# Summary Numbers

| Callset | SNPs | | | indels | | MNPs | others |
|---|---|---|---|---|---|---|---|
| | n | ts/tv | (1st ALT) | n | frm* | | |
| 22mbl | 4,077,704 | 1.93 | 1.94 | 944,152 | – | 0 | 0 |
| | | | | | * frameshift ratio: out/(out+in) | | |

| Callset | singletons (AC=1) | | | multiallelic | |
|---|---|---|---|---|---|
| | SNPs | ts/tv | indels | sites | SNPs |
| 22mbl | 63.1% | 1.91 | 67.8% | 96,978 | 2,092 |

- 22mbl .. `/ngc/projects2/gm/data/archive/2022/variants/snv/22mbltomf-103876802690-Normal_B lood_noinfo-WGS_v1_IlluminaDNAPCRFree_X-220601_A00559_BHJ5WHDSX3-RHGM_LABKA_WGSA KUT-WGSAKUT04386_22RKG013090x01_snv_germline_raw.haplotype_caller.vcf.gz`
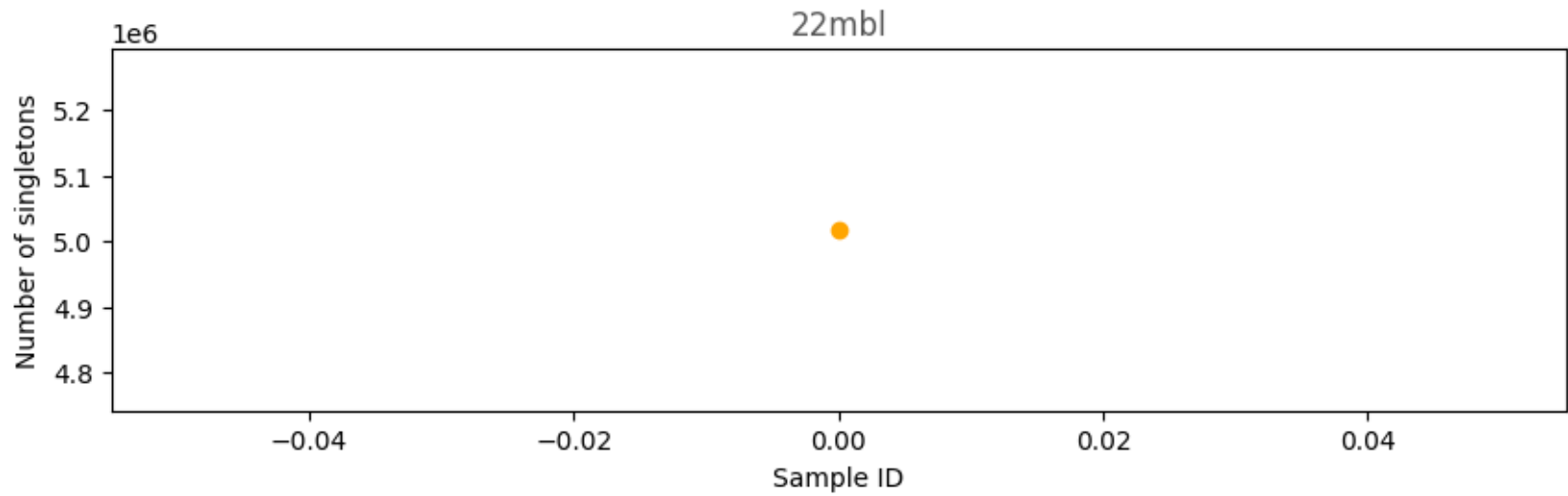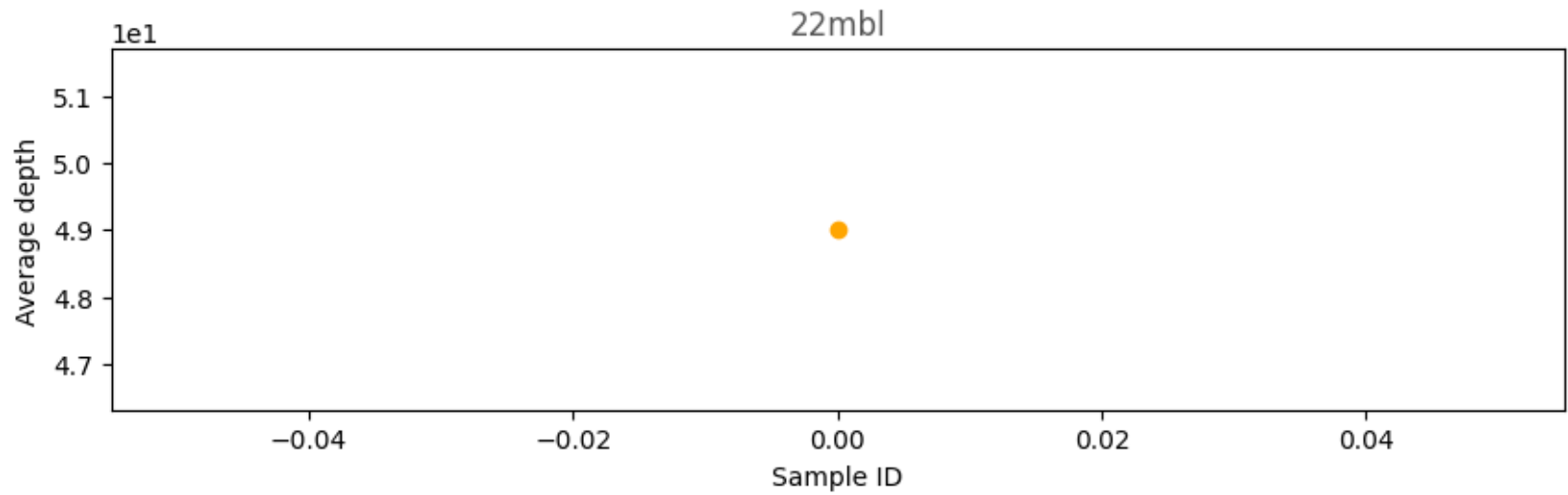
# Ts/Tv by sample
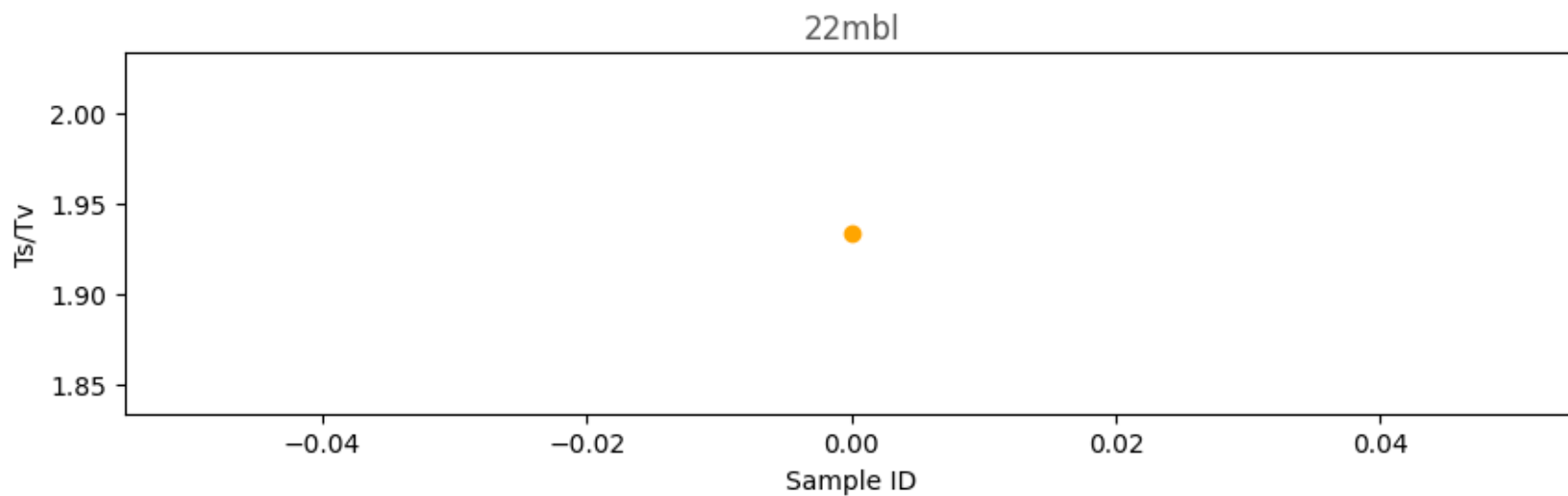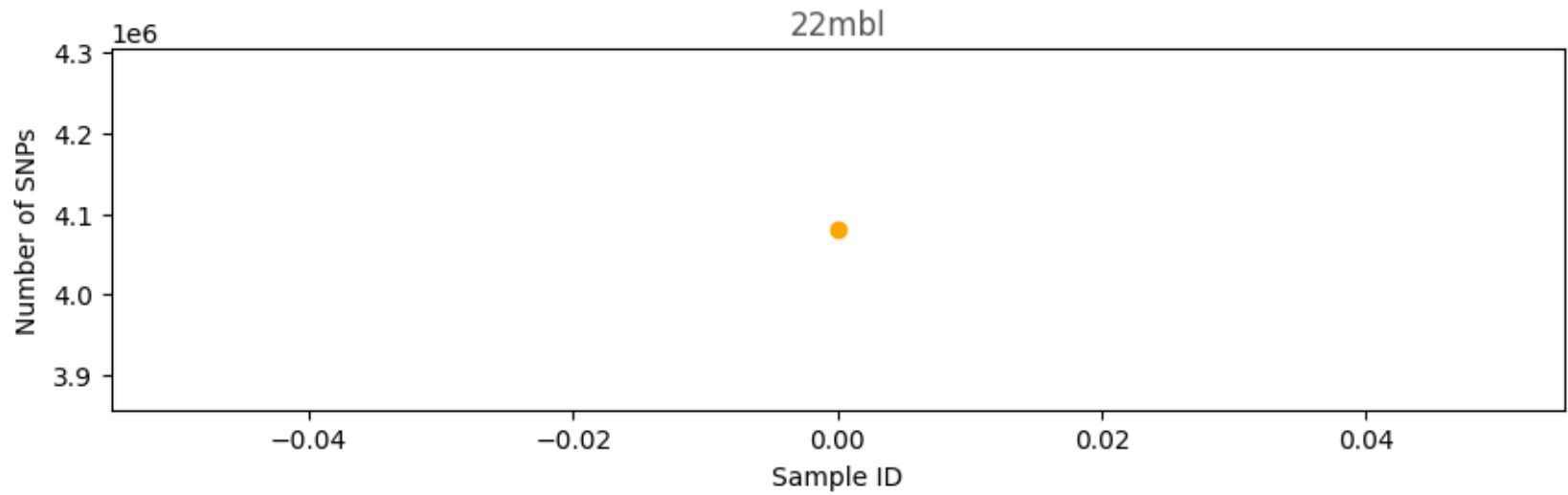
# Hets vs non-ref Homs by sample
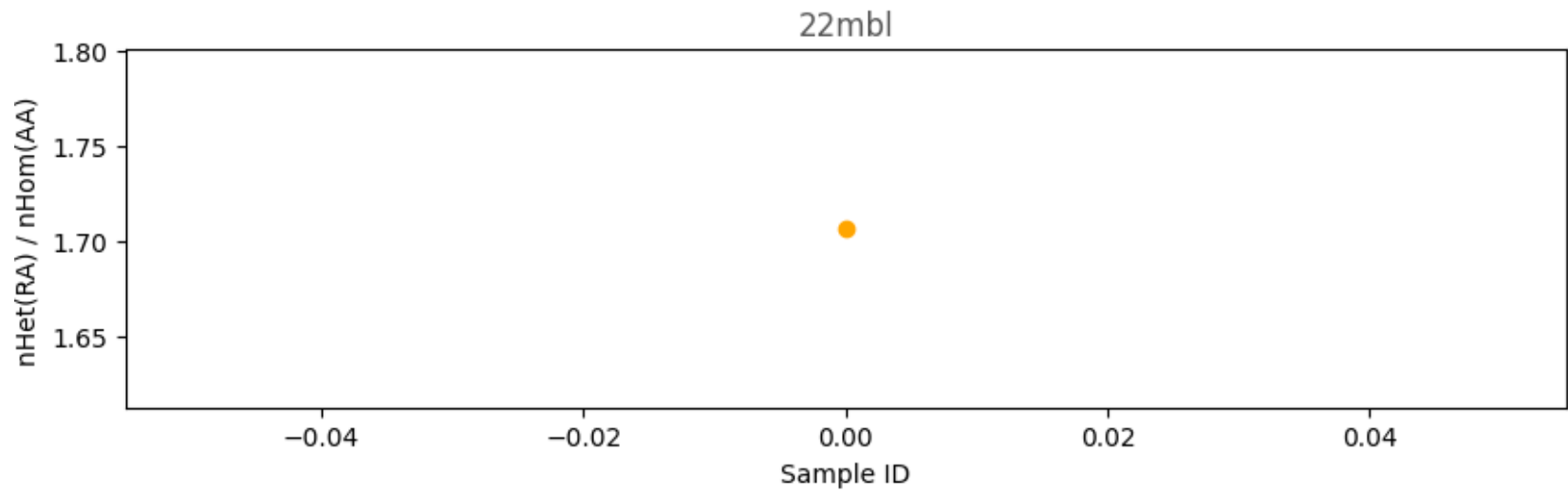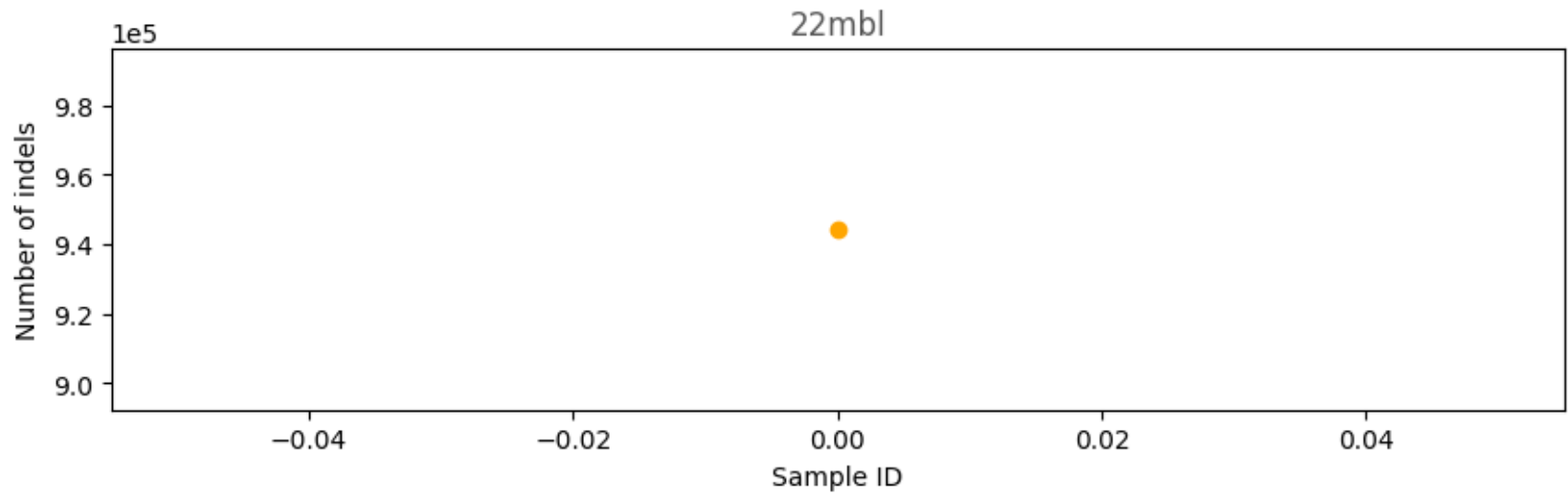
# Singletons by sample (hets and homs)
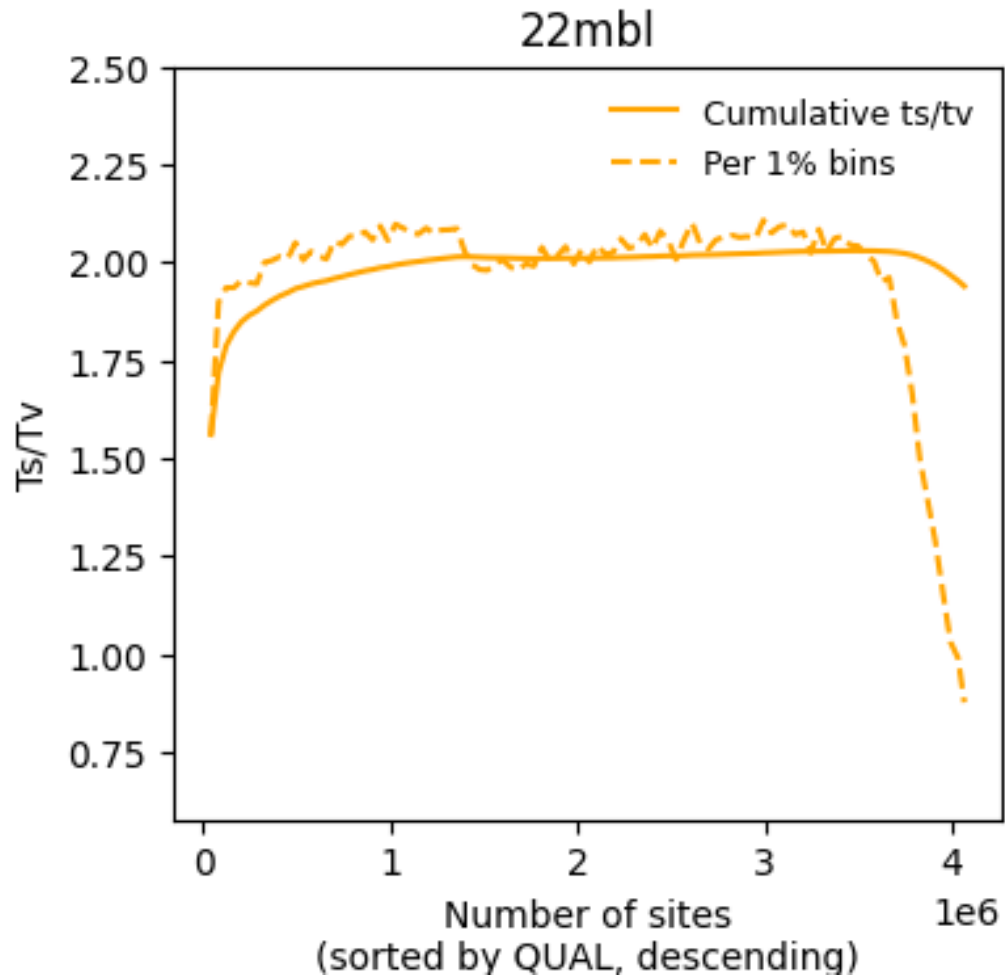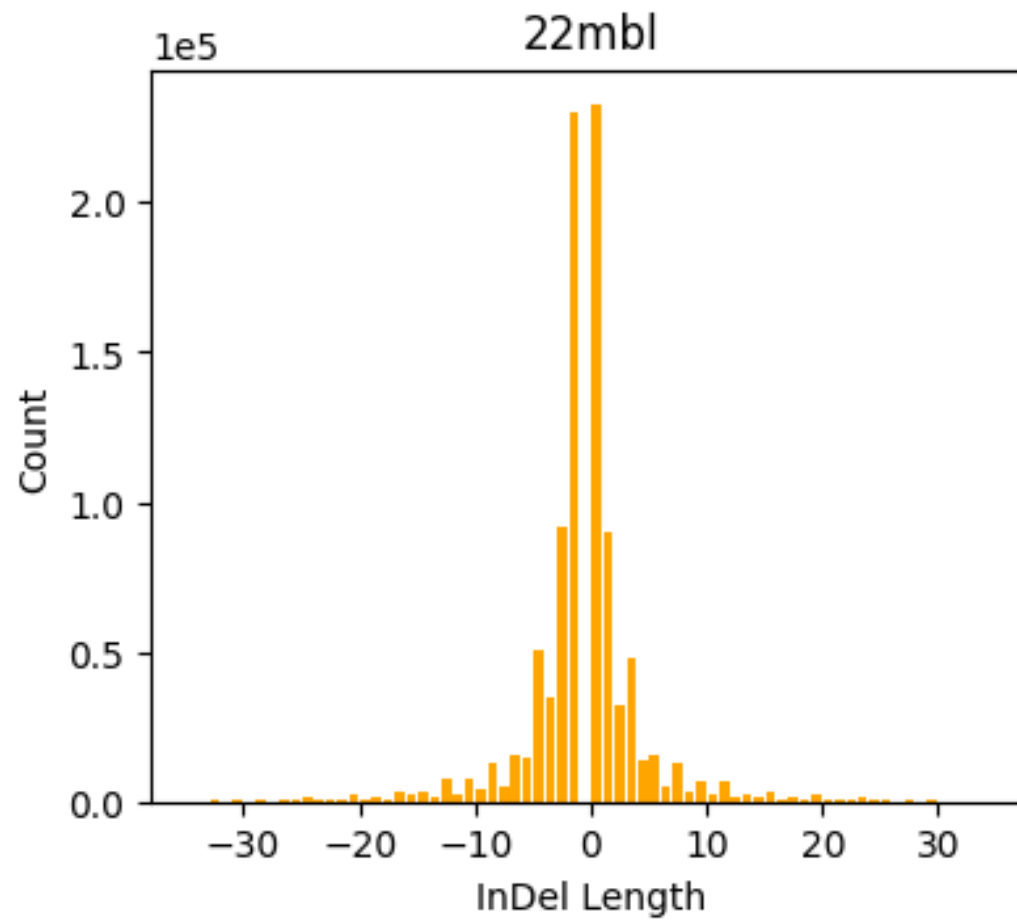
# Average depth by sample

# Number of SNPs by sample

# Number of indels by sample

# Ts/Tv stratified by QUAL

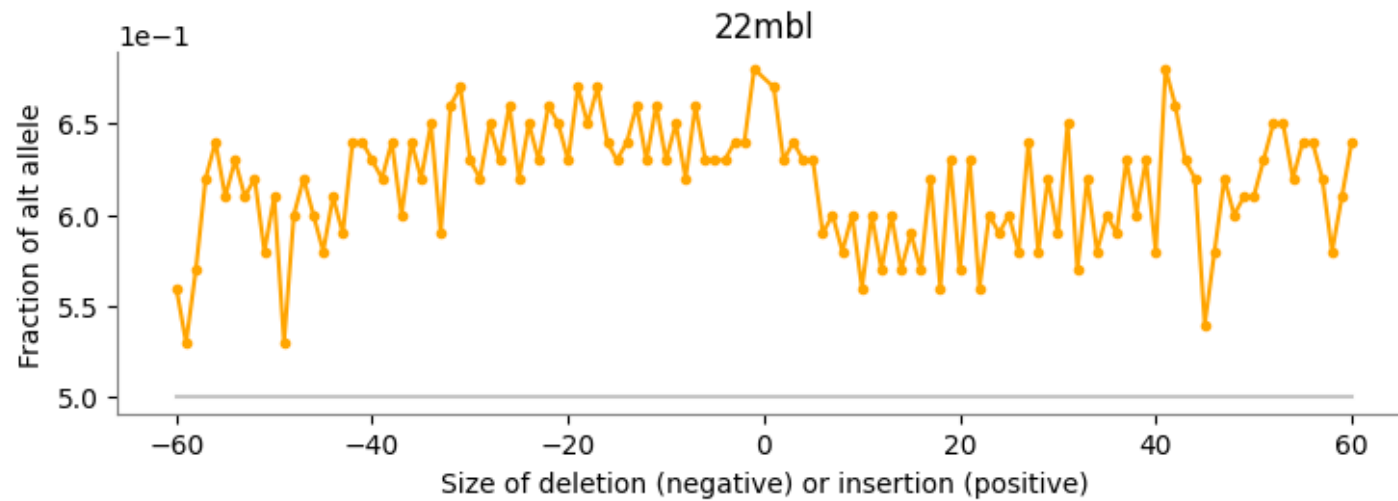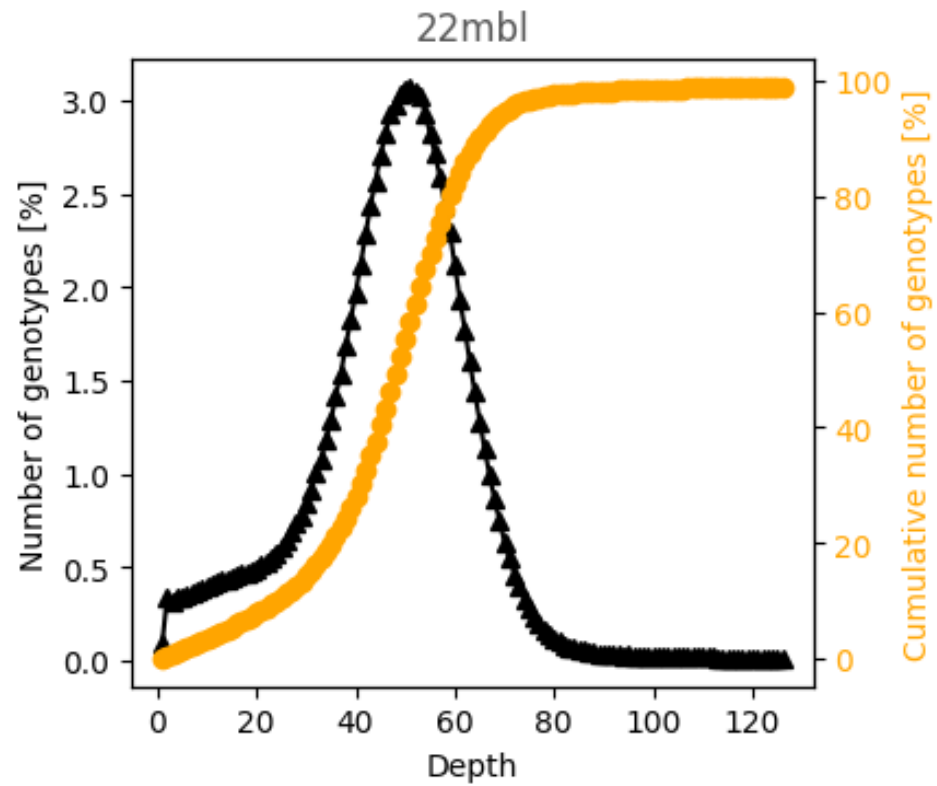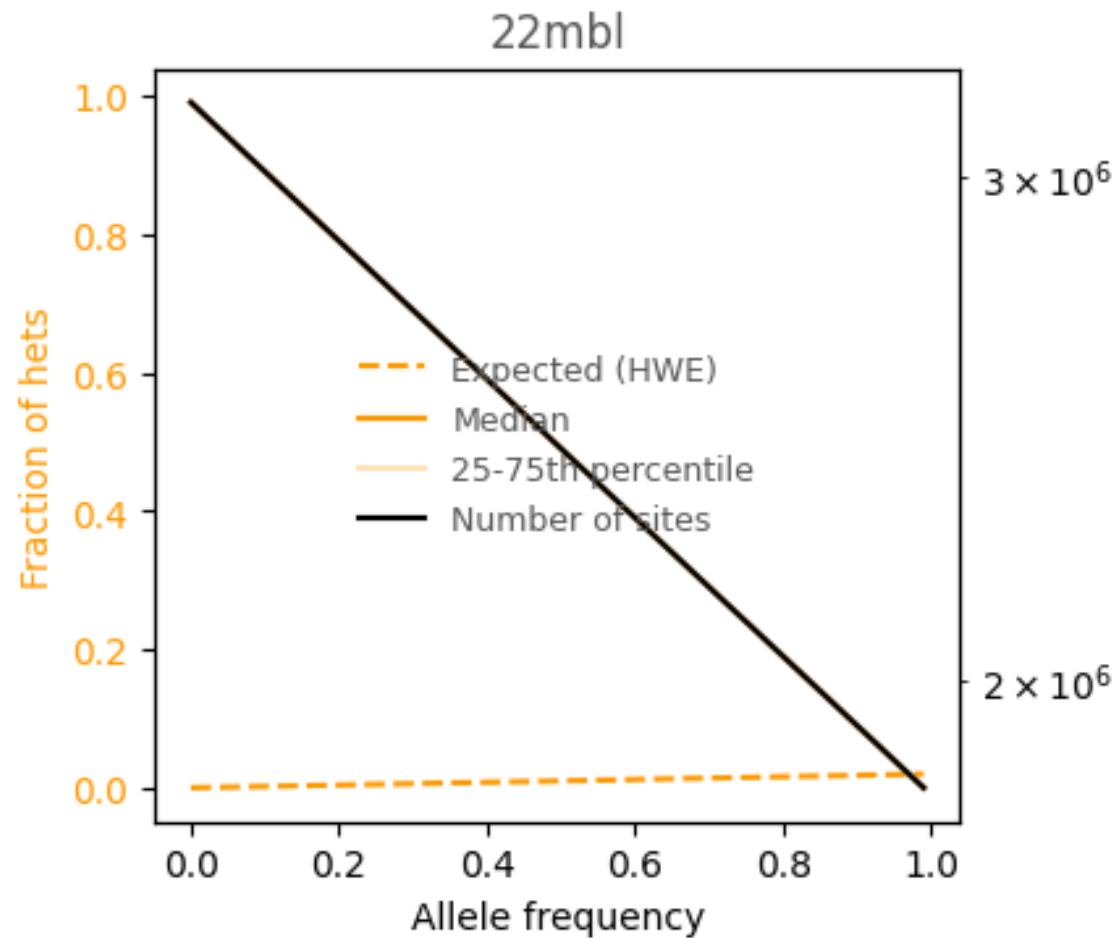# Indel distribution

# Fraction of alternate indel allele

# Depth distribution

# Number of HETs by AF

# Substitution types