Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 19:55:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716150.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_SRR9716150 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716150.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 19:55:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716150.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	680,917
Mapped reads	499,868 / 73.41%
Unmapped reads	181,049 / 26.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	529 / 0.08%
Read min/max/mean length	30 / 76 / 76.03
Duplicated reads (estimated)	24,866 / 3.65%
Duplication rate	4.41%
Clipped reads	499,339 / 73.33%

2.2. ACGT Content

Number/percentage of A's	5,331,710 / 20.42%
Number/percentage of C's	5,018,449 / 19.22%
Number/percentage of T's	8,760,633 / 33.55%
Number/percentage of G's	7,003,565 / 26.82%
Number/percentage of N's	421 / 0%
GC Percentage	46.04%

2.3. Coverage

Mean	0.0084

Standard Deviation	0.1078

2.4. Mapping Quality

Mean Mapping Quality	42.98

2.5. Mismatches and indels

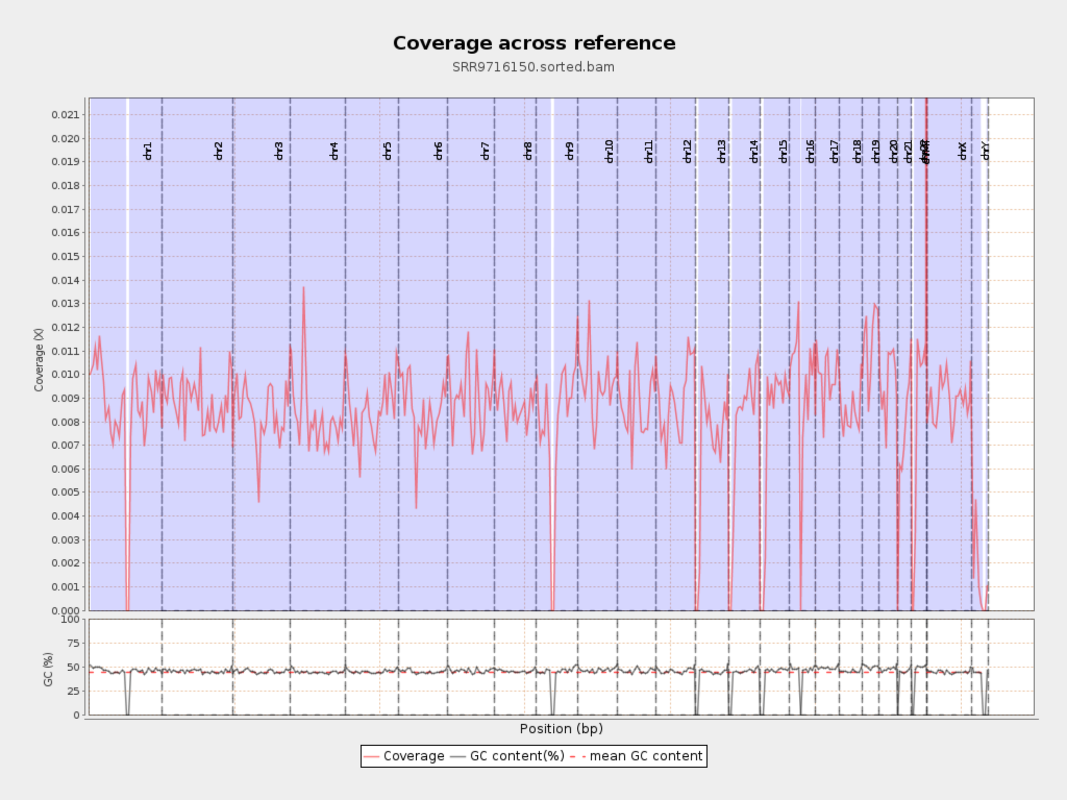
General error rate	0.7%
Mismatches	178,642
Insertions	1,639
Mapped reads with at least one insertion	0.33%
Deletions	4,169
Mapped reads with at least one deletion	0.83%
Homopolymer indels	40.81%

2.6. Chromosome stats

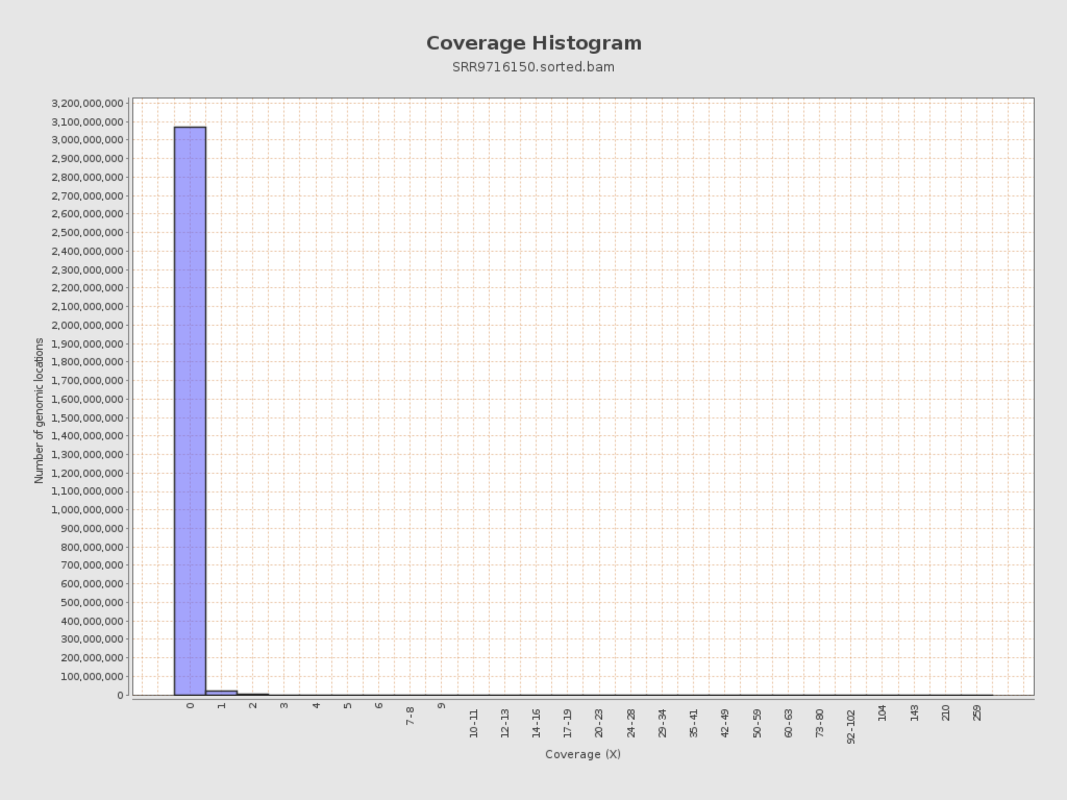
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2114422	0.0085	0.1085
chr2	243199373	2160346	0.0089	0.1481
chr3	198022430	1650619	0.0083	0.0995
chr4	191154276	1572591	0.0082	0.101
chr5	180915260	1533281	0.0085	0.0999
chr6	171115067	1457407	0.0085	0.1084
chr7	159138663	1418536	0.0089	0.1134

chr8	146364022	1278318	0.0087	0.1032
chr9	141213431	1085059	0.0077	0.0988
chr10	135534747	1292618	0.0095	0.1133
chr11	135006516	1188946	0.0088	0.1059
chr12	133851895	1191925	0.0089	0.1032
chr13	115169878	780203	0.0068	0.0899
chr14	107349540	813718	0.0076	0.0951
chr15	102531392	771728	0.0075	0.0945
chr16	90354753	858977	0.0095	0.1116
chr17	81195210	812660	0.01	0.1108
chr18	78077248	653965	0.0084	0.1079
chr19	59128983	674176	0.0114	0.1286
chr20	63025520	608775	0.0097	0.1086
chr21	48129895	348150	0.0072	0.098
chr22	51304566	382296	0.0075	0.0957
chrMT	16571	1927	0.1163	0.3659
chrX	155270560	1381514	0.0089	0.1029
chrY	59373566	89718	0.0015	0.0506

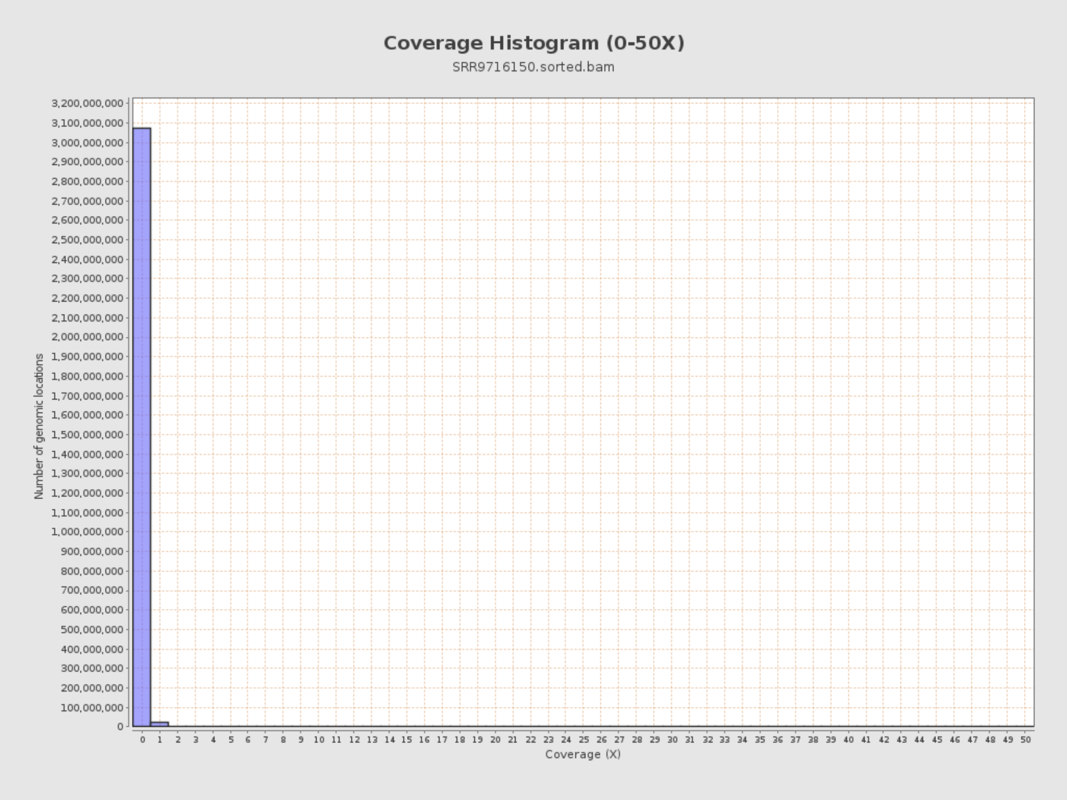
3. Results : Coverage across reference



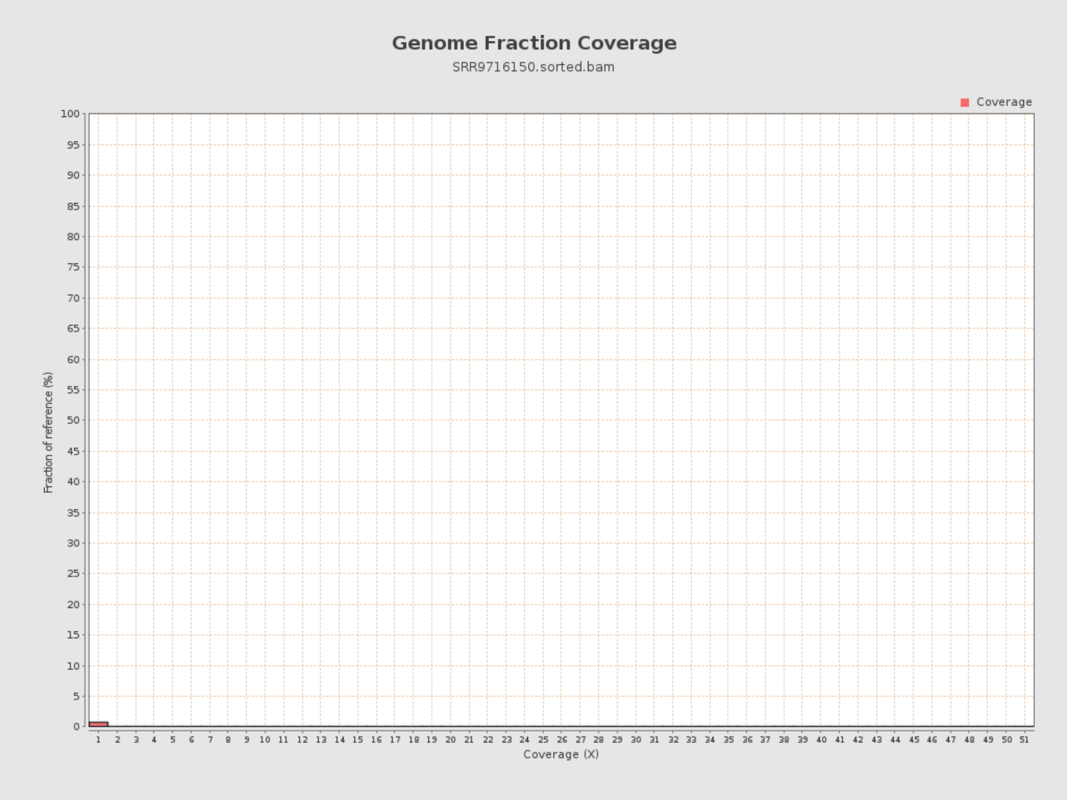
4. Results : Coverage Histogram



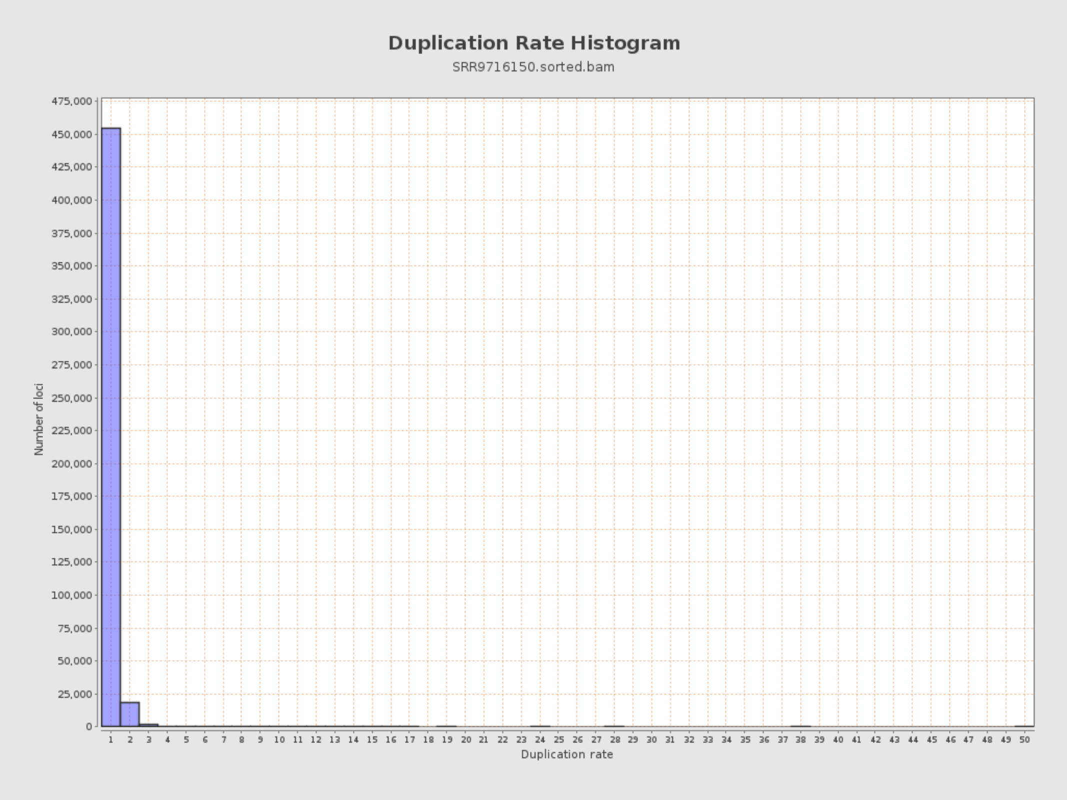
5. Results : Coverage Histogram (0-50X)



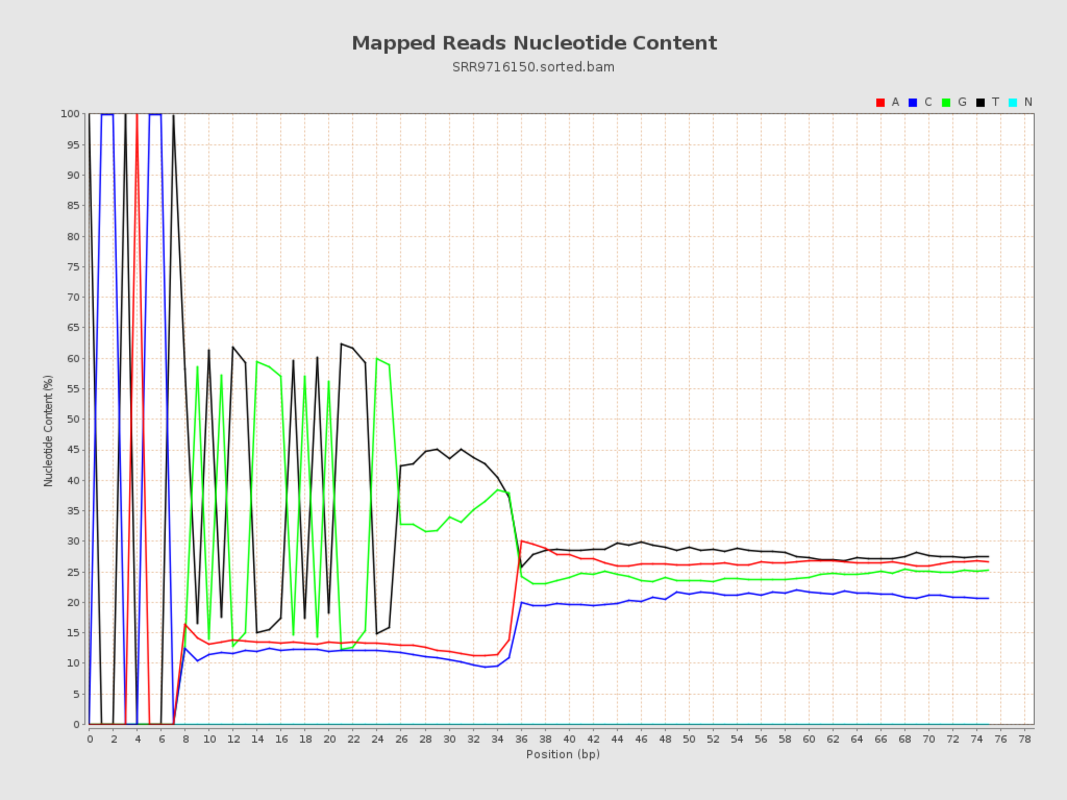
6. Results : Genome Fraction Coverage



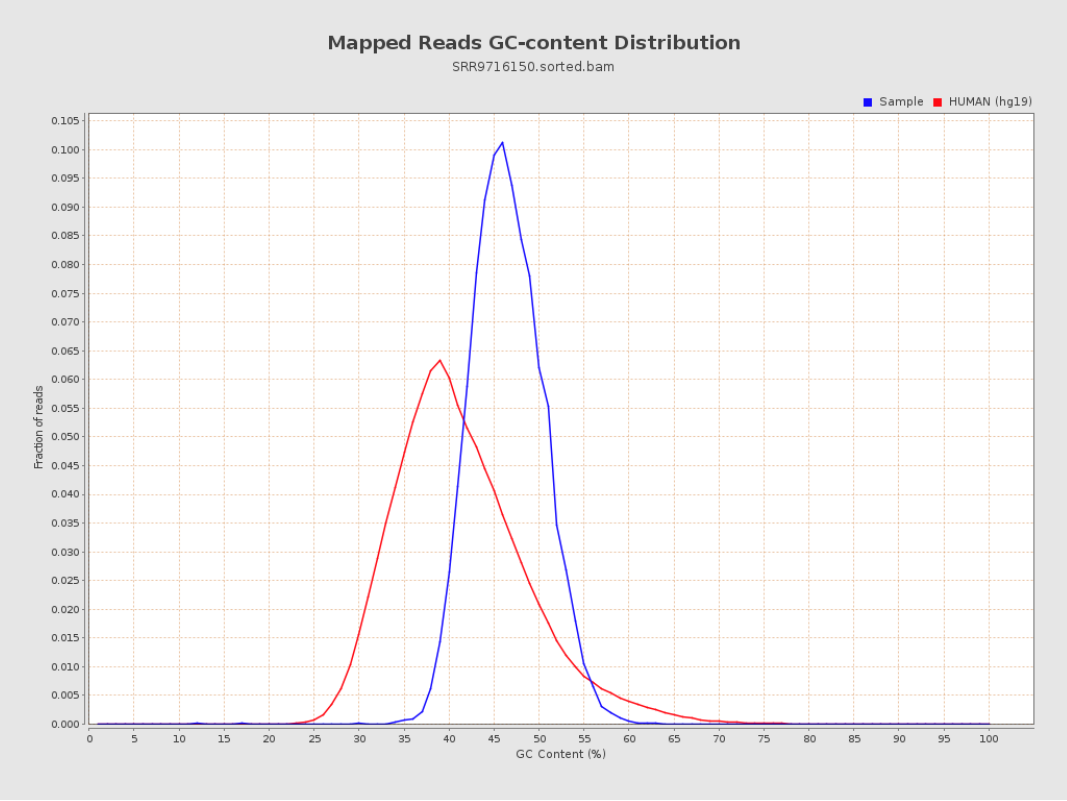
7. Results : Duplication Rate Histogram



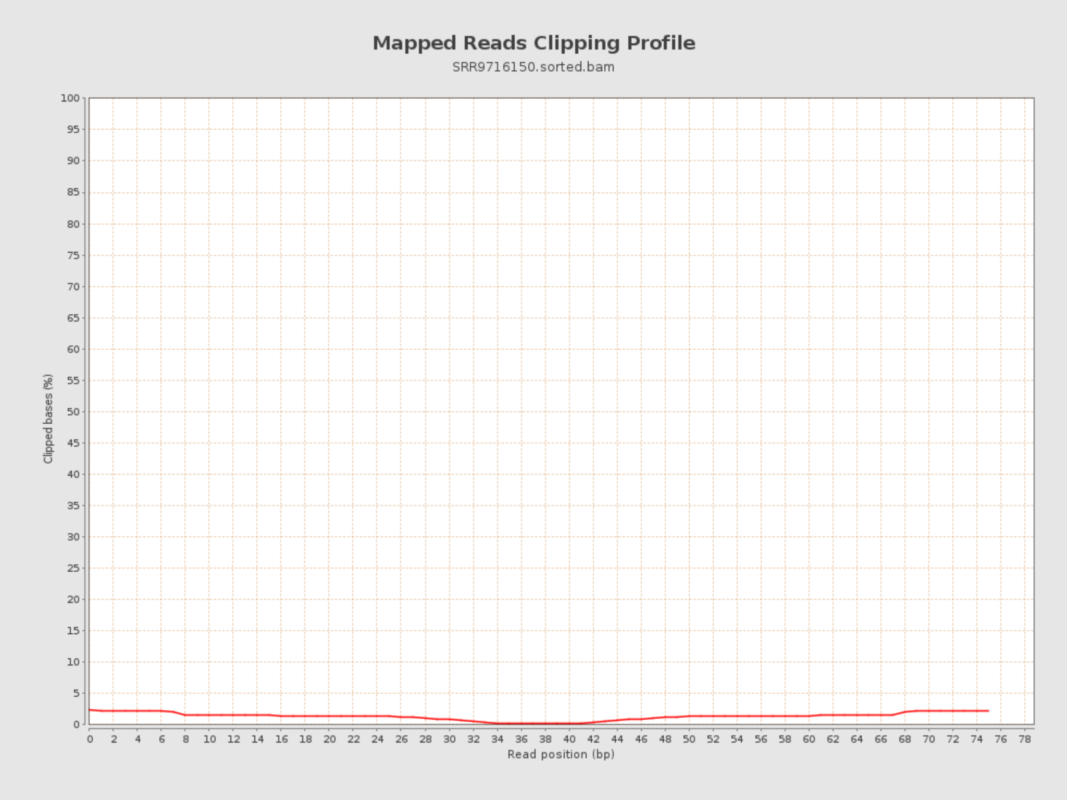
8. Results : Mapped Reads Nucleotide Content



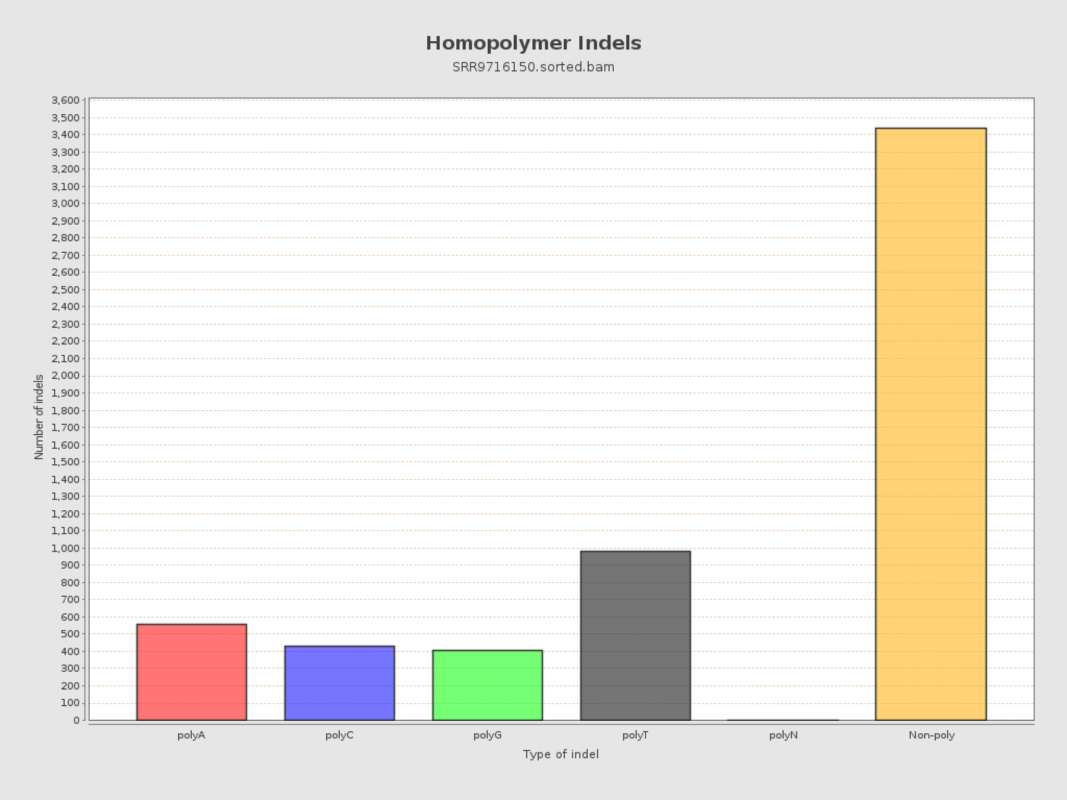
9. Results : Mapped Reads GC-content Distribution



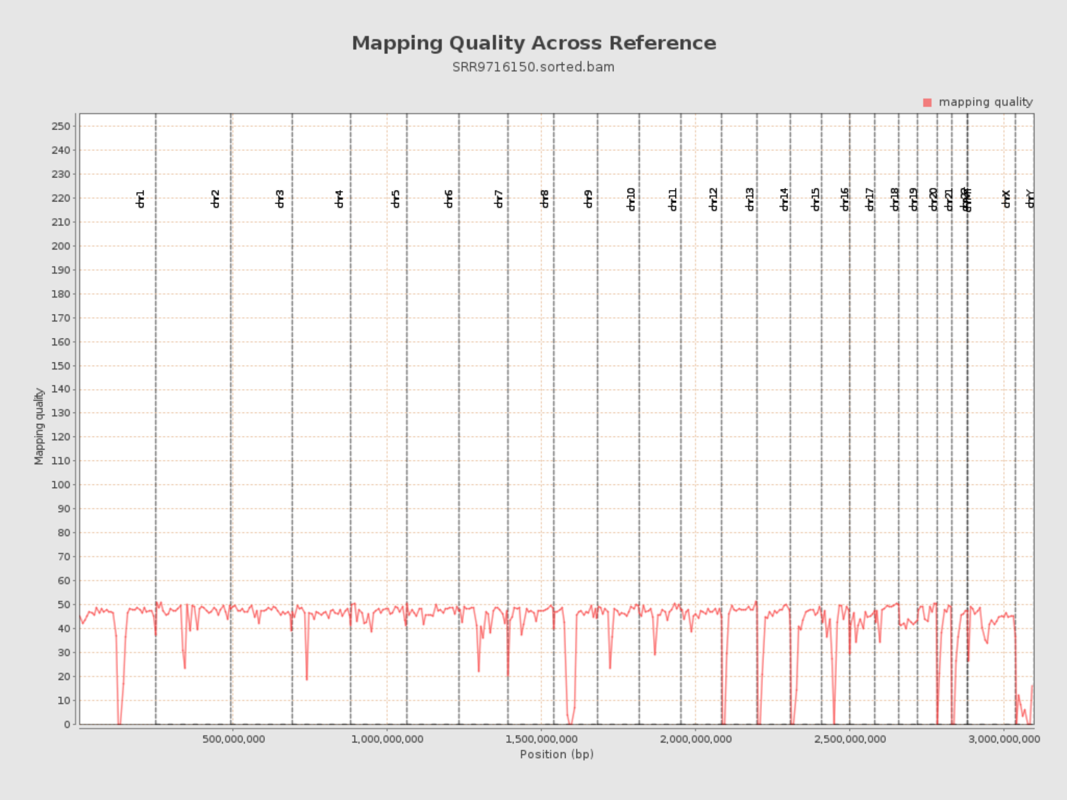
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram