Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 02:46:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716251.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_SRR9716251 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716251.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 02:46:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716251.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,626,533
Mapped reads	1,531,098 / 94.13%
Unmapped reads	95,435 / 5.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,533 / 1.82%
Read min/max/mean length	30 / 101 / 101.66
Duplicated reads (estimated)	71,987 / 4.43%
Duplication rate	3.72%
Clipped reads	1,557,906 / 95.78%

2.2. ACGT Content

Number/percentage of A's	29,653,666 / 25.17%
Number/percentage of C's	24,330,968 / 20.65%
Number/percentage of T's	35,010,319 / 29.72%
Number/percentage of G's	28,807,000 / 24.45%
Number/percentage of N's	4,562 / 0%
GC Percentage	45.11%

2.3. Coverage

Mean	0.0381

Standard Deviation	0.3264

2.4. Mapping Quality

Mean Mapping Quality	46.72

2.5. Mismatches and indels

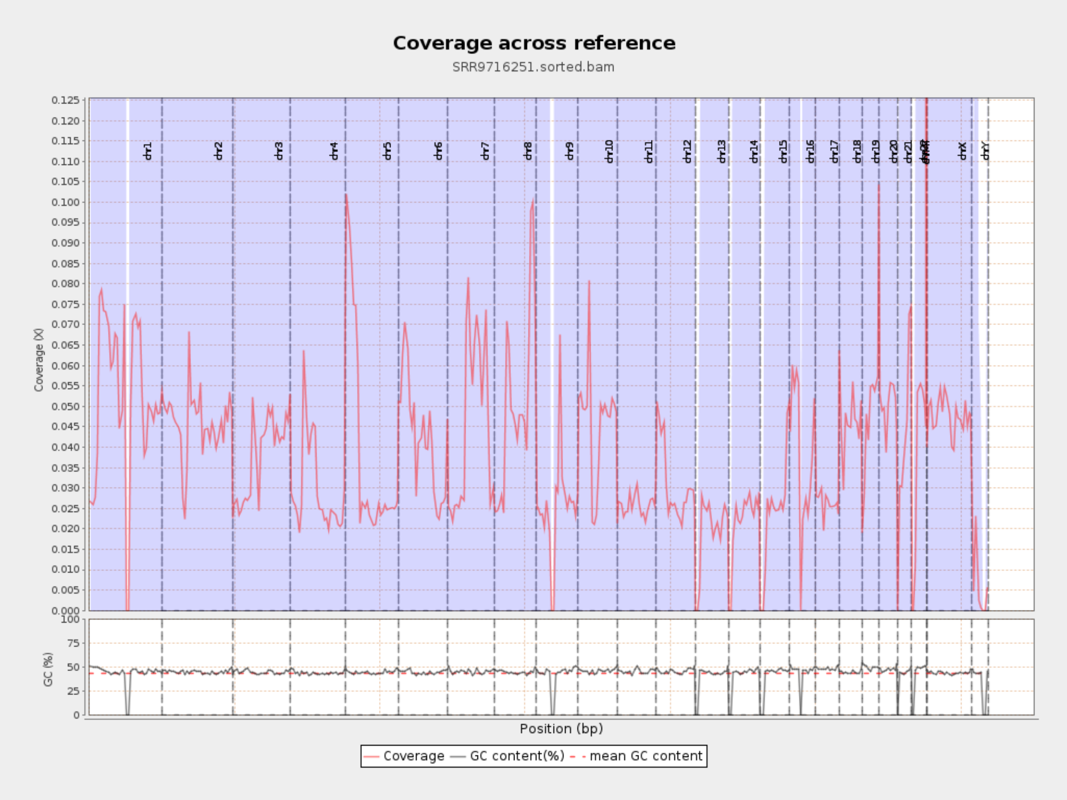
General error rate	0.65%
Mismatches	741,441
Insertions	9,487
Mapped reads with at least one insertion	0.61%
Deletions	21,095
Mapped reads with at least one deletion	1.36%
Homopolymer indels	37.54%

2.6. Chromosome stats

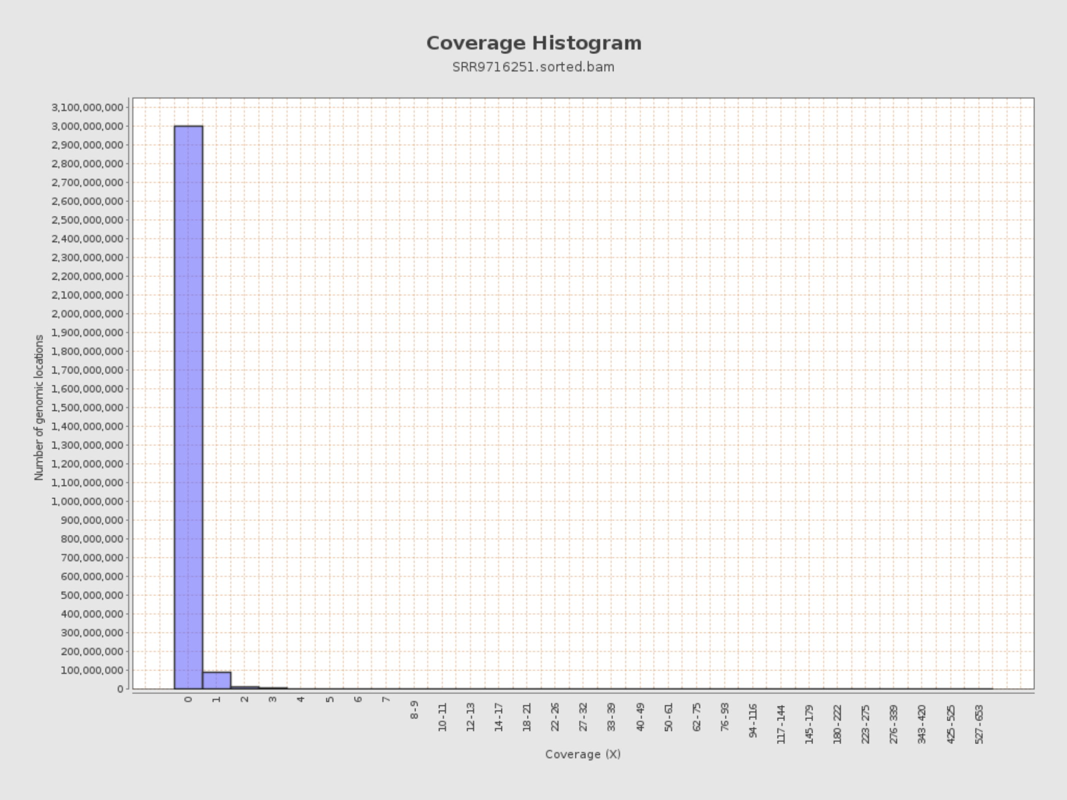
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13015963	0.0522	0.6273
chr2	243199373	11128816	0.0458	0.3479
chr3	198022430	7509446	0.0379	0.2253
chr4	191154276	5652191	0.0296	0.2566
chr5	180915260	7109428	0.0393	0.2341
chr6	171115067	7217511	0.0422	0.2533
chr7	159138663	7411580	0.0466	0.4274

chr8	146364022	7412333	0.0506	0.3659
chr9	141213431	3574988	0.0253	0.2395
chr10	135534747	6248179	0.0461	0.3947
chr11	135006516	3467137	0.0257	0.2565
chr12	133851895	4138610	0.0309	0.2019
chr13	115169878	2230300	0.0194	0.1581
chr14	107349540	2288138	0.0213	0.1808
chr15	102531392	2400273	0.0234	0.1757
chr16	90354753	3488279	0.0386	0.239
chr17	81195210	2129036	0.0262	0.2093
chr18	78077248	3593307	0.046	0.361
chr19	59128983	2897990	0.049	0.4653
chr20	63025520	3162638	0.0502	0.2709
chr21	48129895	2045086	0.0425	0.273
chr22	51304566	1828518	0.0356	0.2244
chrMT	16571	91539	5.524	4.1462
chrX	155270560	7423535	0.0478	0.2671
chrY	59373566	384925	0.0065	0.1933

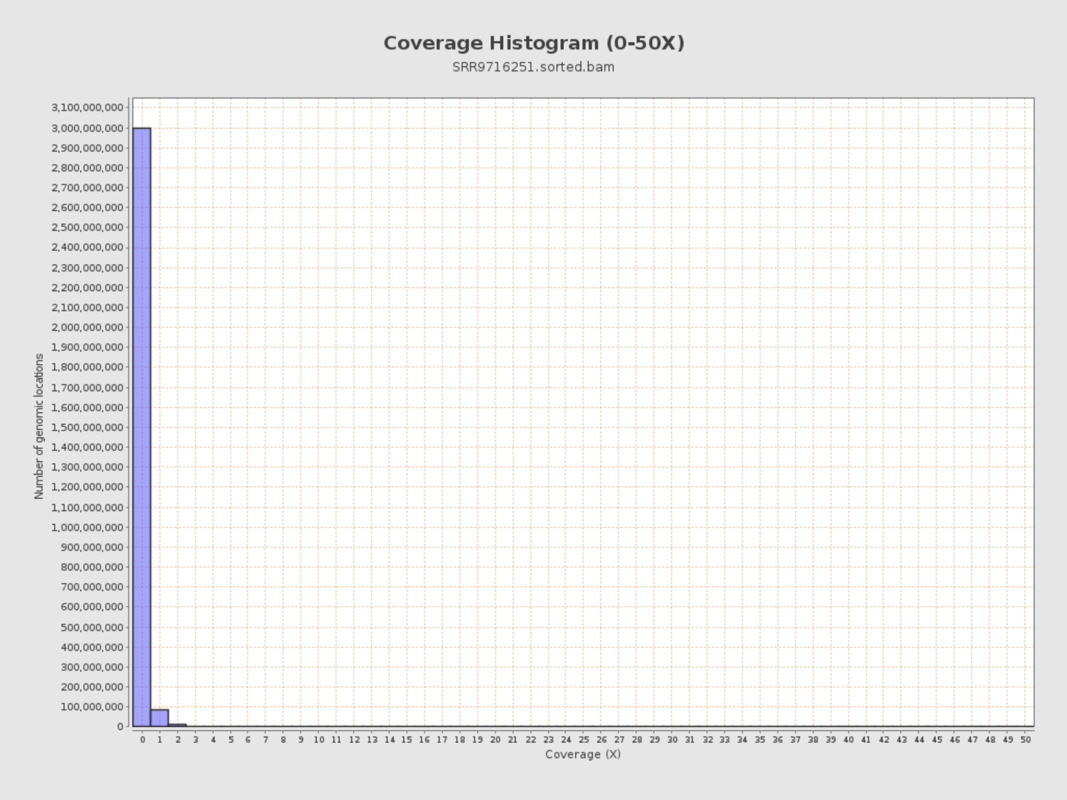
3. Results : Coverage across reference



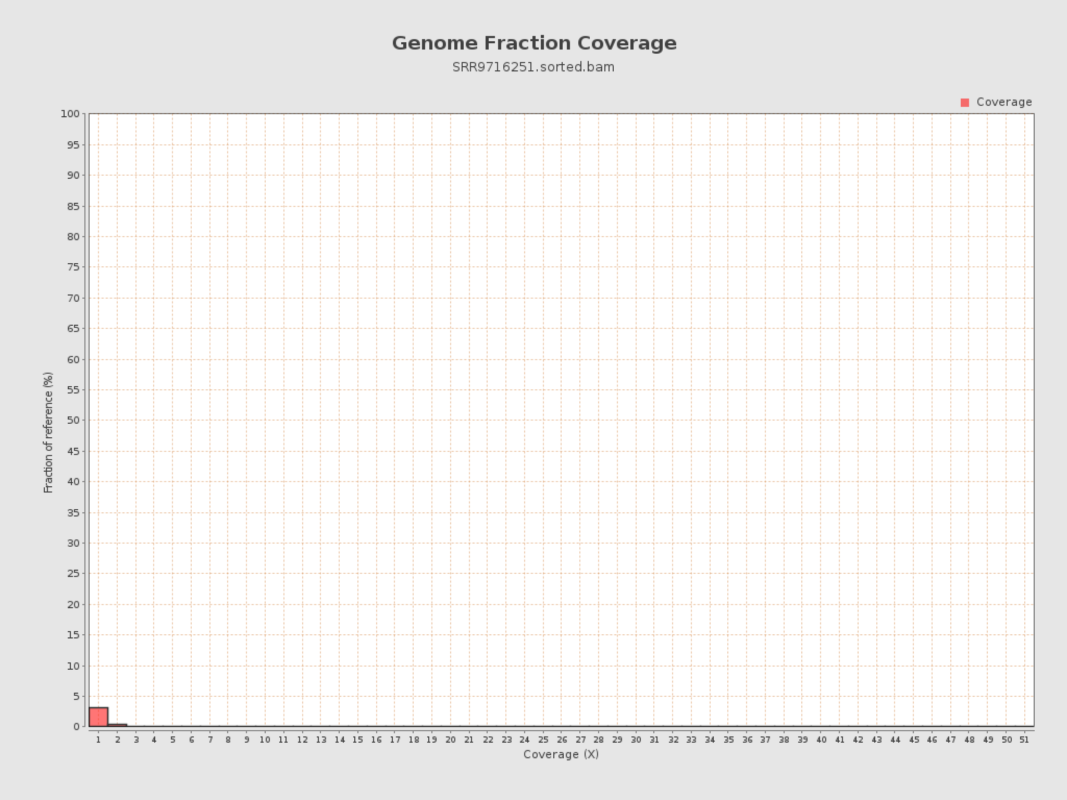
4. Results : Coverage Histogram



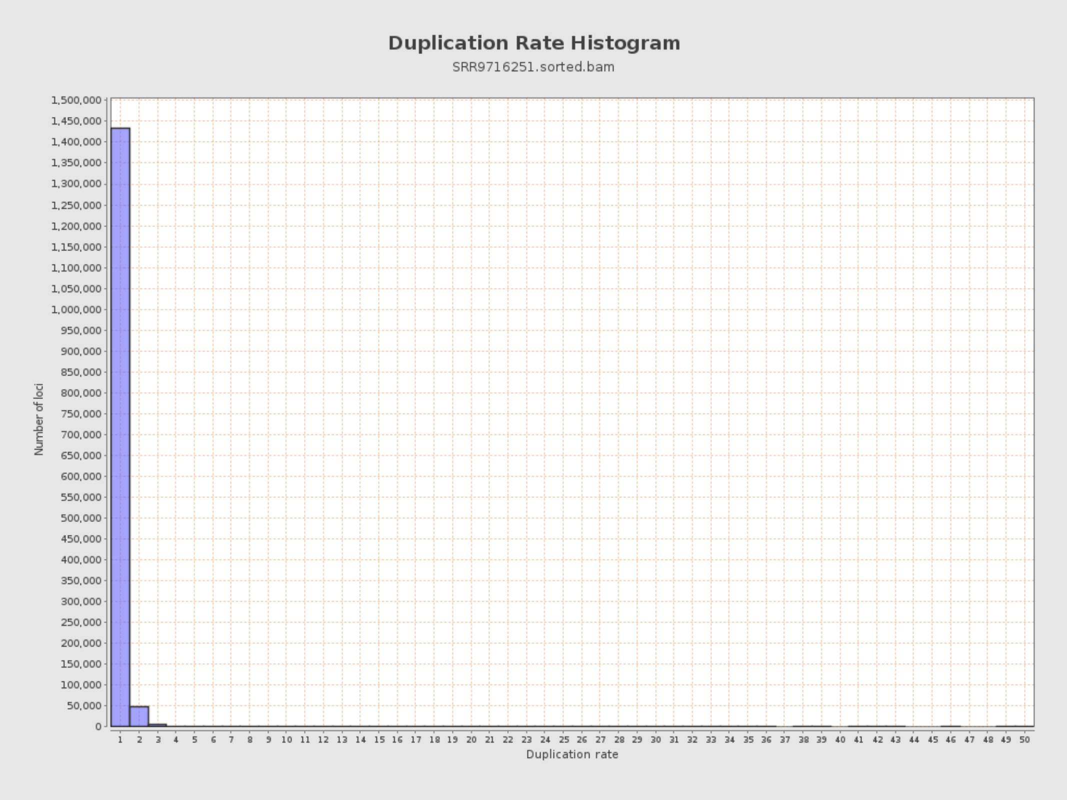
5. Results : Coverage Histogram (0-50X)



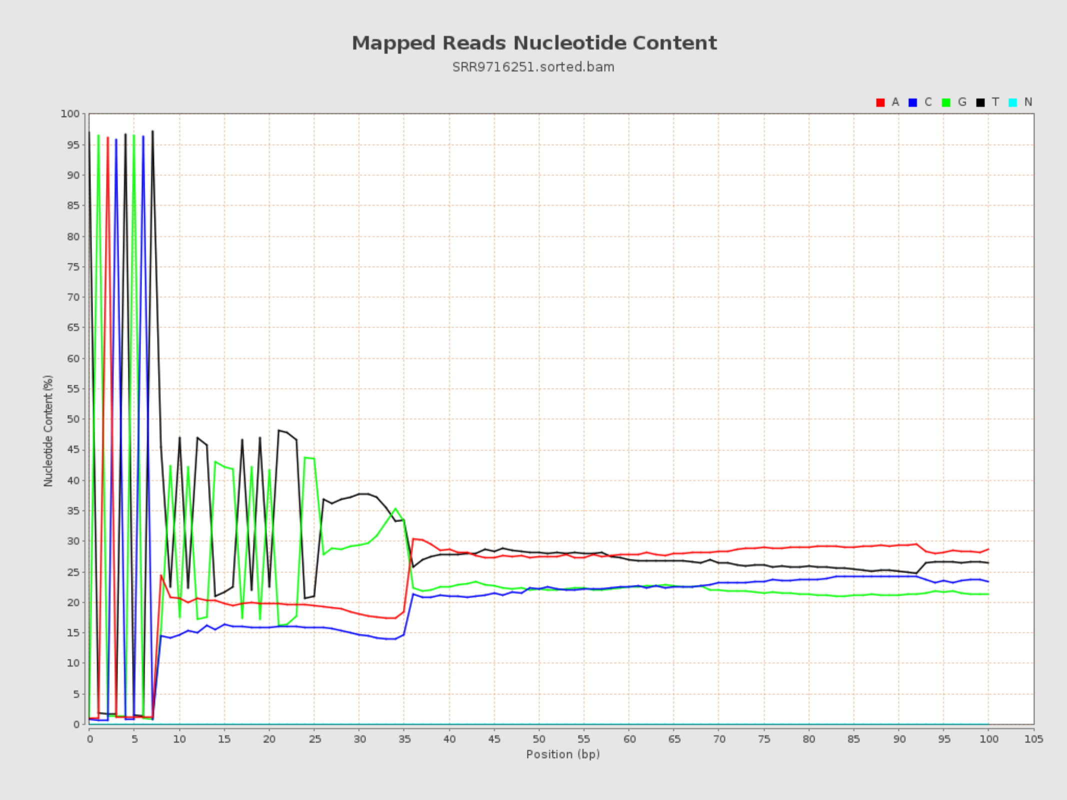
6. Results : Genome Fraction Coverage



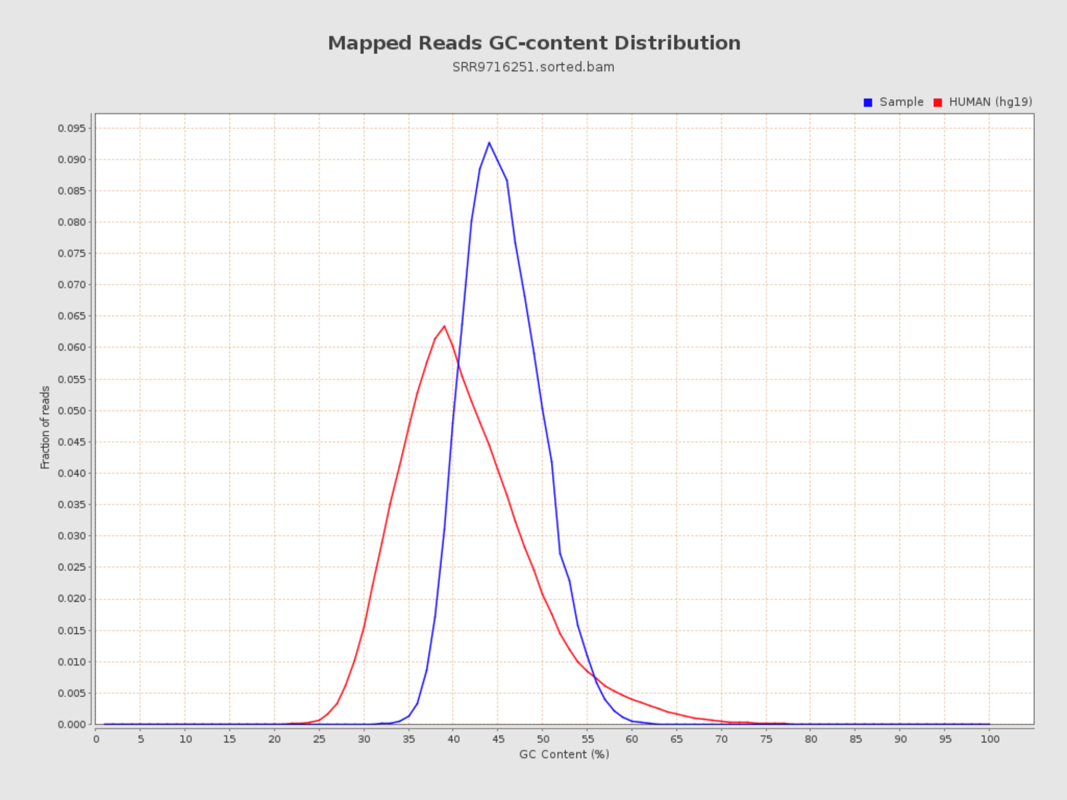
7. Results : Duplication Rate Histogram



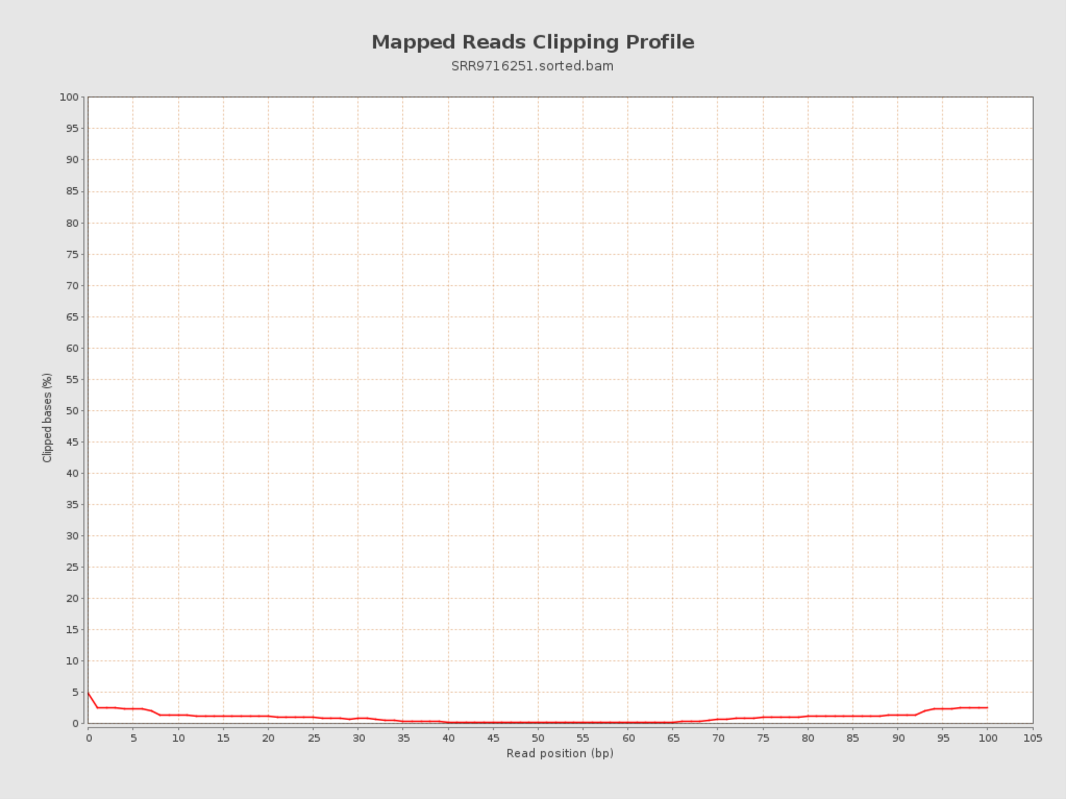
8. Results : Mapped Reads Nucleotide Content



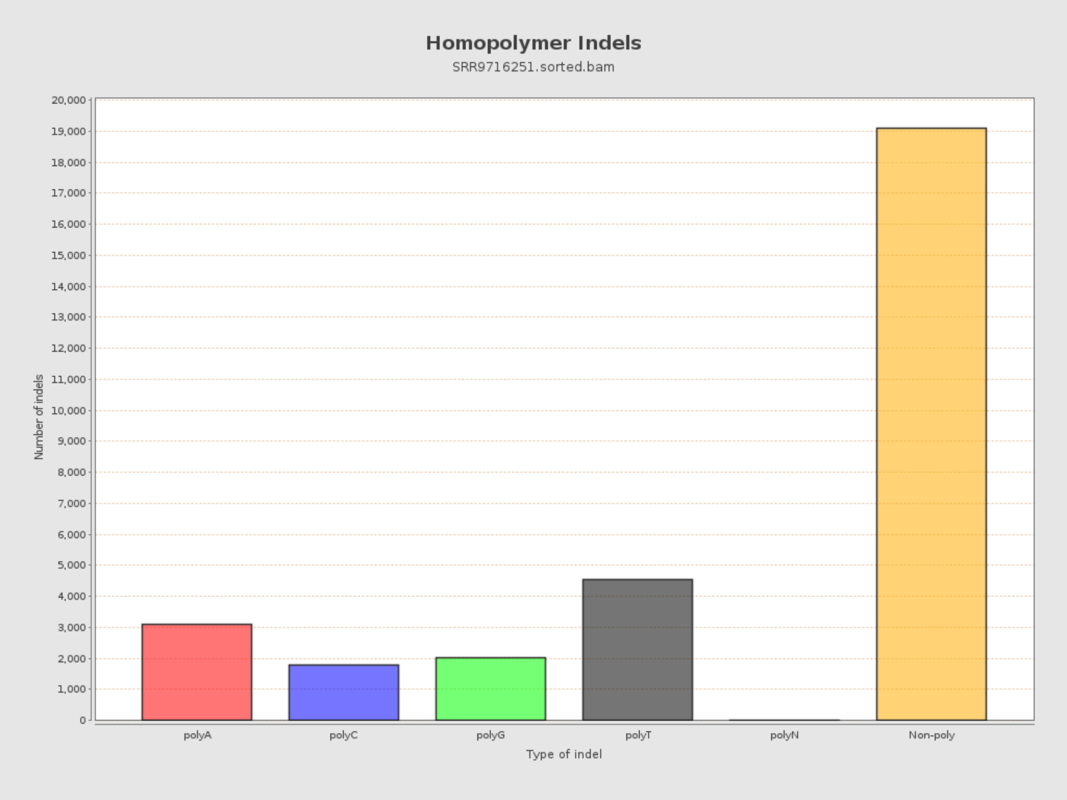
9. Results : Mapped Reads GC-content Distribution



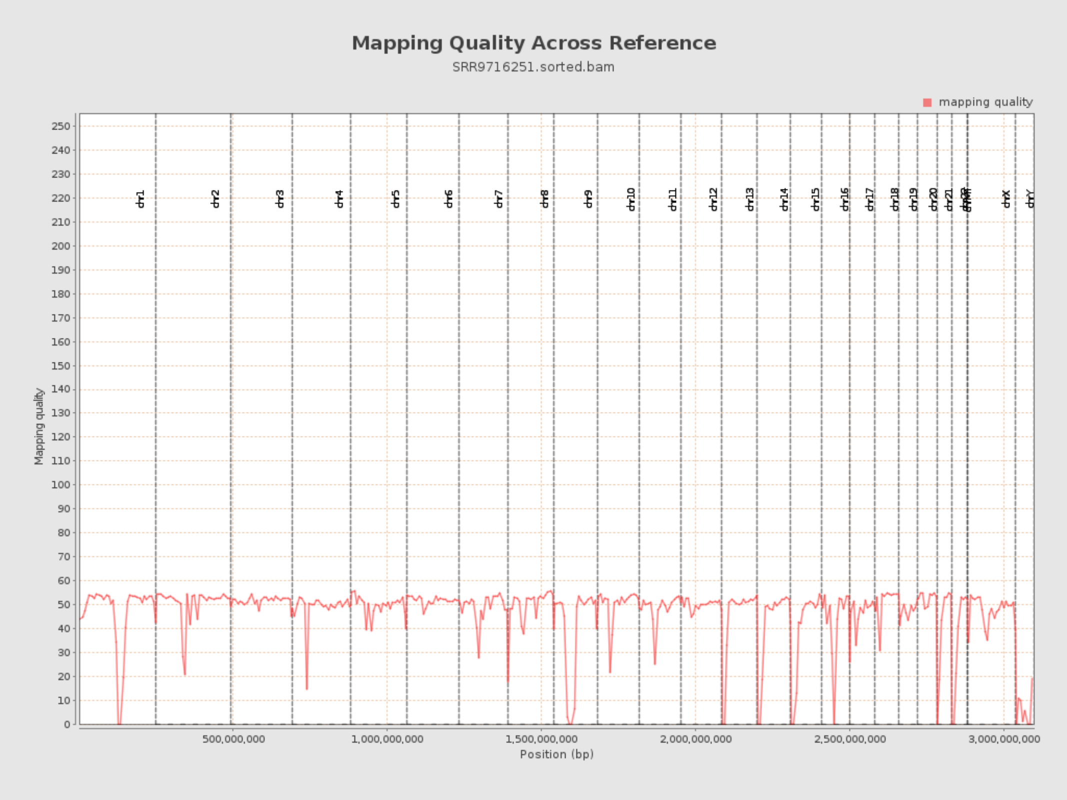
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram