Table S1 - Identified candidates among abiotic stress responsive gene categories in soybean and *Medicago* genomes based on selected arabidopsis seed sequences, as well as number of other hits, e-value and score, against the respective database of *Medicago truncatula* (Mt) and *Glycine max* (Gm).

Arabidopsis Information		**Blast Result**				
Category	**Query Sequence**	**Best Hit**	**Organism**	**Other Hits**	**E-value**	**Score**
bZIP Transcription Factor	At1g42990	Mt_bZIP_1	*M. truncatula*	2	7,00 e-12	67.4
Carbohydrate Metabolism	At3g10740	Mt_Carb_Met_1	*M. truncatula*	7	0.0	959
		Gm_Carb_Met_1	*G. max*	8	0.0	947
	At3g06500	Gm_Carb_Met_2	*G. max*	7	6,00 e-121	430
		Mt_Carb_Met_2	*M. truncatula*	6	0.0	788
	At3g60130	Gm_Carb_Met_3	*G. max*	2	8,00 e-76	280
		Mt_Carb_Met_3	*M. truncatula*	5	1,00 e-107	386
	At5g18670	Gm_Carb_Met_4	*G. max*	3	1,00 e-166	582
		Mt_Carb_Met_4	*M. truncatula*	3	8,00 e-141	496
	At3g04240	Gm_Carb_Met_5	*G. max*	19	0.0	919
		Mt_Carb_Met_5	*M. truncatula*	17	0.0	1166
	At2g43820	Gm_Carb_Met_6	*G. max*	5	5,00 e-98	353
		Mt_Carb_Met_6	*M. truncatula*	10	2,00 e-106	382
Cellular Metabolism	At3g53180	Gm_Cell_Met_1	*G. max*	1	8,00 e-83	304
		Mt_Cell_Met_1	*M. truncatula*	7	9,00 e-175	610
	At3g45300	Gm_Cell_Met_2	*G. max*	4	2,00 e-60	229
		Mt_Cell_Met_2	*M. truncatula*	7	6,00 e-153	536
	At2g39210	Gm_Cell_Met_3	*G. max*	14	2,00 e-156	352
		Mt_Cell_Met_3	*M. truncatula*	8	1,00 e-91	333
	At2g42970	Gm_Cell_Met_4	*G. max*	2	3,00 e-91	331
		Mt_Cell_Met_4	*M. truncatula*	11	7,00 e-145	510
	At1g68620	Gm_Cell_Met_5	*G. max*	19	1,00 e-38	155
		Mt_Cell_Met_5	*M. truncatula*	19	7,00 e-40	159
Cellular Structure Organization and Biogenesis	At1g03220	Gm_Cell_Stru_Org_Biog_1	*G. max*	16	4,00 e-110	394
		Mt_Cell_Stru_Org_Biog_1	*M. truncatula*	19	4,00 e-145	510
	At3g10720	Gm_Cell_Stru_Org_Biog_2	*G. max*	7	1,00 e-123	437
		Mt_Cell_Stru_Org_Biog_2	*M. truncatula*	7	1,00 e-87	318
	At5g62350	Gm_Cell_Stru_Org_Biog_3	*G. max*	16	1,00 e-47	184
		Mt_Cell_Stru_Org_Biog_3	*M. truncatula*	18	9,00 e-47	182
	At5g20230	Gm_Cell_Stru_Org_Biog_4	*G. max*	19	7,00 e-21	95.9
		Mt_Cell_Stru_Org_Biog_4	*M. truncatula*	18	1,00 e-22	102
Cytochrome P450	At2g34500	Gm_Cytoch_P450_1	*G. max*	11	2,00 e-101	365
		Mt_Cytoch_P450_1	*M. truncatula*	12	0.0	684
	At3g26220	Gm_Cytoch_P450_2	*G. max*	4	2,00 e-85	311
		Mt_Cytoch_P450_2	*M. truncatula*	10	8,00 e-97	350
Detoxification Enzyme	At2g31570	Gm_Detox_Enz_1	*G. max*	14	4,00 e-43	169
		Mt_Detox_Enz_1	*M. truncatula*	17	9,00 e-40	157
	At2g29450	Gm_Detox_Enz_2	*G. max*	19	4,00 e-51	196
		Mt_Detox_Enz_2	*M. truncatula*	19	2,00 e-50	194

	At5g44070	Gm_Detox_Enz_3	*G. max*	6	4,00 e-107	374
		Mt_Detox_Enz_3	*M. truncatula*	2	1,00 e-95	346
DNA Nucleus	At2g18050	Gm_DNA_Nuc_1	*G. max*	5	3,00 e-11	63.2
		Mt_DNA_Nuc_1	*M. truncatula*	8	1,00 e-11	65.1
DREB/ERF Transcription Factor	At1g22190	Gm_DREB_ERF_TF_1	*G. max*	19	2,00 e-41	164
		Mt_DREB_ERF_TF_1	*M. truncatula*	18	2,00 e-37	152
	At4g17500	Gm_DREB_ERF_TF_2	*G. max*	19	6,00 e-33	136
		Mt_DREB_ERF_TF_2	*M. truncatula*	19	2,00 e-52	202
Ethylene Biosynthesis	At5g43450	Gm_Ethyl_Bios_1	*G. max*	7	1,00 e-112	402
		Mt_Ethyl_Bios_1	*M. truncatula*	19	4,00 e-106	380
	At1g17020	Gm_Ethyl_Bios_2	*G. max*	8	5,00 e-61	230
		Mt_Ethyl_Bios_2	*M. truncatula*	16	7,00 e-101	363
Fatty Acid Metabolism	At1g73480	Gm_Fatty_Acid_Met_1	*G. max*	14	6,00 e-96	347
		Mt_ Fatty_Acid_Met_1	*M. truncatula*	18	5,00 e-26	115
	At4g09760	Gm_Fatty_Acid_Met_2	*G. max*	8	3,00 e-94	340
		Mt_ Fatty_Acid_Met_2	*M. truncatula*	6	3,00 e-124	441
	At1g73920	Gm_Fatty_Acid_Met_3	*G. max*	3	2,00 e-58	222
		Mt_ Fatty_Acid_Met_3	*M. truncatula*	1	3,00 e-134	446
	At1g07720	Gm_Fatty_Acid_Met_4	*G. max*	19	2,00 e-92	335
		Mt_ Fatty_Acid_Met_4	*M. truncatula*	19	8,00 e-168	586
Ferritin	At5g01600	Gm_Ferritin_1	*G. max*	6	1,00 e-85	311
		Mt_ Ferritin_1	*M. truncatula*	13	1,00 e-87	318
Heat Shock Protein	At3g46230	Gm_HSF_1	*G. max*	19	2,00 e-51	197
		Mt_ HSF_1	*M. truncatula*	19	1,00 e-51	198
	At1g16030	Gm_HSF_2	*G. max*	8	0.0	996
		Mt_ HSF_2	*M. truncatula*	5	0.0	994
Homeodomain Transcription Factor	At2g35940	Gm_Homeodom_TF_1	*G. max*	19	8,00 e-88	320
		Mt_Homeodom_TF_1	*M. truncatula*	19	4,00 e-116	415
LEA Protein	At4g02380	Gm_LEA_1	*G. max*	6	6,00 e-09	55.5
		Mt_LEA_1	*M. truncatula*	4	2,00 e-07	50.4
Membrane Protein	At5g54170	Gm_Memb_Prot_1	*G. max*	7	1,00 e-116	415
		Mt_Memb_Prot_1	*M. truncatula*	6	3,00 e-113	332
	At1g30360	Gm_Memb_Prot_2	*G. max*	8	6,00 e-44	174
		Mt_Memb_Prot_2	*M. truncatula*	17	0.0	855
MYB Transcription Factor	At1g01060	Gm_MYB_TF_1	*G. max*	18	8,00 e-57	217
		Mt_MYB_TF_1	*M. truncatula*	11	4,00 e-25	112
NAC Transcription Factor	At5g63790	Gm_NAC_TF_1	*G. max*	10	1,00 e-89	325
		Mt_NAC_TF_1	*M. truncatula*	11	4,00 e-91	330
	At4g27410	Gm_NAC_TF_2	*G. max*	9	2,00 e-95	344
		Mt_NAC_TF_2	*M. truncatula*	10	2,00 e-94	341
Osmoprotectant	At2g47180	Gm_Osmoprot_1	*G. max*	4	2,00 e-142	500
		Mt_Osmoprot_1	*M. truncatula*	4	3,00 e-157	550
	At1g09350	Gm_Osmoprot_2	*G. max*	-	2,00 e-11	65.5
	At1g60470	Gm_Osmoprot_3	*G. max*	-	5,00 e-09	57.8
		Mt_Osmoprot_2	*M. truncatula*	-	9,00 e-16	80.9

	At3g57520	Gm_Osmoprot_4	*G. max*	8	9,00 e-155	543
		Mt_Osmoprot_3	*M. truncatula*	9	0.0	865
	At5g20830	Gm_Osmoprot_5	*G. max*	10	0.0	1410
		Mt_Osmoprot_4	*M. truncatula*	17	0.0	1384
Photosynthesis	At4g15530	Gm_Photosynt_1	*G. max*	7	6,00 e-143	504
		Mt_ Photosynt_1	*M. truncatula*	5	0.0	1102
Plant Defense	At3g55430	Gm_Plant_Defen_1	*G. max*	19	6,00 e-86	313
		Mt_Plant_Defen_1	*M. truncatula*	19	2,00 e-133	472
	At4g13580	Gm_Plant_Defen_2	*G. max*	19	4,00 e-42	166
		Mt_Plant_Defen_2	*M. truncatula*	19	1,00 e-67	252
	At2g40000	Gm_Plant_Defen_3	*G. max*	-	1,00 e-53	206
		Mt_Plant_Defen_3	*M. truncatula*	5	9,00 e-130	459
	At5g06860	Gm_Plant_Defen_4	*G. max*	18	6,00 e-109	389
		Mt_Plant_Defen_4	*M. truncatula*	19	2,00 e-100	362
Protein degradation	At1g47128	Gm_Prot_Degrad_1	*G. max*	19	0.0	634
		Mt_Prot_Degrad_1	*M. truncatula*	19	7,00 e-161	330
Protein Kinase	At2g31880	Gm_Prot_Kinase_1	*G. max*	15	7,00 e-166	309
		Mt_Prot_Kinase_1	*M. truncatula*	14	9,00 e-114	407
	At5g25110	Gm_Prot_Kinase_2	*G. max*	16	5,00 e-146	242
		Mt_Prot_Kinase_2	*M. truncatula*	13	3,00 e-143	504
Protein Phosphatase	At4g26080	Gm_Prot_Phosphat_1	*G. max*	13	3,00 e-108	387
		Mt_Prot_Phosphat_1	*M. truncatula*	13	7,00 e-98	353
	At3g11410	Gm_Prot_Phosphat_1	*G. max*	9	1,00 e-50	196
		Mt_Prot_Phosphat_1	*M. truncatula*	11	2,00 e-91	332
Reproductive Development	At5g56750	Gm_Reprod_Develop_1	*G. max*	14	3,00 e-162	566
		Mt_Reprod_Develop_1	*M. truncatula*	4	5,00 e-74	274
	At3g22370	Gm_Reprod_Develop_2	*G. max*	1	3,00 e-142	500
		Mt_Reprod_Develop_2	*M. truncatula*	13	9,00 e-143	502
Secondary Metabolism	At2g38240	Gm_Second_Metabol_1	*G. max*	13	3,00 e-67	251
		Mt_Second_Metabol_1	*M. truncatula*	7	1,00 e-125	445
Senescence-Related	At5g13170	Gm_Senesc_Relat_1	*G. max*	19	4,00 e-69	257
		Mt_Senesc_Relat_1	*M. truncatula*	19	1,00 e-74	275
Signalling	At5g33380	Gm_Siganlling_1	*G. max*	7	8,00 e-57	215
		Mt_Siganlling_1	*M. truncatula*	5	2,00 e-43	171
Transport Protein Ion Channel Carrier	At1g58360	Gm_Transp_Prot_Ion_1	*G. max*	19	4,00 e-116	414
		Mt_Transp_Prot_Ion_1	*M. truncatula*	19	1,00 e-180	629
	At1g08930	Gm_Transp_Prot_Ion_2	*G. max*	19	3,00 e-81	298
	At5g20380	Gm_Transp_Prot_Ion_3	*G. max*	5	5,00 e-93	337
		Mt_Transp_Prot_Ion_2	*M. truncatula*	12	1,00 e-86	317
	At2g22500	Gm_Transp_Prot_Ion_4	*G. max*	13	2,00 e-117	417
		Mt_Transp_Prot_Ion_3	*M. truncatula*	10	1,00 e-112	402
Unknown Protein	At5g22290	Gm_Unknown_1	*G. max*	7	6,00 e-42	167
		Mt_Unknown_1	*M. truncatula*	11	4,00 e-62	234
	At1g11210	Mt_Unknown_2	*M. truncatula*	-	8,00 e-11	64.3
	At1g15430	Gm_Unknown_2	*G. max*	3	5,00 e-28	120

	Mt_Unknown_3	*M. truncatula*	7	1,00 e-31	132
At1g55280	Gm_Unknown_3	*G. max*	-	9,00 e-34	140
	Mt_Unknown_4	*M. truncatula*	-	6,00 e-39	157
At1g63720	Gm_Unknown_4	*G. max*	5	2,00 e-20	95.5
	Mt_Unknown_5	*M. truncatula*	1	2,00 e-28	122
At1g69890	Gm_Unknown_5	*G. max*	1	2,00 e-76	281
	Mt_Unknown_6	*M. truncatula*	7	2,00 e-66	248
At1g76600	Gm_Unknown_6	*G. max*	1	4,00 e-16	80.5
	Mt_Unknown_7	*M. truncatula*	2	1,00 e-14	75.9
At2g26560	Gm_Unknown_7	*G. max*	4	3,00 e-124	441
	Mt_Unknown_8	*M. truncatula*	19	3,00 e-147	518
At2g32240	Gm_Unknown_8	*G. max*	1	2,00 e-39	160
	Mt_Unknown_9	*M. truncatula*	2	2,00 e-67	254
At2g38820	Gm_Unknown_9	*G. max*	14	2,00 e-56	214
	Mt_Unknown_10	*M. truncatula*	19	3,00 e-81	298
At2g41190	Gm_Unknown_10	*G. max*	15	1,00 e-61	233
	Mt_Unknown_11	*M. truncatula*	11	6,00 e-50	154
At3g17800	Gm_Unknown_11	*G. max*	12	6,00 e-79	290
	Mt_Unknown_12	*M. truncatula*	9	1,00 e-87	320
At4g21570	Gm_Unknown_12	*G. max*	13	3,00 e-106	380
	Mt_Unknown_13	*M. truncatula*	4	4,00 e-58	202
At4g25670	Gm_Unknown_13	*G. max*	3	5,00 e-29	123
	Mt_Unknown_14	*M. truncatula*	1	1,00 e-25	112
At4g27520	Gm_Unknown_14	*G. max*	7	7,00 e-20	94.0
	Mt_Unknown_15	*M. truncatula*	12	3,00 e-30	129
At4g30650	Gm_Unknown_15	*G. max*	6	2,00 e-13	70.1
	Mt_Unknown_16	*M. truncatula*	6	4,00 e-18	86.3
At4g38060	Gm_Unknown_16	*G. max*	-	9,00 e-18	84.7
	Mt_Unknown_17	*M. truncatula*	3	2,00 e-15	77.8
At5g02020	Gm_Unknown_17	*G. max*	1	8,00 e-10	58.2
	Mt_Unknown_18	*M. truncatula*	3	2,00 e-07	50.8
At5g42050	Gm_Unknown_18	*G. max*	8	8,00 e-66	246
	Mt_Unknown_19	*M. truncatula*	17	2,00 e-70	262
At5g50100	Gm_Unknown_19	*G. max*	1	3,00 e-60	197
	Mt_Unknown_20	*M. truncatula*	1	2,00 e-46	181
At3g61060	Gm_Unknown_20	*G. max*	19	5,00 e-102	366
	Mt_Unknown_21	*M. truncatula*	19	2,00 e-101	365
At4g37390	Gm_Unknown_21	*G. max*	5	0.0	510
	Mt_Unknown_22	*M. truncatula*	12	0.0	754
At5g630160	Gm_Unknown_22	*G. max*	3	3,00 e-20	95.1
	Mt_Unknown_23	*M. truncatula*	4	5,00 e-32	134
At5g43260	Mt_Unknown_24	*M. truncatula*	1	3,00 e-36	146
At1g76650	Gm_Unknown_23	*G. max*	1	4,00 e-11	63.5
	Mt_Unknown_25	*M. truncatula*	5	6,00 e-25	109
At1g29395	Mt_Unknown_26	*M. truncatula*	-	2,00 e-40	161

	At2g40140	Gm_Unknown_24	*G. max*	19	1,00 e-161	565
		Mt_Unknown_27	*M. truncatula*	19	5,00 e-153	537
	At4g36040	Gm_Unknown_25	*G. max*	20	1,00 e-28	121
		Mt_Unknown_28	*M. truncatula*	19	2,00 e-26	114
	At4g33050	Gm_Unknown_26	*G. max*	9	1,00 e-59	225
		Mt_Unknown_29	*M. truncatula*	14	7,00 e-74	273
	At5g09440	Gm_Unknown_27	*G. max*	18	3,00 e-87	317
		Mt_Unknown_30	*M. truncatula*	19	2,00 e-79	291
	At1g19180	Gm_Unknown_28	*G. max*	9	9,00 e-38	152
		Mt_Unknown_31	*M. truncatula*	14	3,00 e-23	105
	At1g17380	Gm_Unknown_29	*G. max*	1	4,00 e-11	64.3
		Mt_Unknown_32	*M. truncatula*	1	7,00 e-14	74.3
	At1g02660	Gm_Unknown_30	*G. max*	4	4,00 e-59	224
		Mt_Unknown_33	*M. truncatula*	5	7,00 e-168	587
	At2g21620	Gm_Unknown_31	*G. max*	2	6,00 e-66	245
		Mt_Unknown_34	*M. truncatula*	1	2,00 e-65	244
	At1g27760	Gm_Unknown_32	*G. max*	7	2,00 e-126	448
		Mt_Unknown_35	*M. truncatula*	1	6,00 e-107	384
	At1g63010	Gm_Unknown_33	*G. max*	4	3,00 e-77	285
		Mt_Unknown_36	*M. truncatula*	3	8,00 e-89	324
	At2g41640	Gm_Unknown_34	*G. max*	1	1,00 e-56	216
		Mt_Unknown_37	*M. truncatula*	2	9,00 e-160	559
	At1g11360	Gm_Unknown_35	*G. max*	14	5,00 e-67	249
		Mt_Unknown_38	*M. truncatula*	19	1,00 e-59	225
Water Channel Protein	At2g37180	Gm_Water_Chan_1	*G. max*	19	2,00 e-116	414
		Mt_Water_Chan_1	*M. truncatula*	19	3,00 e-115	410
WRKY Transcription Factor	At2g30250	Gm_WRKY_TF_1	*G. max*	10	4,00 e-65	244
		Mt_WRKY_TF_1	*M. truncatula*	15	3,00 e-62	235
	At5g13080	Gm_WRKY_TF_2	*G. max*	12	9,00 e-43	167
		Mt_WRKY_TF_2	*M. truncatula*	8	1,00 e-40	161
Zinc Finger Transcription Factor	At2g19580	Gm_ZF_TF_1	*G. max*	7	9,00 e-31	129
		Mt_ZF_TF_1	*M. truncatula*	15	4,00 e-32	134
	At5g59820	Gm_ZF_TF_2	*G. max*	11	1,00 e-24	107
	At2g31380	Gm_ZF_TF_3	*G. max*	17	7,00 e-68	252
		Mt_ZF_TF_2	*M. truncatula*	16	4,00 e-67	250