Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 00:13:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549093.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_SRR1549093 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549093.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 00:13:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549093.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,526,871
Mapped reads	10,063,453 / 87.3%
Unmapped reads	1,463,418 / 12.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	488,203 / 4.24%
Duplication rate	2.61%
Clipped reads	576,628 / 5%

2.2. ACGT Content

Number/percentage of A's	119,415,398 / 29.91%
Number/percentage of C's	80,105,324 / 20.07%
Number/percentage of T's	121,074,028 / 30.33%
Number/percentage of G's	78,490,337 / 19.66%
Number/percentage of N's	101,070 / 0.03%
GC Percentage	39.73%

2.3. Coverage

Mean	0.129
Standard Deviation	1.6839

2.4. Mapping Quality

Mean Mapping Quality	41.86

2.5. Mismatches and indels

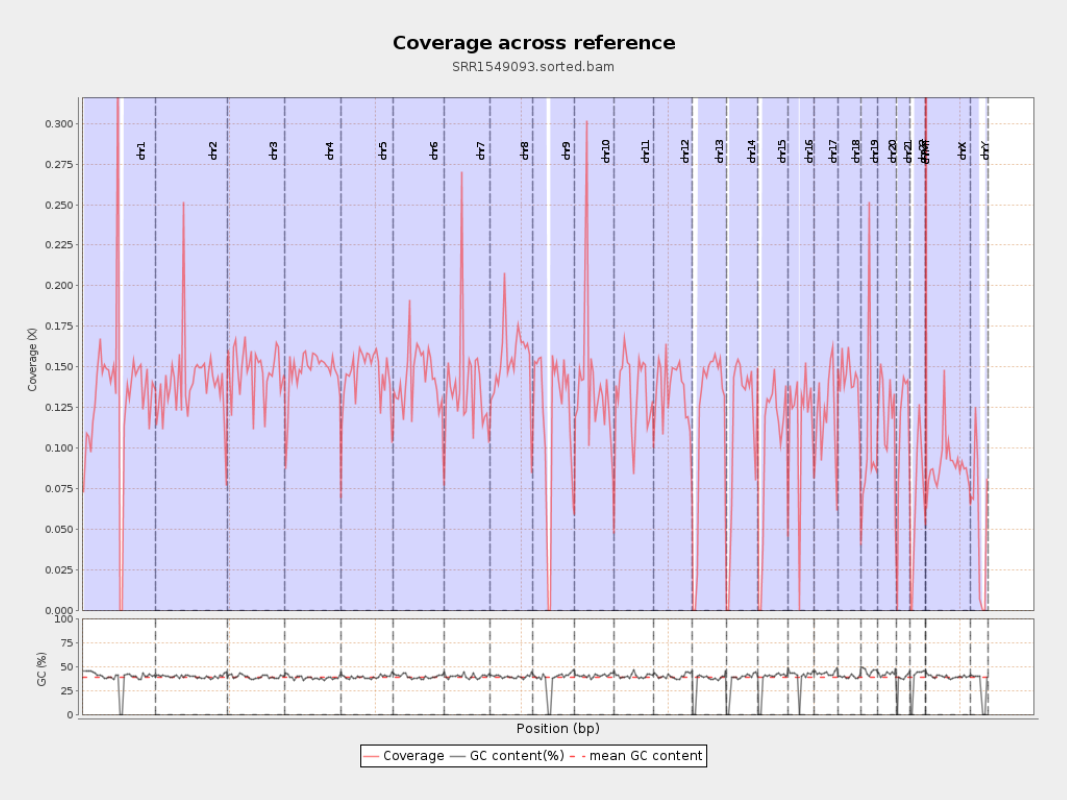
General error rate	0.43%
Mismatches	1,698,514
Insertions	10,272
Mapped reads with at least one insertion	0.1%
Deletions	28,523
Mapped reads with at least one deletion	0.28%
Homopolymer indels	43.59%

2.6. Chromosome stats

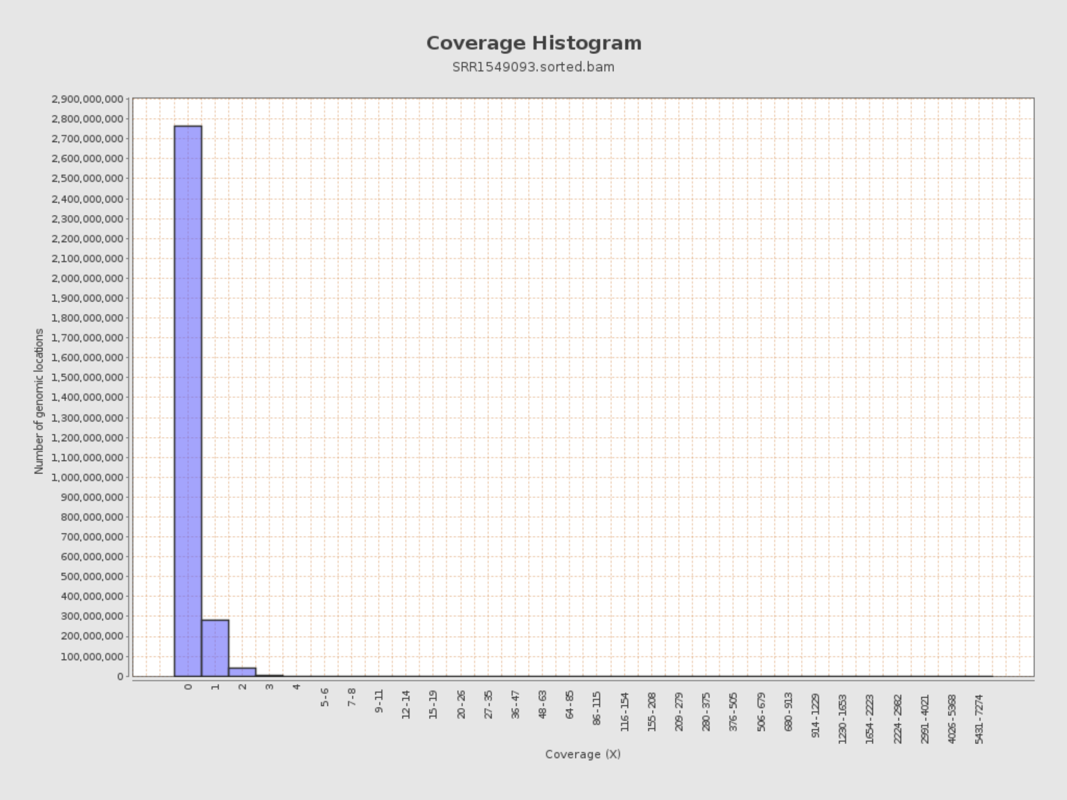
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	33059806	0.1326	4.6873
chr2	243199373	34157033	0.1404	1.0906
chr3	198022430	29288779	0.1479	0.4771
chr4	191154276	28121891	0.1471	0.4725
chr5	180915260	26078286	0.1441	0.493
chr6	171115067	24546654	0.1435	0.6241
chr7	159138663	21904271	0.1376	1.5777
chr8	146364022	22463366	0.1535	1.426

chr9	141213431	16975091	0.1202	1.0808
chr10	135534747	18708851	0.138	1.4526
chr11	135006516	18100458	0.1341	0.9897
chr12	133851895	18102937	0.1352	0.5311
chr13	115169878	13770304	0.1196	0.3825
chr14	107349540	12231225	0.1139	0.6146
chr15	102531392	10376760	0.1012	0.3658
chr16	90354753	10334609	0.1144	0.703
chr17	81195210	9911382	0.1221	0.5088
chr18	78077248	11124833	0.1425	2.3581
chr19	59128983	6228208	0.1053	3.7308
chr20	63025520	7759722	0.1231	0.4481
chr21	48129895	5210632	0.1083	0.5313
chr22	51304566	3525773	0.0687	0.3694
chrMT	16571	39122	2.3609	2.8466
chrX	155270560	13942729	0.0898	0.6172
chrY	59373566	3258560	0.0549	0.44

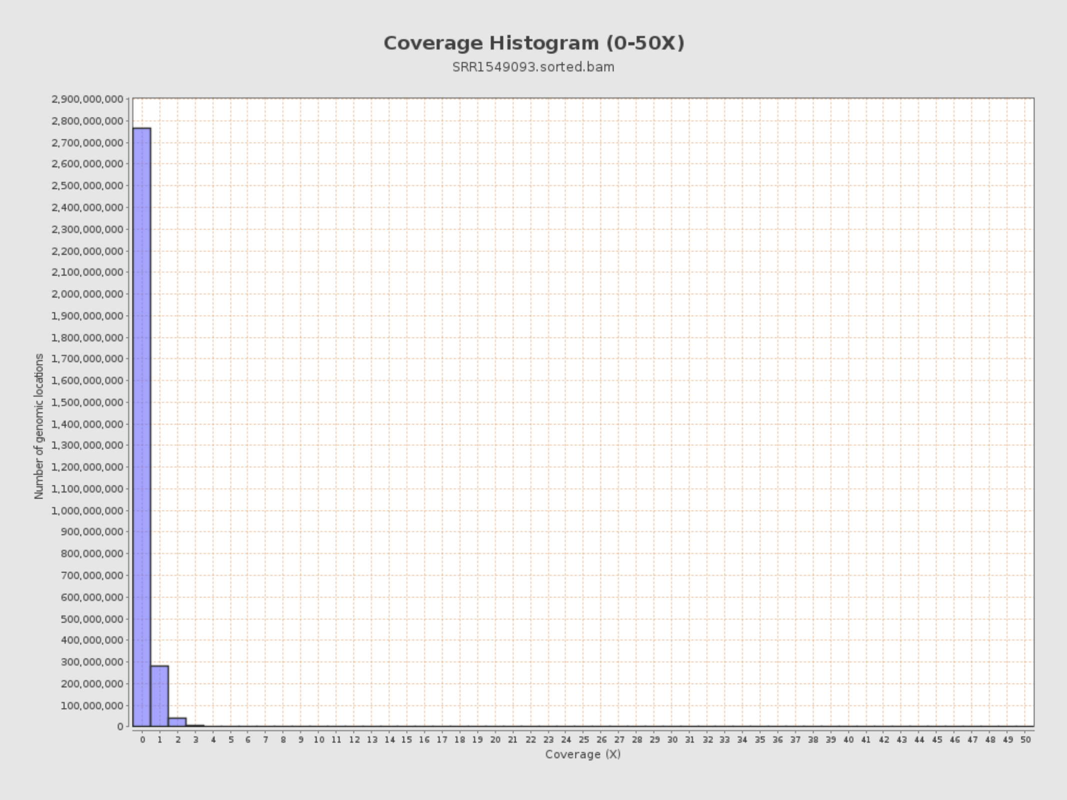
3. Results : Coverage across reference



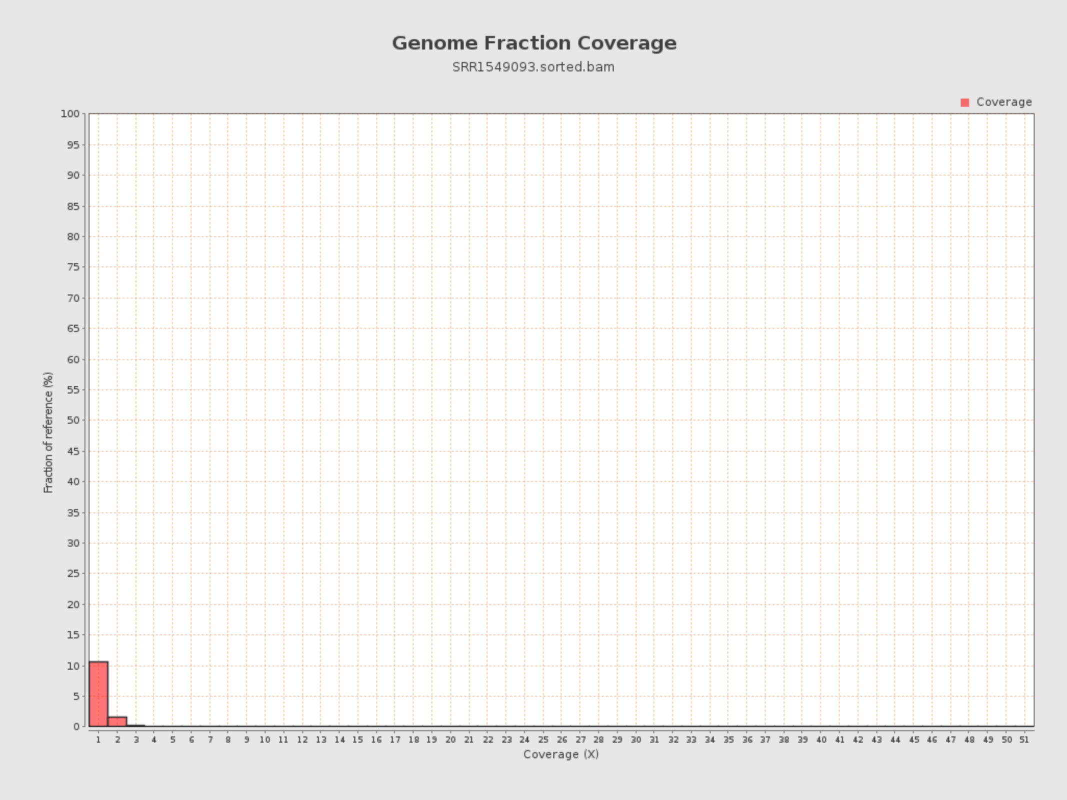
4. Results : Coverage Histogram



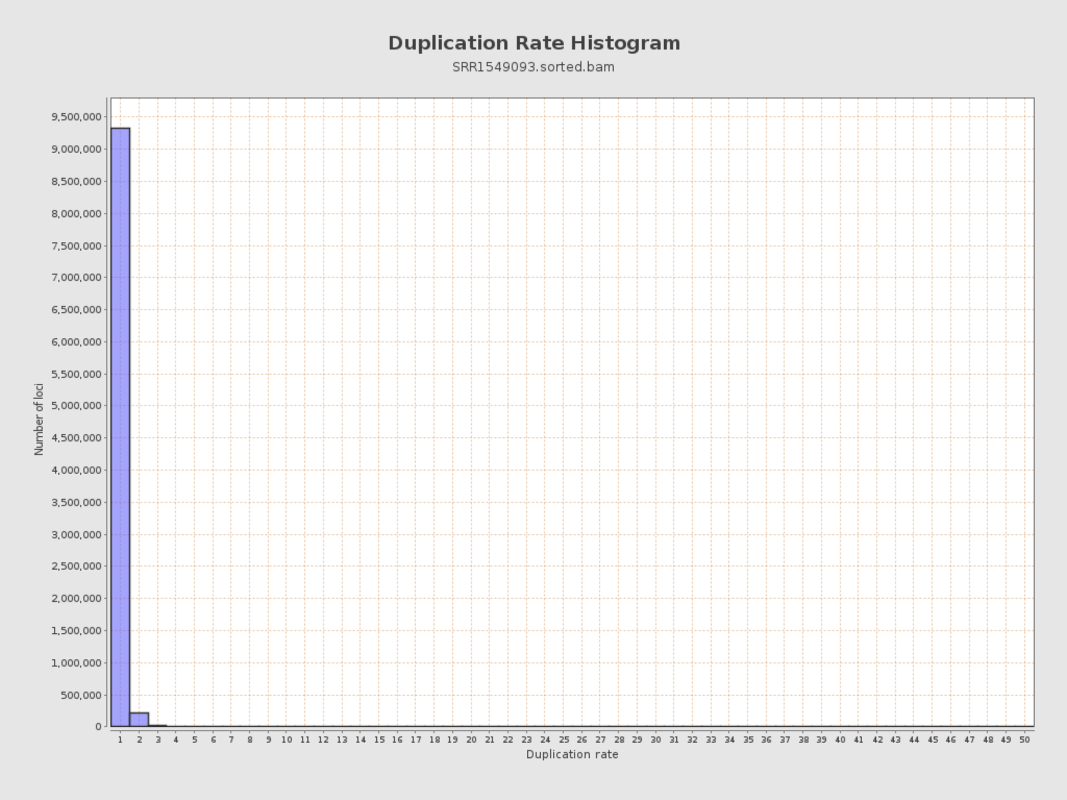
5. Results : Coverage Histogram (0-50X)



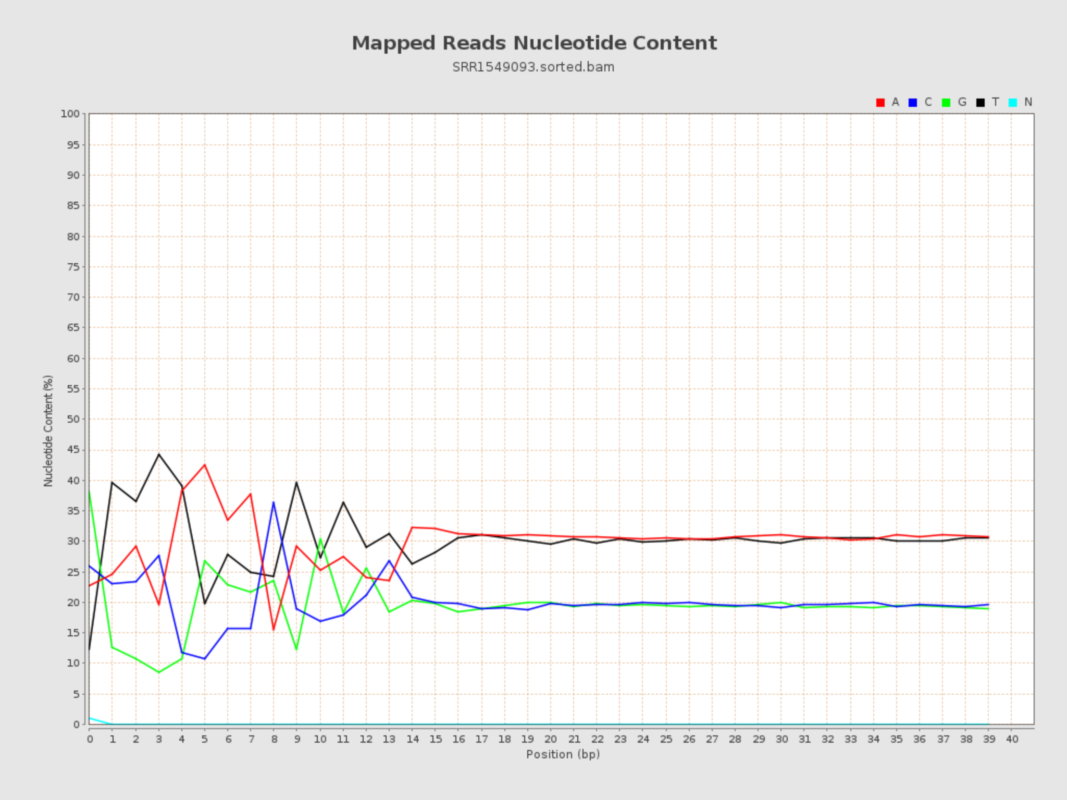
6. Results : Genome Fraction Coverage



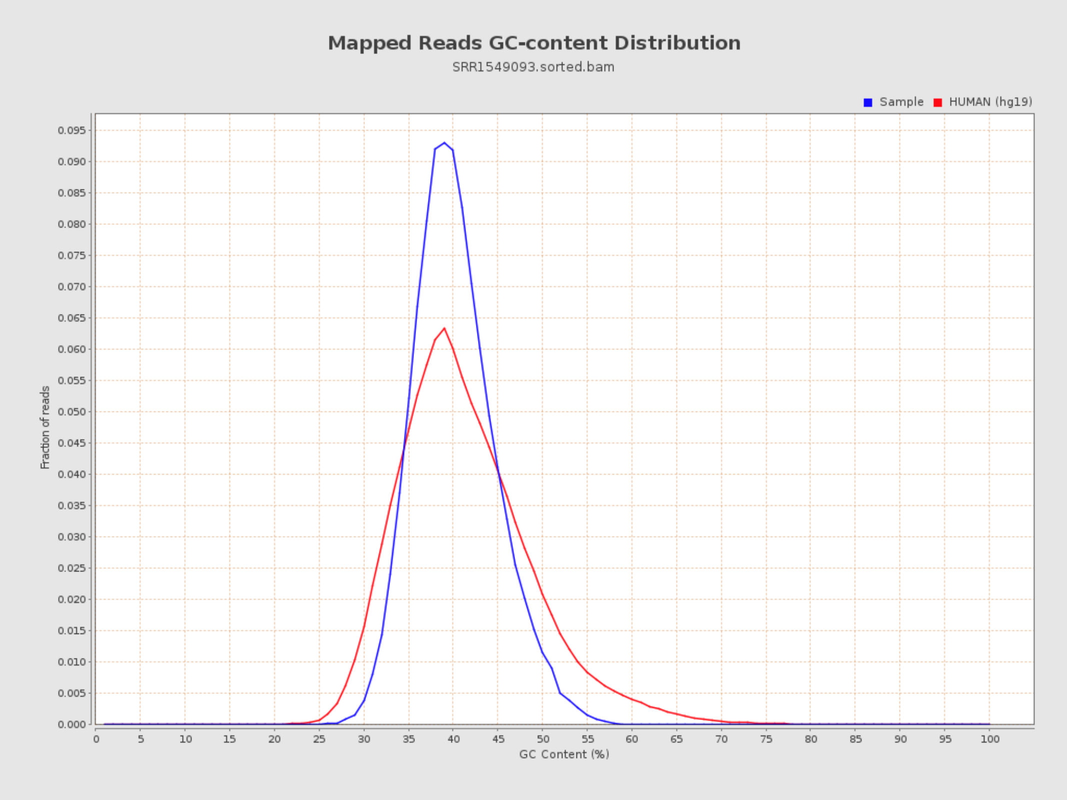
7. Results : Duplication Rate Histogram



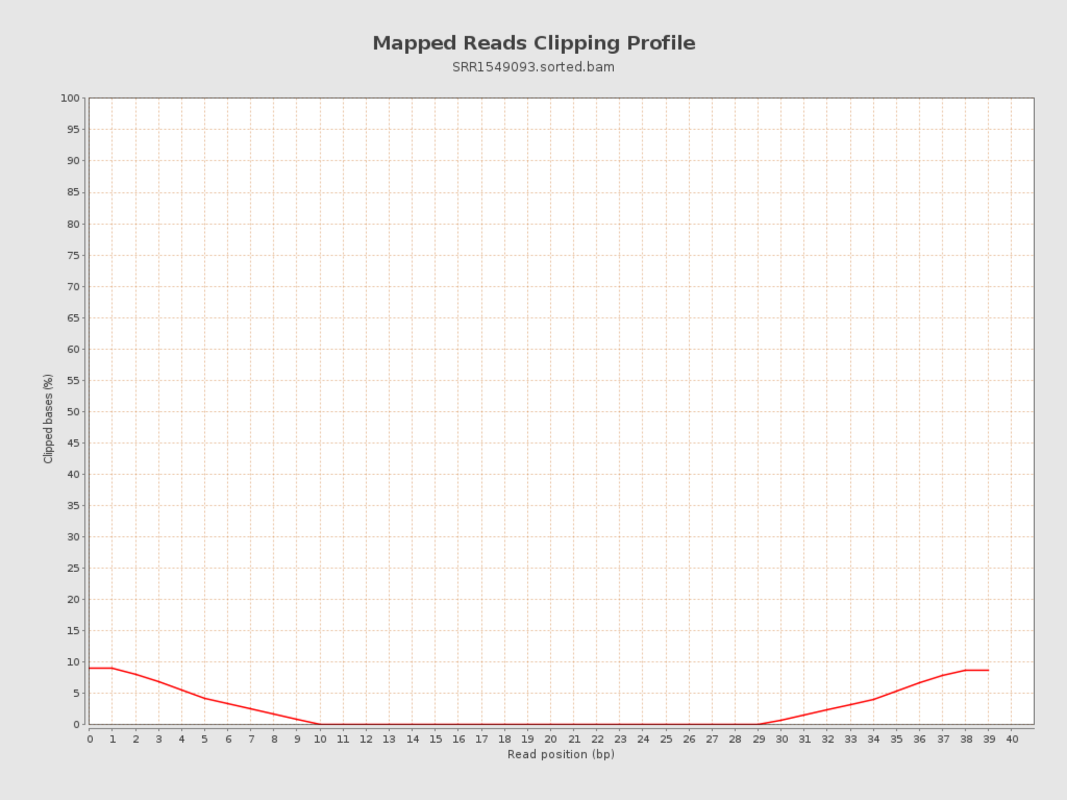
8. Results : Mapped Reads Nucleotide Content



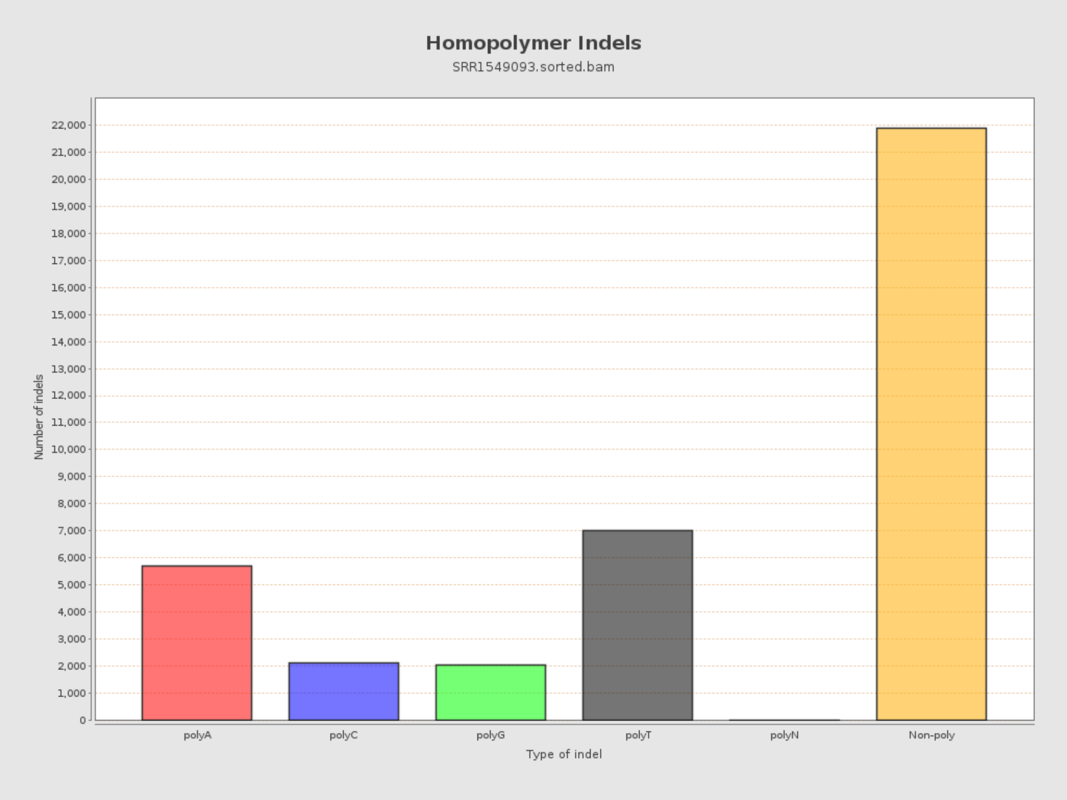
9. Results : Mapped Reads GC-content Distribution



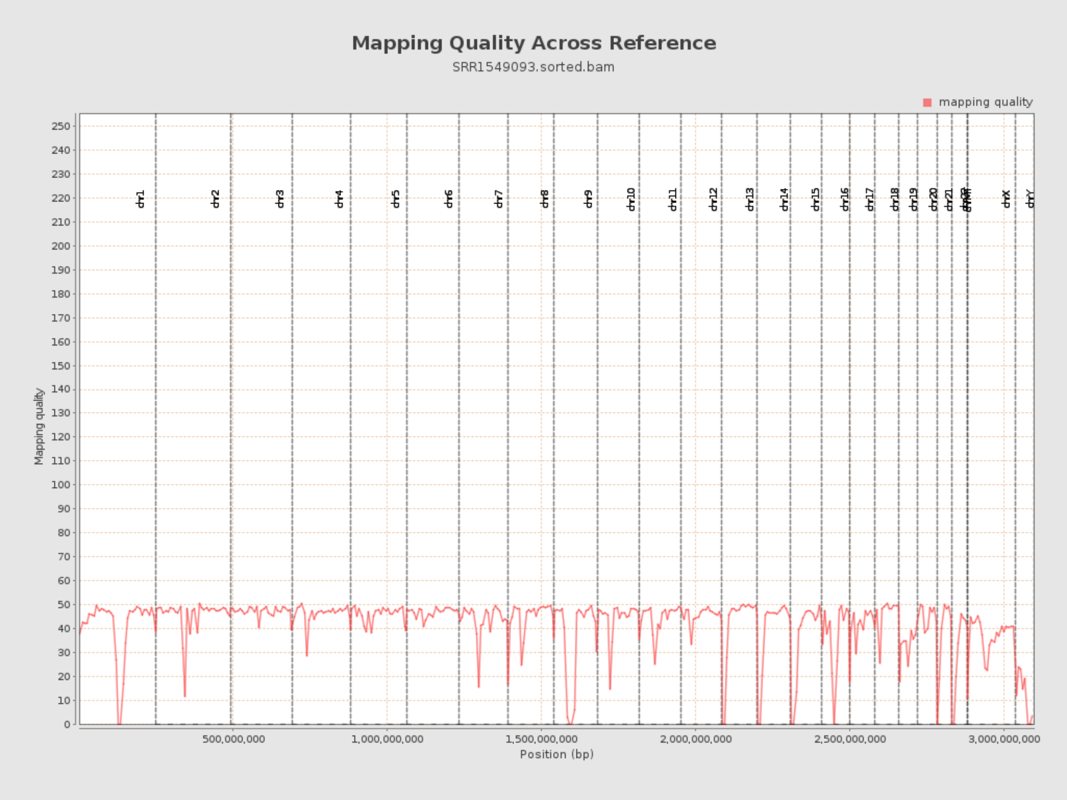
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram