Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 16:21:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716483.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_SRR9716483 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716483.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 16:21:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716483.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	604,305
Mapped reads	486,613 / 80.52%
Unmapped reads	117,692 / 19.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,573 / 0.26%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	7,779 / 1.29%
Duplication rate	1.11%
Clipped reads	487,021 / 80.59%

2.2. ACGT Content

Number/percentage of A's	6,574,873 / 23.94%
Number/percentage of C's	5,171,406 / 18.83%
Number/percentage of T's	8,803,275 / 32.06%
Number/percentage of G's	6,909,556 / 25.16%
Number/percentage of N's	445 / 0%
GC Percentage	44%

2.3. Coverage

Mean	0.0089

Standard Deviation	0.1171

2.4. Mapping Quality

Mean Mapping Quality	42.65

2.5. Mismatches and indels

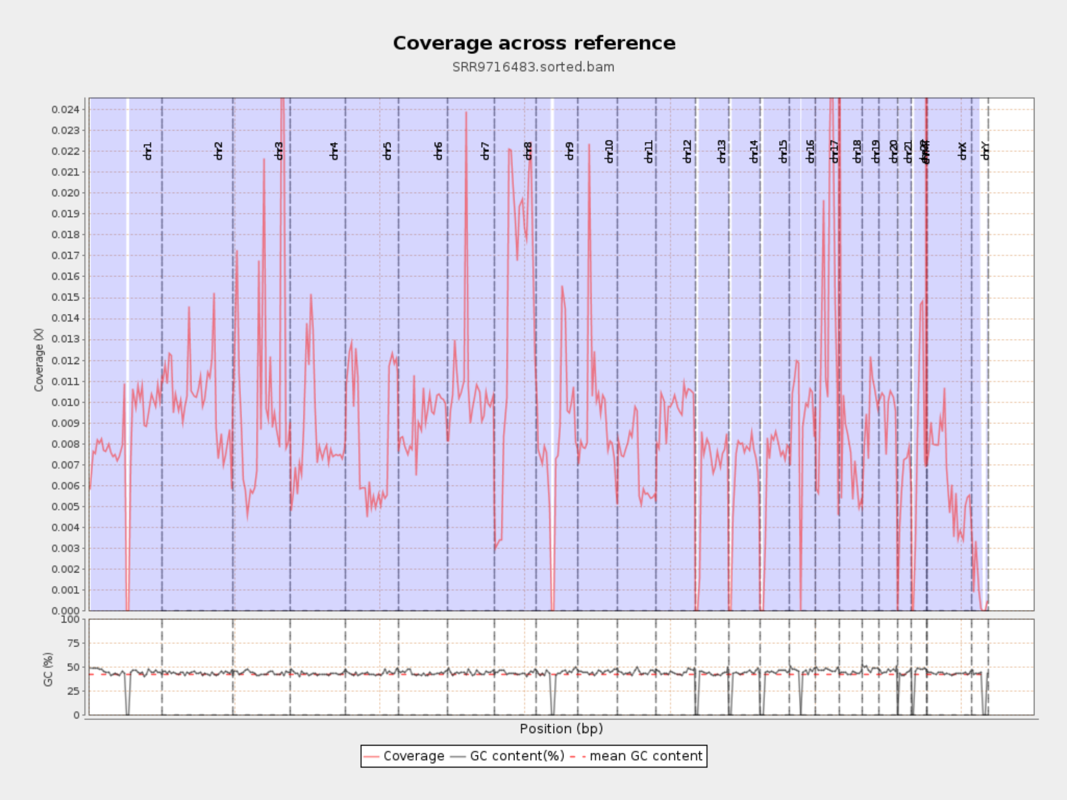
General error rate	0.53%
Mismatches	141,634
Insertions	1,825
Mapped reads with at least one insertion	0.37%
Deletions	5,437
Mapped reads with at least one deletion	1.11%
Homopolymer indels	41.17%

2.6. Chromosome stats

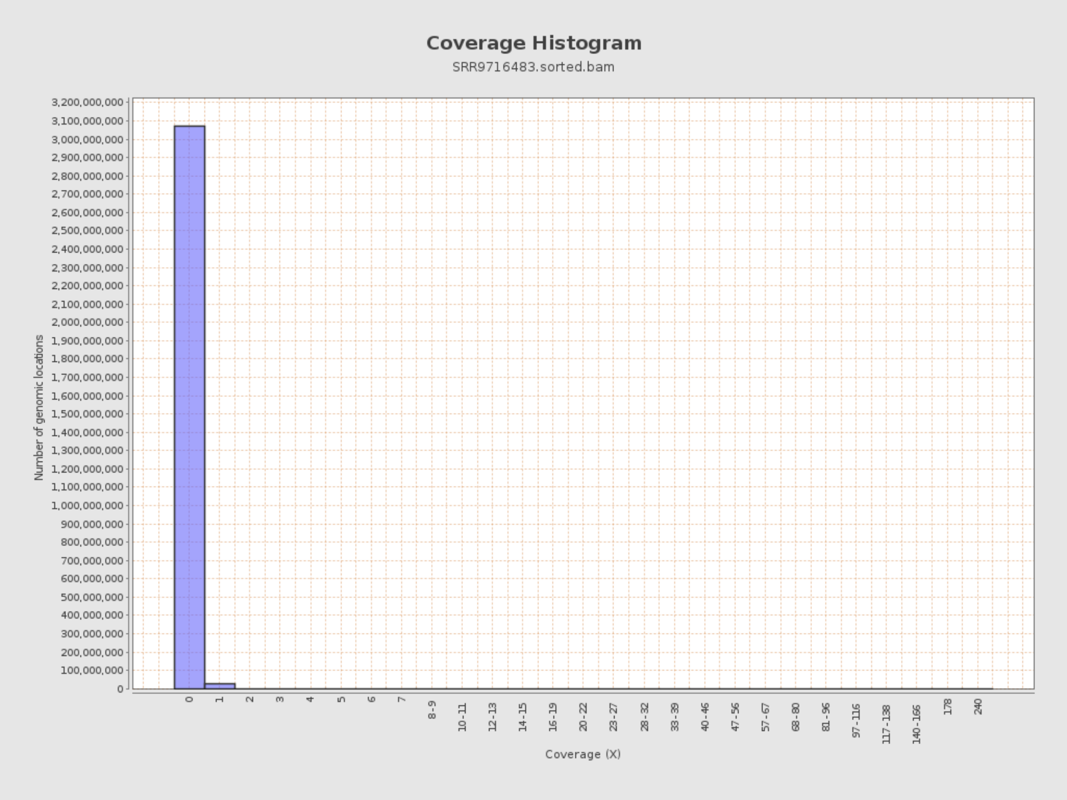
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2044032	0.0082	0.1198
chr2	243199373	2485712	0.0102	0.146
chr3	198022430	2138645	0.0108	0.1099
chr4	191154276	1585429	0.0083	0.0954
chr5	180915260	1489549	0.0082	0.0933
chr6	171115067	1555857	0.0091	0.1029
chr7	159138663	1735370	0.0109	0.2193

chr8	146364022	2152573	0.0147	0.1344
chr9	141213431	1132525	0.008	0.0965
chr10	135534747	1300810	0.0096	0.1398
chr11	135006516	938835	0.007	0.0932
chr12	133851895	1300014	0.0097	0.104
chr13	115169878	731907	0.0064	0.0827
chr14	107349540	698874	0.0065	0.0842
chr15	102531392	657285	0.0064	0.0834
chr16	90354753	837493	0.0093	0.1017
chr17	81195210	1124382	0.0138	0.1228
chr18	78077248	652253	0.0084	0.1189
chr19	59128983	563766	0.0095	0.1329
chr20	63025520	608022	0.0096	0.1016
chr21	48129895	278790	0.0058	0.0788
chr22	51304566	385042	0.0075	0.0896
chrMT	16571	12129	0.7319	0.9865
chrX	155270560	999045	0.0064	0.0883
chrY	59373566	59865	0.001	0.0374

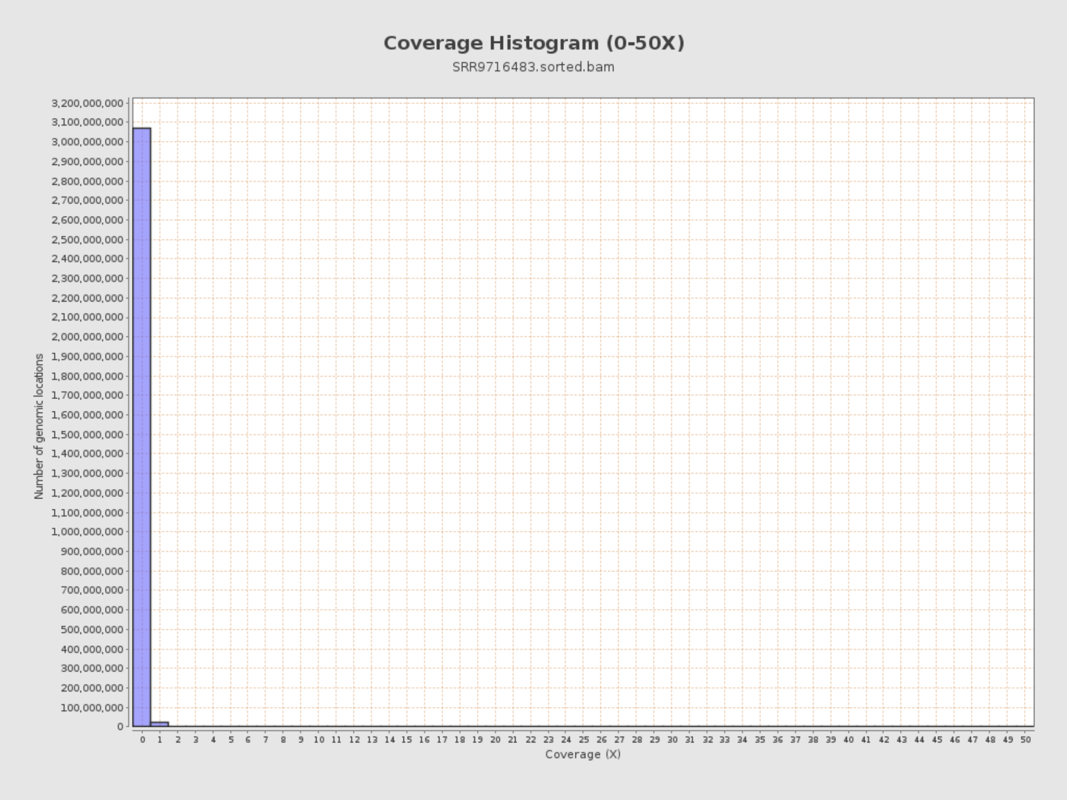
3. Results : Coverage across reference



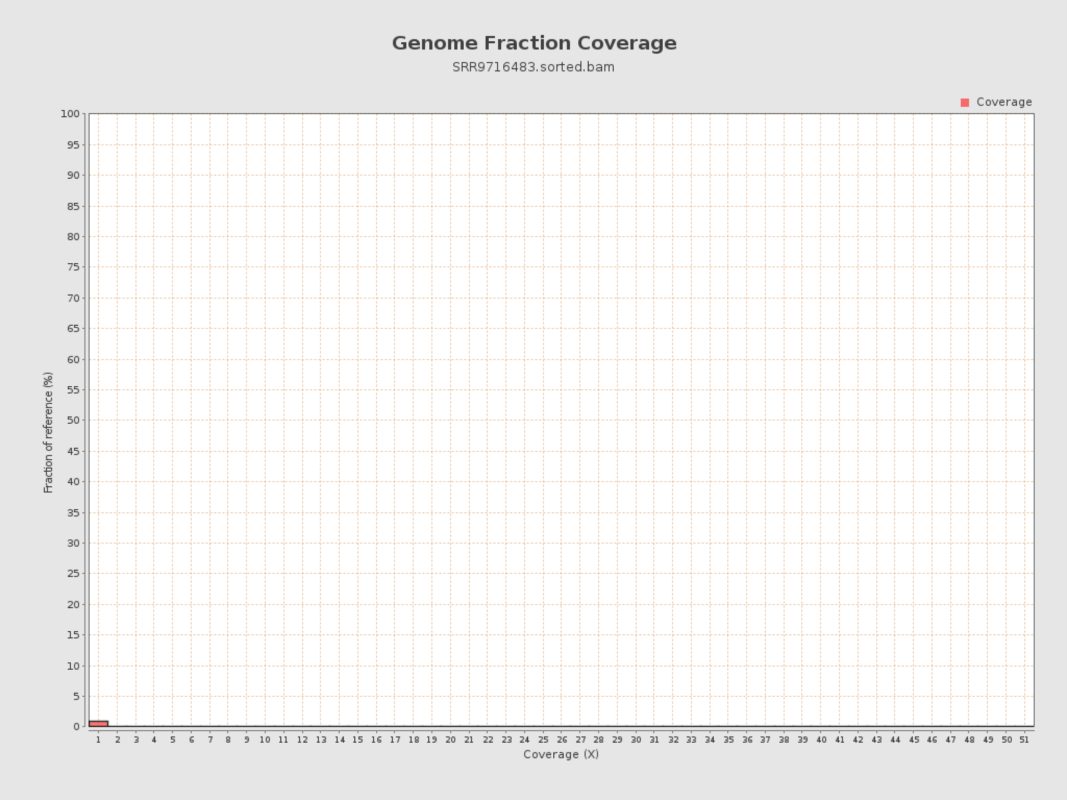
4. Results : Coverage Histogram



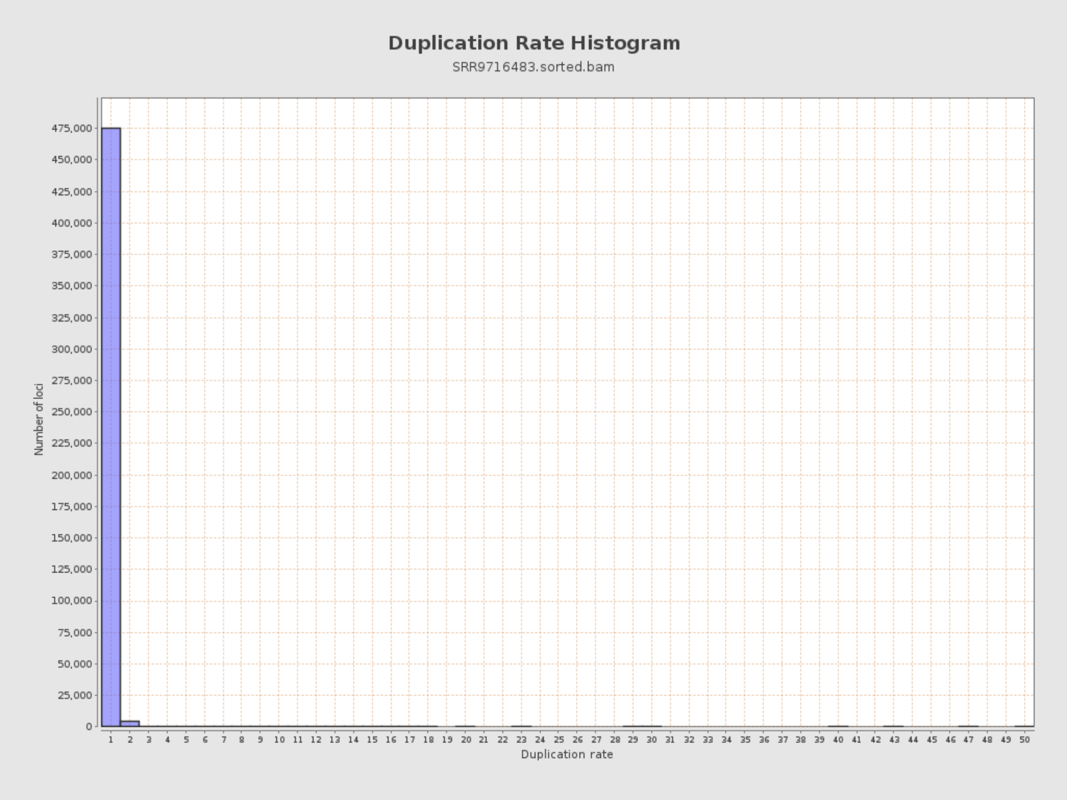
5. Results : Coverage Histogram (0-50X)



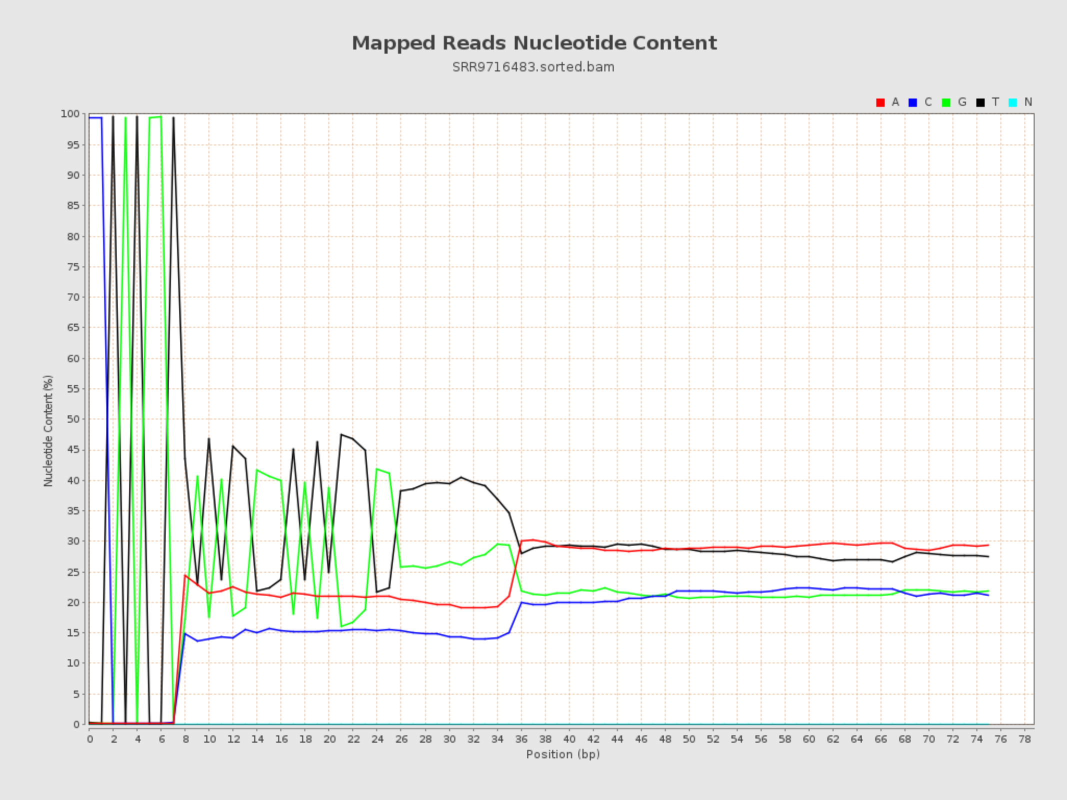
6. Results : Genome Fraction Coverage



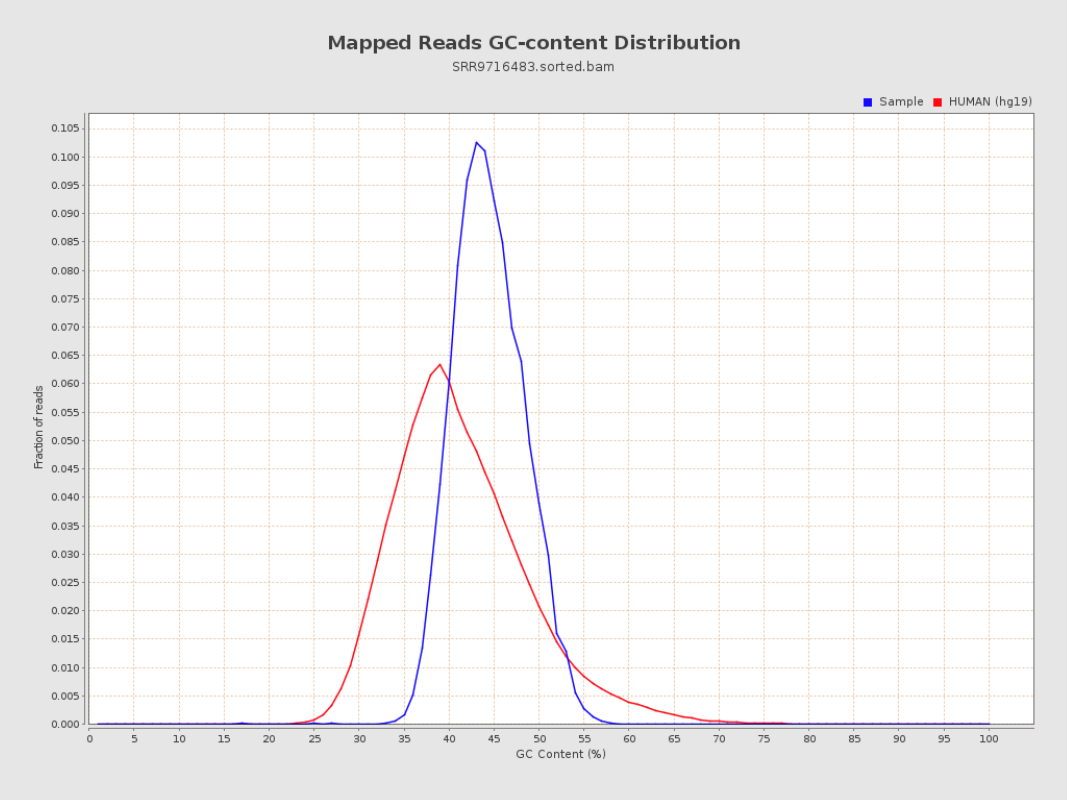
7. Results : Duplication Rate Histogram



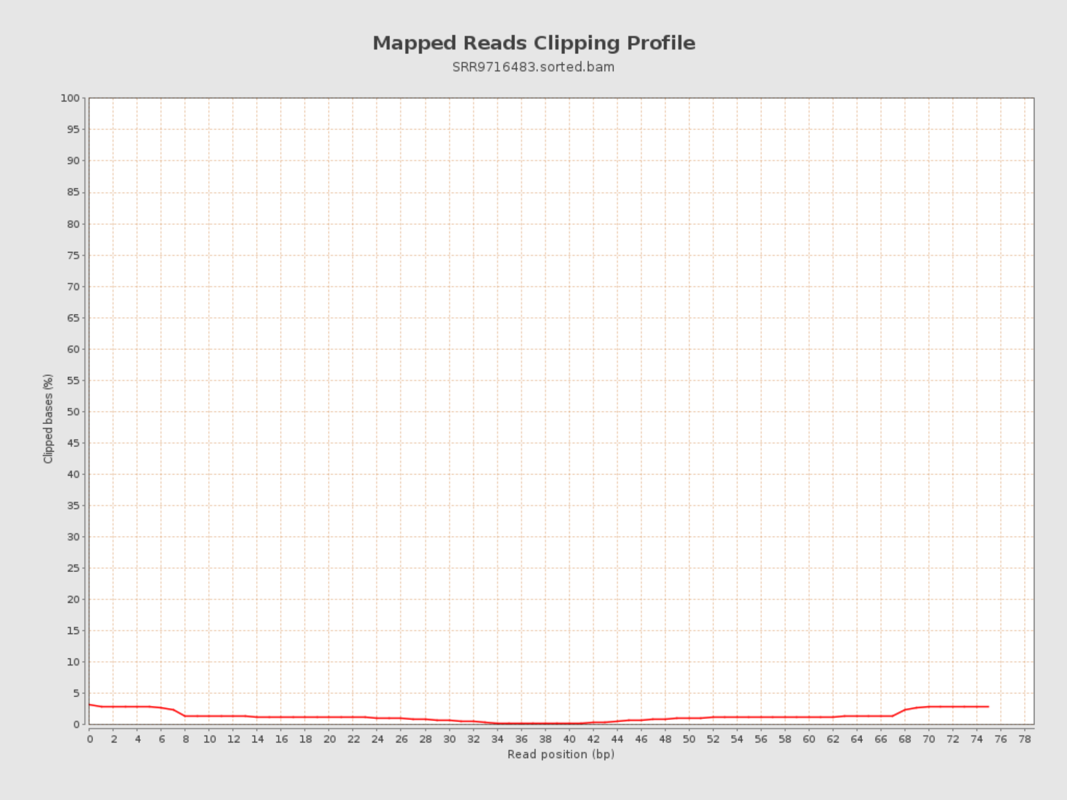
8. Results : Mapped Reads Nucleotide Content



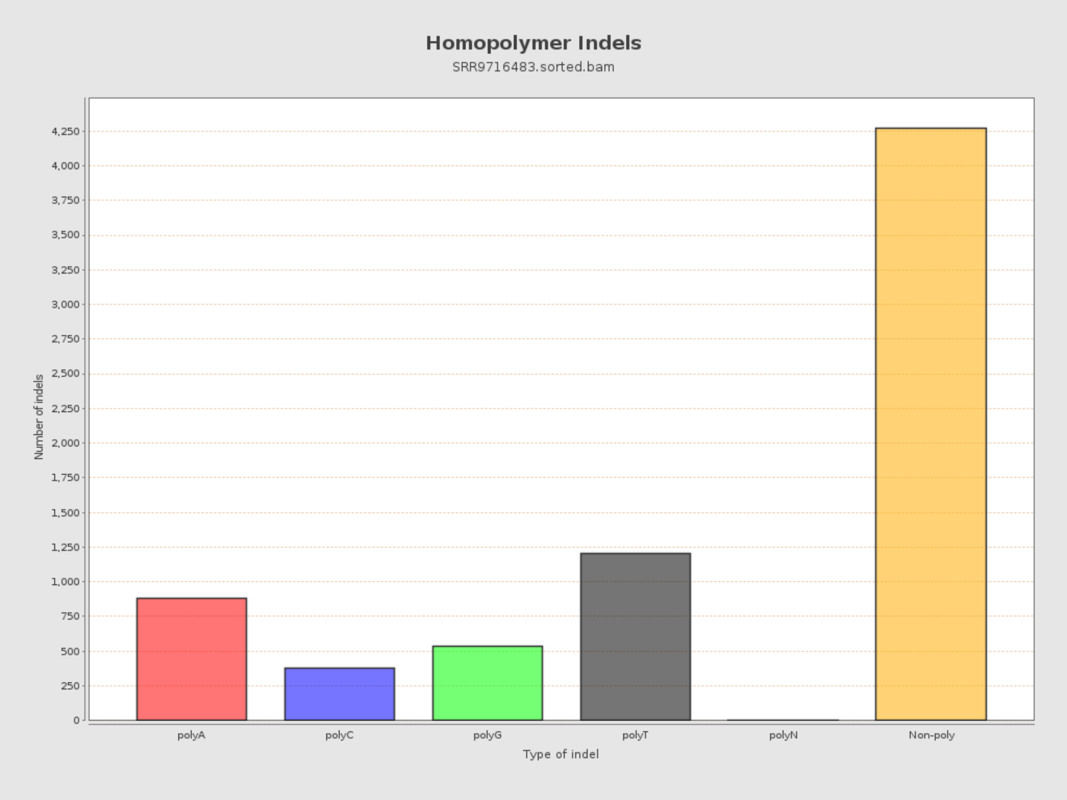
9. Results : Mapped Reads GC-content Distribution



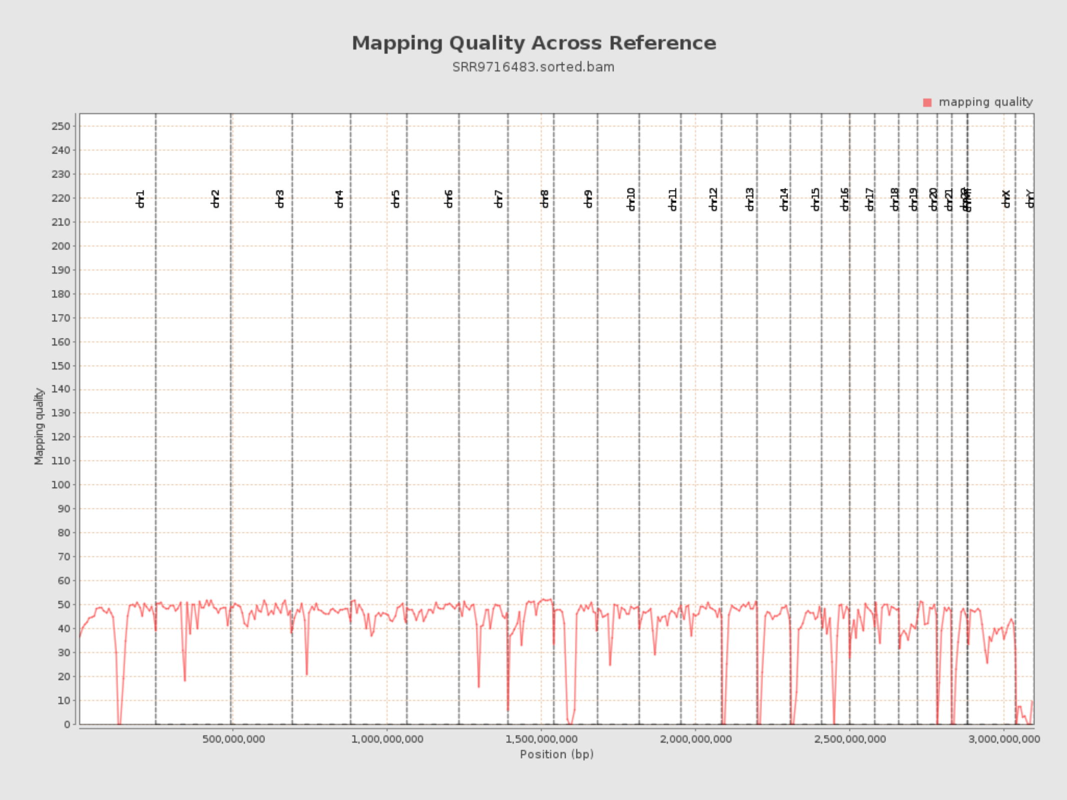
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram