

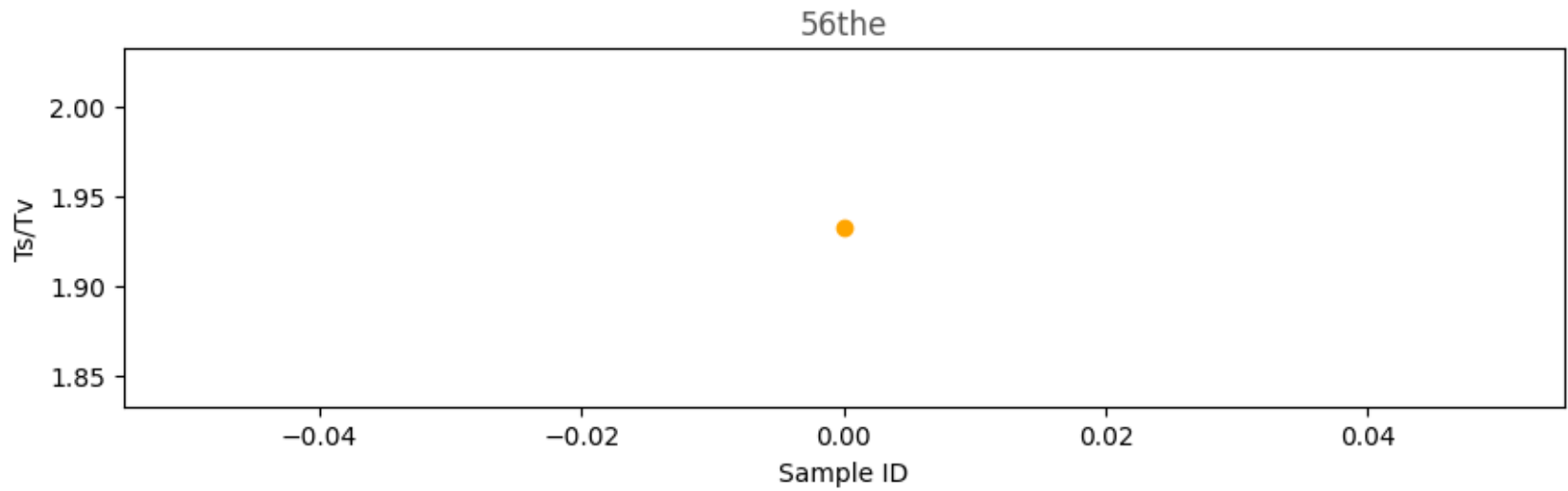
Summary Numbers

| Callset | SNPs | | | indels | | MNPs | others |
|----------------------------------|-----------|-------|-----------|---------|------|------|--------|
| | n | ts/tv | (1st ALT) | n | frm* | | |
| 56the | 4,041,630 | 1.93 | 1.94 | 943,260 | – | 0 | 0 |
| * frameshift ratio: out/(out+in) | | | | | | | |

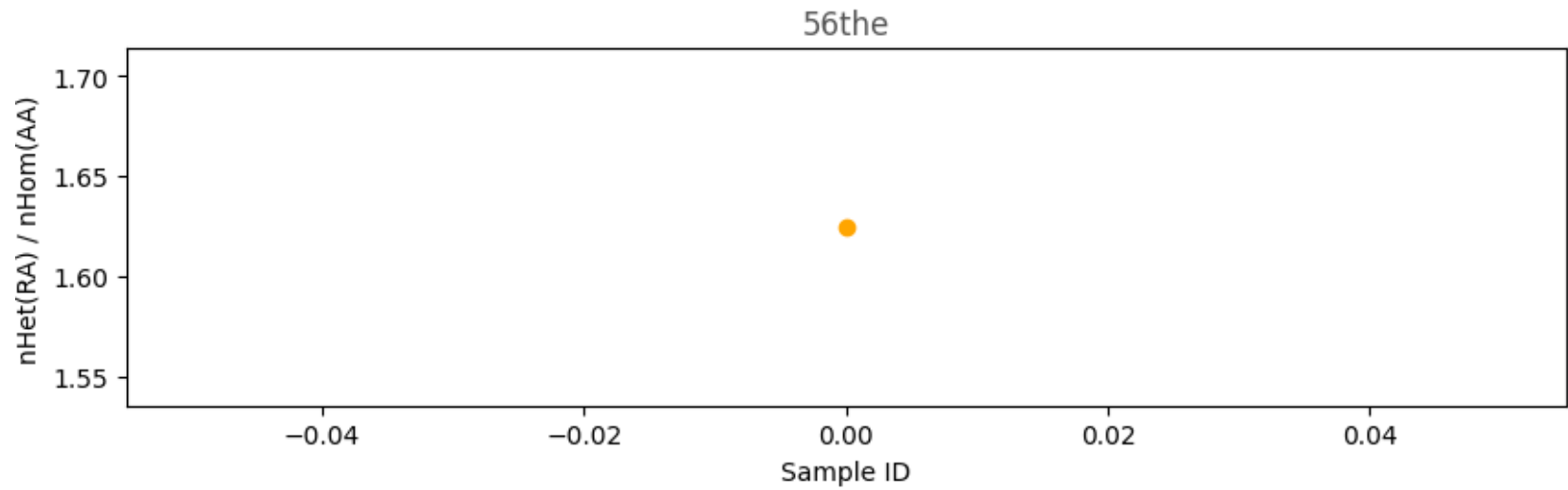
| Callset | singletons (AC=1) | | | multiallelic | |
|---------|-------------------|-------|--------|--------------|-------|
| | SNPs | ts/tv | indels | sites | SNPs |
| 56the | 61.9% | 1.90 | 66.7% | 97,322 | 1,938 |

- 56the .. /ngc/projects2/gm/data/archive/2022/variants/snv/56thensqm-103859456290-Normal_B
 lood_noinfo-WGS_v1_IlluminaDNAPCRFree_RHGM00729-220422_A01176_BH2CKMDSX3-EXT_LAB
 KA_NGCWGS-NGCWGS04162-snv_germline_raw.haplotype_caller.vcf.gz

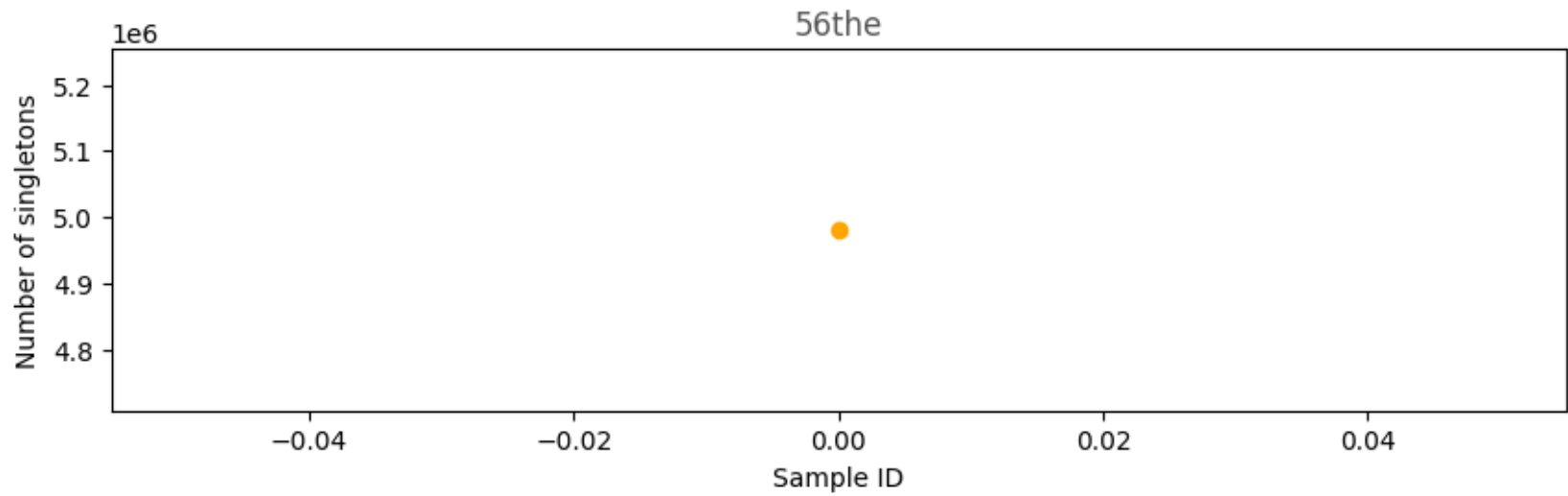
Ts/Tv by sample



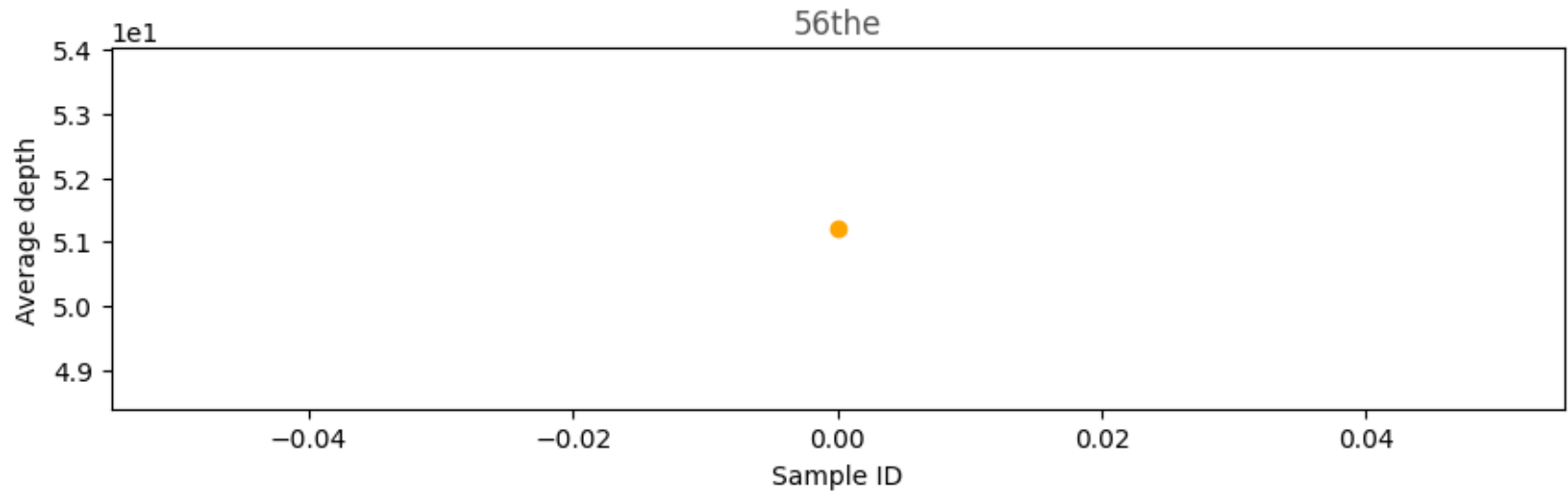
Hets vs non-ref Homs by sample



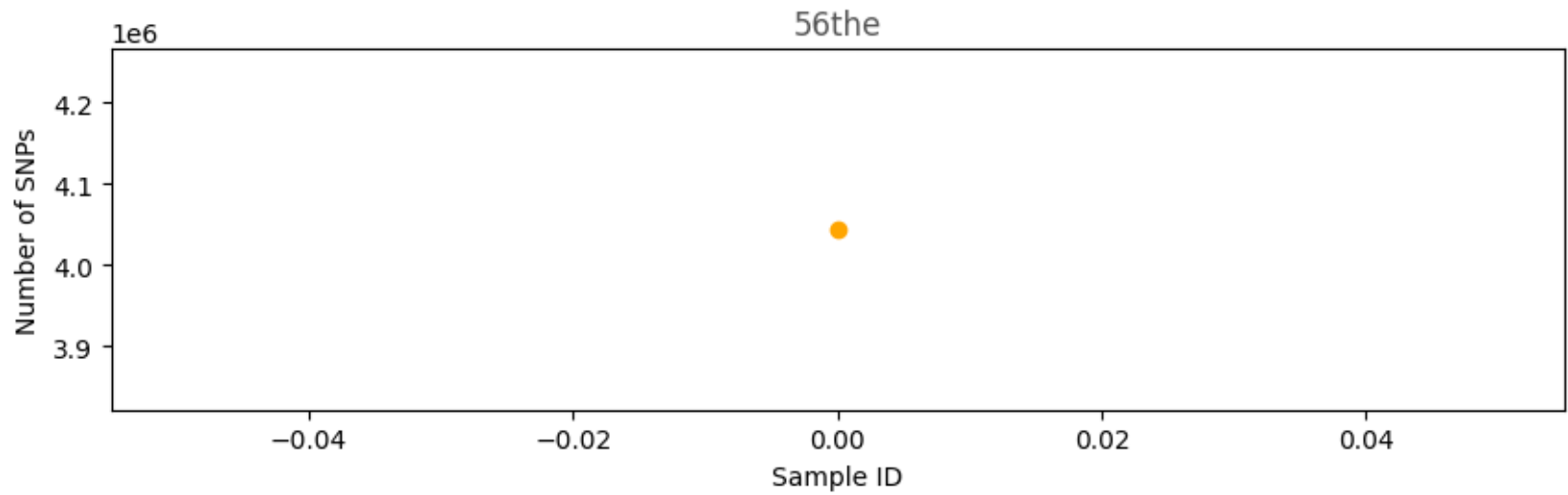
Singletons by sample (hets and homs)



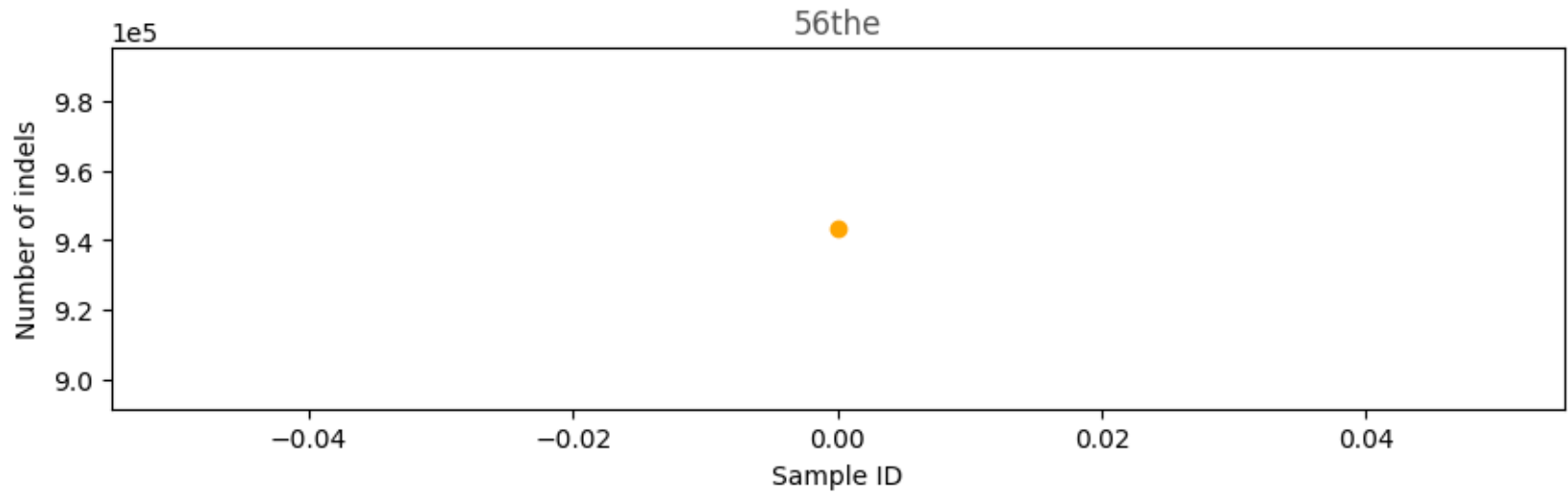
Average depth by sample



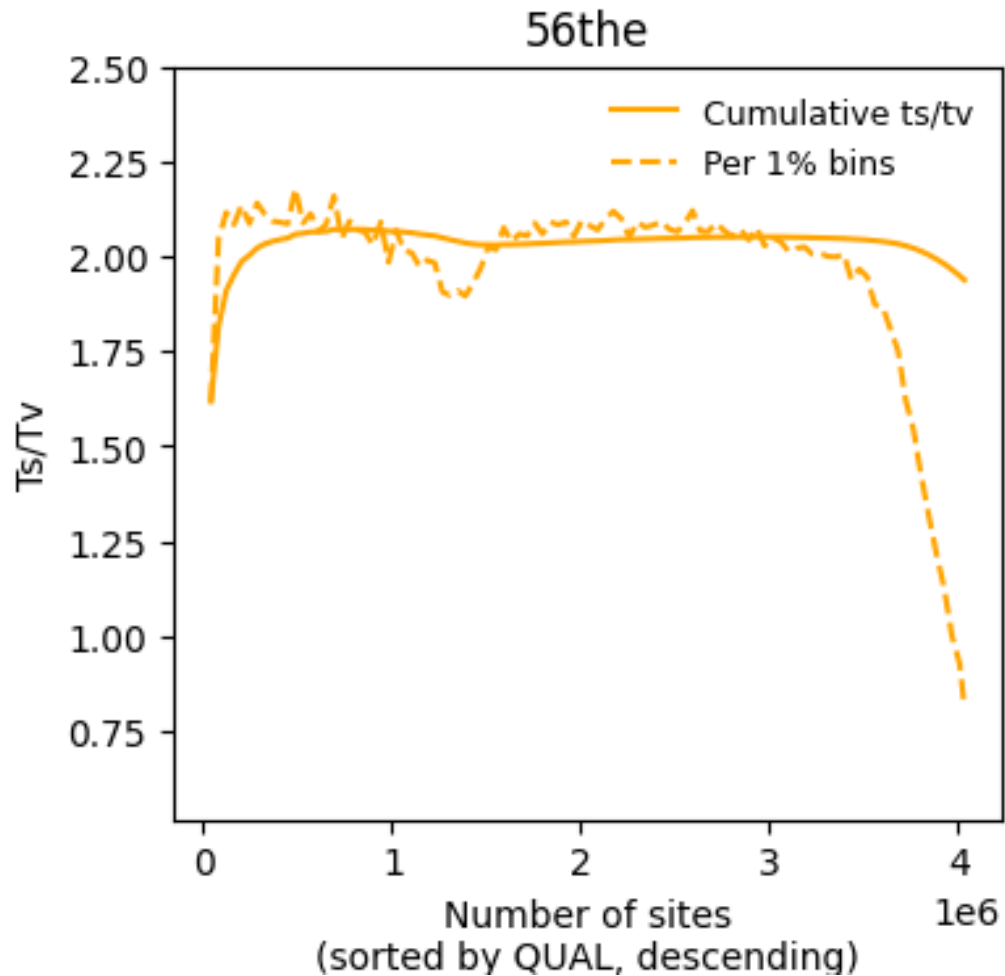
Number of SNPs by sample



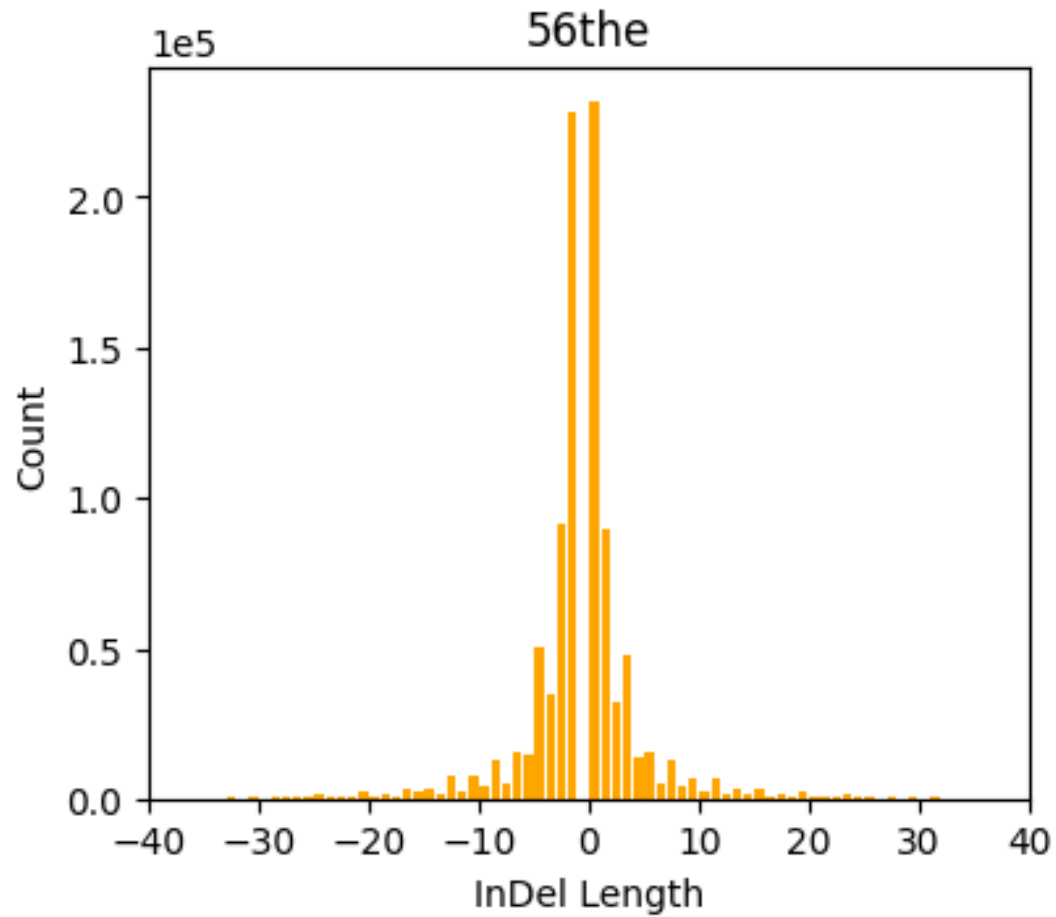
Number of indels by sample



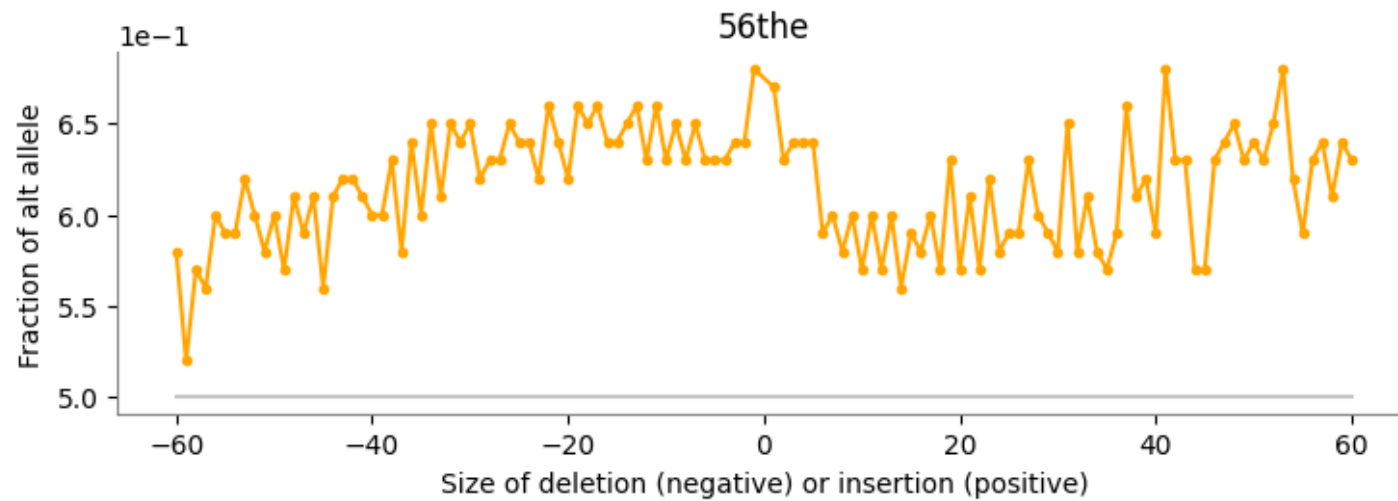
Ts/Tv stratified by QUAL



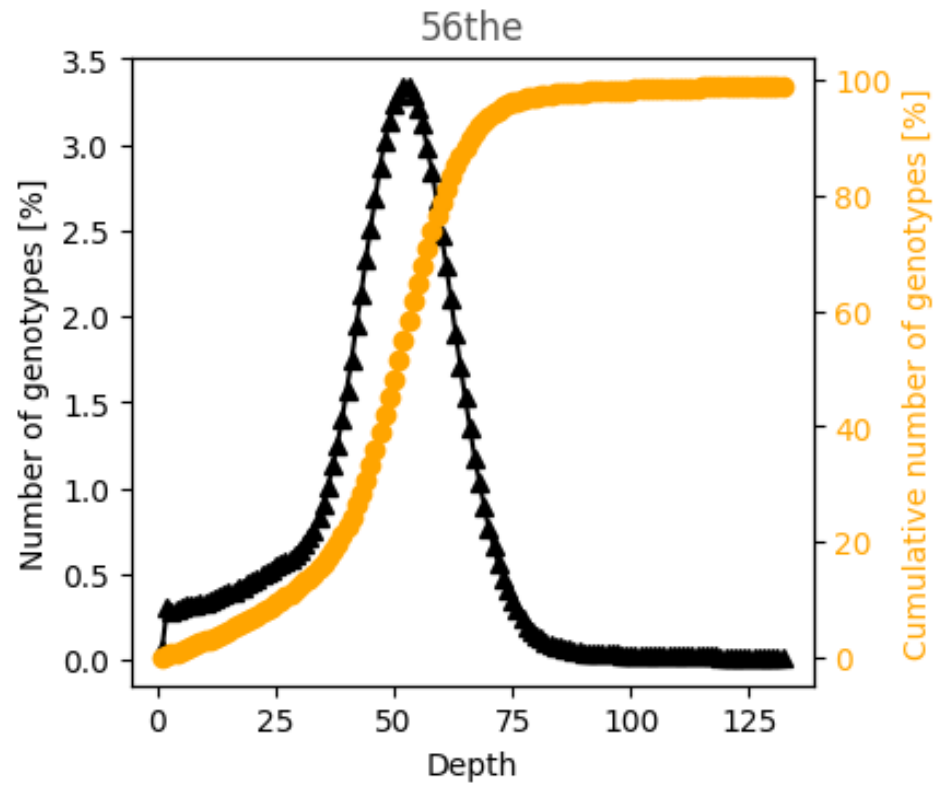
Indel distribution



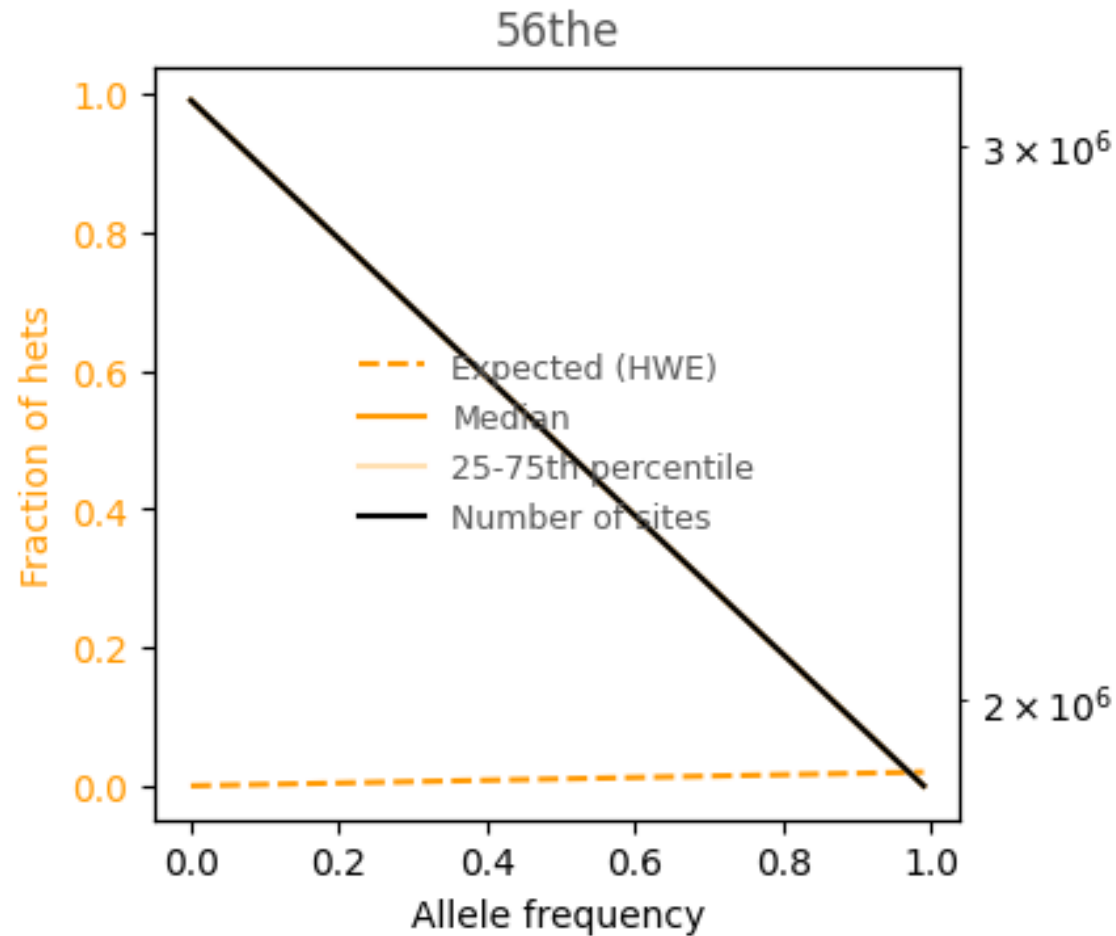
Fraction of alternate indel allele



Depth distribution



Number of HETs by AF



Substitution types

