

Supplementary information

Genetic analyses of autoimmune mutants uncover the *MPK3/6-CHR5-SNC1* module in *Arabidopsis*

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Table S1. Pairwise comparisons, using Student's *t*-tests, of qRT-PCR results presented in **Fig. 3**.

In red, *p*-value < 0.05

<i>PAD3</i>	0 h WT	0 h chr5-1	0 h MPK3- CA	0 h MPK3- CA chr5-1	2 h WT	2 h chr5-1	2 h MPK3- CA	2 h MPK3- CA chr5-1	8 h WT	8 h chr5-1	8 h MPK3- CA
0 h chr5-1	0.4283	-	-	-	-	-	-	-	-	-	-
0 h MPK3-CA	0.2014	0.2144	-	-	-	-	-	-	-	-	-
0 h MPK3-CA chr5-1	0.2820	0.4595	0.2454	-	-	-	-	-	-	-	-
2 h WT	0.0087	0.0074	0.4389	0.0301	-	-	-	-	-	-	-
2 h chr5-1	0.0155	0.0165	0.3644	0.0953	0.3566	-	-	-	-	-	-
2 h MPK3-CA	0.0029	0.0029	0.0014	0.0028	0.0033	0.0032	-	-	-	-	-
2 h MPK3-CA chr5-1	0.0115	0.0117	0.0536	0.0117	0.0170	0.0153	0.0114	-	-	-	-
8 h WT	0.0879	0.2431	0.2461	0.9829	0.0156	0.0481	0.0030	0.0125	-	-	-
8 h chr5-1	0.5456	0.7031	0.2079	0.3577	0.0088	0.0166	0.0029	0.0116	0.1343	-	-
8 h MPK3-CA	0.0047	0.0047	0.0299	0.0042	0.0063	0.0057	0.0142	0.7430	0.0050	0.0048	-
8 h MPK3-CA chr5-1	0.0207	0.0216	0.7134	0.0222	0.0596	0.0434	0.0027	0.0418	0.0254	0.0214	0.0116

<i>SNCI</i>	0 h WT	0 h chr5-1	0 h MPK3- CA	0 h MPK3- CA chr5-1	2 h WT	2 h chr5-1	2 h MPK3- CA	2 h MPK3- CA chr5-1	8 h WT	8 h chr5-1	8 h MPK3- CA
0 h chr5-1	0.35853	-	-	-	-	-	-	-	-	-	-
0 h MPK3-CA	0.48754	0.23882	-	-	-	-	-	-	-	-	-
0 h MPK3-CA chr5-1	0.96790	0.40934	0.52393	-	-	-	-	-	-	-	-
2 h WT	0.03596	0.01965	0.14341	0.03890	-	-	-	-	-	-	-
2 h chr5-1	0.11214	0.06160	0.32269	0.12075	0.64895	-	-	-	-	-	-
2 h MPK3-CA	0.00029	0.00011	0.01559	0.00090	0.13018	0.09151	-	-	-	-	-
2 h MPK3-CA chr5-1	0.00181	0.00046	0.07488	0.00620	0.80369	0.45862	0.03266	-	-	-	-
8 h WT	0.02600	0.07011	0.07201	0.05452	0.01136	0.02889	0.00015	9.7e-05	-	-	-
8 h chr5-1	0.03275	0.09191	0.08052	0.06534	0.01253	0.03152	0.00021	0.00014	0.68590	-	-
8 h MPK3-CA	0.03247	0.10379	0.08089	0.06607	0.01131	0.03047	8.4e-05	6.0e-05	0.68155	0.93493	-
8 h MPK3-CA chr5-1	0.01004	0.01730	0.03946	0.02258	0.00815	0.01920	0.00022	0.00014	0.02597	0.01056	0.03335

<i>PRI</i>	0 h WT	0 h chr5-1	0 h MPK3- CA	0 h MPK3- CA chr5-1	2 h WT	2 h chr5-1	2 h MPK3- CA	2 h MPK3- CA chr5-1	8 h WT	8 h chr5-1	8 h MPK3- CA
0 h chr5-1	0.71	-	-	-	-	-	-	-	-	-	-
0 h MPK3-CA	0.27	0.26	-	-	-	-	-	-	-	-	-
0 h MPK3-CA chr5-1	0.90	0.85	0.27	-	-	-	-	-	-	-	-
2 h WT	0.46	0.61	0.25	0.61	-	-	-	-	-	-	-
2 h chr5-1	0.47	0.64	0.25	0.62	1.00	-	-	-	-	-	-
2 h MPK3-CA	0.19	0.18	0.98	0.18	0.17	0.17	-	-	-	-	-
2 h MPK3-CA chr5-1	0.73	0.94	0.26	0.88	0.42	0.50	0.18	-	-	-	-
8 h WT	0.20	0.17	0.41	0.18	0.15	0.15	0.32	0.17	-	-	-
8 h chr5-1	0.34	0.41	0.25	0.47	0.60	0.66	0.17	0.26	0.13	-	-
8 h MPK3-CA	0.36	0.34	0.85	0.35	0.33	0.33	0.85	0.34	0.53	0.32	-
8 h MPK3-CA chr5-1	0.31	0.34	0.25	0.44	0.44	0.56	0.17	0.15	0.13	0.98	0.32

Table S2. List of all the primers used in this work.

Gene	Forward primer sequence (5'→3')	Reverse primer sequence (5'→3')	T-DNA LB primer name/sequence (5'→3') or other comment	Usage
<i>ACTIN2</i>	CGTTTCTATGATGCACTTGTGTG	GGGAACAAAAGGAATAAAGAGG	/	qRT-PCR
<i>CHR5/chr5-1</i>	TCCATAGCAACTCAAGGACT	GCTGCGAACTTCACTACTCT	LB3/TAGCATCTGAATTCATAACCAATCTCGATACAC	Genotyping
<i>CHR5/chr5-2</i>	TCTTCCTAAGAGAGATGCGC	CGTTTGCTTTAACTGGCACA	LBb1.3/ATTTTGCCGATTTCGGAAC	Genotyping
<i>MPK3/mpk3-1</i>	TCTGCCTTTTCACGGAATATG	ATTTTGTCAACAATGGCCTG	LBb1.3/ATTTTGCCGATTTCGGAAC	Genotyping
<i>MPK4/mpk4-3</i>	CGCTCTAACCAACCCTTAAGT	TTACCGGGAAACAAGGGCTC	PCR + sequencing	Genotyping
<i>MPK4/mpk4-3</i>	TAGCAATTTGCTCCTGAATGCAAATGTGATCTAAAGCTCG	AGGGTACTGTGGAAGCTGTCTAAC	dCAPS with XhoI	Genotyping
<i>MPK6/mpk6-2</i>	GAATTCTGAAACTAACGAGAGCGTTG	CTGGTGACGGTACCATCTCGTGAC	LBb1.3/ATTTTGCCGATTTCGGAAC	Genotyping
<i>PAD3</i>	CTTTAAGCTCGTGGTCAAGGAGAC	TGGGAGCAAGAGTGGAGTTGTTG	/	qRT-PCR
<i>PR1</i>	GATCCTCGTGGGAATTATGTG	TTCTCGTAATCTCAGCTCTTATTTG	/	qRT-PCR
<i>SAND</i>	AACTCTATGCAGCATTGATCCACT	TGATTGCATATCTTTATCGCCATC	/	qRT-PCR
<i>SNC1/snc1-1</i>	CAGAACTCTTCTTGGAATACGTTTGCC	GATTCCAAGTTGAGATCGGTTGG	PCR + sequencing	Genotyping
<i>SNC1/snc1-1</i>	CAGAACTCTTCTTGGAATACGTTTGCC	GATTCCAAGTTGAGATCGGTTGG	CAPS with XbaI	Genotyping
<i>SNC1</i>	ACCGGCGAATTTGAAAGGTCT	TCCGAAGATCATATCCGGCCATAAC	/	qRT-PCR
<i>SUMM2/summ2-8</i>	AAGGTTTATGCATCAACGTGG	GAAACATGGTTTCACCTGCTC	LB3/TAGCATCTGAATTCATAACCAATCTCGATACAC	Genotyping

Figure S1

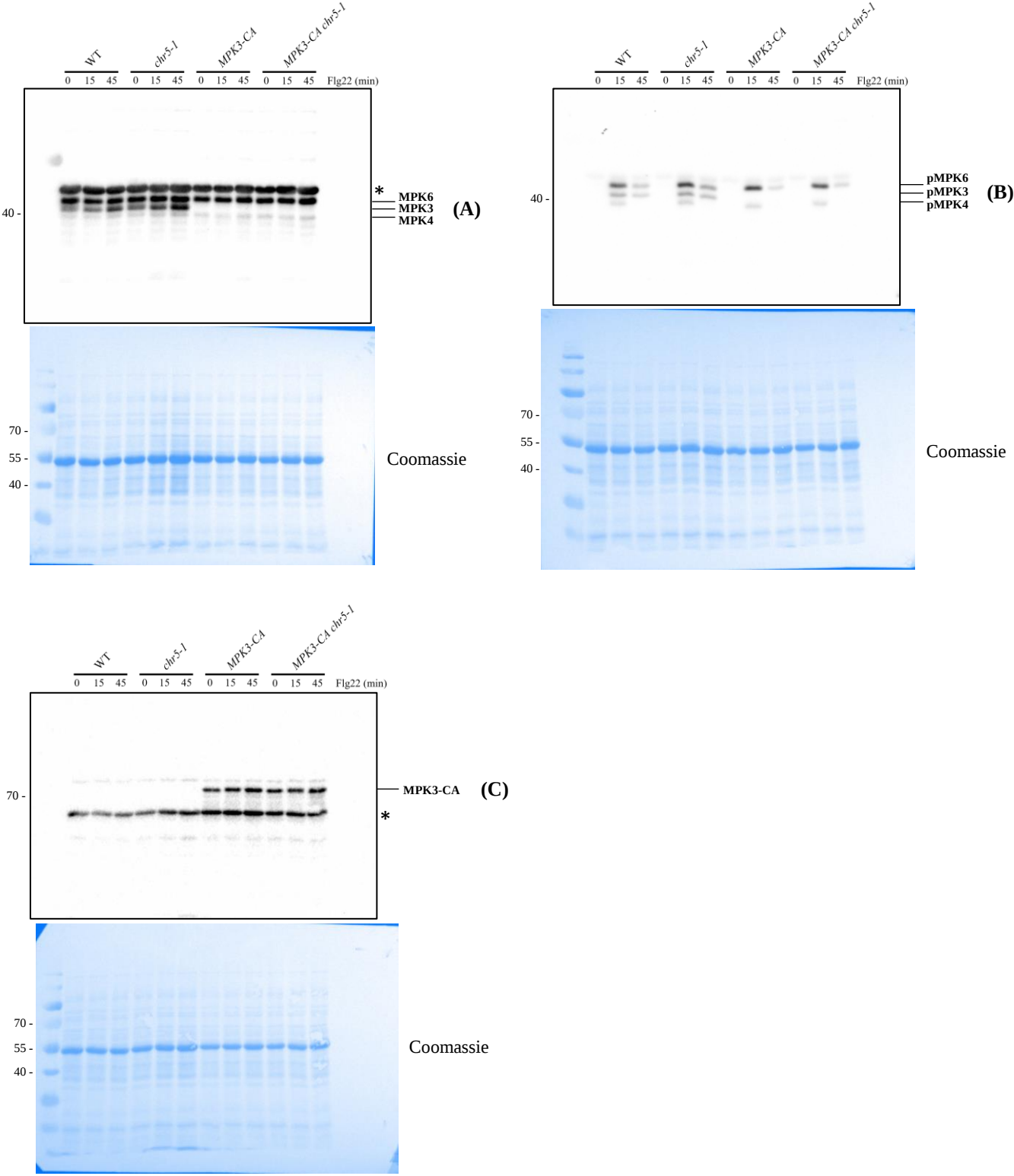


Fig. S1. Original blots of results presented in **Fig. 4.** (A) MPK i proteins were detected together with specific anti-MPK3, anti-MPK4 and anti-MPK6 antibodies. (B) pMPK i stands for the activated form of MAPKs as revealed by their phosphorylated state using the anti-phospho-p44/42 MAPK (Erk1/2) (Thr202/Tyr204) antibody. (C) The multi-tagged MPK3-CA protein was detected with a specific anti-Myc antibody. (A, B, C) Coomassie blue staining (Coomassie) of blots indicates the equal loading of protein samples. Molecular weights are indicated in kDa on the left of blots. Unspecific protein bands recognized by some antibodies are indicated with an asterisk (*).

Figure S2

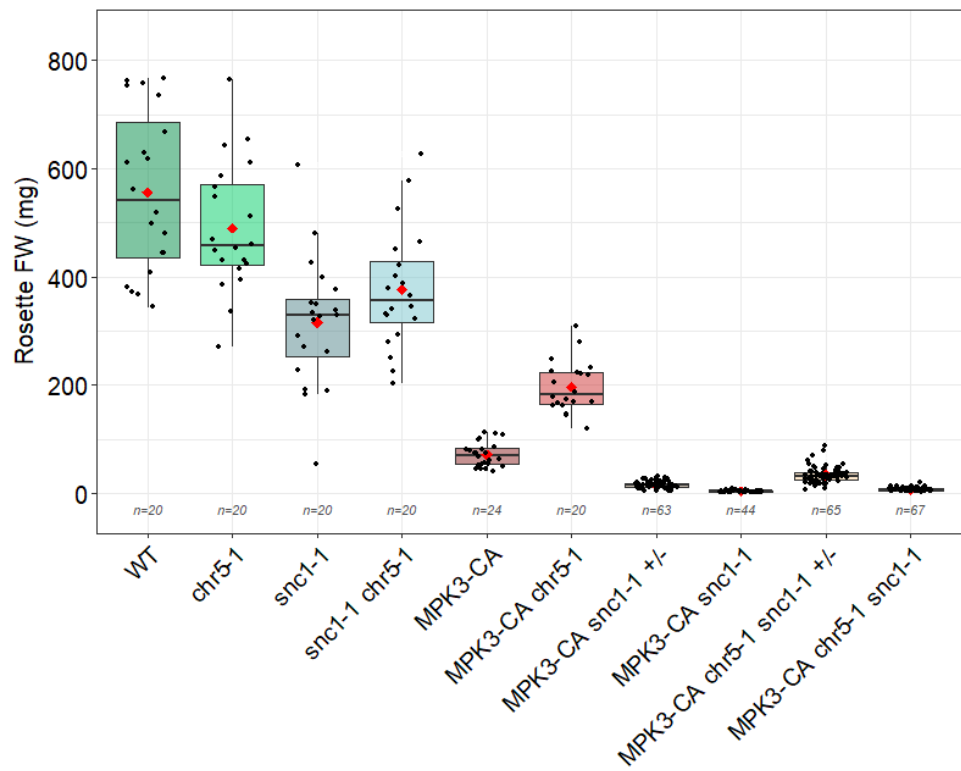


Fig. S2. Combined representation of all the genotypes presented in Fig. 5B-C.

Figure S3

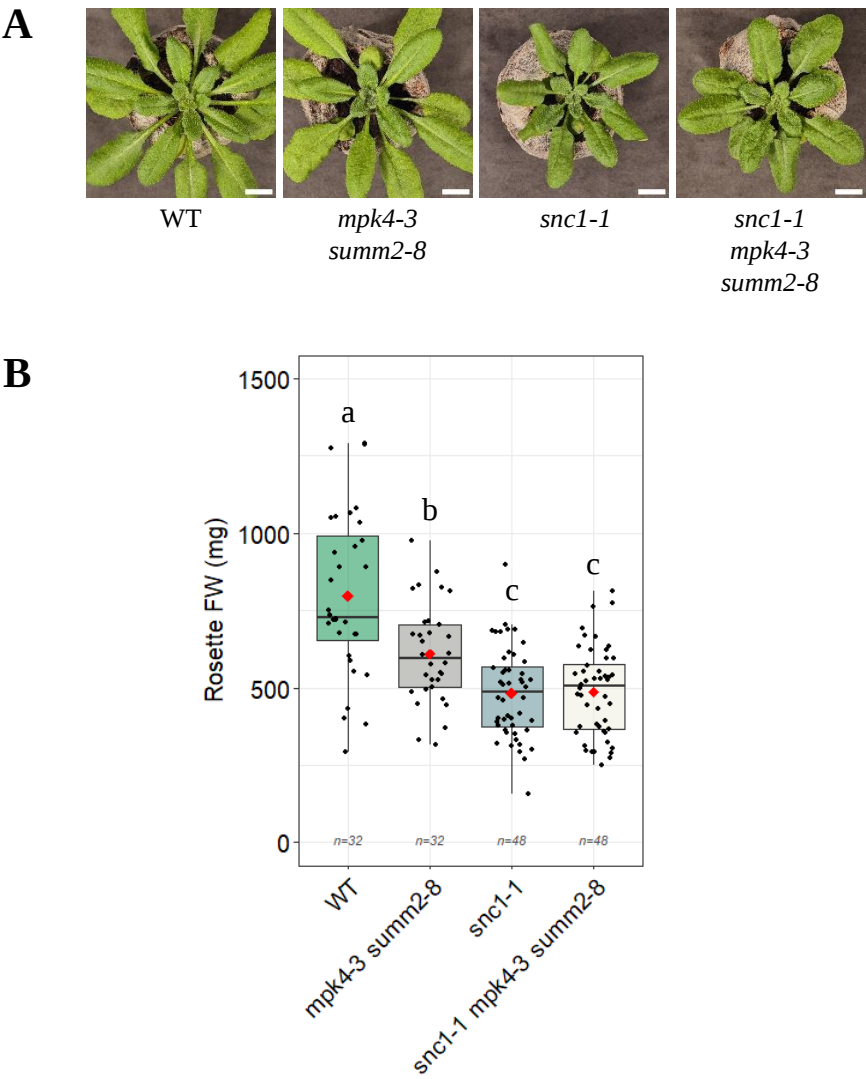


Fig. S3. Evaluation of *mpk4-3 summ2-8* mutant on *snc1-1* phenotype. (A) Representative pictures of 35-day-old plants of indicated genotypes. Scale bars represent 1 cm. (B) Rosette fresh weight (FW) of 35-day-old plants. For each boxplot, boundaries represent the first and third quartiles, a horizontal black line represents the median, a red diamond represents the mean, and *n* indicates the number of samples. Multiple comparisons were tested with the Kruskal-Wallis rank sum test followed by Dunn post-hoc tests using the Benjamini-Hochberg method for *p*-values adjustment. Different letters above boxplots indicate a statistical difference (*p*-value < 0.05) between the corresponding genotypes.