Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 10:59:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716769.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_SRR9716769 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716769.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 10:59:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716769.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,489,130
Mapped reads	1,387,606 / 93.18%
Unmapped reads	101,524 / 6.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,138 / 1.96%
Read min/max/mean length	30 / 101 / 101.7
Duplicated reads (estimated)	59,212 / 3.98%
Duplication rate	3.33%
Clipped reads	1,414,524 / 94.99%

2.2. ACGT Content

Number/percentage of A's	26,770,353 / 25.08%
Number/percentage of C's	22,400,962 / 20.99%
Number/percentage of T's	31,358,181 / 29.38%
Number/percentage of G's	26,206,142 / 24.55%
Number/percentage of N's	3,719 / 0%
GC Percentage	45.54%

2.3. Coverage

Mean	0.0345

Standard Deviation	0.298

2.4. Mapping Quality

Mean Mapping Quality	46.14

2.5. Mismatches and indels

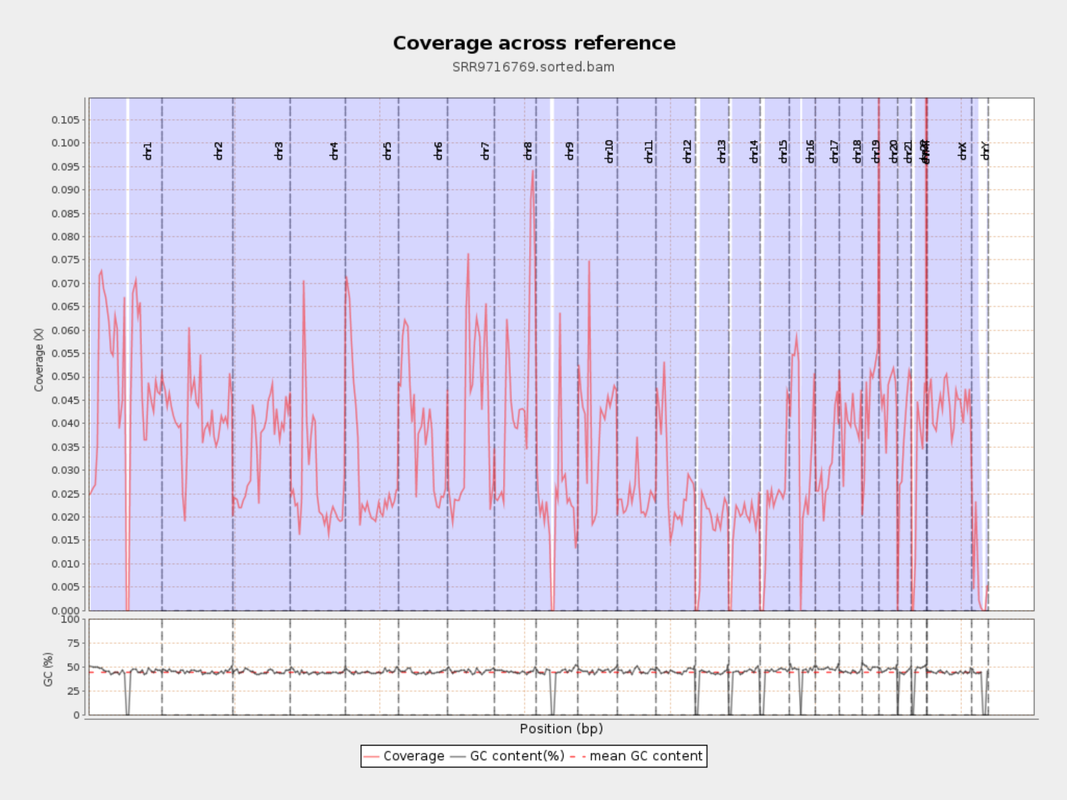
General error rate	0.68%
Mismatches	698,347
Insertions	8,926
Mapped reads with at least one insertion	0.63%
Deletions	19,767
Mapped reads with at least one deletion	1.4%
Homopolymer indels	39.25%

2.6. Chromosome stats

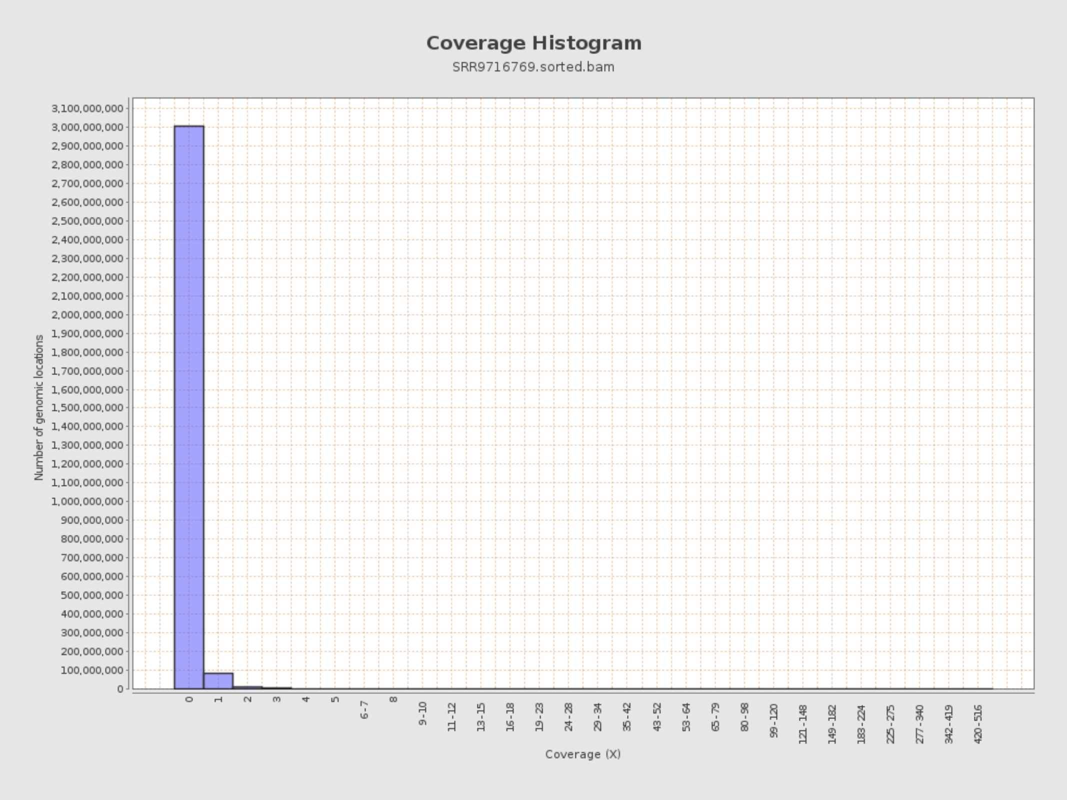
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12069266	0.0484	0.5366
chr2	243199373	10091707	0.0415	0.32
chr3	198022430	6943991	0.0351	0.2148
chr4	191154276	5113714	0.0268	0.2602
chr5	180915260	5491181	0.0304	0.2015
chr6	171115067	6680339	0.039	0.2376
chr7	159138663	6606560	0.0415	0.3889

chr8	146364022	6743015	0.0461	0.3225
chr9	141213431	3159252	0.0224	0.2145
chr10	135534747	5504395	0.0406	0.4224
chr11	135006516	3252268	0.0241	0.2306
chr12	133851895	3812960	0.0285	0.1921
chr13	115169878	2035002	0.0177	0.15
chr14	107349540	1923768	0.0179	0.1644
chr15	102531392	2264637	0.0221	0.1685
chr16	90354753	3322938	0.0368	0.2315
chr17	81195210	2516737	0.031	0.2258
chr18	78077248	3148717	0.0403	0.3139
chr19	59128983	2784951	0.0471	0.3996
chr20	63025520	2921625	0.0464	0.2586
chr21	48129895	1701223	0.0353	0.2562
chr22	51304566	1462542	0.0285	0.2003
chrMT	16571	35477	2.1409	2.0261
chrX	155270560	6823435	0.0439	0.2524
chrY	59373566	371221	0.0063	0.215

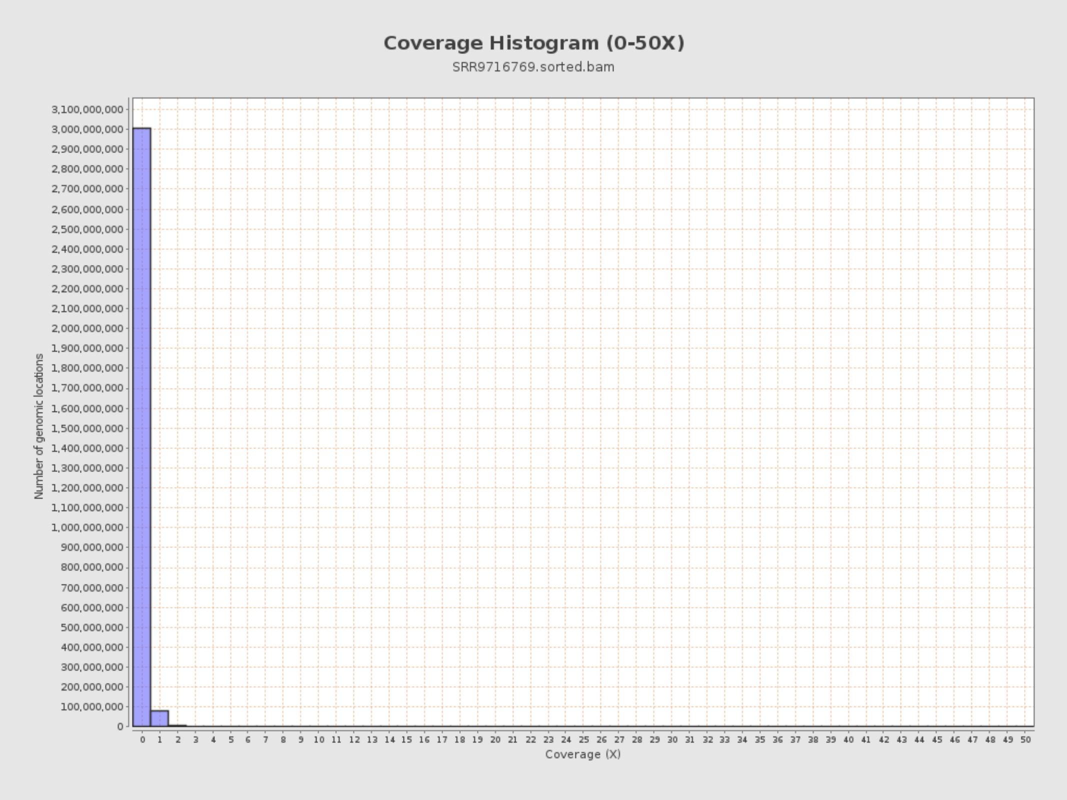
3. Results : Coverage across reference



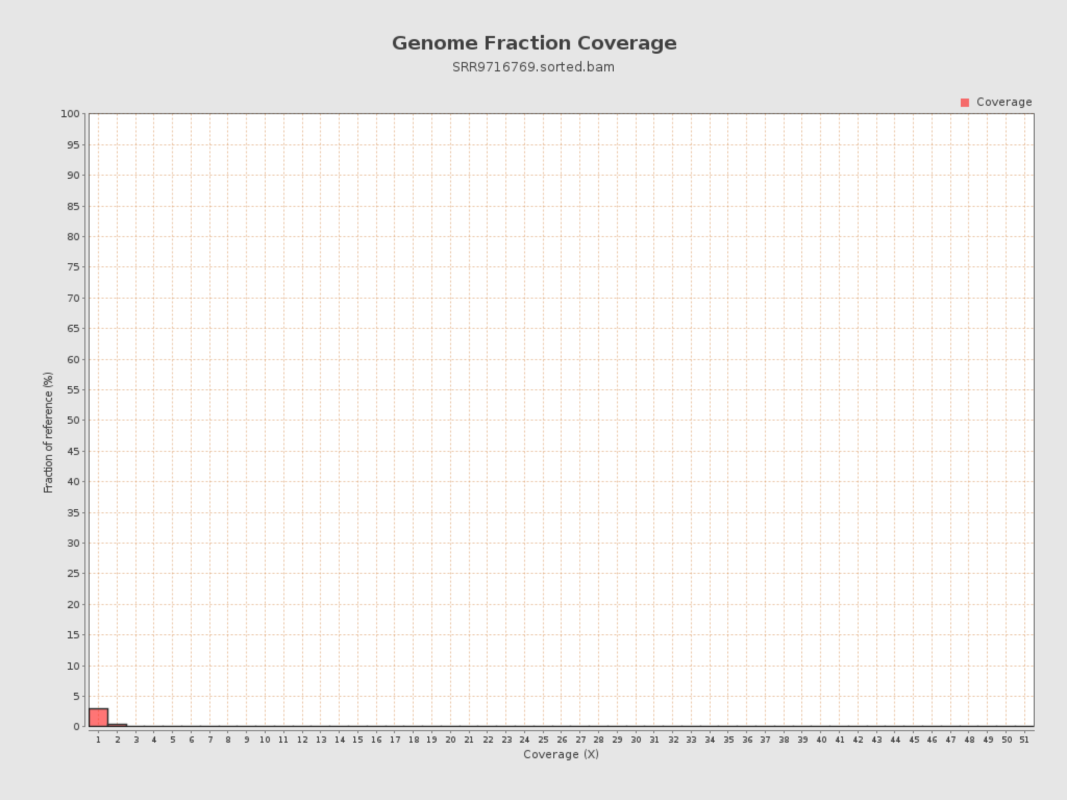
4. Results : Coverage Histogram



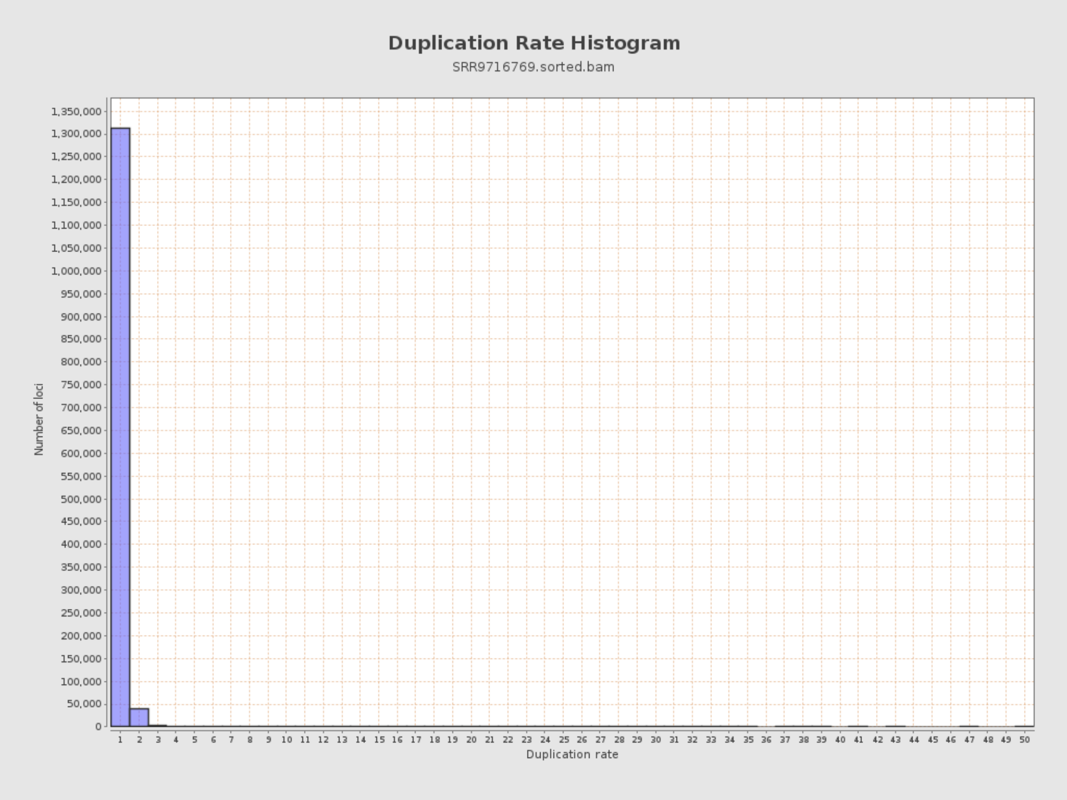
5. Results : Coverage Histogram (0-50X)



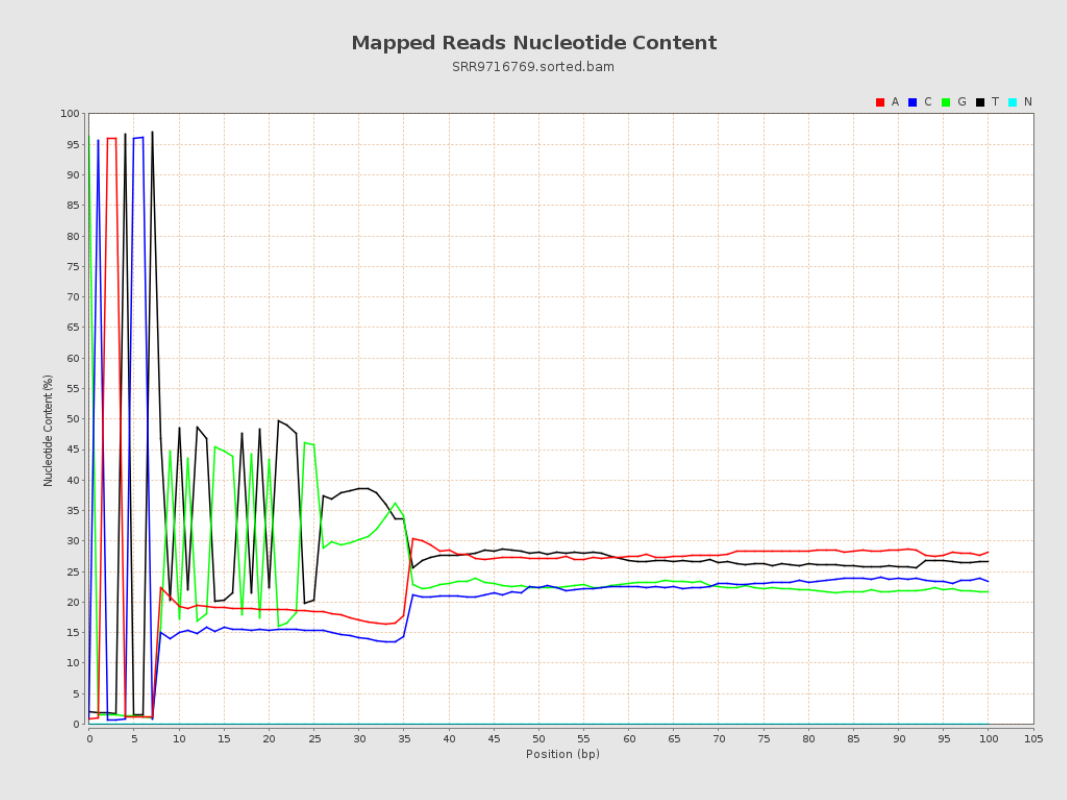
6. Results : Genome Fraction Coverage



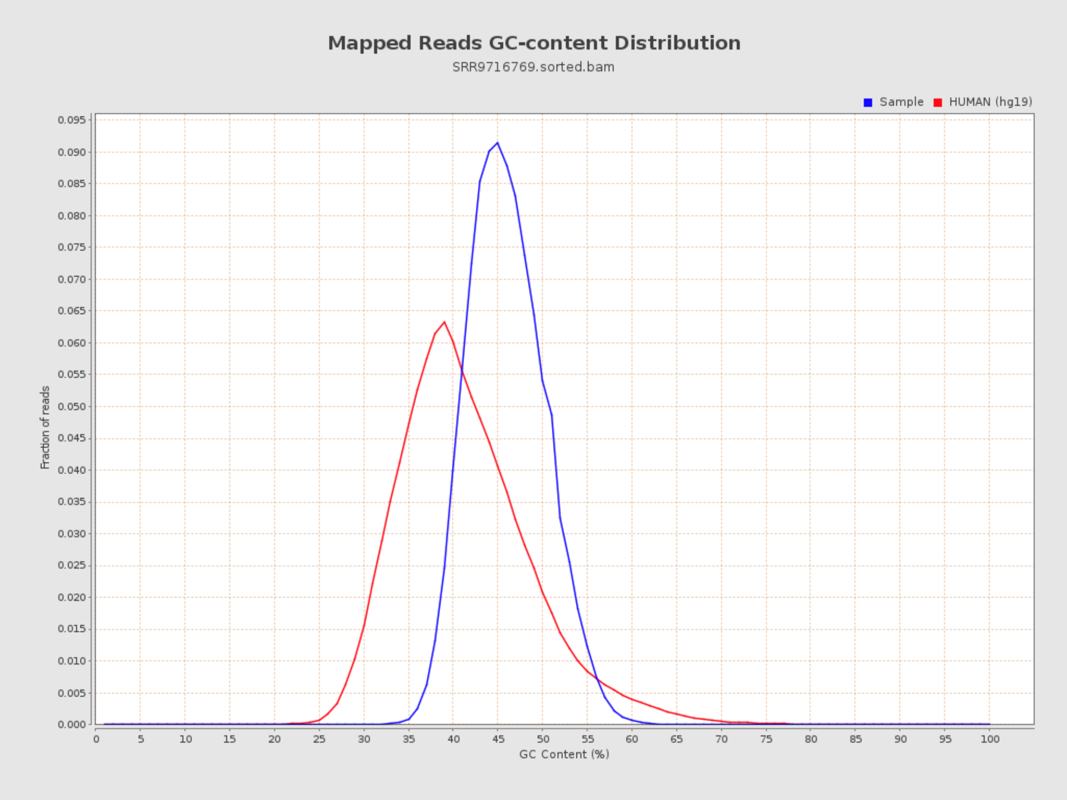
7. Results : Duplication Rate Histogram



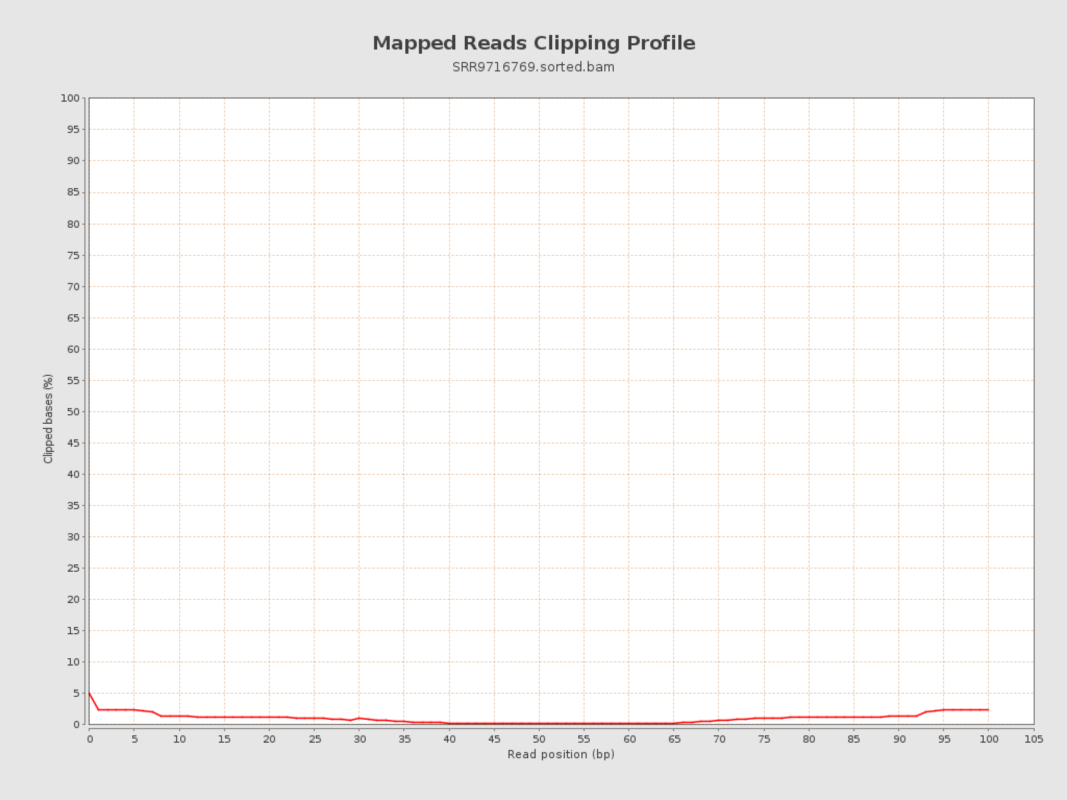
8. Results : Mapped Reads Nucleotide Content



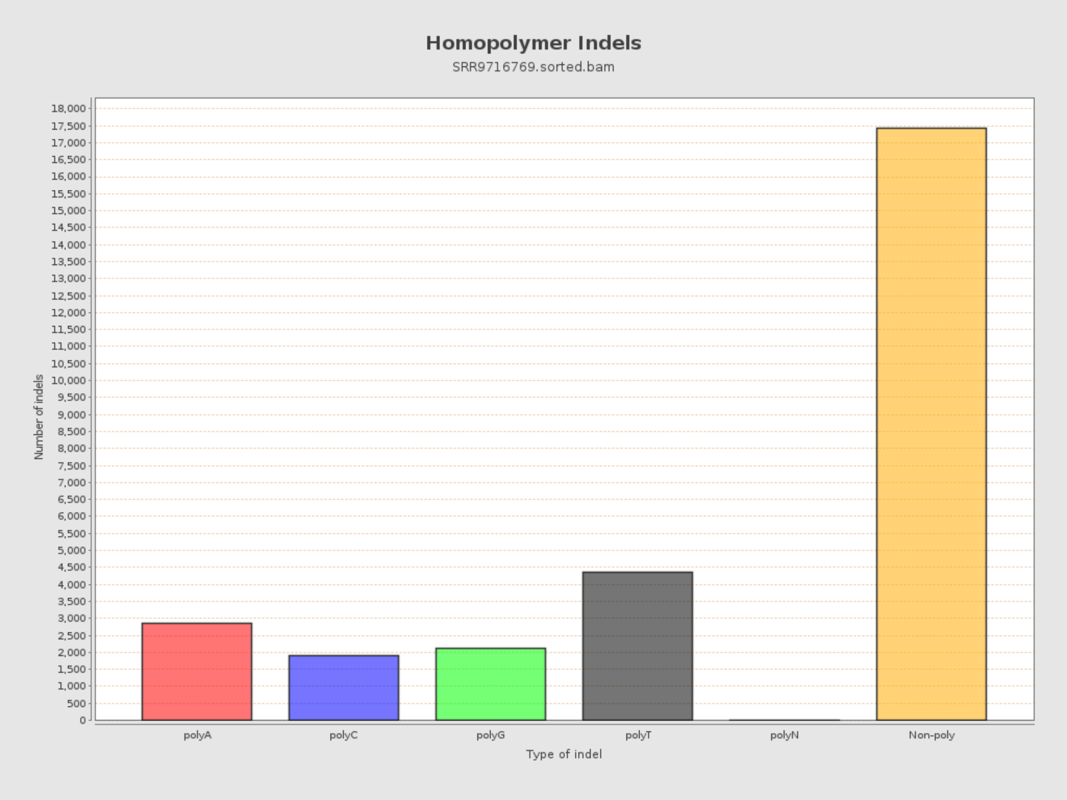
9. Results : Mapped Reads GC-content Distribution



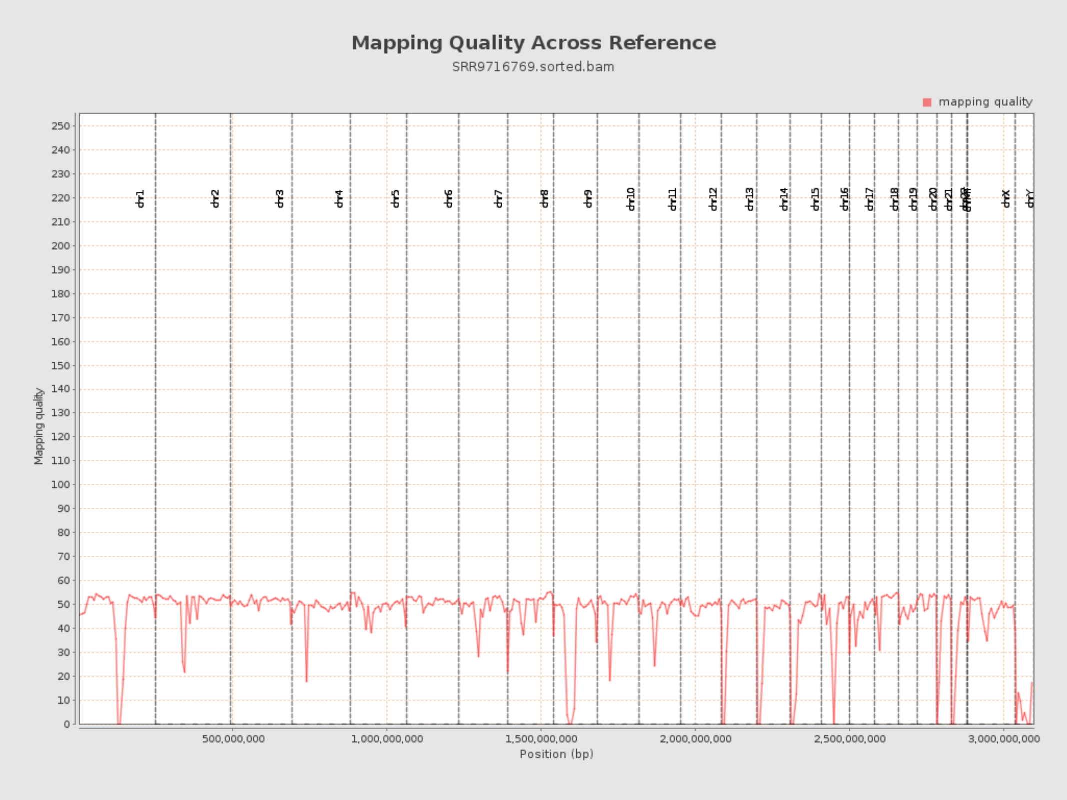
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram