Table 1: My caption

GEO Number	Reference	Tissue	Sample Size	Note
GSE36626	[18]	leaves	4	
GSE39463	[10]	leaves	12	48 samples (repeated measure)
GSE51304	[17]	leaves	18	
GSE54677	[12]	leaves	20	
GSE48235	[9]	leaves	6	
GSE51119	[19]	seedling	10	
GSE32202	NA	seedling	6	
GSE37159	NA	seedling	8	
GSE38400	[20]	seedling	12	
GSE41766	[1]	seedling	6	
GSE43703	[8]	seedling	4	8 samples (the removed 4 have low mapping quality $< 50\%$)
GSE43865	[16]	seedling	6	42 samples (repeated measure)
GSE51772	[14]	seedling	8	
GSE53078	[5]	seedling	4	
GSE60835	[4]	seedling	6	12 samples(not sure about the ecotype of the other 6)
GSE35288	[13]	flower	6	
GSE35408	[2]	hypocotyl	10	
GSE52966	[3]	primary root	18	
GSE56326	NA	carpels	8	
GSE59167	[15]	root tip tissue	11	
GSE59637	[11]	inflorescences and siliques	4	
GSE62799	[6]	aerial tissue	6	
GSE63355	[7]	shoot apical meristem	16	

Table 2: My caption

GEO Number	Reference	Tissue	N	Note	Map quality(≥)
GSE36626	[18]	leaves	4		85.50%
GSE39463	[10]	leaves	12	it contains 48 samples (Used One time point)	74.50%
GSE51304	[17]	leaves	18	18 RNA-Seq	88.40%
GSE54677	[12]	leaves	20	20 RNA-Seq	85.20%
GSE48235	[9]	leaves	6		90.40%
GSE51119	[19]	seedling	10		70.50%
GSE32202	NA	seedling	6		84.30%
GSE37159	NA	seedling	8		82.50%
GSE38400	[20]	seedling	12	PCA	45.90%–59.6%
GSE41766	[1]	seedling	6		85.20%
GSE43703	[8]	seedling	4	8 samples (mapping quality 23-46% removed)	55.50%–68.4%
GSE43865	[16]	seedling	6	42 samples (one time point)	92.50%
GSE51772	[14]	seedling	8		90.60%
GSE53078	[5]	seedling	4		86.10%
GSE60835	[4]	seedling	6	12 samples(not sure about the ecotype of the other 6)	65.60%–85.6%
GSE35288	[13]	flower	6	removed duplicated column	76.50%
GSE35408	[2]	hypocotyl	10		77.00%
GSE52966	[3]	primary root	18		87.20%
GSE56326	NA	carpels	8		92.40%
GSE59167	[15]	root tip tissue	11		87.10%
GSE59637	[11]	inflorescences and siliques	4		71.70%
GSE62799	[6]	aerial tissue	6		89.30%
GSE63355	[7]	shoot apical meristem	16		87.90%

References

[1] M.-Y. Bai, M. Fan, E. Oh, and Z.-Y. Wang. A triple helix-loop-helix/basic helix-loop-helix cascade controls cell elongation downstream of multiple hormonal and environmental signaling pathways in arabidopsis. *The Plant Cell*, 24(12):4917–4929, 2012.

[2] M.-Y. Bai, J.-X. Shang, E. Oh, M. Fan, Y. Bai, R. Zentella, T.-p. Sun, and Z.-Y. Wang. Brassinosteroid, gibberellin and phytochrome impinge on a common transcription module in arabidopsis. *Nat. Cell Biol.*, 14(8):810–817, 2012.

[3] J. Chaiwanon and Z.-Y. Wang. Spatiotemporal brassinosteroid signaling and antagonism with auxin pattern stem cell dynamics in arabidopsis roots. *Curr. Biol.*, 25(8):1031–1042, 2015.

[4] J. Dong, D. Tang, Z. Gao, R. Yu, K. Li, H. He, W. Terzaghi, X. W. Deng, and H. Chen. Arabidopsis de-etiolated1 represses photomorphogenesis by positively regulating phytochrome-interacting factors in the dark. *The Plant Cell*, 26(9):3630–3645, 2014.

[5] M. Fan, M.-Y. Bai, J.-G. Kim, T. Wang, E. Oh, L. Chen, C. H. Park, S.-H. Son, S.-K. Kim, M. B. Mudgett, et al. The bhlh transcription factor hbi1 mediates the trade-off between growth and pathogen-associated molecular pattern–triggered immunity in arabidopsis. *The Plant Cell*, 26(2):828–841, 2014.

[6] M. Groth, H. Stroud, S. Feng, M. V. Greenberg, A. A. Vashisht, J. A. Wohlschlegel, S. E. Jacobsen, and I. Ausin. SNF2 chromatin remodeler-family proteins FRG1 and-2 are required for RNA-directed DNA methylation. *P. Natl. Acad. Sci. USA*, 111(49):17666–17671, 2014.

[7] C.-H. Liu, A. Finke, M. Díaz, W. Rozhon, B. Poppenberger, T. Baubec, and A. Pecinka. Repair of dna damage induced by the cytidine analog zebularine requires atr and atm in arabidopsis. *The Plant Cell*, 27(6):1788–1800, 2015.

[8] M.-J. Liu, S.-H. Wu, J.-F. Wu, W.-D. Lin, Y.-C. Wu, T.-Y. Tsai, H.-L. Tsai, and S.-H. Wu. Translational landscape of photomorphogenic arabidopsis. *The Plant Cell*, 25(10):3699–3710, 2013.

[9] N. Liu, Y. Ding, M. Fromm, and Z. Avramova. Different gene-specific mechanisms determine the revised-responsememory transcription patterns of a subset of A. thaliana dehydration stress responding genes. *Nuc. Acids Res.*, 42(9):5556–5566, 2014.

[10] T. Maekawa, B. Kracher, S. Vernaldi, E. V. L. van Themaat, and P. Schulze-Lefert. Conservation of NLR-triggered immunity across plant lineages. *P. Natl. Acad. Sci. USA*, 109(49):20119–20123, 2012.

[11] C. Mizzotti, I. Ezquer, D. Paolo, P. Rueda-Romero, R. F. Guerra, R. Battaglia, I. Rogachev, A. Aharoni, M. M. Kater, E. Caporali, et al. SEEDSTICK is a master regulator of development and metabolism in the Arabidopsis seed coat. *PLoS Genet.*, 10(12):e1004856, 2014.

[12] G. Moissiard, S. Bischof, D. Husmann, W. A. Pastor, C. J. Hale, L. Yen, H. Stroud, A. Papikian, A. A. Vashisht, J. A. Wohlschlegel, et al. Transcriptional gene silencing by Arabidopsis microrchidia homologues involves the formation of heteromers. *P. Natl. Acad. Sci. USA*, 111(20):7474–7479, 2014.

[13] C. E. Niederhuth, O. R. Patharkar, and J. C. Walker. Transcriptional profiling of the Arabidopsis abscission mutant hae hsl2 by RNA-Seq. *BMC Genomics*, 14(1):37, 2013.

[14] E. Oh, J.-Y. Zhu, M.-Y. Bai, R. A. Arenhart, Y. Sun, and Z.-Y. Wang. Cell elongation is regulated through a central circuit of interacting transcription factors in the arabidopsis hypocotyl. *Elife*, 3:e03031, 2014.

[15] H. Pallakies and R. Simon. The CLE40 and CRN/CLV2 signaling pathways antagonistically control root meristem growth in arabidopsis. *Mol. Plant*, 7(11):1619–1636, 2014.

[16] M. L. Rugnone, A. F. Soverna, S. E. Sanchez, R. G. Schlaen, C. E. Hernando, D. K. Seymour, E. Mancini, A. Chernomoretz, D. Weigel, P. Más, et al. Lnk genes integrate light and clock signaling networks at the core of the arabidopsis oscillator. *P. Natl. Acad. Sci. USA*, 110(29):12120–12125, 2013.

[17] H. Stroud, T. Do, J. Du, X. Zhong, S. Feng, L. Johnson, D. J. Patel, and S. E. Jacobsen. Non-CG methylation patterns shape the epigenetic landscape in Arabidopsis. *Nat. Struct. Mol. Biol.*, 21(1):64–72, 2014.

[18] H. Wollmann, S. Holec, K. Alden, N. D. Clarke, P.-E. Jacques, and F. Berger. Dynamic deposition of histone variant H3. 3 accompanies developmental remodeling of the Arabidopsis transcriptome. *PLoS Genet.*, 8(5):e1002658, 2012.

[19] M. K. Zhiponova, K. Morohashi, I. Vanhoutte, K. Machemer-Noonan, M. Revalska, M. Van Montagu, E. Grotewold, and E. Russinova. Helix–loop–helix/basic helix–loop–helix transcription factor network represses cell elongation in Arabidopsis through an apparent incoherent feed-forward loop. *P. Natl. Acad. Sci. USA*, 111(7):2824–2829, 2014.

[20] Y. Zhu, M. J. Rowley, G. Böhmdorfer, and A. T. Wierzbicki. A swi/snf chromatin-remodeling complex acts in noncoding rna-mediated transcriptional silencing. *Mol. Cell*, 49(2):298–309, 2013.