Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 01:19:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085111.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_SRR3085111 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085111.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 01:19:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085111.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,085,656
Mapped reads	852,631 / 78.54%
Unmapped reads	233,025 / 21.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,528 / 0.6%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	13,553 / 1.25%
Duplication rate	1.39%
Clipped reads	344,810 / 31.76%

2.2. ACGT Content

Number/percentage of A's	17,450,013 / 30.23%
Number/percentage of C's	10,412,732 / 18.04%
Number/percentage of T's	17,240,407 / 29.86%
Number/percentage of G's	12,625,025 / 21.87%
Number/percentage of N's	1,197 / 0%
GC Percentage	39.91%

2.3. Coverage

Mean	0.0187

Standard Deviation	0.161

2.4. Mapping Quality

Mean Mapping Quality	48.03

2.5. Mismatches and indels

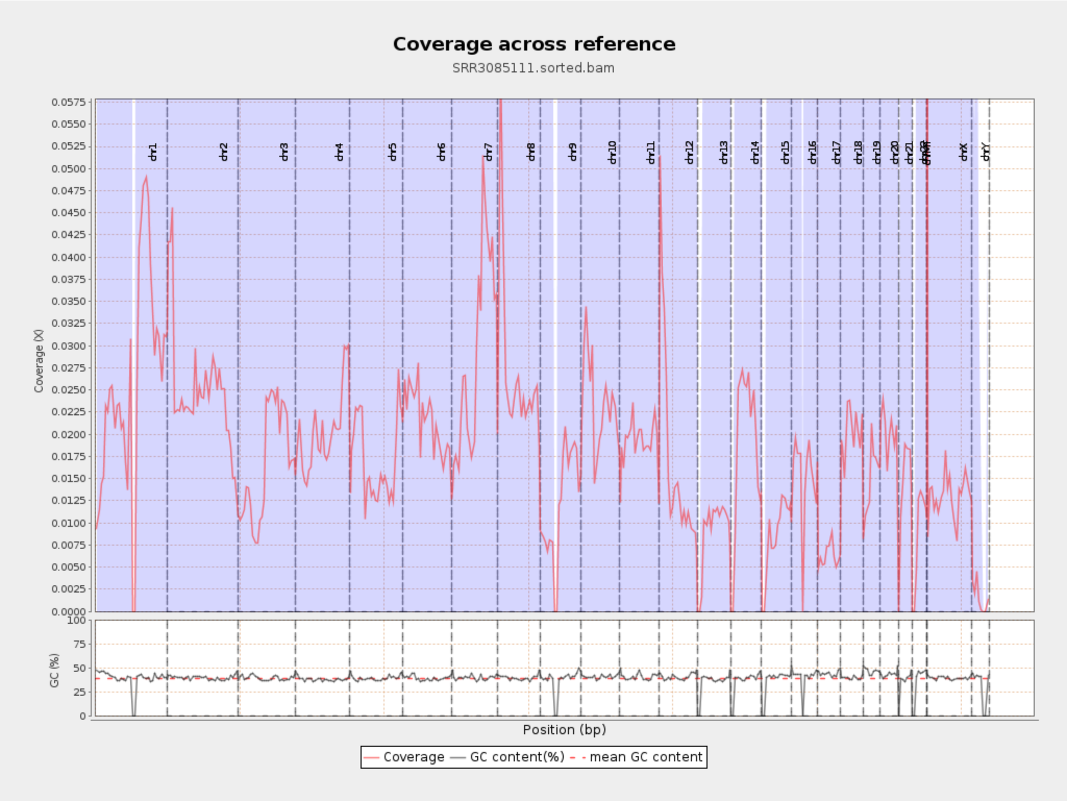
General error rate	1%
Mismatches	569,068
Insertions	4,367
Mapped reads with at least one insertion	0.51%
Deletions	12,598
Mapped reads with at least one deletion	1.46%
Homopolymer indels	47.64%

2.6. Chromosome stats

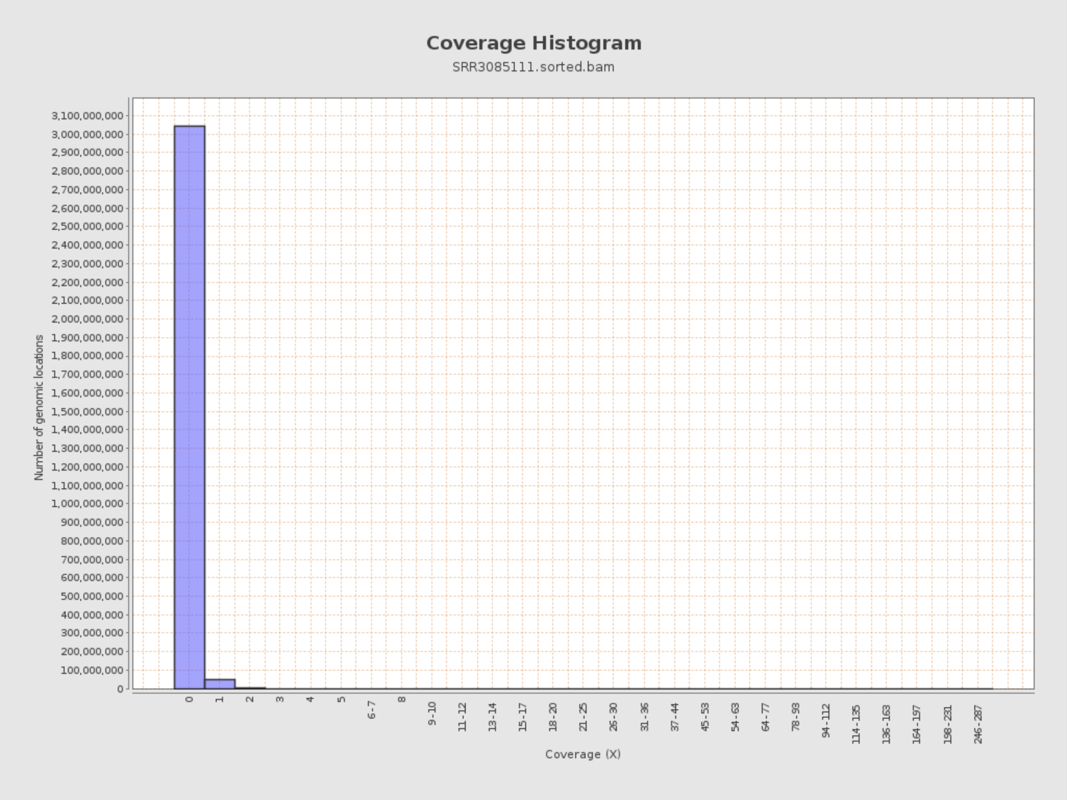
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6445949	0.0259	0.2373
chr2	243199373	6091581	0.025	0.1762
chr3	198022430	3290843	0.0166	0.1352
chr4	191154276	3864686	0.0202	0.1482
chr5	180915260	3084126	0.017	0.1357
chr6	171115067	3693779	0.0216	0.1644
chr7	159138663	4681346	0.0294	0.186

chr8	146364022	3985960	0.0272	0.2448
chr9	141213431	1691128	0.012	0.1223
chr10	135534747	3202800	0.0236	0.1885
chr11	135006516	2632625	0.0195	0.1631
chr12	133851895	2302628	0.0172	0.1371
chr13	115169878	1038321	0.009	0.0984
chr14	107349540	2019677	0.0188	0.1435
chr15	102531392	854160	0.0083	0.0943
chr16	90354753	1339006	0.0148	0.1286
chr17	81195210	506229	0.0062	0.0833
chr18	78077248	1589151	0.0204	0.1821
chr19	59128983	887024	0.015	0.1601
chr20	63025520	1260011	0.02	0.1476
chr21	48129895	697895	0.0145	0.1264
chr22	51304566	452131	0.0088	0.0975
chrMT	16571	4688	0.2829	0.5828
chrX	155270560	2043823	0.0132	0.1227
chrY	59373566	90251	0.0015	0.0446

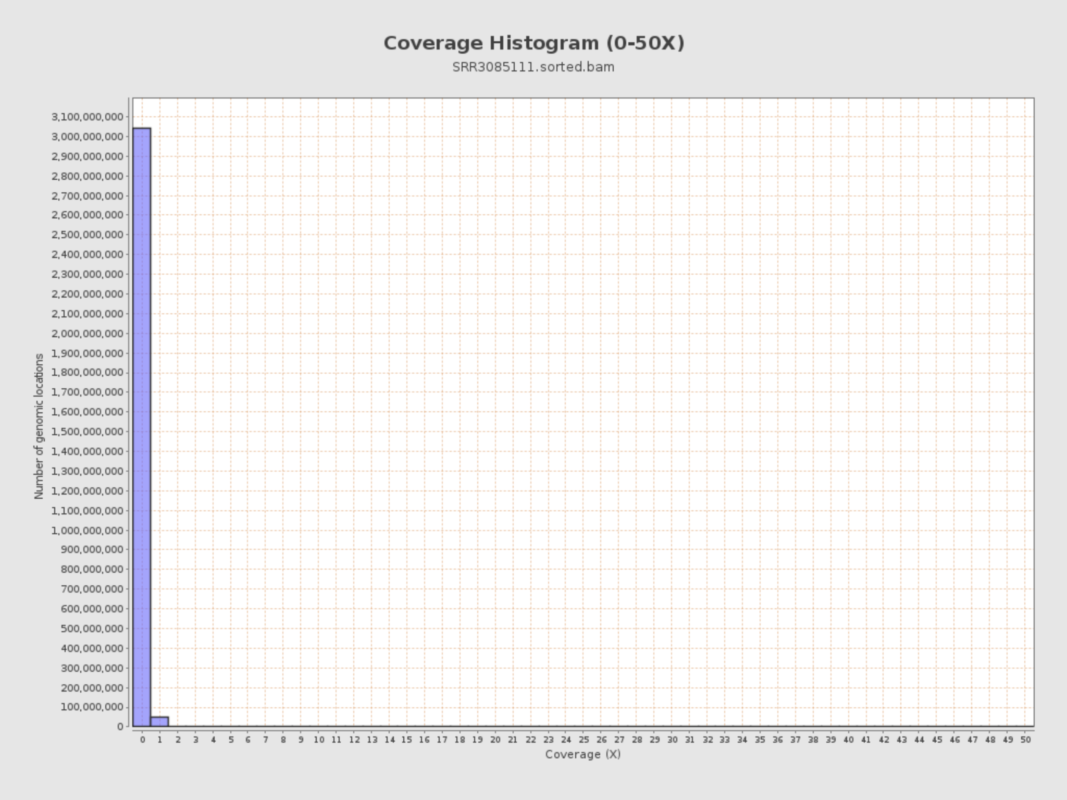
3. Results : Coverage across reference



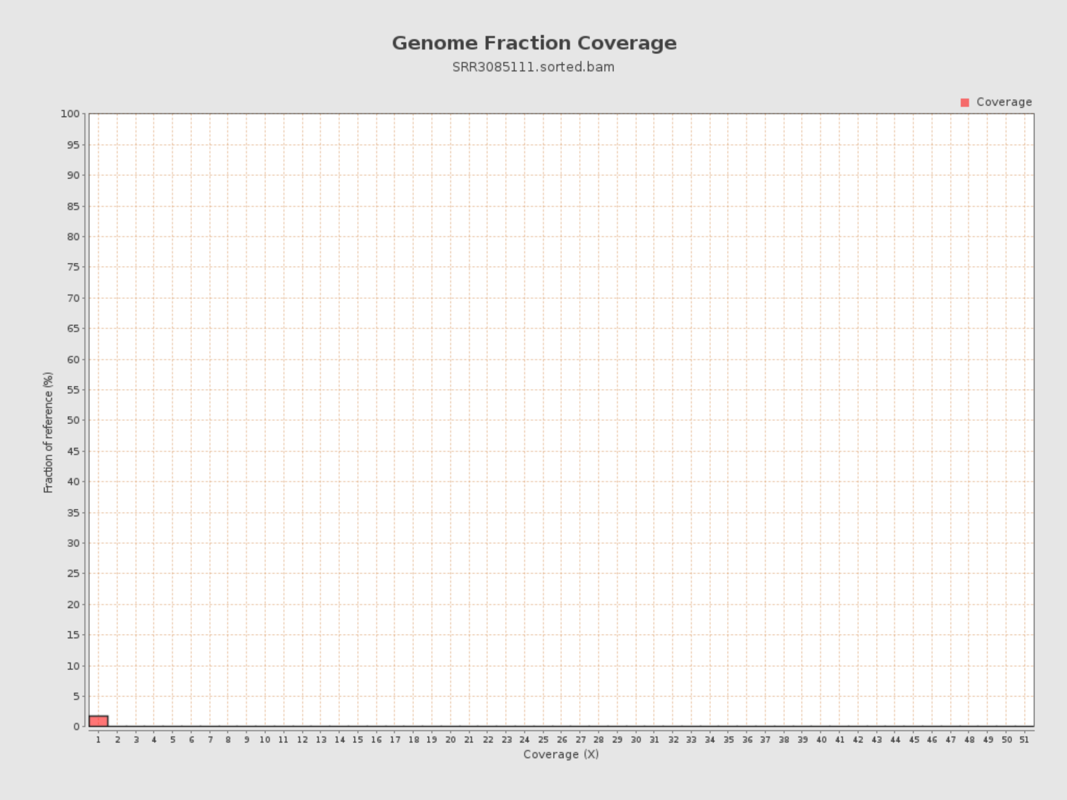
4. Results : Coverage Histogram



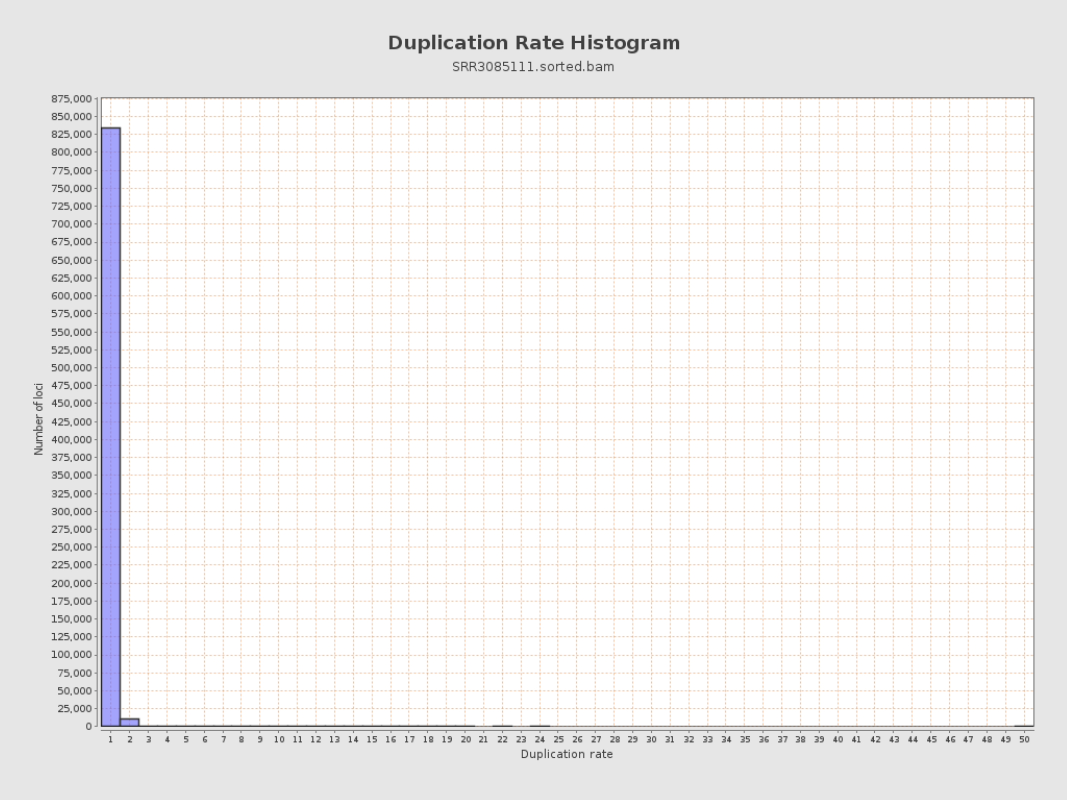
5. Results : Coverage Histogram (0-50X)



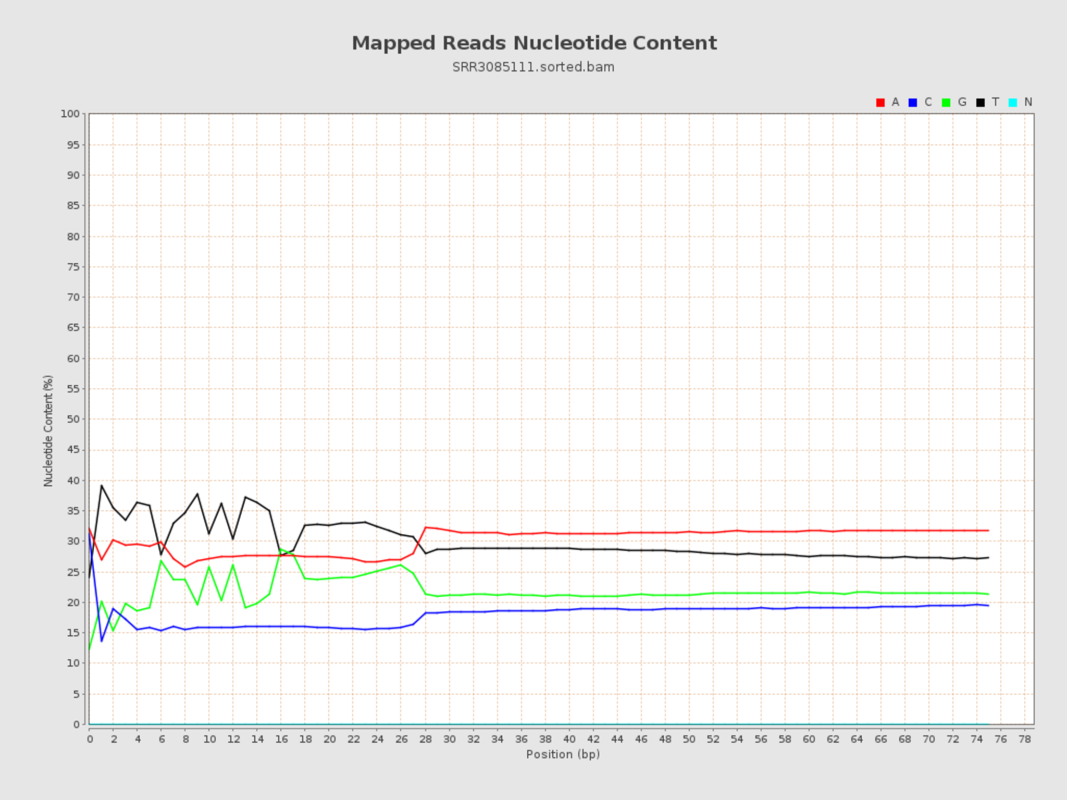
6. Results : Genome Fraction Coverage



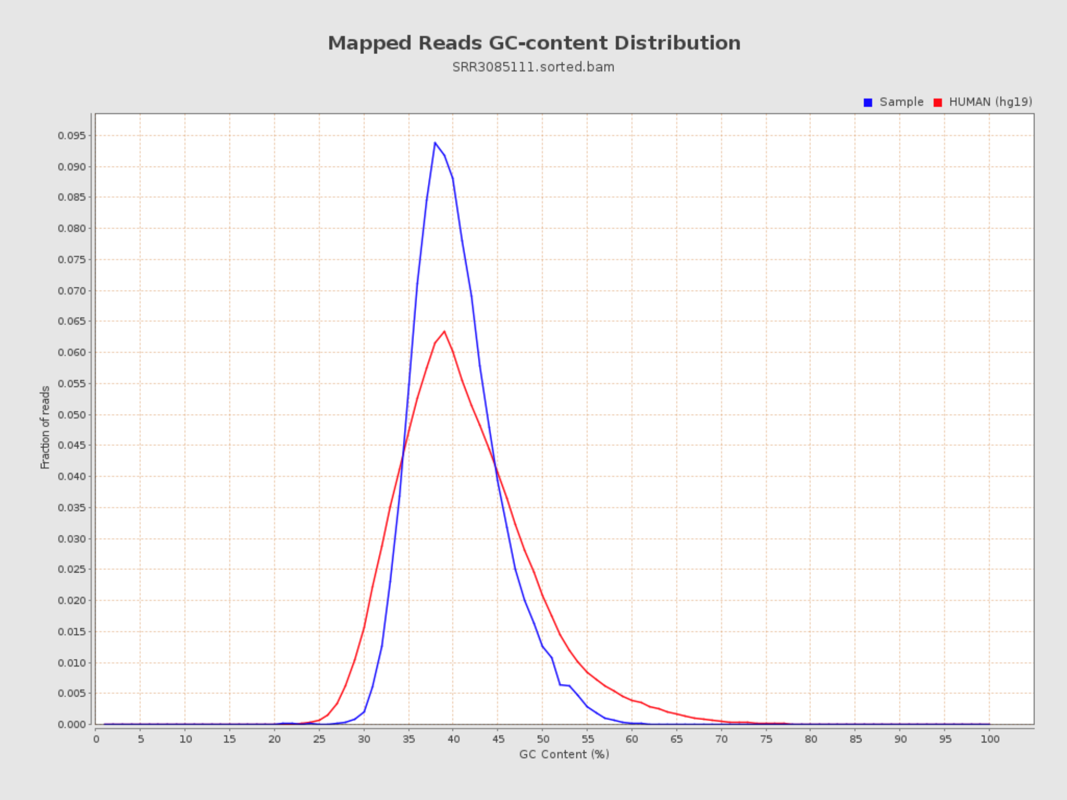
7. Results : Duplication Rate Histogram



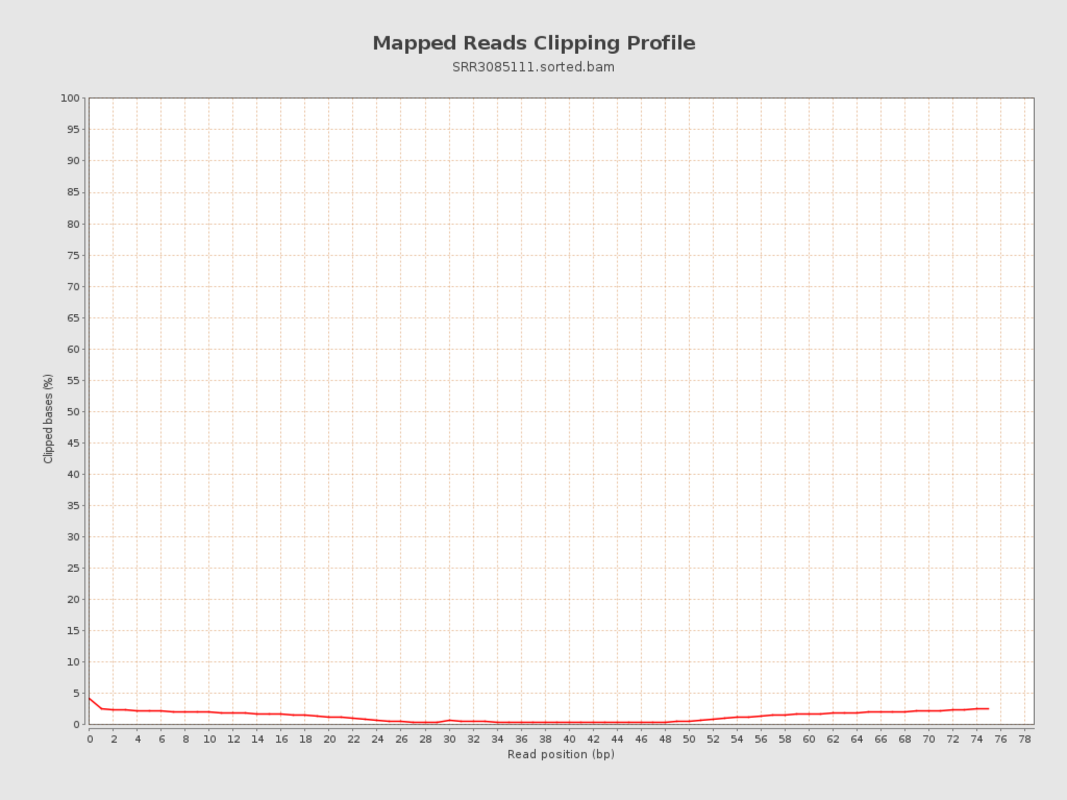
8. Results : Mapped Reads Nucleotide Content



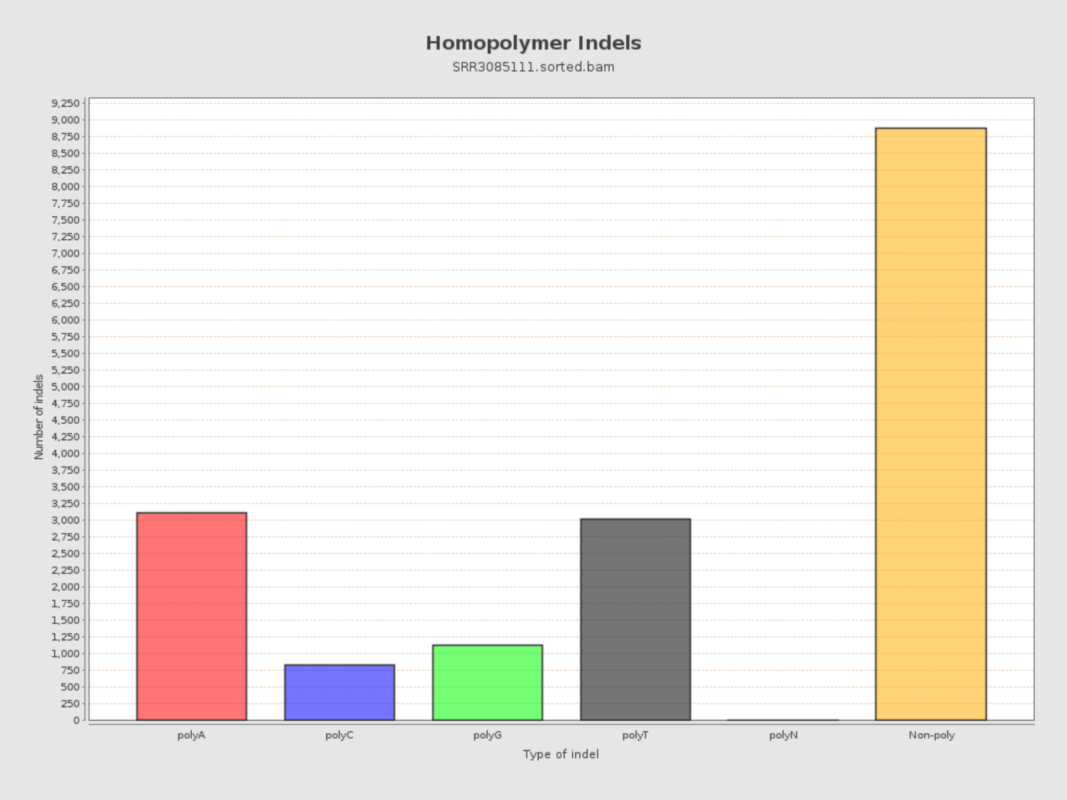
9. Results : Mapped Reads GC-content Distribution



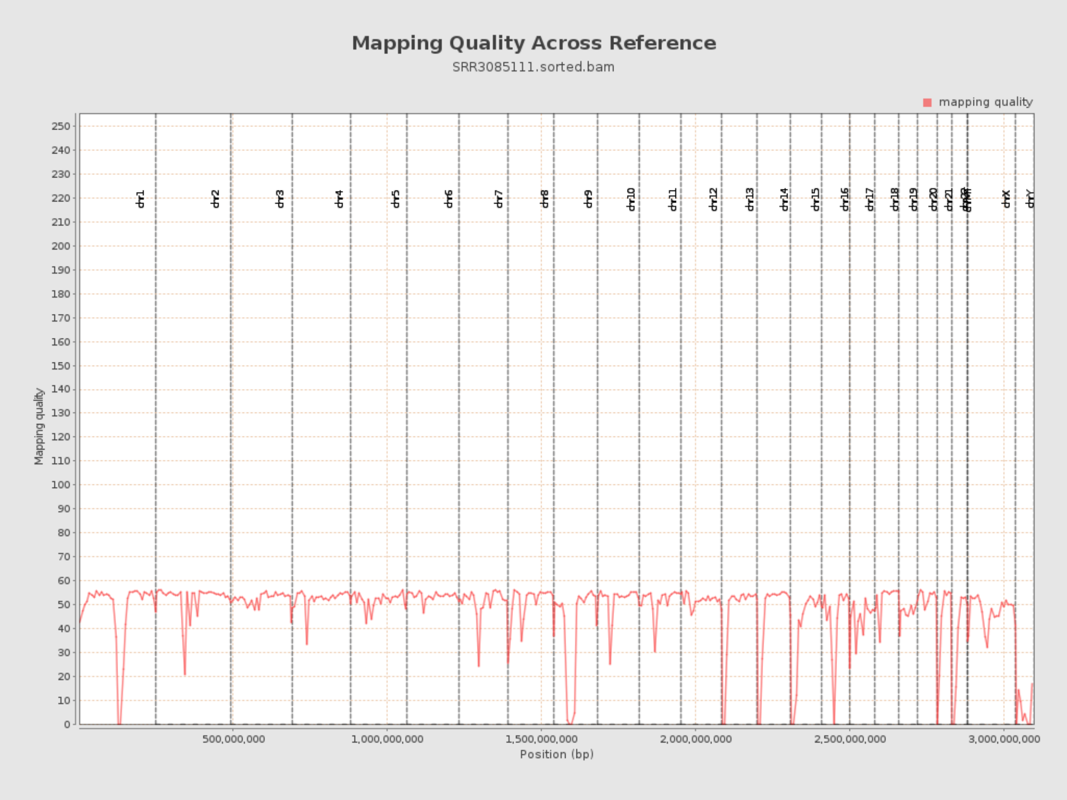
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram