Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 15:35:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716469.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_SRR9716469 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716469.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 15:35:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716469.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	590,680
Mapped reads	539,564 / 91.35%
Unmapped reads	51,116 / 8.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,743 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	11,581 / 1.96%
Duplication rate	1.51%
Clipped reads	541,027 / 91.59%

2.2. ACGT Content

Number/percentage of A's	7,578,930 / 24.37%
Number/percentage of C's	6,011,167 / 19.33%
Number/percentage of T's	9,814,312 / 31.56%
Number/percentage of G's	7,695,287 / 24.74%
Number/percentage of N's	594 / 0%
GC Percentage	44.07%

2.3. Coverage

Mean	0.01

Standard Deviation	0.1297

2.4. Mapping Quality

Mean Mapping Quality	44.23

2.5. Mismatches and indels

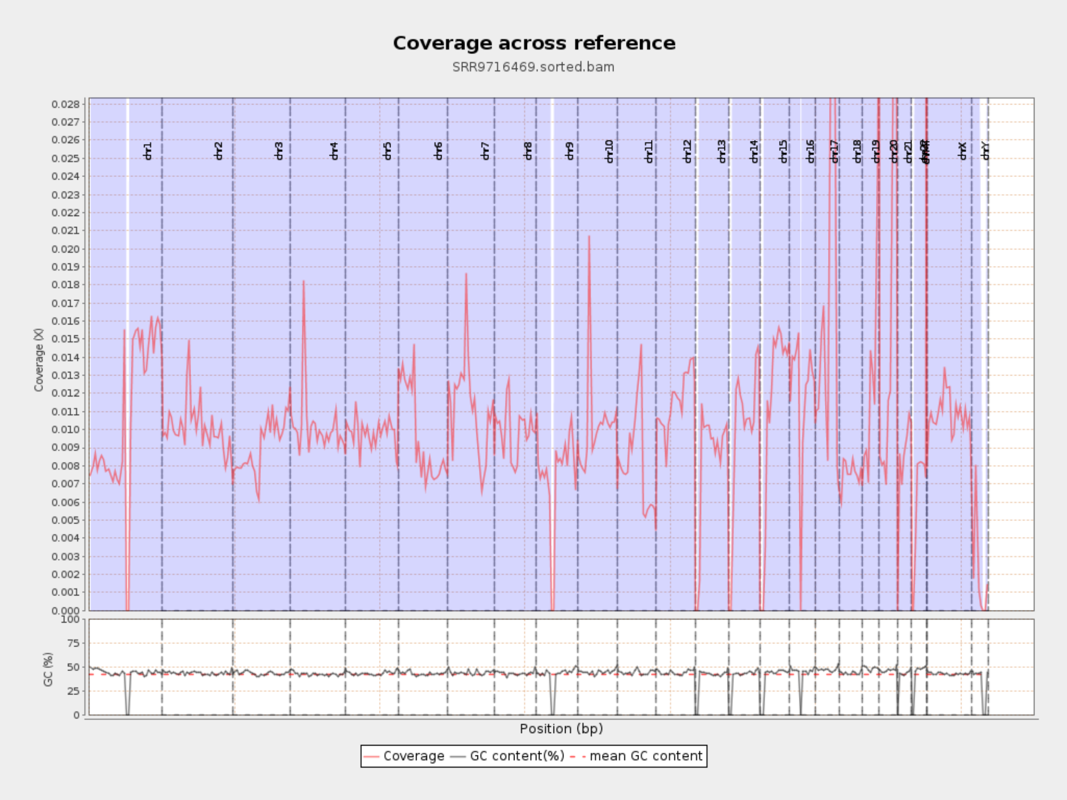
General error rate	0.52%
Mismatches	156,721
Insertions	1,963
Mapped reads with at least one insertion	0.36%
Deletions	5,568
Mapped reads with at least one deletion	1.02%
Homopolymer indels	42.94%

2.6. Chromosome stats

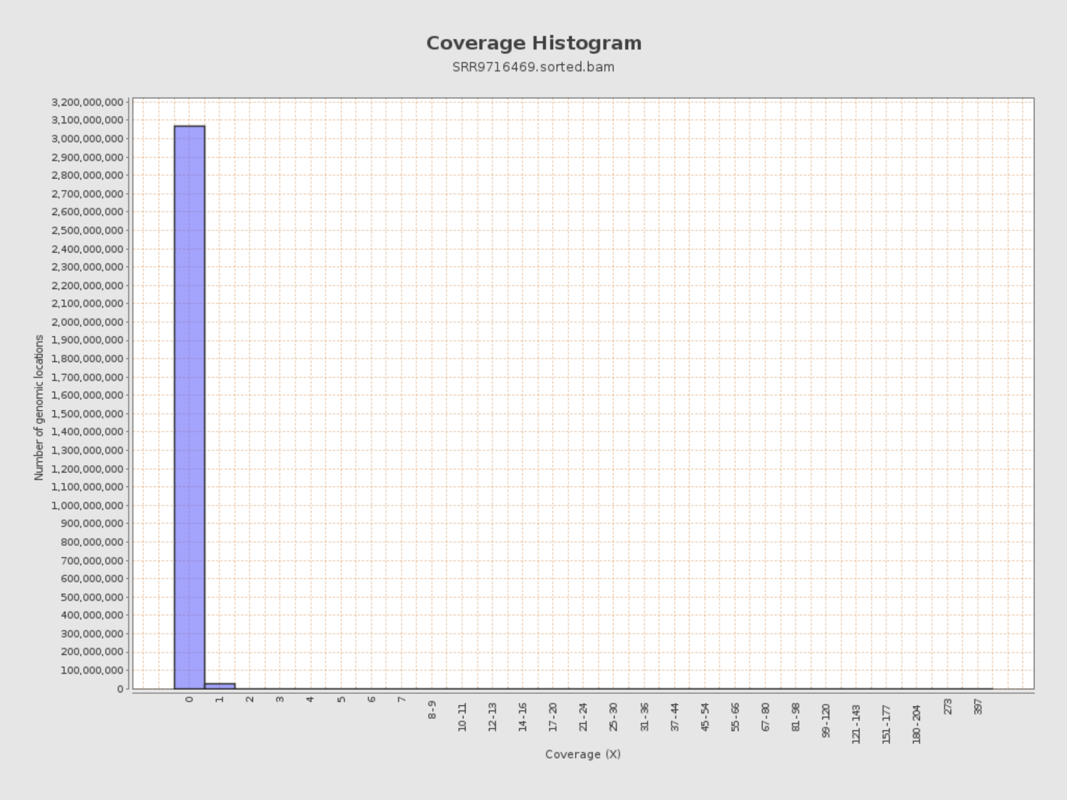
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2641168	0.0106	0.1768
chr2	243199373	2467493	0.0101	0.187
chr3	198022430	1797111	0.0091	0.0991
chr4	191154276	1939943	0.0101	0.1129
chr5	180915260	1775712	0.0098	0.1026
chr6	171115067	1656760	0.0097	0.1104
chr7	159138663	1784555	0.0112	0.1521

chr8	146364022	1448824	0.0099	0.1571
chr9	141213431	1037941	0.0074	0.0986
chr10	135534747	1382420	0.0102	0.1338
chr11	135006516	1116283	0.0083	0.1032
chr12	133851895	1551630	0.0116	0.112
chr13	115169878	936224	0.0081	0.0936
chr14	107349540	1048603	0.0098	0.1022
chr15	102531392	1135491	0.0111	0.1092
chr16	90354753	1085755	0.012	0.1158
chr17	81195210	1383024	0.017	0.1373
chr18	78077248	590738	0.0076	0.1309
chr19	59128983	796984	0.0135	0.1532
chr20	63025520	1039488	0.0165	0.1349
chr21	48129895	397595	0.0083	0.1026
chr22	51304566	293206	0.0057	0.0777
chrMT	16571	1617	0.0976	0.3333
chrX	155270560	1681682	0.0108	0.1116
chrY	59373566	118983	0.002	0.0894

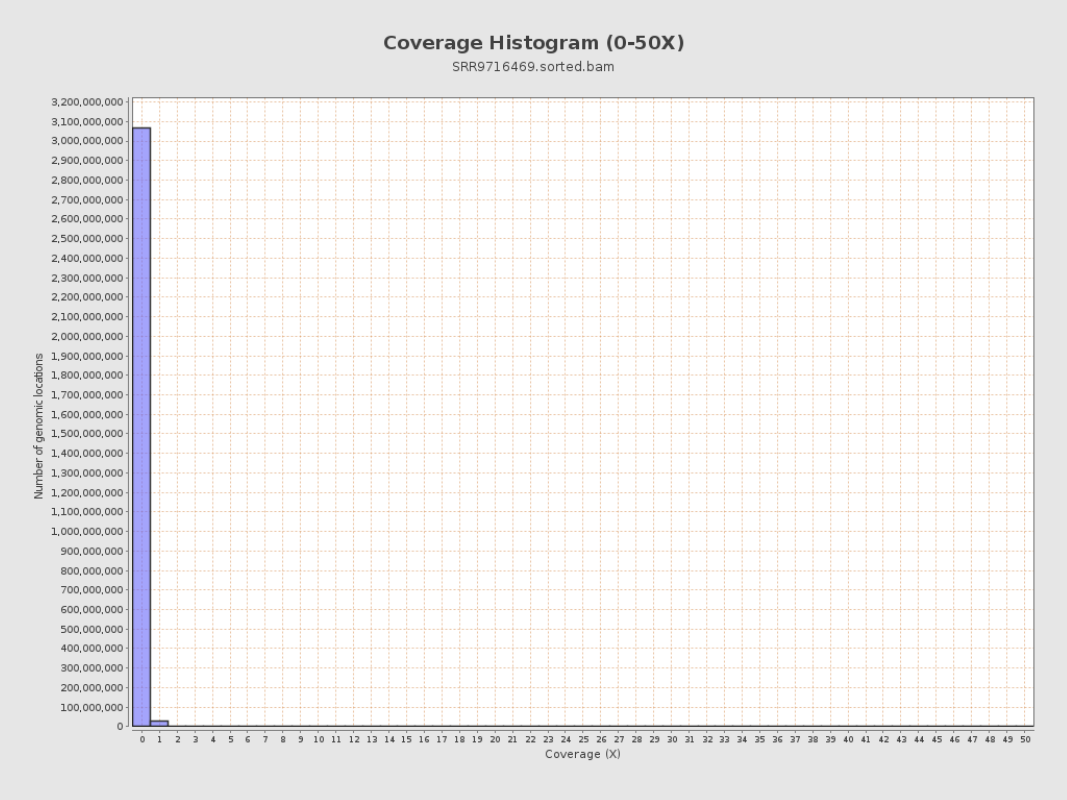
3. Results : Coverage across reference



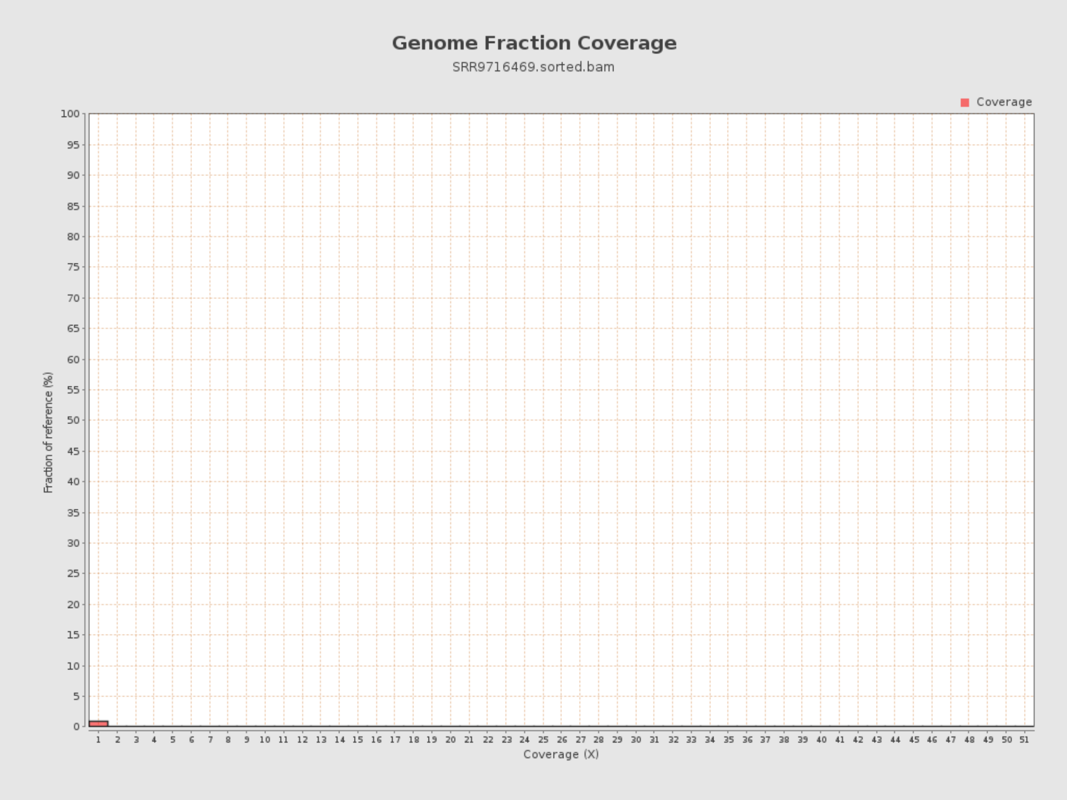
4. Results : Coverage Histogram



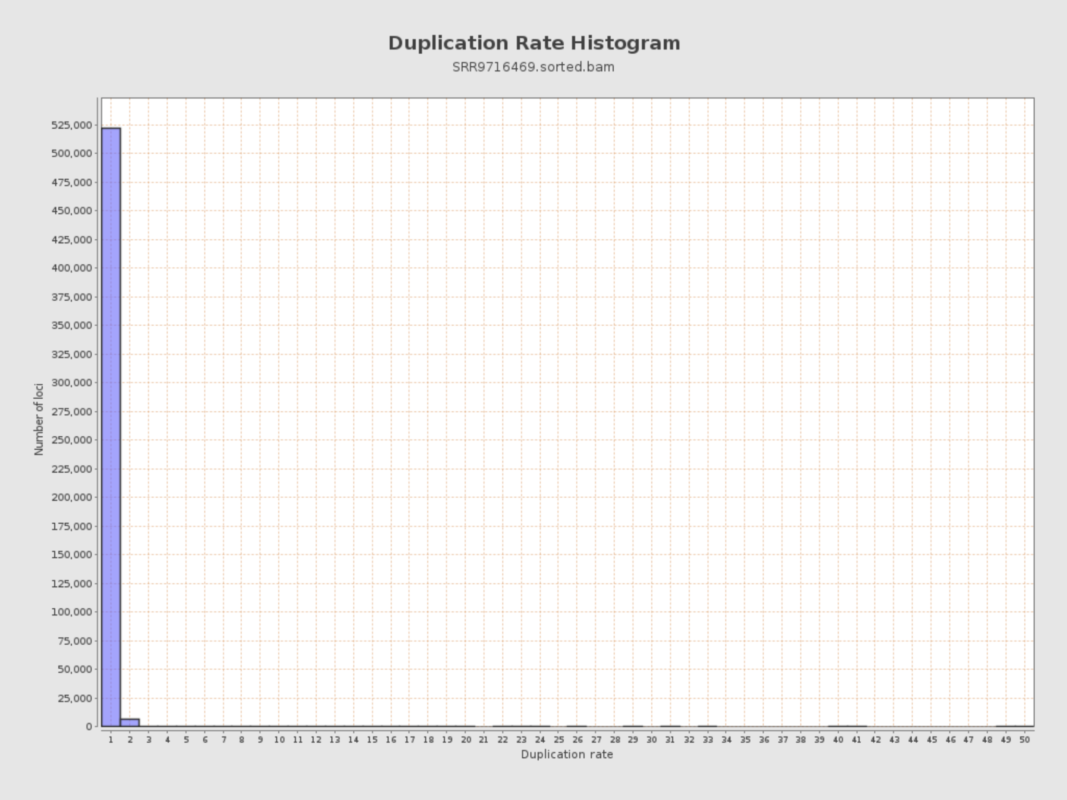
5. Results : Coverage Histogram (0-50X)



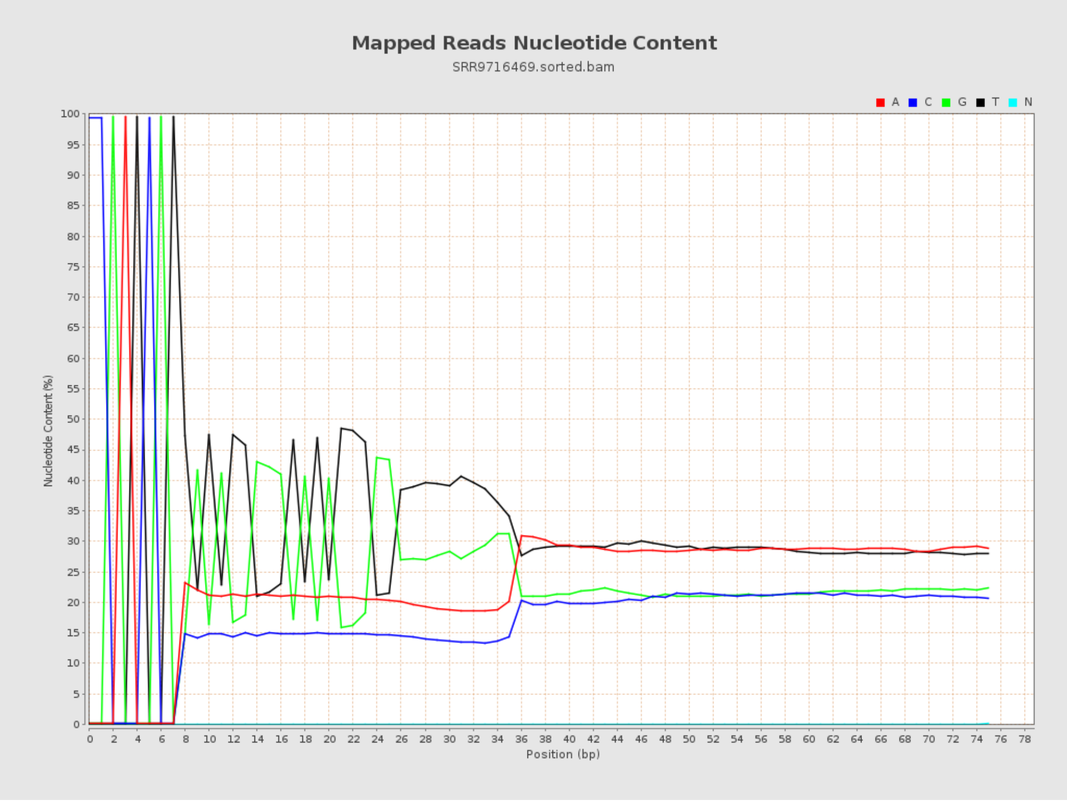
6. Results : Genome Fraction Coverage



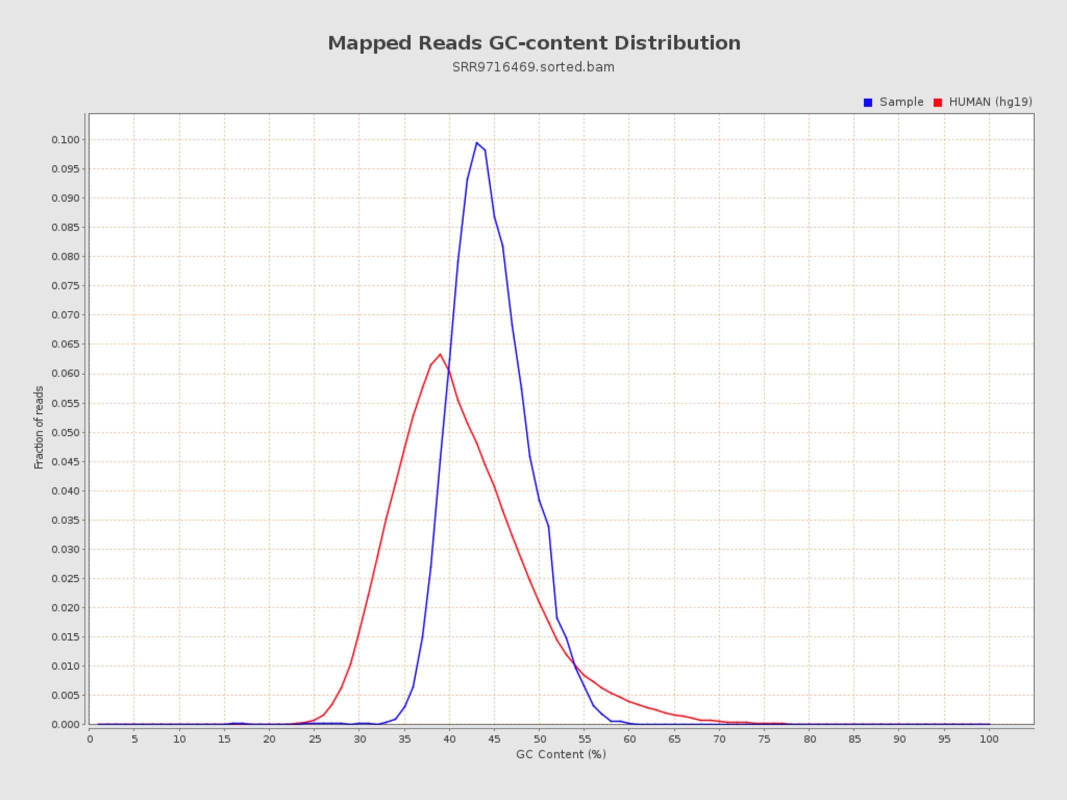
7. Results : Duplication Rate Histogram



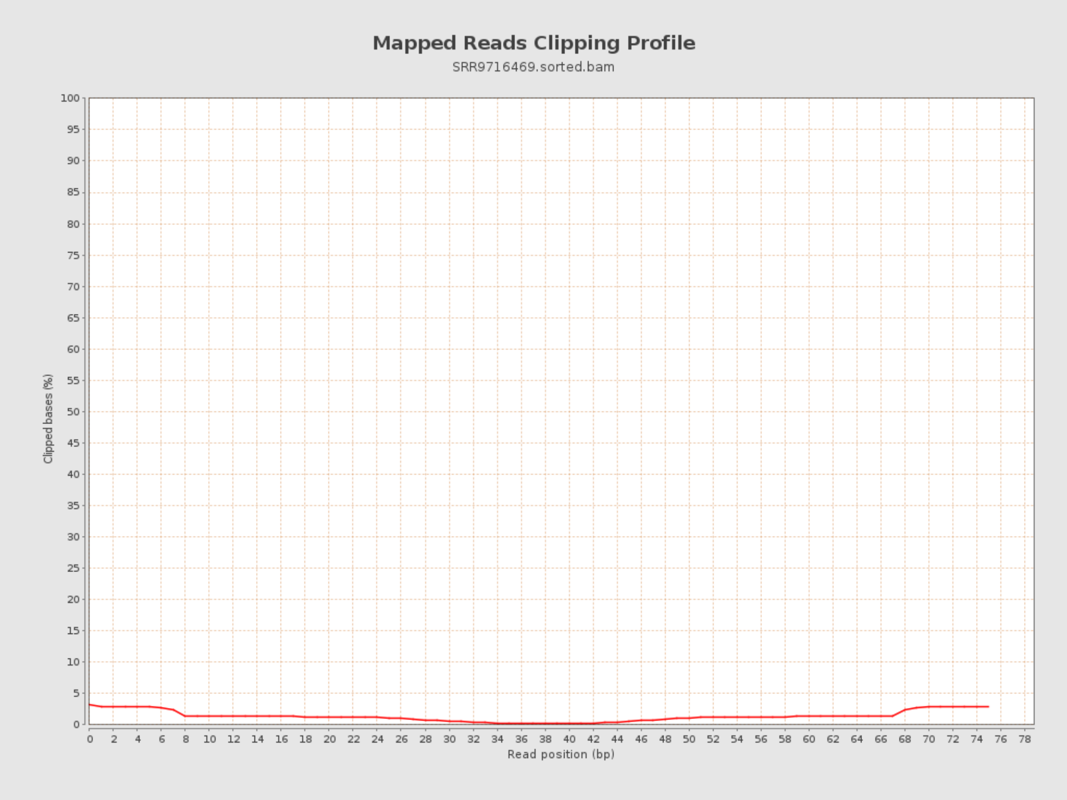
8. Results : Mapped Reads Nucleotide Content



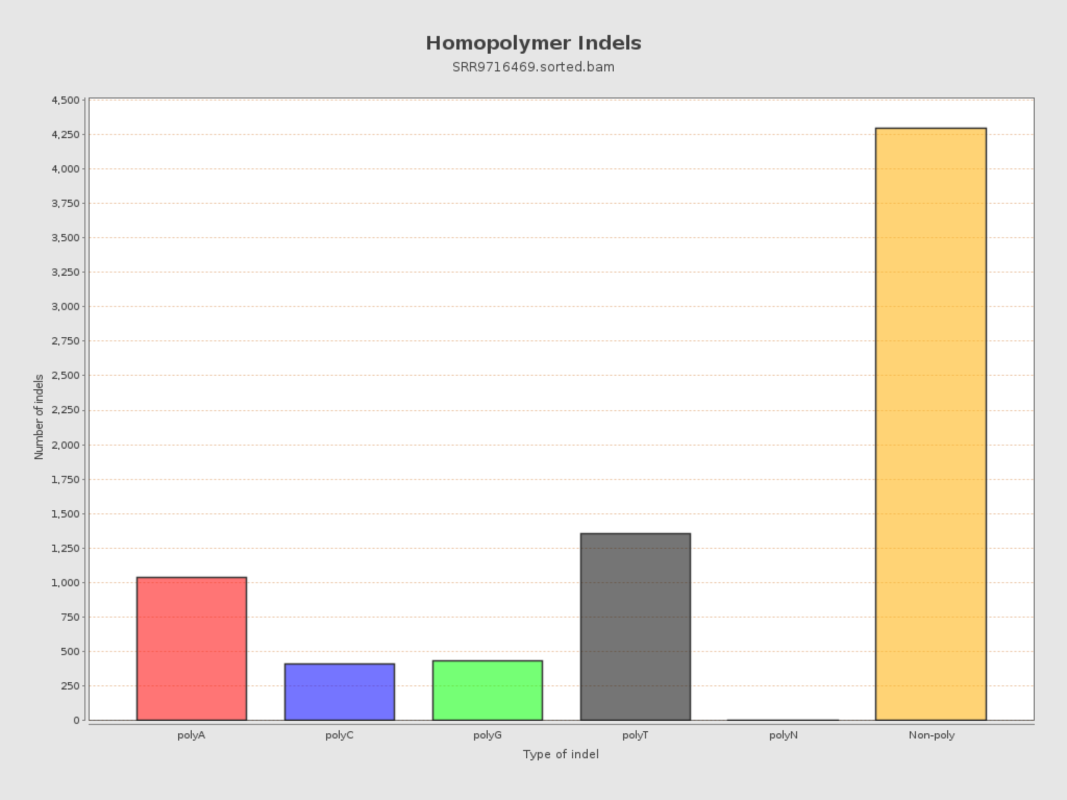
9. Results : Mapped Reads GC-content Distribution



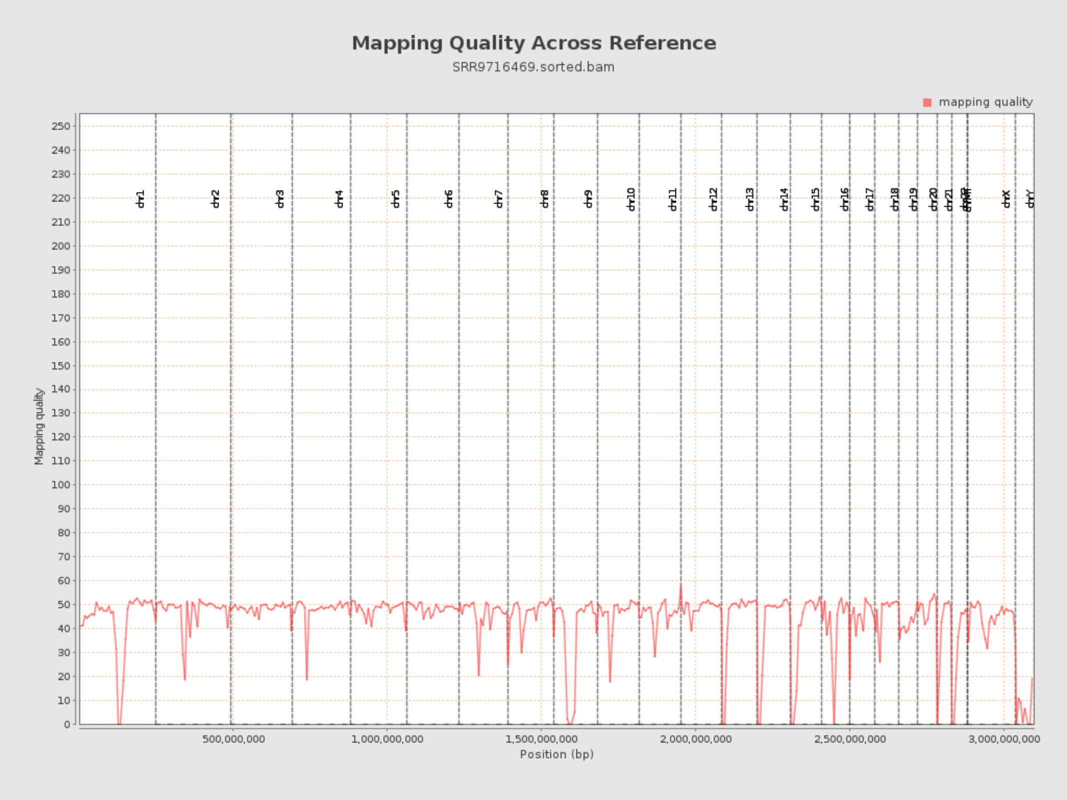
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram