

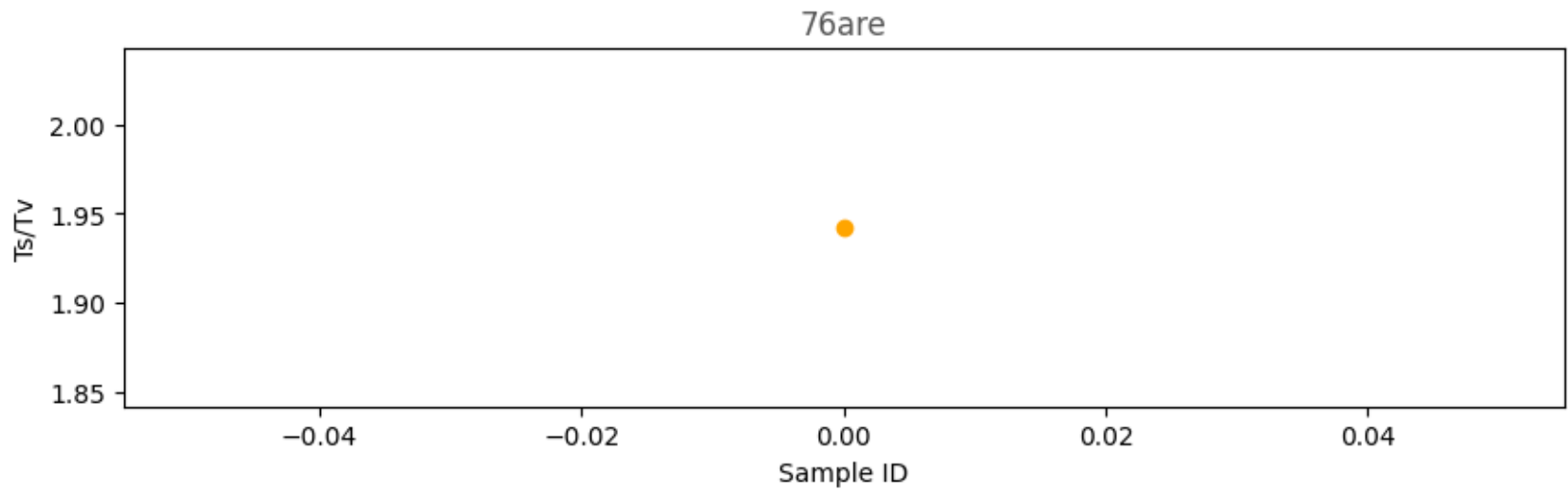
Summary Numbers

Callset	SNPs			indels		MNPs	others
	n	ts/tv	(1st ALT)	n	frm*		
76are	4,111,910	1.94	1.95	953,184	–	0	0
* frameshift ratio: out/(out+in)							

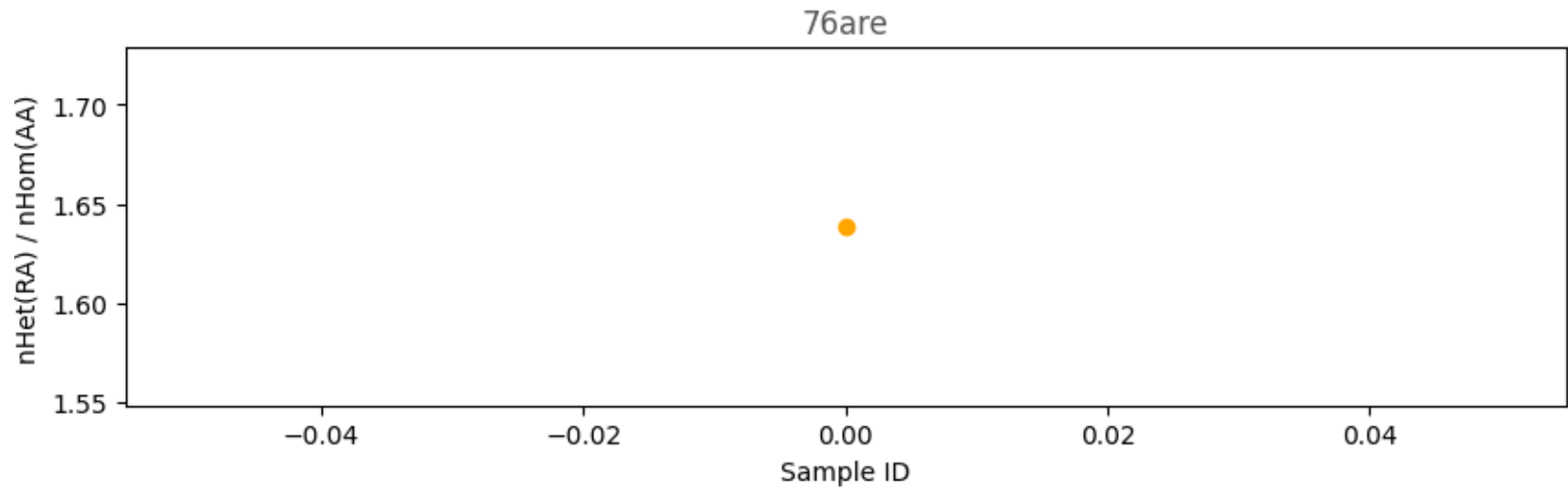
Callset	singletons (AC=1)			multiallelic	
	SNPs	ts/tv	indels	sites	SNPs
76are	62.1%	1.91	66.5%	96,092	1,870

- 76are .. /ngc/projects2/gm/data/archive/2022/variants/snv/76aressom-103913394797-Normal_B
 lood_noinfo-WGS_v1_IlluminaDNAPCRFree_RHGM01743-220923_A01176_BHTNN3DSX3-EXT_LAB
 KA_NGCWGS-NGCWGS05504_18RKG000711_snv_germline_raw.haplotype_caller.vcf.gz

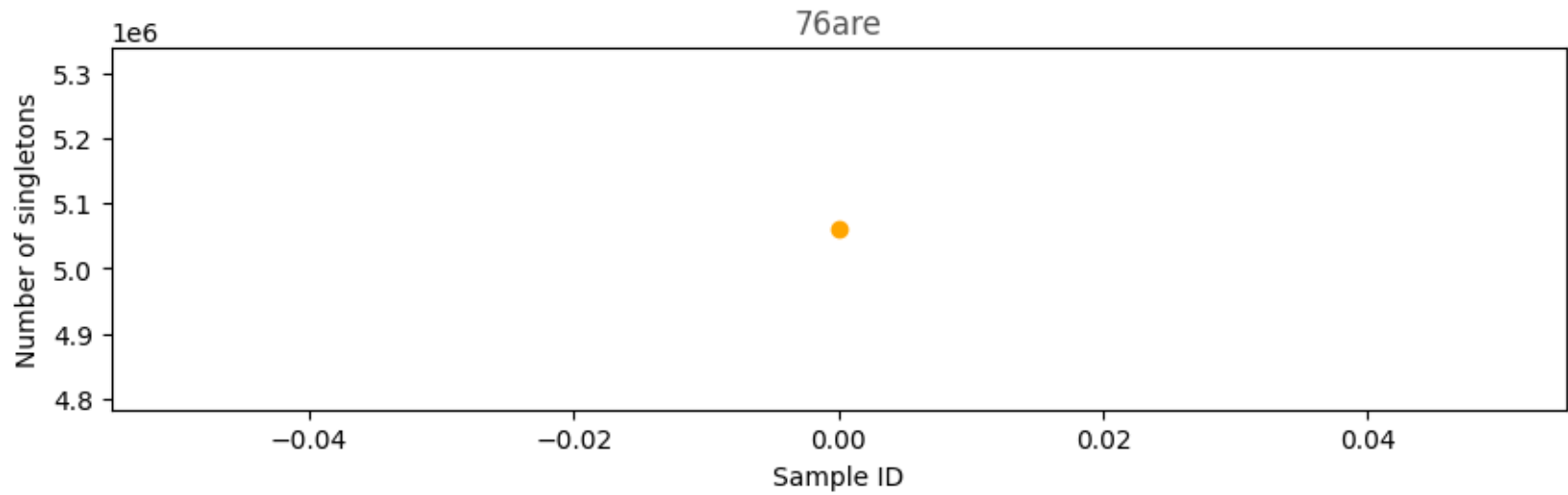
Ts/Tv by sample



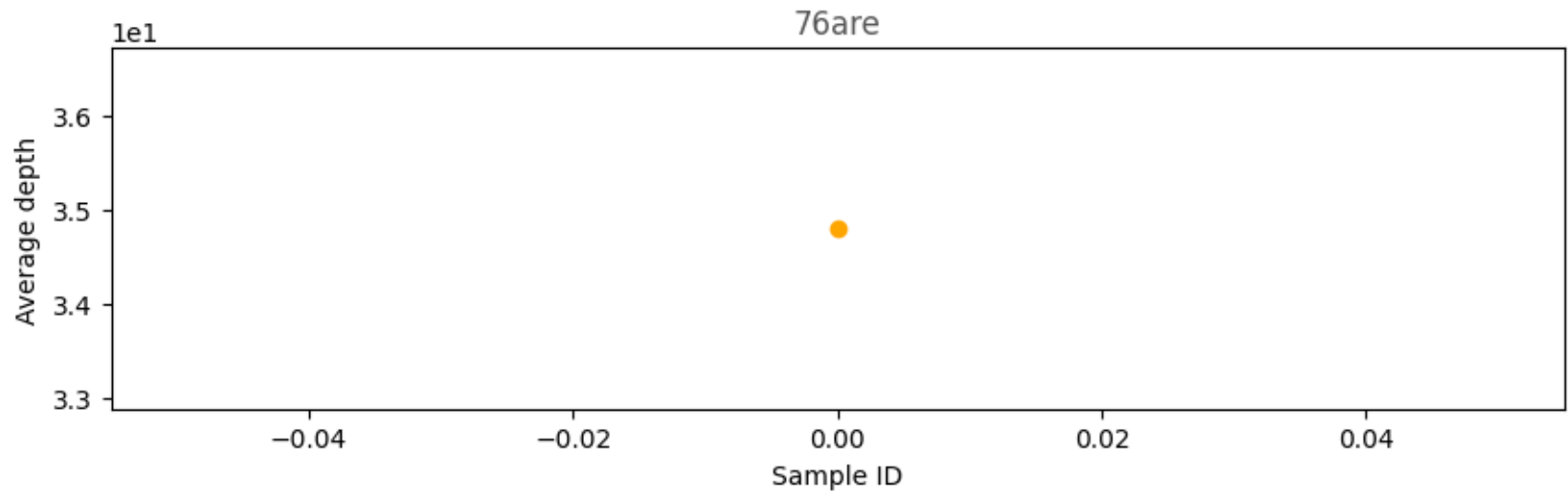
Hets vs non-ref Homs by sample



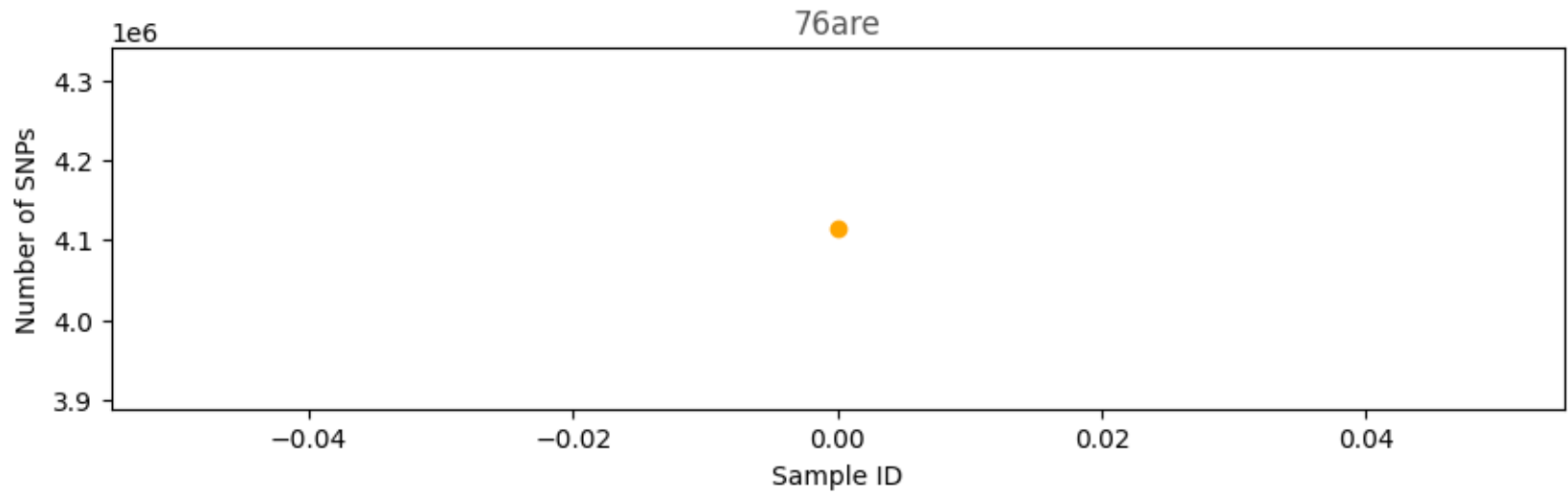
Singletons by sample (hets and homs)



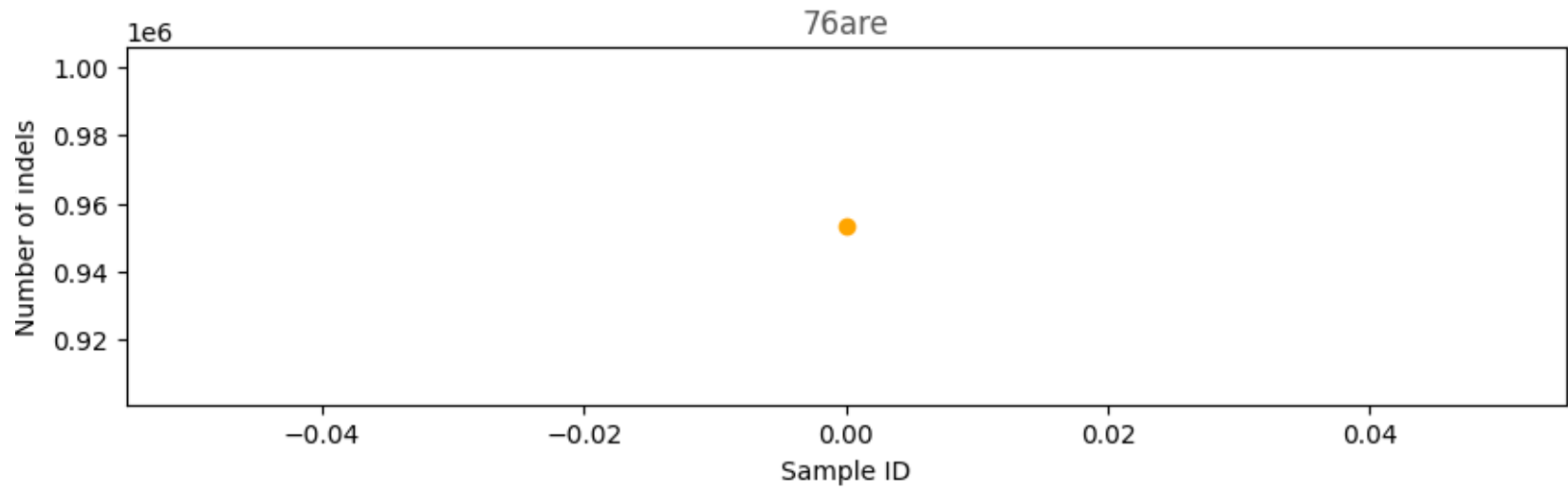
Average depth by sample



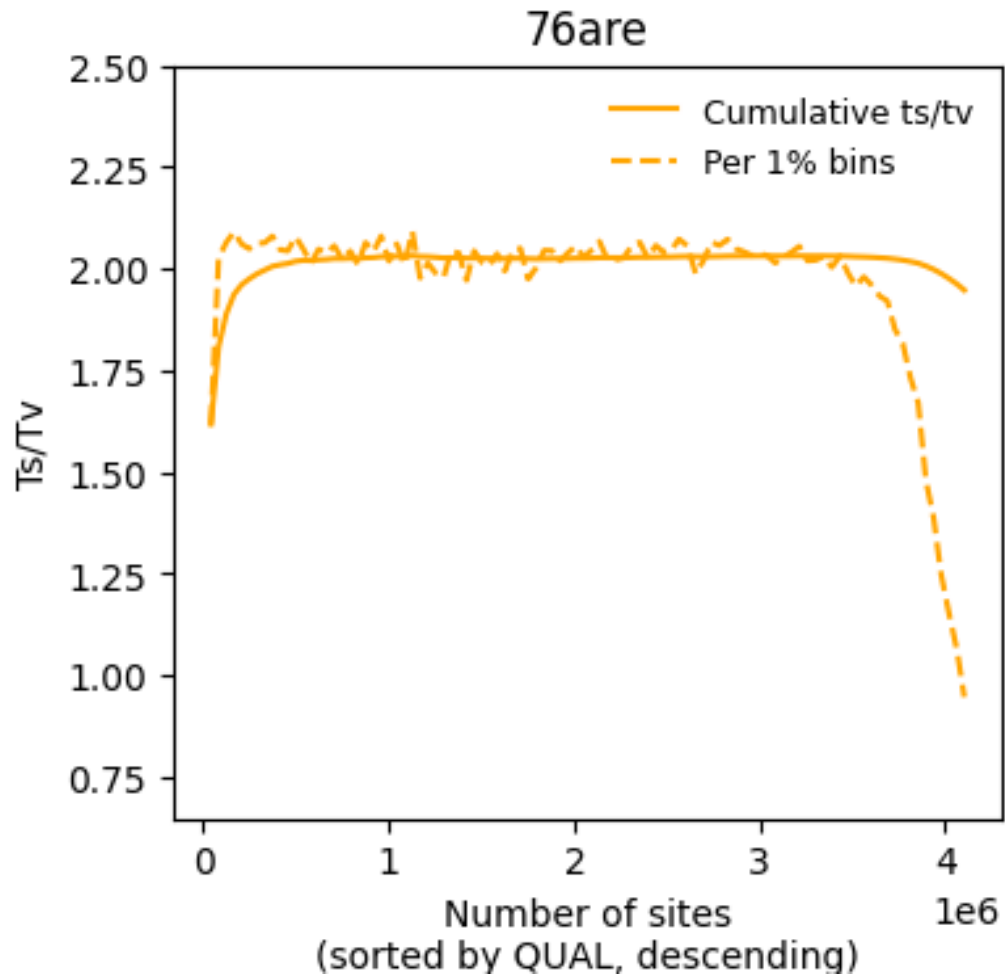
Number of SNPs by sample



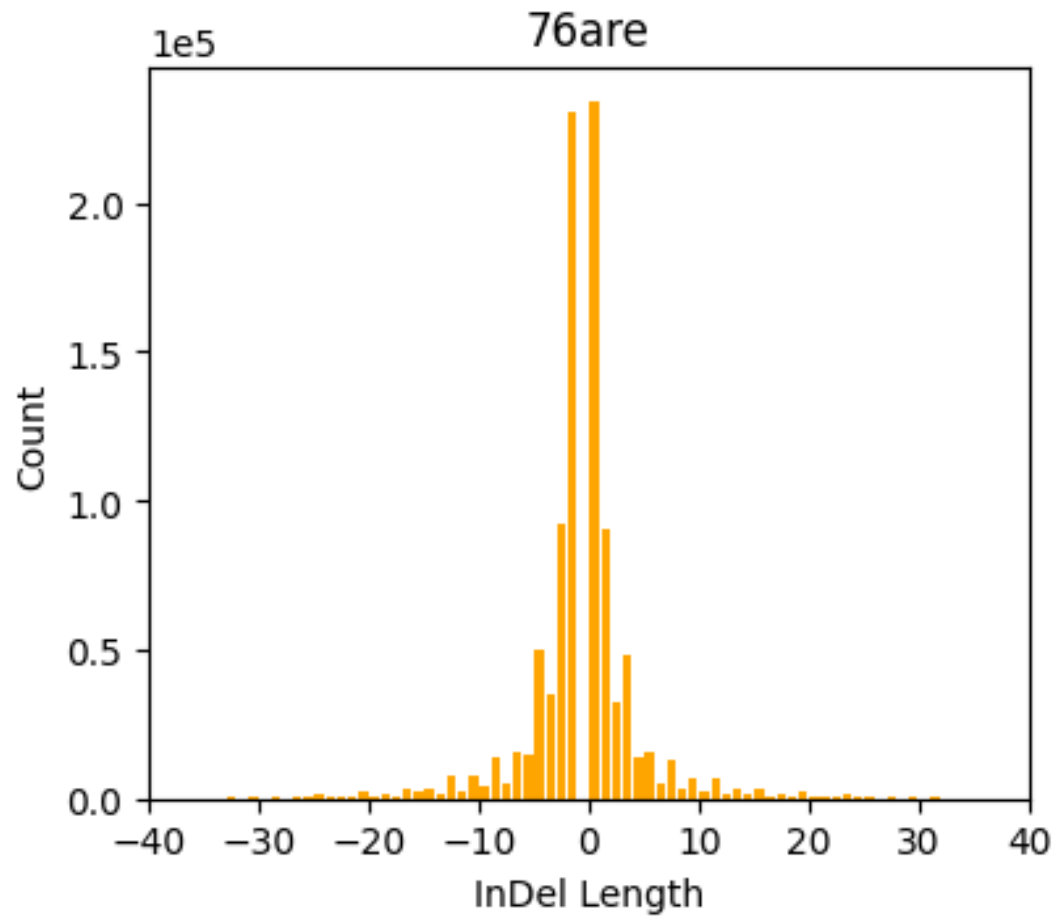
Number of indels by sample



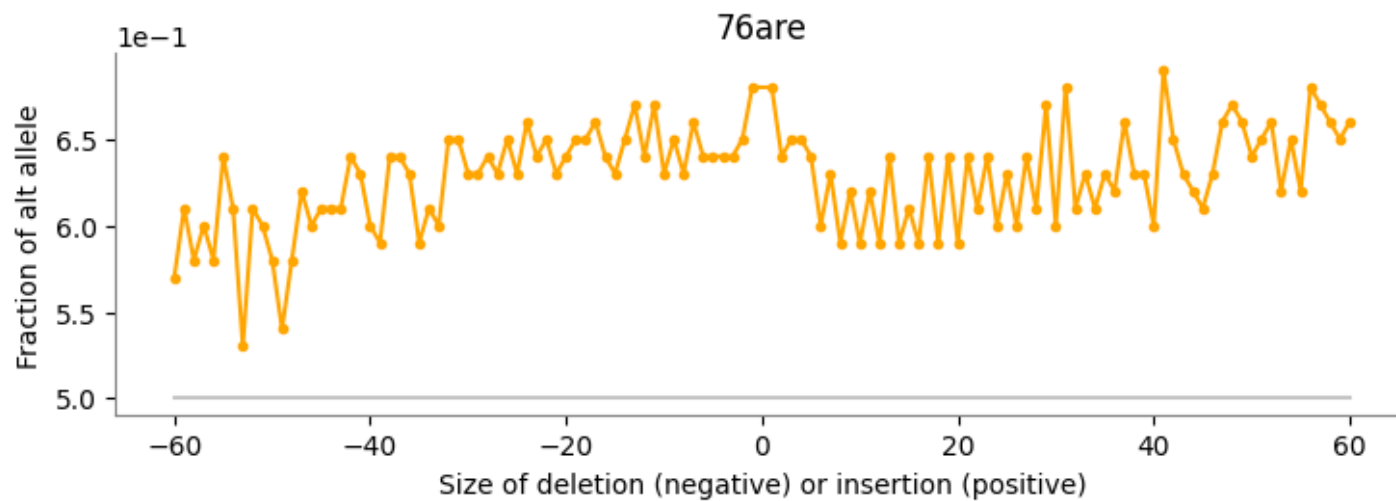
Ts/Tv stratified by QUAL



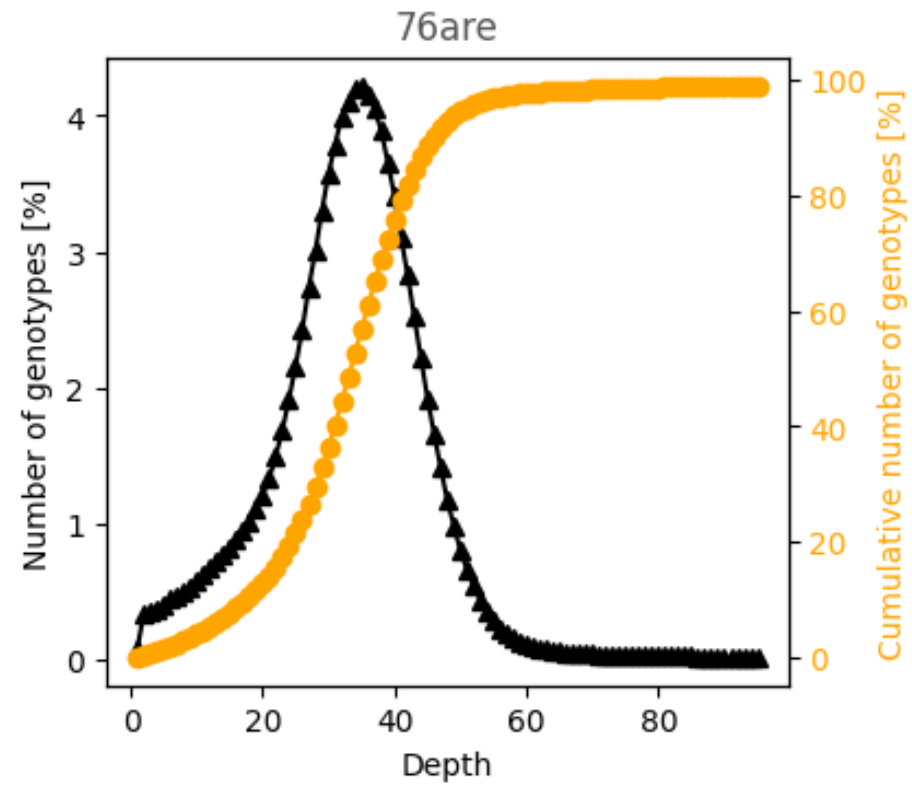
Indel distribution



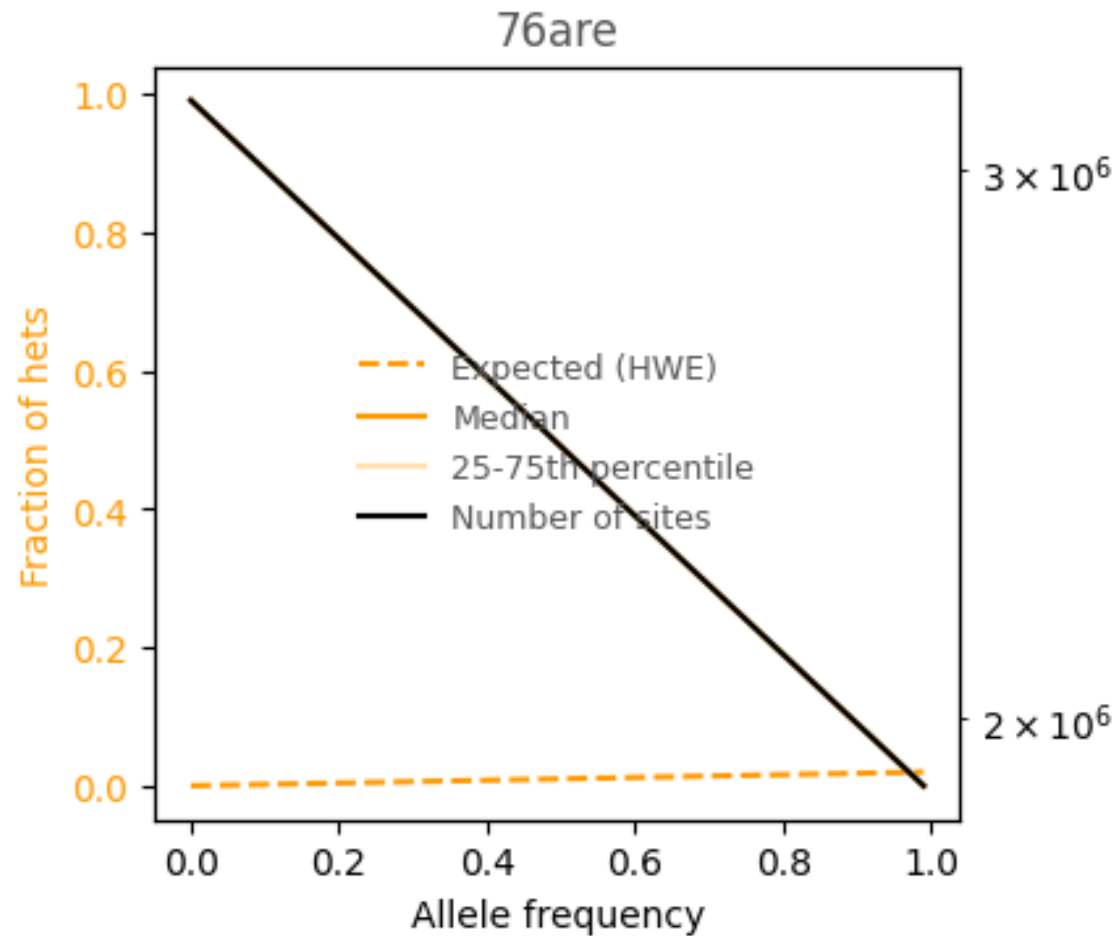
Fraction of alternate indel allele



Depth distribution



Number of HETs by AF



Substitution types

