Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 06:40:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716695.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_SRR9716695 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716695.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 06:40:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716695.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,414,041
Mapped reads	1,302,926 / 92.14%
Unmapped reads	111,115 / 7.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,528 / 1.52%
Read min/max/mean length	30 / 101 / 101.56
Duplicated reads (estimated)	47,153 / 3.33%
Duplication rate	2.2%
Clipped reads	1,321,887 / 93.48%

2.2. ACGT Content

Number/percentage of A's	26,020,877 / 25.35%
Number/percentage of C's	20,052,600 / 19.53%
Number/percentage of T's	30,647,743 / 29.86%
Number/percentage of G's	25,923,242 / 25.25%
Number/percentage of N's	6,237 / 0.01%
GC Percentage	44.79%

2.3. Coverage

Mean	0.0332

Standard Deviation	0.4037

2.4. Mapping Quality

Mean Mapping Quality	43.07

2.5. Mismatches and indels

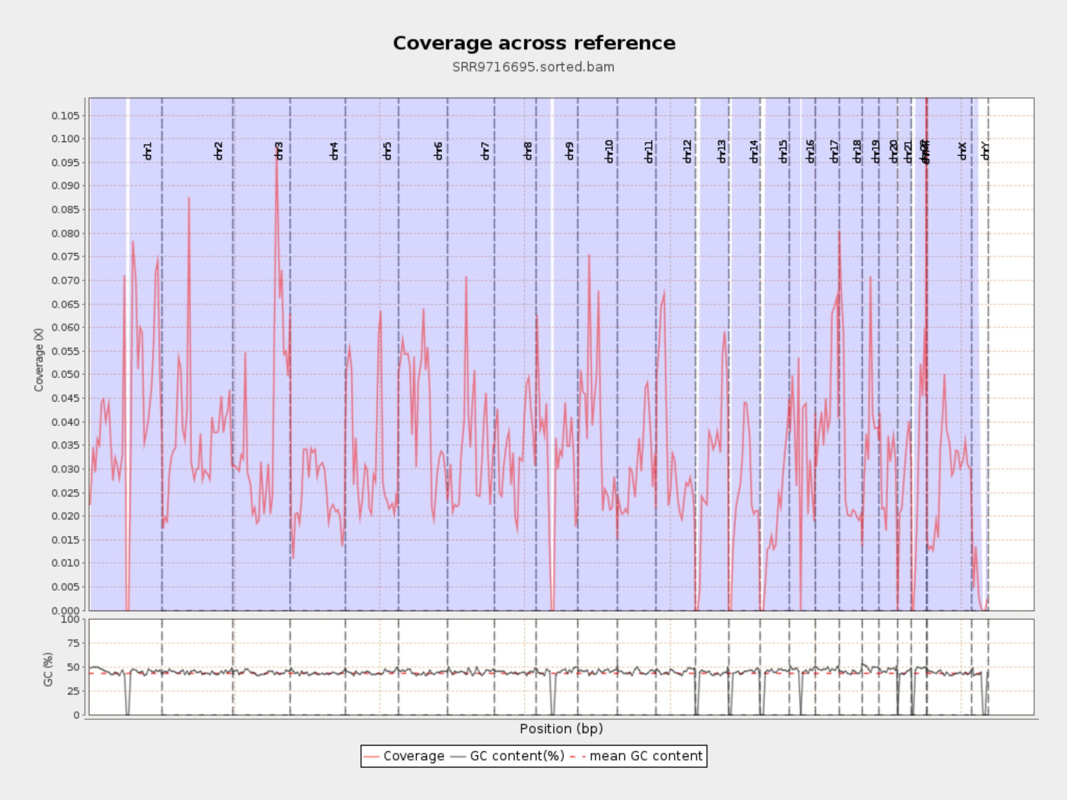
General error rate	0.83%
Mismatches	832,805
Insertions	9,801
Mapped reads with at least one insertion	0.74%
Deletions	24,224
Mapped reads with at least one deletion	1.83%
Homopolymer indels	42.57%

2.6. Chromosome stats

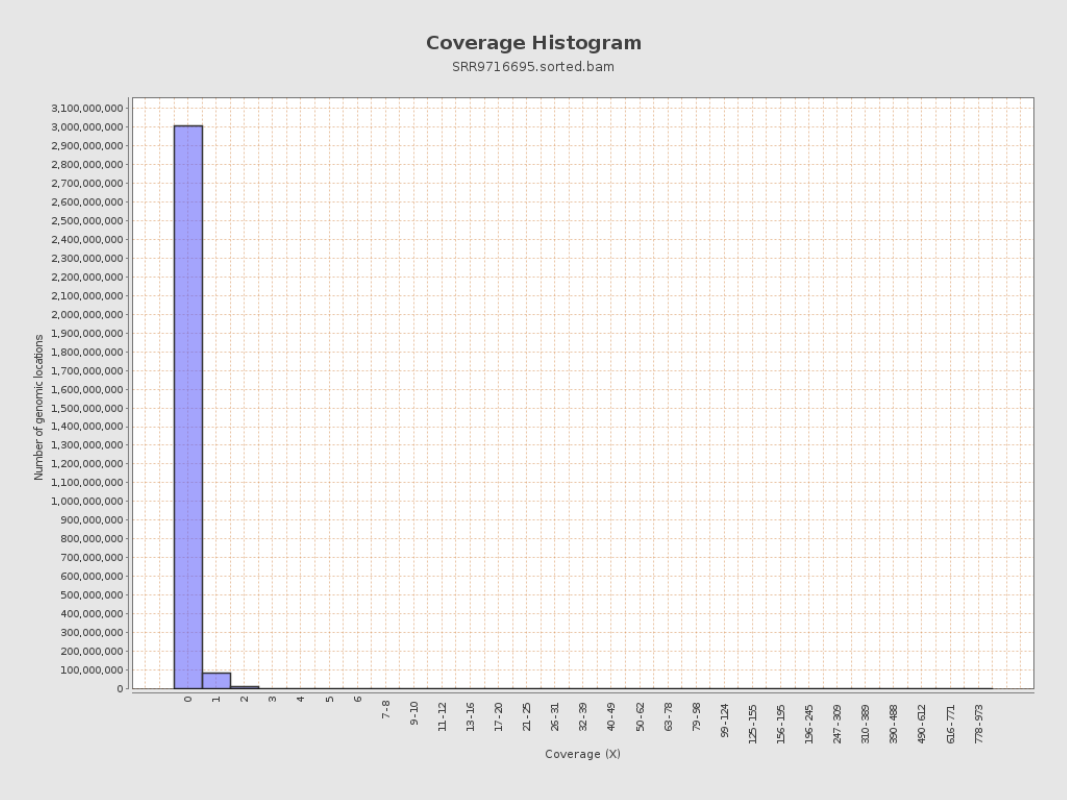
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10542701	0.0423	0.7375
chr2	243199373	8900509	0.0366	0.6956
chr3	198022430	7598938	0.0384	0.2214
chr4	191154276	4708205	0.0246	0.187
chr5	180915260	5764689	0.0319	0.1994
chr6	171115067	7391786	0.0432	0.2835
chr7	159138663	5464250	0.0343	0.5633

chr8	146364022	4992618	0.0341	0.4743
chr9	141213431	4461509	0.0316	0.3579
chr10	135534747	5304633	0.0391	0.4053
chr11	135006516	4063285	0.0301	0.2924
chr12	133851895	4566374	0.0341	0.2093
chr13	115169878	3604668	0.0313	0.1951
chr14	107349540	2562631	0.0239	0.1934
chr15	102531392	1853794	0.0181	0.1539
chr16	90354753	2928940	0.0324	0.2192
chr17	81195210	3738503	0.046	0.2867
chr18	78077248	2487352	0.0319	0.4531
chr19	59128983	2345292	0.0397	0.5715
chr20	63025520	1831096	0.0291	0.1946
chr21	48129895	1290410	0.0268	0.1886
chr22	51304566	1548802	0.0302	0.1967
chrMT	16571	4396	0.2653	0.5645
chrX	155270560	4482271	0.0289	0.2307
chrY	59373566	256503	0.0043	0.138

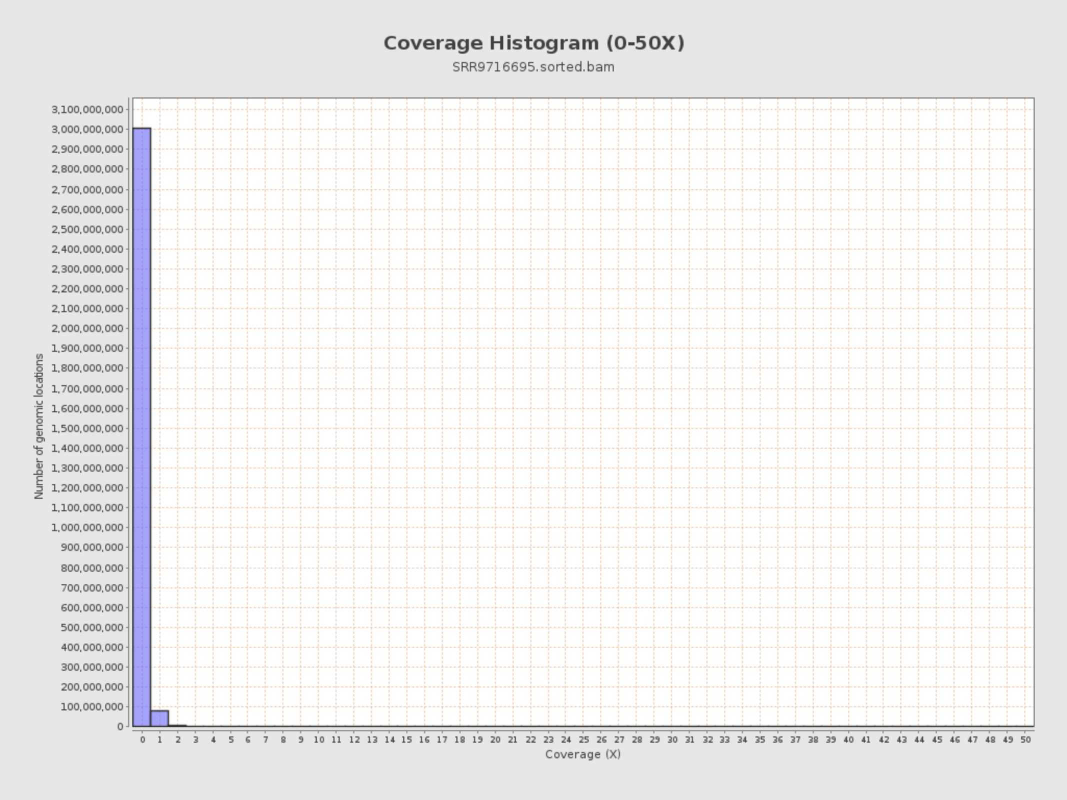
3. Results : Coverage across reference



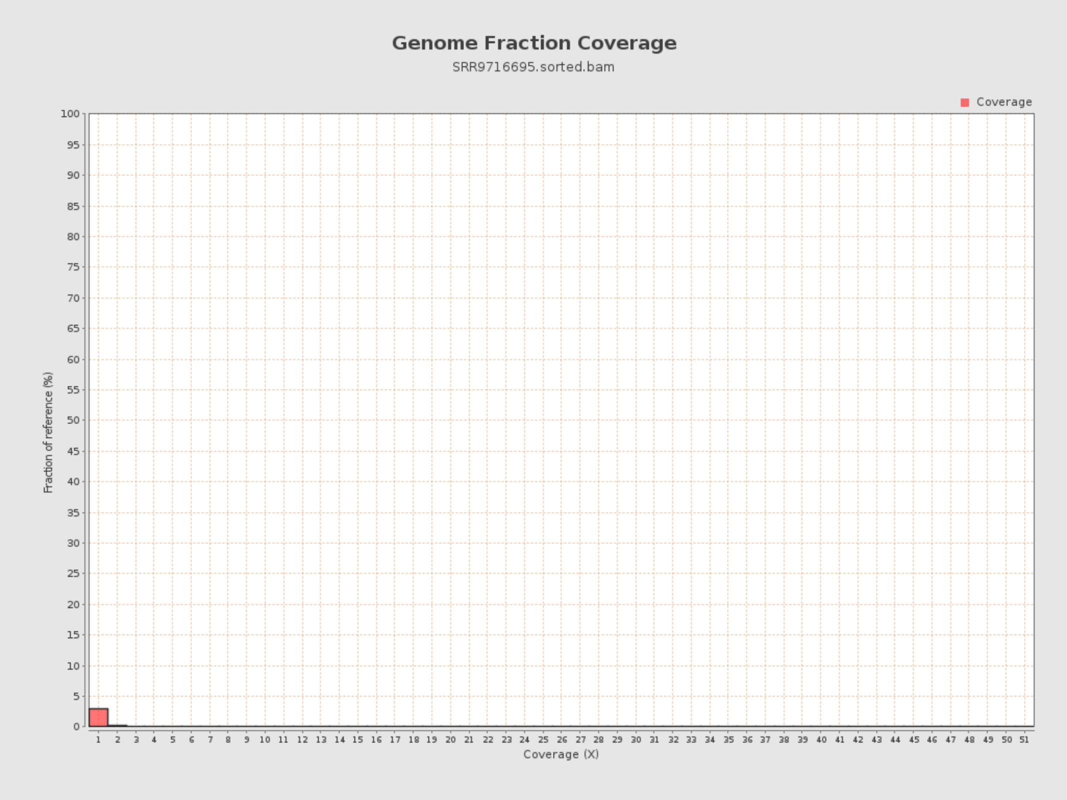
4. Results : Coverage Histogram



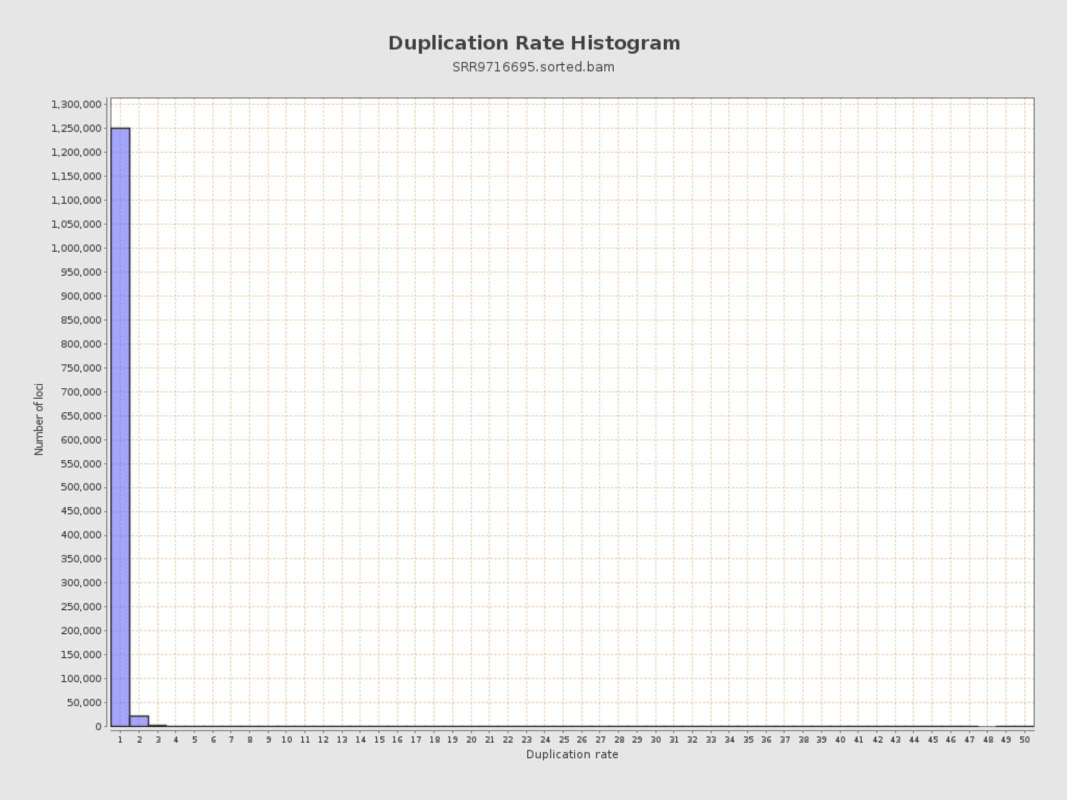
5. Results : Coverage Histogram (0-50X)



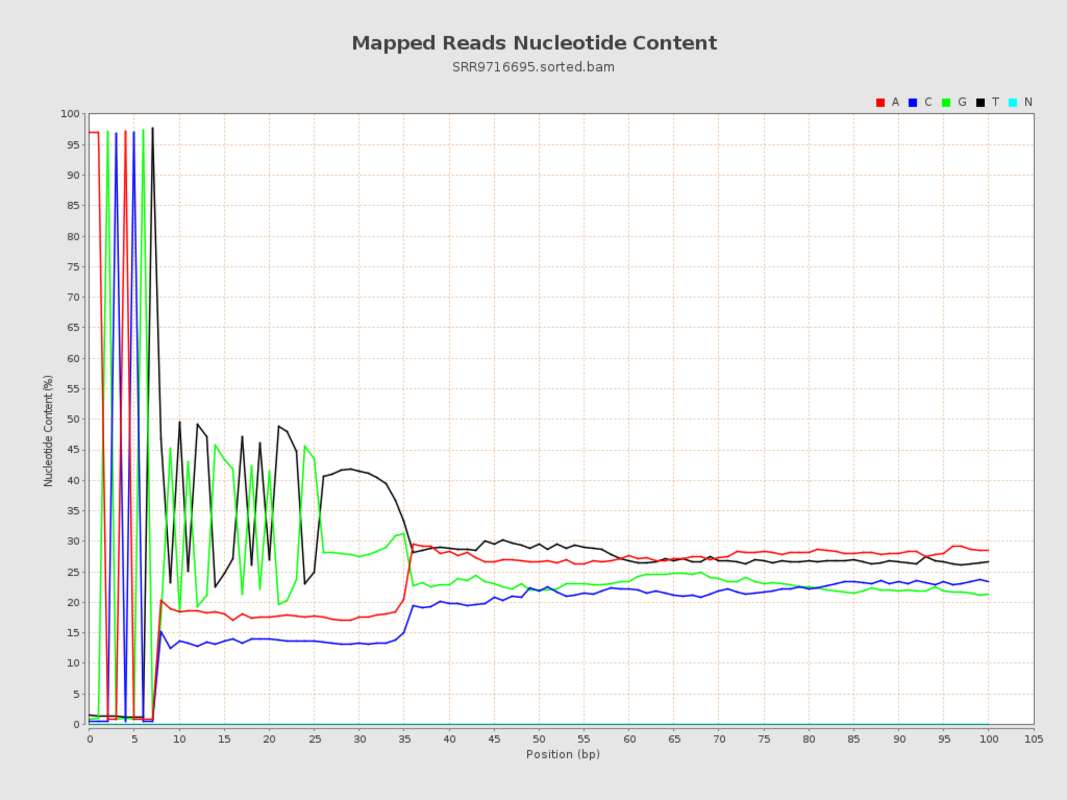
6. Results : Genome Fraction Coverage



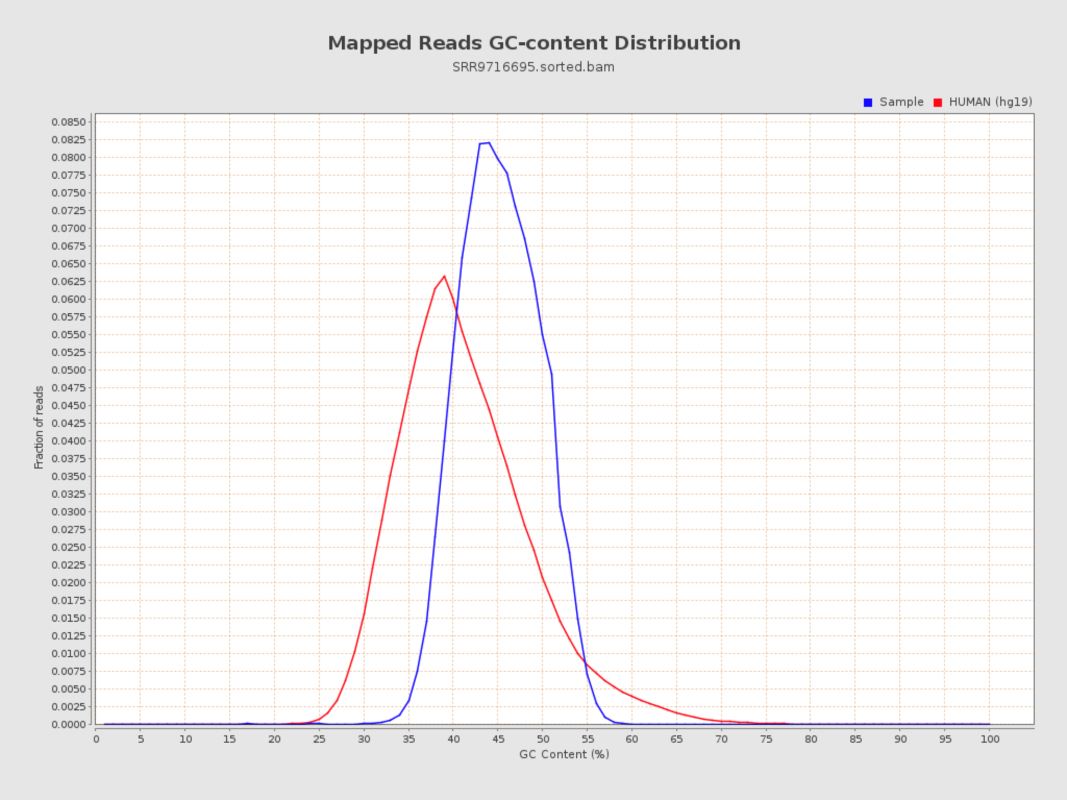
7. Results : Duplication Rate Histogram



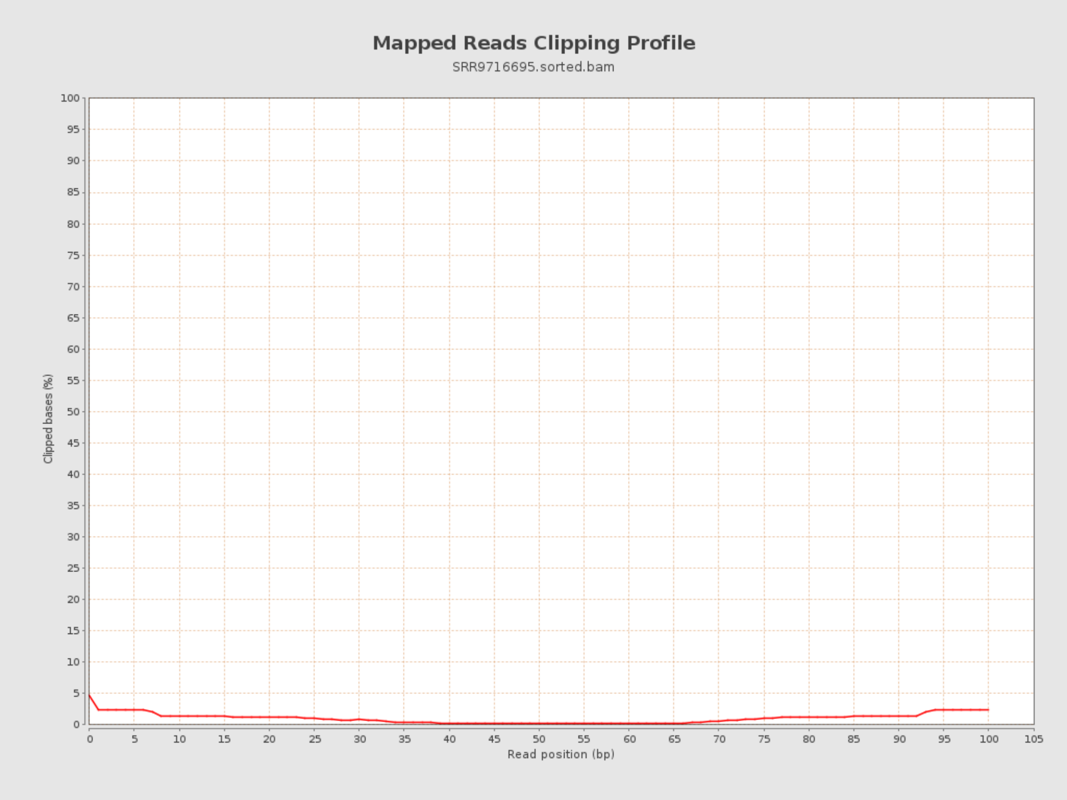
8. Results : Mapped Reads Nucleotide Content



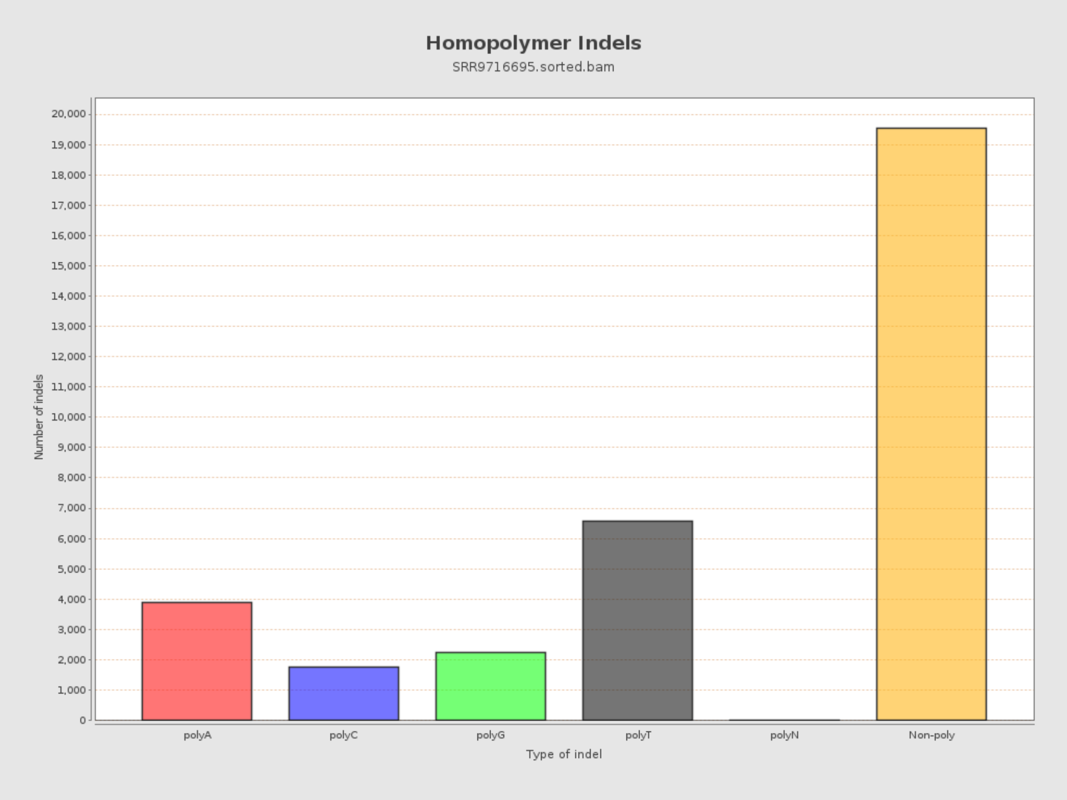
9. Results : Mapped Reads GC-content Distribution



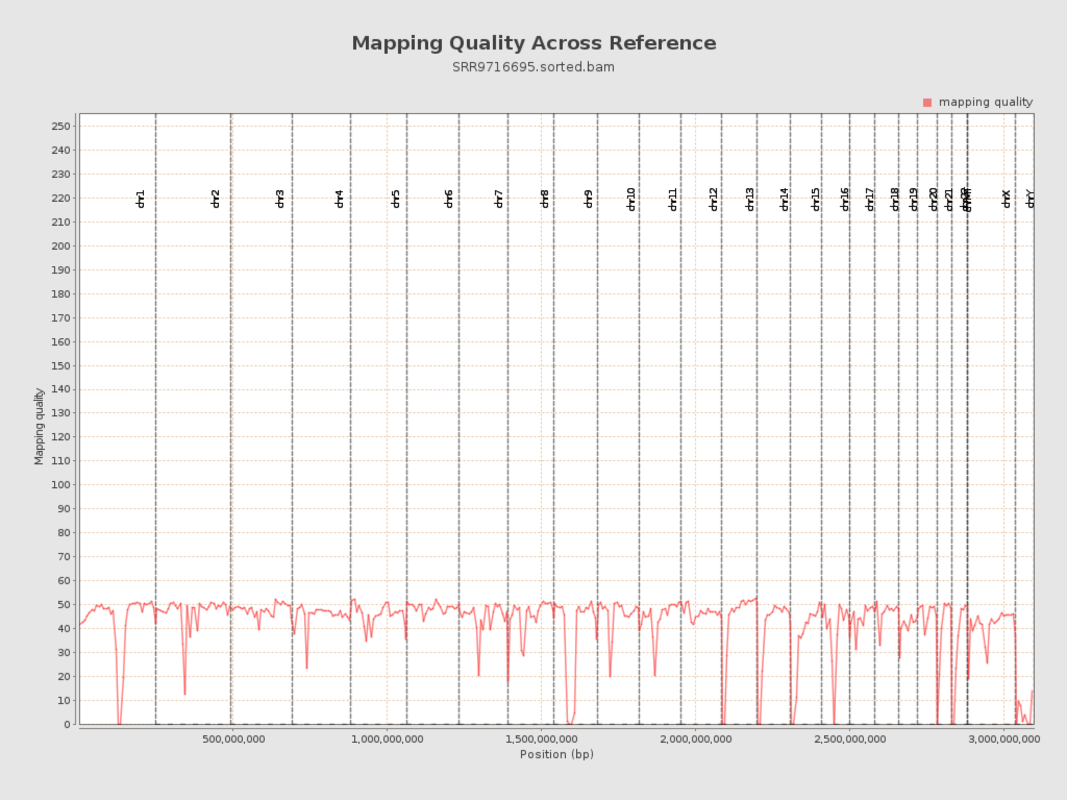
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram