

Cultivar name	Origin	Sequence variation in cDNA of <i>DRO1</i>							Haplotype group ^b	
		5'-UTR	5'-UTR	Exon3	Exon3	Exon4	Exon4	3'-UTR		
		A/G	C/T	T/C	A/C	A/-	C/A	CT/--		
		S.S.			Leu/Phe	Stop	Asp/Gly			
		27 ^a	150	617	752	943	962	1133-4		
SNP	SNP	SNP	SNP	INDEL	SNP	INDEL				
Kinandang Patong	Philippines	A	C	T	A	A	C	CT	I	
Bekogonomi	Japan	A	C	T	A	A	C	CT	I	
Fukuhibiki	Japan	A	C	T	A	A	C	CT	I	
Hoshiaoba	Japan	A	C	T	A	A	C	CT	I	
Kusahonami	Japan	A	C	T	A	A	C	CT	I	
Leafstar	Japan	A	C	T	A	A	C	CT	I	
Mizuhochikara	Japan	A	C	T	A	A	C	CT	I	
Momiroman	Japan	A	C	T	A	A	C	CT	I	
Natsuaoba	Japan	A	C	T	A	A	C	CT	I	
Tachisugata	Japan	A	C	T	A	A	C	CT	I	
Yumeaoba	Japan	A	C	T	A	A	C	CT	I	
Yumesakari	Japan	A	C	T	A	A	C	CT	I	
Habataki	Japan	A	T	T/C	C	A	C	-	VII	
Hokuriku 193	Japan	A	T	T/C	C	A	C	-	VII	
Minamiyutaka	Japan	A	T	T/C	C	A	C	-	VII	
Takanari	Japan	A	T	T/C	C	A	C	-	VII	

Figure S1. Sequence polymorphism in the transcribed region of *DRO1* among 16 rice cultivars

S.S., synonymous substitution. ^a In/del or SNP position from the start of the 5' UTR. T/C in exon 3 of four accessions indicates heterozygous allele. ^b Numbering of each accession is based on the classification described in Uga et al. (2013a).