

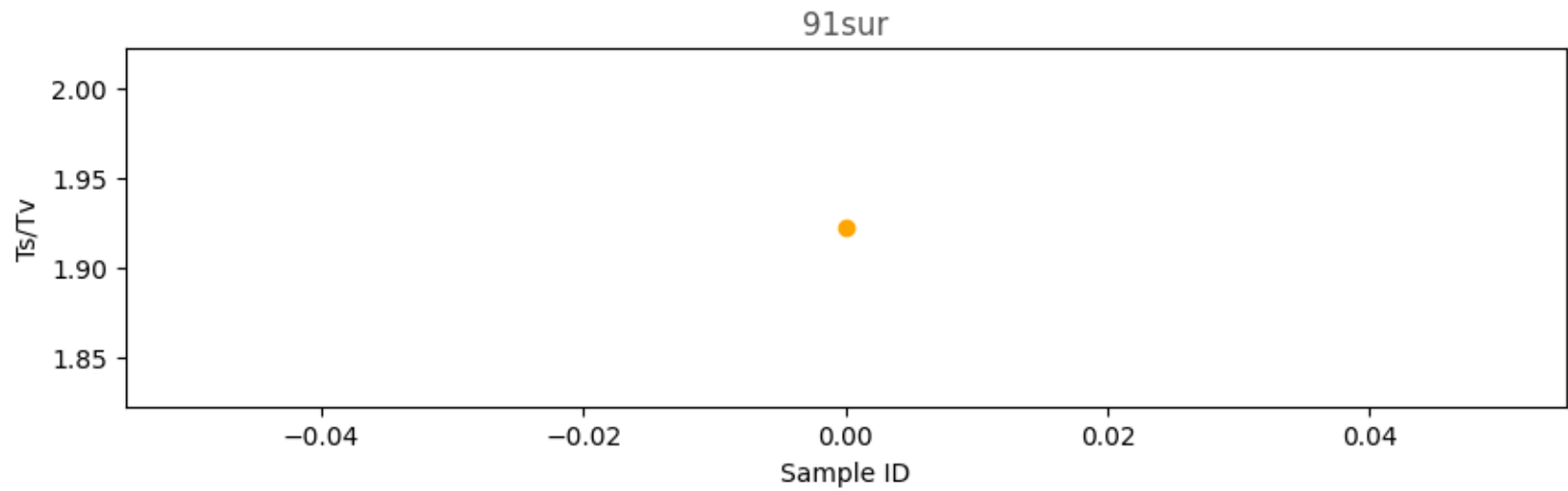
# Summary Numbers

Callset	SNPs			indels		MNPs	others
	n	ts/tv	(1st ALT)	n	frm*		
91sur	4,117,902	1.92	1.93	964,160	–	0	0
* frameshift ratio: out/(out+in)							

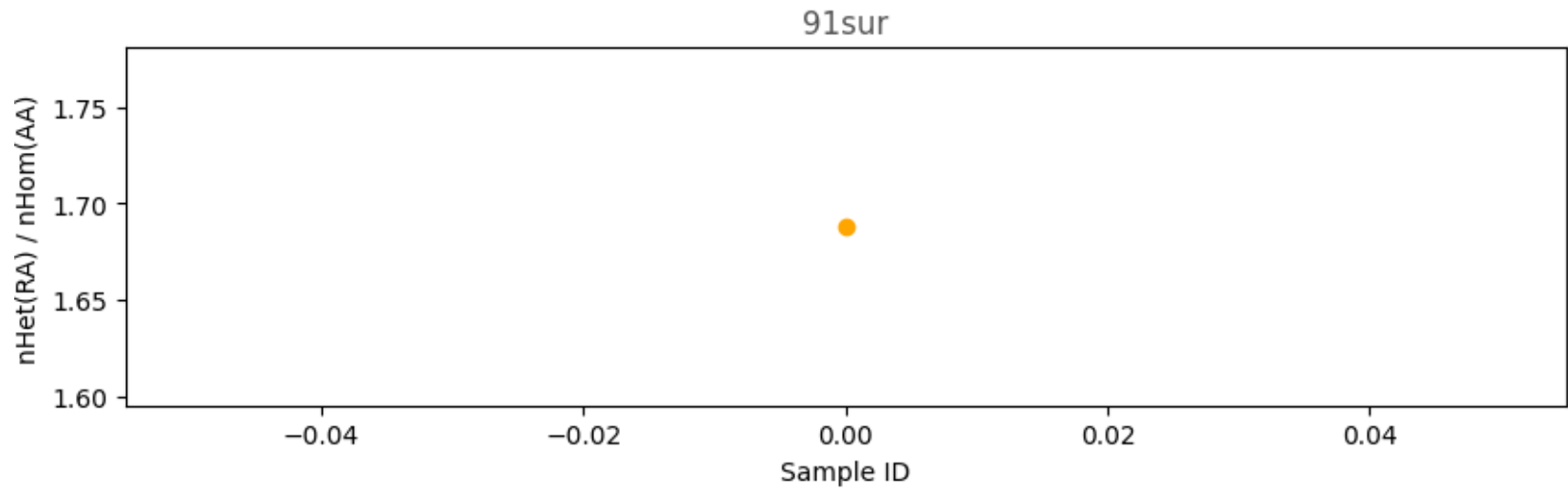
Callset	singletons (AC=1)			multiallelic	
	SNPs	ts/tv	indels	sites	SNPs
91sur	62.8%	1.89	68.2%	106,107	2,367

- 91sur .. /ngc/projects2/gm/data/archive/2022/variants/snv/91surelaf-110297310465-Normal\_Blood\_noinfo-WGS\_v1\_IlluminaDNAPCRFree\_X-221014\_A00559\_AH3F23DSX5-RHGM\_LABKA\_WGSA\_KUT-WGSAKUT05828\_22RKG024667x01\_snv\_germline\_raw.haplotype\_caller.vcf.gz

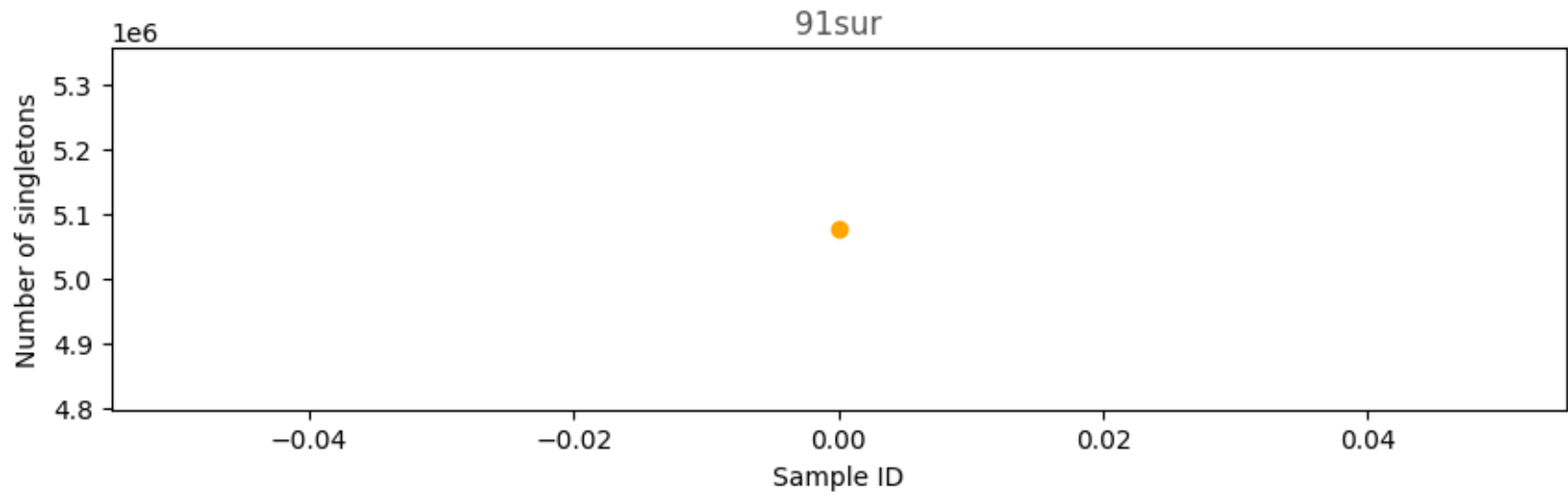
# Ts/Tv by sample



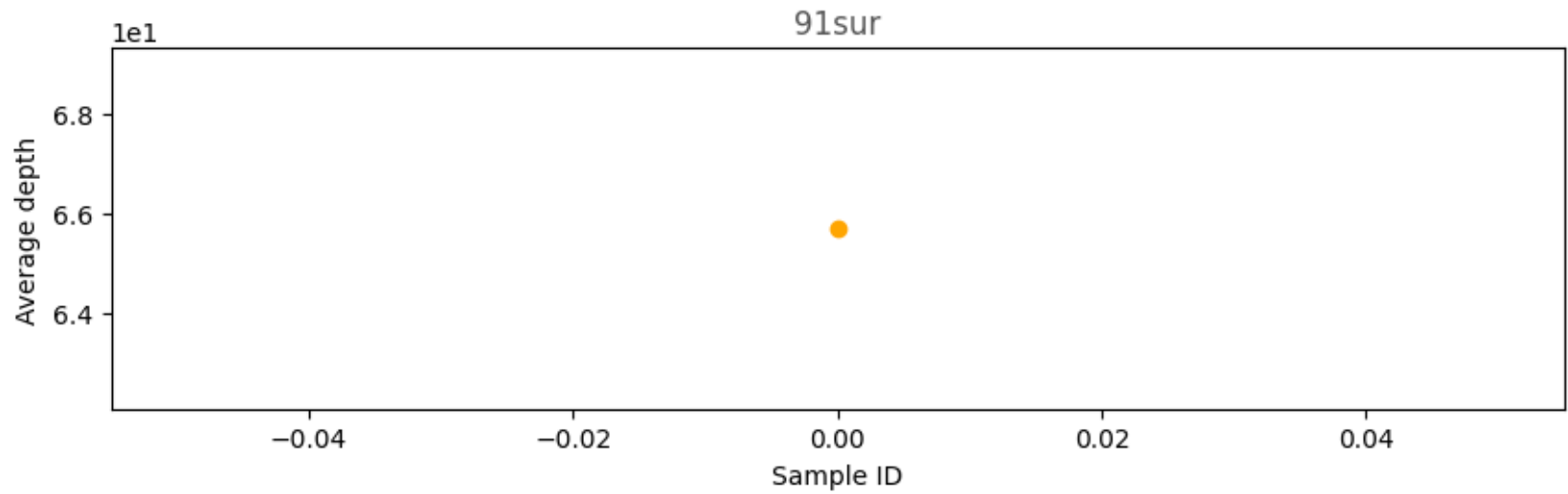
# Hets vs non-ref Homs by sample



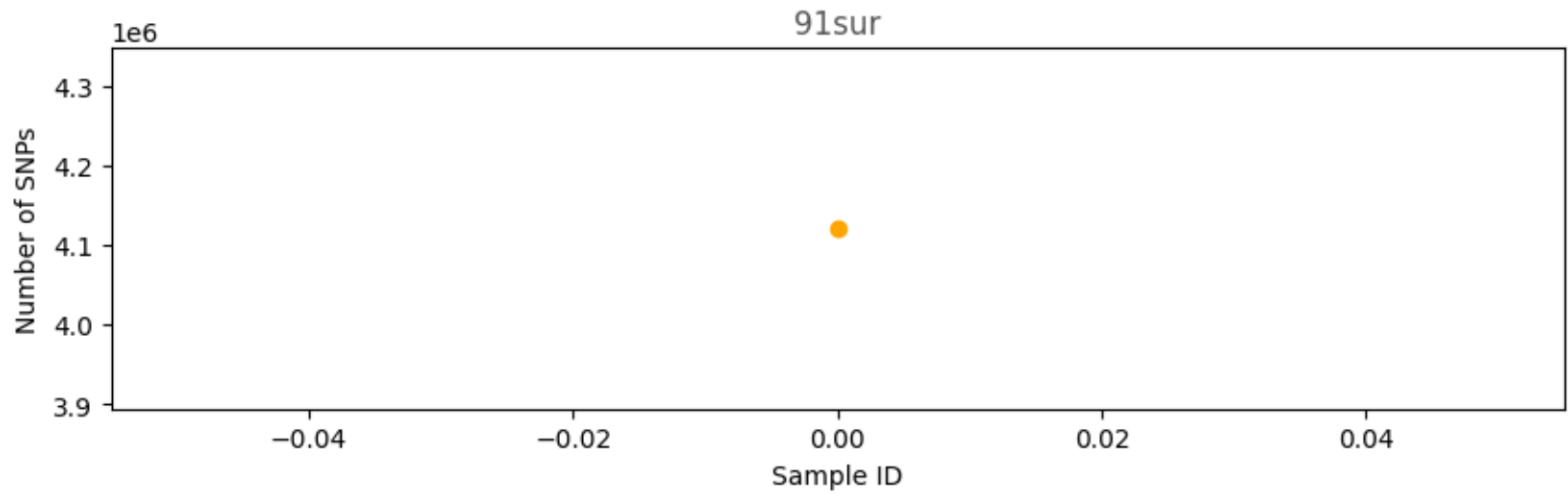
# Singletons by sample (hets and homs)



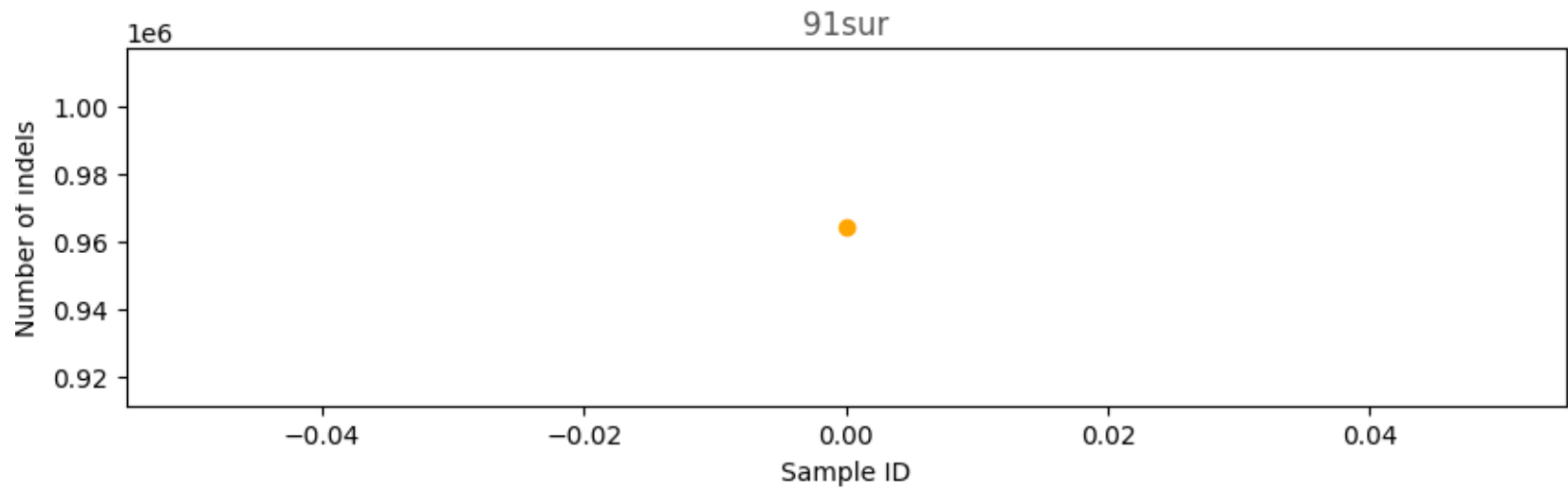
# Average depth by sample



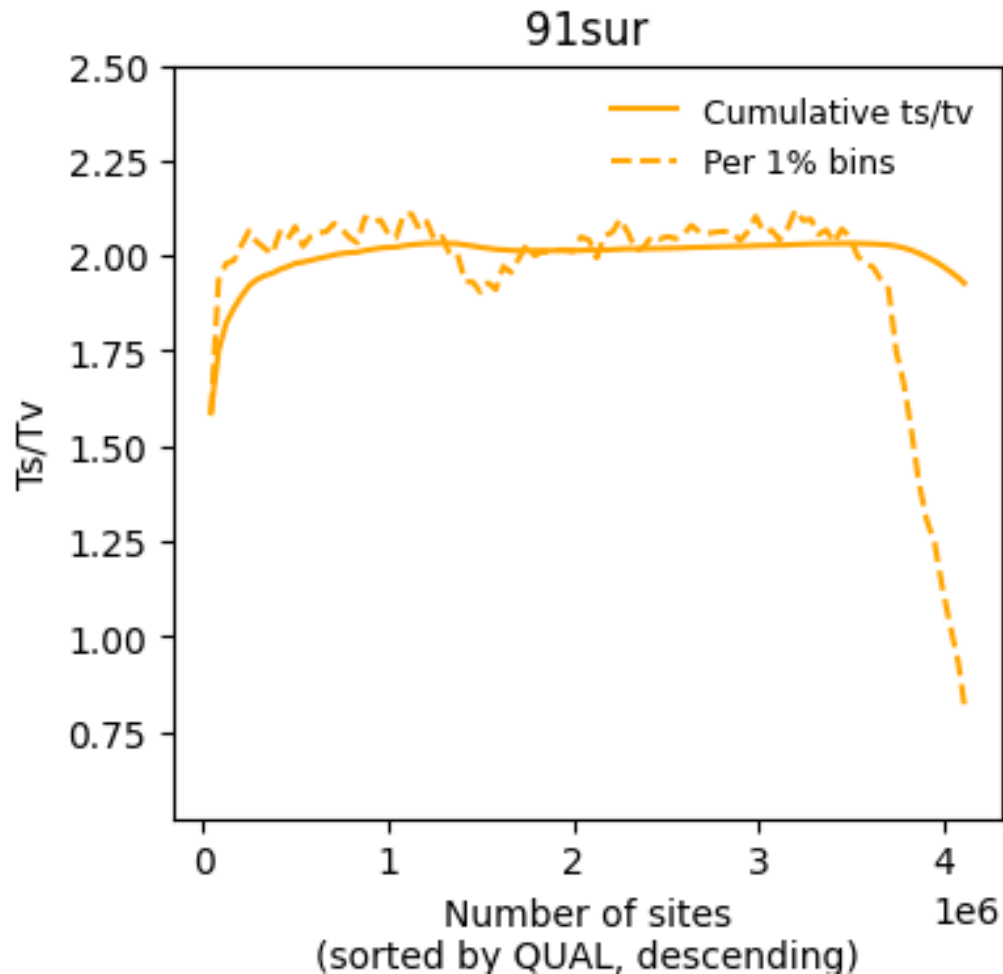
# Number of SNPs by sample



# Number of indels by sample

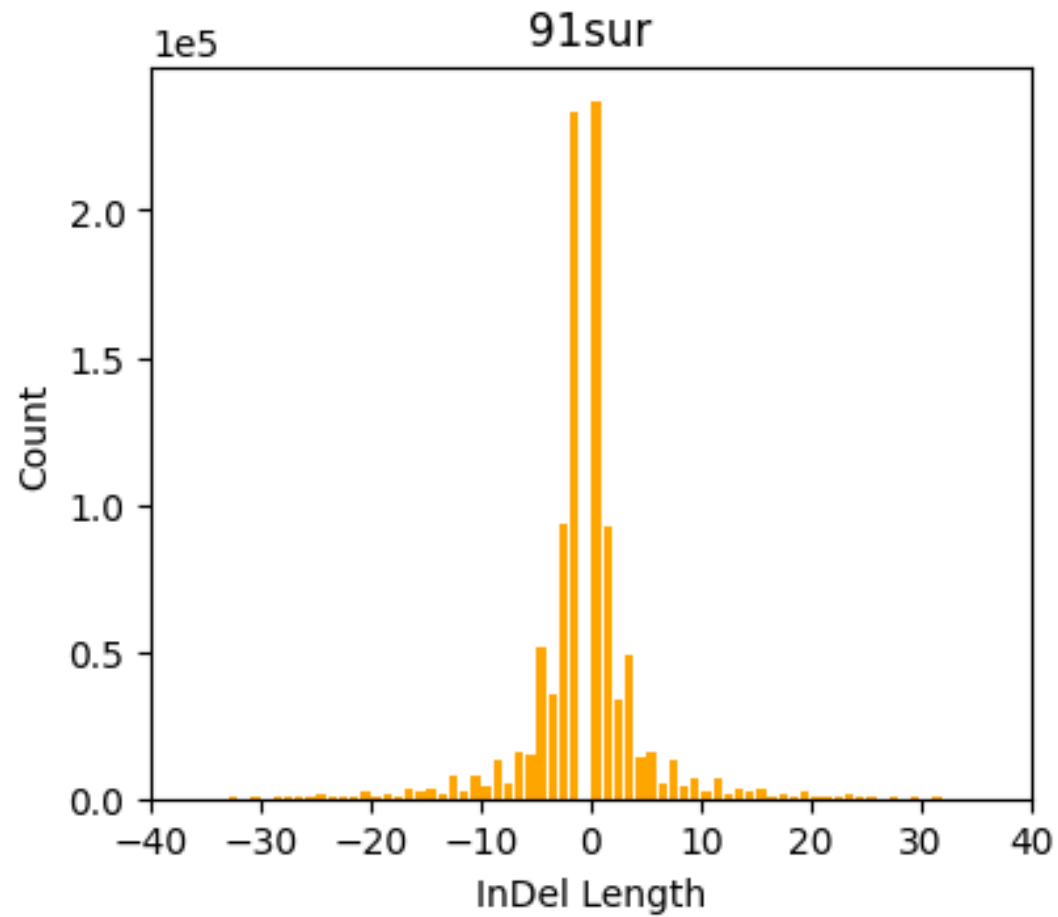


## Ts/Tv stratified by QUAL

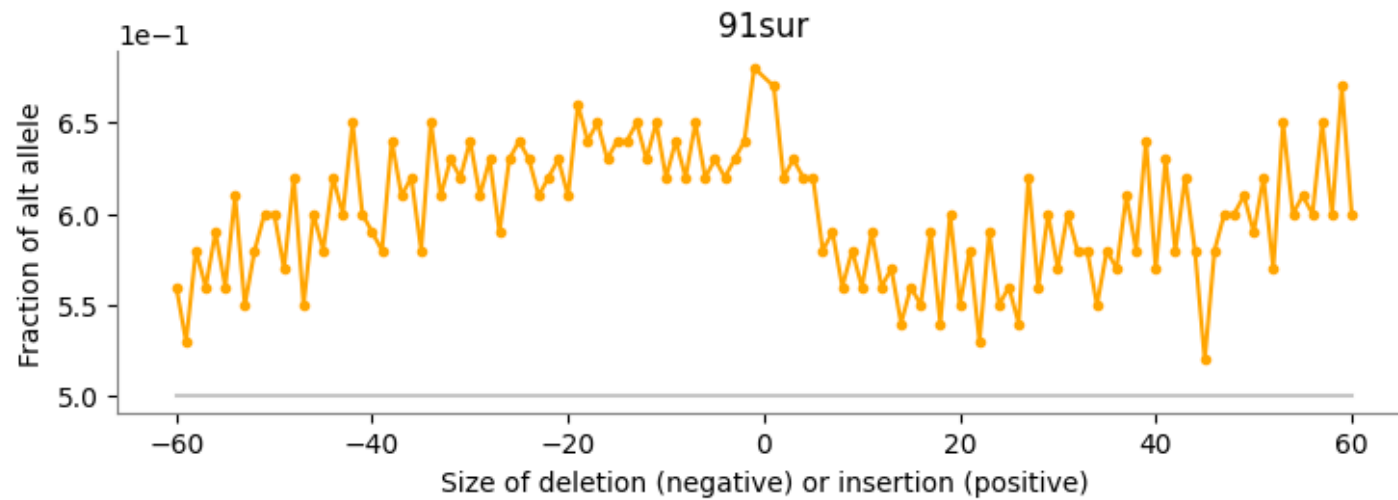




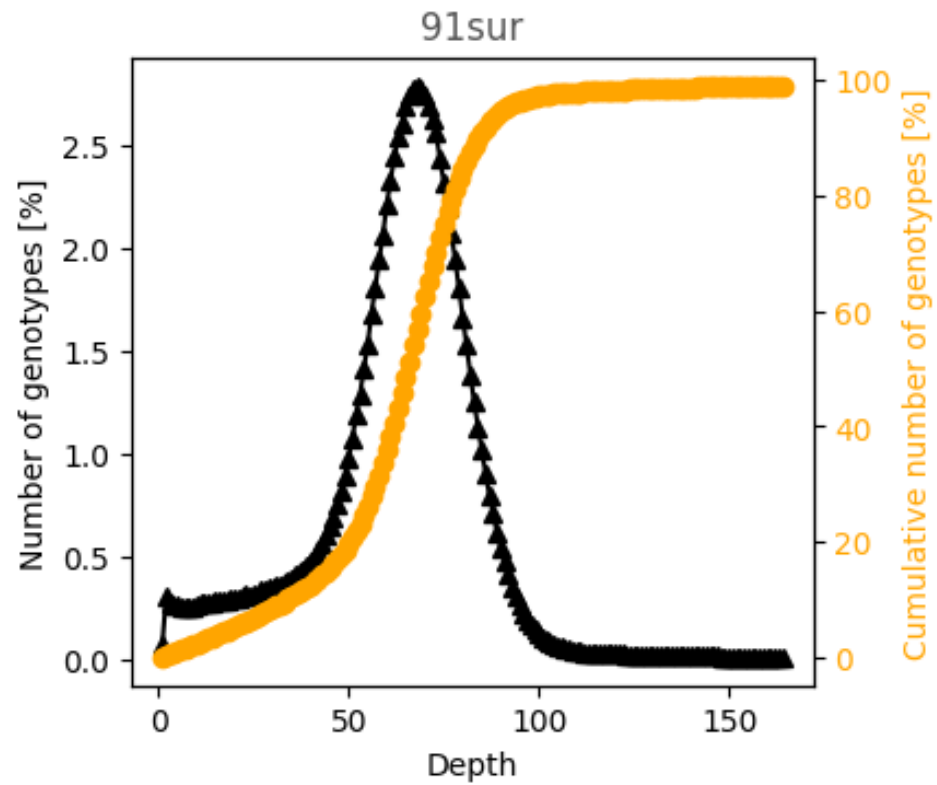
# Indel distribution



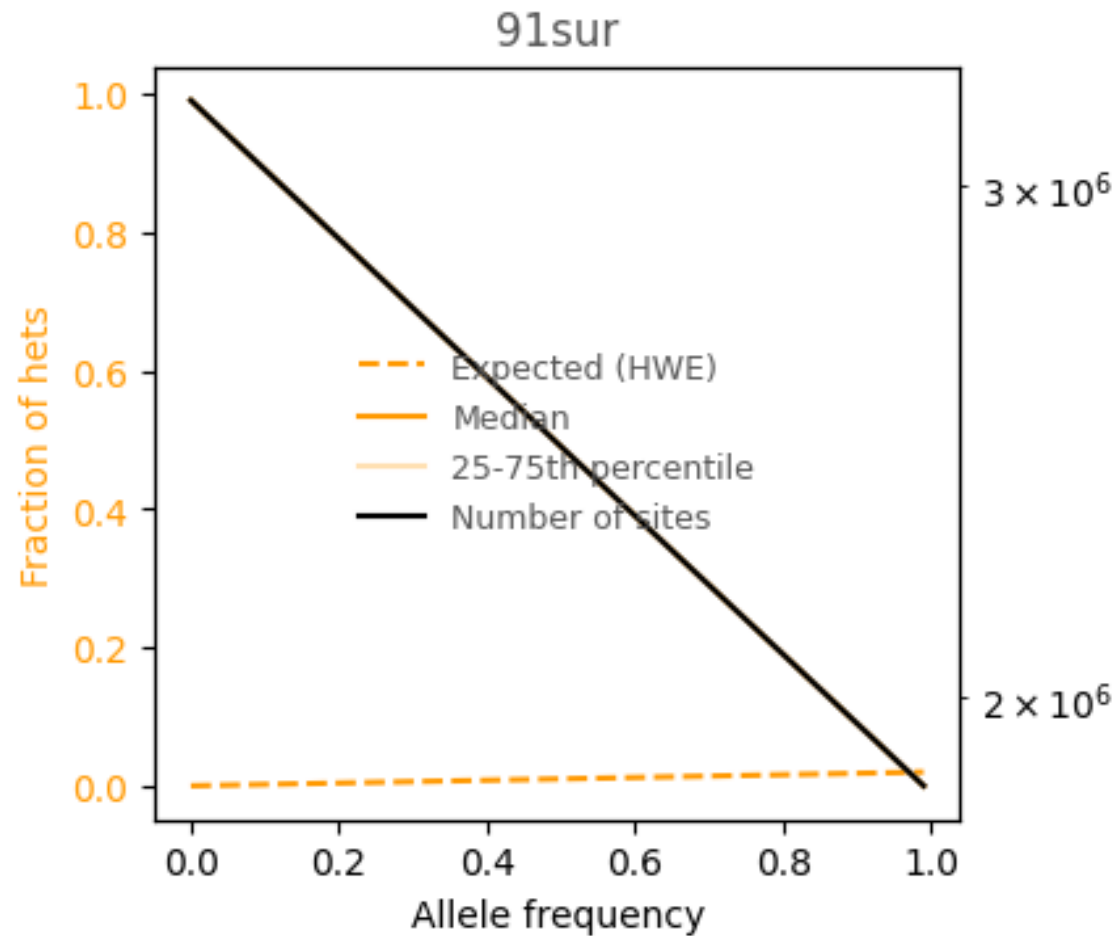
# Fraction of alternate indel allele



# Depth distribution



# Number of HETs by AF



# Substitution types

