# Summary Numbers

| Callset | SNPs | | | indels | | MNPs | others |
|---|---|---|---|---|---|---|---|
| | n | ts/tv | (1st ALT) | n | frm* | | |
| 90dor | 4,059,332 | 1.92 | 1.93 | 950,089 | – | 0 | 0 |
| | | | | | * frameshift ratio: out/(out+in) | | |

| Callset | singletons (AC=1) | | | multiallelic | |
|---|---|---|---|---|---|
| | SNPs | ts/tv | indels | sites | SNPs |
| 90dor | 61.9% | 1.89 | 66.9% | 101,609 | 2,164 |

- 90dor .. `/ngc/projects2/gm/data/archive/2022/variants/snv/90dormrem-110298852873-Normal_B`
`lood_noinfo-WGS_v1_IlluminaDNAPCRFree_RHGM02128-221026_A01961_AH3TGFDSX5-EXT_LAB`
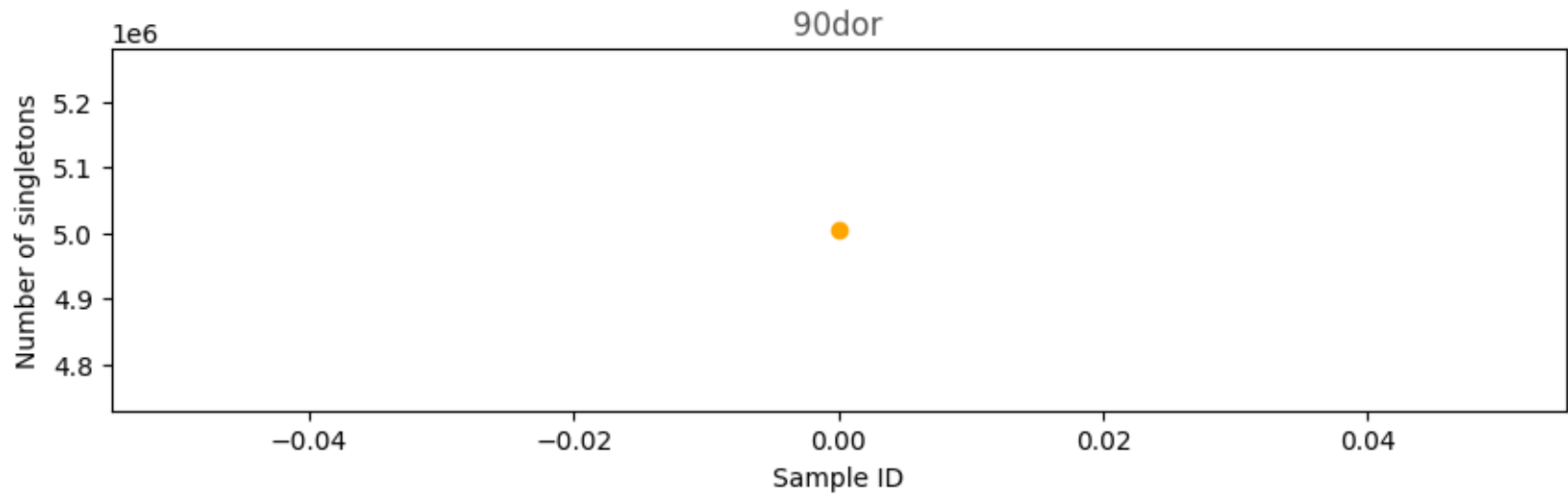`KA_NGCWGS-NGCWGS05976_snv_germline_raw.haplotype_caller.vcf.gz`
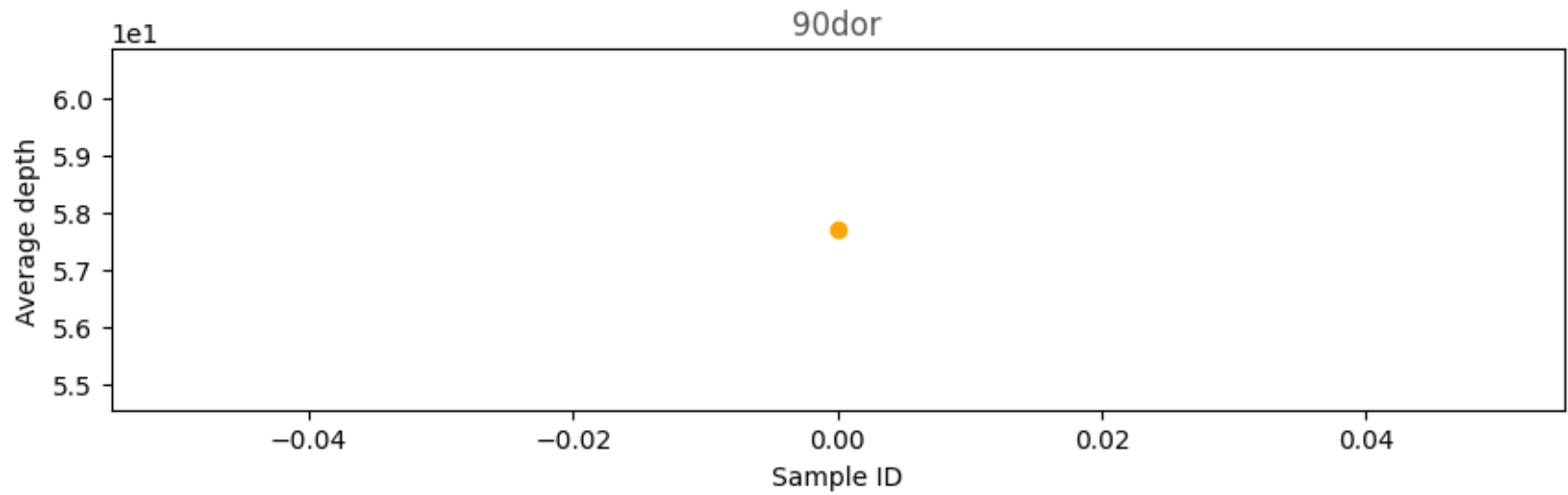
# Ts/Tv by sample
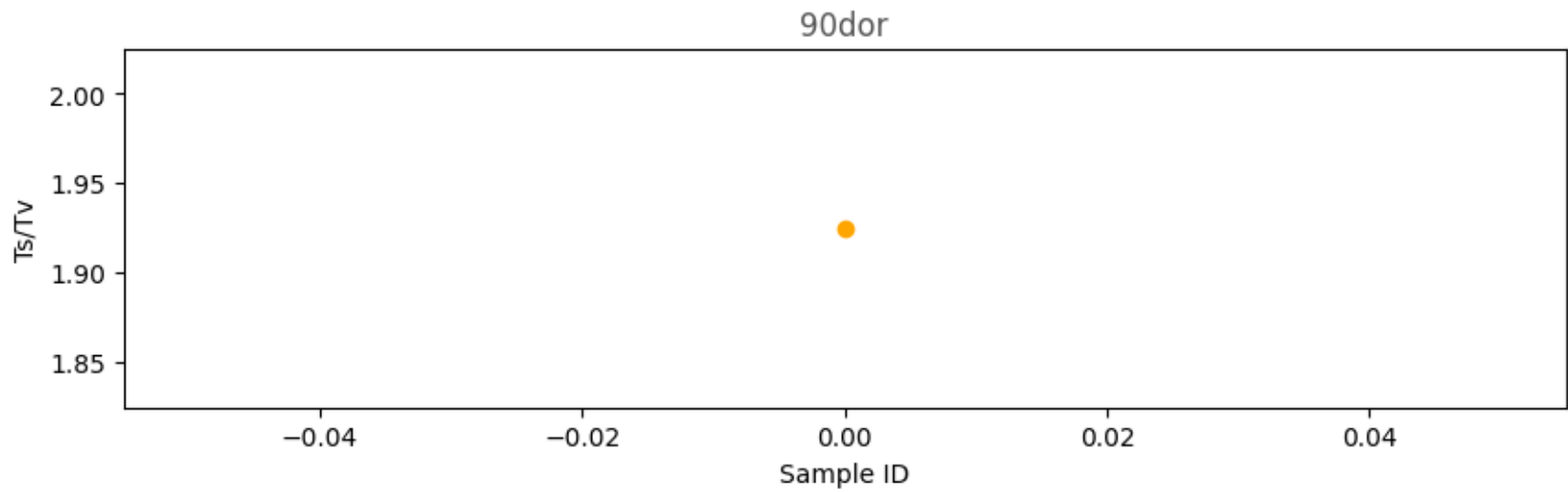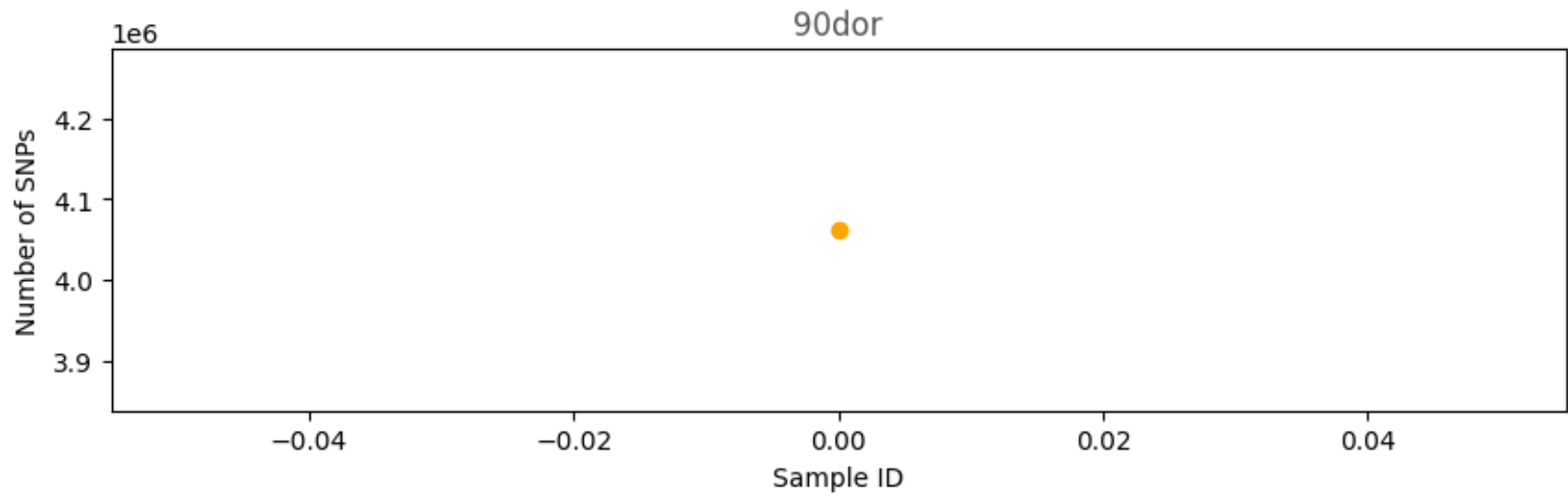
# Hets vs non-ref Homs by sample
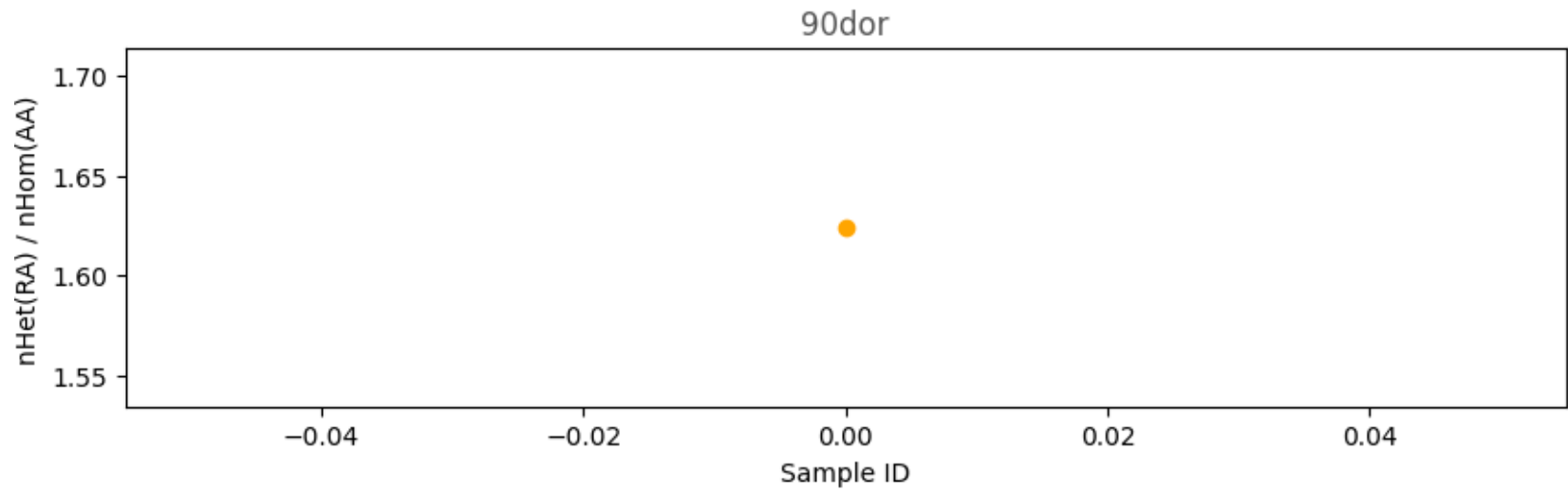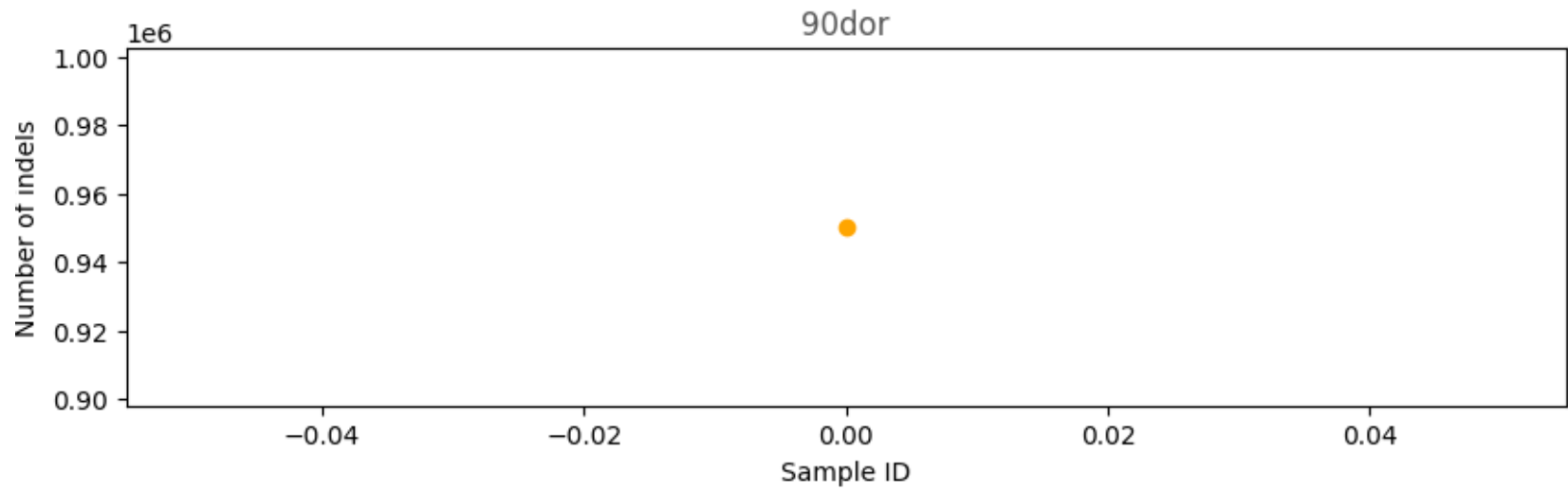
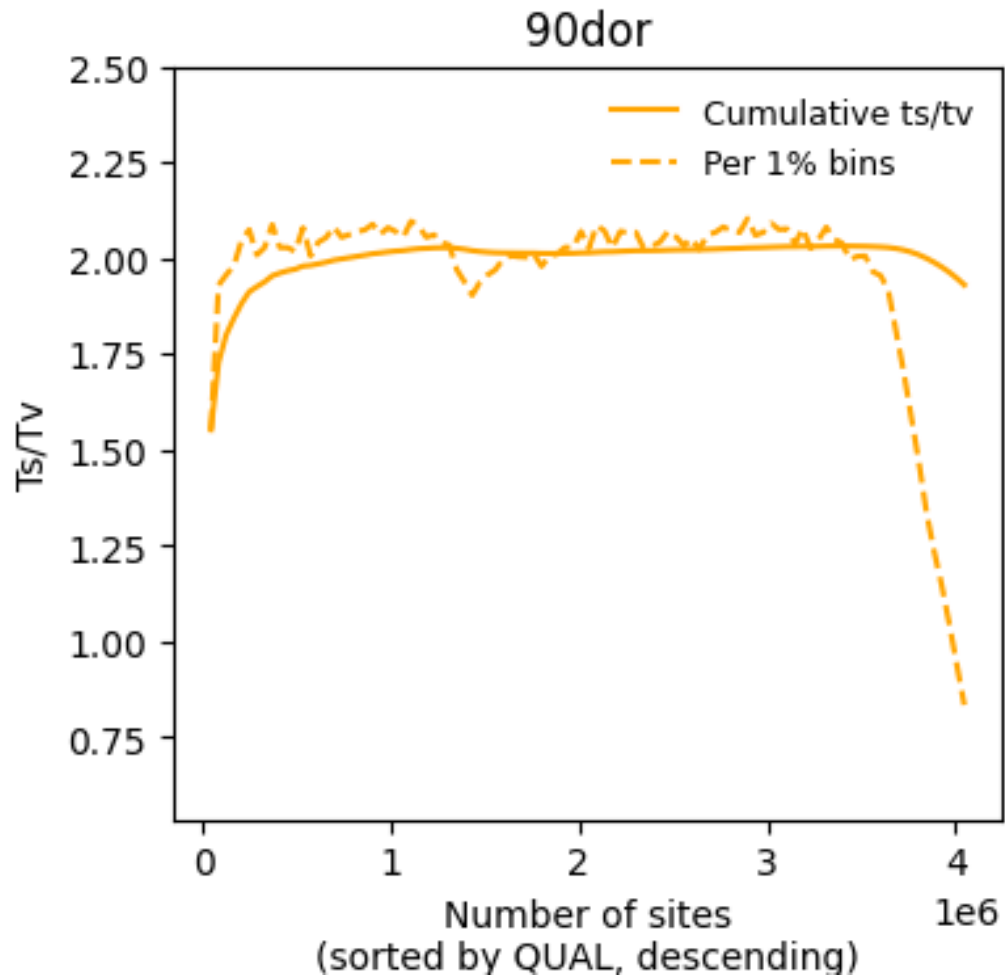# Singletons by sample (hets and homs)

# Average depth by sample
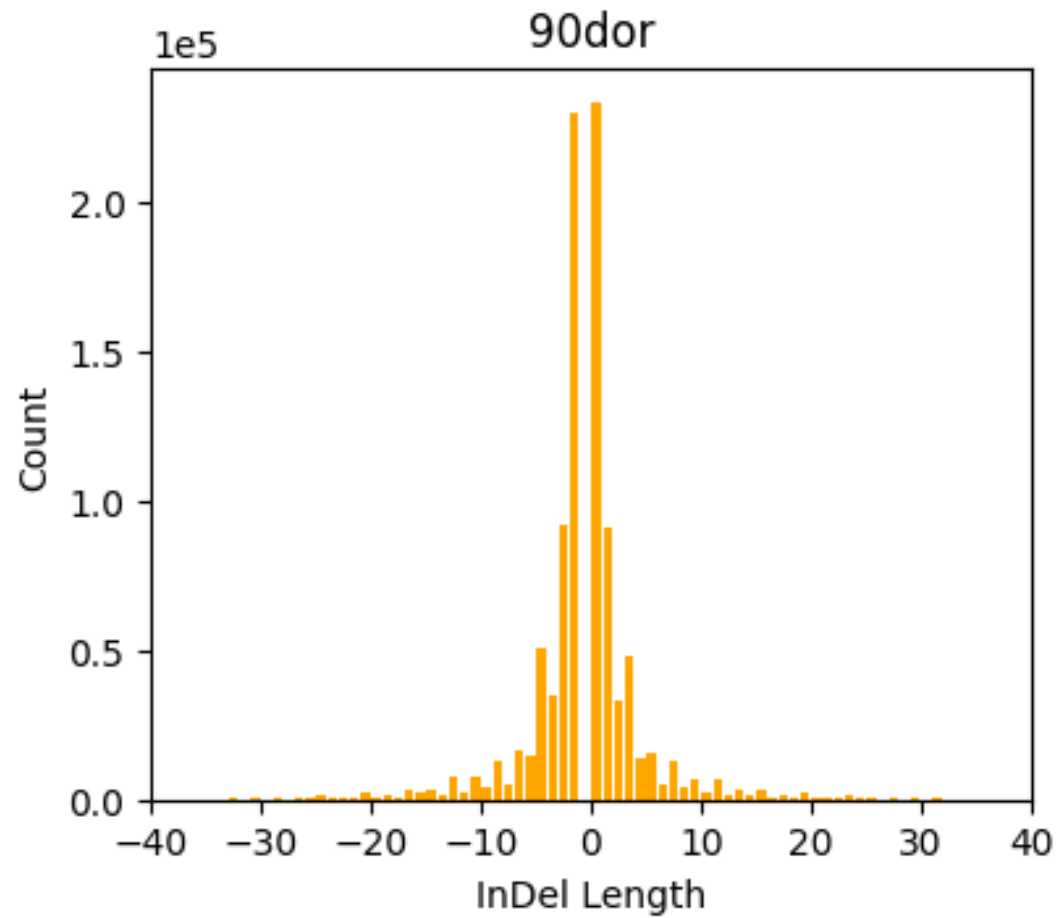
# Number of SNPs by sample

# Number of indels by sample
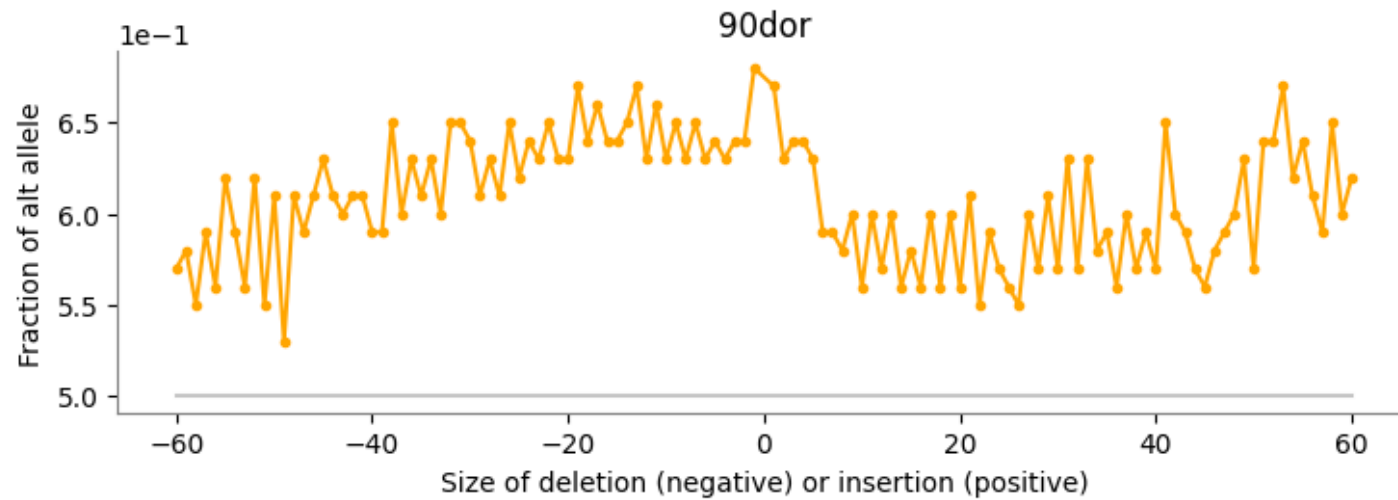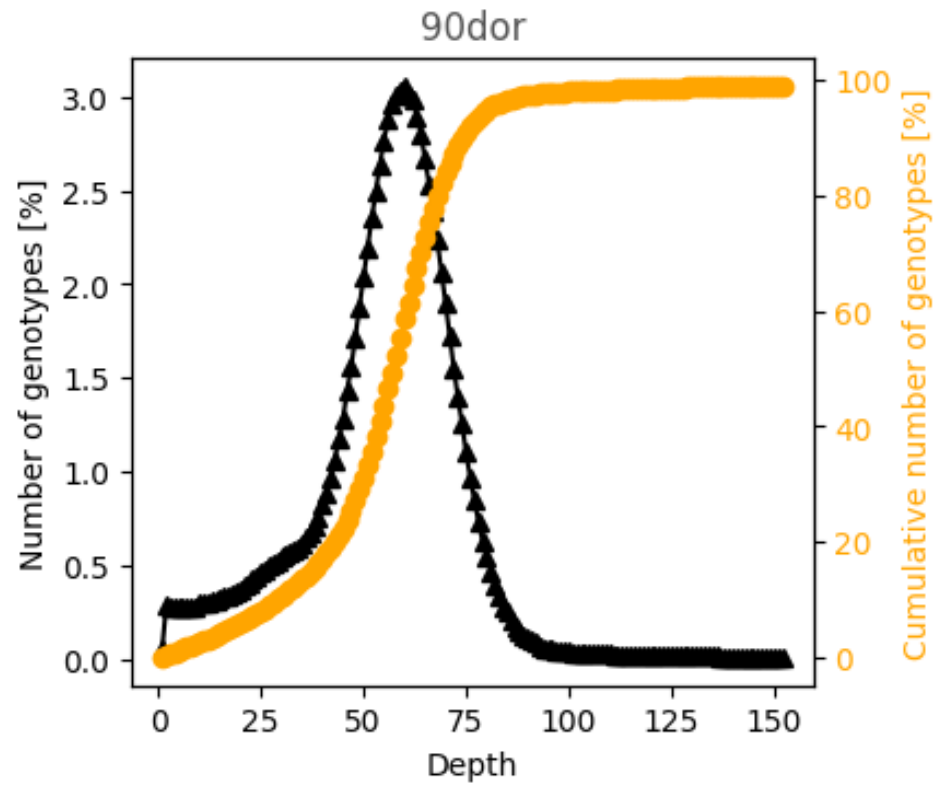
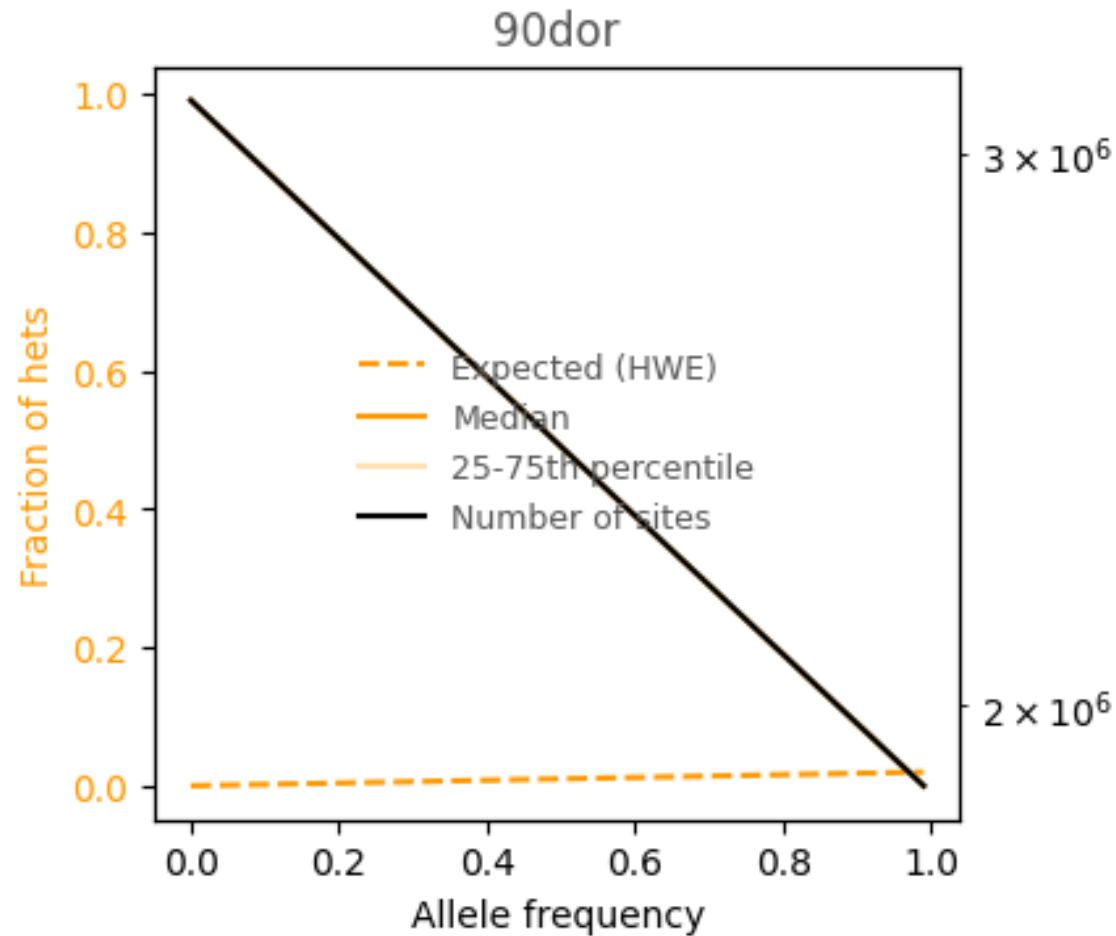# Ts/Tv stratified by QUAL

# Indel distribution

# Fraction of alternate indel allele

# Depth distribution

# Number of HETs by AF

# Substitution types



90dor