

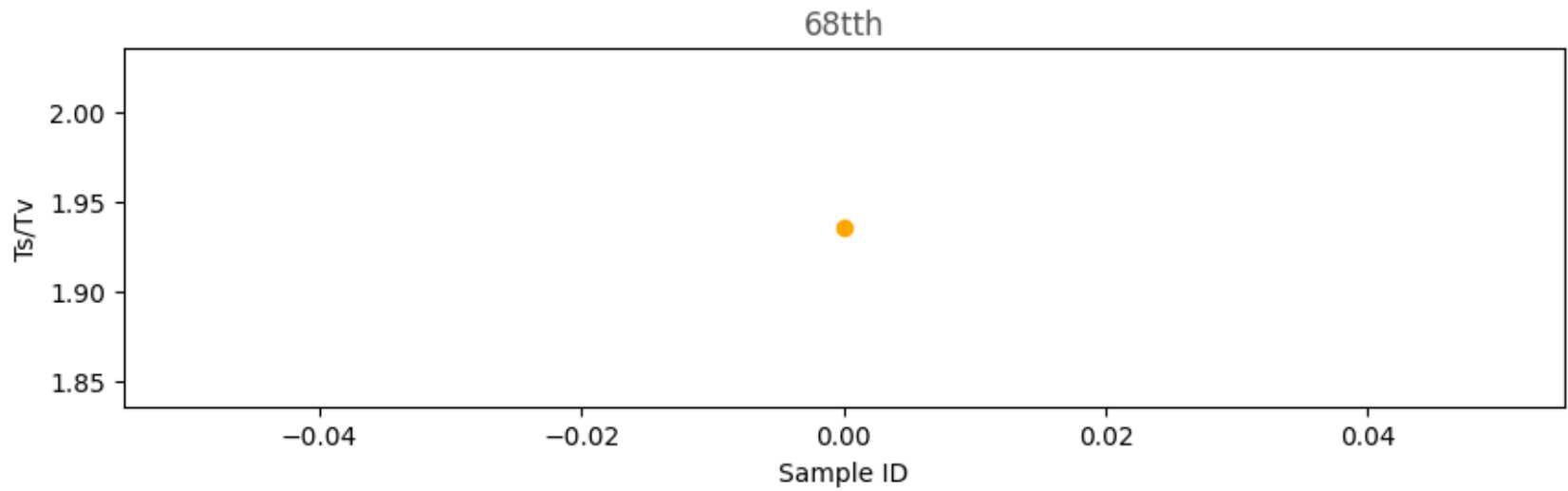
Summary Numbers

| Callset | SNPs | | | indels | | MNPs | others |
|----------------------------------|-----------|-------|-----------|---------|------|------|--------|
| | n | ts/tv | (1st ALT) | n | frm* | | |
| 68tth | 4,083,050 | 1.94 | 1.94 | 947,274 | – | 0 | 0 |
| * frameshift ratio: out/(out+in) | | | | | | | |

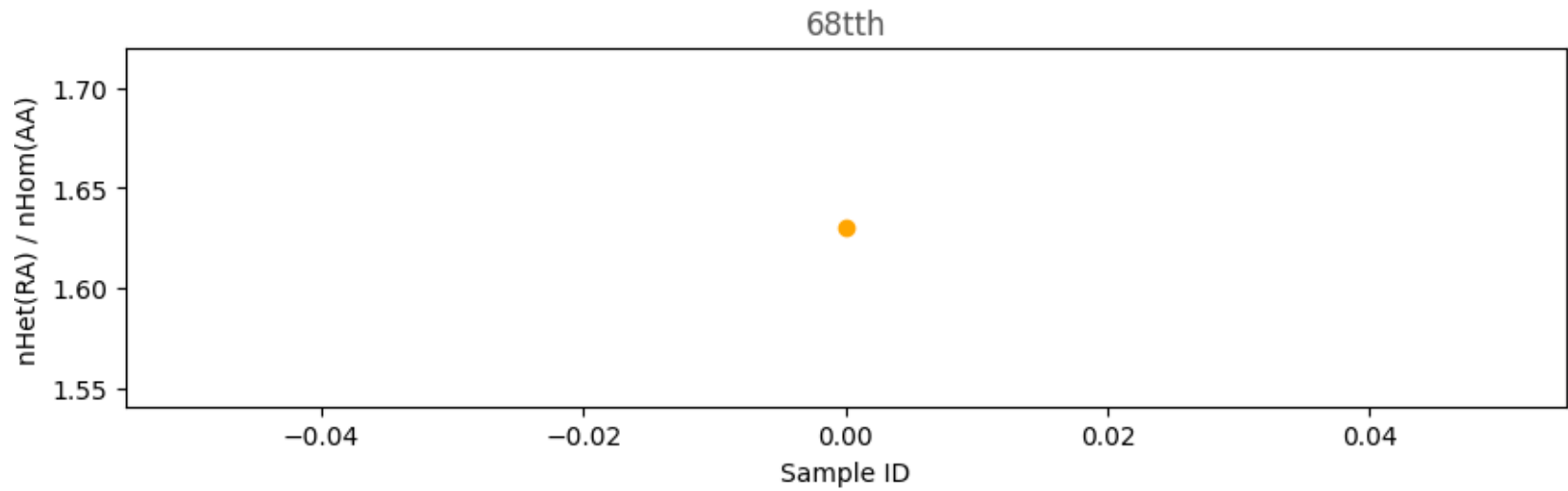
| Callset | singletons (AC=1) | | | multiallelic | |
|---------|-------------------|-------|--------|--------------|-------|
| | SNPs | ts/tv | indels | sites | SNPs |
| 68tth | 62.0% | 1.91 | 66.3% | 96,480 | 2,117 |

- 68tth .. /ngc/projects2/gm/data/archive/2022/variants/snv/68tthallm-103905114152-Normal_Blood_noinfo-WGS_v1_IlluminaDNAPCRFree_RHGM01495-220914_A01176_BHTNVLDSX3-EXT_LAB_KA_NGCWGS-NGCWGS05269_22RKG020484_snv_germline_raw.haplotype_caller.vcf.gz

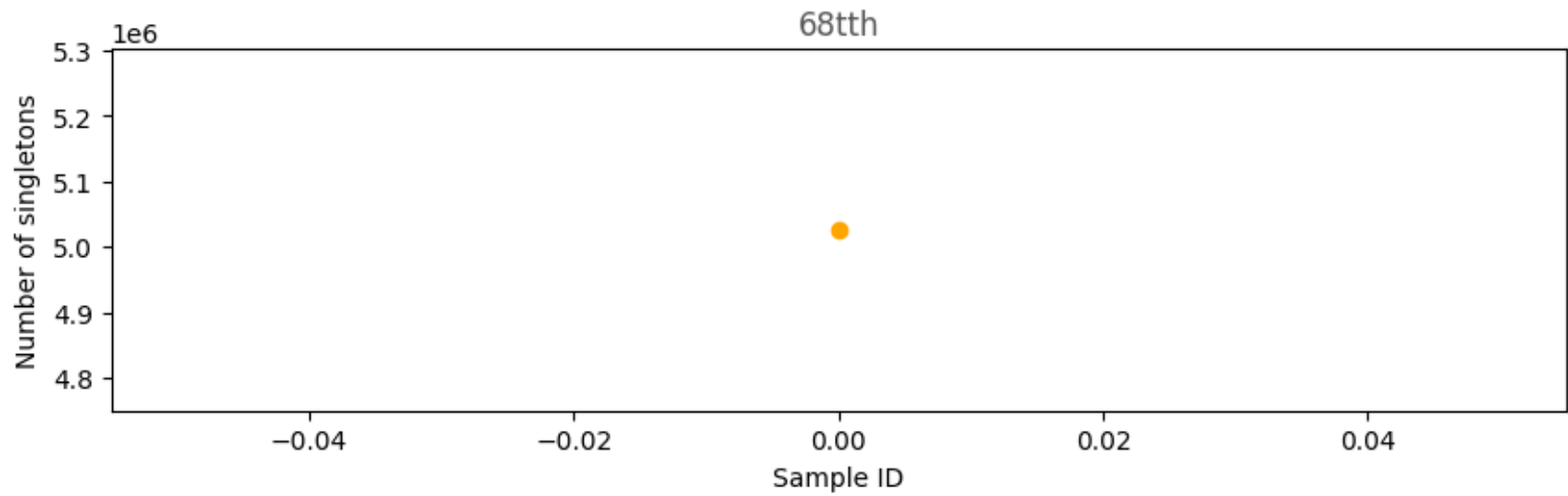
Ts/Tv by sample



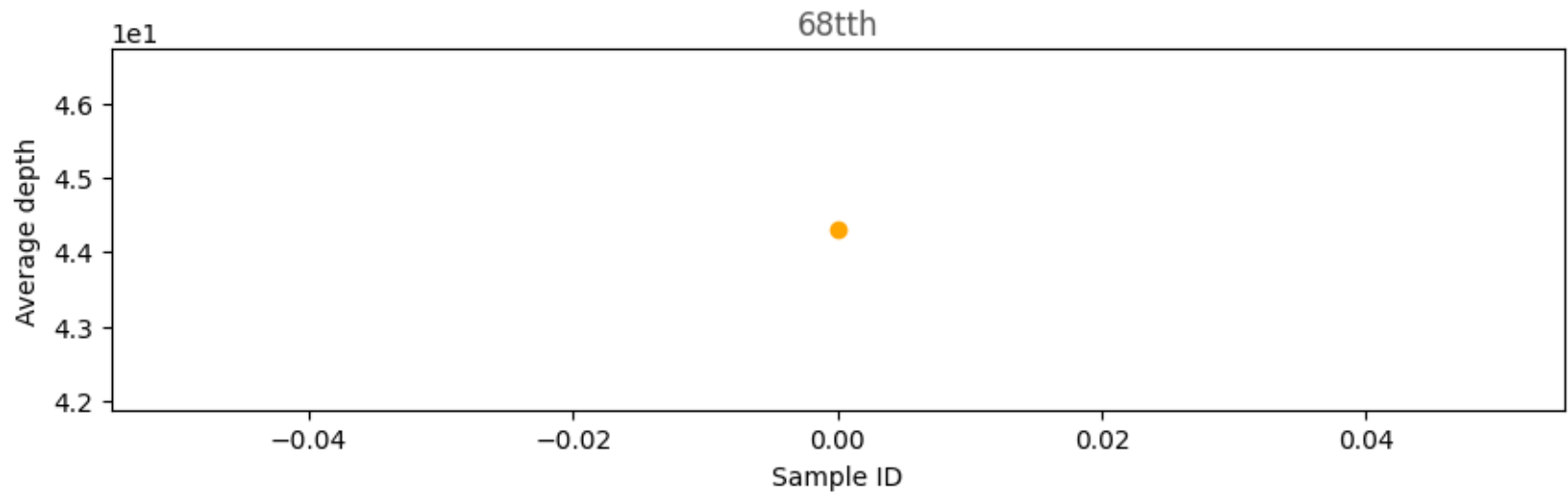
Hets vs non-ref Homs by sample



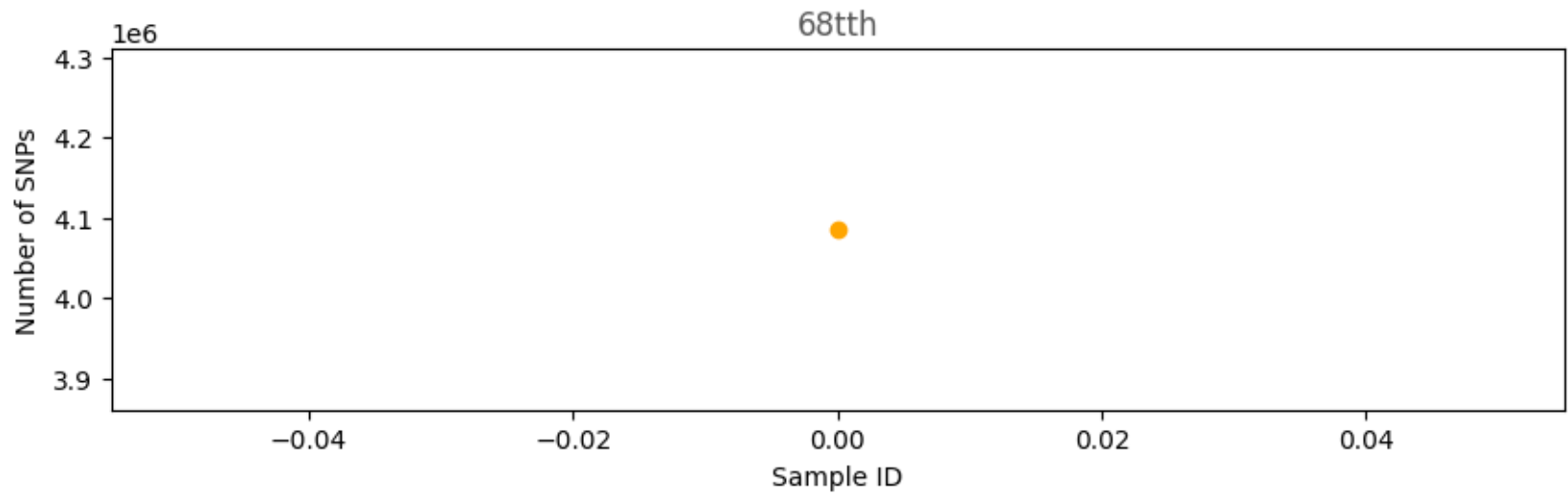
Singletons by sample (hets and homs)



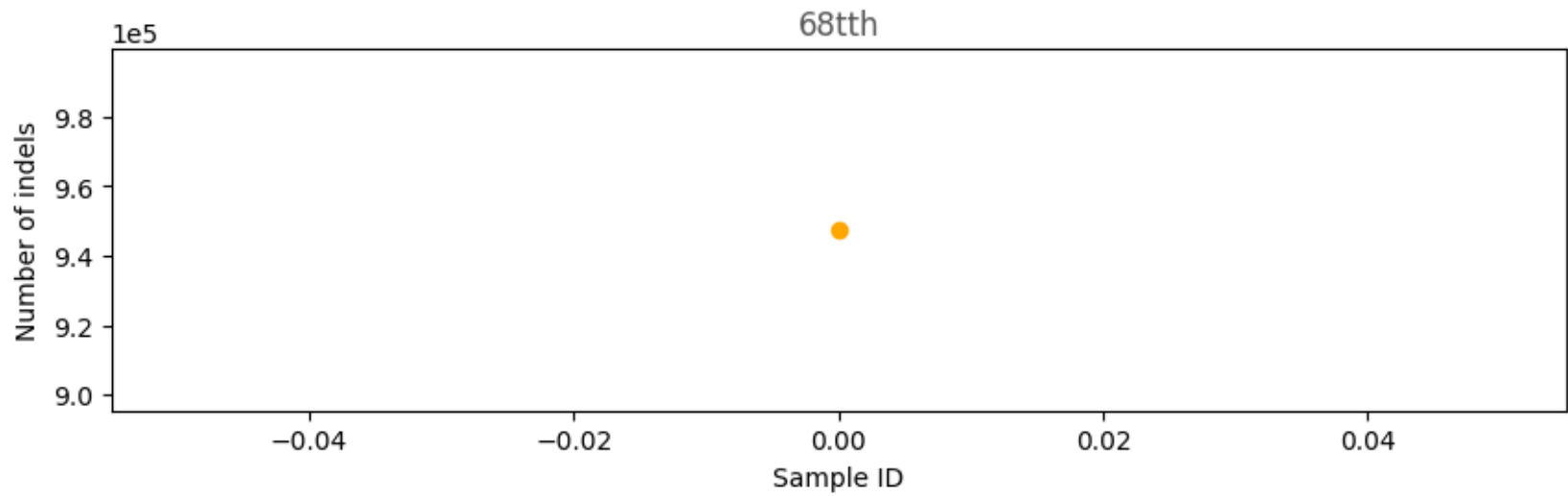
Average depth by sample



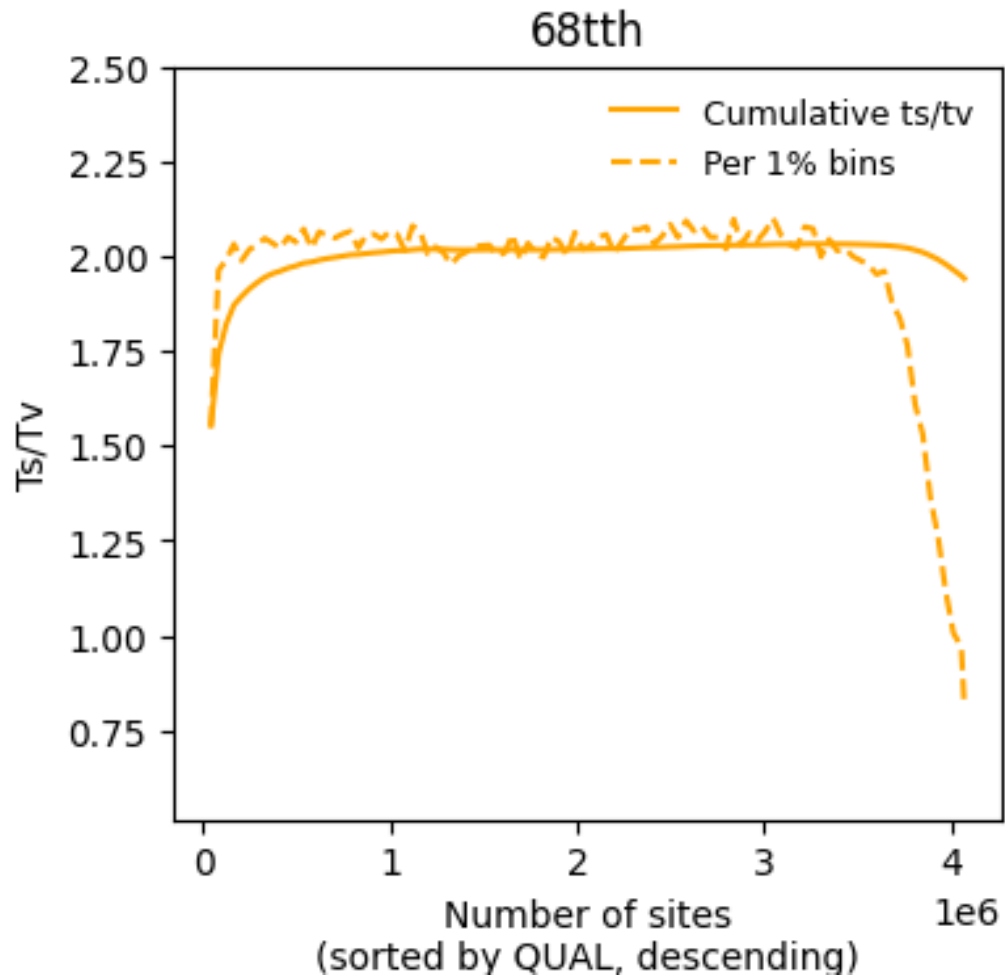
Number of SNPs by sample



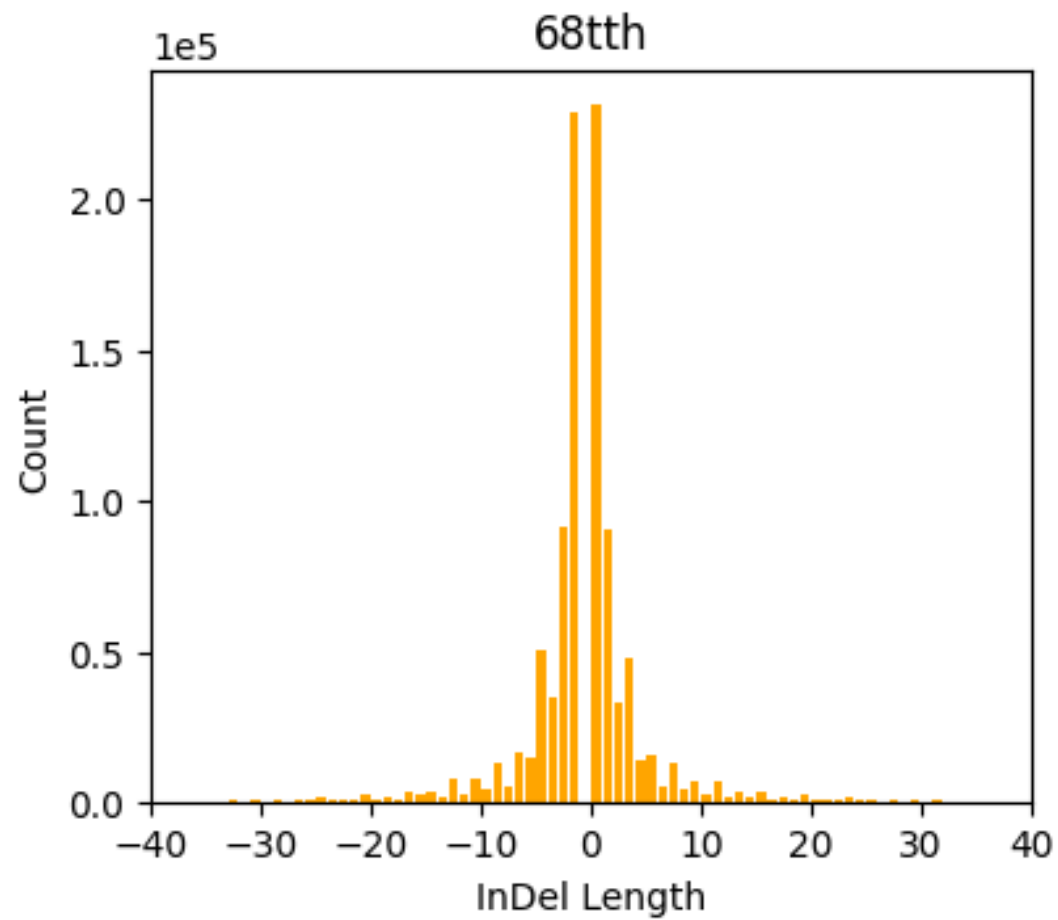
Number of indels by sample



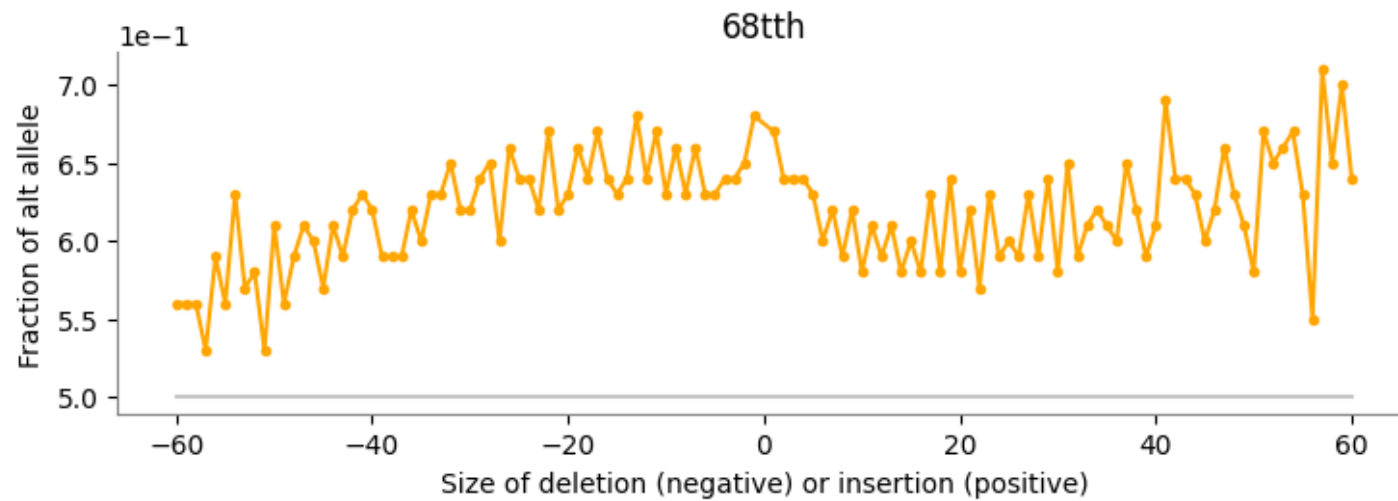
Ts/Tv stratified by QUAL



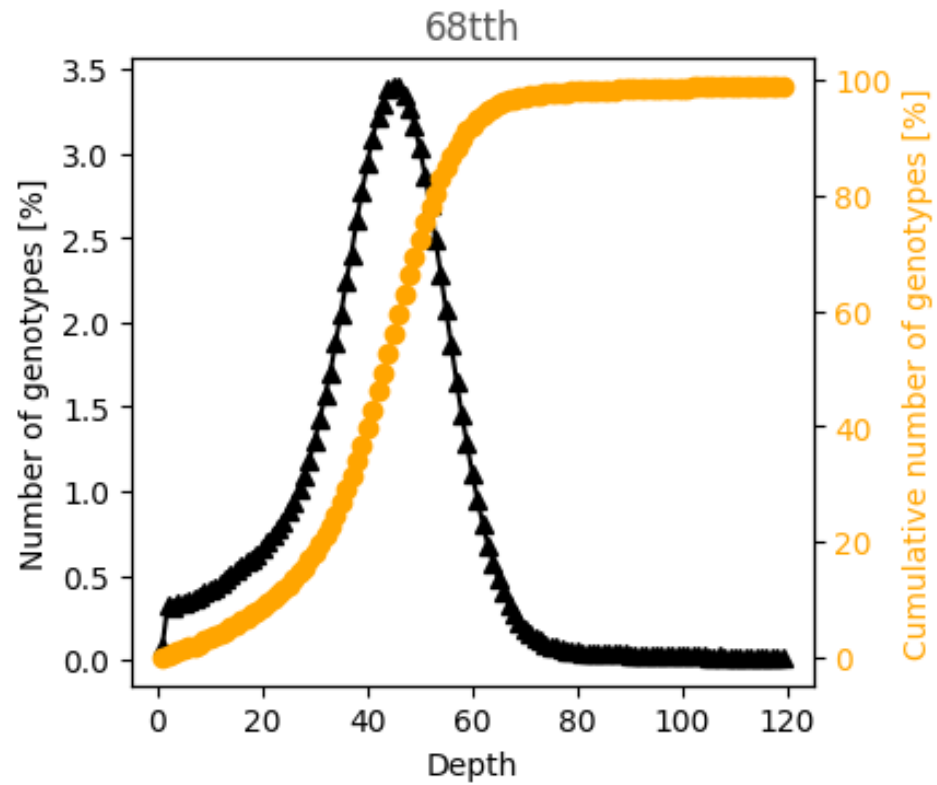
Indel distribution



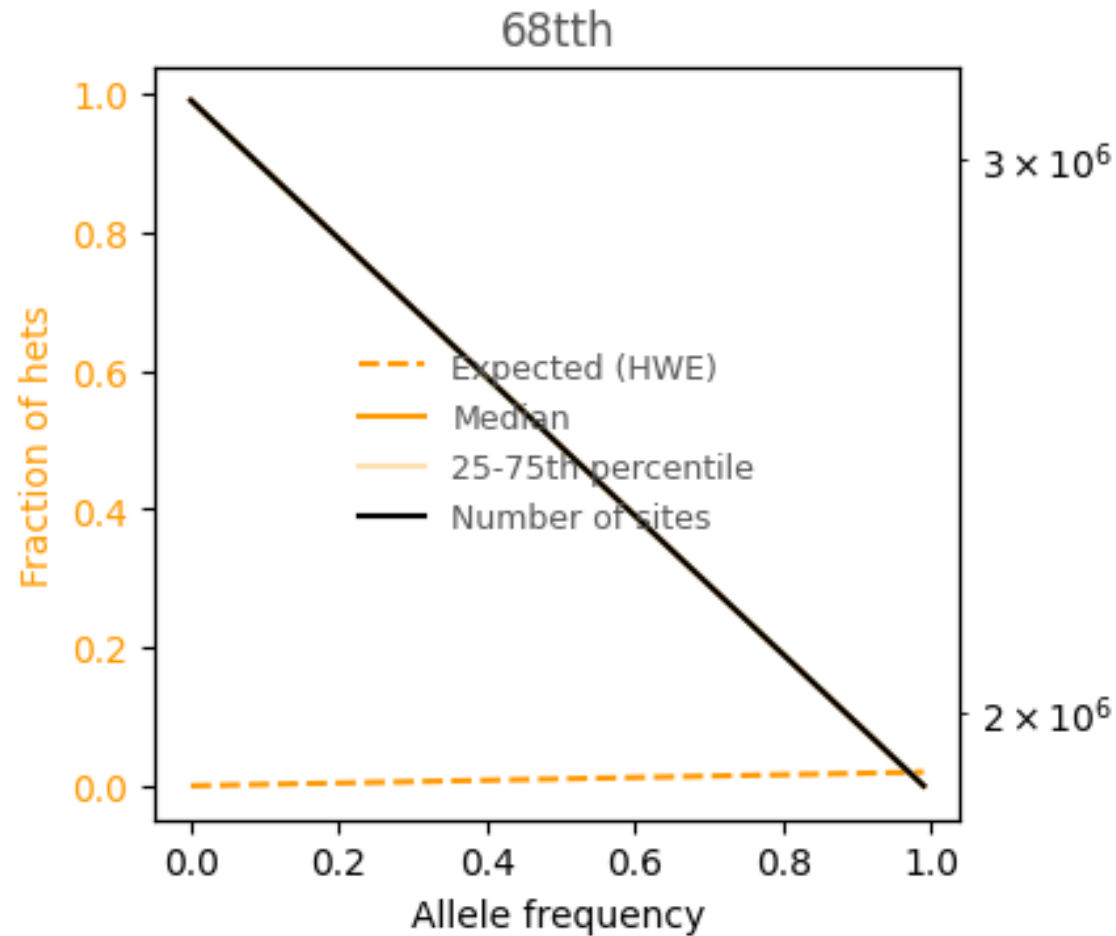
Fraction of alternate indel allele



Depth distribution



Number of HETs by AF



Substitution types

