35	5.6	39	7.0
Protein catabolism											
35	Proteasome subunit beta type-6	Nicotiana tabacum	PSB6_TOB AC	SwissProt	54	1	6	25	5.2	25	5.8
59	Probable protein phosphatase 2C 57	Oryza sativa subsp. japonica	P2C57_OR YSJ	SwissProt	32	1	2	40	5.3	29	8.2
Organelle											
185	Putative UPF0496 protein 5	Oryza sativa subsp. indica	U496E_OR YSI	SwissProt	43	1	1	48	6.5	15	7.3
95	Putative UPF0496 protein 5	Oryza sativa subsp. indica	U496E_OR YSI	SwissProt	33	2	1	48	6.5	35	5.7
Protein synthesis/ Here ambiguous function											
84	Rubber elongation factor protein	Hevea brasiliensis	P15252	SwissProt	44	2	7	15	5.0	32	7.4

Table S1. Continued

Spot	Identification	Taxonomy	Accession number	Database	Mascot scores	Matched peptide	Protein sequence coverage (%)	Theoretical		Experimental	
								Mass (kDa)	pI	Mass (kDa)	pI
5	Rubber elongation factor protein	<i>Hevea brasiliensis</i>	P15252	SwissProt	35	2	15	15	5.0	14	5.9