Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 17:20:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716892.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_SRR9716892 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716892.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 17:20:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716892.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,728,570
Mapped reads	4,224,177 / 89.33%
Unmapped reads	504,393 / 10.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	99,100 / 2.1%
Read min/max/mean length	30 / 101 / 101.75
Duplicated reads (estimated)	222,014 / 4.7%
Duplication rate	3.72%
Clipped reads	4,313,673 / 91.23%

2.2. ACGT Content

Number/percentage of A's	80,828,508 / 25.61%
Number/percentage of C's	66,361,914 / 21.03%
Number/percentage of T's	95,237,944 / 30.17%
Number/percentage of G's	73,158,389 / 23.18%
Number/percentage of N's	37,967 / 0.01%
GC Percentage	44.2%

2.3. Coverage

Mean	0.102

Standard Deviation	0.7159

2.4. Mapping Quality

Mean Mapping Quality	46.15

2.5. Mismatches and indels

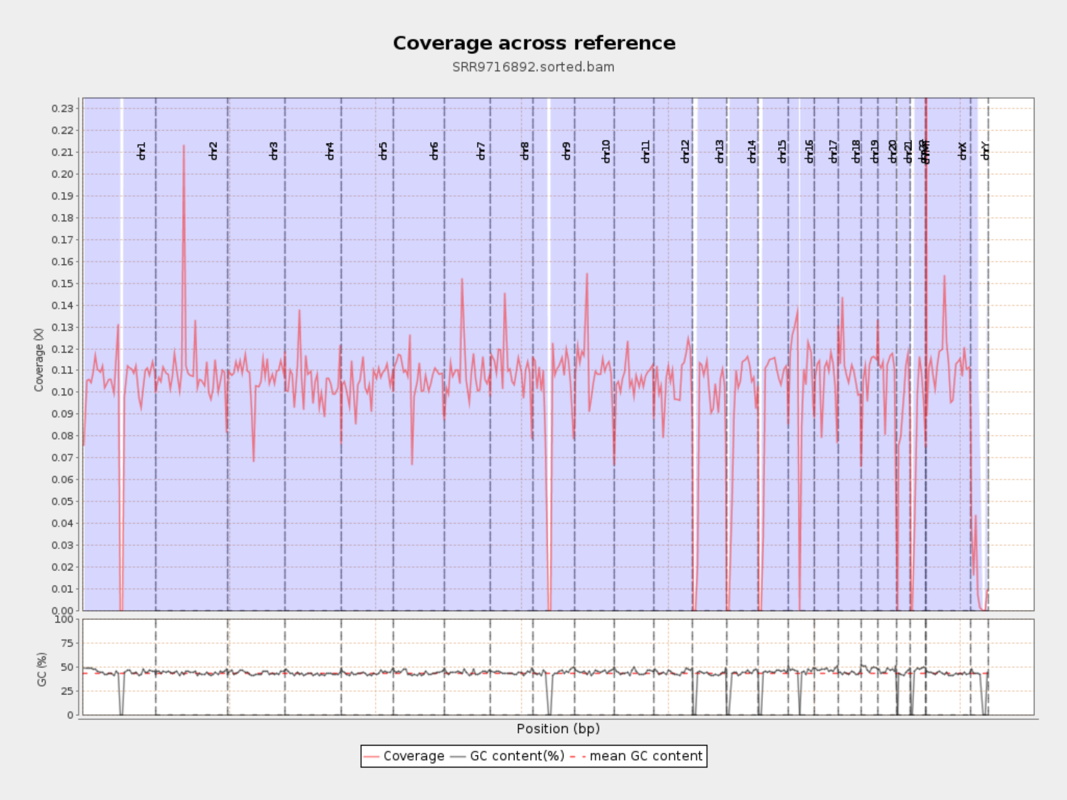
General error rate	0.74%
Mismatches	2,280,277
Insertions	28,576
Mapped reads with at least one insertion	0.67%
Deletions	65,618
Mapped reads with at least one deletion	1.53%
Homopolymer indels	39.96%

2.6. Chromosome stats

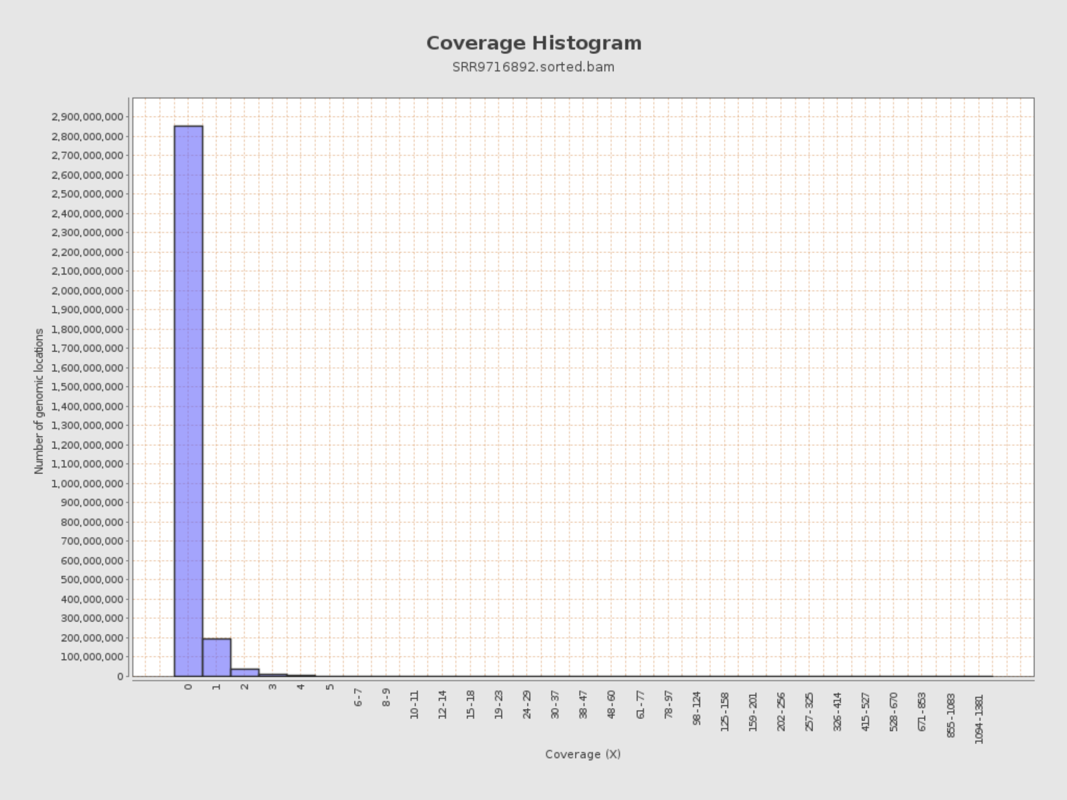
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	25036102	0.1004	0.8446
chr2	243199373	26879659	0.1105	1.1154
chr3	198022430	21228302	0.1072	0.4099
chr4	191154276	20071058	0.105	0.4683
chr5	180915260	18883019	0.1044	0.4128
chr6	171115067	18280249	0.1068	0.5146
chr7	159138663	17371380	0.1092	0.9316

chr8	146364022	16198222	0.1107	0.9667
chr9	141213431	13438344	0.0952	0.7882
chr10	135534747	15123554	0.1116	0.7067
chr11	135006516	14286310	0.1058	0.8012
chr12	133851895	14176624	0.1059	0.4203
chr13	115169878	9974203	0.0866	0.3669
chr14	107349540	9532163	0.0888	0.5039
chr15	102531392	9184626	0.0896	0.3793
chr16	90354753	9315213	0.1031	0.4892
chr17	81195210	8672503	0.1068	0.4858
chr18	78077248	8735617	0.1119	1.5487
chr19	59128983	6456042	0.1092	0.7548
chr20	63025520	6758018	0.1072	0.4455
chr21	48129895	4187799	0.087	0.4314
chr22	51304566	3662629	0.0714	0.338
chrMT	16571	10638	0.642	1.6864
chrX	155270560	17471858	0.1125	0.6213
chrY	59373566	801686	0.0135	0.3457

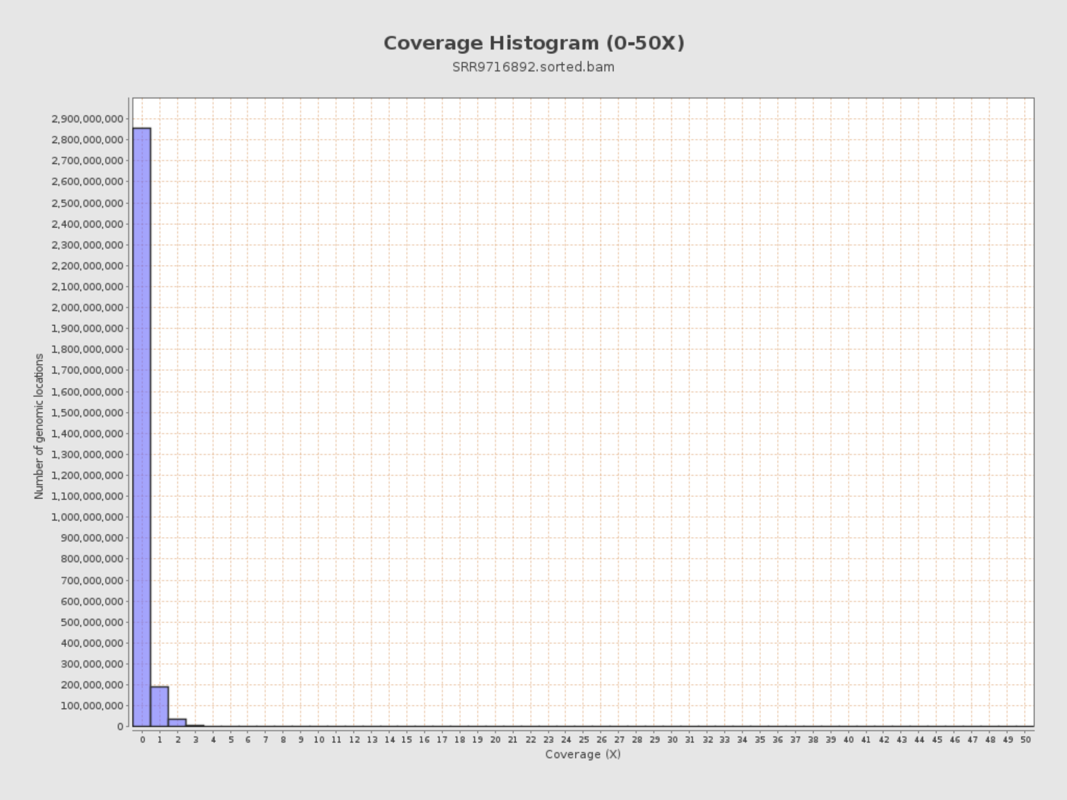
3. Results : Coverage across reference



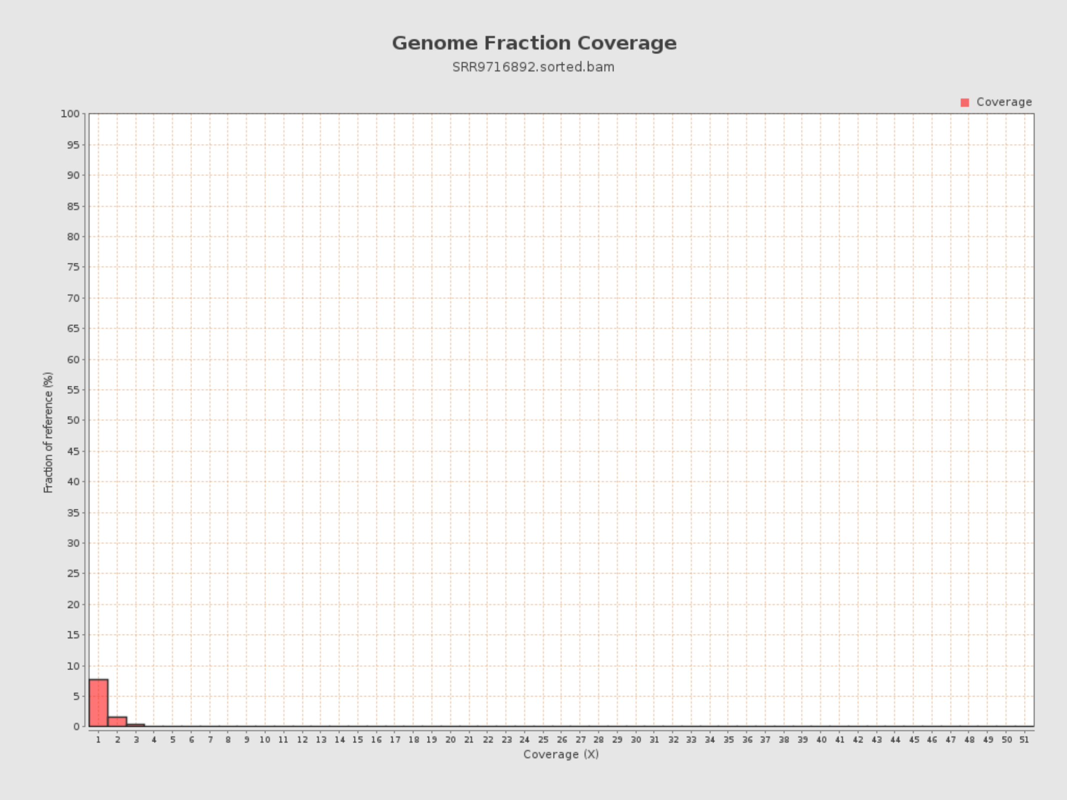
4. Results : Coverage Histogram



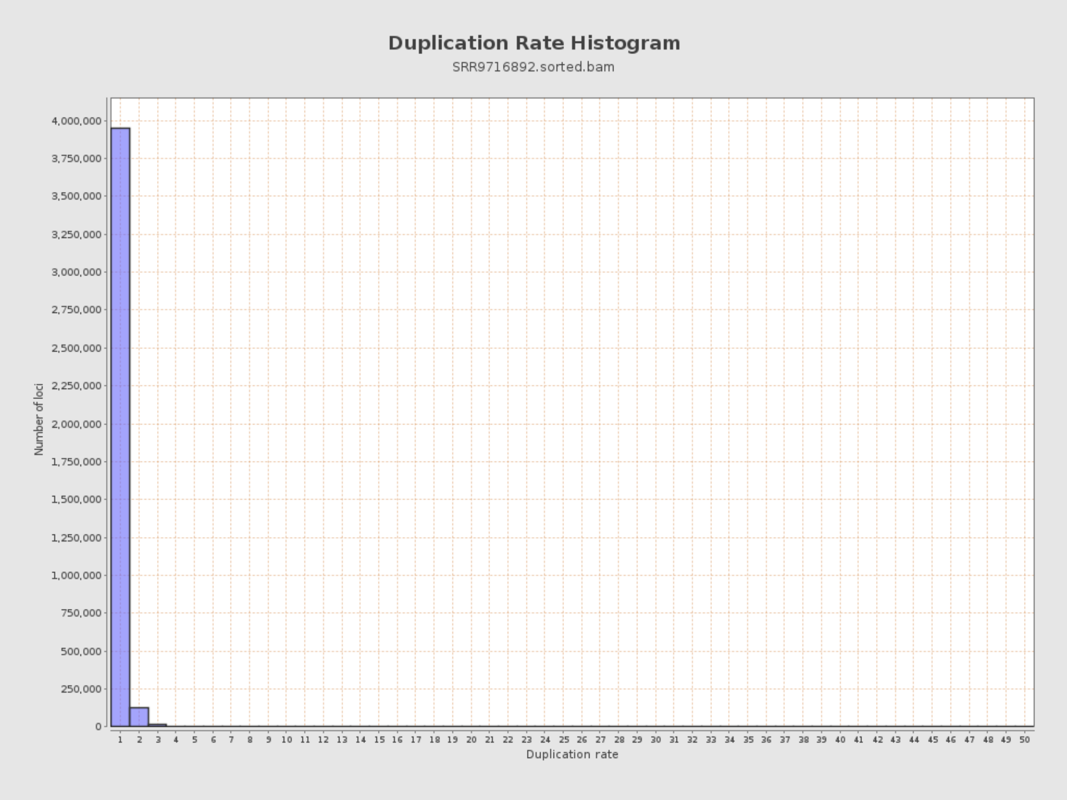
5. Results : Coverage Histogram (0-50X)



