

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 13:28:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080670.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_SRR3080670 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080670.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 13:28:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080670.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,603,166
Mapped reads	1,449,998 / 90.45%
Unmapped reads	153,168 / 9.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,383 / 0.77%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	52,124 / 3.25%
Duplication rate	3.03%
Clipped reads	680,090 / 42.42%

2.2. ACGT Content

Number/percentage of A's	25,764,813 / 26.88%
Number/percentage of C's	17,886,432 / 18.66%
Number/percentage of T's	30,035,067 / 31.33%
Number/percentage of G's	22,167,626 / 23.13%
Number/percentage of N's	4,135 / 0%
GC Percentage	41.78%

2.3. Coverage

Mean	0.031

Standard Deviation	0.2606
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2.4. Mapping Quality

Mean Mapping Quality	45.05
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2.5. Mismatches and indels

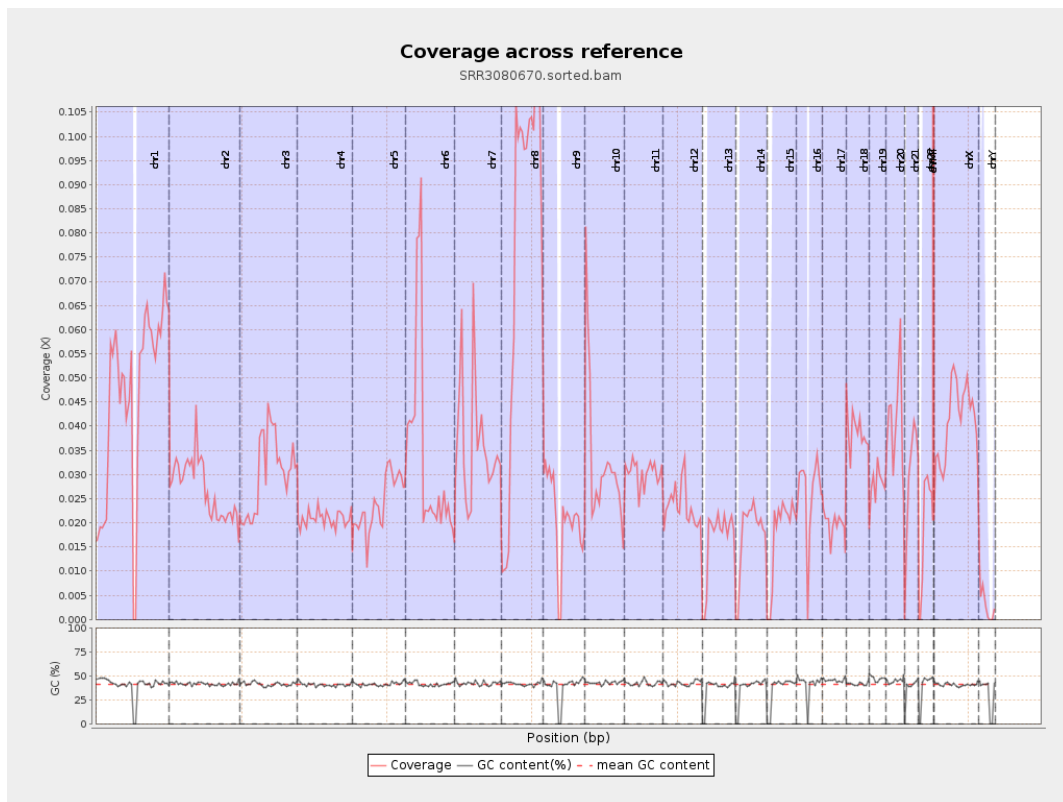
General error rate	0.69%
Mismatches	650,740
Insertions	7,318
Mapped reads with at least one insertion	0.5%
Deletions	22,499
Mapped reads with at least one deletion	1.54%
Homopolymer indels	47.76%

2.6. Chromosome stats

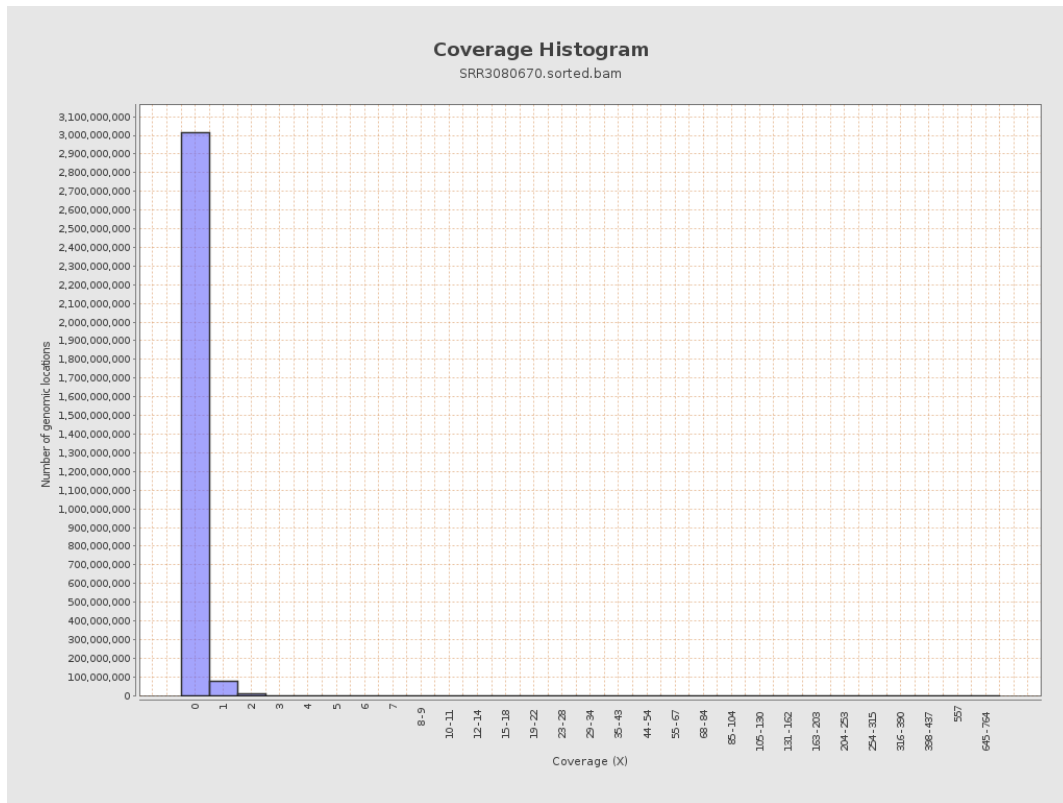
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11510765	0.0462	0.3207
chr2	243199373	6578352	0.027	0.3779
chr3	198022430	6002339	0.0303	0.1929
chr4	191154276	3982380	0.0208	0.1637
chr5	180915260	4359856	0.0241	0.1723
chr6	171115067	5818442	0.034	0.2538
chr7	159138663	5882010	0.037	0.5334

chr8	146364022	11312943	0.0773	0.3432
chr9	141213431	2934731	0.0208	0.1918
chr10	135534747	4481491	0.0331	0.2125
chr11	135006516	4099538	0.0304	0.2114
chr12	133851895	3095998	0.0231	0.1701
chr13	115169878	1884392	0.0164	0.1421
chr14	107349540	1889670	0.0176	0.1504
chr15	102531392	1812390	0.0177	0.1602
chr16	90354753	2362175	0.0261	0.1813
chr17	81195210	1586143	0.0195	0.1592
chr18	78077248	3028761	0.0388	0.2669
chr19	59128983	1669315	0.0282	0.2214
chr20	63025520	2571311	0.0408	0.2267
chr21	48129895	1407301	0.0292	0.1921
chr22	51304566	968973	0.0189	0.151
chrMT	16571	117860	7.1124	4.1757
chrX	155270560	6348934	0.0409	0.2299
chrY	59373566	188145	0.0032	0.0671

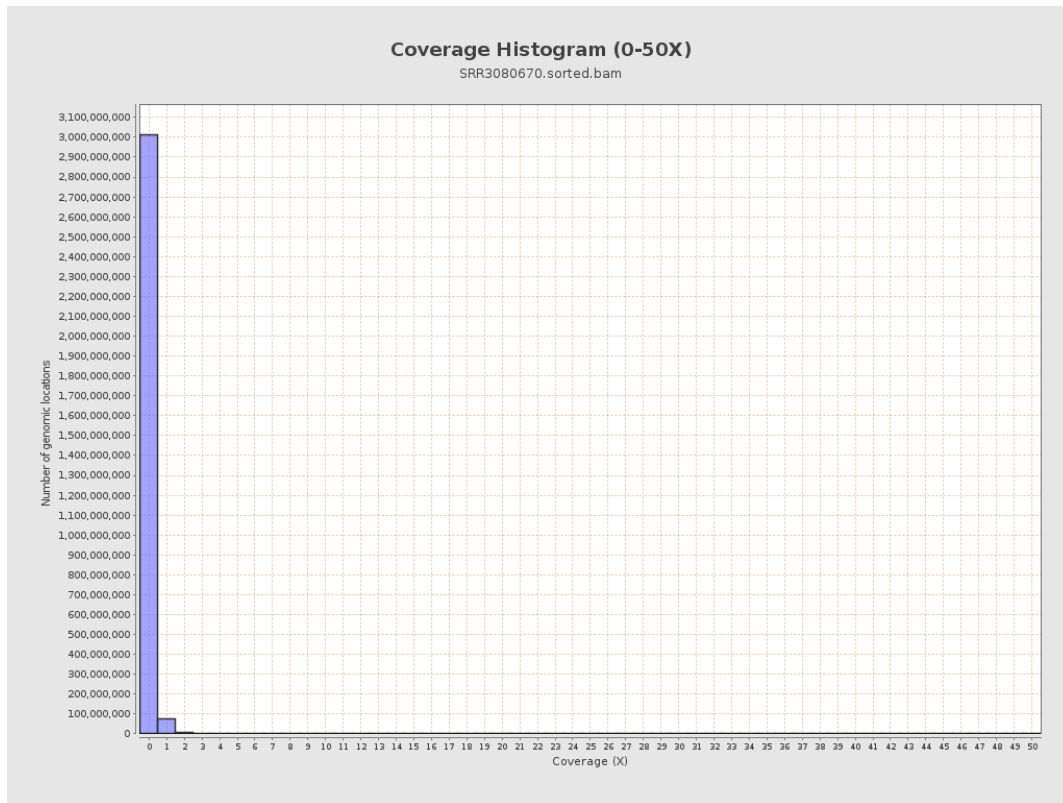
3. Results : Coverage across reference



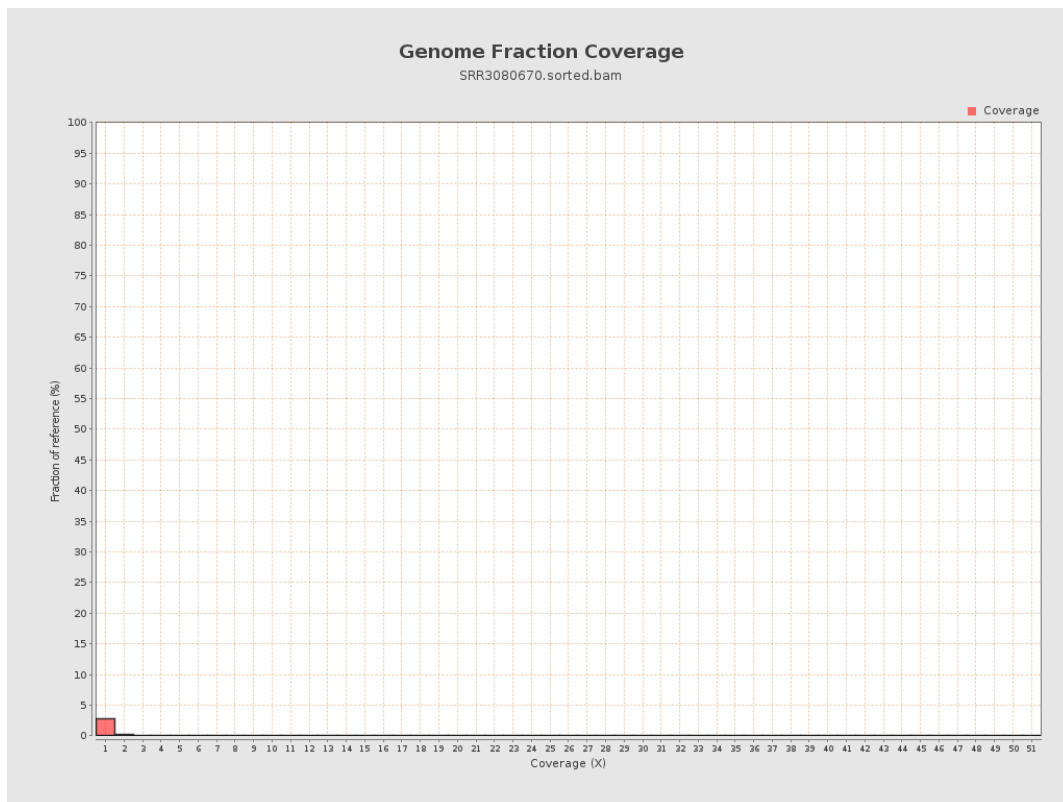
4. Results : Coverage Histogram



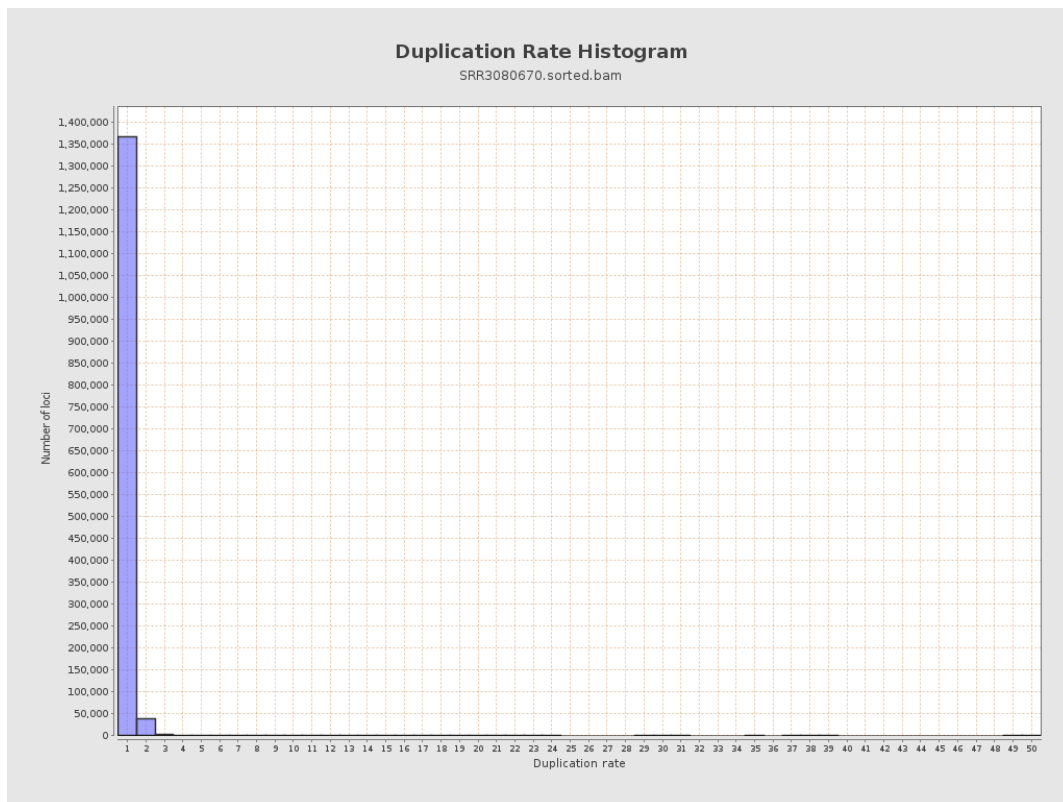
5. Results : Coverage Histogram (0-50X)



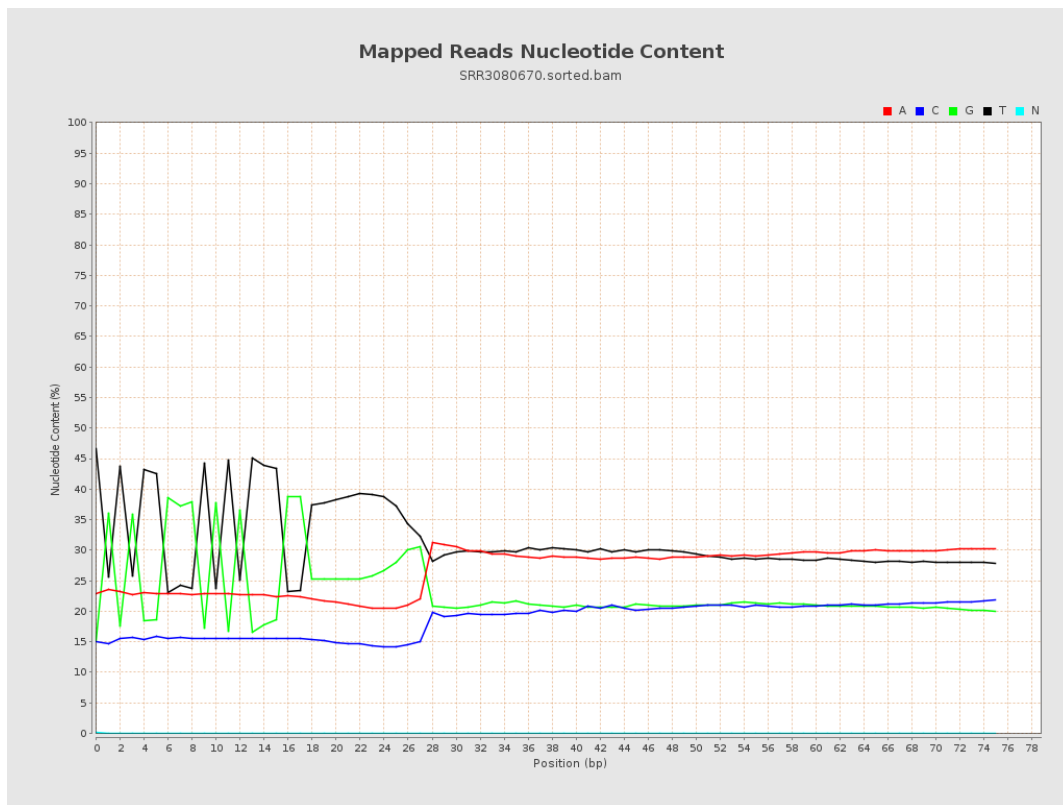
6. Results : Genome Fraction Coverage



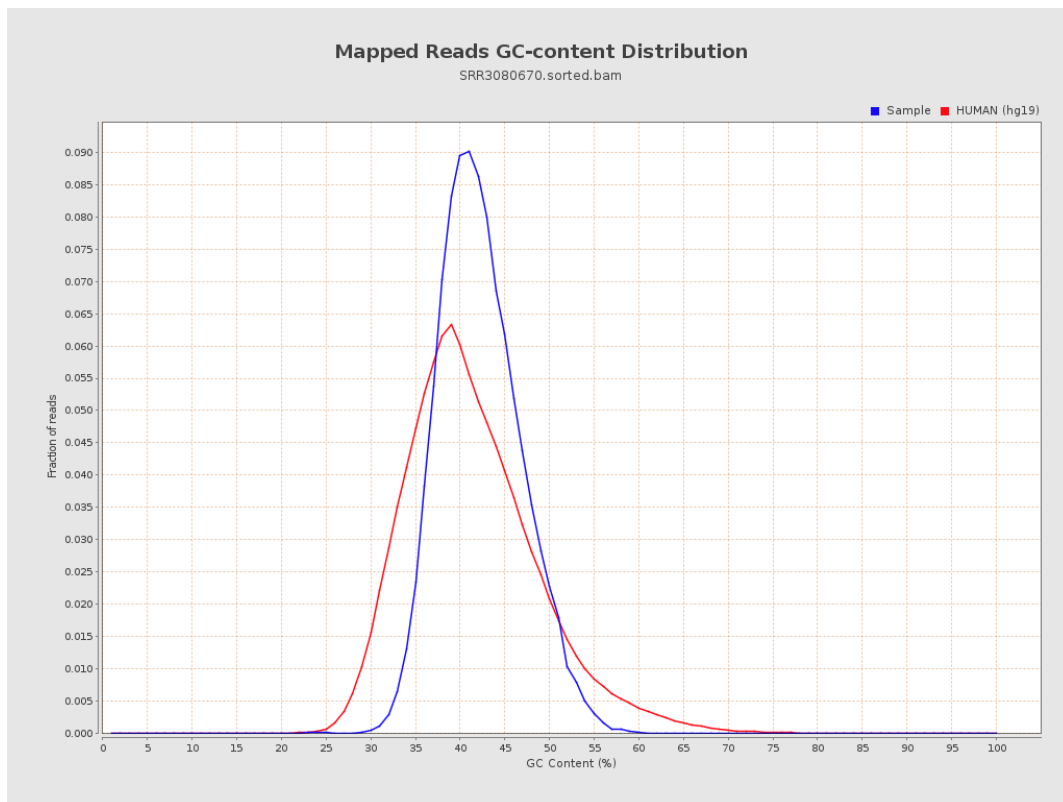
7. Results : Duplication Rate Histogram



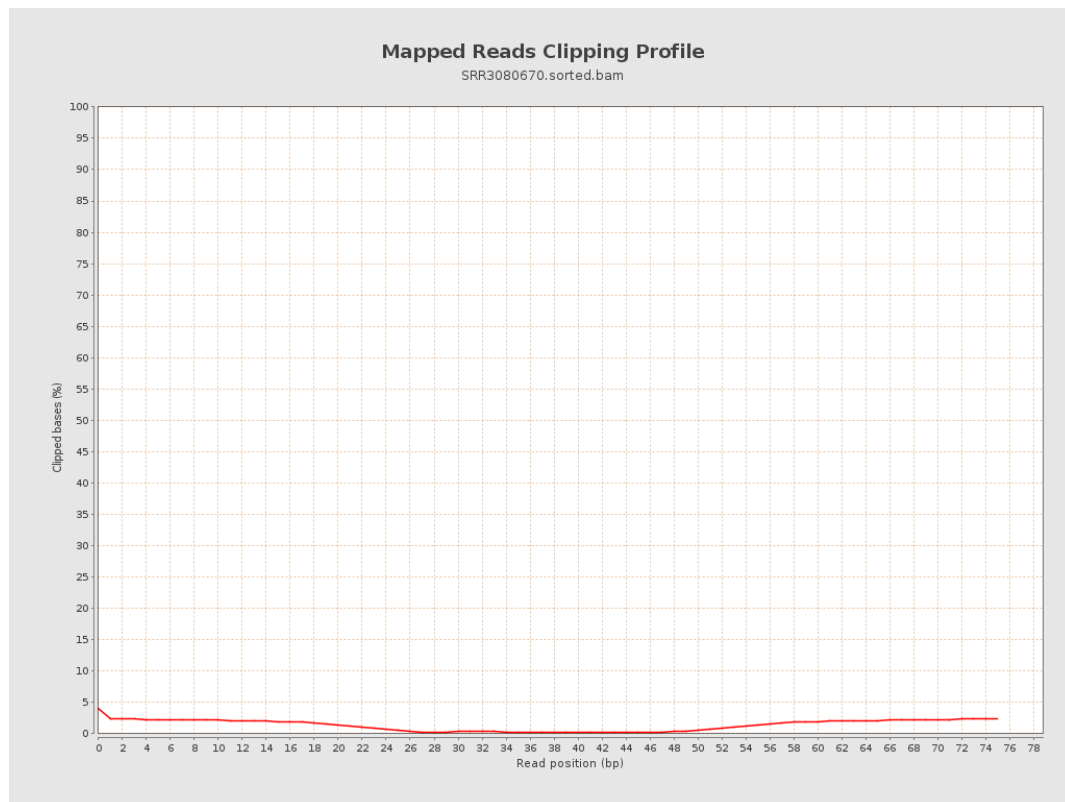
8. Results : Mapped Reads Nucleotide Content



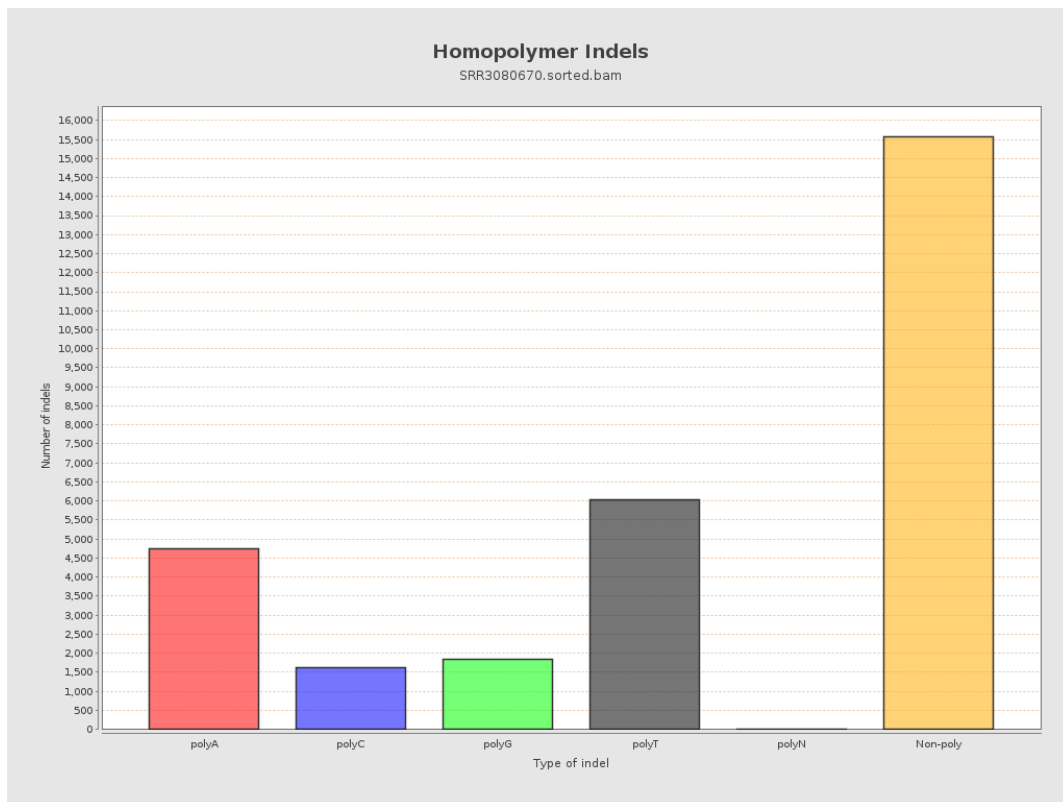
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

