

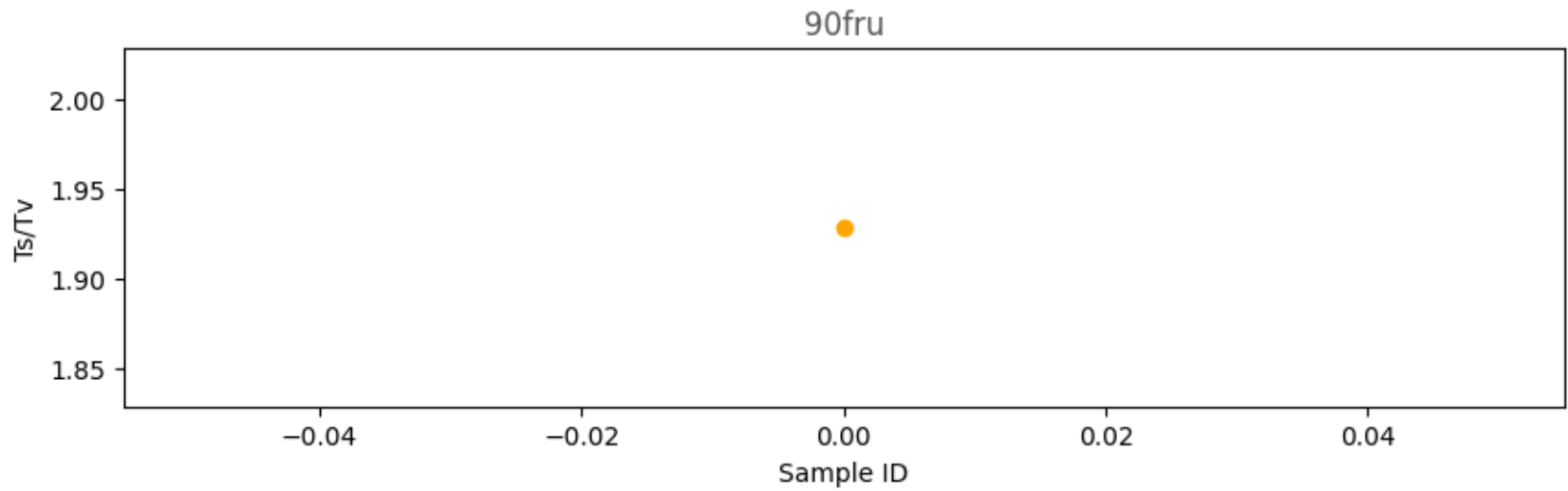
Summary Numbers

| Callset | SNPs | | | indels | | MNPs | others |
|----------------------------------|-----------|-------|-----------|---------|------|------|--------|
| | n | ts/tv | (1st ALT) | n | frm* | | |
| 90fru | 4,062,329 | 1.93 | 1.93 | 936,044 | – | 0 | 0 |
| * frameshift ratio: out/(out+in) | | | | | | | |

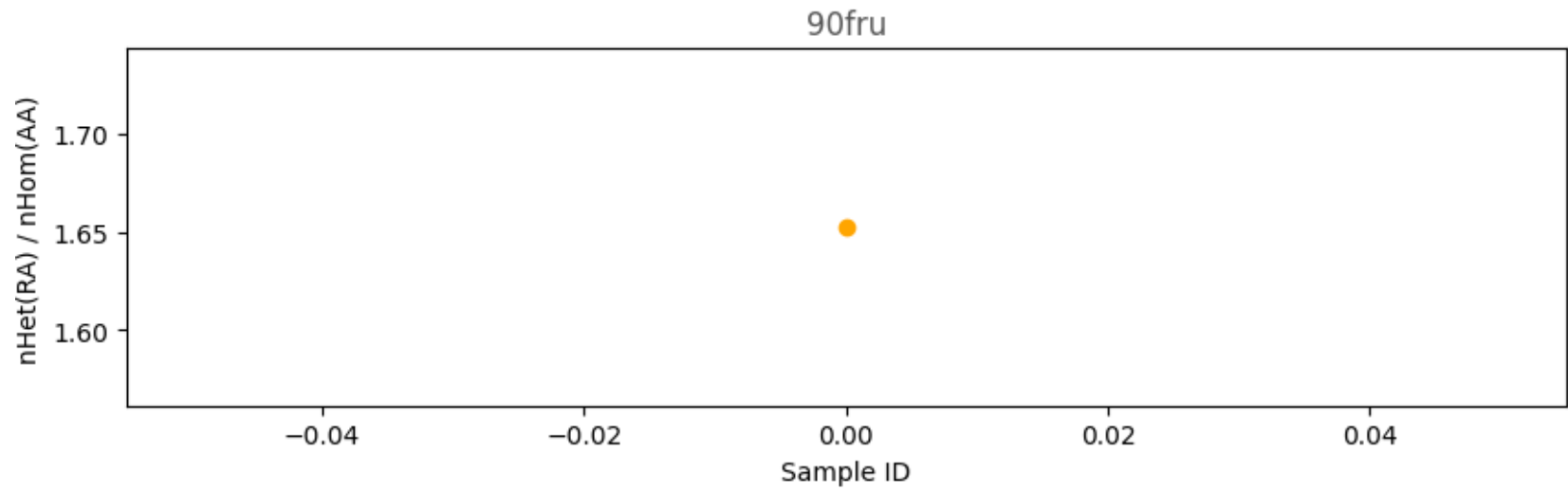
| Callset | singletons (AC=1) | | | multiallelic | |
|---------|-------------------|-------|--------|--------------|-------|
| | SNPs | ts/tv | indels | sites | SNPs |
| 90fru | 62.3% | 1.90 | 66.6% | 94,015 | 2,097 |

- 90fru .. /ngc/projects2/gm/data/archive/2022/variants/snv/90fruceam-103900084174-Normal_B
 lood_noinfo-WGS_v1_IlluminaDNAPCRFree_RHGM01081-220817_A00559_AHNKFVDSX3-EXT_LAB
 KA_NGCWGS-NGCWGS04806_snv_germline_raw.haplotype_caller.vcf.gz

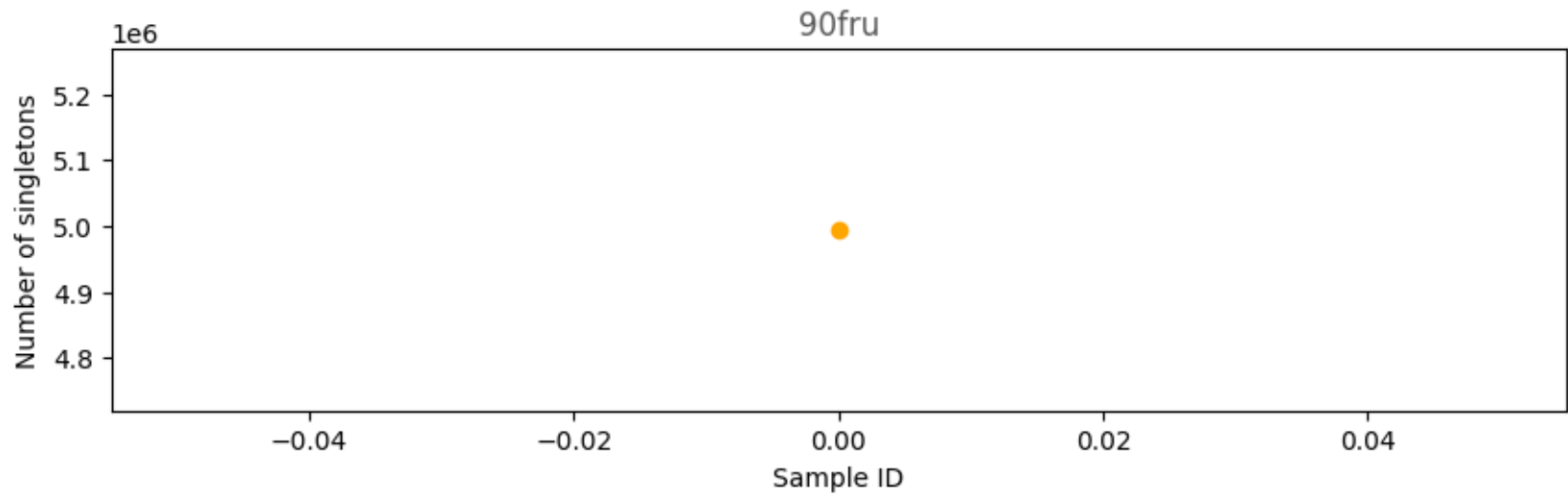
Ts/Tv by sample



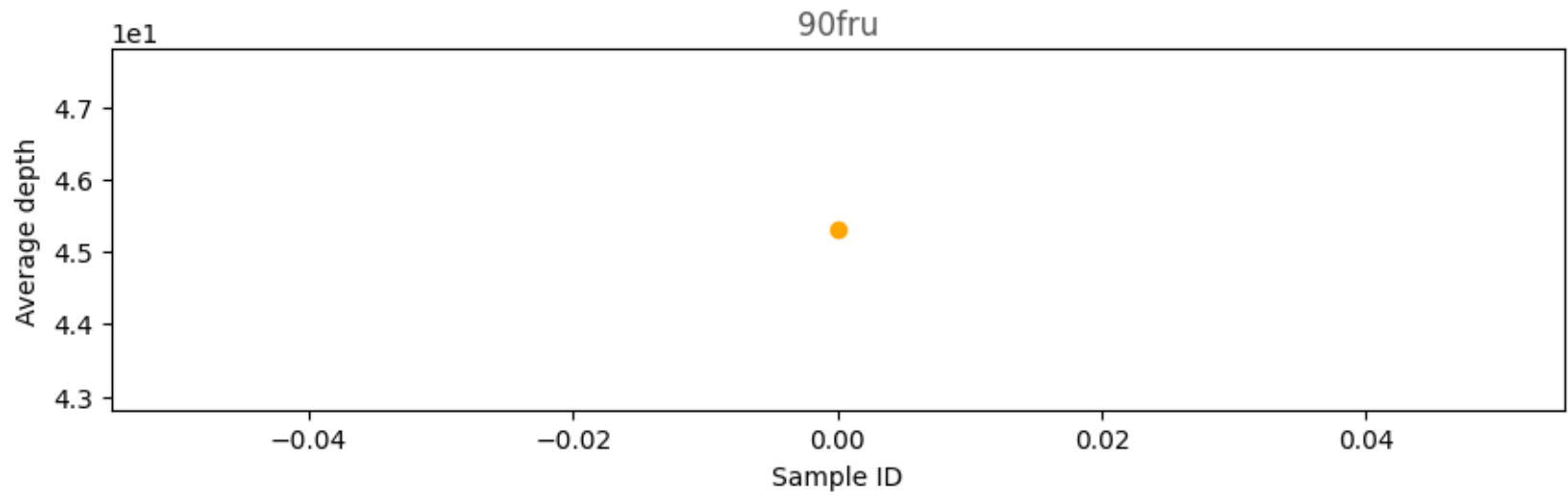
Hets vs non-ref Homs by sample



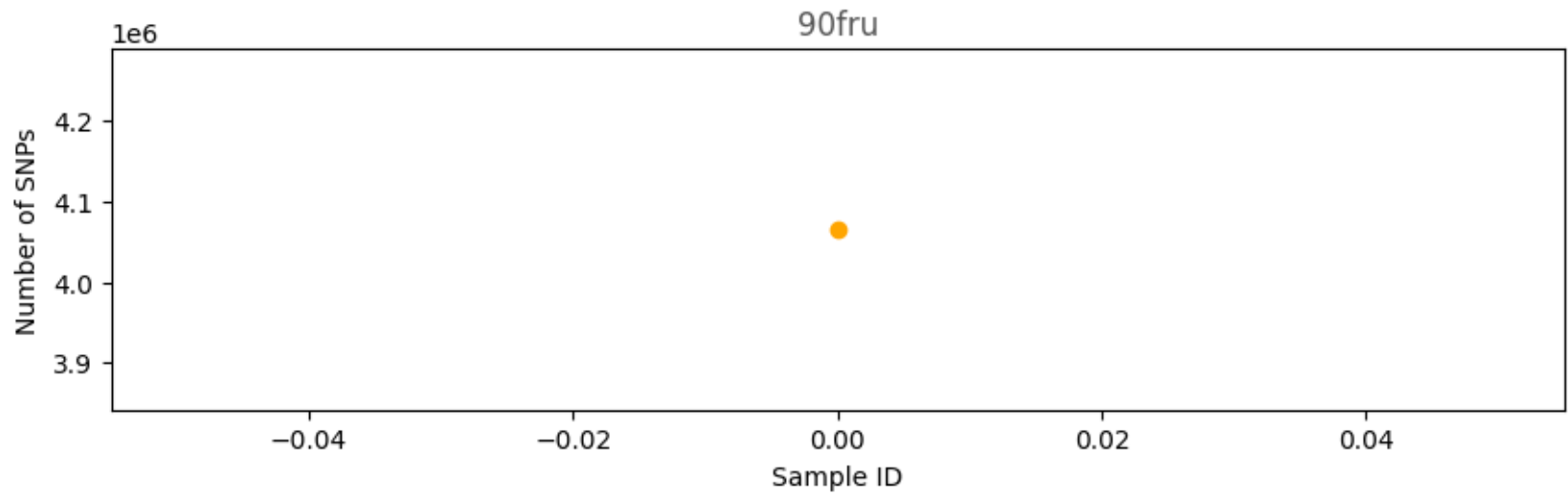
Singletons by sample (hets and homs)



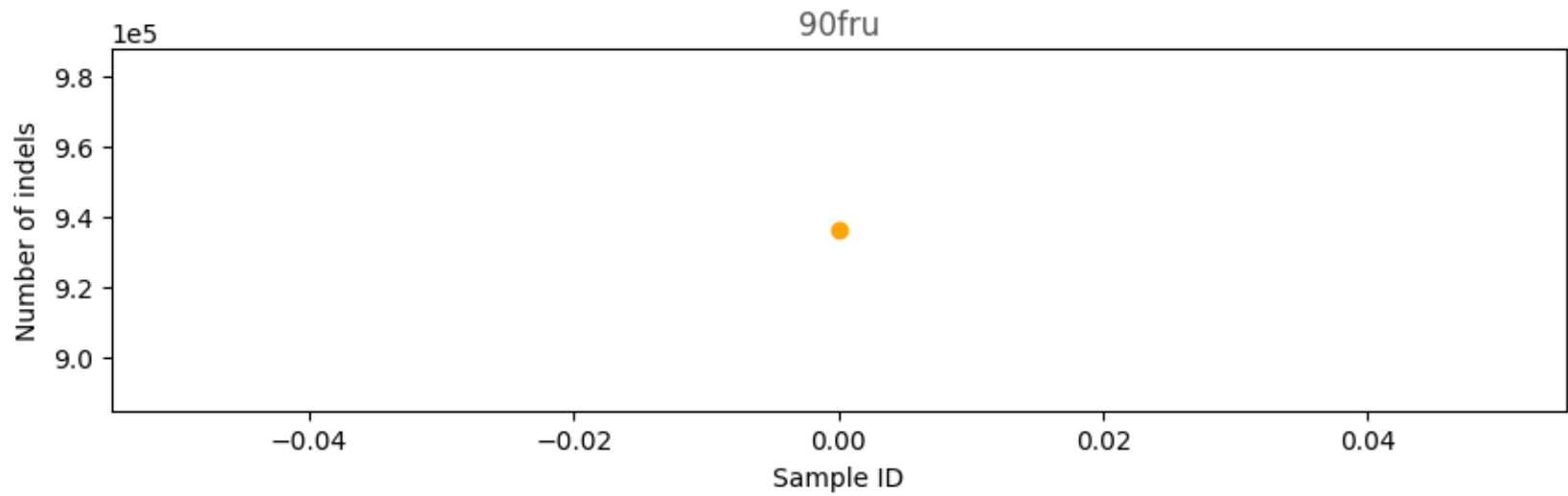
Average depth by sample



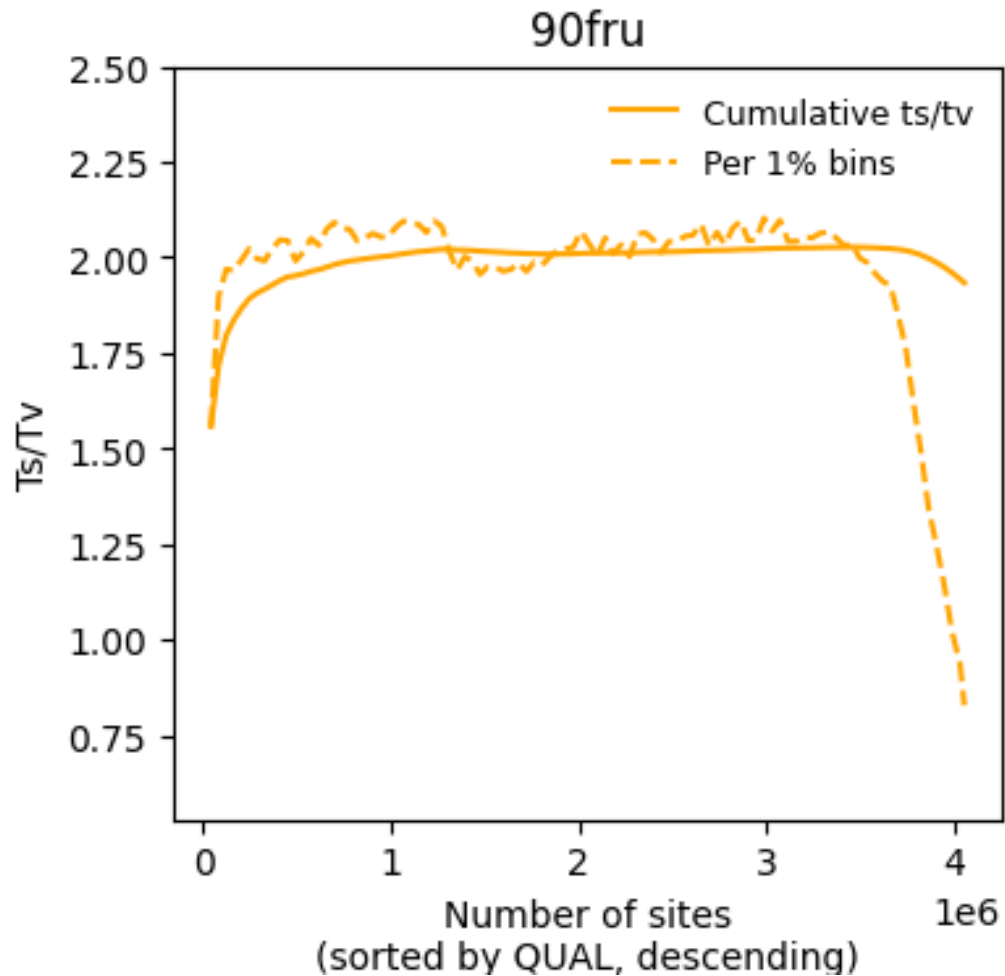
Number of SNPs by sample



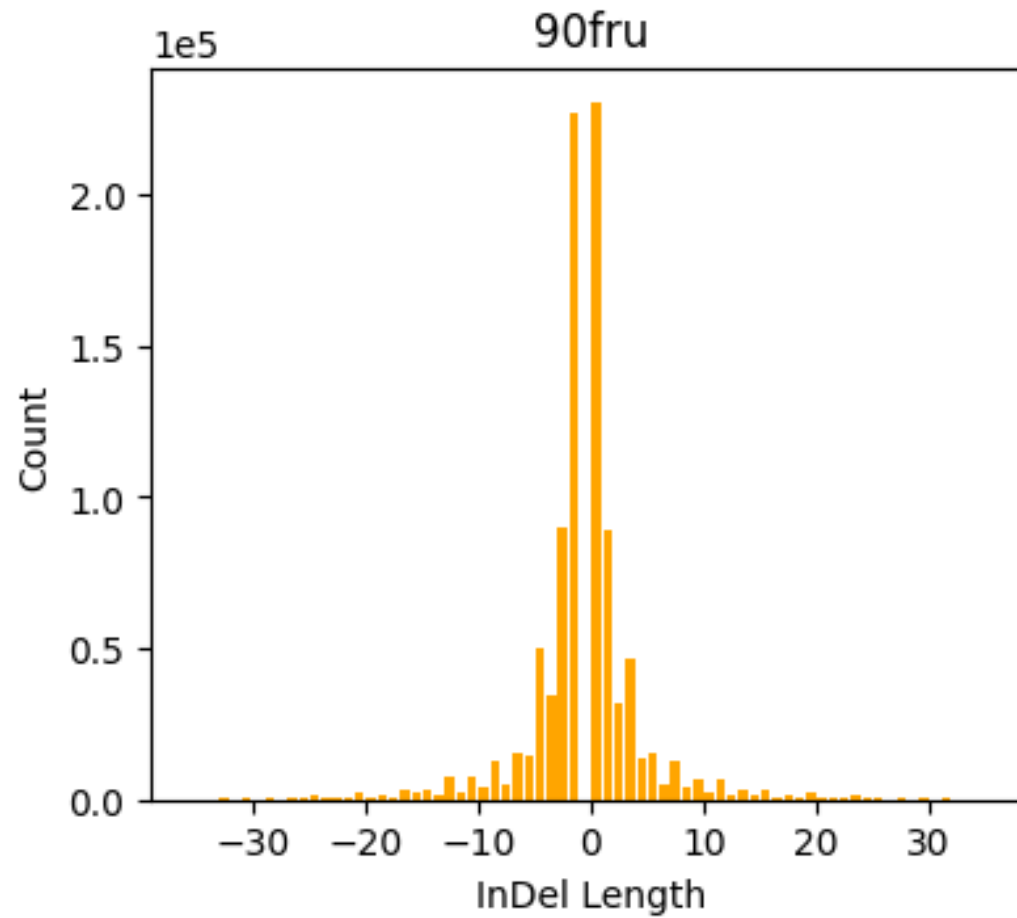
Number of indels by sample



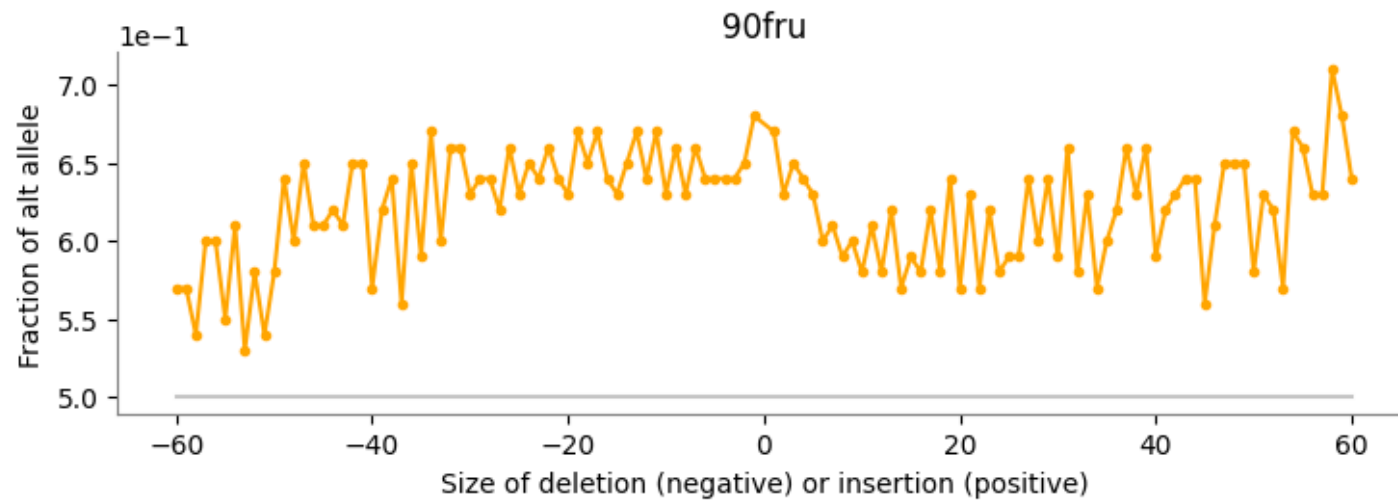
Ts/Tv stratified by QUAL



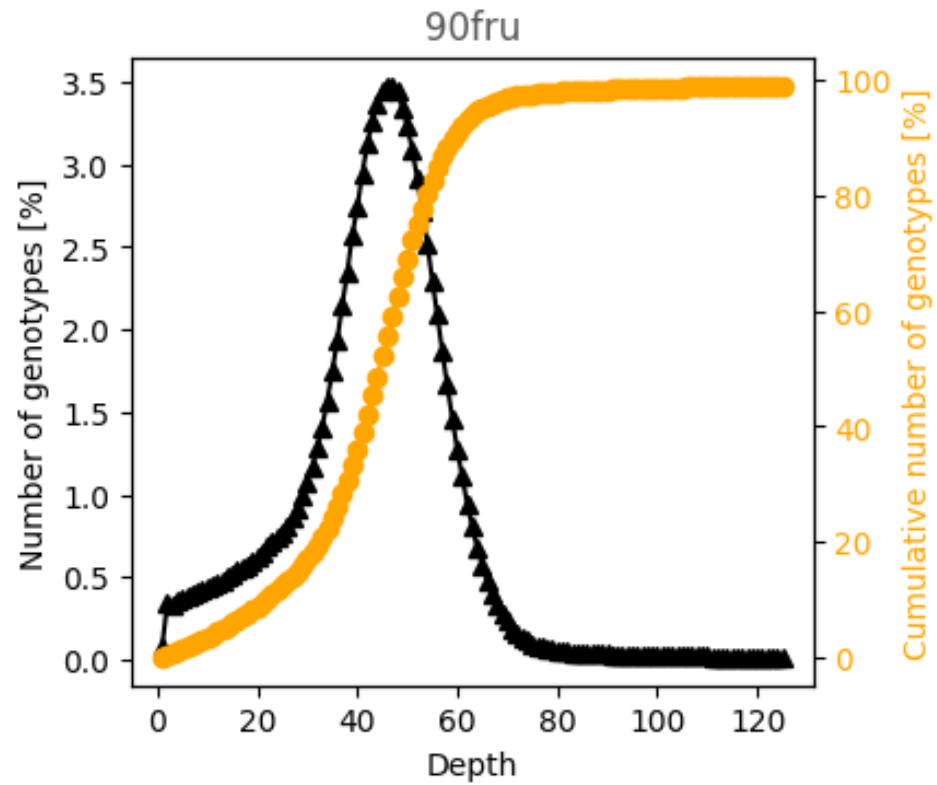
Indel distribution



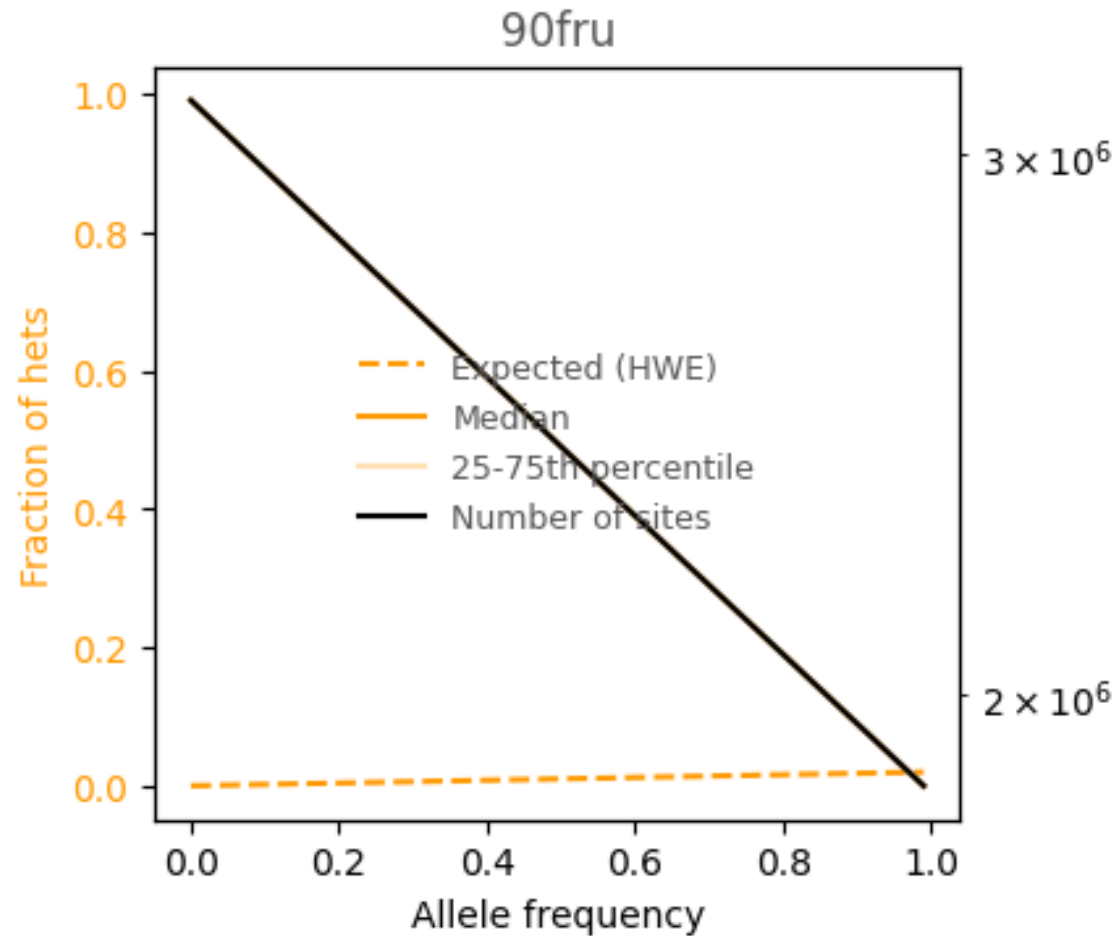
Fraction of alternate indel allele



Depth distribution



Number of HETs by AF



Substitution types

