

**Table S6. SNP/indel calling accuracy for real (experimental) and simulated reads.**

Read	SNP/indel	SNP/indel calling accuracy	
		True positives rate	False positives rate
Real	SNP	658,735 (89.0%)	3,771 (0.57%)
	Indel	49,152 (64.6%)	1,901 (3.72%)
Simulated (dwgsim)	SNP	679,856 (91.8%)	198 (0.03%)
	Indel	54,777 (72.0%)	78 (0.14%)
Simulated (pIRS)	SNP	672,398 (90.8%)	404 (0.06%)
	Indel	53,574 (70.4%)	77 (0.14%)

Using BWA,  $6.3 \times 10^7$  experimentally obtained 75 bp paired-end reads of Nipponbare (real) were aligned to the simulated rice Nipponbare reference genome containing 0.2% artificial SNPs and 0.02% artificial indels. The same number of artificial simulated reads (75 bp paired-end) were generated using dwgsim and pIRS simulation tools with the simulated rice genome as a template. The simulated reads were aligned to the wild-type Nipponbare reference sequence, which contained no artificial SNPs/indels. SNPs and indels were called using the Coval-Call tool with  $\geq 0.8$  of variant frequency and a minimum of two supported reads at the called site.