

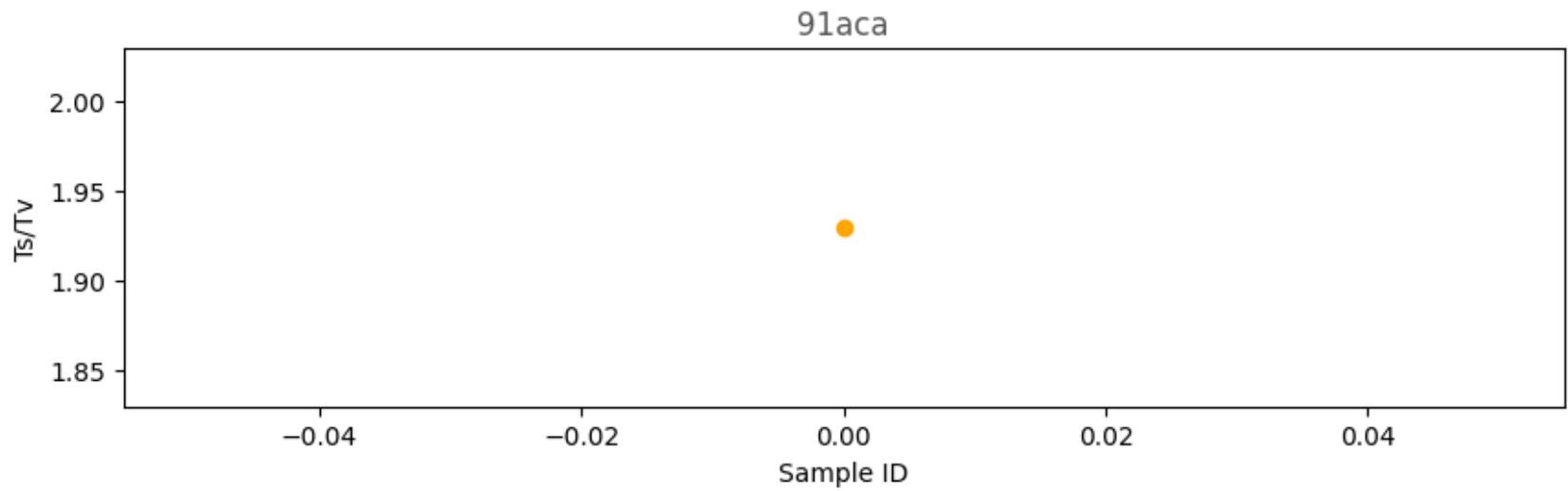
# Summary Numbers

| Callset                          | SNPs      |       |           | indels  |      | MNPs | others |
|----------------------------------|-----------|-------|-----------|---------|------|------|--------|
|                                  | n         | ts/tv | (1st ALT) | n       | frm* |      |        |
| 91aca                            | 4,078,751 | 1.93  | 1.93      | 951,508 | –    | 0    | 0      |
| * frameshift ratio: out/(out+in) |           |       |           |         |      |      |        |

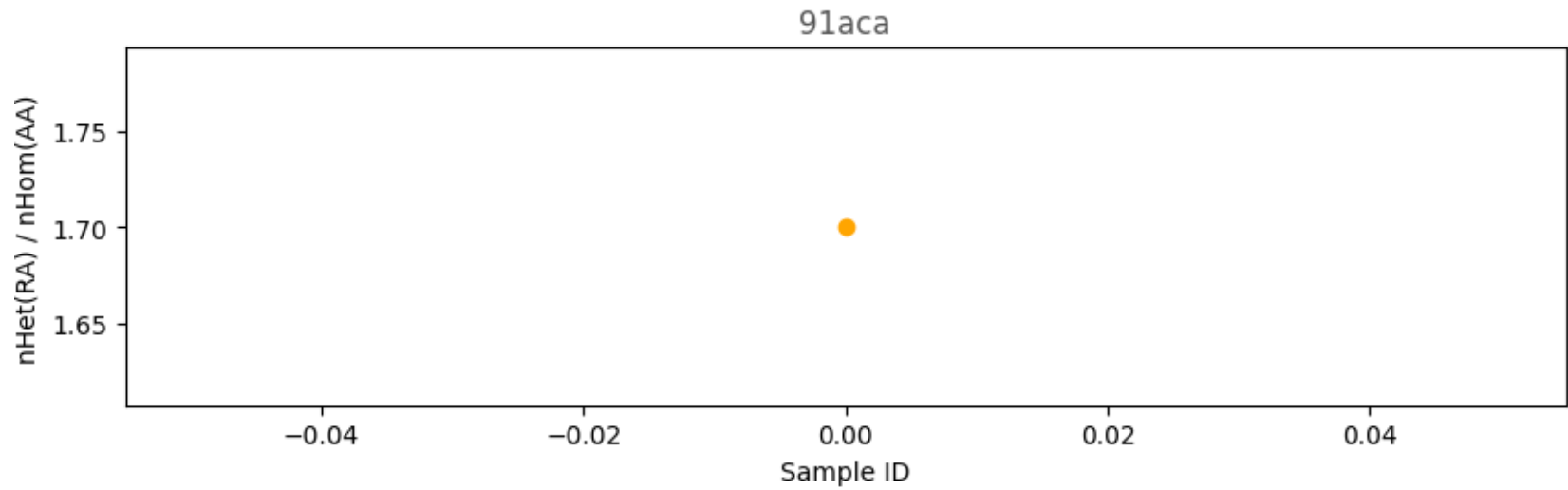
| Callset | singletons (AC=1) |       |        | multiallelic |       |
|---------|-------------------|-------|--------|--------------|-------|
|         | SNPs              | ts/tv | indels | sites        | SNPs  |
| 91aca   | 63.0%             | 1.90  | 68.2%  | 102,128      | 2,070 |

- 91aca .. /ngc/projects2/gm/data/archive/2022/variants/snv/91acasurf-103890246480-Normal\_B  
 lood\_noinfo-WGS\_v1\_IlluminaDNAPCRFree\_X-220708\_A01176\_BHK5MGDSX3-RHGM\_LABKA\_WGSA  
 KUT-WGSAKUT04609\_22RKG016425x01\_snv\_germline\_raw.haplotype\_caller.vcf.gz

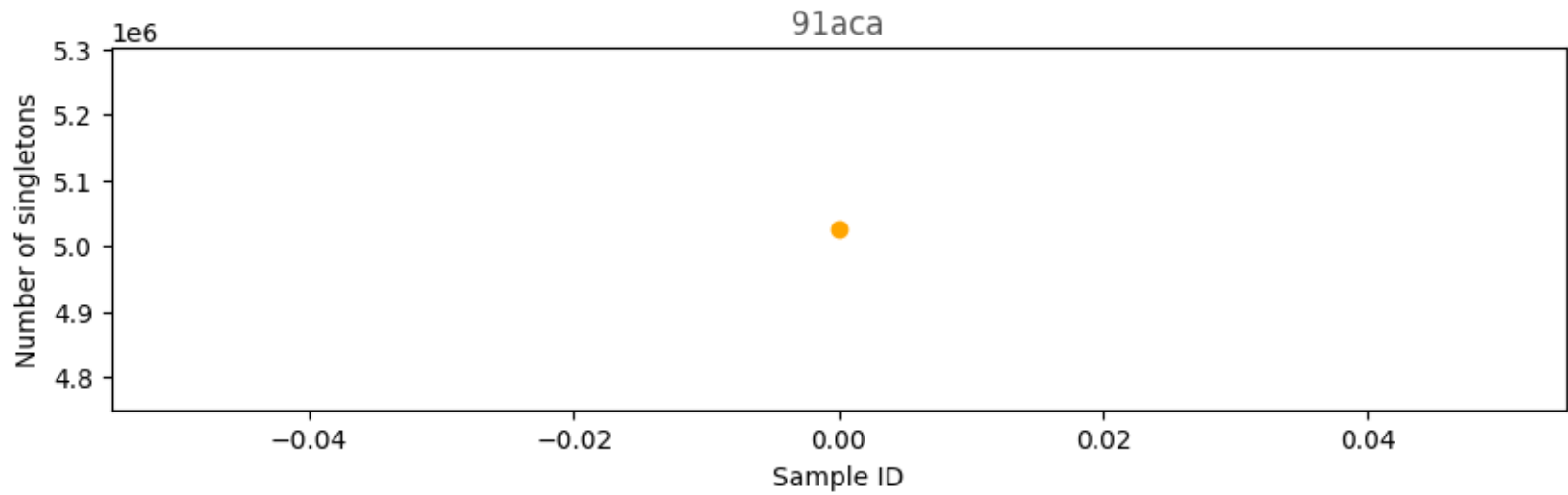
# Ts/Tv by sample



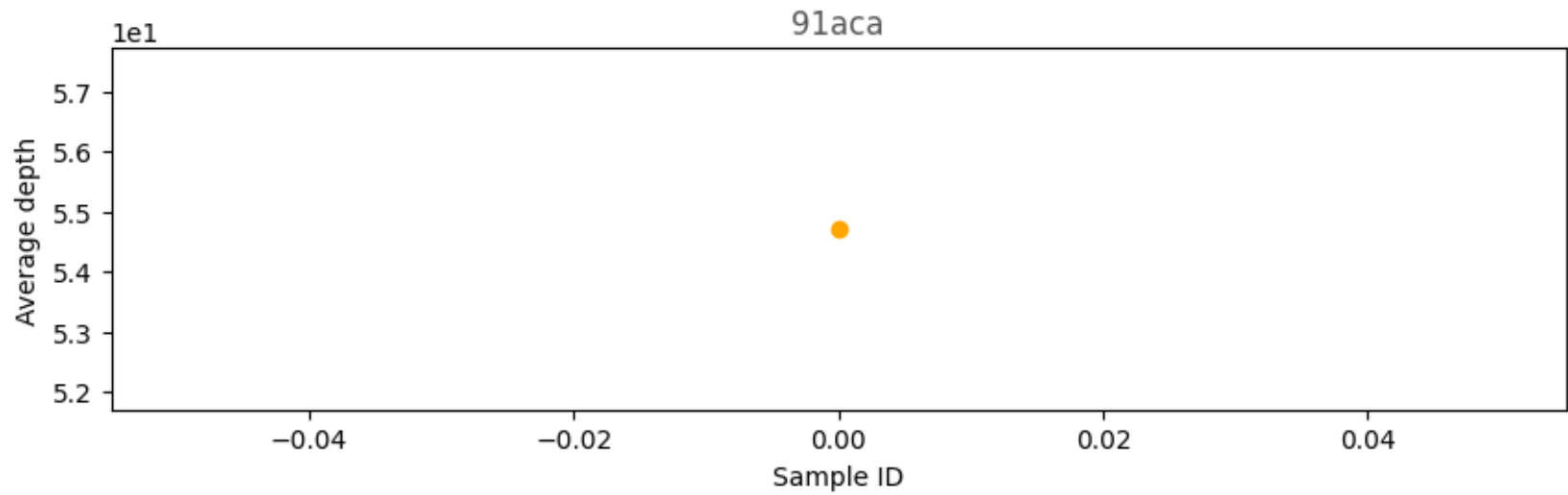
# Hets vs non-ref Homs by sample



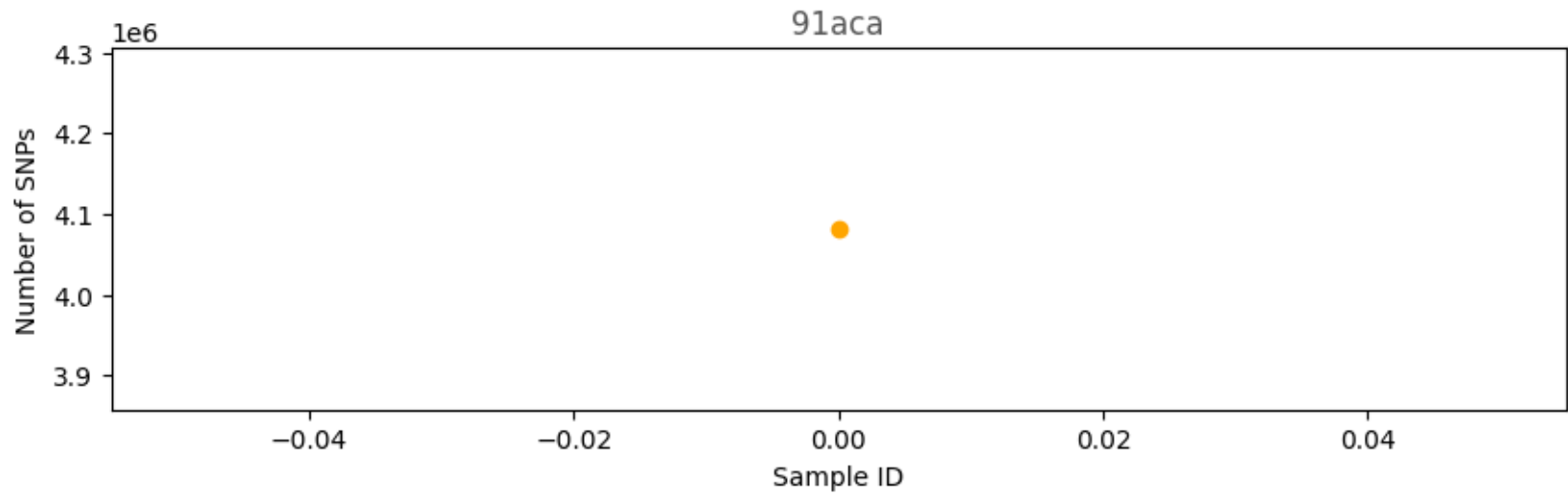
# Singletons by sample (hets and homs)



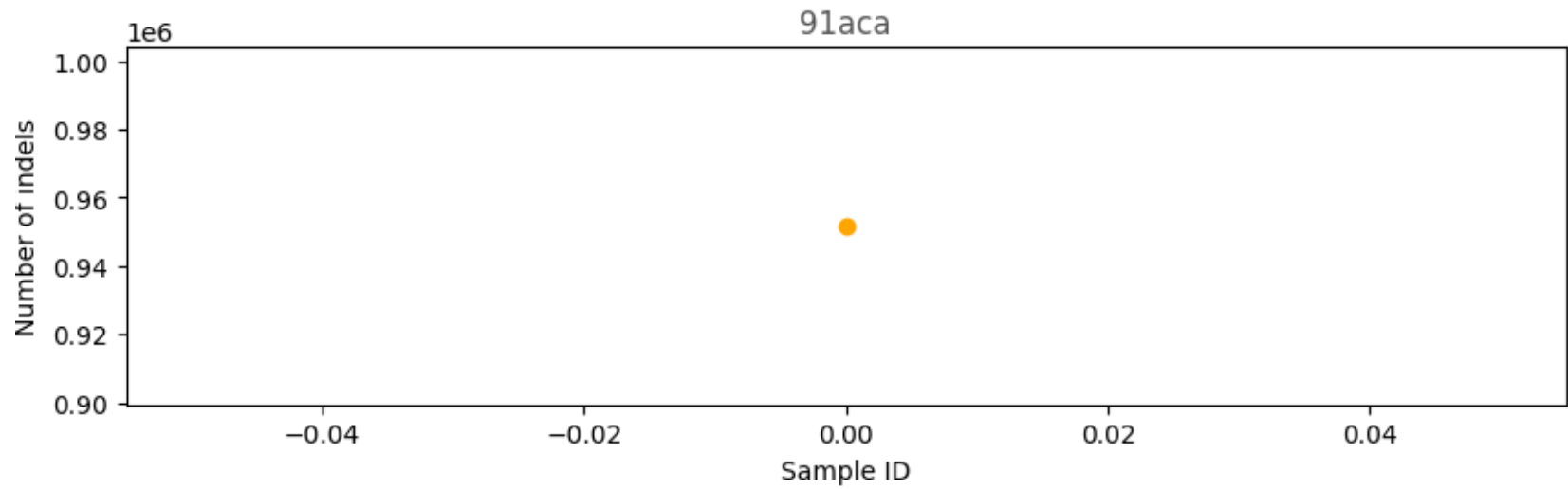
# Average depth by sample



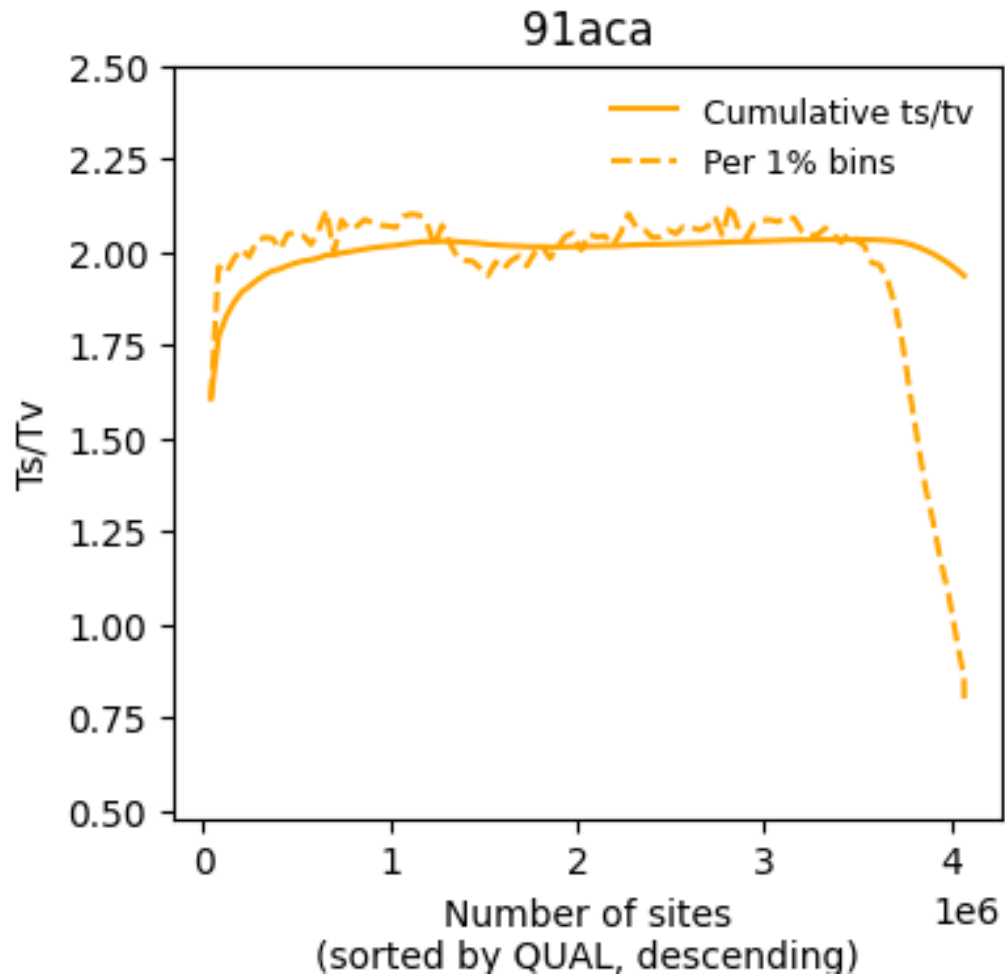
# Number of SNPs by sample



# Number of indels by sample

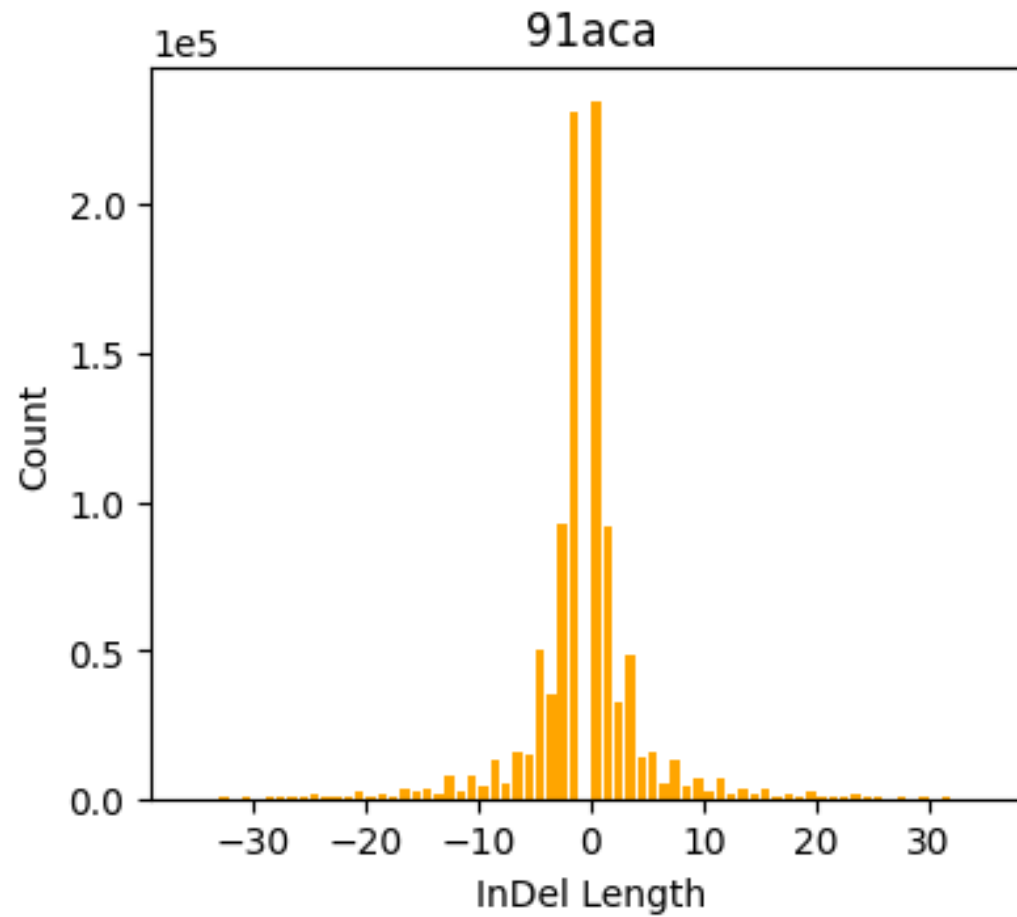


## Ts/Tv stratified by QUAL

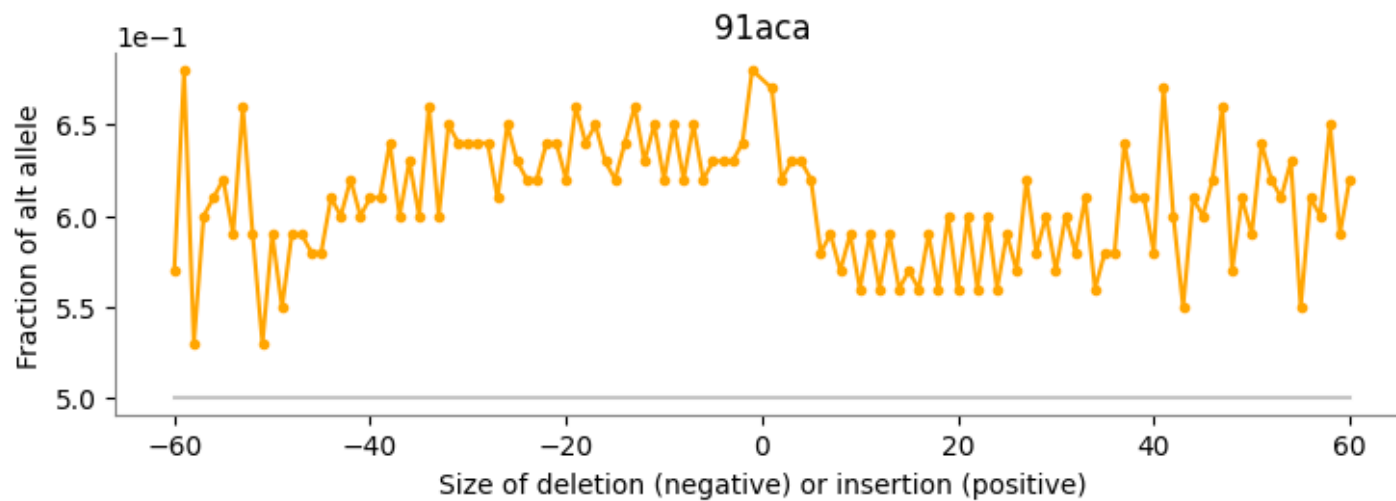




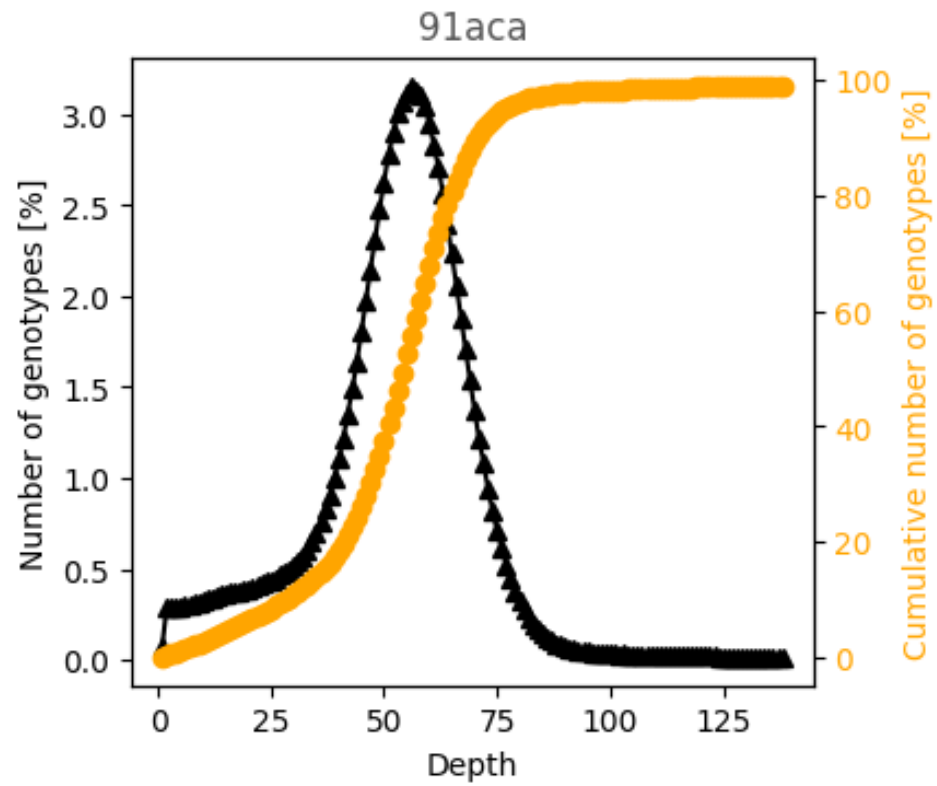
# Indel distribution



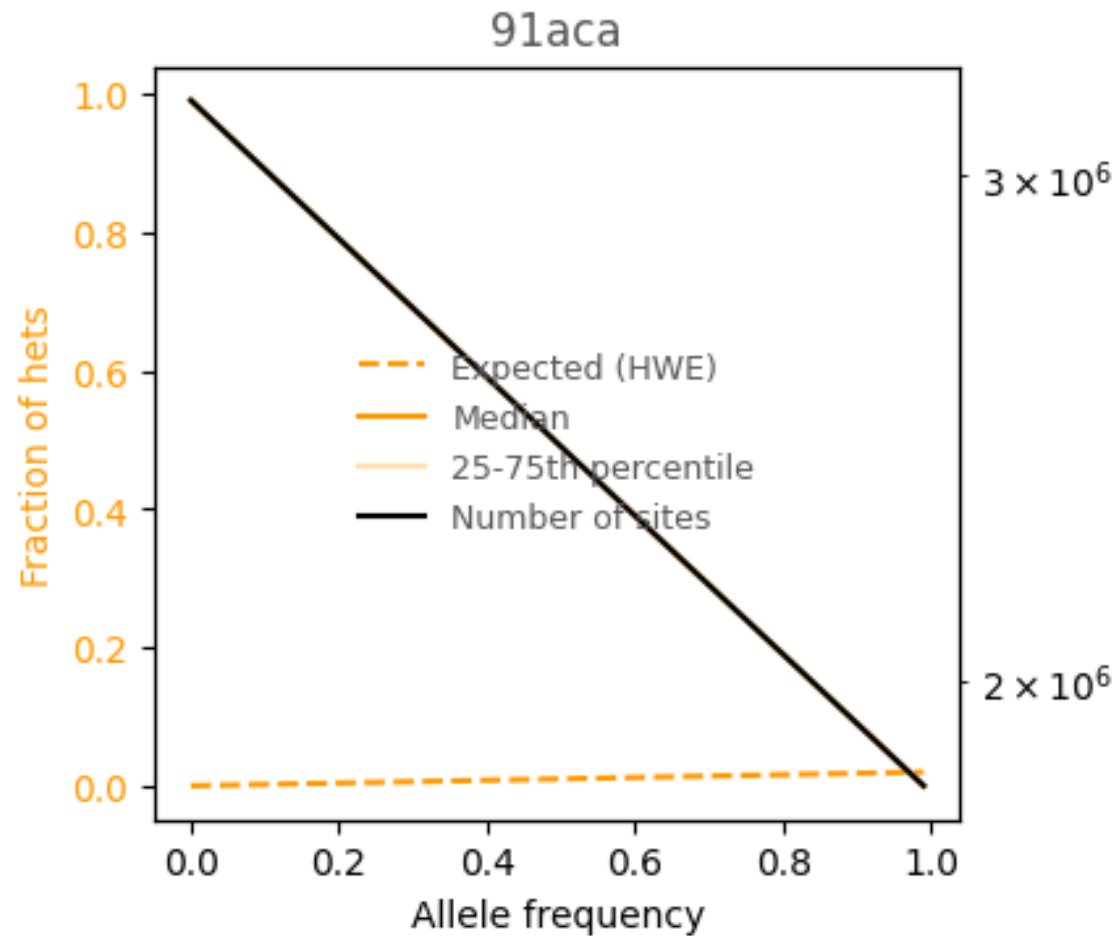
# Fraction of alternate indel allele



# Depth distribution



# Number of HETs by AF



# Substitution types

