

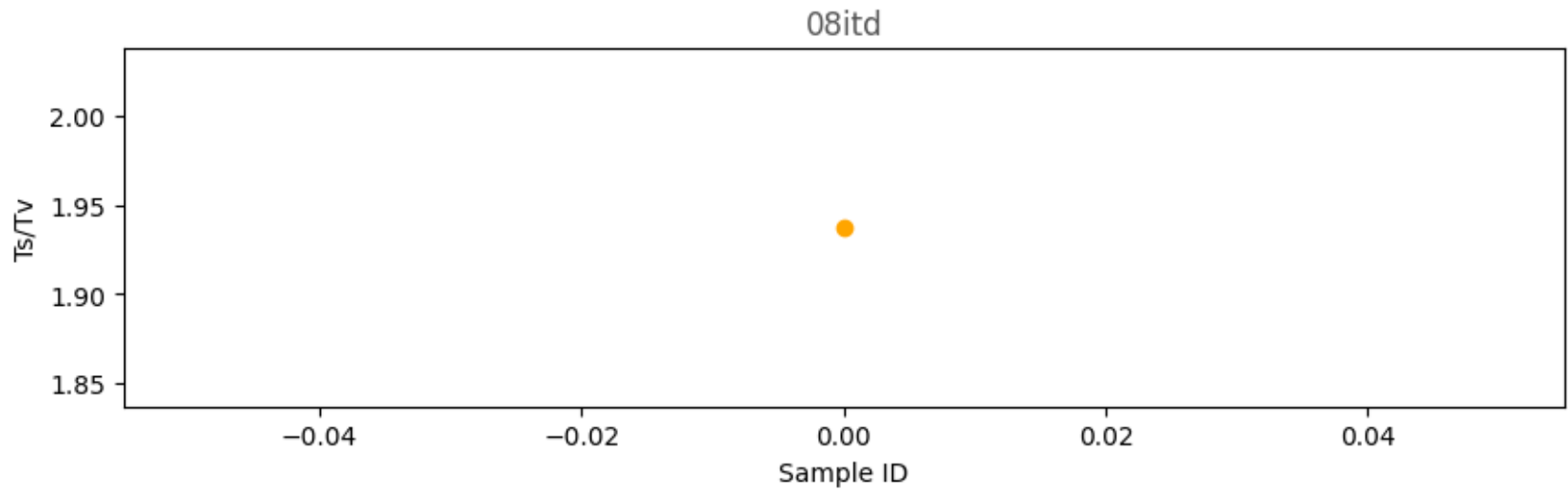
Summary Numbers

| Callset | SNPs | | | indels | | MNPs | others |
|----------------------------------|-----------|-------|-----------|---------|------|------|--------|
| | n | ts/tv | (1st ALT) | n | frm* | | |
| 08itd | 4,084,946 | 1.94 | 1.94 | 949,748 | – | 0 | 0 |
| * frameshift ratio: out/(out+in) | | | | | | | |

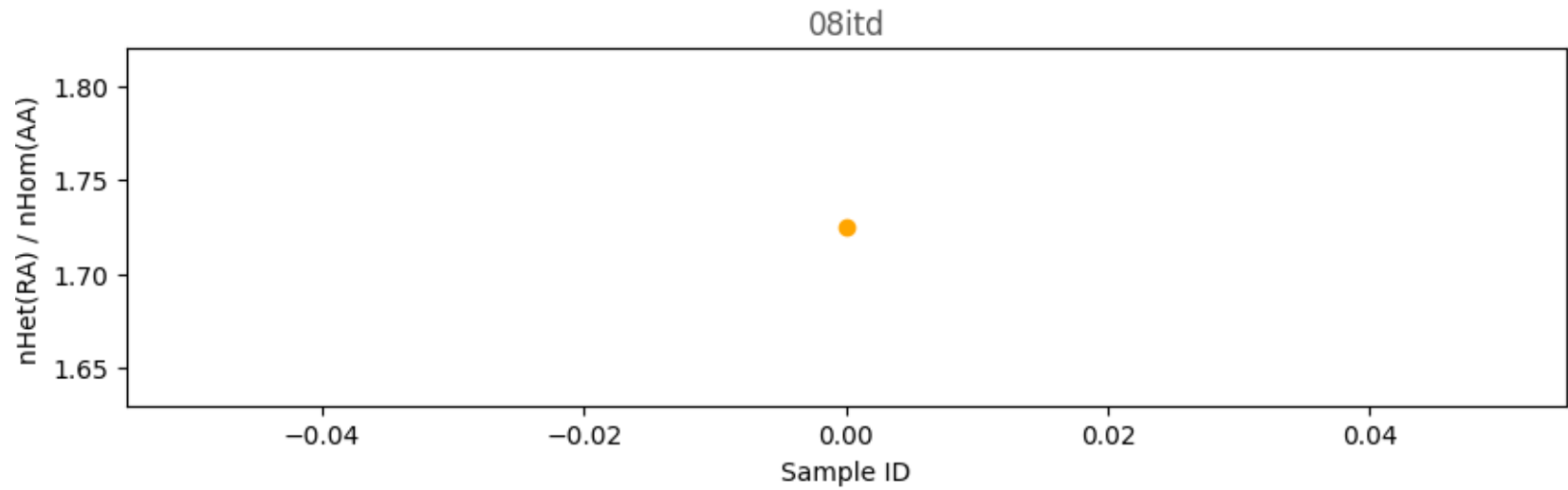
| Callset | singletons (AC=1) | | | multiallelic | |
|---------|-------------------|-------|--------|--------------|-------|
| | SNPs | ts/tv | indels | sites | SNPs |
| 08itd | 63.3% | 1.91 | 68.2% | 99,574 | 2,063 |

- 08itd .. /ngc/projects2/gm/data/archive/2022/variants/snv/08itdiolf-110306404052-Normal_Blood_noinfo-WGS_v1_IlluminaDNAPCRFree_RHGM02352-221116_A01176_AHF53VDSX5-EXT_LAB
KA_NGCWGS-NGCWGS06249_snv_germline_raw.haplotype_caller.vcf.gz

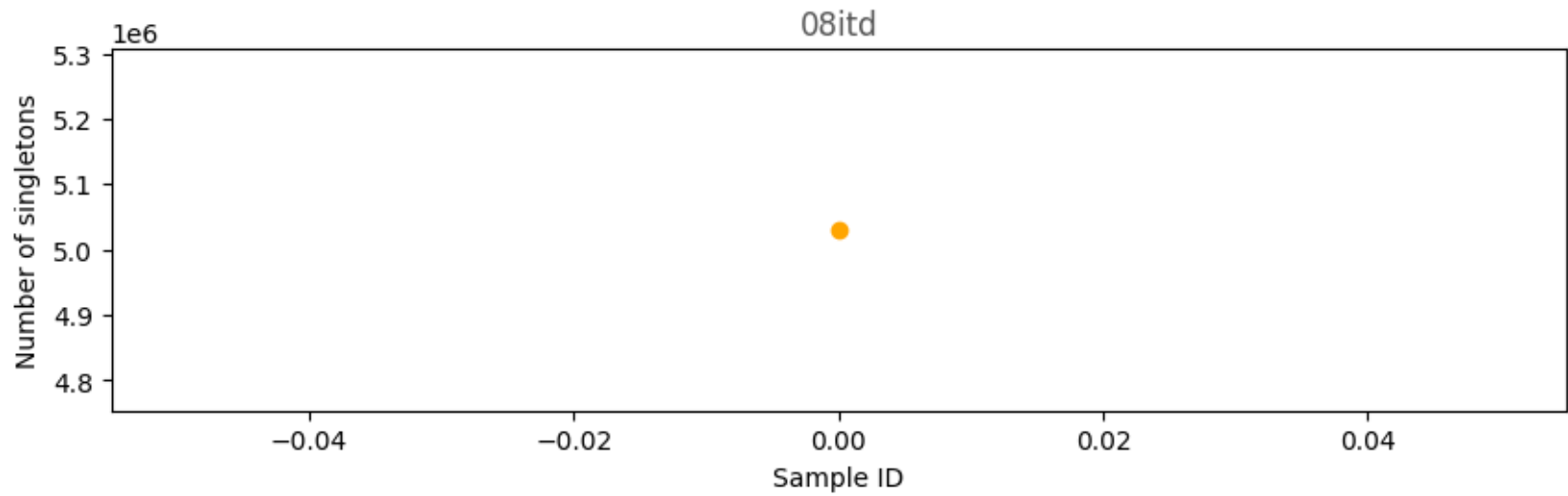
Ts/Tv by sample



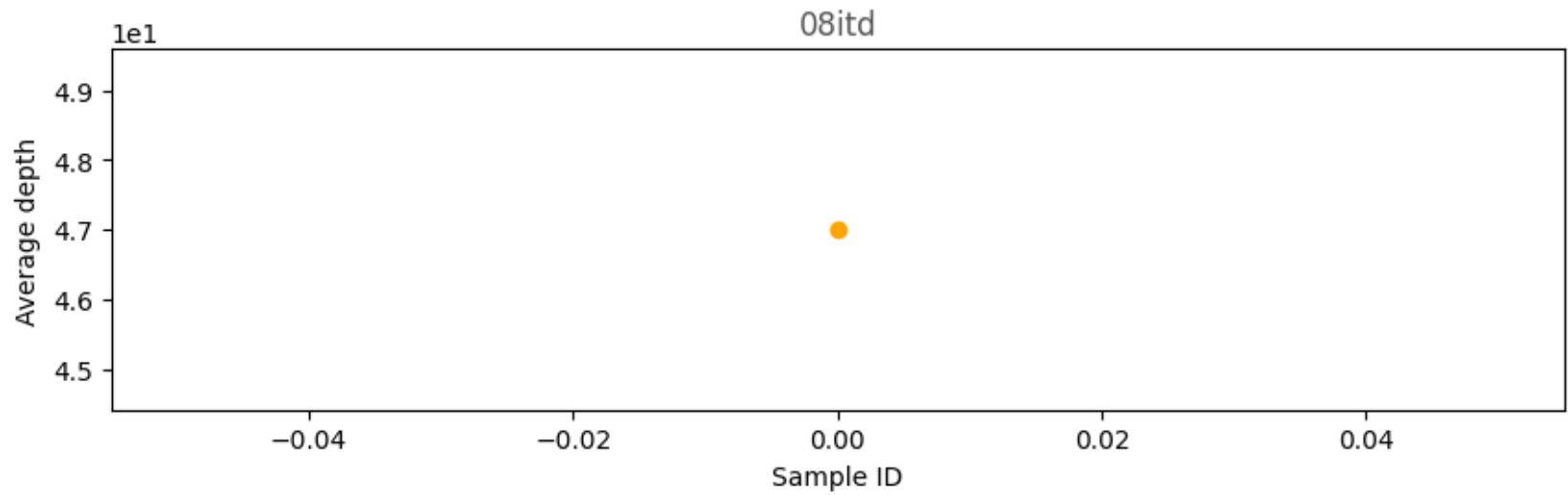
Hets vs non-ref Homs by sample



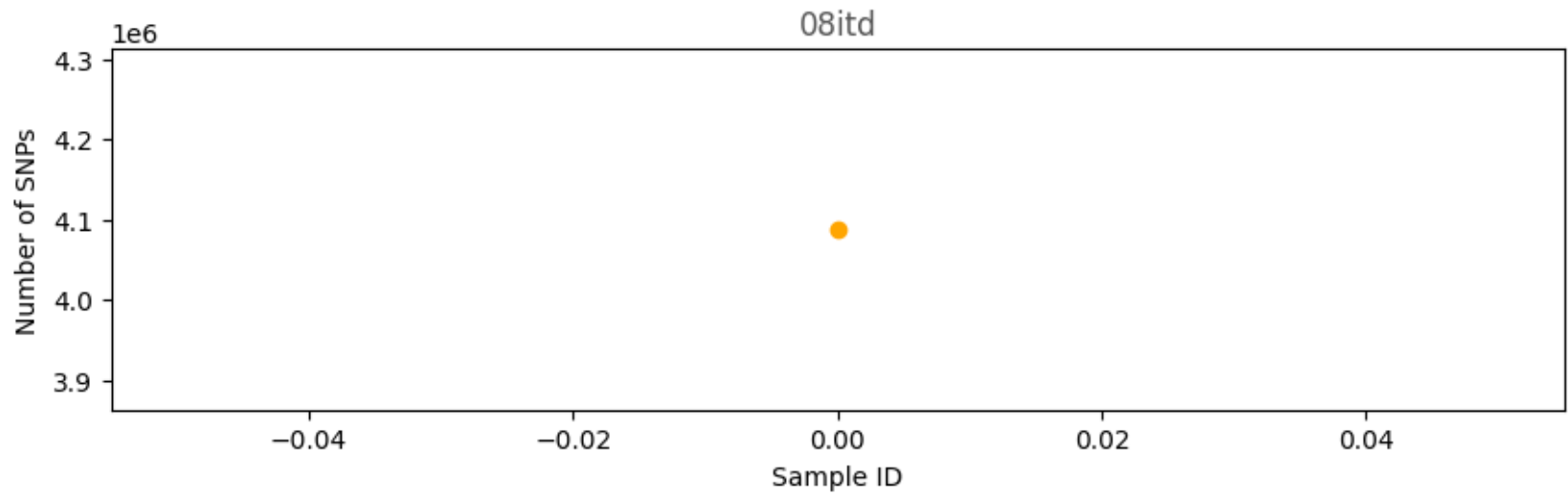
Singletons by sample (hets and homs)



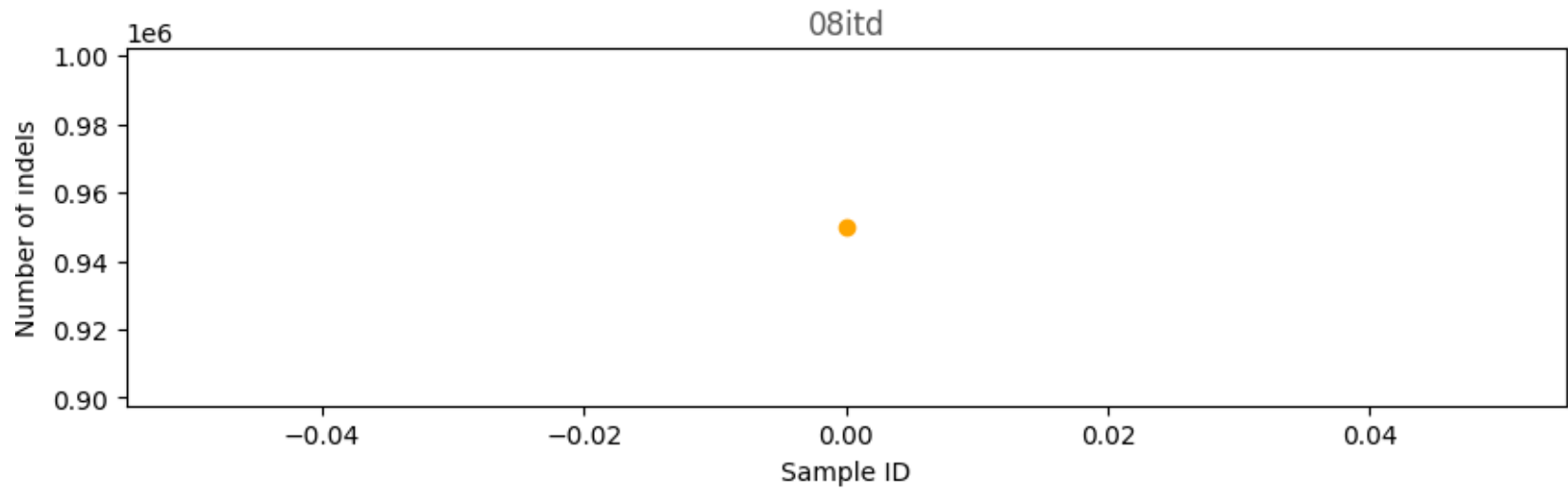
Average depth by sample



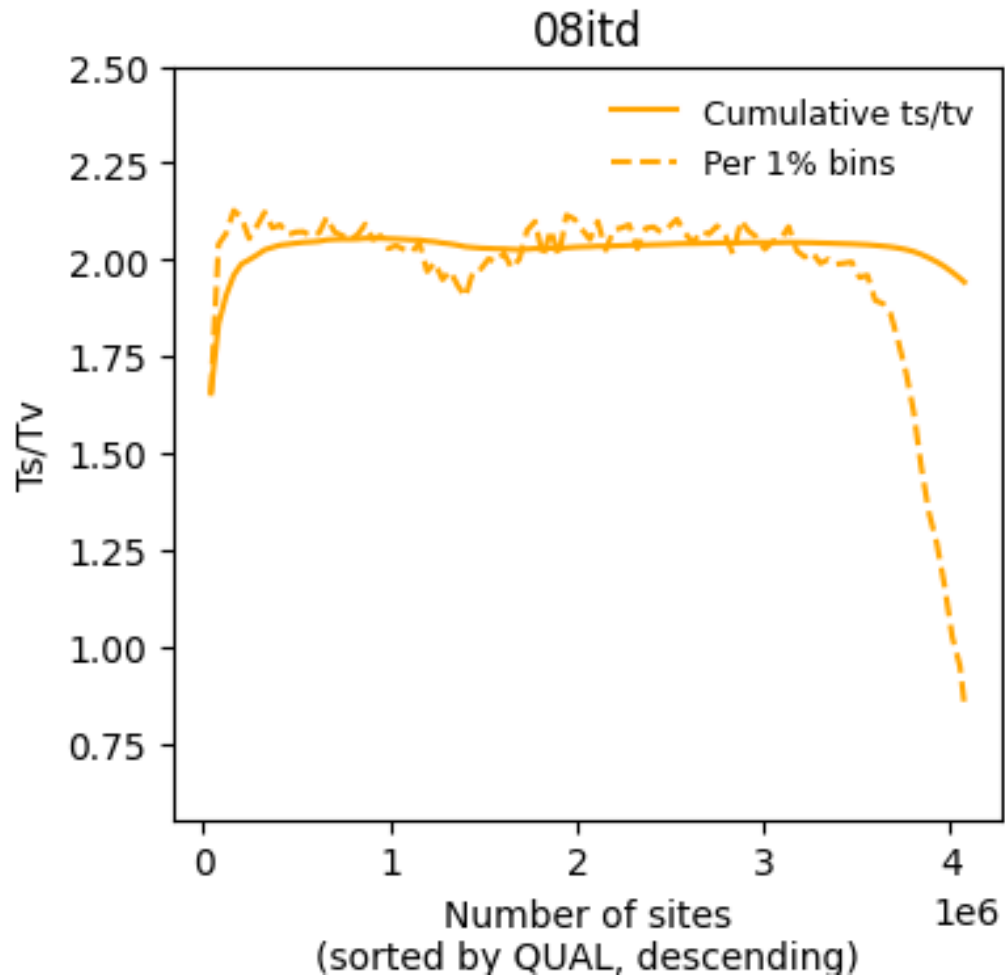
Number of SNPs by sample



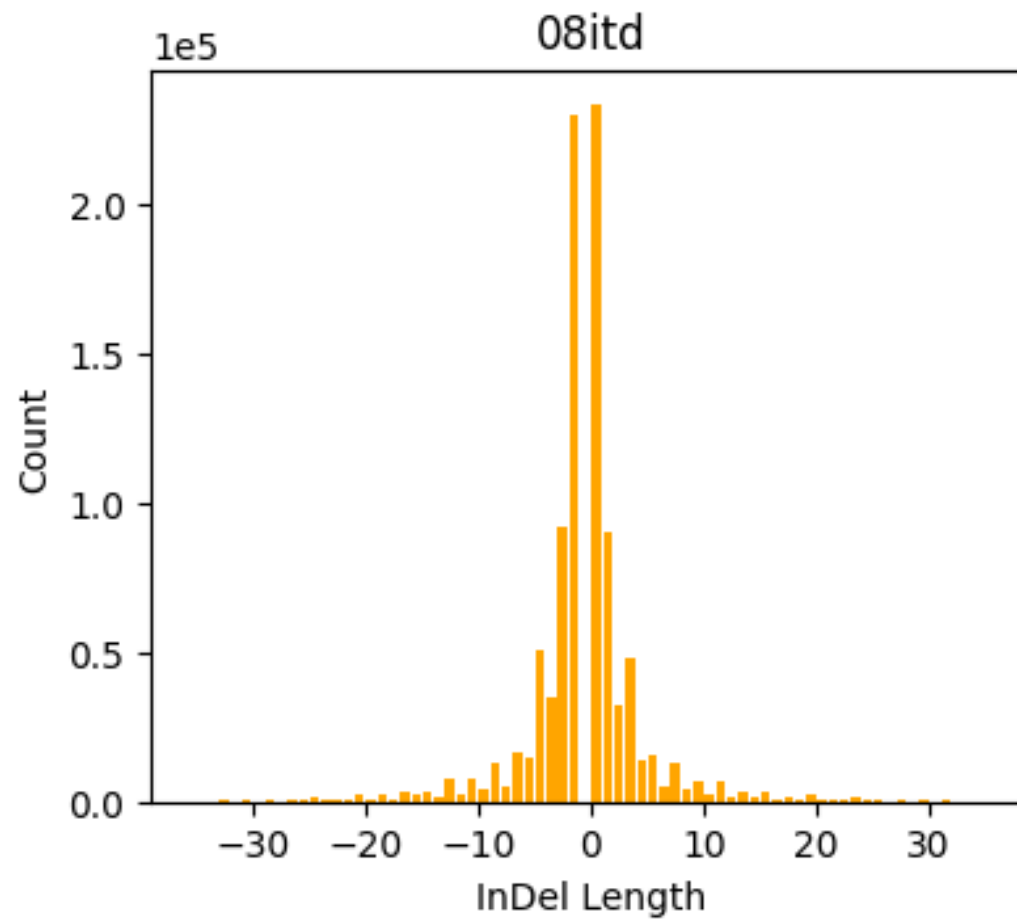
Number of indels by sample



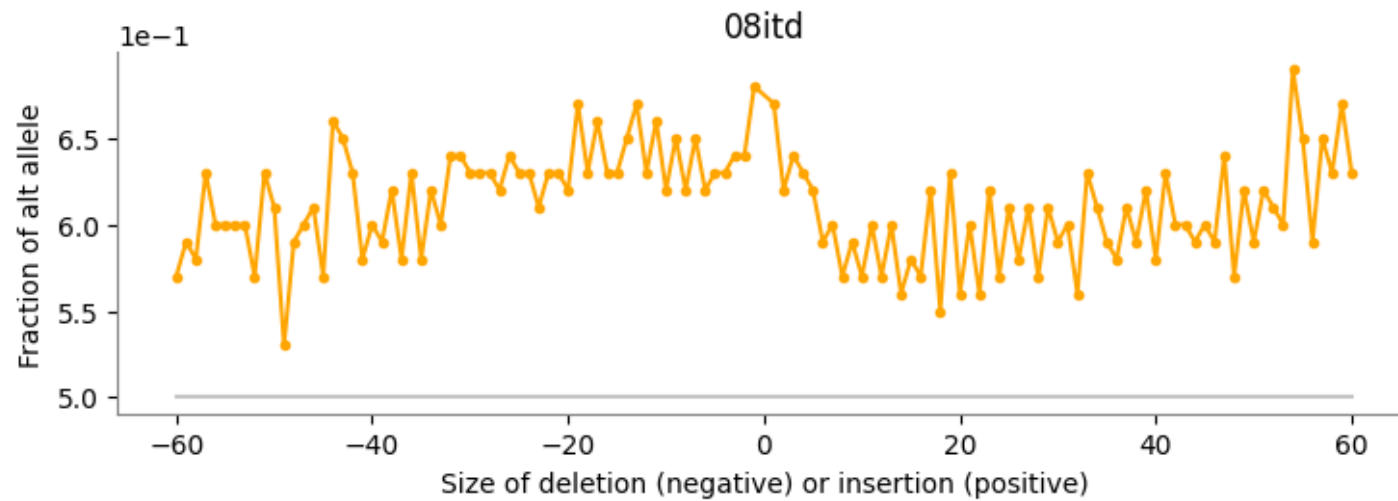
Ts/Tv stratified by QUAL



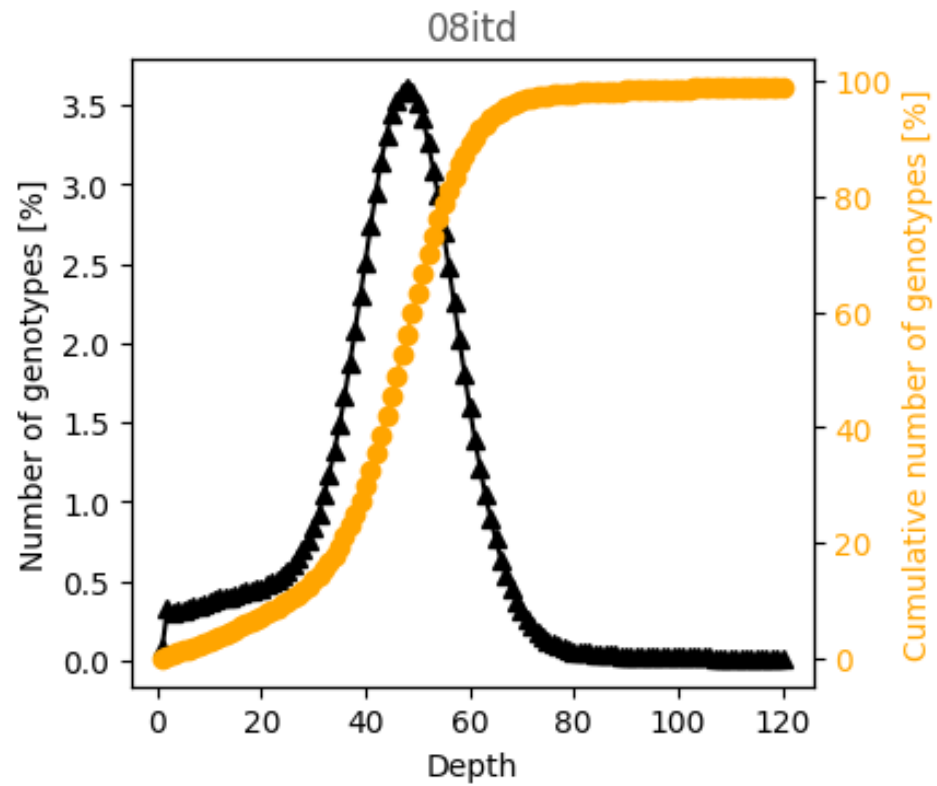
Indel distribution



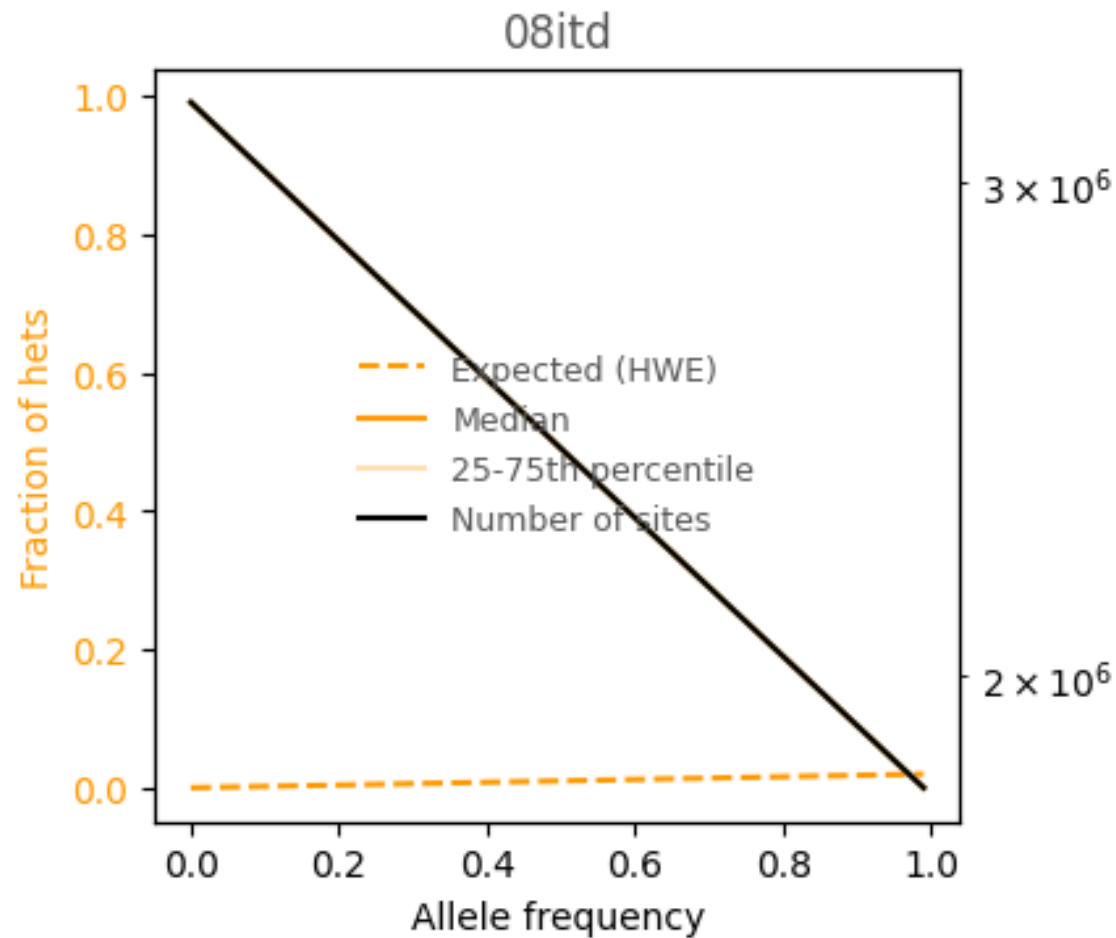
Fraction of alternate indel allele



Depth distribution



Number of HETs by AF



Substitution types

