

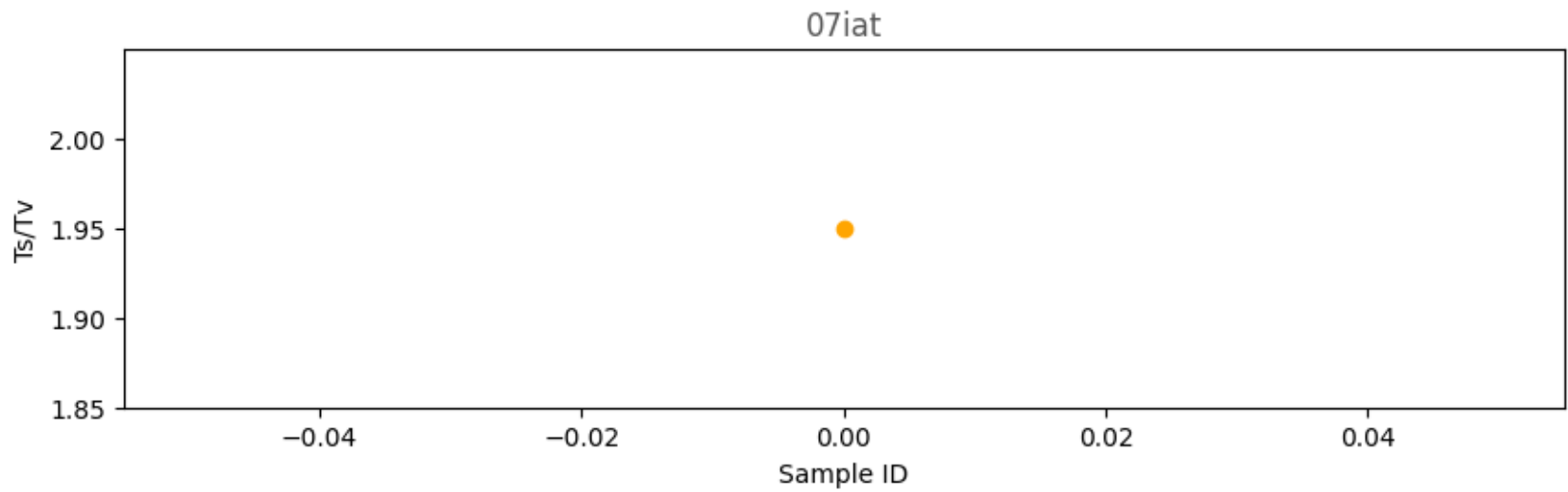
# Summary Numbers

| Callset                          | SNPs      |       |           | indels    |      | MNPs | others |
|----------------------------------|-----------|-------|-----------|-----------|------|------|--------|
|                                  | n         | ts/tv | (1st ALT) | n         | frm* |      |        |
| 07iat                            | 4,355,307 | 1.95  | 1.96      | 1,012,028 | –    | 0    | 0      |
| * frameshift ratio: out/(out+in) |           |       |           |           |      |      |        |

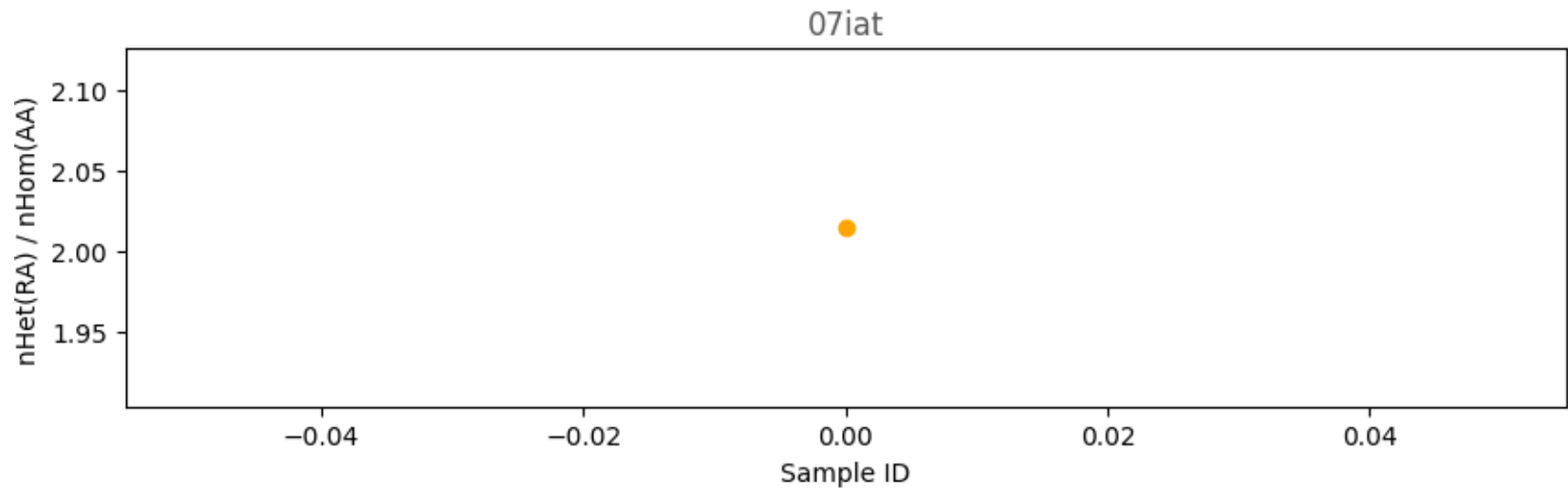
| Callset | singletons (AC=1) |       |        | multiallelic |       |
|---------|-------------------|-------|--------|--------------|-------|
|         | SNPs              | ts/tv | indels | sites        | SNPs  |
| 07iat   | 66.8%             | 1.93  | 72.2%  | 114,215      | 2,335 |

- 07iat .. /ngc/projects2/gm/data/archive/2022/variants/snv/07iathepf-103825455674-Normal\_Blood\_noinfo-WGS\_v1\_IlluminaDNAPCRFree\_RHGM00514-220119\_A01176\_BH2CT5DSX3-EXT\_LAB\_KA\_NGCWGS-NGCWGS03687\_21RKG030669x01\_snv\_germline\_raw.haplotype\_caller.vcf.gz

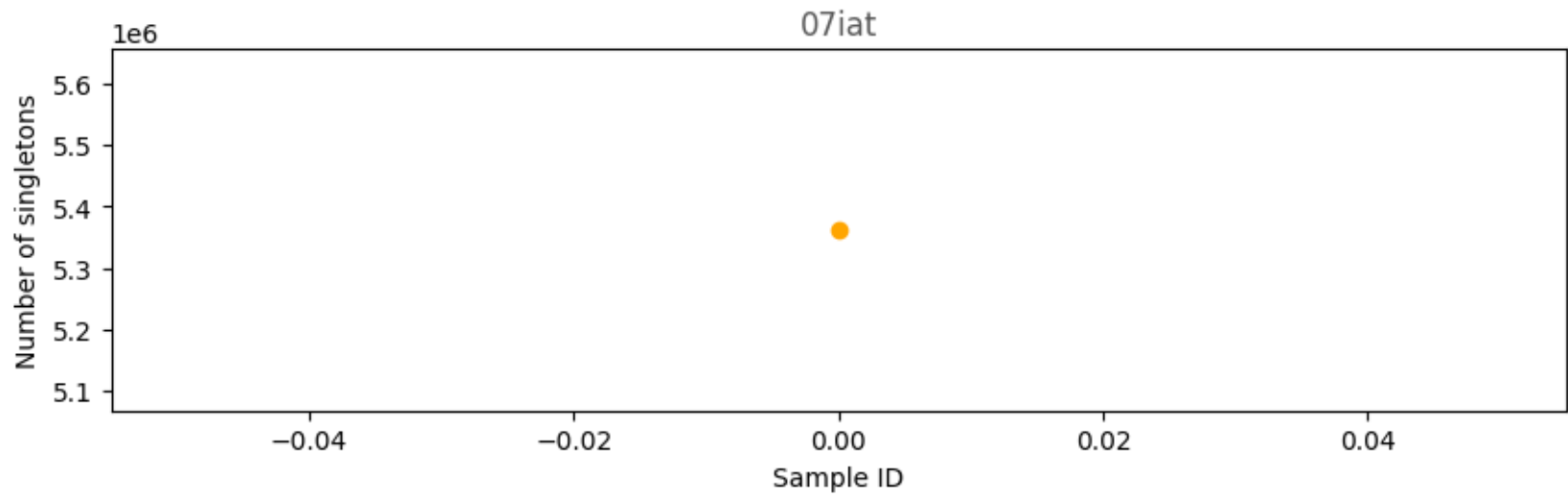
# Ts/Tv by sample



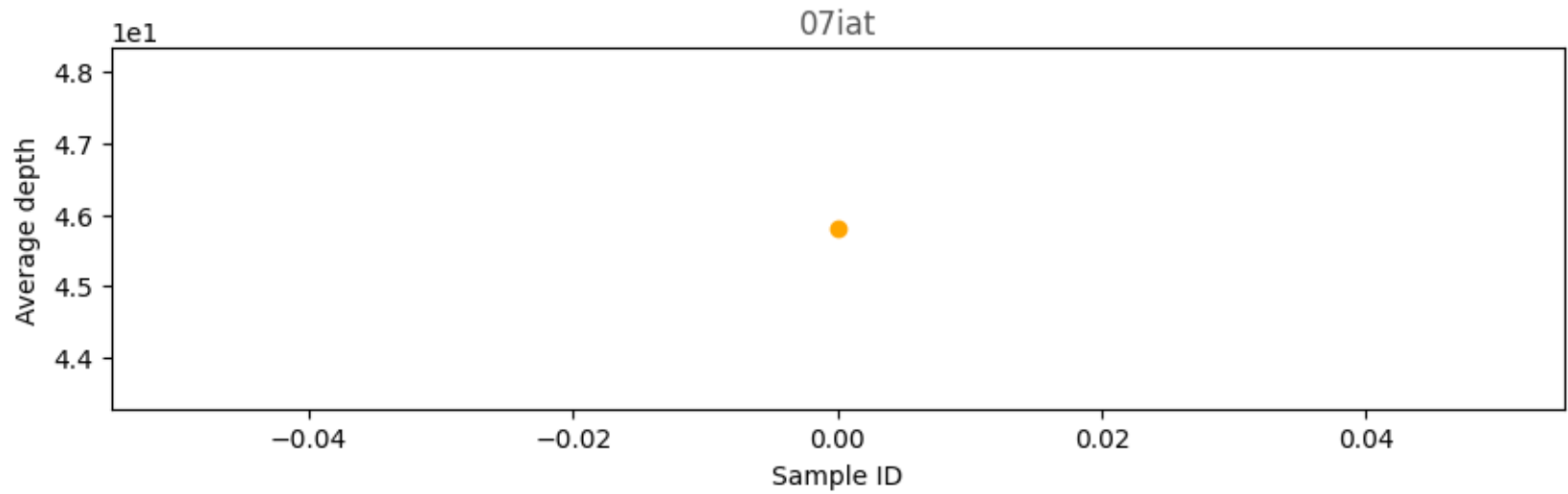
# Hets vs non-ref Homs by sample



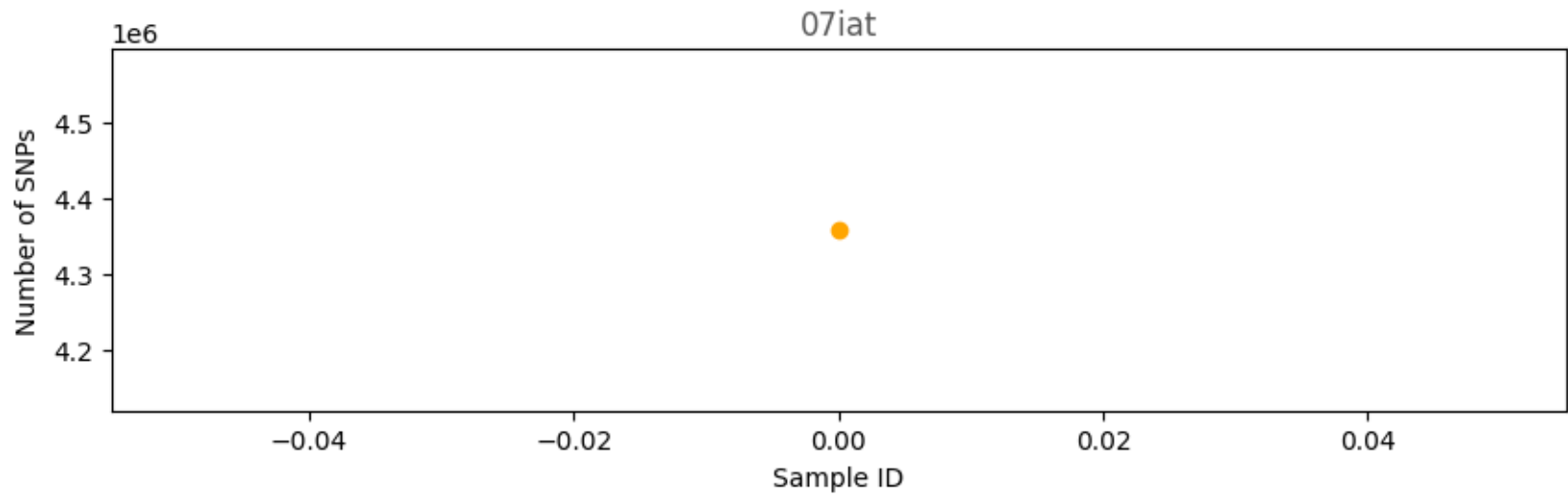
# Singletons by sample (hets and homs)



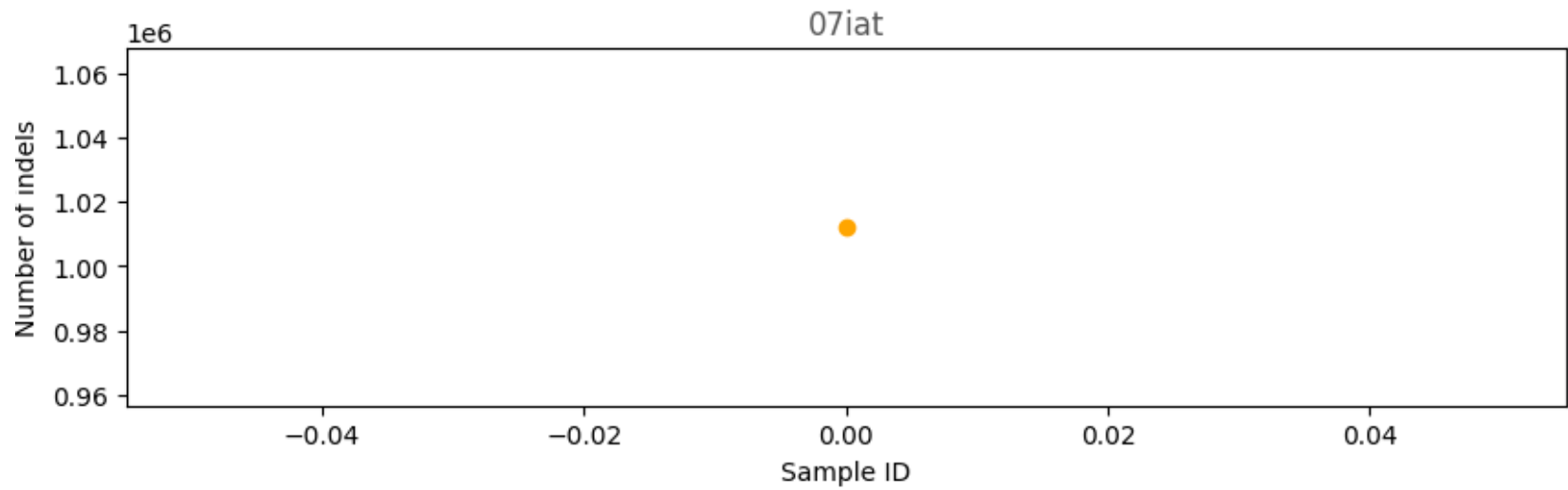
# Average depth by sample



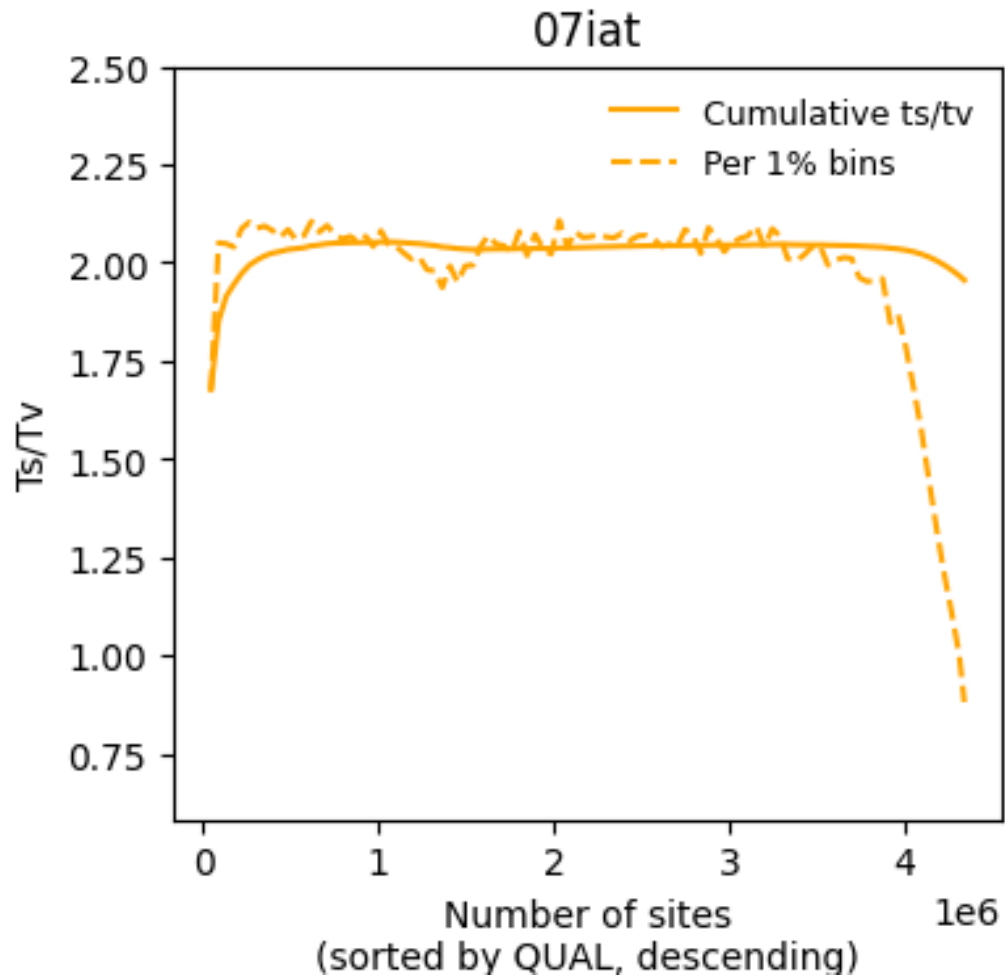
# Number of SNPs by sample



# Number of indels by sample

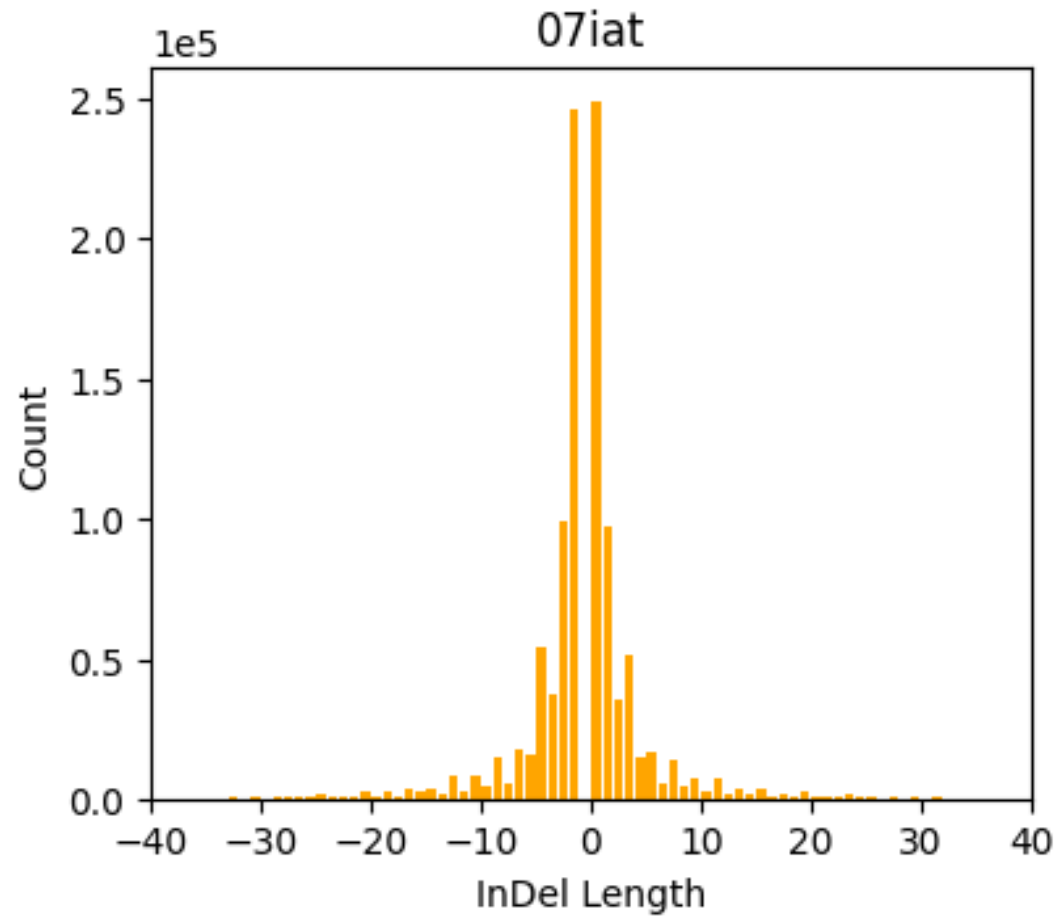


## Ts/Tv stratified by QUAL

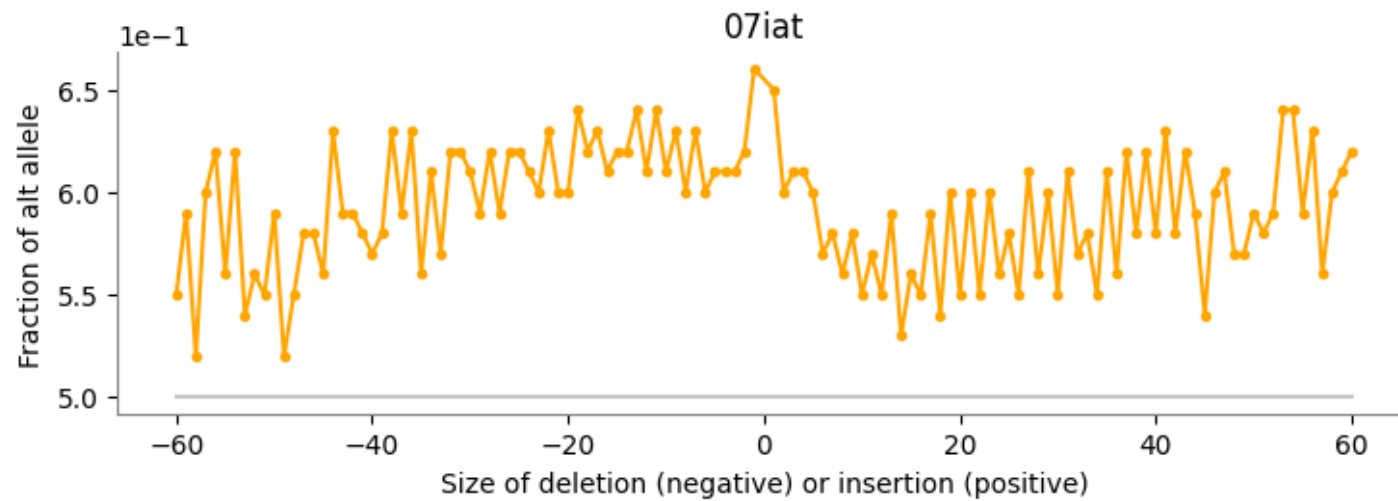




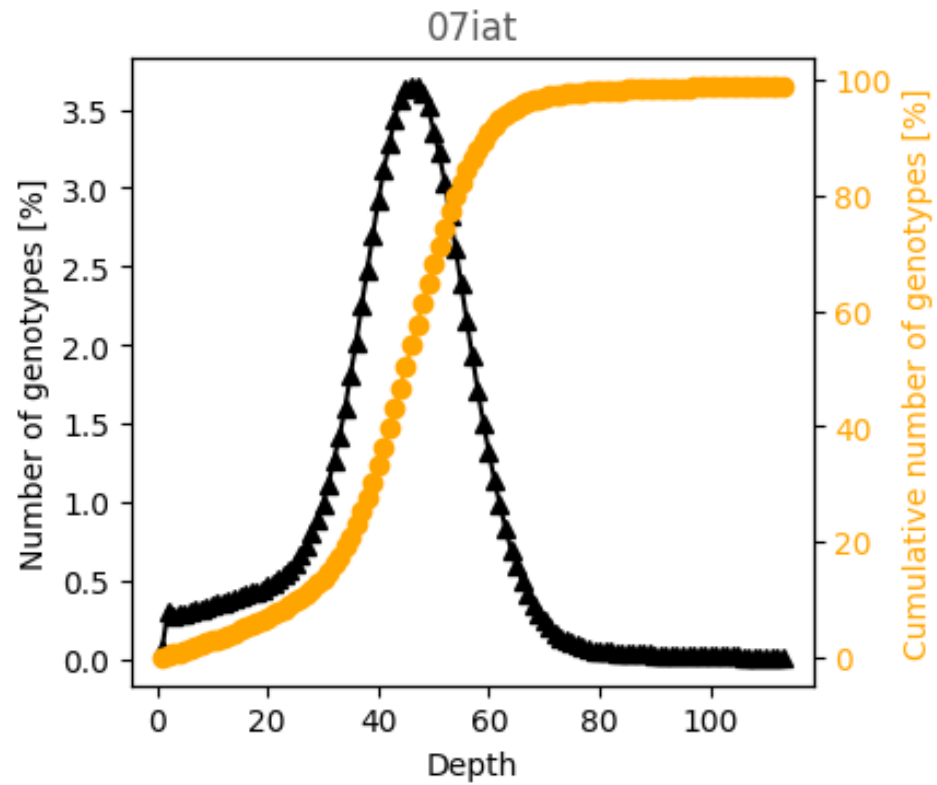
# Indel distribution



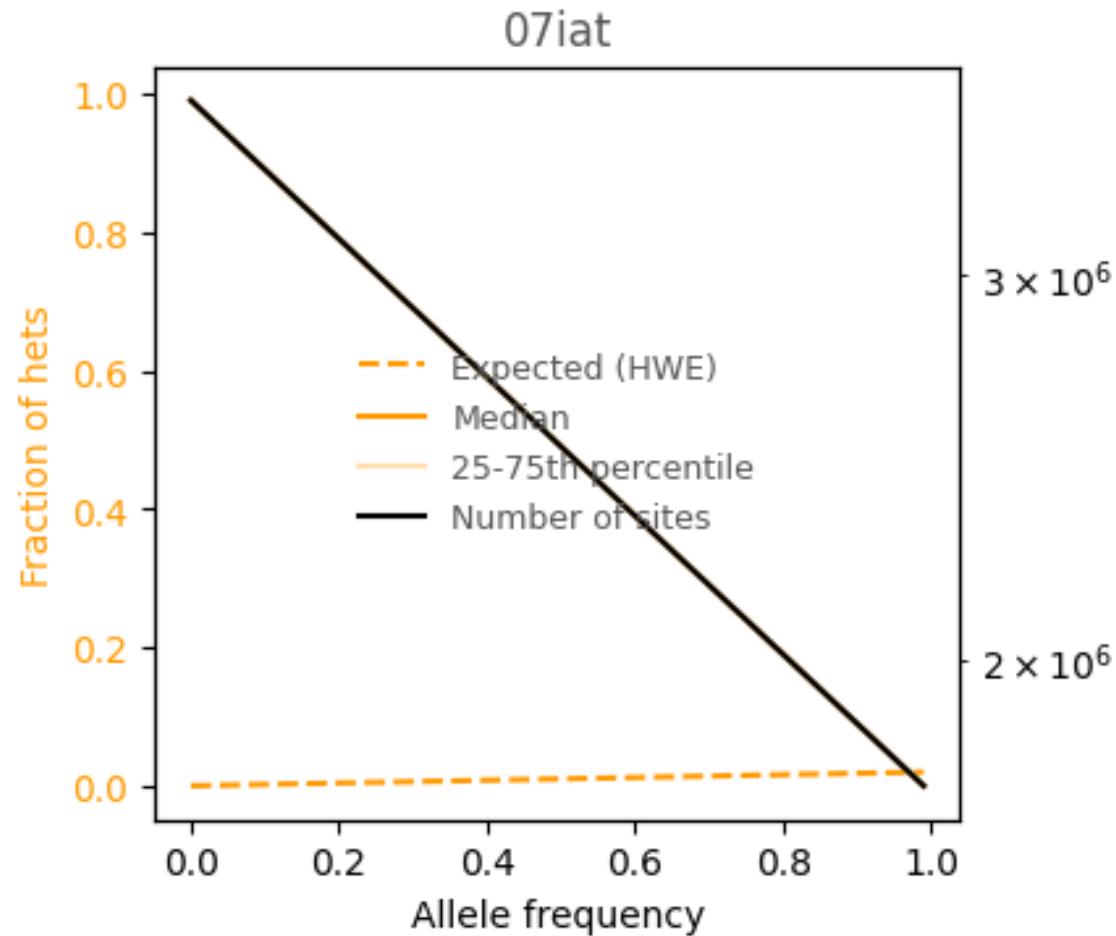
# Fraction of alternate indel allele



# Depth distribution



# Number of HETs by AF



# Substitution types

