

Additional file 4

Supplemental Table 3. Estimation of background-mutation rates from intron mutations of four genomes (*Or*, *On*, *Indica* (I) and Nipponbare (J)).

Locus	Intron surveyed	Number of shared mutation between I and J	Mutations specific to I	Mutations specific to J	Length of intron ^a (bp)
<i>SH4</i>	Intron 1	3	0	0	863
<i>AN-2</i>	Intron 1	2	0	0	965
<i>AN-1</i>	Intron 3	0	0	0	832
<i>DAHPS2</i>	Intron 1	1	0	0	1001
<i>SSY3</i>	Intron 1	0	1	1	1095
<i>Rc</i>	Intron 2	1	0	0	2717
<i>GS5</i>	Intron 4	0	0	0	939
<i>Chalk5</i>	Intron 1	0	6	0	1561
<i>Lc</i>	Intron 1	0	0	1	2487
Sum		7	7	2	12460
Mutation Rate^b		0.56	0.56	0.16	

^a The length of the longest intron in the case of unequal intron lengths among orthologs.

^b The unit is number of mutations per 1K nucleotides over the historical period implicated.