

S2 Table. Concordance and error rates for ANGSD/Beagle genotype calls at different dosage r^2 thresholds

	DR²>=0.9	DR²>=0.8	DR²>=0.7
Total called and imputed by ANGSD/Beagle	2,274,118	2,274,118	2,274,118
SNPs passing dosage r^2 filter	305,779	427,123	541,622
SNPs passing MAF ≥ 0.01 filter	244,586	326,550	393,569
SNPs passing HWE 10^{-7} filter	204,104	259,111	305,660
Mean Pearson correlation of dosages (n=381)	0.983	0.969	0.957
Rate of concordance of hard calls (n=381)	0.983	0.972	0.963
Rate of discordance (1 – concordance)	0.017	0.028	0.037
Error rate (Rate of discordance/2)*100	0.85%	1.4%	1.85%