Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 01:05:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716623.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_SRR9716623 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716623.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 01:05:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716623.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	624,001
Mapped reads	571,346 / 91.56%
Unmapped reads	52,655 / 8.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,503 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	9,048 / 1.45%
Duplication rate	1.22%
Clipped reads	572,463 / 91.74%

2.2. ACGT Content

Number/percentage of A's	8,040,011 / 24.5%
Number/percentage of C's	6,305,643 / 19.22%
Number/percentage of T's	10,371,715 / 31.61%
Number/percentage of G's	8,098,086 / 24.68%
Number/percentage of N's	768 / 0%
GC Percentage	43.89%

2.3. Coverage

Mean	0.0106

Standard Deviation	0.1204

2.4. Mapping Quality

Mean Mapping Quality	44.95

2.5. Mismatches and indels

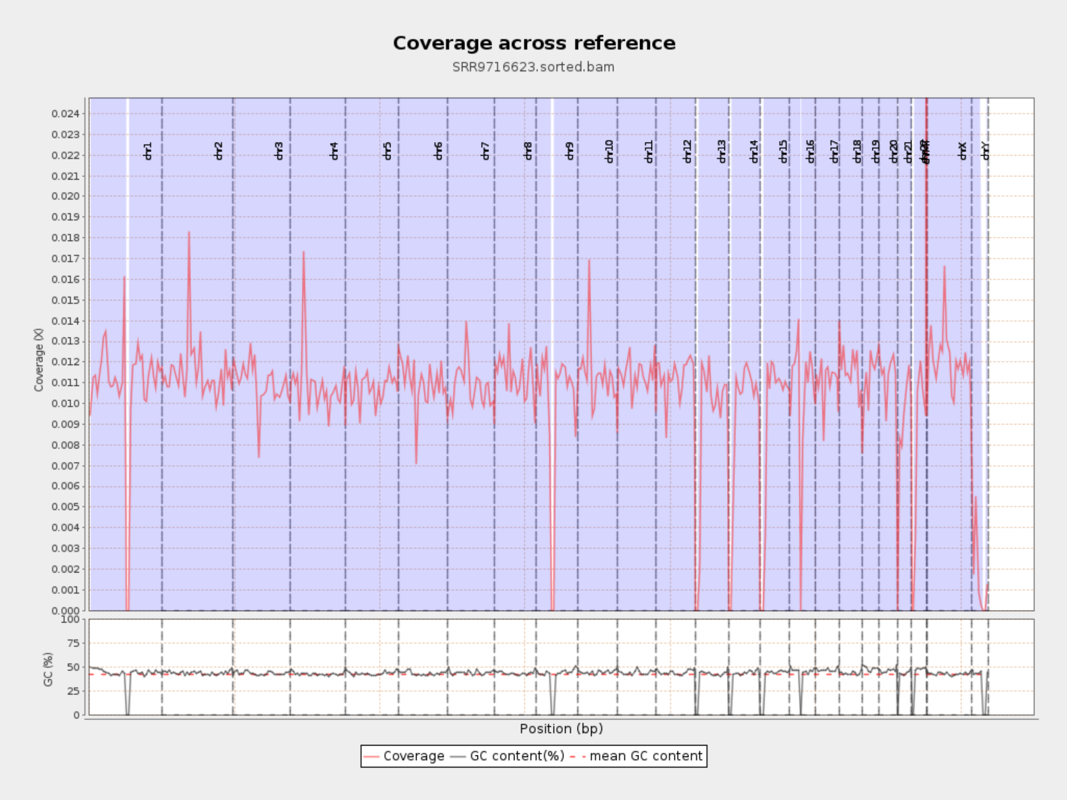
General error rate	0.5%
Mismatches	159,514
Insertions	2,020
Mapped reads with at least one insertion	0.35%
Deletions	5,230
Mapped reads with at least one deletion	0.91%
Homopolymer indels	41.17%

2.6. Chromosome stats

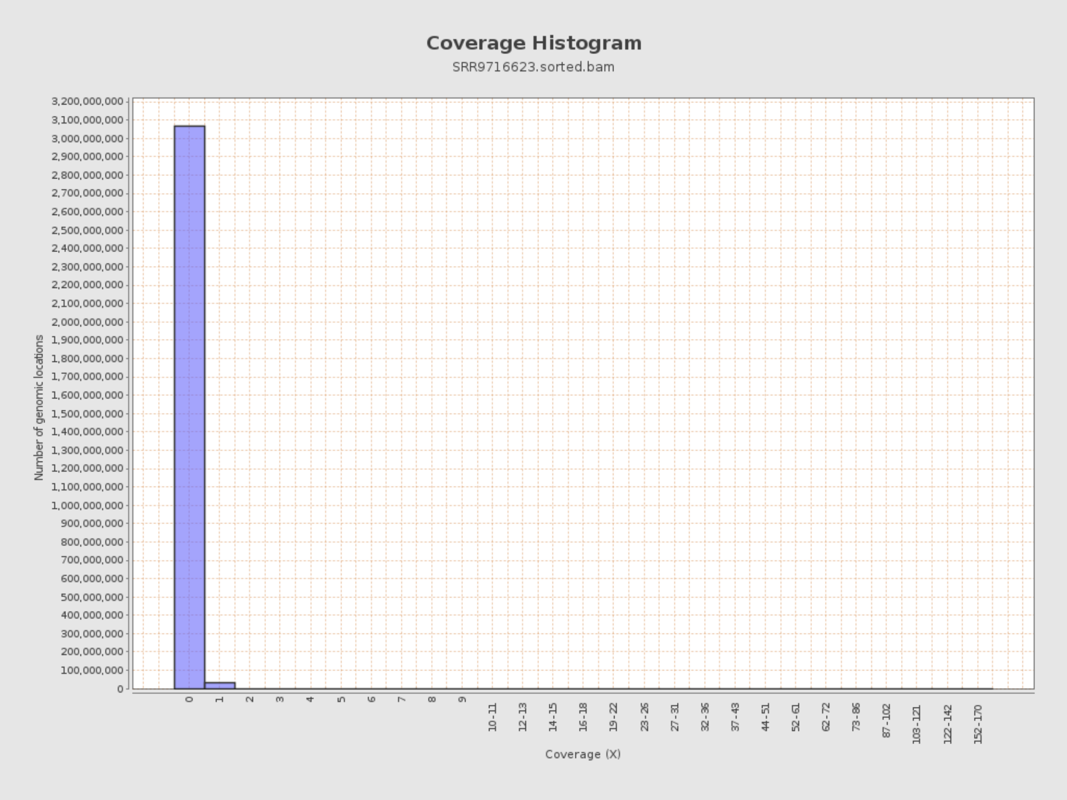
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2693922	0.0108	0.1683
chr2	243199373	2801894	0.0115	0.1291
chr3	198022430	2177970	0.011	0.1084
chr4	191154276	2085452	0.0109	0.1111
chr5	180915260	1949344	0.0108	0.1076
chr6	171115067	1879059	0.011	0.1106
chr7	159138663	1729548	0.0109	0.1261

chr8	146364022	1664980	0.0114	0.1178
chr9	141213431	1389448	0.0098	0.1167
chr10	135534747	1548728	0.0114	0.1233
chr11	135006516	1537138	0.0114	0.121
chr12	133851895	1506132	0.0113	0.1094
chr13	115169878	1029067	0.0089	0.0975
chr14	107349540	982072	0.0091	0.102
chr15	102531392	927523	0.009	0.0986
chr16	90354753	949665	0.0105	0.1107
chr17	81195210	893658	0.011	0.1106
chr18	78077248	915051	0.0117	0.1754
chr19	59128983	669269	0.0113	0.1307
chr20	63025520	706980	0.0112	0.111
chr21	48129895	427258	0.0089	0.1004
chr22	51304566	380226	0.0074	0.0888
chrMT	16571	1943	0.1173	0.3561
chrX	155270560	1880639	0.0121	0.1199
chrY	59373566	98197	0.0017	0.051

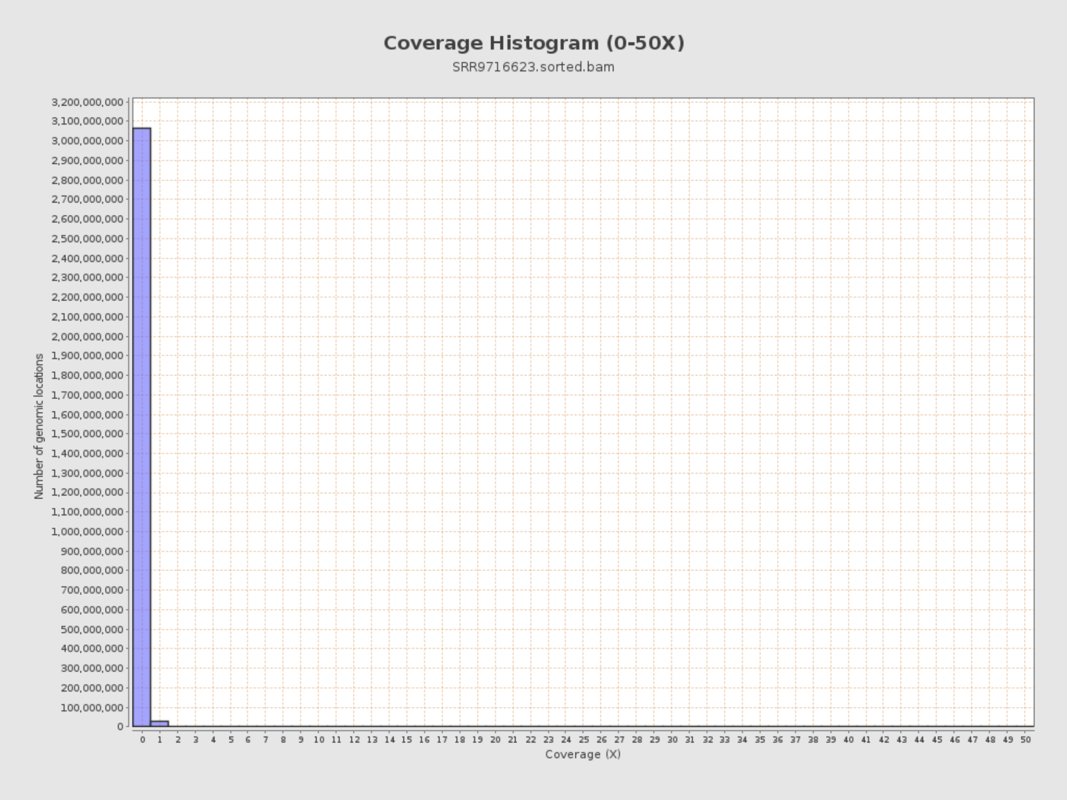
3. Results : Coverage across reference



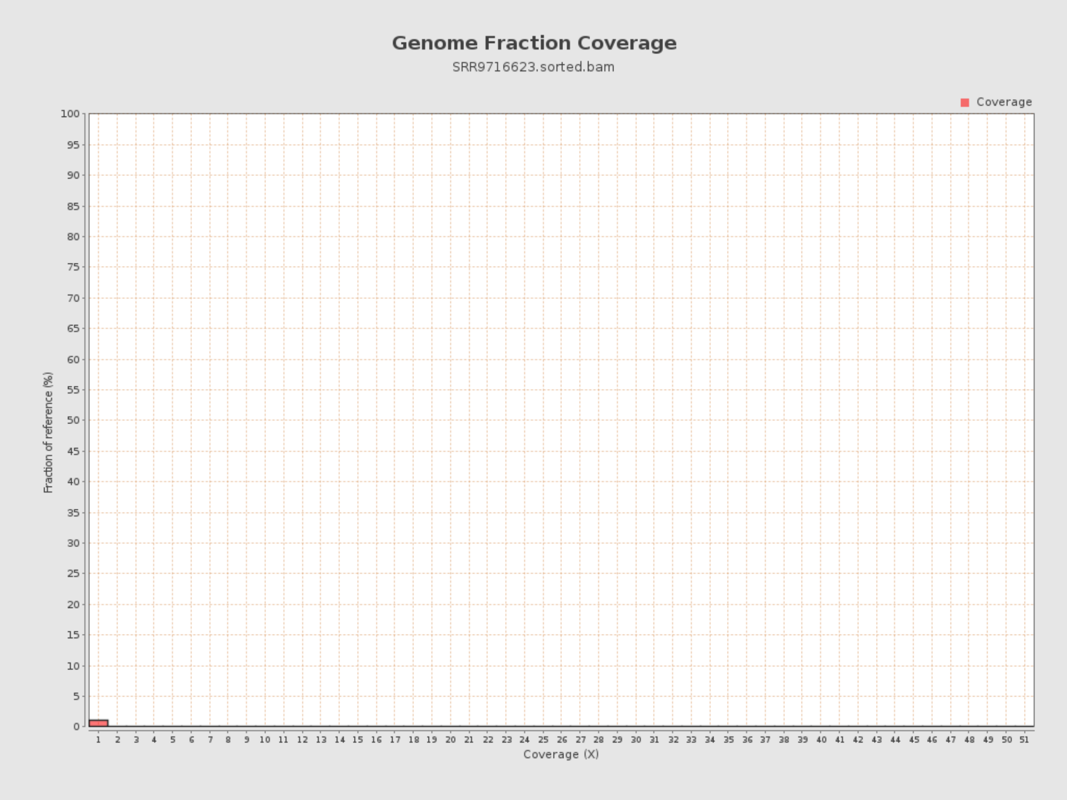
4. Results : Coverage Histogram



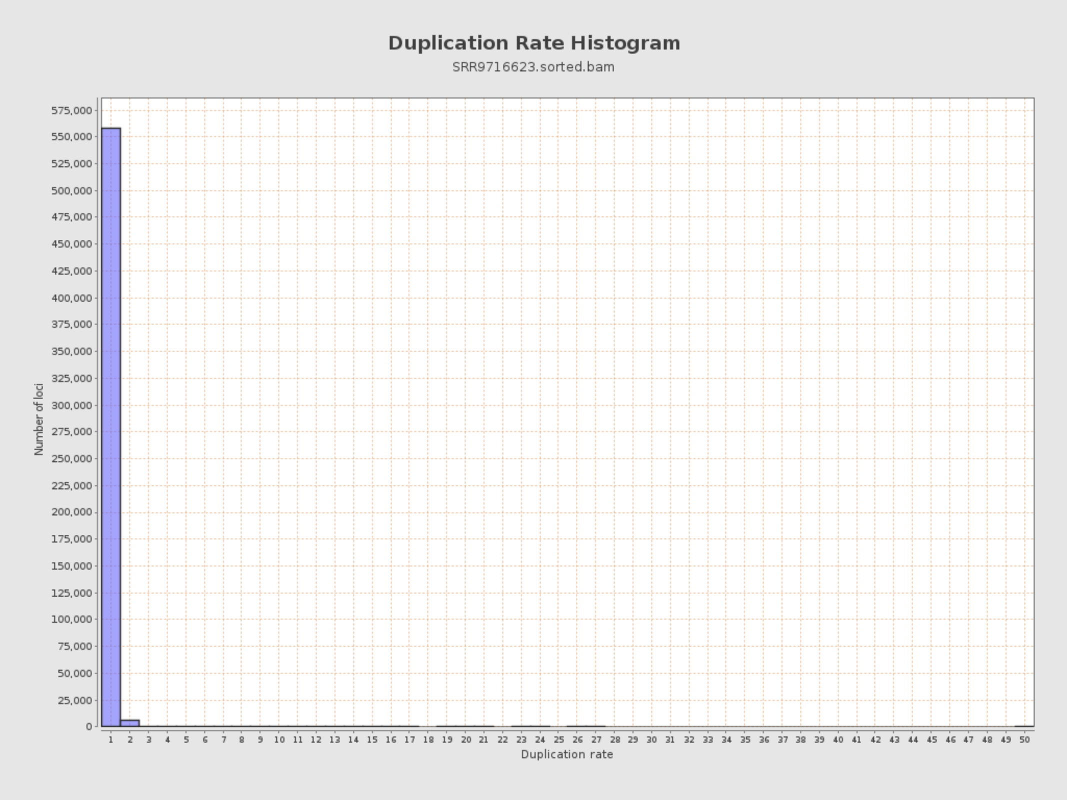
5. Results : Coverage Histogram (0-50X)



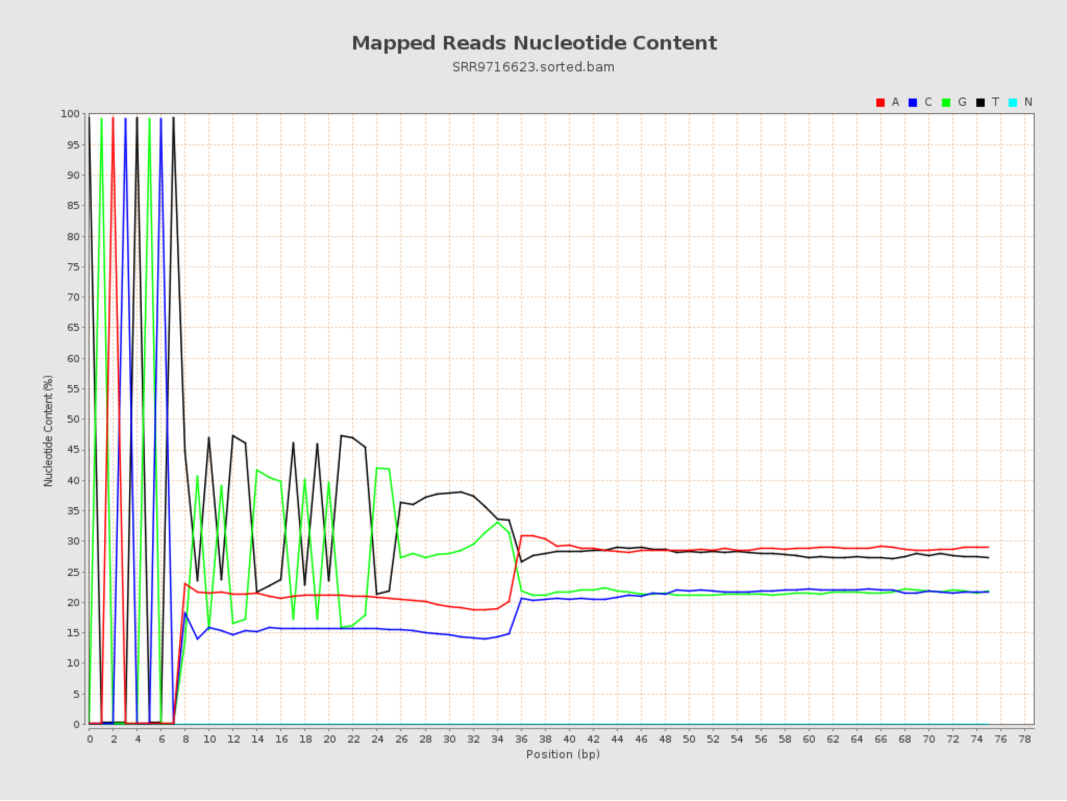
6. Results : Genome Fraction Coverage



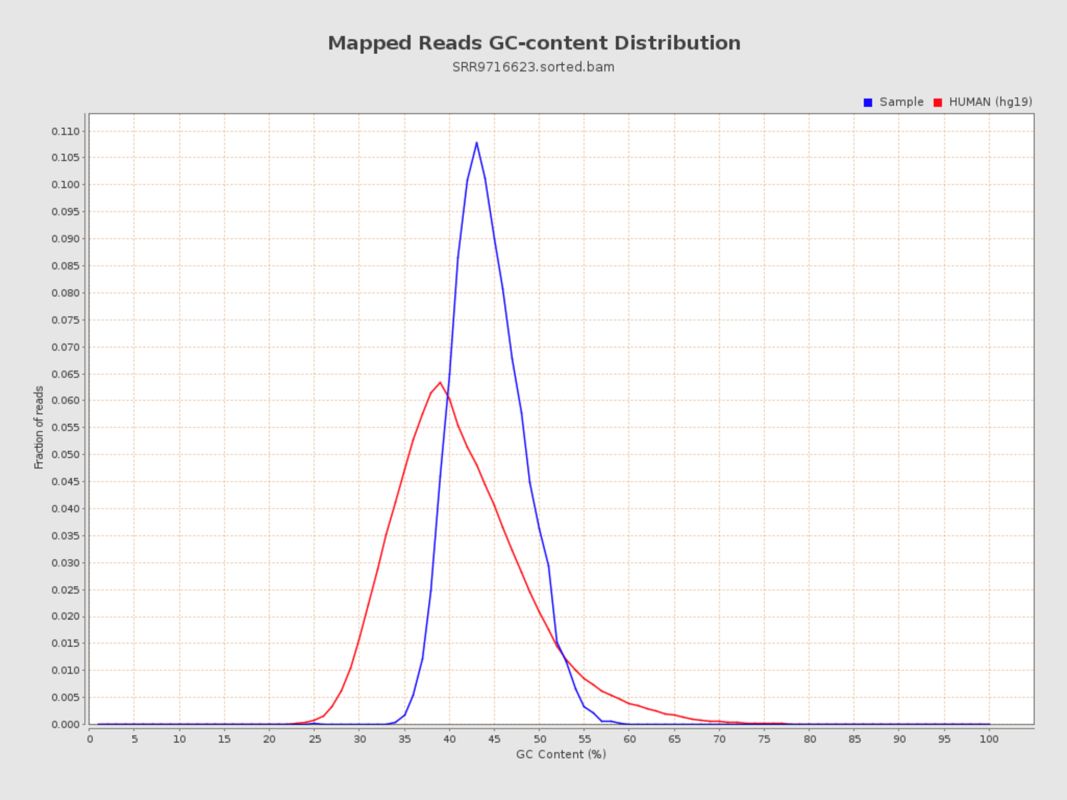
7. Results : Duplication Rate Histogram



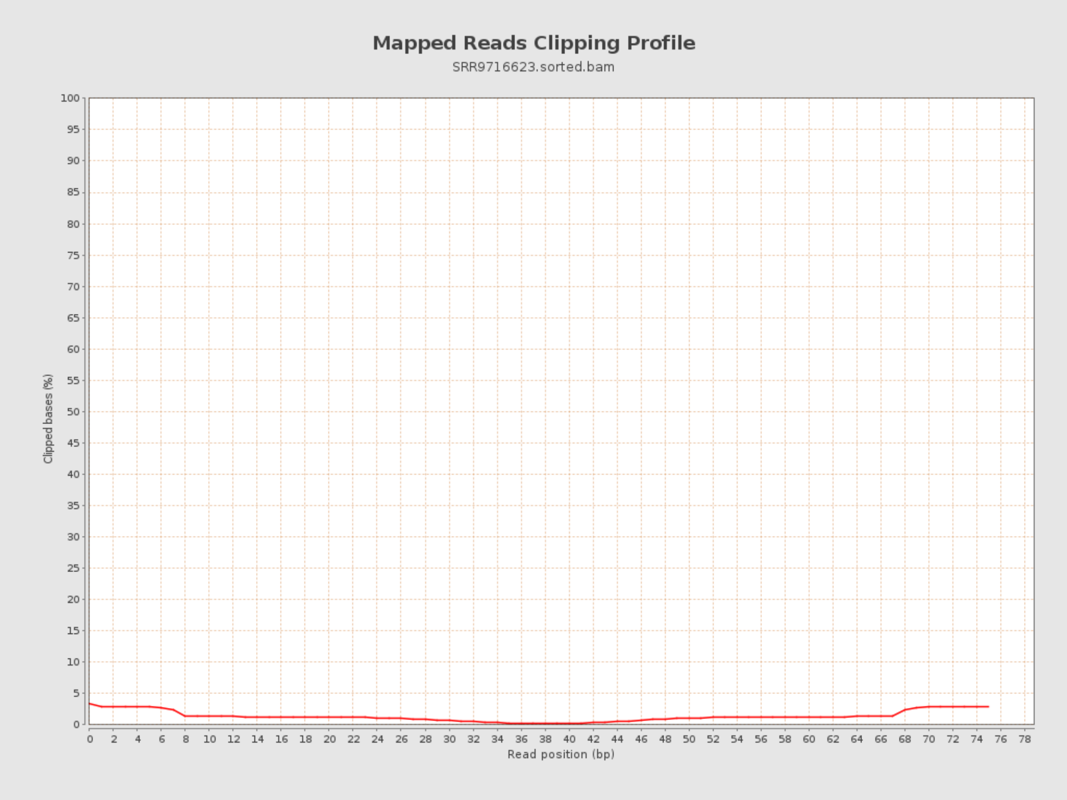
8. Results : Mapped Reads Nucleotide Content



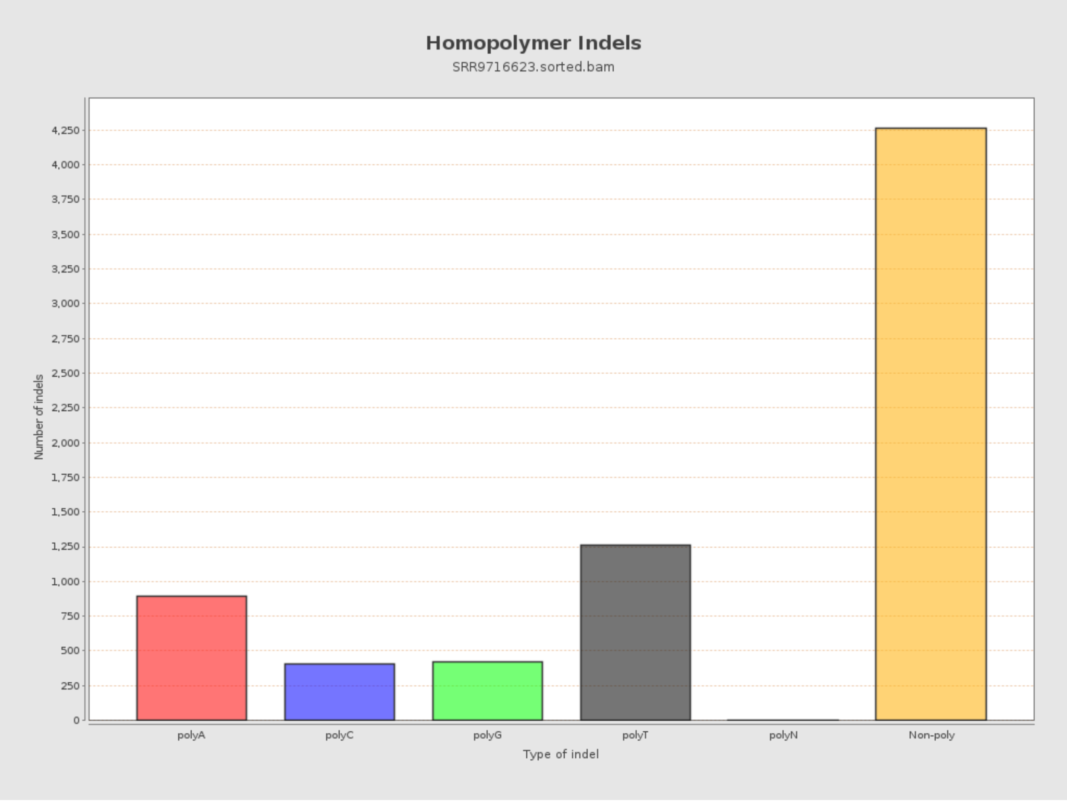
9. Results : Mapped Reads GC-content Distribution



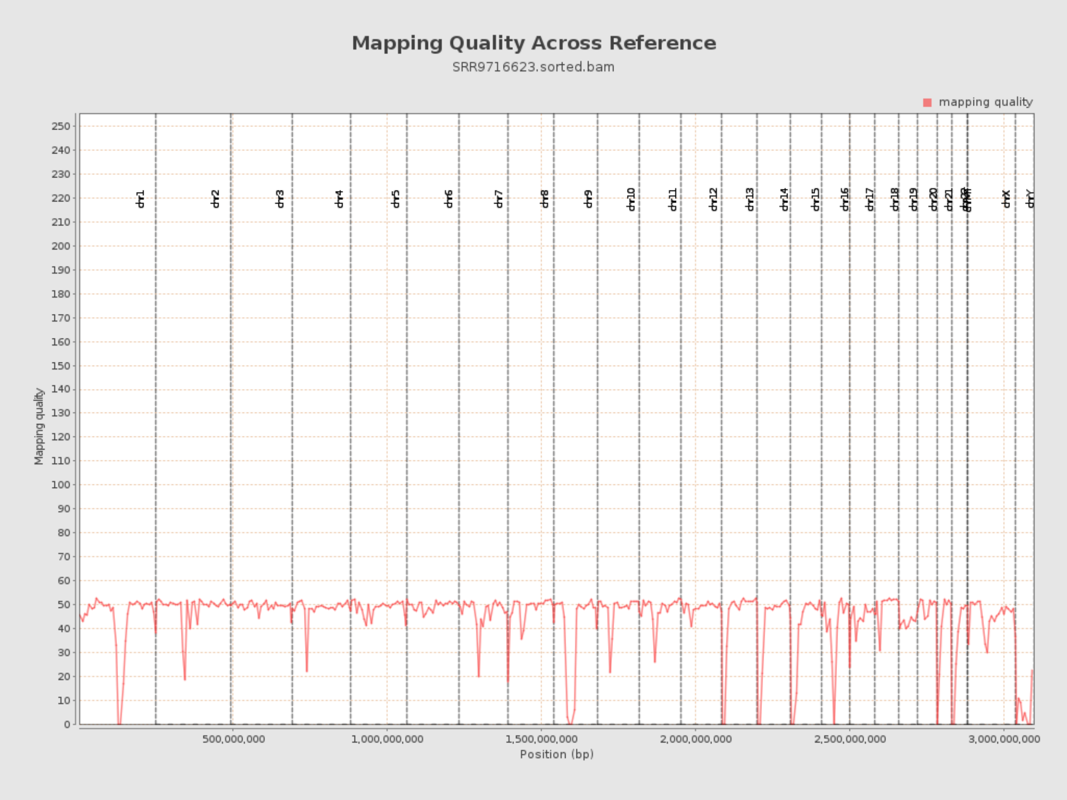
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram