Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 19:38:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716945.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_SRR9716945 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716945.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 19:38:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716945.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,083,444
Mapped reads	1,433,890 / 68.82%
Unmapped reads	649,554 / 31.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,025 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	52,196 / 2.51%
Duplication rate	2.82%
Clipped reads	1,439,982 / 69.12%

2.2. ACGT Content

Number/percentage of A's	21,234,331 / 25.83%
Number/percentage of C's	15,317,448 / 18.63%
Number/percentage of T's	25,181,517 / 30.63%
Number/percentage of G's	20,483,039 / 24.91%
Number/percentage of N's	1,236 / 0%
GC Percentage	43.54%

2.3. Coverage

Mean	0.0266

Standard Deviation	0.2406

2.4. Mapping Quality

Mean Mapping Quality	44.28

2.5. Mismatches and indels

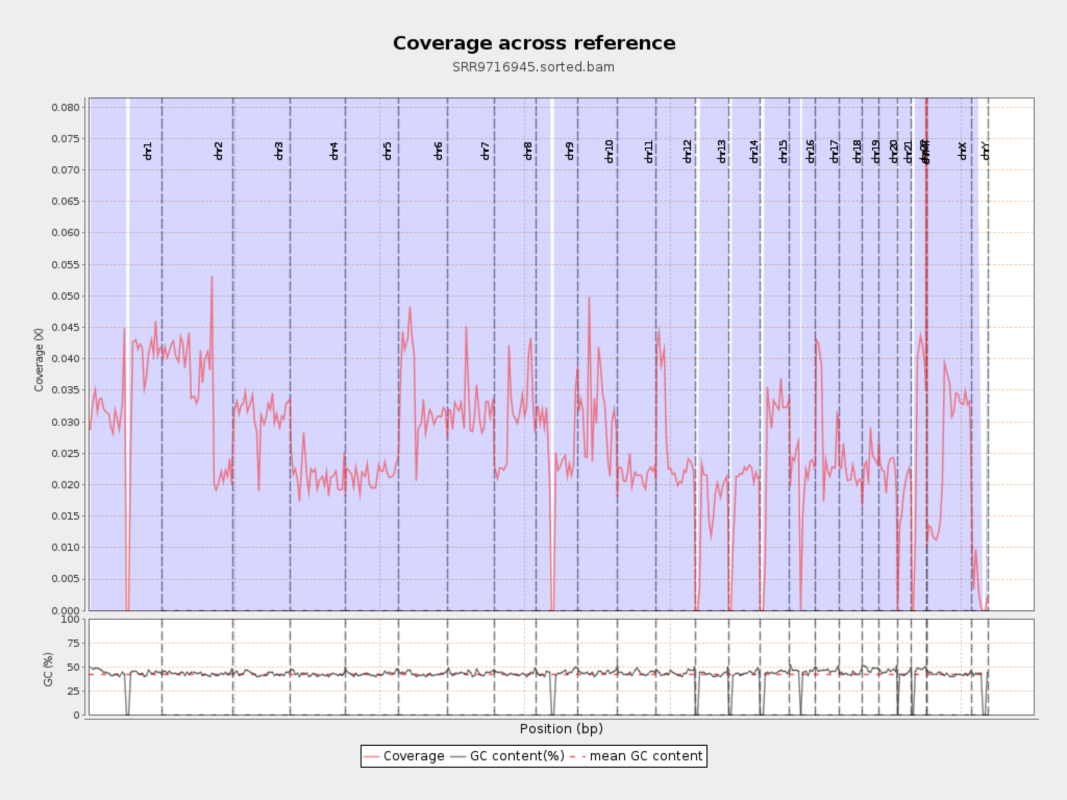
General error rate	0.49%
Mismatches	390,836
Insertions	4,513
Mapped reads with at least one insertion	0.31%
Deletions	13,273
Mapped reads with at least one deletion	0.92%
Homopolymer indels	43.39%

2.6. Chromosome stats

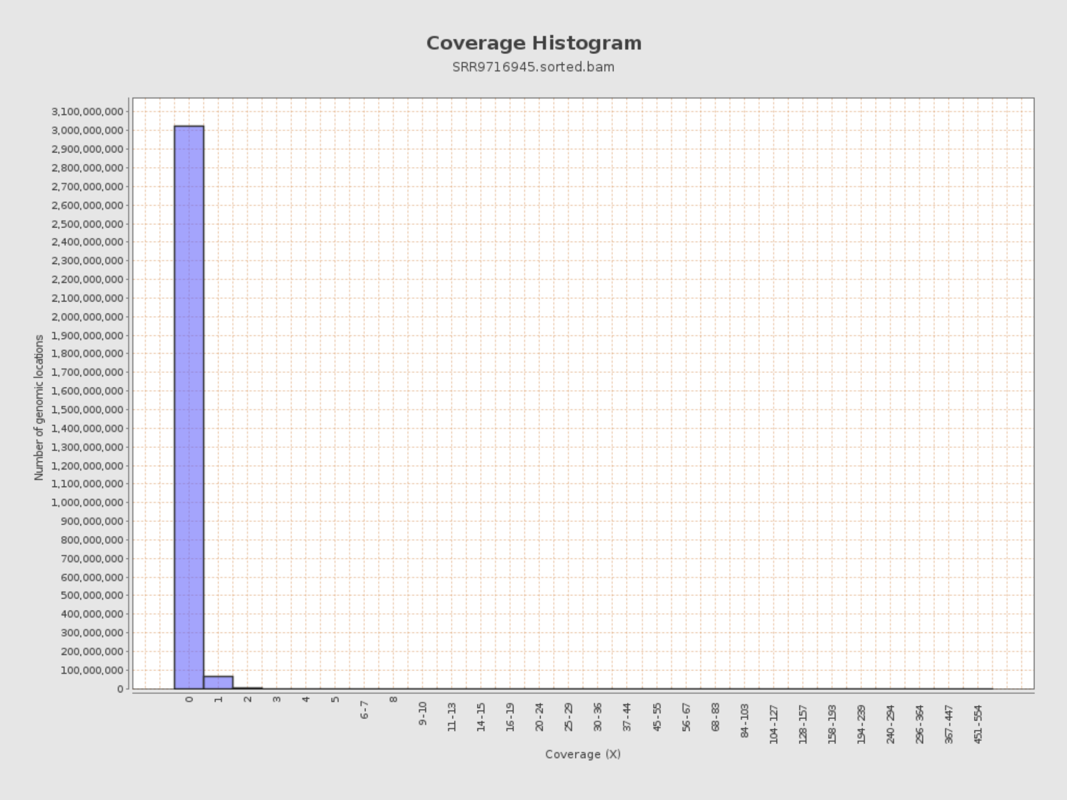
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8415273	0.0338	0.3977
chr2	243199373	8496675	0.0349	0.3117
chr3	198022430	6173586	0.0312	0.1938
chr4	191154276	4082943	0.0214	0.1707
chr5	180915260	3895813	0.0215	0.1613
chr6	171115067	5785119	0.0338	0.243
chr7	159138663	5112415	0.0321	0.3257

chr8	146364022	4440955	0.0303	0.2161
chr9	141213431	3317241	0.0235	0.2119
chr10	135534747	4272569	0.0315	0.2429
chr11	135006516	2916211	0.0216	0.215
chr12	133851895	3568111	0.0267	0.1823
chr13	115169878	1810815	0.0157	0.1364
chr14	107349540	1957907	0.0182	0.1592
chr15	102531392	2702144	0.0264	0.1822
chr16	90354753	1885658	0.0209	0.1685
chr17	81195210	2323842	0.0286	0.193
chr18	78077248	1718728	0.022	0.3552
chr19	59128983	1403581	0.0237	0.2723
chr20	63025520	1405400	0.0223	0.1659
chr21	48129895	812182	0.0169	0.1482
chr22	51304566	1438421	0.028	0.1848
chrMT	16571	55569	3.3534	2.6555
chrX	155270560	4063410	0.0262	0.1989
chrY	59373566	183604	0.0031	0.0789

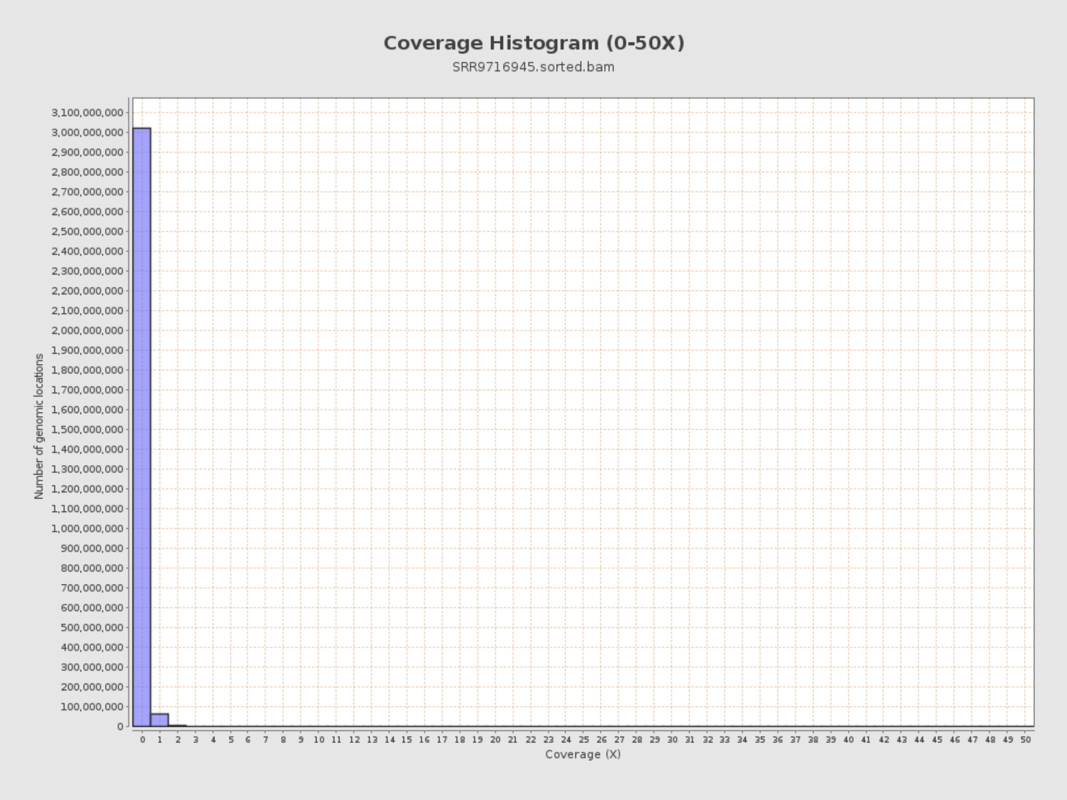
3. Results : Coverage across reference



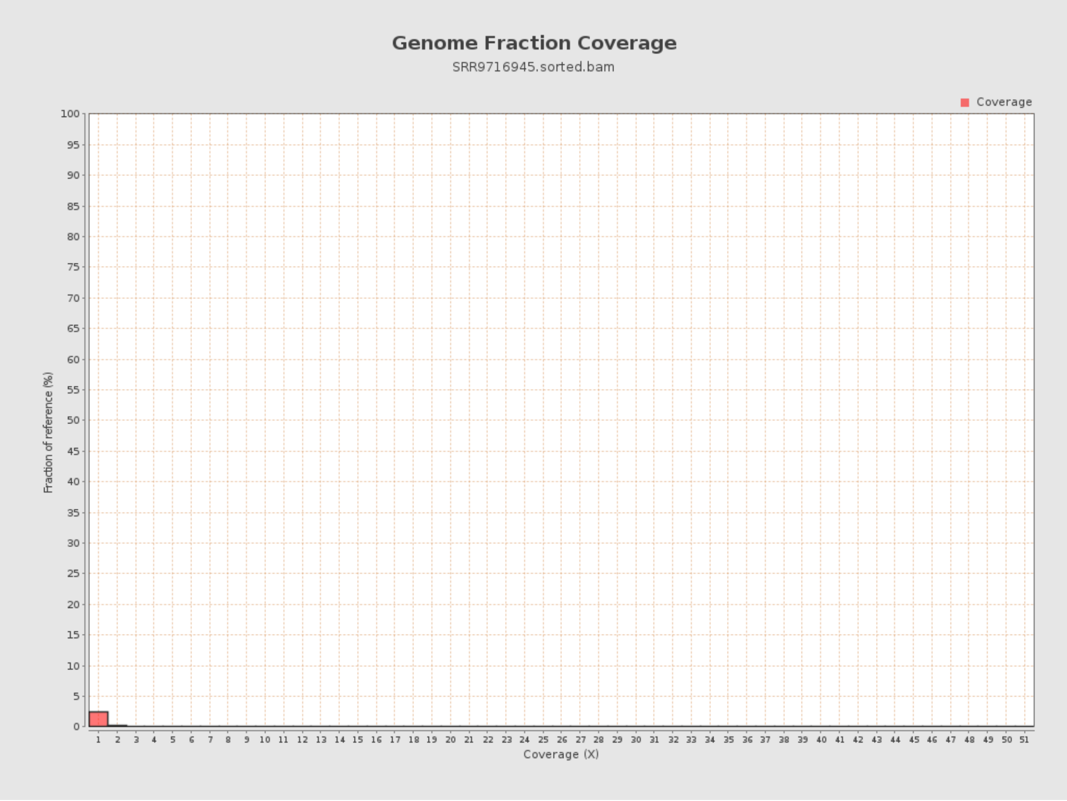
4. Results : Coverage Histogram



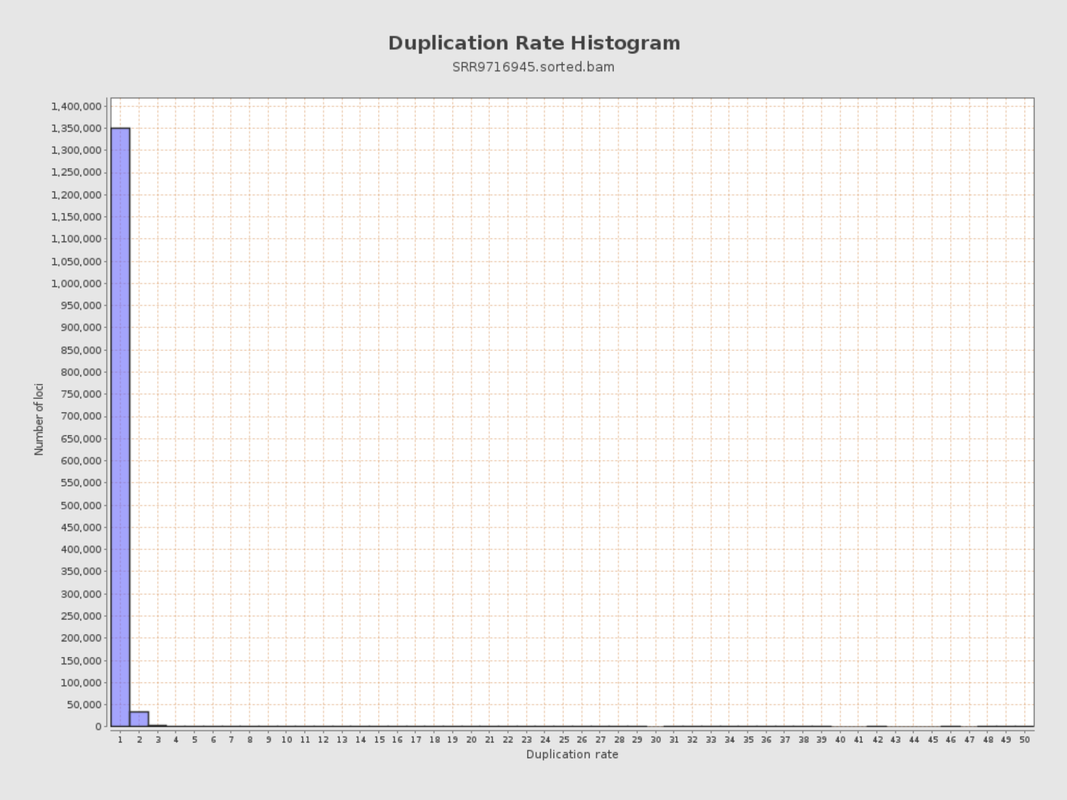
5. Results : Coverage Histogram (0-50X)



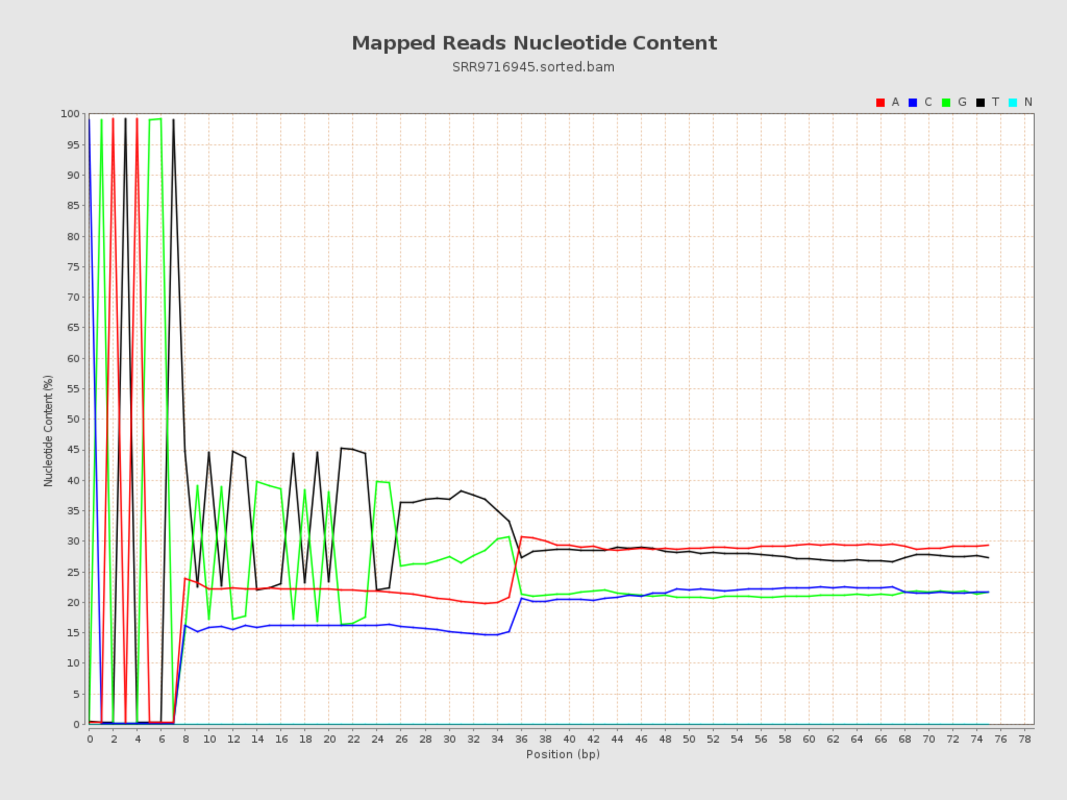
6. Results : Genome Fraction Coverage



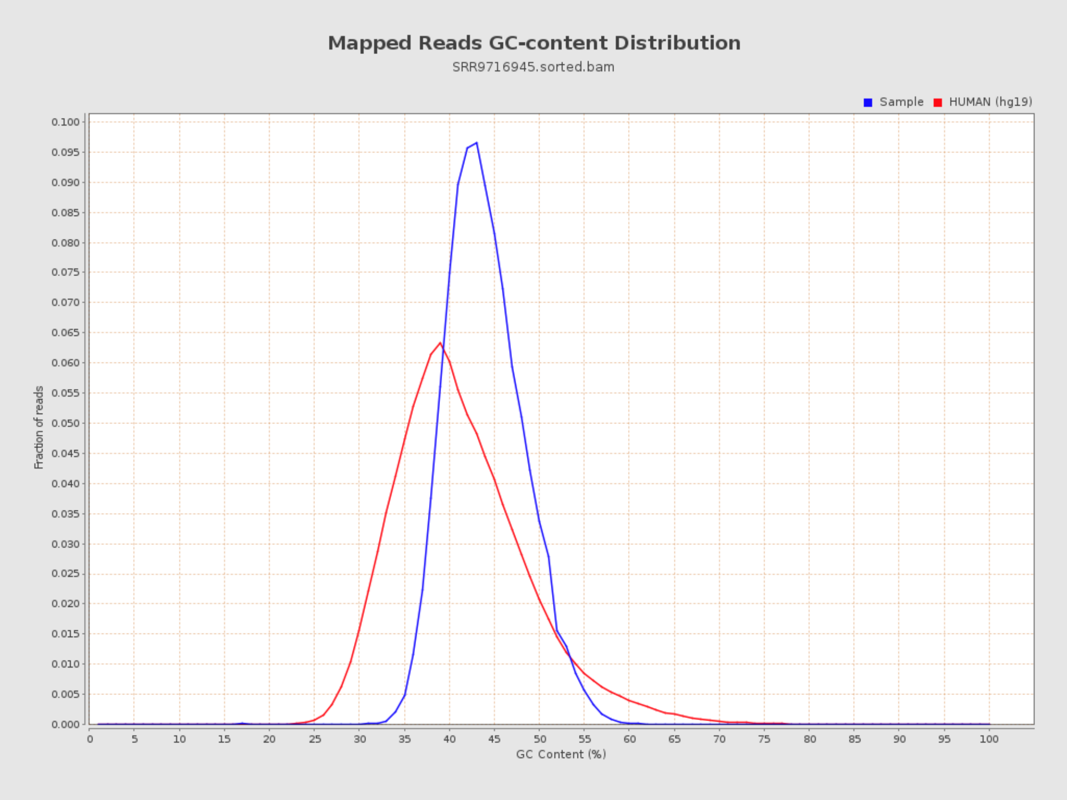
7. Results : Duplication Rate Histogram



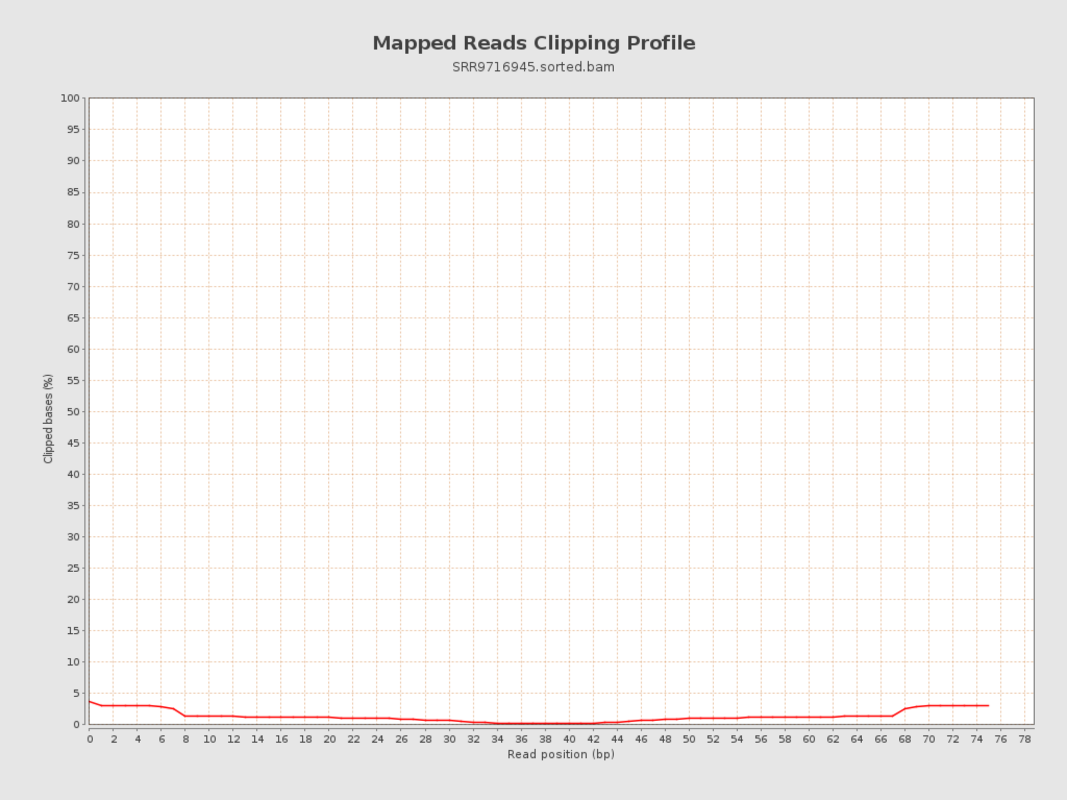
8. Results : Mapped Reads Nucleotide Content



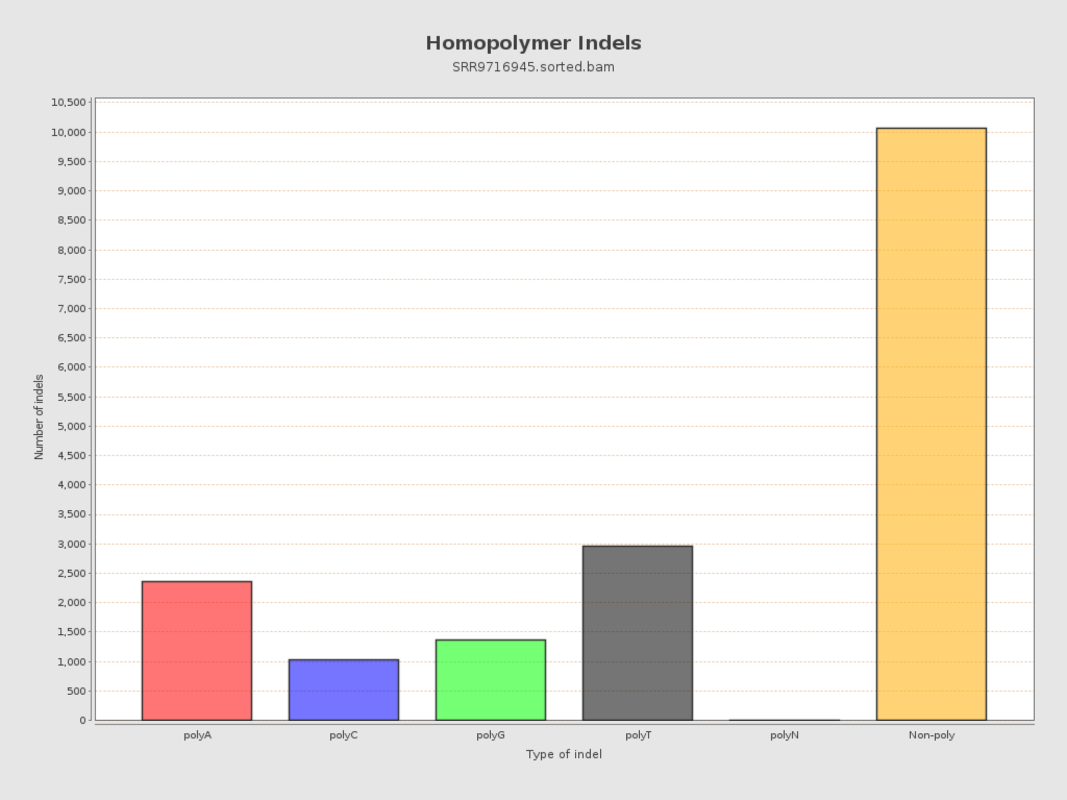
9. Results : Mapped Reads GC-content Distribution



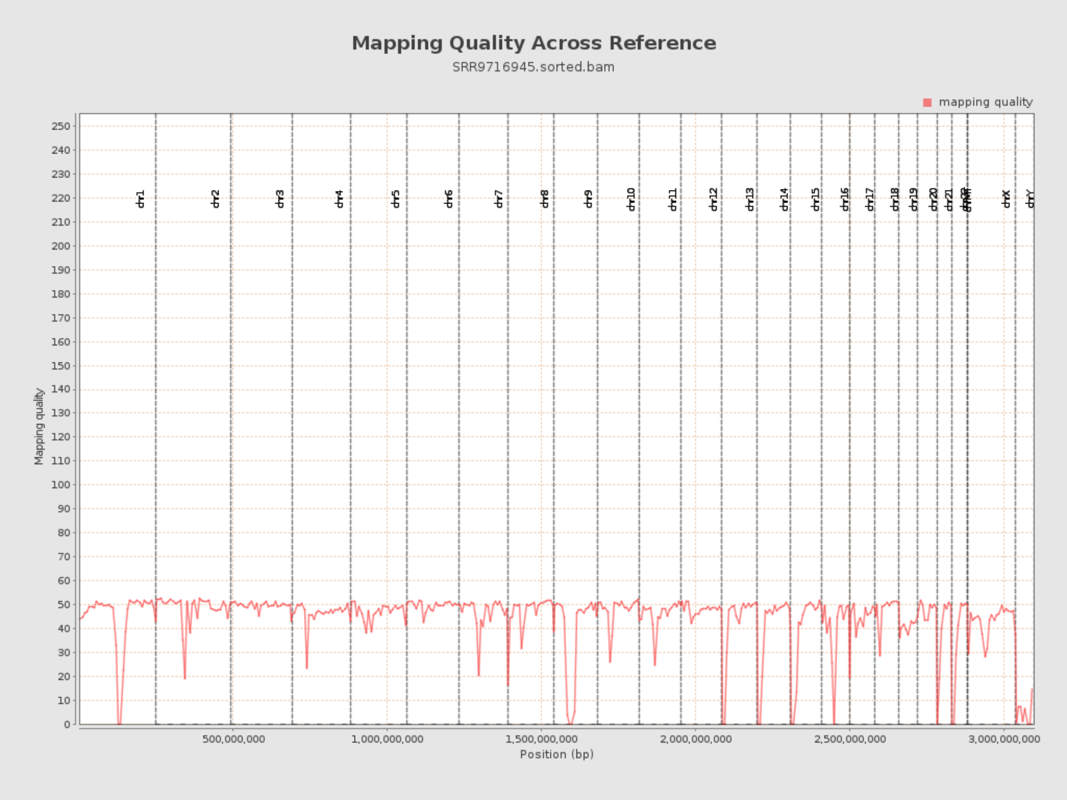
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram