

Additional file 4 (a) : Non-synonymous SNPs in Sdr4 and GA2ox3 genes

<i>Sdr4</i>	<i>SNP ID</i>	<i>sf0723795969</i>	<i>sf0723796436</i>	<i>sf0723796212</i>
	<i>Chromosome</i>	7	7	7
	<i>Position (bp)</i>	23795969	23796436	23796212
	<i>Major Allele</i>	A	G	C
	<i>Minor Allele</i>	G	C	T
	<i>Amino Acid change</i>	T to A	A to P	A to V
	<i>Hap1</i>	A	G	C
	<i>Hap2</i>	G	C	C
	<i>Hap3</i>	G	C	T
<i>GA2ox3</i>	<i>SNP ID</i>	<i>sf0131794745</i>	<i>sf0131794598</i>	<i>sf0131795793</i>
	<i>Chromosome</i>	1	1	1
	<i>Position (bp)</i>	31794745	31794598	31795793
	<i>Major Allele</i>	C	G	C
	<i>Minor Allele</i>	G	A	T
	<i>Amino Acid change</i>	L to V	V to I	A to V
	<i>Hap1</i>	C	G	C
	<i>Hap2</i>	C	G	T
	<i>Hap3</i>	G	G	C

Additional file 4: (a) Non-synonymous SNPs in Sdr4 and GA2ox3 genes in 350 accessions used in our study. Amino acid changes are indicated in relation to the nucleotide change from major to minor alleles. The SNPs in each gene resulted into three haplotypes (Hap1-3).

Additional file 4 (b): Number of Accessions in sub-populations and their individual haplotypes in Sdr4 and GA2ox3

<i>Gene</i>	<i>Haplotype</i>	<i>IndI</i>	<i>IndII</i>	<i>Aus</i>	<i>Tej</i>	<i>Trj</i>
		Number of accessions	Number of accessions	Number of accessions	Number of accessions	Number of accessions
<i>Sdr4</i>	<i>Hap1</i>	57	20	21	45	37
	<i>Hap2</i>	3	47	9		
	<i>Hap3</i>	1	14			
<i>GA2ox3</i>	<i>Hap1</i>	34	82	20	11	
	<i>Hap2</i>	24		10		
	<i>Hap3</i>	1			45	26

Additional file 4: (b) The number of accessions in sub-populations of indica, Aus and japonica rice possessing any of the three haplotypes of *Sdr4* and *GA2ox3*. IndI, indica I; IndII, indica II; Tej, temperate japonica; Trj, tropical japonica.