Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 22:57:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716987.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_SRR9716987 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716987.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 22:57:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716987.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,199,678
Mapped reads	2,005,694 / 91.18%
Unmapped reads	193,984 / 8.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,012 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	67,467 / 3.07%
Duplication rate	2.27%
Clipped reads	2,011,091 / 91.43%

2.2. ACGT Content

Number/percentage of A's	30,100,723 / 25.78%
Number/percentage of C's	21,556,229 / 18.46%
Number/percentage of T's	35,958,821 / 30.79%
Number/percentage of G's	29,156,216 / 24.97%
Number/percentage of N's	1,515 / 0%
GC Percentage	43.43%

2.3. Coverage

Mean	0.0377

Standard Deviation	0.3606

2.4. Mapping Quality

Mean Mapping Quality	44.09

2.5. Mismatches and indels

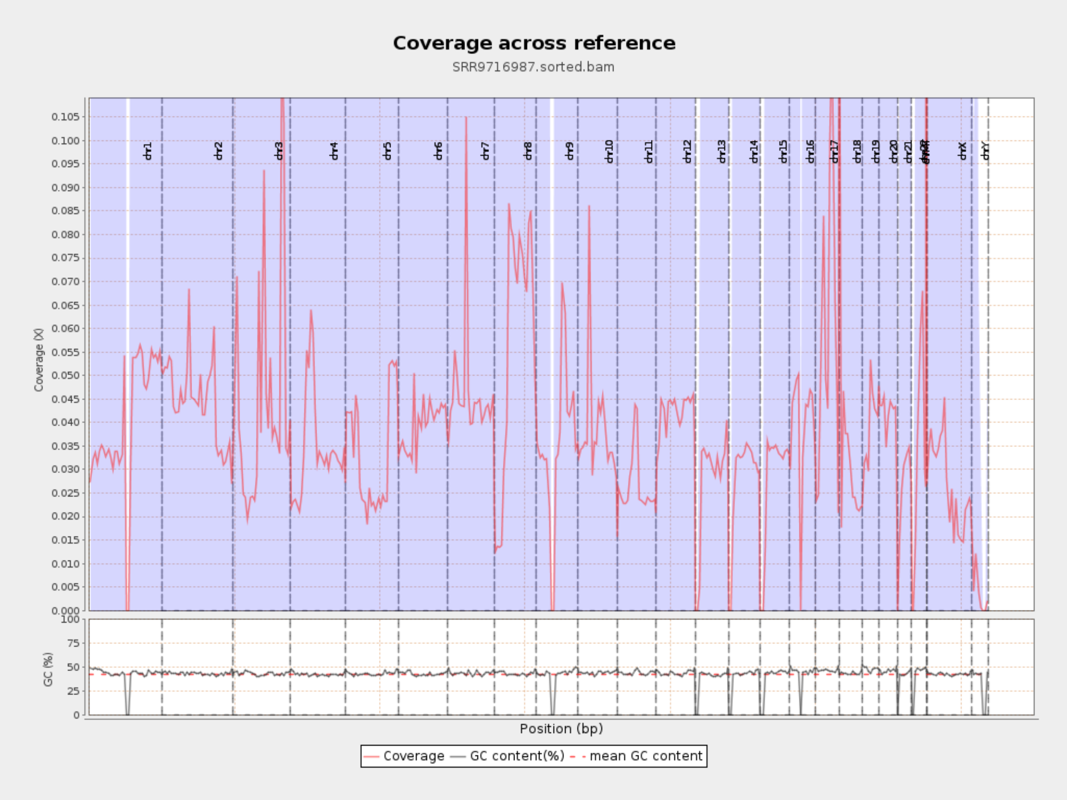
General error rate	0.51%
Mismatches	586,884
Insertions	7,749
Mapped reads with at least one insertion	0.38%
Deletions	22,117
Mapped reads with at least one deletion	1.1%
Homopolymer indels	41.09%

2.6. Chromosome stats

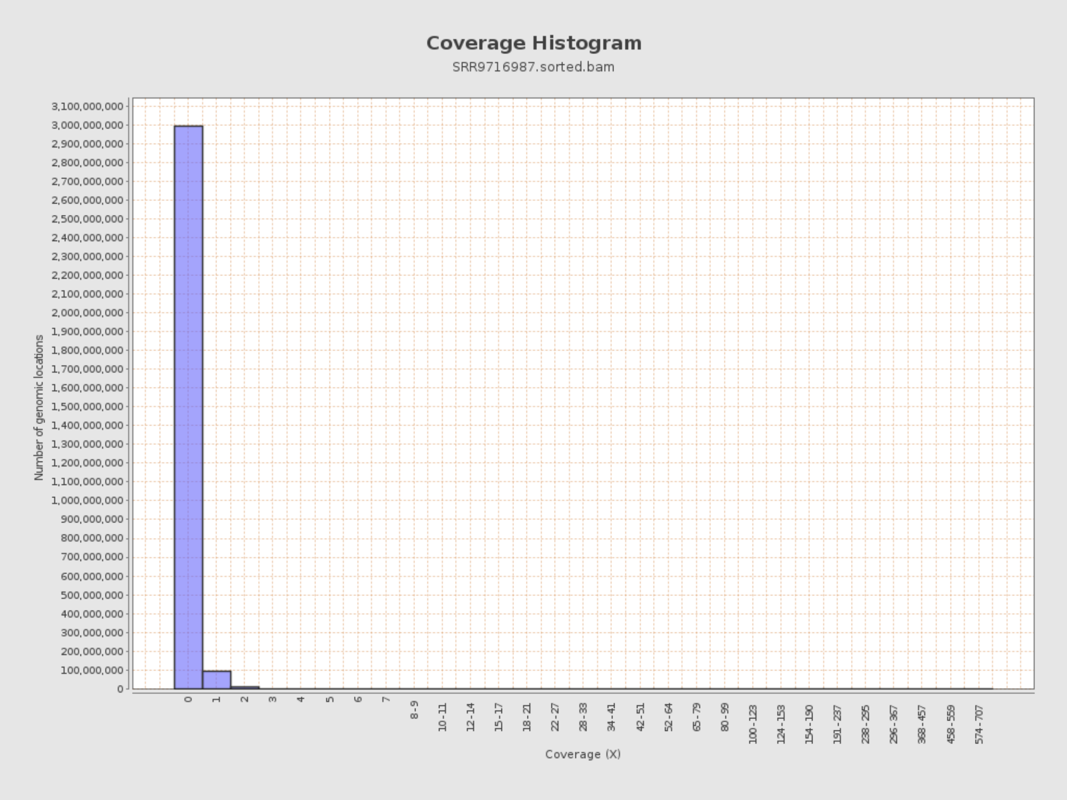
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9881284	0.0396	0.5228
chr2	243199373	10892803	0.0448	0.3887
chr3	198022430	8929689	0.0451	0.2539
chr4	191154276	6612926	0.0346	0.2172
chr5	180915260	5996239	0.0331	0.1999
chr6	171115067	6736828	0.0394	0.2403
chr7	159138663	7458694	0.0469	0.8771

chr8	146364022	8419480	0.0575	0.3526
chr9	141213431	4959003	0.0351	0.2475
chr10	135534747	5236268	0.0386	0.4679
chr11	135006516	3560558	0.0264	0.2311
chr12	133851895	5631164	0.0421	0.2526
chr13	115169878	3134290	0.0272	0.1799
chr14	107349540	2973190	0.0277	0.1907
chr15	102531392	2838516	0.0277	0.1932
chr16	90354753	3575575	0.0396	0.2341
chr17	81195210	4850557	0.0597	0.2836
chr18	78077248	2679784	0.0343	0.381
chr19	59128983	2316399	0.0392	0.4708
chr20	63025520	2629703	0.0417	0.2382
chr21	48129895	1225284	0.0255	0.1825
chr22	51304566	1664174	0.0324	0.1975
chrMT	16571	127185	7.6752	4.7861
chrX	155270560	4235993	0.0273	0.2167
chrY	59373566	242799	0.0041	0.0952

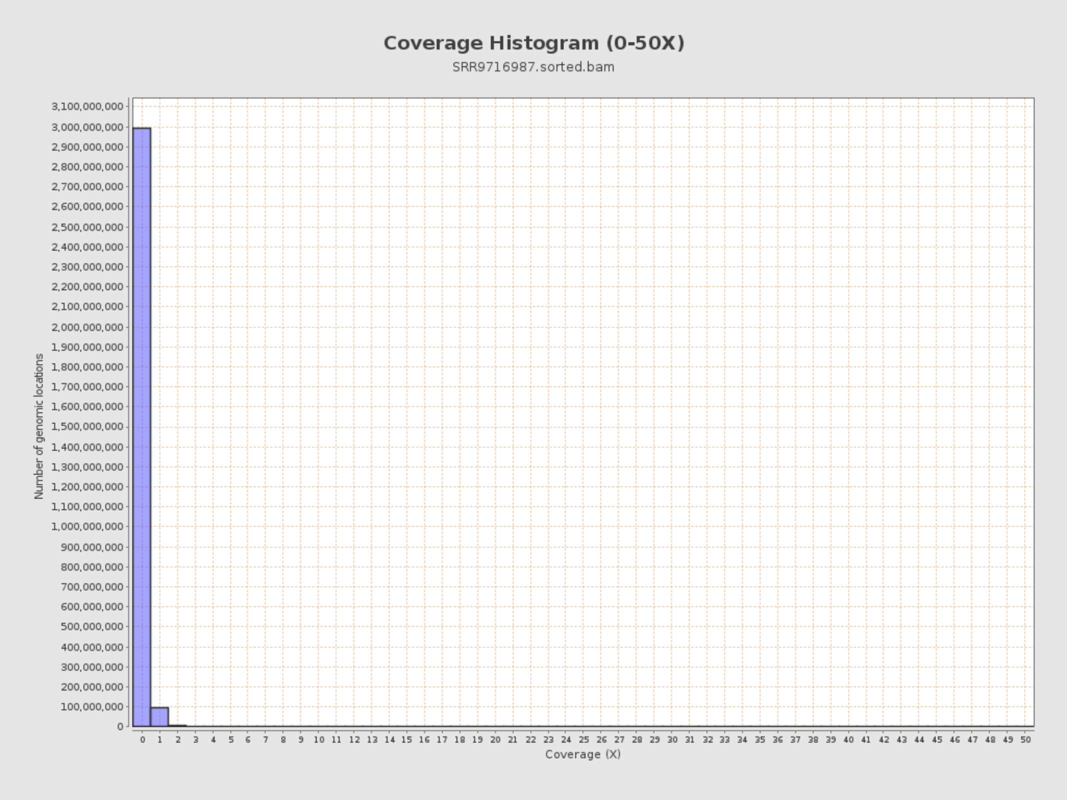
3. Results : Coverage across reference



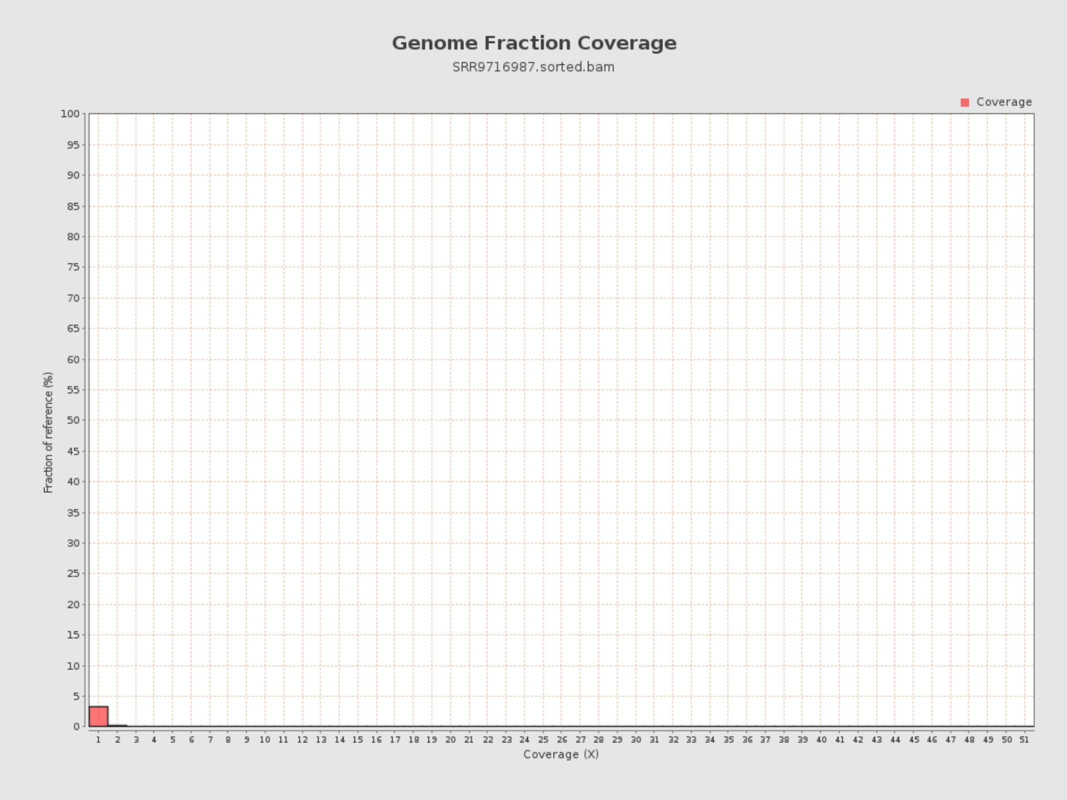
4. Results : Coverage Histogram



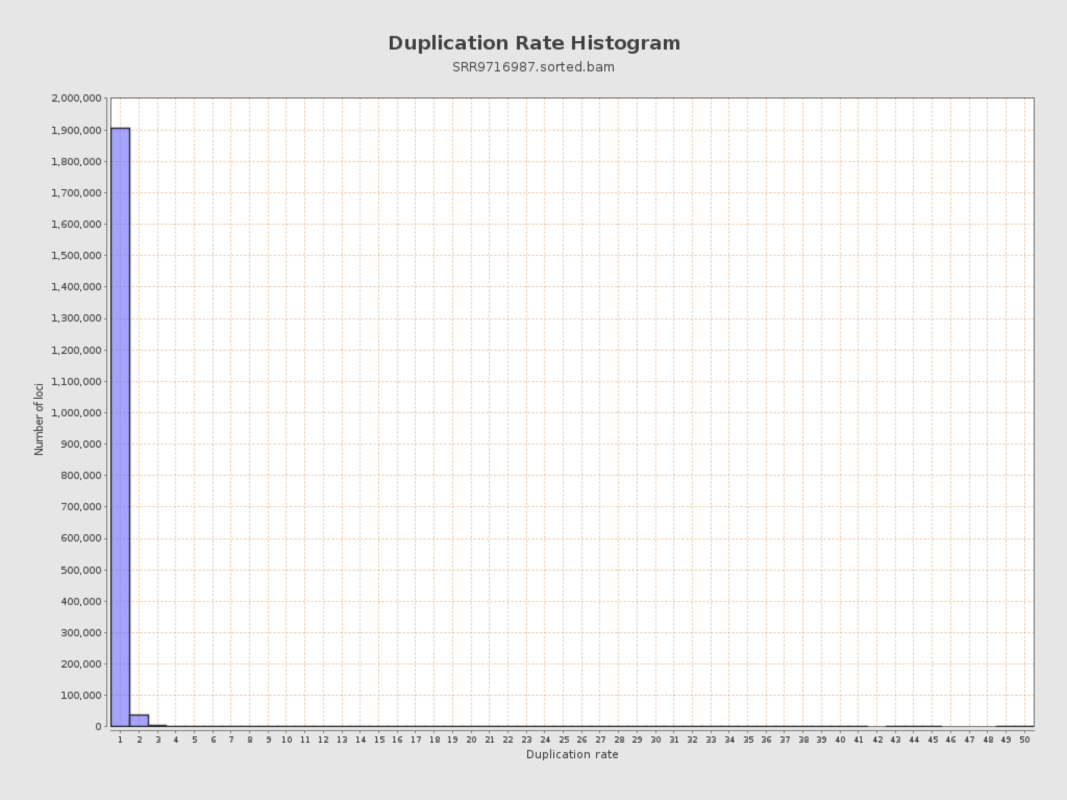
5. Results : Coverage Histogram (0-50X)



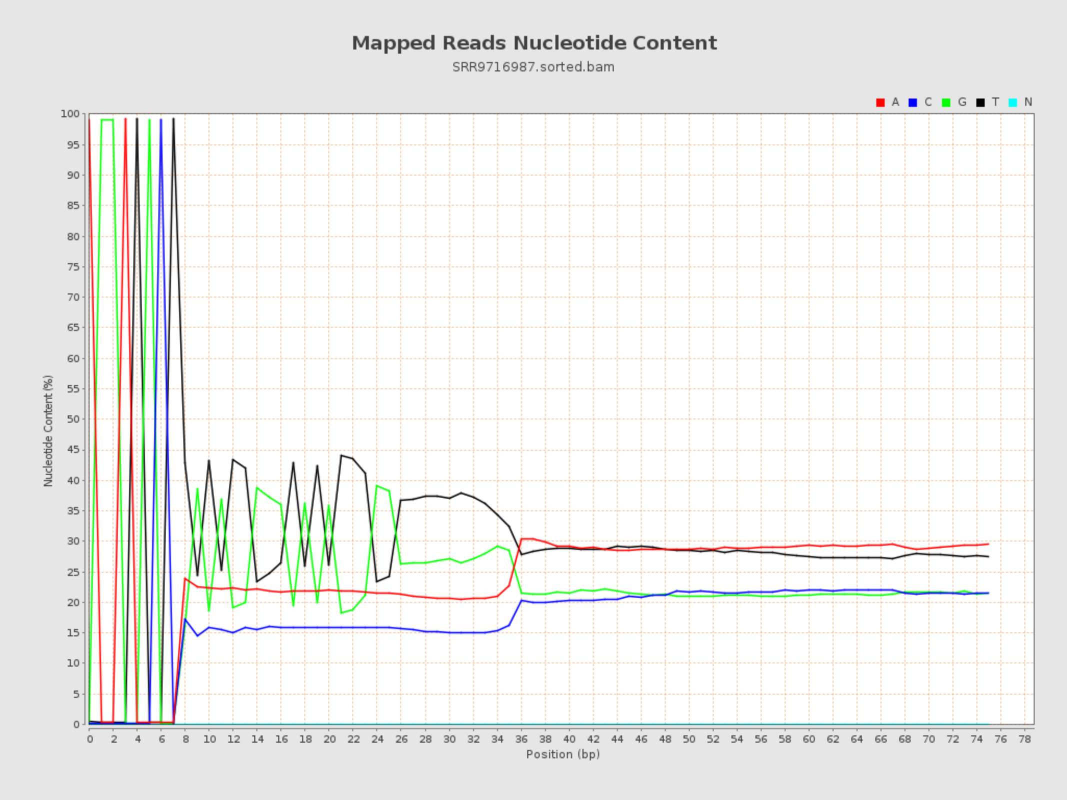
6. Results : Genome Fraction Coverage



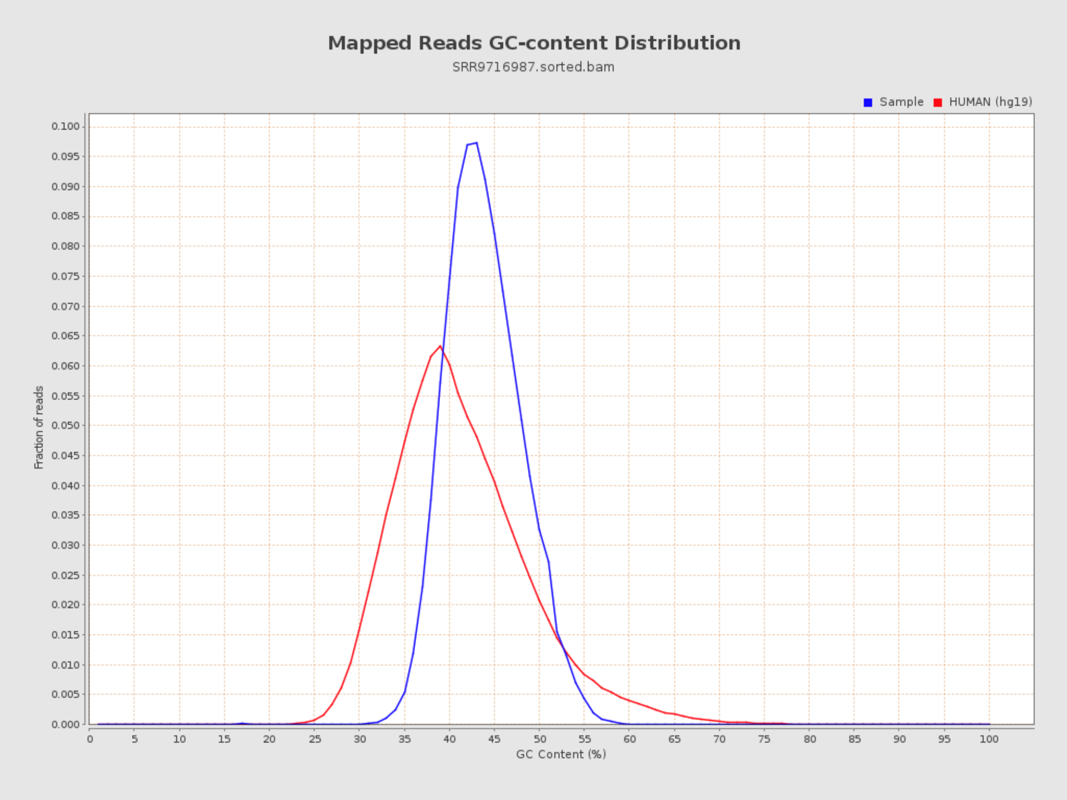
7. Results : Duplication Rate Histogram



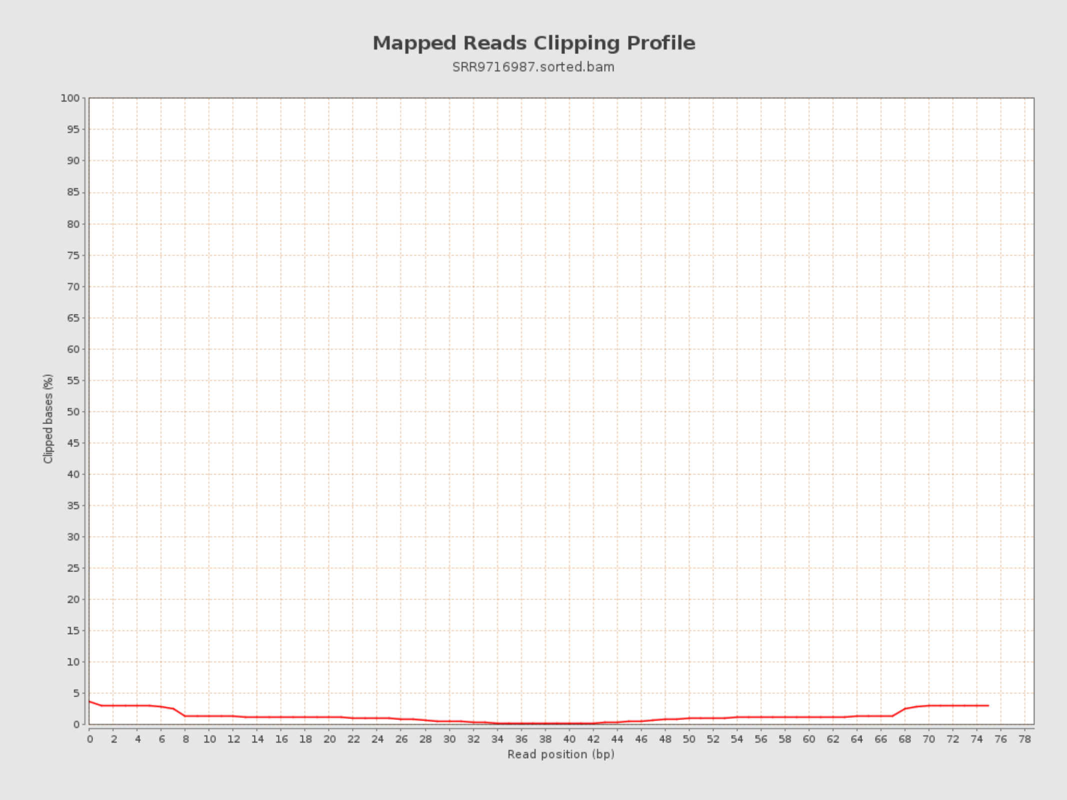
8. Results : Mapped Reads Nucleotide Content



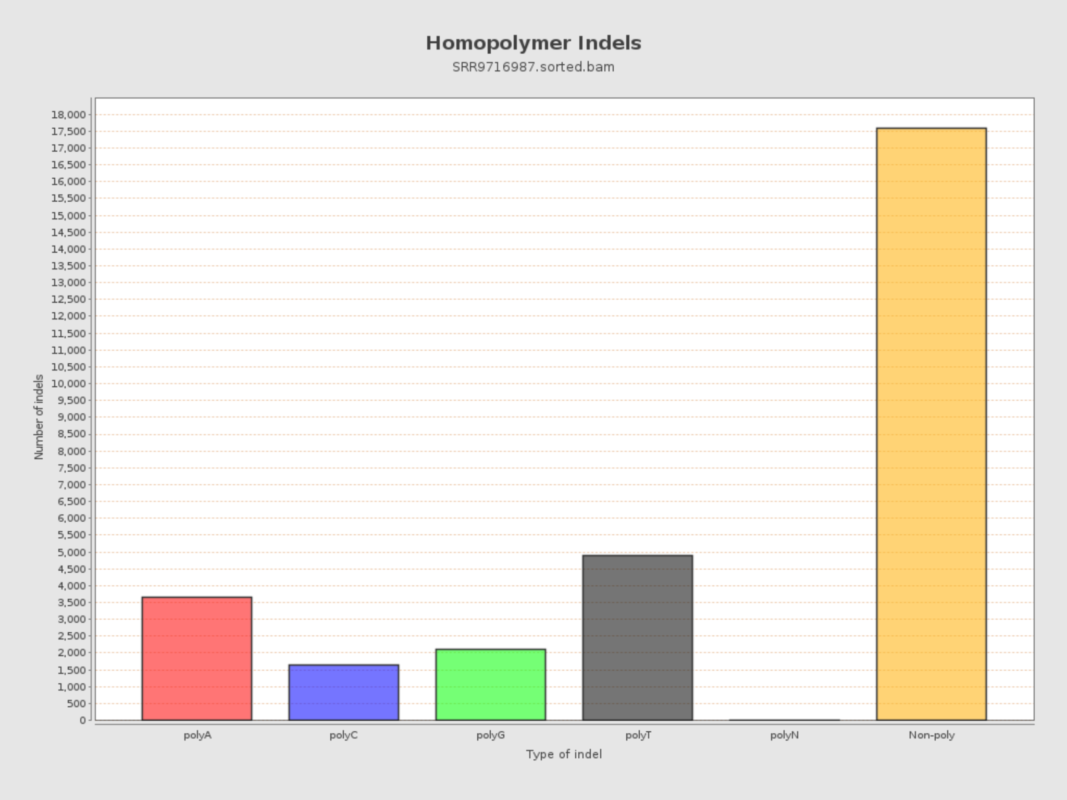
9. Results : Mapped Reads GC-content Distribution



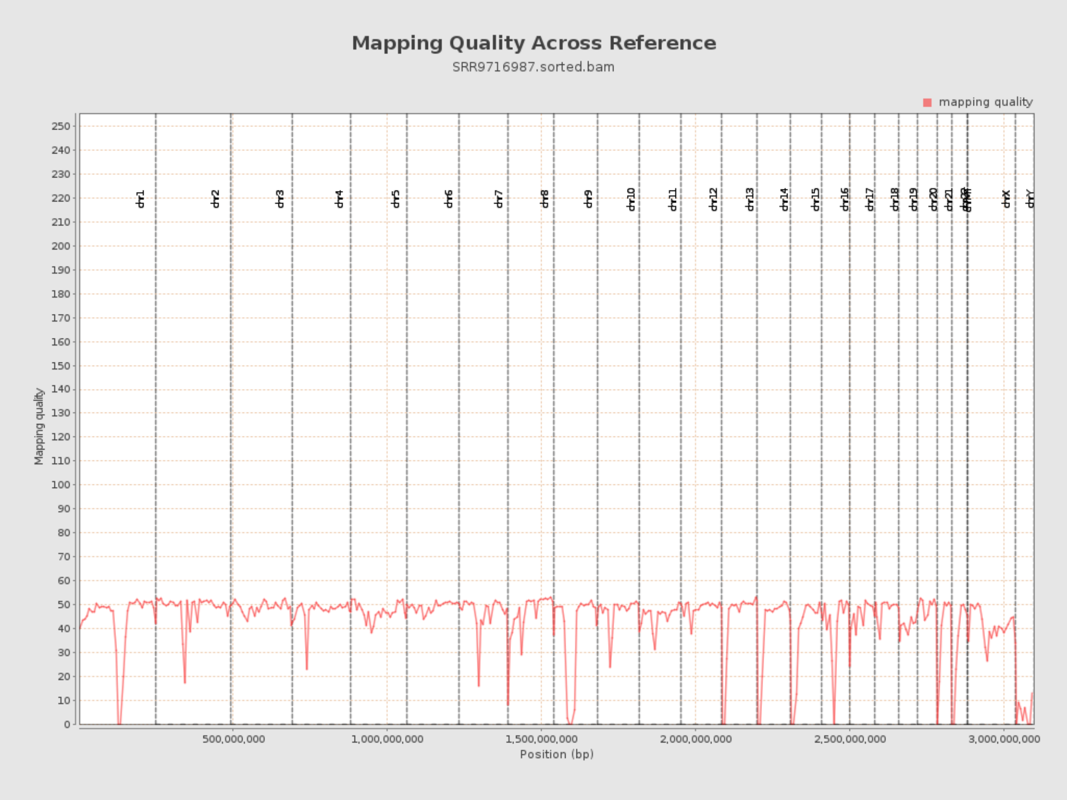
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram