Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 23:45:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085046.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_SRR3085046 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085046.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 23:45:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085046.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,347,587
Mapped reads	3,057,985 / 91.35%
Unmapped reads	289,602 / 8.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,086 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	123,665 / 3.69%
Duplication rate	3.22%
Clipped reads	1,381,109 / 41.26%

2.2. ACGT Content

Number/percentage of A's	59,176,867 / 28.92%
Number/percentage of C's	39,068,221 / 19.09%
Number/percentage of T's	63,056,334 / 30.82%
Number/percentage of G's	43,288,784 / 21.16%
Number/percentage of N's	22,779 / 0.01%
GC Percentage	40.25%

2.3. Coverage

Mean	0.0661

Standard Deviation	0.4548

2.4. Mapping Quality

Mean Mapping Quality	46.13

2.5. Mismatches and indels

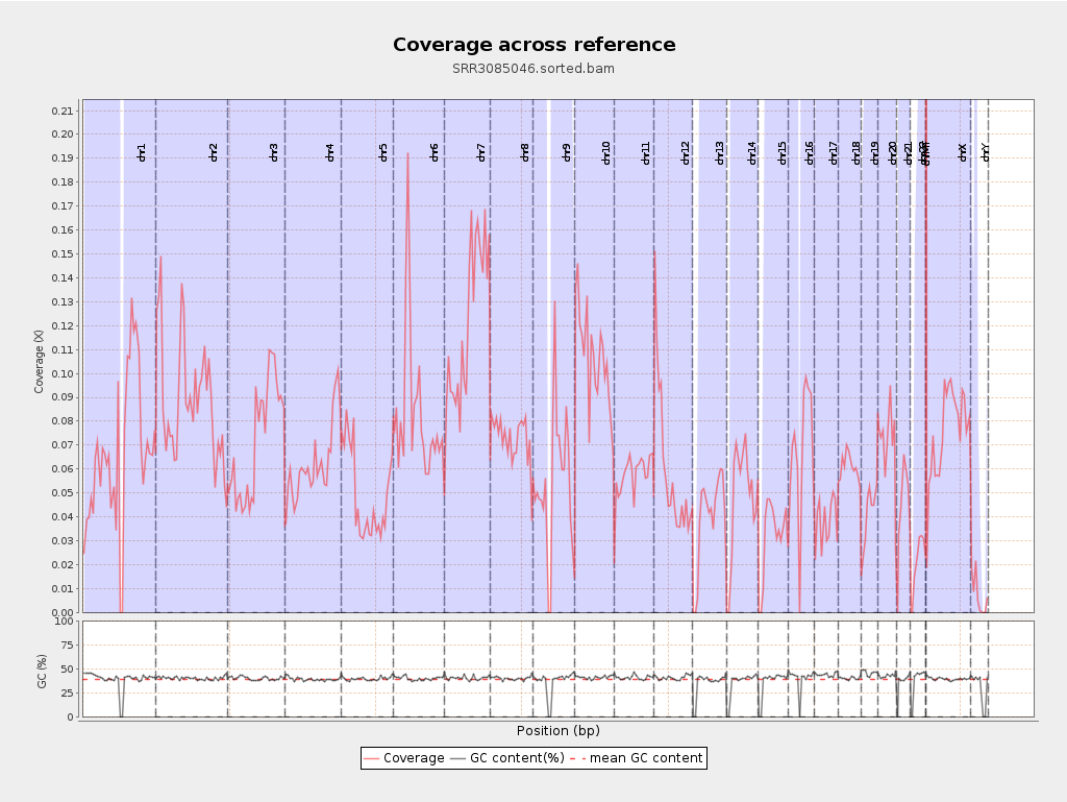
General error rate	0.91%
Mismatches	1,831,427
Insertions	14,469
Mapped reads with at least one insertion	0.47%
Deletions	43,122
Mapped reads with at least one deletion	1.4%
Homopolymer indels	47.46%

2.6. Chromosome stats

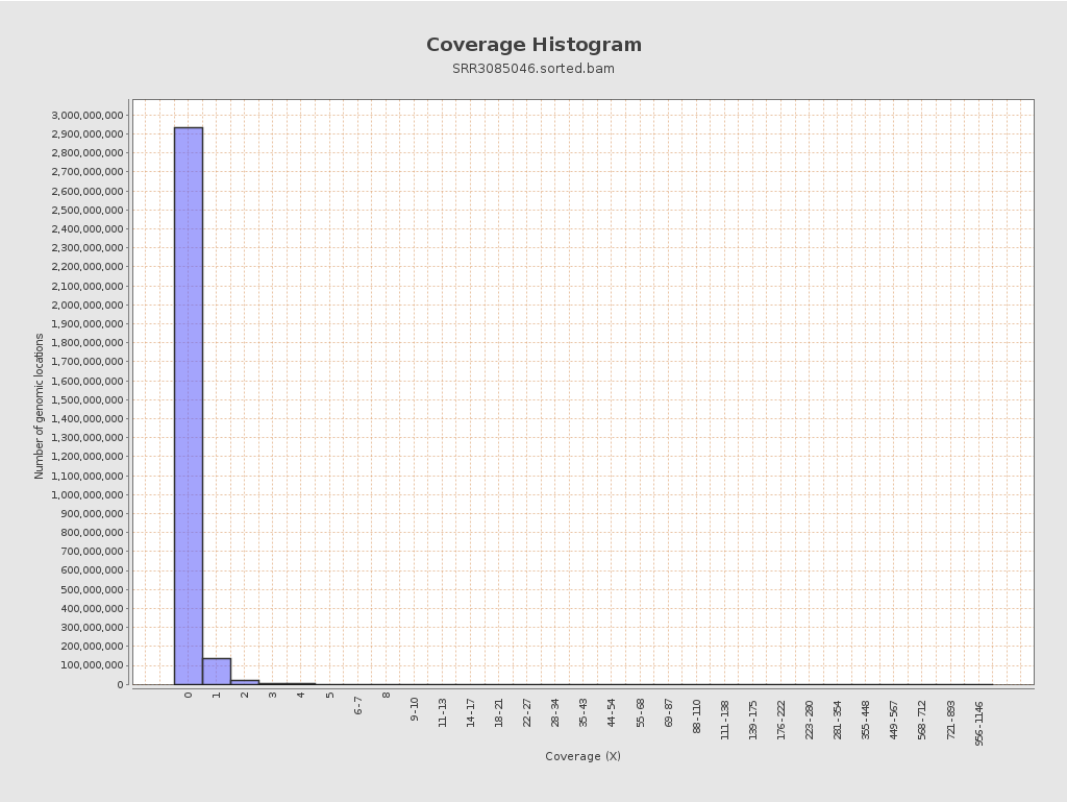
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	16427016	0.0659	0.6184
chr2	243199373	21681907	0.0892	0.5758
chr3	198022430	14099744	0.0712	0.3294
chr4	191154276	11957364	0.0626	0.314
chr5	180915260	8949966	0.0495	0.2652
chr6	171115067	14468596	0.0846	0.4085
chr7	159138663	19271262	0.1211	0.5881

chr8	146364022	10616176	0.0725	0.7566
chr9	141213431	7693849	0.0545	0.4081
chr10	135534747	14445898	0.1066	0.6357
chr11	135006516	7785333	0.0577	0.5137
chr12	133851895	8039406	0.0601	0.3021
chr13	115169878	4526201	0.0393	0.2354
chr14	107349540	5211299	0.0485	0.2898
chr15	102531392	3209869	0.0313	0.2147
chr16	90354753	5955148	0.0659	0.3237
chr17	81195210	3092742	0.0381	0.3098
chr18	78077248	4769871	0.0611	0.6363
chr19	59128983	2521522	0.0426	0.4377
chr20	63025520	4557893	0.0723	0.3254
chr21	48129895	2135456	0.0444	0.2725
chr22	51304566	1081237	0.0211	0.1683
chrMT	16571	18114	1.0931	1.3782
chrX	155270560	11751313	0.0757	0.383
chrY	59373566	420511	0.0071	0.1511

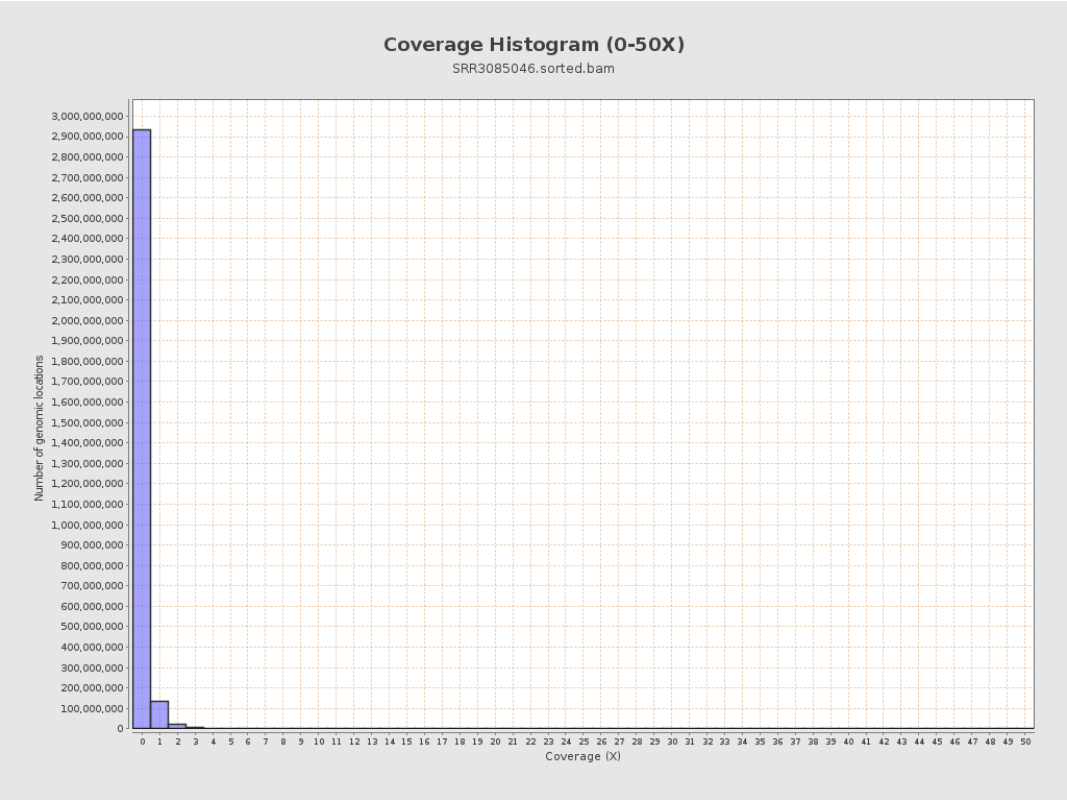
3. Results : Coverage across reference



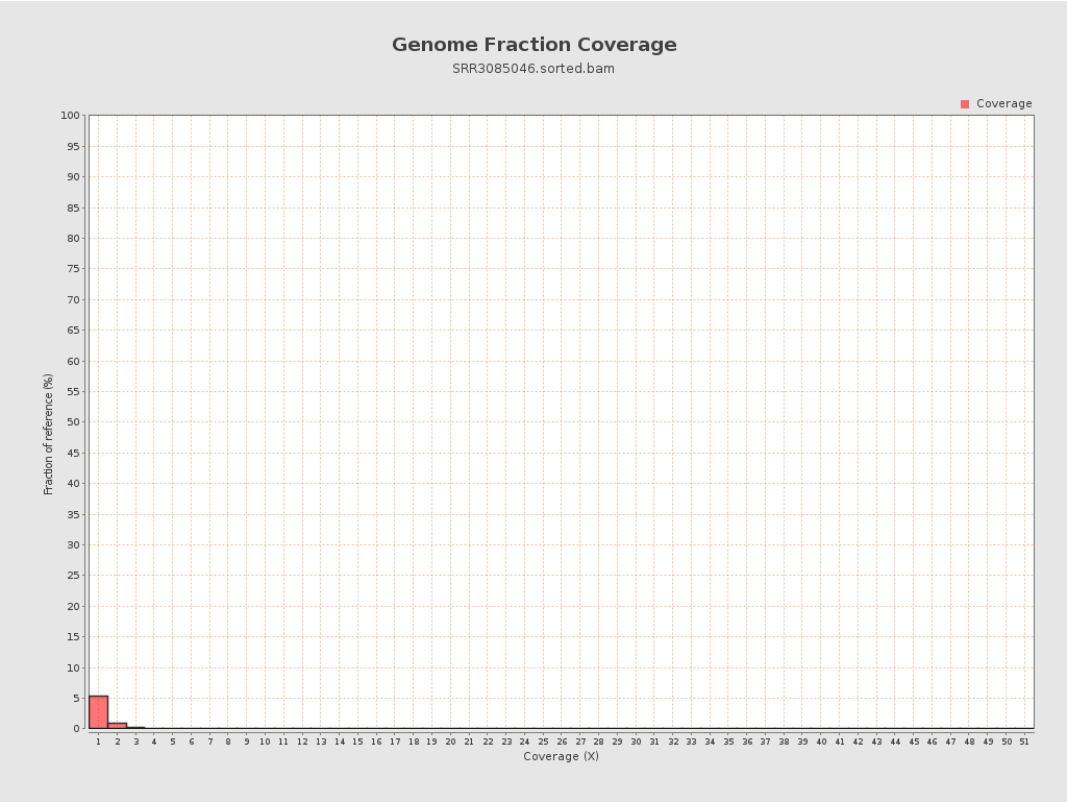
4. Results : Coverage Histogram



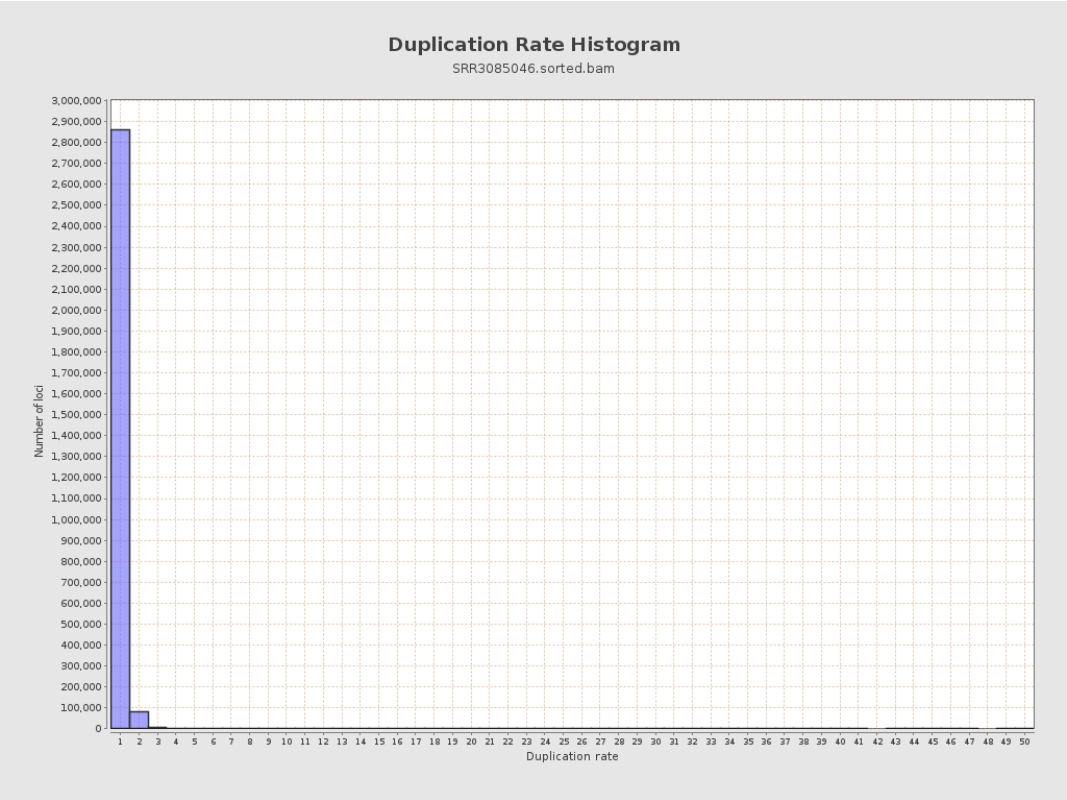
5. Results : Coverage Histogram (0-50X)



