

Table S4. Number of mismatches in rice reads aligned with different alignment tools.

Mismatch number	Percentage of mismatch reads in aligned reads (%) ^a				
	BWA	MAQ	NovoAlign	SOAP2	Bowtie ^b
1	8.6	8.5	8.8	3.4	10.5
2	2.7	2.6	2.6	1.1	4.3
3	1.6	0.78	1.4	0	0
4	1.2	0.49	0.89	0	0
5	0.4	0.35	0.59	0	0
>5	0.8	0.98	1.8	0	0

Sixty-three million Illumina paired-end reads of *O. sativa* cv. Nipponbare were aligned to the rice reference (IRGSP build 5) genome using the indicated alignment tools in a seeding mode, which allows at most two mismatches within a 20–30 bp seed of reads.

^a The percentage of reads with the indicated number of mismatches out of the total number of rice reads aligned to the rice reference genome.

^b Version 0.12.7, which is not the latest version (Bowtie 2).