Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 01:59:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085116.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_SRR3085116 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085116.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 01:59:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085116.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	953,170
Mapped reads	711,514 / 74.65%
Unmapped reads	241,656 / 25.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,991 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	9,983 / 1.05%
Duplication rate	1.13%
Clipped reads	268,272 / 28.15%

2.2. ACGT Content

Number/percentage of A's	15,304,725 / 31.46%
Number/percentage of C's	8,919,867 / 18.33%
Number/percentage of T's	13,905,940 / 28.58%
Number/percentage of G's	10,518,363 / 21.62%
Number/percentage of N's	1,143 / 0%
GC Percentage	39.96%

2.3. Coverage

Mean	0.0157

Standard Deviation	0.1542

2.4. Mapping Quality

Mean Mapping Quality	47.66

2.5. Mismatches and indels

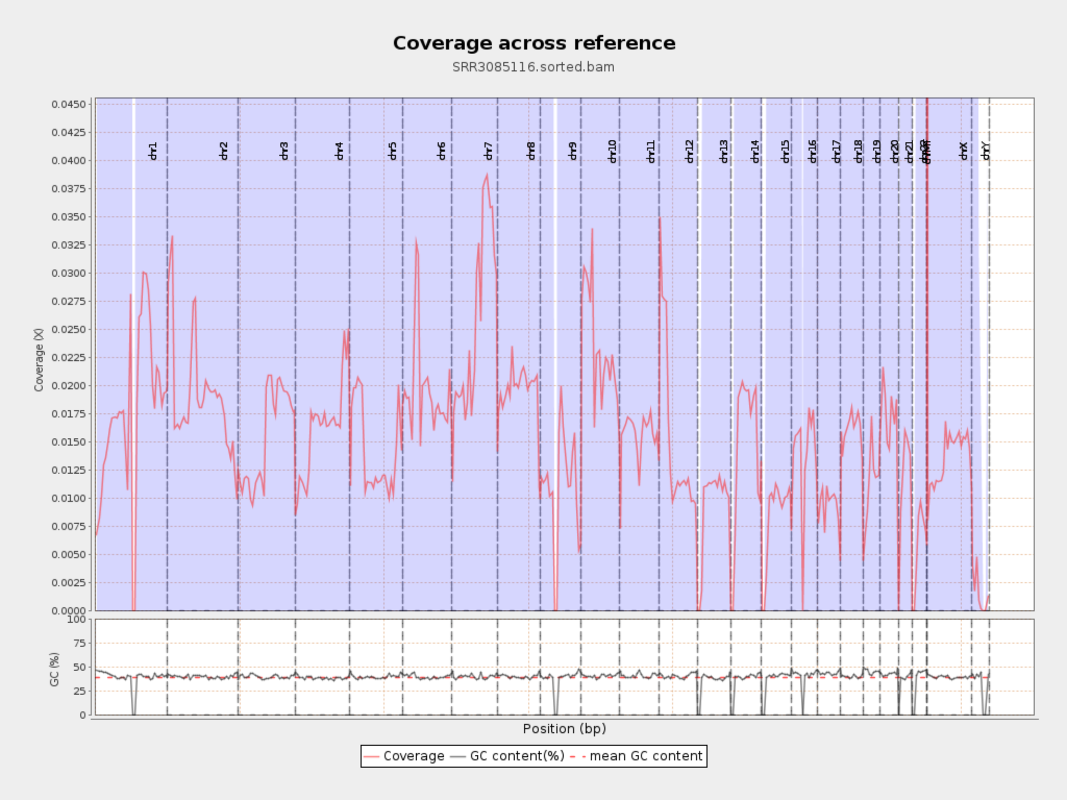
General error rate	0.92%
Mismatches	443,603
Insertions	3,497
Mapped reads with at least one insertion	0.49%
Deletions	8,585
Mapped reads with at least one deletion	1.19%
Homopolymer indels	44.57%