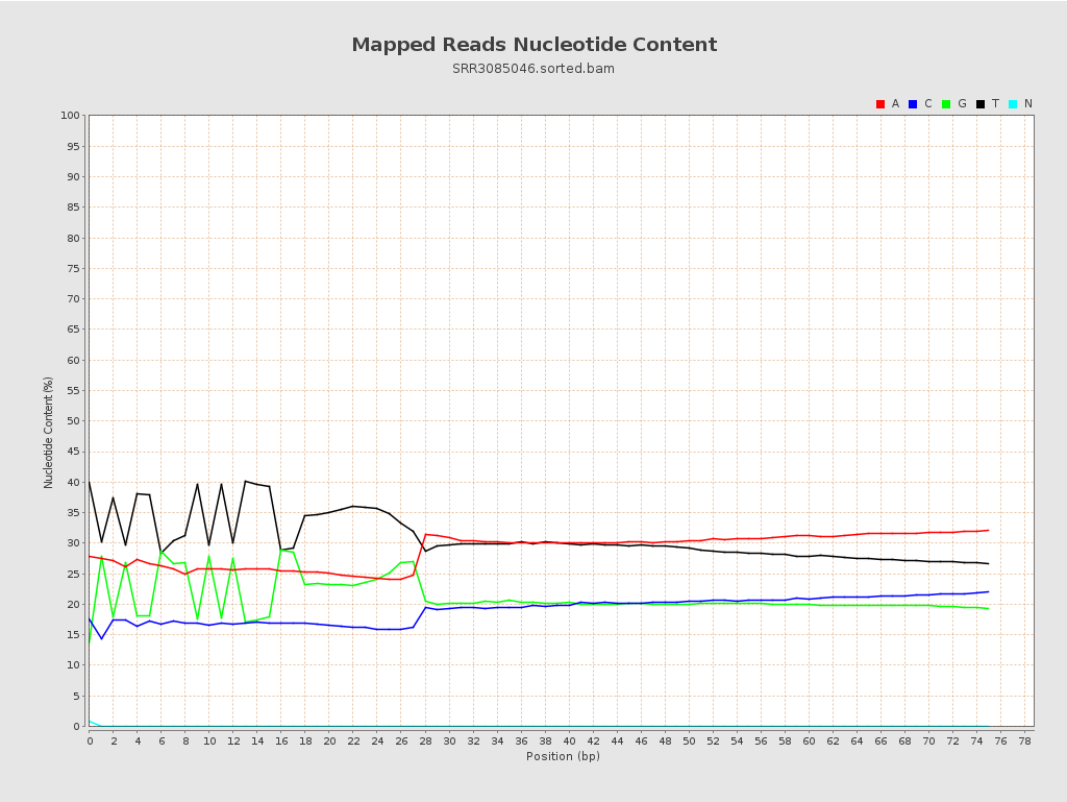
6. Results : Genome Fraction Coverage



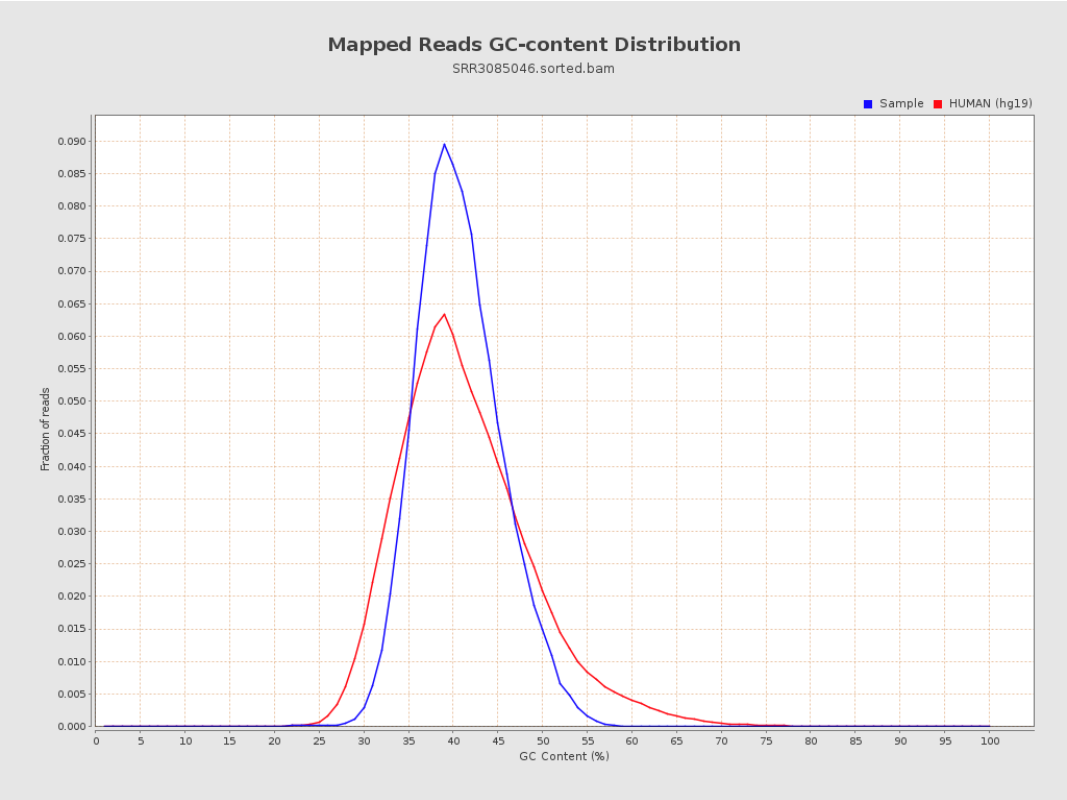
7. Results : Duplication Rate Histogram



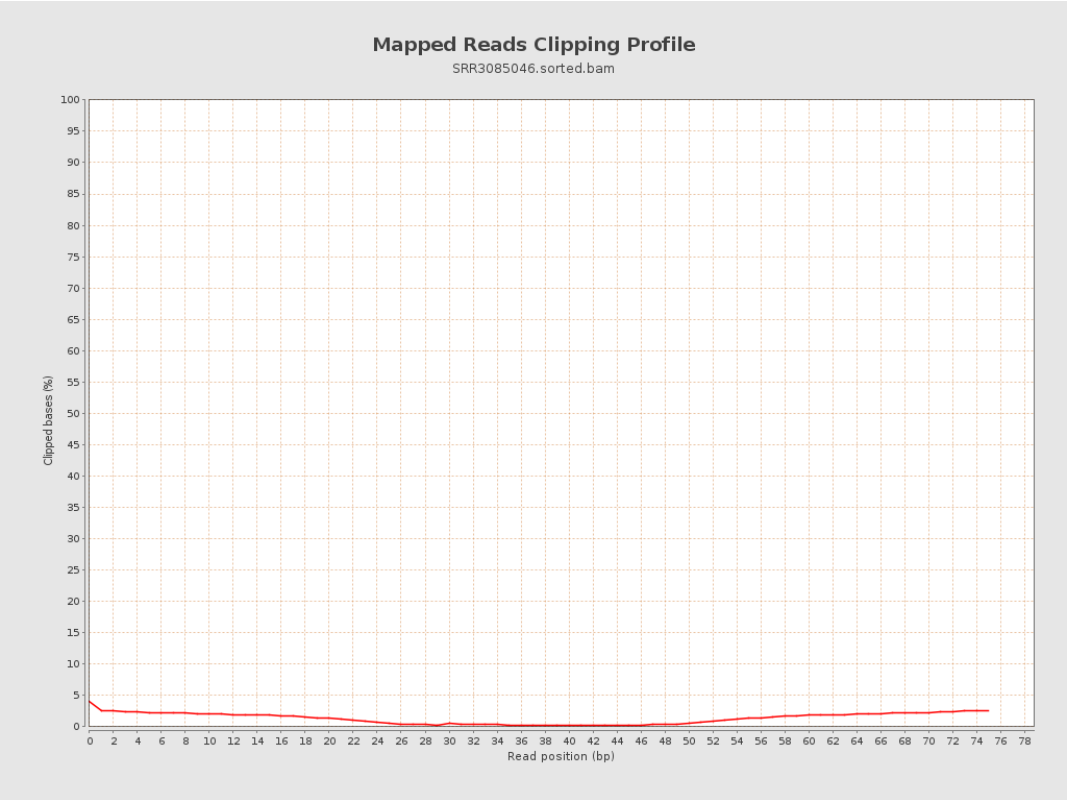
8. Results : Mapped Reads Nucleotide Content



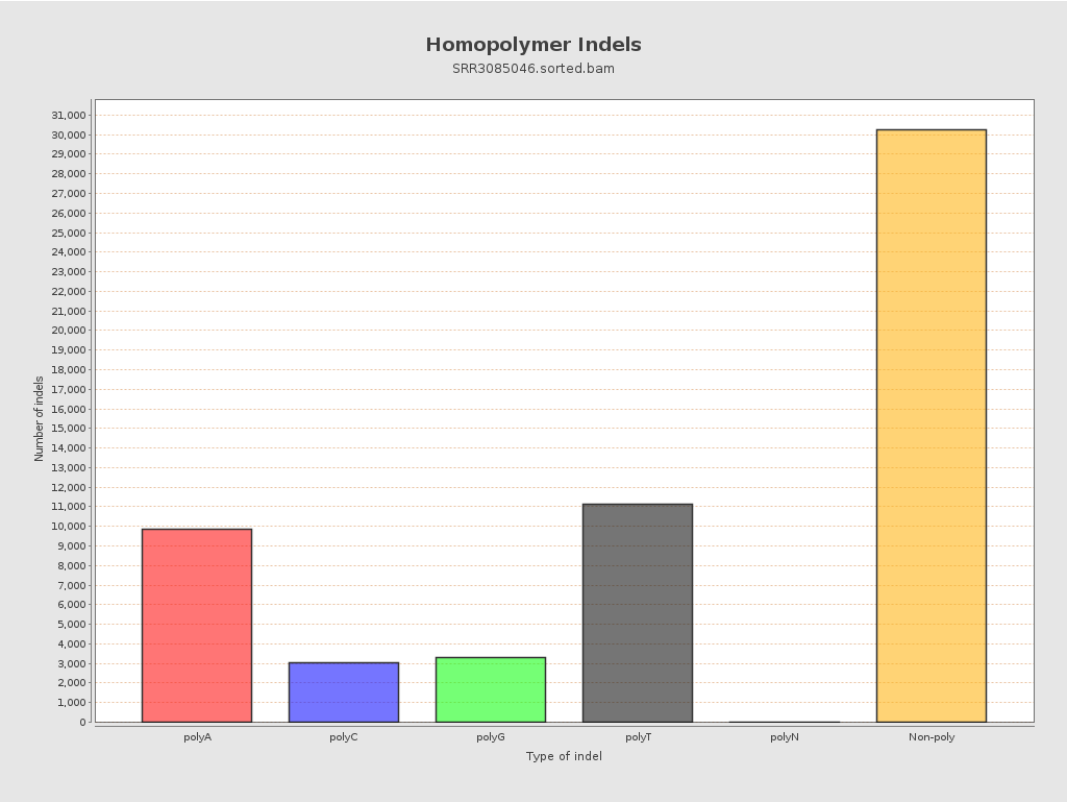
9. Results : Mapped Reads GC-content Distribution



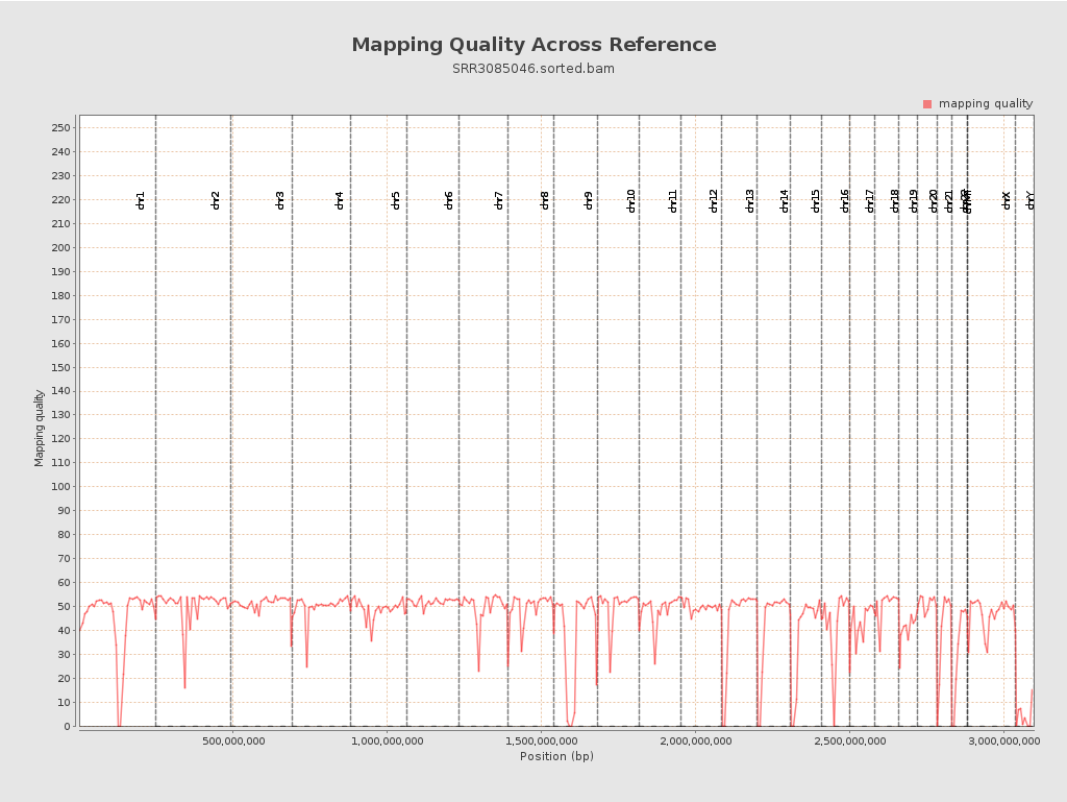
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram