

**Supplemental Table S1:** Impact of base quality score recalibration by Lacer and GATK on SNP calls from NA12878 chr19 (GATK HaplotypeCaller).

Call Set	No. of SNPs		Ti/Tv	
	Lacer	GATK	Lacer	GATK
Raw reads, all calls	88,335	88,335	2.10	2.10
Unique to raw read calls	813	1,462	0.69	0.64
Unique to +recal/+LRA calls	503	443	0.96	1.12
+recal/+LRA, all calls	88,025	87,316	2.11	2.14
Filtered by VQSR	17,155	16,107	1.57	1.64
Final call set	70,870	71,209	2.28	2.28
Unique to final call set	2,518	2,857	1.95	1.95

recal: recalibration; LRA: local realignment; VQSR: variant quality score recalibration