

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 15:48:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819017.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR1819017 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819017.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 15:48:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819017.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,770,889
Mapped reads	2,722,565 / 98.26%
Unmapped reads	48,324 / 1.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	37,253 / 1.34%
Read min/max/mean length	30 / 101 / 101.52
Duplicated reads (estimated)	1,445,097 / 52.15%
Duplication rate	42.17%
Clipped reads	2,743,894 / 99.03%

2.2. ACGT Content

Number/percentage of A's	74,417,562 / 29.54%
Number/percentage of C's	53,381,829 / 21.19%
Number/percentage of T's	69,287,970 / 27.5%
Number/percentage of G's	54,828,422 / 21.76%
Number/percentage of N's	12,378 / 0%
GC Percentage	42.95%

2.3. Coverage

Mean	0.0814

Standard Deviation	1.0568
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2.4. Mapping Quality

Mean Mapping Quality	49.16
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2.5. Mismatches and indels

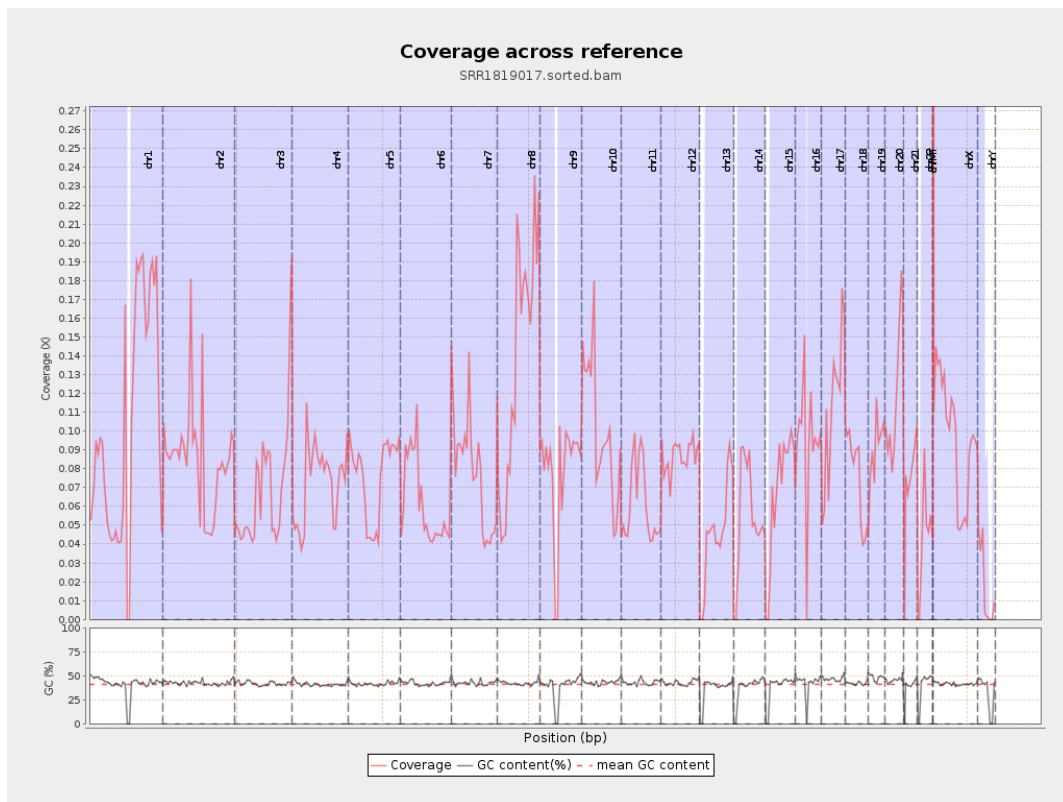
General error rate	0.67%
Mismatches	1,591,917
Insertions	41,254
Mapped reads with at least one insertion	1.47%
Deletions	79,808
Mapped reads with at least one deletion	2.87%
Homopolymer indels	40.03%

2.6. Chromosome stats

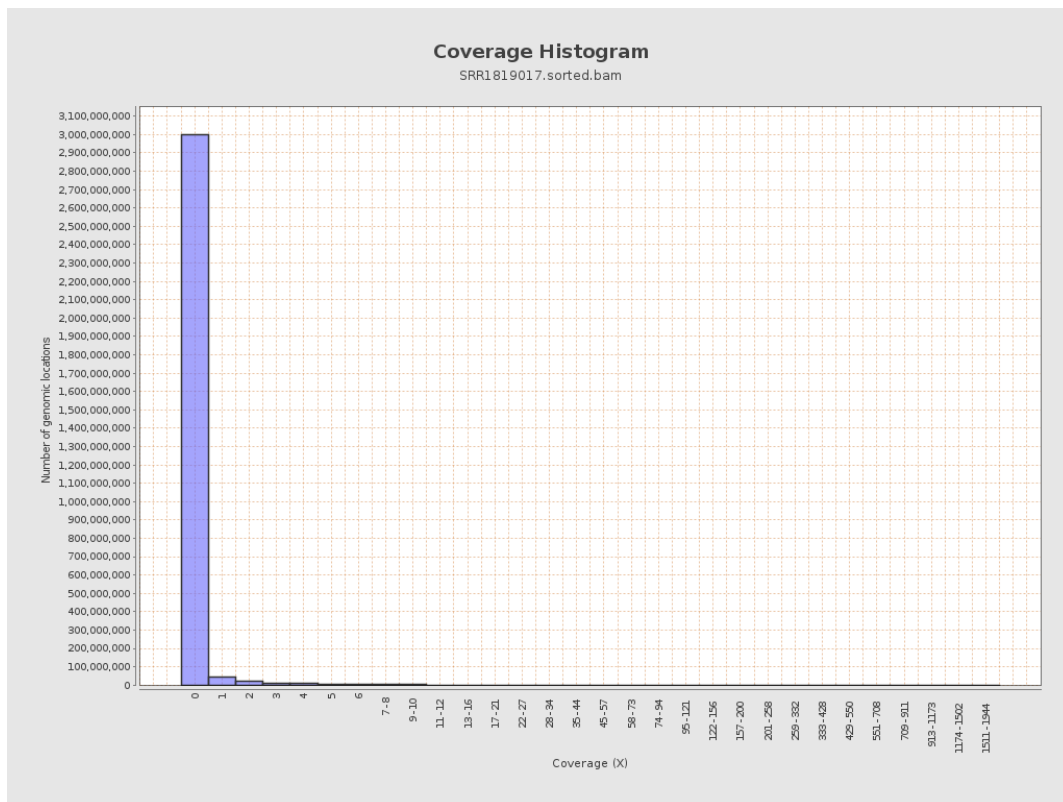
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	25735044	0.1032	1.747
chr2	243199373	20775514	0.0854	1.7247
chr3	198022430	13542228	0.0684	0.5656
chr4	191154276	13952524	0.073	0.6652
chr5	180915260	13743198	0.076	0.6247
chr6	171115067	10590596	0.0619	0.6496
chr7	159138663	12427158	0.0781	1.193

chr8	146364022	20549453	0.1404	0.9034
chr9	141213431	11043568	0.0782	0.9532
chr10	135534747	13449485	0.0992	1.3269
chr11	135006516	8215194	0.0609	0.6232
chr12	133851895	11644871	0.087	0.6582
chr13	115169878	5401331	0.0469	0.4654
chr14	107349540	5964726	0.0556	0.5541
chr15	102531392	6759620	0.0659	0.568
chr16	90354753	8458621	0.0936	1.3752
chr17	81195210	9071156	0.1117	0.8347
chr18	78077248	5886600	0.0754	1.0683
chr19	59128983	5377421	0.0909	1.6702
chr20	63025520	7564706	0.12	0.8391
chr21	48129895	3591681	0.0746	0.6708
chr22	51304566	2179798	0.0425	0.5175
chrMT	16571	38775	2.3399	3.2637
chrX	155270560	15103372	0.0973	0.8118
chrY	59373566	1014493	0.0171	1.3148

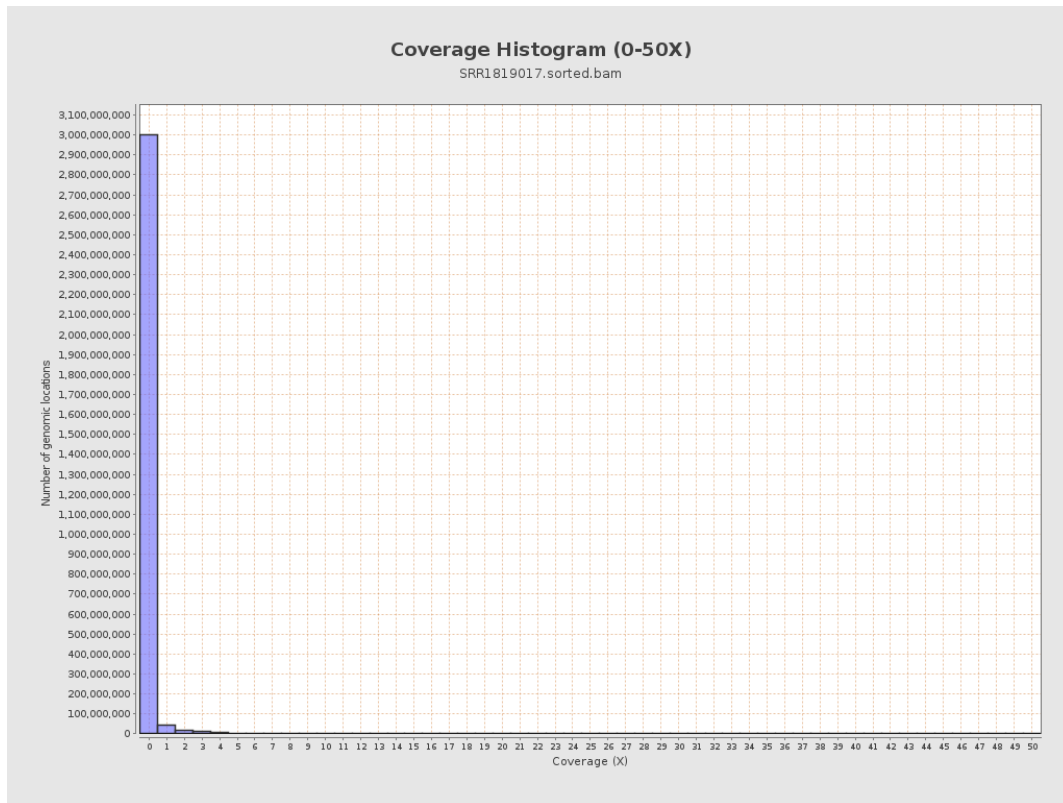
3. Results : Coverage across reference



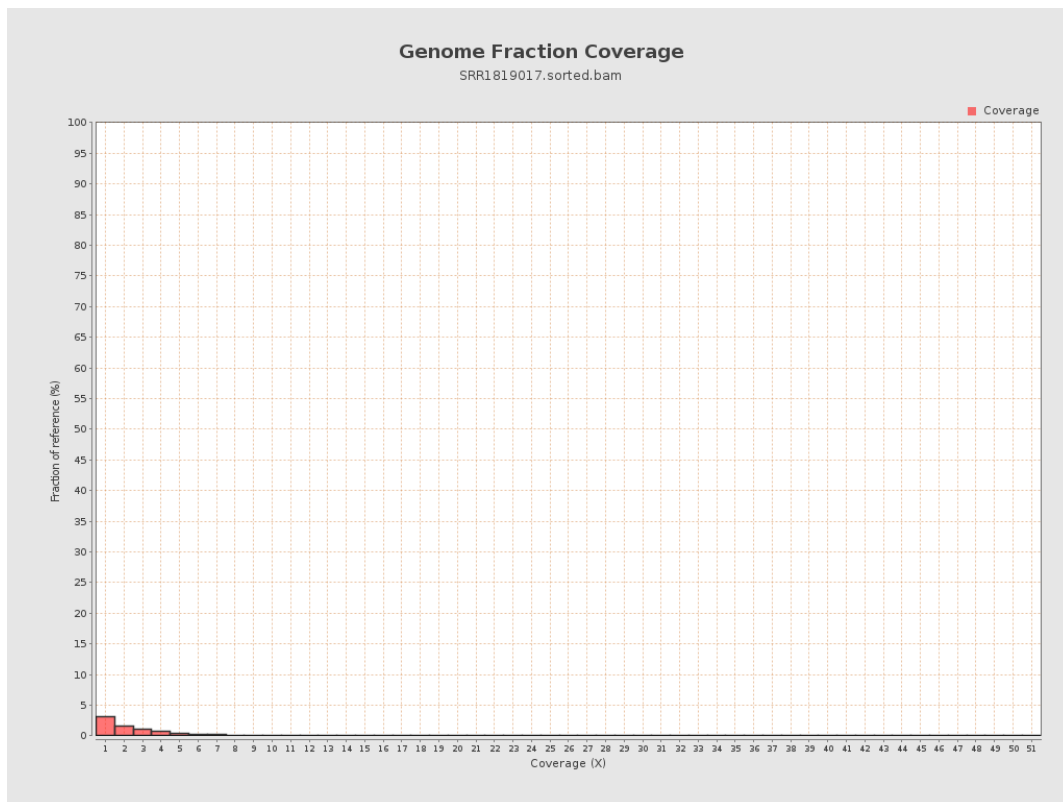
4. Results : Coverage Histogram



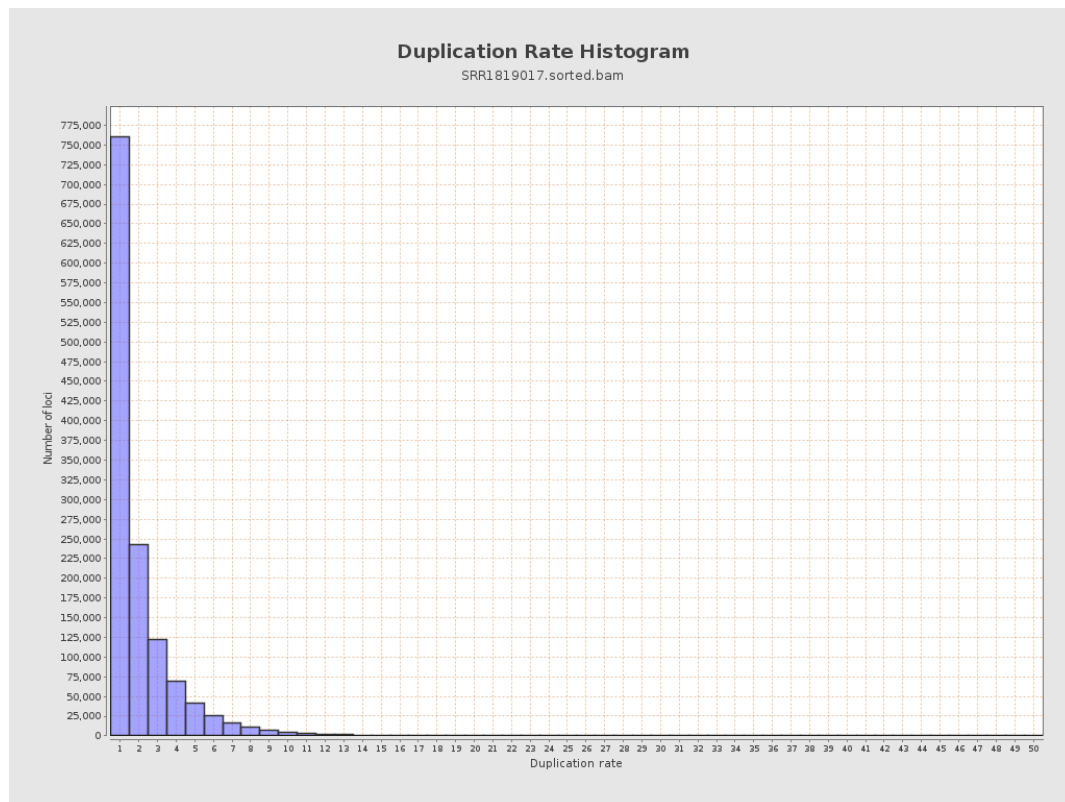
5. Results : Coverage Histogram (0-50X)



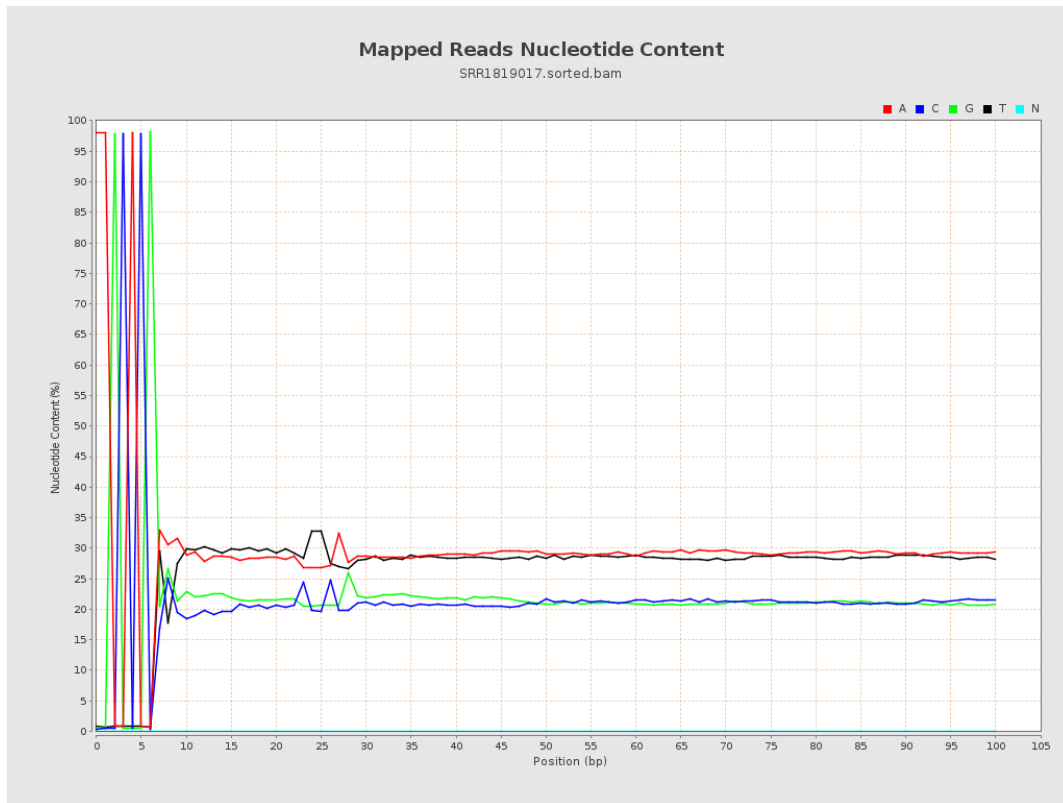
6. Results : Genome Fraction Coverage



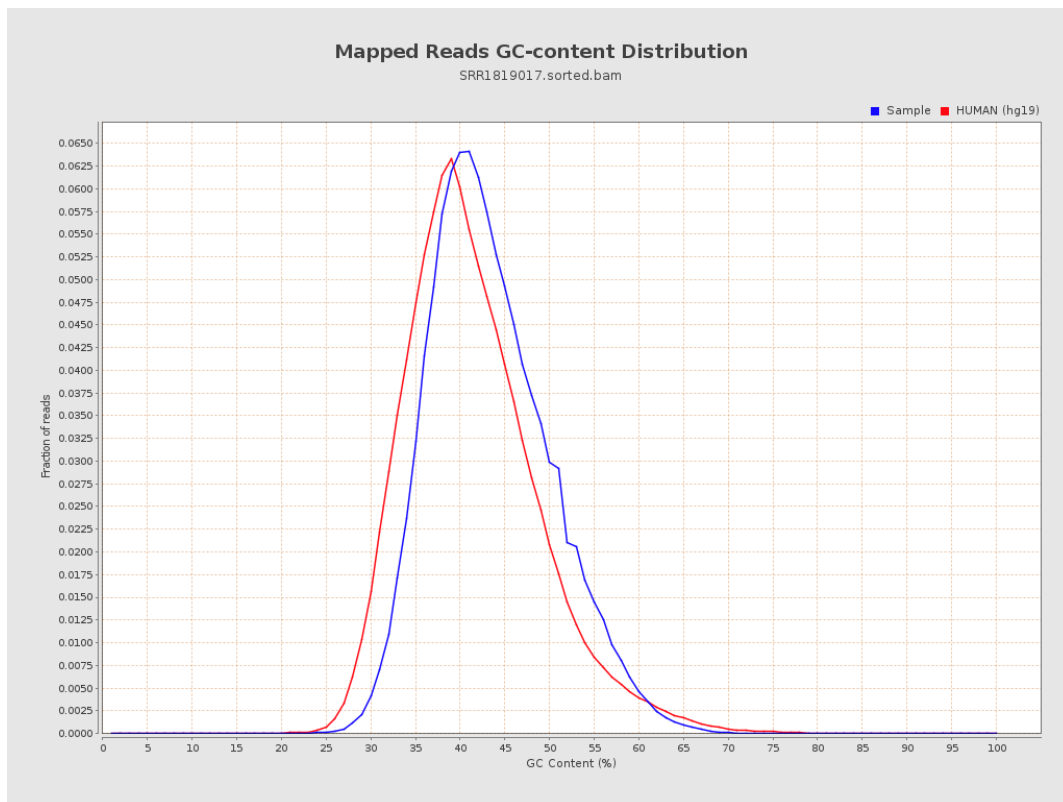
7. Results : Duplication Rate Histogram



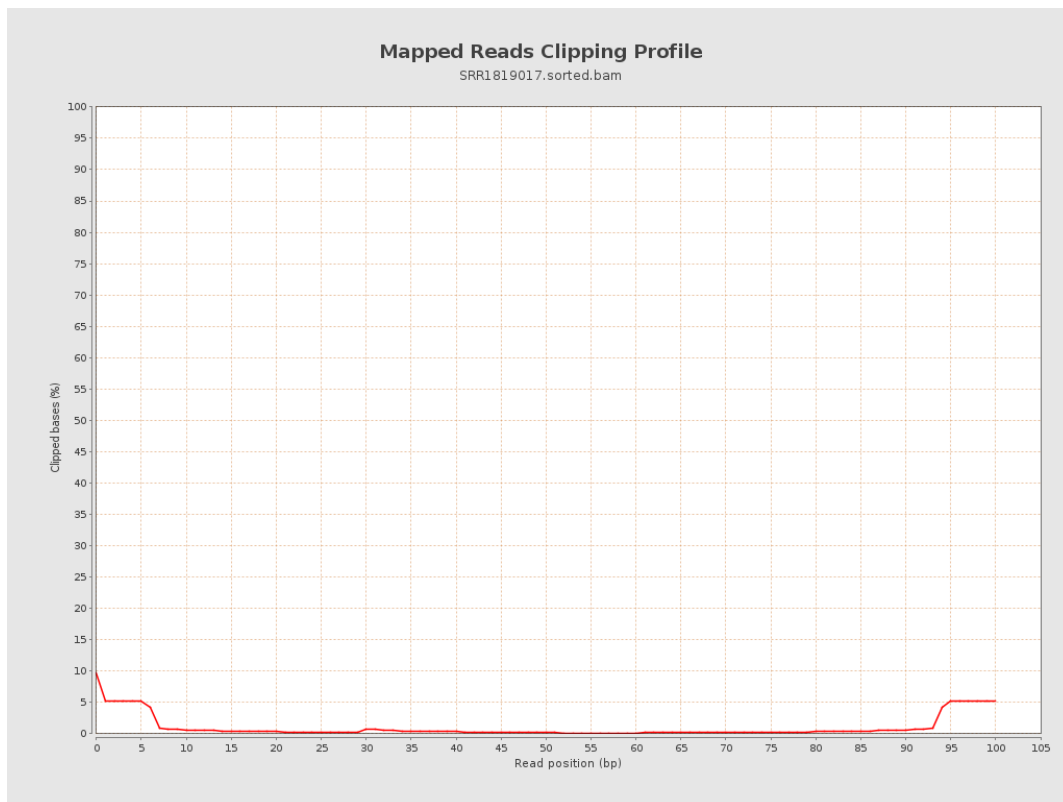
8. Results : Mapped Reads Nucleotide Content



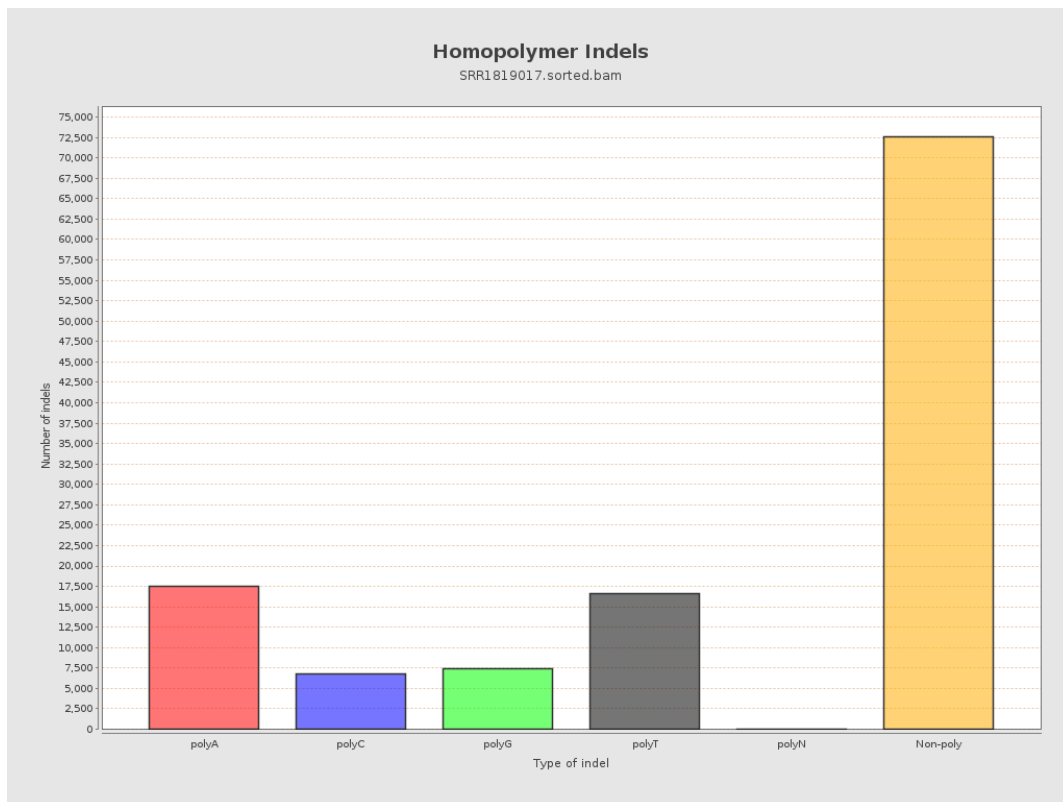
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

