Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 23:00:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716189.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_SRR9716189 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716189.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 23:00:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716189.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	497,856
Mapped reads	441,512 / 88.68%
Unmapped reads	56,344 / 11.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,703 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	5,205 / 1.05%
Duplication rate	0.85%
Clipped reads	442,033 / 88.79%

2.2. ACGT Content

Number/percentage of A's	6,094,072 / 23.88%
Number/percentage of C's	4,867,353 / 19.07%
Number/percentage of T's	8,033,573 / 31.48%
Number/percentage of G's	6,528,131 / 25.58%
Number/percentage of N's	171 / 0%
GC Percentage	44.65%

2.3. Coverage

Mean	0.0082

Standard Deviation	0.1033

2.4. Mapping Quality

Mean Mapping Quality	42

2.5. Mismatches and indels

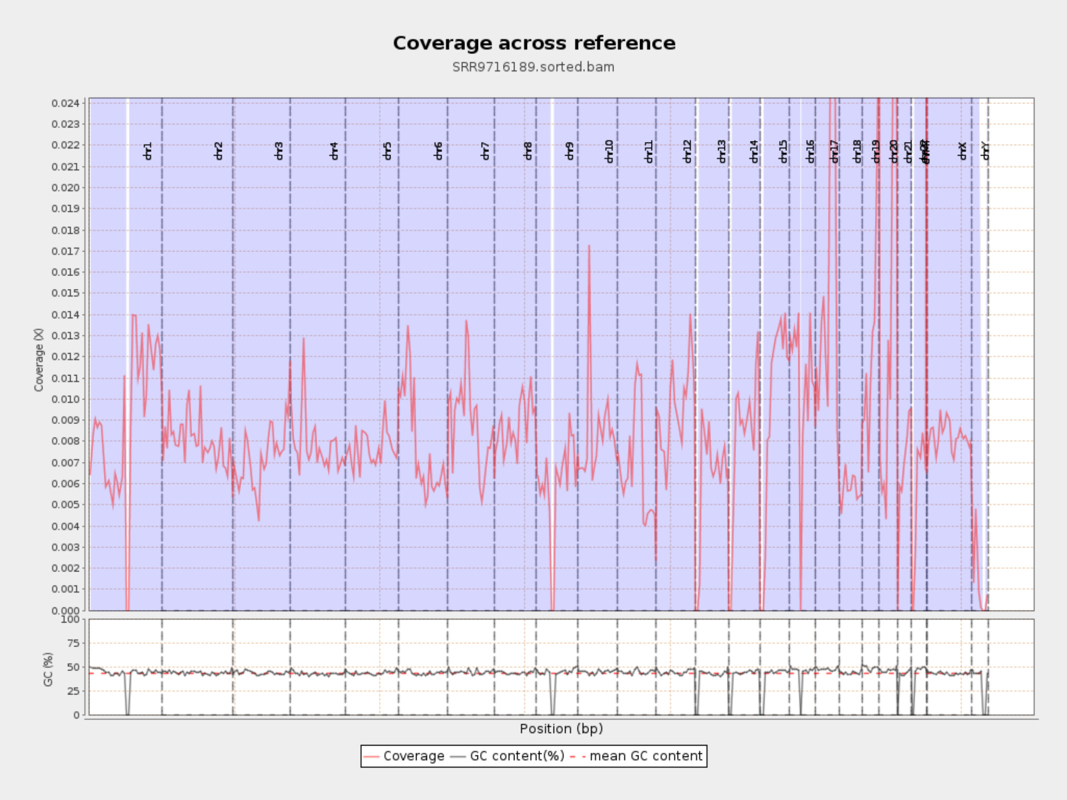
General error rate	0.54%
Mismatches	135,619
Insertions	1,913
Mapped reads with at least one insertion	0.43%
Deletions	4,976
Mapped reads with at least one deletion	1.12%
Homopolymer indels	39.13%

2.6. Chromosome stats

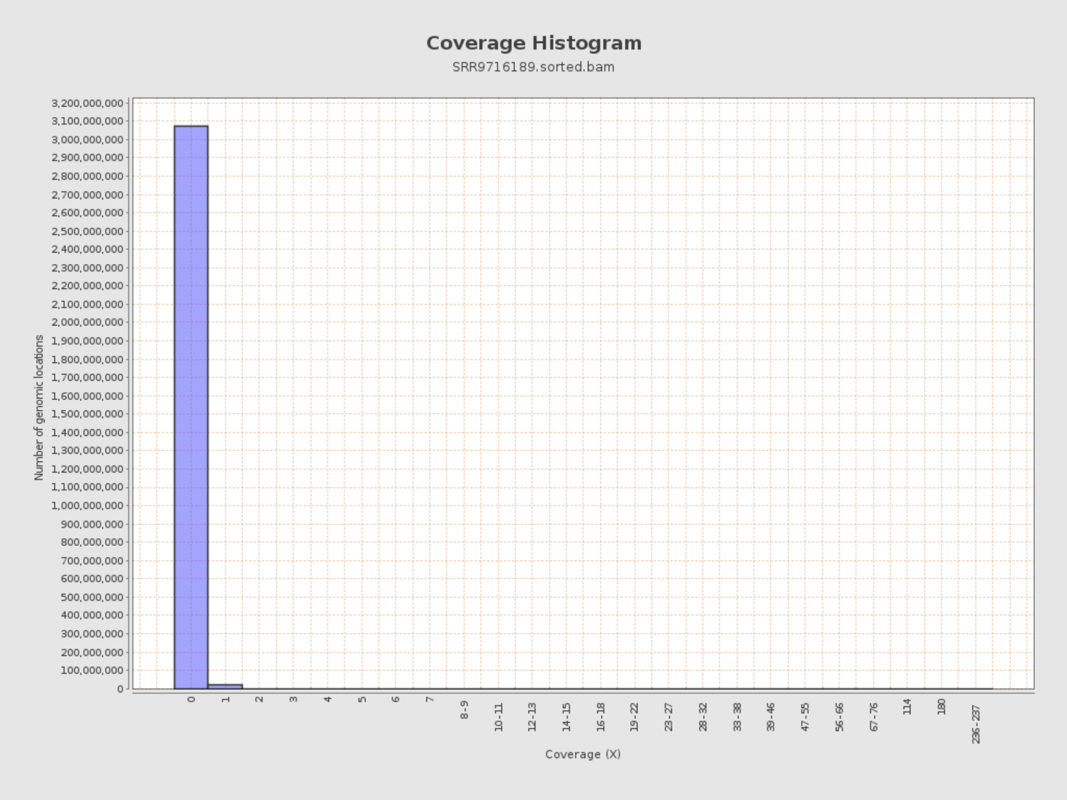
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2202054	0.0088	0.1142
chr2	243199373	1958243	0.0081	0.1328
chr3	198022430	1421407	0.0072	0.0875
chr4	191154276	1492161	0.0078	0.0934
chr5	180915260	1389290	0.0077	0.0896
chr6	171115067	1333829	0.0078	0.0959
chr7	159138663	1417870	0.0089	0.1215

chr8	146364022	1286851	0.0088	0.1017
chr9	141213431	835771	0.0059	0.0829
chr10	135534747	1124582	0.0083	0.1191
chr11	135006516	924657	0.0068	0.0902
chr12	133851895	1280225	0.0096	0.1002
chr13	115169878	711401	0.0062	0.0803
chr14	107349540	863599	0.008	0.0929
chr15	102531392	972991	0.0095	0.0999
chr16	90354753	968546	0.0107	0.109
chr17	81195210	1278780	0.0157	0.1311
chr18	78077248	449982	0.0058	0.0974
chr19	59128983	784943	0.0133	0.1304
chr20	63025520	884627	0.014	0.1239
chr21	48129895	325295	0.0068	0.087
chr22	51304566	271834	0.0053	0.0744
chrMT	16571	1122	0.0677	0.2669
chrX	155270560	1271421	0.0082	0.0941
chrY	59373566	80048	0.0013	0.0551

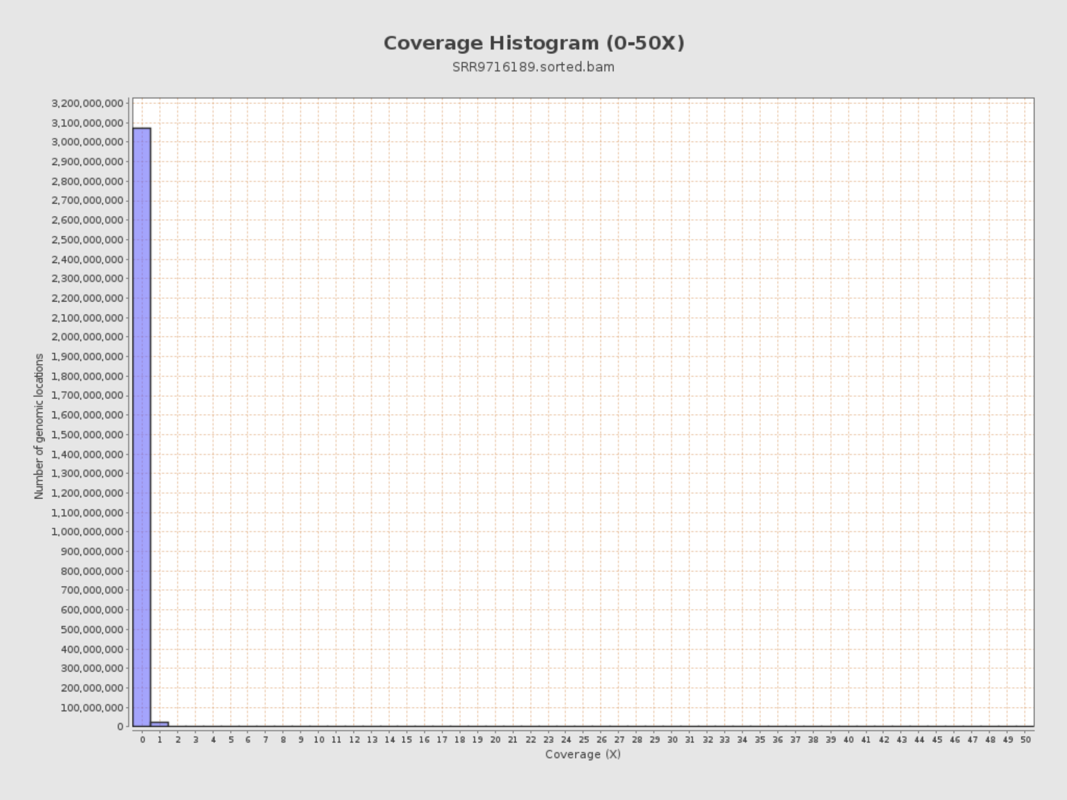
3. Results : Coverage across reference



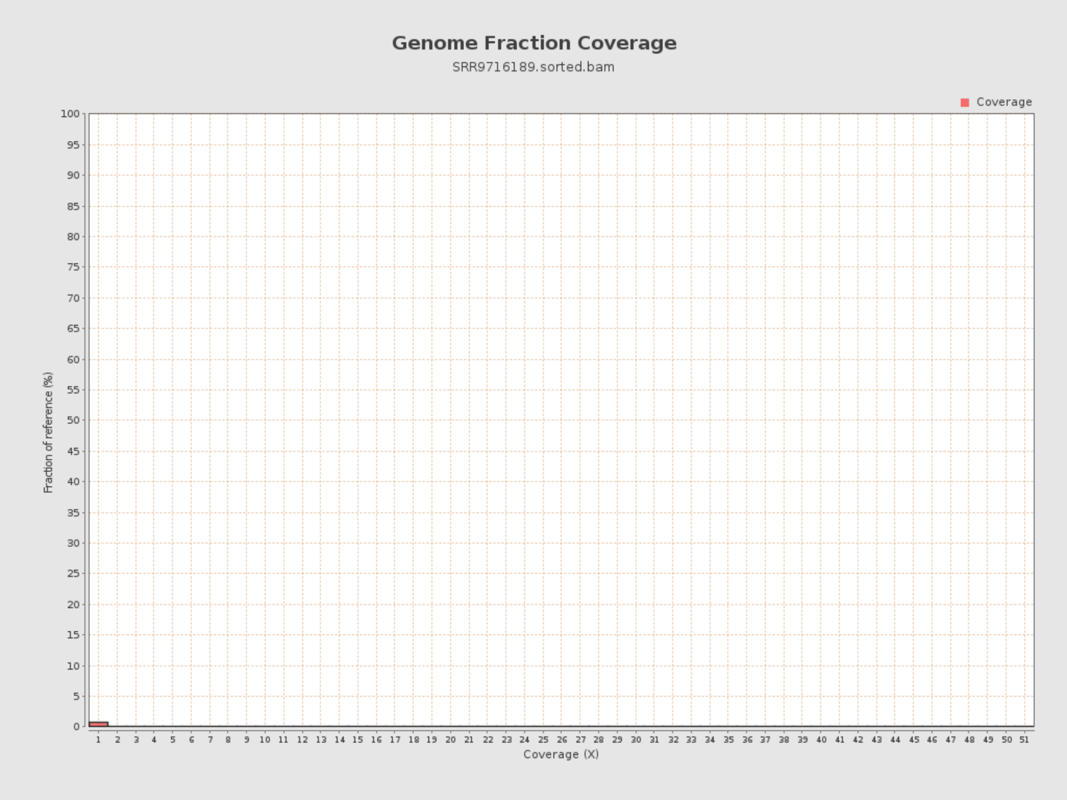
4. Results : Coverage Histogram



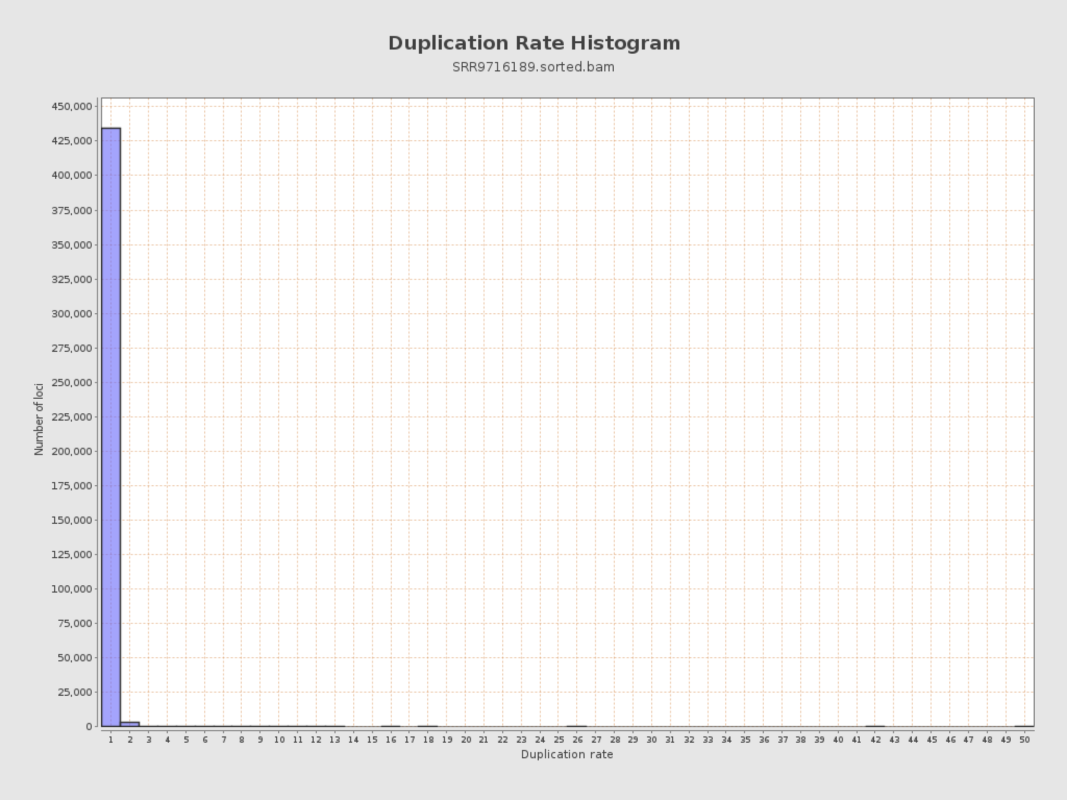
5. Results : Coverage Histogram (0-50X)



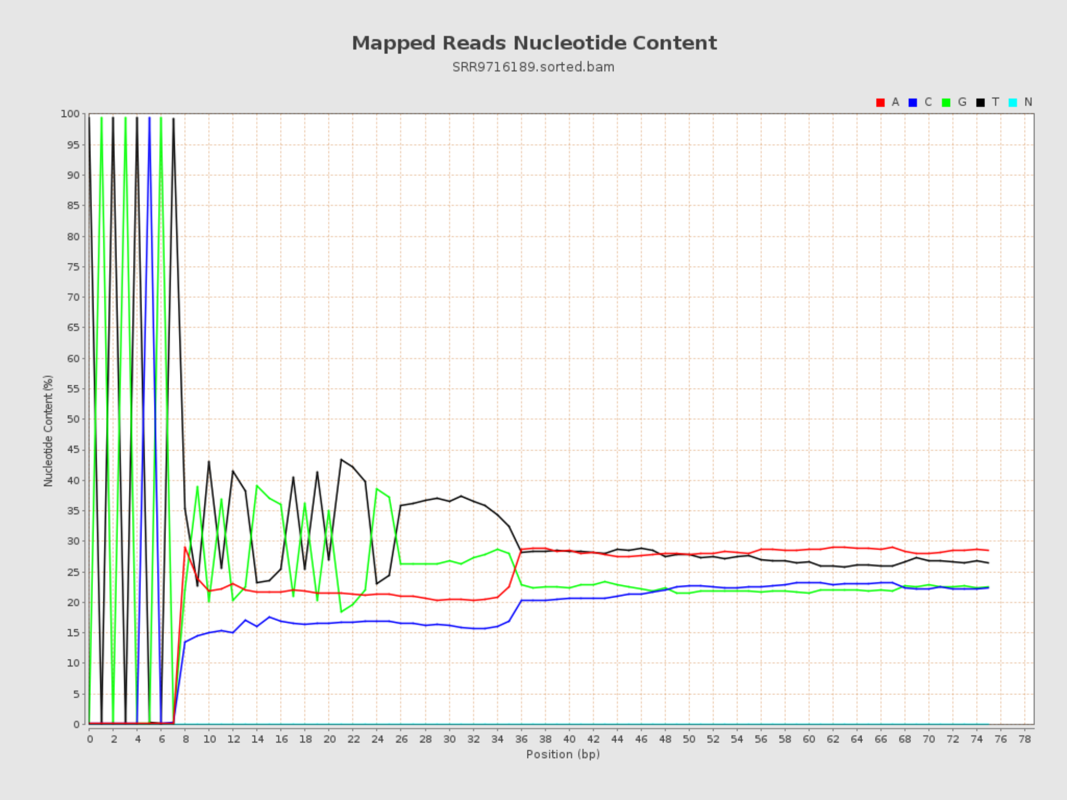
6. Results : Genome Fraction Coverage



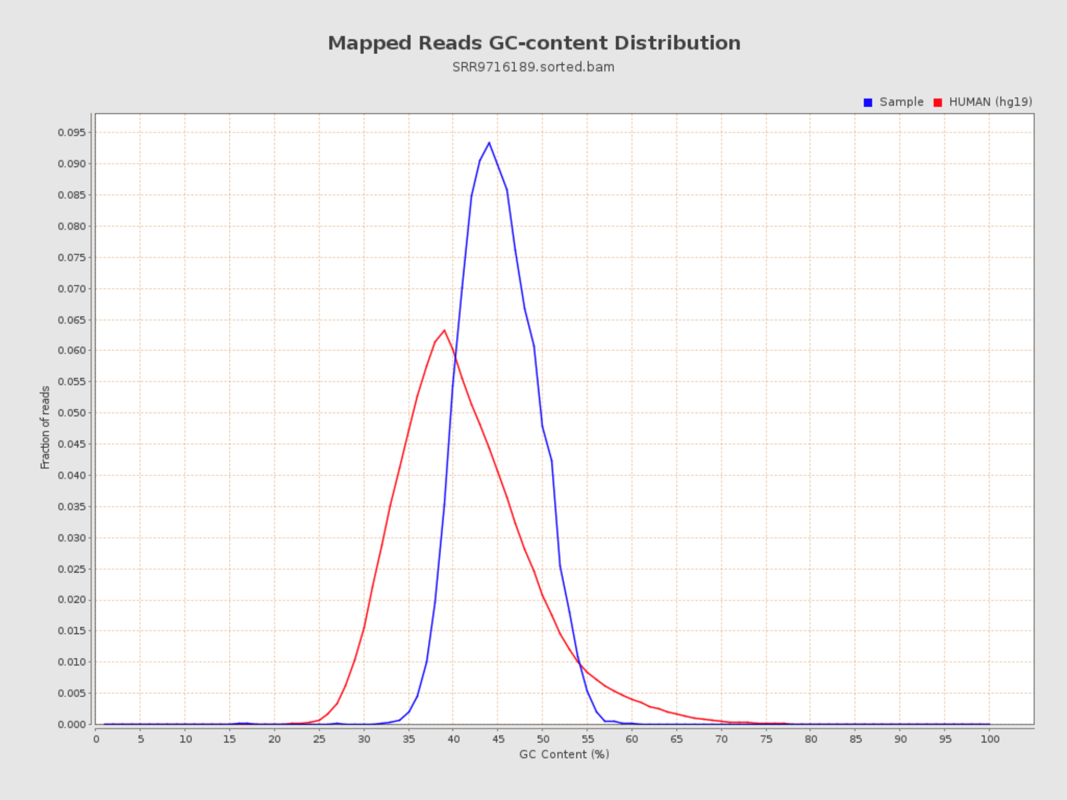
7. Results : Duplication Rate Histogram



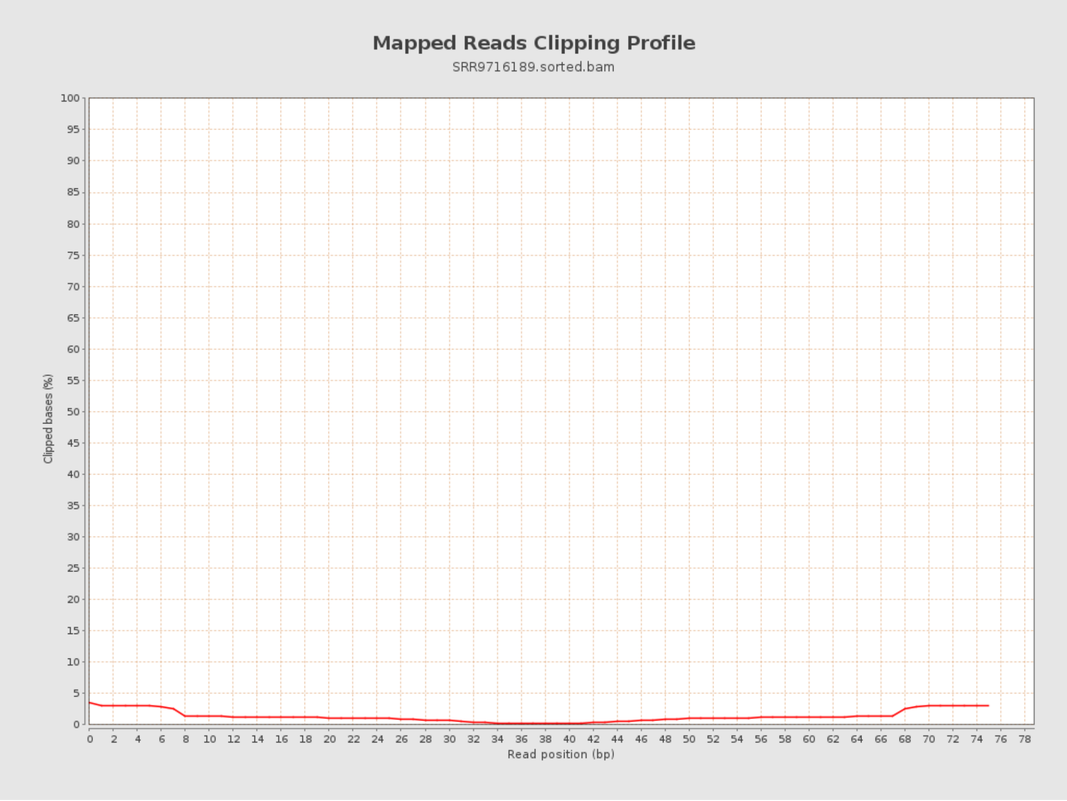
8. Results : Mapped Reads Nucleotide Content



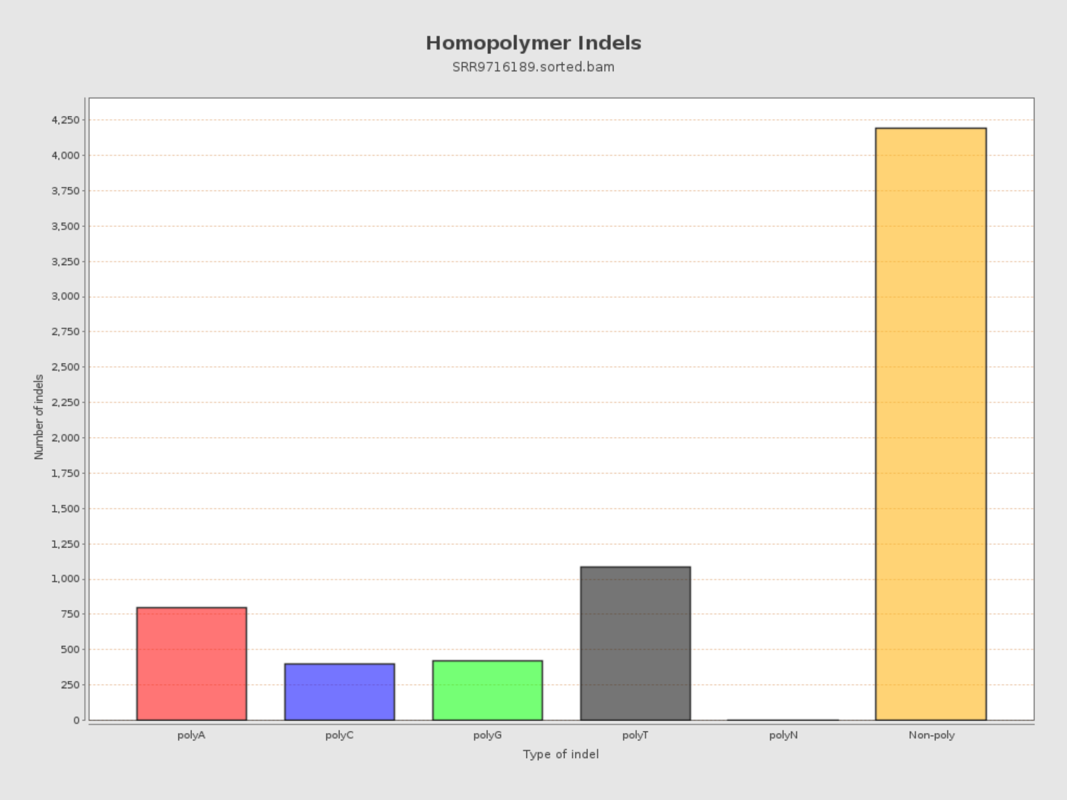
9. Results : Mapped Reads GC-content Distribution



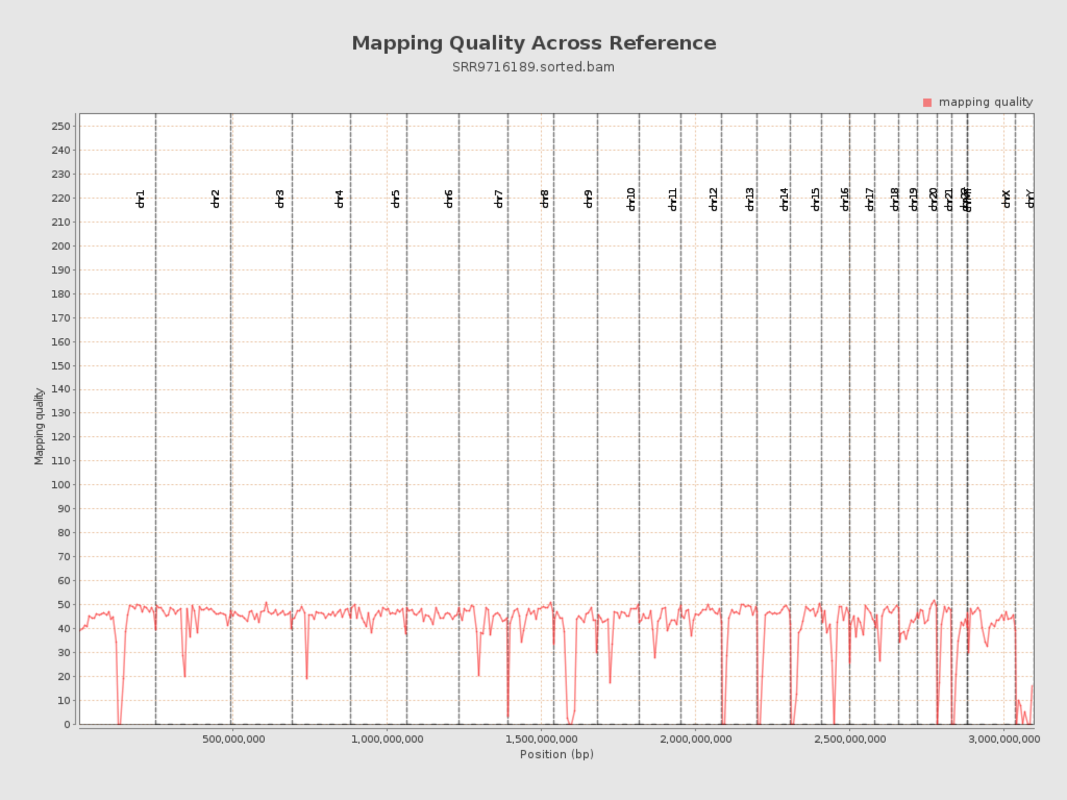
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram