Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 20:20:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716957.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_SRR9716957 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716957.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 20:20:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716957.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,556,047
Mapped reads	1,419,366 / 91.22%
Unmapped reads	136,681 / 8.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,160 / 0.59%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	51,858 / 3.33%
Duplication rate	2.83%
Clipped reads	1,426,908 / 91.7%

2.2. ACGT Content

Number/percentage of A's	20,705,579 / 24.88%
Number/percentage of C's	15,505,653 / 18.63%
Number/percentage of T's	25,336,151 / 30.45%
Number/percentage of G's	21,660,696 / 26.03%
Number/percentage of N's	1,068 / 0%
GC Percentage	44.67%

2.3. Coverage

Mean	0.0269

Standard Deviation	0.2387

2.4. Mapping Quality

Mean Mapping Quality	45.02

2.5. Mismatches and indels

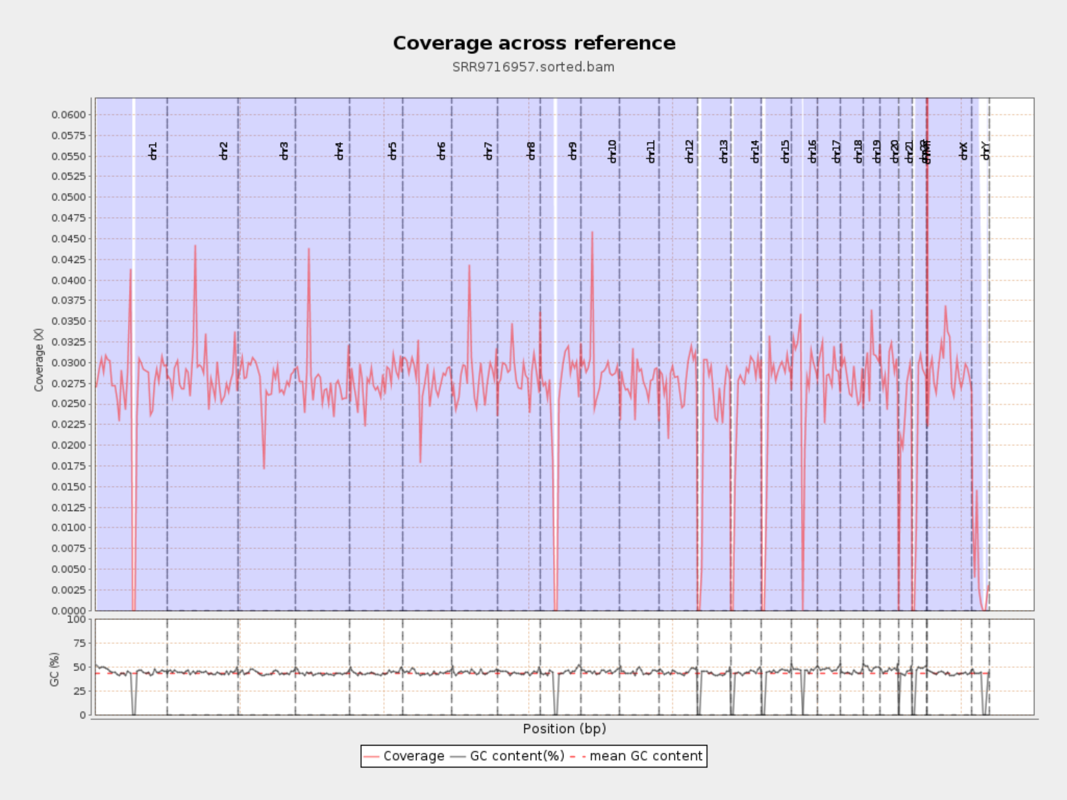
General error rate	0.51%
Mismatches	415,217
Insertions	4,889
Mapped reads with at least one insertion	0.34%
Deletions	14,940
Mapped reads with at least one deletion	1.05%
Homopolymer indels	42.68%

2.6. Chromosome stats

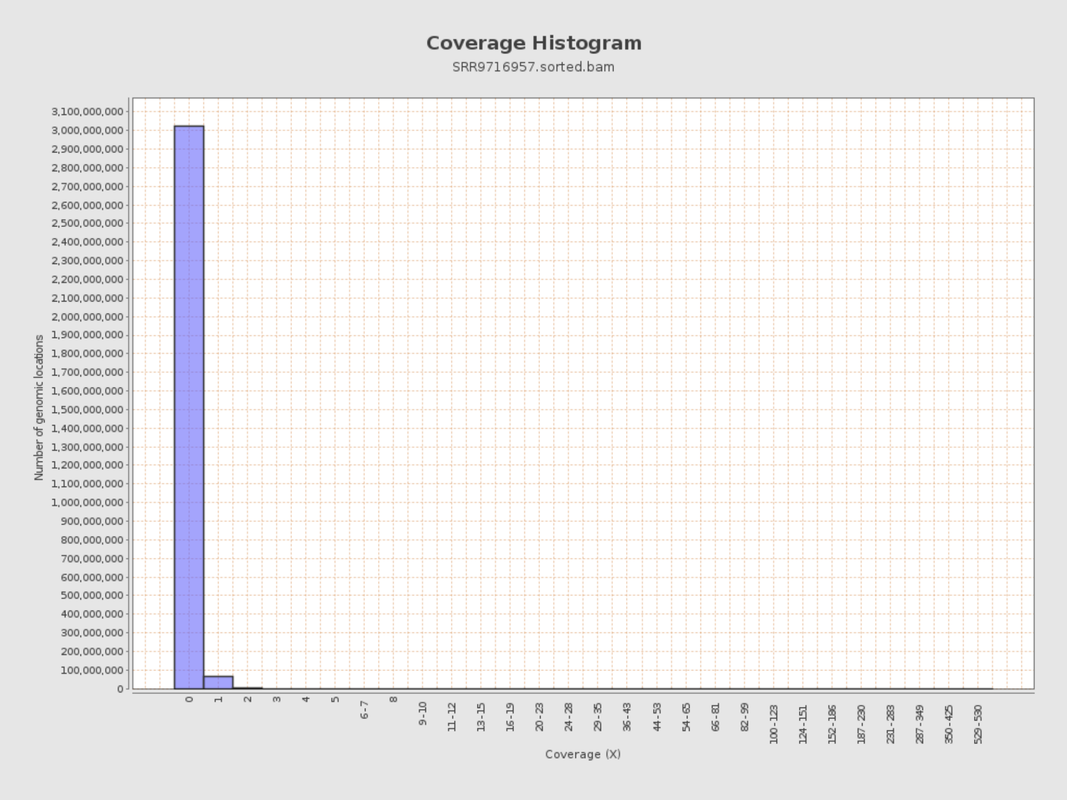
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6655092	0.0267	0.3788
chr2	243199373	6991326	0.0287	0.3069
chr3	198022430	5482218	0.0277	0.1817
chr4	191154276	5313034	0.0278	0.2032
chr5	180915260	5022337	0.0278	0.182
chr6	171115067	4803848	0.0281	0.1984
chr7	159138663	4530643	0.0285	0.2996

chr8	146364022	4197158	0.0287	0.243
chr9	141213431	3520500	0.0249	0.2026
chr10	135534747	4006298	0.0296	0.2501
chr11	135006516	3744277	0.0277	0.2169
chr12	133851895	3733005	0.0279	0.1847
chr13	115169878	2620361	0.0228	0.1648
chr14	107349540	2609767	0.0243	0.1754
chr15	102531392	2475134	0.0241	0.1727
chr16	90354753	2447205	0.0271	0.1883
chr17	81195210	2347606	0.0289	0.2014
chr18	78077248	2170606	0.0278	0.3353
chr19	59128983	1793629	0.0303	0.3059
chr20	63025520	1820777	0.0289	0.1881
chr21	48129895	1080604	0.0225	0.1788
chr22	51304566	1041570	0.0203	0.156
chrMT	16571	17958	1.0837	1.2872
chrX	155270560	4554934	0.0293	0.1994
chrY	59373566	253201	0.0043	0.1219

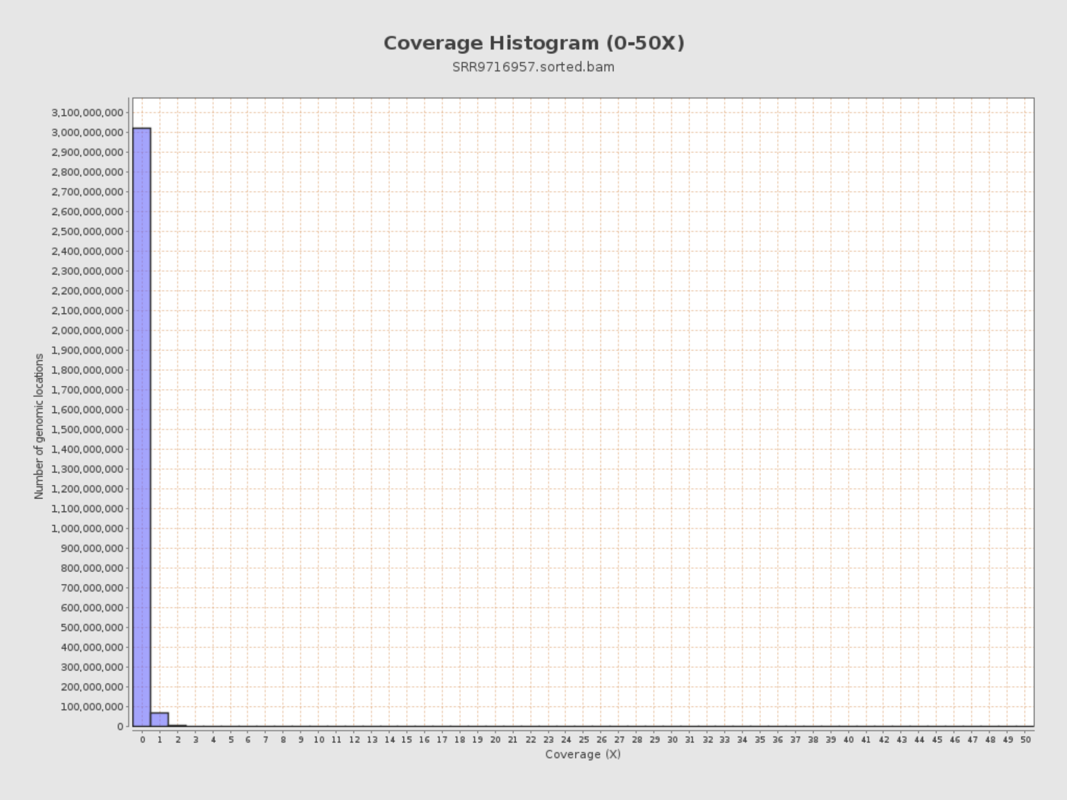
3. Results : Coverage across reference



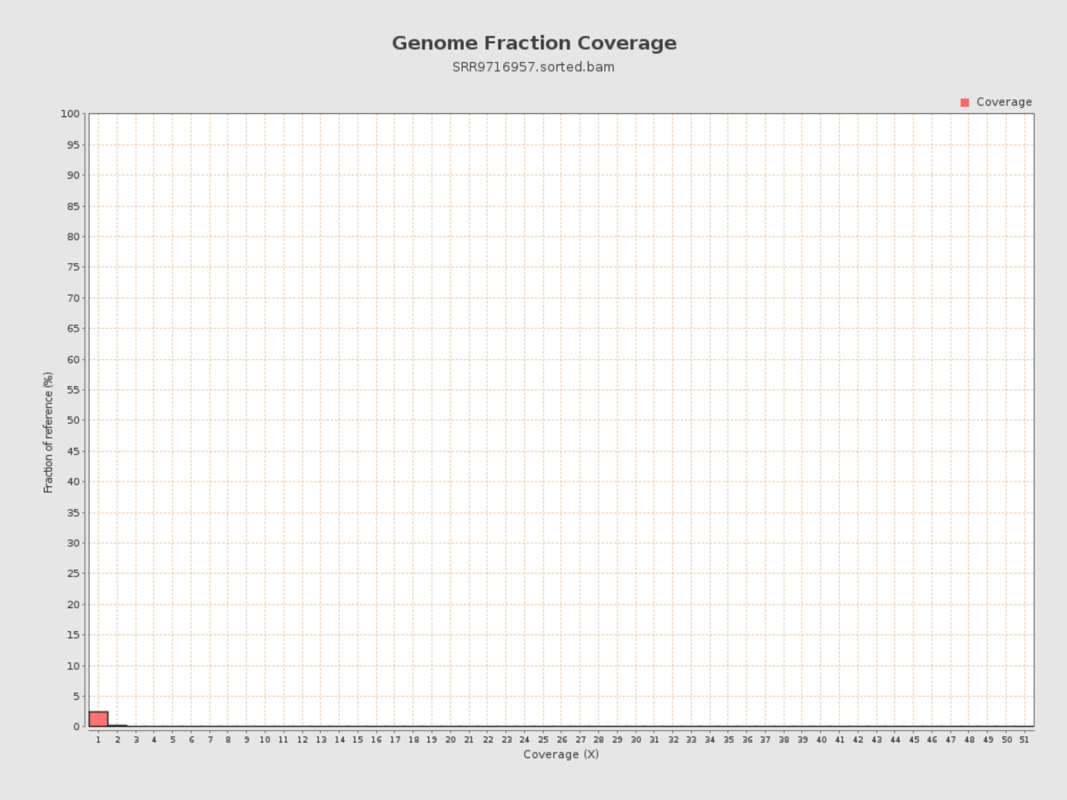
4. Results : Coverage Histogram



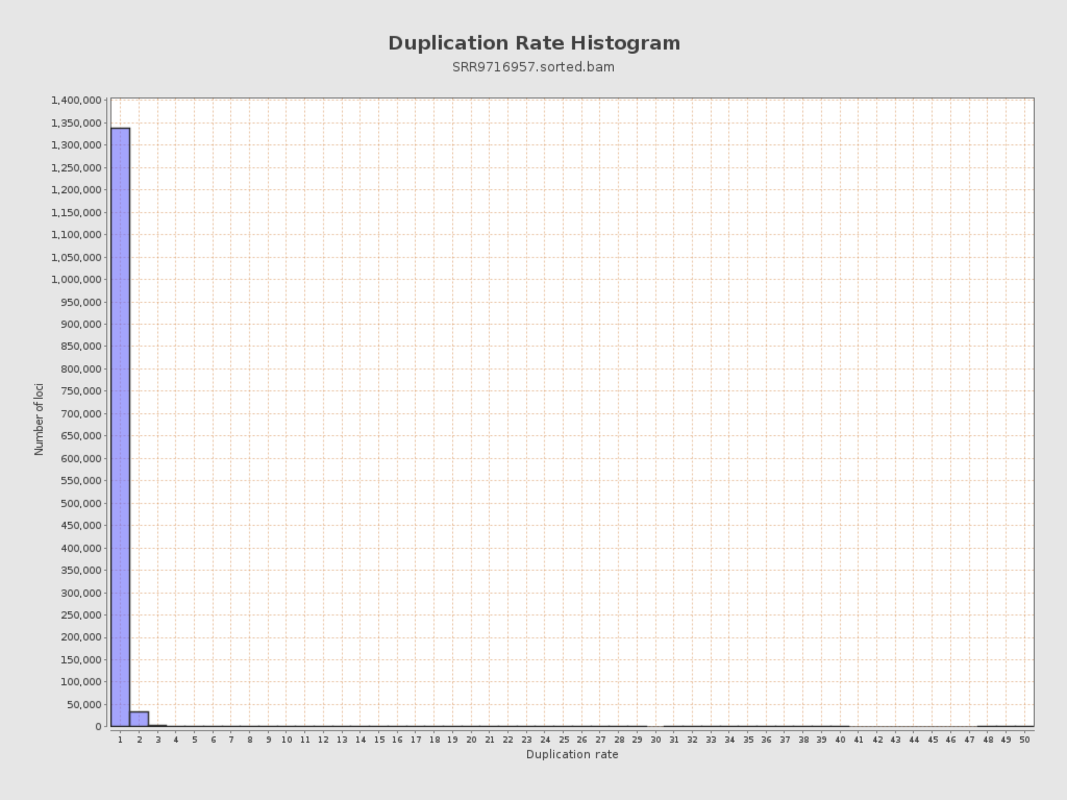
5. Results : Coverage Histogram (0-50X)



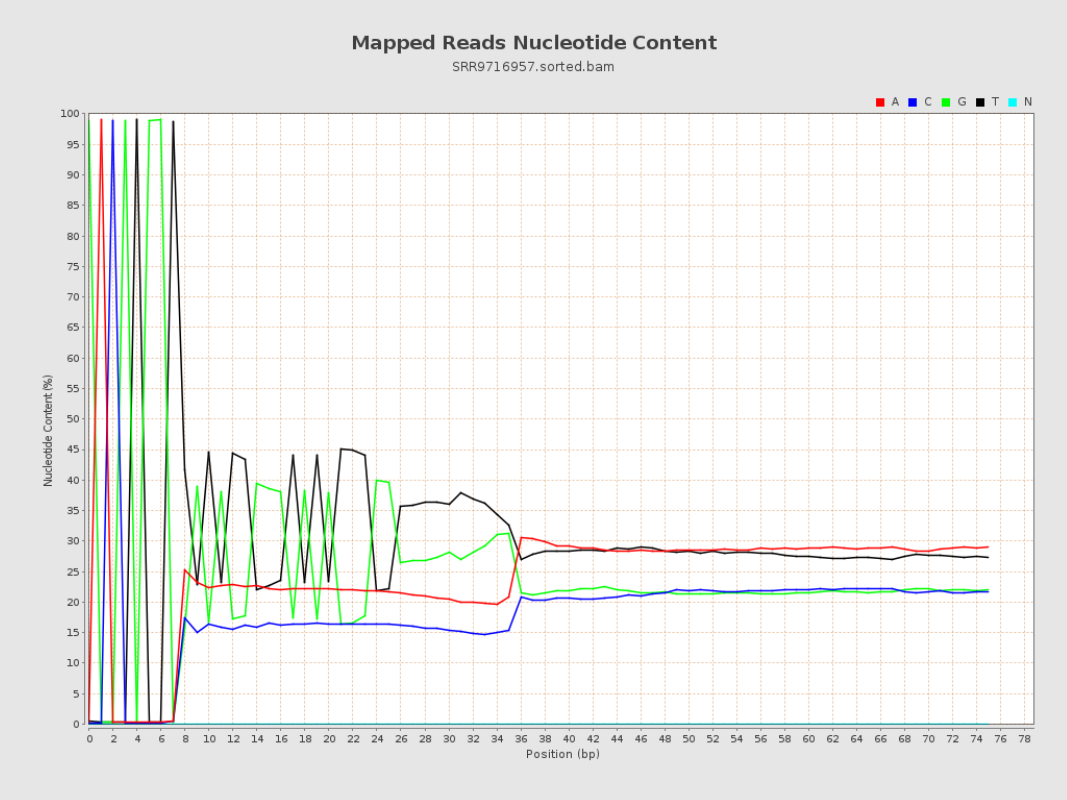
6. Results : Genome Fraction Coverage



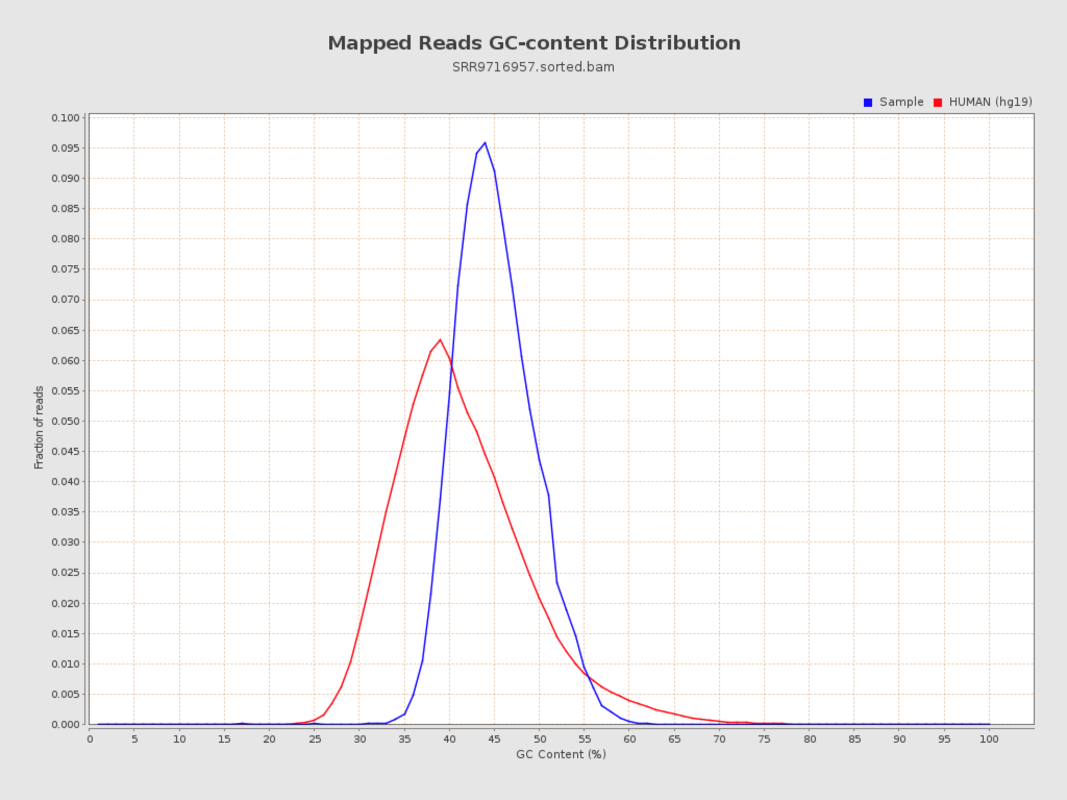
7. Results : Duplication Rate Histogram



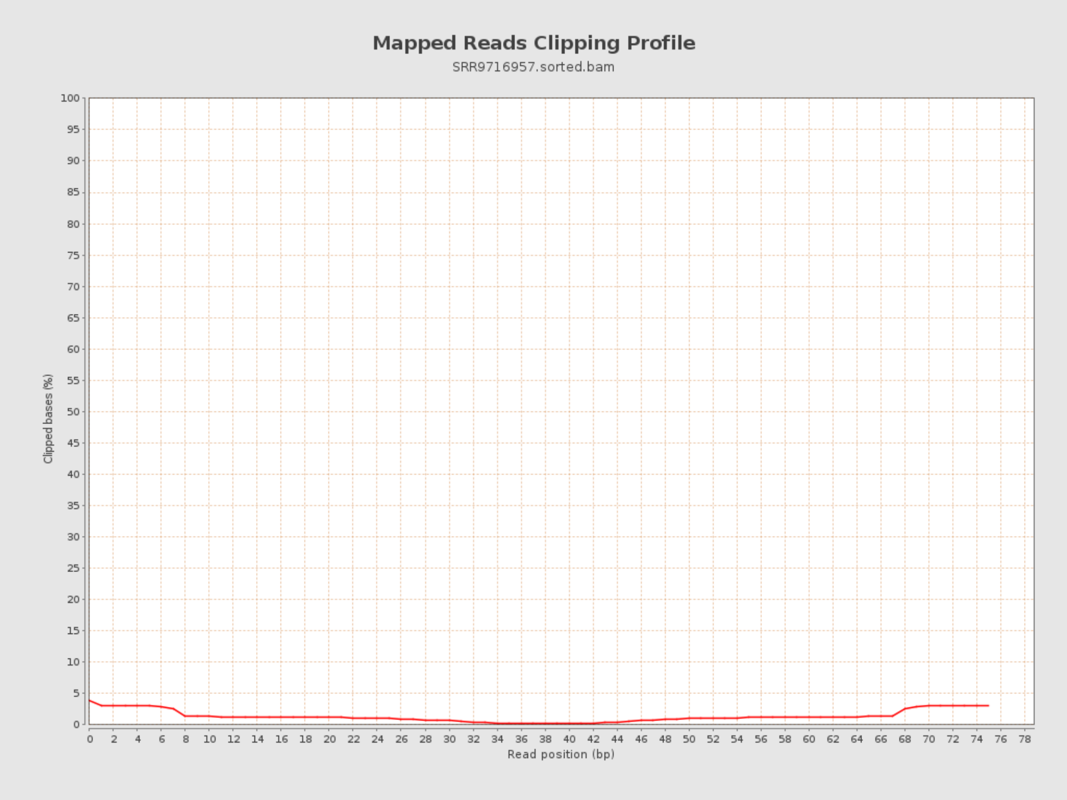
8. Results : Mapped Reads Nucleotide Content



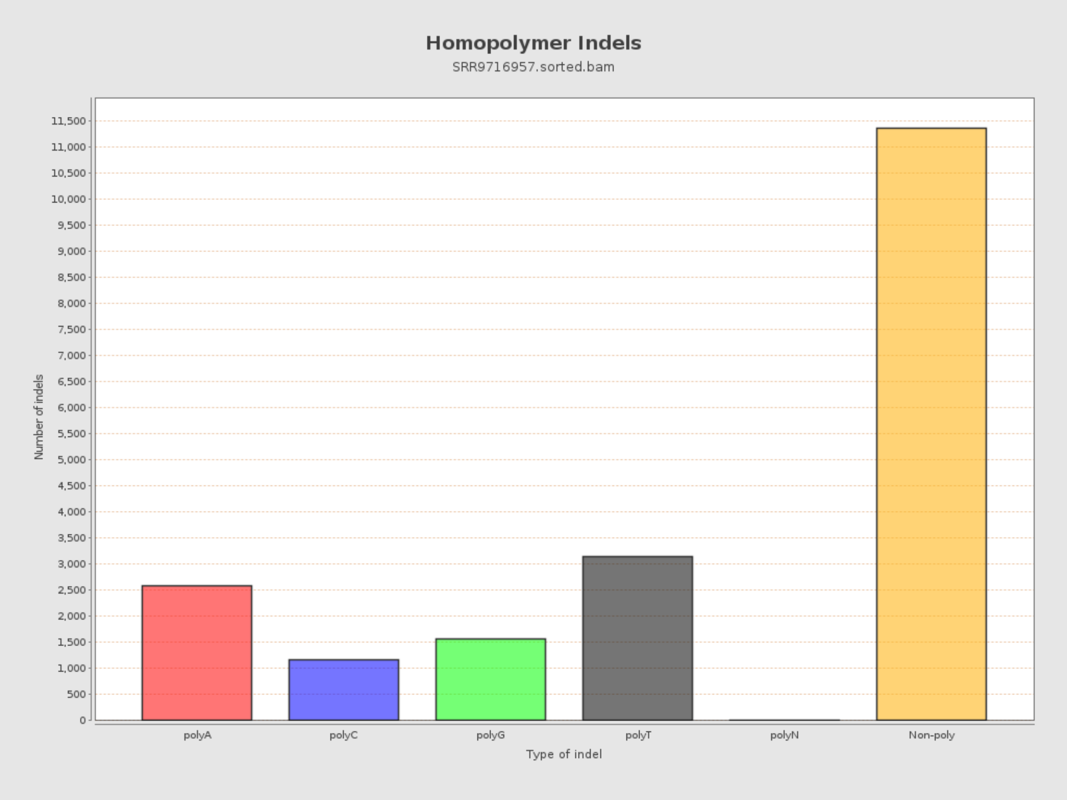
9. Results : Mapped Reads GC-content Distribution



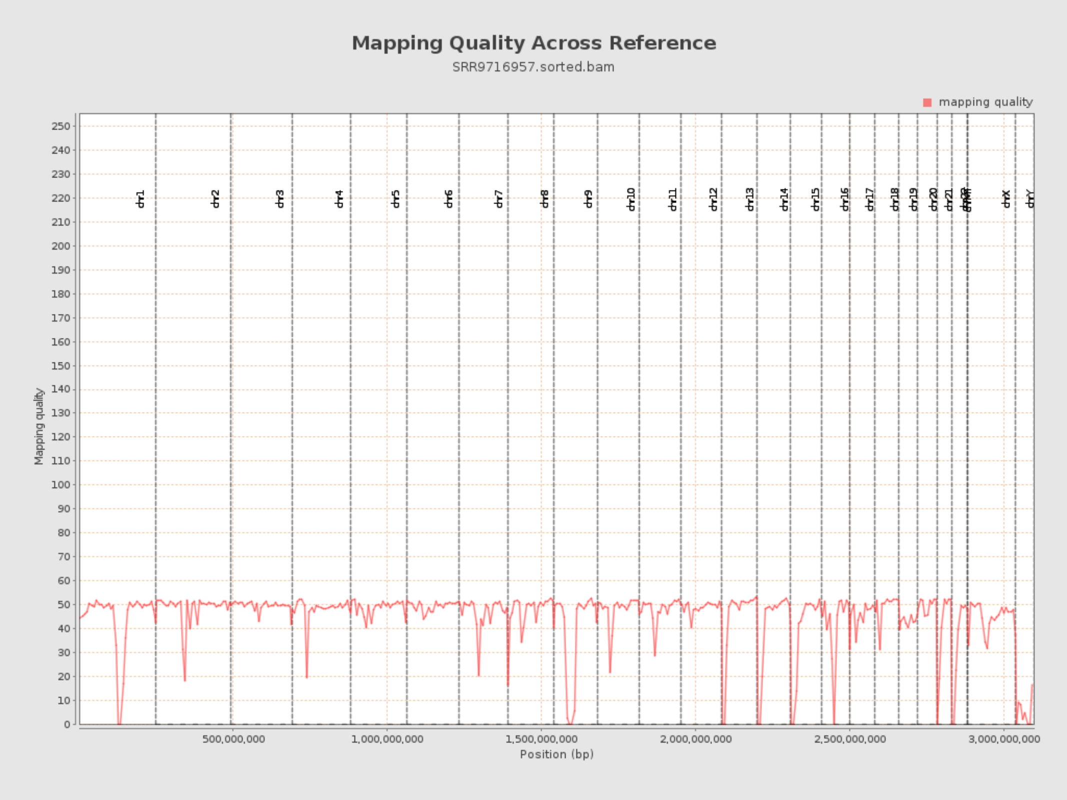
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram