Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 18:50:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716529.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_SRR9716529 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716529.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 18:50:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716529.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,347,880
Mapped reads	1,264,073 / 93.78%
Unmapped reads	83,807 / 6.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,478 / 1.96%
Read min/max/mean length	30 / 101 / 101.71
Duplicated reads (estimated)	40,265 / 2.99%
Duplication rate	2.21%
Clipped reads	1,287,921 / 95.55%

2.2. ACGT Content

Number/percentage of A's	25,742,963 / 25.72%
Number/percentage of C's	19,603,594 / 19.59%
Number/percentage of T's	30,883,977 / 30.86%
Number/percentage of G's	23,839,332 / 23.82%
Number/percentage of N's	6,643 / 0.01%
GC Percentage	43.41%

2.3. Coverage

Mean	0.0323

Standard Deviation	0.3194

2.4. Mapping Quality

Mean Mapping Quality	47.28

2.5. Mismatches and indels

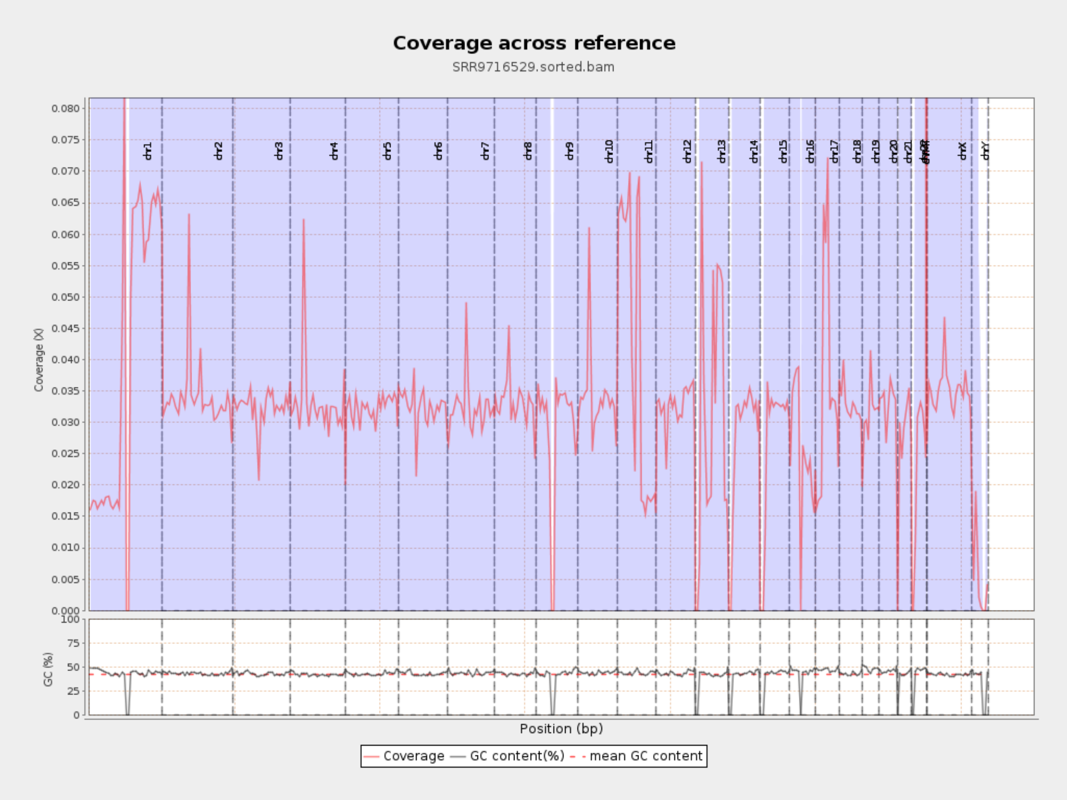
General error rate	0.66%
Mismatches	642,715
Insertions	8,386
Mapped reads with at least one insertion	0.65%
Deletions	23,879
Mapped reads with at least one deletion	1.86%
Homopolymer indels	42.07%

2.6. Chromosome stats

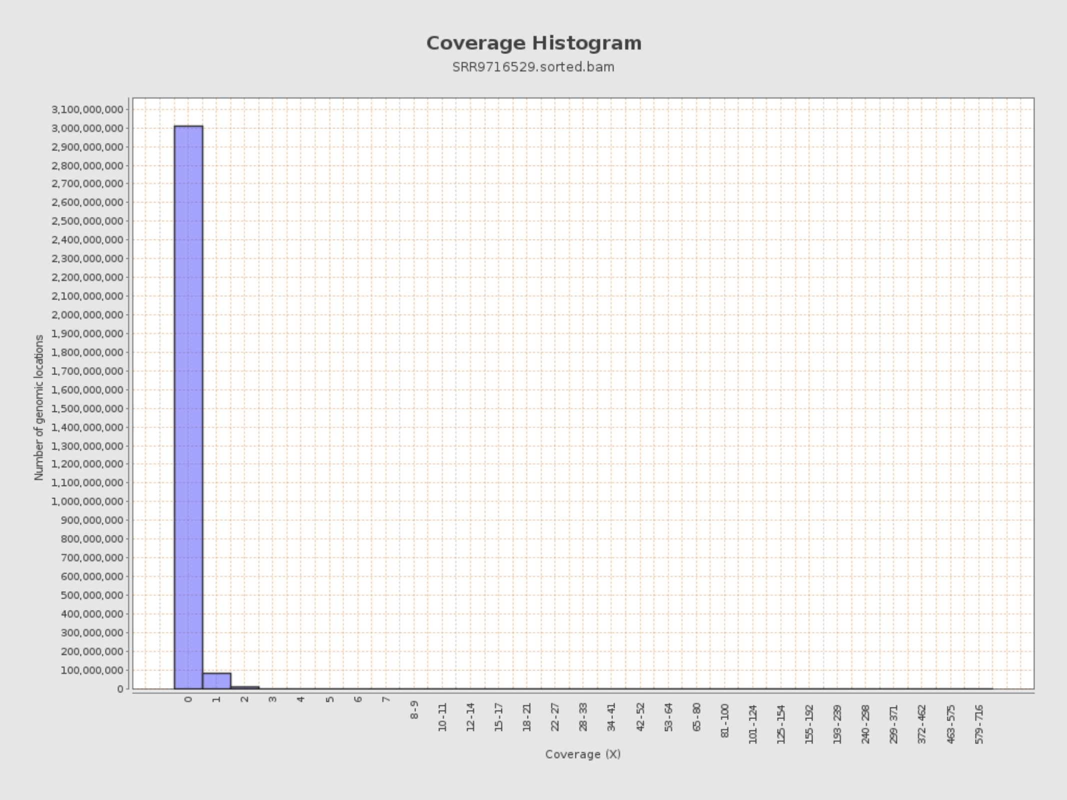
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9768851	0.0392	0.6494
chr2	243199373	8291472	0.0341	0.3418
chr3	198022430	6416415	0.0324	0.1958
chr4	191154276	6325070	0.0331	0.235
chr5	180915260	5854891	0.0324	0.1977
chr6	171115067	5557538	0.0325	0.2114
chr7	159138663	5178367	0.0325	0.3752

chr8	146364022	4854251	0.0332	0.3536
chr9	141213431	4072597	0.0288	0.2655
chr10	135534747	4606038	0.034	0.3162
chr11	135006516	5596183	0.0415	0.3542
chr12	133851895	4375843	0.0327	0.1985
chr13	115169878	3533620	0.0307	0.1923
chr14	107349540	2912408	0.0271	0.1939
chr15	102531392	2748762	0.0268	0.1778
chr16	90354753	2280466	0.0252	0.1901
chr17	81195210	3010048	0.0371	0.2419
chr18	78077248	2586065	0.0331	0.438
chr19	59128983	1872140	0.0317	0.4483
chr20	63025520	2063615	0.0327	0.2058
chr21	48129895	1309030	0.0272	0.2016
chr22	51304566	1094290	0.0213	0.159
chrMT	16571	57379	3.4626	2.765
chrX	155270560	5459169	0.0352	0.2372
chrY	59373566	297468	0.005	0.1615

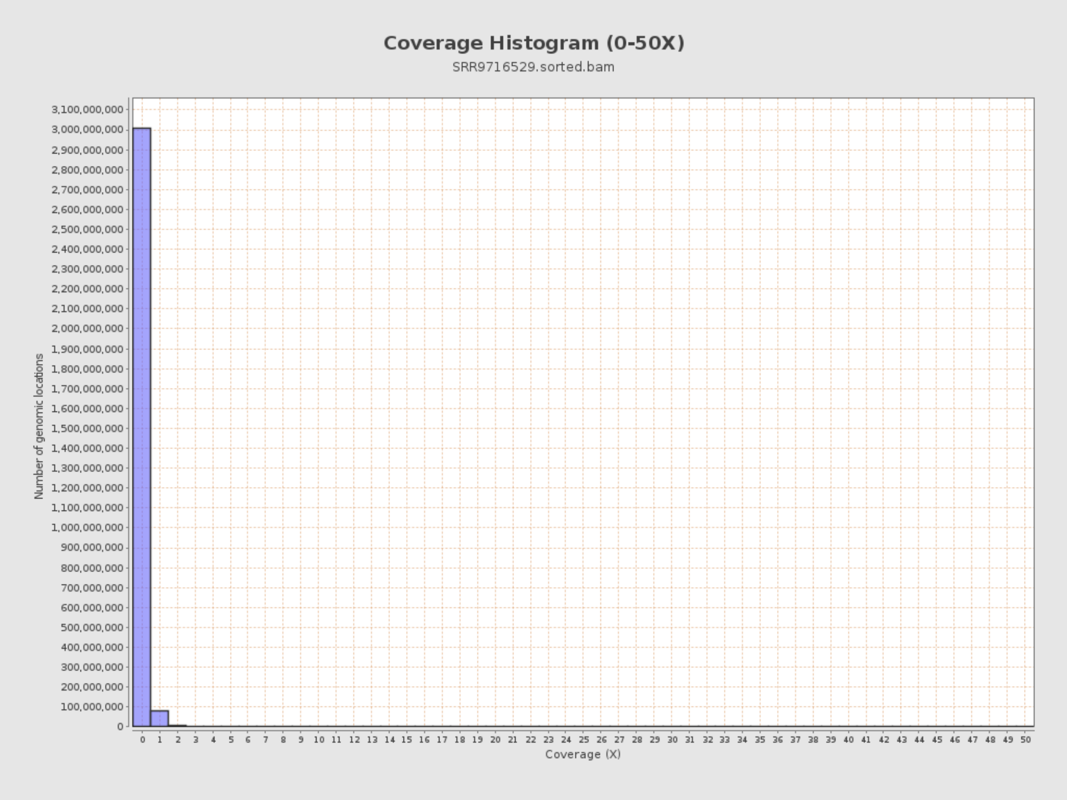
3. Results : Coverage across reference



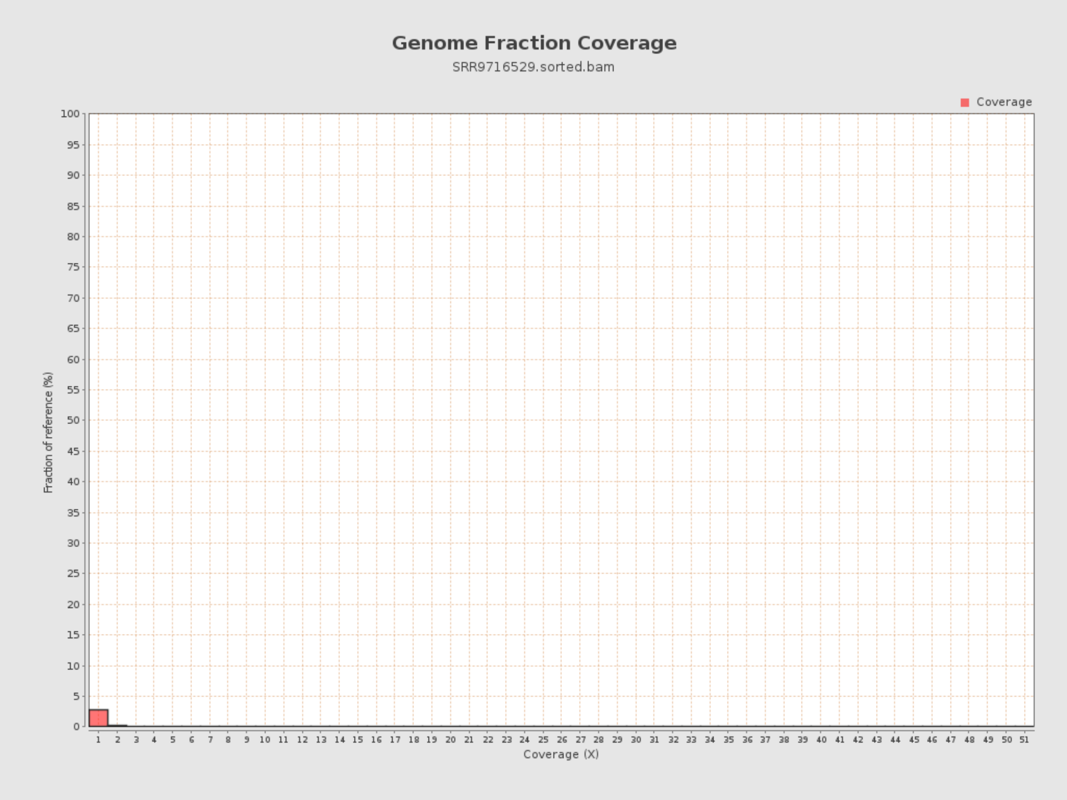
4. Results : Coverage Histogram



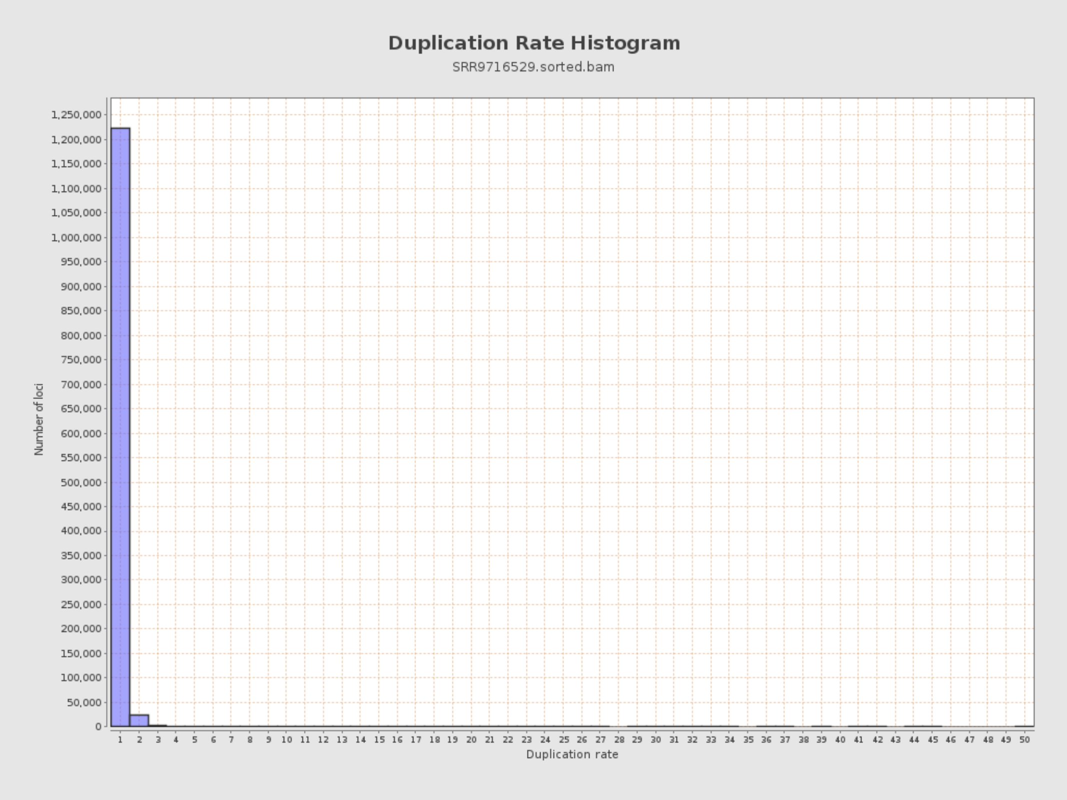
5. Results : Coverage Histogram (0-50X)



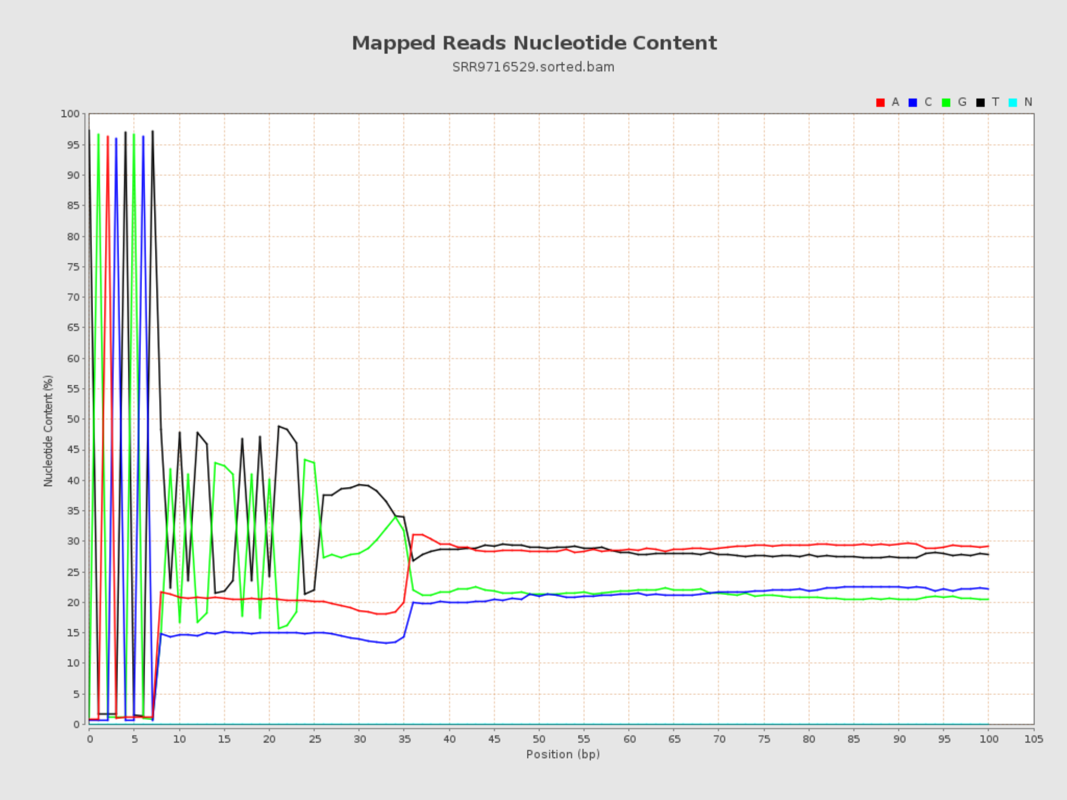
6. Results : Genome Fraction Coverage



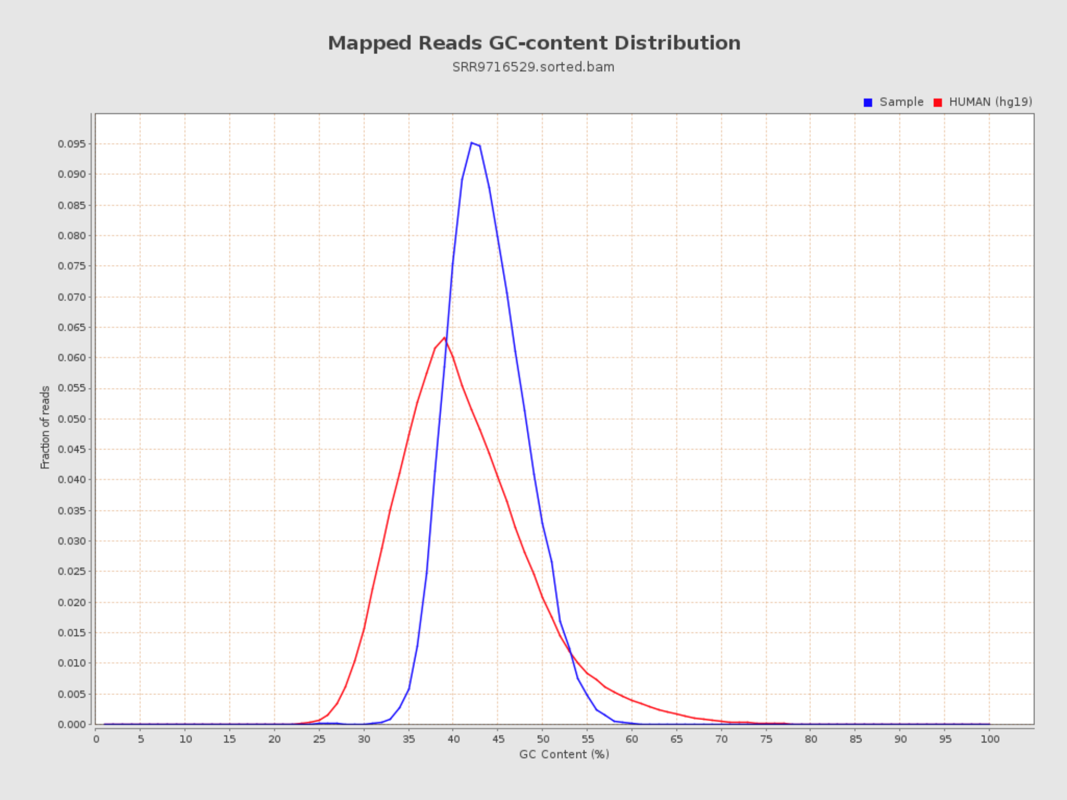
7. Results : Duplication Rate Histogram



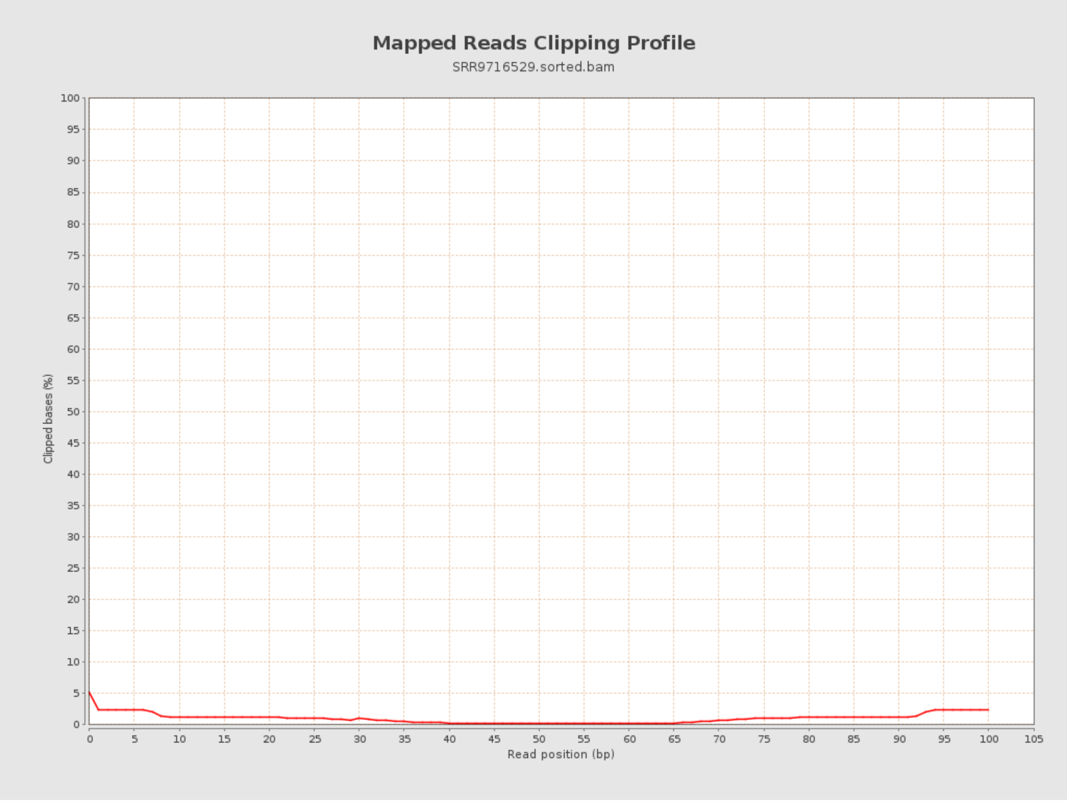
8. Results : Mapped Reads Nucleotide Content



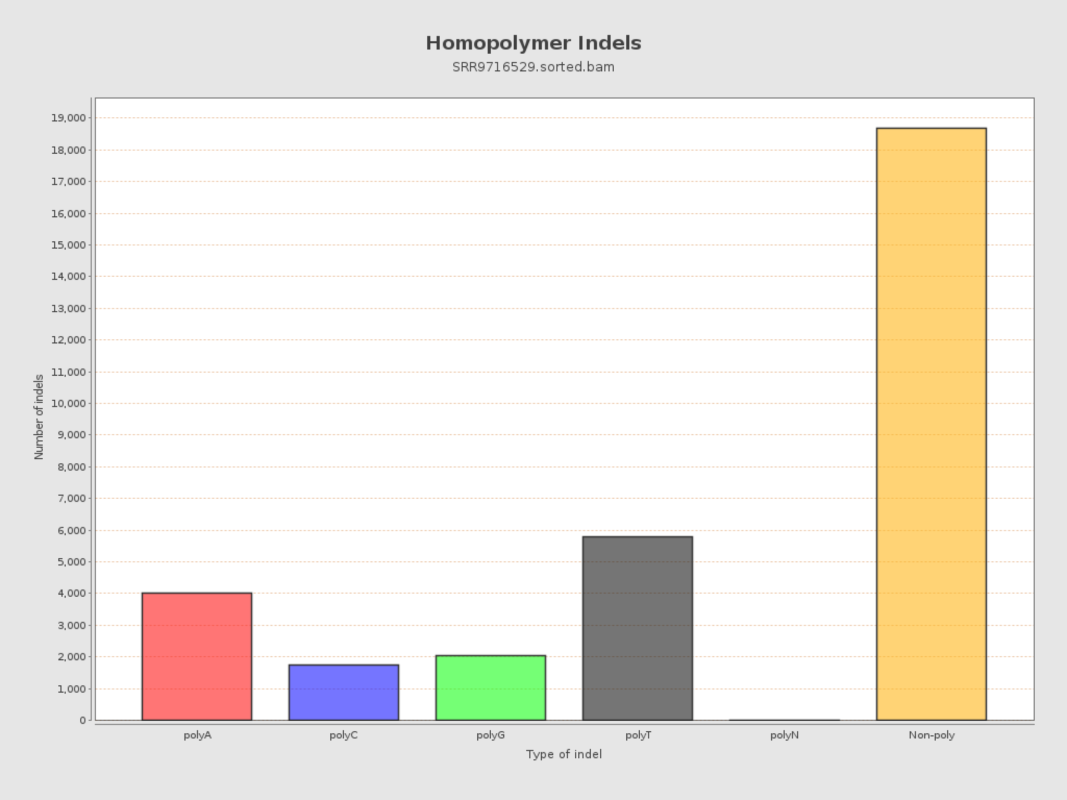
9. Results : Mapped Reads GC-content Distribution



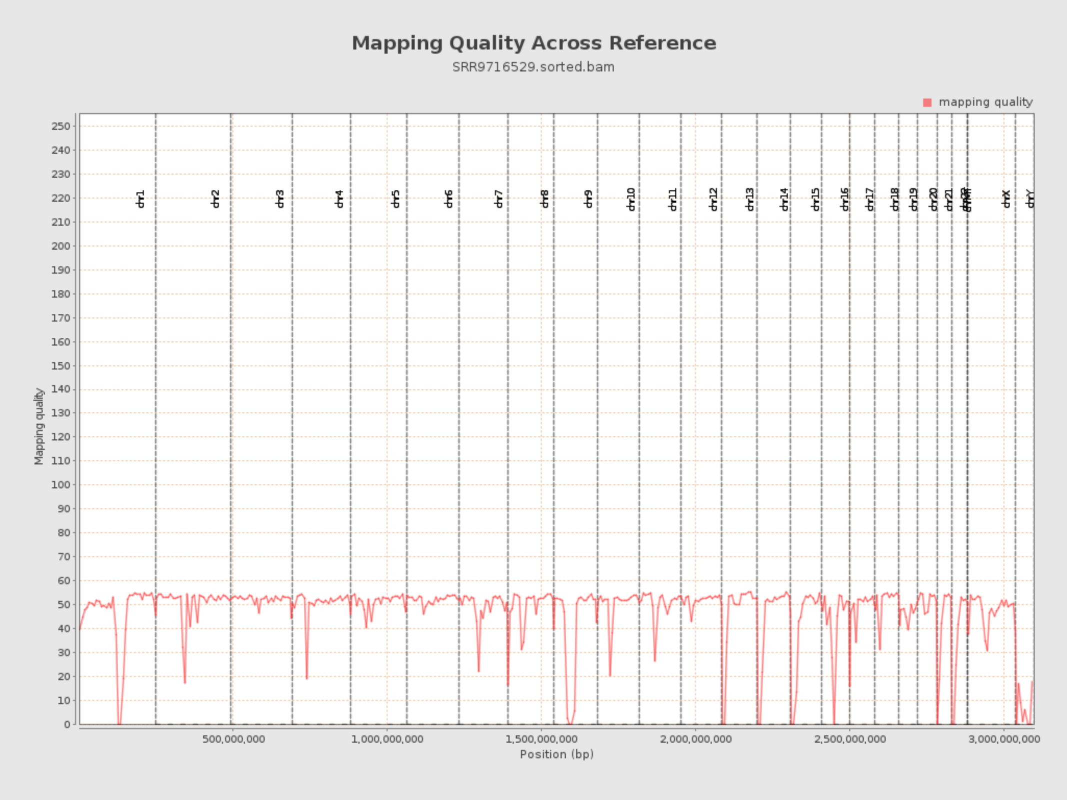
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram