Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 23:20:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716196.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_SRR9716196 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716196.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 23:20:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716196.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,970,741
Mapped reads	1,767,067 / 89.67%
Unmapped reads	203,674 / 10.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	43,763 / 2.22%
Read min/max/mean length	30 / 101 / 101.8
Duplicated reads (estimated)	57,173 / 2.9%
Duplication rate	2.25%
Clipped reads	1,808,133 / 91.75%

2.2. ACGT Content

Number/percentage of A's	33,893,007 / 25.68%
Number/percentage of C's	27,122,543 / 20.55%
Number/percentage of T's	39,442,943 / 29.89%
Number/percentage of G's	31,498,768 / 23.87%
Number/percentage of N's	15,826 / 0.01%
GC Percentage	44.42%

2.3. Coverage

Mean	0.0426

Standard Deviation	0.3386

2.4. Mapping Quality

Mean Mapping Quality	45.84

2.5. Mismatches and indels

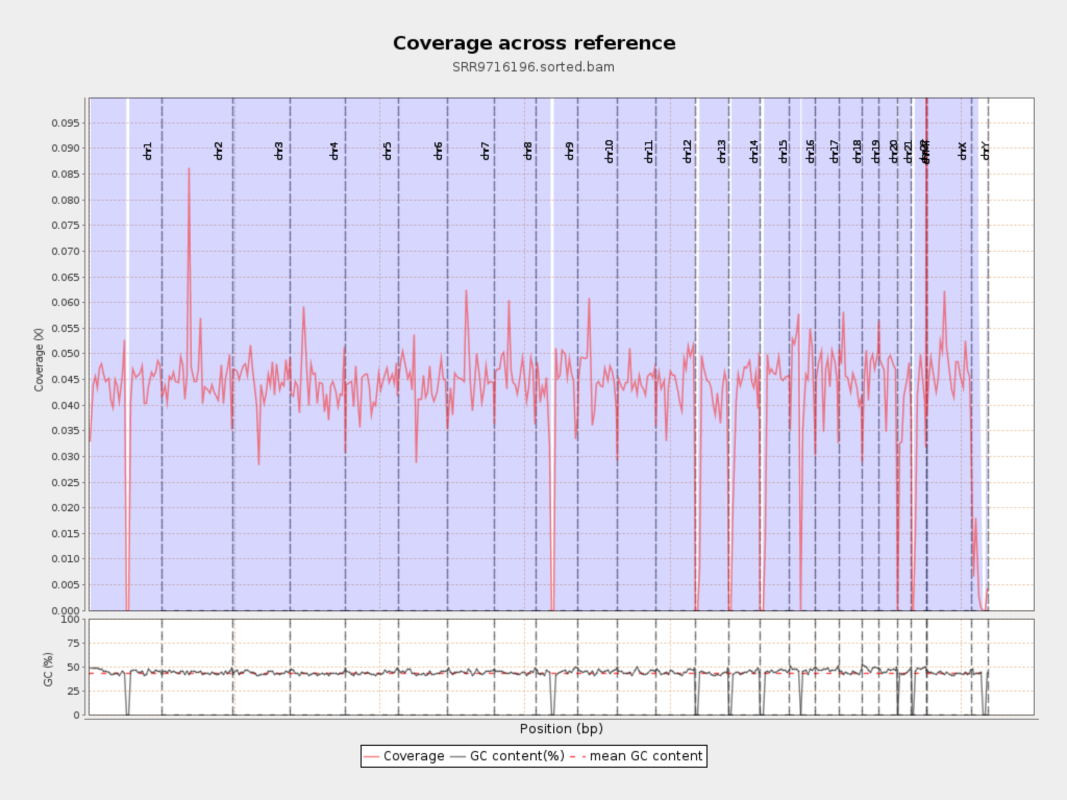
General error rate	0.76%
Mismatches	972,753
Insertions	11,845
Mapped reads with at least one insertion	0.66%
Deletions	25,632
Mapped reads with at least one deletion	1.43%
Homopolymer indels	40.76%

2.6. Chromosome stats

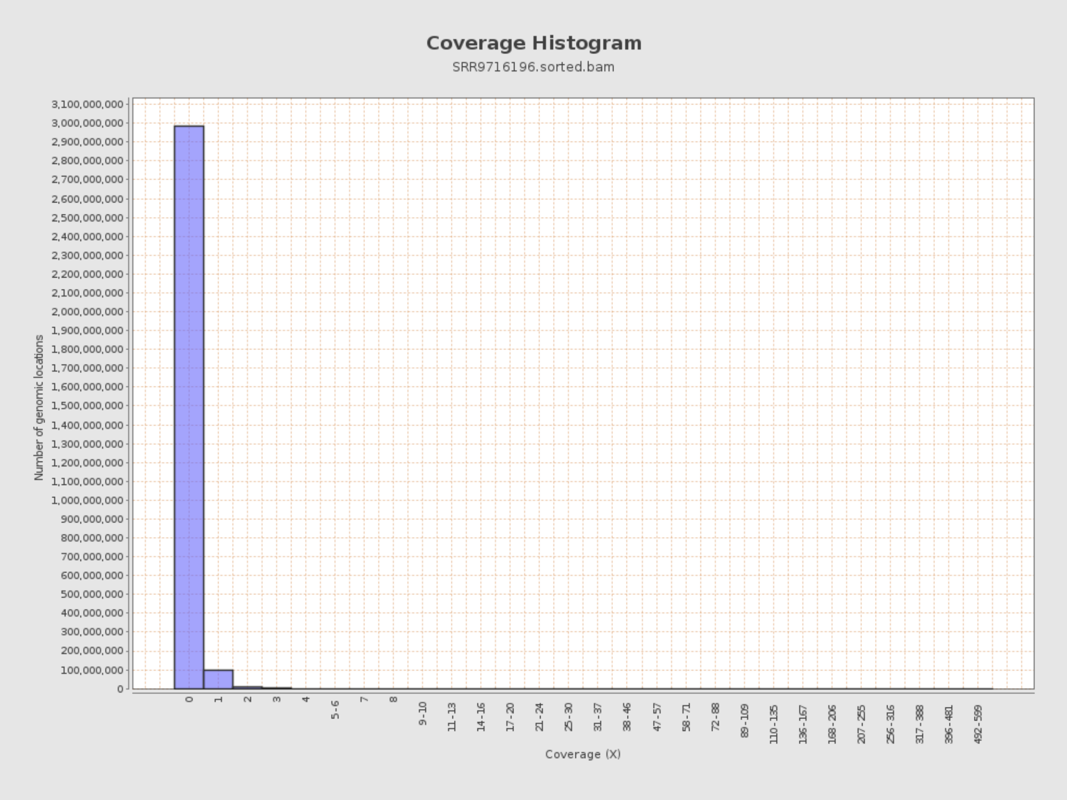
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10418827	0.0418	0.3682
chr2	243199373	11195075	0.046	0.51
chr3	198022430	8851379	0.0447	0.2396
chr4	191154276	8401510	0.044	0.2578
chr5	180915260	7906685	0.0437	0.2377
chr6	171115067	7584607	0.0443	0.2716
chr7	159138663	7224140	0.0454	0.4152

chr8	146364022	6766202	0.0462	0.4334
chr9	141213431	5591468	0.0396	0.364
chr10	135534747	6225469	0.0459	0.323
chr11	135006516	5992019	0.0444	0.3763
chr12	133851895	5996941	0.0448	0.2441
chr13	115169878	4155266	0.0361	0.2152
chr14	107349540	4019201	0.0374	0.2595
chr15	102531392	3843971	0.0375	0.2217
chr16	90354753	3953951	0.0438	0.2605
chr17	81195210	3692625	0.0455	0.2637
chr18	78077248	3590549	0.046	0.6642
chr19	59128983	2777102	0.047	0.3505
chr20	63025520	2868279	0.0455	0.2527
chr21	48129895	1738491	0.0361	0.2392
chr22	51304566	1549409	0.0302	0.1987
chrMT	16571	3775	0.2278	0.5747
chrX	155270560	7334758	0.0472	0.3061
chrY	59373566	336271	0.0057	0.1594

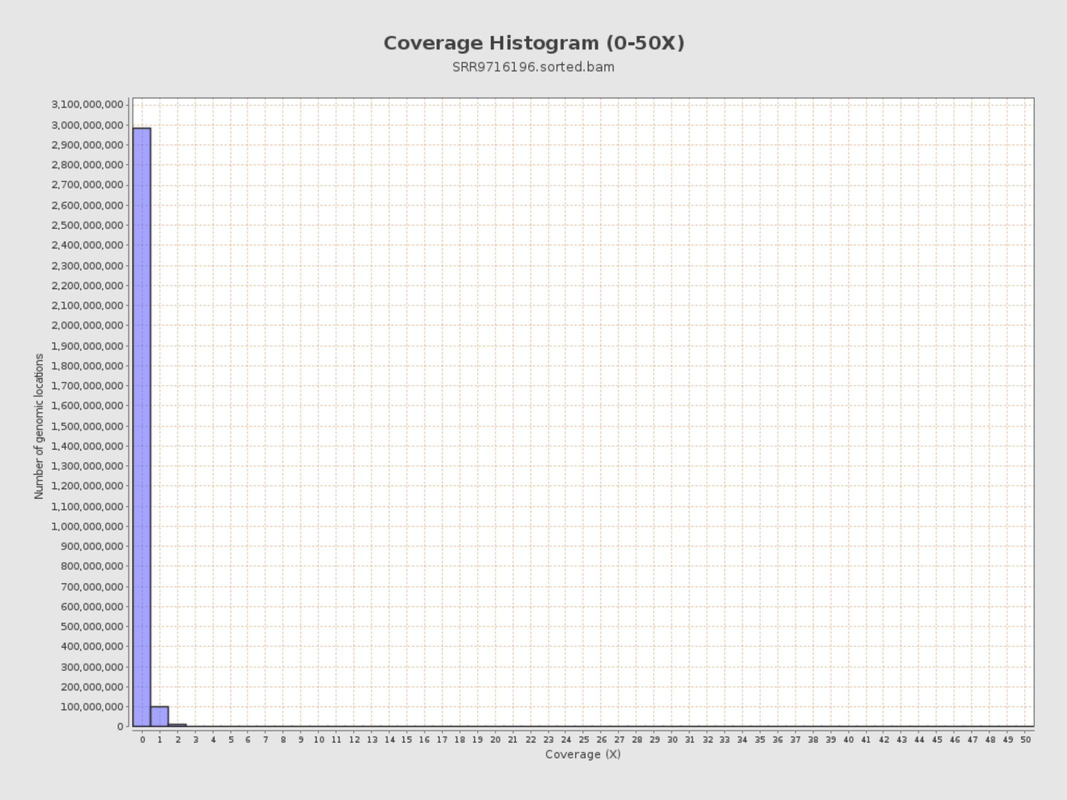
3. Results : Coverage across reference



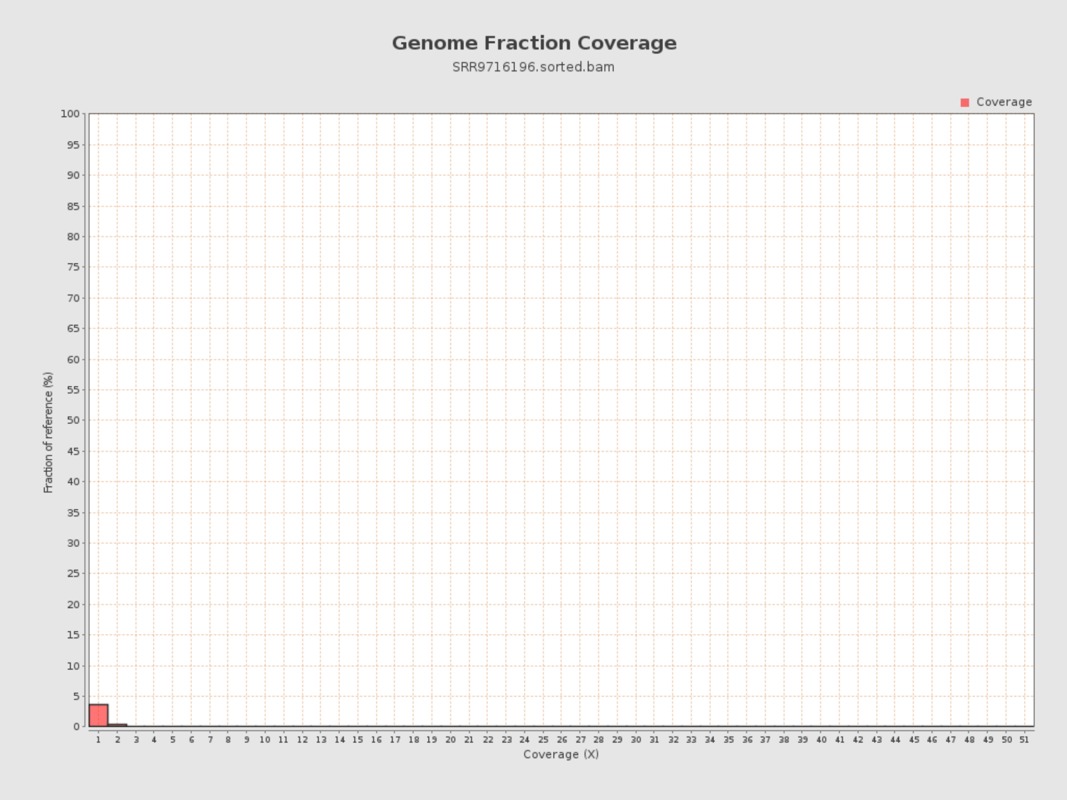
4. Results : Coverage Histogram



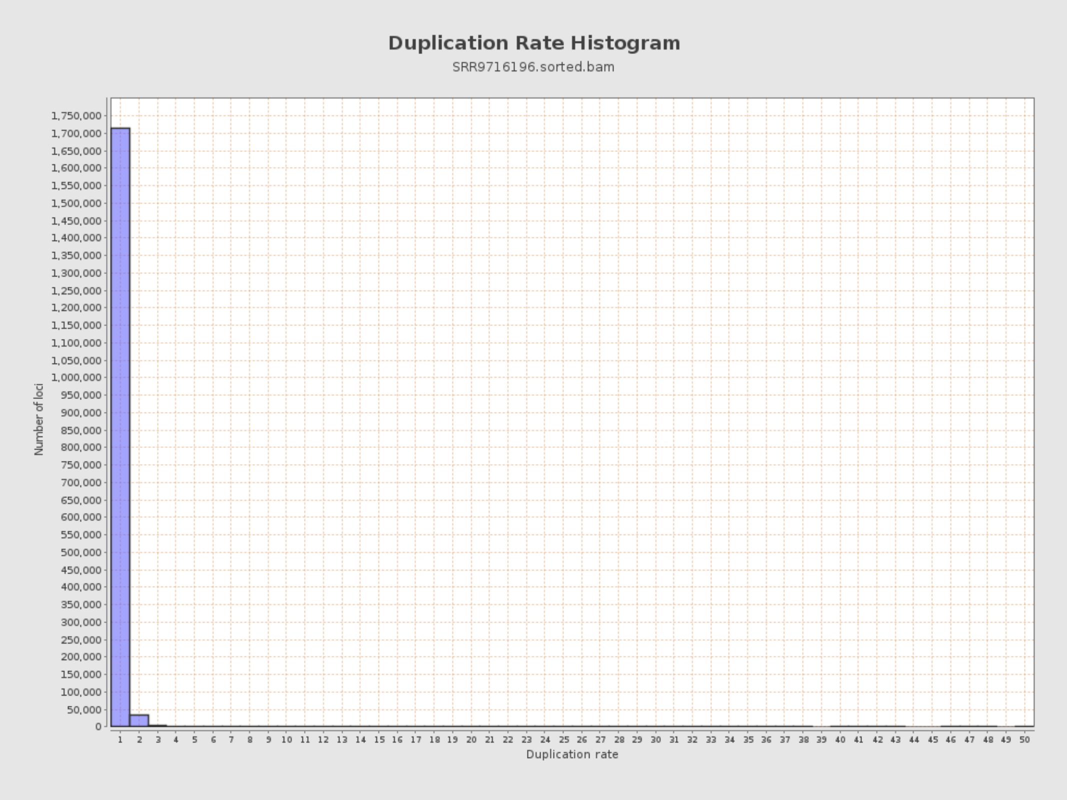
5. Results : Coverage Histogram (0-50X)



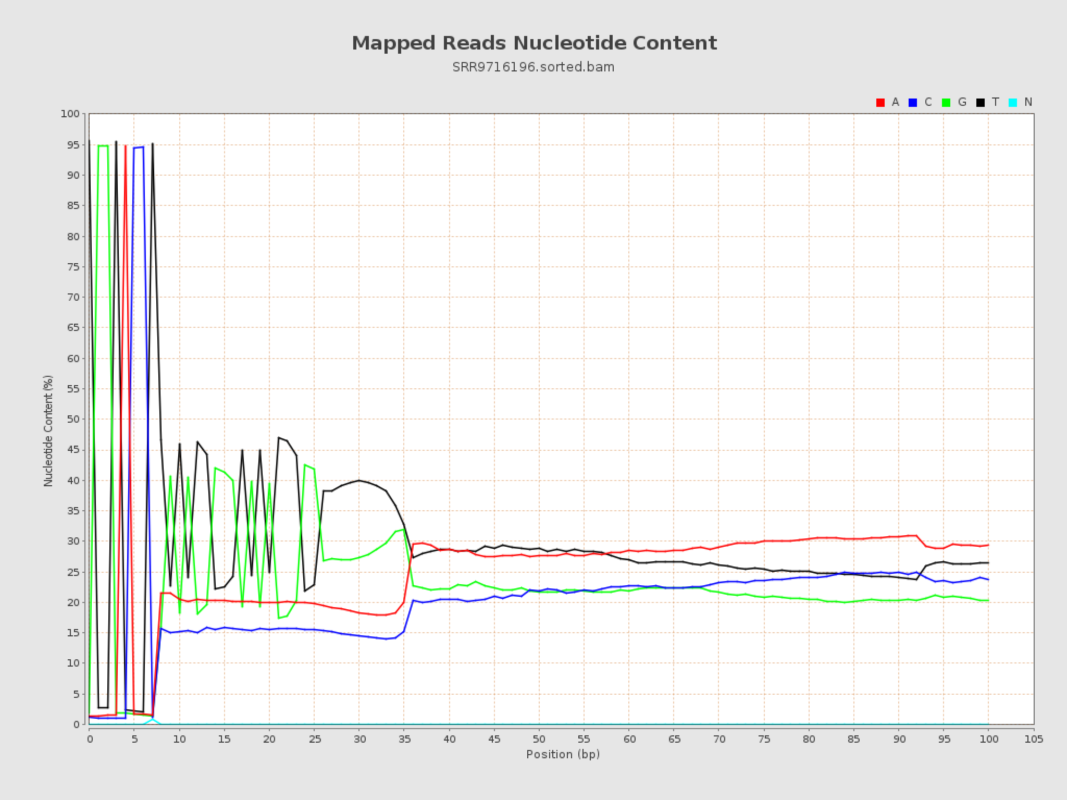
6. Results : Genome Fraction Coverage



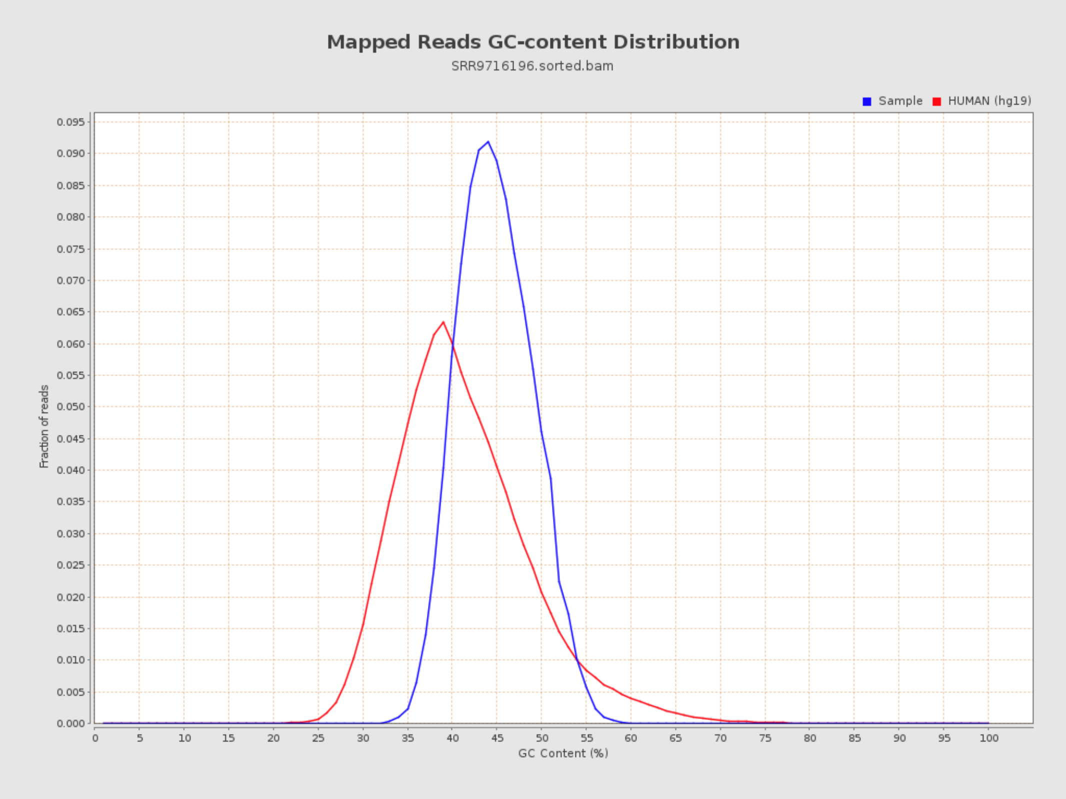
7. Results : Duplication Rate Histogram



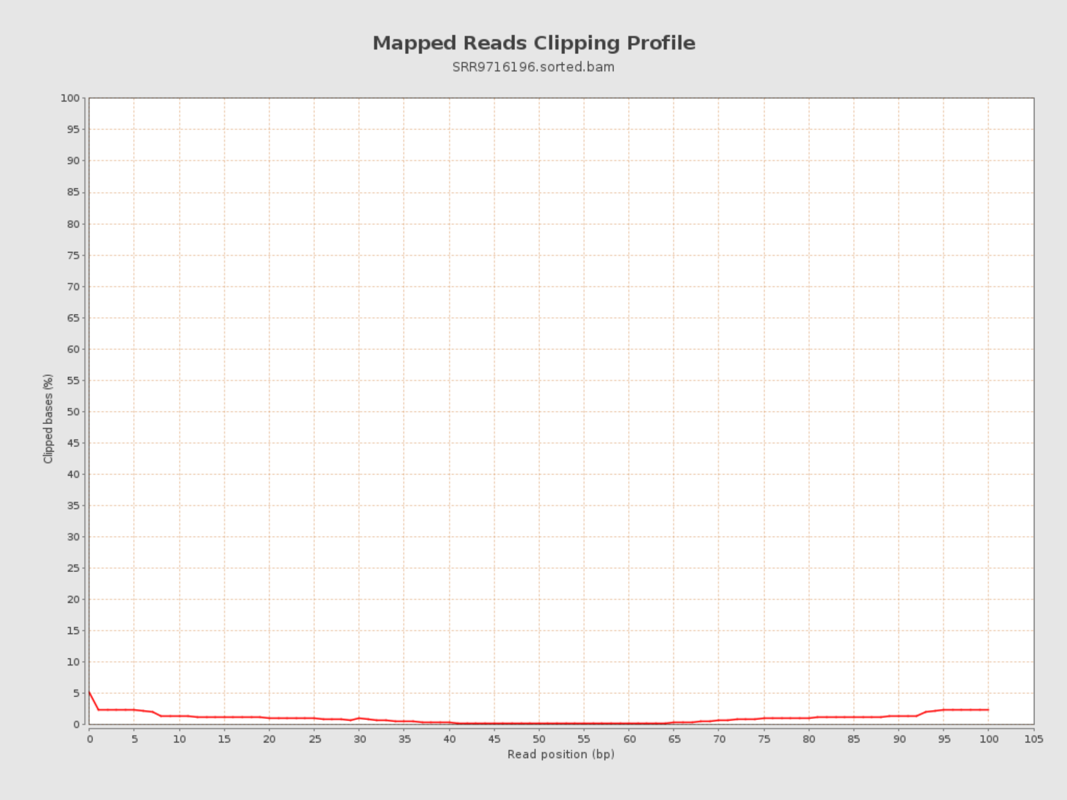
8. Results : Mapped Reads Nucleotide Content



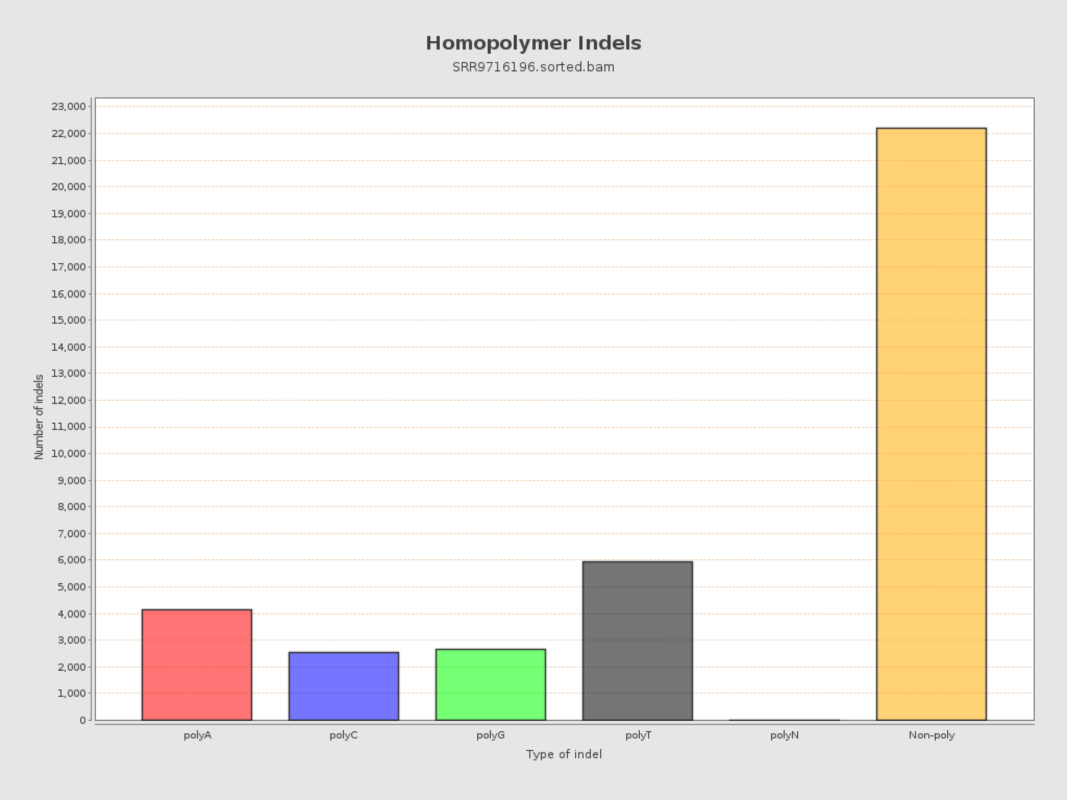
9. Results : Mapped Reads GC-content Distribution



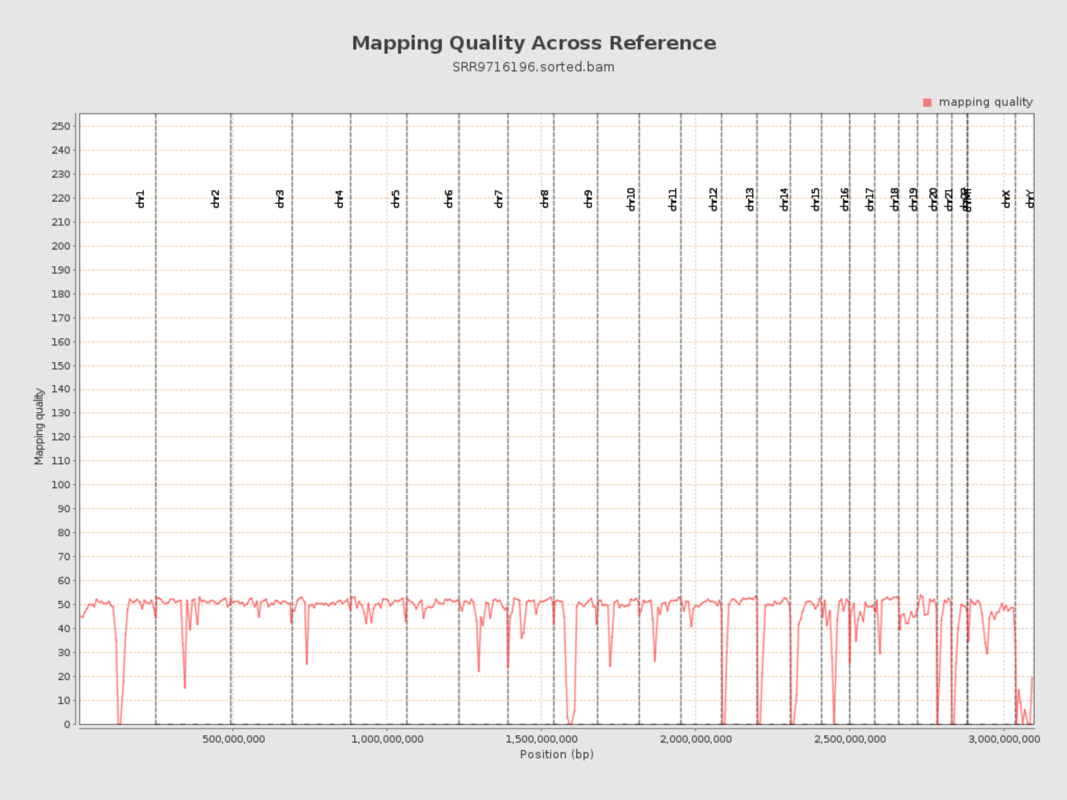
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram