

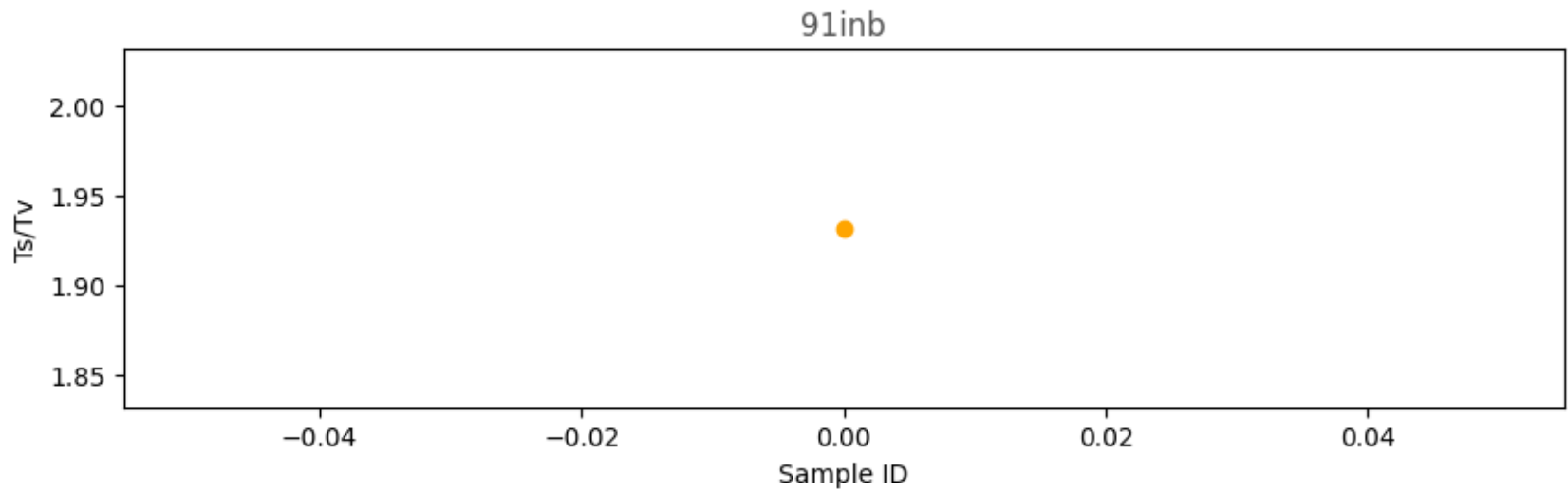
# Summary Numbers

Callset	SNPs			indels		MNPs	others
	n	ts/tv	(1st ALT)	n	frm*		
91inb	4,027,980	1.93	1.94	937,954	–	0	0
* frameshift ratio: out/(out+in)							

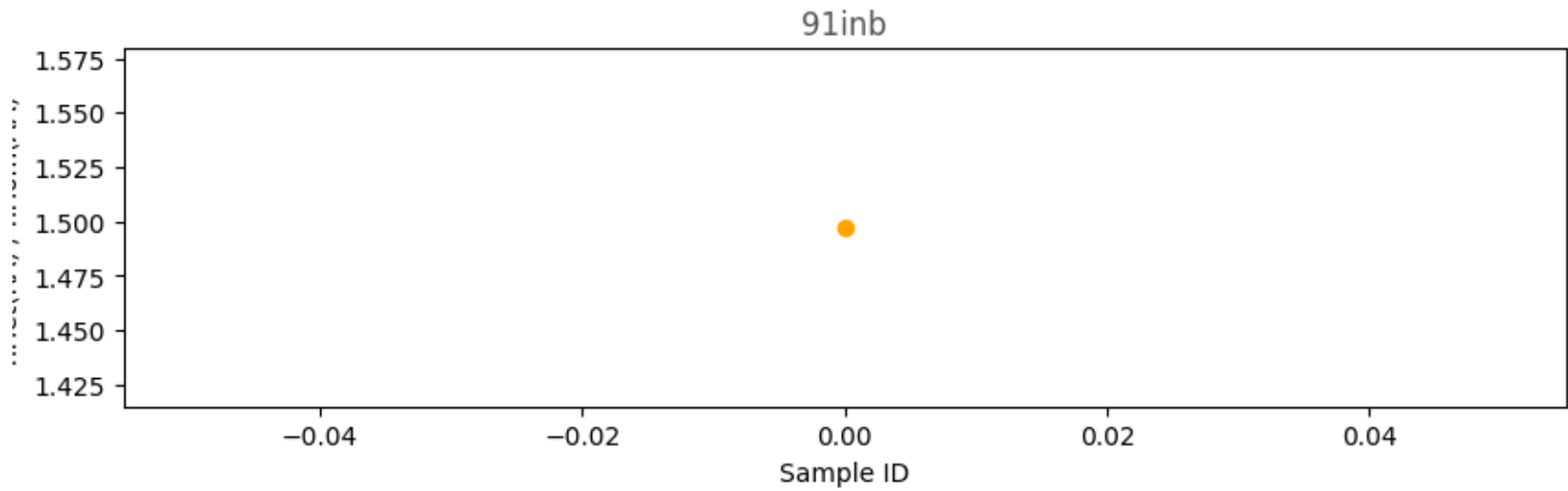
Callset	singletons (AC=1)			multiallelic	
	SNPs	ts/tv	indels	sites	SNPs
91inb	60.0%	1.89	64.2%	93,513	1,807

- 91inb .. /ngc/projects2/gm/data/archive/2022/variants/snv/91inbryrm-103836014445-Normal\_B  
 lood\_noinfo-WGS\_v1\_IlluminaDNAPCRFree\_RHGM00599-220225\_A01176\_AH7CT5DSX3-EXT\_LAB  
 KA\_NGCWGS-NGCWGS03876\_21RKG031957x01\_snv\_germline\_raw.haplotype\_caller.vcf.gz

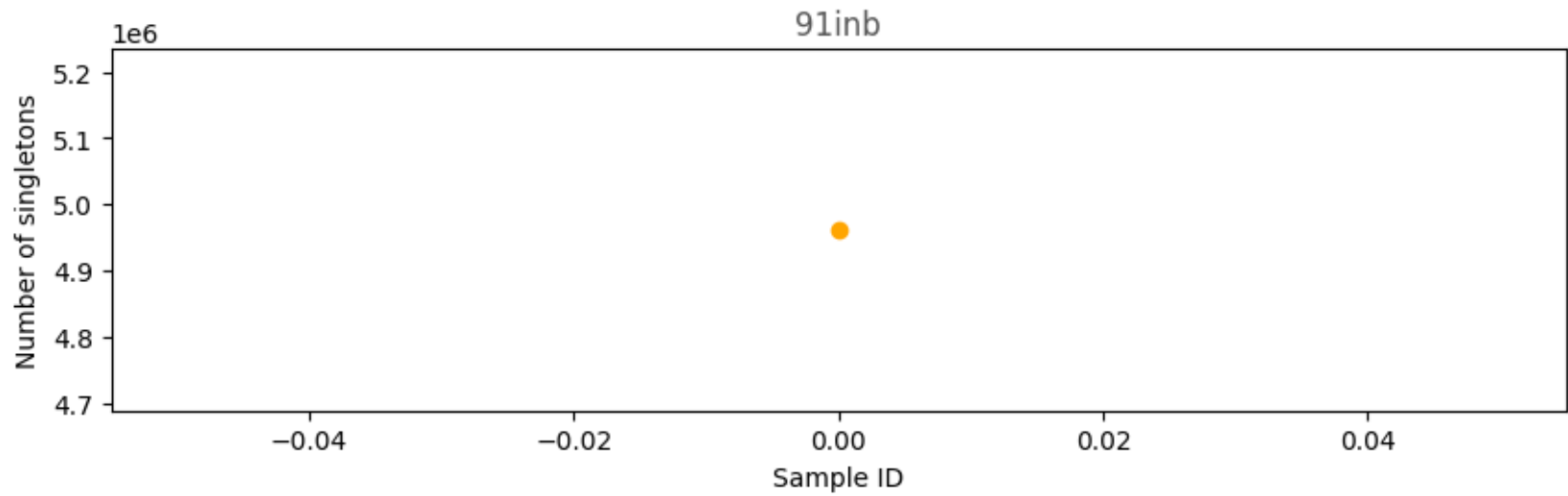
# Ts/Tv by sample



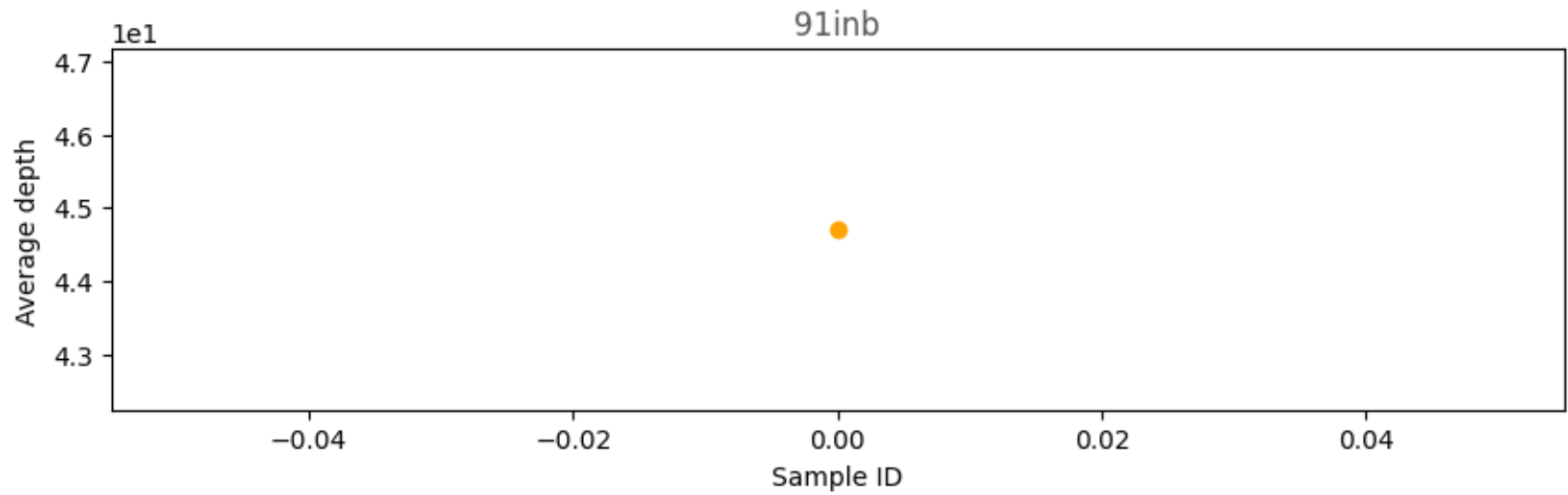
# Hets vs non-ref Homs by sample



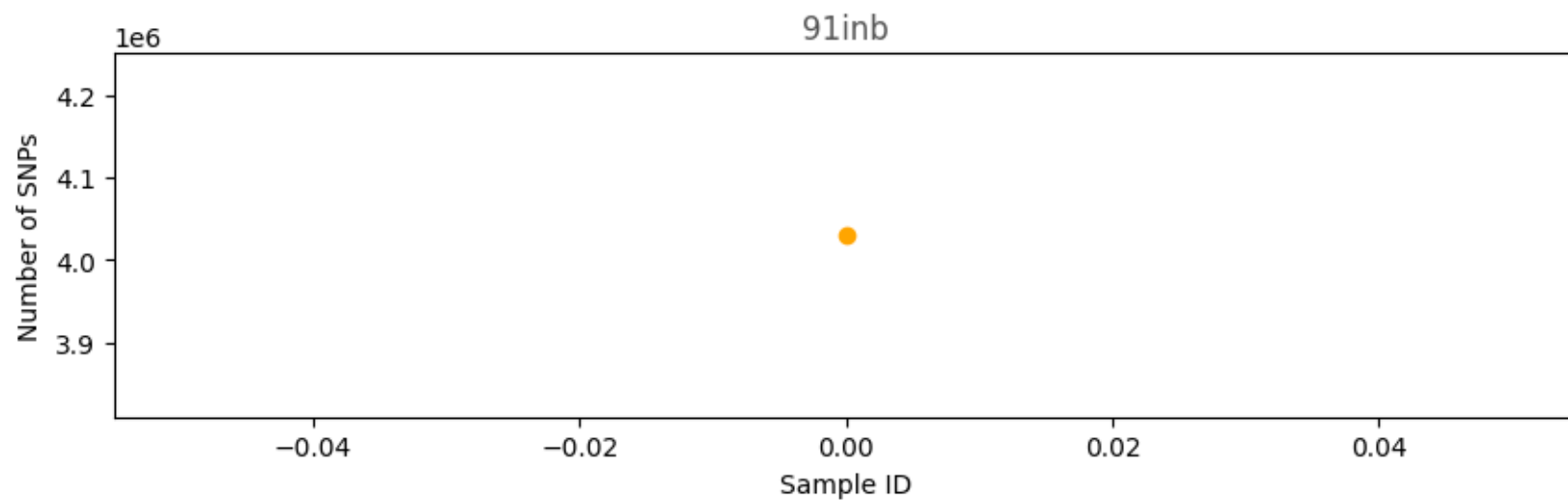
# Singletons by sample (hets and homs)



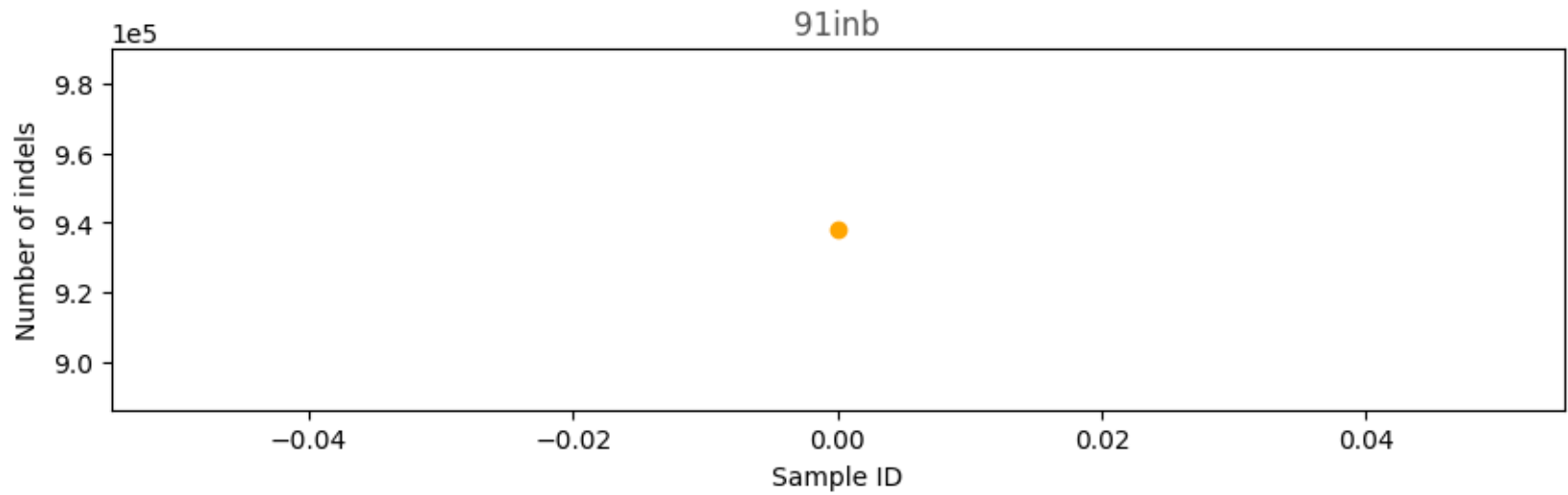
# Average depth by sample



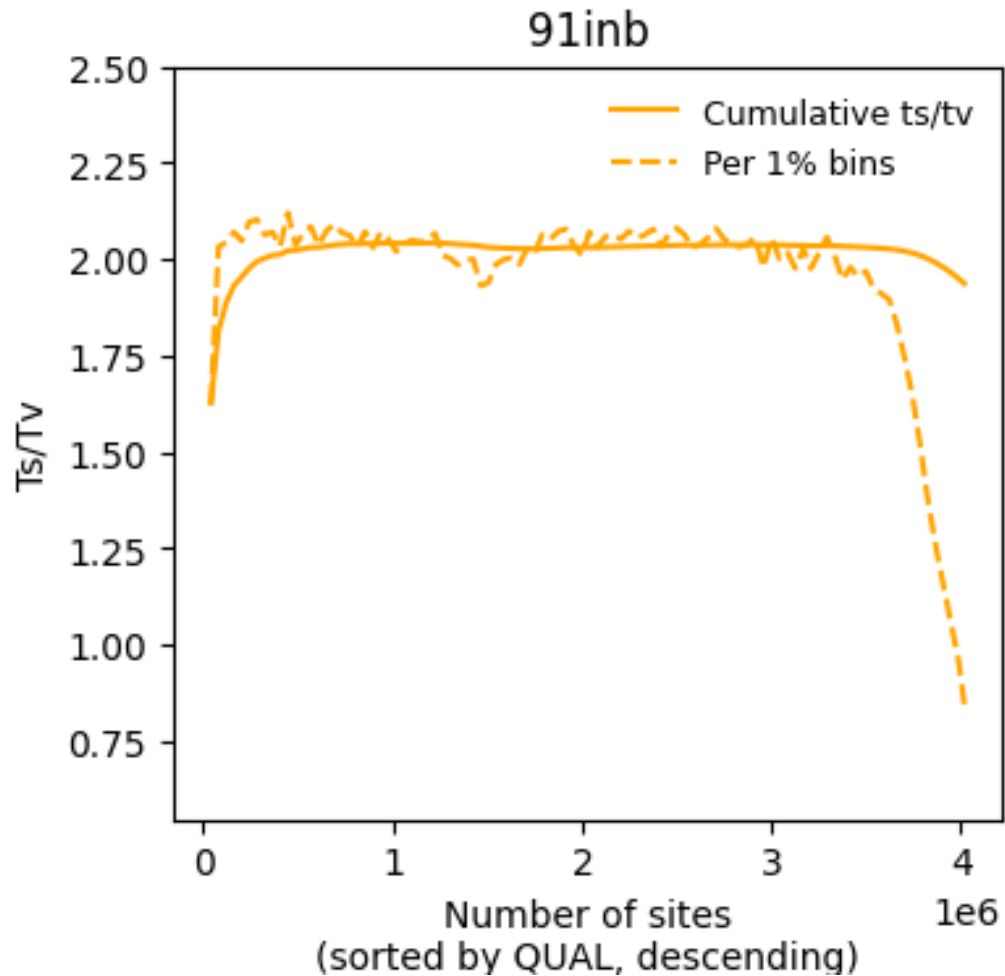
# Number of SNPs by sample



# Number of indels by sample

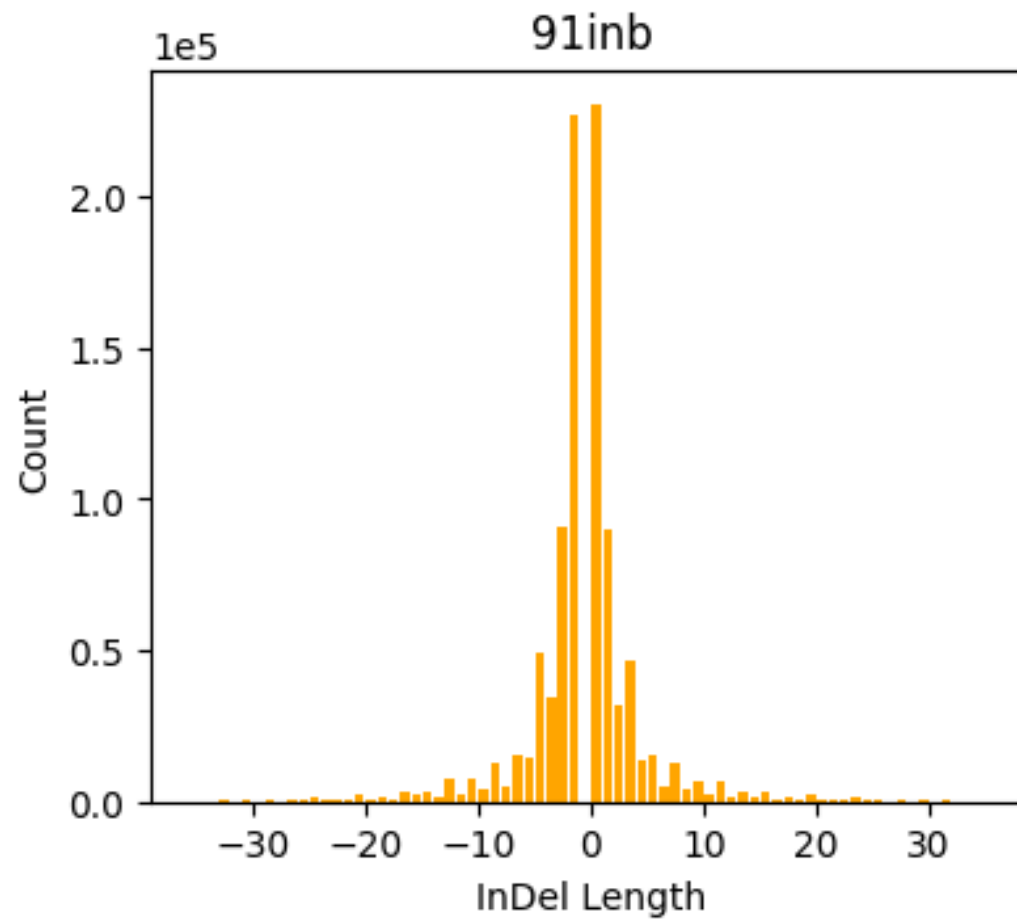


## Ts/Tv stratified by QUAL

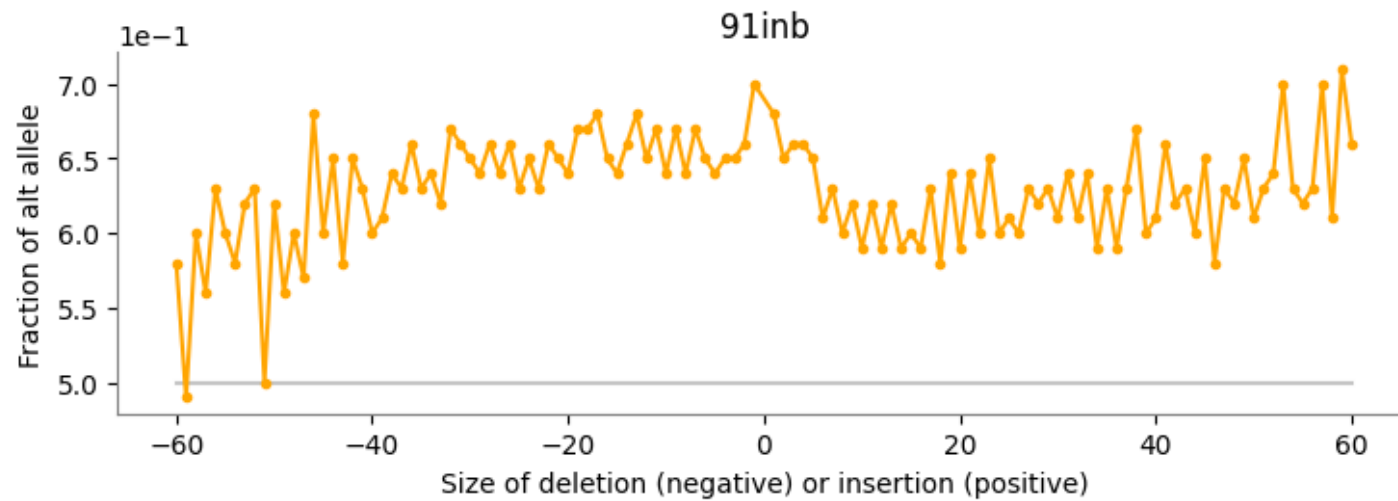




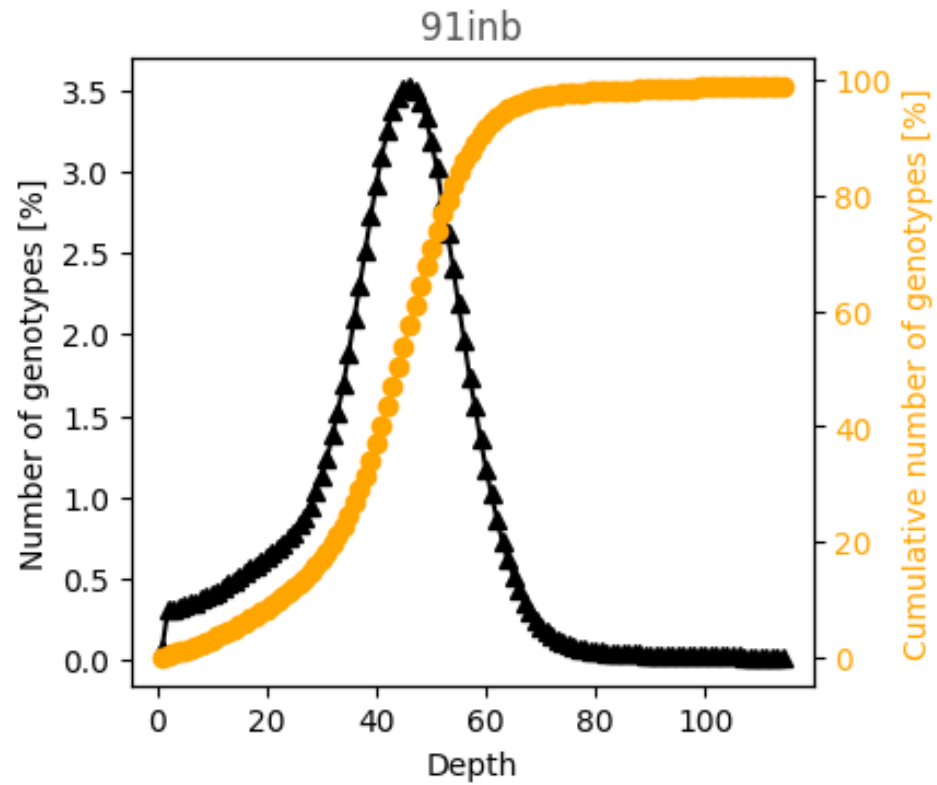
# Indel distribution



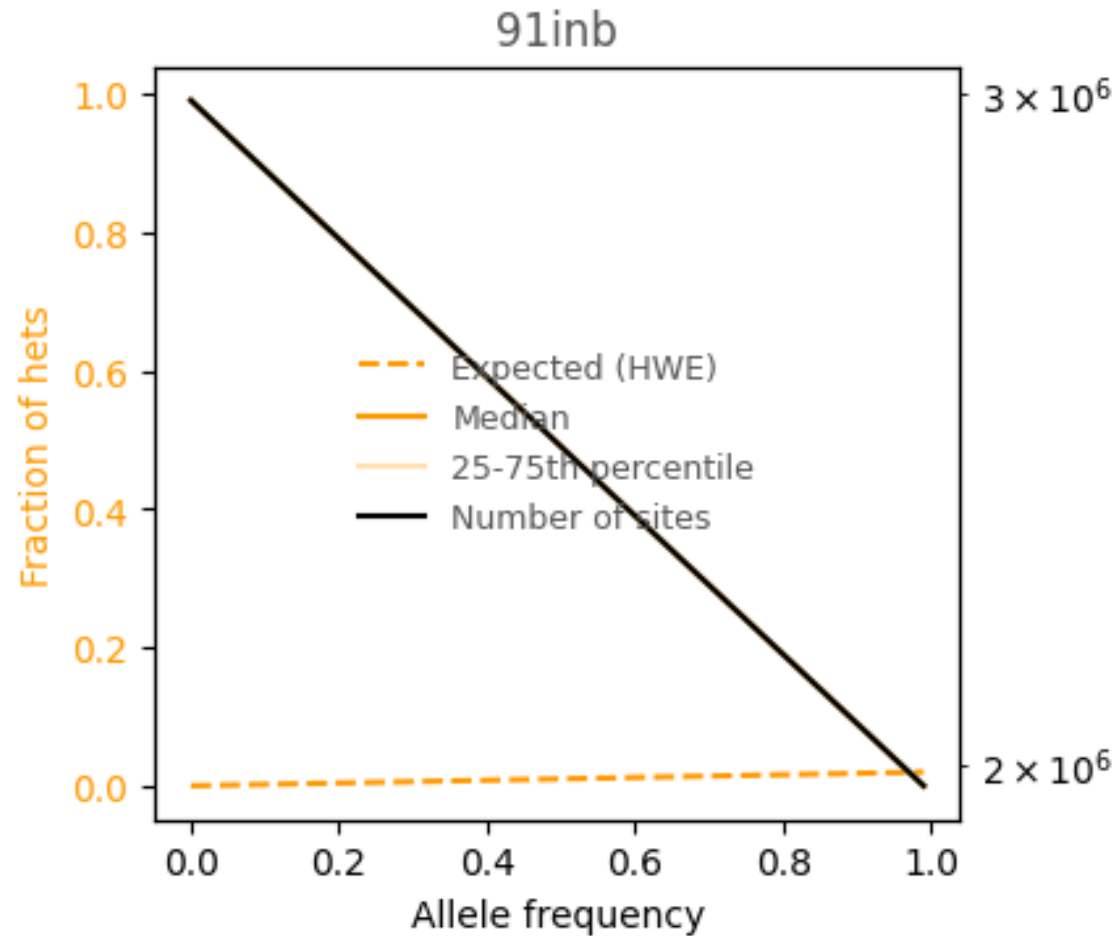
# Fraction of alternate indel allele



# Depth distribution



# Number of HETs by AF



# Substitution types

