Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 08:55:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716357.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_SRR9716357 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716357.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 08:55:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716357.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,531,959
Mapped reads	1,385,030 / 90.41%
Unmapped reads	146,929 / 9.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,930 / 0.52%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	63,462 / 4.14%
Duplication rate	3.66%
Clipped reads	1,389,717 / 90.72%

2.2. ACGT Content

Number/percentage of A's	20,623,215 / 25.7%
Number/percentage of C's	16,070,704 / 20.03%
Number/percentage of T's	24,625,288 / 30.69%
Number/percentage of G's	18,930,869 / 23.59%
Number/percentage of N's	571 / 0%
GC Percentage	43.62%

2.3. Coverage

Mean	0.0259

Standard Deviation	0.2402

2.4. Mapping Quality

Mean Mapping Quality	44.7

2.5. Mismatches and indels

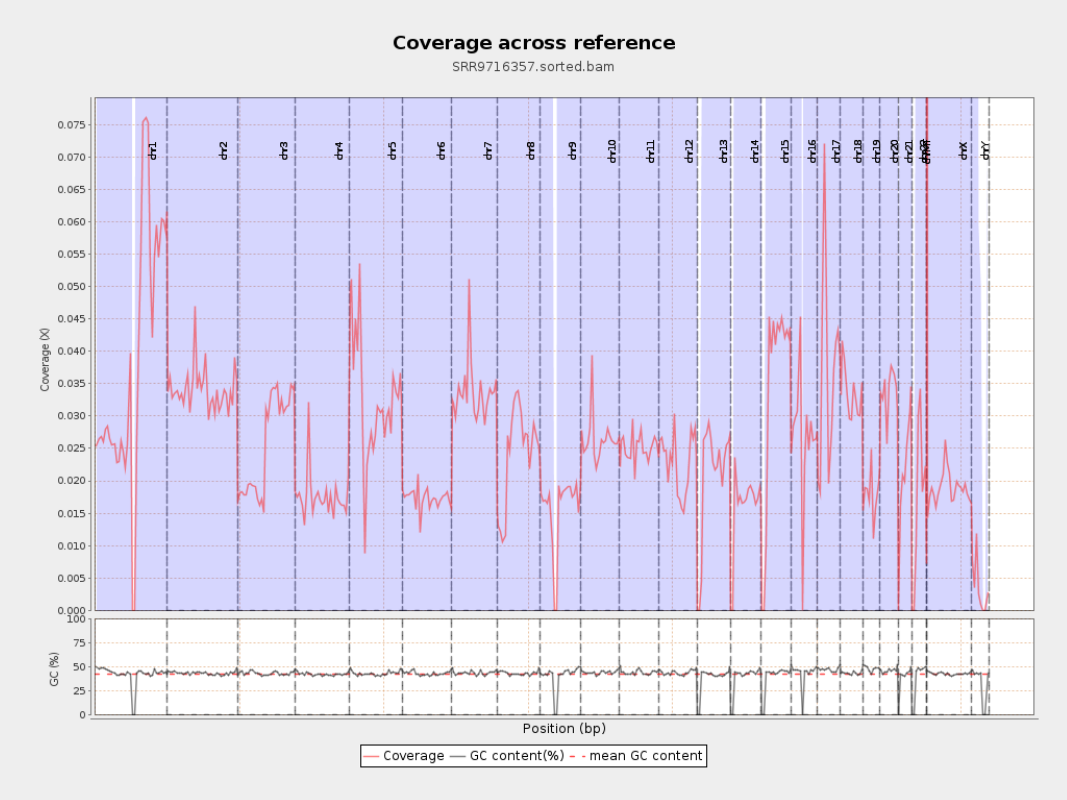
General error rate	0.51%
Mismatches	397,807
Insertions	5,238
Mapped reads with at least one insertion	0.38%
Deletions	14,417
Mapped reads with at least one deletion	1.03%
Homopolymer indels	42.54%

2.6. Chromosome stats

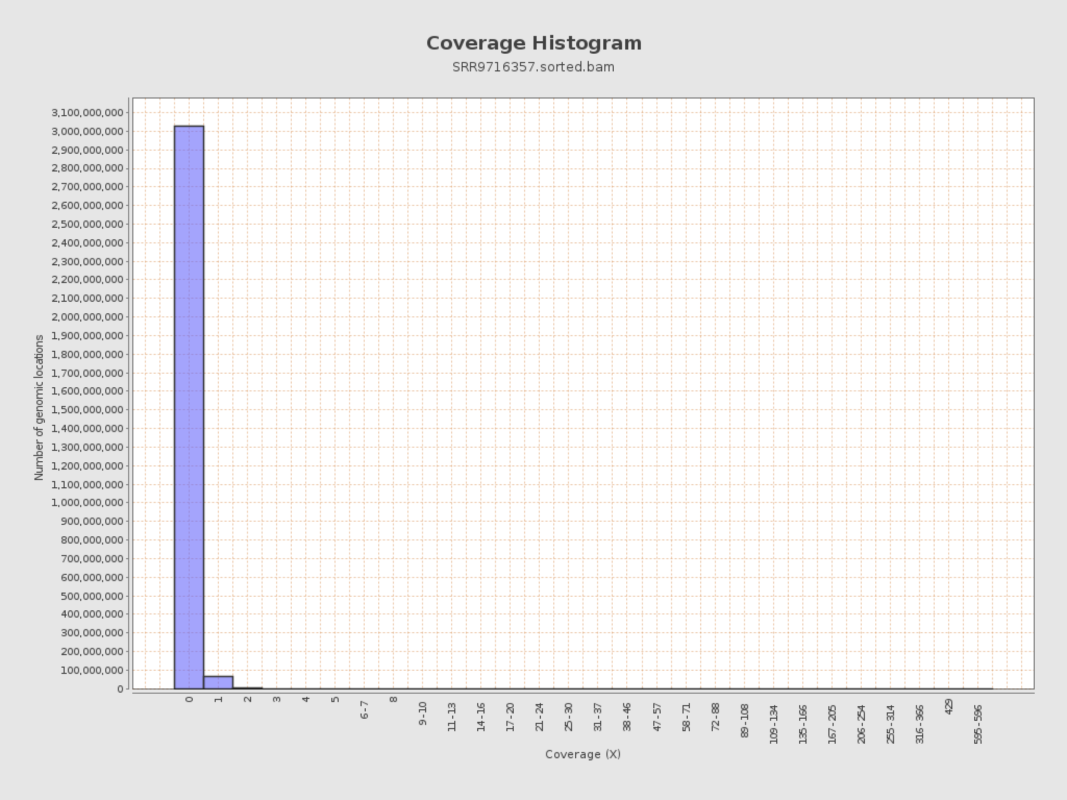
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9508944	0.0382	0.3752
chr2	243199373	8282524	0.0341	0.3377
chr3	198022430	5049568	0.0255	0.177
chr4	191154276	3367266	0.0176	0.1706
chr5	180915260	5879633	0.0325	0.2013
chr6	171115067	2955506	0.0173	0.1609
chr7	159138663	5373502	0.0338	0.3621

chr8	146364022	3587622	0.0245	0.2341
chr9	141213431	2197460	0.0156	0.1754
chr10	135534747	3599894	0.0266	0.2238
chr11	135006516	3397939	0.0252	0.2137
chr12	133851895	3039641	0.0227	0.1688
chr13	115169878	2372321	0.0206	0.1605
chr14	107349540	1696373	0.0158	0.1452
chr15	102531392	3543047	0.0346	0.2073
chr16	90354753	2404462	0.0266	0.1872
chr17	81195210	3061179	0.0377	0.232
chr18	78077248	2619457	0.0335	0.3586
chr19	59128983	1064981	0.018	0.2741
chr20	63025520	2131698	0.0338	0.2081
chr21	48129895	1044071	0.0217	0.1796
chr22	51304566	905743	0.0177	0.1468
chrMT	16571	43570	2.6293	2.1772
chrX	155270560	2940917	0.0189	0.1668
chrY	59373566	205904	0.0035	0.0972

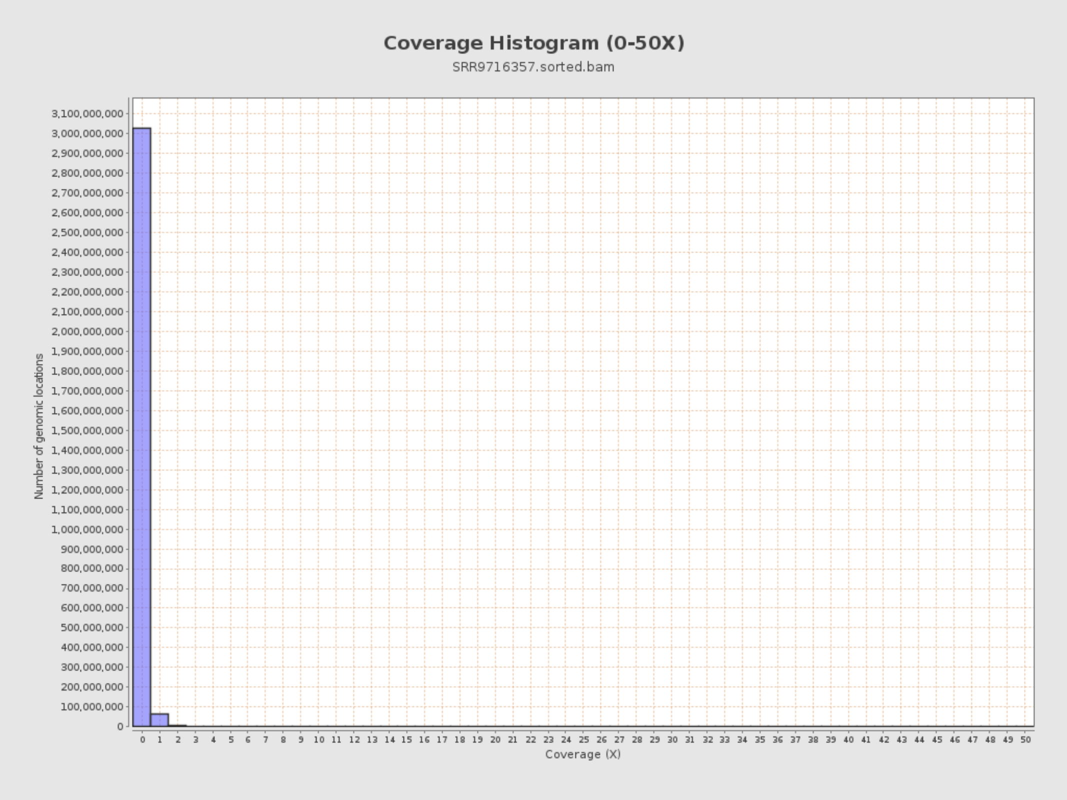
3. Results : Coverage across reference



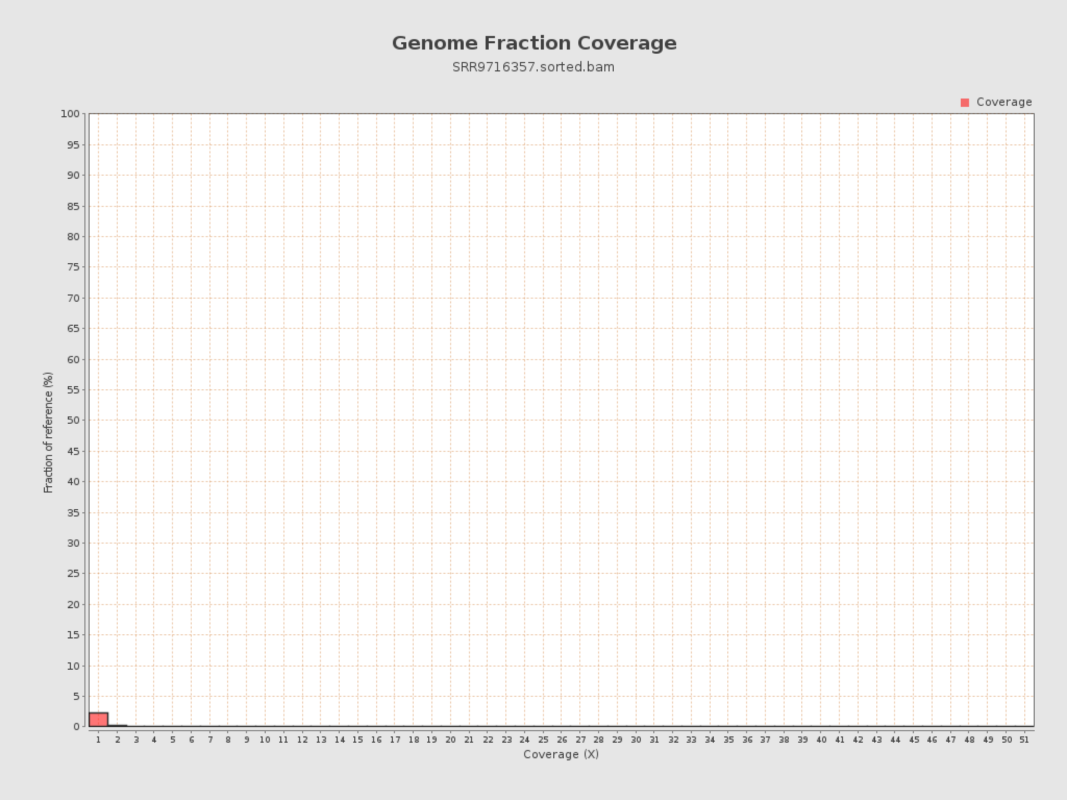
4. Results : Coverage Histogram



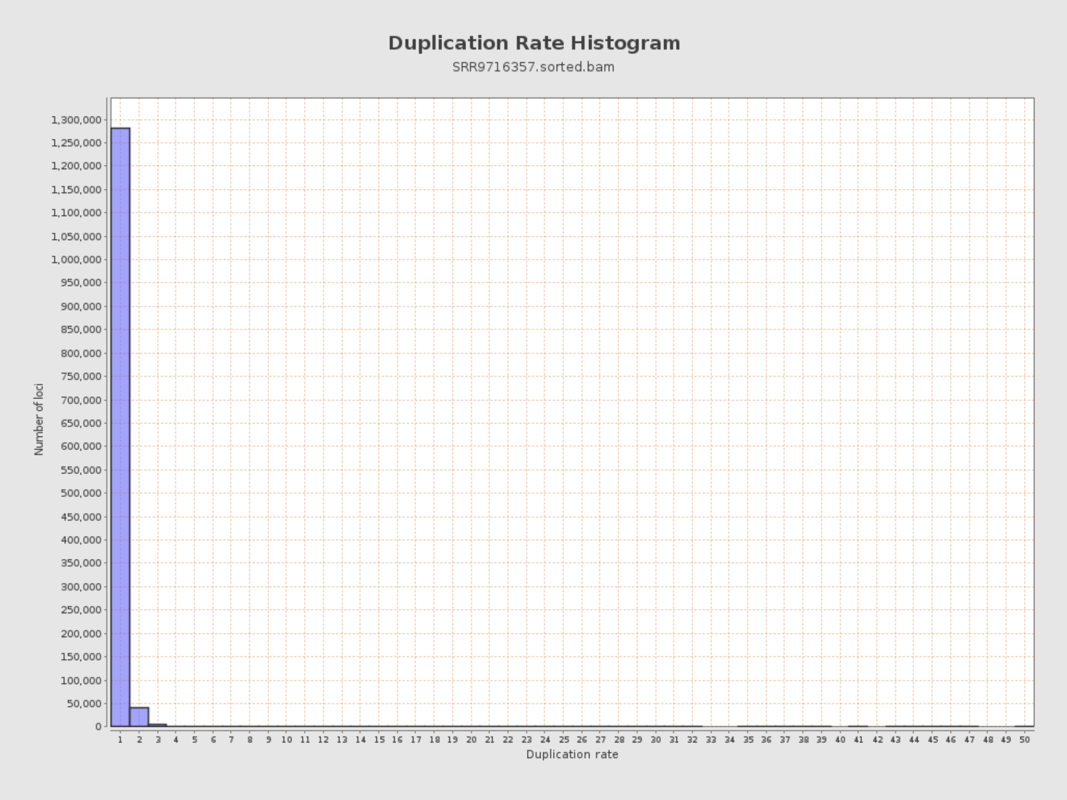
5. Results : Coverage Histogram (0-50X)



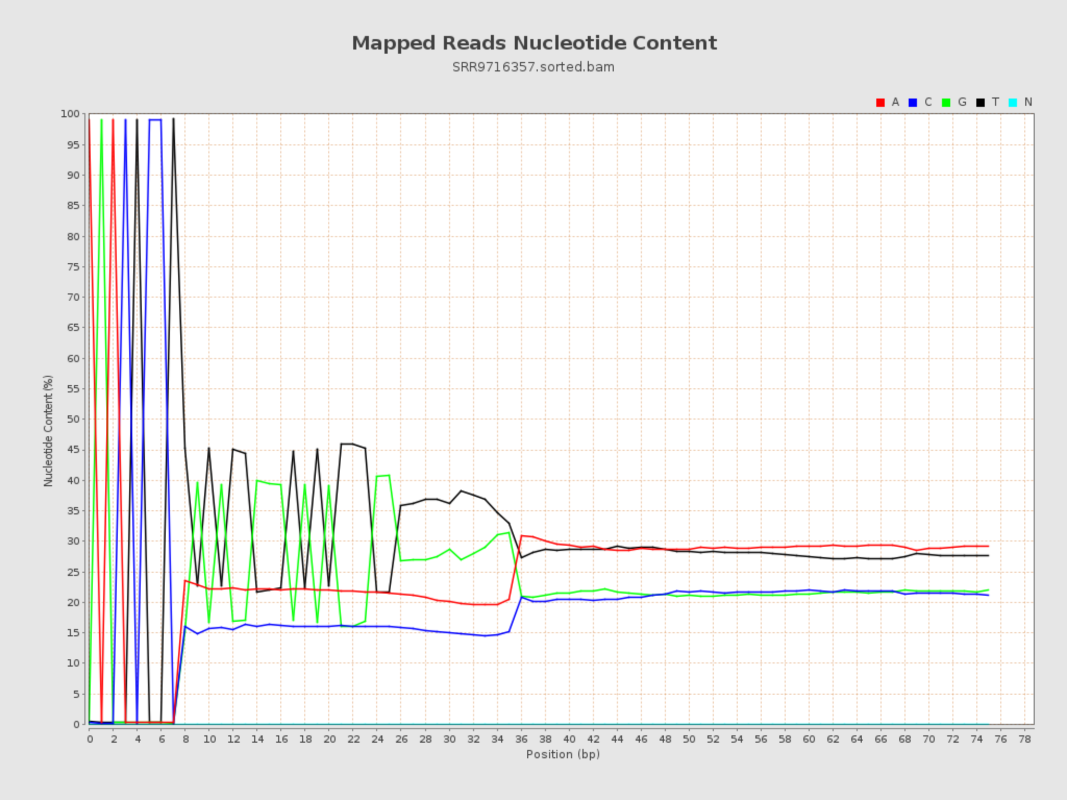
6. Results : Genome Fraction Coverage



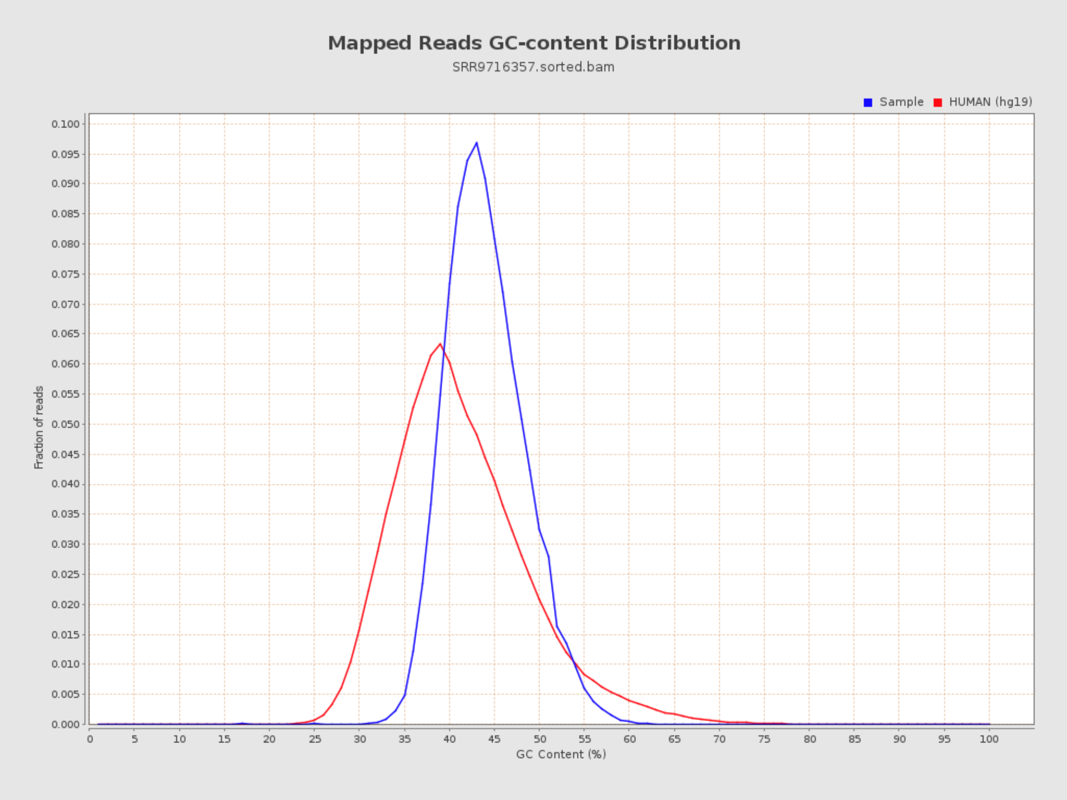
7. Results : Duplication Rate Histogram



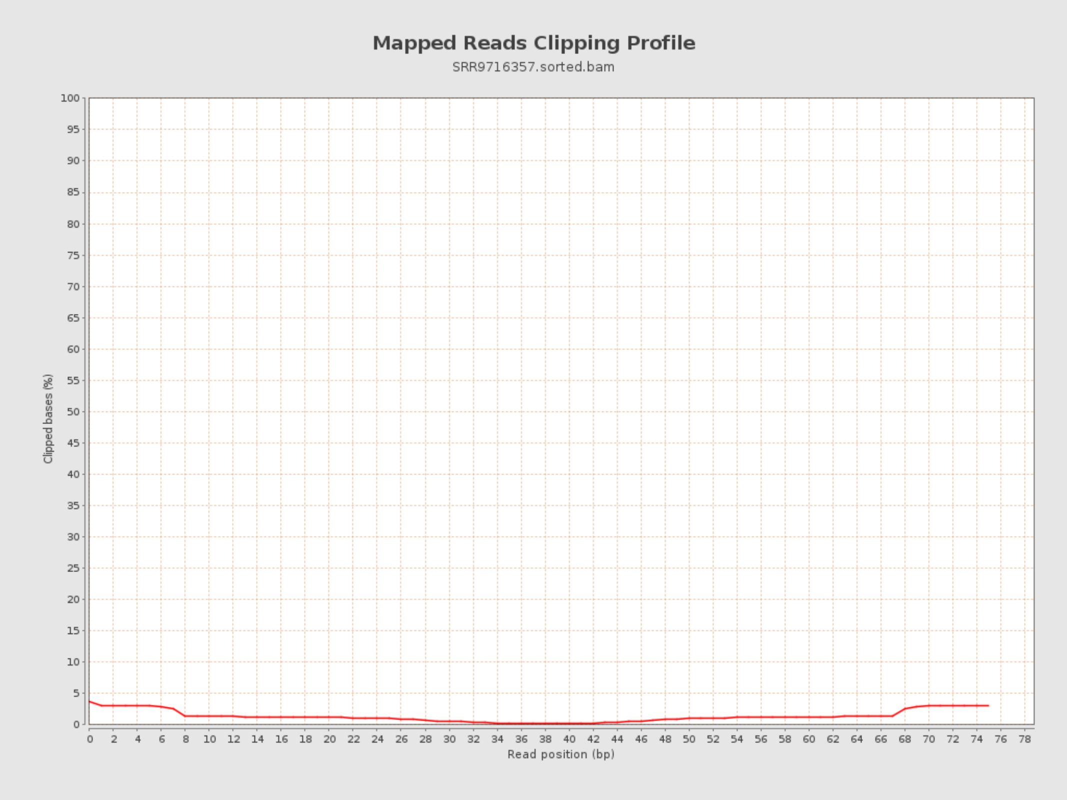
8. Results : Mapped Reads Nucleotide Content



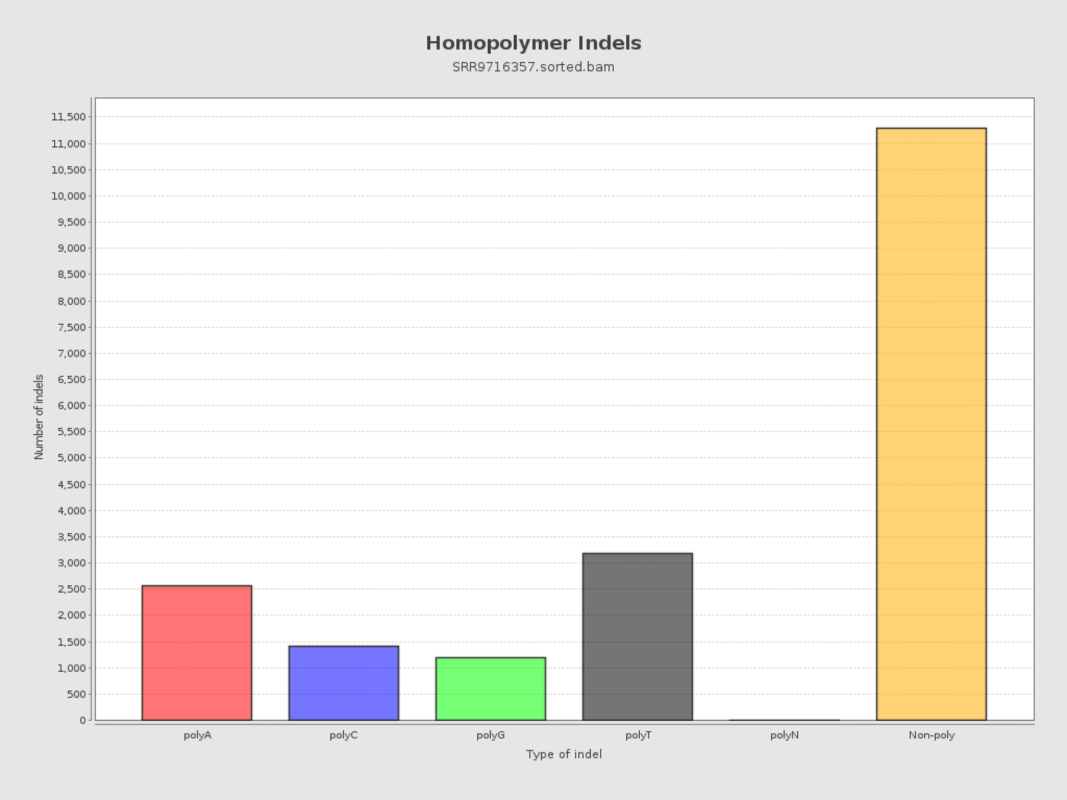
9. Results : Mapped Reads GC-content Distribution



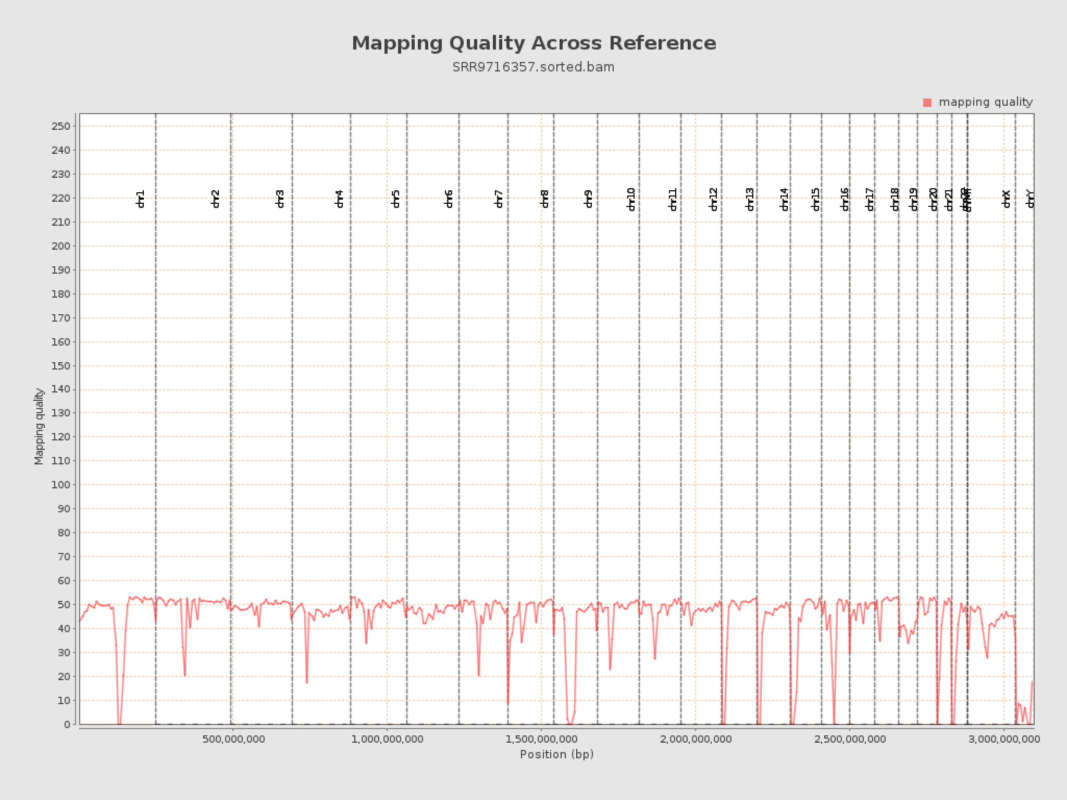
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram