

Supplementary Table 3. Sequence analysis of nucleotide variations involved in the function of candidate genes.

Var ID	Variants type	Chromosome	Position (bp)	Reference allele	Alternative allele	Koshihikari genotype	IS592BB genotype	HGVS ^z (protein)	Candidate gene
vg0333002789	SNP	3	33,002,789	G	A	A	ref. allele	p.Ala331Thr	<i>Hd16</i>
vg0602235191	SNP	6	2,235,191	C	T	T	ref. allele	p.Leu558Ser	<i>Hd17</i>
vg082388554	SNP	8	2,388,554	T	C	ref. allele	C	p.Thr225Ala	<i>Hd18</i>
vg0138385083	SNP	1	38,385,083	G	C	C	ref. allele	p.Asp349His	<i>SD1</i>
vg1118744679	SNP	11	18,744,679	C	A	ref. allele	A	p.Ala618Ser	<i>OsCPL3</i>
vg1118744841	SNP	11	18,744,841	G	A	ref. allele	A	p.Pro564Ser	<i>OsCPL3</i>
vg1118745356	SNP	11	18,745,356	T	G	ref. allele	G	p.Lys392Thr	<i>OsCPL3</i>
vg1118745357	SNP	11	18,745,357	T	C	ref. allele	C	p.Lys392Glu	<i>OsCPL3</i>
vg1118746332	SNP	11	18,746,332	A	C	ref. allele	C	p.Tyr186Asp	<i>OsCPL3</i>
vg0328428721	Indel	3	28,428,721	C	CTGTG	ref. allele	CTGTG	p.Ala111dup	<i>OsTB1</i>
vg0724669233	Indel	7	24669233	CTATCACTTTCT	C	ref. allele	C	MODIFIER	<i>GW7</i>

^zHGVS: Human Genome Variation Society.

Supplementary Table 4. ANOVA analysis with *F*-values for the effects of *SD1*, *OsCPL3*, and their interaction on the phenotype variation of yield-related traits.

Source of variance	df ^z	HD ^y	CL	PL	PN	NS	TGW	RRG	BRR	Yield
<i>SD1</i>	1	0.0 ^{ns}	38.2 ^{**}	42.2 ^{**}	0.8 ^{ns}	4.5 [*]	6.3 [*]	0.1 ^{ns}	1.0 ^{ns}	7.6 ^{**}
<i>OsCPL3</i>	1	2.7 ^{ns}	16.7 ^{**}	0.2 ^{ns}	1.9 ^{ns}	5.1 [*]	0.2 ^{ns}	1.7 ^{ns}	38.1 ^{**}	2.3 ^{ns}
<i>SD1*OsCPL3</i>	1	1.0 ^{ns}	0.2 ^{ns}	0.6 ^{ns}	1.5 ^{ns}	1.7 ^{ns}	0.4 ^{ns}	0.3 ^{ns}	0.7 ^{ns}	0.0 ^{ns}

^zDegree of freedom.

^yHD: heading date, CL: culm length, PL: panicle length, PN: number of panicles per hill, NS: number of spikelets per panicle, TGW: 1,000-grain weight, RRG: ratio of ripened grain, BRR: brown/rough rice ratio.

ns, *, and ** mean no significant, significant $p < 0.05$, and $p < 0.01$ by two-way ANOVA, respectively.