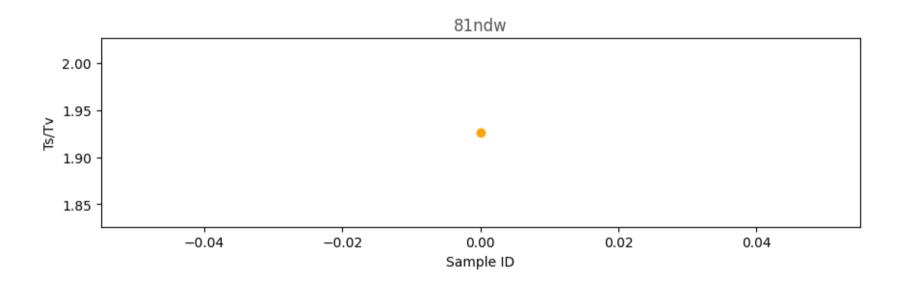
#### **Summary Numbers**

|                                  | SNPs      |       |           | indels  |      | MNPs | others |  |  |  |
|----------------------------------|-----------|-------|-----------|---------|------|------|--------|--|--|--|
| Callset                          | n         | ts/tv | (1st ALT) | n       | frm* |      |        |  |  |  |
| 81ndw                            | 4,071,785 | 1.93  | 1.93      | 947,146 | 1    | 0    | 0      |  |  |  |
| * frameshift ratio: out/(out+in) |           |       |           |         |      |      |        |  |  |  |

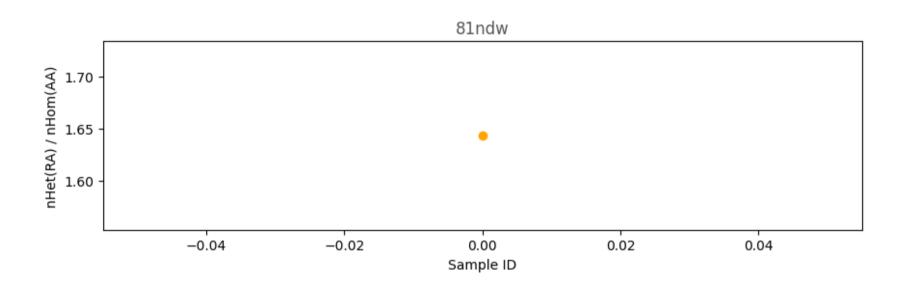
|         | singl | etons (A | multiallelic |        |       |
|---------|-------|----------|--------------|--------|-------|
| Callset | SNPs  | ts/tv    | indels       | sites  | SNPs  |
| 81ndw   | 62.2% | 1.89     | 67.0%        | 99,713 | 2,140 |

- 81ndw .. /ngc/projects2/gm/data/archive/2022/variants/snv/81ndwimum-110304078026-Normal\_B lood\_noinfo-WGS\_v1\_IlluminaDNAPCRFree\_RHGM02284-221109\_A01961\_AH3KN7DSX5-EXT\_LAB KA\_NGCWGS-NGCWGS06169\_snv\_germline\_raw.haplotype\_caller.vcf.gz

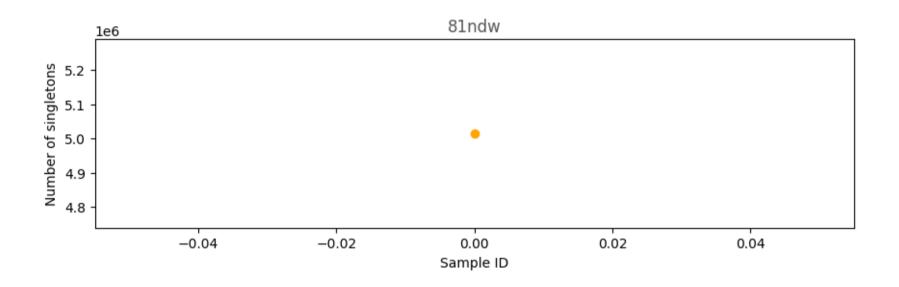
# Ts/Tv by sample



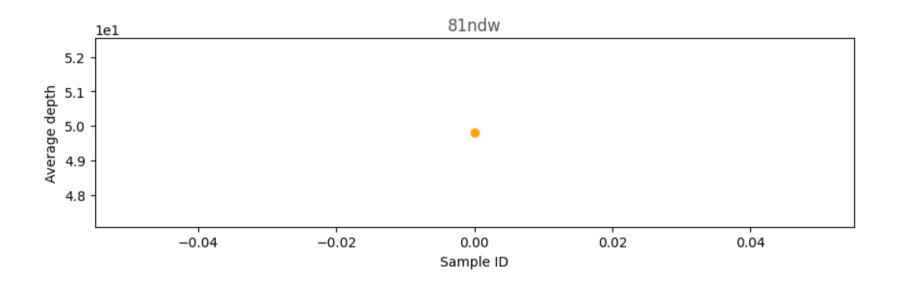
### Hets vs non-ref Homs by sample



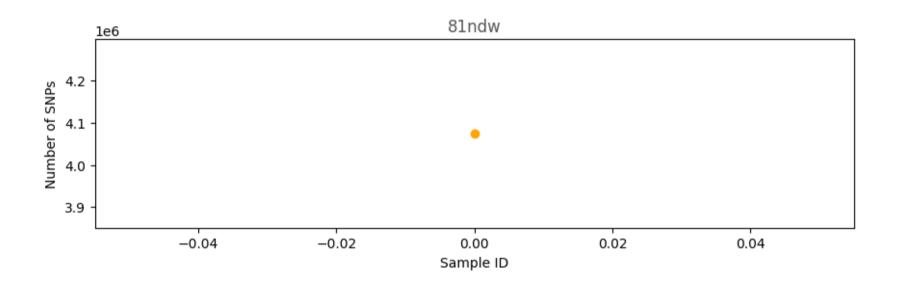
### Singletons by sample (hets and homs)



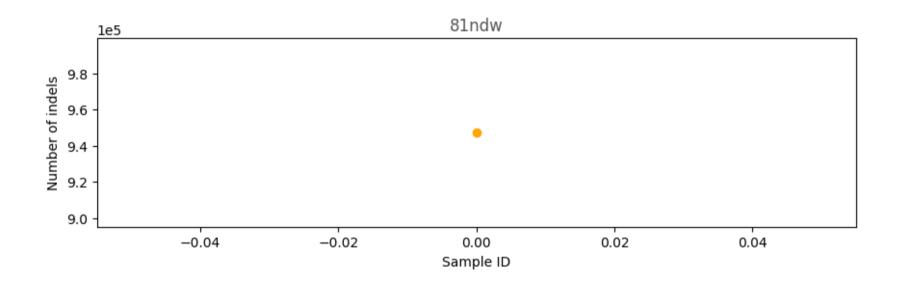
# Average depth by sample



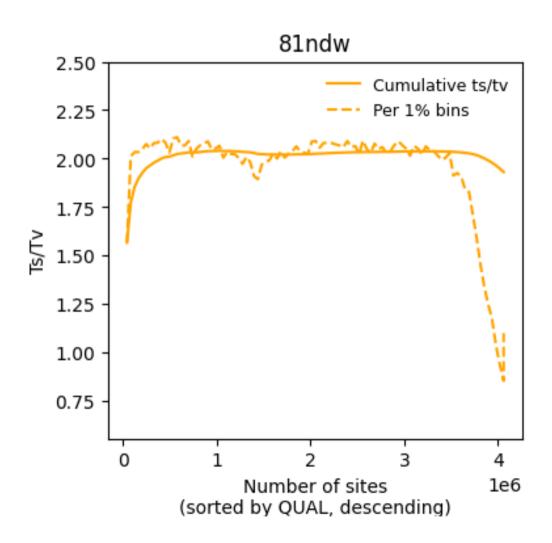
# Number of SNPs by sample



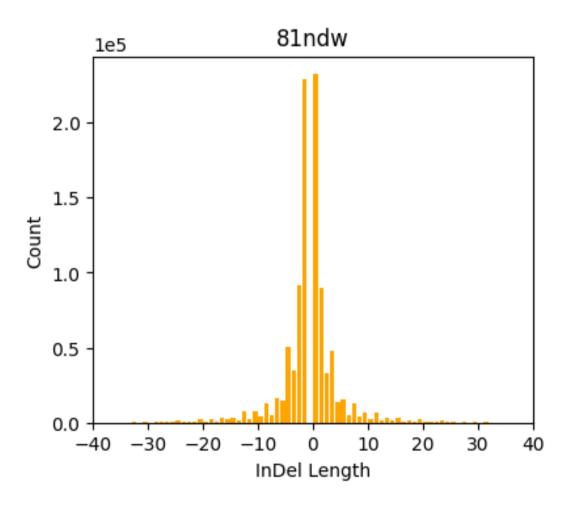
# Number of indels by sample



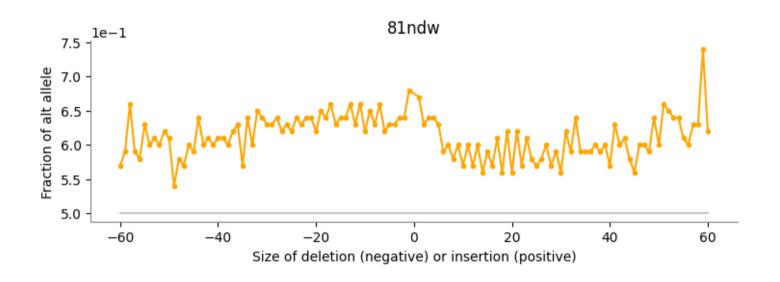
### Ts/Tv stratified by QUAL



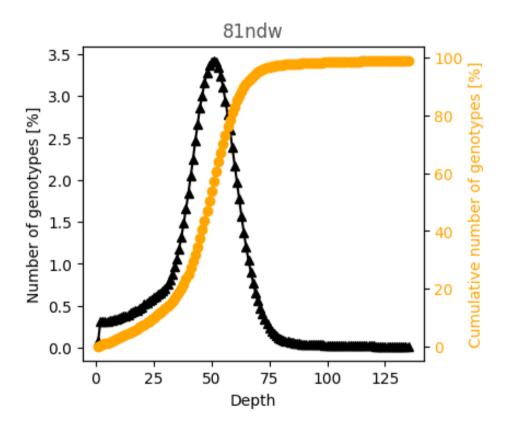
#### Indel distribution



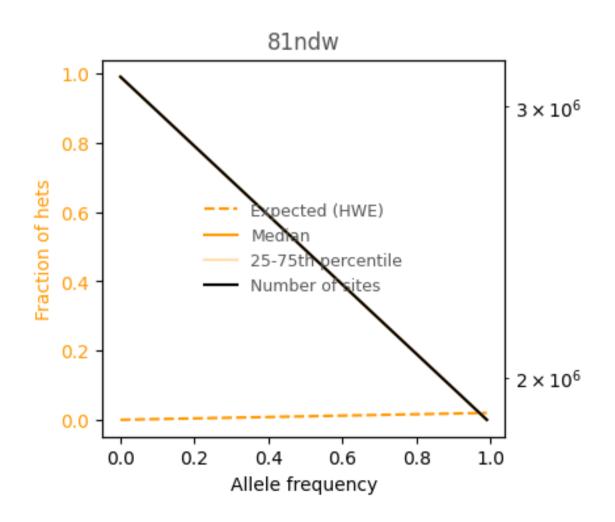
#### Fraction of alternate indel allele



# Depth distribution



### Number of HETs by AF



### Substitution types

