Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 23:36:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716200.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_SRR9716200 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716200.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 23:36:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716200.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,459,559
Mapped reads	1,137,048 / 77.9%
Unmapped reads	322,511 / 22.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,136 / 1.65%
Read min/max/mean length	30 / 101 / 101.61
Duplicated reads (estimated)	27,505 / 1.88%
Duplication rate	1.67%
Clipped reads	1,159,566 / 79.45%

2.2. ACGT Content

Number/percentage of A's	22,437,495 / 26.18%
Number/percentage of C's	17,779,607 / 20.74%
Number/percentage of T's	25,465,667 / 29.71%
Number/percentage of G's	20,027,059 / 23.36%
Number/percentage of N's	10,617 / 0.01%
GC Percentage	44.1%

2.3. Coverage

Mean	0.0277

Standard Deviation	0.2388

2.4. Mapping Quality

Mean Mapping Quality	46.02

2.5. Mismatches and indels

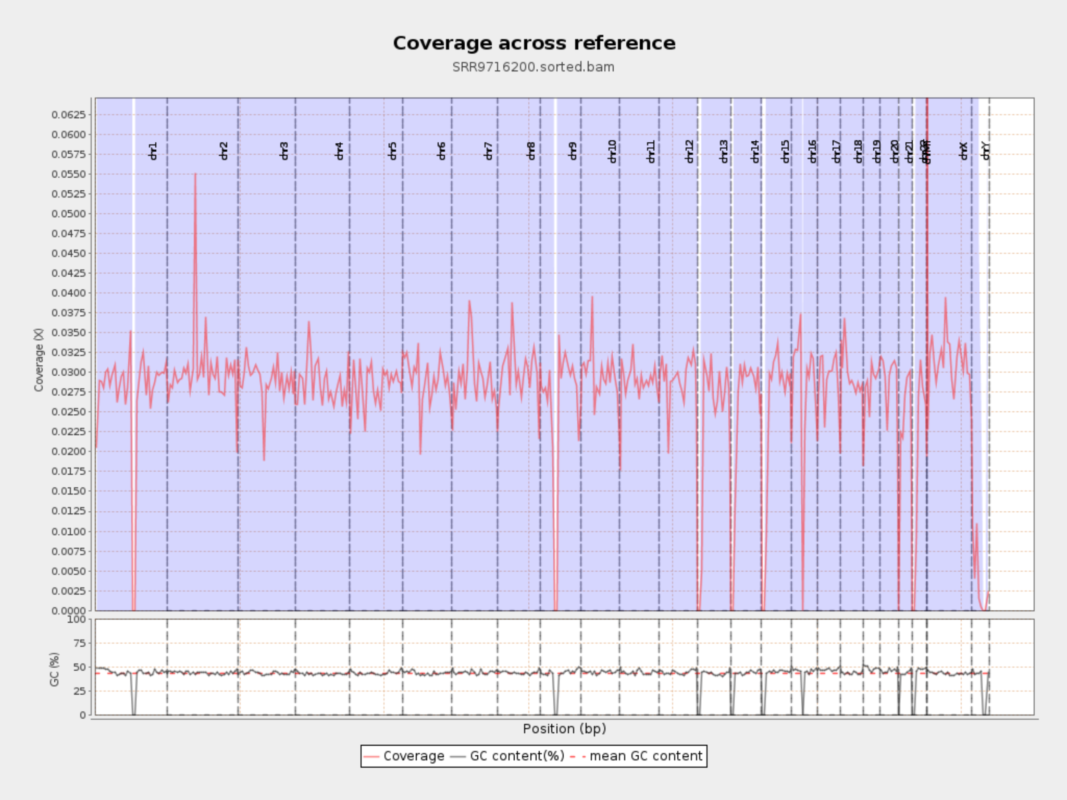
General error rate	0.76%
Mismatches	639,658
Insertions	7,404
Mapped reads with at least one insertion	0.64%
Deletions	17,253
Mapped reads with at least one deletion	1.5%
Homopolymer indels	40.37%

2.6. Chromosome stats

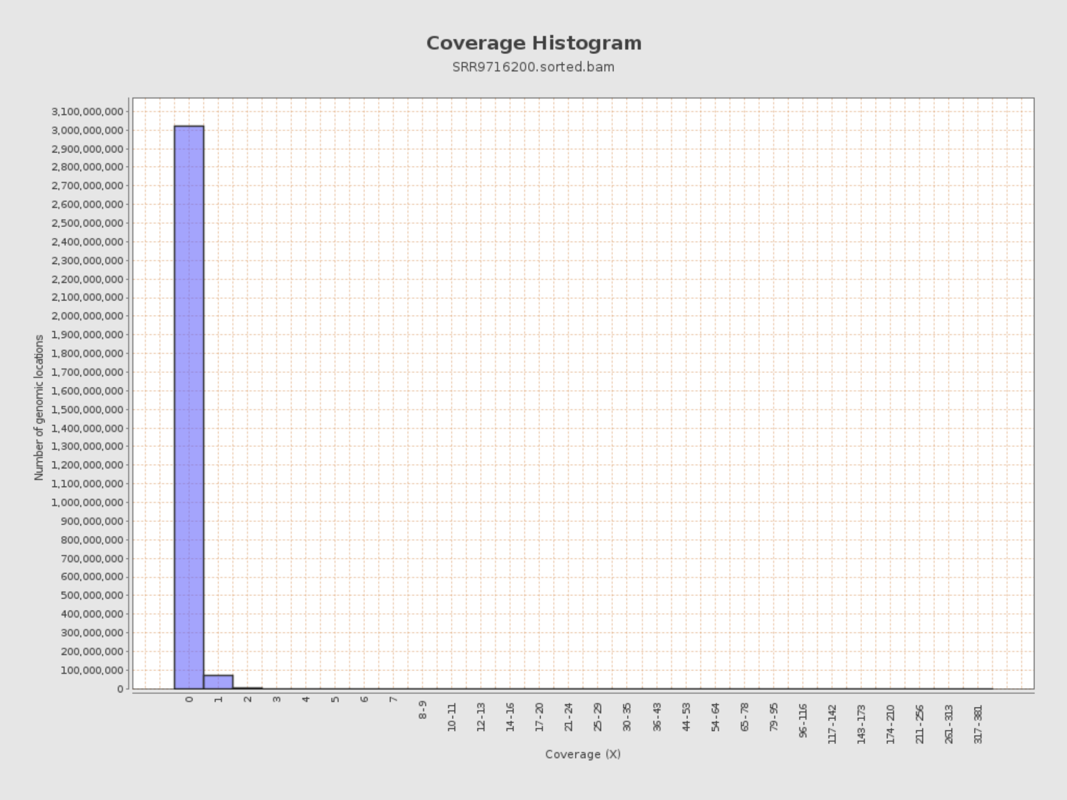
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6769975	0.0272	0.2594
chr2	243199373	7388189	0.0304	0.3438
chr3	198022430	5745603	0.029	0.185
chr4	191154276	5485900	0.0287	0.1962
chr5	180915260	5146041	0.0284	0.1836
chr6	171115067	4977802	0.0291	0.1987
chr7	159138663	4656565	0.0293	0.2811

chr8	146364022	4403144	0.0301	0.2895
chr9	141213431	3606420	0.0255	0.2568
chr10	135534747	4037398	0.0298	0.2405
chr11	135006516	3923220	0.0291	0.2488
chr12	133851895	3910219	0.0292	0.1884
chr13	115169878	2714372	0.0236	0.1665
chr14	107349540	2610831	0.0243	0.196
chr15	102531392	2492193	0.0243	0.1695
chr16	90354753	2481690	0.0275	0.1963
chr17	81195210	2360204	0.0291	0.196
chr18	78077248	2327140	0.0298	0.4385
chr19	59128983	1683890	0.0285	0.2427
chr20	63025520	1840662	0.0292	0.192
chr21	48129895	1120393	0.0233	0.181
chr22	51304566	979487	0.0191	0.1503
chrMT	16571	3536	0.2134	0.5228
chrX	155270560	4879629	0.0314	0.2264
chrY	59373566	205363	0.0035	0.0963

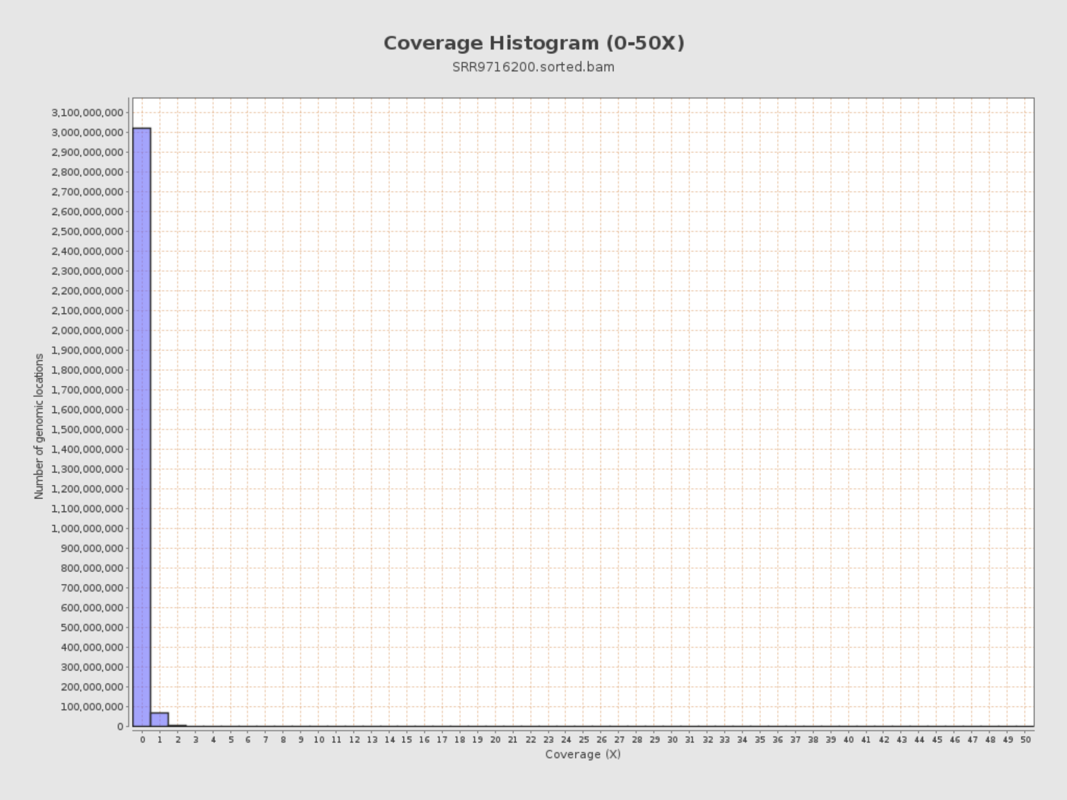
3. Results : Coverage across reference



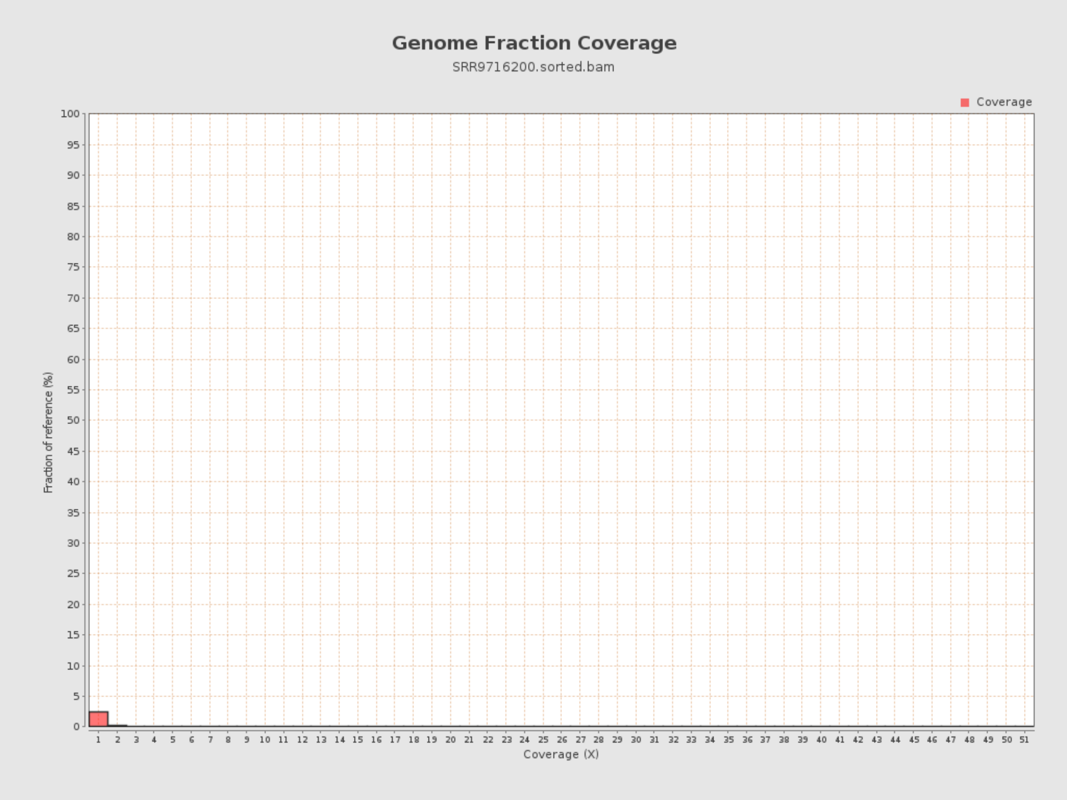
4. Results : Coverage Histogram



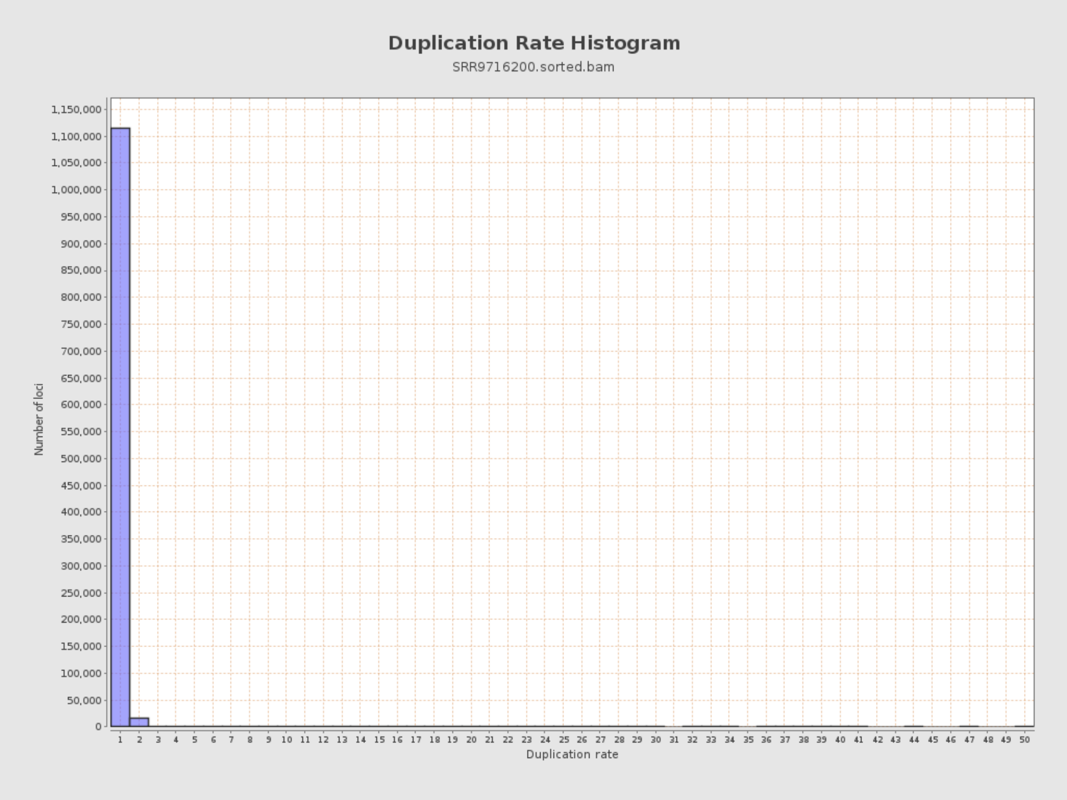
5. Results : Coverage Histogram (0-50X)



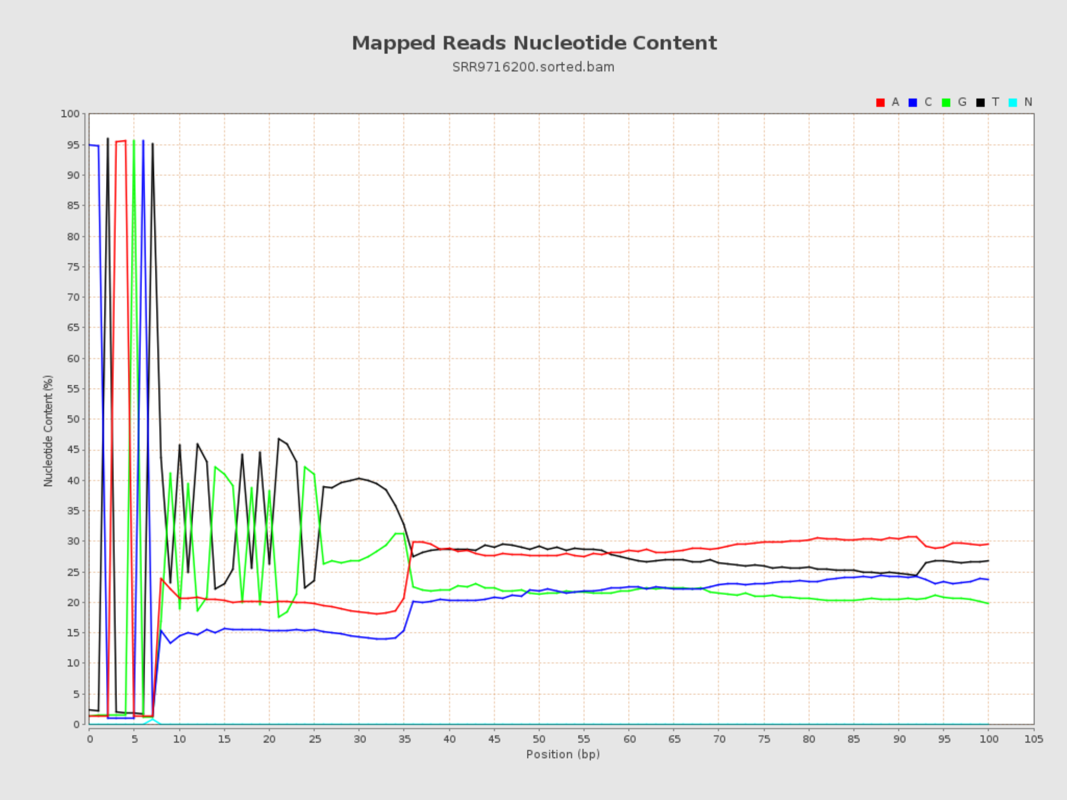
6. Results : Genome Fraction Coverage



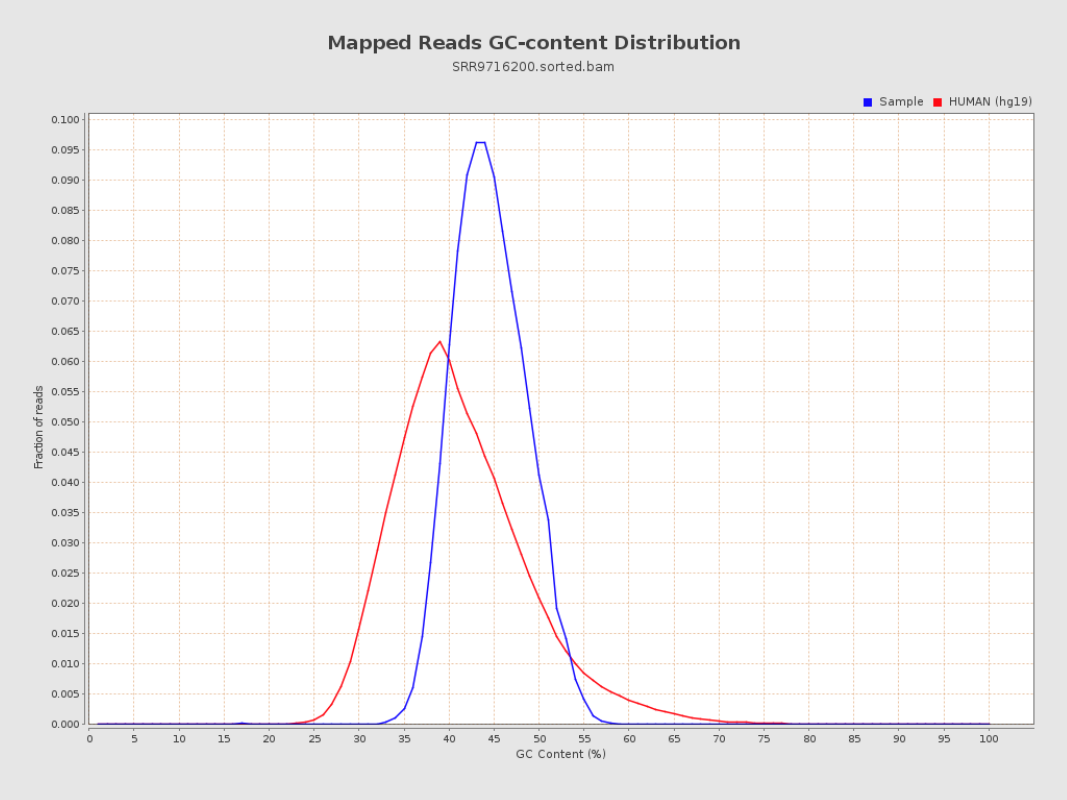
7. Results : Duplication Rate Histogram



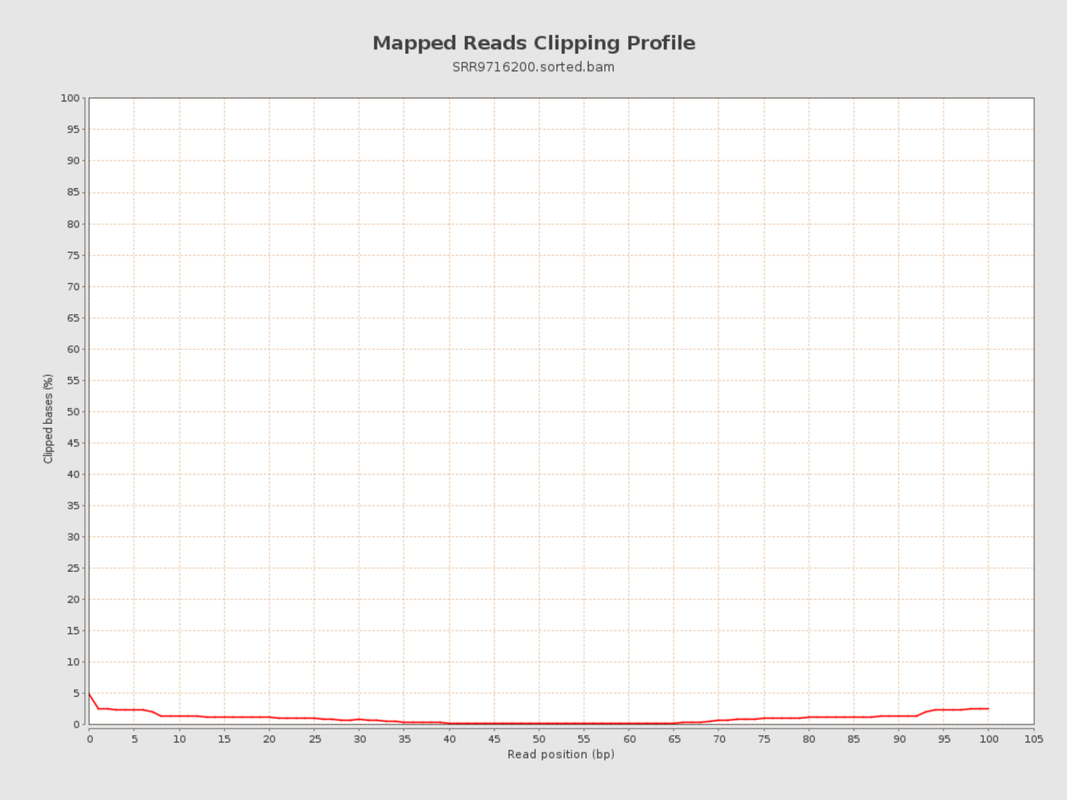
8. Results : Mapped Reads Nucleotide Content



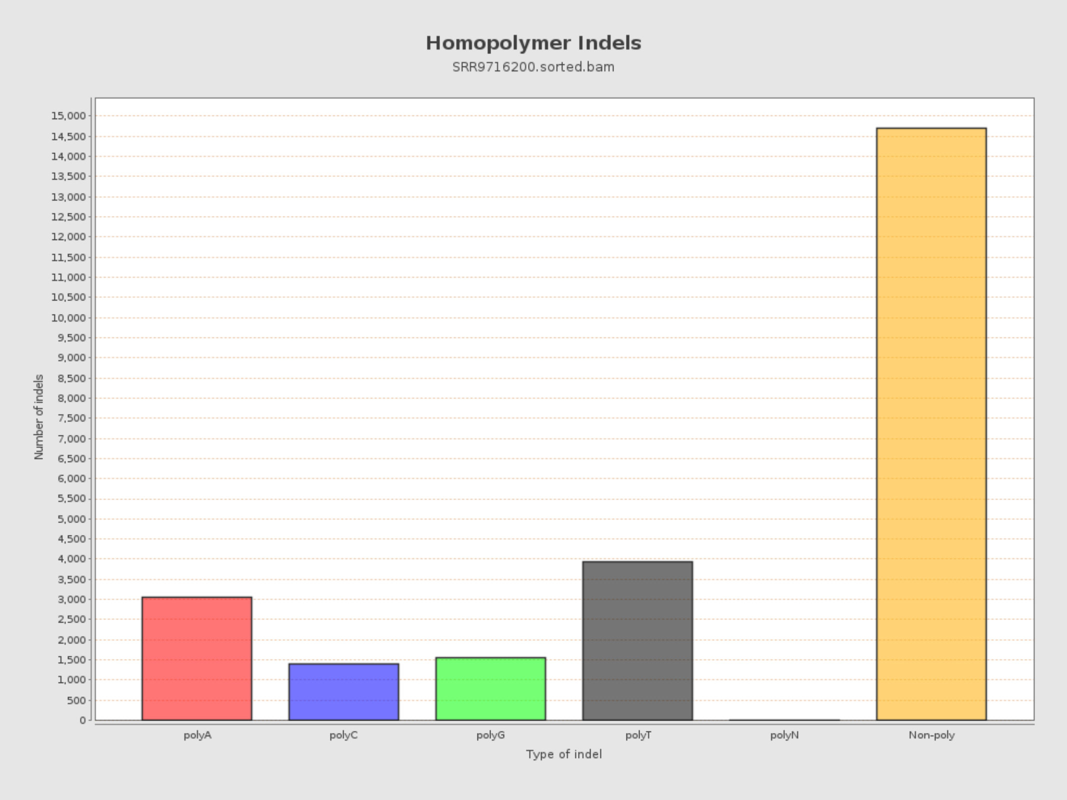
9. Results : Mapped Reads GC-content Distribution



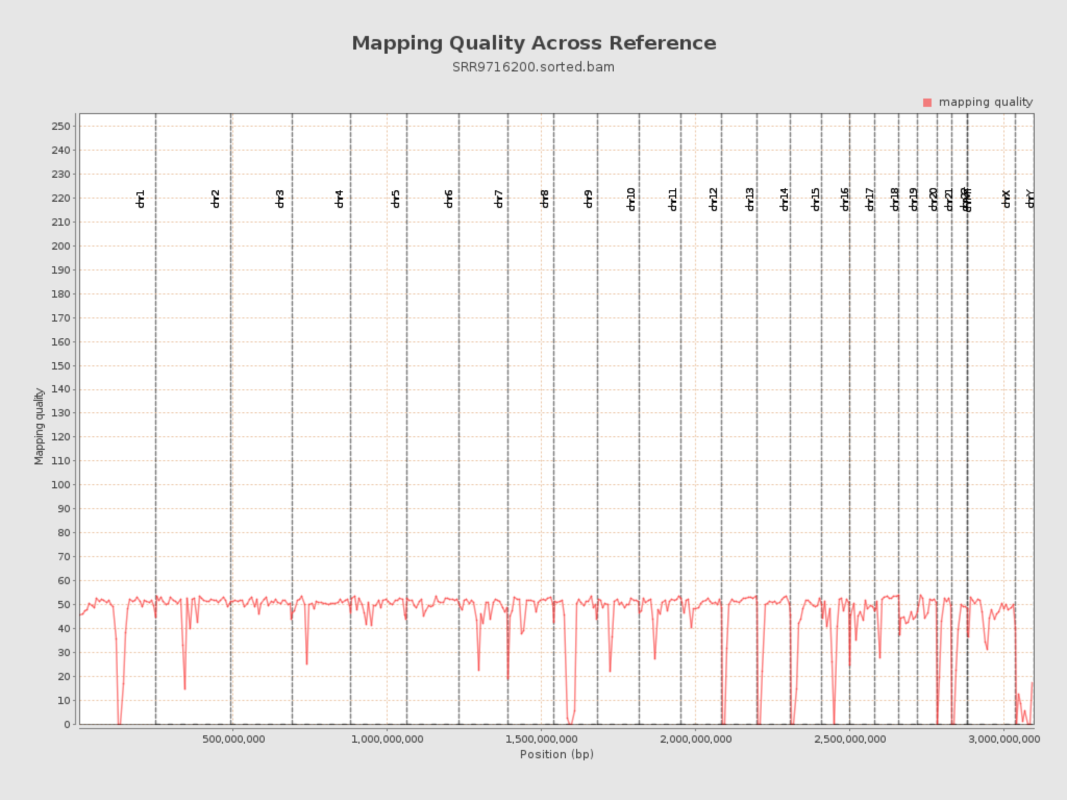
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram