**Figure S1** Breeding scheme used to dissect the qSD7-1/qPC7 cluster. IL_{qSD7-1/qPC7} is the introgression line having only the QTL-containing segment introduced from the weedy rice S518-2 into the background of the cultivated rice EM93-1. A single seed (F_3) was pooled from each of the F_2 plants to form the red and white F_3 seed subpopulations. Numbers in parentheses indicate individual plants checked for pericarp color and/or marker genotypes to select for red (Rrec) or white (Wrec) pericarp recombinants. F_4 and F_6 lines were derived from the selected recombinants and evaluated for seed dormancy by progeny testing. SD7-1^d_1 and SD7-1^d_2 are isogenic lines for dormancy-enhancing and –reducing alleles, respectively, at the SD7-1 locus.
Figure S2  Germination profile of three genotypes at SD7-1. Germination was evaluated with 1- to 16-d after-ripened (DAR) seeds. Data shown are genotypic means (circles) and s.d. of 15 plants selected from the intragenic recombinant Rrec² (figure 1B)-derived progeny population. The genotypes homozygous for the dormancy-enhancing allele (dark circles) or heterozygous (gray circles) at SD7-1 displayed red pericarp color, and the genotype homozygous for the dormancy-reducing allele at SD7-1 exhibited white pericarp color (open circles). Gene additive (a) and dominance (d) effects and degree of dominance (d/a) were estimated for cumulative germination after 10 (D10) or 2 (D2) days of incubation. A significant (*) or non-significant (ns) gene effect was determined at the probability level of 5%.
Table S1  List of PCR primers used for marker genotyping, cDNA cloning, or expression analysis

<table>
<thead>
<tr>
<th>Name or locus</th>
<th>Forward (5' to 3')</th>
<th>Reverse (5' to 3')</th>
<th>Predicted size (bp)</th>
<th>Genomic position or predicted function</th>
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<tbody>
<tr>
<td><strong>New markers for fine mapping</strong></td>
<td></td>
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</tr>
<tr>
<td>AP5098-15</td>
<td>gtggacctacagccctcct</td>
<td>ctgcacctacccgtcactt</td>
<td>431</td>
<td>Ch7: 6061943-6062373</td>
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<tr>
<td>AP5779-8</td>
<td>cagctgatactgcatgtggt</td>
<td>cgtatgtgtgcctcctgtg</td>
<td>217</td>
<td>Ch7: 6136216-6136432</td>
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<tr>
<td><strong>Isolation of SD7-1 full-length and fragment cDNAs</strong></td>
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<tr>
<td>5' fragment</td>
<td>atggccgggctggcagcaagcg</td>
<td>ggtggctgaatcaacct (13)</td>
<td>1466</td>
<td>From the start codon to 1466 bp</td>
</tr>
<tr>
<td>3' fragment</td>
<td>gcgtttcacctggcatt (13)</td>
<td>gggtgaatatataaatcagattcag</td>
<td>997</td>
<td>From 1065 bp to 45 bp downstream the stop codon TAA</td>
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<tr>
<td>Full length</td>
<td>cttacttatcgtcatcgactcc</td>
<td>ggggtgaatatataaatcagattcag</td>
<td>2061</td>
<td>49 bp upstream the start codon ATG to 45 bp downstream the stop codon TAA</td>
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<td><strong>qRT-PCR for transcripts from selected genes</strong></td>
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<tr>
<td>Os07g11020</td>
<td>cacccacctactcatcactcacat</td>
<td>caaagctgacacaggtctcatctg</td>
<td>402</td>
<td>SD7-1 or Rc</td>
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<tr>
<td>Os10g17260</td>
<td>atcaagacacgtttcggccctc</td>
<td>tggcagctcaagctgtacacat</td>
<td>313</td>
<td>F3'H: Flavonoid 3'-monooxygenase</td>
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<tr>
<td>Os03g15360</td>
<td>gtggcgtacacttctcatgctctg</td>
<td>gcgtcagtgaagcgactatgct</td>
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<td>LAR: Leucoanthocyanidin reductase</td>
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<td>ggcacattctcgtatcctgaa</td>
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<td>gggctcagctcagatccgcagag</td>
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<td>tgtatgacccacactctctc</td>
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<td>attccatgagccgctgctcag</td>
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<td>ctctcagtgagggtccattcata</td>
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Table S2  Allelic variation among SD7-1 alleles from the parental line SS18-2 and EM93-1, and the isogenic line SD7-1<sup>0</sup>

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<th>No.</th>
<th>Site (bp)</th>
<th>SS18-2</th>
<th>SD7-1&lt;sup&gt;0&lt;/sup&gt;</th>
<th>EM93-1 (SD7-1&lt;sup&gt;0&lt;/sup&gt;)</th>
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</table>

Note: Mutant sites are numbered from the 5´ end of the SD7-1 dormancy locus. Upper or lowercase letter(s) indicate the mutation occurred in exons or introns. The weedy red rice line SS18-2 is the donor of the dormancy gene. SD7-1<sup>0</sup> was derived from the intragenic recombinant Rrec<sup>5</sup> (Figure 1B) and is isogenic to the recipient line EM93-1 (SD7-1<sup>0</sup>). Gray color-depicted background indicates the sequence from SS18-2.
Table S3  Statistic test for difference in 100-seed weight between the isogenic lines SD7-1\textsuperscript{D} and SD7-1\textsuperscript{d} in three greenhouse experiments

<table>
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<tr>
<th>Line</th>
<th>Experiment 1</th>
<th></th>
<th>Experiment 2</th>
<th></th>
<th>Experiment 3</th>
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<tbody>
<tr>
<td></td>
<td>N</td>
<td>Mean</td>
<td>Stddev</td>
<td>N</td>
<td>Mean</td>
<td>Stddev</td>
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<td>SD7-1\textsuperscript{D}</td>
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<td>1.832</td>
<td>0.028</td>
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<td>2.234</td>
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<td>SD7-1\textsuperscript{d}</td>
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<td>0.010</td>
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