SUPPLEMENTARY DATA

FIG. S1. Natural variation for hypocotyl length in WL (A) and EOD (B) for 108 accessions of *Arabidopsis thaliana*. The linear correlation equation and the Pearson correlation index (*r*) with *P*-value are shown in the graphs.

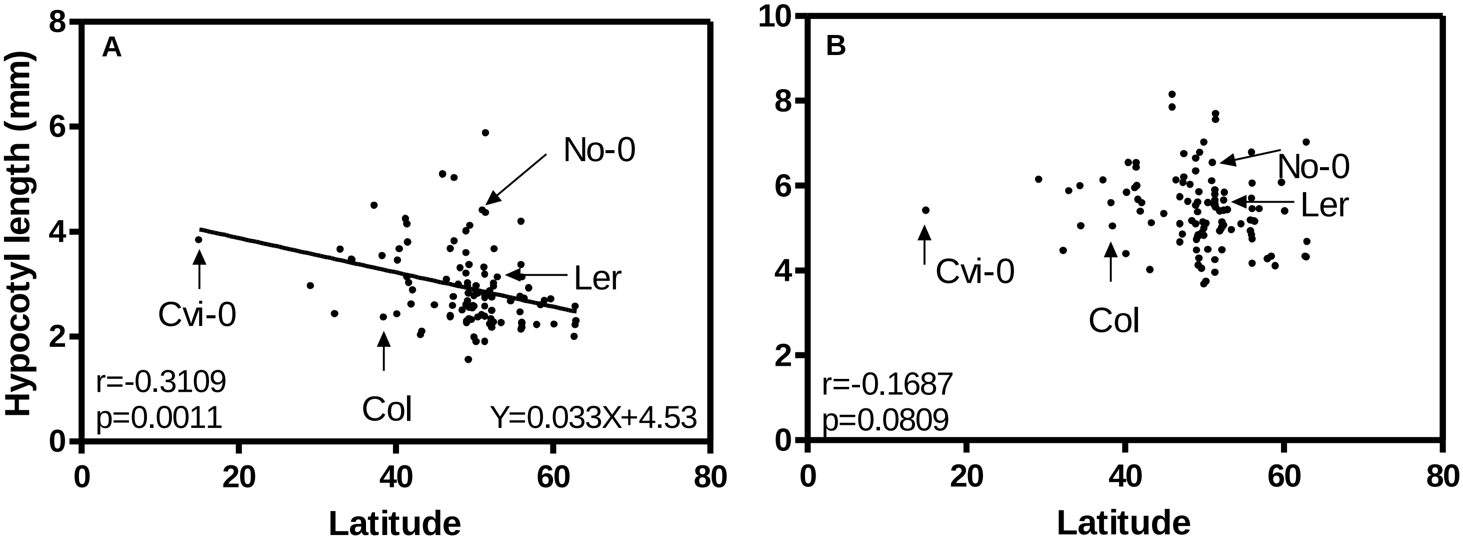


FIG. S2. Shade-avoidance response for hypocotyl growth in WT, *phy*A and *phy*B. Seedlings were grown in WL or EOD for 4 d in short-day conditions (A) and the EOD response was calculated (B). Each bar represents mean ± s.e.m. Significant differences between means were determined using Student's *t*-test:*$P < 0.05$;** $P < 0.001$.

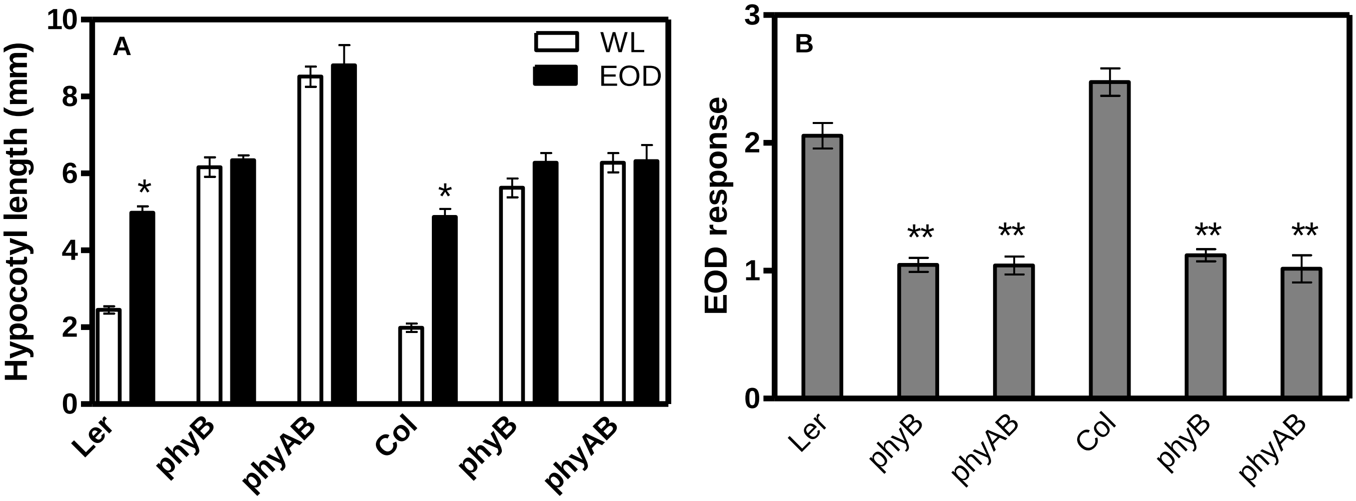


FIG. S3. Frequency distribution in WL, EOD and EOD response for Ler × Cvi-0 (A, B), Ler × Col (C, D) and Ler × No-0 (E, F) RIL populations. The average response of parental genotypes is indicated with arrows in each light condition.

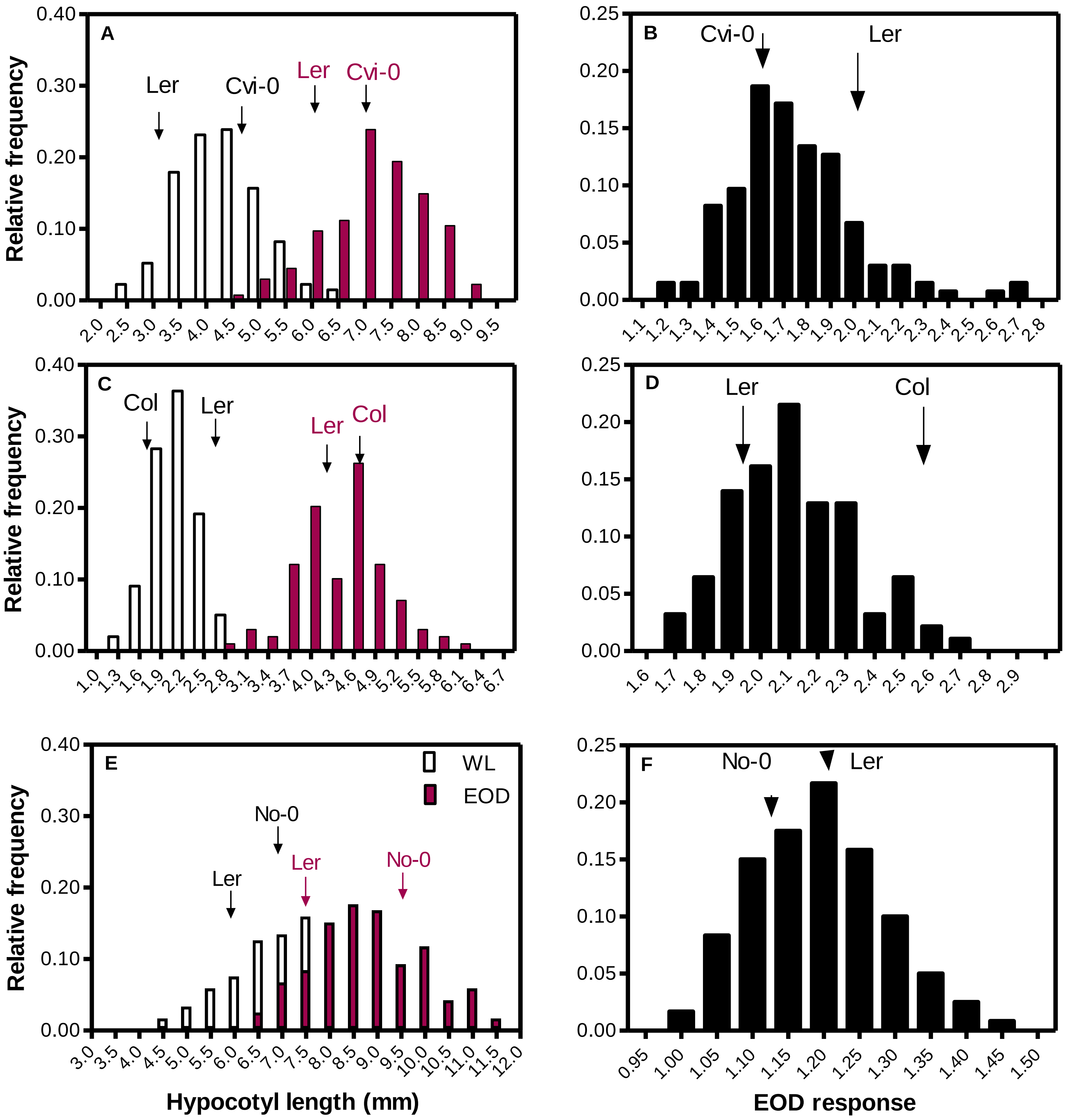


FIG. S4. *EODRATIO1* in WL (A) and EOD (B) is confirmed by HIF and rHIF polymorphics between CIW3 and NGA1126 markers at chromosome 2. Each bar represents mean ± s.e.m. Significant differences between means of the same HIF or rHIF were dstermined using Student's *t*-test: *$P < 0.05$; **$P < 0.001$.

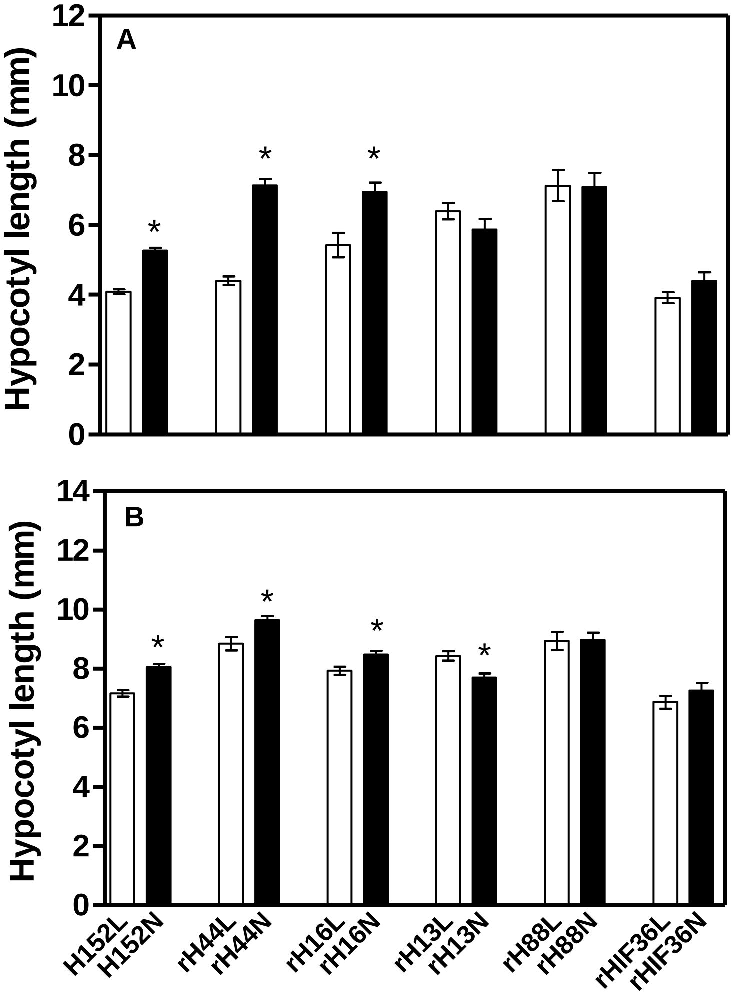
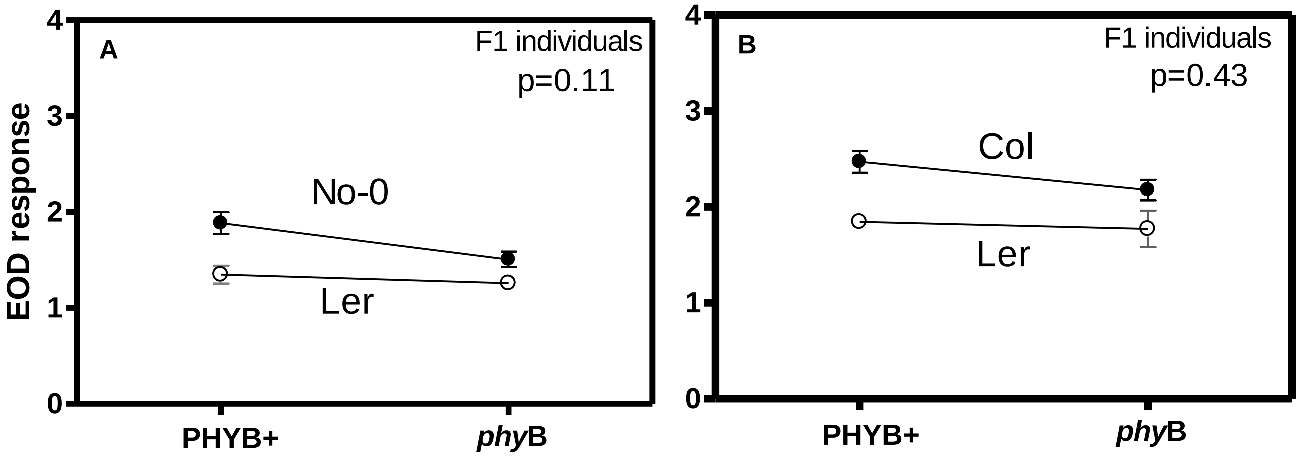


FIG. S5. *PHYB* gene is not responsible for *EODRATIO1* and *EODRATIO2*. In each graph the *P*-value of the interaction between tester genotype (genotype factor) and *phyB* mutation (phyB factor) is indicated. Quantitative complementation test with phyB mutant was done in Ler (A) and in Col (B) backgrounds.



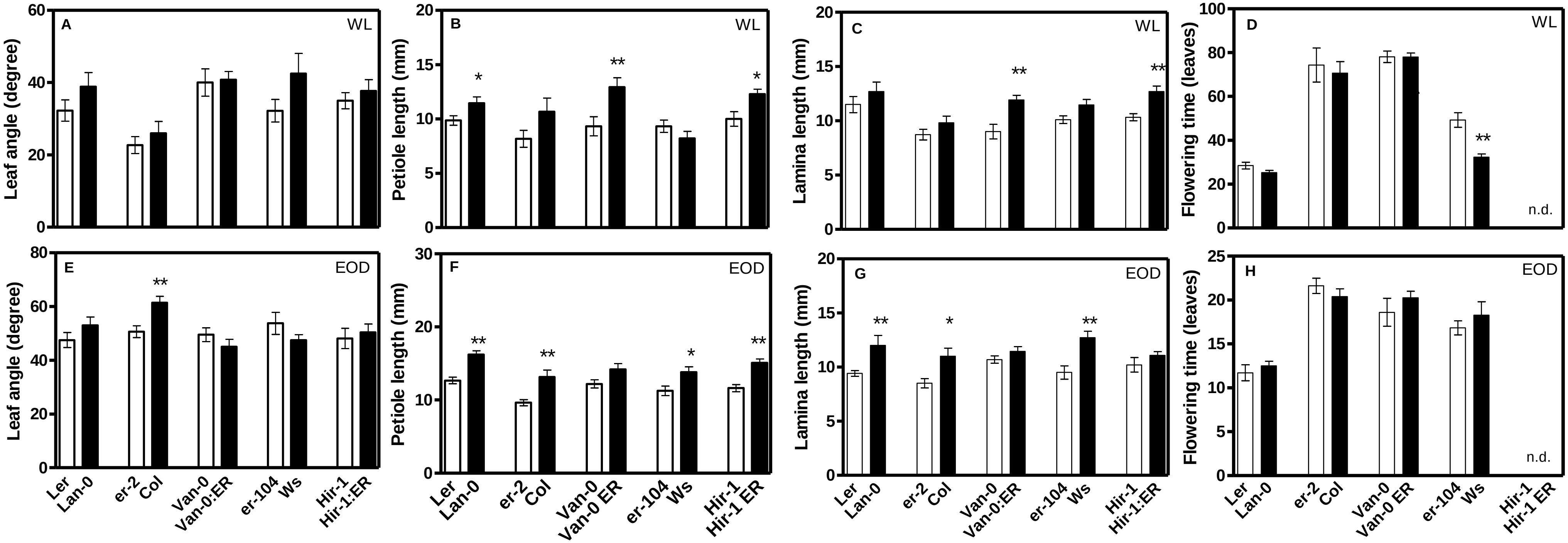


FIG. 6. *ERECTA* function in the shade-avoidance syndrome is pleiotropic. Leaf angle (A, E), petiole length (B, F), lamina length (C, G), and number of leaves at flowering (D, H) were measured in plants cultivated in WL and EOD. Each bar represents mean ± s.e.m. Significant differences between means were determined using Student's *t*-test: $^{*}P < 0.05$; $^{**}P < 0.001$. nd: not determined.

TABLE S1. Summary statistics for hypocotyl length under WL, EOD and EOD response. WL irradiation was 30 µmol m^{-2} s^{-1} for the Ler × No-0 experiment, 70 µmol m^{-2} s^{-1} for the Ler × Cvi-0 experiment, and 110 µmol m^{-2} s^{-1} for the Ler × Col experiment. Data are means (mm) ± s.e.m.

	WL	EOD	EOD response
Ler x No-0			
Ler	6.21 ± 0.15	7.53 ± 0.18	1.21 ± 0.02
No-0	8.67 ± 0.31	9.73 ± 0.26	1.13 ± 0.05
RIL mean	7.41 ± 0.25	8.78 ± 0.25	1.20 ± 0.02
RIL max – min	10.93 – 4.47	11.80 – 6.28	1.71 – 1.00
[Vg][1]	2.011	1.675	0.019
[Ve][2]	0.312	0.262	0.007
[H2][3]	0.845	0.844	0.633
[CVg][4]	19.14	14.73	11.53
Ler x Col			
Ler	2.05 ± 0.15	4.03 ± 0.32	1.89 ± 0.10
Col	1.77 ± 0.10	4.33 ± 0.12	2.47 ± 0.19
RIL mean	2.10 ± 0.12	4.40 ± 0.05	2.13 ± 0.12
RIL max - min	3.10 – 1.28	5.98 – 2.88	2.68 – 1.52
[Vg]	0.180	0.633	0.161
[Ve]	0.057	0.212	0.111
[H2]	0.684	0.664	0.312
[CVg]	20.21	18.08	18.83
Ler x Cvi-0			
Ler	3.47 ± 0.14	6.94 ± 0.42	2.02 ± 0.17
Cvi-0	5.38 ± 0.47	8.26 ± 0.10	1.56 ± 0.11

RIL mean	4.20 ± 0.22	7.13 ± 0.17	1.75 ± 0.11
RIL max - min	6.31 – 2.40	8.97 – 4.71	2.72 – 1.16
[Vg]	1.110	1.500	0.240
[Ve]	0.516	0.619	0.169
[H2]	0.540	0.590	0.300
[CVg]	25.14	17.20	27.94

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[1] Vg is the among RIL line variance component for each trait.

[2] Ve is the residual (error) variance component.

[3] H2 is defined as broad sense heritability calculated as $\sigma G2/\sigma z2$. H2 is the proportion of the total phenotypic variance that is genetic $(Vg/(Vg+Ve))$.

[4] Coefficient of genetic variation calculated as $(100 \times \sqrt{Vg})/media$.

Table S2. QTL mapping for hypocotyl length (mm) in WL and EOD and EOD response in three RIL populations sharing Ler as a common parental.

			WL				EOD				EOD response			
QTL	Closest marker	Pos cM[1] (Accum.. distance)	LOD	Interval	ADD	%	LOD	Interval	ADD	%	LOD	Interval	ADD	%
Ler x No-0														
WL1	C4_CIW7	52 (304)	3.58	45-61	0.82	9	2.45	36-68	0.65	6				
EOD1	C1_NGA111	99 (99)	2.93	88-102	-0.9	11	2.99	87-100	-0.77	10				
EOD2	C2_NGA1126	43 (145)					12.48	37-47	-1.5	37				
EODRATIO1	C2_PSL5	31 (133)	9.38	26-40	-1.49	33					3.58	2-35	0.096	17
Ler x Col														
WL2	C1_GAPB	61 (61)	3.55	35-65	0.26	14								
WL3	C3_g4708	24 (213)	5.38	0-25	-0.3	17	4.18	0-25	-0.48	13				
WL4	C4_PG11	75 (331)	2.65	40-102	-0.21	9								
WL5	C5_O6569	18 (369)	4.11	0-28	0.26	12	3.68	0-22	0.44	10				
WL6	C5_m435	109 (460)	2.95	82-109	-0.26	13								
EOD3	C1_m315	97 (97)					2.55	77-107	0.41	9				
EOD4	C2_g6842	47(168)					6.92	44-51	0.75	20				
EODRATIO2	C2_m216	34 (156)									4.35	25-46	0.18	15
EODRATIO3	C5_m247	74 (426)									5.5	60-84	0.27	33
Ler x Cvi-0														
WL7	C5_DF119L	110 (470)	3.00	105-112	-0.45	7.5	2.4	90-112	-0.45	6				
EOD5	C1_GH157L	104 (104)					2.5	102-105	0.16	6				
EOD6	C2_*ERECTA*	47 (172)	2.67	39-49	-041	6.4	3.67	39-49	-0.91	11				
EODRATIO4	C1_EC.66C	28 (28)									4.62	14-30	0.068	14
EODRATIO5	C2_FD81L	15 (140)									2.41	6-19	0.07	7

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[1] Accumulative distance of the five chromosomes of Arabidopsis is indicated between parentheses.