Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 01:14:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085109.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_SRR3085109 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085109.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 01:14:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085109.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,171,129
Mapped reads	943,025 / 80.52%
Unmapped reads	228,104 / 19.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,238 / 0.7%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	18,006 / 1.54%
Duplication rate	1.47%
Clipped reads	495,235 / 42.29%

2.2. ACGT Content

Number/percentage of A's	18,587,287 / 30.23%
Number/percentage of C's	11,572,129 / 18.82%
Number/percentage of T's	18,337,727 / 29.82%
Number/percentage of G's	12,989,384 / 21.13%
Number/percentage of N's	1,276 / 0%
GC Percentage	39.95%

2.3. Coverage

Mean	0.0199

Standard Deviation	0.2007

2.4. Mapping Quality

Mean Mapping Quality	46.6

2.5. Mismatches and indels

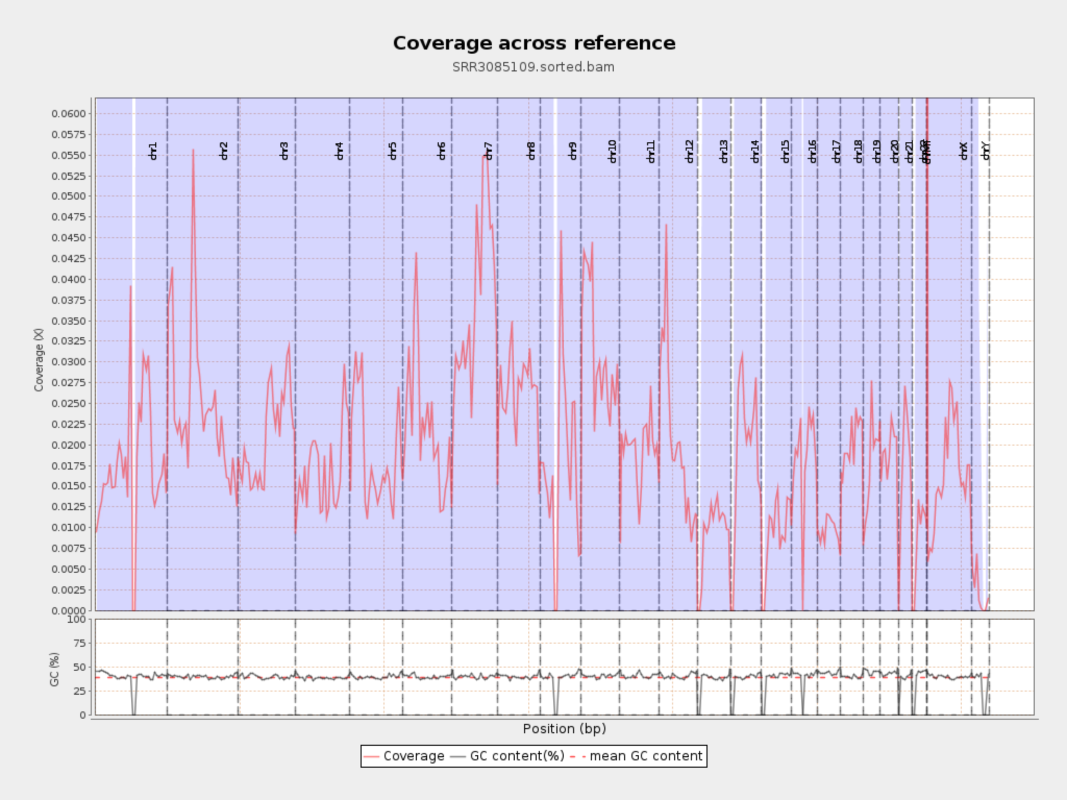
General error rate	0.97%
Mismatches	585,869
Insertions	4,845
Mapped reads with at least one insertion	0.51%
Deletions	13,371
Mapped reads with at least one deletion	1.4%
Homopolymer indels	45.86%

2.6. Chromosome stats

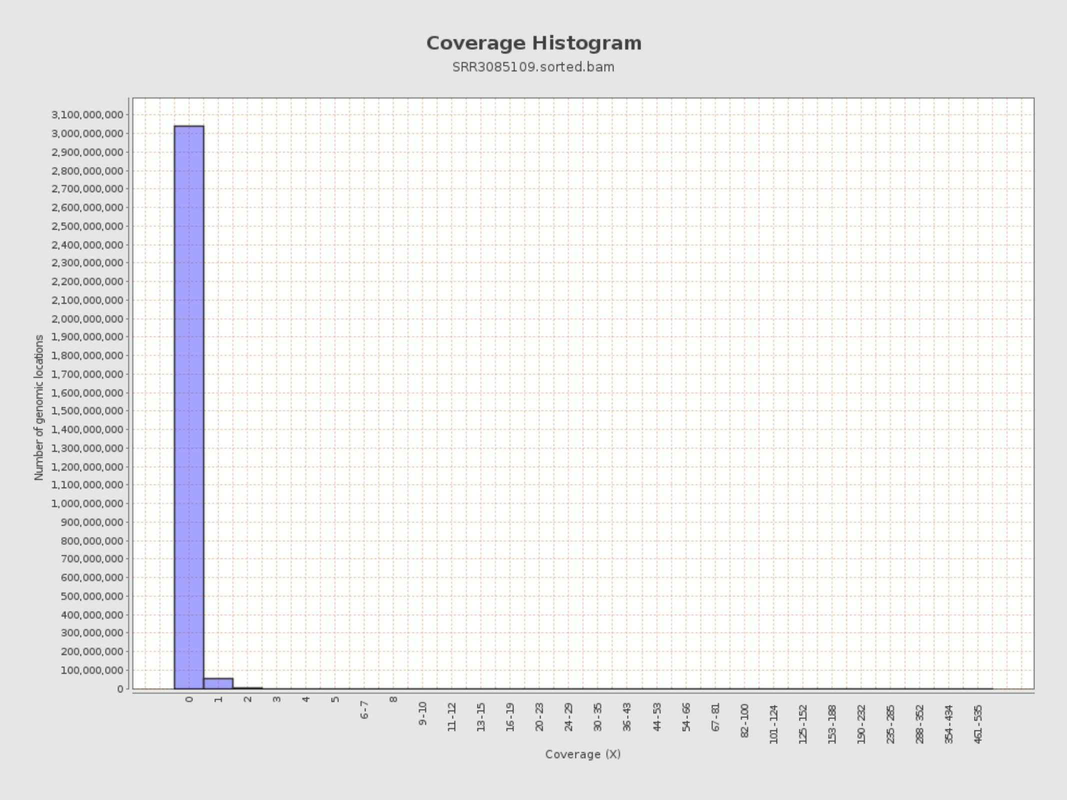
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4360427	0.0175	0.3316
chr2	243199373	6062284	0.0249	0.2062
chr3	198022430	4173761	0.0211	0.1531
chr4	191154276	3230659	0.0169	0.1386
chr5	180915260	3463483	0.0191	0.1449
chr6	171115067	3838028	0.0224	0.1742
chr7	159138663	6004811	0.0377	0.235

chr8	146364022	3925320	0.0268	0.3576
chr9	141213431	2519367	0.0178	0.1678
chr10	135534747	4278318	0.0316	0.2548
chr11	135006516	2610283	0.0193	0.1803
chr12	133851895	2795321	0.0209	0.153
chr13	115169878	1067774	0.0093	0.1001
chr14	107349540	2070136	0.0193	0.1481
chr15	102531392	938666	0.0092	0.0995
chr16	90354753	1607457	0.0178	0.145
chr17	81195210	783706	0.0097	0.1097
chr18	78077248	1585051	0.0203	0.264
chr19	59128983	1050017	0.0178	0.2142
chr20	63025520	1184690	0.0188	0.1437
chr21	48129895	838589	0.0174	0.1414
chr22	51304566	441352	0.0086	0.096
chrMT	16571	8854	0.5343	0.7611
chrX	155270560	2548367	0.0164	0.1419
chrY	59373566	122834	0.0021	0.0594

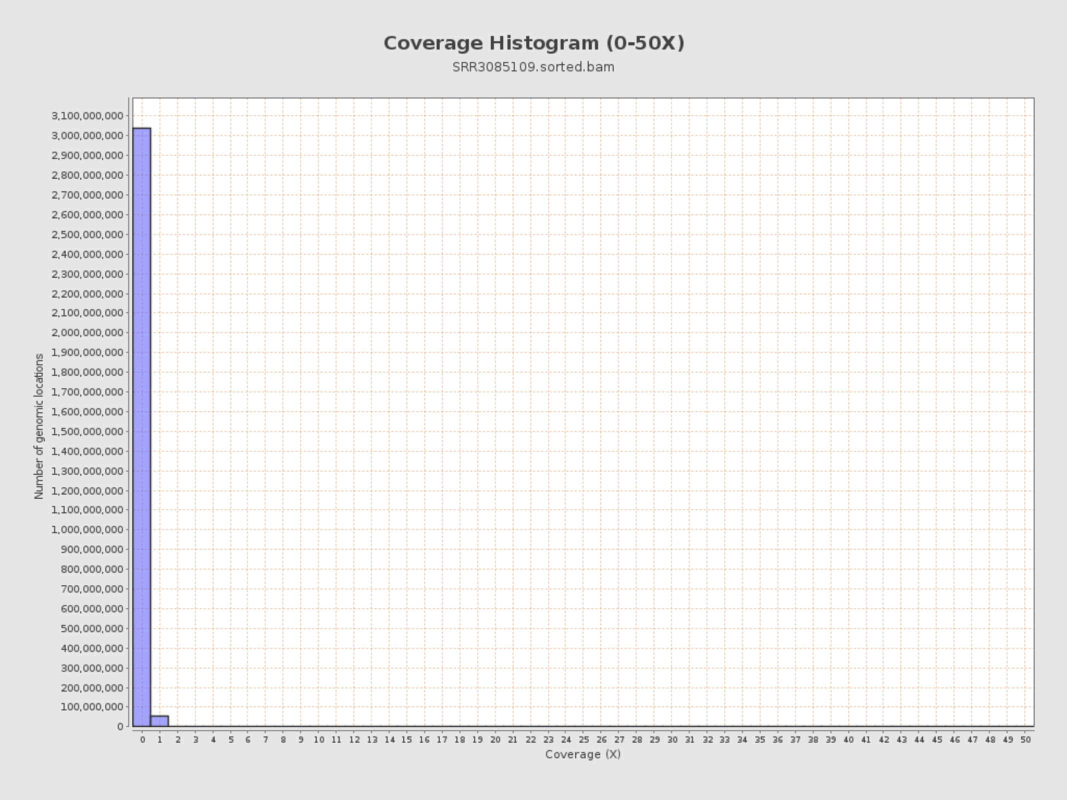
3. Results : Coverage across reference



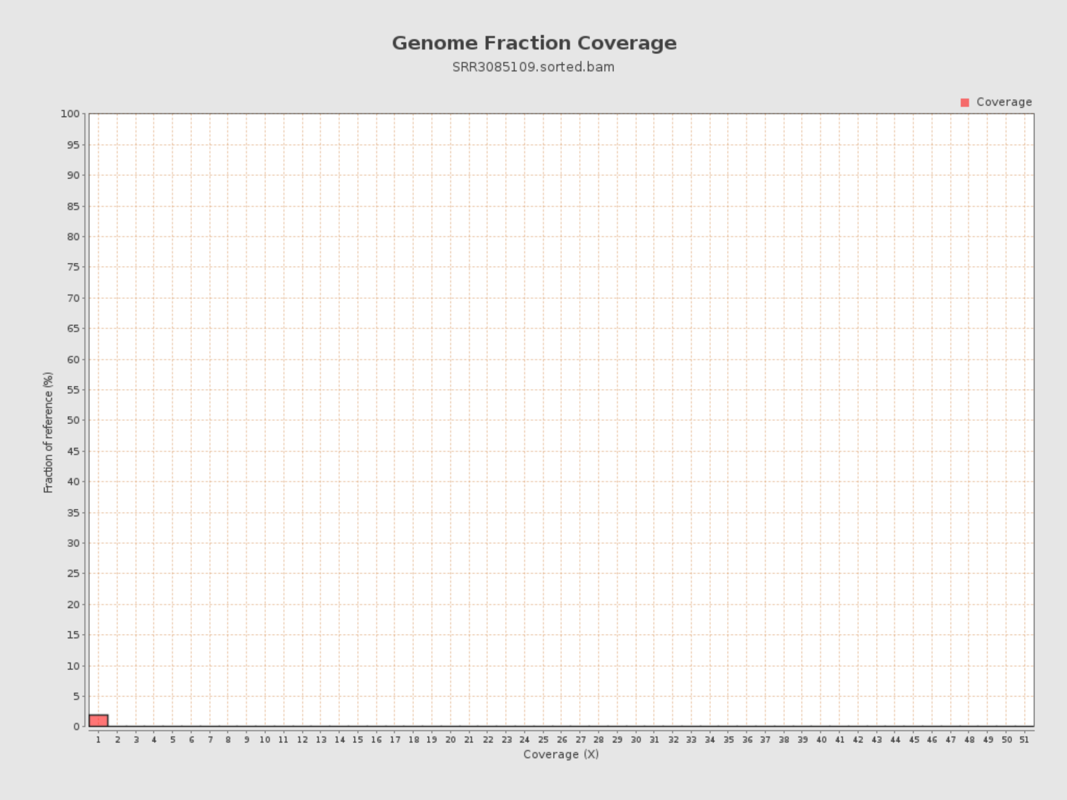
4. Results : Coverage Histogram



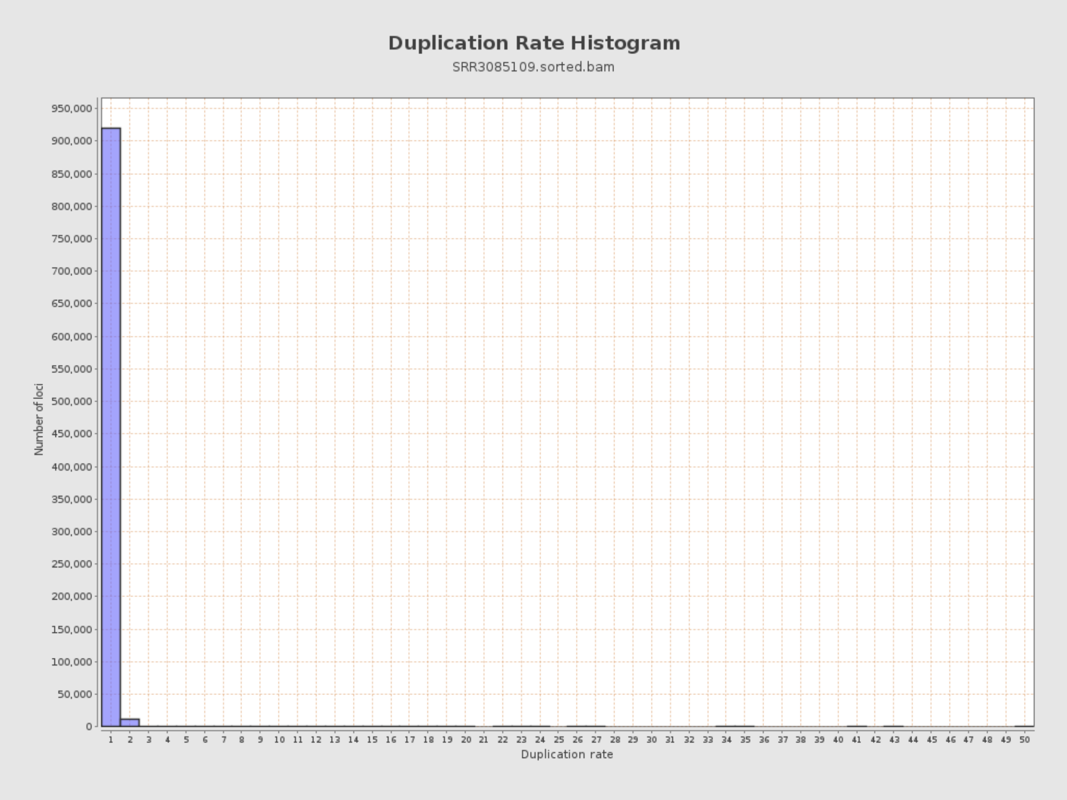
5. Results : Coverage Histogram (0-50X)



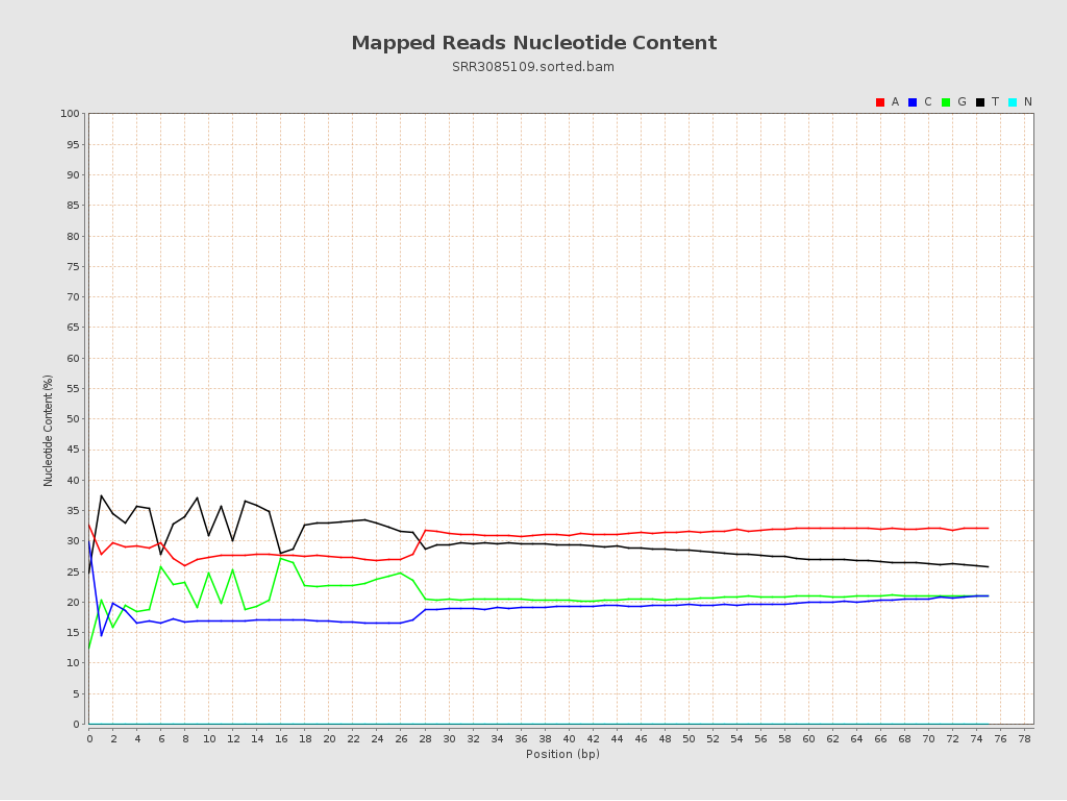
6. Results : Genome Fraction Coverage



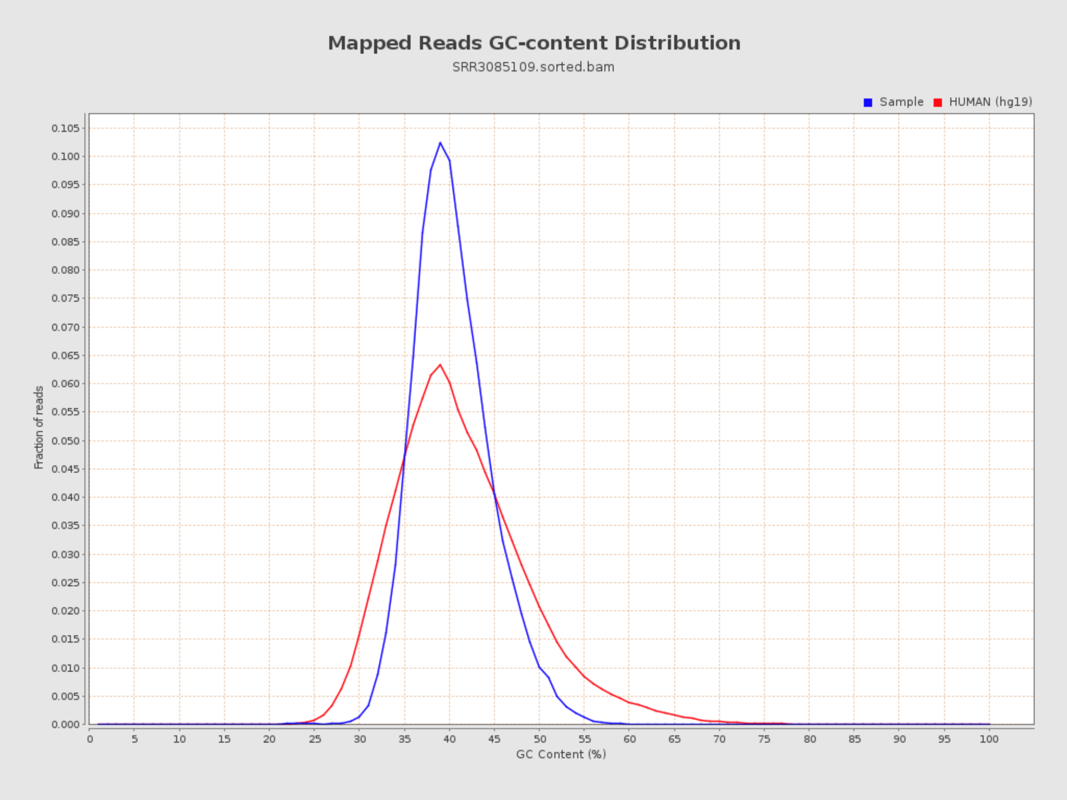
7. Results : Duplication Rate Histogram



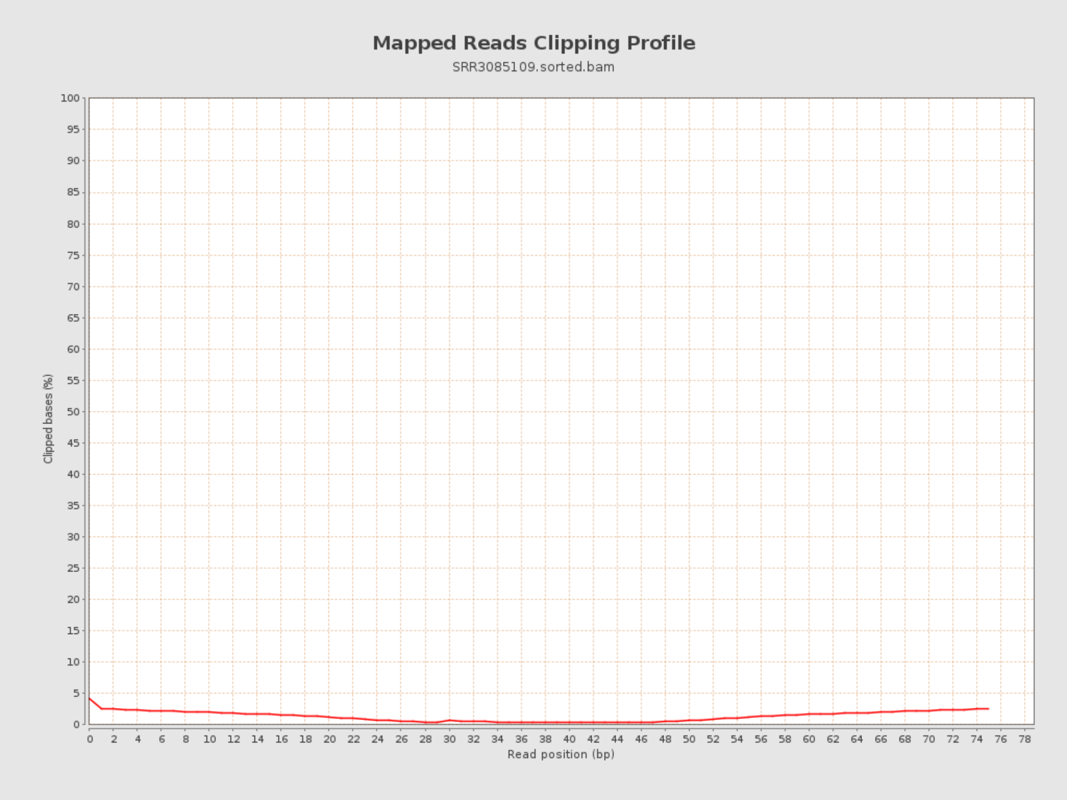
8. Results : Mapped Reads Nucleotide Content



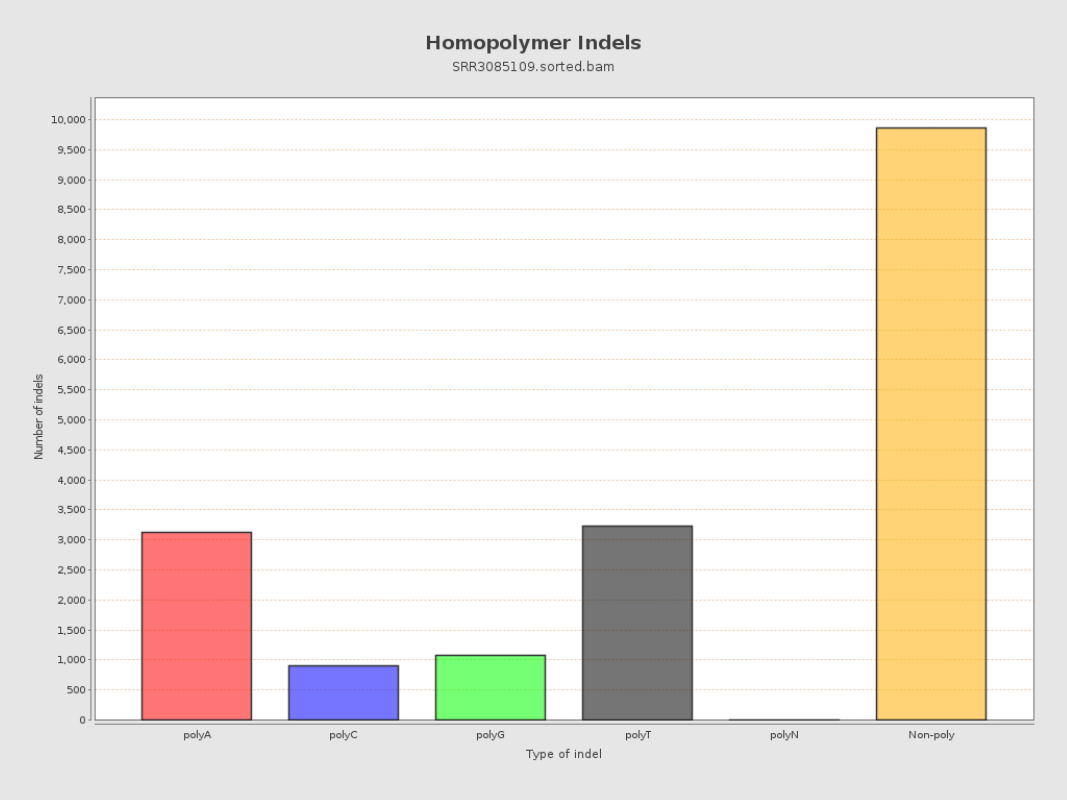
9. Results : Mapped Reads GC-content Distribution



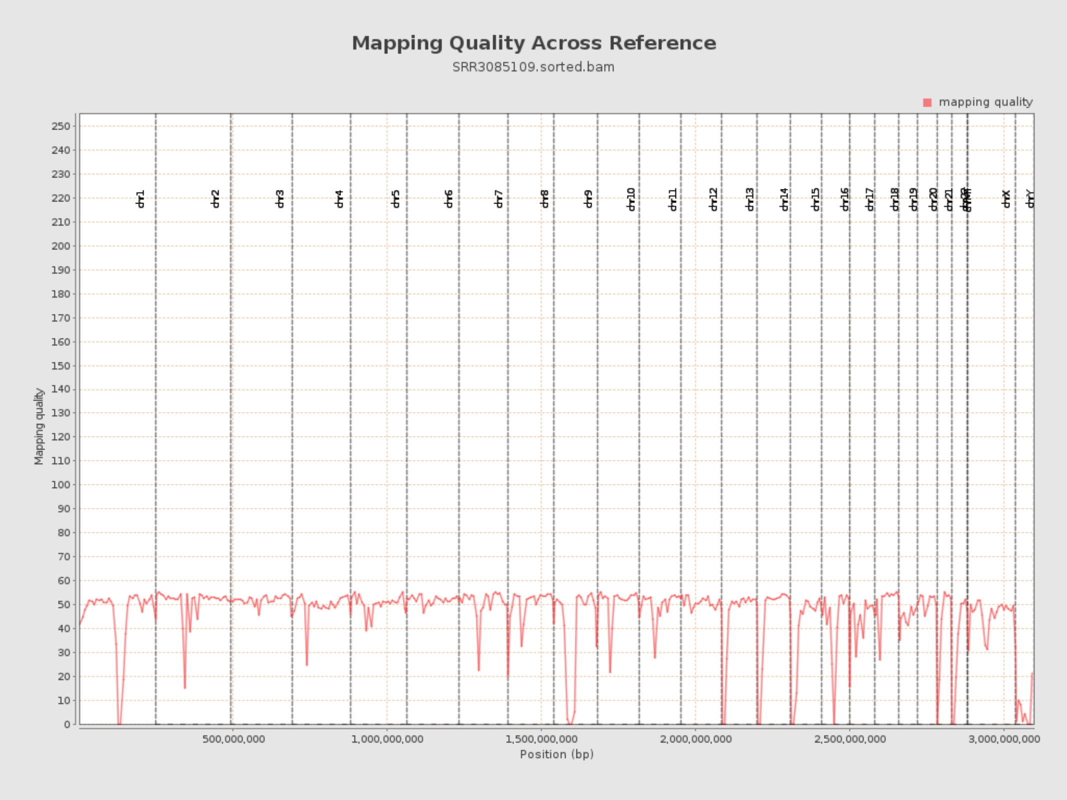
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram