

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/20 06:29:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618646.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_SRR618646 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618646.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Jan 20 06:29:29 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618646.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	101,279,821
Mapped reads	95,490,822 / 94.28%
Unmapped reads	5,788,999 / 5.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	337,347 / 0.33%
Read min/max/mean length	30 / 100 / 100.12
Duplicated reads (estimated)	79,235,377 / 78.23%
Duplication rate	63.54%
Clipped reads	14,612,093 / 14.43%

2.2. ACGT Content

Number/percentage of A's	2,461,898,581 / 26.79%
Number/percentage of C's	2,159,940,082 / 23.51%
Number/percentage of T's	2,786,315,067 / 30.33%
Number/percentage of G's	1,779,478,688 / 19.37%
Number/percentage of N's	445,387 / 0%
GC Percentage	42.88%

2.3. Coverage

Mean	2.9703

Standard Deviation	91.7895
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2.4. Mapping Quality

Mean Mapping Quality	49.61
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2.5. Mismatches and indels

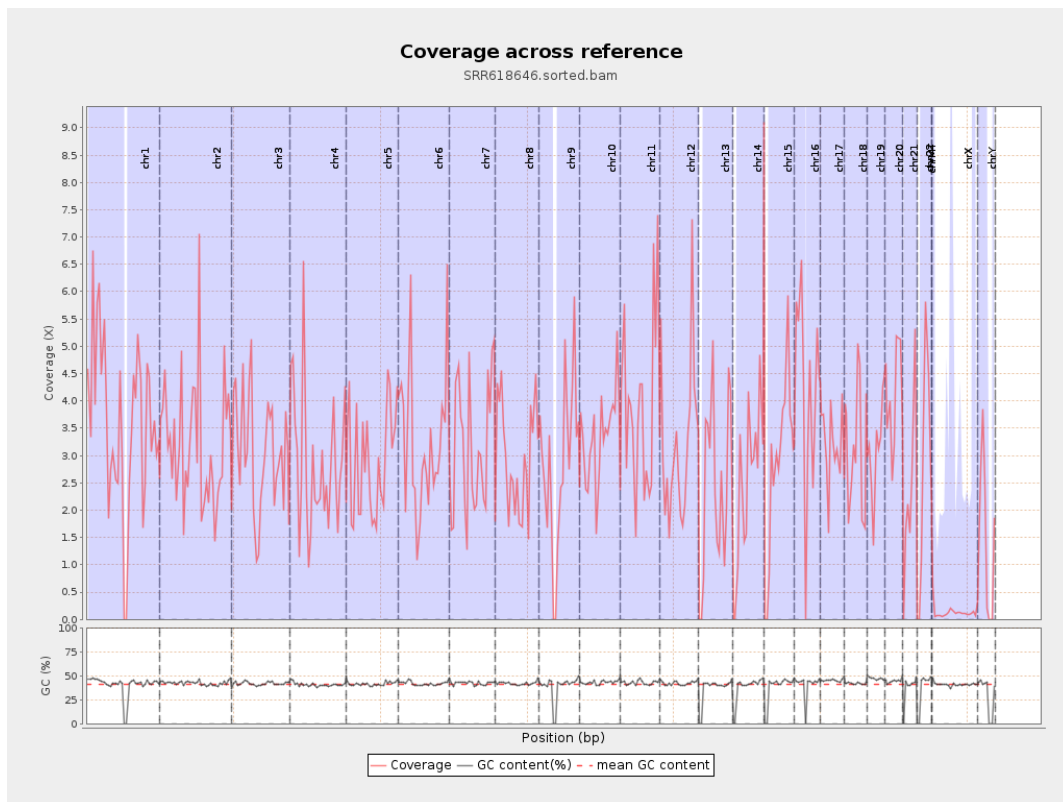
General error rate	0.93%
Mismatches	82,327,233
Insertions	1,785,907
Mapped reads with at least one insertion	1.83%
Deletions	4,305,414
Mapped reads with at least one deletion	4.39%
Homopolymer indels	50.17%

2.6. Chromosome stats

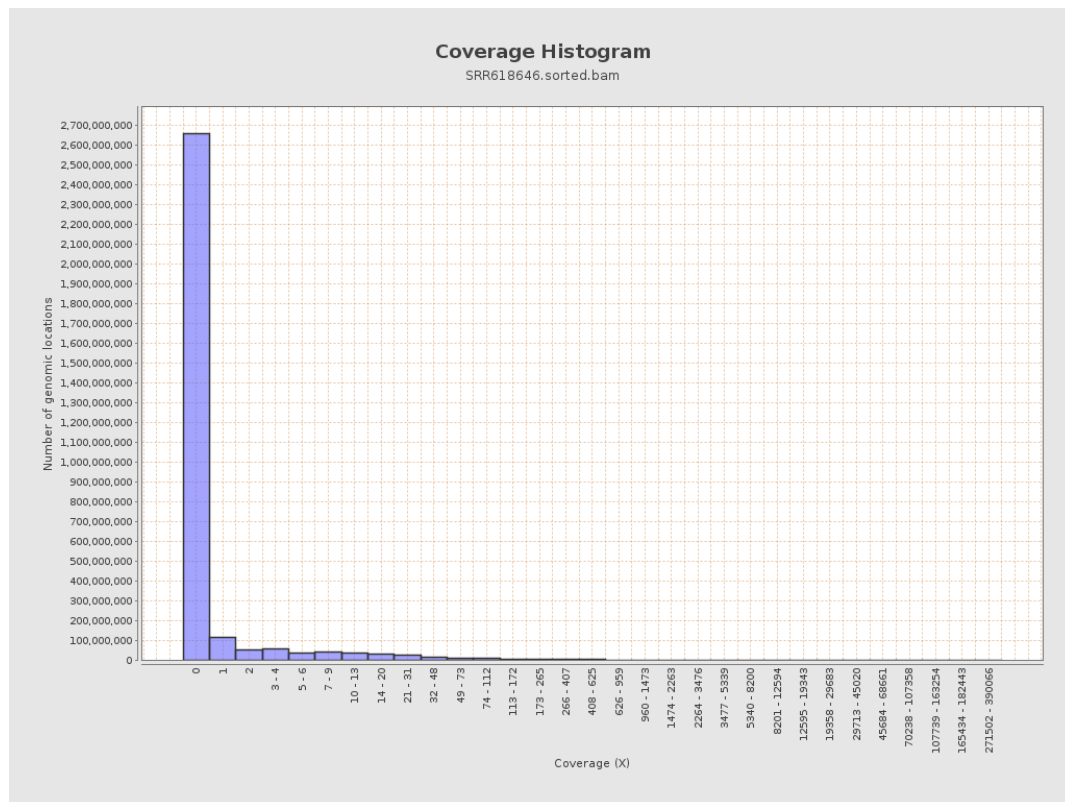
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	893791194	3.5859	59.6691
chr2	243199373	779537453	3.2053	115.2376
chr3	198022430	608701669	3.0739	47.8003
chr4	191154276	540046677	2.8252	209.755
chr5	180915260	529288780	2.9256	53.9858
chr6	171115067	558717360	3.2652	46.1996
chr7	159138663	499628502	3.1396	58.4979

chr8	146364022	435173024	2.9732	52.8903
chr9	141213431	403072786	2.8544	44.9452
chr10	135534747	459510484	3.3904	79.5323
chr11	135006516	525911502	3.8955	63.5565
chr12	133851895	426243778	3.1844	235.6548
chr13	115169878	281614679	2.4452	42.398
chr14	107349540	272098163	2.5347	38.4615
chr15	102531392	291621807	2.8442	45.1606
chr16	90354753	373300938	4.1315	75.3676
chr17	81195210	257784654	3.1749	45.2883
chr18	78077248	245271213	3.1414	46.4114
chr19	59128983	182040789	3.0787	51.9955
chr20	63025520	260094916	4.1268	48.3533
chr21	48129895	118921272	2.4708	49.208
chr22	51304566	141167556	2.7516	45.4761
chrMT	16571	28090	1.6951	8.3355
chrX	155270560	19221948	0.1238	11.4261
chrY	59373566	92373700	1.5558	51.8819

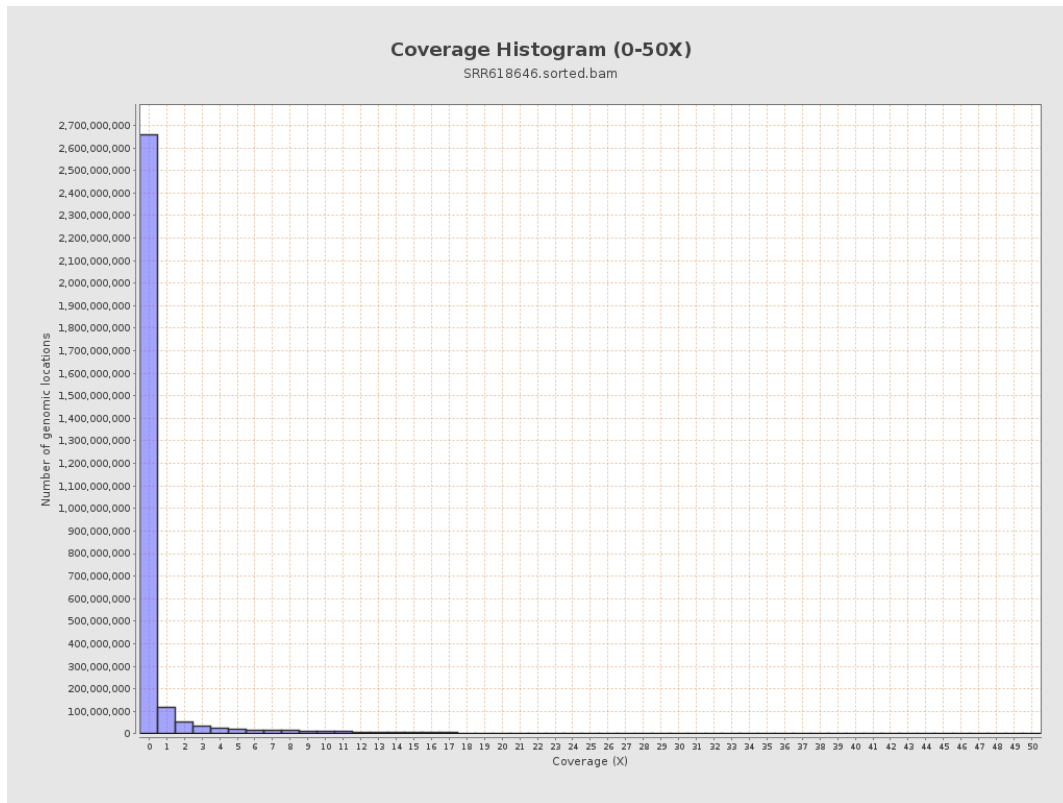
3. Results : Coverage across reference



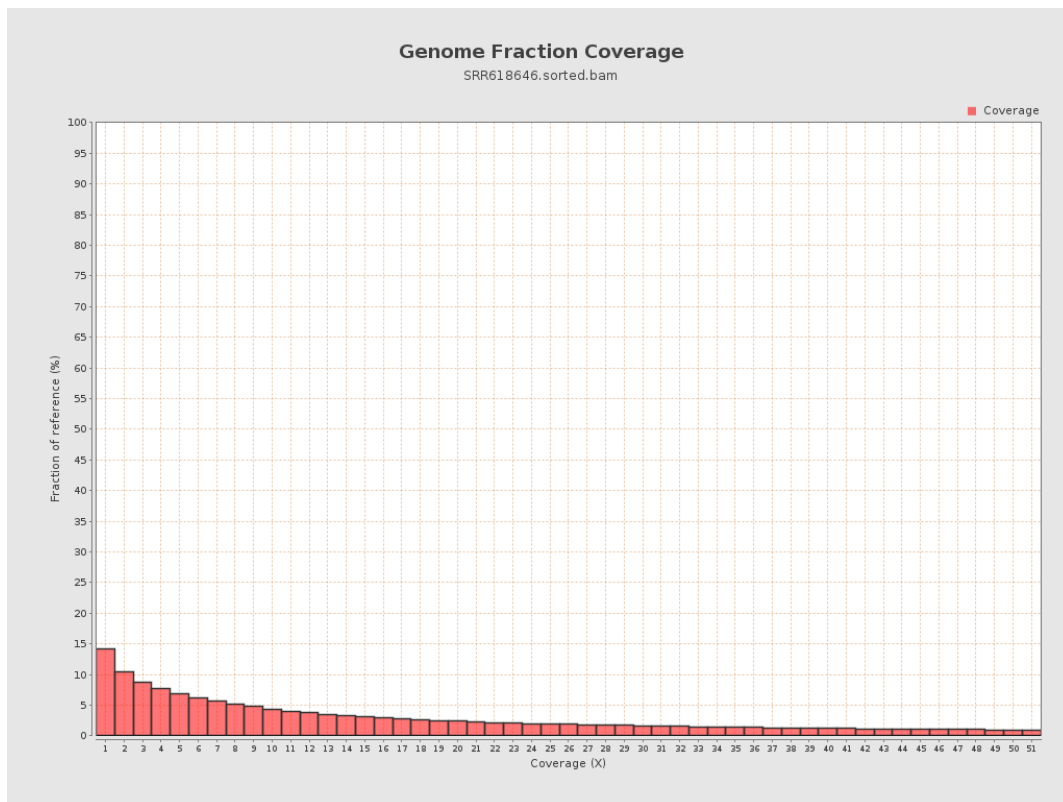
4. Results : Coverage Histogram



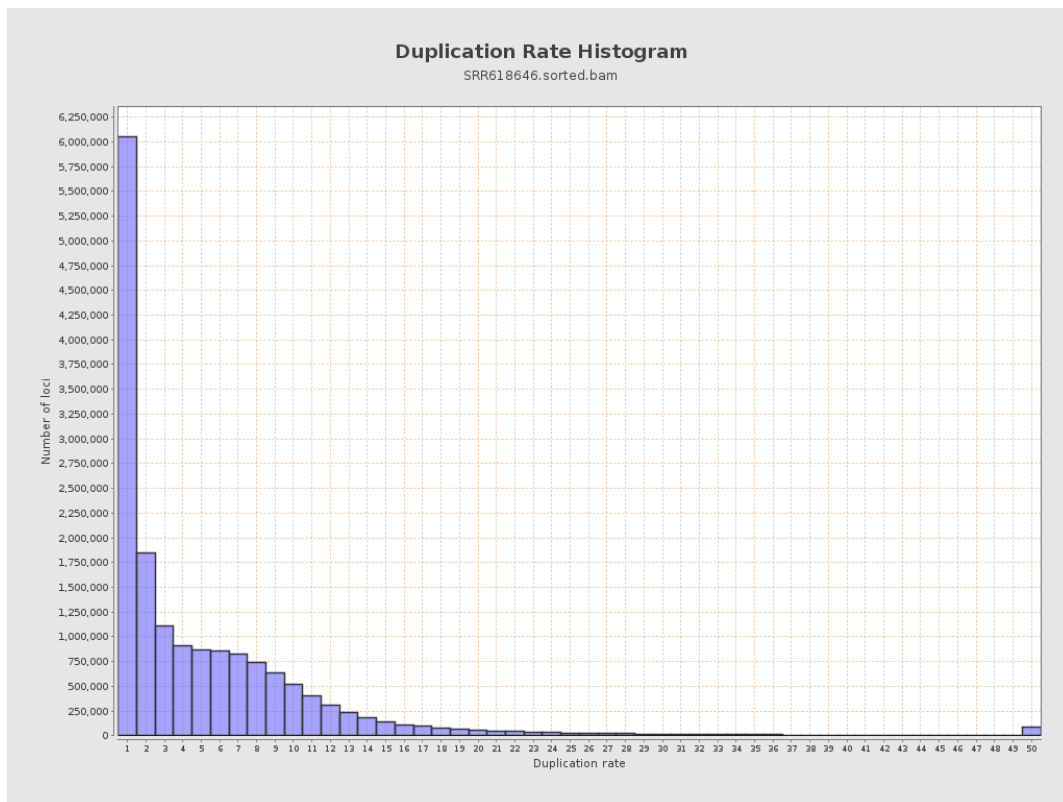
5. Results : Coverage Histogram (0-50X)



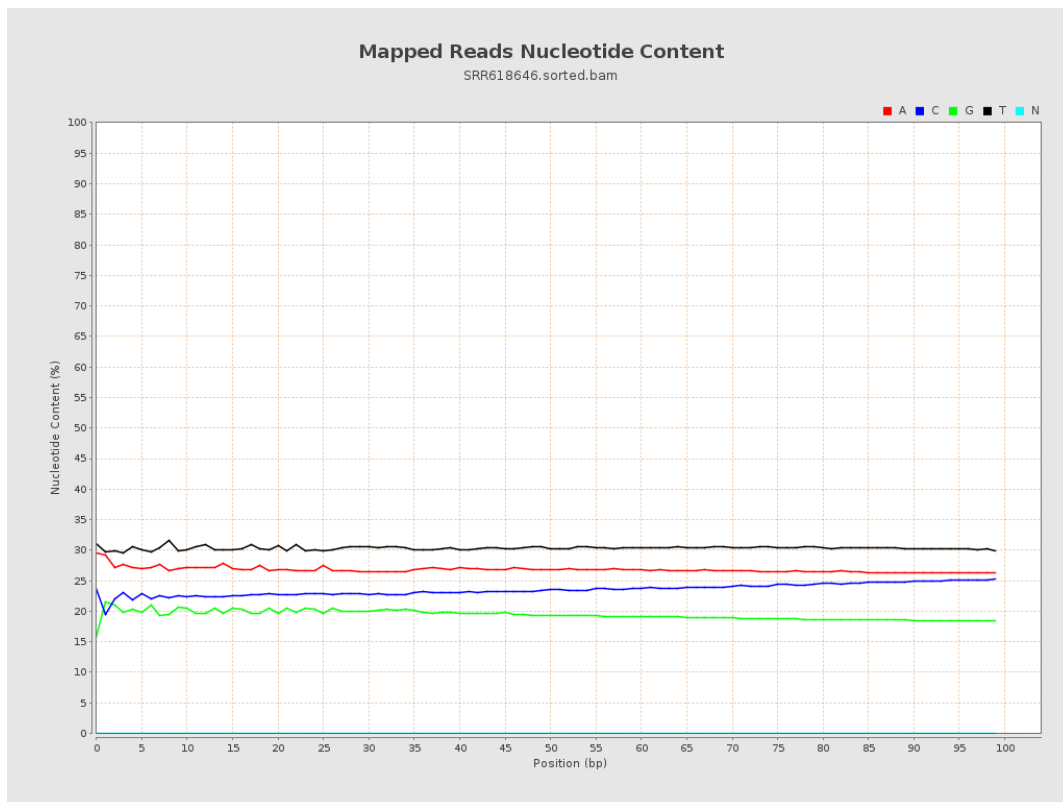
6. Results : Genome Fraction Coverage



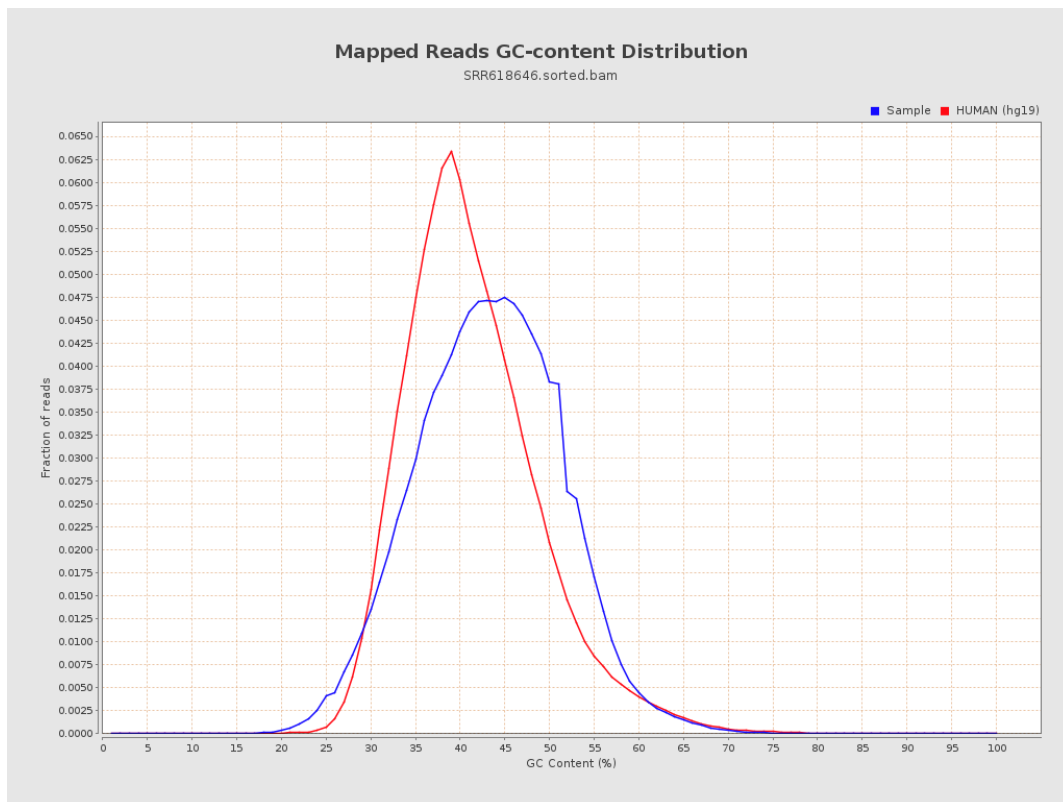
7. Results : Duplication Rate Histogram



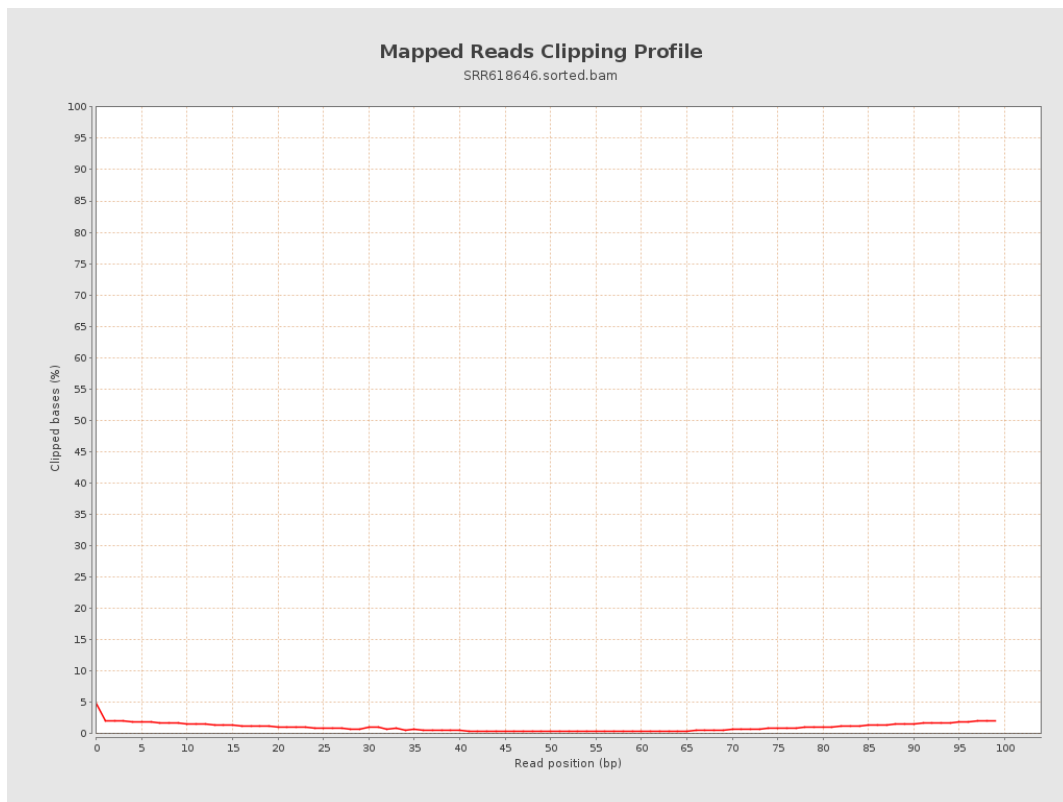
8. Results : Mapped Reads Nucleotide Content



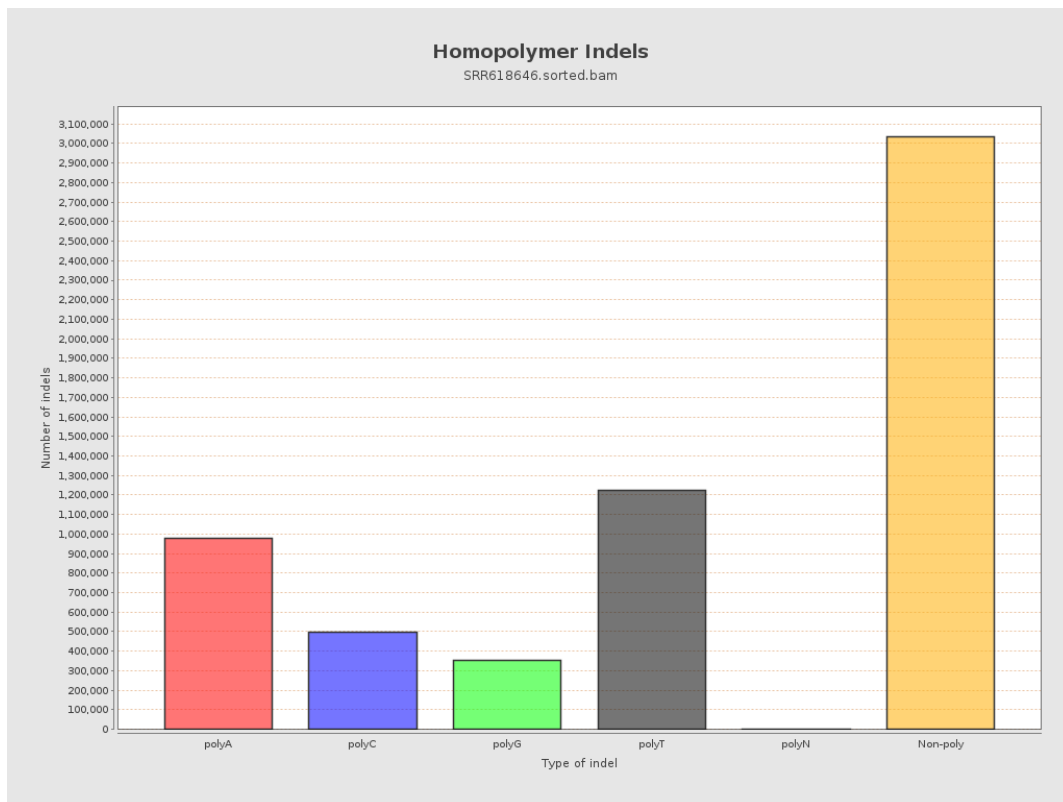
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

