Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 02:50:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549109.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_SRR1549109 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549109.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 02:50:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549109.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,604,583
Mapped reads	10,024,114 / 86.38%
Unmapped reads	1,580,469 / 13.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	496,078 / 4.27%
Duplication rate	3.97%
Clipped reads	718,932 / 6.2%

2.2. ACGT Content

Number/percentage of A's	110,683,234 / 27.9%
Number/percentage of C's	87,586,719 / 22.08%
Number/percentage of T's	110,891,416 / 27.95%
Number/percentage of G's	87,596,880 / 22.08%
Number/percentage of N's	1,550 / 0%
GC Percentage	44.15%

2.3. Coverage

Mean	0.1282
Standard Deviation	0.6932

2.4. Mapping Quality

Mean Mapping Quality	41.14

2.5. Mismatches and indels

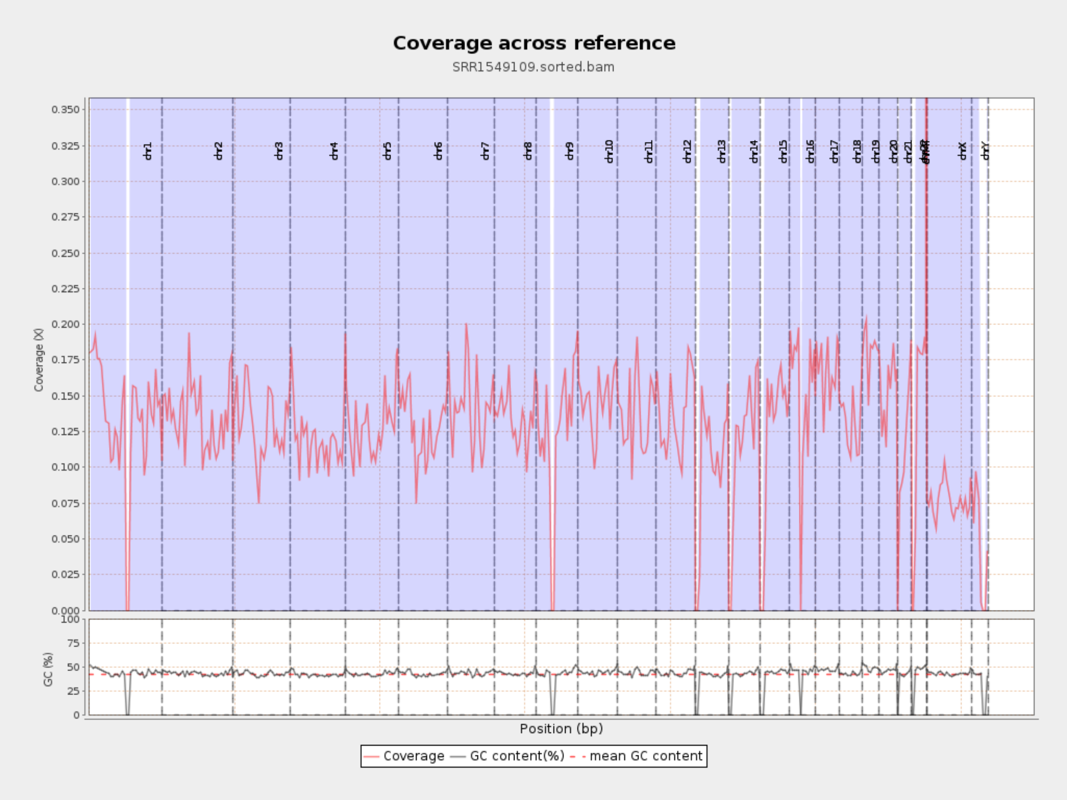
General error rate	0.34%
Mismatches	1,322,011
Insertions	13,068
Mapped reads with at least one insertion	0.13%
Deletions	34,903
Mapped reads with at least one deletion	0.35%
Homopolymer indels	45.69%

2.6. Chromosome stats

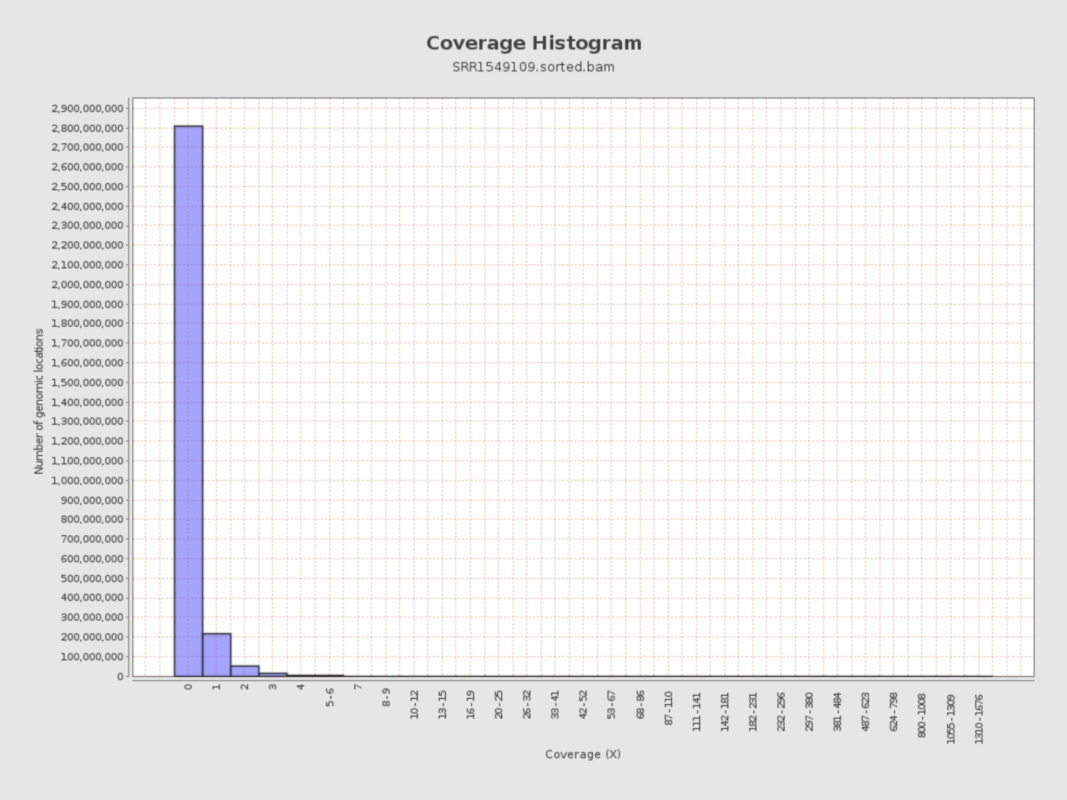
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	33293472	0.1336	1.0686
chr2	243199373	33043567	0.1359	0.7077
chr3	198022430	25723254	0.1299	0.4786
chr4	191154276	22733576	0.1189	0.4728
chr5	180915260	23198764	0.1282	0.49
chr6	171115067	22007660	0.1286	0.524
chr7	159138663	22414522	0.1408	0.8963
chr8	146364022	19684753	0.1345	0.988

chr9	141213431	17207285	0.1219	0.6872
chr10	135534747	19720808	0.1455	0.6336
chr11	135006516	18563456	0.1375	0.6104
chr12	133851895	18461021	0.1379	0.5173
chr13	115169878	11555282	0.1003	0.4151
chr14	107349540	12304331	0.1146	0.6431
chr15	102531392	12516477	0.1221	0.4586
chr16	90354753	13645567	0.151	0.5502
chr17	81195210	13654201	0.1682	0.5553
chr18	78077248	10183560	0.1304	1.263
chr19	59128983	10797290	0.1826	1.0955
chr20	63025520	9618920	0.1526	0.5495
chr21	48129895	5307305	0.1103	0.5255
chr22	51304566	6439783	0.1255	0.5116
chrMT	16571	168460	10.166	14.6138
chrX	155270560	11950777	0.077	0.4561
chrY	59373566	2609458	0.0439	0.3245

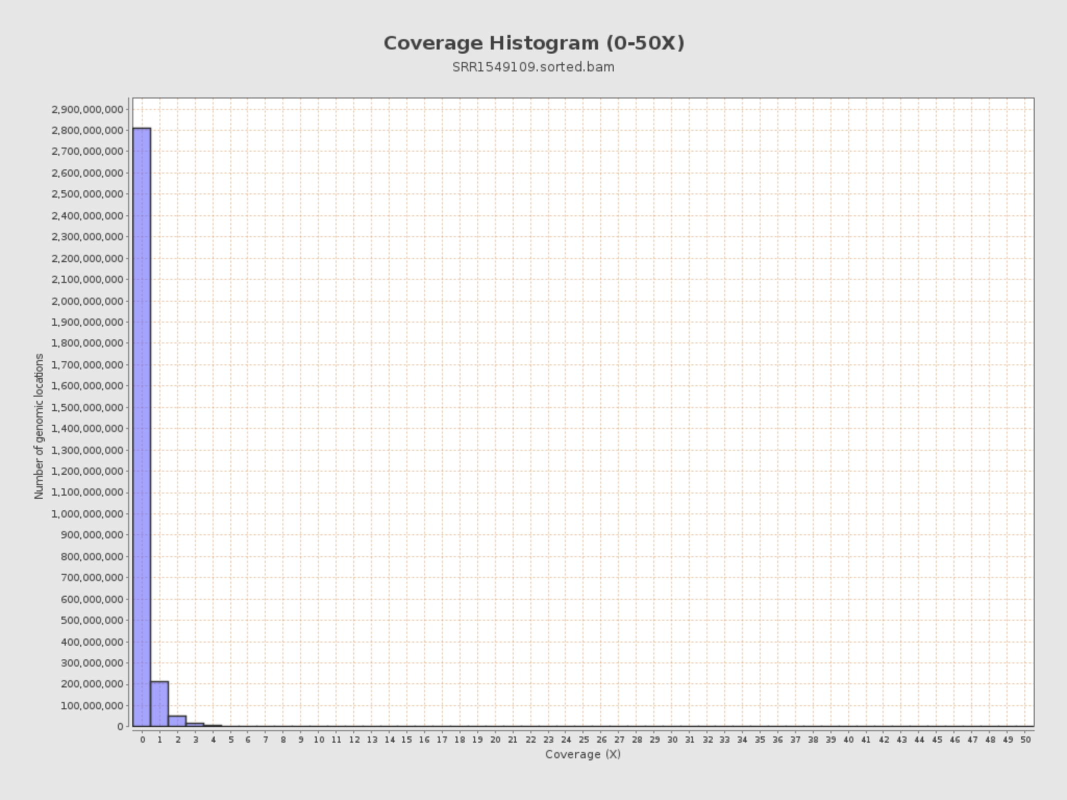
3. Results : Coverage across reference



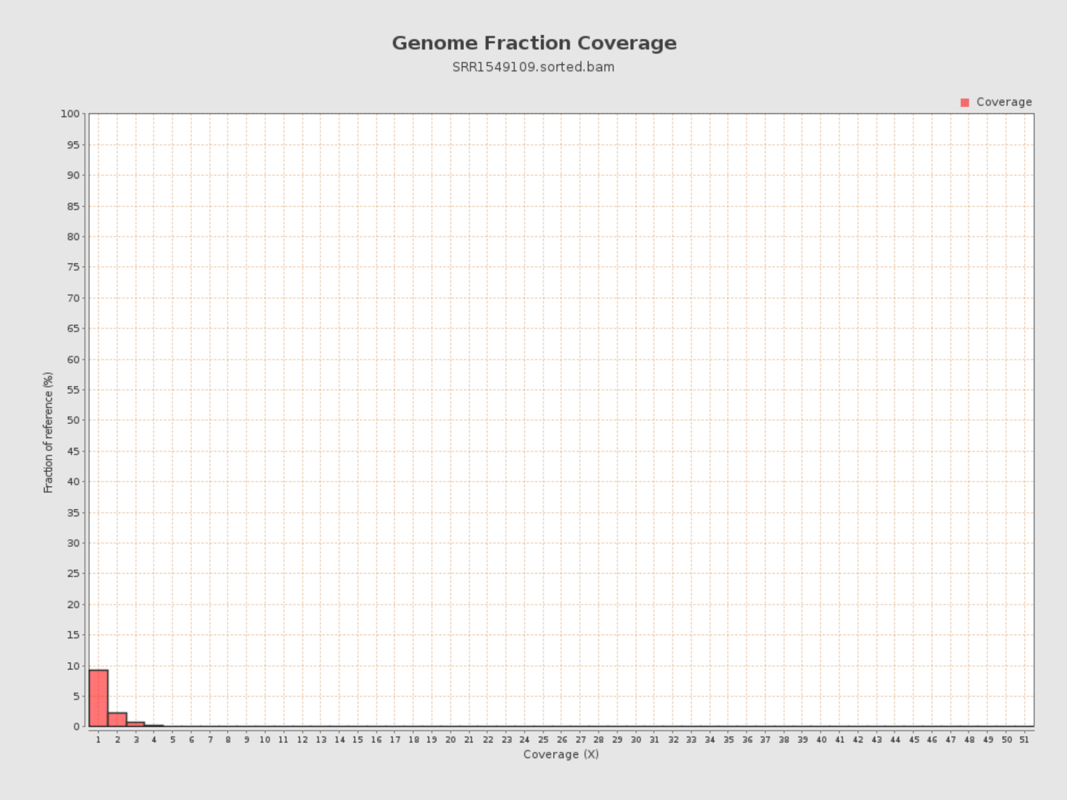
4. Results : Coverage Histogram



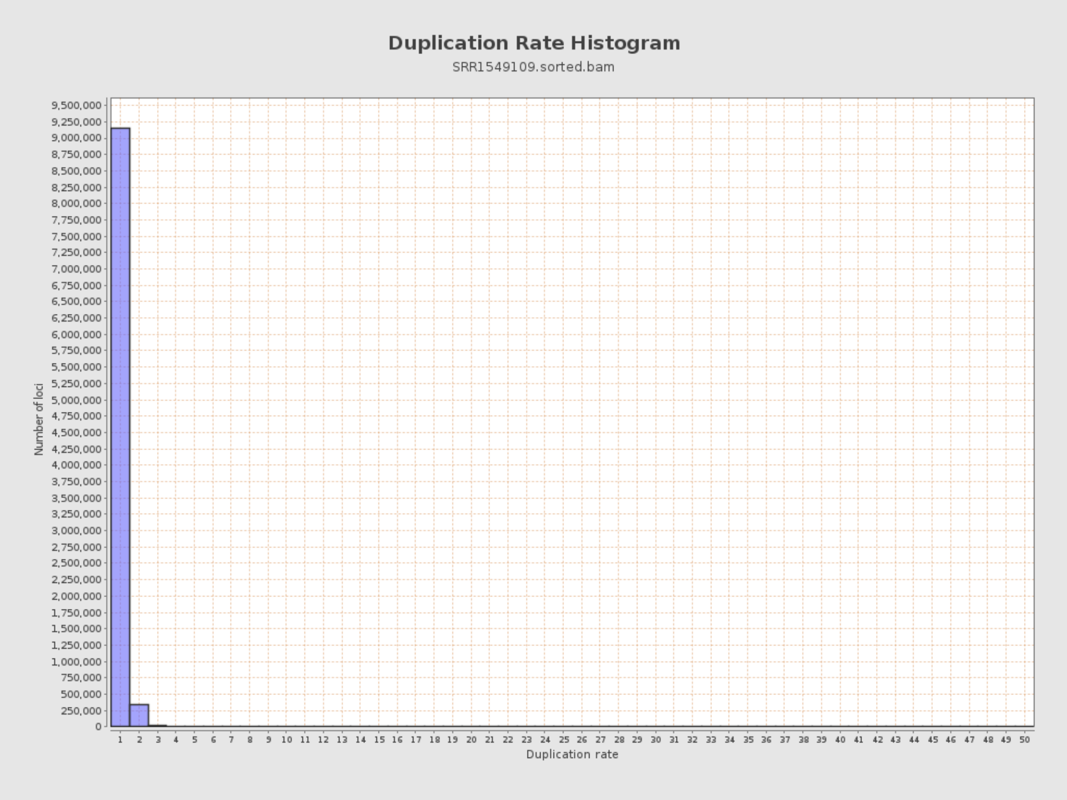
5. Results : Coverage Histogram (0-50X)



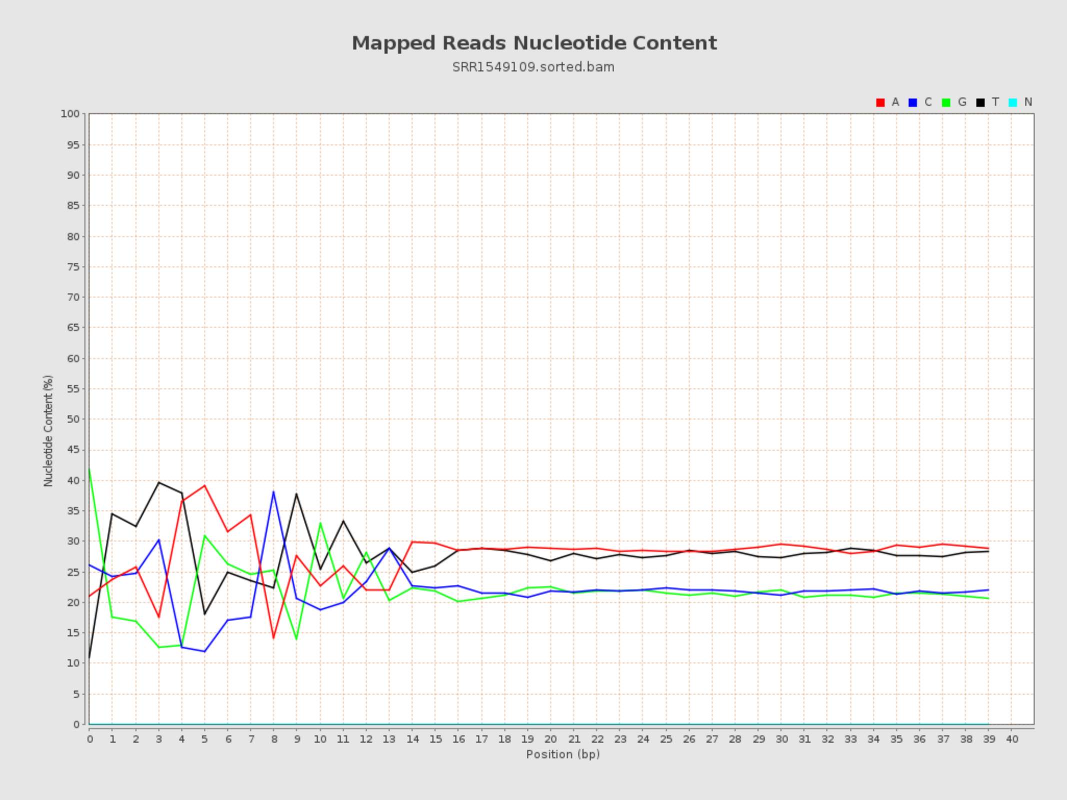
6. Results : Genome Fraction Coverage



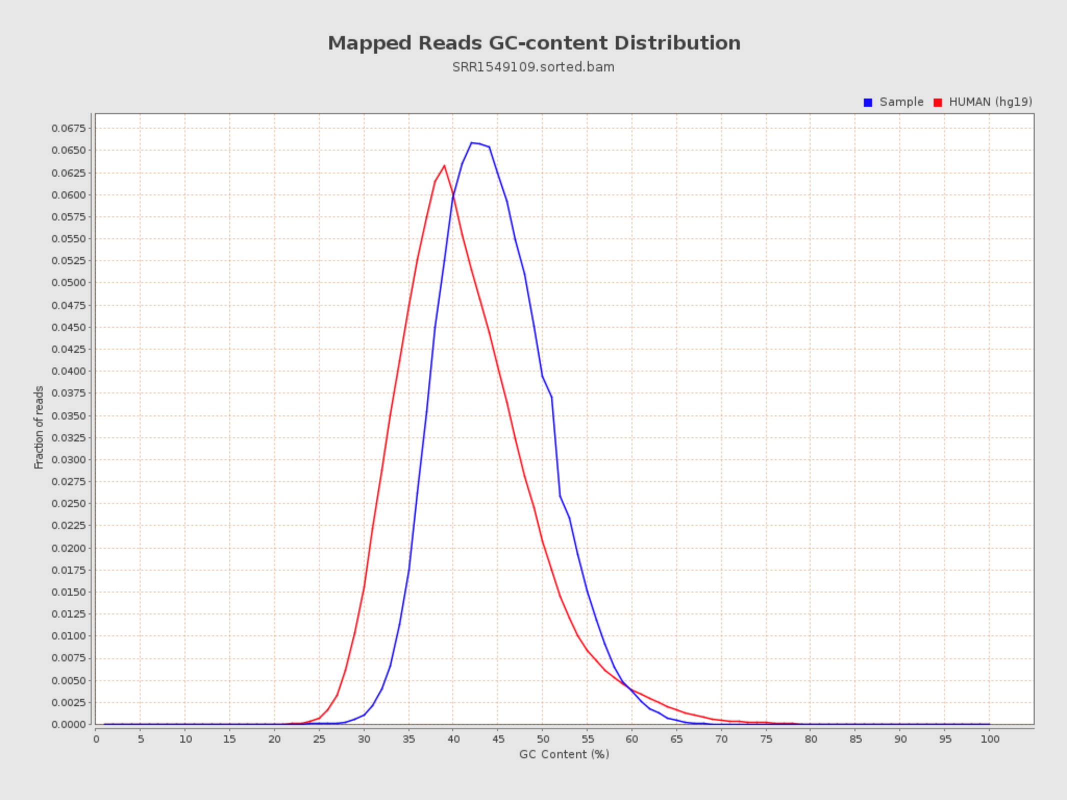
7. Results : Duplication Rate Histogram



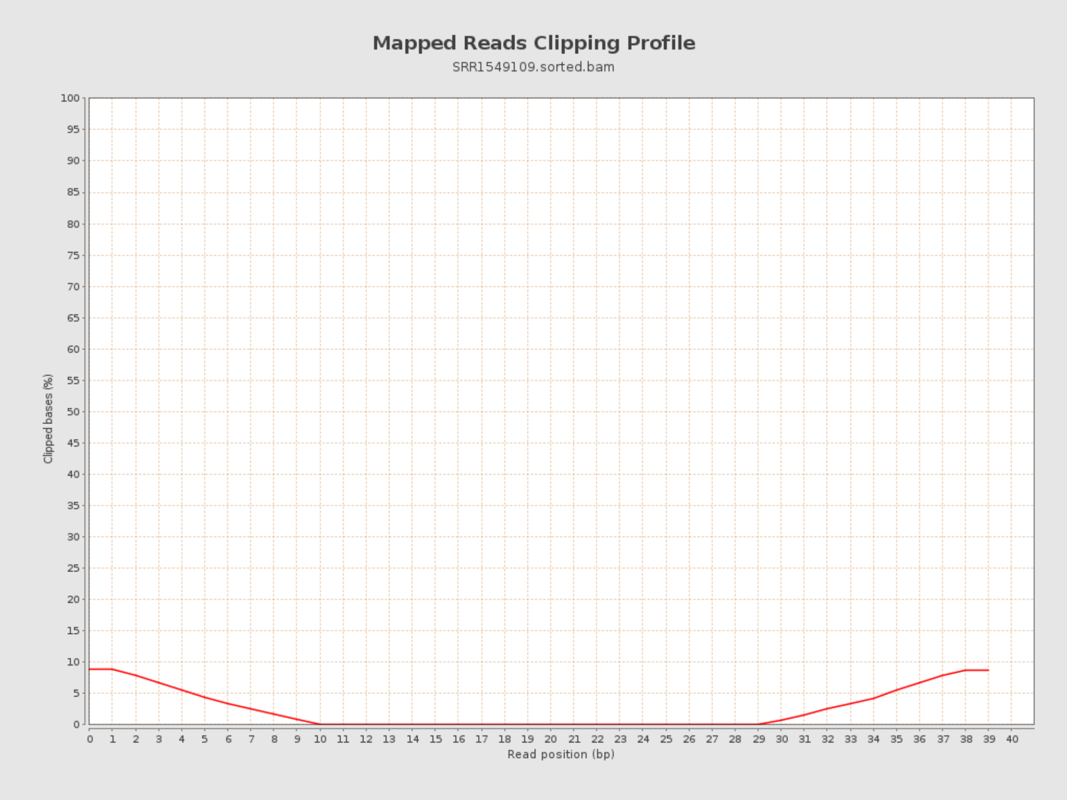
8. Results : Mapped Reads Nucleotide Content



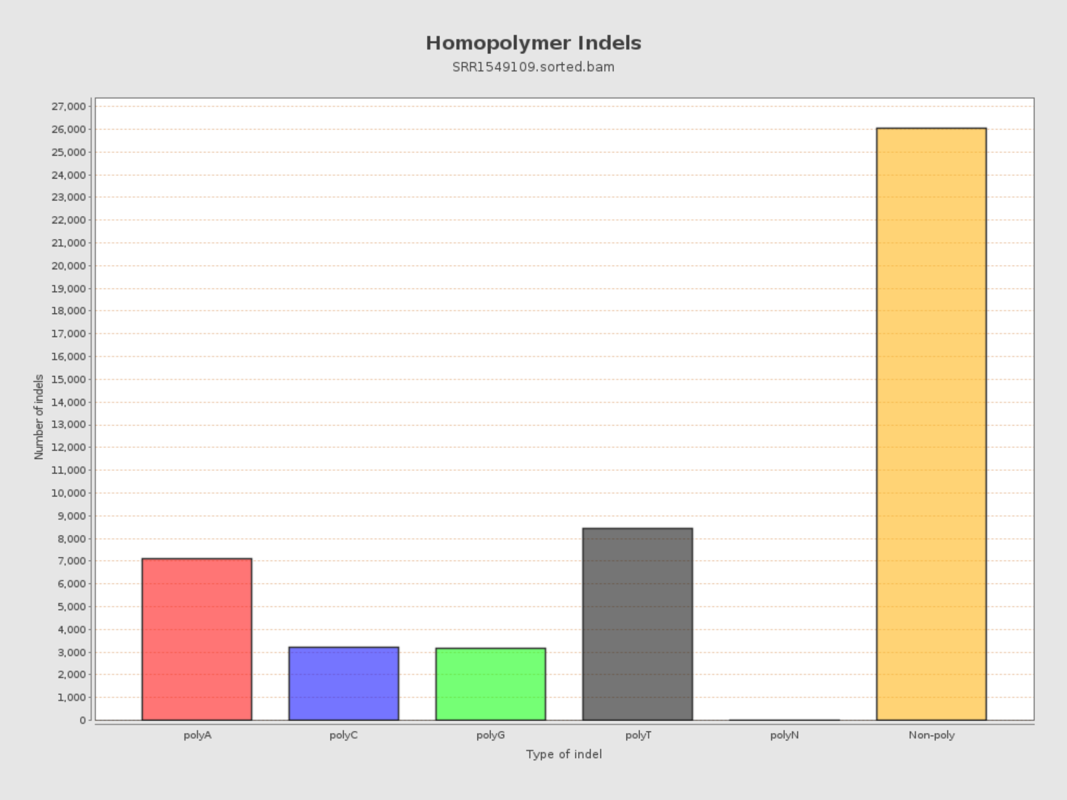
9. Results : Mapped Reads GC-content Distribution



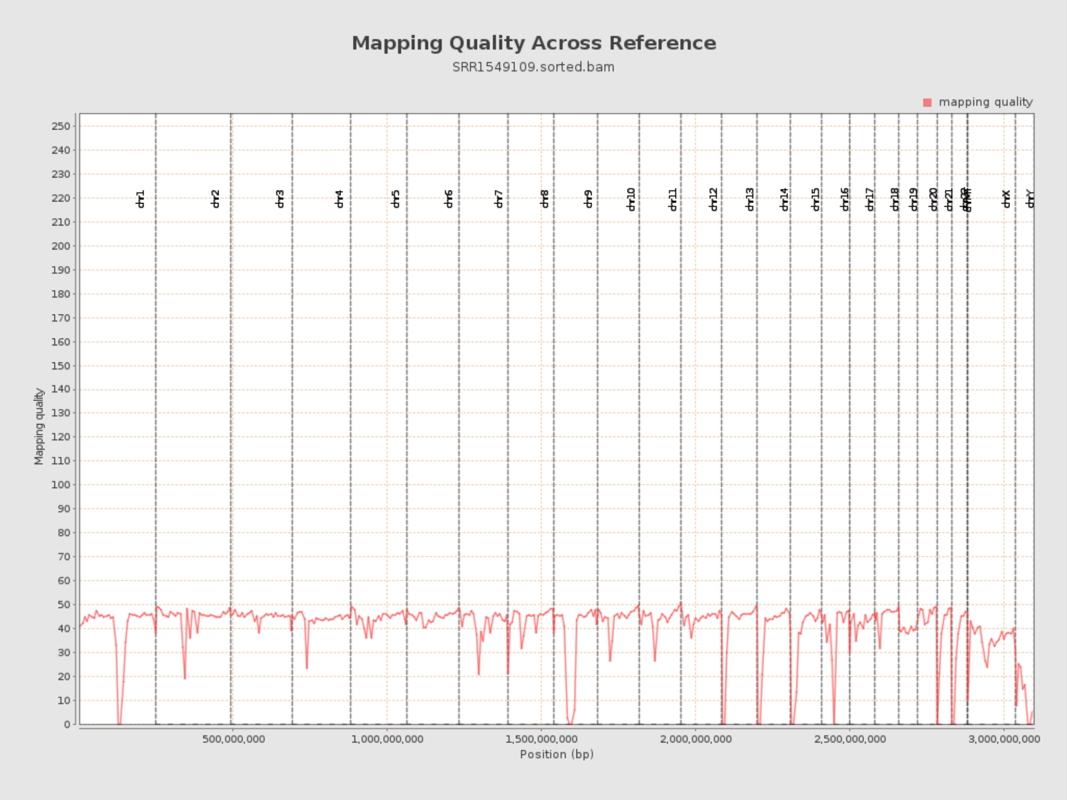
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram