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.