

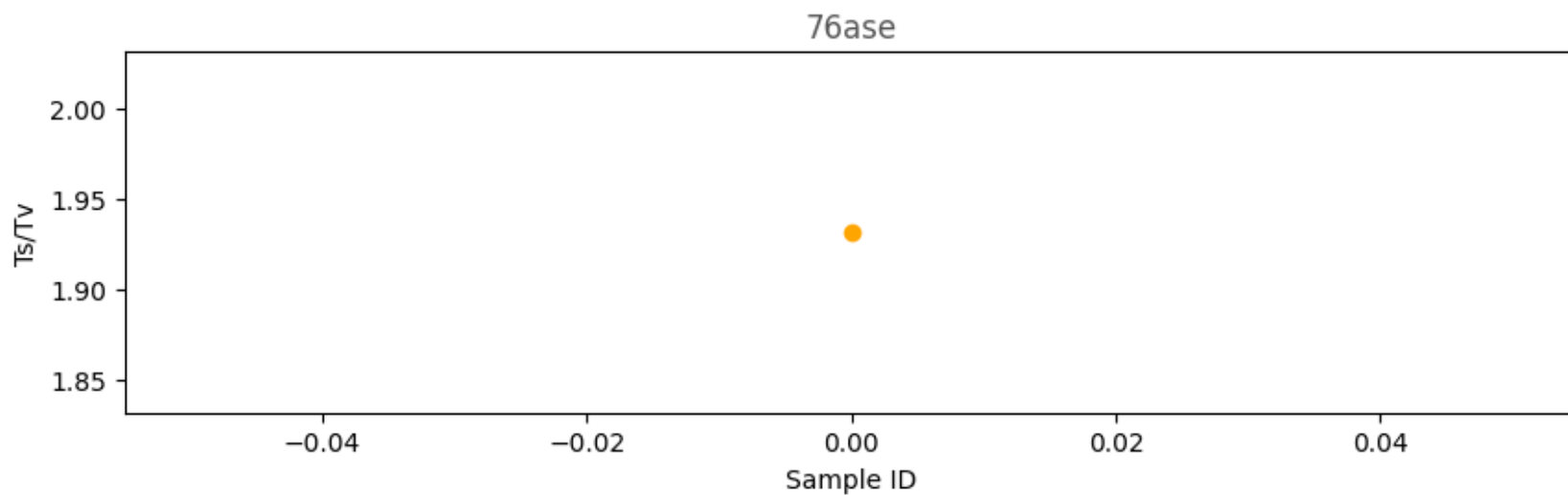
Summary Numbers

| Callset | SNPs | | | indels | | MNPs | others |
|----------------------------------|-----------|-------|-----------|---------|------|------|--------|
| | n | ts/tv | (1st ALT) | n | frm* | | |
| 76ase | 4,111,941 | 1.93 | 1.94 | 962,609 | – | 0 | 0 |
| * frameshift ratio: out/(out+in) | | | | | | | |

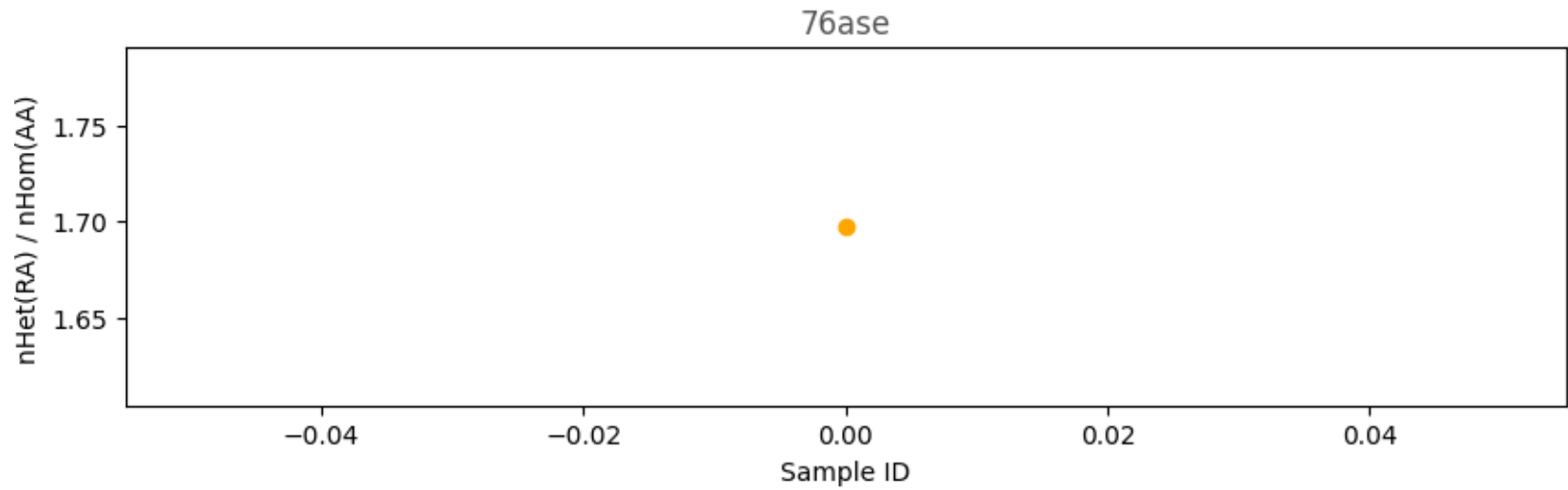
| Callset | singletons (AC=1) | | | multiallelic | |
|---------|-------------------|-------|--------|--------------|-------|
| | SNPs | ts/tv | indels | sites | SNPs |
| 76ase | 62.9% | 1.90 | 68.3% | 104,669 | 2,192 |

- 76ase .. /ngc/projects2/gm/data/archive/2022/variants/snv/76aseletf-103907814429-Normal_B
 lood_noinfo-WGS_v1_IlluminaDNAPCRFree_RHGM01277-220907_A01411_AHYN3VDSX3-EXT_LAB
 KA_NGCWGS-NGCWGS05053_22RKG011851x01_snv_germline_raw.haplotype_caller.vcf.gz

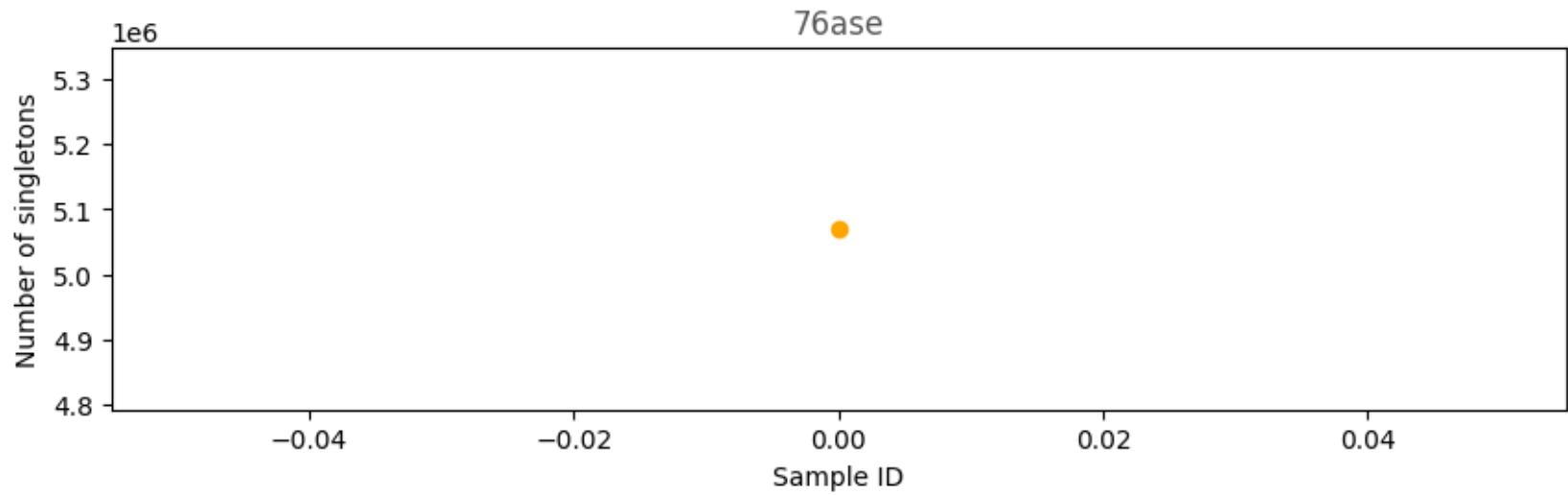
Ts/Tv by sample



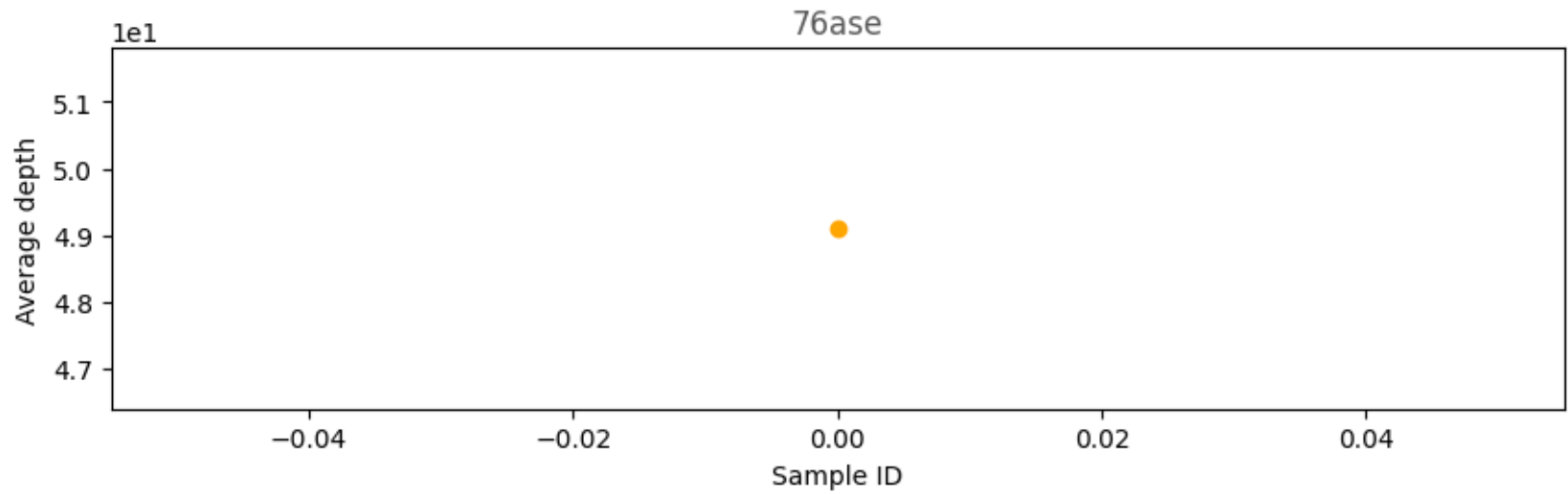
Hets vs non-ref Homs by sample



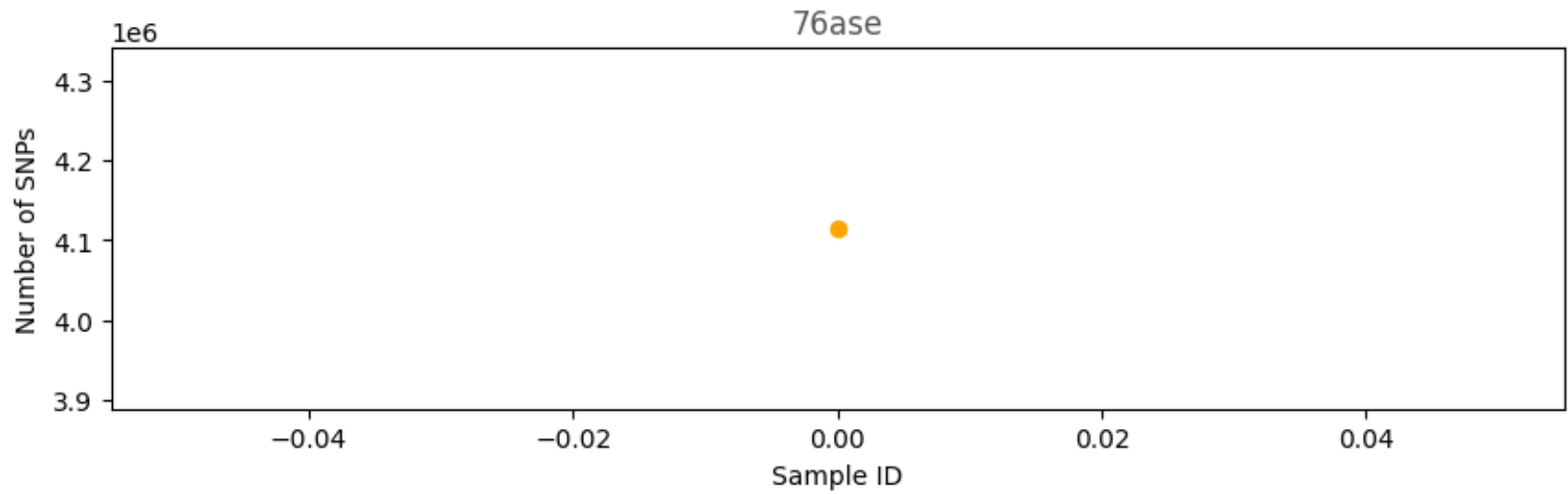
Singletons by sample (hets and homs)



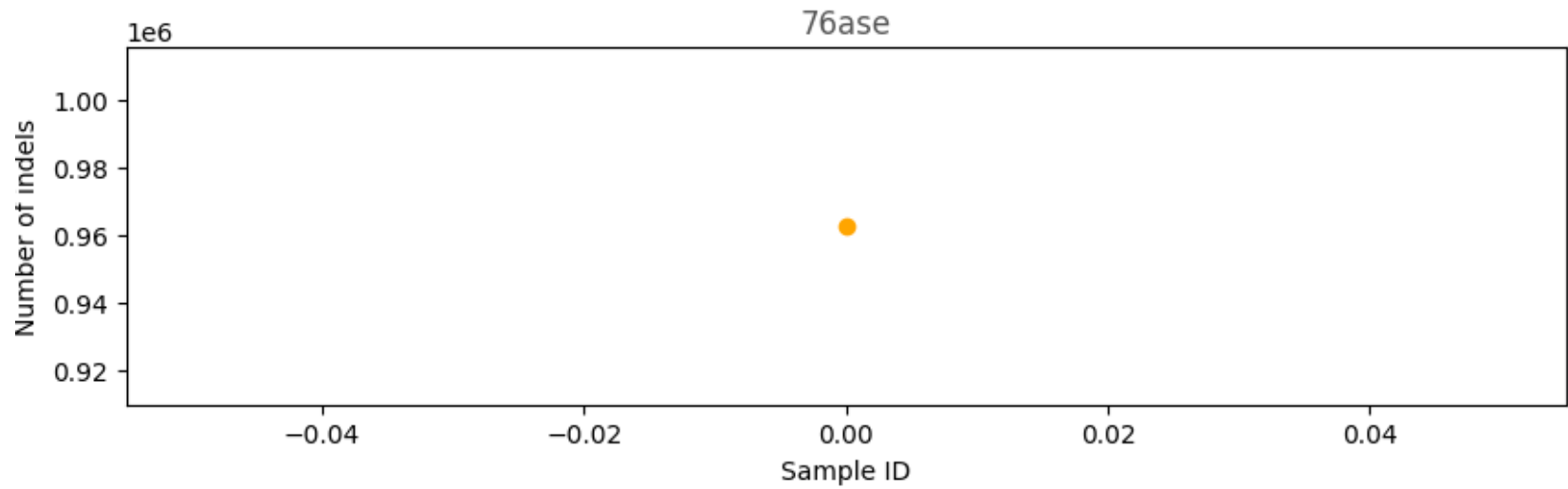
Average depth by sample



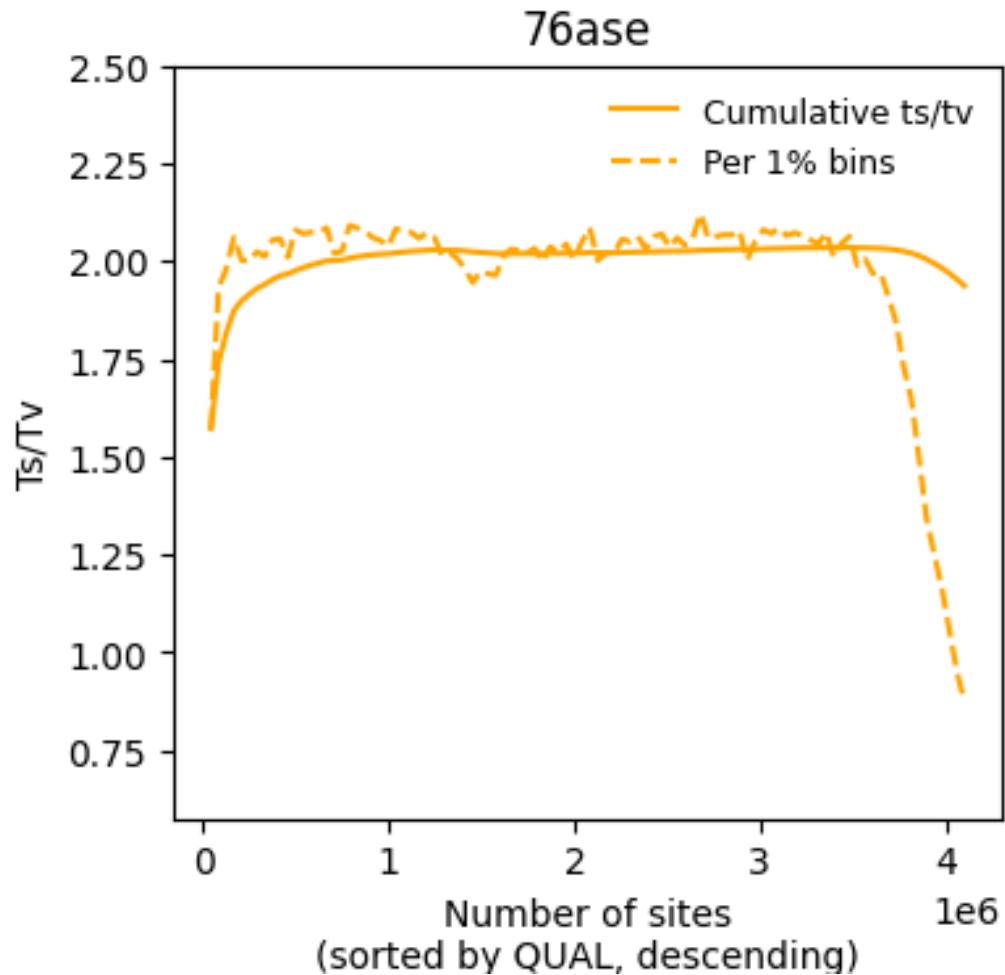
Number of SNPs by sample



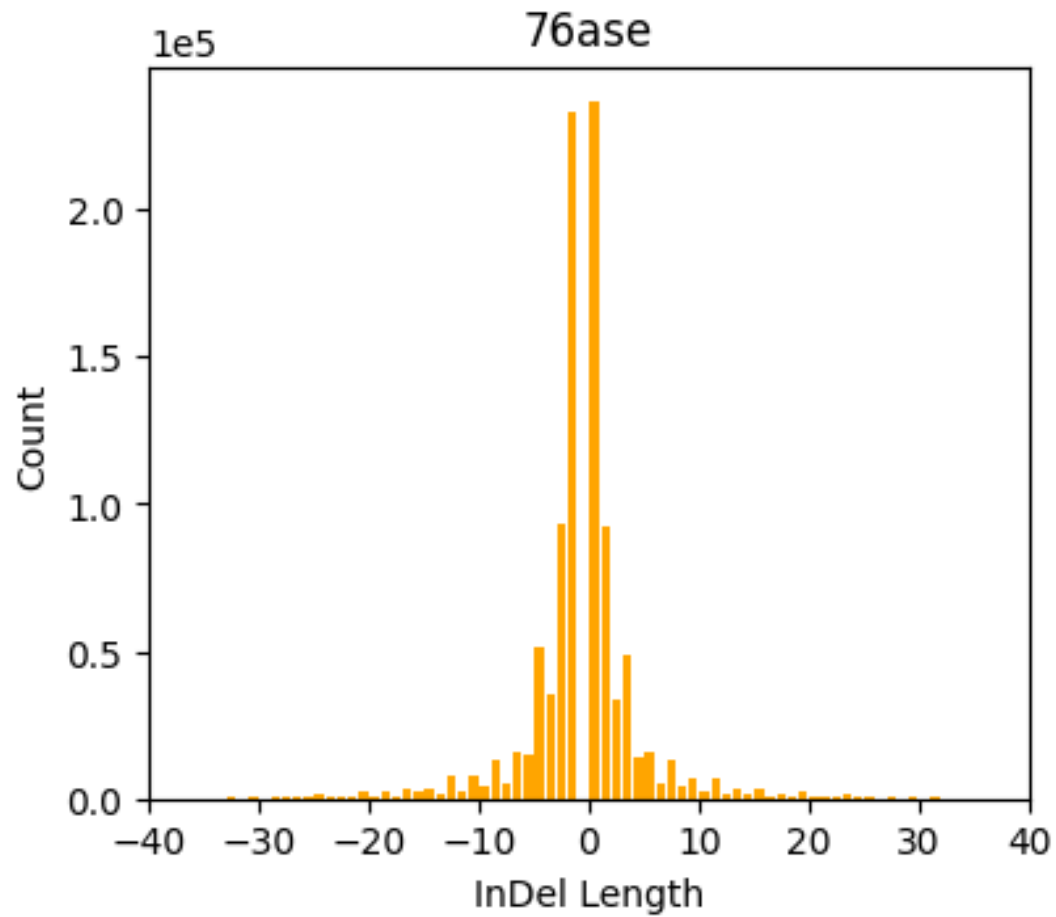
Number of indels by sample



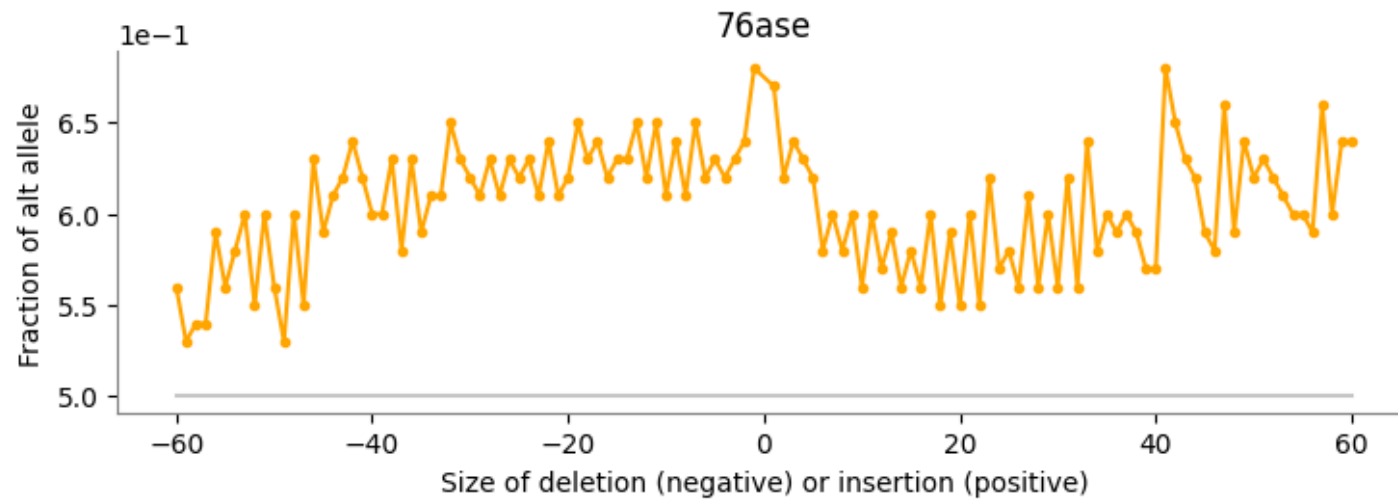
Ts/Tv stratified by QUAL



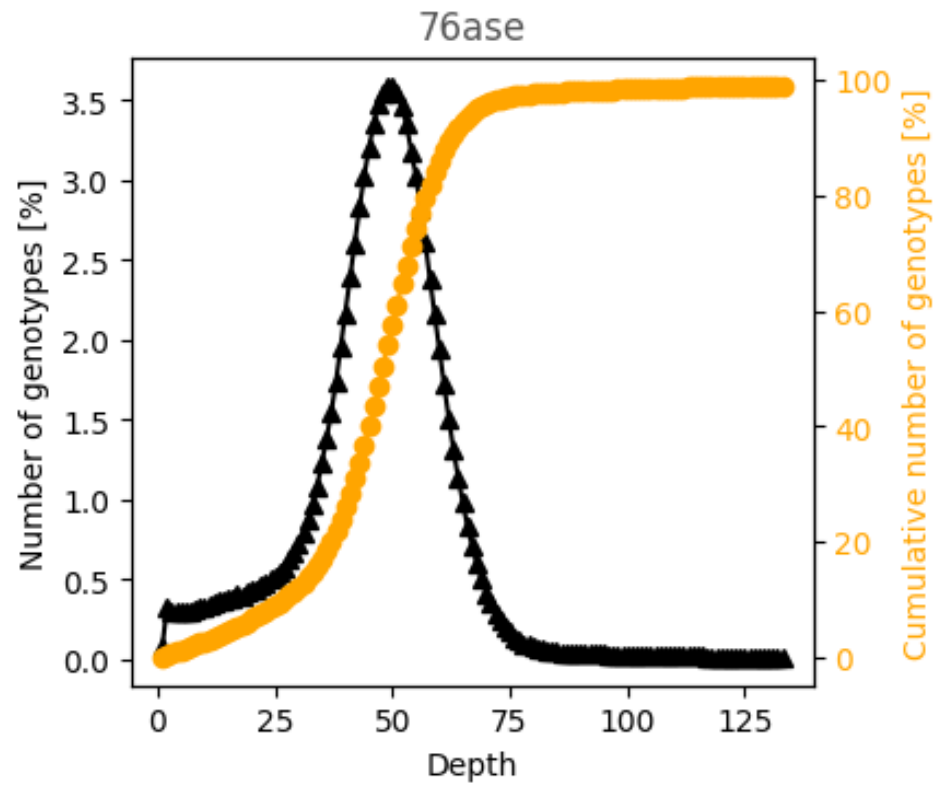
Indel distribution



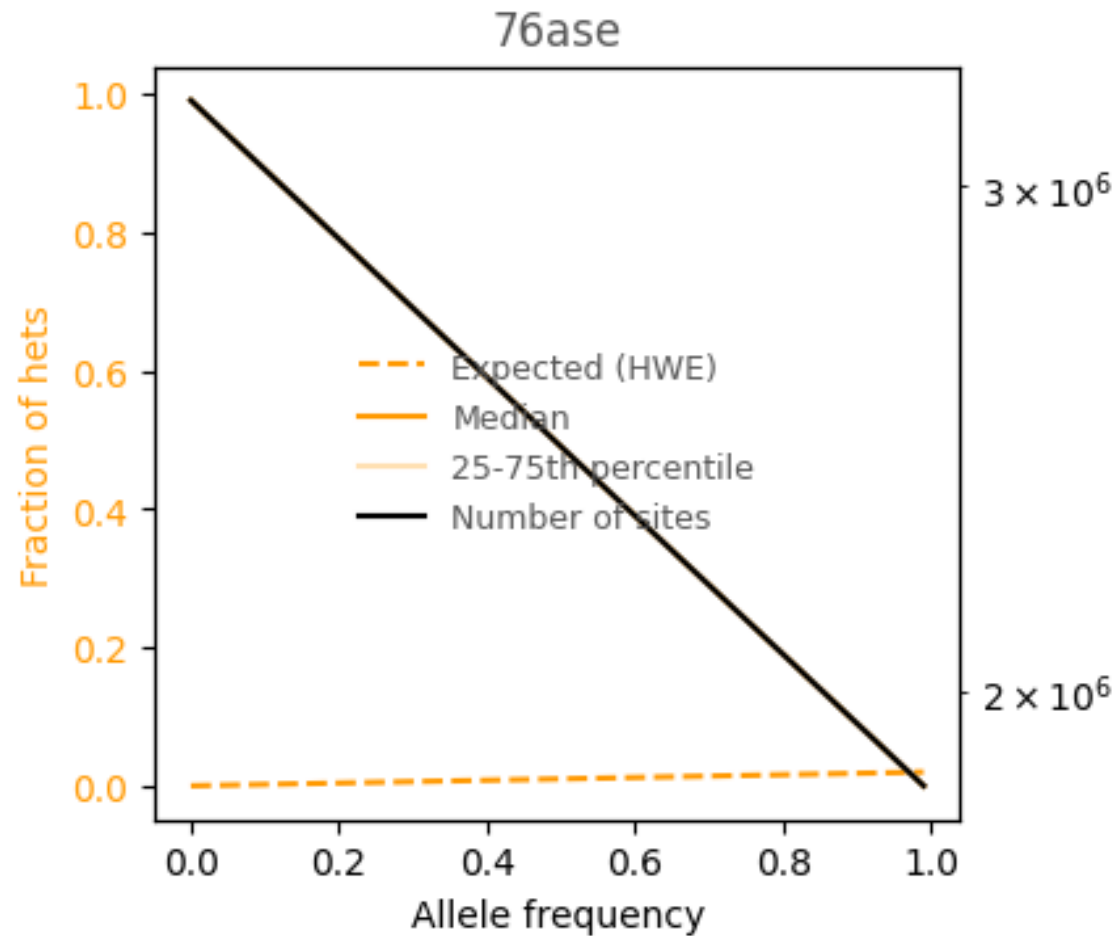
Fraction of alternate indel allele



Depth distribution



Number of HETs by AF



Substitution types

