Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 07:14:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081739.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_SRR3081739 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081739.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 07:14:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081739.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,634,100
Mapped reads	2,394,075 / 90.89%
Unmapped reads	240,025 / 9.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,197 / 0.65%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	99,856 / 3.79%
Duplication rate	3.38%
Clipped reads	998,382 / 37.9%

2.2. ACGT Content

Number/percentage of A's	44,772,686 / 27.81%
Number/percentage of C's	30,287,901 / 18.81%
Number/percentage of T's	50,528,428 / 31.38%
Number/percentage of G's	35,424,928 / 22%
Number/percentage of N's	1,855 / 0%
GC Percentage	40.81%

2.3. Coverage

Mean	0.052

Standard Deviation	0.3779

2.4. Mapping Quality

Mean Mapping Quality	46.29

2.5. Mismatches and indels

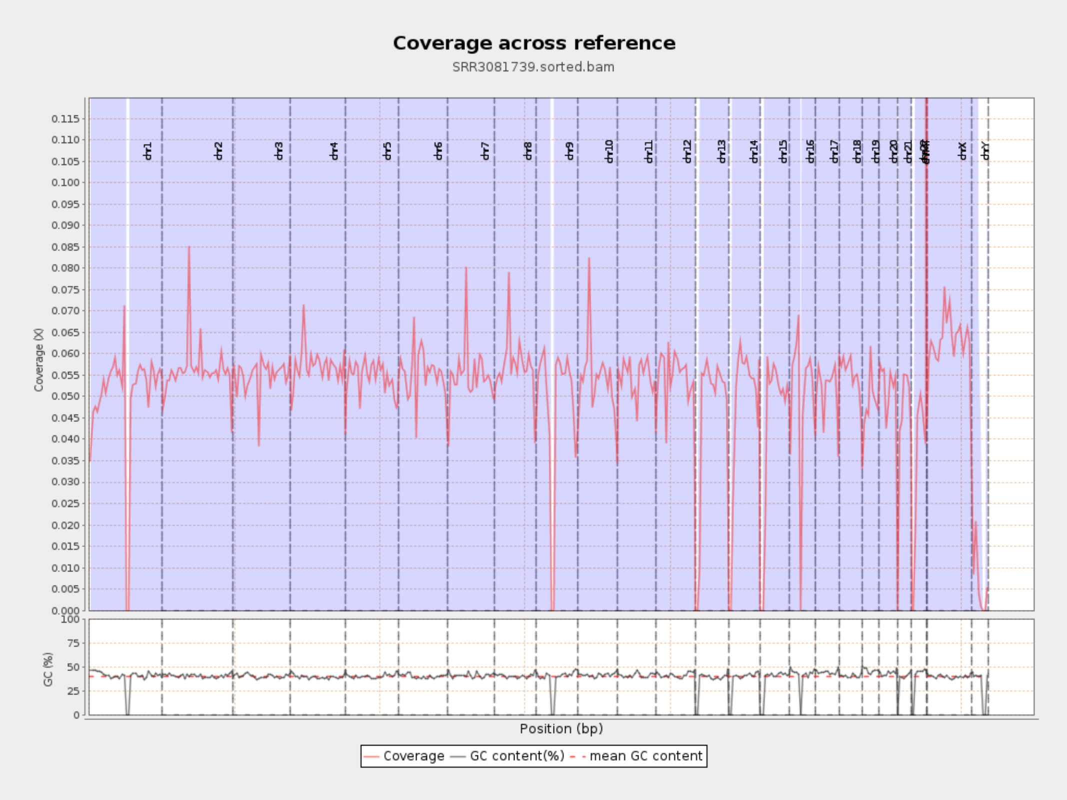
General error rate	0.8%
Mismatches	1,260,092
Insertions	11,416
Mapped reads with at least one insertion	0.47%
Deletions	32,240
Mapped reads with at least one deletion	1.33%
Homopolymer indels	47.46%

2.6. Chromosome stats

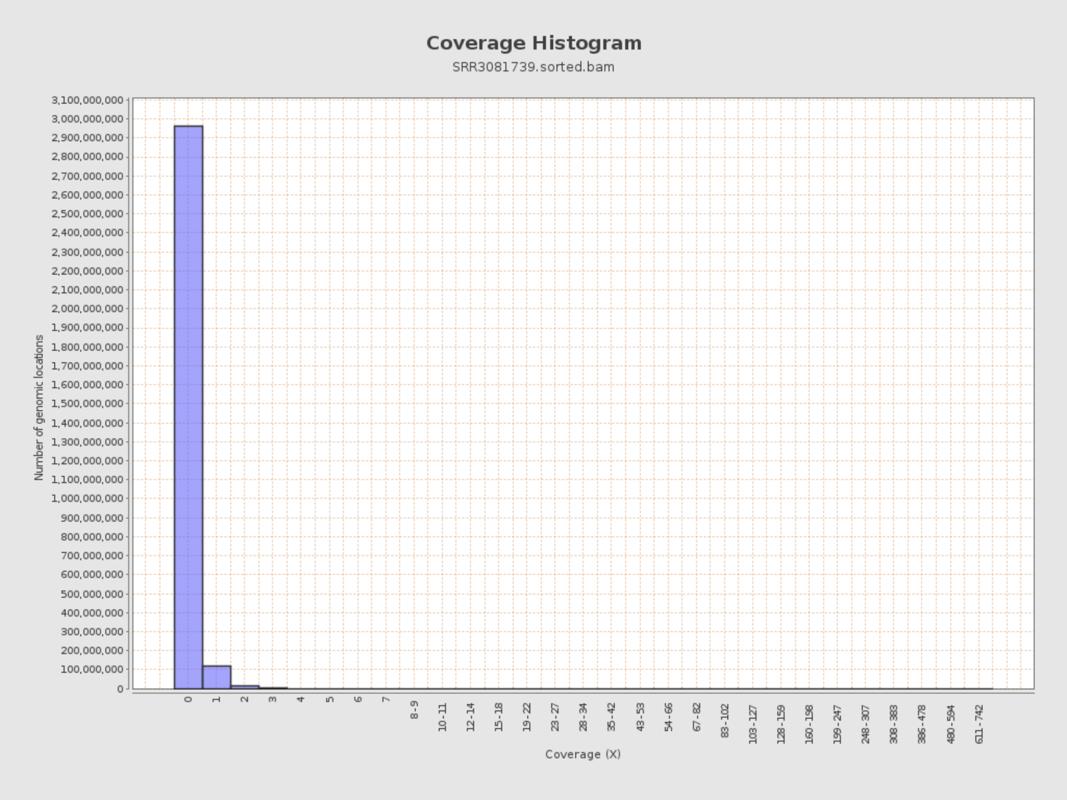
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12481695	0.0501	0.5701
chr2	243199373	13699567	0.0563	0.453
chr3	198022430	10874993	0.0549	0.2719
chr4	191154276	10924834	0.0572	0.2921
chr5	180915260	9879727	0.0546	0.268
chr6	171115067	9487096	0.0554	0.3093
chr7	159138663	8809169	0.0554	0.5037

chr8	146364022	8378419	0.0572	0.5379
chr9	141213431	6763982	0.0479	0.3556
chr10	135534747	7394256	0.0546	0.4061
chr11	135006516	7338457	0.0544	0.3324
chr12	133851895	7301020	0.0545	0.2699
chr13	115169878	5160985	0.0448	0.243
chr14	107349540	4956053	0.0462	0.2576
chr15	102531392	4450885	0.0434	0.2417
chr16	90354753	4573578	0.0506	0.2923
chr17	81195210	4161771	0.0513	0.2776
chr18	78077248	4331238	0.0555	0.6235
chr19	59128983	2879657	0.0487	0.4587
chr20	63025520	3255834	0.0517	0.2693
chr21	48129895	2121238	0.0441	0.2623
chr22	51304566	1640978	0.032	0.2027
chrMT	16571	31653	1.9101	2.0635
chrX	155270560	9771265	0.0629	0.3093
chrY	59373566	404637	0.0068	0.1585

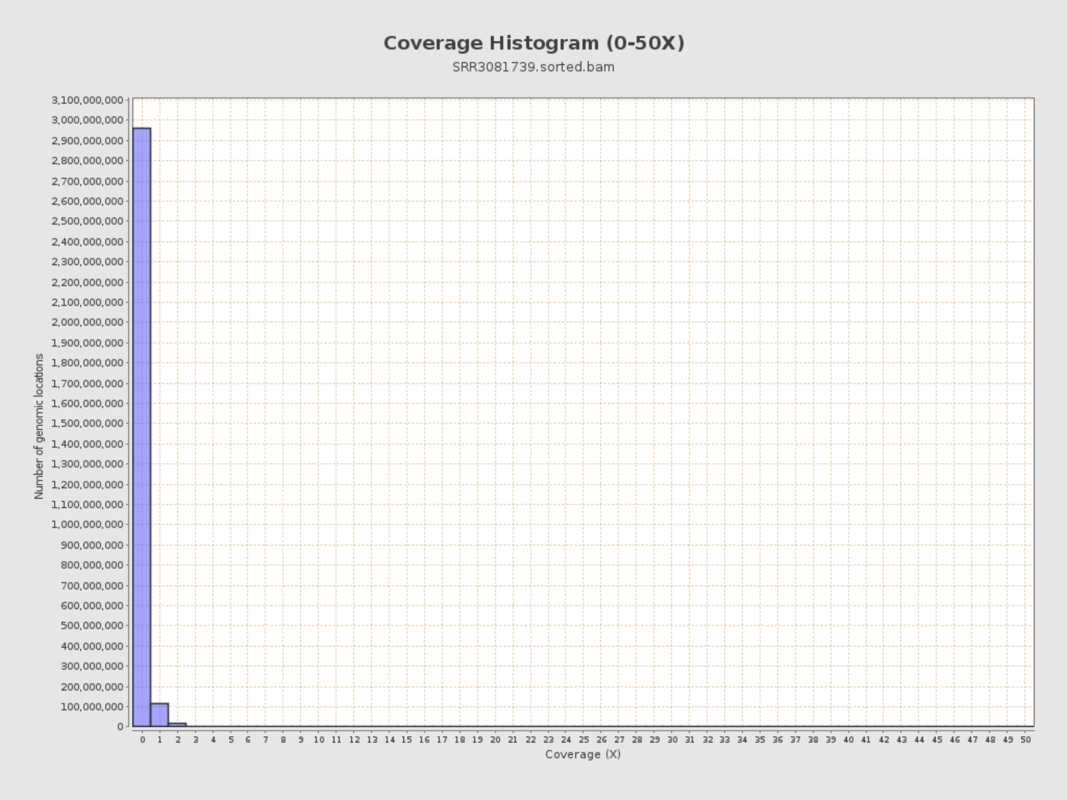
3. Results : Coverage across reference



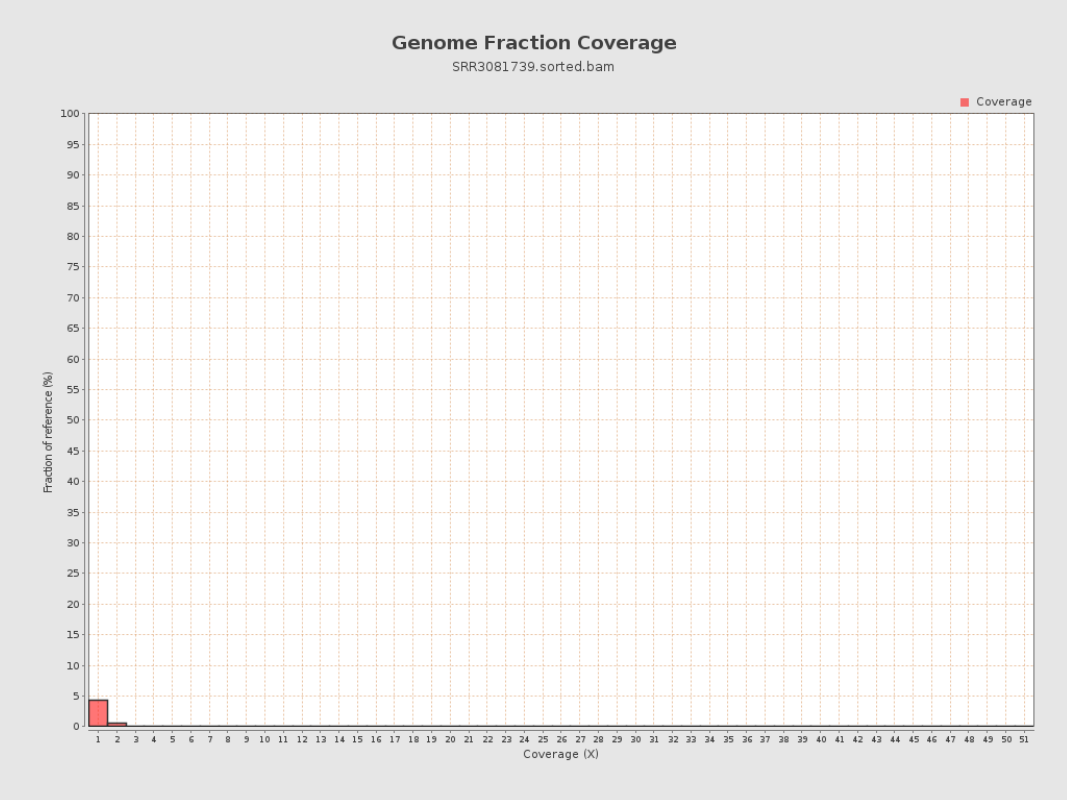
4. Results : Coverage Histogram



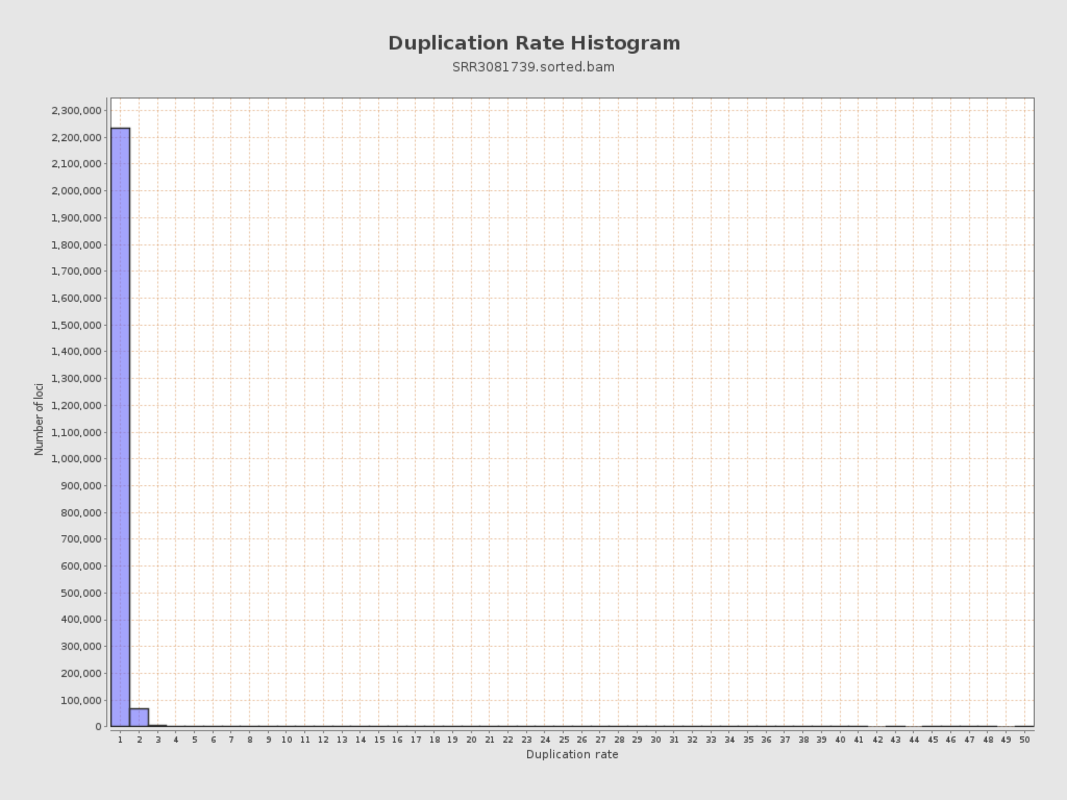
5. Results : Coverage Histogram (0-50X)



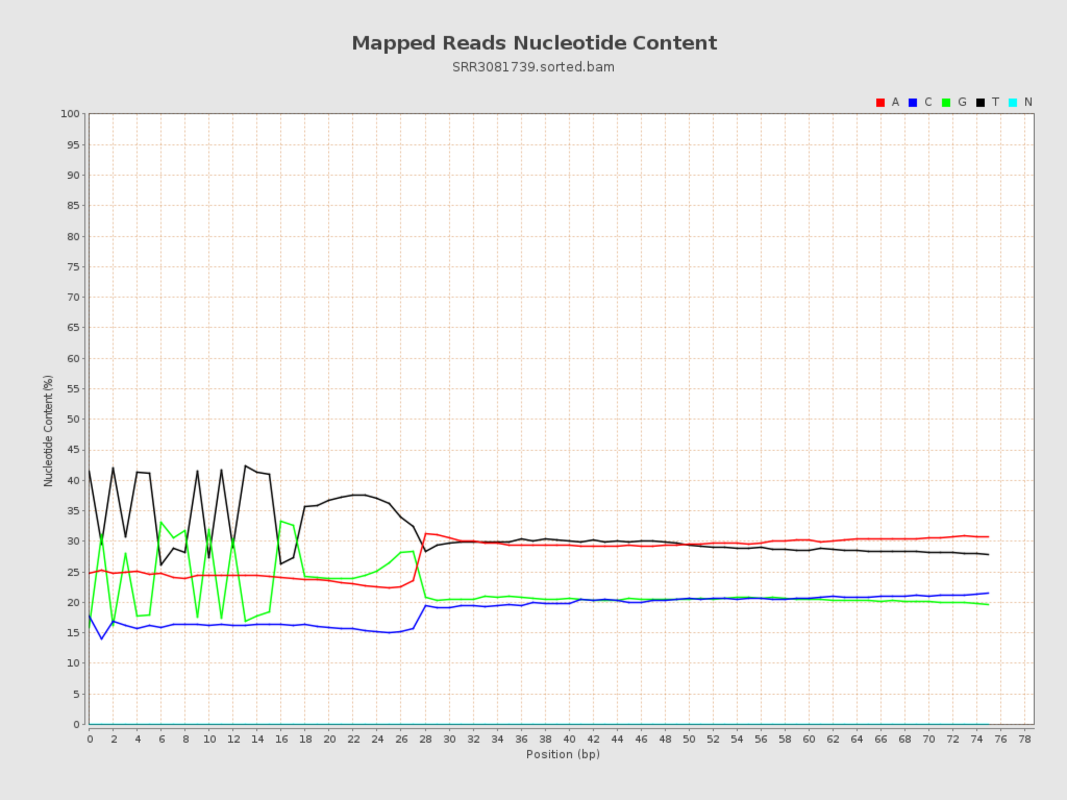
6. Results : Genome Fraction Coverage



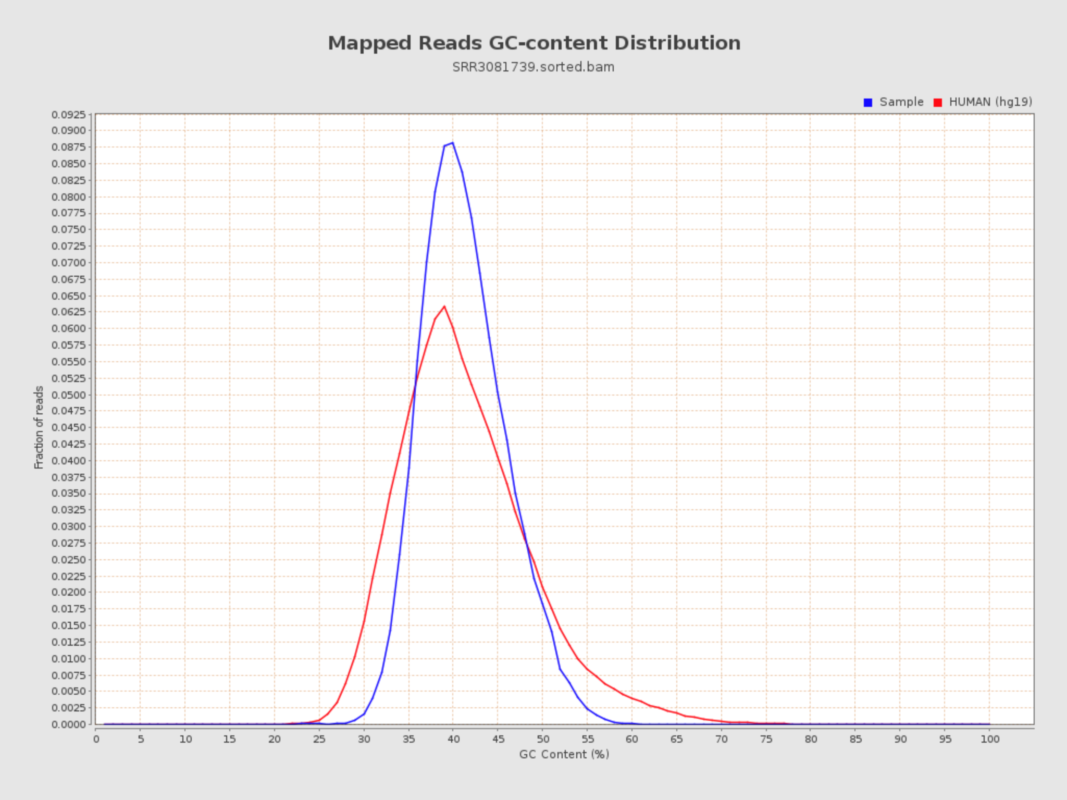
7. Results : Duplication Rate Histogram



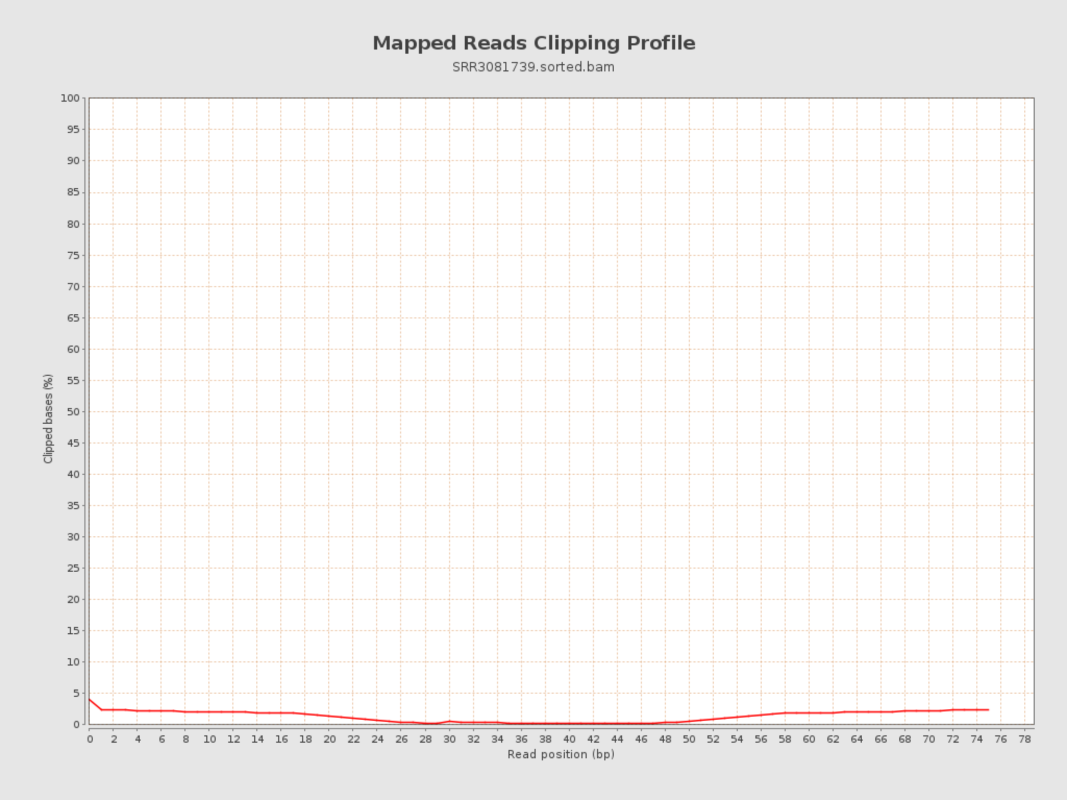
8. Results : Mapped Reads Nucleotide Content



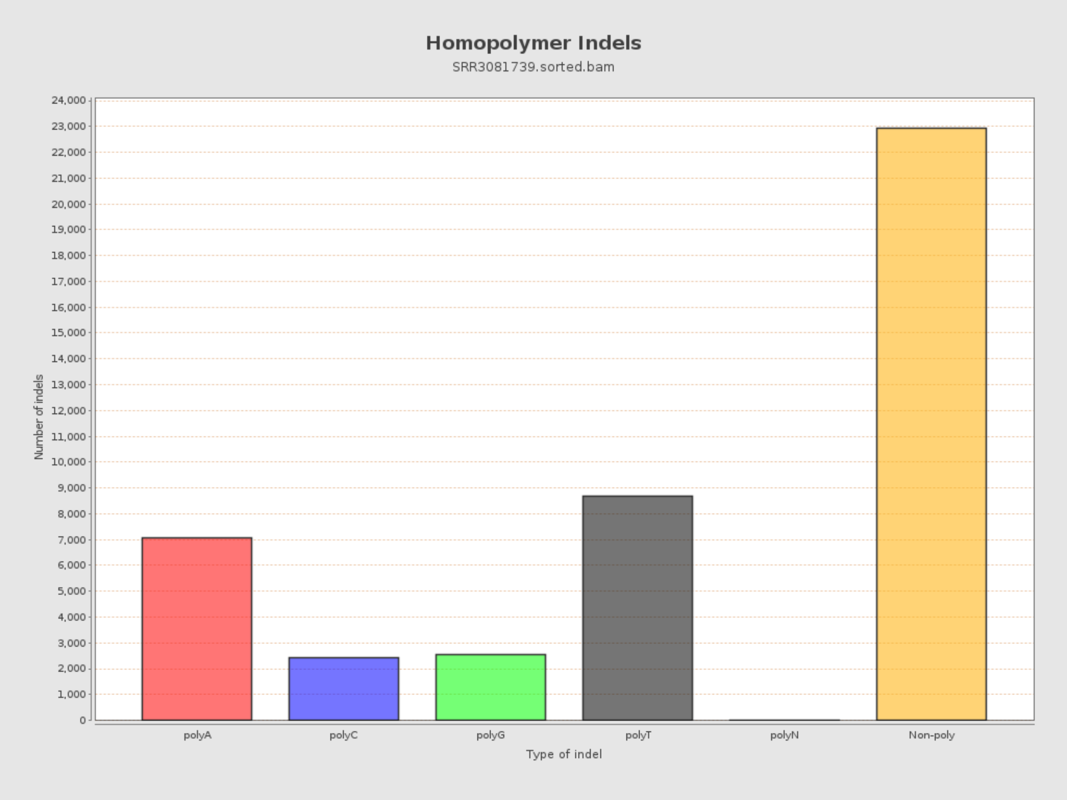
9. Results : Mapped Reads GC-content Distribution



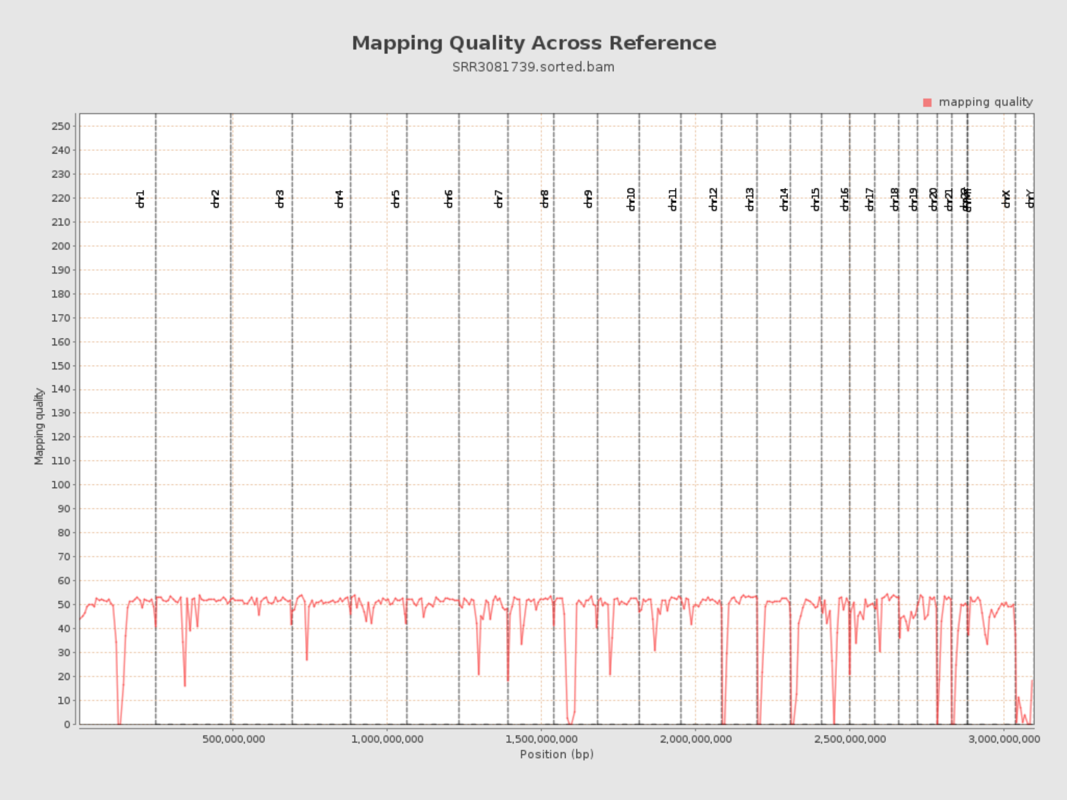
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram