Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 18:32:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716916.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_SRR9716916 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716916.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 18:32:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716916.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,057,213
Mapped reads	735,960 / 69.61%
Unmapped reads	321,253 / 30.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,504 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	13,570 / 1.28%
Duplication rate	1.31%
Clipped reads	737,921 / 69.8%

2.2. ACGT Content

Number/percentage of A's	9,788,337 / 23.89%
Number/percentage of C's	8,439,573 / 20.6%
Number/percentage of T's	11,837,135 / 28.89%
Number/percentage of G's	10,901,974 / 26.61%
Number/percentage of N's	1,149 / 0%
GC Percentage	47.21%

2.3. Coverage

Mean	0.0132

Standard Deviation	0.1391

2.4. Mapping Quality

Mean Mapping Quality	39.14

2.5. Mismatches and indels

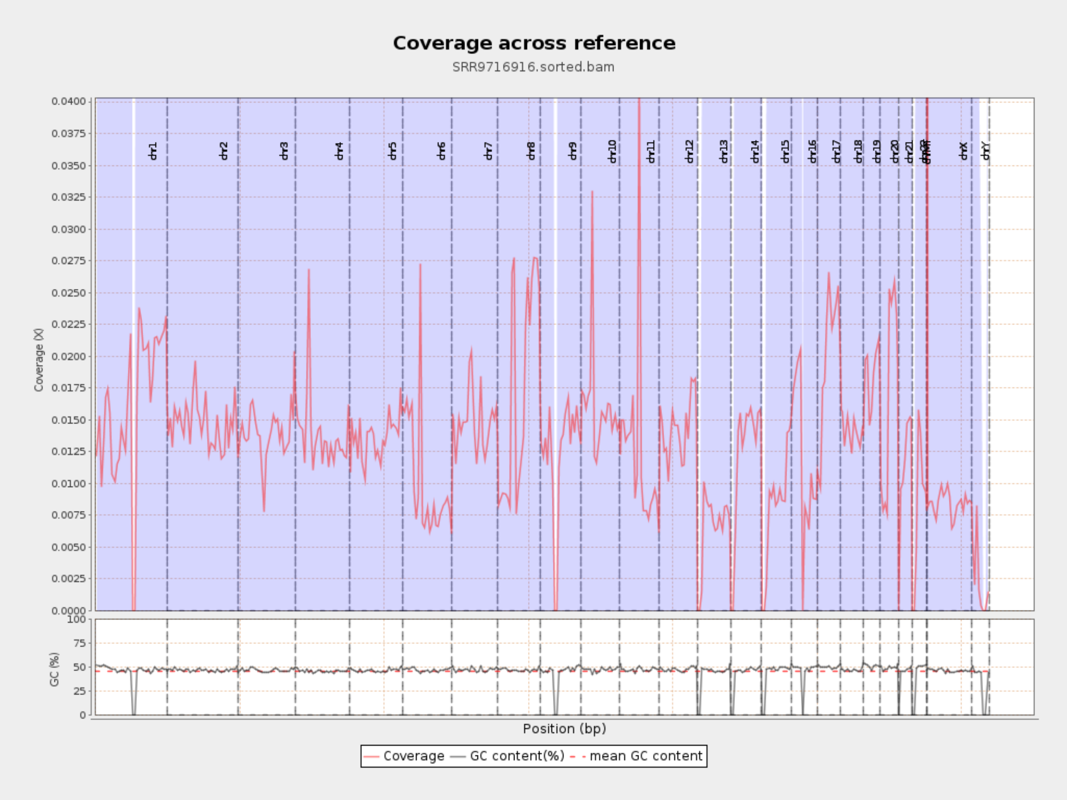
General error rate	0.55%
Mismatches	218,728
Insertions	3,363
Mapped reads with at least one insertion	0.45%
Deletions	7,216
Mapped reads with at least one deletion	0.97%
Homopolymer indels	33.62%

2.6. Chromosome stats

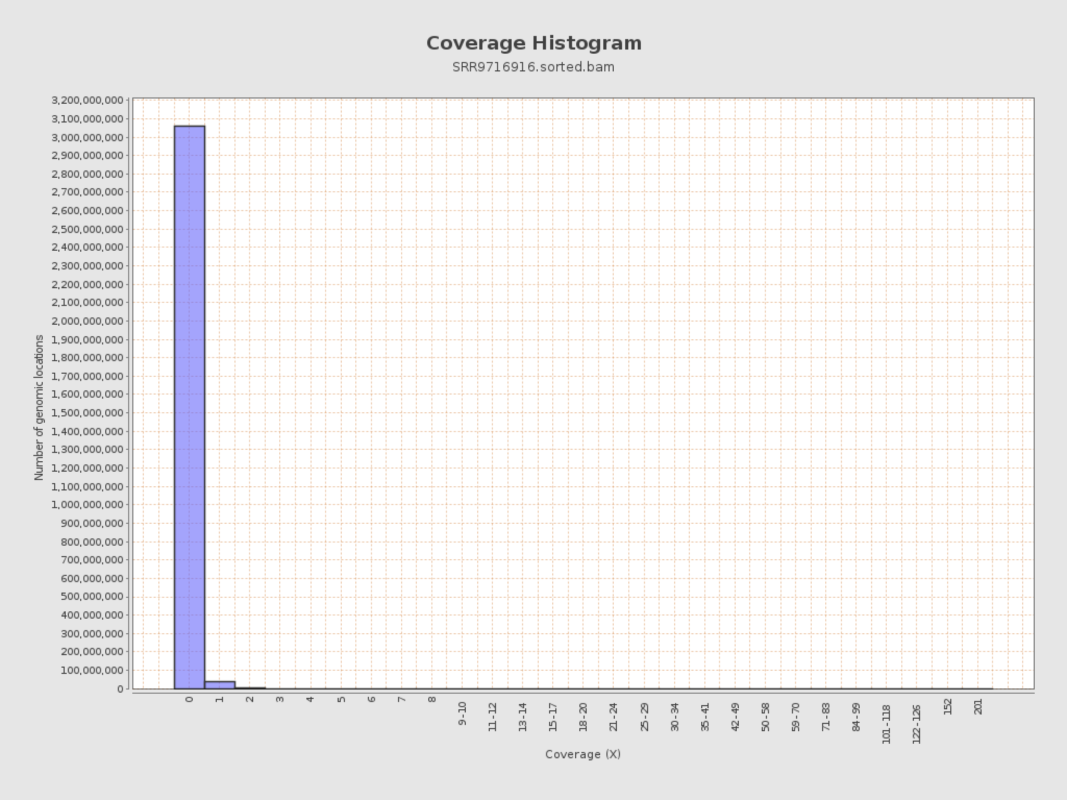
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3999434	0.016	0.1675
chr2	243199373	3573560	0.0147	0.1652
chr3	198022430	2741396	0.0138	0.1317
chr4	191154276	2669164	0.014	0.1371
chr5	180915260	2479924	0.0137	0.1245
chr6	171115067	1760538	0.0103	0.11
chr7	159138663	2366557	0.0149	0.1541

chr8	146364022	2516391	0.0172	0.1446
chr9	141213431	1730580	0.0123	0.1254
chr10	135534747	2199549	0.0162	0.2068
chr11	135006516	1740307	0.0129	0.1375
chr12	133851895	1921594	0.0144	0.1277
chr13	115169878	741943	0.0064	0.0857
chr14	107349540	1311426	0.0122	0.1199
chr15	102531392	830303	0.0081	0.0974
chr16	90354753	1055462	0.0117	0.1211
chr17	81195210	1629635	0.0201	0.1565
chr18	78077248	1098331	0.0141	0.15
chr19	59128983	1085939	0.0184	0.1634
chr20	63025520	1067148	0.0169	0.1449
chr21	48129895	548907	0.0114	0.1229
chr22	51304566	432795	0.0084	0.0988
chrMT	16571	34106	2.0582	1.9793
chrX	155270560	1311170	0.0084	0.1048
chrY	59373566	134206	0.0023	0.074

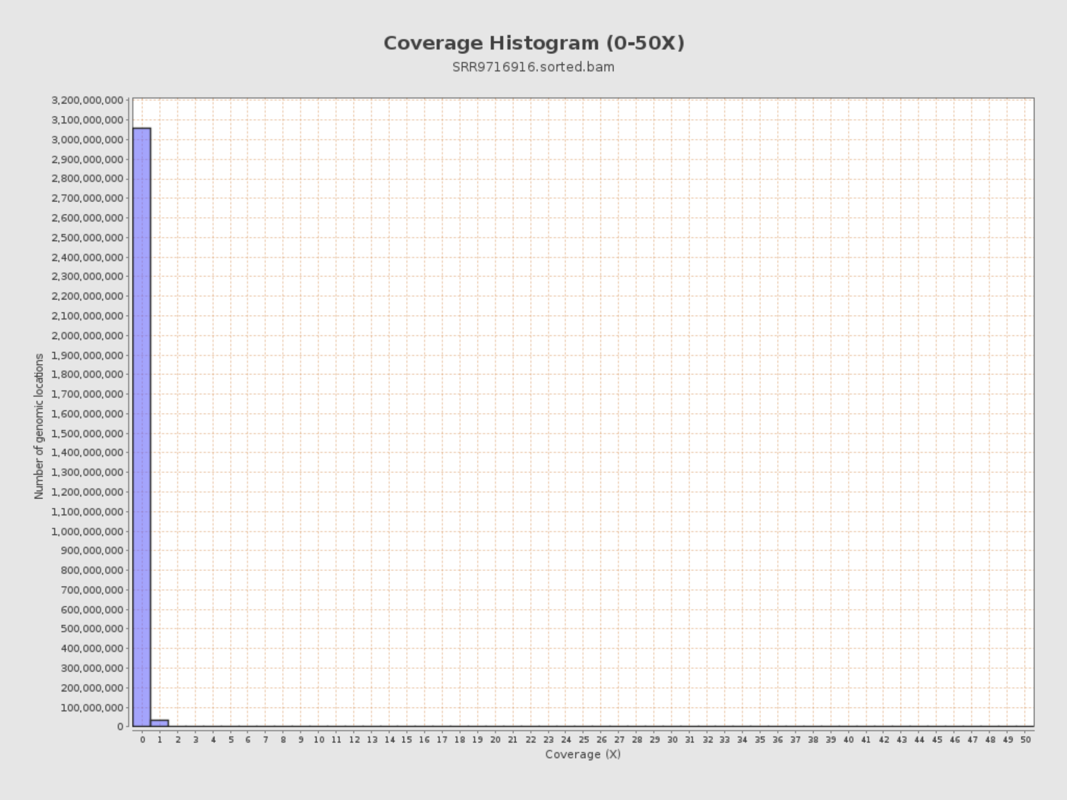
3. Results : Coverage across reference



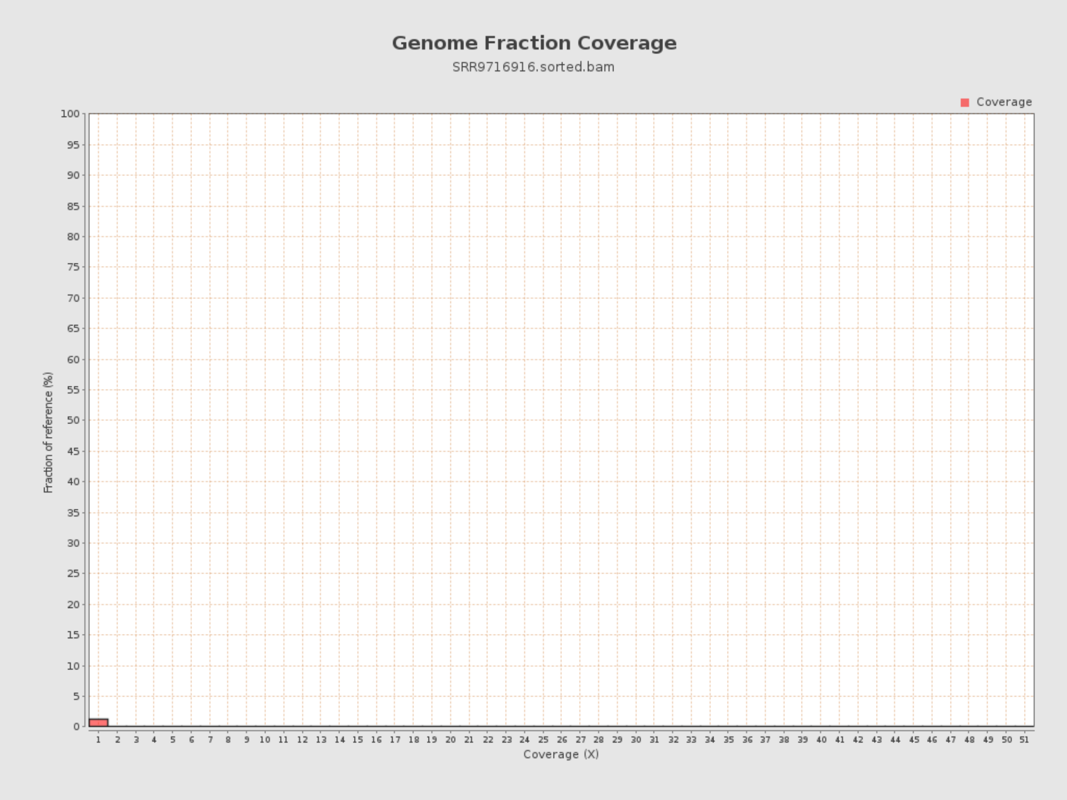
4. Results : Coverage Histogram



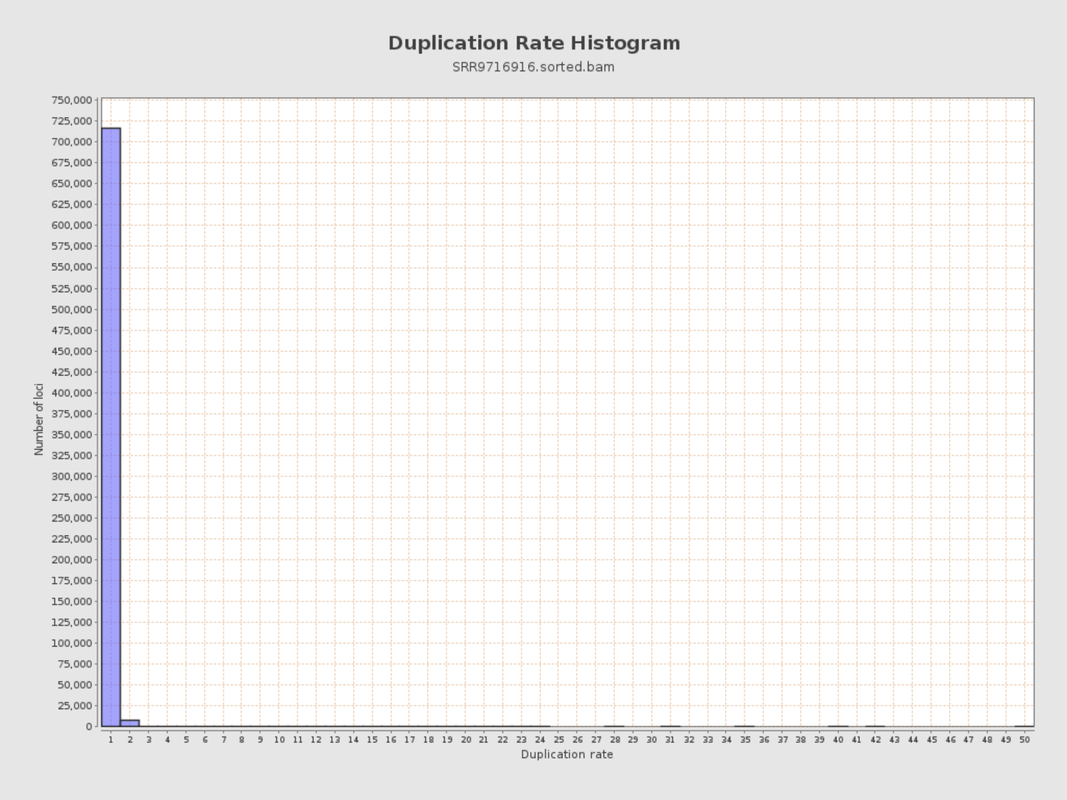
5. Results : Coverage Histogram (0-50X)



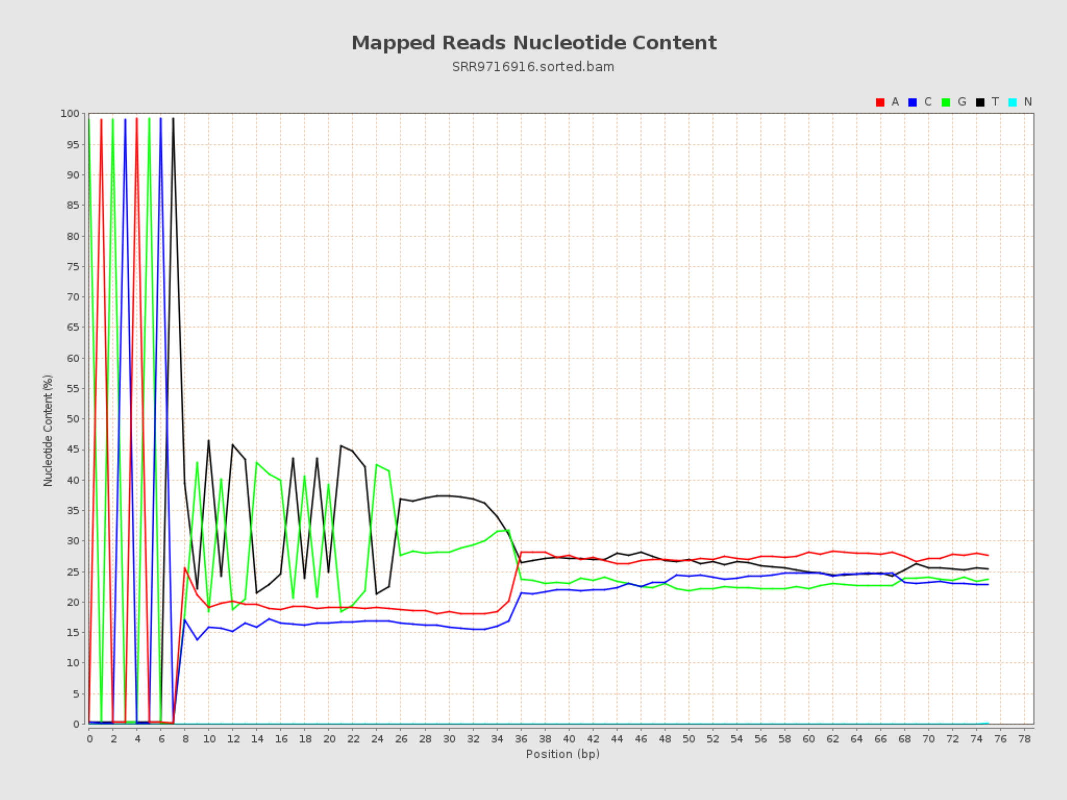
6. Results : Genome Fraction Coverage



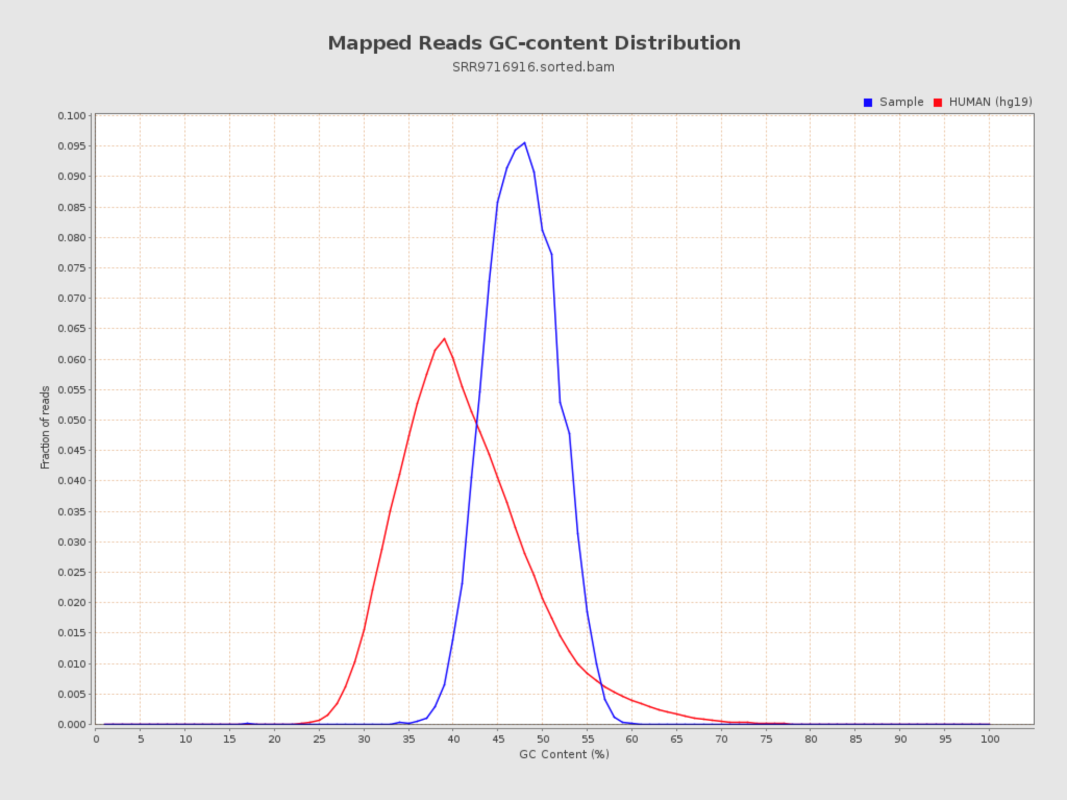
7. Results : Duplication Rate Histogram



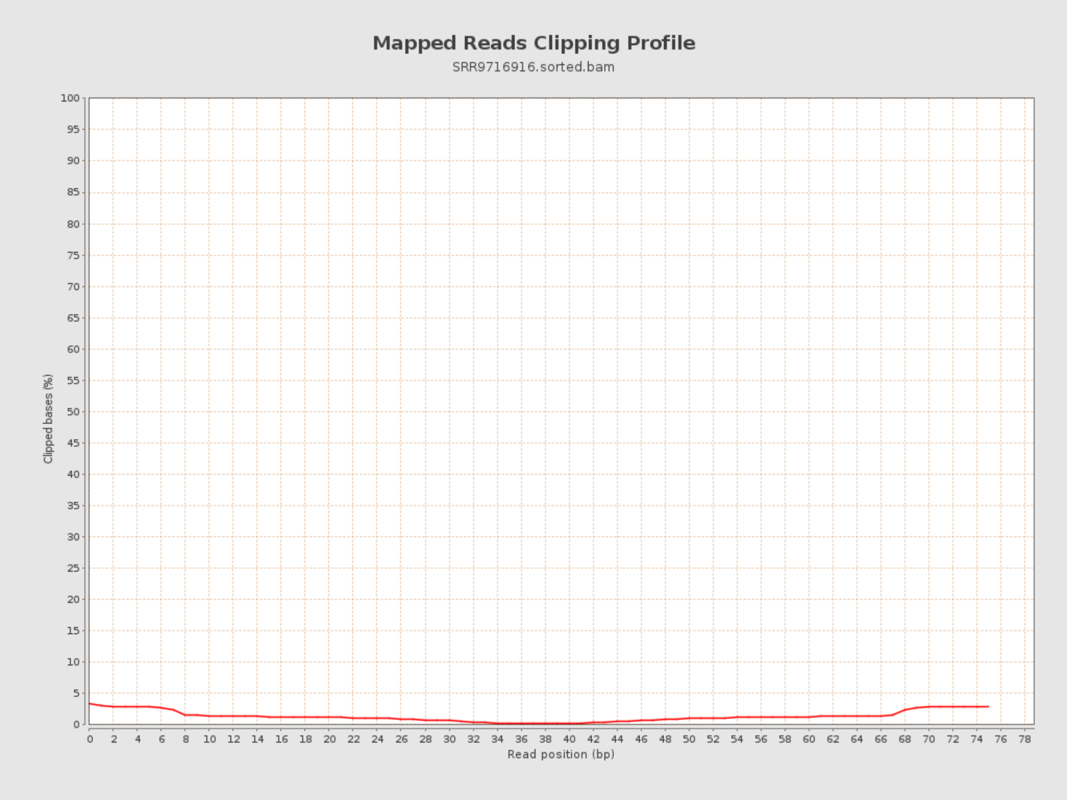
8. Results : Mapped Reads Nucleotide Content



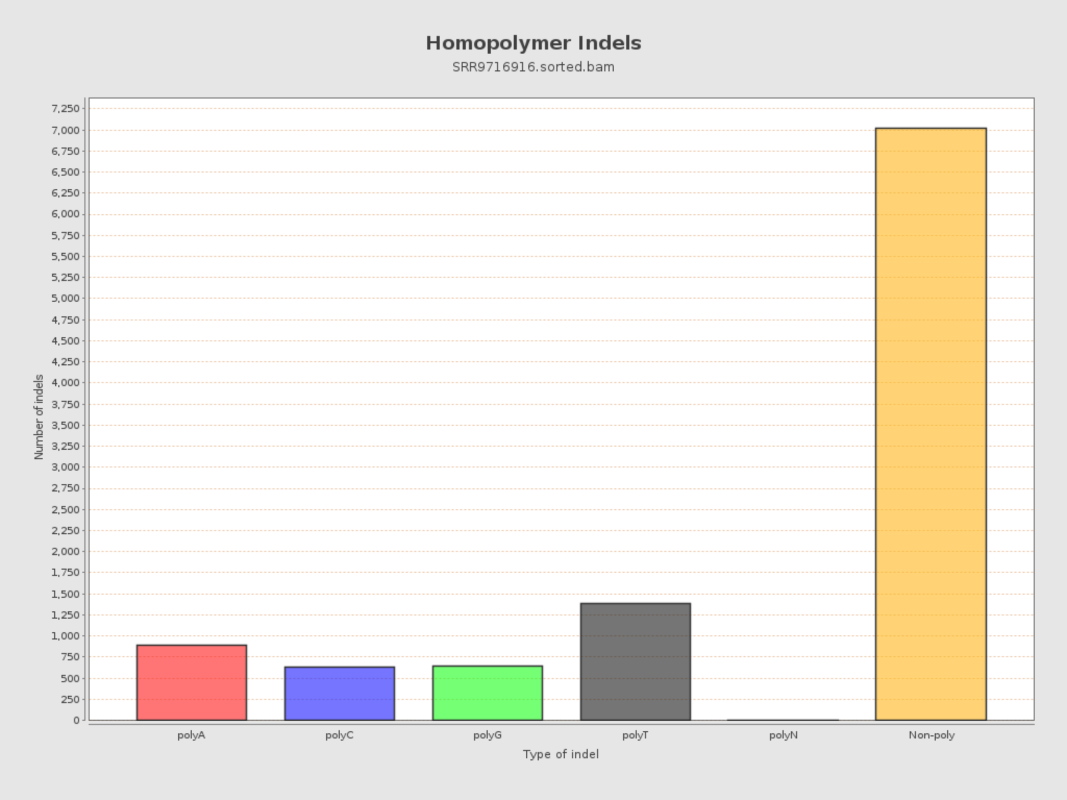
9. Results : Mapped Reads GC-content Distribution



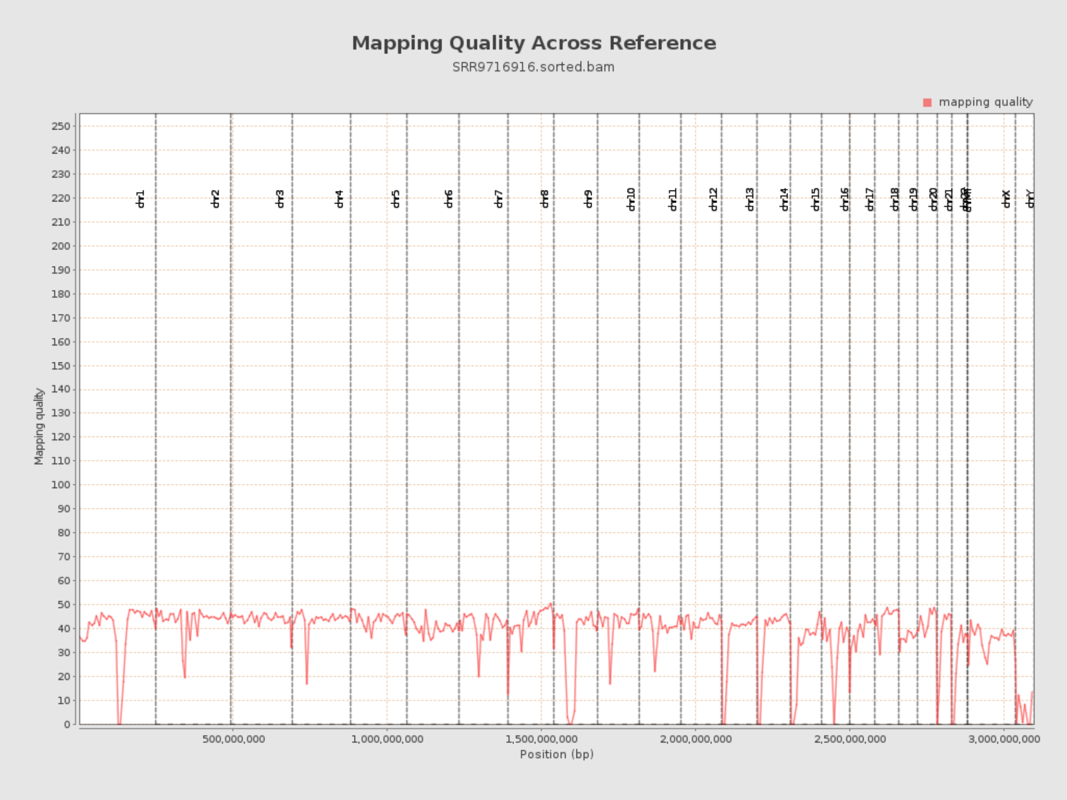
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram