

Additional file 5:

We test the performance of vi-HMM with homopolymers on a simulated dataset with $30\times$ coverage depth. vi-HMM produces high calling accuracies of SNPs and INDELS, which are only slightly smaller than those in the general situation. One potential explanation for the lower INDEL calling accuracy is that the INDELS are redundant in the output[1].

SNP and INDEL callings by vi-HMM using simulated data with homopolymers at $30\times$ depths.

Caller	SNP			INDEL		
	Sensitivity	Precision	F_1 score	Sensitivity	Precision	F_1 score
Bowtie2	88.39%	87.46%	87.92%	59.16%	57.47%	58.30%
BWA-MEM	79.76%	88.52%	83.91%	58.13%	53.14%	55.52%

References

- [1] Hasan, M.S., Wu, X., Watson, L.T., Li, Z., Zhang, L.: Ups-indel: A better approach for finding indel redundancy. In: Computational Advances in Bio and Medical Sciences (ICCABS), 2016 IEEE 6th International Conference On, pp. 1–1 (2016). IEEE