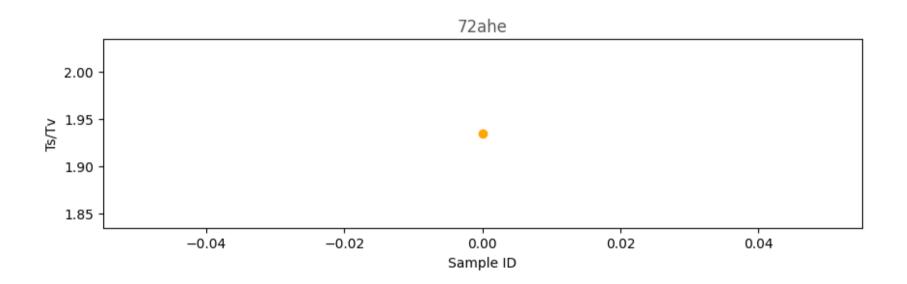
#### **Summary Numbers**

|                                  | SNPs      |       |           | indels  |      | MNPs | others |  |  |
|----------------------------------|-----------|-------|-----------|---------|------|------|--------|--|--|
| Callset                          | n         | ts/tv | (1st ALT) | n       | frm* |      |        |  |  |
| 72ahe                            | 4,098,876 | 1.93  | 1.94      | 979,980 | -    | 0    | 0      |  |  |
| * frameshift ratio: out/(out+in) |           |       |           |         |      |      |        |  |  |

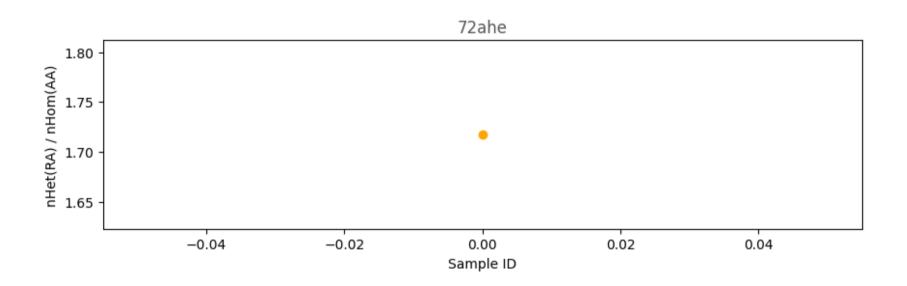
|         | singl | etons (A | multiallelic |         |       |
|---------|-------|----------|--------------|---------|-------|
| Callset | SNPs  | ts/tv    | indels       | sites   | SNPs  |
| 72ahe   | 63.2% | 1.90     | 69.3%        | 107,746 | 1,877 |

- 72ahe .. /ngc/projects2/gm/data/archive/2022/variants/snv/72ahenttf-103761016890-Normal\_B lood\_noinfo-WGS\_v1\_IlluminaDNAPCRFree\_RHGM00282-210720\_A01176\_BH2VTTDMXY-EXT\_LAB KA\_NGCWGS-NGCWGS00175\_72tge55q0\_snv\_germline\_raw.haplotype\_caller.vcf.gz

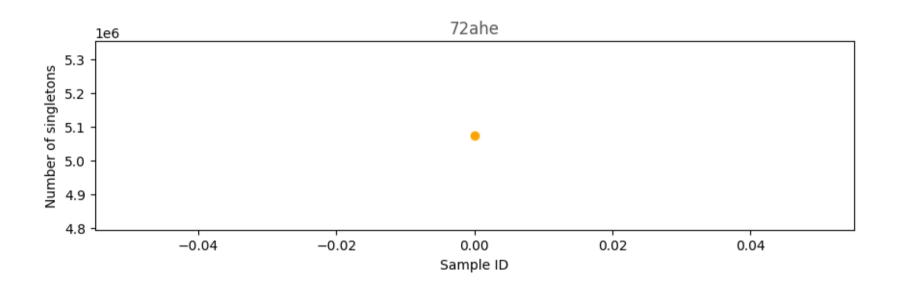
# Ts/Tv by sample



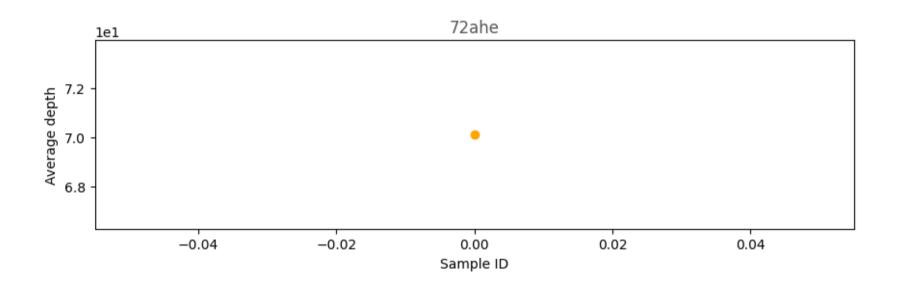
### Hets vs non-ref Homs by sample



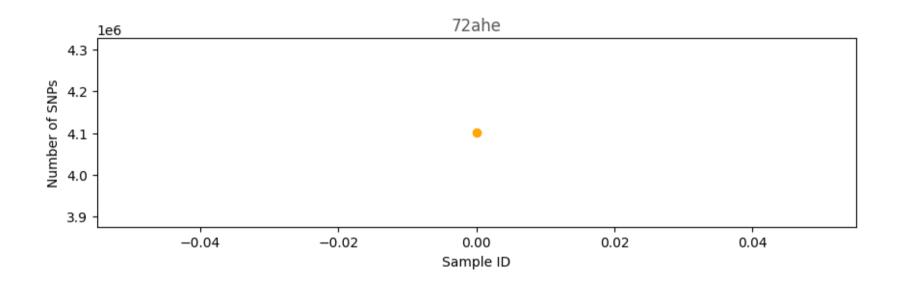
### Singletons by sample (hets and homs)



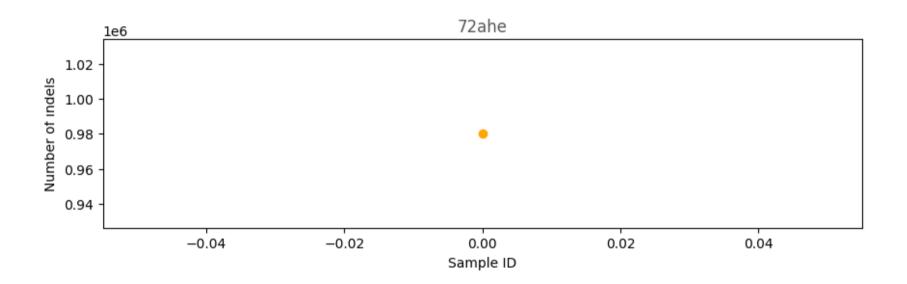
# Average depth by sample



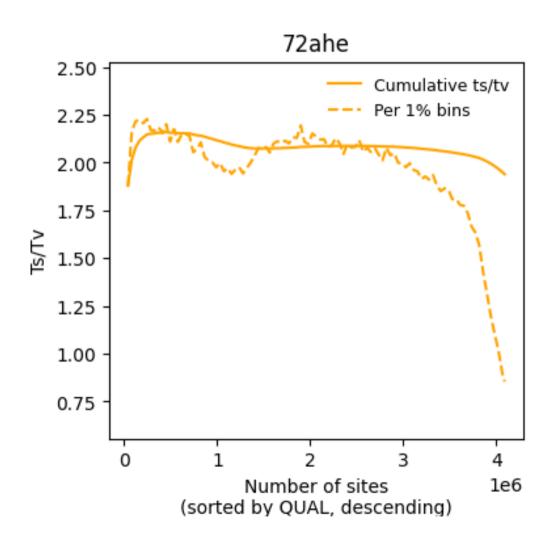
# Number of SNPs by sample



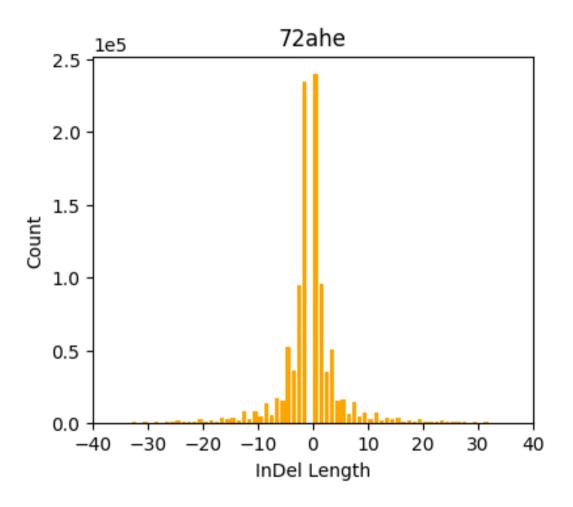
### Number of indels by sample



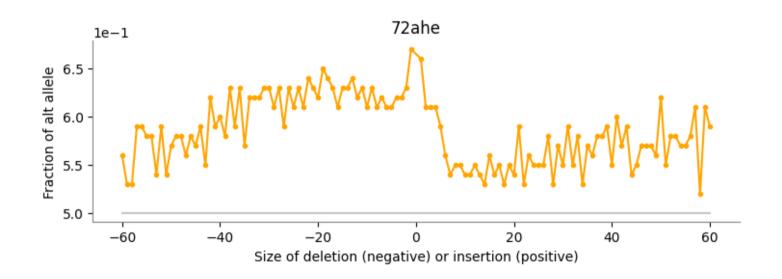
### Ts/Tv stratified by QUAL



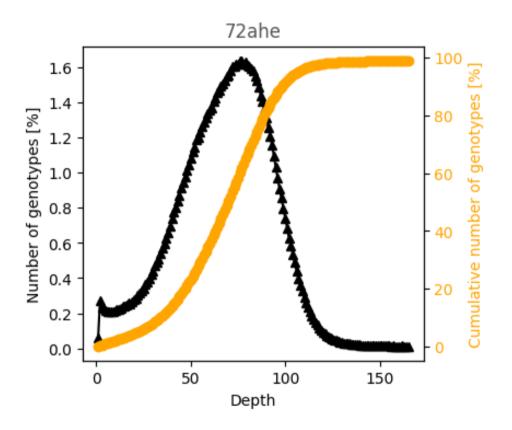
#### Indel distribution



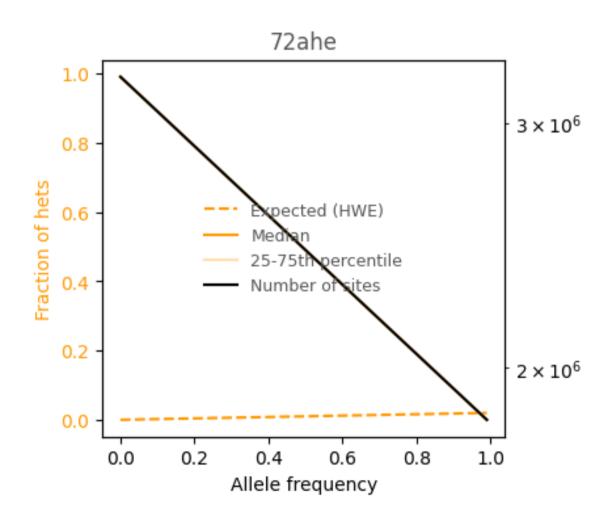
#### Fraction of alternate indel allele



# Depth distribution



### Number of HETs by AF



### Substitution types

