Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 22:52:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085031.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_SRR3085031 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085031.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 22:52:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085031.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,305,238
Mapped reads	2,117,904 / 91.87%
Unmapped reads	187,334 / 8.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,680 / 0.59%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	66,169 / 2.87%
Duplication rate	2.45%
Clipped reads	895,208 / 38.83%

2.2. ACGT Content

Number/percentage of A's	39,681,465 / 27.8%
Number/percentage of C's	27,559,614 / 19.31%
Number/percentage of T's	43,684,780 / 30.61%
Number/percentage of G's	31,795,931 / 22.28%
Number/percentage of N's	7,192 / 0.01%
GC Percentage	41.59%

2.3. Coverage

Mean	0.0461

Standard Deviation	0.345

2.4. Mapping Quality

Mean Mapping Quality	44.99

2.5. Mismatches and indels

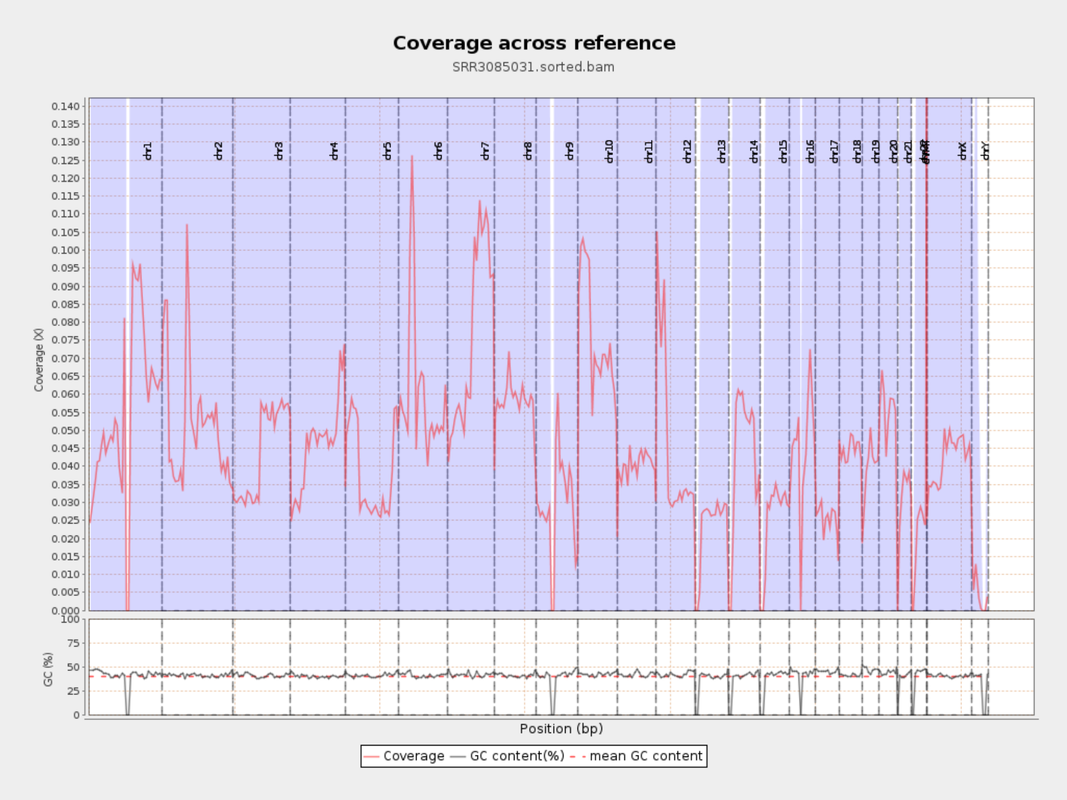
General error rate	0.83%
Mismatches	1,162,480
Insertions	9,806
Mapped reads with at least one insertion	0.46%
Deletions	29,741
Mapped reads with at least one deletion	1.39%
Homopolymer indels	46.54%

2.6. Chromosome stats

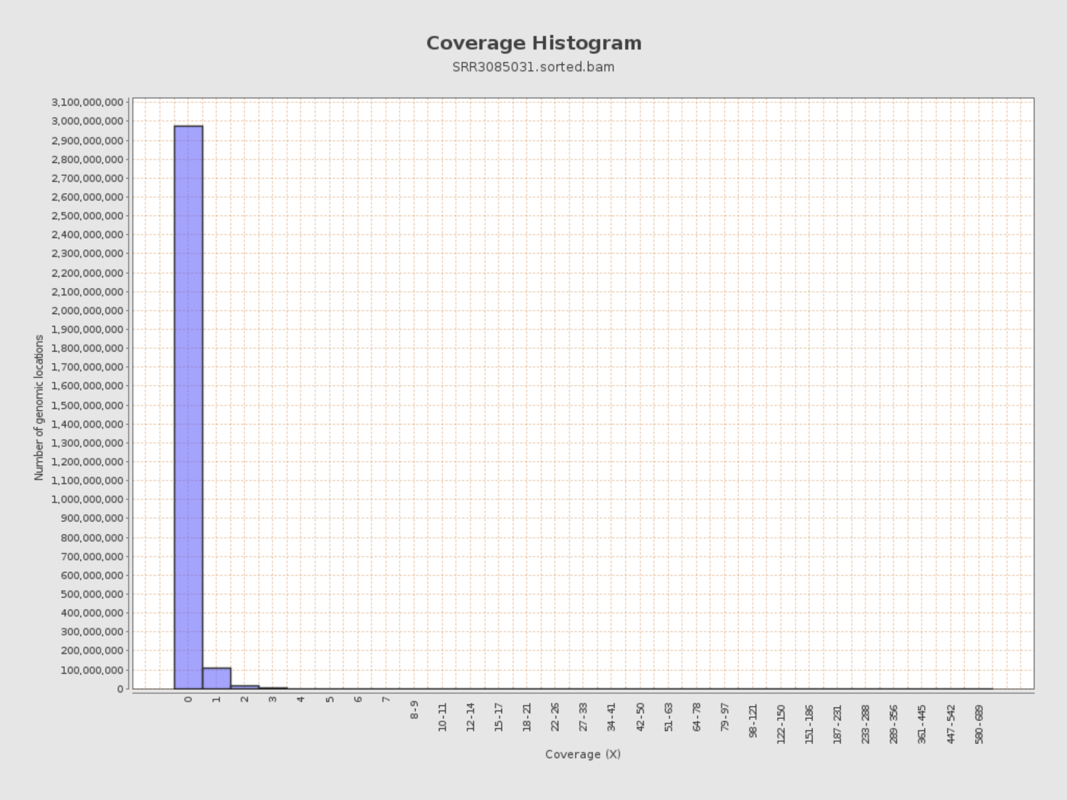
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13695473	0.0549	0.5321
chr2	243199373	12726367	0.0523	0.4601
chr3	198022430	8672201	0.0438	0.2428
chr4	191154276	8829367	0.0462	0.2431
chr5	180915260	6902084	0.0382	0.2182
chr6	171115067	10444580	0.061	0.3559
chr7	159138663	12255357	0.077	0.3665

chr8	146364022	8544659	0.0584	0.5084
chr9	141213431	4152257	0.0294	0.3003
chr10	135534747	10427396	0.0769	0.4859
chr11	135006516	5430348	0.0402	0.3065
chr12	133851895	6170040	0.0461	0.2479
chr13	115169878	2649751	0.023	0.1698
chr14	107349540	4640439	0.0432	0.2443
chr15	102531392	2562518	0.025	0.1819
chr16	90354753	4134406	0.0458	0.2522
chr17	81195210	2030146	0.025	0.1962
chr18	78077248	3500385	0.0448	0.4725
chr19	59128983	2363065	0.04	0.4087
chr20	63025520	3473982	0.0551	0.2651
chr21	48129895	1455748	0.0302	0.2045
chr22	51304566	950750	0.0185	0.1506
chrMT	16571	4006	0.2417	0.5336
chrX	155270560	6496763	0.0418	0.2555
chrY	59373566	268308	0.0045	0.0884

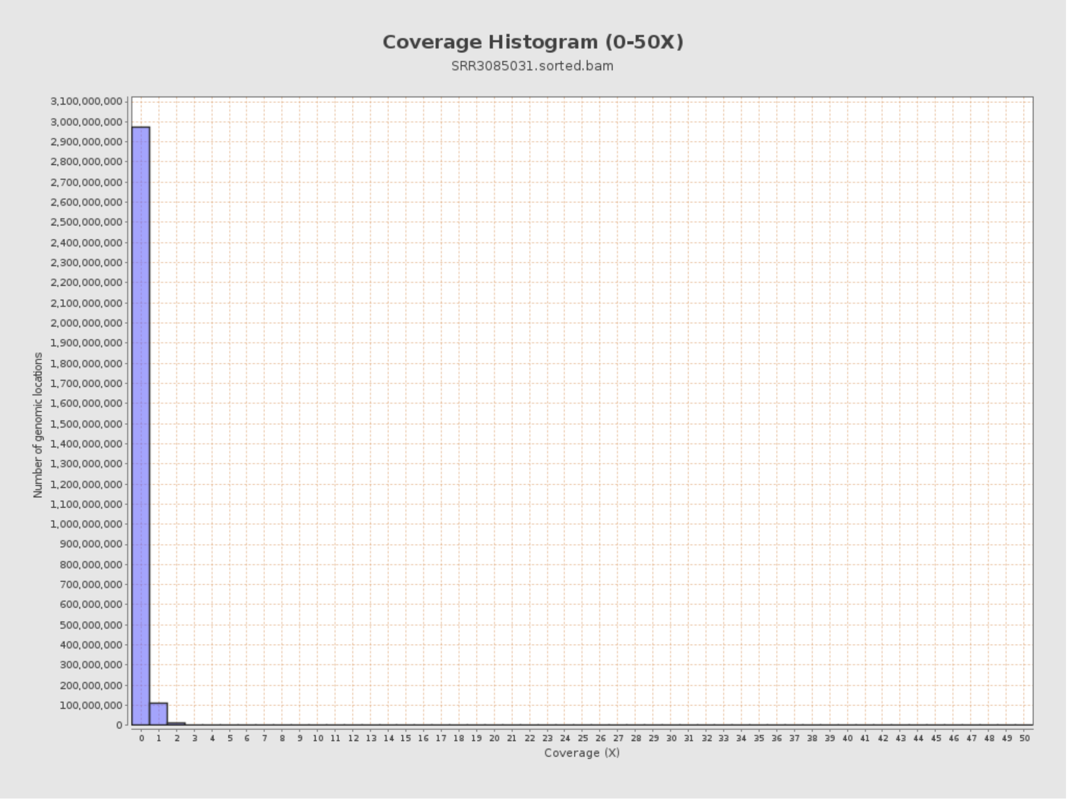
3. Results : Coverage across reference



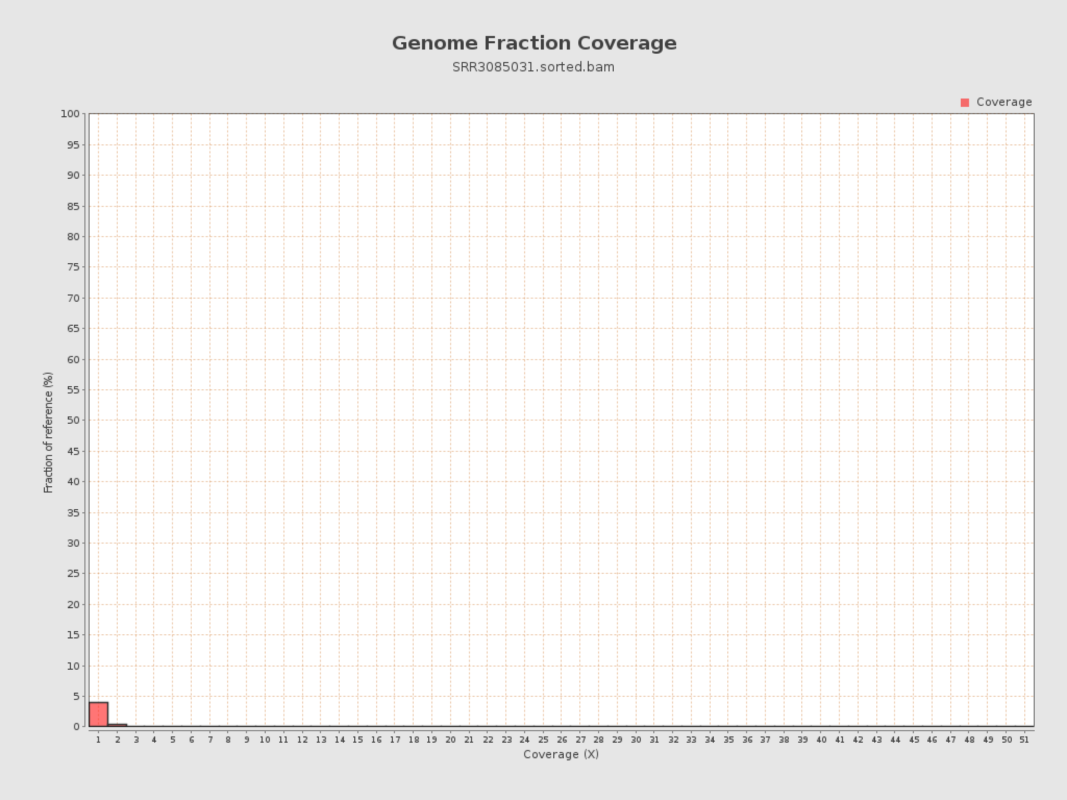
4. Results : Coverage Histogram



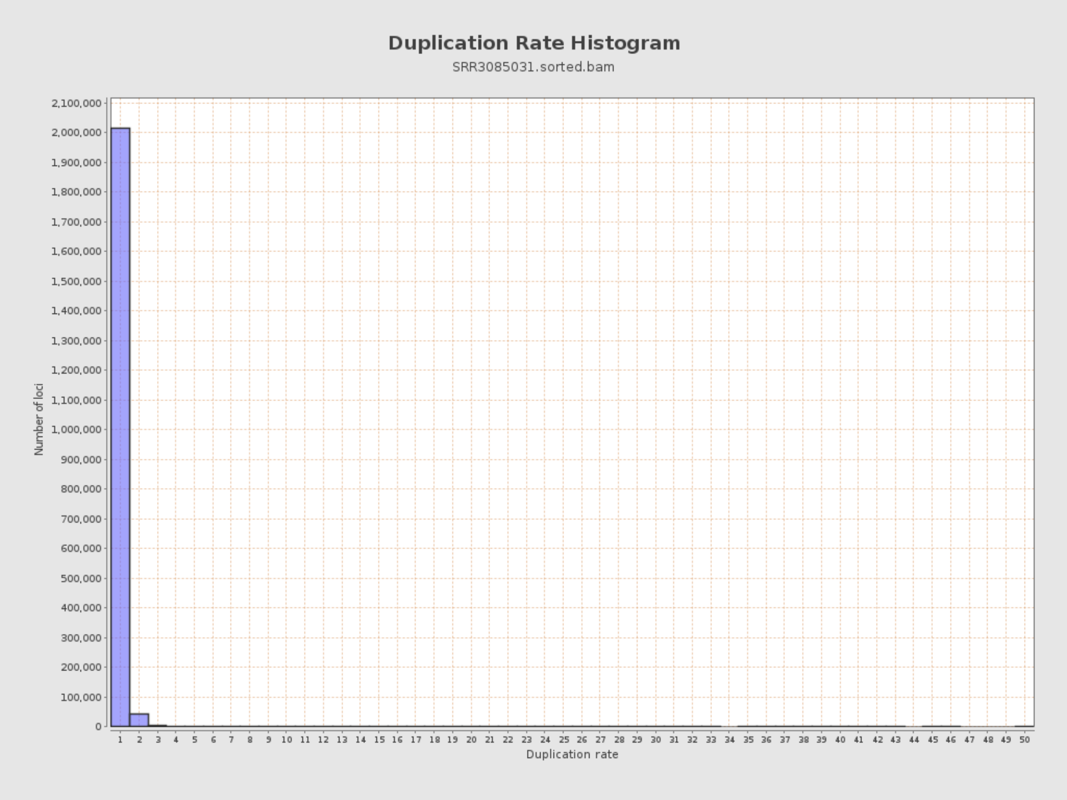
5. Results : Coverage Histogram (0-50X)



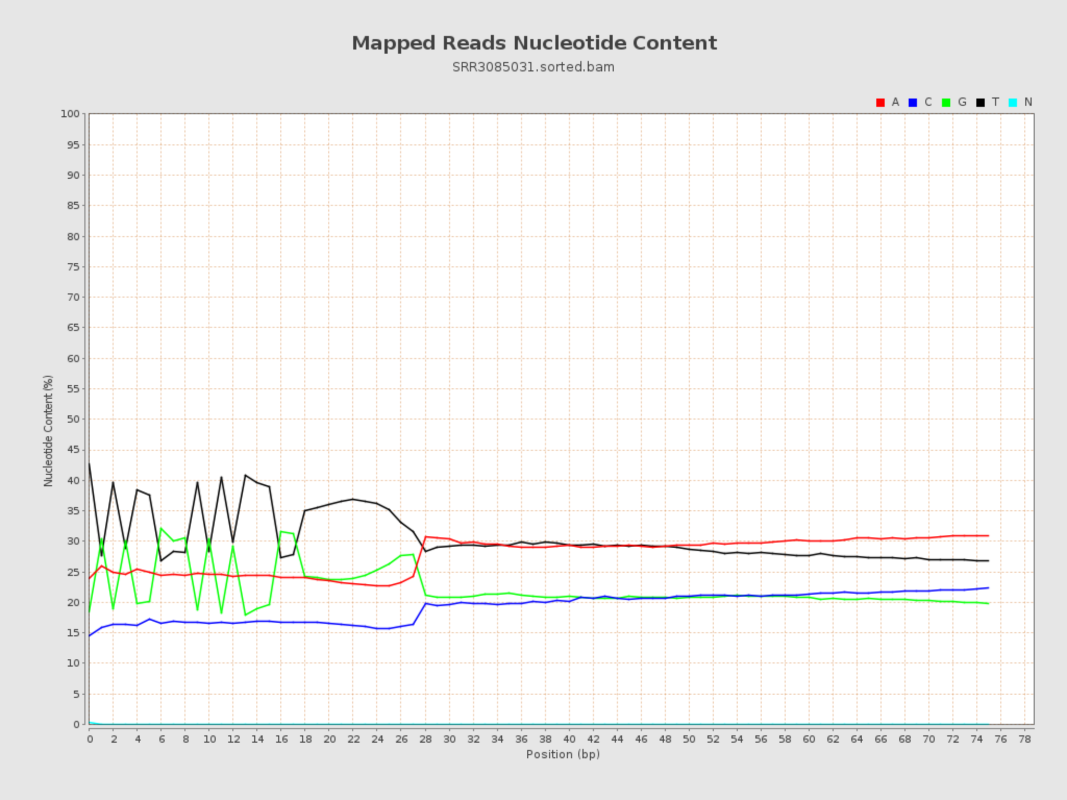
6. Results : Genome Fraction Coverage



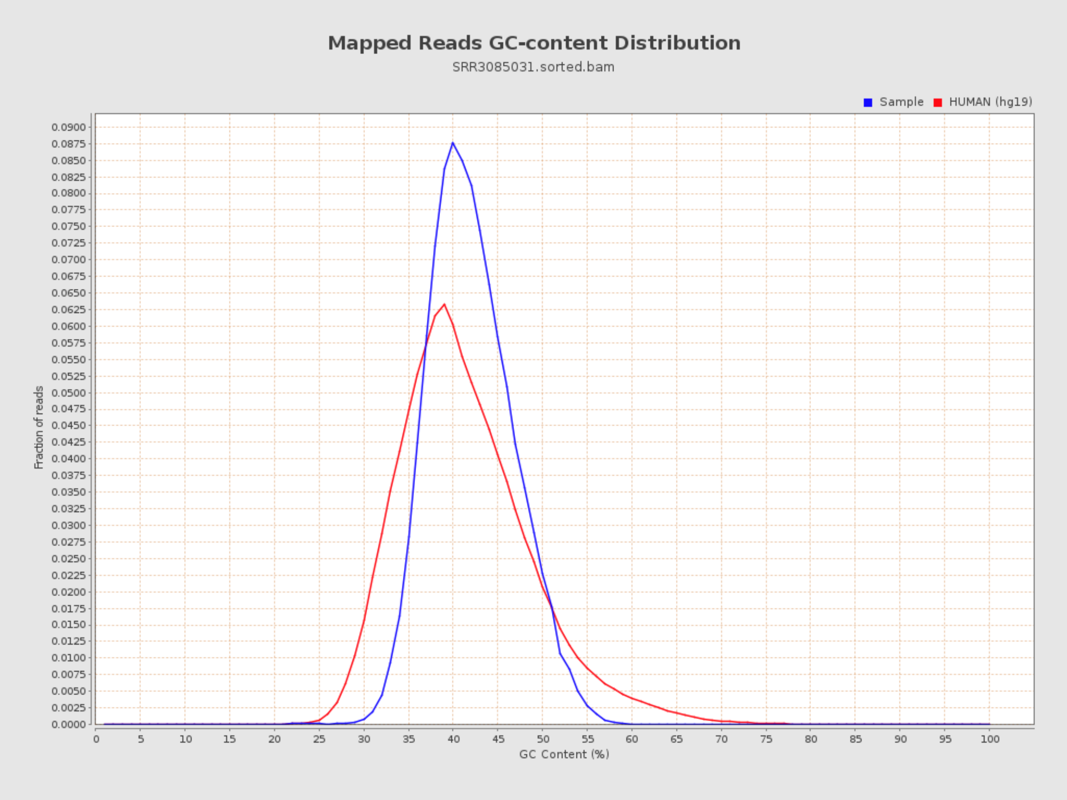
7. Results : Duplication Rate Histogram



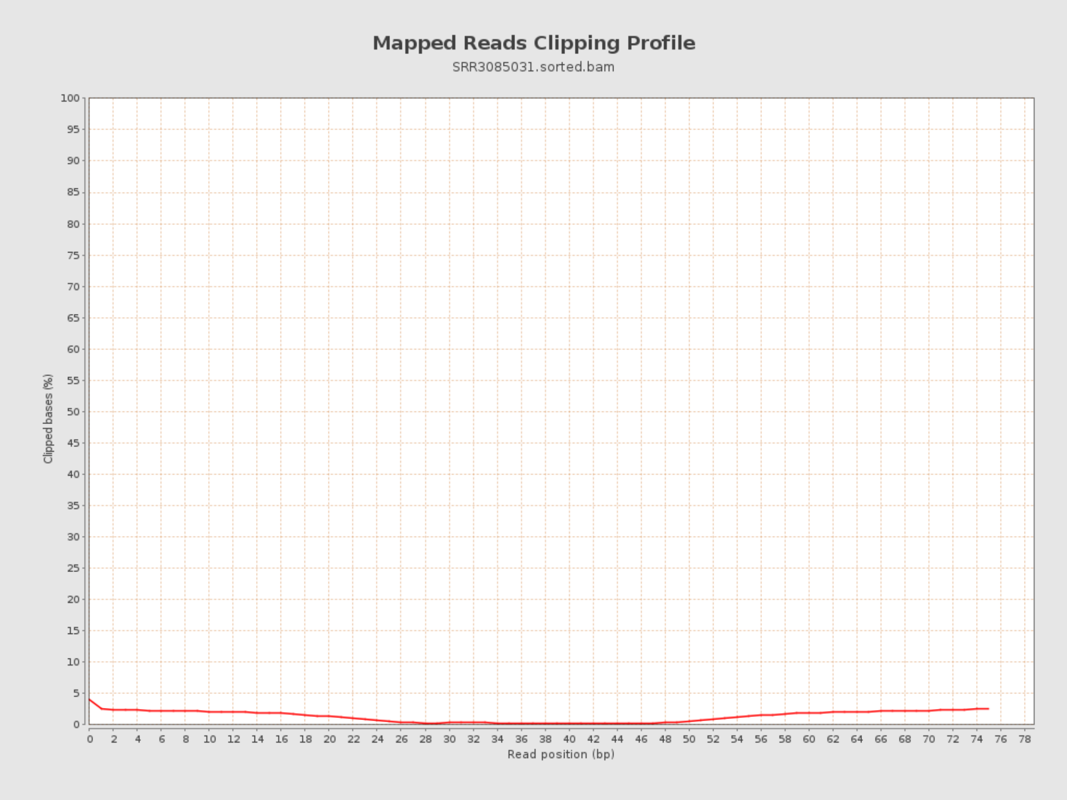
8. Results : Mapped Reads Nucleotide Content



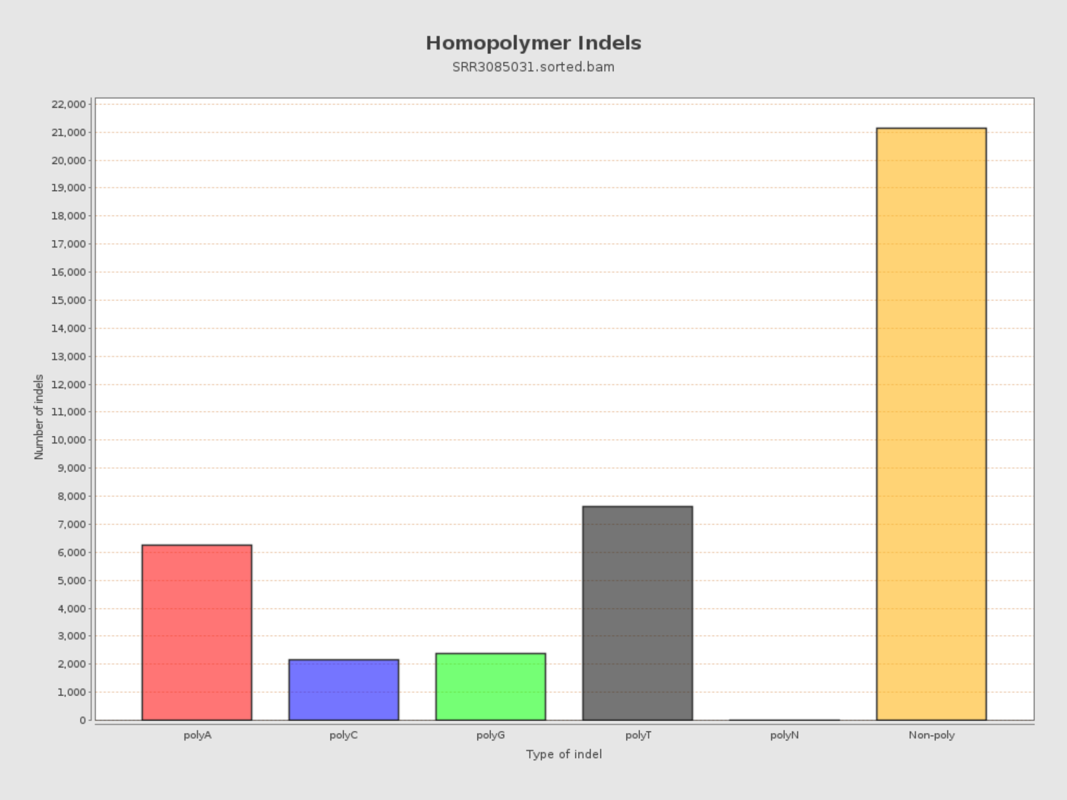
9. Results : Mapped Reads GC-content Distribution



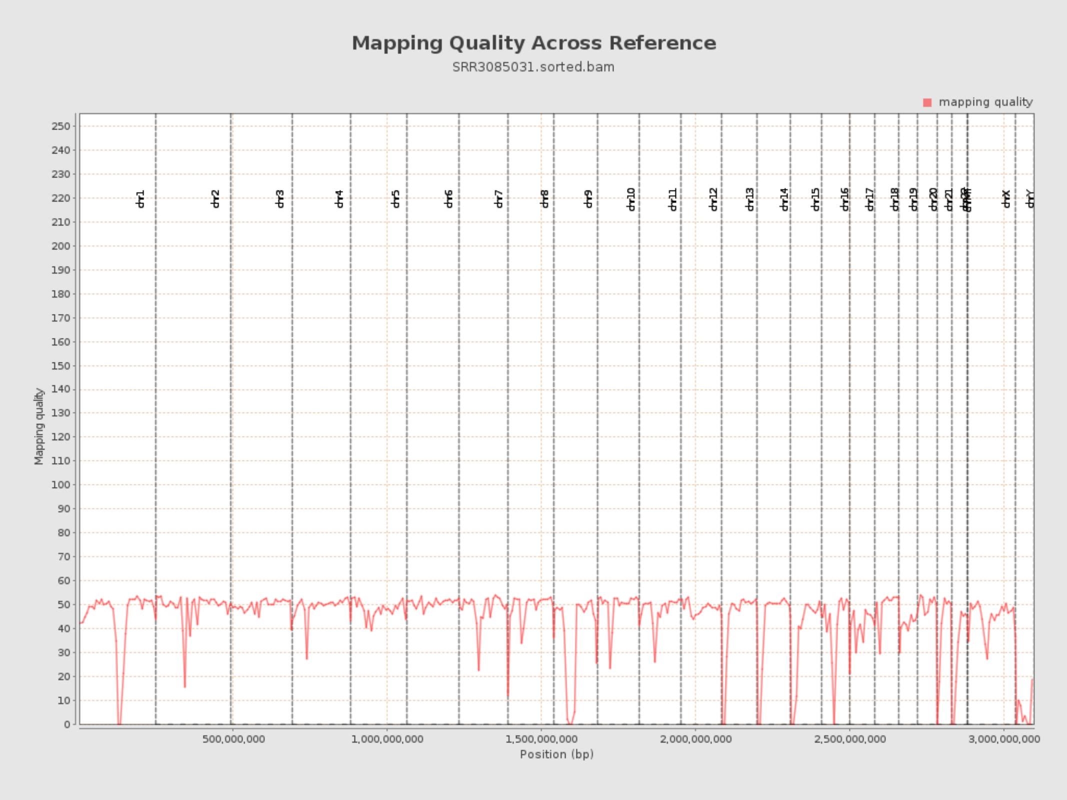
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram