

Feature	STRkit	LongTR	TRGT	Straglr	STRdust	Notes
Copy number output	✓	-	✓	✓	-	
Allele size confidence intervals	✓	-	✓	✓	-	
Allele consensus sequence output	✓	✓	✓	-	✓	
<i>De novo</i> proximate SNV phasing	✓ + output	-	✓	-	-	STRkit and TRGT can use heterozygous SNVs to cluster STR alleles; STRkit can output them to VCF.
Existing phased SNV incorporation	-	✓✓	-	-	-	
Haplotagged alignment file support	✓	✓	✓	-	✓	All but Straglr can use phased read data (from, e.g., WhatsHap) to call STR alleles.
Methylation handling	-	-	✓✓	-	-	
ONT read support	✓	✓	<u>Explicitly forbidden</u>	✓	-	Theoretically works on ONT data, but forbidden by software license.
Read-level data	✓	-	Partial	✓	✓	<b>STRkit</b> : JSON output with read-level peak ID + sequence data; <b>TRGT</b> : overlapping reads in BAM; <b>Straglr</b> : TSV output with read-level copy numbers; <b>STRdust</b> : read-level sequence output in VCF.
Mendelian inheritance calculation tool	✓✓	-	-	-	-	STRkit includes a tool to output loci which do not respect Mendelian inheritance in a set of trio VCFs.
Free and open-source software license	Yes (GPLv3)	Yes (GPLv2)	-	Yes (GPLv3)	Yes (MIT)	TRGT's license restricts it to be only used with PacBio sequencing data, and the software cannot be forked and subsequently re-distributed.
Multi-threading/processing	✓	-	✓	✓	✓	
Pre-built Docker image	✓✓	-	-	-	-	STRkit is available as a pre-built Docker image, which can be incorporated into pipelines/workflow definitions (e.g., Nextflow, WDL).