

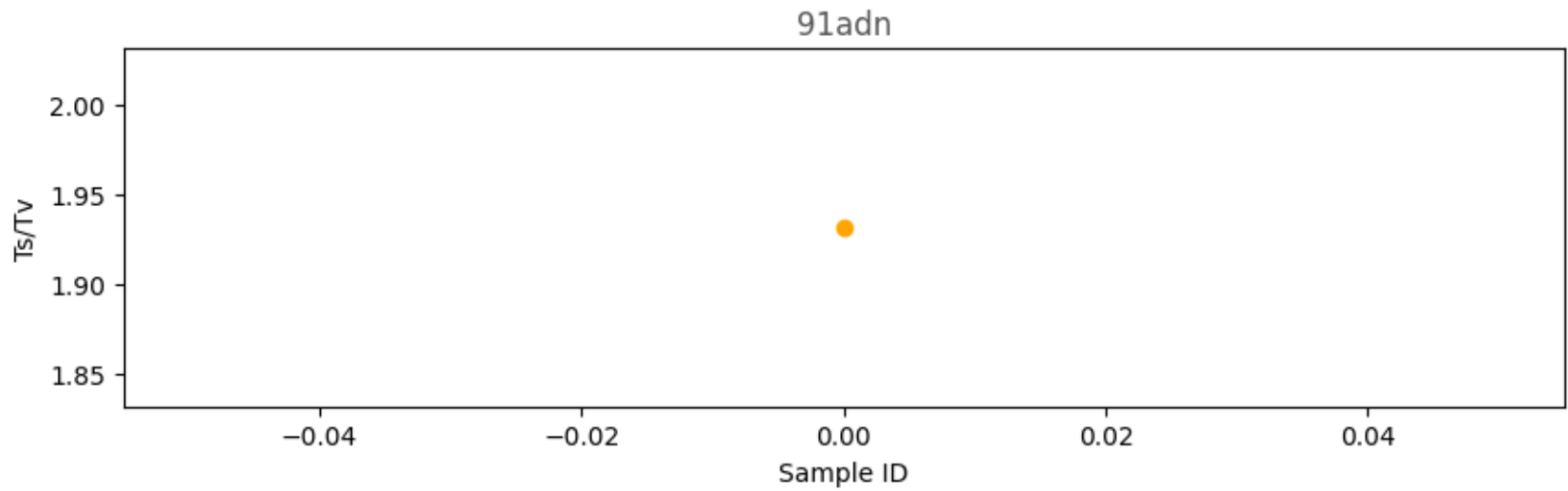
# Summary Numbers

Callset	SNPs			indels		MNPs	others
	n	ts/tv	(1st ALT)	n	frm*		
91adn	4,057,384	1.93	1.94	938,197	–	0	0
* frameshift ratio: out/(out+in)							

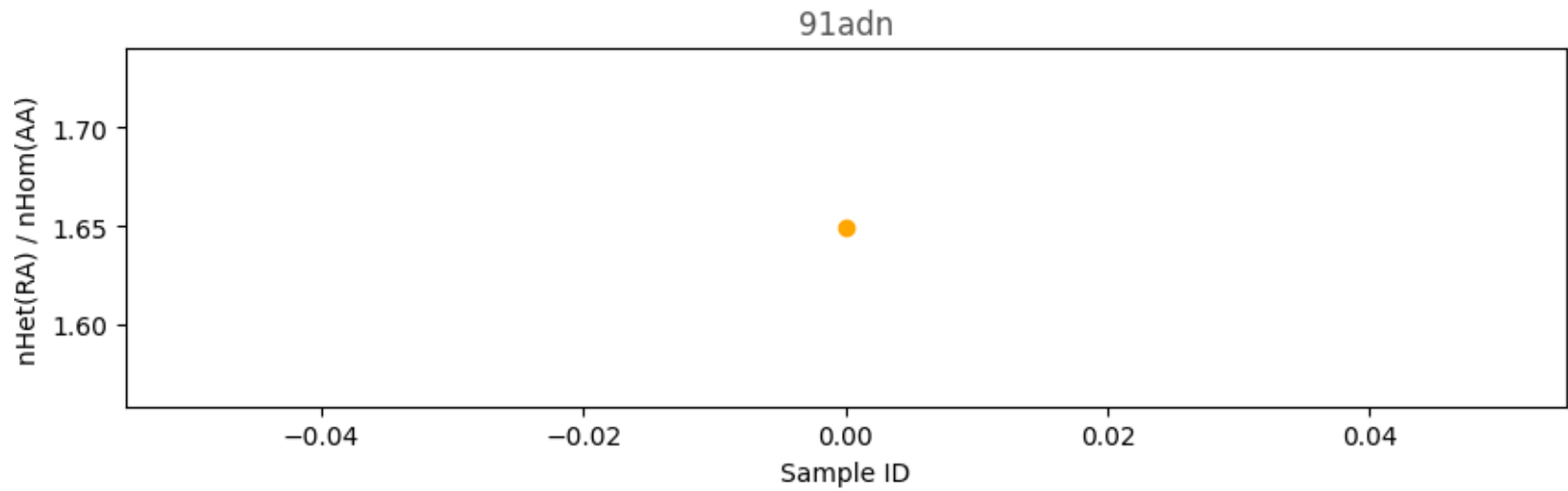
Callset	singletons (AC=1)			multiallelic	
	SNPs	ts/tv	indels	sites	SNPs
91adn	62.3%	1.90	66.4%	93,519	1,953

- 91adn .. /ngc/projects2/gm/data/archive/2022/variants/snv/91adntthm-103853915323-Normal\_B  
 lood\_noinfo-WGS\_v1\_IlluminaDNAPCRFree\_X-220330\_A00559\_BHCF7CDSX3-RHGM\_LABKA\_WGSA  
 KUT-WGSAKUT04037\_22RKG007098x01\_snv\_germline\_raw.haplotype\_caller.vcf.gz

