Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 00:17:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716608.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_SRR9716608 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716608.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 00:17:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716608.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,046,879
Mapped reads	914,113 / 87.32%
Unmapped reads	132,766 / 12.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,181 / 2.6%
Read min/max/mean length	30 / 101 / 101.94
Duplicated reads (estimated)	18,175 / 1.74%
Duplication rate	1.24%
Clipped reads	940,783 / 89.87%

2.2. ACGT Content

Number/percentage of A's	17,673,168 / 25.64%
Number/percentage of C's	14,216,519 / 20.63%
Number/percentage of T's	20,683,873 / 30.01%
Number/percentage of G's	16,339,293 / 23.71%
Number/percentage of N's	8,439 / 0.01%
GC Percentage	44.33%

2.3. Coverage

Mean	0.0223

Standard Deviation	0.2135

2.4. Mapping Quality

Mean Mapping Quality	44.62

2.5. Mismatches and indels

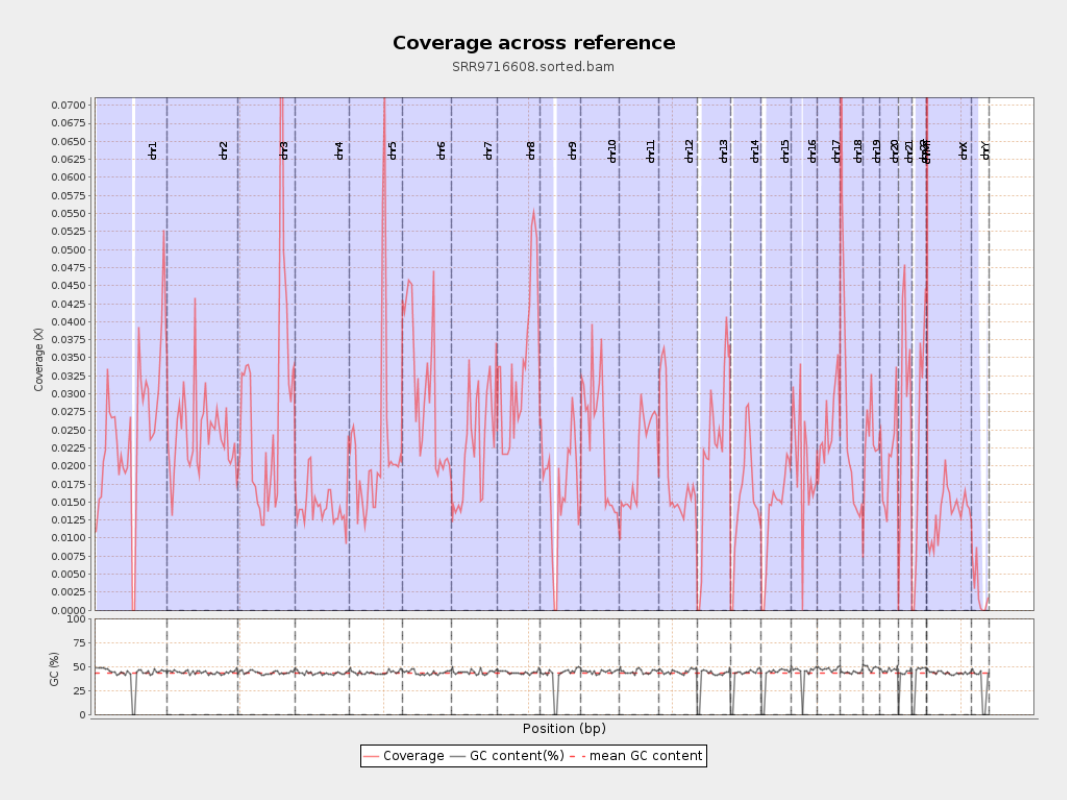
General error rate	0.8%
Mismatches	542,733
Insertions	5,391
Mapped reads with at least one insertion	0.58%
Deletions	15,329
Mapped reads with at least one deletion	1.65%
Homopolymer indels	41.59%

2.6. Chromosome stats

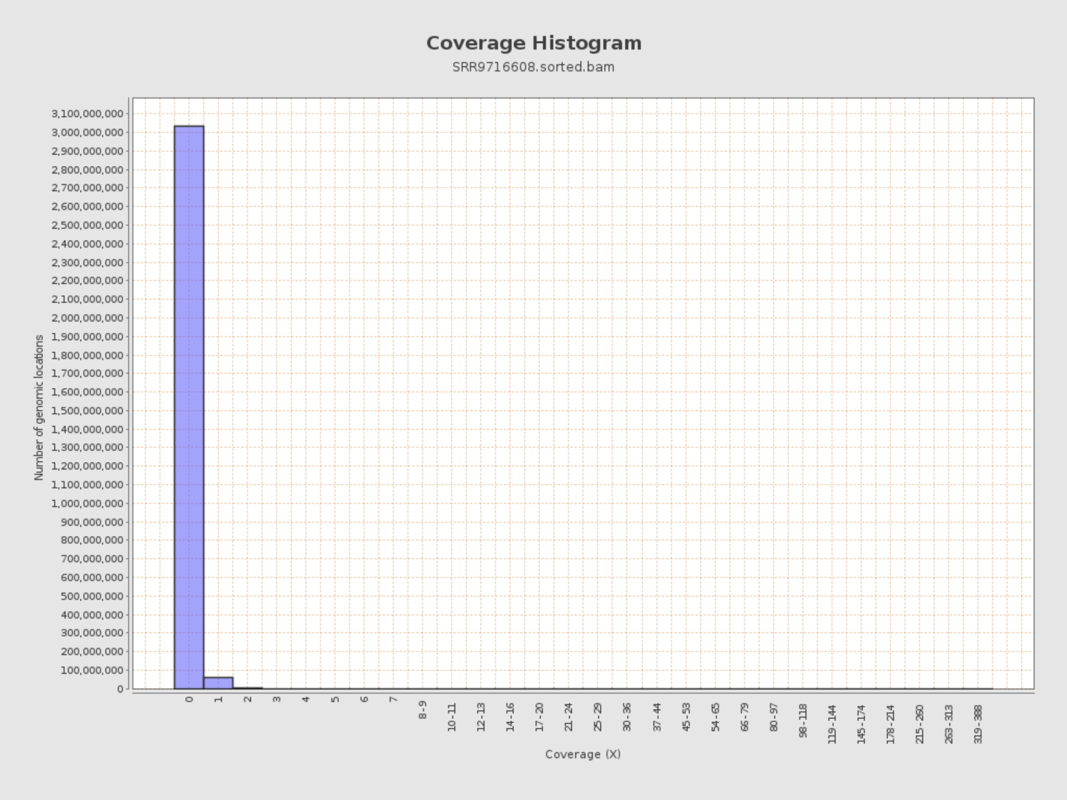
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6192971	0.0248	0.2789
chr2	243199373	5923736	0.0244	0.3217
chr3	198022430	5632414	0.0284	0.1807
chr4	191154276	2820067	0.0148	0.1336
chr5	180915260	4133434	0.0228	0.1611
chr6	171115067	5165827	0.0302	0.1978
chr7	159138663	3654903	0.023	0.2665

chr8	146364022	4955817	0.0339	0.2683
chr9	141213431	2418453	0.0171	0.1977
chr10	135534747	3251987	0.024	0.2104
chr11	135006516	2820563	0.0209	0.1874
chr12	133851895	2616099	0.0195	0.1493
chr13	115169878	2613748	0.0227	0.1593
chr14	107349540	1648087	0.0154	0.141
chr15	102531392	1393074	0.0136	0.1244
chr16	90354753	1828395	0.0202	0.1646
chr17	81195210	2077428	0.0256	0.1813
chr18	78077248	2135415	0.0274	0.3576
chr19	59128983	1418498	0.024	0.255
chr20	63025520	1319753	0.0209	0.1628
chr21	48129895	1468320	0.0305	0.1902
chr22	51304566	1169374	0.0228	0.1627
chrMT	16571	12368	0.7464	1.0712
chrX	155270560	2121091	0.0137	0.1438
chrY	59373566	156431	0.0026	0.0847

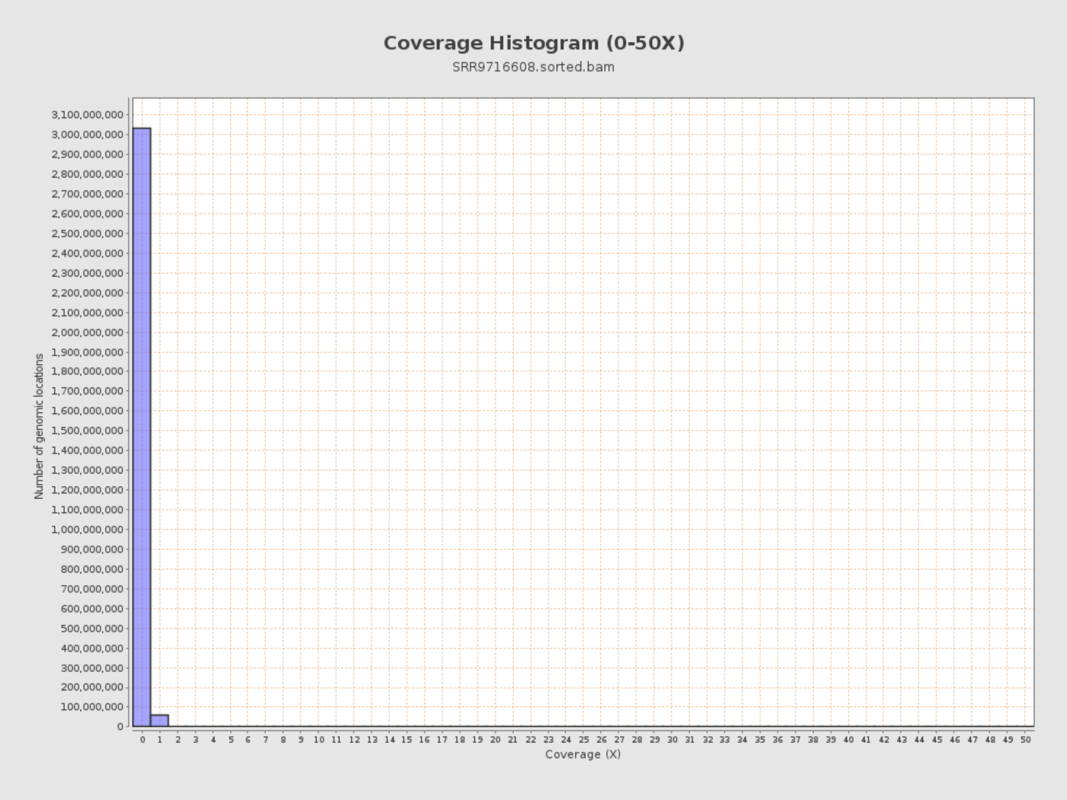
3. Results : Coverage across reference



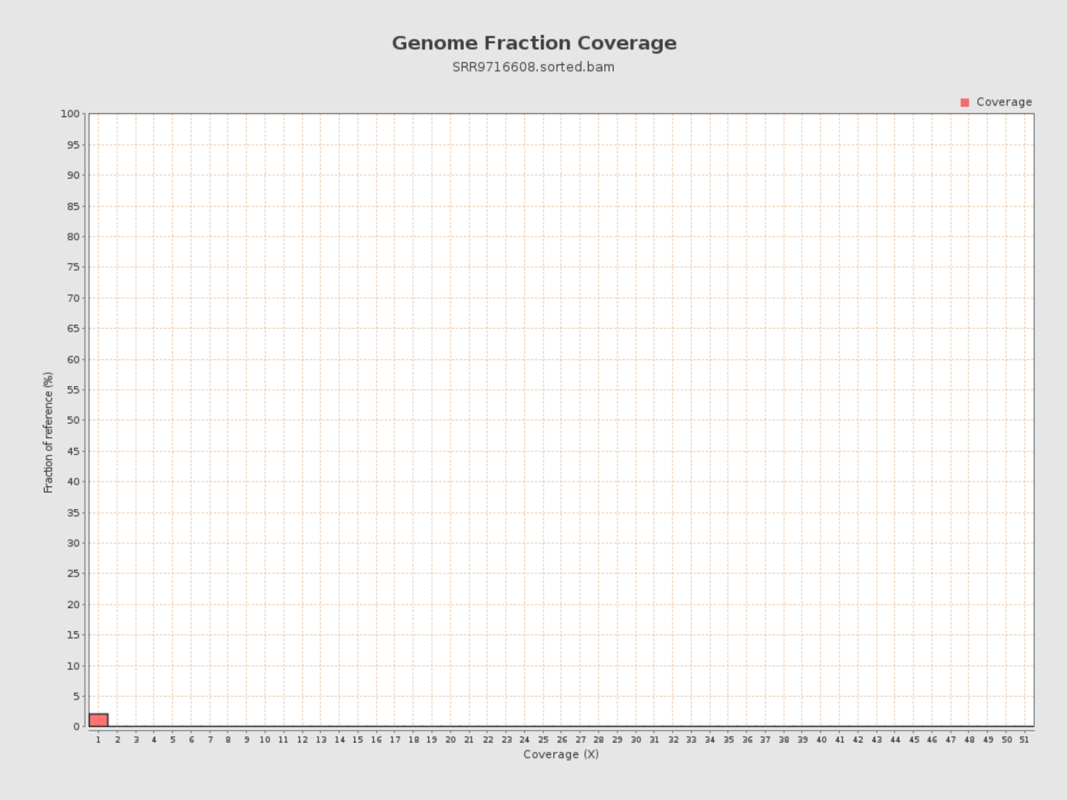
4. Results : Coverage Histogram



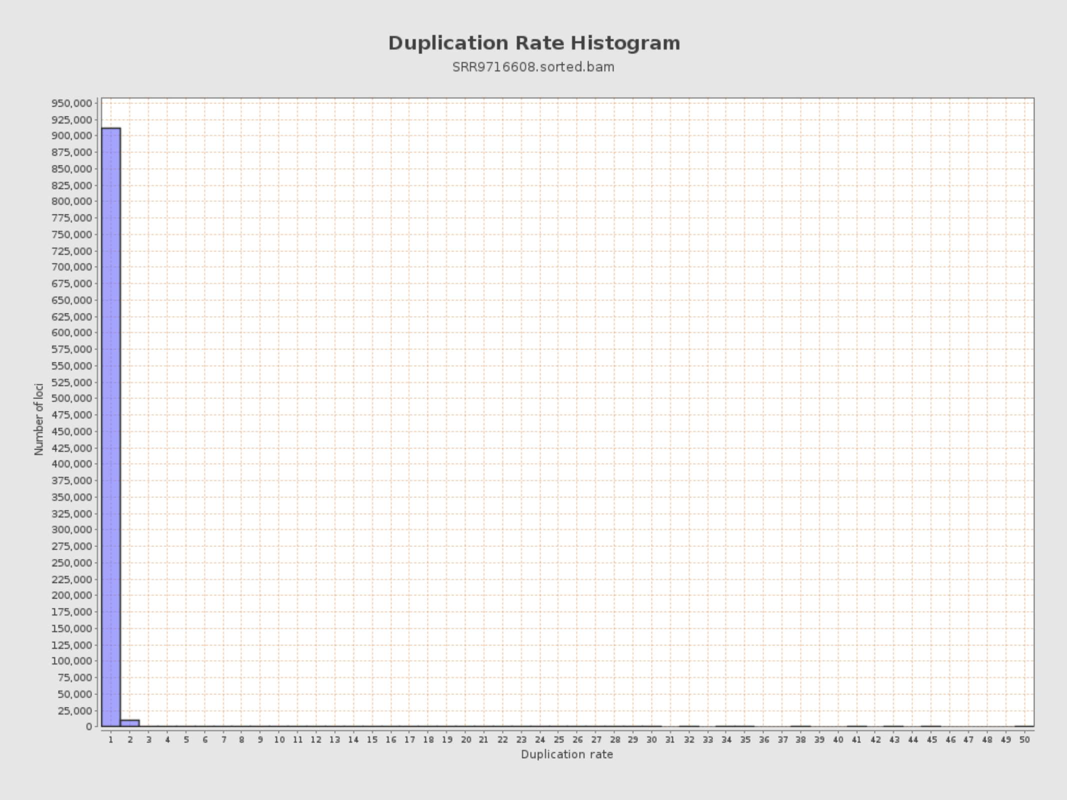
5. Results : Coverage Histogram (0-50X)



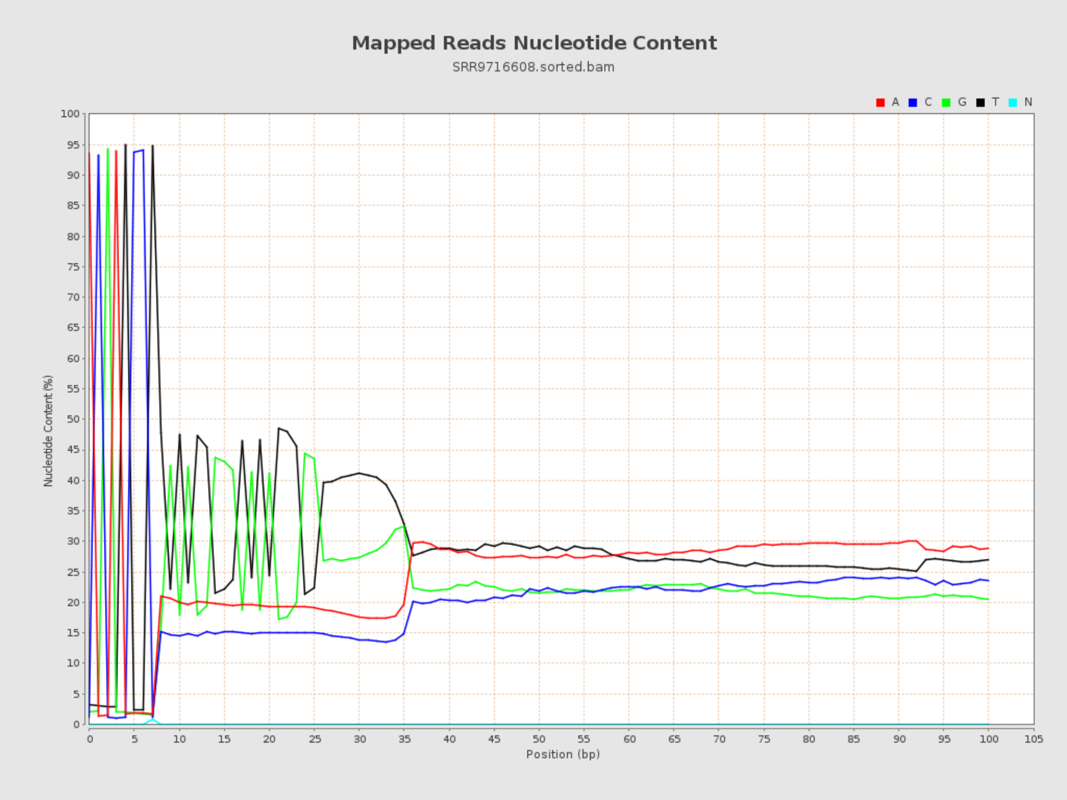
6. Results : Genome Fraction Coverage



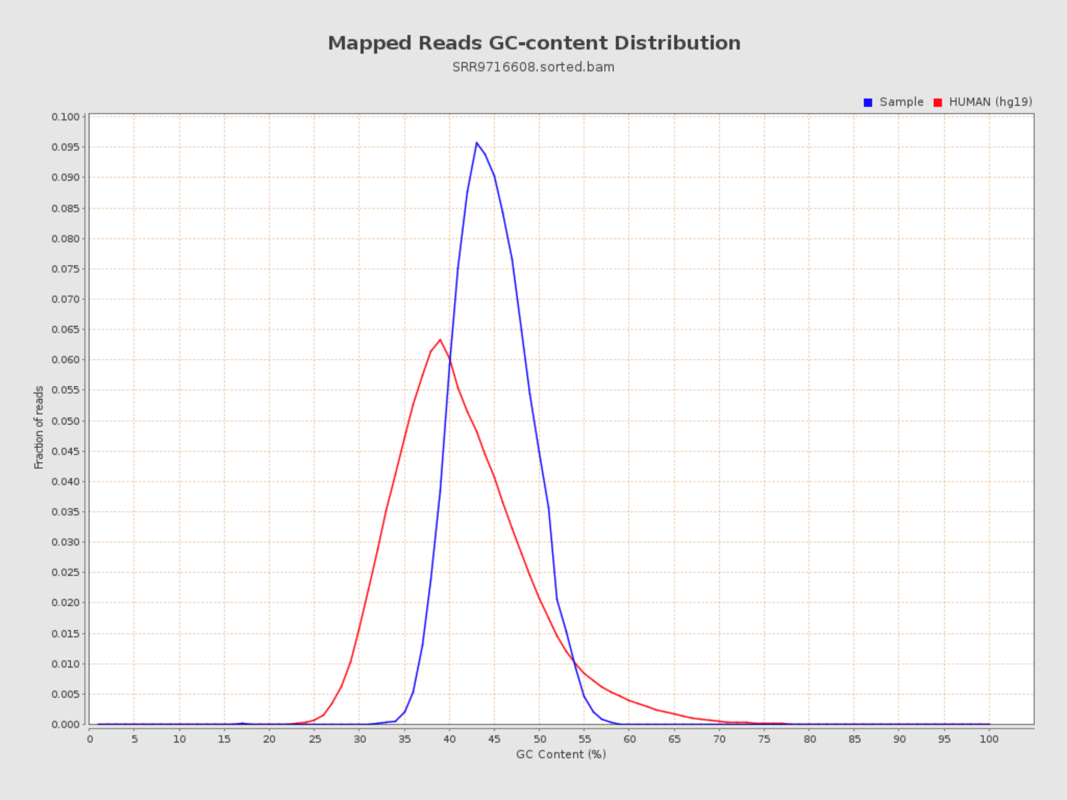
7. Results : Duplication Rate Histogram



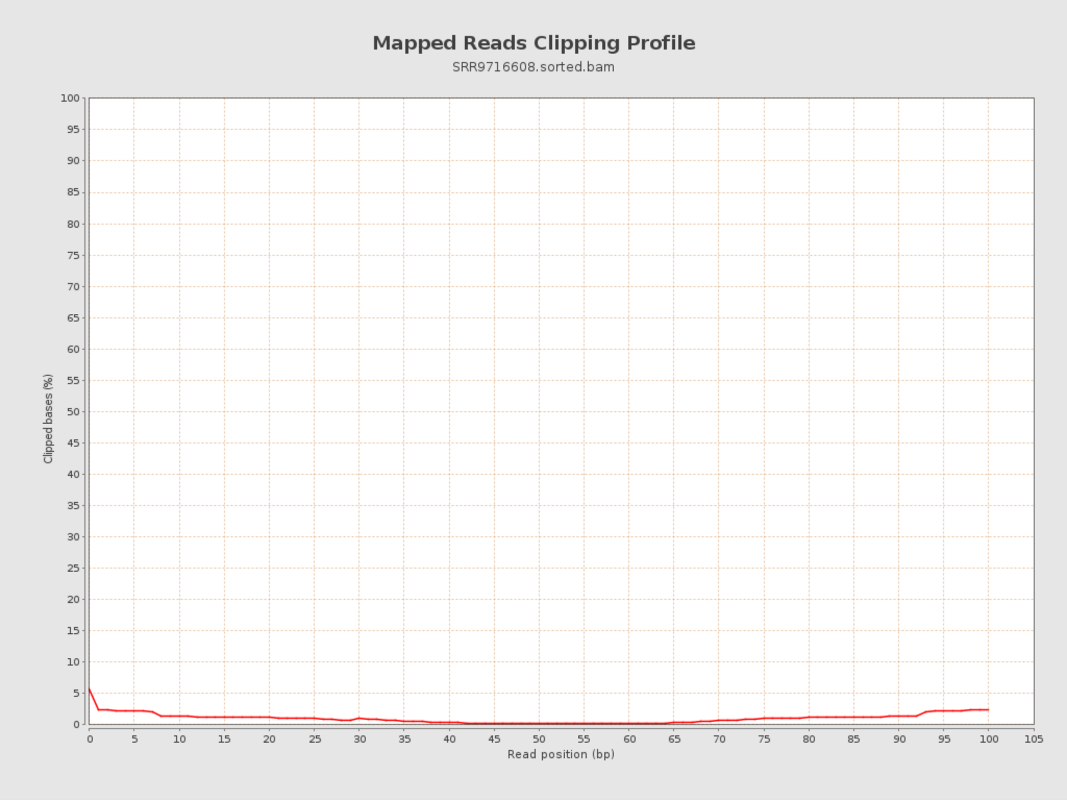
8. Results : Mapped Reads Nucleotide Content



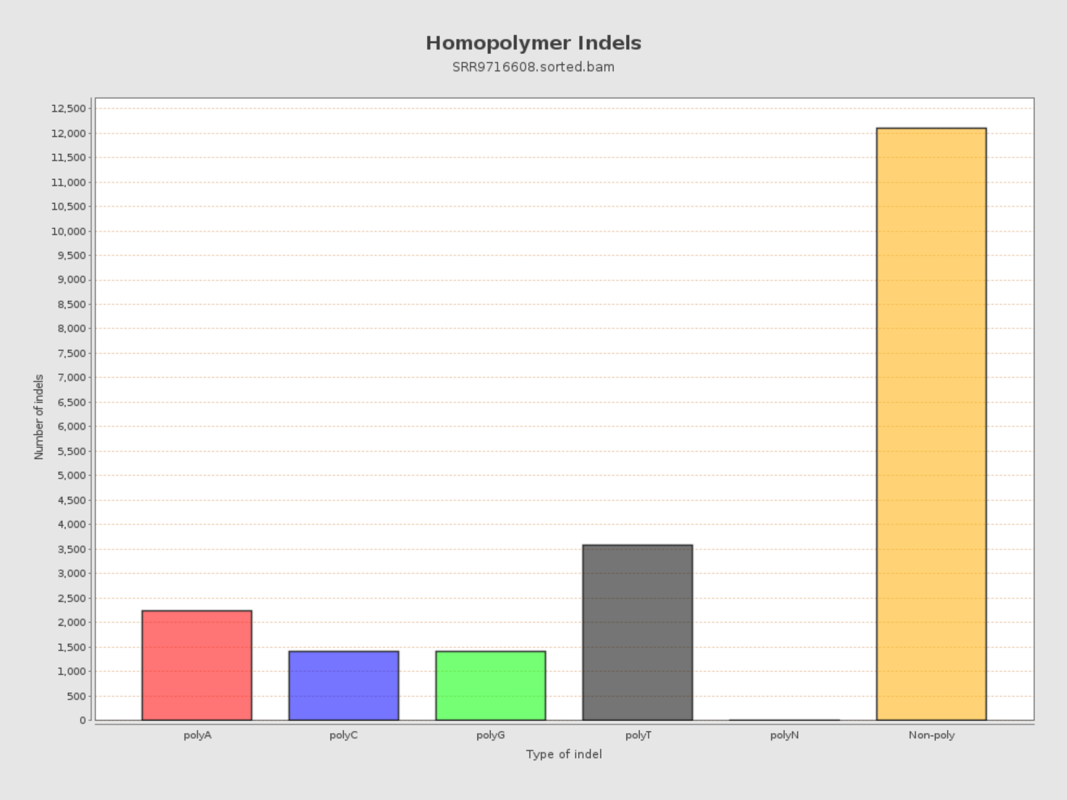
9. Results : Mapped Reads GC-content Distribution



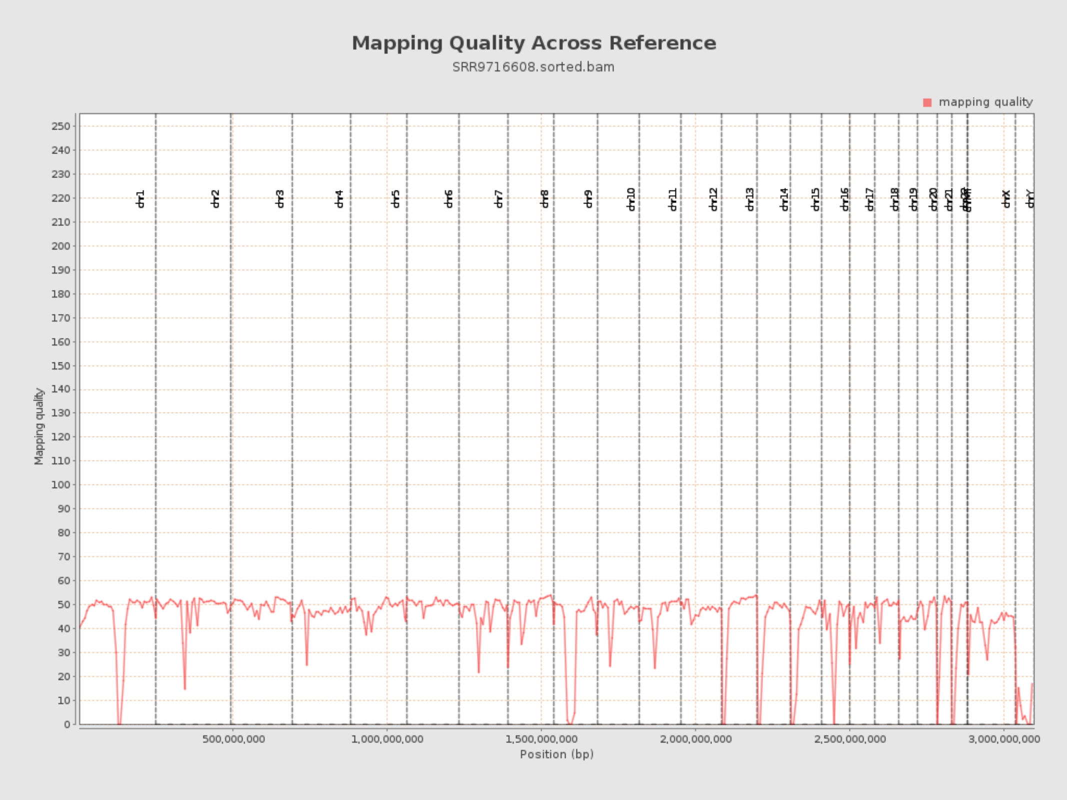
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram