Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 22:22:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085023.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_SRR3085023 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085023.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 22:22:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085023.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,930,689
Mapped reads	2,674,072 / 91.24%
Unmapped reads	256,617 / 8.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,479 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	99,281 / 3.39%
Duplication rate	2.95%
Clipped reads	1,170,380 / 39.94%

2.2. ACGT Content

Number/percentage of A's	50,268,927 / 28.03%
Number/percentage of C's	34,555,459 / 19.27%
Number/percentage of T's	54,955,542 / 30.64%
Number/percentage of G's	39,552,714 / 22.05%
Number/percentage of N's	7,050 / 0%
GC Percentage	41.32%

2.3. Coverage

Mean	0.058

Standard Deviation	0.399

2.4. Mapping Quality

Mean Mapping Quality	45.22

2.5. Mismatches and indels

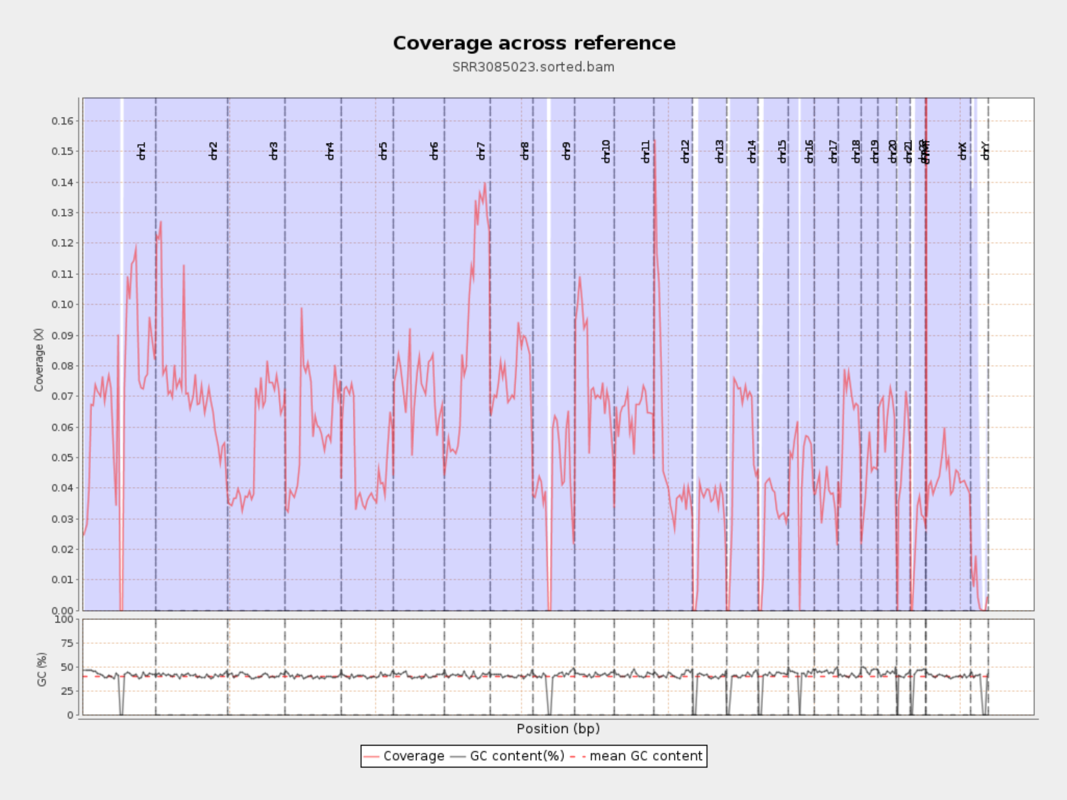
General error rate	0.86%
Mismatches	1,520,541
Insertions	12,797
Mapped reads with at least one insertion	0.47%
Deletions	36,826
Mapped reads with at least one deletion	1.36%
Homopolymer indels	46.74%

2.6. Chromosome stats

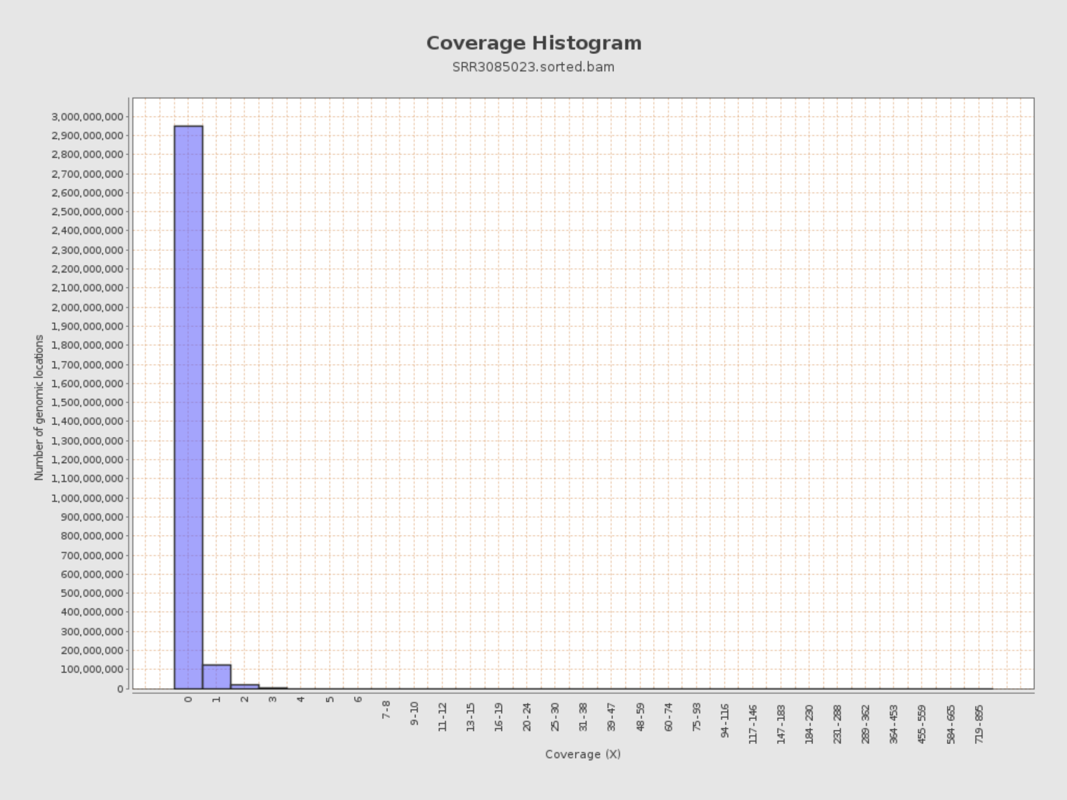
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17579908	0.0705	0.561
chr2	243199373	18010069	0.0741	0.5354
chr3	198022430	10877776	0.0549	0.2746
chr4	191154276	11468408	0.06	0.2927
chr5	180915260	8829413	0.0488	0.2564
chr6	171115067	12497500	0.073	0.3828
chr7	159138663	14603462	0.0918	0.4714

chr8	146364022	11265229	0.077	0.6314
chr9	141213431	5876259	0.0416	0.3828
chr10	135534747	10498471	0.0775	0.4783
chr11	135006516	8696187	0.0644	0.4104
chr12	133851895	7265520	0.0543	0.2797
chr13	115169878	3574059	0.031	0.2025
chr14	107349540	5986308	0.0558	0.301
chr15	102531392	2965706	0.0289	0.2072
chr16	90354753	4205049	0.0465	0.265
chr17	81195210	3075311	0.0379	0.2595
chr18	78077248	4940061	0.0633	0.6418
chr19	59128983	2587808	0.0438	0.4114
chr20	63025520	4039612	0.0641	0.2995
chr21	48129895	2347261	0.0488	0.2731
chr22	51304566	1196944	0.0233	0.1739
chrMT	16571	10869	0.6559	0.9561
chrX	155270560	6662069	0.0429	0.2813
chrY	59373566	343399	0.0058	0.1182

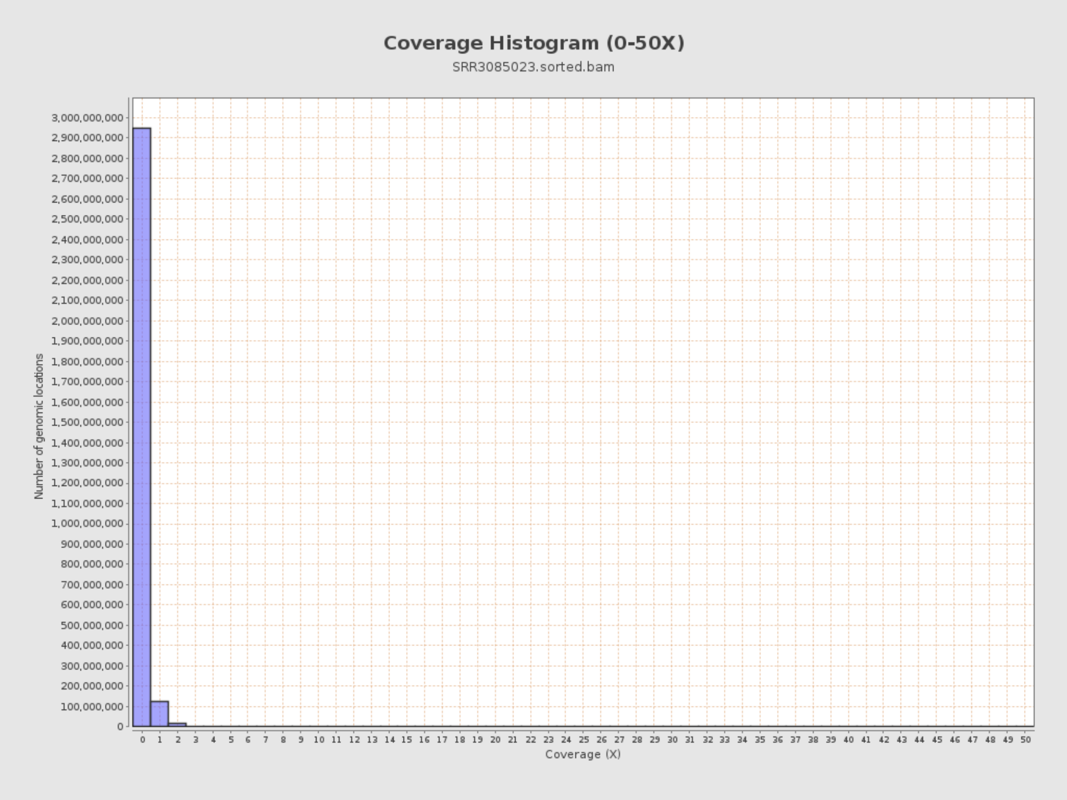
3. Results : Coverage across reference



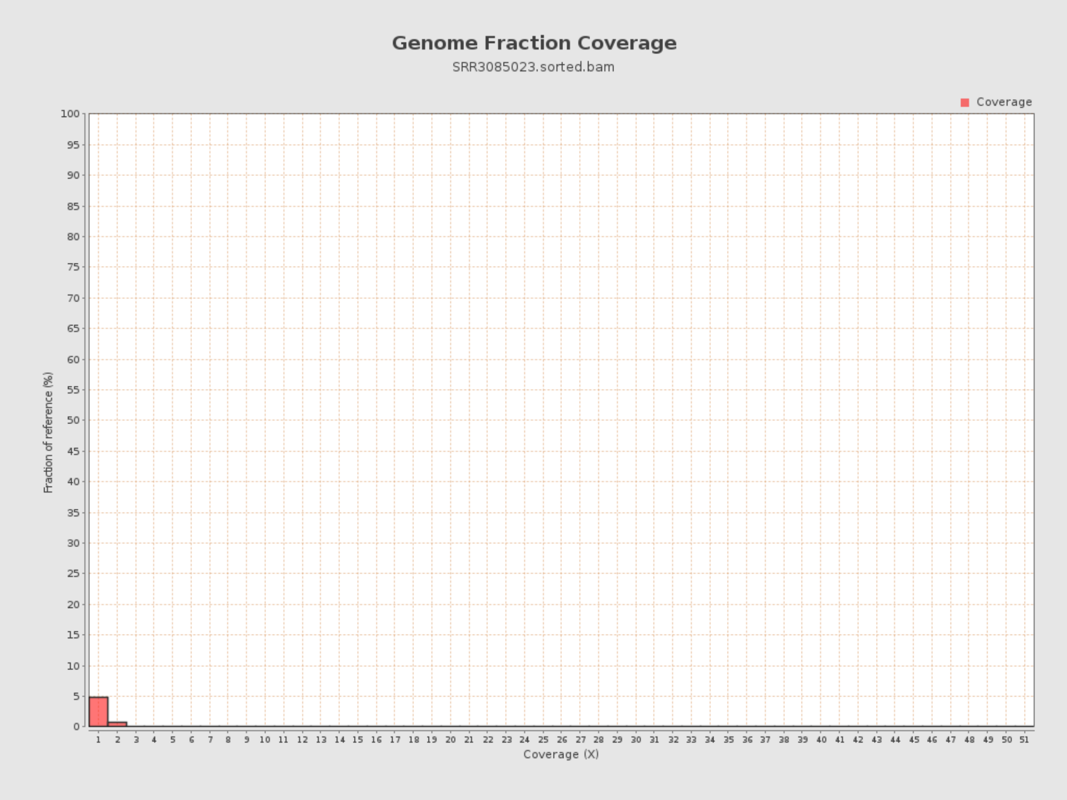
4. Results : Coverage Histogram



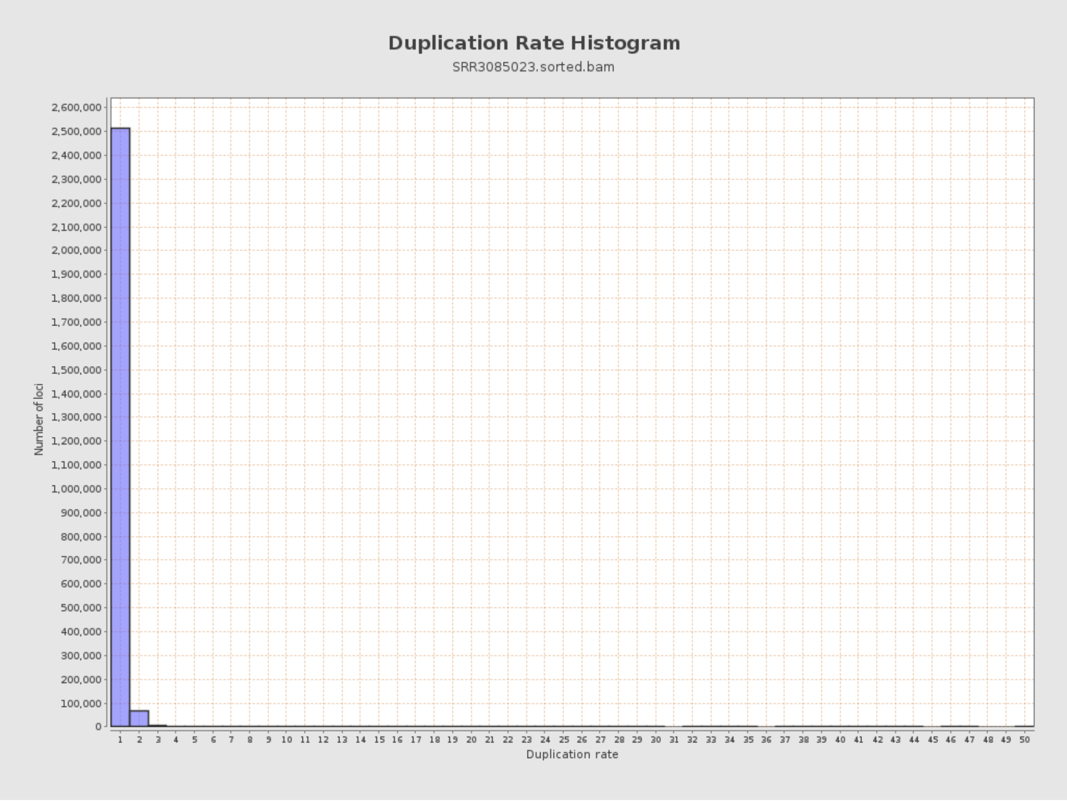
5. Results : Coverage Histogram (0-50X)



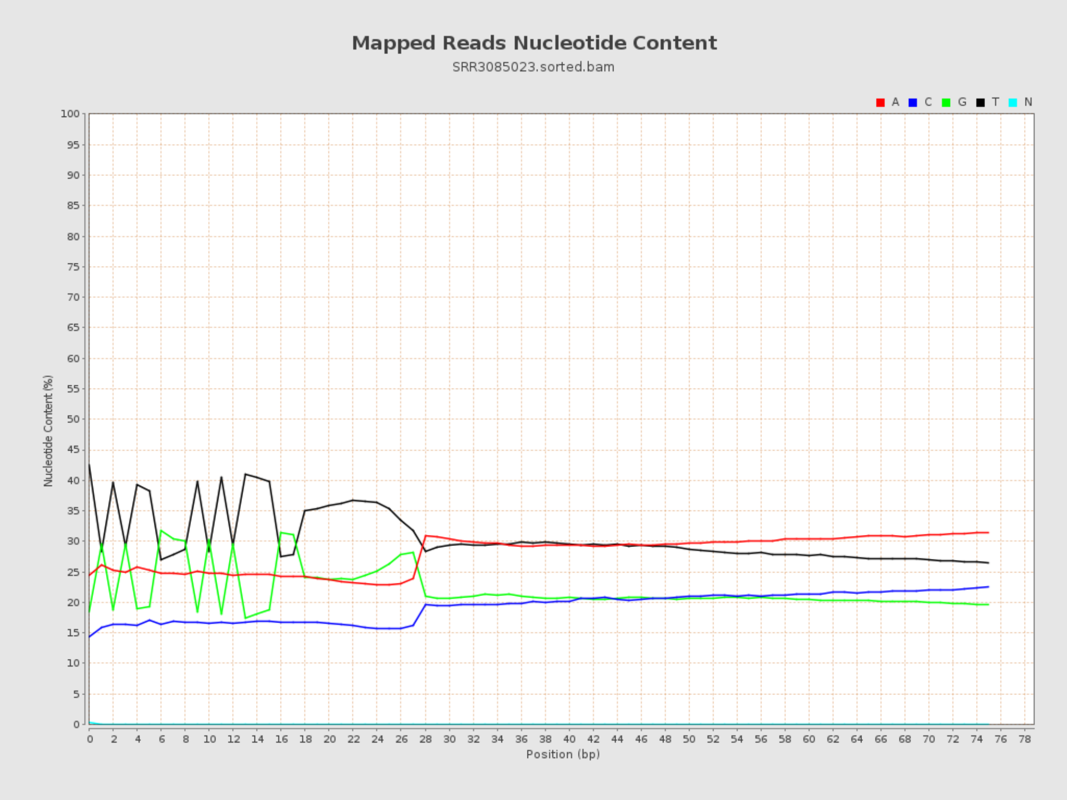
6. Results : Genome Fraction Coverage



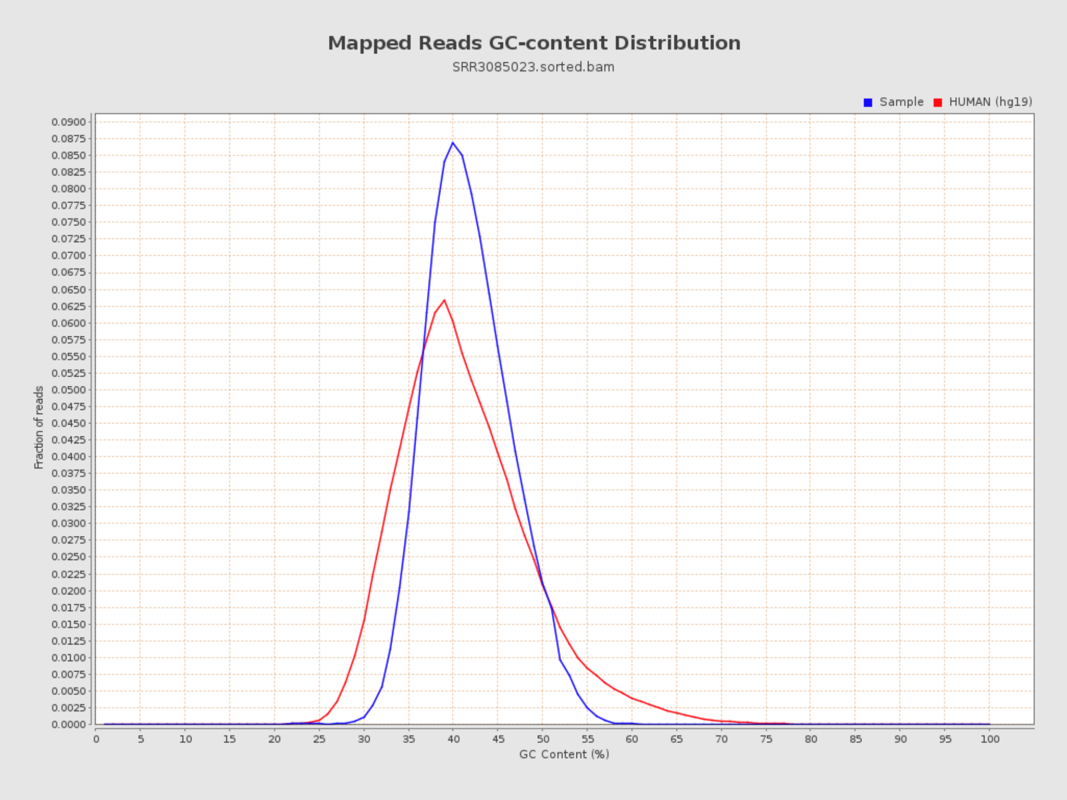
7. Results : Duplication Rate Histogram



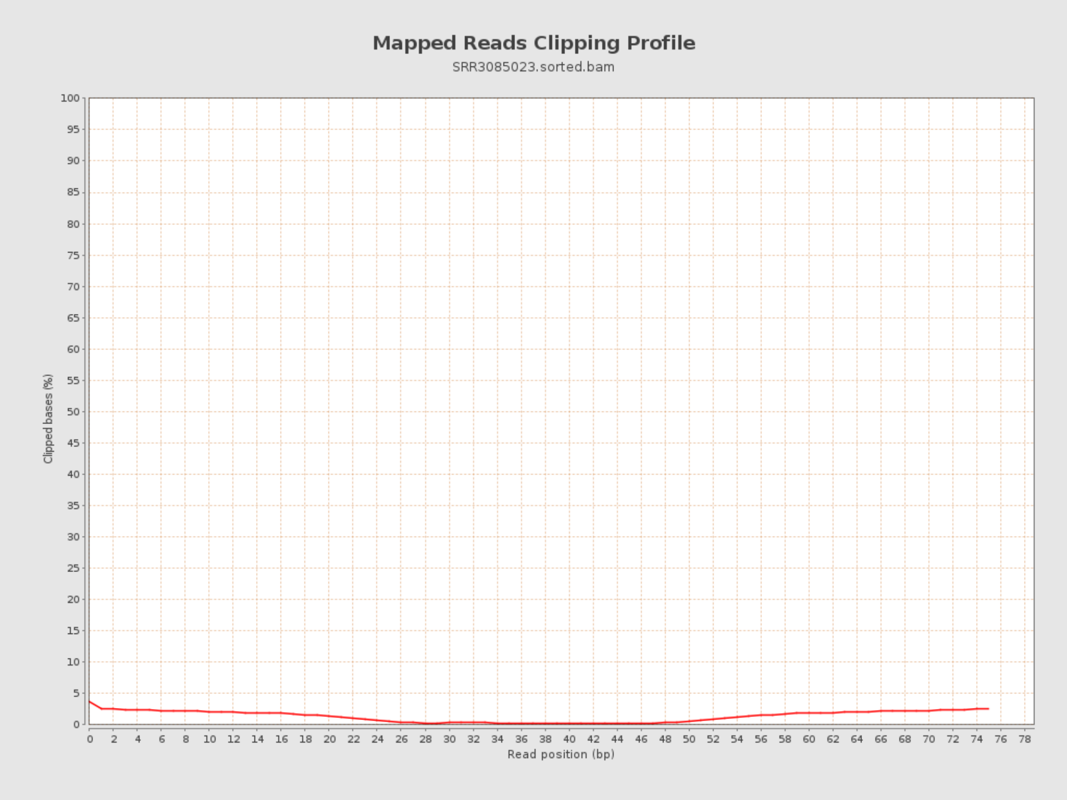
8. Results : Mapped Reads Nucleotide Content



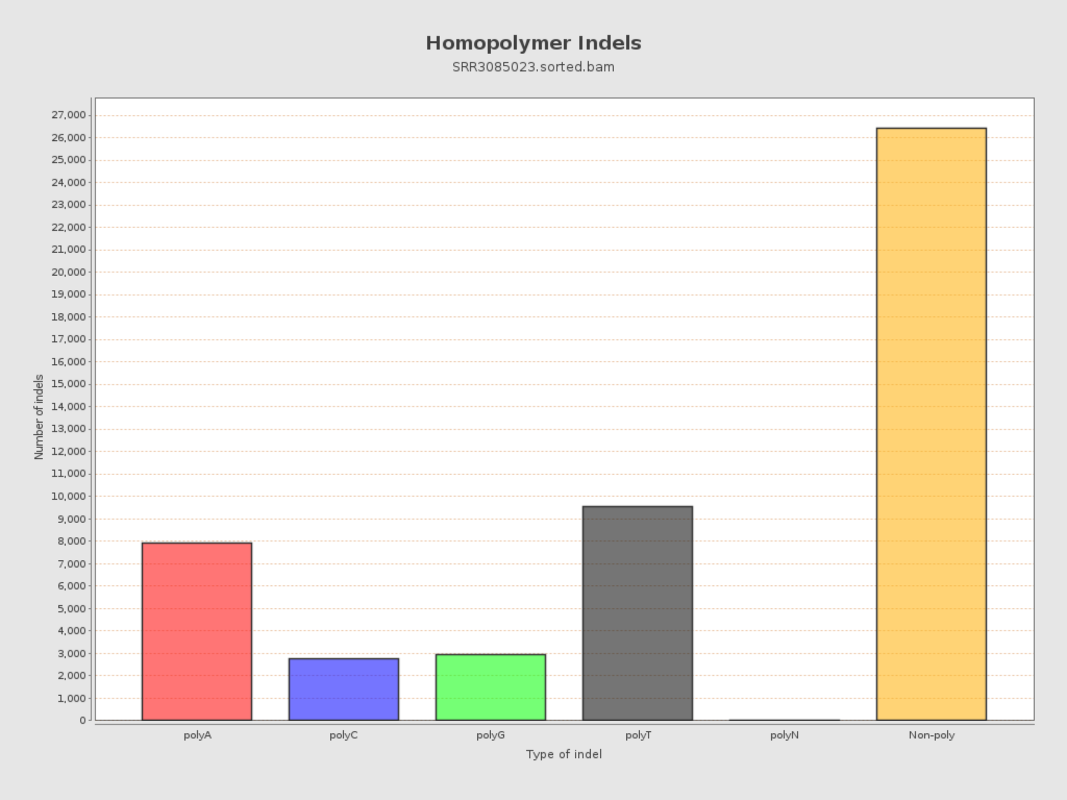
9. Results : Mapped Reads GC-content Distribution



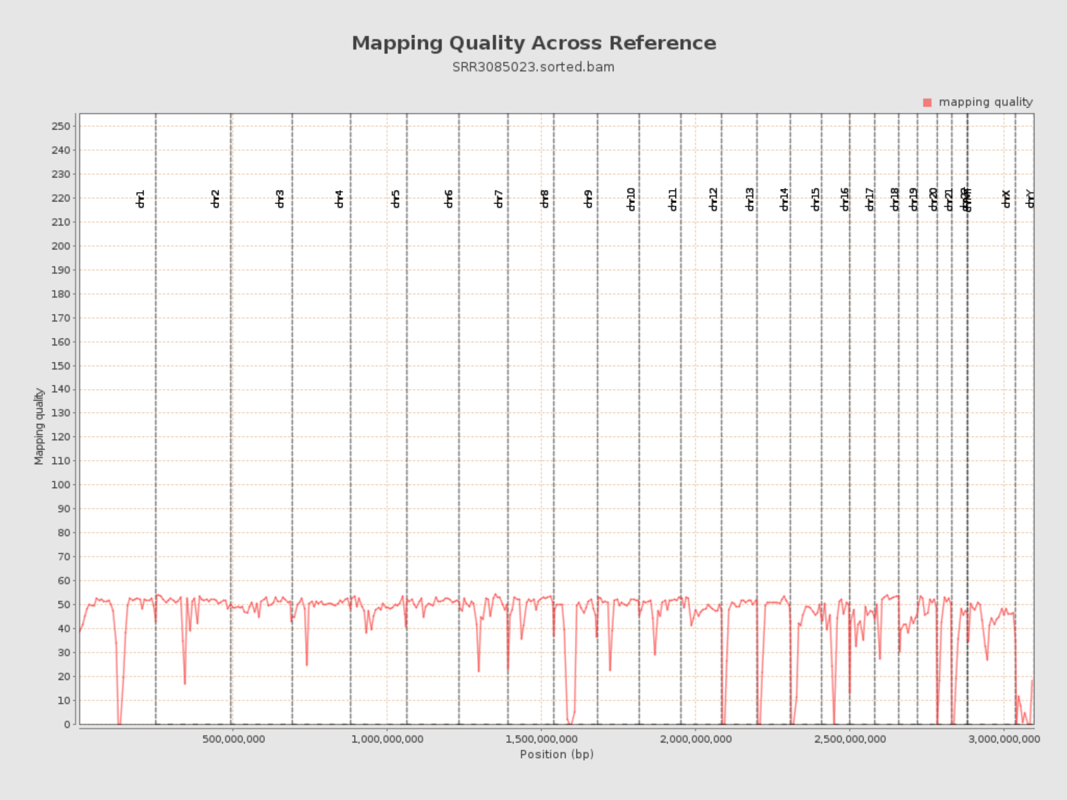
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram