

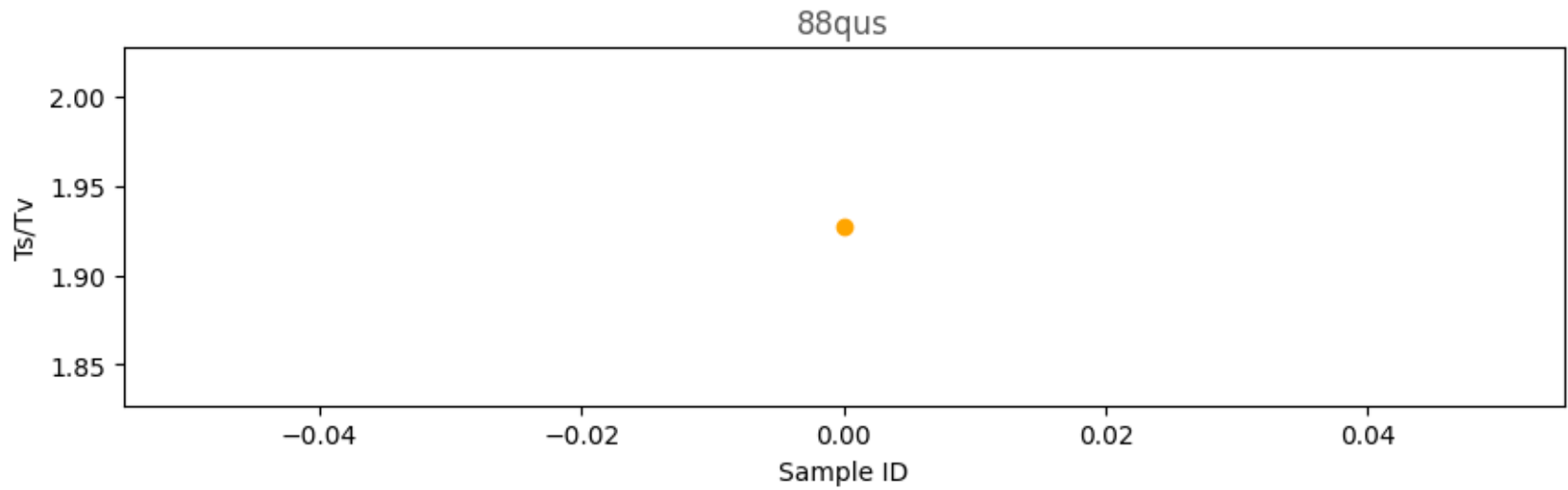
# Summary Numbers

Callset	SNPs			indels		MNPs	others
	n	ts/tv	(1st ALT)	n	frm*		
88qus	4,152,896	1.93	1.93	970,626	–	0	0
* frameshift ratio: out/(out+in)							

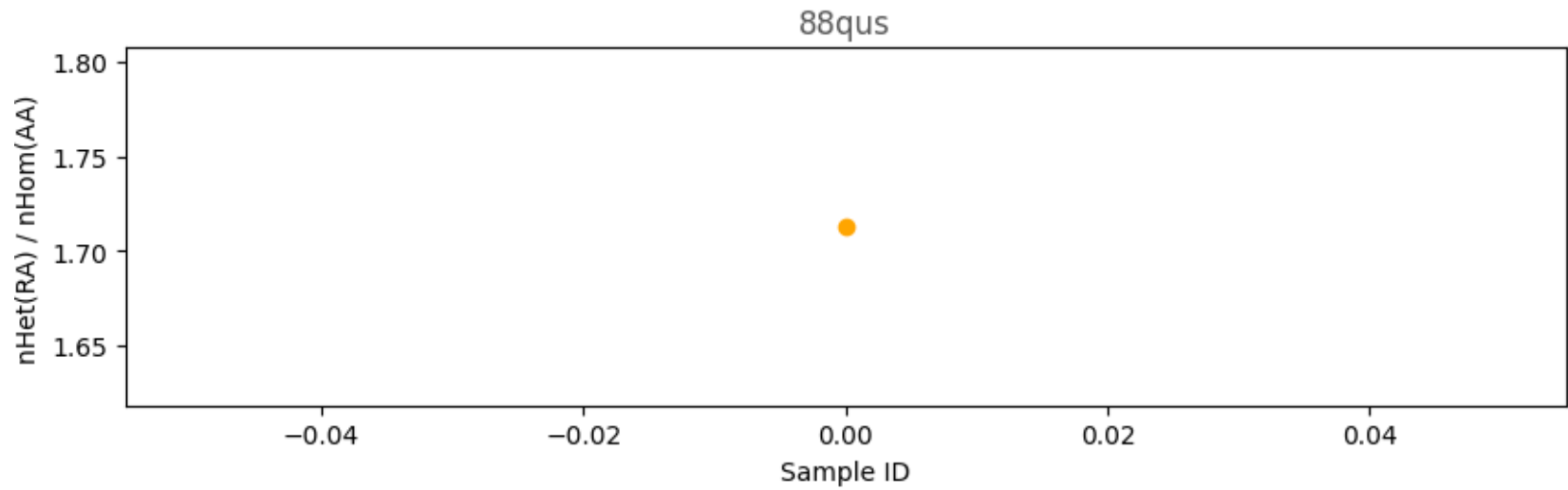
Callset	singletons (AC=1)			multiallelic	
	SNPs	ts/tv	indels	sites	SNPs
88qus	63.2%	1.90	68.4%	106,800	2,306

- 88qus .. /ngc/projects2/gm/data/archive/2022/variants/snv/88qusinaf-103904432894-Normal\_Blood\_noinfo-WGS\_v1\_IlluminaDNAPCRFree\_RHGM01157-220824\_A01961\_BHMWKTDSX3-EXT\_LAB  
KA\_NGCWGS-NGCWGS04908\_22RKG011845x01\_snv\_germline\_raw.haplotype\_caller.vcf.gz

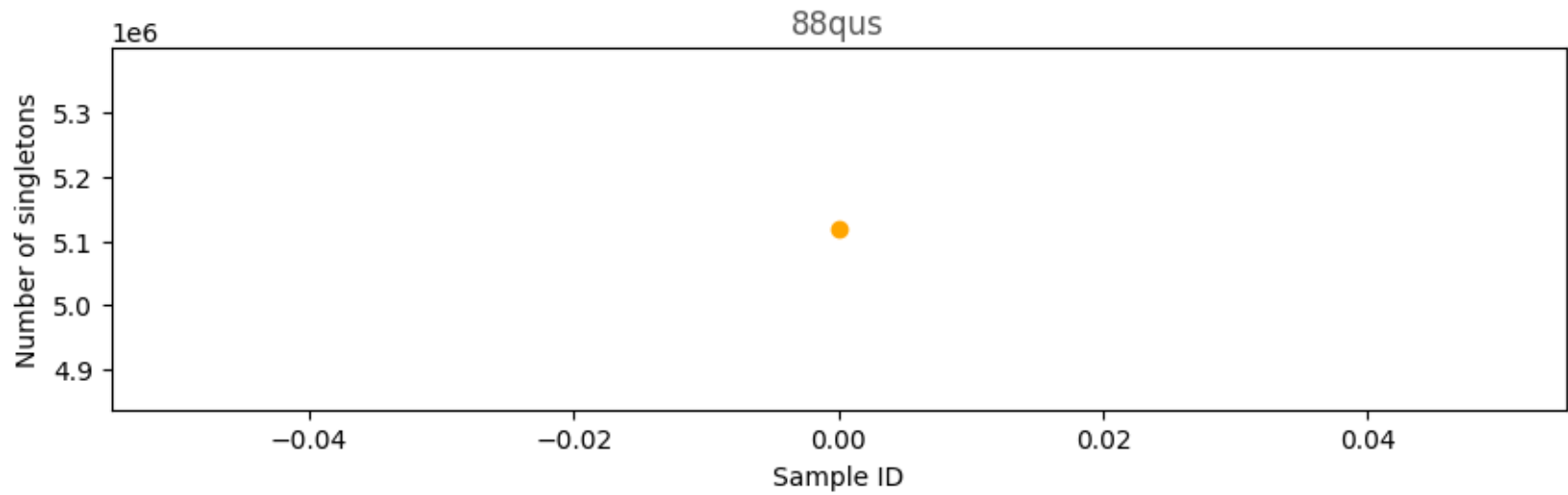
# Ts/Tv by sample



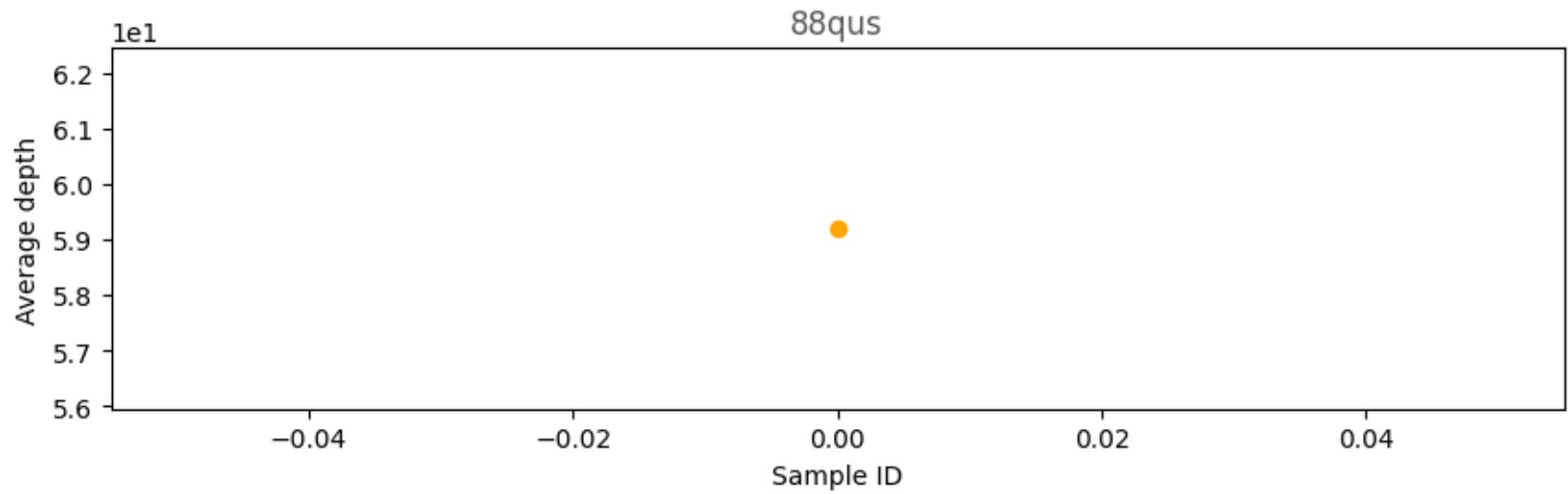
# Hets vs non-ref Homs by sample



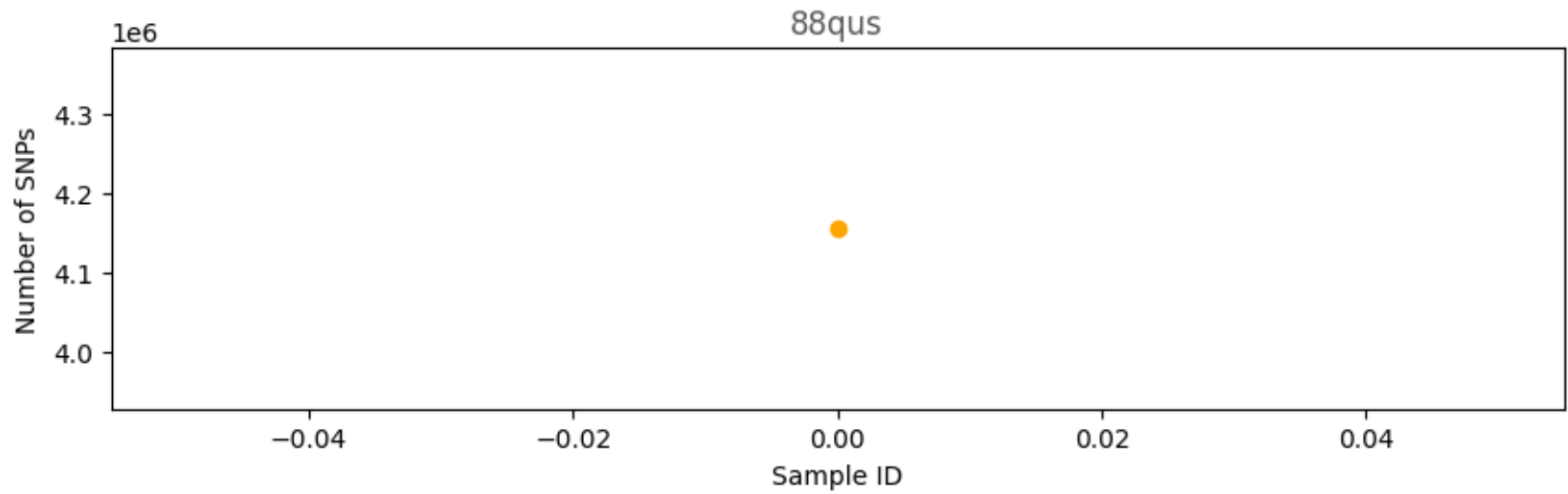
# Singletons by sample (hets and homs)



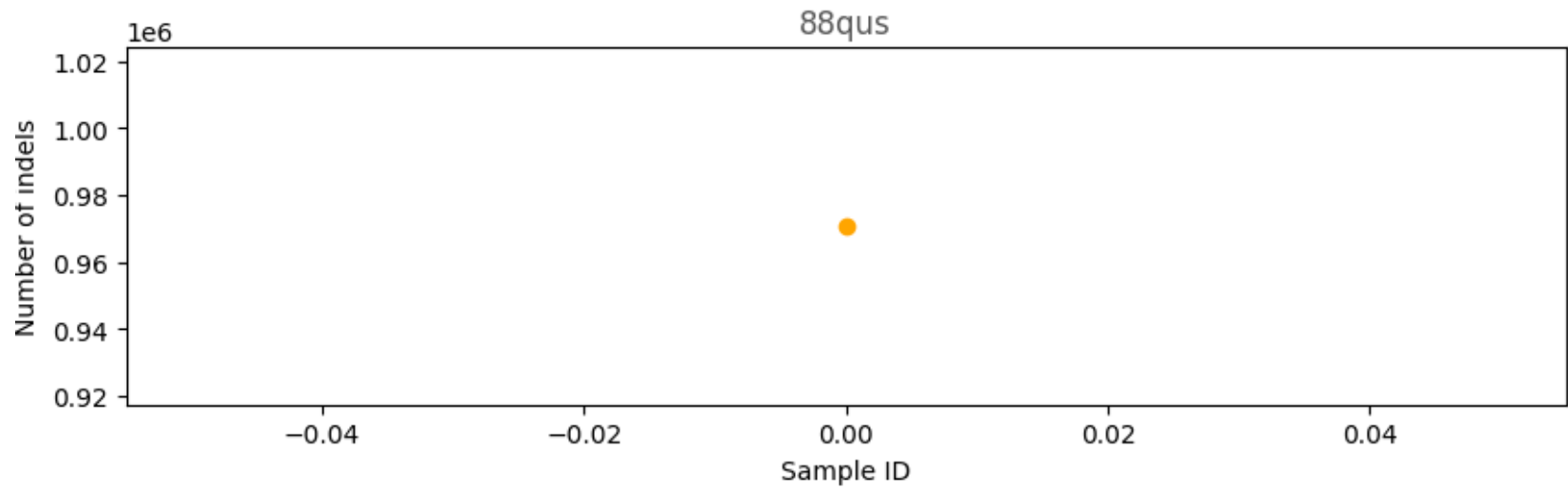
# Average depth by sample



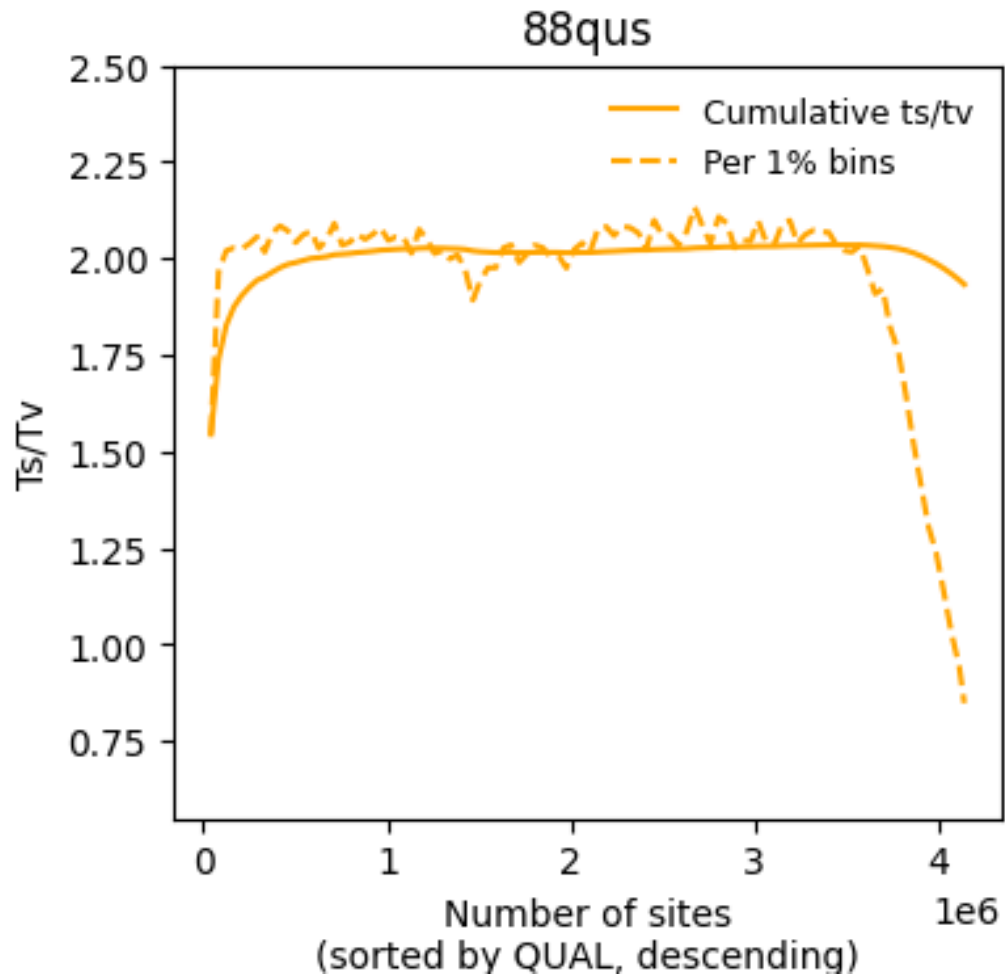
# Number of SNPs by sample



# Number of indels by sample

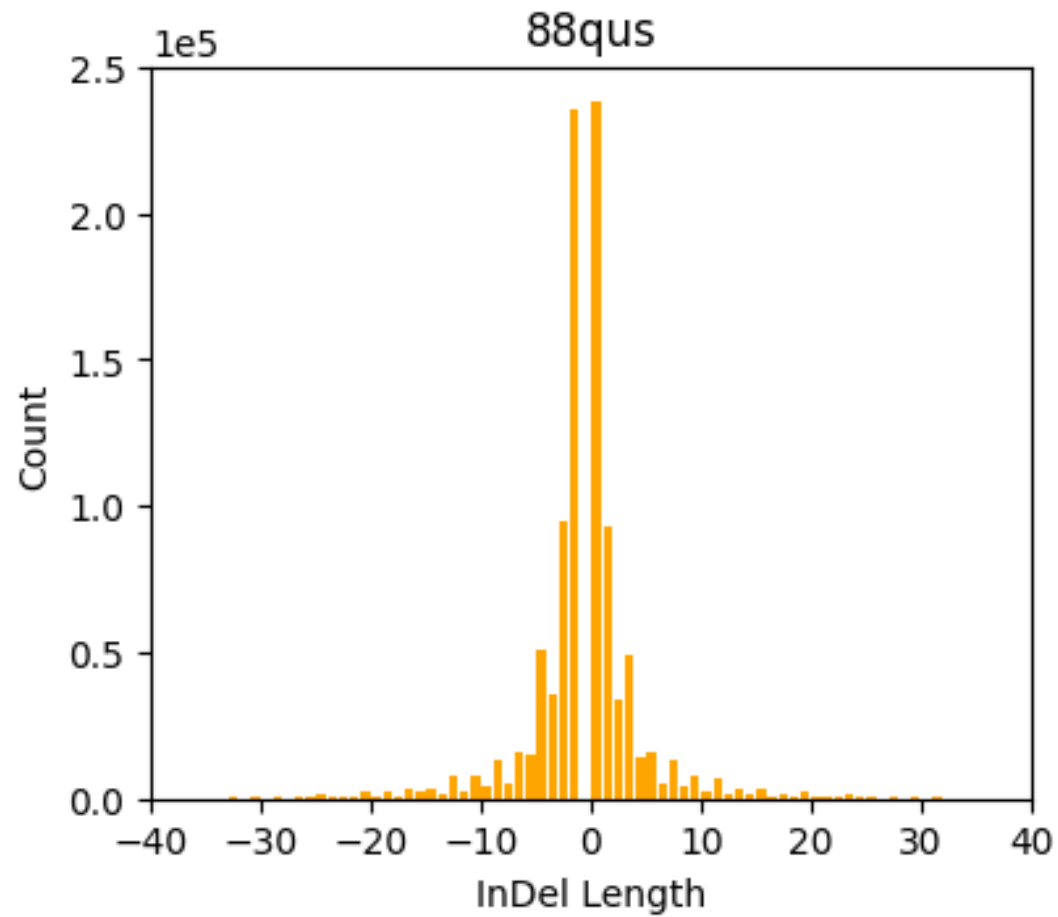


# Ts/Tv stratified by QUAL

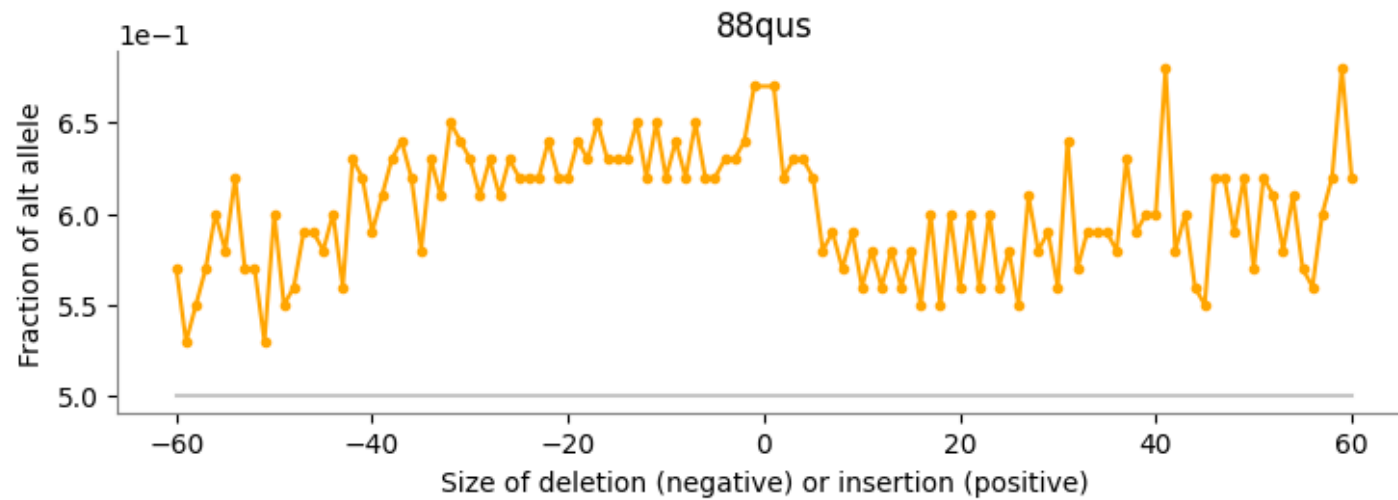




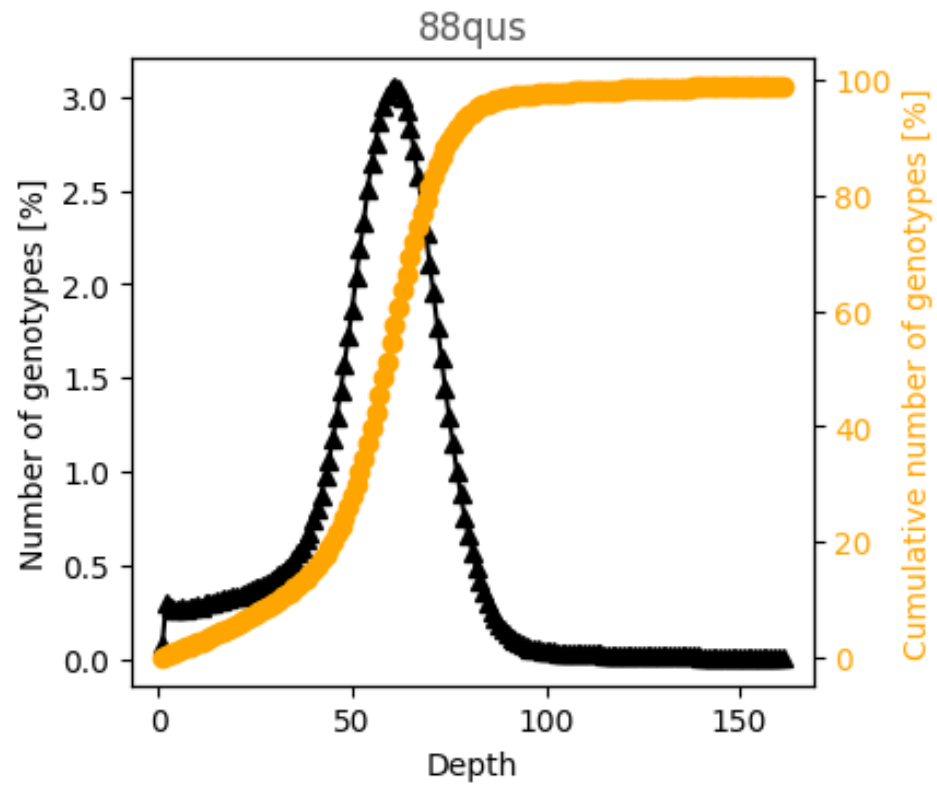
# Indel distribution



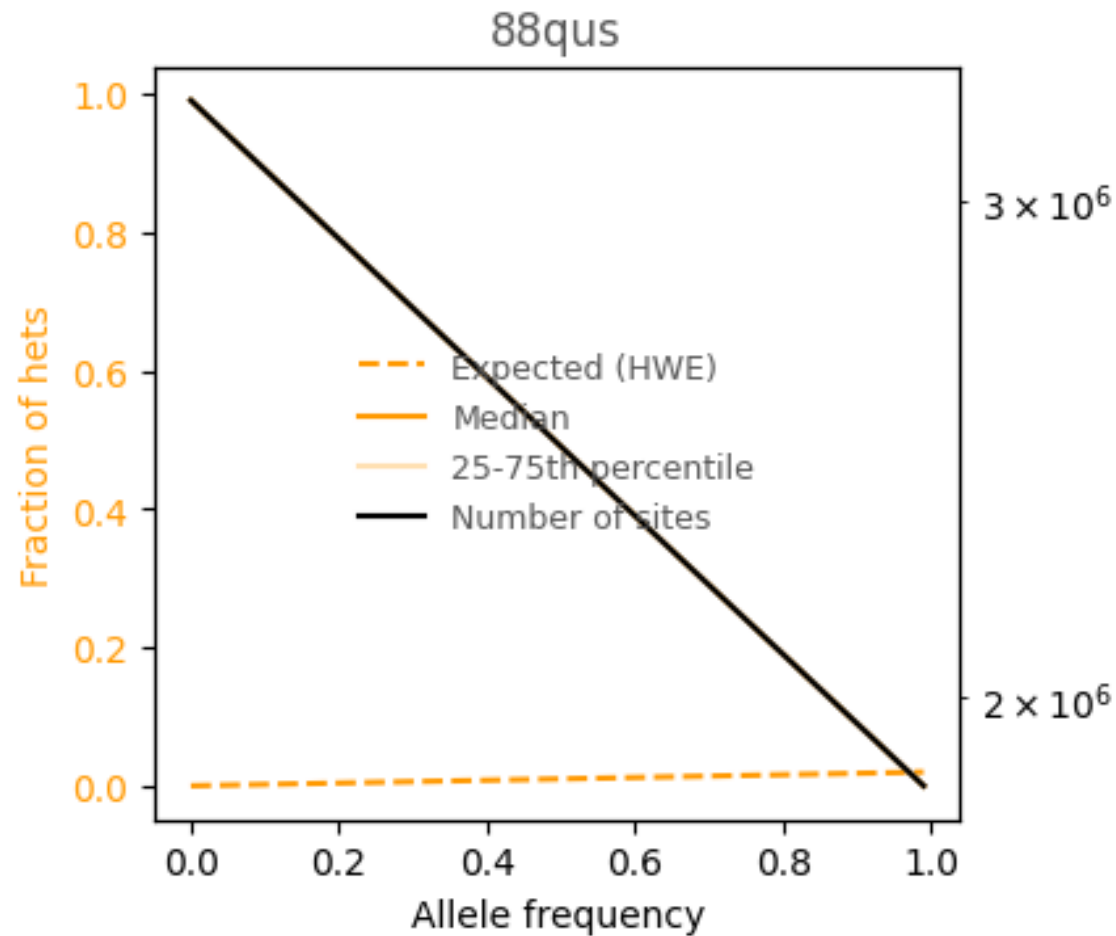
# Fraction of alternate indel allele



# Depth distribution



# Number of HETs by AF



# Substitution types

