

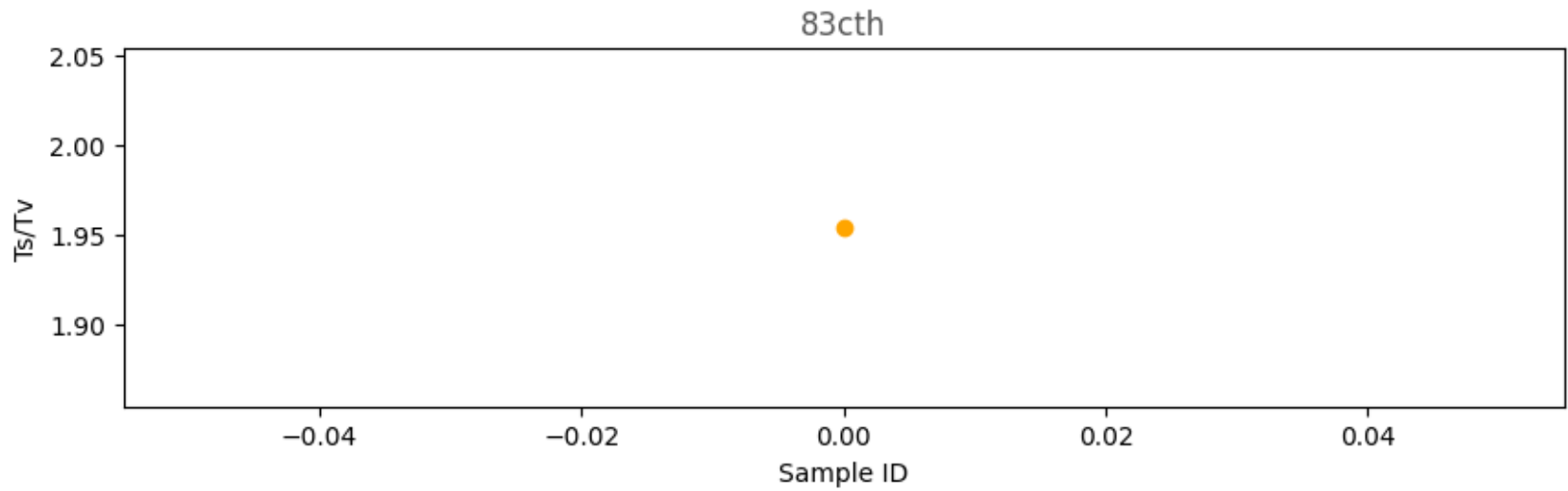
Summary Numbers

| Callset | SNPs | | | indels | | MNPs | others |
|----------------------------------|-----------|-------|-----------|---------|------|------|--------|
| | n | ts/tv | (1st ALT) | n | frm* | | |
| 83cth | 4,112,071 | 1.95 | 1.96 | 955,664 | – | 0 | 0 |
| * frameshift ratio: out/(out+in) | | | | | | | |

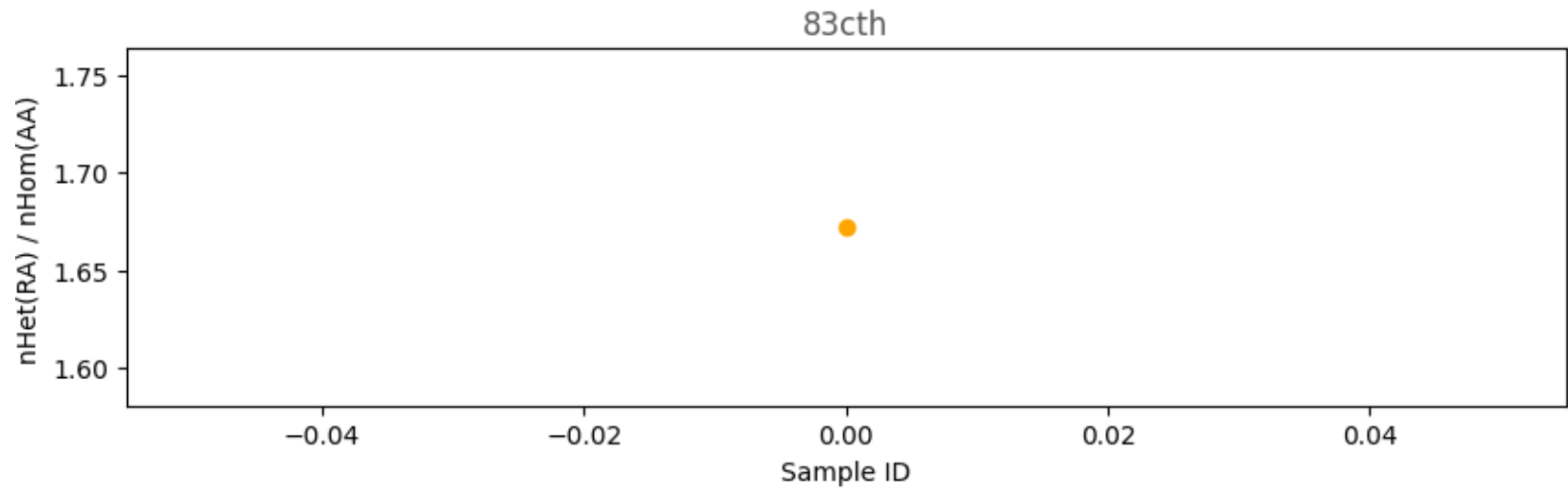
| Callset | singletons (AC=1) | | | multiallelic | |
|---------|-------------------|-------|--------|--------------|-------|
| | SNPs | ts/tv | indels | sites | SNPs |
| 83cth | 62.6% | 1.93 | 67.3% | 99,425 | 1,953 |

- 83cth .. /ngc/projects2/gm/data/archive/2022/variants/snv/83cthsssf-103754933742-Normal_B
 lood_noinfo-WGS_v1_IlluminaDNAPCRFree_RHGM00195-210629_A00559_AHFHNHDSX2-EXT_LAB
 KA_NGCWGS-NGCWGS00111-83h7vnxb2-snv_germline_raw.haplotype_caller.vcf.gz

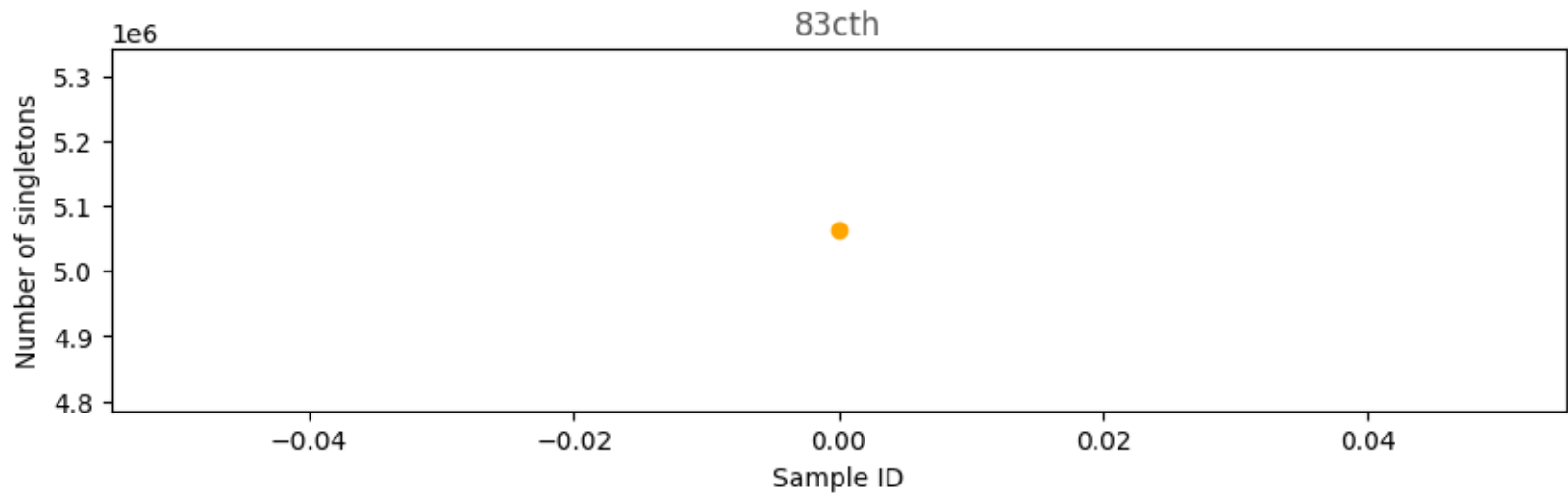
Ts/Tv by sample



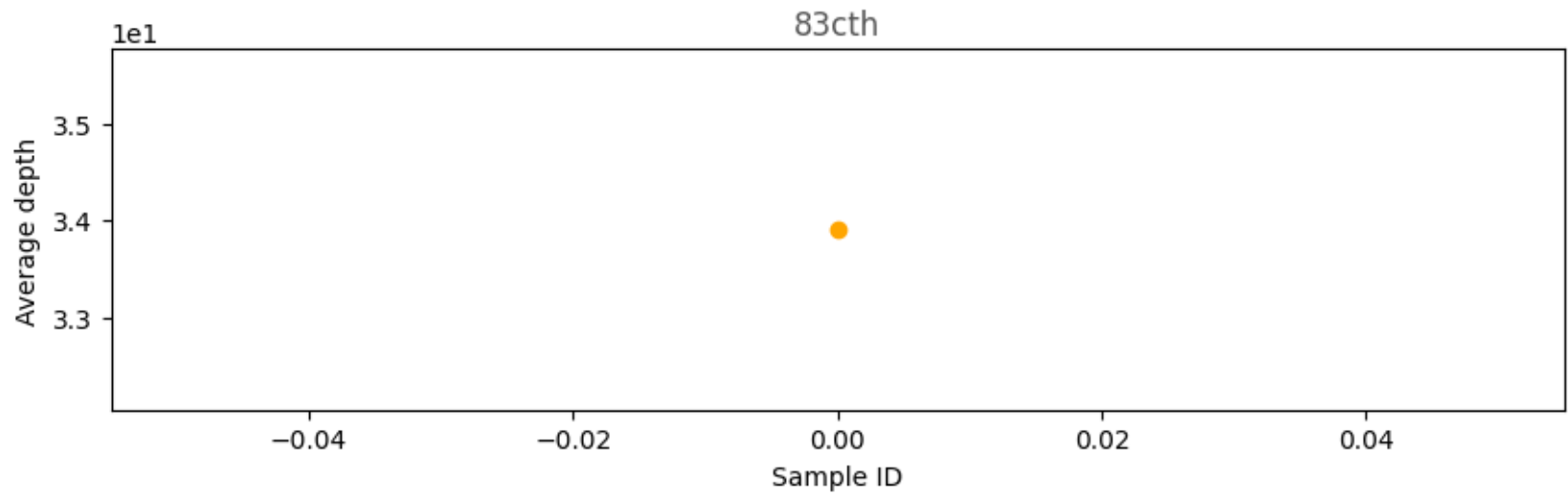
Hets vs non-ref Homs by sample



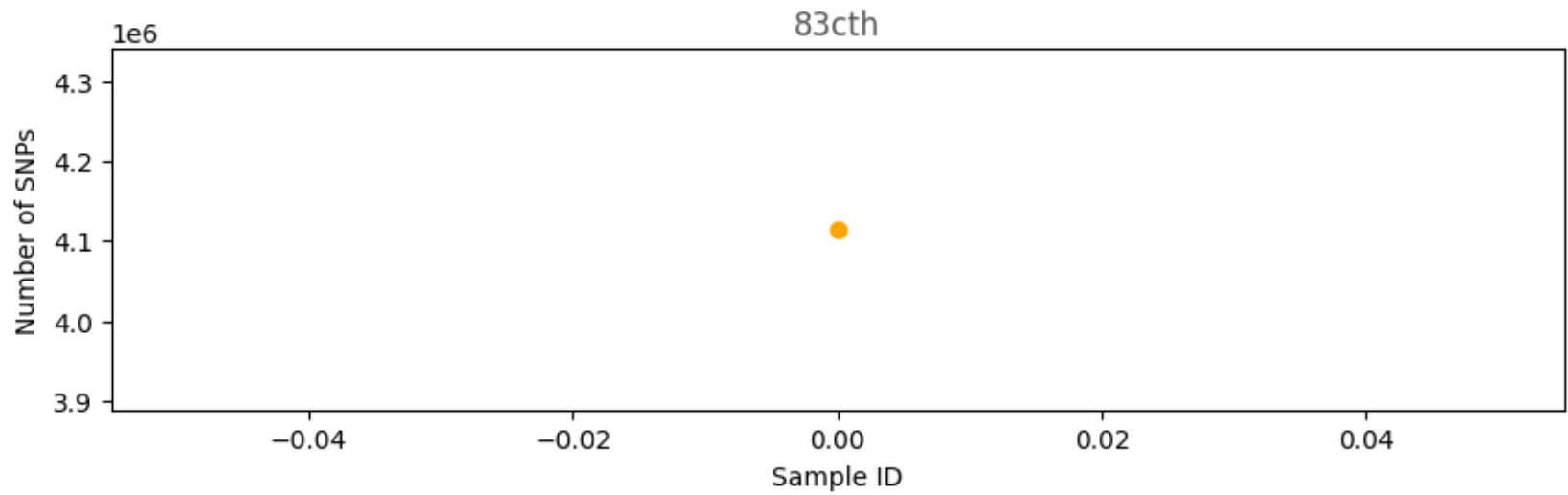
Singletons by sample (hets and homs)



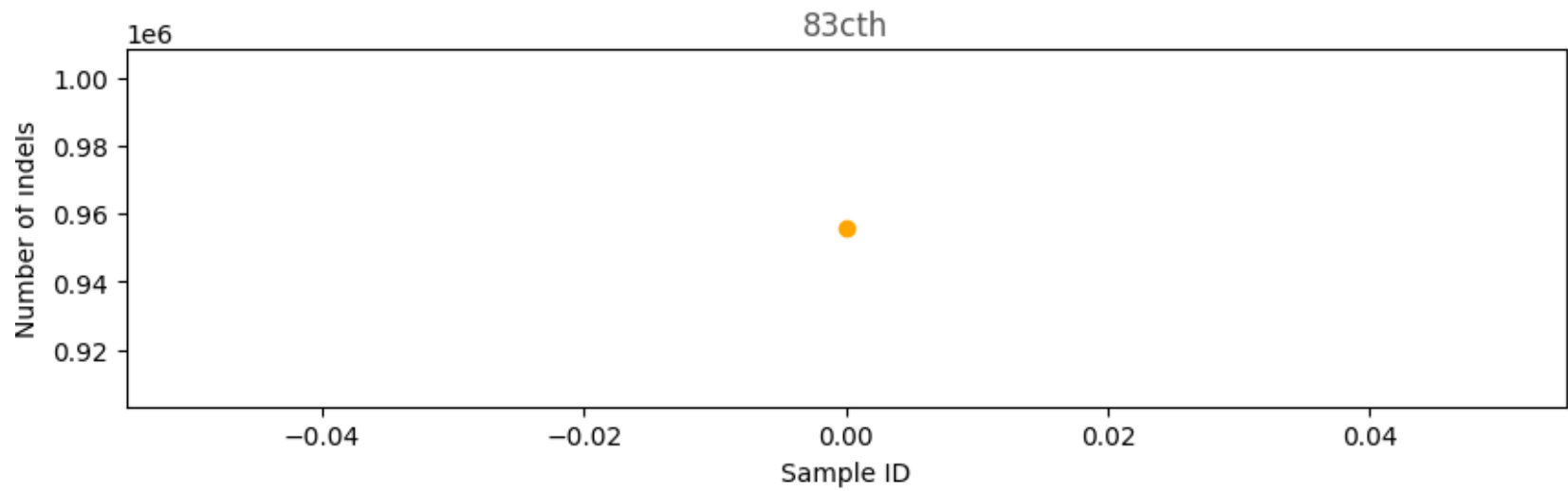
Average depth by sample



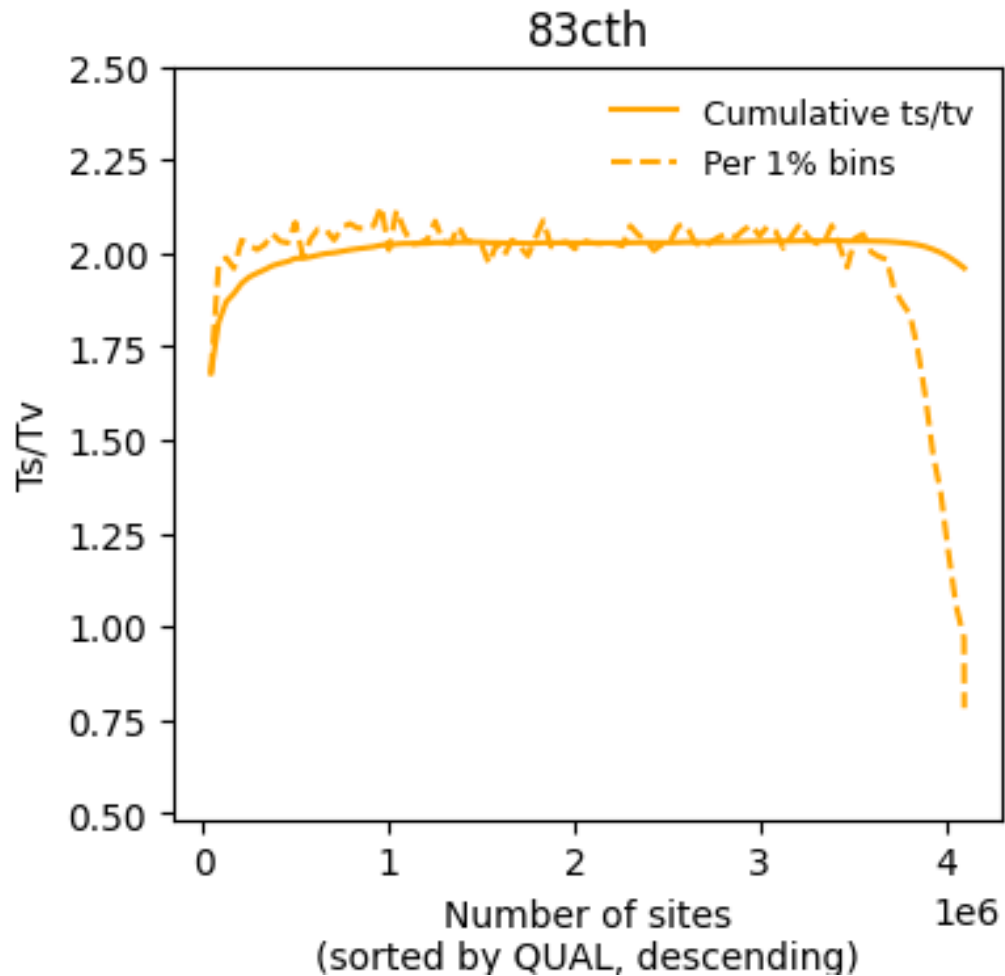
Number of SNPs by sample



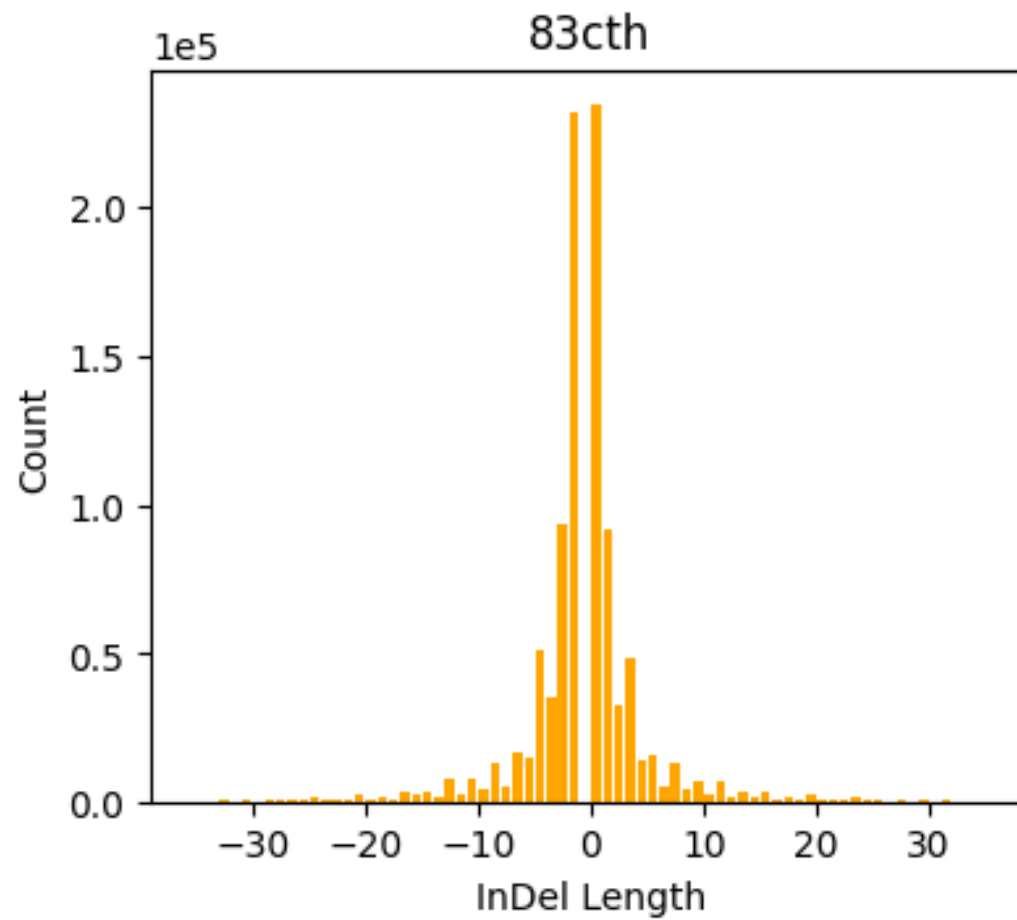
Number of indels by sample



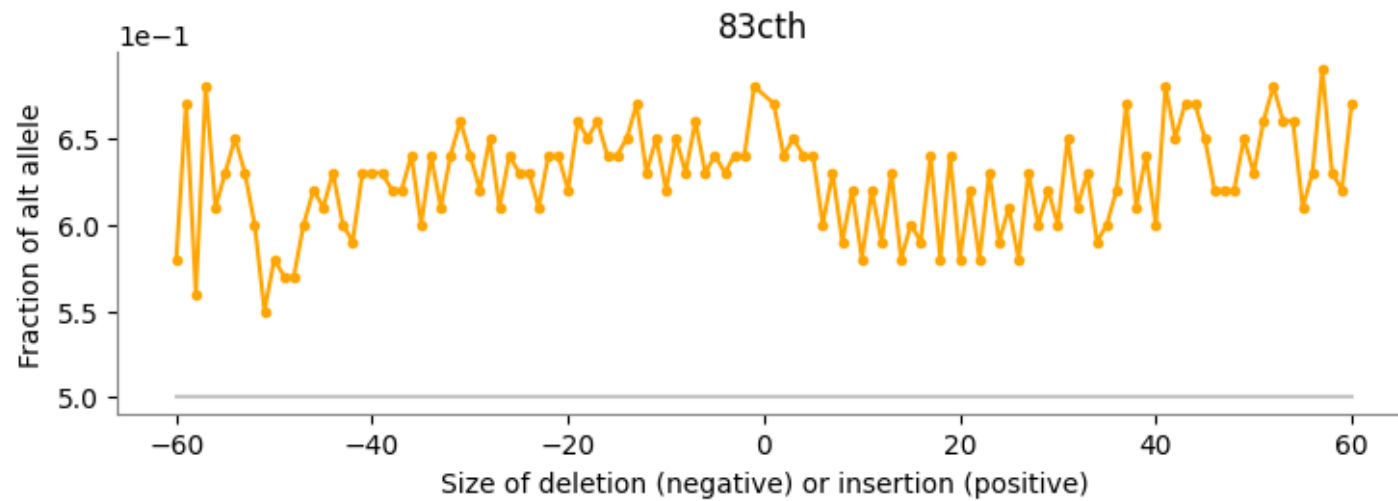
Ts/Tv stratified by QUAL



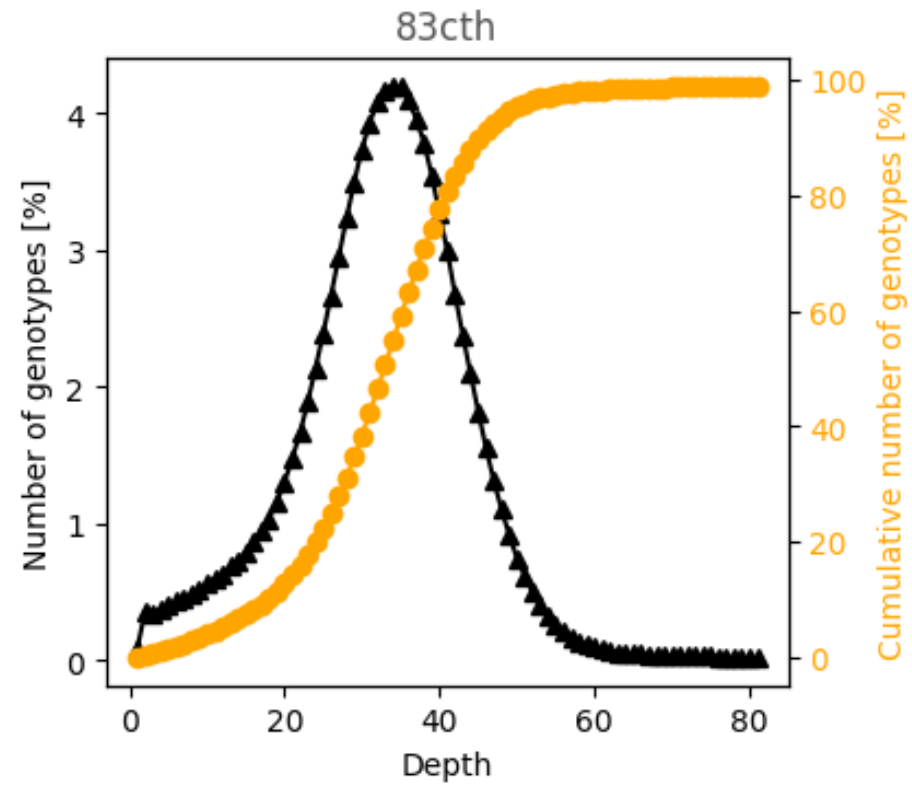
Indel distribution



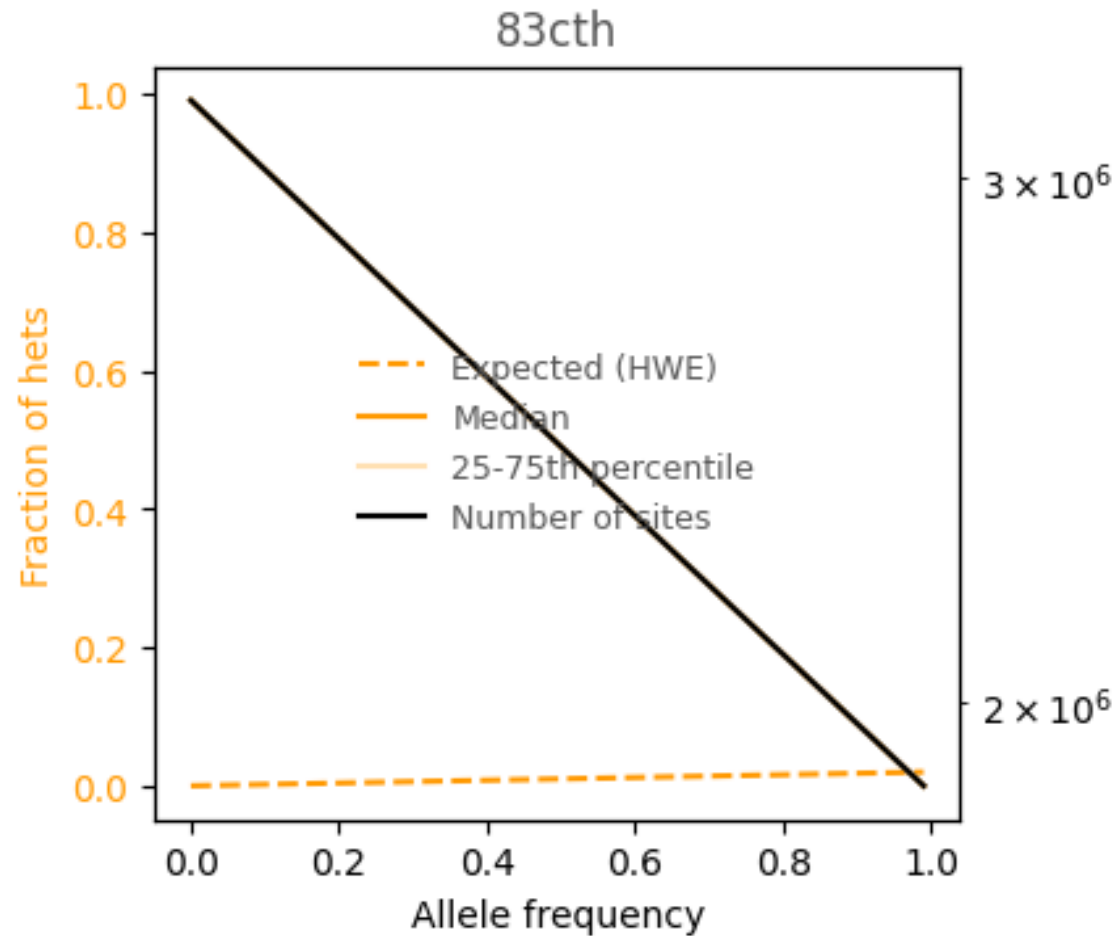
Fraction of alternate indel allele



Depth distribution



Number of HETs by AF



Substitution types

