

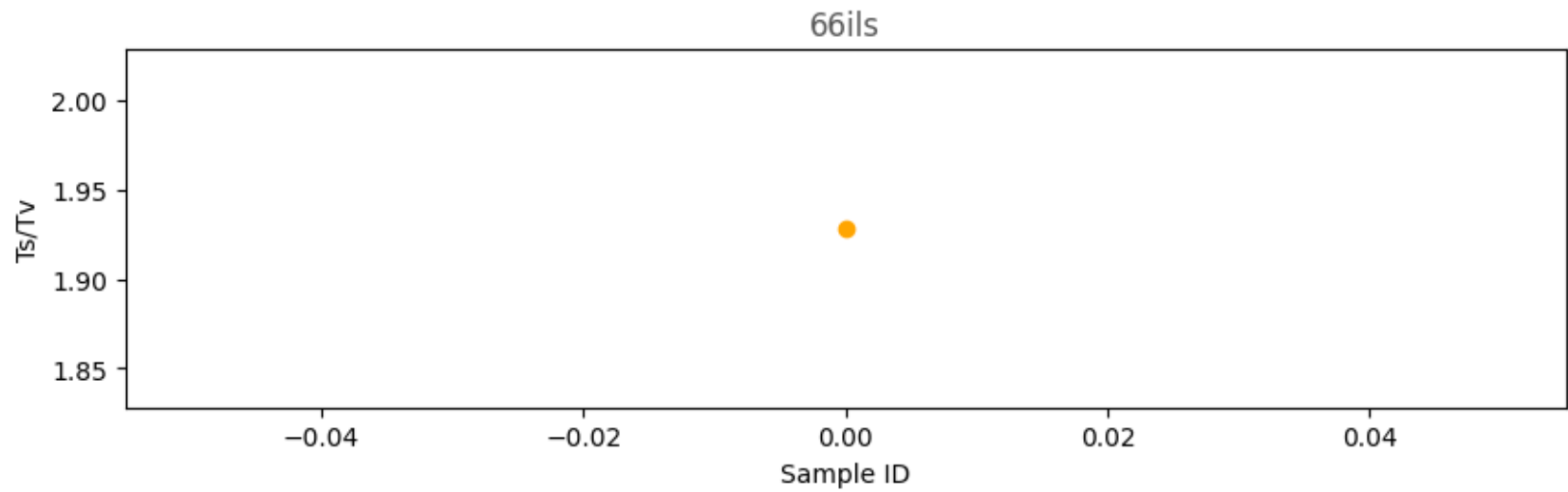
Summary Numbers

| Callset | SNPs | | | indels | | MNPs | others |
|----------------------------------|-----------|-------|-----------|---------|------|------|--------|
| | n | ts/tv | (1st ALT) | n | frm* | | |
| 66ils | 4,102,771 | 1.93 | 1.93 | 958,972 | – | 0 | 0 |
| * frameshift ratio: out/(out+in) | | | | | | | |

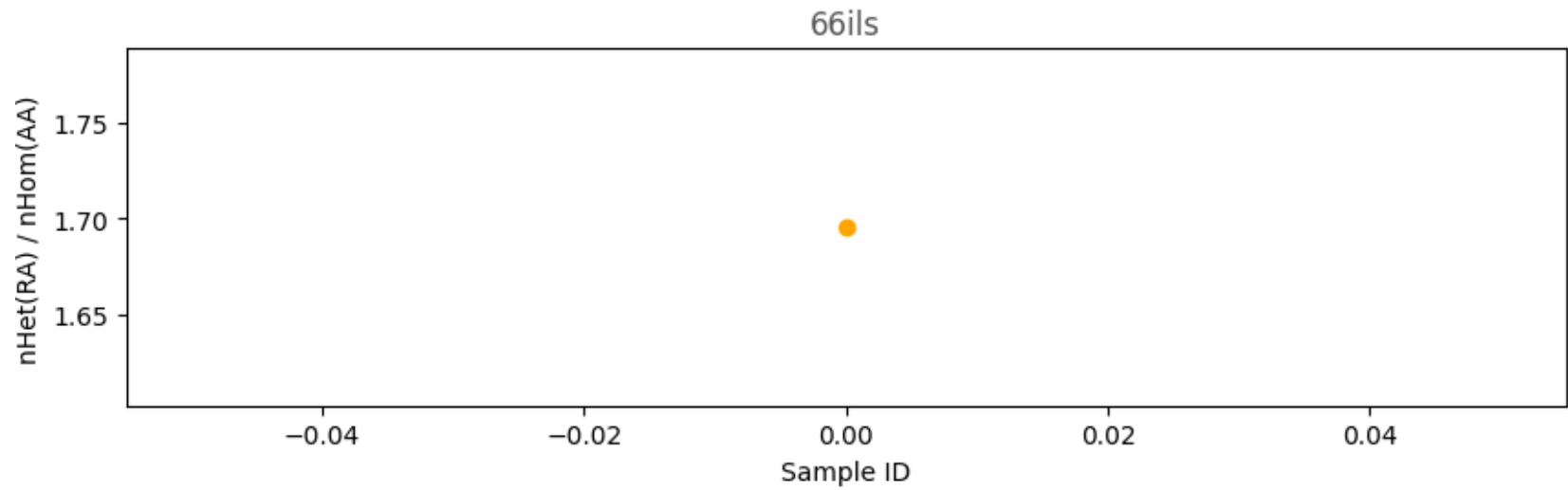
| Callset | singletons (AC=1) | | | multiallelic | |
|---------|-------------------|-------|--------|--------------|-------|
| | SNPs | ts/tv | indels | sites | SNPs |
| 66ils | 62.9% | 1.90 | 68.4% | 104,139 | 2,113 |

- 66ils .. /ngc/projects2/gm/data/archive/2022/variants/snv/66ilsconf-110297594382-Normal_Blood_noinfo-WGS_v1_IlluminaDNAPCRFree_RHGM02091-221021_A00559_BH3FHJDSX5-EXT_LAB_KA_NGCWGS-NGCWGS05946_snv_germline_raw.haplotype_caller.vcf.gz

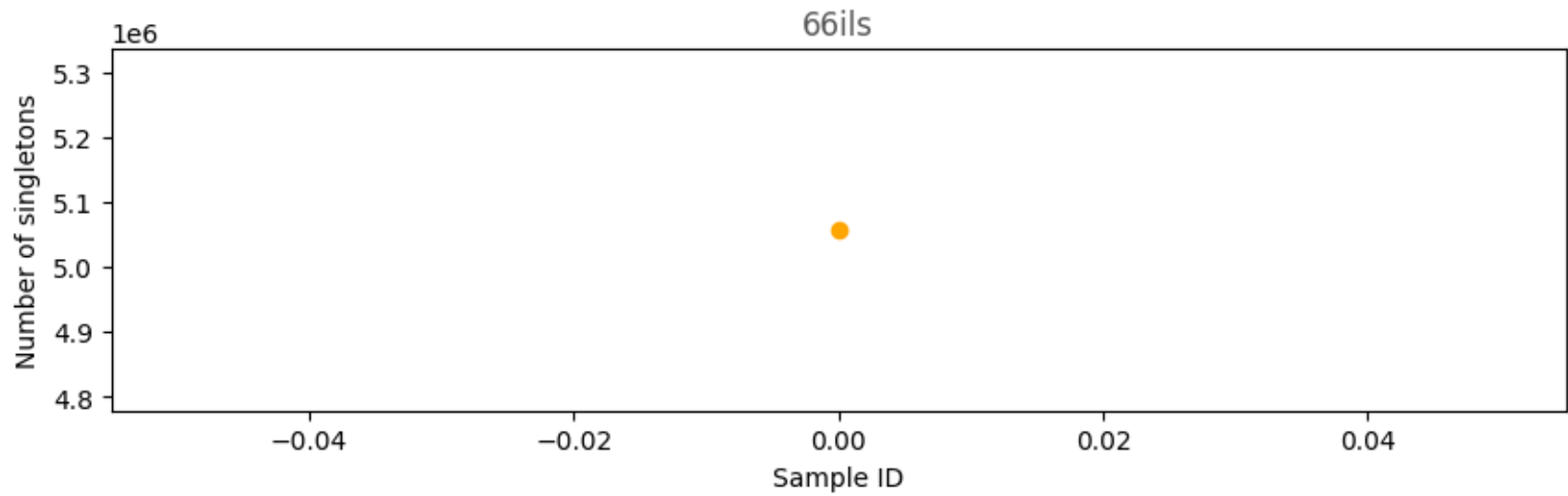
Ts/Tv by sample



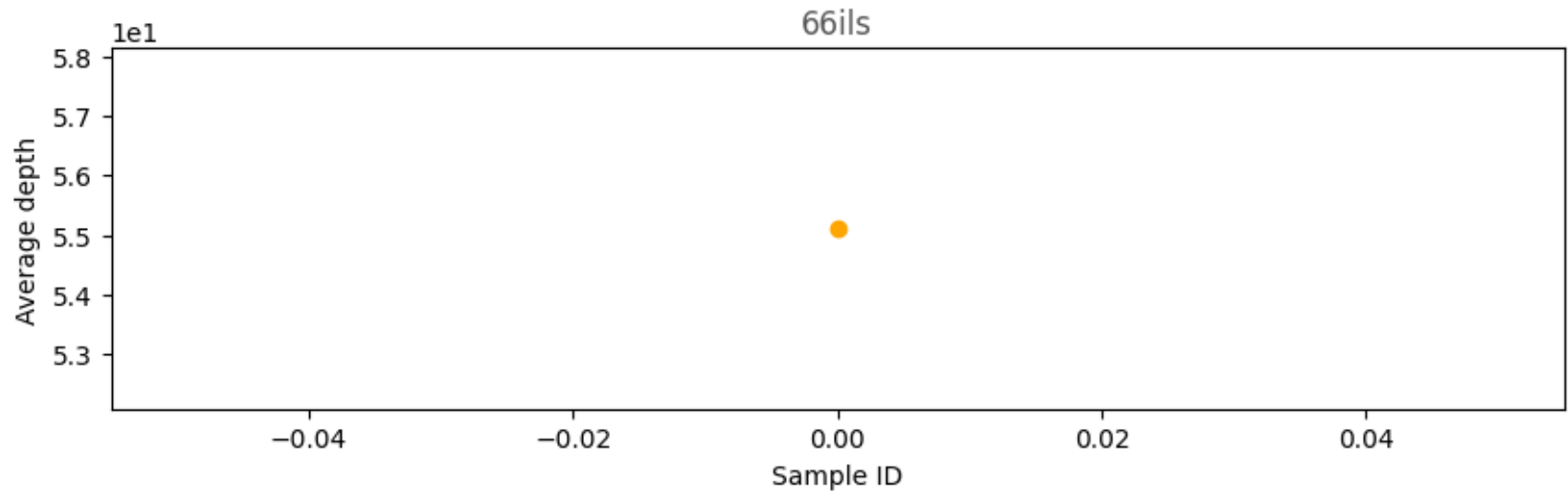
Hets vs non-ref Homs by sample



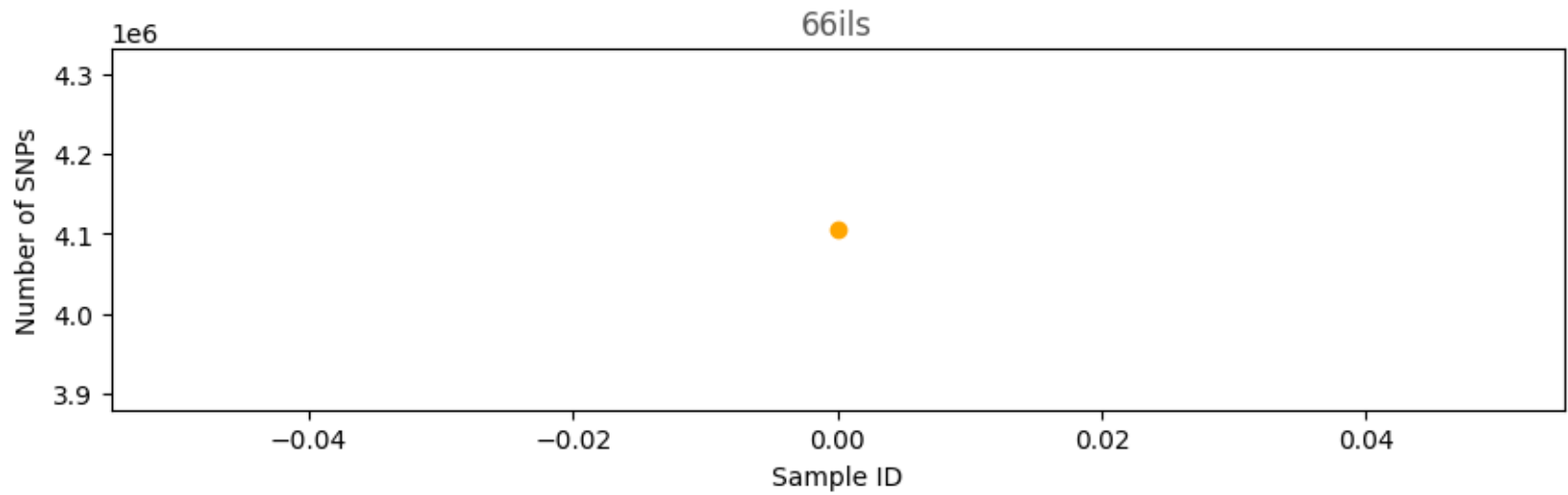
Singletons by sample (hets and homs)



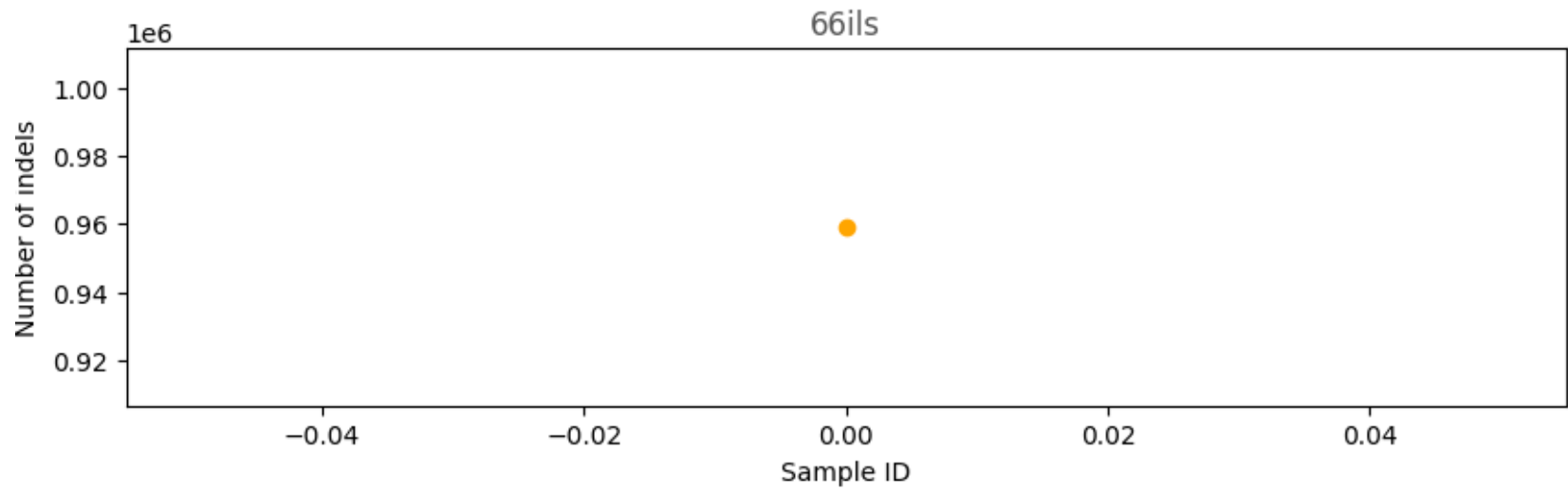
Average depth by sample



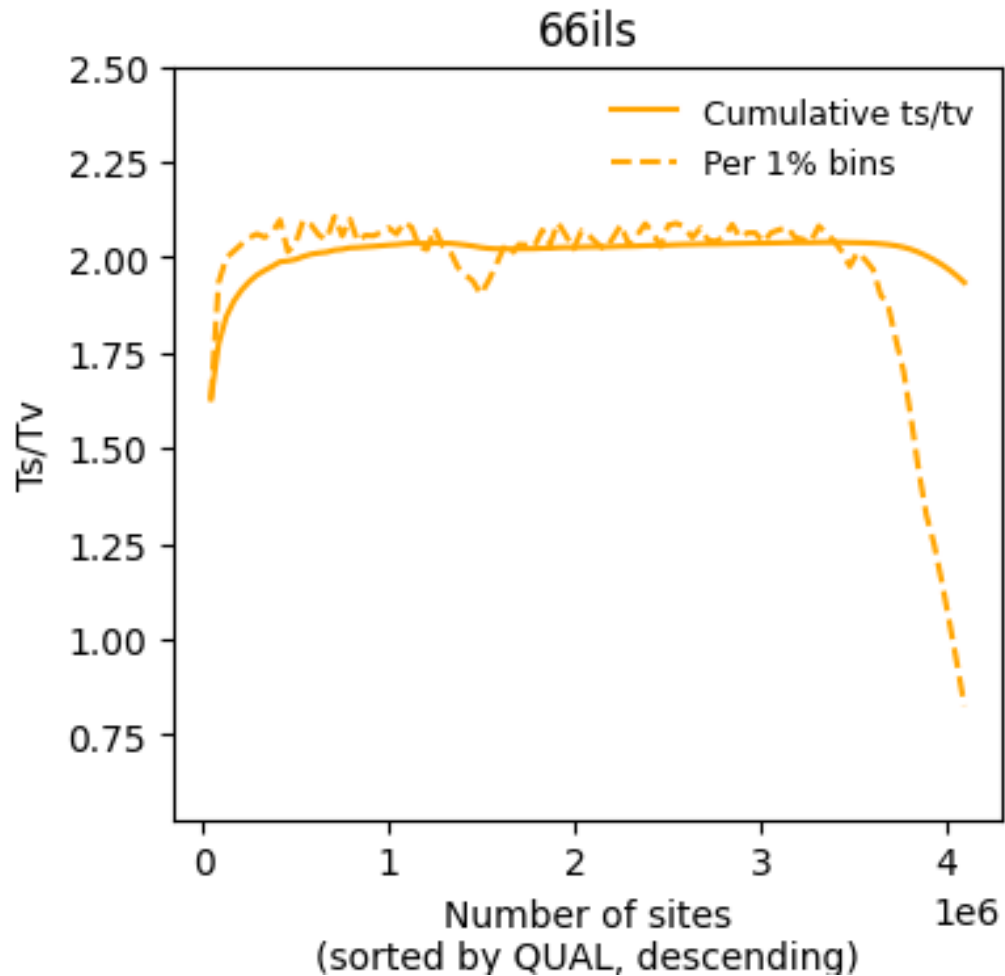
Number of SNPs by sample



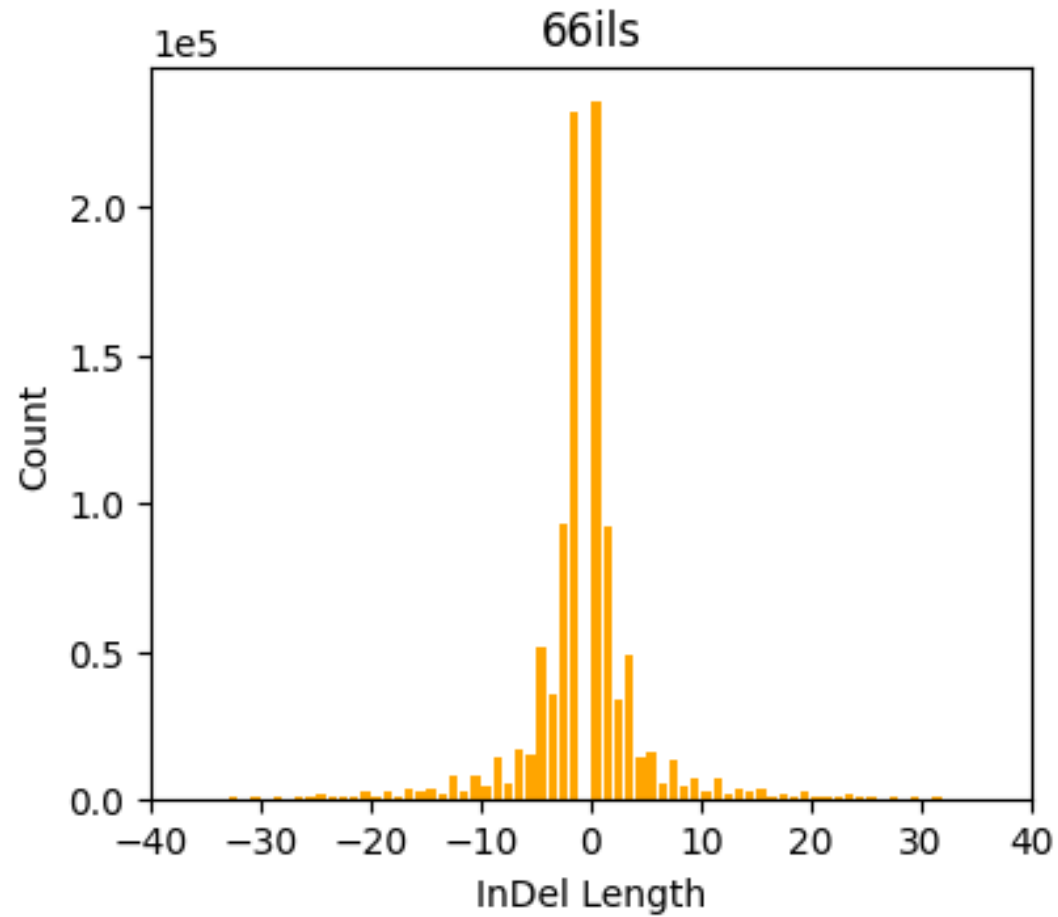
Number of indels by sample



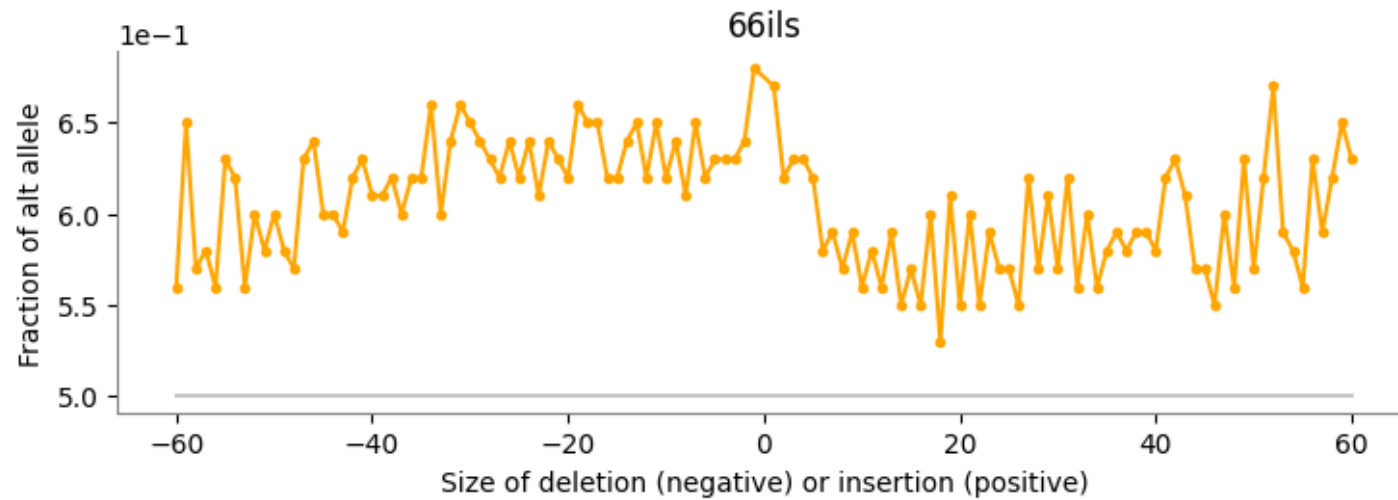
Ts/Tv stratified by QUAL



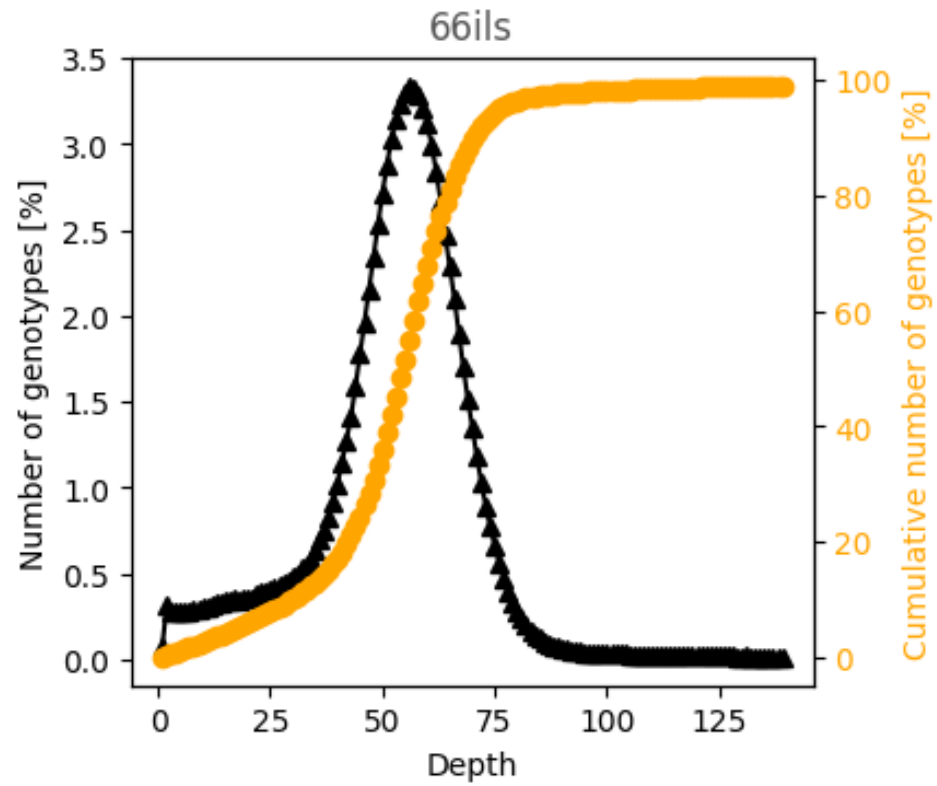
Indel distribution



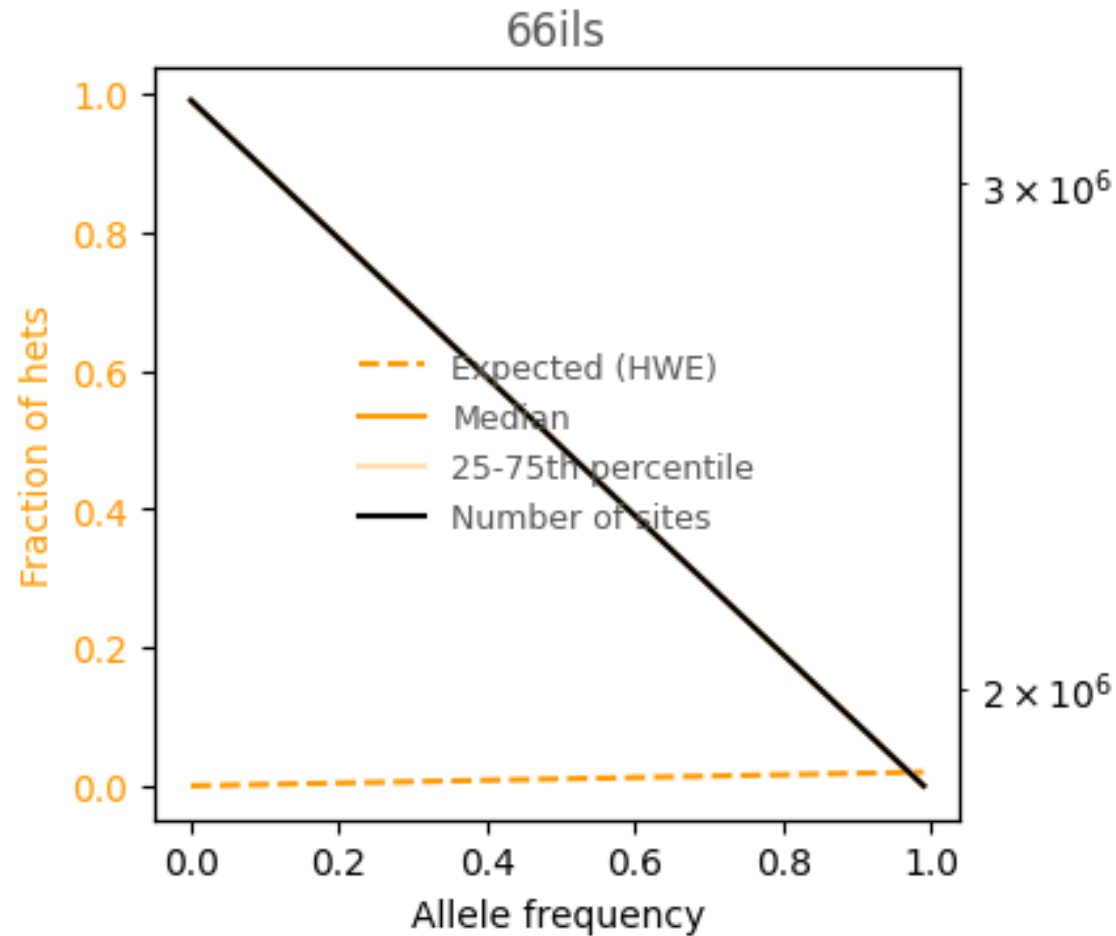
Fraction of alternate indel allele



Depth distribution



Number of HETs by AF



Substitution types

