Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 00:24:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085084.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_SRR3085084 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085084.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 00:24:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085084.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,043,545
Mapped reads	2,738,131 / 89.97%
Unmapped reads	305,414 / 10.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,060 / 0.95%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	113,563 / 3.73%
Duplication rate	3.08%
Clipped reads	1,330,752 / 43.72%

2.2. ACGT Content

Number/percentage of A's	50,695,989 / 28.05%
Number/percentage of C's	34,538,597 / 19.11%
Number/percentage of T's	54,889,501 / 30.37%
Number/percentage of G's	40,601,012 / 22.46%
Number/percentage of N's	24,522 / 0.01%
GC Percentage	41.57%

2.3. Coverage

Mean	0.0584

Standard Deviation	0.4861

2.4. Mapping Quality

Mean Mapping Quality	44.77

2.5. Mismatches and indels

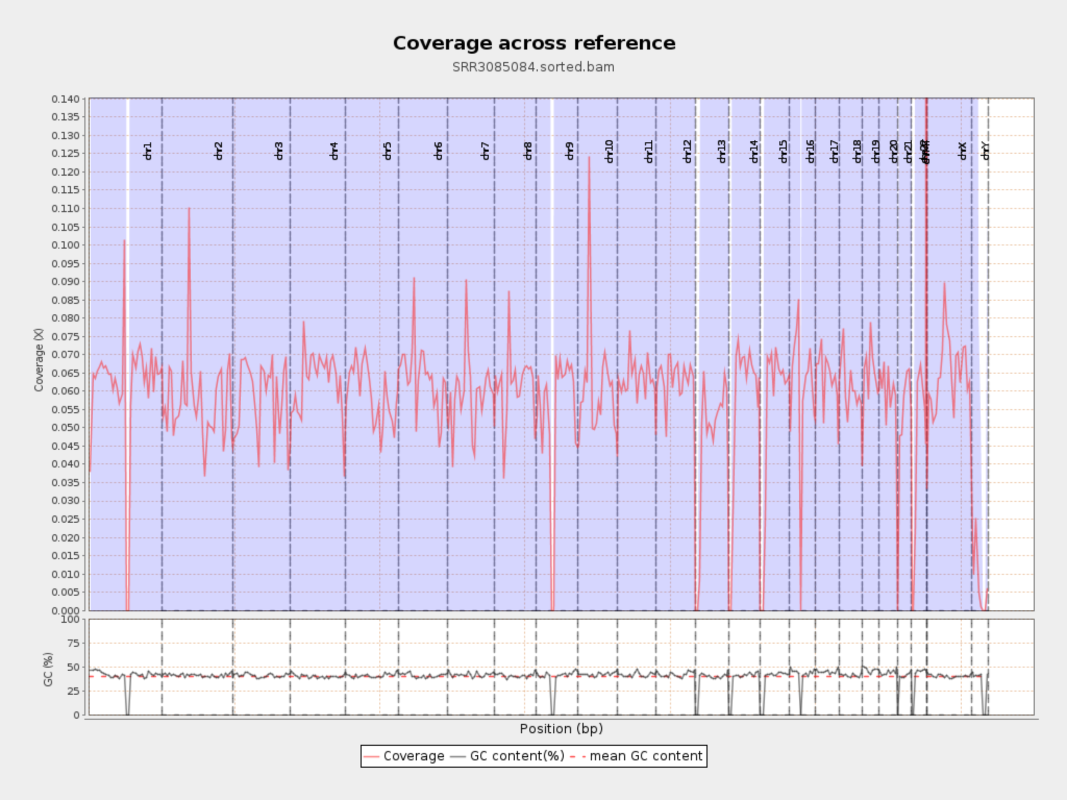
General error rate	0.87%
Mismatches	1,537,969
Insertions	14,963
Mapped reads with at least one insertion	0.54%
Deletions	43,199
Mapped reads with at least one deletion	1.56%
Homopolymer indels	45.94%

2.6. Chromosome stats

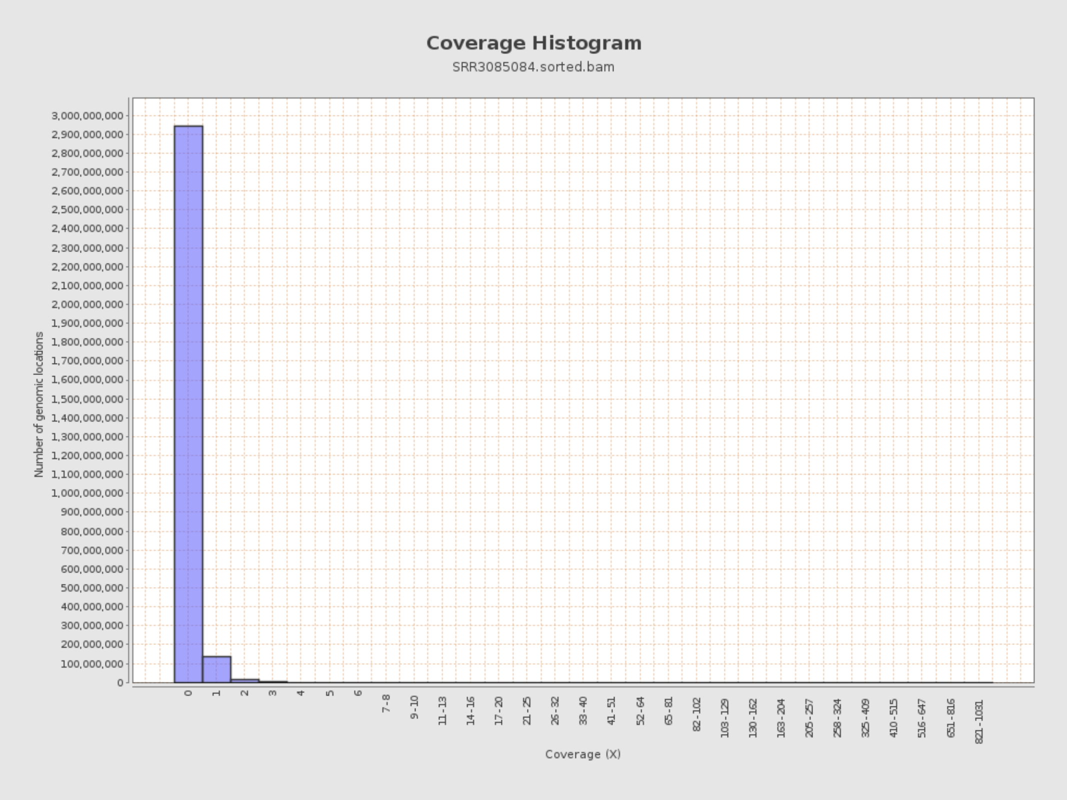
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15236765	0.0611	0.9192
chr2	243199373	14044807	0.0578	0.5773
chr3	198022430	11556529	0.0584	0.2834
chr4	191154276	11922079	0.0624	0.3081
chr5	180915260	10729665	0.0593	0.2776
chr6	171115067	10889780	0.0636	0.414
chr7	159138663	9480595	0.0596	0.4639

chr8	146364022	9089725	0.0621	0.5852
chr9	141213431	7630803	0.054	0.4186
chr10	135534747	8323664	0.0614	0.6448
chr11	135006516	8543446	0.0633	0.4934
chr12	133851895	8462746	0.0632	0.2912
chr13	115169878	5229289	0.0454	0.2408
chr14	107349540	5965384	0.0556	0.3066
chr15	102531392	5486068	0.0535	0.2688
chr16	90354753	5488660	0.0607	0.3317
chr17	81195210	5182321	0.0638	0.3428
chr18	78077248	4820065	0.0617	0.8057
chr19	59128983	3849597	0.0651	0.6578
chr20	63025520	3766352	0.0598	0.2934
chr21	48129895	2488246	0.0517	0.2886
chr22	51304566	2174746	0.0424	0.233
chrMT	16571	18566	1.1204	1.1735
chrX	155270560	9979146	0.0643	0.3453
chrY	59373566	461203	0.0078	0.1763

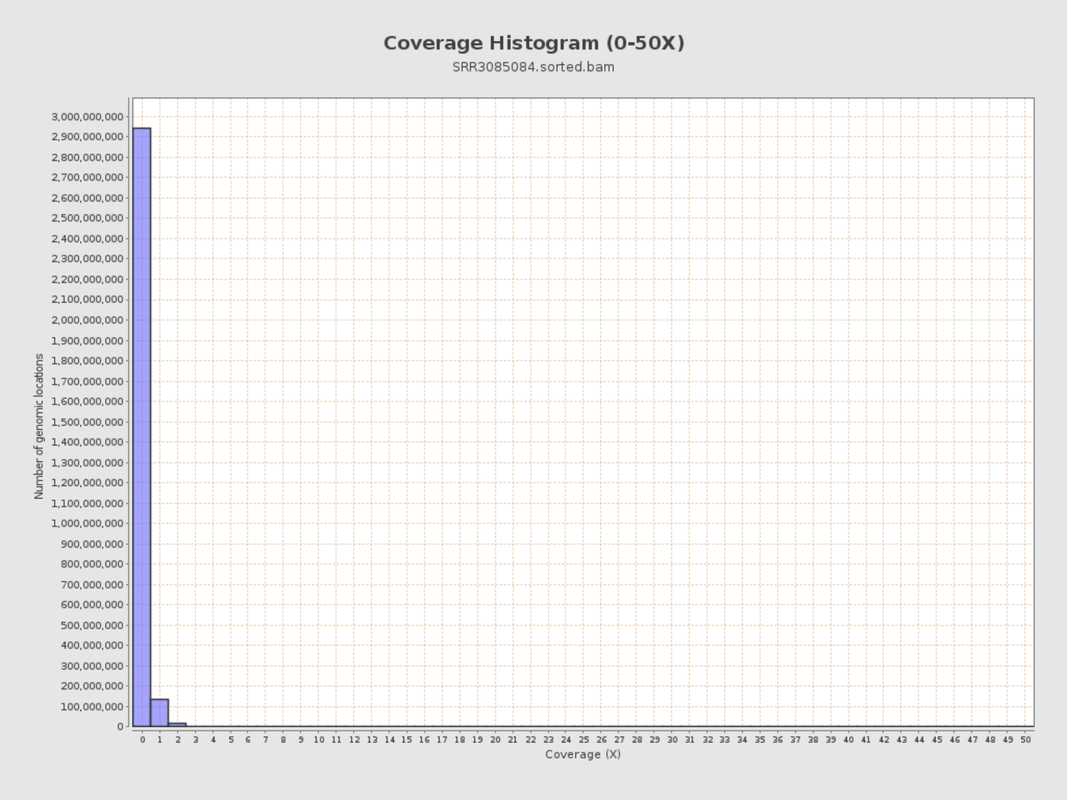
3. Results : Coverage across reference



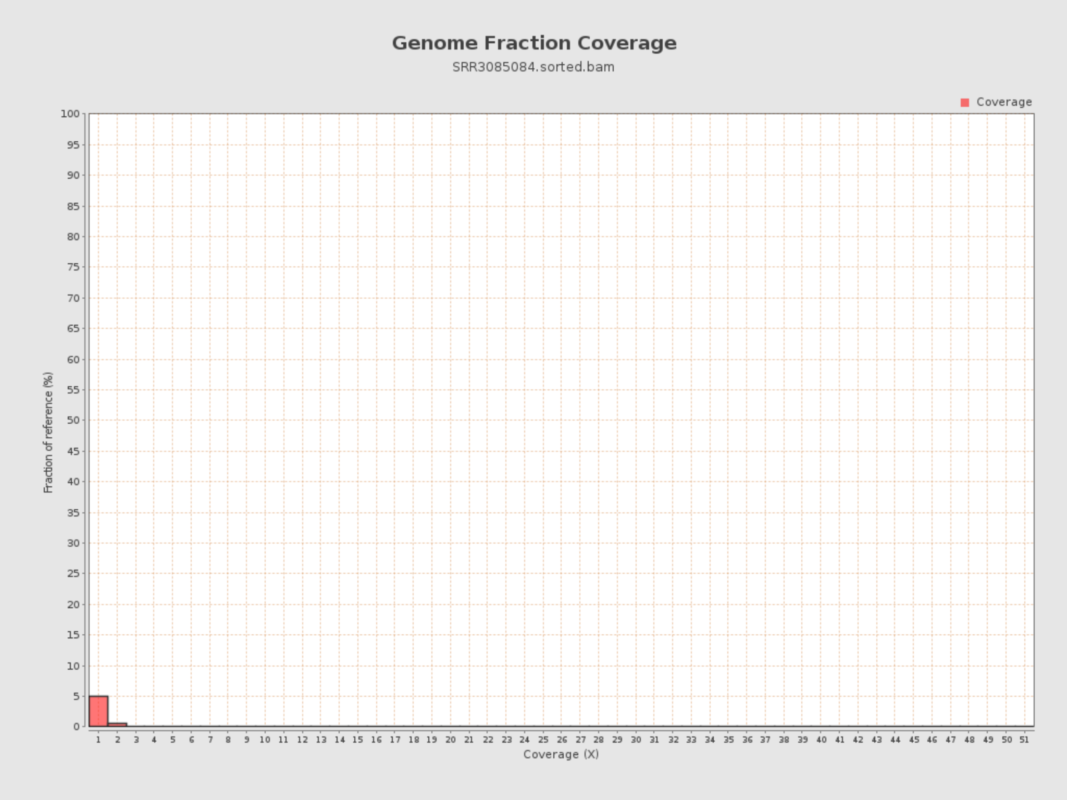
4. Results : Coverage Histogram



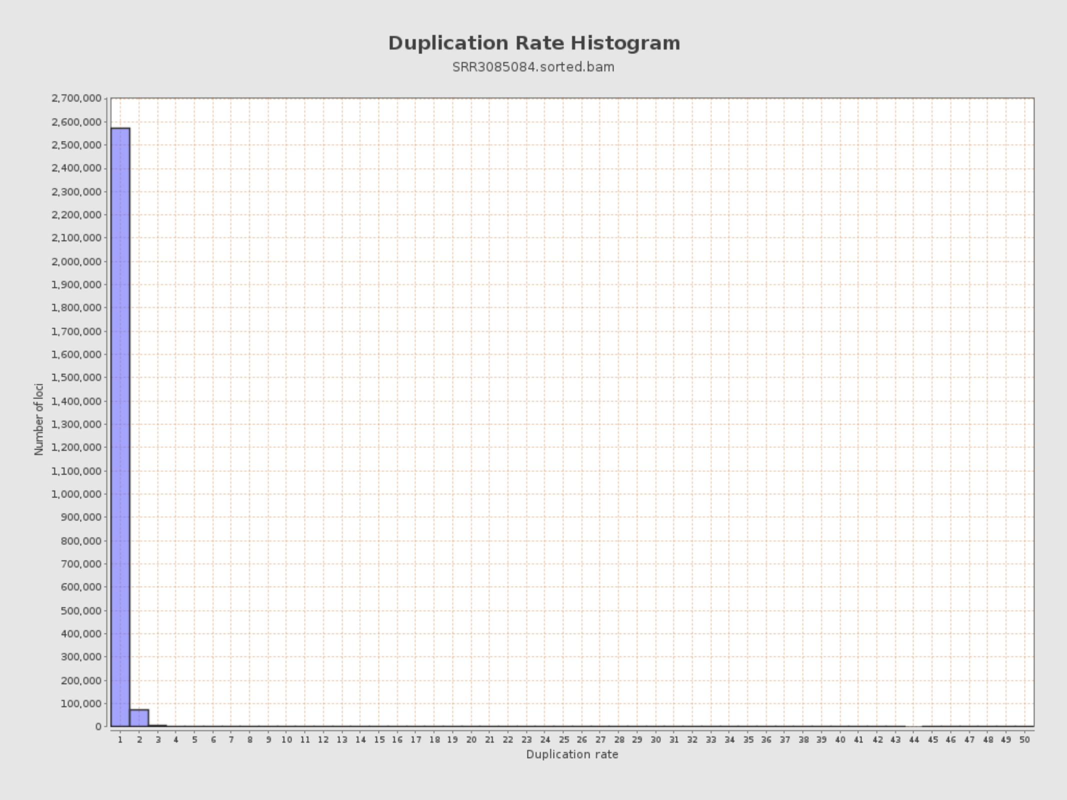
5. Results : Coverage Histogram (0-50X)



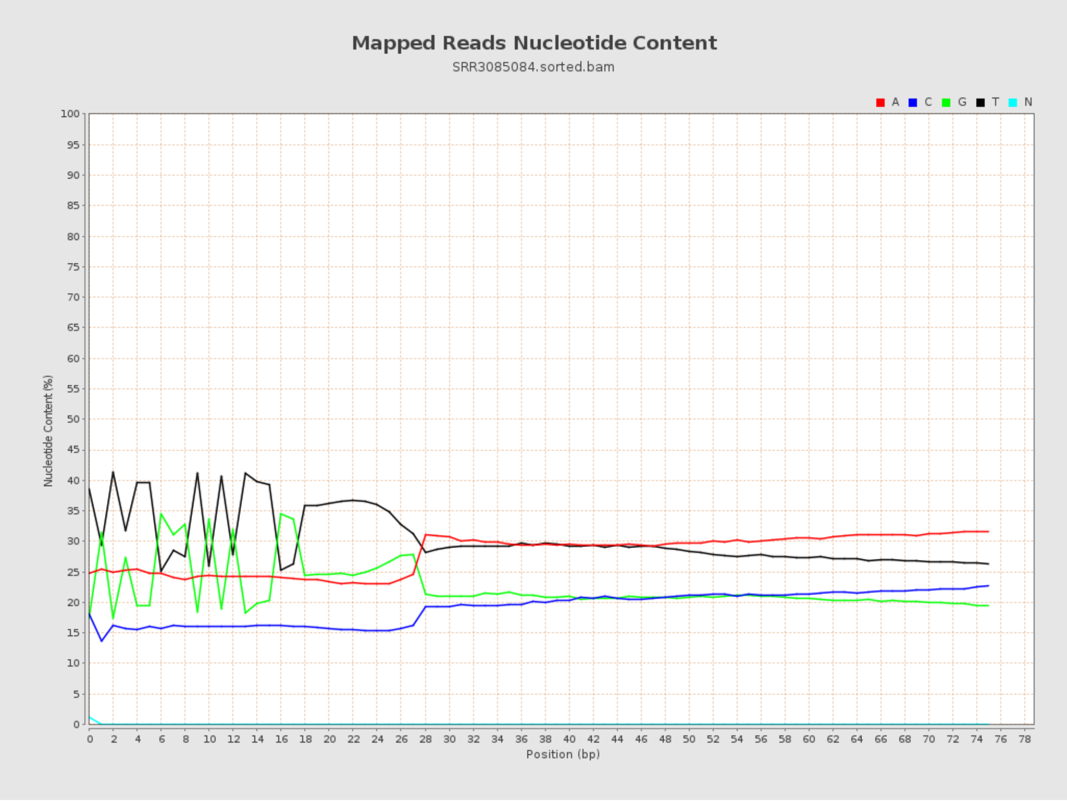
6. Results : Genome Fraction Coverage



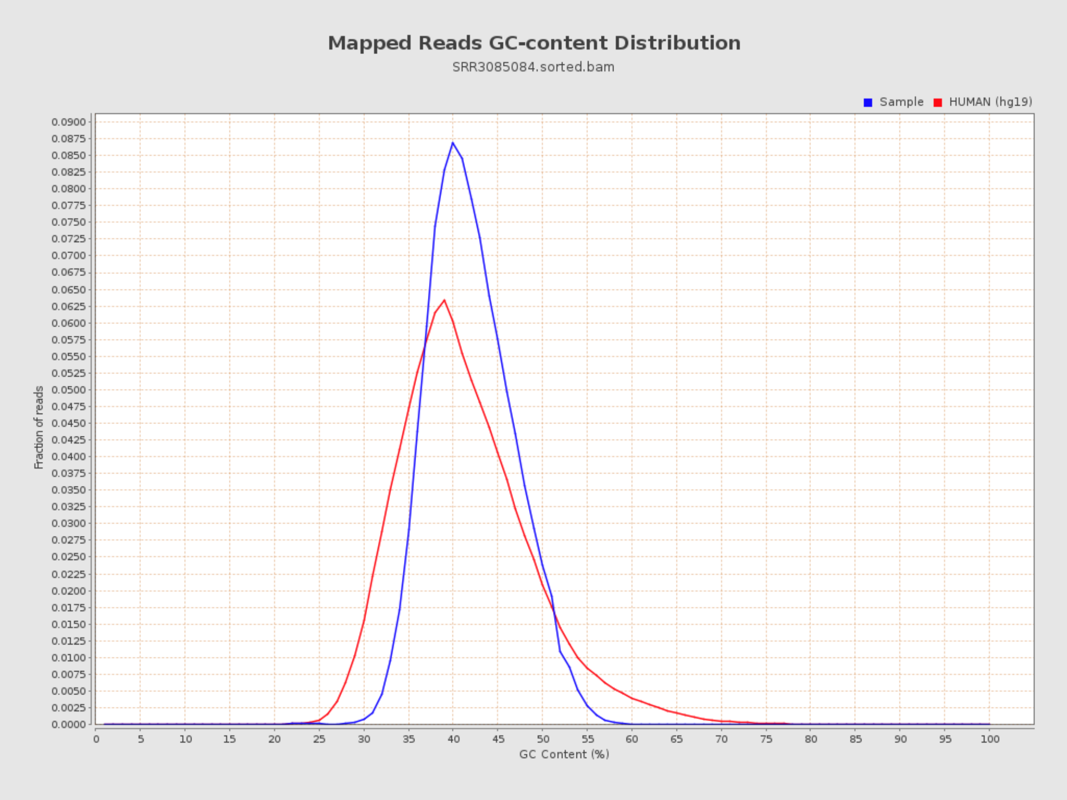
7. Results : Duplication Rate Histogram



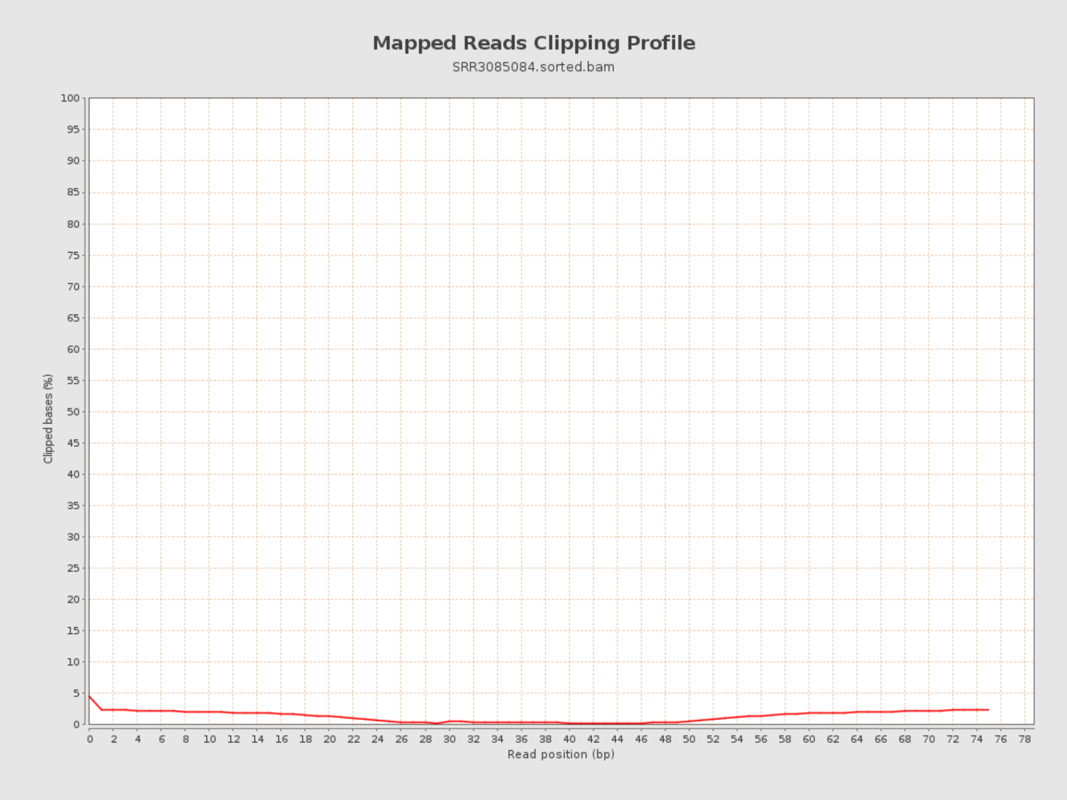
8. Results : Mapped Reads Nucleotide Content



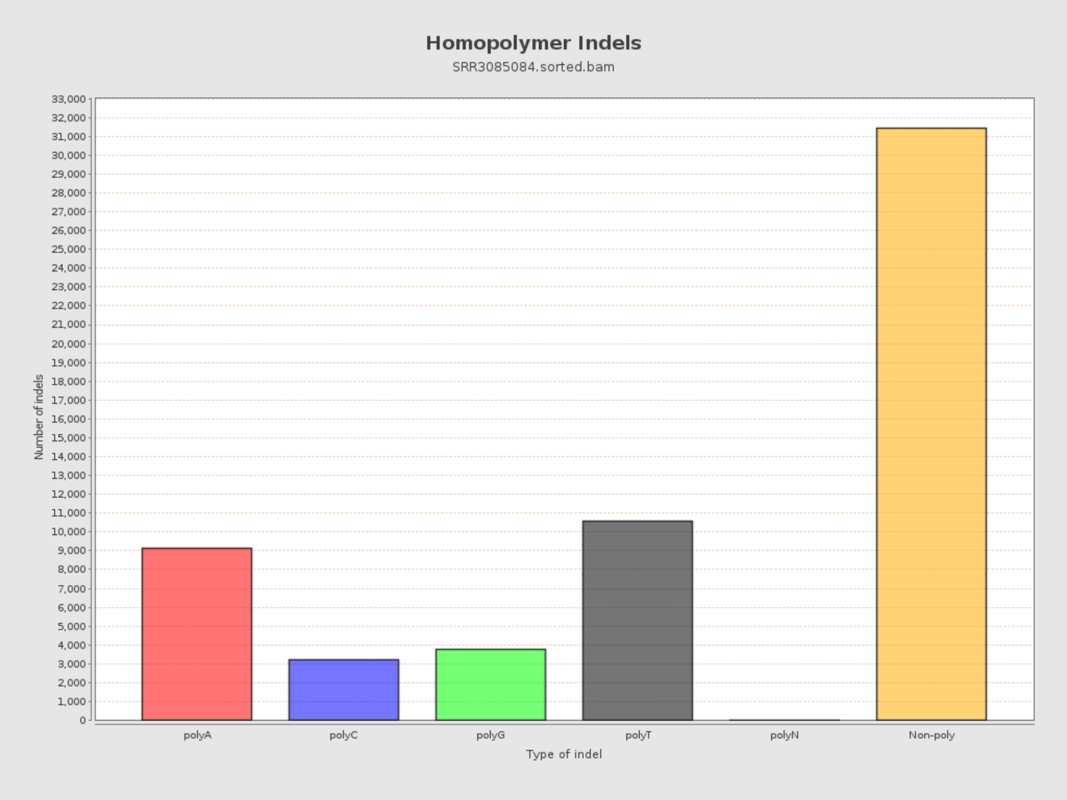
9. Results : Mapped Reads GC-content Distribution



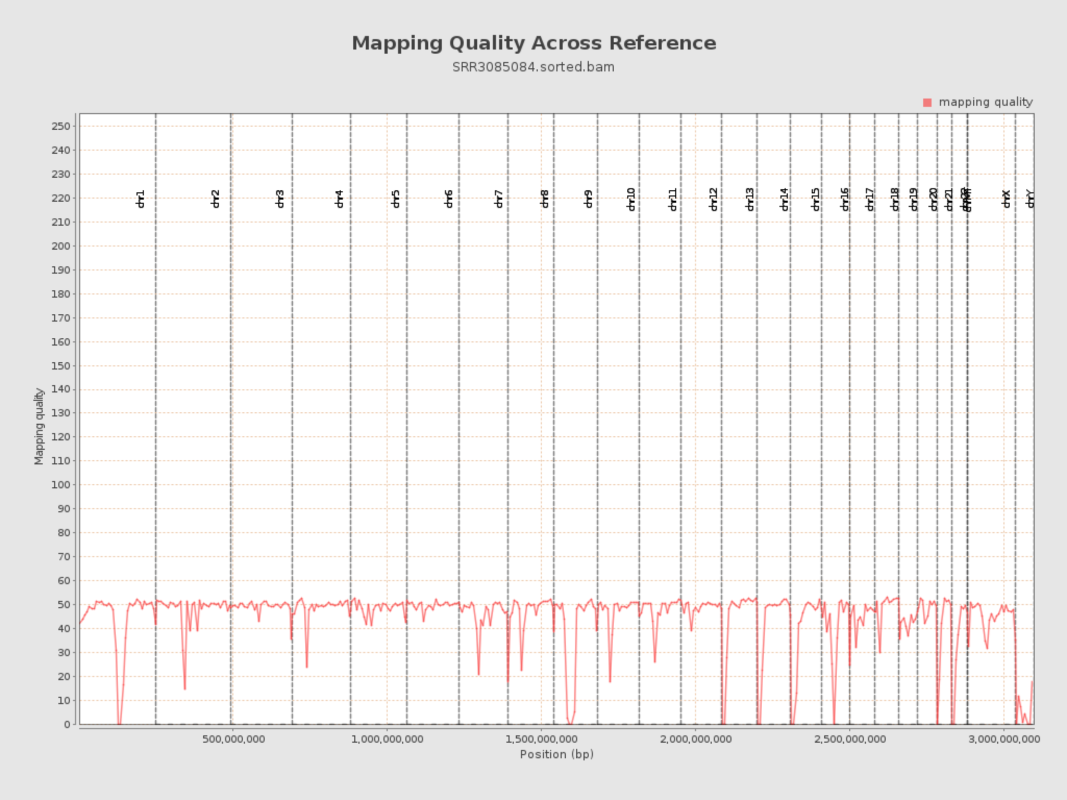
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram