

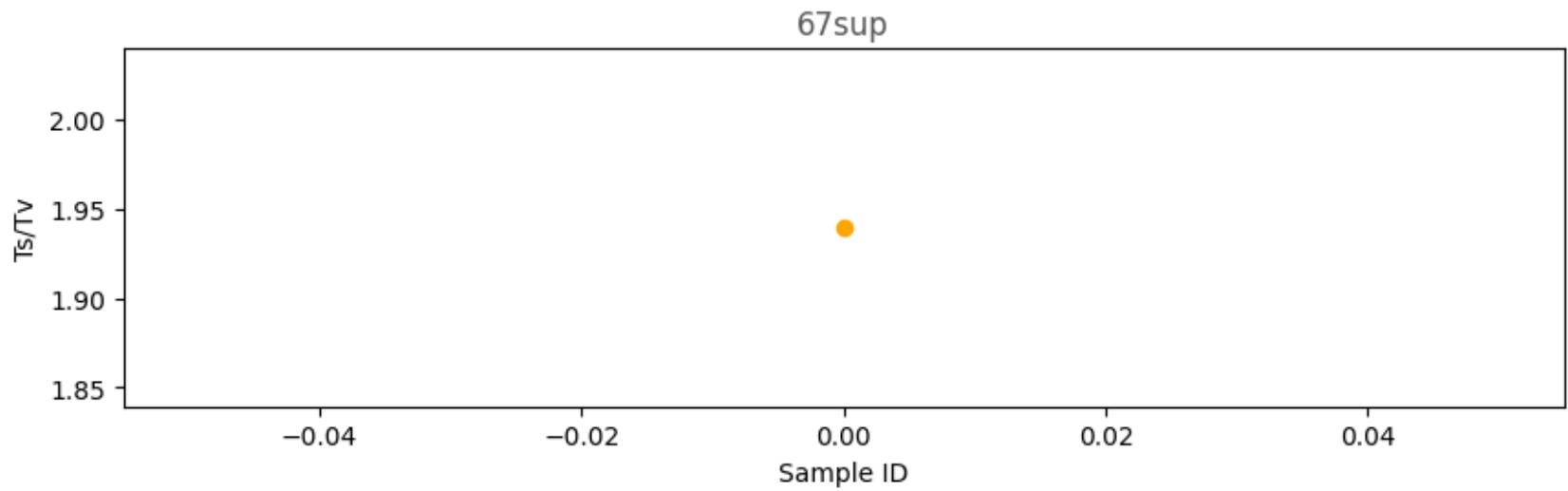
Summary Numbers

| Callset | SNPs | | | indels | | MNPs | others |
|----------------------------------|-----------|-------|-----------|---------|------|------|--------|
| | n | ts/tv | (1st ALT) | n | frm* | | |
| 67sup | 4,079,571 | 1.94 | 1.94 | 949,052 | – | 0 | 0 |
| * frameshift ratio: out/(out+in) | | | | | | | |

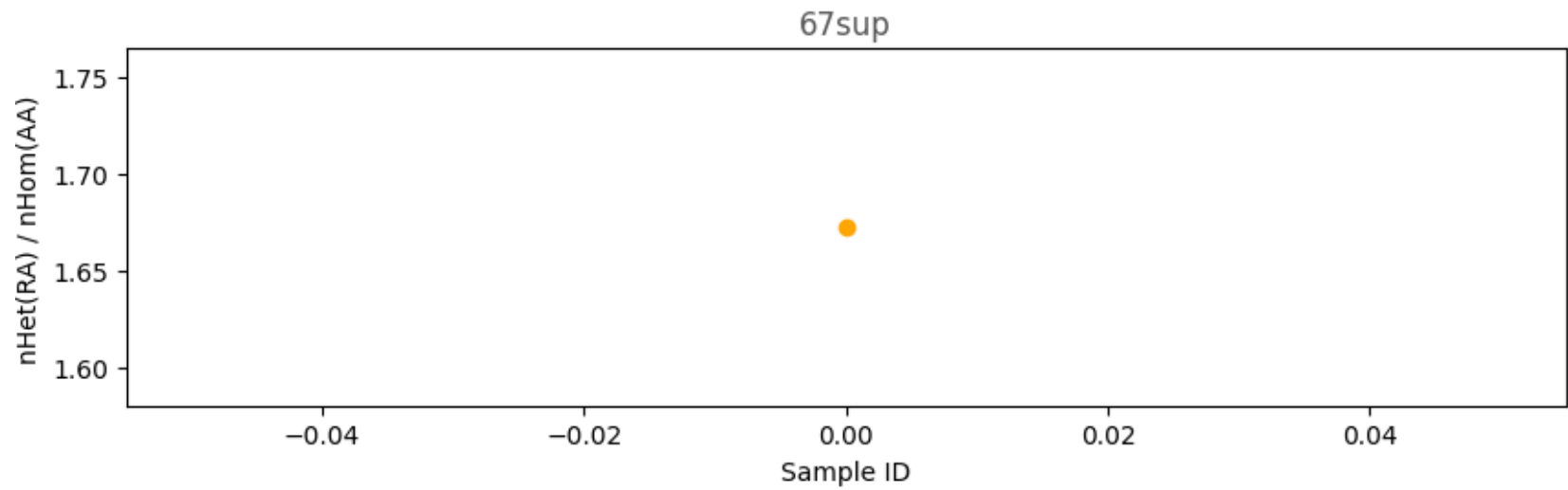
| Callset | singletons (AC=1) | | | multiallelic | |
|---------|-------------------|-------|--------|--------------|-------|
| | SNPs | ts/tv | indels | sites | SNPs |
| 67sup | 62.6% | 1.91 | 67.5% | 98,377 | 2,122 |

- 67sup .. /ngc/projects2/gm/data/archive/2022/variants/snv/67supoinf-103892393502-Normal_Blood_noinfo-WGS_v1_IlluminaDNAPCRFree_X-220727_A01176_BHNV7KDSX3-RHGM_LABKA_WGS-WGS04718_snv_germline_raw.haplotype_caller.vcf.gz

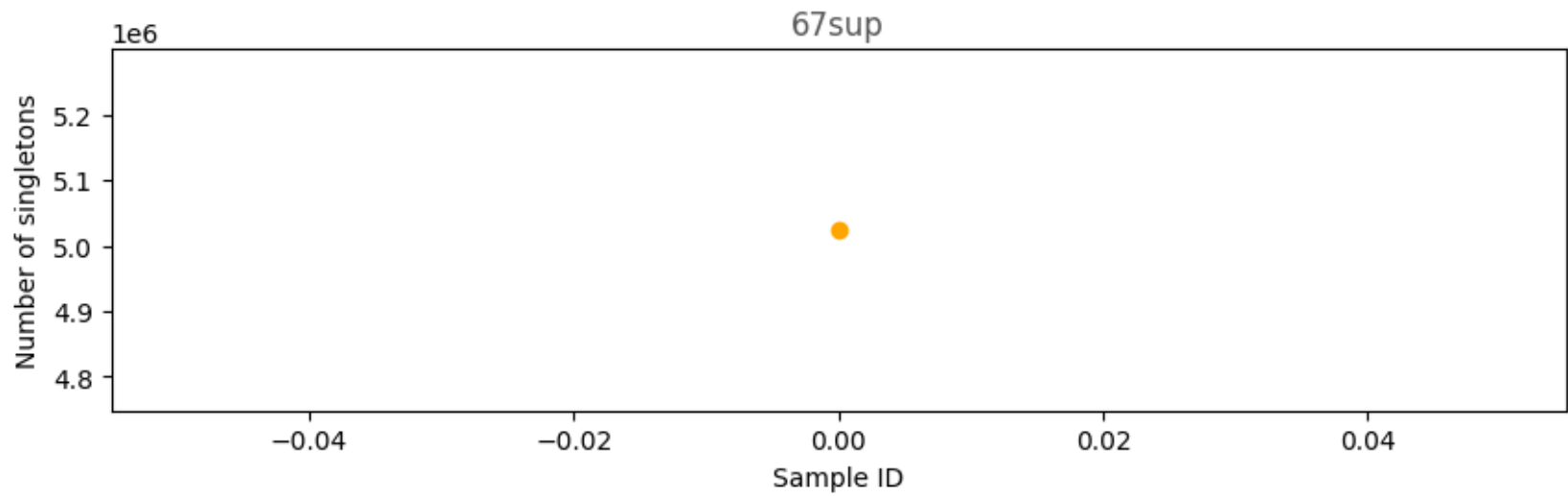
Ts/Tv by sample



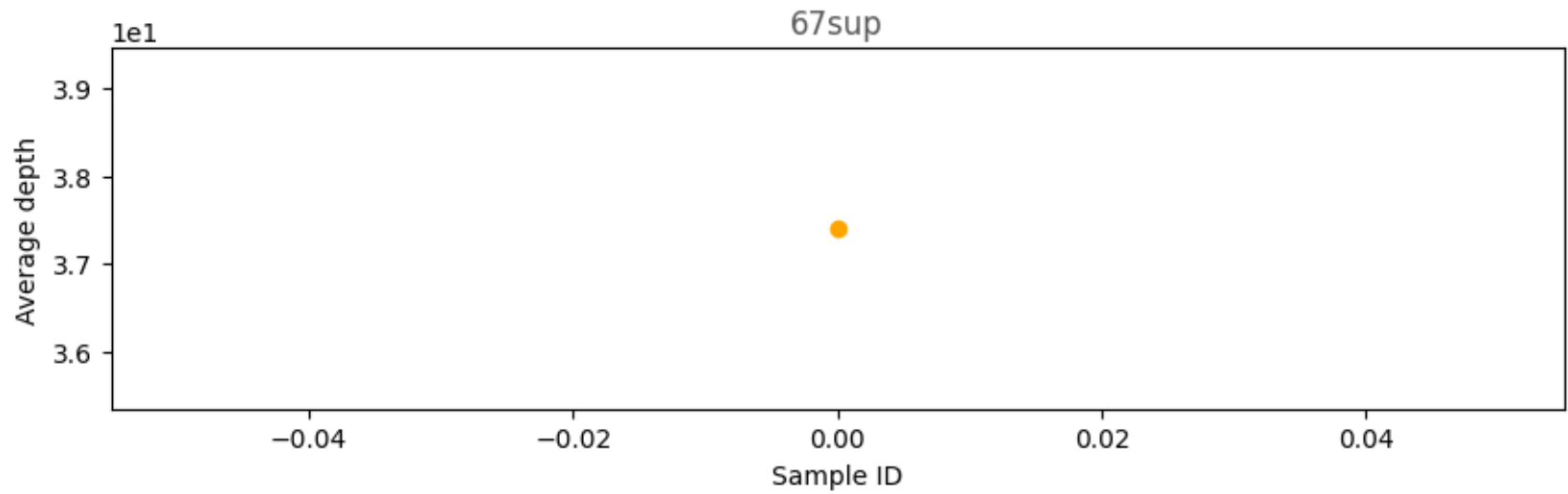
Hets vs non-ref Homs by sample



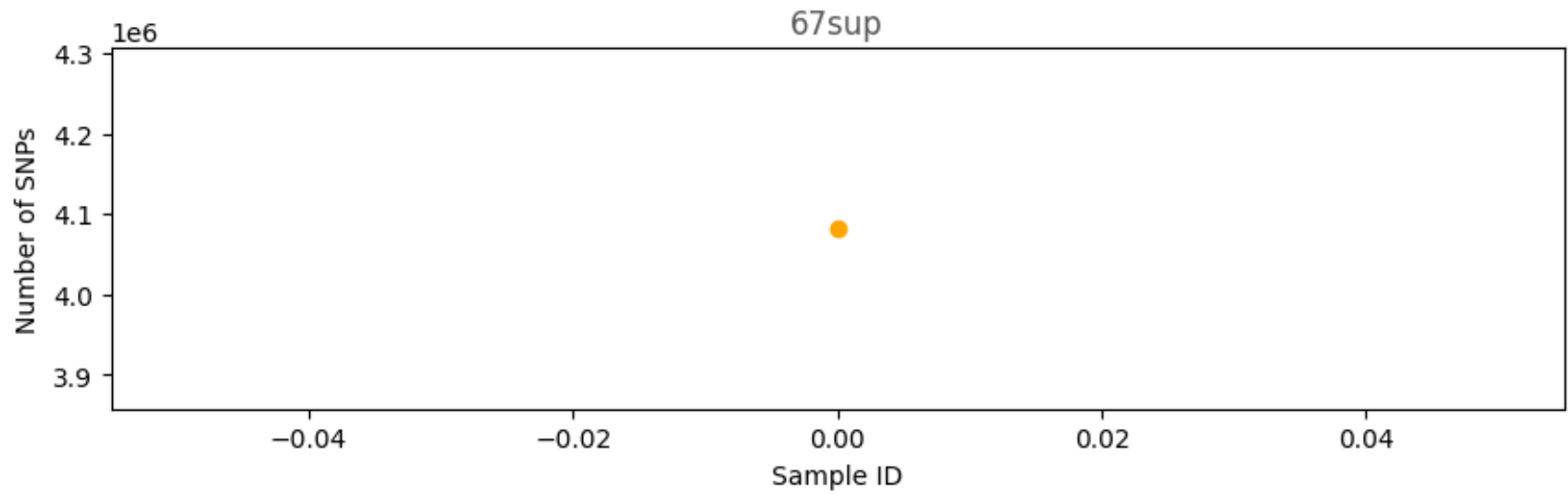
Singletons by sample (hets and homs)



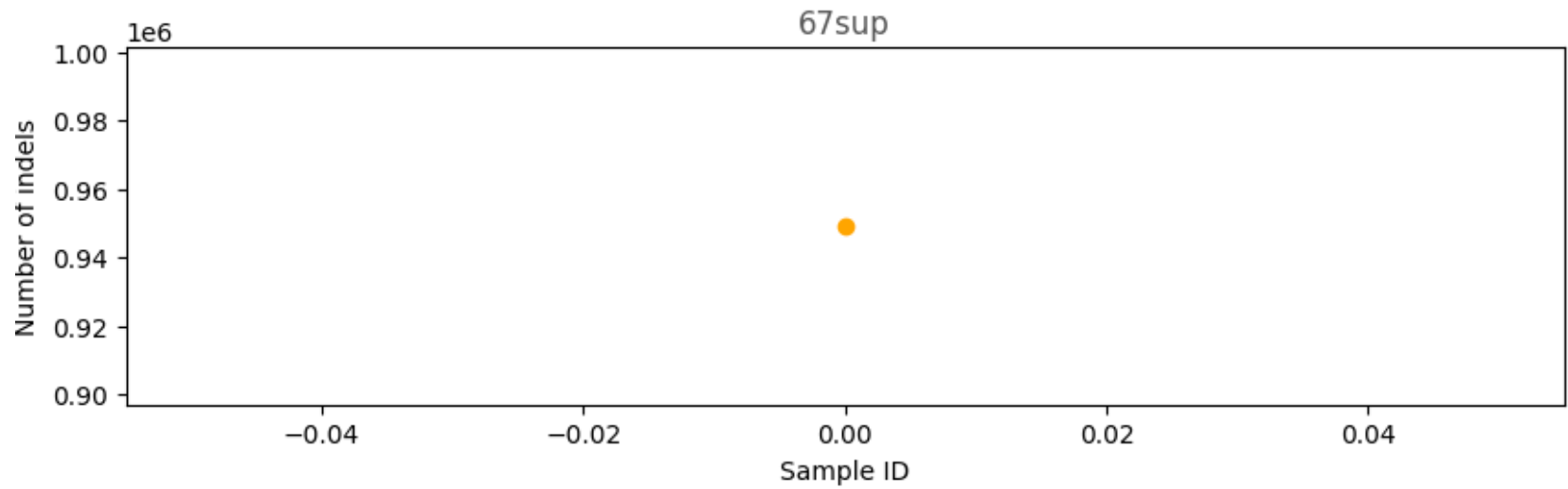
Average depth by sample



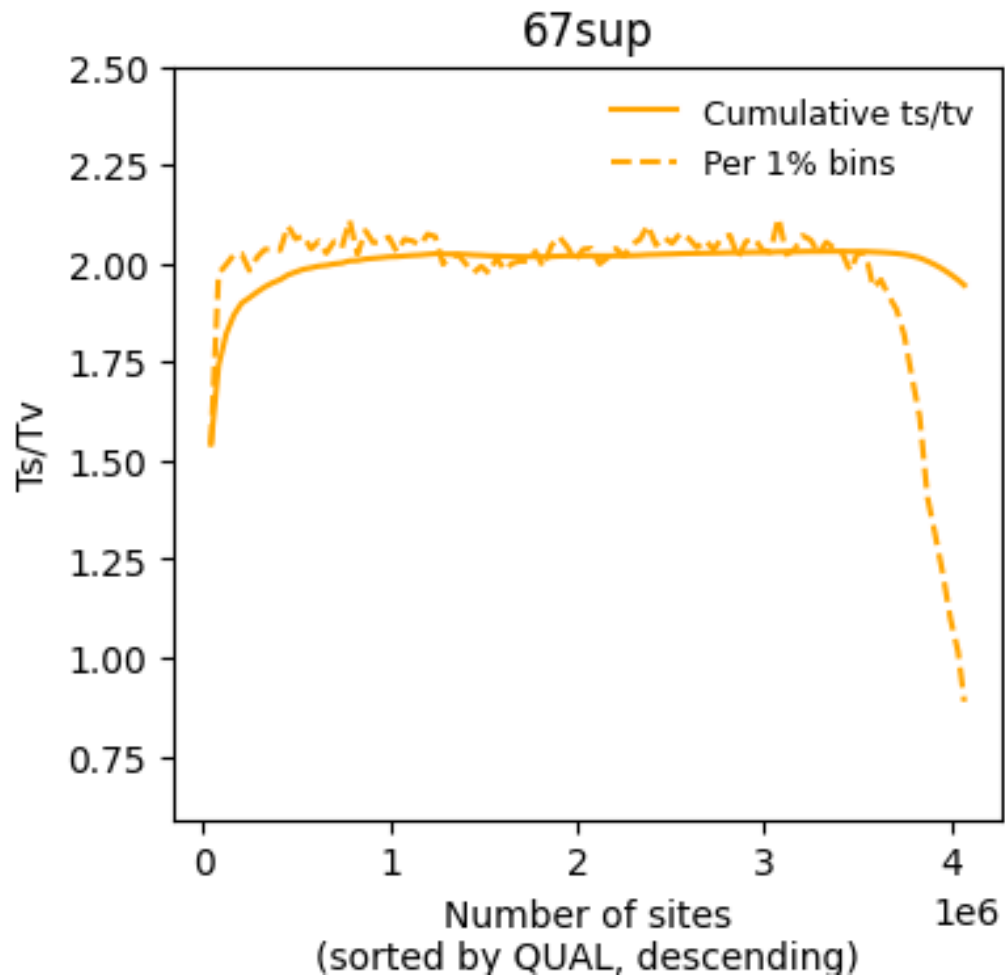
Number of SNPs by sample



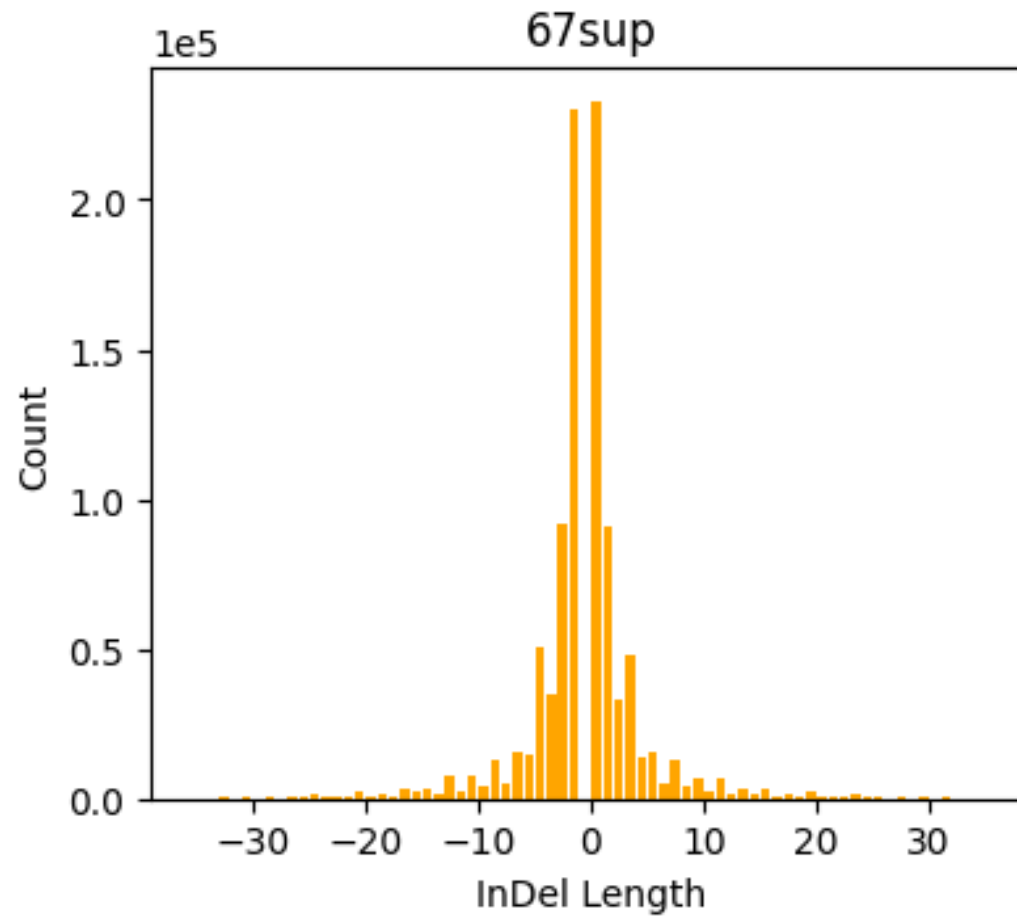
Number of indels by sample



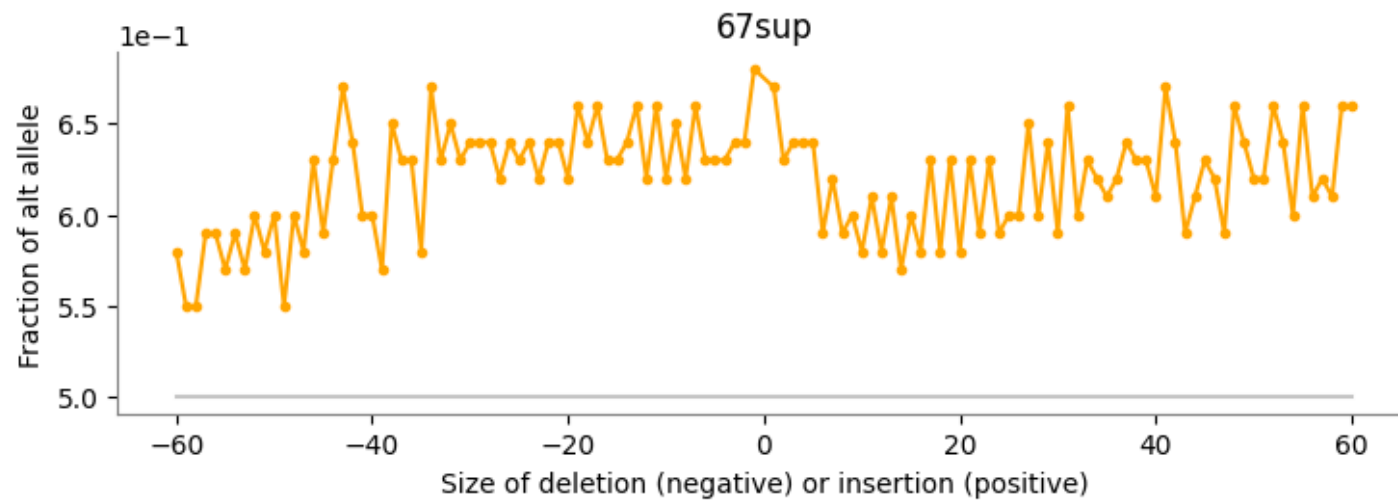
Ts/Tv stratified by QUAL



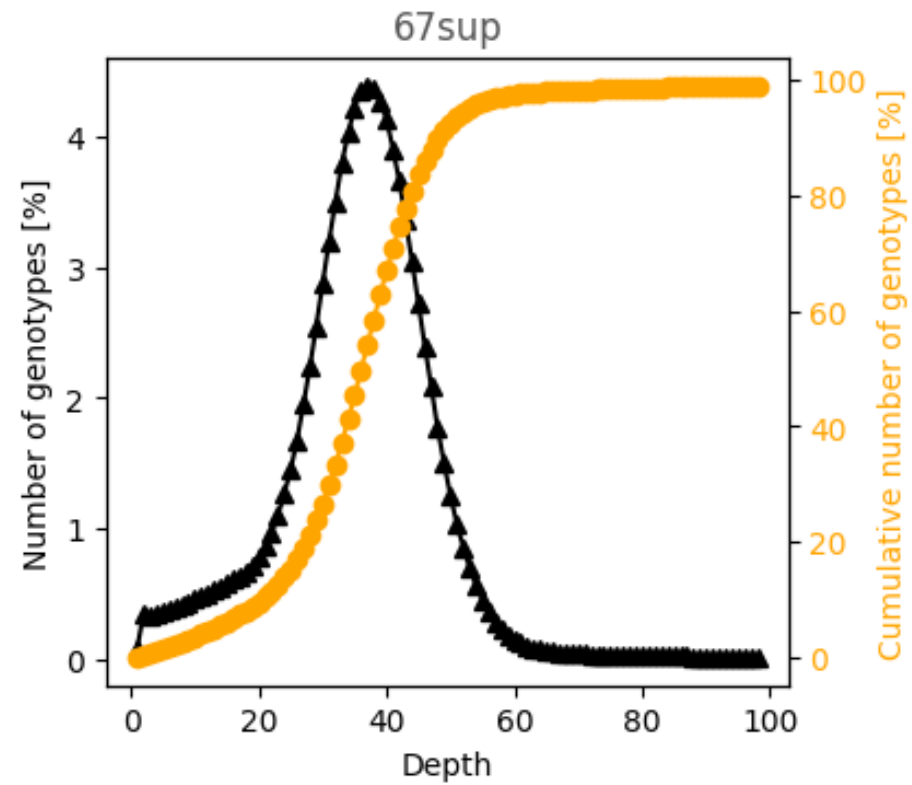
Indel distribution



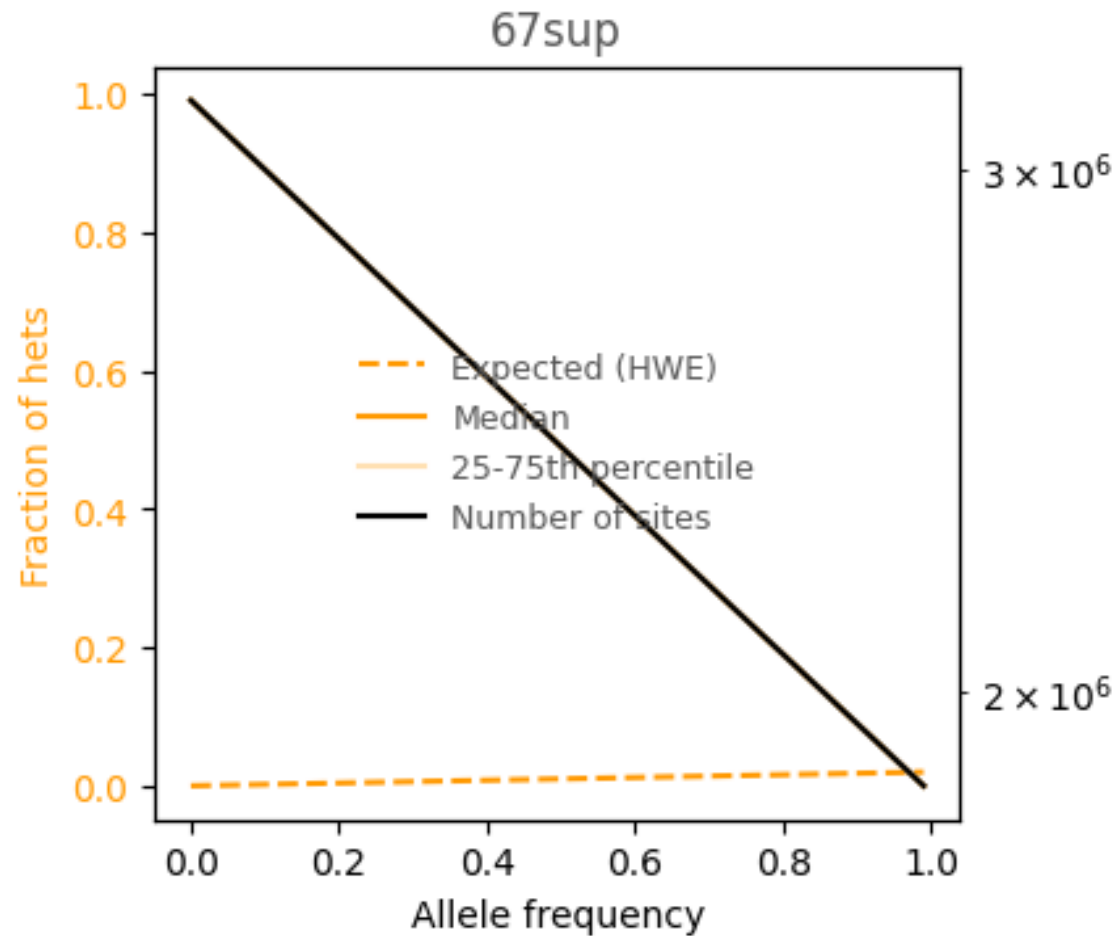
Fraction of alternate indel allele



Depth distribution



Number of HETs by AF



Substitution types

