

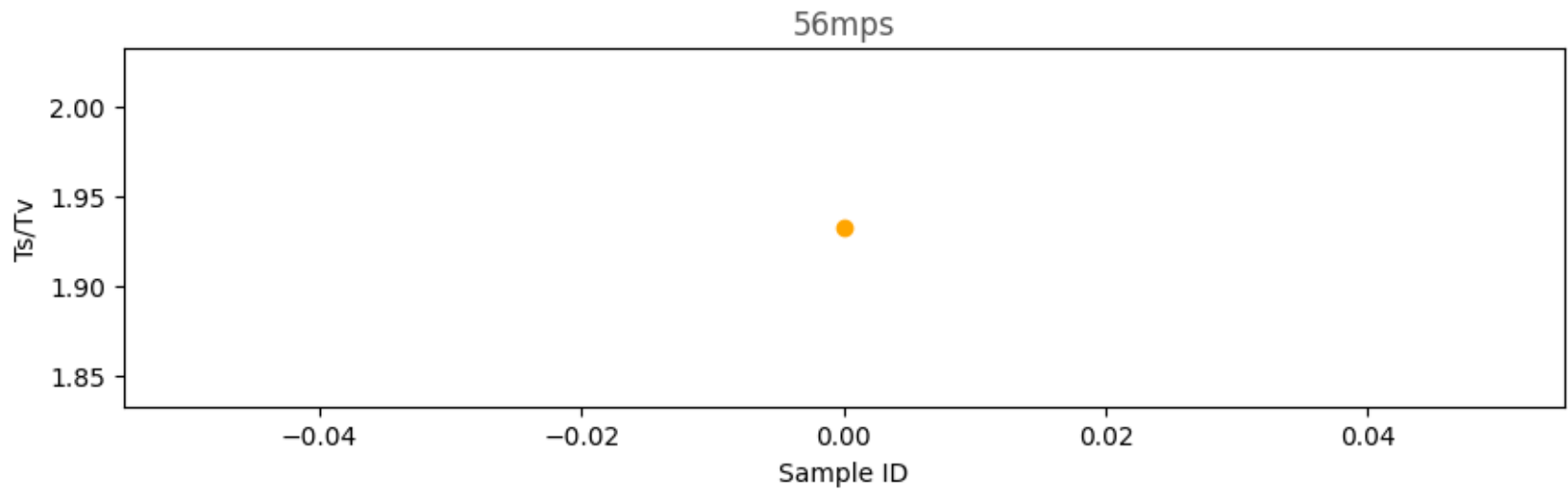
# Summary Numbers

Callset	SNPs			indels		MNPs	others
	n	ts/tv	(1st ALT)	n	frm*		
56mps	4,059,756	1.93	1.94	941,923	–	0	0
* frameshift ratio: out/(out+in)							

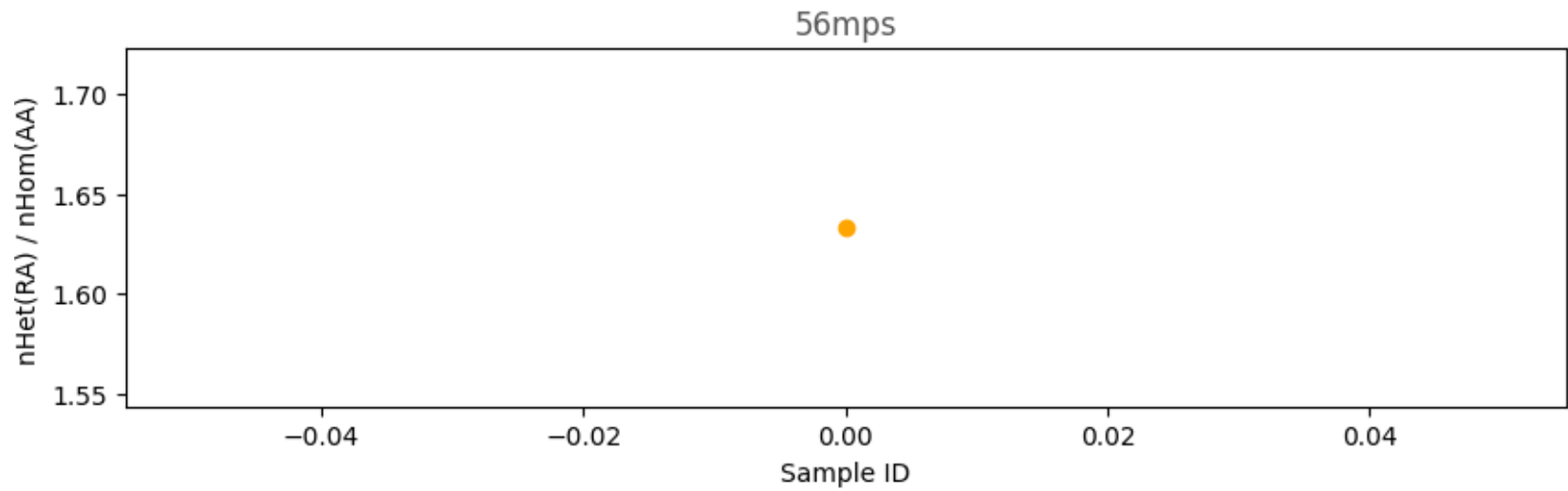
Callset	singletons (AC=1)			multiallelic	
	SNPs	ts/tv	indels	sites	SNPs
56mps	62.0%	1.90	66.5%	95,887	1,997

- 56mps .. /ngc/projects2/gm/data/archive/2022/variants/snv/56mpssom-103911873167-Normal\_B  
 lood\_noinfo-WGS\_v1\_IlluminaDNAPCRFree\_RHGM01631-220921\_A00559\_BHYLJMDSX3-EXT\_LAB  
 KA\_NGCWGS-NGCWGS05421\_22RKG022048\_snv\_germline\_raw.haplotype\_caller.vcf.gz

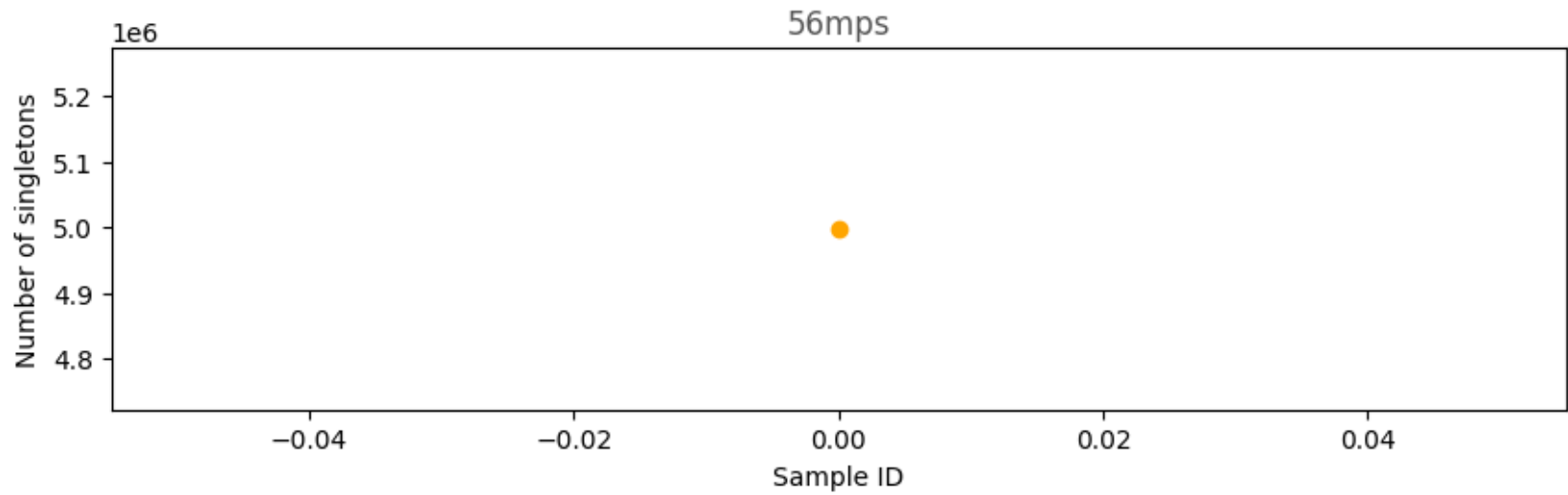
# Ts/Tv by sample



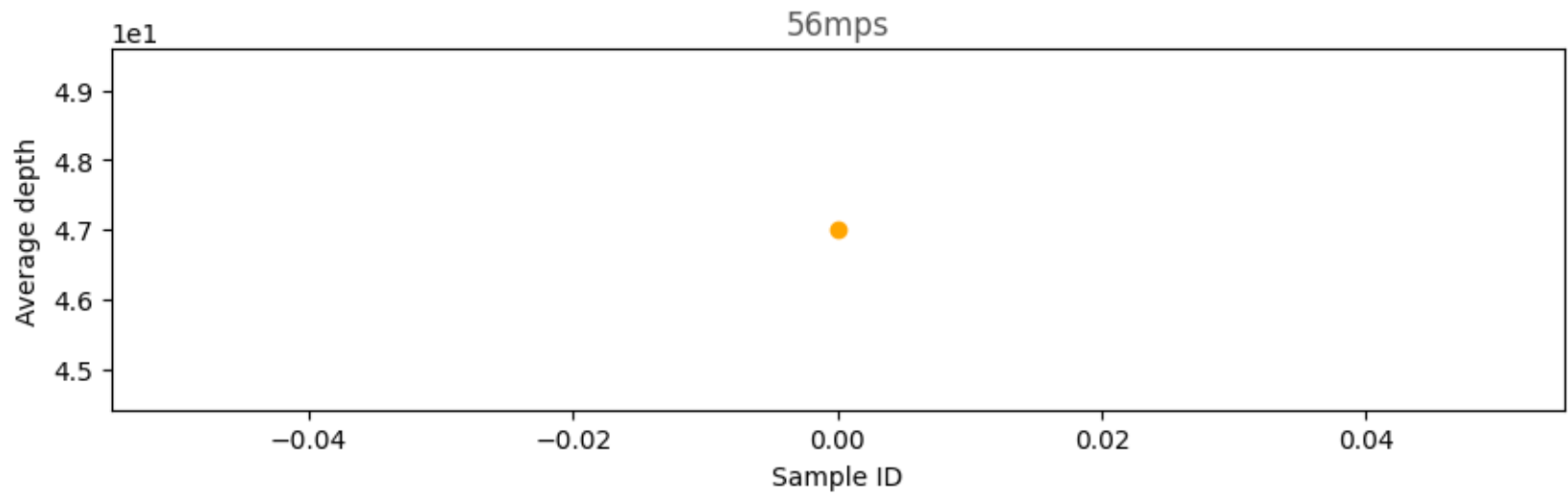
# Hets vs non-ref Homs by sample



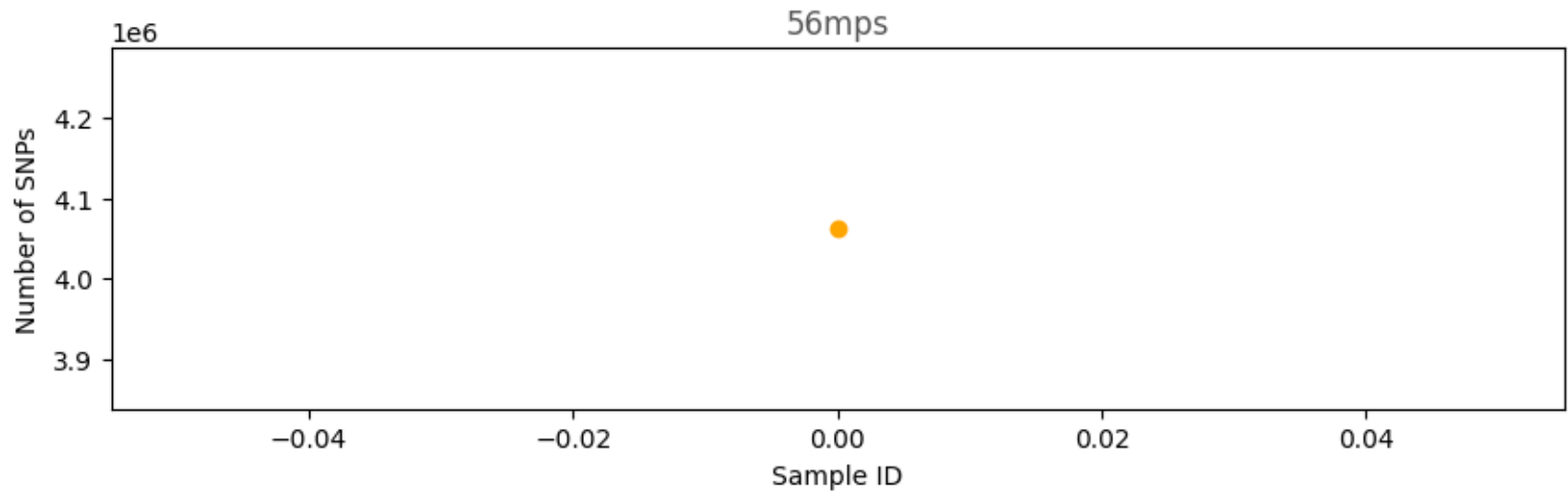
# Singletons by sample (hets and homs)



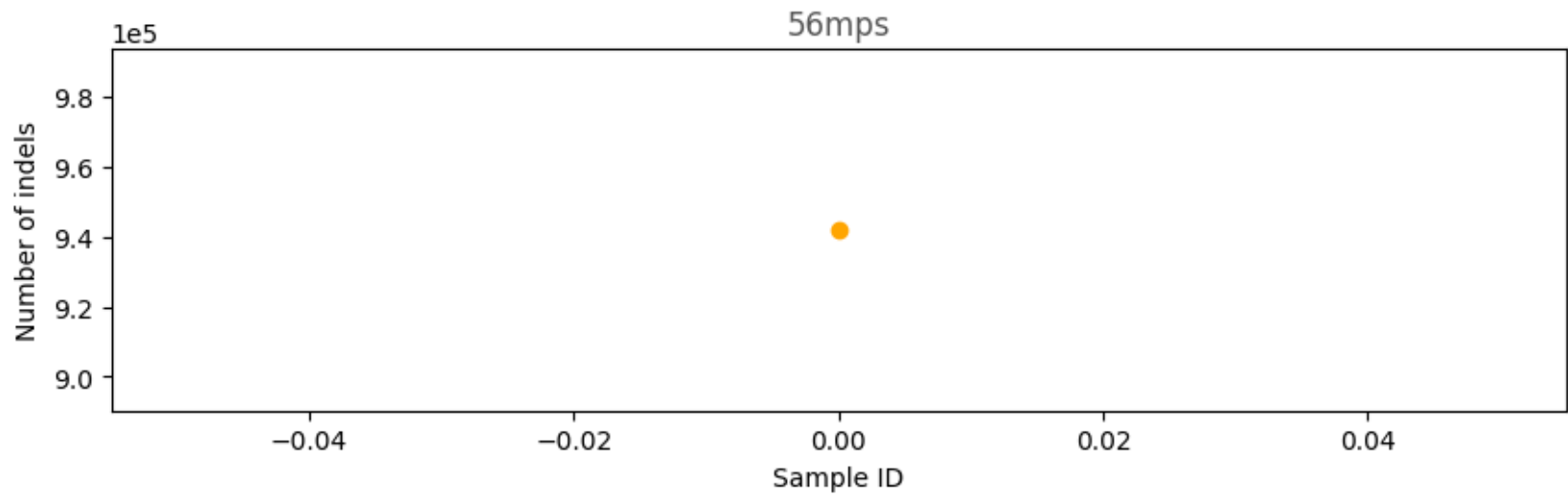
# Average depth by sample



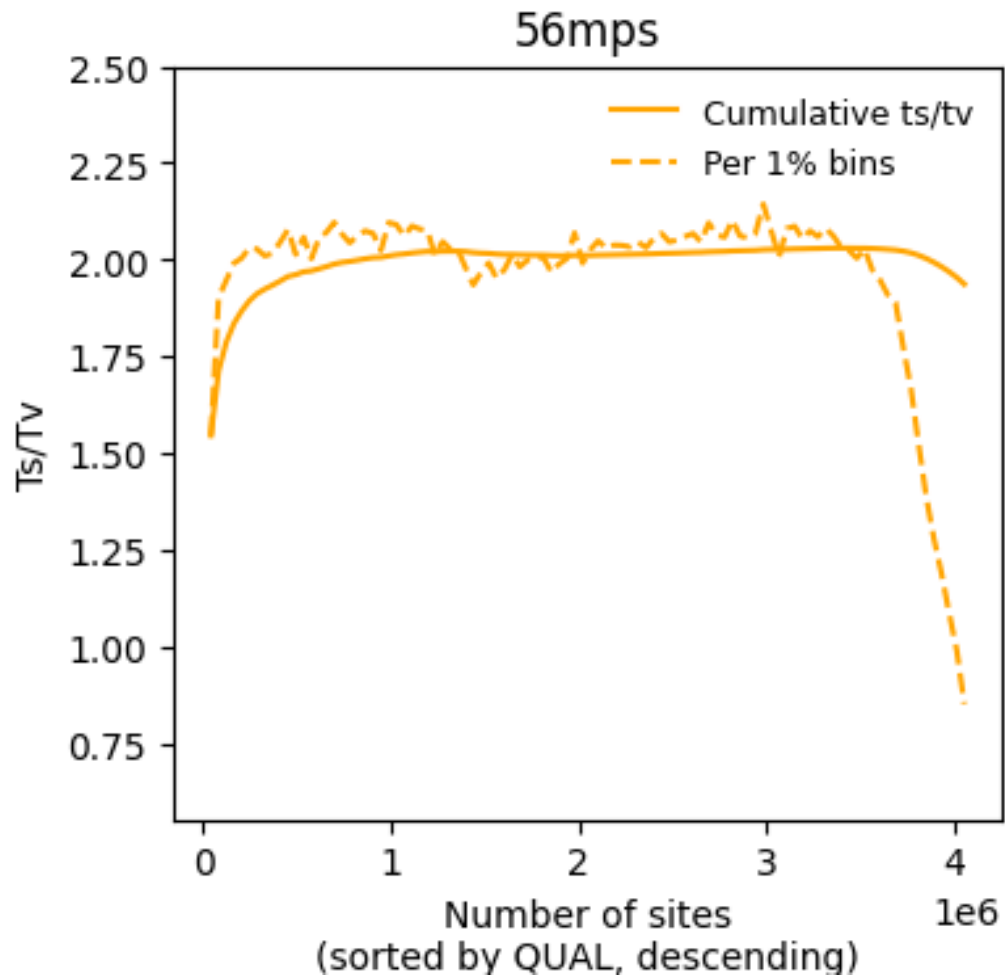
# Number of SNPs by sample



# Number of indels by sample

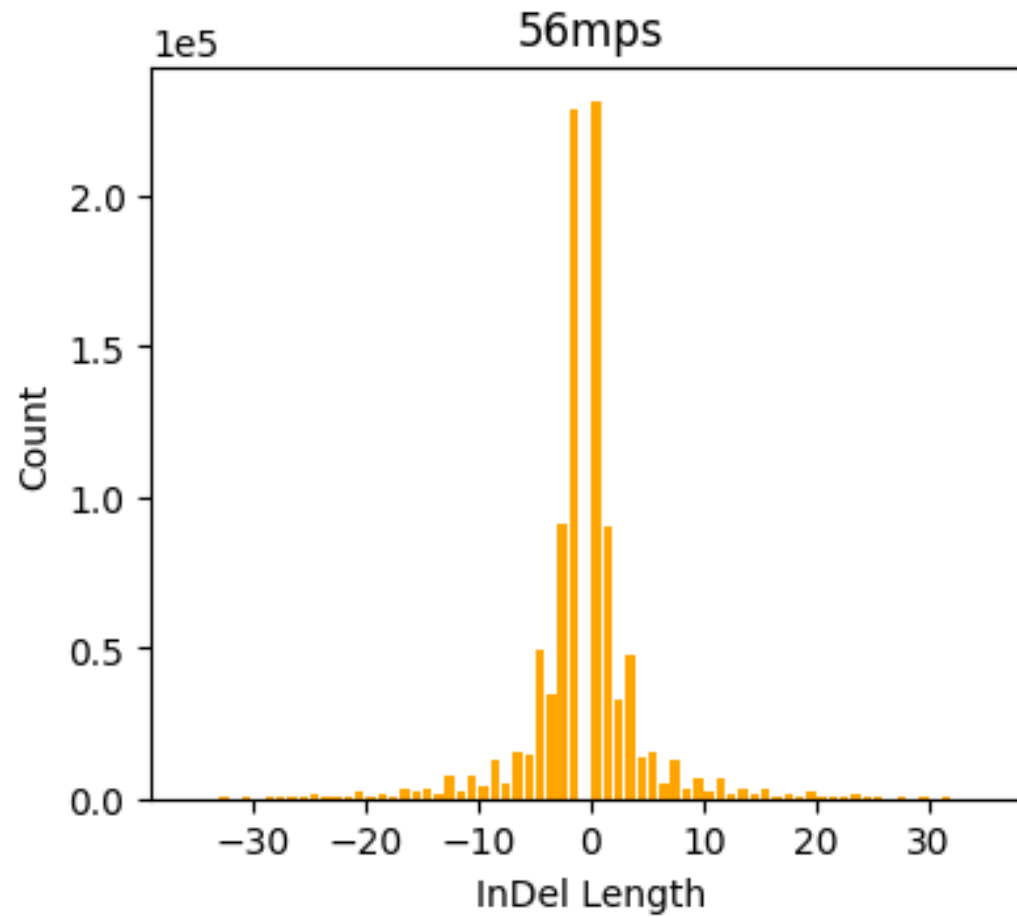


## Ts/Tv stratified by QUAL

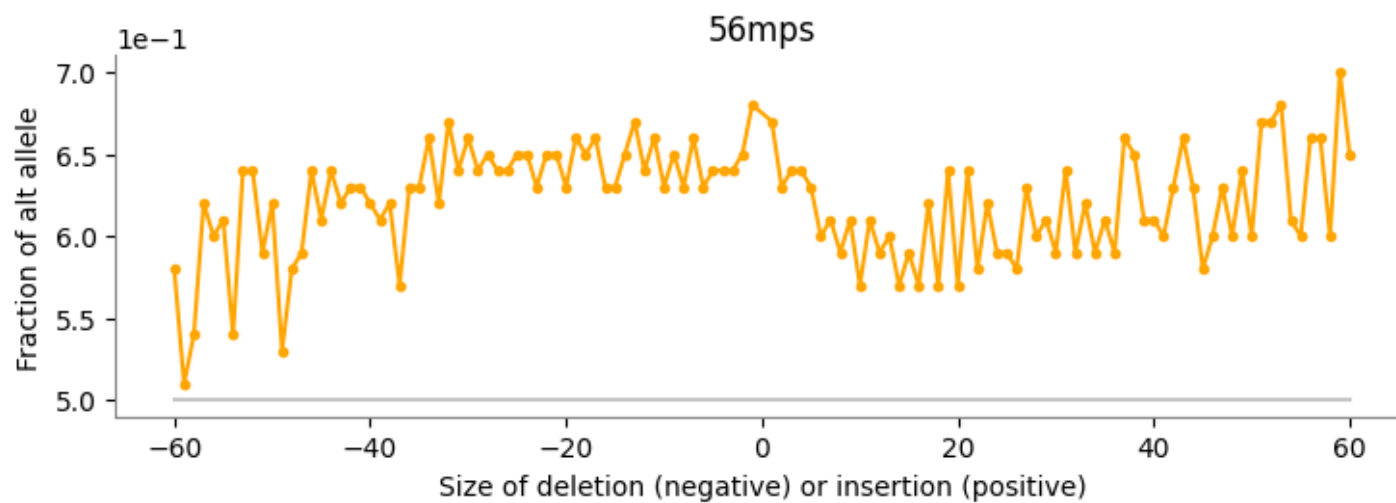




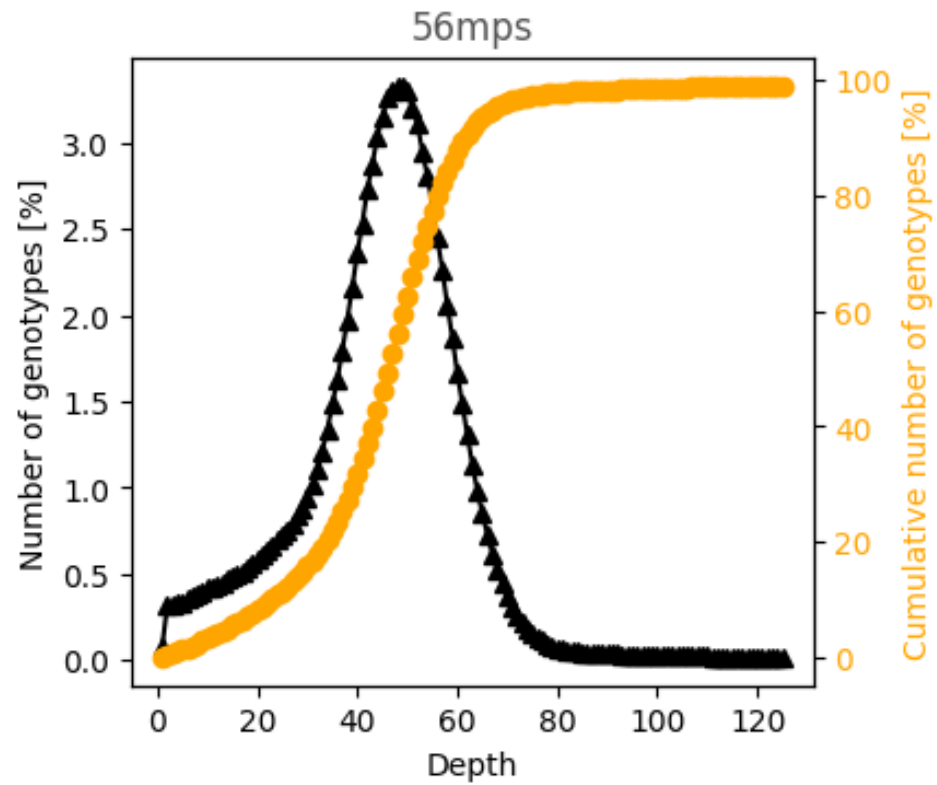
# Indel distribution



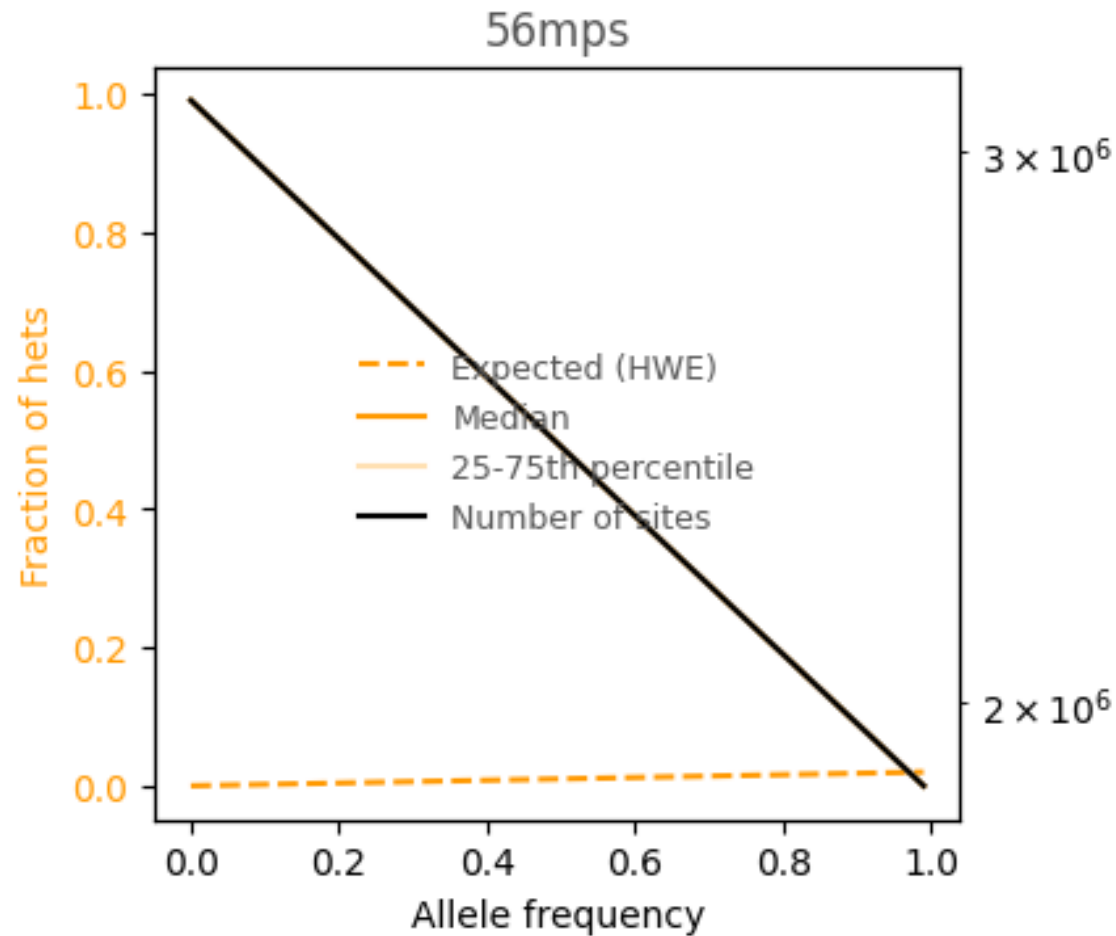
# Fraction of alternate indel allele



# Depth distribution



# Number of HETs by AF



# Substitution types

