Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 19:21:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716938.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_SRR9716938 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716938.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 19:21:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716938.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	502,432
Mapped reads	344,643 / 68.59%
Unmapped reads	157,789 / 31.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	359 / 0.07%
Read min/max/mean length	30 / 76 / 76.02
Duplicated reads (estimated)	15,914 / 3.17%
Duplication rate	4.11%
Clipped reads	344,352 / 68.54%

2.2. ACGT Content

Number/percentage of A's	3,682,982 / 20.51%
Number/percentage of C's	3,280,232 / 18.27%
Number/percentage of T's	6,237,238 / 34.74%
Number/percentage of G's	4,754,760 / 26.48%
Number/percentage of N's	261 / 0%
GC Percentage	44.75%

2.3. Coverage

Mean	0.0058

Standard Deviation	0.0887

2.4. Mapping Quality

Mean Mapping Quality	42.13

2.5. Mismatches and indels

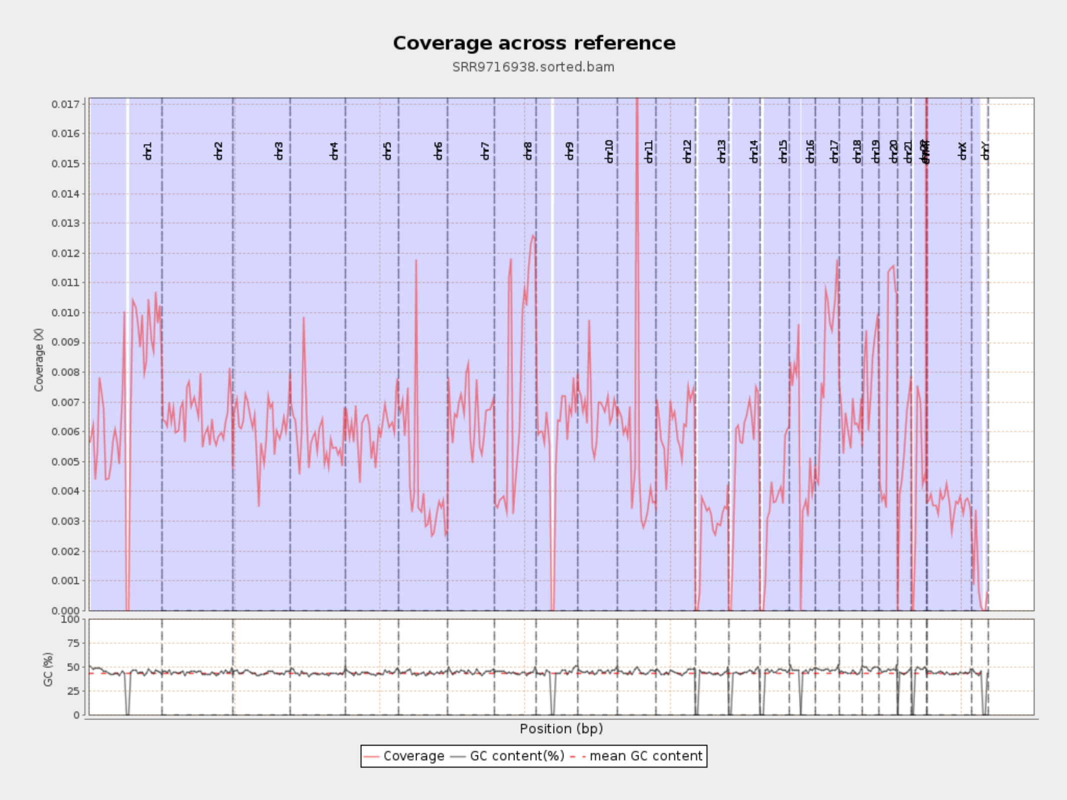
General error rate	0.75%
Mismatches	132,669
Insertions	1,089
Mapped reads with at least one insertion	0.31%
Deletions	2,882
Mapped reads with at least one deletion	0.83%
Homopolymer indels	39.41%

2.6. Chromosome stats

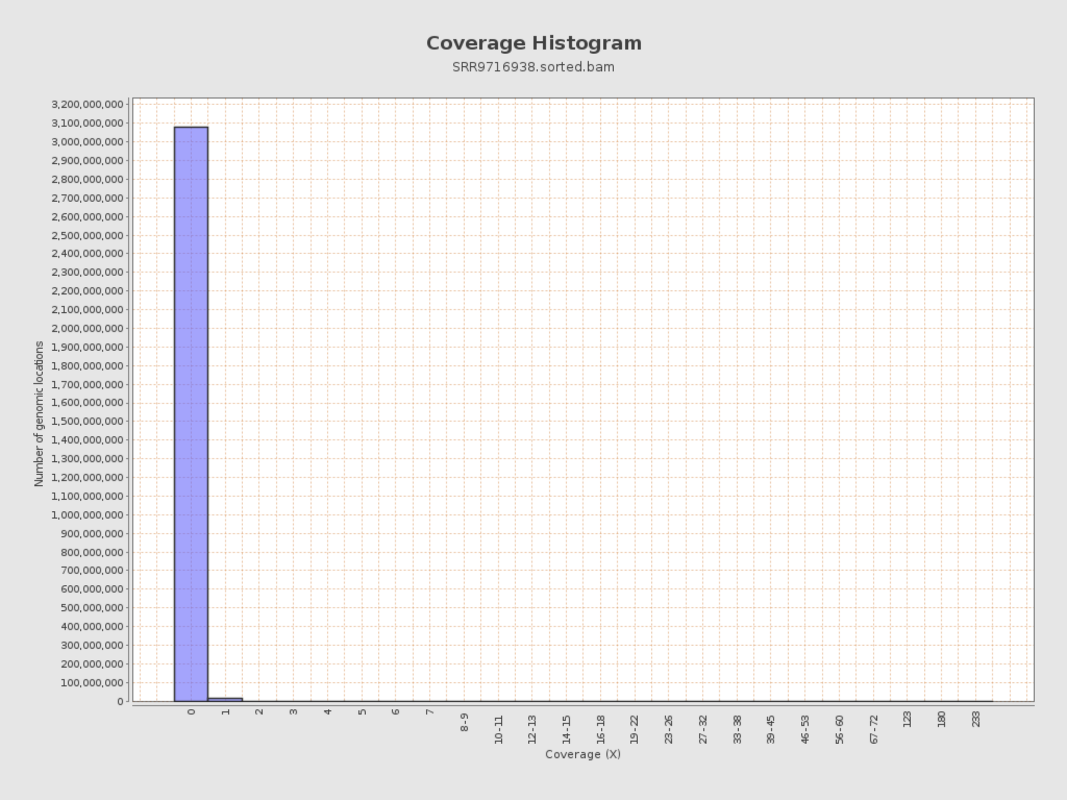
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1773855	0.0071	0.0994
chr2	243199373	1575386	0.0065	0.1256
chr3	198022430	1218093	0.0062	0.0842
chr4	191154276	1116855	0.0058	0.0838
chr5	180915260	1106015	0.0061	0.0836
chr6	171115067	756135	0.0044	0.0787
chr7	159138663	1044331	0.0066	0.0927

chr8	146364022	1097317	0.0075	0.0944
chr9	141213431	799394	0.0057	0.0853
chr10	135534747	918162	0.0068	0.0943
chr11	135006516	756551	0.0056	0.083
chr12	133851895	830459	0.0062	0.0847
chr13	115169878	312219	0.0027	0.0567
chr14	107349540	568509	0.0053	0.079
chr15	102531392	347996	0.0034	0.0627
chr16	90354753	483847	0.0054	0.0834
chr17	81195210	707909	0.0087	0.1023
chr18	78077248	496017	0.0064	0.0902
chr19	59128983	485386	0.0082	0.1104
chr20	63025520	493232	0.0078	0.0974
chr21	48129895	250772	0.0052	0.0808
chr22	51304566	206572	0.004	0.0701
chrMT	16571	1550	0.0935	0.3247
chrX	155270560	559716	0.0036	0.0655
chrY	59373566	54082	0.0009	0.0363

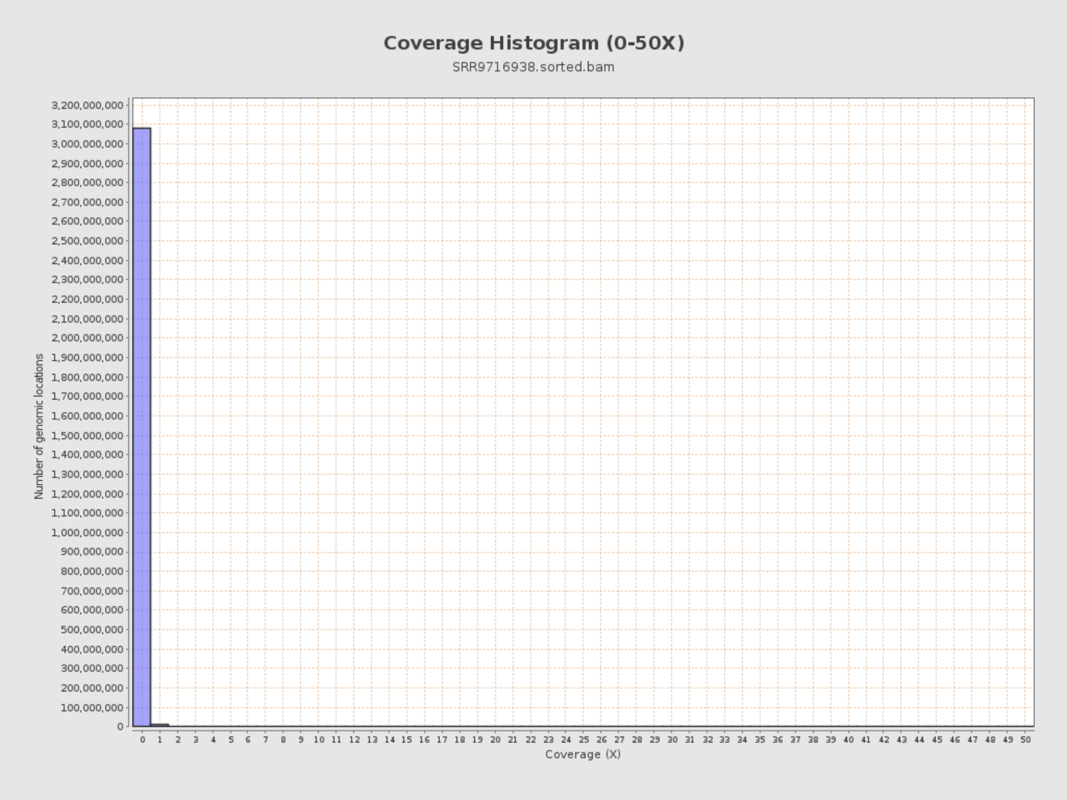
3. Results : Coverage across reference



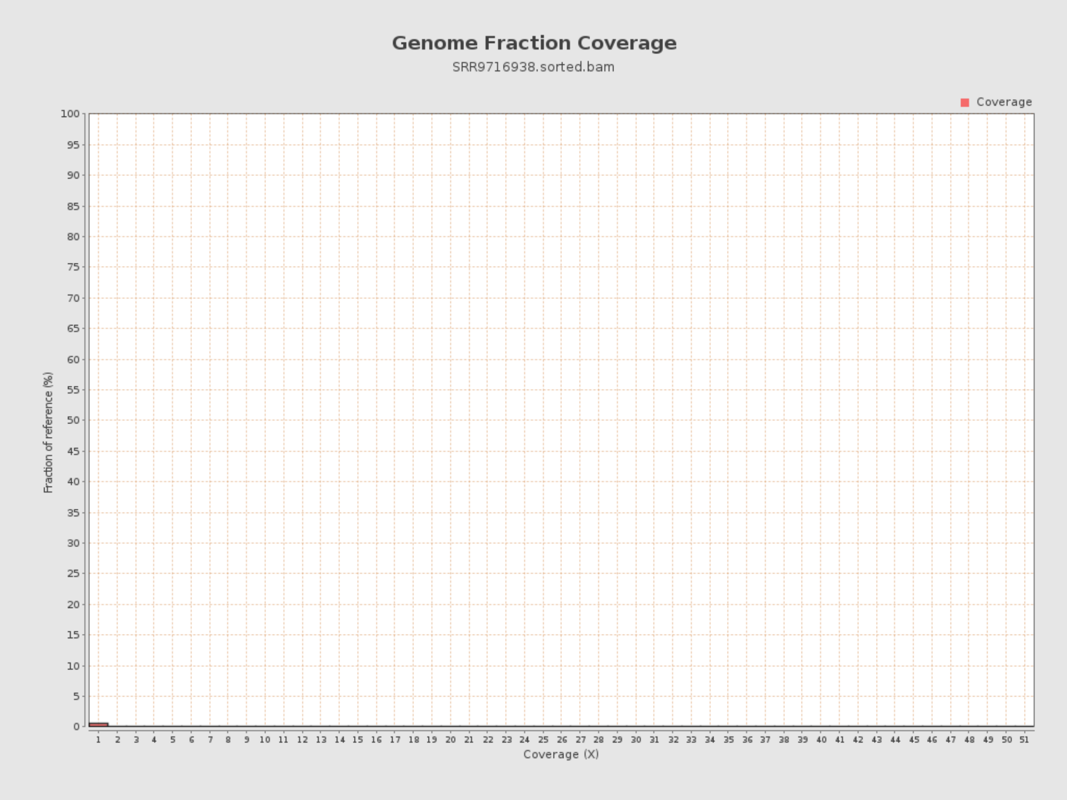
4. Results : Coverage Histogram



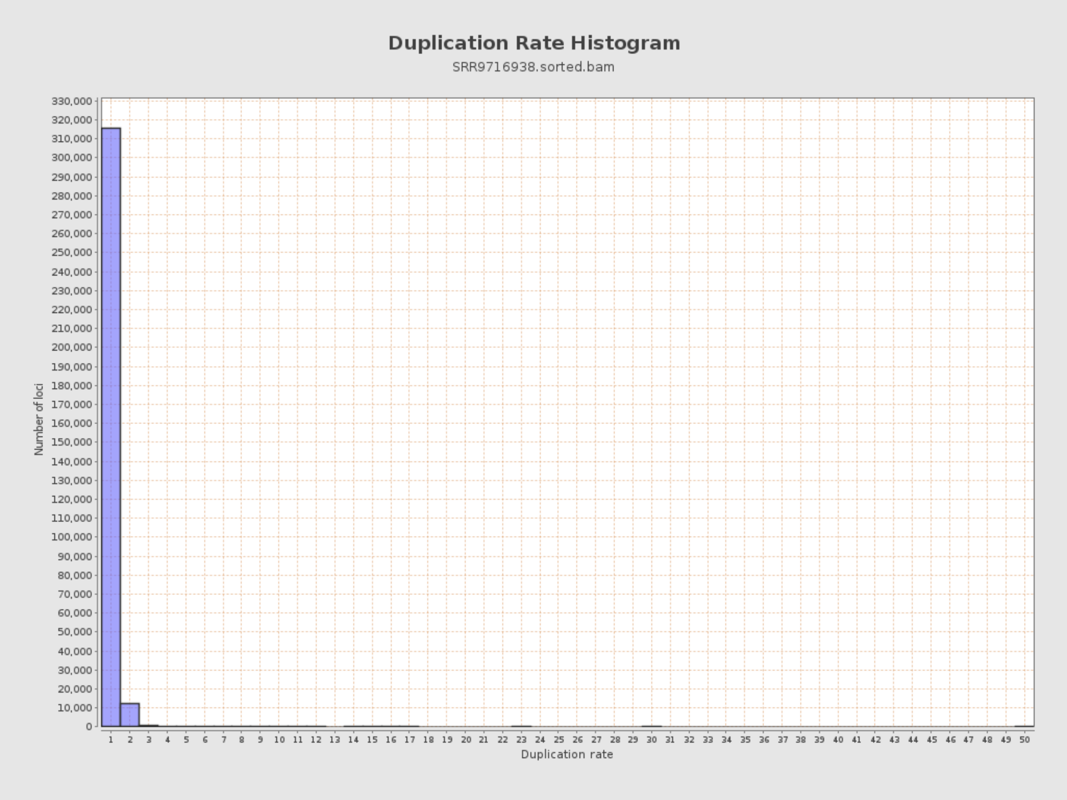
5. Results : Coverage Histogram (0-50X)



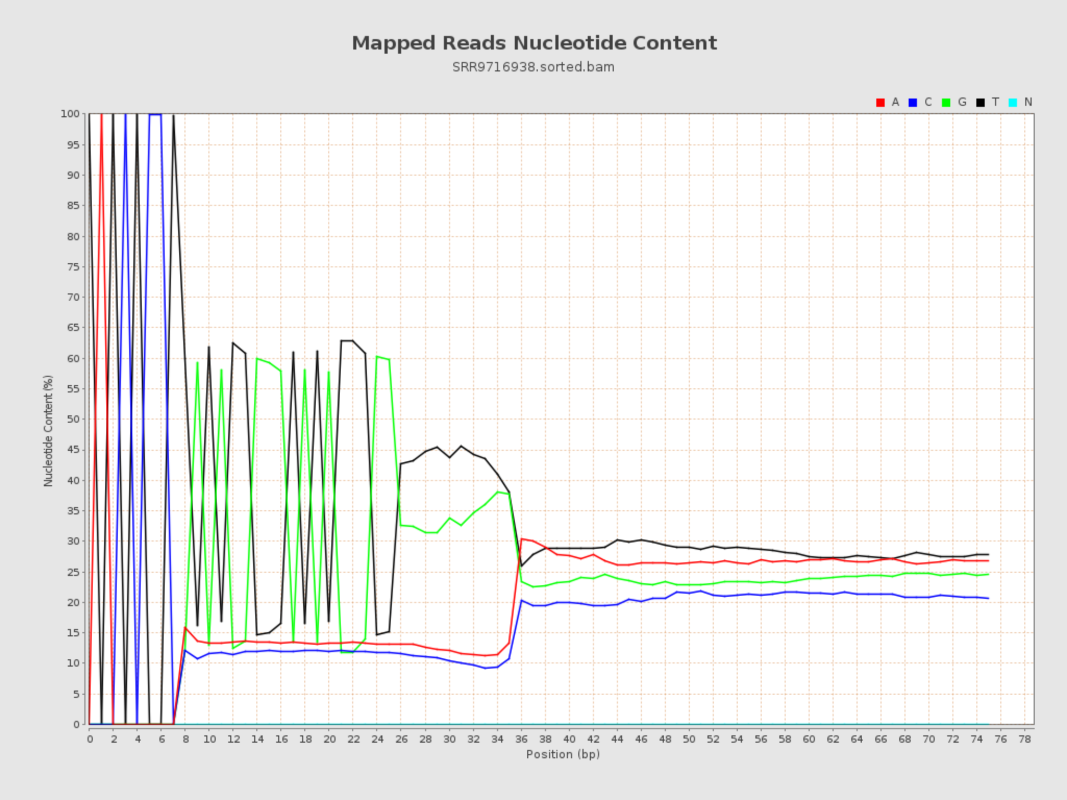
6. Results : Genome Fraction Coverage



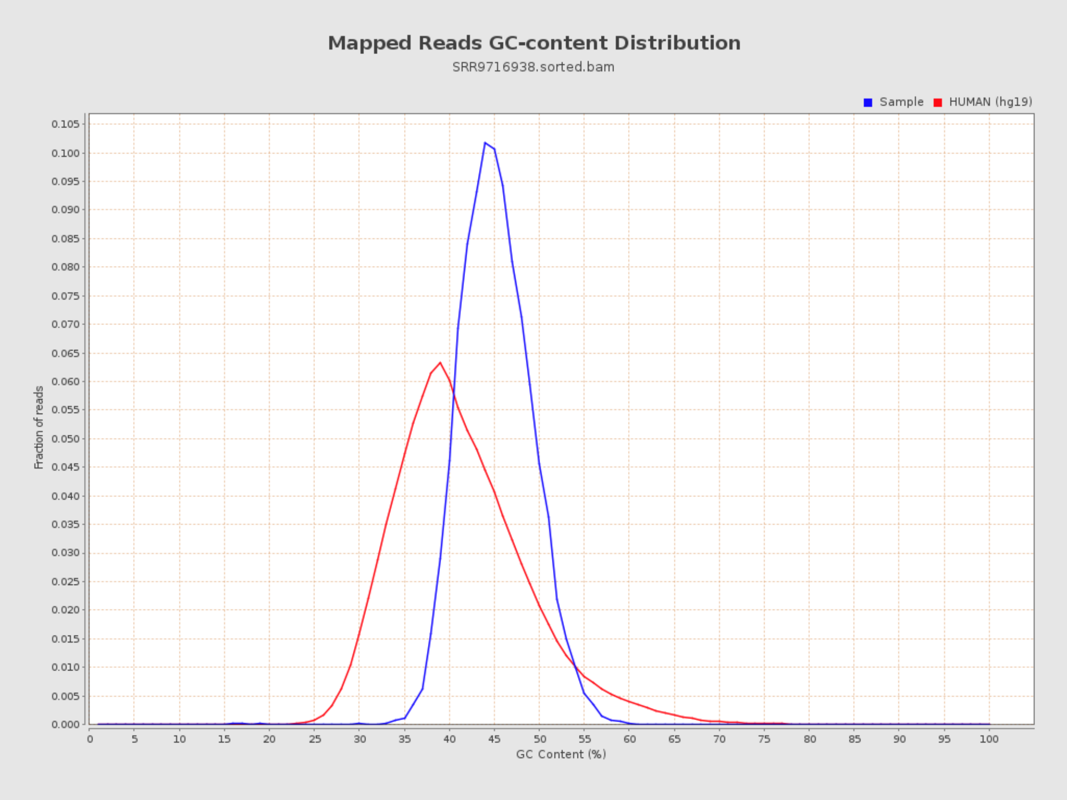
7. Results : Duplication Rate Histogram



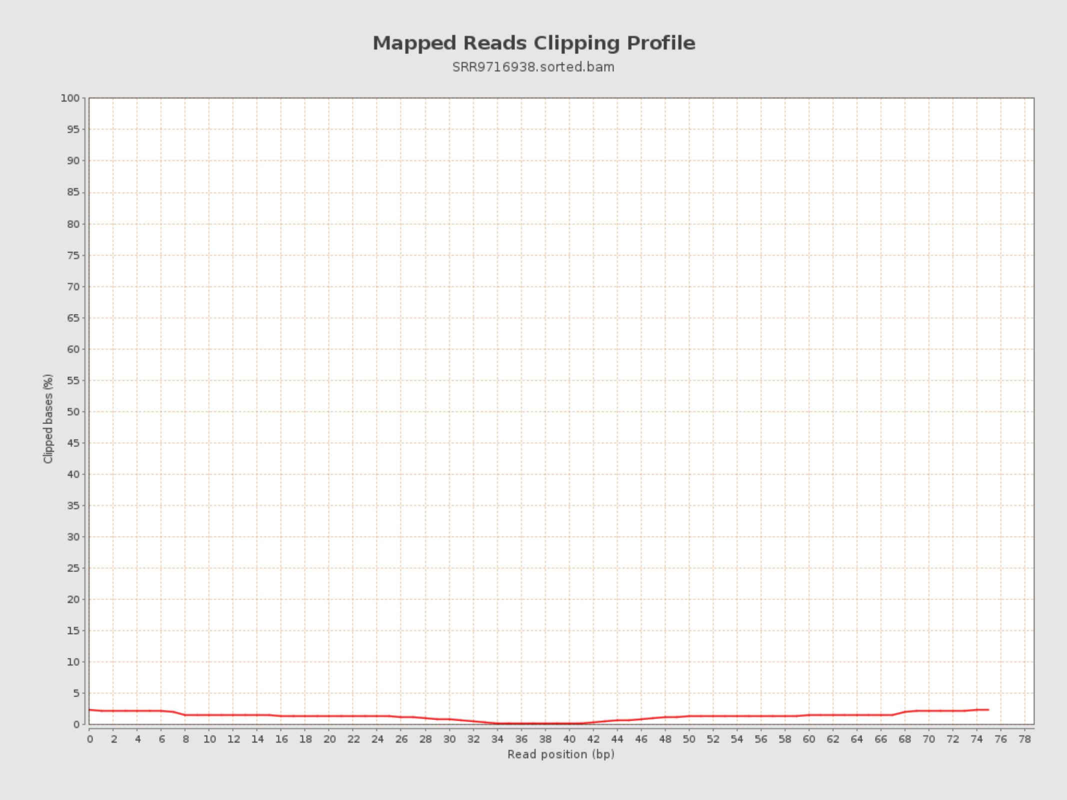
8. Results : Mapped Reads Nucleotide Content



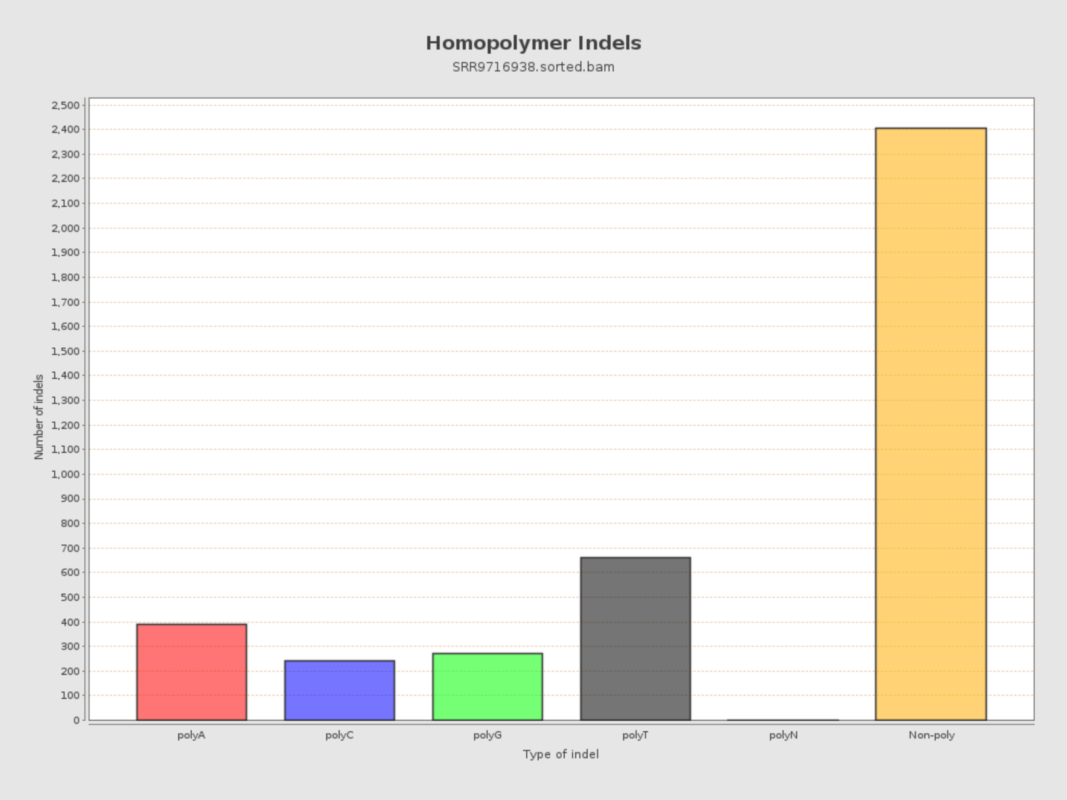
9. Results : Mapped Reads GC-content Distribution



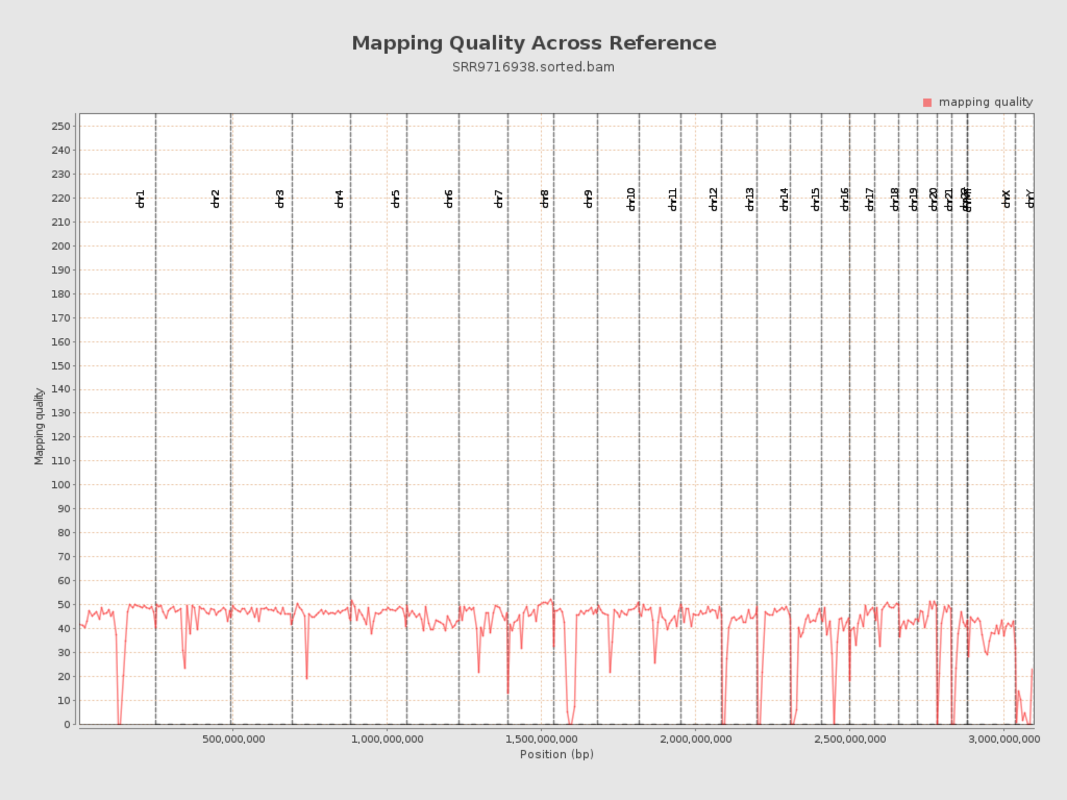
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram