

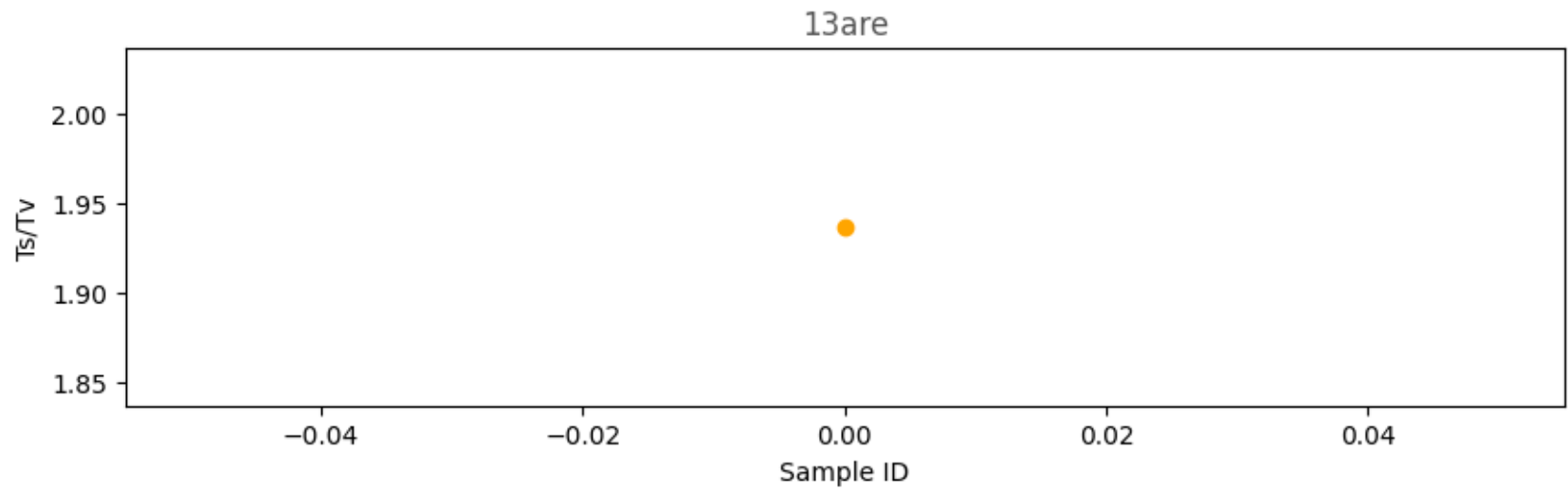
# Summary Numbers

Callset	SNPs			indels		MNPs	others
	n	ts/tv	(1st ALT)	n	frm*		
13are	4,099,041	1.94	1.94	958,120	–	0	0
* frameshift ratio: out/(out+in)							

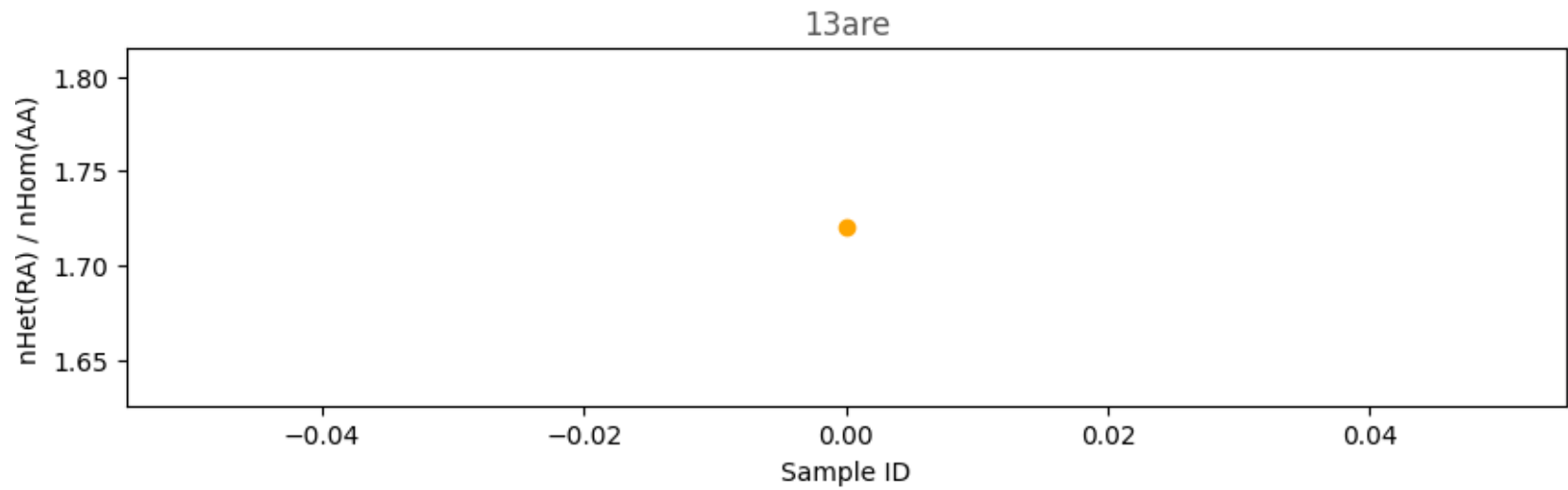
Callset	singletons (AC=1)			multiallelic	
	SNPs	ts/tv	indels	sites	SNPs
13are	63.3%	1.91	68.5%	102,007	2,090

- 13are .. /ngc/projects2/gm/data/archive/2022/variants/snv/13arenerf-103910794875-Normal\_B  
 lood\_noinfo-WGS\_v1\_IlluminaDNAPCRFree\_RHGM01548-220916\_A01411\_AHTJ7JDSX3-EXT\_LAB  
 KA\_NGCWGS-NGCWGS05391\_22RKG017111\_snv\_germline\_raw.haplotype\_caller.vcf.gz

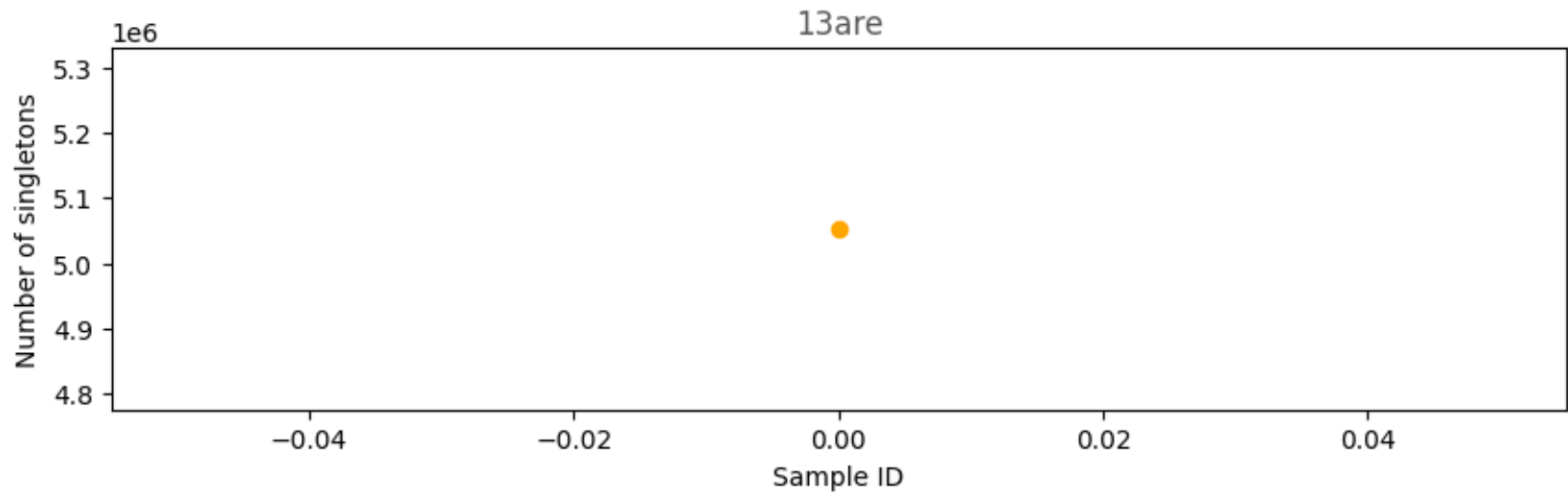
# Ts/Tv by sample



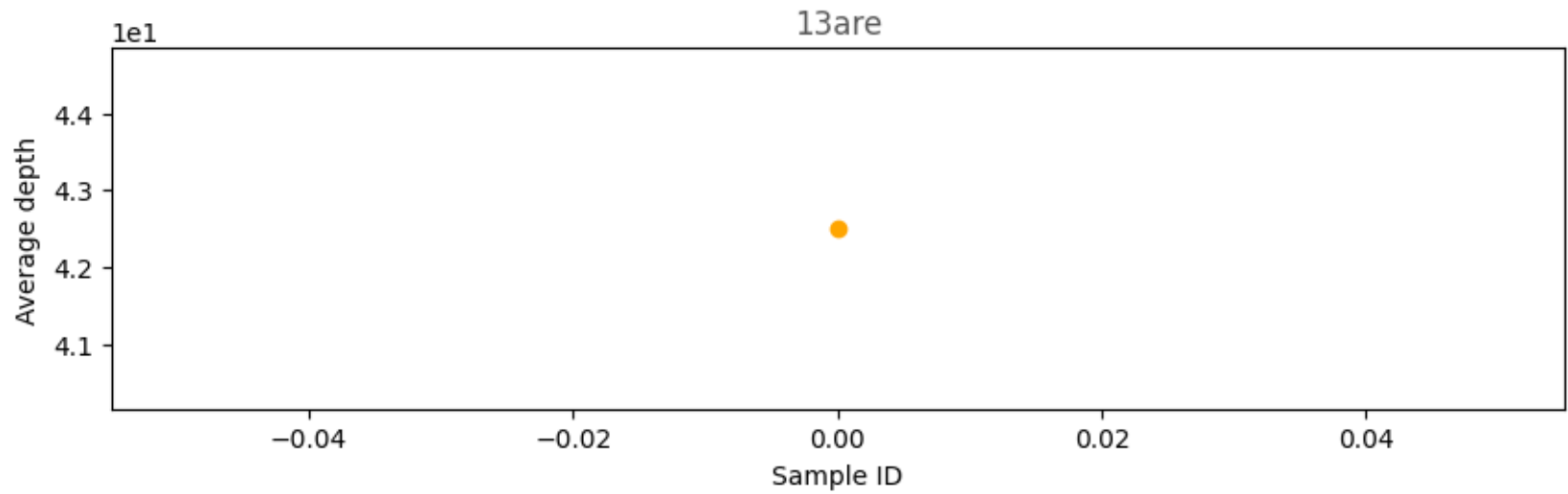
# Hets vs non-ref Homs by sample



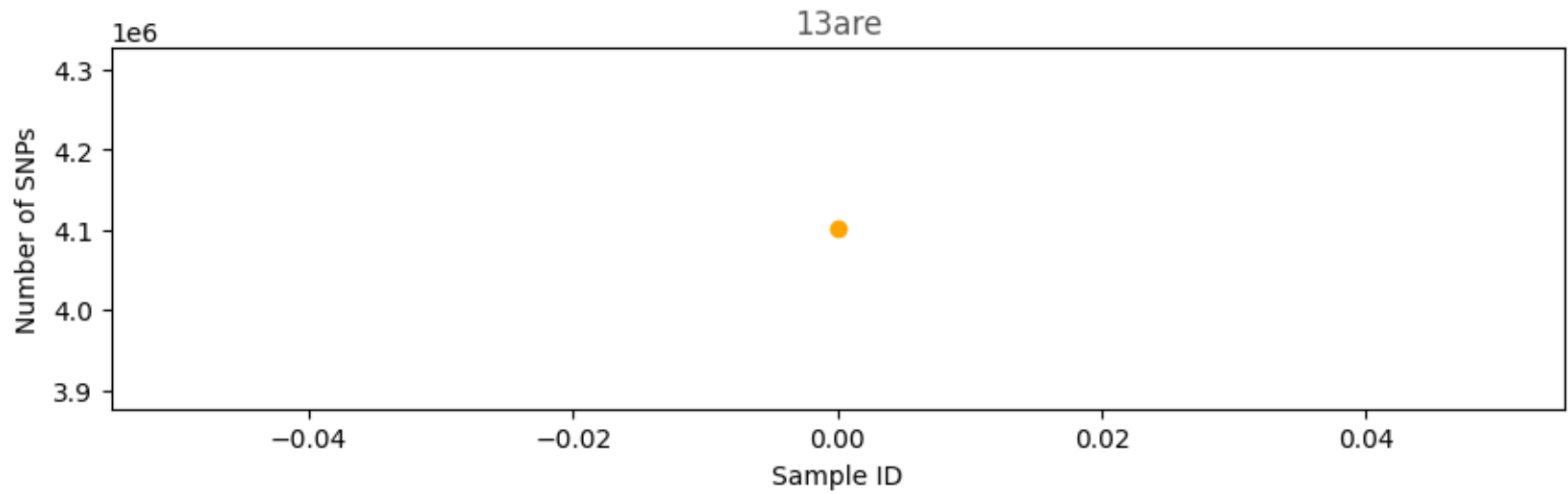
# Singletons by sample (hets and homs)



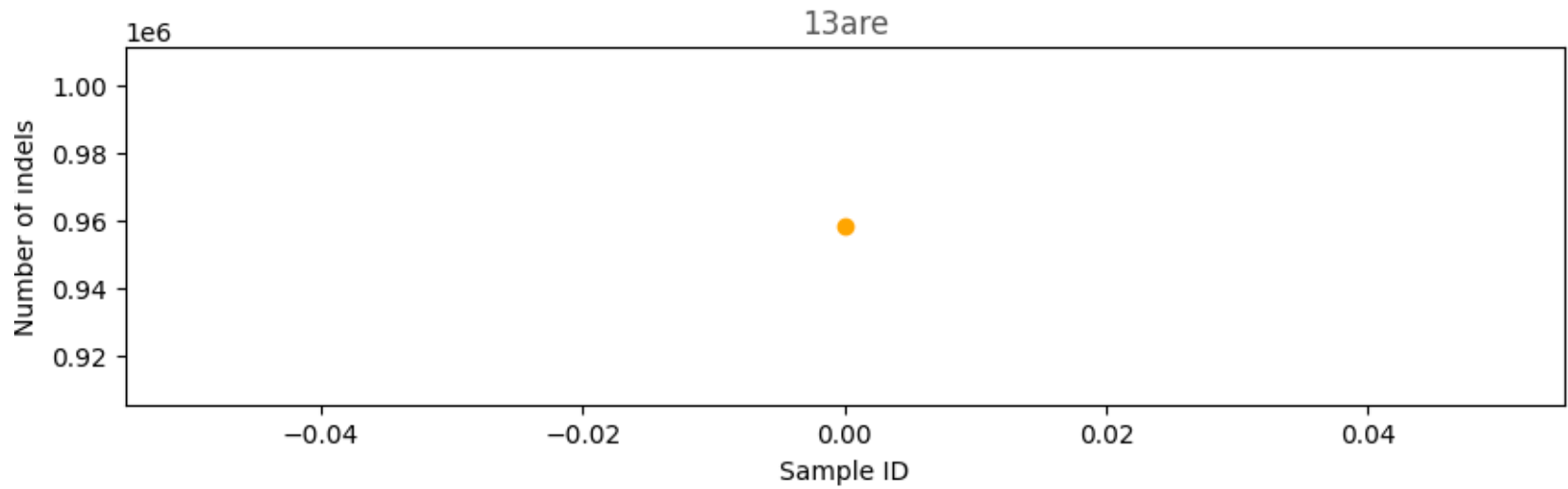
# Average depth by sample



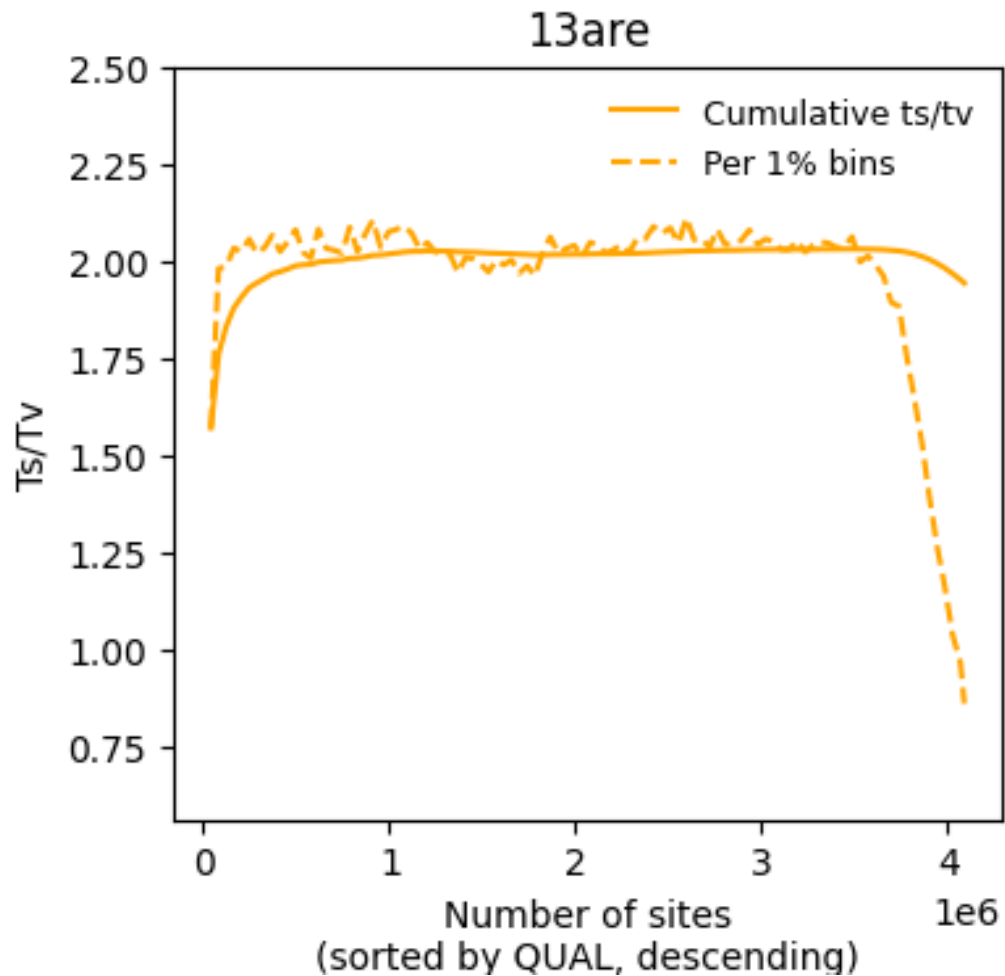
# Number of SNPs by sample



# Number of indels by sample

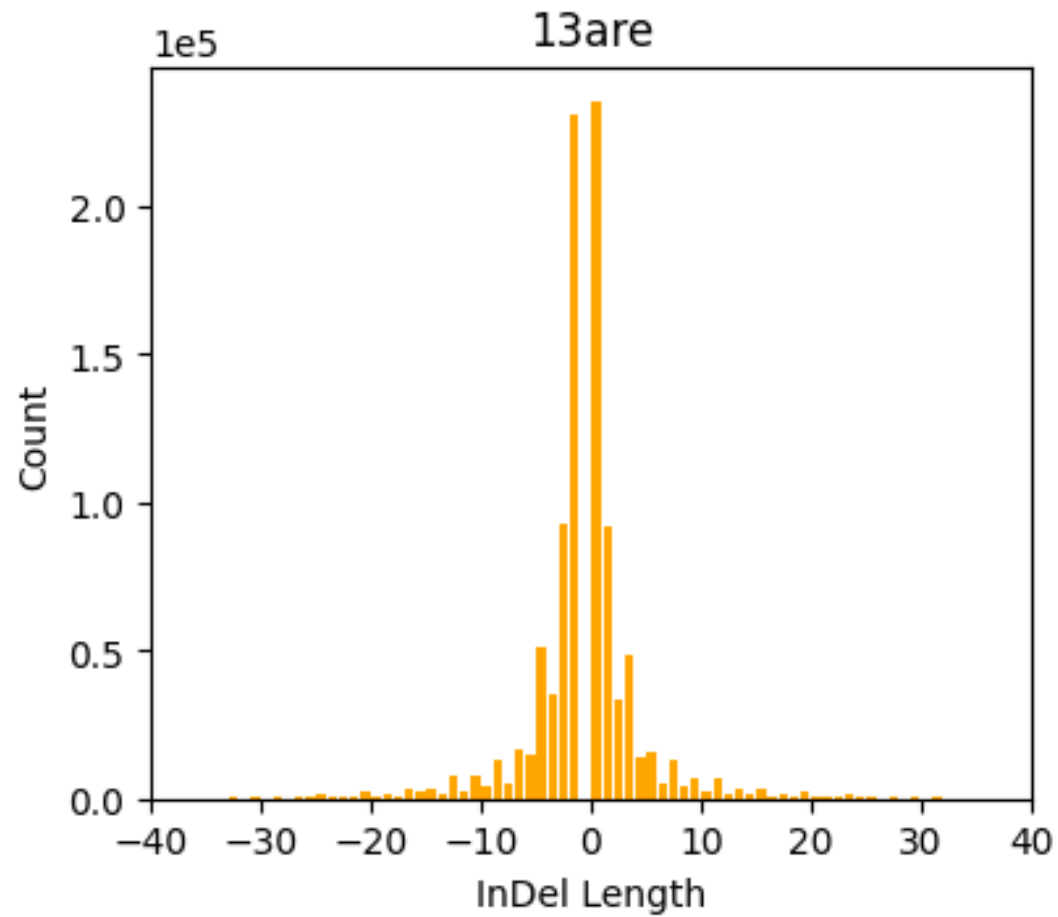


## Ts/Tv stratified by QUAL

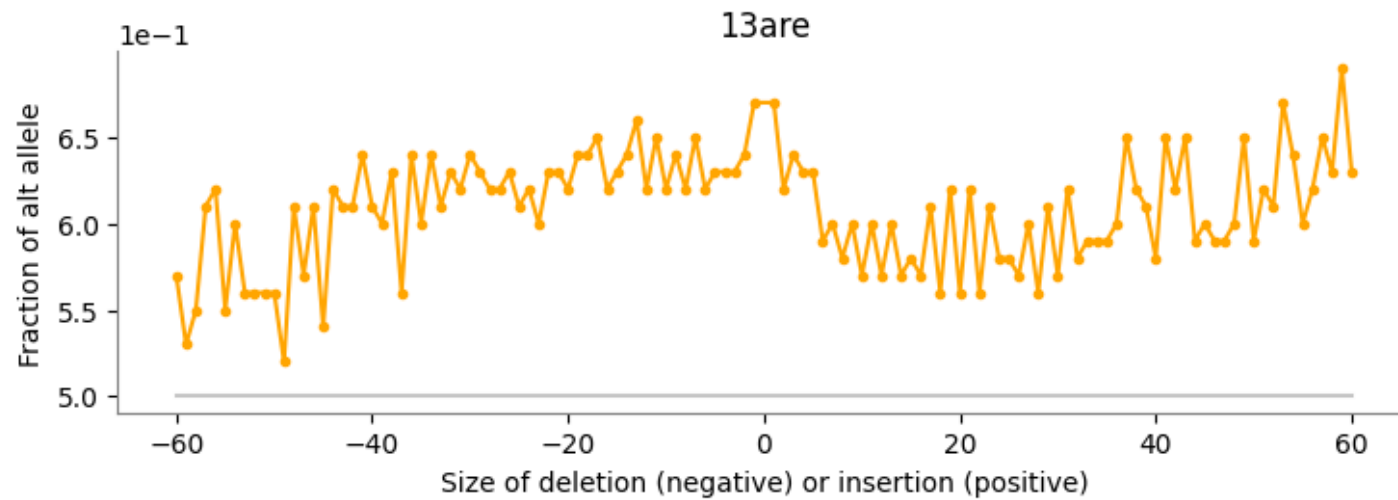




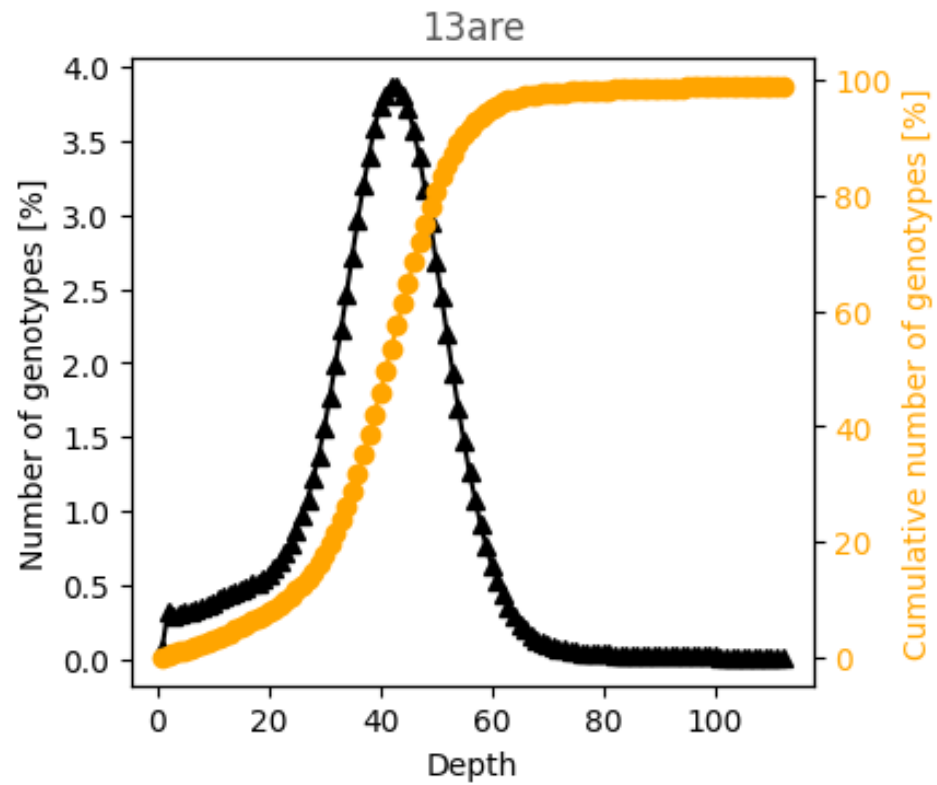
# Indel distribution



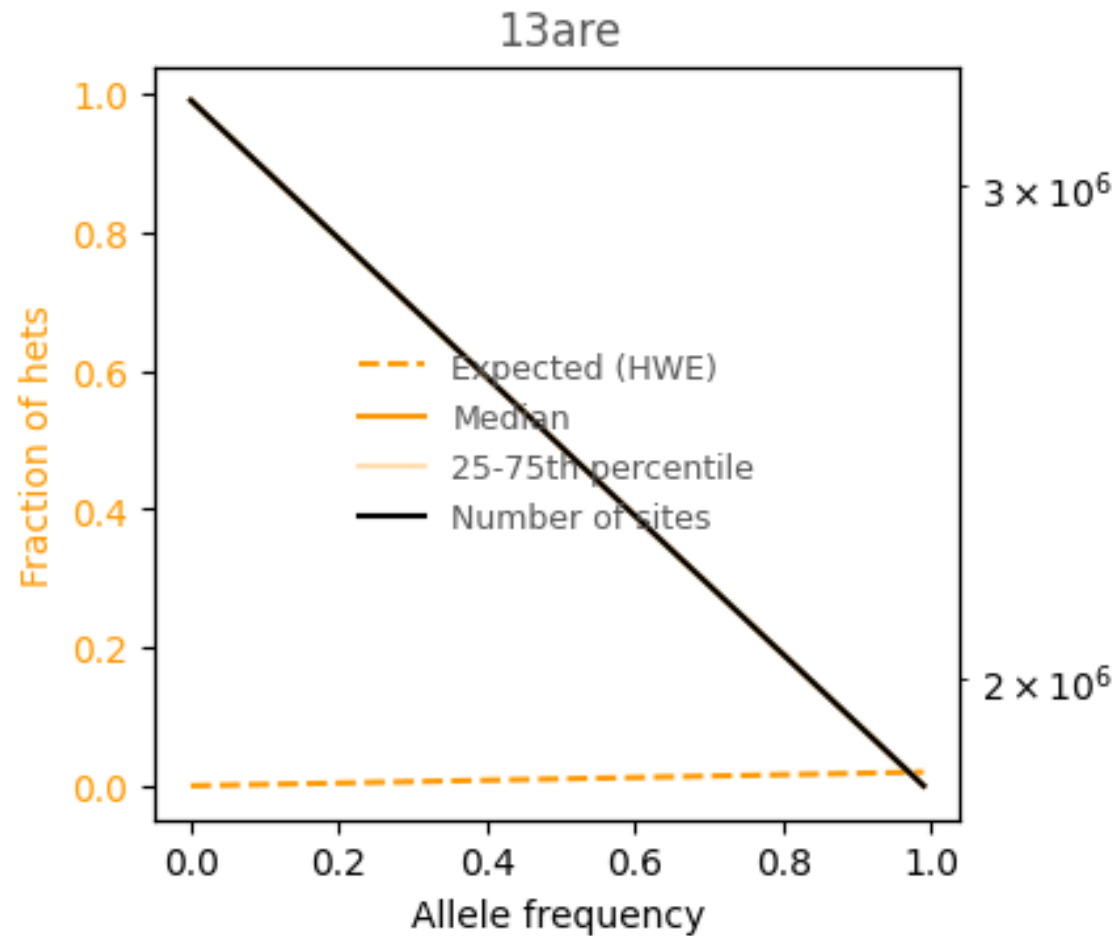
# Fraction of alternate indel allele



# Depth distribution



# Number of HETs by AF



# Substitution types

