Supplemental Table 2. Description of transcripts with a significant [CO_2] x developmental stage interaction. Genes were clustered into four groups using k-means clustering (see Figure 3). Annotations are based first on the BLASTX hit of the 3′ end EST if sequence information was available, and second on the 5′ end EST.

	Clone ID	**Annotation**	**E**
Cluster 1	Gm-r1070-6478	DAG [Antirrhinum majus]	6.6E-71
	Gm-r1088-5307	putative growth-on protein GRO10 [Oryza sativa]	2.0E-18
	Gm-r1088-8361	DNA-binding protein PD1 [Pisum sativum]	2.7E-34
	Gm-r1070-8398	chloroplast RNA binding protein [Phaseolus vulgaris]	5.8E-48
	Gm-r1088-7127	No Hits	
	Gm-r1070-1656	At5g39570/MIJ24_40 [Arabidopsis thaliana]	8.0E-21
	Gm-r1070-3608	unknown [Arabidopsis thaliana]	6.6E-17
	Gm-r1070-7604	At1g36050 [Arabidopsis thaliana]	2.9E-32
	Gm-r1088-7685	T6D22.8 [Arabidopsis thaliana]	1.5E-15
	Gm-r1070-4312	putative Mob1-like protein [Oryza sativa]	6.6E-103
	Gm-r1070-874	triosephosphate isomerase [Glycine max]	2.1E-25
	Gm-r1088-8178	lipoxygenase [Citrus jambhiri]	1.9E-63
	Gm-r1070-7482	phosphatidylserine decarboxylase-like [Oryza sativa]	3.7E-38
	Gm-r1070-8754	acetyl-CoA carboxylase [Glycine max]	1.4E-90
	Gm-r1070-6484	ATP synthase (gamma subunit, chloroplast precursor) [Pisum sativum]	1.5E-79
	Gm-r1070-8315	photosystem I reaction center subunit III [Vigna radiata]	1.5E-81
	Gm-r1070-4121	casein kinase II alpha subunit [Sinapis alba]	1.2E-30
	Gm-r1070-4296	putative CBL-interacting protein kinase 23 [Oryza sativa]	5.5E-34
	Gm-r1070-7416	LEC1-like protein [Phaseolus coccineus]	9.9E-76
	Gm-r1070-8950	Helicase, C-terminal; Zinc finger, CCHC-type [Medicago truncatula]	8.0E-70
	Gm-r1070-7242	rpoC2 [Glycine max]	9.8E-50
	Gm-r1070-8885	aspartyl protease family protein [Arabidopsis thaliana]	1.2E-08
	Gm-r1070-5304	calcium dependent protein kinase	3.9E-07
	Gm-r1088-7022	MDR-like p-glycoprotein [Arabidopsis thaliana]	3.4E-58
	Gm-r1070-8550	plasma membrane H+ ATPase [Prunus persica]	4.0E-15
	Gm-r1070-7680	putative plastid triose phophate translocator [Glycine max]	1.9E-41
	Gm-r1070-5372	No Hits	
	Gm-r1070-3541	No Hits	
	Gm-r1070-5874	unknown protein [Arabidopsis thaliana]	8.2E-21
	Gm-r1070-7217	No Hits	
	Gm-r1070-8604	KH domain-containing protein [Betula platyphylla]	1.6E-52
	Gm-r1088-6856	At3g09980 [Arabidopsis thaliana]	1.7E-43
Cluster 2	Gm-r1070-3758	ribosomal protein small subunit 28 [Helianthus annuus]	4.9E-20
	Gm-r1070-6640	ribosomal protein L38-like [Solanum tuberosum]	2.0E-28
	Gm-r1070-8751	ribosomal protein L29 [Panax ginseng]	1.1E-21
	Gm-r1070-5946	No Hits	

	Gm-r1070-4689	No Hits	
	Gm-r1070-5287	No Hits	
	Gm-r1070-5896	No Hits	
	Gm-r1070-6662	unknown [Arabidopsis thaliana]	2.2E-22
	Gm-r1070-8744	allantoinase [Robinia pseudoacacia]	2.0E-55
	Gm-r1070-7989	BiP [Glycine max]	4.7E-60
	Gm-r1070-9103	protein phosphatase 2C [Medicago sativa]	1.6E-27
	Gm-r1070-8375	DNAJ protein-like [Arabidopsis thaliana]	1.2E-32
	Gm-r1070-4491	No Hits	
	Gm-r1070-9110	AT5g55220/MCO15_17 [Arabidopsis thaliana]	6.3E-31
	Gm-r1070-2402	No Hits	
	Gm-r1070-1266	No Hits	
	Gm-r1070-4147	AT5g55940/MYN21_5 [Arabidopsis thaliana]	9.0E-61
	Gm-r1070-5320	expressed protein [Arabidopsis thaliana]	2.5E-23
	Gm-r1070-8574	expressed protein [Arabidopsis thaliana]	5.3E-18
	Gm-r1070-9170	3-oxoacyl-[acyl-carrier protein] reductase; beta-ketoacyl-ACP reductase [Cuphea lanceolata]	2.9E-30
	Gm-r1070-6846	NADPH-protochlorophyllide oxidoreductase [Cucumis sativus]	1.7E-77
	Gm-r1070-8056	putative TIP120 protein [Oryza sativa (japonica cultivar-group)]	3.7E-45
	Gm-r1070-5692	26S proteasome regulatory subunit, putative (RPN5) [Arabidopsis thaliana]	9.1E-35
	Gm-r1070-8184	20S proteasome beta subunit PBB2 [Arabidopsis thaliana]	2.1E-72
	Gm-r1070-3694	40S ribosomal protein S19-like [Arabidopsis thaliana]	5.1E-22
	Gm-r1070-6638	eIF3e [Arabidopsis thaliana]	2.5E-89
	Gm-r1070-6140	putative RING3 protein [Oryza sativa]	1.1E-08
	Gm-r1070-7982	putative small nuclear ribonucleoprotein polypeptide E [Oryza sativa (japonica cultivar-group)]	2.4E-36
	Gm-r1070-8620	MAP kinase PsMAPK2 [Pisum sativum]	5.3E-49
	Gm-r1070-9097	calnexin [Glycine max]	4.2E-77
	Gm-r1070-7474	stress related protein, putative [Arabidopsis thaliana]	4.7E-32
	Gm-r1070-7772	putative protein [Arabidopsis thaliana]	7.6E-81
	Gm-r1070-8984	No Hits	
	Gm-r1070-3130	chaperonin precursor [Pisum sativum]	9.0E-32
	Gm-r1070-3018	putative Lysyl-tRNA synthetase [Oryza sativa]	3.9E-25
	Gm-r1070-7104	At1g31850/68069_m00154 [Arabidopsis thaliana]	1.7E-43
	Gm-r1070-8602	putative triosephosphate isomerase [Arabidopsis thaliana]	1.7E-76
	Gm-r1070-5700	putative acetyltransferase [Arabidopsis thaliana]	5.5E-44
	Gm-r1070-5948	No Hits	
	Gm-r1070-6086	unknown protein [Oryza sativa]	2.9E-23
	Gm-r1070-8994	transcription factor lim1 [Eucalyptus camaldulensis]	2.7E-76
Cluster 3	Gm-r1070-2069	cullin [Arabidopsis thaliana]	3.2E-29
	Gm-r1070-1591	probable ubiquitin-like protein [imported] - Arabidopsis thaliana	6.8E-26

Gm-r1070-257	ubiquitin fusion protein [Arachis hypogaea]	1.1E-39
Gm-r1070-3911	ribosomal protein S5 [Spinacia oleracea]	2.9E-10
Gm-r1070-4267	carbonic anhydrase 2 [Flaveria bidentis]	4.2E-42
Gm-r1070-921	No Hits	
Gm-r1070-6562	No Hits	
Gm-r1070-795	No Hits	
Gm-r1070-829	No Hits	
Gm-r1088-8096	No Hits	
Gm-r1070-4803	fiber protein Fb12 [Gossypium barbadense]	6.1E-37
Gm-r1070-3835	putative beta-phosphoglucomutase [Arabidopsis thaliana]	9.8E-49
Gm-r1070-1020	Similar to dTDP-D-glucose 4,6-dehydratase [Arabidopsis thaliana]	1.3E-18
Gm-r1070-1390	glycinin [Glycine max]	6.0E-26
Gm-r1070-2259	putative ethanolamine kinase 1 [Oryza sativa]	8.2E-16
Gm-r1070-1399	annexin [Cicer arietinum]	4.7E-14
Gm-r1070-801	asparaginyl endopeptidase (VmPE-1) [Vigna mungo]	0
Gm-r1088-3109	putative CAAX amino terminal protease family protein [Solanum demissum]	1.9E-62
Gm-r1070-261	protein phosphatase type 2C [Lotus japonicus]	2.9E-23
Gm-r1070-395	putative integral membrane protein [Phaseolus vulgaris]	9.8E-90
Gm-r1070-4675	60S ribosomal protein L21 [Oryza sativa (japonica cultivar-group)]	4.2E-84
Gm-r1088-7328	ascorbate oxidase precursor [Glycine max]	6.2E-47
Gm-r1088-2433	helicase-like protein [Arabidopsis thaliana]	1.1E-20
Gm-r1070-4035	Sali3-2 [Glycine max]	3.6E-95
Gm-r1070-4157	Chain 1, Bean Pod Mottle Virus (Bpmv), Top Component	3.0E-6
Gm-r1070-1765	adenosine 5'-phosphosulfate reductase [Glycine max]	2.1E-74
Gm-r1070-909	oligouridylate binding protein [Nicotiana plumbaginifolia]	2.1E-29
Gm-r1070-3845	No Hits	
Gm-r1070-473	SAM (and some other nucleotide) binding motif [Medicago truncatula]	3.0 E-17
Gm-r1070-1935	At1g75460/F1B16_22 [Arabidopsis thaliana]	1.7E-28
Gm-r1070-917	No Hits	
Gm-r1070-919	No Hits	
Gm-r1070-823	No Hits	
Gm-r1070-1013	No Hits	
Gm-r1070-1019	No Hits	
Gm-r1070-1395	No Hits	
Gm-r1070-1793	expressed protein [Arabidopsis thaliana]	3.3E-17
Gm-r1070-2327	No Hits	
Gm-r1070-241	putative protein [Arabidopsis thaliana]	2.5E-55
Gm-r1070-3851	No Hits	
Gm-r1070-6401	unknown [Arabidopsis thaliana]	3.2E-19
Gm-r1070-997	No Hits	
Gm-r1070-39	Similar to phosphoribosylanthranilate transferase from	6.1E-26

		Pisum sativum [Arabidopsis thaliana]	
Cluster 4	Gm-r1070-6804	No Hits	
	Gm-r1088-751	At1g51580 [Arabidopsis thaliana]	8.8E-27
	Gm-r1088-839	unnamed protein product [Arabidopsis thaliana]	9.1E-35
	Gm-r1070-2173	No Hits	
	Gm-r1070-6303	unnamed protein product [Arabidopsis thaliana]	1.9E-17
	Gm-r1070-9038	Ni-binding urease accessory protein UreG [Glycine max]	4.7E-68
	Gm-r1088-3825	kinesin heavy chain, putative [Arabidopsis thaliana]	6.9E-46
	Gm-r1070-5796	putative NAD dependent epimerase [Arabidopsis thaliana]	2.2E-90
	Gm-r1088-767	glycosyl hydrolase family 17 protein [Arabidopsis thaliana]	4.0E-62
	Gm-r1070-5263	putative protein phosphatase [Oryza sativa (japonica cultivar-group)]	2.5E-20
	Gm-r1070-2913	putative ribophorin I [Arabidopsis thaliana]	5.0E-82
	Gm-r1070-6083	cysteine protease [Ipomoea batatas]	1.1E-49
	Gm-r1070-2921	putative ribosomal protein L7 [Arabidopsis thaliana]	1.3E-33
	Gm-r1088-4199	plastid-specific ribosomal protein 2 precursor [Spinacia oleracea]	1.3E-52
	Gm-r1088-2243	putative cyclic nucleotide and calmodulin-regulated ion channel protein [Arabidopsis thaliana]	1.7E-32
	Gm-r1088-1027	No Hits	
	Gm-r1088-953	No Hits	
	Gm-r1070-5026	No Hits	
	Gm-r1070-2665	No Hits	
	Gm-r1088-941	No Hits	
	Gm-r1070-4051	fiber protein Fb33 [Gossypium barbadense]	9.7E-56
	Gm-r1070-6383	No Hits	
	Gm-r1070-2555	apyrase GS52 [Glycine soja]	8.9E-26