Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 06:56:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716314.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_SRR9716314 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716314.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 06:56:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716314.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,120,572
Mapped reads	2,929,715 / 93.88%
Unmapped reads	190,857 / 6.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	60,508 / 1.94%
Read min/max/mean length	30 / 101 / 101.7
Duplicated reads (estimated)	160,295 / 5.14%
Duplication rate	3.99%
Clipped reads	2,985,365 / 95.67%

2.2. ACGT Content

Number/percentage of A's	59,532,540 / 25.67%
Number/percentage of C's	45,858,175 / 19.77%
Number/percentage of T's	70,709,881 / 30.48%
Number/percentage of G's	55,837,495 / 24.07%
Number/percentage of N's	16,561 / 0.01%
GC Percentage	43.84%

2.3. Coverage

Mean	0.075

Standard Deviation	0.6325

2.4. Mapping Quality

Mean Mapping Quality	47.42

2.5. Mismatches and indels

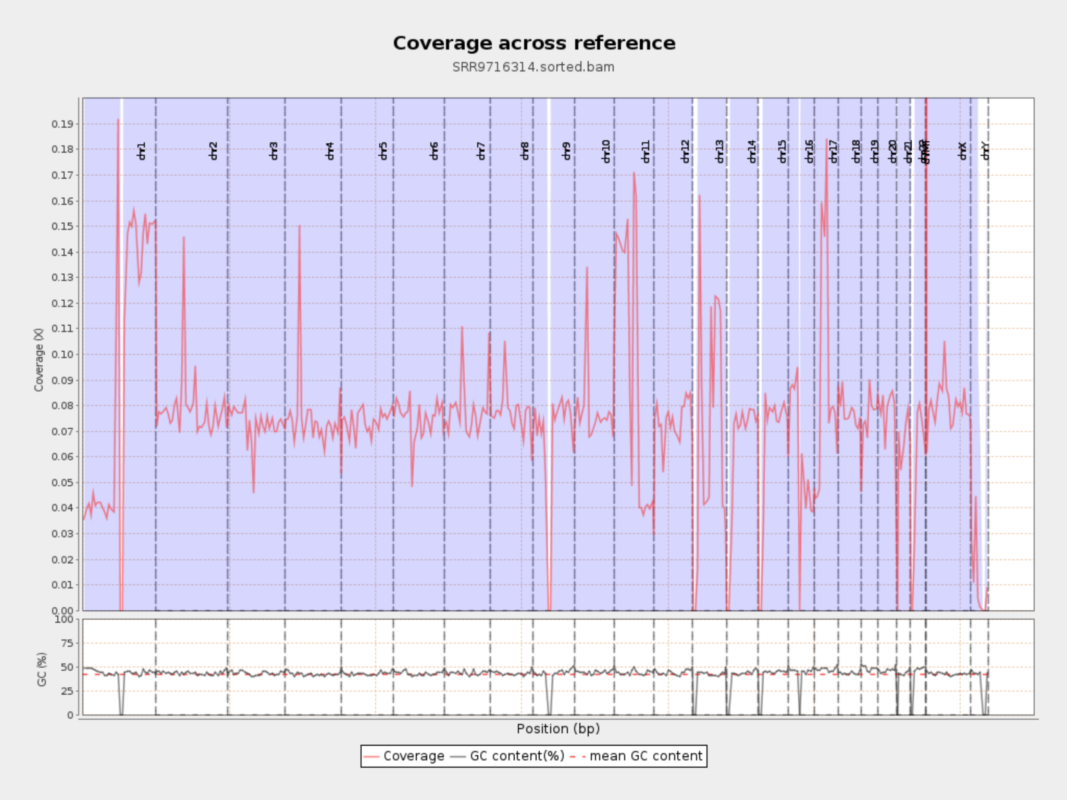
General error rate	0.65%
Mismatches	1,465,735
Insertions	19,411
Mapped reads with at least one insertion	0.65%
Deletions	52,461
Mapped reads with at least one deletion	1.76%
Homopolymer indels	43.38%

2.6. Chromosome stats

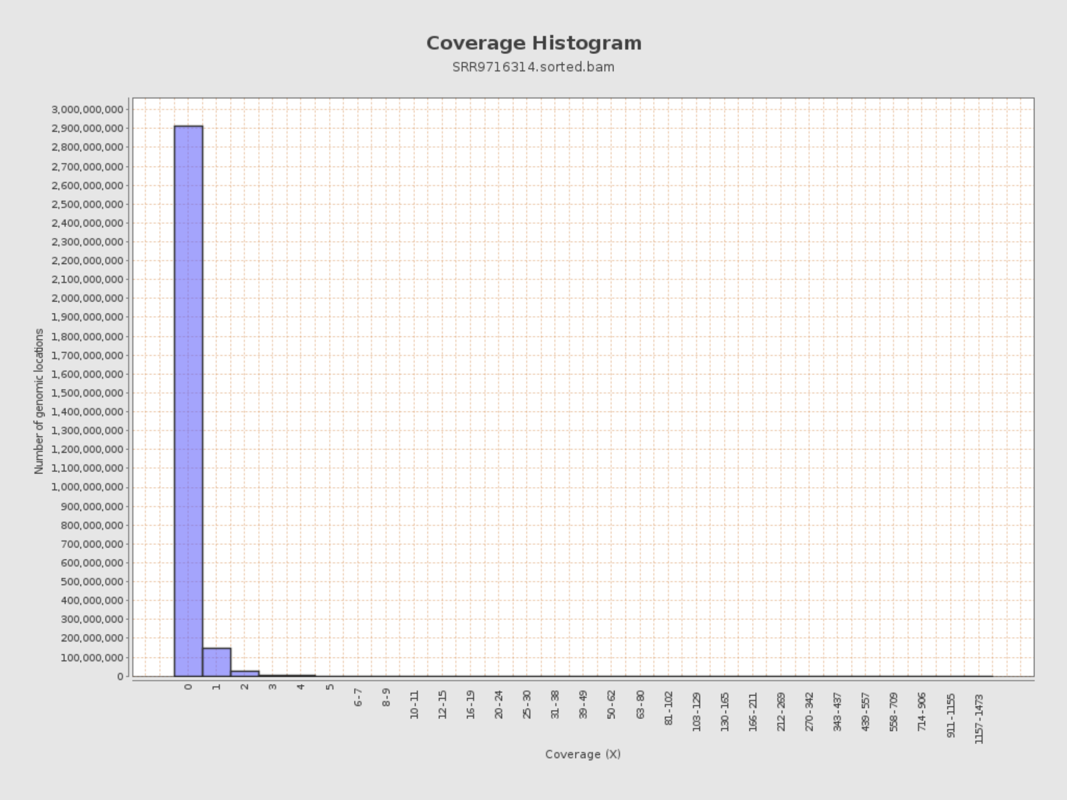
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	22629719	0.0908	1.3237
chr2	243199373	19274270	0.0793	0.7125
chr3	198022430	14423494	0.0728	0.3244
chr4	191154276	14508427	0.0759	0.4614
chr5	180915260	13381218	0.074	0.3335
chr6	171115067	12804670	0.0748	0.3748
chr7	159138663	12559025	0.0789	0.7909

chr8	146364022	11324826	0.0774	0.7094
chr9	141213431	9360085	0.0663	0.5053
chr10	135534747	10588372	0.0781	0.6078
chr11	135006516	12841563	0.0951	0.7219
chr12	133851895	9991453	0.0746	0.3335
chr13	115169878	8060930	0.07	0.324
chr14	107349540	6733770	0.0627	0.3337
chr15	102531392	6494979	0.0633	0.304
chr16	90354753	5236960	0.058	0.3391
chr17	81195210	7470484	0.092	0.4848
chr18	78077248	6054804	0.0775	0.9047
chr19	59128983	4500134	0.0761	0.8579
chr20	63025520	4924687	0.0781	0.3649
chr21	48129895	2971232	0.0617	0.3906
chr22	51304566	2648612	0.0516	0.277
chrMT	16571	73954	4.4629	3.2949
chrX	155270560	12512286	0.0806	0.4247
chrY	59373566	685499	0.0115	0.3834

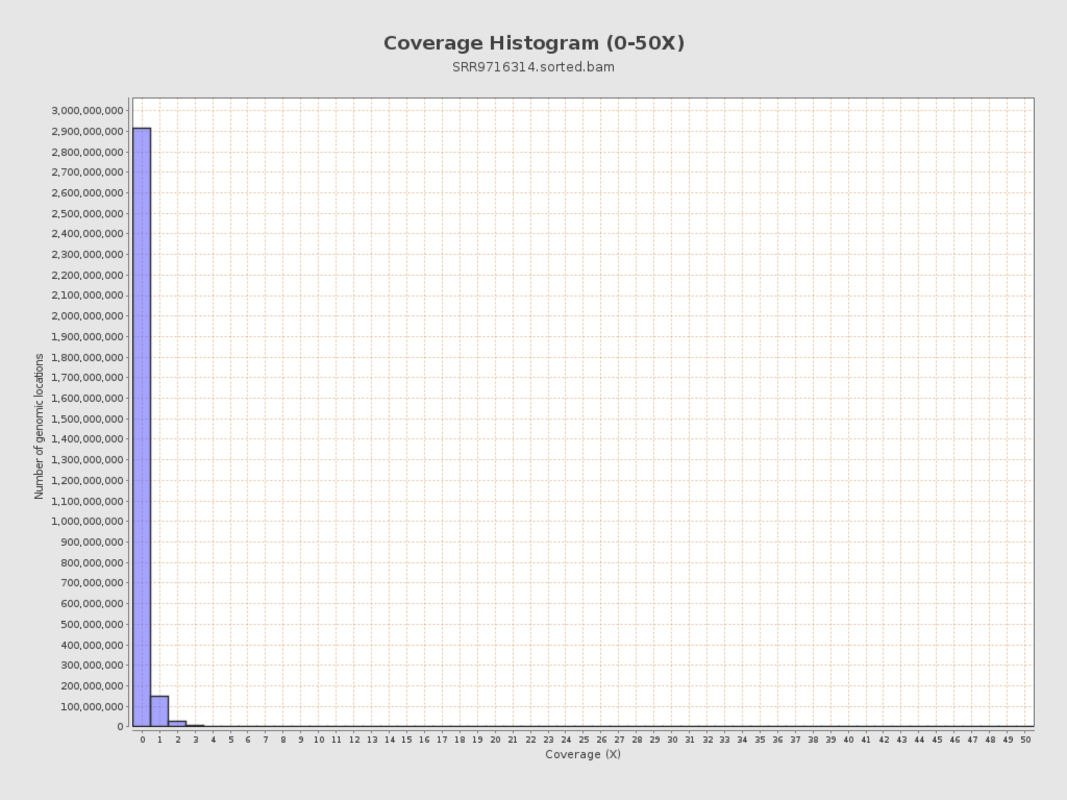
3. Results : Coverage across reference



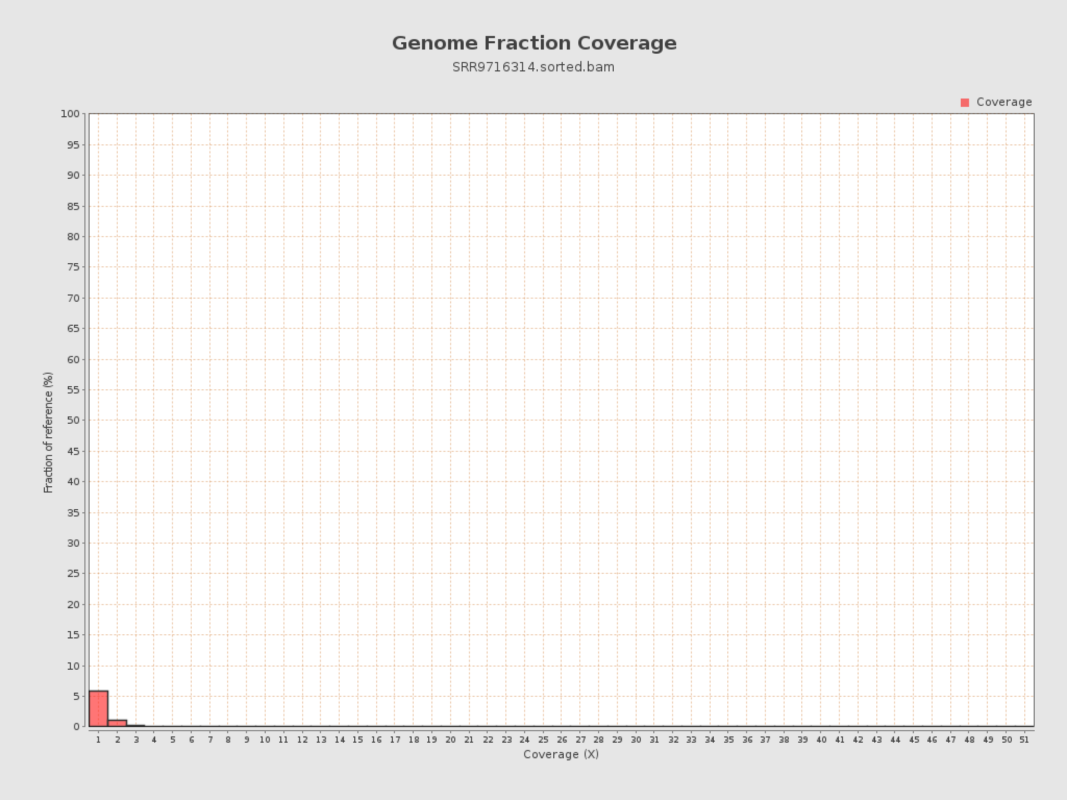
4. Results : Coverage Histogram



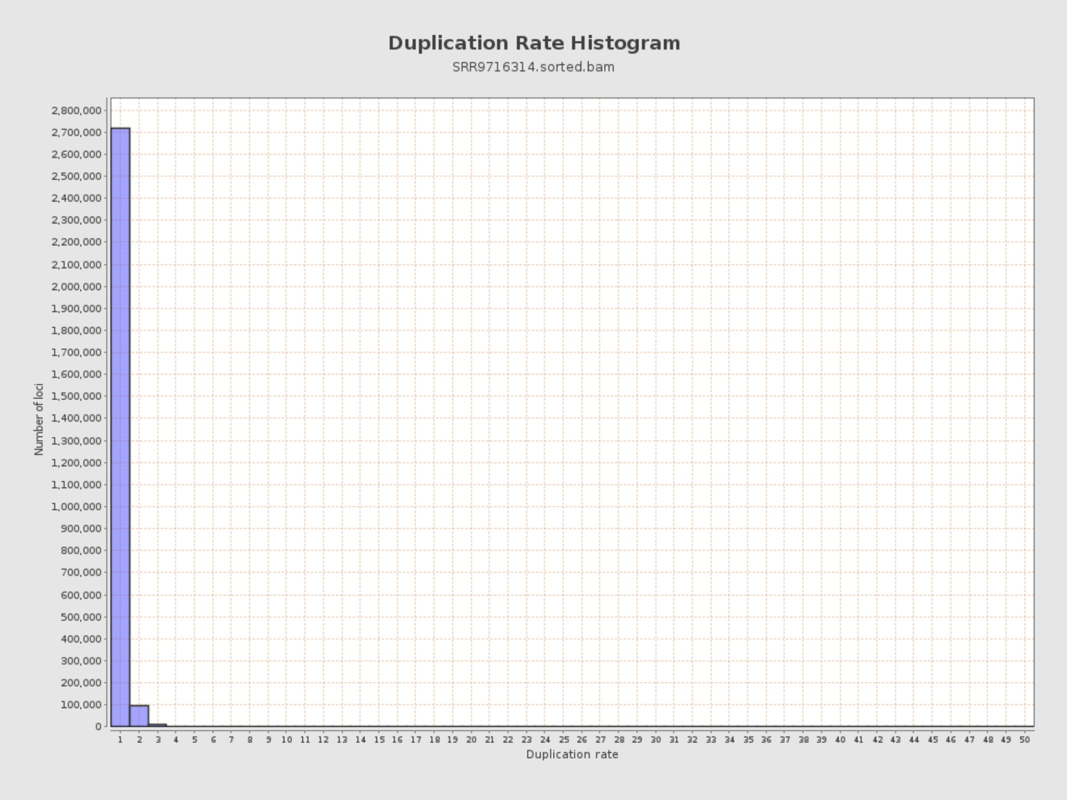
5. Results : Coverage Histogram (0-50X)



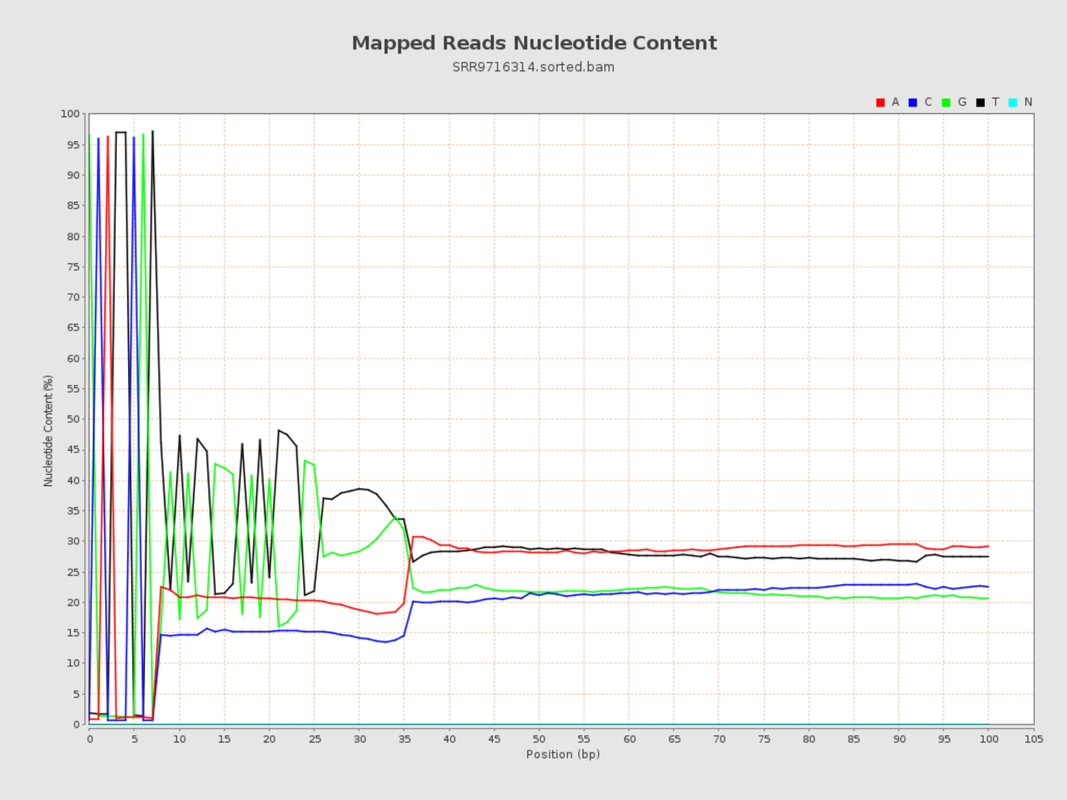
6. Results : Genome Fraction Coverage



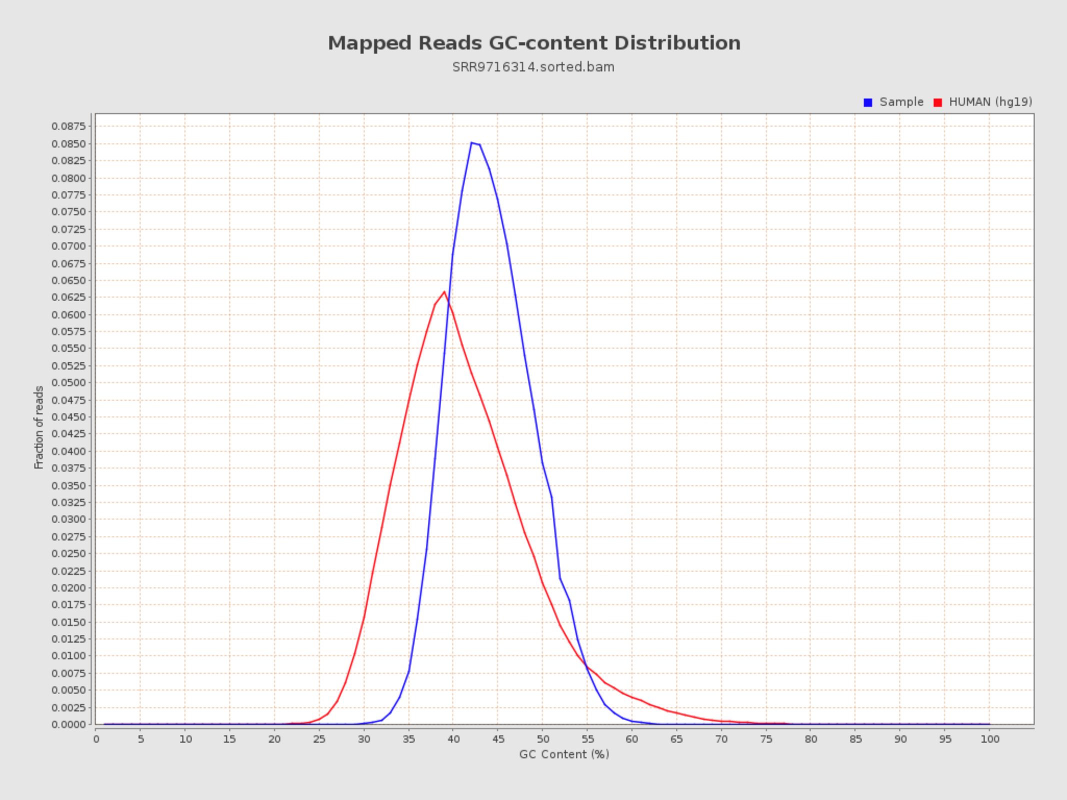
7. Results : Duplication Rate Histogram



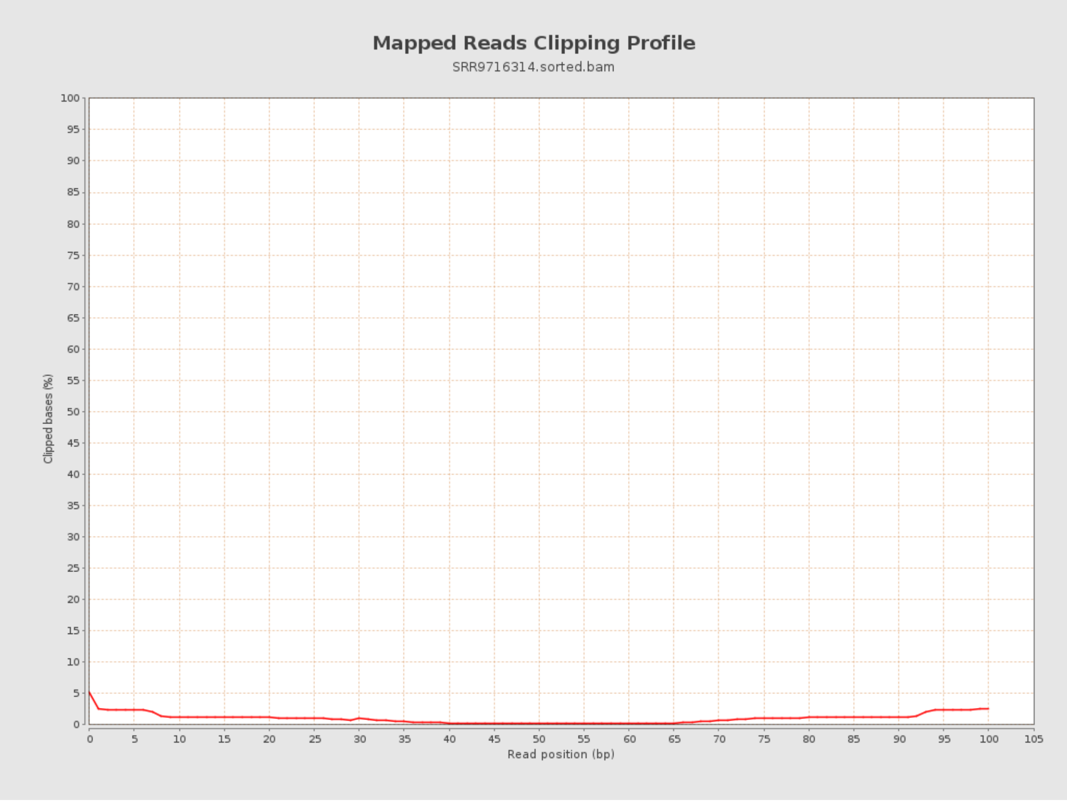
8. Results : Mapped Reads Nucleotide Content



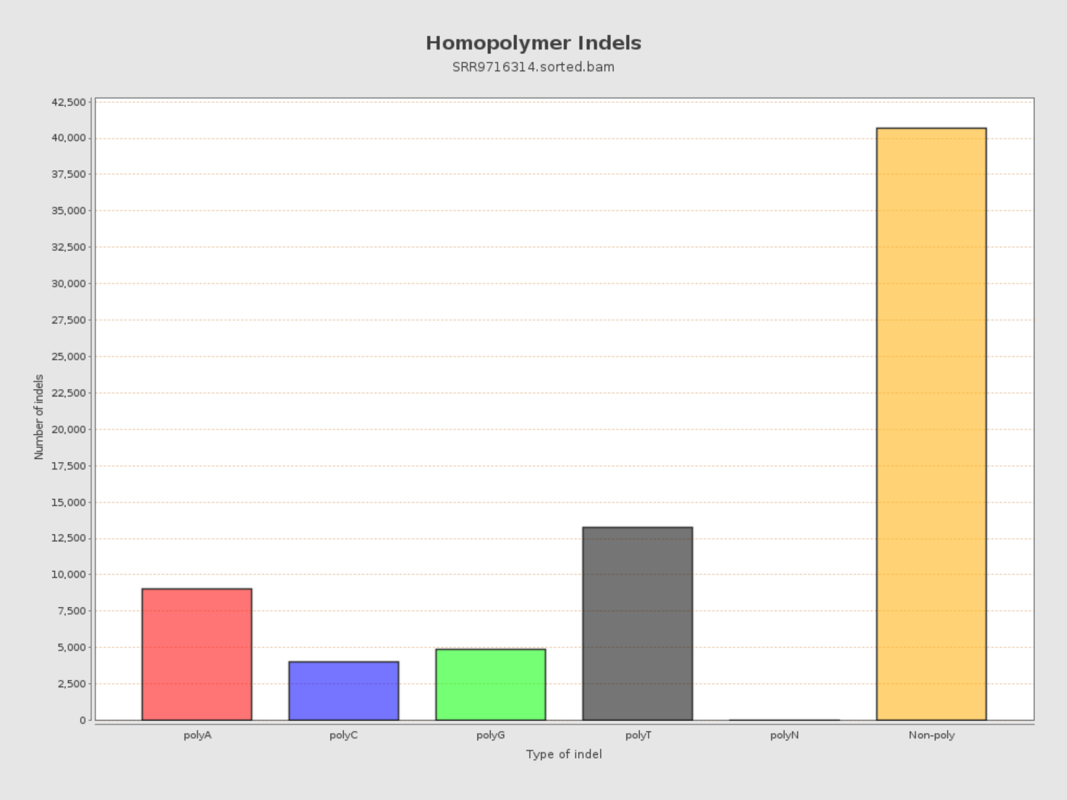
9. Results : Mapped Reads GC-content Distribution



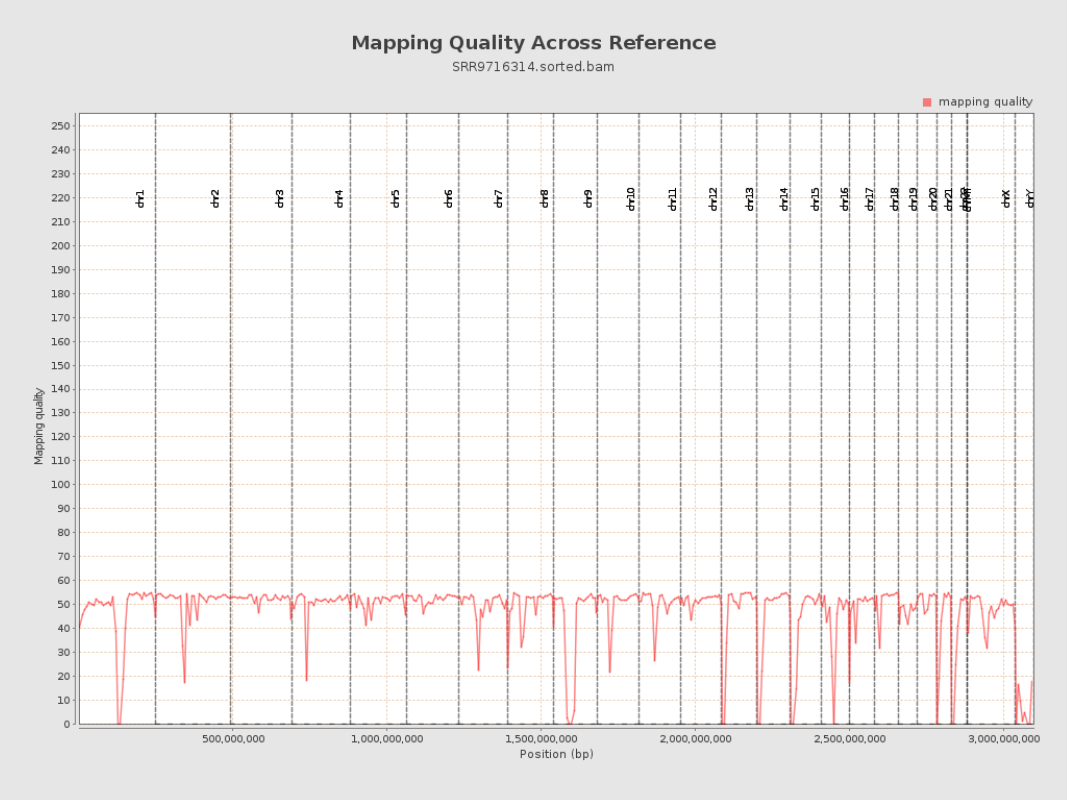
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram