Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 18:56:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716926.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_SRR9716926 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716926.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 18:56:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716926.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,781,454
Mapped reads	1,649,770 / 92.61%
Unmapped reads	131,684 / 7.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,394 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	57,891 / 3.25%
Duplication rate	2.62%
Clipped reads	1,654,420 / 92.87%

2.2. ACGT Content

Number/percentage of A's	24,056,448 / 25.02%
Number/percentage of C's	19,580,834 / 20.37%
Number/percentage of T's	29,296,911 / 30.47%
Number/percentage of G's	23,208,810 / 24.14%
Number/percentage of N's	2,673 / 0%
GC Percentage	44.51%

2.3. Coverage

Mean	0.0311

Standard Deviation	0.274

2.4. Mapping Quality

Mean Mapping Quality	44.88

2.5. Mismatches and indels

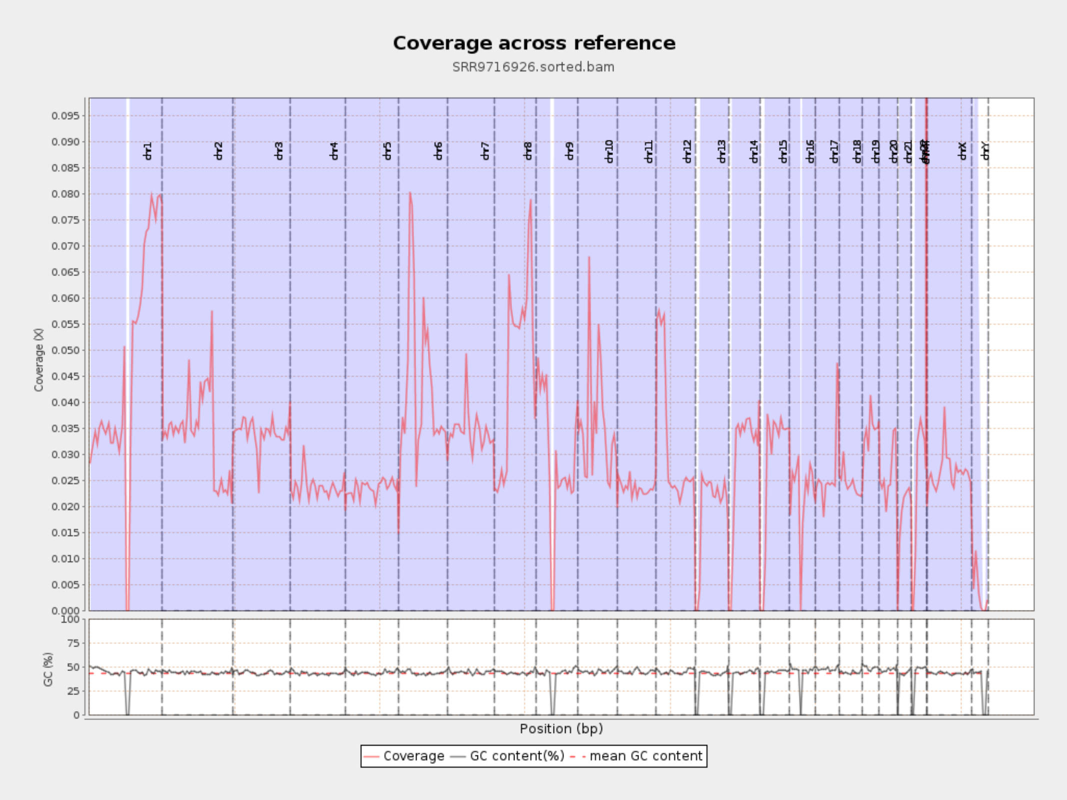
General error rate	0.49%
Mismatches	460,821
Insertions	6,575
Mapped reads with at least one insertion	0.4%
Deletions	16,148
Mapped reads with at least one deletion	0.97%
Homopolymer indels	42.86%

2.6. Chromosome stats

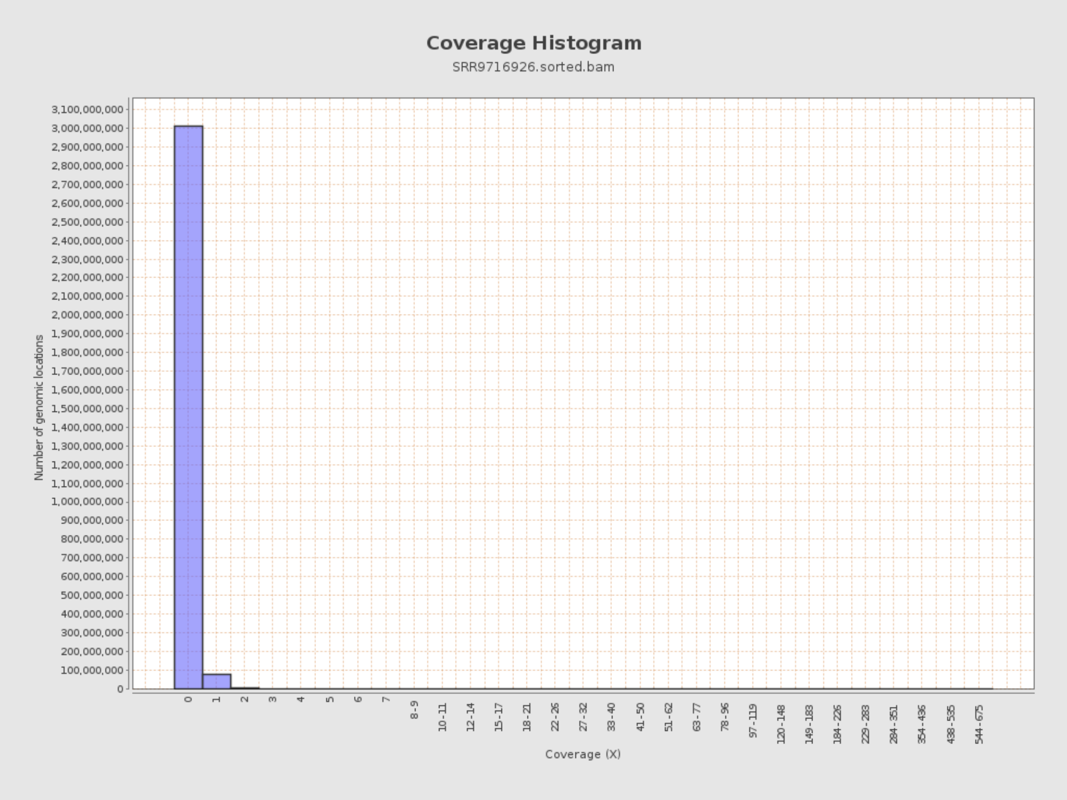
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11601093	0.0465	0.4768
chr2	243199373	8309730	0.0342	0.3495
chr3	198022430	6747169	0.0341	0.2059
chr4	191154276	4521333	0.0237	0.1752
chr5	180915260	4265428	0.0236	0.1716
chr6	171115067	7349867	0.043	0.2985
chr7	159138663	5536635	0.0348	0.3382

chr8	146364022	6983072	0.0477	0.268
chr9	141213431	4020070	0.0285	0.2386
chr10	135534747	4883160	0.036	0.3163
chr11	135006516	3166544	0.0235	0.2166
chr12	133851895	4281622	0.032	0.2027
chr13	115169878	2240999	0.0195	0.1538
chr14	107349540	3088673	0.0288	0.202
chr15	102531392	2886391	0.0282	0.1839
chr16	90354753	2036606	0.0225	0.1853
chr17	81195210	2195847	0.027	0.1855
chr18	78077248	1911626	0.0245	0.4165
chr19	59128983	2042734	0.0345	0.3422
chr20	63025520	1651905	0.0262	0.1786
chr21	48129895	888072	0.0185	0.1672
chr22	51304566	1188709	0.0232	0.1675
chrMT	16571	15349	0.9263	1.1172
chrX	155270560	4140939	0.0267	0.2051
chrY	59373566	217652	0.0037	0.0899

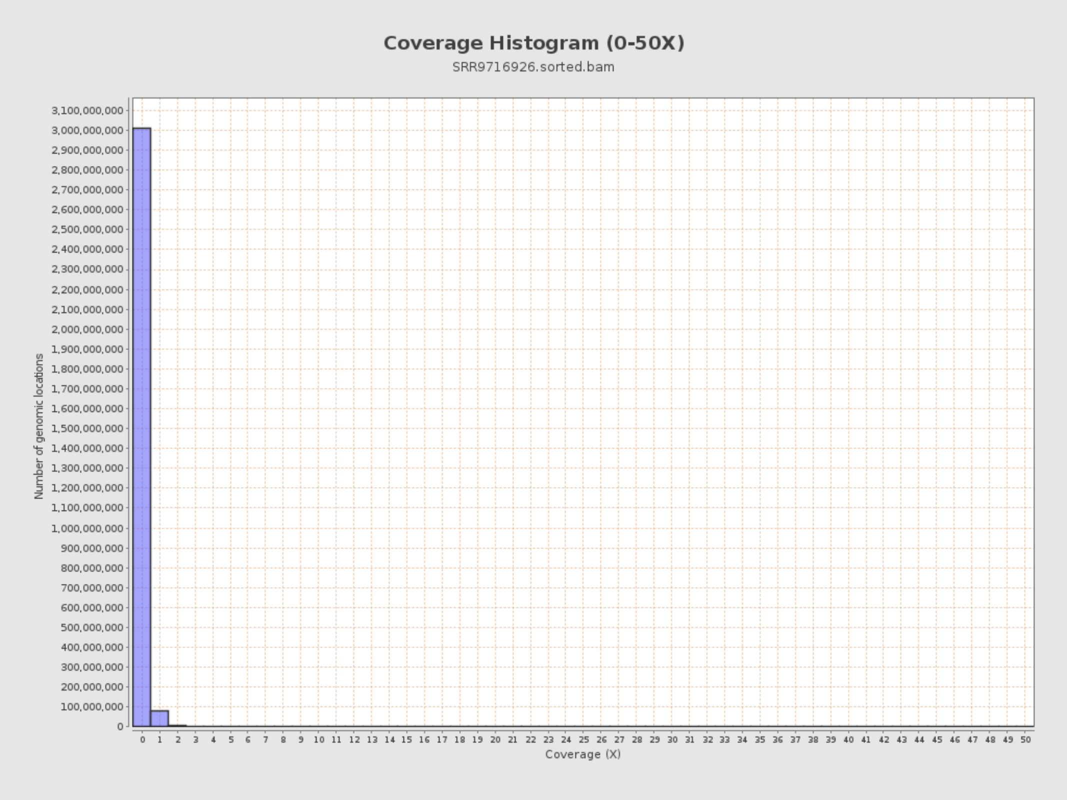
3. Results : Coverage across reference



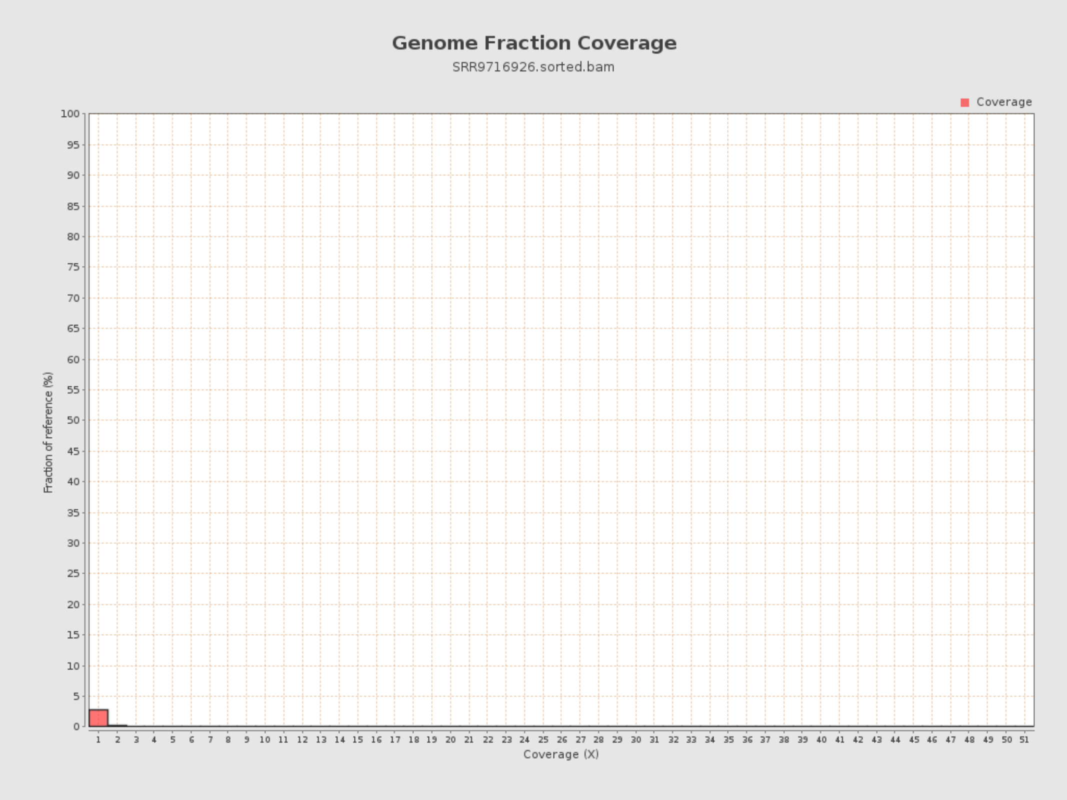
4. Results : Coverage Histogram



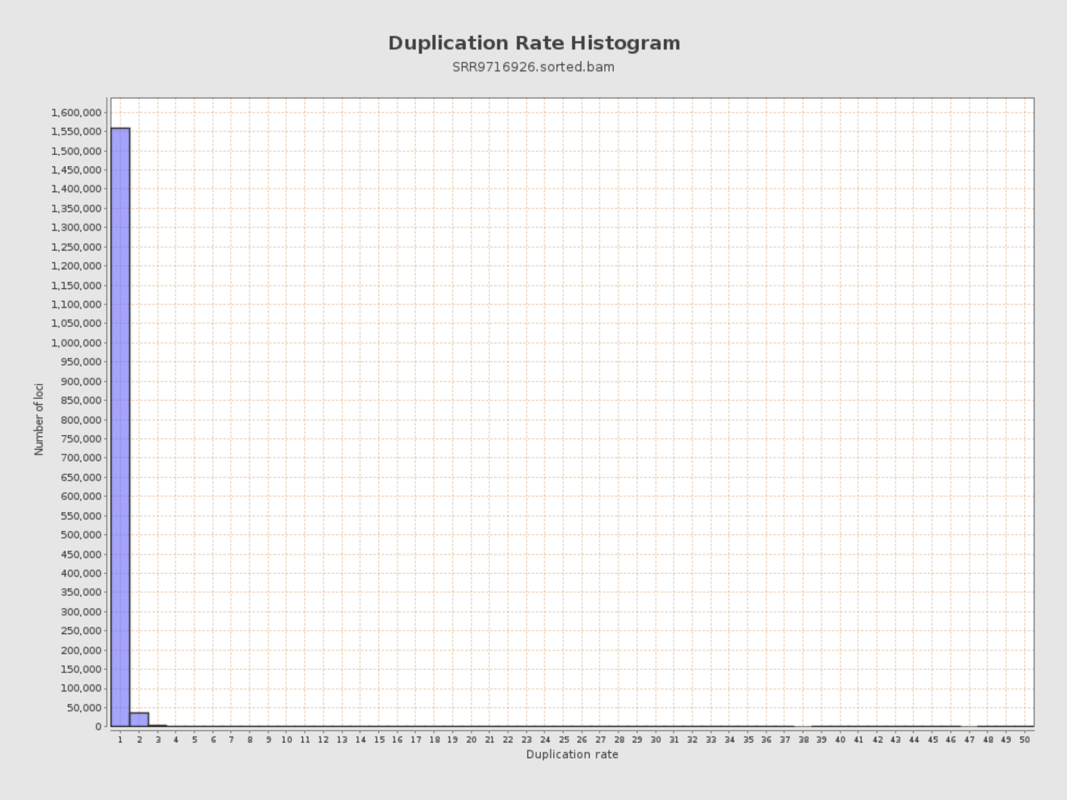
5. Results : Coverage Histogram (0-50X)



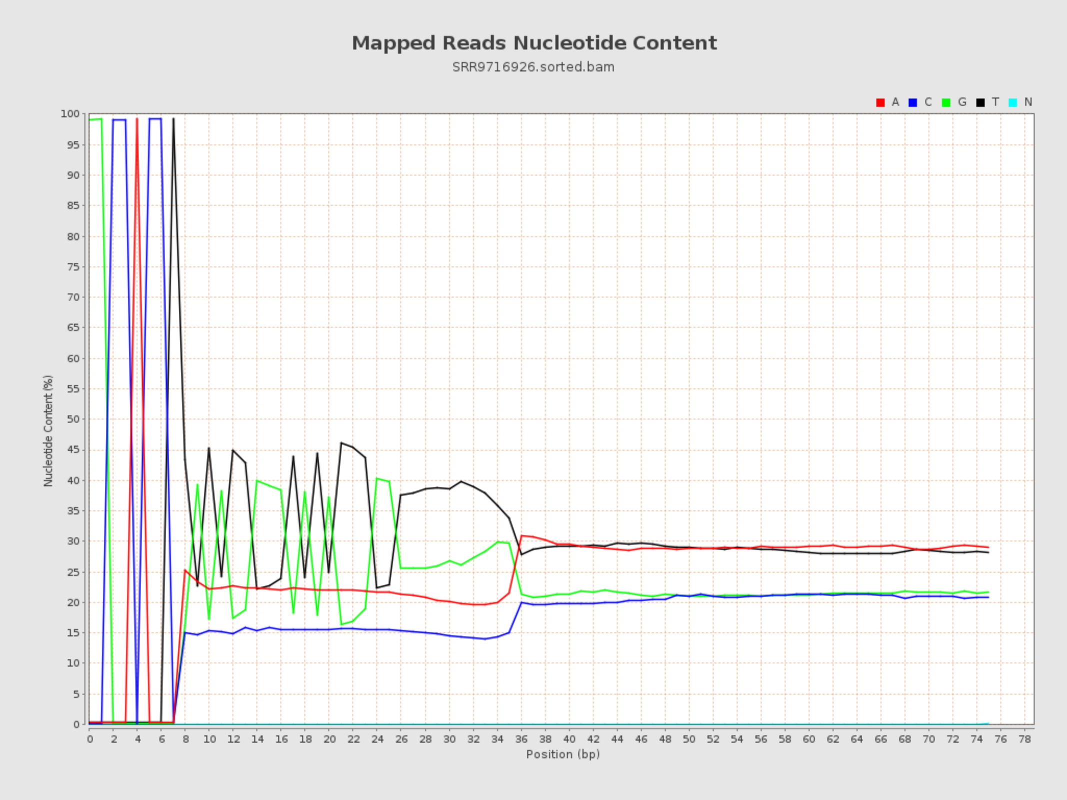
6. Results : Genome Fraction Coverage



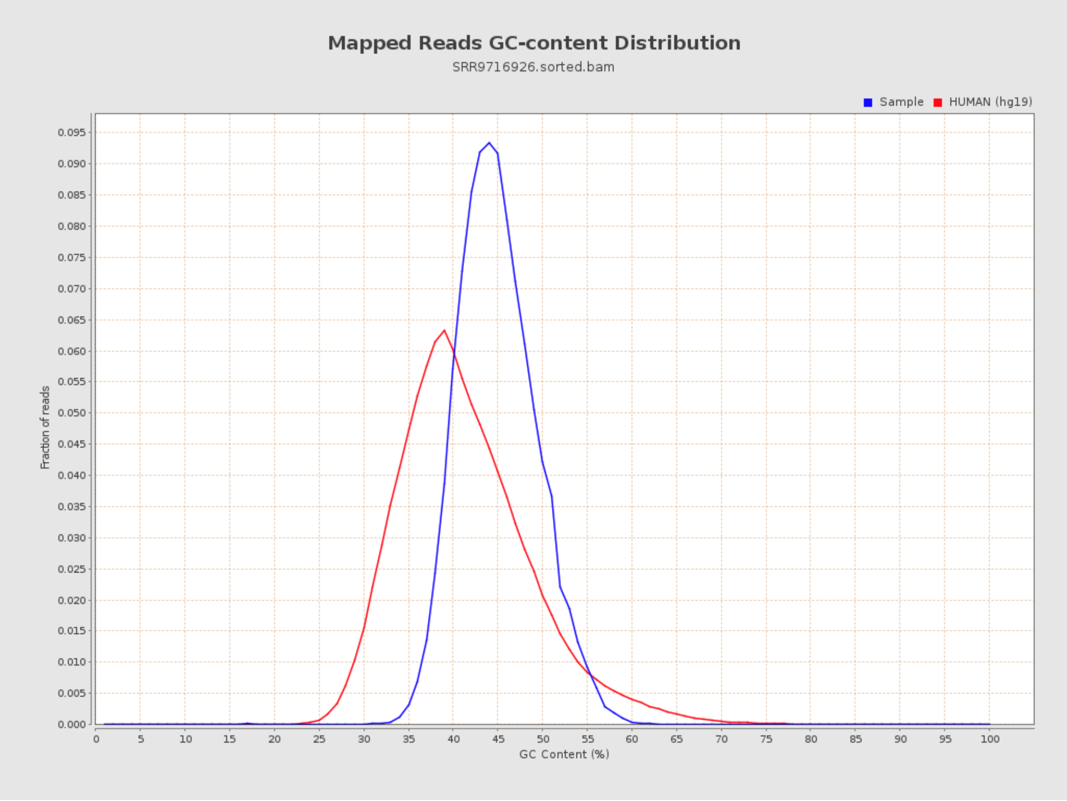
7. Results : Duplication Rate Histogram



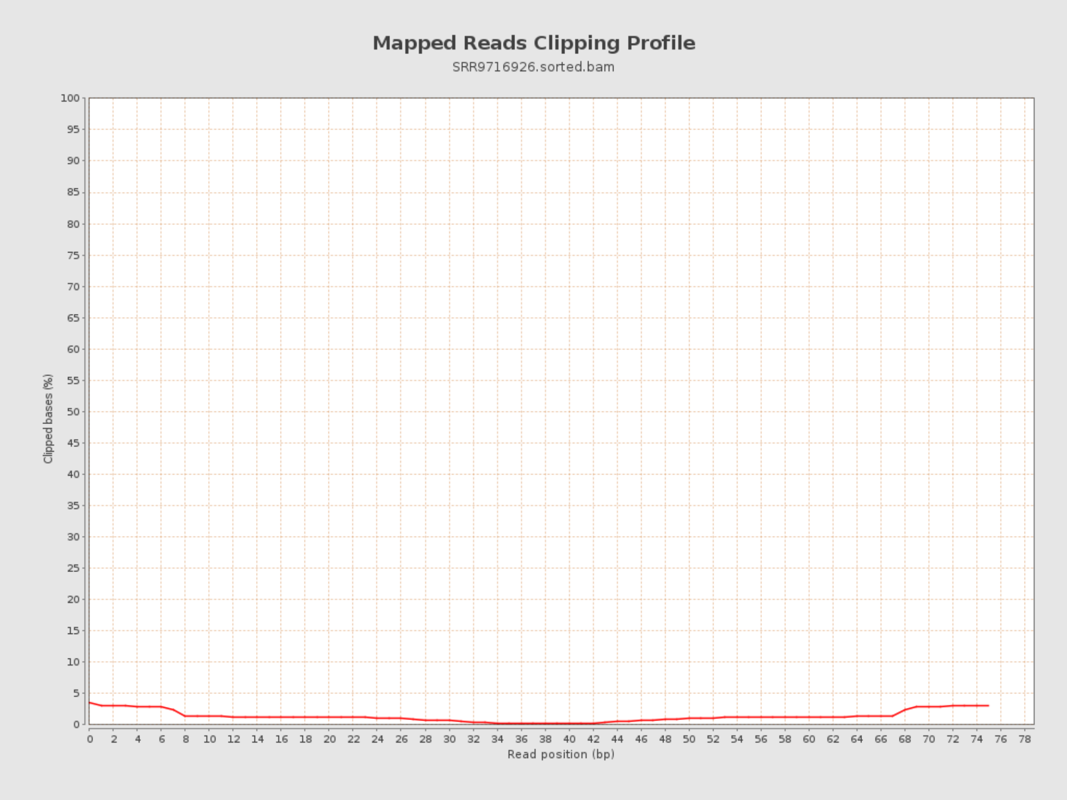
8. Results : Mapped Reads Nucleotide Content



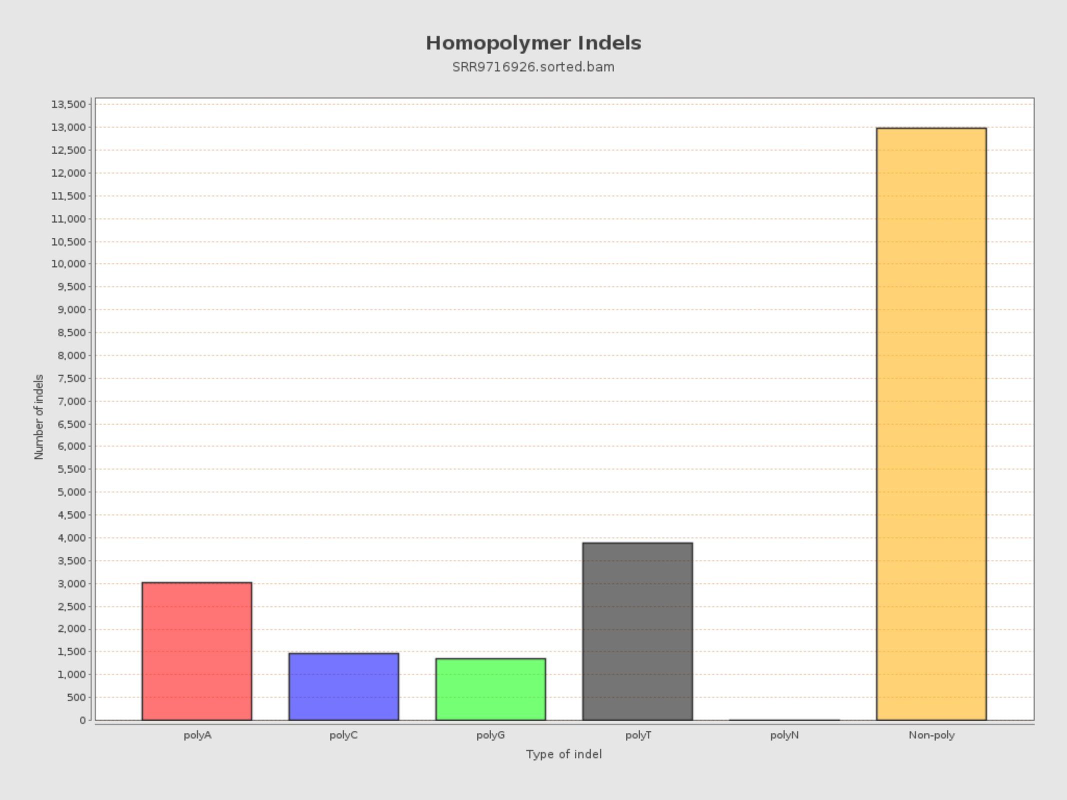
9. Results : Mapped Reads GC-content Distribution



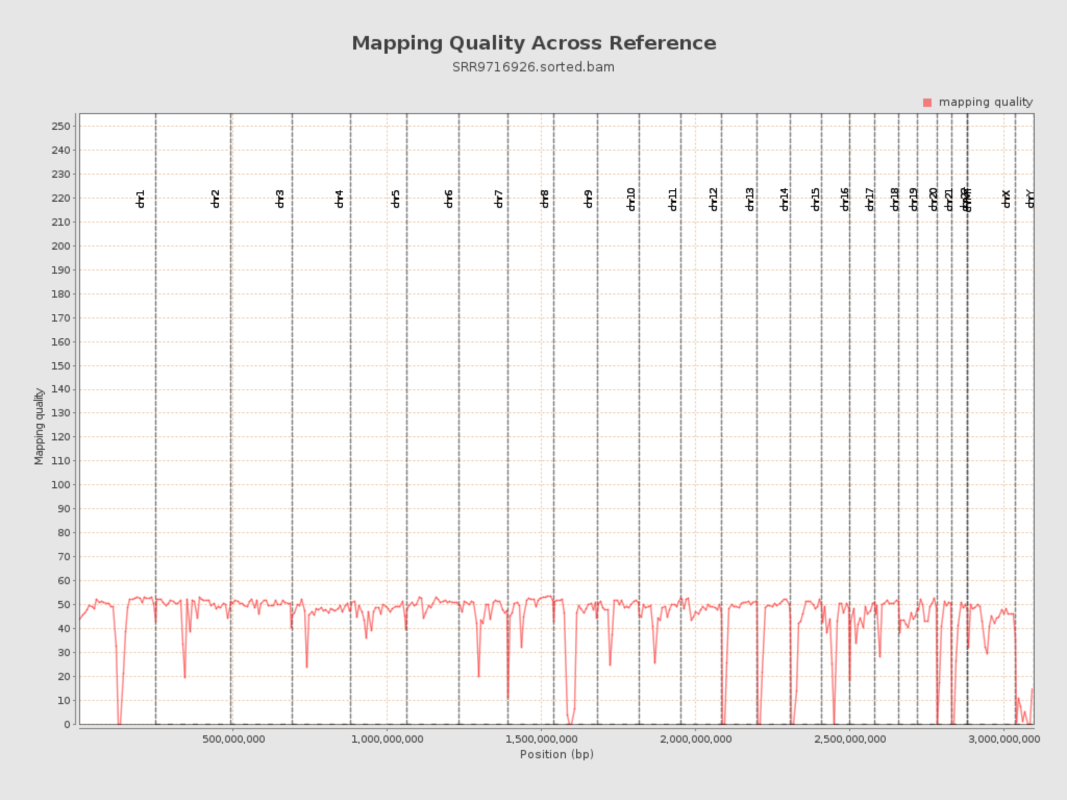
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram