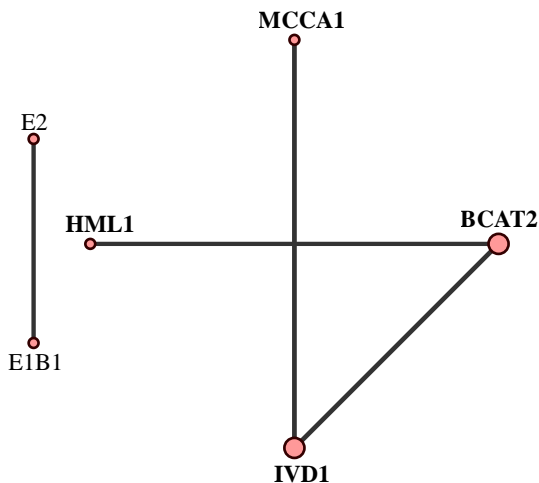
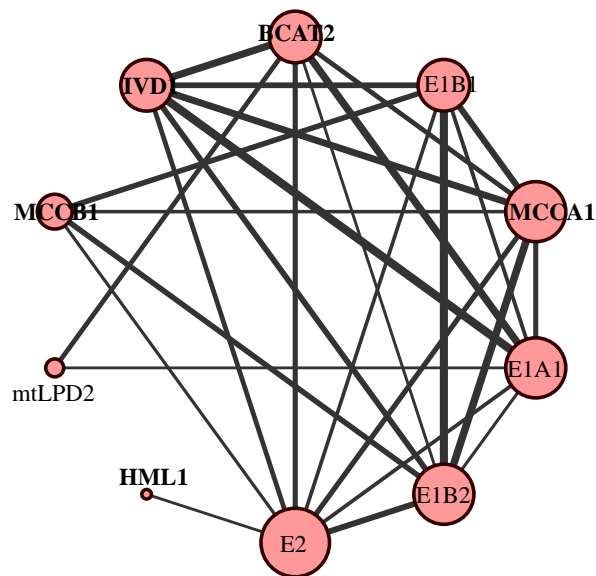


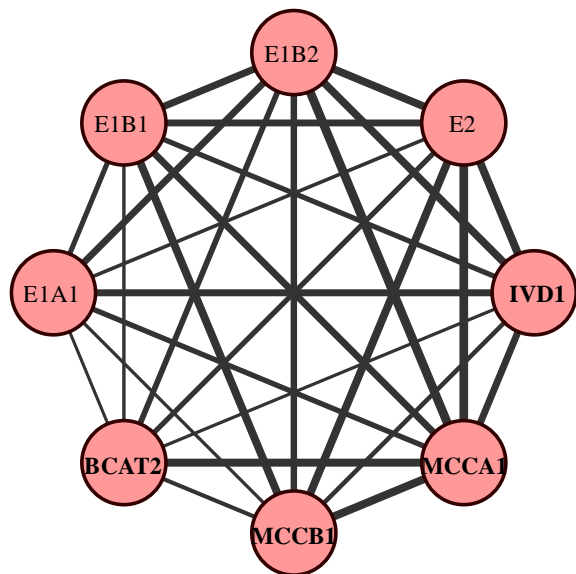
## Development



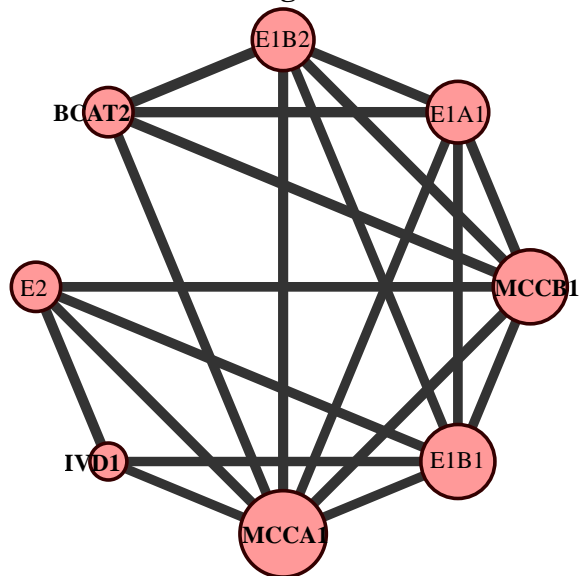
## Stress



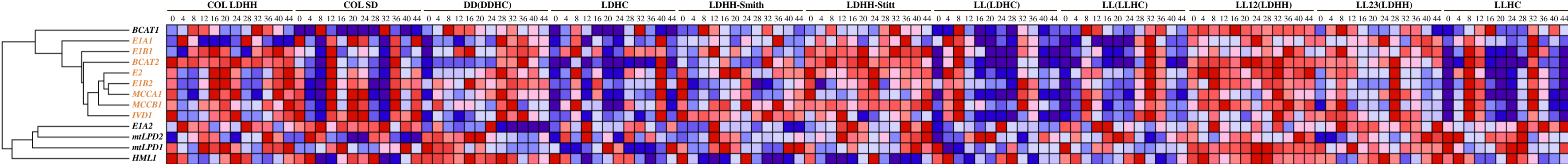
## Diurnal/circadian



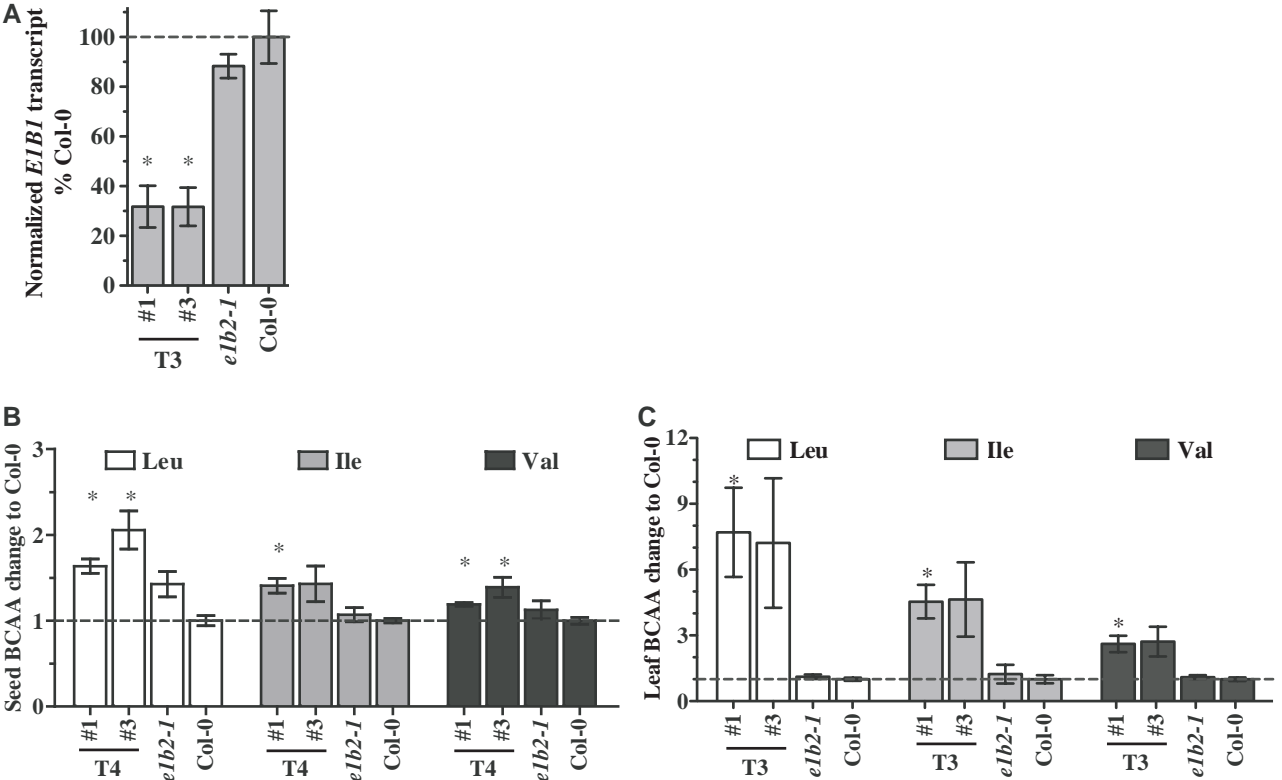
## Light



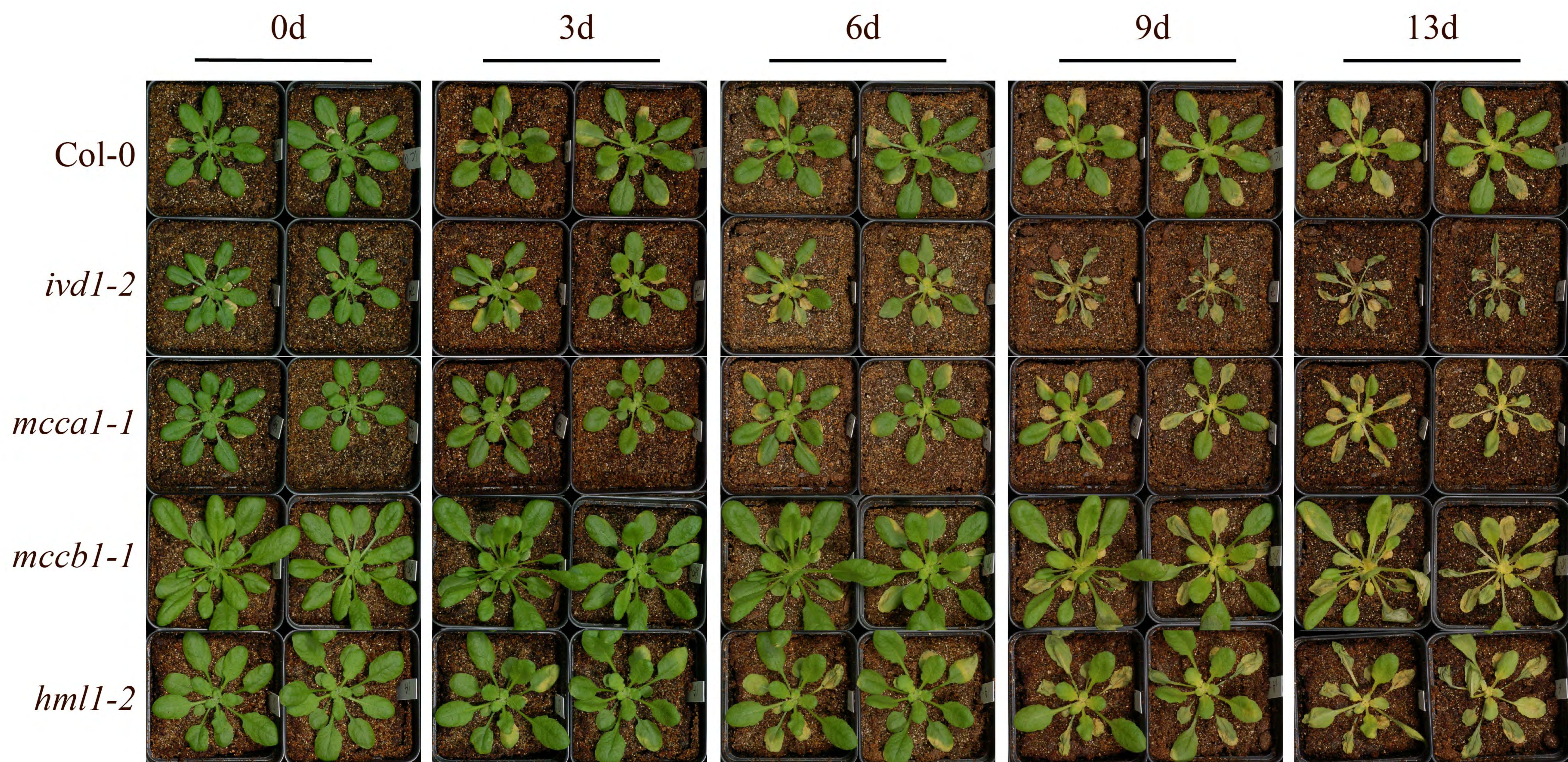
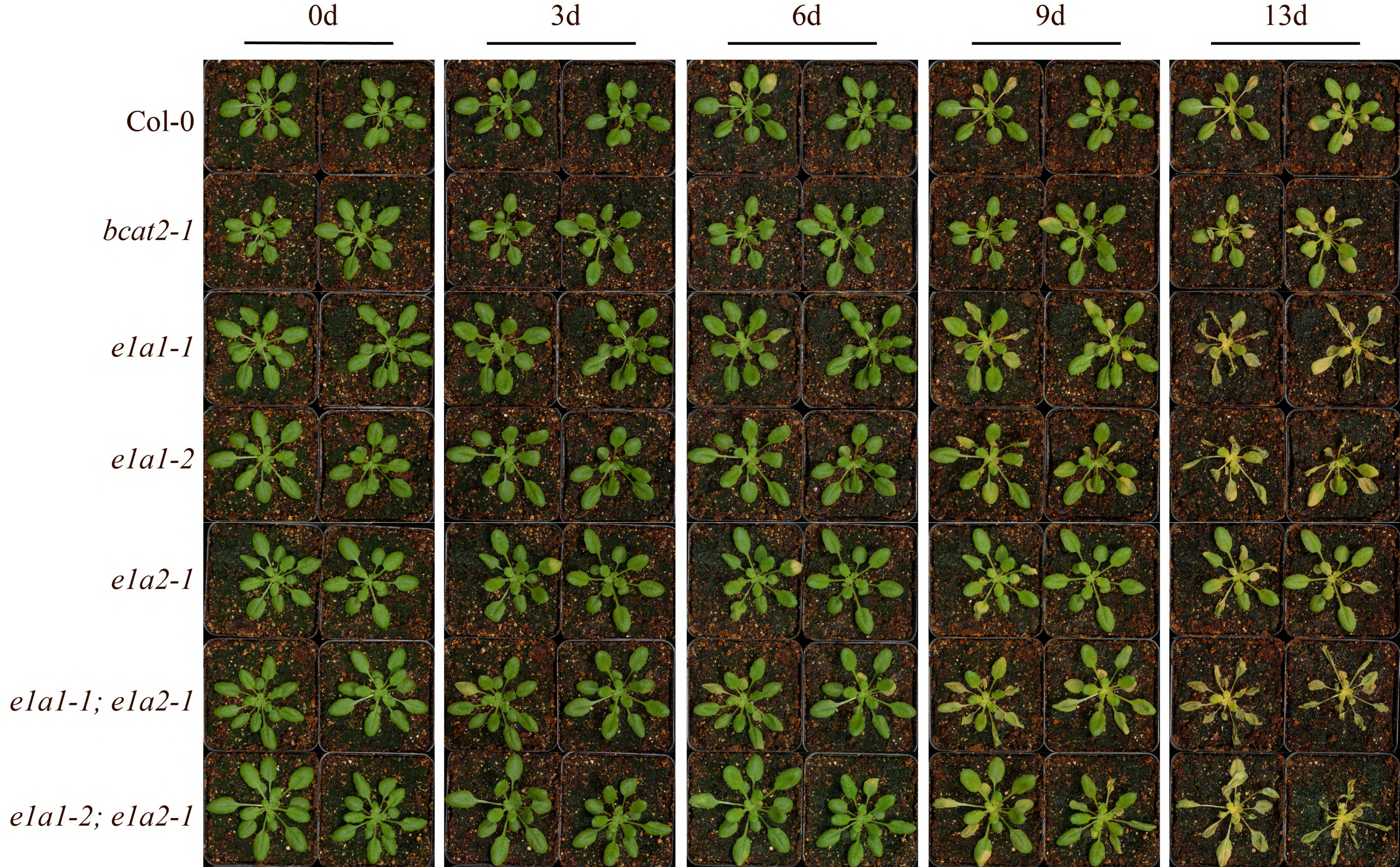
**Supplemental Figure S1.** Graphical representation of transcript correlation modules among the four datasets. Graphs were constructed using development (top left), stress (top right), diurnal/circadian (bottom left), and light (bottom right) datasets. Nodes represent transcripts and edges indicate pairwise PCC values exceeding the threshold in each database. Transcript names of validated genes are in bold, and proposed genes in regular font. The size of nodes corresponds to the connectivity of the transcript (smaller node indicates fewer significant correlations with other transcripts, and *vice versa*). The thickness of edges correlates with their PCC values. See Supplemental Table S1 for PCC values and the corresponding threshold in each dataset. The network graphs were created using Cytoscape.



**Supplemental Figure S2.** Transcript profiles for known and proposed BCAA catabolism genes under diurnal/circadian conditions. Microarray data were obtained from the Diurnal database (Mockler et al., 2007), and normalized to the maximum expression levels of each gene in every treatment. Pearson's Correlation Coefficient and average linkage were used for gene clustering. Gene names in orange text represent members of the highly coexpressed module identified from the diurnal/circadian dataset. Refer to the Diurnal database website (<http://diurnal.mocklerlab.org/>) for detailed information on each condition. COL, Col-0; LDHH, 12h light/12h dark and 24h hot; SD, 8h light/16h dark; DD(DDHC), entrained on 24h dark and 12h hot/12h cold, and subjected to 24h dark and 24h hot; LDHC, 12h light/12h dark and 12h hot/12h cold; LDHH-Smith, 12h light/12h dark and 24h hot (Smith et al., 2004); LDHH-Stitt, 12h light/12h dark and 24h hot (Bläsing et al., 2005); LL(LDHC), entrained on LDHC and subjected to 24h light and 24h hot; LL(LLHC), entrained on 24h light and 12h hot/12h cold, and subjected to 24h light and 24h hot; LL12(LDHH), entrained on LDHH and subjected to 24h light and 24h hot; LL23(LDHH), entrained on LDHH and subjected to 24h light and 24h hot; LLHC, 24h light and 12h hot/12h cold.



**Supplemental Figure S4.** Transcript and mutant analyses of *EIB1*-silenced *e1b2-1* lines. (A) Relative *EIB1* transcript abundance in two homozygous *EIB1*-silenced *e1b2-1* T3 lines (progeny seed pools of independent primary transformants #1 and #3) by qPCR. The y axis values represent the normalized *EIB1* transcript levels relative to Col-0 (shown as the horizontal dashed line, n=5, mean  $\pm$  SE). The *EIB1* transcript levels were normalized to *ACT2* transcript levels. An asterisk indicates a significant difference from the wild type, determined by the Student's *t*-test ( $p < 0.05$ ). Leaf tissues were harvested by the end of night on a 16h light/8h dark photoperiod. (B) Relative levels of seed free BCAAs in homozygous *EIB1*-silenced *e1b2-1* T4 seeds (progeny seed pools of #1 and #3). The y axis values represent the amino acid levels relative to Col-0 (shown as the dashed line, n=4, mean  $\pm$  SE). An asterisk indicates a significant difference from the wild type, determined by the Student's *t*-test ( $p < 0.05$ ). (C) Relative levels of leaf free BCAAs in homozygous *EIB1*-silenced *e1b2-1* T3 lines (progeny seed pools of #1 and #3) after 6 days in prolonged darkness. The y axis values represent the amino acid levels relative to Col-0 (shown as the dashed line, n=5, mean  $\pm$  SE). An asterisk indicates a significant difference from the wild type, determined by the Student's *t*-test ( $p < 0.05$ ).



**Supplemental Figure S5.** Phenotypes of BCAA mutants subjected to prolonged darkness. Photographs of 5-week-old, short-day-grown *Arabidopsis* plants taken prior to (0d) and after 3, 6, 9 and 13 days of prolonged darkness. The leaves of *elal-1*, *elal-2*, both *elal; ela2* double mutants, *ivd1-2*, *mcca1-1*, *mccb1-1*, and *hml1-2* were visibly yellowed and dehydrated following 13 days of prolonged darkness compared to the wild type. The *ivd1-2* mutant started showing visible senescence symptoms at day 6. The experiments were done at least three times with similar results, and representative results are shown. Plants in the upper and lower panels were grown and assayed in individual experiments. Two replicates were shown for each mutant at every time point.

**Supplemental Table S1. Pairwise Pearson's Correlation Coefficients (PCCs) for transcripts of BCAA catabolism genes**

PCCs above the 95<sup>th</sup> percentile threshold for each dataset are highlighted in red, and the values are indicated below.

Genes that have PCCs above threshold with one or more other genes are highlighted in yellow.

**Development**

95th percentile of random PCC distribution = 0.60

	BCAT1	BCAT2	E1A1	E1A2	E1B1	E1B2	E2	mtLPD1	mtLPD2	IVD1	MCCA1	MCCB1	HML1
BCAT1	1.000	0.031	0.586	0.576	0.454	0.379	0.433	-0.049	-0.426	-0.124	-0.123	-0.034	-0.006
BCAT2	0.031	1.000	0.550	-0.173	0.356	0.177	0.138	-0.280	0.220	0.704	0.580	0.044	0.666
E1A1	0.586	0.550	1.000	0.196	0.436	0.315	0.359	-0.216	-0.216	0.387	0.241	0.113	0.251
E1A2	0.576	-0.173	0.196	1.000	0.370	-0.049	0.408	-0.516	-0.335	-0.241	-0.325	-0.133	-0.289
E1B1	0.454	0.356	0.436	0.370	1.000	0.410	0.673	-0.544	0.008	0.443	0.411	0.140	0.163
E1B2	0.379	0.177	0.315	-0.049	0.410	1.000	0.600	0.191	-0.261	0.440	0.511	0.510	0.307
E2	0.433	0.138	0.359	0.408	0.673	0.600	1.000	-0.420	-0.058	0.407	0.458	0.330	-0.029
mtLPD1	-0.049	-0.280	-0.216	-0.516	-0.544	0.191	-0.420	1.000	-0.105	-0.282	-0.075	0.206	0.018
mtLPD2	-0.426	0.220	-0.216	-0.335	0.008	-0.261	-0.058	-0.105	1.000	0.301	0.201	-0.257	0.084
IVD1	-0.124	0.704	0.387	-0.241	0.443	0.440	0.407	-0.282	0.301	1.000	0.706	0.251	0.599
MCCA1	-0.123	0.580	0.241	-0.325	0.411	0.511	0.458	-0.075	0.201	0.706	1.000	0.548	0.322
MCCB1	-0.034	0.044	0.113	-0.133	0.140	0.510	0.330	0.206	-0.257	0.251	0.548	1.000	-0.041
HML1	-0.006	0.666	0.251	-0.289	0.163	0.307	-0.029	0.018	0.084	0.599	0.322	-0.041	1.000

**Stress**

95th percentile of random PCC distribution = 0.47

	BCAT1	BCAT2	E1A1	E1A2	E1B1	E1B2	E2	mtLPD1	mtLPD2	IVD1	MCCA1	MCCB1	HML1
BCAT1	1.000	-0.133	0.005	-0.027	0.120	0.134	-0.417	0.102	-0.284	0.011	0.094	0.081	-0.385
BCAT2	-0.133	1.000	0.777	-0.064	0.425	0.487	0.631	-0.538	0.607	0.767	0.608	0.125	0.275
E1A1	0.005	0.777	1.000	-0.149	0.545	0.497	0.543	-0.462	0.477	0.839	0.622	0.282	0.464
E1A2	-0.027	-0.064	-0.149	1.000	0.173	0.110	0.200	0.293	-0.032	-0.142	-0.113	0.236	-0.270
E1B1	0.120	0.425	0.545	0.173	1.000	0.825	0.535	-0.298	0.009	0.668	0.701	0.653	0.288
E1B2	0.134	0.487	0.497	0.110	0.825	1.000	0.685	-0.287	0.022	0.669	0.787	0.656	0.239
E2	-0.417	0.631	0.543	0.200	0.535	0.685	1.000	-0.250	0.357	0.605	0.634	0.504	0.480
mtLPD1	0.102	-0.538	-0.462	0.293	-0.298	-0.287	-0.250	1.000	-0.478	-0.432	-0.340	0.300	-0.249
mtLPD2	-0.284	0.607	0.477	-0.032	0.009	0.022	0.357	-0.478	1.000	0.393	0.113	-0.330	0.202
IVD1	0.011	0.767	0.839	-0.142	0.668	0.669	0.605	-0.432	0.393	1.000	0.742	0.449	0.380
MCCA1	0.094	0.608	0.622	-0.113	0.701	0.787	0.634	-0.340	0.113	0.742	1.000	0.524	0.328
MCCB1	0.081	0.125	0.282	0.236	0.653	0.656	0.504	0.300	-0.330	0.449	0.524	1.000	0.125
HML1	-0.385	0.275	0.464	-0.270	0.288	0.239	0.480	-0.249	0.202	0.380	0.328	0.125	1.000

**Diurnal/circadian**

95th percentile of random PCC distribution = 0.45

	BCAT1	BCAT2	E1A1	E1A2	E1B1	E1B2	E2	mtLPD1	mtLPD2	IVD1	MCCA1	MCCB1	HML1
BCAT1	1.000	0.195	-0.017	-0.109	0.287	0.155	0.186	0.059	-0.392	-0.002	0.227	0.298	-0.278
BCAT2	0.195	1.000	0.497	-0.222	0.515	0.670	0.633	-0.152	-0.334	0.506	0.816	0.565	-0.092
E1A1	-0.017	0.497	1.000	-0.363	0.629	0.740	0.533	-0.286	-0.409	0.750	0.644	0.511	-0.068
E1A2	-0.109	-0.222	-0.363	1.000	-0.240	-0.284	0.031	-0.070	0.379	-0.115	-0.190	-0.090	-0.155
E1B1	0.287	0.515	0.629	-0.240	1.000	0.756	0.745	-0.173	-0.487	0.635	0.746	0.811	-0.005
E1B2	0.155	0.670	0.740	-0.284	0.756	1.000	0.797	-0.354	-0.399	0.794	0.874	0.717	-0.039
E2	0.186	0.633	0.533	0.031	0.745	0.797	1.000	-0.435	-0.320	0.816	0.862	0.810	-0.046
mtLPD1	0.059	-0.152	-0.286	-0.070	-0.173	-0.354	-0.435	1.000	-0.107	-0.627	-0.320	-0.110	0.204
mtLPD2	-0.392	-0.334	-0.409	0.379	-0.487	-0.399	-0.320	-0.107	1.000	-0.239	-0.385	-0.482	-0.050
IVD1	-0.002	0.506	0.750	-0.115	0.635	0.794	0.816	-0.627	-0.239	1.000	0.748	0.591	-0.161
MCCA1	0.227	0.816	0.644	-0.190	0.746	0.874	0.862	-0.320	-0.385	0.748	1.000	0.820	-0.006
MCCB1	0.298	0.565	0.511	-0.090	0.811	0.717	0.810	-0.110	-0.482	0.591	0.820	1.000	0.071
HML1	-0.278	-0.092	-0.068	-0.155	-0.005	-0.039	-0.046	0.204	-0.050	-0.161	-0.006	0.071	1.000

**Light**

95th percentile of random PCC distribution = 0.90

	BCAT1	BCAT2	E1A1	E1A2	E1B1	E1B2	E2	mtLPD1	mtLPD2	IVD1	MCCA1	MCCB1	HML1
BCAT1	1.000	0.622	0.589	-0.146	0.612	0.618	0.510	-0.388	-0.398	0.520	0.589	0.555	-0.210
BCAT2	0.622	1.000	0.972	0.101	0.894	0.983	0.843	-0.762	-0.328	0.785	0.931	0.958	-0.752
E1A1	0.589	0.972	1.000	0.134	0.927	0.952	0.855	-0.667	-0.349	0.816	0.908	0.958	-0.722
E1A2	-0.146	0.101	0.134	1.000	-0.021	0.072	-0.172	0.292	0.621	-0.314	-0.144	0.017	-0.462
E1B1	0.612	0.894	0.927	-0.021	1.000	0.908	0.935	-0.630	-0.544	0.912	0.906	0.923	-0.567
E1B2	0.618	0.983	0.952	0.072	0.908	1.000	0.885	-0.780	-0.397	0.818	0.958	0.969	-0.738
E2	0.510	0.843	0.855	-0.172	0.935	0.885	1.000	-0.710	-0.680	0.964	0.941	0.927	-0.587
mtLPD1	-0.388	-0.762	-0.667	0.292	-0.630	-0.780	-0.710	1.000	0.328	-0.664	-0.796	-0.738	0.472
mtLPD2	-0.398	-0.328	-0.349	0.621	-0.544	-0.397	-0.680	0.328	1.000	-0.776	-0.586	-0.517	0.068
IVD1	0.520	0.785	0.816	-0.314	0.912	0.818	0.964	-0.664	-0.776	1.000	0.907	0.886	-0.452
MCCA1	0.589	0.931	0.908	-0.144	0.906	0.958	0.941	-0.796	-0.586	0.907	1.000	0.973	-0.645
MCCB1	0.555	0.958	0.958	0.017	0.923	0.969	0.927	-0.738	-0.517	0.886	0.973	1.000	-0.722
HML1	-0.210	-0.752	-0.722	-0.462	-0.567	-0.738	-0.587	0.472	0.068	-0.452	-0.645	-0.722	1.000

**Supplemental Table S2. Mutant seed free amino acid profiles**

Amino acid	<i>bcat1-1</i>			<i>bcat2-1</i>			<i>elal-1</i>	
	Mean	SE	<i>t</i> -test	Mean	SE	<i>t</i> -test	Mean	SE
Ala	0.797	0.053	0.235	0.976	0.171	0.922	0.730	0.111
Arg	1.191	0.077	0.373	1.014	0.160	0.948	1.358	0.180
Asn	0.970	0.072	0.905	0.722	0.095	0.294	0.860	0.051
Asp	1.783	0.320	0.347	0.943	0.090	0.756	0.898	0.109
Gln	1.154	0.043	0.470	0.889	0.140	0.784	0.887	0.205
Glu	1.170	0.068	0.504	0.874	0.105	0.507	1.036	0.298
Gly	1.559	0.120	0.128	0.749	0.200	0.499	0.798	0.074
His	1.084	0.021	0.482	1.562	0.183	0.052	2.276	0.444
Ile	1.088	0.051	0.575	2.790	0.411	0.017	5.411	0.307
Leu	1.086	0.025	0.345	3.832	0.633	0.015	1.486	0.029
Lys	0.994	0.032	0.952	1.528	0.338	0.237	1.064	0.076
Met	1.030	0.044	0.869	1.582	0.512	0.373	1.089	0.091
Phe	1.072	0.046	0.634	1.461	0.275	0.192	1.040	0.034
Pro	1.060	0.211	0.948	1.796	0.575	0.284	1.099	0.069
Ser	1.012	0.063	0.950	1.342	0.239	0.249	0.973	0.160
Thr	0.605	0.081	0.296	1.244	0.243	0.582	1.131	0.107
Trp	1.235	0.065	0.204	1.267	0.168	0.387	0.947	0.056
Tyr	1.040	0.052	0.777	1.305	0.366	0.546	1.098	0.060
Val	1.045	0.057	0.821	2.389	0.315	0.016	1.319	0.075

The mean represents the fold change between the averages of five biological replicates of mutant and wild type. The '*t*-test' indicates the value at which the mean measurement deviates from expectation (for exam

<i>t</i> -test	<i>ela1-2</i>			<i>ela2-1</i>			<i>ela1-1;ela2-1</i>		
	Mean	SE	<i>t</i> -test	Mean	SE	<i>t</i> -test	Mean	SE	<i>t</i> -test
0.304	0.816	0.127	0.478	0.794	0.231	0.528	0.604	0.077	0.146
0.177	1.156	0.069	0.126	0.925	0.064	0.401	2.183	0.204	0.000
0.494	0.813	0.052	0.374	0.965	0.094	0.870	0.621	0.035	0.119
0.455	0.802	0.086	0.100	1.136	0.160	0.464	0.595	0.040	0.000
0.644	0.711	0.051	0.018	1.026	0.092	0.832	0.442	0.049	0.002
0.915	0.689	0.092	0.035	1.339	0.214	0.212	0.433	0.052	0.000
0.272	0.514	0.068	0.034	0.925	0.123	0.704	0.625	0.057	0.072
0.098	2.441	0.188	0.002	0.968	0.095	0.805	6.780	0.652	0.000
0.003	5.832	0.223	0.000	0.972	0.040	0.787	25.395	1.064	0.000
0.050	1.251	0.059	0.210	0.836	0.043	0.376	56.961	3.316	0.000
0.641	0.873	0.075	0.363	0.872	0.087	0.384	1.405	0.135	0.019
0.561	0.984	0.098	0.919	0.984	0.063	0.903	2.181	0.136	0.000
0.570	0.978	0.032	0.749	1.001	0.056	0.991	1.714	0.081	0.000
0.399	1.043	0.075	0.714	0.996	0.097	0.976	1.214	0.062	0.073
0.890	0.772	0.039	0.074	1.077	0.071	0.518	2.165	0.166	0.000
0.344	0.848	0.036	0.020	1.081	0.125	0.563	0.642	0.089	0.001
0.527	1.164	0.105	0.232	0.869	0.044	0.113	1.077	0.087	0.411
0.453	1.083	0.123	0.626	0.902	0.070	0.467	1.259	0.077	0.082
0.027	1.315	0.081	0.023	1.004	0.055	0.964	8.355	0.399	0.000

nts and Col-0 grown at the same time.

ple '0.01' means significant at <0.01).

<i>el1-2;ela2-1</i>			<i>elb2-1</i>			<i>ivd1-2</i>			
Mean	SE	<i>t</i> -test	Mean	SE	<i>t</i> -test	Mean	SE	<i>t</i> -test	Mean
0.618	0.060	0.156	1.284	0.071	0.023	3.178	0.145	0.002	0.781
2.394	0.164	0.000	1.843	0.226	0.030	10.673	0.325	0.000	1.085
0.578	0.029	0.094	1.421	0.121	0.035	1.392	0.046	0.015	0.541
0.638	0.027	0.000	1.212	0.079	0.137	0.681	0.051	0.056	0.817
0.491	0.042	0.001	1.236	0.115	0.156	2.604	0.103	0.001	0.684
0.484	0.059	0.000	1.297	0.107	0.100	0.627	0.034	0.011	0.424
0.835	0.100	0.380	0.962	0.081	0.894	4.004	0.119	0.000	0.579
6.935	0.495	0.000	1.641	0.117	0.016	13.354	0.690	0.001	2.234
27.915	1.419	0.000	1.675	0.096	0.001	15.962	0.319	0.000	4.325
59.784	2.448	0.000	1.591	0.110	0.005	19.107	0.375	0.000	5.811
1.597	0.160	0.011	1.419	0.127	0.041	4.869	0.140	0.000	0.852
2.268	0.120	0.000	1.704	0.146	0.009	5.218	0.205	0.001	1.076
1.803	0.069	0.000	1.421	0.135	0.049	3.123	0.106	0.000	0.969
1.346	0.099	0.024	1.232	0.113	0.180	2.515	0.223	0.125	0.852
2.337	0.183	0.000	1.443	0.100	0.022	5.049	0.217	0.001	1.514
0.759	0.073	0.013	1.037	0.193	0.888	1.648	0.077	0.039	0.785
1.138	0.071	0.155	1.536	0.081	0.002	7.164	0.267	0.000	0.939
1.447	0.093	0.013	1.520	0.133	0.022	3.946	0.144	0.000	0.857
8.928	0.407	0.000	1.596	0.115	0.007	11.116	0.332	0.000	2.323



<i>mcca1-1</i>		<i>mccb1-1</i>			<i>hml1-2</i>		
SE	<i>t</i> -test	Mean	SE	<i>t</i> -test	Mean	SE	<i>t</i> -test
0.053	0.072	0.915	0.101	0.526	1.433	0.178	0.088
0.072	0.321	1.209	0.177	0.324	2.998	0.382	0.014
0.033	0.021	0.612	0.086	0.025	1.244	0.123	0.165
0.085	0.269	0.720	0.073	0.116	1.057	0.136	0.762
0.033	0.110	0.747	0.086	0.164	1.348	0.042	0.087
0.018	0.007	0.485	0.067	0.002	1.475	0.102	0.012
0.133	0.432	0.892	0.035	0.824	1.668	0.298	0.272
0.325	0.031	2.056	0.152	0.004	3.305	0.204	0.001
0.657	0.015	4.522	0.454	0.004	5.818	0.427	0.001
0.777	0.008	6.405	0.798	0.006	6.591	0.410	0.001
0.053	0.061	0.912	0.156	0.613	1.258	0.064	0.022
0.109	0.553	1.127	0.147	0.458	1.765	0.227	0.041
0.053	0.781	1.139	0.133	0.426	1.268	0.109	0.115
0.216	0.600	0.886	0.117	0.581	2.038	0.475	0.114
0.139	0.027	1.416	0.142	0.054	2.257	0.216	0.008
0.113	0.225	0.834	0.053	0.256	1.207	0.224	0.449
0.116	0.649	1.054	0.083	0.583	2.378	0.245	0.010
0.084	0.219	0.940	0.046	0.456	1.423	0.173	0.088
0.230	0.009	2.726	0.222	0.003	3.645	0.305	0.003

**Supplemental Table S3. Mutant leaf free amino acid profiles in prolonged darkness**The mean represents the average of five biological replicates ( $\mu\text{mol/mg}$ ).Significance by Student's *t*-test:*p*<0.05*p*<0.01*p*<0.001**0d in dark**

Amino acid	Col-0		<i>bcat2-1</i>			<i>e1a1-1</i>			Mean
	Mean	SE	Mean	SE	<i>t</i> -test	Mean	SE	<i>t</i> -test	
Ala	1.370	0.086	1.557	0.202	0.412	1.312	0.071	0.607	1.392
Arg	0.032	0.006	0.051	0.010	0.123	0.041	0.008	0.369	0.030
Asn	0.123	0.010	0.115	0.015	0.641	0.114	0.008	0.475	0.122
Asp	1.551	0.194	1.411	0.163	0.587	1.284	0.122	0.260	1.472
Gln	0.877	0.053	0.966	0.115	0.496	0.904	0.072	0.773	0.989
Glu	6.200	0.309	5.765	0.362	0.373	5.374	0.346	0.092	5.958
Gly	0.271	0.034	0.241	0.046	0.608	0.231	0.044	0.478	0.225
His	0.078	0.003	0.116	0.012	<b>0.010</b>	0.093	0.004	<b>0.013</b>	0.089
Ile	0.042	0.004	0.059	0.009	0.108	0.031	0.003	0.060	0.036
Leu	0.070	0.007	0.138	0.027	<b>0.036</b>	0.073	0.006	0.779	0.068
Lys	0.106	0.007	0.123	0.009	0.153	0.108	0.008	0.873	0.111
Met	0.023	0.002	0.023	0.002	0.991	0.024	0.003	0.767	0.027
Phe	0.122	0.004	0.144	0.010	0.061	0.120	0.004	0.765	0.124
Pro	0.168	0.014	0.177	0.013	0.643	0.167	0.008	0.935	0.171
Ser	0.413	0.020	0.535	0.062	0.086	0.332	0.031	<b>0.044</b>	0.374
Thr	0.367	0.036	0.422	0.058	0.431	0.275	0.021	<b>0.043</b>	0.354
Trp	0.021	0.001	0.031	0.003	<b>0.008</b>	0.022	0.002	0.526	0.020
Tyr	0.030	0.002	0.045	0.007	0.056	0.027	0.002	0.392	0.025
Val	0.155	0.007	0.232	0.032	<b>0.042</b>	0.167	0.007	0.277	0.166

**3d in dark**

Amino acid	Col-0		<i>bcat2-1</i>			<i>e1a1-1</i>			Mean
	Mean	SE	Mean	SE	<i>t</i> -test	Mean	SE	<i>t</i> -test	
Ala	2.477	0.130	2.216	0.195	0.283	1.738	0.079	<b>0.000</b>	2.008
Arg	2.361	0.137	2.508	0.145	0.472	2.356	0.218	0.983	2.291
Asn	1.366	0.064	1.453	0.109	0.496	1.429	0.096	0.593	1.675
Asp	0.588	0.068	0.998	0.100	<b>0.004</b>	0.985	0.073	<b>0.001</b>	1.083
Gln	0.780	0.036	0.779	0.075	0.987	0.722	0.061	0.427	0.857
Glu	6.654	0.432	5.955	0.458	0.282	5.431	0.134	<b>0.021</b>	6.128
Gly	0.297	0.043	0.267	0.041	0.622	0.226	0.016	0.150	0.252
His	1.423	0.073	1.460	0.114	0.793	1.323	0.068	0.328	1.370
Ile	1.444	0.163	2.065	0.272	0.069	2.261	0.315	<b>0.038</b>	2.062
Leu	1.345	0.058	4.589	0.323	<b>0.000</b>	5.377	0.206	<b>0.000</b>	5.184
Lys	1.347	0.084	1.413	0.157	0.714	1.308	0.089	0.753	1.401
Met	0.072	0.005	0.085	0.008	0.167	0.087	0.005	<b>0.047</b>	0.085
Phe	2.685	0.121	2.773	0.219	0.728	2.664	0.101	0.896	2.662
Pro	0.163	0.017	0.230	0.021	<b>0.022</b>	0.170	0.016	0.749	0.187

Ser	0.914	0.070	1.155	0.174	0.222	1.022	0.082	0.330	1.035
Thr	0.823	0.101	0.988	0.144	0.361	0.831	0.039	0.938	0.864
Trp	0.836	0.031	0.813	0.024	0.580	0.837	0.041	0.976	0.804
Tyr	0.996	0.059	0.980	0.069	0.858	0.972	0.056	0.772	0.969
Val	3.172	0.165	3.662	0.289	0.162	3.818	0.165	<b>0.013</b>	3.836

### 6d in dark

Amino acid	Col-0		<i>bcat2-1</i>			<i>ela1-1</i>			Mean
	Mean	SE	Mean	SE	<i>t</i> -test	Mean	SE	<i>t</i> -test	
Ala	2.538	0.244	1.458	0.127	<b>0.002</b>	1.017	0.106	<b>0.000</b>	1.342
Arg	3.696	0.342	3.888	0.169	0.624	3.863	0.402	0.756	4.299
Asn	2.684	0.201	2.639	0.189	0.872	2.920	0.330	0.551	3.496
Asp	0.971	0.084	1.362	0.084	<b>0.004</b>	1.580	0.160	<b>0.005</b>	1.614
Gln	1.056	0.107	0.877	0.078	0.194	0.896	0.101	0.291	1.121
Glu	7.951	0.630	6.966	0.452	0.222	6.192	0.552	0.050	6.683
Gly	0.354	0.049	0.174	0.027	<b>0.006</b>	0.222	0.042	0.055	0.200
His	2.143	0.134	2.076	0.133	0.727	2.035	0.207	0.668	2.225
Ile	1.571	0.162	2.699	0.279	<b>0.003</b>	3.291	0.355	<b>0.001</b>	1.675
Leu	1.258	0.127	6.244	0.299	<b>0.000</b>	8.002	0.774	<b>0.000</b>	8.223
Lys	2.019	0.186	1.600	0.105	0.069	1.395	0.186	<b>0.029</b>	1.572
Met	0.119	0.009	0.141	0.012	0.153	0.158	0.017	0.055	0.183
Phe	4.114	0.244	3.947	0.215	0.613	4.031	0.338	0.845	4.365
Pro	0.093	0.011	0.100	0.009	0.651	0.086	0.009	0.635	0.104
Ser	1.753	0.213	1.480	0.149	0.311	1.457	0.265	0.397	1.344
Thr	0.774	0.142	0.816	0.111	0.818	0.748	0.121	0.892	0.613
Trp	1.334	0.088	1.162	0.072	0.150	1.288	0.079	0.700	1.443
Tyr	1.213	0.131	1.142	0.105	0.679	1.077	0.179	0.549	1.275
Val	3.860	0.285	4.731	0.263	<b>0.037</b>	5.475	0.459	<b>0.009</b>	6.242

### 9d in dark

Amino acid	Col-0		<i>bcat2-1</i>			<i>ela1-1</i>			Mean
	Mean	SE	Mean	SE	<i>t</i> -test	Mean	SE	<i>t</i> -test	
Ala	3.171	0.238	1.661	0.186	<b>0.000</b>	0.861	0.076	<b>0.000</b>	0.757
Arg	4.141	0.422	4.035	0.382	0.854	4.011	0.197	0.784	3.615
Asn	4.179	0.341	4.220	0.443	0.943	3.999	0.268	0.683	5.433
Asp	0.832	0.039	1.256	0.106	<b>0.003</b>	1.380	0.072	<b>0.000</b>	1.532
Gln	1.526	0.101	1.462	0.165	0.746	1.167	0.063	<b>0.009</b>	1.554
Glu	9.048	0.398	9.372	0.810	0.725	7.713	0.557	0.069	8.139
Gly	0.356	0.046	0.467	0.089	0.291	0.417	0.053	0.399	0.456
His	2.377	0.097	2.601	0.199	0.330	2.348	0.094	0.827	2.892
Ile	1.056	0.069	2.555	0.330	<b>0.001</b>	3.215	0.478	<b>0.001</b>	3.576
Leu	0.838	0.065	6.663	0.416	<b>0.000</b>	9.405	0.178	<b>0.000</b>	11.447
Lys	1.943	0.150	1.611	0.149	0.134	1.130	0.105	<b>0.000</b>	1.007
Met	0.146	0.012	0.178	0.021	0.210	0.225	0.015	<b>0.001</b>	0.381
Phe	4.289	0.216	4.367	0.264	0.823	4.427	0.121	0.588	5.454
Pro	0.092	0.009	0.114	0.010	0.137	0.109	0.007	0.163	0.113
Ser	1.979	0.140	1.823	0.242	0.586	1.215	0.064	<b>0.000</b>	1.912
Thr	0.568	0.041	0.656	0.084	0.363	0.540	0.049	0.662	1.084

Trp	1.543	0.072	1.618	0.098	0.543	1.640	0.092	0.416	2.406
Tyr	1.456	0.147	1.340	0.229	0.676	1.065	0.156	0.084	1.444
Val	3.482	0.142	5.158	0.287	<b>0.000</b>	6.082	0.148	<b>0.000</b>	7.260

---

<i>ela1-2</i>		<i>ela2-1</i>			<i>ela1-1;ela2-1</i>			<i>ela1-2;ela2</i>	
SE	<i>t</i> -test	Mean	SE	<i>t</i> -test	Mean	SE	<i>t</i> -test	Mean	SE
0.100	0.868	1.299	0.107	0.610	1.331	0.134	0.809	1.566	0.072
0.006	0.790	0.036	0.006	0.618	0.037	0.007	0.570	0.057	0.008
0.009	0.909	0.123	0.010	0.966	0.135	0.016	0.555	0.118	0.009
0.153	0.753	1.455	0.159	0.706	1.672	0.201	0.671	1.665	0.194
0.076	0.244	0.889	0.078	0.901	0.996	0.069	0.191	1.004	0.050
0.361	0.617	5.799	0.334	0.390	6.500	0.294	0.491	6.393	0.272
0.024	0.286	0.201	0.038	0.182	0.206	0.036	0.205	0.196	0.024
0.006	0.126	0.094	0.004	<b>0.012</b>	0.094	0.007	0.060	0.108	0.008
0.004	0.271	0.048	0.004	0.319	0.048	0.007	0.475	0.044	0.007
0.003	0.785	0.088	0.009	0.125	0.085	0.008	0.175	0.115	0.015
0.010	0.707	0.113	0.009	0.567	0.114	0.009	0.532	0.127	0.012
0.002	0.137	0.021	0.001	0.363	0.025	0.003	0.527	0.027	0.002
0.004	0.699	0.132	0.004	0.103	0.127	0.007	0.507	0.128	0.006
0.013	0.856	0.165	0.011	0.872	0.178	0.014	0.593	0.192	0.015
0.031	0.305	0.501	0.056	0.162	0.520	0.088	0.263	0.584	0.059
0.035	0.804	0.377	0.027	0.826	0.457	0.083	0.335	0.499	0.075
0.001	0.393	0.025	0.002	0.083	0.024	0.001	0.104	0.027	0.002
0.002	0.124	0.029	0.002	0.820	0.031	0.003	0.722	0.035	0.003
0.006	0.280	0.175	0.012	0.188	0.174	0.012	0.213	0.212	0.019

<i>ela1-2</i>		<i>ela2-1</i>			<i>ela1-1;ela2-1</i>			<i>ela1-2;ela2</i>	
SE	<i>t</i> -test	Mean	SE	<i>t</i> -test	Mean	SE	<i>t</i> -test	Mean	SE
0.150	<b>0.030</b>	3.625	0.402	<b>0.022</b>	2.668	0.207	0.448	2.820	0.299
0.231	0.799	2.549	0.300	0.580	2.309	0.241	0.853	2.659	0.329
0.119	<b>0.038</b>	1.842	0.176	<b>0.029</b>	1.777	0.145	<b>0.023</b>	1.959	0.200
0.098	<b>0.001</b>	1.029	0.116	<b>0.006</b>	1.337	0.062	<b>0.000</b>	1.545	0.123
0.061	0.301	1.148	0.138	<b>0.030</b>	0.975	0.077	<b>0.040</b>	1.180	0.171
0.201	0.291	7.925	0.481	0.066	7.001	0.249	0.497	7.250	0.358
0.042	0.464	0.327	0.030	0.569	0.291	0.044	0.932	0.298	0.048
0.070	0.602	1.569	0.082	0.203	1.507	0.060	0.388	1.524	0.083
0.329	0.116	1.528	0.206	0.751	2.404	0.374	<b>0.036</b>	2.169	0.502
0.143	<b>0.000</b>	1.779	0.177	<b>0.043</b>	6.083	0.195	<b>0.000</b>	6.480	0.261
0.074	0.632	1.767	0.176	0.053	1.474	0.112	0.374	1.747	0.097
0.005	0.079	0.091	0.012	0.159	0.112	0.010	<b>0.002</b>	0.114	0.008
0.117	0.892	3.016	0.198	0.176	2.861	0.117	0.309	2.965	0.103
0.018	0.325	0.227	0.033	0.105	0.269	0.027	<b>0.004</b>	0.273	0.028

0.068	0.230	1.814	0.241	<b>0.005</b>	1.456	0.120	<b>0.002</b>	1.589	0.150
0.049	0.716	1.526	0.229	<b>0.017</b>	1.485	0.177	<b>0.006</b>	1.470	0.199
0.035	0.510	0.906	0.035	0.153	0.799	0.021	0.342	0.831	0.027
0.080	0.788	1.174	0.128	0.234	1.035	0.064	0.657	1.190	0.107
0.173	<b>0.013</b>	3.636	0.210	0.102	3.957	0.184	<b>0.005</b>	4.310	0.185

<i>ela1-2</i>		<i>ela2-1</i>			<i>ela1-1;ela2-1</i>			<i>ela1-2;ela2</i>	
SE	<i>t</i> -test	Mean	SE	<i>t</i> -test	Mean	SE	<i>t</i> -test	Mean	SE
0.171	<b>0.001</b>	3.070	0.321	0.253	1.261	0.076	<b>0.000</b>	1.412	0.129
0.232	0.164	3.905	0.224	0.533	4.353	0.233	0.066	4.679	0.333
0.357	0.067	3.546	0.305	<b>0.032</b>	3.486	0.311	0.051	3.786	0.340
0.226	<b>0.021</b>	1.252	0.137	0.059	1.740	0.141	<b>0.000</b>	1.988	0.190
0.173	0.752	1.299	0.146	0.145	1.135	0.140	0.520	1.281	0.155
0.970	0.290	8.700	0.868	0.415	6.671	0.536	0.212	7.415	0.632
0.040	<b>0.027</b>	0.261	0.030	0.106	0.229	0.020	<b>0.029</b>	0.303	0.017
0.189	0.729	2.321	0.136	0.271	2.250	0.156	0.420	2.402	0.175
0.162	0.654	1.666	0.256	0.594	1.632	0.242	0.567	1.413	0.094
0.664	<b>0.000</b>	1.477	0.156	0.239	8.944	0.669	<b>0.000</b>	9.992	0.689
0.180	0.101	2.257	0.198	0.325	1.778	0.131	0.454	1.921	0.142
0.016	<b>0.004</b>	0.154	0.013	<b>0.037</b>	0.185	0.013	<b>0.001</b>	0.183	0.018
0.339	0.557	4.412	0.292	0.299	4.394	0.270	0.253	4.526	0.282
0.011	0.500	0.116	0.013	0.156	0.102	0.006	0.491	0.109	0.007
0.245	0.227	2.352	0.283	0.097	1.773	0.224	0.786	2.046	0.261
0.103	0.373	1.068	0.150	0.143	0.851	0.101	0.509	1.063	0.139
0.066	0.338	1.415	0.069	0.616	1.259	0.067	0.347	1.359	0.070
0.139	0.750	1.414	0.084	0.312	1.523	0.088	0.085	1.839	0.135
0.428	<b>0.000</b>	4.473	0.240	0.106	6.250	0.424	<b>0.000</b>	6.551	0.341

<i>ela1-2</i>		<i>ela2-1</i>			<i>ela1-1;ela2-1</i>			<i>ela1-2;ela2</i>	
SE	<i>t</i> -test	Mean	SE	<i>t</i> -test	Mean	SE	<i>t</i> -test	Mean	SE
0.100	<b>0.000</b>	3.310	0.283	0.712	1.277	0.164	<b>0.000</b>	1.236	0.142
0.478	0.420	4.286	0.261	0.774	4.568	0.185	0.372	4.217	0.153
0.796	0.173	4.489	0.393	0.558	4.669	0.277	0.279	4.399	0.380
0.158	<b>0.002</b>	0.885	0.073	0.538	1.709	0.077	<b>0.000</b>	1.443	0.099
0.165	0.888	1.766	0.245	0.384	1.367	0.067	0.209	1.256	0.096
0.874	0.362	9.361	0.691	0.700	8.618	0.515	0.517	7.467	0.557
0.086	0.331	0.472	0.048	0.101	0.233	0.033	<b>0.045</b>	0.325	0.062
0.294	0.128	2.606	0.160	0.241	2.630	0.124	0.128	2.434	0.059
0.814	<b>0.015</b>	0.979	0.084	0.491	1.761	0.201	<b>0.007</b>	1.600	0.141
1.252	<b>0.000</b>	1.067	0.084	<b>0.046</b>	10.571	0.373	<b>0.000</b>	10.432	0.272
0.101	<b>0.000</b>	2.366	0.136	0.052	1.600	0.110	0.084	1.241	0.079
0.075	<b>0.014</b>	0.165	0.016	0.374	0.245	0.017	<b>0.000</b>	0.234	0.018
0.605	0.100	4.460	0.216	0.584	4.742	0.161	0.113	4.636	0.120
0.015	0.270	0.096	0.009	0.803	0.154	0.014	<b>0.003</b>	0.112	0.010
0.377	0.870	2.580	0.287	0.082	1.791	0.115	0.313	1.377	0.157
0.317	0.140	0.816	0.123	0.083	0.825	0.081	<b>0.014</b>	0.685	0.074

0.343	<b>0.037</b>	1.875	0.179	0.111	1.758	0.116	0.136	1.805	0.112
0.303	0.973	2.145	0.230	<b>0.023</b>	1.626	0.131	0.398	1.372	0.162
0.492	<b>0.000</b>	3.970	0.266	0.128	6.954	0.164	<b>0.000</b>	6.543	0.199

---

<i>-I</i>	<i>e1b2-1</i>			<i>ivd1-2</i>			<i>mcca1-1</i>		
	<i>t</i> -test	Mean	SE	<i>t</i> -test	Mean	SE	<i>t</i> -test	Mean	SE
0.099	1.253	0.088	0.352	1.581	0.137	0.210	1.308	0.070	0.584
<b>0.021</b>	0.047	0.005	0.078	0.046	0.008	0.182	0.046	0.008	0.172
0.679	0.100	0.011	0.116	0.131	0.011	0.594	0.121	0.008	0.843
0.682	1.336	0.136	0.376	1.656	0.150	0.674	1.582	0.160	0.904
0.098	0.832	0.075	0.629	1.050	0.072	0.071	0.929	0.040	0.453
0.645	5.767	0.372	0.382	6.869	0.258	0.115	5.732	0.203	0.224
0.087	0.243	0.041	0.600	0.237	0.033	0.485	0.188	0.026	0.067
<b>0.003</b>	0.088	0.004	0.097	0.110	0.008	<b>0.003</b>	0.094	0.008	0.088
0.810	0.038	0.003	0.484	0.055	0.006	0.074	0.037	0.003	0.323
<b>0.016</b>	0.077	0.006	0.461	0.117	0.018	<b>0.033</b>	0.086	0.016	0.382
0.148	0.109	0.008	0.786	0.133	0.008	<b>0.021</b>	0.109	0.008	0.800
0.202	0.024	0.002	0.883	0.028	0.002	0.130	0.027	0.003	0.330
0.426	0.119	0.007	0.722	0.138	0.006	<b>0.043</b>	0.123	0.005	0.861
0.249	0.183	0.013	0.436	0.214	0.009	<b>0.013</b>	0.179	0.016	0.615
<b>0.018</b>	0.354	0.037	0.189	0.543	0.055	<b>0.046</b>	0.376	0.032	0.346
0.137	0.370	0.037	0.952	0.495	0.070	0.126	0.364	0.048	0.967
<b>0.030</b>	0.024	0.001	0.096	0.030	0.003	<b>0.018</b>	0.022	0.003	0.783
0.207	0.025	0.001	0.111	0.040	0.006	0.103	0.029	0.002	0.959
<b>0.016</b>	0.160	0.006	0.658	0.215	0.021	<b>0.022</b>	0.175	0.015	0.258

<i>-I</i>	<i>e1b2-1</i>			<i>ivd1-2</i>			<i>mcca1-1</i>		
	<i>t</i> -test	Mean	SE	<i>t</i> -test	Mean	SE	<i>t</i> -test	Mean	SE
0.318	2.603	0.155	0.554	0.881	0.067	<b>0.000</b>	3.071	0.286	0.082
0.423	2.303	0.157	0.514	2.509	0.209	0.563	2.579	0.237	0.440
<b>0.021</b>	1.364	0.125	0.468	2.177	0.179	<b>0.001</b>	1.735	0.149	<b>0.041</b>
<b>0.000</b>	0.731	0.053	0.066	1.754	0.177	<b>0.000</b>	1.484	0.169	<b>0.000</b>
0.053	0.774	0.068	0.543	0.725	0.047	0.364	0.757	0.065	0.761
0.304	6.780	0.335	0.460	5.153	0.269	<b>0.010</b>	5.560	0.312	0.056
0.977	0.256	0.039	0.486	0.156	0.024	<b>0.012</b>	0.249	0.033	0.390
0.377	1.330	0.057	0.680	1.479	0.123	0.700	1.518	0.137	0.552
0.205	1.291	0.136	0.930	1.768	0.178	0.195	2.476	0.284	<b>0.007</b>
<b>0.000</b>	1.892	0.123	<b>0.001</b>	2.721	0.110	<b>0.000</b>	5.710	0.389	<b>0.000</b>
<b>0.007</b>	1.233	0.100	0.719	1.625	0.145	0.117	1.256	0.127	0.561
<b>0.001</b>	0.069	0.005	0.561	0.071	0.004	0.963	0.102	0.010	<b>0.015</b>
0.096	2.548	0.120	0.638	2.727	0.186	0.852	2.833	0.184	0.512
<b>0.006</b>	0.179	0.018	0.677	0.185	0.009	0.261	0.186	0.018	0.341



<b>0.002</b>	0.929	0.088	0.356	1.456	0.206	<b>0.030</b>	1.332	0.170	<b>0.042</b>
<b>0.015</b>	0.794	0.108	0.710	0.860	0.084	0.781	0.831	0.077	0.947
0.919	0.770	0.031	0.843	0.821	0.032	0.748	0.810	0.027	0.533
0.139	0.934	0.076	0.907	1.130	0.081	0.199	1.009	0.074	0.890
<b>0.000</b>	3.416	0.132	0.136	3.925	0.205	<b>0.011</b>	4.258	0.306	<b>0.008</b>

<i>-I</i>	<i>eIb2-1</i>			<i>ivd1-2</i>			<i>mcca1-1</i>		
<i>t</i> -test	Mean	SE	<i>t</i> -test	Mean	SE	<i>t</i> -test	Mean	SE	<i>t</i> -test
<b>0.001</b>	2.361	0.147	0.580	3.489	0.581	<b>0.012</b>	1.357	0.133	<b>0.001</b>
<b>0.015</b>	3.764	0.089	0.907	5.723	0.525	<b>0.003</b>	4.003	0.163	0.399
<b>0.011</b>	2.448	0.189	0.248	4.998	0.589	<b>0.006</b>	3.130	0.140	0.127
<b>0.000</b>	1.014	0.041	0.559	2.209	0.265	<b>0.001</b>	1.729	0.135	<b>0.000</b>
0.168	0.748	0.045	<b>0.018</b>	1.016	0.178	0.911	0.681	0.041	<b>0.008</b>
0.730	6.648	0.328	0.100	5.668	1.098	0.181	5.015	0.337	<b>0.002</b>
0.348	0.183	0.026	<b>0.005</b>	0.425	0.104	0.379	0.299	0.032	0.255
0.102	1.878	0.067	0.112	5.400	1.039	<b>0.011</b>	2.161	0.067	0.868
0.518	1.637	0.214	0.833	1.553	0.295	0.959	2.995	0.420	<b>0.007</b>
<b>0.000</b>	1.782	0.077	<b>0.003</b>	3.917	0.808	<b>0.014</b>	8.198	0.328	<b>0.000</b>
0.953	1.649	0.087	0.088	1.957	0.304	0.822	1.238	0.073	<b>0.003</b>
<b>0.008</b>	0.104	0.006	0.192	0.704	0.188	<b>0.013</b>	0.179	0.013	<b>0.003</b>
0.135	3.774	0.153	0.292	10.098	1.931	<b>0.012</b>	4.349	0.182	0.336
0.193	0.091	0.005	0.698	0.633	0.165	<b>0.010</b>	0.073	0.006	0.156
0.298	1.254	0.113	0.051	3.666	0.706	<b>0.016</b>	1.644	0.160	0.801
0.140	0.573	0.073	0.265	1.128	0.205	0.118	0.498	0.081	0.129
0.867	1.198	0.057	0.187	3.221	0.616	<b>0.016</b>	1.376	0.082	0.804
<b>0.001</b>	1.291	0.062	0.573	2.931	0.506	<b>0.004</b>	1.209	0.100	0.902
<b>0.000</b>	4.046	0.213	0.609	9.901	1.862	<b>0.010</b>	5.923	0.241	<b>0.000</b>

<i>-I</i>	<i>eIb2-1</i>			<i>ivd1-2</i>			<i>mcca1-1</i>		
<i>t</i> -test	Mean	SE	<i>t</i> -test	Mean	SE	<i>t</i> -test	Mean	SE	<i>t</i> -test
<b>0.000</b>	2.936	0.247	0.503	10.334	2.264	<b>0.011</b>	0.798	0.109	<b>0.000</b>
0.869	3.726	0.314	0.441	8.915	0.943	<b>0.001</b>	4.747	0.221	0.225
0.671	3.761	0.332	0.392	12.034	1.219	<b>0.000</b>	5.142	0.479	0.121
<b>0.000</b>	0.849	0.068	0.833	3.914	0.548	<b>0.000</b>	1.582	0.110	<b>0.000</b>
0.069	1.430	0.160	0.619	1.910	0.151	0.051	1.102	0.081	<b>0.004</b>
<b>0.034</b>	9.769	0.716	0.394	11.304	1.458	0.165	5.917	0.382	<b>0.000</b>
0.688	0.434	0.067	0.357	1.679	0.543	<b>0.038</b>	0.361	0.071	0.955
0.626	2.270	0.158	0.571	14.187	1.465	<b>0.000</b>	2.881	0.100	<b>0.002</b>
<b>0.006</b>	1.461	0.153	<b>0.032</b>	2.594	0.481	<b>0.013</b>	3.128	0.586	<b>0.006</b>
<b>0.000</b>	1.063	0.076	<b>0.037</b>	9.303	1.335	<b>0.000</b>	10.612	0.319	<b>0.000</b>
<b>0.001</b>	1.711	0.183	0.340	3.751	0.642	<b>0.021</b>	0.871	0.073	<b>0.000</b>
<b>0.001</b>	0.135	0.012	0.512	1.929	0.281	<b>0.000</b>	0.297	0.022	<b>0.000</b>
0.183	4.079	0.264	0.545	26.226	2.542	<b>0.000</b>	5.329	0.248	<b>0.006</b>
0.160	0.094	0.013	0.910	2.129	0.350	<b>0.000</b>	0.111	0.006	0.115
<b>0.010</b>	1.789	0.225	0.485	11.198	1.480	<b>0.000</b>	1.535	0.135	<b>0.035</b>
0.189	0.581	0.072	0.878	3.217	0.562	<b>0.001</b>	0.547	0.058	0.763

0.068	1.560	0.082	0.873	10.017	1.150	<i>0.000</i>	1.911	0.101	<i>0.009</i>
0.706	1.076	0.105	0.051	7.680	1.272	<i>0.001</i>	1.167	0.146	0.179
<i>0.000</i>	3.481	0.231	0.999	24.924	3.016	<i>0.000</i>	7.505	0.274	<i>0.000</i>

<i>mccb1-1</i>			<i>hml1-2</i>		
Mean	SE	<i>t</i> -test	Mean	SE	<i>t</i> -test
1.396	0.102	0.851	1.475	0.089	0.409
0.043	0.005	0.154	0.073	0.008	<b>0.001</b>
0.153	0.013	0.095	0.116	0.009	0.569
1.655	0.185	0.702	1.458	0.107	0.679
1.164	0.083	<b>0.011</b>	0.834	0.074	0.639
6.678	0.290	0.275	5.201	0.295	<b>0.032</b>
0.224	0.035	0.345	0.187	0.029	0.076
0.114	0.006	<b>0.000</b>	0.096	0.008	0.076
0.035	0.005	0.299	0.042	0.010	0.962
0.083	0.010	0.320	0.116	0.017	<b>0.031</b>
0.120	0.012	0.315	0.128	0.010	0.100
0.031	0.003	<b>0.017</b>	0.029	0.005	0.329
0.129	0.008	0.450	0.131	0.008	0.330
0.231	0.015	<b>0.007</b>	0.176	0.012	0.649
0.420	0.030	0.847	0.447	0.031	0.368
0.365	0.041	0.973	0.357	0.031	0.830
0.025	0.001	<b>0.012</b>	0.027	0.002	<b>0.034</b>
0.028	0.002	0.495	0.037	0.005	0.171
0.182	0.013	0.091	0.200	0.019	0.051

<i>mccb1-1</i>			<i>hml1-2</i>		
Mean	SE	<i>t</i> -test	Mean	SE	<i>t</i> -test
3.054	0.266	0.073	2.654	0.166	0.412
2.727	0.151	0.090	2.545	0.132	0.346
1.695	0.083	<b>0.006</b>	1.314	0.095	0.657
1.395	0.130	<b>0.000</b>	1.376	0.078	<b>0.000</b>
0.755	0.049	0.689	0.594	0.067	<b>0.027</b>
5.492	0.207	<b>0.031</b>	4.625	0.219	<b>0.001</b>
0.228	0.031	0.209	0.186	0.029	<b>0.047</b>
1.504	0.091	0.497	1.383	0.070	0.693
2.024	0.300	0.112	2.027	0.256	0.074
5.827	0.321	<b>0.000</b>	5.308	0.234	<b>0.000</b>
1.333	0.094	0.916	1.093	0.092	0.056
0.104	0.006	<b>0.000</b>	0.091	0.004	<b>0.011</b>
2.888	0.131	0.270	2.622	0.105	0.701
0.198	0.022	0.230	0.140	0.009	0.243

1.259	0.087	<b>0.007</b>	1.123	0.098	0.101
0.824	0.055	0.992	0.841	0.137	0.913
0.870	0.039	0.499	0.849	0.052	0.823
1.139	0.070	0.137	0.963	0.127	0.815
4.066	0.245	<b>0.008</b>	3.745	0.139	<b>0.016</b>

<i>mccb1-1</i>			<i>hml1-2</i>		
Mean	SE	<i>t</i> -test	Mean	SE	<i>t</i> -test
1.618	0.099	<b>0.005</b>	1.301	0.087	<b>0.001</b>
4.681	0.337	<b>0.032</b>	3.852	0.195	0.848
3.355	0.229	<b>0.027</b>	2.379	0.221	0.174
1.819	0.095	<b>0.000</b>	1.694	0.078	<b>0.000</b>
0.855	0.066	0.165	0.469	0.035	<b>0.000</b>
5.715	0.461	<b>0.014</b>	4.214	0.177	<b>0.000</b>
0.270	0.040	0.126	0.137	0.034	<b>0.002</b>
2.353	0.131	0.213	1.902	0.094	0.161
2.669	0.399	<b>0.048</b>	1.683	0.148	0.614
9.063	0.543	<b>0.000</b>	7.511	0.324	<b>0.000</b>
1.591	0.095	0.093	1.194	0.084	<b>0.001</b>
0.190	0.015	<b>0.001</b>	0.153	0.006	<b>0.008</b>
4.586	0.265	0.117	3.892	0.156	0.464
0.081	0.004	0.302	0.066	0.005	<b>0.047</b>
1.915	0.215	0.542	1.321	0.089	0.089
0.720	0.129	0.904	0.367	0.034	<b>0.026</b>
1.432	0.088	0.635	1.367	0.069	0.820
1.569	0.160	0.086	1.472	0.112	0.190
6.659	0.352	<b>0.000</b>	5.433	0.251	<b>0.001</b>

<i>mccb1-1</i>			<i>hml1-2</i>		
Mean	SE	<i>t</i> -test	Mean	SE	<i>t</i> -test
1.044	0.067	<b>0.000</b>	0.752	0.098	<b>0.000</b>
5.025	0.172	0.076	5.634	0.557	<b>0.049</b>
5.045	0.304	0.075	4.647	0.342	0.346
1.755	0.090	<b>0.000</b>	1.695	0.287	<b>0.015</b>
1.221	0.069	<b>0.024</b>	1.390	0.224	0.590
7.496	0.465	<b>0.021</b>	6.751	0.693	<b>0.015</b>
0.295	0.047	0.366	0.217	0.037	<b>0.032</b>
2.820	0.127	<b>0.013</b>	3.607	0.669	0.105
2.389	0.475	<b>0.021</b>	2.929	0.616	<b>0.016</b>
10.061	0.265	<b>0.000</b>	10.667	0.590	<b>0.000</b>
1.251	0.054	<b>0.001</b>	1.305	0.145	<b>0.007</b>
0.277	0.012	<b>0.000</b>	0.333	0.040	<b>0.002</b>
5.130	0.132	<b>0.005</b>	5.355	0.357	<b>0.025</b>
0.113	0.009	0.124	0.118	0.013	0.142
2.017	0.165	0.862	1.985	0.270	0.984
0.666	0.089	0.339	0.788	0.142	0.171

1.947	0.102	<b>0.005</b>	2.593	0.417	<b>0.037</b>
2.022	0.311	0.124	2.035	0.235	0.056
7.891	0.350	<b>0.000</b>	9.091	1.480	<b>0.005</b>

---

**Supplemental Table S4.** *Leaf amino acid profiles of ivd1-2 relative to Col-0 at 6d and 9*

Amino acid	6d in dark			Mean
	Mean	SE	<i>t</i> -test	
Ala	1.375	0.229	0.012	3.259
Arg	1.548	0.142	0.003	2.153
Asn	1.862	0.219	0.006	2.880
Asp	2.274	0.273	0.001	4.704
Gln	0.962	0.169	0.911	1.252
Glu	0.713	0.138	0.181	1.249
Gly	1.202	0.294	0.379	4.712
His	2.520	0.485	0.011	5.967
Ile	0.989	0.188	0.959	2.456
Leu	3.114	0.642	0.014	11.103
Lys	0.969	0.150	0.822	1.930
Met	5.922	1.583	0.013	13.169
Phe	2.454	0.469	0.012	6.114
Pro	6.796	1.768	0.010	23.072
Ser	2.092	0.403	0.016	5.657
Thr	1.457	0.265	0.118	5.659
Trp	2.415	0.462	0.016	6.494
Tyr	2.417	0.417	0.004	5.275
Val	2.565	0.482	0.010	7.159

The mean represents the fold change between the averages of five biological replicates of time point.

*d in prolonged darkness*

---

<b>9d in dark</b>	
<b>SE</b>	<b>t-test</b>
0.714	0.011
0.228	0.001
0.292	0.000
0.659	0.000
0.099	0.051
0.161	0.165
1.524	0.038
0.616	0.000
0.455	0.013
1.593	0.000
0.330	0.021
1.916	0.000
0.593	0.000
3.794	0.000
0.748	0.000
0.988	0.001
0.746	0.000
0.873	0.001
0.866	0.000

---

*f ivdI-2 and Col-0 at the same*

**Supplemental Table S5. Primers for genotyping, qPCR and amiRNA generation**

<b>Primer</b>	<b>Sequence</b>
LP_SALK_138630	TGAACCTGTATGTGGAGGAGG
RP_SALK_138630	TTCAAAAGCTTTTGATGGGTG
LP_SALK_037854	CAAATTCAACGATTTGCCAAG
RP_SALK_037854	TTTTACCCAACGTTTGTTC
LP_SALK_071680C	ACCTTTACCATGACTTGTGCG
RP_SALK_071680C	AGTTGGAGATGGATACGGATG
LP_SALK_098054	GATGTTGGATTTGGTGGTGTG
RP_SALK_098054	TGGAACCTATATACCTCTGCCTC
LP_SALK_027039	TTGTTCTCGTTGCATATGCTG
RP_SALK_027039	CATCTTCTTCGGCTTTGTGAG
LP_SALK_137966	AATATCTTGCTCATGGCCATG
RP_SALK_137966	TGCAGCCTTTCTTAATGCTTC
LP_SALK_117349	CATATTTT TAGCAGGACCGCC
RP_SALK_117349	AGCACAGGATACTGCCATCAC
LP_SALK_145226	TTCTTTGCACCTGCAGATAC
RP_SALK_145226	GAAGTTGGTCCAAGAGATGGC
LBa1	TGGTTCACGTAGTGGGCCATCG
P1_At1g21400	GGTTTGCTAGATCCAAAACCC
P2_At1g21400	AGAACCCGGTAACATGGAATC
p745	AACGTCCGCAATGTGTTATTAAGTTGTC
LP_SAIL_113_D07	TTTTTACAGACGAAGGCCTTG
RP_SAIL_113_D07	CTCTTCACCGATTGCAGTAGC
LB3	TAGCATCTGAATTT CATAACCAATCTCGATACAC
GABI_756G02-LP	LPAATCTGCAAAGCAACCACAAC
GABI_756G02-RP	RPACCTGCAGAGGAATATGGAGG
LB-GABI-KAT-o8409	ATATTGACCATCATACTCATTGC
AT1G21400L3	CGTATTTGAGTCCCTTCGGTA
AT1G21400R3	TTTCATCTCCGATGTGTAACC
AT5G09300L2	CACGAATACGCCAACAATCA
AT5G09300R2	TCATCAAGAACACGGTAGCA
At3g13450L	AGGTTCCGACATAACTCTTG
At3g13450R	CACTGAGGTCTCAACGATTT
LPD2_At3g17240L	CTCGGTGGTACTTGTCTTAA
LPD2_At3g17240R	CAACCGAAGAGACCTTAACA
amiRNA A cacc	CACCCTGCAAGGCGATTAAGTTGGGTAAC
amiRNA B	GCGGATAACAATTT CACACAGGAAACAG
amiE1B1-1 I	gaTATGCGATTACATTAGTCCTTtctctctttgtattcc
amiE1B1-1 II	gaAAGGACTAATGTAATCGCATAtcaaagagaatcaatga
amiE1B1-1 III	gaAAAGACTAATGTATTTCGCATTtcacaggtcgtgatatg
amiE1B1-1 IV	gaAATGCGAATACATTAGTCTTTtctacatatattcct
amiE1B1-2 I	gaTAACTACAGATAGTACGCCTAtctctctttgtattcc
amiE1B1-2 II	gaTAGGCGTACTATCTGTAGTTAtcaaagagaatcaatga
amiE1B1-2 III	gaTAAGCGTACTATCAGTAGTTTtcacaggtcgtgatatg
amiE1B1-2 IV	gaAAACTACTGATAGTACGCTTAtctacatatattcct
pEARLEY-100 For	CATCGTGGAAAAAGAAGACGT
pEARLEY-100 Rev	AGGATCTGAGCTACACATGCT



<b>Note</b>
Genotyping primer for <i>bcat1-1</i>
Genotyping primer for <i>bcat1-1</i>
Genotyping primer for <i>bcat2-1</i>
Genotyping primer for <i>bcat2-1</i>
Genotyping primer for <i>e1a1-1</i>
Genotyping primer for <i>e1a1-1</i>
Genotyping primer for <i>e1b2-1</i>
Genotyping primer for <i>e1b2-1</i>
Genotyping primer for <i>mtlpd2-2</i>
Genotyping primer for <i>mtlpd2-2</i>
Genotyping primer for <i>mcca1-1</i>
Genotyping primer for <i>mcca1-1</i>
Genotyping primer for <i>mccb1-1</i>
Genotyping primer for <i>mccb1-1</i>
Genotyping primer for <i>hml1-2</i>
Genotyping primer for <i>hml1-2</i>
Universal left genotyping primer for SALK lines
Genotyping primer for <i>e1a1-2</i>
Genotyping primer for <i>e1a1-2</i>
Universal left genotyping primer for WiscDsLox lines
Genotyping primer for <i>e1a2-1</i>
Genotyping primer for <i>e1a2-1</i>
Universal left genotyping primer for SAIL lines
Genotyping primer for <i>ivd1-2</i>
Genotyping primer for <i>ivd1-2</i>
Insertion specific genotyping left primer for <i>ivd1-2</i>
qPCR primer for <i>EIA1</i>
qPCR primer for <i>EIA1</i>
qPCR primer for <i>EIA2</i>
qPCR primer for <i>EIA2</i>
qPCR primer for <i>E1B2</i>
qPCR primer for <i>E1B2</i>
qPCR primer for <i>mtLPD2</i>
qPCR primer for <i>mtLPD2</i>
amiRNA a primer with cacc at 5', for amiRNA inserts cloning into pENTR-d/topo
amiRNA B, for amiRNA inserts cloning into pENTR-d/topo
I miR-s primer designed for amiE1B1-1
II miR-a primer designed for amiE1B1-1
III miR*s primer designed for amiE1B1-1
IV miR*a primer designed for amiE1B1-1
I miR-s primer designed for amiE1B1-2
II miR-a primer designed for amiE1B1-2
III miR*s primer designed for amiE1B1-2
IV miR*a primer designed for amiE1B1-2
Forward primer for amplifying/genotyping insert on pEarleyGate100 vector
Reverse primer for amplifying/genotyping insert on pEarleyGate100 vector

1 **Supplemental Material**

2

3 **Supplemental Figure S1.** Graphical representation of transcript correlation modules  
4 among the four datasets.

5 Graphs were constructed using development (top left), stress (top right), diurnal/circadian  
6 (bottom left), and light (bottom right) datasets. Nodes represent transcripts and edges  
7 indicate pairwise PCC values exceeding the threshold in each database. Transcript names  
8 of validated genes are in bold, and proposed genes in regular font. The size of nodes  
9 corresponds to the connectivity of the transcript (smaller node indicates fewer significant  
10 correlations with other transcripts, and *vice versa*). The thickness of edges correlates with  
11 their PCC values. See Supplemental Table S1 for PCC values and the corresponding  
12 threshold in each dataset. The network graphs were created using Cytoscape.

13

14 **Supplemental Figure S2.** Transcript profiles for known and proposed BCAA catabolism  
15 genes under diurnal/circadian conditions.

16 Microarray data were obtained from the Diurnal database (Mockler et al., 2007), and  
17 normalized to the maximum expression levels of each gene in every treatment. Pearson's  
18 Correlation Coefficient and average linkage were used for gene clustering. Gene names  
19 in orange text represent members of the highly coexpressed module identified from the  
20 diurnal/circadian dataset. Refer to the Diurnal database website  
21 (<http://diurnal.mocklerlab.org/>) for detailed information on each condition. COL, Col-0;  
22 LDHH, 12h light/12h dark and 24h hot; SD, 8h light/16h dark; DD(DDHC), entrained on  
23 24h dark and 12h hot/12h cold, and subjected to 24h dark and 24h hot; LDHC, 12h  
24 light/12h dark and 12h hot/12h cold; LDHH-Smith, 12h light/12h dark and 24h hot  
25 (Smith et al., 2004); LDHH-Stitt, 12h light/12h dark and 24h hot (Bläsing et al., 2005);  
26 LL(LDHC), entrained on LDHC and subjected to 24h light and 24h hot; LL(LLHC),  
27 entrained on 24h light and 12h hot/12h cold, and subjected to 24h light and 24h hot;  
28 LL12(LDHH), entrained on LDHH and subjected to 24h light and 24h hot;  
29 LL23(LDHH), entrained on LDHH and subjected to 24h light and 24h hot; LLHC, 24h  
30 light and 12h hot/12h cold.

31

32 **Supplemental Figure S3.** Characterization of BCKDH complex subunit mutants.

33 (A) Schematic representations of the T-DNA insertion sites of newly characterized  
34 BCAA catabolic mutants. Exons are shown as white rectangles, UTRs as grey rectangles,  
35 and introns as solid lines. The sites of T-DNA insertion confirmed in this study are  
36 indicated by black triangles.

37 (B) Decreased BCAA catabolic enzyme transcript accumulation in *e1a1-1*, *e1a1-2*, *e1a2-*  
38 *1*, *e1b2-1*, and *mtlpd2-2* mutants. Values represent mean  $\pm$  SE from four biological  
39 replicates. An asterisk indicates a significant difference determined by the Student's *t*-test  
40 ( $p < 0.05$ ). ND, not detectable. The normalized *E1B2* transcript level in *e1b2-1* is less than  
41 0.5% relative to Col-0.

42

43 **Supplemental Figure S4.** Transcript and mutant analyses of *E1B1*-silenced *e1b2-1* lines.

44 (A) Relative *E1B1* transcript abundance in two homozygous *E1B1*-silenced *e1b2-1* T3  
45 lines (progeny seed pools of independent primary transformants #1 and #3) by qPCR.  
46 The y axis values represent the normalized *E1B1* transcript levels relative to Col-0  
47 (shown as the horizontal dashed line,  $n=5$ , mean  $\pm$  SE). The *E1B1* transcript levels were  
48 normalized to *ACT2* transcript levels. An asterisk indicates a significant difference from  
49 the wild type, determined by the Student's *t*-test ( $p < 0.05$ ). Leaf tissue samples were  
50 harvested by the end of night on a 16h light/8h dark photoperiod.

51 (B) Relative levels of seed free BCAAs in homozygous *E1B1*-silenced *e1b2-1* T4 seeds  
52 (progeny seed pools of #1 and #3). The y axis values represent the amino acid levels  
53 relative to Col-0 (shown as the dashed line,  $n=4$ , mean  $\pm$  SE). An asterisk indicates a  
54 significant difference from the wild type, determined by the Student's *t*-test ( $p < 0.05$ ).

55 (C) Relative levels of leaf free BCAAs in homozygous *E1B1*-silenced *e1b2-1* T3 lines  
56 (progeny seed pools of #1 and #3) after 6 days in prolonged darkness. The y axis values  
57 represent the amino acid levels relative to Col-0 (shown as the dashed line,  $n=5$ , mean  $\pm$   
58 SE). An asterisk indicates a significant difference from the wild type, determined by the  
59 Student's *t*-test ( $p < 0.05$ ).

60

61 **Supplemental Figure S5.** Phenotypes of BCAA mutants subjected to prolonged  
62 darkness.

63 Photographs of 5-week-old, short-day-grown Arabidopsis plants taken prior to (0d) and  
64 after 3, 6, 9 and 13 days of prolonged darkness. The leaves of *elal-1*, *elal-2*, both *elal*;  
65 *ela2* double mutants, *ivdl-2*, *mccal-1*, *mccb1-1*, and *hml1-2* were visibly yellowed and  
66 dehydrated following 13 days of prolonged darkness compared to the wild type. The  
67 *ivdl-2* mutant started showing visible senescence symptoms at day 6. The experiments  
68 were done at least three times with similar results, and representative results are shown.  
69 Plants in the upper and lower panels were grown and assayed in individual experiments.  
70 Two replicates were shown for each mutant at every time point.

71

72 **Supplemental Table S1.** Pairwise Pearson's Correlation Coefficients (PCCs) for  
73 transcripts of BCAA catabolism genes.

74 PCCs above the 95<sup>th</sup> percentile threshold for each dataset are highlighted in red, and the  
75 values are indicated below. Genes that have PCCs above threshold with at least one other  
76 gene are highlighted in yellow.

77

78 **Supplemental Table S2.** Mutant seed free amino acid profiles.

79 The mean represents the fold change between the averages of five biological replicates of  
80 mutants and Col-0 grown at the same time.

81 't-test' indicates the value at which the mean measurement deviates from expectation (for  
82 example '0.01' means significant at <0.01).

83

84 **Supplemental Table S3.** Mutant leaf free amino acid profiles in prolonged darkness.

85 The mean represents the average of five biological replicates ( $\mu\text{mol/mg}$ ).

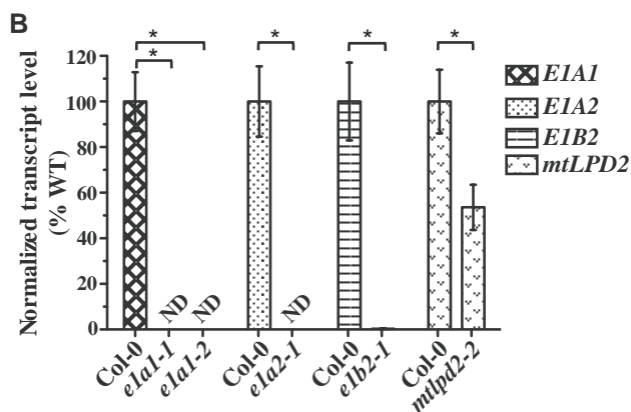
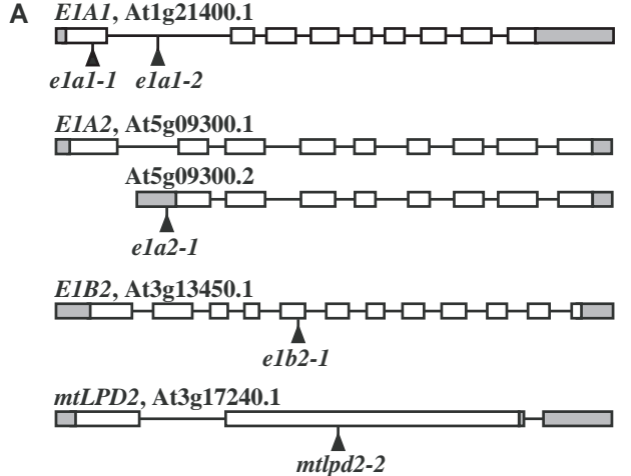
86

87 **Supplemental Table S4.** Leaf amino acid profiles of *ivdl-2* relative to Col-0 at 6d and  
88 9d in prolonged darkness.

89 The mean represents the fold change between the averages of five biological replicates of  
90 *ivdl-2* and Col-0 at the same time point.

91

92 **Supplemental Table S5.** Primers for genotyping, qPCR and amiRNA generation.



**Supplemental Figure S3.** Characterization of BCKDH complex subunit mutants. (A) Schematic representations of the T-DNA insertion sites of newly characterized BCAA catabolic mutants. Exons are shown as white rectangles, UTRs as grey rectangles, and introns as solid lines. The sites of T-DNA insertion confirmed in this study are indicated by black triangles. At5g09300.1 and At5g09300.2 correspond to alternatively spliced gene models. (B) Decreased BCAA catabolic enzyme transcript accumulation in *eia1-1*, *eia1-2*, *eia2-1*, *eib2-1*, and *mtlpd2-2* mutants. Values represent mean  $\pm$  SE from four biological replicates. An asterisk indicates a significant difference determined by the Student's *t*-test ( $p < 0.05$ ). ND, not detectable. The normalized *EIB2* transcript level in *eib2-1* is less than 0.5% relative to Col-0.