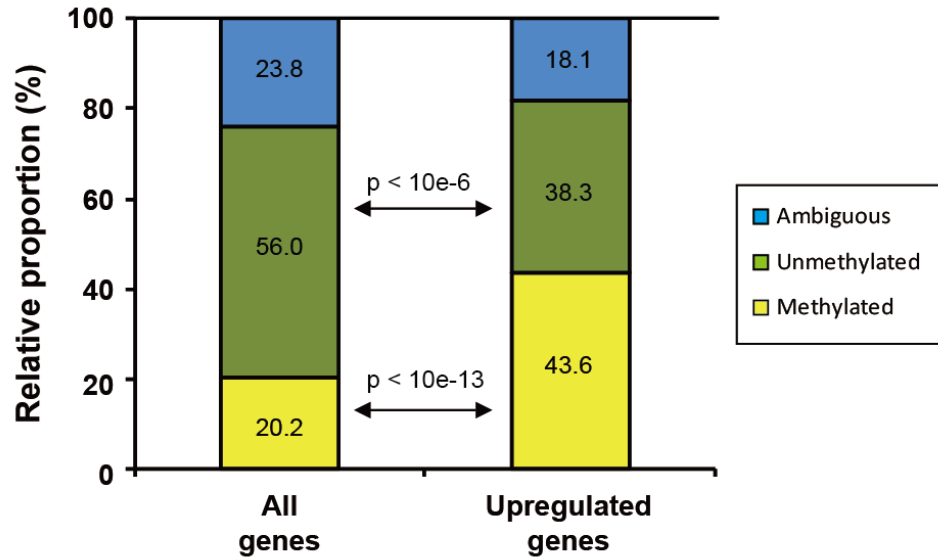
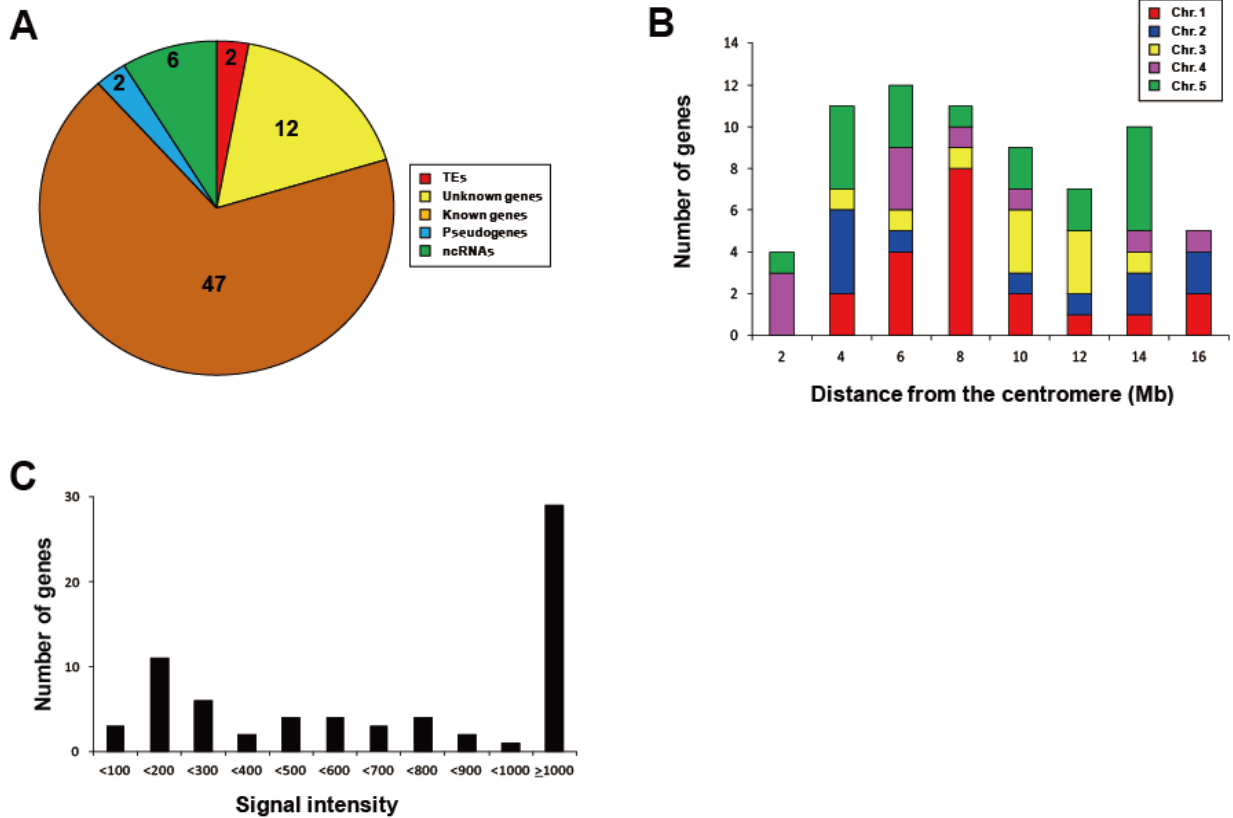


Supplemental Figure 1. Relationship between DNA methylation and transcriptional activation in *vim1/2/3*.



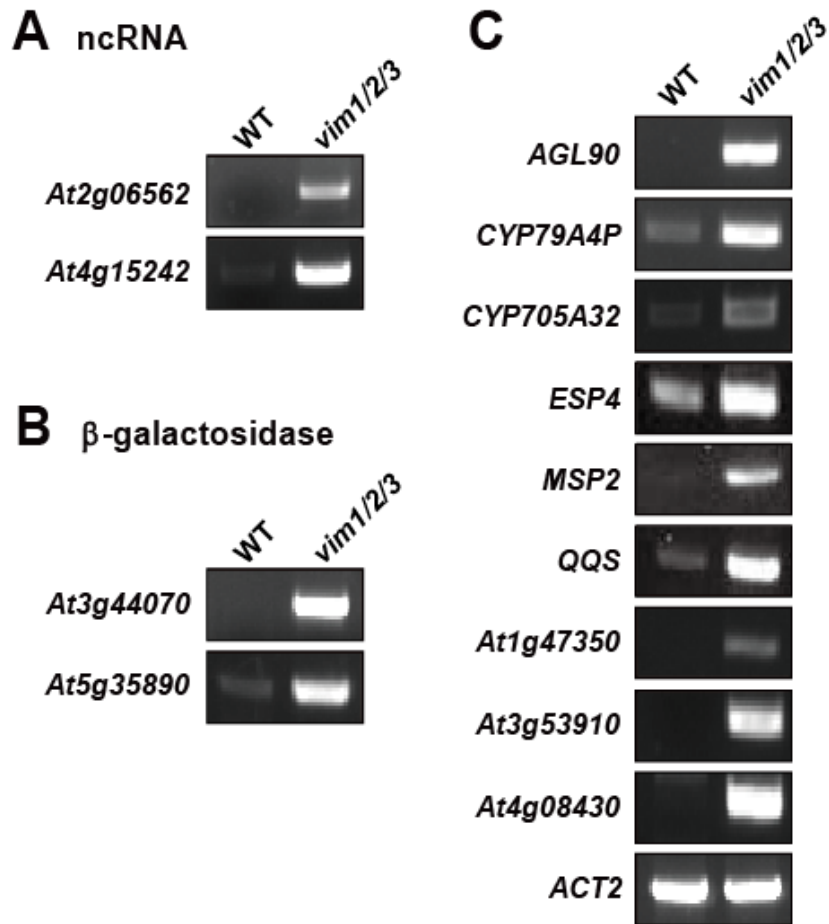
Relative portions of methylated genes and unmethylated genes among the upregulated genes in *vim1/2/3* and the all annotated *Arabidopsis* genes included in the microarray analyses were compared. The p-value of enrichment for methylated genes or unmethylated genes was calculated using the hypergeometric distribution, based on the list of genes with or without DNA methylation (Zilberman *et al.*, 2007). It is noted that pseudogenes and TEs among genes with DNA methylation were not included as background for enrichment test of methylated genes.

Supplemental Figure 2. Genes whose transcripts were decreased in the *vim1/2/3* mutant.



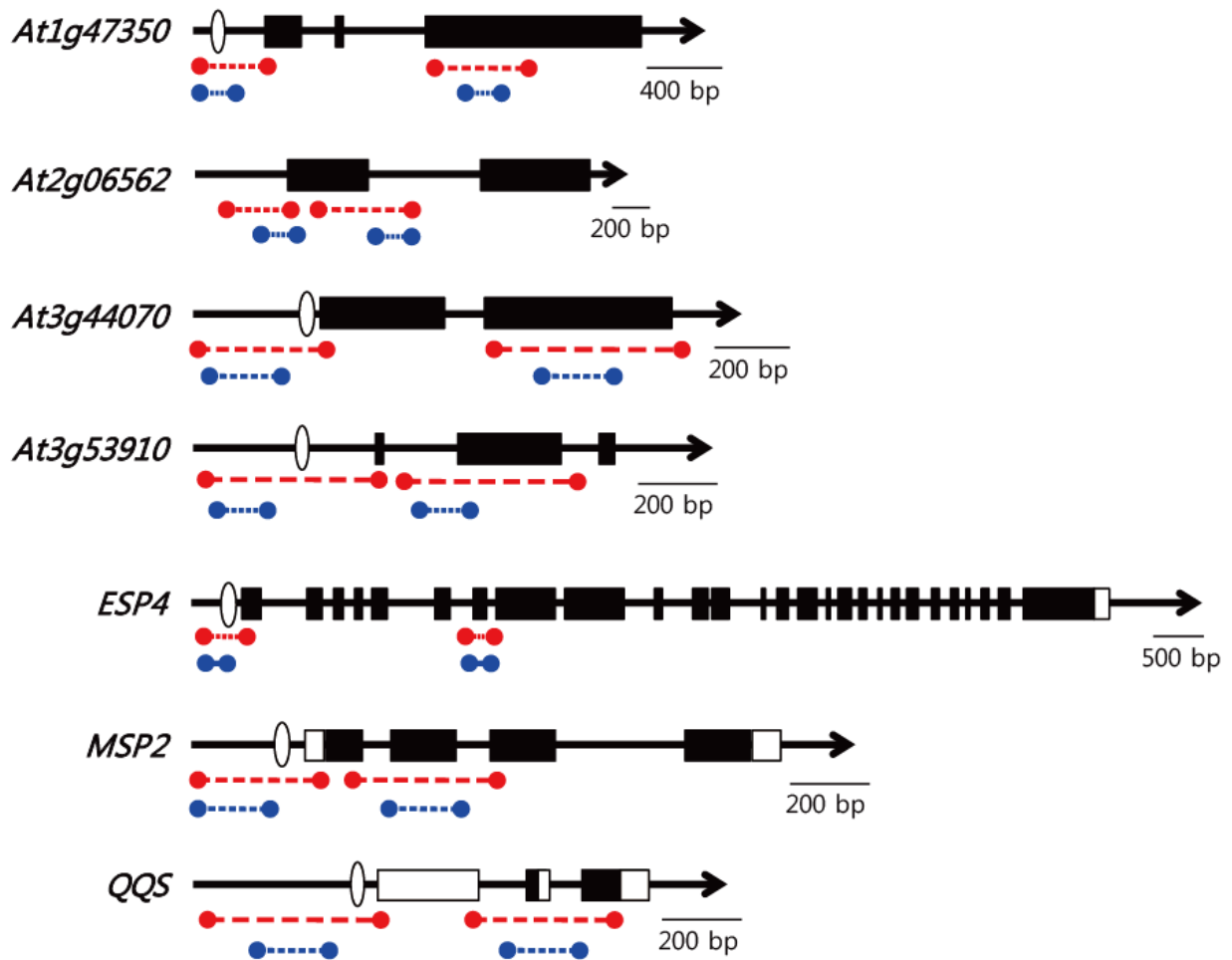
(A) Categorization of genes downregulated in the *vim1/2/3* mutant in comparison with WT. Transposons or related elements (TEs) (red); genes for unknown proteins (yellow); genes for known proteins (orange); pseudogenes (blue); ncRNAs (green). (B) Chromosomal positions of downregulated genes with respect to the centromere. Results for individual chromosomes are shown with the indicated colors. (C) Transcript levels of genes downregulated in *vim1/2/3* in comparison with WT plants. The number of genes within the indicated ranges of signal intensity from the microarray data in WT plants is shown.

Supplemental Figure 3. Validation of transcriptional derepression of the putative targets of the VIM proteins.



Reverse transcription polymerase chain reaction (RT-PCR) was used to validate microarray gene expression data in wild type (WT) and *vim1/2/3*. RT-PCR analysis of two ncRNAs selected from thirteen upregulated ncRNAs (**A**), two genes selected from ten upregulated putative β -galactosidase genes (**B**), and nine genes chosen from 133 upregulated genes of known function or those similar to known genes (**C**). Total RNA for RT-PCR analysis was isolated from 14-day-old WT and *vim1/2/3* plants. *ACT2* was used as an internal control. Results were consistent in three biological replicates.

Supplemental Figure 4. Schematic of VIM1 target genes showing regions amplified by the primers used for bisulfite sequencing and ChIP-qPCR analyses.



The positions and sizes of the amplified fragments for bisulfite sequencing (red dashed line) and ChIP-qPCR (blue dashed line) analyses from promoter and transcribed areas are indicated. Black boxes indicate exons and black lines indicate introns and intergenic regions. White ovals and boxes represent putative TATA boxes and known 5' or 3' untranslated regions, respectively.

Supplemental Table 1. AGI annotated genes upregulated in *vim1/2/3*.

The AGI genes that were transcriptionally upregulated in *vim1/2/3* compared with wild-type (WT) plants (fold-change ≥ 5.0 , $p < 0.05$) are listed.

At number	<i>vim1/2/3</i> intensity	WT intensity	<i>vim1/2/3</i> / WT	p-value	Gene_Name
AT1G01530	164.67	18.12	9.60	3.08E-04	AGL28
AT1G02580	1294.23	156.78	17.12	6.10E-03	MEA
AT1G02920	707.65	153.31	5.32	3.42E-03	ATGSTF7
AT1G02930	11148.01	2603.43	5.48	2.06E-02	ATGSTF6
AT1G06135	2611.13	687.27	7.35	1.50E-02	Unknown
AT1G08105	293.78	58.26	5.55	2.60E-05	TE
AT1G10710	2613.13	451.13	5.19	2.13E-05	PHS1
AT1G12064	1784.06	268.42	6.75	2.47E-05	Unknown
AT1G12667	421.35	15.55	19.79	1.77E-03	Pseudogene
AT1G13470	4154.28	770.28	6.08	3.88E-02	Unknown
AT1G16225	527.63	71.06	7.44	8.09E-05	Unknown
AT1G18130	13323.74	329.90	37.59	3.73E-05	ClassII aaRS and biotin synthetase
AT1G20390	2504.48	83.44	30.10	3.91E-05	TE
AT1G20400	5726.73	201.16	28.36	3.91E-05	Unknown
AT1G20795	160.54	13.76	6.39	4.27E-02	F-box family protein
AT1G22590	6961.18	828.14	8.08	6.21E-05	AGL87
AT1G24060	358.14	16.85	15.11	1.05E-04	Unknown
AT1G24110	23190.27	3183.81	6.95	7.08E-05	Putative peroxidase
AT1G24380	5455.88	332.26	18.61	1.51E-06	Unknown
AT1G25430	2584.14	339.32	8.01	3.21E-06	TE
AT1G26558	428.99	89.12	5.04	2.59E-03	ncRNA
AT1G27990	366.09	38.03	9.96	2.73E-05	Unknown
AT1G28000	2423.71	228.15	11.42	1.72E-04	PPR superfamily protein
AT1G28695	2019.89	181.67	10.80	5.41E-05	Unknown
AT1G30810	42217.85	7286.37	5.95	8.39E-05	Transcription factor
AT1G31166	435.94	39.47	5.77	1.27E-02	TE
AT1G31900	2093.18	408.24	5.89	2.24E-05	Pseudogene
AT1G32000	4550.93	308.16	15.55	1.89E-06	Unknown
AT1G32010	1700.53	79.95	19.17	1.06E-05	Myosin heavy chain-related
AT1G33460	3030.22	93.20	32.64	3.84E-05	TE
AT1G33840	941.80	53.37	12.53	8.38E-03	Unknown
AT1G34042	9985.44	1838.56	5.14	9.19E-05	Unknown
AT1G34440	397.27	24.26	17.55	1.21E-04	Unknown
AT1G34545	245.83	20.79	13.79	1.20E-05	TE
AT1G34680	296.60	33.07	7.22	5.28E-04	Pseudogene
AT1G34810	364.31	17.20	18.51	6.07E-04	Plant thionin family protein
AT1G34860	113.13	17.70	6.21	6.83E-04	Plant thionin family protein
AT1G35500	1141.06	70.64	15.58	1.78E-06	Unknown

AT1G35614	504.79	27.33	19.05	3.22E-05	Unknown
AT1G35617	958.05	40.49	26.04	1.50E-06	Unknown
AT1G35647	1225.52	39.19	37.14	1.47E-06	TE
AT1G36020	1252.80	87.58	9.59	3.34E-03	Unknown
AT1G36100	315.26	22.44	19.00	1.74E-03	Myosin heavy chain-related
AT1G36190	36707.22	1167.50	32.01	3.85E-05	TE
AT1G36210	102.00	10.00	9.44	1.01E-03	TE
AT1G36272	2707.48	239.36	11.64	5.28E-05	Unknown
AT1G36360	10140.64	267.91	37.17	3.72E-05	TE
AT1G36580	6317.15	271.05	23.31	4.08E-05	Unknown
AT1G36630	12509.42	400.47	29.90	3.86E-05	TE
AT1G36640	5590.33	819.07	8.43	4.14E-03	Unknown
AT1G36680	293.86	11.90	16.13	2.83E-03	TE
AT1G36910	274.49	13.41	18.49	1.48E-04	TE
AT1G37000	69.17	12.86	5.05	6.27E-03	Beta-galactosidase
AT1G37030	151.87	11.29	7.76	3.26E-02	TE
AT1G37057	6667.10	231.71	29.57	3.88E-05	TE
AT1G37063	244.48	15.78	17.35	1.32E-04	TE
AT1G37080	371.52	15.14	22.21	2.23E-05	TE
AT1G37100	157.89	13.55	11.09	3.57E-04	TE
AT1G37180	78.52	10.00	7.29	2.21E-03	TE
AT1G37735	292.21	38.25	8.58	3.35E-05	TE
AT1G38280	4180.16	226.79	18.93	1.80E-06	TE
AT1G38410	185.30	23.42	11.00	1.05E-02	TE
AT1G38460	380.44	45.28	11.48	1.81E-04	TE
AT1G41750	637.77	33.90	12.72	1.25E-03	TE
AT1G42110	1674.37	86.82	19.17	4.51E-05	TE
AT1G42200	2407.35	75.58	28.38	4.04E-05	TE
AT1G42210	1541.85	77.18	20.23	4.37E-05	TE
AT1G42410	32642.32	2532.83	15.61	8.47E-05	TE
AT1G42420	104.70	10.60	6.52	1.94E-02	TE
AT1G42595	1495.15	182.30	8.18	6.36E-05	TE
AT1G42680	1456.26	217.43	6.71	7.47E-05	Myosin-related
AT1G43920	770.49	116.06	6.76	8.50E-05	TE
AT1G44040	2704.18	147.04	18.79	4.38E-05	Pseudogene
AT1G44890	1292.39	86.98	12.48	1.06E-04	Unknown
AT1G47265	570.37	47.25	12.42	1.29E-04	Unknown
AT1G47350	589.48	39.32	15.54	2.91E-06	F-box family protein-related
AT1G47660	162.36	10.00	13.29	7.05E-04	Unknown
AT1G48625	43010.92	7346.82	5.89	8.47E-05	Pseudogene
AT1G49680	13749.41	896.48	15.00	4.62E-05	Unknown
AT1G49715	70.77	10.13	5.69	3.57E-03	DEFL family protein
AT1G50350	98.02	11.92	6.25	4.48E-03	Unknown
AT1G50660	38819.23	3008.14	12.95	5.04E-05	Unknown
AT1G50735	781.19	85.69	7.67	4.47E-05	TE
AT1G51172	85.28	10.47	5.86	1.38E-02	Unknown
AT1G51920	3648.01	778.16	6.03	6.16E-04	Unknown
AT1G52460	2041.22	210.43	9.01	2.72E-06	Hydrolase

AT1G53480	27140.57	917.20	30.32	3.86E-05	MRD1
AT1G53490	37524.04	1656.01	23.24	4.16E-05	DNA binding
AT1G57670	402.52	20.84	19.84	7.72E-05	TIR domain-containing protein
AT1G59770	143.74	22.52	6.53	1.27E-03	TE
AT1G59920	24102.31	663.48	36.17	3.73E-05	Unknown
AT1G59930	30550.85	797.96	38.44	3.71E-05	Unknown
AT1G60570	39339.06	4487.29	8.80	6.19E-05	Kelch repeat/F-box family protein
AT1G64790	12815.44	589.99	22.75	4.09E-05	ILA
AT1G65483	271.45	57.82	5.63	6.29E-03	Unknown
AT1G67105	44043.90	3413.92	14.50	1.80E-06	ncRNA
AT1G67635	685.99	131.40	8.25	2.49E-02	Unknown
AT1G72060	6020.17	974.60	6.53	4.83E-03	Serine-type endopeptidase inhibitor
AT1G73603	888.16	42.92	23.66	1.68E-06	LCR64
AT1G73607	244.81	14.28	17.19	1.45E-04	LCR65
AT1G78095	502.33	71.43	6.87	3.55E-05	TE
AT1G79100	93.89	11.75	6.40	3.79E-03	Arginine/serine-rich protein-related
AT2G01310	11020.64	1725.23	6.25	2.60E-05	Unknown
AT2G02030	175.35	14.96	10.14	3.35E-04	F-box family protein
AT2G03720	8177.98	490.46	17.34	1.26E-05	MRH6
AT2G03970	1360.23	97.57	13.68	1.85E-06	TE
AT2G04020	494.74	86.63	6.58	2.35E-03	GDSL-motif lipase family protein
AT2G04031	2666.93	232.83	11.47	5.24E-05	ECA1-related family protein
AT2G04037	945.01	48.08	18.68	4.81E-06	Unknown
AT2G04600	3221.33	325.86	12.90	4.07E-04	TE
AT2G05660	5343.94	200.80	24.30	4.13E-05	TE
AT2G05752	178.19	18.26	11.53	4.29E-05	Unknown
AT2G05915	19330.70	516.56	38.69	3.68E-05	Unknown
AT2G05995	16795.60	2271.97	8.46	5.32E-03	ncRNA
AT2G06002	36269.68	3061.08	12.08	3.54E-05	ncRNA
AT2G06420	5504.01	295.19	17.16	4.48E-05	Unknown
AT2G06480	1272.36	81.51	16.21	4.77E-05	TE
AT2G06490	7979.87	249.83	31.67	3.81E-05	TE
AT2G06562	33002.31	794.81	41.27	3.66E-05	ncRNA
AT2G06908	1635.23	68.56	33.22	1.81E-03	Unknown
AT2G07213	2986.38	83.23	35.12	3.80E-05	ncRNA
AT2G07215	3131.95	113.58	30.12	3.96E-05	Unknown
AT2G07635	42441.73	4748.89	9.00	6.14E-05	TE
AT2G07710	404.53	65.74	6.38	1.47E-04	TE
AT2G07730	117.35	10.75	7.50	1.46E-02	TE
AT2G09838	756.04	30.85	18.43	5.50E-04	Unknown
AT2G10080	88.35	11.38	5.65	3.02E-02	TE
AT2G10100	92.61	10.40	8.52	1.11E-03	TE
AT2G10510	2956.40	167.50	17.75	4.40E-05	TE
AT2G10540	1460.22	100.18	16.70	7.22E-06	TE
AT2G10550	230.28	32.59	10.08	5.81E-04	Uracil DNA glycosylase family
AT2G10650	6024.19	611.90	9.52	5.62E-05	TE
AT2G10890	589.15	47.38	12.28	6.09E-05	TE
AT2G10900	339.69	12.75	15.03	4.11E-02	TE

AT2G10960	1992.01	84.11	23.84	4.16E-05	TE
AT2G10965	1202.75	49.08	24.83	4.28E-05	Unknown
AT2G10980	2871.63	89.59	30.95	3.91E-05	TE
AT2G11015	125.37	18.92	5.57	1.14E-02	Unknown
AT2G11100	122.31	15.58	6.85	8.46E-03	TE
AT2G11320	290.61	17.98	16.38	3.16E-04	TE
AT2G11550	7610.45	775.75	8.93	2.33E-03	TE
AT2G11590	289.80	18.53	15.70	1.09E-04	TE
AT2G11620	1659.03	71.50	20.93	5.59E-05	Unknown
AT2G11630	303.02	21.13	14.38	3.74E-05	Pseudogene
AT2G11650	236.86	13.31	16.51	1.79E-05	TE
AT2G11651	698.46	96.86	9.70	1.56E-03	Unknown
AT2G11700	202.36	28.26	6.13	1.39E-02	TE
AT2G11775	6906.58	202.87	34.40	3.77E-05	TE
AT2G11778	7025.43	486.26	14.72	4.63E-05	Unknown
AT2G11780	7570.69	294.95	26.86	1.34E-06	TE
AT2G11790	322.78	19.71	17.58	3.57E-04	TE
AT2G12050	643.49	37.09	18.67	6.92E-05	Pseudogene
AT2G12340	439.75	18.83	18.36	8.97E-03	TE
AT2G12420	5394.64	171.96	31.18	3.85E-05	TE
AT2G12500	400.59	13.45	30.35	7.48E-05	TE
AT2G12570	159.76	20.92	7.85	1.61E-03	TE
AT2G12935	4975.87	294.24	17.81	4.40E-05	Unknown
AT2G13118	356.62	28.43	13.17	1.65E-05	TE
AT2G13410	2051.58	75.01	26.16	4.44E-05	Pseudogene
AT2G13463	5304.19	357.33	14.60	4.67E-05	Unknown
AT2G13547	4734.63	200.37	24.75	4.05E-05	Unknown
AT2G13760	2118.25	142.28	16.54	2.37E-06	Unknown
AT2G13770	306.40	50.51	6.69	1.08E-05	Unknown
AT2G13865	32361.27	10871.53	5.35	1.48E-02	TE
AT2G13980	1446.69	61.86	21.53	4.47E-05	Nucleic acid binding
AT2G14405	576.46	37.32	12.22	3.12E-04	Pseudogene
AT2G14410	833.62	24.45	28.50	7.66E-05	Pseudogene
AT2G14430	124.55	17.16	5.35	3.70E-02	TE
AT2G14560	12729.27	2367.81	5.63	2.74E-02	LURP1
AT2G14610	8838.10	1071.75	8.05	4.02E-03	PR1
AT2G14970	3550.32	93.45	36.00	3.80E-05	TE
AT2G15410	2736.72	83.18	32.84	3.85E-05	TE
AT2G15555	45088.84	3152.07	18.08	1.49E-03	ncRNA
AT2G15750	441.21	35.92	14.15	1.87E-05	TE
AT2G15800	131.81	14.25	7.72	6.13E-04	TE
AT2G15940	1704.55	87.18	19.99	4.36E-05	TE
AT2G16020	7321.82	233.48	31.55	3.82E-05	Unknown
AT2G16050	23438.71	2189.97	11.88	2.80E-05	Cys/His-rich C1 domain family
AT2G16310	419.85	74.08	5.69	1.27E-04	Pseudogene
AT2G17690	18671.70	371.63	33.87	7.44E-04	SDC
AT2G17910	385.11	57.46	5.85	1.08E-03	TE
AT2G18540	42701.81	4220.12	10.53	5.64E-05	Cupin family protein

AT2G18570	5935.37	1112.63	5.62	7.10E-06	UDP-glucosyl transferase family
AT2G18610	928.91	66.80	13.38	7.32E-05	Unknown
AT2G18660	11166.49	2131.70	6.24	3.61E-02	EXLB3
AT2G19010	312.95	28.37	10.14	6.75E-04	GDSL-motif lipase family protein
AT2G19850	3764.84	116.84	33.64	3.81E-05	Unknown
AT2G24735	189.88	41.83	5.44	9.64E-03	Unknown
AT2G24780	647.40	58.56	14.59	6.59E-05	Unknown
AT2G25735	7145.64	1627.66	5.21	2.29E-02	Unknown
AT2G26630	1413.31	112.82	12.60	5.13E-05	TE
AT2G27540	465.50	19.59	9.06	4.68E-02	Unknown
AT2G28980	576.22	70.55	8.21	8.28E-05	TE
AT2G31080	4892.72	99.48	47.97	3.60E-05	TE
AT2G32510	39737.47	4246.57	9.54	1.40E-05	MAPKKK17
AT2G34120	624.15	30.78	19.57	5.11E-05	Unknown
AT2G36710	452.21	109.41	7.52	1.75E-02	Pectinesterase family protein
AT2G41400	1655.75	69.78	24.04	4.38E-05	Unknown
AT2G41650	6679.33	1423.88	5.31	5.24E-05	Unknown
AT2G44240	14019.33	1269.24	10.75	5.97E-04	Unknown
AT2G45580	261.54	71.90	5.10	3.24E-03	CYP76C3
AT3G01345	884.05	66.57	13.19	5.31E-05	Unknown
AT3G01830	5654.39	664.29	5.10	6.97E-03	Putative calmodulin-related protein
AT3G02100	3841.26	391.18	9.49	6.78E-04	UDP-glucosyl transferase family
AT3G03400	871.66	87.88	8.08	9.80E-06	Putative calmodulin-related protein
AT3G09800	1430.43	107.87	12.54	1.69E-05	SNARE-like superfamily protein
AT3G10510	40101.98	5089.81	8.07	6.60E-05	Kelch repeat/F-box family protein
AT3G10595	306.34	46.40	7.77	9.69E-03	Myb family transcription factor
AT3G11080	573.28	130.89	5.85	1.02E-03	AtRLP35
AT3G11990	2120.97	165.71	12.72	2.26E-06	Unknown
AT3G14670	9558.76	396.91	23.31	4.04E-05	Unknown
AT3G14981	360.68	35.48	11.45	7.75E-05	Unknown
AT3G15320	701.07	61.39	9.51	8.20E-03	TE
AT3G15330	2176.04	287.44	6.94	1.35E-03	Pseudogene
AT3G16100	27231.60	4268.40	6.31	3.92E-05	ATRABG3C
AT3G18720	358.87	49.30	8.06	8.27E-04	F-box family protein
AT3G19020	7172.29	1281.97	5.95	5.05E-04	Leucine-rich repeat family protein
AT3G20950	1761.15	72.42	25.31	4.18E-05	CYP705A32
AT3G21450	646.56	63.52	8.58	1.19E-05	Protein kinase family protein
AT3G21570	419.07	24.72	17.12	1.55E-04	Unknown
AT3G22022	185.89	10.00	15.64	1.29E-04	Unknown
AT3G22937	296.43	20.62	16.25	2.96E-04	Pseudogene
AT3G23060	183.42	21.55	5.80	3.21E-02	Zinc finger family protein
AT3G23085	88.67	11.46	6.00	4.05E-03	TE
AT3G24516	2057.28	176.12	12.11	5.15E-05	Unknown
AT3G24517	3056.02	66.72	46.22	3.62E-05	Unknown
AT3G24518	6443.18	151.39	42.65	3.63E-05	ncRNA
AT3G24542	1610.37	73.15	22.41	4.32E-05	Beta-galactosidase
AT3G25719	38674.21	4743.71	8.14	6.51E-05	Unknown
AT3G25720	134.67	28.32	5.25	2.31E-03	Unknown

AT3G27250	3043.34	311.06	9.51	7.69E-04	Unknown
AT3G28153	6790.56	210.89	29.85	1.38E-18	TE
AT3G28291	2402.39	322.85	7.14	7.16E-05	Unknown
AT3G28830	510.57	38.47	11.94	9.32E-04	Unknown
AT3G28899	39595.43	1781.64	22.98	4.19E-05	Unknown
AT3G28918	1090.37	109.70	9.13	3.09E-05	Unknown
AT3G29610	2996.44	254.54	11.65	5.14E-05	TE
AT3G29612	7363.29	285.67	25.11	4.00E-05	TE
AT3G29618	1232.43	107.94	9.27	3.64E-04	TE
AT3G29634	379.90	39.94	10.10	2.00E-03	TE
AT3G29636	266.59	16.20	14.34	3.38E-03	TE
AT3G29639	38629.43	3183.60	12.64	5.15E-05	Unknown
AT3G29641	159.36	17.40	6.67	9.21E-03	TE
AT3G29738	4834.77	606.15	8.41	6.01E-05	TE
AT3G29767	2681.28	93.59	28.32	1.50E-06	TE
AT3G29787	775.97	71.04	10.44	6.38E-05	TE
AT3G29790	306.84	25.01	14.89	9.53E-06	Unknown
AT3G30187	5013.94	335.89	14.55	4.67E-05	Pseudogene
AT3G30218	474.78	17.88	30.97	3.15E-06	TE
AT3G30390	520.64	85.26	5.09	5.87E-04	TE
AT3G30433	182.38	13.87	12.02	4.21E-04	TE
AT3G30710	500.38	15.30	31.03	5.12E-05	TE
AT3G30720	7985.36	854.06	9.24	4.07E-06	QQS
AT3G30746	1327.73	31.85	38.43	4.49E-05	TE
AT3G30751	208.59	22.77	7.64	8.23E-04	TE
AT3G30820	95.34	11.96	6.92	1.49E-03	Unknown
AT3G31310	335.41	26.83	13.24	8.72E-05	TE
AT3G31314	5200.93	328.15	15.93	4.50E-05	TE
AT3G31356	688.14	43.87	18.83	4.74E-04	TE
AT3G31390	102.68	15.21	5.50	7.78E-03	TE
AT3G31406	7423.30	656.17	11.38	5.12E-05	TE
AT3G31422	131.08	13.26	8.07	7.71E-03	TE
AT3G31442	2737.89	200.18	13.94	4.77E-05	SADHU7-2 TE
AT3G31908	127.08	12.01	8.09	7.65E-04	Pseudogene
AT3G31909	511.38	26.48	11.59	1.88E-03	TE
AT3G31910	676.18	32.76	19.39	5.22E-05	Unknown
AT3G31915	861.48	48.99	18.59	4.84E-05	TE
AT3G31950	2253.01	71.79	31.25	4.61E-05	Unknown
AT3G32160	185.55	19.20	6.32	1.27E-02	Unknown
AT3G32200	330.31	12.19	16.14	8.02E-03	Unknown
AT3G32230	4830.35	145.05	34.02	3.81E-05	TE
AT3G32240	39852.31	2287.16	18.12	4.49E-05	TE
AT3G32377	2455.58	113.95	21.59	4.33E-05	Pseudogene
AT3G32902	1530.79	50.06	32.98	2.30E-06	TE
AT3G32914	109.15	10.93	6.95	3.06E-02	TE
AT3G32966	1857.98	60.31	32.38	3.96E-05	TE
AT3G33045	1988.99	63.73	31.37	3.96E-05	TE
AT3G33197	40038.31	2189.55	21.89	4.73E-05	TE

AT3G33528	2481.02	171.93	14.31	4.74E-05	Unknown
AT3G42083	222.82	25.03	13.22	1.14E-03	TE
AT3G42206	705.07	54.11	11.75	8.57E-19	TE
AT3G42310	1175.31	83.07	10.29	6.06E-05	Unknown
AT3G42350	28379.21	822.04	31.03	3.87E-05	TE
AT3G42624	168.77	12.55	13.68	1.78E-04	TE
AT3G42650	49167.51	2161.98	22.57	4.23E-05	TE
AT3G42658	39486.81	1921.51	20.94	4.28E-05	SADHU3-2 TE
AT3G42712	9522.66	283.42	34.44	3.75E-05	TE
AT3G43020	291.82	14.49	15.76	3.19E-05	TE
AT3G43148	709.98	50.78	16.32	9.87E-05	Unknown
AT3G43150	858.65	47.14	13.58	3.73E-04	Unknown
AT3G43290	948.85	84.63	6.02	3.50E-02	Unknown
AT3G43420	85.06	11.60	5.59	2.77E-02	Unknown
AT3G43436	658.09	23.78	29.26	4.51E-05	TE
AT3G43571	4682.04	180.74	26.27	3.99E-05	TE
AT3G43572	8973.01	206.16	43.27	3.62E-05	Unknown
AT3G43574	23416.68	1160.96	21.30	4.18E-05	Unknown
AT3G43580	2050.22	197.93	11.07	3.66E-05	Beta-galactosidase
AT3G43826	410.36	98.83	5.54	7.19E-03	Pseudogene
AT3G43833	41427.92	1448.22	29.07	3.96E-05	Unknown
AT3G43880	400.18	24.52	16.53	6.49E-05	Unknown
AT3G44006	5981.57	447.59	13.71	4.74E-05	Unknown
AT3G44042	37602.31	1464.23	25.69	4.05E-05	SADHU3-1 TE
AT3G44070	1231.81	42.68	28.98	4.03E-05	Beta-galactosidase
AT3G44093	13933.81	433.33	32.43	3.77E-05	TE
AT3G44261	11624.94	355.24	32.93	3.78E-05	Unknown
AT3G44325	713.33	99.93	5.73	3.64E-03	TE
AT3G44790	1879.04	153.27	12.22	5.27E-05	MATH domain-containing protein
AT3G45093	28059.80	1446.20	20.52	4.27E-05	TE
AT3G45510	82.31	10.55	6.37	2.96E-03	Zinc finger family protein
AT3G45525	320.35	38.43	14.43	1.74E-02	Unknown
AT3G45800	1043.38	55.08	21.25	5.42E-05	Unknown
AT3G45820	27949.40	1027.30	27.74	3.95E-05	Unknown
AT3G46390	183.88	27.25	5.92	4.72E-04	Unknown
AT3G48130	8740.34	900.86	9.44	2.68E-04	RSU1
AT3G48526	268.77	56.02	5.19	2.29E-02	TE
AT3G48650	9654.28	2079.07	5.70	3.95E-02	Pseudogene
AT3G49230	670.69	81.26	6.60	1.18E-02	Unknown
AT3G49850	10494.98	1756.24	5.78	3.82E-03	TRB3
AT3G50320	6679.23	190.76	34.91	3.82E-05	Unknown
AT3G52620	5097.89	755.60	6.59	7.13E-05	Unknown
AT3G52830	38582.83	5180.16	7.92	6.72E-05	Unknown
AT3G53910	2045.23	56.15	37.21	3.80E-05	Malate dehydrogenase-related
AT3G54730	33393.54	964.48	34.16	3.78E-05	Unknown
AT3G56630	7591.34	1025.40	7.13	6.75E-05	CYP94D2
AT3G60170	526.35	108.32	9.78	2.94E-02	TE
AT3G60260	36319.97	5736.53	6.57	7.72E-05	ELMO1-related protein

AT3G60870	2744.96	334.94	7.48	6.93E-05	DNA-binding protein-related
AT4G00700	3466.13	687.29	5.06	4.69E-02	C2 domain-containing protein
AT4G01140	17891.45	1628.05	10.59	5.33E-05	Unknown
AT4G01980	451.71	96.56	8.34	2.39E-02	TE
AT4G02380	29088.44	5900.49	5.62	8.50E-03	SAG21
AT4G02490	150.60	10.57	13.62	3.25E-04	TE
AT4G03156	1285.96	124.88	10.68	5.79E-05	Small GTPase-related
AT4G03723	678.61	41.16	21.77	5.20E-04	Unknown
AT4G03870	2373.24	272.56	8.81	5.93E-05	TE
AT4G03880	230.95	22.60	10.04	8.54E-05	TE
AT4G03913	114.28	14.24	5.59	4.15E-02	Pseudogene
AT4G03923	23500.07	716.15	33.16	3.79E-05	TE
AT4G03950	266.32	16.99	14.86	2.23E-04	Putative G6P /P translocator
AT4G04077	2774.66	118.41	18.97	5.59E-04	ncRNA
AT4G04100	1131.92	48.17	23.32	4.32E-05	TE
AT4G04145	2730.84	129.89	20.62	4.33E-05	Pseudogene
AT4G04250	1998.54	60.72	33.59	3.89E-05	Pseudogene
AT4G04270	2631.55	115.07	21.01	4.57E-05	TE
AT4G04293	37570.27	1258.70	30.77	3.90E-05	TE
AT4G04316	362.42	14.86	18.29	1.80E-03	TE
AT4G04500	99.94	14.47	5.22	2.16E-02	Protein kinase family protein
AT4G04635	838.66	78.26	10.63	5.94E-05	TE
AT4G04980	637.14	57.90	12.66	1.08E-04	Unknown
AT4G05505	20392.78	603.22	33.73	3.77E-05	TE
AT4G05633	74.91	10.04	7.06	2.30E-03	TE
AT4G06474	216.56	14.83	14.71	1.98E-04	TE
AT4G06477	5918.91	573.03	11.88	4.13E-03	TE
AT4G06481	250.25	12.99	18.74	1.75E-05	TE
AT4G06529	7100.64	248.81	23.57	4.14E-05	TE
AT4G06541	228.62	27.08	11.41	1.95E-03	TE
AT4G06572	4516.43	122.41	34.41	3.79E-05	TE
AT4G06582	507.29	13.39	31.01	5.08E-06	Pseudogene
AT4G06584	1496.51	79.54	18.41	8.68E-05	TE
AT4G06597	285.83	25.43	9.98	5.02E-04	Pseudogene
AT4G06613	144.52	10.00	11.55	7.56E-04	TE
AT4G06617	208.31	14.14	15.48	1.30E-04	TE
AT4G06619	324.70	12.93	19.85	1.61E-04	TE
AT4G06627	427.22	20.14	21.43	5.71E-05	TE
AT4G06686	512.86	34.06	20.39	1.06E-03	TE
AT4G06735	18264.05	2656.22	7.15	6.02E-06	TE
AT4G06748	180.20	20.69	9.63	3.40E-04	Pseudogene
AT4G07320	1643.15	97.64	13.19	7.33E-06	Pseudogene
AT4G07526	1062.75	50.52	22.37	4.48E-05	Unknown
AT4G07560	273.36	21.94	13.43	1.01E-04	TE
AT4G07630	1302.43	76.01	17.36	1.25E-05	TE
AT4G07696	223.68	29.17	8.09	1.72E-04	TE
AT4G07868	371.20	18.89	10.20	3.65E-02	Unknown
AT4G07940	31590.61	768.99	41.47	3.66E-05	Unknown

AT4G07965	3646.03	137.76	26.46	3.98E-05	Unknown
AT4G08030	71.05	10.52	5.38	7.53E-03	TE
AT4G08039	319.76	51.10	7.31	9.05E-04	Defensin-like family protein
AT4G08053	79.23	12.53	6.37	1.39E-03	TE
AT4G08078	2170.35	269.66	7.65	5.62E-06	TE
AT4G08105	12469.46	499.39	24.56	4.01E-05	TE
AT4G08131	127.82	13.35	9.59	6.16E-04	TE
AT4G08420	203.30	19.08	9.59	1.25E-04	TE
AT4G08430	2692.75	88.55	30.32	3.91E-05	Ulp1 protease family protein
AT4G08593	40229.78	862.74	46.48	3.63E-05	Unknown
AT4G08691	10277.38	280.05	36.80	3.70E-05	Unknown
AT4G08710	8711.06	495.61	14.41	2.15E-06	TE
AT4G08720	3100.19	261.04	11.69	5.12E-05	TE
AT4G08860	1058.66	88.48	11.84	2.59E-04	TE
AT4G09880	654.96	68.46	11.10	7.44E-06	Unknown
AT4G10655	6486.82	207.35	30.47	3.86E-05	Defensin-like family protein
AT4G10910	10743.77	1425.68	11.36	3.24E-03	Unknown
AT4G10920	14833.58	2635.59	5.71	4.02E-04	KELP
AT4G11890	3201.09	523.57	5.98	2.76E-02	Protein kinase family protein
AT4G13890	798.88	126.58	5.86	2.36E-05	EDA36
AT4G15242	6791.81	199.06	34.12	3.77E-05	ncRNA
AT4G15417	1907.60	448.46	7.08	1.22E-02	ATRTL1
AT4G16215	30458.87	1228.52	24.94	4.05E-05	Unknown
AT4G17585	596.14	39.21	16.34	2.19E-06	Unknown
AT4G17587	285.71	21.18	11.43	9.70E-05	TE
AT4G18150	175.17	10.82	11.35	8.21E-03	Unknown
AT4G18410	2776.47	152.12	17.63	4.45E-05	TE
AT4G19240	613.28	26.71	23.69	5.58E-05	Unknown
AT4G22170	124.73	11.98	7.78	3.63E-03	F-box family protein
AT4G24610	1419.52	72.63	13.24	3.03E-04	Unknown
AT4G24644	33019.03	1112.02	28.42	3.93E-05	Unknown
AT4G25530	5514.40	172.42	31.82	3.82E-05	FWA
AT4G26390	496.33	57.63	10.00	7.66E-06	Putative pyruvate kinase
AT4G28420	1082.67	241.51	8.15	3.56E-02	Putative aminotransferase
AT4G29200	10534.38	228.80	46.34	3.58E-05	Beta-galactosidase
AT4G30040	1684.37	142.59	12.42	7.61E-04	Aspartyl protease family
AT4G30640	549.12	228.28	5.40	3.95E-02	FBL19
AT4G34180	12487.96	2029.91	6.15	5.53E-06	Cyclase family protein
AT4G34680	234.63	40.31	5.72	1.79E-02	Putative GATA transcription factor 3
AT4G34690	195.71	12.60	10.76	3.54E-03	Unknown
AT4G39404	3131.77	352.53	7.83	6.55E-05	ncRNA
AT4G40080	5257.93	453.85	13.92	1.03E-05	ENTH domain-containing protein
AT5G01080	5214.58	231.60	23.45	4.09E-05	Beta-galactosidase
AT5G01400	10466.70	632.79	16.10	4.53E-05	ESP4
AT5G03090	26613.24	691.40	38.64	3.69E-05	Unknown
AT5G05870	40434.88	3065.78	14.47	1.93E-06	UGT76C1
AT5G06320	3766.37	783.45	5.27	1.55E-02	NHL3

AT5G07570	489.99	23.03	8.42	2.79E-02	Glycine/proline-rich protein
AT5G07572	729.82	69.97	5.97	1.65E-02	Unknown
AT5G07620	162.22	22.82	6.03	2.35E-03	Protein kinase family protein
AT5G10760	2161.50	303.22	7.78	2.36E-03	Aspartyl protease family protein
AT5G14460	41039.54	2952.26	13.88	4.94E-05	Pseudogene
AT5G15110	1299.12	38.69	37.62	1.82E-06	Lyase/ pectate lyase
AT5G15360	17633.74	568.57	31.96	3.83E-05	Unknown
AT5G15420	4654.29	100.81	45.22	3.63E-05	Unknown
AT5G15690	6230.23	234.77	26.64	3.95E-05	Unknown
AT5G16500	221.57	39.37	6.05	6.44E-04	Protein kinase family protein
AT5G22570	803.60	125.25	5.02	2.28E-02	WRKY38
AT5G24240	10119.06	636.27	18.25	1.52E-06	PI3- and 4-kinase family protein
AT5G24250	1649.33	75.88	23.76	4.32E-05	Unknown
AT5G24480	2165.30	224.33	8.92	6.17E-06	Beta-galactosidase
AT5G25955	13008.88	542.53	23.44	4.06E-05	TE
AT5G26170	4315.39	726.15	5.63	1.12E-02	WRKY50
AT5G26270	44130.70	1950.85	24.85	4.15E-05	Unknown
AT5G26970	8749.04	1112.03	8.53	2.54E-06	Unknown
AT5G27170	5224.63	181.22	28.24	3.92E-05	Unknown
AT5G27340	166.11	16.74	11.47	1.49E-03	Unknown
AT5G27345	3019.25	189.11	14.83	3.69E-04	TE
AT5G27927	2290.78	117.12	19.08	4.42E-05	SADHU5-2 TE
AT5G27960	198.84	18.77	9.75	4.37E-04	AGL90
AT5G28085	185.62	24.50	8.10	1.10E-02	TE
AT5G28090	2358.08	83.22	27.22	4.02E-05	Unknown
AT5G28100	1781.57	88.05	20.86	4.99E-05	TE
AT5G28200	1117.25	33.37	31.86	3.15E-05	TE
AT5G28232	1788.46	152.77	11.52	5.35E-05	TE
AT5G28235	642.97	16.58	36.91	5.16E-05	Ulp1 protease family protein
AT5G28360	16002.32	2219.90	6.49	1.03E-03	ACS3
AT5G28464	2609.04	73.51	34.73	3.83E-05	TE
AT5G28526	15427.30	432.94	35.63	3.74E-05	TE
AT5G28560	1529.40	104.92	14.10	1.82E-06	Unknown
AT5G28696	310.35	22.31	16.64	8.13E-05	TE
AT5G28760	1630.09	82.00	18.72	4.71E-05	TE
AT5G28810	293.84	23.21	16.44	2.06E-04	Unknown
AT5G28824	86.77	10.71	7.73	1.76E-03	ncRNA
AT5G28880	7756.46	245.41	26.95	4.12E-05	TE
AT5G28888	4315.68	330.44	10.98	4.62E-04	TE
AT5G28890	115.43	12.94	6.60	5.19E-03	TE
AT5G28927	2387.03	284.36	8.28	6.55E-05	TE
AT5G29020	166.53	13.47	7.05	4.70E-02	TE
AT5G29026	138.40	10.58	10.58	1.22E-03	TE
AT5G29028	540.01	46.08	10.00	7.61E-06	TE
AT5G29034	252.04	12.45	16.34	1.04E-04	TE
AT5G29035	1235.87	132.46	8.47	3.22E-06	TE
AT5G29050	5106.51	87.43	54.55	3.55E-05	Unknown
AT5G29337	118.74	12.44	8.76	9.63E-04	TE

AT5G29560	458.00	10.36	39.89	4.76E-06	Calcium ion binding
AT5G29720	613.29	16.80	37.71	3.68E-06	TE
AT5G29807	832.25	32.47	25.27	4.63E-05	Unknown
AT5G30341	13626.37	966.54	13.76	4.76E-05	Unknown
AT5G30400	1346.89	76.06	16.18	5.17E-05	TE
AT5G30450	1018.44	128.76	7.77	7.04E-05	TE
AT5G30520	169.34	26.49	6.77	7.47E-04	Unknown
AT5G31685	214.74	16.89	13.99	1.28E-04	TE
AT5G31702	743.00	47.36	19.78	1.24E-05	TE
AT5G31758	721.31	57.38	13.07	5.53E-05	TE
AT5G31821	2235.80	85.77	25.52	4.16E-05	TE
AT5G32487	1153.66	30.34	40.95	4.09E-05	TE
AT5G32580	698.24	64.45	9.51	9.36E-05	TE
AT5G32590	221.34	14.52	14.53	1.78E-04	Myosin heavy chain-related
AT5G32620	730.53	47.72	12.21	4.53E-03	TE
AT5G32623	2879.77	66.00	39.75	2.70E-05	TE
AT5G32627	163.41	15.55	9.81	7.48E-05	TE
AT5G32654	120.87	10.25	10.44	5.04E-04	TE
AT5G33226	279.59	15.78	17.59	1.27E-05	TE
AT5G33250	1383.99	42.29	33.14	4.05E-05	TE
AT5G33251	39285.11	1441.64	27.76	3.99E-05	Pseudogene
AT5G33393	302.58	17.64	15.23	3.37E-05	Unknown
AT5G33404	1049.02	28.10	36.73	4.63E-05	TE
AT5G33898	1211.56	75.33	16.00	6.71E-06	Unknown
AT5G34501	1192.66	84.70	13.30	1.74E-04	TE
AT5G34665	196.02	33.47	5.33	3.54E-03	TE
AT5G34829	98.48	14.71	6.91	1.31E-03	Unknown
AT5G34845	111.55	10.00	10.72	8.23E-04	TE
AT5G34869	5863.09	204.89	28.71	3.89E-05	Unknown
AT5G34920	271.00	27.78	10.96	7.26E-04	TE
AT5G35048	145.61	19.18	7.69	5.91E-04	TE
AT5G35069	4189.89	257.16	15.80	4.57E-05	Unknown
AT5G35070	572.60	27.09	22.51	3.61E-04	Pseudogene
AT5G35120	6722.43	660.62	9.76	2.48E-06	Unknown
AT5G35205	10494.96	588.93	17.94	4.34E-05	TE
AT5G35375	1897.82	159.05	11.99	5.40E-05	Unknown
AT5G35416	1773.43	76.89	23.49	4.24E-05	TE
AT5G35490	27295.20	4748.18	5.72	5.12E-06	ATMRU1
AT5G35535	743.13	46.82	12.68	2.34E-04	TE
AT5G35760	144.13	17.94	8.41	6.64E-04	Beta-galactosidase
AT5G35798	5620.30	120.95	44.51	3.64E-05	TE
AT5G35800	608.25	29.38	18.28	3.93E-05	TE
AT5G35870	969.53	194.38	6.06	5.24E-04	Unknown
AT5G35890	847.17	28.38	27.04	7.89E-05	Beta-galactosidase
AT5G35917	10931.47	678.76	16.93	1.87E-06	CYP79A3P
AT5G35918	4106.63	245.97	15.21	1.84E-06	TE
AT5G35920	4520.76	224.16	19.32	1.42E-05	CYP79A4P
AT5G36140	1408.82	176.38	6.75	1.85E-05	CYP716A2

AT5G36900	10530.13	340.36	30.06	3.83E-05	Unknown
AT5G37200	357.80	10.83	28.08	1.52E-05	Zinc finger family protein
AT5G37280	2868.36	102.35	26.59	4.03E-05	Zinc finger family protein
AT5G38190	2097.61	118.06	17.19	4.53E-05	Myosin heavy chain-related
AT5G39270	1367.92	21.09	65.55	3.56E-05	ATEXPA22
AT5G40605	267.81	10.57	23.31	1.35E-04	TE
AT5G41280	190.71	19.19	6.39	1.94E-02	Unknown
AT5G41660	9975.79	533.76	18.84	4.25E-05	Unknown
AT5G41830	3297.11	127.33	27.16	3.97E-05	F-box family protein-related
AT5G43630	44145.99	7690.27	5.65	8.74E-05	TZP
AT5G44585	22486.11	4792.33	8.15	1.64E-02	Unknown
AT5G45095	6150.39	456.01	14.38	3.33E-04	Unknown
AT5G45576	1774.05	166.75	10.82	5.42E-05	TE
AT5G45890	1851.26	98.00	17.99	4.53E-05	SAG12
AT5G46295	2866.25	489.79	6.66	2.10E-03	Unknown
AT5G46795	441.07	33.68	13.11	1.20E-02	MSP2
AT5G49250	787.43	28.36	31.00	3.95E-06	Beta-galactosidase
AT5G49465	5642.54	513.16	11.02	2.96E-06	TE
AT5G52340	27389.77	1047.44	26.55	3.99E-05	ATEXO70A2 A2)
AT5G52750	4755.29	659.32	6.51	2.24E-02	Heavy metal transport superfamily
AT5G52760	4673.28	725.75	6.17	4.78E-02	Heavy metal transport superfamily
AT5G54700	87.67	13.62	5.51	1.09E-03	Ankyrin repeat family protein
AT5G57735	424.74	16.29	16.95	1.73E-03	ncRNA
AT5G59620	350.35	24.47	17.93	1.15E-03	TE
AT5G63225	1152.76	147.62	9.71	1.63E-02	Glycosyl hydrolase family protein 17
AT5G65300	41301.20	4493.33	9.49	6.00E-05	Unknown
AT5G66380	866.56	147.32	5.26	4.57E-04	ATFOLT1

Supplemental Table 2. ncRNAs upregulated in the *vim1/2/3* mutant.

ncRNA genes that were transcriptionally upregulated in *vim1/2/3* compared with wild-type (WT) plants (fold-change ≥ 5.0 , $p < 0.05$) are listed.

Gene	<i>vim1/2/3</i> /WT	p-value	Signal intensity in WT	TE existence *
<i>AT1G26558</i>	5.04	3.00E-03	89.12	Y
<i>AT1G67105</i>	14.50	1.80E-06	3413.92	Y
<i>AT2G05995</i>	8.46	5.00E-03	2271.97	Y
<i>AT2G06002</i>	12.08	3.54E-05	3061.08	Y
<i>AT2G06562</i>	41.27	3.66E-05	794.81	Y
<i>AT2G07213</i>	35.12	3.80E-05	83.23	Y
<i>AT2G15555</i>	18.08	1.49E-03	3152.07	Y
<i>AT3G24518</i>	42.65	3.63E-05	151.39	N
<i>AT4G04077</i>	18.97	5.59E-04	118.41	Y
<i>AT4G15242</i>	34.12	3.77E-05	199.06	N
<i>AT4G39404</i>	7.83	6.55E-05	352.53	N
<i>AT5G28824</i>	7.73	2.00E-03	10.71	Y
<i>AT5G57735</i>	16.95	2.00E-03	16.29	Y

* Y, at least one TE was positioned proximately to or inside of the gene; N, no TE was positioned proximately to or inside of the gene.

Supplemental Table 3. Genes for known function or genes similar to known proteins upregulated in *vim1/2/3*.

Genes that were transcriptionally upregulated in *vim1/2/3* compared with wild-type (WT) plants (fold-change ≥ 5.0 , $p < 0.05$) are listed.

Gene	<i>vim1/2/3</i> / WT	p-value	Description	Signal intensity in WT	Expression pattern in WT (Genevestigator)
<i>AT1G01530</i>	9.60	3.08E-04	AGL28	18.12	Endosperm
<i>AT1G02580</i>	17.12	6.10E-03	MEA	156.78	Endosperm
<i>AT1G02920</i>	5.32	3.42E-03	ATGSTF7	153.31	
<i>AT1G02930</i>	5.48	2.06E-02	ATGSTF6	2603.43	
<i>AT1G10710</i>	5.19	2.13E-05	PHS1	451.13	
<i>AT1G18130</i>	37.59	3.73E-05	Class II aaRS synthetases	329.90	
<i>AT1G20795</i>	6.39	4.27E-02	F-box family protein	13.76	N.D.
<i>AT1G22590</i>	8.08	6.21E-05	AGL87	828.14	Endosperm
<i>AT1G24110</i>	6.95	7.08E-05	Putative peroxidase	3183.81	Stamen
<i>AT1G28000</i>	11.42	1.72E-04	PPR superfamily protein	228.15	N.D.
<i>AT1G30810</i>	5.95	8.39E-05	Transcription factor	7286.37	Ubiquitous
<i>AT1G32010</i>	19.17	1.06E-05	Myosin heavy chain-related	79.95	
<i>AT1G34810</i>	18.51	6.07E-04	Plant thionin family protein	17.20	N.D.
<i>AT1G34860</i>	6.21	6.83E-04	Plant thionin family protein	17.70	N.D.
<i>AT1G36100</i>	19.00	1.74E-03	Myosin heavy chain-related	22.44	
<i>AT1G37000</i>	5.05	6.27E-03	β -galactosidase-related	12.86	
<i>AT1G42680</i>	6.71	7.47E-05	Myosin-related	217.43	
<i>AT1G47350</i>	15.54	2.91E-06	F-box family protein-related	39.32	
<i>AT1G49715</i>	5.69	3.57E-03	DEFL family protein	10.13	N.D.
<i>AT1G52460</i>	9.01	2.72E-06	Hydrolase	210.43	Seed
<i>AT1G53490</i>	23.24	4.16E-05	DNA binding	1656.01	Endosperm
<i>AT1G53480</i>	30.32	3.86E-05	MRD1	917.20	N.D.
<i>AT1G57670</i>	19.84	7.72E-05	TIR domain-containing protein	20.84	Root
<i>AT1G60570</i>	8.80	6.19E-05	F-box family protein	4487.29	Endosperm, Cell culture
<i>AT1G64790</i>	22.75	4.09E-05	ILA	589.99	
<i>AT1G72060</i>	6.53	4.83E-03	Endopeptidase inhibitor	974.60	
<i>AT1G73603</i>	23.66	1.68E-06	LCR64	42.92	N.D.
<i>AT1G73607</i>	17.19	1.45E-04	LCR65	14.28	N.D.
<i>AT1G79100</i>	6.40	3.79E-03	Arg/Ser-rich protein-related	11.75	
<i>AT2G02030</i>	10.14	3.35E-04	F-box family protein	14.96	N.D.
<i>AT2G03720</i>	17.34	1.26E-05	MRH6	490.46	Root
<i>AT2G04020</i>	6.58	2.35E-03	GDSL-motif lipase family	86.63	Stamen
<i>AT2G04031</i>	11.47	5.24E-05	ECA1 gametogenesis related	232.83	N.D.

<i>AT2G10550</i>	10.08	5.81E-04	Uracil DNA glycosylase family	32.59	N.D.
<i>AT2G13980</i>	21.53	4.47E-05	Nucleic acid binding	61.86	N.D.
<i>AT2G14560</i>	5.63	2.74E-02	LURP1	2367.81	
<i>AT2G14610</i>	8.05	4.02E-03	PR1	1071.75	
<i>AT2G16050</i>	11.88	2.80E-05	Cys/His-rich C1 domain family	2189.97	N.D.
<i>AT2G17690</i>	33.87	7.44E-04	SDC	371.63	N.D.
<i>AT2G18540</i>	10.53	5.64E-05	Cupin family protein	4220.12	Endosperm
<i>AT2G18570</i>	5.62	7.10E-06	UDP-glucosyl transferase	1112.63	
<i>AT2G18660</i>	6.24	3.61E-02	EXLB3	2131.70	
<i>AT2G19010</i>	10.14	6.75E-04	GDSL-motif lipase family	28.37	Stamen
<i>AT2G32510</i>	9.54	1.40E-05	MAPKKK17	4246.57	Seed, cell culture
<i>AT2G36710</i>	7.52	1.75E-02	Pectinesterase family protein	109.41	Silique
<i>AT2G45580</i>	5.10	3.24E-03	CYP76C3	71.90	Petal
<i>AT3G01830</i>	5.10	6.97E-03	Putative calmodulin-related	664.29	Cell culture
<i>AT3G02100</i>	9.49	6.78E-04	UDP-glucosyl transferase	391.18	
<i>AT3G03400</i>	8.08	9.80E-06	Putative calmodulin-related	87.88	Endosperm
<i>AT3G09800</i>	12.54	1.69E-05	SNARE-like superfamily	107.87	
<i>AT3G10510</i>	8.07	6.60E-05	F-box family protein	5089.81	N.D.
<i>AT3G10595</i>	7.77	9.69E-03	Myb family transcription factor	46.40	N.D.
<i>AT3G11080</i>	5.85	1.02E-03	AtRLP35	130.89	
<i>AT3G16100</i>	6.31	3.92E-05	ATRABG3C	4268.40	
<i>AT3G18720</i>	8.06	8.27E-04	F-box family protein	49.30	Cell culture
<i>AT3G19020</i>	5.95	5.05E-04	Leucine-rich repeat family	1281.97	Stamen
<i>AT3G20950</i>	25.31	4.18E-05	CYP705A32	72.42	Endosperm
<i>AT3G21450</i>	8.58	1.19E-05	Protein kinase family protein	63.52	N.D.
<i>AT3G23060</i>	5.80	3.21E-02	Zinc finger family protein	21.55	Endosperm
<i>AT3G24542</i>	22.41	4.32E-05	β -galactosidase-related	73.15	N.D.
<i>AT3G30720</i>	9.24	4.07E-06	QQS	854.06	
<i>AT3G43580</i>	11.07	3.66E-05	β -galactosidase-related	197.93	N.D.
<i>AT3G44070</i>	28.98	4.03E-05	β -galactosidase-related	42.68	Stamen
<i>AT3G44790</i>	12.22	5.27E-05	MATH domain-containing	153.27	N.D.
<i>AT3G45510</i>	6.37	2.96E-03	Zinc finger family protein	10.55	
<i>AT3G48130</i>	9.44	2.68E-04	RSU1	900.86	Cell culture
<i>AT3G49850</i>	5.78	3.823e-03	TRB3	1756.24	
<i>AT3G53910</i>	37.21	3.80E-05	Malate dehydrogenase-related	56.15	
<i>AT3G56630</i>	7.13	6.75E-05	CYP94D2	1025.40	
<i>AT3G60260</i>	6.57	7.72E-05	ELMO1-related	5736.53	
<i>AT3G60870</i>	7.48	6.93E-05	DNA-binding protein-related	334.94	N.D.
<i>AT4G00700</i>	5.06	4.69E-02	C2 domain-containing protein	687.29	
<i>AT4G02380</i>	5.62	8.50E-03	SAG21	5900.49	
<i>AT4G03156</i>	10.68	5.79E-05	Small GTPase-related	124.88	Endosperm
<i>AT4G03950</i>	14.86	2.23E-04	Putative G6P translocator	16.99	
<i>AT4G04500</i>	5.22	2.16E-02	Protein kinase family protein	14.47	

<i>AT4G08039</i>	7.31	9.05E-04	DEFL family protein	51.10	N.D.
<i>AT4G08430</i>	30.32	3.91E-05	Ulp1 protease family protein	88.55	
<i>AT4G10655</i>	30.47	3.86E-05	DEFL family protein	207.35	N.D.
<i>AT4G10920</i>	5.71	4.02E-04	KELP	2635.59	
<i>AT4G11890</i>	5.98	2.76E-02	Protein kinase family protein	523.57	
<i>AT4G13890</i>	5.86	2.36E-05	EDA36	126.58	
<i>AT4G15417</i>	7.08	1.22E-02	ATRTL1	448.46	N.D.
<i>AT4G22170</i>	7.78	3.63E-03	F-box family protein	11.98	N.D.
<i>AT4G25530</i>	31.82	3.82E-05	FWA	172.42	Endosperm
<i>AT4G26390</i>	10.00	7.66E-06	Putative pyruvate kinase	57.63	Cell culture
<i>AT4G28420</i>	8.15	3.56E-02	Putative aminotransferase	241.51	
<i>AT4G29200</i>	46.34	3.58E-05	β -galactosidase-related	228.80	Root
<i>AT4G30040</i>	12.42	7.61E-04	Aspartyl protease family	142.59	
<i>AT4G30640</i>	5.40	3.95E-02	FBL19	228.28	
<i>AT4G34180</i>	6.15	5.53E-06	Cyclase family protein	2029.91	
<i>AT4G34680</i>	5.72	1.78E-02	GATA transcription factor 3	40.31	
<i>AT4G40080</i>	13.92	1.03E-05	ENTH domain-containing	453.85	Root
<i>AT5G01080</i>	23.45	4.09E-05	β -galactosidase-related	231.60	
<i>AT5G01400</i>	16.10	4.53E-05	ESP4	632.79	
<i>AT5G05870</i>	14.47	1.93E-06	UGT76C1	3065.78	
<i>AT5G06320</i>	5.27	1.55E-02	NHL3	783.45	
<i>AT5G07570</i>	8.42	2.79E-02	Glycine/proline-rich protein	23.03	
<i>AT5G07620</i>	6.03	2.35E-03	Protein kinase family protein	22.82	
<i>AT5G10760</i>	7.78	2.36E-03	Aspartyl protease family protein	303.22	
<i>AT5G15110</i>	37.62	1.82E-06	Lyase/pectate lyase	38.69	Stamen
<i>AT5G16500</i>	6.05	6.44E-04	Protein kinase family protein	39.37	Stamen
<i>AT5G22570</i>	5.02	2.28E-02	WRKY38	125.25	
<i>AT5G24240</i>	18.25	1.52E-06	PI3- and 4-kinase family	636.27	Stamen
<i>AT5G24480</i>	8.92	6.17E-06	β -galactosidase-related	224.33	Shoot apex
<i>AT5G26170</i>	5.63	1.12E-02	WRKY50	726.15	N.D.
<i>AT5G27960</i>	9.75	4.37E-04	AGL90	18.77	Endosperm
<i>AT5G28235</i>	36.91	5.16E-05	Ulp1 protease family protein	16.58	N.D.
<i>AT5G28360</i>	6.49	1.03E-03	ACS3	2219.90	
<i>AT5G29560</i>	39.89	4.76E-06	Calcium ion binding	10.36	N.D.
<i>AT5G32590</i>	14.53	1.78E-04	Myosin heavy chain-related	14.52	
<i>AT5G35490</i>	5.72	5.12E-06	ATMRU1	4748.18	
<i>AT5G35760</i>	8.41	6.64E-04	β -galactosidase-related	17.94	
<i>AT5G35890</i>	27.04	7.89E-05	β -galactosidase-related	28.38	
<i>AT5G35917</i>	16.93	1.87E-06	CYP79A3P	678.76	N.D.
<i>AT5G35920</i>	19.32	1.42E-05	CYP79A4P	224.16	
<i>AT5G36140</i>	6.75	1.85E-05	CYP716A2	176.38	Root
<i>AT5G37200</i>	28.08	1.52E-05	Zinc finger family protein	10.83	N.D.
<i>AT5G37280</i>	26.59	4.03E-05	Zinc finger family protein	102.35	

<i>AT5G38190</i>	17.19	4.53E-05	Myosin heavy chain-related	118.06	
<i>AT5G39270</i>	65.55	3.56E-05	ATEXPA22	21.09	Endoseprm
<i>AT5G41830</i>	27.16	3.97E-05	F-box family protein-related	127.33	Embryo
<i>AT5G43630</i>	5.65	8.74E-05	TZP	7690.27	N.D.
<i>AT5G45890</i>	17.99	4.53E-05	SAG12	98.00	Senescing leaf
<i>AT5G46795</i>	13.11	1.20E-02	MSP2	33.68	Stamen
<i>AT5G49250</i>	31.00	3.95E-06	β -galactosidase-related	28.36	
<i>AT5G52340</i>	26.55	3.99E-05	ATEXO70A2	1047.44	Cell culture
<i>AT5G52750</i>	6.51	2.24E-02	Heavy-metal-associated domain	659.32	
<i>AT5G52760</i>	6.17	4.78E-02	Heavy-metal-associated domain	725.75	
<i>AT5G54700</i>	5.51	1.09E-03	Ankyrin repeat family protein	13.62	
<i>AT5G63225</i>	9.71	1.63E-02	Glycosyl hydrolase family	147.62	N.D.
<i>AT5G66380</i>	5.26	4.57E-04	ATFOLT1	147.32	

Supplemental Table 4. AGI annotated genes downregulated in *vim1/2/3*.

The AGI genes whose transcripts were decreased in *vim1/2/3* compared with wild-type (WT) plants (fold-change ≤ 0.2 , $p < 0.05$) are listed.

Gene	<i>vim1,2,3</i> intensity	WT intensity	<i>vim1/2/3</i> / WT	p-value	Gene_Name
AT1G05550	68.06	333.63	0.18	8.39E-03	Unknown
AT1G19500	105.00	550.90	0.14	1.20E-02	Unknown
AT1G20480	70.05	271.81	0.19	2.25E-02	4-coumarate--CoA ligase family
AT1G21980	255.44	1394.18	0.18	1.56E-03	ATPIP5K1
AT1G23940	20.90	142.05	0.14	1.25E-04	Adaptin family protein
AT1G26310	19.64	103.21	0.19	1.23E-03	CAL
AT1G26790	890.59	5036.02	0.16	1.09E-02	Zinc finger domain-containing protein
AT1G29610	221.50	2066.55	0.10	5.71E-05	Unknown
AT1G47655	115.76	790.80	0.14	7.97E-05	Zinc finger domain-containing protein
AT1G47840	773.19	2492.97	0.19	4.04E-02	HXK3
AT1G52000	153.33	1543.26	0.08	9.41E-04	Jacalin lectin family protein
AT1G58430	17.71	155.92	0.17	2.62E-02	RXF26; carboxylesterase/ hydrolase
AT1G58520	16.95	120.73	0.15	1.89E-04	RXW8
AT1G59406	33.35	168.56	0.17	3.10E-03	Putative GDSL-motif lipase
AT1G61270	13.74	111.33	0.14	1.89E-04	Putative Lys and His-specific transporter
AT1G62230	13.65	85.37	0.18	2.44E-03	Pseudogene
AT1G66100	4103.39	29874.67	0.14	3.15E-03	Putative thionin
AT1G68540	133.21	756.71	0.18	1.92E-05	Oxidoreductase family protein
AT1G77870	292.25	2374.74	0.12	2.86E-05	MUB5
AT1G77880	196.80	1116.10	0.19	1.04E-02	F-box family protein
AT2G04110	3476.19	33132.05	0.10	5.28E-05	Pseudogene
AT2G13550	787.63	8044.10	0.10	5.46E-05	Unknown
AT2G15128	735.59	4572.39	0.16	7.62E-05	ncRNA
AT2G16367	3302.59	23244.44	0.16	2.41E-02	DEFL family protein
AT2G20870	256.11	1841.60	0.14	5.84E-06	Putative cell wall protein precursor
AT2G28180	47.29	261.08	0.15	2.35E-02	ATCHX8
AT2G36490	142.24	2598.14	0.05	1.11E-05	DML1
AT2G37555	13.94	99.12	0.20	2.91E-02	ncRNA
AT2G39950	138.70	804.11	0.16	1.41E-05	Unknown
AT2G45540	658.07	4175.13	0.13	2.17E-03	WD-40 repeat family protein
AT2G46375	115.03	505.97	0.16	1.42E-02	Unknown
AT3G03840	13.28	70.02	0.20	2.30E-03	Putative auxin-responsive protein
AT3G06435	700.65	5045.30	0.13	5.47E-06	Unknown
AT3G07610	285.35	1755.54	0.16	7.15E-05	IBM1
AT3G09160	728.85	4967.44	0.15	4.20E-06	RRM-containing protein
AT3G12460	15.74	100.09	0.17	3.34E-04	Polynucleotidyl transferase

AT3G16120	472.71	2956.60	0.18	1.98E-03	Putative dynein light chain
AT3G21020	67.97	575.94	0.14	3.79E-03	TE
AT3G25795	129.29	622.29	0.17	2.16E-02	ncRNA
AT3G46490	104.35	1182.98	0.09	5.57E-05	Fe(II)-dependent oxygenase superfamily
AT3G62570	233.07	989.65	0.18	2.56E-03	TPR-like superfamily protein
AT4G03298	26.67	232.18	0.13	2.01E-02	Unknown
AT4G03935	358.27	2135.43	0.18	5.33E-05	ncRNA
AT4G06701	90.24	858.78	0.12	2.74E-04	ncRNA
AT4G08570	298.31	1894.32	0.18	2.86E-04	Heavy metal transport superfamily protein
AT4G08874	85.75	404.37	0.18	4.42E-04	Unknown
AT4G09430	32.15	239.58	0.16	1.06E-04	Putative TIR-NBS-LRR class protein
AT4G13690	61.04	617.99	0.10	4.55E-02	Unknown
AT4G15200	25.56	339.11	0.10	7.98E-03	Actin binding
AT4G25010	110.21	446.03	0.15	1.90E-02	Nodulin MtN3 family protein
AT4G33790	573.62	3228.48	0.17	3.90E-03	CER4
AT5G03250	25.48	133.26	0.19	6.04E-04	NPH3 family protein
AT5G10140	32.34	171.98	0.19	1.46E-04	FLC
AT5G15800	78.49	418.56	0.20	1.13E-02	SEP1
AT5G20240	170.29	1078.50	0.10	1.52E-02	PI
AT5G22430	54.74	736.57	0.07	1.02E-05	Unknown
AT5G23970	13.58	105.55	0.19	3.46E-02	Transferase family protein
AT5G24770	4205.83	29227.68	0.13	3.80E-03	VSP2
AT5G24780	833.38	6905.88	0.11	4.56E-04	VSP1
AT5G28440	1097.59	5668.56	0.19	3.54E-05	Unknown
AT5G38120	186.61	1120.24	0.15	2.79E-03	4-coumarate--CoA ligase family protein
AT5G39190	3943.27	22899.74	0.19	3.51E-05	GER2
AT5G49615	137.63	587.36	0.18	3.84E-02	ncRNA
AT5G57420	116.27	650.79	0.12	5.58E-03	IAA33
AT5G59100	60.06	249.65	0.20	2.03E-02	Subtilase family protein
AT5G59130	89.63	413.68	0.16	4.33E-02	Subtilase family protein
AT5G60142	45.08	266.23	0.18	6.01E-03	DNA binding
AT5G60910	34.06	193.72	0.16	2.42E-03	AGL8
AT5G62080	38.62	722.68	0.11	4.72E-02	Protease inhibitor family protein

Supplemental Table 5. Putative β -galactosidase genes upregulated in *vim1/2/3*.

β -galactosidase genes that were transcriptionally upregulated in *vim1/2/3* compared with wild-type type (WT) plants (fold-change ≥ 5.0 , $p < 0.05$) are listed.

Gene	<i>vim1/2/3</i> /WT	p-value	Signal intensity in WT	TE existence*
<i>AT1G37000</i>	5.05	6.27E-03	12.86	Y
<i>AT3G24542</i>	22.41	4.32E-05	73.15	N
<i>AT3G43580</i>	11.07	3.66E-05	197.93	Y
<i>AT3G44070</i>	28.98	4.03E-05	42.68	Y
<i>AT4G29200</i>	46.34	3.58E-05	228.80	N
<i>AT5G01080</i>	23.45	4.09E-05	231.60	N
<i>AT5G24480</i>	8.92	6.17E-06	224.33	Y
<i>AT5G35760</i>	8.41	1.00E-03	17.94	Y
<i>AT5G35890</i>	27.04	7.89E-05	28.38	Y
<i>AT5G49250</i>	31.00	3.95E-06	28.36	Y

* Y, at least one TE was positioned proximately to or inside of the gene; N, no TE was positioned proximately to or inside of the gene.

Supplemental Table 6. Oligonucleotide primers used in this study

Name	Sequence (5'→3')	Description
AT1G47350-F	TGT TTC GGT AGT TGG AGT GA	RT-PCR, qRT-PCR
AT1G47350-R1	TTC GTC GTG GTC TGA TTG TT	RT-PCR
AT1G47350-R2	TTC TAC GCT TTA GCA GAC CA	qRT-PCR
AT1G47350BI-F1	TTC TCA CTC TAA TCT CTC TC	Bisulfite sequencing
AT1G47350BI-R1	TAA AYG TGA GTA GTA GGT AG	Bisulfite sequencing
AT1G47350BI-F2	ATY GAA AAT AAT GGY TTG TGA AG	Bisulfite sequencing
AT1G47350BI-R2	CAC ATC AAA RCA AAC TAC CAC	Bisulfite sequencing
AT1G47350IP-F1	TTC TCA CTC TAA TCT CTC TC	ChIP-qPCR
AT1G47350IP-R1	AGT TCG GTA ATT TCG GTG TT	ChIP-qPCR
AT1G47350IP-F2	AGA GGA TGA TTA CGA TGG AG	ChIP-qPCR
AT1G47350IP-R2	GTC AAT CGG ATC ATA CCC GA	ChIP-qPCR
AT2G06562-F1	ATC GAA TTC TGA TGC GTC GA	RT-PCR, qRT-PCR
AT2G06562-R1	GTA CTT CAG CAG CTG ACG GA	RT-PCR
AT2G06562-F2	ATC GAA TTC TGA TGC GTC GA	qRT-PCR
AT2G06562BI-F1	GTT GTT GAG ATY GTA TAT ATT TYA	Bisulfite sequencing
AT2G06562BI-R1	AAT TTG AGC CCT CTT GTC TAC AAC	Bisulfite sequencing
AT2G06562BI-F2	CCC RCC ATC ATC RAT TCA TCA A	Bisulfite sequencing
AT2G06562BI-R2	GGG GAA TTT GGG GAT GYA TAG A	Bisulfite sequencing
AT2G06562IP-F1	AGT GTT GGC TTC TCT GTT ACC TCA	ChIP-qPCR
AT2G06562IP-R1	GTA GAT CAA GGG AAA ATC TCC	ChIP-qPCR
AT2G06562IP-F2	AGC ACT TAT GTT ATG CAC GG	ChIP-qPCR
AT2G06562IP-R2	GGG AAT TTG GGG ATG CAT AG	ChIP-qPCR
AT3G44070-F1	ACC GTA ACT TCC TCG ACC TC	RT-PCR
AT3G44070-R1	AGA CGA AGT GGC GTT GGT GT	RT-PCR, ChIP-qPCR
AT3G44070-F2	GCT TTA TTA CCC GAC ATT TAC G	qRT-PCR
AT3G44070-R2	GCG AAT GGA AGT AGT GTA GAG	qRT-PCR
AT3G44070BI-F1	CRT TCA TTR ARA CCC ACC CCT TTA	Bisulfite sequencing
AT3G44070BI-R1	GGG ATA TGG AGA TAA GAG GTY GAG	Bisulfite sequencing
AT3G44070BI-F2	RAC TAC CTT TCA TCA ARC TCT CTA	Bisulfite sequencing
AT3G44070BI-R2	AYA AAG ATG GAG GGG AAA TGA ATT	Bisulfite sequencing
AT3G44070IP-F1	TTC ATT GAG ACC CAC CCC TT	ChIP-qPCR
AT3G44070IP-R1	TTG GTT CCA TAG ATC GAC AC	ChIP-qPCR
AT3G44070IP-F2	ATC GGA GTA CCG TCT TTG CT	ChIP-qPCR
AT3G53910-F1	CCC ATA CGC TAT GAT ATC GT	RT-PCR

AT3G53910-R1	GCA ACA AAA GTC CTC TGT AG	RT-PCR
AT3G53910-F2	AGA GAA TTG AGG AAG TGA TAG ATT	qRT-PCR, ChIP-qPCR
AT3G53910-R2	TCT GTA GCA AAG TGA TGT CTT	qRT-PCR, ChIP-qPCR
AT3G53910BI-F1	AAC CAC CTA ACR ACA ACT CC	Bisulfite sequencing
AT3G53910BI-R1	GAG GAY AAA GAY GAG AAG GA	Bisulfite sequencing
AT3G53910BI-F2	GGG TTG GAA GTG AAT YGG ATG ATA	Bisulfite sequencing
AT3G53910BI-R2	ACA ACA CAC ATA RTT CCA TRT CTT	Bisulfite sequencing
AT3G53910IP-F1	AAC CAC CTA ACG ACA ACT CC	ChIP-qPCR
AT3G53910IP-R1	CTT CGC AAA AGG TAA TCG GA	ChIP-qPCR
ESP4-F1	CAG CCA GCC AGA GAT TCA ATC TTC	RT-PCR
ESP4-R1	AGA CTG GCC AGT ACC AAT AGG ACT	RT-PCR, qRT-PCR
ESP4-F2	GAG TCA GTC TCA GAA CAG TC	qRT-PCR
ESP4BI-F1	CCC ACA TCR RCC CAT TAT TAC T	Bisulfite sequencing
ESP4BI-R1	TGA TTT GGY GGA ATT YGY GAG A	Bisulfite sequencing
ESP4BI-F2	GAT GGT GTA TTY TYY ATG GAG	Bisulfite sequencing
ESP4BI-R2	TTC TCT TCC ACT RAT ACC TR	Bisulfite sequencing
ESP4IP-F1	CCC ACA TCG GCC CAT TAT TA	ChIP-qPCR
ESP4IP-R1	GTT ACA CTA CGT CGT TTG GA	ChIP-qPCR
ESP4IP-F2	TTC AGG ACA AAG ACA GTG TAG AAG	ChIP-qPCR
ESP4IP-R2	TTC TCT TCC ACT GAT ACC TG	ChIP-qPCR
MSP2-F1	ACC TTC CGA AAT GGA AAG ACG AAA	RT-PCR
MSP2-R1	GCA GCC CAA TAA GCT AAA ACG AGA	RT-PCR
MSP2-F2	TCC TTT TCA TGT CCC CTT AC	qRT-PCR
MSP2-R2	CTC CAG TAA TGG CTT CTC TAC	qRT-PCR
MSP2BI-F1	GGT TTA TAA ATT GGA GTT AAT ATT TA	Bisulfite sequencing
MSP2BI-R1	CAA TTT ACA ACR AAA TCC AAR TRT TC	Bisulfite sequencing
MSP2BI-F2	ATG GAG AYG ATT GAG YAA CAA	Bisulfite sequencing
MSP2BI-R2	TTC ACC ARA CCC TCC ART TRA A	Bisulfite sequencing
MSP2IP-F1	GGT TTA TAA ATT GGA GTT AAT A	ChIP-qPCR
MSP2IP-R1	TTT CCT GTT GAC ACT CTC TA	ChIP-qPCR
MSP2IP-F2	ACC TTC CGA AAT GGA AAG ACG AAA	ChIP-qPCR
MSP2IP-R2	GCG ATT CGA TCT AGT AAC GA	ChIP-qPCR
QQS-F1	CCT CTC ATT ACC TCT CAT CAA ACA	RT-PCR
QQS-R1	ACC CAT GAT ATG ACC CTC ATT TTG	RT-PCR
QQS-F2	CCT TAT TTC TCG CTT TGT CT	qRT-PCR
QQS-R2	AGA ACC AAA CAC CAA CTG GT	qRT-PCR, ChIP-qPCR
QQSBI-F1	TCT RTA CCC AAA CCT TAT CCC	Bisulfite sequencing
QQSBI-R1	GAT GTA GAA GTG TGA GGY AAA	Bisulfite sequencing
QQSBI-F2	AGG TTA TAG AAG ATY TGG GTT G	Bisulfite sequencing

QQSBI-R2	CCT TTC AAT RTC CAT CAA ATT C	Bisulfite sequencing
QQSIP-F1	TCT GTA CCC AAA CCT TAT CCC	ChIP-qPCR
QQSIP-R1	ACC TGT GGA GAA AAT GAA GC	ChIP-qPCR
QQSIP-F2	AGG TTA TAG AAG ATC TGG GTT G	ChIP-qPCR
AT4G08430-F1	AGA ATG CAA GCA GCA GAT TG	RT-PCR
AT4G08430-R1	CCT TTA CAG CTG TCT TCT TC	RT-PCR
AT4G08430-F2	TCA CAA TTA GTG ACA TGG AC	qRT-PCR
AT4G08430-R2	GCT TCA TTG CAT ACT ACA AG	qRT-PCR
AT4G15242-F1	ATC TAG AGA TTC TGC GAT CTG	RT-PCR, qRT-PCR
AT4G15242-R1	TCT GAT GTG GTT GAG CTT AG	RT-PCR
AT4G15242-R2	AGC ACT ACA AGC TAC ACC TA	qRT-PCR
AT5G35890-F1	GGT TAT GGA CTC CGC TTA AGC CAT	RT-PCR, qRT-PCR
AT5G35890-R1	AAT GCT ACG GAG CCG ACT GGT ACC	RT-PCR
AT5G35890-R2	CAC CAA GTC CAT TAG CCT AAA GC	qRT-PCR
AGL90-F1	ACC CAT CTT ATG GAG AGG AT	RT-PCR
AGL90-R1	TCA TAT TCG CAT TTG CGT CC	RT-PCR, qRT-PCR
AGL90-F2	TCG TTT TCC GAC TCT CCT AT	qRT-PCR
CYP79A4P-F1	TGT CCA CTA CTG ATG TTG TG	RT-PCR, qRT-PCR
CYP79A4P-R1	GAT CAC TCT TGC TTA CTG AA	RT-PCR
CYP79A4P -R2	CAG GAT CAA ACT TAA GCG GT	qRT-PCR
CYP705A32-F1	GTT CAA GAA ACC GAT CTA CC	RT-PCR
CYP705A32-R1	AGC AGC CTC GTT CAT GTT TA	RT-PCR, qRT-PCR
CYP705A32-F2	TAC ATG CCT TTC TCA ACT GG	qRT-PCR
ACT2-F1	TTC CGC TCT TTC TTT CCA AGC TCA	RT-PCR
ACT2-R1	AAG AGG CAT CAA TTC GAT CAC TCA	RT-PCR
ACT2-F2	TCC CTC AGC ACA TTC CAG CAG AT	qRT-PCR
ACT2-R2	AAC GAT TCC TGG ACC TGC CTC ATC	qRT-PCR
UBQ10-F1	TGT TTA GTG CAG TTC TGC GAA AC	qRT-PCR
UBQ10-R1	CAG CTC AAC ACT TTC GCT ACA TCT	qRT-PCR
