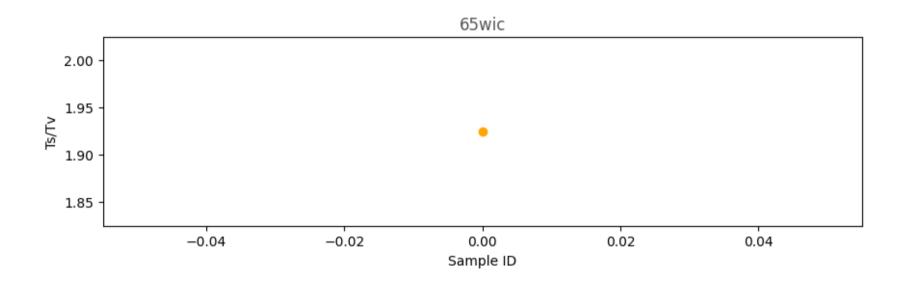
#### **Summary Numbers**

|                                  | SNPs      |       |           | indels  |      | MNPs | others |  |  |
|----------------------------------|-----------|-------|-----------|---------|------|------|--------|--|--|
| Callset                          | n         | ts/tv | (1st ALT) | n       | frm* |      |        |  |  |
| 65wic                            | 4,064,231 | 1.92  | 1.93      | 951,691 | -    | 0    | 0      |  |  |
| * frameshift ratio: out/(out+in) |           |       |           |         |      |      |        |  |  |

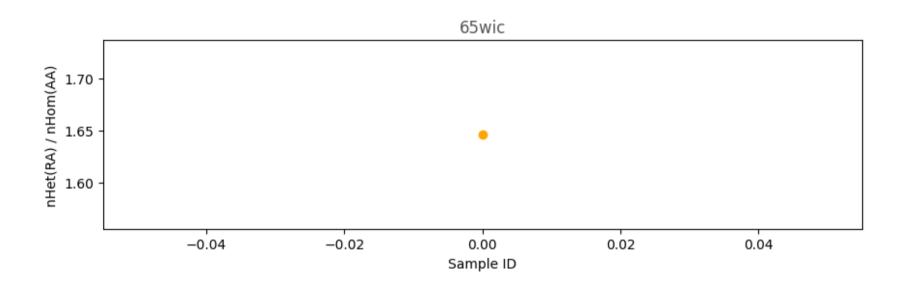
|         | singl | etons (A | multiallelic |         |       |
|---------|-------|----------|--------------|---------|-------|
| Callset | SNPs  | ts/tv    | indels       | sites   | SNPs  |
| 65wic   | 62.2% | 1.89     | 67.3%        | 102,133 | 2,104 |

- 65wic.../ngc/projects2/gm/data/archive/2022/variants/snv/65wicawnm-103755220650-Normal\_B lood\_noinfo-WGS\_v1\_IlluminaDNAPCRFree\_RHGM00201-210629\_A00559\_AHFHNHDSX2-EXT\_LAB KA\_NGCWGS-NGCWGS00117\_65wtu30b5\_snv\_germline\_raw.haplotype\_caller.vcf.gz

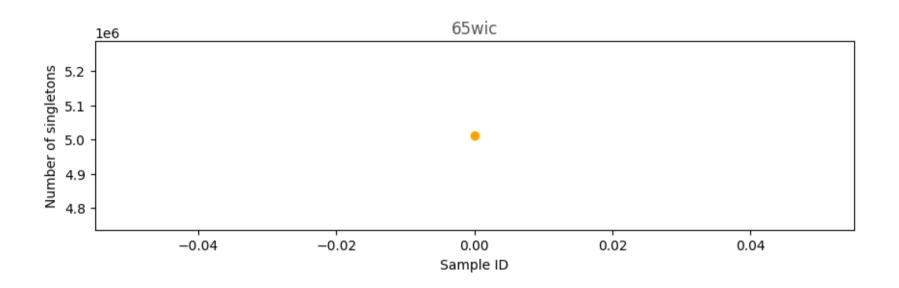
# Ts/Tv by sample



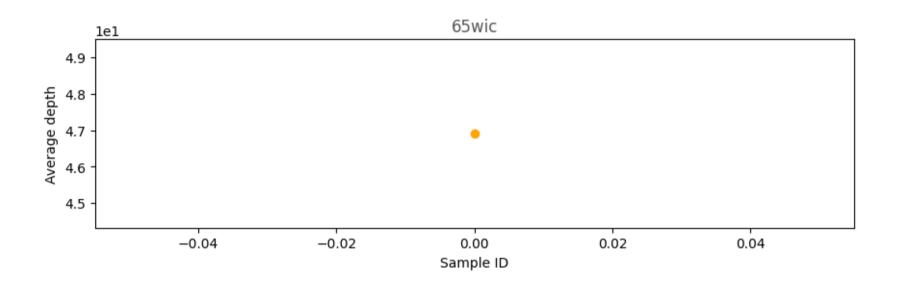
## Hets vs non-ref Homs by sample



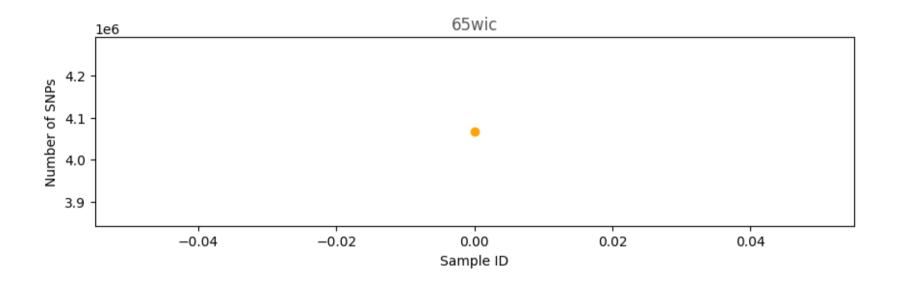
## Singletons by sample (hets and homs)



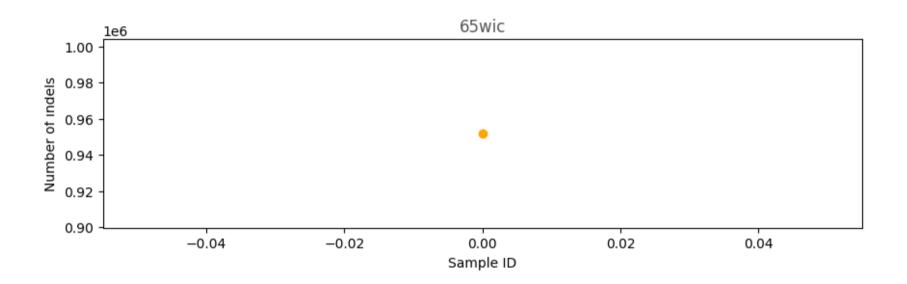
# Average depth by sample



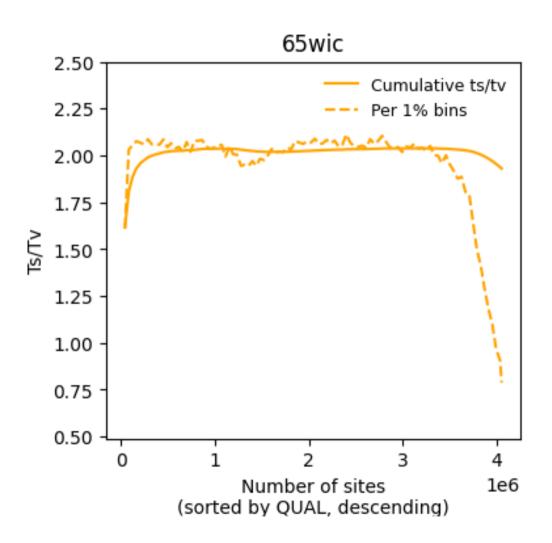
# Number of SNPs by sample



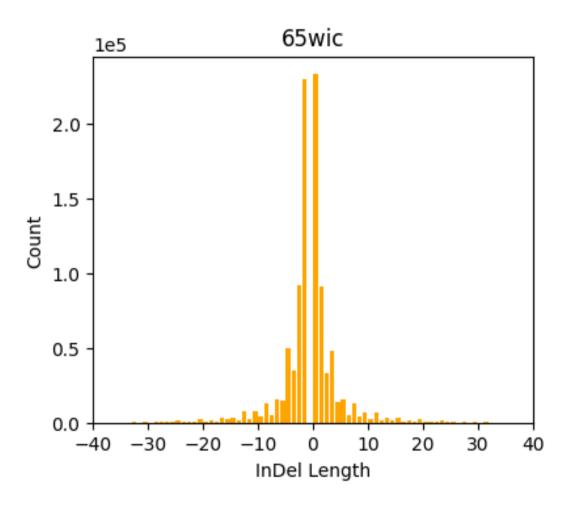
## Number of indels by sample



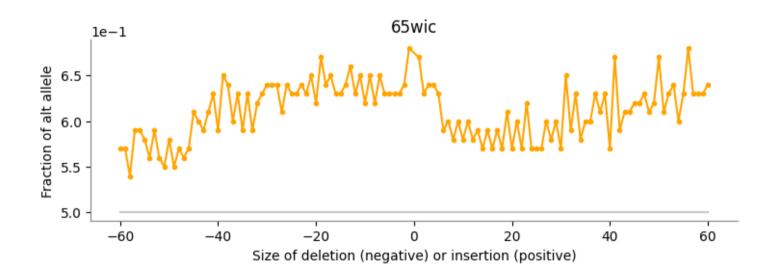
### Ts/Tv stratified by QUAL



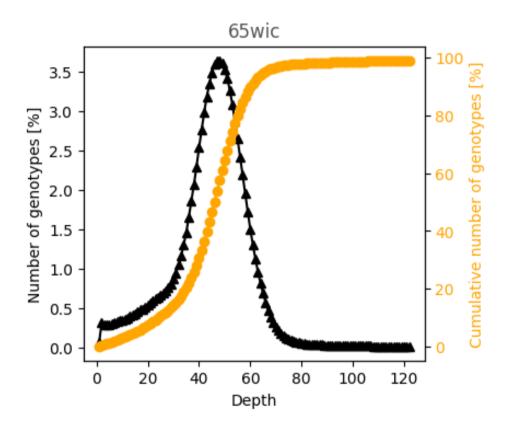
#### Indel distribution



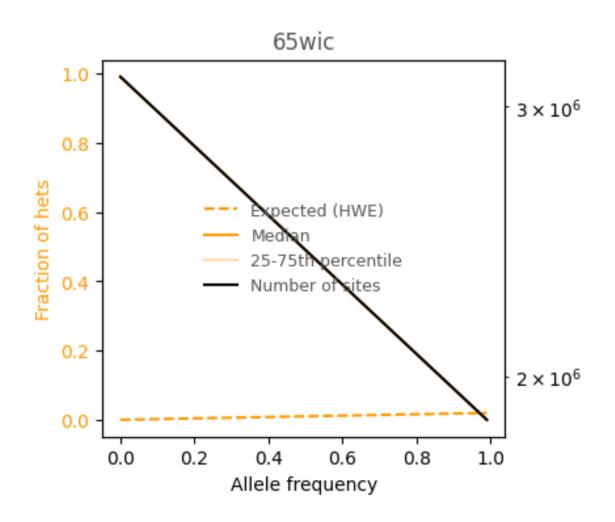
#### Fraction of alternate indel allele



# Depth distribution



### Number of HETs by AF



### Substitution types

