Figure S1. Multiple sequence alignment of the *Arabidopsis thaliana* and *Citrus sinensis* ABA signalling core components. (A) START-like domain of the ABA-receptors, delimited by black triangles below the alignment. ABA-binding sites are indicated by arrows and PP2Cs interaction sites by asterisks. Boxes indicate *Gate* and *Latch* loops. (B) PP2C-like domain of the clade-A PP2Cs proteins, delimited by black triangles below the alignment. Metal-binding sites are pointed out by asterisks and phosphatase activity regulatory sequences are underlined. (C) Subclass III SnRK2s full protein sequences. Black triangles below the alignment delimit protein kinase domain, asterisk indicate ATP binding site and plus symbol highlights the proton acceptor active site.

A pi1250042534P1L5 90 KHF 92-110 REVRVSGLPAFSUE -139 FSVVGGDHRIMNYSS -114 ESVV -192 FADTI VR A pi12517092/APPL5 90 KHF 92-110 REVRVSGLPAFSUE -112 INI GGDHRIMNYSS -144 ESVV -103 FVSLTV gi175170450/APPL5 61 KPF 63-79 REVNVKSGLPATSUE -110 INI GGDHRIMNYSS -144 ESVV -103 FVSLTV gi1751704570/APPL10 63 KPF 65-81 REVNVKSGLPATSUE -104 IPVGGDHRIMNYSS -143 ESFVV -105 FVALUS gi175170958/APPL110 56 KPF 58-75 REVDVKSGLPATSUE -104 IPVGGDHRIMNYSS -137 ESFVV -135 FVALUS gi175170958/APPL110 56 KPF 58-75 REVDVKSGLPATSUE -104 IPVGGDHRIMNYSS -137 ESFVV -135 FVALUS gi175170957/APPL12 39 KHF 41-58 REVTVVSGLPAFSUE -87 ISI GGDHRIMNYSS -137 ESFVV -135 FADT VG gi175170957/APPL13 39 KHF 41-58 REVTVVSGLPASTSTE -92 VSI GGCHRIMNYSS -145 ESVVV -143 FVDT VK GRMZM2G134731_P01-ZmPYL1 38 OKHF 82-100 REVTVVSGLPASTSTE -125 FSI GGCHRIMNYSS<	299952299
B B B b b c c c c c c c c c c c c c	▼ 413D 402D 492D 492D 492D 402D 402D 351D 402D 380D 383D 393D 454D 381D 385D
ATP bingding Activation loop Motif I	-
snRk2gi75337420lAtSnRk2.79GSGNFG15-149SVLHS OPKSTVGTPAY LAPEVLSR.5-286EKCRÖSVEE I V.K.1EEARKmi753336098lAtSnRk2.89GSGNFG15-149SVLHS OPK TVGTPAYI APEVLSR.5-277GPS TO TVEEI V.WIEEARKmi75333550lAtSnRk2.99GSGNFG15-149SVLHS OPK TVGTPAYI APEVLSR.5-278NFS PG EVELI V.WIEEARKmi75333556lAtSnRk2.109GAGNFG15-149SVLHS OPK STVGTPAYI APEVLSR.5-283TISLOSVEEI MKI V GEARTImi1955495552mSnRk2.19GAGNFG15-149SVLHS OPK STVGTPAYI APEVLSR.5-282NTGOS LEEV MAI OEARKmi1955495552mSnRk2.29GSGNFG15-149SVLHS OPK STVGTPAYI APEVLSR.5-282NTGOS LEEV MAI OEARKmi1955495552mSnRk2.39GAGNFG15-149SVLHS OPK STVGTPAYI APEVLSR.5-283AEPAOA DEI MRI VE EARTINGmi1955495632mSnRk2.39GAGNFG15-149SVLHS OPK STVGTPAYI APEVLSR.5-285SDO ISEEV MKI VOLARTINGmi1955495632mSnRk2.49GSGNFG15-149SVLHS PKSTVGTPAYI APEVLSR.5-285SDO ISEEV MKI VOLARTINGmi1955495632mSnRk2.69GAGNFG15-149SVLHS PKSTVGTPAYI APEVLSR.5-285SDO ISEEV MKI VOLARTINGmi1955495632mSnRk2.69GAGNFG15-149SVLHS PKSTVGTPAYI APEVLSR.5-285SDO ISEEV MKI VERARTINGmi1955495672mSnRk2.79GAGNFG15-149SVLHS PKSTVGTPAYI APEVLSR.5-285TSDO IVEEII MKI VERARTINGmi1955495672mSnRk2.79GAGNFG15-149SS	ITV AV PP AP GVN IT PN AR GGD GD PK VPK PO PP AA

∇ Mn/Mg**

Phosphate