Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 07:05:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716701.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_SRR9716701 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716701.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 07:05:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716701.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,264,925
Mapped reads	2,040,371 / 90.09%
Unmapped reads	224,554 / 9.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,890 / 1.32%
Read min/max/mean length	30 / 101 / 101.49
Duplicated reads (estimated)	91,663 / 4.05%
Duplication rate	3.14%
Clipped reads	2,067,237 / 91.27%

2.2. ACGT Content

Number/percentage of A's	37,156,819 / 23.41%
Number/percentage of C's	32,863,513 / 20.7%
Number/percentage of T's	48,927,443 / 30.82%
Number/percentage of G's	39,773,639 / 25.06%
Number/percentage of N's	8,893 / 0.01%
GC Percentage	45.76%

2.3. Coverage

Mean	0.0513

Standard Deviation	0.466

2.4. Mapping Quality

Mean Mapping Quality	41.93

2.5. Mismatches and indels

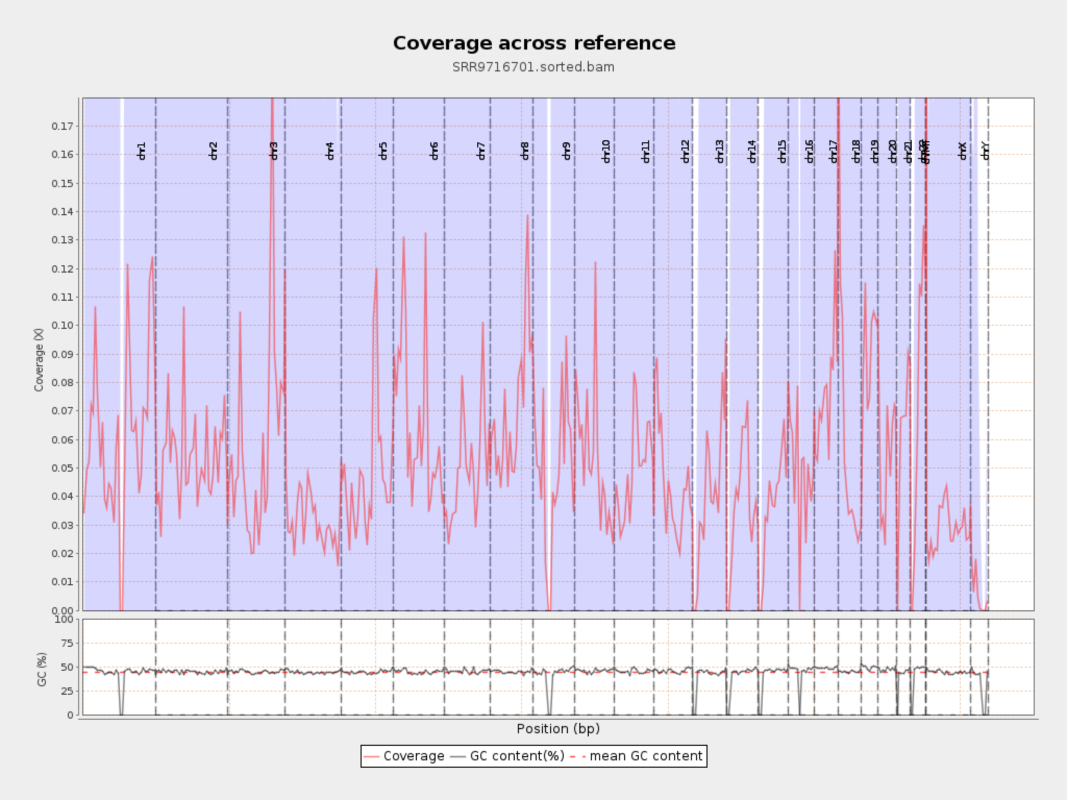
General error rate	0.88%
Mismatches	1,367,040
Insertions	14,716
Mapped reads with at least one insertion	0.71%
Deletions	37,274
Mapped reads with at least one deletion	1.8%
Homopolymer indels	44.35%

2.6. Chromosome stats

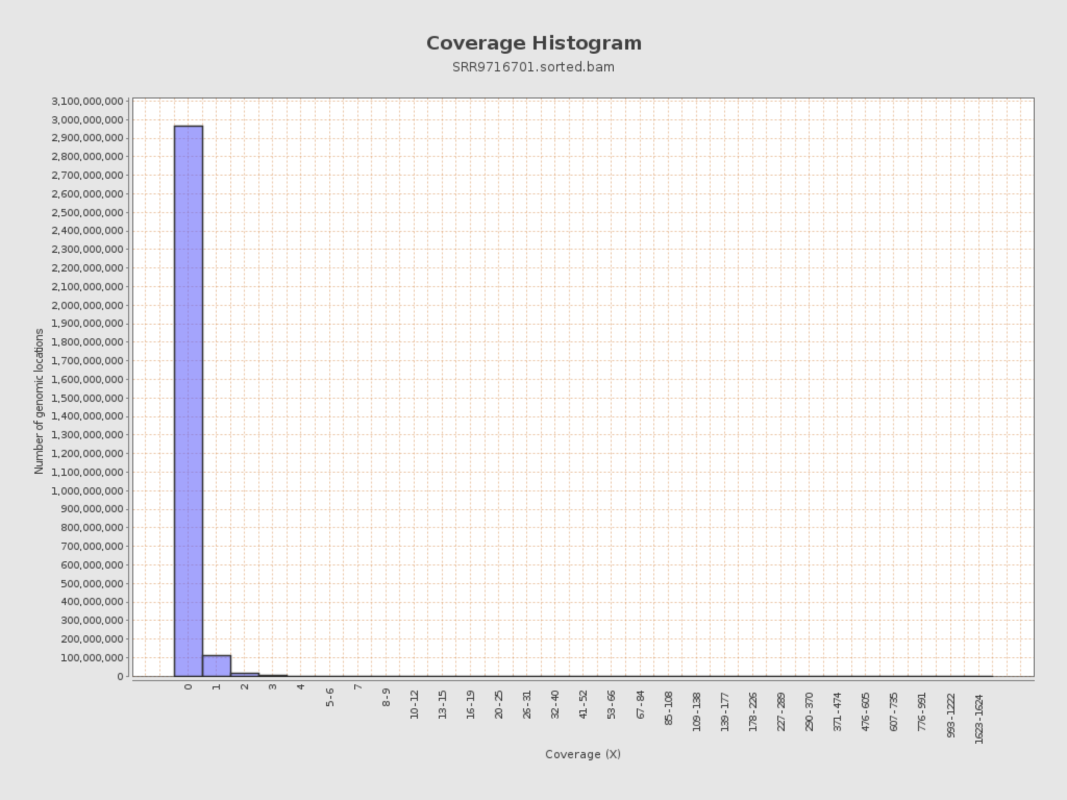
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15403775	0.0618	0.5761
chr2	243199373	13193601	0.0543	0.9146
chr3	198022430	11406202	0.0576	0.2938
chr4	191154276	5978914	0.0313	0.2379
chr5	180915260	8547772	0.0472	0.2608
chr6	171115067	11297781	0.066	0.3691
chr7	159138663	7957413	0.05	0.5736

chr8	146364022	10351445	0.0707	0.6115
chr9	141213431	6843450	0.0485	0.4361
chr10	135534747	7334481	0.0541	0.4063
chr11	135006516	6640482	0.0492	0.3284
chr12	133851895	6069057	0.0453	0.2533
chr13	115169878	4643855	0.0403	0.239
chr14	107349540	4013537	0.0374	0.2541
chr15	102531392	3638569	0.0355	0.2427
chr16	90354753	4390607	0.0486	0.2962
chr17	81195210	6184031	0.0762	0.3559
chr18	78077248	4551637	0.0583	0.82
chr19	59128983	5343934	0.0904	0.5475
chr20	63025520	3325671	0.0528	0.2989
chr21	48129895	2927362	0.0608	0.3056
chr22	51304566	3636201	0.0709	0.3332
chrMT	16571	286846	17.3101	11.5155
chrX	155270560	4478996	0.0288	0.2515
chrY	59373566	351199	0.0059	0.1632

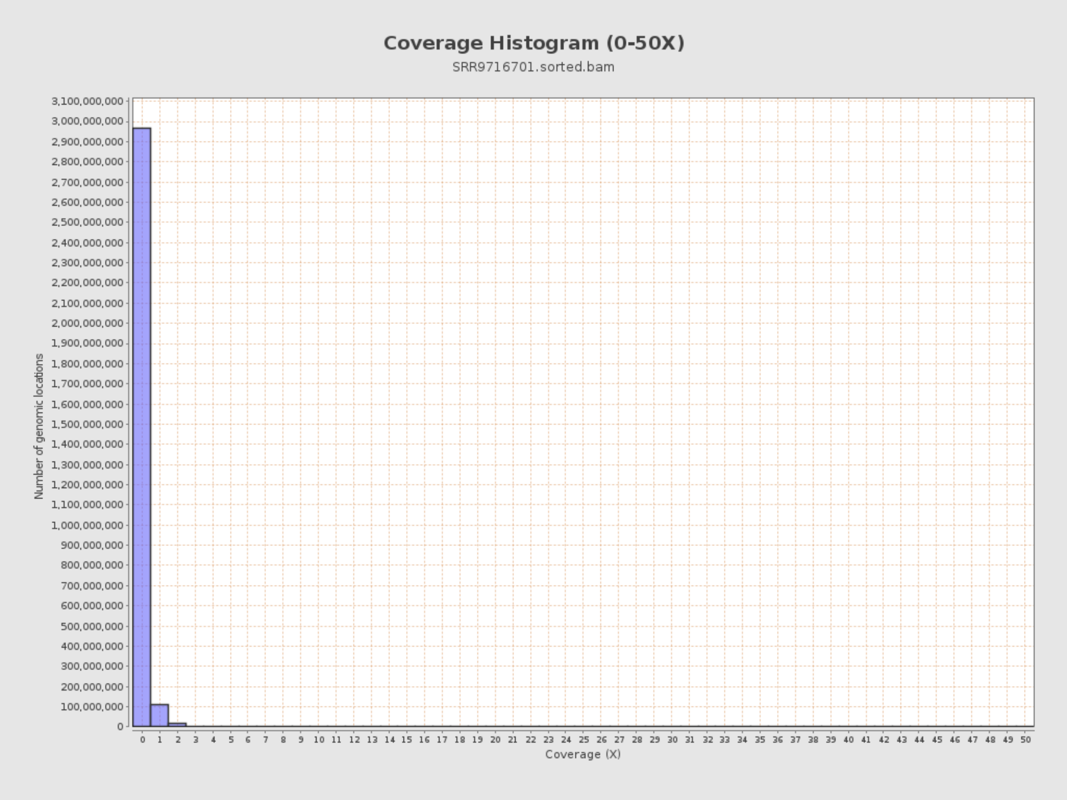
3. Results : Coverage across reference



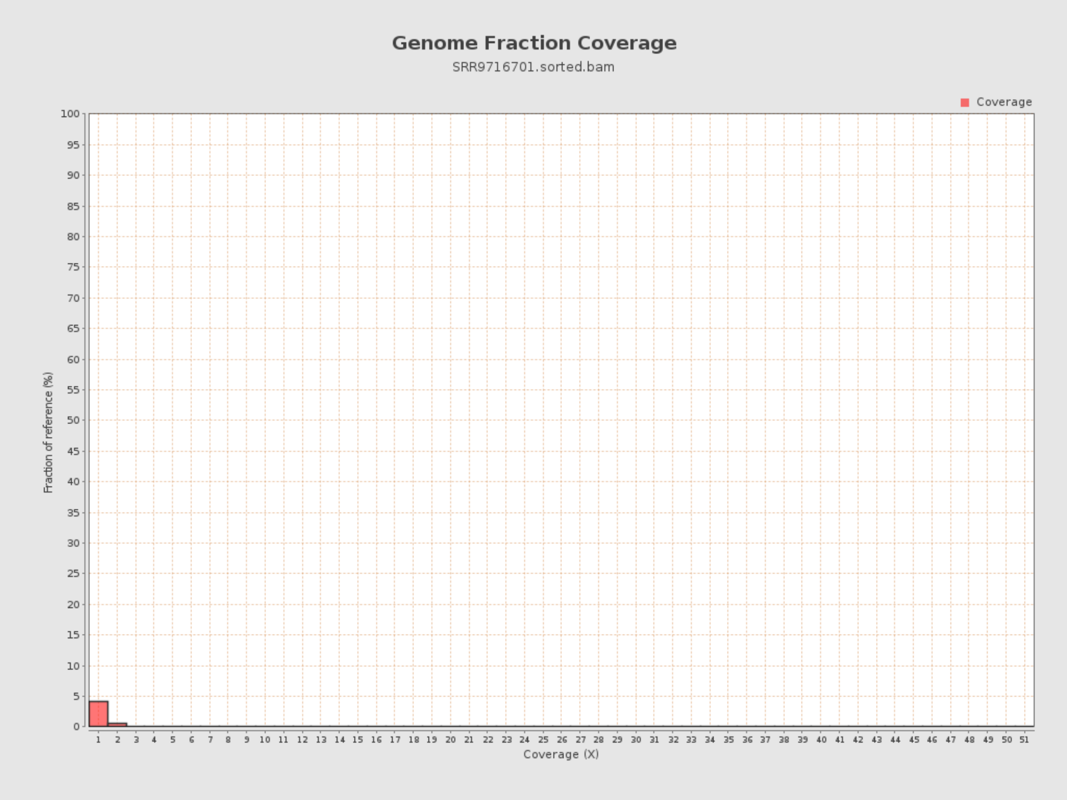
4. Results : Coverage Histogram



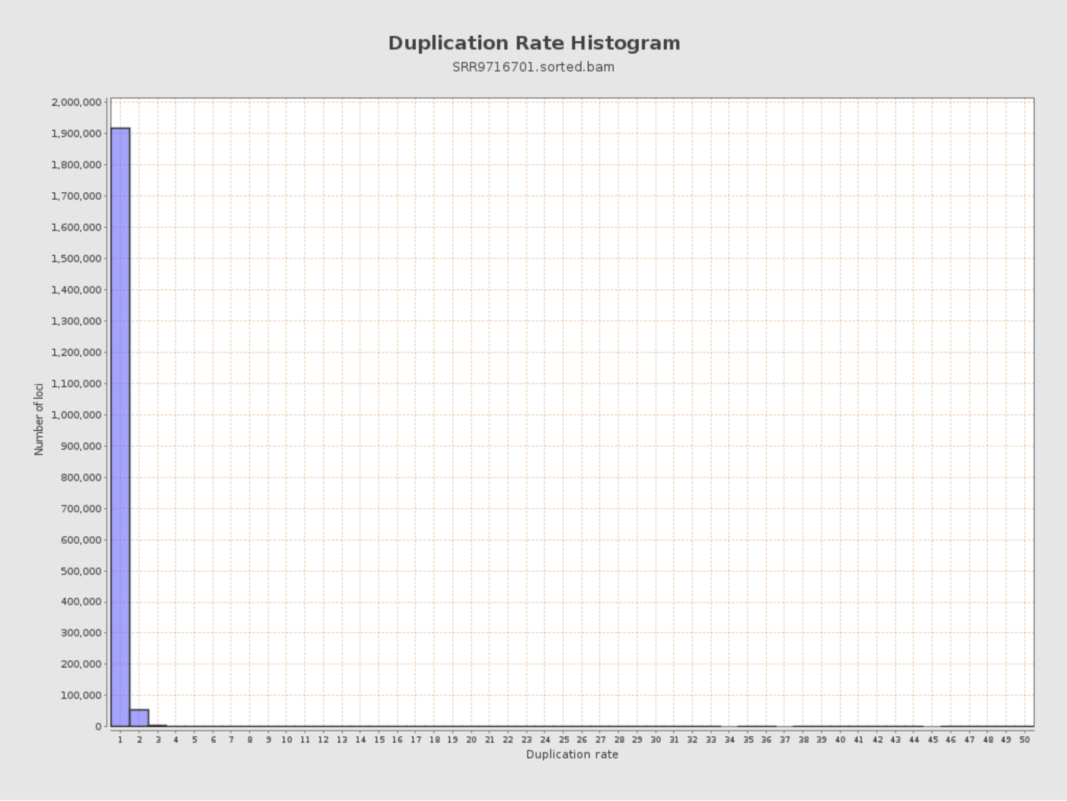
5. Results : Coverage Histogram (0-50X)



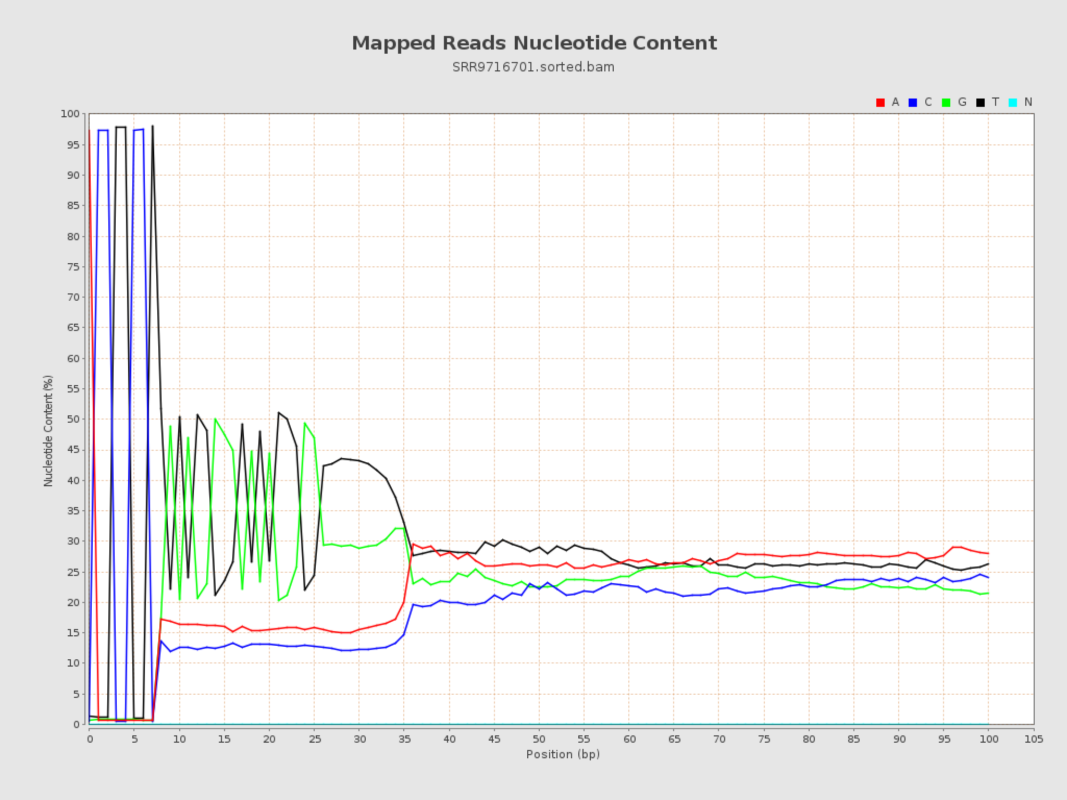
6. Results : Genome Fraction Coverage



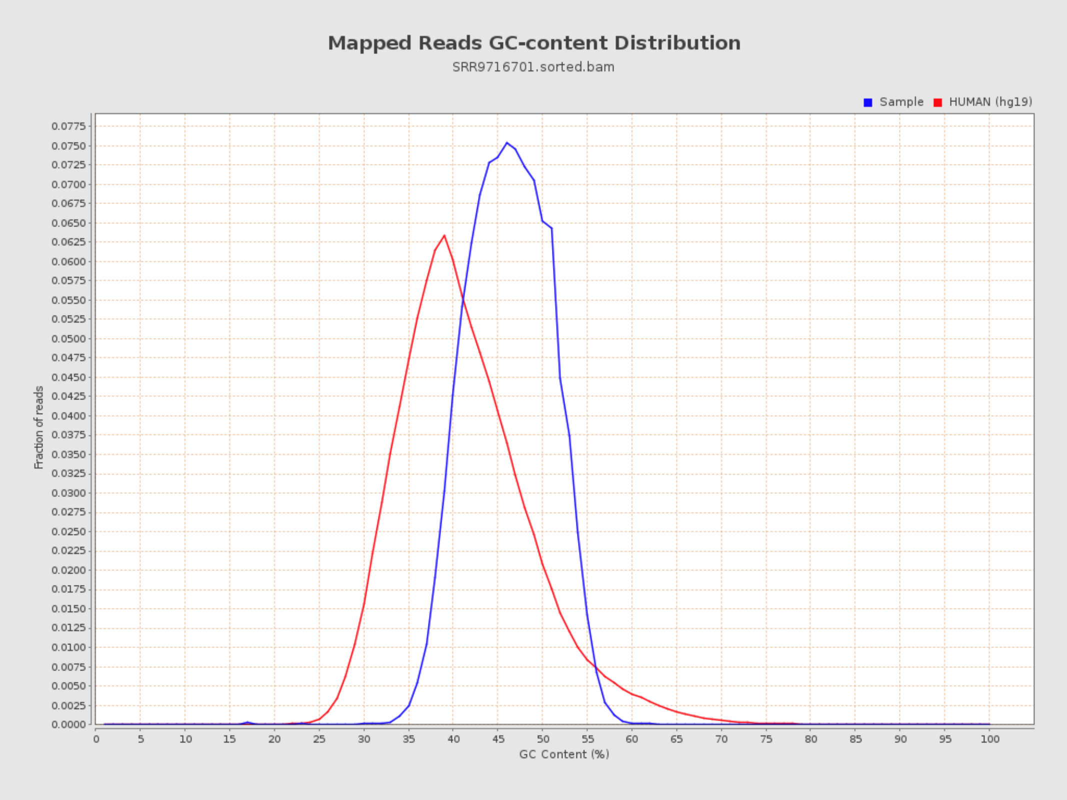
7. Results : Duplication Rate Histogram



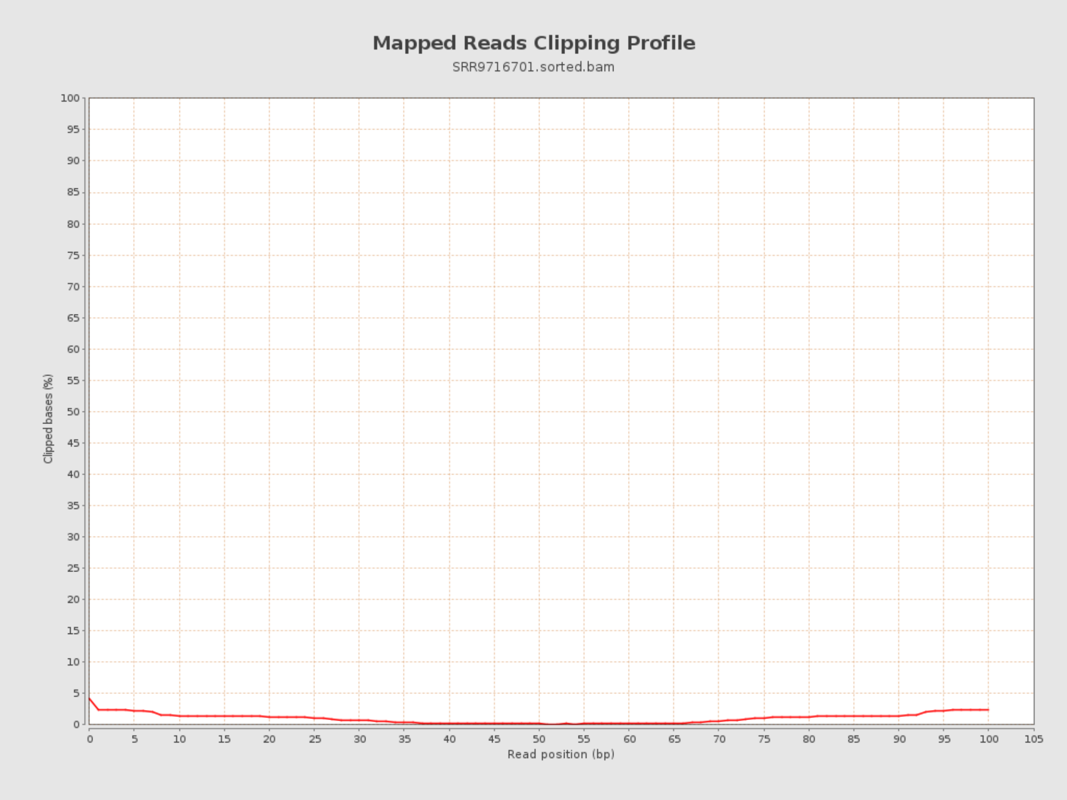
8. Results : Mapped Reads Nucleotide Content



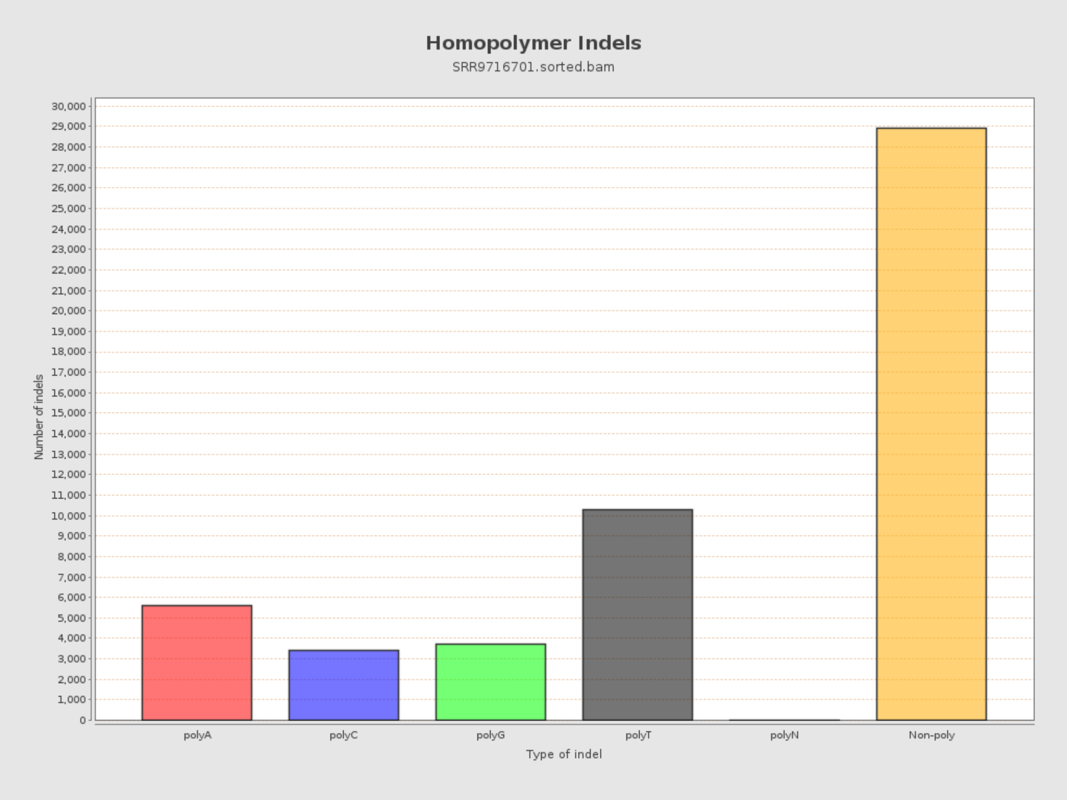
9. Results : Mapped Reads GC-content Distribution



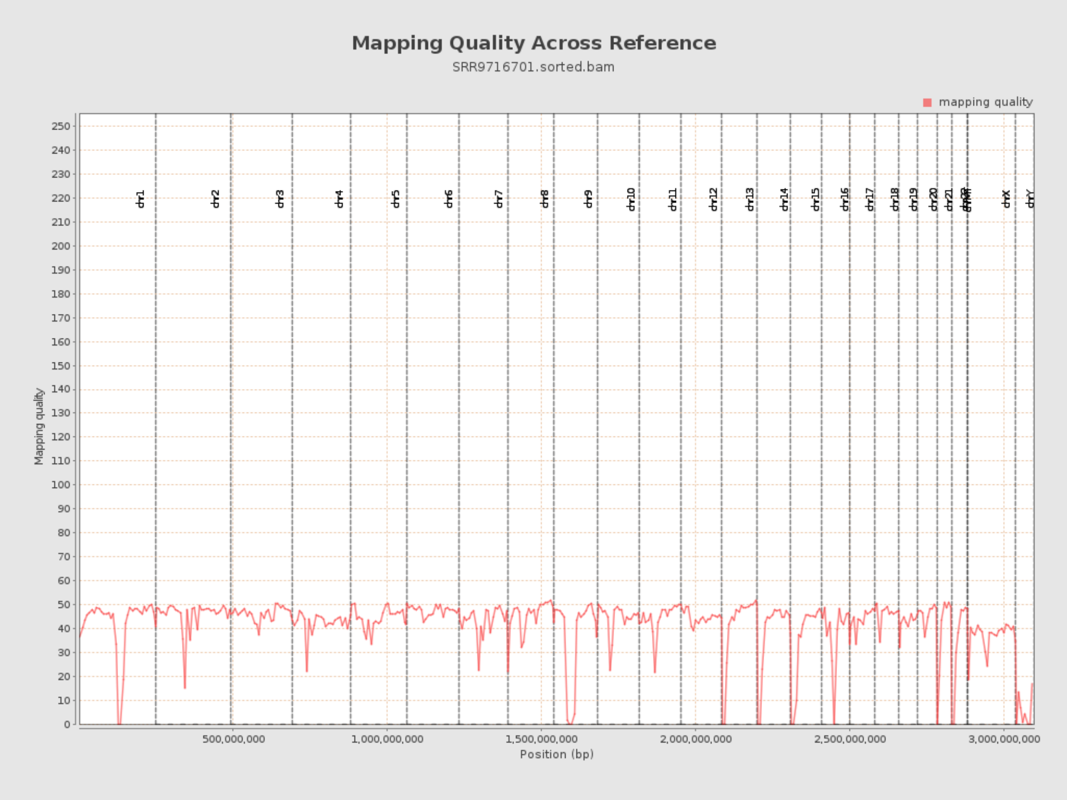
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram