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

<table>
<thead>
<tr>
<th>Target</th>
<th>F primer (5'→3')</th>
<th>R primer (5'→3')</th>
<th>Efficiency (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>CPS</td>
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<td>GAGATTTCAAGACGCTCCAG</td>
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<tr>
<td>KS</td>
<td>CTCCATGCTCTCCCTCAATGT</td>
<td>TGGCCAAGATCTCCATTTCTC</td>
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<td>KO</td>
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<tr>
<td>KAO</td>
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<td>CACCAGGAGTGTAGGTAGTGT</td>
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<tr>
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<tr>
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<tr>
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</tr>
<tr>
<td>GID2</td>
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</tr>
<tr>
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<tr>
<td>ACTIN</td>
<td>ACCTTCAGTTGCCAGCAAT</td>
<td>CAGAGTGGACACAAATACCATG</td>
<td>97.7</td>
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</tbody>
</table>

### 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.