

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 00:27:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085085.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_SRR3085085 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085085.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 00:27:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085085.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,387,733
Mapped reads	1,057,776 / 76.22%
Unmapped reads	329,957 / 23.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,232 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	22,250 / 1.6%
Duplication rate	1.68%
Clipped reads	656,543 / 47.31%

2.2. ACGT Content

Number/percentage of A's	19,469,142 / 29.66%
Number/percentage of C's	12,490,624 / 19.03%
Number/percentage of T's	19,124,585 / 29.14%
Number/percentage of G's	14,552,385 / 22.17%
Number/percentage of N's	1,528 / 0%
GC Percentage	41.2%

2.3. Coverage

Mean	0.0212

Standard Deviation	0.1905
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2.4. Mapping Quality

Mean Mapping Quality	45.42
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2.5. Mismatches and indels

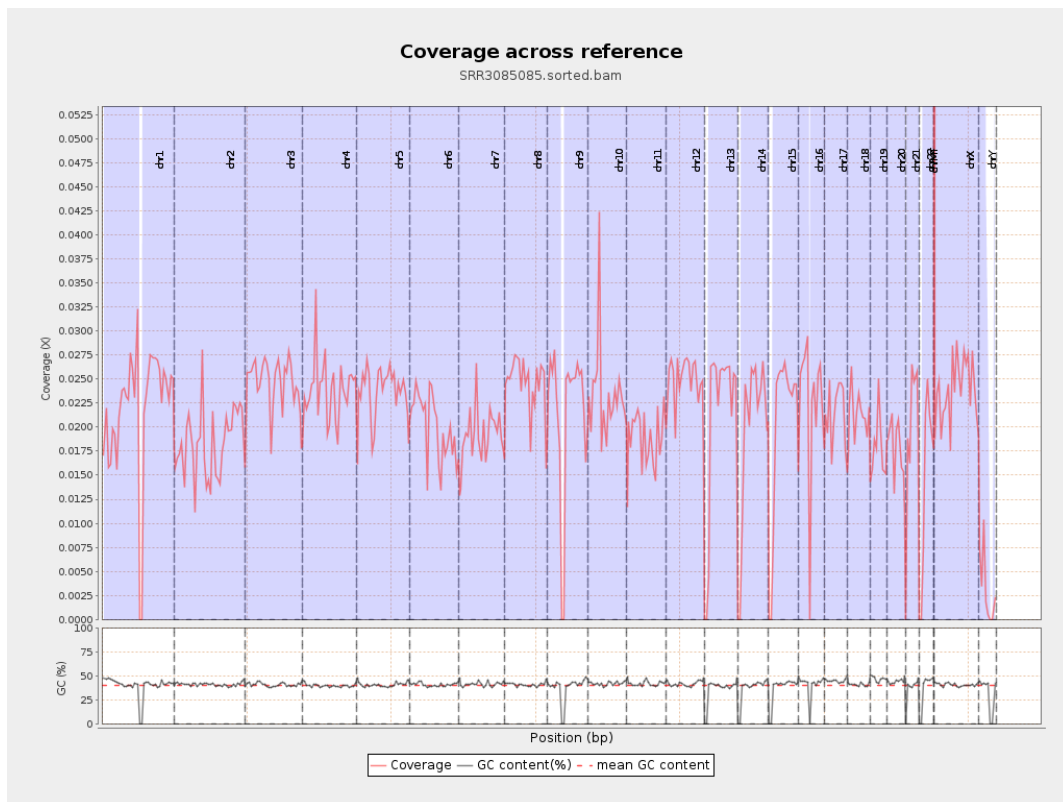
General error rate	0.95%
Mismatches	614,477
Insertions	5,285
Mapped reads with at least one insertion	0.5%
Deletions	14,383
Mapped reads with at least one deletion	1.35%
Homopolymer indels	45.62%

2.6. Chromosome stats

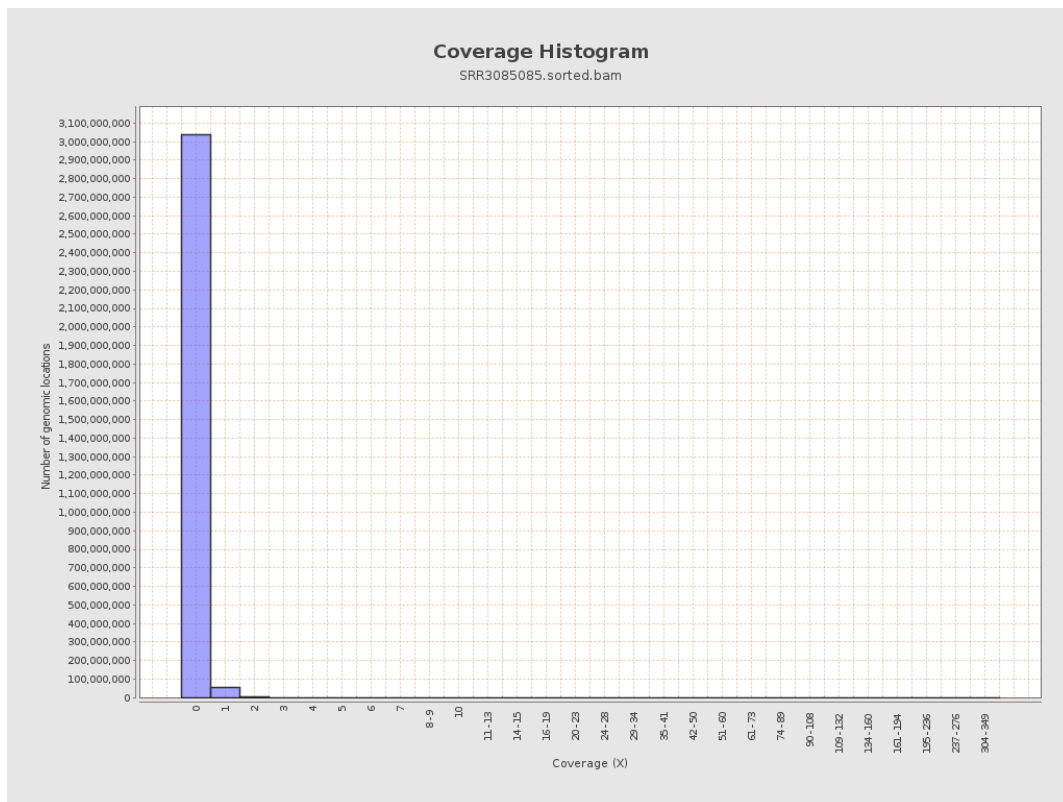
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5455499	0.0219	0.2652
chr2	243199373	4456691	0.0183	0.1789
chr3	198022430	4886318	0.0247	0.1662
chr4	191154276	4545195	0.0238	0.1705
chr5	180915260	4330803	0.0239	0.1631
chr6	171115067	3416153	0.02	0.1638
chr7	159138663	3049987	0.0192	0.1815

chr8	146364022	3591077	0.0245	0.2626
chr9	141213431	3036360	0.0215	0.189
chr10	135534747	3175709	0.0234	0.2227
chr11	135006516	2550205	0.0189	0.164
chr12	133851895	3331588	0.0249	0.1679
chr13	115169878	2419429	0.021	0.1526
chr14	107349540	2113333	0.0197	0.1555
chr15	102531392	2065964	0.0201	0.1493
chr16	90354753	2001191	0.0221	0.1679
chr17	81195210	1730909	0.0213	0.1611
chr18	78077248	1677043	0.0215	0.3388
chr19	59128983	1067235	0.018	0.2107
chr20	63025520	1118486	0.0177	0.1439
chr21	48129895	960118	0.0199	0.1587
chr22	51304566	759987	0.0148	0.1281
chrMT	16571	17237	1.0402	1.2537
chrX	155270560	3724090	0.024	0.1702
chrY	59373566	181042	0.003	0.0792

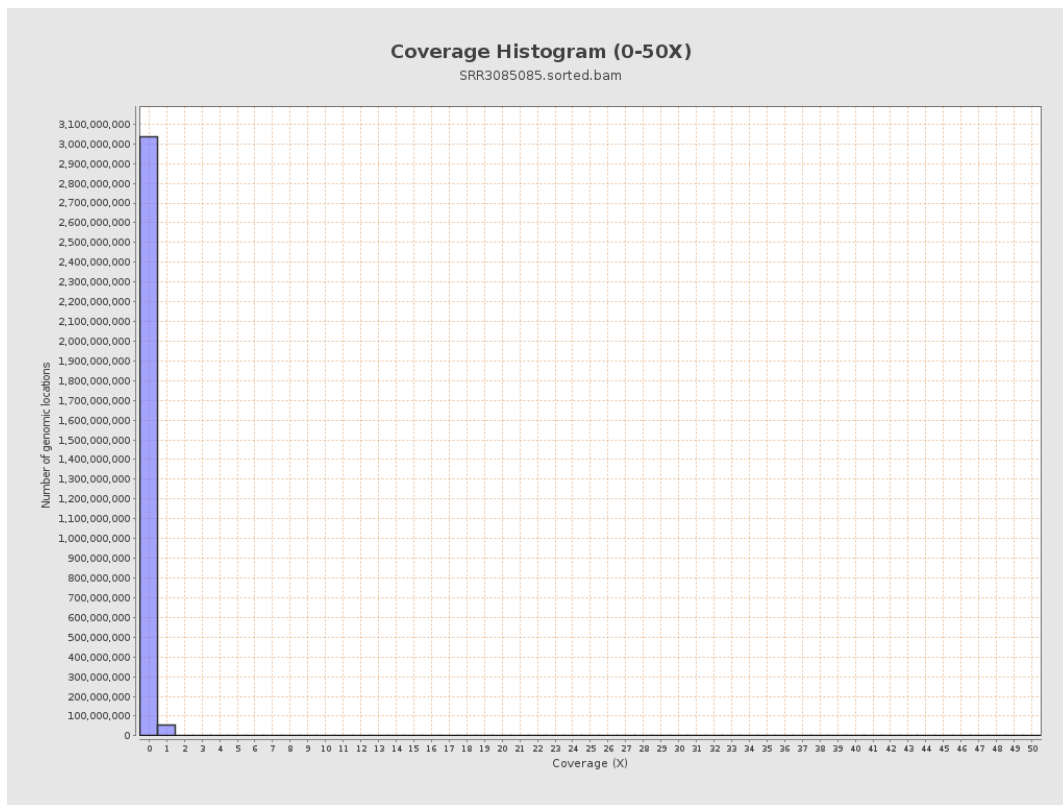
3. Results : Coverage across reference



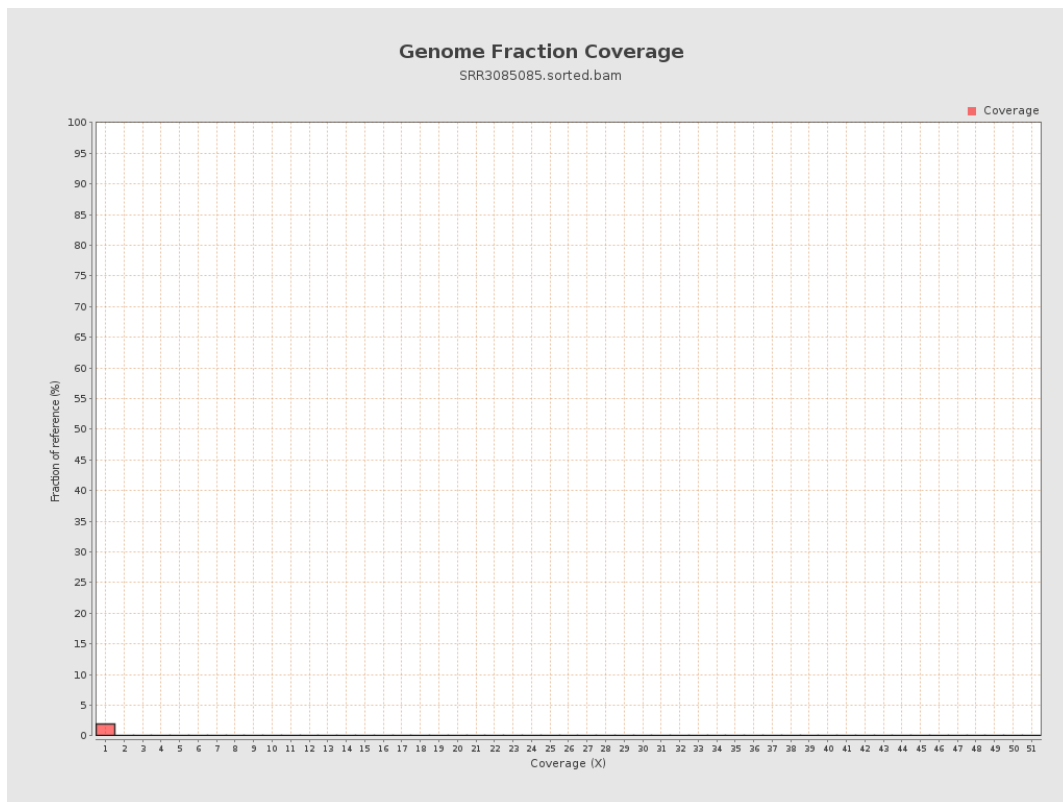
4. Results : Coverage Histogram



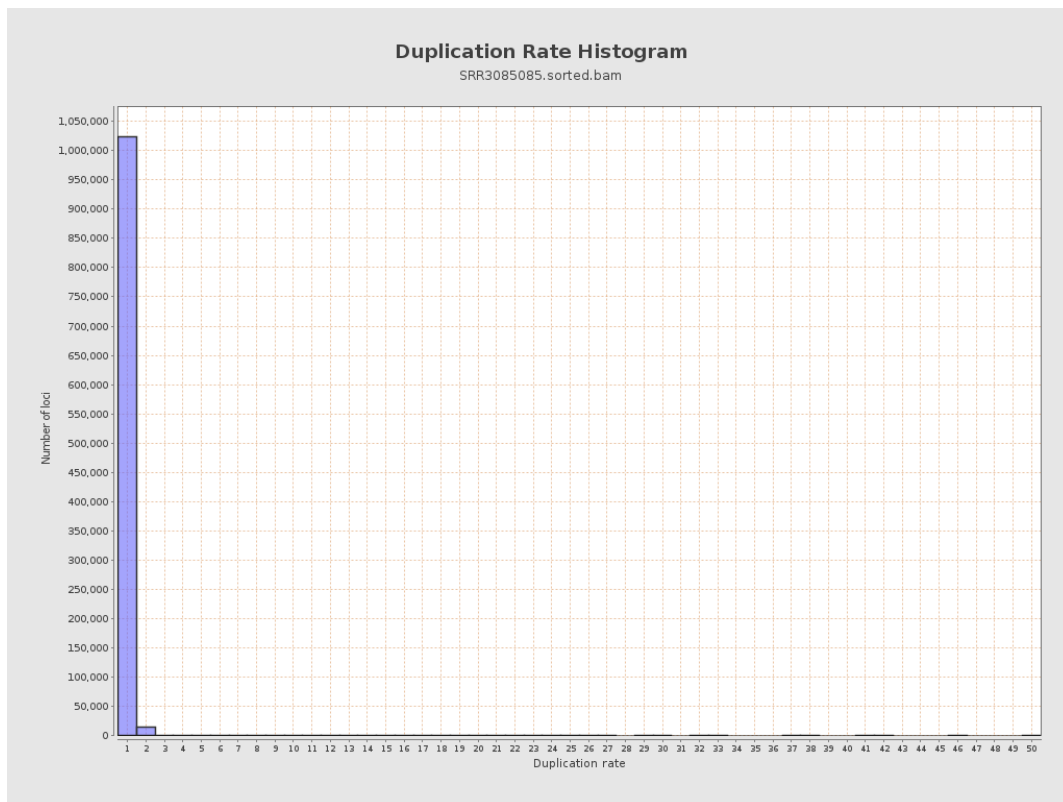
5. Results : Coverage Histogram (0-50X)



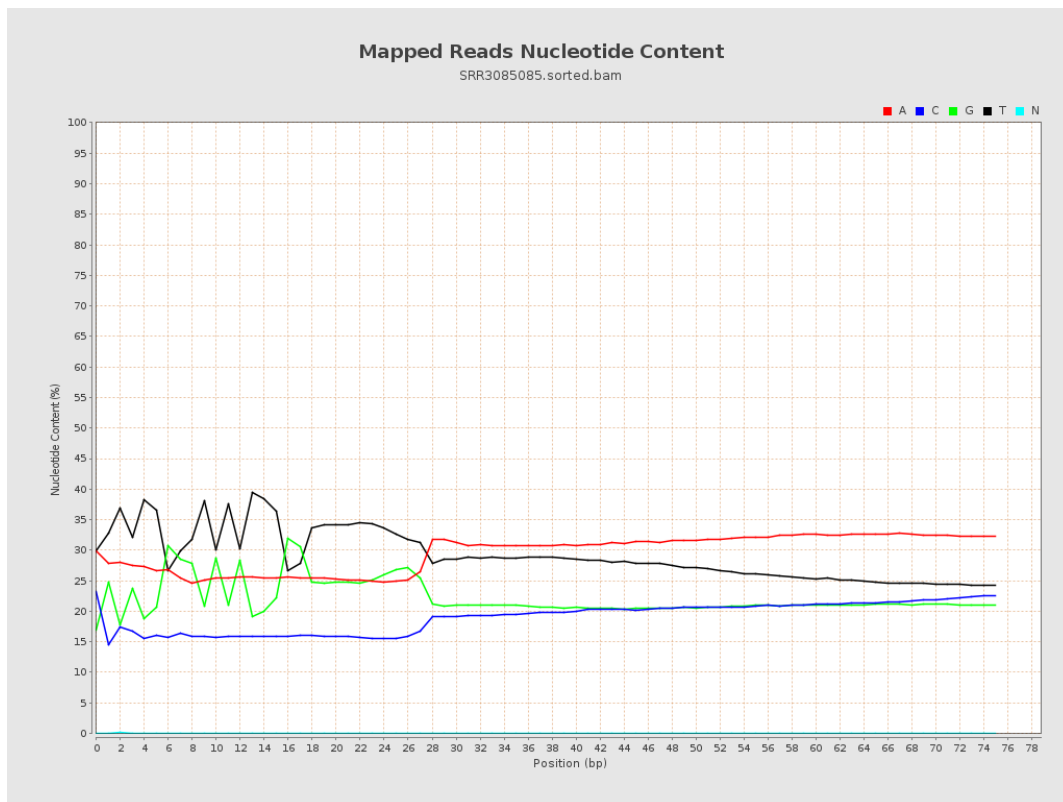
6. Results : Genome Fraction Coverage



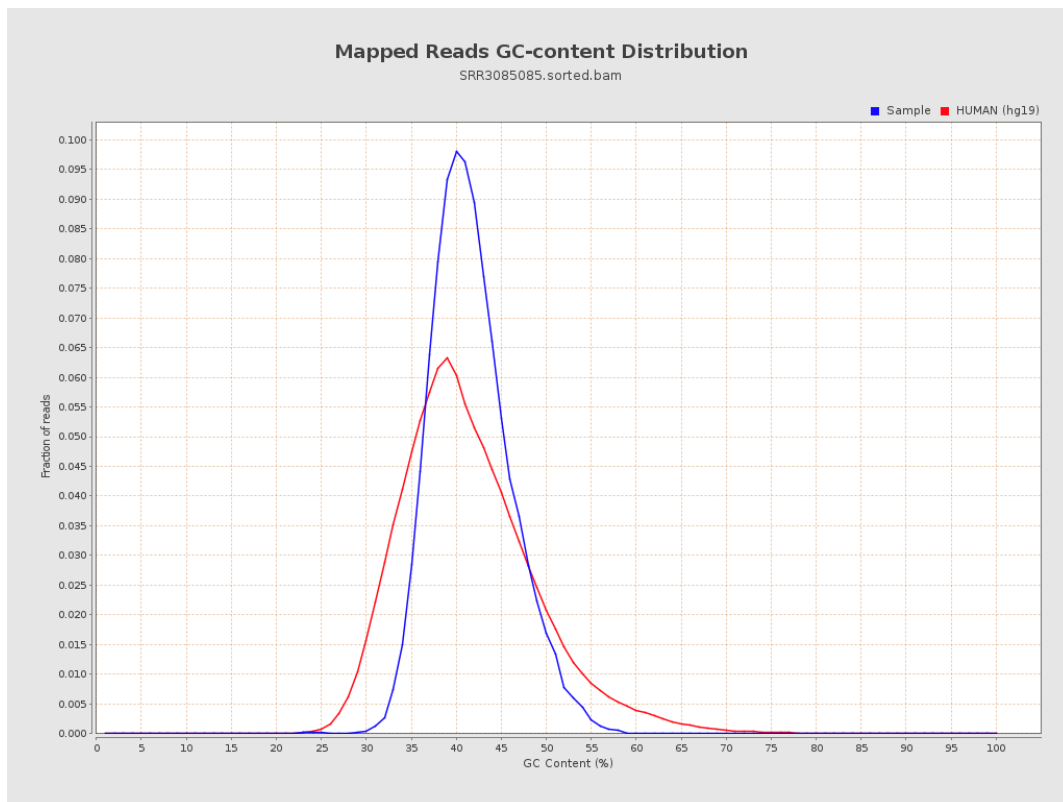
7. Results : Duplication Rate Histogram



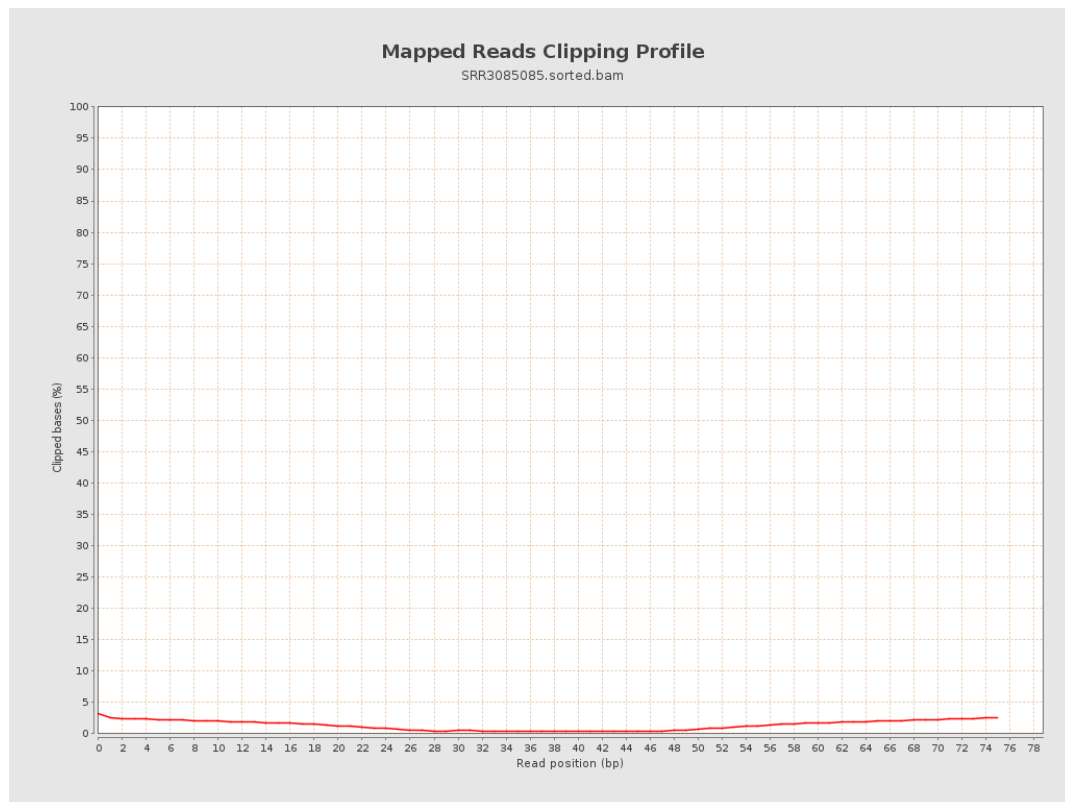
8. Results : Mapped Reads Nucleotide Content



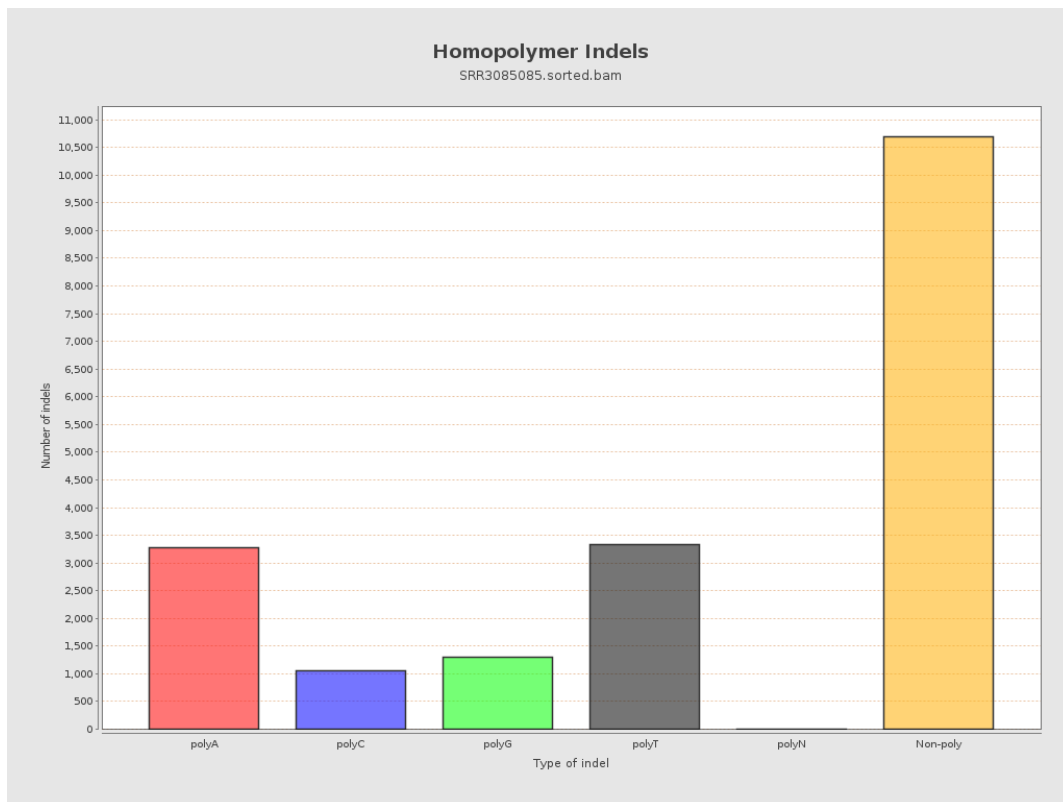
9. Results : Mapped Reads GC-content Distribution



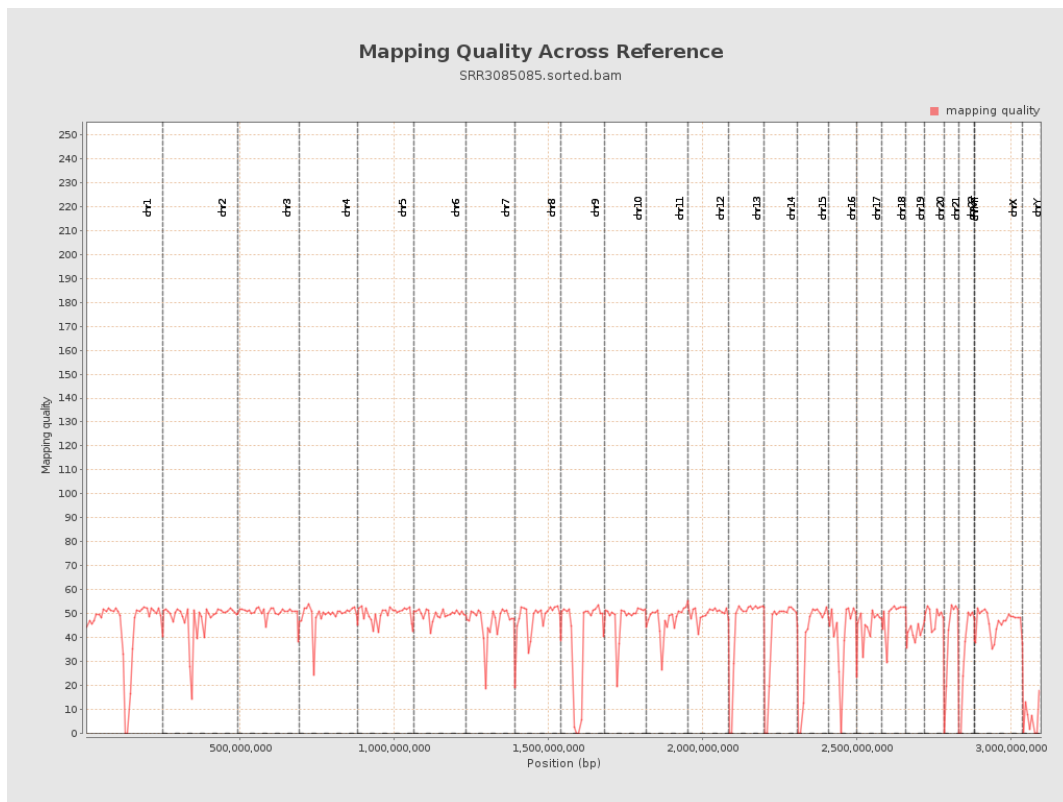
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

