Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 20:03:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716953.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_SRR9716953 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716953.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 20:03:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716953.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,824,480
Mapped reads	1,626,847 / 89.17%
Unmapped reads	197,633 / 10.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,641 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	53,582 / 2.94%
Duplication rate	2.42%
Clipped reads	1,628,722 / 89.27%

2.2. ACGT Content

Number/percentage of A's	24,156,287 / 25.8%
Number/percentage of C's	18,734,434 / 20.01%
Number/percentage of T's	28,800,429 / 30.76%
Number/percentage of G's	21,927,338 / 23.42%
Number/percentage of N's	1,193 / 0%
GC Percentage	43.43%

2.3. Coverage

Mean	0.0303

Standard Deviation	0.2739

2.4. Mapping Quality

Mean Mapping Quality	43.79

2.5. Mismatches and indels

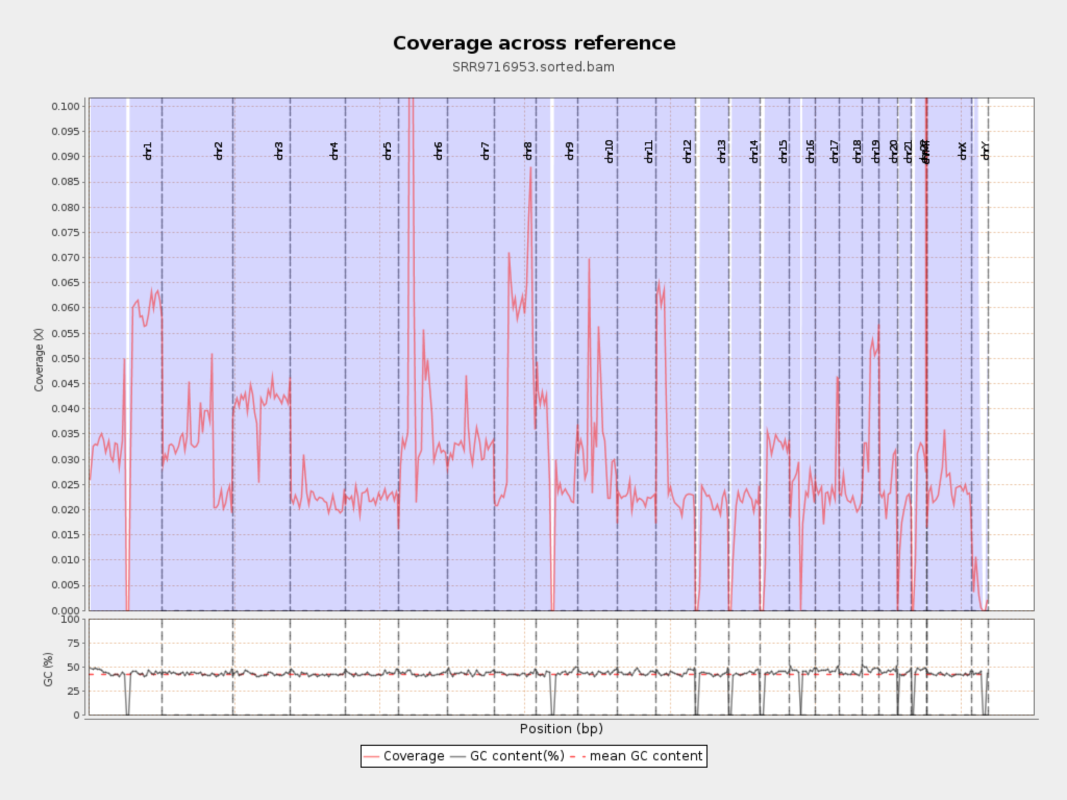
General error rate	0.52%
Mismatches	469,134
Insertions	7,205
Mapped reads with at least one insertion	0.44%
Deletions	16,992
Mapped reads with at least one deletion	1.04%
Homopolymer indels	40.86%

2.6. Chromosome stats

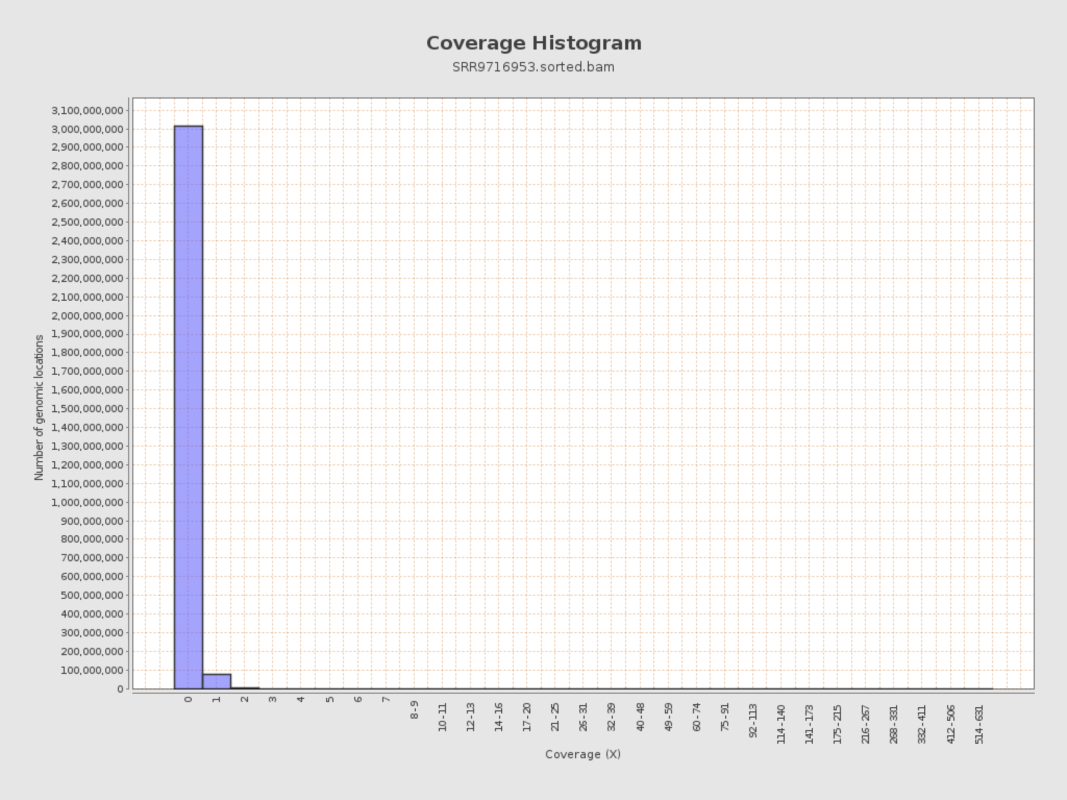
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10505631	0.0421	0.4996
chr2	243199373	7668993	0.0315	0.3246
chr3	198022430	8154283	0.0412	0.2247
chr4	191154276	4217190	0.0221	0.172
chr5	180915260	4068008	0.0225	0.1655
chr6	171115067	7788995	0.0455	0.3007
chr7	159138663	5269986	0.0331	0.329

chr8	146364022	7320500	0.05	0.2707
chr9	141213431	3818436	0.027	0.2402
chr10	135534747	4676063	0.0345	0.3115
chr11	135006516	3024896	0.0224	0.2141
chr12	133851895	4342979	0.0324	0.2042
chr13	115169878	2108745	0.0183	0.1488
chr14	107349540	1976734	0.0184	0.1865
chr15	102531392	2741962	0.0267	0.1847
chr16	90354753	2006712	0.0222	0.1834
chr17	81195210	2120906	0.0261	0.1856
chr18	78077248	1734701	0.0222	0.3809
chr19	59128983	2519093	0.0426	0.3672
chr20	63025520	1546952	0.0245	0.1749
chr21	48129895	833537	0.0173	0.1653
chr22	51304566	1112854	0.0217	0.1617
chrMT	16571	90224	5.4447	3.5874
chrX	155270560	3794808	0.0244	0.2033
chrY	59373566	202911	0.0034	0.0887

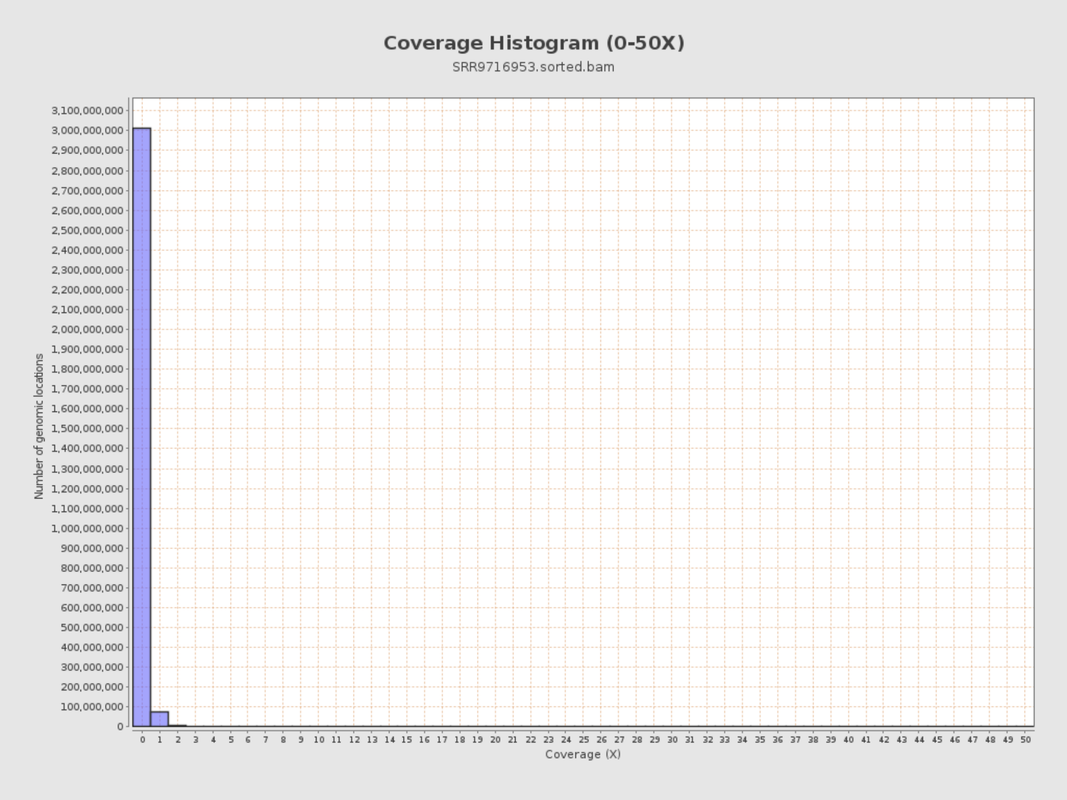
3. Results : Coverage across reference



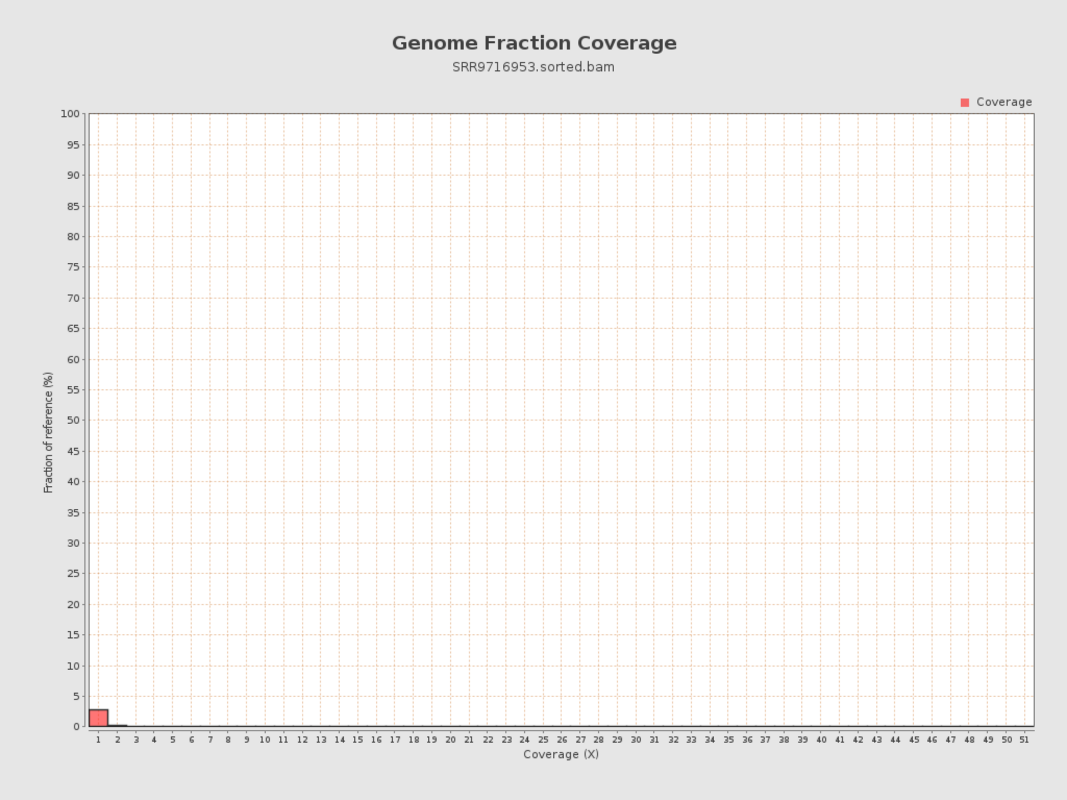
4. Results : Coverage Histogram



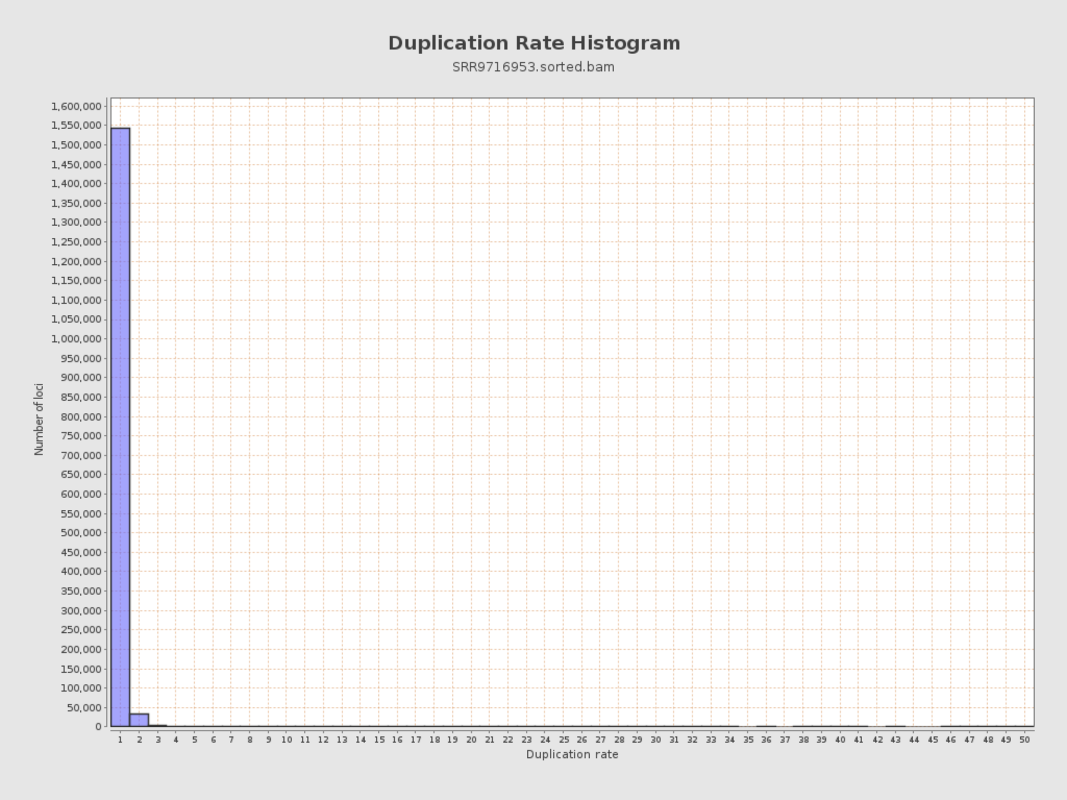
5. Results : Coverage Histogram (0-50X)



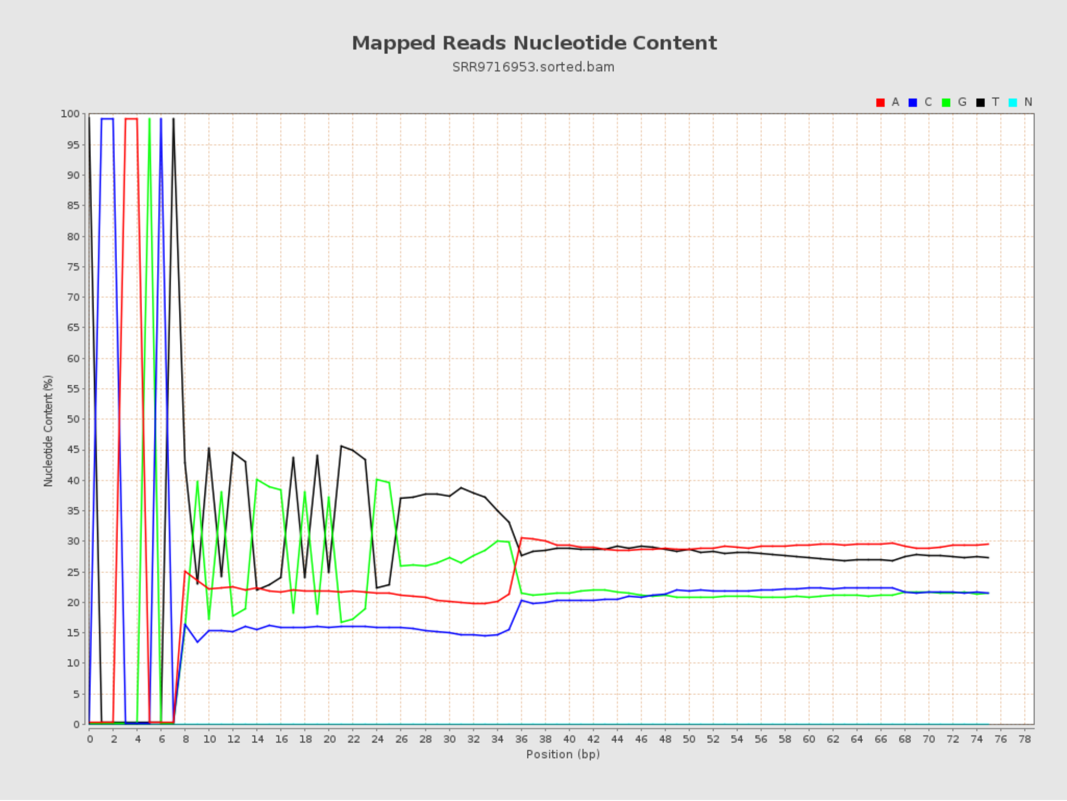
6. Results : Genome Fraction Coverage



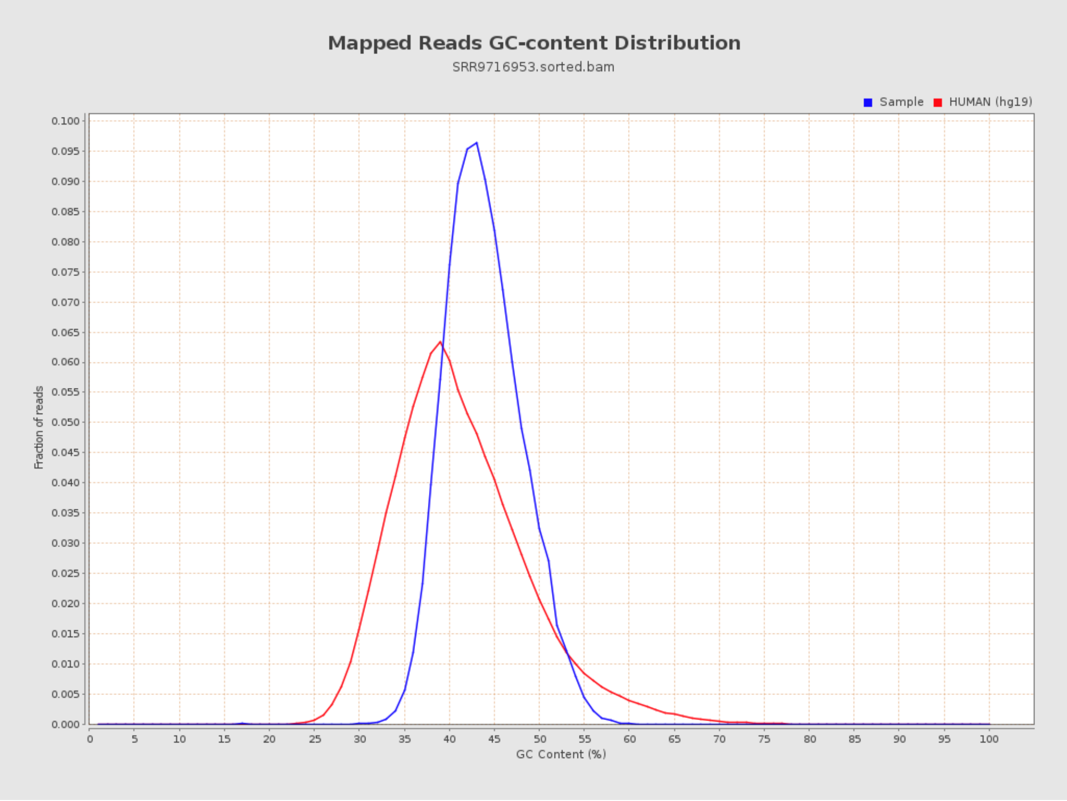
7. Results : Duplication Rate Histogram



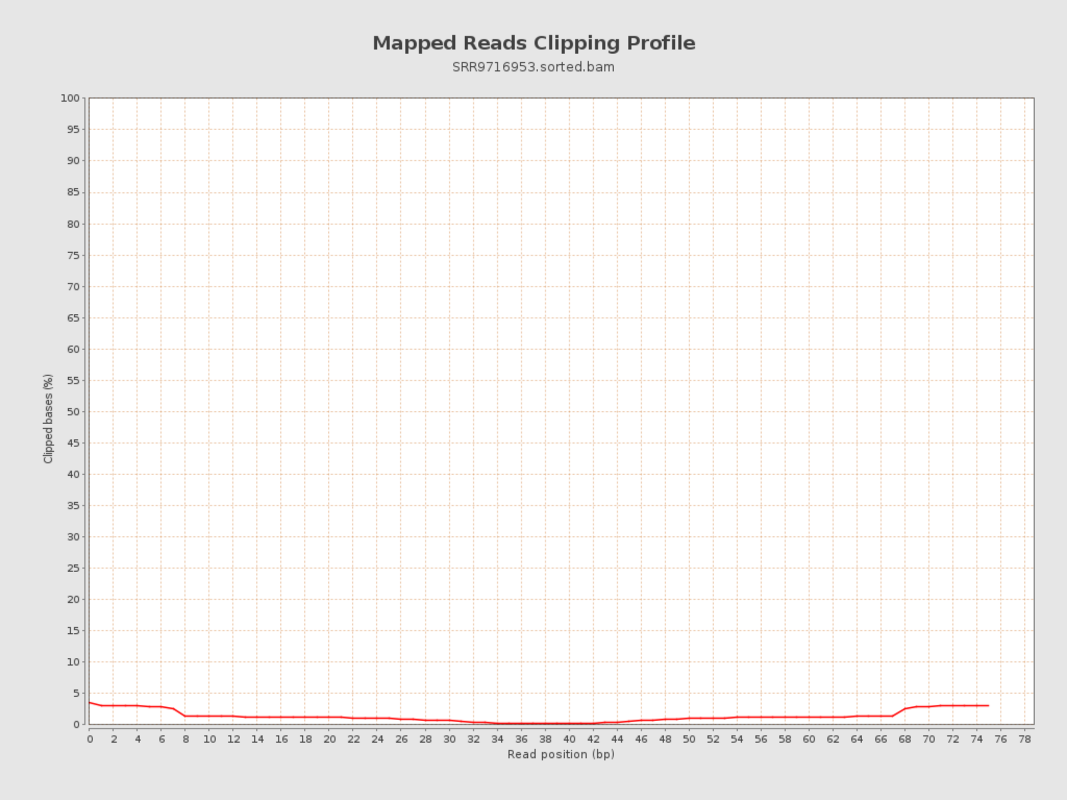
8. Results : Mapped Reads Nucleotide Content



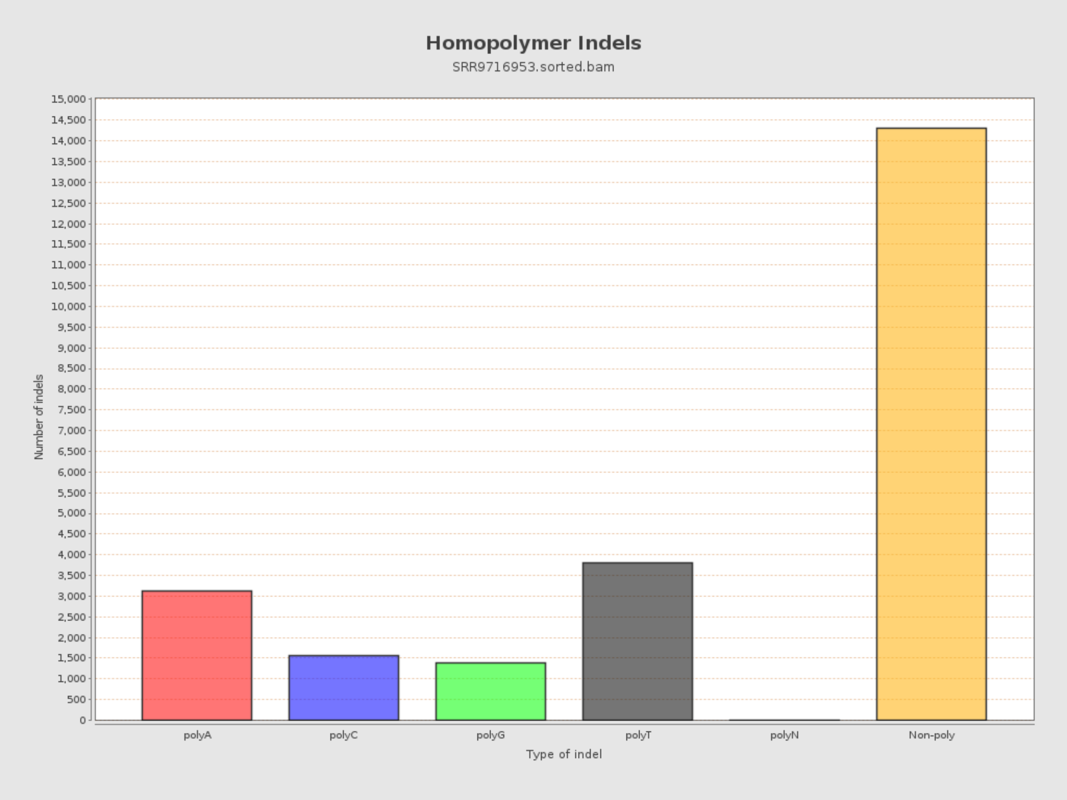
9. Results : Mapped Reads GC-content Distribution



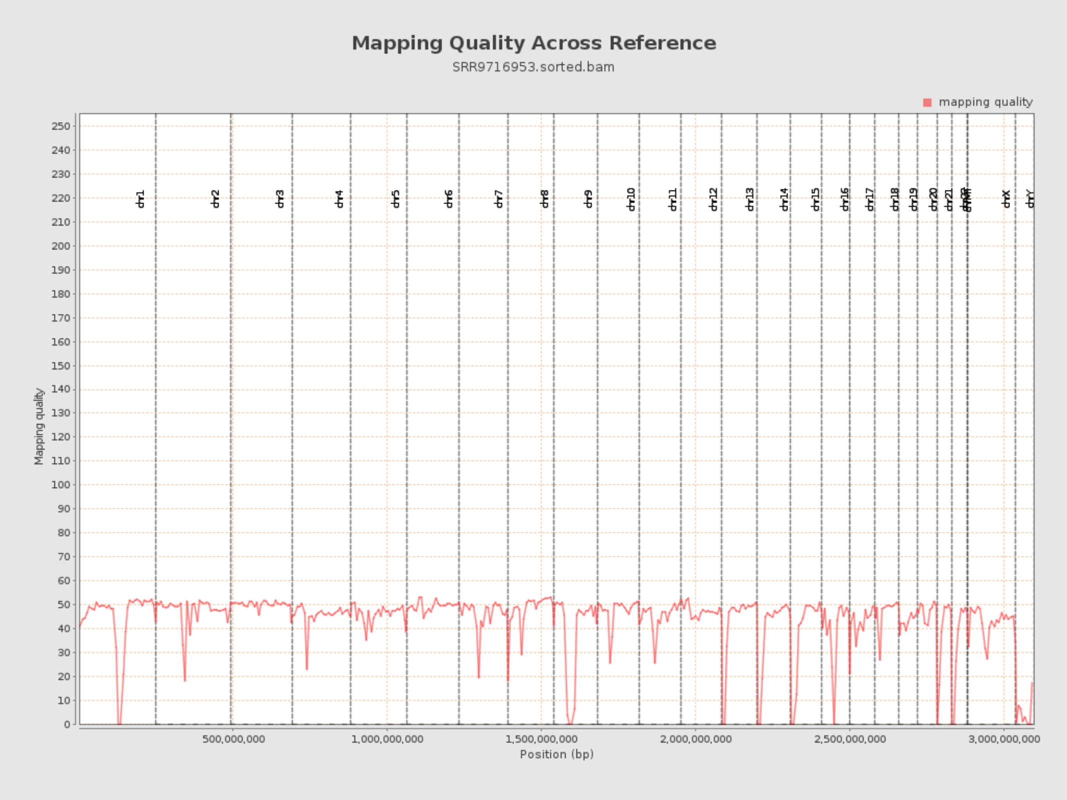
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram