Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 18:35:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081059.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_SRR3081059 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081059.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 18:35:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081059.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,758,463
Mapped reads	2,506,883 / 90.88%
Unmapped reads	251,580 / 9.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,769 / 1.08%
Read min/max/mean length	30 / 76 / 76.38
Duplicated reads (estimated)	122,284 / 4.43%
Duplication rate	3.81%
Clipped reads	1,101,669 / 39.94%

2.2. ACGT Content

Number/percentage of A's	47,507,549 / 28.17%
Number/percentage of C's	31,942,023 / 18.94%
Number/percentage of T's	52,555,199 / 31.16%
Number/percentage of G's	36,646,633 / 21.73%
Number/percentage of N's	1,922 / 0%
GC Percentage	40.67%

2.3. Coverage

Mean	0.0545

Standard Deviation	0.4466

2.4. Mapping Quality

Mean Mapping Quality	45.84

2.5. Mismatches and indels

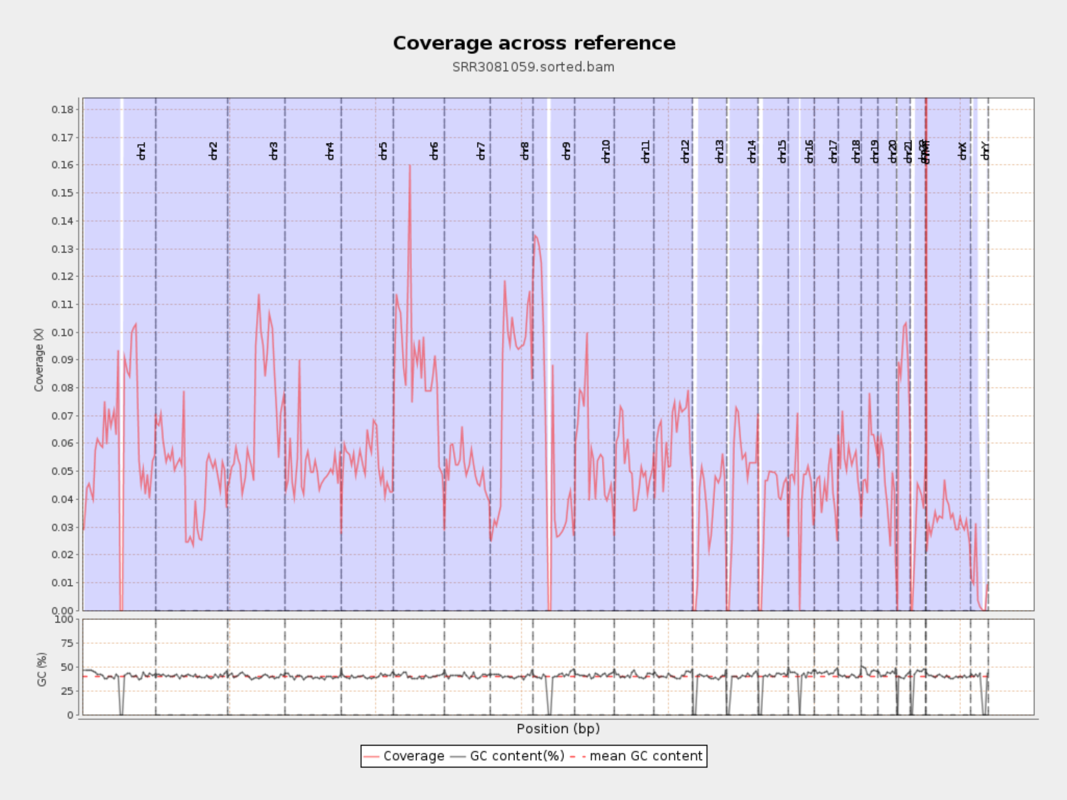
General error rate	0.92%
Mismatches	1,530,002
Insertions	13,500
Mapped reads with at least one insertion	0.53%
Deletions	37,082
Mapped reads with at least one deletion	1.46%
Homopolymer indels	46.63%

2.6. Chromosome stats

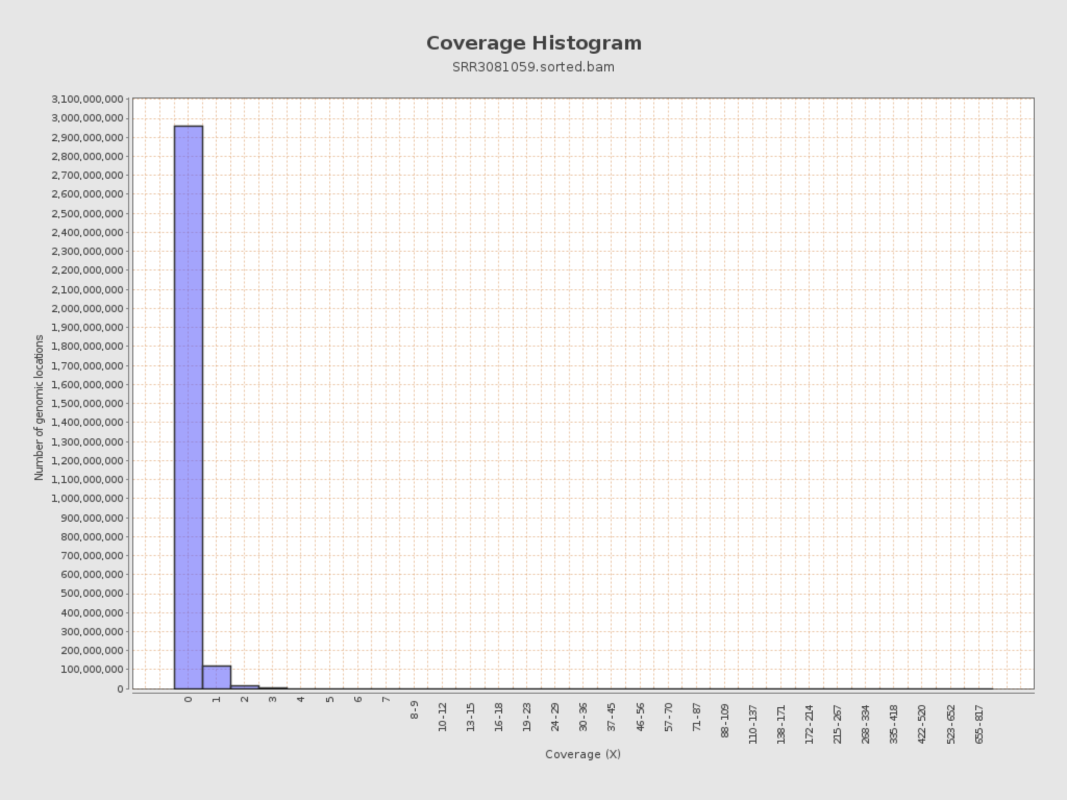
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14789275	0.0593	0.7608
chr2	243199373	11629187	0.0478	0.4587
chr3	198022430	13909672	0.0702	0.3119
chr4	191154276	9786670	0.0512	0.2999
chr5	180915260	9605163	0.0531	0.2682
chr6	171115067	15353383	0.0897	0.6237
chr7	159138663	8032866	0.0505	0.3479

chr8	146364022	11980853	0.0819	0.5353
chr9	141213431	8432980	0.0597	0.5061
chr10	135534747	7726378	0.057	0.451
chr11	135006516	6978707	0.0517	0.357
chr12	133851895	8466988	0.0633	0.3059
chr13	115169878	4088235	0.0355	0.2198
chr14	107349540	5192368	0.0484	0.3334
chr15	102531392	3891873	0.038	0.2281
chr16	90354753	3865755	0.0428	0.3353
chr17	81195210	3554106	0.0438	0.2581
chr18	78077248	4268591	0.0547	0.9236
chr19	59128983	3302314	0.0558	0.5506
chr20	63025520	2813324	0.0446	0.2766
chr21	48129895	3938276	0.0818	0.3936
chr22	51304566	1537789	0.03	0.1995
chrMT	16571	88776	5.3573	3.608
chrX	155270560	4995868	0.0322	0.2492
chrY	59373566	484604	0.0082	0.2167

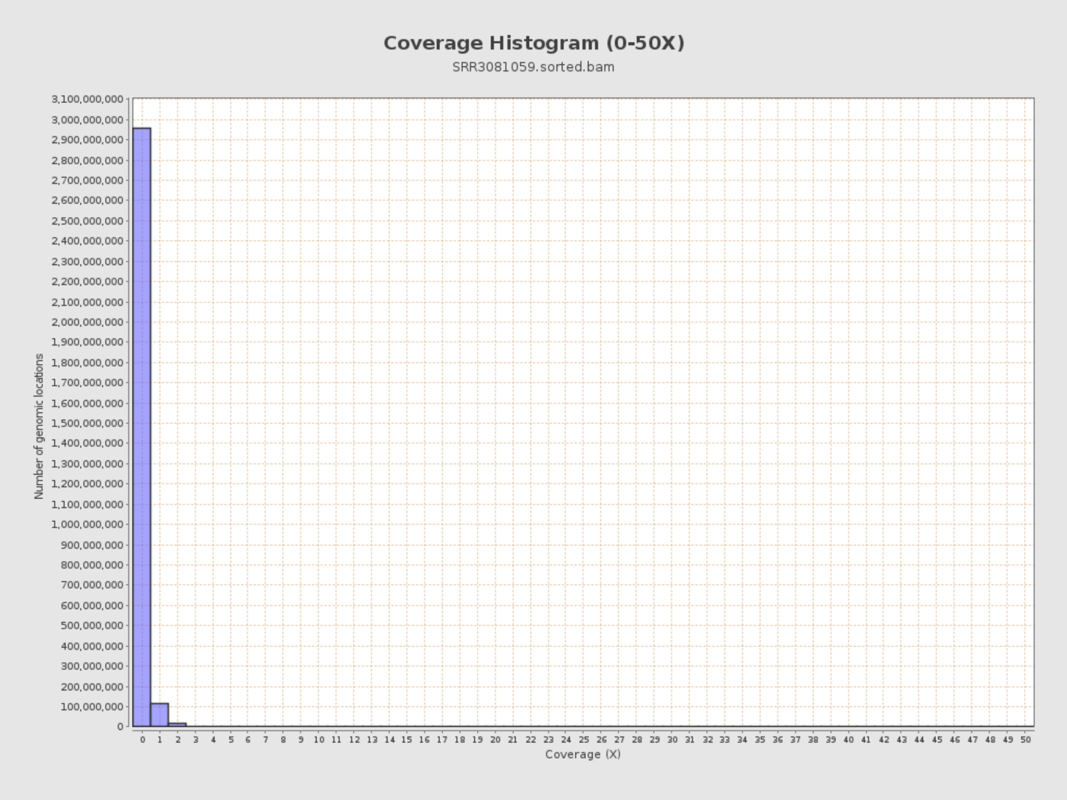
3. Results : Coverage across reference



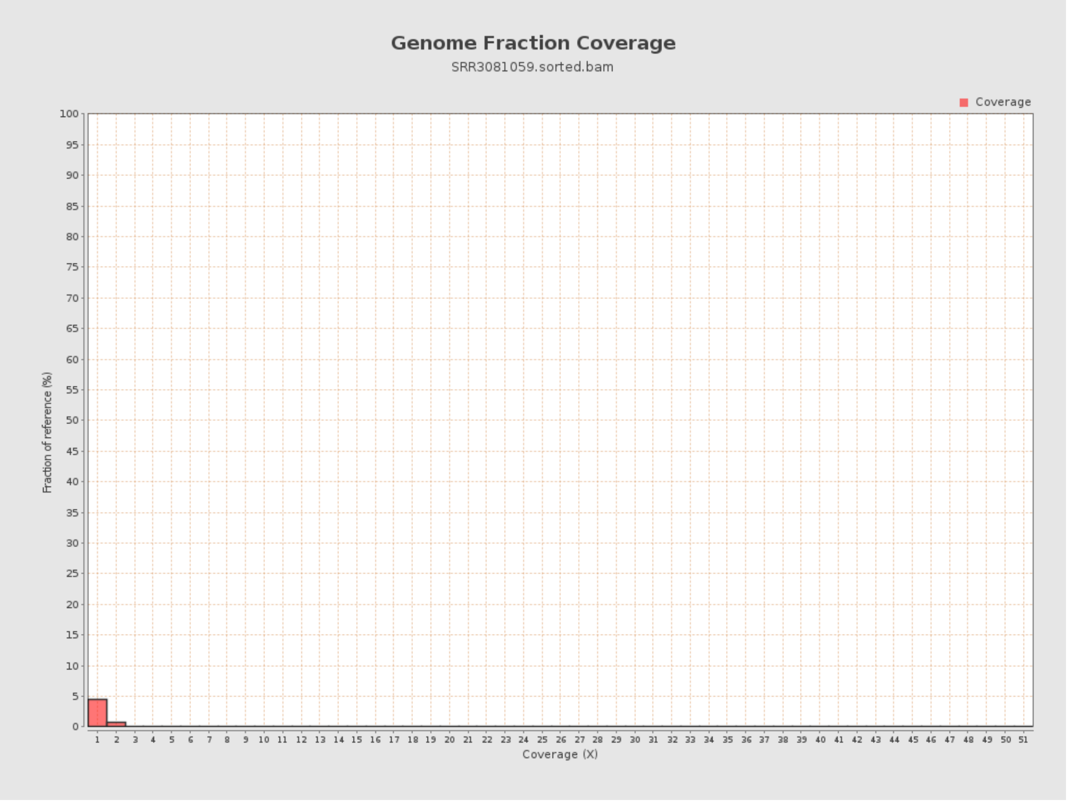
4. Results : Coverage Histogram



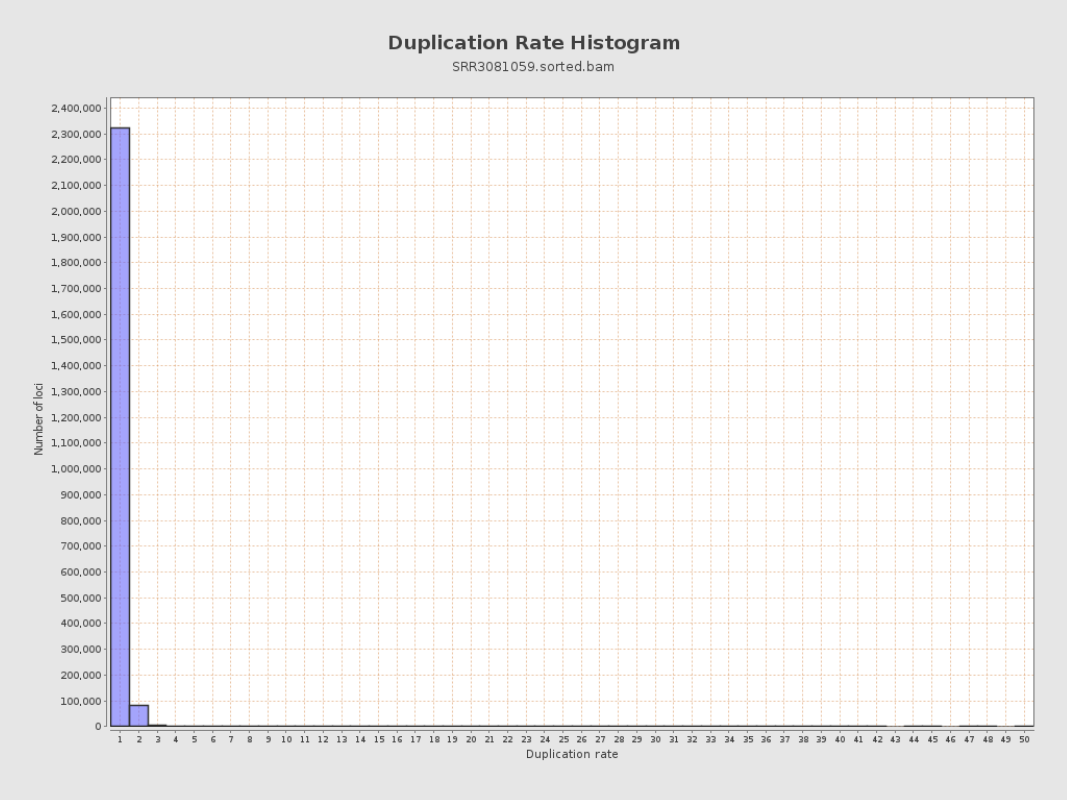
5. Results : Coverage Histogram (0-50X)



6. Results : Genome Fraction Coverage



7. Results : Duplication Rate Histogram



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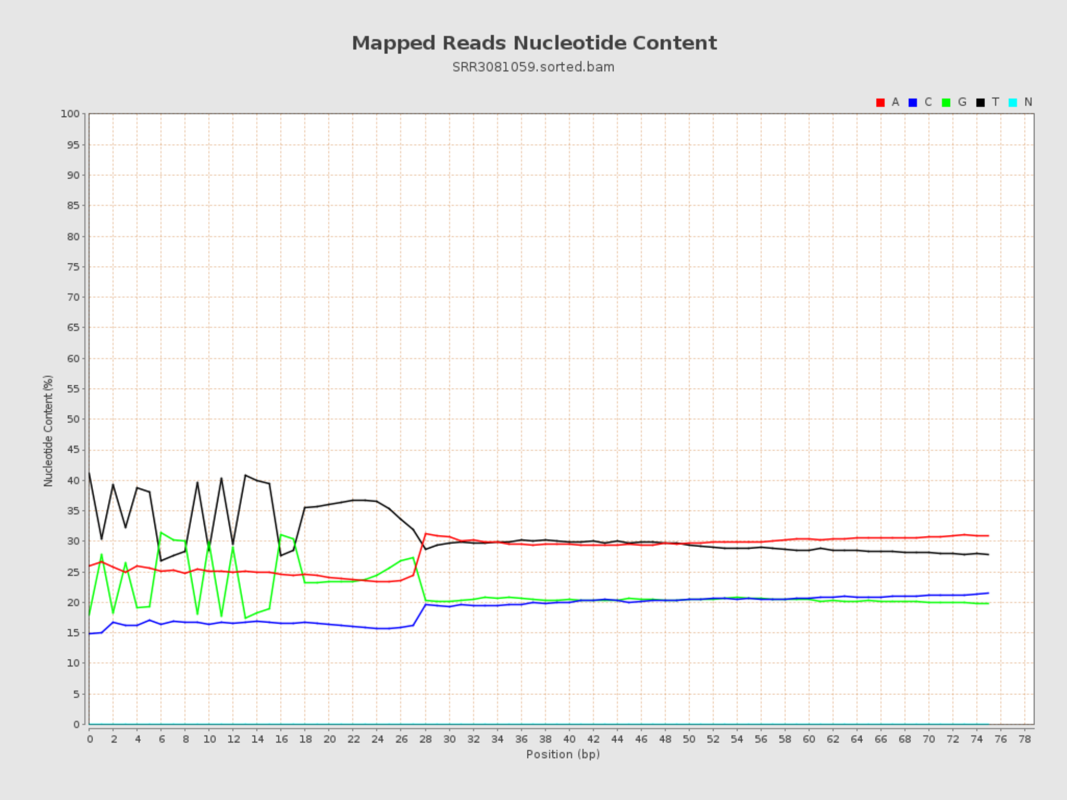
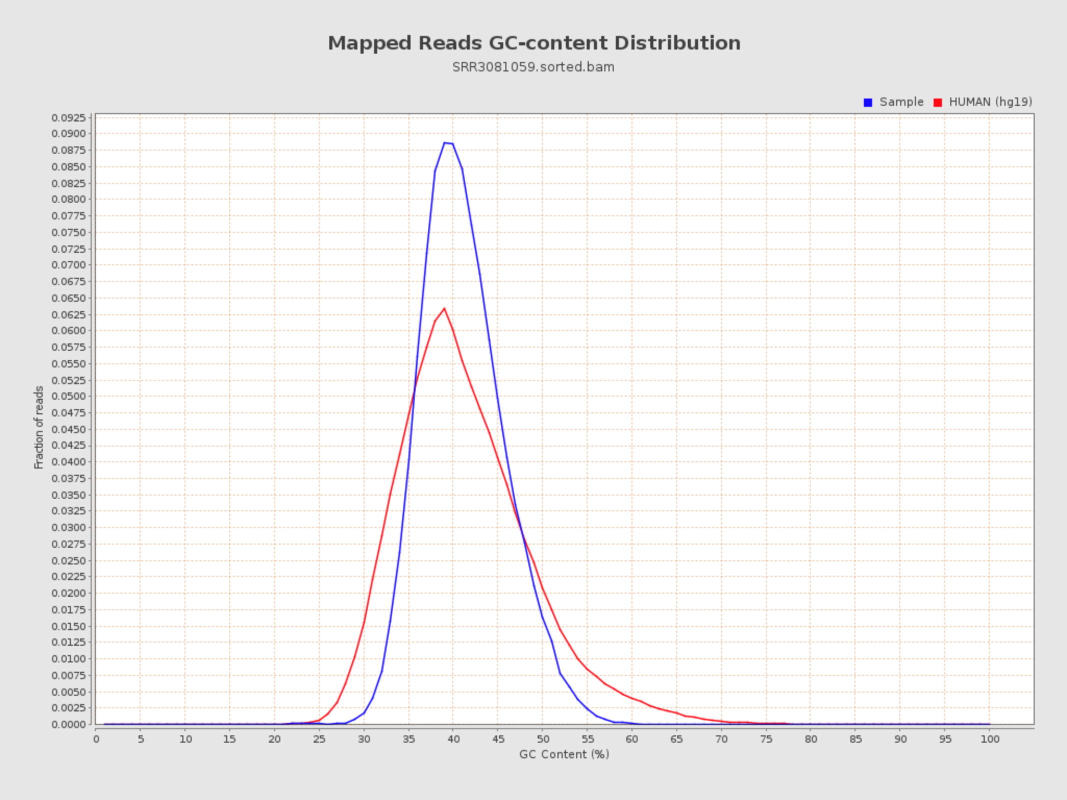
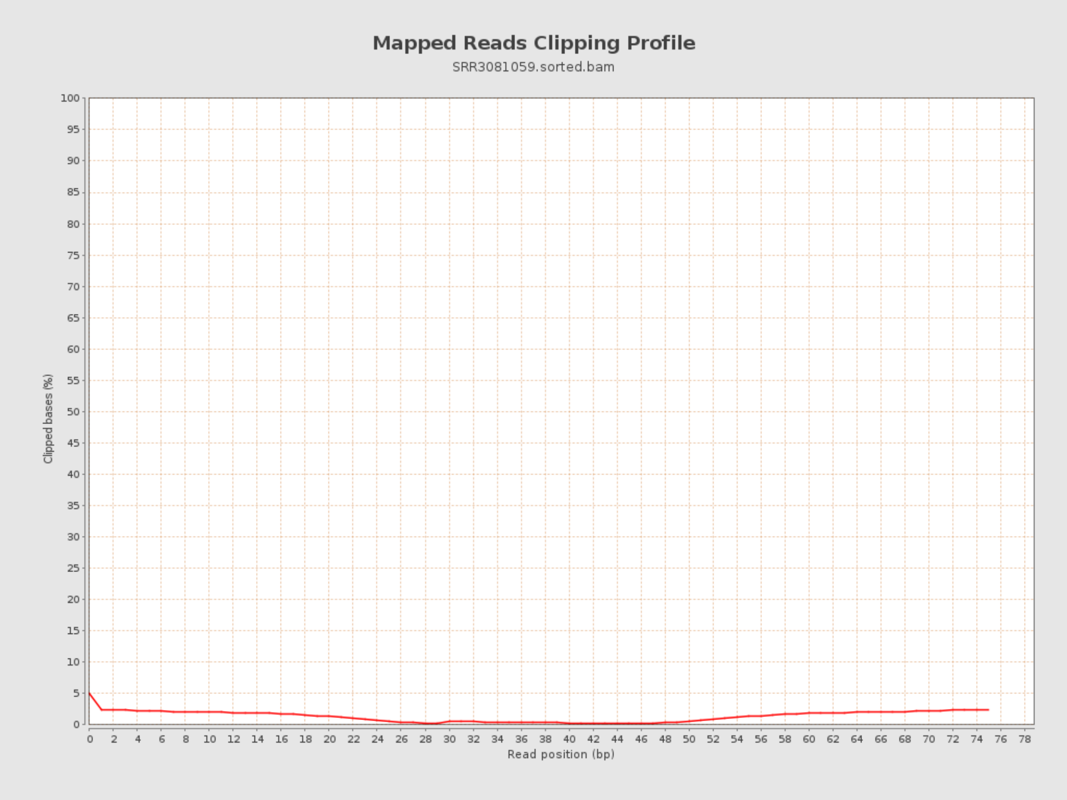
8. Results : Mapped Reads Nucleotide Content



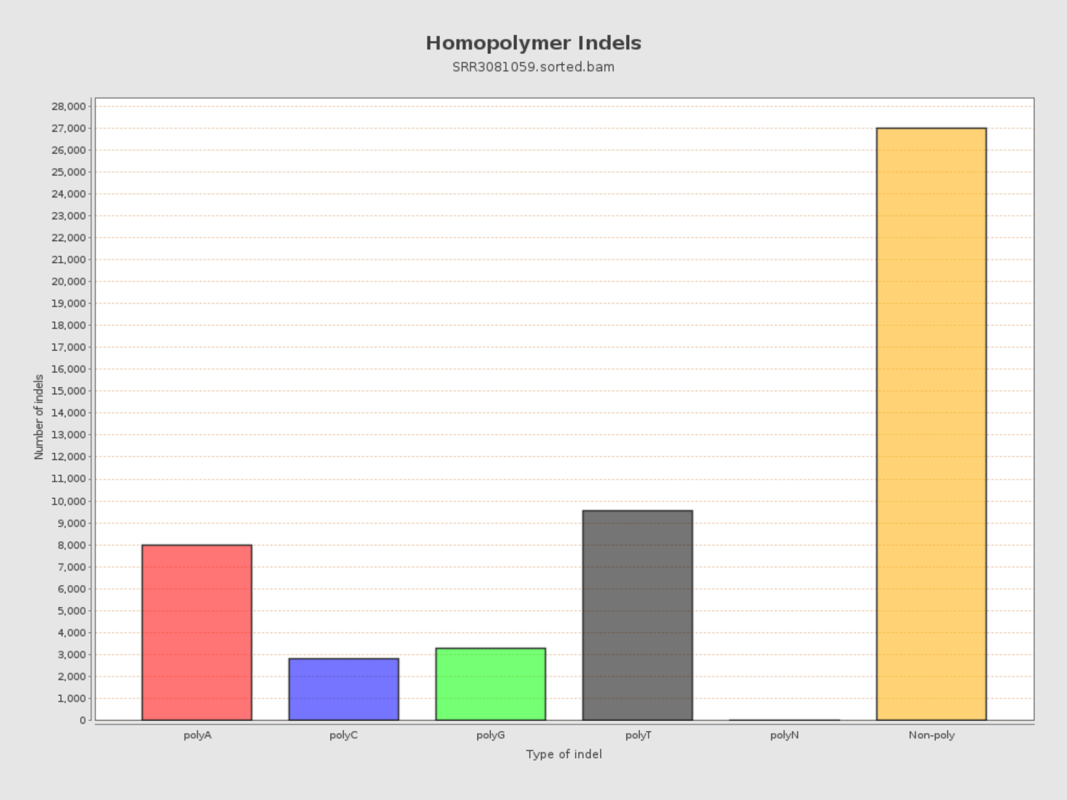
9. Results : Mapped Reads GC-content Distribution



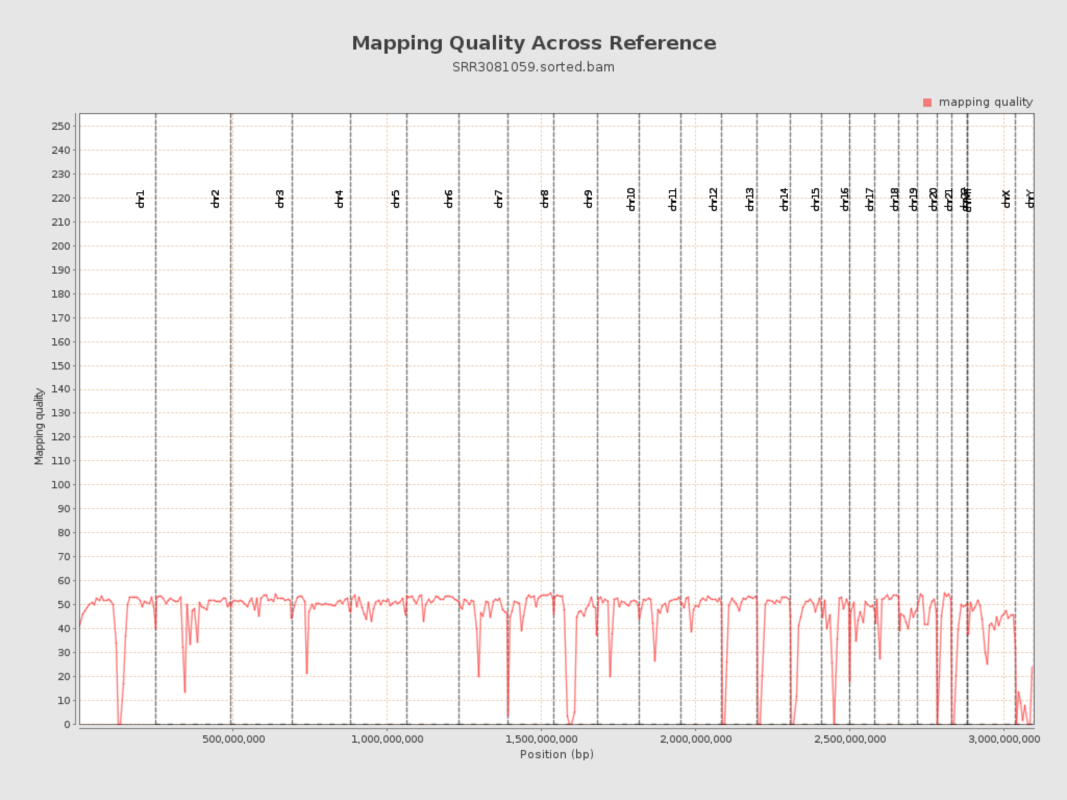
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram