# Summary Numbers

| Callset | SNPs | | | indels | | MNPs | others |
|---|---|---|---|---|---|---|---|
| | n | ts/tv | (1st ALT) | n | frm* | | |
| 21hat | 4,022,797 | 1.94 | 1.95 | 927,330 | – | 0 | 0 |
| | | | | | | * frameshift ratio: out/(out+in) | |

| Callset | singletons (AC=1) | | | multiallelic | |
|---|---|---|---|---|---|
| | SNPs | ts/tv | indels | sites | SNPs |
| 21hat | 61.6% | 1.91 | 65.5% | 90,561 | 1,904 |

- 21hat .. `/ngc/projects2/gm/data/archive/2022/variants/snv/21hathanm-103915646963-Normal_B`
`lood_noinfo-WGS_v1_IlluminaDNAPCRFree_RHGM01772-220928_A01176_BH3FHLDSX5-EXT_LAB`
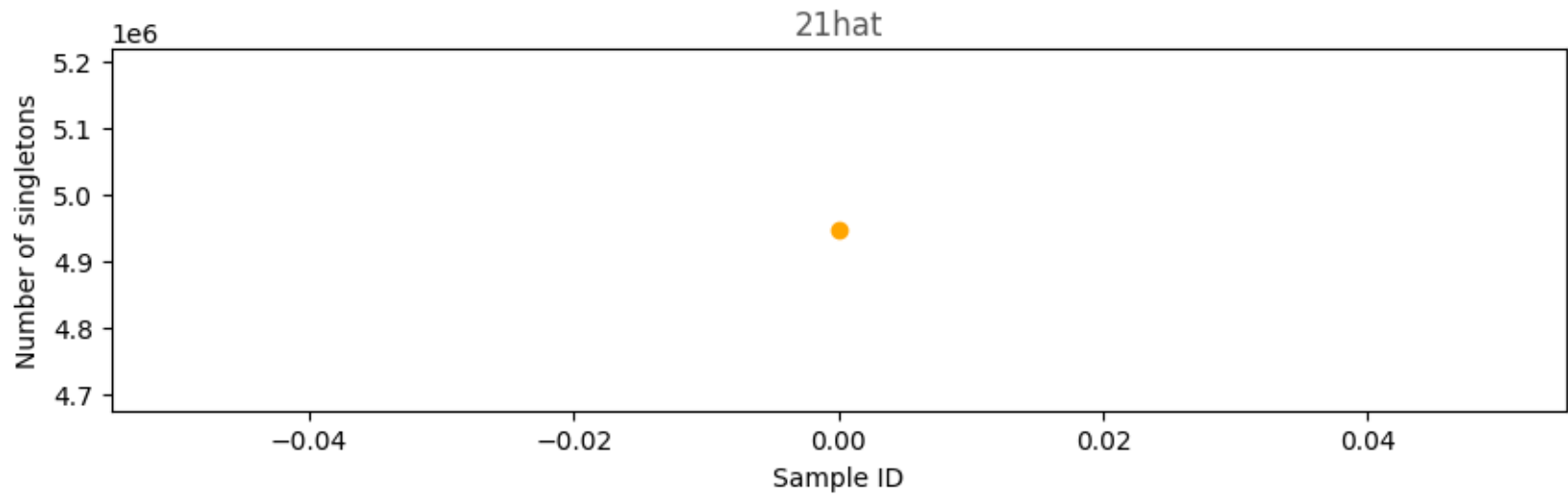`KA_NGCWGS-NGCWGS05606_22RKG012909_snv_germline_raw.haplotype_caller.vcf.gz`
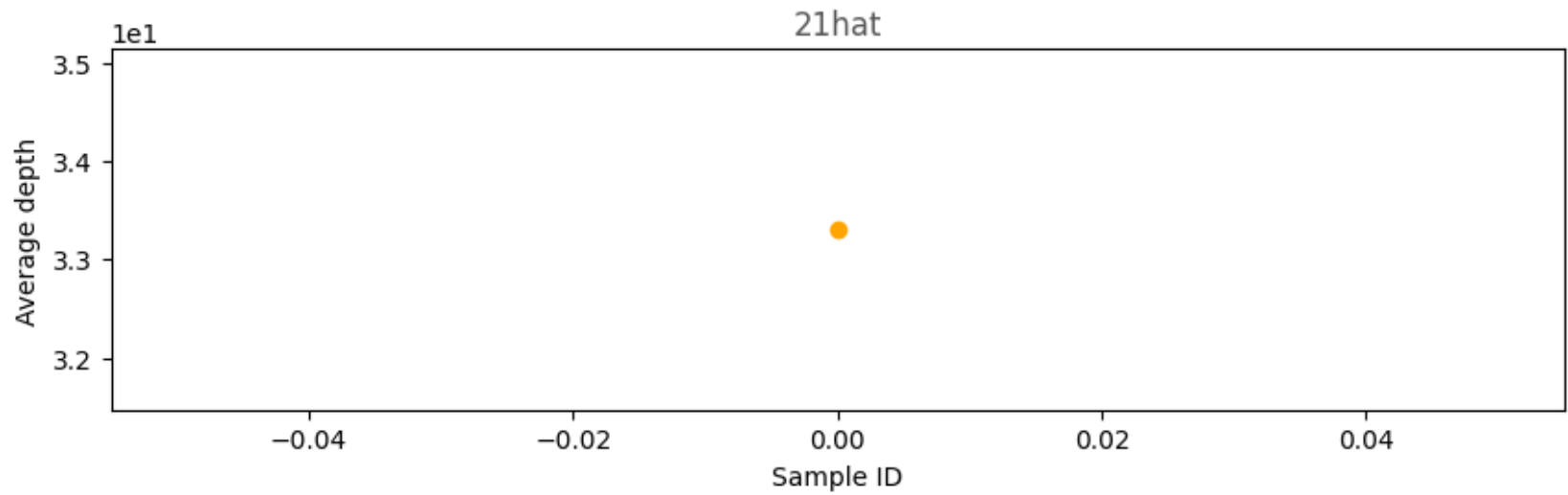
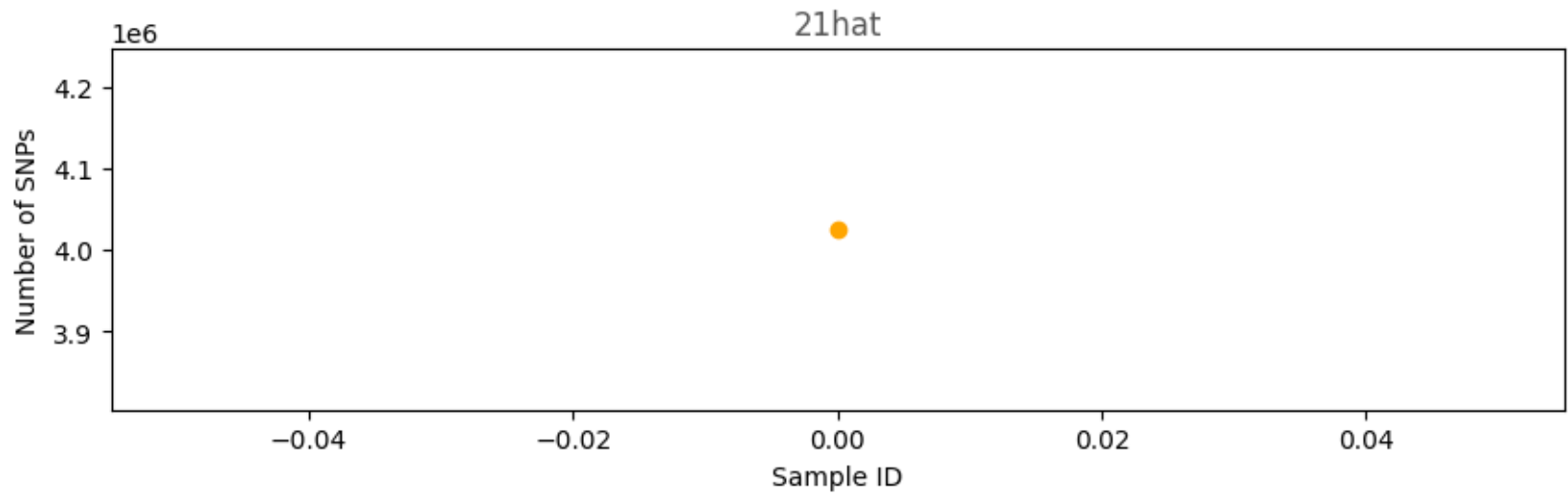# Ts/Tv by sample
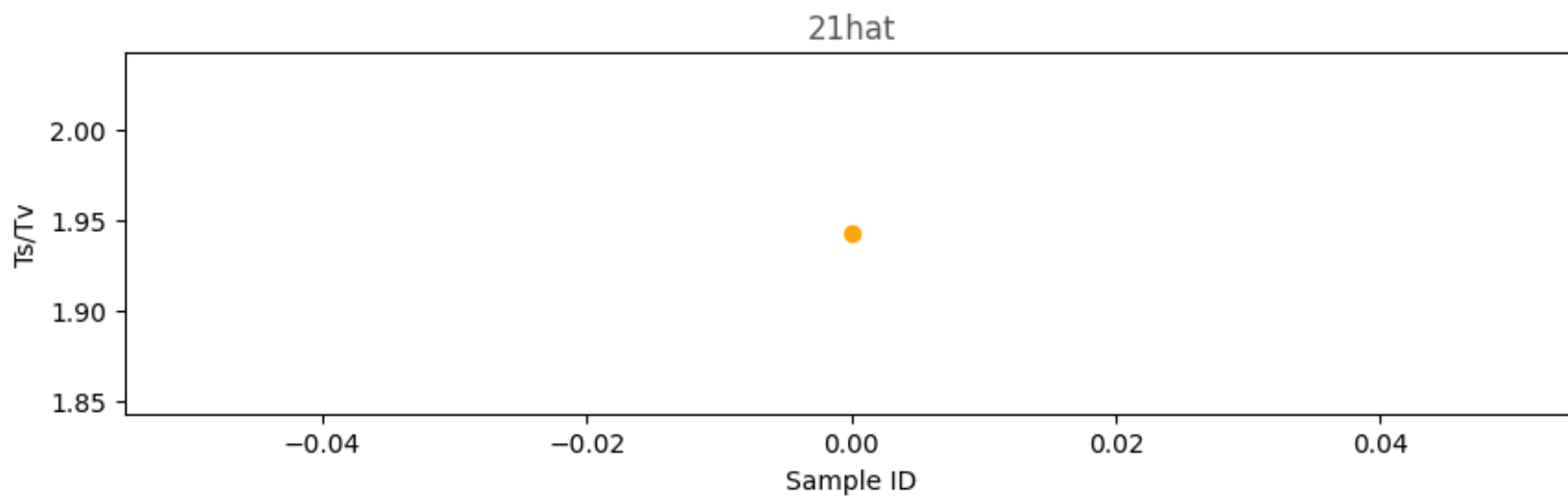
# Hets vs non-ref Homs by sample
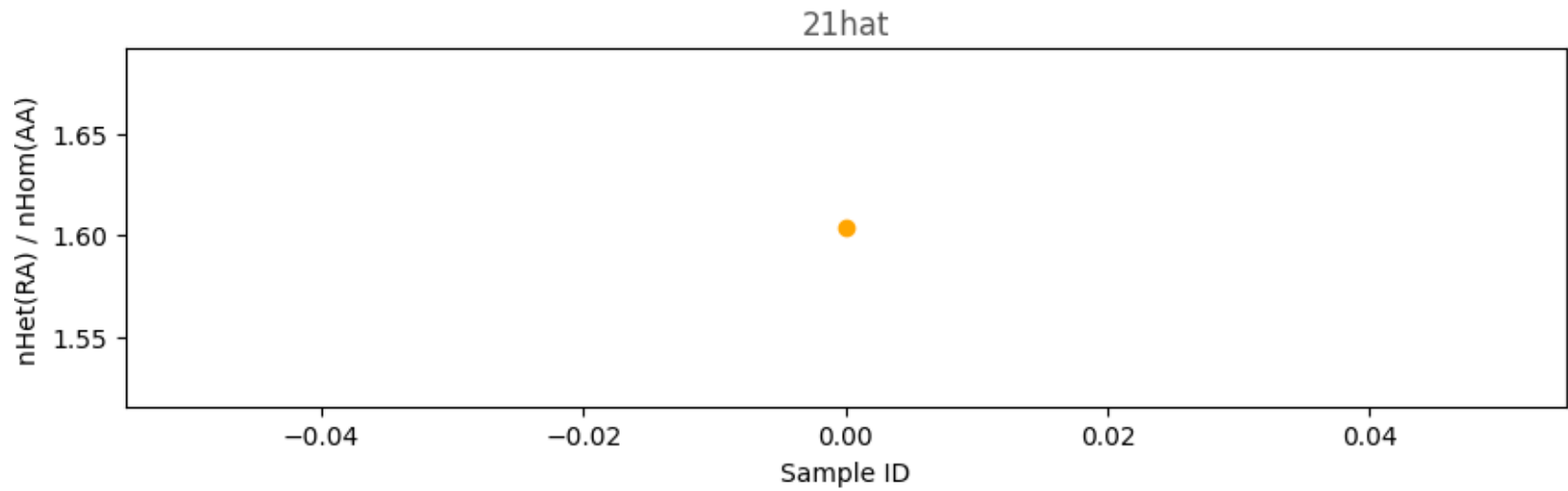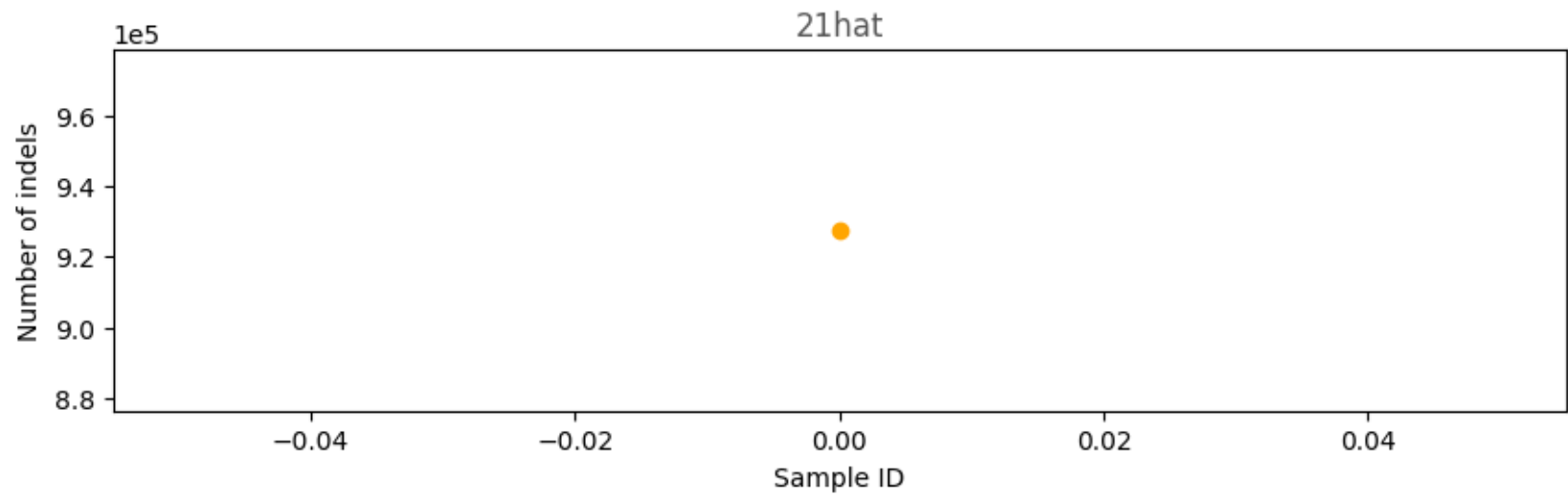
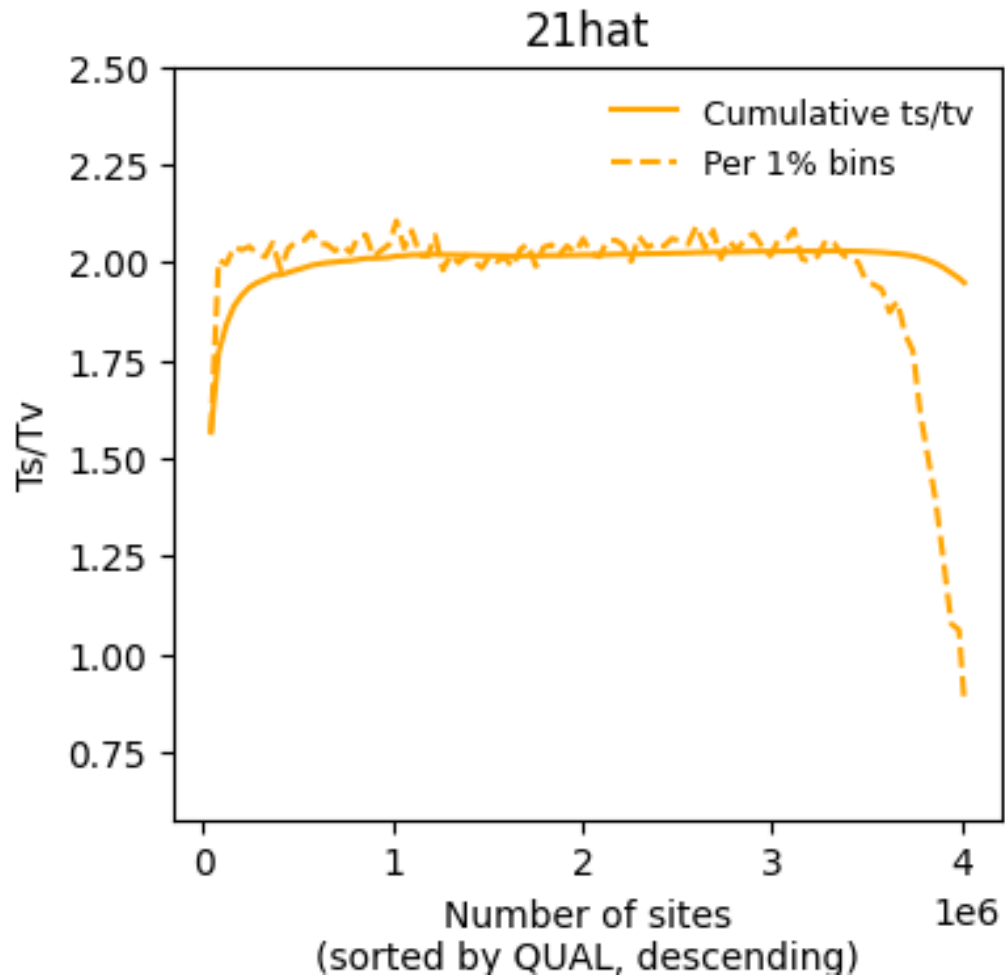# Singletons by sample (hets and homs)
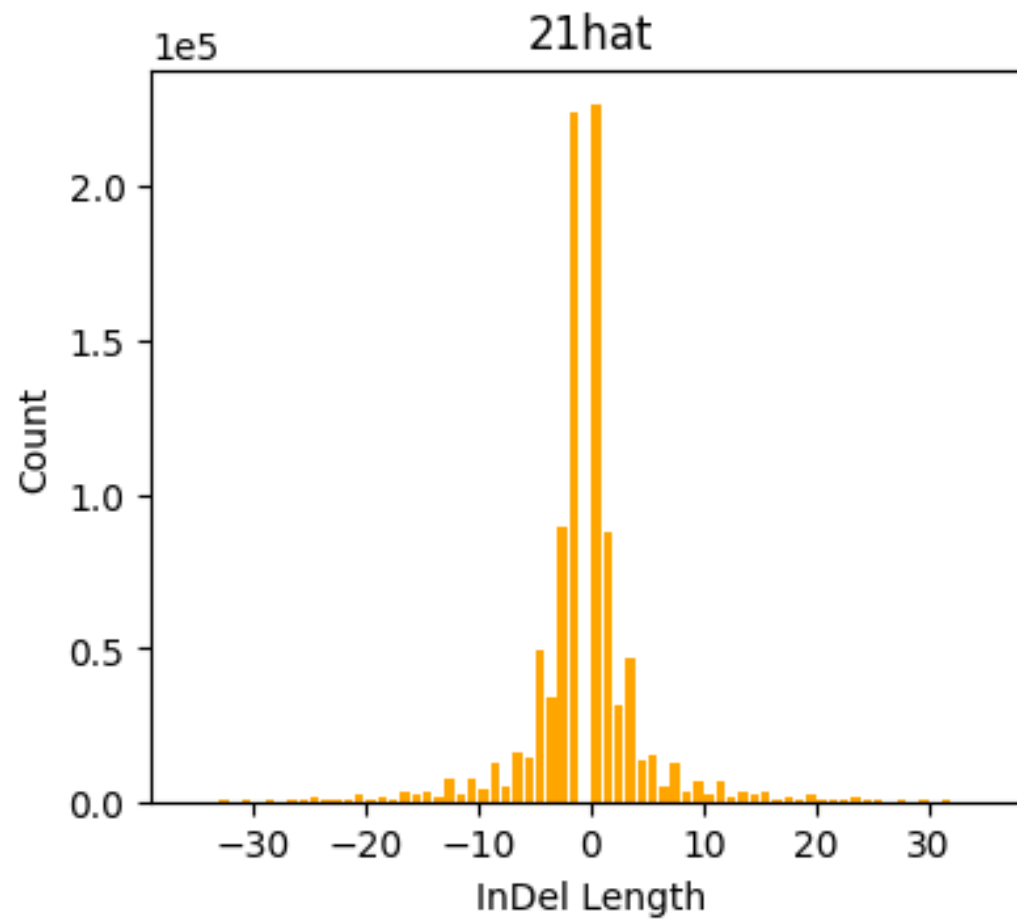
# Average depth by sample

# Number of SNPs by sample

# Number of indels by sample

# Ts/Tv stratified by QUAL

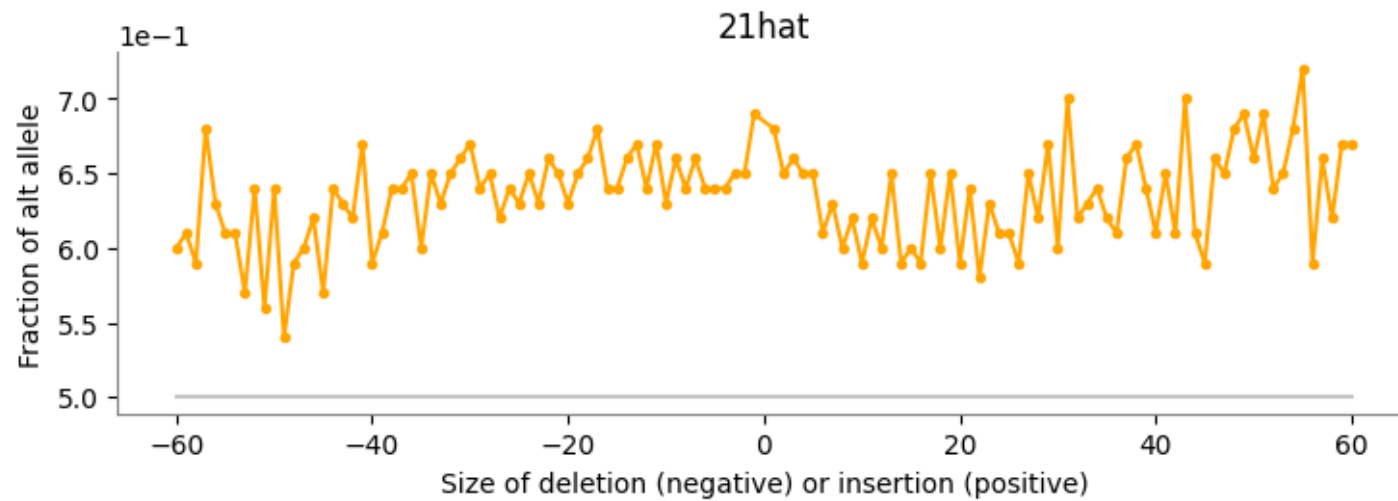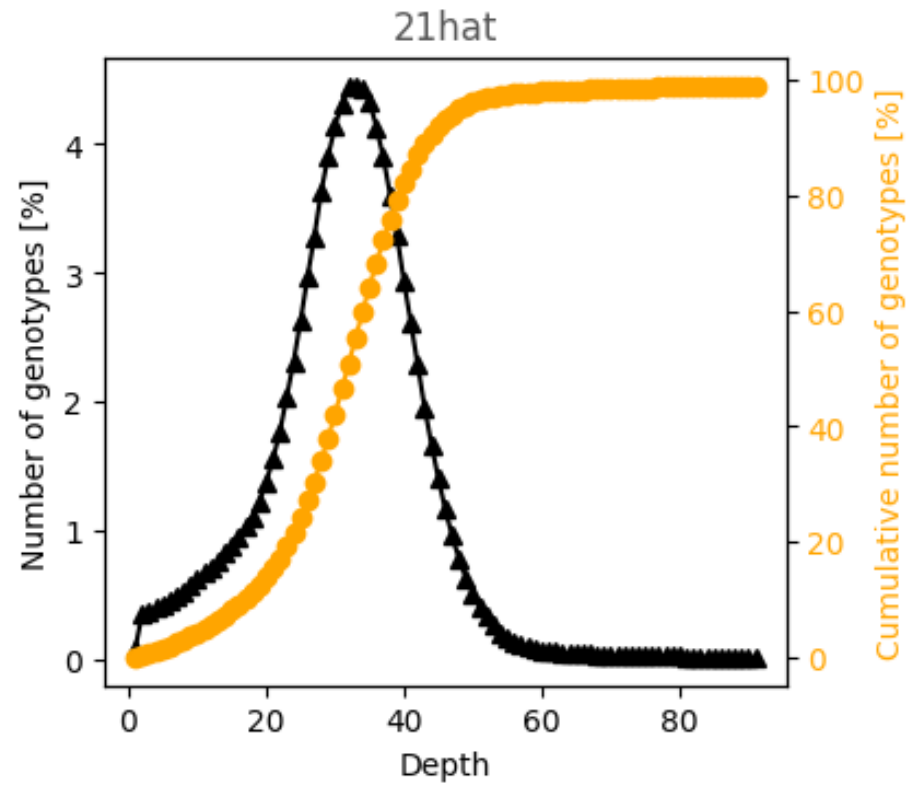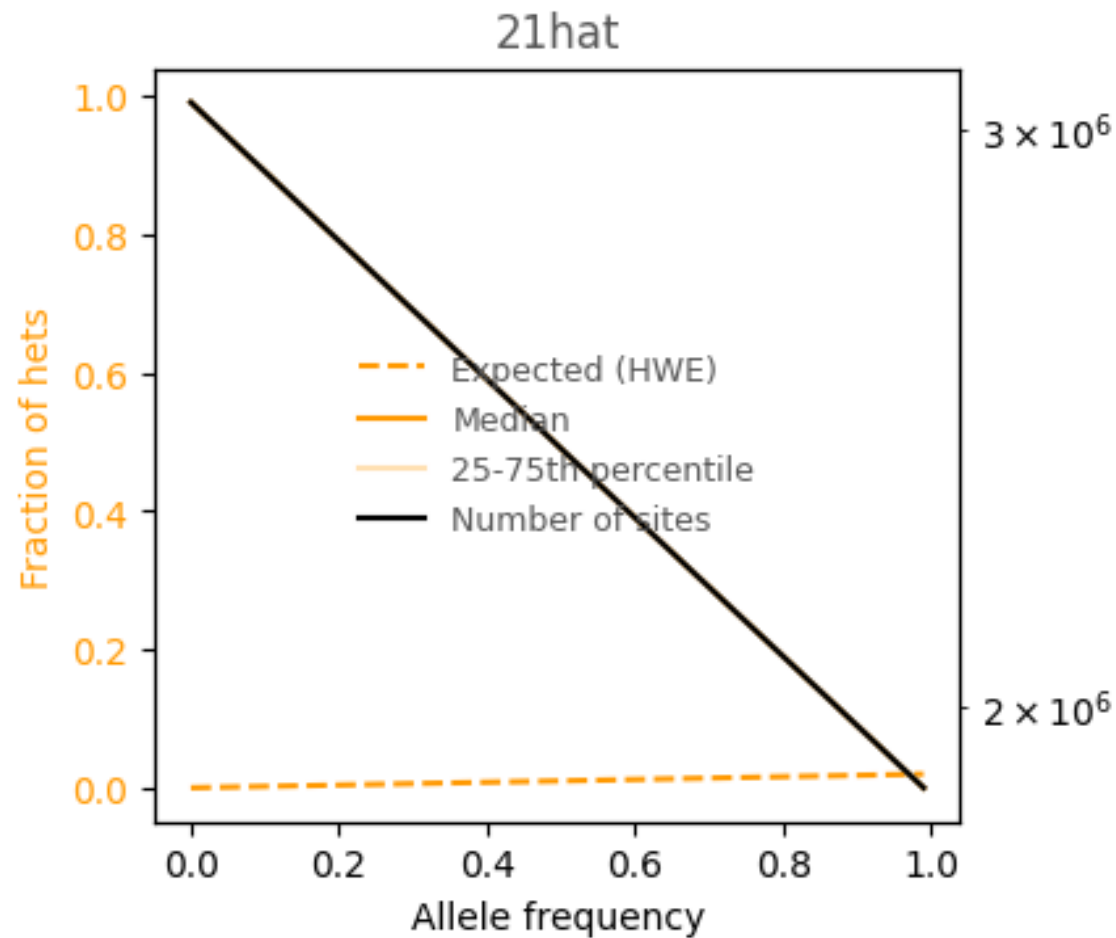# Indel distribution

# Fraction of alternate indel allele

# Depth distribution

# Number of HETs by AF

# Substitution types