Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 08:09:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716336.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_SRR9716336 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716336.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 08:09:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716336.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	456,662
Mapped reads	411,903 / 90.2%
Unmapped reads	44,759 / 9.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,507 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	8,207 / 1.8%
Duplication rate	1.63%
Clipped reads	411,982 / 90.22%

2.2. ACGT Content

Number/percentage of A's	6,513,051 / 27.15%
Number/percentage of C's	4,470,834 / 18.64%
Number/percentage of T's	7,294,631 / 30.41%
Number/percentage of G's	5,708,724 / 23.8%
Number/percentage of N's	364 / 0%
GC Percentage	42.44%

2.3. Coverage

Mean	0.0078

Standard Deviation	0.1046

2.4. Mapping Quality

Mean Mapping Quality	46.11

2.5. Mismatches and indels

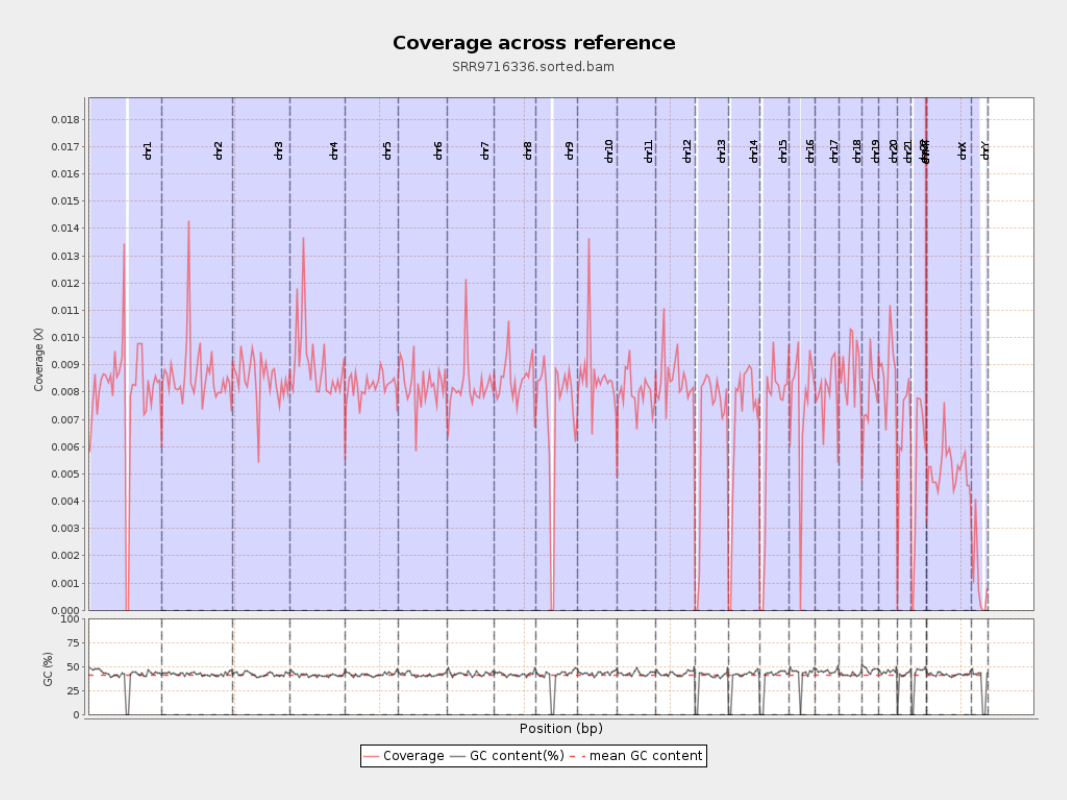
General error rate	0.54%
Mismatches	125,785
Insertions	1,890
Mapped reads with at least one insertion	0.46%
Deletions	3,957
Mapped reads with at least one deletion	0.95%
Homopolymer indels	43.25%

2.6. Chromosome stats

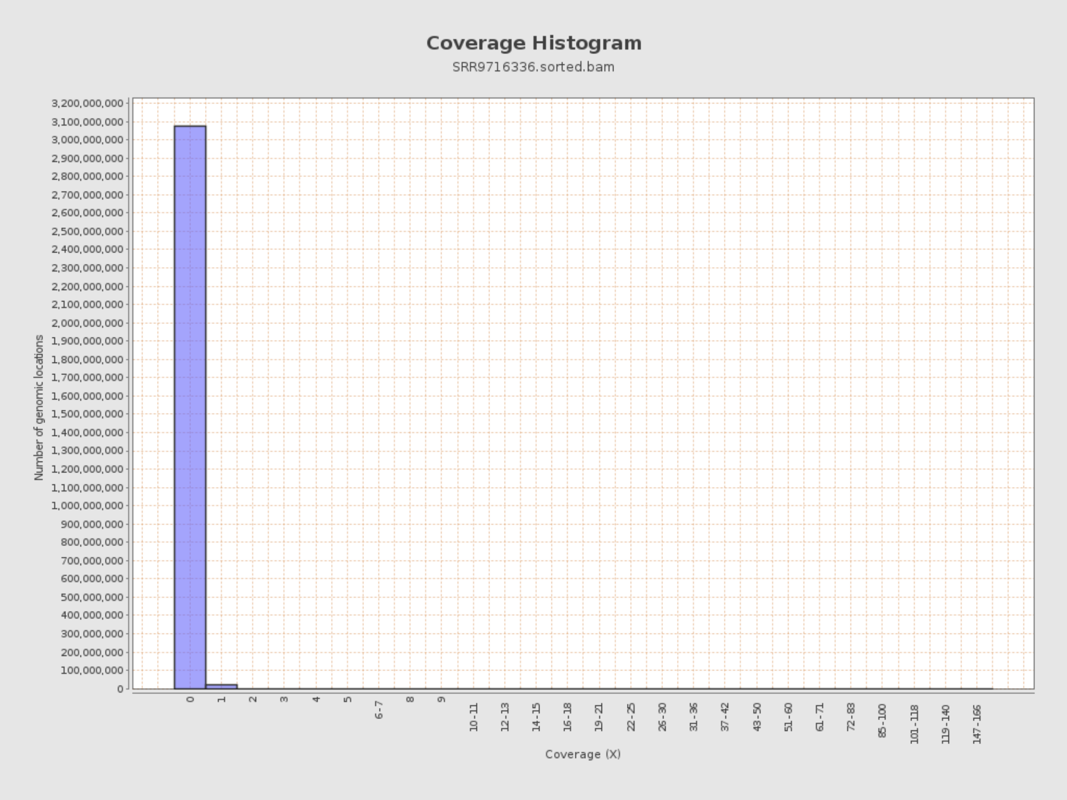
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1984857	0.008	0.1522
chr2	243199373	2099360	0.0086	0.1106
chr3	198022430	1681428	0.0085	0.0949
chr4	191154276	1722388	0.009	0.0992
chr5	180915260	1490919	0.0082	0.0939
chr6	171115067	1414258	0.0083	0.0958
chr7	159138663	1315472	0.0083	0.1135

chr8	146364022	1238985	0.0085	0.1193
chr9	141213431	1015483	0.0072	0.0993
chr10	135534747	1163217	0.0086	0.106
chr11	135006516	1076523	0.008	0.1021
chr12	133851895	1125034	0.0084	0.0952
chr13	115169878	762803	0.0066	0.0836
chr14	107349540	731577	0.0068	0.0874
chr15	102531392	687904	0.0067	0.0839
chr16	90354753	690374	0.0076	0.0916
chr17	81195210	644498	0.0079	0.0931
chr18	78077248	694659	0.0089	0.1419
chr19	59128983	464285	0.0079	0.1283
chr20	63025520	552565	0.0088	0.0972
chr21	48129895	309402	0.0064	0.0847
chr22	51304566	258110	0.005	0.0726
chrMT	16571	8292	0.5004	0.764
chrX	155270560	800722	0.0052	0.0777
chrY	59373566	61139	0.001	0.0404

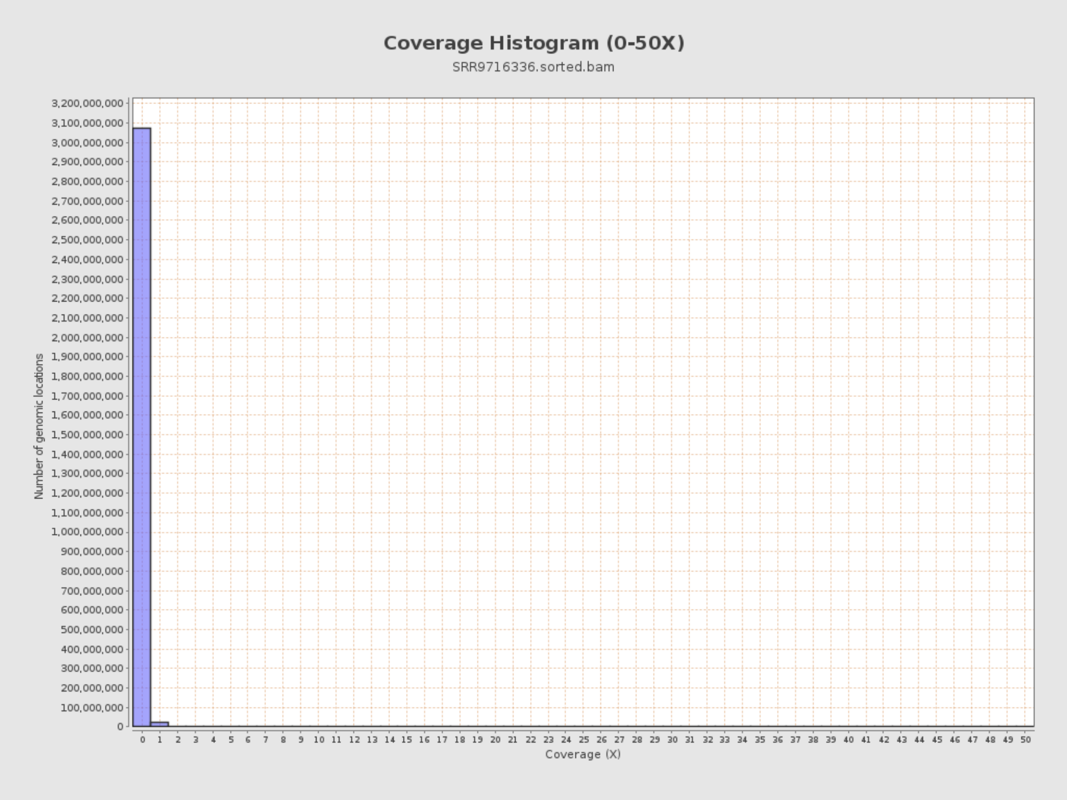
3. Results : Coverage across reference



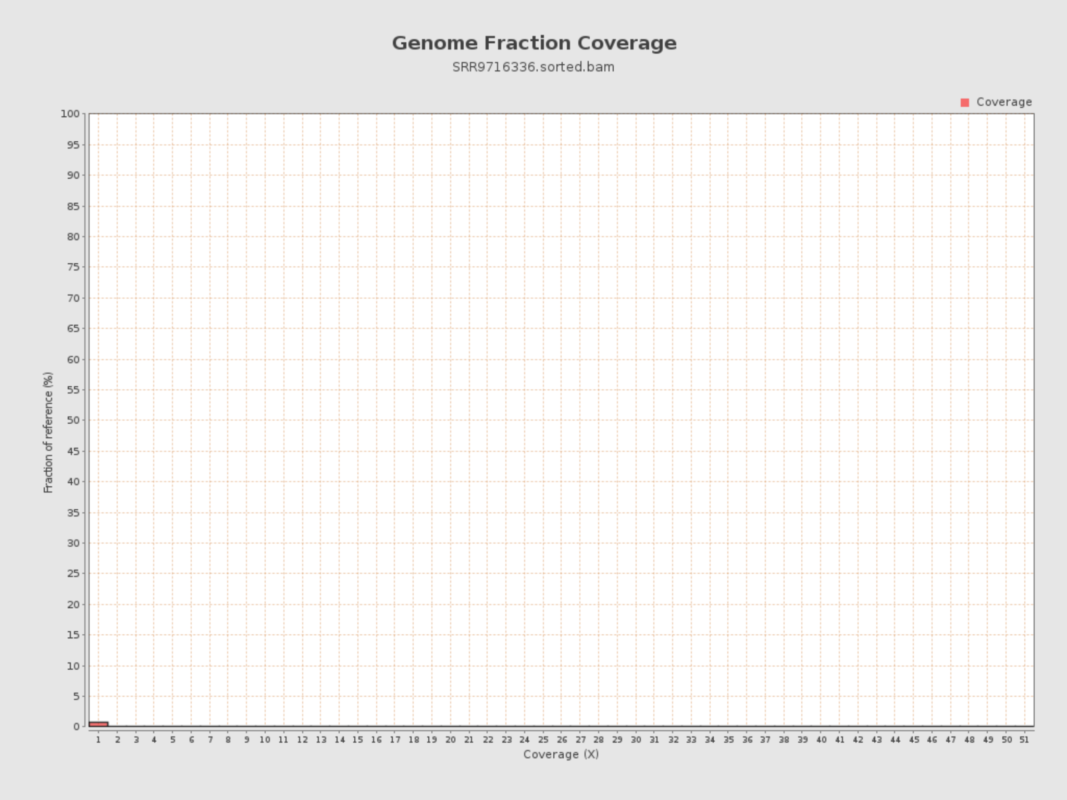
4. Results : Coverage Histogram



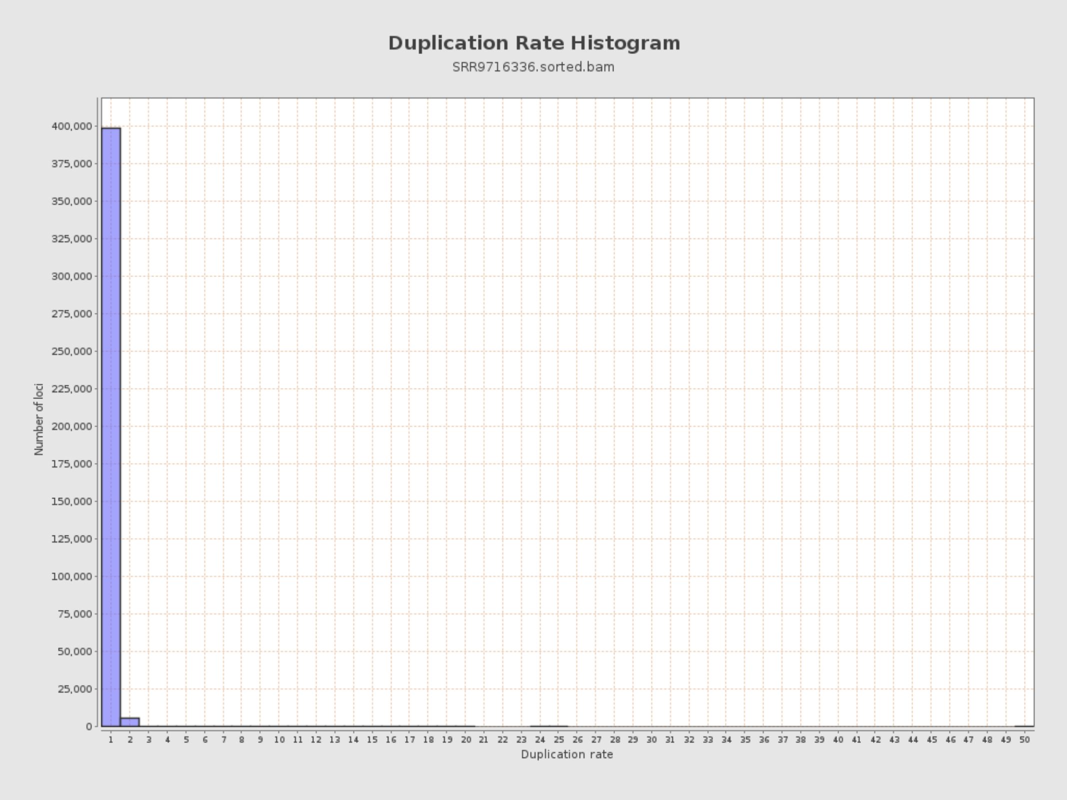
5. Results : Coverage Histogram (0-50X)



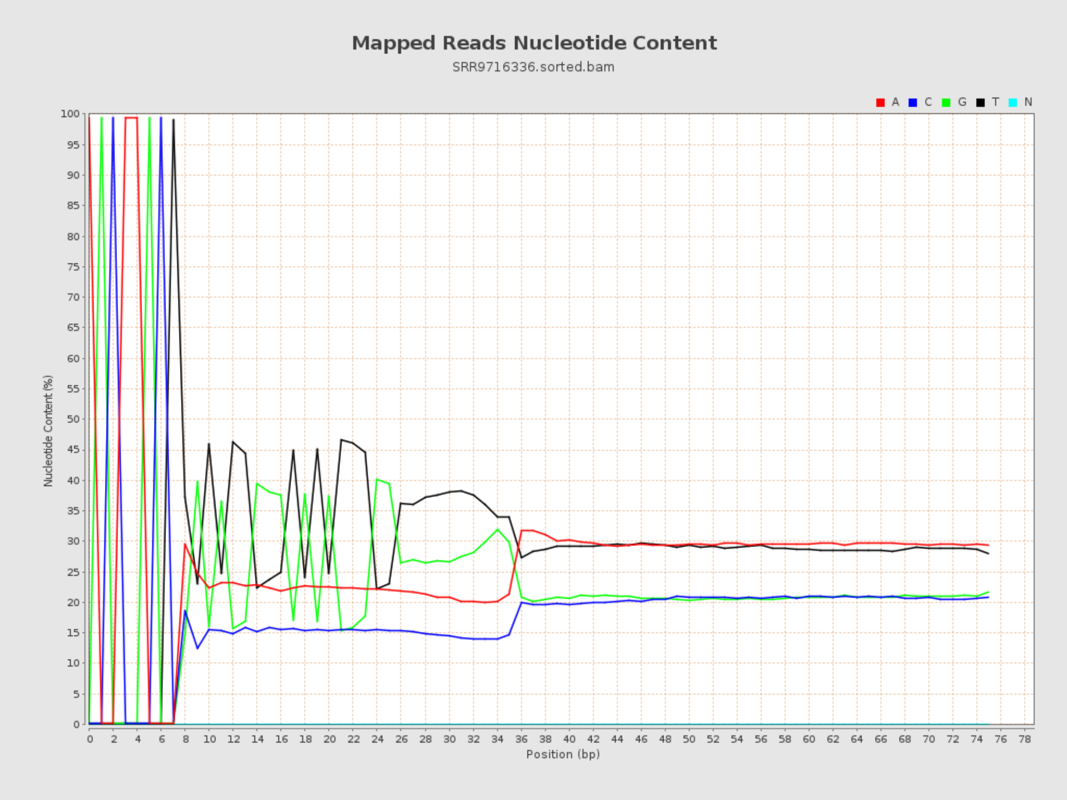
6. Results : Genome Fraction Coverage



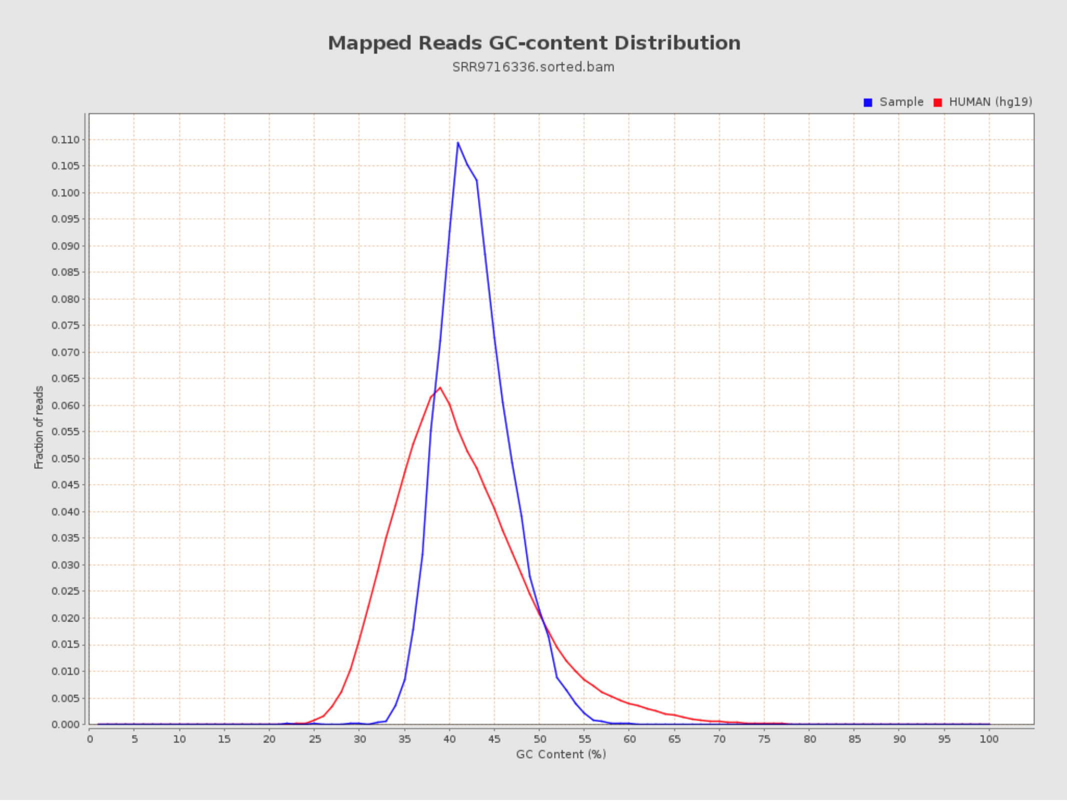
7. Results : Duplication Rate Histogram



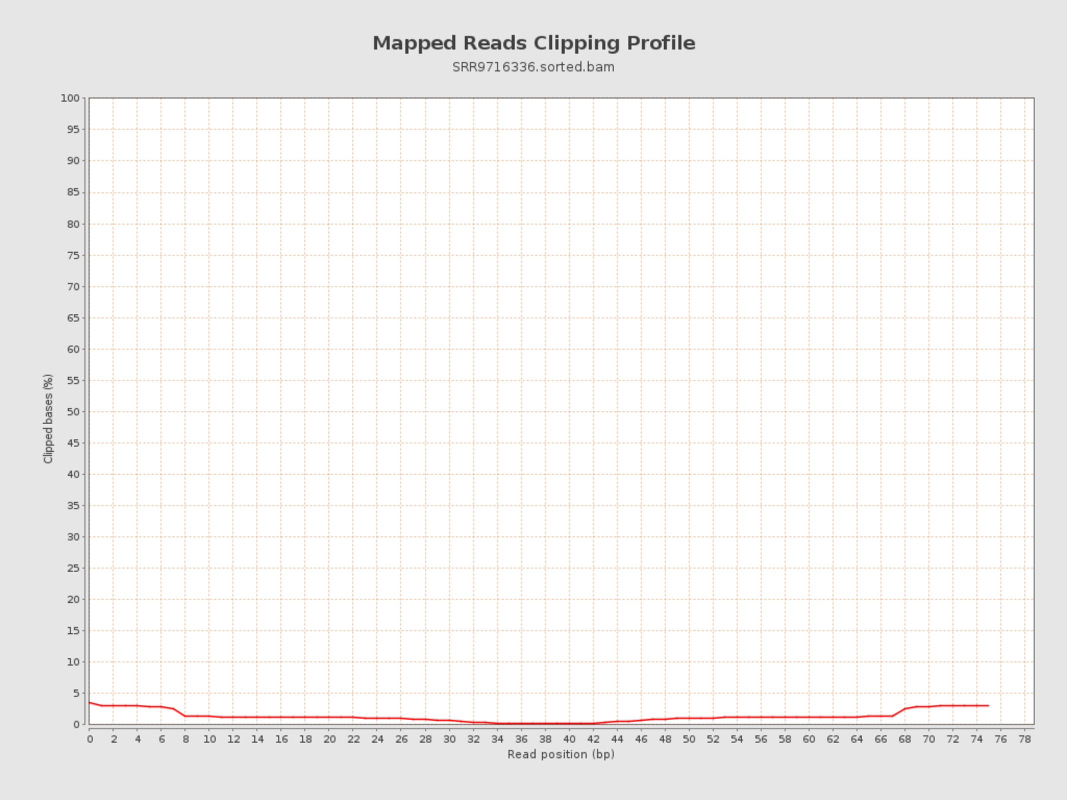
8. Results : Mapped Reads Nucleotide Content



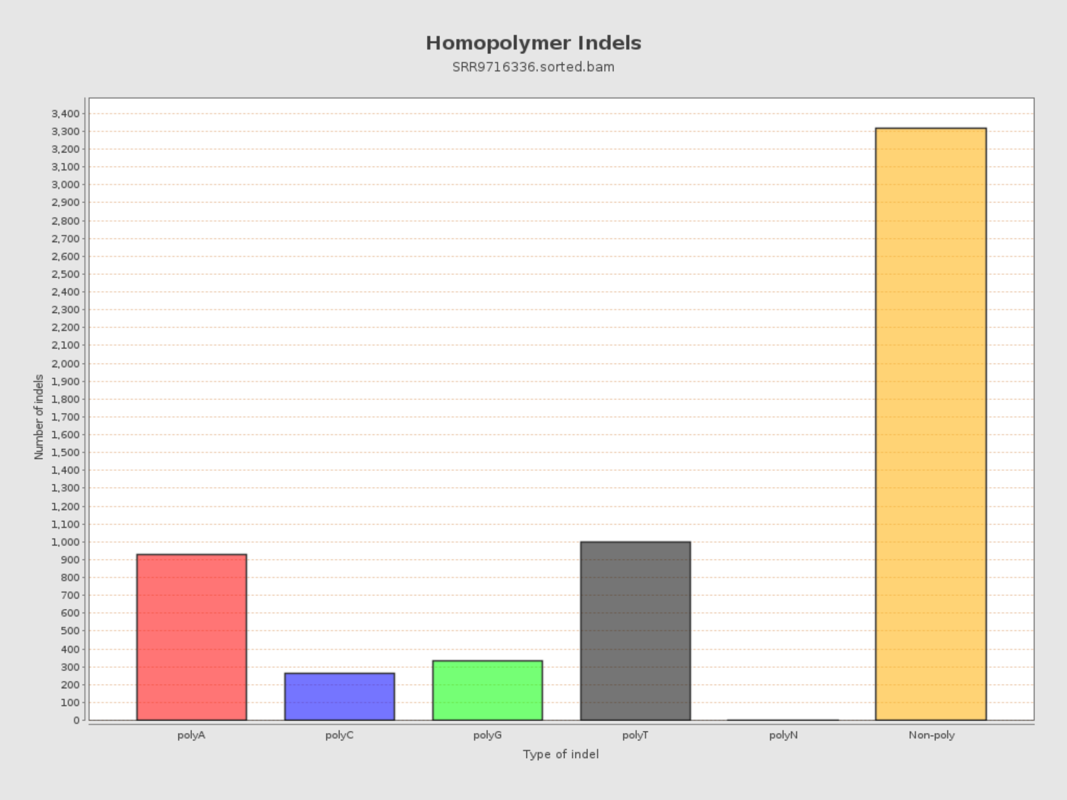
9. Results : Mapped Reads GC-content Distribution



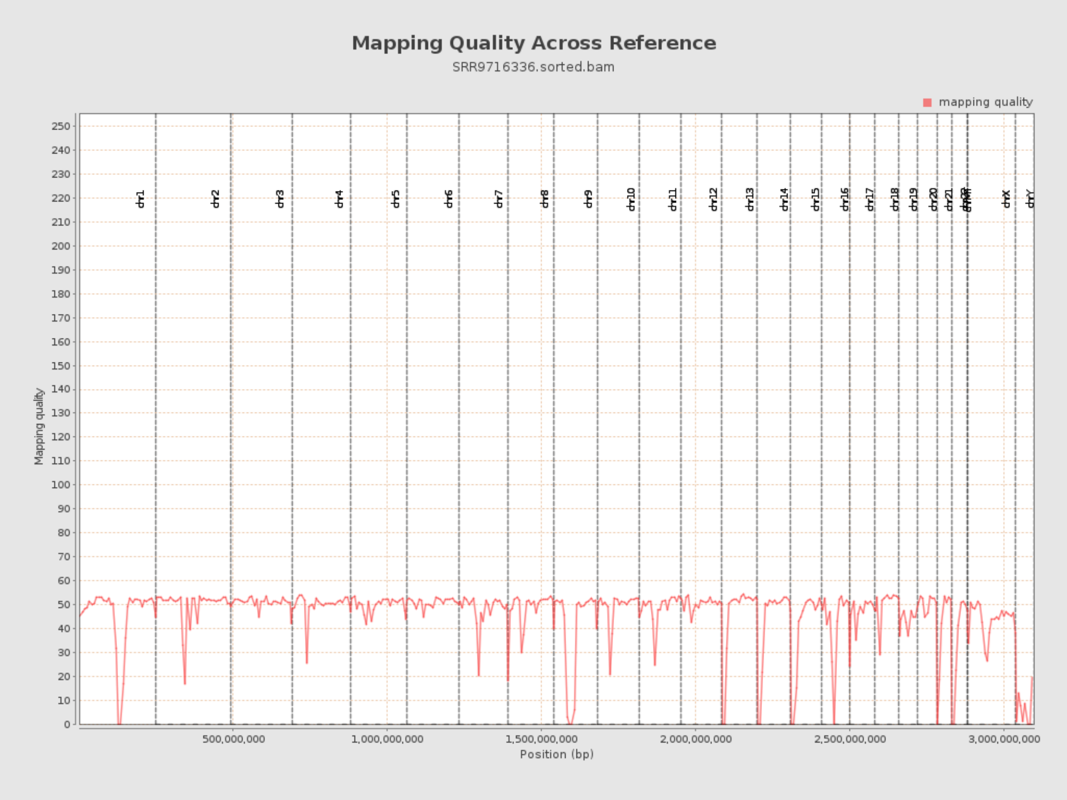
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram