

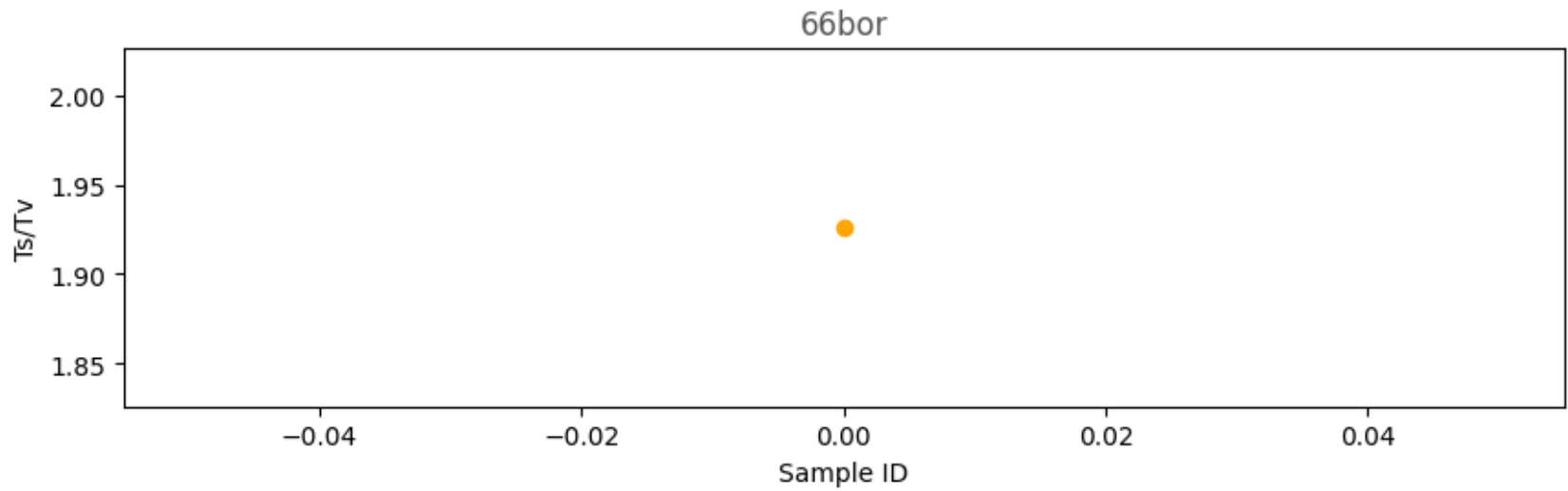
Summary Numbers

| Callset | SNPs | | | indels | | MNPs | others |
|----------------------------------|-----------|-------|-----------|---------|------|------|--------|
| | n | ts/tv | (1st ALT) | n | frm* | | |
| 66bor | 4,098,569 | 1.93 | 1.93 | 955,977 | – | 0 | 0 |
| * frameshift ratio: out/(out+in) | | | | | | | |

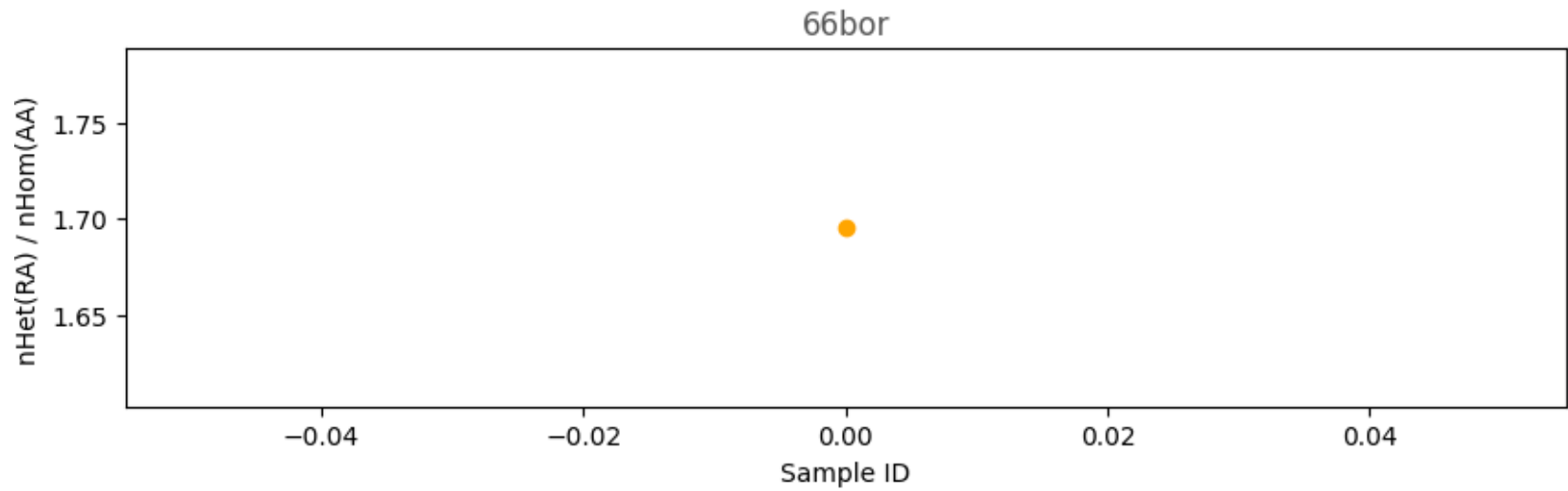
| Callset | singletons (AC=1) | | | multiallelic | |
|---------|-------------------|-------|--------|--------------|-------|
| | SNPs | ts/tv | indels | sites | SNPs |
| 66bor | 62.9% | 1.89 | 68.1% | 101,834 | 2,158 |

- 66bor .. /ngc/projects2/gm/data/archive/2022/variants/snv/66boreref-103760986321-Normal_B
 lood_noinfo-WGS_v1_IlluminaDNAPCRFree_RHGM00279-210720_A01411_BHGMTTDSX2-EXT_LAB
 KA_NGCWGS-NGCWGS00172-666hwrqj2-snv_germline_raw.haplotype_caller.vcf.gz

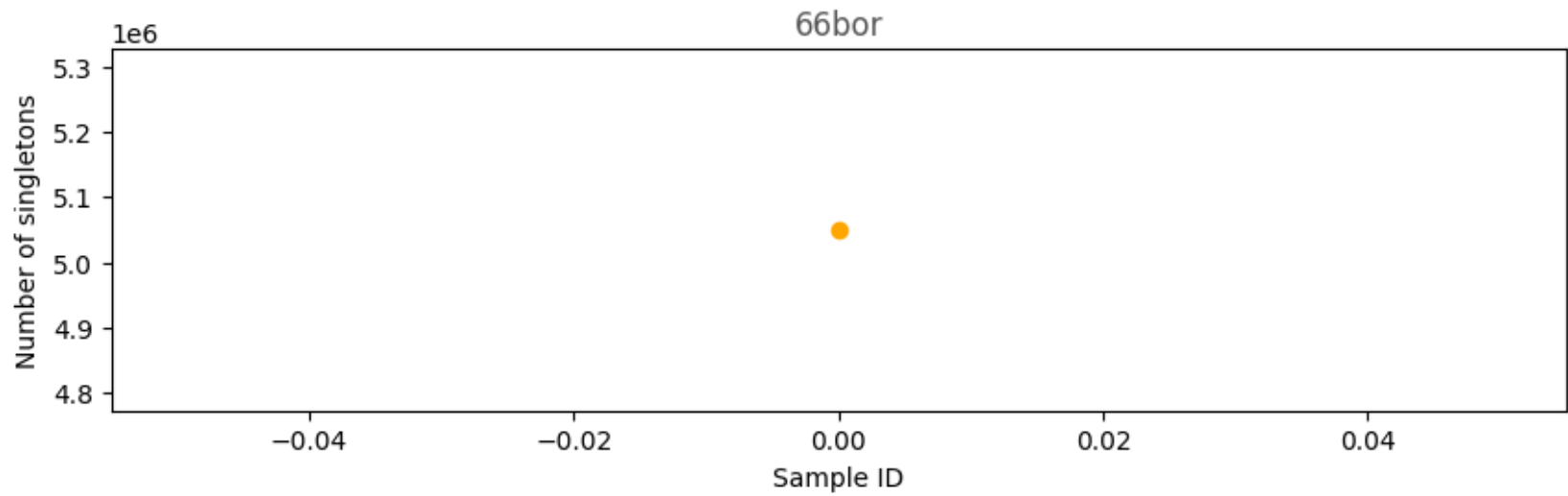
Ts/Tv by sample



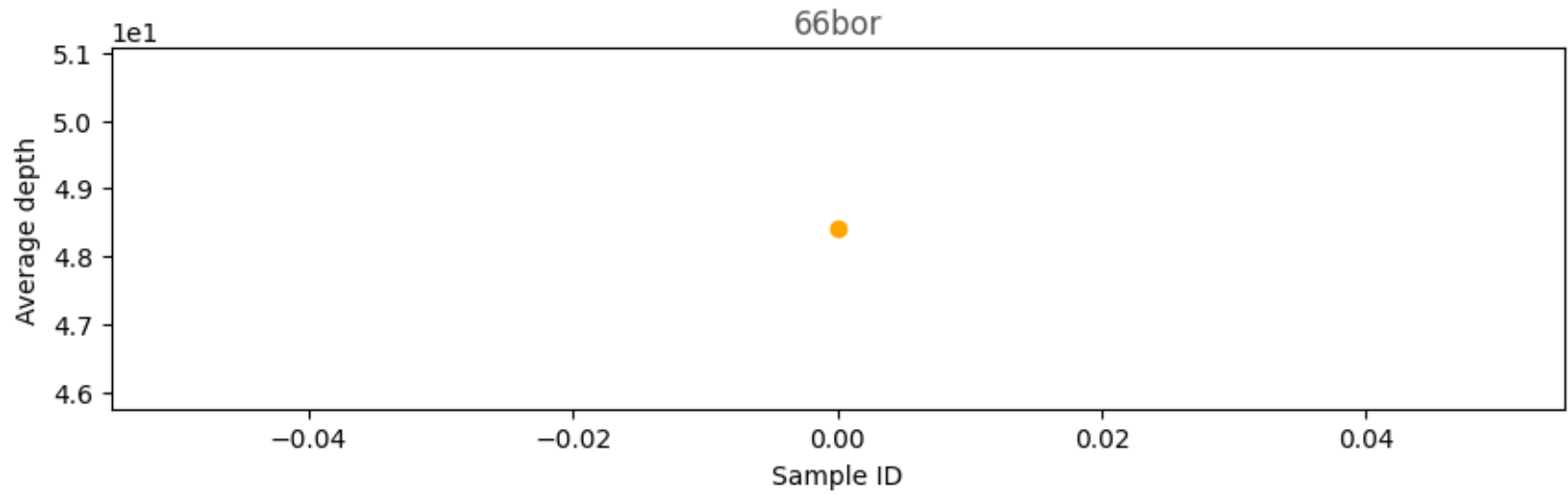
Hets vs non-ref Homs by sample



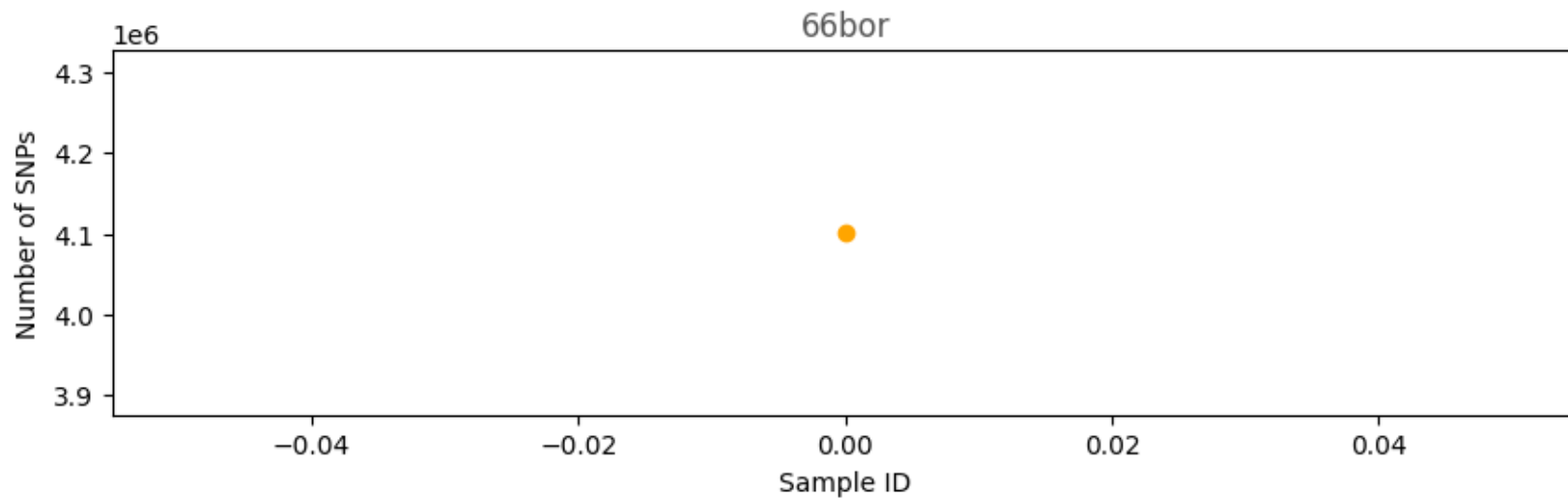
Singletons by sample (hets and homs)



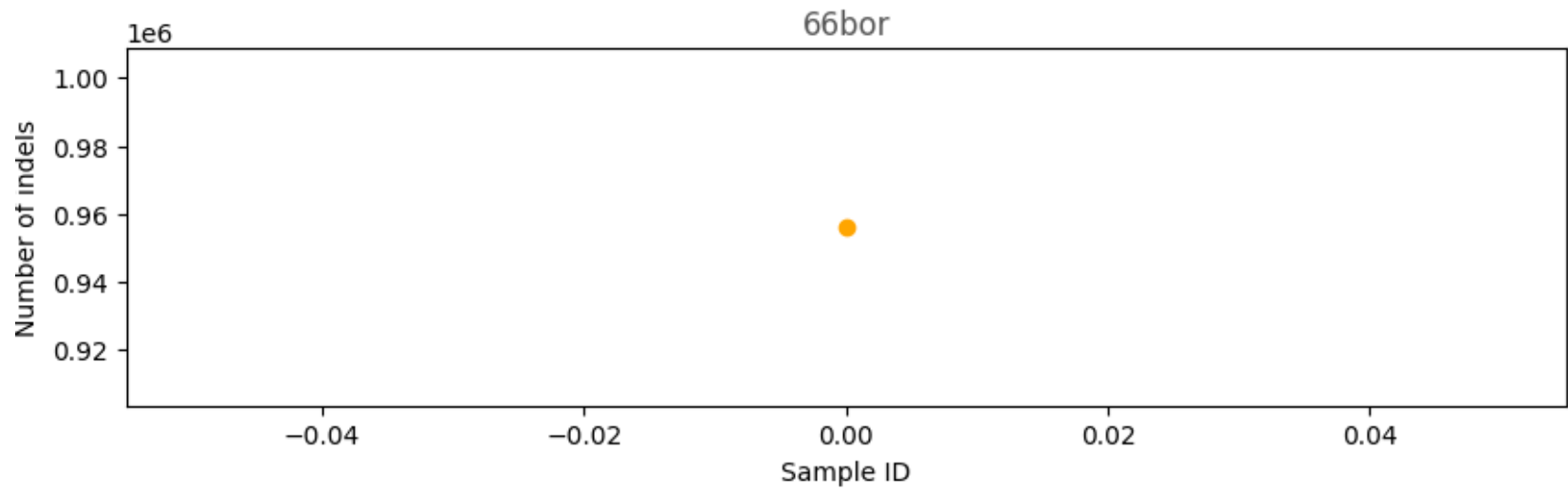
Average depth by sample



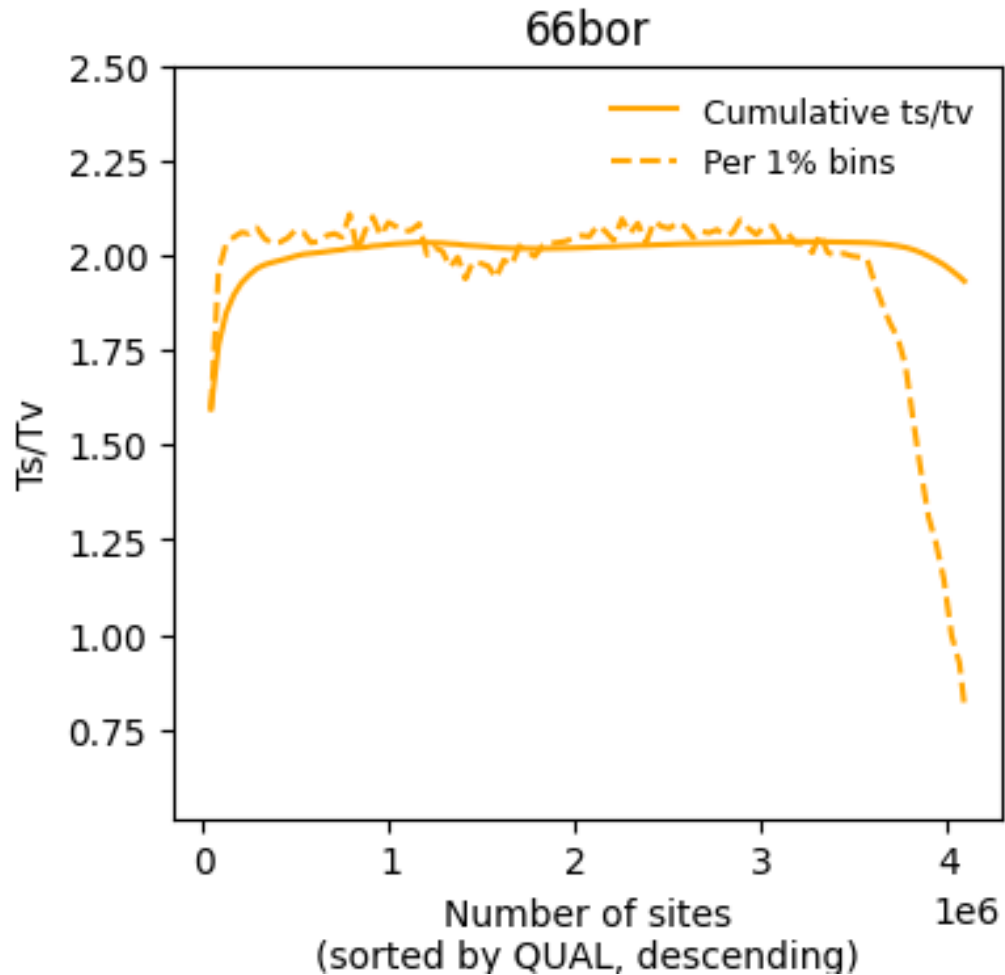
Number of SNPs by sample



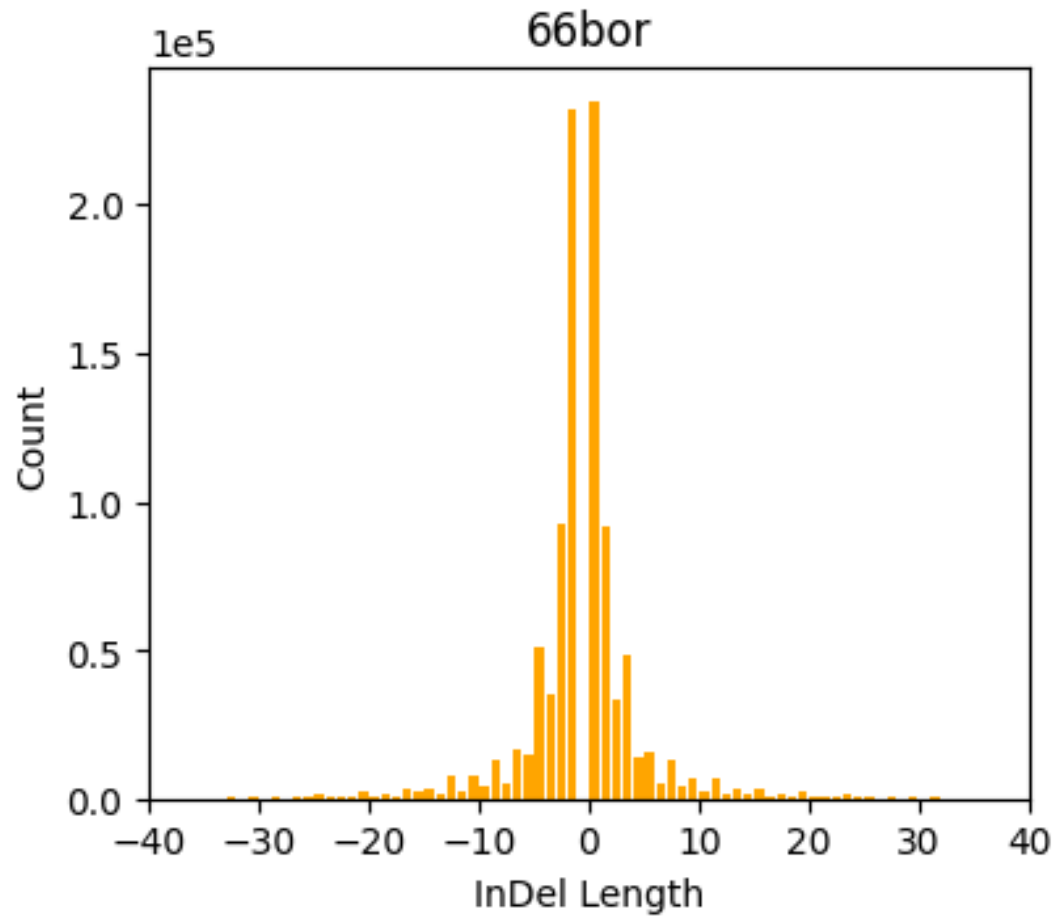
Number of indels by sample



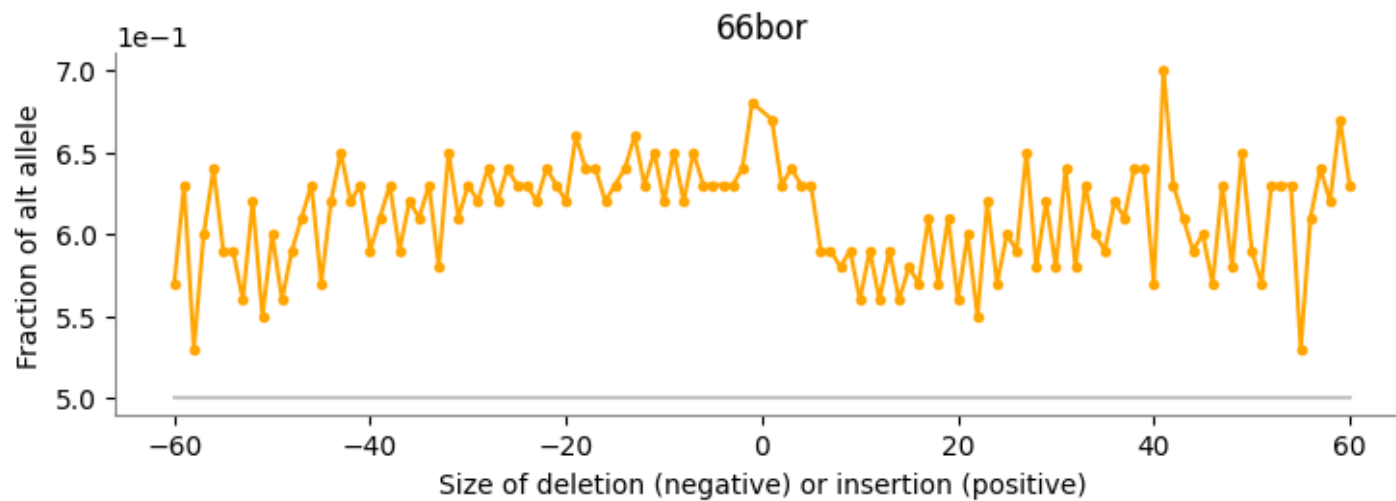
Ts/Tv stratified by QUAL



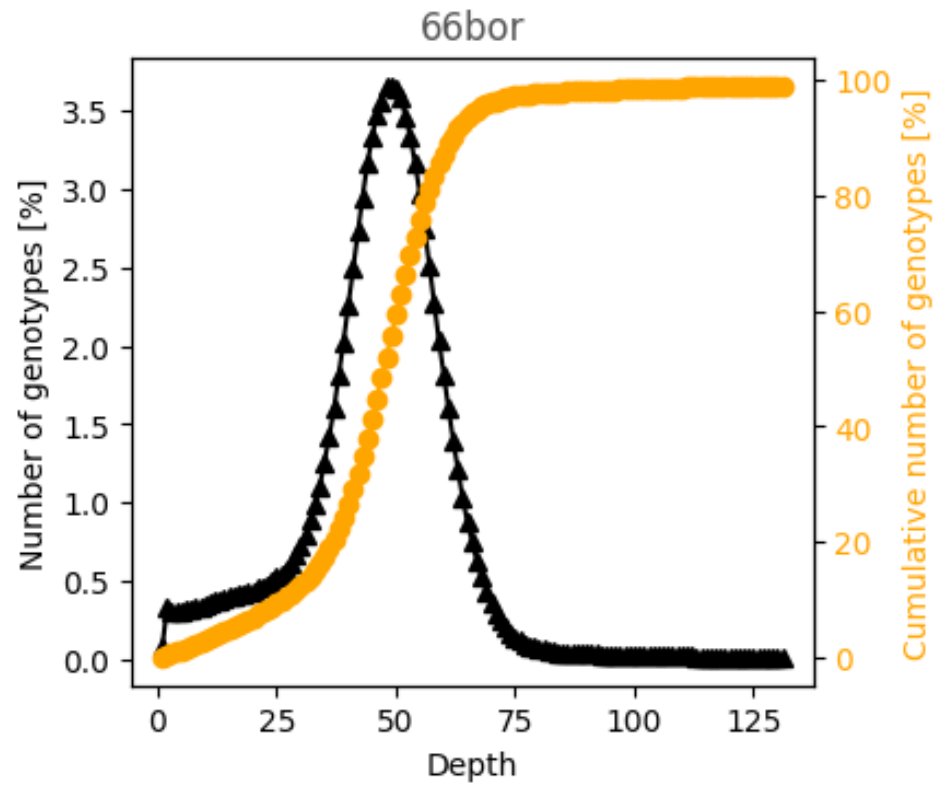
Indel distribution



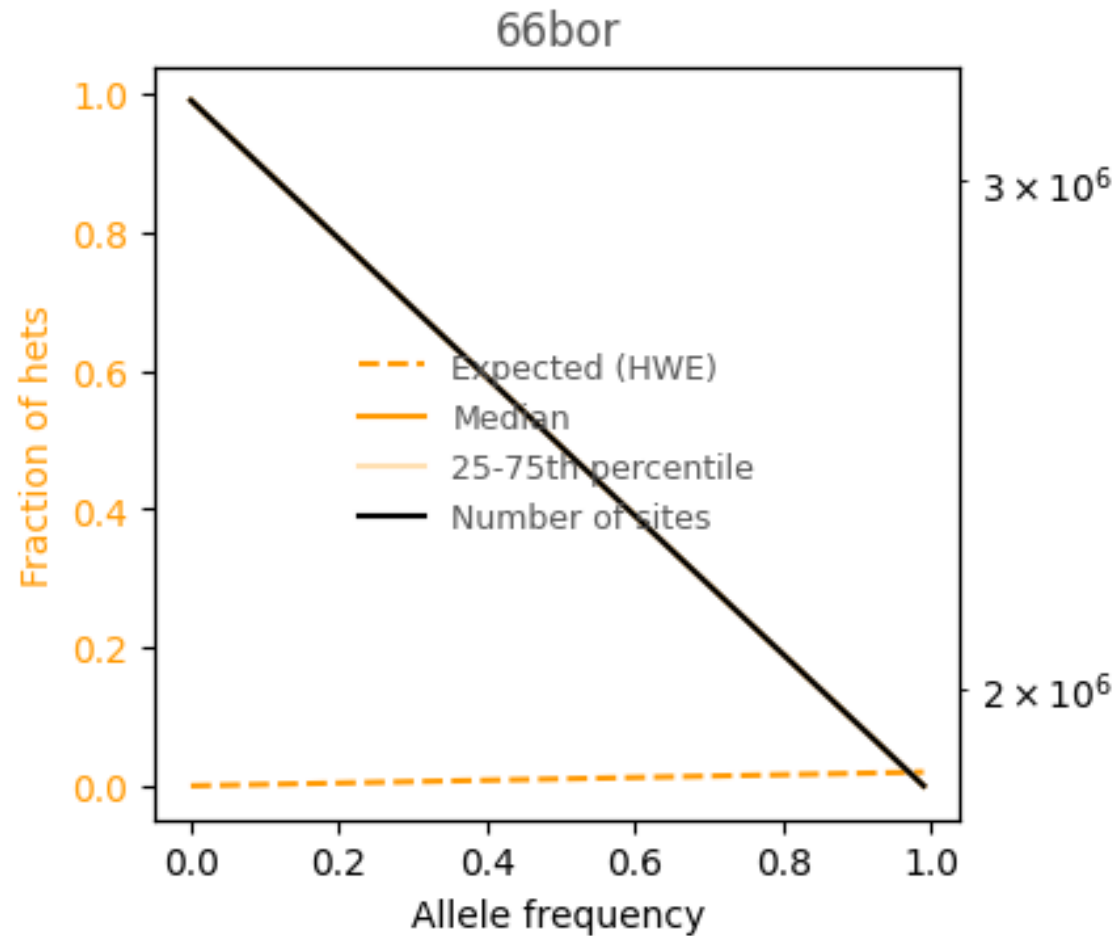
Fraction of alternate indel allele



Depth distribution



Number of HETs by AF



Substitution types

