Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 23:56:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085050.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_SRR3085050 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085050.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 23:56:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085050.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,051,077
Mapped reads	1,847,033 / 90.05%
Unmapped reads	204,044 / 9.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,698 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	54,871 / 2.68%
Duplication rate	2.21%
Clipped reads	809,181 / 39.45%

2.2. ACGT Content

Number/percentage of A's	35,921,767 / 28.97%
Number/percentage of C's	23,541,810 / 18.98%
Number/percentage of T's	37,980,086 / 30.63%
Number/percentage of G's	26,548,059 / 21.41%
Number/percentage of N's	13,855 / 0.01%
GC Percentage	40.39%

2.3. Coverage

Mean	0.0401

Standard Deviation	0.3399

2.4. Mapping Quality

Mean Mapping Quality	45.74

2.5. Mismatches and indels

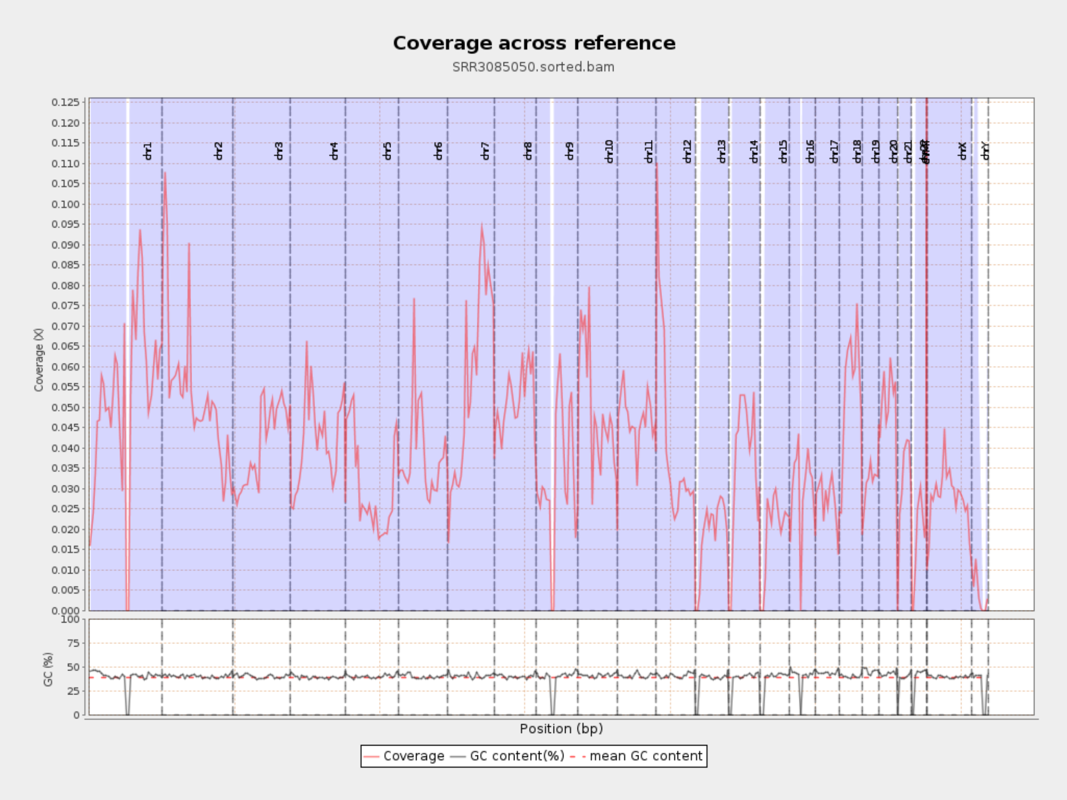
General error rate	0.91%
Mismatches	1,115,377
Insertions	9,048
Mapped reads with at least one insertion	0.49%
Deletions	25,914
Mapped reads with at least one deletion	1.39%
Homopolymer indels	45.61%

2.6. Chromosome stats

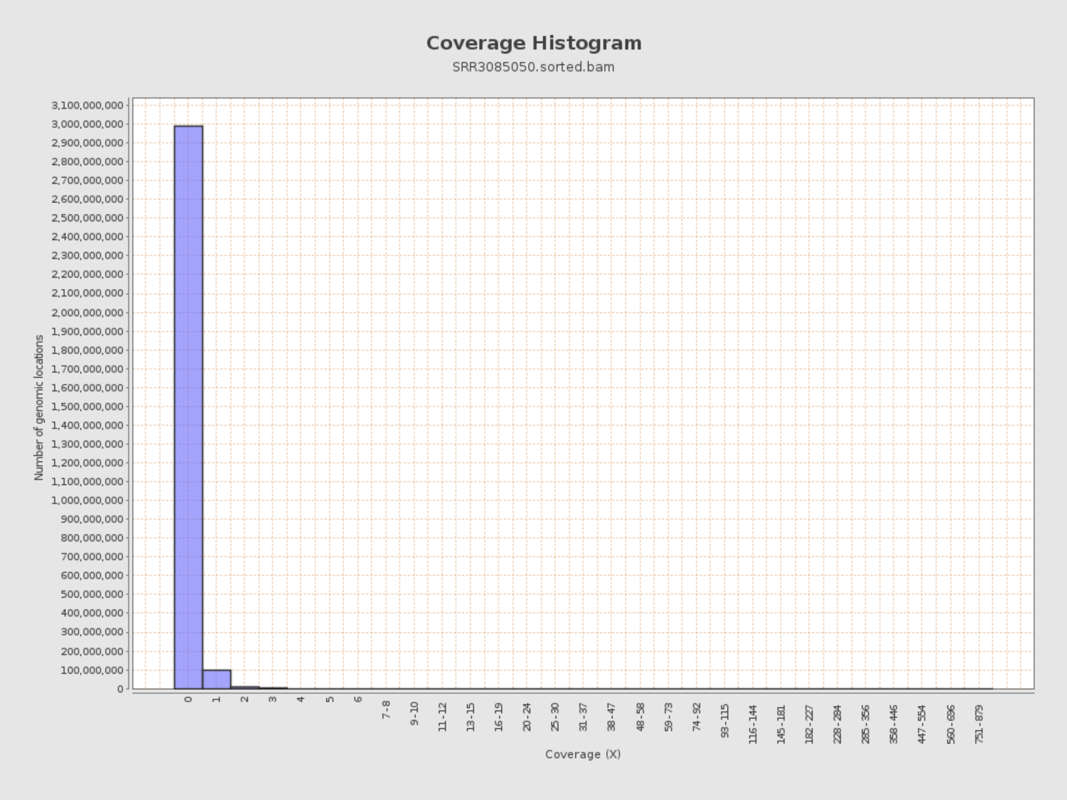
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13182352	0.0529	0.4936
chr2	243199373	13062961	0.0537	0.4212
chr3	198022430	8022332	0.0405	0.2276
chr4	191154276	8077253	0.0423	0.2344
chr5	180915260	5518104	0.0305	0.1937
chr6	171115067	6572761	0.0384	0.2918
chr7	159138663	9205254	0.0578	0.4511

chr8	146364022	7639668	0.0522	0.5864
chr9	141213431	4689310	0.0332	0.3173
chr10	135534747	6814302	0.0503	0.4261
chr11	135006516	6303048	0.0467	0.3419
chr12	133851895	5627991	0.042	0.2339
chr13	115169878	2163015	0.0188	0.1498
chr14	107349540	3939432	0.0367	0.2303
chr15	102531392	2014047	0.0196	0.157
chr16	90354753	2706726	0.03	0.2137
chr17	81195210	2208357	0.0272	0.2098
chr18	78077248	4285362	0.0549	0.5759
chr19	59128983	1882218	0.0318	0.3401
chr20	63025520	3240123	0.0514	0.2544
chr21	48129895	1499436	0.0312	0.2121
chr22	51304566	872654	0.017	0.1417
chrMT	16571	2902	0.1751	0.4435
chrX	155270560	4286336	0.0276	0.2195
chrY	59373566	233757	0.0039	0.101

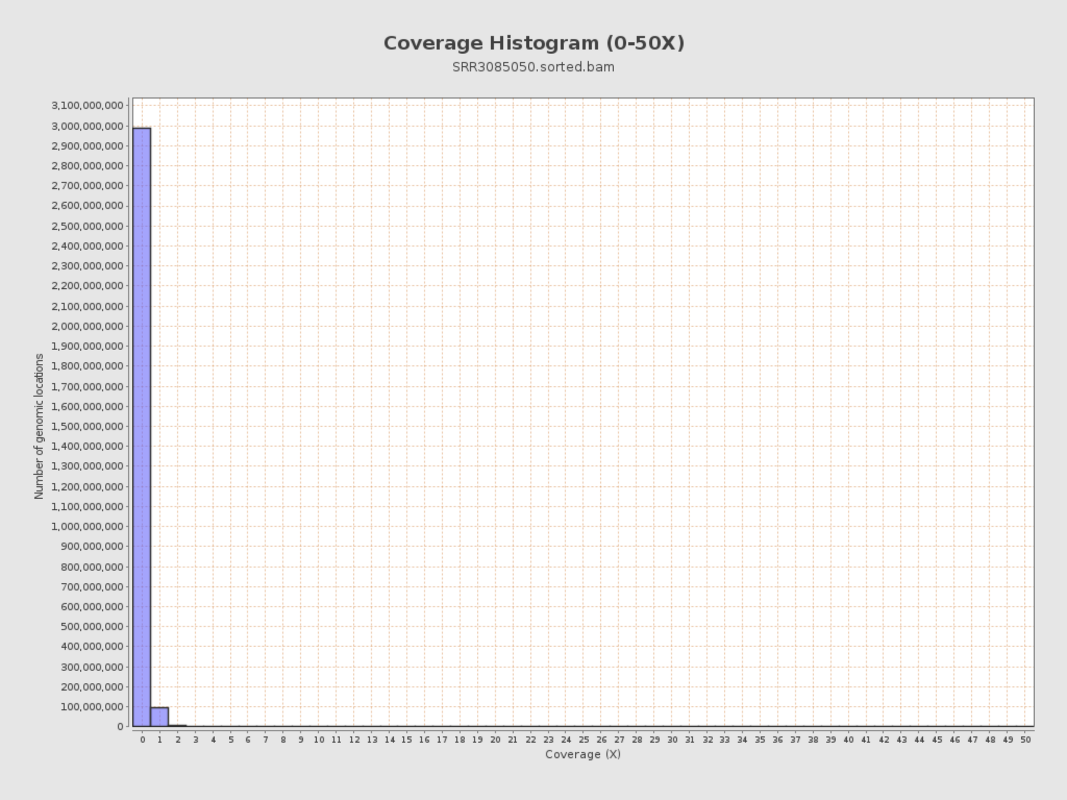
3. Results : Coverage across reference



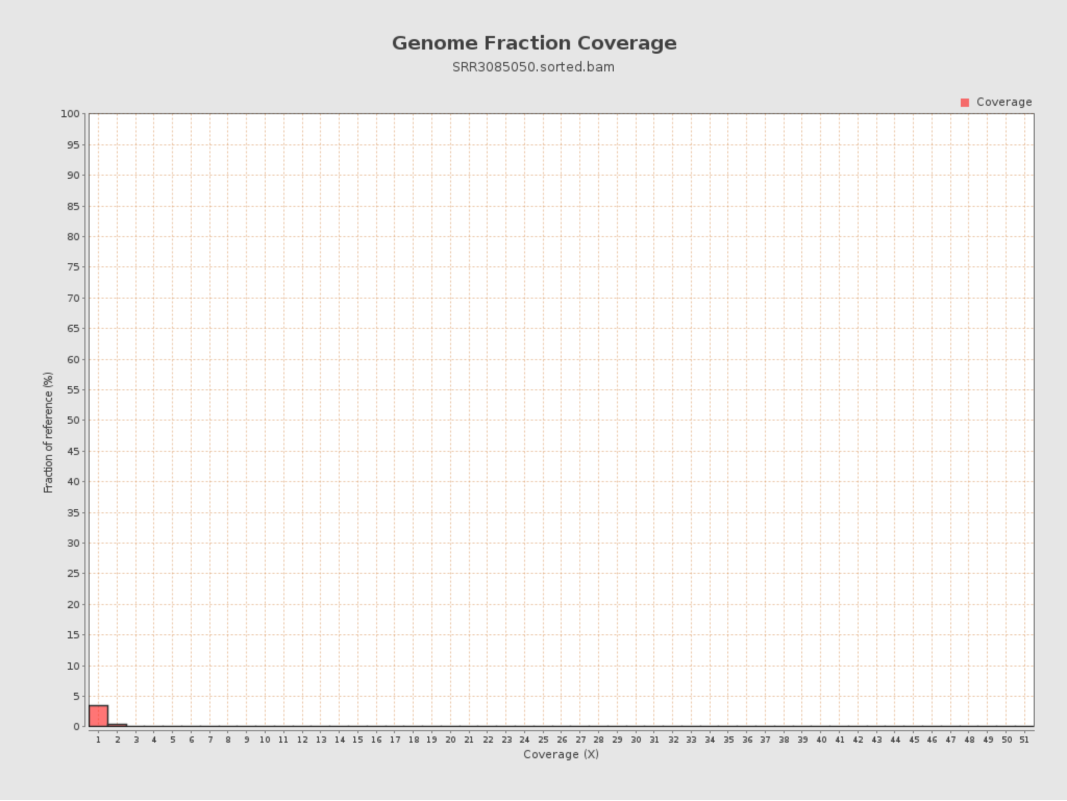
4. Results : Coverage Histogram



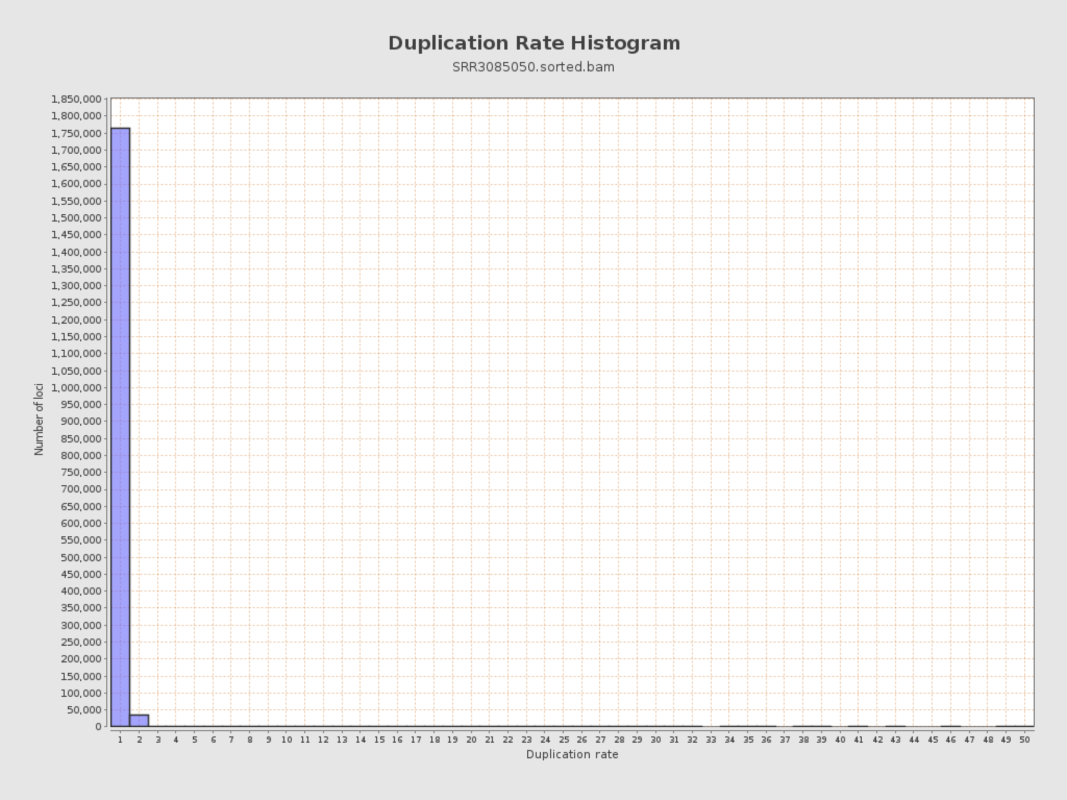
5. Results : Coverage Histogram (0-50X)



6. Results : Genome Fraction Coverage



7. Results : Duplication Rate Histogram



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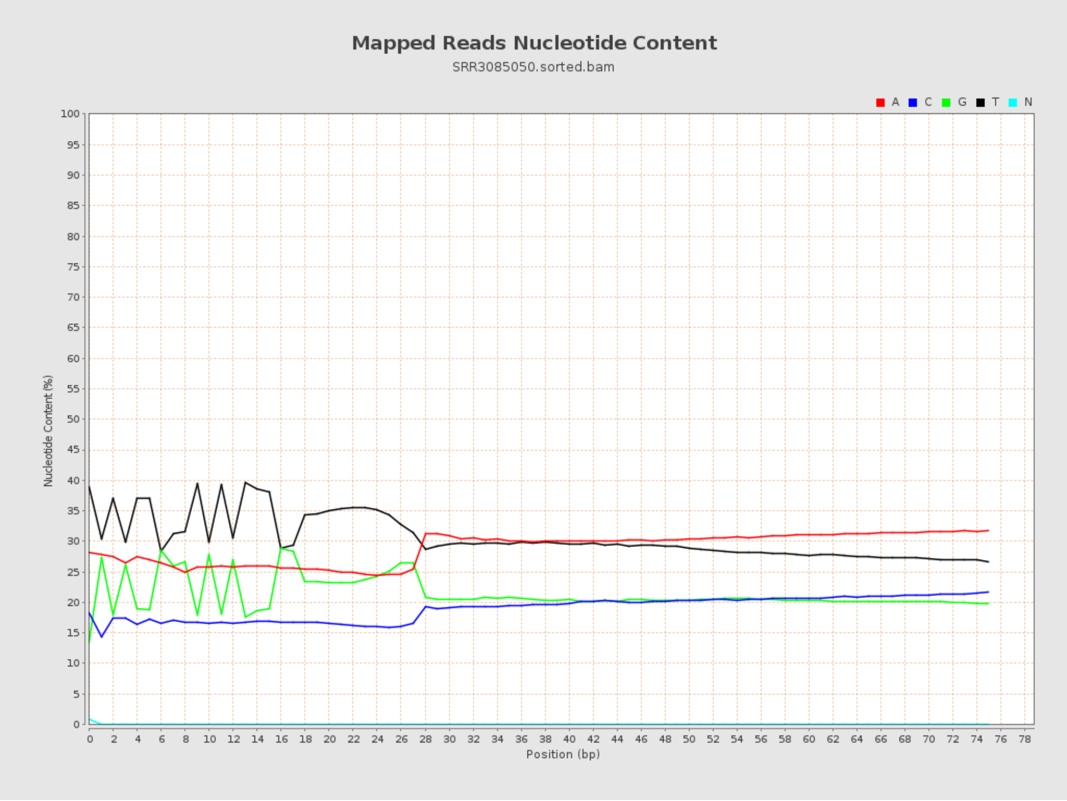
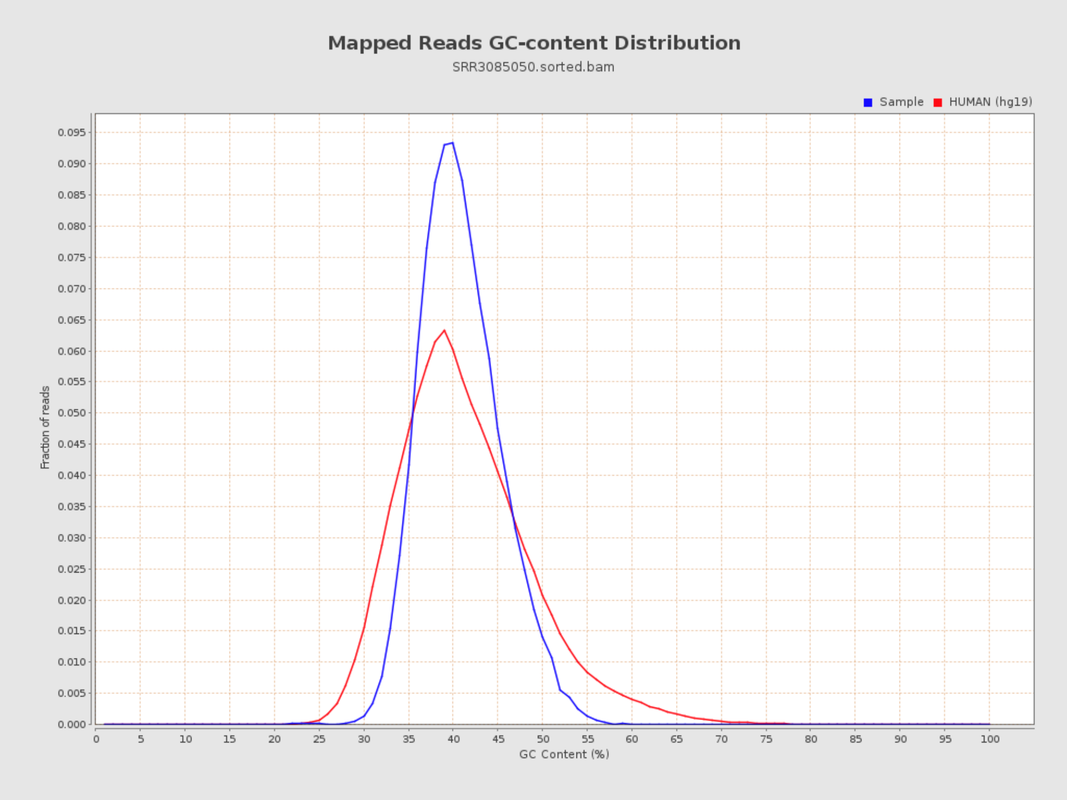
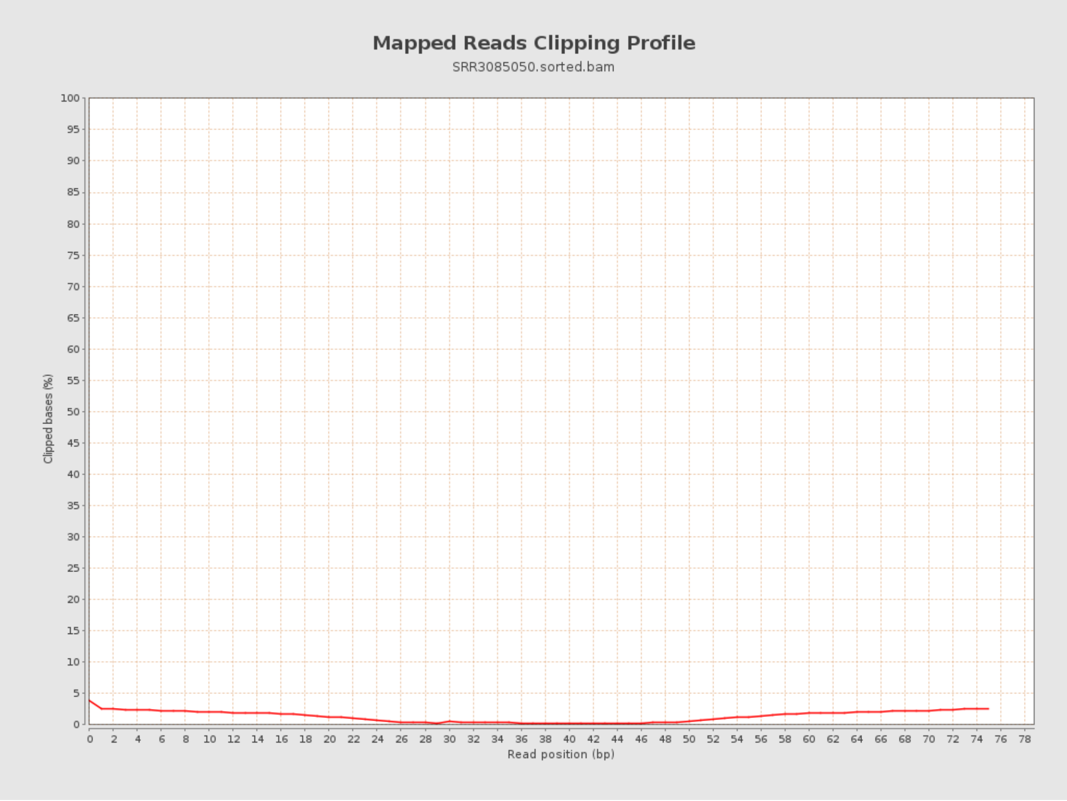
8. Results : Mapped Reads Nucleotide Content



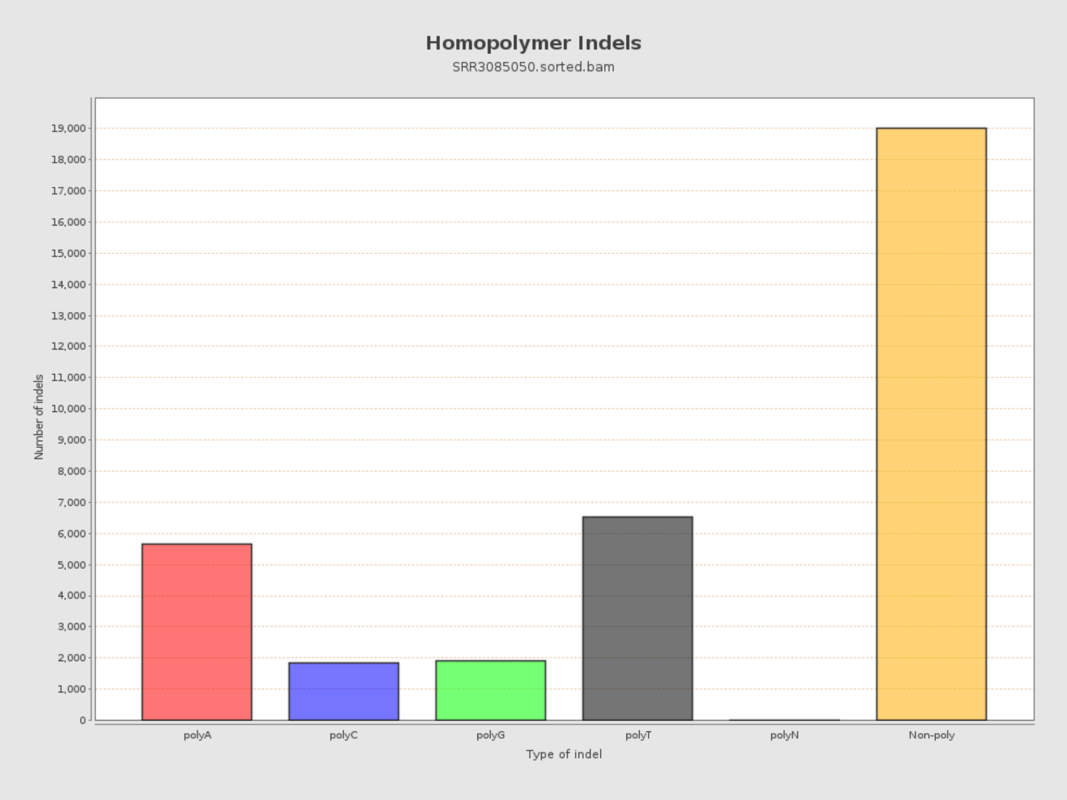
9. Results : Mapped Reads GC-content Distribution



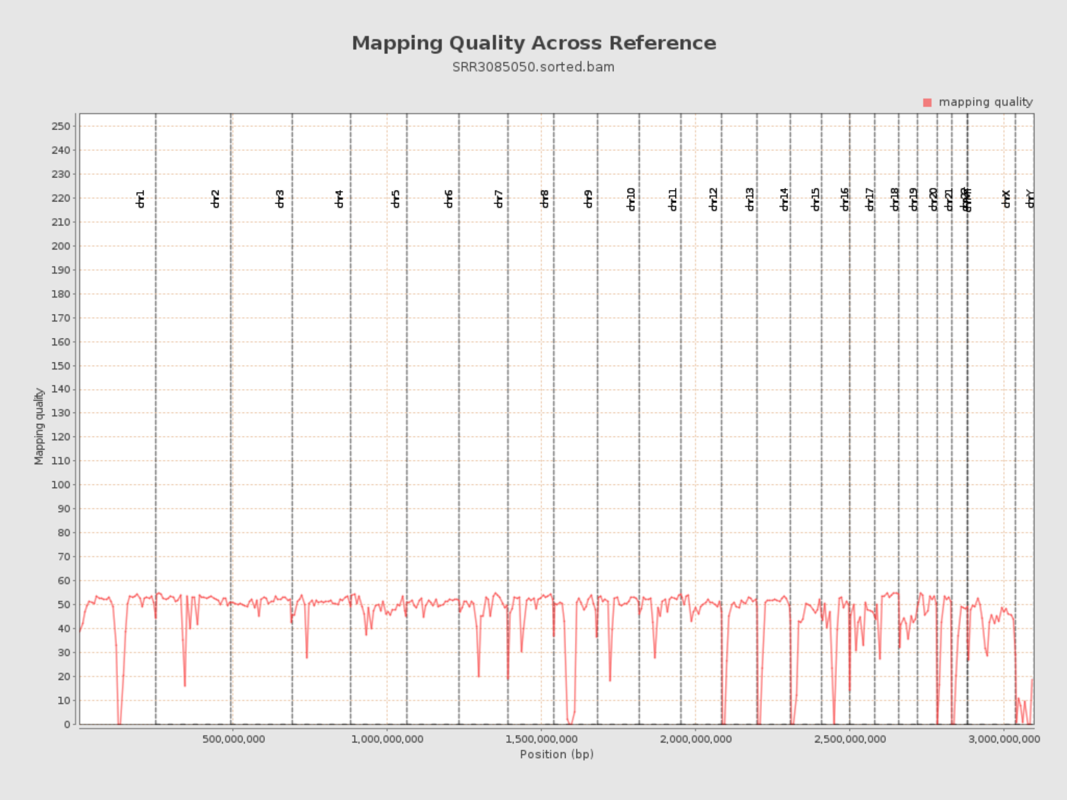
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram