

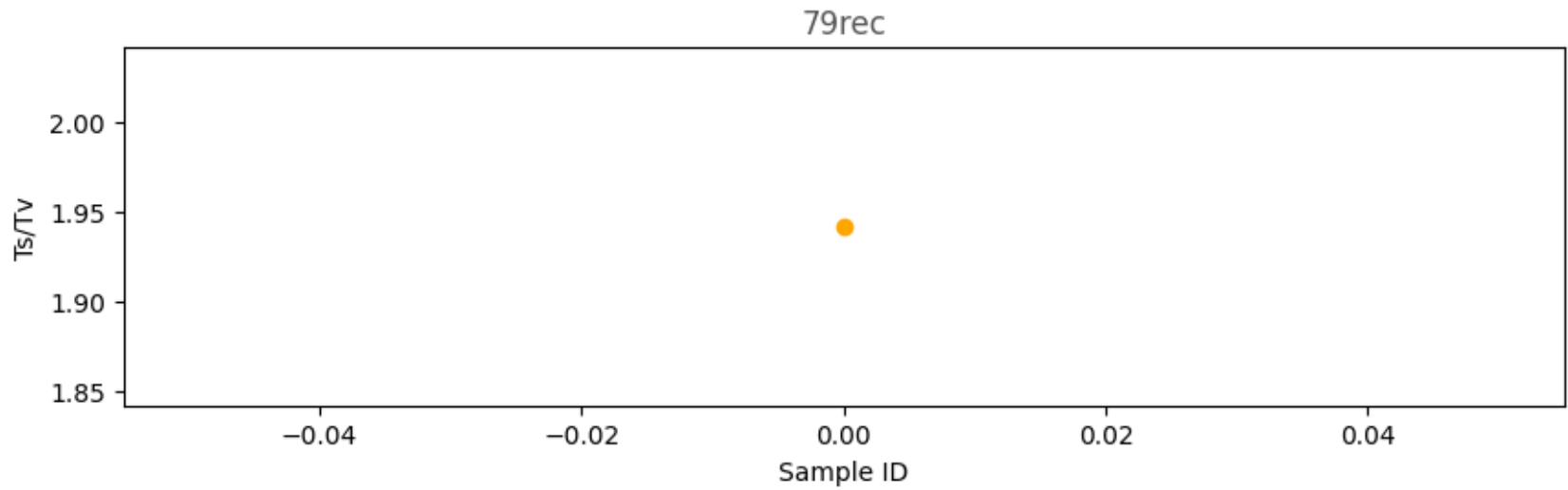
# Summary Numbers

| Callset                          | SNPs      |       |           | indels  |      | MNPs | others |
|----------------------------------|-----------|-------|-----------|---------|------|------|--------|
|                                  | n         | ts/tv | (1st ALT) | n       | frm* |      |        |
| 79rec                            | 4,036,375 | 1.94  | 1.95      | 954,707 | –    | 0    | 0      |
| * frameshift ratio: out/(out+in) |           |       |           |         |      |      |        |

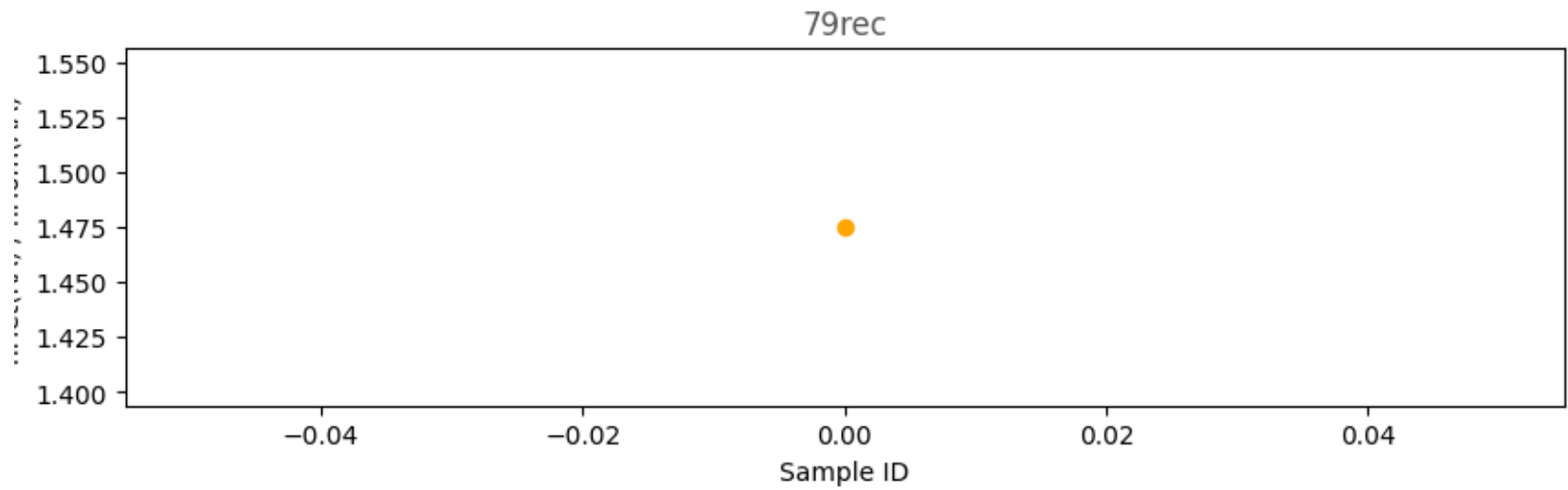
| Callset | singletons (AC=1) |       |        | multiallelic |       |
|---------|-------------------|-------|--------|--------------|-------|
|         | SNPs              | ts/tv | indels | sites        | SNPs  |
| 79rec   | 59.6%             | 1.91  | 64.8%  | 101,088      | 1,934 |

- 79rec .. /ngc/projects2/gm/data/archive/2022/variants/snv/79rechacf-103719164410-Normal\_B  
 lood\_noinfo-WGS\_v1\_IlluminaDNAPCRFree\_RHGM00110-210323\_A01176\_AH27F5DSX2-EXT\_LAB  
 KA\_NGCWGS-NGCWGS00025\_794572cd0\_snv\_germline\_raw.haplotype\_caller.vcf.gz

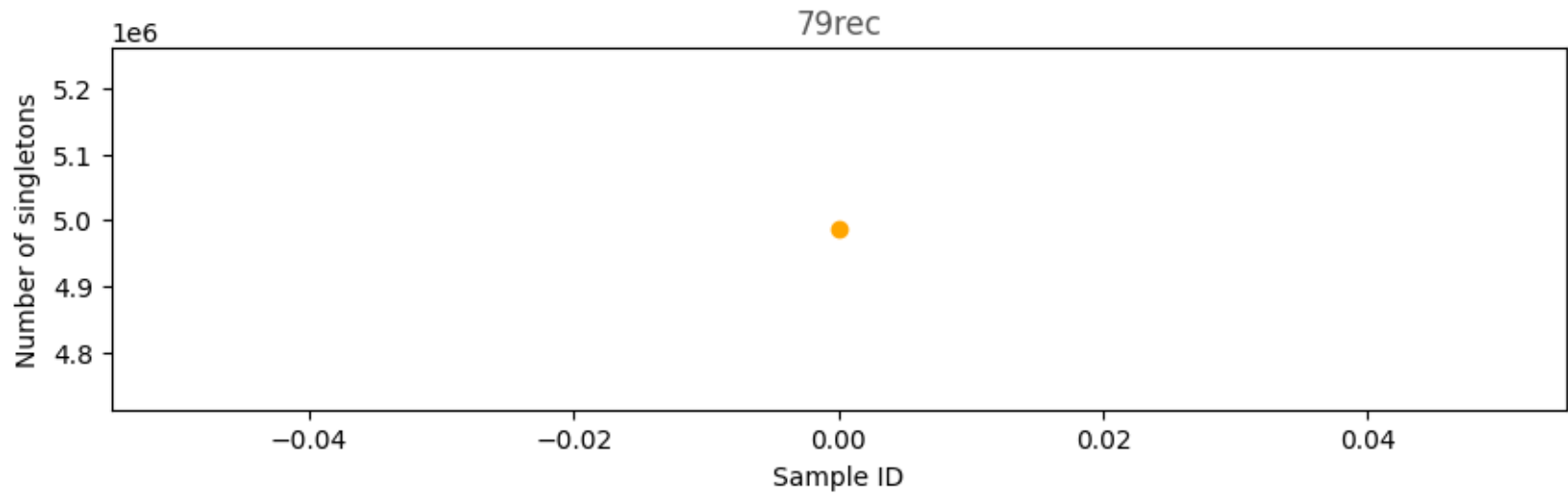
# Ts/Tv by sample



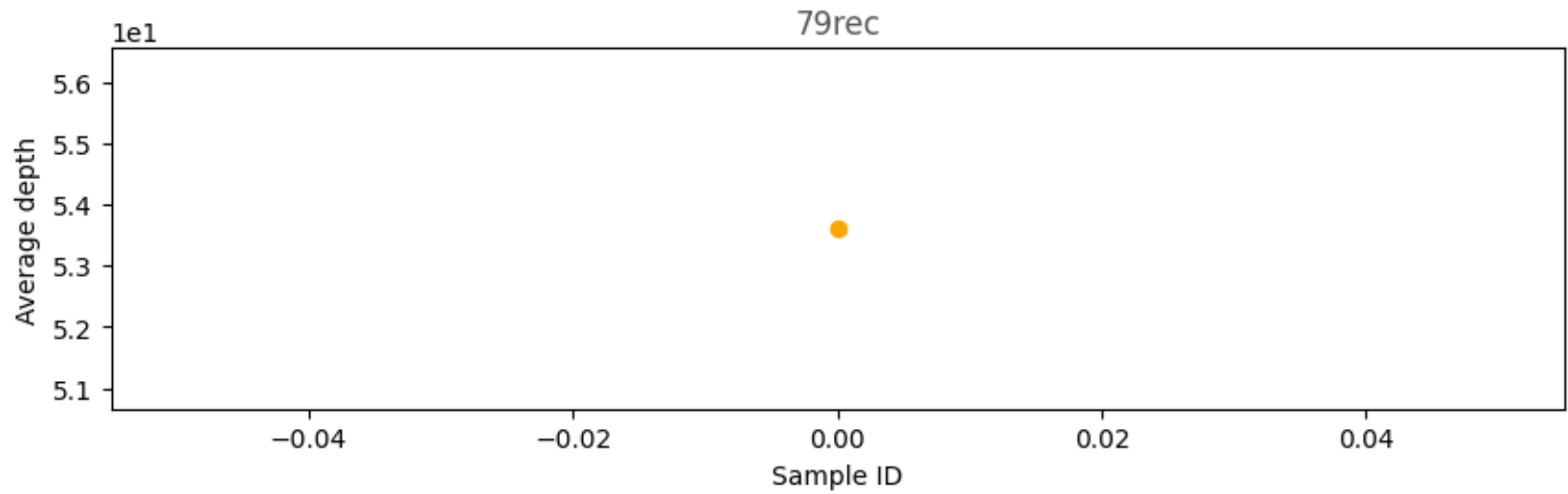
# Hets vs non-ref Homs by sample



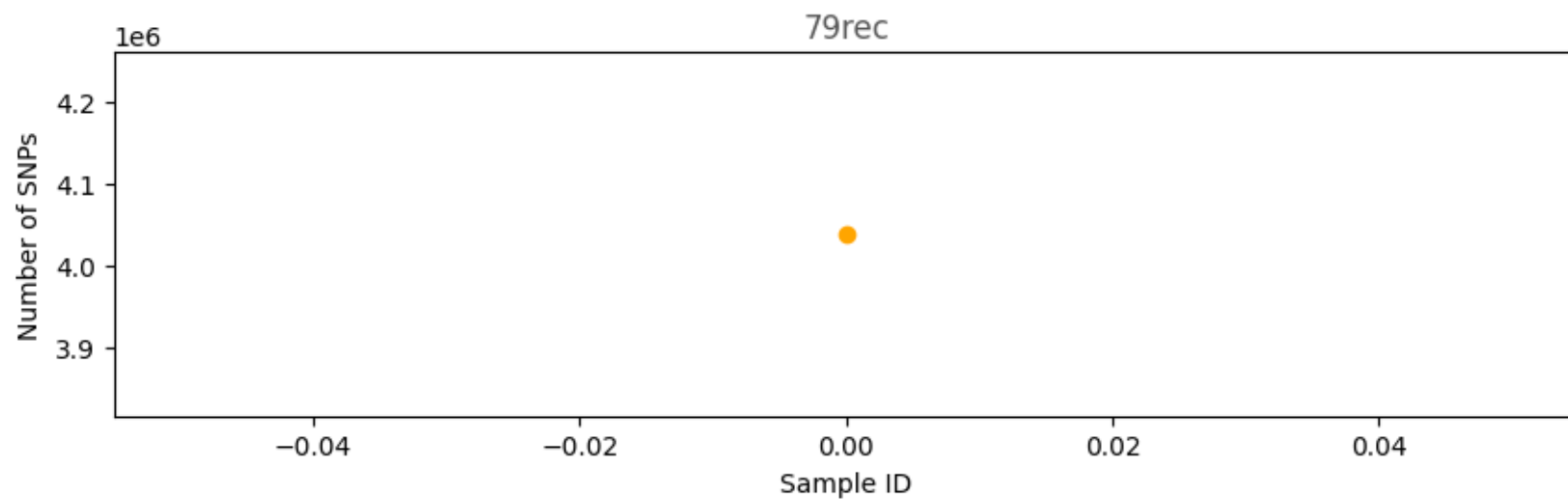
# Singletons by sample (hets and homs)



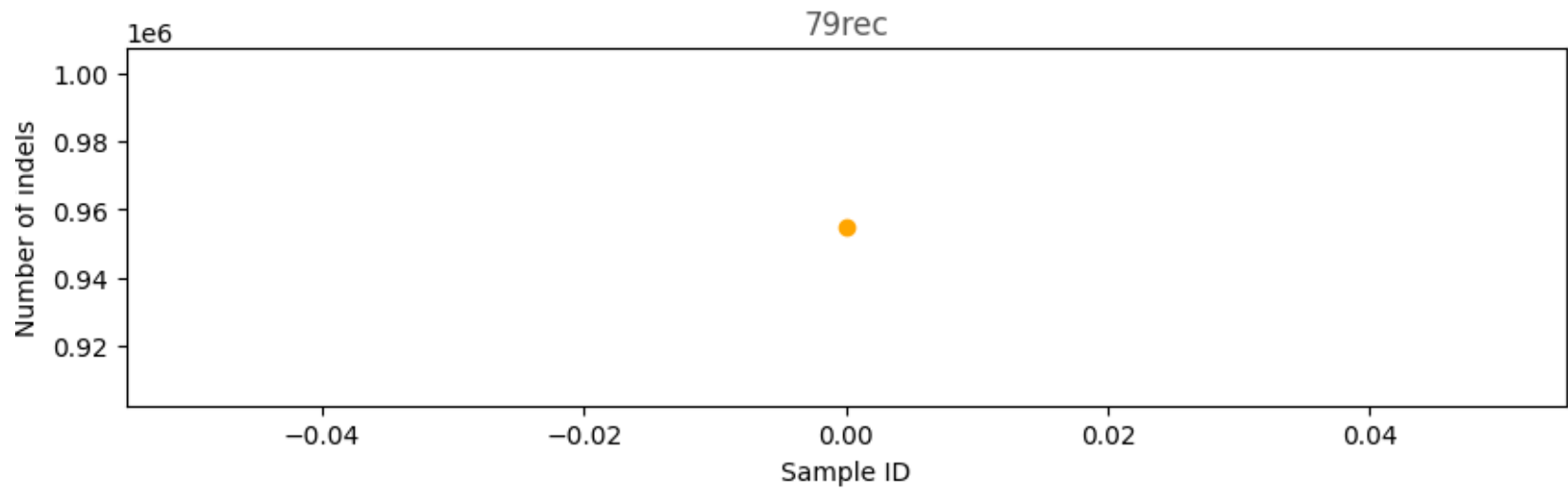
# Average depth by sample



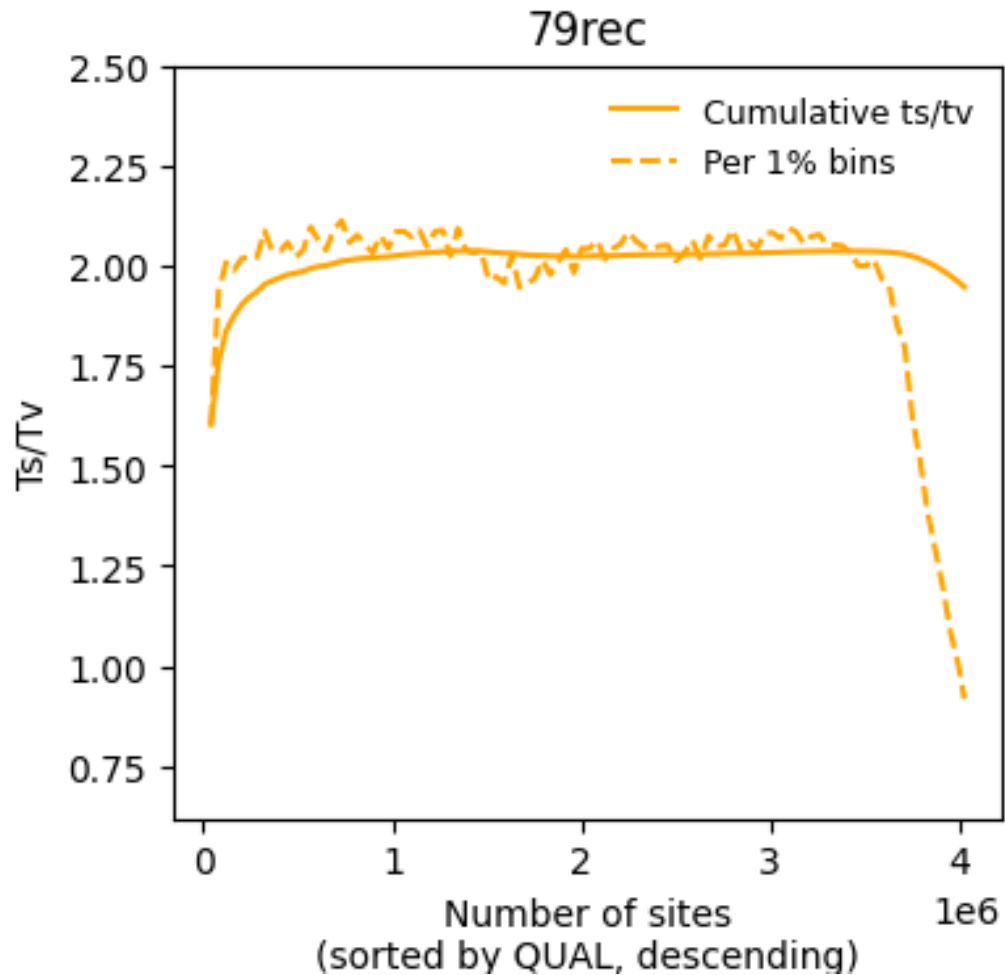
# Number of SNPs by sample



# Number of indels by sample

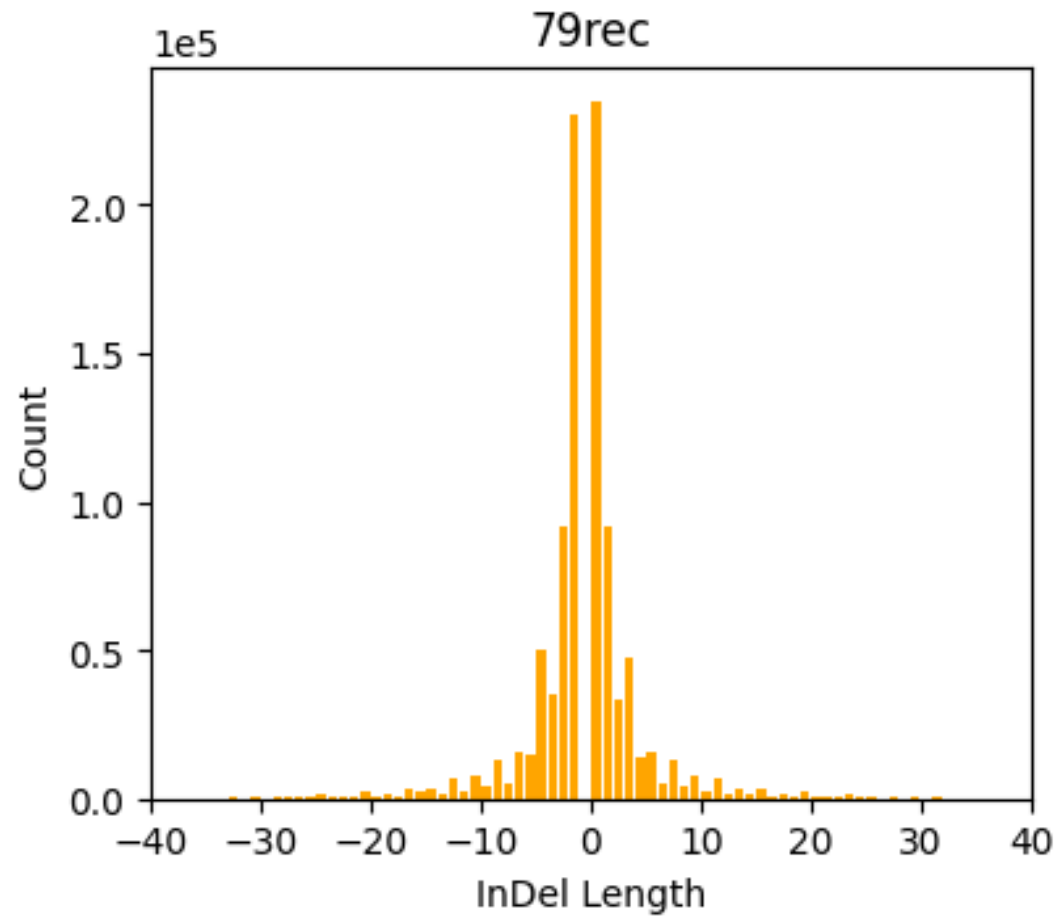


## Ts/Tv stratified by QUAL

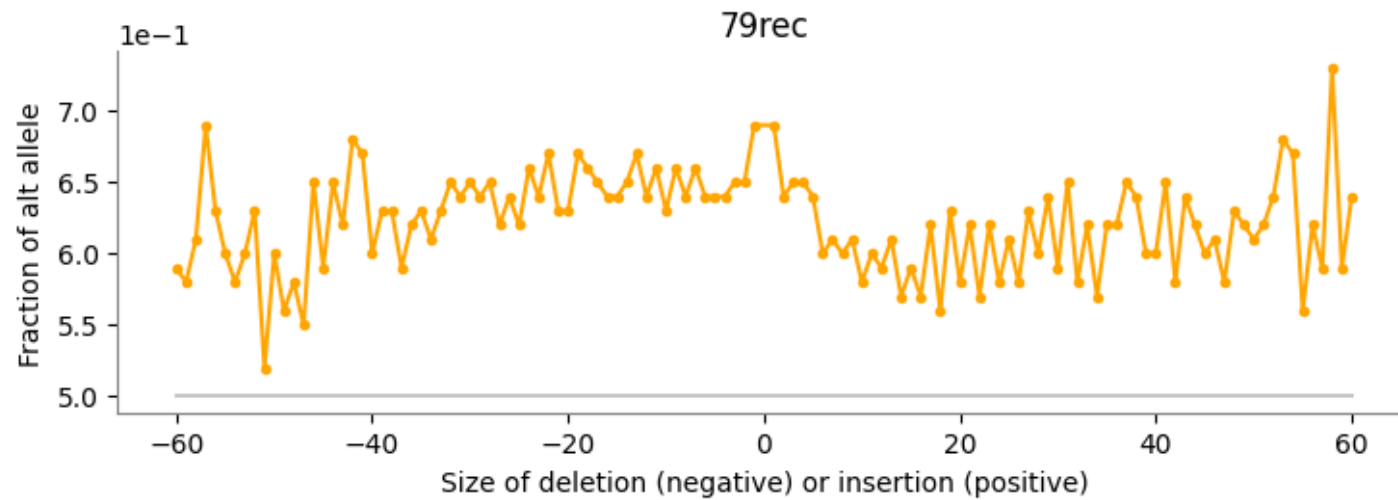




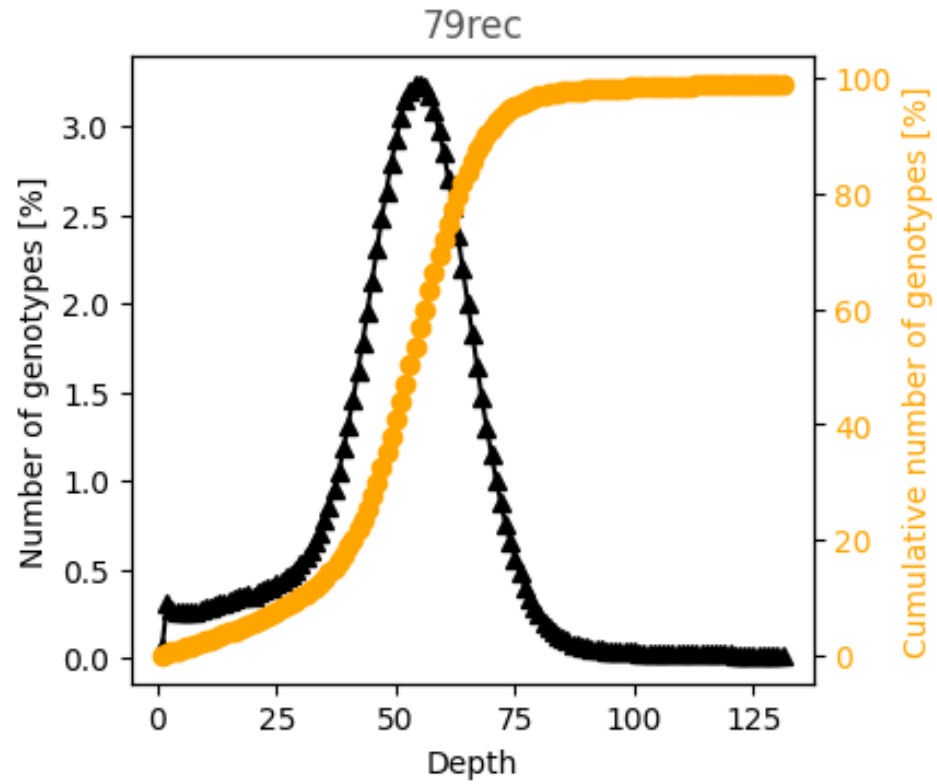
# Indel distribution



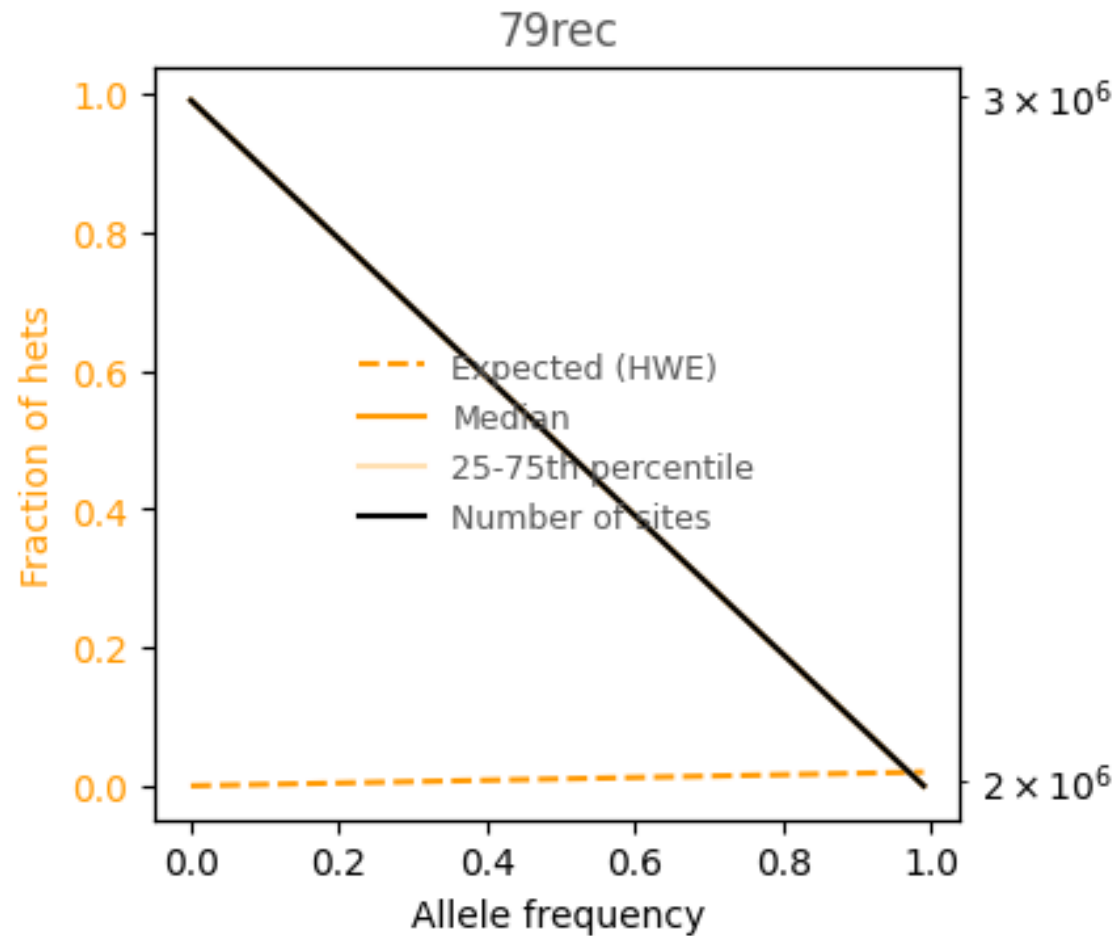
# Fraction of alternate indel allele



# Depth distribution



# Number of HETs by AF



# Substitution types

