Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 22:14:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716172.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_SRR9716172 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716172.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 22:14:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716172.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	552,945
Mapped reads	514,205 / 92.99%
Unmapped reads	38,740 / 7.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,743 / 1.94%
Read min/max/mean length	30 / 101 / 101.7
Duplicated reads (estimated)	10,146 / 1.83%
Duplication rate	1.41%
Clipped reads	524,528 / 94.86%

2.2. ACGT Content

Number/percentage of A's	10,387,297 / 25.66%
Number/percentage of C's	7,700,683 / 19.03%
Number/percentage of T's	12,199,021 / 30.14%
Number/percentage of G's	10,183,129 / 25.16%
Number/percentage of N's	3,188 / 0.01%
GC Percentage	44.19%

2.3. Coverage

Mean	0.0131

Standard Deviation	0.153

2.4. Mapping Quality

Mean Mapping Quality	47.31

2.5. Mismatches and indels

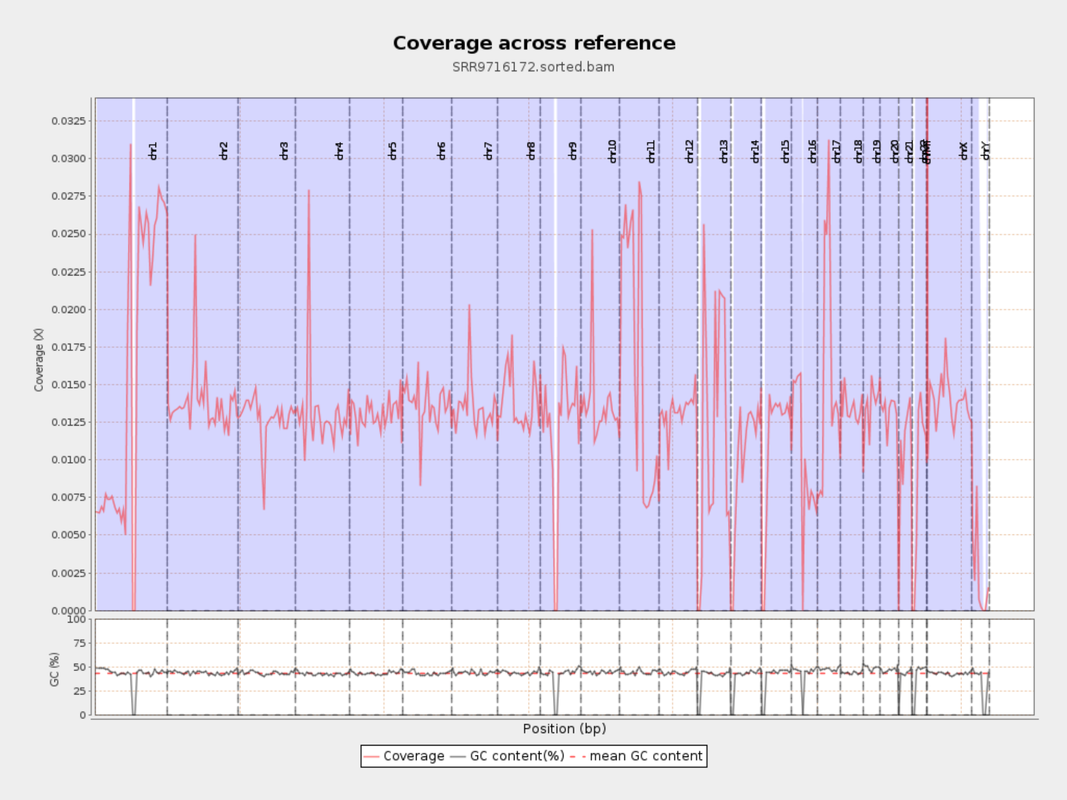
General error rate	0.66%
Mismatches	257,514
Insertions	3,199
Mapped reads with at least one insertion	0.61%
Deletions	9,164
Mapped reads with at least one deletion	1.75%
Homopolymer indels	44.72%

2.6. Chromosome stats

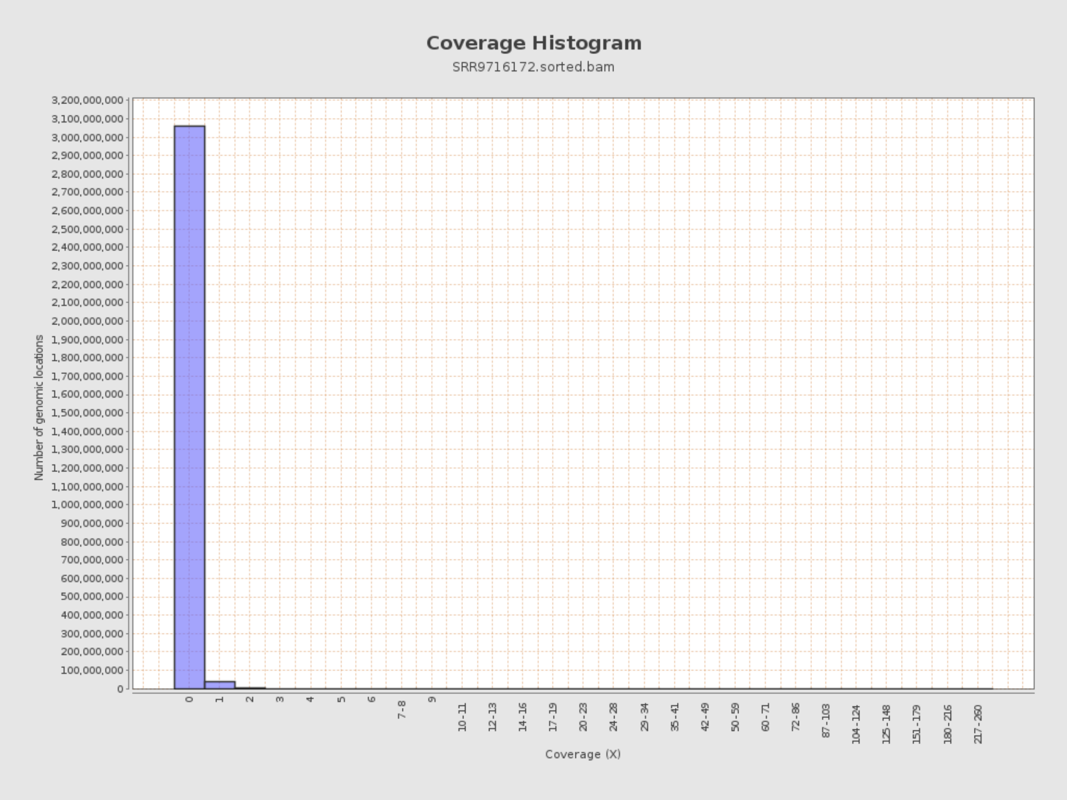
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3889986	0.0156	0.2659
chr2	243199373	3376999	0.0139	0.1616
chr3	198022430	2526363	0.0128	0.1174
chr4	191154276	2524808	0.0132	0.1346
chr5	180915260	2374920	0.0131	0.1194
chr6	171115067	2339347	0.0137	0.1262
chr7	159138663	2156917	0.0136	0.1771

chr8	146364022	2018953	0.0138	0.1612
chr9	141213431	1713297	0.0121	0.1359
chr10	135534747	1862948	0.0137	0.1561
chr11	135006516	2287642	0.0169	0.167
chr12	133851895	1772587	0.0132	0.1196
chr13	115169878	1349588	0.0117	0.1124
chr14	107349540	1076082	0.01	0.106
chr15	102531392	1128447	0.011	0.1091
chr16	90354753	897562	0.0099	0.107
chr17	81195210	1260775	0.0155	0.1388
chr18	78077248	1049899	0.0134	0.1873
chr19	59128983	807499	0.0137	0.1944
chr20	63025520	822573	0.0131	0.1211
chr21	48129895	507819	0.0106	0.1172
chr22	51304566	454586	0.0089	0.0976
chrMT	16571	2897	0.1748	0.4177
chrX	155270560	2164273	0.0139	0.1295
chrY	59373566	124356	0.0021	0.0867

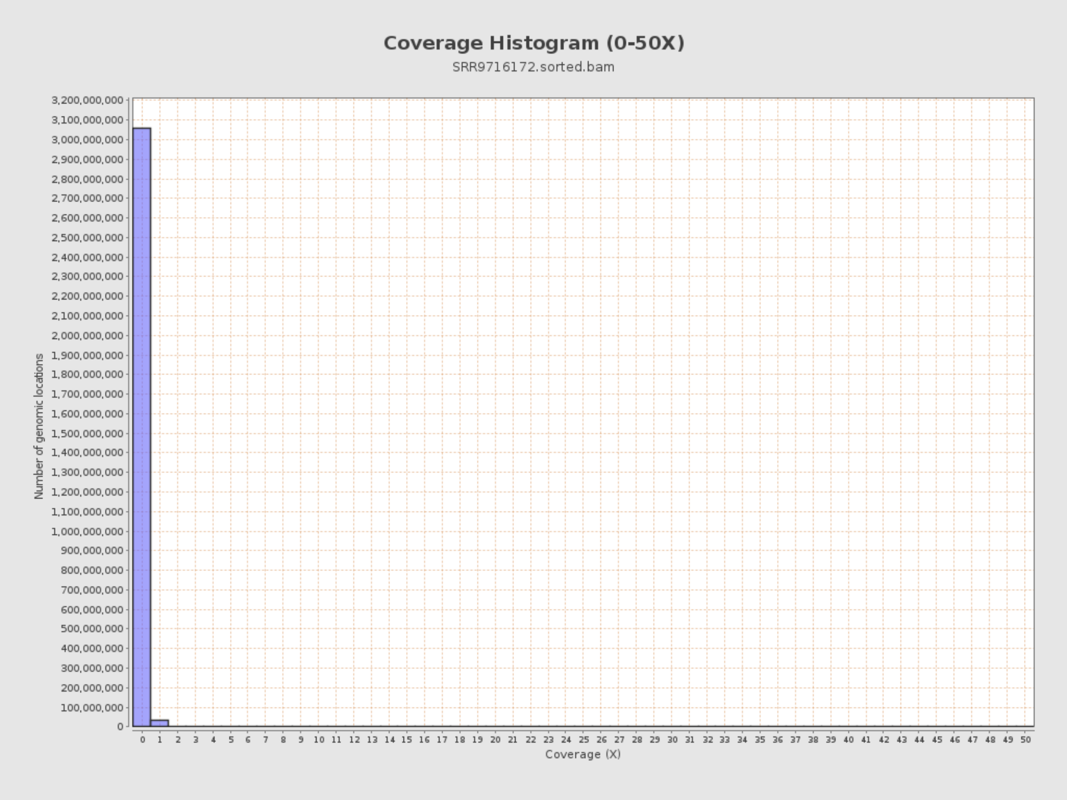
3. Results : Coverage across reference



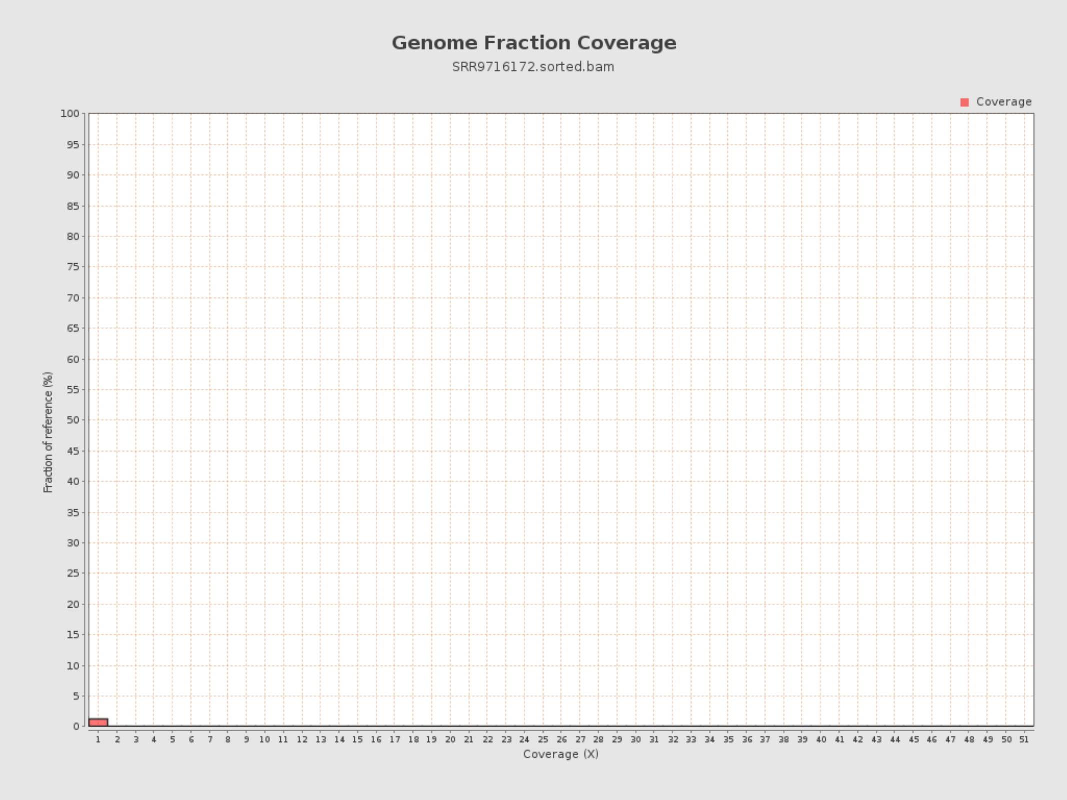
4. Results : Coverage Histogram



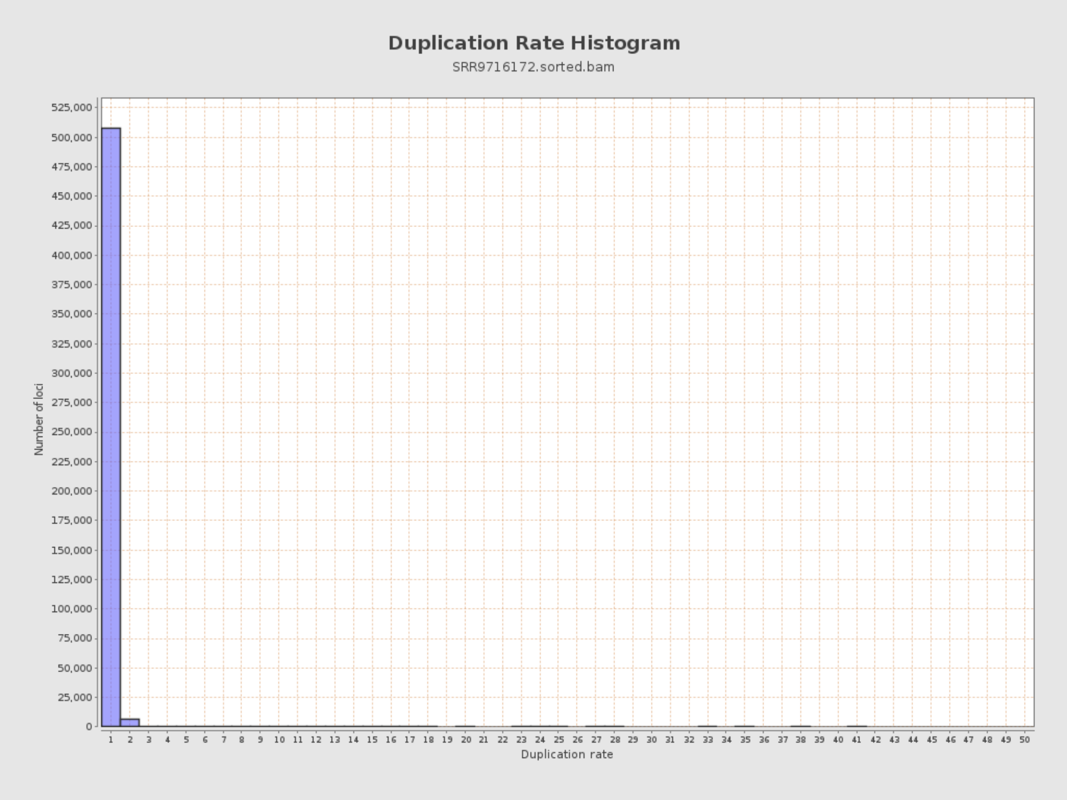
5. Results : Coverage Histogram (0-50X)



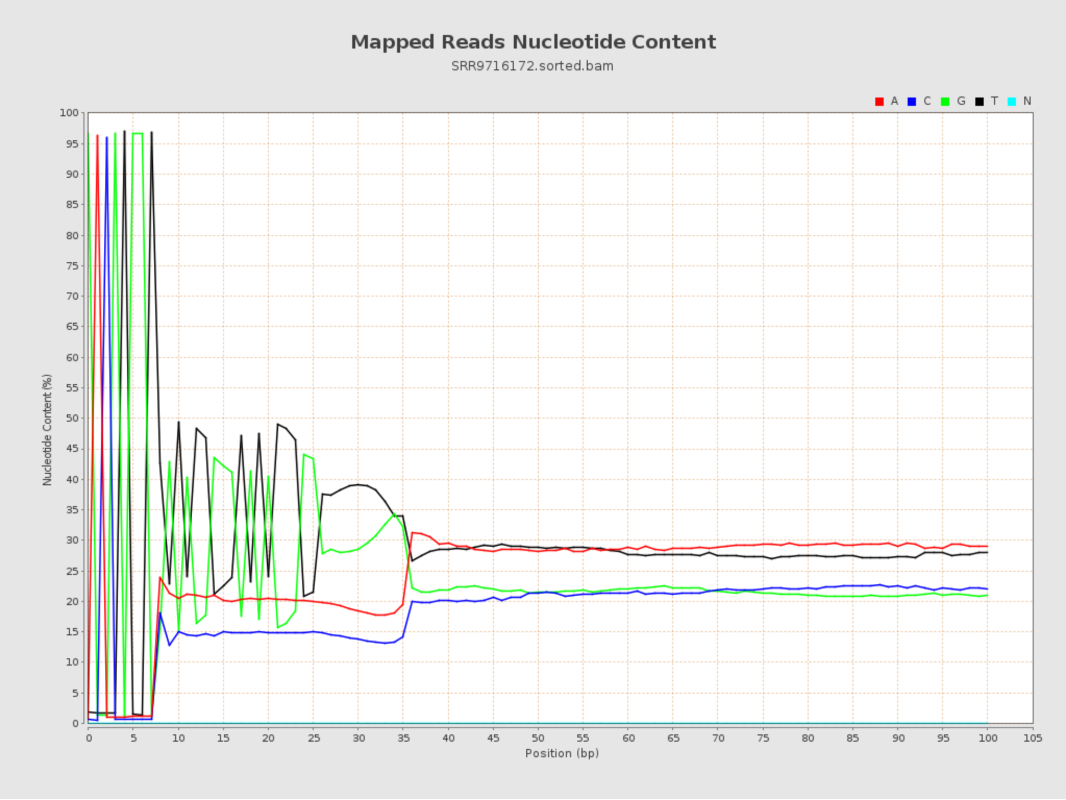
6. Results : Genome Fraction Coverage



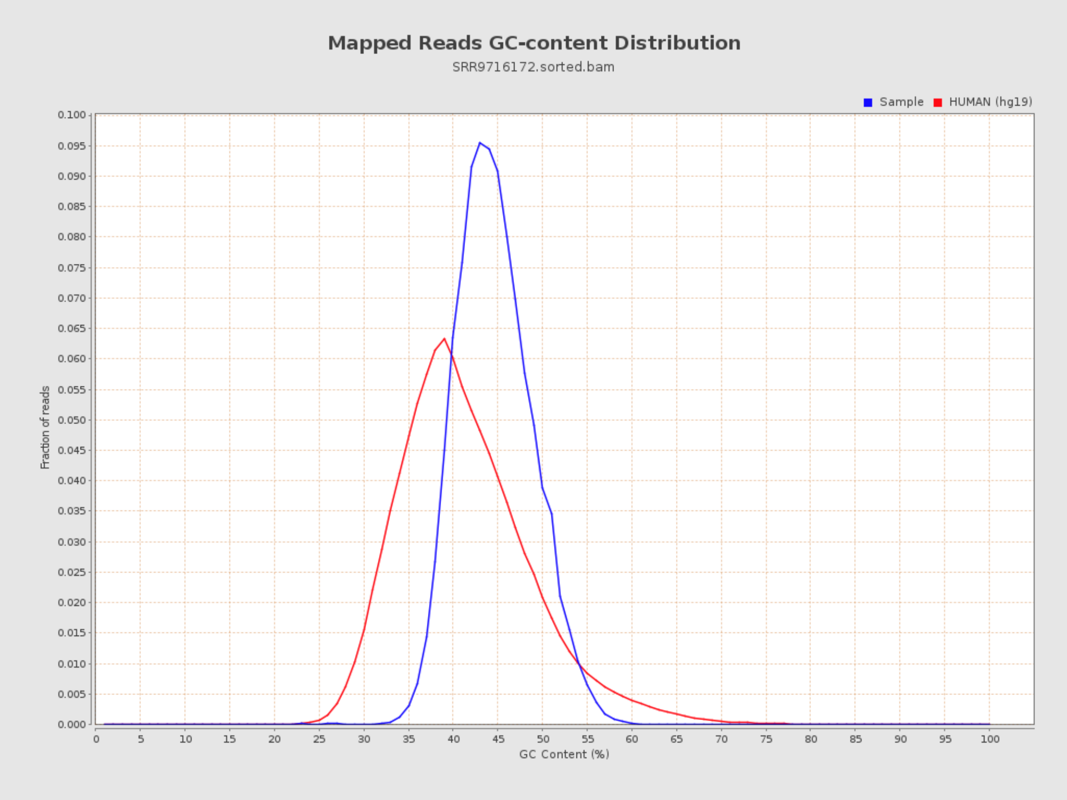
7. Results : Duplication Rate Histogram



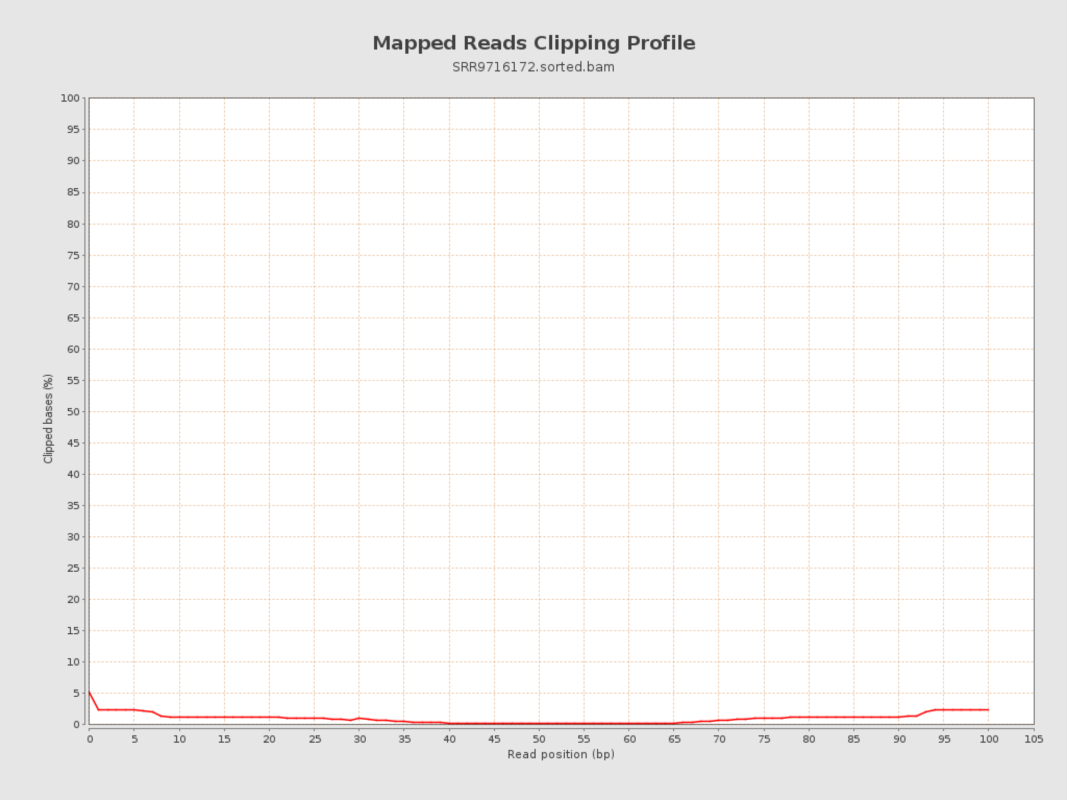
8. Results : Mapped Reads Nucleotide Content



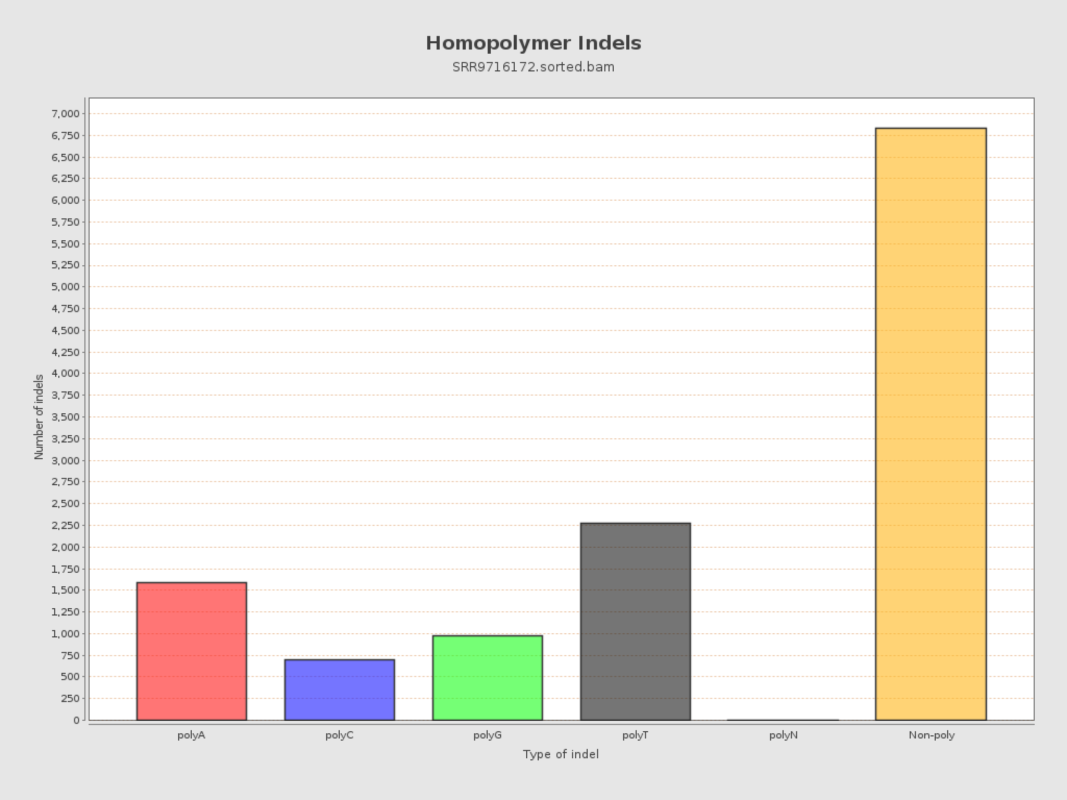
9. Results : Mapped Reads GC-content Distribution



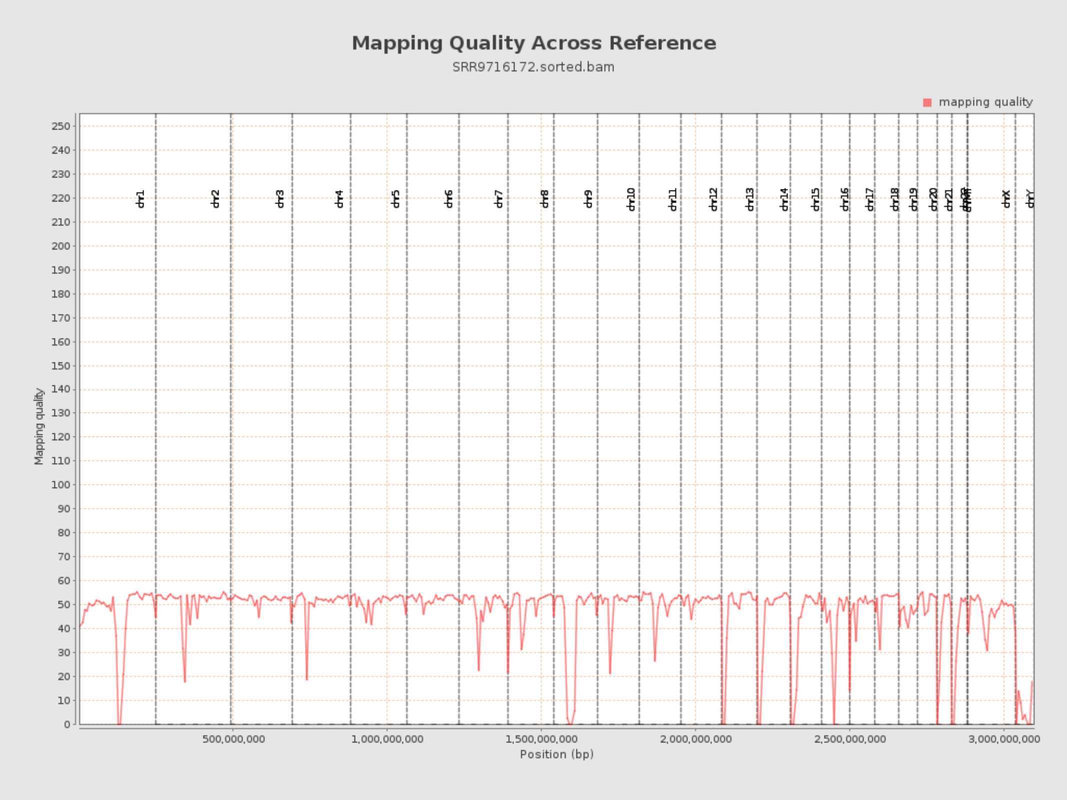
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram