Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 08:53:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716356.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_SRR9716356 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716356.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 08:53:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716356.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	461,603
Mapped reads	407,096 / 88.19%
Unmapped reads	54,507 / 11.81%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,689 / 0.58%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	15,550 / 3.37%
Duplication rate	3.29%
Clipped reads	409,005 / 88.61%

2.2. ACGT Content

Number/percentage of A's	5,596,230 / 24.68%
Number/percentage of C's	4,490,335 / 19.8%
Number/percentage of T's	7,029,881 / 31%
Number/percentage of G's	5,562,095 / 24.53%
Number/percentage of N's	179 / 0%
GC Percentage	44.33%

2.3. Coverage

Mean	0.0073

Standard Deviation	0.1037

2.4. Mapping Quality

Mean Mapping Quality	43.85

2.5. Mismatches and indels

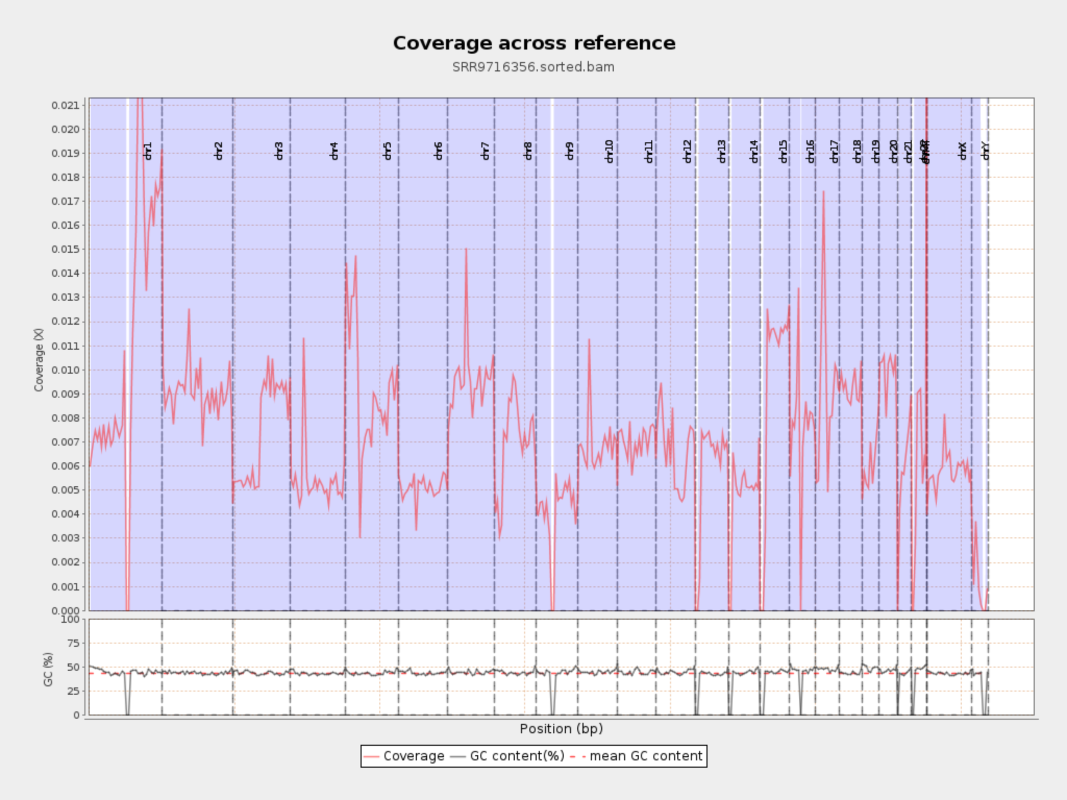
General error rate	0.56%
Mismatches	124,485
Insertions	1,522
Mapped reads with at least one insertion	0.37%
Deletions	4,775
Mapped reads with at least one deletion	1.17%
Homopolymer indels	40.46%

2.6. Chromosome stats

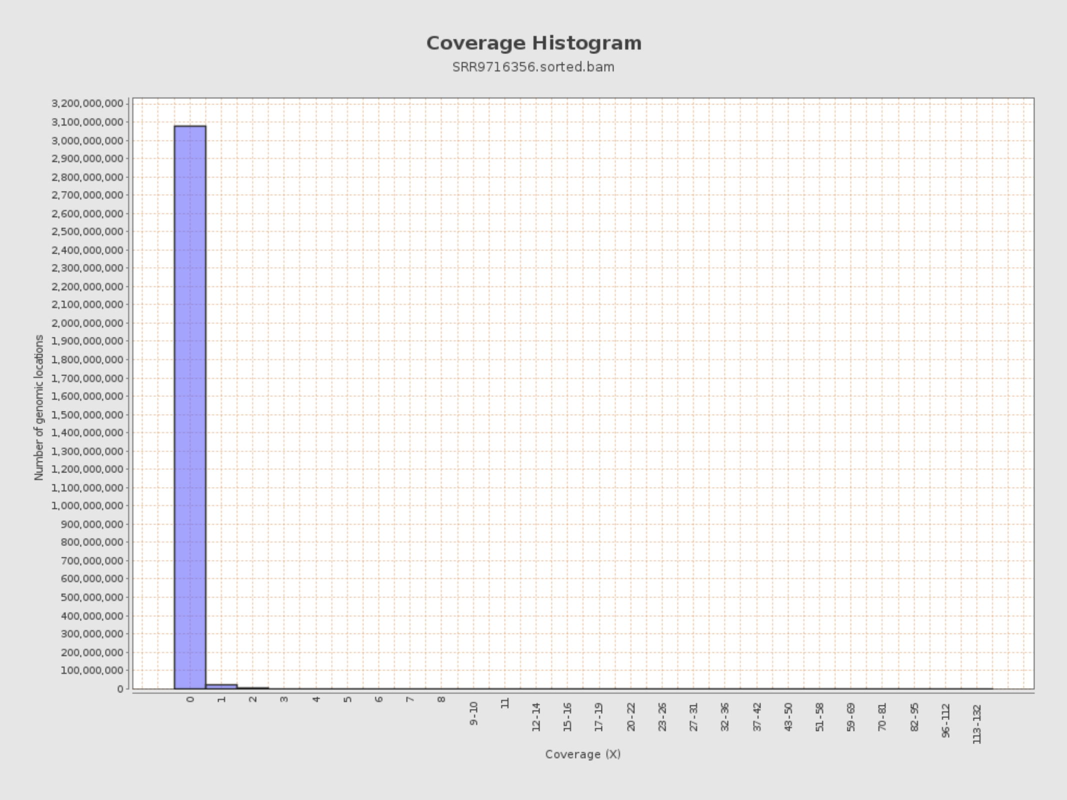
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2747420	0.011	0.1406
chr2	243199373	2218016	0.0091	0.1252
chr3	198022430	1460396	0.0074	0.0935
chr4	191154276	1029045	0.0054	0.0871
chr5	180915260	1661987	0.0092	0.1049
chr6	171115067	875016	0.0051	0.0807
chr7	159138663	1536521	0.0097	0.1377

chr8	146364022	1021937	0.007	0.1038
chr9	141213431	571128	0.004	0.0767
chr10	135534747	931679	0.0069	0.1
chr11	135006516	946600	0.007	0.1002
chr12	133851895	888734	0.0066	0.0895
chr13	115169878	669516	0.0058	0.0829
chr14	107349540	498137	0.0046	0.075
chr15	102531392	963258	0.0094	0.1065
chr16	90354753	685484	0.0076	0.0963
chr17	81195210	756811	0.0093	0.1083
chr18	78077248	723972	0.0093	0.1363
chr19	59128983	361742	0.0061	0.0997
chr20	63025520	627849	0.01	0.1093
chr21	48129895	278904	0.0058	0.0849
chr22	51304566	265328	0.0052	0.0785
chrMT	16571	616	0.0372	0.21
chrX	155270560	900851	0.0058	0.0855
chrY	59373566	65180	0.0011	0.0414

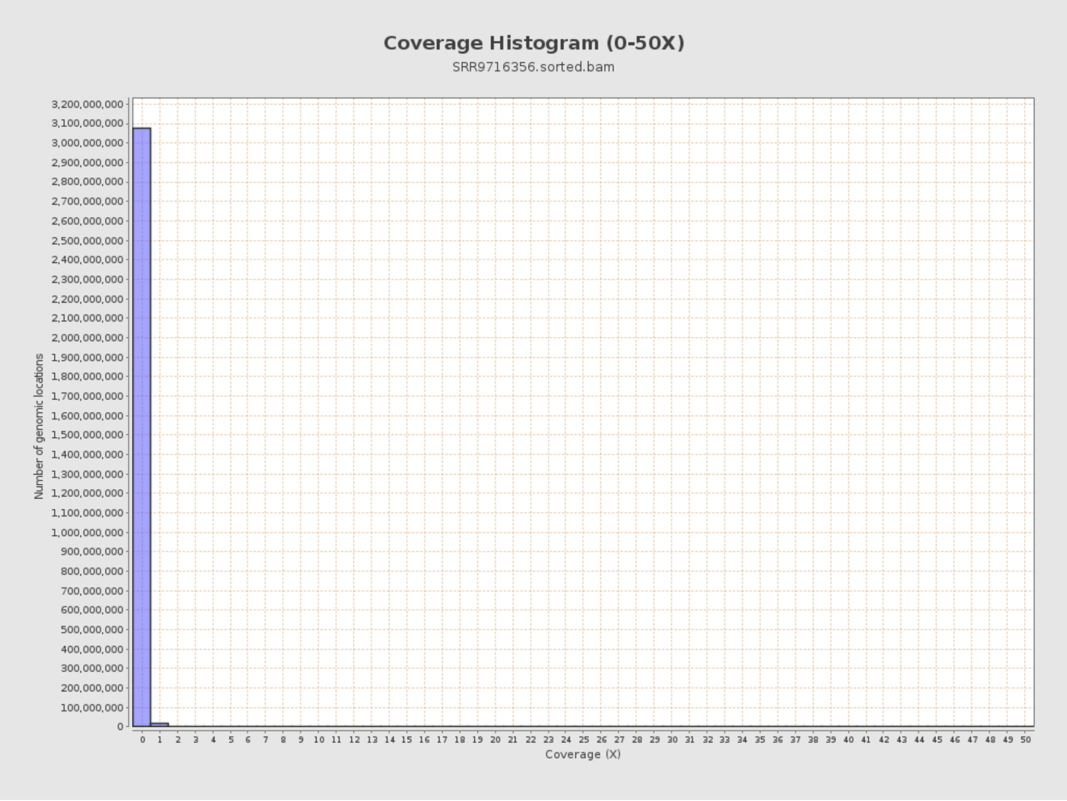
3. Results : Coverage across reference



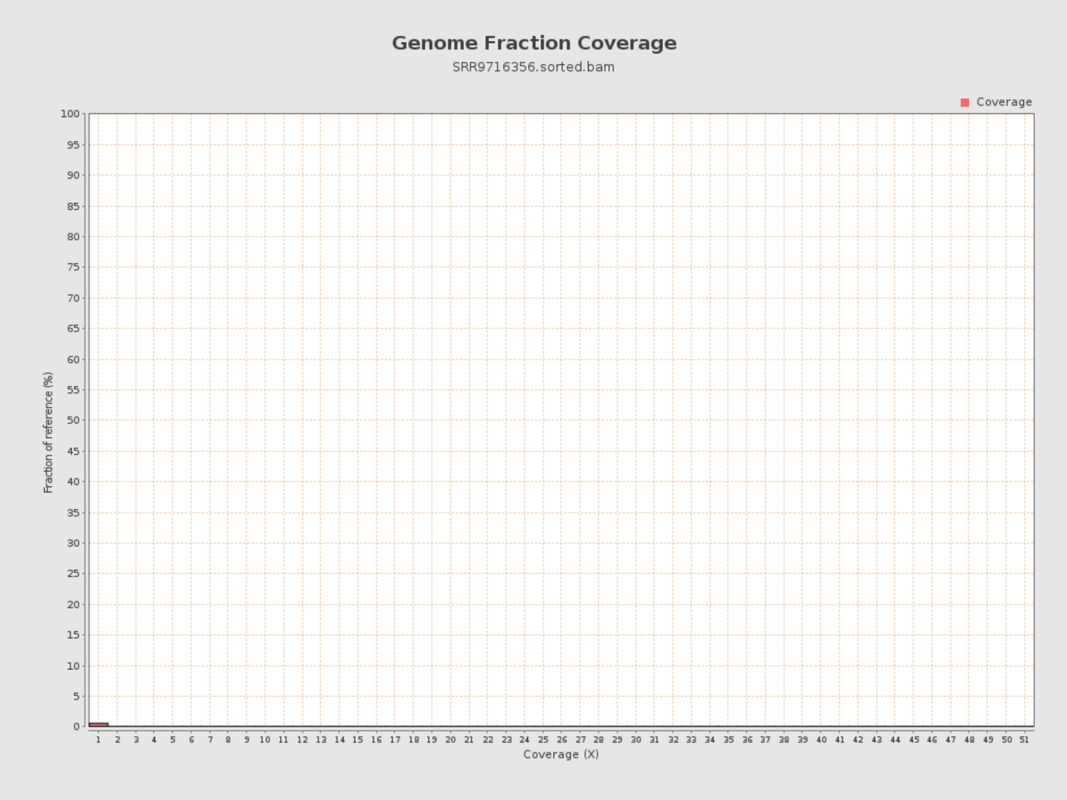
4. Results : Coverage Histogram



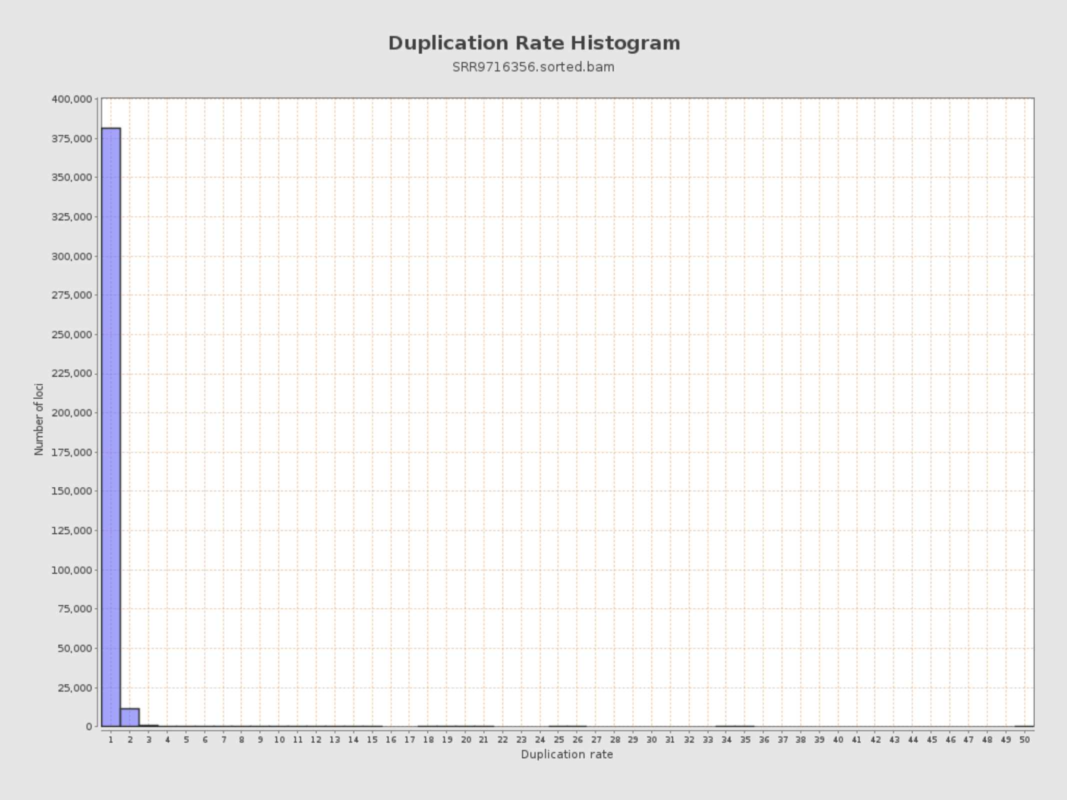
5. Results : Coverage Histogram (0-50X)



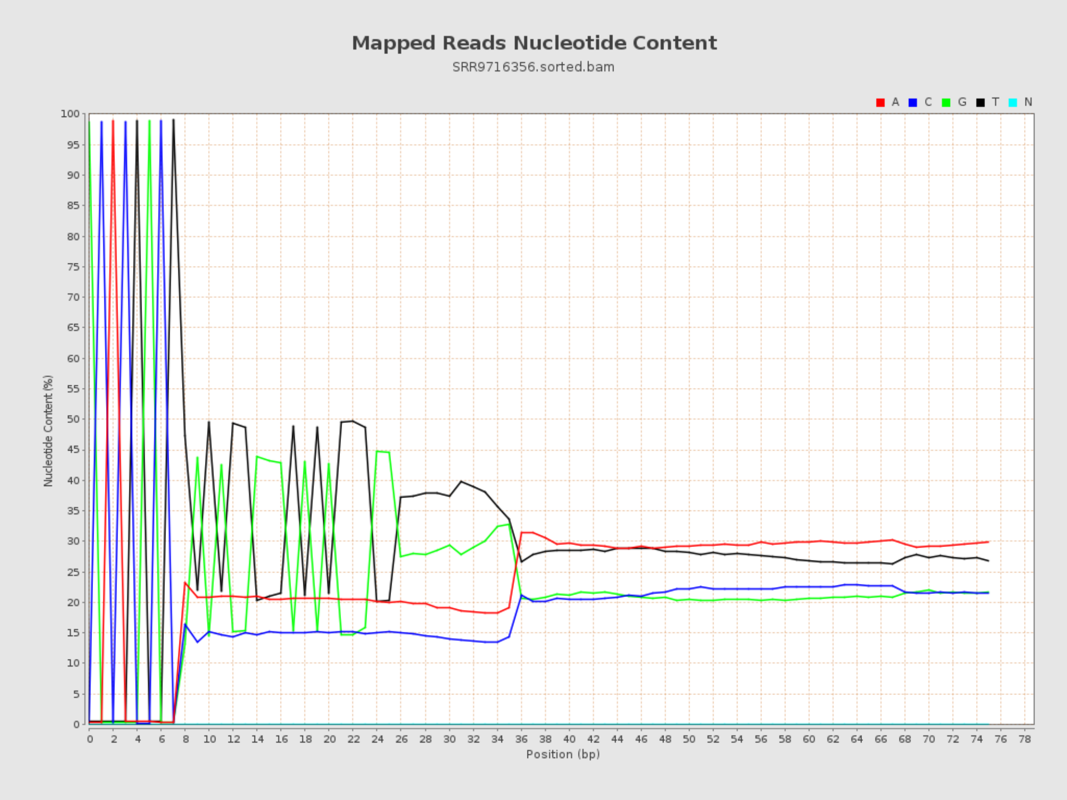
6. Results : Genome Fraction Coverage



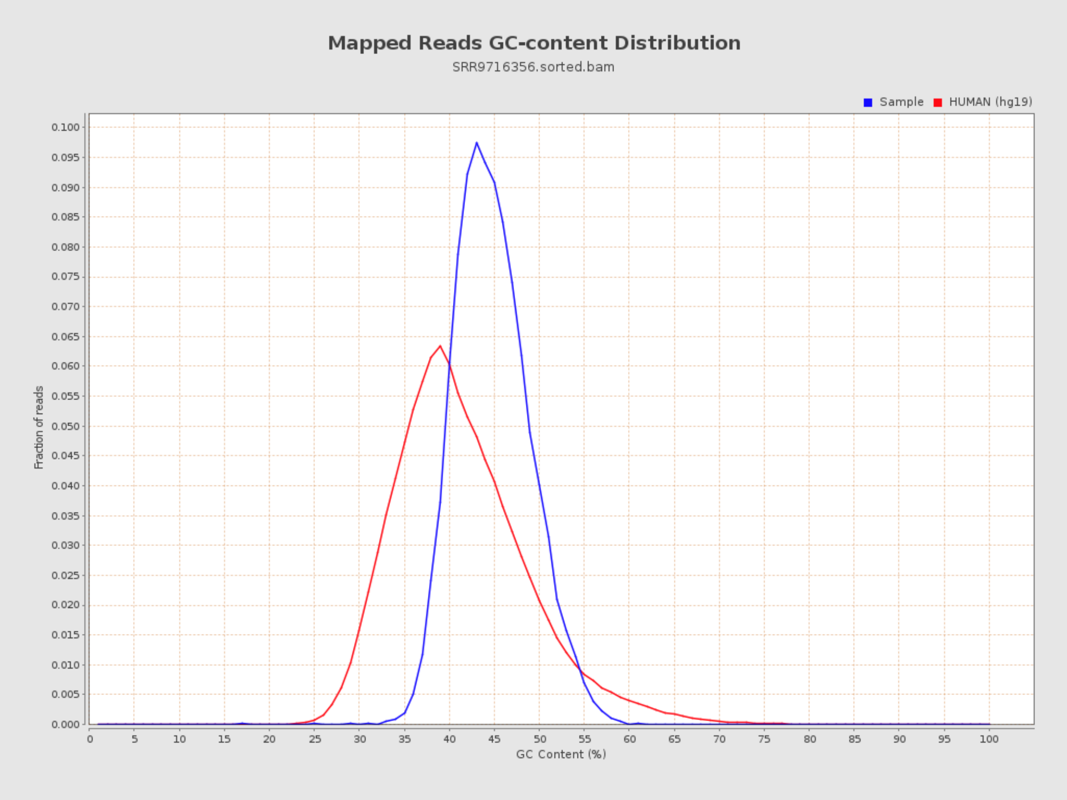
7. Results : Duplication Rate Histogram



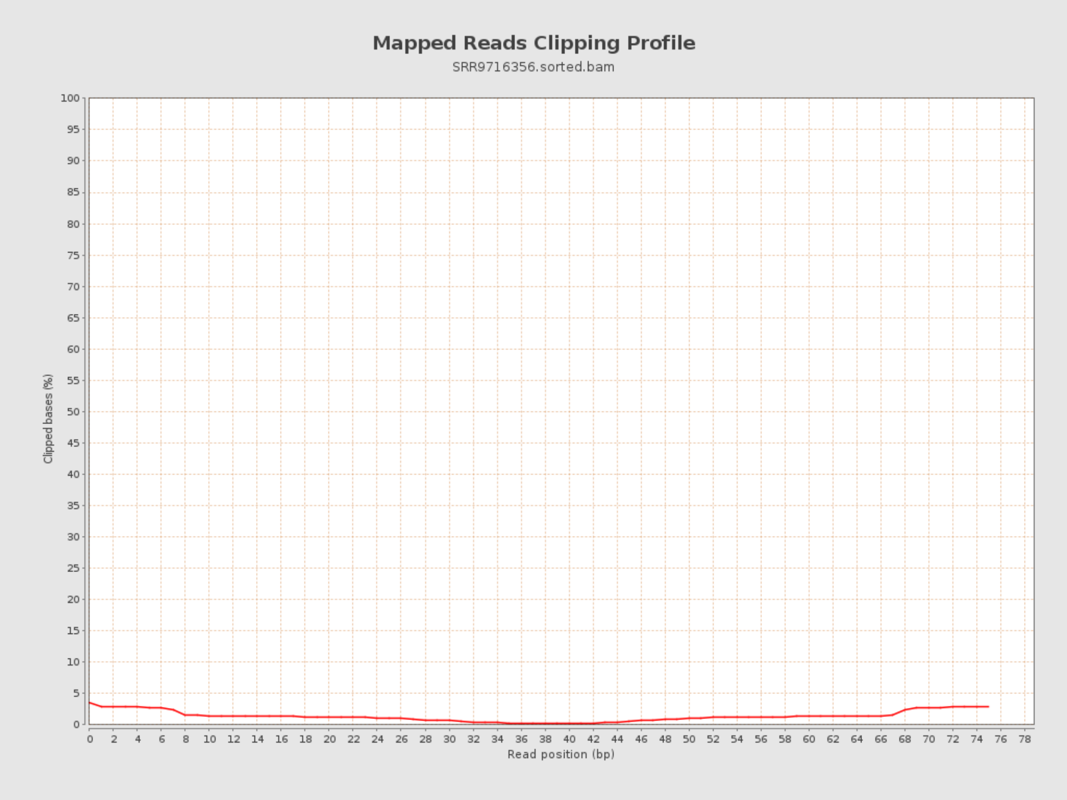
8. Results : Mapped Reads Nucleotide Content



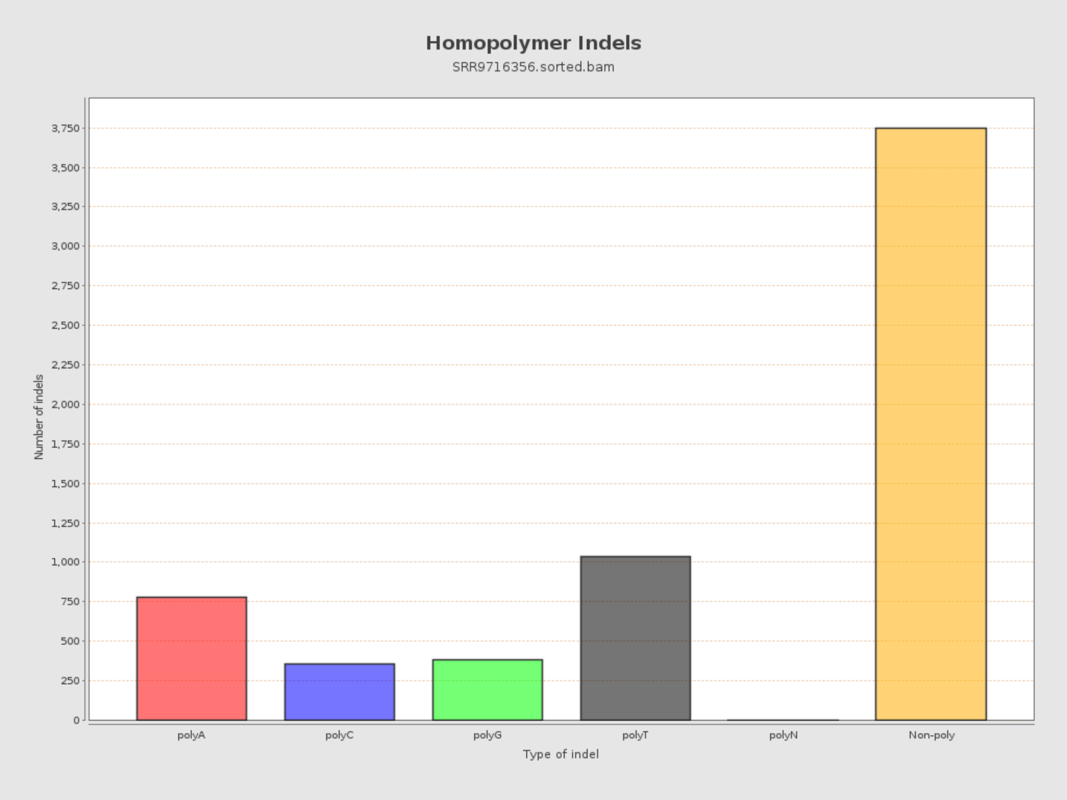
9. Results : Mapped Reads GC-content Distribution



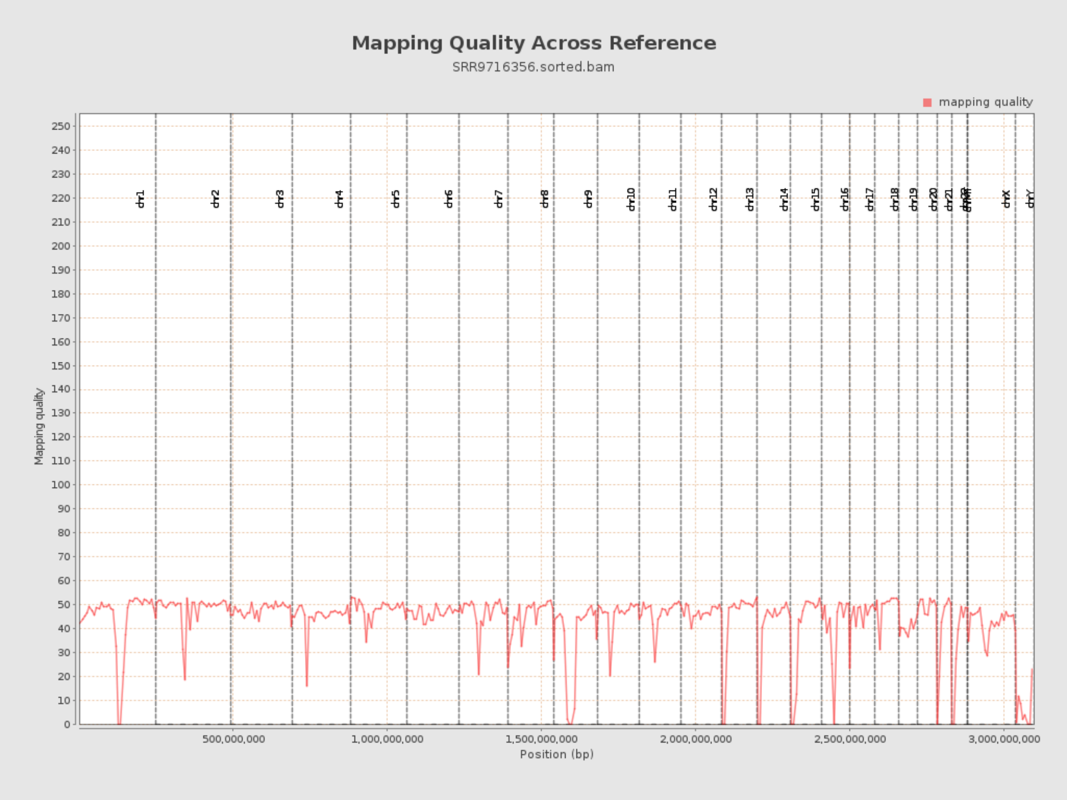
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram