

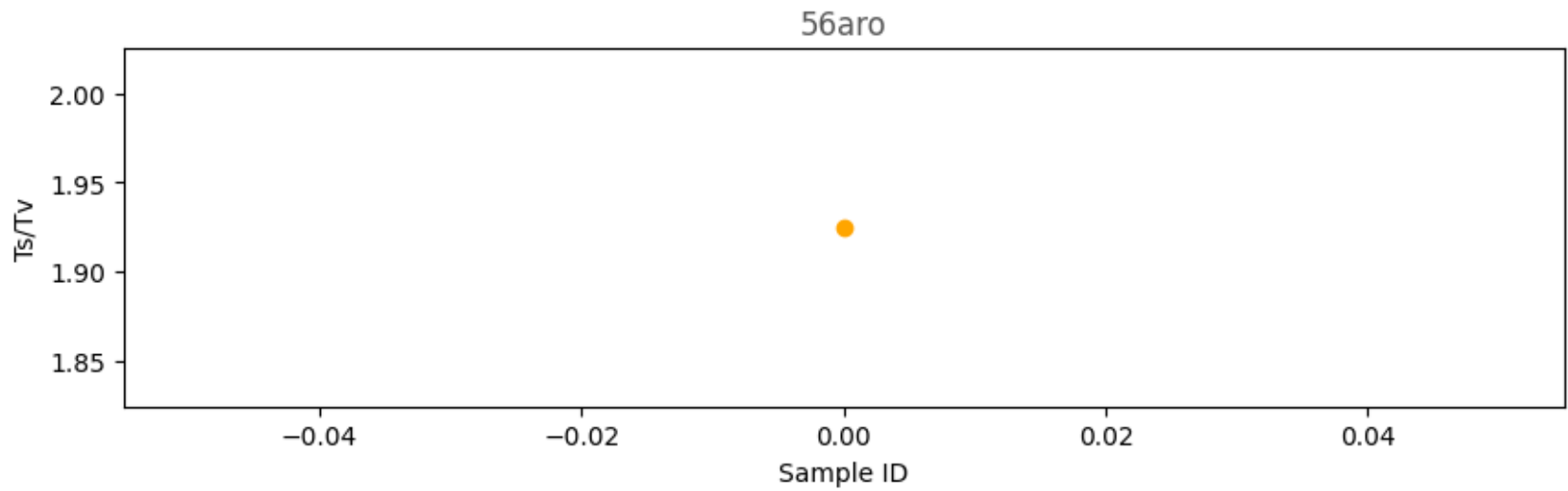
Summary Numbers

Callset	SNPs			indels		MNPs	others
	n	ts/tv	(1st ALT)	n	frm*		
56aro	4,061,551	1.92	1.93	943,544	–	0	0
* frameshift ratio: out/(out+in)							

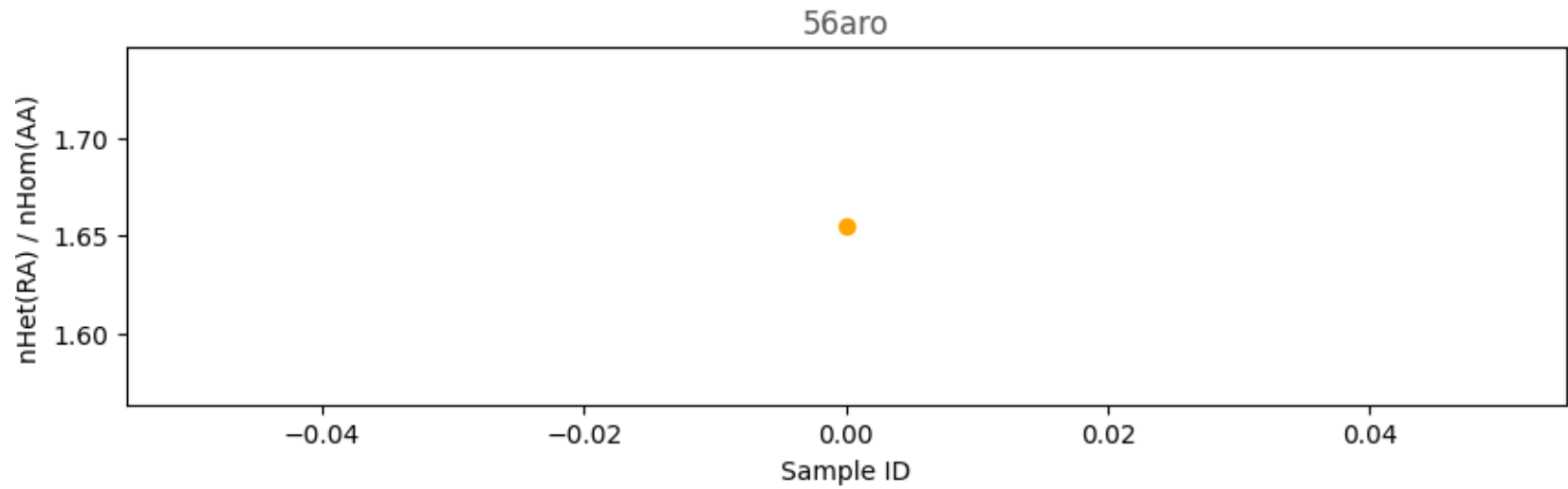
Callset	singletons (AC=1)			multiallelic	
	SNPs	ts/tv	indels	sites	SNPs
56aro	62.3%	1.89	67.0%	97,550	1,865

- 56aro .. /ngc/projects2/gm/data/archive/2022/variants/snv/56arortom-103844796350-Normal_B
 lood_noinfo-WGS_v1_IlluminaDNAPCRFree_X-220413_A00559_AHGTFCDSX3-RHGM_LABKA_WGS-
 WGS04146_snv_germline_raw.haplotype_caller.vcf.gz

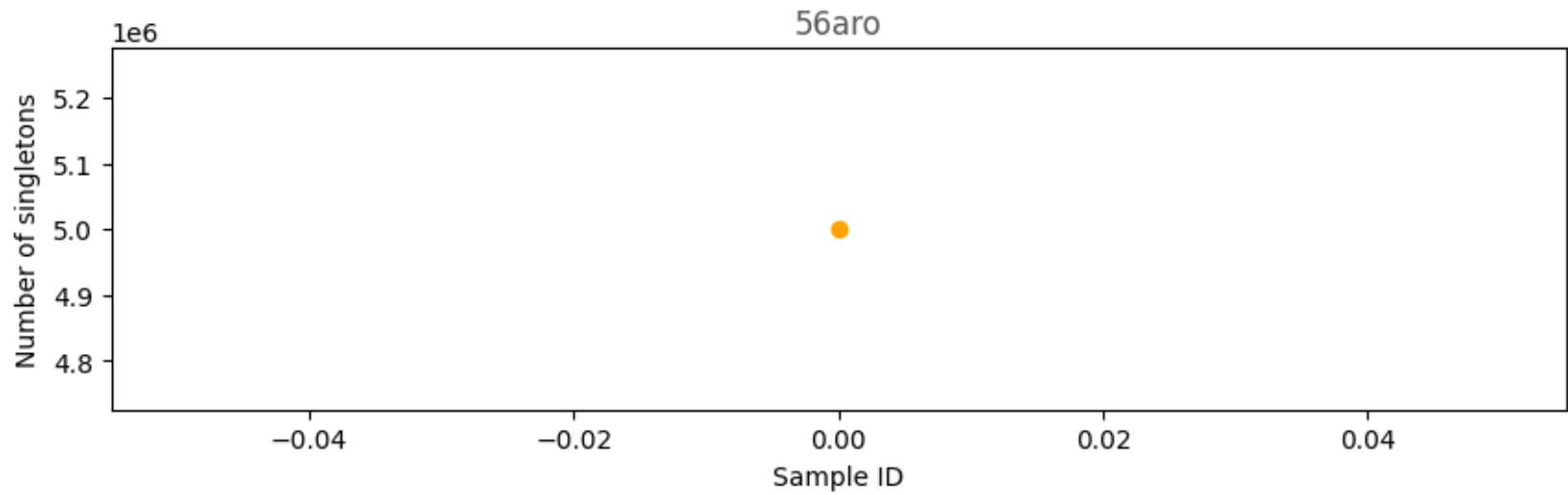
Ts/Tv by sample



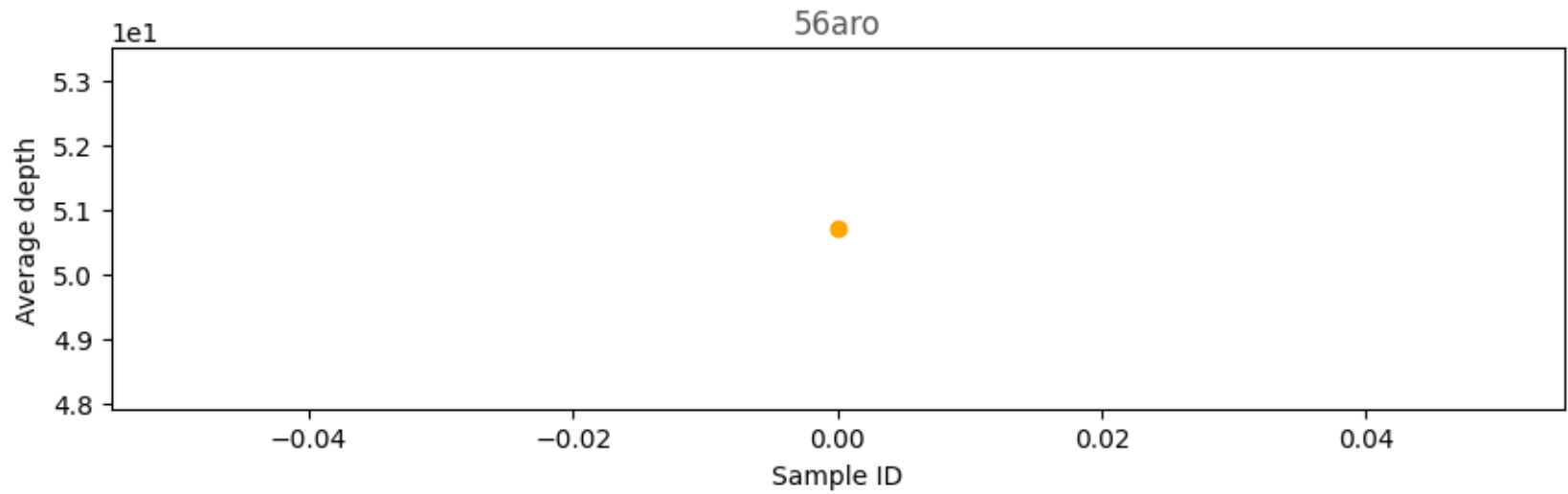
Hets vs non-ref Homs by sample



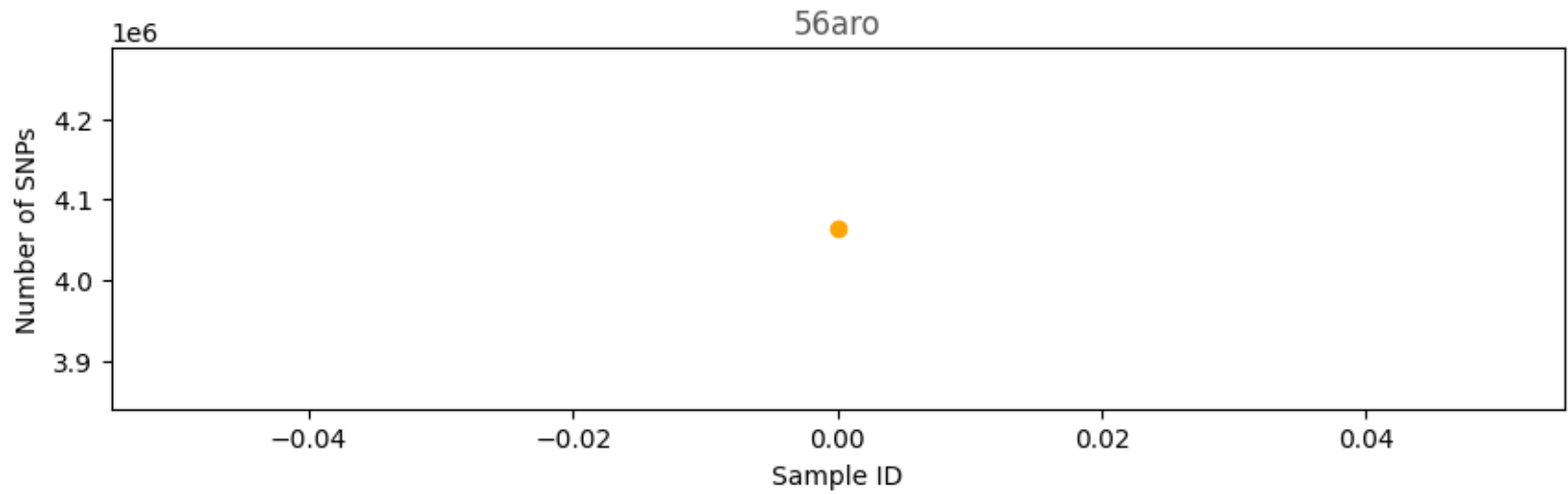
Singletons by sample (hets and homs)



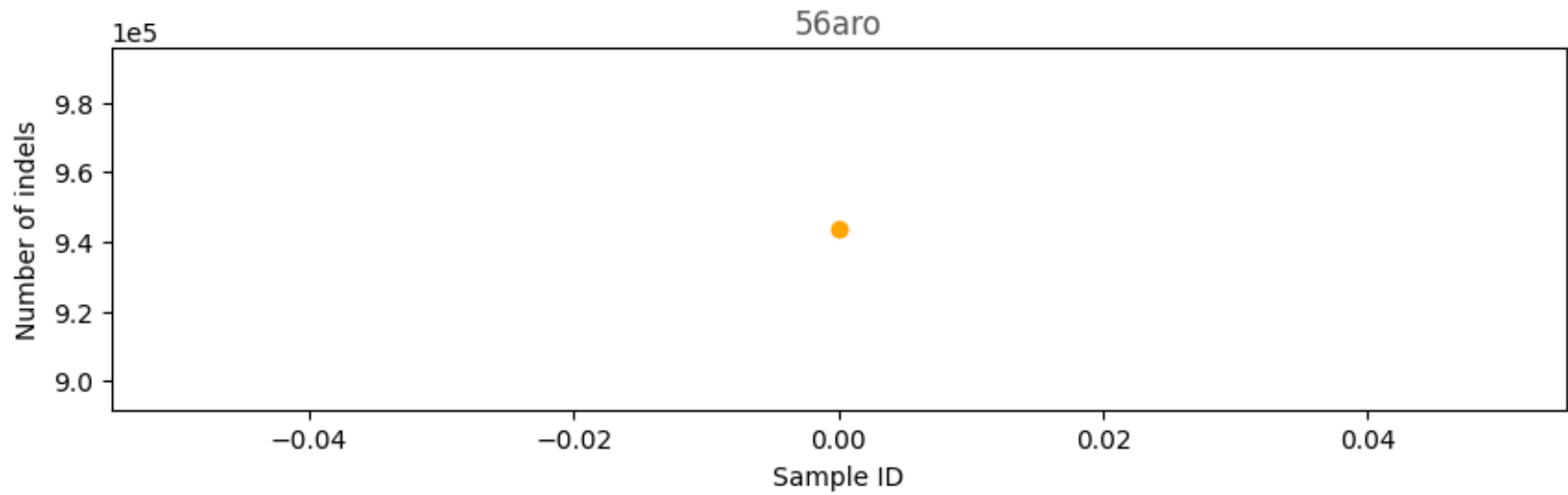
Average depth by sample



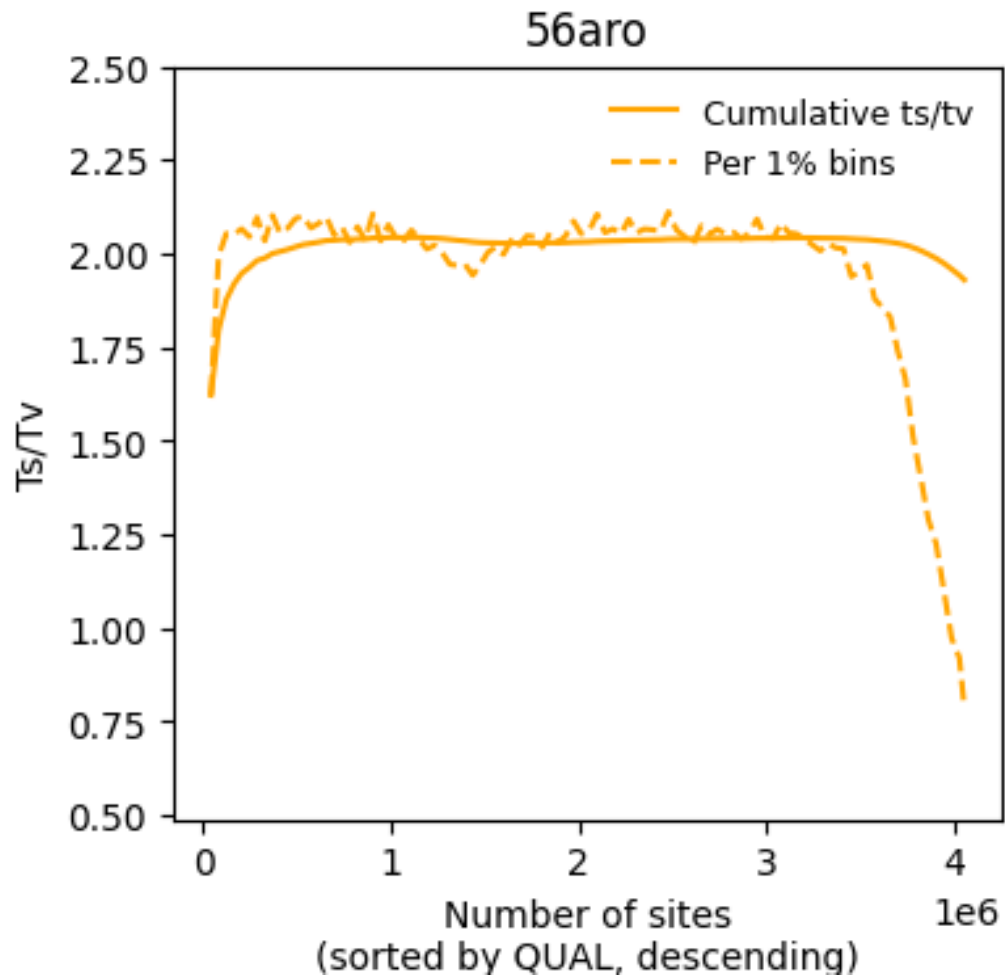
Number of SNPs by sample



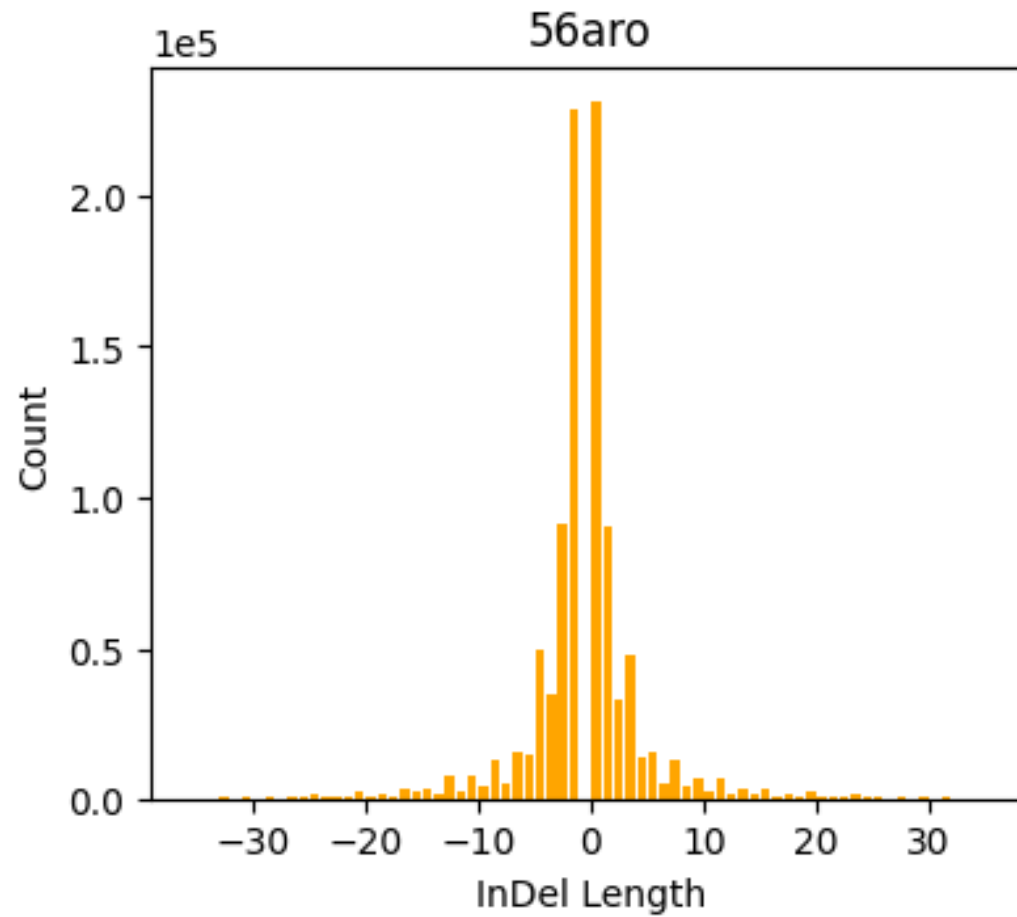
Number of indels by sample



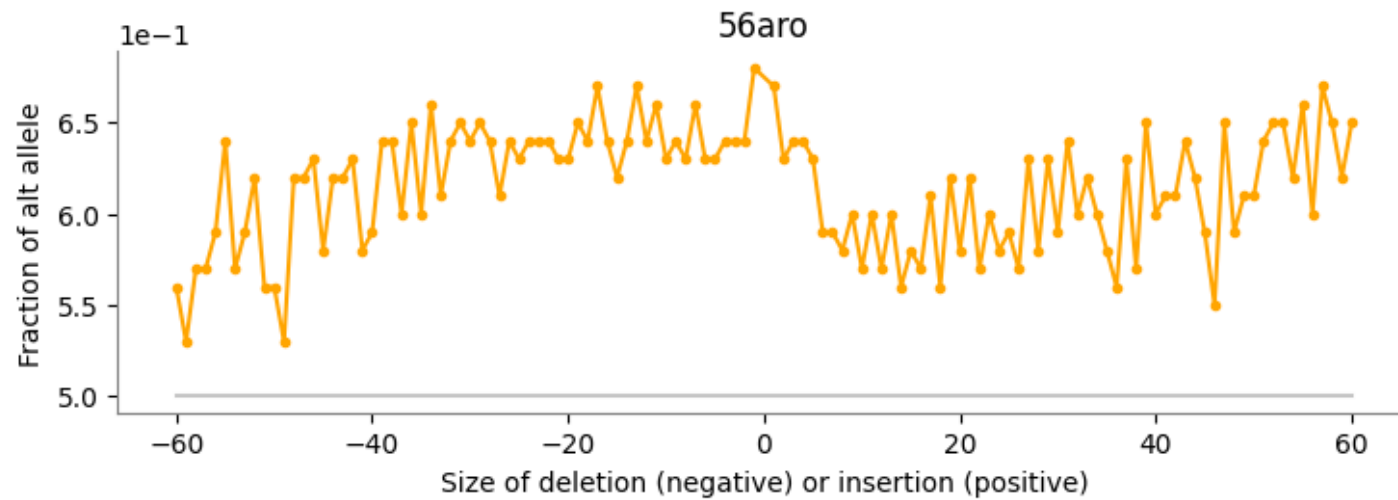
Ts/Tv stratified by QUAL



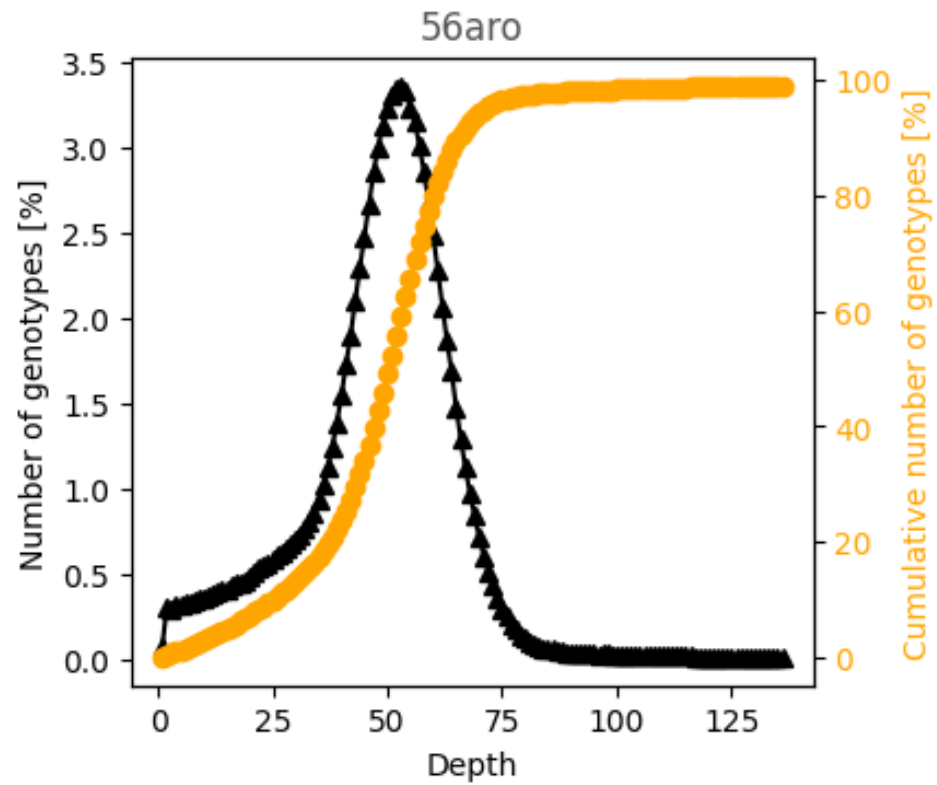
Indel distribution



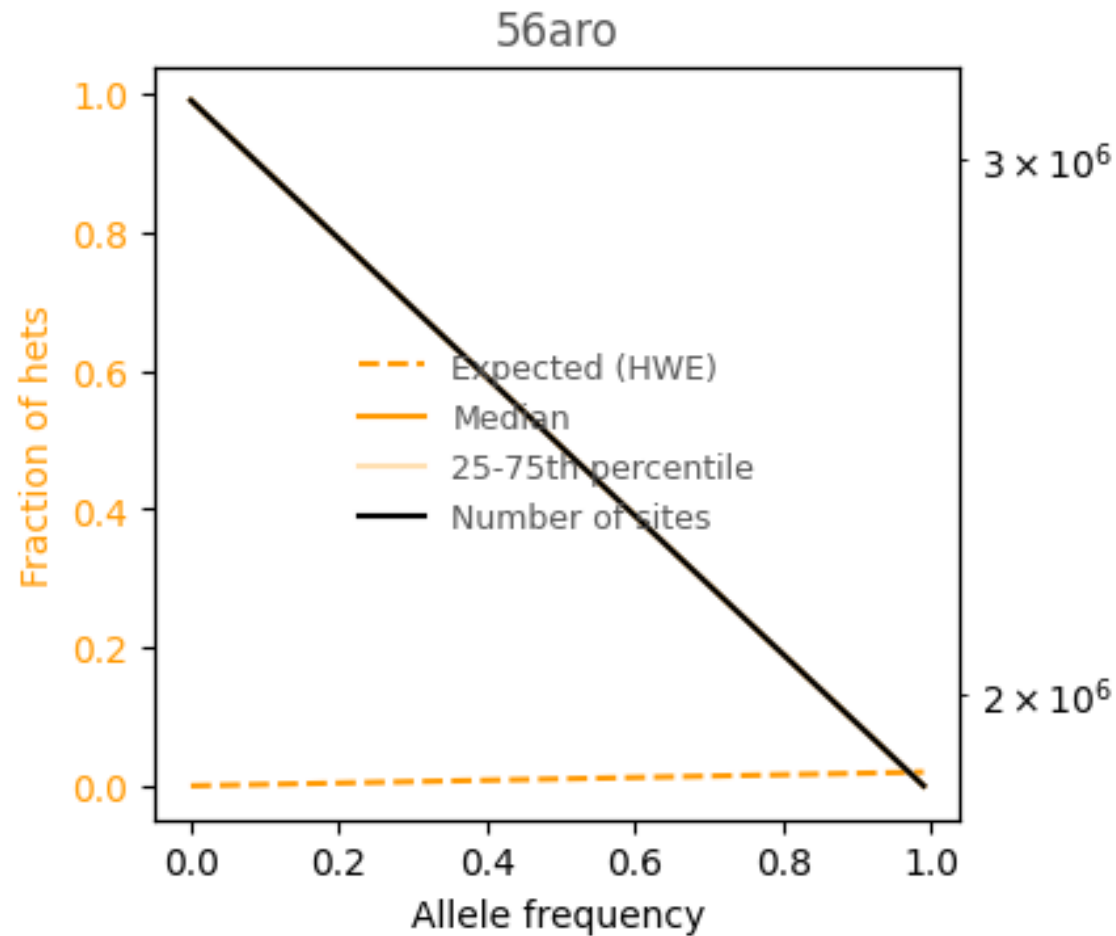
Fraction of alternate indel allele



Depth distribution



Number of HETs by AF



Substitution types