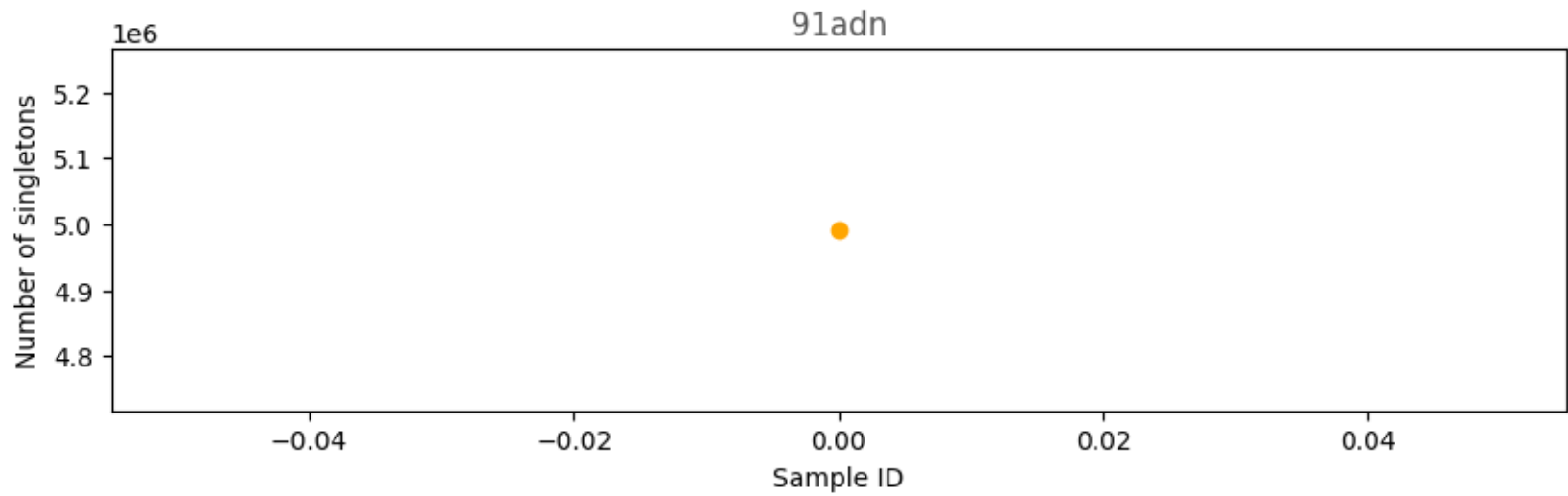
# Ts/Tv by sample



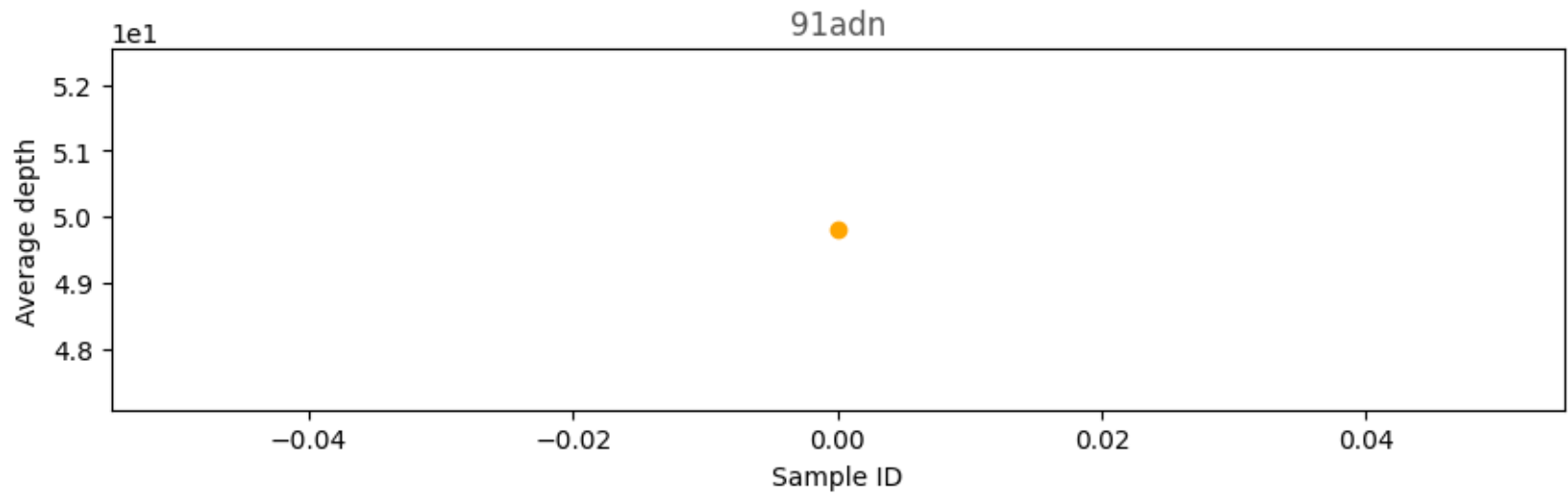
# Hets vs non-ref Homs by sample



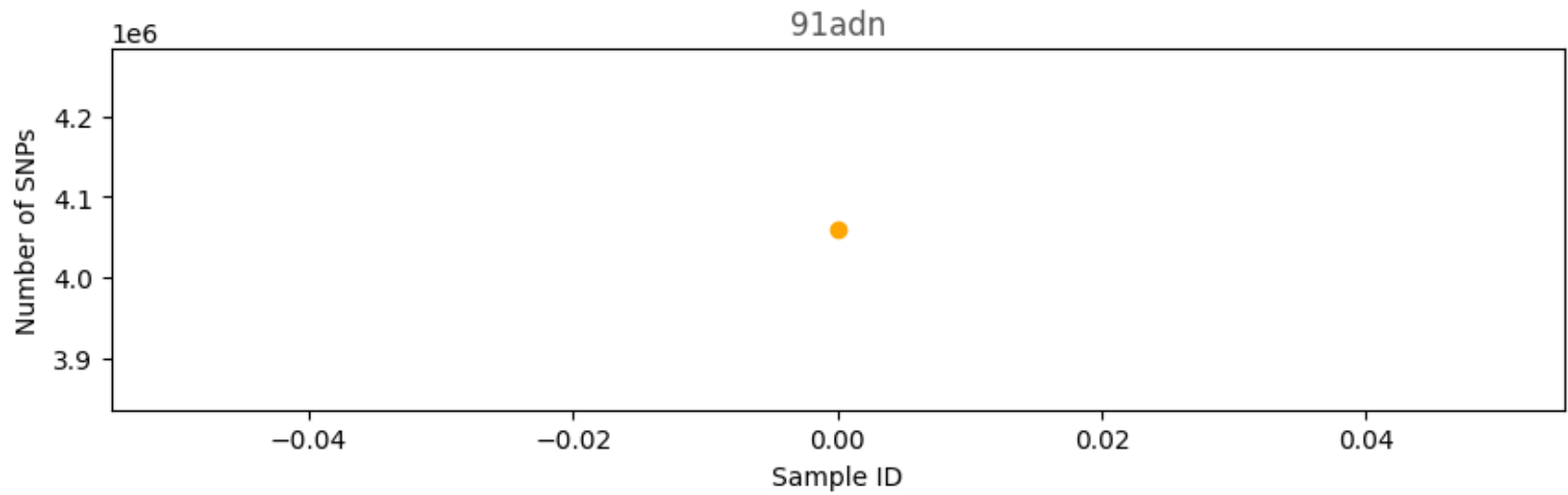
# Singletons by sample (hets and homs)



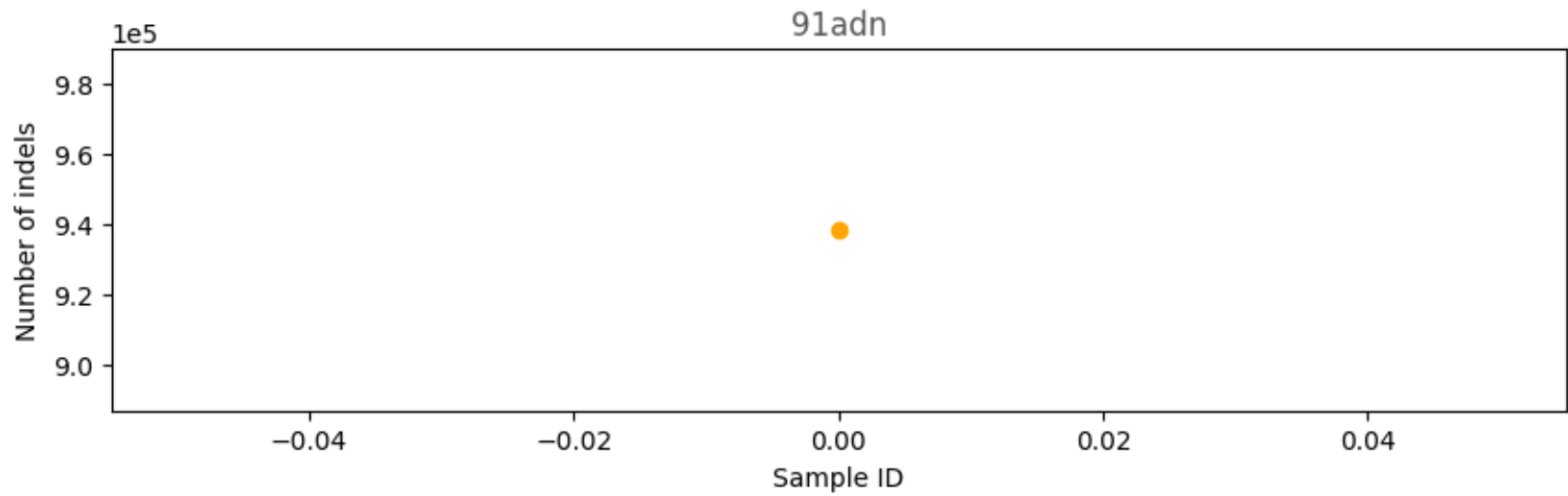
# Average depth by sample



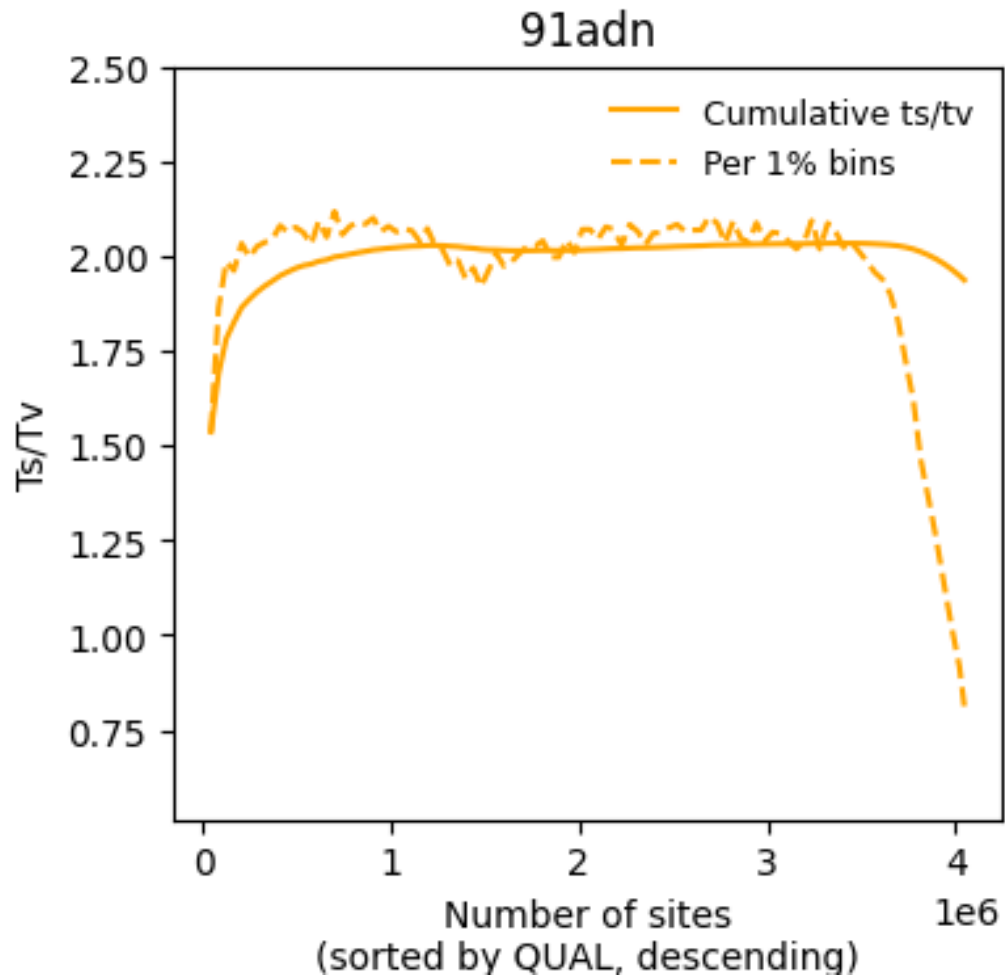
# Number of SNPs by sample



# Number of indels by sample

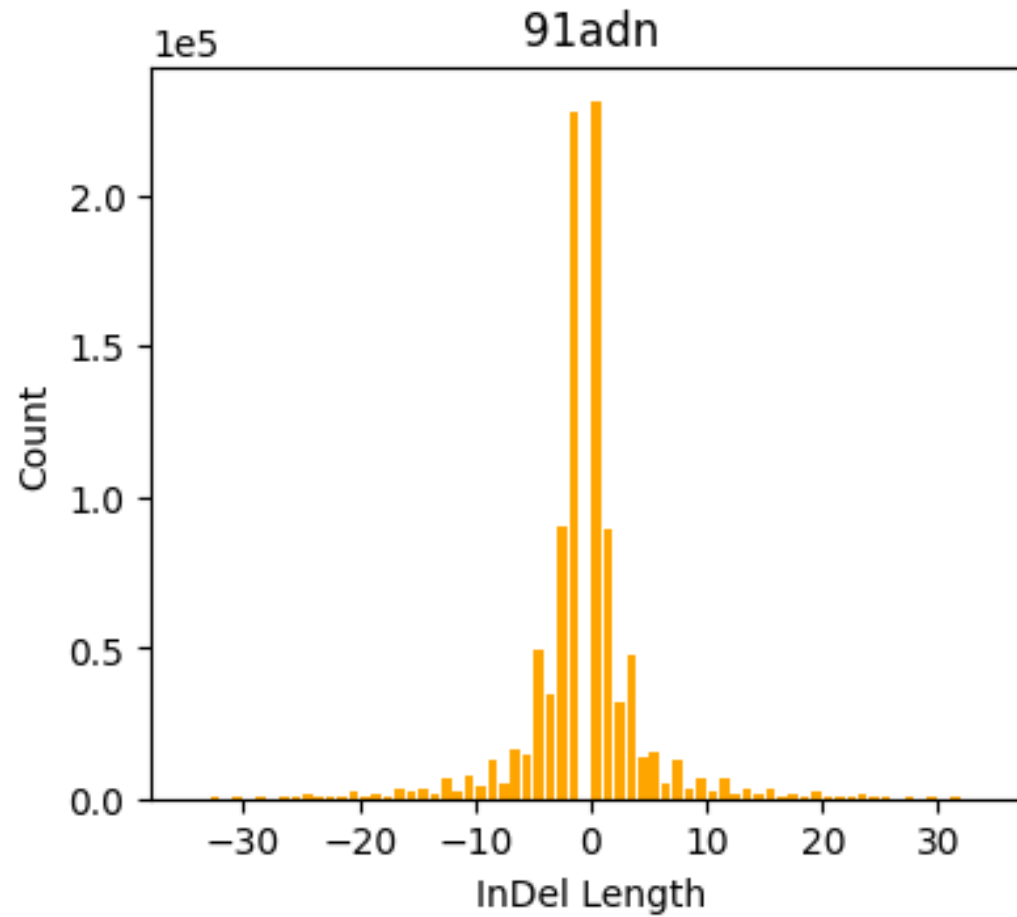


# Ts/Tv stratified by QUAL

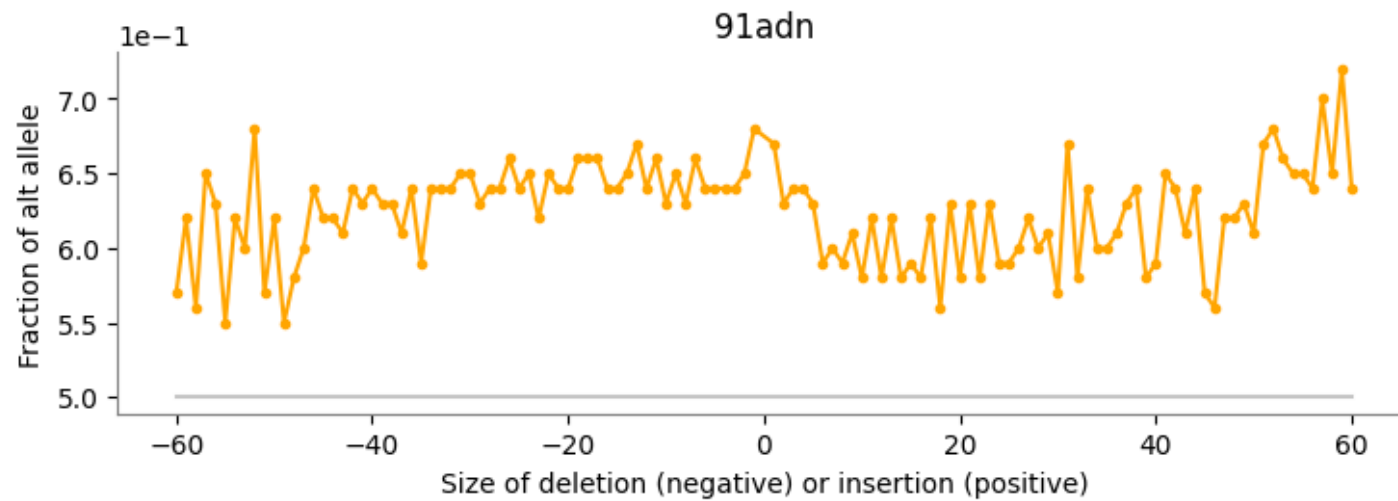




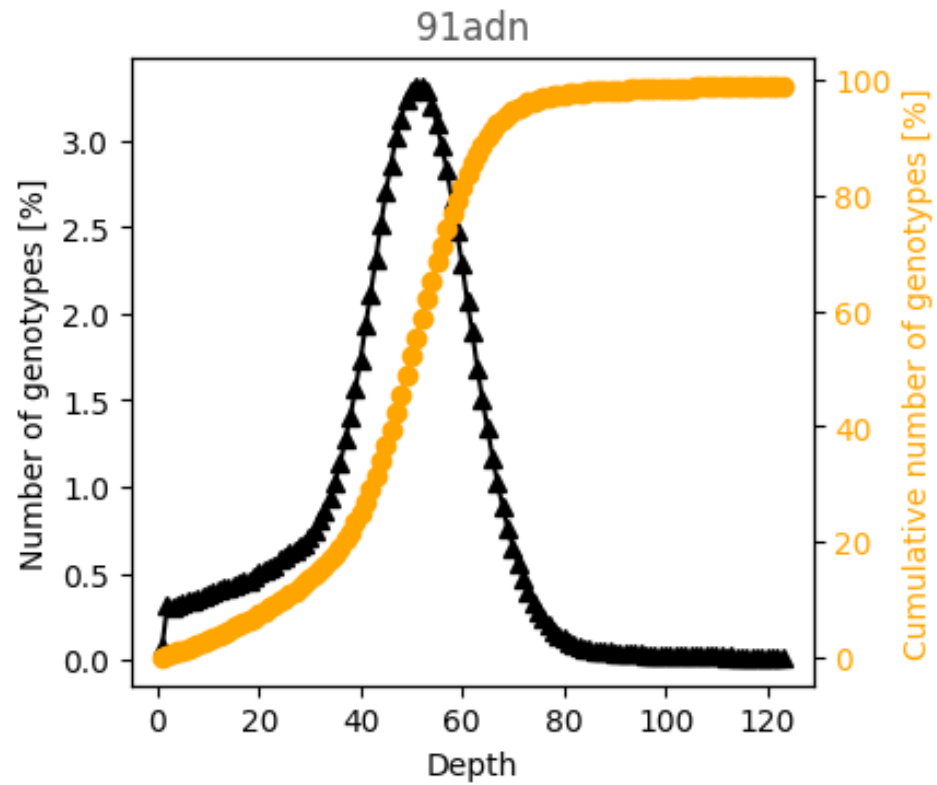
# Indel distribution



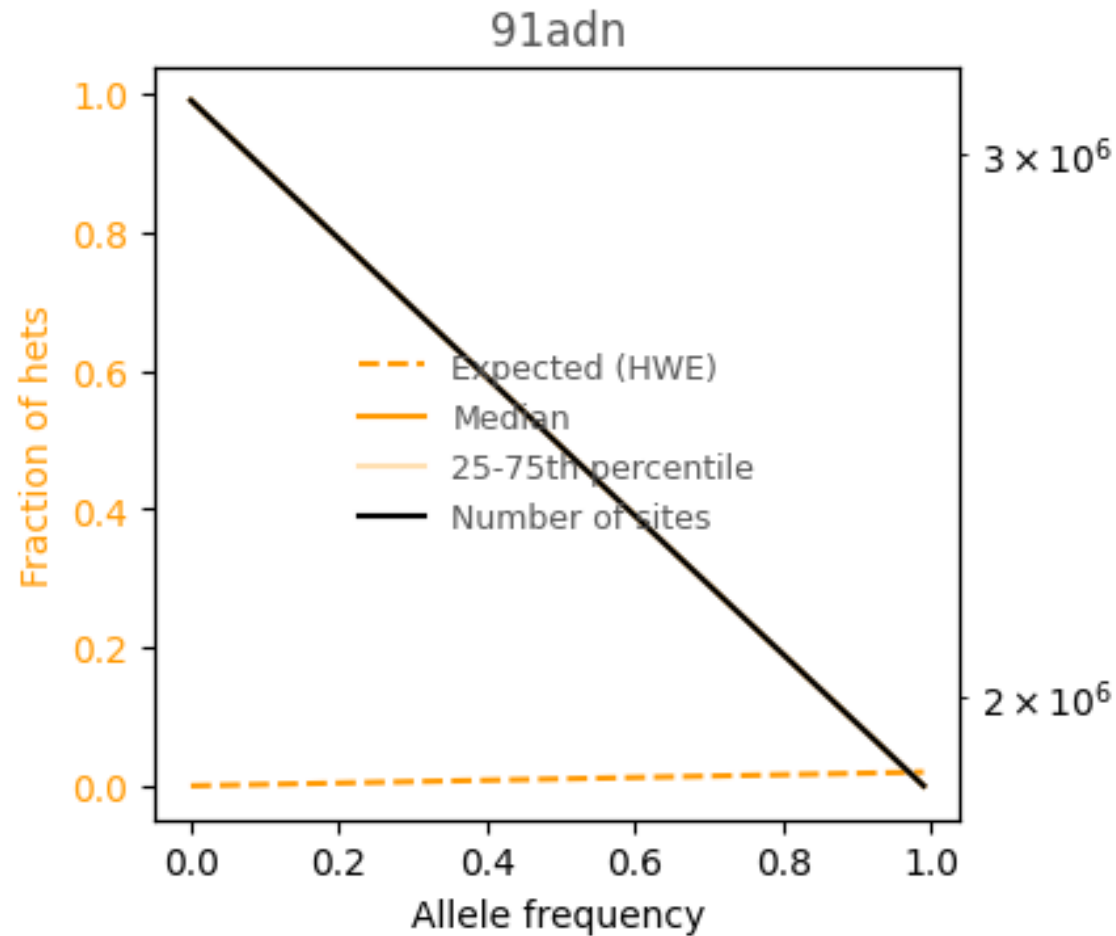
# Fraction of alternate indel allele



# Depth distribution



# Number of HETs by AF



# Substitution types

