

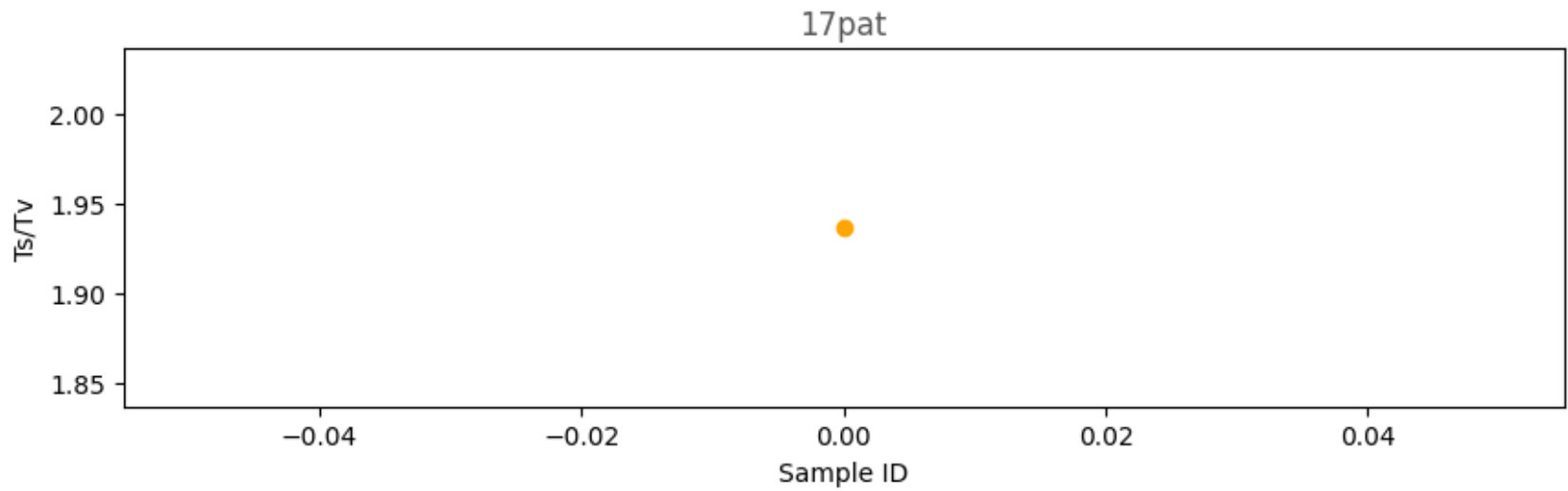
Summary Numbers

| Callset | SNPs | | | indels | | MNPs | others |
|----------------------------------|-----------|-------|-----------|---------|------|------|--------|
| | n | ts/tv | (1st ALT) | n | frm* | | |
| 17pat | 4,041,205 | 1.94 | 1.94 | 935,022 | – | 0 | 0 |
| * frameshift ratio: out/(out+in) | | | | | | | |

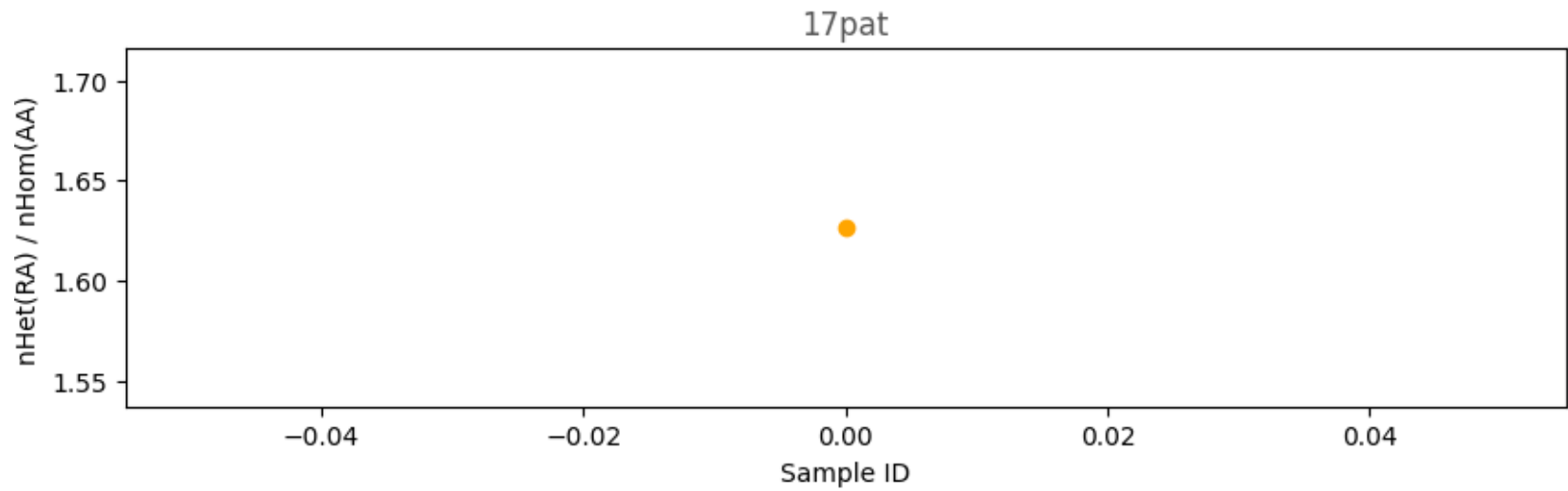
| Callset | singletons (AC=1) | | | multiallelic | |
|---------|-------------------|-------|--------|--------------|-------|
| | SNPs | ts/tv | indels | sites | SNPs |
| 17pat | 61.9% | 1.91 | 65.9% | 93,067 | 1,753 |

- 17pat .. /ngc/projects2/gm/data/archive/2022/variants/snv/17patibm-103794069402-Normal_B
 lood_noinfo-WGS_v1_IlluminaDNAPCRFree_RHGM00355-211019_A01411_AHHHWJDSX2-EXT_LAB
 KA_NGCWGS-NGCWGS00254_21RKG022419x01_snv_germline_raw.haplotype_caller.vcf.gz

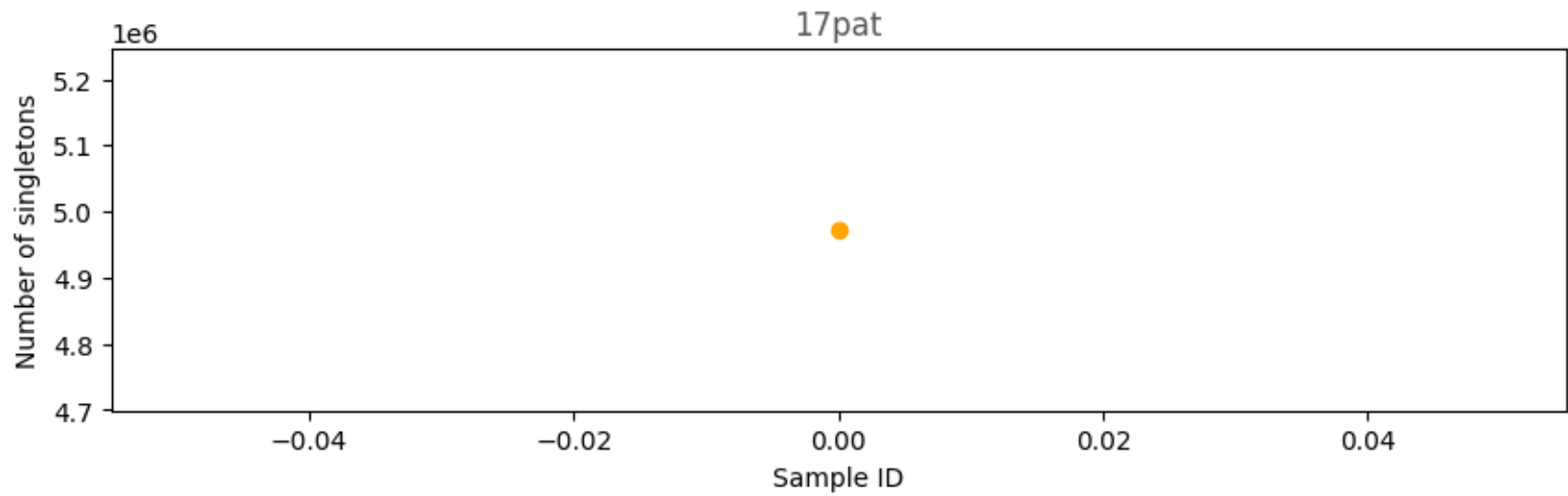
Ts/Tv by sample



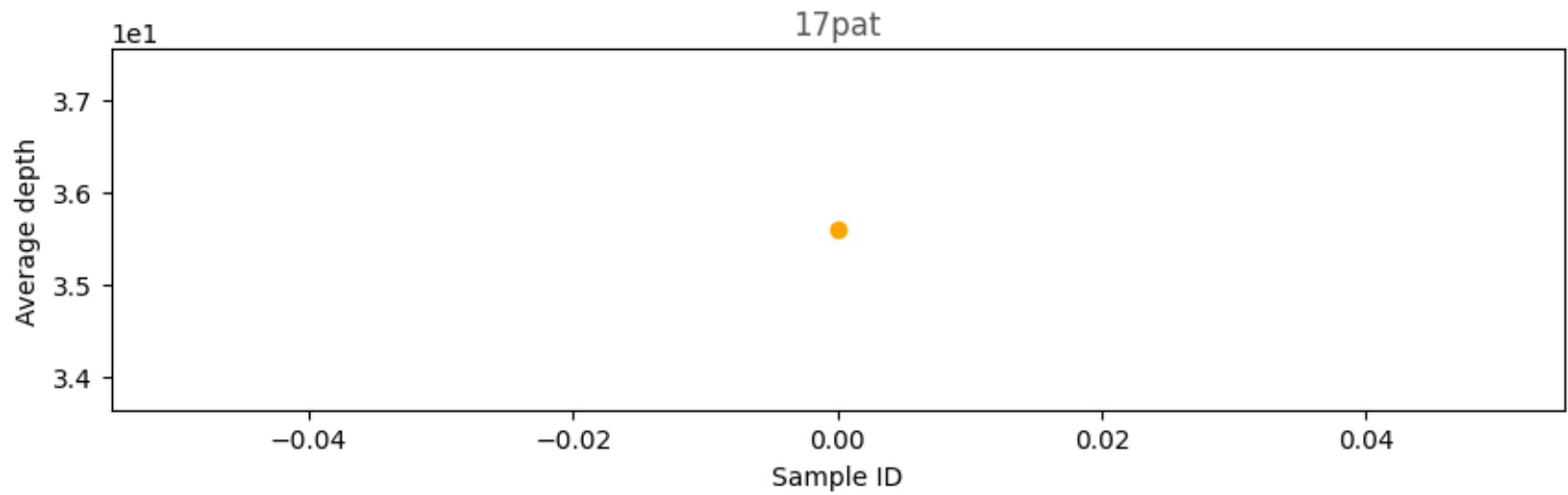
Hets vs non-ref Homs by sample



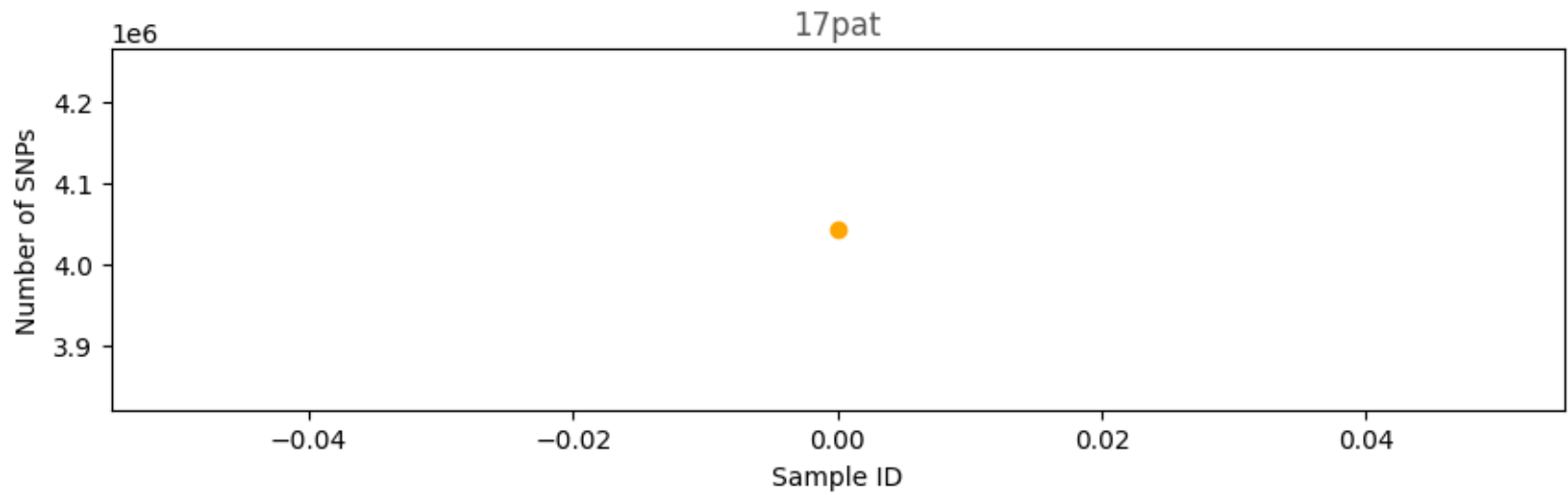
Singletons by sample (hets and homs)



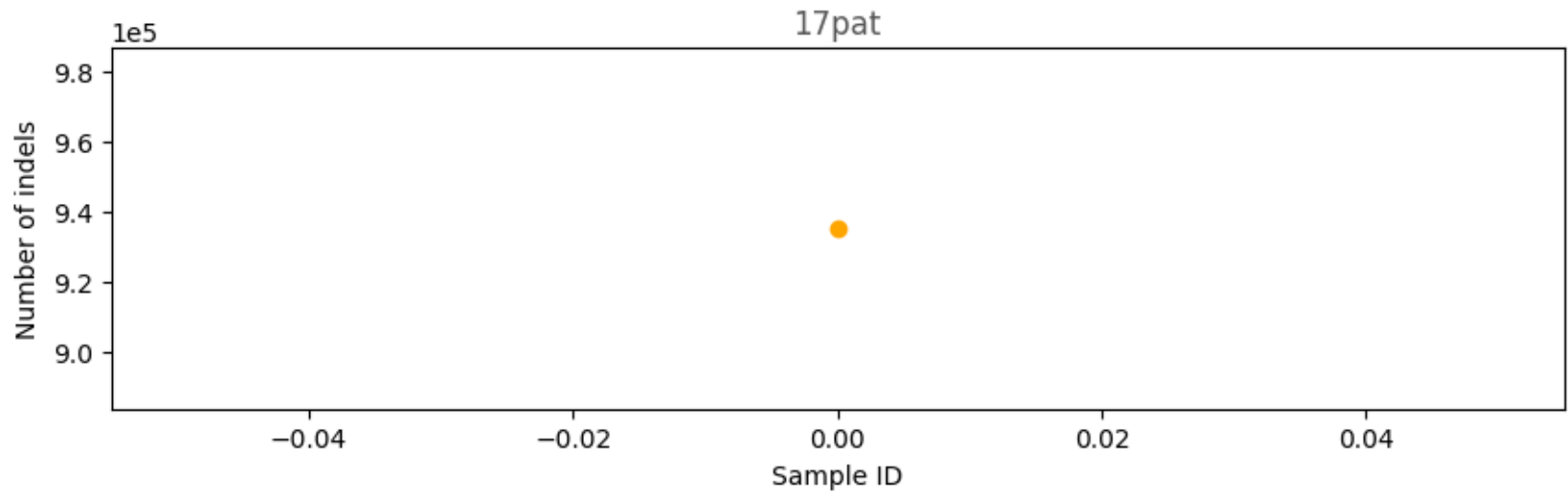
Average depth by sample



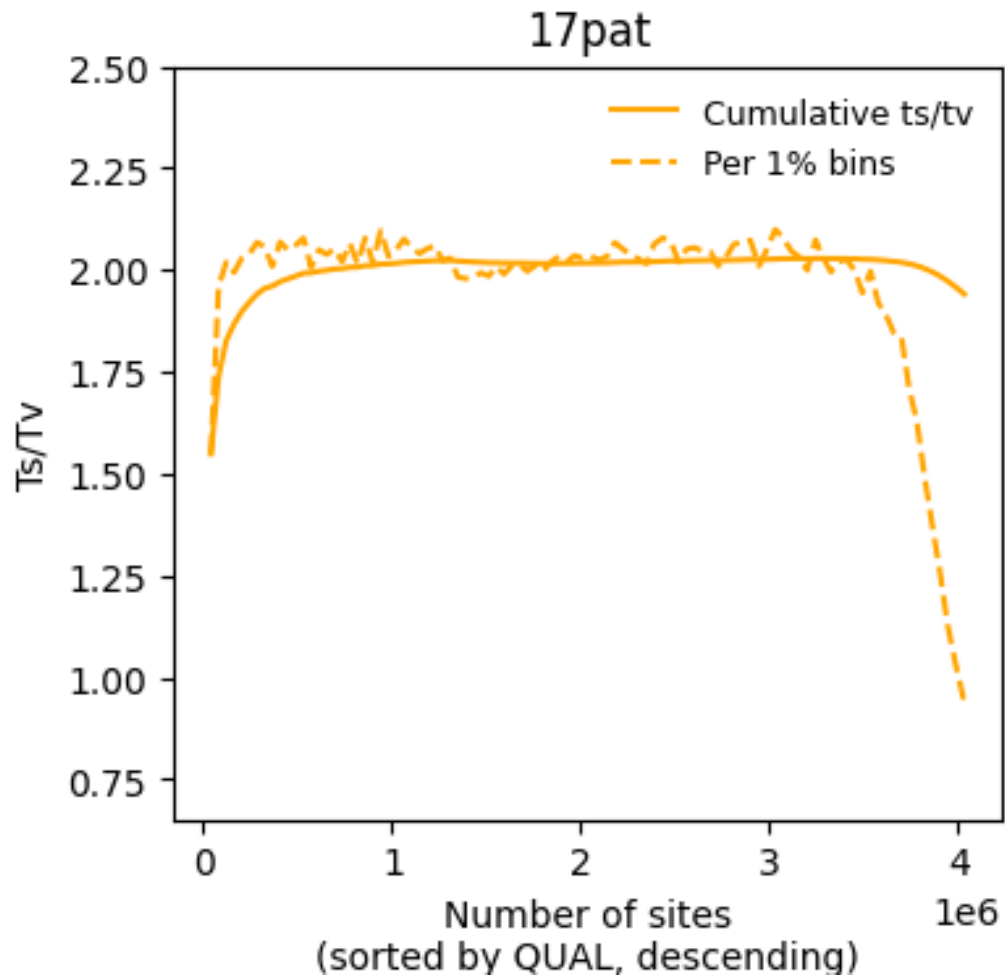
Number of SNPs by sample



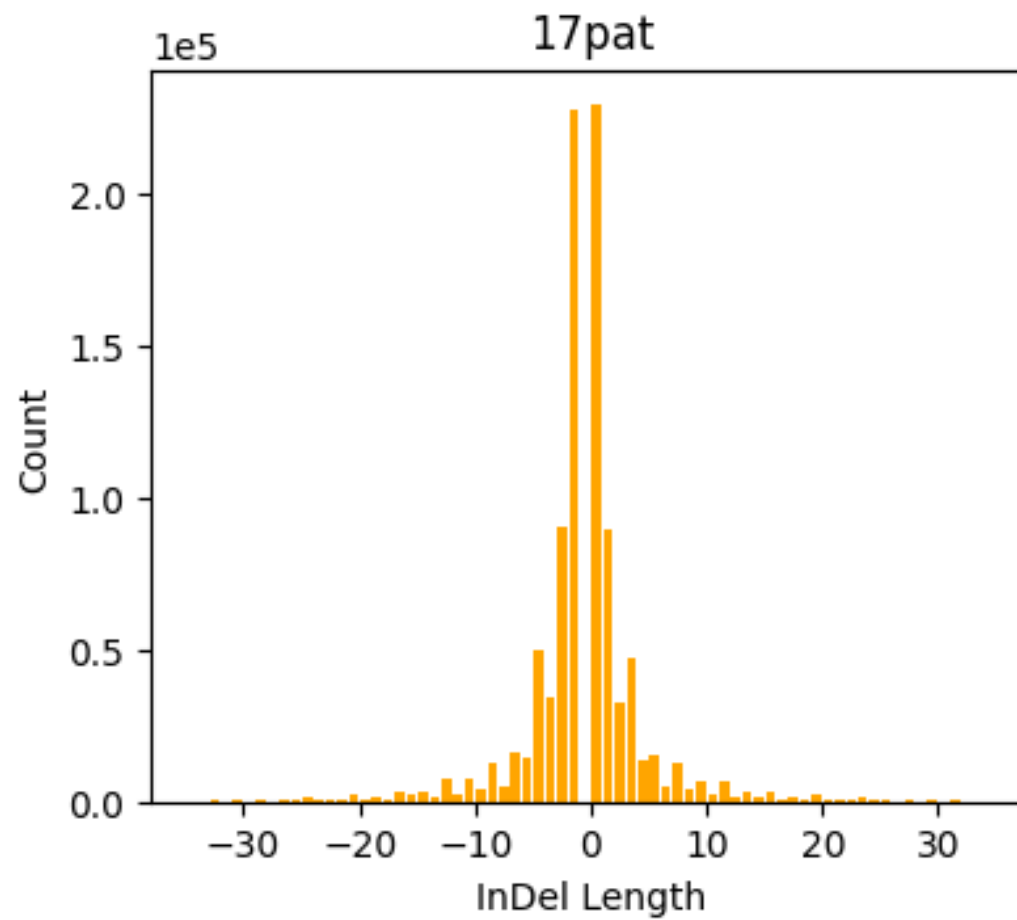
Number of indels by sample



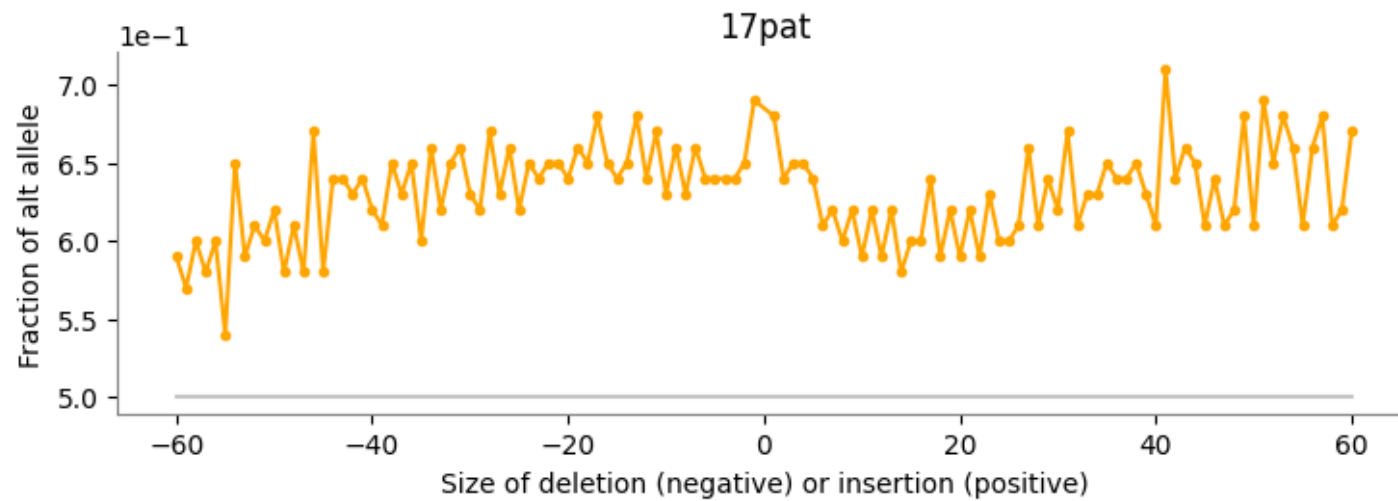
Ts/Tv stratified by QUAL



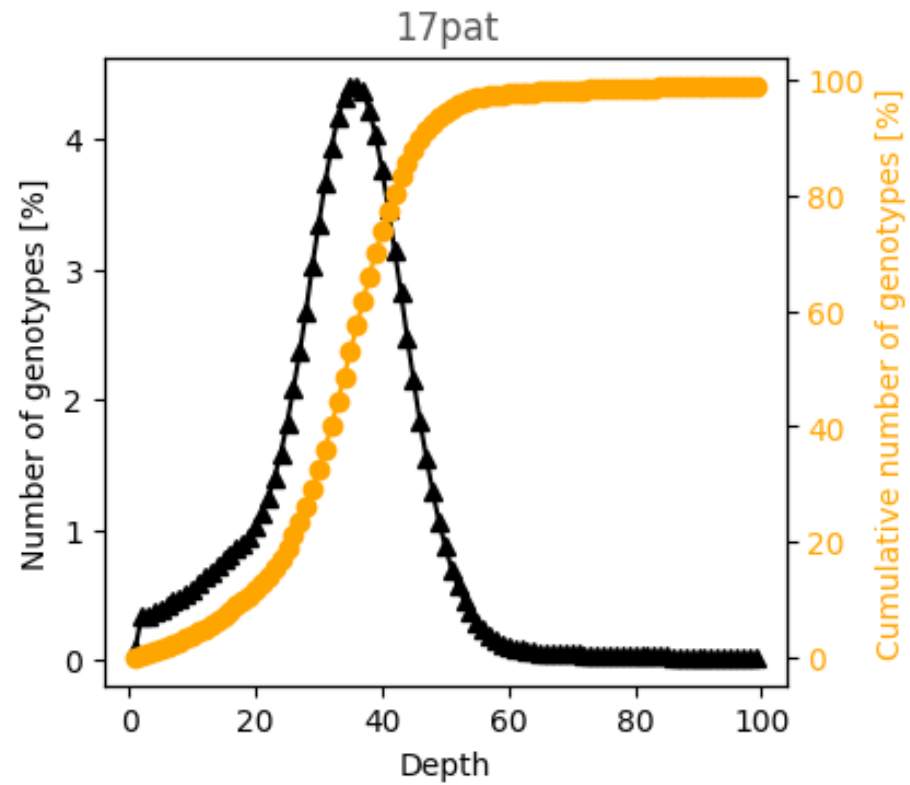
Indel distribution



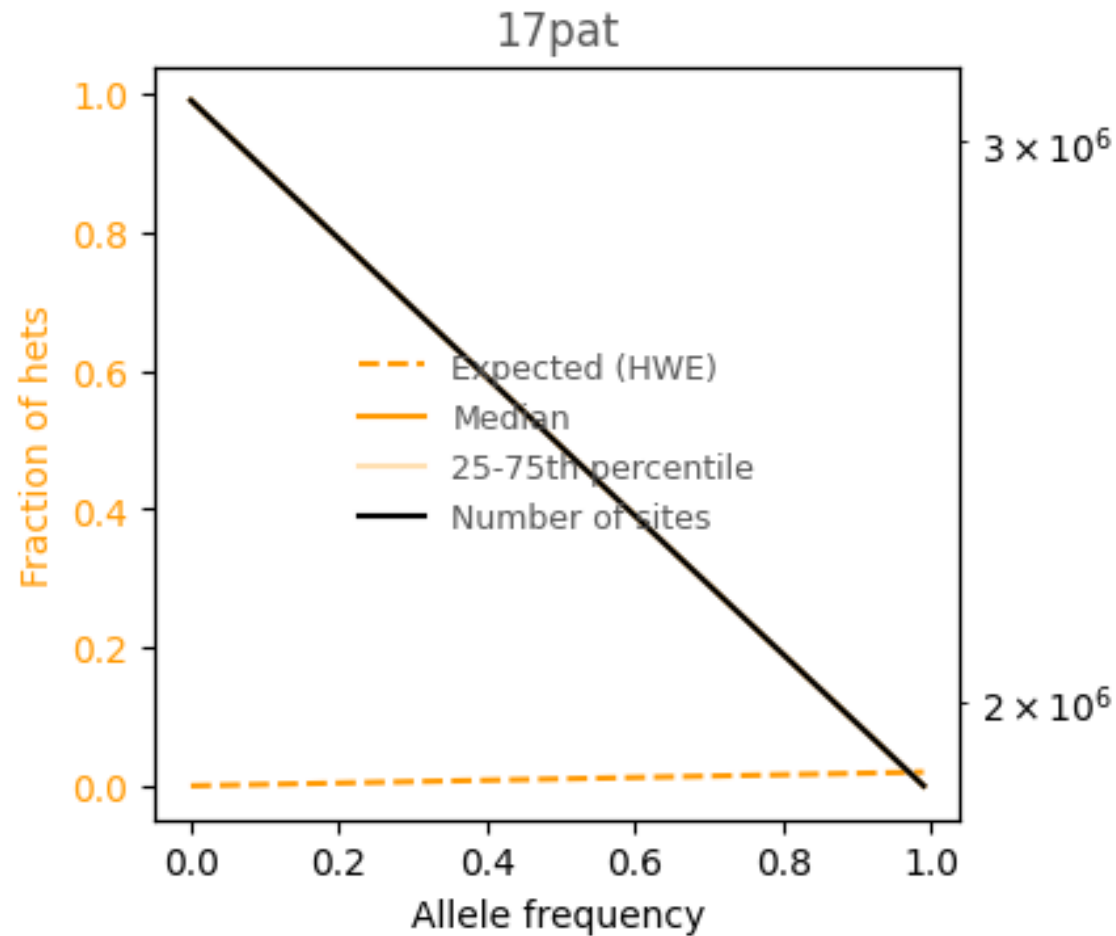
Fraction of alternate indel allele



Depth distribution



Number of HETs by AF



Substitution types

