

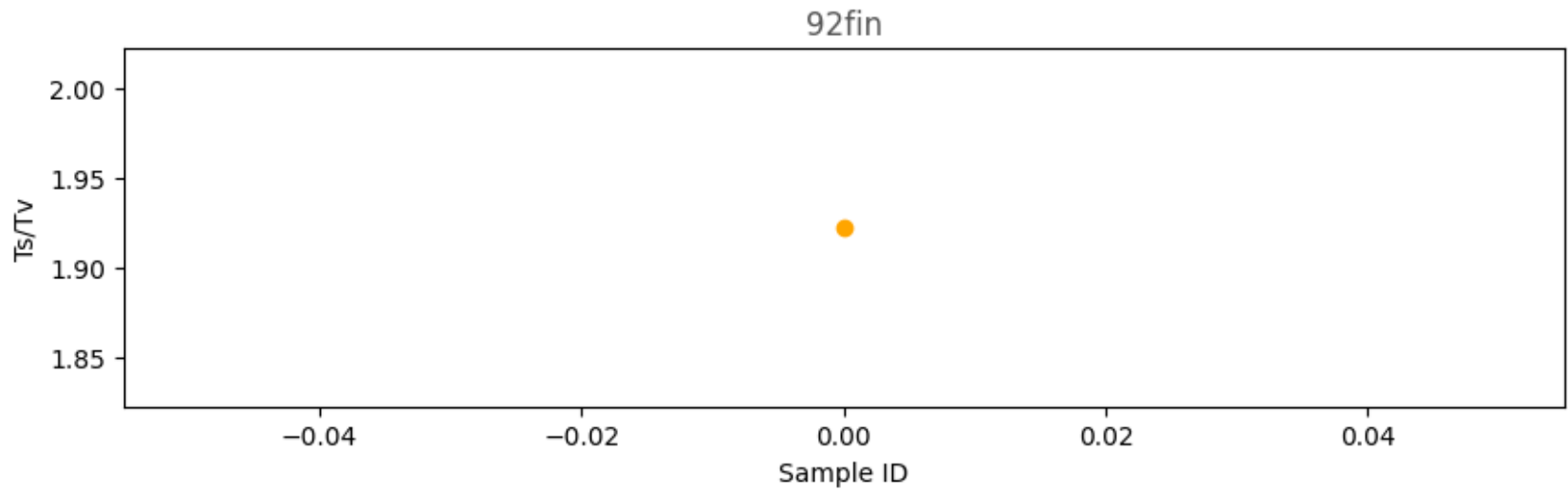
# Summary Numbers

Callset	SNPs			indels		MNPs	others
	n	ts/tv	(1st ALT)	n	frm*		
92fin	4,092,383	1.92	1.93	958,942	–	0	0
* frameshift ratio: out/(out+in)							

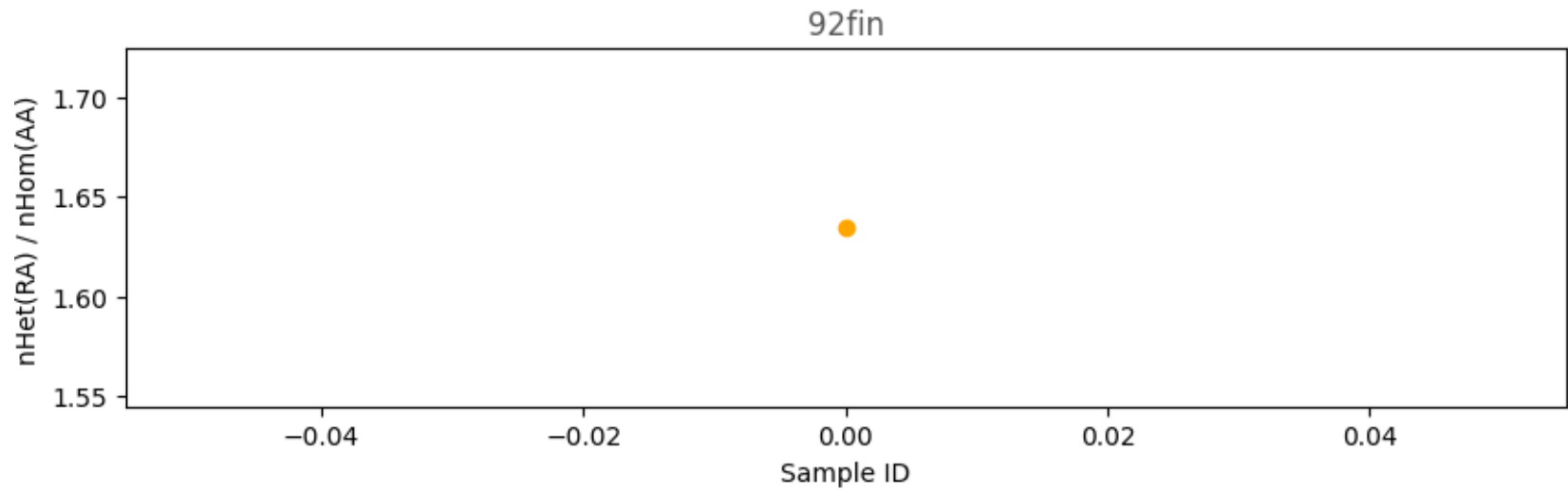
Callset	singletons (AC=1)			multiallelic	
	SNPs	ts/tv	indels	sites	SNPs
92fin	62.1%	1.89	67.4%	104,145	2,046

- 92fin .. /ngc/projects2/gm/data/archive/2022/variants/snv/92finprem-103825131445-Normal\_Blood\_noinfo-WGS\_v1\_IlluminaDNAPCRFree\_X-220107\_A01176\_BH5TGWDSX3-RHGM\_LABKA\_WGSA\_KUT-WGSAKUT03639\_22RKG000122x01\_snv\_germline\_raw.haplotype\_caller.vcf.gz

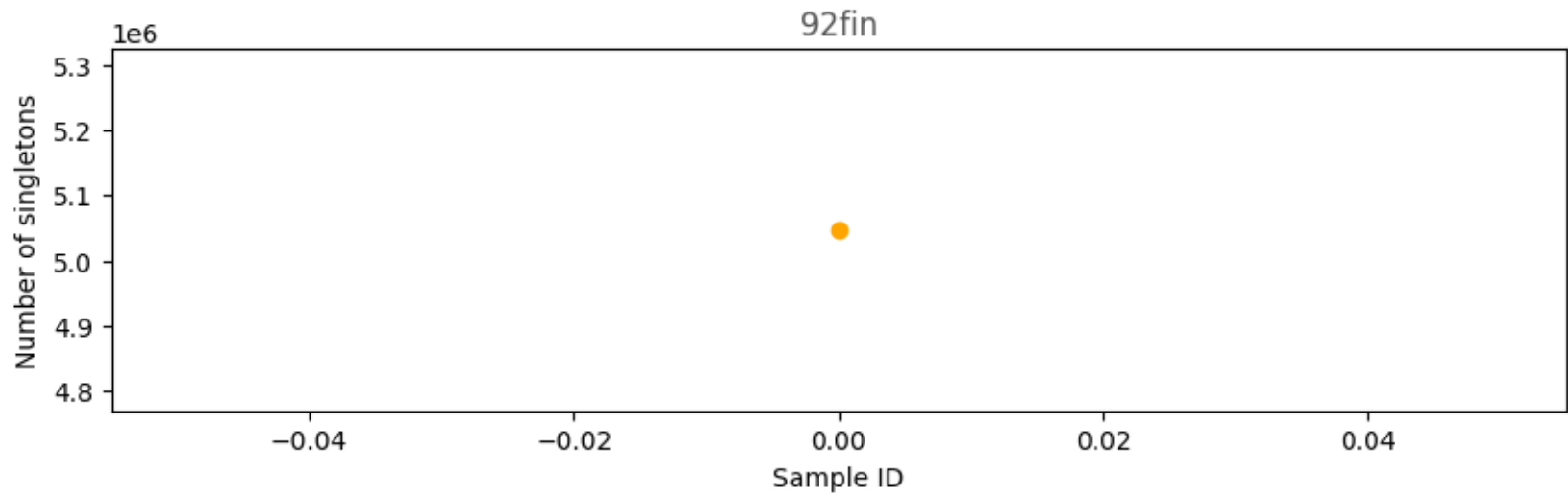
# Ts/Tv by sample



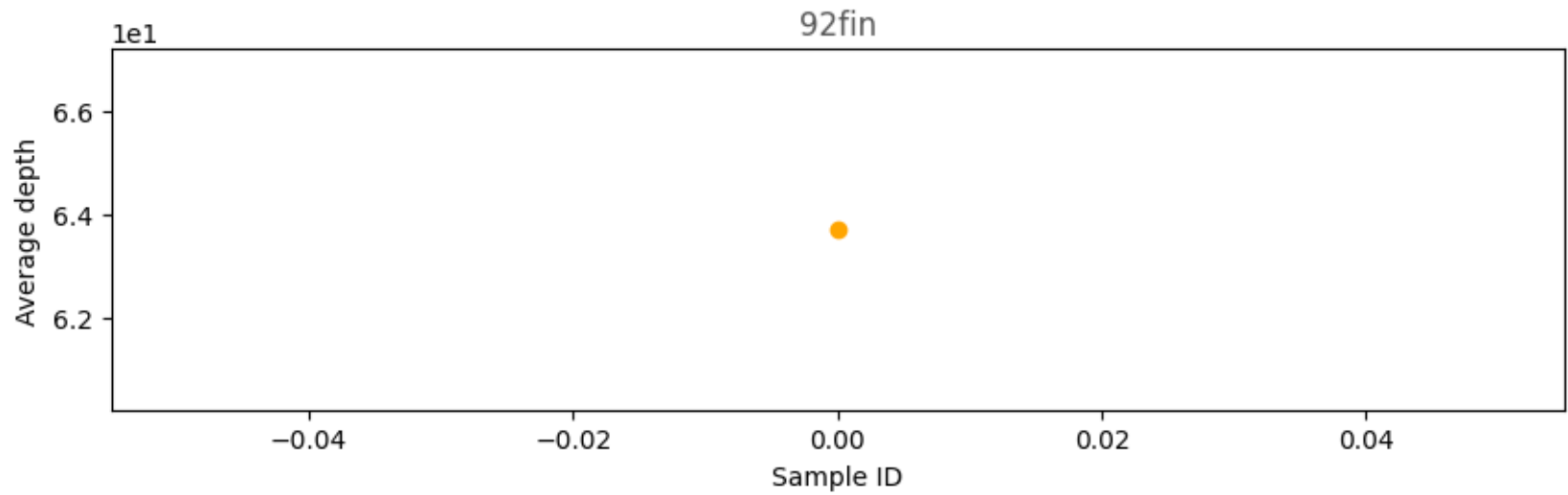
# Hets vs non-ref Homs by sample



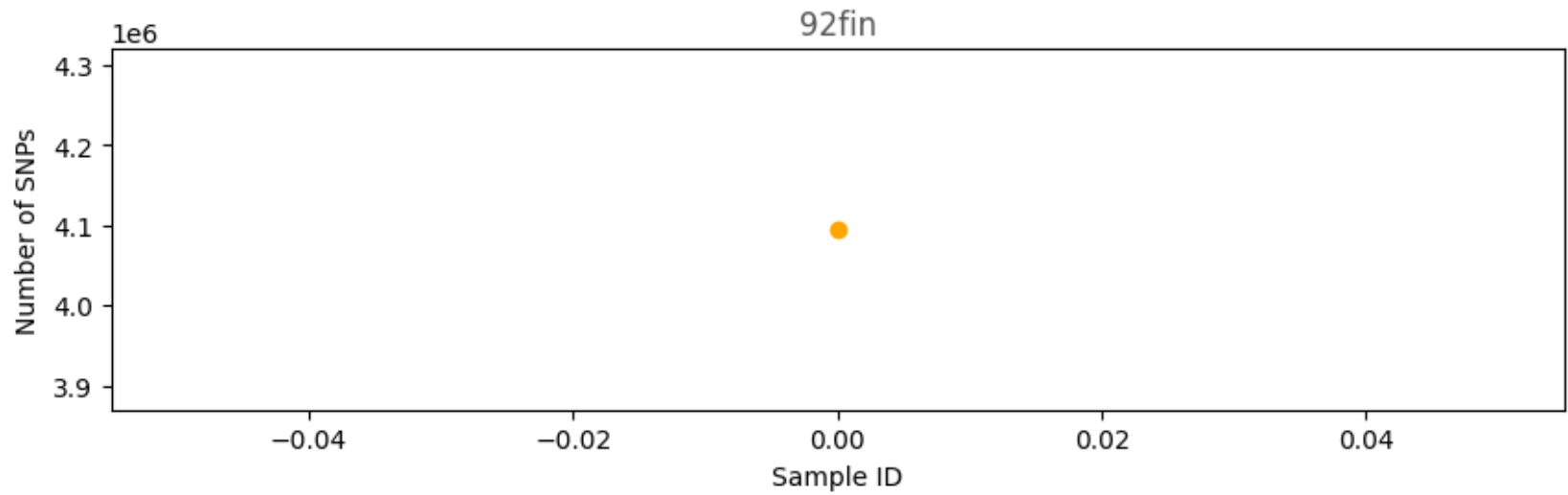
# Singletons by sample (hets and homs)



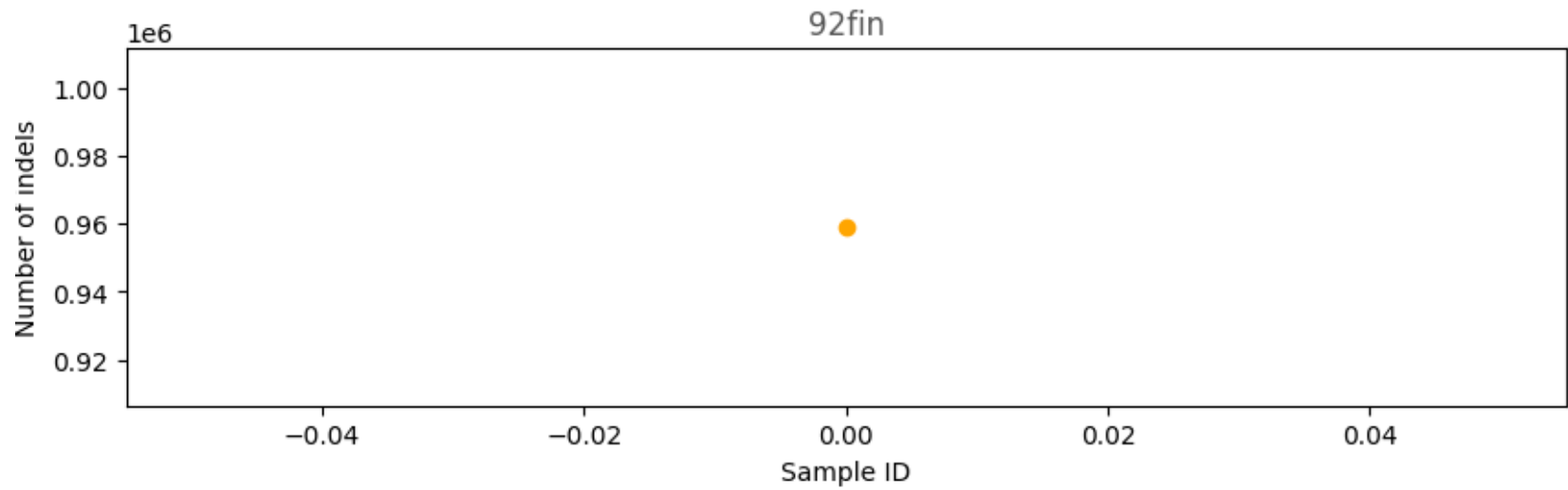
# Average depth by sample



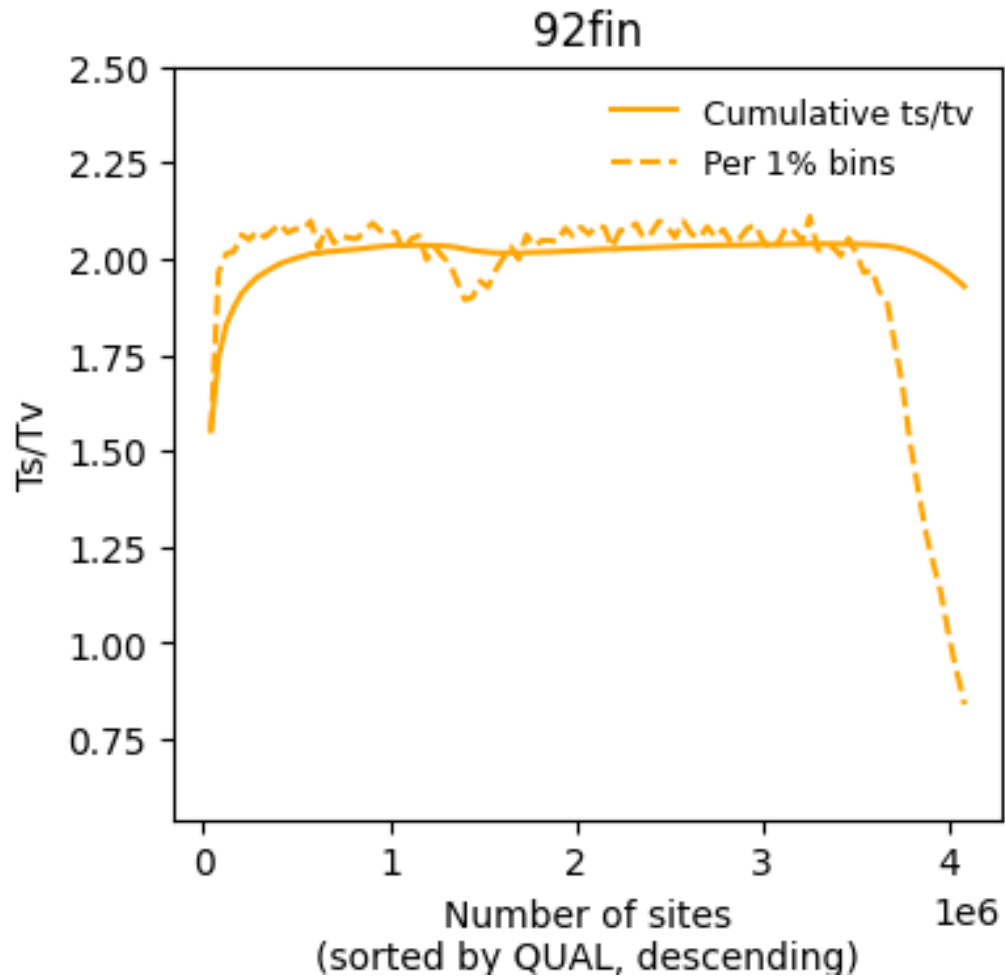
# Number of SNPs by sample



# Number of indels by sample

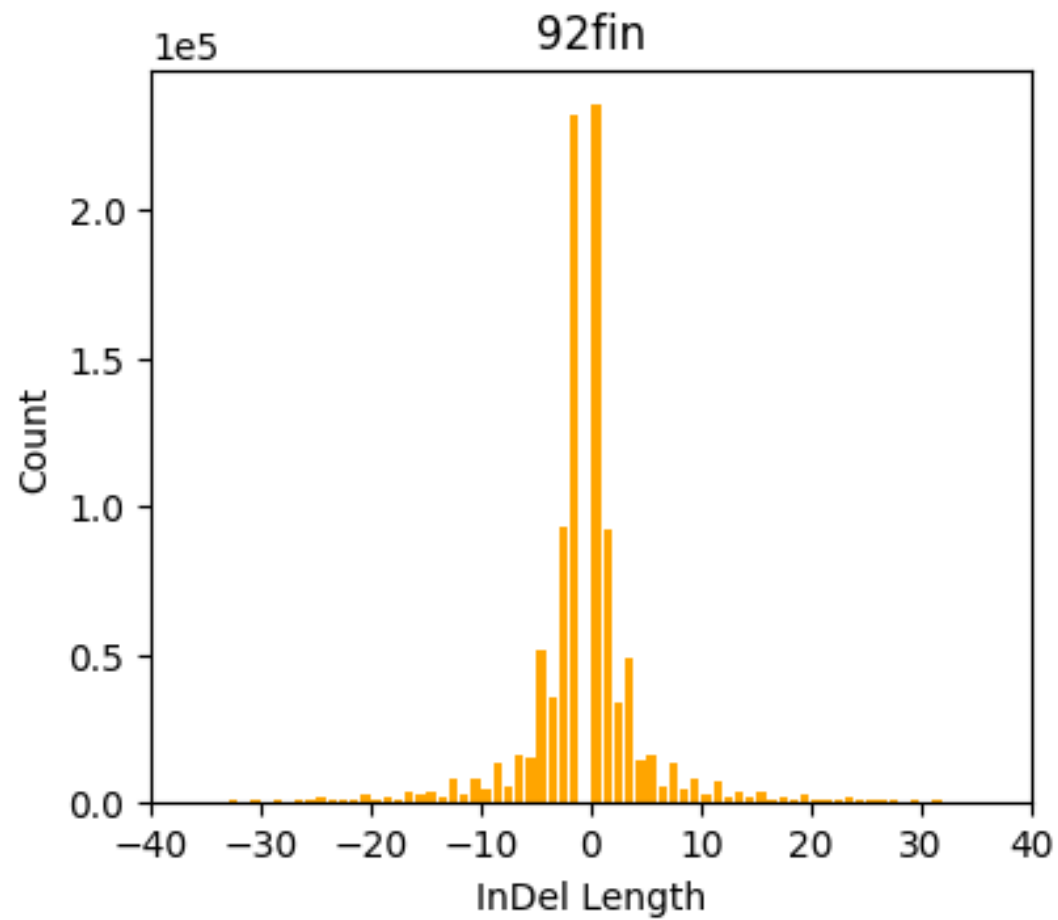


## Ts/Tv stratified by QUAL

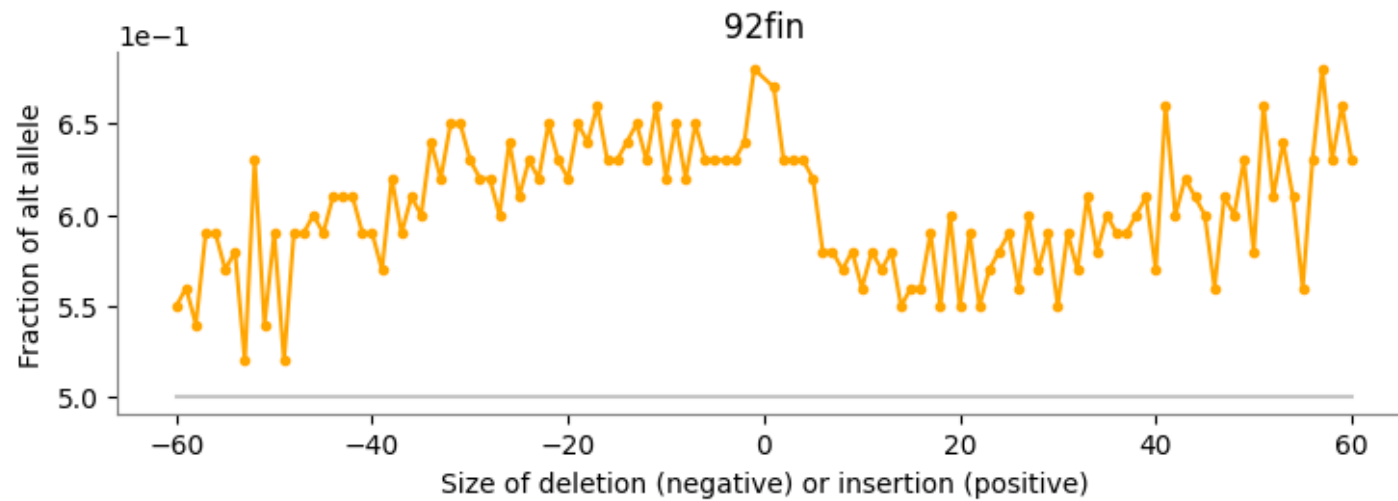




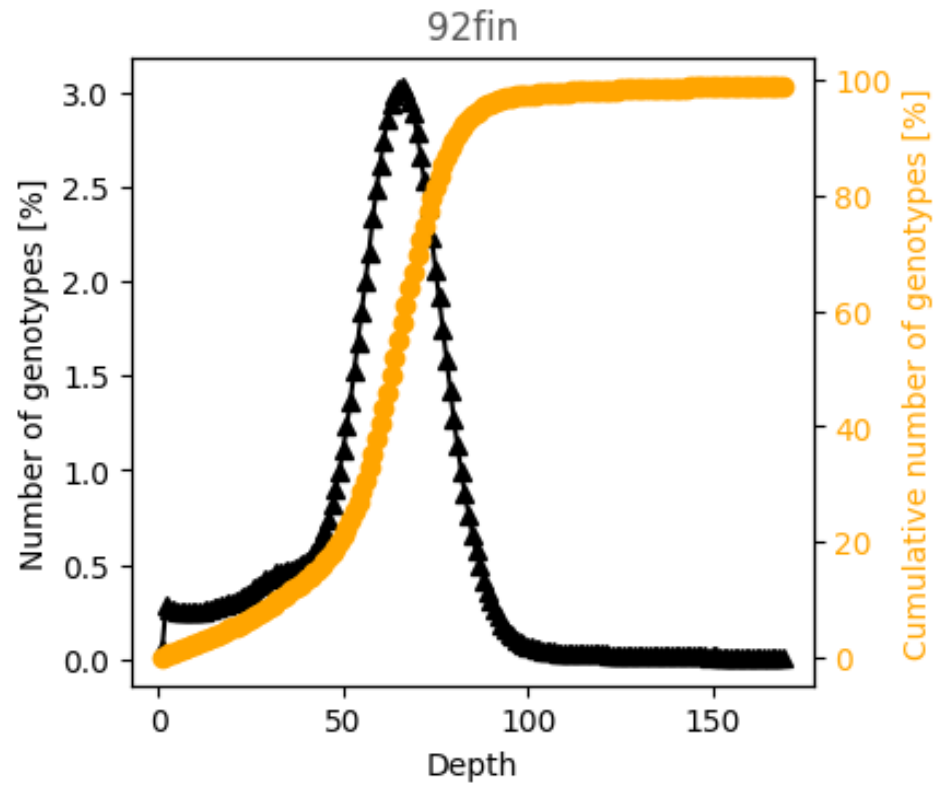
# Indel distribution



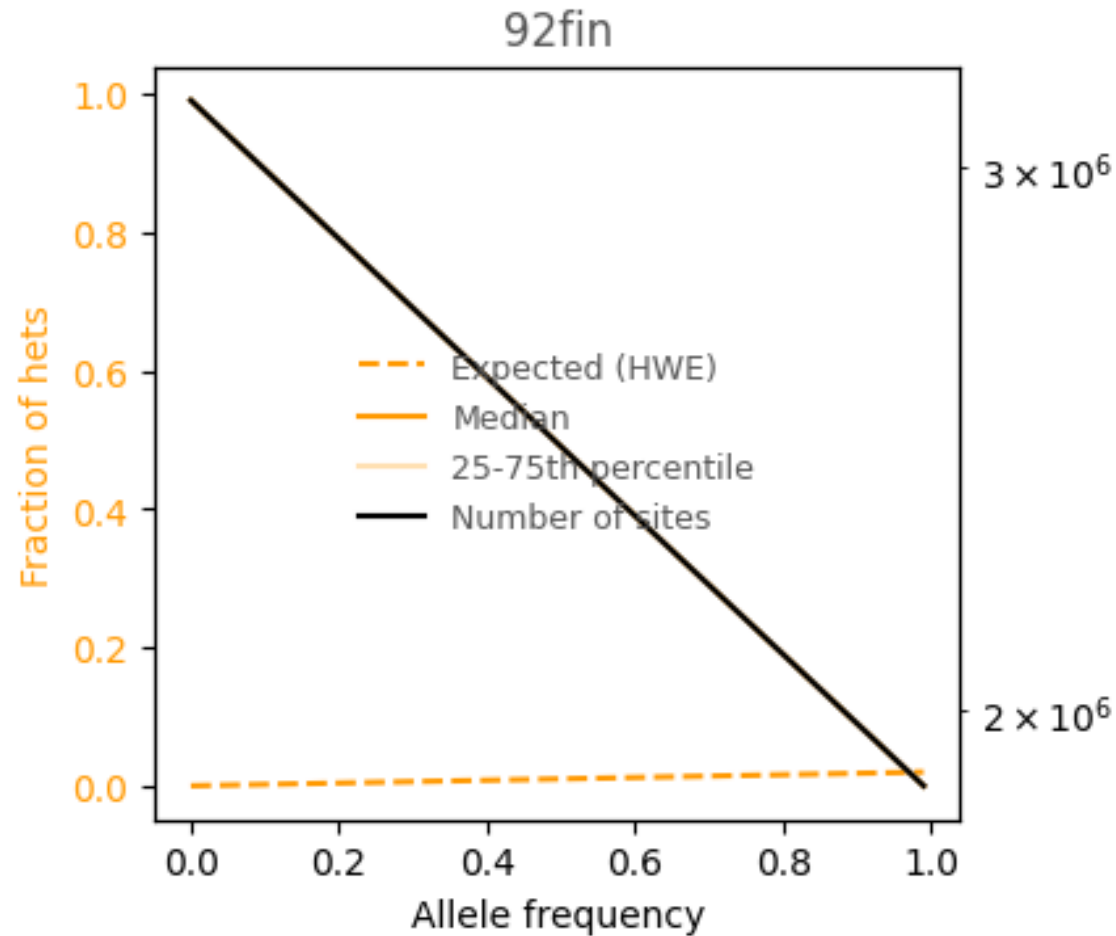
# Fraction of alternate indel allele



# Depth distribution



# Number of HETs by AF



# Substitution types

