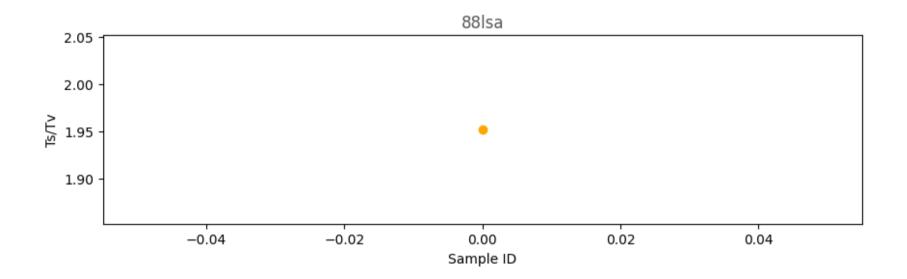
#### **Summary Numbers**

|                                  | SNPs      |       |           | indels  |      | MNPs | others |  |  |
|----------------------------------|-----------|-------|-----------|---------|------|------|--------|--|--|
| Callset                          | n         | ts/tv | (1st ALT) | n       | frm* |      |        |  |  |
| 88lsa                            | 4,034,258 | 1.95  | 1.96      | 919,092 | _    | 0    | 0      |  |  |
| * frameshift ratio: out/(out+in) |           |       |           |         |      |      |        |  |  |

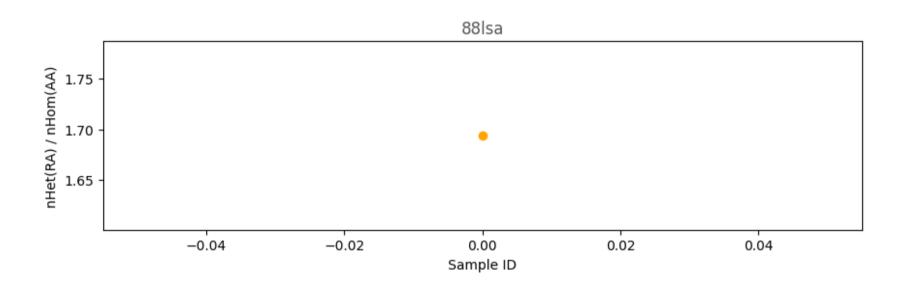
|         | singl | etons (A | multiallelic |        |       |
|---------|-------|----------|--------------|--------|-------|
| Callset | SNPs  | ts/tv    | indels       | sites  | SNPs  |
| 88lsa   | 62.9% | 1.93     | 66.2%        | 85,420 | 1,897 |

- 88lsa .. /ngc/projects2/gm/data/archive/2022/variants/snv/88lsagblf-103799143520-Normal\_B lood\_noinfo-WGS\_v1\_IlluminaDNAPCRFree\_X-211103\_A01466\_BHT575DSX2-RHGM\_LABKA\_WGS-WGS03284\_snv\_germline\_raw.haplotype\_caller.vcf.gz

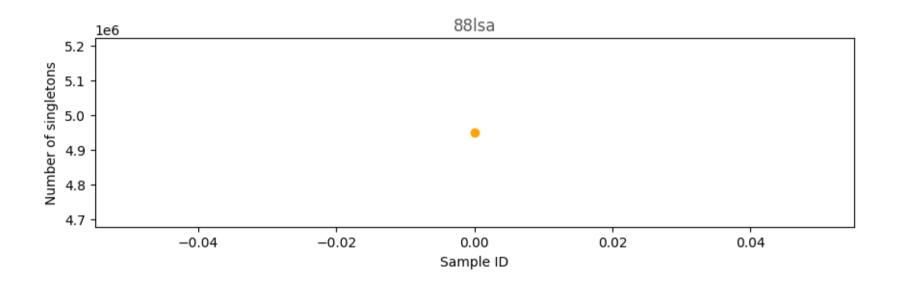
# Ts/Tv by sample



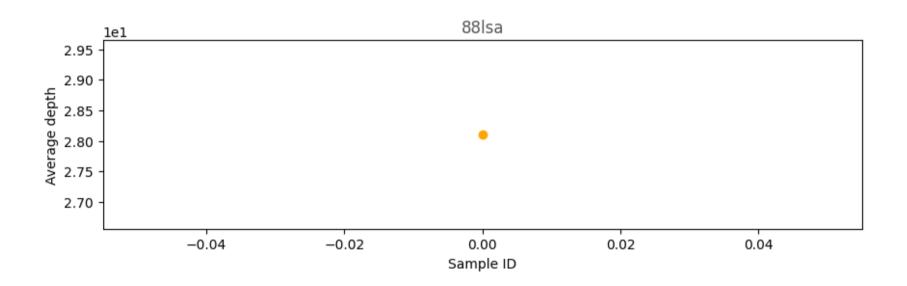
### Hets vs non-ref Homs by sample



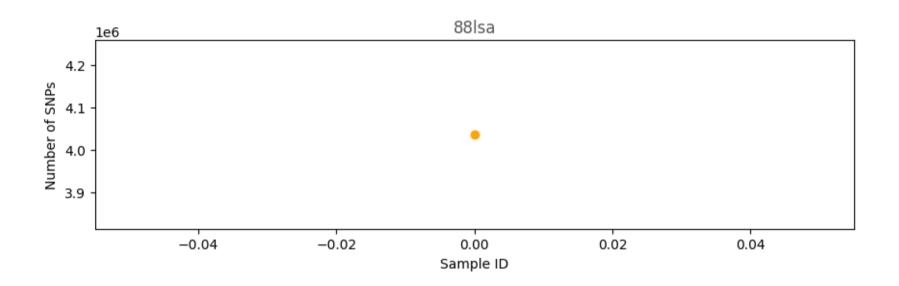
### Singletons by sample (hets and homs)



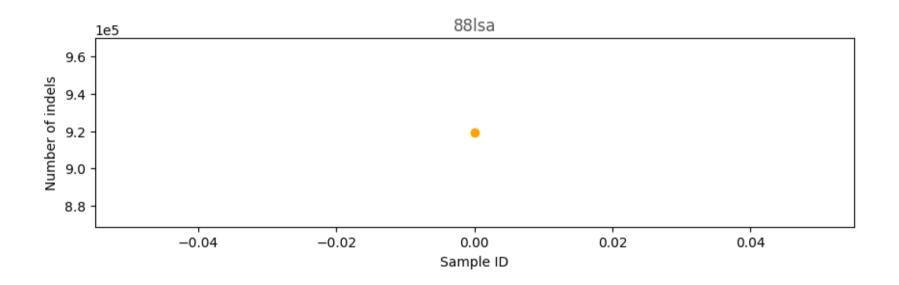
### Average depth by sample



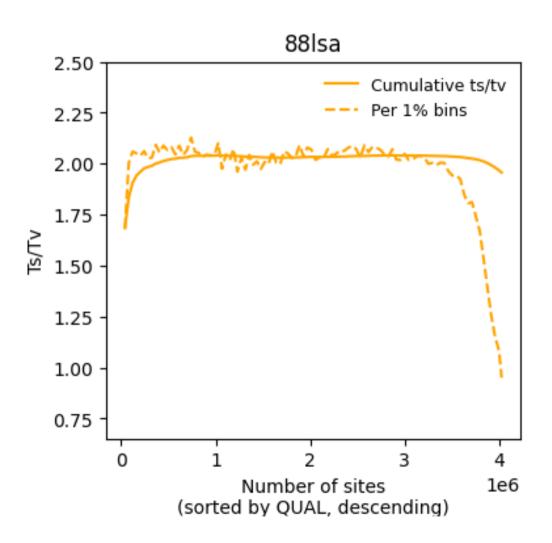
### Number of SNPs by sample



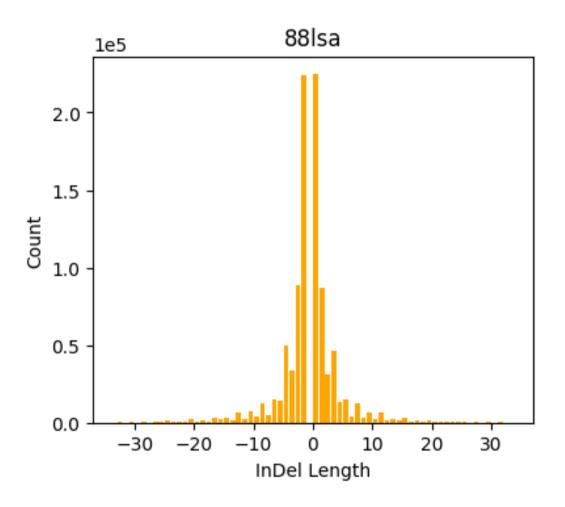
### Number of indels by sample



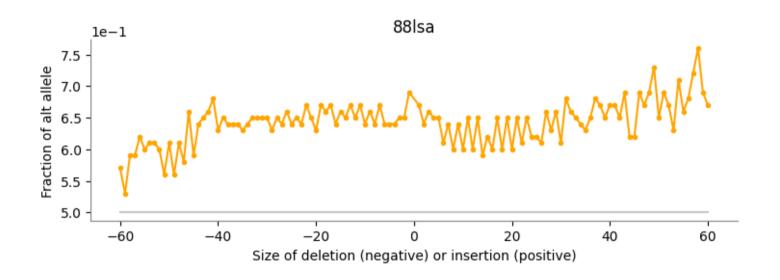
#### Ts/Tv stratified by QUAL



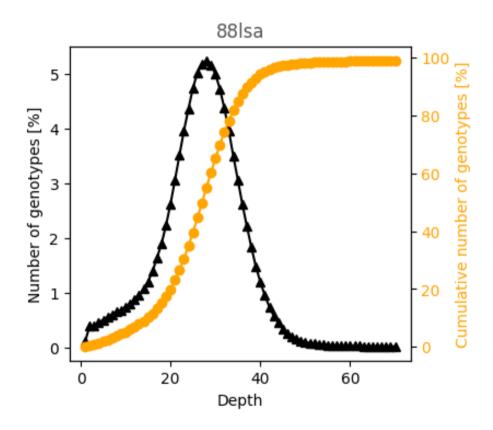
#### Indel distribution



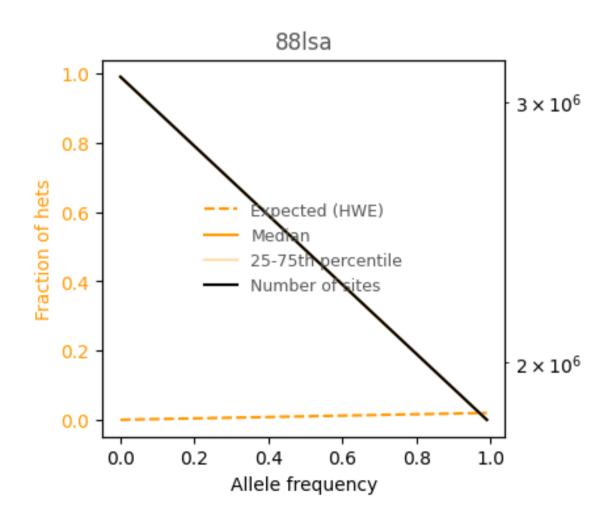
#### Fraction of alternate indel allele



## Depth distribution



#### Number of HETs by AF



### Substitution types

