

**TABLE S6 Comparison of the performance of the triploid genotype caller to that of GATK**

Method	Coverage	Genotype	Correct-call Rate	Correct-call Rate among Called Genotypes
TRI	10	Homozygote	0.999	0.999
GATK	10	Homozygote	0.963	0.963
TRI	10	Heterozygote with two different nucleotides	0.685	0.786
GATK	10	Heterozygote with two different nucleotides	0.770	0.770
TRI	10	Heterozygote with three different nucleotides	0.665	0.678
GATK	10	Heterozygote with three different nucleotides	0.765	0.765
TRI	20	Homozygote	1.000	1.000
GATK	20	Homozygote	0.997	0.997
TRI	20	Heterozygote with two different nucleotides	0.881	0.926
GATK	20	Heterozygote with two different nucleotides	0.904	0.904
TRI	20	Heterozygote with three different nucleotides	0.892	0.901
GATK	20	Heterozygote with three different nucleotides	0.977	0.977
TRI	30	Homozygote	1.000	1.000
GATK	30	Homozygote	0.996	0.996
TRI	30	Heterozygote with two different nucleotides	0.953	0.973
GATK	30	Heterozygote with two different nucleotides	0.958	0.958

TRI	30	Heterozygote with three different nucleotides	0.952	0.952
GATK	30	Heterozygote with three different nucleotides	0.998	0.998

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Correct-call rate and that among called genotypes are calculated among 10,000 simulation replications and those with called genotypes, respectively. Error rate  $\epsilon = 0.01$ .