Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 17:37:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716507.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_SRR9716507 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716507.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 17:37:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716507.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,348,065
Mapped reads	2,078,214 / 88.51%
Unmapped reads	269,851 / 11.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,393 / 0.49%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	83,535 / 3.56%
Duplication rate	2.8%
Clipped reads	2,086,923 / 88.88%

2.2. ACGT Content

Number/percentage of A's	30,848,300 / 25.83%
Number/percentage of C's	24,525,463 / 20.54%
Number/percentage of T's	35,791,369 / 29.97%
Number/percentage of G's	28,261,562 / 23.66%
Number/percentage of N's	1,756 / 0%
GC Percentage	44.2%

2.3. Coverage

Mean	0.0386

Standard Deviation	0.3748

2.4. Mapping Quality

Mean Mapping Quality	43.28

2.5. Mismatches and indels

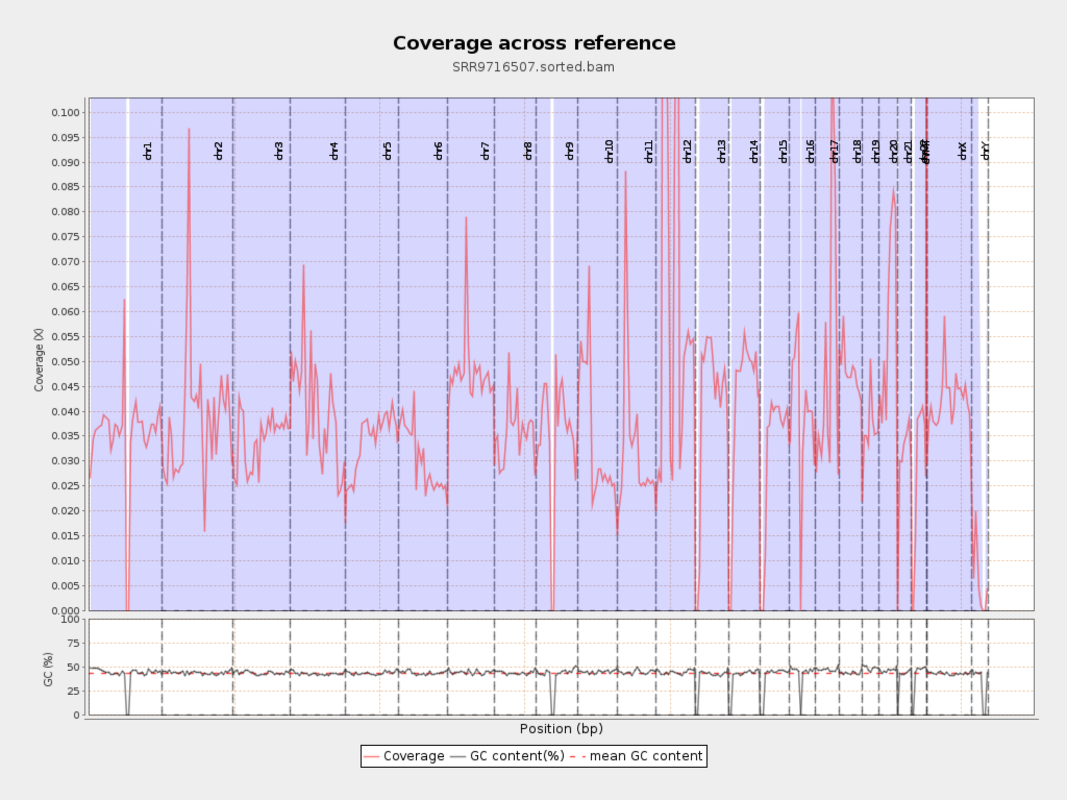
General error rate	0.56%
Mismatches	650,042
Insertions	7,464
Mapped reads with at least one insertion	0.36%
Deletions	19,462
Mapped reads with at least one deletion	0.93%
Homopolymer indels	42.42%

2.6. Chromosome stats

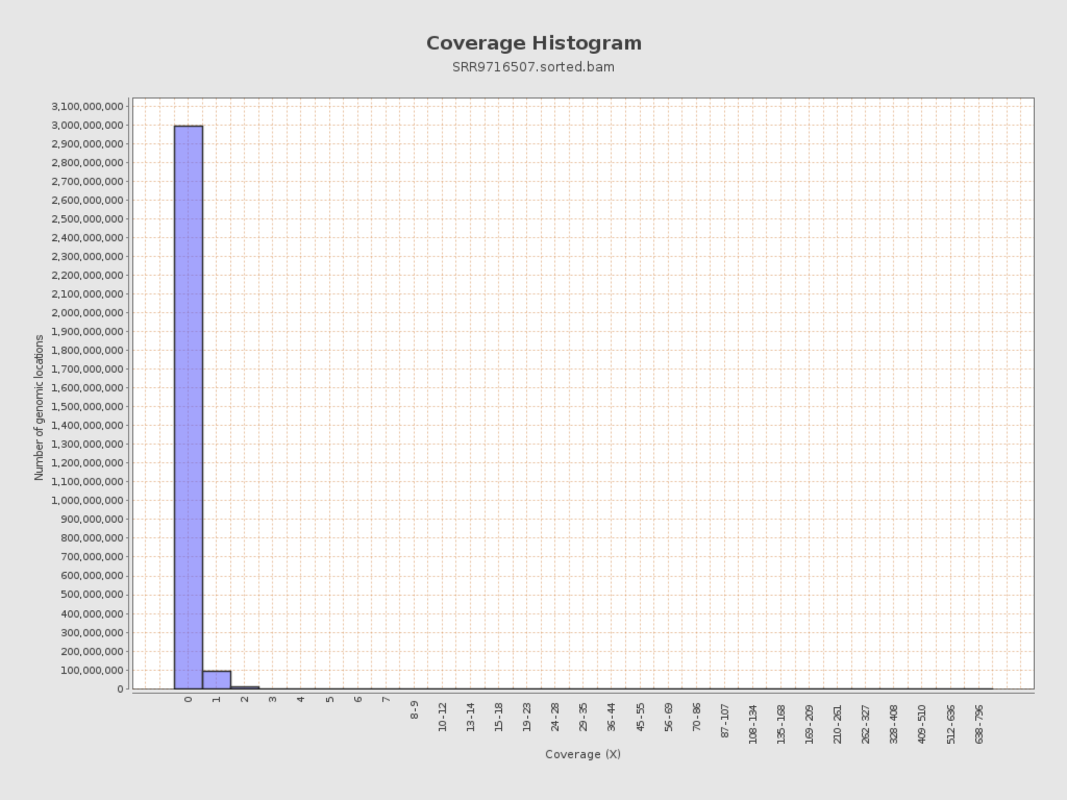
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8715751	0.035	0.6514
chr2	243199373	9435320	0.0388	0.4522
chr3	198022430	6823716	0.0345	0.2039
chr4	191154276	7718691	0.0404	0.2551
chr5	180915260	6197340	0.0343	0.2094
chr6	171115067	5204227	0.0304	0.2272
chr7	159138663	7690285	0.0483	0.5274

chr8	146364022	5242948	0.0358	0.324
chr9	141213431	4868900	0.0345	0.3964
chr10	135534747	4706054	0.0347	0.3624
chr11	135006516	4485620	0.0332	0.3119
chr12	133851895	9137497	0.0683	0.3321
chr13	115169878	4644318	0.0403	0.22
chr14	107349540	4456548	0.0415	0.2668
chr15	102531392	3220584	0.0314	0.1969
chr16	90354753	3605640	0.0399	0.254
chr17	81195210	3941335	0.0485	0.256
chr18	78077248	3768018	0.0483	0.7721
chr19	59128983	2183467	0.0369	0.5124
chr20	63025520	3726967	0.0591	0.2811
chr21	48129895	1442992	0.03	0.2293
chr22	51304566	1372792	0.0268	0.1778
chrMT	16571	4368	0.2636	0.5331
chrX	155270560	6514332	0.042	0.2943
chrY	59373566	353865	0.006	0.1332

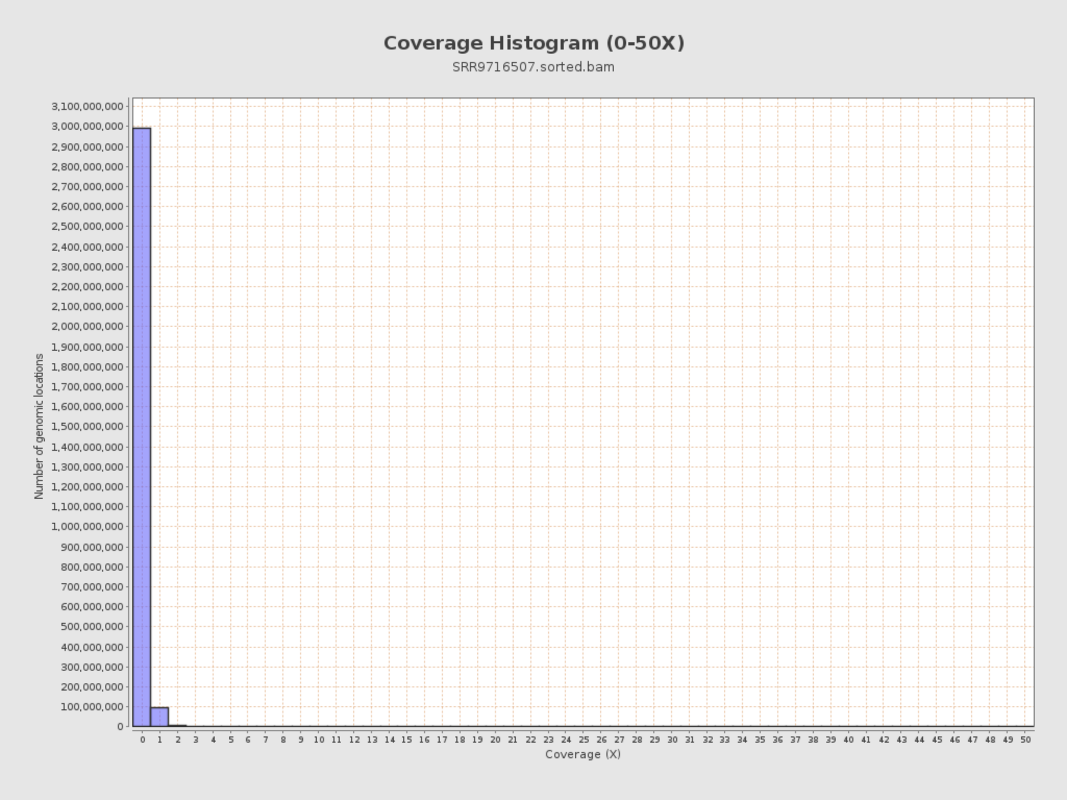
3. Results : Coverage across reference



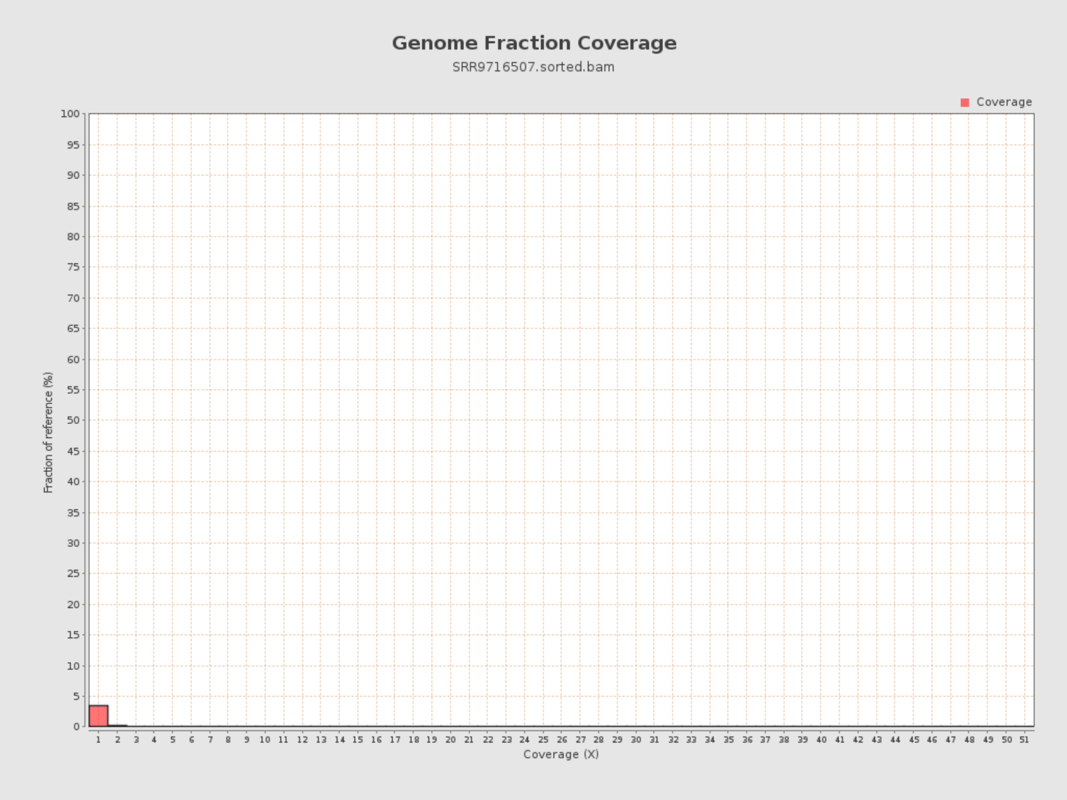
4. Results : Coverage Histogram



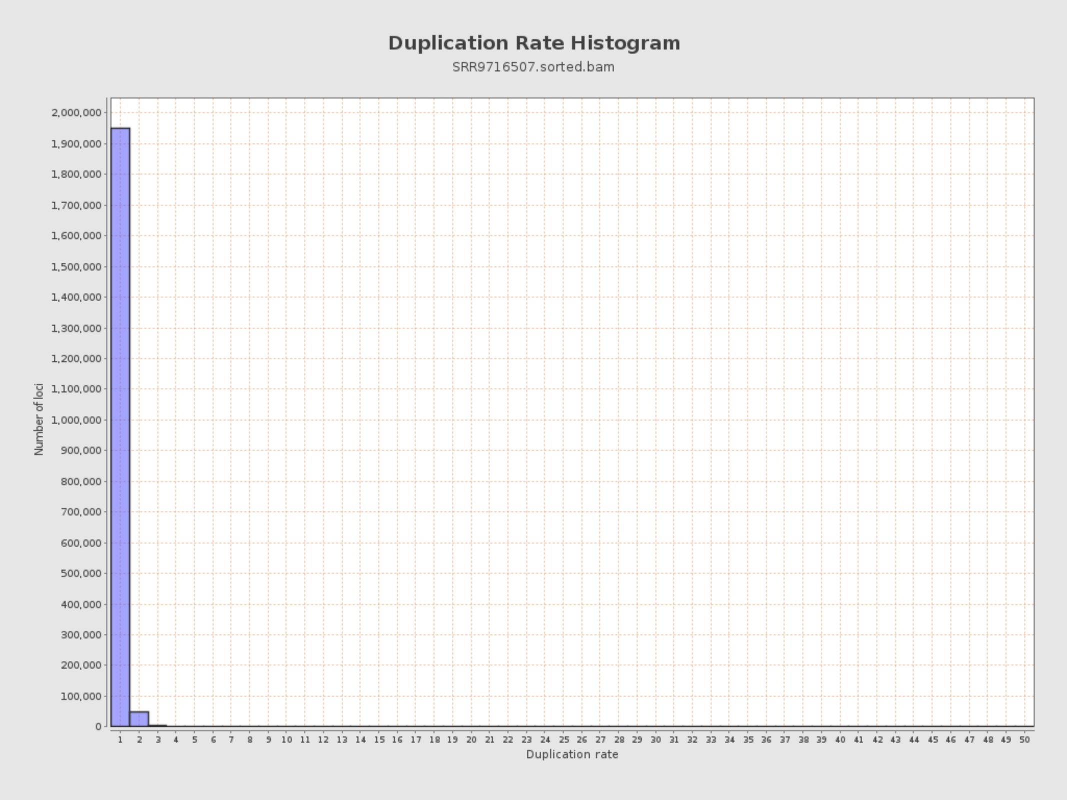
5. Results : Coverage Histogram (0-50X)



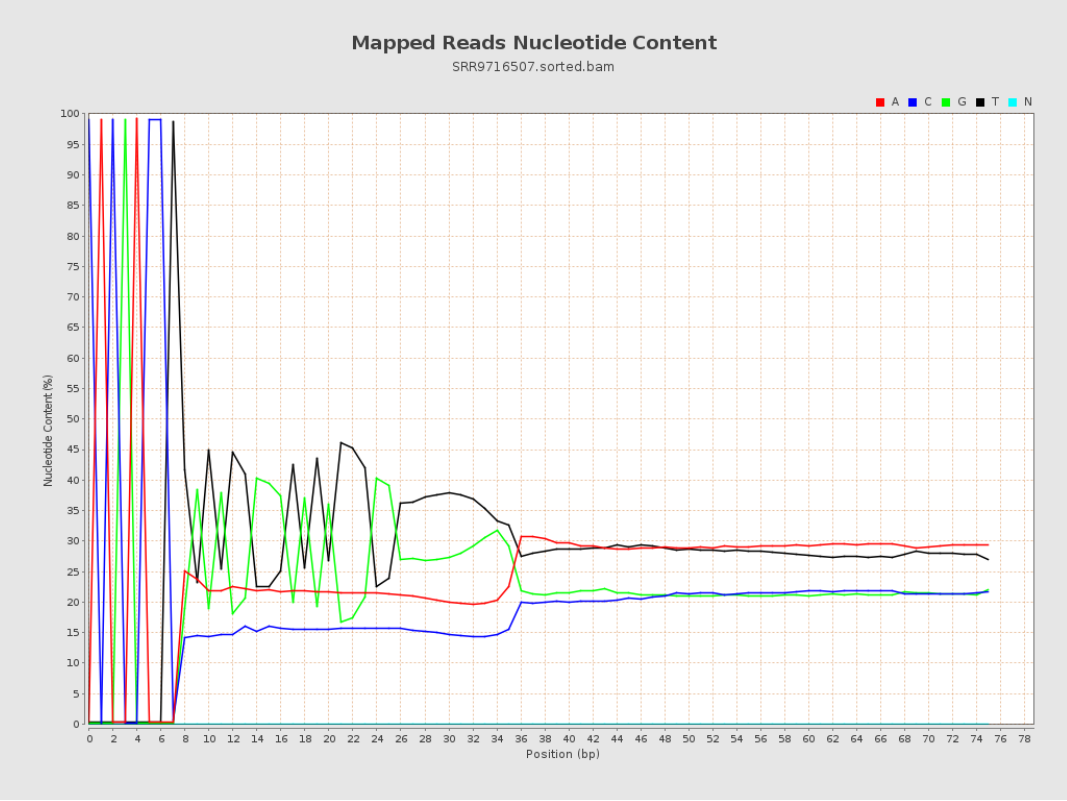
6. Results : Genome Fraction Coverage



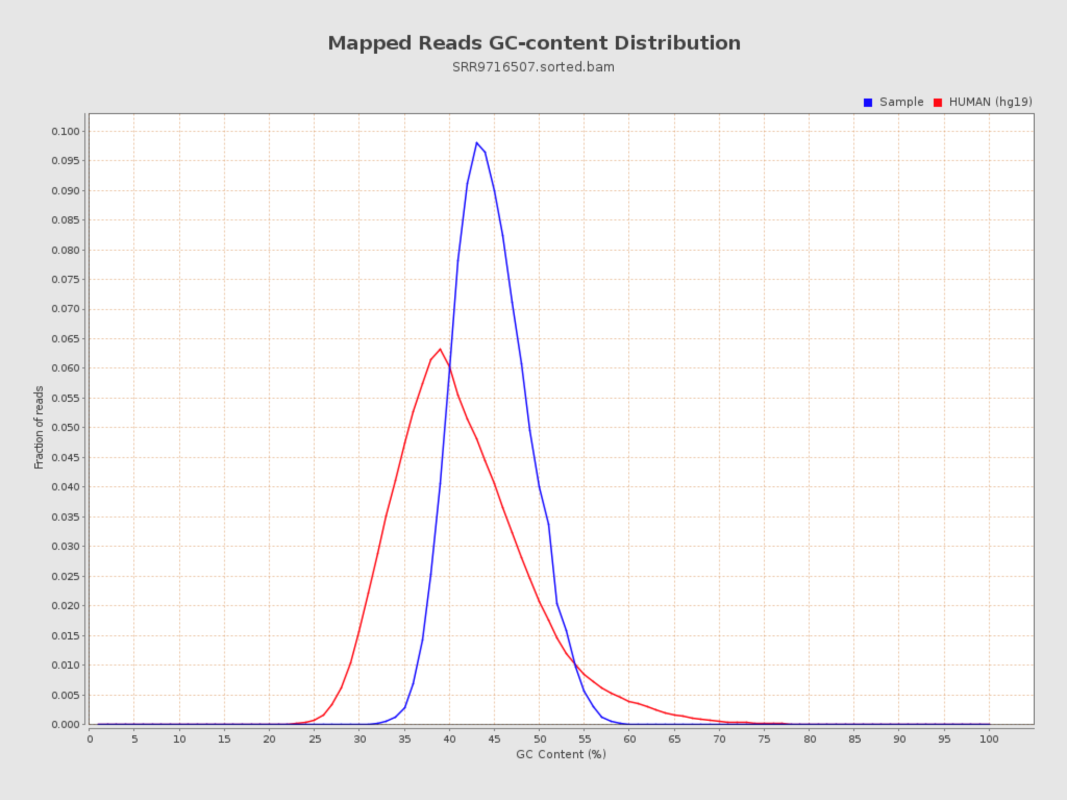
7. Results : Duplication Rate Histogram



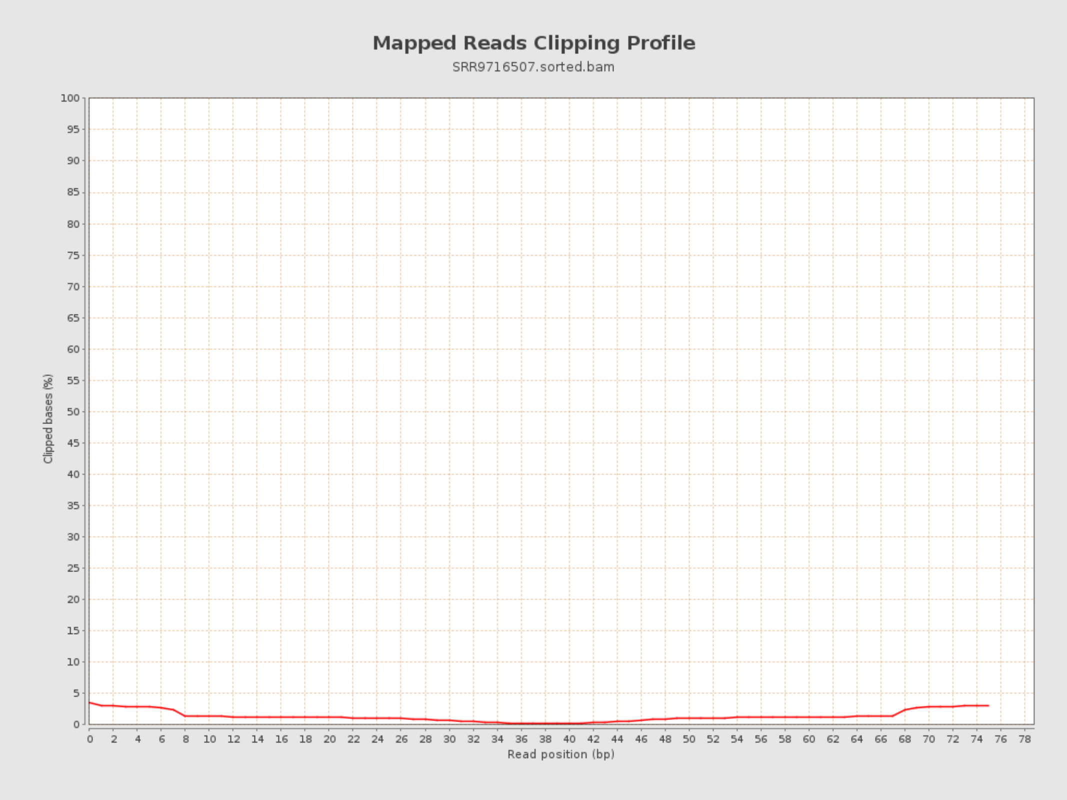
8. Results : Mapped Reads Nucleotide Content



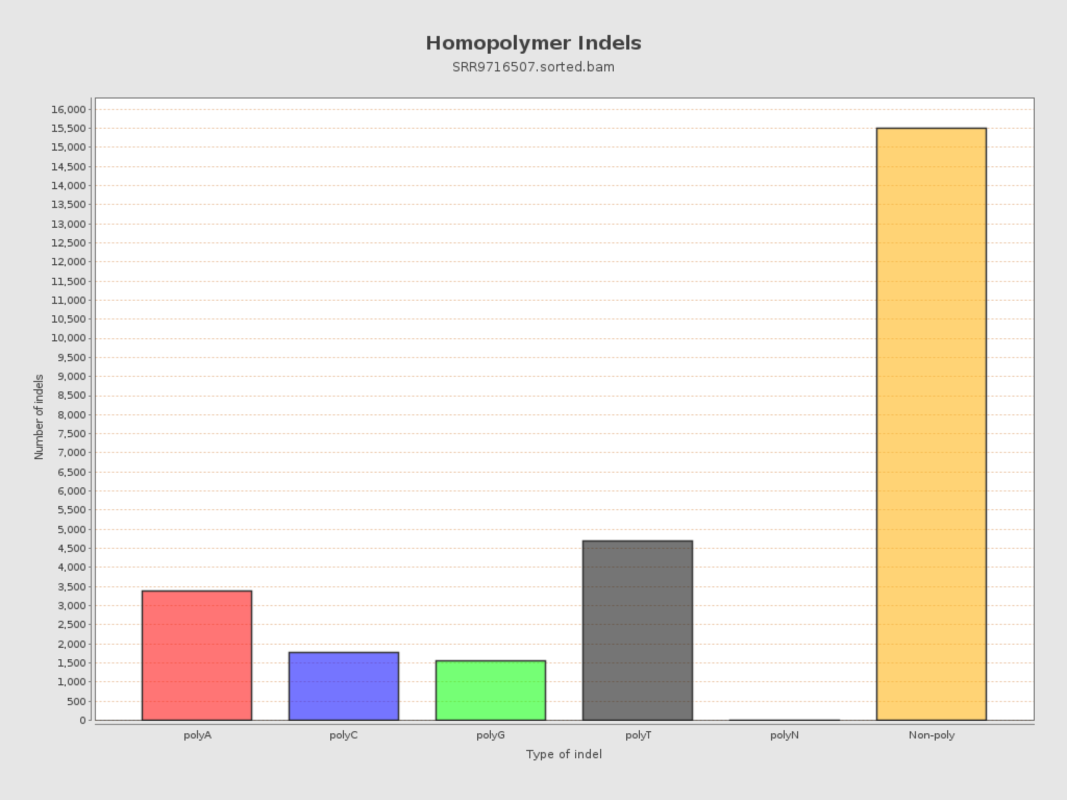
9. Results : Mapped Reads GC-content Distribution



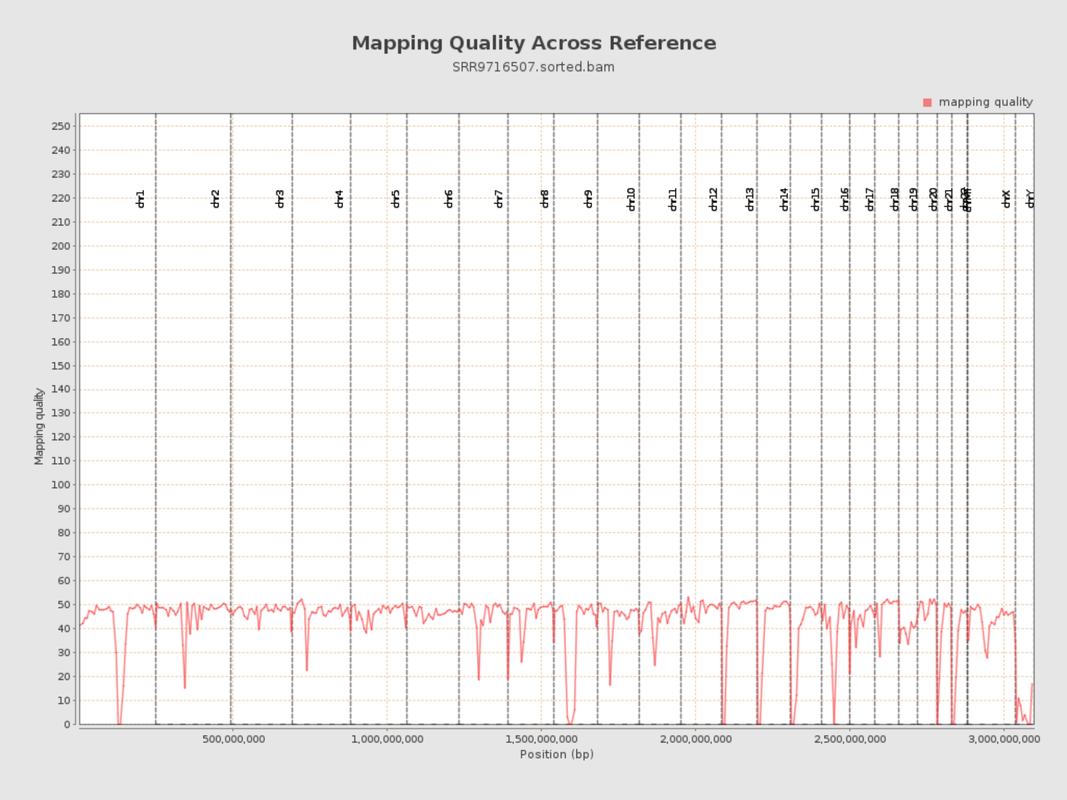
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram