

Supporting evidence for applicability of QQ-SNV on Illumina NGS data of any read length

Reference sequence: KC866600

Illumina Miseq 250bp

Analysis on all paired-end reads

True variants: 334C>T, 625A>T (data from [28])

QQ-SNV predicted SNV probability for the true variants for plasmid mix ratios 95:5, 99:1 and 99.9:0.1

	95:5	99:1	99.9:0.1	
Average coverage depth (number of reads)	26,663	23,659	29,090	
	P(SNV)	P(SNV)	P(SNV)	
334C>T	0.9999761488	0.9997707282	0.5613726795	
625A>T	0.9999456703	0.9992583561	0.9989070416	625A>T filtered by frequency for QQ-SNV _{HS-P80} at mix ratio 99.9:0.1

