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2 **Supplemental Figure S1. Transcription profiles of *LecRK-VIII.2* during plant growth and**
3 **development.**

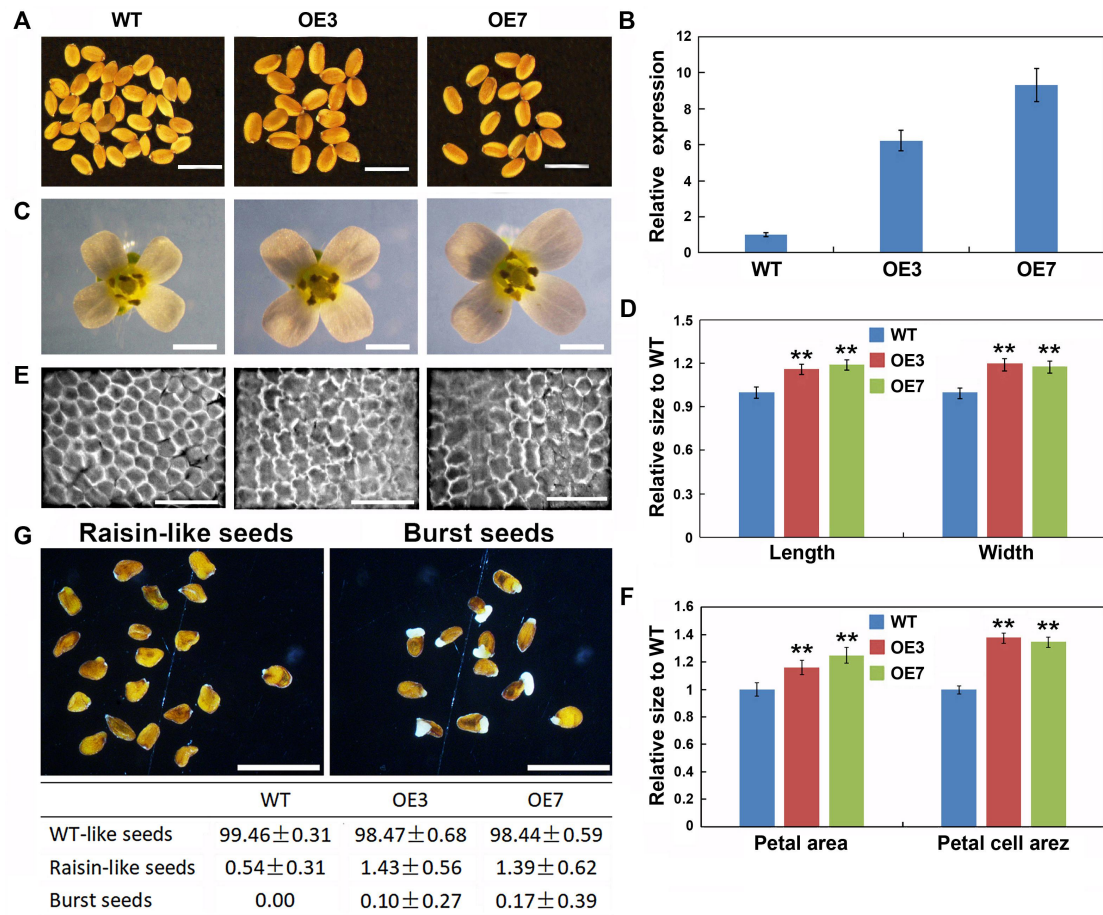
4 **A** *LecRK-VIII.2* is strongly expressed in developing seed, especially at the stage 6 and 7.

5 **B** *LecRK-VIII.2* is highly expressed in seed coat.

6 **C** The primers P1/P2 is qualified for checking *LecRK-VIII.2* expression. The gDNA-free RNA
7 samples were obtained using the RNA-miniprep kit containing gDNA wiper, which was checked
8 by P3/P4 primers.

9 **D** The expression level of *LecRK-VIII.2* in dry seeds, seedlings, roots, rosettes, cauline leaves,
10 flowers at the 15th stage, siliques and developing seeds. Values are means \pm SE relative to the
11 *LecRK-VIII.2* level in dry seeds, which is set at 1 (primers in Supplemental Table 1, n=three
12 biological replicates).

13 These transcriptional patterns were retrieved from the *Arabidopsis* eFP Browser
14 (<http://bar.utoronto.ca/>).



15

16 **Supplemental Figure S2. Overexpression of *LecRK-VIII.2* affects organ size and seed**
 17 **development.**

18 **A** Mature seeds of WT, OE3 and OE7, bar=500 μ m.

19 **B** Relative expression level of *LecRK-VIII.2* in 7-day-old seedlings of WT, OE3 and OE7.

20 **C** flowers (bar=1 mm) of WT, OE3 and OE7 plants.

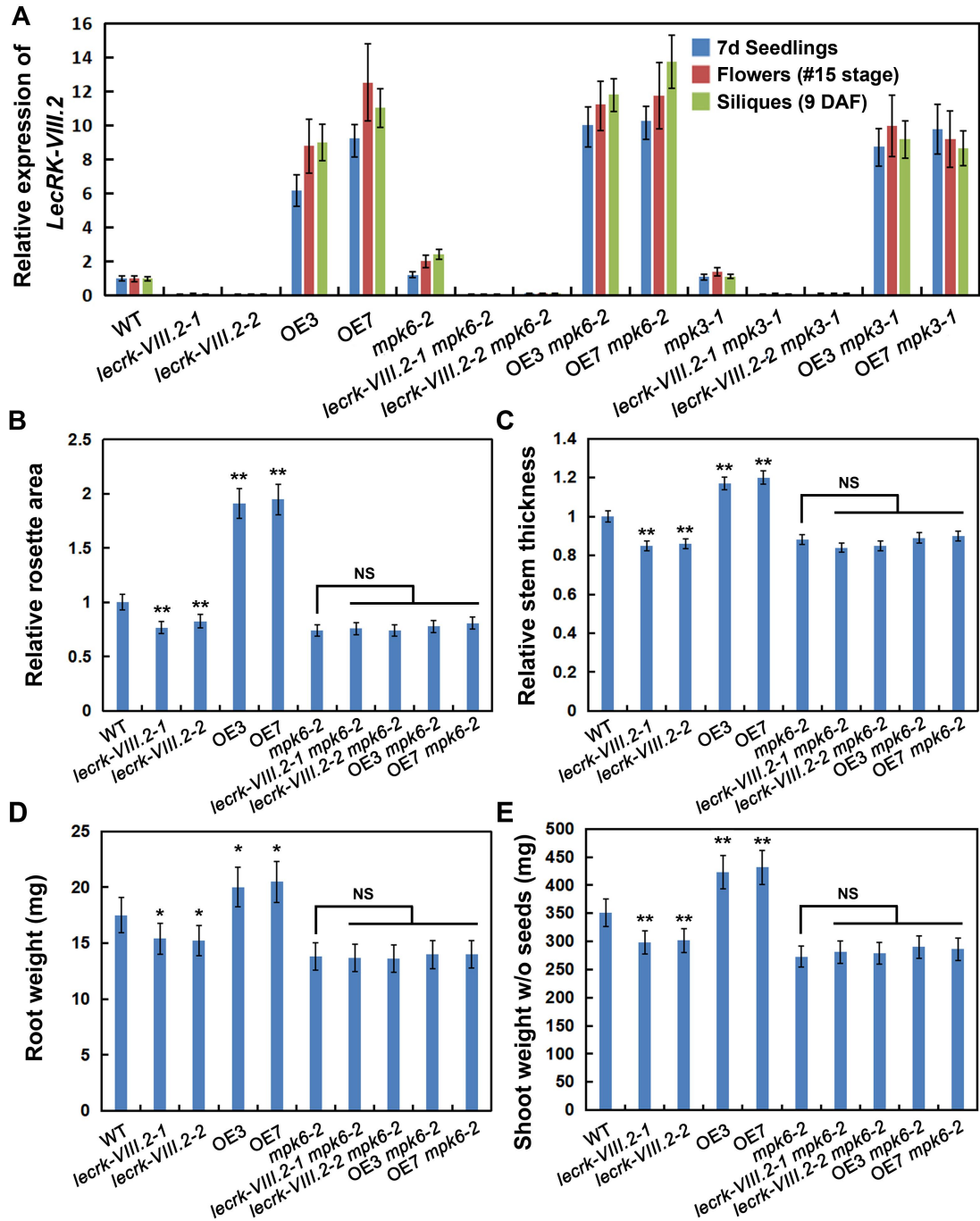
21 **D** Relative seed length and width of WT, OE3 and OE7 plants.

22 **E** Epidemic cells in petal of WT, OE3 and OE7 plants, bar=40 μ m.

23 **F** Relative size of petal and petal epidermic cells from WT, OE3 and OE7.

24 **G** OE plants develops raisin-like seeds and burst seeds, bar=600 μ m.

25 Values are means \pm SE (**B**, n= three biological replicates; **D**, n>300 seeds; **F**, n>20 petals and
 26 n>120 cells) relative to the WT value that is set at 1. ******P < 0.01 compared with the WT (Student's
 27 *t* test).

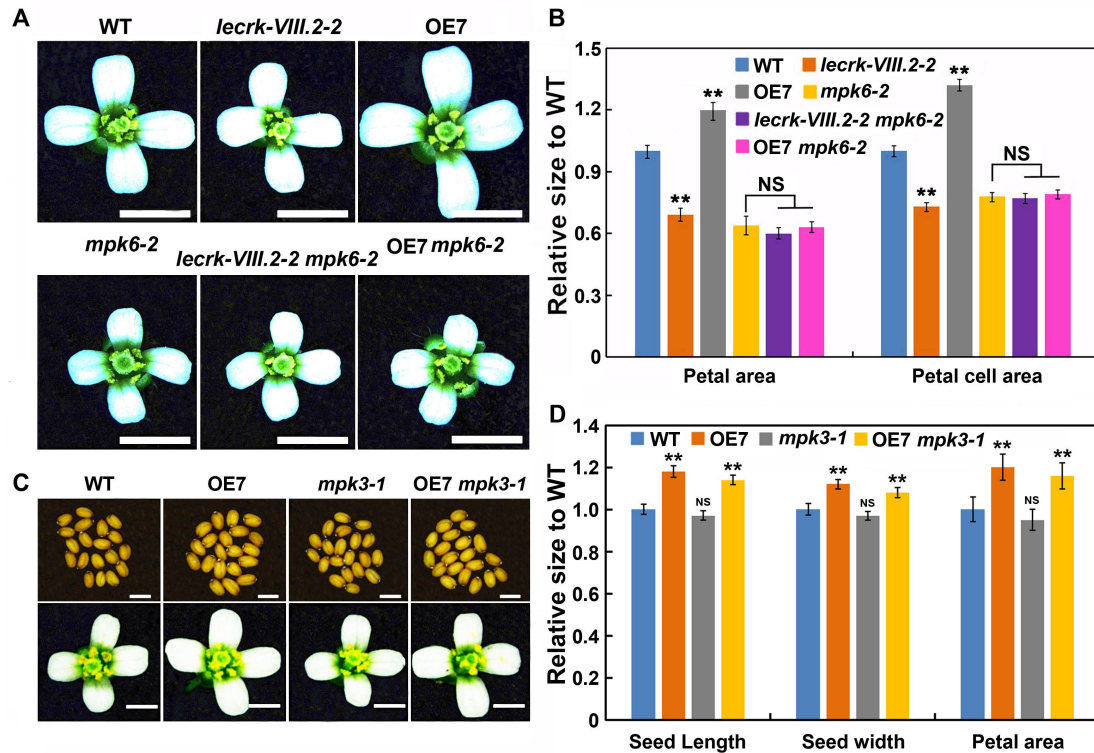


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29 **Supplemental Figure S3. *LecRK-VIII.2* acts upstream of *MPK6* to control the growth of**
 30 **rosette and stem.**

31 A Relative expression of *LecRK-VIII.2* in 7-day-old seedlings, flowers (#15 stage) and siliques (9
 32 DAF) of WT, *lecrk-VIII.2-1*, *lecrk-VIII.2-2*, OE3, OE7, *mpk6-2*, *lecrk-VIII.2-1 mpk6-2*,
 33 *lecrk-VIII.2-2 mpk6-2*, OE3 *mpk6-2*, OE7 *mpk6-2*, *mpk3-1*, *lecrk-VIII.2-1 mpk3-1*, *lecrk-VIII.2-2*
 34 *mpk3-1*, OE3 *mpk3-1*, OE7 *mpk3-1* plants (n=three biological replicates).

35 **B-E** Relative rosettes size, relative stem thickness, root weight and shoot weight (35d plants, n=12)
 36 of *lecrk-VIII.2-1*, *lecrk-VIII.2-2*, OE3, OE7, *mpk6-2*, *lecrk-VIII.2-1 mpk6-2*, *lecrk-VIII.2-2 mpk6-2*,
 37 OE3 *mpk6-2* and OE7 *mpk6-2* to WT. Values are means \pm SE relative to the WT value that is set at
 38 1 (B, C). ** $P < 0.01$ compared with the WT, NS means no significance (Student's *t* test).



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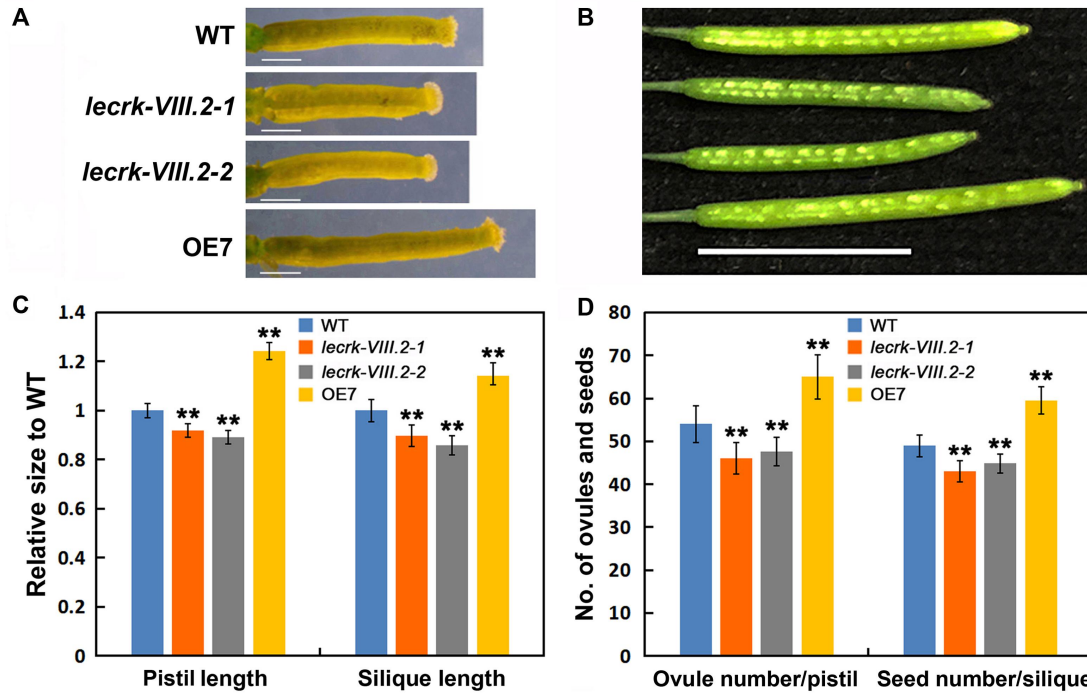
40 **Supplemental Figure S4. *LecRK-VIII.2* controls the size of seeds and flowers in an**
 41 ***MPK6*-dependent manner, but independent of *MPK3*.**

42 **A** The flowers of WT, *lecrk-VIII.2-2*, OE7, *mpk6-2*, *lecrk-VIII.2-2 mpk6-2*, OE7 *mpk6-2*, bar=1
 43 mm.

44 **B** Relative petal area and petal cell size of *lecrk-VIII.2-2*, OE7, *mpk6-2*, *lecrk-VIII.2-2 mpk6-2* and
 45 OE7 *mpk6-2* to WT.

46 **C** The seeds (bar=500 μ m) and flowers (bar=500 μ m) of WT, OE7, *mpk3-1* and OE7 *mpk3-1*
 47 plants.

48 **D** Relative seed size and petal area of OE7, *mpk3-1* and OE7 *mpk3-1* to WT. Values are means \pm
 49 SE (**B**, n>20 petals and n>120 cells; **D**, n>300 seeds and n>20 petals) relative to the WT value that
 50 is set at 1. ****** $P < 0.01$ compared with WT (Student's *t* test). NS means no significance (Student's *t*
 51 test).



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53 **Supplemental Figure S5. *LecRK-VIII.2* regulates the development of flowers and siliques.**

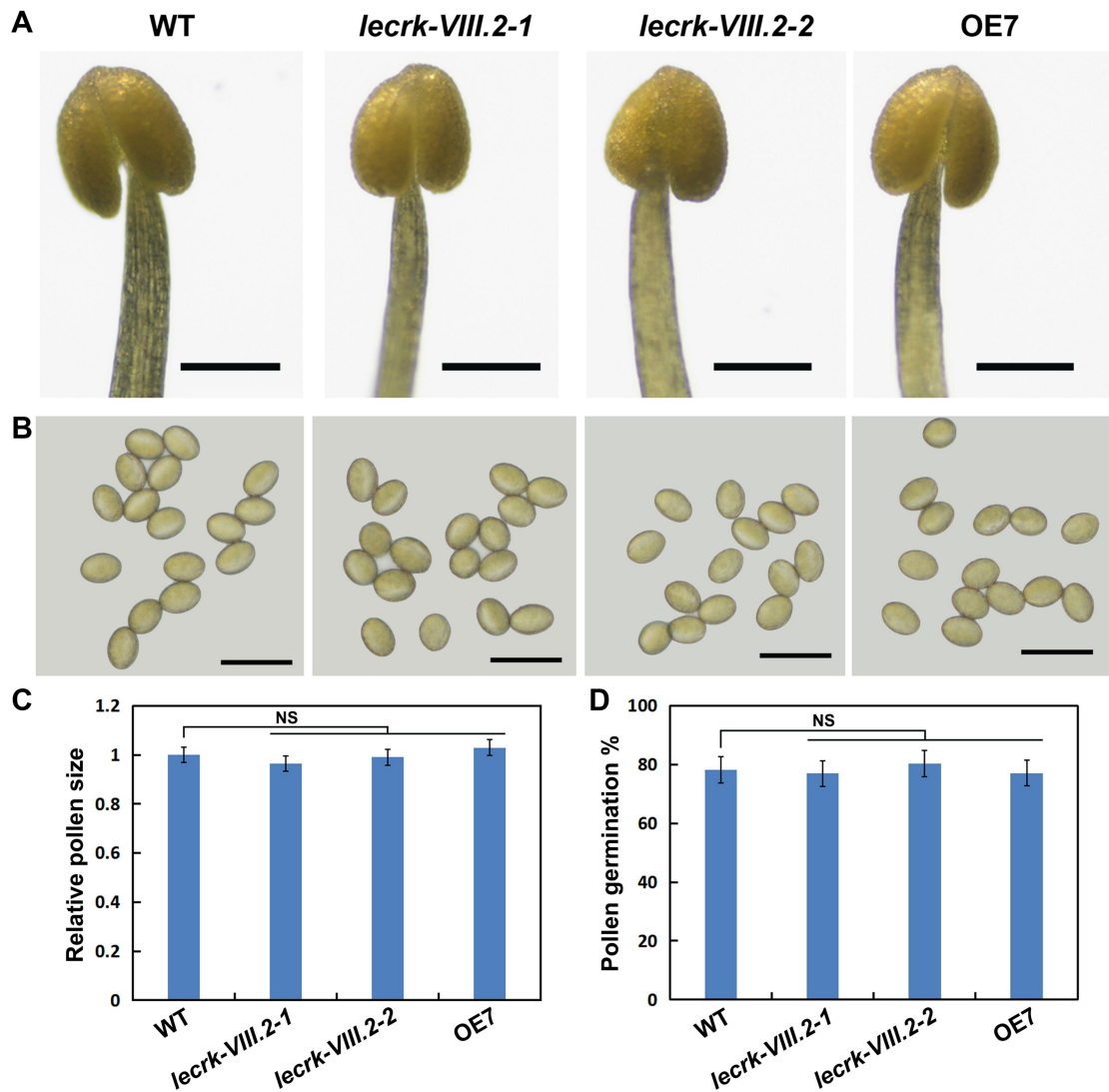
54 **A-B** Pistils (bar=250 μ m) and siliques (bar=1 cm) of WT, *lecrk-VIII.2-1*, *lecrk-VIII.2-2* and OE7
 55 plants.

56 **C** Relative pistil and silique length of *lecrk-VIII.2-1*, *lecrk-VIII.2-2* and OE7 to WT.

57 **D** The No. of ovules per pistil and No. of seeds per silique of WT, *lecrk-VIII.2-1*, *lecrk-VIII.2-2*
 58 and OE7 plants.

59 Values are means \pm SE (**C**, n=20 pistils and **D**, n=30 siliques) relative to the WT value, set at 1.

60 ** $P < 0.01$ compared with the WT, NS means no significance (Student's *t* test).



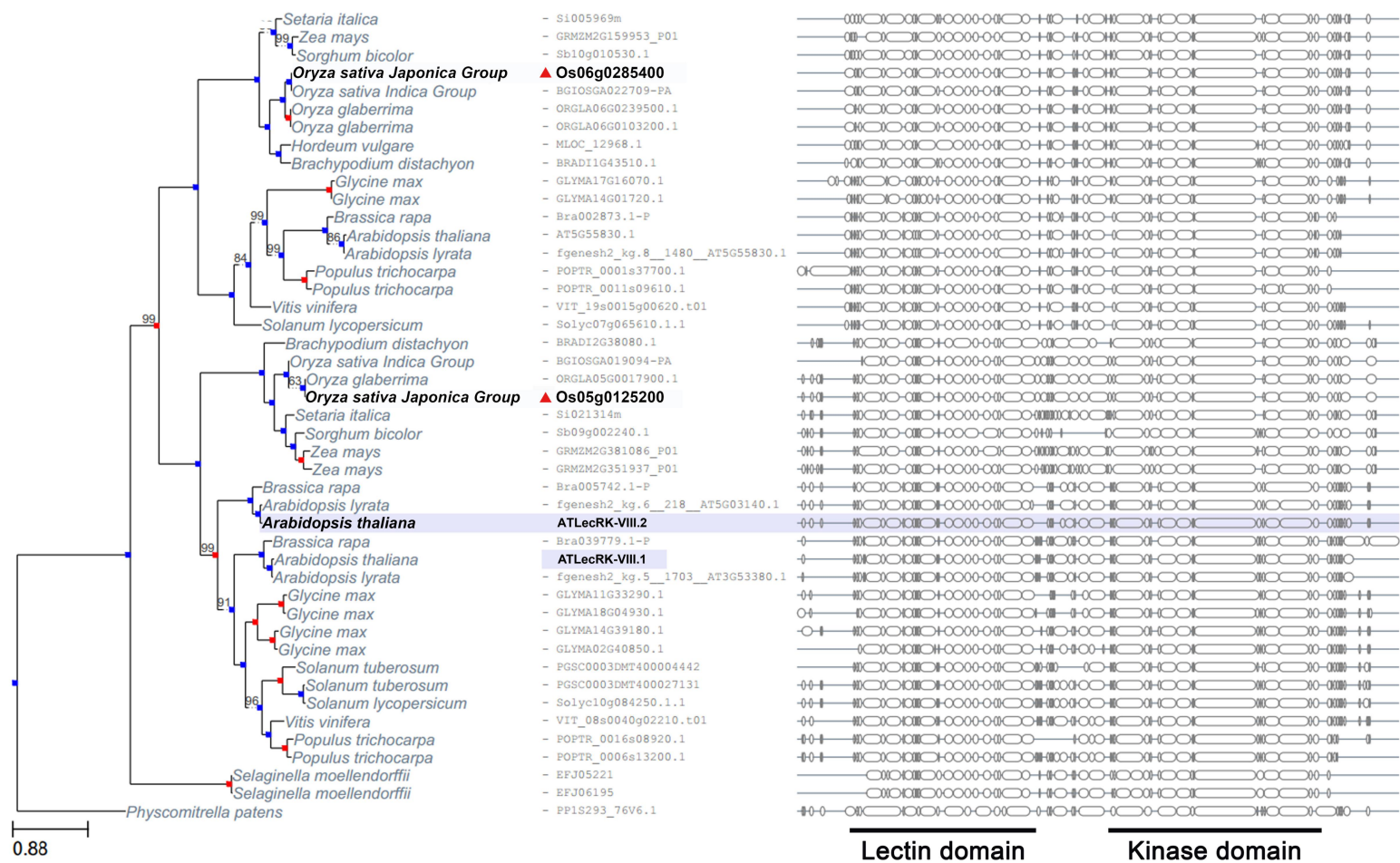
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62 **Supplemental Figure S6. *LecRK-VIII.2* exhibits no effect on the development of stamen and**
 63 **pollen.**

64 **A, B** The stamens and pollens of WT, *lecrk-VIII.2-1*, *lecrk-VIII.2-2* and OE7 plants.

65 **C** Relative pollen size (n>100) of *lecrk-VIII.2-1*, *lecrk-VIII.2-2* and OE7 to WT. Values are
 66 means±SE relative to the WT value that is set at 1.

67 **D** Pollen germination (n>200) of WT, *lecrk-VIII.2-1*, *lecrk-VIII.2-2* and OE7 plants. Values are
 68 means±SE (C, n>200 pollens; D, n=three biological repeats). NS means no significance (Student's
 69 *t* test).

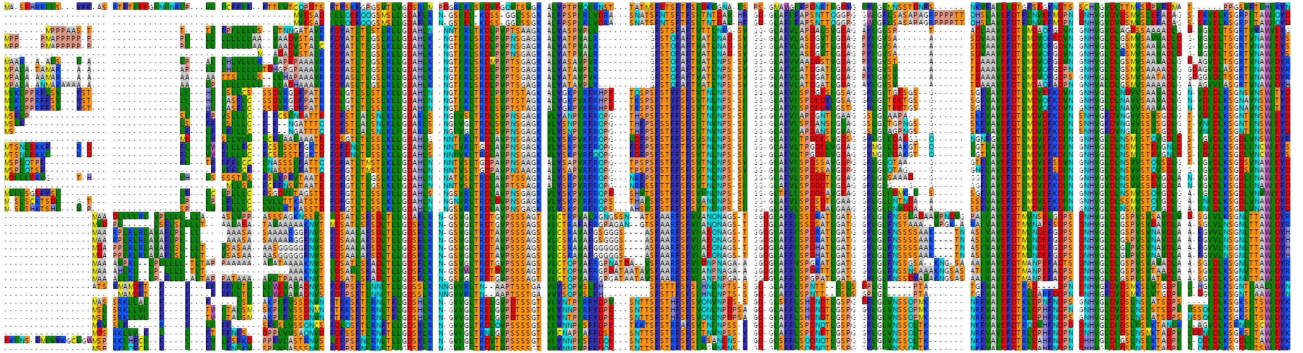


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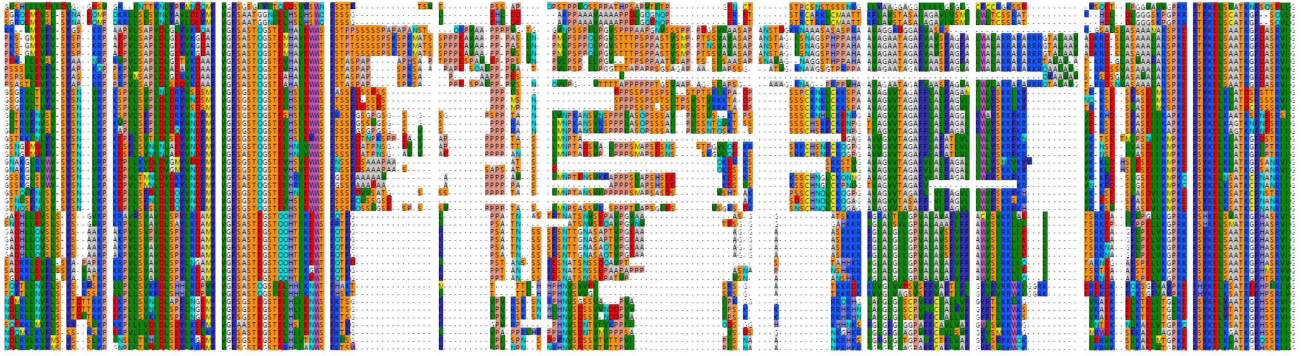
71 **Supplemental Figure S7. Phylogenetic analysis of AtLecRK-VIII.2 homologs in crops.**

72 The phylogenetic analysis was performed by the EggNOG v4.5.1. The amino acid sequence of AtLecRK-VIII.2 was searched against the dataset of *Viridiplantae* 45
 73 homologs, L-type lectin-domain containing receptor kinase, in 18 species were extracted and generated to be a set, named as the ENOG411DVC7.

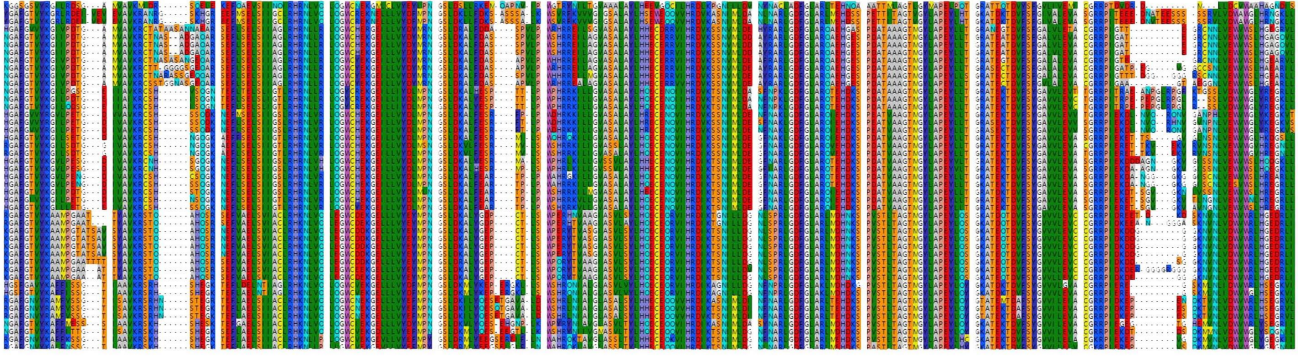
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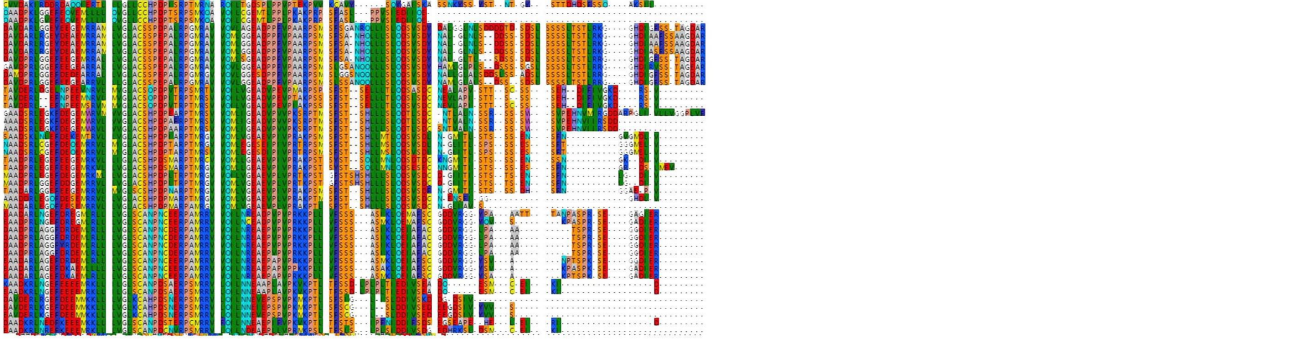
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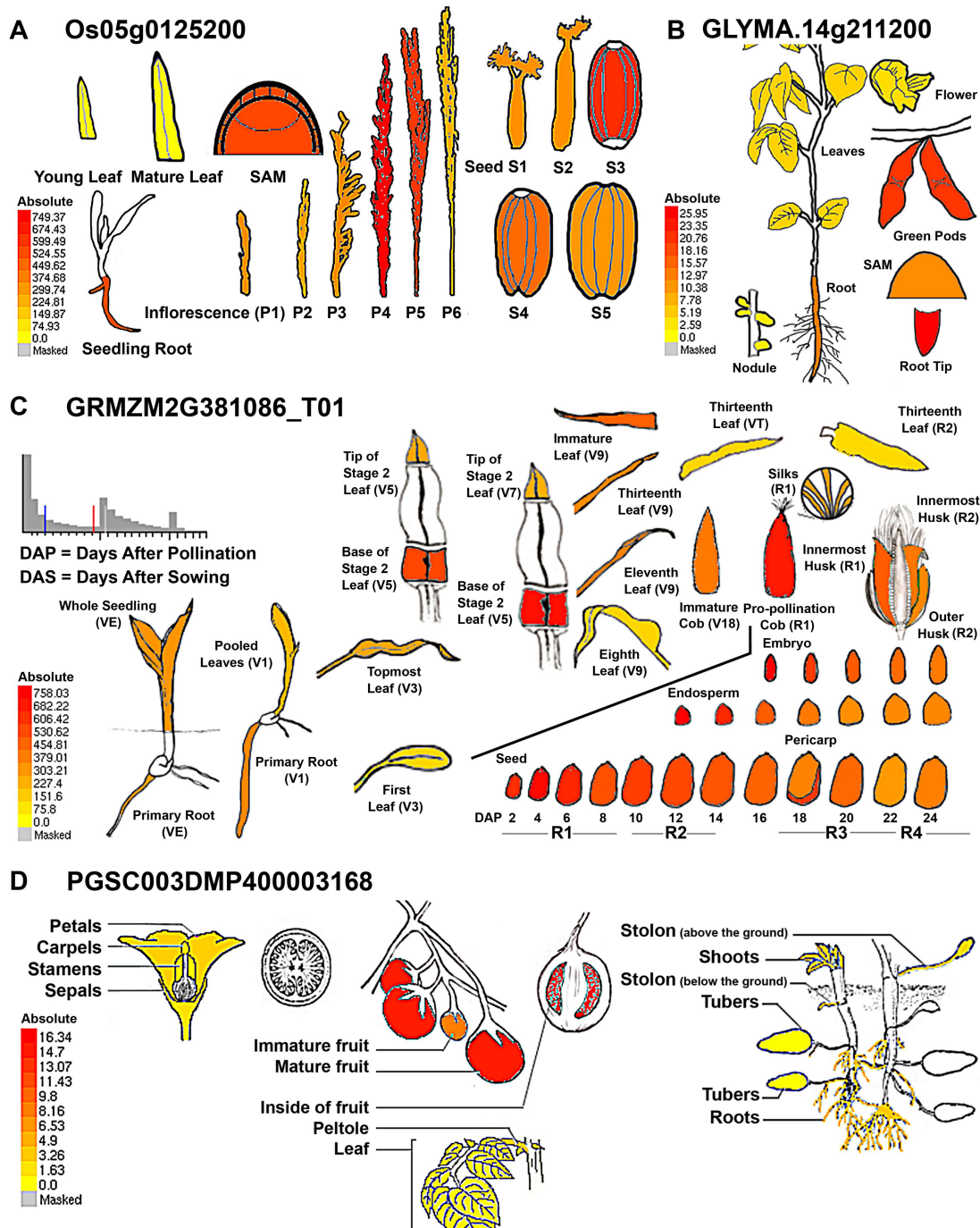
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80 **Supplemental Figure S8. Alignment of amino acid sequences of AtLecRK-VIII.2 and its**
81 **homologs in higher plants.**

82 The Alignment for amino acid sequences of AtLecRK-VIII.2 and its homologs were performed by
83 the EggNOG v4.5.1. *Arabidopsis thaliana*: AT3G53380.1, AT5G03140.1 and AT5G55830.1;
84 *Brassica rapa*: BRA002873.1-P, BRA005742.1-P and BRA039779.1-P; *Brachypodium*
85 *distachyon*: BRADI1G43510.1 and BRADI2G38080.1; *Selaginella moellendorffii*: EFJ05221 and
86 EFJ06195; *Arabidopsis lyrata*: fgenes2_kg.5_1703_AT3G53380.1,
87 fgenes2_kg.6_218_AT5G03140.1 and fgenes2_kg.8_1480_AT5G55830.1; *Glycine max*:
88 GLYMA02G40850.1, GLYMA11G33290.1, GLYMA14G01720.1, GLYMA14G39180.1,
89 GLYMA17G16070.1 and GLYMA18G04930.1; *Zea mays*: GRMZM2G159953_P01,
90 GRMZM2G351937_P01 and GRMZM2G381086_P01; *Hordeum vulgare*: MLOC_12968.1;
91 *Oryza glaberrima*: ORGLA05G0017900.1, ORGLA06G0103200.1 and ORGLA06G0239500.1;
92 *Oryza sativa Indica*: BGIOSGA019094-PA and BGIOSGA022709-PA; *Oryza sativa Japonica*:
93 Os05g0125200 and Os06g0285400; *Physcomitrella patens*: PP1S293_76V6.1; *Sorghum bicolor*:
94 SB09G002240.1 and SB10G010530.1; *Populus trichocarpa*: POPTR_0001S37700.1,
95 POPTR_0006S13200.1, POPTR_0011S09610.1 and POPTR_0016S08920.1; *Setaria italica*:
96 SI005969M and SI021314M; *Solanum lycopersicum*: SOLYC07G065610.1.1 and
97 SOLYC10G084250.1.1; *Solanum tuberosum*: PGSC0003DMT400004442 and
98 PGSC0003DMT400027131; *Vitis vinifera*: VIT_08S0040G02210.t01 and
99 VIT_19S0015G00620.t01.



100
 101 **Supplemental Figure S9. The expression profiles of the homologous genes of *AtLecRK-VIII.2*.**
 102 **A-D** *Os05g0125200* (A), *GLYMA.14g211200* (B), *GRMZM2G381086* (C) and
 103 *PGSC003DMP400003168* (D) are homologous genes of *AtLecRK-VIII.2* in rice, soybean, maize
 104 and potato, respectively. They show common high expression in grain (or fruit), suggesting their
 105 conserved roles during plant development in these crops. These transcriptional patterns were
 106 retrieved from the Arabidopsis eFP Browser (<http://bar.utoronto.ca/>).
 107
 108
 109

110 **Supplemental Table 1. Primers used in this work.**

111

LB3	GGAACCACCATCAAACAGGA
<i>lecrk-VIII.2-1</i> -TF	GGAATCTTACAAGATTCCGGC
<i>lecrk-VIII.2-1</i> -TR	TCTTGAGGTTCCAAAACCAAG
<i>lecrk-VIII.2-2</i> -TF	GACCAATTTCCAAACCCTTTC
<i>lecrk-VIII.2-2</i> -TR	CTGCTTTGGCTTATTTGCATC
<i>LecRK-VIII.2</i> -qF-(P1)	GCTACGGAGCCGTTGTTTTA
<i>LecRK-VIII.2</i> -qR-(P2)	CCACCATCATAACCCGACTC
<i>LecRK-VIII.2</i> -qF-(P3)	TCAAACAGAAGCCAACACGC
<i>LLecRK-VIII.2</i> -qR-(P4)	TCTGCTGATTGACACGTGGA
<i>LecRK-VIII.2</i> -CDS-F	CAAAAAAGCAGGCTTCGAGAACCCAACAACCTCCA
<i>LecRK-VIII.2</i> -CDS-R	CAAGAAAGCTGGGTCCGTACAAAATTGTGCTTCGT
<i>mpk3-1</i> -TF	ATTTTTGTCAACAATGGCCTG
<i>mpk3-1</i> -TR	TCTGCCTTTTACGGAATATG
<i>mpk6-2</i> -TF	CTCTGGCTCATCGCTTATGTC
<i>mpk6-2</i> -TR	ATCTATGTTGGCGTTTGCAAC
<i>EXPA1</i> -qF	ACGGAAACCTATATAGCCAAGG
<i>EXPA1</i> -qR	AGCACCACAACCTTAGACCATTA
<i>EXPA5</i> -qF	GCTCTCTACAAATCCGGTATCA
<i>EXPA5</i> -qR	CAAGTTAAAGTATGAGTGGCCG
<i>EXPA15</i> -qF	CTTAAACGGTCAAGCATTGTCA
<i>EXPA15</i> -qR	TAGCTGGAGCAATGTTGTTAGA
<i>ACTIN2</i> -qF	CACTGTGCCAATCTACGAGGGT
<i>ACTIN2</i> -qR	CACAAACGAGGGCTGGAACAAG

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