Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 17:53:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716898.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_SRR9716898 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716898.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 17:53:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716898.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,077,144
Mapped reads	964,311 / 89.52%
Unmapped reads	112,833 / 10.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,401 / 1.99%
Read min/max/mean length	30 / 101 / 101.72
Duplicated reads (estimated)	21,078 / 1.96%
Duplication rate	1.44%
Clipped reads	984,328 / 91.38%

2.2. ACGT Content

Number/percentage of A's	19,062,358 / 26.3%
Number/percentage of C's	15,137,276 / 20.88%
Number/percentage of T's	21,475,089 / 29.63%
Number/percentage of G's	16,796,717 / 23.17%
Number/percentage of N's	8,807 / 0.01%
GC Percentage	44.06%

2.3. Coverage

Mean	0.0234

Standard Deviation	0.2161

2.4. Mapping Quality

Mean Mapping Quality	46.29

2.5. Mismatches and indels

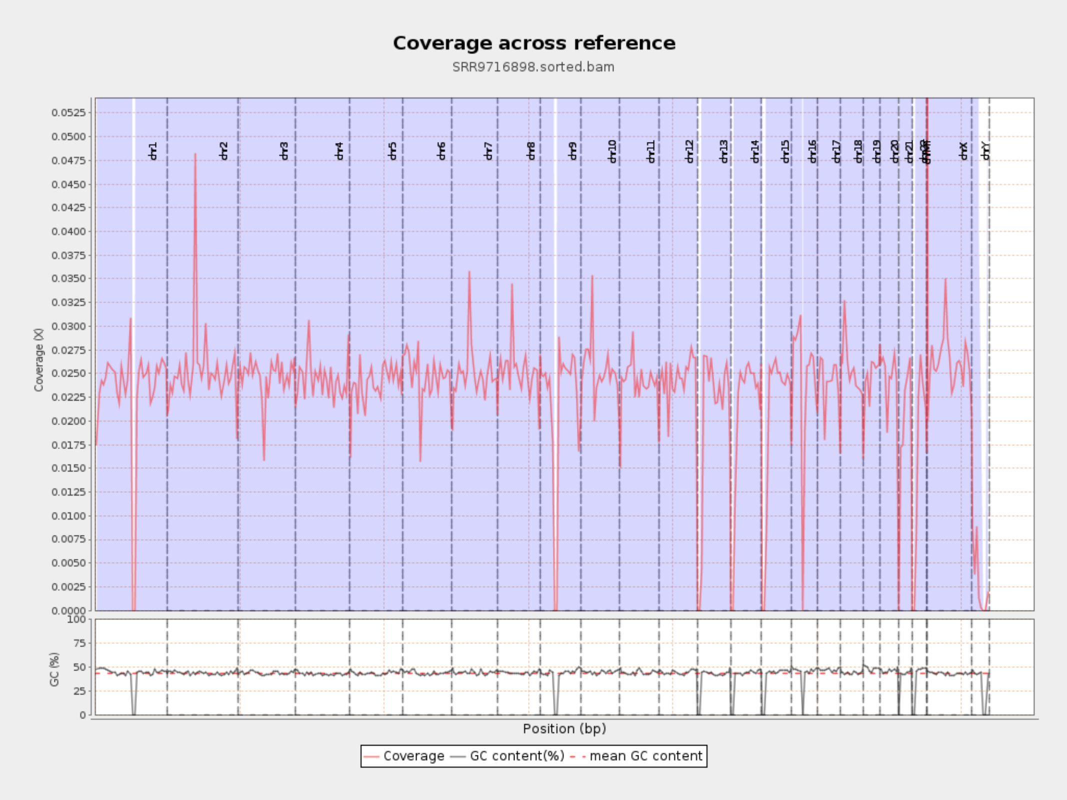
General error rate	0.77%
Mismatches	544,332
Insertions	5,784
Mapped reads with at least one insertion	0.59%
Deletions	15,195
Mapped reads with at least one deletion	1.56%
Homopolymer indels	40.83%

2.6. Chromosome stats

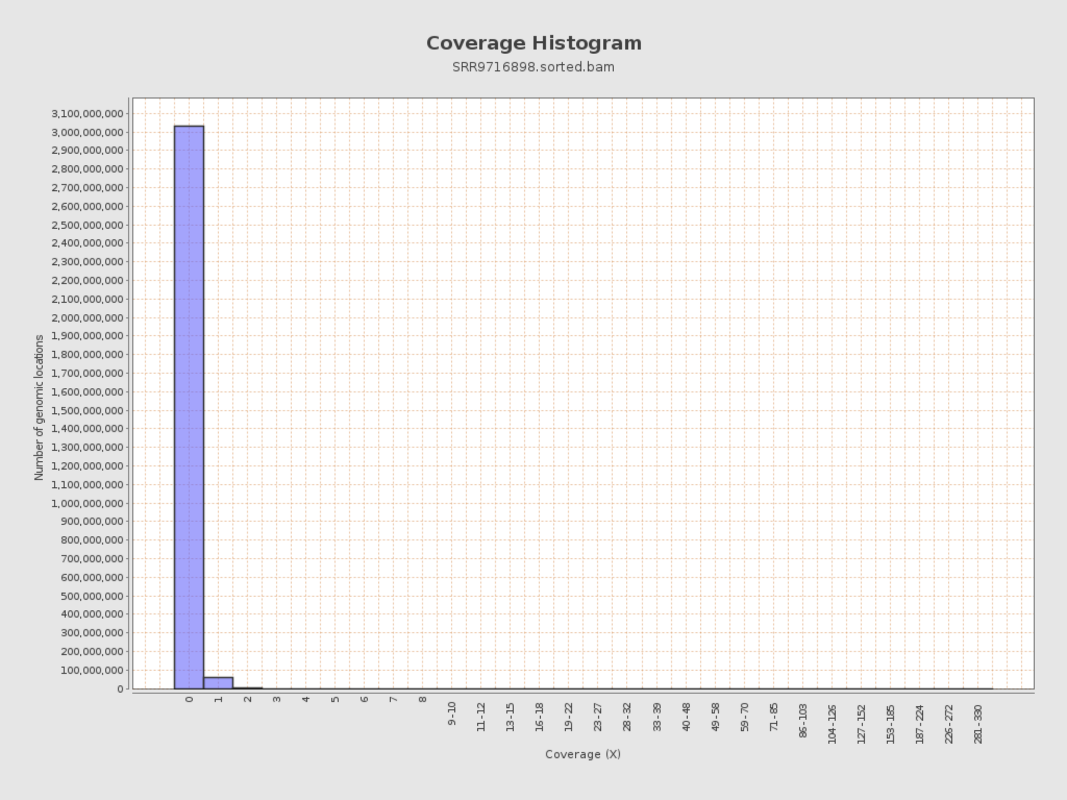
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5727096	0.023	0.2461
chr2	243199373	6197965	0.0255	0.2974
chr3	198022430	4884782	0.0247	0.1679
chr4	191154276	4664423	0.0244	0.1756
chr5	180915260	4371547	0.0242	0.1681
chr6	171115067	4233522	0.0247	0.1835
chr7	159138663	3986608	0.0251	0.2698

chr8	146364022	3703292	0.0253	0.2589
chr9	141213431	3065198	0.0217	0.2251
chr10	135534747	3445576	0.0254	0.2133
chr11	135006516	3287212	0.0243	0.2303
chr12	133851895	3281662	0.0245	0.1697
chr13	115169878	2332628	0.0203	0.1519
chr14	107349540	2183629	0.0203	0.1755
chr15	102531392	2069587	0.0202	0.1521
chr16	90354753	2139652	0.0237	0.175
chr17	81195210	1938634	0.0239	0.179
chr18	78077248	1992008	0.0255	0.3926
chr19	59128983	1455859	0.0246	0.2292
chr20	63025520	1522081	0.0242	0.1715
chr21	48129895	933022	0.0194	0.1571
chr22	51304566	832800	0.0162	0.1367
chrMT	16571	4085	0.2465	0.4848
chrX	155270560	4082930	0.0263	0.2058
chrY	59373566	170177	0.0029	0.0873

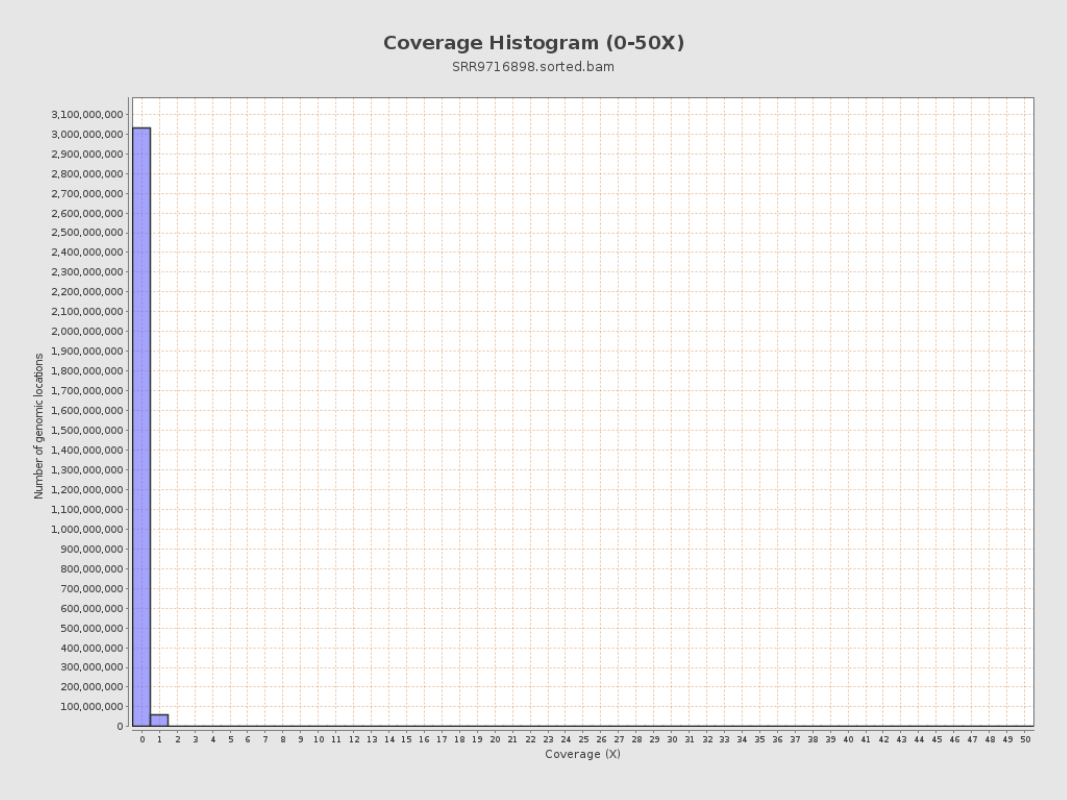
3. Results : Coverage across reference



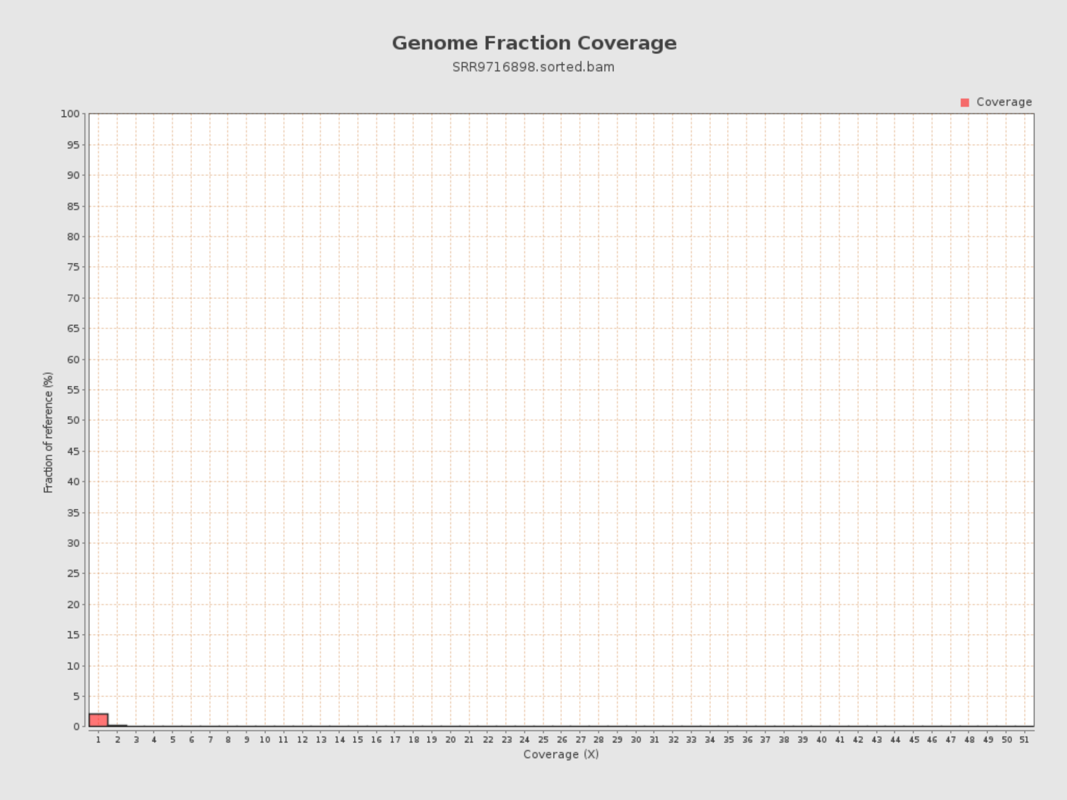
4. Results : Coverage Histogram



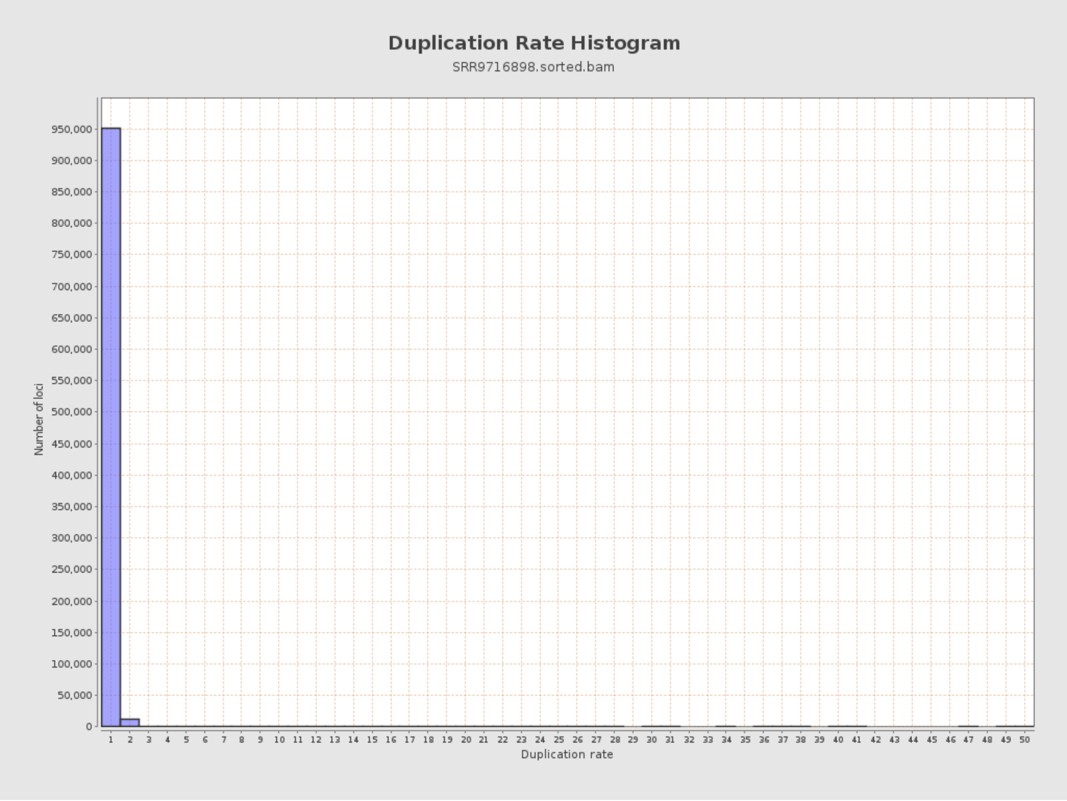
5. Results : Coverage Histogram (0-50X)



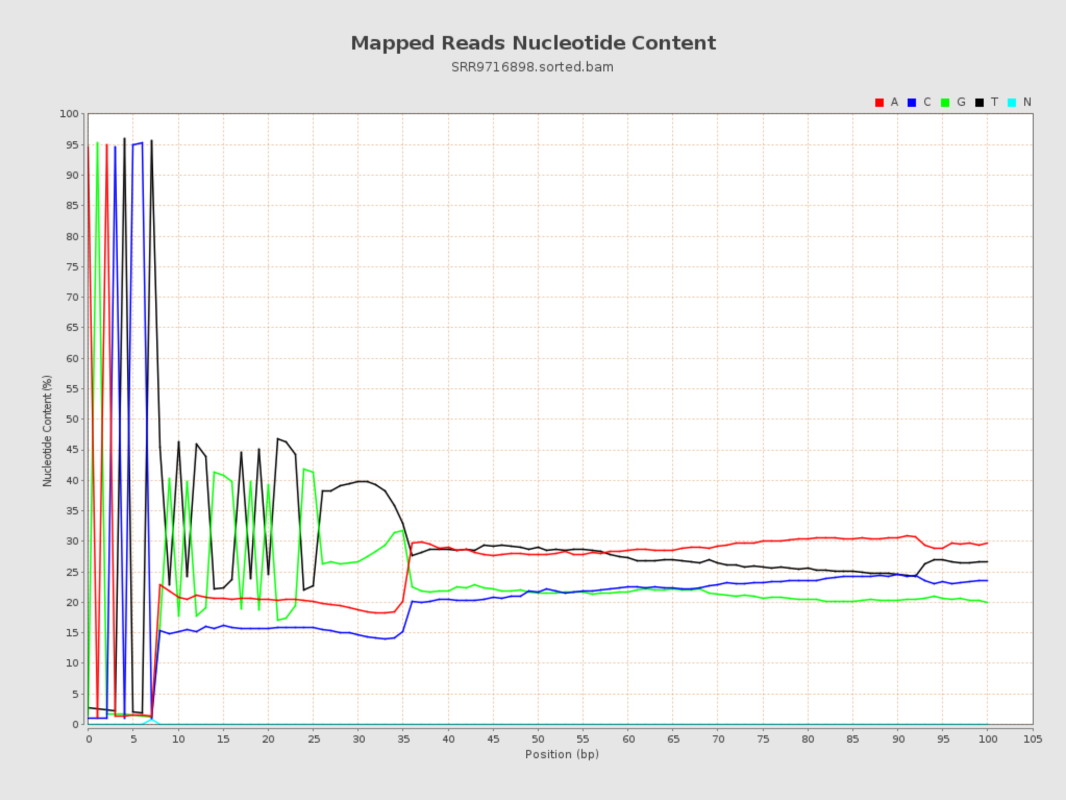
6. Results : Genome Fraction Coverage



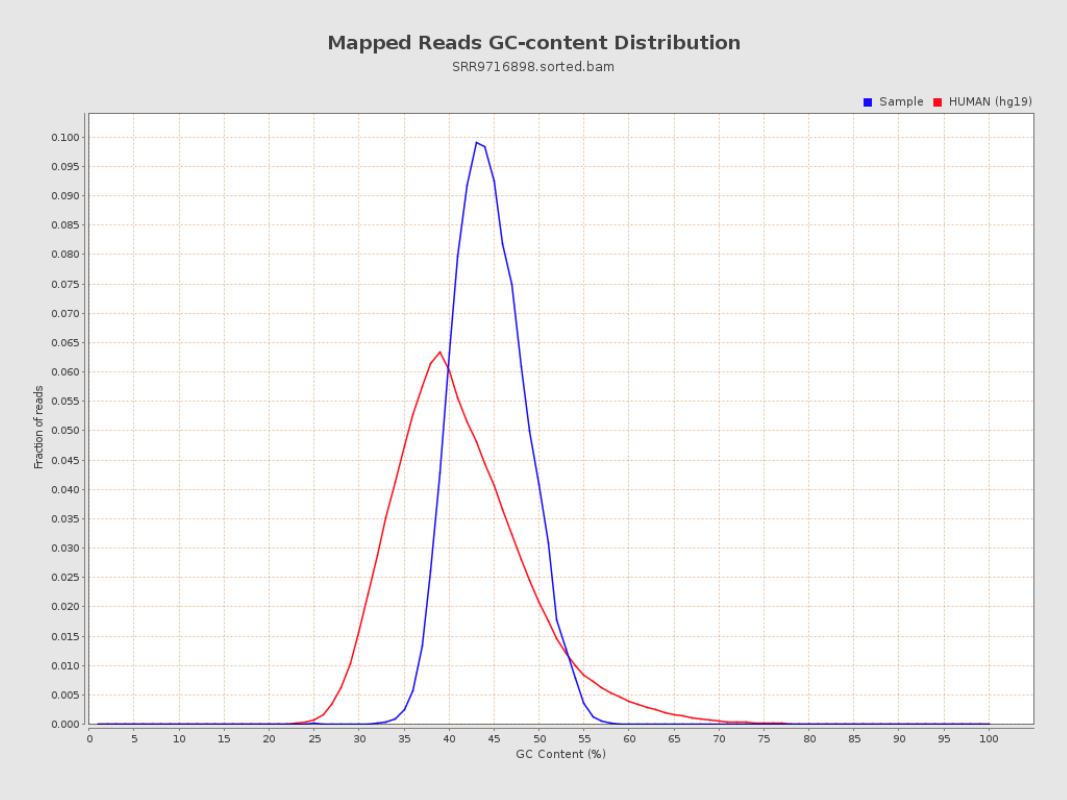
7. Results : Duplication Rate Histogram



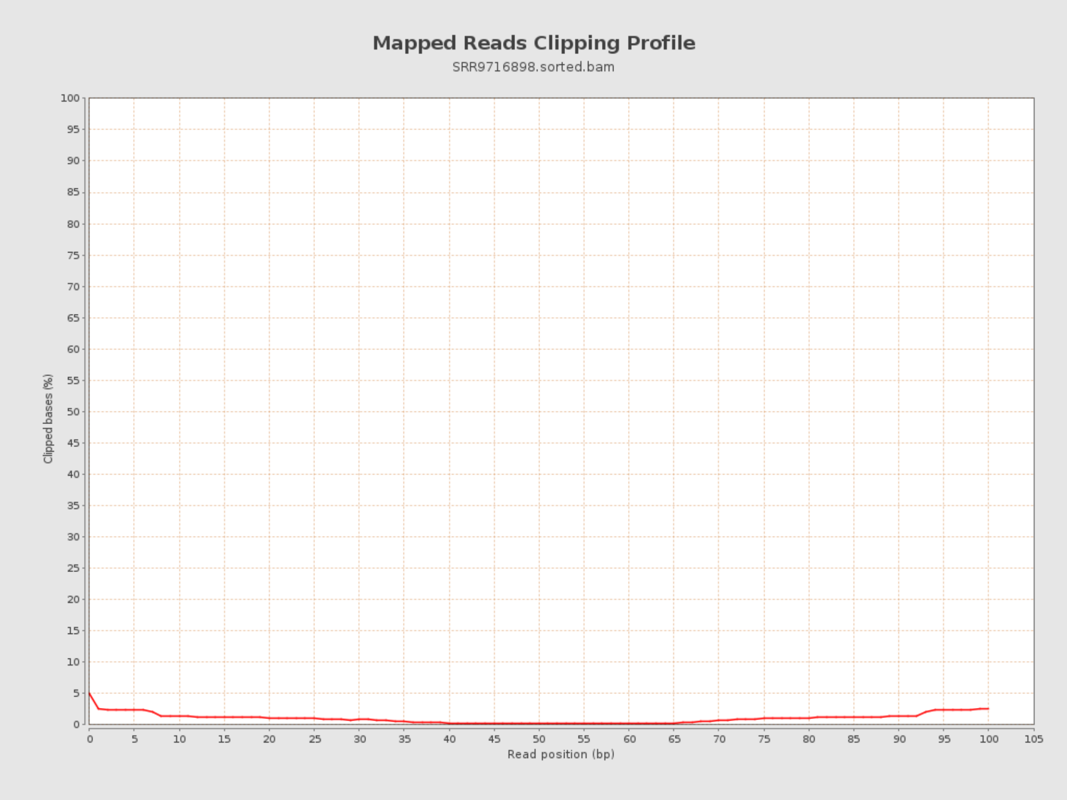
8. Results : Mapped Reads Nucleotide Content



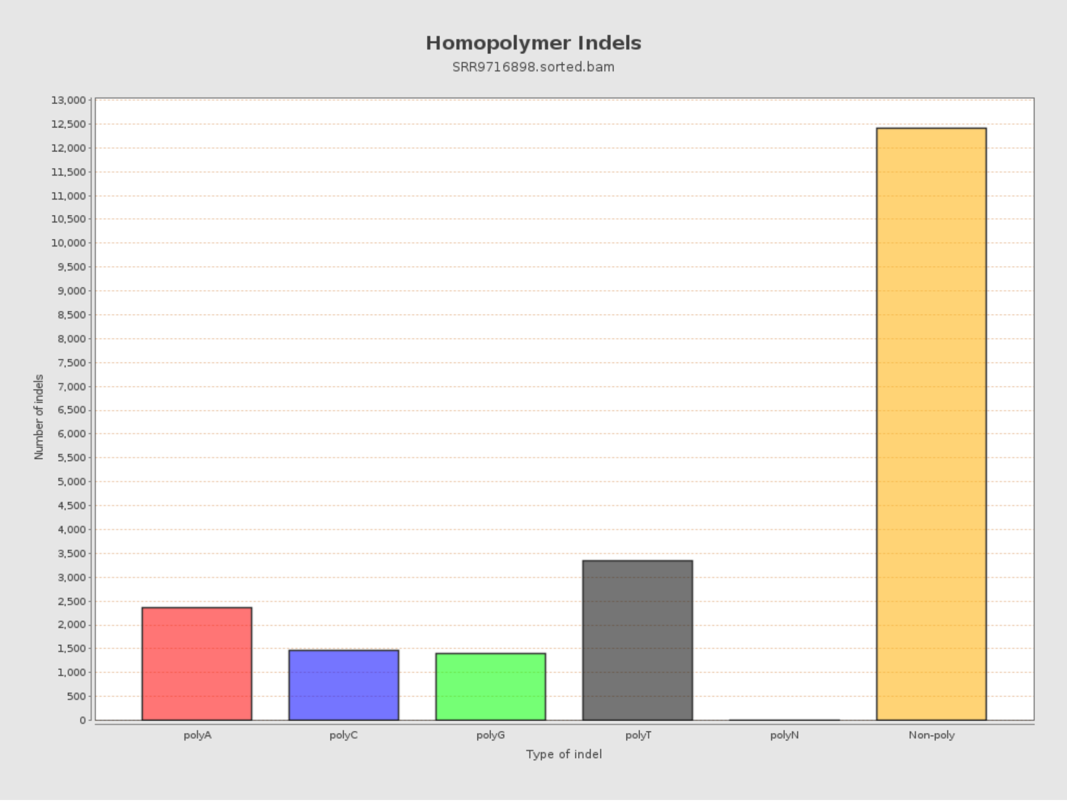
9. Results : Mapped Reads GC-content Distribution



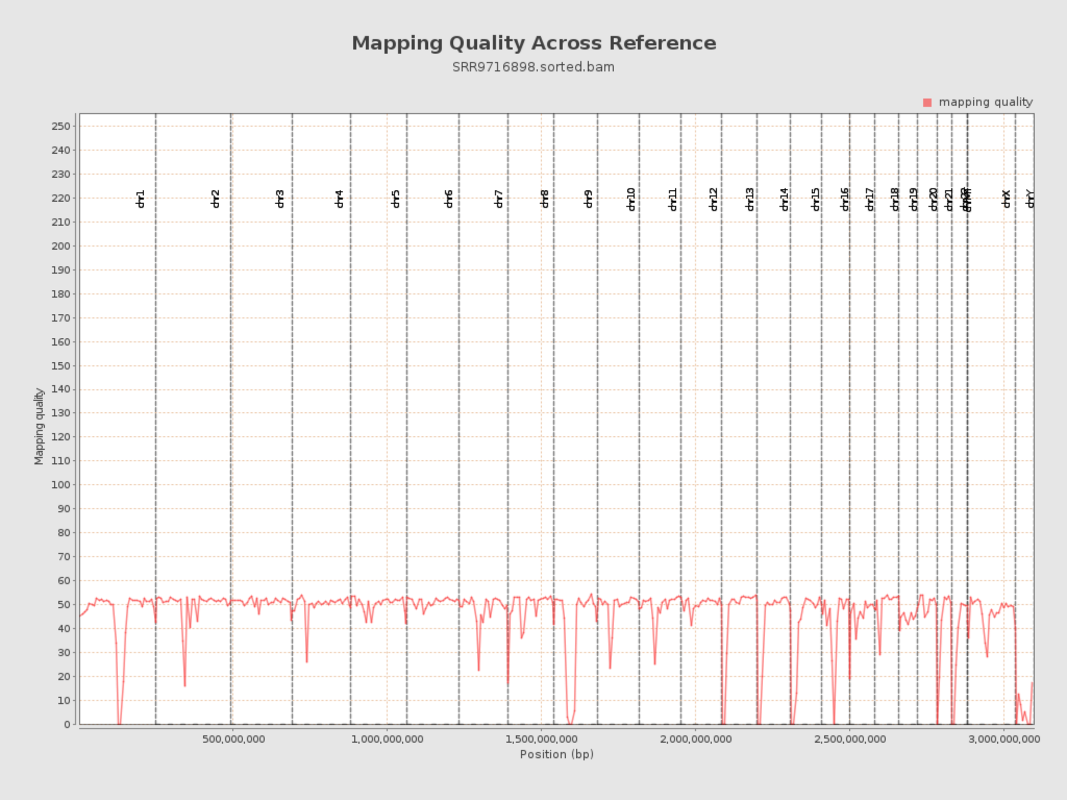
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram