

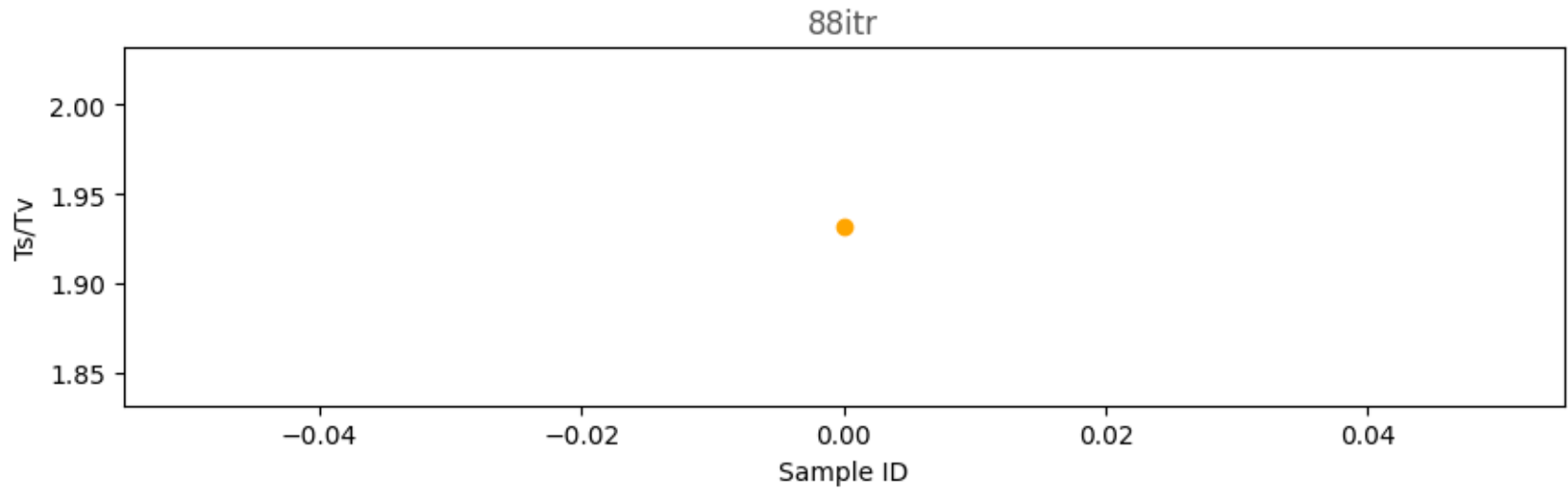
Summary Numbers

| | SNPs | | | indels | MNPs | others |
|----------------------------------|-----------|-------|-----------|---------|------|--------|
| Callset | n | ts/tv | (1st ALT) | n | frm* | |
| 88itr | 4,089,056 | 1.93 | 1.94 | 952,782 | – | 0 |
| * frameshift ratio: out/(out+in) | | | | | | |

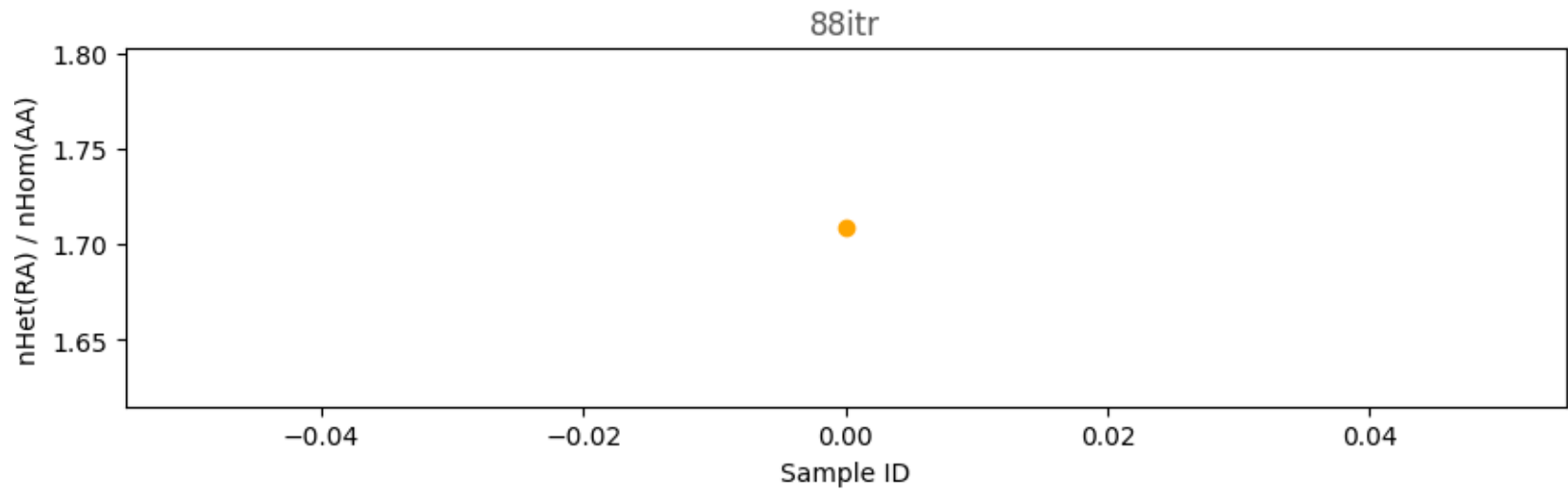
| | singletons (AC=1) | | | multiallelic | |
|---------|-------------------|-------|--------|--------------|-------|
| Callset | SNPs | ts/tv | indels | sites | SNPs |
| 88itr | 63.1% | 1.90 | 68.2% | 101,021 | 2,119 |

- 88itr .. /ngc/projects2/gm/data/archive/2022/variants/snv/88itrymaf-103910139346-Normal_Blood_noinfo-WGS_v1_IlluminaDNAPCRFree_RHGM01609-220921_A00559_AHYM7WDSX3-EXT_LAB_KA_NGCWGS-NGCWGS05399_22RKG020401_snv_germline_raw.haplotype_caller.vcf.gz

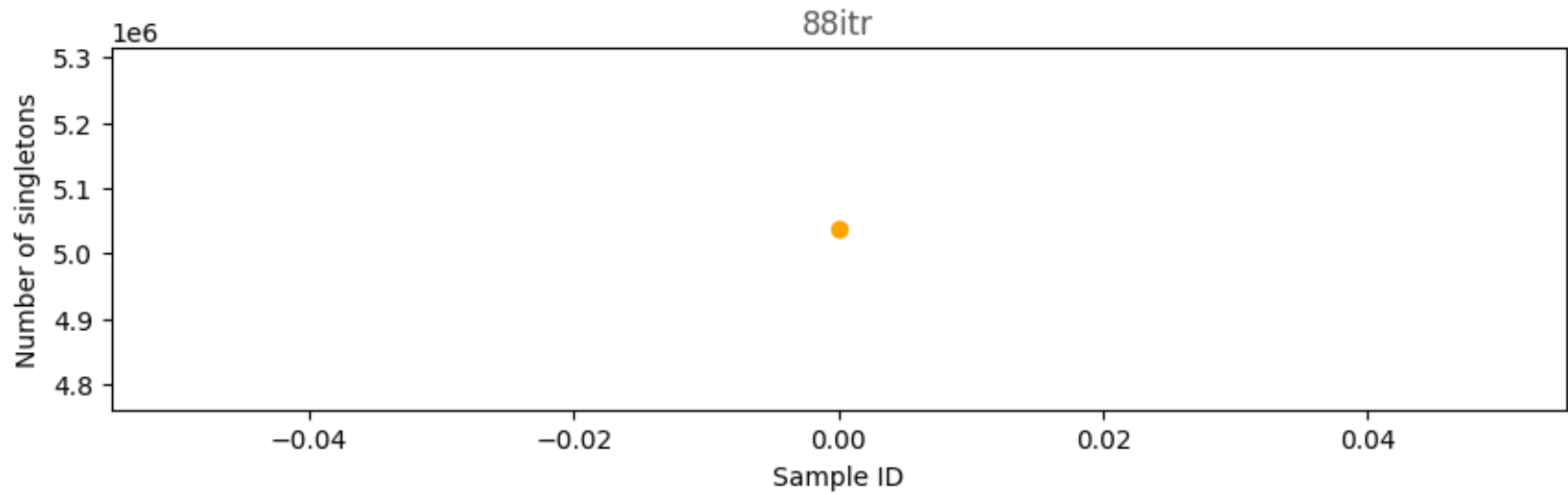
Ts/Tv by sample



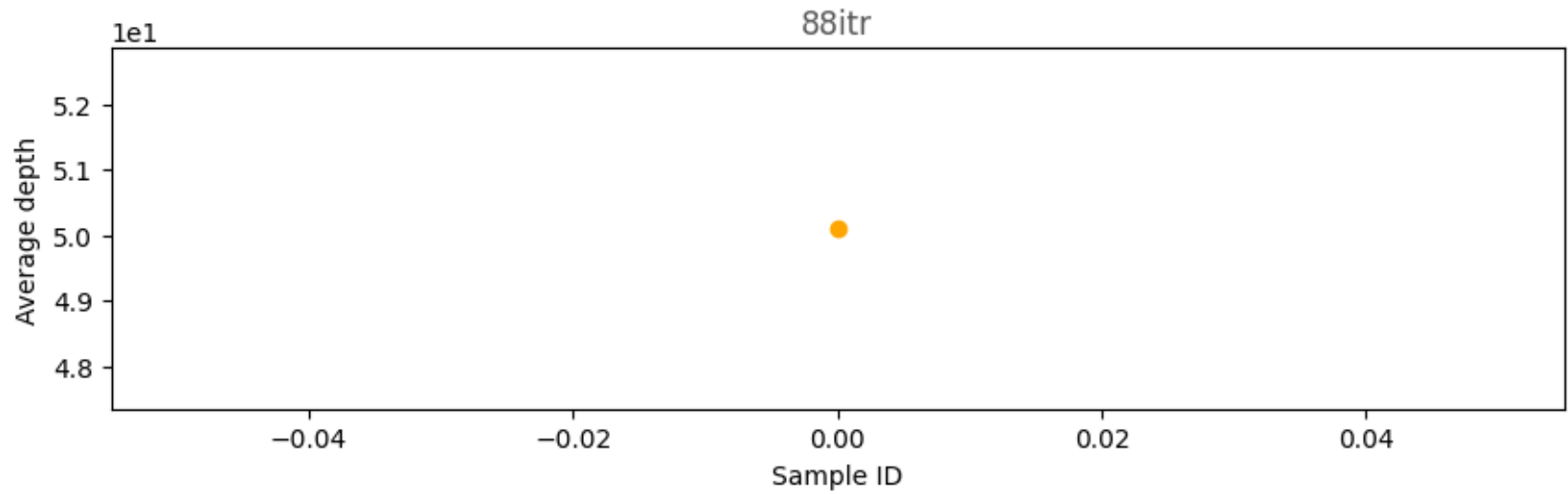
Hets vs non-ref Homs by sample



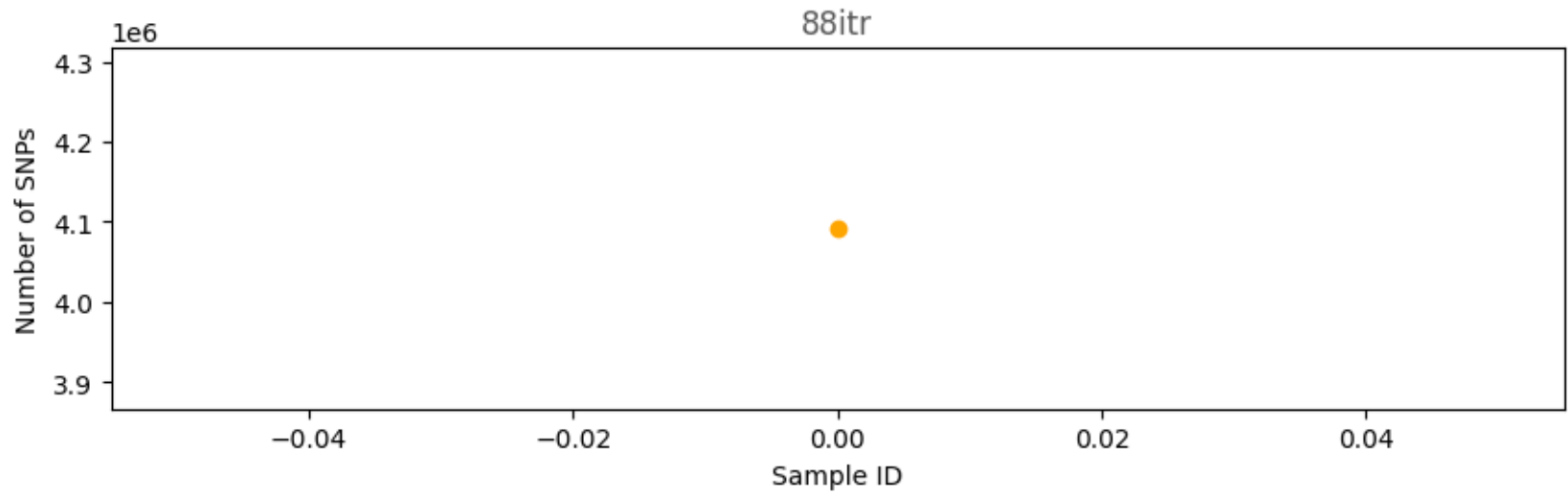
Singletons by sample (hets and homs)



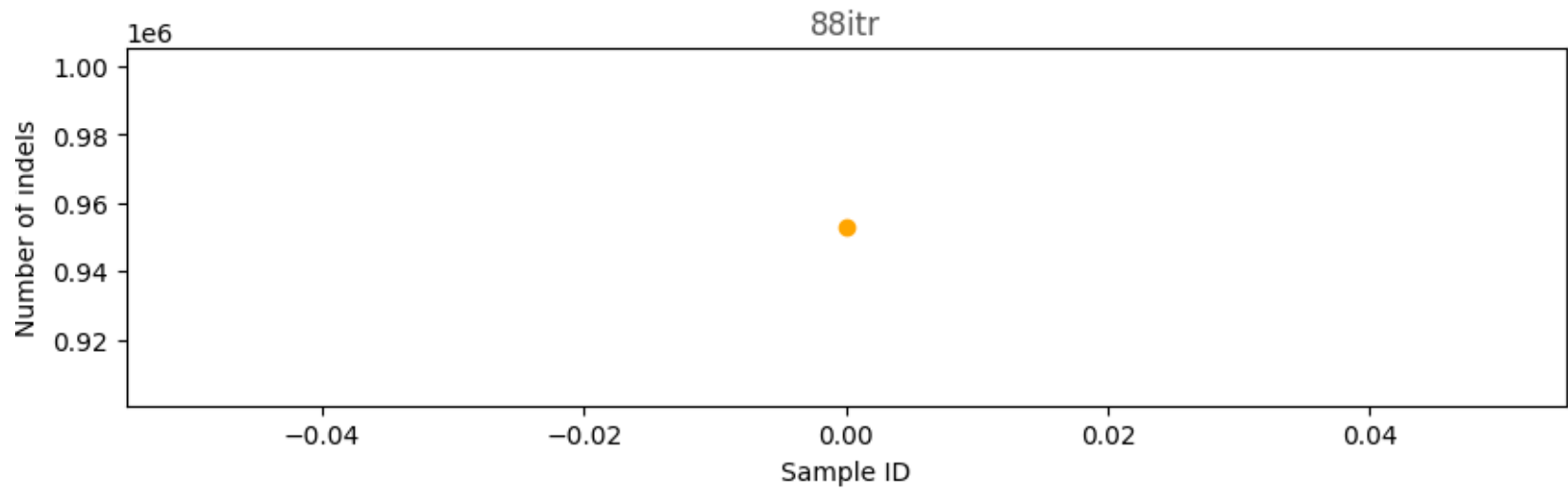
Average depth by sample



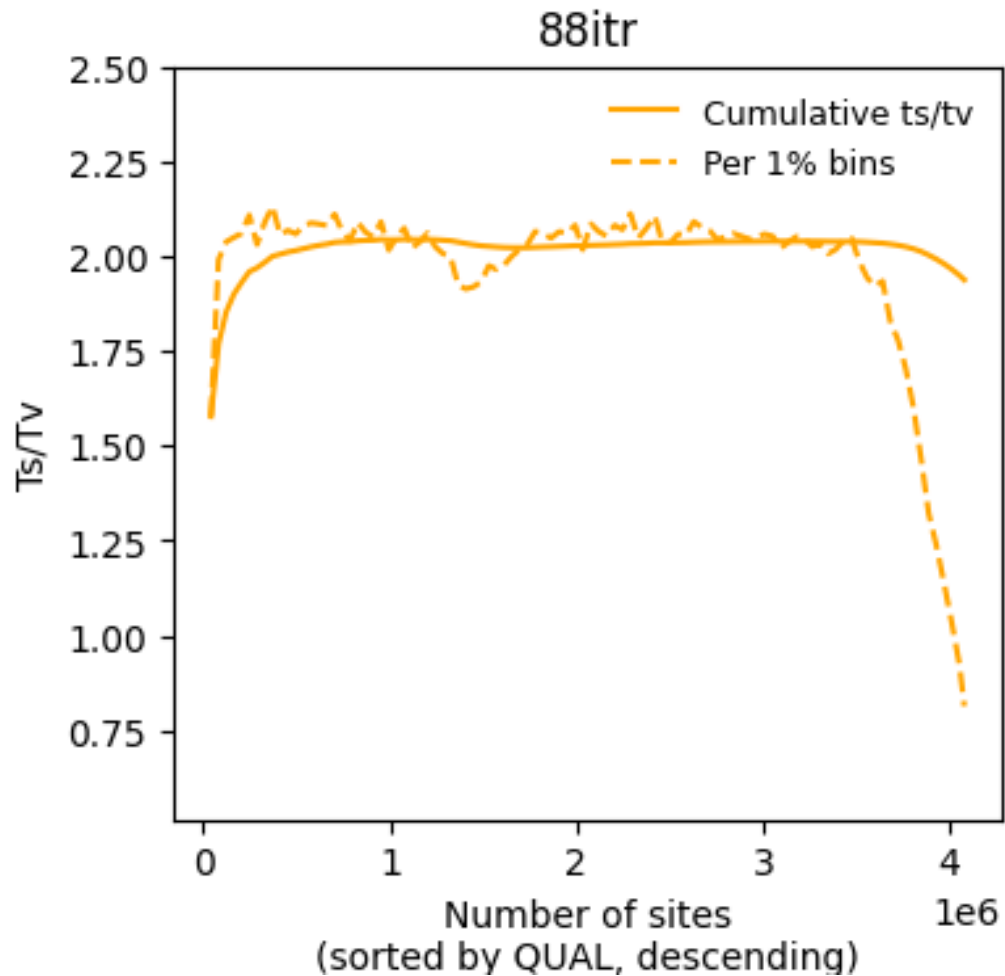
Number of SNPs by sample



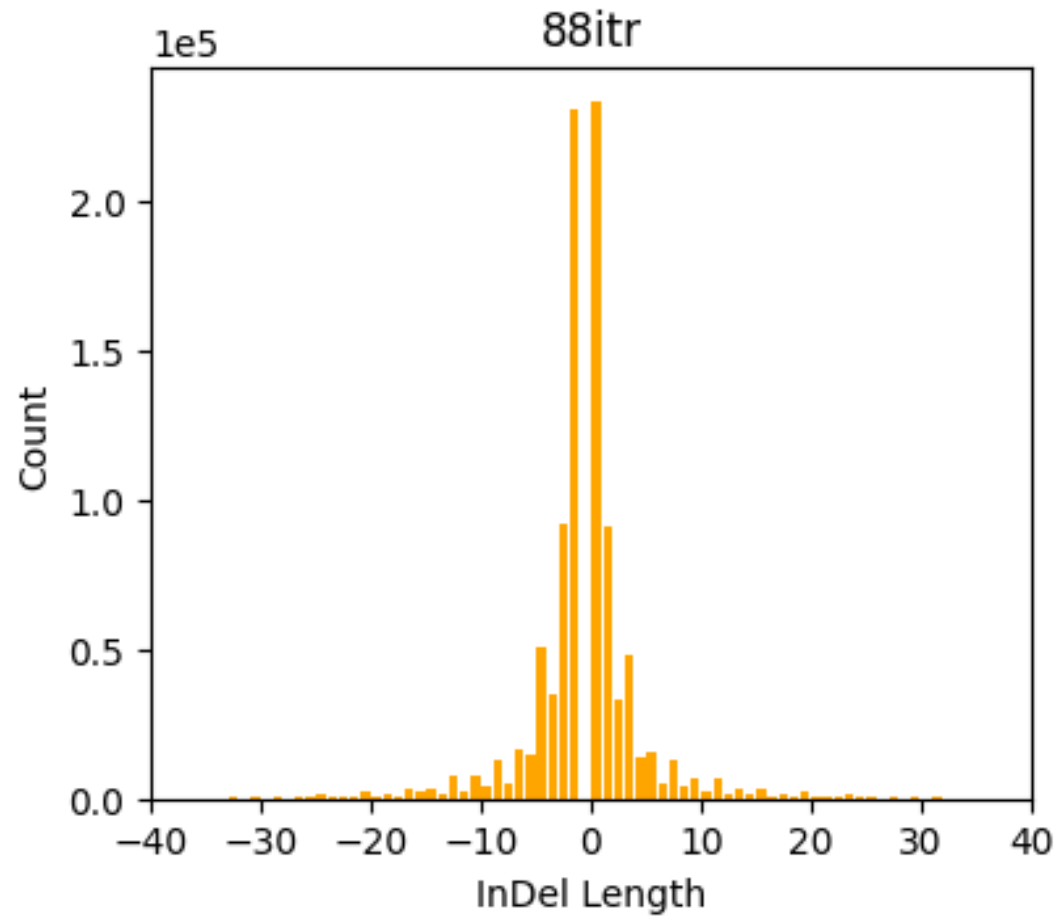
Number of indels by sample



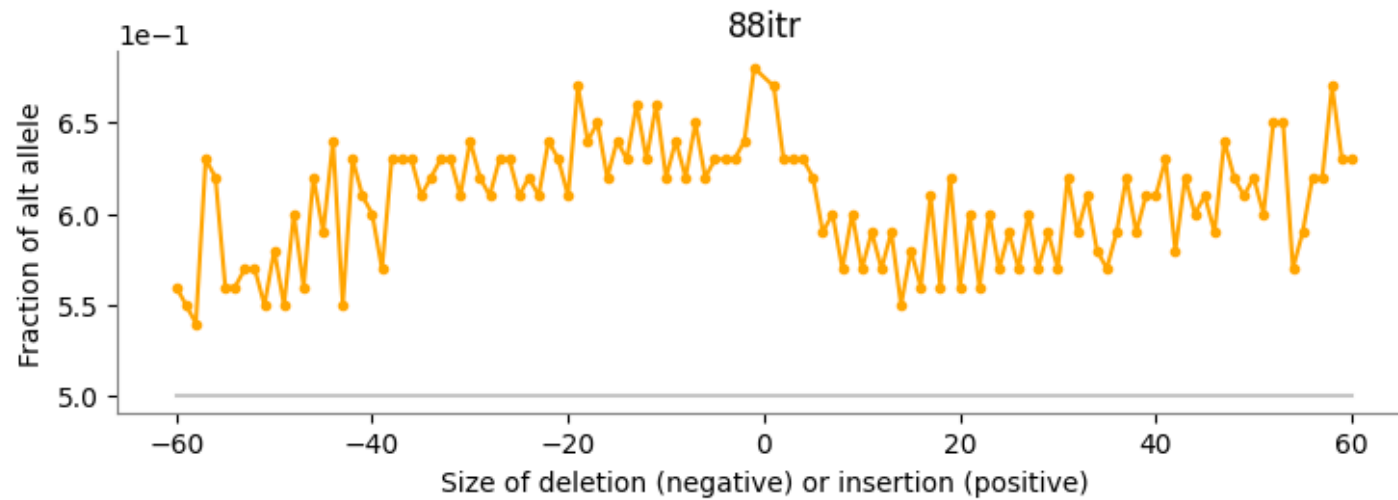
Ts/Tv stratified by QUAL



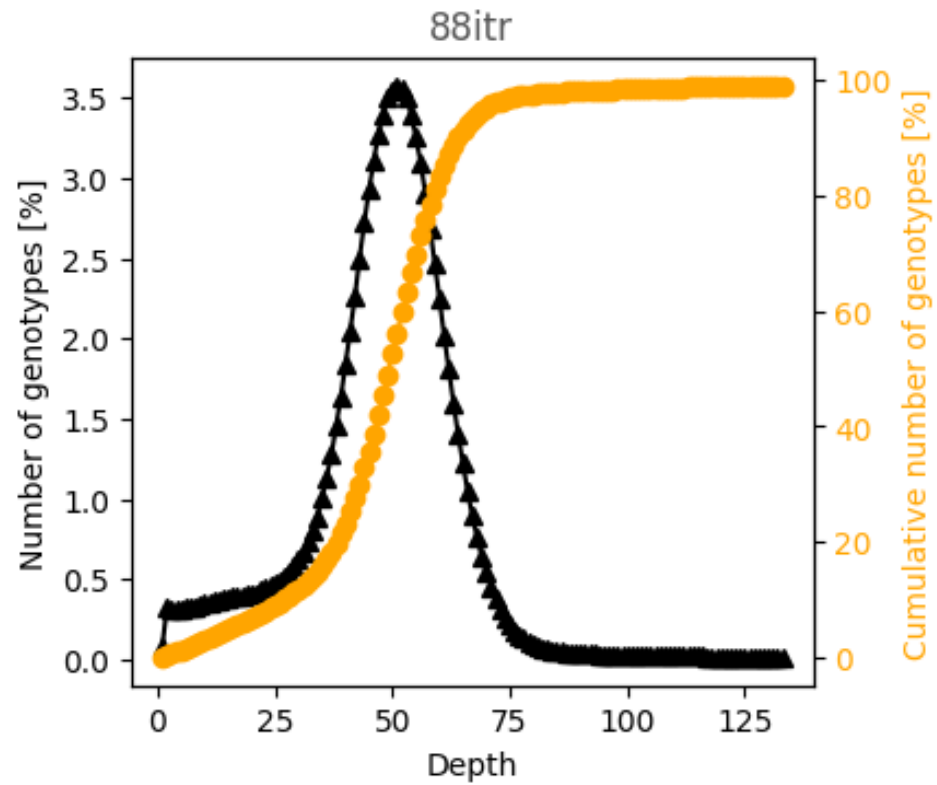
Indel distribution



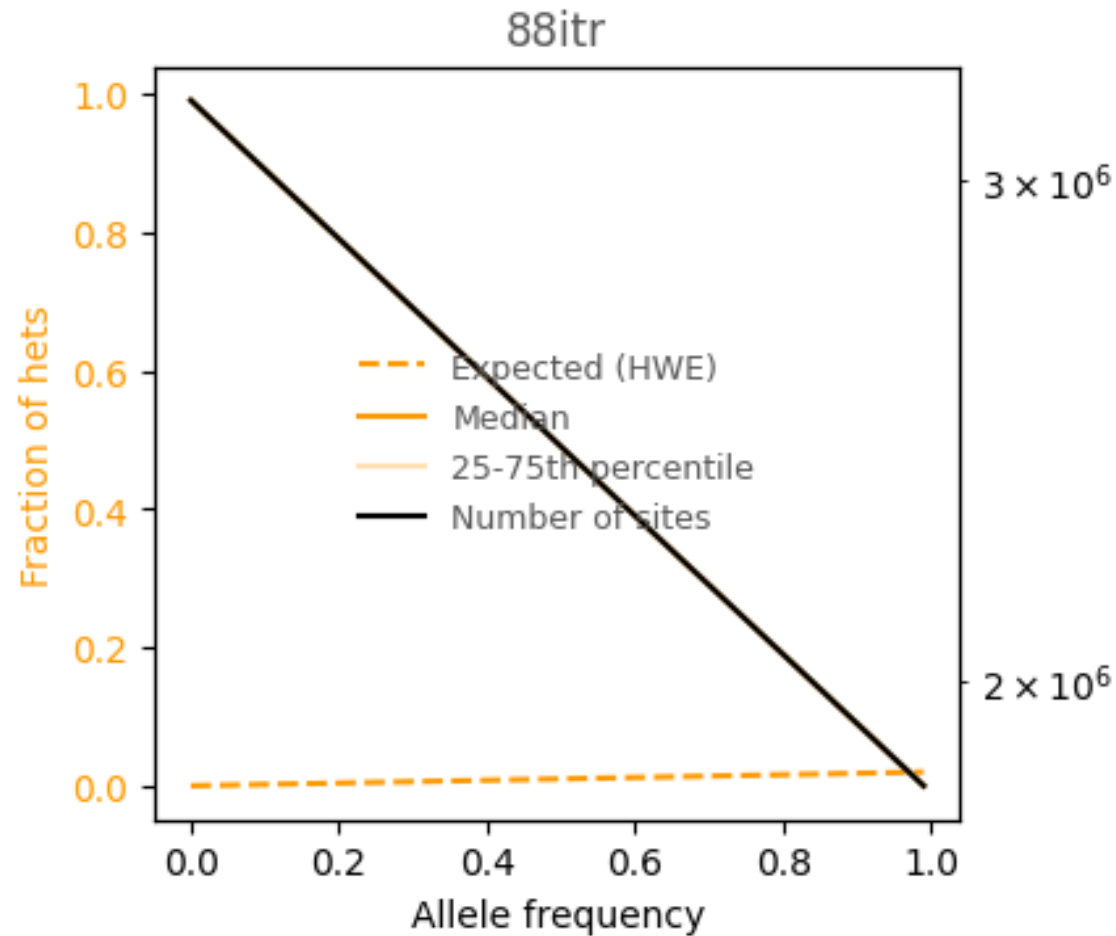
Fraction of alternate indel allele



Depth distribution



Number of HETs by AF



Substitution types

