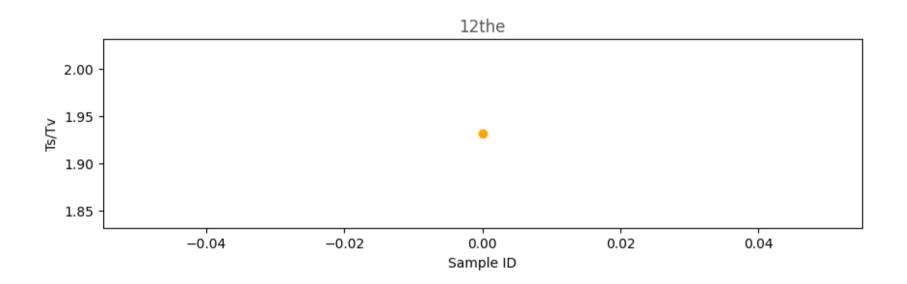
### **Summary Numbers**

|                                  | SNPs      |       |           | indels  |      | MNPs | others |  |  |
|----------------------------------|-----------|-------|-----------|---------|------|------|--------|--|--|
| Callset                          | n         | ts/tv | (1st ALT) | n       | frm* |      |        |  |  |
| 12the                            | 4,075,436 | 1.93  | 1.94      | 934,148 | 1    | 0    | 0      |  |  |
| * frameshift ratio: out/(out+in) |           |       |           |         |      |      |        |  |  |

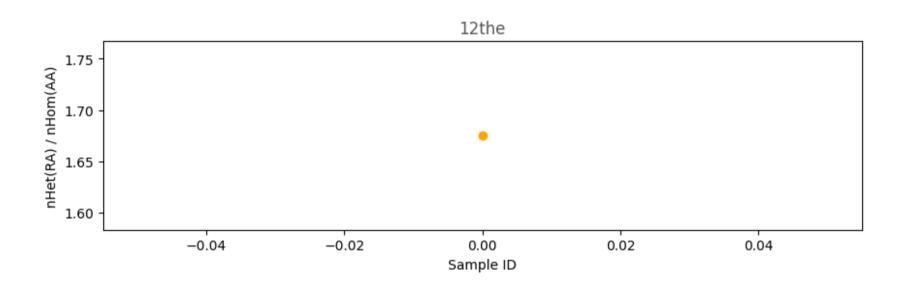
|         | singl | etons (A | multiallelic |        |       |
|---------|-------|----------|--------------|--------|-------|
| Callset | SNPs  | ts/tv    | indels       | sites  | SNPs  |
| 12the   | 62.6% | 1.90     | 66.9%        | 92,380 | 2,076 |

- 12the../ngc/projects2/gm/data/archive/2022/variants/snv/12thedtyf-110301698880-Normal\_B lood\_noinfo-WGS\_v1\_IlluminaDNAPCRFree\_RHGM02223-221109\_A01176\_BH3N2MDSX5-EXT\_LAB KA\_NGCWGS-NGCWGS06105\_snv\_germline\_raw.haplotype\_caller.vcf.gz

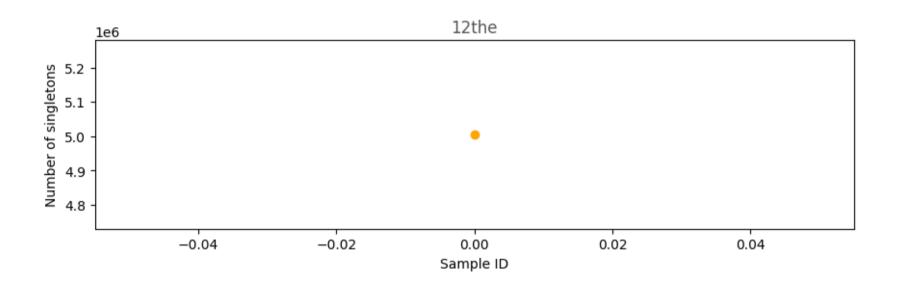
# Ts/Tv by sample



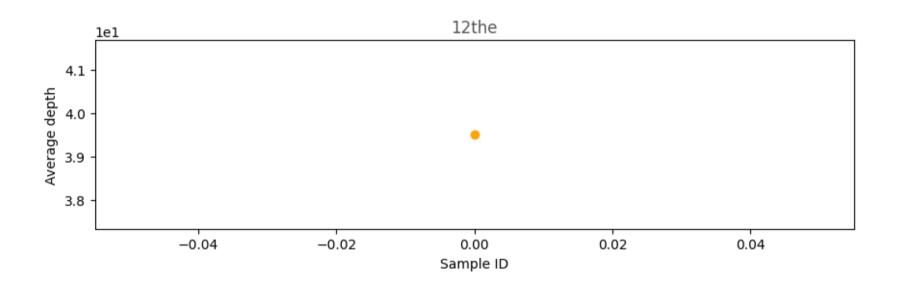
### Hets vs non-ref Homs by sample



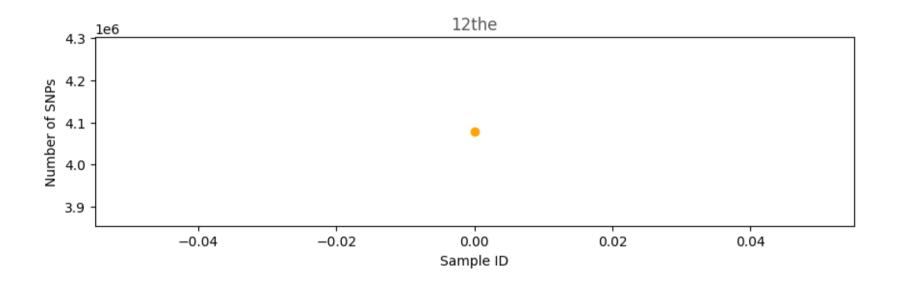
### Singletons by sample (hets and homs)



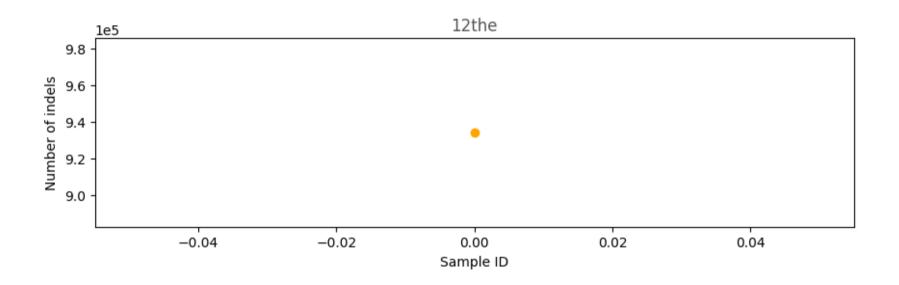
## Average depth by sample



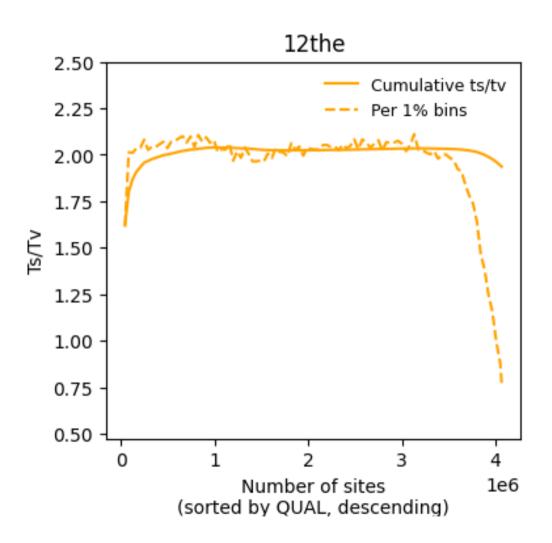
## Number of SNPs by sample



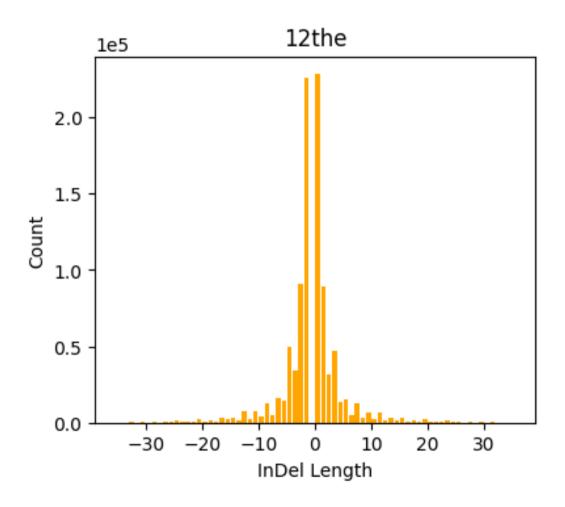
## Number of indels by sample



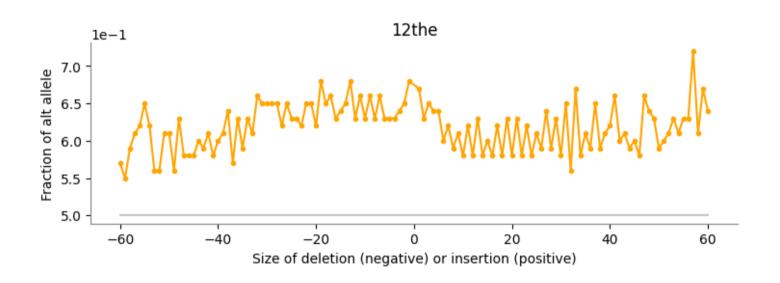
#### Ts/Tv stratified by QUAL



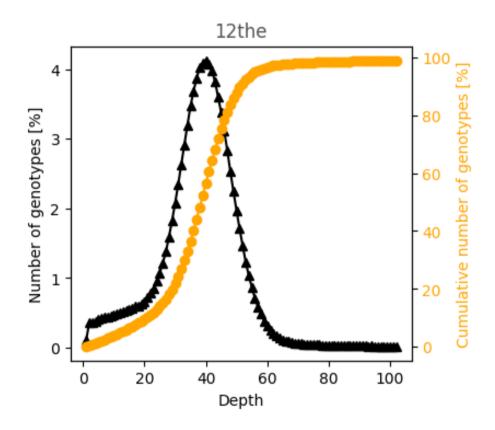
#### Indel distribution



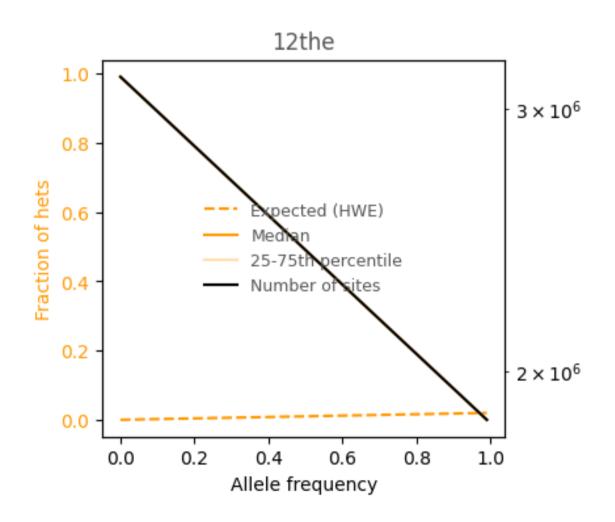
#### Fraction of alternate indel allele



# Depth distribution



#### Number of HETs by AF



### Substitution types

