Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 17:30:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716505.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_SRR9716505 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716505.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 17:30:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716505.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	547,475
Mapped reads	415,001 / 75.8%
Unmapped reads	132,474 / 24.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	773 / 0.14%
Read min/max/mean length	30 / 76 / 76.05
Duplicated reads (estimated)	7,373 / 1.35%
Duplication rate	1.32%
Clipped reads	414,649 / 75.74%

2.2. ACGT Content

Number/percentage of A's	5,586,557 / 23.41%
Number/percentage of C's	4,180,690 / 17.52%
Number/percentage of T's	8,000,424 / 33.53%
Number/percentage of G's	6,093,093 / 25.54%
Number/percentage of N's	227 / 0%
GC Percentage	43.06%

2.3. Coverage

Mean	0.0077

Standard Deviation	0.1041

2.4. Mapping Quality

Mean Mapping Quality	43.97

2.5. Mismatches and indels

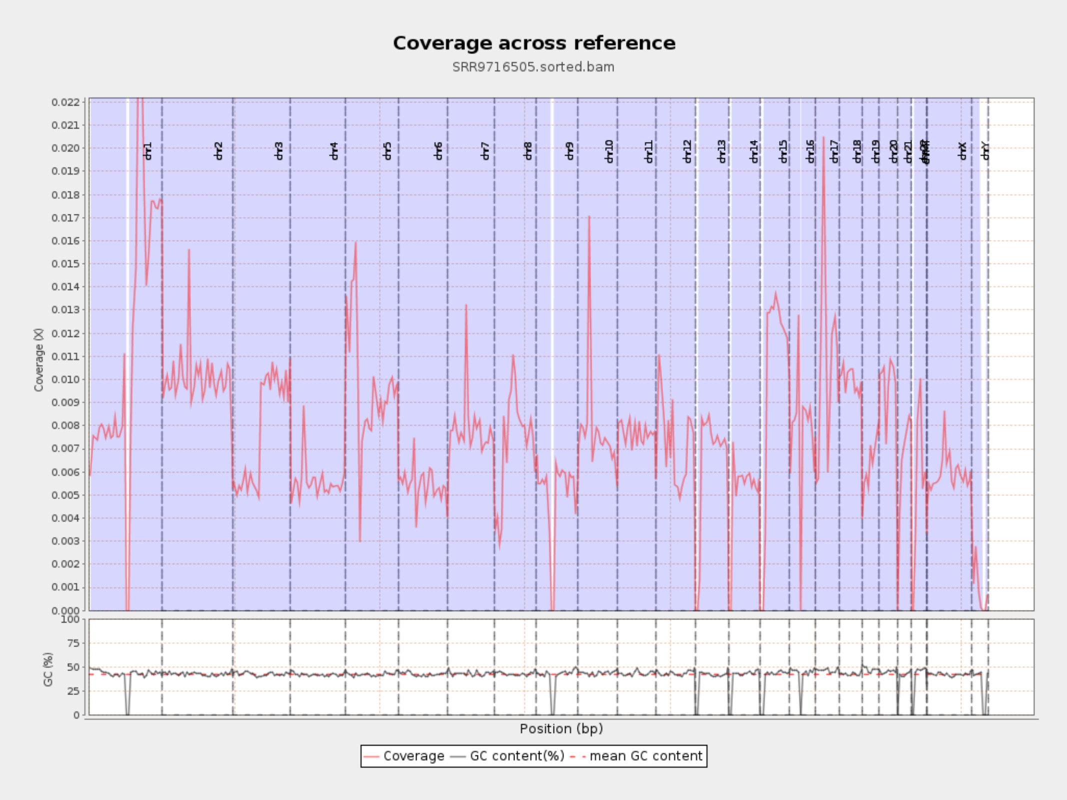
General error rate	0.51%
Mismatches	119,146
Insertions	1,532
Mapped reads with at least one insertion	0.37%
Deletions	4,788
Mapped reads with at least one deletion	1.15%
Homopolymer indels	43.56%

2.6. Chromosome stats

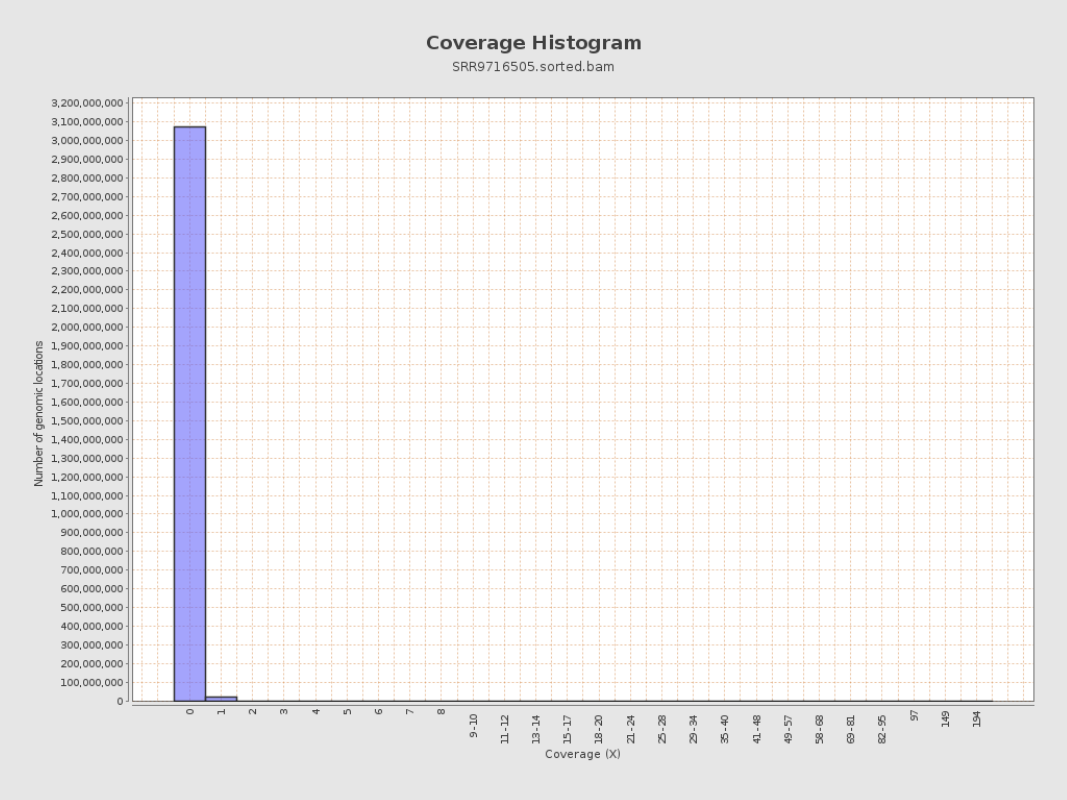
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2849576	0.0114	0.1369
chr2	243199373	2457838	0.0101	0.1385
chr3	198022430	1532522	0.0077	0.0919
chr4	191154276	1057040	0.0055	0.0781
chr5	180915260	1766340	0.0098	0.1019
chr6	171115067	931460	0.0054	0.0804
chr7	159138663	1255039	0.0079	0.1234

chr8	146364022	1065640	0.0073	0.0945
chr9	141213431	693251	0.0049	0.083
chr10	135534747	1065084	0.0079	0.1229
chr11	135006516	1032084	0.0076	0.1035
chr12	133851895	966184	0.0072	0.0876
chr13	115169878	727744	0.0063	0.082
chr14	107349540	535223	0.005	0.0741
chr15	102531392	1039988	0.0101	0.1041
chr16	90354753	696756	0.0077	0.0959
chr17	81195210	886755	0.0109	0.1104
chr18	78077248	780756	0.01	0.1483
chr19	59128983	376708	0.0064	0.1065
chr20	63025520	610997	0.0097	0.1012
chr21	48129895	304392	0.0063	0.0829
chr22	51304566	263602	0.0051	0.0738
chrMT	16571	55	0.0033	0.0575
chrX	155270560	917841	0.0059	0.086
chrY	59373566	55797	0.0009	0.0345

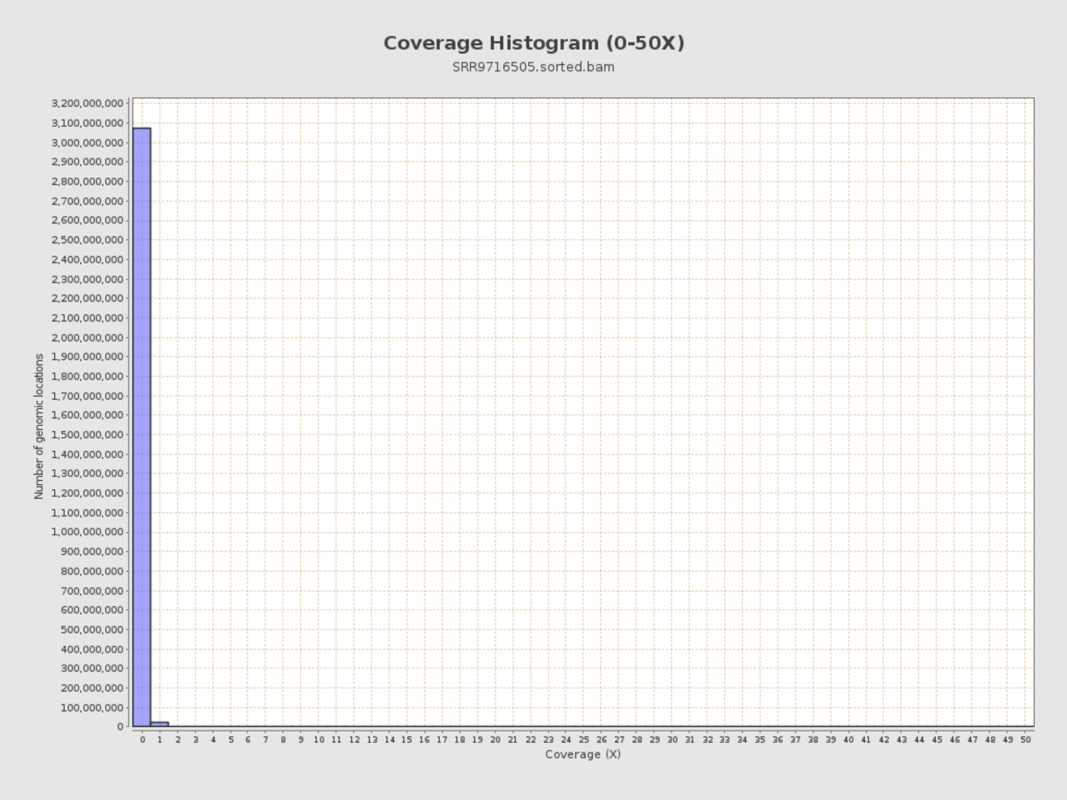
3. Results : Coverage across reference



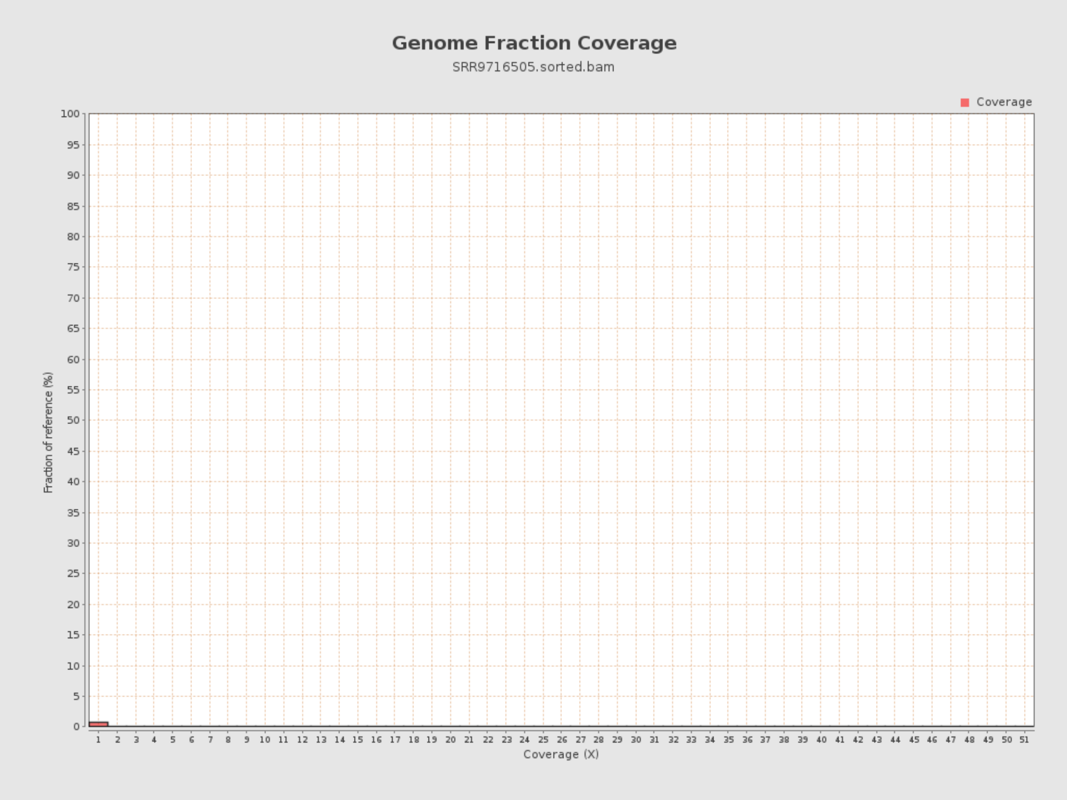
4. Results : Coverage Histogram



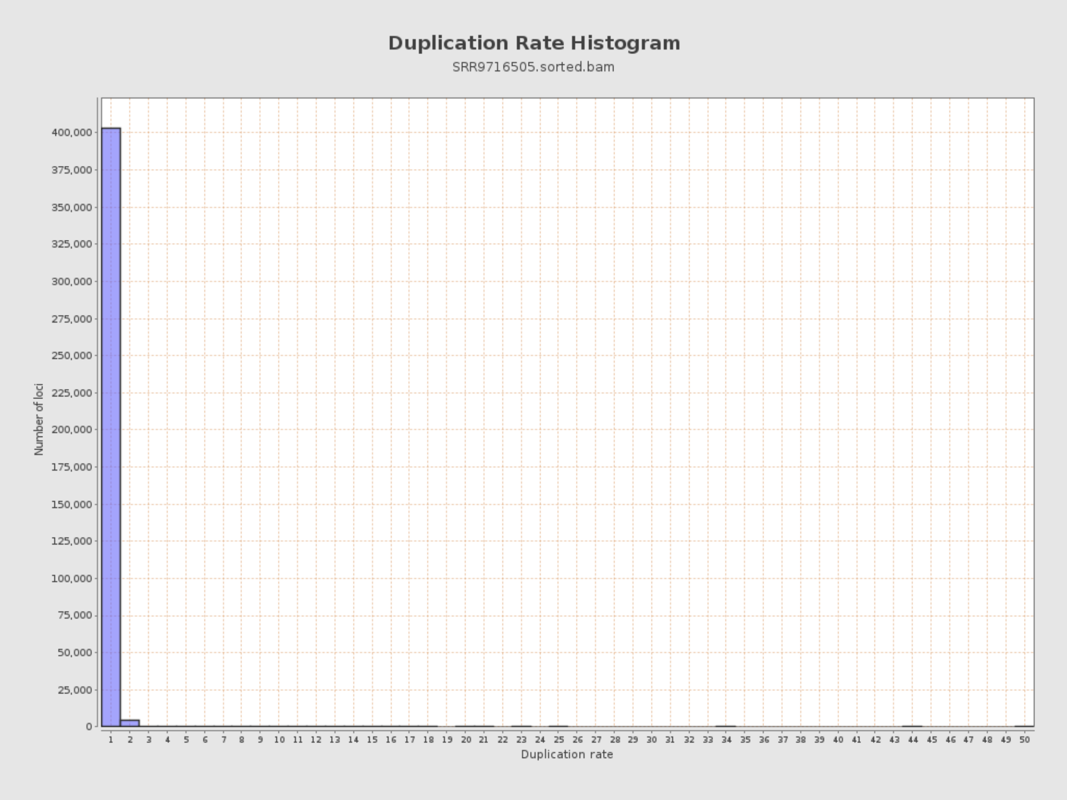
5. Results : Coverage Histogram (0-50X)



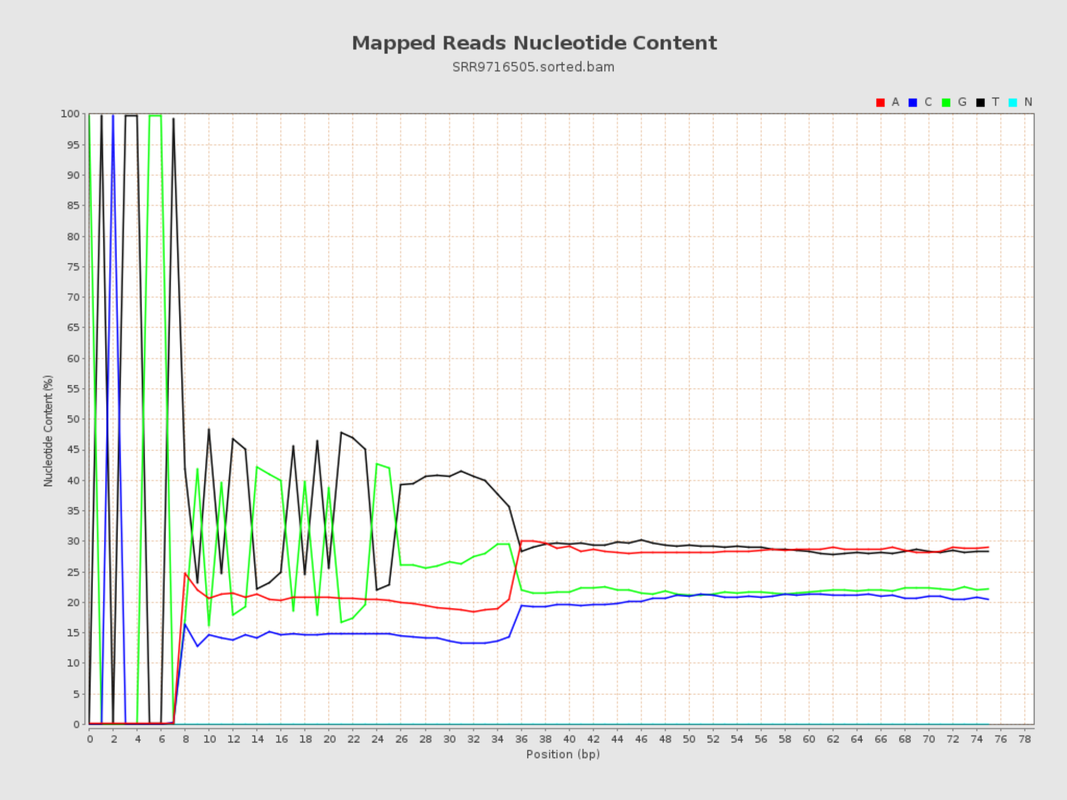
6. Results : Genome Fraction Coverage



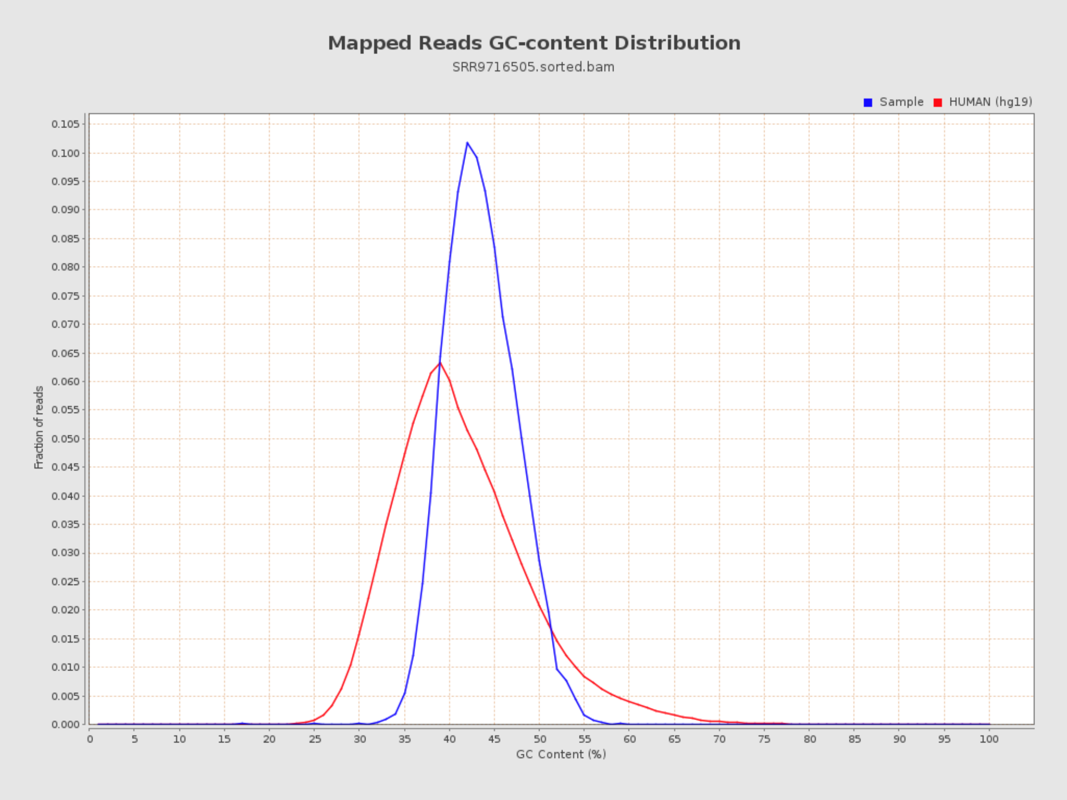
7. Results : Duplication Rate Histogram



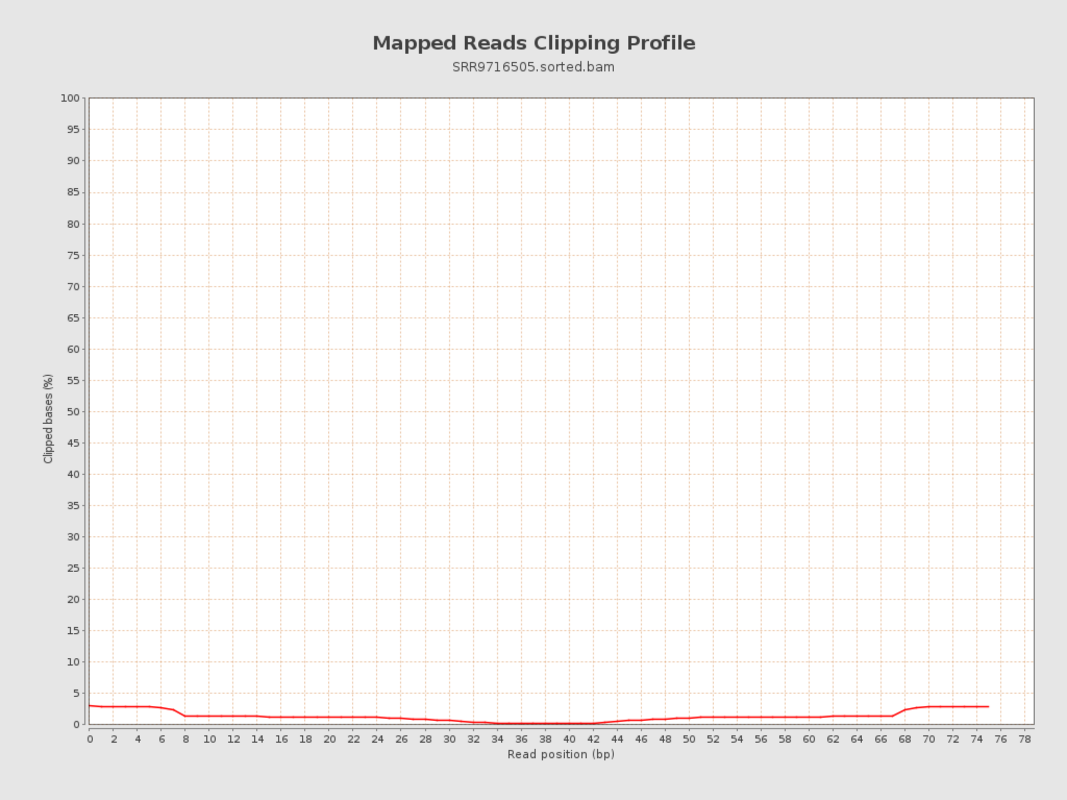
8. Results : Mapped Reads Nucleotide Content



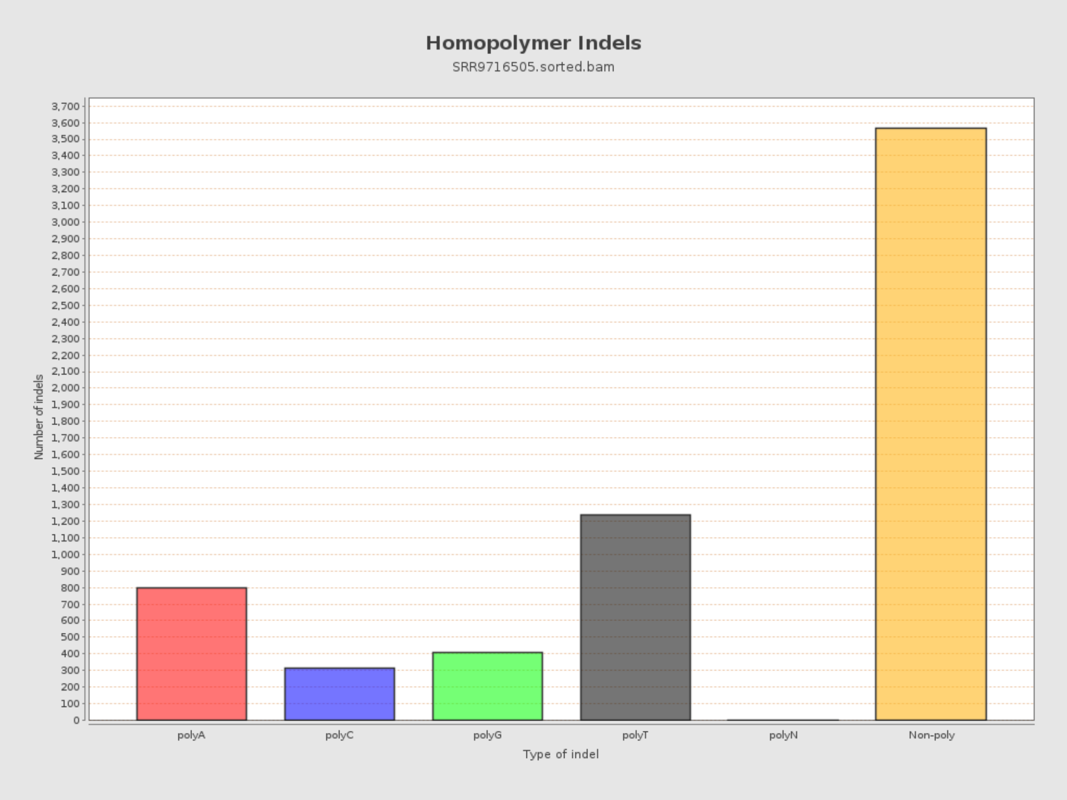
9. Results : Mapped Reads GC-content Distribution



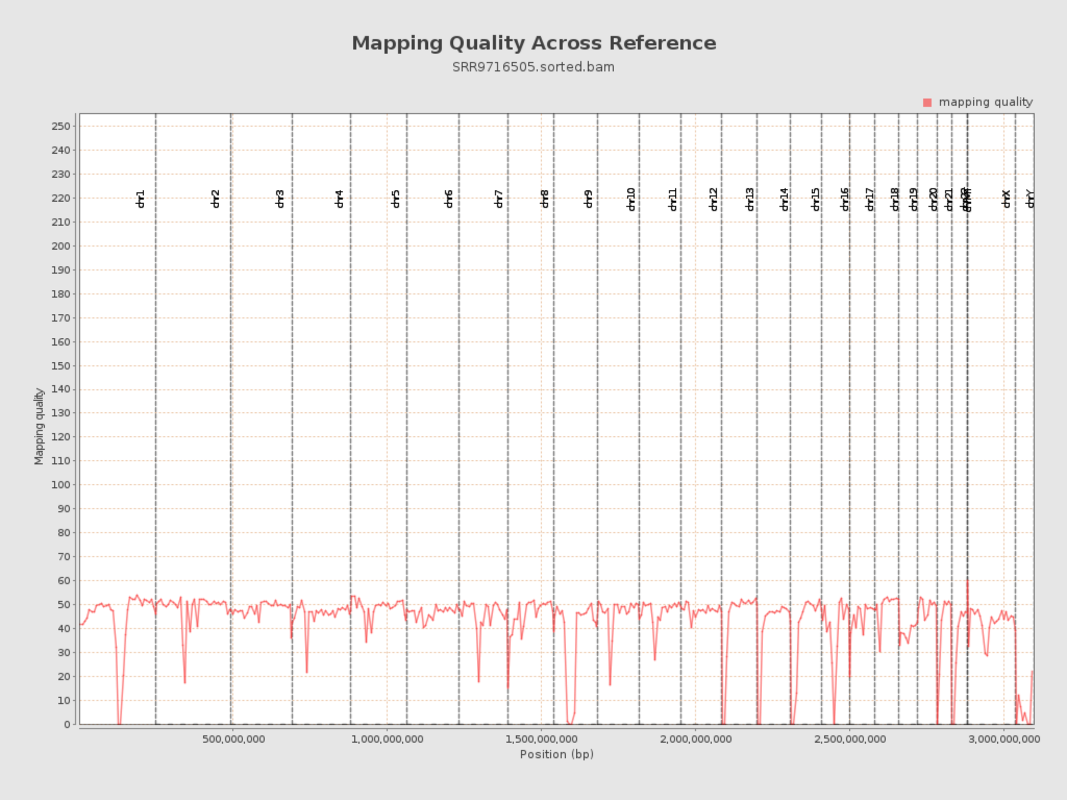
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram