Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 20:33:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716963.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_SRR9716963 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716963.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 20:33:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716963.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	640,611
Mapped reads	604,514 / 94.37%
Unmapped reads	36,097 / 5.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,151 / 2.37%
Read min/max/mean length	30 / 101 / 101.86
Duplicated reads (estimated)	13,947 / 2.18%
Duplication rate	1.76%
Clipped reads	618,159 / 96.5%

2.2. ACGT Content

Number/percentage of A's	11,980,936 / 25.5%
Number/percentage of C's	9,799,302 / 20.86%
Number/percentage of T's	13,399,911 / 28.52%
Number/percentage of G's	11,793,890 / 25.11%
Number/percentage of N's	2,058 / 0%
GC Percentage	45.97%

2.3. Coverage

Mean	0.0152

Standard Deviation	0.155

2.4. Mapping Quality

Mean Mapping Quality	46.57

2.5. Mismatches and indels

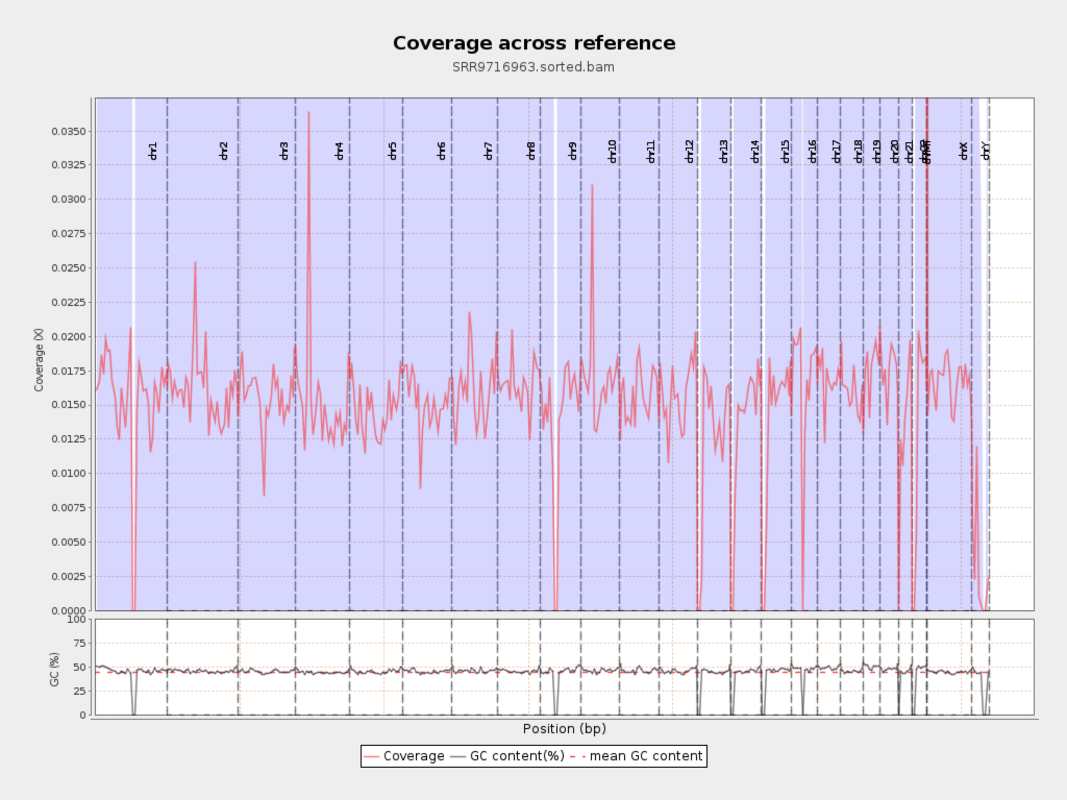
General error rate	0.68%
Mismatches	305,191
Insertions	4,712
Mapped reads with at least one insertion	0.77%
Deletions	9,167
Mapped reads with at least one deletion	1.49%
Homopolymer indels	37.63%

2.6. Chromosome stats

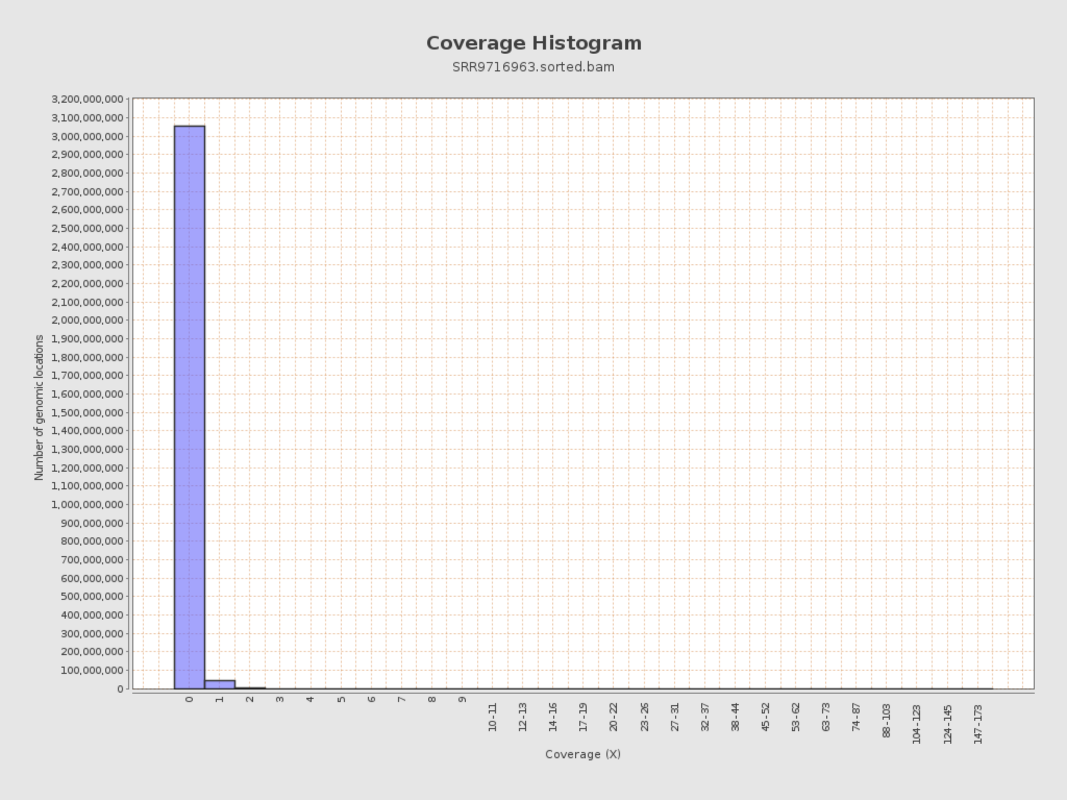
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3782798	0.0152	0.19
chr2	243199373	3942431	0.0162	0.1695
chr3	198022430	3078399	0.0155	0.1317
chr4	191154276	2933931	0.0153	0.1659
chr5	180915260	2656450	0.0147	0.1283
chr6	171115067	2606697	0.0152	0.1332
chr7	159138663	2561895	0.0161	0.1817

chr8	146364022	2411364	0.0165	0.1573
chr9	141213431	1933543	0.0137	0.1417
chr10	135534747	2321366	0.0171	0.2078
chr11	135006516	2139738	0.0158	0.157
chr12	133851895	2108760	0.0158	0.1344
chr13	115169878	1408197	0.0122	0.1166
chr14	107349540	1421280	0.0132	0.1275
chr15	102531392	1368018	0.0133	0.122
chr16	90354753	1476795	0.0163	0.1423
chr17	81195210	1373177	0.0169	0.1462
chr18	78077248	1240766	0.0159	0.1971
chr19	59128983	1048268	0.0177	0.1672
chr20	63025520	1099618	0.0174	0.1444
chr21	48129895	645799	0.0134	0.1464
chr22	51304566	664011	0.0129	0.123
chrMT	16571	6898	0.4163	0.6654
chrX	155270560	2592459	0.0167	0.1407
chrY	59373566	172939	0.0029	0.1348

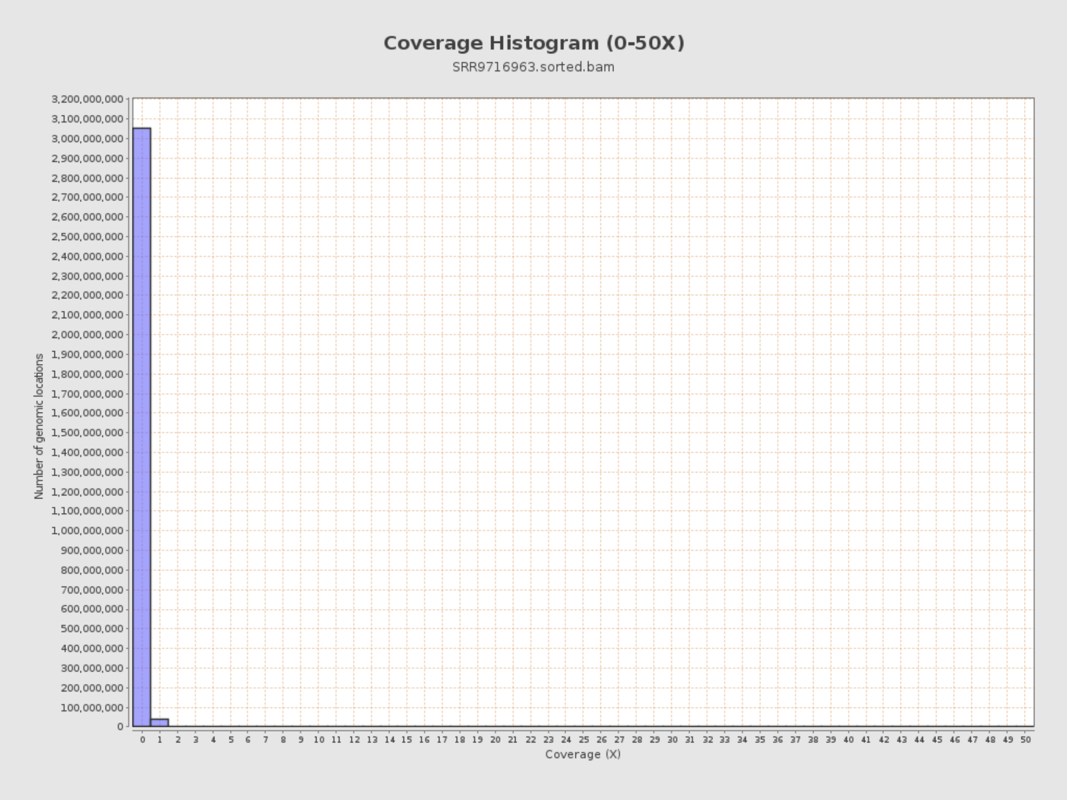
3. Results : Coverage across reference



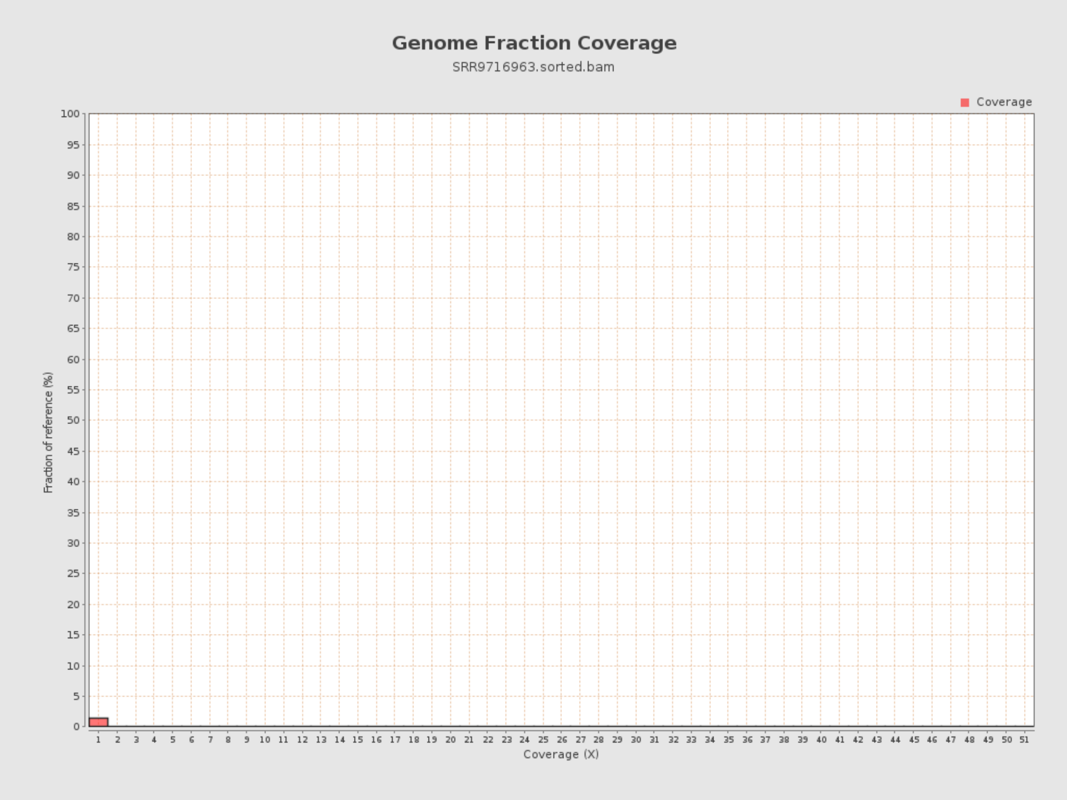
4. Results : Coverage Histogram



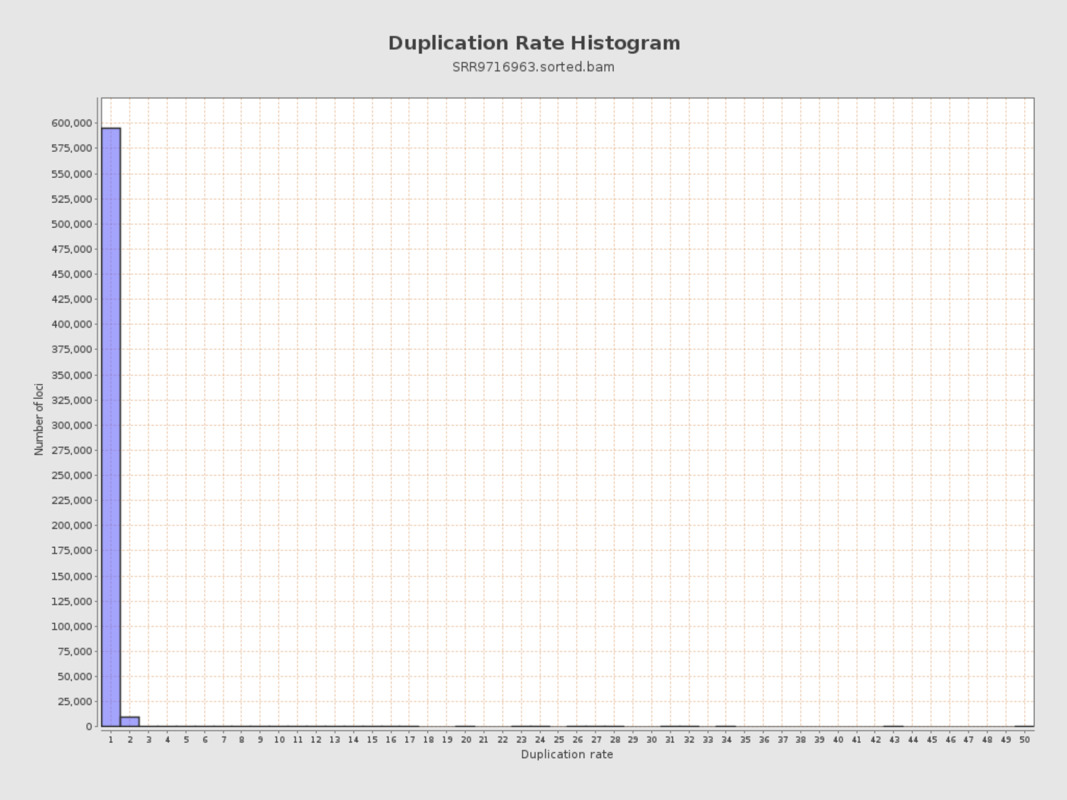
5. Results : Coverage Histogram (0-50X)



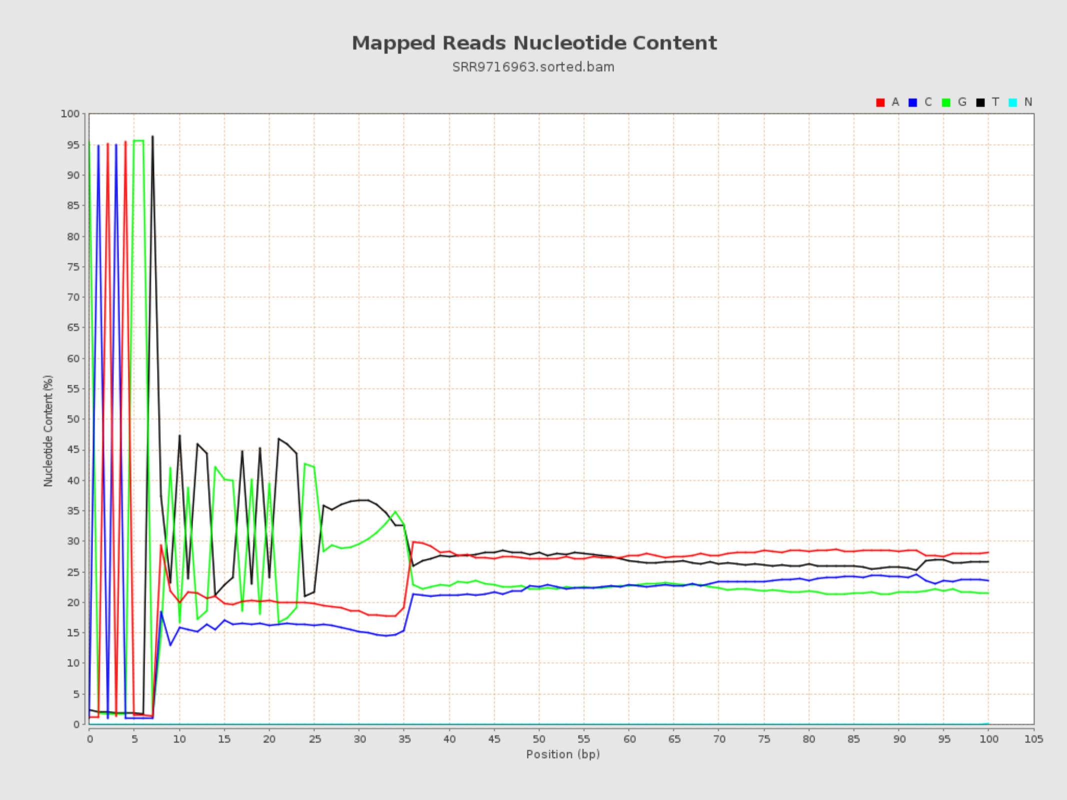
6. Results : Genome Fraction Coverage



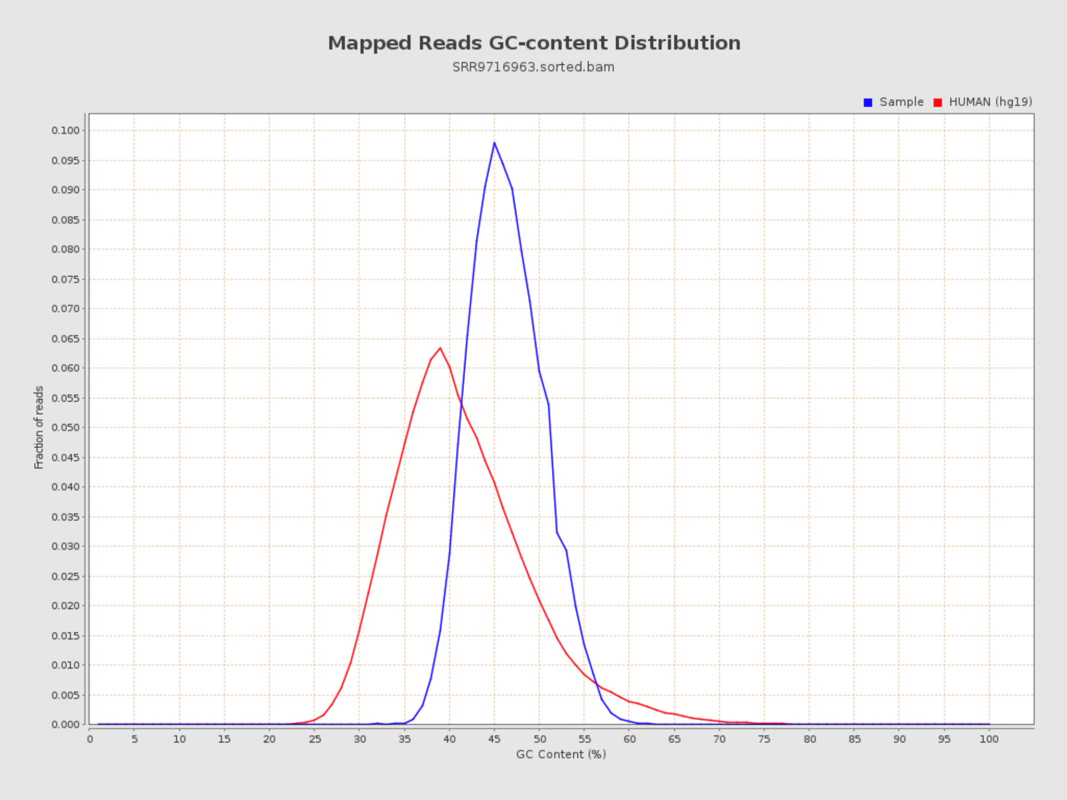
7. Results : Duplication Rate Histogram



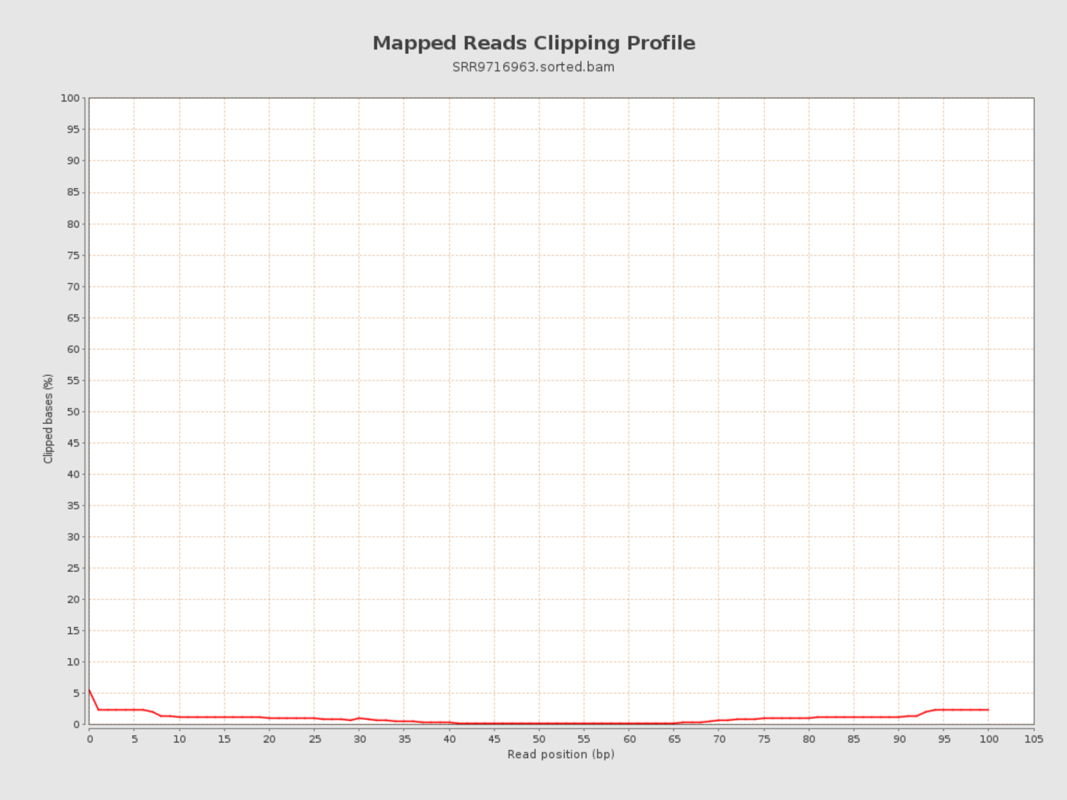
8. Results : Mapped Reads Nucleotide Content



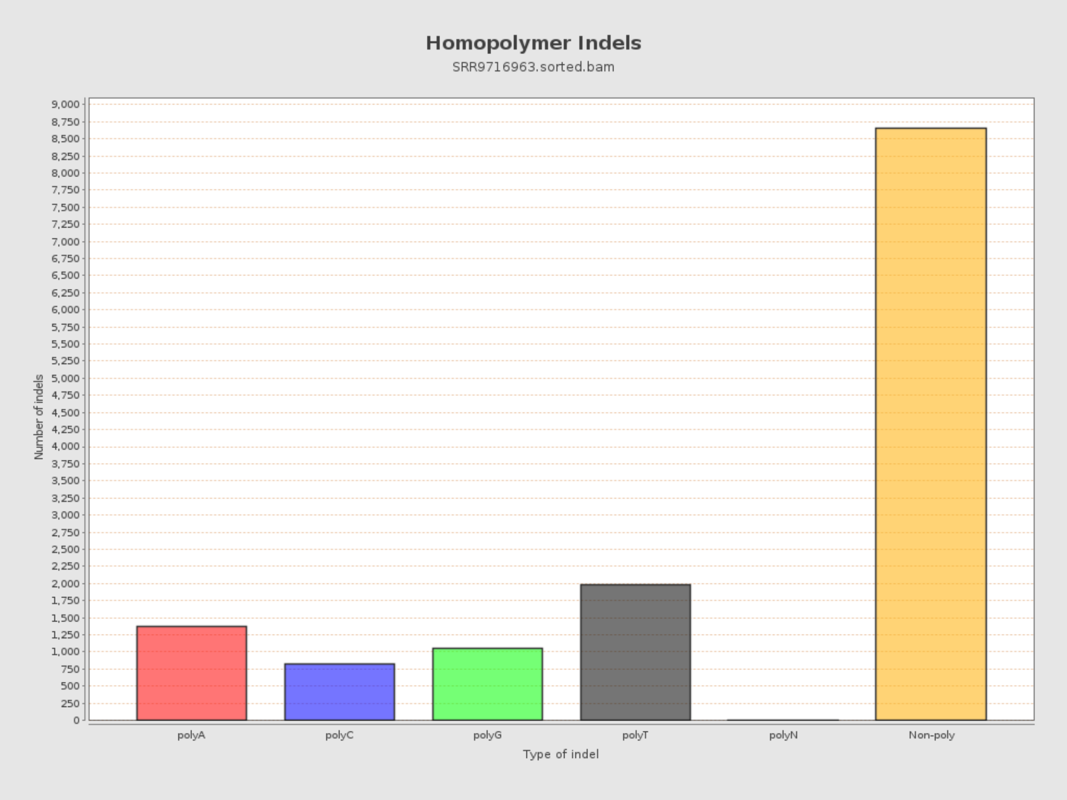
9. Results : Mapped Reads GC-content Distribution



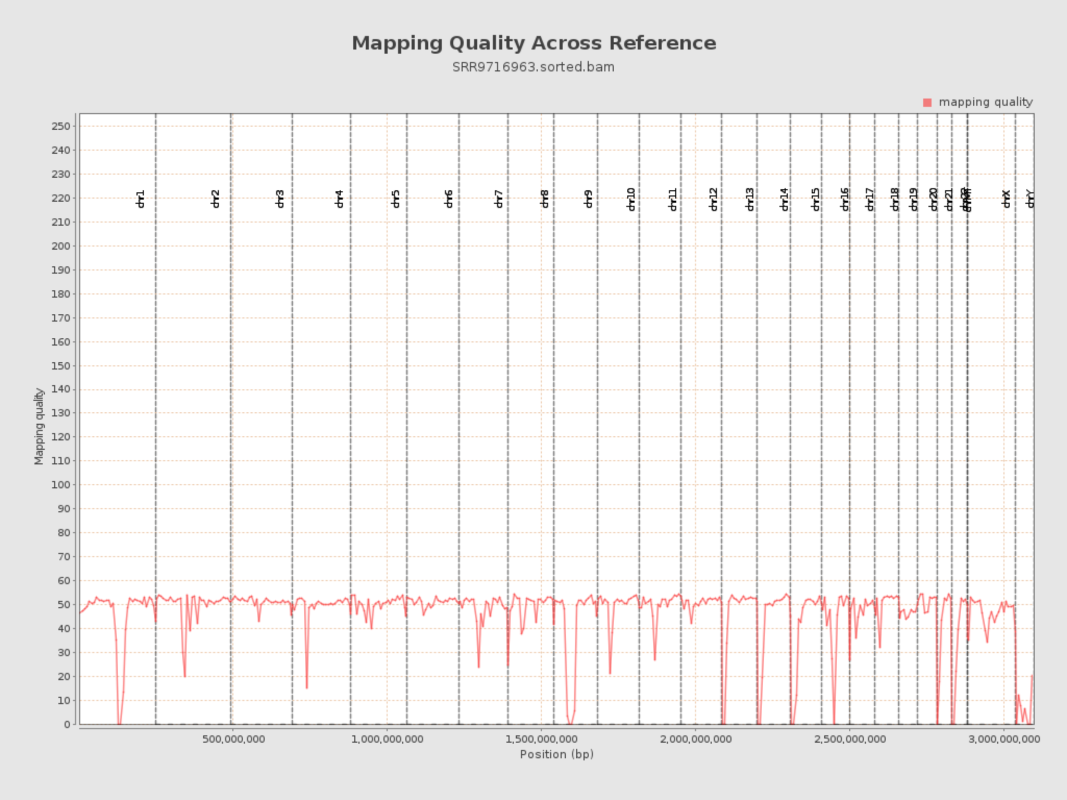
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram