Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 12:43:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716797.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_SRR9716797 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716797.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 12:43:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716797.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,434,915
Mapped reads	1,042,168 / 72.63%
Unmapped reads	392,747 / 27.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,063 / 0.07%
Read min/max/mean length	30 / 76 / 76.02
Duplicated reads (estimated)	77,722 / 5.42%
Duplication rate	6.4%
Clipped reads	1,042,237 / 72.63%

2.2. ACGT Content

Number/percentage of A's	11,116,977 / 20.43%
Number/percentage of C's	9,514,349 / 17.49%
Number/percentage of T's	18,142,733 / 33.34%
Number/percentage of G's	15,638,700 / 28.74%
Number/percentage of N's	842 / 0%
GC Percentage	46.23%

2.3. Coverage

Mean	0.0176

Standard Deviation	0.1807

2.4. Mapping Quality

Mean Mapping Quality	42.2

2.5. Mismatches and indels

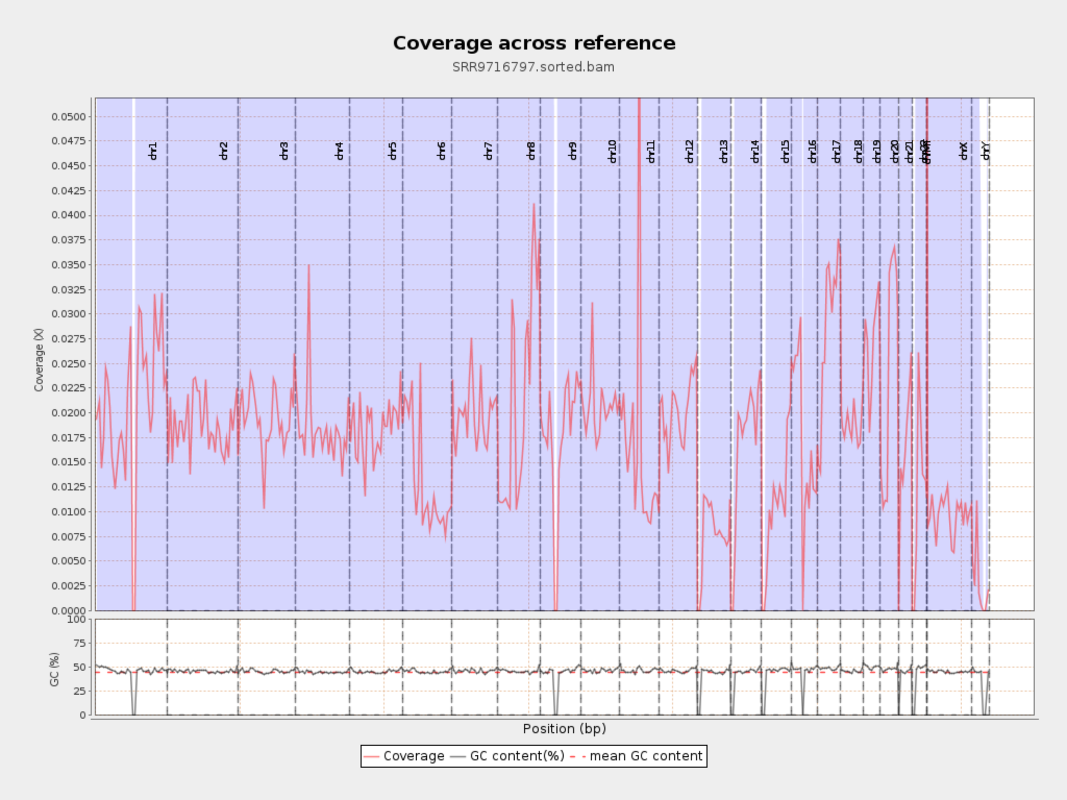
General error rate	0.73%
Mismatches	389,087
Insertions	3,102
Mapped reads with at least one insertion	0.3%
Deletions	8,711
Mapped reads with at least one deletion	0.83%
Homopolymer indels	40.02%

2.6. Chromosome stats

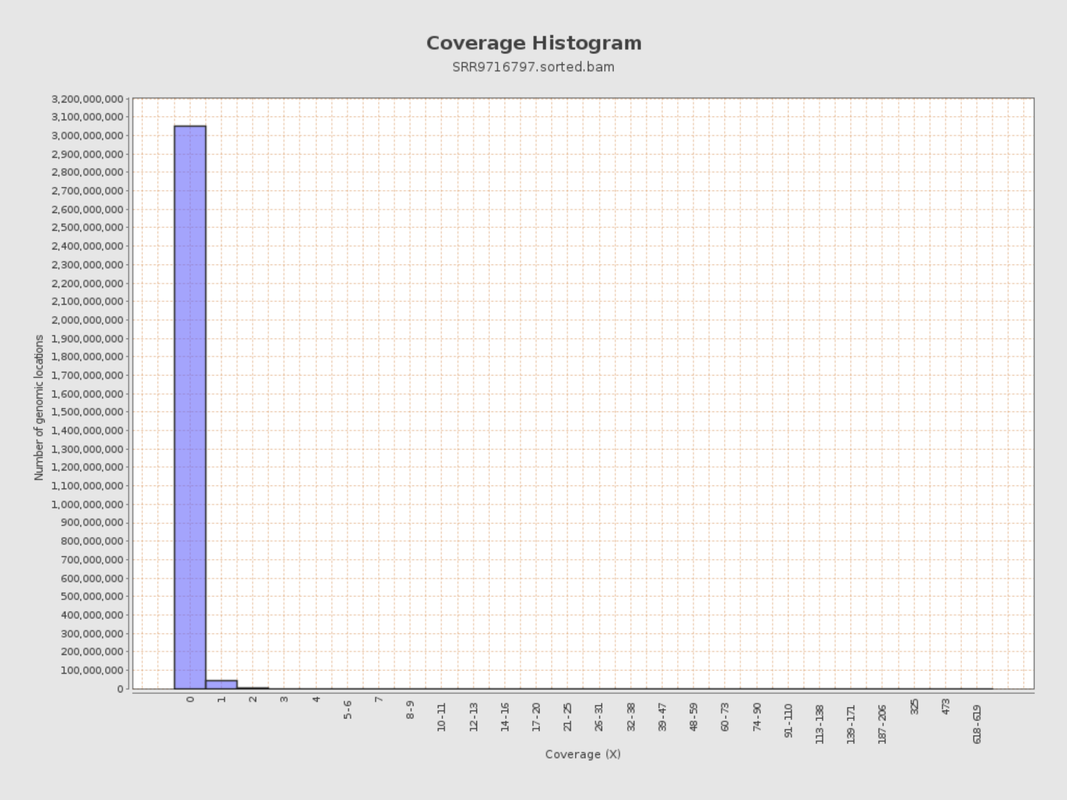
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5114423	0.0205	0.1981
chr2	243199373	4569329	0.0188	0.2963
chr3	198022430	3845554	0.0194	0.1605
chr4	191154276	3558208	0.0186	0.1688
chr5	180915260	3346357	0.0185	0.1552
chr6	171115067	2222814	0.013	0.1621
chr7	159138663	3181402	0.02	0.1871

chr8	146364022	3110001	0.0212	0.1749
chr9	141213431	2442182	0.0173	0.1662
chr10	135534747	2809163	0.0207	0.2028
chr11	135006516	2297737	0.017	0.1654
chr12	133851895	2696608	0.0201	0.1641
chr13	115169878	858263	0.0075	0.1017
chr14	107349540	1791374	0.0167	0.153
chr15	102531392	1057431	0.0103	0.117
chr16	90354753	1519744	0.0168	0.1656
chr17	81195210	2335403	0.0288	0.2032
chr18	78077248	1455169	0.0186	0.1797
chr19	59128983	1590126	0.0269	0.2308
chr20	63025520	1517739	0.0241	0.1877
chr21	48129895	793423	0.0165	0.1605
chr22	51304566	639497	0.0125	0.1332
chrMT	16571	1705	0.1029	0.3745
chrX	155270560	1507605	0.0097	0.1181
chrY	59373566	167153	0.0028	0.0883

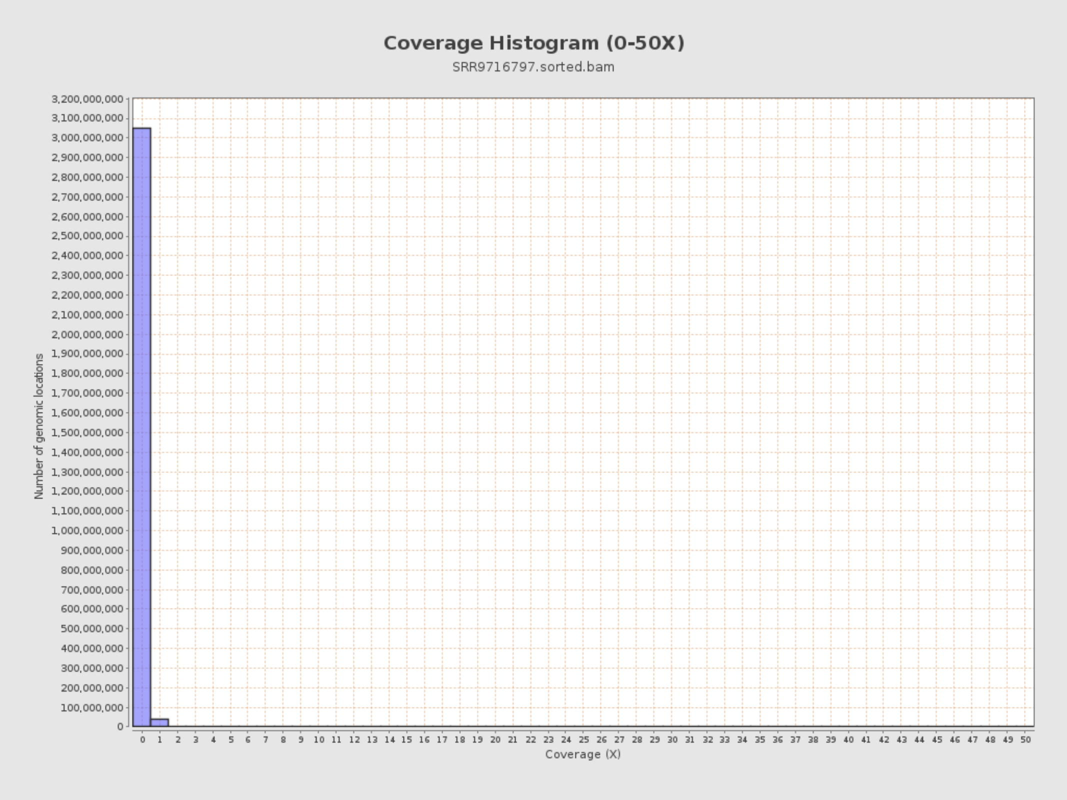
3. Results : Coverage across reference



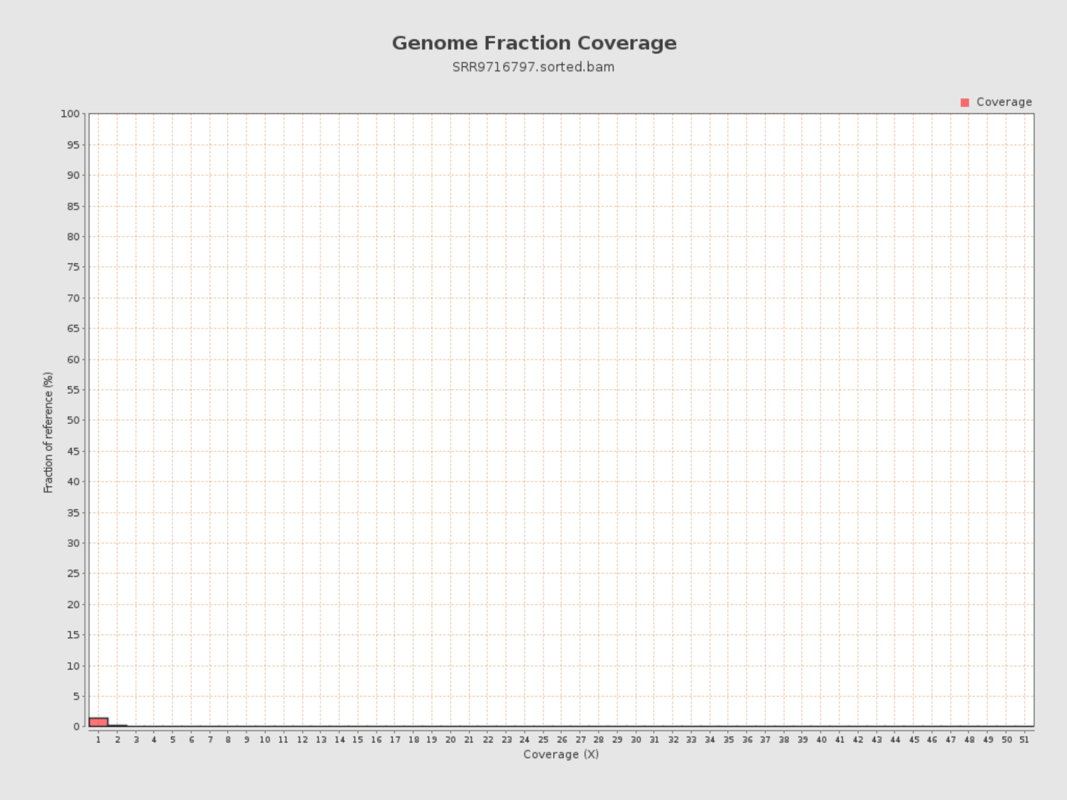
4. Results : Coverage Histogram



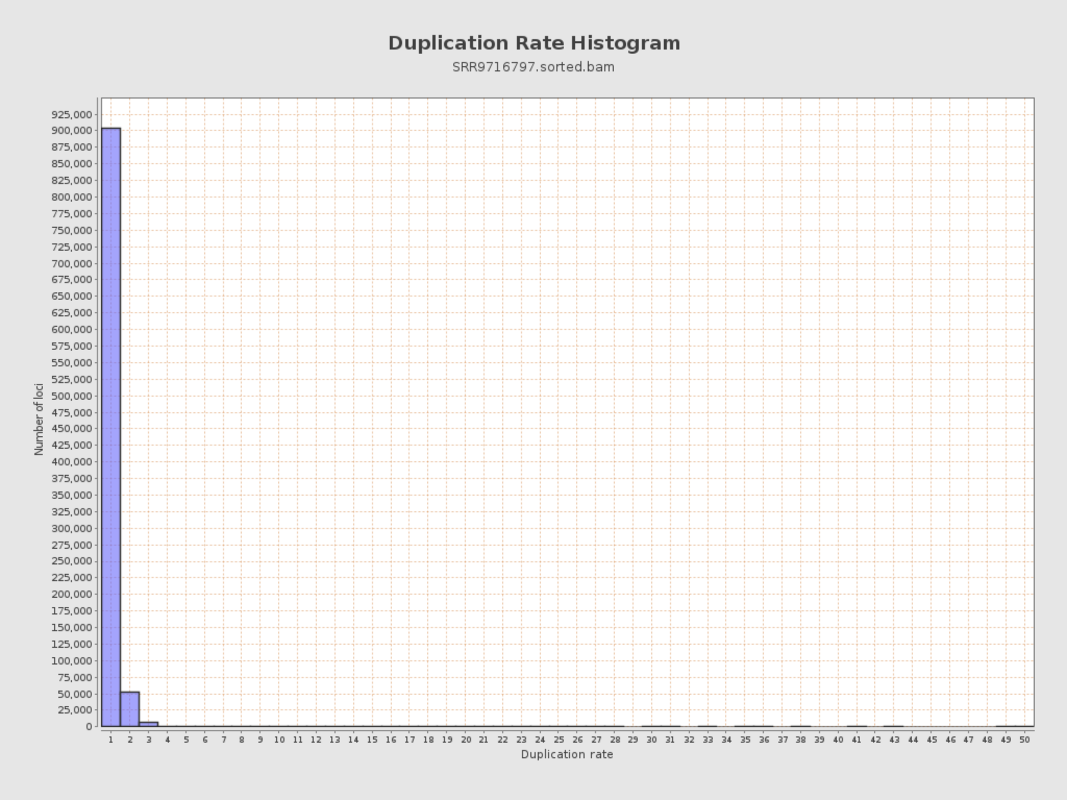
5. Results : Coverage Histogram (0-50X)



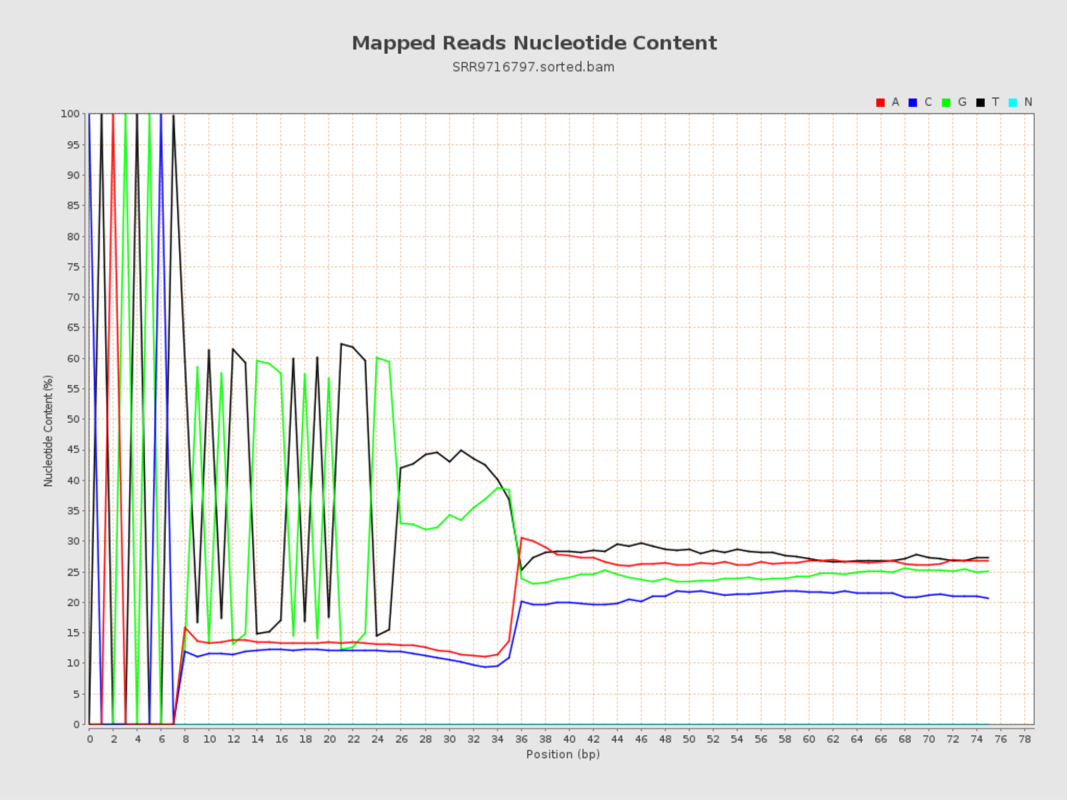
6. Results : Genome Fraction Coverage



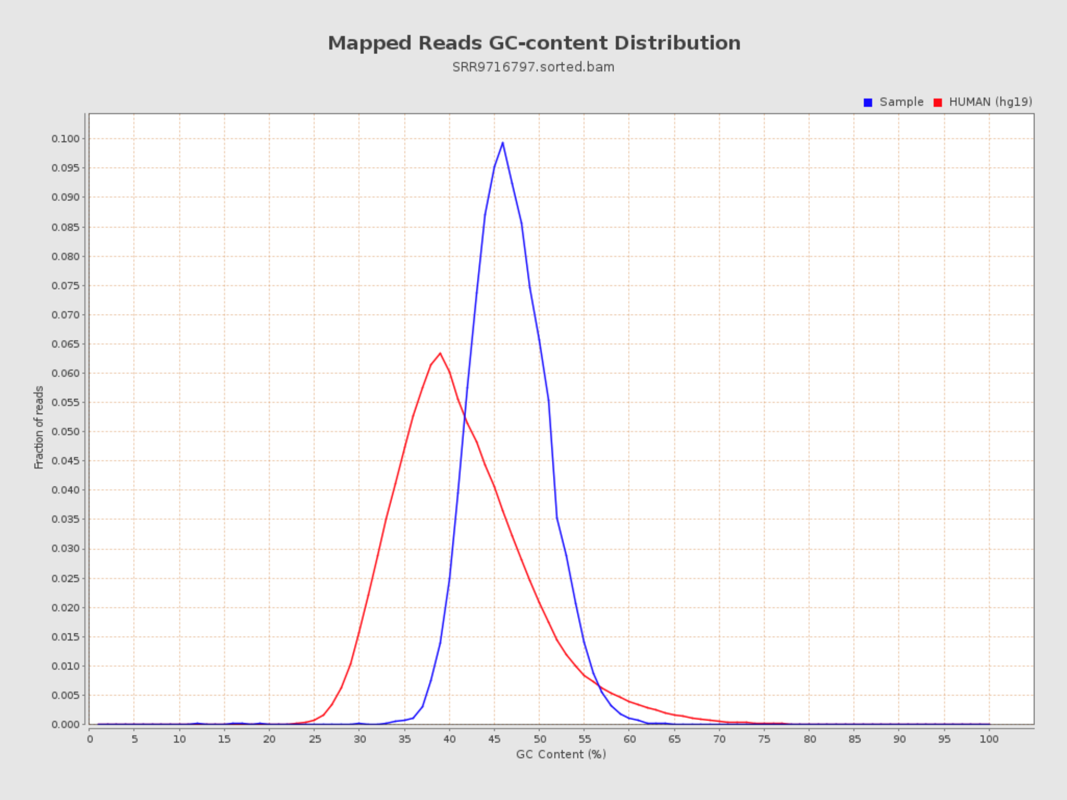
7. Results : Duplication Rate Histogram



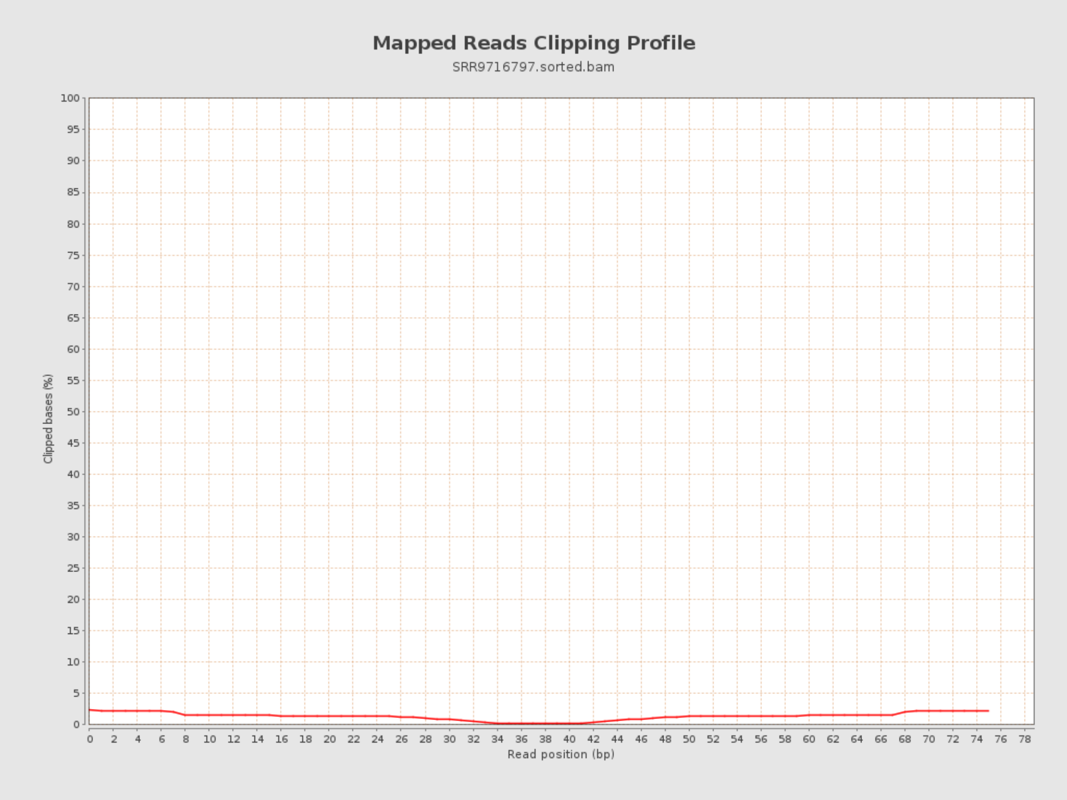
8. Results : Mapped Reads Nucleotide Content



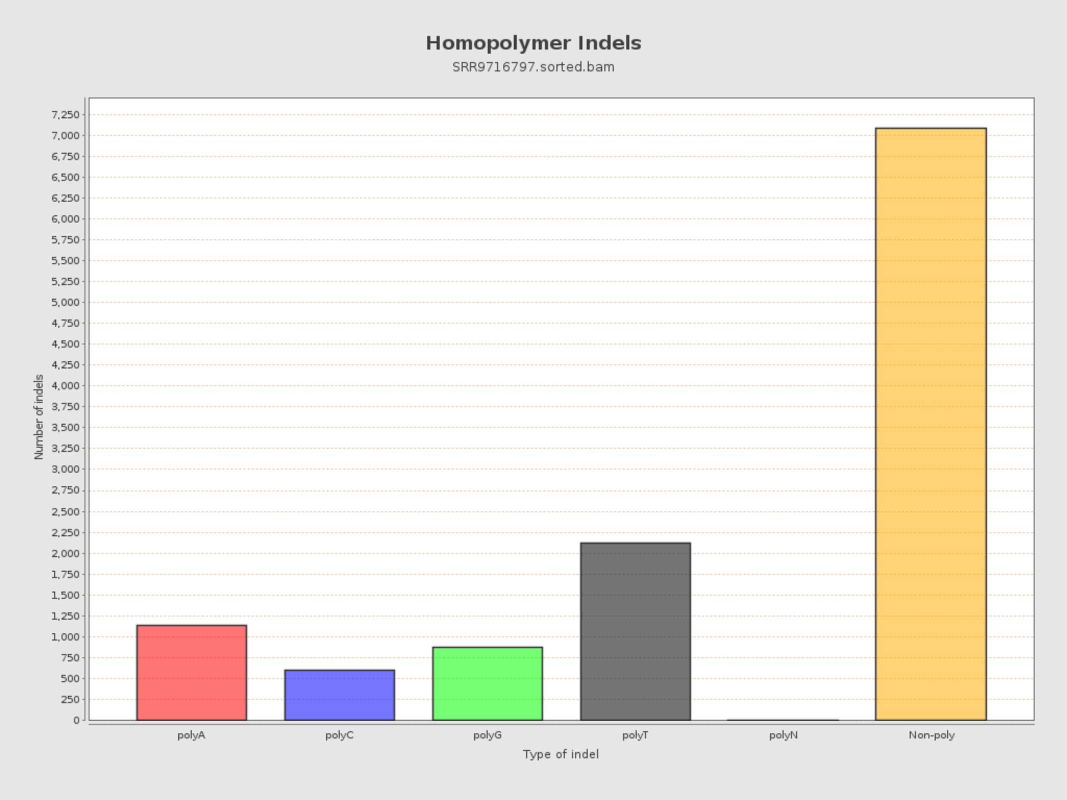
9. Results : Mapped Reads GC-content Distribution



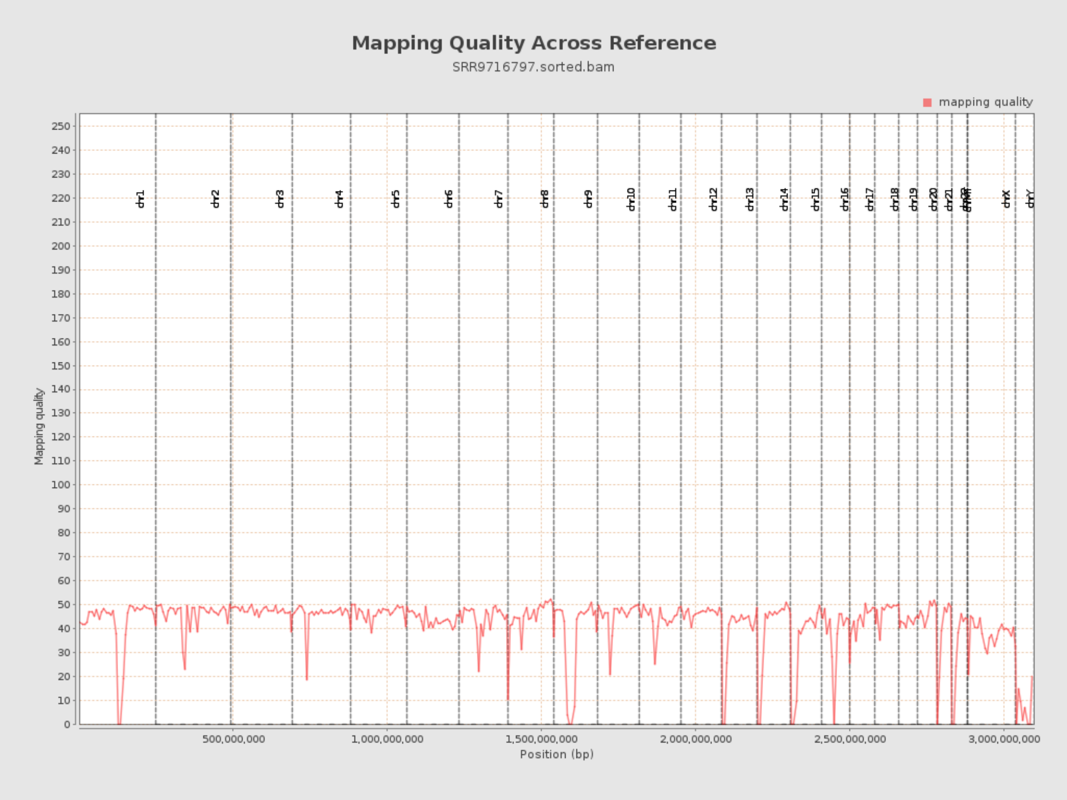
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram