Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 12:08:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716409.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_SRR9716409 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716409.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 12:08:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716409.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,197,750
Mapped reads	996,897 / 83.23%
Unmapped reads	200,853 / 16.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,718 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	27,624 / 2.31%
Duplication rate	2.02%
Clipped reads	999,224 / 83.43%

2.2. ACGT Content

Number/percentage of A's	14,452,467 / 25.21%
Number/percentage of C's	11,367,271 / 19.83%
Number/percentage of T's	17,807,299 / 31.06%
Number/percentage of G's	13,695,701 / 23.89%
Number/percentage of N's	813 / 0%
GC Percentage	43.72%

2.3. Coverage

Mean	0.0185

Standard Deviation	0.2027

2.4. Mapping Quality

Mean Mapping Quality	44.09

2.5. Mismatches and indels

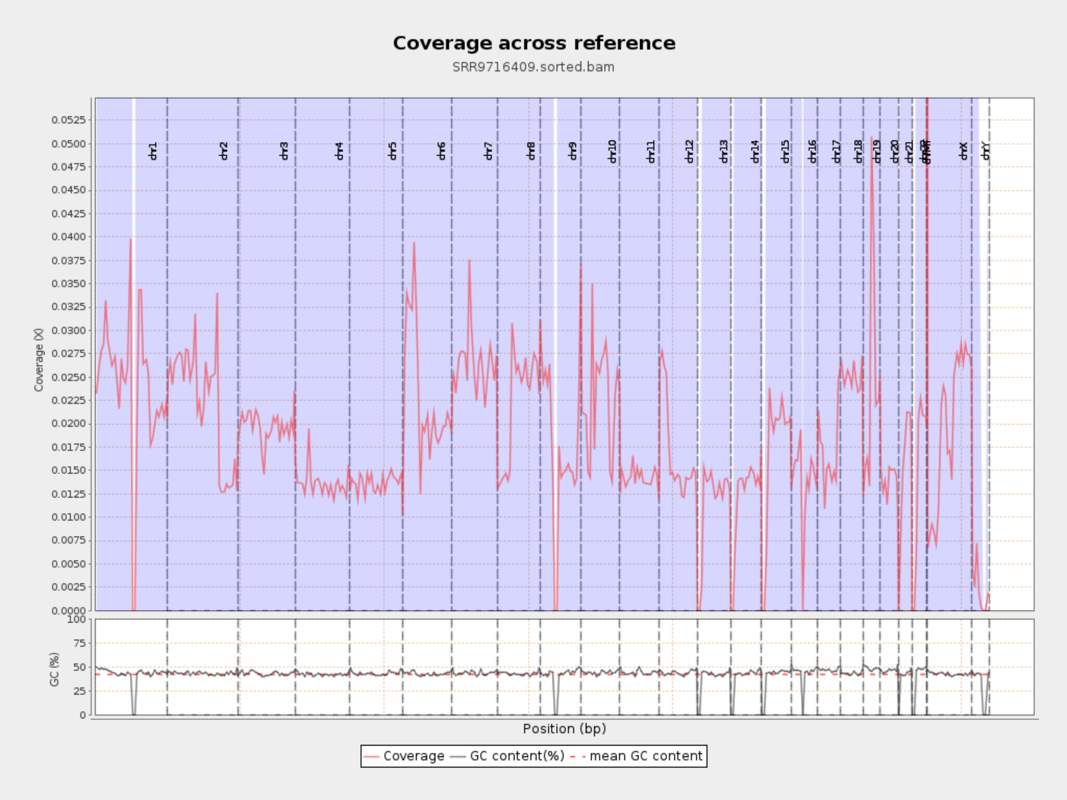
General error rate	0.51%
Mismatches	285,571
Insertions	3,711
Mapped reads with at least one insertion	0.37%
Deletions	10,367
Mapped reads with at least one deletion	1.03%
Homopolymer indels	43.49%

2.6. Chromosome stats

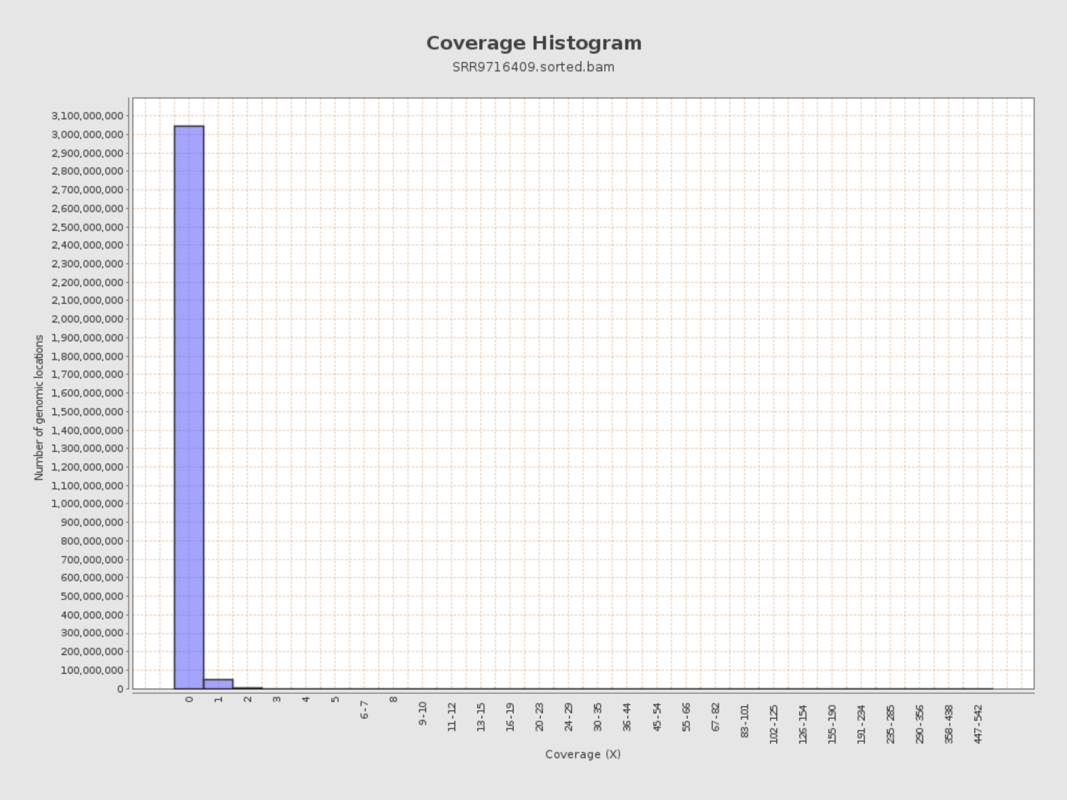
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5973758	0.024	0.3958
chr2	243199373	5449939	0.0224	0.2626
chr3	198022430	3888286	0.0196	0.1492
chr4	191154276	2612753	0.0137	0.1292
chr5	180915260	2485329	0.0137	0.1258
chr6	171115067	3888818	0.0227	0.1724
chr7	159138663	4222890	0.0265	0.2725

chr8	146364022	3255182	0.0222	0.1738
chr9	141213431	2393604	0.017	0.1641
chr10	135534747	3061195	0.0226	0.193
chr11	135006516	1933120	0.0143	0.1587
chr12	133851895	2298012	0.0172	0.1419
chr13	115169878	1309203	0.0114	0.1146
chr14	107349540	1266312	0.0118	0.1239
chr15	102531392	1718152	0.0168	0.139
chr16	90354753	1225003	0.0136	0.1316
chr17	81195210	1384711	0.0171	0.1415
chr18	78077248	1955331	0.025	0.2607
chr19	59128983	1489312	0.0252	0.2585
chr20	63025520	879260	0.014	0.1263
chr21	48129895	737516	0.0153	0.136
chr22	51304566	746135	0.0145	0.1282
chrMT	16571	8163	0.4926	0.7292
chrX	155270560	3027004	0.0195	0.1617
chrY	59373566	130740	0.0022	0.0607

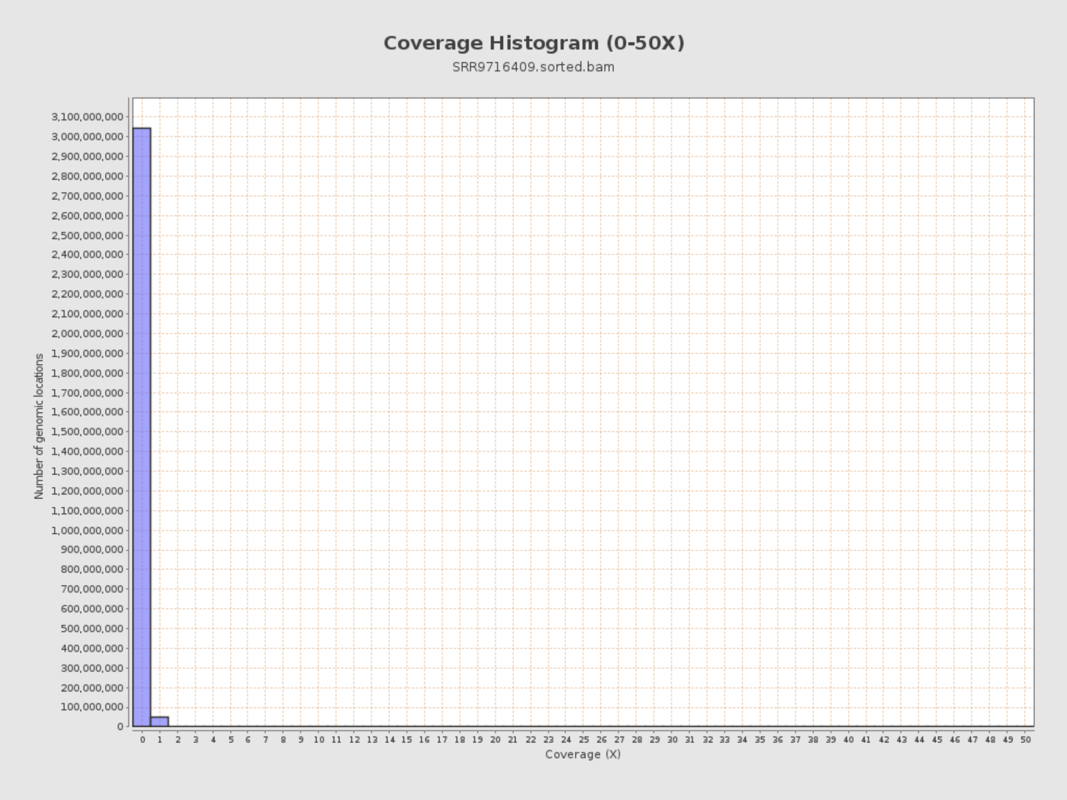
3. Results : Coverage across reference



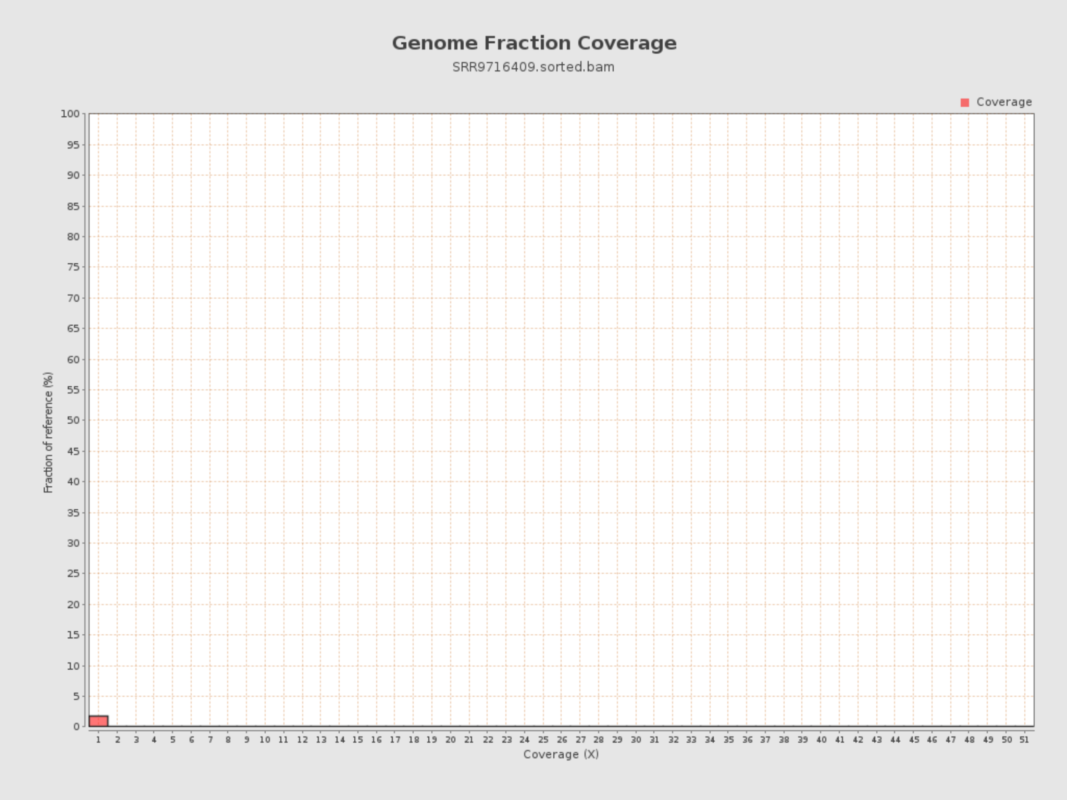
4. Results : Coverage Histogram



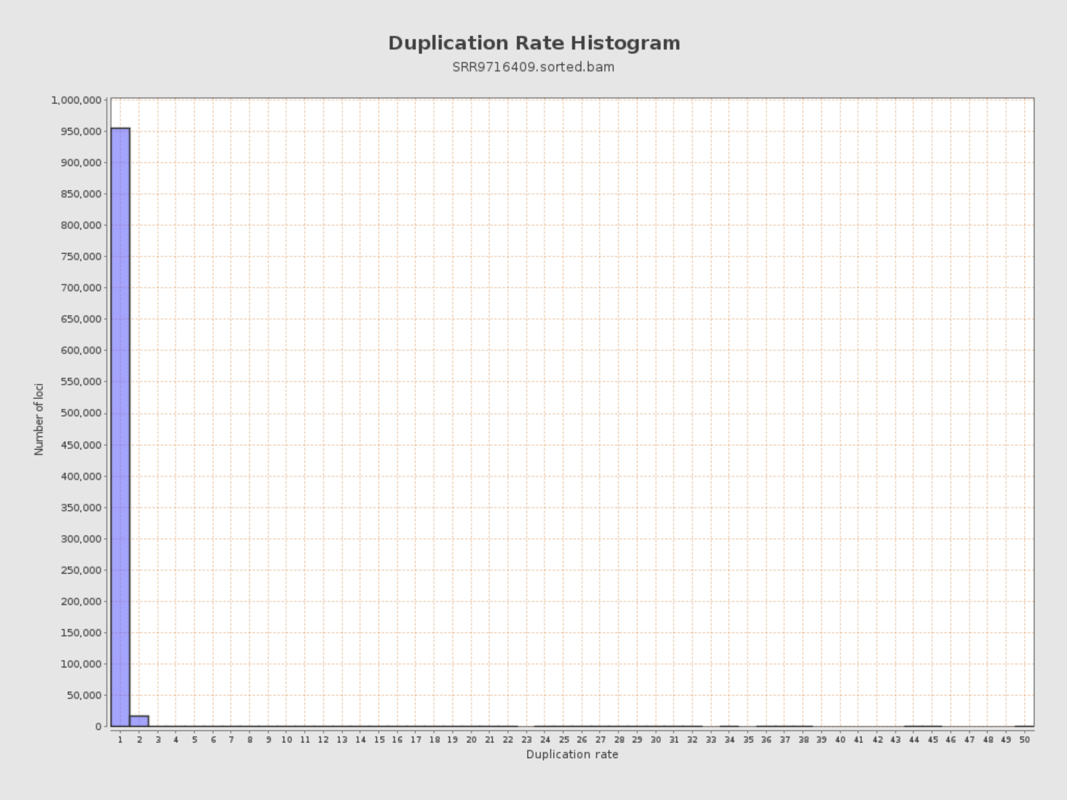
5. Results : Coverage Histogram (0-50X)



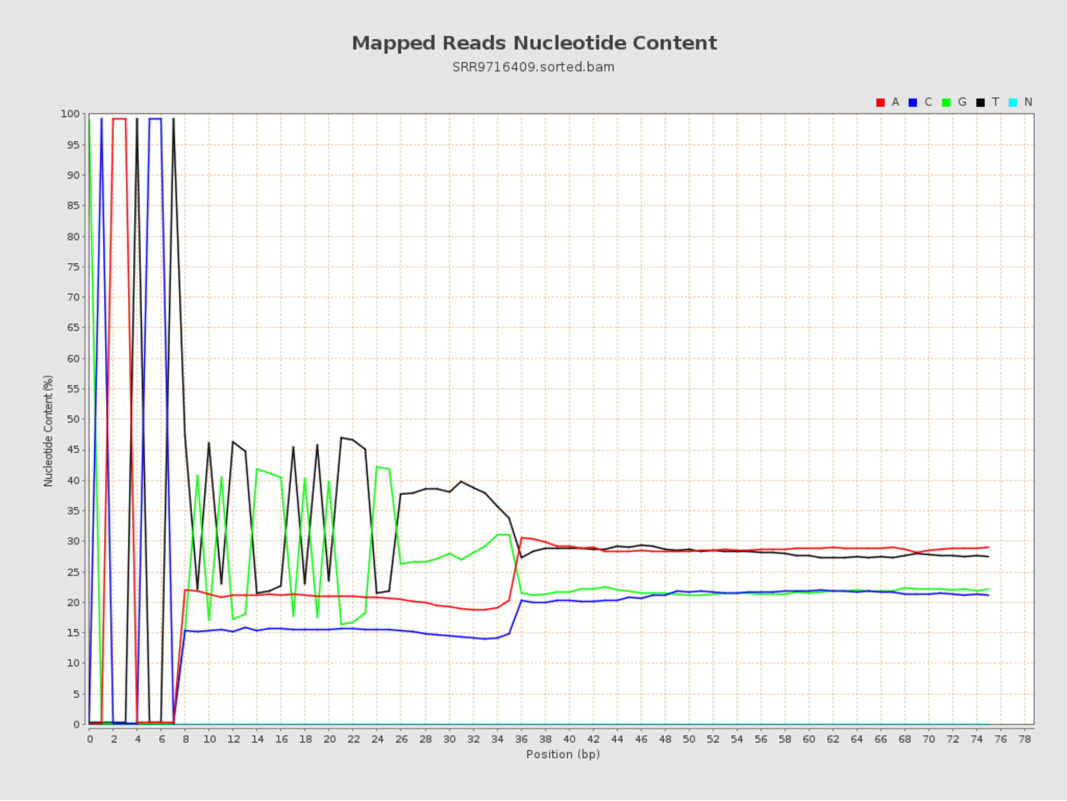
6. Results : Genome Fraction Coverage



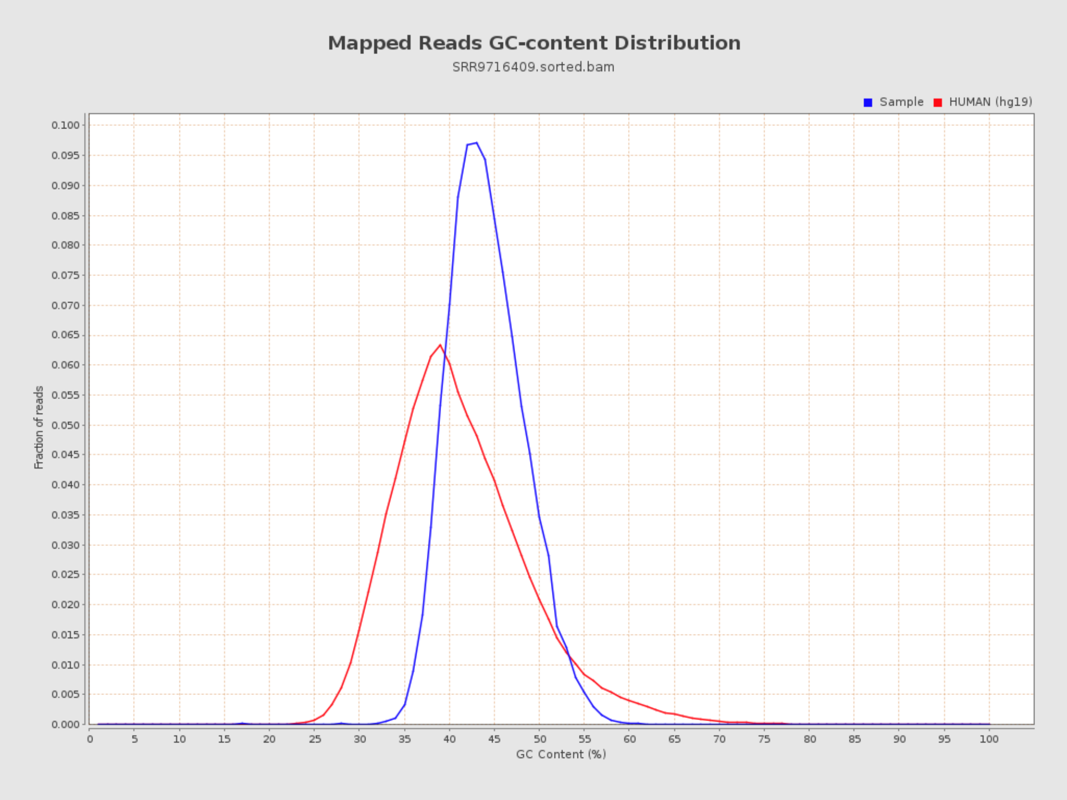
7. Results : Duplication Rate Histogram



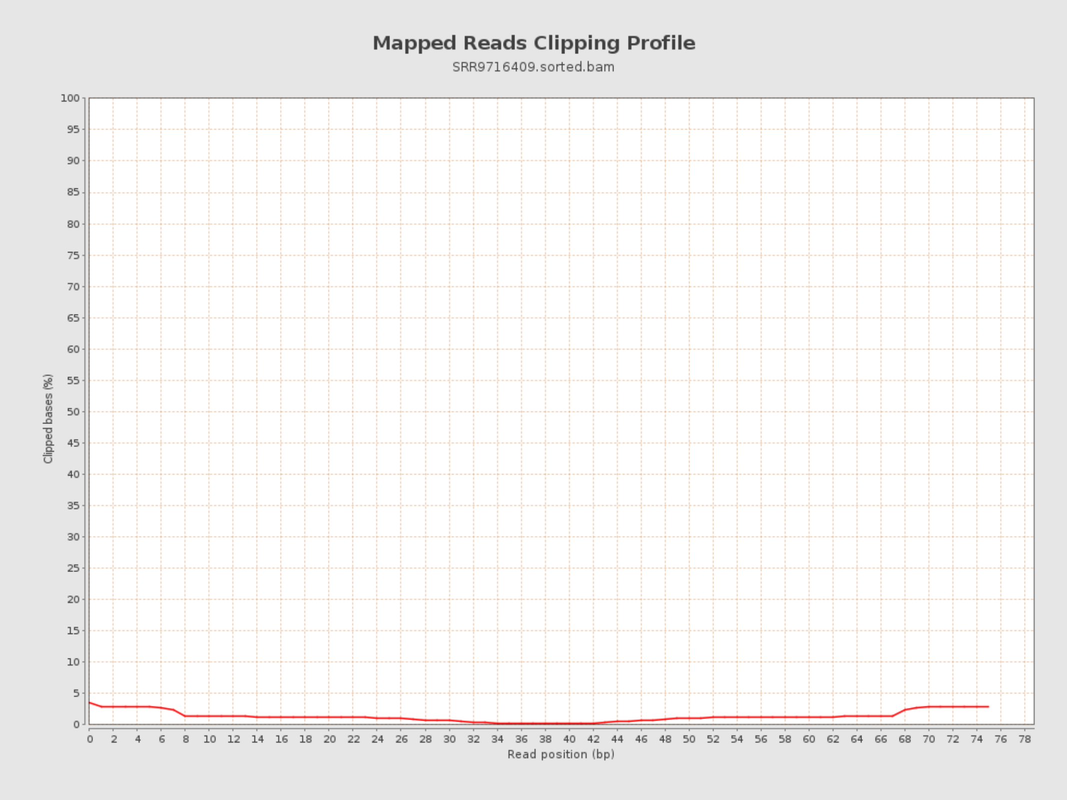
8. Results : Mapped Reads Nucleotide Content



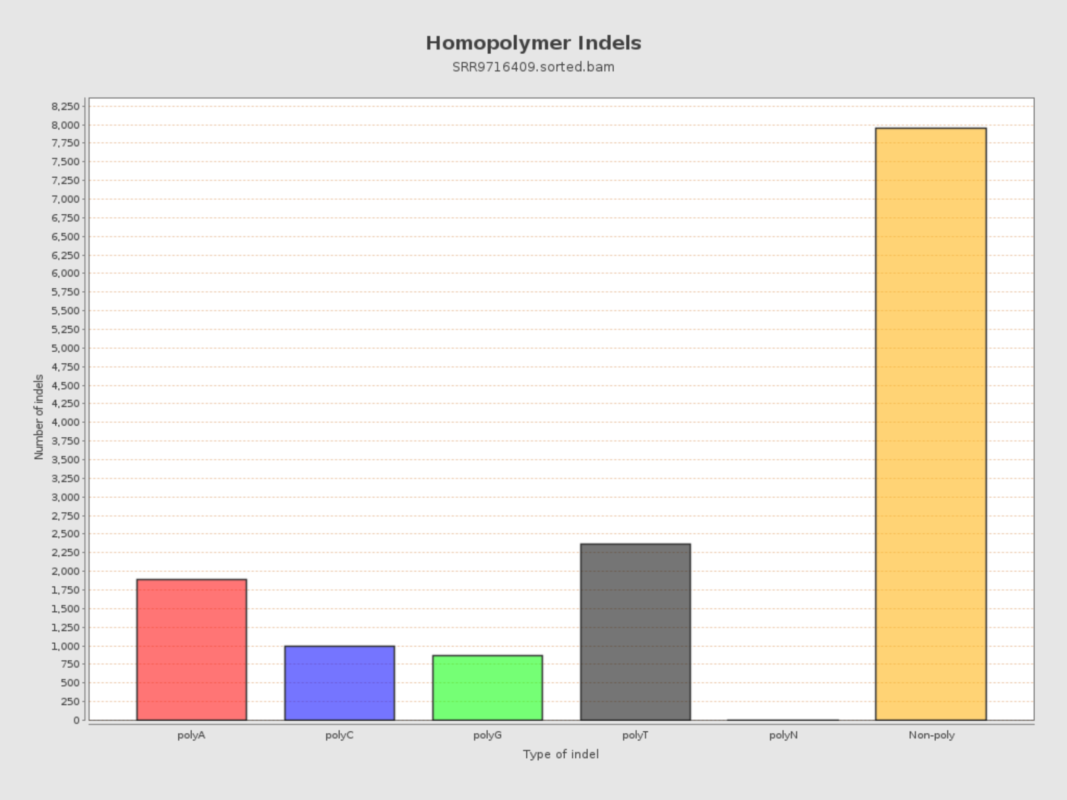
9. Results : Mapped Reads GC-content Distribution



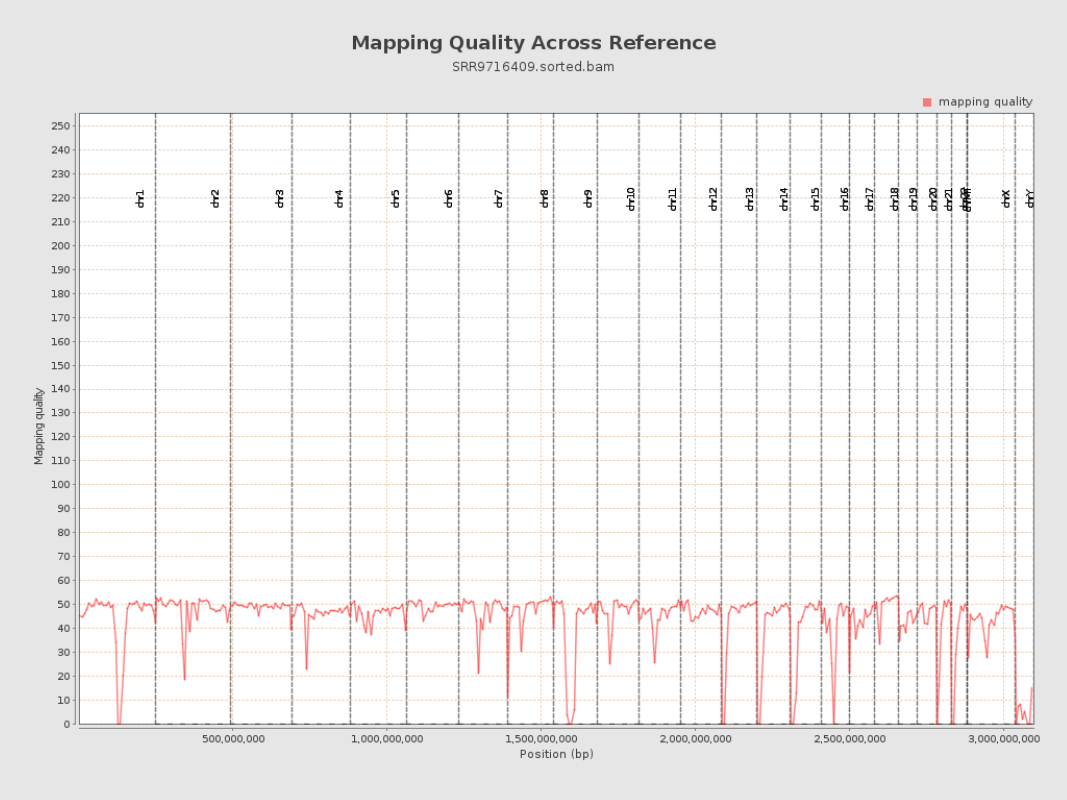
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram