Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 18:01:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716902.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_SRR9716902 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716902.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 18:01:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716902.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	957,218
Mapped reads	827,769 / 86.48%
Unmapped reads	129,449 / 13.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,888 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	15,654 / 1.64%
Duplication rate	1.37%
Clipped reads	828,634 / 86.57%

2.2. ACGT Content

Number/percentage of A's	10,806,160 / 23.14%
Number/percentage of C's	10,171,649 / 21.78%
Number/percentage of T's	13,591,833 / 29.11%
Number/percentage of G's	12,120,638 / 25.96%
Number/percentage of N's	1,404 / 0%
GC Percentage	47.74%

2.3. Coverage

Mean	0.0151

Standard Deviation	0.1513

2.4. Mapping Quality

Mean Mapping Quality	39.91

2.5. Mismatches and indels

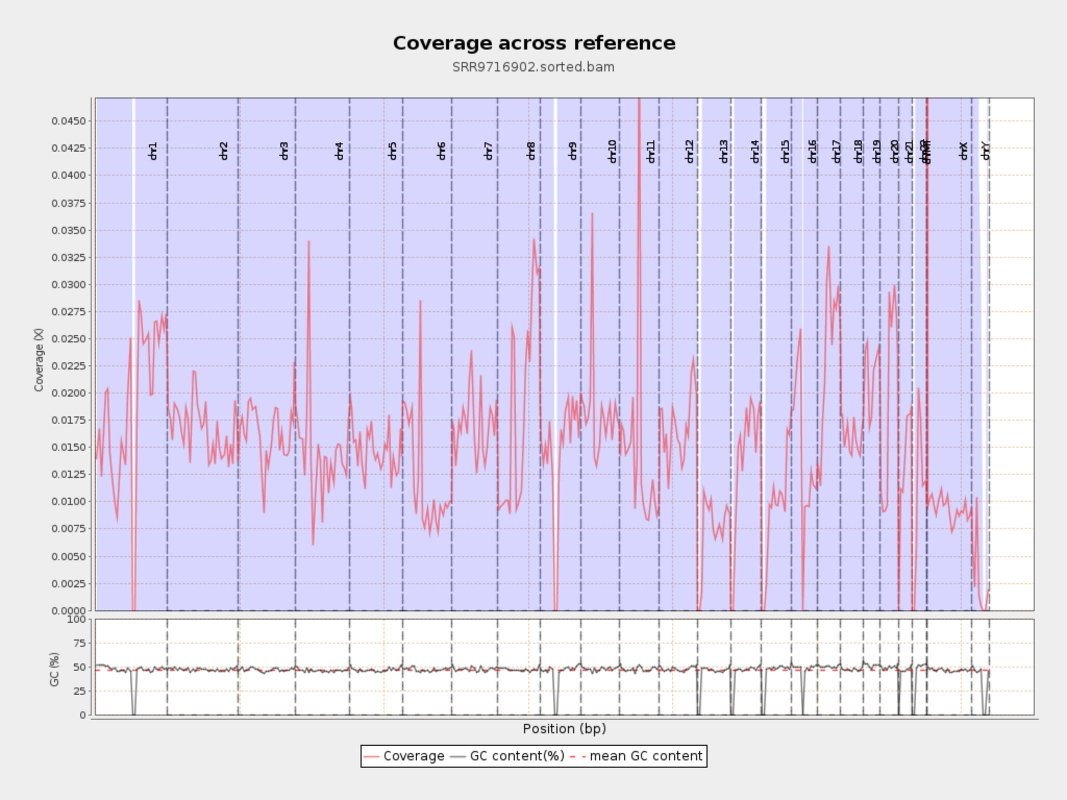
General error rate	0.54%
Mismatches	245,573
Insertions	3,728
Mapped reads with at least one insertion	0.45%
Deletions	8,076
Mapped reads with at least one deletion	0.96%
Homopolymer indels	34.37%

2.6. Chromosome stats

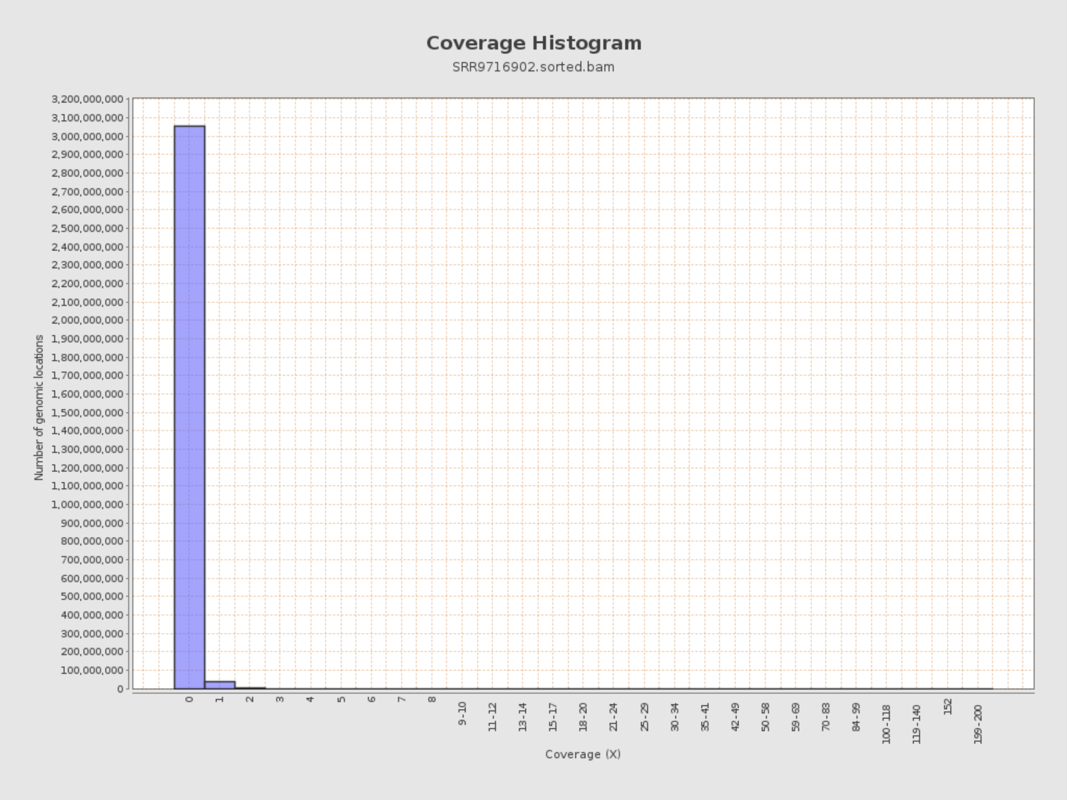
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4617823	0.0185	0.1821
chr2	243199373	4058943	0.0167	0.1809
chr3	198022430	3211357	0.0162	0.1401
chr4	191154276	2792062	0.0146	0.1497
chr5	180915260	2671542	0.0148	0.1301
chr6	171115067	2055679	0.012	0.1201
chr7	159138663	2720651	0.0171	0.168

chr8	146364022	2701460	0.0185	0.1517
chr9	141213431	2034021	0.0144	0.1357
chr10	135534747	2489442	0.0184	0.227
chr11	135006516	2023210	0.015	0.1496
chr12	133851895	2268557	0.0169	0.1403
chr13	115169878	831460	0.0072	0.0914
chr14	107349540	1491224	0.0139	0.1288
chr15	102531392	945974	0.0092	0.1032
chr16	90354753	1277034	0.0141	0.1358
chr17	81195210	1941968	0.0239	0.1745
chr18	78077248	1242214	0.0159	0.1681
chr19	59128983	1277223	0.0216	0.1829
chr20	63025520	1222018	0.0194	0.1556
chr21	48129895	649276	0.0135	0.1439
chr22	51304566	541416	0.0106	0.1129
chrMT	16571	32105	1.9374	1.9929
chrX	155270560	1452929	0.0094	0.1077
chrY	59373566	155735	0.0026	0.094

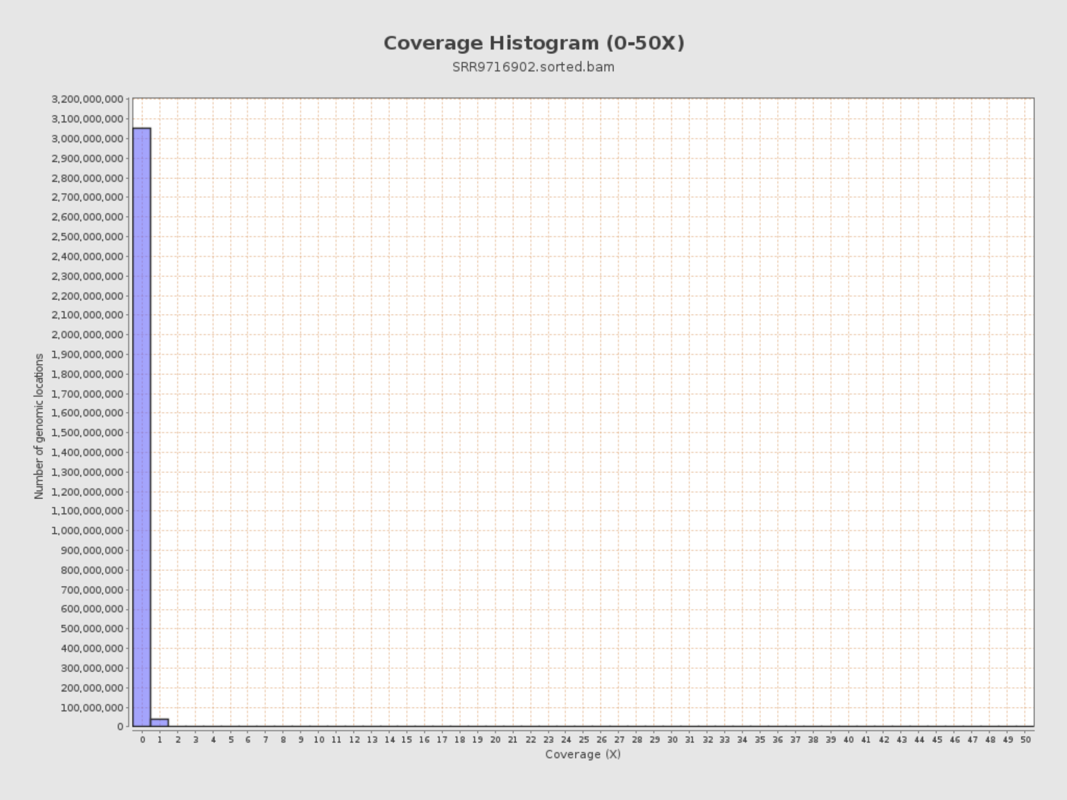
3. Results : Coverage across reference



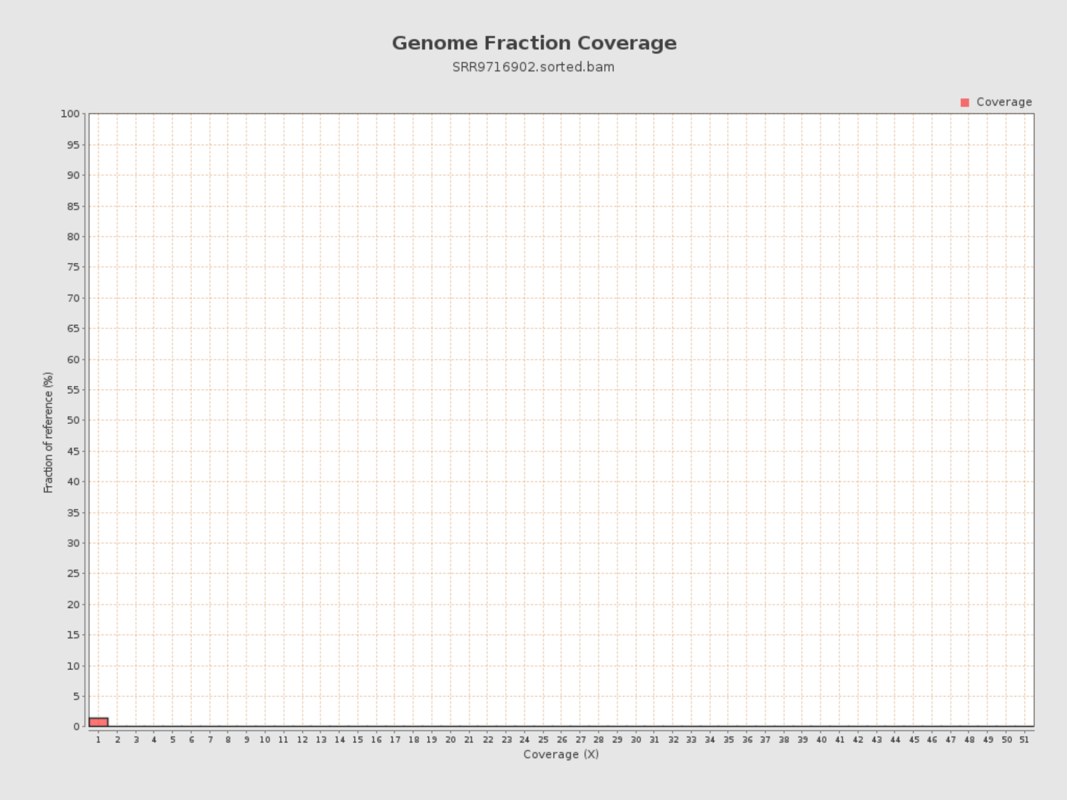
4. Results : Coverage Histogram



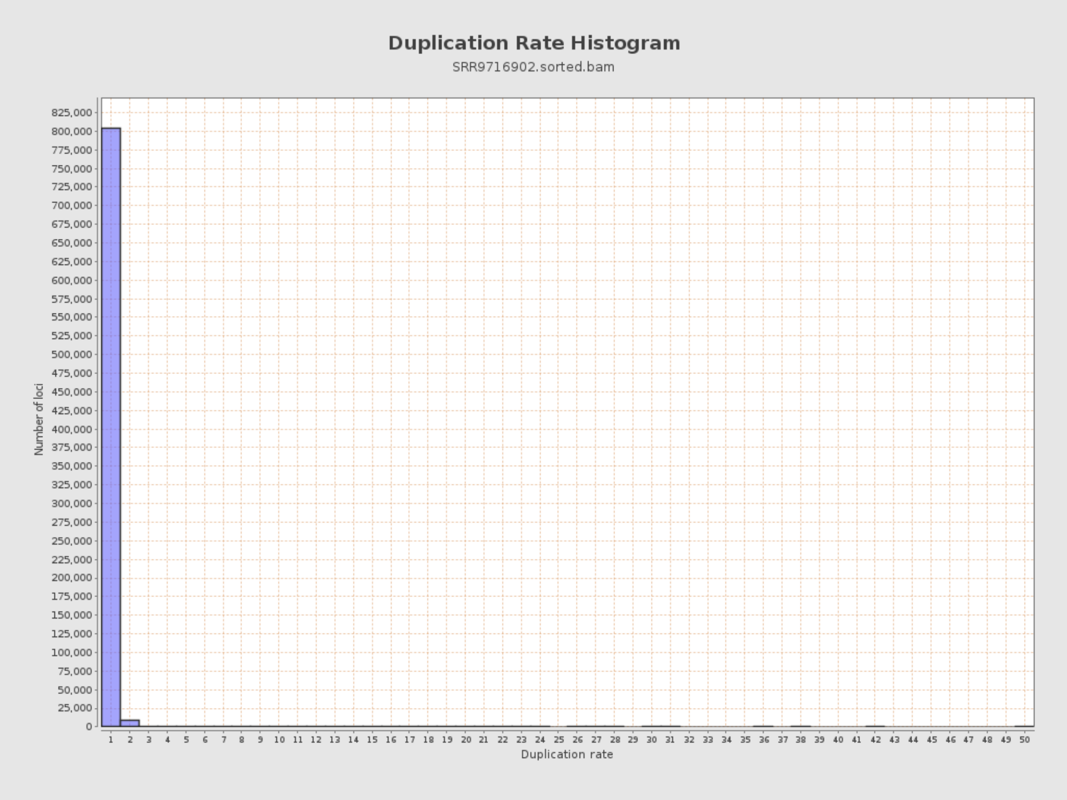
5. Results : Coverage Histogram (0-50X)



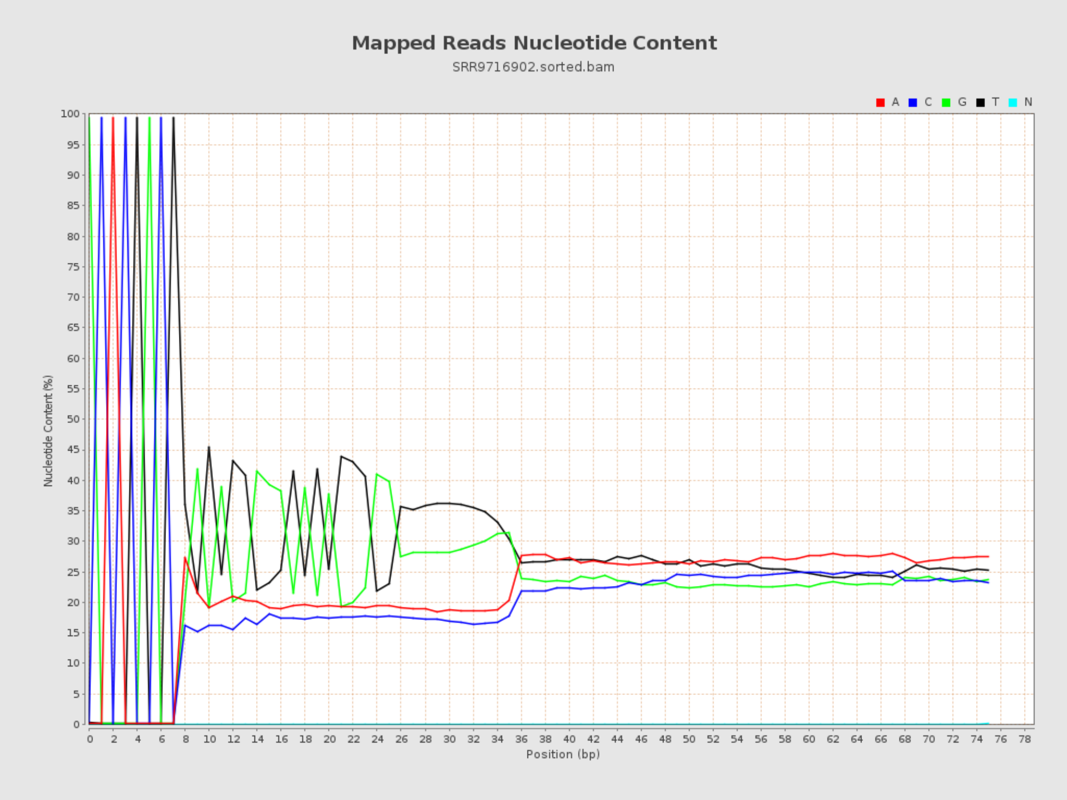
6. Results : Genome Fraction Coverage



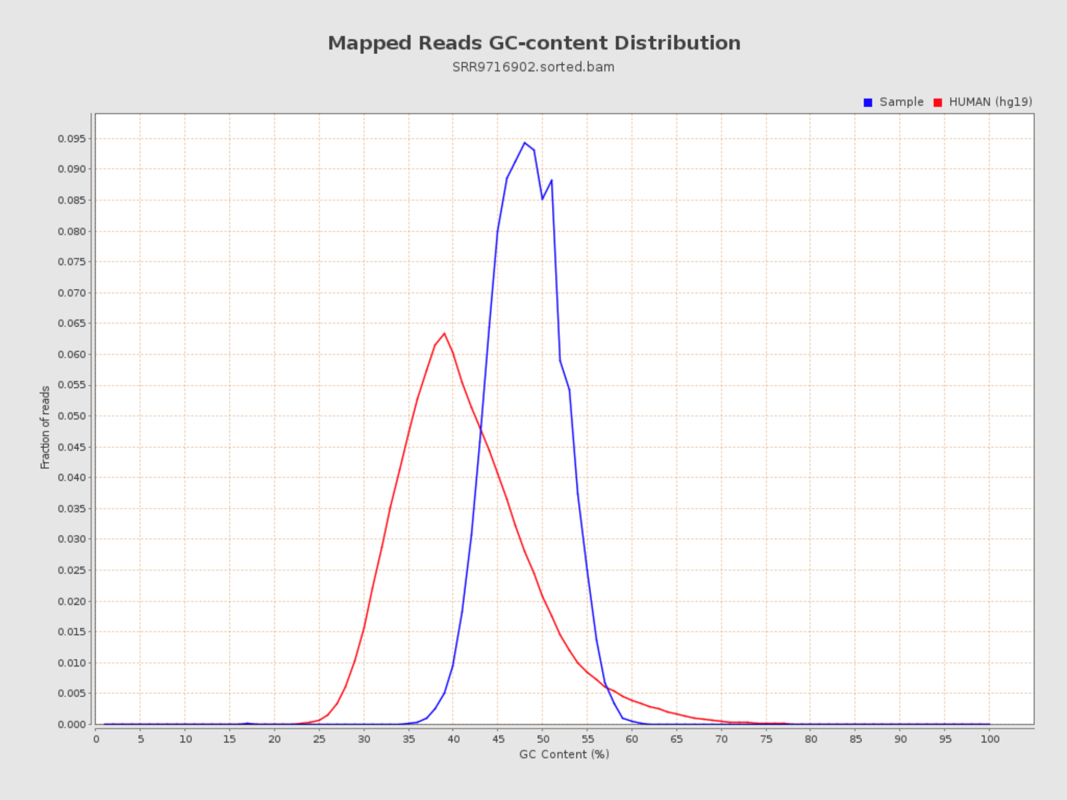
7. Results : Duplication Rate Histogram



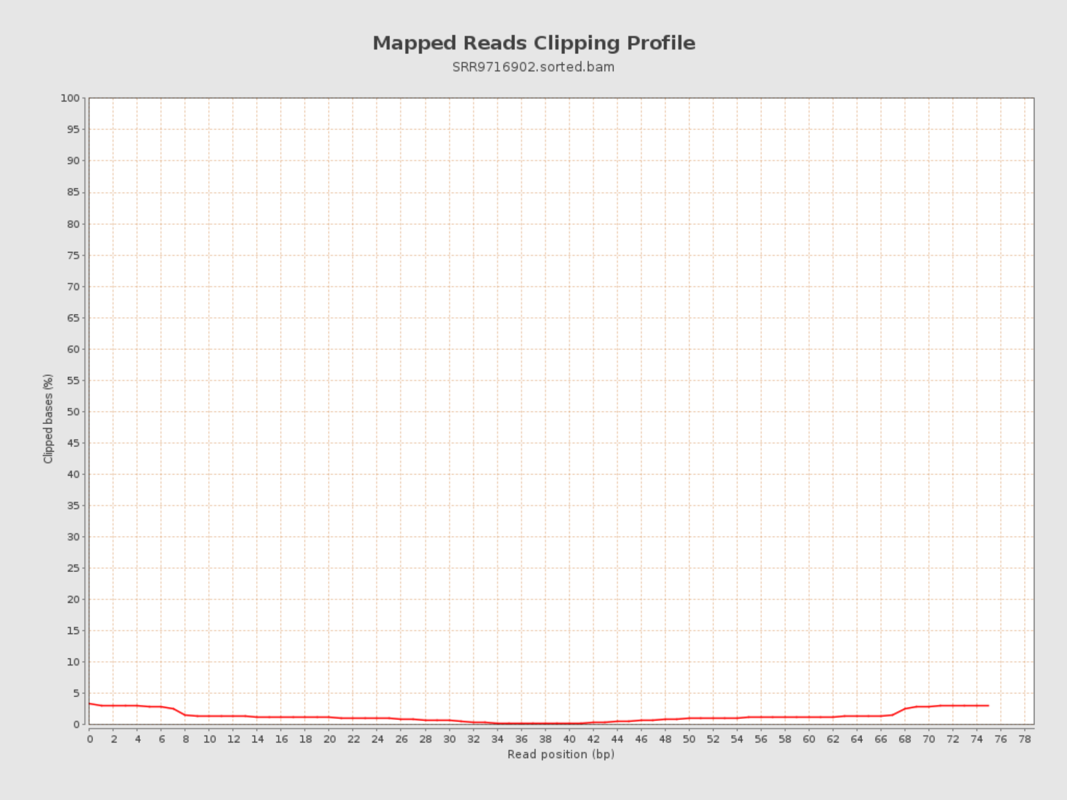
8. Results : Mapped Reads Nucleotide Content



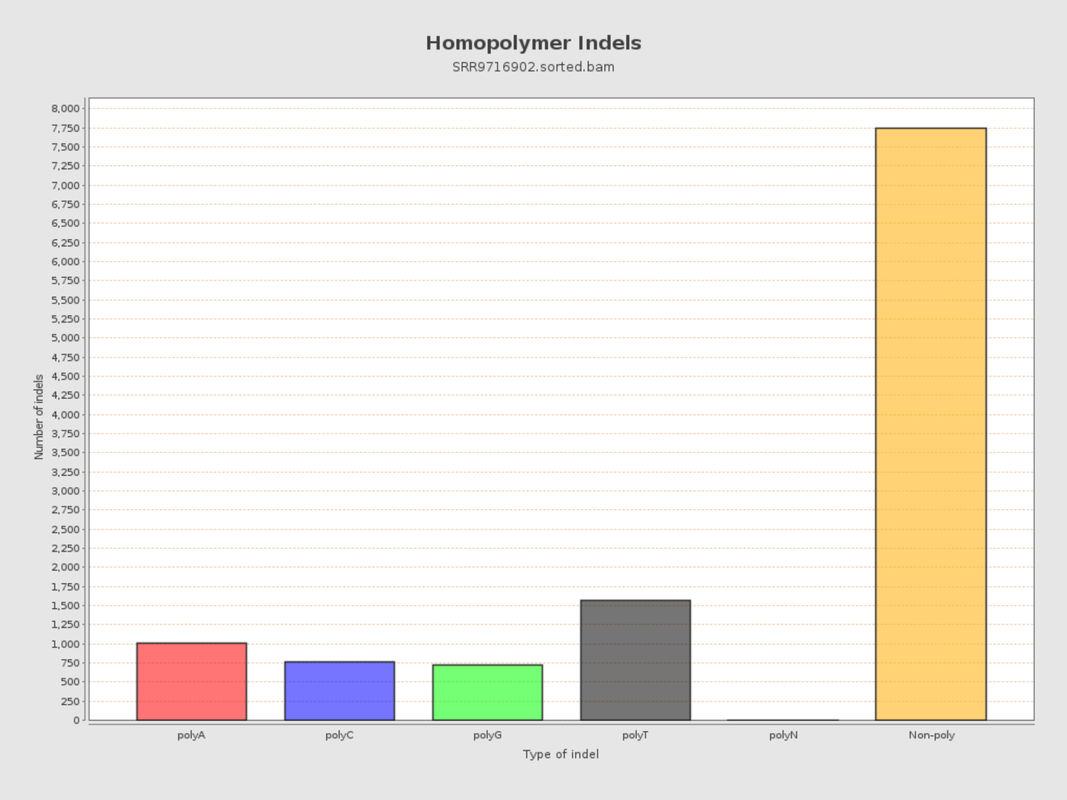
9. Results : Mapped Reads GC-content Distribution



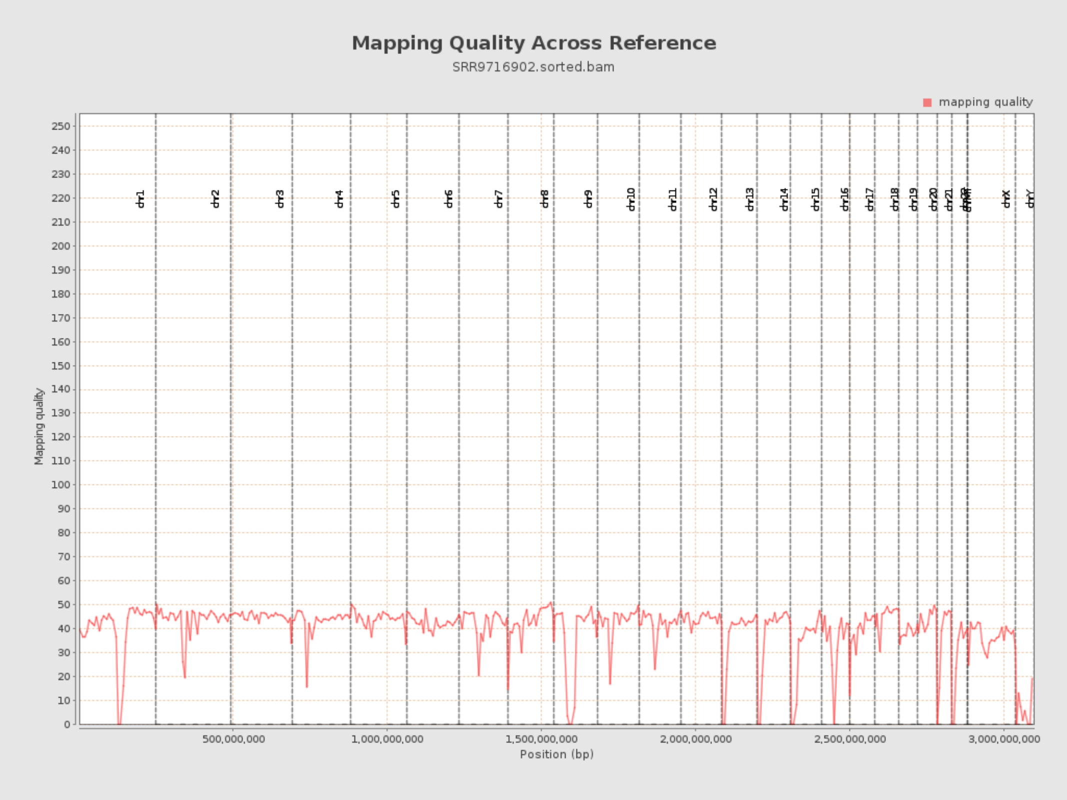
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram