SUPPLEMENTARY DATA

Figure S1. Protein sequence alignment of AtMob1A and AtMob1B proteins.

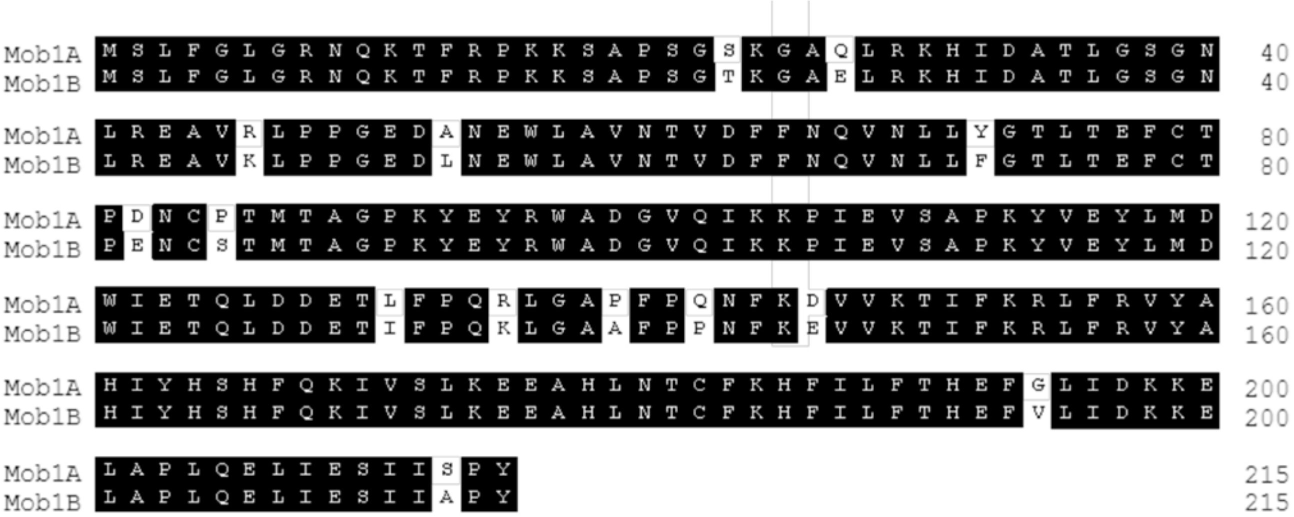


Figure S2: Genevestigator Anatomy expression profile of *Mob1A*.

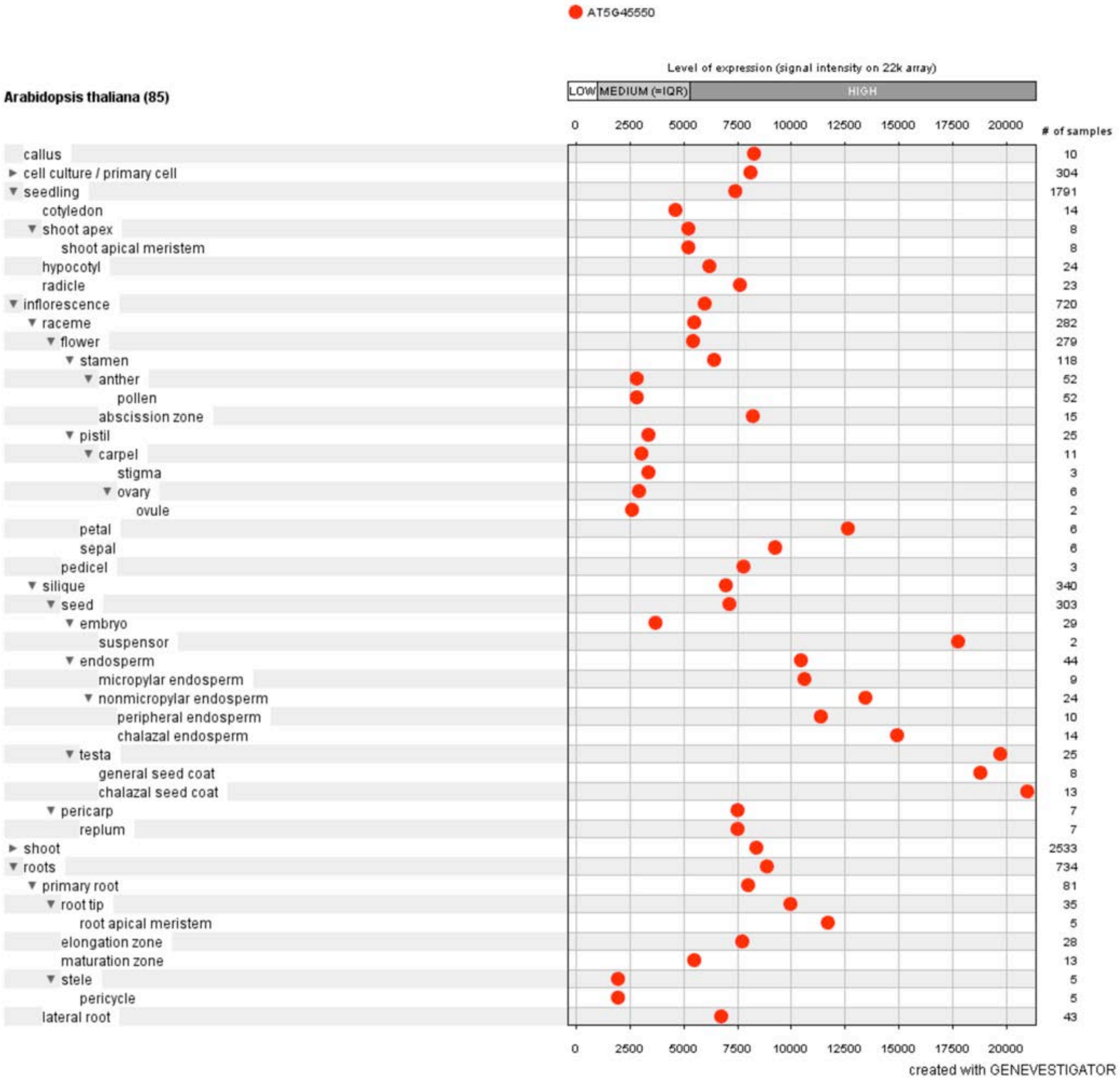
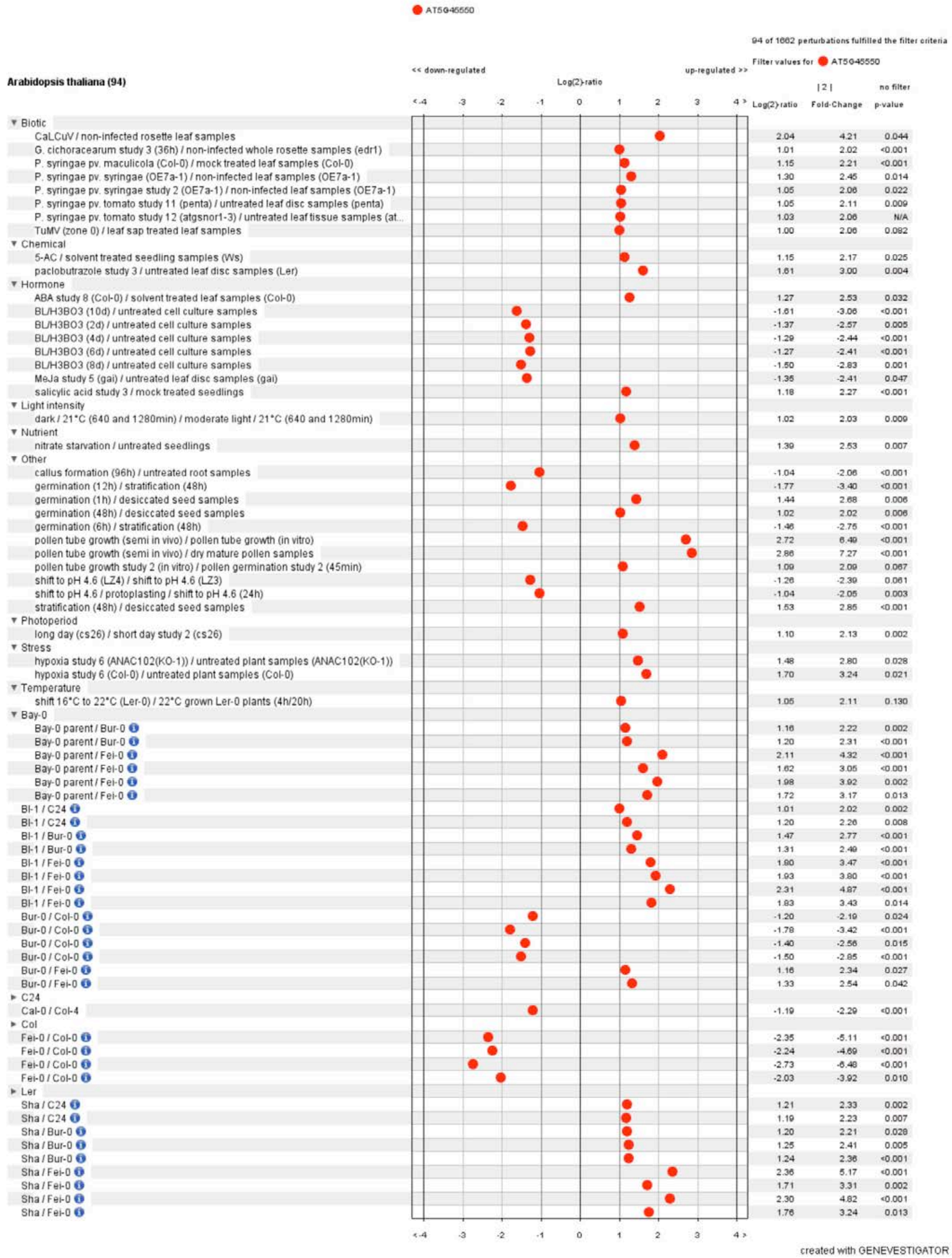


Figure S3. Genevestigator Perturbation expression profile of *Mob1A*.

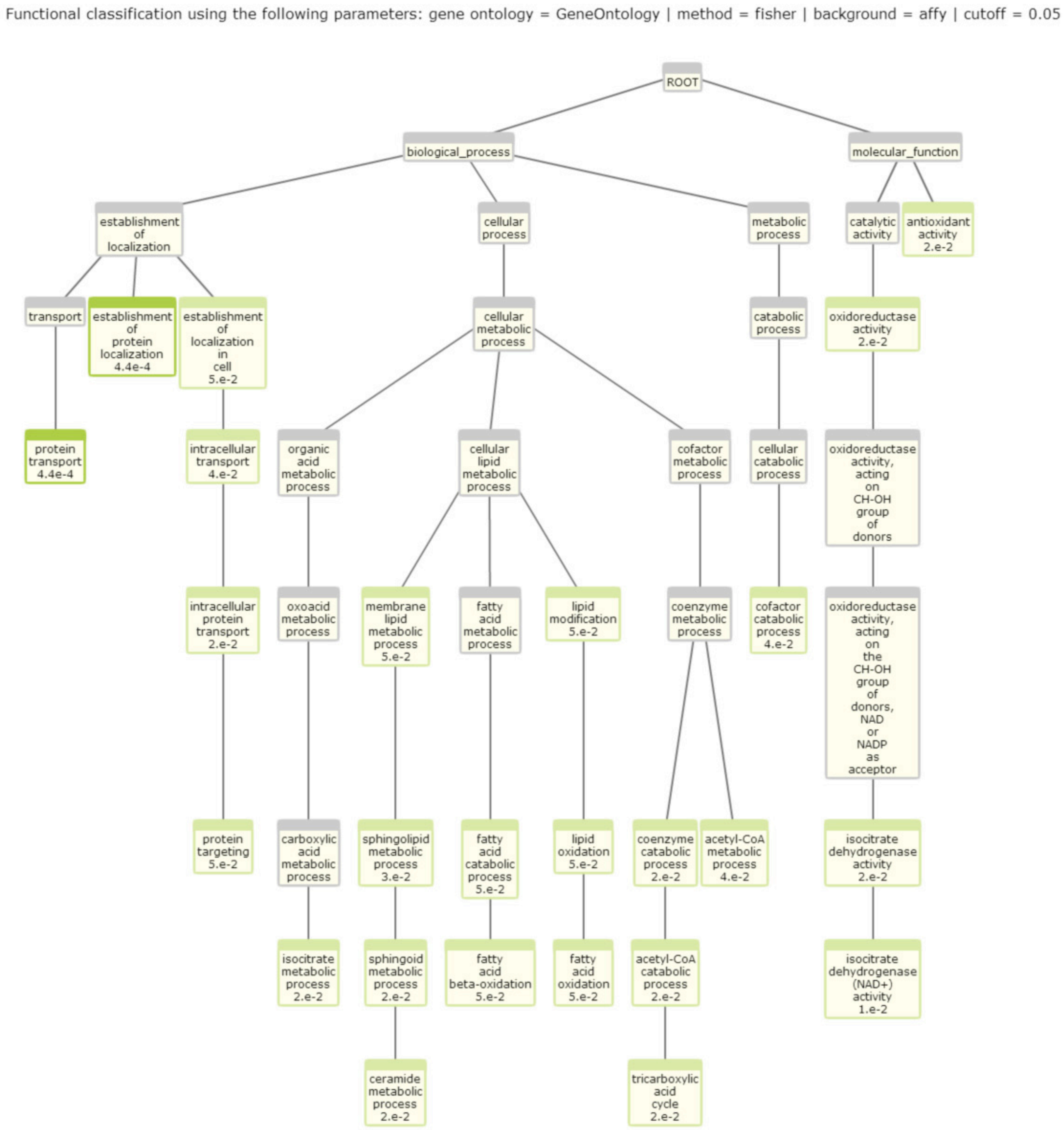


94 of 1662 perturbations fulfilled the filter criteria

Filter values for ● AT5G45550

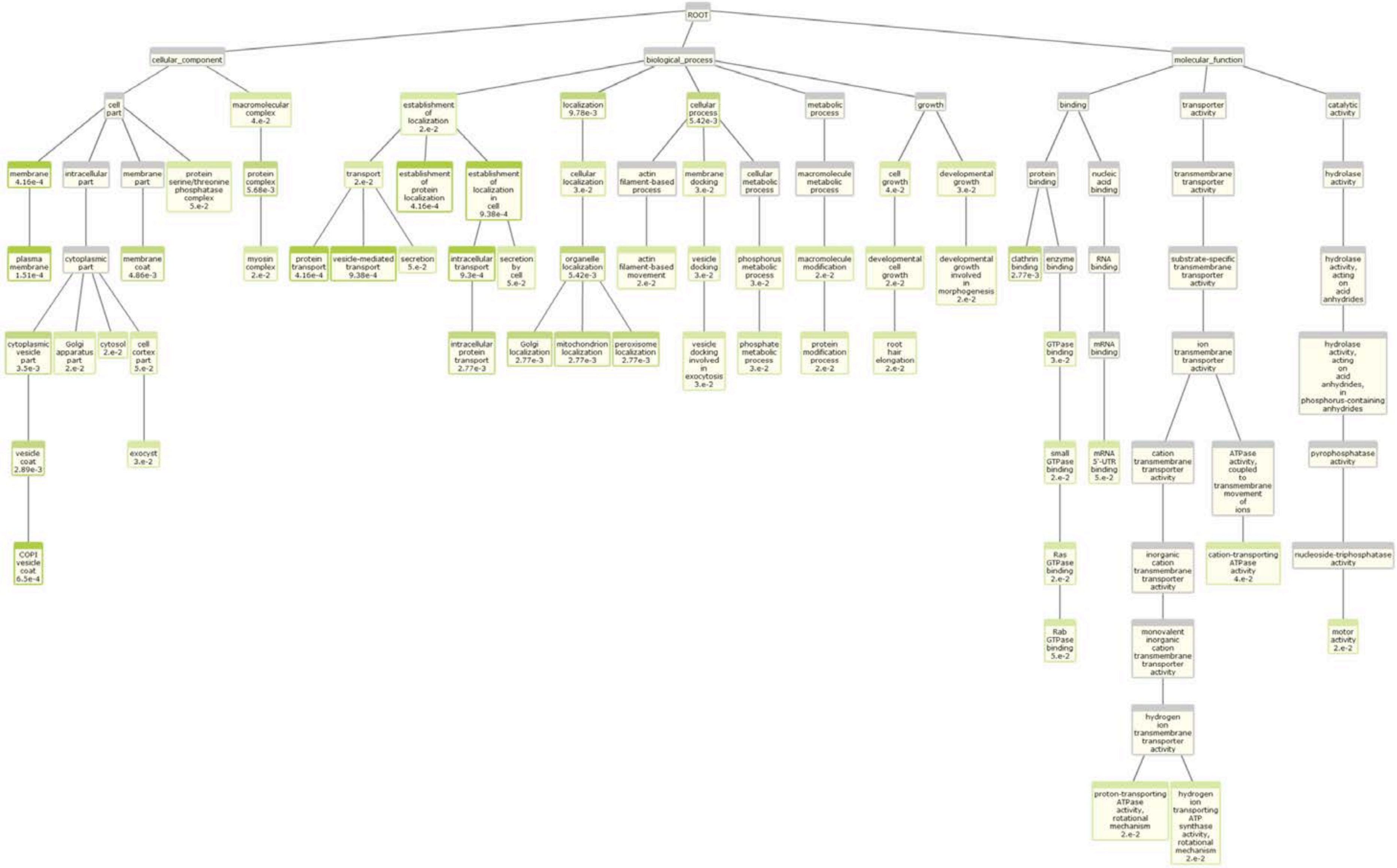
Arabidopsis thaliana (94)	Log(2)-ratio	|2| Fold-Change	no filter p-value
▼ Biotic			
CaLCuV / non-infected rosette leaf samples	2.04	4.21	0.044
G. cichoracearum study 3 (36h) / non-infected whole rosette samples (edr1)	1.01	2.02	<0.001
P. syringae pv. maculicola (Col-0) / mock treated leaf samples (Col-0)	1.15	2.21	<0.001
P. syringae pv. syringae (OE7a-1) / non-infected leaf samples (OE7a-1)	1.30	2.46	0.014
P. syringae pv. syringae study 2 (OE7a-1) / non-infected leaf samples (OE7a-1)	1.05	2.06	0.022
P. syringae pv. tomato study 11 (penta) / untreated leaf disc samples (penta)	1.05	2.11	0.009
P. syringae pv. tomato study 12 (atgsnor1-3) / untreated leaf tissue samples (at...	1.03	2.06	N/A
TuMV (zone 0) / leaf sap treated leaf samples	1.00	2.06	0.082
▼ Chemical			
5-AC / solvent treated seedling samples (Ws)	1.15	2.17	0.025
paclobutrazole study 3 / untreated leaf disc samples (Ler)	1.61	3.00	0.004
▼ Hormone			
ABA study 8 (Col-0) / solvent treated leaf samples (Col-0)	1.27	2.53	0.032
BL/H3BO3 (10d) / untreated cell culture samples	-1.61	-3.06	<0.001
BL/H3BO3 (2d) / untreated cell culture samples	-1.37	-2.57	0.005
BL/H3BO3 (4d) / untreated cell culture samples	-1.29	-2.44	<0.001
BL/H3BO3 (6d) / untreated cell culture samples	-1.27	-2.41	<0.001
BL/H3BO3 (8d) / untreated cell culture samples	-1.50	-2.83	0.001
MeJa study 5 (gai) / untreated leaf disc samples (gai)	-1.35	-2.41	0.047
salicylic acid study 3 / mock treated seedlings	1.18	2.27	<0.001
▼ Light intensity			
dark / 21°C (640 and 1280min) / moderate light / 21°C (640 and 1280min)	1.02	2.03	0.009
▼ Nutrient			
nitrate starvation / untreated seedlings	1.39	2.53	0.007
▼ Other			
callus formation (96h) / untreated root samples	-1.04	-2.06	<0.001
germination (12h) / stratification (48h)	-1.77	-3.40	<0.001
germination (1h) / desiccated seed samples	1.44	2.68	0.006
germination (48h) / desiccated seed samples	1.02	2.02	0.006
germination (6h) / stratification (48h)	-1.46	-2.75	<0.001
pollen tube growth (semi in vivo) / pollen tube growth (in vitro)	2.72	6.49	<0.001
pollen tube growth (semi in vivo) / dry mature pollen samples	2.86	7.27	<0.001
pollen tube growth study 2 (in vitro) / pollen germination study 2 (45min)	1.09	2.09	0.067
shift to pH 4.6 (LZ4) / shift to pH 4.6 (LZ3)	-1.26	-2.39	0.061
shift to pH 4.6 / protoplasting / shift to pH 4.6 (24h)	-1.04	-2.05	0.003
stratification (48h) / desiccated seed samples	1.53	2.85	<0.001
▼ Photoperiod			
long day (cs26) / short day study 2 (cs26)	1.10	2.13	0.002
▼ Stress			
hypoxia study 6 (ANAC102(KO-1)) / untreated plant samples (ANAC102(KO-1))	1.48	2.80	0.028
hypoxia study 6 (Col-0) / untreated plant samples (Col-0)	1.70	3.24	0.021
▼ Temperature			
shift 16°C to 22°C (Ler-0) / 22°C grown Ler-0 plants (4h/20h)	1.05	2.11	0.130
▼ Bay-0			
Bay-0 parent / Bur-0 ⓘ	1.16	2.22	0.002
Bay-0 parent / Bur-0 ⓘ	1.20	2.31	<0.001
Bay-0 parent / Fei-0 ⓘ	2.11	4.32	<0.001
Bay-0 parent / Fei-0 ⓘ	1.62	3.05	<0.001
Bay-0 parent / Fei-0 ⓘ	1.98	3.92	0.002
Bay-0 parent / Fei-0 ⓘ	1.72	3.17	0.013
Bl-1 / C24 ⓘ	1.01	2.02	0.002
Bl-1 / C24 ⓘ	1.20	2.26	0.008
Bl-1 / Bur-0 ⓘ	1.47	2.77	<0.001
Bl-1 / Bur-0 ⓘ	1.31	2.49	<0.001
Bl-1 / Fei-0 ⓘ	1.80	3.47	<0.001
Bl-1 / Fei-0 ⓘ	1.93	3.80	<0.001
Bl-1 / Fei-0 ⓘ	2.31	4.87	<0.001
Bl-1 / Fei-0 ⓘ	1.83	3.43	0.014
Bur-0 / Col-0 ⓘ	-1.20	-2.19	0.024
Bur-0 / Col-0 ⓘ	-1.78	-3.42	<0.001
Bur-0 / Col-0 ⓘ	-1.40	-2.56	0.015
Bur-0 / Col-0 ⓘ	-1.50	-2.85	<0.001
Bur-0 / Fei-0 ⓘ	1.16	2.34	0.027
Bur-0 / Fei-0 ⓘ	1.33	2.54	0.042
▸ C24			
Cal-0 / Col-4	-1.19	-2.29	<0.001
▸ Col			
Fei-0 / Col-0 ⓘ	-2.35	-5.11	<0.001
Fei-0 / Col-0 ⓘ	-2.24	-4.69	<0.001
Fei-0 / Col-0 ⓘ	-2.73	-6.48	<0.001
Fei-0 / Col-0 ⓘ	-2.03	-3.92	0.010
▸ Ler			
Sha / C24 ⓘ	1.21	2.33	0.002
Sha / C24 ⓘ	1.19	2.23	0.007
Sha / Bur-0 ⓘ	1.20	2.21	0.028
Sha / Bur-0 ⓘ	1.25	2.41	0.005
Sha / Bur-0 ⓘ	1.24	2.36	<0.001
Sha / Fei-0 ⓘ	2.36	5.17	<0.001
Sha / Fei-0 ⓘ	1.71	3.31	0.002
Sha / Fei-0 ⓘ	2.30	4.82	<0.001
Sha / Fei-0 ⓘ	1.76	3.24	0.013

Figure S4. Gene ontology (GO) analysis of 54 genes with highest co-expression to At5g45550 based on 1662 perturbation (Genevestigator: Co-expression tool).



Functional classification using the following parameters: gene ontology = GeneOntology | method = fisher | background = affy | cutoff = 0.05

Figure S5. Gene ontology (GO) analysis of 55 genes with highest co-expression to At5g45550 based on 74 anatomical parts (Genevestigator: Co-expression tool).



Functional classification using the following parameters: gene ontology = GeneOntology | method = fisher | background = affy | cutoff = 0.05

Figure S6. *Mob1A* expression in floral tissues.

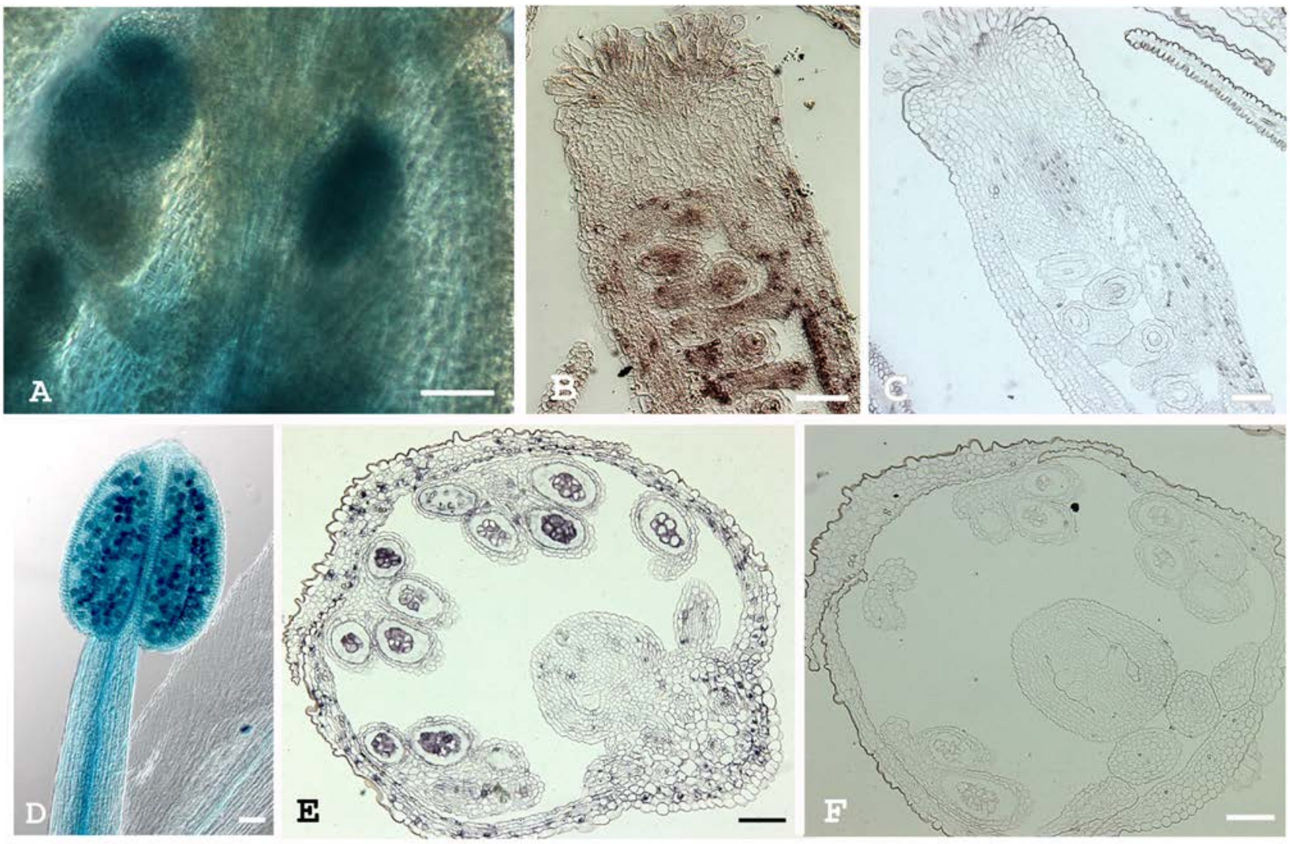


Figure S7. comparison of *Mob1A* and *Mob1B* spatial expression in arabidopsis seedlings.

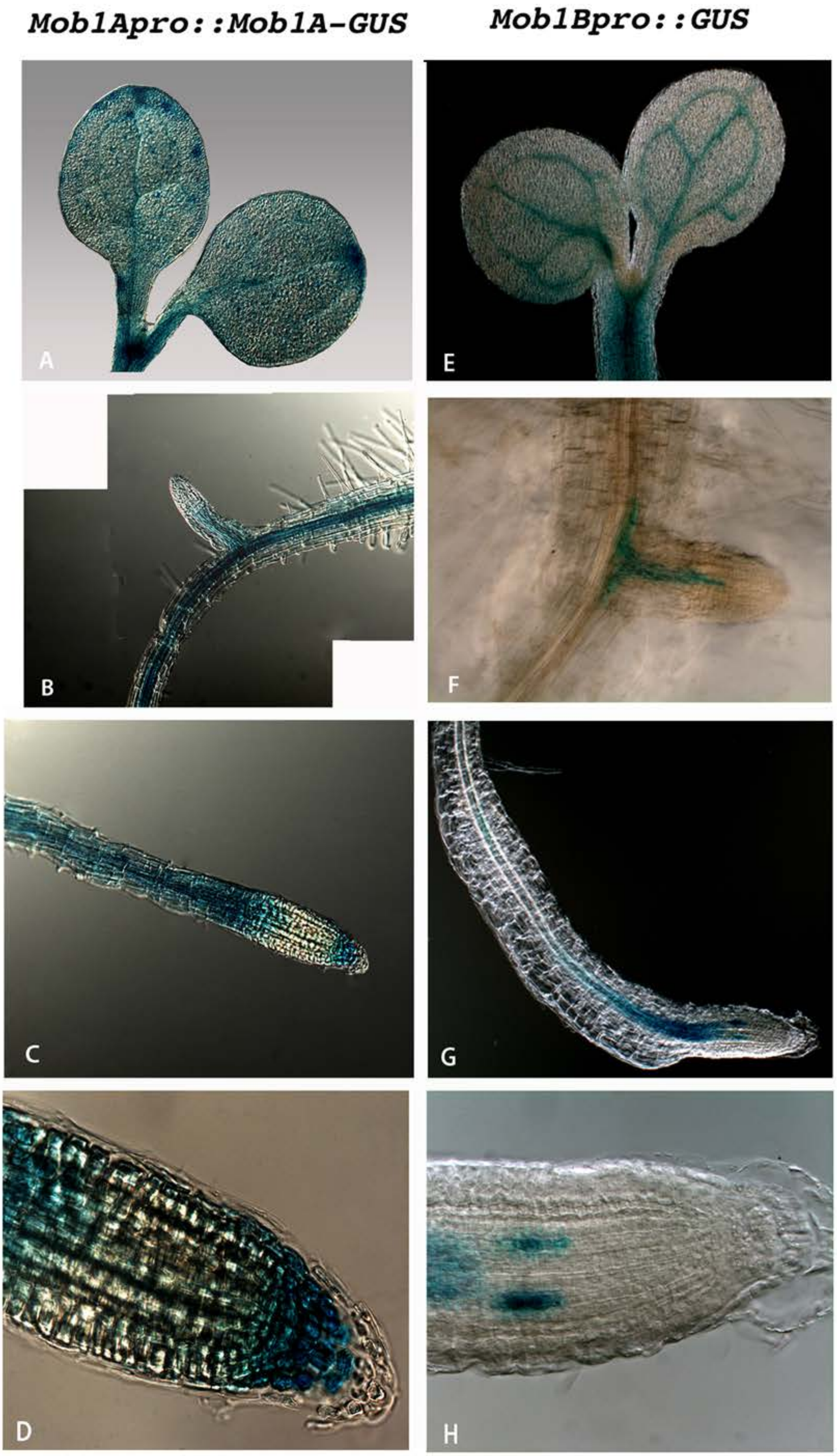


Figure S8. Absence of visible phenotypes for *mob1B-1* plants.

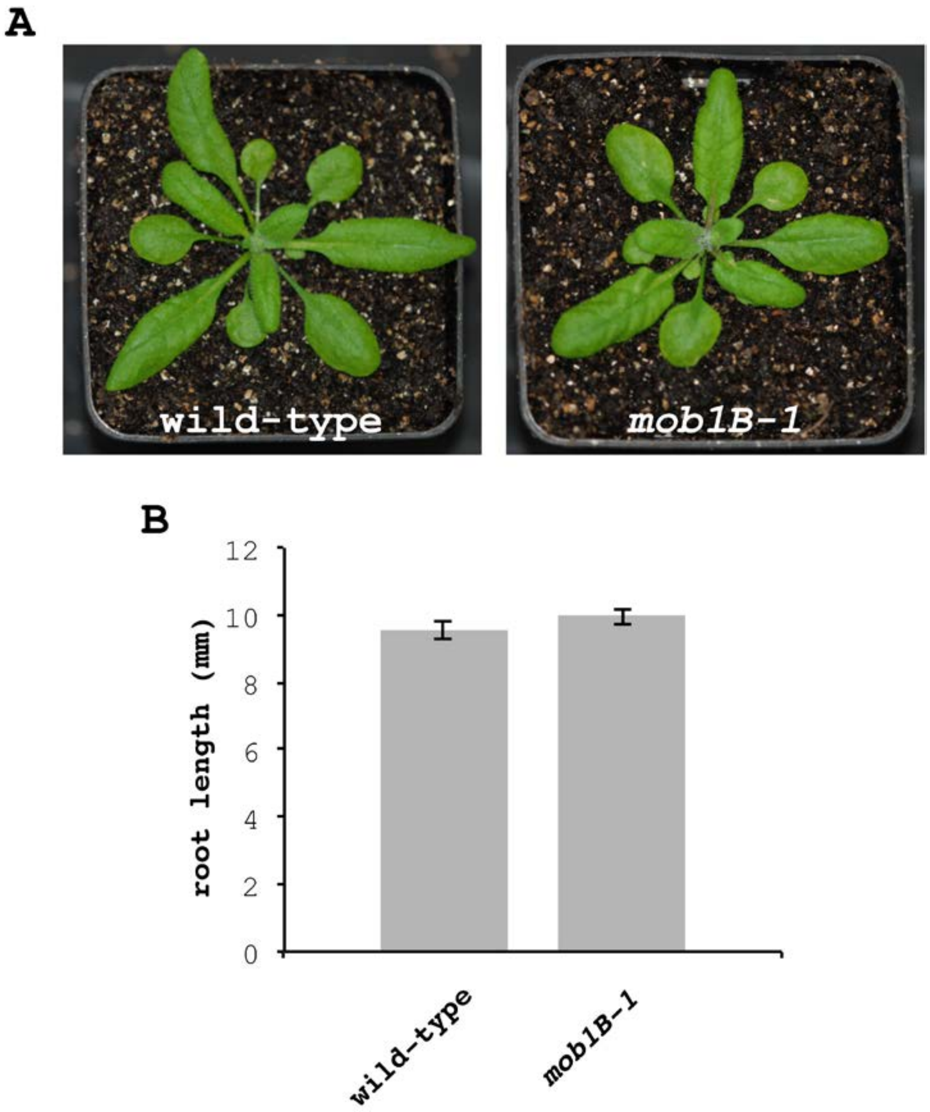
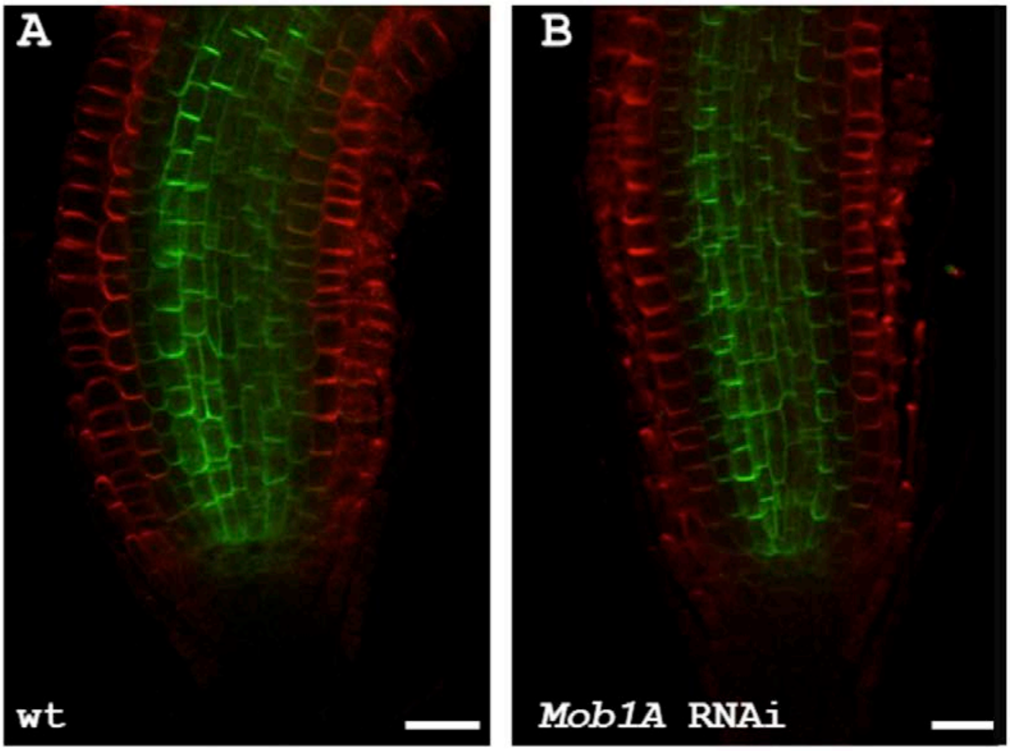


Figure S9. Flowers of wild-type and *mob1A-1* plants.

Figure S10. PIN1 and PIN2 immunolocalisation in roots of wild-type and *Mob1A* RNAi plants.



Also available:

Video – confocal microscopy *z*-stack of a *Mob1A* RNAi root tip with double staining of cell borders and starch granules.