Summary Numbers

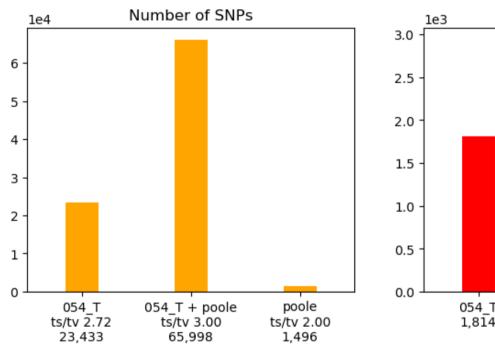
| | SNPs | | | indels | | MNPs | others | | | |
|----------------------------------|--------|-------|-----------|--------|------|------|--------|--|--|--|
| Callset | n | ts/tv | (1st ALT) | n | frm* | | | | | |
| 054_T | 23,433 | 2.72 | 2.72 | 1,814 | _ | 0 | 0 | | | |
| poole | 1,496 | 1.99 | 2.00 | 397 | _ | 0 | 0 | | | |
| 054_T + poole | 65,998 | 3.00 | 3.00 | 2,936 | _ | 0 | 0 | | | |
| * frameshift ratio: out/(out+in) | | | | | | | | | | |

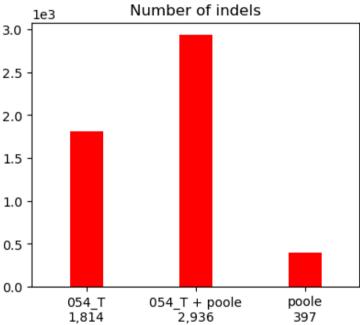
| | singl | etons (A | multiallelic | | |
|---------------|-------|----------|--------------|-------|------|
| Callset | SNPs | ts/tv | indels | sites | SNPs |
| 054_T | 0.7% | 0.69 | 8.5% | 26 | 0 |
| poole | 10.4% | 1.00 | 43.1% | 20 | 2 |
| 054_T + poole | 0.1% | 2.73 | 1.9% | 6 | 0 |

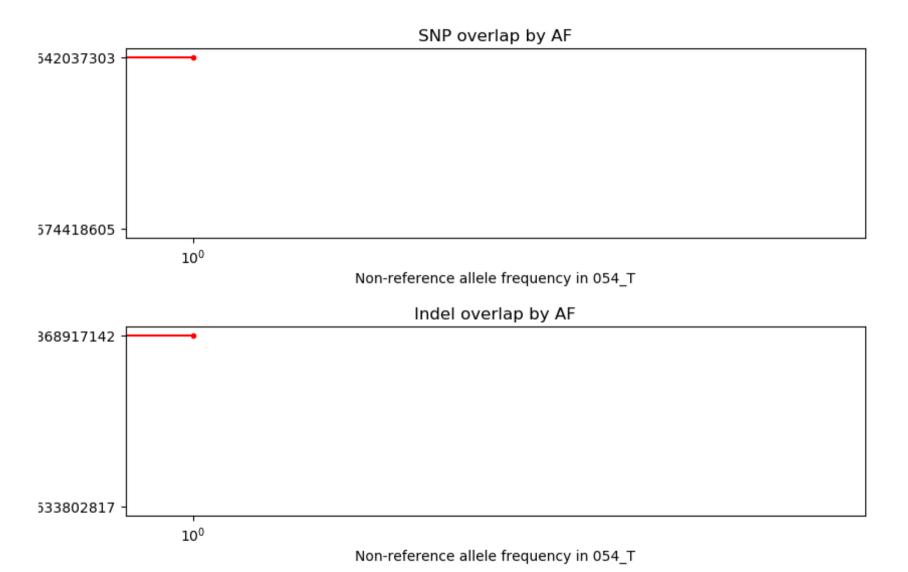
⁻ 054_T . 054_T 4.g.vcf.gz.RGsorted.HaplotypeCaller.all.snp.filtered.vcf.gz.pass.vcf.gz

⁻ poole . pooled.RGsorted.dedupped.HaplotypeCaller.all.snp.filtered.pass.vcf.gz

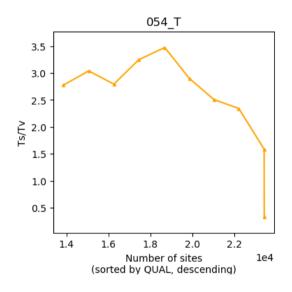
Total counts

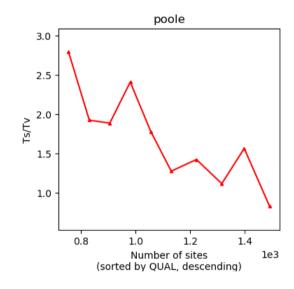


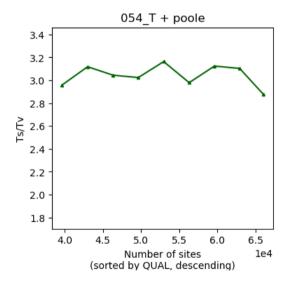




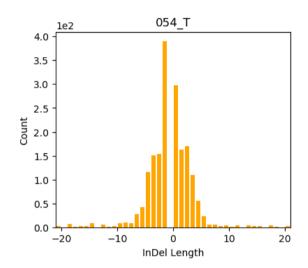
Ts/Tv stratified by QUAL

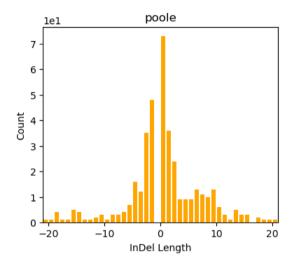


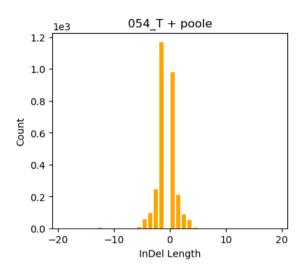




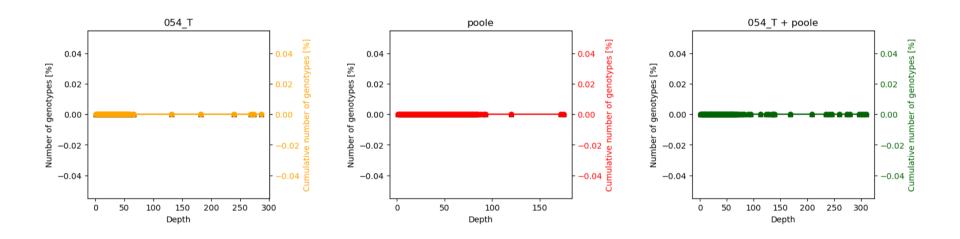
Indel distribution







Depth distribution



Substitution types

