Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 18:01:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716101.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_SRR9716101 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716101.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 18:01:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716101.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,809,476
Mapped reads	2,577,906 / 91.76%
Unmapped reads	231,570 / 8.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,121 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	123,378 / 4.39%
Duplication rate	3.41%
Clipped reads	2,584,736 / 92%

2.2. ACGT Content

Number/percentage of A's	37,480,635 / 25.12%
Number/percentage of C's	28,850,043 / 19.34%
Number/percentage of T's	47,214,396 / 31.65%
Number/percentage of G's	35,646,691 / 23.89%
Number/percentage of N's	2,935 / 0%
GC Percentage	43.23%

2.3. Coverage

Mean	0.0482

Standard Deviation	0.4202

2.4. Mapping Quality

Mean Mapping Quality	44.11

2.5. Mismatches and indels

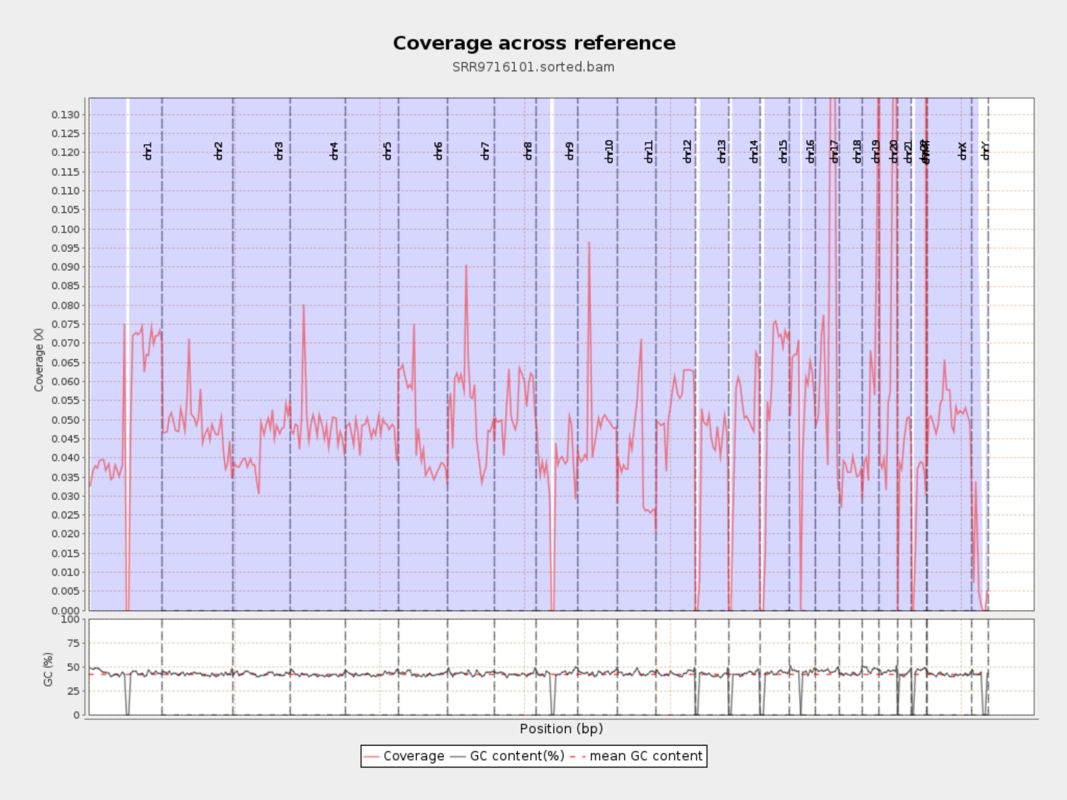
General error rate	0.52%
Mismatches	756,811
Insertions	8,849
Mapped reads with at least one insertion	0.34%
Deletions	28,871
Mapped reads with at least one deletion	1.11%
Homopolymer indels	44.24%

2.6. Chromosome stats

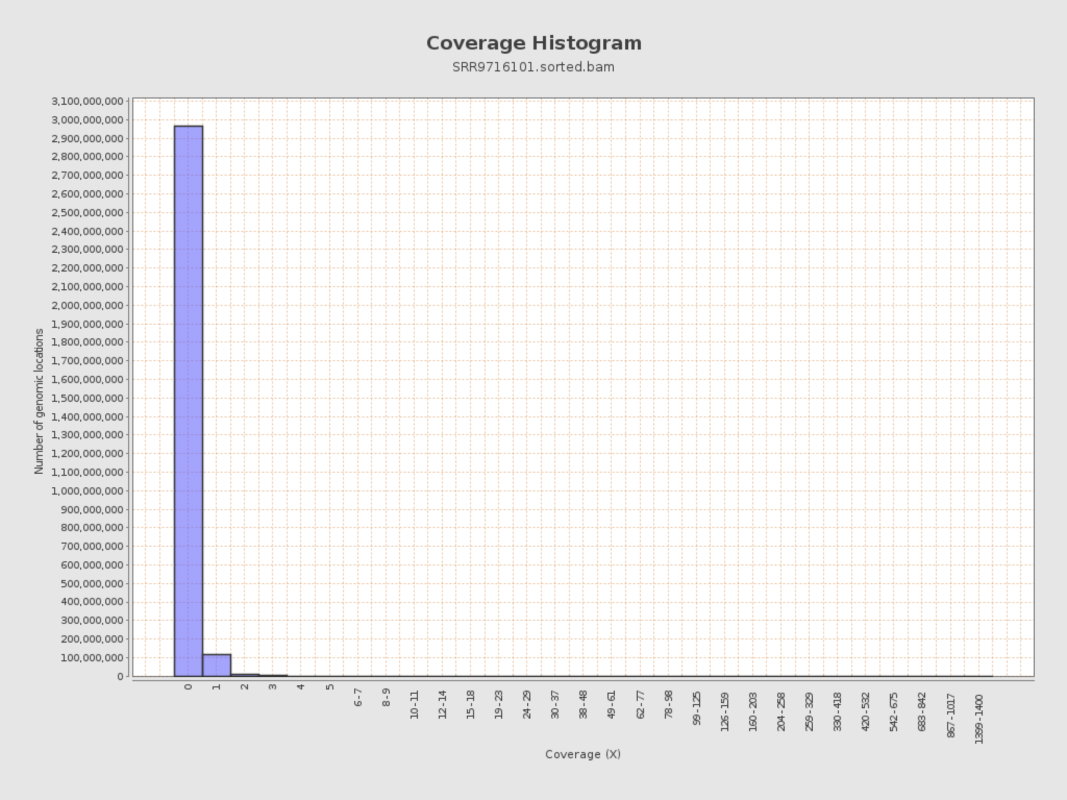
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12517947	0.0502	0.7014
chr2	243199373	11749423	0.0483	0.6207
chr3	198022430	8602756	0.0434	0.2405
chr4	191154276	9294460	0.0486	0.303
chr5	180915260	8547918	0.0472	0.2462
chr6	171115067	8014677	0.0468	0.315
chr7	159138663	8450576	0.0531	0.5907

chr8	146364022	7920963	0.0541	0.5473
chr9	141213431	4940460	0.035	0.2843
chr10	135534747	6555771	0.0484	0.4369
chr11	135006516	5301870	0.0393	0.3202
chr12	133851895	7395452	0.0553	0.2713
chr13	115169878	4511604	0.0392	0.2266
chr14	107349540	4999135	0.0466	0.2532
chr15	102531392	5530956	0.0539	0.2725
chr16	90354753	5047033	0.0559	0.2943
chr17	81195210	6422191	0.0791	0.3421
chr18	78077248	2815432	0.0361	0.5306
chr19	59128983	3771602	0.0638	0.5475
chr20	63025520	4861442	0.0771	0.3345
chr21	48129895	1927782	0.0401	0.28
chr22	51304566	1342603	0.0262	0.1835
chrMT	16571	173051	10.443	6.6858
chrX	155270560	8036445	0.0518	0.2931
chrY	59373566	510416	0.0086	0.335

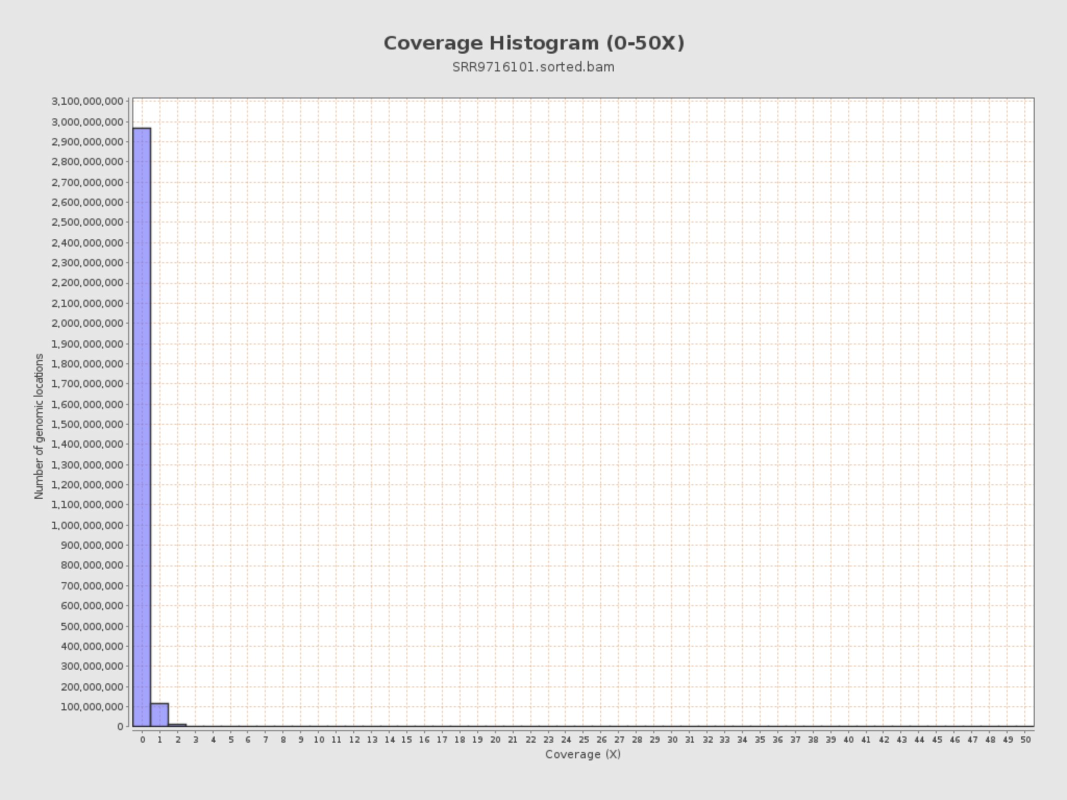
3. Results : Coverage across reference



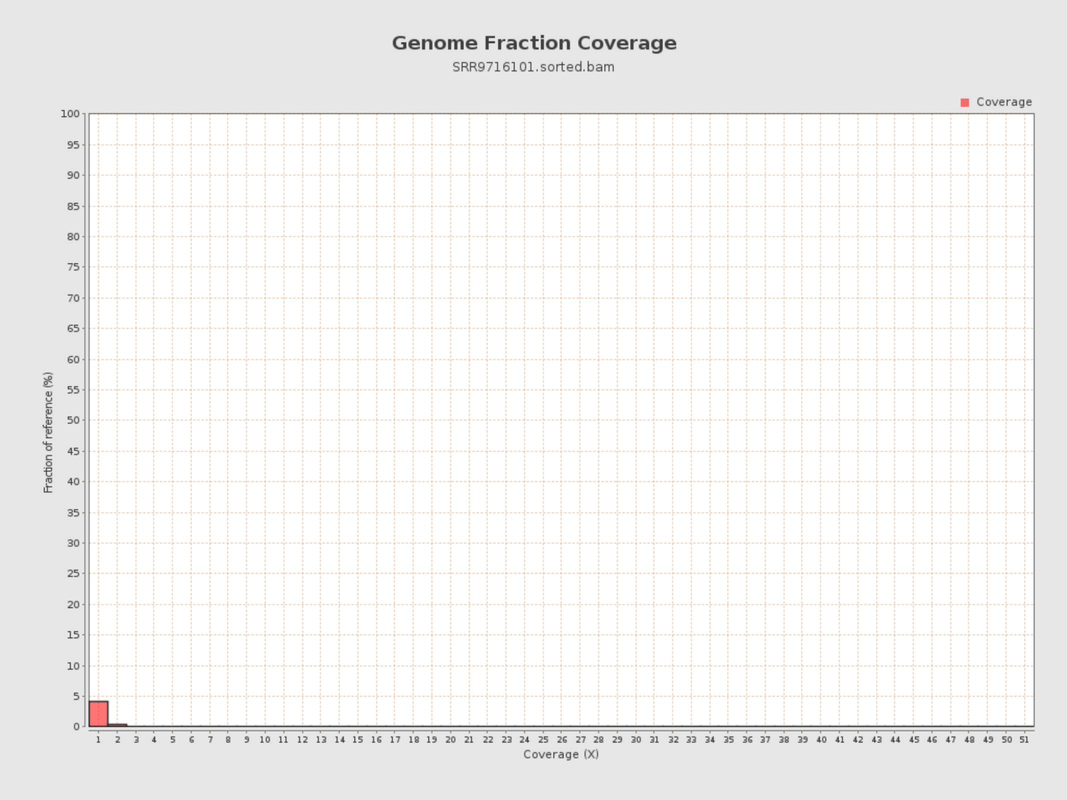
4. Results : Coverage Histogram



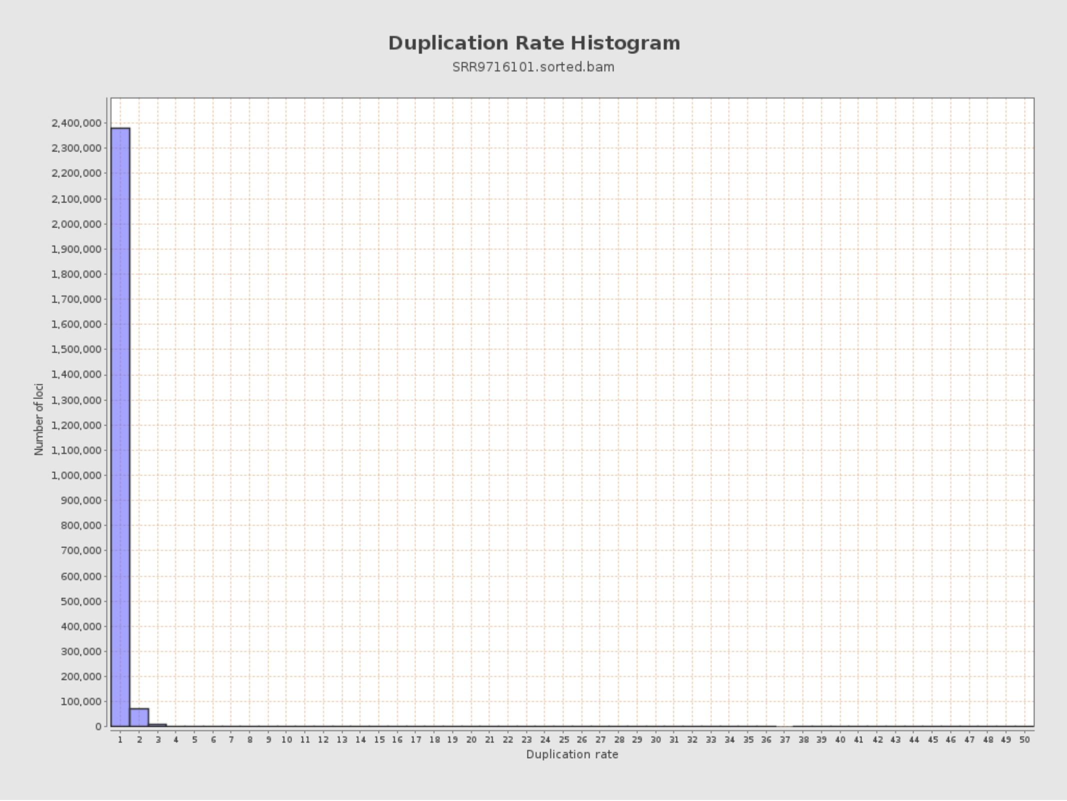
5. Results : Coverage Histogram (0-50X)



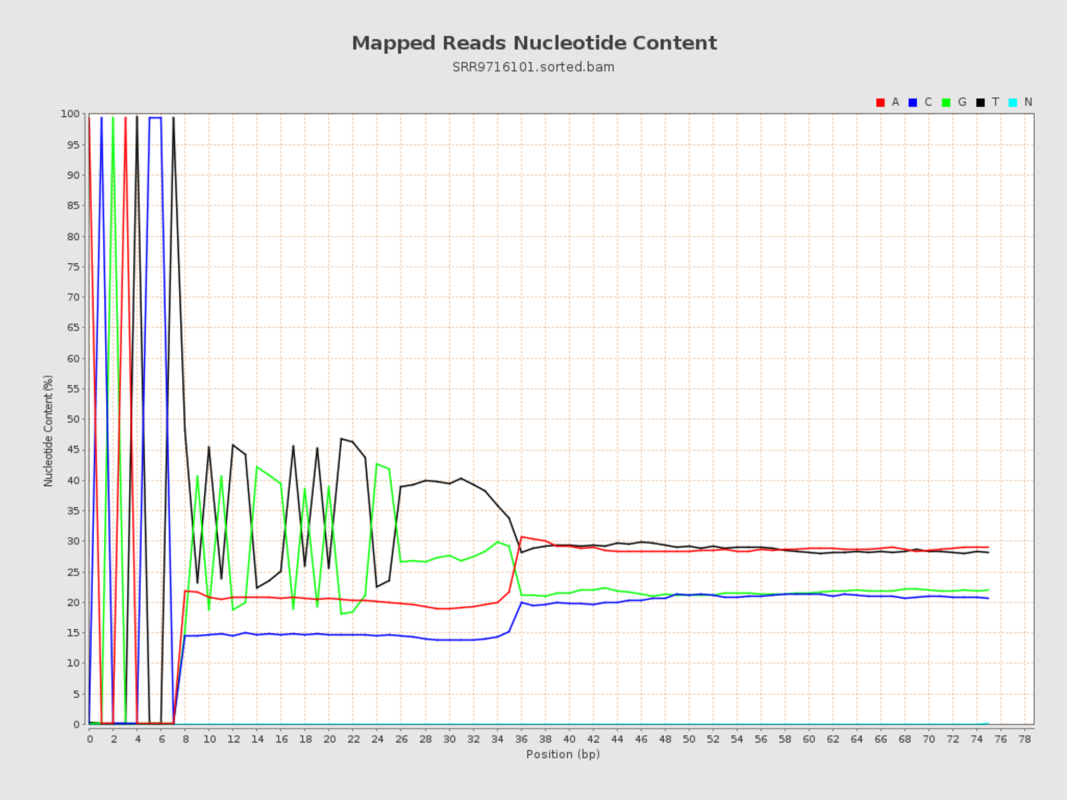
6. Results : Genome Fraction Coverage



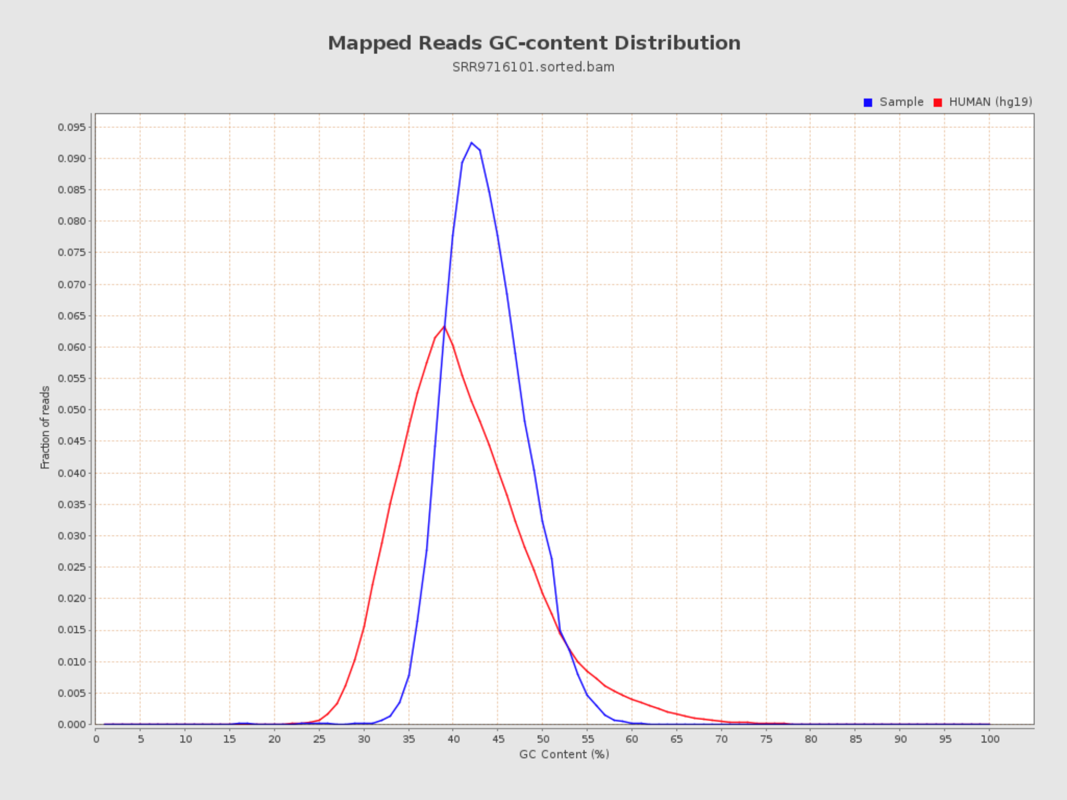
7. Results : Duplication Rate Histogram



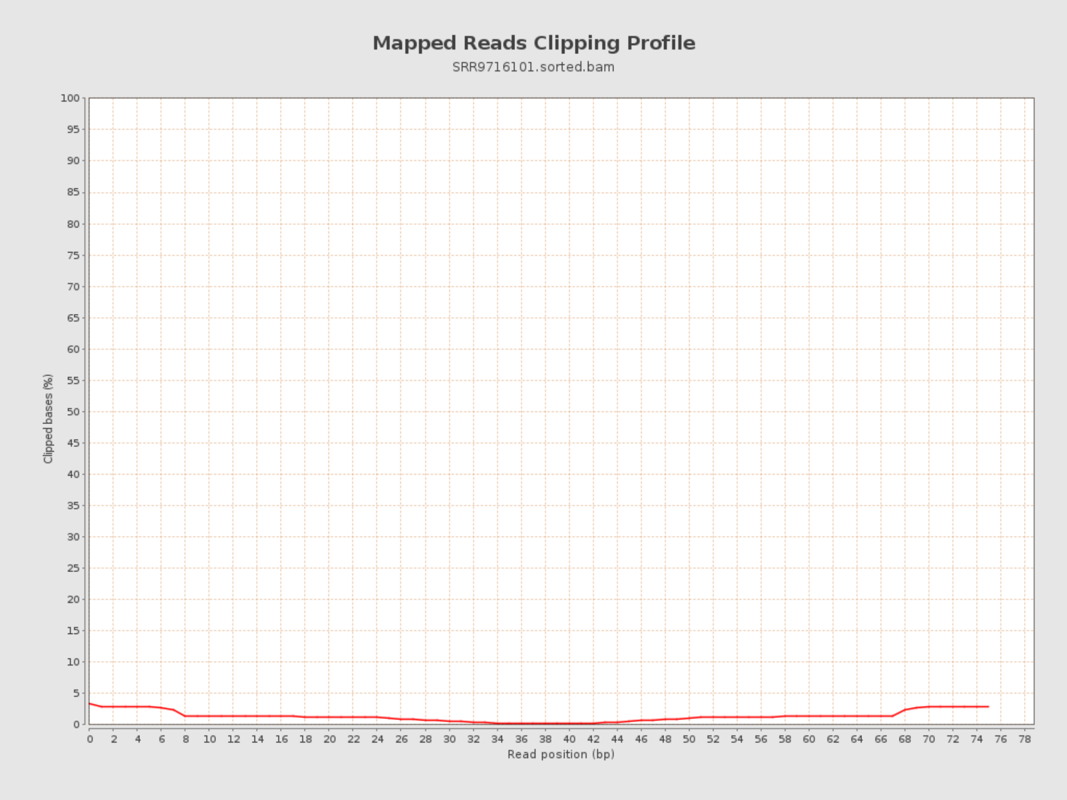
8. Results : Mapped Reads Nucleotide Content



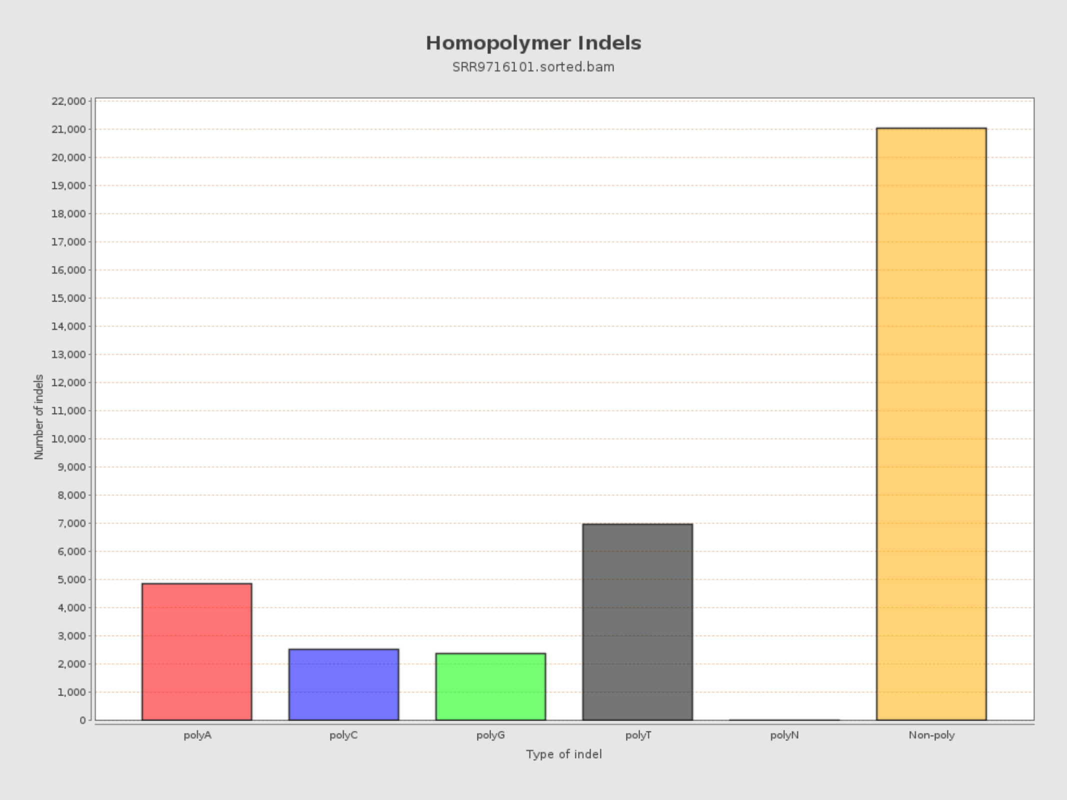
9. Results : Mapped Reads GC-content Distribution



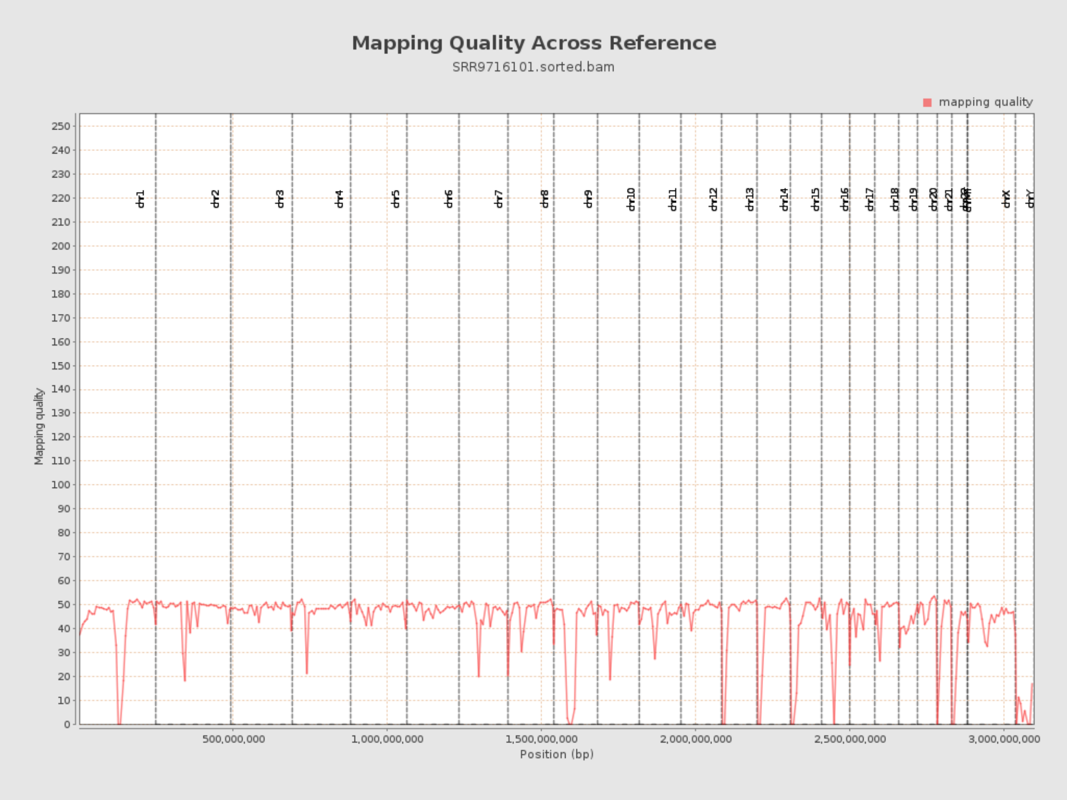
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram