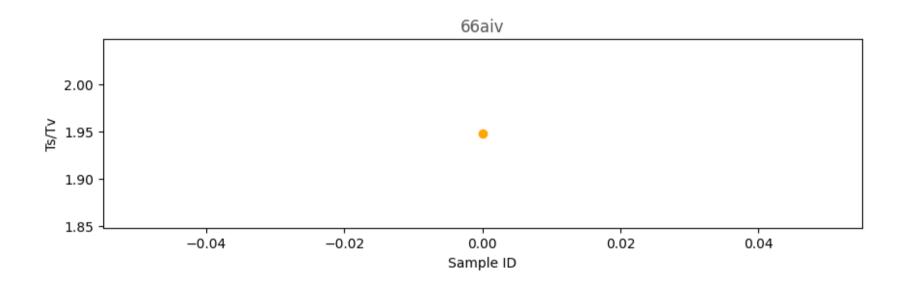
#### **Summary Numbers**

|                                  | SNPs      |       |           | indels  |      | MNPs | others |  |  |
|----------------------------------|-----------|-------|-----------|---------|------|------|--------|--|--|
| Callset                          | n         | ts/tv | (1st ALT) | n       | frm* |      |        |  |  |
| 66aiv                            | 4,069,470 | 1.95  | 1.95      | 953,236 | 1    | 0    | 0      |  |  |
| * frameshift ratio: out/(out+in) |           |       |           |         |      |      |        |  |  |

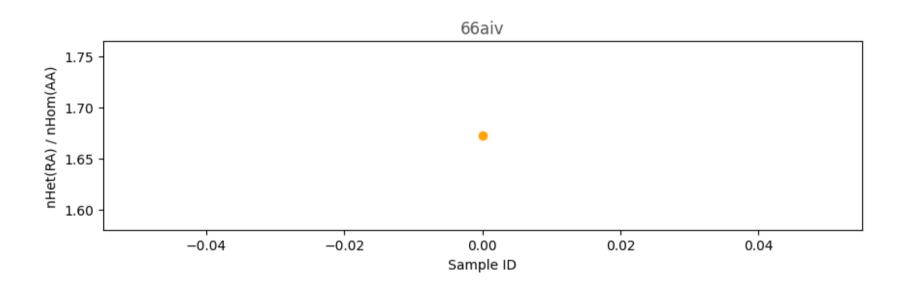
|         | singl | etons (A | multiallelic |         |       |
|---------|-------|----------|--------------|---------|-------|
| Callset | SNPs  | ts/tv    | indels       | sites   | SNPs  |
| 66aiv   | 62.6% | 1.93     | 67.7%        | 100,647 | 2,123 |

- 66aiv .. /ngc/projects2/gm/data/archive/2022/variants/snv/66aivecuf-103913369989-Normal\_B lood\_noinfo-WGS\_v1\_IlluminaDNAPCRFree\_RHGM01741-220923\_A01176\_BHTNN3DSX3-EXT\_LAB KA\_NGCWGS-NGCWGS05502\_20RKG029610\_snv\_germline\_raw.haplotype\_caller.vcf.gz

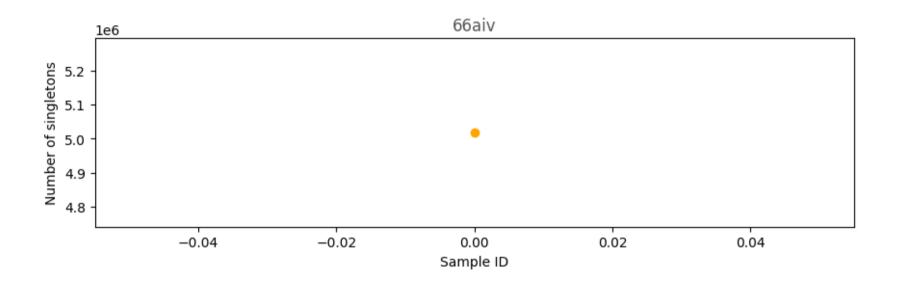
# Ts/Tv by sample



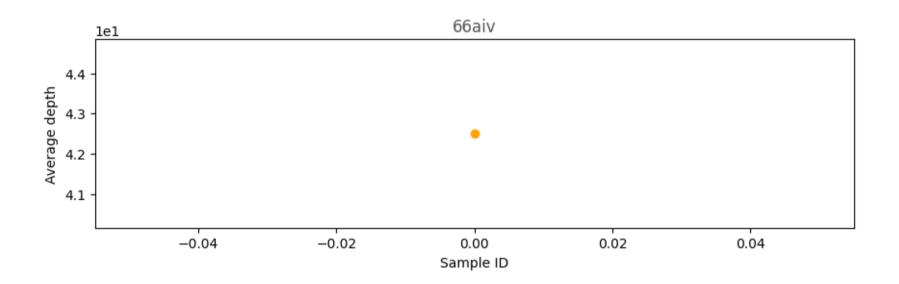
## Hets vs non-ref Homs by sample



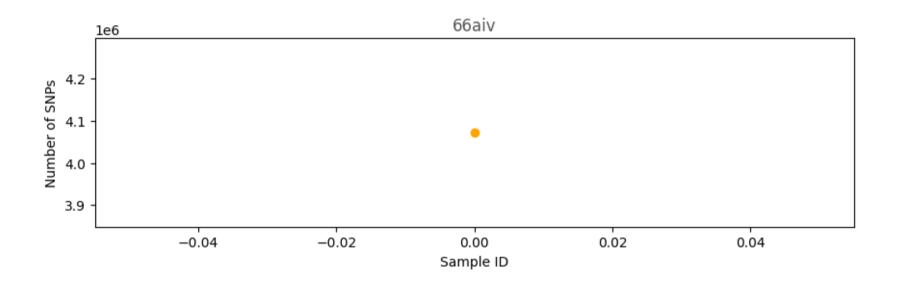
## Singletons by sample (hets and homs)



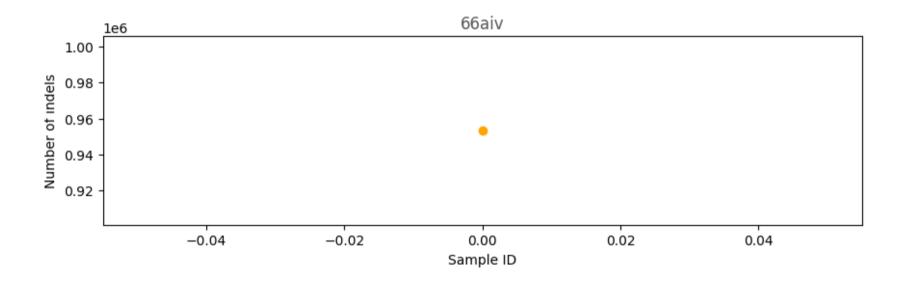
# Average depth by sample



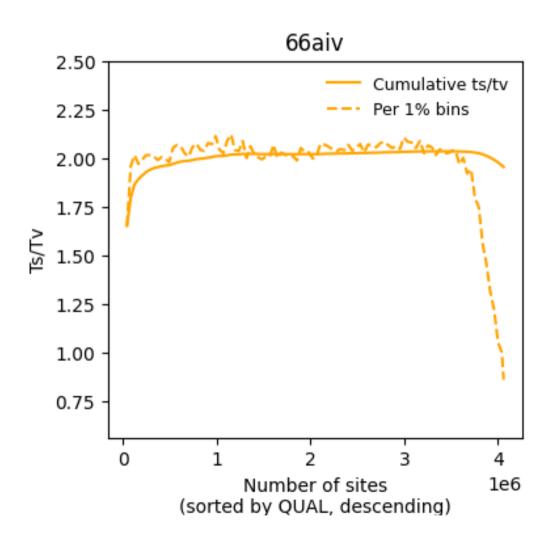
# Number of SNPs by sample



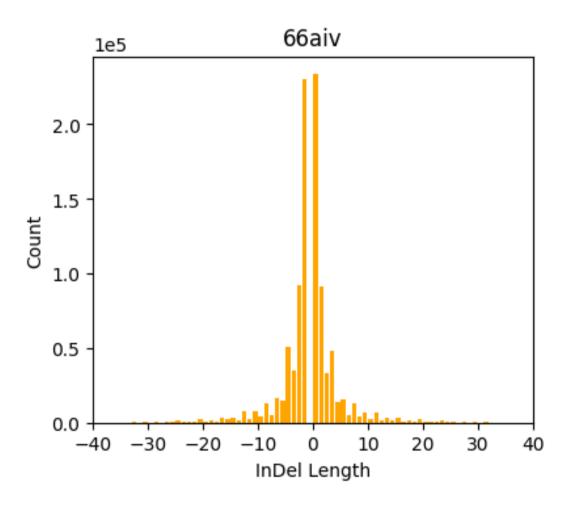
## Number of indels by sample



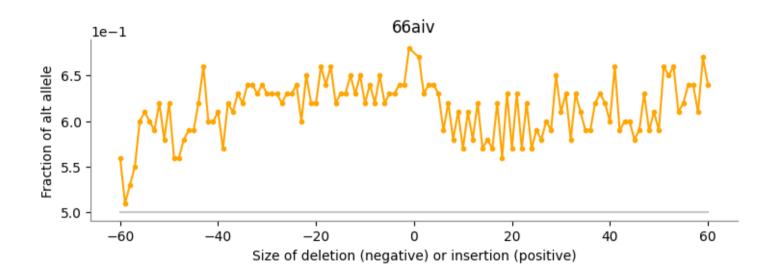
### Ts/Tv stratified by QUAL



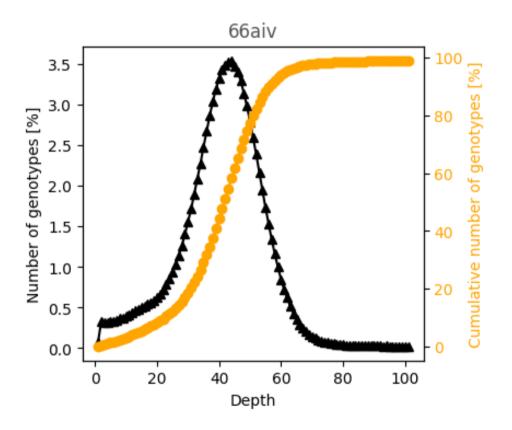
#### Indel distribution



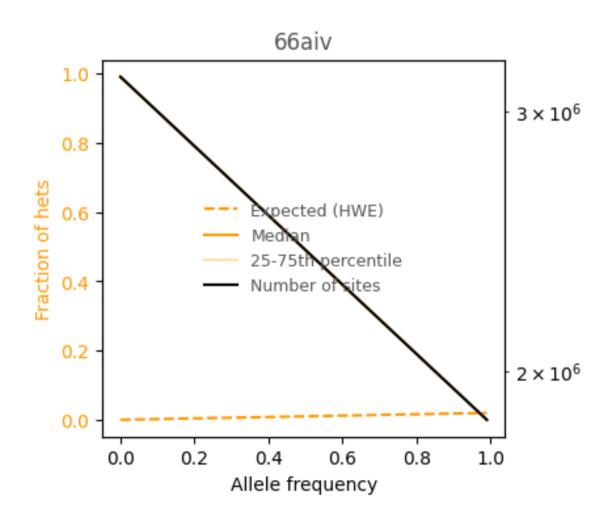
#### Fraction of alternate indel allele



# Depth distribution



#### Number of HETs by AF



### Substitution types