2.6. Chromosome stats

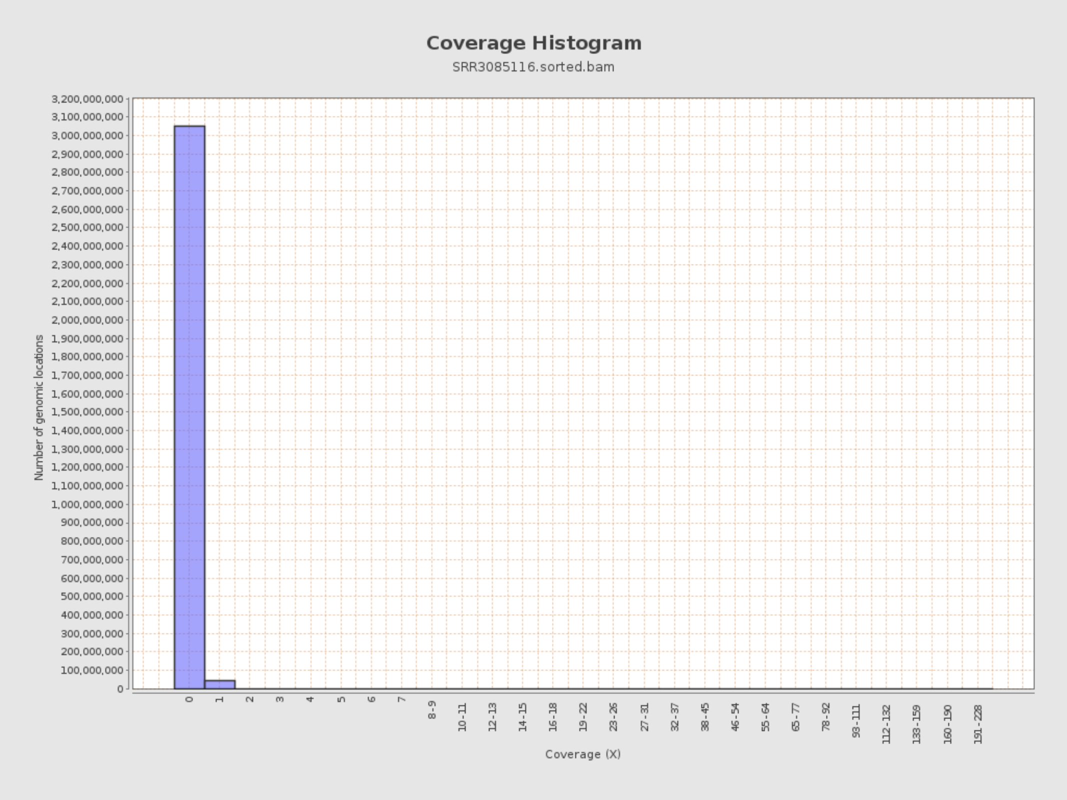
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4388092	0.0176	0.2307
chr2	243199373	4663271	0.0192	0.1671
chr3	198022430	3055036	0.0154	0.128
chr4	191154276	3103474	0.0162	0.1305
chr5	180915260	2574247	0.0142	0.1217
chr6	171115067	3377783	0.0197	0.163
chr7	159138663	4135042	0.026	0.1872

chr8	146364022	2879568	0.0197	0.1991
chr9	141213431	1570547	0.0111	0.1292
chr10	135534747	3194855	0.0236	0.2059
chr11	135006516	2117920	0.0157	0.1494
chr12	133851895	2046029	0.0153	0.1265
chr13	115169878	1058554	0.0092	0.0971
chr14	107349540	1569428	0.0146	0.125
chr15	102531392	846681	0.0083	0.0922
chr16	90354753	1224969	0.0136	0.1231
chr17	81195210	751472	0.0093	0.1031
chr18	78077248	1267103	0.0162	0.2025
chr19	59128983	677006	0.0114	0.1557
chr20	63025520	1085791	0.0172	0.1339
chr21	48129895	560878	0.0117	0.1129
chr22	51304566	300854	0.0059	0.0779
chrMT	16571	6887	0.4156	0.6861
chrX	155270560	2118572	0.0136	0.1245
chrY	59373566	89969	0.0015	0.0451

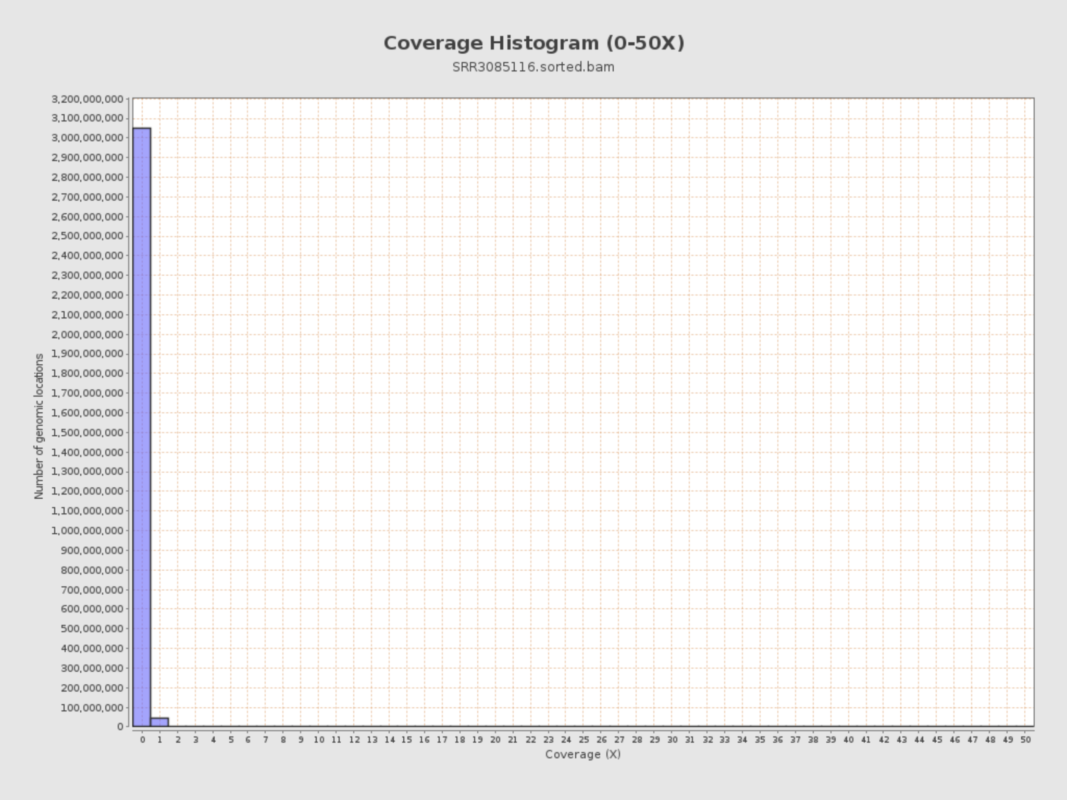
3. Results : Coverage across reference



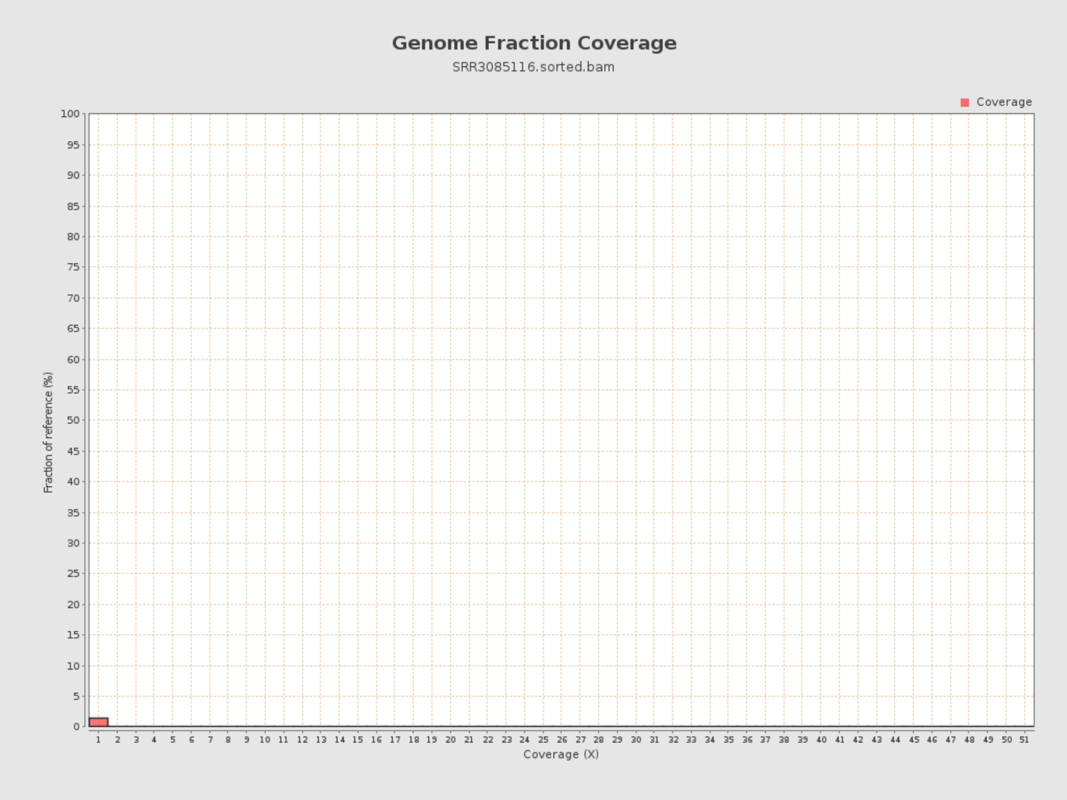
4. Results : Coverage Histogram



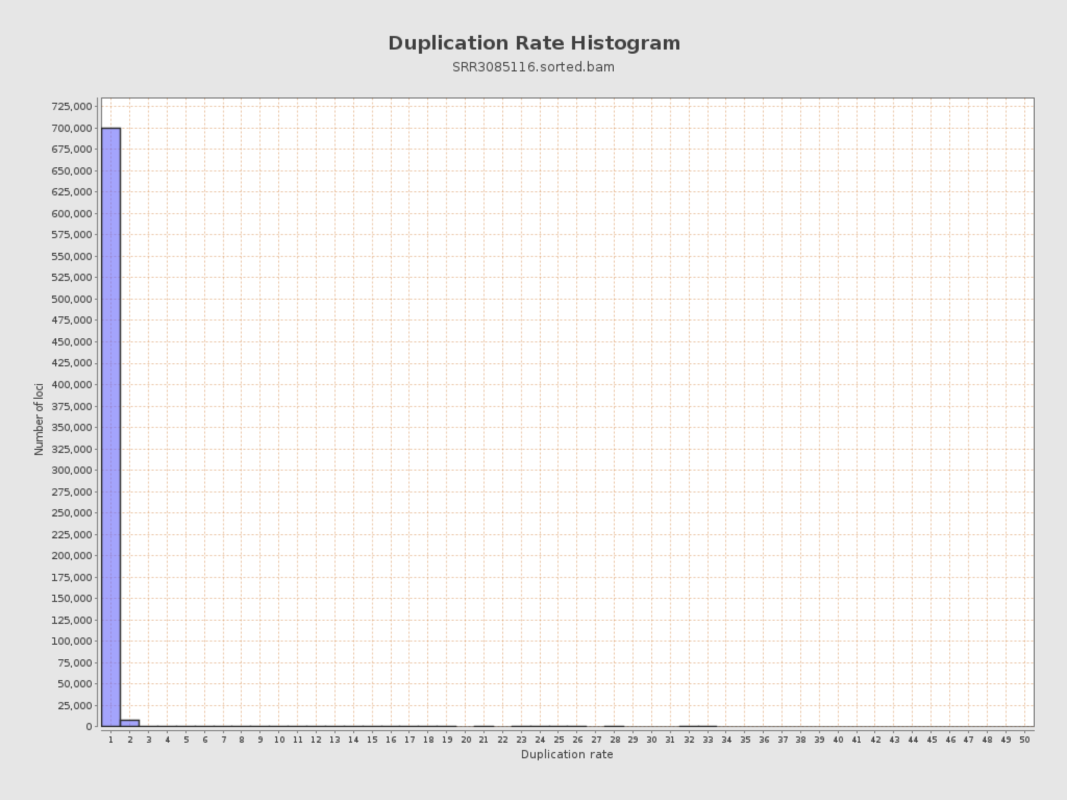
5. Results : Coverage Histogram (0-50X)



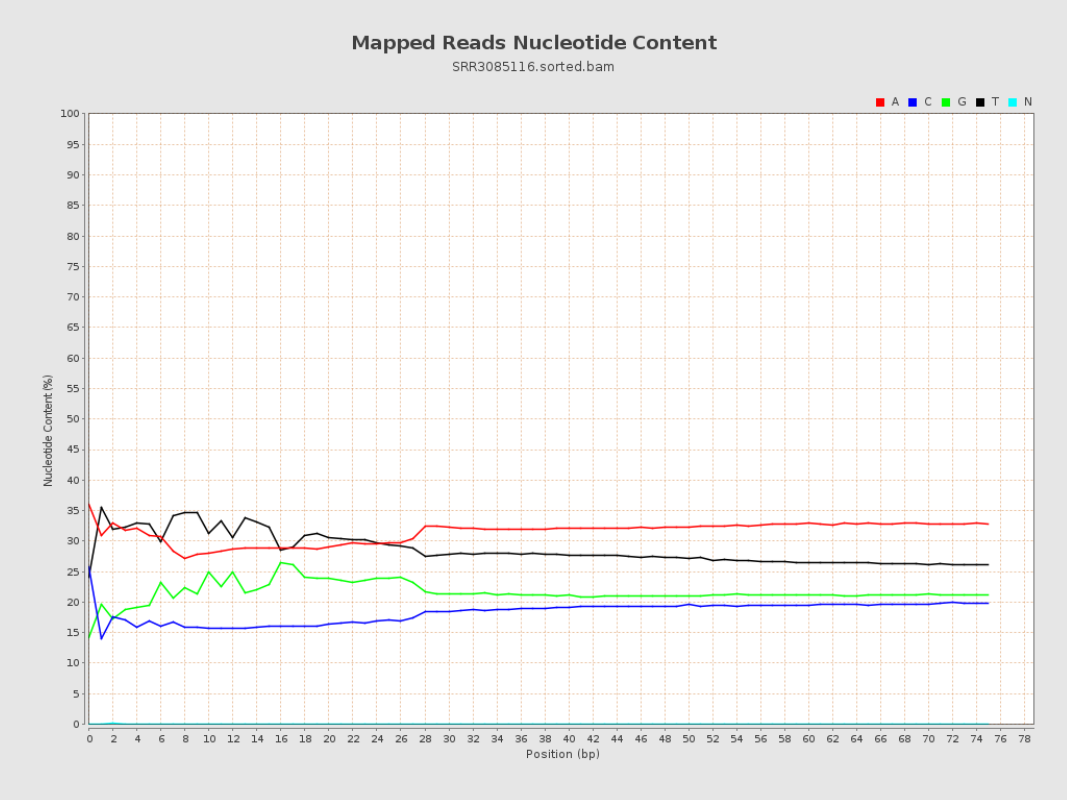
6. Results : Genome Fraction Coverage



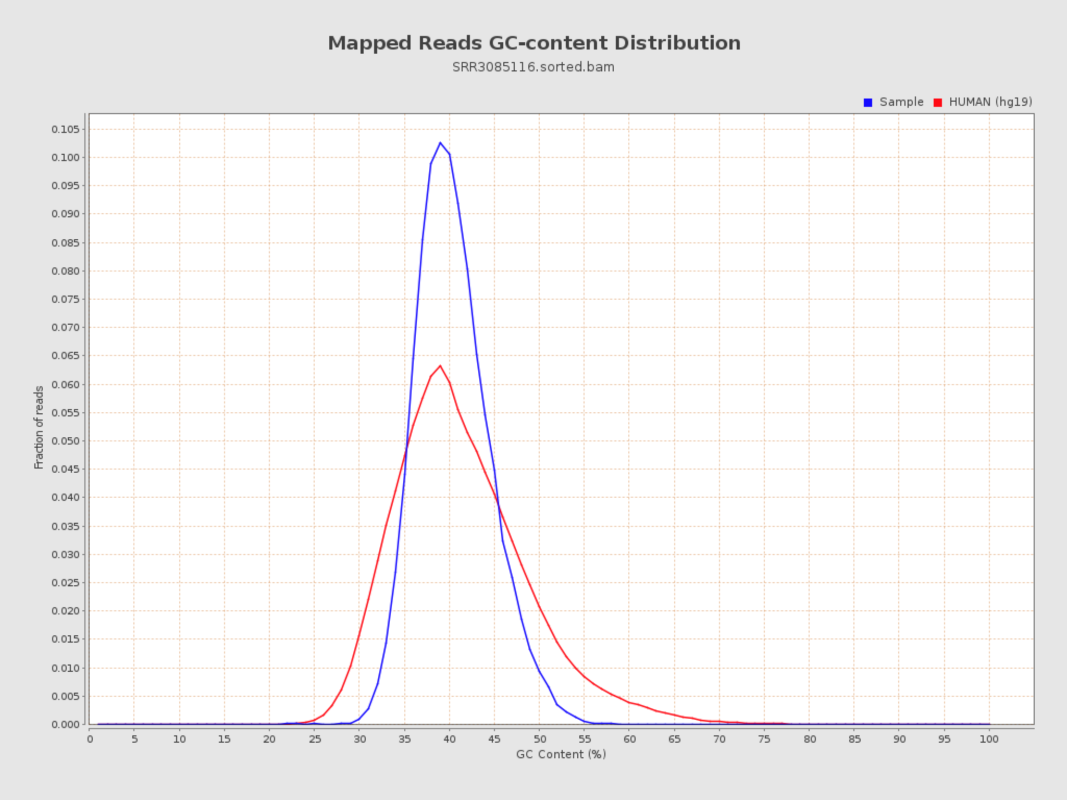
7. Results : Duplication Rate Histogram



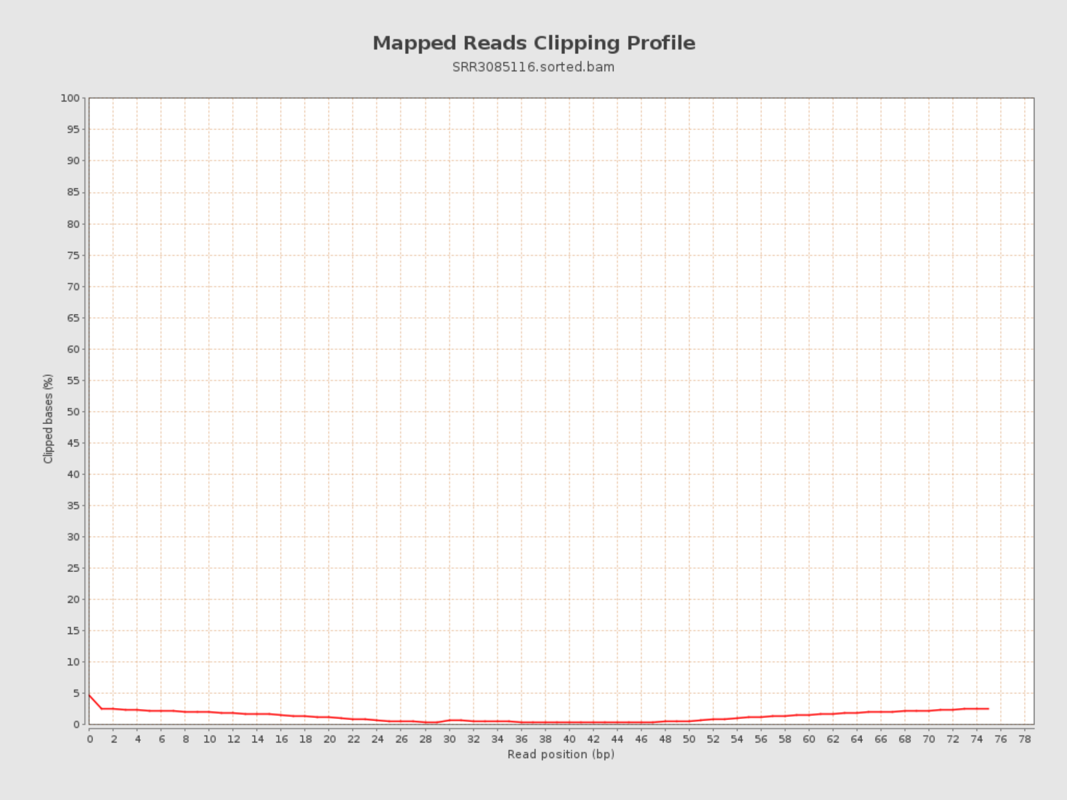
8. Results : Mapped Reads Nucleotide Content



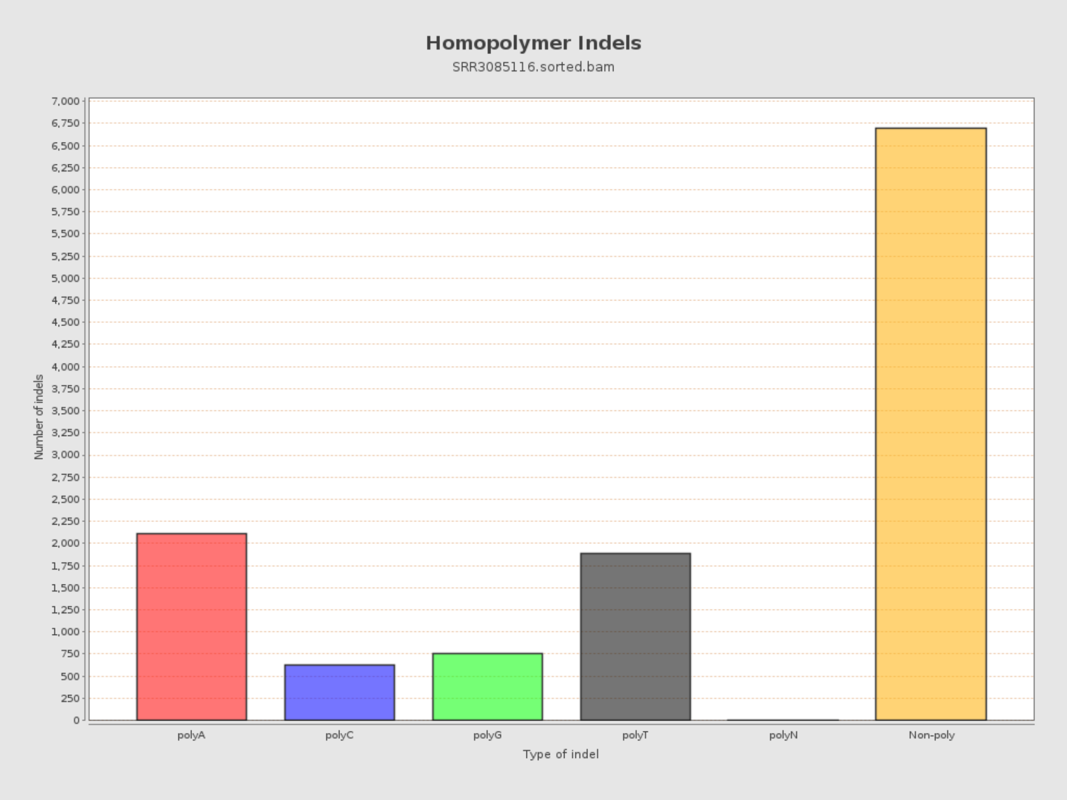
9. Results : Mapped Reads GC-content Distribution



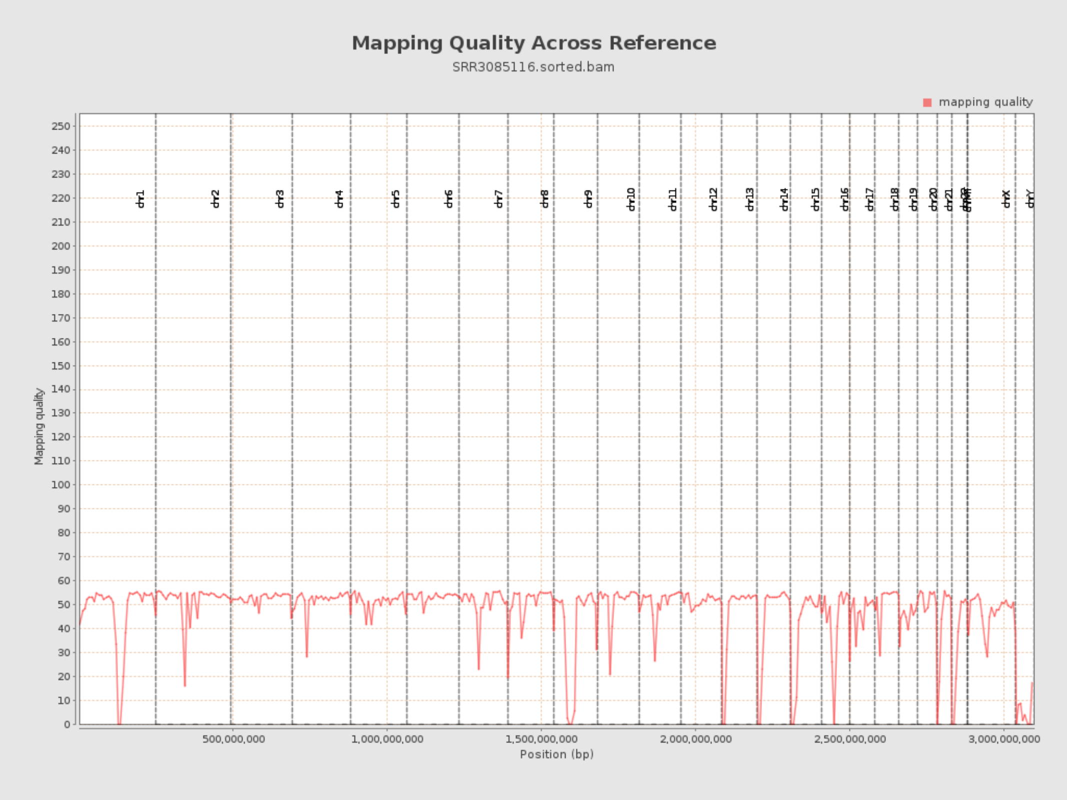
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram