

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 15:03:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080679.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_SRR3080679 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080679.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 15:02:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080679.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,376,687
Mapped reads	1,265,184 / 91.9%
Unmapped reads	111,503 / 8.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,523 / 0.76%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	45,445 / 3.3%
Duplication rate	3.16%
Clipped reads	569,705 / 41.38%

2.2. ACGT Content

Number/percentage of A's	22,888,175 / 27.24%
Number/percentage of C's	15,326,787 / 18.24%
Number/percentage of T's	26,881,474 / 31.99%
Number/percentage of G's	18,923,414 / 22.52%
Number/percentage of N's	4,104 / 0%
GC Percentage	40.76%

2.3. Coverage

Mean	0.0272

Standard Deviation	0.2181
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2.4. Mapping Quality

Mean Mapping Quality	45.85
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2.5. Mismatches and indels

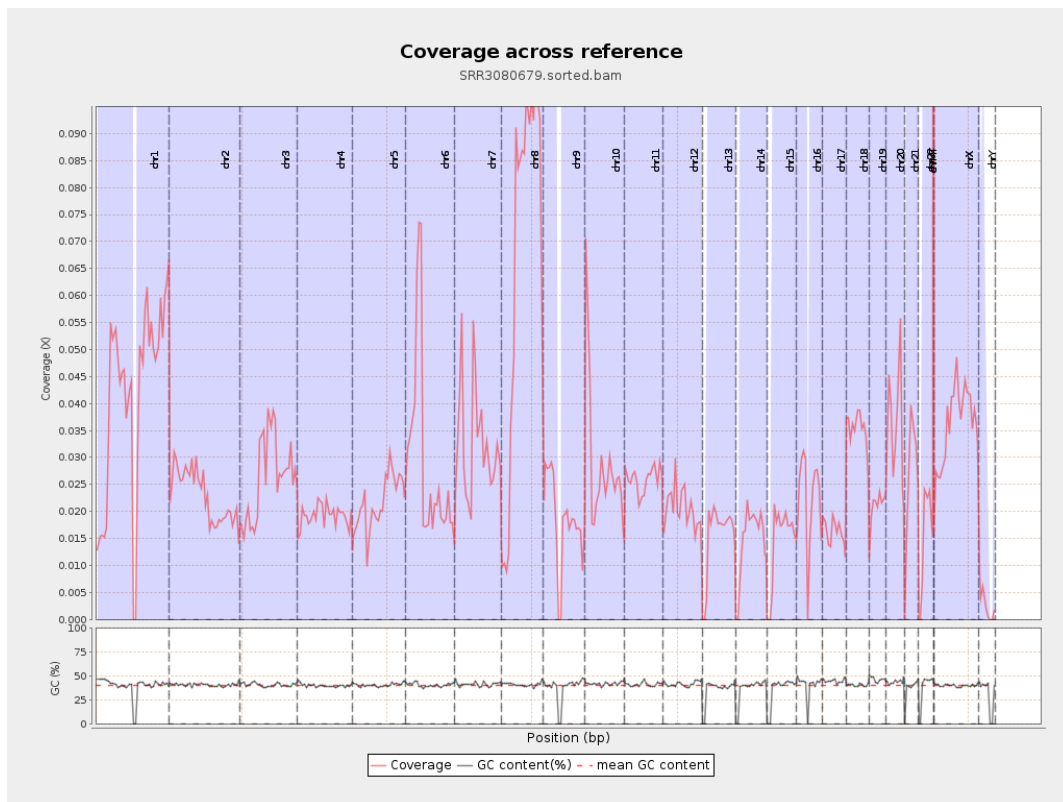
General error rate	0.69%
Mismatches	568,449
Insertions	6,264
Mapped reads with at least one insertion	0.49%
Deletions	19,101
Mapped reads with at least one deletion	1.5%
Homopolymer indels	48.13%

2.6. Chromosome stats

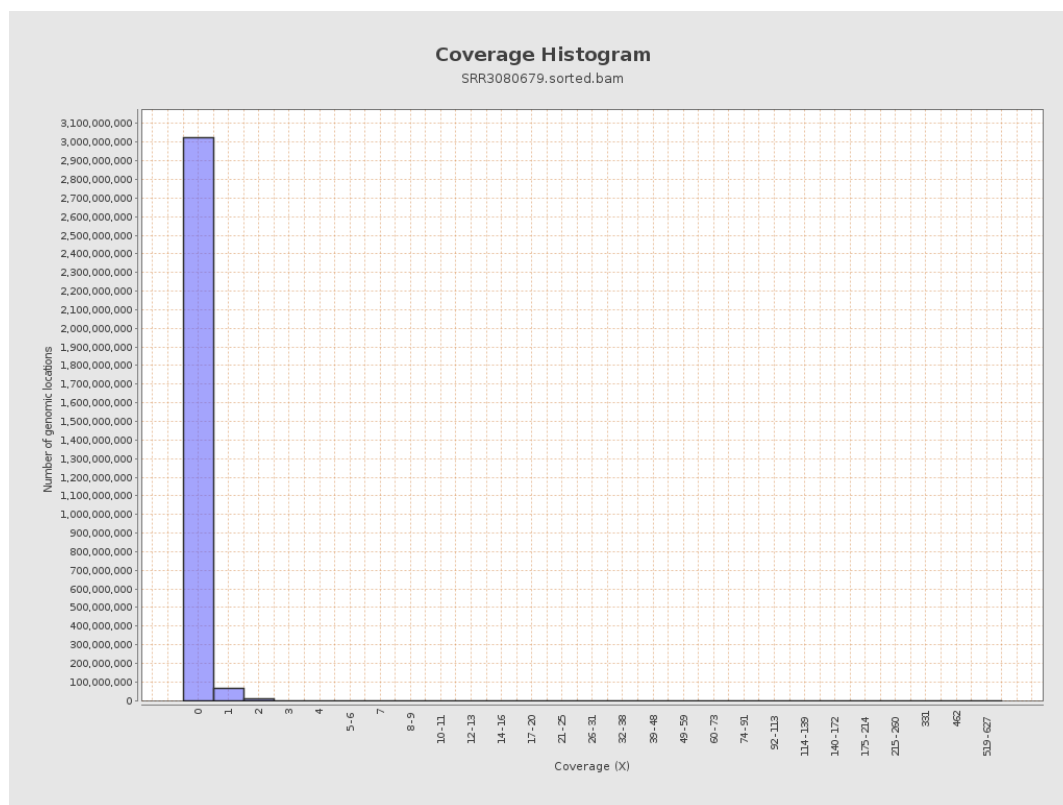
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10292463	0.0413	0.2501
chr2	243199373	5580619	0.0229	0.3101
chr3	198022430	5230343	0.0264	0.1804
chr4	191154276	3680691	0.0193	0.1558
chr5	180915260	3937975	0.0218	0.1636
chr6	171115067	5032683	0.0294	0.2295
chr7	159138663	5249863	0.033	0.3591

chr8	146364022	9928616	0.0678	0.3135
chr9	141213431	2580558	0.0183	0.1694
chr10	135534747	4004790	0.0295	0.1981
chr11	135006516	3485517	0.0258	0.1936
chr12	133851895	2727300	0.0204	0.1598
chr13	115169878	1774963	0.0154	0.1387
chr14	107349540	1588362	0.0148	0.1369
chr15	102531392	1492095	0.0146	0.1395
chr16	90354753	2024323	0.0224	0.1676
chr17	81195210	1318796	0.0162	0.1435
chr18	78077248	2774014	0.0355	0.2486
chr19	59128983	1261164	0.0213	0.1773
chr20	63025520	2276226	0.0361	0.2135
chr21	48129895	1279090	0.0266	0.1837
chr22	51304566	767560	0.015	0.1348
chrMT	16571	7994	0.4824	0.8281
chrX	155270560	5598938	0.0361	0.218
chrY	59373566	159401	0.0027	0.0597

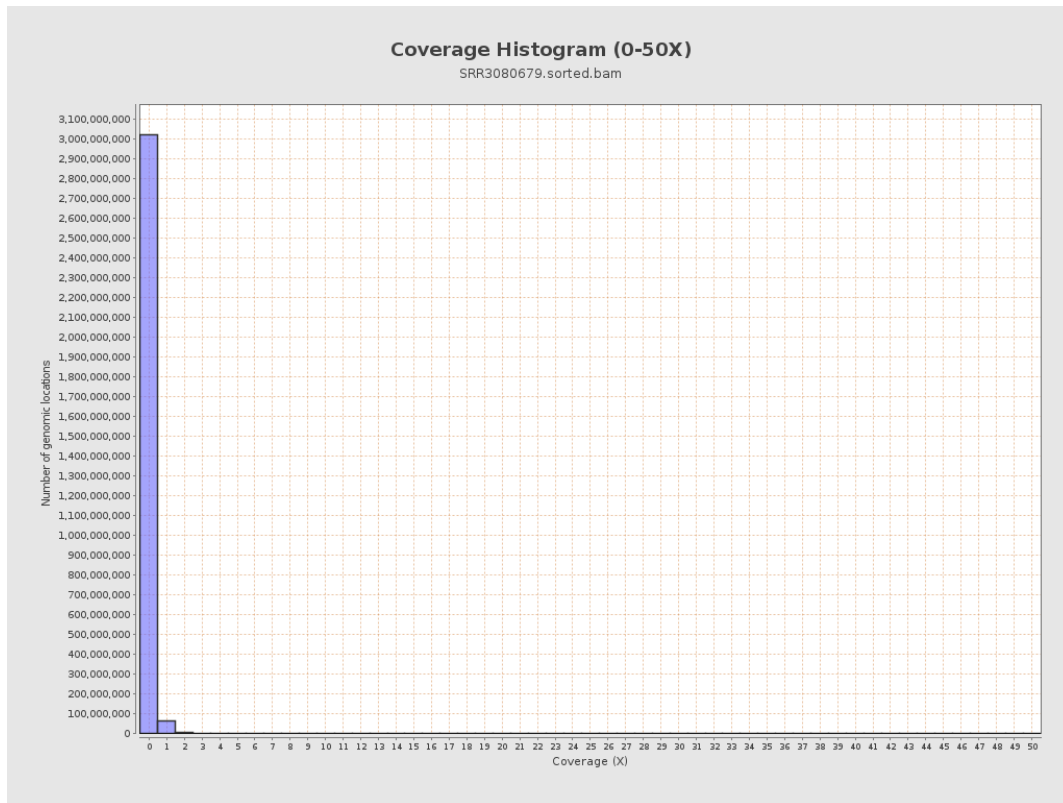
3. Results : Coverage across reference



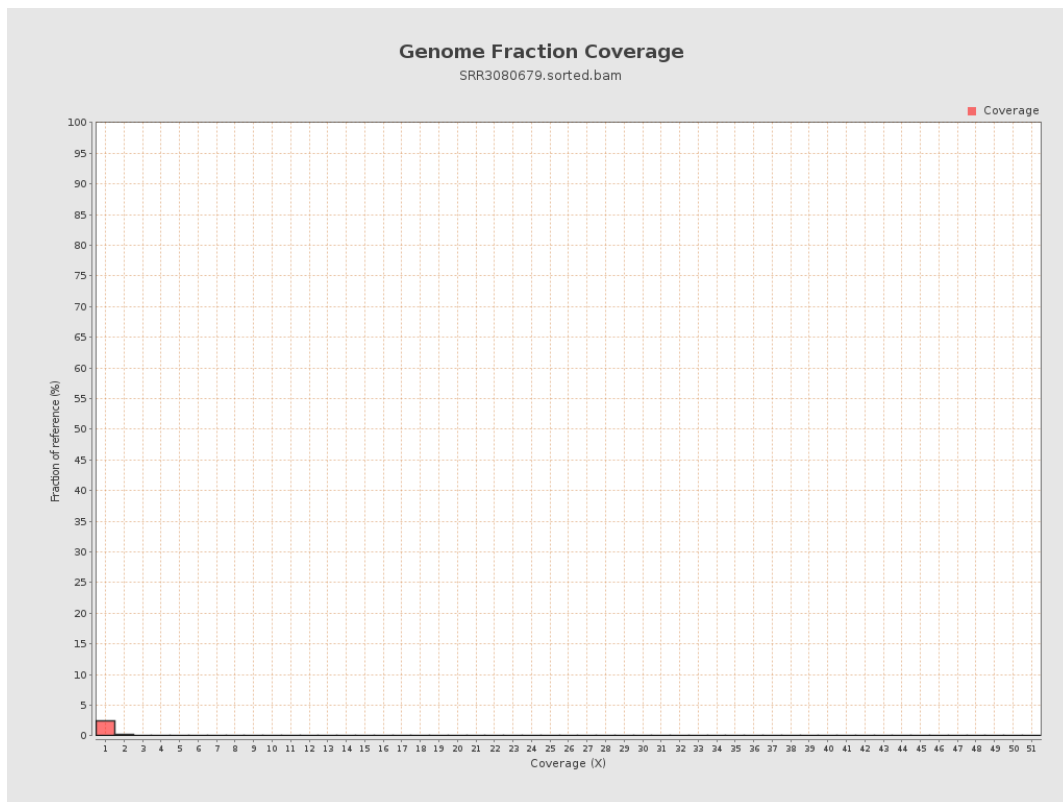
4. Results : Coverage Histogram



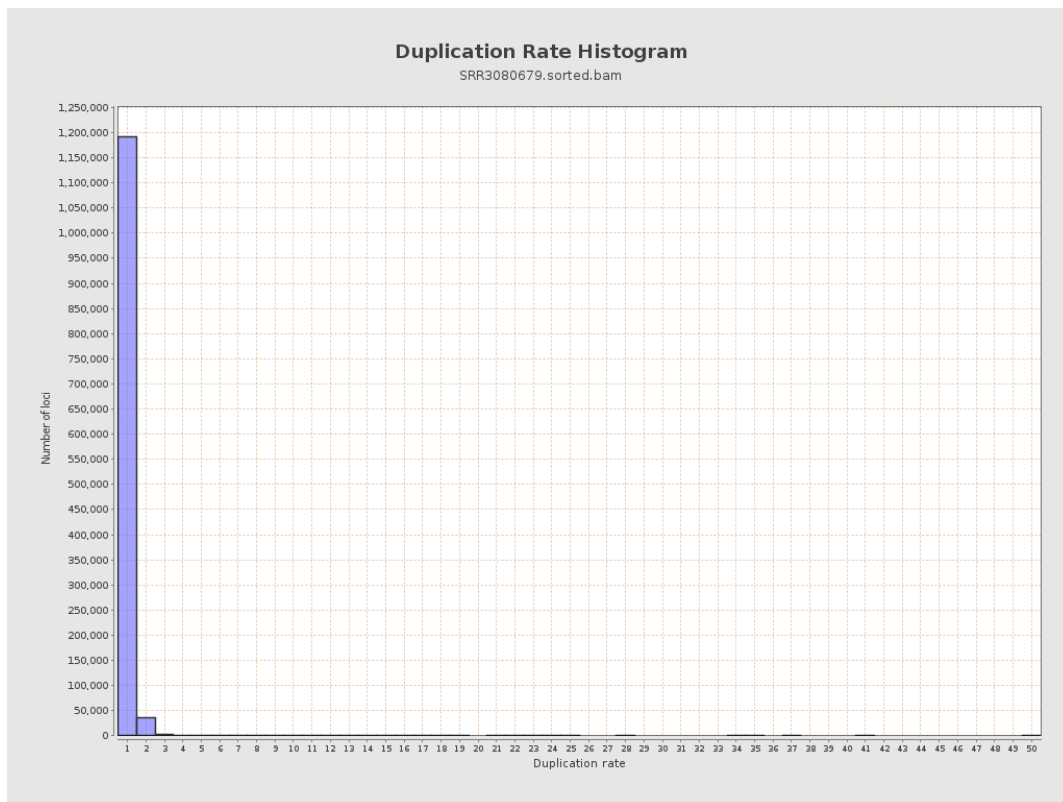
5. Results : Coverage Histogram (0-50X)



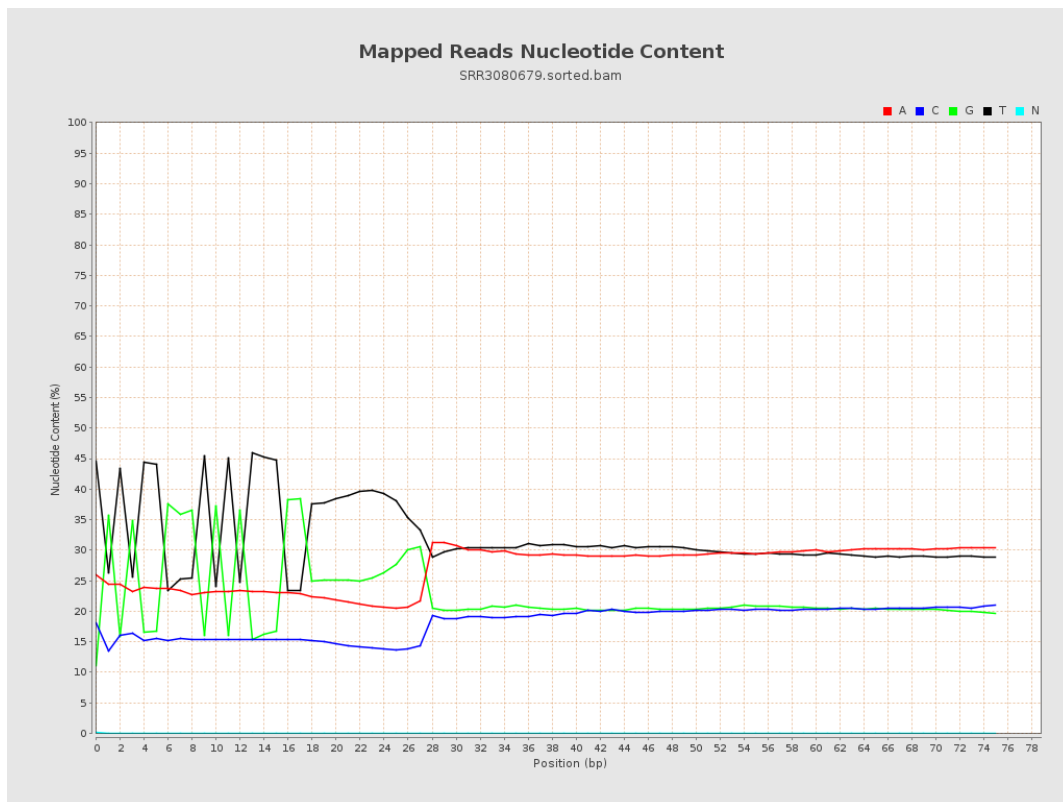
6. Results : Genome Fraction Coverage



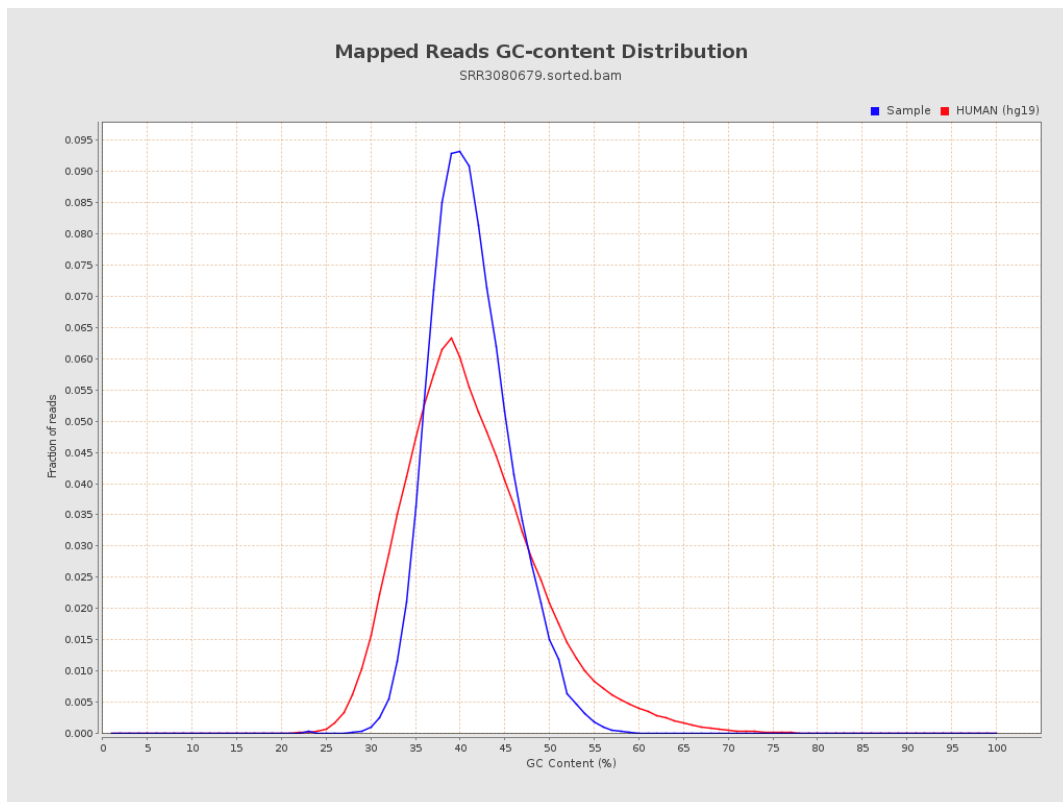
7. Results : Duplication Rate Histogram



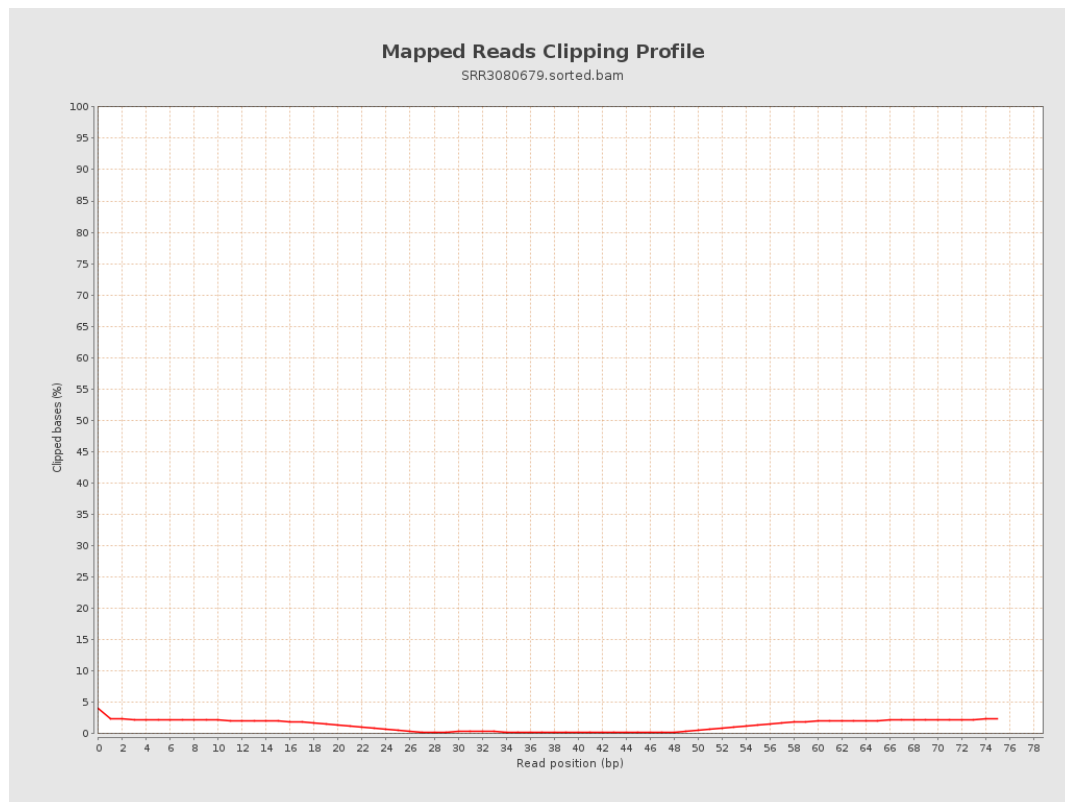
8. Results : Mapped Reads Nucleotide Content



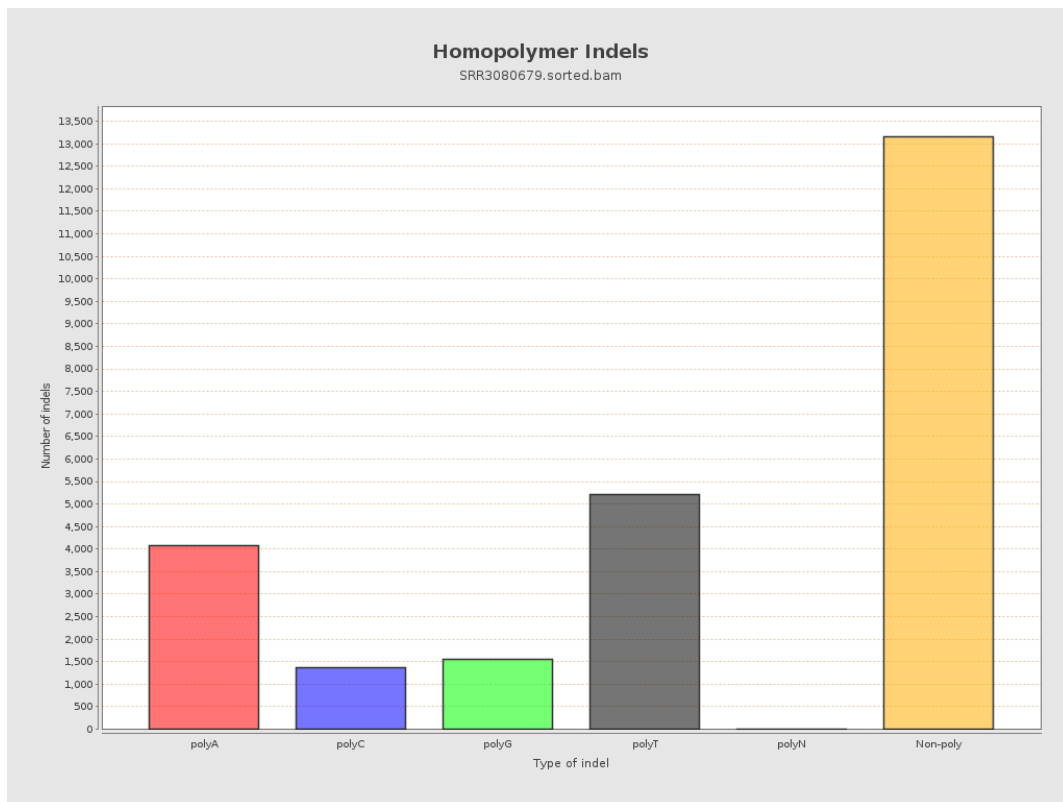
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

