

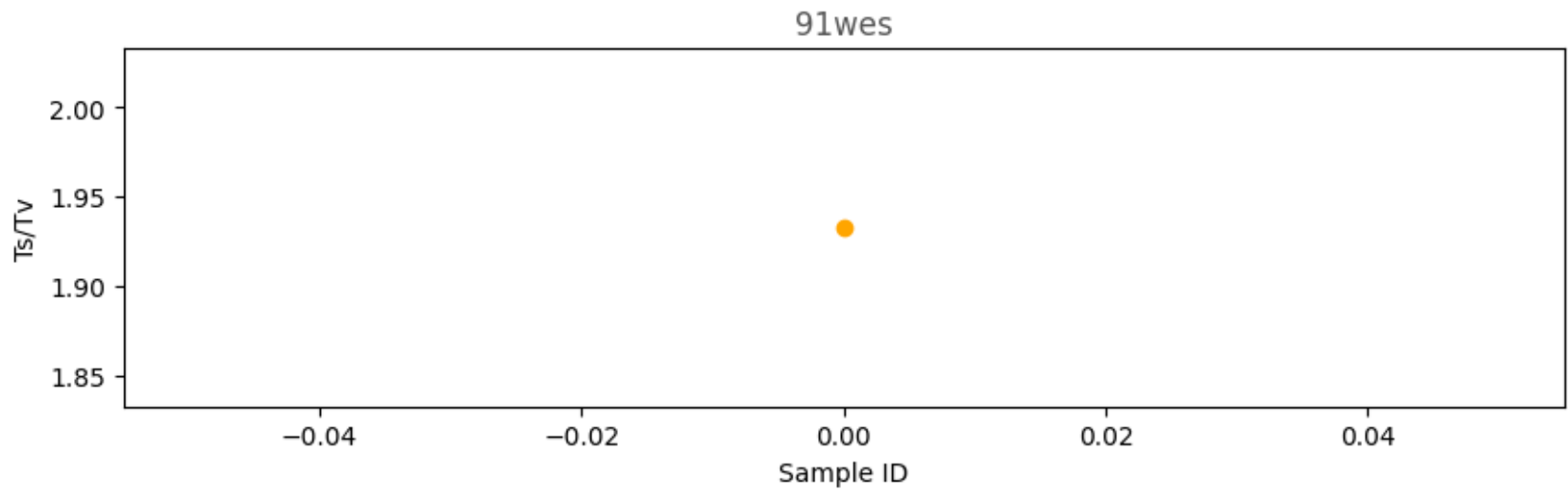
# Summary Numbers

Callset	SNPs			indels		MNPs	others
	n	ts/tv	(1st ALT)	n	frm*		
91wes	4,042,597	1.93	1.94	941,782	–	0	0
* frameshift ratio: out/(out+in)							

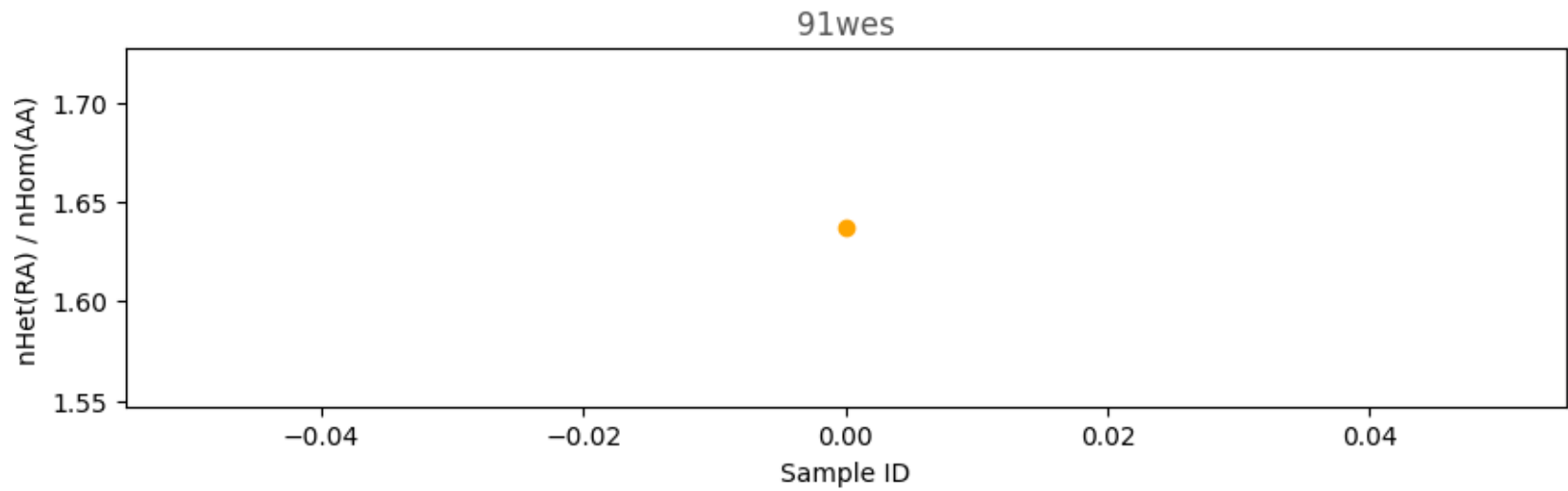
Callset	singletons (AC=1)			multiallelic	
	SNPs	ts/tv	indels	sites	SNPs
91wes	62.1%	1.90	66.6%	97,699	1,815

- 91wes .. /ngc/projects2/gm/data/archive/2022/variants/snv/91wesechm-110297146932-Normal\_Blood\_noinfo-WGS\_v1\_IlluminaDNAPCRFree\_X-221014\_A00559\_BH3FK3DSX5-RHGM\_LABKA\_WGSA\_KUT-WGSAKUT05837\_22RKG024485x01\_snv\_germline\_raw.haplotype\_caller.vcf.gz

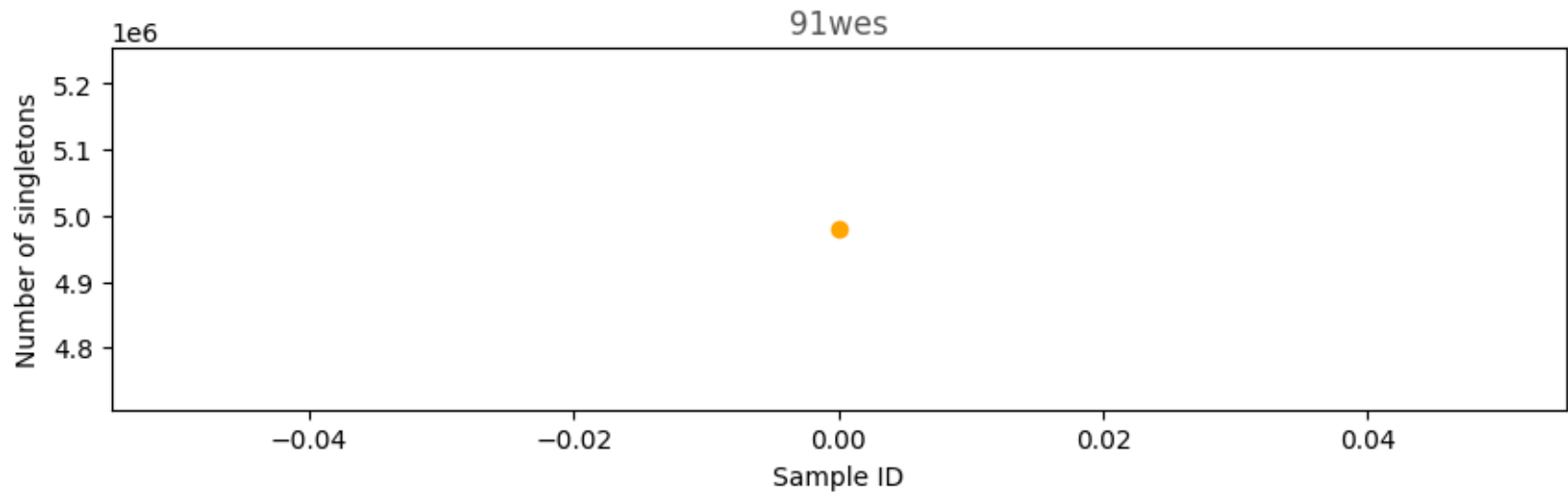
# Ts/Tv by sample



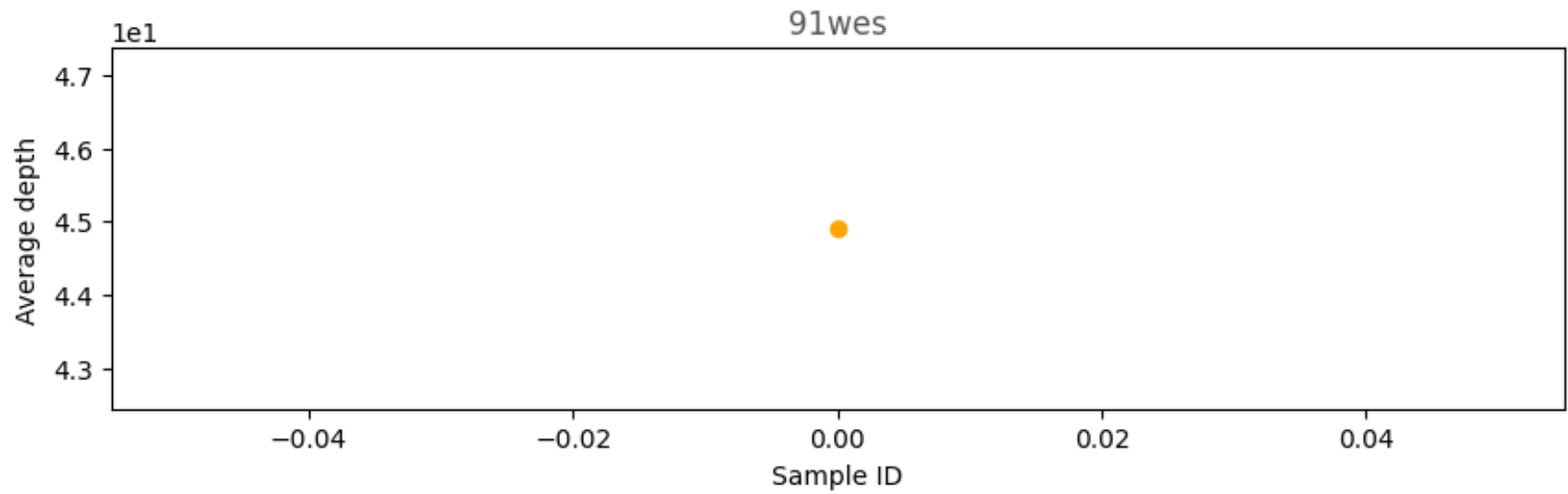
# Hets vs non-ref Homs by sample



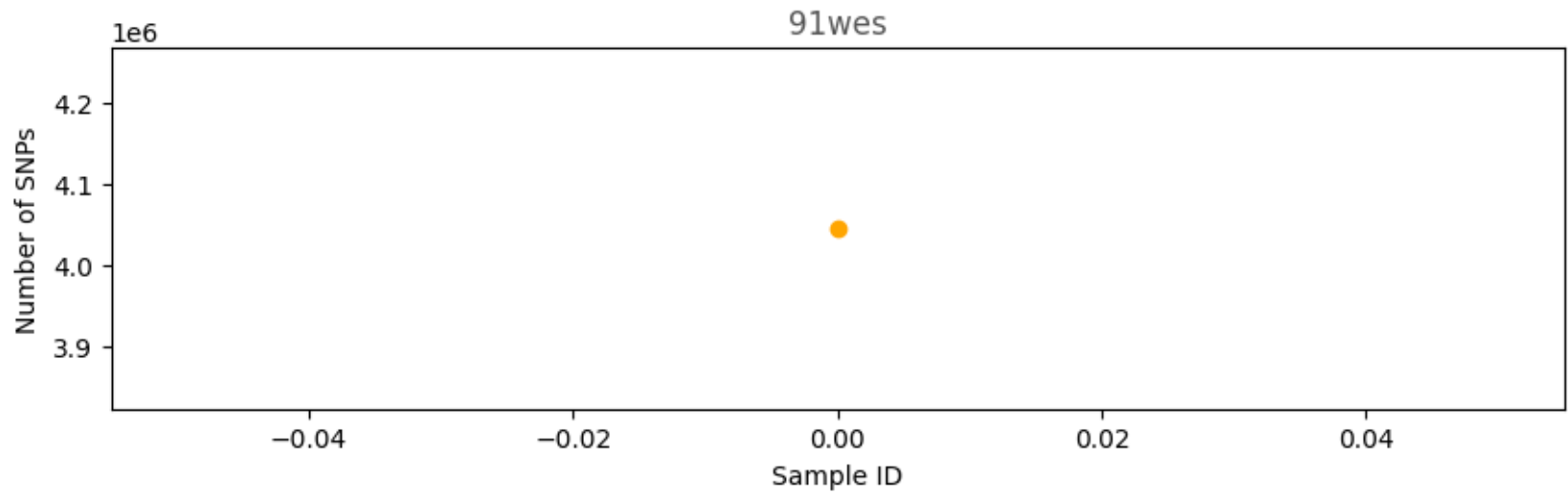
# Singletons by sample (hets and homs)



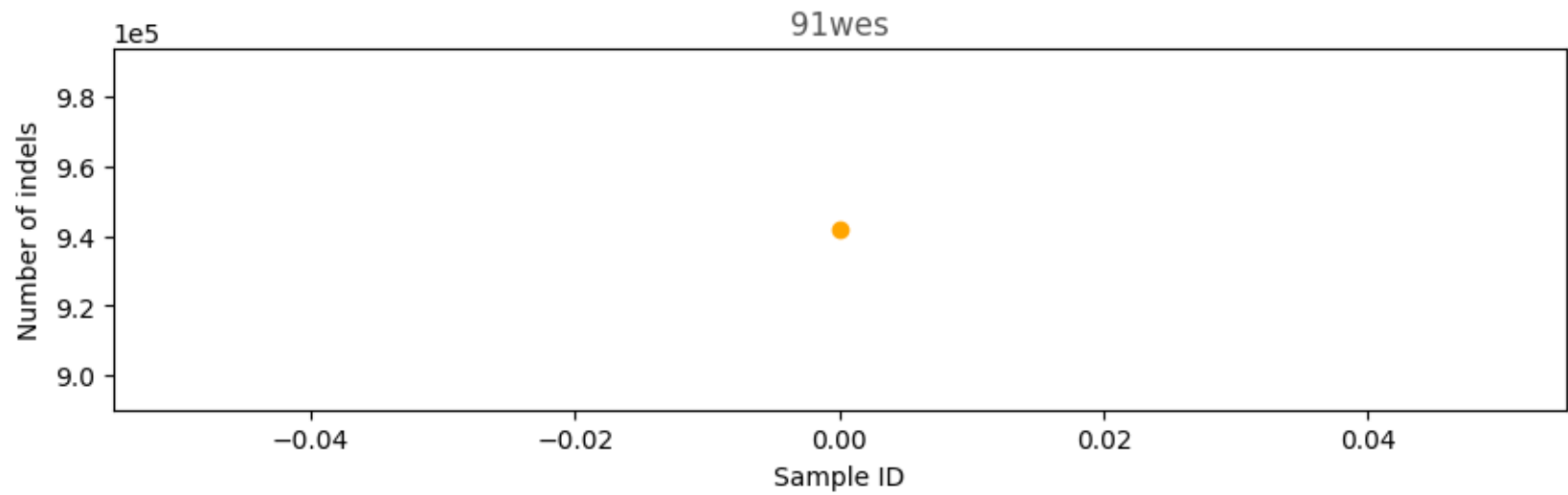
# Average depth by sample



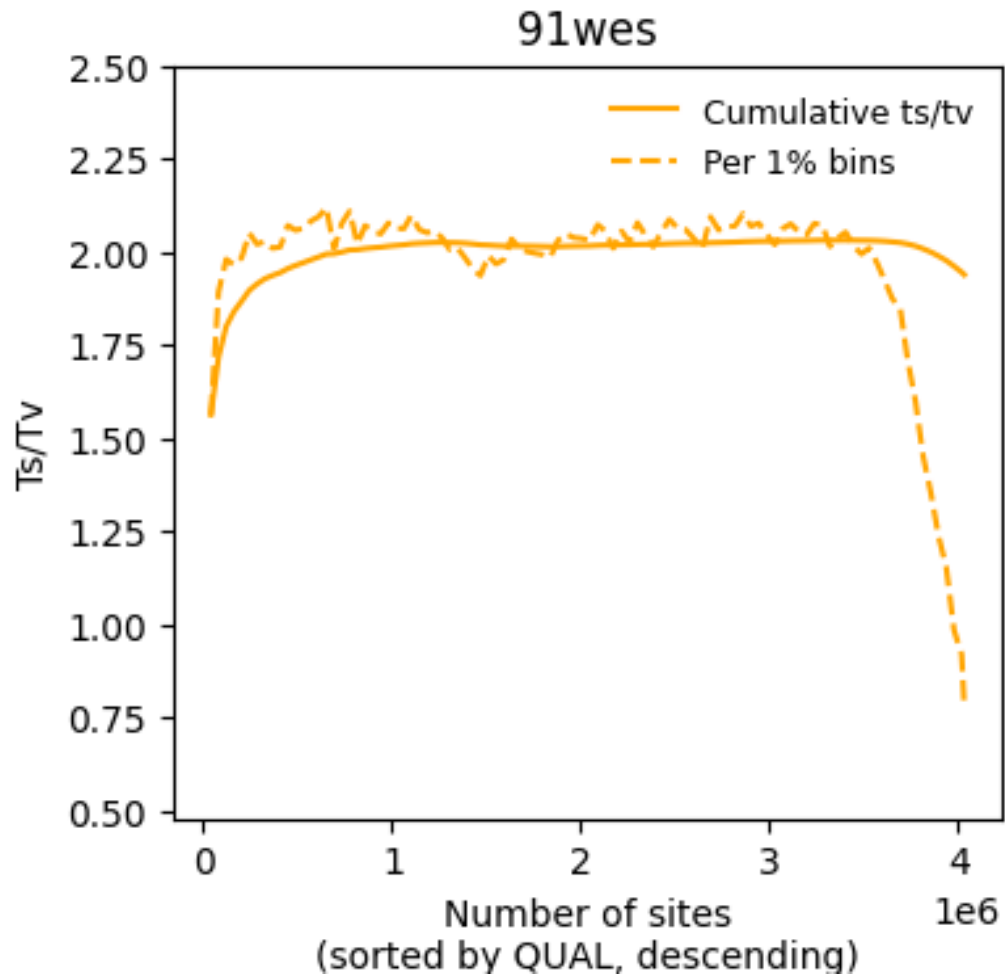
# Number of SNPs by sample



# Number of indels by sample

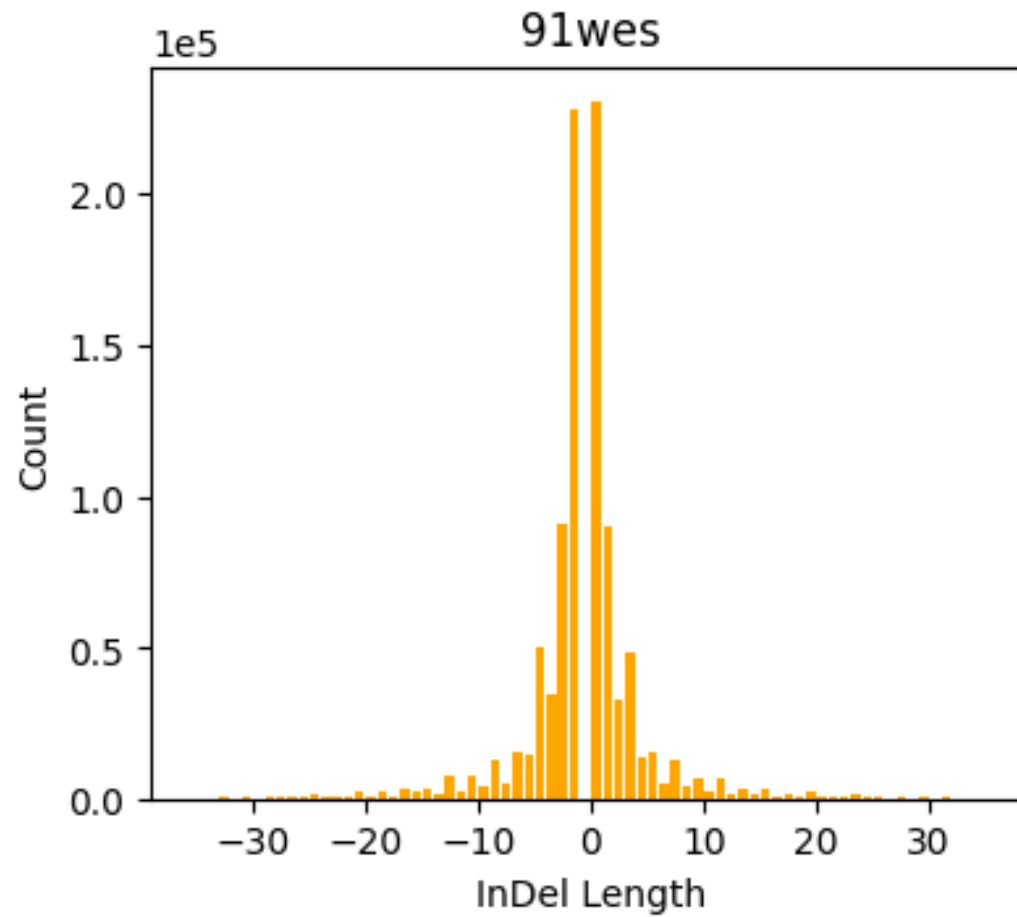


# Ts/Tv stratified by QUAL

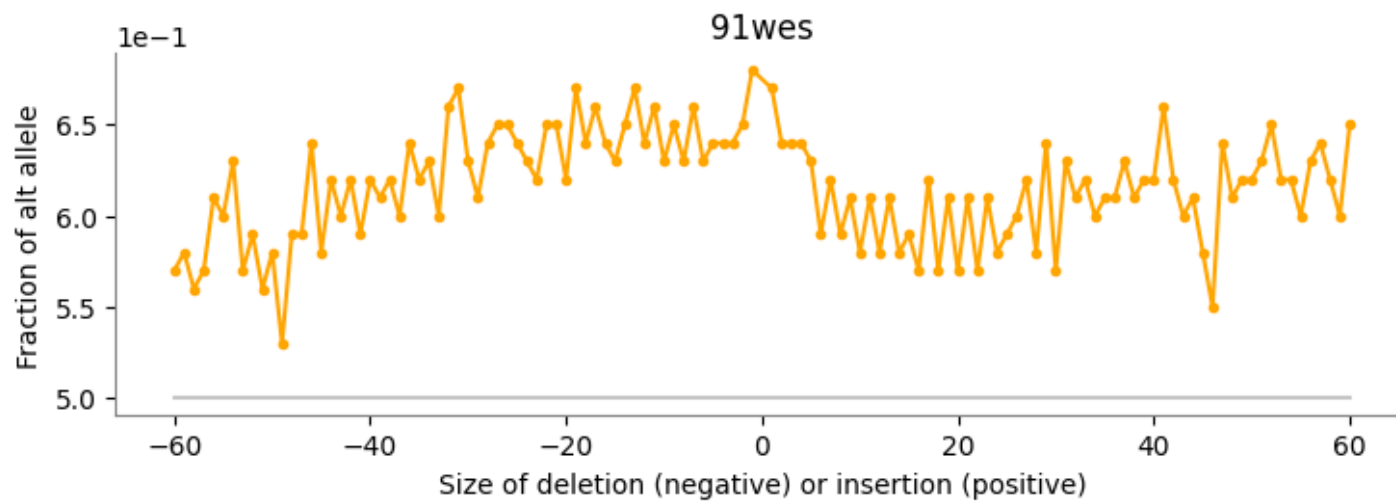




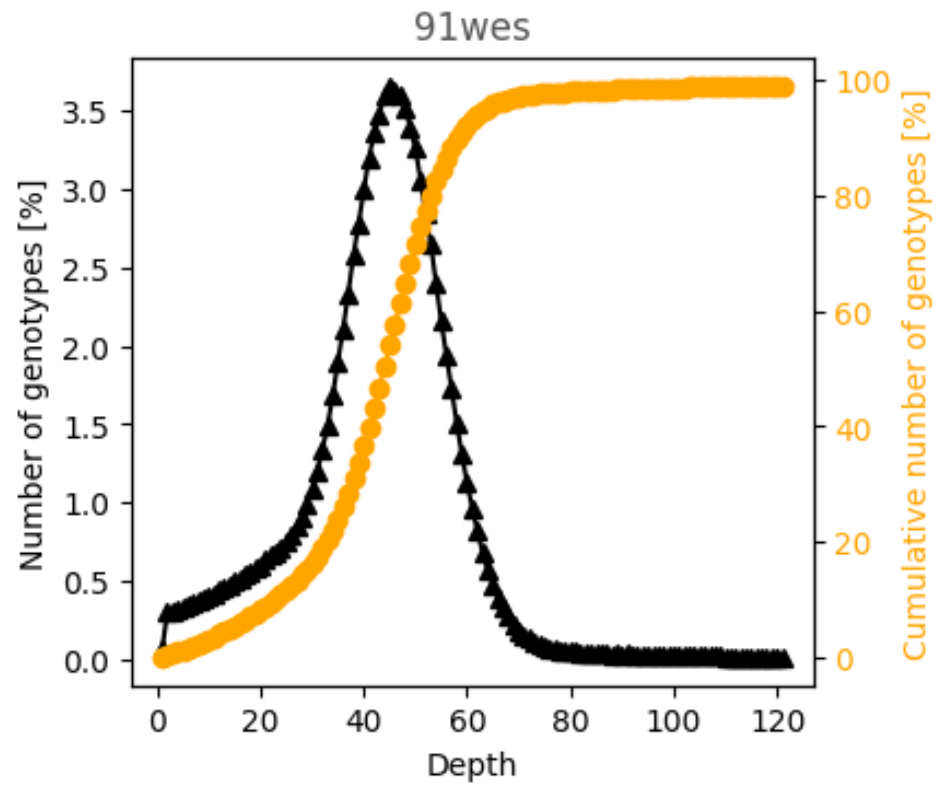
# Indel distribution



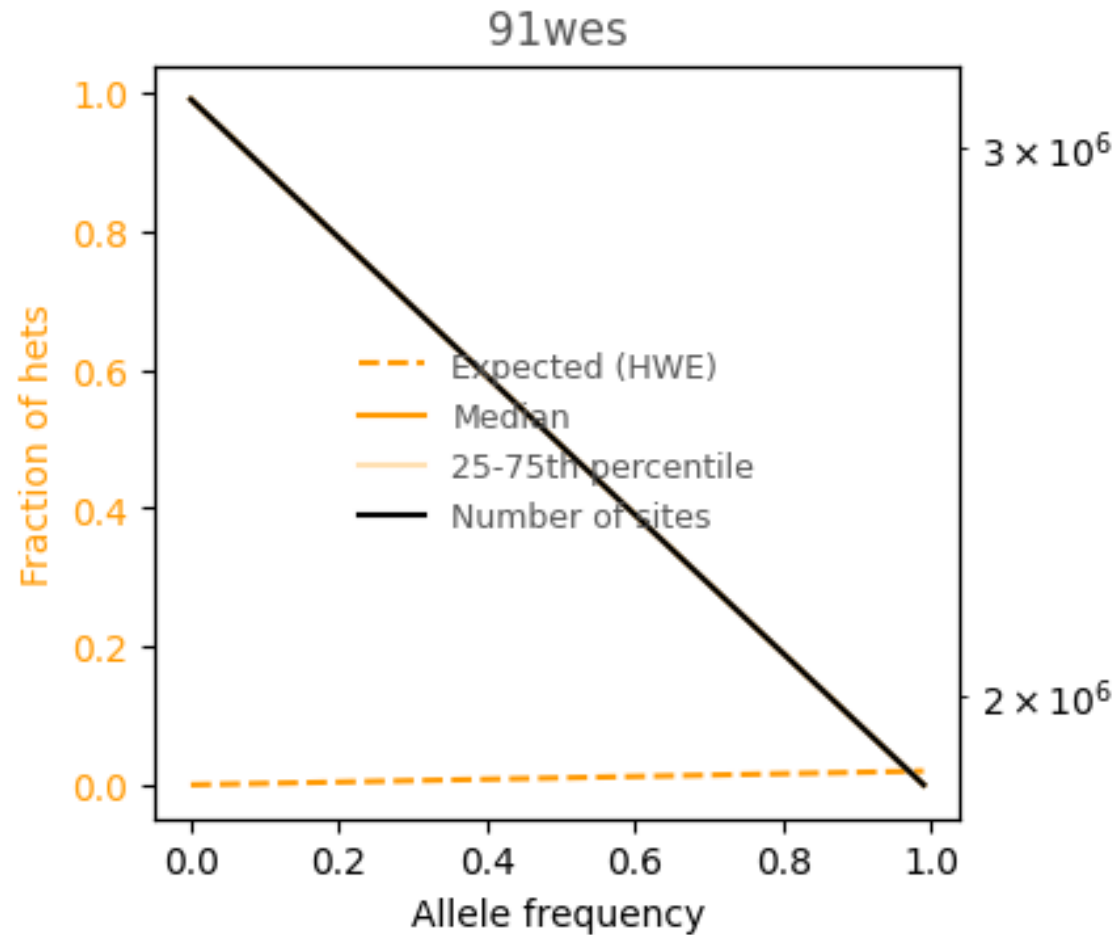
# Fraction of alternate indel allele



# Depth distribution



# Number of HETs by AF



# Substitution types

