

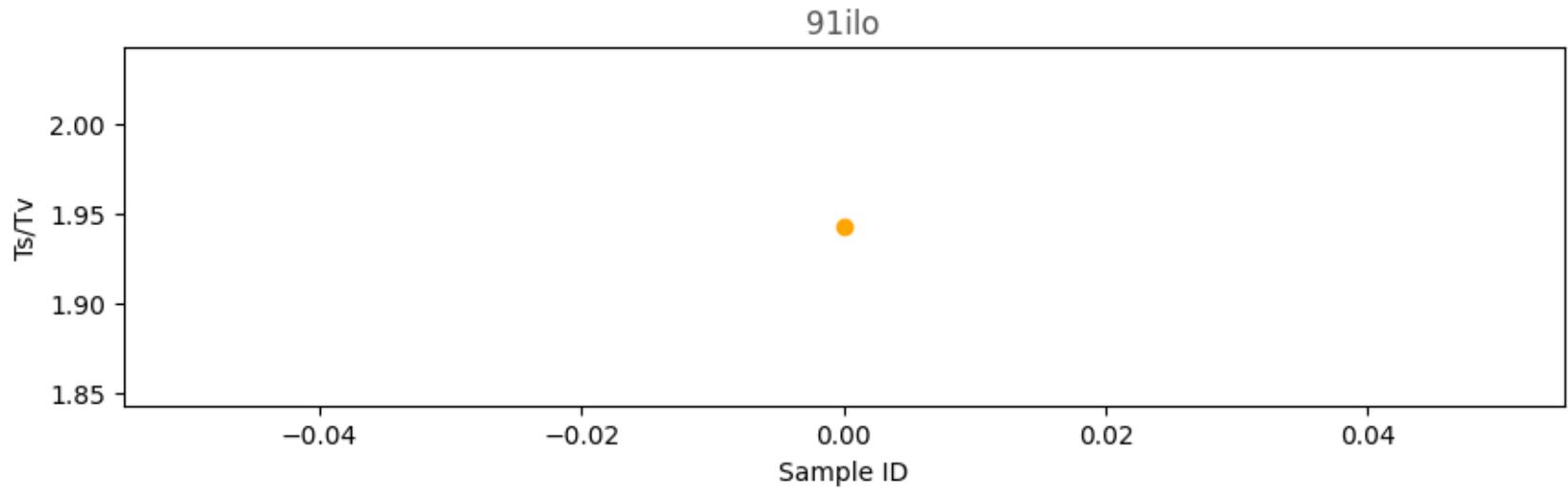
Summary Numbers

| Callset | SNPs | | | indels | | MNPs | others |
|----------------------------------|-----------|-------|-----------|---------|------|------|--------|
| | n | ts/tv | (1st ALT) | n | frm* | | |
| 91ilo | 4,055,921 | 1.94 | 1.95 | 941,516 | – | 0 | 0 |
| * frameshift ratio: out/(out+in) | | | | | | | |

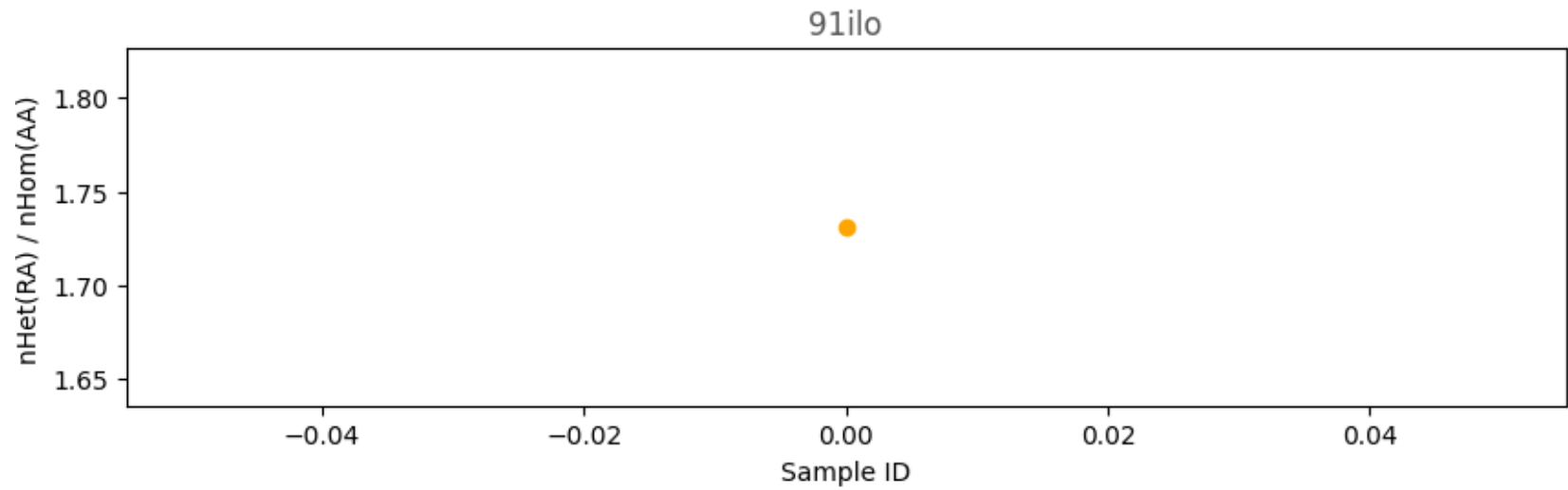
| Callset | singletons (AC=1) | | | multiallelic | |
|---------|-------------------|-------|--------|--------------|-------|
| | SNPs | ts/tv | indels | sites | SNPs |
| 91ilo | 63.4% | 1.92 | 67.8% | 96,023 | 1,926 |

- 91ilo .. /ngc/projects2/gm/data/archive/2022/variants/snv/91iloclyf-103870182088-Normal_Blood_noinfo-WGS_v1_IlluminaDNAPCRFree_RHGM00820-220525_A01176_AHJ5HGDSX3-EXT_LAB_KA_NGCWGS-NGCWGS04326_snv_germline_raw.haplotype_caller.vcf.gz

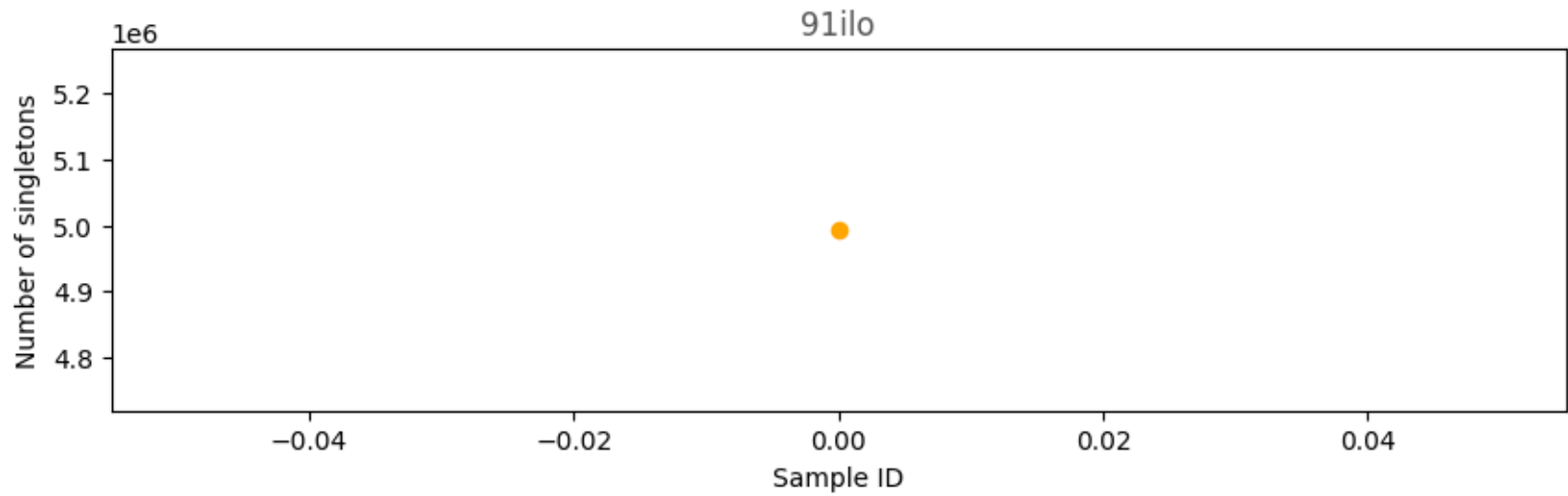
Ts/Tv by sample



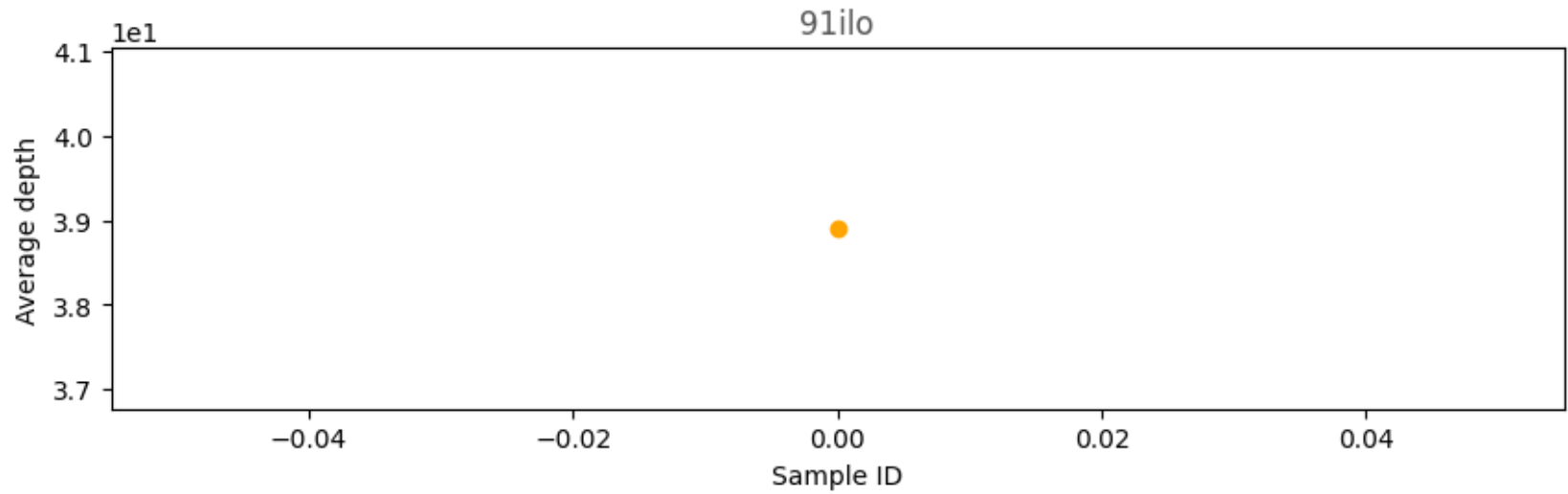
Hets vs non-ref Homs by sample



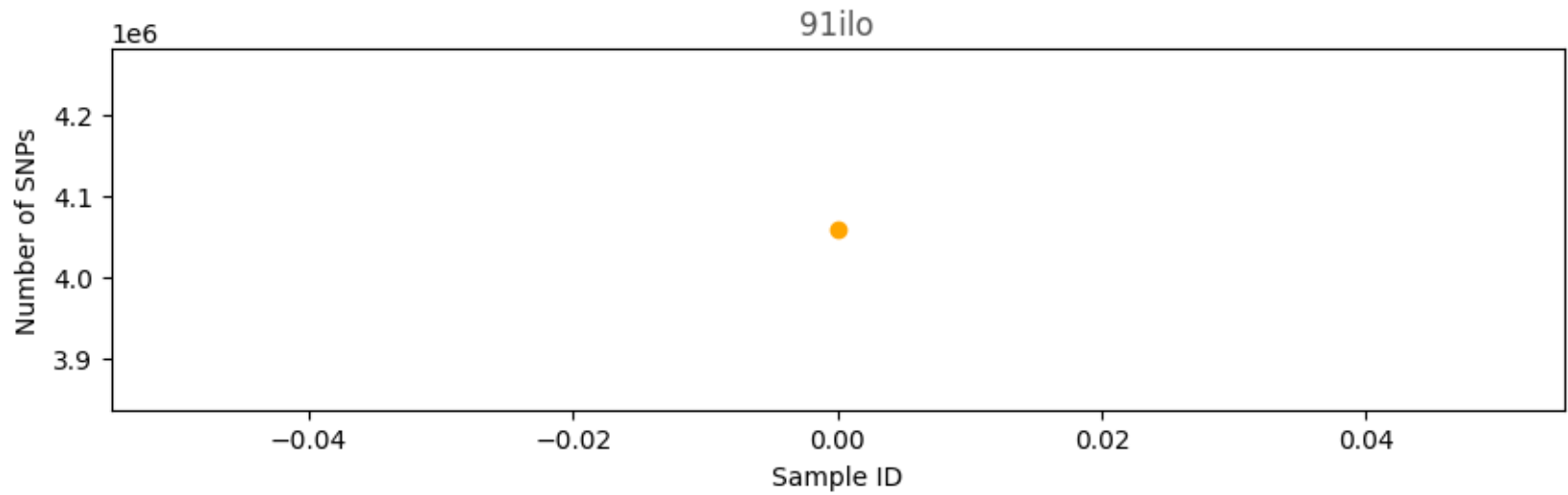
Singletons by sample (hets and homs)



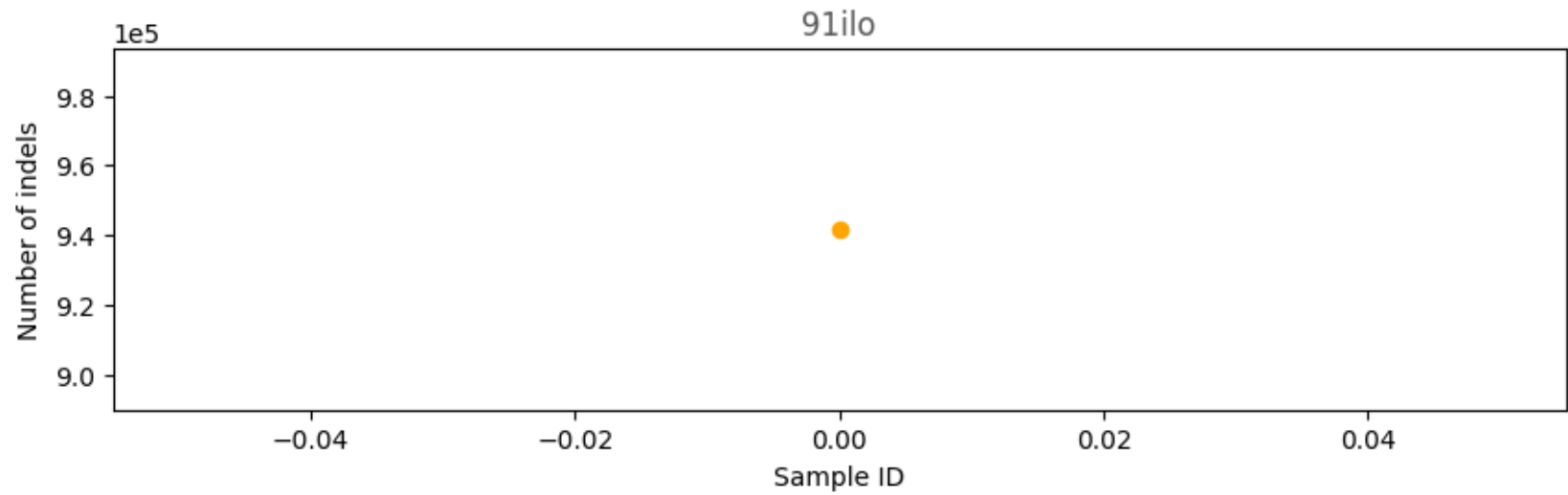
Average depth by sample



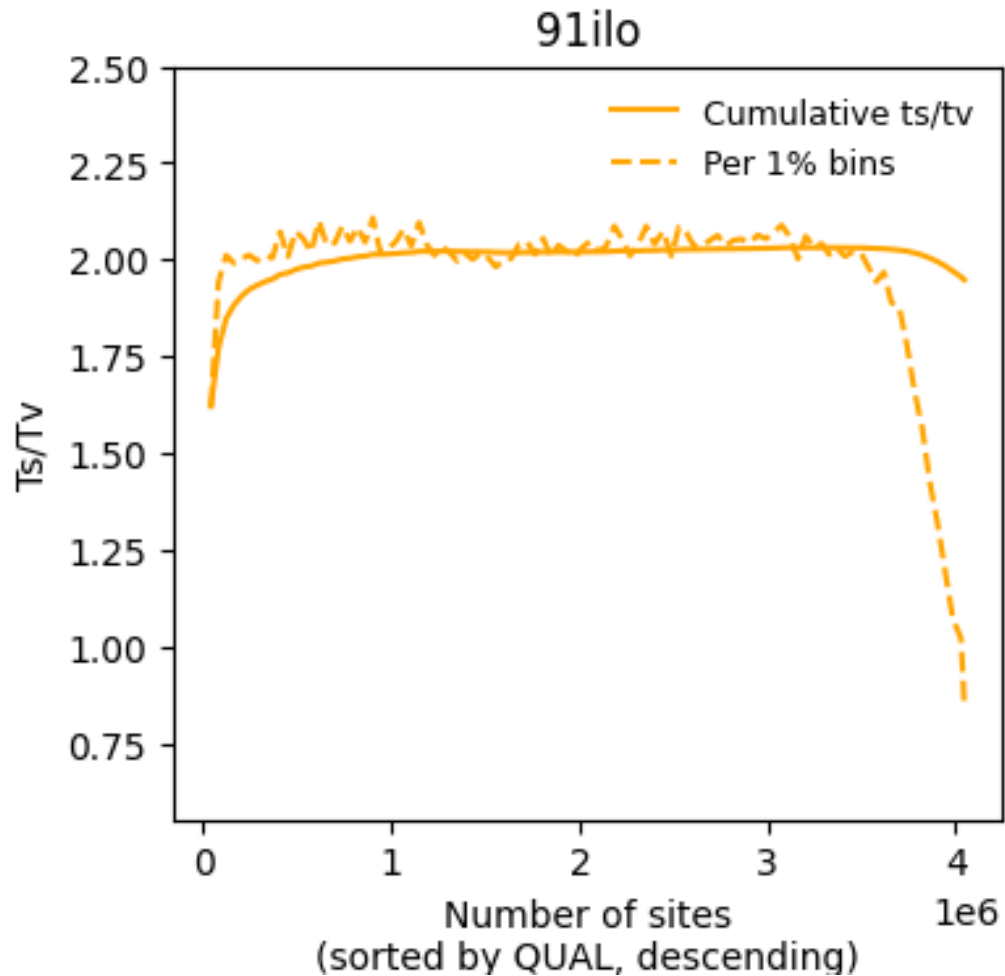
Number of SNPs by sample



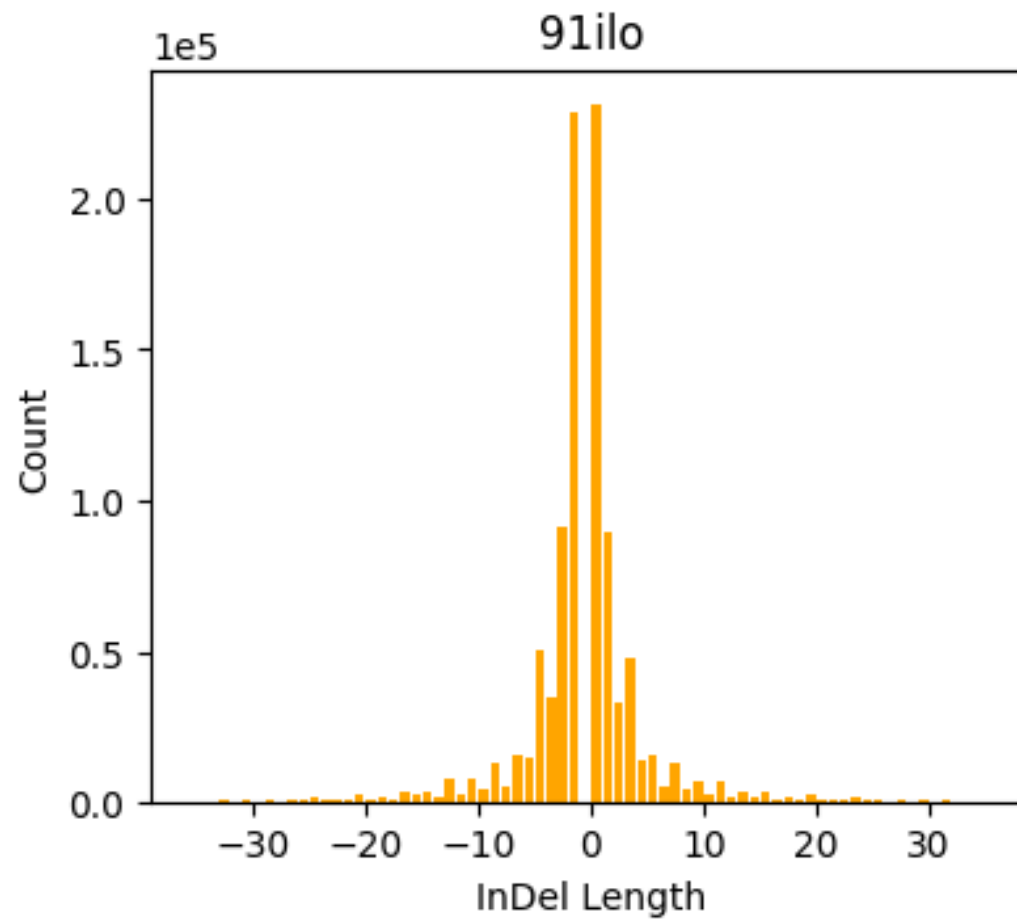
Number of indels by sample



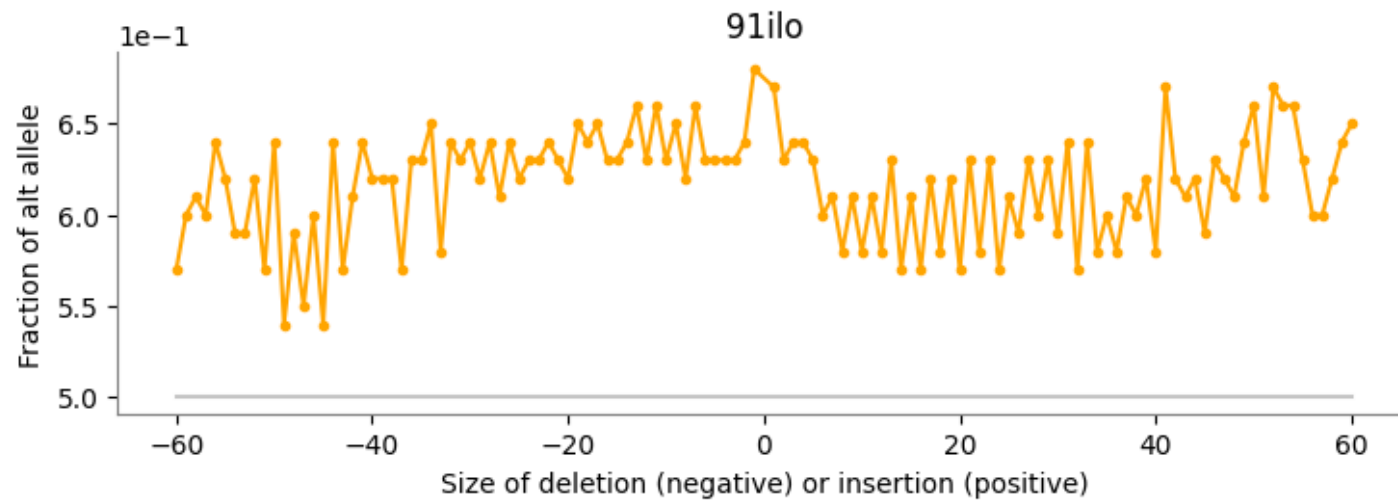
Ts/Tv stratified by QUAL



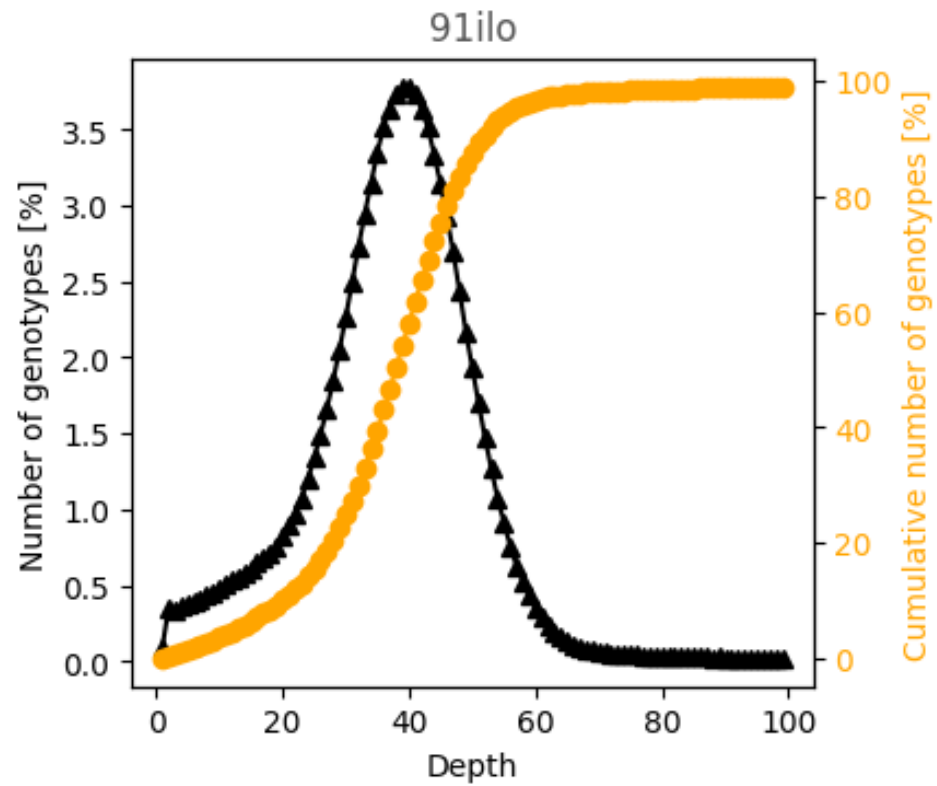
Indel distribution



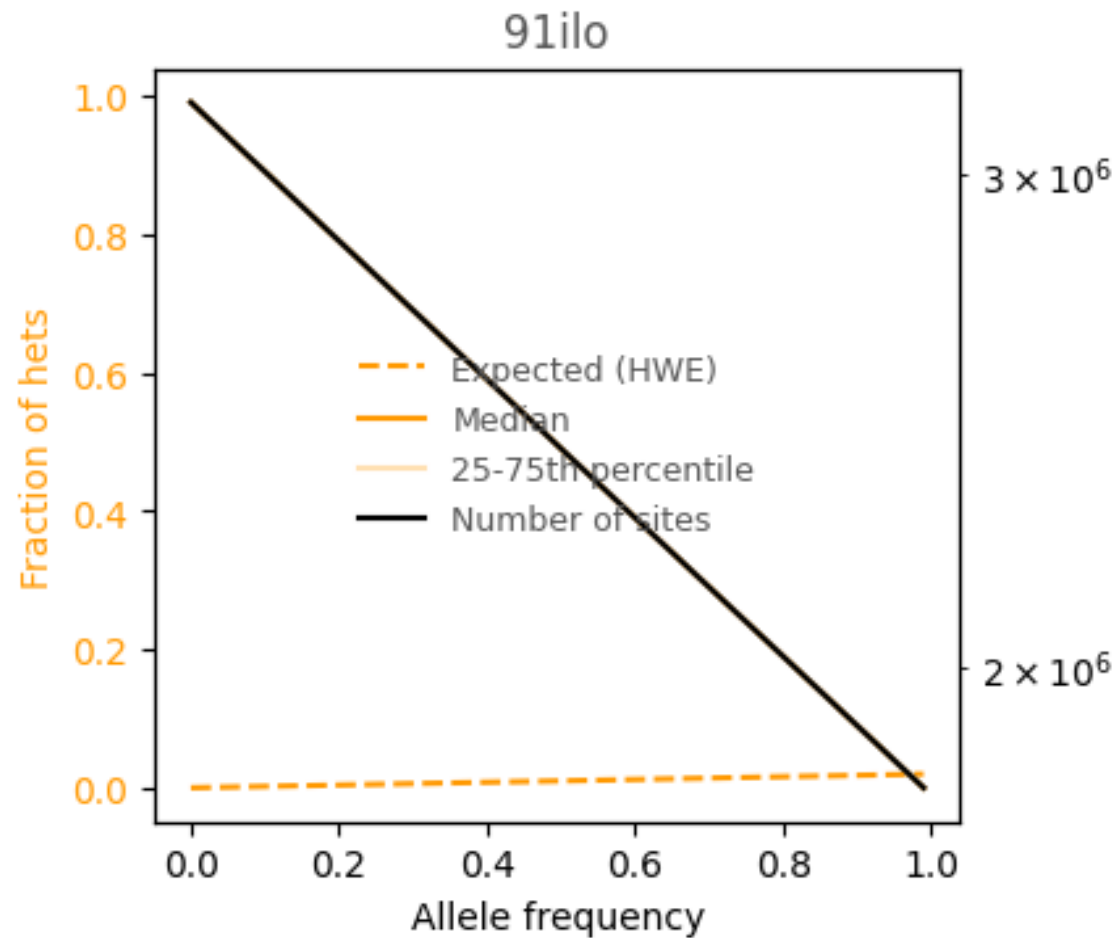
Fraction of alternate indel allele



Depth distribution



Number of HETs by AF



Substitution types

