Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 23:39:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716201.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_SRR9716201 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716201.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 23:39:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716201.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,231,791
Mapped reads	1,927,688 / 86.37%
Unmapped reads	304,103 / 13.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	52,703 / 2.36%
Read min/max/mean length	30 / 101 / 101.85
Duplicated reads (estimated)	61,472 / 2.75%
Duplication rate	2.13%
Clipped reads	1,976,772 / 88.57%

2.2. ACGT Content

Number/percentage of A's	37,917,611 / 26.28%
Number/percentage of C's	29,939,856 / 20.75%
Number/percentage of T's	41,741,381 / 28.93%
Number/percentage of G's	34,668,354 / 24.03%
Number/percentage of N's	17,331 / 0.01%
GC Percentage	44.78%

2.3. Coverage

Mean	0.0466

Standard Deviation	0.3662

2.4. Mapping Quality

Mean Mapping Quality	45.55

2.5. Mismatches and indels

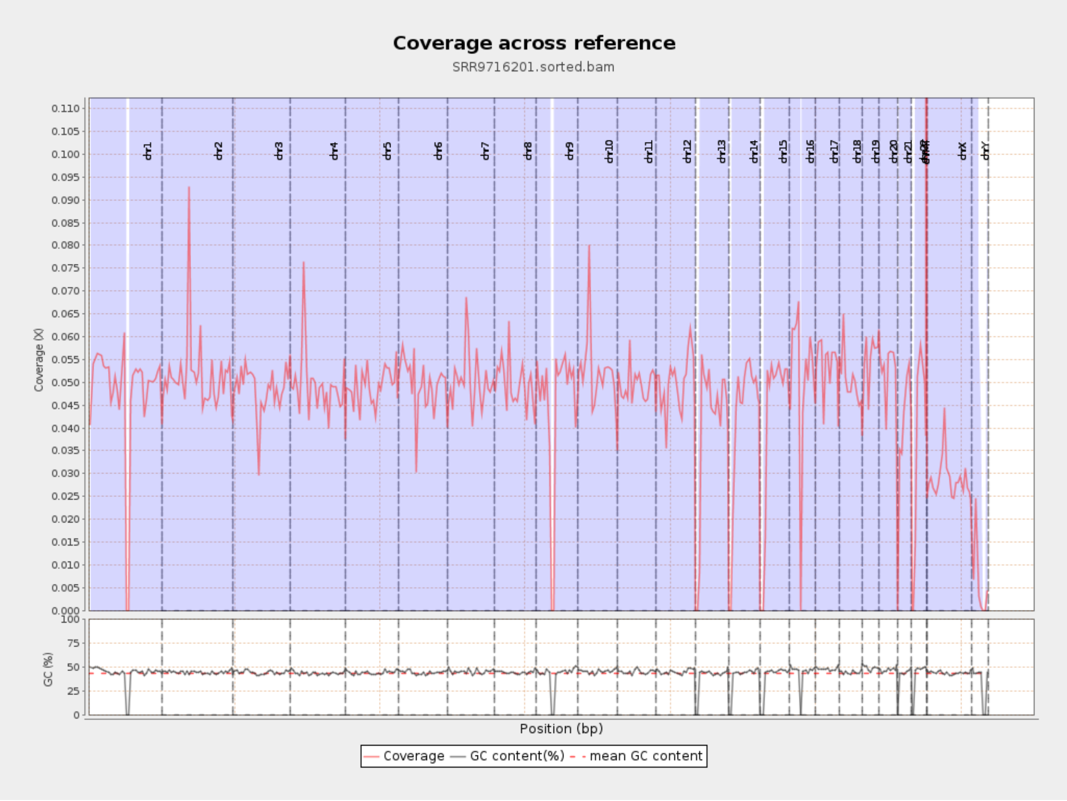
General error rate	0.78%
Mismatches	1,101,533
Insertions	13,787
Mapped reads with at least one insertion	0.71%
Deletions	30,067
Mapped reads with at least one deletion	1.54%
Homopolymer indels	40.33%

2.6. Chromosome stats

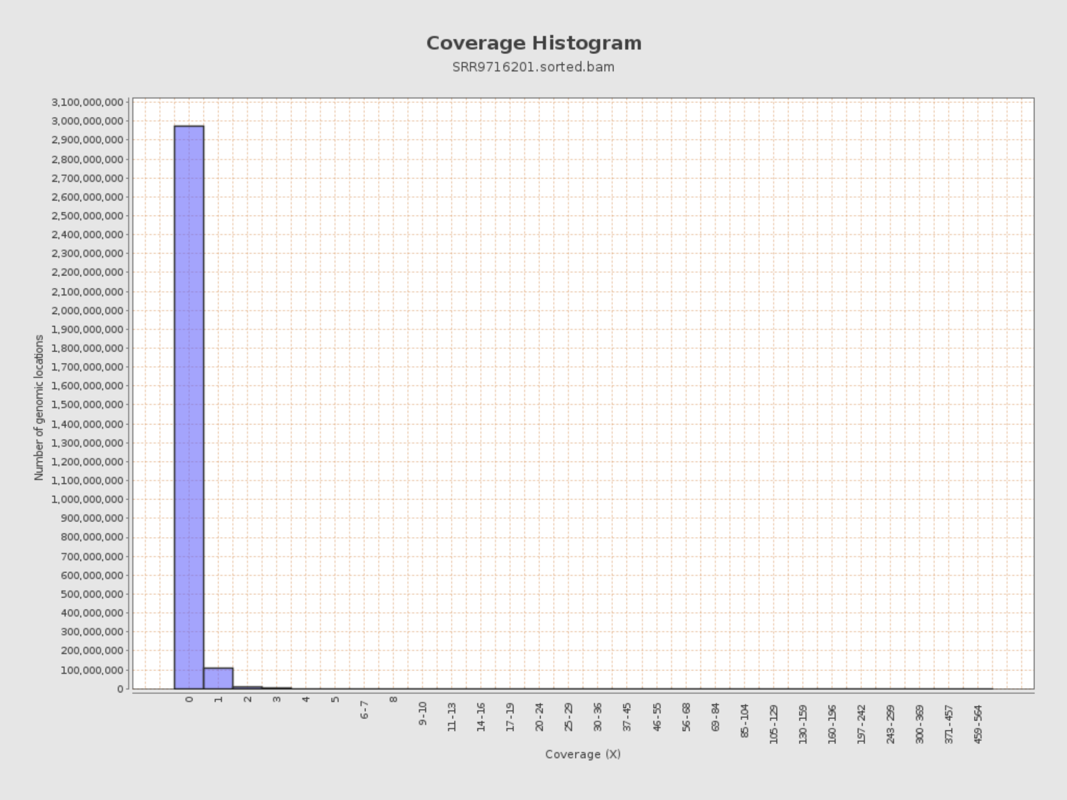
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11943738	0.0479	0.4367
chr2	243199373	12575786	0.0517	0.5293
chr3	198022430	9565955	0.0483	0.2477
chr4	191154276	9417337	0.0493	0.2941
chr5	180915260	8926344	0.0493	0.2536
chr6	171115067	8498618	0.0497	0.2878
chr7	159138663	8012656	0.0504	0.446

chr8	146364022	7248714	0.0495	0.4568
chr9	141213431	6291569	0.0446	0.3771
chr10	135534747	7129410	0.0526	0.4116
chr11	135006516	6656348	0.0493	0.4083
chr12	133851895	6673875	0.0499	0.2562
chr13	115169878	4604661	0.04	0.2249
chr14	107349540	4440201	0.0414	0.2881
chr15	102531392	4277216	0.0417	0.2321
chr16	90354753	4626177	0.0512	0.293
chr17	81195210	4347161	0.0535	0.2877
chr18	78077248	3966787	0.0508	0.7294
chr19	59128983	3243994	0.0549	0.386
chr20	63025520	3280182	0.052	0.2724
chr21	48129895	1907672	0.0396	0.2488
chr22	51304566	1845671	0.036	0.2157
chrMT	16571	18695	1.1282	1.4227
chrX	155270560	4477983	0.0288	0.2559
chrY	59373566	360624	0.0061	0.2181

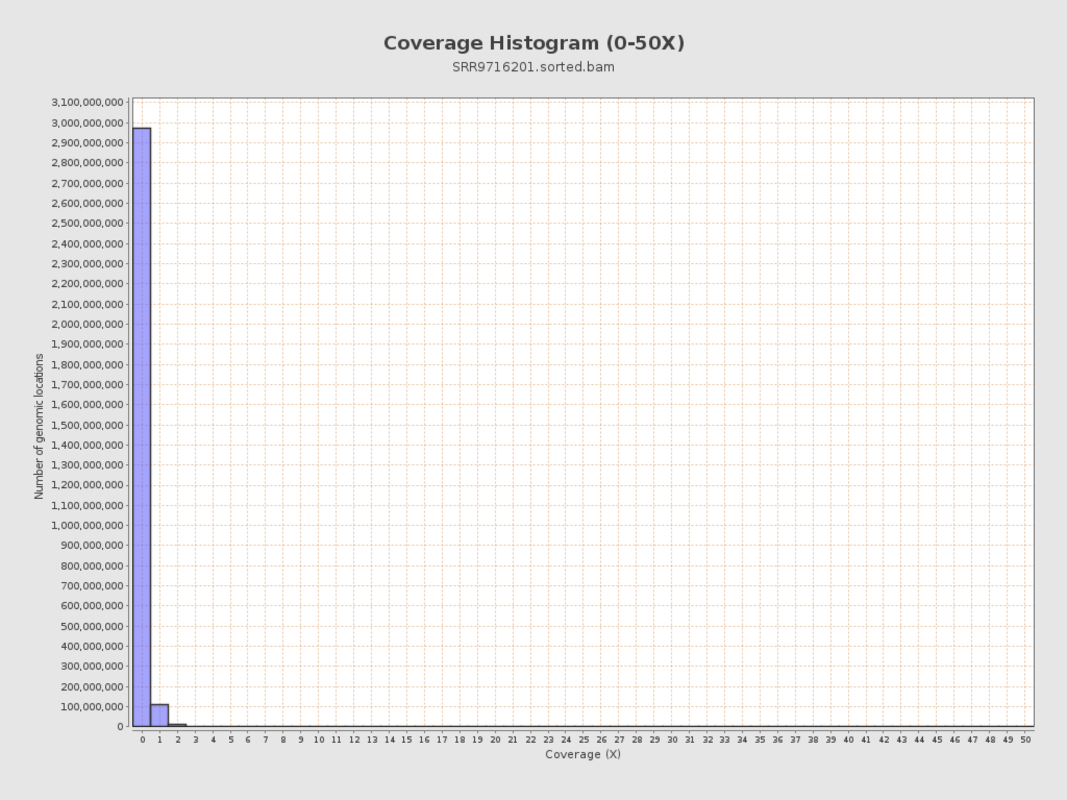
3. Results : Coverage across reference



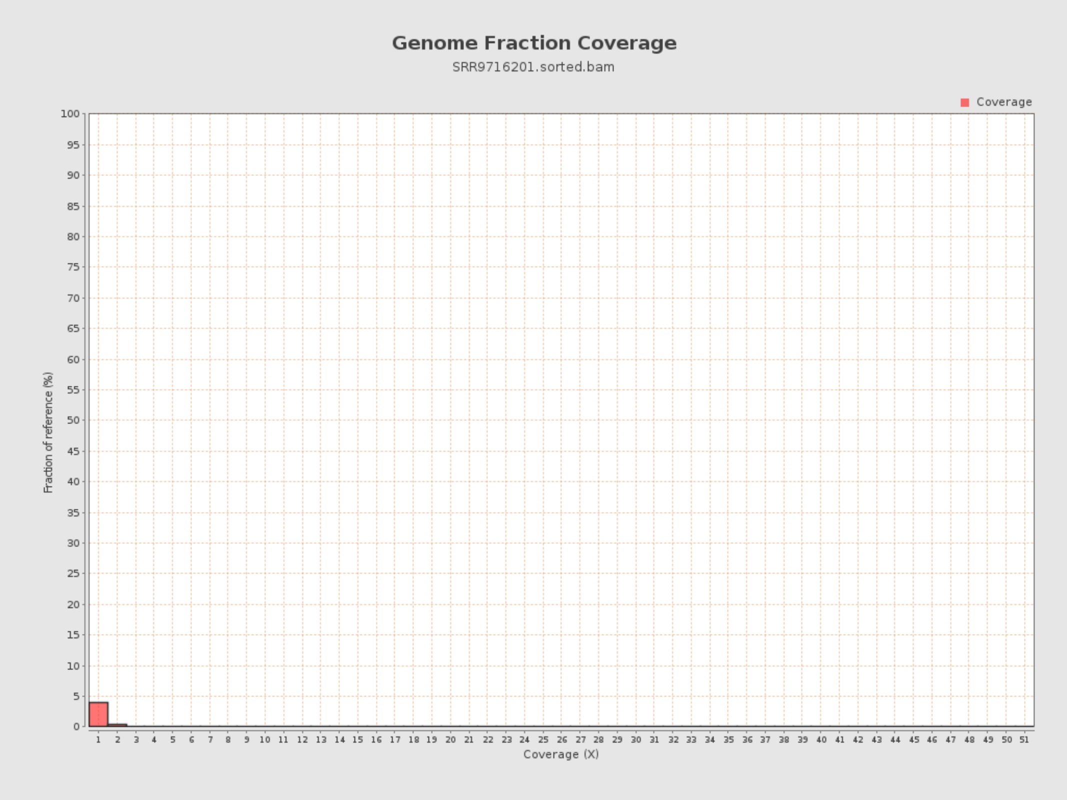
4. Results : Coverage Histogram



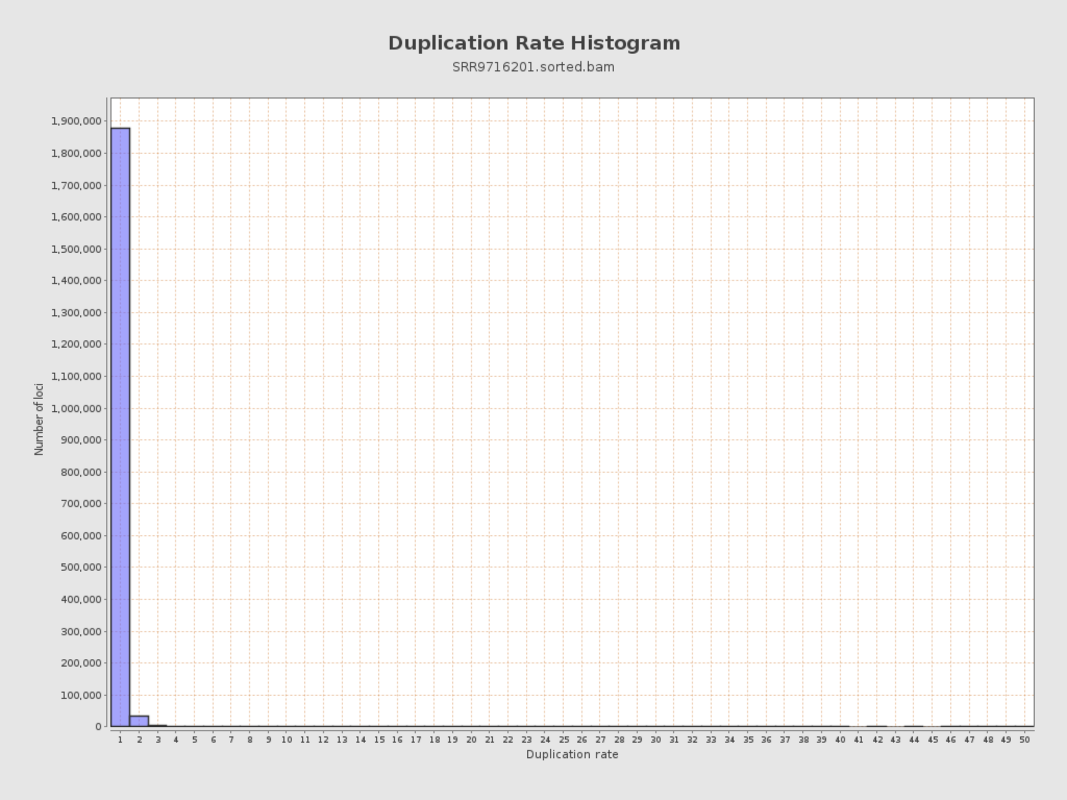
5. Results : Coverage Histogram (0-50X)



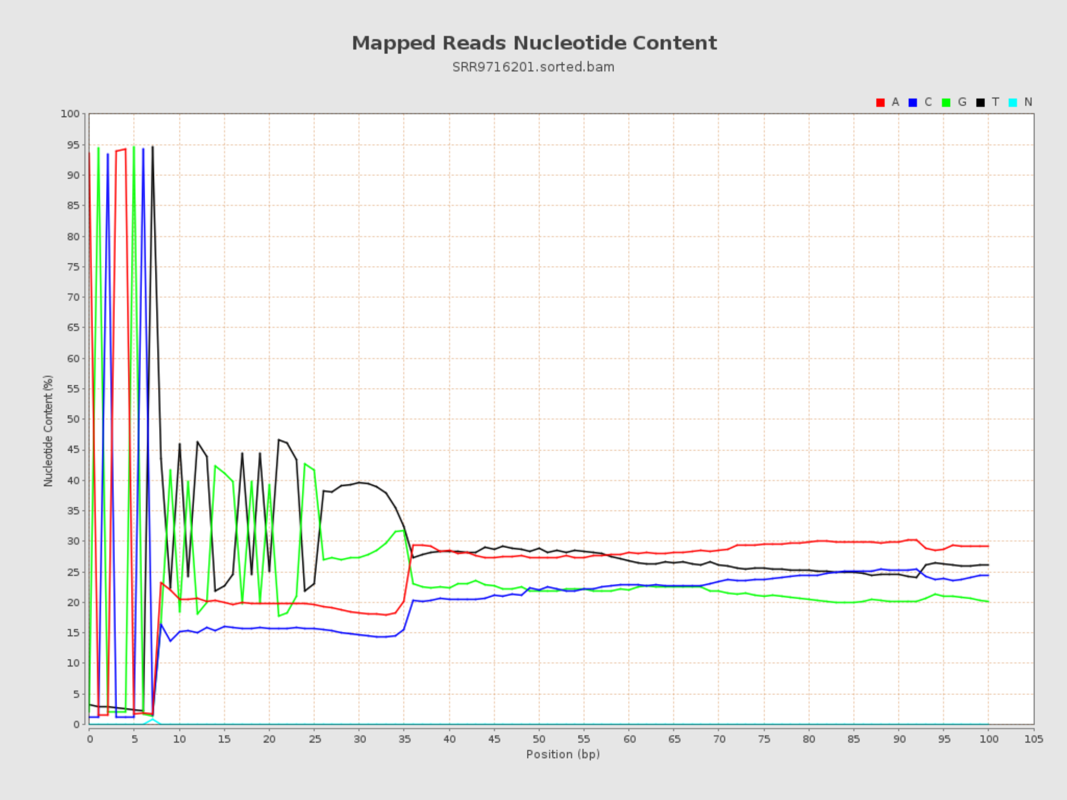
6. Results : Genome Fraction Coverage



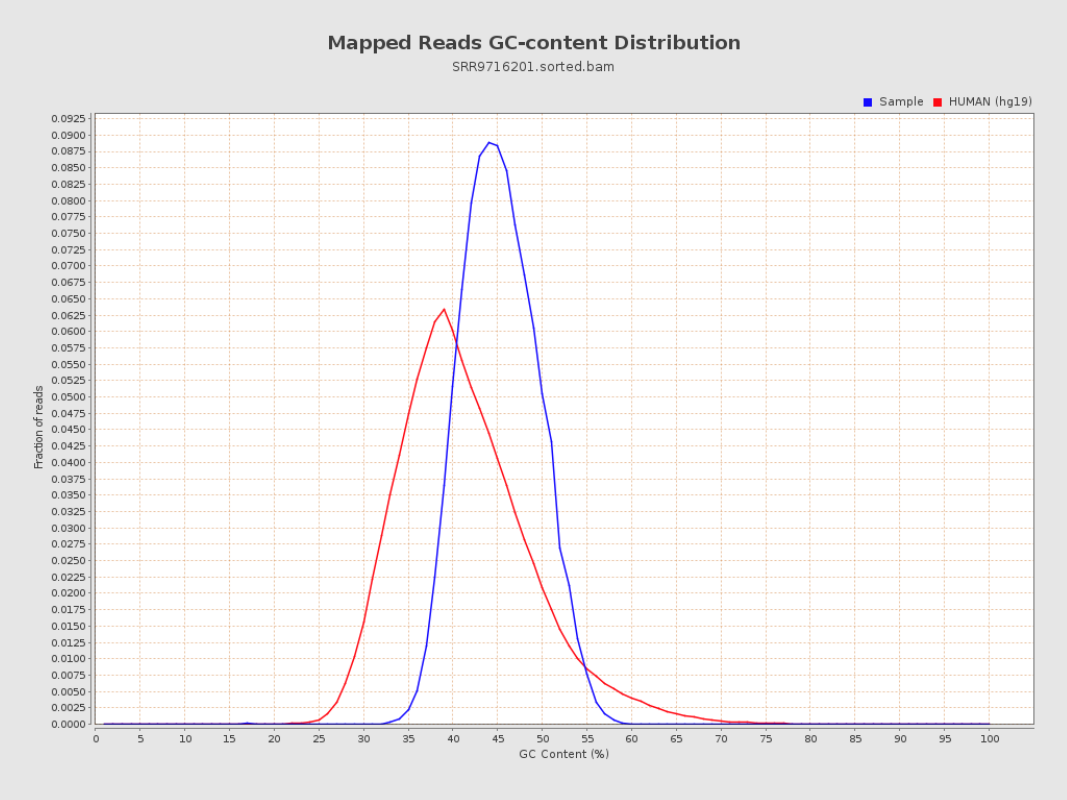
7. Results : Duplication Rate Histogram



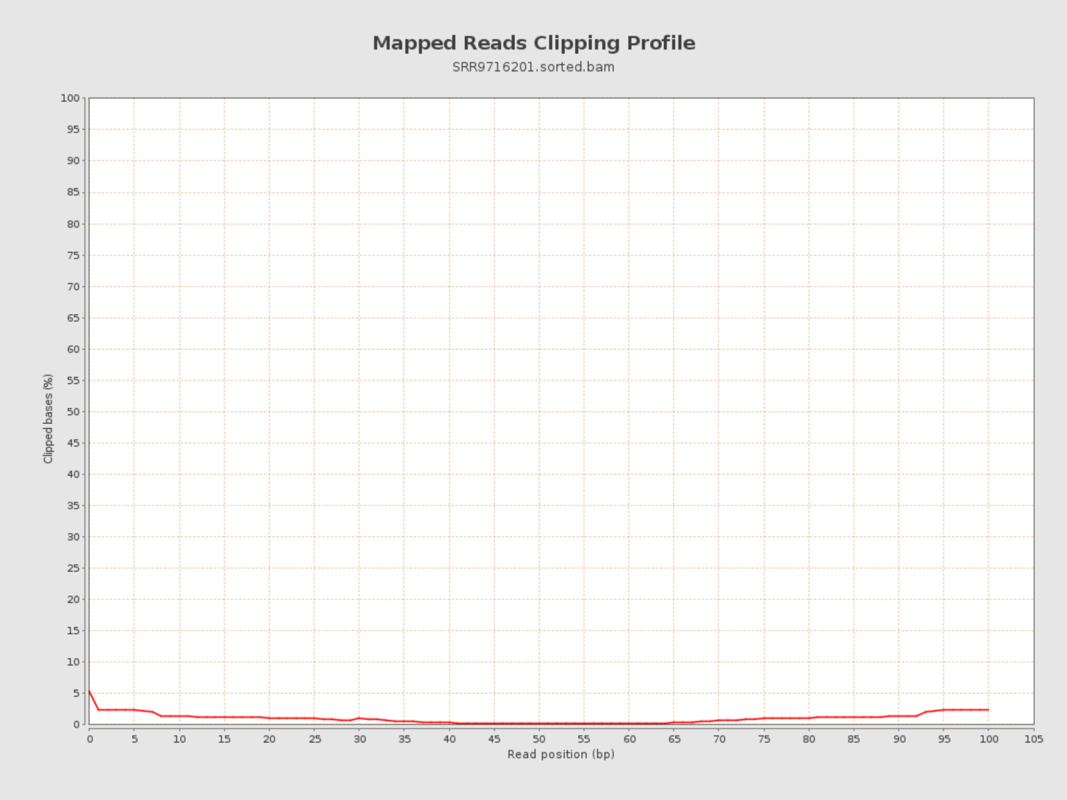
8. Results : Mapped Reads Nucleotide Content



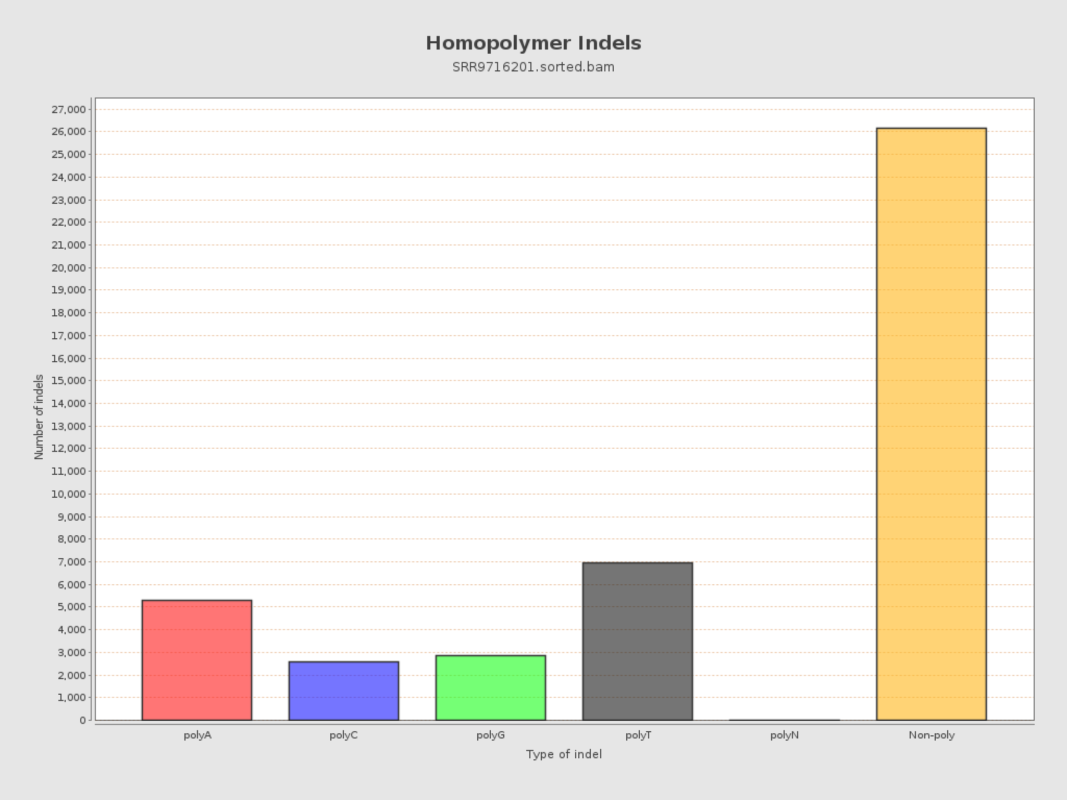
9. Results : Mapped Reads GC-content Distribution



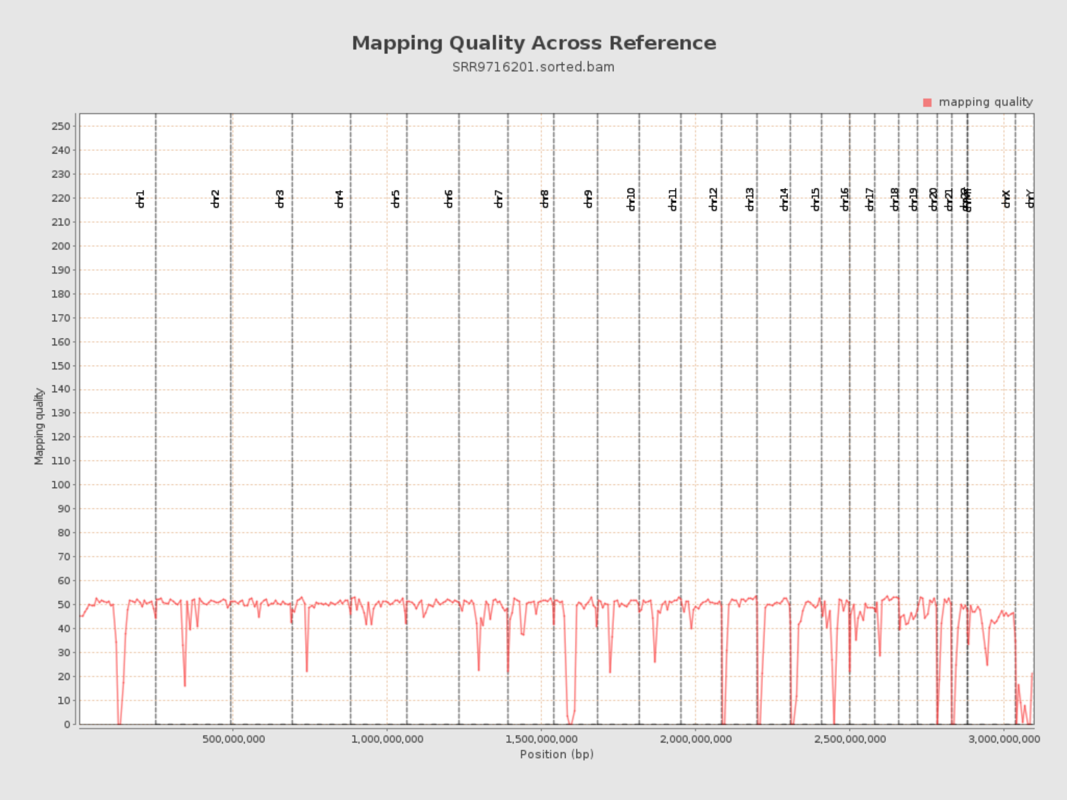
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram