# Summary Numbers

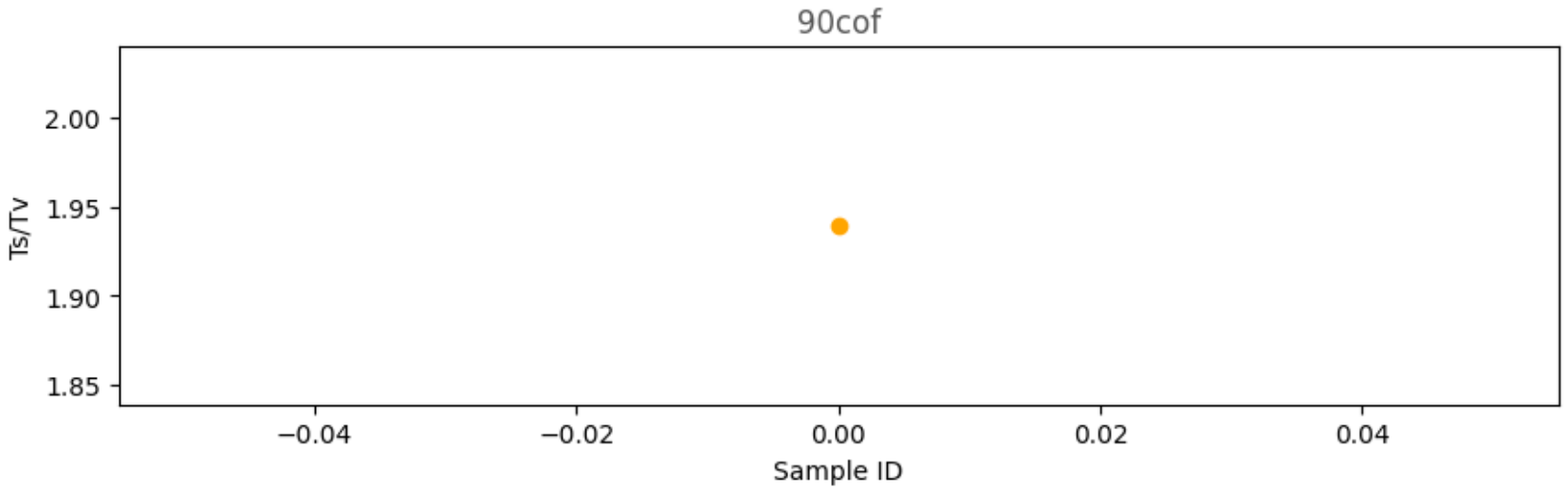
| | SNPs | | | indels | | MNPs | others |
|---|---|---|---|---|---|---|---|
| Callset | n | ts/tv | (1st ALT) | n | frm* | | |
| 90cof | 4,133,269 | 1.94 | 1.94 | 963,556 | – | 0 | 0 |

* frameshift ratio: out/(out+in)

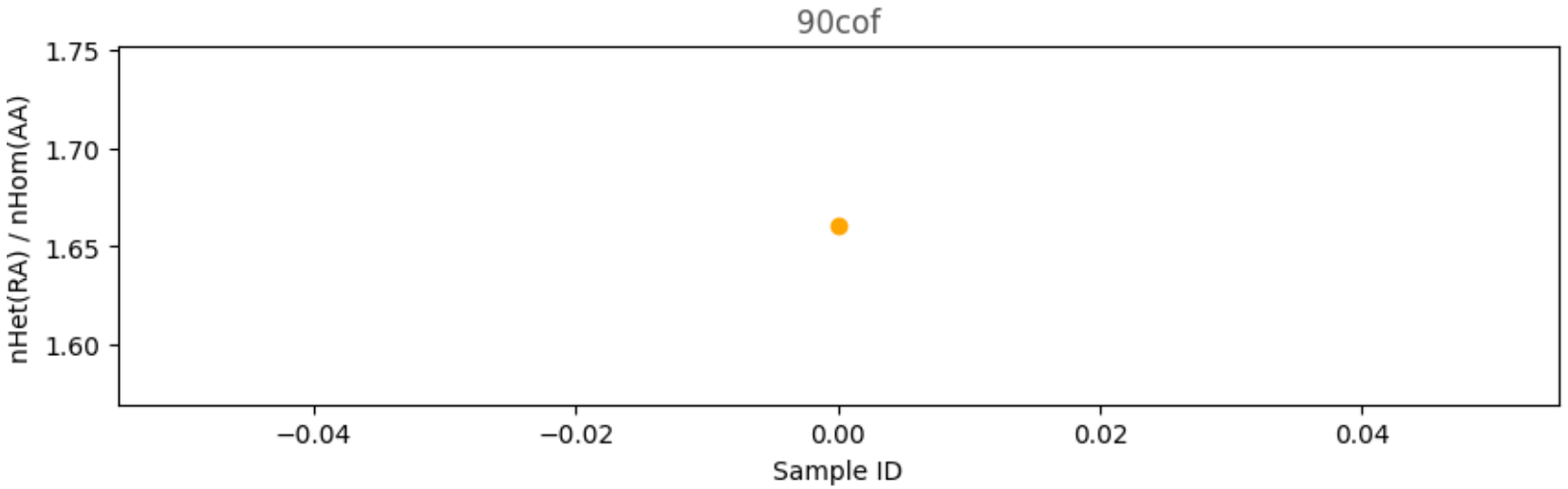
| | singletons (AC=1) | | | multiallelic | |
|---|---|---|---|---|---|
| Callset | SNPs | ts/tv | indels | sites | SNPs |
| 90cof | 62.4% | 1.91 | 67.2% | 100,846 | 2,104 |

- 90cof .. `/ngc/projects2/gm/data/archive/2022/variants/snv/90cofofof-103838574995-Normal_Blood_noinfo-WGS_v1_IlluminaDNAPCRFree_RHGM00601-220225_A01176_AH7CT5DSX3-EXT_LABKA_NGCWGS-NGCWGS03878_22RKG000471x01_snv_germline_raw.haplotype_caller.vcf.gz`

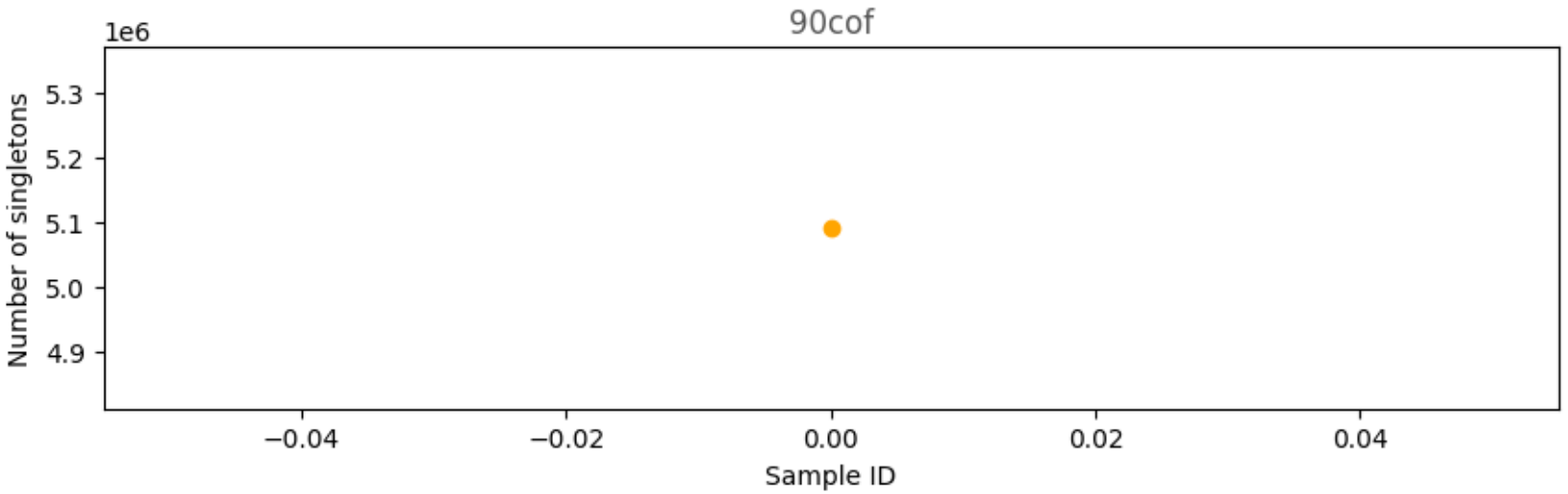
# Ts/Tv by sample



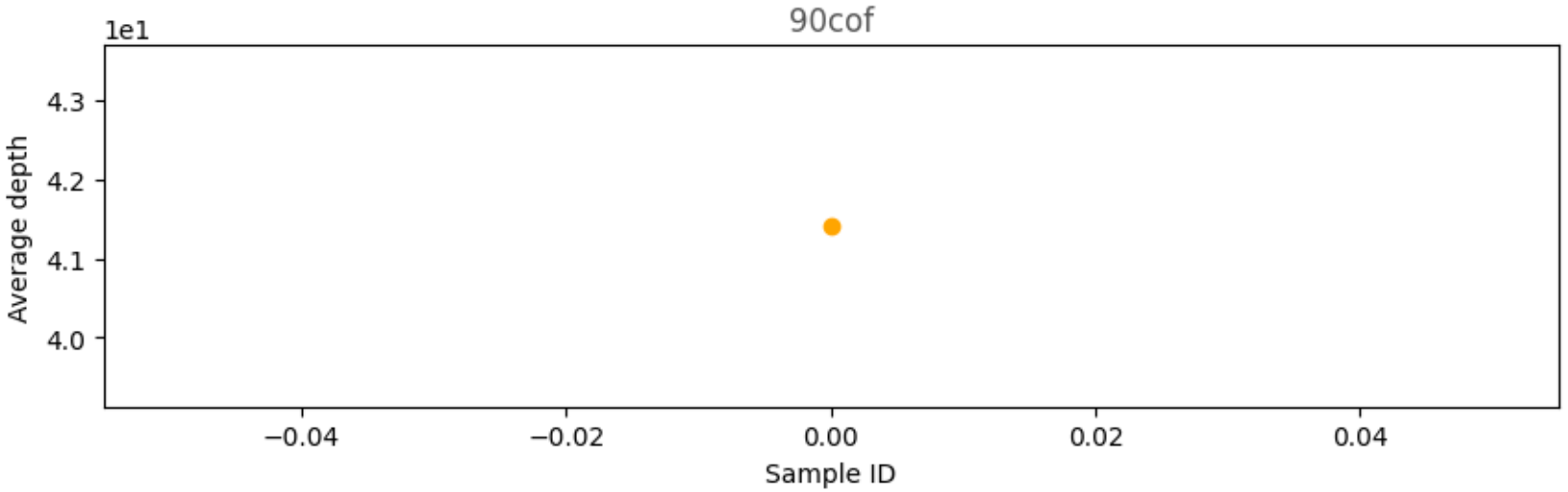
# Hets vs non-ref Homs by sample



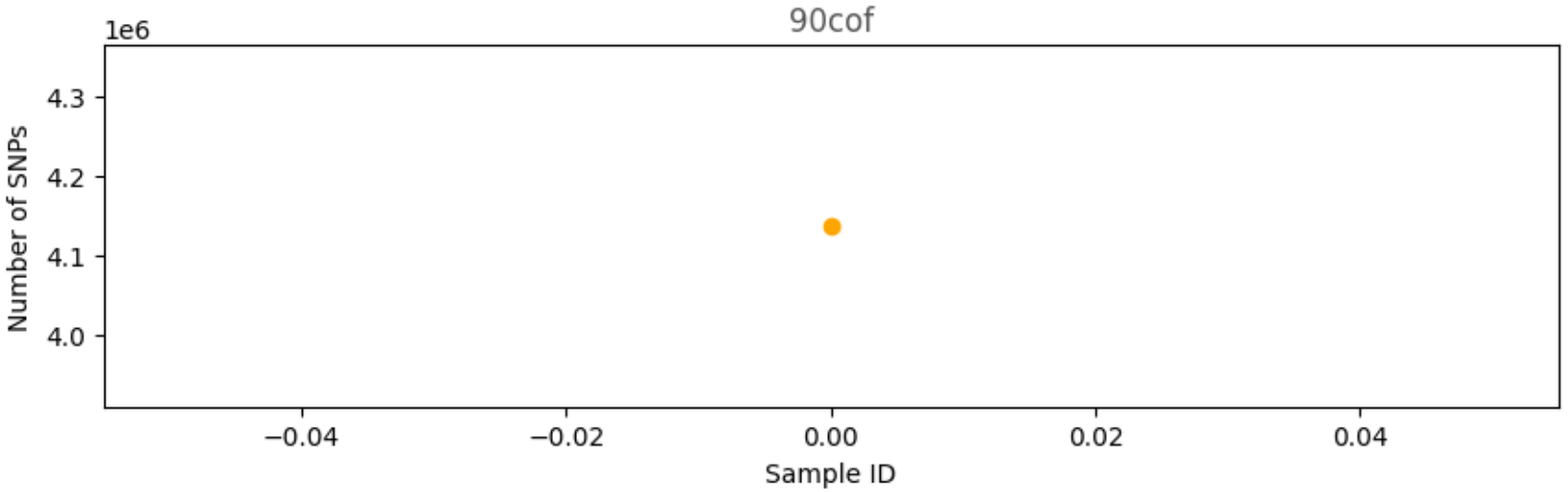
# Singletons by sample (hets and homs)



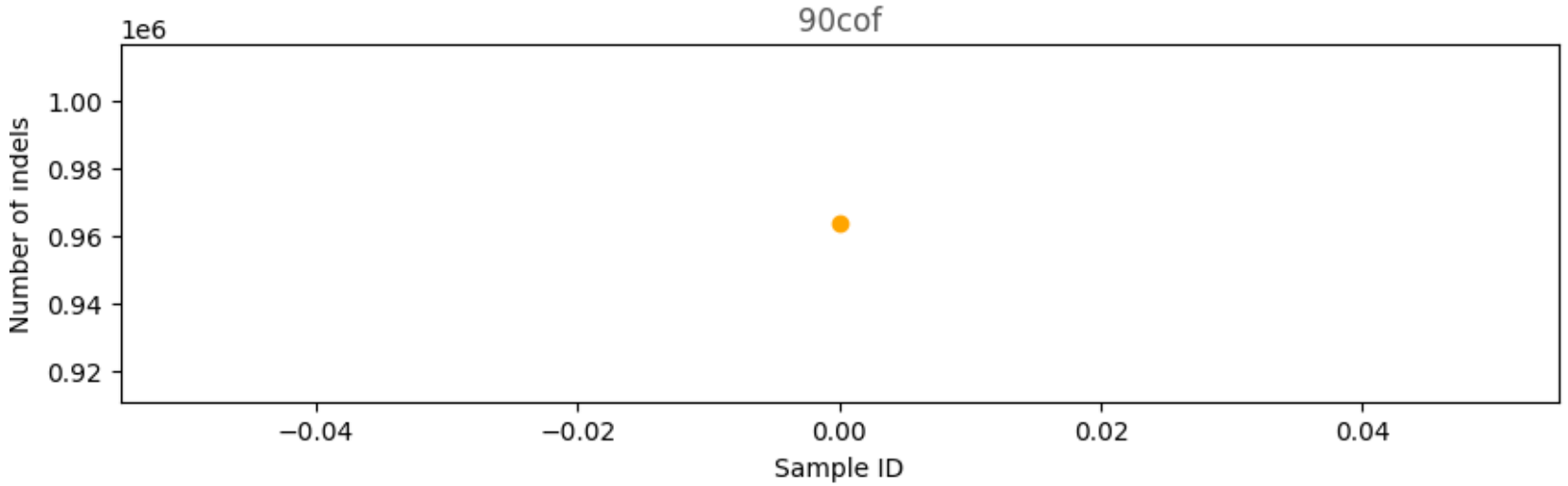
# Average depth by sample



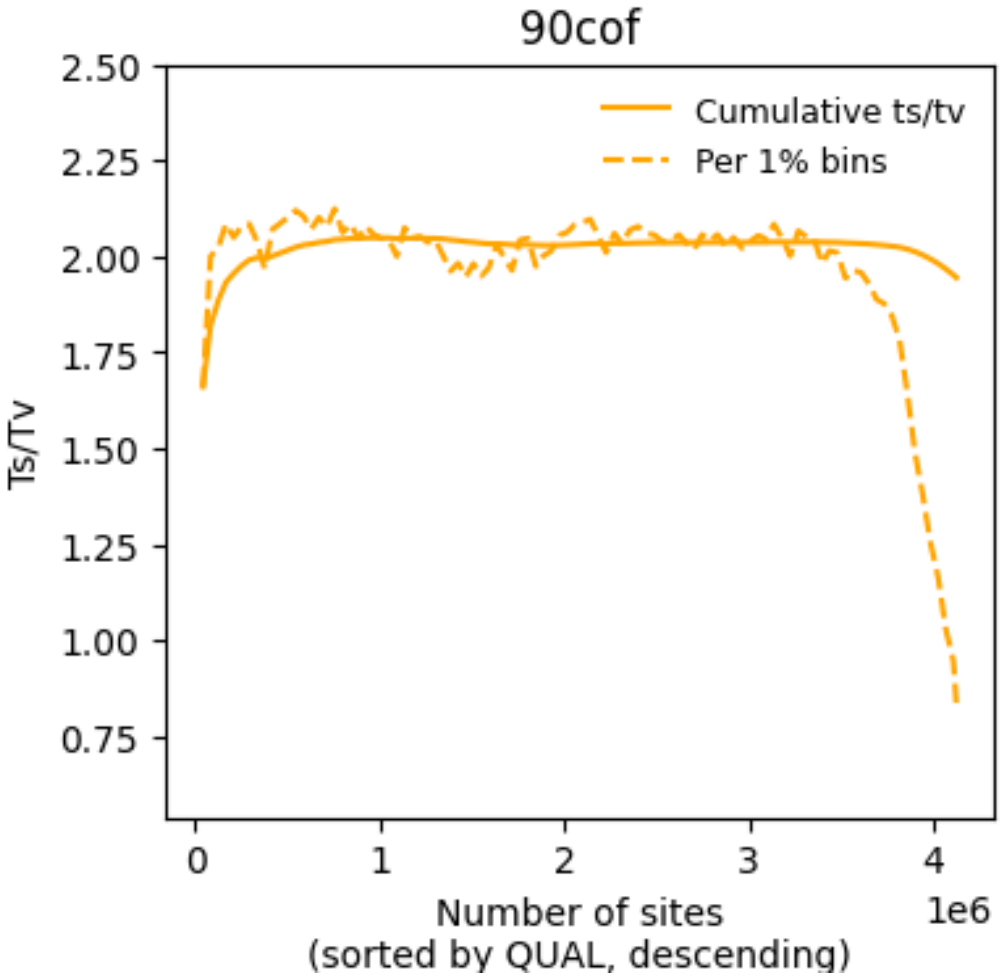
# Number of SNPs by sample



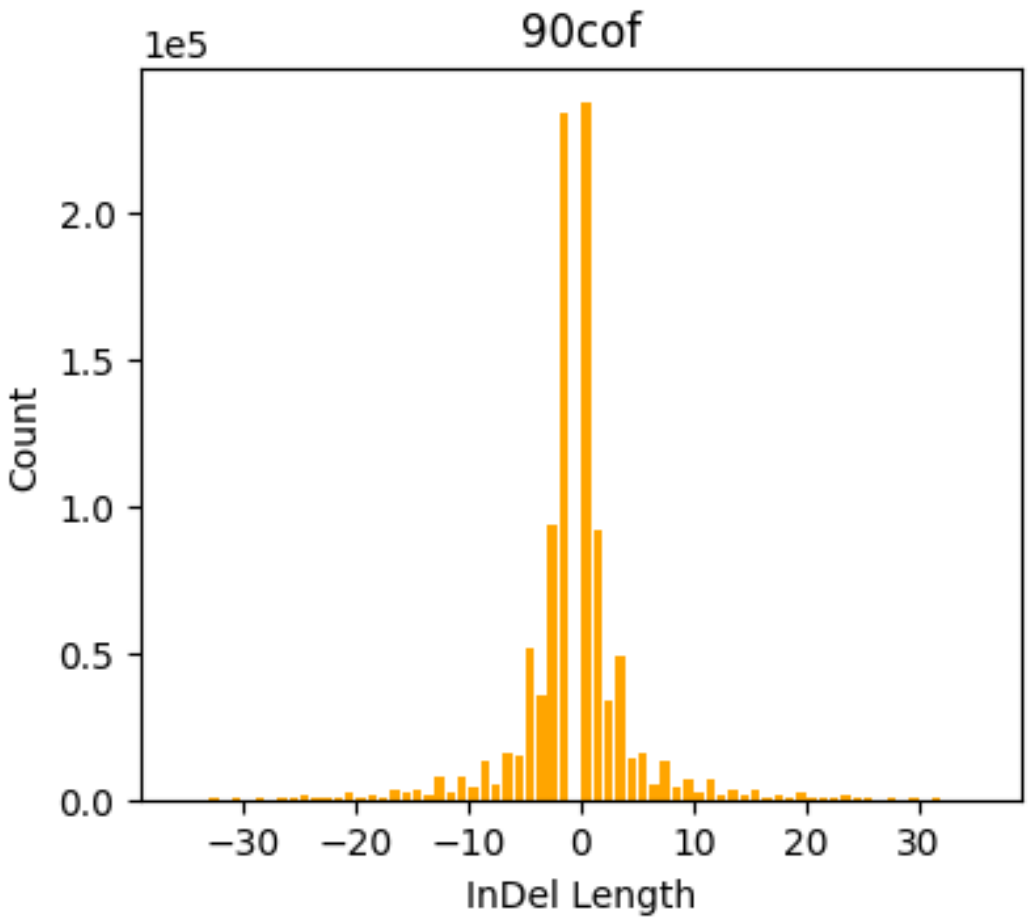
# Number of indels by sample



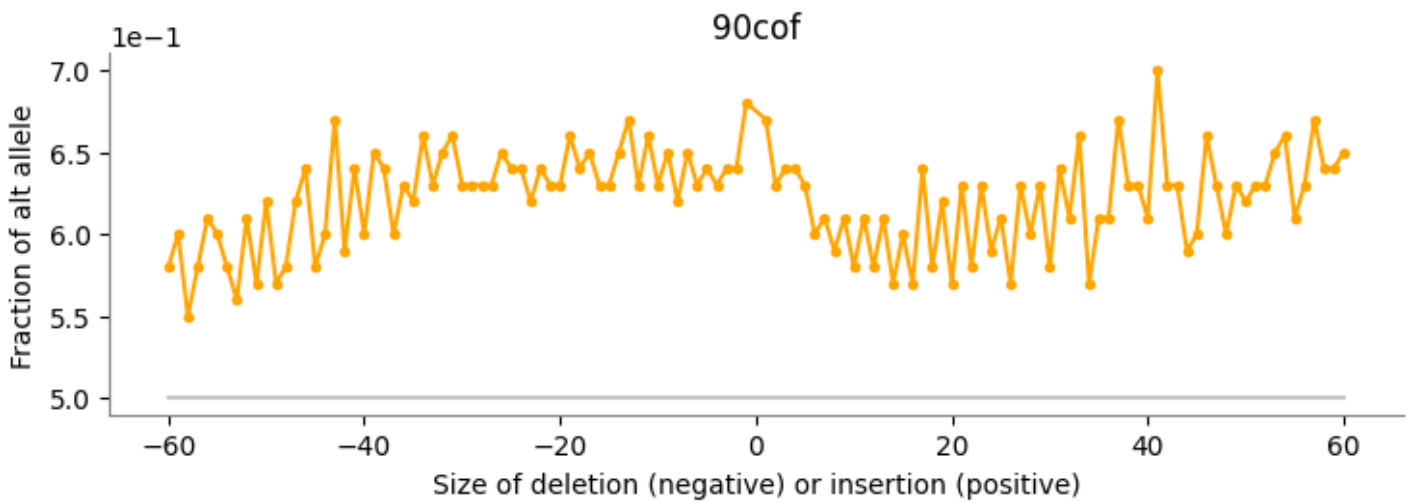
# Ts/Tv stratified by QUAL



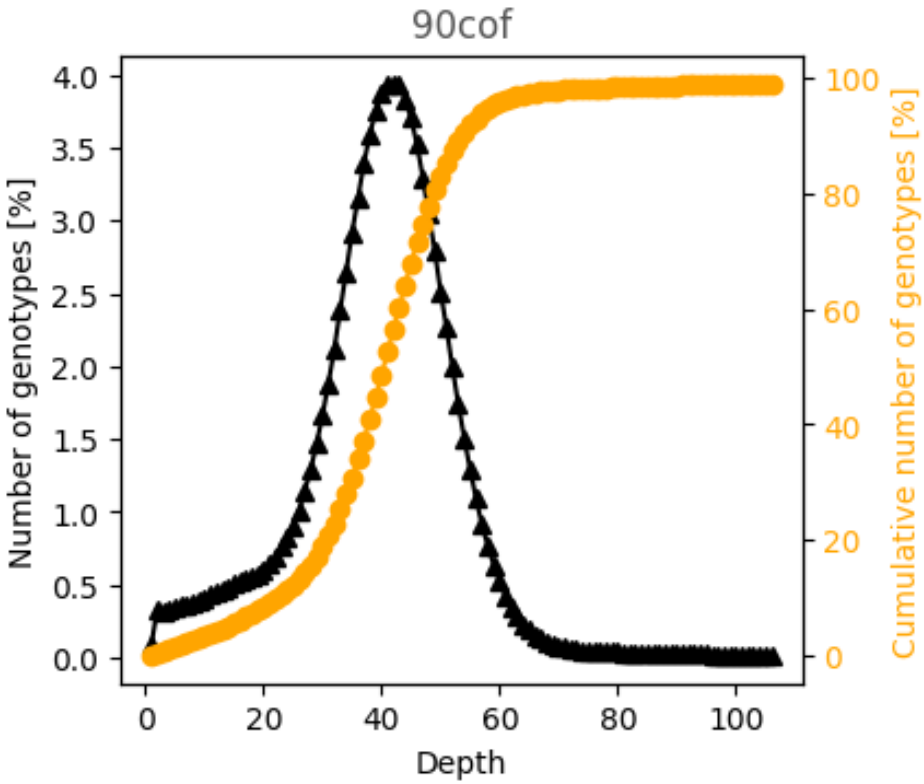
# Indel distribution



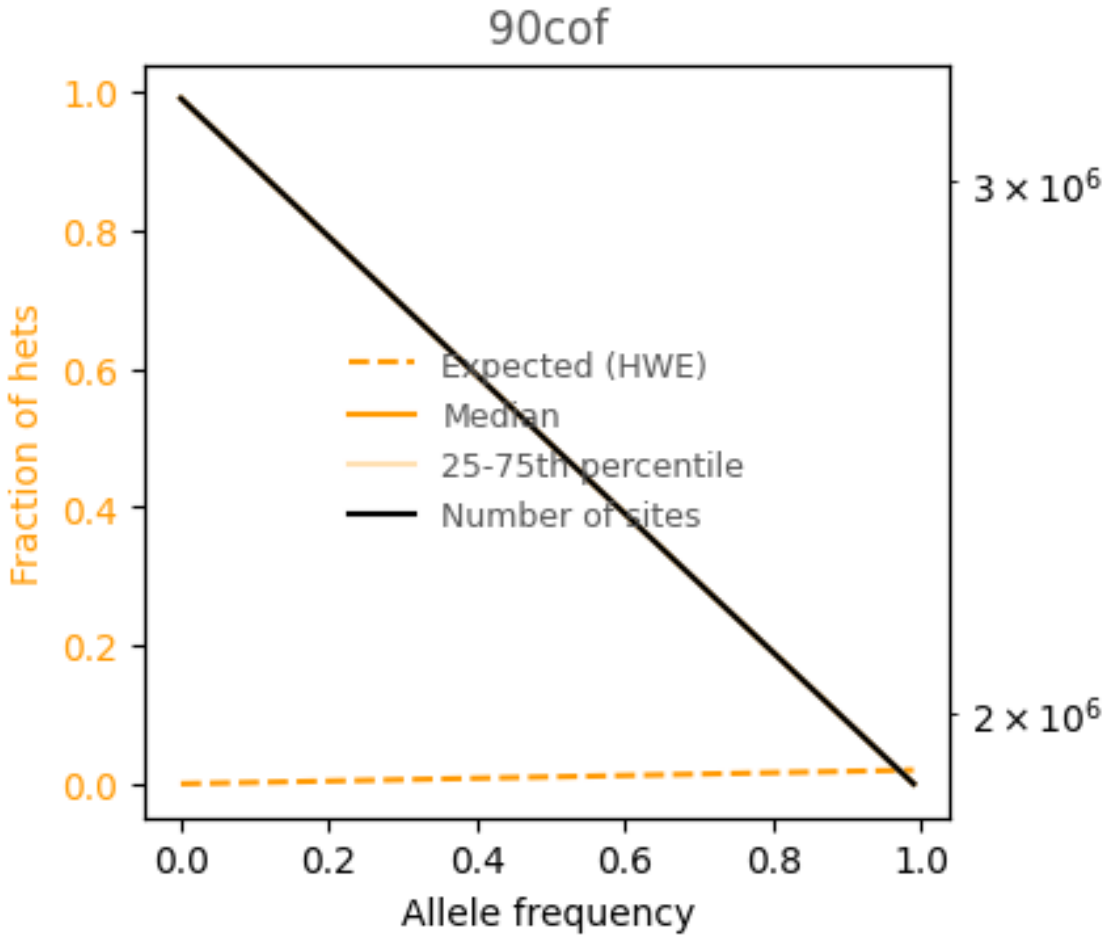
# Fraction of alternate indel allele



# Depth distribution



# Number of HETs by AF



# Substitution types