Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 15:15:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716856.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_SRR9716856 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716856.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 15:15:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716856.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	649,310
Mapped reads	583,850 / 89.92%
Unmapped reads	65,460 / 10.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,668 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	11,404 / 1.76%
Duplication rate	1.46%
Clipped reads	585,870 / 90.23%

2.2. ACGT Content

Number/percentage of A's	8,095,321 / 24.16%
Number/percentage of C's	6,401,483 / 19.1%
Number/percentage of T's	10,633,511 / 31.73%
Number/percentage of G's	8,381,292 / 25.01%
Number/percentage of N's	414 / 0%
GC Percentage	44.11%

2.3. Coverage

Mean	0.0108

Standard Deviation	0.1278

2.4. Mapping Quality

Mean Mapping Quality	43.86

2.5. Mismatches and indels

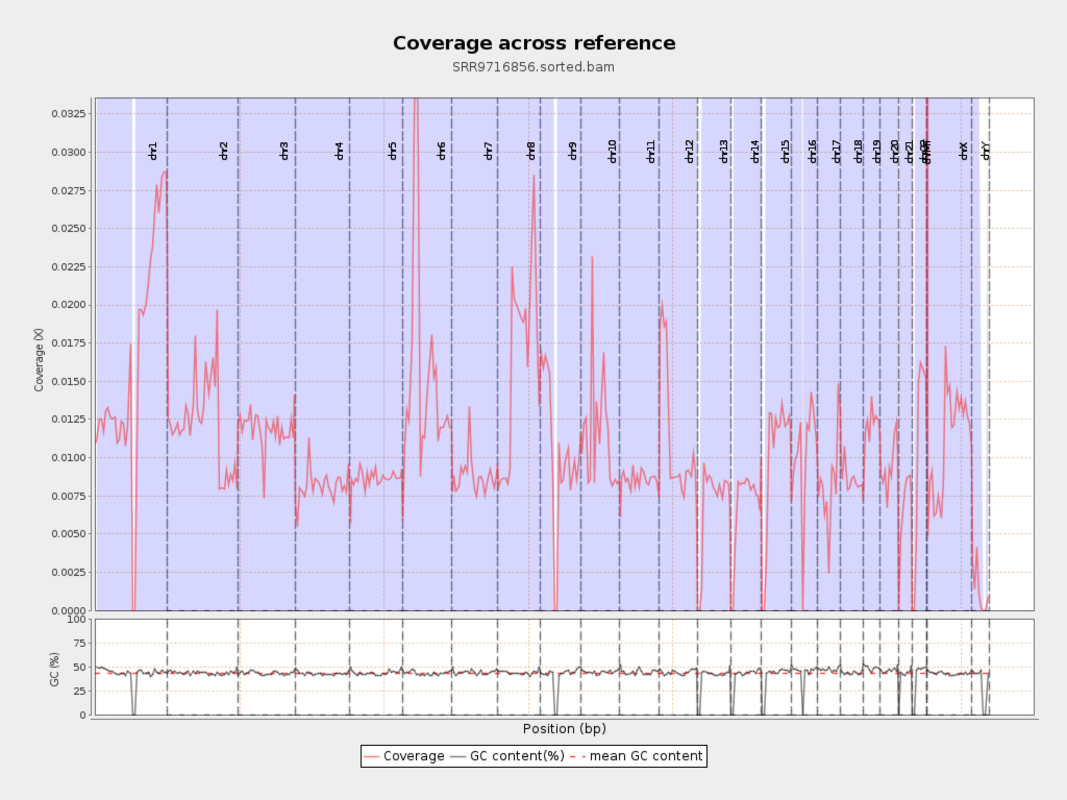
General error rate	0.51%
Mismatches	168,187
Insertions	1,899
Mapped reads with at least one insertion	0.32%
Deletions	5,422
Mapped reads with at least one deletion	0.92%
Homopolymer indels	41.54%

2.6. Chromosome stats

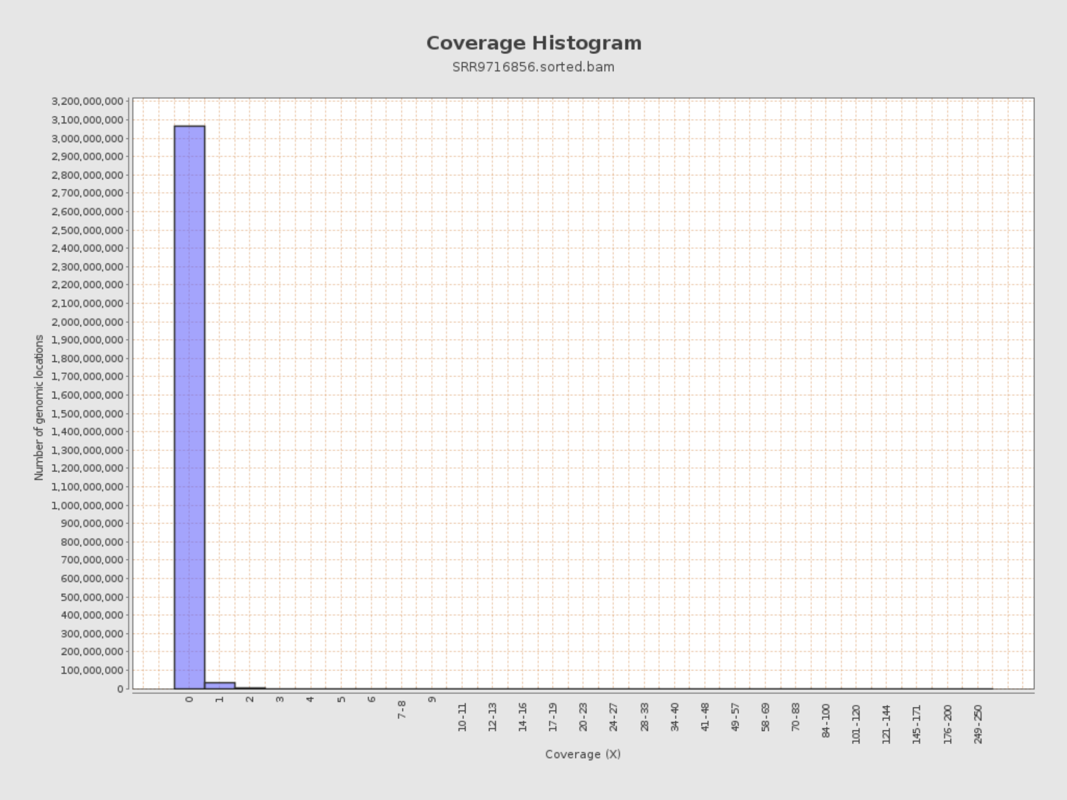
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4083967	0.0164	0.1971
chr2	243199373	2966713	0.0122	0.1563
chr3	198022430	2341913	0.0118	0.1133
chr4	191154276	1563514	0.0082	0.0966
chr5	180915260	1571523	0.0087	0.0976
chr6	171115067	2700095	0.0158	0.1504
chr7	159138663	1402017	0.0088	0.1187

chr8	146364022	2406619	0.0164	0.1386
chr9	141213431	1443885	0.0102	0.1207
chr10	135534747	1565431	0.0116	0.1339
chr11	135006516	1161410	0.0086	0.1091
chr12	133851895	1519137	0.0113	0.1123
chr13	115169878	795388	0.0069	0.0861
chr14	107349540	724400	0.0067	0.0921
chr15	102531392	1015803	0.0099	0.1049
chr16	90354753	908897	0.0101	0.108
chr17	81195210	679515	0.0084	0.0972
chr18	78077248	670985	0.0086	0.1637
chr19	59128983	715125	0.0121	0.1569
chr20	63025520	596185	0.0095	0.1013
chr21	48129895	321421	0.0067	0.0881
chr22	51304566	540459	0.0105	0.107
chrMT	16571	27990	1.6891	1.552
chrX	155270560	1722253	0.0111	0.117
chrY	59373566	75835	0.0013	0.0421

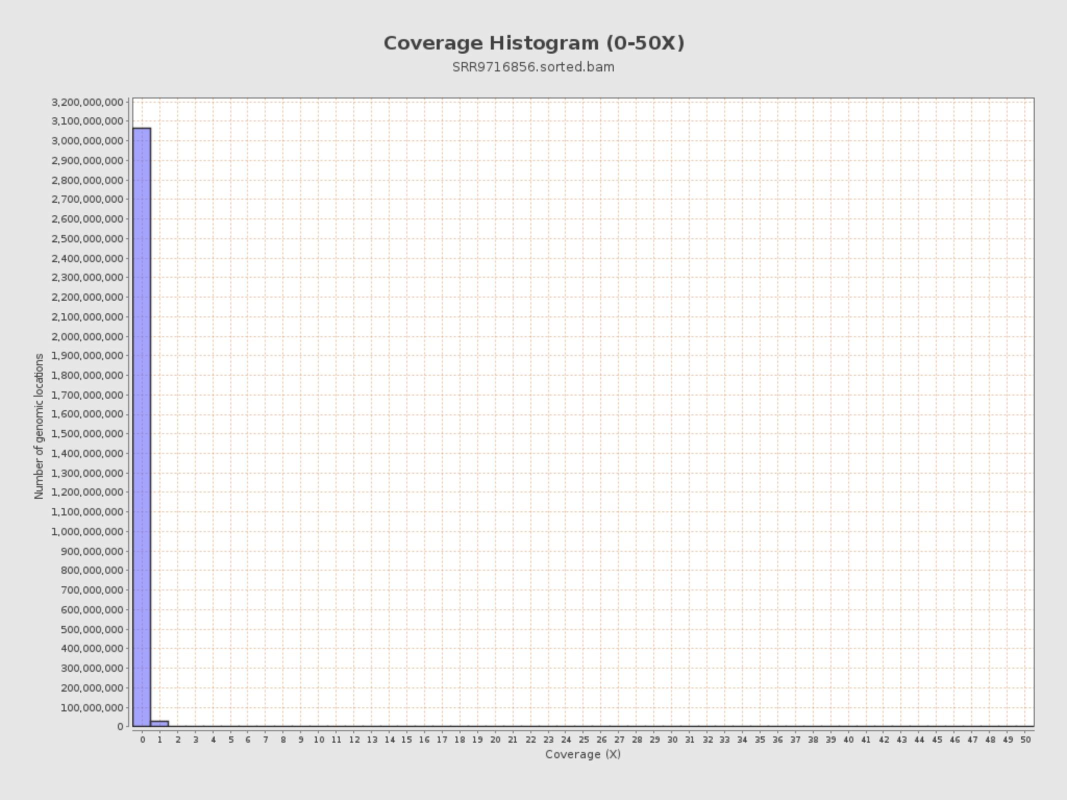
3. Results : Coverage across reference



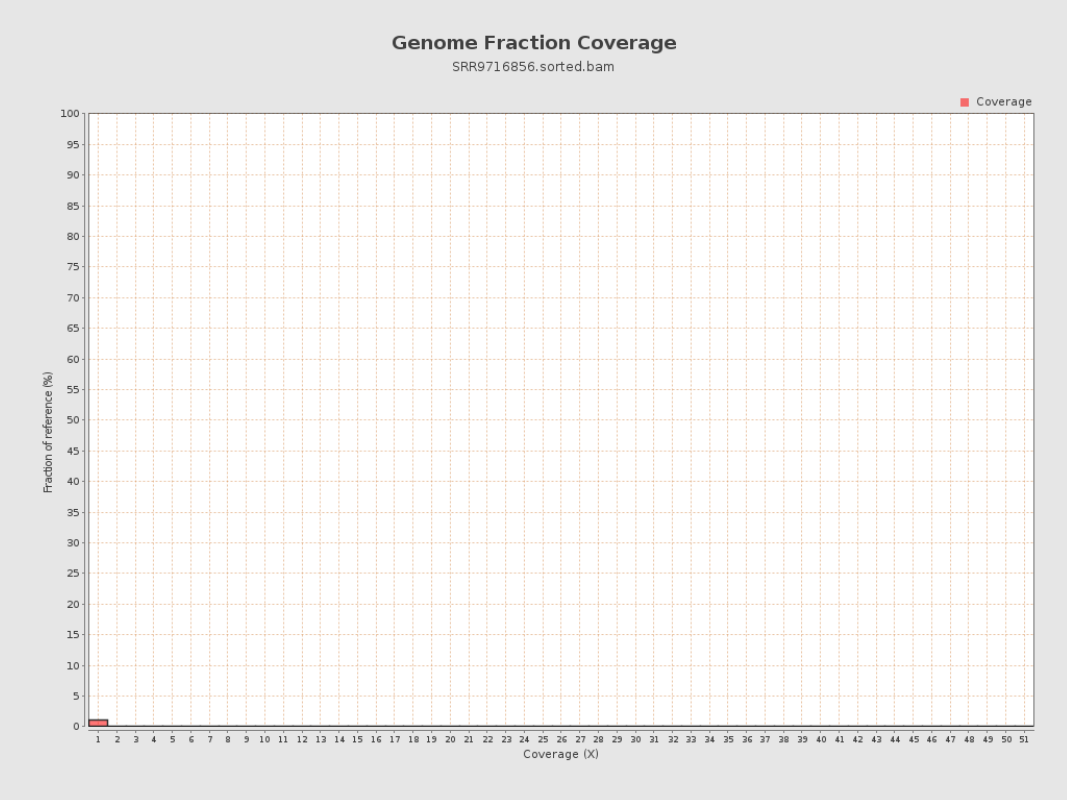
4. Results : Coverage Histogram



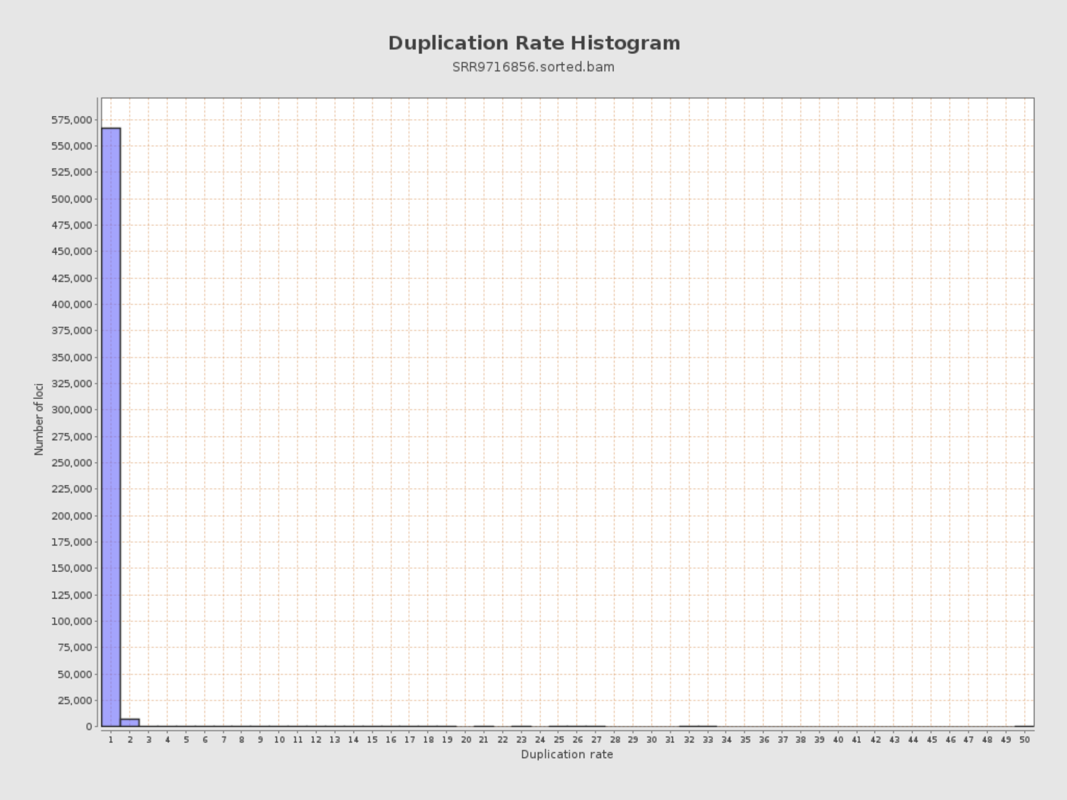
5. Results : Coverage Histogram (0-50X)



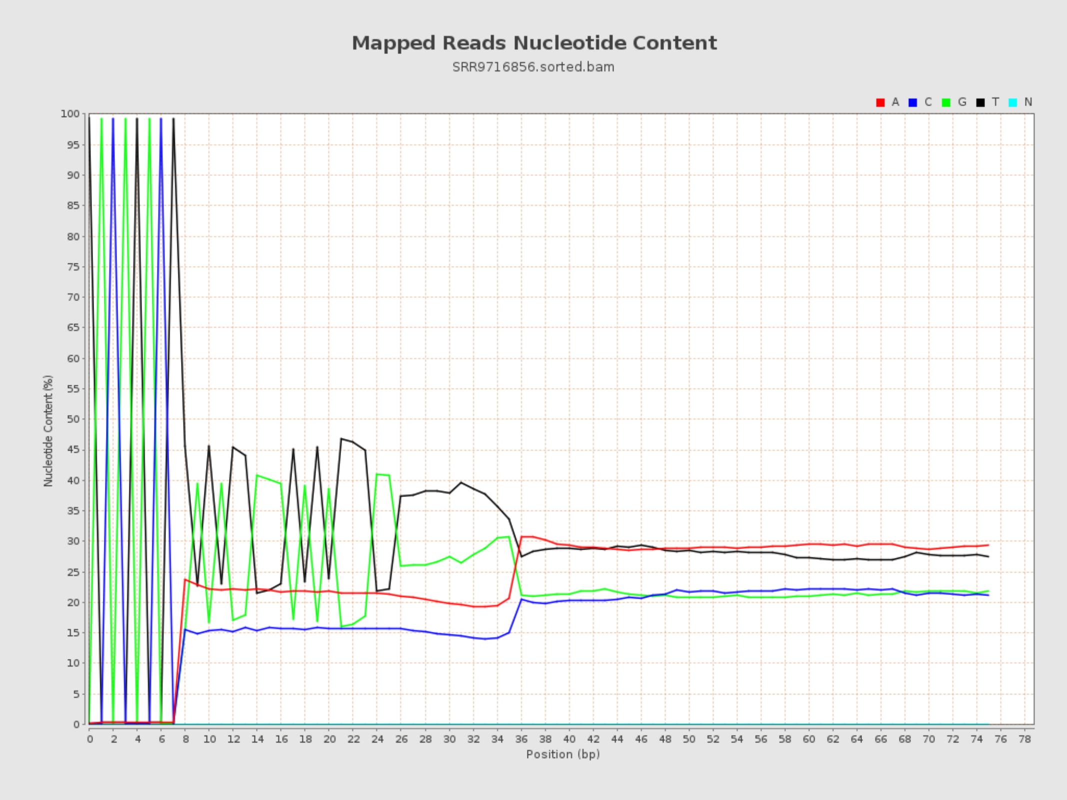
6. Results : Genome Fraction Coverage



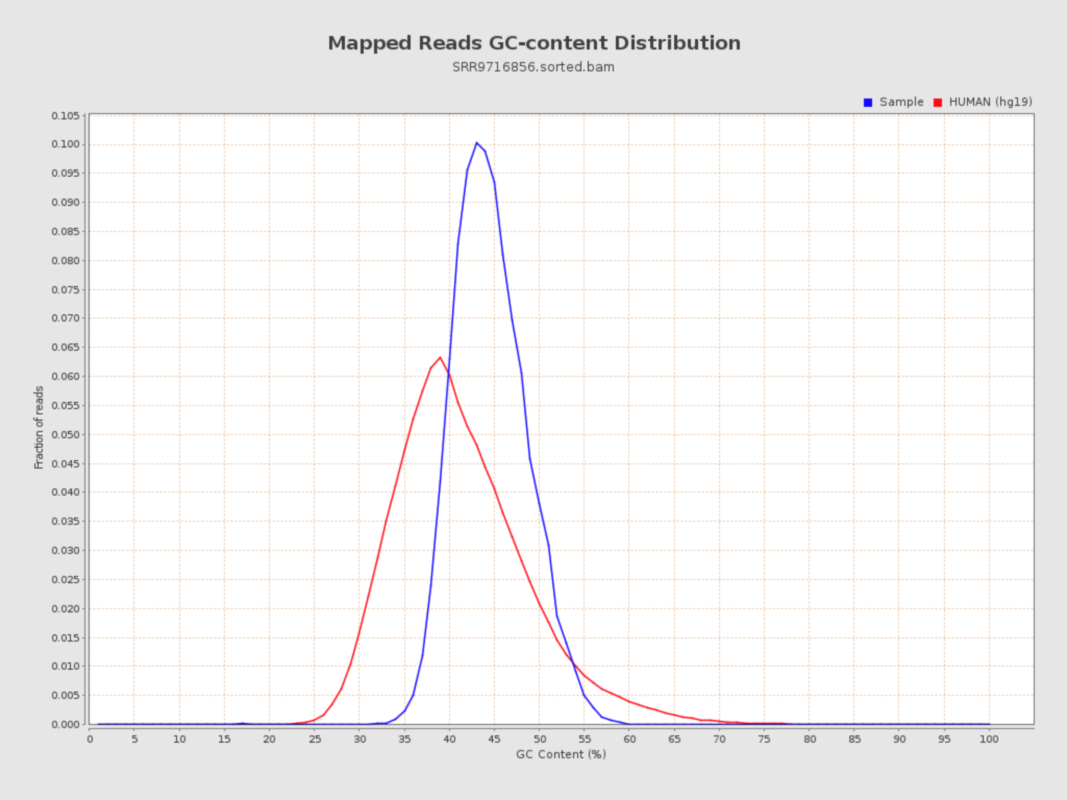
7. Results : Duplication Rate Histogram



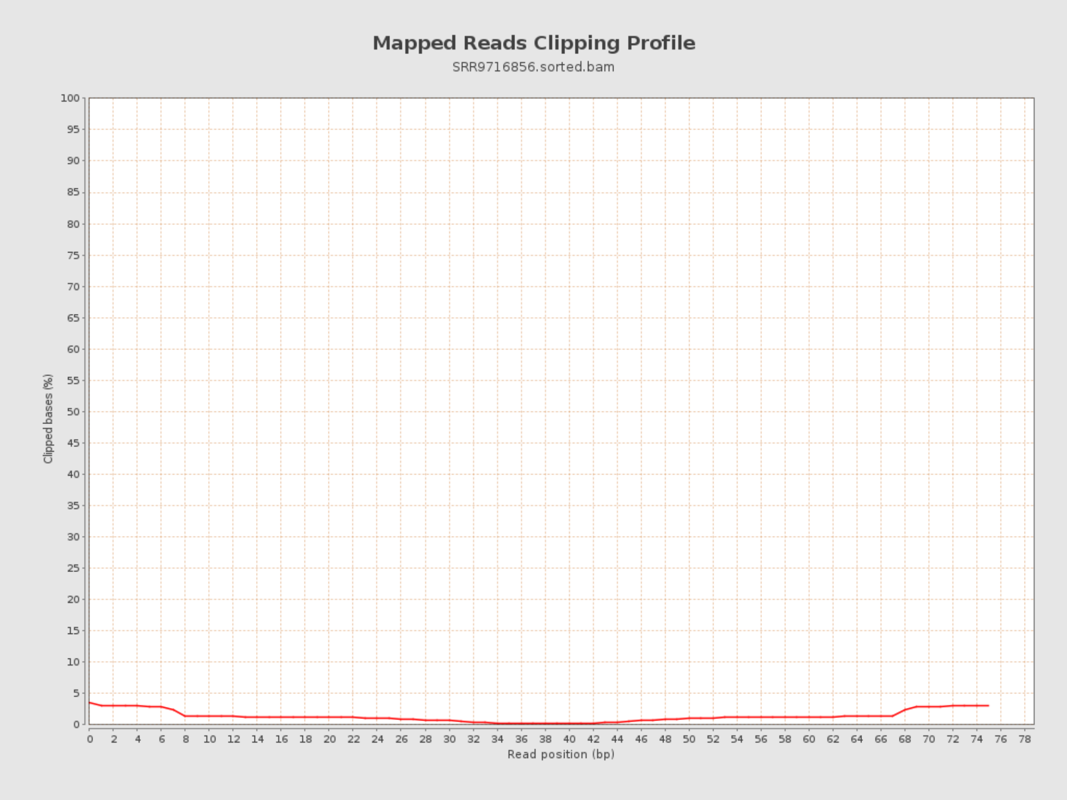
8. Results : Mapped Reads Nucleotide Content



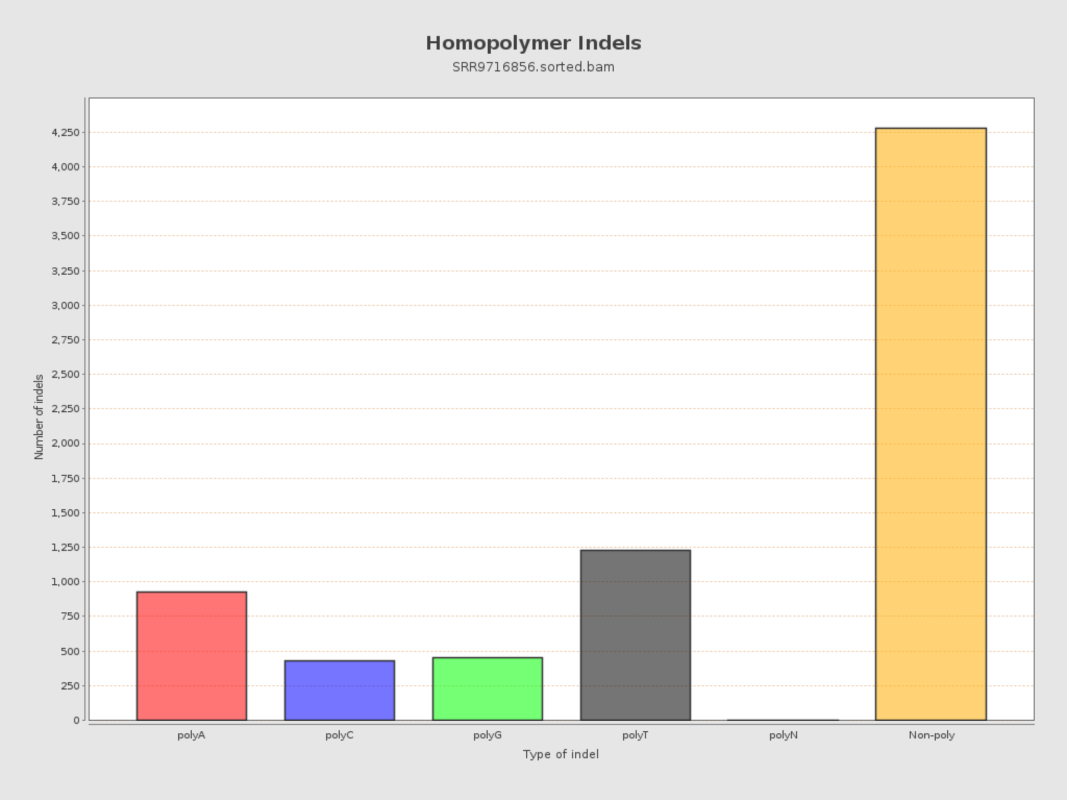
9. Results : Mapped Reads GC-content Distribution



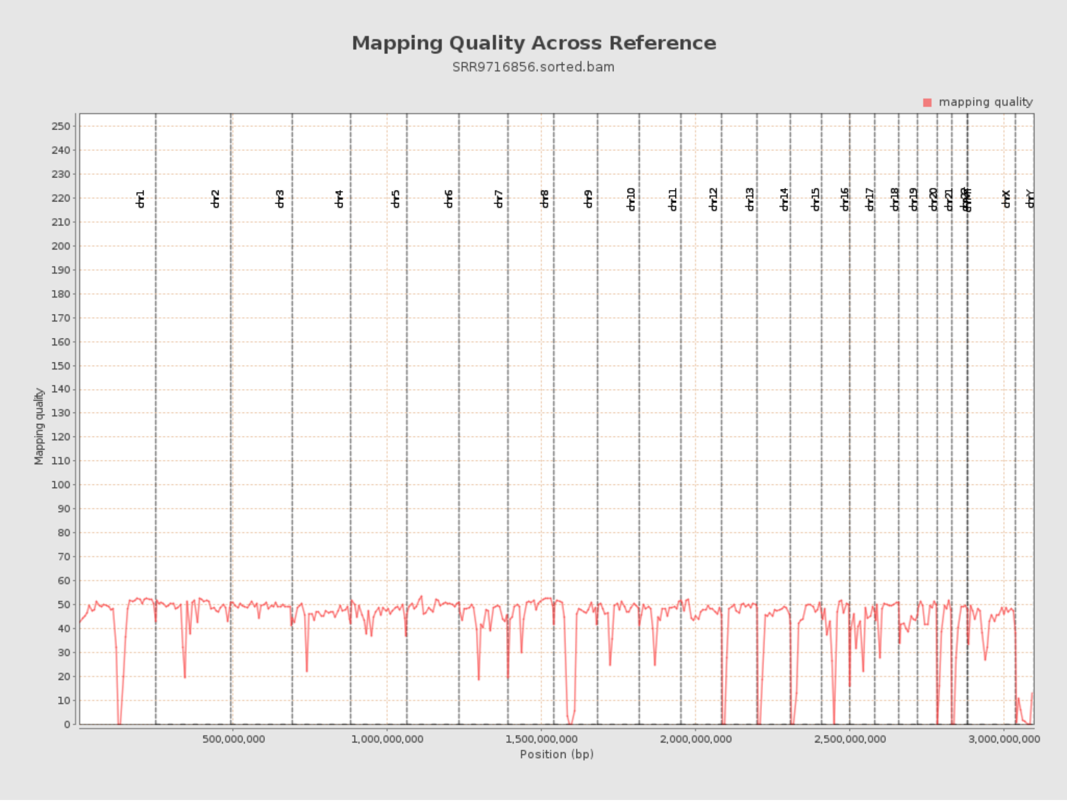
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram