

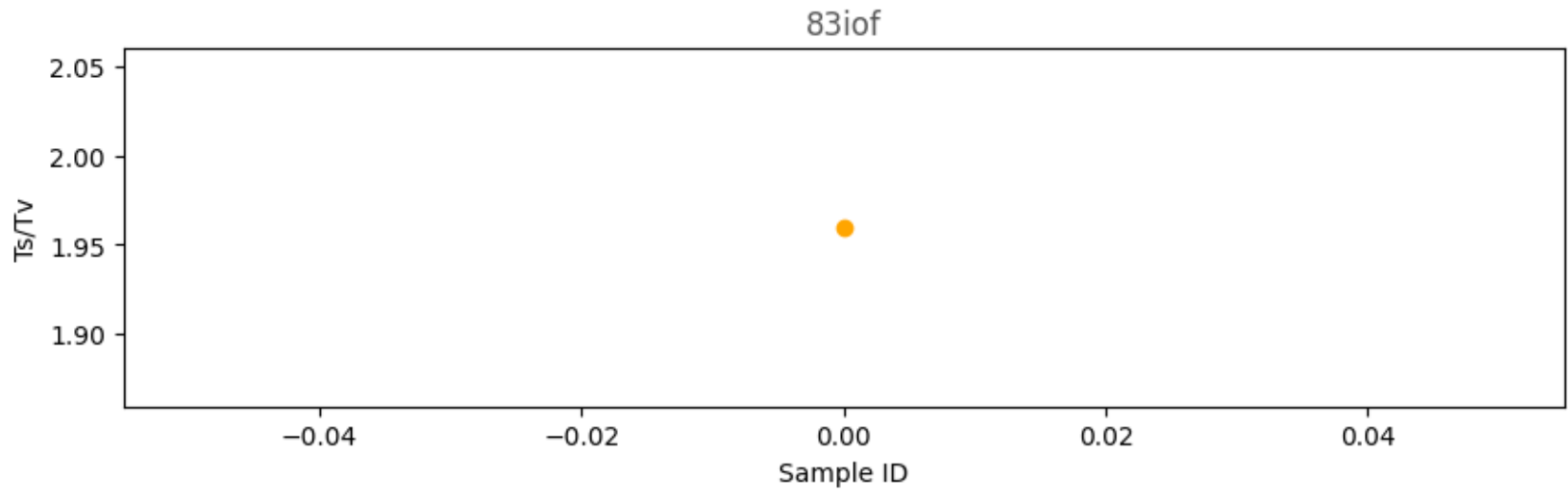
Summary Numbers

| Callset | SNPs | | | indels | | MNPs | others |
|----------------------------------|-----------|-------|-----------|---------|------|------|--------|
| | n | ts/tv | (1st ALT) | n | frm* | | |
| 83iof | 4,047,036 | 1.96 | 1.96 | 952,061 | – | 0 | 0 |
| * frameshift ratio: out/(out+in) | | | | | | | |

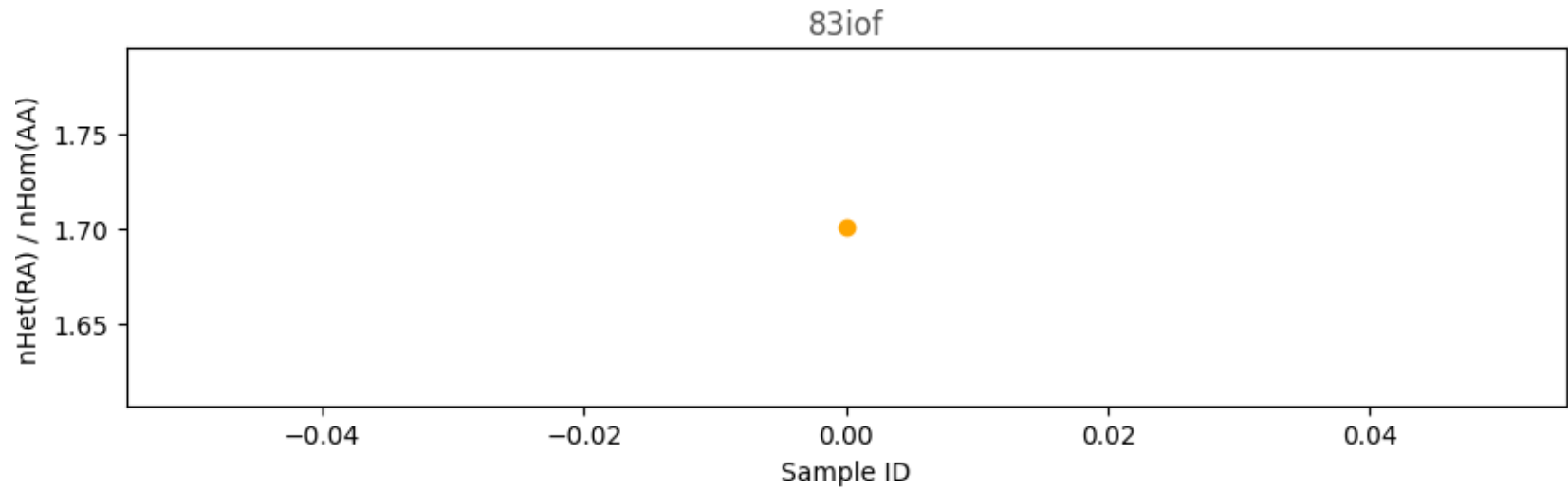
| Callset | singletons (AC=1) | | | multiallelic | |
|---------|-------------------|-------|--------|--------------|-------|
| | SNPs | ts/tv | indels | sites | SNPs |
| 83iof | 63.0% | 1.94 | 68.1% | 99,293 | 1,930 |

- 83iof .. /ngc/projects2/gm/data/archive/2022/variants/snv/83iofelaf-103805108227-Normal_Blood_noinfo-WGS_v1_IlluminaDNAPCRFree-X-211117_A01411_BHT773DSX2-RHGM_LABKA_WGS-WGS03343_snv_germline_raw.haplotype_caller.vcf.gz

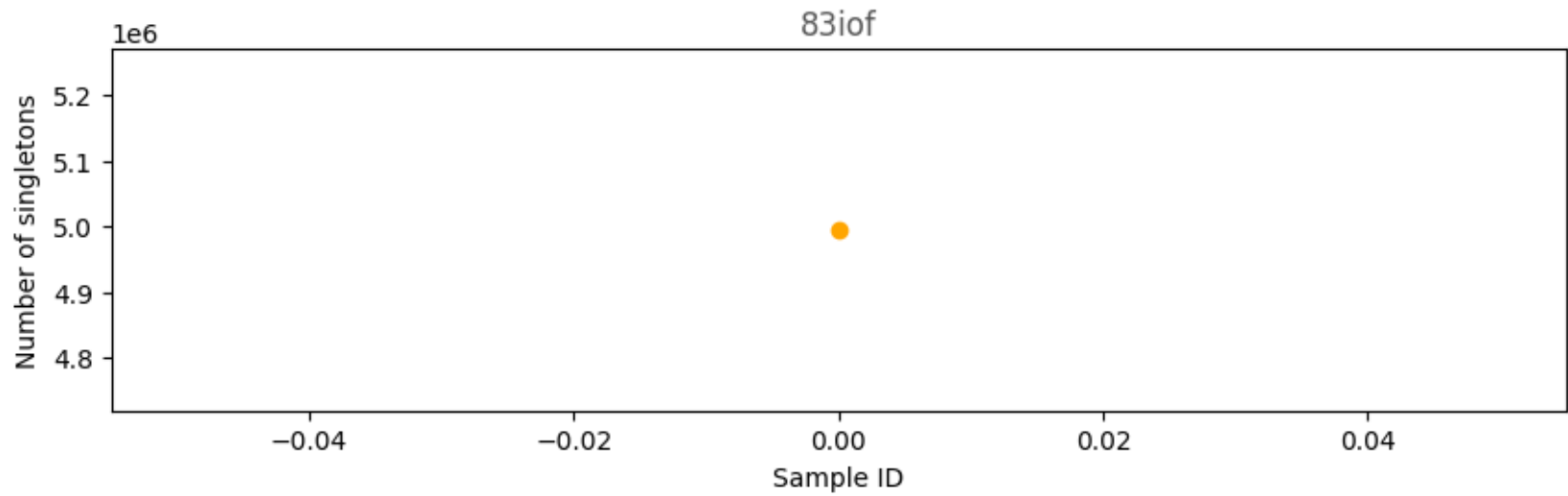
Ts/Tv by sample



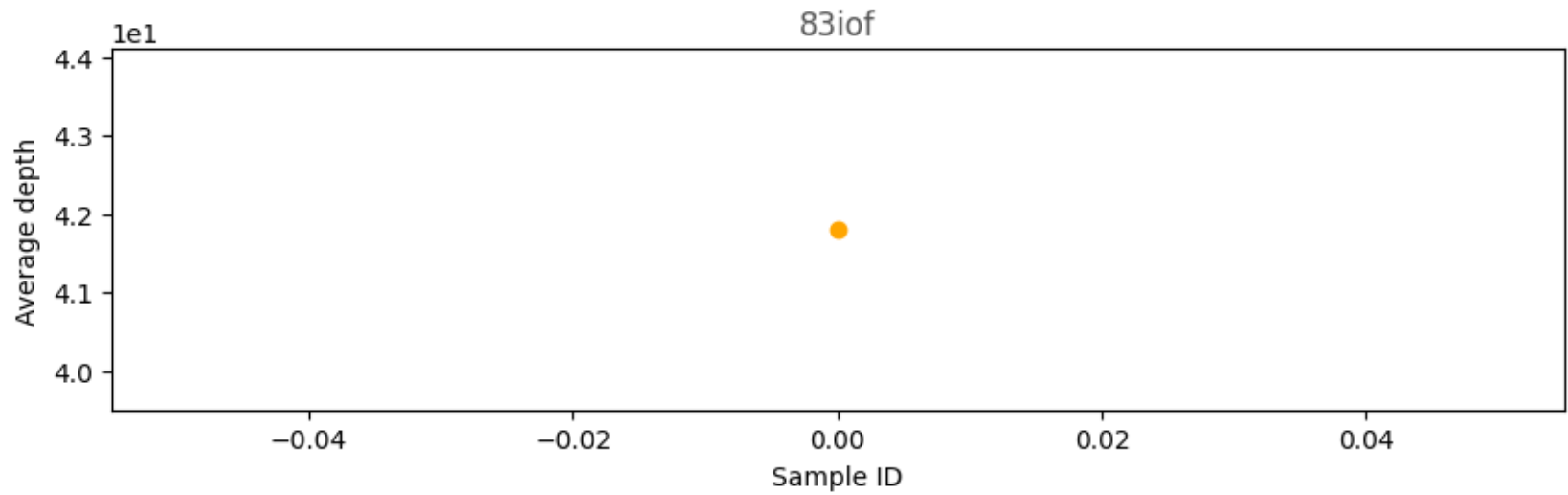
Hets vs non-ref Homs by sample



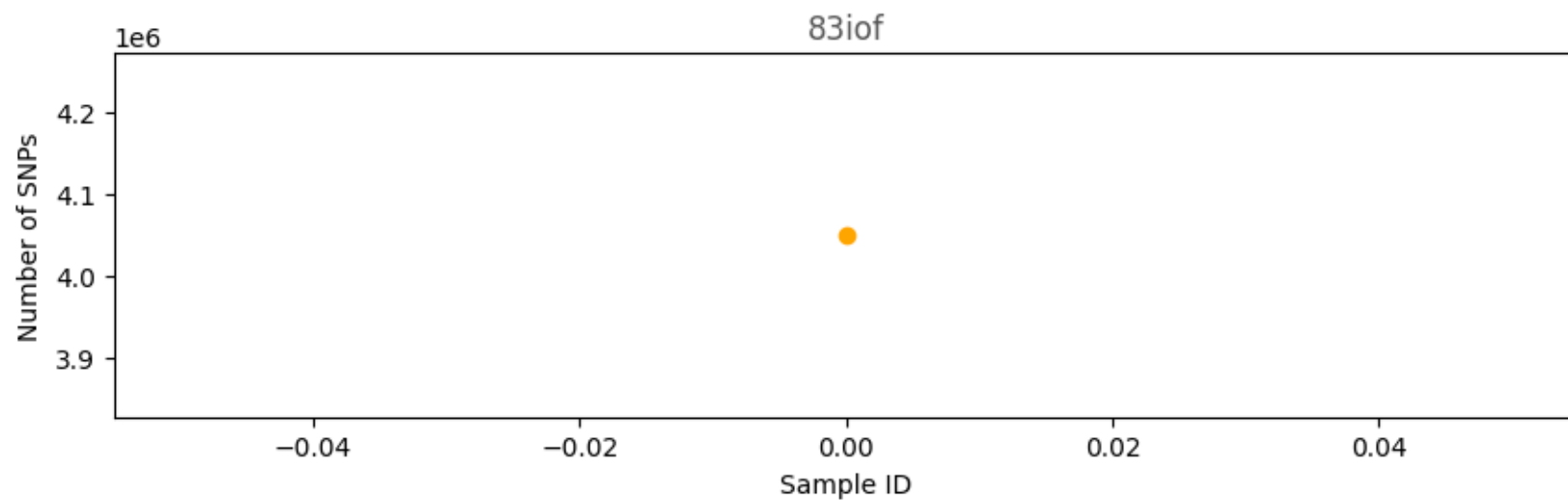
Singletons by sample (hets and homs)



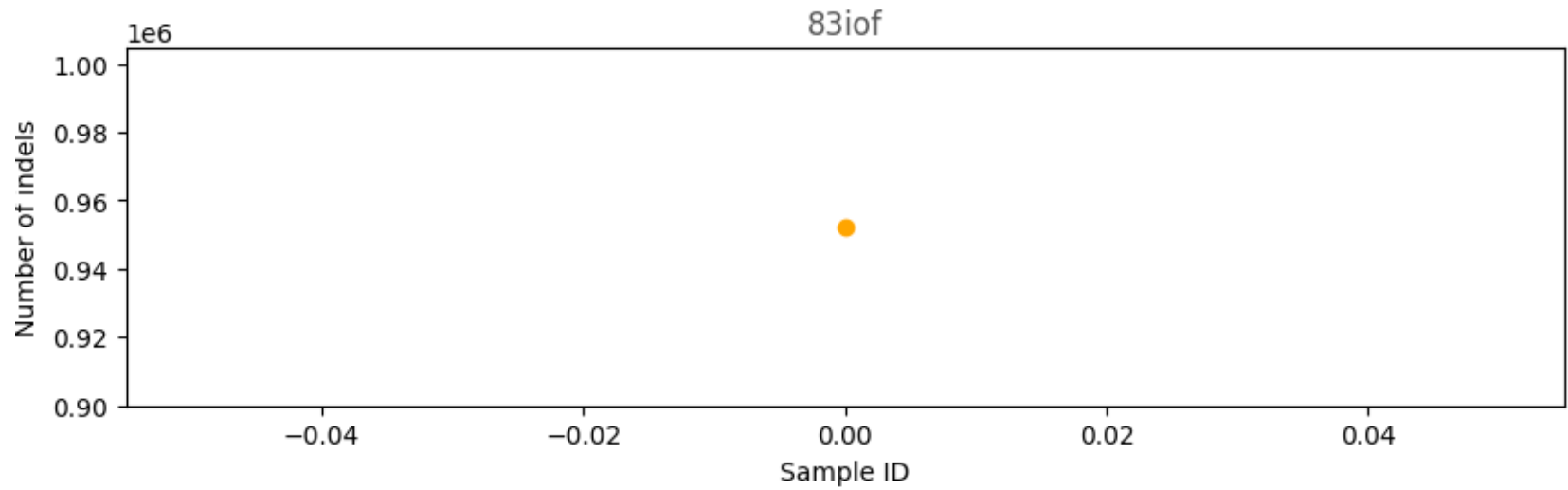
Average depth by sample



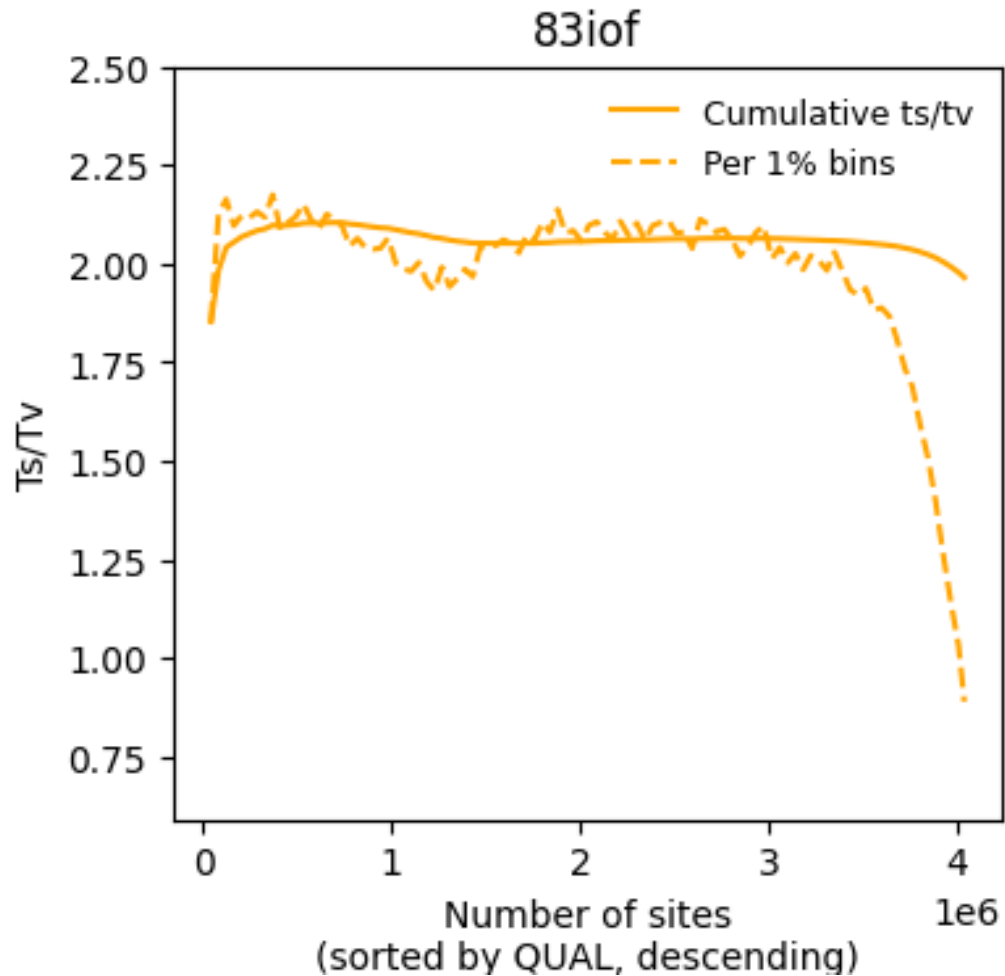
Number of SNPs by sample



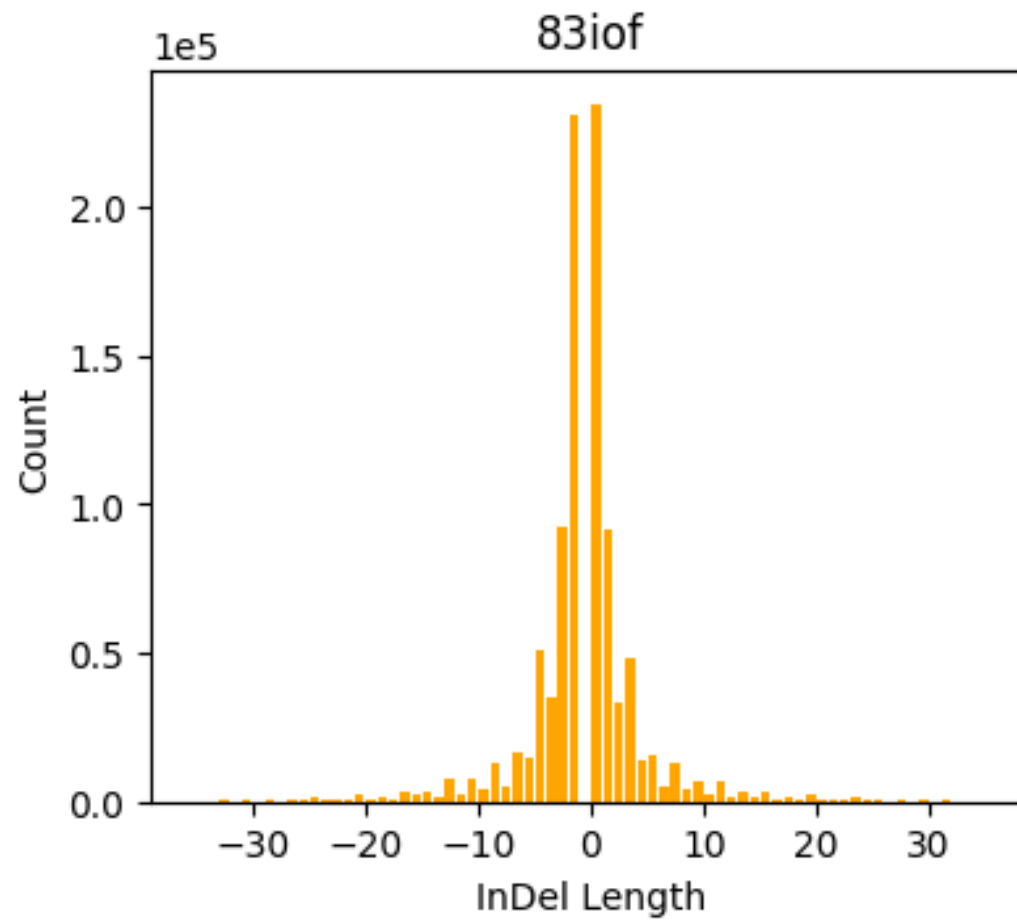
Number of indels by sample



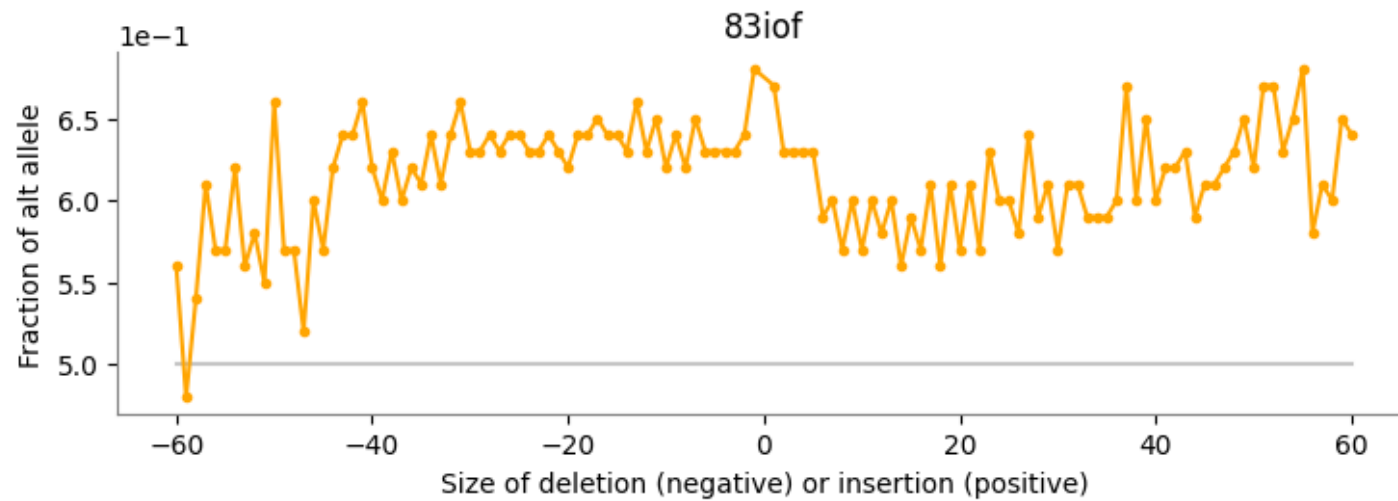
Ts/Tv stratified by QUAL



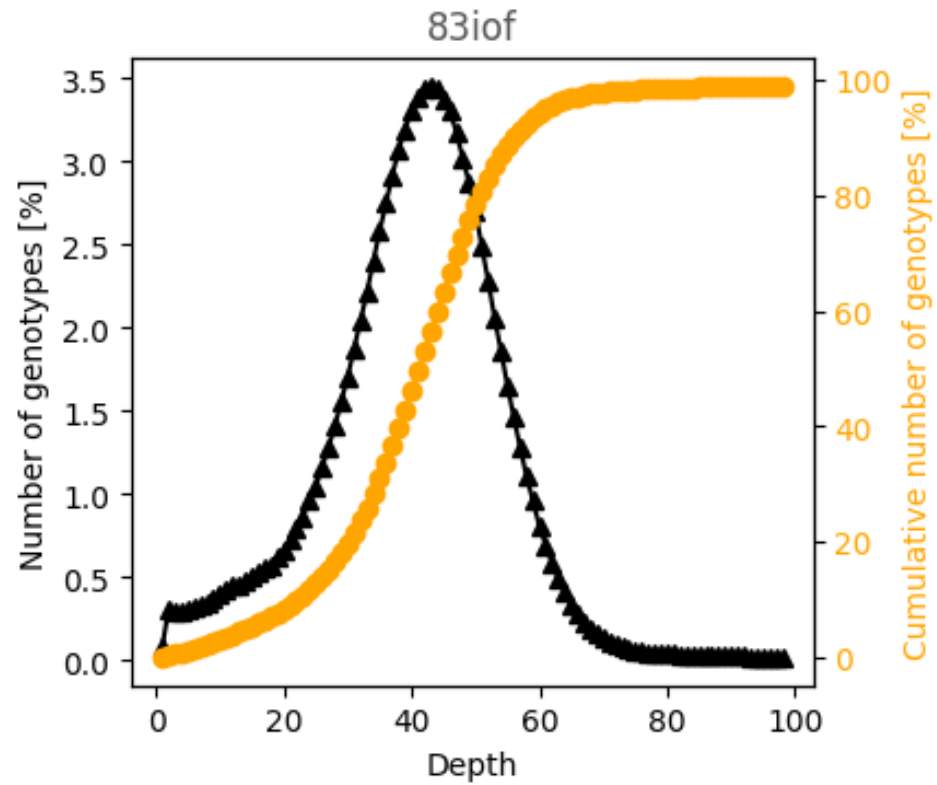
Indel distribution



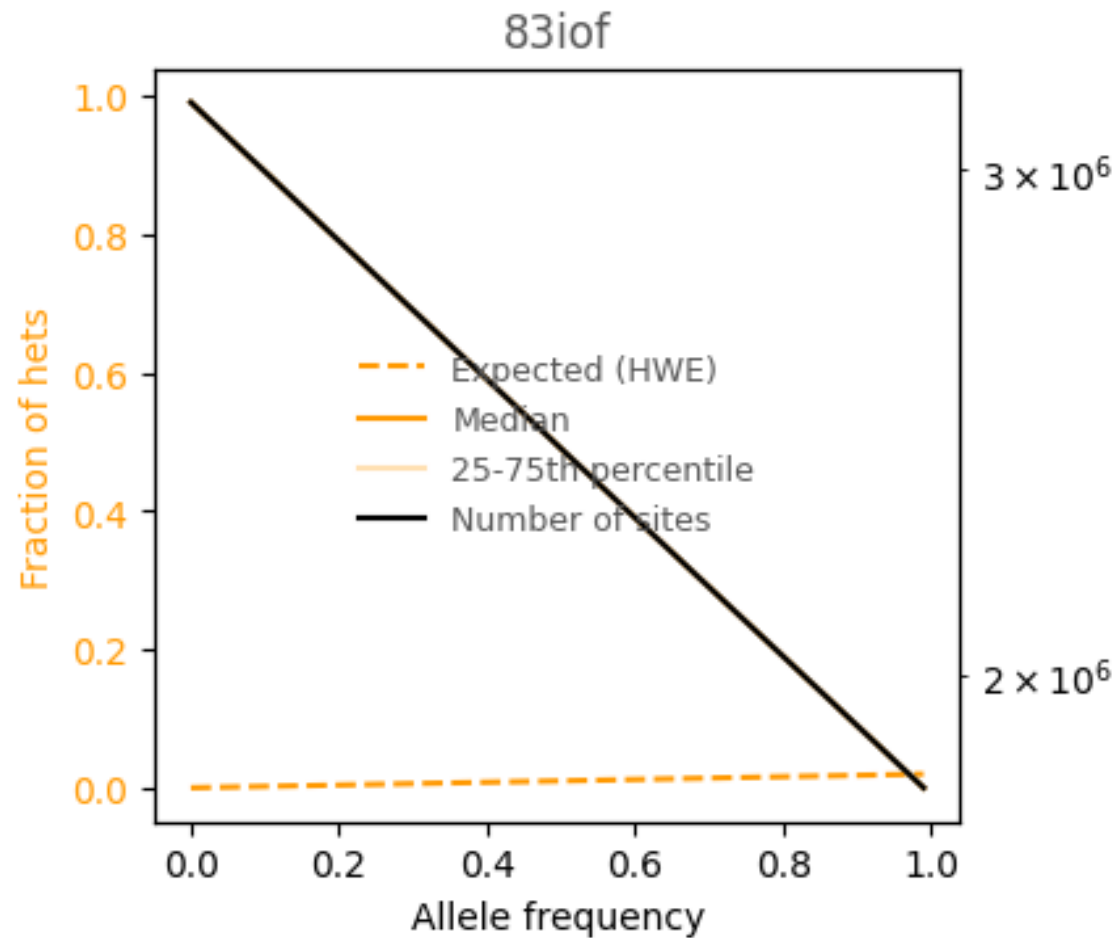
Fraction of alternate indel allele



Depth distribution



Number of HETs by AF



Substitution types

