Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 23:03:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716190.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_SRR9716190 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716190.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 23:03:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716190.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,732,823
Mapped reads	1,529,781 / 88.28%
Unmapped reads	203,042 / 11.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,439 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	37,884 / 2.19%
Duplication rate	1.69%
Clipped reads	1,531,531 / 88.38%

2.2. ACGT Content

Number/percentage of A's	21,744,807 / 24.99%
Number/percentage of C's	16,122,788 / 18.53%
Number/percentage of T's	26,837,101 / 30.84%
Number/percentage of G's	22,304,675 / 25.63%
Number/percentage of N's	678 / 0%
GC Percentage	44.16%

2.3. Coverage

Mean	0.0281

Standard Deviation	0.239

2.4. Mapping Quality

Mean Mapping Quality	42.1

2.5. Mismatches and indels

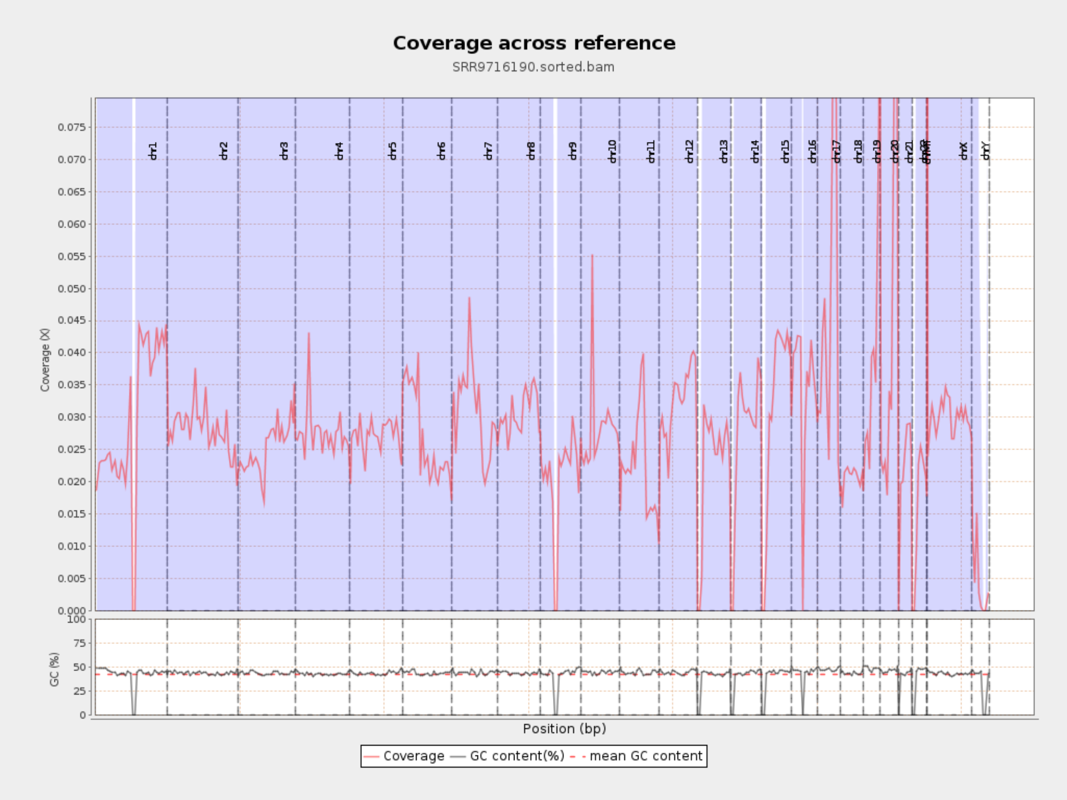
General error rate	0.54%
Mismatches	455,143
Insertions	6,050
Mapped reads with at least one insertion	0.39%
Deletions	16,966
Mapped reads with at least one deletion	1.1%
Homopolymer indels	40.56%

2.6. Chromosome stats

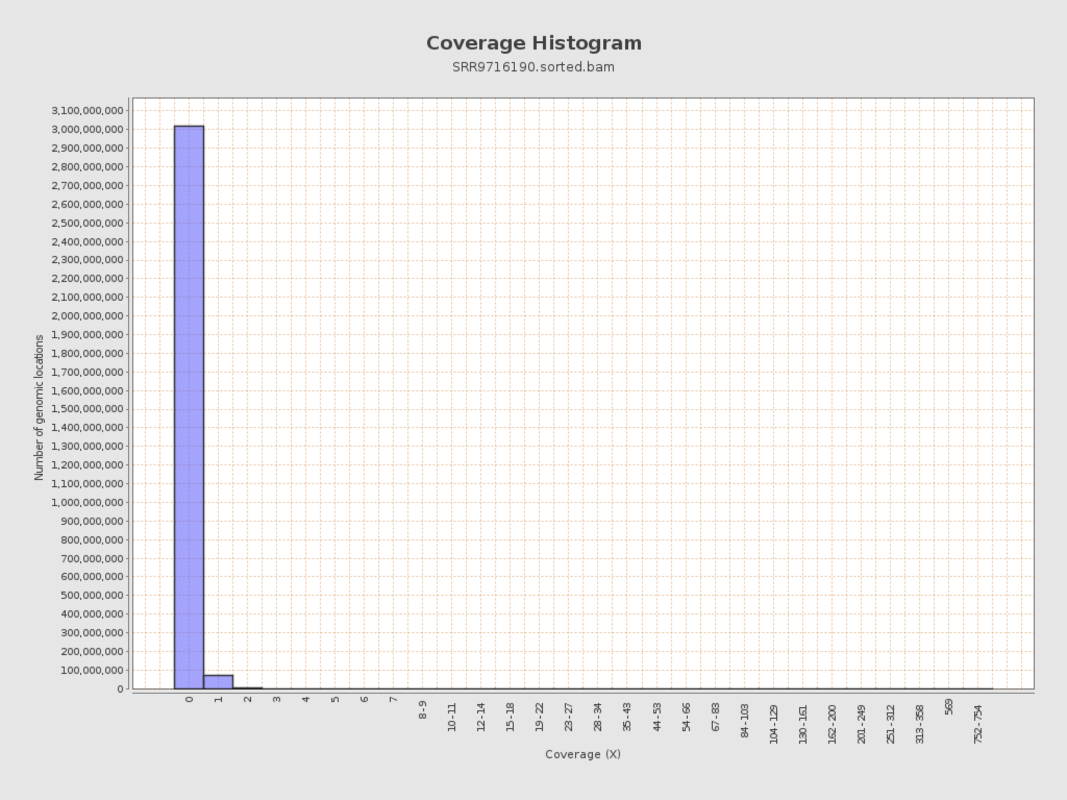
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7357741	0.0295	0.3052
chr2	243199373	6848634	0.0282	0.355
chr3	198022430	4990577	0.0252	0.1756
chr4	191154276	5301000	0.0277	0.1941
chr5	180915260	4952275	0.0274	0.1781
chr6	171115067	4633039	0.0271	0.2091
chr7	159138663	4963863	0.0312	0.3239

chr8	146364022	4492503	0.0307	0.2334
chr9	141213431	2887444	0.0204	0.1793
chr10	135534747	3836713	0.0283	0.2968
chr11	135006516	3065491	0.0227	0.2024
chr12	133851895	4354467	0.0325	0.1964
chr13	115169878	2612109	0.0227	0.1637
chr14	107349540	2937870	0.0274	0.1889
chr15	102531392	3209455	0.0313	0.1945
chr16	90354753	3063673	0.0339	0.214
chr17	81195210	3909603	0.0482	0.2494
chr18	78077248	1610321	0.0206	0.2718
chr19	59128983	2366347	0.04	0.2999
chr20	63025520	2786091	0.0442	0.2392
chr21	48129895	1067870	0.0222	0.1708
chr22	51304566	824149	0.0161	0.1382
chrMT	16571	39887	2.407	2.1842
chrX	155270560	4666938	0.0301	0.1999
chrY	59373566	258905	0.0044	0.1277

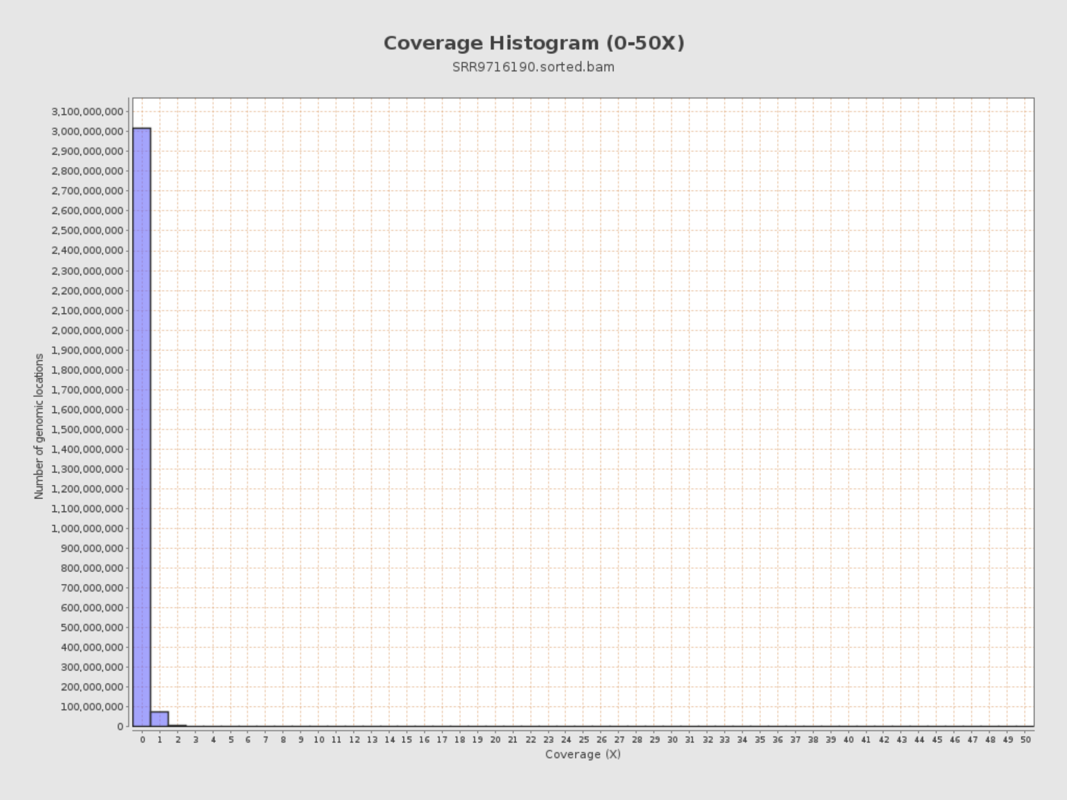
3. Results : Coverage across reference



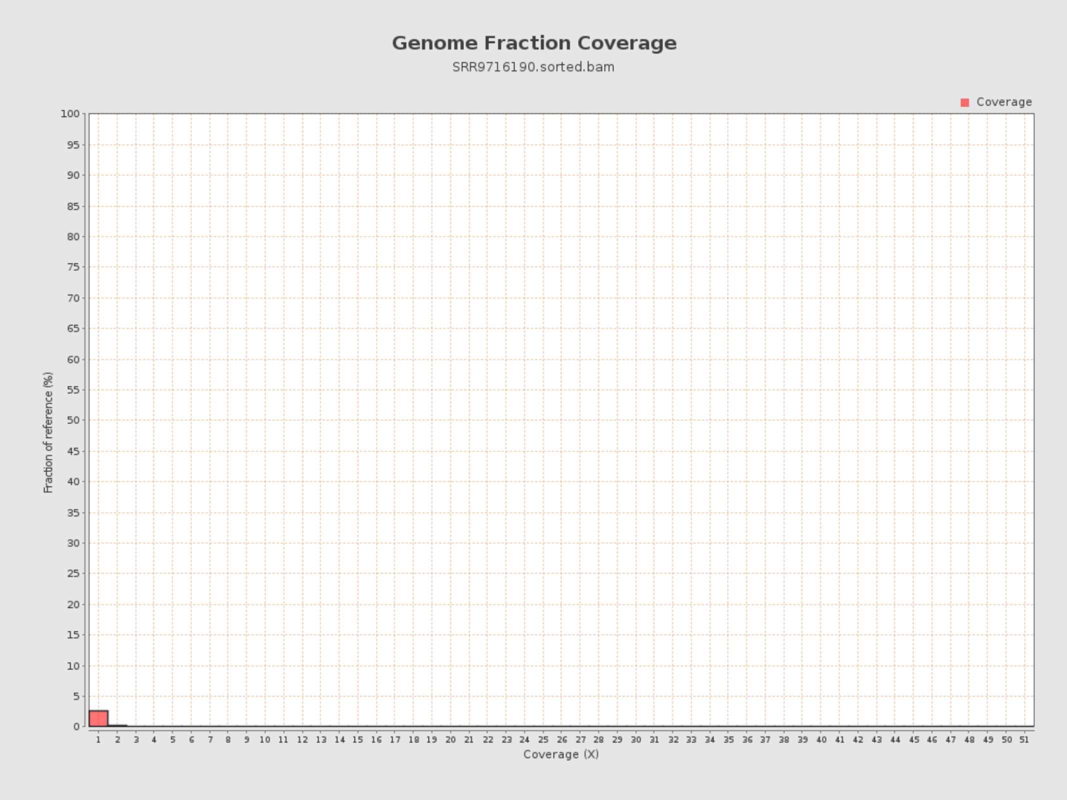
4. Results : Coverage Histogram



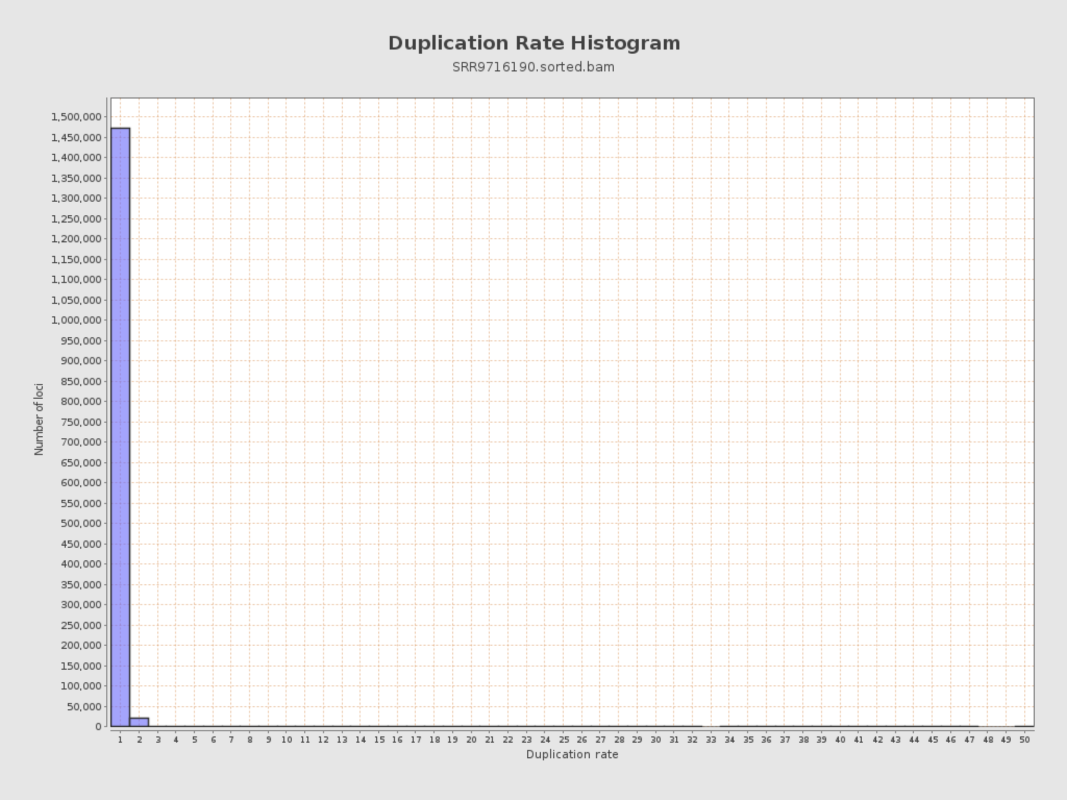
5. Results : Coverage Histogram (0-50X)



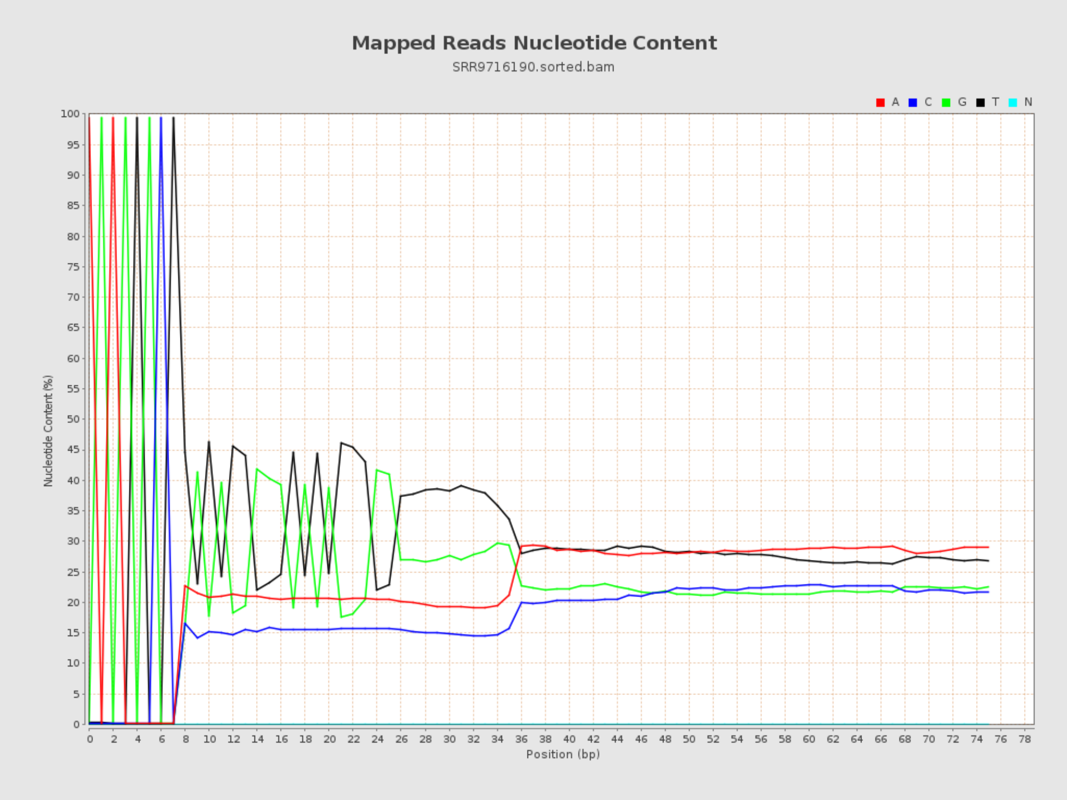
6. Results : Genome Fraction Coverage



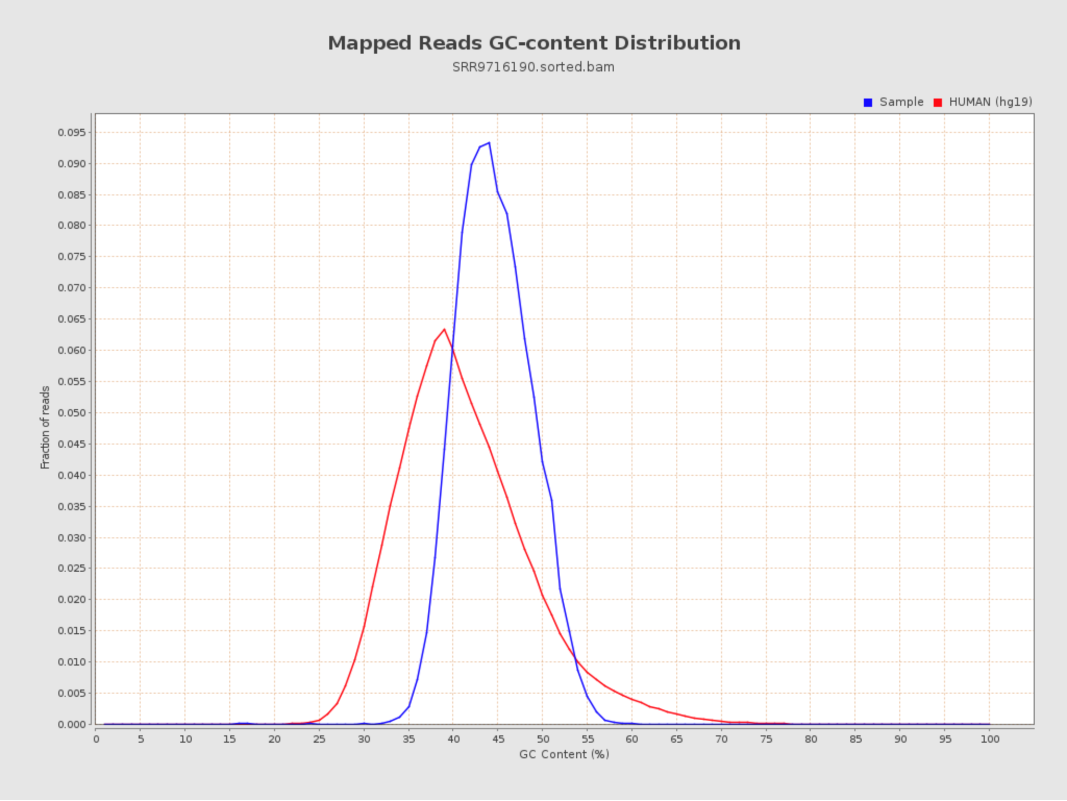
7. Results : Duplication Rate Histogram



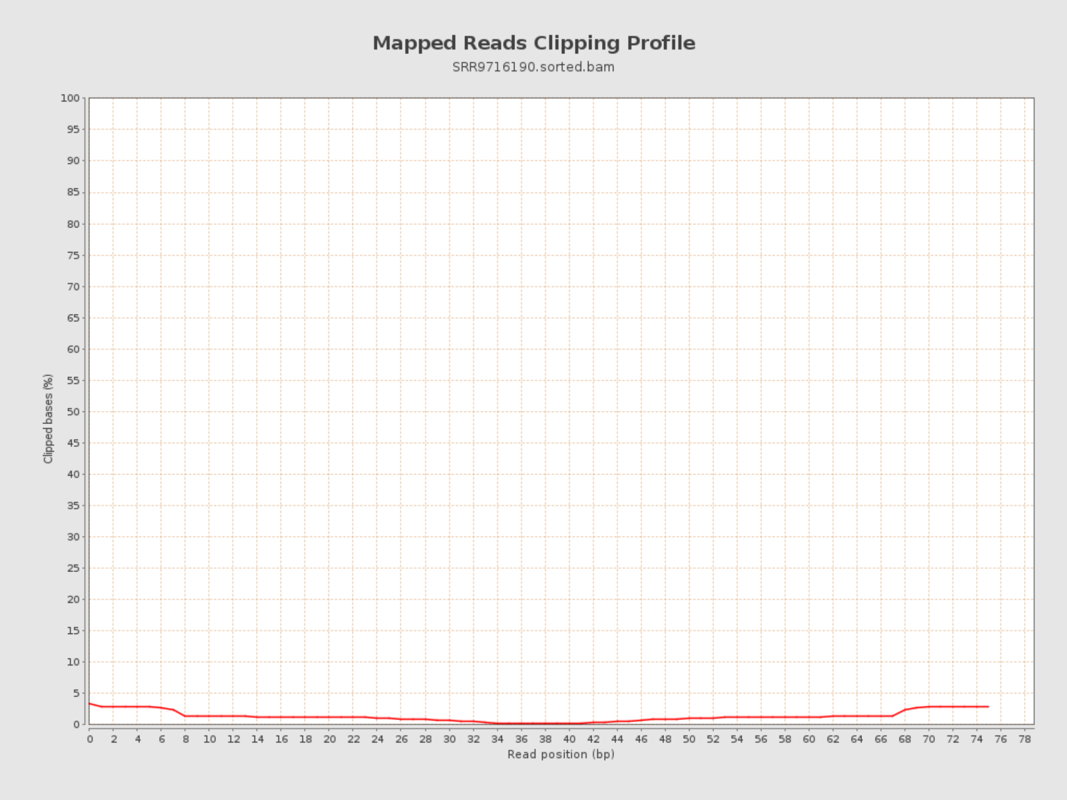
8. Results : Mapped Reads Nucleotide Content



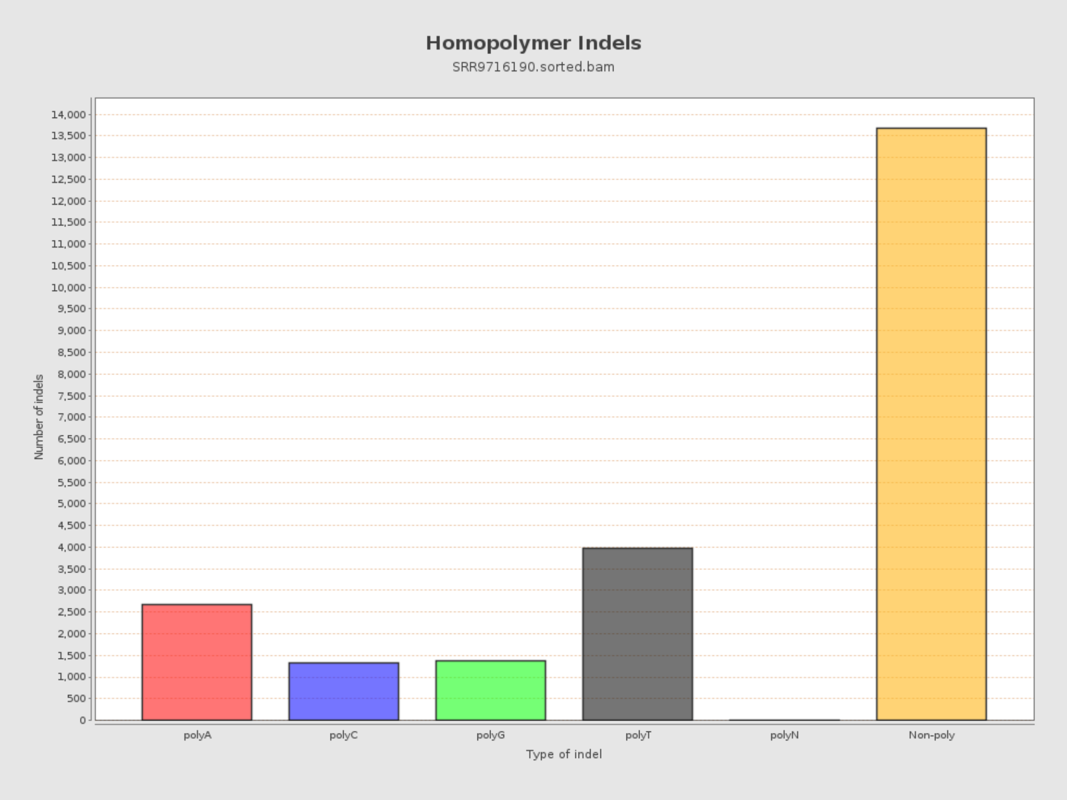
9. Results : Mapped Reads GC-content Distribution



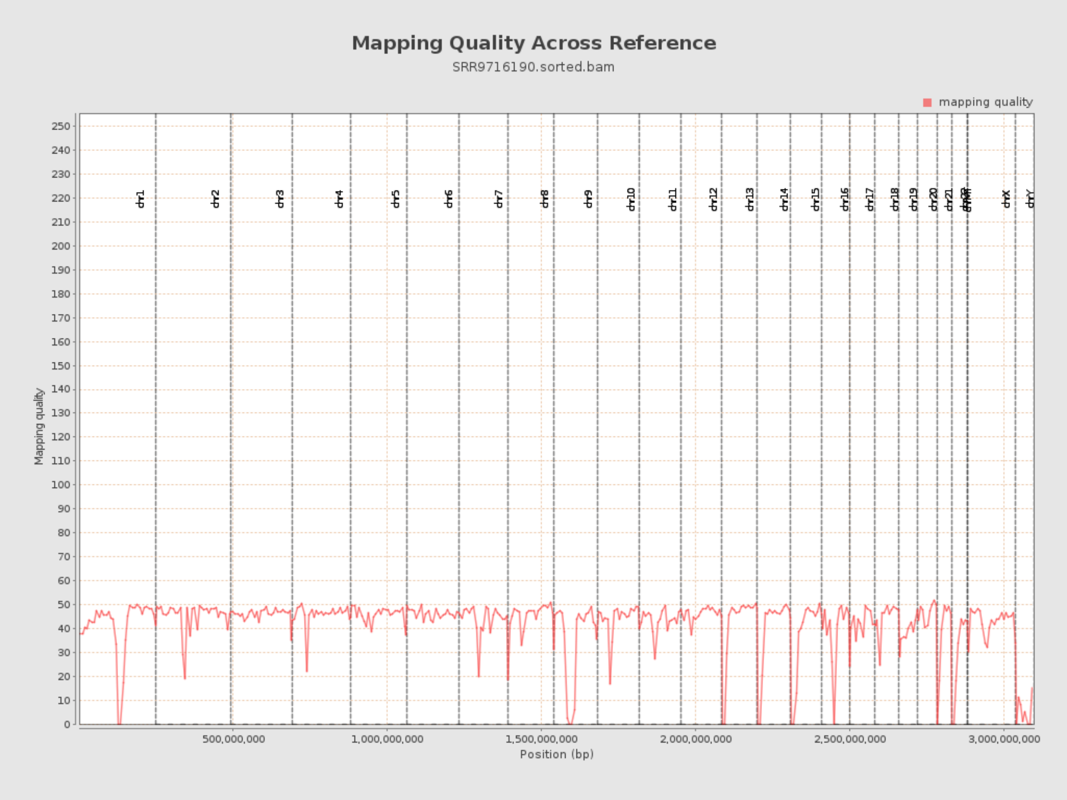
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram