Supplementary table 1 Differential protein spots between GCF and WCF identified by MS/MS

Spot no.	Protein name	GenBank acc. no.	Protein score	species	Matched peptides	Sequence coverage	Change		
							12	15	24
				Secondary metabolism					
14	PCBER	ABN12322	127	*Gossypium hirsutum*	8	38%	-3.44	-2.11	
19	**PCBER**	ABN12322	167	*Gossypium hirsutum*	8	35%		NDW	NDW
17	Flavanone-3-hydroxylase	ABM64799	325	*Gossypium hirsutum*	16	63%		-2.10	
				Energy/carbohydrate metabolism					
13	Phosphoglycerate kinase	ACJ11718	364	*Gossypium hirsutum*	14	53%	-2.65	-2.79	
16	Triosephosphate isomerase	AAP40643	281	*Gossypium barbadense*	6	89%	-2.35	-1.64	
7	Phosphoglycerate dehydrogenase	ACJ11736	495	*Gossypium hirsutum*	19	42%	-2.08	-3.61	
6	Phosphoglycerate dehydrogenase	ACJ11736	495	*Gossypium hirsutum*	19	54%	-2.65		
				Cell wall related proteins					
22	Alpha-1,4-glucan-protein synthase	AAB88408	193	*Pisum sativum*	8	35%			-1.96
9	UDP-D-glucose pyrophosphorylase	ACJ11710	517	*Gossypium hirsutum*	12	47%	-2.92		-1.73
23	RGP-like protein	ABG75999	172	*Gossypium hirsutum*	9	31%			-1.94
12	RGP-like protein	ABG76000	318	*Gossypium hirsutum*	13	54%	-2.41		-9.40
5	Phosphoglucomutase	EEF34593	156	*Ricinus communis*	12	29%	-2.11		-3.35
				Cytoskeleton					
15	Actin (fragment)	CAN86935	77	*Cynara scolymus*	6	51%	-2.32	NDG	NDG
				Protein metabolism					
8	Rubisco subunit binding- protein beta subunit	AAA66365	410	*Pisum sativum*	14	34%	NDG		
20	Heat shock protein	EEF49244	331	*Ricinus communis*	16	37%			NDG
21	Heat shock protein	ACJ11742	397	*Gossypium hirsutum*	23	53%			NDG
4	Heat shock protein 70Kda	AAO17017	167	*Oryza sativa Japonica Group*	12	32%	NDG		NDG
10	Acyl-[acyl-carrier-protein] desaturase	CAB75356	91	*Gossypium hirsutum*	10	28%	-4.06		
				Amino acid metabolism					
11	*s*-adenosylmethionine synthase	ADN96174	381	*Gossypium hirsutum*	15	46%	NDG	NDG	NDG
25	*s*-adenosylmethionine synthase	ABO80948	460	*Medicago truncatula*	14	43%			2.56
				Cell response					
24	Betaine aldehyde dehydrogenase	BAE07176	94	*Beta vulgaris*	3	9%			1.80

Spot no.	**Protein name**	**GenBank acc. no.**	**Protein score**	**species**	**Matched peptides**	**Sequence coverage**	**Change** 12	15	24
				Lipid metabolism					
18	Phospholipase D	ACV70146	412	*Gossypium arboreum*	33	55%		5.89	2.68
3	Phospholipase D	ACG63795	851	*Gossypium raimondii*	36	56%	-3.15		-3.20
2	Transitional endoplasmic reticulum ATPase	EEF43196	970	*Ricinus communis*	30	12	-5.89		
1	Transitional endoplasmic reticulum ATPase	EEF43196	489	*Ricinus communis*	31	12	-5.89		

"Change" in table head represents a ratio of the protein spots %volume ratio between the GCF and WCF. Negative and positive values in the column indicate decreases and increases in abundance in GCF, respectively. The ratio for some spots cannot be calculated due to their absence in either GCF or WCF; NDW: not detectable in the 2-DE maps of WCF; NDG: not detectable in the 2-DE maps of GCF.