Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 22:58:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716582.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_SRR9716582 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716582.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 22:58:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716582.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	787,775
Mapped reads	714,525 / 90.7%
Unmapped reads	73,250 / 9.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,778 / 0.48%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	18,061 / 2.29%
Duplication rate	1.9%
Clipped reads	716,593 / 90.96%

2.2. ACGT Content

Number/percentage of A's	10,482,466 / 25.31%
Number/percentage of C's	8,290,766 / 20.02%
Number/percentage of T's	12,761,235 / 30.81%
Number/percentage of G's	9,879,356 / 23.85%
Number/percentage of N's	495 / 0%
GC Percentage	43.87%

2.3. Coverage

Mean	0.0134

Standard Deviation	0.1512

2.4. Mapping Quality

Mean Mapping Quality	44.52

2.5. Mismatches and indels

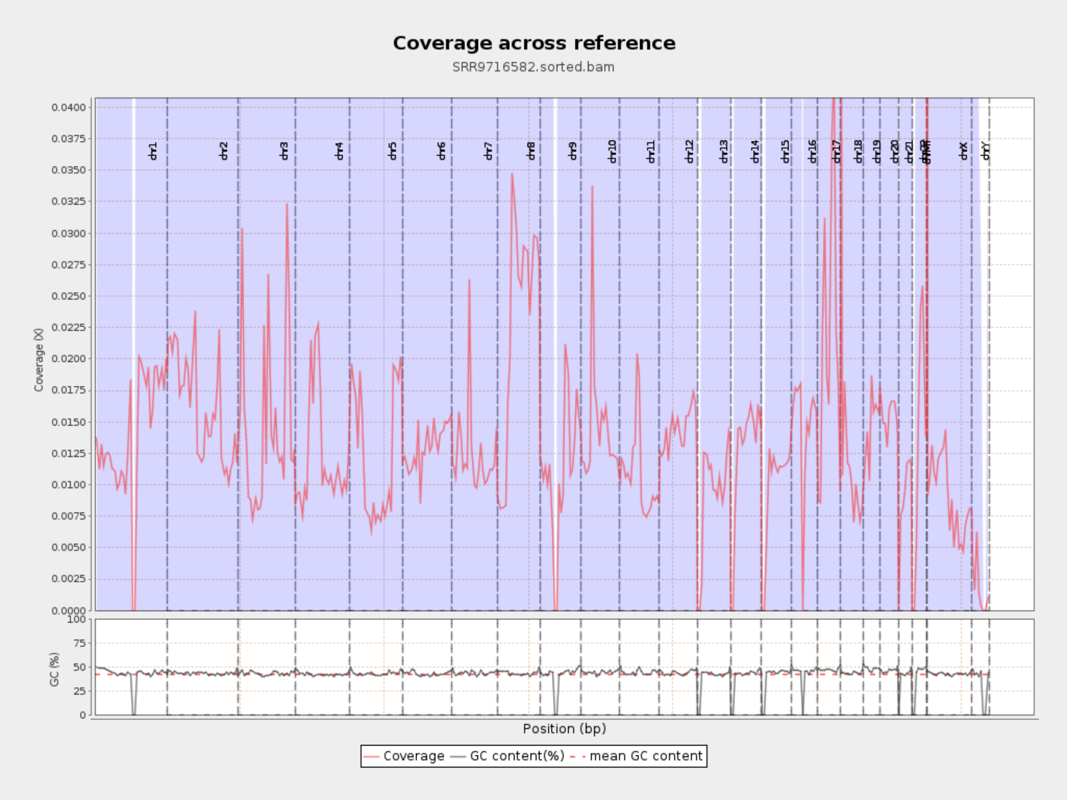
General error rate	0.5%
Mismatches	203,936
Insertions	2,779
Mapped reads with at least one insertion	0.39%
Deletions	7,506
Mapped reads with at least one deletion	1.04%
Homopolymer indels	42.03%

2.6. Chromosome stats

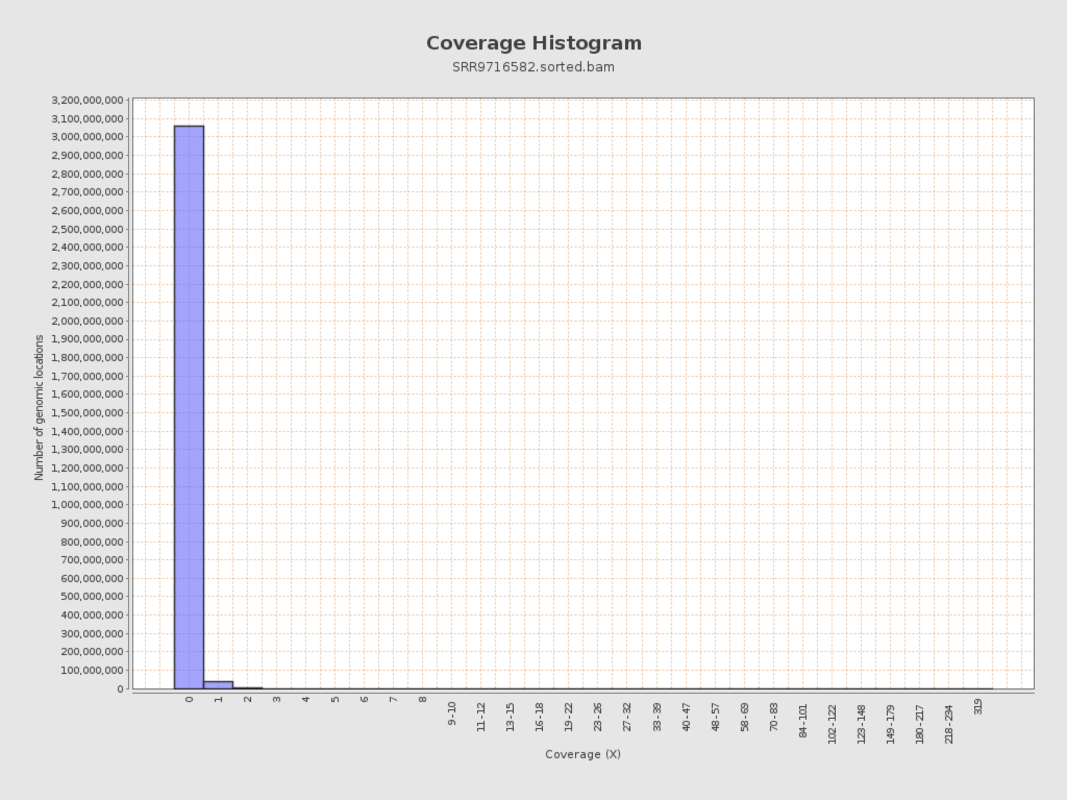
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3452826	0.0139	0.2021
chr2	243199373	3931672	0.0162	0.1902
chr3	198022430	2902231	0.0147	0.129
chr4	191154276	2335478	0.0122	0.1251
chr5	180915260	2233890	0.0123	0.1172
chr6	171115067	2229892	0.013	0.1246
chr7	159138663	1980204	0.0124	0.2084

chr8	146364022	3415327	0.0233	0.1913
chr9	141213431	1551641	0.011	0.1191
chr10	135534747	1968408	0.0145	0.1832
chr11	135006516	1486547	0.011	0.1214
chr12	133851895	1926275	0.0144	0.1312
chr13	115169878	1063826	0.0092	0.1009
chr14	107349540	1334189	0.0124	0.1185
chr15	102531392	982504	0.0096	0.1024
chr16	90354753	1300469	0.0144	0.1287
chr17	81195210	1800118	0.0222	0.1598
chr18	78077248	937080	0.012	0.163
chr19	59128983	864426	0.0146	0.1791
chr20	63025520	971742	0.0154	0.1335
chr21	48129895	435058	0.009	0.1046
chr22	51304566	681737	0.0133	0.1212
chrMT	16571	129792	7.8325	5.3707
chrX	155270560	1407235	0.0091	0.1077
chrY	59373566	103457	0.0017	0.0595

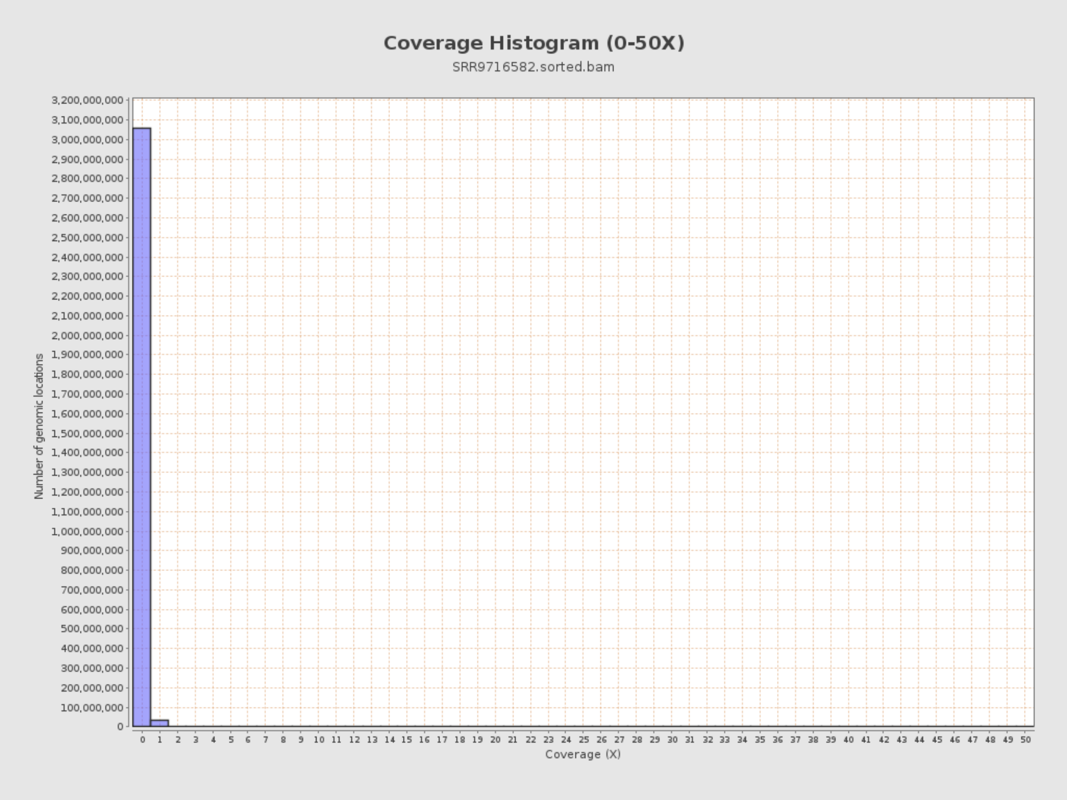
3. Results : Coverage across reference



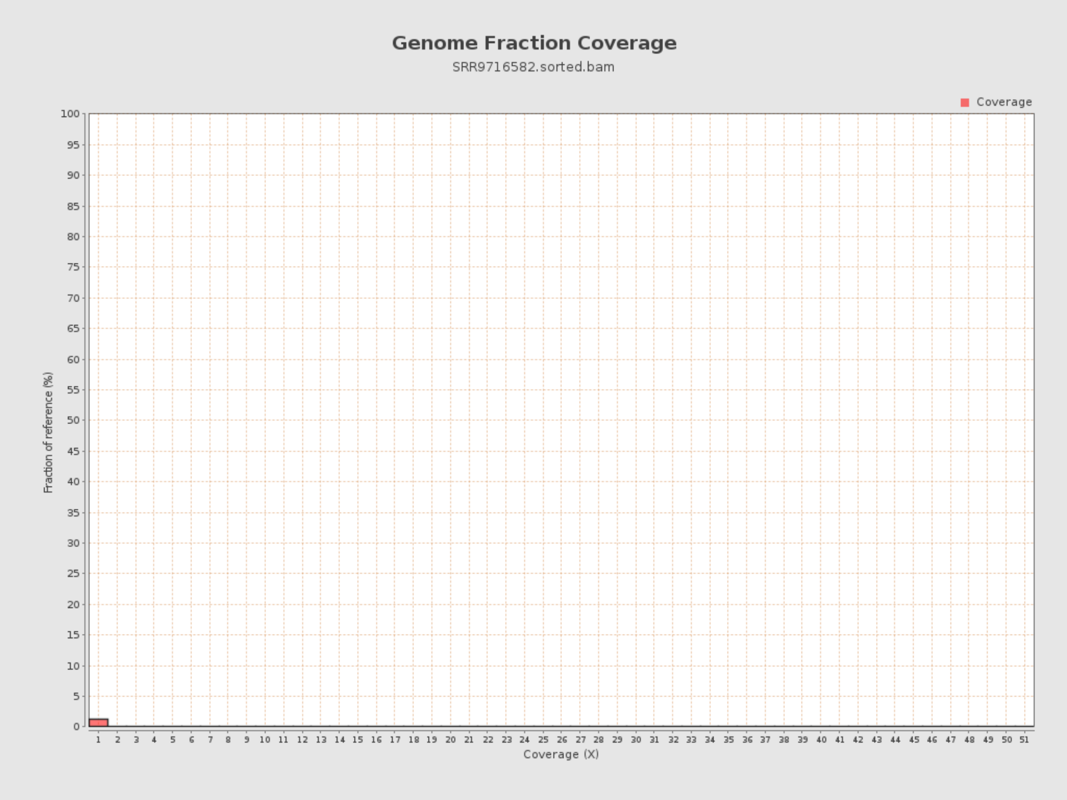
4. Results : Coverage Histogram



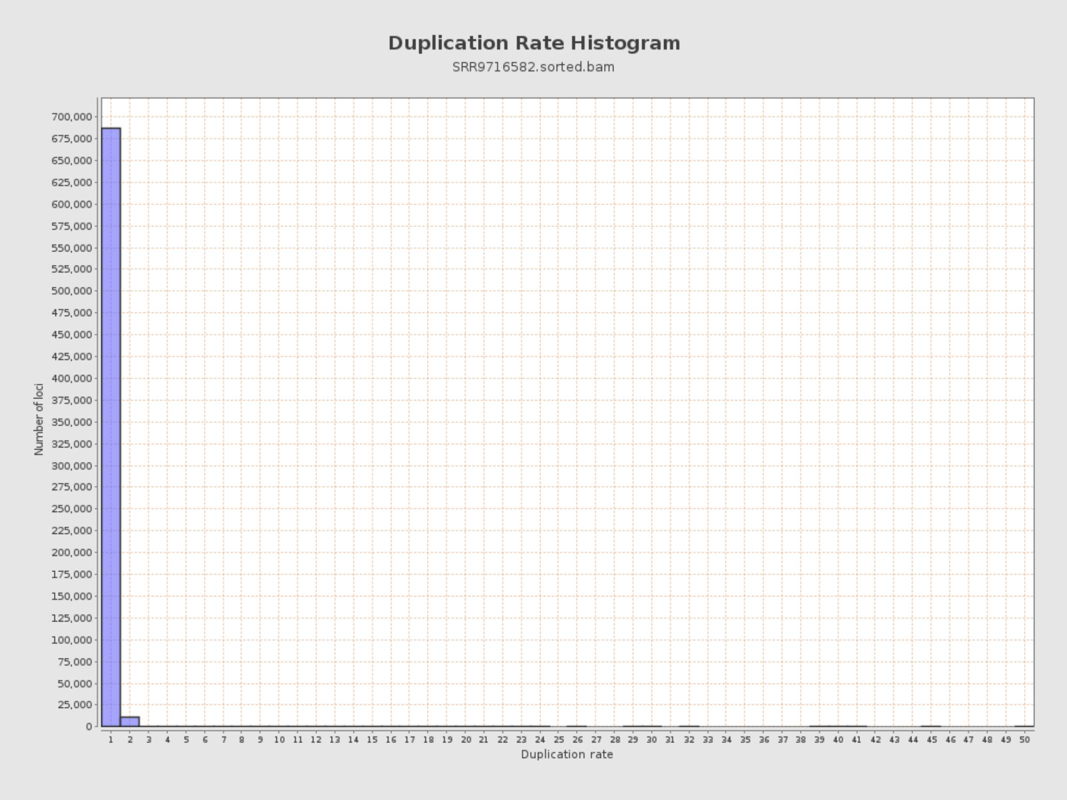
5. Results : Coverage Histogram (0-50X)



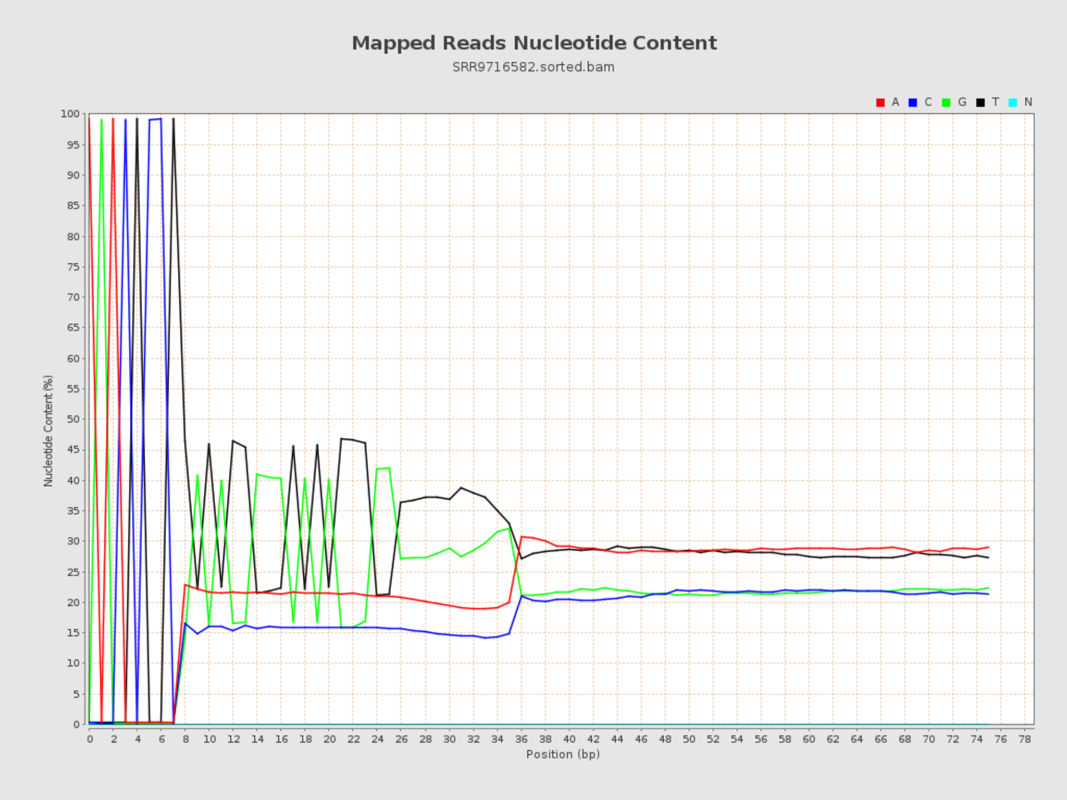
6. Results : Genome Fraction Coverage



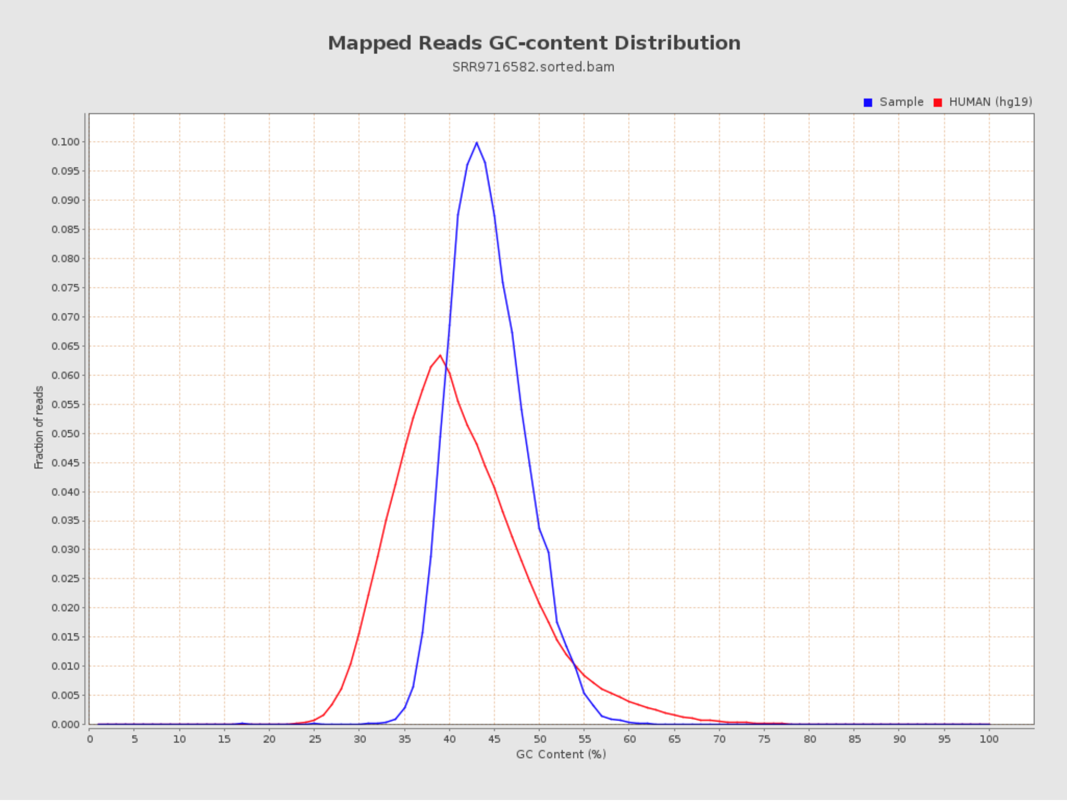
7. Results : Duplication Rate Histogram



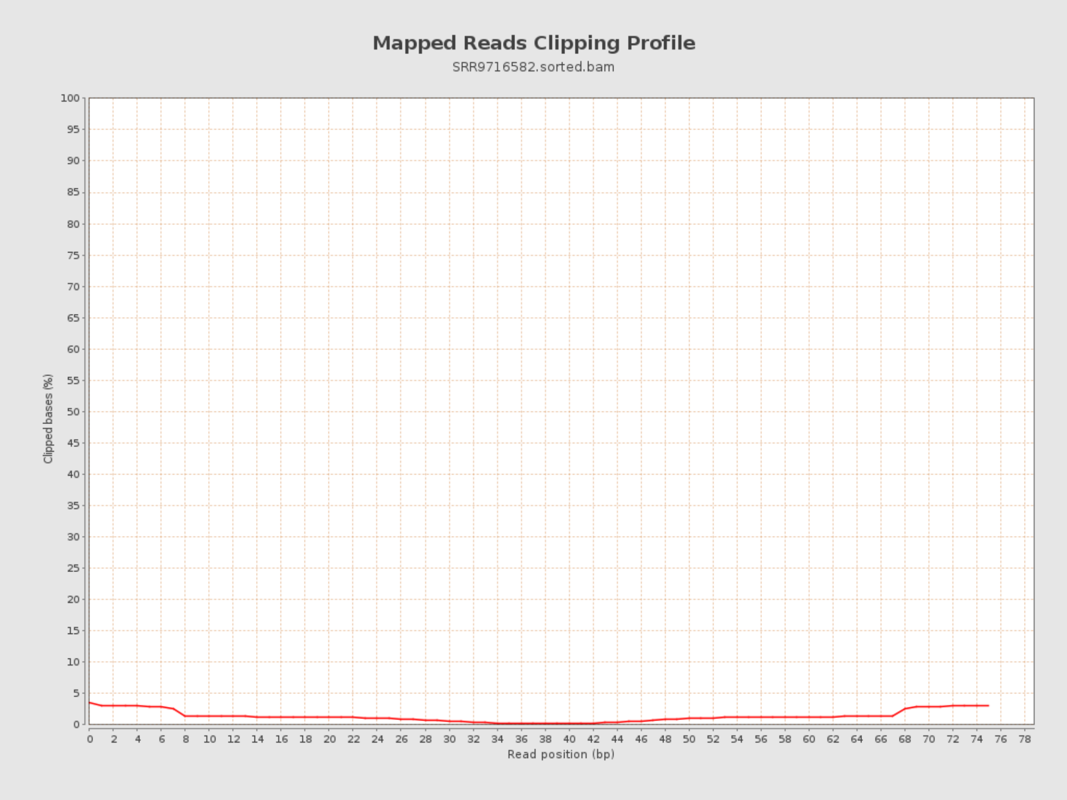
8. Results : Mapped Reads Nucleotide Content



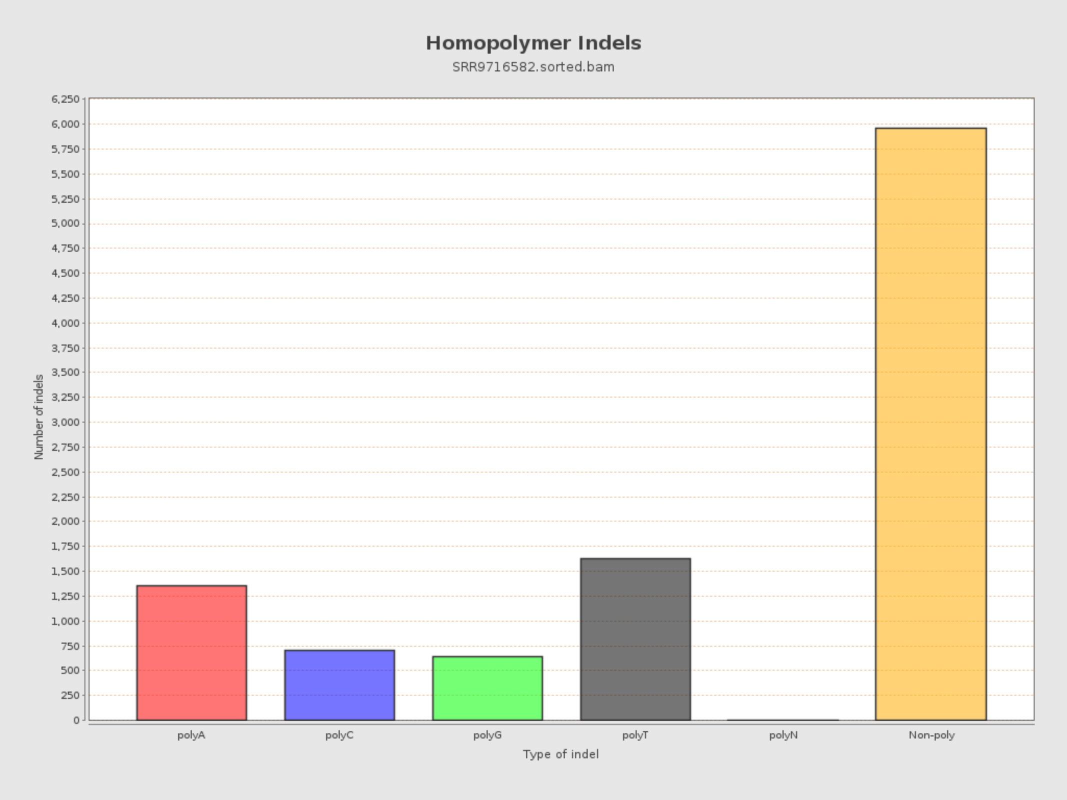
9. Results : Mapped Reads GC-content Distribution



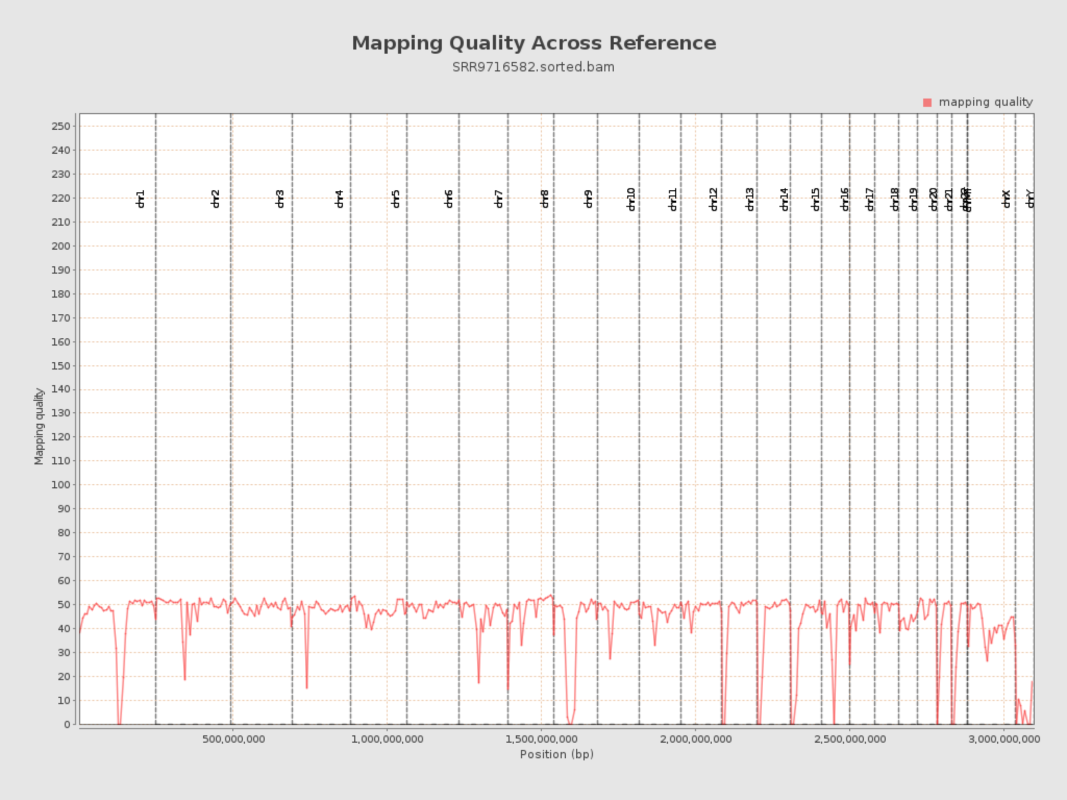
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram