SUPPLEMENTARY FIGURES AND TABLES FOR

WUSCHEL acts as an auxin response rheostat to maintain apical stem cells in *Arabidopsis*

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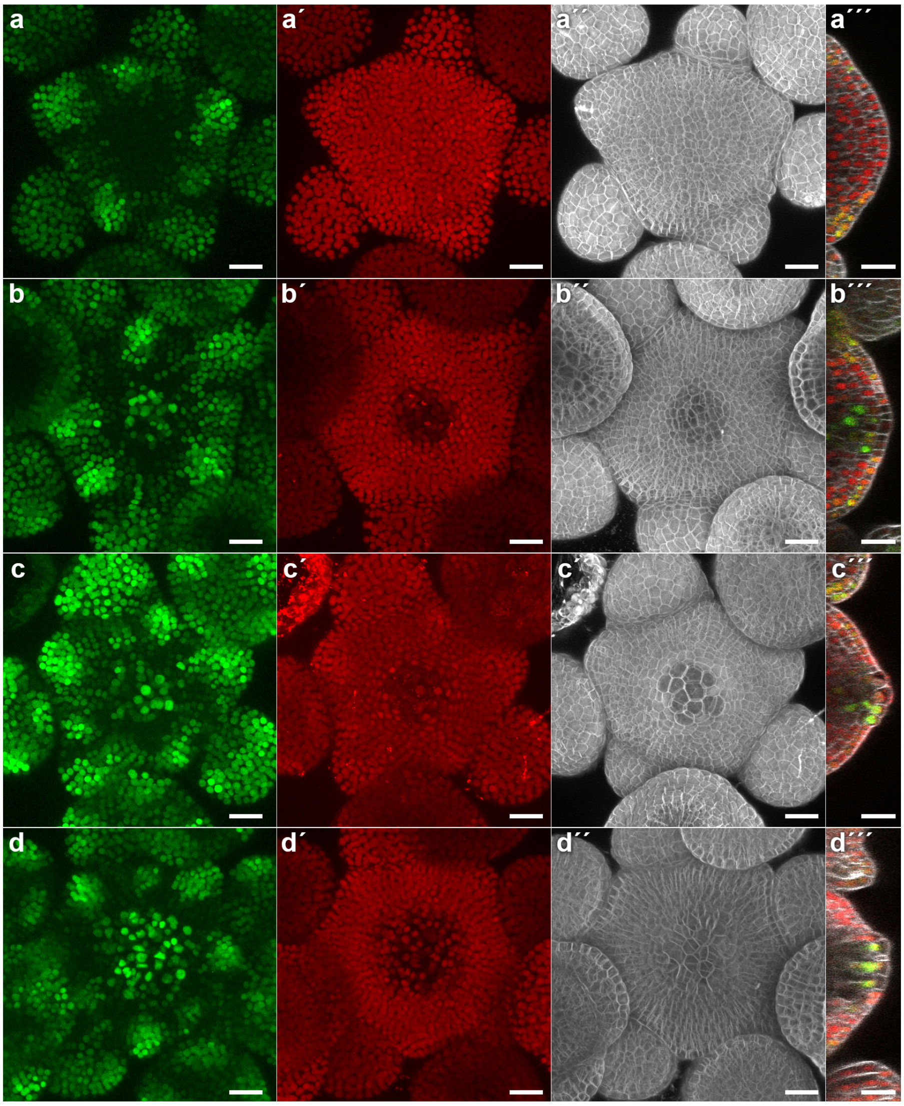
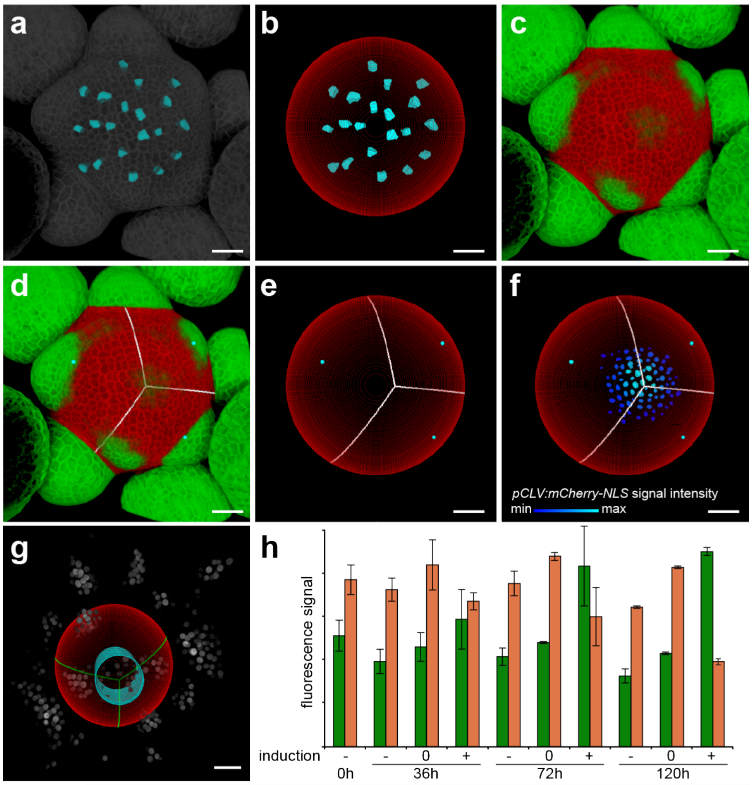


Supplementary Fig. 1: Activation of DR5v2 and differentiation after induced stem cell loss.

Representative SAMs of the imaged cohorts quantified in Fig. 2f and Supplementary Fig 2. A) 0h after induction B) 36h after induction C) 72h after induction D) 120h after induction. Left panels show *pDR5v2:3xVENUS-NLS* signal, middle panels show *pRPS5a:NLS-tdTomato* and right panels show DAPI stained cell walls. Small panels on the far-right show Z-projections of all channels through the center of the SAM. Scale bars 20 μm.



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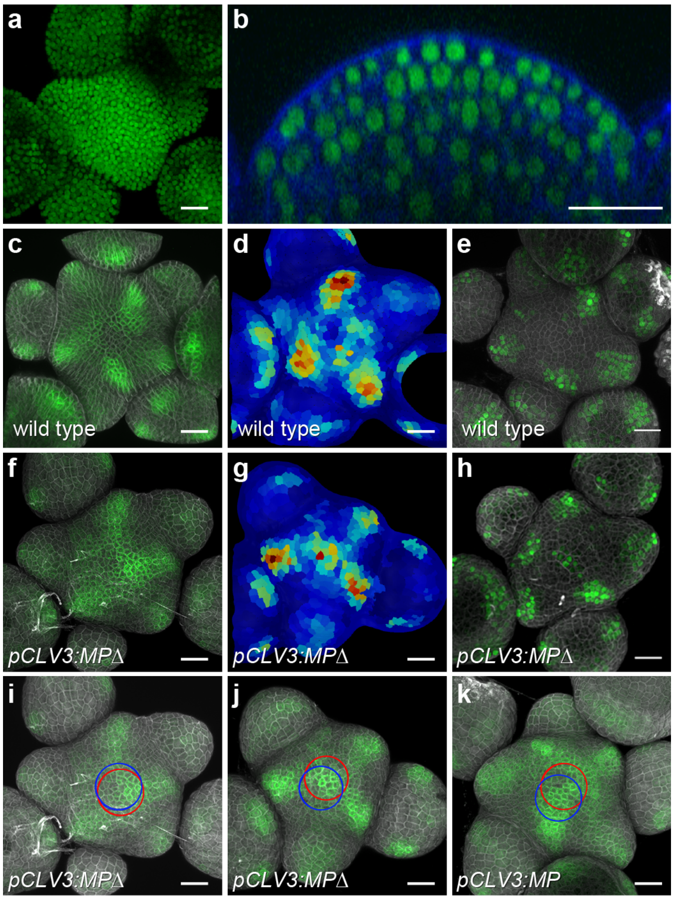
	induced			untreated		
	pRPS5A +	pRPS5A -	DR5v2 +	pRPS5A +	pRPS5A -	DR5v2 +
0h	-	-	-	7	0	0
36h	3	**4**	**4**	7	0	0
72h	2	**5**	**5**	7	0	0
120h	2	**2**	**2**	4	0	0

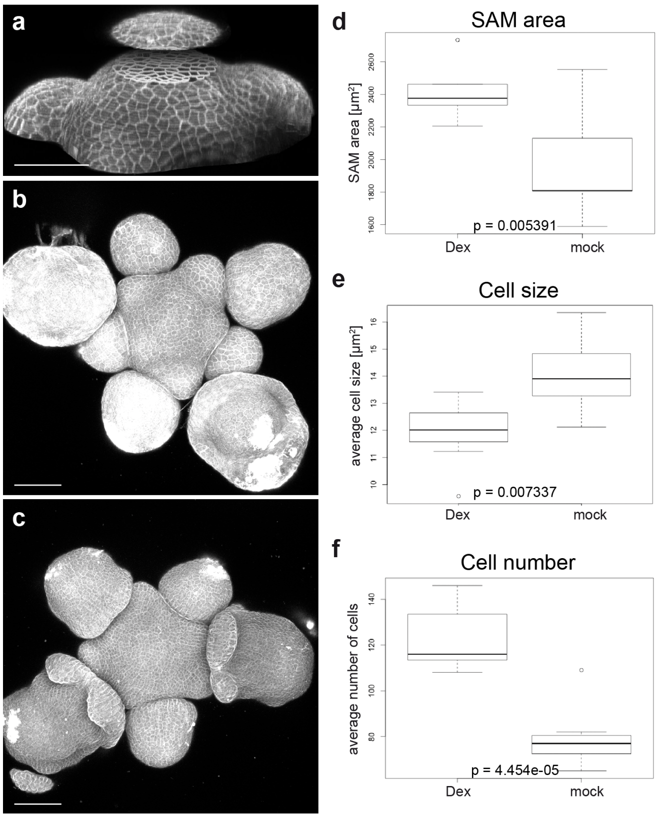
Supplementary Figure 2: Computational strategy to identify stem cells and DR5v2 quantification.

a) In a first step, cells across the L1 of the SAM are segmented. **b)** Based on the position of segmented cells, a perfect sphere is fitted to the SAM. **c)** The sphere is applied to the SAM and organ primordia are identified by emergence through the sphere. **d, e)** Equidistant points between the primordia are calculated and used to triangulate the center of the SAM. **f)** The triangulated center was benchmarked against SAMs harboring *pCLV3* reporter labelled stem cells (n=9). The triangulation invariantly identified one of the most central *pCLV3* positive cells. See also Methods. **g)** For signal quantification in the stem cell domain, a cylinder with radius r_{cyl} (= 1/3 * r_{sphere}) mimicking the average size of the *CLV3* domain was placed into the computationally identified center of the SAM and fluorescence intensities were quantified within this narrowly defined subdomain. DR5v2-NLS signals are shown in grey, SAM sphere derived from segmentation in red, triangulation lines in green and quantification cylinder in cyan. **h)** Quantification of fluorescent signals from all SAMs of the stem cell loss experiment described in Fig. 2 and Supplementary Fig. 1. Total fluorescence signal intensities for *pDR5v2:3xVENUS-NLS* and *pRPS5a:NLS-tdTomato* for the inner region (I_{cyl}) and for the peripheral region (I_{sphere}) were extracted from respective image volumes. I_{cyl} was averaged over all plants for each time-point and condition and normalized to the overall signal ($I_{cyl} + I_{sphere}$). Green bars: DR5v2:3xVENUS-NLS signal, orange bars: pRPS5a:NLS-tdTomato signal. - : mock treated, 0: ethanol induced, but no observable stem cell loss, + : ethanol induced and stem cell loss. **i)** Quantification of DR5v2 response to induction of iCalSm at the per plant level. Number of plants scored for loss of *RPS5a* promoter activity from stem cells and DR5v2 expression are shown. Stem cell loss and associated DR5v2 activation exclusively occurred in induced plants. All plants with stem cell loss as shown by reduced *pRPS5a* activity expressed DR5v2. *pRPS5a* + denotes plants with uncompromised *pRPS5a* promoter activity in stem cells. *pRPS5a* - denotes plants with reduced *pRPS5a* promoter activity in stem cells. DR5v2 + denotes plants with DR5v2 activity in stem cells. Scale bars 20 μm.



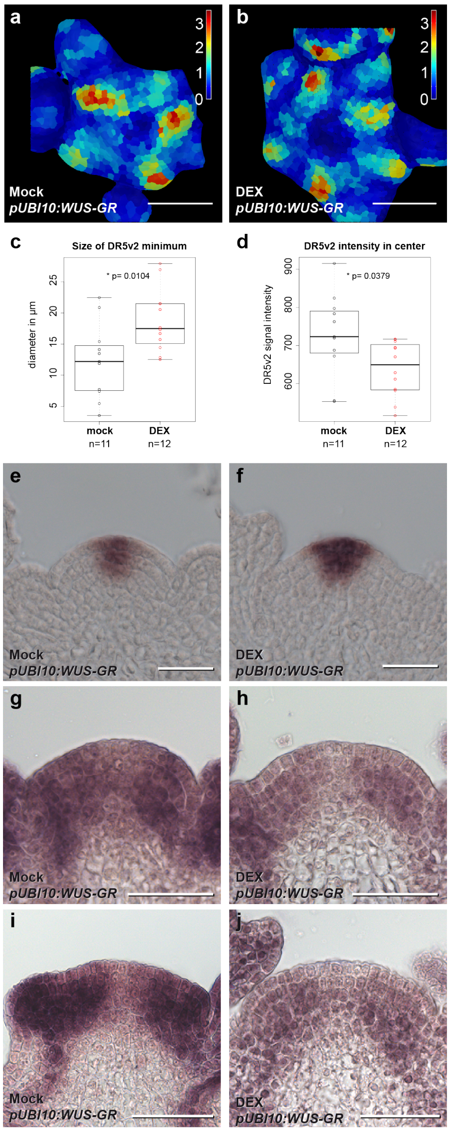
Supplementary Figure 3: Activity of the *pHMG* promoter, behavior of nuclear and ER localized DR5v2 reporters and auxin signaling output in wild type and *pCLV3:MPΔ* lines.

a, b) Transgenic line carrying 1347 bp upstream of the At1g76110 locus fused to the *GFP-NLS* coding sequence. **a)** GFP channel in top view. **b)** Side view though a representative SAM showing DAPI and GFP channel. **c)** *pDR5v2:ER-EYFP-HDEL* in wild type. **d)** Per cell quantification of an independent *pDR5v2:ER-EYFP-HDEL* wild-type SAM. **e)** *pDR5v2:3xVENUS-NLS* in wild type. **f-k)** Auxin signaling output was present in the center of *pCLV3:MP* and *pCLV3:MPΔ* lines, indicated by two independent reporters *pDR5v2:ER-EYFP-HDEL* (6 out of 8 independent T1 plants) (F) and *pDR5v2:3xVENUS-NLS* (6 out of 7 independent T1 plants) (H). **g)** Per cell quantification of *pDR5v2:ER-EYFP-HDEL* in an independent *pCLV3:MPΔ* SAM. DR5v2 activity was not observed in the center of wild-type SAMs grown in the same experiments. **i-k)** Computationally derived central zone in L1 (red) and L3 (blue) are superimposed to SAMs of *pDR5v2:ER-EYFP-HDEL* carrying *pCLV3:MPΔ* (I, J) and *pCLV3:MP* (K). DR5v2 signal clearly coincides with central zone. Scale bars 20 μm.



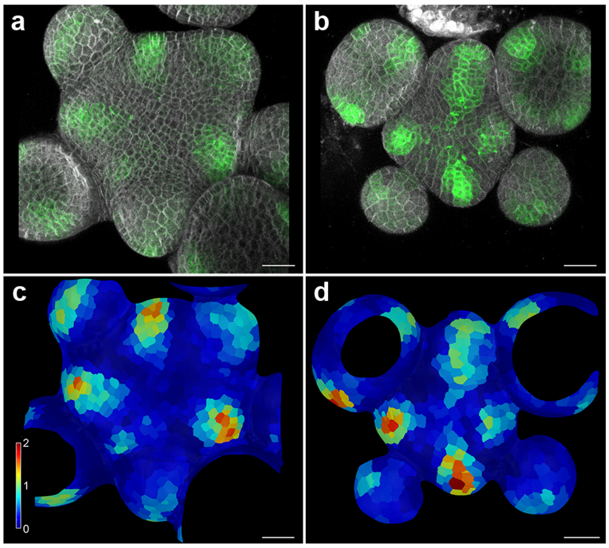
Supplementary Figure 4: Morphological effects of WUS-GR induction.

a) Visualization of meristem morphology analysis strategy. Meristem size, cell count and average cell size were measured at a constant relative position defined by the image plane in which the L1 to L2 transition became visible. **b)** Mock treated and **c)** DEX induced *pUBI:mCherry-GR-linker-WUS* SAMs four days after local application. Following WUS induction, SAM size increased **(d)**, cell size decreased **(e)** and cell number strongly increased **(f)** n= 7 and 8 meristems, respectively. p-values derived by t-test. Scale bars 50 *µ*m.



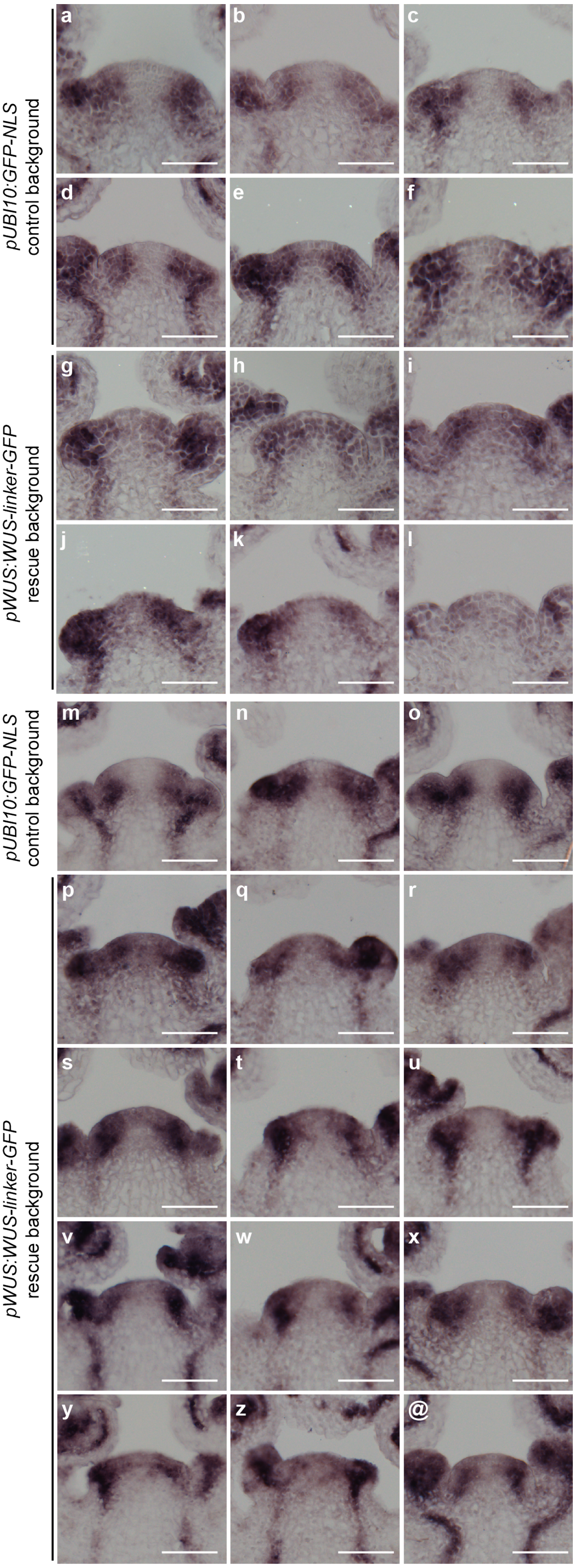
Supplementary Figure 5: SAM specific molecular responses to ectopic WUS induction in *pUBI10:WUS-GR lines*.

24 hours after induction of ectopic WUS-GR activity, DR5v2 signal in the central zone was suppressed and *CLV3* mRNA expression was enhanced. Representative in situ quantifications of DR5v2 signal after mock **(a)** and DEX **(b)** treatments. **c)** Quantification of the size of the central DR5v2 minimum. **d)** Quantification of the average DR5v2 signal intensity in the central zone. p-values derived by t-test. **e)** *CLV3* mRNA expression after 24 hours of mock treatment. **f)** *CLV3* mRNA expression after 24 hours of DEX treatment. **g)** *TIR1* mRNA expression after 24 hours of mock treatment. **h)** *TIR1* mRNA expression after 24 hours of DEX treatment. **i)** *MP* mRNA expression after 24 hours of mock treatment. **j)** *MP* mRNA expression after 24 hours of DEX treatment. SAMs of both treatment types were hybridized on the same microscopic slide and imaged under identical settings. Scale bars 50 μm.



Supplementary Figure 6: SAMs of *wus-7* plants show auxin signaling output in the stem cell domain.

a) Representative image of *pDR5v2:ER-eYFP-HDEL* signal in the SAM of L*er* wild-type plants. Only 16% of plants showed DR5v2 activity in the center of the SAM (n=38). **b)** Representative image of *pDR5v2:ER-eYFP-HDEL* signal in a *wus-7* SAM before termination. 61% of *wus-7* plants showed DR5v2 activity in the center of the SAM (n=13). Per cell quantification of DR5v2 signal in wild type (**c**) and *wus-7* (**d**). Scale bars 20 μm.

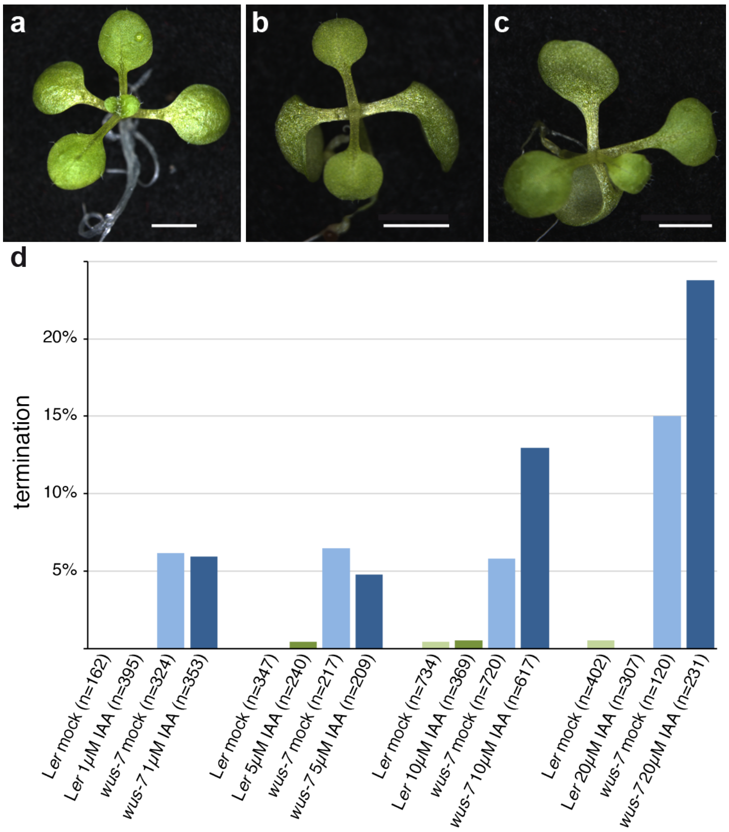


Supplementary Figure 7: *MP* mRNA expression after induced WUS loss of function in two independent experiments.

a-l) Experiment I. a-f) In situ detection of *MP* mRNA in *pUBQ10:GFP-NLS* control plants carrying *pCLV3:AlcR/AlcA:NSlmb-vhhGFP4* after 24h of ethanol treatment. **g-l)** In situ detection of *MP* mRNA in stable *pWUS:WUS-linker-GFP wus* rescue plants carrying *pCLV3:AlcR/AlcA:NSlmb-vhhGFP4* after 24h of ethanol treatment.

m-@) Experiment II. m-o) In situ detection of *MP* mRNA in *pUBQ10:GFP-NLS* control plants carrying *pCLV3:AlcR/AlcA:NSlmb-vhhGFP4* after 24h of ethanol treatment. **p-@)** In situ detection of *MP* mRNA in stable *pWUS:WUS-linker-GFP wus* rescue plants carrying *pCLV3:AlcR/AlcA:NSlmb-vhhGFP4* after 24h of ethanol treatment.

SAMs of both genotypes were hybridized in sets of two independent experiments and imaged under identical settings. Unadjusted images are shown. Scale bars 50 μm.



Supplementary Figure 8: Seedling phenotypes eleven days after germination on auxin supplemented plates and SAM termination frequencies on increasing auxin concentrations.

Phenotypes of seedlings grown on plates containing 10 µm IAA ranged from **a)** unaffected, to **b)** arrested at four leaves stage, or **c)** arrested at five leaves stage with a terminal leaf. **d)** Quantification of terminated seedlings grown on plates containing various concentrations of auxin. Wild-type L*er* and *wus-7* seedlings were tested on 1-20 µM IAA, termination in wus-7 starts to occur on 10µM IAA, wild type is resistant to even 20 µM IAA. Scale bars 1 mm.

	GO ID	Term	Annotated genes	Significant genes	Expected	p-Value
1	GO:0010200	response to chitin	393	145	55.45	2.80E-30
2	GO:0009611	response to wounding	313	109	44.16	1.00E-20
3	GO:0010363	regulation of plant-type hypersensitive response	336	111	47.41	4.60E-19
4	GO:0006612	protein targeting to membrane	340	111	47.97	1.30E-18
5	GO:0009414	response to water deprivation	374	130	52.77	5.70E-18
6	GO:0009867	jasmonic acid mediated signaling pathway	256	89	36.12	1.20E-15
7	GO:0009733	response to auxin	354	107	49.95	2.30E-15
8	GO:0002679	respiratory burst involved in defense response	114	50	16.09	1.10E-14
9	GO:0009737	response to abscisic acid	548	174	77.32	1.10E-14
10	GO:0009738	abscisic acid-activated signaling pathway	232	78	32.74	1.10E-12
11	GO:0009651	response to salt stress	704	187	99.33	2.60E-12
12	GO:0009695	jasmonic acid biosynthetic process	125	49	17.64	3.40E-12
13	GO:0006857	oligopeptide transport	97	41	13.69	1.10E-11
14	GO:0050832	defense response to fungus	303	84	42.75	3.30E-10
15	GO:0009862	systemic acquired resistance. salicylic acid mediated signaling pathway	222	66	31.32	1.20E-09
16	GO:0042538	hyperosmotic salinity response	152	50	21.45	2.90E-09
17	GO:0009612	response to mechanical stimulus	59	27	8.32	4.50E-09
18	GO:0042742	defense response to bacterium	344	93	48.54	4.90E-09
19	GO:0009684	indoleacetic acid biosynthetic process	94	36	13.26	5.20E-09
20	GO:0006569	tryptophan catabolic process	67	29	9.45	6.00E-09
21	GO:0009723	response to ethylene	325	101	45.86	1.20E-08
22	GO:0009753	response to jasmonic acid	427	141	60.25	1.20E-08
23	GO:0009873	ethylene-activated signaling pathway	118	41	16.65	1.30E-08
24	GO:0009620	response to fungus	440	132	62.08	2.50E-08
25	GO:0000165	MAPK cascade	197	57	27.8	4.50E-08
26	GO:0009963	positive regulation of flavonoid biosynthetic process	93	34	13.12	5.30E-08
27	GO:0006355	regulation of transcription. DNA-templated	1588	296	224.07	7.10E-08
28	GO:0043069	negative regulation of programmed cell death	158	48	22.29	1.00E-07
29	GO:0009739	response to gibberellin	143	49	20.18	1.10E-07
30	GO:0031348	negative regulation of defense response	246	65	34.71	2.30E-07
31	GO:0009409	response to cold	539	118	76.05	4.20E-07
32	GO:0009750	response to fructose	127	39	17.92	1.10E-06
33	GO:0030968	endoplasmic reticulum unfolded protein response	171	48	24.13	1.30E-06
34	GO:0009693	ethylene biosynthetic process	110	35	15.52	1.60E-06
35	GO:0009805	coumarin biosynthetic process	51	21	7.2	2.00E-06
36	GO:0010310	regulation of hydrogen peroxide metabolic process	159	45	22.43	2.20E-06
37	GO:0030003	cellular cation homeostasis	146	42	20.6	3.00E-06
38	GO:0007623	circadian rhythm	156	44	22.01	3.20E-06
39	GO:0006833	water transport	118	36	16.65	3.40E-06
40	GO:0009741	response to brassinosteroid	102	37	14.39	3.60E-06
41	GO:0080167	response to karrikin	114	35	16.09	4.00E-06
42	GO:0002237	response to molecule of bacterial origin	97	31	13.69	5.60E-06
43	GO:0006979	response to oxidative stress	407	90	57.43	6.50E-06
44	GO:0006813	potassium ion transport	35	16	4.94	6.60E-06
45	GO:0046777	protein autophosphorylation	131	37	18.48	1.80E-05
46	GO:0006598	polyamine catabolic process	34	15	4.8	2.20E-05
47	GO:0035556	intracellular signal transduction	446	133	62.93	2.30E-05
48	GO:0009269	response to desiccation	31	14	4.37	3.00E-05
49	GO:0031347	regulation of defense response	485	146	68.43	3.00E-05
50	GO:0009825	multidimensional cell growth	96	29	13.55	3.70E-05
51	GO:0009697	salicylic acid biosynthetic process	181	46	25.54	3.70E-05
52	GO:0019344	cysteine biosynthetic process	181	46	25.54	3.70E-05
53	GO:0006970	response to osmotic stress	749	207	105.68	4.10E-05
54	GO:0070838	divalent metal ion transport	184	53	25.96	6.90E-05
55	GO:0009627	systemic acquired resistance	395	109	55.73	7.70E-05
56	GO:0006949	syncytium formation	19	10	2.68	8.30E-05
57	GO:0042398	cellular modified amino acid biosynthetic process	50	18	7.06	9.10E-05
58	GO:0009751	response to salicylic acid	423	122	59.69	9.80E-05
59	GO:0042631	cellular response to water deprivation	59	20	8.32	1.00E-04
60	GO:0009965	leaf morphogenesis	186	49	26.24	1.10E-04
61	GO:0010583	response to cyclopentenone	132	35	18.63	1.20E-04
62	GO:0001666	response to hypoxia	74	23	10.44	1.40E-04
63	GO:0007030	Golgi organization	160	40	22.58	1.70E-04
64	GO:0016126	sterol biosynthetic process	150	38	21.17	1.80E-04
65	GO:0019748	secondary metabolic process	527	133	74.36	2.20E-04
66	GO:0006468	protein phosphorylation	620	157	87.48	2.40E-04
67	GO:0006995	cellular response to nitrogen starvation	21	10	2.96	2.40E-04
68	GO:0009863	salicylic acid mediated signaling pathway	315	92	44.45	2.80E-04
69	GO:0009407	toxin catabolic process	180	43	25.4	2.90E-04
70	GO:0009595	detection of biotic stimulus	92	26	12.98	3.00E-04

	GO ID	Term	Annotated genes	Significant genes	Expected	p-Value
71	GO:0046686	response to cadmium ion	415	84	58.56	3.30E-04
72	GO:0006816	calcium ion transport	108	29	15.24	3.60E-04
73	GO:0042335	cuticle development	42	15	5.93	3.80E-04
74	GO:0009617	response to bacterium	499	140	70.41	4.00E-04
75	GO:0010264	myo-inositol hexakisphosphate biosynthetic process	51	17	7.2	4.10E-04
76	GO:0010119	regulation of stomatal movement	47	16	6.63	4.60E-04
77	GO:0043900	regulation of multi-organism process	115	30	16.23	4.90E-04
78	GO:0010017	red or far-red light signaling pathway	39	14	5.5	5.60E-04
79	GO:0010260	animal organ senescence	27	11	3.81	6.30E-04
80	GO:0009740	gibberellic acid mediated signaling pathway	72	21	10.16	7.00E-04
81	GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	113	29	15.94	8.00E-04
82	GO:0015824	proline transport	68	20	9.59	8.30E-04
83	GO:0010227	floral organ abscission	32	12	4.52	8.80E-04
84	GO:0052541	plant-type cell wall cellulose metabolic process	24	10	3.39	9.00E-04
85	GO:0010158	abaxial cell fate specification	7	5	0.99	9.10E-04
86	GO:0009742	brassinosteroid mediated signaling pathway	37	13	5.22	1.10E-03
87	GO:0048767	root hair elongation	164	38	23.14	1.17E-03
88	GO:0010118	stomatal movement	86	32	12.13	1.68E-03
89	GO:0009694	jasmonic acid metabolic process	147	58	20.74	1.71E-03
90	GO:0033500	carbohydrate homeostasis	12	8	1.69	1.74E-03
91	GO:0007231	osmosensory signaling pathway	5	4	0.71	1.75E-03
92	GO:2000022	regulation of jasmonic acid mediated signaling pathway	5	4	0.71	1.75E-03
93	GO:0010037	response to carbon dioxide	5	4	0.71	1.75E-03
94	GO:0009624	response to nematode	72	20	10.16	1.80E-03
95	GO:0006766	vitamin metabolic process	77	21	10.86	1.80E-03
96	GO:0006865	amino acid transport	228	61	32.17	2.09E-03
97	GO:0000038	very long-chain fatty acid metabolic process	44	14	6.21	2.14E-03
98	GO:0046885	regulation of hormone biosynthetic process	8	5	1.13	2.15E-03
99	GO:0050801	ion homeostasis	205	59	28.93	2.26E-03
100	GO:0052546	cell wall pectin metabolic process	40	13	5.64	2.47E-03

Supplementary Table 1: GO category enrichment analysis of direct WUS targets. Top 100 enriched categories are shown. As a background set for calculating enrichment, we used genes in open chromatin[28].

		ChIP-seq					RNA-seq	
AGI	**Gene Name**	**peaks**	Ac	deAc	Me	deMe	**Log2FC**	**p adj.**
AT1G59750	ARF1	0	-	+	-	-	-0.09	4.26E-01
AT5G62000	ARF2	1	+	-	-	-	-0.14	7.01E-02
AT2G33860	ARF3	1	+	-	-	-	0.78	2.11E-06
AT5G60450	ARF4	1	-	+	-	-	-1.26	4.76E-18
AT1G19850	ARF5	1	-	-	-	-	0.86	1.25E-04
AT1G30330	ARF6	5	+	+	-	-	0.29	1.40E-02
AT5G20730	ARF7	0	+	-	-	-	0.17	2.46E-01
AT5G37020	ARF8	1	-	-	-	-	-1.58	8.52E-20
AT4G23980	ARF9	1	-	-	-	-	1.15	5.92E-25
AT2G28350	ARF10	2	+	-	-	-	0.85	9.49E-04
AT2G46530	ARF11	1	-	-	-	+	0.93	4.27E-07
AT1G34310*	ARF12	0	-	-	-	-	0	1
AT1G34170*	ARF13	0	-	-	-	-	0	1
AT1G35540*	ARF14	0	-	-	-	-	0	1
AT1G35520*	ARF15	0	-	-	-	-	0	1
AT4G30080	ARF16	0	+	-	-	-	0.14	6.29E-01
AT1G77850	ARF17	0	+	-	-	-	0.87	4.19E-05
AT3G61830*	ARF18	0	+	+	-	-	0.99	7.48E-15
AT1G19220	ARF19	0	+	-	-	-	1.12	2.96E-09
AT1G35240*	ARF20	0	-	-	-	-	0	1
AT1G34410*	ARF21	0	-	-	-	-	0	1
AT1G34390*	ARF22	0	-	-	-	-	0	1
AT1G43950*	ARF23	0	-	-	-	-	0	1
AT4G14560	IAA1	1	-	-	-	-	-0.03	9.48E-01
AT3G23030	IAA2	2	-	+	-	-	-0.76	2.39E-21
AT1G04240	SHY2	2	-	-	-	-	3.22	4.66E-121
AT5G43700	ATAUX2-11	1	-	+	-	-	-0.45	2.15E-05
AT1G15580*	IAA5	0	-	-	-	-	0	1
AT1G52830	IAA6	2	-	+	-	-	0	1
AT3G23050	IAA7	1	-	-	-	+	0.57	4.02E-07
AT2G22670	IAA8	2	-	+	-	-	1.39	6.40E-43
AT5G65670	IAA9	2	-	-	-	-	0.12	1.41E-01
AT1G04100*	IAA10	0	-	-	-	-	-1.71	2.57E-14
AT4G28640	IAA11	0	-	-	-	-	-0.68	1.26E-02
AT1G04550	IAA12	1	-	-	-	-	-0.56	1.27E-02
AT2G33310	IAA13	1	-	+	-	-	-1.00	2.41E-15
AT4G14550	IAA14	2	-	-	-	-	-0.58	6.37E-03
AT1G80390	IAA15	0	-	-	-	+	0	1
AT3G04730	IAA16	1	-	+	-	-	-0.39	2.49E-09
AT1G04250	AXR3	1	-	-	-	+	0.67	1.70E-04
AT1G51950	IAA18	3	-	+	-	-	-0.75	2.02E-11
AT3G15540	IAA19	2	+	-	-	+	1.44	1.10E-03
AT2G46990	IAA20	1	-	-	-	+	1.93	4.30E-16
AT3G16500	PAP1	2	+	-	-	-	-1.48	1.32E-35
AT4G29080	PAP2	1	-	-	-	-	0.88	7.44E-07
AT5G25890	IAA28	0	-	+	-	-	-0.28	2.54E-01
AT4G32280	IAA29	0	-	-	-	-	1.97	3.36E-07
AT3G62100	IAA30	0	-	-	-	-	1.18	9.73E-04
AT3G17600*	IAA31	0	-	-	-	-	0	1
AT2G01200*	IAA32	0	-	-	-	-	2.88	8.13E-02
AT1G15050*	IAA34	0	+	-	-	-	-0.44	4.35E-01
AT4G03190	AFB1	0	+	-	-	-	-1.55	3.32E-12
AT3G26810	AFB2	2	-	+	-	-	-0.15	3.61E-01
AT1G12820	AFB3	0	+	+	-	-	1.20	1.29E-40
AT4G24390	AFB4	0	-	-	-	-	0.58	1.03E-03
AT5G49980	AFB5	1	+	-	-	-	0.48	4.95E-05
AT3G62980	TIR1	1	-	+	-	-	-0.87	4.91E-18
AT1G73590	PIN1	1	+	+	-	-	0.13	7.71E-01
AT5G57090	PIN2	0	-	-	-	-	0.68	7.34E-02
AT1G70940	PIN3	2	+	+	-	-	-1.17	1.85E-27
AT2G01420	PIN4	3	+	+	+	-	0.36	2.92E-05
AT5G16530*	PIN5	0	-	-	-	-	-0.98	7.92E-01
AT1G77110	PIN6	1	-	+	-	+	1.57	5.68E-02
AT1G23080	PIN7	2	-	-	-	-	-0.17	3.05E-01
AT5G15100	PIN8	0	-	-	-	+	0	1
AT2G38120	AUX1	2	-	-	-	+	0.91	3.36E-10
AT5G01240	LAX1	2	-	-	-	+	0.16	2.08E-01
AT2G21050	LAX2	0	-	-	-	-	0.46	1.45E-01
AT1G77690	LAX3	1	-	-	-	-	0.01	9.65E-01
AT2G34650	PID	2	-	-	-	+	0.35	1.04E-01
AT2G26700	PID2	0	-	-	-	-	-0.11	8.31E-01

Supplementary Table 2: Response of genes with activities in auxin signaling to WUS.

Adjusted p-value for RNA-seq data (WUS-GR, DEX vs. mock) was calculated using the Benjamini-Hochberg method in DESeq2. Asterisks denote genes in regions with closed chromatin[28]. ChIP-seq results for WUS binding, acetylation and methylation are given. Peaks column denotes number of WUS binding events at the locus; Ac denotes increase of acetylation at the locus, deAc denotes reduction in acetylation at the locus; Me denotes increase of methylation at the locus, deMe denotes reduction in methylation at the locus. Processed raw data including read counts can be found in Supplementary File 1.

AGI	Gene Name	WUS peaks	Ac	deAc	Me	deMe	Log2FC	p adj.
AT3G28970	AAR3	0	-	+	-	-	-0.15	6.05E-01
AT2G36910	ABCB1	1	-	-	-	-	0.29	1.89E-01
AT1G10680	ABCB10	1	-	+	-	+	0	1
AT1G27940	ABCB13	0	-	-	-	-	0	1
AT1G28010	ABCB14	0	+	+	-	-	0.22	3.46E-01
AT3G28345	ABCB15	0	-	-	-	+	2.29	2.67E-14
AT3G28360	ABCB16	0	-	-	+	+	0	1
AT3G28380	ABCB17	0	-	+	-	-	-0.69	8.20E-01
AT3G28390	ABCB18	0	-	-	-	+	0	1
AT3G28860	ABCB19	2	+	+	-	-	-0.55	4.02E-04
AT4G25960	ABCB2	0	+	-	-	-	0.75	3.93E-07
AT3G55320	ABCB20	0	-	-	-	-	0.48	8.69E-03
AT3G62150	ABCB21	0	-	-	-	-	-2.94	2.89E-108
AT3G28415	ABCB22	0	-	-	-	+	0	1
AT5G03910	ABCB29	0	-	+	-	-	-0.15	1.77E-01
AT2G47000	ABCB4	1	+	-	-	-	-0.26	3.71E-01
AT2G39480	ABCB6	2	-	-	-	-	-0.47	1.12E-03
AT1G59870	ABCG36	1	-	-	-	-	-1.90	3.99E-66
AT3G53480	ABCG37	0	+	-	-	-	-0.82	3.26E-03
AT1G15520	ABCG40	0	-	-	-	-	0.40	5.02E-02
AT4G26080	ABI1	0	-	+	-	-	-0.80	2.21E-18
AT3G24650	ABI3	1	+	-	-	+	1.14	4.23E-01
AT2G05710	ACO3	0	-	+	-	-	-0.82	6.22E-18
AT2G22810	ACS4	1	-	-	-	+	0	1
AT4G11280	ACS6	3	-	-	-	-	-0.49	5.50E-04
AT5G09810	ACT7	2	+	-	-	-	0.09	2.64E-01
AT4G16420	ADA2B	0	+	-	-	-	0.22	1.55E-02
AT1G69260	AFP1	1	-	-	-	-	0.55	6.83E-02
AT5G13300	AGD3	1	-	+	-	-	0.32	1.14E-03
AT5G13790	AGL15	1	-	-	-	-	-1.01	8.44E-05
AT1G48410	AGO1	1	-	-	-	+	0.49	2.22E-07
AT2G35270	AHL21	0	-	-	-	-	-1.04	3.21E-01
AT2G46510	AIB	1	-	-	-	-	0.38	1.73E-02
AT5G57390	AIL5	0	-	-	-	+	-0.04	9.04E-01
AT5G10510	AIL6	1	-	-	-	+	-0.55	2.46E-01
AT5G65510	AIL7	1	-	-	-	-	-0.21	9.10E-01
AT4G12550	AIR1	0	-	-	-	+	-5.02	6.48E-03
AT3G07390	AIR12	2	-	-	-	-	1.13	9.55E-24
AT2G04160	AIR3	2	-	-	-	+	-1.50	1.00E-13
AT2G34680	AIR9	0	-	-	-	-	-0.05	8.38E-01
AT1G54100	ALDH7B4	1	-	+	-	-	1.12	2.98E-82
AT2G17800	ARAC1	0	-	-	-	-	-0.05	8.48E-01
AT1G59750	ARF1	0	-	+	-	-	-0.09	4.26E-01
AT2G28350	ARF10	2	+	-	-	-	0.85	9.49E-04
AT4G30080	ARF16	0	+	-	-	-	0.14	6.29E-01
AT1G77850	ARF17	0	+	-	-	-	0.87	4.19E-05
AT1G19220	ARF19	0	+	-	-	-	1.12	2.96E-09
AT2G33860	ARF3	1	+	-	-	-	0.78	2.11E-06
AT1G19850	ARF5	1	-	-	-	-	0.86	1.25E-04
AT1G30330	ARF6	5	+	+	-	-	0.29	1.40E-02
AT5G37020	ARF8	1	-	-	-	-	-1.58	8.52E-20
AT3G59900	ARGOS	1	-	-	-	-	-4.69	4.35E-18
AT2G37630	AS1	1	+	-	-	-	0.30	4.03E-01
AT5G05730	ASA1	1	-	-	-	-	-1.38	6.94E-19
AT1G54060	ASIL1	0	-	-	-	-	-0.16	3.42E-01
AT4G18710	ASK7	3	-	-	-	-	-0.92	2.63E-35
AT5G19140	ATAILP1	2	-	-	-	-	0.69	2.82E-15
AT3G01220	ATHB-20	0	-	+	-	+	-0.29	7.71E-01
AT5G66700	ATHB-53	1	-	-	-	-	-2.31	1.35E-06
AT4G32880	ATHB-8	0	-	+	-	+	-0.50	1.44E-02
AT5G27420	ATL31	1	-	-	-	-	-0.32	5.80E-03
AT2G46070	ATMPK12	0	-	-	-	-	0.77	8.82E-08
AT4G21440	ATMYB102	2	-	-	-	+	0.24	5.42E-01
AT5G15310	ATMYB16	1	-	-	-	-	1.70	6.56E-29
AT2G47190	ATMYB2	1	-	-	-	-	-0.70	5.42E-03
AT1G57560	AtMYB50	0	-	-	-	-	0	1
AT4G05100	AtMYB74	2	-	-	+	-	-0.35	6.17E-01
AT1G34670	AtMYB93	0	-	-	+	-	2.03	3.11E-01
AT2G26740	ATSEH	1	-	-	-	-	-1.97	5.66E-95
AT3G22650	ATSFL61	0	-	-	-	-	0	1
AT2G38120	AUX1	2	-	-	-	+	0.91	3.36E-10
AT2G32410	AXL1	1	-	-	-	-	-0.24	3.72E-01
AT1G05180	AXR1	0	-	+	-	-	-0.23	1.58E-02
AT1G54990	AXR4	1	-	+	-	-	-1.52	3.09E-06
AT3G19580	AZF2	1	-	-	-	-	1.53	4.36E-16
AT1G27740	BHLH54	0	-	+	-	-	0	1
AT4G33880	BHLH85	0	-	-	-	-	0	1
AT3G02260	BIG	1	-	-	-	+	-0.26	5.70E-01
AT2G35940	BLH1	4	-	+	-	-	-1.72	2.08E-30
AT2G01950	BRL2	0	-	-	-	-	-0.03	9.11E-01

AGI	Gene Name	WUS peaks	Ac	deAc	Me	deMe	Log2FC	p adj.
AT5G63160	BT1	4	-	-	-	-	-0.33	1.01E-03
AT3G48360	BT2	3	+	-	-	-	0.45	4.86E-09
AT5G67480	BT4	1	-	-	-	-	1.37	3.24E-30
AT4G37610	BT5	2	+	-	-	-	1.26	1.14E-21
AT2G02560	CAND1	0	-	+	-	-	0.25	4.26E-02
AT5G01490	CAX4	0	-	-	+	+	-2.48	2.56E-03
AT4G17615	CBL1	2	-	-	-	-	-1.32	1.65E-14
AT2G46830	CCA1	0	-	-	-	-	-0.78	1.23E-10
AT4G32810	CCD8	0	-	-	-	-	-0.72	7.05E-02
AT2G20000	CDC27B	0	-	+	-	-	0.61	2.63E-06
AT3G55120	CHI1	1	-	-	-	-	0.76	1.46E-02
AT3G07370	CHIP	1	-	+	-	-	0.42	2.20E-06
AT5G13930	CHS	1	+	-	+	-	0.63	4.65E-01
AT5G65940	CHY1	0	-	-	-	-	-0.10	4.00E-01
AT5G37770	CML24	0	+	-	-	-	0.94	4.28E-04
AT5G20990	CNX1	0	-	-	-	-	-0.79	7.46E-22
AT4G10100	CNX7	0	+	-	-	-	-0.99	2.03E-08
AT1G18890	CPK10	0	+	+	-	-	0.22	3.83E-02
AT3G57530	CPK32	3	-	-	-	-	-0.51	6.10E-08
AT2G17290	CPK6	2	+	-	-	-	0.32	2.70E-03
AT5G01270	CPL2	1	-	-	-	-	0.16	3.04E-01
AT1G22920	CSN5A	1	-	+	-	-	-0.54	1.59E-06
AT1G71230	CSN5B	0	-	-	-	-	2.56	2.36E-03
AT4G02570	CUL1	0	+	-	-	-	-0.26	1.44E-03
AT2G26710	CYP734A1	2	+	-	-	-	1.32	6.53E-29
AT5G07990	CYP75B1	1	+	+	-	-	0.47	3.03E-01
AT2G27690	CYP94C1	0	-	-	-	-	-0.30	1.61E-01
AT4G03400	DFL2	2	-	+	-	-	-3.71	1.80E-83
AT3G50410	DOF3.4	0	-	+	-	-	-1.09	1.64E-03
AT1G09700	DRB1	0	-	-	-	-	0.82	1.29E-03
AT5G22220	E2FB	0	-	-	-	-	-0.04	8.48E-01
AT5G14960	E2FD	0	-	-	-	-	1.65	3.47E-08
AT4G14430	ECI2	1	-	+	-	-	0.36	4.75E-03
AT2G19560	EER5	0	-	-	-	-	-0.03	8.60E-01
AT1G73730	EIL3	0	-	-	-	-	0.55	6.23E-05
AT3G20770	EIN3	0	-	-	-	-	0.23	4.34E-03
AT2G25930	ELF3	0	-	-	-	-	0.31	3.39E-03
AT5G13680	ELP1	0	+	-	-	-	0.20	2.61E-01
AT3G11220	ELP4	0	+	-	-	-	0.12	6.05E-01
AT1G28370	ERF11	1	+	-	-	-	2.24	2.86E-27
AT2G44840	ERF13	1	-	+	-	+	2.11	9.22E-13
AT1G24590	ESR2	0	+	-	-	+	-1.42	4.50E-01
AT1G66340	ETR1	0	-	-	-	-	-0.30	9.46E-04
AT1G27340	FBX6	1	-	+	-	-	-2.18	7.88E-41
AT1G26870	FEZ	0	+	-	-	-	0	1
AT5G08640	FLS1	0	-	-	-	-	1.95	1.51E-01
AT5G54500	FQR1	2	-	-	-	-	0.89	1.04E-16
AT3G26790	FUS3	0	-	+	-	-	2.16	9.74E-02
AT2G46270	GBF3	0	+	-	-	-	0.63	1.33E-07
AT1G61120	GES	0	-	-	-	-	-2.64	1.24E-03
AT2G39550	GGB	1	-	-	-	-	-0.32	1.45E-02
AT2G14960	GH3.1	0	-	-	-	+	-0.28	9.15E-01
AT1G28130	GH3.17	2	-	-	-	-	-0.39	9.13E-03
AT2G23170	GH3.3	0	-	+	-	-	-0.93	1.67E-05
AT1G59500	GH3.4	0	-	-	-	-	0	1
AT4G27260	GH3.5	3	-	-	-	-	-0.48	4.82E-07
AT5G54510	GH3.6	1	-	+	-	-	2.81	2.19E-46
AT2G47750	GH3.9	0	-	-	-	-	0.96	9.34E-02
AT3G63010	GID1B	3	-	-	-	-	-1.83	2.95E-51
AT4G32690	GLB3	1	-	-	-	-	-1.08	7.55E-08
AT4G03190	GRH1	0	+	-	-	-	-1.55	3.32E-12
AT1G28480	GRXC9	1	-	-	-	-	1.82	1.35E-17
AT5G50320	HAG3	0	+	+	-	-	-0.46	2.86E-05
AT5G47370	HAT2	3	-	-	-	-	0.31	1.55E-01
AT4G16780	HAT4	3	-	-	-	-	-1.77	3.79E-24
AT4G36740	HB-5	0	-	+	-	-	2.90	6.73E-07
AT4G37580	HLS1	2	+	-	-	-	-0.26	3.16E-01
AT5G45710	HSFA4C	0	-	-	-	-	0.08	6.97E-01
AT4G14560	IAA1	1	-	-	-	-	-0.03	9.48E-01
AT1G04100	IAA10	0	-	-	-	-	-1.71	2.57E-14
AT4G28640	IAA11	0	-	-	-	-	-0.68	1.26E-02
AT1G04550	IAA12	1	-	-	-	-	-0.56	1.27E-02
AT2G33310	IAA13	1	-	+	-	-	-1.00	2.41E-15
AT4G14550	IAA14	2	-	-	-	-	-0.58	6.37E-03
AT1G80390	IAA15	0	-	-	-	+	0	1
AT3G04730	IAA16	1	-	+	-	-	-0.39	2.49E-09
AT1G04250	IAA17	1	-	-	-	+	0.67	1.70E-04
AT1G51950	IAA18	3	-	+	-	-	-0.75	2.02E-11
AT3G15540	IAA19	2	+	-	-	+	1.44	1.10E-03
AT3G23030	IAA2	2	-	+	-	-	-0.76	2.39E-21

AGI	Gene Name	WUS peaks	Ac	deAc	Me	deMe	Log2FC	p adj.
AT2G46990	IAA20	1	-	-	-	+	1.93	4.30E-16
AT3G16500	IAA26	2	+	-	-	-	-1.48	1.32E-35
AT4G29080	IAA27	1	-	-	-	-	0.88	7.44E-07
AT5G25890	IAA28	0	-	+	-	-	-0.28	2.54E-01
AT4G32280	IAA29	0	-	-	-	-	1.97	3.36E-07
AT3G62100	IAA30	0	-	-	-	-	1.18	9.73E-04
AT3G17600	IAA31	0	-	-	-	-	0	1
AT2G01200	IAA32	0	-	-	-	-	2.88	8.13E-02
AT5G57420	IAA33	0	-	+	-	+	0	1
AT1G15050	IAA34	0	+	-	-	-	-0.44	4.35E-01
AT5G43700	IAA4	1	-	+	-	-	-0.45	2.15E-05
AT1G15580	IAA5	0	-	-	-	-	0	1
AT1G52830	IAA6	2	-	+	-	-	0	1
AT3G23050	IAA7	1	-	-	-	+	0.57	4.02E-07
AT2G22670	IAA8	2	-	+	-	-	1.39	6.40E-43
AT5G65670	IAA9	2	-	-	-	-	0.12	1.41E-01
AT2G04550	IBR5	0	-	-	-	-	0.28	1.84E-02
AT1G47510	IP5P11	1	-	-	-	-	-1.90	6.10E-08
AT4G18010	IP5P2	4	-	-	-	-	-1.04	3.42E-12
AT2G22240	IPS2	0	+	-	-	-	1.13	2.29E-14
AT4G19690	IRT1	0	-	-	-	-	0	1
AT2G46370	JAR1	2	-	-	-	-	-0.76	6.78E-13
AT5G13220	JAZ10	1	-	-	-	-	2.12	4.86E-30
AT1G19640	JMT	2	-	-	-	-	0	1
AT5G49720	KOR	1	-	+	-	-	-0.35	2.80E-07
AT1G77690	LAX3	1	-	-	-	-	0.01	9.65E-01
AT3G58190	LBD29	0	-	-	-	-	0	1
AT1G01060	LHY	1	-	-	-	-	-0.20	6.39E-01
AT5G06300	LOG7	5	-	+	-	-	0.01	9.73E-01
AT5G12330	LRP1	2	+	-	-	+	0.09	8.26E-01
AT4G20380	LSD1	0	+	-	-	-	0.39	2.24E-04
AT2G39370	MAKR4	0	-	-	-	-	0	1
AT3G09940	MDAR3	0	-	-	-	+	-2.00	4.29E-02
AT1G74660	MIF1	0	-	-	-	-	1.14	3.39E-03
AT1G10210	MPK1	0	+	-	-	-	-0.16	3.04E-01
AT1G01560	MPK11	0	+	-	-	-	2.01	1.50E-40
AT4G01370	MPK4	0	-	+	-	-	0.28	7.86E-03
AT2G43790	MPK6	1	-	-	-	-	-0.91	3.41E-29
AT3G06490	MYB108	2	-	-	-	-	-2.35	2.86E-09
AT3G55730	MYB109	1	-	-	-	-	1.12	4.18E-05
AT2G47460	MYB12	1	-	-	-	+	0	1
AT2G31180	MYB14	0	-	-	-	+	0	1
AT3G23250	MYB15	2	-	-	-	+	-2.72	1.40E-16
AT1G22640	MYB3	2	-	+	-	-	-1.50	3.49E-16
AT3G28910	MYB30	3	-	-	-	-	1.26	4.36E-16
AT5G67300	MYB44	3	-	-	-	-	1.45	6.93E-22
AT1G18570	MYB51	3	-	+	-	+	-0.88	1.61E-08
AT5G59780	MYB59	2	-	-	-	-	-1.03	2.21E-02
AT1G09540	MYB61	1	-	-	-	-	-0.89	5.37E-01
AT1G56650	MYB75	1	-	-	-	-	1.83	1.39E-01
AT5G07700	MYB76	1	-	+	-	-	0	1
AT3G47600	MYB94	1	-	-	-	+	0.64	2.08E-04
AT1G52890	NAC019	2	-	+	-	-	-0.21	3.78E-01
AT1G56010	NAC021	2	-	-	-	-	-0.47	1.24E-01
AT3G15500	NAC055	2	+	-	-	+	-0.13	3.37E-01
AT5G39610	NAC92	2	-	+	-	-	-0.15	3.46E-01
AT5G63310	NDPK2	0	-	-	-	-	0.68	1.17E-10
AT2G34720	NFYA4	1	+	-	-	+	0.11	5.46E-01
AT1G31880	NLM9	1	-	-	-	-	1.44	2.45E-10
AT1G32450	NPF7.3	0	-	+	-	-	-0.41	2.46E-01
AT5G20730	NPH4	0	+	-	-	-	0.17	2.46E-01
AT1G80680	NUP96	0	-	+	-	-	0.06	7.11E-01
AT2G06050	OPR3	1	+	-	-	-	0.91	1.13E-20
AT5G54490	PBP1	0	-	-	-	-	0.84	4.32E-03
AT5G64890	PEP2	0	-	-	-	-	-4.68	2.22E-02
AT5G56290	PEX5	1	-	-	-	-	-0.28	6.52E-03
AT5G40770	PHB3	0	-	-	-	-	-0.33	5.54E-04
AT2G34650	PID	2	-	-	-	+	0.35	1.04E-01
AT2G43010	PIF4	2	-	-	-	-	1.79	1.26E-75
AT3G59060	PIF5	3	-	-	-	-	-0.75	1.01E-22
AT1G73590	PIN1	1	+	+	-	-	0.13	7.71E-01
AT5G57090	PIN2	0	-	-	-	-	0.68	7.34E-02
AT1G70940	PIN3	2	+	+	-	-	-1.17	1.85E-27
AT5G15100	PIN8	0	-	-	-	+	0	1
AT2G25170	PKL	0	-	+	-	-	0.27	1.60E-02
AT2G19690	PLA2-BETA	0	+	-	-	-	2.18	2.28E-01
AT3G05630	PLPZETA2	1	+	-	-	-	-1.43	1.83E-05
AT4G39403	PLS	3	-	-	-	-	3.03	2.12E-01
AT1G25490	PP2AA1	0	+	+	-	-	-0.27	5.88E-03
AT4G29940	PRH	1	+	+	-	-	-0.13	2.15E-01

AGI	Gene Name	WUS peaks	Ac	deAc	Me	deMe	Log2FC	p adj.
AT3G62680	PRP3	0	-	+	-	+	0	1
AT3G21110	PUR7	0	-	-	-	-	0.21	3.13E-01
AT2G41820	PXC3	2	-	-	-	-	-1.78	1.49E-03
AT1G06400	RABA1A	0	+	-	-	-	-0.09	5.72E-01
AT1G64060	RBOHF	2	+	+	-	-	0.09	7.26E-01
AT1G32230	RCD1	1	-	+	-	-	-0.61	2.11E-09
AT4G36800	RCE1	1	-	-	-	-	-0.61	6.63E-12
AT4G27410	RD26	0	+	-	-	-	2.38	1.17E-113
AT2G01570	RGA	3	+	+	-	-	-2.17	1.11E-44
AT3G26090	RGS1	0	-	-	-	-	-1.33	5.83E-19
AT1G78570	RHM1	1	+	+	-	-	0.41	4.09E-03
AT5G20570	ROC1	0	-	+	-	-	-0.39	4.95E-04
AT1G69270	RPK1	1	-	-	-	-	-1.64	3.08E-05
AT3G53020	RPL24B	0	+	-	-	-	-0.50	4.28E-05
AT4G38630	RPN10	1	-	+	-	-	-0.23	4.87E-03
AT1G64520	RPN12A	1	-	-	-	-	-0.30	7.15E-03
AT3G14050	RSH2	1	-	+	-	-	0.23	3.32E-02
AT1G31340	RUB1	1	-	-	-	-	-1.02	1.11E-16
AT5G17300	RVE1	1	-	+	-	-	-1.13	1.26E-12
AT5G37260	RVE2	1	-	-	-	-	1.64	1.26E-29
AT5G02840	RVE4	0	-	-	-	-	-0.84	1.25E-10
AT4G01280	RVE5	0	-	-	-	-	0.22	9.55E-02
AT3G09600	RVE8	1	-	-	-	-	-1.21	7.36E-20
AT5G59220	SAG113	4	-	-	-	+	-1.48	5.36E-03
AT3G28210	SAP12	1	-	+	-	-	0.72	2.18E-10
AT1G33410	SAR1	0	+	-	-	-	0.24	6.46E-02
AT4G38850	SAUR15	1	-	-	-	-	0	1
AT5G18010	SAUR19	1	-	-	-	-	0	1
AT5G18020	SAUR20	1	-	-	-	-	0	1
AT5G18030	SAUR21	1	-	-	-	-	0.08	9.64E-01
AT5G18050	SAUR22	0	-	-	-	-	0	1
AT5G18060	SAUR23	0	-	-	-	-	0	1
AT5G18080	SAUR24	1	-	-	-	-	0.57	8.41E-01
AT3G03830	SAUR28	1	-	+	-	-	0	1
AT2G46690	SAUR32	1	-	-	-	-	-0.86	1.06E-06
AT2G45210	SAUR36	2	-	-	-	+	-1.82	9.59E-14
AT1G79130	SAUR40	0	-	-	-	-	-2.95	2.72E-01
AT1G16510	SAUR41	1	-	-	-	-	0.41	7.28E-01
AT4G34760	SAUR50	1	-	-	-	-	-1.83	1.42E-02
AT1G29430	SAUR62	0	-	-	-	-	0	1
AT1G29440	SAUR63	1	-	-	-	-	-4.15	7.16E-02
AT1G29450	SAUR64	0	-	-	-	-	-1.41	3.27E-01
AT1G29500	SAUR66	1	-	-	-	-	-0.98	5.70E-01
AT1G29510	SAUR67	0	-	-	-	-	-5.26	6.53E-04
AT1G29490	SAUR68	0	-	-	-	-	0	1
AT1G56150	SAUR71	1	-	-	-	-	1.63	4.98E-02
AT3G12830	SAUR72	2	-	-	-	-	0.47	3.51E-01
AT4G05530	SDRA	0	-	-	-	-	-0.54	1.33E-04
AT4G23570	SGT1A	1	-	-	-	-	-0.38	1.03E-08
AT4G11260	SGT1B	0	-	+	-	-	-0.62	2.20E-14
AT1G04240	SHY2	2	-	-	-	-	3.22	4.66E-121
AT1G16540	SIR3	0	-	-	-	-	0.02	9.13E-01
AT1G21410	SKP2A	0	+	-	-	-	0.74	1.99E-07
AT4G13520	SMAP1	1	-	-	-	-	-0.31	2.47E-02
AT3G24280	SMAP2	0	-	-	-	-	0	1
AT4G16890	SNC1	1	+	+	-	-	0.06	6.58E-01
AT1G74100	SOT16	0	+	-	-	-	0.41	1.82E-01
AT4G34710	SPE2	4	-	+	-	-	-0.58	1.69E-03
AT1G28560	SRD2	0	-	-	-	-	0.37	5.95E-01
AT3G11820	SYP121	1	-	+	-	-	0.43	7.88E-07
AT3G52400	SYP122	1	-	-	-	-	-0.31	5.37E-02
AT2G24850	TAT3	0	-	-	-	-	0.93	5.57E-01
AT1G53230	TCP3	1	-	-	-	-	-0.19	8.18E-01
AT3G16640	TCTP1	0	-	-	-	-	-0.29	1.07E-02
AT5G06960	TGA5	0	-	-	-	-	0.60	8.92E-06
AT2G34600	TIFY	1	-	-	-	-	-0.28	2.89E-01
AT1G19180	TIFY10A	2	-	-	-	-	1.45	1.83E-18
AT1G74950	TIFY10B	1	-	-	-	-	-0.83	1.73E-22
AT1G17380	TIFY11A	1	+	-	-	-	1.46	3.54E-11
AT3G62980	TIR1	1	-	+	-	-	-0.87	4.91E-18
AT1G15750	TPL	1	+	-	-	-	-0.30	2.25E-03
AT1G08030	TPST	1	+	-	-	-	-0.05	7.43E-01
AT1G49950	TRB1	0	-	-	-	-	0.23	3.47E-02
AT5G67580	TRB2	0	+	-	-	-	1.04	1.93E-28
AT3G49850	TRB3	0	-	-	-	-	-0.02	9.45E-01
AT5G59430	TRP1	1	-	+	-	-	0.96	4.91E-20
AT5G42980	TRX3	0	-	-	-	-	-0.47	7.51E-10
AT5G24520	TTG1	1	+	-	-	-	-0.45	6.43E-06
AT2G42580	TTL3	1	+	-	-	-	-0.12	2.04E-01
AT3G20830	UCNL	2	+	-	-	+	1.28	1.88E-08

AGI	Gene Name	WUS peaks	Ac	deAc	Me	deMe	Log2FC	p adj.
AT4G00080	UNE11	0	-	-	-	-	0	1
AT3G63300	VAB	0	-	+	-	-	-2.48	3.84E-15
AT3G13300	VCS	0	-	-	-	-	0.11	4.17E-01
AT1G14000	VIK	0	-	+	-	-	0.22	7.50E-02
AT5G55120	VTC5	1	+	-	-	-	1.37	2.91E-23
AT3G11260	WOX5	0	-	-	-	+	-1.19	5.39E-01
AT2G47260	WRKY23	2	+	+	-	-	-0.68	6.96E-02
AT5G57740	XBAT32	0	-	+	-	-	0.92	1.18E-03
AT4G34390	XLG2	0	+	-	-	-	0.10	5.00E-01
AT5G57560	XTH22	3	+	-	-	-	-0.30	5.39E-02
AT2G06850	XTH4	2	-	-	-	-	-0.47	5.33E-08
AT4G37390	YDK1	1	-	-	-	-	3.61	3.69E-169
AT5G51640	YLS7	0	-	-	-	-	0.22	3.22E-01
AT1G27730	ZAT10	3	+	-	-	-	-1.81	1.46E-35
AT5G51470		0	-	+	+	+	0	1
AT3G20220		0	-	-	-	-	0	1
AT2G37030		0	-	-	-	-	1.35	4.92E-01
AT4G34810		0	-	-	-	-	-6.84	6.66E-14
AT1G19840		0	+	-	-	-	1.30	5.24E-01
AT4G34770		1	-	-	-	-	-5.89	8.70E-10
AT1G63720		1	+	-	-	-	0.68	9.03E-05
AT3G43120		0	-	-	-	-	0	1
AT1G19830		0	-	-	-	+	-3.36	6.43E-02
AT4G38840		1	-	-	-	-	-3.31	2.26E-03
AT3G26760		0	-	+	-	+	-1.92	2.90E-17
AT1G48670		0	-	+	-	-	0	1
AT1G17520		0	-	-	-	-	-0.18	1.36E-01
AT1G70000		1	-	-	-	-	-2.22	1.93E-11
AT5G20820		0	-	-	-	-	0	1
AT3G51200		0	-	-	-	-	0	1
AT5G13380		0	-	-	-	-	0	1
AT2G21210		2	-	-	-	-	-0.47	4.87E-01
AT5G42410		0	-	-	-	-	0	1
AT1G17345		2	-	-	-	-	-1.15	2.31E-02
AT1G74840		0	-	-	-	-	1.11	8.83E-35
AT3G03840		0	-	-	-	-	0	1
AT1G76190		0	-	-	-	-	0	1
AT1G15430		1	-	+	-	-	-0.19	2.29E-01
AT4G33940		1	-	-	-	-	0.53	2.59E-07
AT2G21200		1	-	-	-	-	0.73	7.99E-01
AT3G25880		1	-	-	-	-	-1.92	8.85E-02
AT1G49010		1	-	+	-	-	-1.59	4.17E-06
AT1G48660		0	-	-	-	-	0	1
AT4G18950		1	-	+	-	-	0.61	3.38E-06
AT4G34780		0	-	+	-	-	0	1
AT5G13350		0	-	-	-	-	0	1
AT2G36210		0	+	-	-	-	0.93	3.14E-01
AT2G18010		1	-	-	-	+	0	1
AT1G75590		0	-	-	-	-	0.40	8.58E-01
AT5G50120		0	-	-	-	-	0	1
AT2G24400		0	-	-	-	-	-0.60	2.35E-01
AT3G61900		0	-	-	-	-	-0.70	1.41E-01
AT1G43040		0	-	-	-	-	0	1
AT2G21220		1	-	-	-	-	-0.32	9.19E-01
AT4G34790		1	-	-	-	-	-5.25	3.70E-04
AT3G03850		0	-	-	-	-	0	1
AT4G12410		0	-	-	-	-	-0.77	4.08E-01
AT4G00880		1	-	-	-	+	-0.91	2.56E-01
AT4G13790		0	-	-	-	-	0	1
AT4G09530		0	-	-	-	+	0	1
AT5G38895		0	-	-	-	-	0.09	5.32E-01
AT3G60690		3	-	-	-	-	-2.32	2.18E-09
AT4G31320		0	-	-	-	-	0	1
AT3G09980		1	-	-	-	-	0.85	9.78E-16
AT5G10990		0	+	-	-	-	-0.18	9.60E-01
AT5G53590		1	-	-	-	-	1.10	1.17E-02
AT4G36110		0	-	-	-	+	-0.04	9.56E-01
AT5G66260		0	-	-	-	-	0	1
AT4G22620		2	-	-	-	-	2.38	1.16E-01
AT5G50760		0	+	-	-	-	0.99	1.60E-02
AT3G09870		0	-	-	-	-	0	1
AT3G16350		0	+	-	-	-	-0.62	8.84E-02
AT1G63840		2	-	+	-	-	-0.84	1.91E-14
AT4G35030		0	-	-	+	-	1.46	2.20E-02
AT3G03847		1	-	-	-	-	0	1
AT1G20470		0	-	-	-	-	0.28	8.72E-01
AT3G03820		0	-	-	-	-	0	1
AT4G38860		2	-	-	-	-	1.83	1.27E-01
AT1G78100		4	+	-	-	-	1.72	2.64E-13
AT4G15430		1	-	+	-	-	-0.86	7.50E-02

AGI	Gene Name	WUS peaks	Ac	deAc	Me	deMe	Log2FC	p adj.
AT5G20810		0	-	-	-	+	2.68	1.42E-01
AT2G28085		0	-	-	+	-	0	1
AT2G28780		0	-	-	-	-	-1.96	1.01E-01
AT3G53250		0	+	-	-	-	-0.87	4.57E-01
AT1G29460		0	-	-	-	-	-1.63	2.59E-01
AT2G25790		1	-	-	-	+	-0.37	4.07E-03
AT3G12955		0	-	-	-	+	3.97	1.40E-02
AT4G25030		1	-	-	-	-	-2.87	4.89E-254
AT1G78990		0	-	-	-	-	3.66	1.99E-01
AT4G37295		1	-	-	-	-	2.44	6.80E-09
AT1G29420		1	-	-	-	-	0	1
AT5G27780		0	-	-	-	-	0	1
AT5G13370		1	-	-	-	-	0.70	9.58E-13
AT5G03310		1	-	-	-	-	0	1
AT1G72430		2	+	-	-	-	0.63	1.40E-03
AT4G26400		0	+	-	-	-	0.04	7.06E-01
AT1G23160		0	-	-	-	+	-4.47	3.10E-05
AT5G13360		1	-	-	-	-	-1.23	3.64E-08
AT5G63190		0	+	-	-	-	0.48	3.00E-08
AT2G16580		0	-	-	-	-	-1.66	4.98E-01
AT4G34750		2	-	+	-	-	-1.25	2.55E-03
AT1G75580		2	-	-	-	-	-1.85	6.28E-04
AT1G48690		0	-	-	-	+	0	1
AT4G34800		1	-	+	-	-	-6.31	4.05E-05

Supplementary Table 3: Response of genes with annotated activities in "auxin response" to WUS.

Adjusted p-value for RNA-seq data (WUS-GR, DEX vs. mock) was calculated using the Benjamini-Hochberg method in DESeq2. ChIP-seq results for WUS binding, acetylation and methylation are given. Peaks column denotes number of WUS binding events at the locus; Ac denotes increase of acetylation at the locus, deAc denotes reduction in acetylation at the locus; Me denotes increase of methylation at the locus, deMe denotes reduction in methylation at the locus. Processed raw data including read counts can be found in Supplementary File 1.

Supplementary Data 1: Processed raw data of genomic datasets.

Supplementary Data 2: Interactive HTML file allowing intersections of genomic datasets.