Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 22:09:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085020.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_SRR3085020 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085020.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 22:09:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085020.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,705,773
Mapped reads	2,471,516 / 91.34%
Unmapped reads	234,257 / 8.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,201 / 0.67%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	92,149 / 3.41%
Duplication rate	2.94%
Clipped reads	1,091,466 / 40.34%

2.2. ACGT Content

Number/percentage of A's	46,515,637 / 28.04%
Number/percentage of C's	32,102,835 / 19.35%
Number/percentage of T's	50,833,005 / 30.64%
Number/percentage of G's	36,433,862 / 21.96%
Number/percentage of N's	18,279 / 0.01%
GC Percentage	41.31%

2.3. Coverage

Mean	0.0536

Standard Deviation	0.4057

2.4. Mapping Quality

Mean Mapping Quality	45.51

2.5. Mismatches and indels

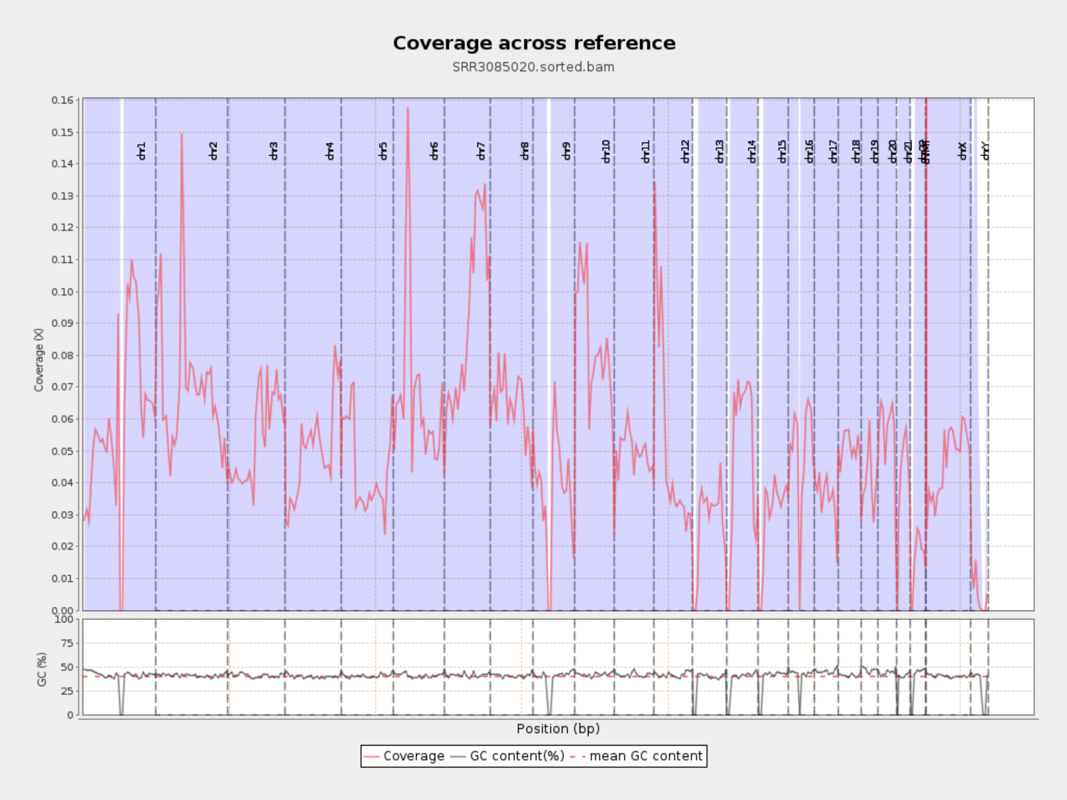
General error rate	0.88%
Mismatches	1,433,789
Insertions	11,496
Mapped reads with at least one insertion	0.46%
Deletions	33,800
Mapped reads with at least one deletion	1.35%
Homopolymer indels	46.07%

2.6. Chromosome stats

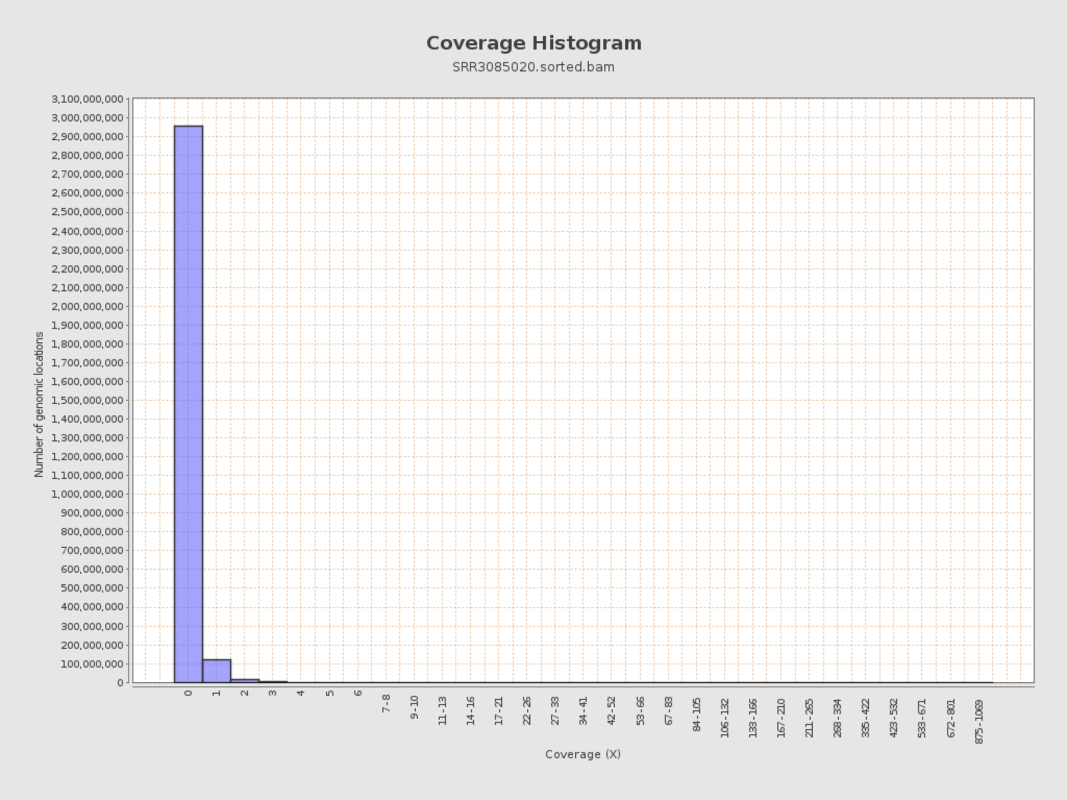
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14829619	0.0595	0.6195
chr2	243199373	17191220	0.0707	0.5106
chr3	198022430	10638246	0.0537	0.2721
chr4	191154276	9643909	0.0505	0.265
chr5	180915260	8109689	0.0448	0.244
chr6	171115067	11801452	0.069	0.4158
chr7	159138663	14627977	0.0919	0.4797

chr8	146364022	9344837	0.0638	0.6923
chr9	141213431	5294551	0.0375	0.331
chr10	135534747	11501829	0.0849	0.5564
chr11	135006516	6695803	0.0496	0.4207
chr12	133851895	7101526	0.0531	0.2725
chr13	115169878	3160732	0.0274	0.1884
chr14	107349540	5352642	0.0499	0.2673
chr15	102531392	2993290	0.0292	0.2042
chr16	90354753	4360501	0.0483	0.2678
chr17	81195210	2924597	0.036	0.2574
chr18	78077248	4023518	0.0515	0.5379
chr19	59128983	2433436	0.0412	0.424
chr20	63025520	3608481	0.0573	0.2783
chr21	48129895	1957759	0.0407	0.2421
chr22	51304566	819853	0.016	0.1426
chrMT	16571	10664	0.6435	0.9641
chrX	155270560	7209384	0.0464	0.2847
chrY	59373566	325705	0.0055	0.1083

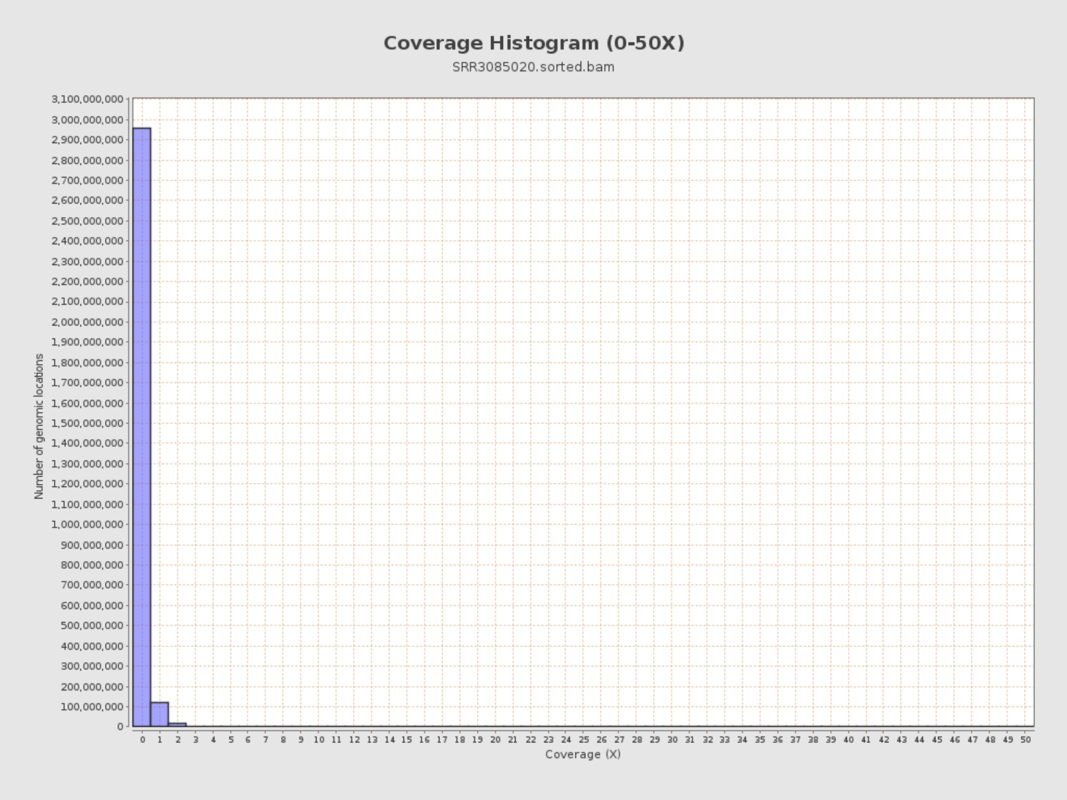
3. Results : Coverage across reference



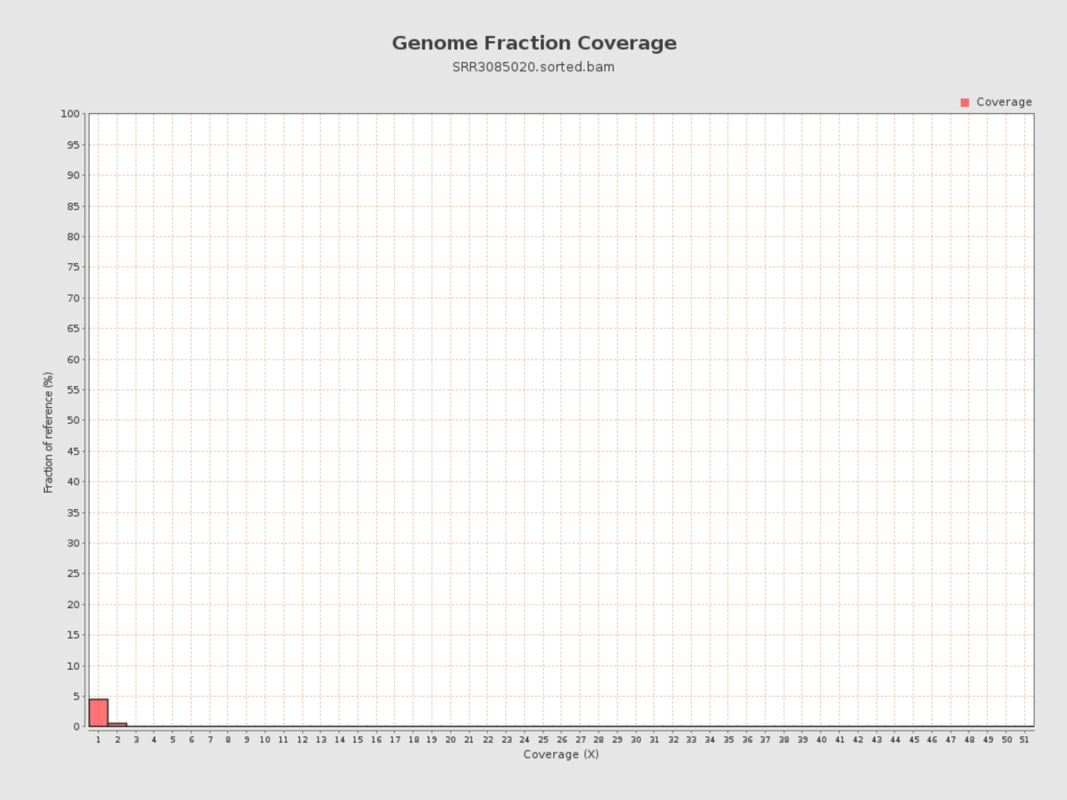
4. Results : Coverage Histogram



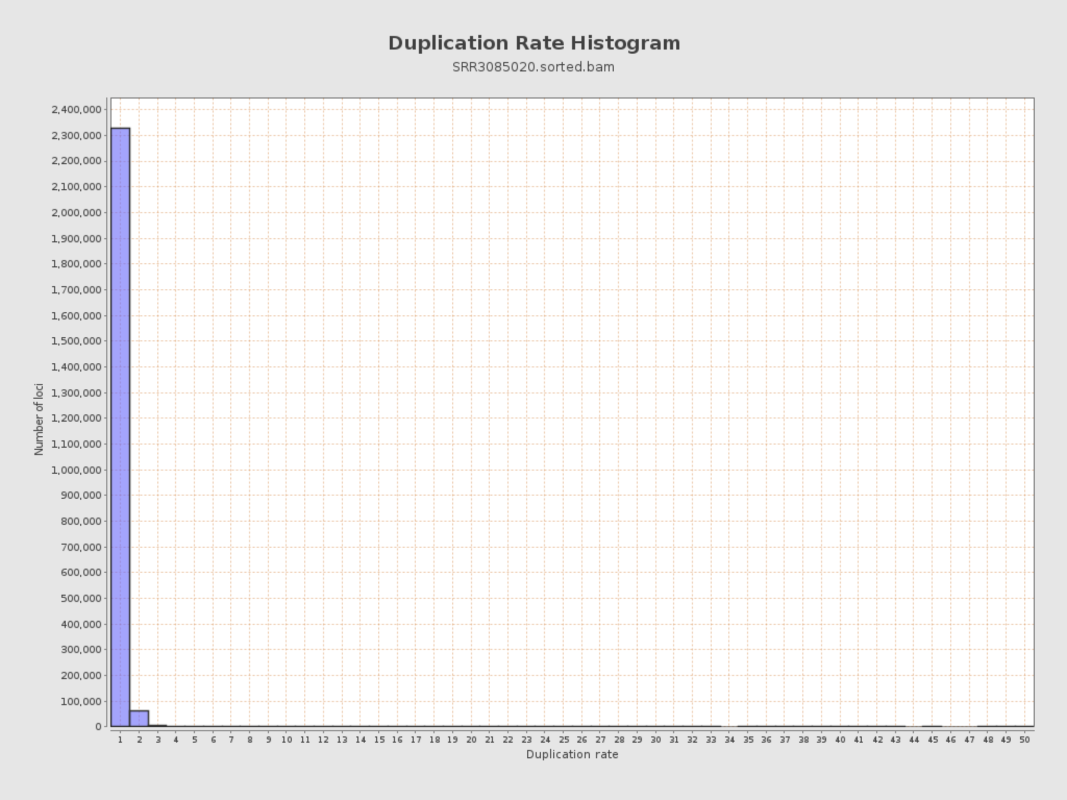
5. Results : Coverage Histogram (0-50X)



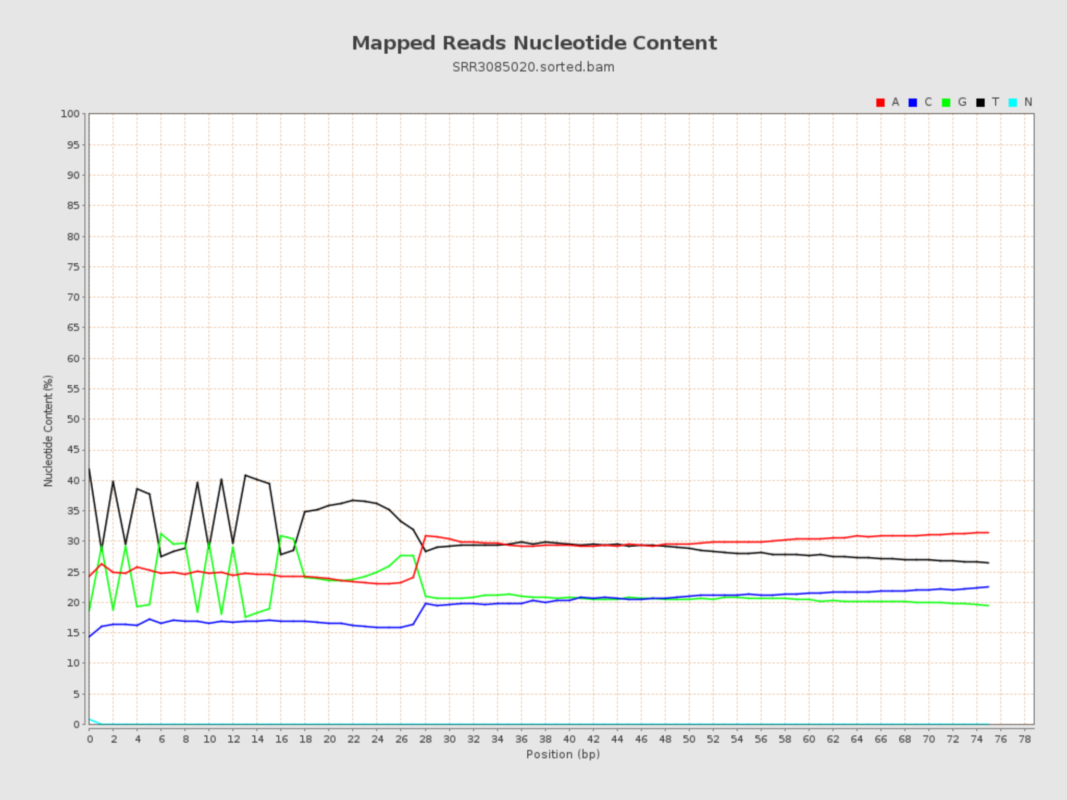
6. Results : Genome Fraction Coverage



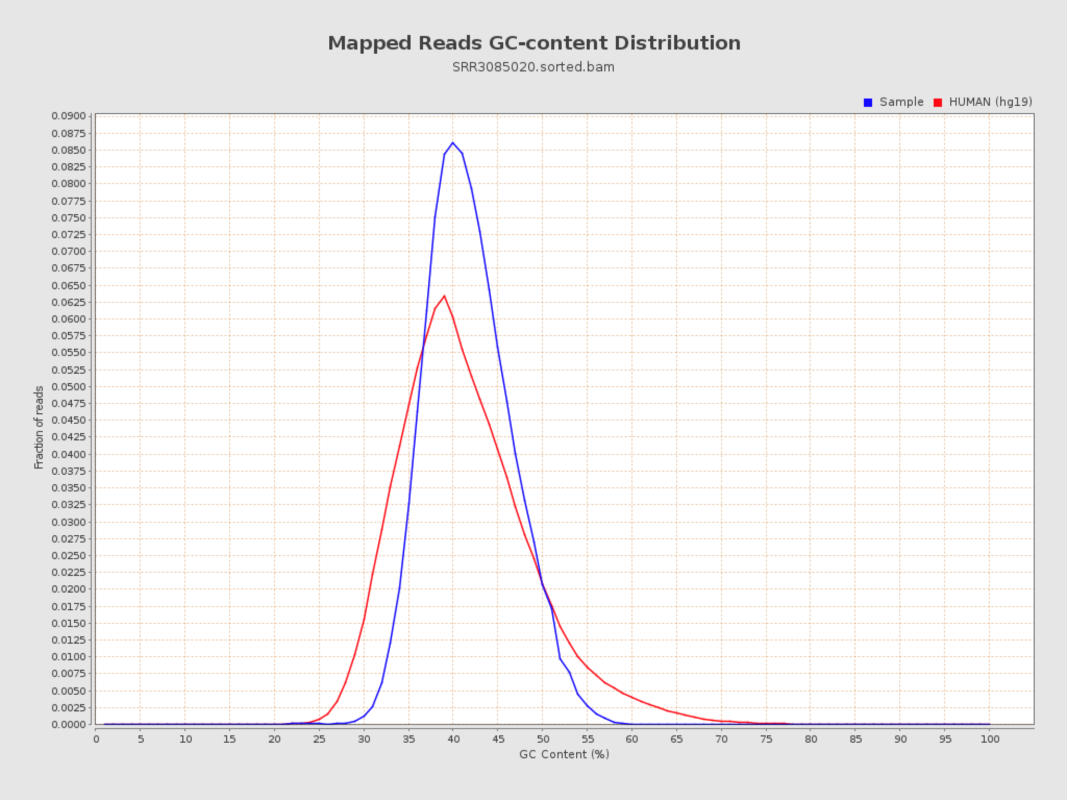
7. Results : Duplication Rate Histogram



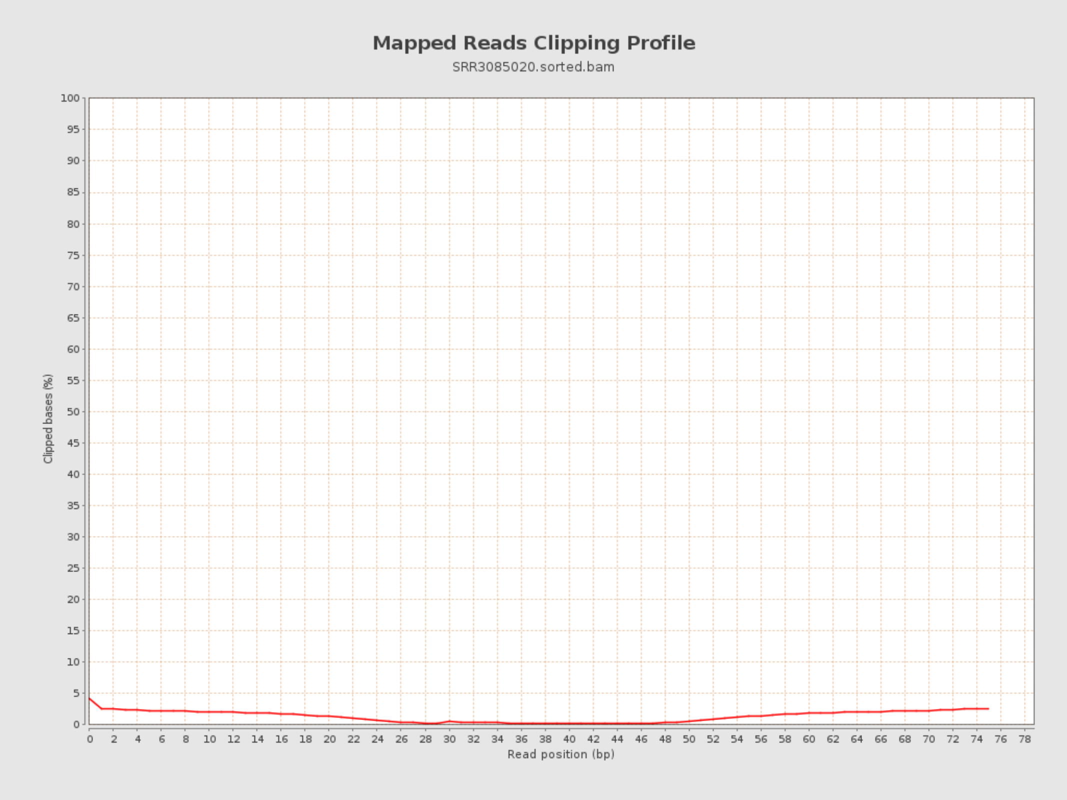
8. Results : Mapped Reads Nucleotide Content



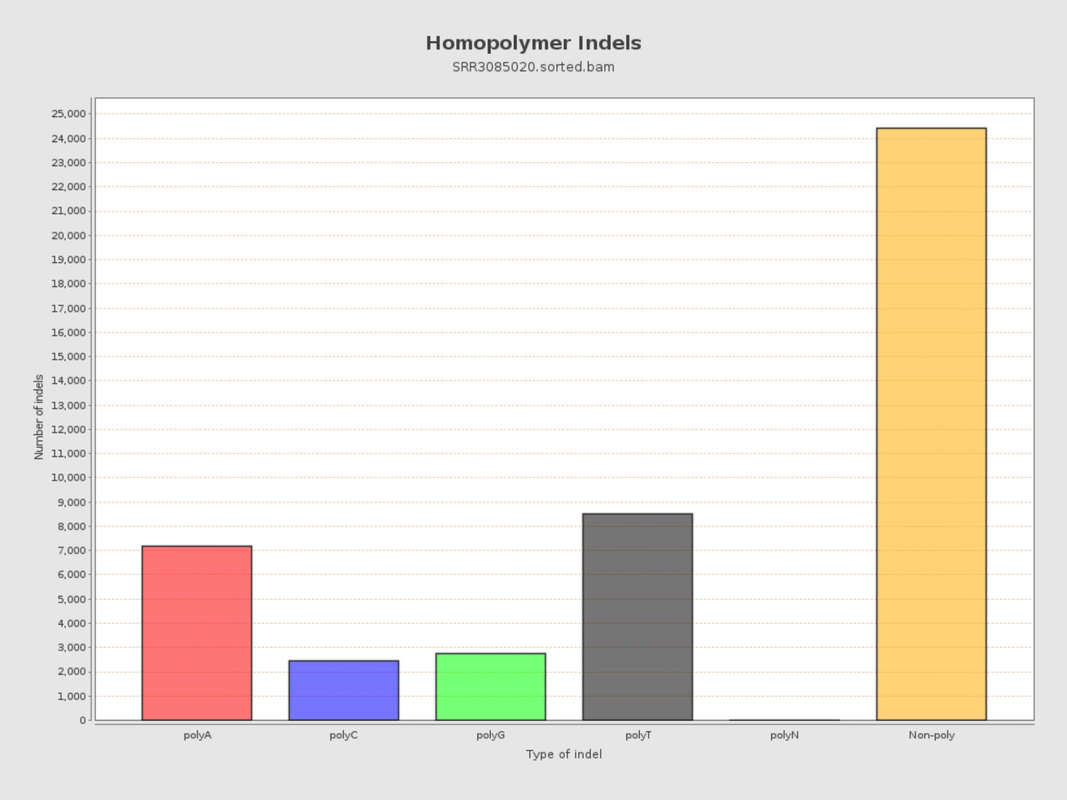
9. Results : Mapped Reads GC-content Distribution



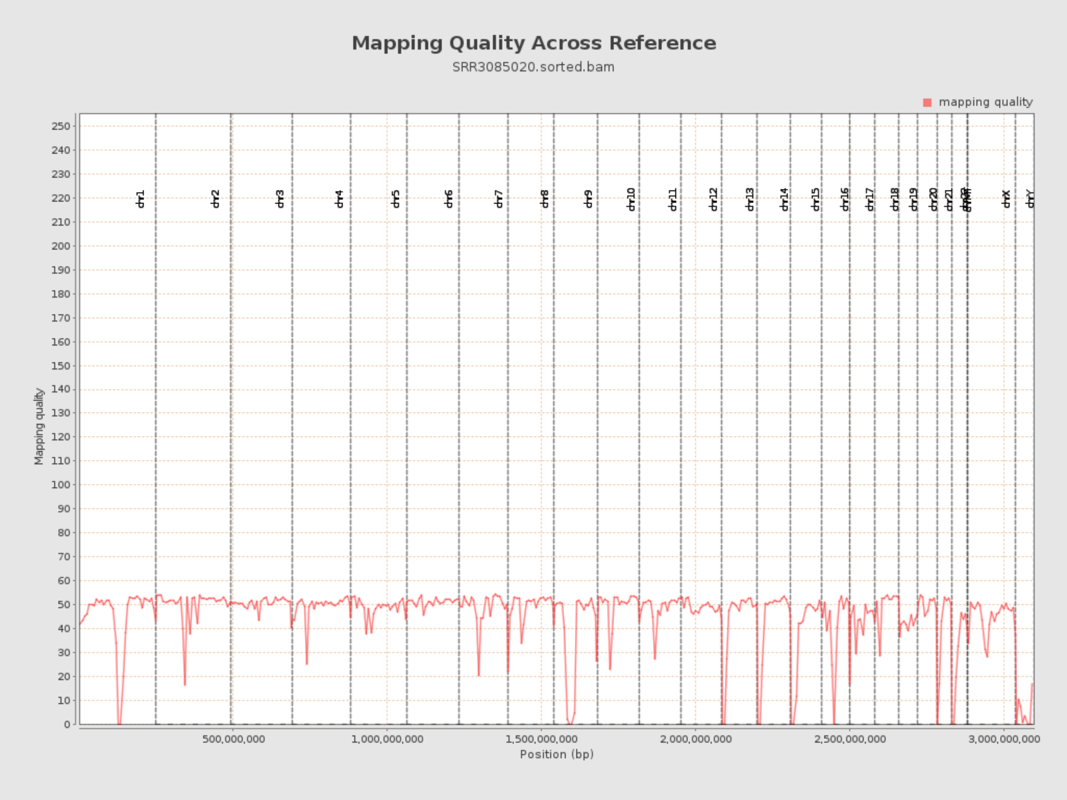
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram