

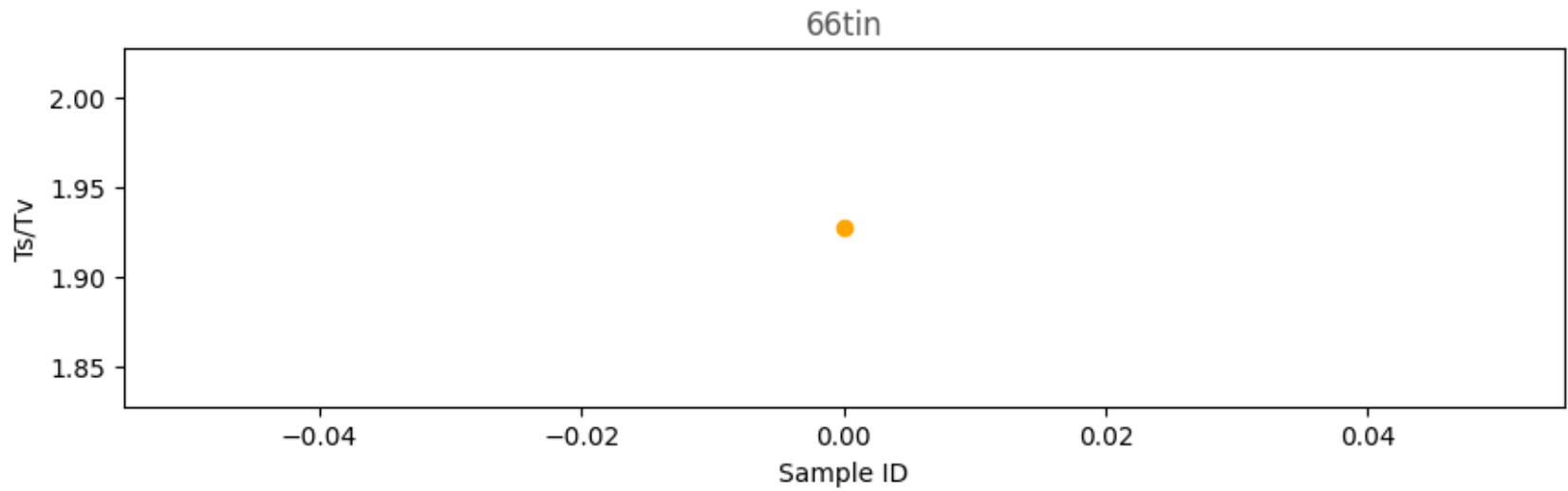
Summary Numbers

Callset	SNPs			indels		MNPs	others
	n	ts/tv	(1st ALT)	n	frm*		
66tin	4,055,352	1.93	1.93	950,702	–	0	0
* frameshift ratio: out/(out+in)							

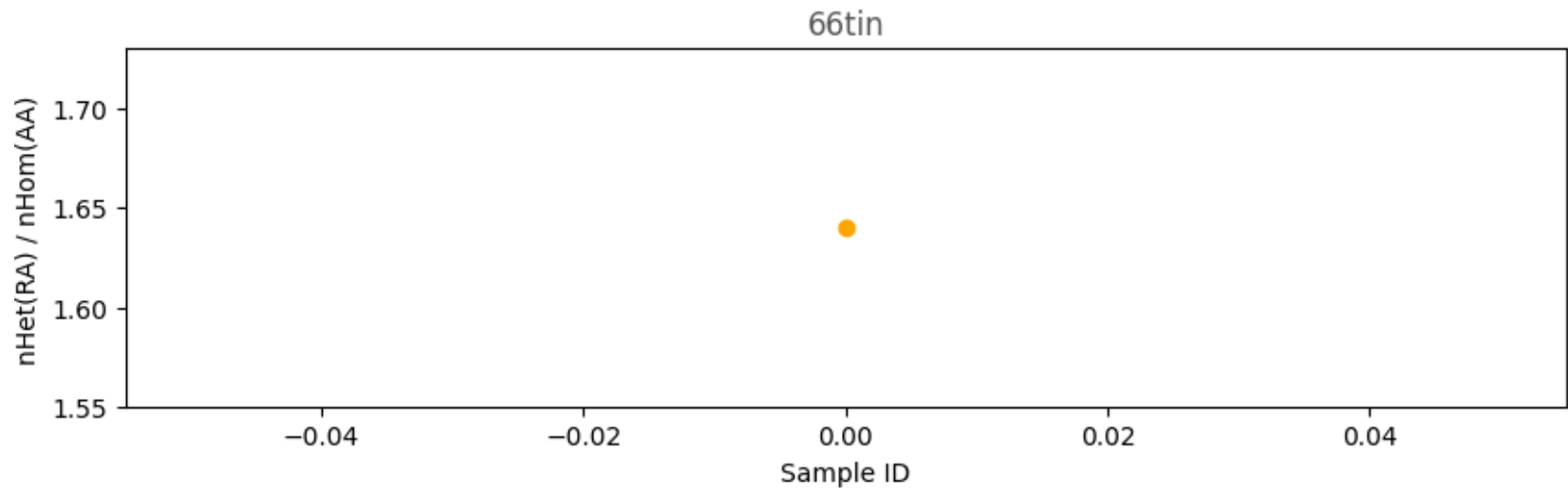
Callset	singletons (AC=1)			multiallelic	
	SNPs	ts/tv	indels	sites	SNPs
66tin	62.1%	1.90	67.2%	102,016	1,960

- 66tin .. /ngc/projects2/gm/data/archive/2022/variants/snv/66tinsusm-103806330624-Normal_Blood_noinfo-WGS_v1_IlluminaDNAPCRFree_X-211117_A01411_BHT773DSX2-RHGM_LABKA_WGSA_KUT-WGSAKUT03357_21RKG028160x01_snv_germline_raw.haplotype_caller.vcf.gz

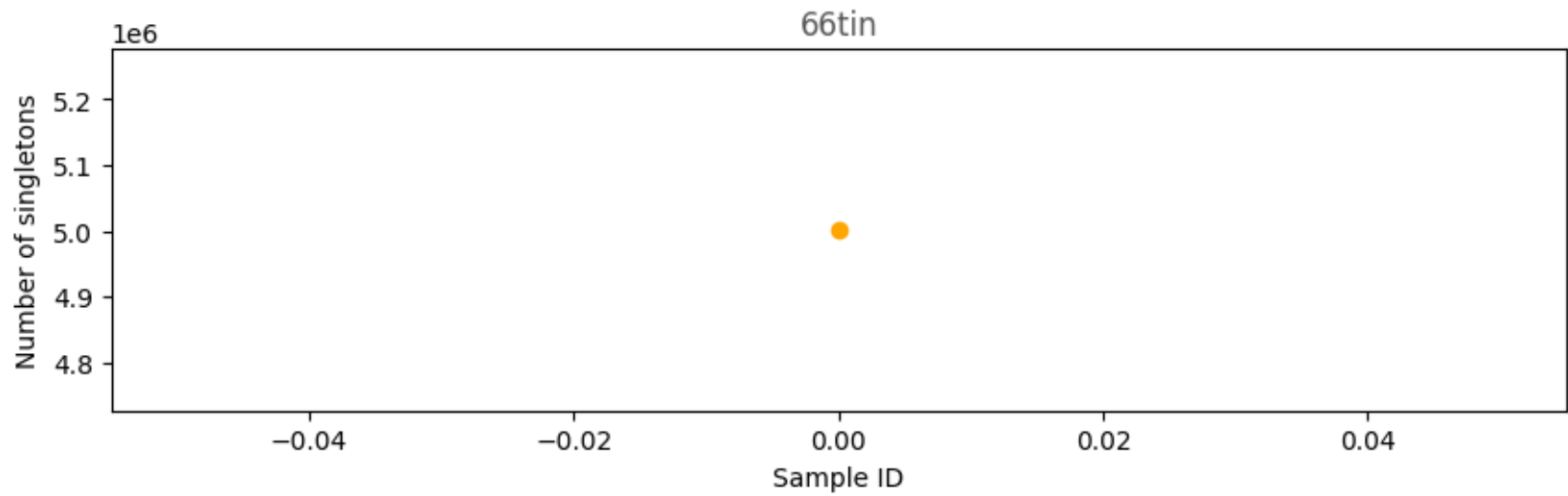
Ts/Tv by sample



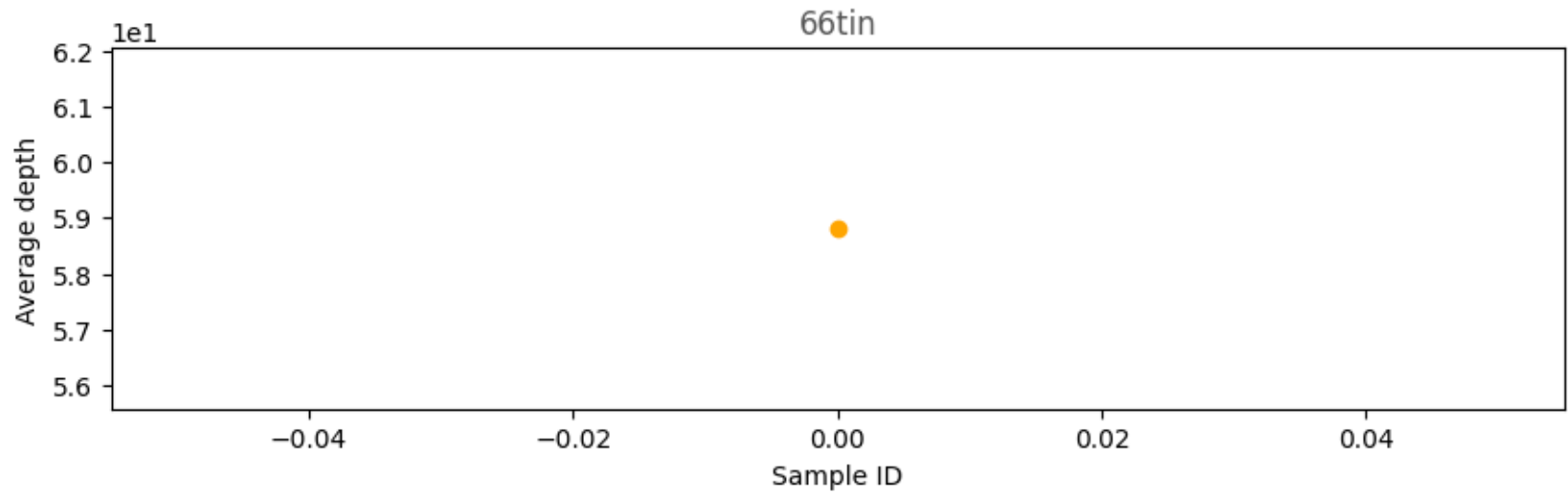
Hets vs non-ref Homs by sample



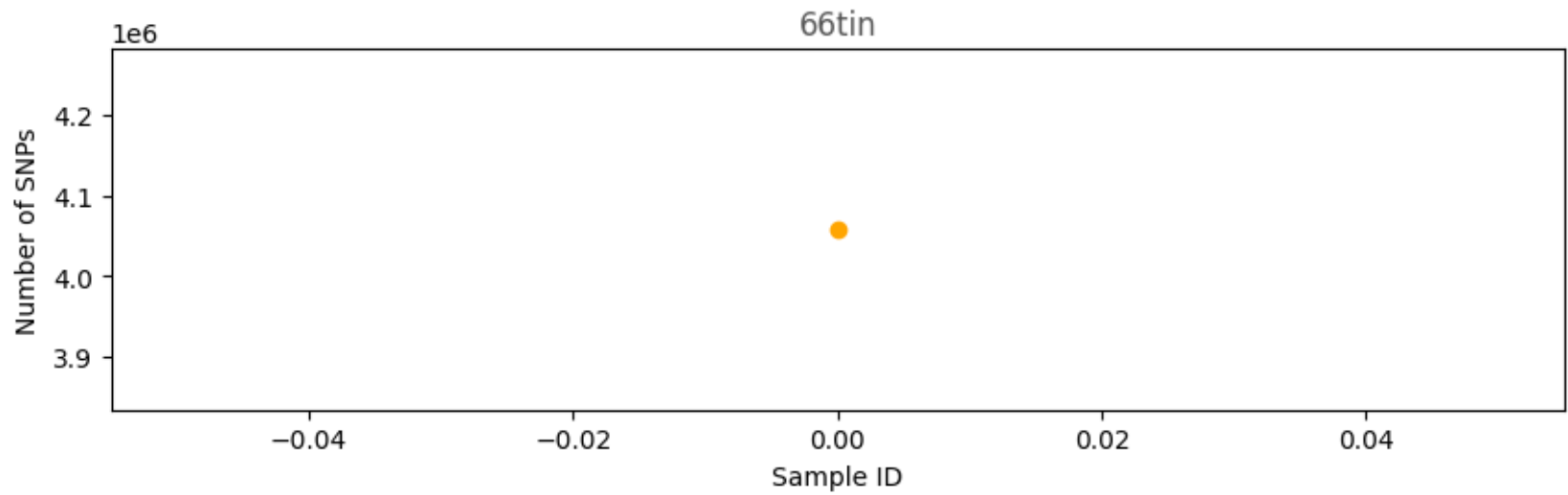
Singletons by sample (hets and homs)



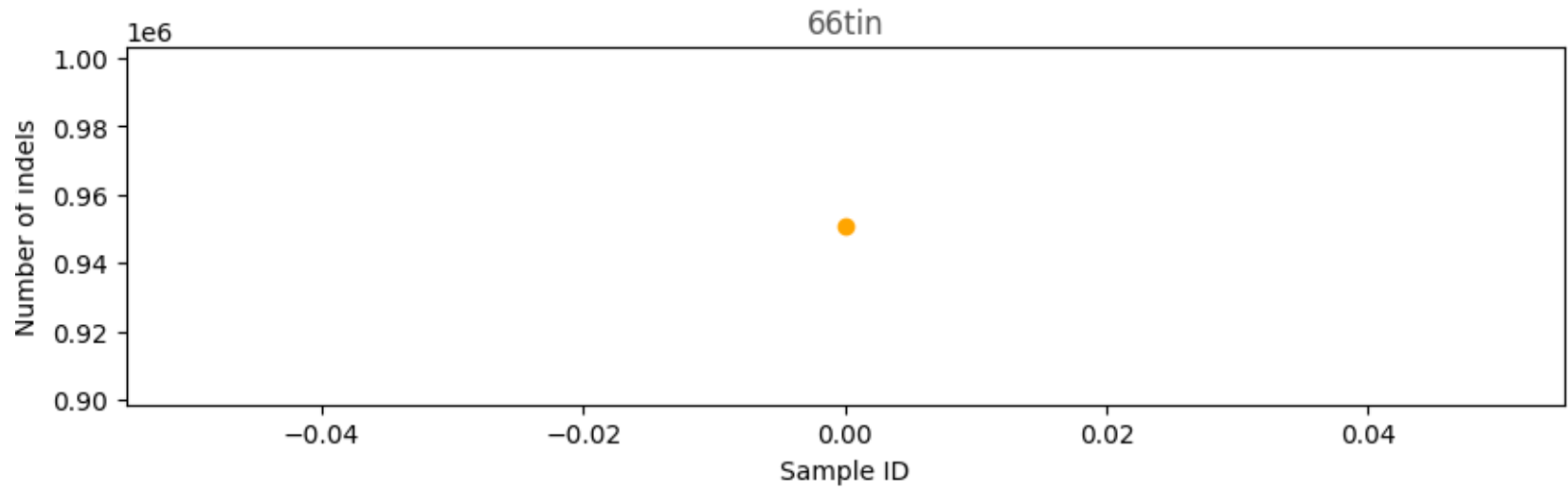
Average depth by sample



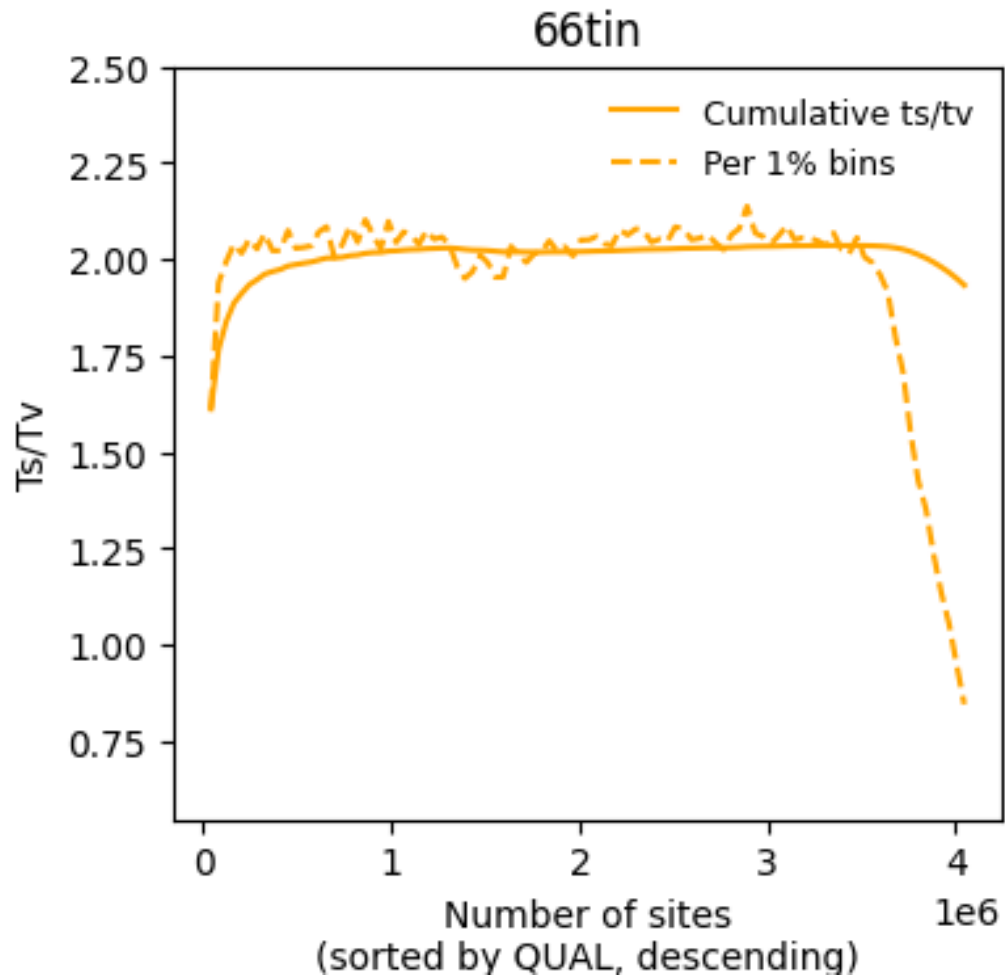
Number of SNPs by sample



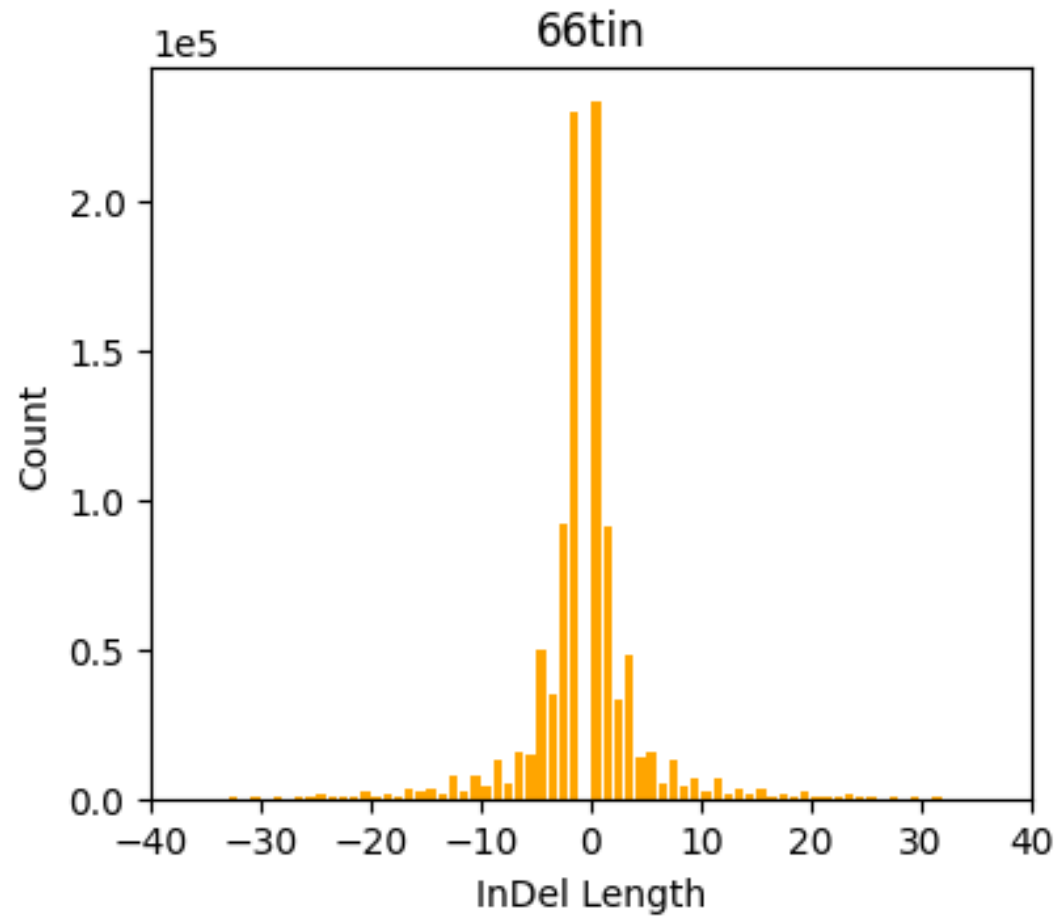
Number of indels by sample



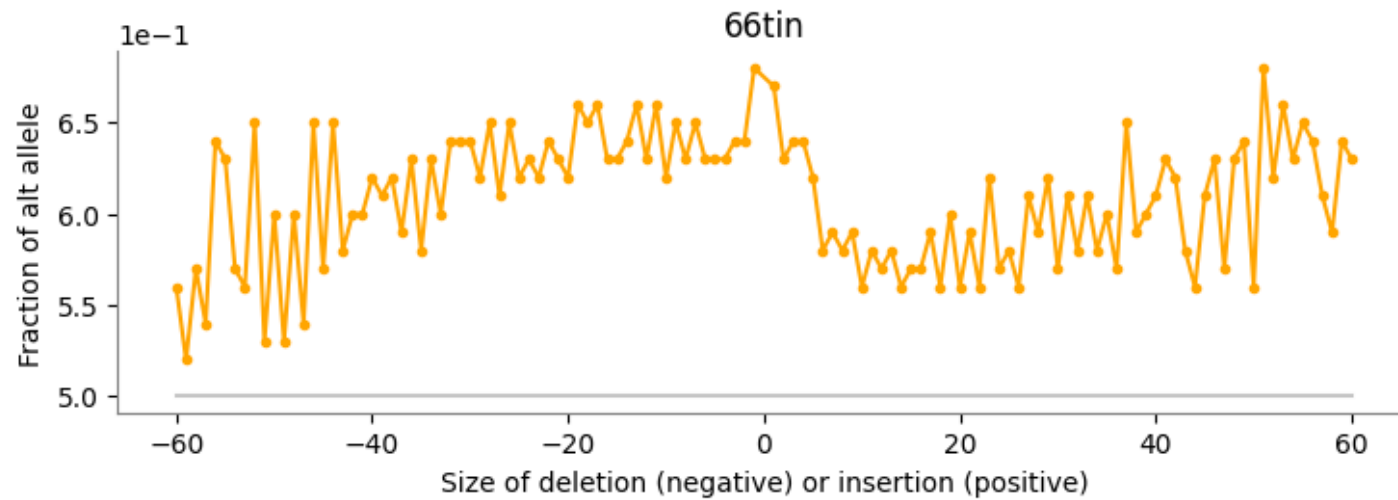
Ts/Tv stratified by QUAL



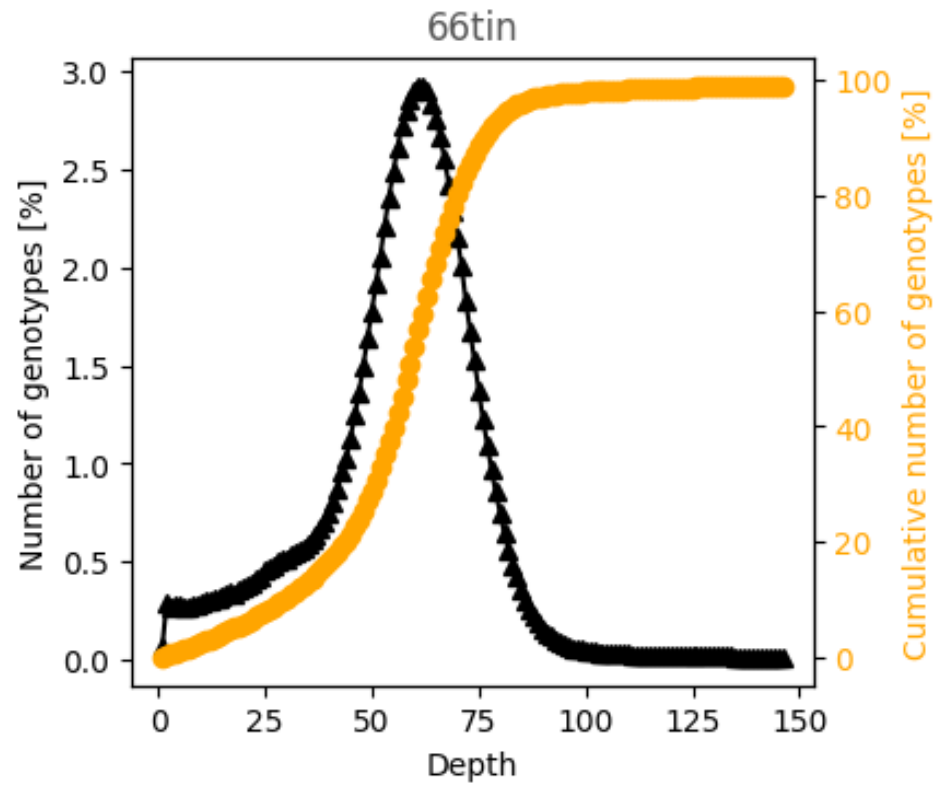
Indel distribution



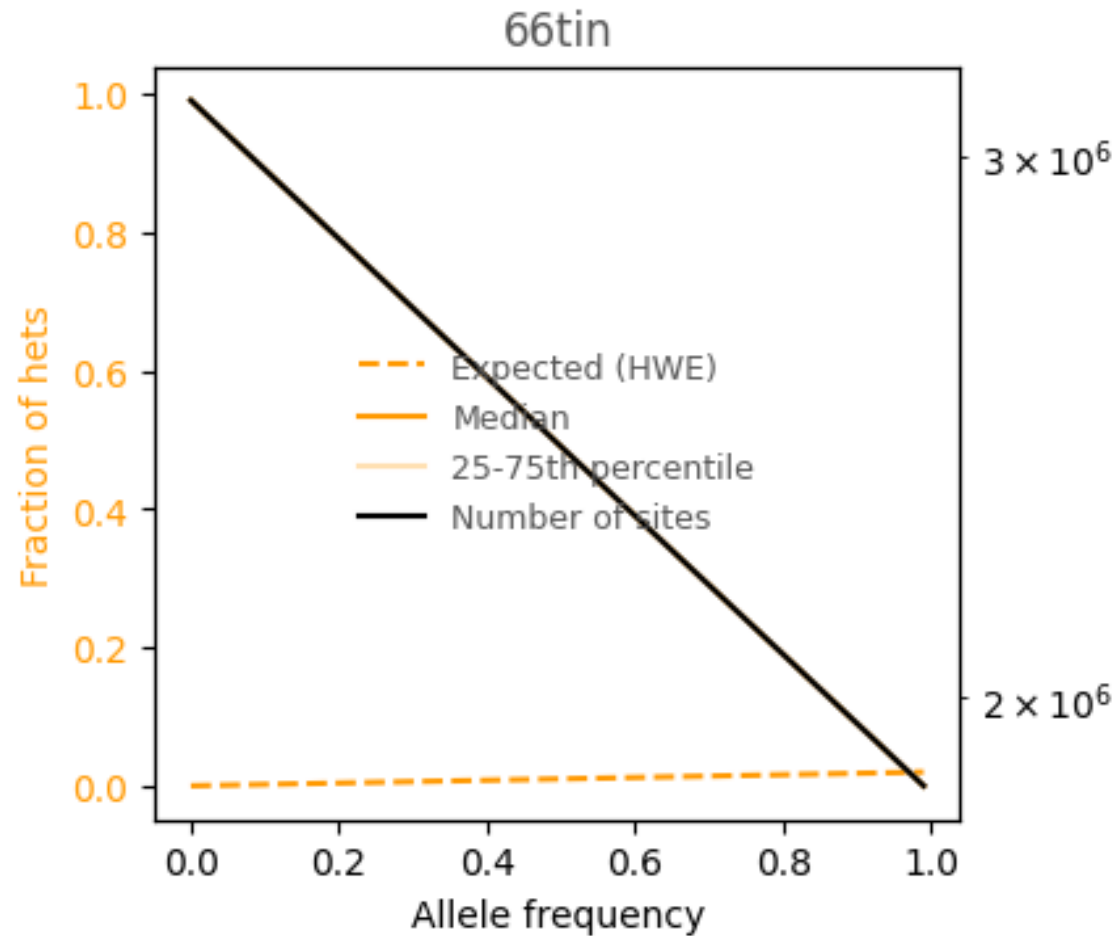
Fraction of alternate indel allele



Depth distribution



Number of HETs by AF



Substitution types

