

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 11:32:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818962.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_SRR1818962 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818962.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 11:32:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818962.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	423,234
Mapped reads	407,630 / 96.31%
Unmapped reads	15,604 / 3.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,224 / 1.47%
Read min/max/mean length	30 / 101 / 101.56
Duplicated reads (estimated)	62,847 / 14.85%
Duplication rate	13.48%
Clipped reads	409,844 / 96.84%

2.2. ACGT Content

Number/percentage of A's	11,092,052 / 29.49%
Number/percentage of C's	7,692,523 / 20.45%
Number/percentage of T's	10,577,513 / 28.12%
Number/percentage of G's	8,251,895 / 21.94%
Number/percentage of N's	1,667 / 0%
GC Percentage	42.39%

2.3. Coverage

Mean	0.0122

Standard Deviation	0.1936
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2.4. Mapping Quality

Mean Mapping Quality	48.77
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2.5. Mismatches and indels

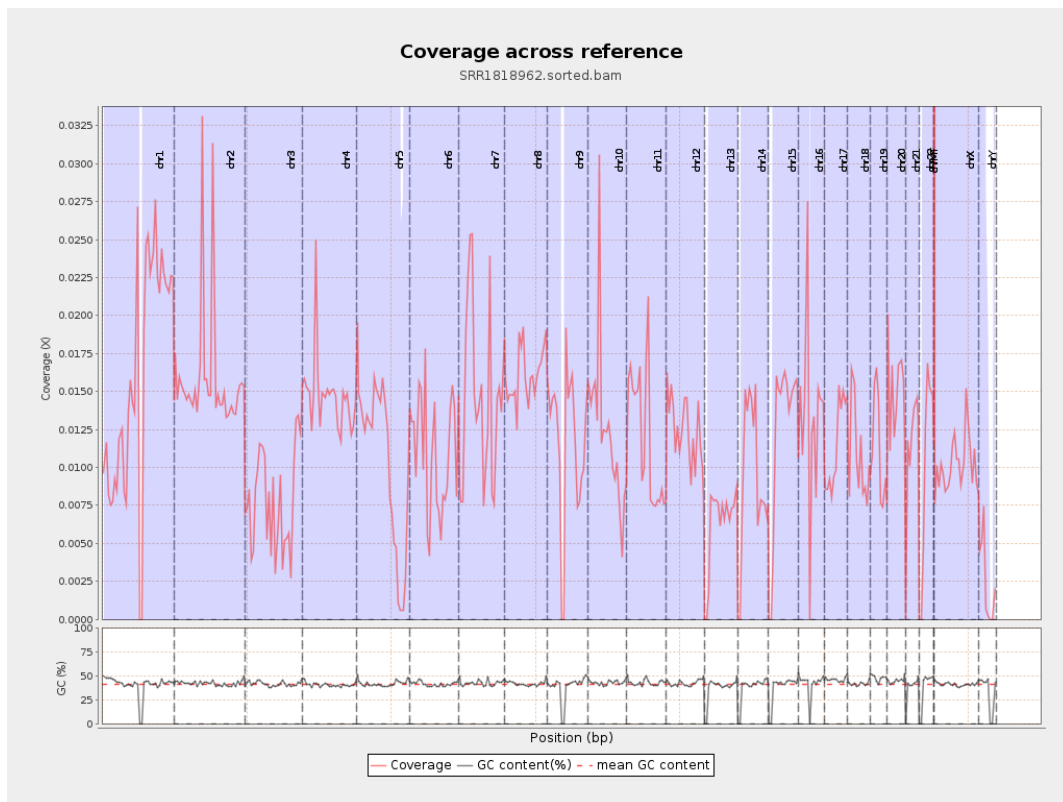
General error rate	0.72%
Mismatches	258,072
Insertions	5,896
Mapped reads with at least one insertion	1.39%
Deletions	12,740
Mapped reads with at least one deletion	3.03%
Homopolymer indels	39.55%

2.6. Chromosome stats

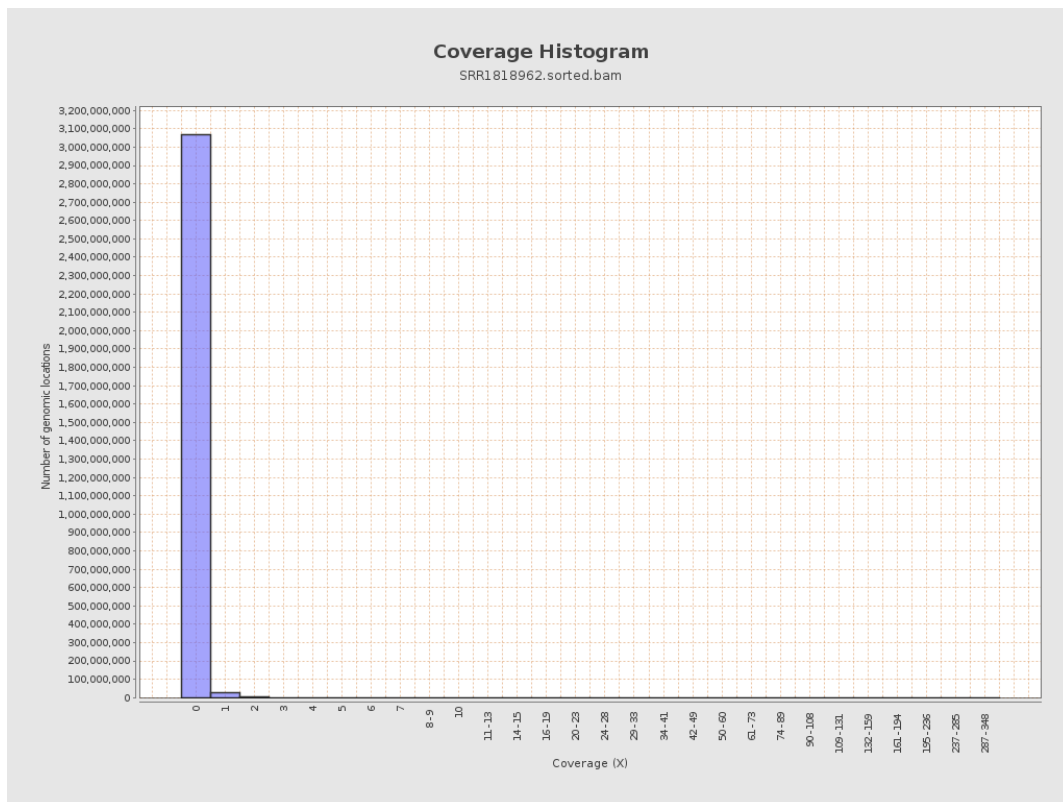
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3979350	0.016	0.3231
chr2	243199373	3859699	0.0159	0.2951
chr3	198022430	1545442	0.0078	0.1062
chr4	191154276	2816604	0.0147	0.1578
chr5	180915260	1855402	0.0103	0.126
chr6	171115067	1861456	0.0109	0.1357
chr7	159138663	2318361	0.0146	0.1698

chr8	146364022	2358458	0.0161	0.1669
chr9	141213431	1632968	0.0116	0.1888
chr10	135534747	1689640	0.0125	0.2444
chr11	135006516	1640226	0.0121	0.1448
chr12	133851895	1659546	0.0124	0.1372
chr13	115169878	720668	0.0063	0.0925
chr14	107349540	1011068	0.0094	0.1295
chr15	102531392	1271386	0.0124	0.1332
chr16	90354753	1183943	0.0131	0.2328
chr17	81195210	926533	0.0114	0.1333
chr18	78077248	826260	0.0106	0.2353
chr19	59128983	675924	0.0114	0.2773
chr20	63025520	950413	0.0151	0.1511
chr21	48129895	551426	0.0115	0.1379
chr22	51304566	520981	0.0102	0.1261
chrMT	16571	40398	2.4379	2.0529
chrX	155270560	1599789	0.0103	0.1428
chrY	59373566	143886	0.0024	0.1995

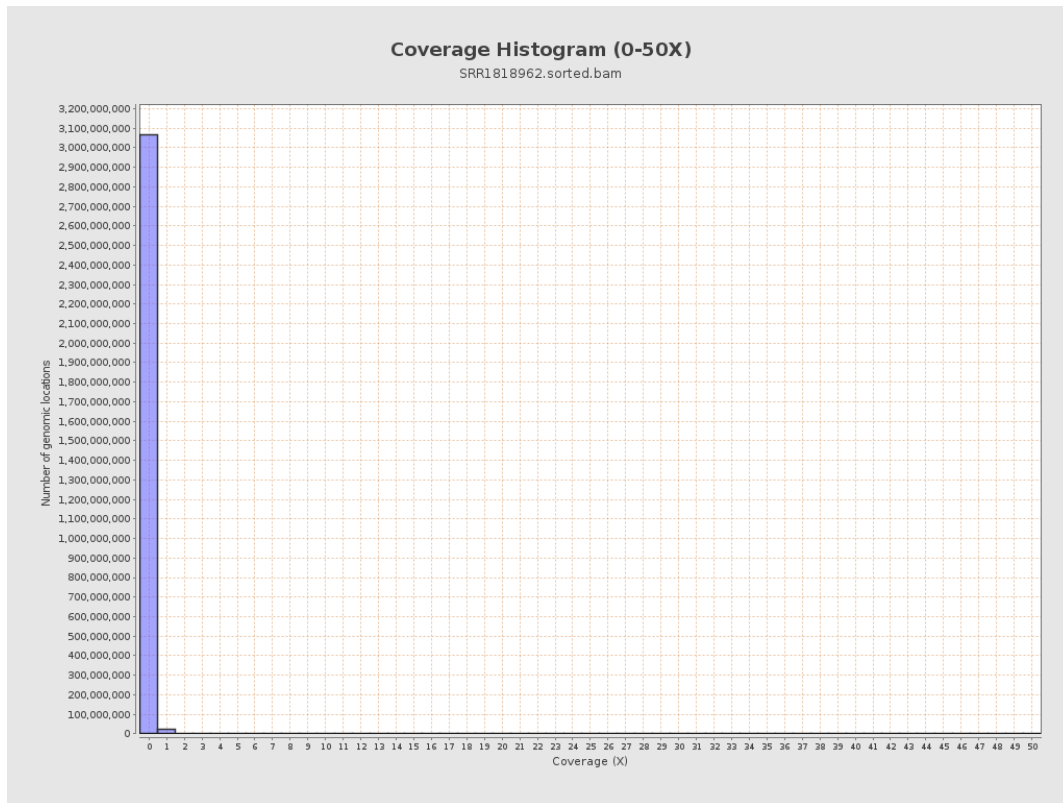
3. Results : Coverage across reference



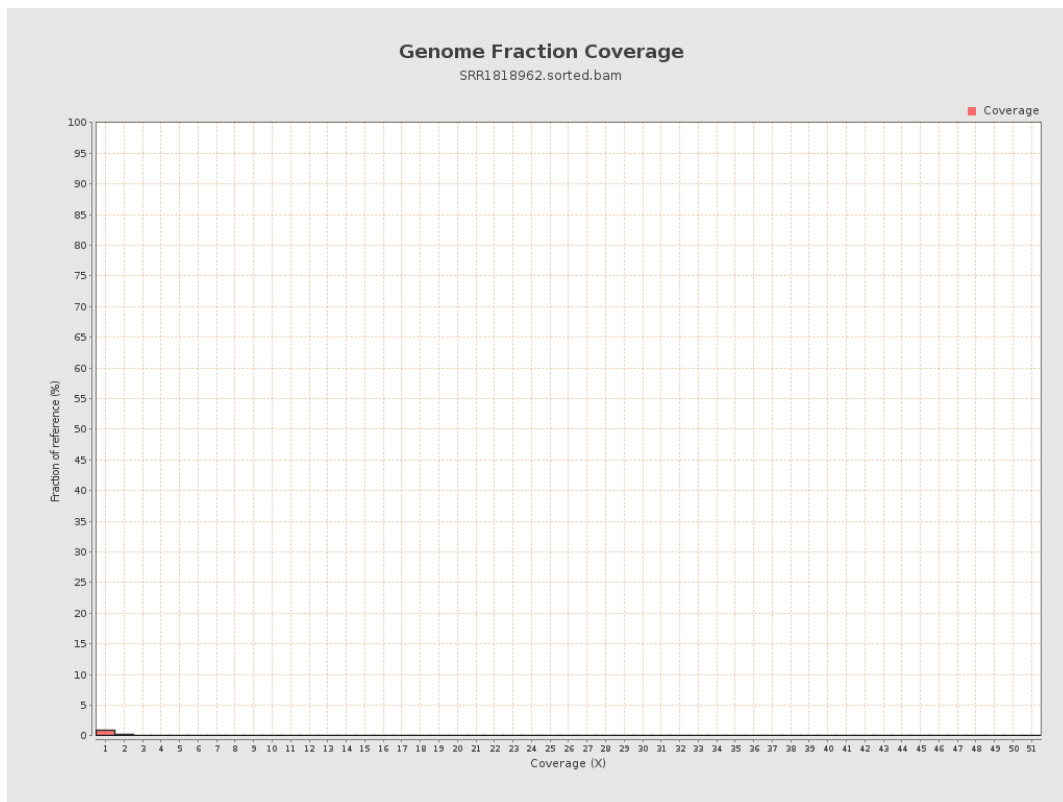
4. Results : Coverage Histogram



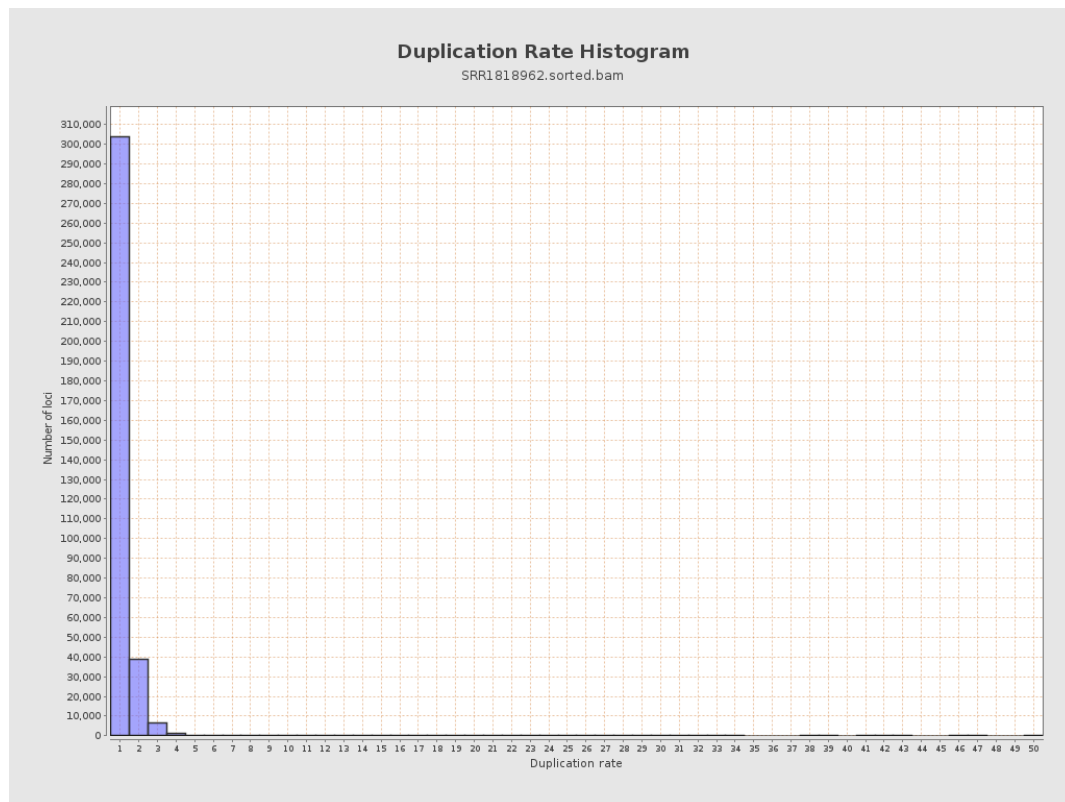
5. Results : Coverage Histogram (0-50X)



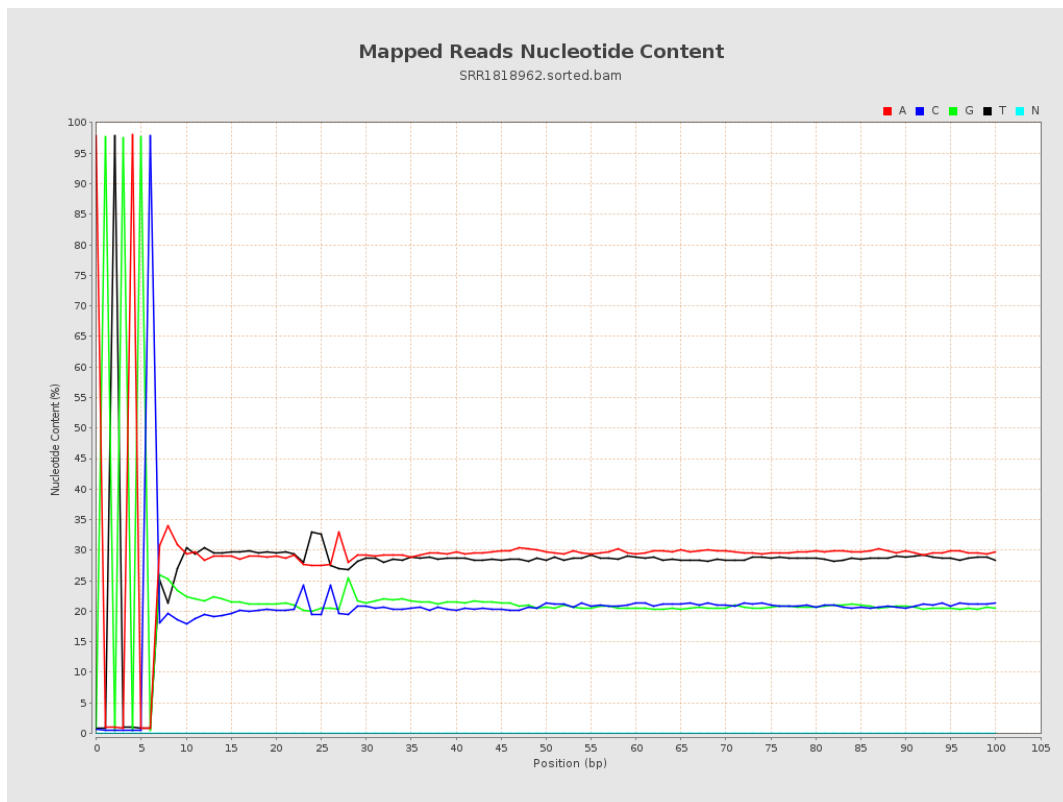
6. Results : Genome Fraction Coverage



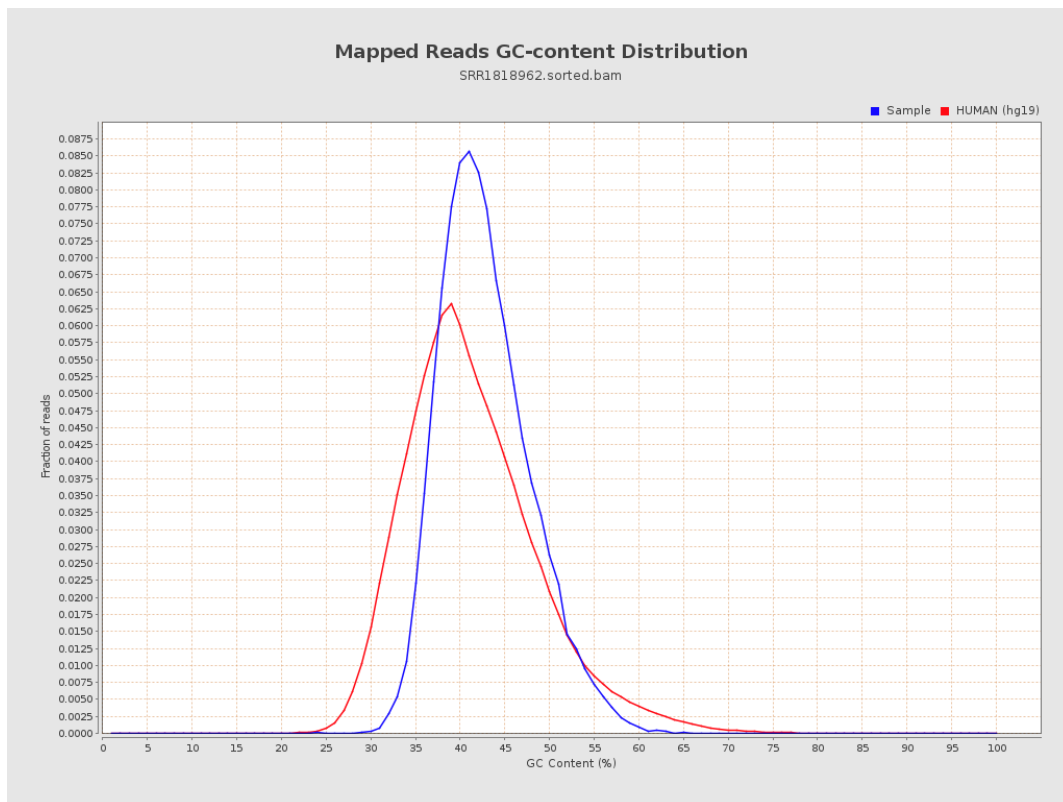
7. Results : Duplication Rate Histogram



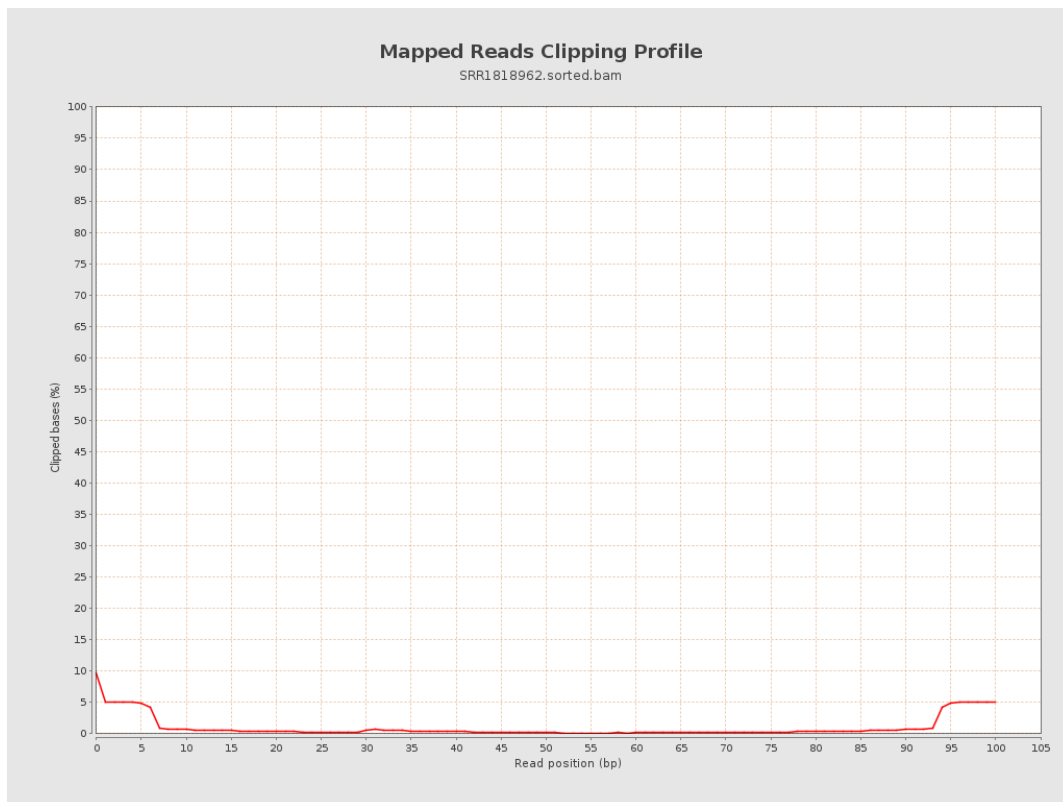
8. Results : Mapped Reads Nucleotide Content



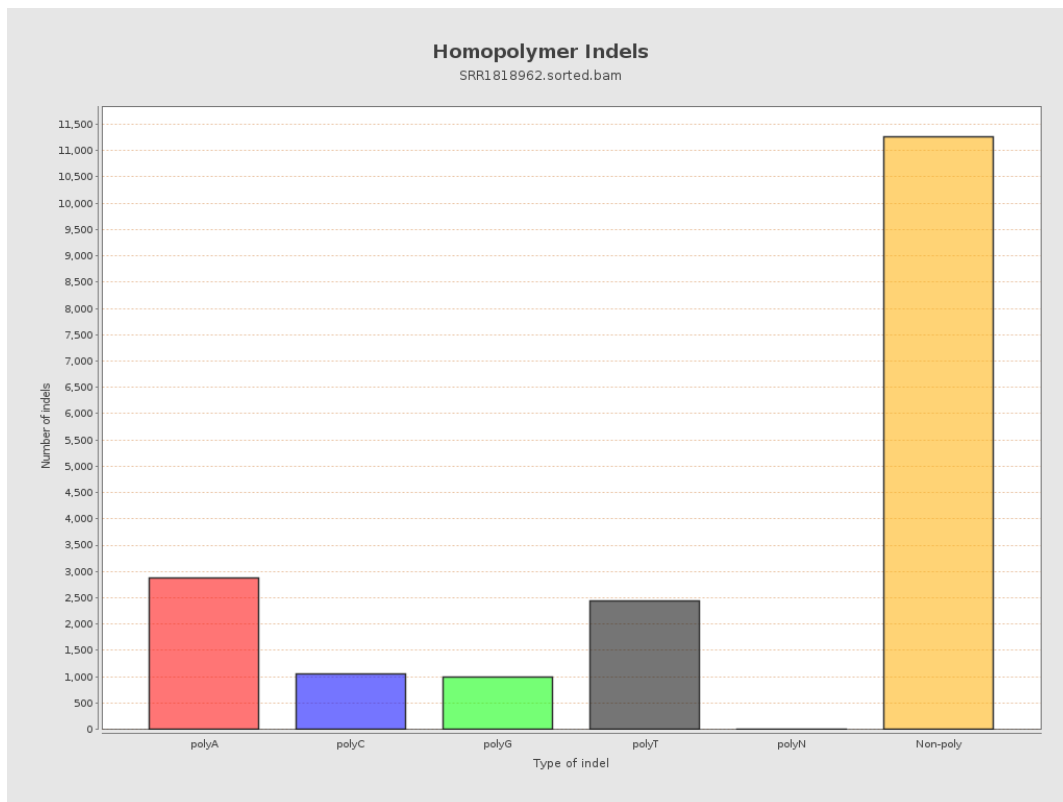
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

