

Additional file 4: qRT-PCR primers used in this study.

Target	F primer (5'- 3')	R primer (5'- 3')	Efficiency (%)
<i>CPS</i>	CGCAAAATGCTTCGAGTACA	GAGATTCCAAGACGCTCCAG	91.3
<i>KS</i>	CTCCATGCTTCCCTCAATGT	TGGCCAAGATTCCATTTCTC	96.3
<i>KO</i>	CAGAAAAACAGGATCGGCTC	ACCAGTGGGACAGGAGAATG	97.1
<i>KAO</i>	TCGTCAACATCTCCTTCGTG	TGAGGGTACACCTGAGGGTC	99.1
<i>GA13ox1</i>	GAGCCTACTCCGCAGATGTC	AGAACCTTAGGCCGGTCATT	94.6
<i>GA13ox2</i>	GAGCTCAAGGTGCTGCTCTC	CACCGGCGAGTGTAGGTAGT	93.4
<i>GA20ox1</i>	GACCATCCTCCACCAGGAC	TGGAGGCAGCTCTTGTACCT	92.4
<i>GA20ox2</i>	CCCTGGAAGGAGACCCTCT	GGGTGCTGGTGAAGTAGTCC	93.5
<i>GA20ox3</i>	ACCGTGCCTTCAACTGCTC	CCCATGTCACGGTACTCCTC	98.0
<i>GA20ox4</i>	GTAAACATCGGCGACACCTT	GTGGAGGCAGCTCTTGTACC	93.0
<i>GA3ox2</i>	AGGTCGCCGCCGTCGAGTCC	CAGTTGAGGTGCATTGTGGC	91.8
<i>GA3ox3</i>	GTGATGCAGAGCCACGTC	TGAGGATCTGGAAGAGGTCA	97.6
<i>GA1ox1</i>	AGTAGGGCCGCTTAAGGAAG	GGTTGATGGAGACCATCTCG	92.5
<i>GA2ox1</i>	AATGTACTCGCTCCGCCTAA	ATTTTCCTTTGCTGCCATTG	91.8
<i>GA2ox3</i>	GACCCCGGGGACTACTTCT	TTGACGAGCTTGAAGAACC	99.5
<i>GA2ox4</i>	AGCAGATCACGCTGCTGAG	GTTACAGACGCTGAAGAACC	96.2
<i>GA2ox6</i>	GTTCGACACCAAGGAGAAGG	GAGCTGAGCTTCCCGTAGTC	98.2
<i>GA2ox7</i>	CTTCGCGTCCCTGGACATTG	ACTCCTCCAGAAGATCCCGT	98.8
<i>GA2ox8</i>	GCACAAGAGCAAGCTGGAG	CCGACGGAGAGAAGGATGTA	89.2
<i>GA2ox9</i>	TCTCAACGACTCCTACCGCT	ATGGAAGGCCTCAGACCAG	89.5
<i>GA2ox10</i>	TCGAGTATCTCCTGCTCGGT	ACGACCTCCGTGTACTCGTT	99.6
<i>GID1</i>	CACACATGGGTGCTCATCTC	GATGAAGTGGTCAAGGAGG	93.3
<i>GID2</i>	GAGGACGTGATGTTTCGAGGT	GAGCAGCTGTTCCGAGAAG	96.2
<i>Rht-1</i>	GAAGCAGATACCCTTGCTGG	GGGCAGGACTCGTAGAAGTG	94.6
<i>ACTIN</i>	ACCTTCAGTTGCCAGCAAT	CAGAGTCGAGCACAAATACCAGTTG	97.7

Expression analysis by qRT-PCR

RNA was extracted from shoot, root, spike and grain tissues from the tetraploid cv. 'Kronos' as described in Krasileva et al. (2013). Total RNA was extracted from ground tissues using the Spectrum™ Plant Total RNA kit (Sigma-Aldrich, St. Louis, MO) and 1 µg of the RNA equivalent of cDNA was synthesized using Quantitect Reverse Transcription Kit (Qiagen, Valencia, CA). qRT-PCR reactions were performed on an Applied Biosystems 7500 Fast Real-Time PCR System machine (Applied Biosystems, Foster City, CA). Each reaction was carried out in a 20 µl volume and consisted of 1x USB® VeriQuest™ SYBR® Green qPCR Master Mix (Affymetrix, Santa Clara, CA), 0.5 µM of F and R primers and 10 ng of cDNA. *ACTIN* was used as an endogenous control gene and all qRT-PCR primers used in this study and their efficiencies are above. All primers were checked for efficiency and specificity by analyzing their amplification in a four-fold dilution series and checking that each reaction yielded a single product by studying the derived dissociation curve. Transcript levels are reported as the proportional distribution of transcripts from each gene across the four tissues.