

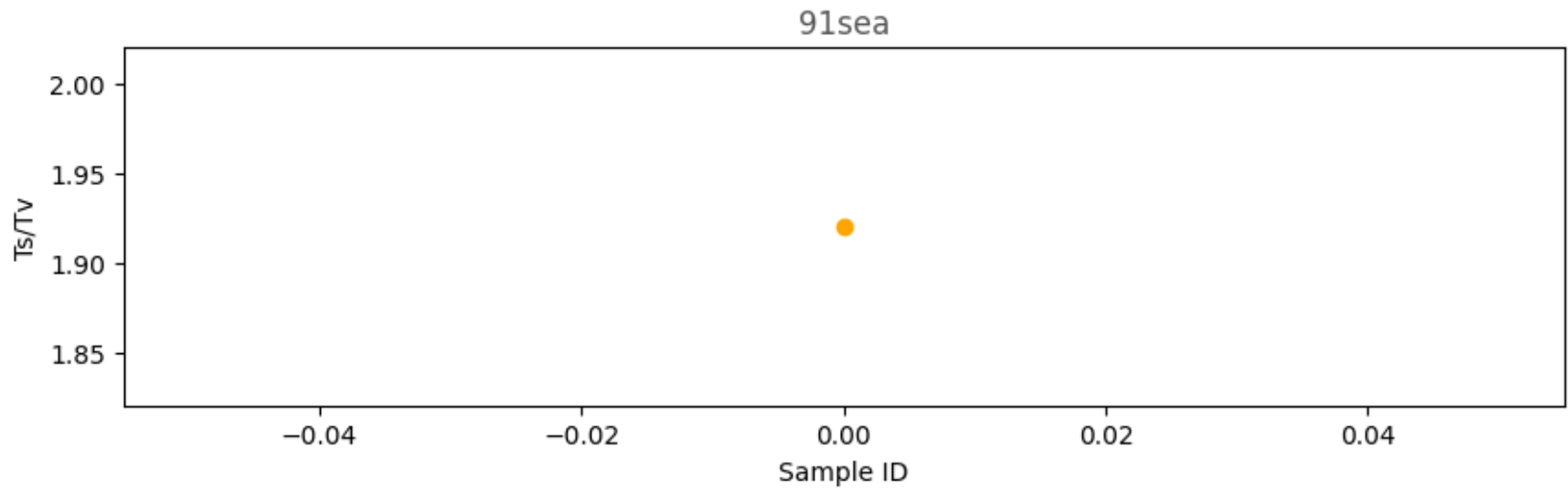
# Summary Numbers

Callset	SNPs			indels		MNPs	others
	n	ts/tv	(1st ALT)	n	frm*		
91sea	4,108,010	1.92	1.93	961,742	–	0	0
* frameshift ratio: out/(out+in)							

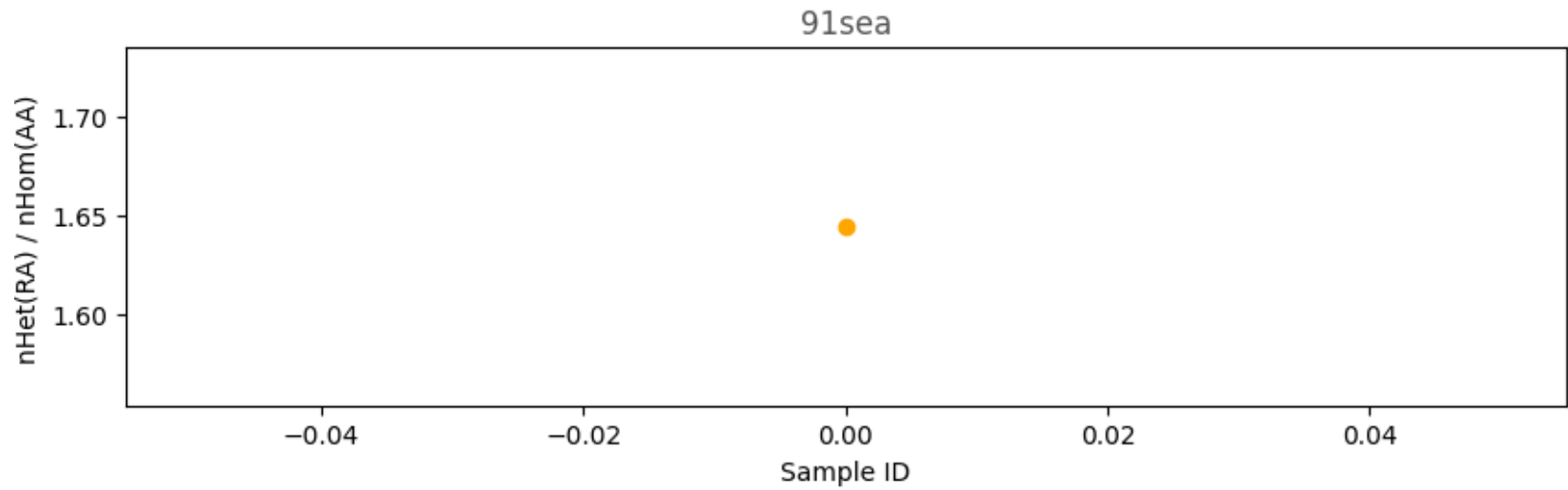
Callset	singletons (AC=1)			multiallelic	
	SNPs	ts/tv	indels	sites	SNPs
91sea	62.2%	1.89	67.5%	104,857	2,122

- 91sea .. /ngc/projects2/gm/data/archive/2022/variants/snv/91seandmm-103830365238-Normal\_B  
 lood\_noinfo-WGS\_v1\_IlluminaDNAPCRFree\_X-220124\_A00559\_AH2CKHDSX3-RHGM\_LABKA\_WGSA  
 KUT-WGSAKUT03709\_22RKG000619x01\_snv\_germline\_raw.haplotype\_caller.vcf.gz

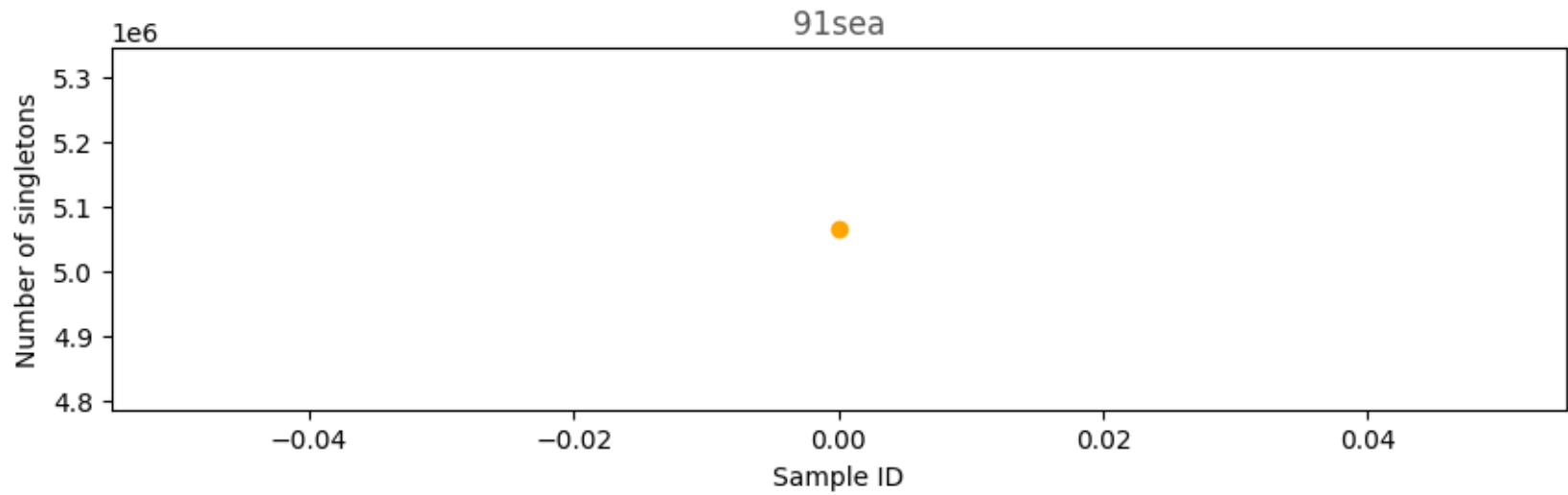
# Ts/Tv by sample



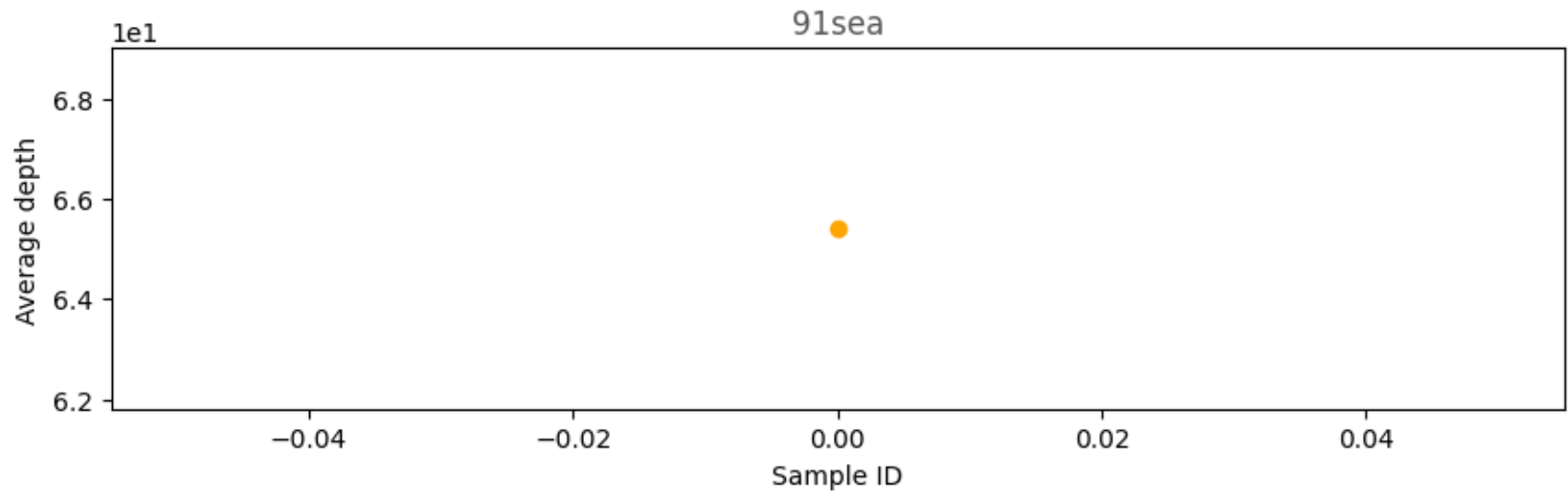
# Hets vs non-ref Homs by sample



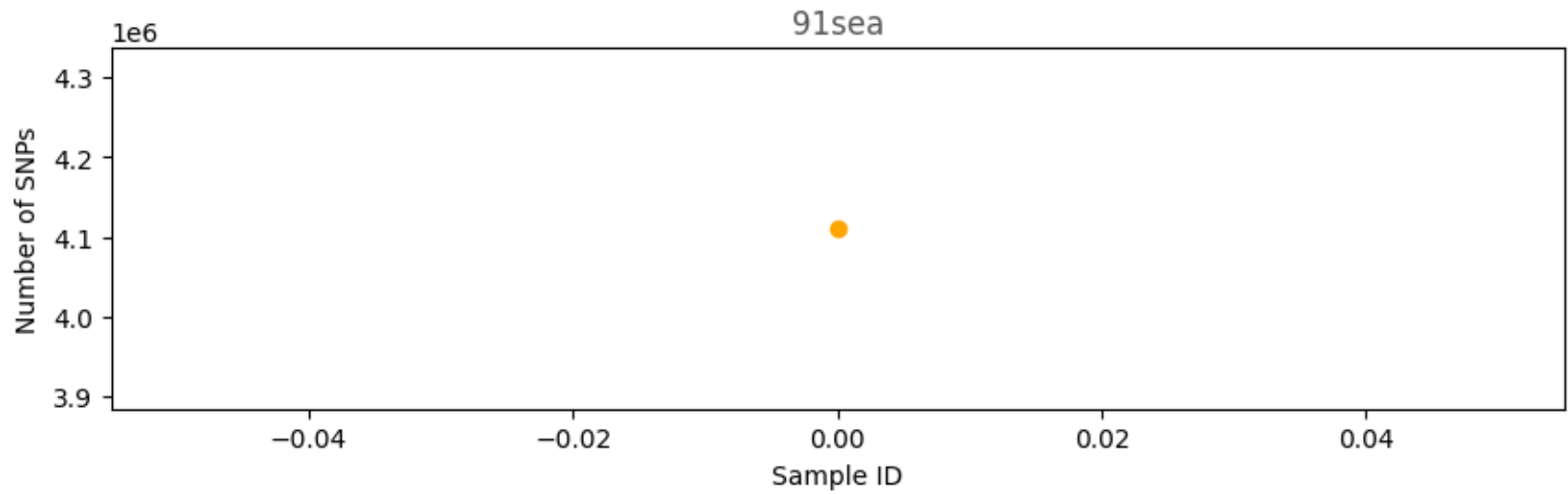
# Singletons by sample (hets and homs)



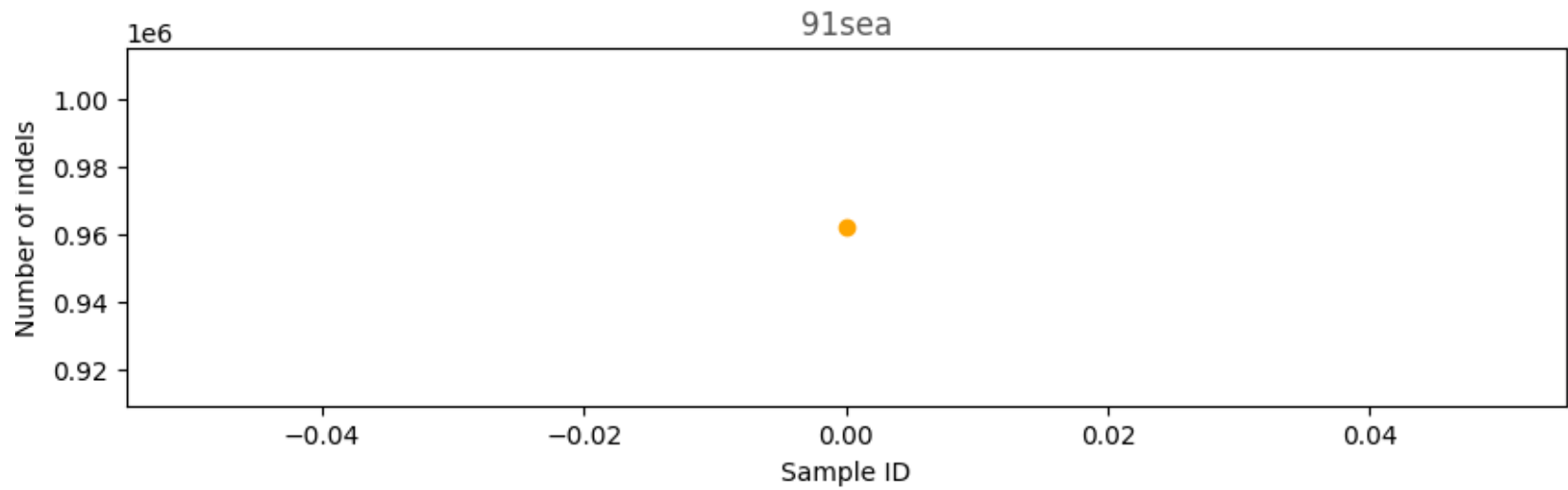
# Average depth by sample



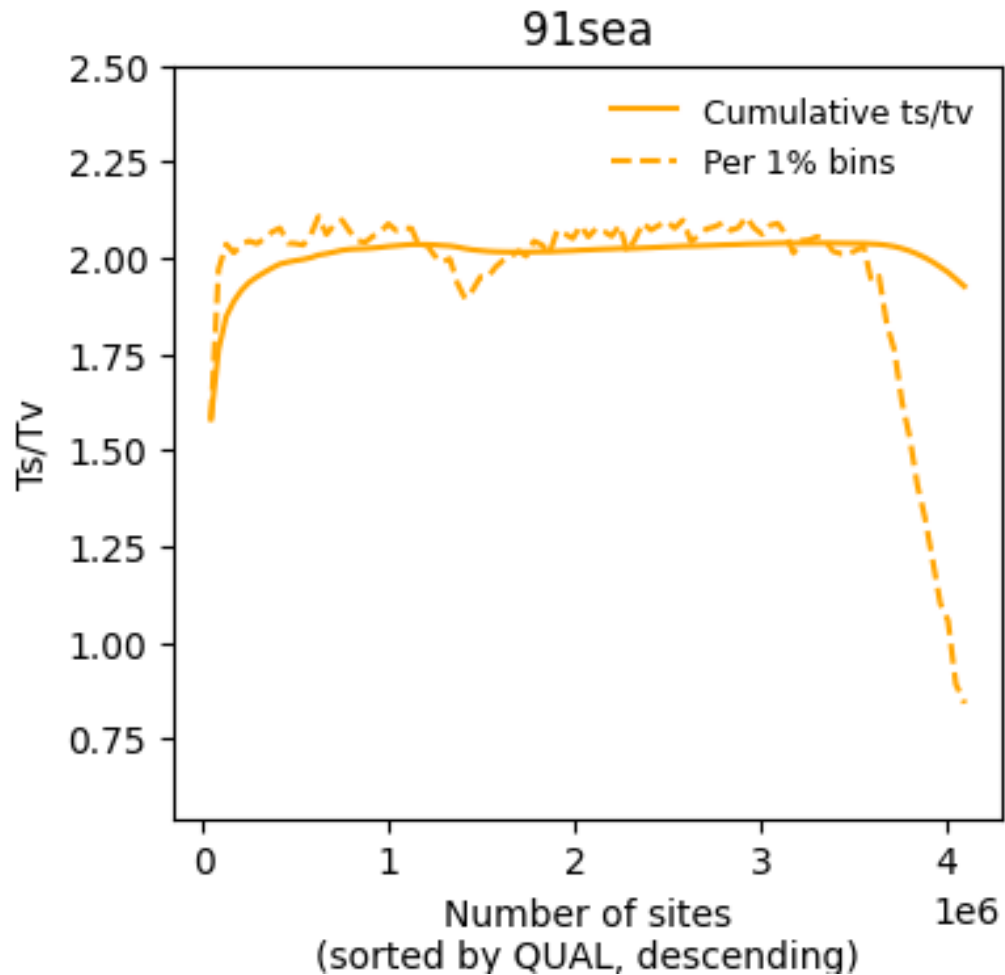
# Number of SNPs by sample



# Number of indels by sample

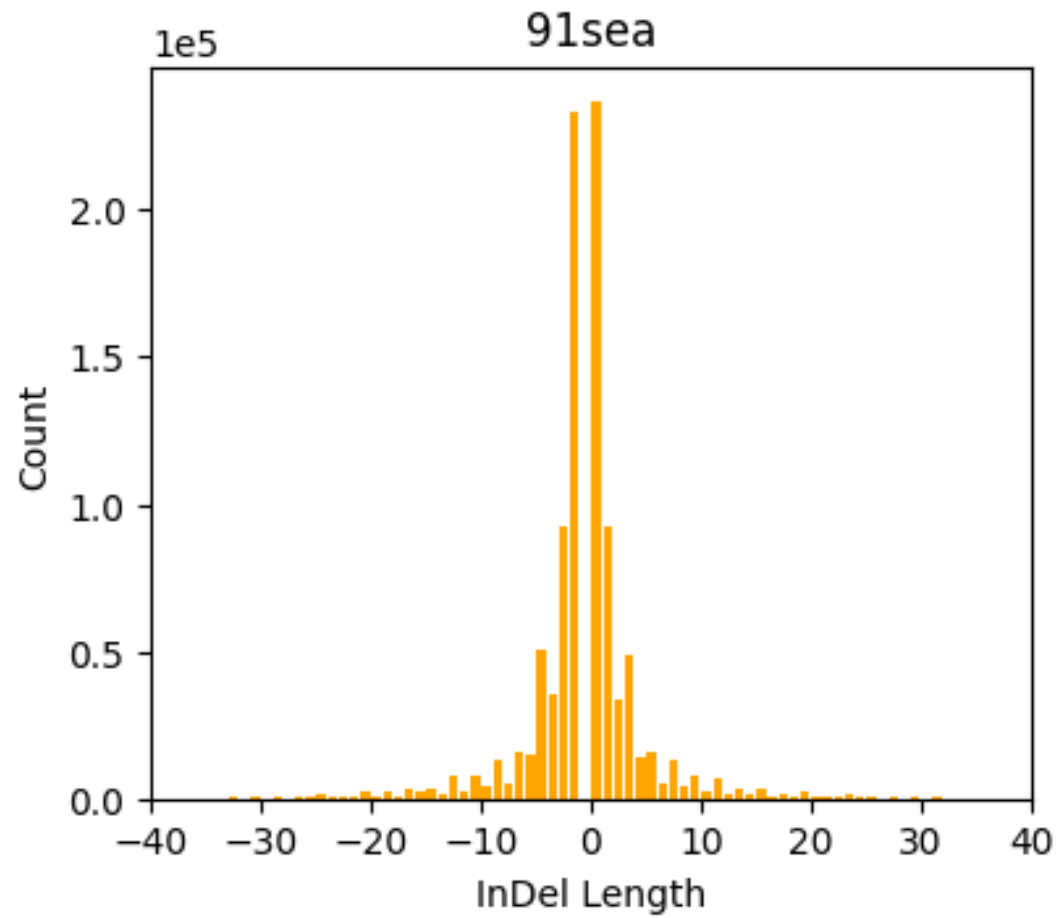


# Ts/Tv stratified by QUAL

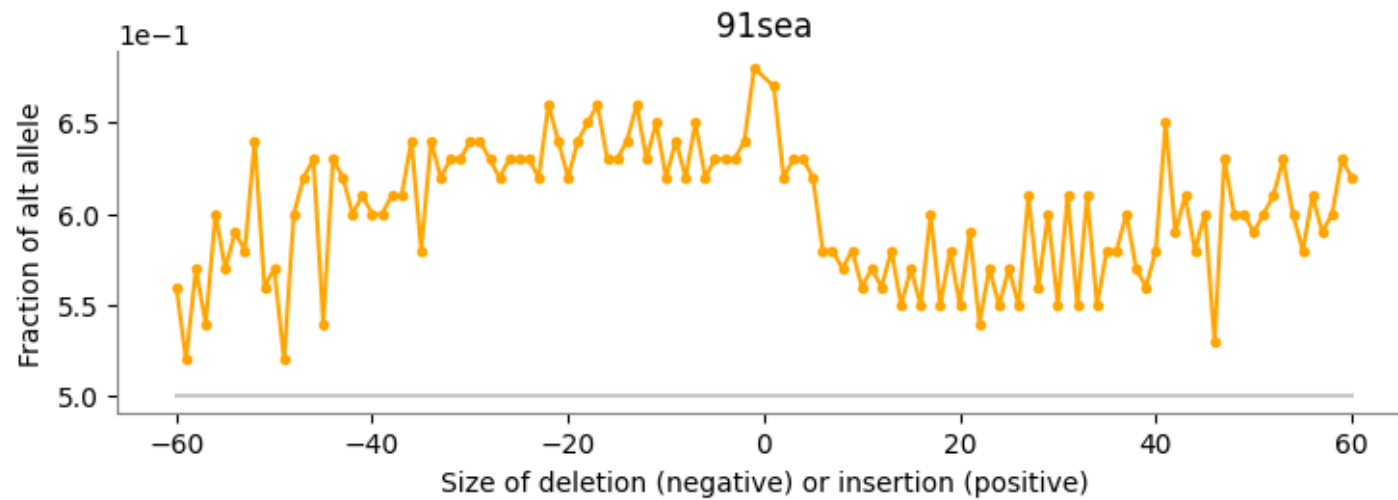




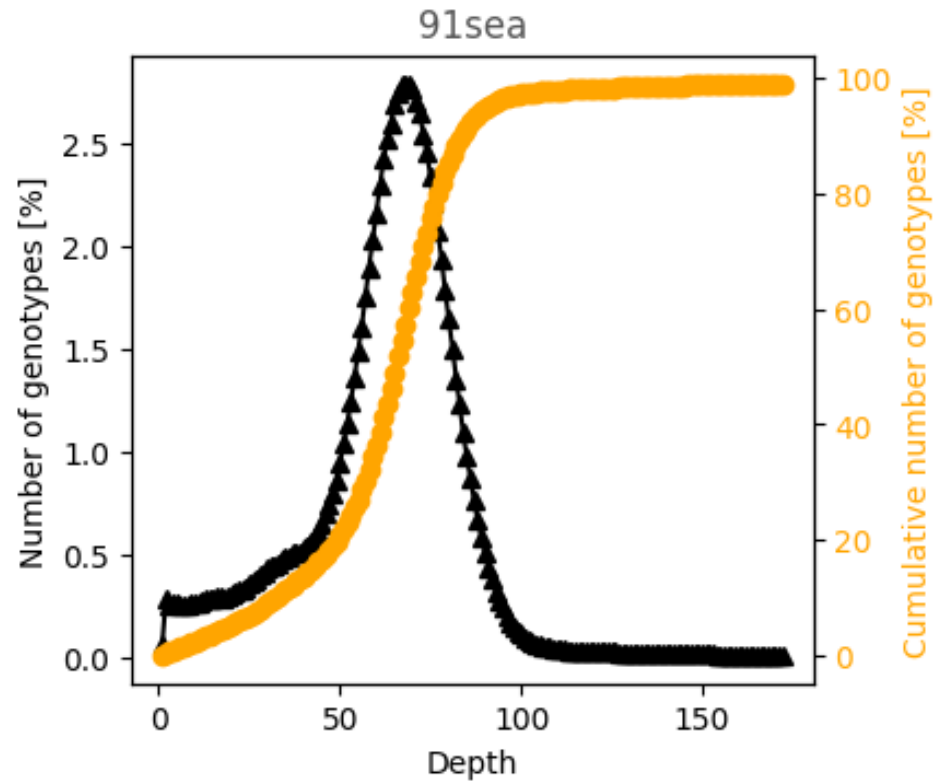
# Indel distribution



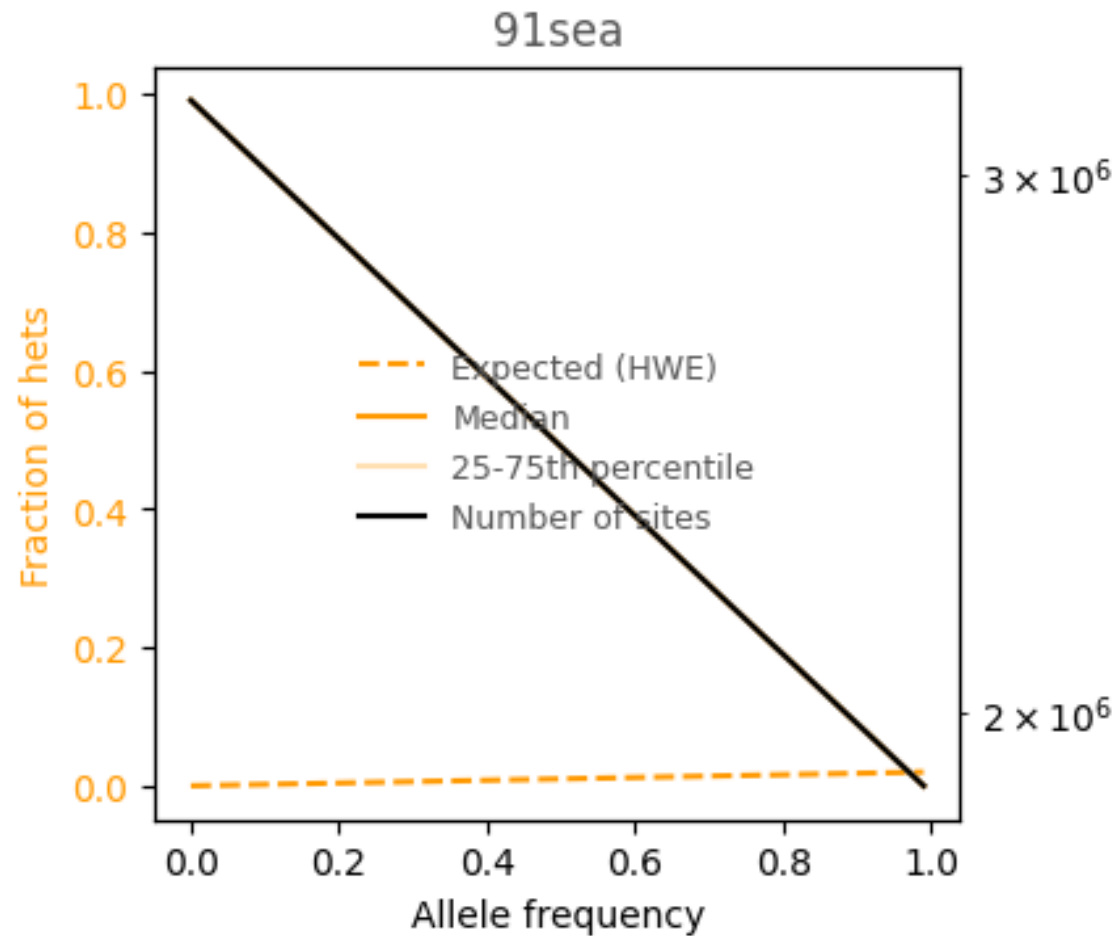
# Fraction of alternate indel allele



# Depth distribution



# Number of HETs by AF



# Substitution types

