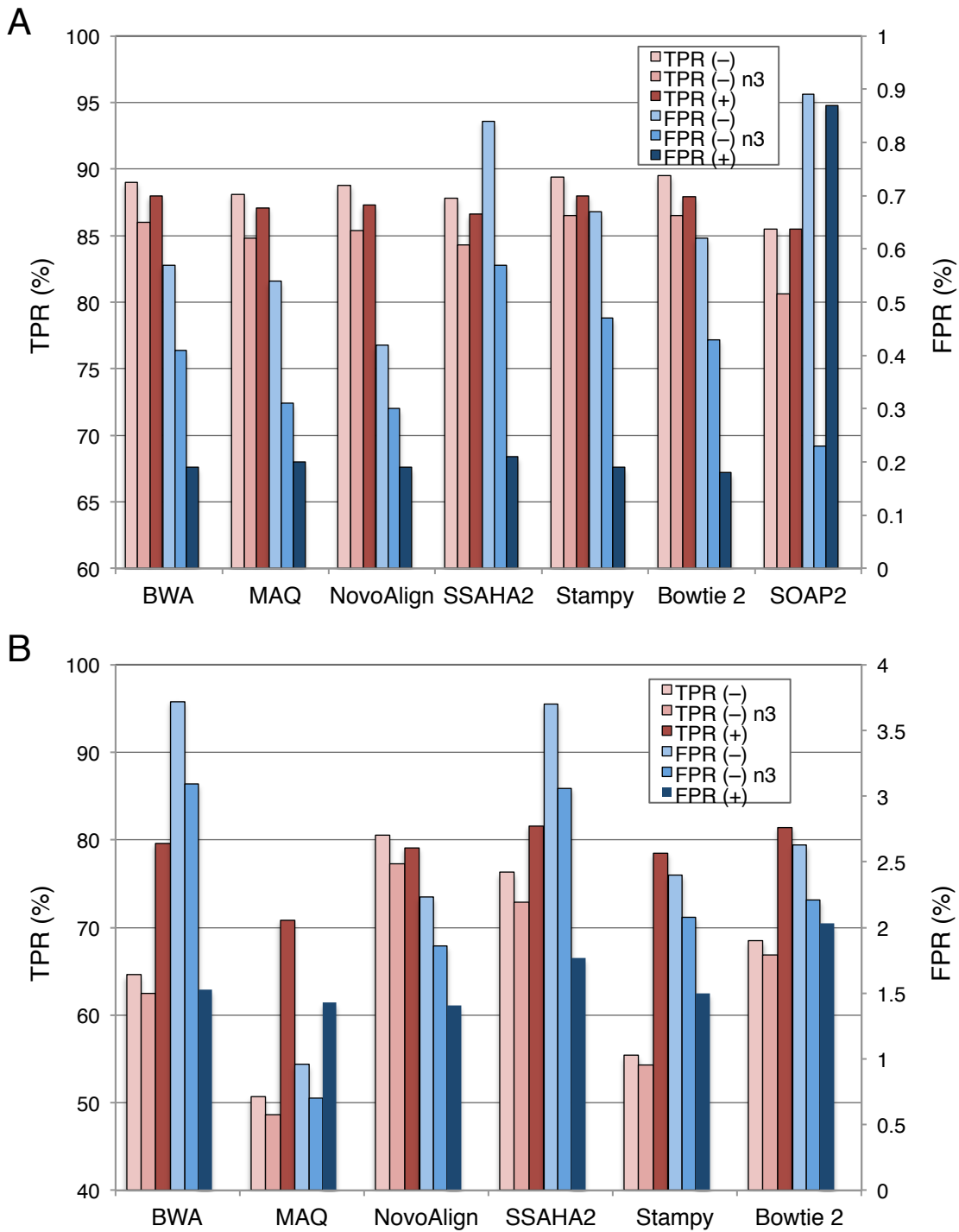


Figure S7



**Figure S7. SNP/indel calling performance of Coval for alignment data generated by different aligners.**

(A) SNP calling accuracy with or without Coval-Refine. (B) Indel calling accuracy with or without Coval-Refine. The simulated rice genome was aligned with the rice real (experimental) sequence data using the indicated alignment tools. The alignments were filtered (+, bars in dark red and in dark blue) or not filtered (-, bars in light- and middle-red and in light- and middle-blue) with Coval-Refine in the error correction mode (except for Novoalign in the basic mode), and SNPs and indels were called using Coval-Call with “minimum allele frequency=0.8” and “minimum number of reads supporting non-reference allele=2”. For another calling condition (n3, bars in middle-red and in middle-blue), SNPs/indels were called with “minimum number of reads supporting non-reference allele=3”, and the same for the other options. TPR and FPR for the called SNPs are shown with red and blue bars, respectively.