Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 19:06:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6003985.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_SRR6003985 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6003985.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 19:06:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6003985.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,306,422
Mapped reads	3,646,966 / 84.69%
Unmapped reads	659,456 / 15.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,046 / 0.65%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	325,443 / 7.56%
Duplication rate	7.14%
Clipped reads	1,601,082 / 37.18%

2.2. ACGT Content

Number/percentage of A's	68,543,429 / 28.08%
Number/percentage of C's	43,400,198 / 17.78%
Number/percentage of T's	81,223,026 / 33.28%
Number/percentage of G's	50,875,519 / 20.84%
Number/percentage of N's	26,831 / 0.01%
GC Percentage	38.63%

2.3. Coverage

Mean	0.0789

Standard Deviation	0.6596

2.4. Mapping Quality

Mean Mapping Quality	46.12

2.5. Mismatches and indels

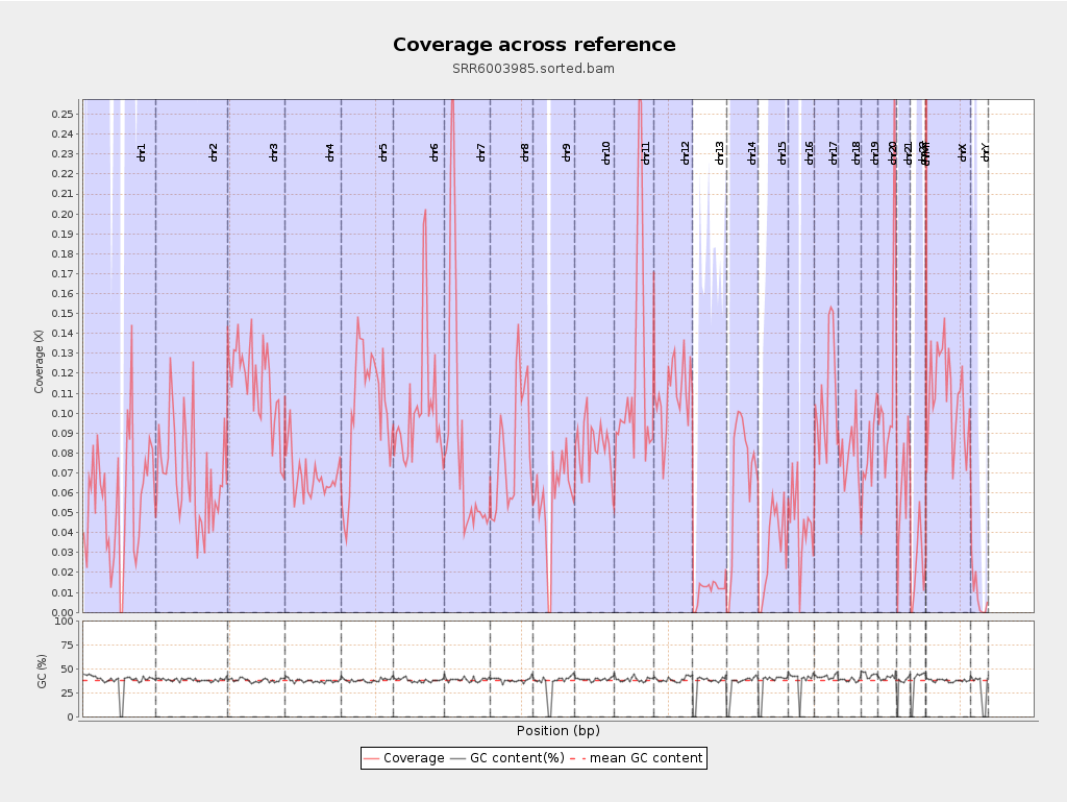
General error rate	1.01%
Mismatches	2,415,142
Insertions	21,899
Mapped reads with at least one insertion	0.6%
Deletions	68,427
Mapped reads with at least one deletion	1.85%
Homopolymer indels	47.33%

2.6. Chromosome stats

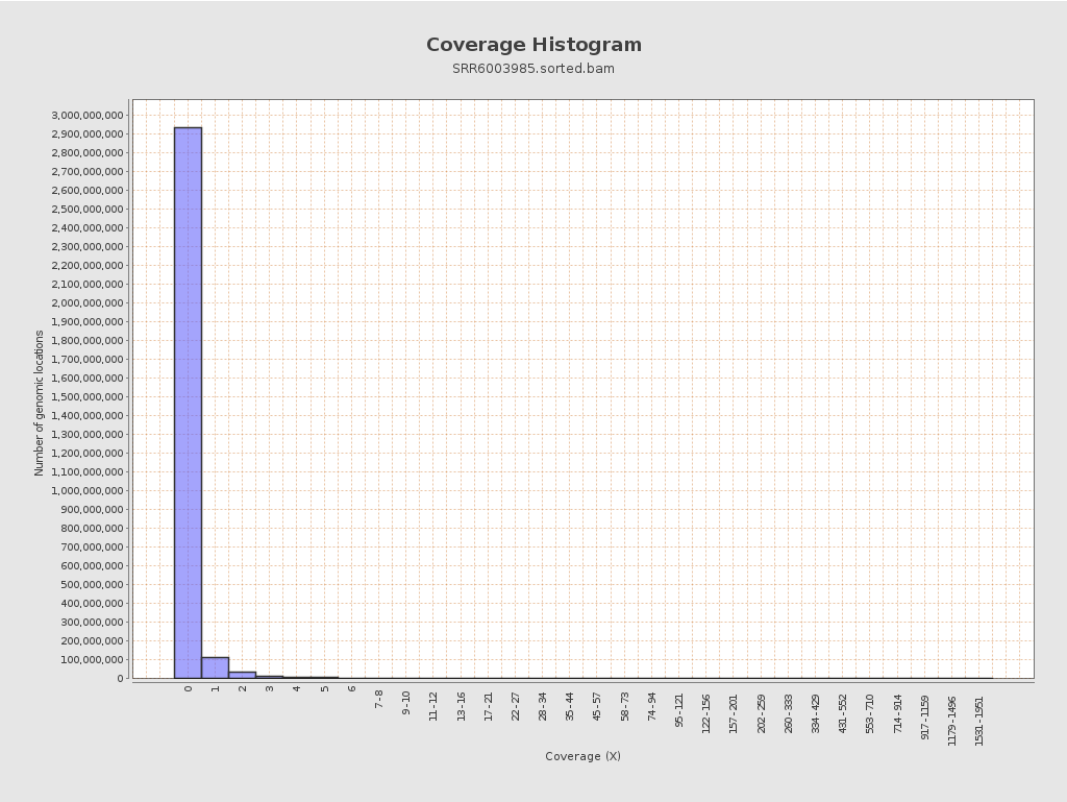
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	14004591	0.0562	0.9654
chr2	243199373	16871295	0.0694	0.8415
chr3	198022430	22855057	0.1154	0.478
chr4	191154276	13183687	0.069	0.3854
chr5	180915260	18577459	0.1027	0.4577
chr6	171115067	17547394	0.1025	0.514
chr7	159138663	13235331	0.0832	0.6937

chr8	146364022	12208301	0.0834	1.2457
chr9	141213431	8078032	0.0572	0.5916
chr10	135534747	11315660	0.0835	0.5749
chr11	135006516	15896789	0.1177	0.7605
chr12	133851895	14742419	0.1101	0.4782
chr13	115169878	1284614	0.0112	0.1539
chr14	107349540	7468392	0.0696	0.4049
chr15	102531392	3193437	0.0311	0.2441
chr16	90354753	3987525	0.0441	0.326
chr17	81195210	9027252	0.1112	0.5316
chr18	78077248	6207557	0.0795	1.0045
chr19	59128983	4795862	0.0811	0.7079
chr20	63025520	7482584	0.1187	0.4975
chr21	48129895	2882266	0.0599	0.3637
chr22	51304566	1185902	0.0231	0.197
chrMT	16571	690137	41.6473	25.2101
chrX	155270560	16960644	0.1092	0.5337
chrY	59373566	498347	0.0084	0.1588

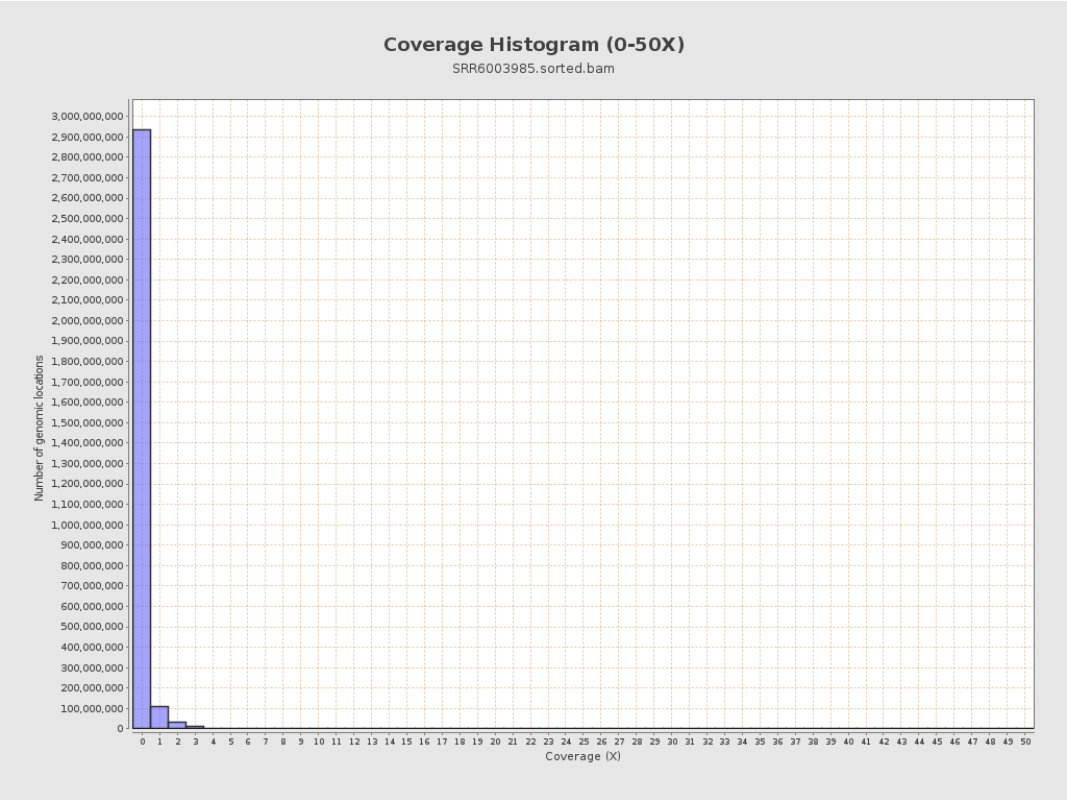
3. Results : Coverage across reference



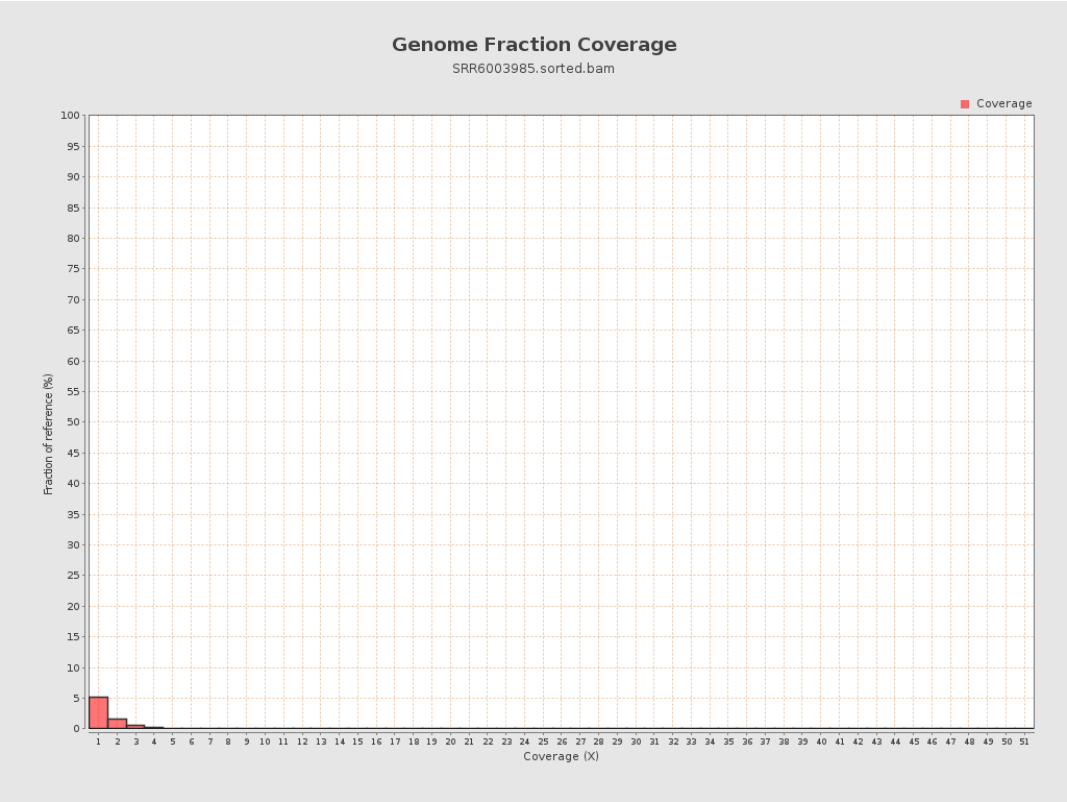
4. Results : Coverage Histogram



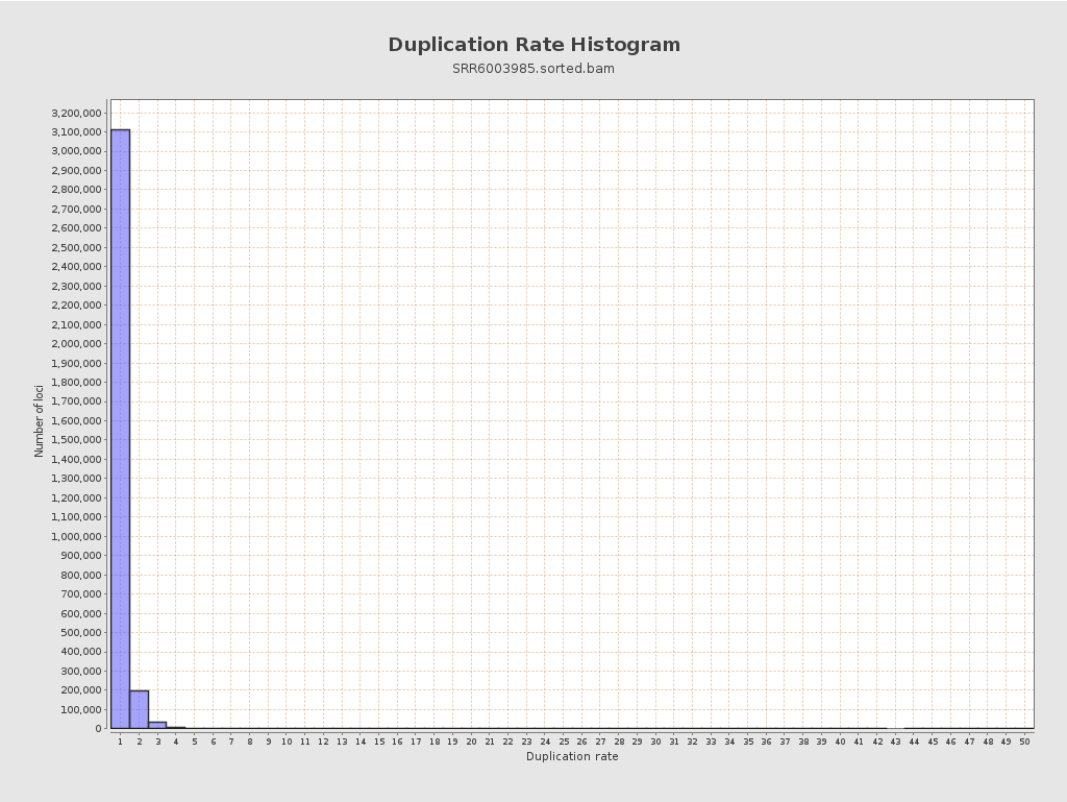
5. Results : Coverage Histogram (0-50X)



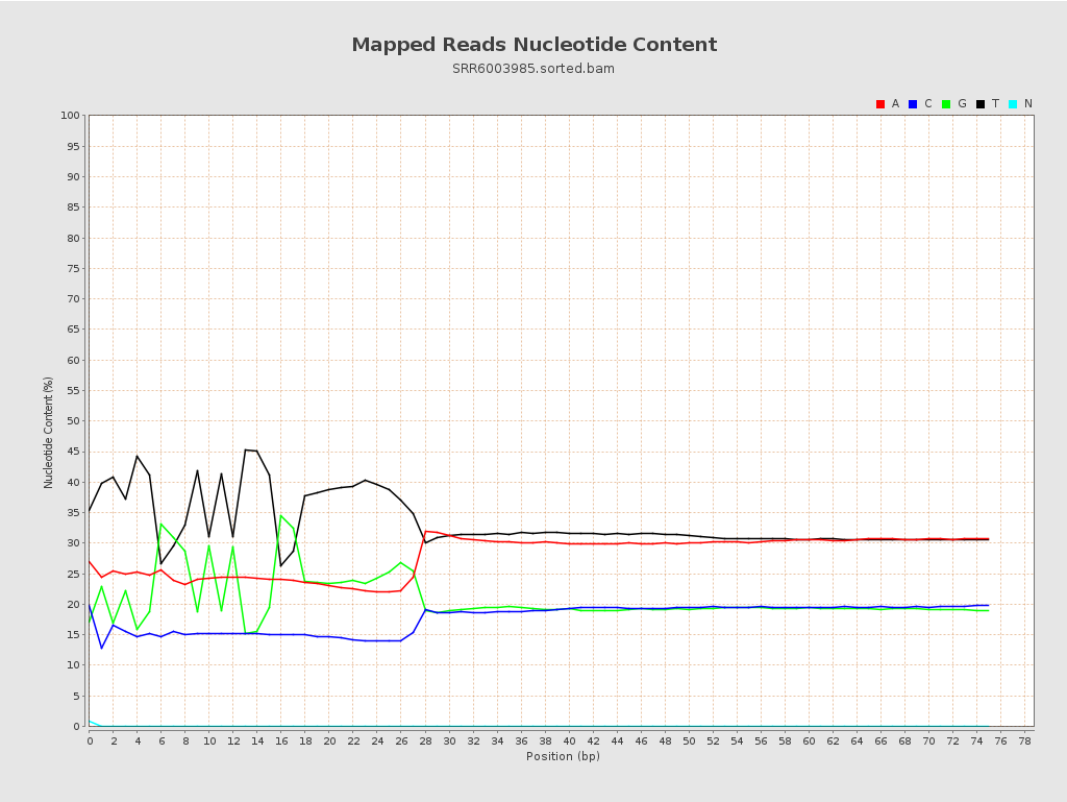
6. Results : Genome Fraction Coverage



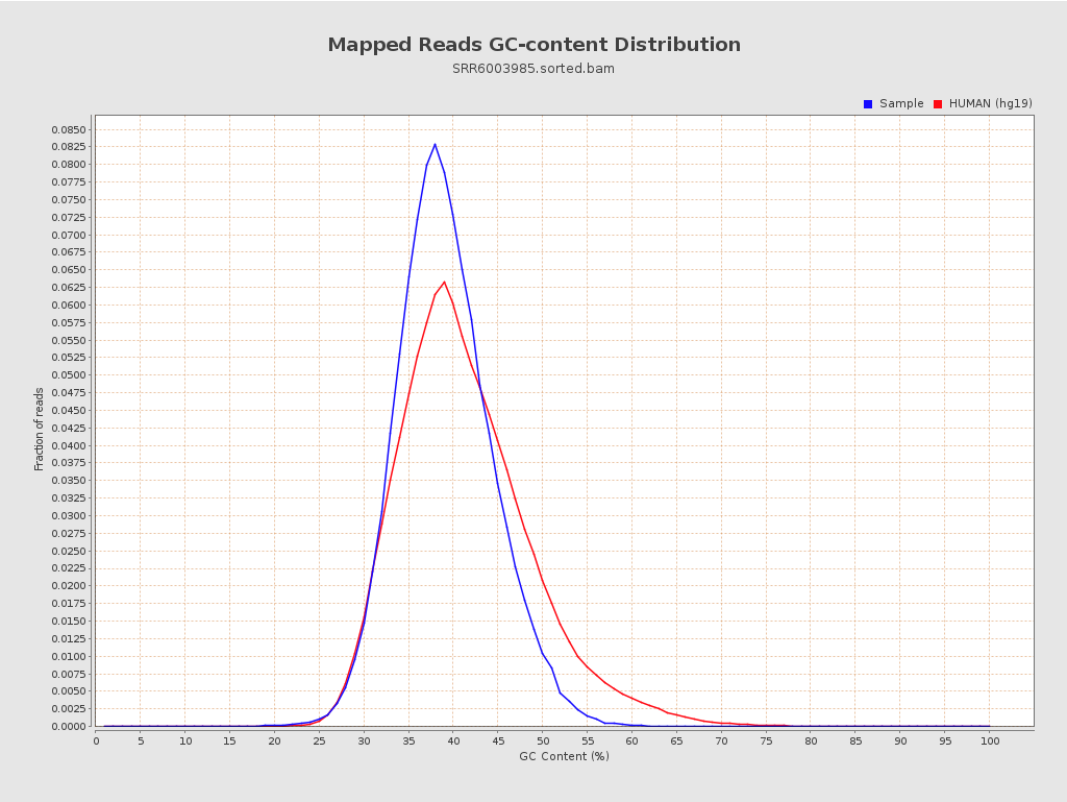
7. Results : Duplication Rate Histogram



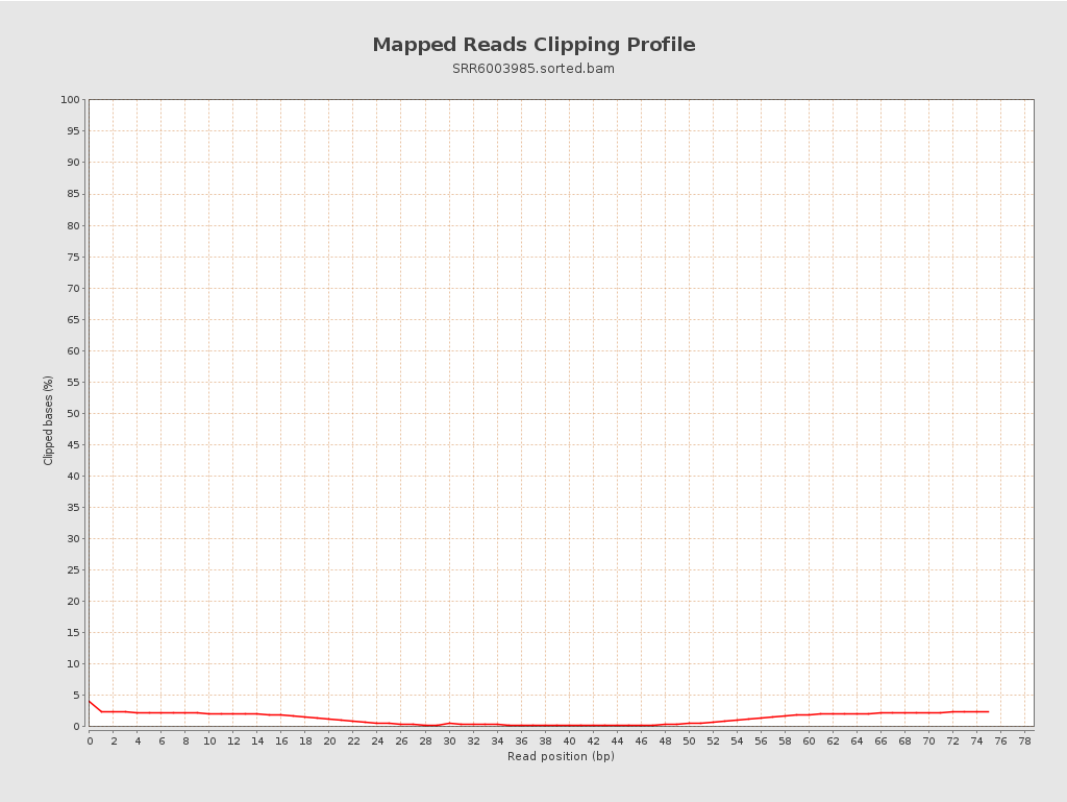
8. Results : Mapped Reads Nucleotide Content



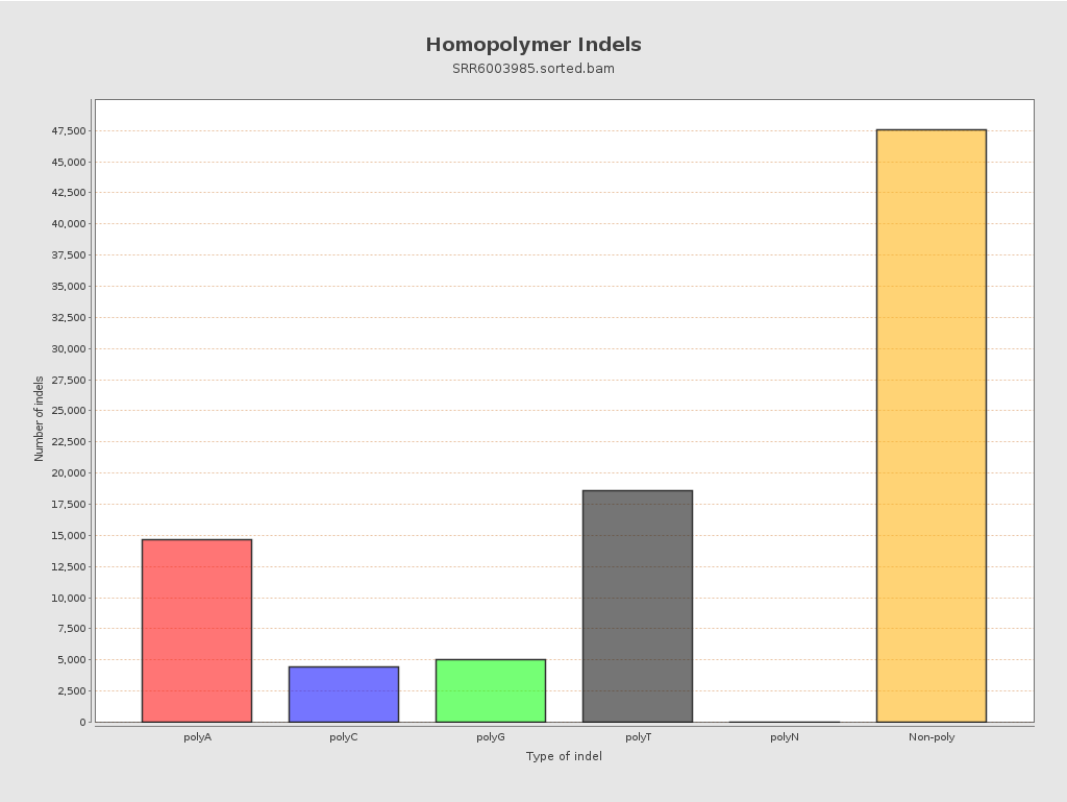
9. Results : Mapped Reads GC-content Distribution



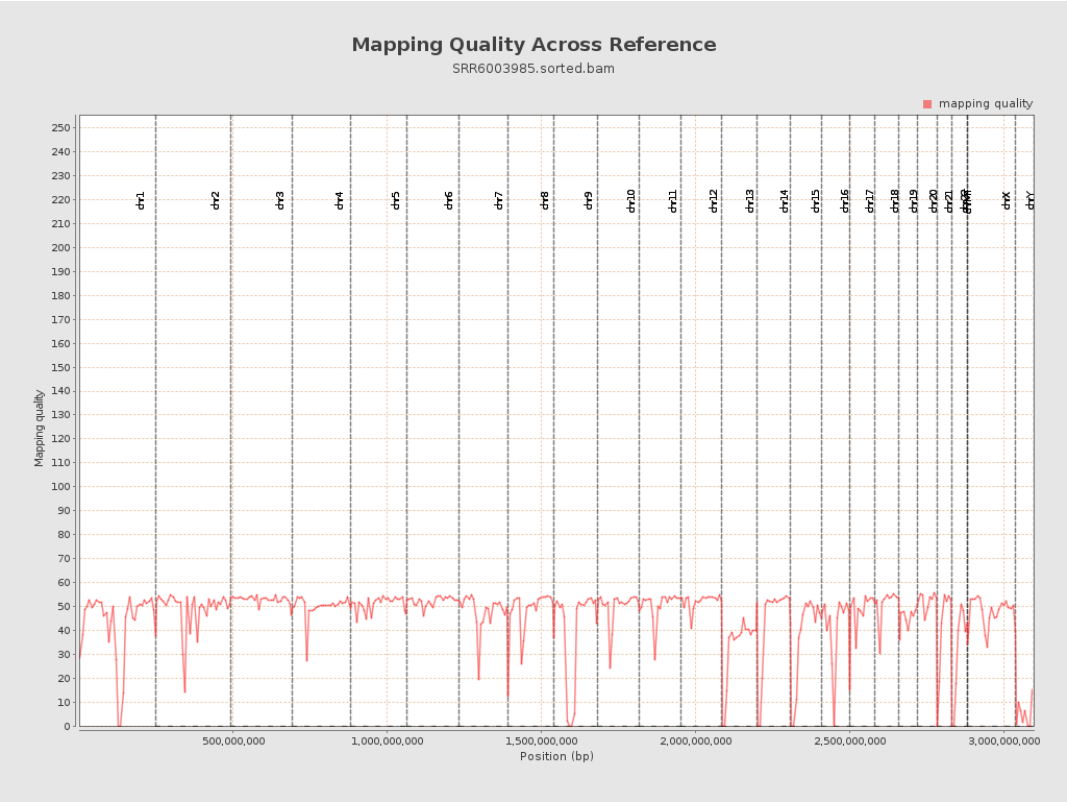
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram