Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 19:26:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716941.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_SRR9716941 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716941.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 19:26:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716941.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	591,590
Mapped reads	449,523 / 75.99%
Unmapped reads	142,067 / 24.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	593 / 0.1%
Read min/max/mean length	30 / 76 / 76.03
Duplicated reads (estimated)	19,871 / 3.36%
Duplication rate	3.98%
Clipped reads	449,867 / 76.04%

2.2. ACGT Content

Number/percentage of A's	5,035,285 / 21.36%
Number/percentage of C's	4,344,053 / 18.43%
Number/percentage of T's	7,649,274 / 32.45%
Number/percentage of G's	6,543,472 / 27.76%
Number/percentage of N's	453 / 0%
GC Percentage	46.19%

2.3. Coverage

Mean	0.0076

Standard Deviation	0.1015

2.4. Mapping Quality

Mean Mapping Quality	42.41

2.5. Mismatches and indels

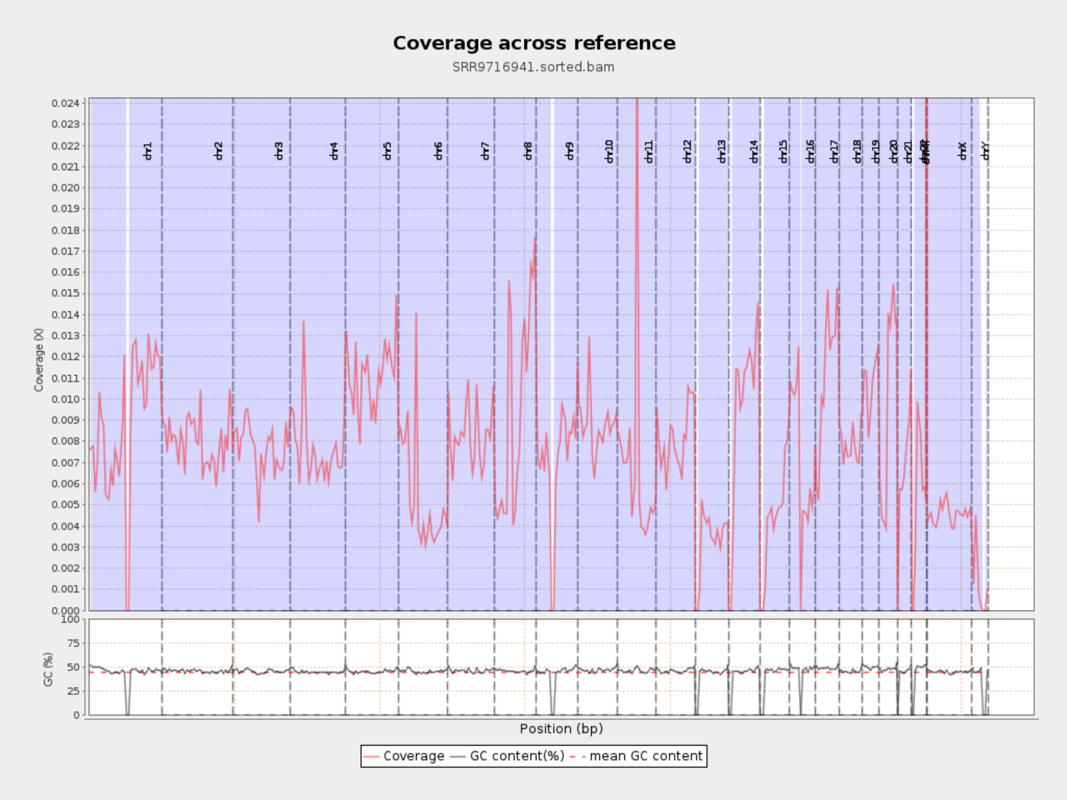
General error rate	0.68%
Mismatches	156,967
Insertions	1,252
Mapped reads with at least one insertion	0.28%
Deletions	3,532
Mapped reads with at least one deletion	0.78%
Homopolymer indels	39.32%

2.6. Chromosome stats

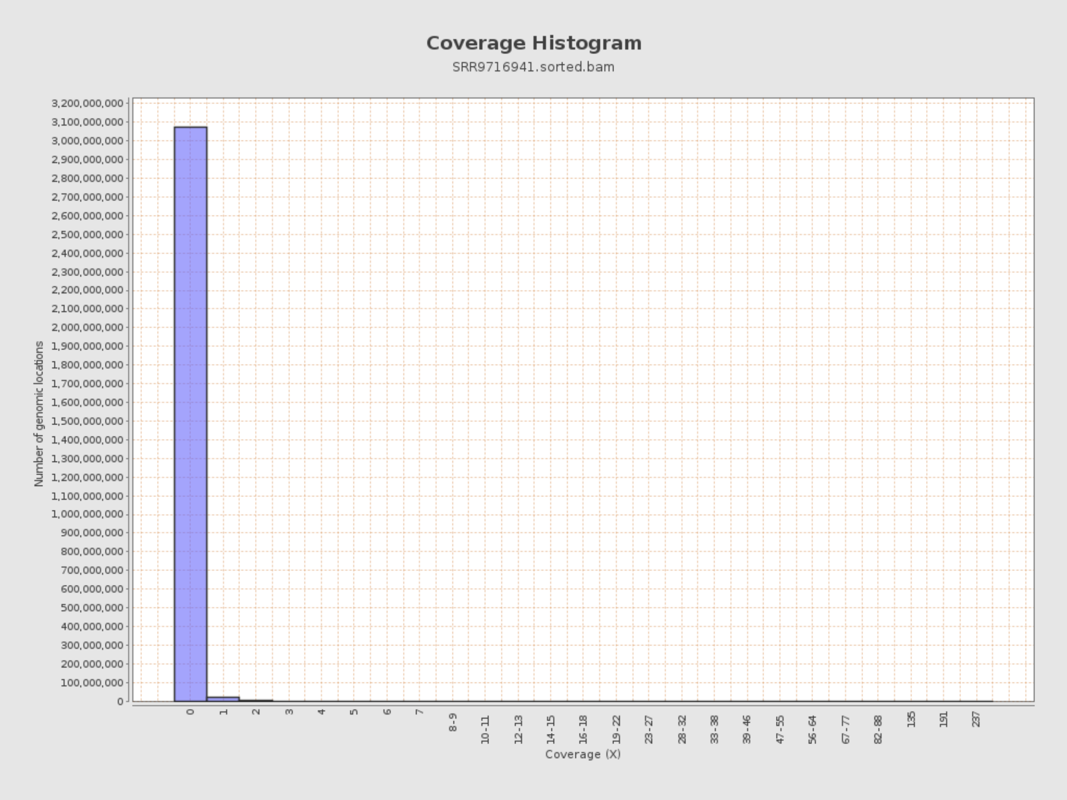
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2192259	0.0088	0.1152
chr2	243199373	1945573	0.008	0.1342
chr3	198022430	1512846	0.0076	0.0935
chr4	191154276	1450906	0.0076	0.0963
chr5	180915260	2012227	0.0111	0.1127
chr6	171115067	926133	0.0054	0.0867
chr7	159138663	1314447	0.0083	0.107

chr8	146364022	1393645	0.0095	0.1069
chr9	141213431	979541	0.0069	0.0925
chr10	135534747	1179778	0.0087	0.1094
chr11	135006516	957295	0.0071	0.0975
chr12	133851895	1088002	0.0081	0.0966
chr13	115169878	379790	0.0033	0.0618
chr14	107349540	1024593	0.0095	0.1051
chr15	102531392	444429	0.0043	0.0705
chr16	90354753	627143	0.0069	0.093
chr17	81195210	930277	0.0115	0.1184
chr18	78077248	606431	0.0078	0.1031
chr19	59128983	627184	0.0106	0.1254
chr20	63025520	611813	0.0097	0.1084
chr21	48129895	325111	0.0068	0.0915
chr22	51304566	263547	0.0051	0.0778
chrMT	16571	2679	0.1617	0.4353
chrX	155270560	709684	0.0046	0.0736
chrY	59373566	73218	0.0012	0.0444

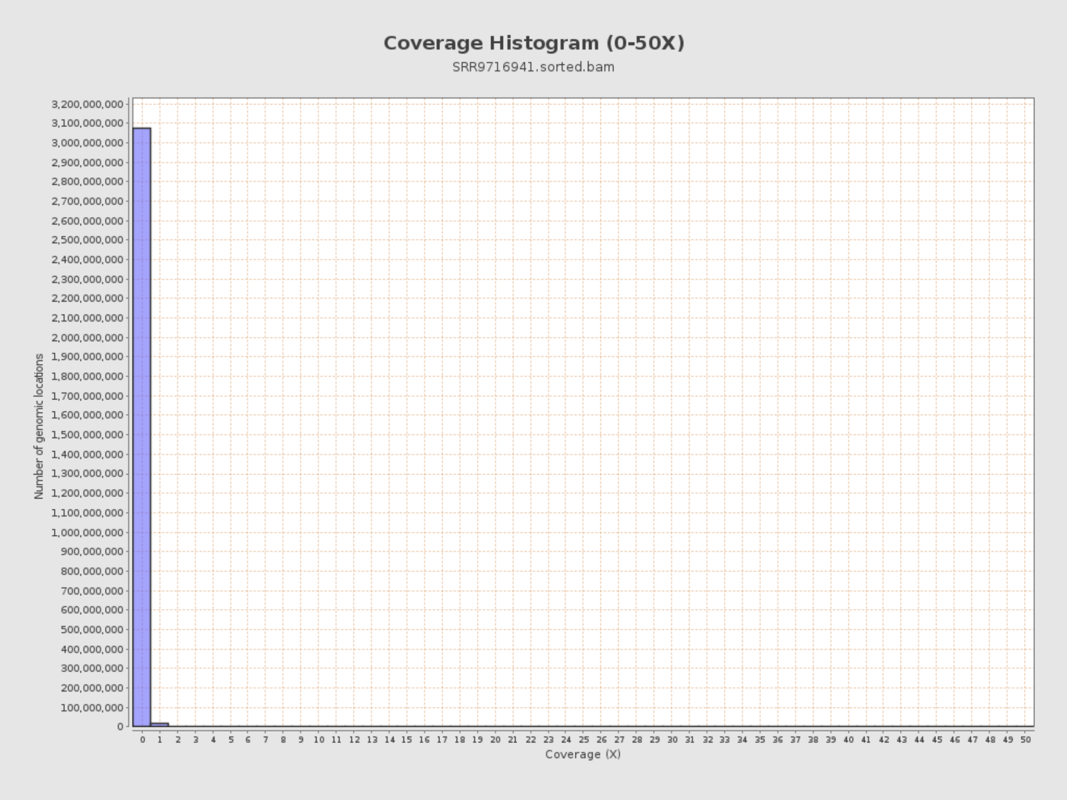
3. Results : Coverage across reference



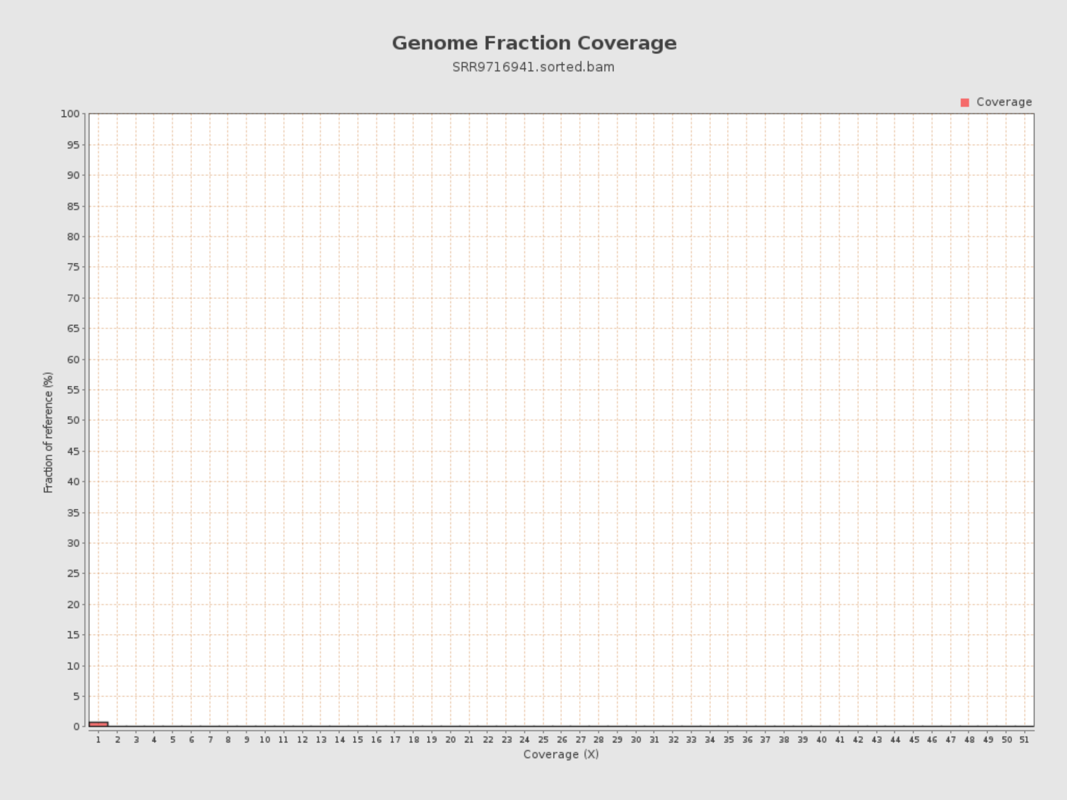
4. Results : Coverage Histogram



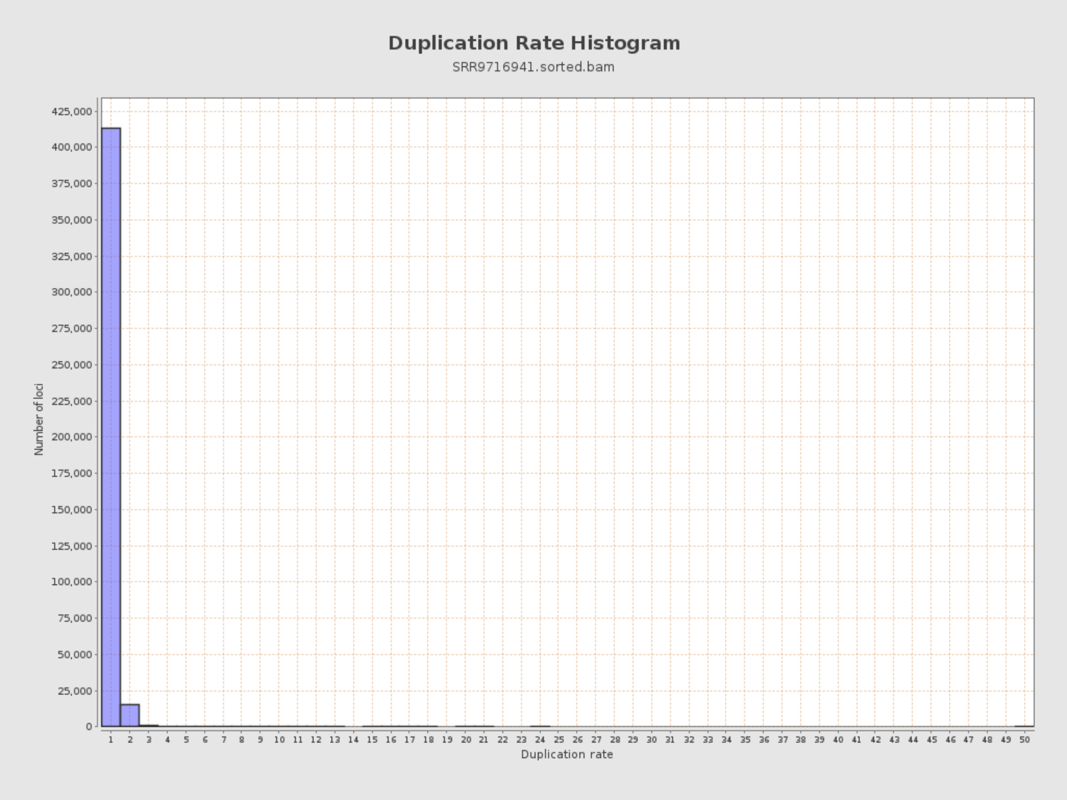
5. Results : Coverage Histogram (0-50X)



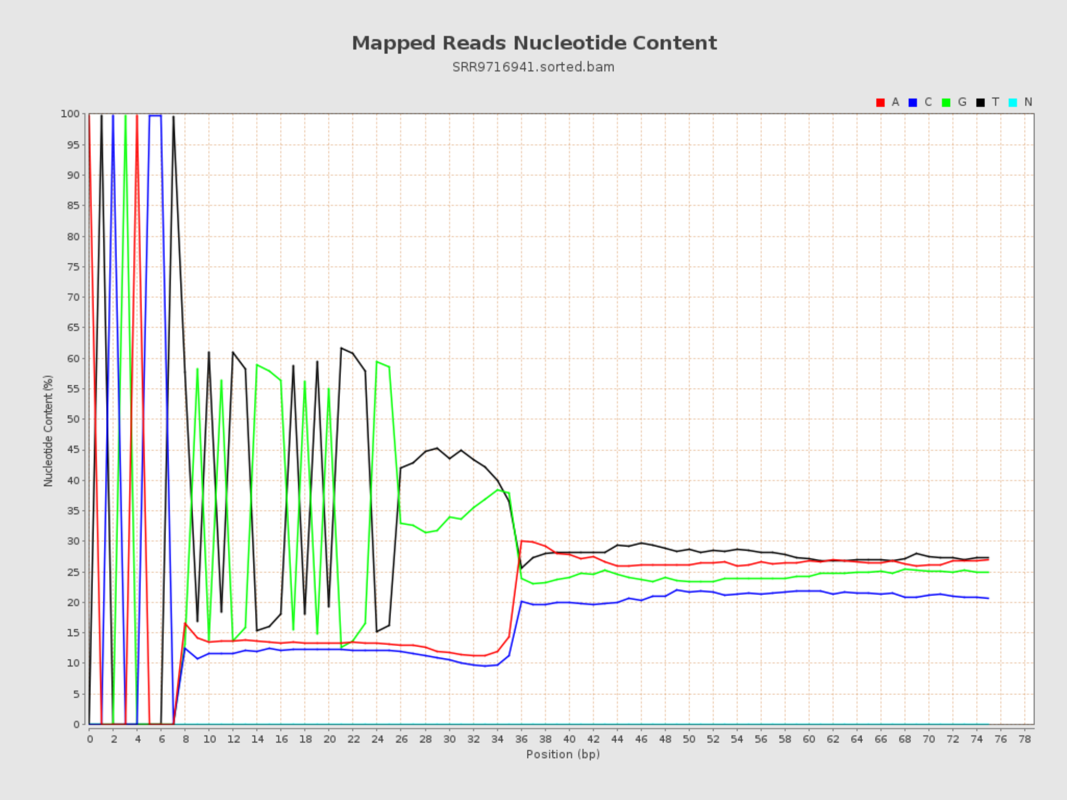
6. Results : Genome Fraction Coverage



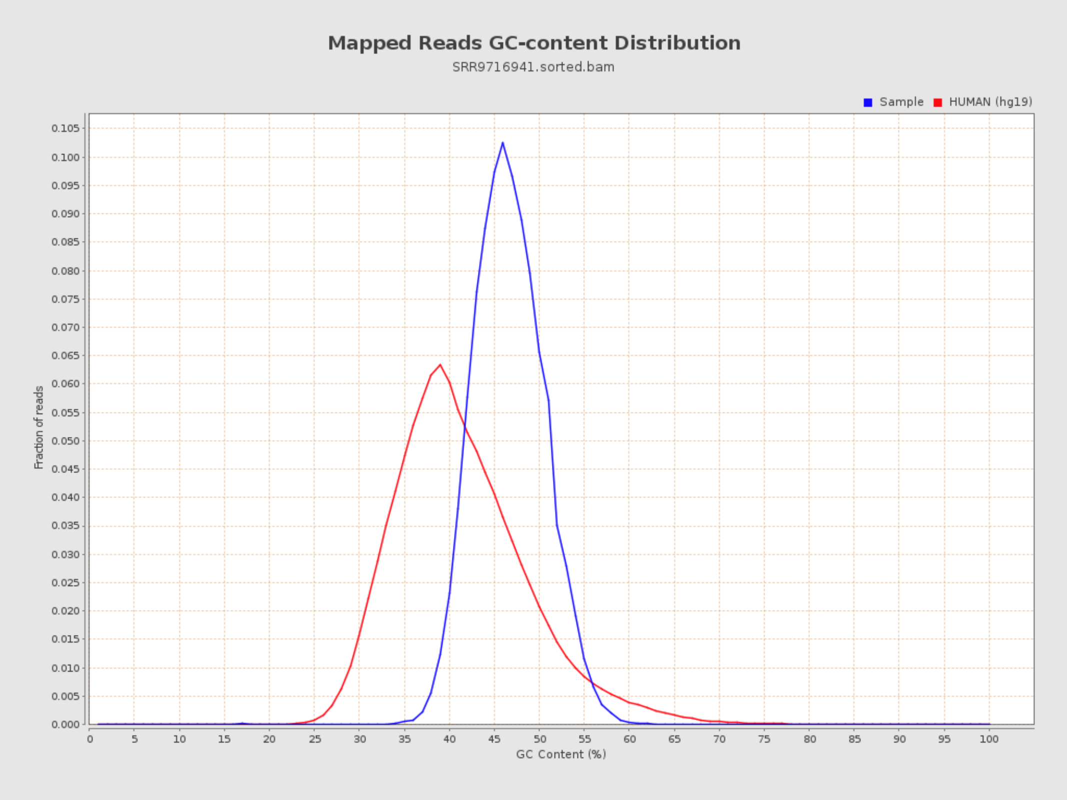
7. Results : Duplication Rate Histogram



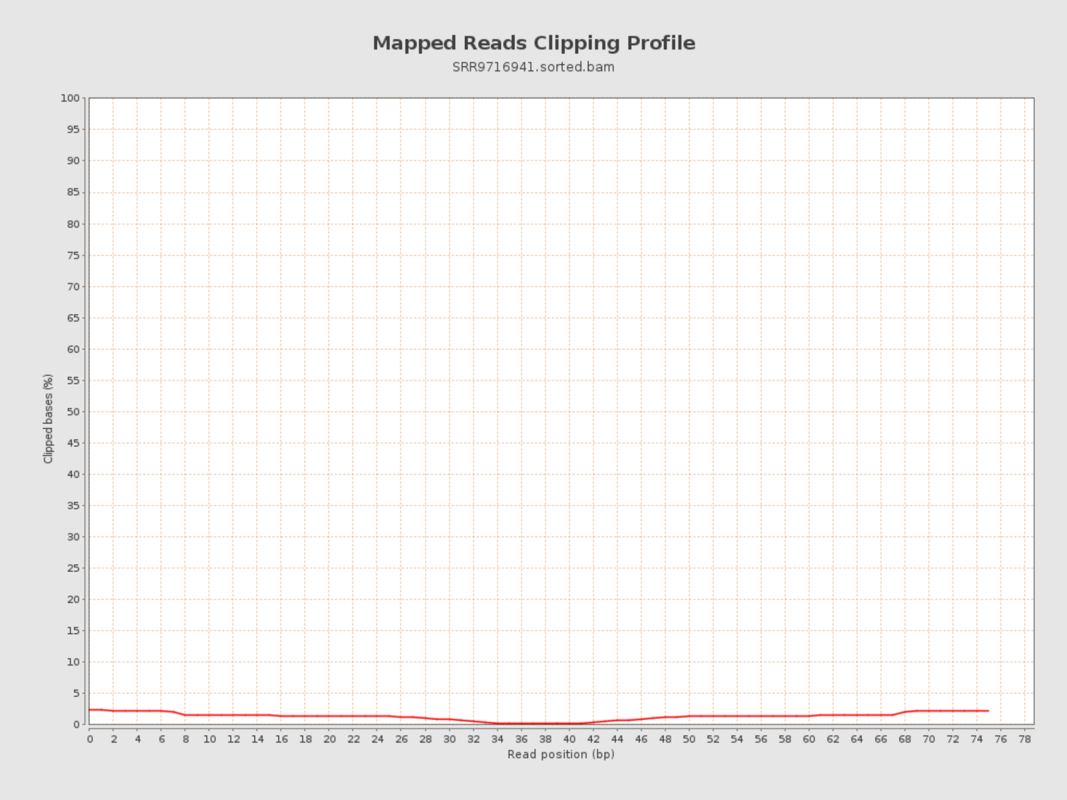
8. Results : Mapped Reads Nucleotide Content



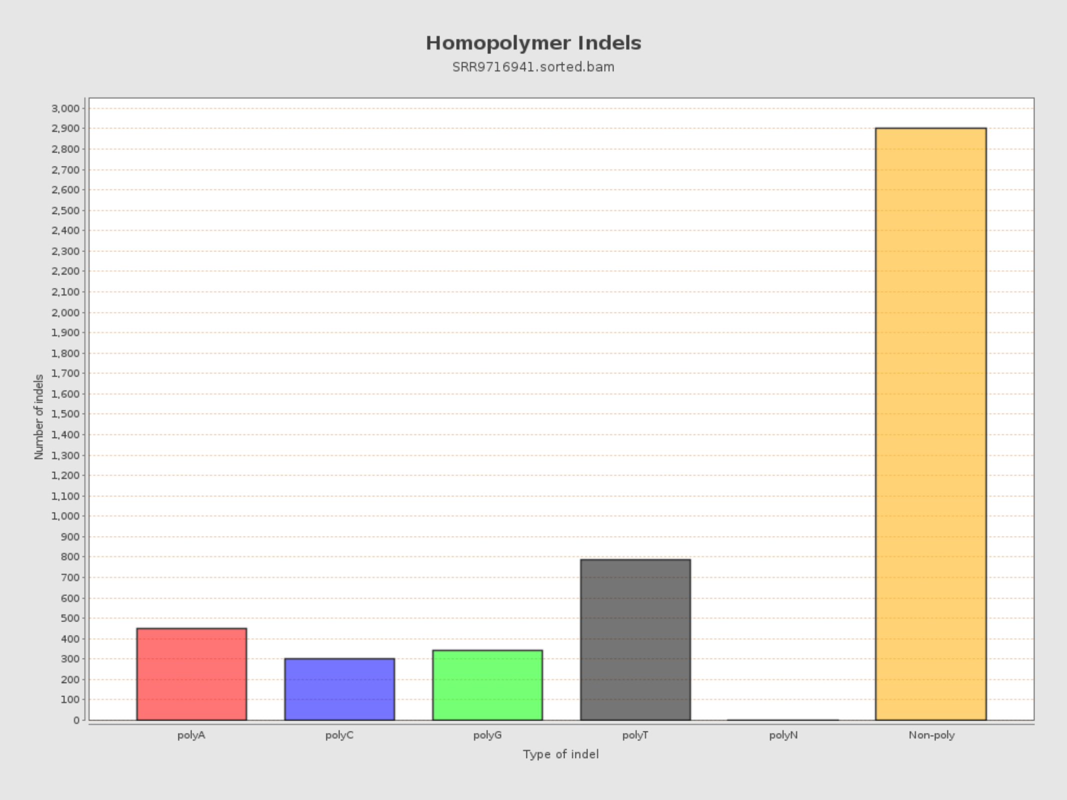
9. Results : Mapped Reads GC-content Distribution



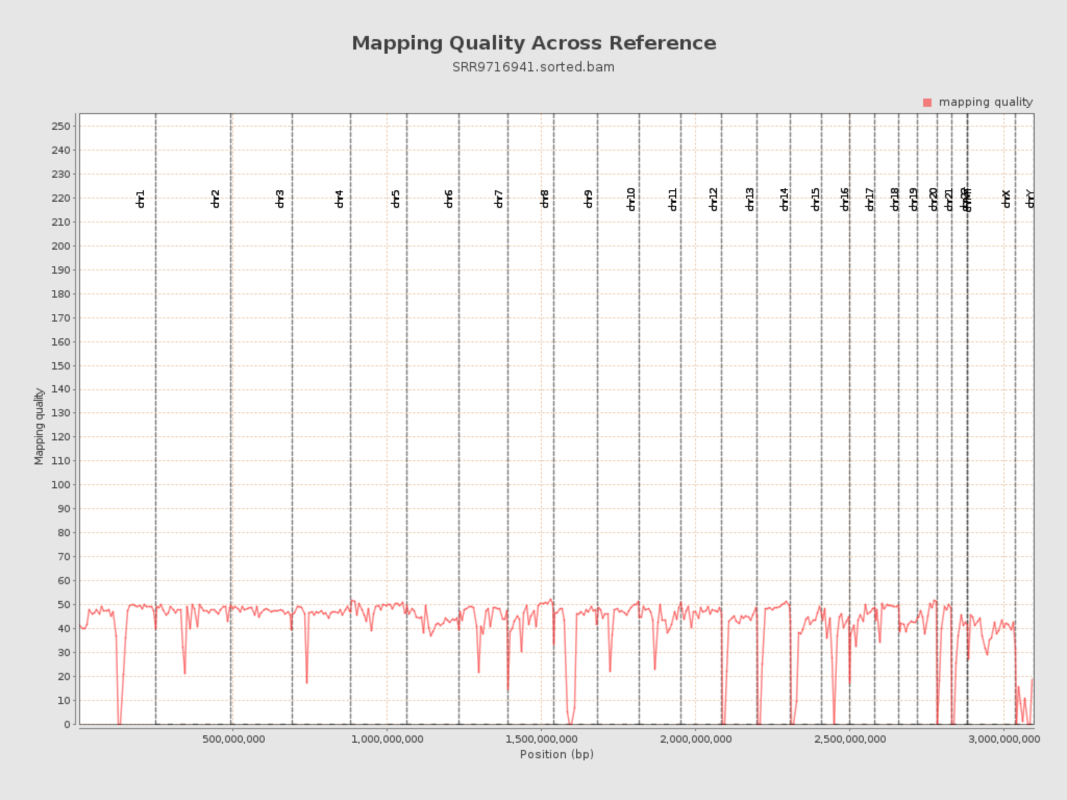
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram