

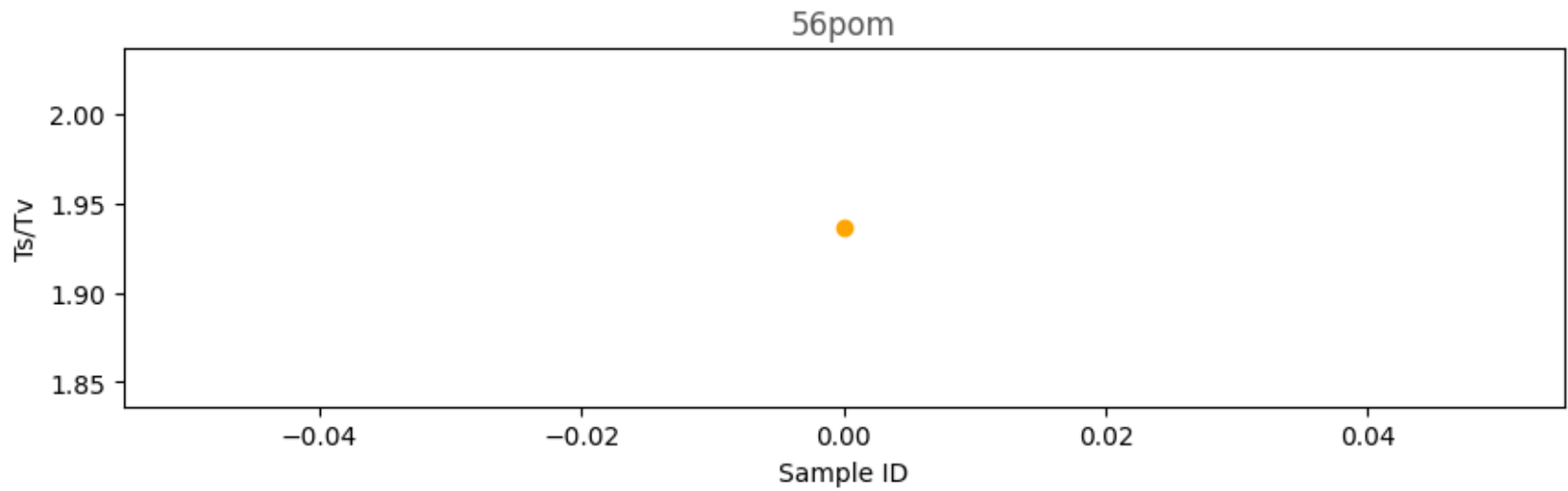
Summary Numbers

Callset	SNPs			indels		MNPs	others
	n	ts/tv	(1st ALT)	n	frm*		
56pom	4,012,070	1.94	1.94	910,038	–	0	0
* frameshift ratio: out/(out+in)							

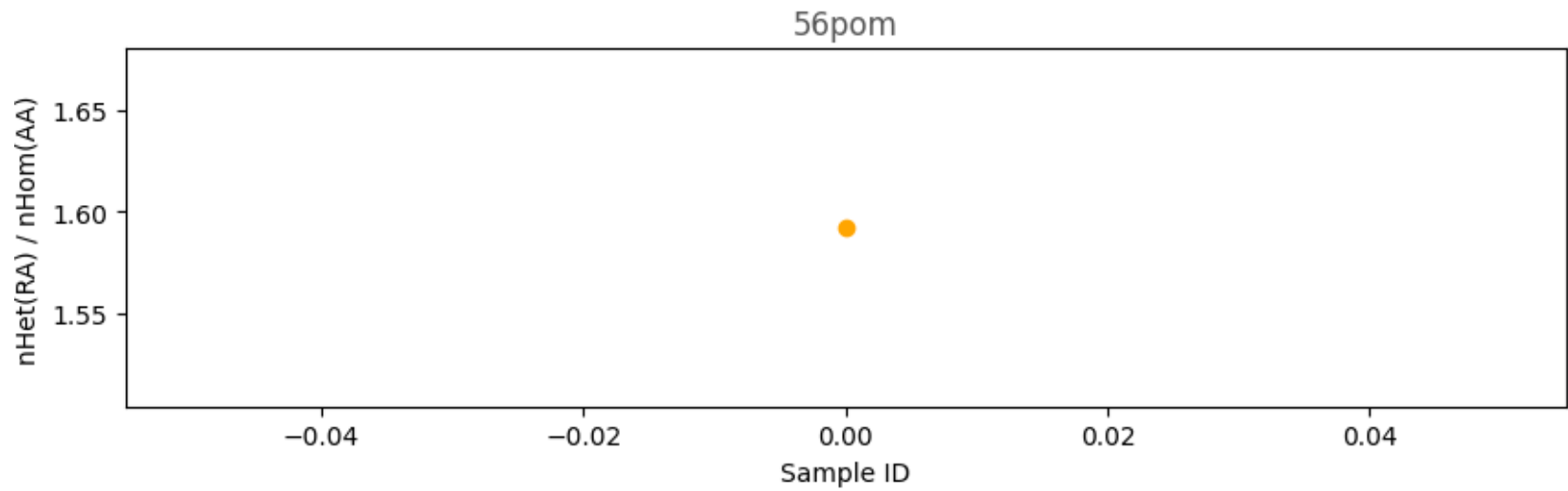
Callset	singletons (AC=1)			multiallelic	
	SNPs	ts/tv	indels	sites	SNPs
56pom	61.4%	1.90	64.6%	82,859	1,667

- 56pom .. /ngc/projects2/gm/data/archive/2022/variants/snv/56pomardm-103844529041-Normal_B
 lood_noinfo-WGS_v1_IlluminaDNAPCRFree_X-220302_A01411_AH5T5WDSX3-RHGM_LABKA_WGS-
 WGS03930_snv_germline_raw.haplotype_caller.vcf.gz

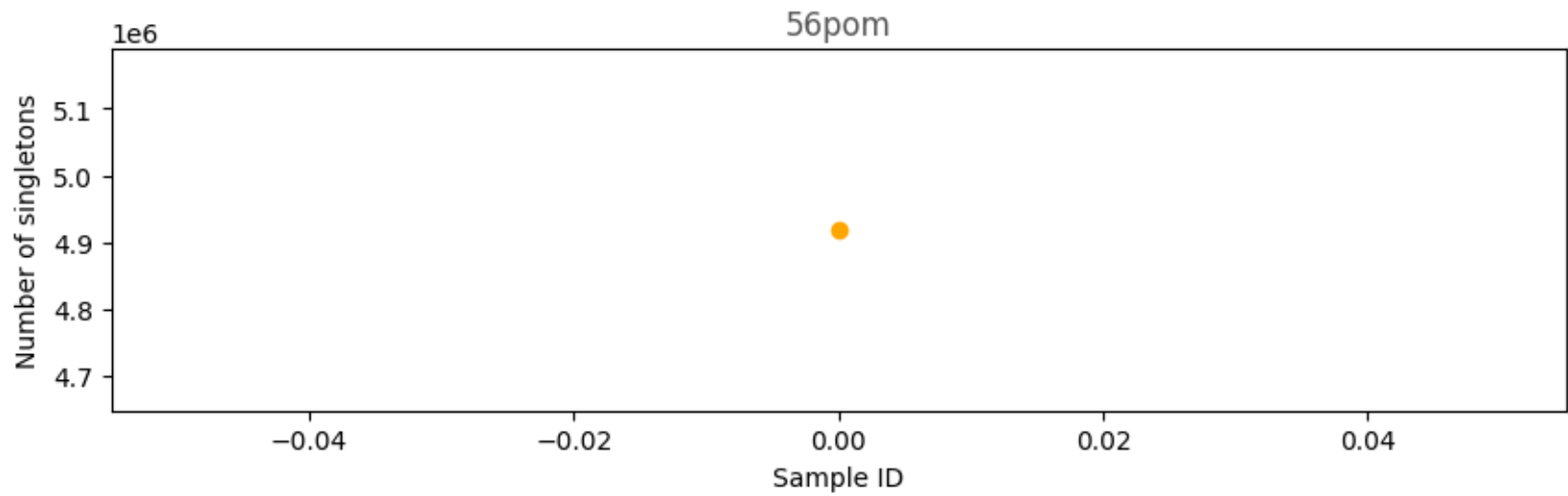
Ts/Tv by sample



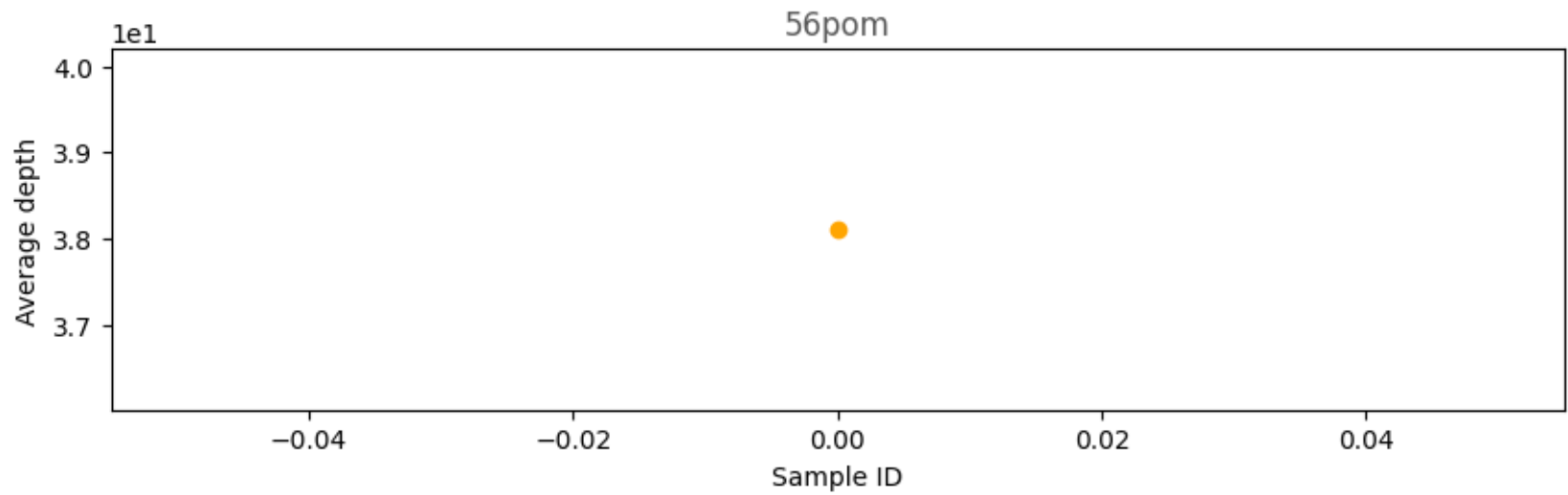
Hets vs non-ref Homs by sample



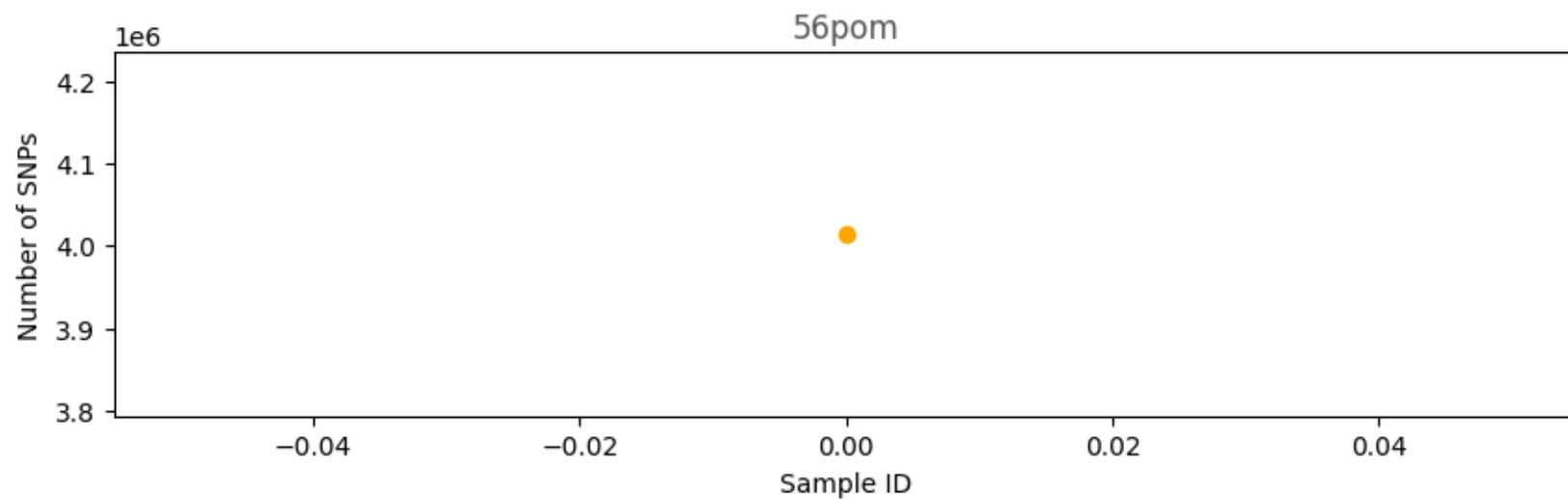
Singletons by sample (hets and homs)



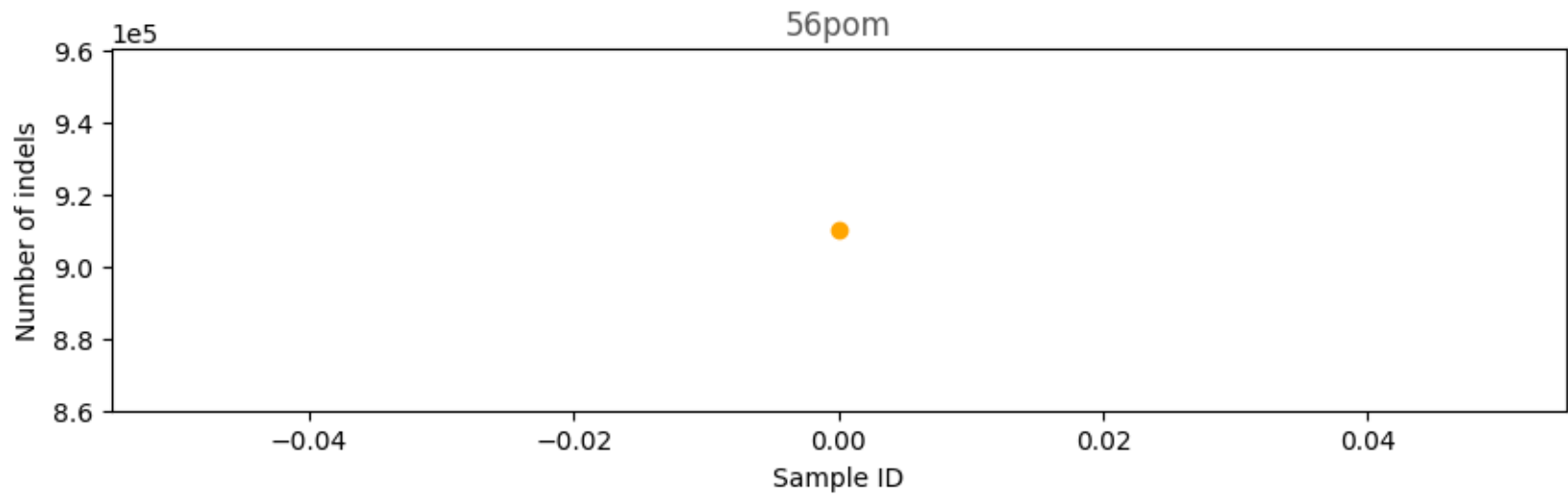
Average depth by sample



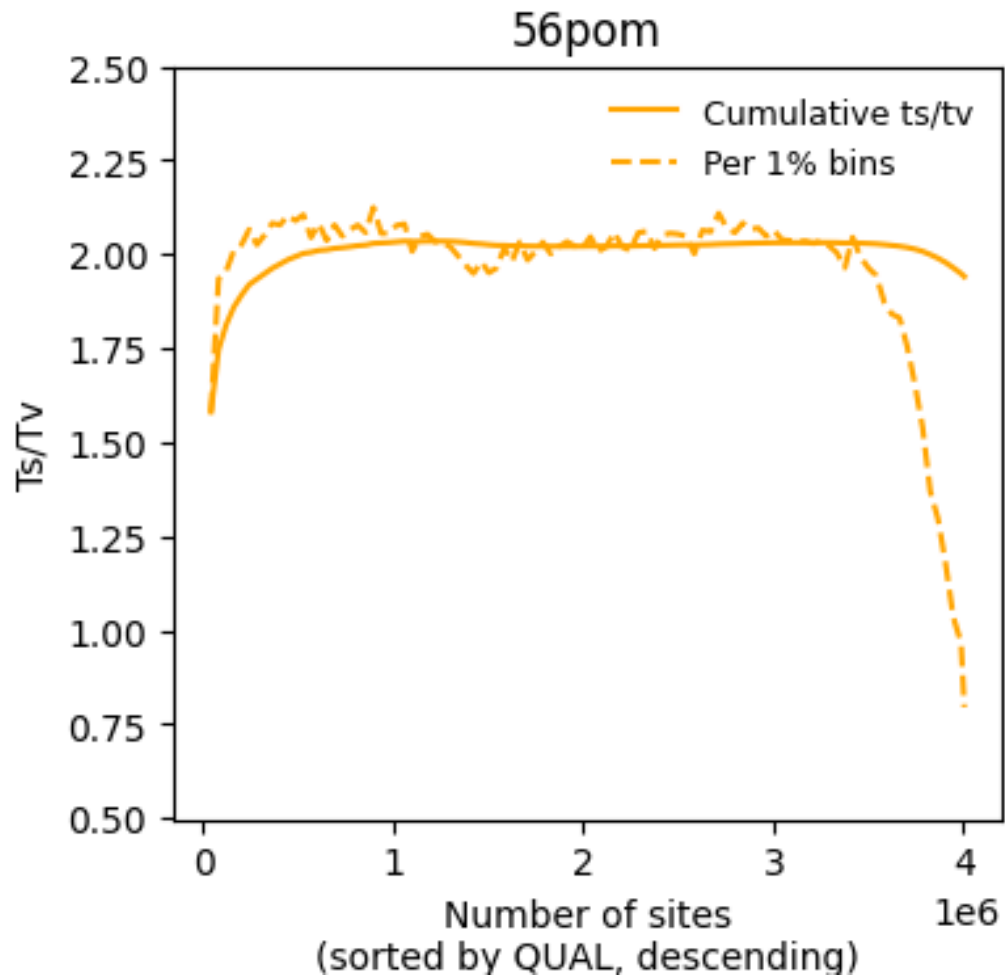
Number of SNPs by sample



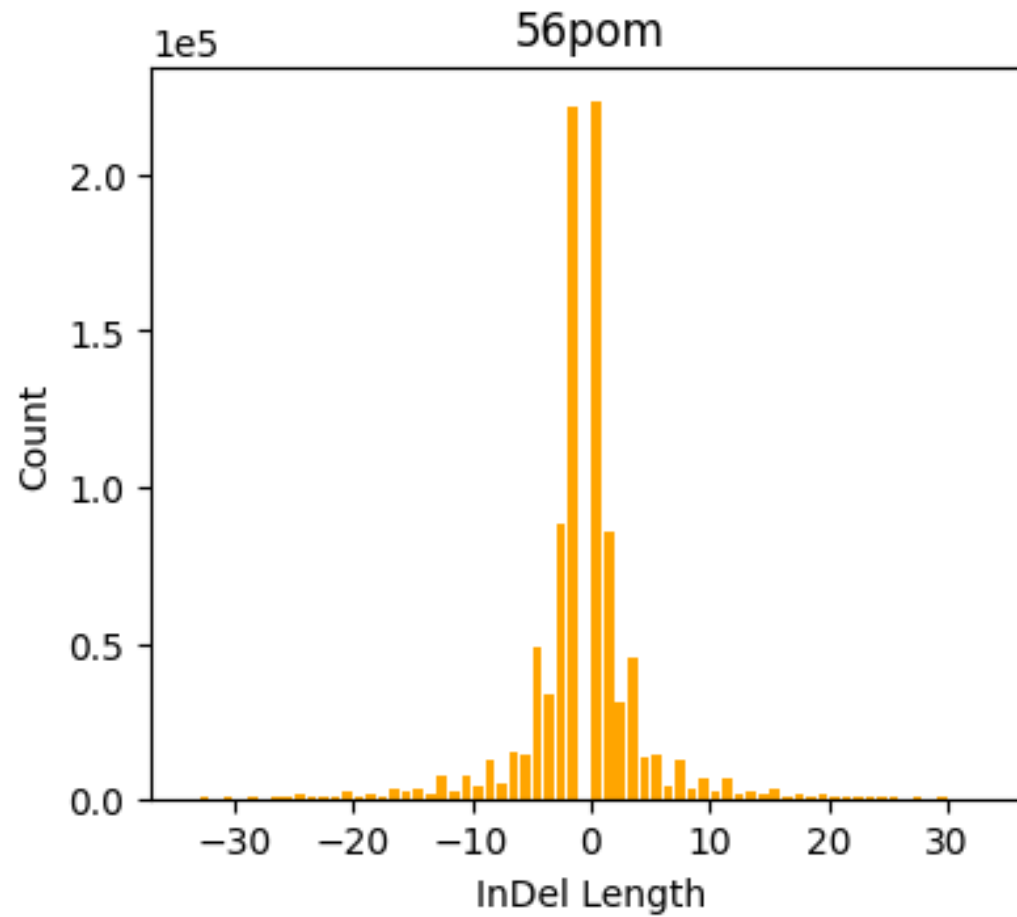
Number of indels by sample



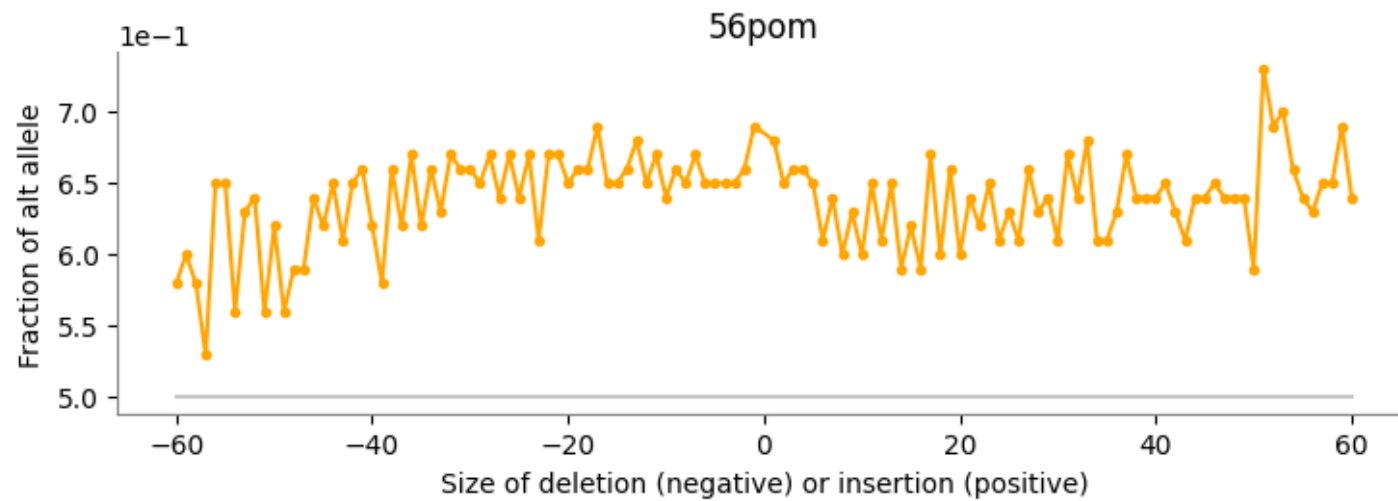
Ts/Tv stratified by QUAL



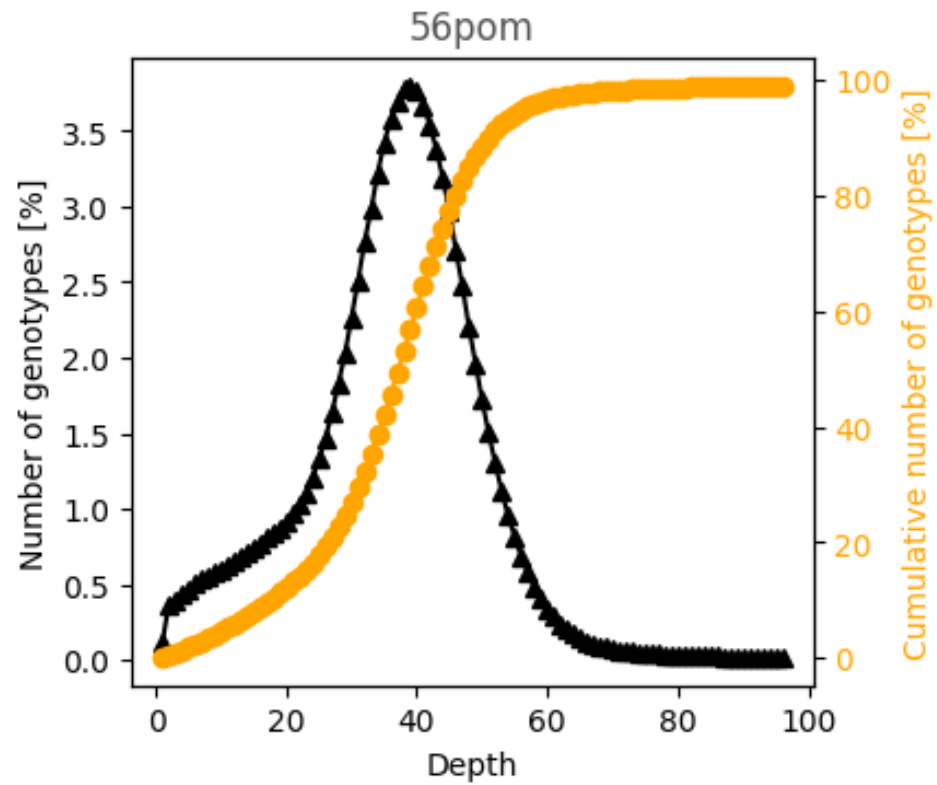
Indel distribution



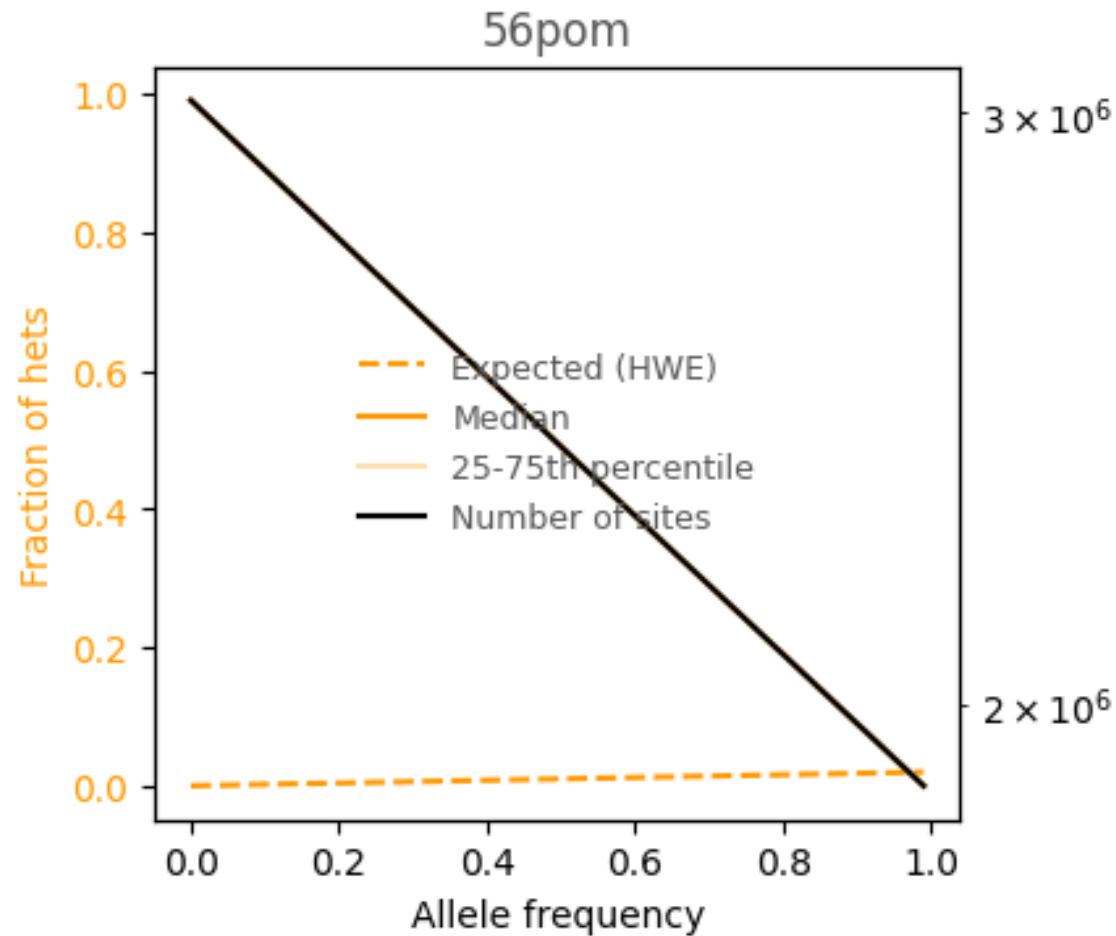
Fraction of alternate indel allele



Depth distribution



Number of HETs by AF



Substitution types

