Supplementary Table S3. Results of mapping simulated reads against the genomes database. 200,000 simulated reads obtained using 'wgsim' simulator were mapped against the genomes in our database (see Supplementary Table S1). Using wgsim_eval.pl we calculated the percentage of reads mapped correctly.

	bowtie2	stampy	bowtie	gassst	bwa	smalt	ssaha2
Single read	98.2	95.5	100	64.8	65.4	66.4	100
Paired-end	96.9	93.4	0.23	-	65.8	62.3	56.1