Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 04:12:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085144.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_SRR3085144 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085144.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 04:11:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085144.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,793,435
Mapped reads	1,590,289 / 88.67%
Unmapped reads	203,146 / 11.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,528 / 0.75%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	52,733 / 2.94%
Duplication rate	2.39%
Clipped reads	734,423 / 40.95%

2.2. ACGT Content

Number/percentage of A's	29,614,486 / 27.95%
Number/percentage of C's	19,865,248 / 18.75%
Number/percentage of T's	32,666,502 / 30.83%
Number/percentage of G's	23,779,519 / 22.44%
Number/percentage of N's	20,760 / 0.02%
GC Percentage	41.2%

2.3. Coverage

Mean	0.0342

Standard Deviation	0.3341

2.4. Mapping Quality

Mean Mapping Quality	44.62

2.5. Mismatches and indels

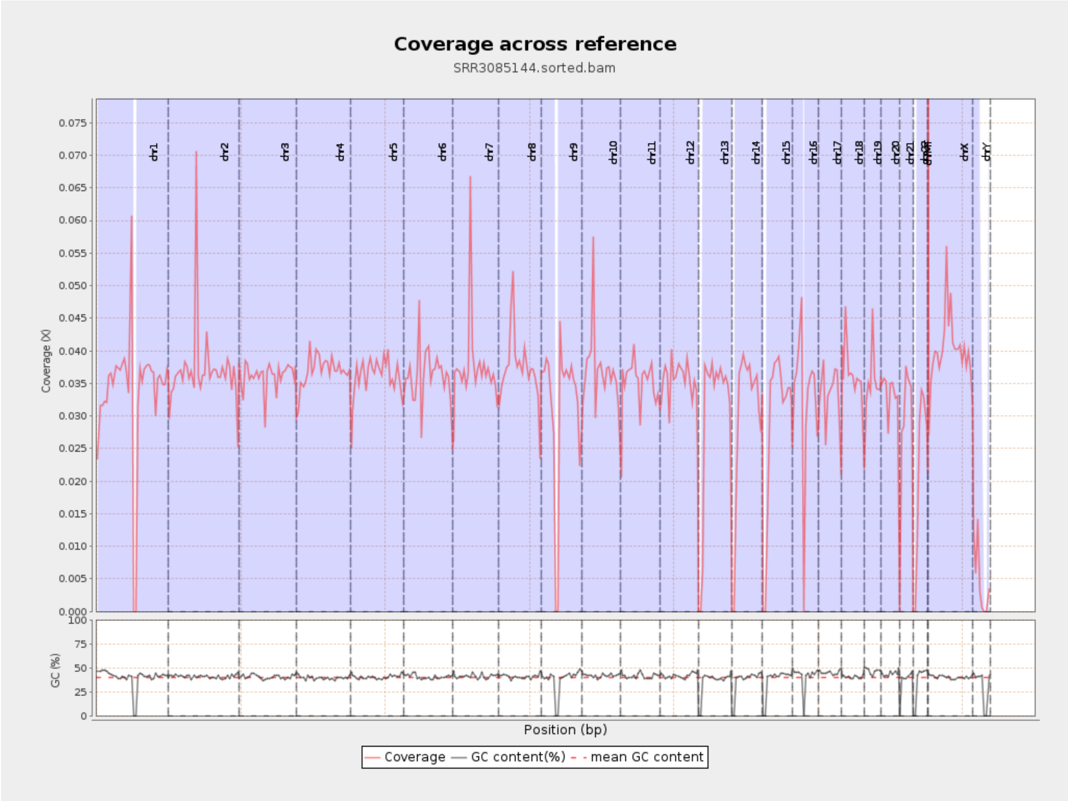
General error rate	0.91%
Mismatches	949,335
Insertions	8,457
Mapped reads with at least one insertion	0.53%
Deletions	23,664
Mapped reads with at least one deletion	1.47%
Homopolymer indels	46.74%

2.6. Chromosome stats

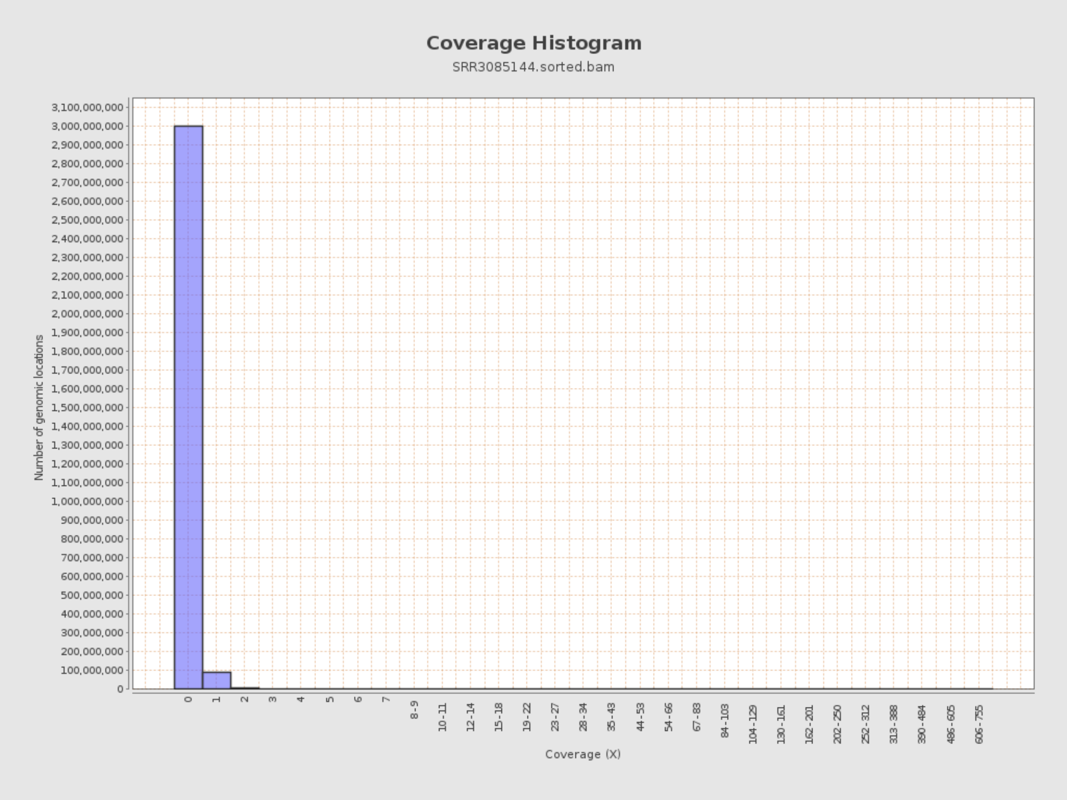
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8403871	0.0337	0.5878
chr2	243199373	9027993	0.0371	0.4078
chr3	198022430	7147786	0.0361	0.2064
chr4	191154276	7041560	0.0368	0.2135
chr5	180915260	6583093	0.0364	0.2067
chr6	171115067	6176003	0.0361	0.2438
chr7	159138663	5975469	0.0375	0.4538

chr8	146364022	5487643	0.0375	0.5039
chr9	141213431	4428344	0.0314	0.3064
chr10	135534747	4982787	0.0368	0.3127
chr11	135006516	4778839	0.0354	0.2829
chr12	133851895	4750580	0.0355	0.2074
chr13	115169878	3425898	0.0297	0.1859
chr14	107349540	3189100	0.0297	0.201
chr15	102531392	2959049	0.0289	0.1902
chr16	90354753	2911127	0.0322	0.2249
chr17	81195210	2685999	0.0331	0.213
chr18	78077248	2845625	0.0364	0.5417
chr19	59128983	2085755	0.0353	0.4517
chr20	63025520	2069667	0.0328	0.2009
chr21	48129895	1392982	0.0289	0.1953
chr22	51304566	1095186	0.0213	0.1569
chrMT	16571	2391	0.1443	0.3847
chrX	155270560	6262699	0.0403	0.2442
chrY	59373566	275642	0.0046	0.1114

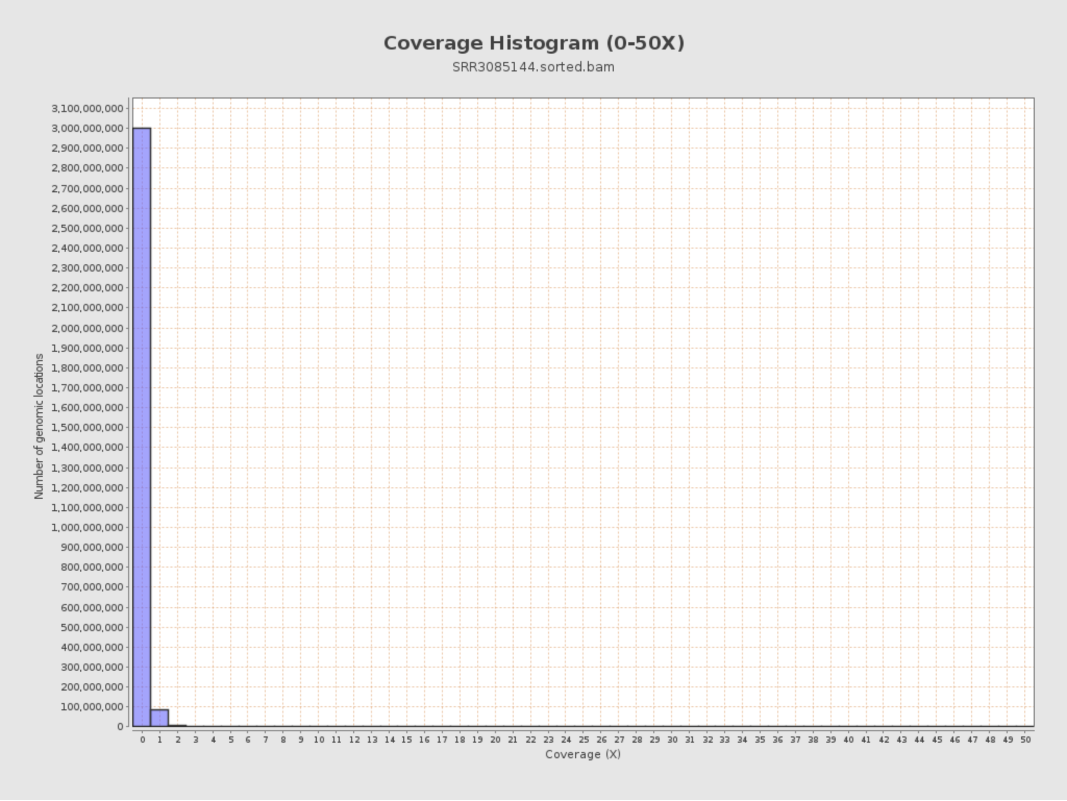
3. Results : Coverage across reference



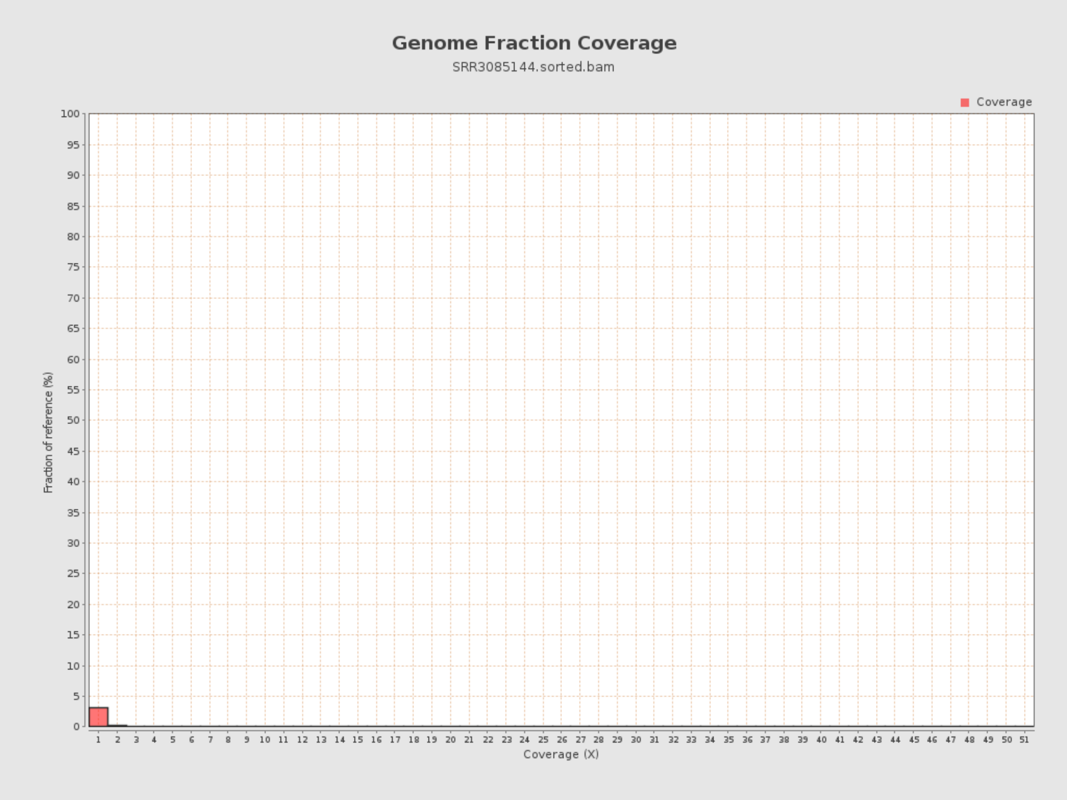
4. Results : Coverage Histogram



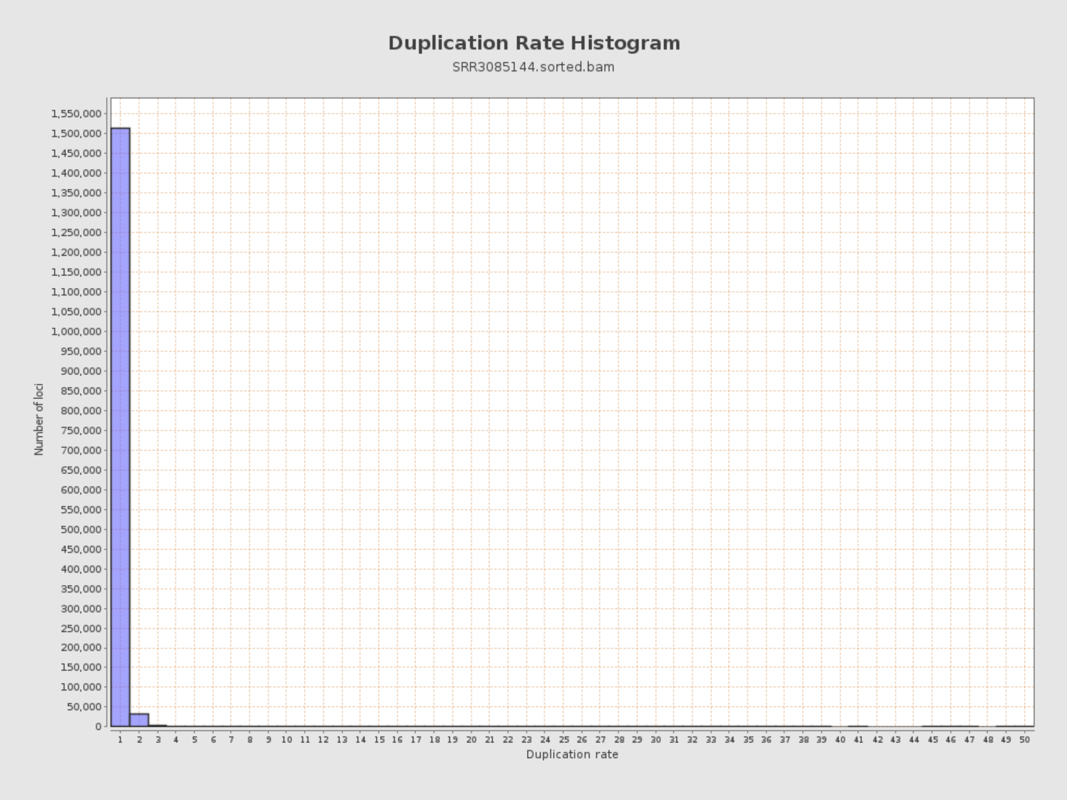
5. Results : Coverage Histogram (0-50X)



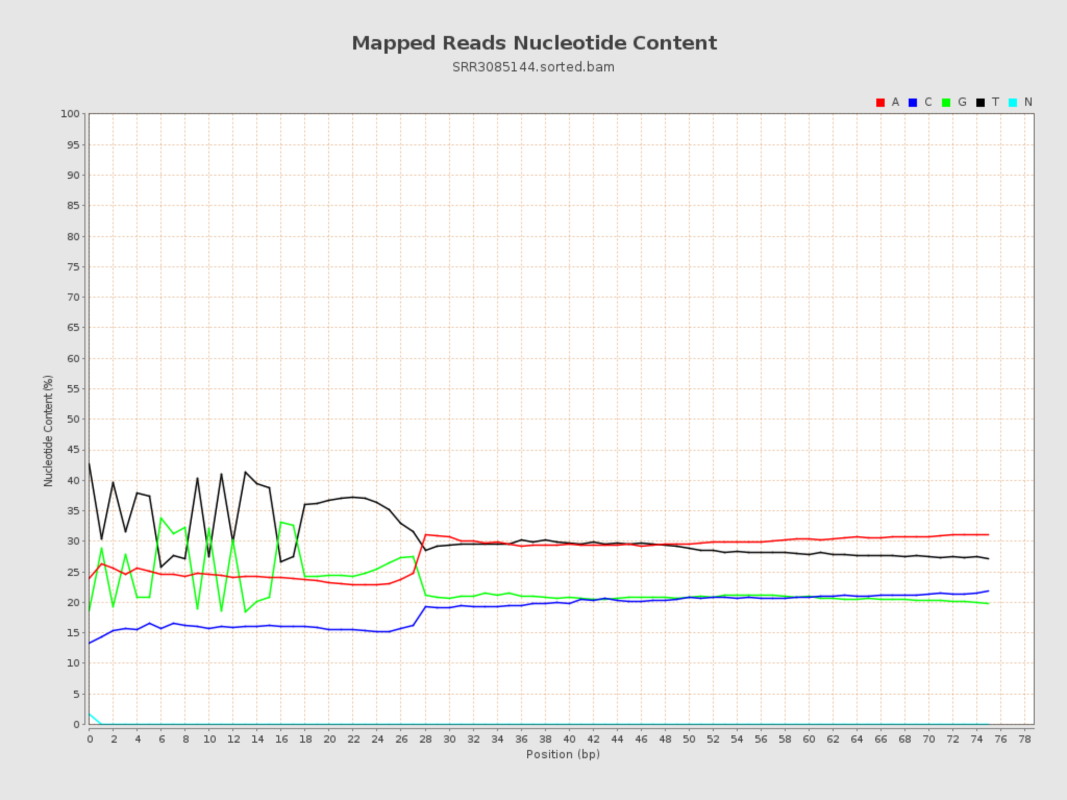
6. Results : Genome Fraction Coverage



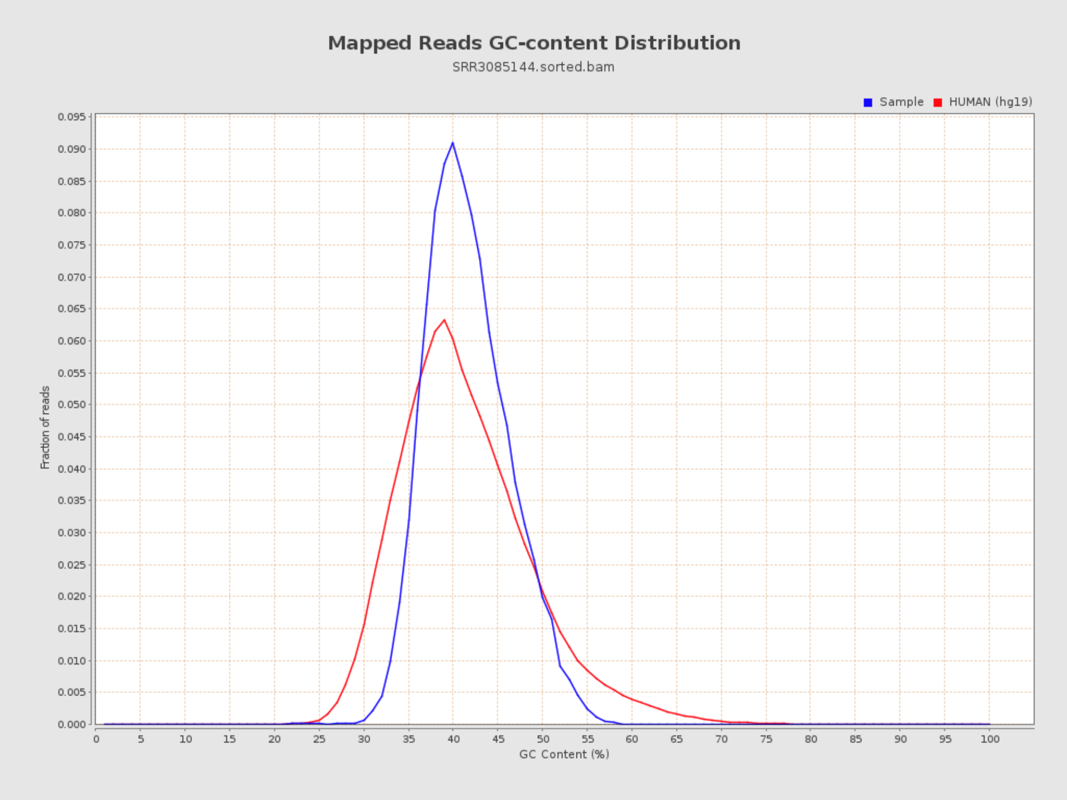
7. Results : Duplication Rate Histogram



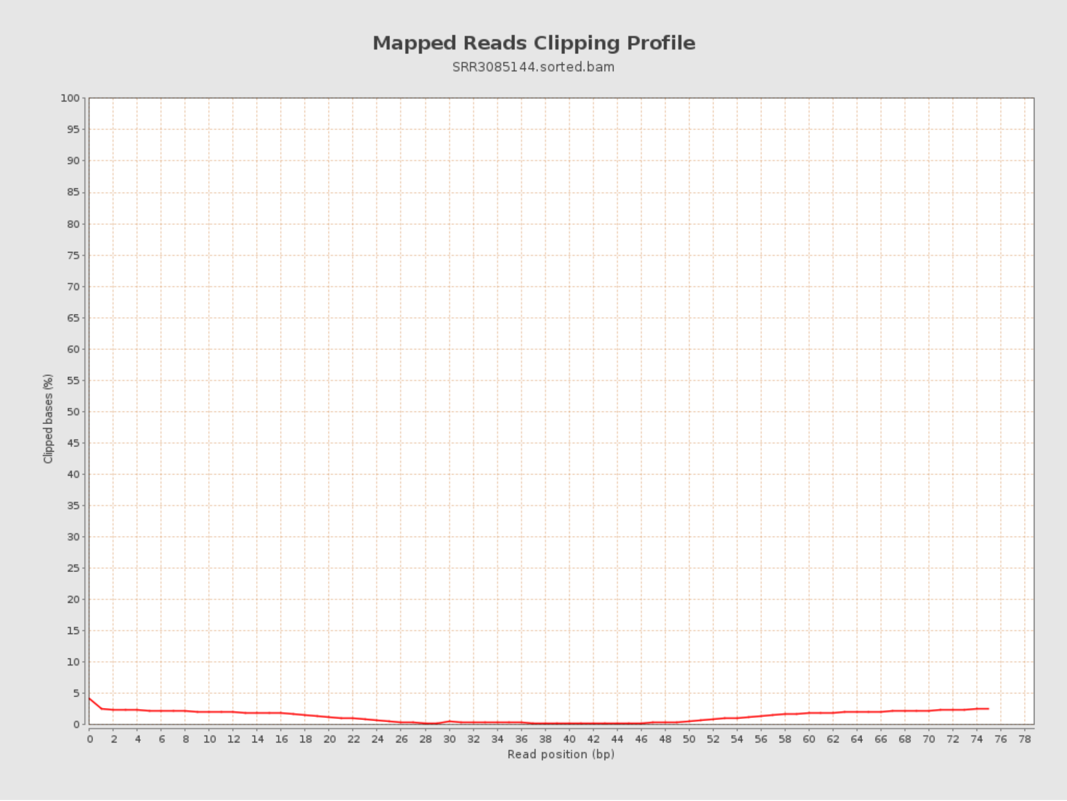
8. Results : Mapped Reads Nucleotide Content



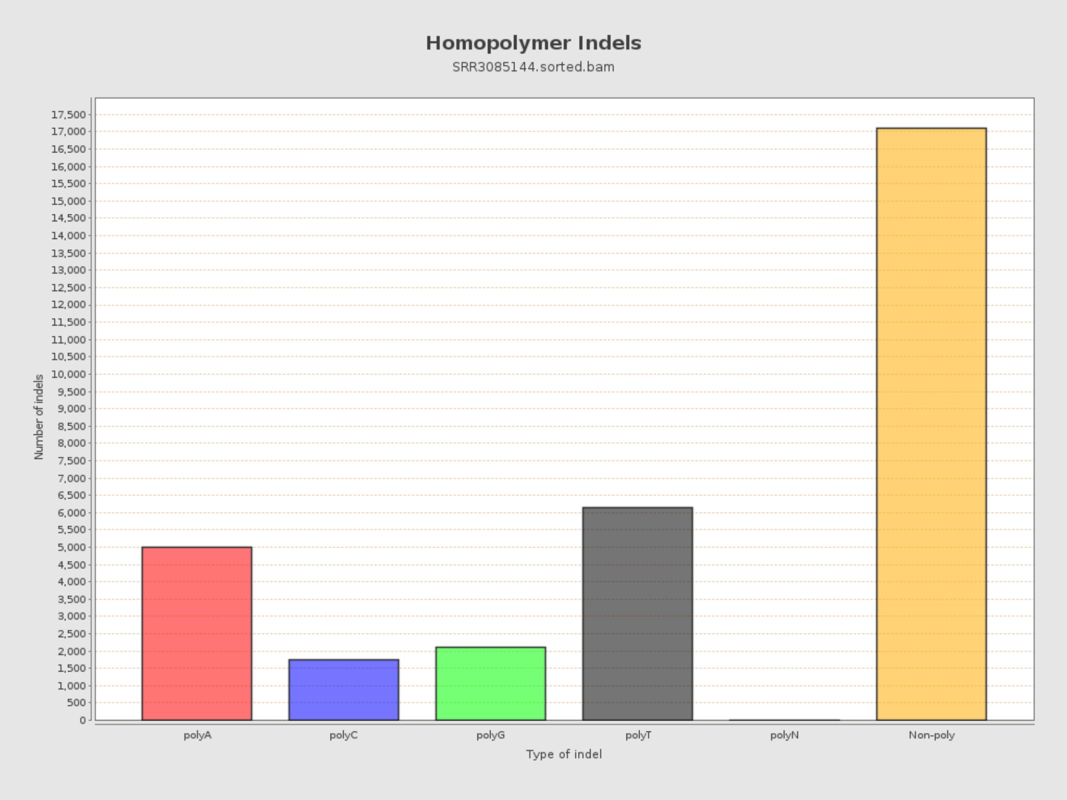
9. Results : Mapped Reads GC-content Distribution



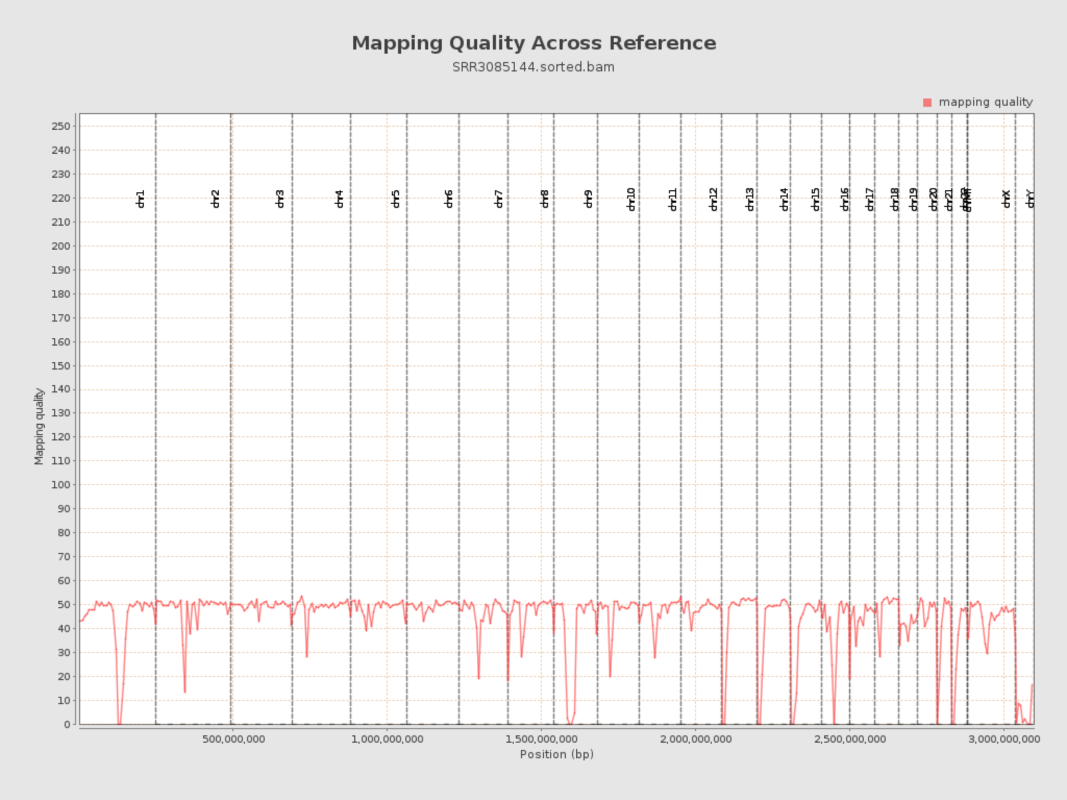
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram