Supplementary Table 3. Mitochondrial integral membrane proteins that did not significantly ($p<0.05$) change in abundance following stress treatment. AGI, Arabidopsis Gene Initiative chromosomal location; ID, Protein identified; C1-C3, number of peptides for Control 1-3 samples; T1-T3, number of peptides for Treatment 1-3 samples; MOWSE C1-C3, MOlecular Weight SEarch score for Control 1-3 samples; MOWSE T1-C3, MOlecular Weight SEarch score for Treatment 1-3 samples; t-test, Students t-test of control versus treatment; Treatment, The treatment that did not significantly change protein abundance.

AGI	ID	C1	C2	C3	T1	T2	T3	MOWSE C1	MOWSE C2	MOWSE C3	MOWSE T1	MOWSE T2	MOWSE T3	t-test	Treatment
AT1G01980.1	SEC1A Reticuline oxidase-like family	0.625	0.625	0.625	2.000	1.000	2.000	0	0	0	43	41	35	0.053	Anti A
AT1G03860.1	ATPHB2 Prohibitin 2	9.000	11.000	9.000	12.000	16.000	15.000	341	482	372	296	475	419	0.100	Anti A
AT1G03860.1	ATPHB2 Prohibitin 2	8.000	11.000	13.000	8.000	8.000	5.000	421	356	386	372	355	58	0.194	CuCl
AT1G03860.1	ATPHB2 Prohibitin 2	8.000	11.000	13.000	7.000	11.000	8.000	421	356	386	232	356	247	0.256	Cold
AT1G03860.1	ATPHB2 Prohibitin 2	8.000	11.000	13.000	9.000	11.000	9.000	421	356	386	341	482	372	0.508	MeOH
AT1G03860.1	ATPHB2 Prohibitin 2	8.000	11.000	13.000	13.000	15.000	9.000	421	356	386	482	469	326	0.519	H202
AT1G03860.1	ATPHB2 Prohibitin 2	9.000	11.000	9.000	8.000	11.000	13.000	341	482	372	451	379	485	0.699	Mena
AT1G04630.1	NADH dehydrogenase B16.6 subunit	5.000	8.000	7.000	5.000	8.000	15.000	138	173	268	158	173	155	0.485	Cold
AT1G04630.1	NADH dehydrogenase B16.6 subunit	5.000	8.000	7.000	5.000	10.000	4.000	138	173	268	141	136	69	0.674	CuCl
AT1G04630.1	NADH dehydrogenase B16.6 subunit	0.625	10.000	8.000	5.000	5.000	6.000	0	167	270	224	153	192	0.682	Mena
AT1G06530.1	Myosin heavy chain-related	2.000	2.000	2.000	6.000	2.000	2.000	73	88	102	92	88	64	0.328	Cold
AT1G06530.1	Myosin heavy chain-related	2.000	4.000	3.000	2.000	3.000	3.000	49	164	104	48	61	118	0.520	Mena
AT1G08480.1	SDH6 Succinate dehydrogenase subunit 6	0.625	1.000	3.000	4.000	3.000	3.000	0	35	87	42	45	34	0.167	Anti A
AT1G08480.1	SDH6 Succinate dehydrogenase subunit 6	5.000	5.000	4.000	2.000	3.000	4.000	64	55	55	35	44	52	0.304	H202
AT1G15220.1	CCMH Cytochrome *c* biogenesis protein	0.625	0.625	2.000	2.000	4.000	4.000	0	0	47	45	75	45	0.064	Anti A
AT1G15220.1	CCMH Cytochrome *c* biogenesis protein	3.000	4.000	2.000	5.000	4.000	5.000	43	96	52	68	95	82	0.236	H202
AT1G27390.1	TOM20-2 Translocase Outer Membrane 20-2	0.625	3.000	3.000	2.000	1.000	2.000	0	48	134	105	71	88	0.883	Mena
AT1G47260.1	γCA2 γCarbonic anhydrase 2	8.000	8.000	9.000	7.000	9.000	5.000	278	362	300	173	255	249	0.416	MeOH
AT1G47260.1	γCA2 γCarbonic anhydrase 2	7.000	9.000	5.000	7.000	10.000	8.000	173	255	249	249	218	335	0.434	Anti A
AT1G47260.1	γCA2 γCarbonic anhydrase 2	8.000	8.000	9.000	9.000	8.000	4.000	278	362	300	259	321	201	0.451	H202
AT1G47260.1	γCA2 γCarbonic anhydrase 2	7.000	9.000	5.000	6.000	8.000	7.000	173	255	249	257	308	384	0.892	Mena
AT1G47260.1	γCA2 γCarbonic anhydrase 2	8.000	8.000	9.000	4.000	8.000	15.000	278	362	300	133	362	153	0.920	Cold
AT1G49410.1	TOM6 Translocase Outer Membrane 6	0.625	1.000	1.000	0.625	0.625	0.625	0	41	50	46	51	61	0.076	Anti A
AT1G49410.1	TOM6 Translocase Outer Membrane 6	0.625	1.000	1.000	1.000	1.000	1.000	0	41	50	46	51	61	0.194	Mena
AT1G50460.1	HKL1 Hexokinase like-1	0.625	3.000	0.625	3.000	3.000	2.000	0	40	0	51	58	62	0.171	H202
AT1G50460.1	HKL1 Hexokinase like-1	3.000	3.000	0.625	2.000	4.000	2.000	62	98	0	79	90	82	0.564	Mena
AT1G50460.1	HKL1 Hexokinase like-1	3.000	3.000	0.625	2.000	2.000	4.000	62	98	0	40	57	105	0.700	Anti A
AT1G51610.1	MTPc4 Metal tolerance protein c4	0.625	4.000	5.000	2.000	4.000	6.000	0	108	53	93	86	217	0.259	Mena
AT1G51980.1	MPPα-1 Mitochondrial processing peptidase 1 α-subunit	6.000	11.000	13.000	10.000	11.000	13.000	164	363	412	269	333	694	0.212	Mena
AT1G51980.1	MPPα-1 Mitochondrial processing peptidase 1 α-subunit	0.625	7.000	16.000	6.000	11.000	13.000	0	245	490	164	363	412	0.329	MeOH
AT1G51980.1	MPPα-1 Mitochondrial processing peptidase 1 α-subunit	0.625	7.000	16.000	15.000	7.000	18.000	0	245	490	568	245	285	0.370	Cold
AT1G51980.1	MPPα-1 Mitochondrial processing peptidase 1 α-subunit	0.625	7.000	16.000	20.000	7.000	10.000	0	245	490	822	119	209	0.478	CuCl
AT1G51980.1	MPPα-1 Mitochondrial processing peptidase 1 α-subunit	0.625	7.000	16.000	2.000	11.000	3.000	0	245	490	38	370	50	0.994	H202
AT1G55160.1	Unknown protein	0.625	1.000	1.000	1.000	2.000	2.000	0	55	73	69	68	65	0.051	Mena
AT1G55160.1	Unknown protein	0.625	1.000	1.000	2.000	2.000	1.000	0	55	73	92	96	69	0.143	Anti A
AT1G55160.1	Unknown protein	1.000	1.000	1.000	2.000	1.000	1.000	78	77	85	96	63	66	0.269	H202
AT1G56410.1	ERD2 Early responsive to dehydration 2, HSP70 like	0.625	0.625	2.000	6.000	3.000	1.000	0	0	63	216	38	38	0.329	Cold

AGI	ID	C1	C2	C3	T1	T2	T3	MOWSE C1	MOWSE C2	MOWSE C3	MOWSE T1	MOWSE T2	MOWSE T3	t-test	Treatment
AT1G65540.1	Mdm38-2 Component of mitochondrial protein export machinery	8.000	12.000	9.000	4.000	11.000	3.000	263	378	183	299	86	243	0.168	H202
AT1G65540.1	Mdm38-2 Component of mitochondrial protein export machinery	8.000	12.000	9.000	3.000	12.000	4.000	263	378	85	378	42	42	0.226	Cold
AT1G65540.1	Mdm38-2 Component of mitochondrial protein export machinery	3.000	11.000	7.000	9.000	10.000	11.000	108	263	243	273	361	354	0.235	Mena
AT1G65540.1	Mdm38-2 Component of mitochondrial protein export machinery	8.000	12.000	9.000	3.000	11.000	7.000	263	378	233	108	263	243	0.339	MeOH
AT1G65540.1	Mdm38-2 Component of mitochondrial protein export machinery	3.000	11.000	7.000	6.000	5.000	6.000	108	263	243	57	98	212	0.869	Anti A
AT1G68680.1	Unknown NADH dehydrogenase associated protein	3.000	4.000	2.000	4.000	8.000	4.000	42	54	90	66	86	79	0.111	H202
AT1G68680.1	Unknown NADH dehydrogenase associated protein	3.000	4.000	2.000	11.000	4.000	4.000	42	54	90	147	54	82	0.178	Cold
AT1G68680.1	Unknown NADH dehydrogenase associated protein	3.000	5.000	2.000	5.000	5.000	4.000	53	69	60	88	87	74	0.205	Anti A
AT1G68680.1	Unknown NADH dehydrogenase associated protein	3.000	4.000	2.000	3.000	6.000	3.000	42	54	90	51	72	63	0.307	CuCl
AT1G68680.1	Unknown NADH dehydrogenase associated protein	3.000	4.000	2.000	3.000	5.000	2.000	42	54	90	53	69	60	0.535	MeOH
AT1G68680.1	Unknown NADH dehydrogenase associated protein	3.000	5.000	2.000	2.000	3.000	3.000	53	69	60	43	85	74	0.691	Mena
AT1G72750.1	TIM23-2 Translocase Inner Membrane 23-2	0.625	2.000	4.000	2.000	2.000	5.000	0	106	132	64	106	48	0.245	Cold
AT1G72750.1	TIM23-2 Translocase Inner Membrane 23-2	0.625	2.000	1.000	1.000	1.000	3.000	0	82	40	38	53	164	0.630	Mena
AT1G73980.1	Putative adenylate cyclase	4.000	4.000	3.000	2.000	3.000	2.000	65	89	69	33	58	46	0.139	H202
AT1G73980.1	Putative adenylate cyclase	0.625	3.000	3.000	6.000	3.000	5.000	0	48	63	81	49	77	0.270	Mena
AT1G73990.1	SPPA Serine-type endopeptidase	1.000	3.000	3.000	8.000	6.000	8.000	35	47	50	130	174	205	0.072	Mena
AT1G73990.1	SPPA Serine-type endopeptidase	1.000	3.000	3.000	4.000	3.000	6.000	35	47	50	41	106	61	0.184	Anti A
AT1G73990.1	SPPA Serine-type endopeptidase	2.000	4.000	3.000	1.000	3.000	3.000	62	74	42	35	47	50	0.372	MeOH
AT2G16460.1	COX X6 Cytochrome *c* oxidase X6 subunit	8.000	12.000	16.000	4.000	8.000	4.000	317	496	553	93	329	87	0.089	H202
AT2G16460.1	COX X6 Cytochrome *c* oxidase X6 subunit	11.000	12.000	7.000	3.000	3.000	6.000	337	411	342	103	178	259	0.175	Anti A
AT2G16460.1	COX X6 Cytochrome *c* oxidase X6 subunit	11.000	12.000	7.000	8.000	9.000	6.000	337	411	342	337	373	291	0.184	Mena
AT2G16460.1	COX X6 Cytochrome *c* oxidase X6 subunit	8.000	12.000	16.000	3.000	12.000	5.000	317	496	553	65	496	147	0.202	Cold
AT2G16460.1	COX X6 Cytochrome *c* oxidase X6 subunit	8.000	12.000	16.000	11.000	12.000	7.000	317	496	553	337	411	342	0.628	MeOH
AT2G19080.1	Met-1 Metaxin-1	3.000	6.000	4.000	1.000	5.000	3.000	105	202	149	47	123	203	0.292	MeOH
AT2G19080.1	Met-1 Metaxin-1	1.000	5.000	3.000	3.000	5.000	1.000	47	123	203	149	274	53	0.984	Mena
AT2G19860.1	HXK2 Hexokinase 2	2.000	4.000	0.625	6.000	6.000	5.000	49	82	0	161	205	184	0.146	Mena
AT2G19860.1	HXK2 Hexokinase 2	2.000	4.000	0.625	6.000	6.000	7.000	49	82	0	80	39	173	0.170	Anti A
AT2G20360.1	NADH dehydrogenase 39 kDa subunit	4.000	6.000	8.000	14.000	12.000	9.000	36	84	103	171	255	213	0.111	Mena
AT2G20360.1	NADH dehydrogenase 39 kDa subunit	0.625	10.000	8.000	0.625	0.625	0.625	0	196	84	214	63	158	0.165	Cold
AT2G20360.1	NADH dehydrogenase 39 kDa subunit	0.625	10.000	8.000	4.000	6.000	8.000	0	196	84	36	84	103	0.554	MeOH
AT2G20360.1	NADH dehydrogenase 39 kDa subunit	0.625	10.000	8.000	11.000	3.000	10.000	0	196	84	214	63	158	0.629	CuCl
AT2G20360.1	NADH dehydrogenase 39 kDa subunit	4.000	6.000	8.000	7.000	3.000	9.000	36	84	103	93	53	147	0.985	Anti A
AT2G20360.1	NADH dehydrogenase 39 kDa subunit	0.625	10.000	8.000	5.000	2.000	5.000	0	196	84	38	34	87	0.991	H202
AT2G20530.1	ATPHB6 Prohibitin 6	6.000	7.000	14.000	4.000	7.000	5.000	263	266	316	214	297	219	0.235	MeOH
AT2G20530.1	ATPHB6 Prohibitin 6	6.000	7.000	14.000	5.000	7.000	7.000	263	266	316	212	266	253	0.258	Cold
AT2G20530.1	ATPHB6 Prohibitin 6	6.000	7.000	14.000	5.000	7.000	2.000	263	266	316	291	433	77	0.348	CuCl
AT2G20530.1	ATPHB6 Prohibitin 6	6.000	7.000	14.000	9.000	8.000	9.000	263	266	316	348	302	230	0.830	H202
AT2G20800.1	NDB4 Alternative NAD(P)H dehydrogenase	4.000	7.000	7.000	13.000	16.000	9.000	128	210	187	265	282	236	0.063	Mena
AT2G20800.1	NDB4 Alternative NAD(P)H dehydrogenase	7.000	9.000	8.000	4.000	7.000	7.000	197	262	207	128	210	187	0.273	MeOH
AT2G20800.1	NDB4 Alternative NAD(P)H dehydrogenase	7.000	9.000	8.000	15.000	10.000	7.000	197	262	207	296	262	87	0.314	Cold
AT2G20800.1	NDB4 Alternative NAD(P)H dehydrogenase	6.000	7.000	9.000	10.000	9.000	7.000	128	210	187	169	163	167	0.366	Anti A

AGI	ID	C1	C2	C3	T1	T2	T3	MOWSE C1	MOWSE C2	MOWSE C3	MOWSE T1	MOWSE T2	MOWSE T3	t-test	Treatment
AT2G20800.1	NDB4 Alternative NAD(P)H dehydrogenase	7.000	9.000	8.000	10.000	8.000	3.000	197	262	207	226	101	56	0.543	CuCl
AT2G20800.1	NDB4 Alternative NAD(P)H dehydrogenase	7.000	9.000	8.000	9.000	8.000	7.000	197	262	207	107	116	193	0.846	H202
AT2G20940.1	Unknown protein	4.000	5.000	5.000	6.000	5.000	5.000	76	185	122	91	185	38	0.159	Cold
AT2G20940.1	Unknown protein	3.000	3.000	7.000	3.000	3.000	4.000	78	81	116	93	75	114	0.342	Anti A
AT2G20940.1	Unknown protein	3.000	3.000	7.000	4.000	4.000	5.000	78	81	116	179	166	103	0.625	Mena
AT2G20940.1	Unknown protein	4.000	5.000	5.000	3.000	3.000	7.000	76	185	122	78	81	116	0.684	MeOH
AT2G20940.1	Unknown protein	4.000	5.000	5.000	5.000	5.000	4.000	76	185	122	101	122	88	0.850	H202
AT2G22500.1	AtDIC1 Dicarboxylate Carrier	2.000	4.000	2.000	1.000	3.000	1.000	78	133	72	45	62	64	0.084	MeOH
AT2G22500.1	AtDIC1 Dicarboxylate Carrier	1.000	3.000	1.000	4.000	2.000	2.000	45	62	64	98	72	144	0.358	Mena
AT2G22500.1	AtDIC1 Dicarboxylate Carrier	2.000	4.000	2.000	3.000	3.000	3.000	78	133	72	44	79	63	0.496	H202
AT2G22500.1	AtDIC1 Dicarboxylate Carrier	1.000	3.000	1.000	4.000	1.000	1.000	45	62	64	65	53	55	0.886	Anti A
AT2G26140.1	FTSH4 ATP-dependent peptidase	2.000	2.000	4.000	2.000	2.000	5.000	42	145	185	92	157	225	0.596	Mena
AT2G26140.1	FTSH4 ATP-dependent peptidase	0.625	2.000	6.000	2.000	2.000	2.000	0	147	262	97	147	69	0.959	Cold
AT2G27730.1	B16 NADH dehydrogenase 16 kDa subunit	1.000	1.000	2.000	0.625	0.625	0.625	95	94	134	0	0	0	0.064	Cold
AT2G27730.1	B16 NADH dehydrogenase 16 kDa subunit	1.000	1.000	2.000	0.625	0.625	0.625	95	94	134	0	0	0	0.064	CuCl
AT2G27730.1	B16 NADH dehydrogenase 16 kDa subunit	1.000	1.000	2.000	1.000	1.000	1.000	95	94	134	81	106	70	0.355	H202
AT2G28430.1	Unknown protein, contains RING-finger-type domain	1.000	2.000	2.000	1.000	2.000	3.000	35	79	42	69	49	37	0.532	Mena
AT2G28430.1	Unknown protein, contains RING-finger-type domain	2.000	2.000	2.000	1.000	2.000	2.000	56	72	57	35	79	42	0.546	MeOH
AT2G29080.1	FTSH3 ATP-dependent peptidase	1.000	2.000	3.000	7.000	6.000	6.000	58	81	125	146	94	196	0.050	Mena
AT2G29080.1	FTSH3 ATP-dependent peptidase	3.000	5.000	2.000	1.000	2.000	3.000	106	119	62	58	81	125	0.432	MeOH
AT2G29080.1	FTSH3 ATP-dependent peptidase	3.000	5.000	2.000	4.000	5.000	1.000	106	119	62	123	119	36	0.642	Cold
AT2G29080.1	FTSH3 ATP-dependent peptidase	1.000	2.000	3.000	1.000	3.000	2.000	58	81	125	73	63	66	0.961	Anti A
AT2G29990.1	NDA2 Alternative NAD(P)H dehydrogenase	0.625	0.625	3.000	4.000	4.000	5.000	0	0	96	69	64	133	0.070	Anti A
AT2G29990.1	NDA2 Alternative NAD(P)H dehydrogenase	0.625	0.625	3.000	3.000	5.000	4.000	0	0	96	105	203	126	0.117	Mena
AT2G29990.1	NDA2 Alternative NAD(P)H dehydrogenase	4.000	3.000	4.000	2.000	1.000	3.000	86	100	78	56	46	67	0.125	H202
AT2G33040.1	ATP3 ATP synthase	19.000	15.000	19.000	17.000	12.000	10.000	650	512	626	716	466	128	0.096	CuCl
AT2G33040.1	ATP3 ATP synthase	19.000	15.000	19.000	17.000	15.000	1.000	650	512	626	398	512	55	0.385	Cold
AT2G33040.1	ATP3 ATP synthase	19.000	20.000	19.000	10.000	19.000	18.000	725	620	551	503	650	711	0.472	Mena
AT2G33040.1	ATP3 ATP synthase	19.000	15.000	19.000	19.000	20.000	19.000	650	512	626	725	620	551	0.504	MeOH
AT2G33040.1	ATP3 ATP synthase	19.000	20.000	19.000	17.000	15.000	20.000	725	620	551	535	512	800	0.534	Anti A
AT2G33040.1	ATP3 ATP synthase	19.000	15.000	19.000	14.000	19.000	13.000	650	512	626	333	747	367	0.591	H202
AT2G33220.1	B16.6 NADH dehydrogenase B16.6 subunit	5.000	8.000	7.000	5.000	8.000	15.000	159	181	285	171	181	268	0.485	Cold
AT2G33220.1	B16.6 NADH dehydrogenase B16.6 subunit	0.625	10.000	8.000	5.000	5.000	7.000	0	187	277	234	150	217	0.637	Mena
AT2G33220.1	B16.6 NADH dehydrogenase B16.6 subunit	5.000	8.000	7.000	8.000	7.000	5.000	159	181	285	170	172	226	0.947	H202
AT2G35720.1	DNAJ heat shock N-terminal domain-containing protein	0.625	2.000	0.625	0.625	0.625	0.625	0	52	0	0	0	0	0.426	Cold
AT2G35720.1	DNAJ heat shock N-terminal domain-containing protein	0.625	2.000	0.625	0.625	0.625	0.625	0	52	0	0	0	0	0.426	CuCl
AT2G36500.1	Unknown protein, Phox/Bemp1 (PB1) domain-containing protein	2.000	2.000	2.000	2.000	2.000	5.000	143	143	140	50	141	142	0.475	Cold
AT2G36500.1	Unknown protein, Phox/Bemp1 (PB1) domain-containing protein	2.000	2.000	2.000	2.000	2.000	2.000	143	143	140	100	136	135	0.884	H202
AT2G36500.1	Unknown protein, Phox/Bemp1 (PB1) domain-containing protein	2.000	2.000	2.000	2.000	2.000	2.000	58	146	132	161	165	173	0.884	Mena
AT2G36500.1	Unknown protein, Phox/Bemp1 (PB1) domain-containing protein	2.000	2.000	2.000	2.000	2.000	2.000	143	143	140	58	146	132	0.884	MeOH
AT2G37410.1	AtTIM17-2 Translocase inner membrane subunit 17-2	2.000	2.000	2.000	3.000	2.000	2.000	42	54	90	82	66	126	0.159	MeOH
AT2G37410.1	AtTIM17-2 Translocase inner membrane subunit 17-2	2.000	2.000	2.000	2.000	1.000	2.000	42	54	90	86	80	95	0.436	H202
AT2G37410.1	AtTIM17-2 Translocase inner membrane subunit 17-2	2.000	2.000	2.000	2.000	2.000	3.000	42	54	90	67	70	66	0.532	Cold

AGI	ID	C1	C2	C3	T1	T2	T3	MOWSE C1	MOWSE C2	MOWSE C3	MOWSE T1	MOWSE T2	MOWSE T3	t-test	Treatment
AT2G37410.1	AtTIM17-2 Translocase inner membrane subunit 17-2	3.000	2.000	2.000	3.000	2.000	2.000	95	75	119	116	116	96	0.884	Anti A
AT2G38280.1	FAC1 Embryonic factor 1, AMP deaminase	0.625	3.000	0.625	0.625	0.625	0.625	0	79	0	55	65	60	0.423	Anti A
AT2G38280.1	FAC1 Embryonic factor 1, AMP deaminase	0.625	2.000	0.625	0.625	0.625	0.625	0	62	0	0	0	0	0.426	Cold
AT2G38280.1	FAC1 Embryonic factor 1, AMP deaminase	0.625	2.000	0.625	0.625	0.625	0.625	0	62	0	0	0	0	0.426	CuCl
AT2G38280.1	FAC1 Embryonic factor 1, AMP deaminase	0.625	2.000	0.625	0.625	0.625	0.625	0	62	0	0	0	0	0.426	H202
AT2G38280.1	FAC1 Embryonic factor 1, AMP deaminase	0.625	3.000	0.625	1.000	2.000	1.000	0	79	0	55	65	60	0.572	Mena
AT2G38670.1	PECT1 Phosphorylethanolamine cytidylyltransferase 1	3.000	1.000	5.000	12.000	8.000	9.000	85	45	148	430	252	342	0.080	Mena
AT2G38670.1	PECT1 Phosphorylethanolamine cytidylyltransferase 1	5.000	7.000	5.000	0.625	0.625	0.625	176	213	100	85	45	148	0.288	CuCl
AT2G38670.1	PECT1 Phosphorylethanolamine cytidylyltransferase 1	5.000	7.000	5.000	3.000	1.000	5.000	176	213	100	85	45	148	0.305	MeOH
AT2G40800.1	Unknown protein, contains mitochondrial import inner membrane translocase domain (Tim21)	1.000	8.000	7.000	8.000	9.000	12.000	120	252	98	233	243	354	0.224	Mena
AT2G40800.1	Unknown protein, contains mitochondrial import inner membrane translocase domain (Tim21)	5.000	8.000	6.000	4.000	8.000	4.000	120	252	98	88	252	119	0.251	Cold
AT2G40800.1	Unknown protein, contains mitochondrial import inner membrane translocase domain (Tim21)	1.000	8.000	7.000	4.000	7.000	7.000	60	146	151	74	116	127	0.411	Anti A
AT2G40800.1	Unknown protein, contains mitochondrial import inner membrane translocase domain (Tim21)	5.000	8.000	6.000	1.000	8.000	7.000	120	252	98	60	146	151	0.536	MeOH
AT2G40800.1	Unknown protein, contains mitochondrial import inner membrane translocase domain (Tim21)	5.000	8.000	6.000	10.000	7.000	5.000	209	289	186	189	181	80	0.581	H202
AT2G42210.1	B14.7 NADH dehydrogenase B14.7 subunit	1.000	7.000	4.000	4.000	6.000	6.000	68	185	216	101	139	147	0.292	Anti A
AT2G42210.1	B14.7 NADH dehydrogenase B14.7 subunit	1.000	7.000	4.000	4.000	5.000	9.000	68	185	216	103	97	223	0.311	Mena
AT2G42210.1	B14.7 NADH dehydrogenase B14.7 subunit	3.000	4.000	4.000	1.000	5.000	3.000	73	137	145	80	163	77	0.488	CuCl
AT2G42210.1	B14.7 NADH dehydrogenase B14.7 subunit	3.000	4.000	4.000	5.000	4.000	1.000	73	137	145	114	80	41	0.633	H202
AT2G42210.1	B14.7 NADH dehydrogenase B14.7 subunit	3.000	4.000	4.000	1.000	7.000	4.000	73	137	145	68	185	216	0.790	MeOH
AT2G45060.1	Unknown protein	5.000	9.000	7.000	6.000	9.000	7.000	128	239	302	130	262	322	0.098	Anti A
AT2G45060.1	Unknown protein	6.000	3.000	6.000	7.000	3.000	8.000	207	231	254	167	231	65	0.331	Cold
AT2G45060.1	Unknown protein	6.000	3.000	6.000	5.000	9.000	7.000	207	231	254	128	239	302	0.475	MeOH
AT2G45060.1	Unknown protein	6.000	3.000	6.000	4.000	5.000	7.000	128	239	302	270	307	332	0.791	Mena
AT2G45060.1	Unknown protein	6.000	3.000	6.000	4.000	7.000	3.000	207	231	254	160	283	139	0.896	H202
AT2G46470.1	OXA1-1	0.625	2.000	3.000	2.000	2.000	3.000	128	123	105	0	0	0	0.334	Mena
AT2G46470.1	OXA1-1	4.000	3.000	3.000	1.000	3.000	3.000	128	123	105	45	83	41	0.489	H202
AT2G47380.1	COX 5C-1 Cytochrome *c* oxidase	0.625	0.625	3.000	3.000	3.000	4.000	0	0	41	45	46	39	0.091	Mena
AT2G47380.1	COX 5C-1 Cytochrome *c* oxidase	0.625	0.625	3.000	0.625	0.625	0.625	0	0	41	0	0	0	0.391	Anti A
AT3G01130.1	Unknown protein	2.000	3.000	2.000	3.000	7.000	6.000	122	135	151	105	149	156	0.103	Cold
AT3G01130.1	Unknown protein	2.000	3.000	2.000	4.000	4.000	2.000	122	135	126	135	145	133	0.116	MeOH
AT3G01130.1	Unknown protein	2.000	3.000	2.000	5.000	3.000	4.000	122	135	151	100	110	96	0.161	H202
AT3G01130.1	Unknown protein	2.000	3.000	2.000	4.000	2.000	3.000	122	135	151	85	39	36	0.504	CuCl
AT3G01130.1	Unknown protein	4.000	4.000	2.000	2.000	4.000	2.000	122	135	151	100	110	113	0.546	Mena
AT3G01130.1	Unknown protein	4.000	4.000	2.000	4.000	3.000	4.000	127	143	130	95	48	106	0.703	Anti A
AT3G01280.1	VDAC1 Porin	11.000	11.000	10.000	14.000	11.000	10.000	384	380	367	371	380	133	0.060	Cold
AT3G01280.1	VDAC1 Porin	11.000	11.000	10.000	10.000	10.000	6.000	384	380	367	335	154	168	0.152	CuCl
AT3G01280.1	VDAC1 Porin	9.000	10.000	15.000	12.000	14.000	14.000	169	284	494	432	500	521	0.179	Mena
AT3G01280.1	VDAC1 Porin	9.000	10.000	15.000	10.000	9.000	11.000	169	284	494	257	339	316	0.206	Anti A
AT3G01280.1	VDAC1 Porin	11.000	11.000	10.000	8.000	12.000	7.000	384	380	367	291	354	310	0.393	H202

AGI	ID	C1	C2	C3	T1	T2	T3	MOWSE C1	MOWSE C2	MOWSE C3	MOWSE T1	MOWSE T2	MOWSE T3	t-test	Treatment
AT3G01280.1	VDAC1 Porin	11.000	11.000	10.000	9.000	10.000	15.000	384	380	367	169	284	494	0.864	MeOH
AT3G02090.1	MPPβ Mitochondrial processing peptidase β-subunit	5.000	6.000	8.000	5.000	4.000	6.000	232	231	374	90	187	291	0.092	Anti A
AT3G02090.1	MPPβ Mitochondrial processing peptidase β-subunit	3.000	7.000	7.000	11.000	7.000	15.000	61	222	343	418	222	228	0.174	Cold
AT3G02090.1	MPPβ Mitochondrial processing peptidase β-subunit	3.000	7.000	7.000	5.000	6.000	8.000	61	222	343	232	231	374	0.353	MeOH
AT3G02090.1	MPPβ Mitochondrial processing peptidase β-subunit	5.000	6.000	8.000	5.000	9.000	8.000	232	231	374	185	345	550	0.474	Mena
AT3G02090.1	MPPβ Mitochondrial processing peptidase β-subunit	3.000	7.000	7.000	2.000	13.000	1.000	61	222	343	87	624	107	0.514	H202
AT3G02090.1	MPPβ Mitochondrial processing peptidase β-subunit	3.000	7.000	7.000	12.000	4.000	6.000	61	222	343	606	211	197	0.698	CuCl
AT3G03060.1	Putative AAA-type ATPase family protein	3.000	4.000	4.000	3.000	4.000	3.000	72	99	178	143	155	171	0.330	Mena
AT3G03060.1	Putative AAA-type ATPase family protein	0.625	4.000	0.625	0.625	0.625	0.625	0	133	0	0	0	0	0.423	Cold
AT3G03060.1	Putative AAA-type ATPase family protein	0.625	4.000	0.625	0.625	0.625	0.625	0	133	0	0	0	0	0.423	CuCl
AT3G07568.1	Unknown protein	0.625	1.000	1.000	1.000	1.000	1.000	0	56	77	56	44	70	0.194	H202
AT3G08580.1	AAC1 ADP/ATP carrier 1	29.000	28.000	58.000	22.000	27.000	14.000	629	762	1293	575	709	295	0.280	CuCl
AT3G08580.1	AAC1 ADP/ATP carrier 1	29.000	28.000	58.000	29.000	28.000	32.000	629	762	1293	439	762	508	0.346	Cold
AT3G08580.1	AAC1 ADP/ATP carrier 1	25.000	23.000	43.000	42.000	30.000	32.000	732	783	811	1032	857	802	0.423	Anti A
AT3G08580.1	AAC1 ADP/ATP carrier 1	25.000	23.000	43.000	21.000	27.000	29.000	732	783	811	652	852	682	0.532	Mena
AT3G08580.1	AAC1 ADP/ATP carrier 1	29.000	28.000	58.000	40.000	50.000	35.000	629	762	1293	837	1083	847	0.669	H202
AT3G08950.1	HCC1 Mitochondrial copper chaperone involved in CV assembly	2.000	3.000	1.000	0.625	0.625	0.625	69	142	42	0	0	0	0.099	Cold
AT3G08950.1	HCC1 Mitochondrial copper chaperone involved in CV assembly	2.000	3.000	1.000	0.625	0.625	0.625	69	142	42	0	0	0	0.099	CuCl
AT3G08950.1	HCC1 Mitochondrial copper chaperone involved in CV assembly	0.625	2.000	2.000	0.625	0.625	0.625	0	78	89	0	0	0	0.138	Anti A
AT3G08950.1	HCC1 Mitochondrial copper chaperone involved in CV assembly	0.625	2.000	2.000	2.000	4.000	2.000	0	78	89	69	127	127	0.143	Mena
AT3G09440.1	HSP70-3 Heat shock protein 3 70 kDa	5.000	4.000	0.625	0.625	0.625	0.625	0	78	89	0	0	0	0.213	Mena
AT3G09440.1	HSP70-3 Heat shock protein 3 70 kDa	10.000	7.000	2.000	2.000	2.000	2.000	169	116	68	100	136	135	0.231	H202
AT3G09440.1	HSP70-3 Heat shock protein 3 70 kDa	5.000	4.000	0.625	5.000	7.000	2.000	38	76	0	78	88	45	0.288	Anti A
AT3G09440.1	HSP70-3 Heat shock protein 3 70 kDa	10.000	7.000	2.000	6.000	7.000	2.000	169	116	68	135	116	35	0.583	Cold
AT3G09440.1	HSP70-3 Heat shock protein 3 70 kDa	10.000	7.000	2.000	9.000	4.000	7.000	169	116	68	173	46	89	0.757	CuCl
AT3G10860.1	UCRQ ubiquinol-cytochrome *c* reductase complex 8.5 kDa protein	0.625	0.625	1.000	1.000	1.000	1.000	0	0	50	42	51	55	0.103	Anti A
AT3G10860.1	UCRQ ubiquinol-cytochrome *c* reductase complex 8.5 kDa protein	0.625	0.625	1.000	1.000	1.000	1.000	0	0	49	56	61	56	0.103	H202
AT3G10860.1	UCRQ ubiquinol-cytochrome *c* reductase complex 8.5 kDa protein	0.625	0.625	1.000	0.625	0.625	0.625	0	0	49	56	61	56	0.332	CuCl
AT3G11070.1	SAM50-1 SAM mitochondrial outer membrane complex 50-1	7.000	7.000	5.000	4.000	2.000	3.000	145	149	92	85	39	36	0.086	CuCl
AT3G11070.1	SAM50-1 SAM mitochondrial outer membrane complex 50-1	7.000	7.000	5.000	7.000	3.000	3.000	145	149	92	146	80	109	0.153	H202
AT3G11070.1	SAM50-1 SAM mitochondrial outer membrane complex 50-1	7.000	7.000	5.000	1.000	4.000	6.000	145	149	92	47	89	73	0.389	MeOH
AT3G11070.1	SAM50-1 SAM mitochondrial outer membrane complex 50-1	7.000	7.000	5.000	3.000	7.000	6.000	145	149	92	105	149	156	0.647	Cold
AT3G11070.1	SAM50-1 SAM mitochondrial outer membrane complex 50-1	1.000	4.000	6.000	4.000	3.000	4.000	47	89	73	95	48	106	0.678	Anti A
AT3G12260.1	NADH dehydrogenase B14 subunit	4.000	2.000	5.000	5.000	5.000	6.000	68	48	73	71	45	145	0.226	Anti A
AT3G12260.1	NADH dehydrogenase B14 subunit	0.625	5.000	0.625	4.000	2.000	5.000	0	70	0	68	48	76	0.398	MeOH
AT3G12260.1	NADH dehydrogenase B14 subunit	0.625	5.000	0.625	0.625	0.625	0.625	0	70	0	68	48	76	0.423	Cold
AT3G12260.1	NADH dehydrogenase B14 subunit	0.625	5.000	0.625	0.625	0.625	0.625	0	70	0	68	48	76	0.423	CuCl
AT3G12260.1	NADH dehydrogenase B14 subunit	4.000	2.000	5.000	5.000	5.000	3.000	68	48	73	93	50	80	0.631	Mena
AT3G17910.1	SURF1 like cytochrome *c* oxidase assembly protein	0.625	3.000	0.625	2.000	3.000	2.000	0	64	0	72	49	40	0.173	Anti A
AT3G17910.1	SURF1 like cytochrome *c* oxidase assembly protein	0.625	0.625	3.000	3.000	1.000	1.000	0	0	123	113	50	81	0.689	H202
AT3G20000.1	TOM40-1 Translocase of the outer mitochondrial membrane	3.000	7.000	4.000	3.000	2.000	2.000	121	199	102	87	121	140	0.179	MeOH
AT3G20000.1	TOM40-1 Translocase of the outer mitochondrial membrane	3.000	7.000	4.000	3.000	1.000	2.000	121	199	102	137	45	118	0.245	H202

AGI	ID	C1	C2	C3	T1	T2	T3	MOWSE C1	MOWSE C2	MOWSE C3	MOWSE T1	MOWSE T2	MOWSE T3	t-test	Treatment
AT3G20000.1	TOM40-1 Translocase of the outer mitochondrial membrane	3.000	2.000	2.000	3.000	6.000	4.000	87	121	140	173	267	219	0.252	Mena
AT3G20000.1	TOM40-1 Translocase of the outer mitochondrial membrane	3.000	7.000	4.000	7.000	7.000	4.000	121	199	102	43	199	96	0.298	Cold
AT3G20000.1	TOM40-1 Translocase of the outer mitochondrial membrane	3.000	7.000	4.000	6.000	4.000	2.000	121	199	102	166	47	59	0.683	CuCl
AT3G22330.1	PMH2 Putative Mitochondrial RNA helicase 2	0.625	4.000	4.000	0.625	0.625	0.625	0	127	40	0	0	0	0.155	Anti A
AT3G22330.1	PMH2 Putative Mitochondrial RNA helicase 2	0.625	4.000	4.000	0.625	0.625	0.625	0	127	40	0	0	0	0.155	Mena
AT3G22330.1	PMH2 Putative Mitochondrial RNA helicase 2	9.000	7.000	5.000	11.000	7.000	7.000	390	419	70	236	419	88	0.289	Cold
AT3G22370.1	AOX1A Alternative oxidase 1A	0.625	2.000	3.000	7.000	6.000	8.000	0	100	105	134	133	243	0.060	Mena
AT3G22370.1	AOX1A Alternative oxidase 1A	6.000	6.000	3.000	2.000	2.000	4.000	70	98	72	56	54	111	0.353	H202
AT3G23150.1	AtETR2 Putative ethylene receptor S/T protein kinase	0.625	14.000	0.625	3.000	1.000	3.000	0	450	0	44	47	35	0.909	CuCl
AT3G23990.1	HSP60-3b chaperonin (CPN60)	0.625	14.000	0.625	3.000	6.000	4.000	0	450	0	95	49	87	0.413	MeOH
AT3G23990.1	HSP60-3b chaperonin (CPN60)	3.000	6.000	4.000	14.000	6.000	3.000	95	49	87	488	83	78	0.475	Mena
AT3G23990.1	HSP60-3b chaperonin (CPN60)	0.625	14.000	0.625	11.000	2.000	5.000	0	450	0	393	42	128	0.561	CuCl
AT3G23990.1	HSP60-3b chaperonin (CPN60)	3.000	6.000	4.000	7.000	6.000	2.000	95	49	87	105	53	73	0.879	Anti A
AT3G27240.1	CYC1-1 Complex III cytochrome *c*1	5.000	8.000	12.000	11.000	11.000	13.000	144	298	372	249	218	501	0.092	Anti A
AT3G27240.1	CYC1-1 Complex III cytochrome *c*1	9.000	8.000	8.000	12.000	9.000	13.000	389	381	337	255	190	417	0.174	H202
AT3G27240.1	CYC1-1 Complex III cytochrome *c*1	5.000	8.000	12.000	7.000	10.000	8.000	144	298	372	312	377	359	0.749	Mena
AT3G27240.1	CYC1-1 Complex III cytochrome *c*1	9.000	8.000	8.000	7.000	13.000	8.000	389	381	337	268	290	145	0.765	CuCl
AT3G27240.1	CYC1-1 Complex III cytochrome *c*1	9.000	8.000	8.000	8.000	8.000	10.000	389	381	337	146	388	146	0.808	Cold
AT3G27240.1	CYC1-1 Complex III cytochrome *c*1	9.000	8.000	8.000	5.000	8.000	12.000	410	388	335	134	311	414	0.906	MeOH
AT3G27280.1	ATPHB4 Prohibitin 4	11.000	16.000	9.000	8.000	7.000	7.000	531	631	471	397	429	343	0.138	Mena
AT3G27280.1	ATPHB4 Prohibitin 4	8.000	7.000	10.000	16.000	15.000	9.000	295	370	467	507	452	378	0.186	H202
AT3G27280.1	ATPHB4 Prohibitin 4	8.000	7.000	10.000	11.000	16.000	9.000	295	370	467	531	631	471	0.303	MeOH
AT3G27280.1	ATPHB4 Prohibitin 4	8.000	7.000	10.000	2.000	7.000	13.000	295	370	467	344	370	231	0.599	Cold
AT3G27280.1	ATPHB4 Prohibitin 4	8.000	7.000	10.000	7.000	16.000	8.000	295	370	467	261	520	146	0.681	CuCl
AT3G27280.1	ATPHB4 Prohibitin 4	11.000	16.000	9.000	12.000	14.000	10.000	531	631	471	433	445	524	0.776	Anti A
AT3G27570.1	Unknown protein, sucrose cleavage-like	2.000	4.000	2.000	1.000	2.000	2.000	176	210	164	93	140	157	0.262	MeOH
AT3G27570.1	Unknown protein, sucrose cleavage-like	1.000	2.000	2.000	1.000	2.000	1.000	93	140	157	93	179	101	0.355	Mena
AT3G27570.1	Unknown protein, sucrose cleavage-like	2.000	4.000	2.000	2.000	1.000	2.000	176	210	164	92	95	59	0.424	CuCl
AT3G27570.1	Unknown protein, sucrose cleavage-like	1.000	2.000	2.000	1.000	2.000	2.000	93	140	157	74	70	157	0.884	Anti A
AT3G46430.1	ATP6 ATP Synthase 6kDA subunit	2.000	5.000	3.000	5.000	4.000	6.000	37	88	62	50	64	66	0.283	Mena
AT3G46430.1	ATP6 ATP Synthase 6kDA subunit	2.000	2.000	2.000	2.000	5.000	3.000	50	64	66	37	88	62	0.290	MeOH
AT3G47833.1	SDH7 Succinate dehydrogenase subunit 7	0.625	2.000	0.625	1.000	2.000	2.000	0	50	0	61	50	42	0.275	Cold
AT3G47833.1	SDH7 Succinate dehydrogenase subunit 7	0.625	4.000	2.000	2.000	2.000	2.000	50	64	66	72	73	80	0.761	Mena
AT3G48680.1	γCAL2 γCarbonic anhydrase 2 like	0.625	4.000	2.000	4.000	6.000	3.000	0	78	58	113	148	82	0.160	Mena
AT3G48680.1	γCAL2 γCarbonic anhydrase 2 like	6.000	4.000	4.000	5.000	6.000	2.000	101	130	158	168	163	84	0.685	H202
AT3G52300.1	ATP7 ATP synthase subunit 7	4.000	3.000	3.000	6.000	2.000	1.000	265	127	144	138	79	46	0.430	H202
AT3G52300.1	ATP7 ATP synthase subunit 7	0.625	6.000	3.000	2.000	5.000	3.000	0	179	112	70	140	89	0.439	Anti A
AT3G52300.1	ATP7 ATP synthase subunit 7	0.625	6.000	3.000	3.000	3.000	4.000	0	179	112	136	96	139	0.575	Mena
AT3G52730.1	QCR9 Complex III ubiquinol-cytochrome *c* reductase 9 kDa subunit	1.000	1.000	2.000	0.625	0.625	0.625	55	67	55	0	0	0	0.064	Cold
AT3G52730.1	QCR9 Complex III ubiquinol-cytochrome *c* reductase 9 kDa subunit	1.000	1.000	2.000	0.625	0.625	0.625	55	67	55	0	0	0	0.064	CuCl
AT3G52730.1	QCR9 Complex III ubiquinol-cytochrome *c* reductase 9 kDa subunit	0.625	1.000	2.000	3.000	2.000	3.000	0	83	66	68	69	70	0.082	Anti A
AT3G52730.1	QCR9 Complex III ubiquinol-cytochrome *c* reductase 9 kDa subunit	1.000	1.000	2.000	2.000	2.000	2.000	55	67	55	55	64	74	0.122	H202

AGI	ID	C1	C2	C3	T1	T2	T3	MOWSE C1	MOWSE C2	MOWSE C3	MOWSE T1	MOWSE T2	MOWSE T3	t-test	Treatment
AT3G52730.1	QCR9 Complex III ubiquinol-cytochrome *c* reductase 9 kDa subunit	0.625	1.000	2.000	2.000	1.000	1.000	0	83	66	60	55	60	0.752	Mena
AT3G52950.1	Unknown protein, Phox/Bemp1 (PB1) domain-containing protein	5.000	9.000	11.000	4.000	4.000	2.000	171	287	392	110	195	60	0.130	CuCl
AT3G52950.1	Unknown protein, Phox/Bemp1 (PB1) domain-containing protein	5.000	9.000	11.000	5.000	7.000	5.000	171	287	392	157	174	267	0.184	H202
AT3G52950.1	Unknown protein, Phox/Bemp1 (PB1) domain-containing protein	5.000	9.000	11.000	2.000	9.000	5.000	171	287	392	140	287	142	0.225	Cold
AT3G52950.1	Unknown protein, Phox/Bemp1 (PB1) domain-containing protein	5.000	7.000	10.000	4.000	7.000	6.000	230	263	318	220	151	232	0.238	Anti A
AT3G52950.1	Unknown protein, Phox/Bemp1 (PB1) domain-containing protein	5.000	9.000	11.000	5.000	7.000	10.000	171	287	392	230	263	318	0.272	MeOH
AT3G54110.1	UCP1 Uncoupling protein 1	16.000	15.000	19.000	21.000	22.000	19.000	485	554	660	550	664	588	0.145	H202
AT3G54110.1	UCP1 Uncoupling protein 1	16.000	15.000	19.000	8.000	18.000	11.000	485	554	660	303	444	226	0.383	CuCl
AT3G54110.1	UCP1 Uncoupling protein 1	16.000	15.000	19.000	3.000	15.000	21.000	485	554	660	282	554	186	0.512	Cold
AT3G54110.1	UCP1 Uncoupling protein 1	13.000	14.000	13.000	12.000	15.000	22.000	431	631	482	415	512	397	0.539	Mena
AT3G54110.1	UCP1 Uncoupling protein 1	16.000	15.000	19.000	13.000	17.000	15.000	485	554	660	431	631	482	0.590	MeOH
AT3G56430.1	Unknown protein, contains mitochondrial import inner membrane translocase domain (Tim21)	0.625	8.000	5.000	8.000	9.000	10.000	0	156	132	152	265	288	0.233	Mena
AT3G56430.1	Unknown protein, contains mitochondrial import inner membrane translocase domain (Tim21)	0.625	8.000	5.000	4.000	6.000	5.000	0	156	132	74	86	112	0.469	Anti A
AT3G56430.1	Unknown protein, contains mitochondrial import inner membrane translocase domain (Tim21)	5.000	9.000	6.000	6.000	8.000	5.000	102	196	98	129	155	80	0.564	H202
AT3G59820.1	Mdm38-1 Component of mitochondrial protein export machinery	5.000	0.625	0.625	10.000	14.000	13.000	139	0	0	508	615	661	0.118	Mena
AT3G59820.1	Mdm38-1 Component of mitochondrial protein export machinery	5.000	0.625	0.625	5.000	4.000	7.000	139	0	0	84	106	207	0.216	Anti A
AT3G59820.1	Mdm38-1 Component of mitochondrial protein export machinery	10.000	13.000	9.000	7.000	11.000	2.000	334	560	333	108	191	60	0.218	H202
AT3G59820.1	Mdm38-1 Component of mitochondrial protein export machinery	10.000	13.000	9.000	1.000	13.000	2.000	334	560	333	65	560	38	0.222	Cold
AT3G63150.1	MIRO2 Miro-related GTPase 2	5.000	5.000	7.000	1.000	6.000	5.000	82	103	151	62	62	93	0.436	MeOH
AT3G63150.1	MIRO2 Miro-related GTPase 2	1.000	6.000	5.000	4.000	5.000	2.000	62	93	93	45	76	69	0.874	Mena
AT4G00860.1	COX X2-1 Cytochrome *c* oxidase X2-1 subunit	2.000	0.625	0.625	4.000	3.000	1.000	36	0	0	178	157	85	0.116	Anti A
AT4G00860.1	COX X2-1 Cytochrome *c* oxidase X2-1 subunit	0.625	0.625	1.000	3.000	5.000	1.000	0	0	68	110	141	74	0.172	H202
AT4G00860.1	COX X2-1 Cytochrome *c* oxidase X2-1 subunit	0.625	0.625	1.000	0.625	0.625	0.625	0	0	68	110	141	74	0.332	Cold
AT4G00860.1	COX X2-1 Cytochrome *c* oxidase X2-1 subunit	0.625	0.625	1.000	0.625	0.625	0.625	0	0	68	110	141	74	0.332	CuCl
AT4G00860.1	COX X2-1 Cytochrome *c* oxidase X2-1 subunit	2.000	0.625	0.625	1.000	1.000	1.000	36	0	0	69	75	38	0.856	Mena
AT4G01100.1	ANT1 Adenine nucleotide transporter 1	7.000	9.000	9.000	7.000	6.000	4.000	317	409	334	369	134	120	0.136	CuCl
AT4G01100.1	ANT1 Adenine nucleotide transporter 1	7.000	9.000	9.000	6.000	8.000	5.000	317	409	334	218	230	216	0.137	MeOH
AT4G01100.1	ANT1 Adenine nucleotide transporter 1	6.000	8.000	5.000	13.000	8.000	8.000	218	230	216	402	405	294	0.155	Anti A
AT4G01100.1	ANT1 Adenine nucleotide transporter 1	7.000	9.000	9.000	3.000	9.000	6.000	317	409	334	163	409	212	0.312	Cold
AT4G01100.1	ANT1 Adenine nucleotide transporter 1	6.000	8.000	5.000	7.000	9.000	13.000	218	230	216	356	347	413	0.331	Mena
AT4G01100.1	ANT1 Adenine nucleotide transporter 1	7.000	9.000	9.000	9.000	8.000	7.000	317	409	334	347	291	297	0.756	H202
AT4G01660.1	ABC1 ABC Transporter 1	1.000	2.000	5.000	0.625	0.625	0.625	74	69	81	0	0	0	0.090	CuCl
AT4G01660.1	ABC1 ABC Transporter 1	1.000	2.000	5.000	0.625	0.625	0.625	74	69	81	0	0	0	0.090	H202
AT4G01660.1	ABC1 ABC Transporter 1	0.625	2.000	0.625	5.000	3.000	3.000	0	58	0	69	64	41	0.098	Anti A
AT4G01660.1	ABC1 ABC Transporter 1	0.625	2.000	0.625	1.000	3.000	3.000	0	58	0	72	108	120	0.196	Mena
AT4G05020.1	NDB2 Alternative NAD(P)H dehydrogenase	10.000	11.000	6.000	6.000	4.000	4.000	369	401	294	203	88	103	0.086	CuCl
AT4G05020.1	NDB2 Alternative NAD(P)H dehydrogenase	6.000	6.000	12.000	11.000	15.000	8.000	63	197	339	371	480	260	0.399	Mena
AT4G05020.1	NDB2 Alternative NAD(P)H dehydrogenase	10.000	11.000	6.000	6.000	11.000	5.000	369	401	294	148	401	65	0.414	Cold

AGI	ID	C1	C2	C3	T1	T2	T3	MOWSE C1	MOWSE C2	MOWSE C3	MOWSE T1	MOWSE T2	MOWSE T3	t-test	Treatment
AT4G05020.1	NDB2 Alternative NAD(P)H dehydrogenase	6.000	6.000	12.000	7.000	10.000	10.000	63	197	339	67	277	310	0.464	Anti A
AT4G05020.1	NDB2 Alternative NAD(P)H dehydrogenase	10.000	11.000	6.000	13.000	9.000	8.000	369	401	294	243	212	234	0.512	H202
AT4G05020.1	NDB2 Alternative NAD(P)H dehydrogenase	10.000	11.000	6.000	6.000	6.000	12.000	369	401	294	63	197	339	0.811	MeOH
AT4G16450.1	B20.9 NADH dehydrogenase 20.9 kDa subunit	3.000	4.000	4.000	3.000	3.000	2.000	153	148	198	128	147	98	0.140	H202
AT4G16450.1	B20.9 NADH dehydrogenase 20.9 kDa subunit	3.000	4.000	4.000	1.000	3.000	2.000	153	148	198	91	148	55	0.144	Cold
AT4G16450.1	B20.9 NADH dehydrogenase 20.9 kDa subunit	1.000	5.000	2.000	3.000	5.000	5.000	52	218	98	140	173	257	0.166	Anti A
AT4G16450.1	B20.9 NADH dehydrogenase 20.9 kDa subunit	1.000	5.000	2.000	4.000	4.000	3.000	52	218	98	170	133	145	0.325	Mena
AT4G16450.1	B20.9 NADH dehydrogenase 20.9 kDa subunit	3.000	4.000	4.000	1.000	5.000	2.000	153	148	198	52	218	98	0.360	MeOH
AT4G17085.1	Unknown protein	0.625	1.000	1.000	1.000	1.000	1.000	0	41	51	75	48	39	0.194	Mena
AT4G20150.1	NADH dehydrogenase plant specific subunit 9kDa	6.000	6.000	3.000	9.000	6.000	6.000	152	253	224	227	224	260	0.239	H202
AT4G20150.1	NADH dehydrogenase plant specific subunit 9kDa	6.000	6.000	3.000	7.000	6.000	7.000	152	253	224	275	250	323	0.383	MeOH
AT4G20150.1	NADH dehydrogenase plant specific subunit 9kDa	6.000	6.000	3.000	5.000	8.000	6.000	152	253	224	134	333	132	0.484	CuCl
AT4G20150.1	NADH dehydrogenase plant specific subunit 9kDa	7.000	6.000	7.000	5.000	8.000	4.000	275	250	323	182	323	191	0.543	Mena
AT4G20150.1	NADH dehydrogenase plant specific subunit 9kDa	7.000	6.000	7.000	6.000	8.000	8.000	323	226	292	252	234	286	0.654	Anti A
AT4G20150.1	NADH dehydrogenase plant specific subunit 9kDa	6.000	6.000	3.000	3.000	6.000	4.000	152	253	224	104	253	70	0.769	Cold
AT4G21105.1	COX X4 Cytochrome *c* oxidase X4 subunit	4.000	1.000	0.625	0.625	0.625	0.625	104	78	0	65	48	76	0.351	Mena
AT4G21105.1	COX X4 Cytochrome *c* oxidase X4 subunit	0.625	1.000	0.625	0.625	0.625	0.625	104	78	0	65	48	76	0.458	Cold
AT4G21105.1	COX X4 Cytochrome *c* oxidase X4 subunit	4.000	1.000	0.625	1.000	2.000	2.000	104	78	0	65	48	76	0.862	Anti A
AT4G21490.1	NDB3 Alternative NAD(P)H dehydrogenase	0.625	3.000	0.625	0.625	0.625	0.625	0	68	0	0	0	0	0.423	Cold
AT4G21490.1	NDB3 Alternative NAD(P)H dehydrogenase	0.625	3.000	0.625	0.625	0.625	0.625	0	68	0	0	0	0	0.423	CuCl
AT4G21490.1	NDB3 Alternative NAD(P)H dehydrogenase	0.625	3.000	0.625	0.625	0.625	0.625	0	68	0	0	0	0	0.423	H202
AT4G26910.1	KDC E2-4α 2-oxoacid dehydrogenase family protein	0.625	3.000	1.000	5.000	5.000	1.000	0	43	43	140	92	53	0.253	Anti A
AT4G26910.1	KDC E2-4α 2-oxoacid dehydrogenase family protein	0.625	3.000	1.000	0.625	0.625	0.625	0	43	43	140	92	53	0.263	Mena
AT4G26910.1	KDC E2-4α 2-oxoacid dehydrogenase family protein	0.625	3.000	3.000	2.000	2.000	2.000	0	117	41	93	50	58	0.801	H202
AT4G27585.1	Stomatin-like protein	22.000	21.000	22.000	13.000	15.000	9.000	601	579	523	512	407	206	0.058	CuCl
AT4G27585.1	Stomatin-like protein	18.000	21.000	21.000	15.000	13.000	18.000	580	678	689	449	320	708	0.161	Anti A
AT4G27585.1	Stomatin-like protein	22.000	21.000	22.000	12.000	21.000	10.000	601	579	523	324	579	214	0.212	Cold
AT4G27585.1	Stomatin-like protein	22.000	21.000	22.000	12.000	20.000	14.000	601	579	523	271	582	443	0.235	H202
AT4G27585.1	Stomatin-like protein	18.000	21.000	21.000	20.000	22.000	13.000	580	678	689	686	733	524	0.546	Mena
AT4G27585.1	Stomatin-like protein	22.000	21.000	22.000	18.000	21.000	21.000	601	579	523	580	678	689	0.647	MeOH
AT4G28390.1	AAC3 ADP/ATP carrier 3	11.000	12.000	16.000	9.000	10.000	12.000	181	276	376	201	292	334	0.074	MeOH
AT4G28390.1	AAC3 ADP/ATP carrier 3	9.000	10.000	12.000	11.000	14.000	12.000	201	292	334	241	332	310	0.186	Mena
AT4G28510.1	ATPHB1 Prohibitin 1	6.000	12.000	15.000	5.000	8.000	7.000	308	410	389	219	370	271	0.050	MeOH
AT4G28510.1	ATPHB1 Prohibitin 1	5.000	8.000	7.000	17.000	12.000	10.000	219	370	271	330	410	271	0.084	Cold
AT4G28510.1	ATPHB1 Prohibitin 1	6.000	12.000	15.000	10.000	9.000	8.000	254	448	418	459	314	305	0.686	H202
AT4G29130.1	HXK1 Hexokinase 1	9.000	14.000	13.000	16.000	14.000	16.000	257	383	459	516	493	594	0.147	Mena
AT4G29130.1	HXK1 Hexokinase 1	0.625	11.000	13.000	9.000	14.000	13.000	0	422	493	257	383	459	0.334	MeOH
AT4G29130.1	HXK1 Hexokinase 1	0.625	11.000	13.000	11.000	13.000	12.000	0	422	493	246	436	356	0.371	H202
AT4G29130.1	HXK1 Hexokinase 1	0.625	11.000	13.000	11.000	11.000	12.000	0	422	493	350	422	181	0.404	Cold
AT4G29130.1	HXK1 Hexokinase 1	0.625	11.000	13.000	9.000	10.000	5.000	0	422	493	269	244	135	0.642	CuCl
AT4G29130.1	HXK1 Hexokinase 1	9.000	14.000	13.000	10.000	11.000	17.000	257	383	459	235	196	523	0.776	Anti A
AT4G32470.1	QCR7-1 Complex III ubiquinol-cytochrome *c* reductase complex 14 kDa subunit	4.000	3.000	6.000	7.000	9.000	8.000	176	185	244	166	346	135	0.112	H202

AGI	ID	C1	C2	C3	T1	T2	T3	MOWSE C1	MOWSE C2	MOWSE C3	MOWSE T1	MOWSE T2	MOWSE T3	t-test	Treatment
AT4G32470.1	QCR7-1 Complex III ubiquinol-cytochrome *c* reductase complex 14 kDa subunit	4.000	3.000	6.000	9.000	3.000	11.000	176	185	244	110	185	230	0.158	Cold
AT4G32470.1	QCR7-1 Complex III ubiquinol-cytochrome *c* reductase complex 14 kDa subunit	5.000	6.000	3.000	7.000	8.000	7.000	100	294	147	117	144	262	0.167	Anti A
AT4G32470.1	QCR7-1 Complex III ubiquinol-cytochrome *c* reductase complex 14 kDa subunit	4.000	3.000	6.000	5.000	6.000	3.000	176	185	244	100	294	147	0.840	MeOH
AT4G32470.1	QCR7-1 Complex III ubiquinol-cytochrome *c* reductase complex 14 kDa subunit	4.000	3.000	6.000	3.000	7.000	4.000	176	185	244	182	125	134	0.892	CuCl
AT4G32470.1	QCR7-1 Complex III ubiquinol-cytochrome *c* reductase complex 14 kDa subunit	5.000	6.000	3.000	6.000	4.000	4.000	100	294	147	257	208	223	0.893	Mena
AT4G33520.2	PAA1 Metal-transporting P-type ATPase 1	5.000	6.000	3.000	3.000	4.000	8.000	100	294	147	102	119	242	0.956	Mena
AT4G35860.1	RAB-B1c RAB-B-class small GTPase	0.625	2.000	0.625	1.000	4.000	4.000	0	95	0	53	109	88	0.175	Mena
AT4G35860.1	RAB-B1c RAB-B-class small GTPase	0.625	2.000	0.625	0.625	0.625	0.625	0	95	0	0	0	0	0.426	Anti A
AT4G35860.1	RAB-B1c RAB-B-class small GTPase	0.625	1.000	0.625	0.625	0.625	0.625	0	81	0	0	0	0	0.458	Cold
AT4G35860.1	RAB-B1c RAB-B-class small GTPase	0.625	1.000	0.625	0.625	0.625	0.625	0	81	0	0	0	0	0.458	CuCl
AT4G37830.1	COX 6a Cytochrome *c* oxidase-related	0.625	0.625	2.000	1.000	1.000	2.000	0	0	40	51	43	69	0.103	Mena
AT4G37830.1	COX 6a Cytochrome *c* oxidase-related	0.625	2.000	1.000	0.625	0.625	0.625	0	62	44	0	0	0	0.217	Cold
AT4G37830.1	COX 6a Cytochrome *c* oxidase-related	0.625	2.000	1.000	0.625	0.625	0.625	0	62	44	0	0	0	0.217	CuCl
AT4G37830.1	COX 6a Cytochrome *c* oxidase-related	0.625	2.000	1.000	0.625	0.625	0.625	0	62	44	0	0	0	0.217	H202
AT4G37910.1	mtHSP70-1 Mitochondrial heat shock protein 70 kDa	0.625	6.000	8.000	0.625	0.625	0.625	0	119	190	0	0	0	0.162	Anti A
AT4G37910.1	mtHSP70-1 Mitochondrial heat shock protein 70 kDa	6.000	13.000	8.000	6.000	13.000	11.000	173	628	173	192	628	176	0.556	Cold
AT4G37910.1	mtHSP70-1 Mitochondrial heat shock protein 70 kDa	0.625	6.000	8.000	12.000	1.000	2.000	0	119	190	386	60	69	0.970	Mena
AT4G39460.1	SAMC1 S-Adenosyl-methionone Carrier 1	0.625	5.000	0.625	0.625	0.625	0.625	0	63	0	98	117	61	0.423	Cold
AT4G39460.1	SAMC1 S-Adenosyl-methionone Carrier 1	0.625	4.000	7.000	4.000	4.000	4.000	0	118	100	98	117	61	0.567	Mena
AT4G39690.1	Unknown protein, contains domain PTHR15415	4.000	6.000	10.000	2.000	6.000	5.000	55	155	398	56	155	38	0.224	Cold
AT4G39690.1	Unknown protein, contains domain PTHR15415	4.000	6.000	10.000	6.000	2.000	2.000	55	155	398	188	105	61	0.290	CuCl
AT4G39690.1	Unknown protein, contains domain PTHR15415	0.625	7.000	9.000	2.000	4.000	9.000	0	265	394	78	108	488	0.681	Mena
AT4G39740.1	HCC2 Mitochondrial copper chaperone involved in CV assembly	1.000	2.000	2.000	3.000	2.000	2.000	42	75	62	33	75	34	0.328	Cold
AT4G39740.1	HCC2 Mitochondrial copper chaperone involved in CV assembly	0.625	3.000	2.000	1.000	2.000	2.000	0	69	53	53	85	70	0.884	Mena
AT5G02500.1	HSP70-1 Heat shock protein 1 70 kDa protein	2.000	4.000	4.000	7.000	6.000	6.000	55	85	120	225	115	168	0.081	Mena
AT5G02500.1	HSP70-1 Heat shock protein 1 70 kDa protein	8.000	6.000	2.000	2.000	4.000	4.000	149	195	106	55	85	120	0.652	MeOH
AT5G05520.1	SAM50-2 SAM mitochondrial outer membrane complex 50-2	1.000	5.000	3.000	4.000	8.000	6.000	61	100	102	180	290	270	0.057	Mena
AT5G05520.1	SAM50-2 SAM mitochondrial outer membrane complex 50-2	1.000	5.000	3.000	5.000	8.000	8.000	61	100	102	82	59	198	0.066	Anti A
AT5G05520.1	SAM50-2 SAM mitochondrial outer membrane complex 50-2	6.000	4.000	5.000	7.000	4.000	7.000	68	141	72	67	141	93	0.340	Cold
AT5G05520.1	SAM50-2 SAM mitochondrial outer membrane complex 50-2	6.000	4.000	5.000	8.000	1.000	3.000	68	141	72	245	33	49	0.354	CuCl
AT5G05520.1	SAM50-2 SAM mitochondrial outer membrane complex 50-2	6.000	4.000	5.000	1.000	5.000	3.000	68	141	72	61	100	102	0.405	MeOH
AT5G05520.1	SAM50-2 SAM mitochondrial outer membrane complex 50-2	6.000	4.000	5.000	7.000	9.000	4.000	68	141	72	130	171	162	0.479	H202
AT5G08040.1	TOM5 Translocase Outer Membrane 5	0.625	2.000	3.000	0.625	0.625	0.625	0	57	96	0	0	0	0.151	Cold
AT5G08040.1	TOM5 Translocase Outer Membrane 5	0.625	2.000	3.000	1.000	2.000	8.000	0	57	96	34	37	139	0.256	H202
AT5G08670.1	ATP2 ATP synthase	14.000	17.000	22.000	6.000	5.000	13.000	493	603	757	178	158	635	0.067	Mena
AT5G08670.1	ATP2 ATP synthase	5.000	5.000	22.000	14.000	17.000	22.000	171	101	914	493	603	757	0.152	MeOH
AT5G08670.1	ATP2 ATP synthase	5.000	5.000	22.000	17.000	8.000	11.000	171	101	914	551	144	292	0.551	CuCl
AT5G09270.1	Unknown protein	2.000	1.000	1.000	0.625	0.625	0.625	111	86	96	0	0	0	0.151	Cold
AT5G09270.1	Unknown protein	2.000	1.000	1.000	0.625	0.625	0.625	111	86	96	0	0	0	0.151	CuCl
AT5G09270.1	Unknown protein	1.000	1.000	1.000	1.000	2.000	1.000	36	63	89	63	123	79	0.445	Anti A
AT5G09270.1	Unknown protein	2.000	1.000	1.000	1.000	1.000	1.000	136	86	96	68	67	66	0.546	H202

AGI	ID	C1	C2	C3	T1	T2	T3	MOWSE C1	MOWSE C2	MOWSE C3	MOWSE T1	MOWSE T2	MOWSE T3	t-test	Treatment
AT5G09270.1	Unknown protein	2.000	1.000	1.000	1.000	1.000	1.000	111	86	96	36	63	89	0.546	MeOH
AT5G09270.1	Unknown protein	1.000	1.000	1.000	1.000	1.000	1.000	36	63	89	91	91	85	0.884	Mena
AT5G13450.1	ATP5 ATP synthase	3.000	8.000	12.000	4.000	10.000	16.000	90	147	265	164	219	360	0.063	MeOH
AT5G13450.1	ATP5 ATP synthase	4.000	10.000	16.000	9.000	5.000	8.000	164	219	360	185	170	214	0.717	Mena
AT5G13450.1	ATP5 ATP synthase	3.000	8.000	12.000	8.000	11.000	4.000	90	147	265	104	129	149	0.898	H202
AT5G13450.1	ATP5 ATP synthase	4.000	10.000	16.000	12.000	8.000	5.000	164	219	360	233	125	100	0.899	Anti A
AT5G13450.1	ATP5 ATP synthase	3.000	8.000	12.000	12.000	6.000	3.000	90	147	265	259	144	73	0.920	CuCl
AT5G13490.1	AAC2 ADP/ATP carrier 1	15.000	18.000	26.000	29.000	28.000	26.000	384	500	651	351	533	706	0.099	Anti A
AT5G13490.1	AAC2 ADP/ATP carrier 1	17.000	23.000	33.000	6.000	23.000	19.000	351	533	706	748	765	679	0.281	Cold
AT5G13490.1	AAC2 ADP/ATP carrier 1	17.000	23.000	33.000	18.000	17.000	8.000	351	533	706	413	303	129	0.290	CuCl
AT5G13490.1	AAC2 ADP/ATP carrier 1	15.000	18.000	26.000	20.000	33.000	22.000	384	500	651	468	696	616	0.343	Mena
AT5G13490.1	AAC2 ADP/ATP carrier 1	17.000	23.000	33.000	38.000	33.000	24.000	351	533	706	881	684	561	0.370	H202
AT5G13610.1	Unknown protein	4.000	2.000	4.000	5.000	2.000	4.000	134	68	105	85	68	45	0.060	Cold
AT5G13610.1	Unknown protein	3.000	6.000	4.000	4.000	6.000	4.000	47	83	115	96	152	152	0.081	Mena
AT5G13610.1	Unknown protein	4.000	2.000	4.000	7.000	6.000	6.000	134	68	105	51	118	80	0.089	H202
AT5G13610.1	Unknown protein	4.000	2.000	4.000	3.000	6.000	4.000	134	68	105	47	83	115	0.600	MeOH
AT5G13610.1	Unknown protein	3.000	6.000	4.000	4.000	2.000	8.000	47	83	115	46	38	159	0.965	Anti A
AT5G14040.1	PiC Phosphate carrier	14.000	16.000	14.000	30.000	16.000	24.000	389	362	300	418	362	256	0.156	Cold
AT5G14040.1	PiC Phosphate carrier	14.000	16.000	14.000	13.000	20.000	13.000	389	362	300	292	302	193	0.810	CuCl
AT5G14040.1	PiC Phosphate carrier	14.000	16.000	14.000	16.000	11.000	18.000	389	362	300	280	287	396	0.945	MeOH
AT5G14040.1	PiC Phosphate carrier	16.000	11.000	18.000	12.000	13.000	20.000	280	287	396	290	381	364	0.976	Mena
AT5G15090.1	VDAC3 Porin	11.000	12.000	13.000	10.000	11.000	5.000	336	512	382	423	345	218	0.265	CuCl
AT5G15090.1	VDAC3 Porin	11.000	12.000	13.000	10.000	10.000	12.000	336	512	382	262	432	393	0.310	MeOH
AT5G15090.1	VDAC3 Porin	11.000	12.000	13.000	4.000	12.000	11.000	336	512	382	289	512	232	0.424	Cold
AT5G15090.1	VDAC3 Porin	11.000	12.000	13.000	12.000	16.000	10.000	336	512	382	410	351	431	0.763	H202
AT5G15090.1	VDAC3 Porin	10.000	10.000	12.000	7.000	13.000	16.000	262	432	393	323	548	467	0.812	Mena
AT5G15090.1	VDAC3 Porin	10.000	10.000	12.000	7.000	12.000	13.000	262	432	393	263	430	376	0.943	Anti A
AT5G15320.1	Unknown protein	3.000	3.000	3.000	2.000	3.000	1.000	89	39	119	51	119	55	0.240	H202
AT5G15320.1	Unknown protein	3.000	3.000	3.000	25.000	3.000	4.000	89	39	119	127	39	73	0.305	Cold
AT5G15320.1	Unknown protein	0.625	5.000	3.000	2.000	2.000	3.000	0	131	113	89	40	159	0.879	Anti A
AT5G15320.1	Unknown protein	3.000	3.000	3.000	3.000	2.000	4.000	89	39	119	56	40	63	0.917	CuCl
AT5G15640.1	Putative mitochondrial substrate carrier family protein (MCSF)	1.000	3.000	2.000	0.625	0.625	0.625	52	83	84	150	158	92	0.058	Cold
AT5G15640.1	Putative mitochondrial substrate carrier family protein (MCSF)	1.000	3.000	2.000	0.625	0.625	0.625	52	83	84	150	158	92	0.058	CuCl
AT5G15640.1	Putative mitochondrial substrate carrier family protein (MCSF)	1.000	3.000	2.000	3.000	4.000	3.000	52	83	84	150	158	92	0.083	H202
AT5G15640.1	Putative mitochondrial substrate carrier family protein (MCSF)	0.625	0.625	2.000	5.000	4.000	2.000	0	0	51	157	117	97	0.158	Anti A
AT5G16930.1	AAA-type ATPase protein	5.000	7.000	4.000	12.000	7.000	5.000	157	195	205	256	189	90	0.202	H202
AT5G16930.1	AAA-type ATPase protein	0.625	8.000	6.000	9.000	8.000	9.000	0	128	243	187	156	305	0.307	Anti A
AT5G16930.1	AAA-type ATPase protein	0.625	8.000	6.000	5.000	7.000	5.000	0	128	243	179	220	200	0.467	Mena
AT5G17770.1	CBR1 NADH:cytochrome b5 reductase	2.000	3.000	1.000	3.000	3.000	3.000	66	77	86	72	107	69	0.290	MeOH
AT5G17770.1	CBR1 NADH:cytochrome b5 reductase	2.000	3.000	1.000	3.000	2.000	3.000	66	77	86	84	89	74	0.496	H202
AT5G17770.1	CBR1 NADH:cytochrome b5 reductase	3.000	3.000	3.000	3.000	3.000	4.000	72	107	69	72	83	144	0.567	Mena
AT5G17770.1	CBR1 NADH:cytochrome b5 reductase	3.000	3.000	3.000	3.000	3.000	3.000	72	107	69	89	73	86	0.884	Anti A
AT5G19760.1	DTC Dicarboxylate/tricarboxylate carrier	4.000	7.000	11.000	5.000	7.000	12.000	254	348	223	298	416	699	0.141	Mena

AGI	ID	C1	C2	C3	T1	T2	T3	MOWSE C1	MOWSE C2	MOWSE C3	MOWSE T1	MOWSE T2	MOWSE T3	t-test	Treatment
AT5G19760.1	DTC Dicarboxylate/tricarboxylate carrier	5.000	5.000	5.000	7.000	3.000	2.000	314	342	382	272	134	172	0.355	H202
AT5G19760.1	DTC Dicarboxylate/tricarboxylate carrier	5.000	5.000	5.000	6.000	5.000	14.000	314	342	382	215	342	236	0.375	Cold
AT5G19760.1	DTC Dicarboxylate/tricarboxylate carrier	4.000	7.000	11.000	7.000	2.000	5.000	254	348	223	231	126	296	0.422	Anti A
AT5G19760.1	DTC Dicarboxylate/tricarboxylate carrier	5.000	5.000	5.000	9.000	8.000	3.000	314	342	382	254	348	223	0.573	MeOH
AT5G19760.1	DTC Dicarboxylate/tricarboxylate carrier	5.000	5.000	5.000	4.000	8.000	5.000	314	342	382	261	226	233	0.743	CuCl
AT5G20090.1	Unknown protein	0.625	2.000	1.000	5.000	3.000	2.000	0	42	47	82	75	69	0.141	Anti A
AT5G20090.1	Unknown protein	0.625	2.000	1.000	2.000	1.000	2.000	0	42	47	42	42	43	0.527	Mena
AT5G23300.1	PYRD (pyrimidine d) Dihydroorotate dehydrogenase	3.000	4.000	4.000	1.000	6.000	2.000	120	204	210	49	159	60	0.455	H202
AT5G23300.1	PYRD (pyrimidine d) Dihydroorotate dehydrogenase	0.625	6.000	5.000	3.000	4.000	6.000	0	192	238	147	229	301	0.472	Mena
AT5G23300.1	PYRD (pyrimidine d) Dihydroorotate dehydrogenase	3.000	4.000	4.000	5.000	4.000	3.000	120	204	210	48	204	83	0.639	Cold
AT5G23300.1	PYRD (pyrimidine d) Dihydroorotate dehydrogenase	0.625	6.000	5.000	2.000	2.000	2.000	0	192	238	108	63	93	0.719	Anti A
AT5G24650.1	AtPRAT2.2 Mitochondrial import inner membrane translocase subunit	0.625	0.625	4.000	2.000	2.000	3.000	0	0	96	59	77	75	0.250	MeOH
AT5G24650.1	AtPRAT2.2 Mitochondrial import inner membrane translocase subunit	0.625	0.625	4.000	2.000	1.000	3.000	0	0	96	52	53	65	0.315	H202
AT5G24650.1	AtPRAT2.2 Mitochondrial import inner membrane translocase subunit	2.000	2.000	3.000	2.000	1.000	3.000	59	77	75	39	63	101	0.436	Mena
AT5G25450.1	QCR7-2 Complex III ubiquinol-cytochrome *c* reductase complex 14 kDa subunit	5.000	4.000	4.000	3.000	1.000	2.000	146	216	91	104	36	65	0.074	CuCl
AT5G25450.1	QCR7-2 Complex III ubiquinol-cytochrome *c* reductase complex 14 kDa subunit	3.000	3.000	5.000	7.000	4.000	5.000	90	36	87	158	139	107	0.153	Anti A
AT5G25450.1	QCR7-2 Complex III ubiquinol-cytochrome *c* reductase complex 14 kDa subunit	5.000	4.000	4.000	5.000	5.000	4.000	146	216	91	80	108	109	0.535	H202
AT5G25450.1	QCR7-2 Complex III ubiquinol-cytochrome *c* reductase complex 14 kDa subunit	5.000	4.000	4.000	3.000	3.000	5.000	146	216	91	90	36	87	0.596	MeOH
AT5G25450.1	QCR7-2 Complex III ubiquinol-cytochrome *c* reductase complex 14 kDa subunit	5.000	4.000	4.000	1.000	4.000	7.000	146	216	91	100	216	108	0.687	Cold
AT5G25450.1	QCR7-2 Complex III ubiquinol-cytochrome *c* reductase complex 14 kDa subunit	3.000	3.000	5.000	4.000	3.000	3.000	90	36	87	121	87	91	0.745	Mena
AT5G25940.1	Unknown protein	2.000	2.000	3.000	6.000	3.000	4.000	64	61	39	61	81	83	0.077	H202
AT5G25940.1	Unknown protein	1.000	3.000	2.000	4.000	4.000	2.000	64	73	109	55	77	60	0.243	Anti A
AT5G25940.1	Unknown protein	2.000	2.000	3.000	2.000	2.000	8.000	64	61	39	47	73	196	0.471	Cold
AT5G25940.1	Unknown protein	2.000	2.000	3.000	1.000	3.000	2.000	64	73	109	64	61	39	0.614	MeOH
AT5G25940.1	Unknown protein	1.000	3.000	2.000	2.000	2.000	2.000	64	73	109	39	68	72	0.723	Mena
AT5G27540.1	MIRO1 Miro-related GTPase 1	13.000	12.000	13.000	11.000	4.000	4.000	378	371	307	375	105	67	0.086	CuCl
AT5G27540.1	MIRO1 Miro-related GTPase 1	13.000	12.000	13.000	8.000	10.000	8.000	378	371	307	148	262	262	0.115	H202
AT5G27540.1	MIRO1 Miro-related GTPase 1	3.000	12.000	11.000	13.000	13.000	14.000	66	363	340	460	556	629	0.242	Mena
AT5G27540.1	MIRO1 Miro-related GTPase 1	13.000	12.000	13.000	3.000	12.000	11.000	378	371	307	66	363	340	0.424	MeOH
AT5G27540.1	MIRO1 Miro-related GTPase 1	13.000	12.000	13.000	3.000	12.000	13.000	378	371	307	174	371	135	0.485	Cold
AT5G27540.1	MIRO1 Miro-related GTPase 1	3.000	12.000	11.000	10.000	6.000	8.000	66	363	340	240	121	319	0.895	Anti A
AT5G39410.1	Putative saccharopine dehydrogenase	0.625	2.000	3.000	3.000	5.000	3.000	0	45	113	136	163	114	0.160	Mena
AT5G39410.1	Putative saccharopine dehydrogenase	0.625	2.000	3.000	1.000	1.000	5.000	0	45	113	82	75	69	0.806	Anti A
AT5G40770.1	ATPHB3 Prohibitin 3	10.000	18.000	13.000	16.000	16.000	15.000	490	640	594	590	552	527	0.296	Anti A
AT5G40770.1	ATPHB3 Prohibitin 3	12.000	13.000	17.000	7.000	13.000	15.000	377	449	750	409	449	266	0.461	Cold
AT5G40770.1	ATPHB3 Prohibitin 3	10.000	18.000	13.000	12.000	14.000	11.000	490	640	594	505	599	522	0.470	Mena
AT5G40770.1	ATPHB3 Prohibitin 3	12.000	13.000	17.000	22.000	22.000	11.000	377	449	750	714	762	499	0.474	H202
AT5G40770.1	ATPHB3 Prohibitin 3	12.000	13.000	17.000	7.000	21.000	12.000	377	449	750	316	641	221	0.757	CuCl
AT5G40770.1	ATPHB3 Prohibitin 3	12.000	13.000	17.000	10.000	18.000	13.000	377	449	750	490	640	594	0.900	MeOH
AT5G40810.1	CYC1-2 Complex III cytochrome *c*1	12.000	13.000	16.000	4.000	8.000	4.000	266	218	227	145	113	119	0.068	CuCl

AGI	ID	C1	C2	C3	T1	T2	T3	MOWSE C1	MOWSE C2	MOWSE C3	MOWSE T1	MOWSE T2	MOWSE T3	t-test	Treatment
AT5G40810.1	CYC1-2 Complex III cytochrome *c*1	12.000	15.000	8.000	4.000	5.000	8.000	161	91	224	165	186	309	0.232	Mena
AT5G40810.1	CYC1-2 Complex III cytochrome *c*1	12.000	15.000	8.000	5.000	6.000	8.000	161	91	224	89	93	233	0.242	Anti A
AT5G40810.1	CYC1-2 Complex III cytochrome *c*1	7.000	6.000	7.000	5.000	5.000	7.000	266	218	227	161	91	224	0.447	MeOH
AT5G46800.1	CAC Mitochondrial carnitine/acyl carrier	0.625	0.625	1.000	2.000	2.000	1.000	0	0	36	78	36	40	0.144	Anti A
AT5G47030.1	ATP16 ATP synthase	0.625	0.625	7.000	4.000	5.000	4.000	0	0	105	89	105	87	0.289	MeOH
AT5G54100.1	Stomatin-like protein	9.000	10.000	13.000	11.000	11.000	14.000	275	313	375	348	316	298	0.066	Anti A
AT5G54100.1	Stomatin-like protein	10.000	14.000	17.000	1.000	14.000	5.000	309	342	434	151	342	120	0.246	Cold
AT5G54100.1	Stomatin-like protein	10.000	14.000	17.000	10.000	13.000	4.000	309	342	434	276	275	85	0.356	CuCl
AT5G54100.1	Stomatin-like protein	10.000	14.000	17.000	11.000	14.000	8.000	309	342	434	318	417	202	0.434	H202
AT5G54100.1	Stomatin-like protein	9.000	10.000	13.000	6.000	12.000	11.000	275	313	375	252	337	351	0.652	Mena
AT5G55610.1	Unknown protein	0.625	0.625	4.000	2.000	2.000	4.000	0	78	0	54	132	81	0.144	H202
AT5G55610.1	Unknown protein	0.625	0.625	4.000	5.000	2.000	4.000	0	78	0	46	35	38	0.175	MeOH
AT5G55610.1	Unknown protein	0.625	0.625	4.000	1.000	2.000	1.000	0	78	0	53	62	36	0.908	CuCl
AT5G57490.1	VDAC4 Porin	4.000	4.000	5.000	6.000	4.000	7.000	166	216	174	109	216	58	0.162	Cold
AT5G57490.1	VDAC4 Porin	4.000	6.000	5.000	6.000	5.000	7.000	117	175	203	233	282	391	0.376	Mena
AT5G57490.1	VDAC4 Porin	4.000	4.000	5.000	4.000	6.000	5.000	166	216	174	117	175	203	0.474	MeOH
AT5G57490.1	VDAC4 Porin	4.000	6.000	5.000	6.000	2.000	4.000	117	175	203	119	38	192	0.536	Anti A
AT5G57490.1	VDAC4 Porin	4.000	4.000	5.000	7.000	5.000	3.000	166	216	174	238	192	134	0.720	H202
AT5G57490.1	VDAC4 Porin	4.000	4.000	5.000	6.000	5.000	2.000	166	216	174	230	129	77	0.836	CuCl
AT5G58270.1	ATM3 ABC-type transporter	0.625	0.625	3.000	3.000	5.000	2.000	0	0	58	85	111	91	0.266	Mena
AT5G58270.1	ATM3 ABC-type transporter	5.000	3.000	5.000	7.000	3.000	2.000	111	80	84	101	80	54	0.619	Cold
AT5G60730.1	Human TRC40 like tail anchored protein targeting factor	1.000	4.000	4.000	8.000	5.000	5.000	39	111	121	148	87	127	0.259	Anti A
AT5G60730.1	Human TRC40 like tail anchored protein targeting factor	4.000	2.000	5.000	7.000	5.000	3.000	117	57	142	96	124	39	0.484	H202
AT5G60730.1	Human TRC40 like tail anchored protein targeting factor	1.000	4.000	4.000	3.000	4.000	3.000	39	111	121	111	93	105	0.502	Mena
AT5G60730.1	Human TRC40 like tail anchored protein targeting factor	4.000	2.000	5.000	1.000	4.000	4.000	117	57	142	39	111	121	0.700	MeOH
AT5G60730.1	Human TRC40 like tail anchored protein targeting factor	4.000	2.000	5.000	3.000	2.000	6.000	117	57	142	43	57	38	0.925	Cold
AT5G61310.1	COX5c Cytochrome *c* oxidase subunit 5c	0.625	0.625	1.000	1.000	1.000	2.000	0	0	37	51	40	40	0.057	Mena
AT5G61310.1	COX5c Cytochrome *c* oxidase subunit 5c	0.625	0.625	1.000	0.625	0.625	0.625	0	0	37	0	0	0	0.332	Anti A
AT5G63510.1	γCAL1 γCarbonic anhydrase 1 like	0.625	4.000	4.000	7.000	5.000	5.000	0	78	106	154	141	111	0.280	Anti A
AT5G63510.1	γCAL1 γCarbonic anhydrase 1 like	0.625	4.000	0.625	0.625	0.625	0.625	0	98	0	0	0	0	0.423	Cold
AT5G63510.1	γCAL1 γCarbonic anhydrase 1 like	0.625	4.000	0.625	0.625	0.625	0.625	0	98	0	0	0	0	0.423	CuCl
AT5G66510.1	γCA3 γCarbonic anhydrase 3	1.000	2.000	3.000	0.625	0.625	0.625	67	133	162	224	100	188	0.050	Cold
AT5G66510.1	γCA3 γCarbonic anhydrase 3	1.000	2.000	3.000	4.000	2.000	3.000	67	133	162	135	169	108	0.349	MeOH
AT5G66510.1	γCA3 γCarbonic anhydrase 3	1.000	2.000	3.000	4.000	3.000	2.000	120	108	156	160	93	96	0.397	H202
AT5G66510.1	γCA3 γCarbonic anhydrase 3	4.000	2.000	3.000	3.000	7.000	4.000	120	108	156	146	142	158	0.477	Anti A
AT5G66510.1	γCA3 γCarbonic anhydrase 3	4.000	2.000	3.000	2.000	3.000	3.000	120	108	156	86	98	179	0.848	Mena
AT5G67500.1	VDAC2 porin	11.000	13.000	12.000	15.000	14.000	11.000	446	513	198	514	599	363	0.115	MeOH
AT5G67500.1	VDAC2 porin	11.000	13.000	12.000	13.000	12.000	4.000	446	513	198	271	462	151	0.424	H202
AT5G67500.1	VDAC2 porin	15.000	14.000	11.000	8.000	8.000	17.000	514	599	363	240	165	430	0.615	Anti A
AT5G67500.1	VDAC2 porin	15.000	14.000	11.000	10.000	9.000	15.000	514	599	363	467	354	504	0.637	Mena
AT5G67500.1	VDAC2 porin	11.000	13.000	12.000	11.000	13.000	14.000	446	513	198	218	513	160	0.643	Cold
AT5G67500.1	VDAC2 porin	11.000	13.000	12.000	11.000	14.000	10.000	446	513	198	542	522	144	0.782	CuCl
ATMG00060.1	ND5A NADH dehydrogenase Subunit 5A	0.625	2.000	0.625	0.625	0.625	0.625	0	40	0	0	0	0	0.426	Cold

AGI	ID	C1	C2	C3	T1	T2	T3	MOWSE C1	MOWSE C2	MOWSE C3	MOWSE T1	MOWSE T2	MOWSE T3	t-test	Treatment
ATMG00070.1	ND9 NADH dehydrogenase subunit 9	2.000	2.000	2.000	3.000	2.000	4.000	84	118	96	70	118	102	0.239	Cold
ATMG00160.1	COX2 Cytochrome *c* oxidase subunit 2	0.625	1.000	1.000	3.000	2.000	1.000	0	66	70	75	71	69	0.181	Anti A
ATMG00285.1	ND2A NADH dehydrogenase Subunit 2A	0.625	0.625	1.000	1.000	3.000	2.000	0	0	34	35	77	41	0.131	Mena
ATMG00285.1	ND2A NADH dehydrogenase Subunit 2A	0.625	0.625	1.000	0.625	0.625	0.625	0	0	34	0	0	0	0.332	Cold
ATMG00285.1	ND2A NADH dehydrogenase Subunit 2A	0.625	0.625	1.000	0.625	0.625	0.625	0	0	34	0	0	0	0.332	CuCl
AtMG00516.1	ND1A NADH dehydrogenase Subunit 1A	3.000	2.000	2.000	4.000	5.000	3.000	204		124	109	154	159	0.142	Anti A
AtMG00516.1	ND1A NADH dehydrogenase Subunit 1A	3.000	2.000	3.000	6.000	4.000	2.000	204	125	124	285	197	141	0.394	Mena
AtMG00516.1	ND1A NADH dehydrogenase Subunit 1A	5.000	2.000	3.000	3.000	2.000	3.000	252	142	130	204	125	124	0.583	MeOH
AtMG00516.1	ND1A NADH dehydrogenase Subunit 1A	5.000	2.000	3.000	4.000	5.000	2.000	252	142	130	161	157	107	0.824	H202
AtMG00516.1	ND1A NADH dehydrogenase Subunit 1A	5.000	2.000	3.000	3.000	4.000	3.000	252	142	130	66	123	61	0.871	CuCl
ATMG01190.1	ATP1 ATP synthase subunit 1	15.000	14.000	21.000	2.000	14.000	6.000	488	541	611	183	541	68	0.231	Cold
ATMG01190.1	ATP1 ATP synthase subunit 1	0.625	10.000	13.000	22.000	9.000	14.000	0	412	467	764	314	440	0.401	Mena