

Supplementary Table S1

Table S1: Summary of data sets used in the three groups: the seedling, the leaf and the multi-tissue groups.

GEO Number	Reference	Tissue	N	Quality ¹ (\geq)
GSE32202	NA	seedling	6	84.30%
GSE37159	NA	seedling	8	82.50%
GSE41766	[1]	seedling	6	85.20%
² GSE43865	[18]	seedling	6	92.50%
GSE51119	[21]	seedling	10	70.50%
GSE51772	[16]	seedling	8	90.60%
GSE53078	[6]	seedling	4	86.10%
³ GSE60835	[5]	seedling	6	65.60%
GSE66666	[3]	seedling	6	91.20%
GSE36626	[20]	leaves	4	85.50%
⁴ GSE39463	[12]	leaves	12	74.50%
GSE48235	[10]	leaves	6	90.40%
⁵ GSE51304	[19]	leaves	18	88.40%
⁶ GSE54677	[14]	leaves	20	85.20%
GSE35288	[15]	flower	6	76.50%
GSE35408	[2]	hypocotyl	10	77.00%
GSE52966	[4]	primary root	18	87.20%
GSE56326	NA	carpels	8	92.40%
GSE59167	[17]	root tip tissue	11	87.10%
GSE59637	[13]	inflorescences and siliques	4	71.70%
GSE60183	[8]	epidermis	6	62.30%
GSE61061	[11]	seed	6	91.60%
GSE62799	[7]	aerial tissue	6	89.30%
GSE63355	[9]	shoot apical meristem	16	87.90%

¹The number of mapped reads divided by the total number of reads in the sample

²We chose all the 6 samples at the onset of treatment out of the 42 samples.

³We chose the samples of ecotype Columbia from the 12 samples.

⁴We chose all samples at 6 hours post inoculation out of the 48 samples.

⁵Out of the 48 samples, the total number of RNA-Seq samples is 18.

⁶Out of the 24 samples, the total number of RNA-Seq samples is 20.

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