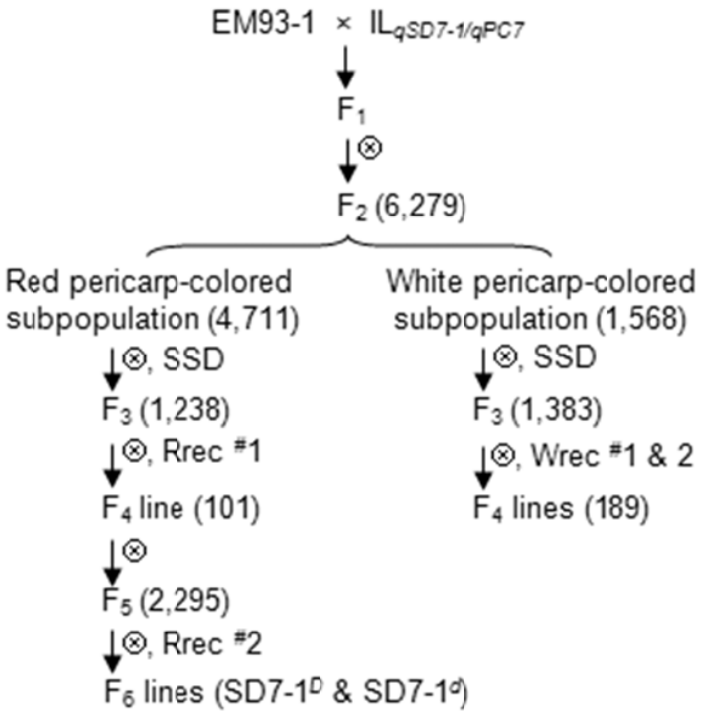

Figure S1 Breeding scheme used to dissect the *qSD7-1/qPC7* cluster. IL$_{qSD7\text{-}1/qPC7}$ is the introgression line having only the QTL-containing segment introduced from the weedy rice SS18-2 into the background of the cultivated rice EM93-1. A single seed (F_3) was pooled from each of the F_2 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 and SD7-1^d are isogenic lines for dormancy-enhancing and –reducing alleles, respectively, at the *SD7-1* locus.

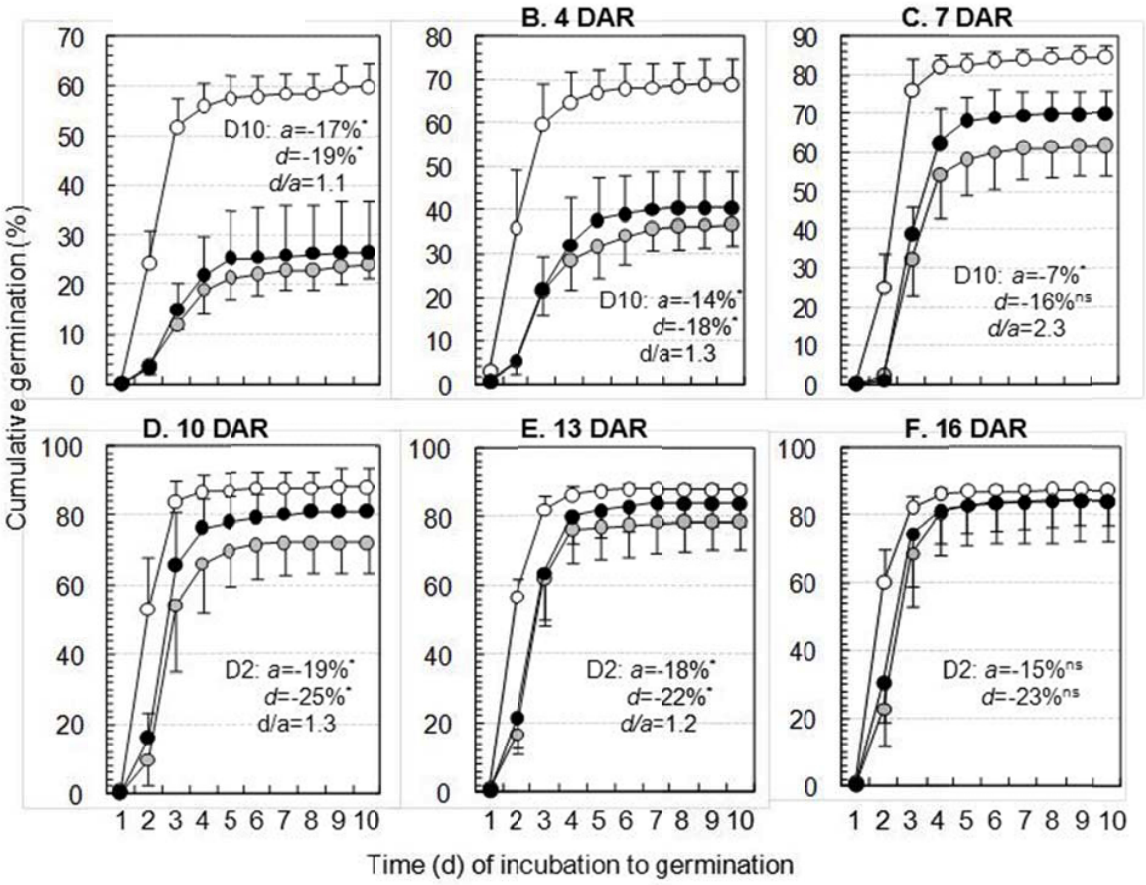

Figure S2 Germination profile of three genotypes at *SD7-1*. Germination was evaluated with 1- to 16-d after-ripened (DAR) seeds. Data shown are genotypic means (circles) and s.d. of 15 plants selected from the intragenic recombinant Rrec$^{\#}$2 (figure 1B)-derived progeny population. The genotypes 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

Name or locus	Forward (5' to 3')	Reverse (5' to 3')	Predicted size (bp)	Genomic position or predicted function
New markers for fine mapping				
AP5098-15	gtggacctacagcctcct	ctgcatcaccgtcgactt	431	Ch7: 6061943-6062373
AP5779-8	ccagctgatactgcatggtg	cgtatgtgtgctccctgatg	217	Ch7: 6136216-6136432
Isolation of *SD7-1* full-length and fragment cDNAs				
5' fragment	atggccggcggcgaggcgcaagcg	ggttggcactgaaatcacct (13)	1466	From the start codon to 1466 bp
3' fragment	gccttgtcactcttggcatt (13)	gggtgaatatataaattcagaattcag	997	From 1065 bp to 45 bp downstream the stop codon TAA
Full length	ctttacttatcgatctcgatcatcc	gggtgaatatataaattcagaattcag	2061	49 bp upstream the start codon ATG to 45 bp downstream the stop codon TAA
qRT-PCR for transcripts from selected genes				
Os07g11020	cacccactgtactcatcagcat	caagagtgacaaggctcatctg	402	*SD7-1* or *Rc*
Os10g17260	atcaaggagacgtttcggcttc	tggcagtcatcagtgtgaccat	313	F3'H: Flavonoid 3'-monooxygenase
Os03g15360	gtgccgtacaccttcatctgct	gcgtcagtgaagcgactatgct	367	LAR: Leucoanthocyanidin reductase
Os11g32650	gtacatgcacctgacggaggag	ctggtacatcatgaggcggttc	280	CHS: Chalcone synthase
Os01g44260	gcccactactcgatcctgaa	cagcgtgtacctgaacctga	250	DFR: Dihydroflavonol 4-reductase
Os04g56700	agggtggcgtacaaccagttc	ggacttcaccgggtacgagaag	333	F3H: Flavanone 3-hydroxylase
Os11g02440	agccattgtcactgcttgct	ggggtggtaggaaagtggaa	396	CHI: Chalcone-flavonone isomerase
Os01g27490	tgacggatgtggagctgaga	tgtatgacgccccactcctc	253	LDOX: Leucoanthocyanidin dioxygenase
Os04g53850	agcctgggcgtacagtgtgt	aggggcttcaggacttcgag	201	ANR: Anthocyanidin reductase
Os03g60509	cgagcagtactcggacaagg	ccttcaggagctgcgagac	340	CHI: Chalcone-flavonone isomerase
Os12g42280	cttcaacgagtcggacgaacac	aggagaggatgtagccgtcgtc	356	NCED1: 9-*cis*-epoxycarotenoid dioxygenase
Os03g44380	ctacttcaacggcaggctcctc	accaccacgtagttctcggtga	315	NCED1
Os04g37619	atcccagcaattcgactgcttc	attcatatgggagcgtgctcag	264	ZEP: Zeaxanthin epoxidase
Os05g33240	attgggacacgtgttgatgc	cttccagtggggcttccata	302	RNA II Polymerase (control)
Os07g13530	aacaaaccagagggtgatgc	aaggaggcacgaggataggt	250	GTP-binding protein (control)

Table S2 Allelic variation among *SD7-1* alleles from the parental line SS18-2 and EM93-1, and the isogenic line SD7-1^{D}

No.	Site (bp)	SS18-2	SD7-1^{D}	EM93-1 (SD7-1^{d})
1	290-323	34-bp deletion	cgaatctaaaaagatgtacatatt ttgattcgta	cgaatctaaaaagatgtacatat tttgattcgta
2	405	T	G	G
3	633	G	T	T
4	956	a	t	t
5	1099	a	1-bp deletion	1-bp deletion
6	1162	t	c	c
7	1201	c	t	t
8	1366	t	c	c
9	1406	g	a	a
10	1473	a	g	g
11	1737	c	t	t
12	1849	c	a	a
13	2197	g	a	a
14	2269	g	a	a
15	2439	a	t	t
16	2441	g	a	a
17	3063	t	a	a
18	3109	g	a	a
19	3206	1-bp deletion	1-bp deletion	a
20	3293-3298	agagag	agagag	6-bp deletion
21	3685	1-bp deletion	1-bp deletion	t
22	3695	c	c	t
23	3808	t	t	g
24	4031	c	c	t
25	4496	G	G	A
26	4960	A	A	G
27	5177-5190	ACGCGAAAA GTCGG	ACGCGAAAAGTCGG	14-bp deletion
28	5401	a	1-bp deletion	1-bp deletion
29	5652	g	a	a
30	6269-6280	CGGCGGCG GCGG	12-bp deletion	12-bp deletion
31	6359	C	T	T
32	6436-6441	6-bp deletion	AAATGC	AAATGC

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^{D} was derived from the intragenic recombinant Rrec $^{\#}$2 (Figure 1B) and is isogenic to the recipient line EM93-1 (SD7-1^{d}). 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^{D} and SD7-1^{d} in three greenhouse experiments

Line	Experiment 1			Experiment 2			Experiment 3		
	N	Mean	Stdev	N	Mean	Stdev	N	Mean	Stdev
SD7-1^{D}	10	1.832	0.028	7	2.234	0.077	16	2.033	0.067
SD7-1^{d}	10	1.778	0.017	8	2.168	0.061	14	1.964	0.059
Difference		0.053	0.010		0.066	0.036		0.070	0.023
t-value		5.18			1.80			3.02	
Probability		0.0001			0.0449			0.0052	
Weight increase (%)		3.01			3.02			3.55	