

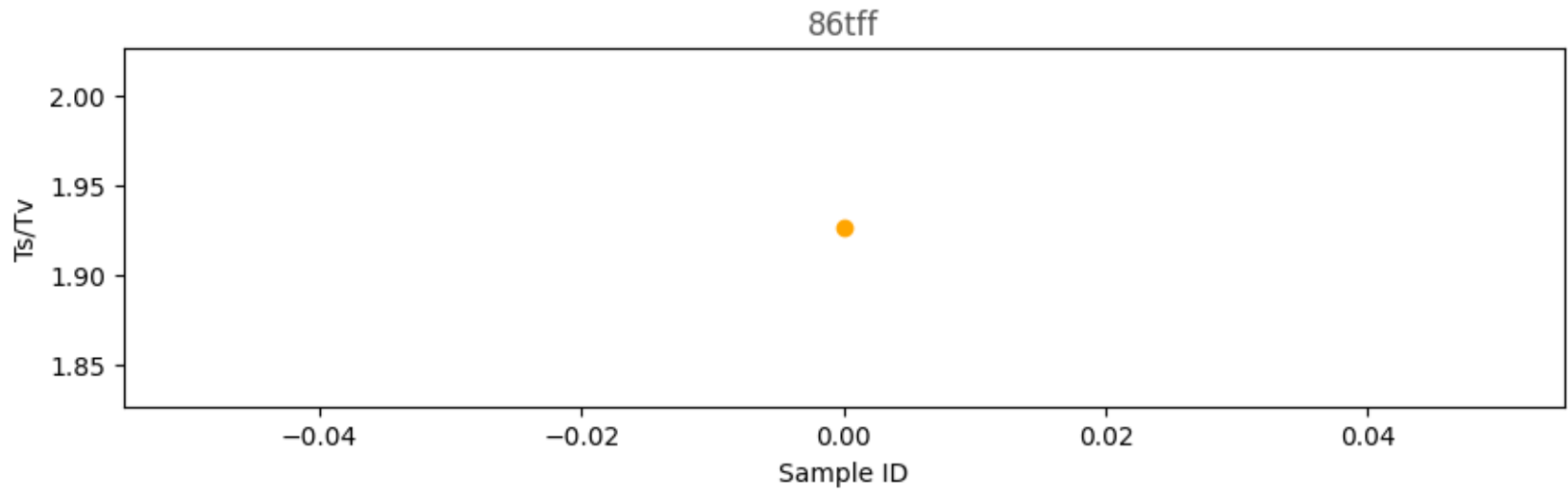
# Summary Numbers

Callset	SNPs			indels		MNPs	others
	n	ts/tv	(1st ALT)	n	frm*		
86tff	4,106,138	1.93	1.93	956,704	–	0	0
* frameshift ratio: out/(out+in)							

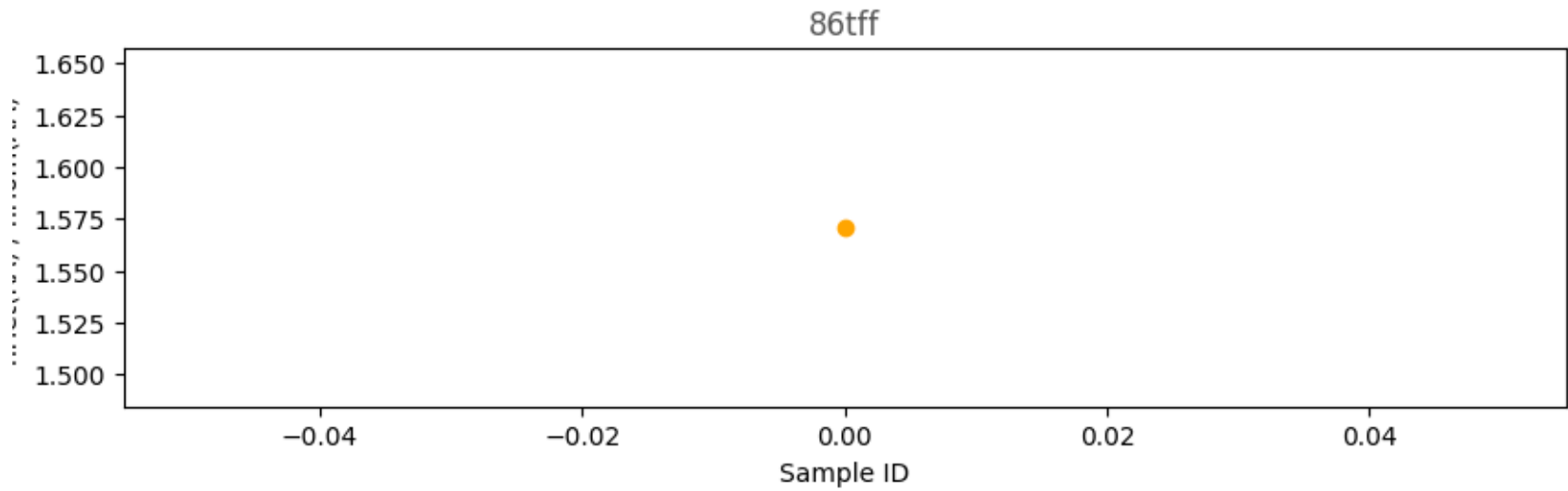
Callset	singletons (AC=1)			multiallelic	
	SNPs	ts/tv	indels	sites	SNPs
86tff	61.1%	1.89	65.9%	99,692	1,891

- 86tff .. /ngc/projects2/gm/data/archive/2022/variants/snv/86tffcthm-103909049673-Normal\_Blood\_noinfo-WGS\_v1\_IlluminaDNAPCRFree\_RHGM01431-220912\_A01411\_BHYMNTDSX3-EXT\_LAB  
KA\_NGCWGS-NGCWGS05210\_22RKG020949\_snv\_germline\_raw.haplotype\_caller.vcf.gz

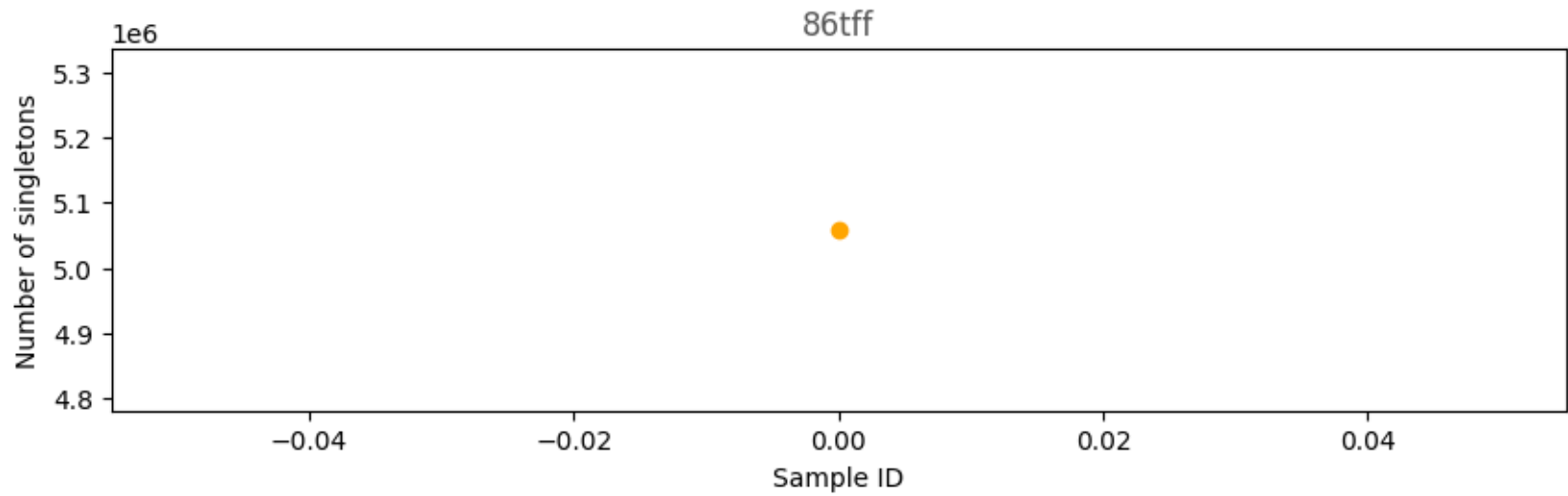
# Ts/Tv by sample



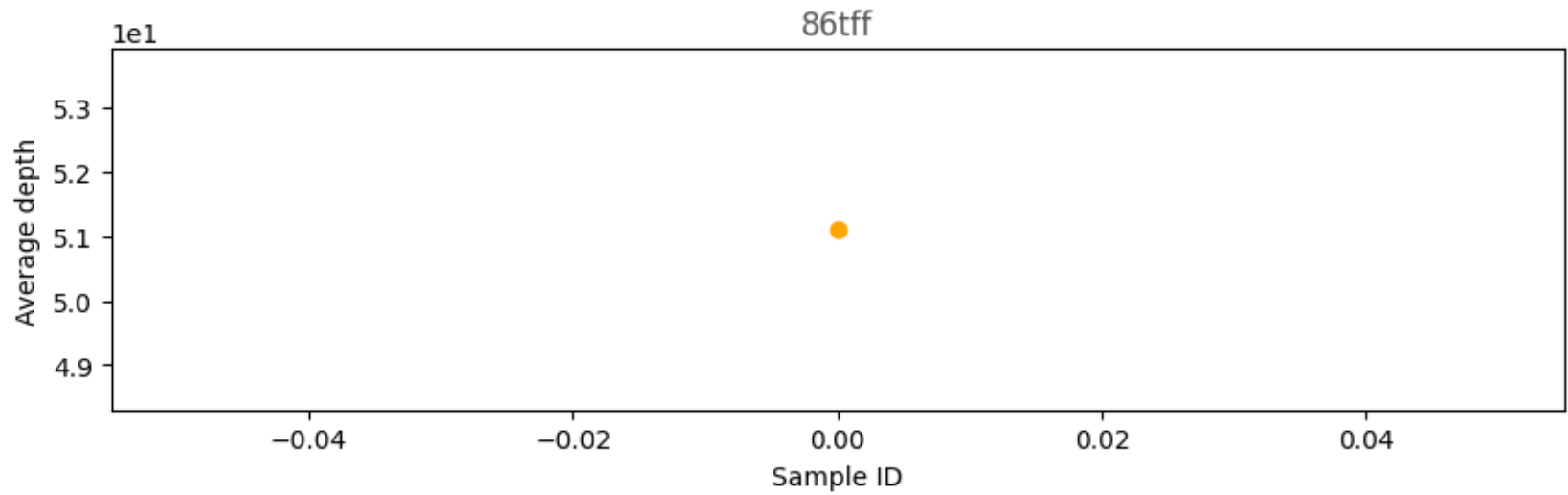
# Hets vs non-ref Homs by sample



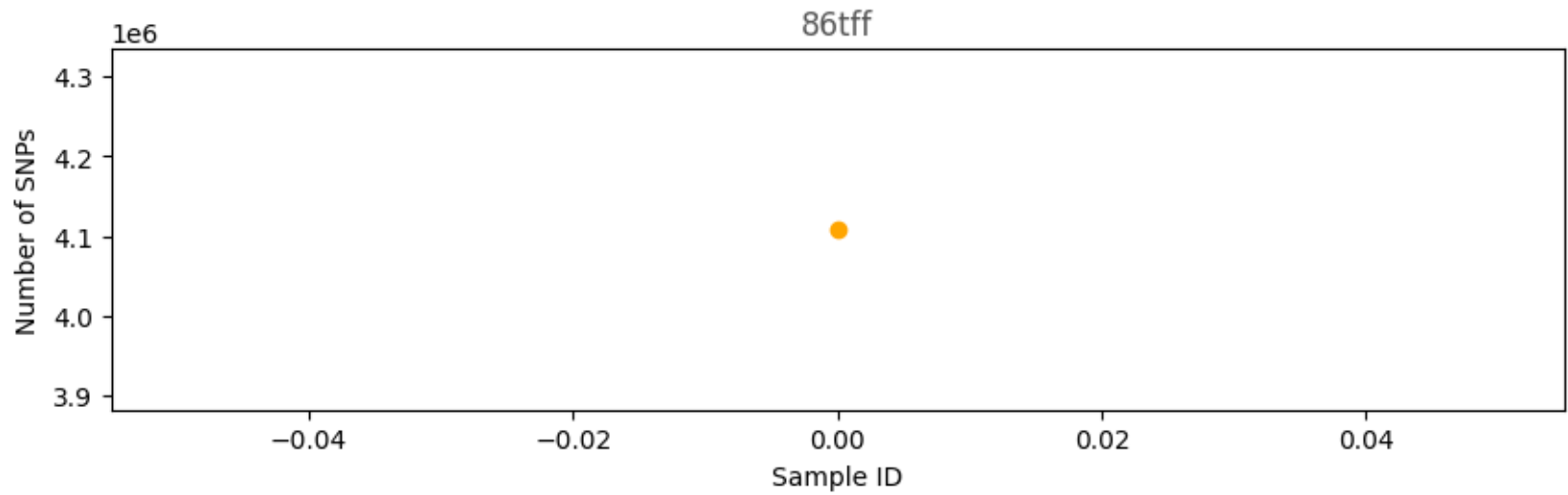
# Singletons by sample (hets and homs)



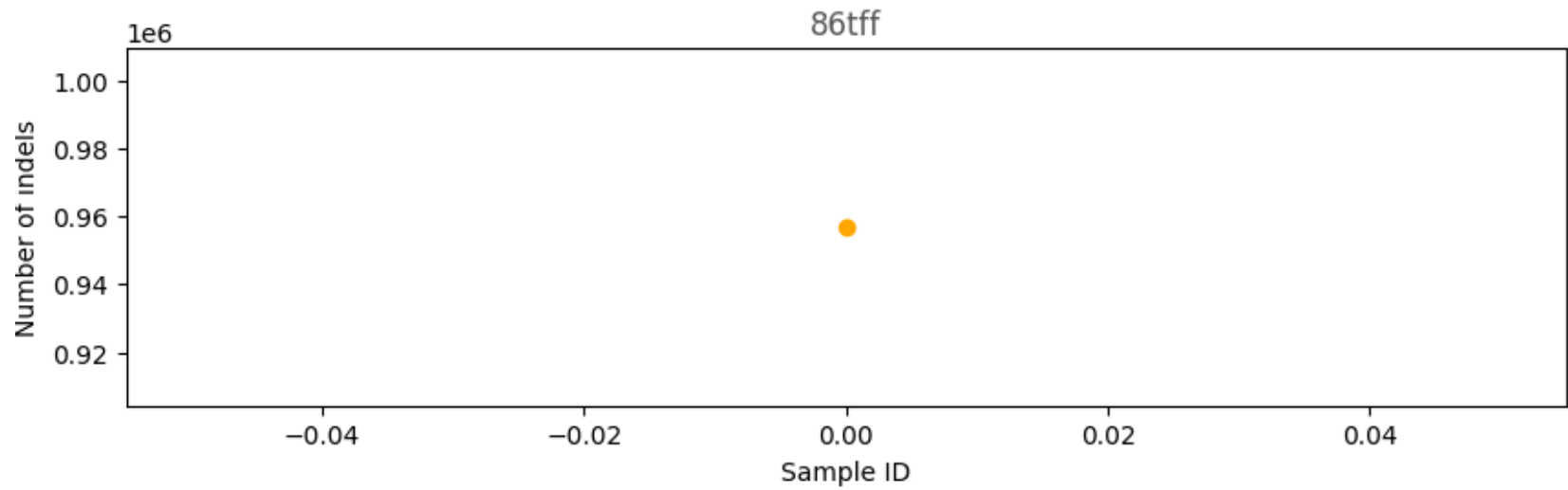
# Average depth by sample



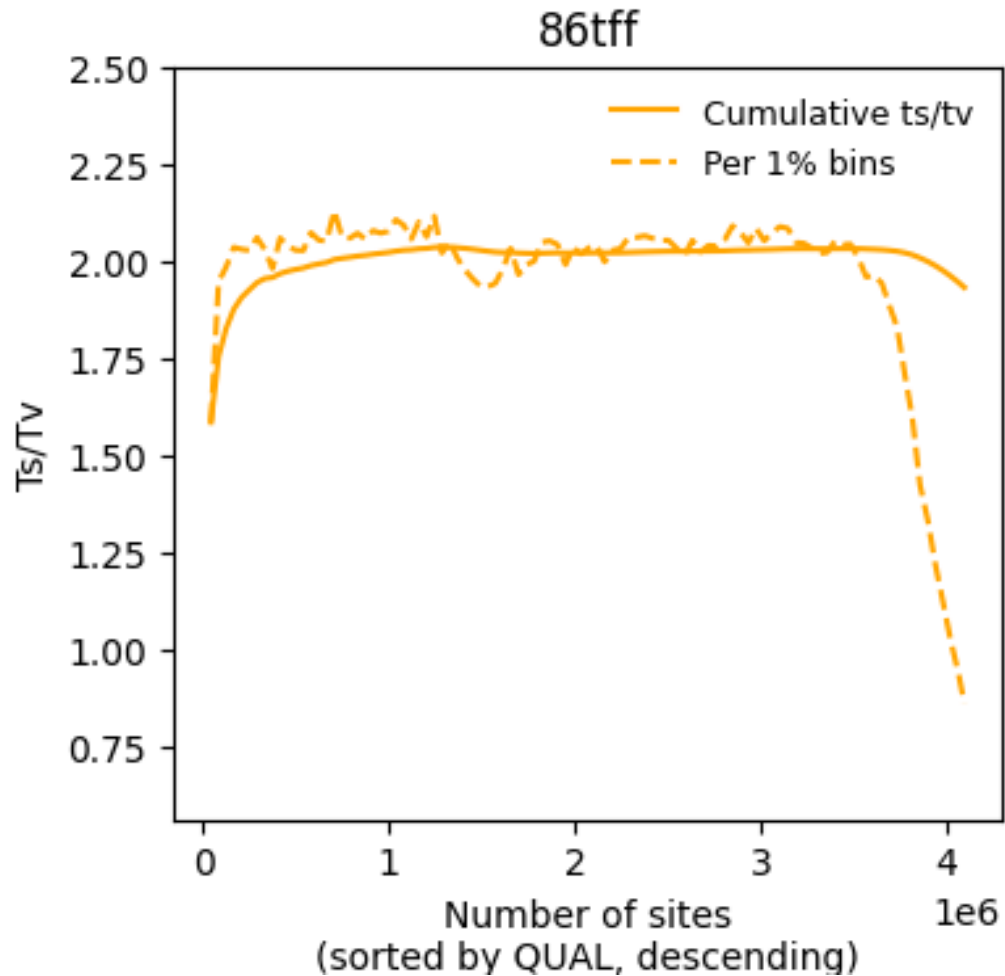
# Number of SNPs by sample



# Number of indels by sample

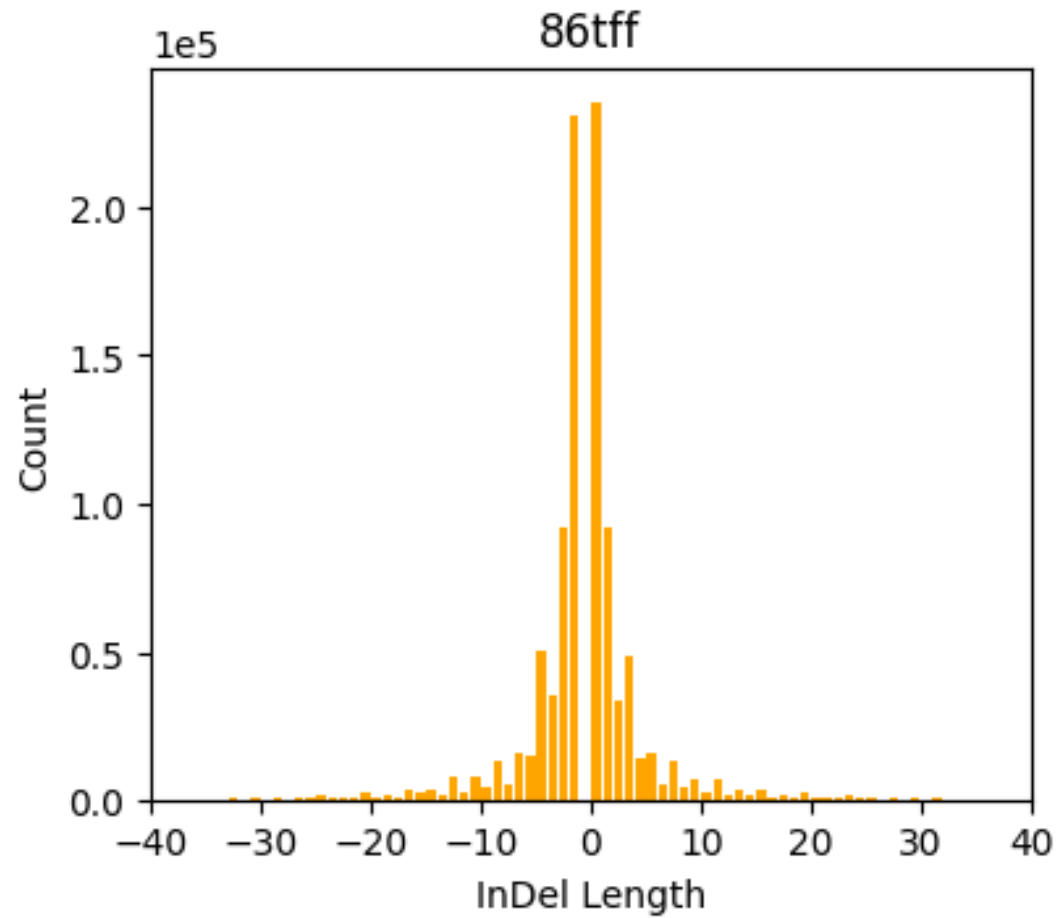


# Ts/Tv stratified by QUAL

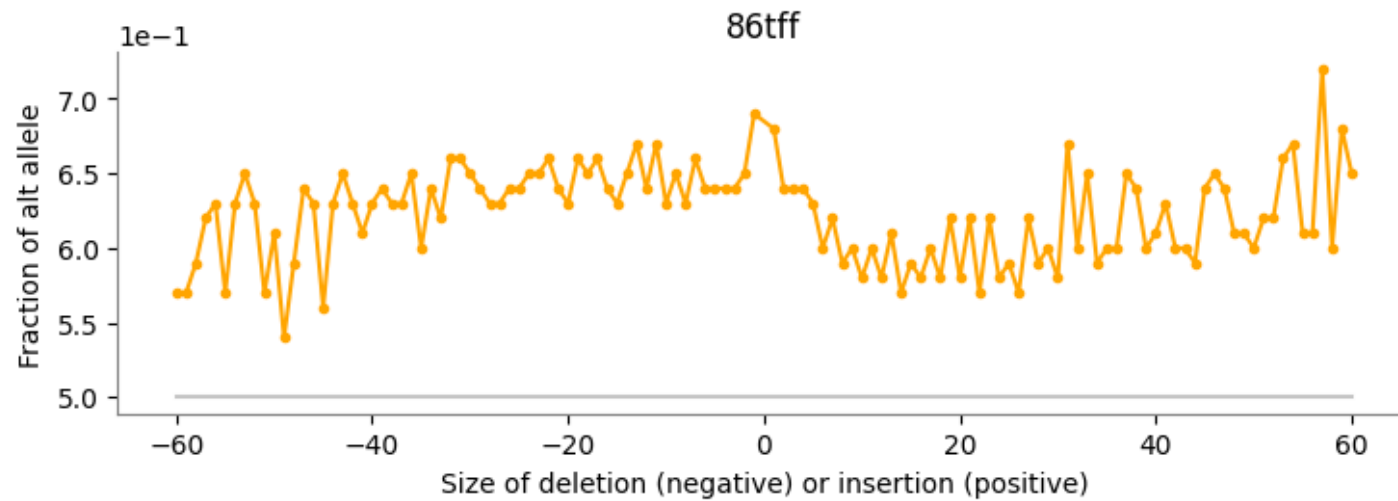




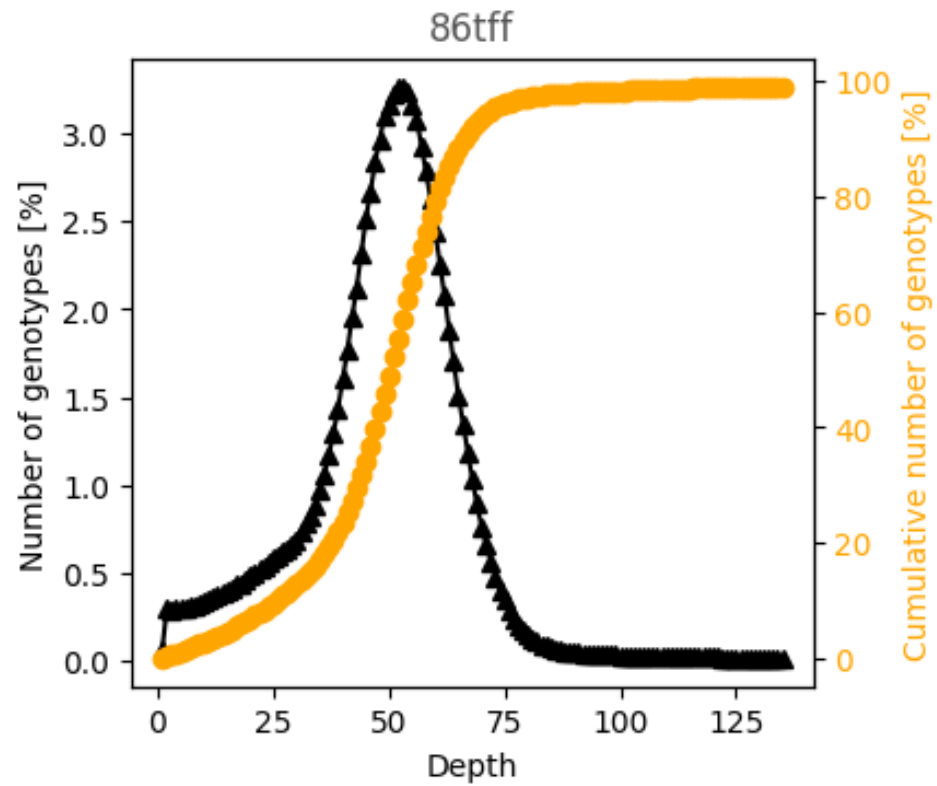
# Indel distribution



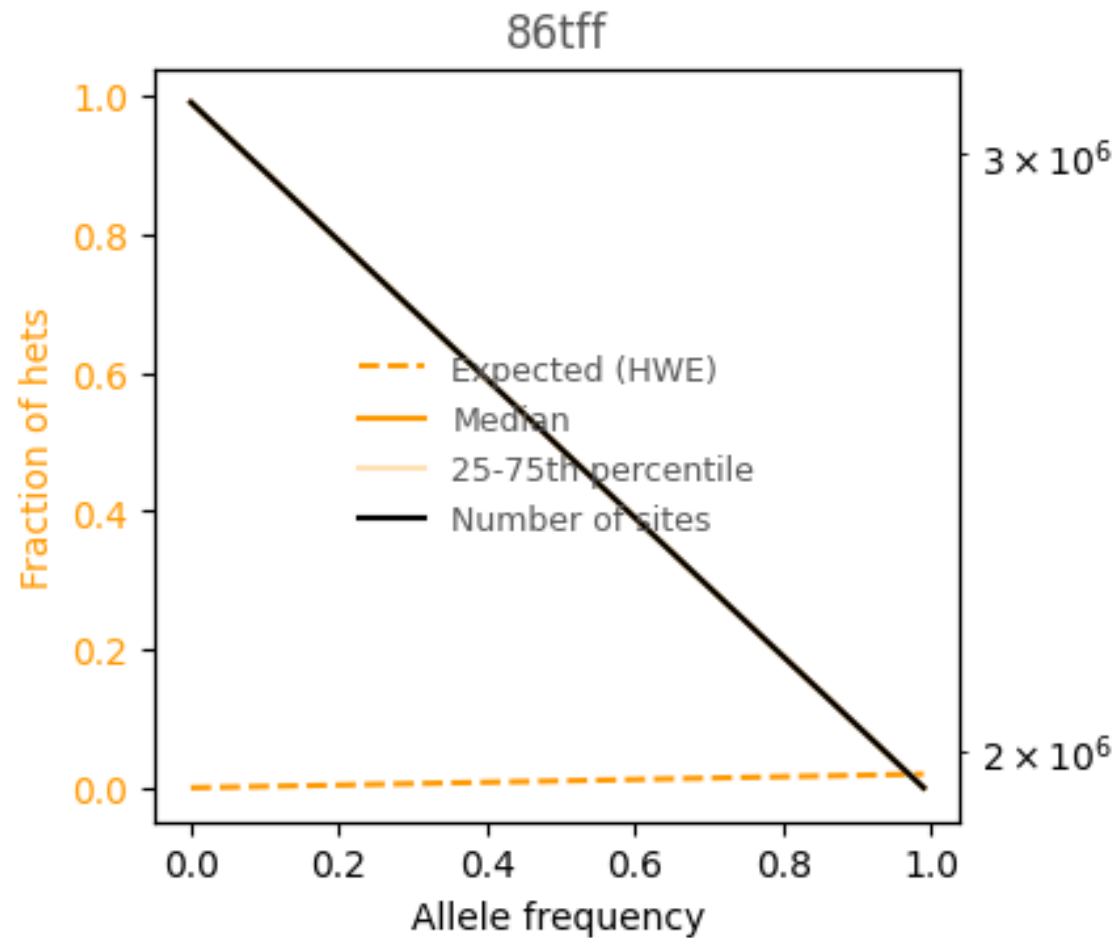
# Fraction of alternate indel allele



# Depth distribution



# Number of HETs by AF



# Substitution types