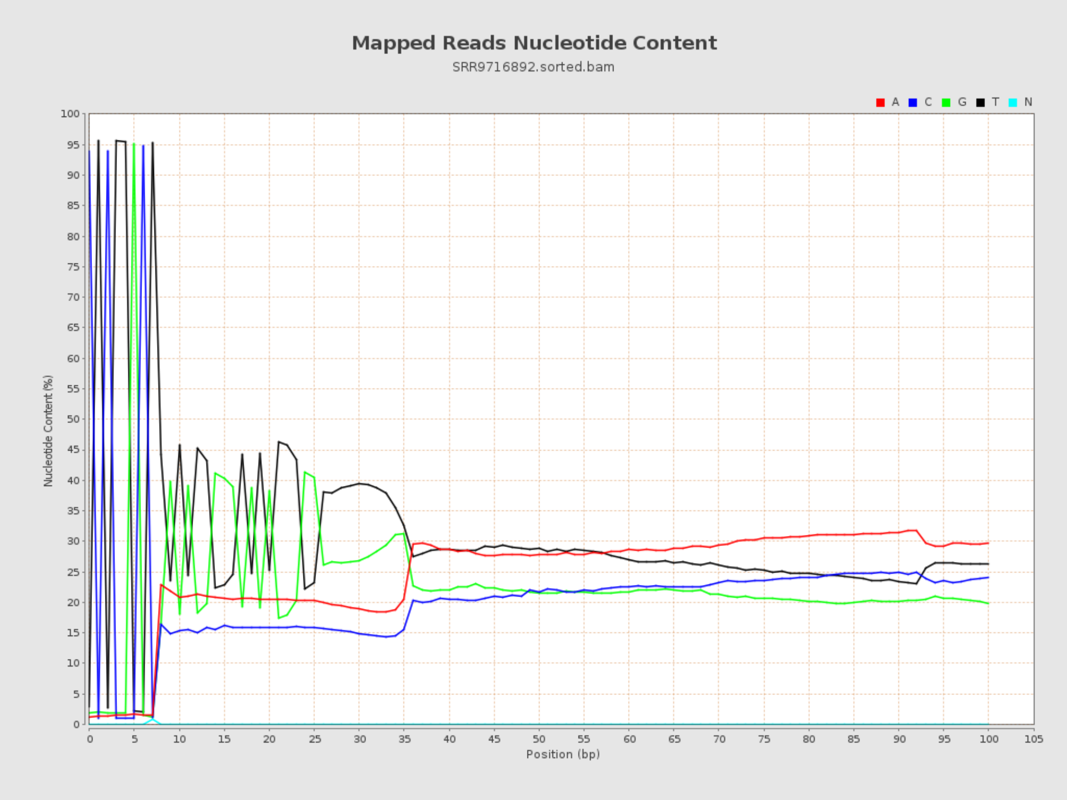
6. Results : Genome Fraction Coverage



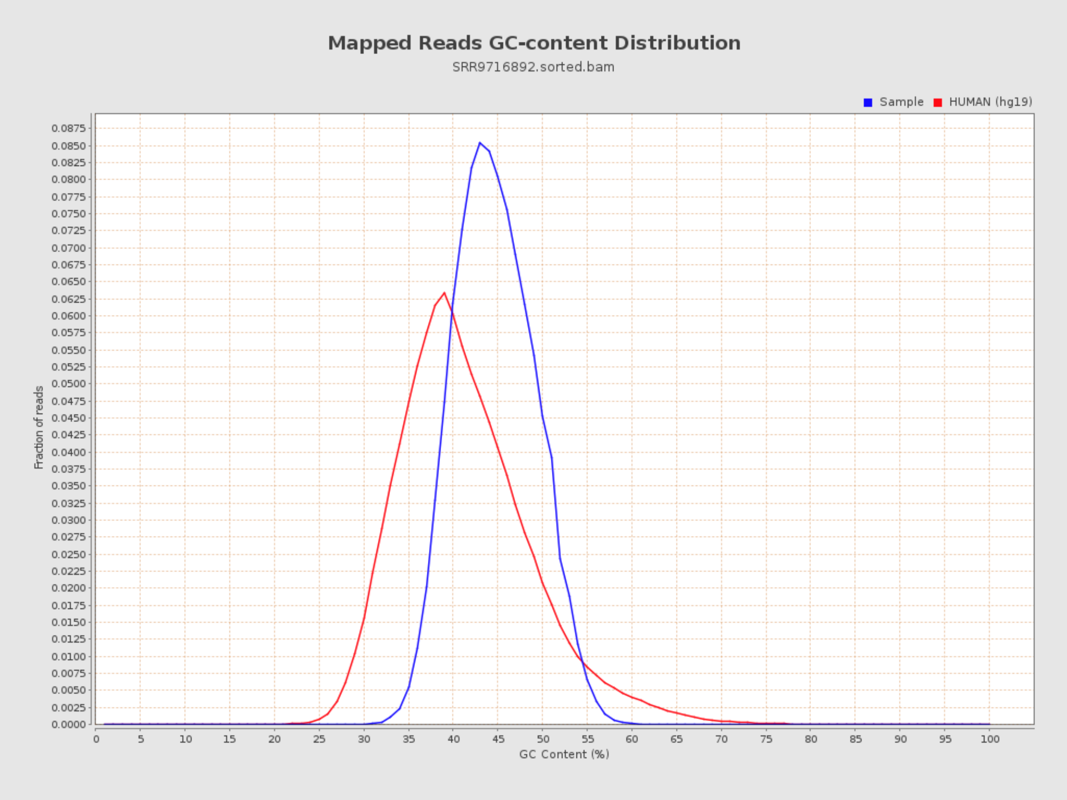
7. Results : Duplication Rate Histogram



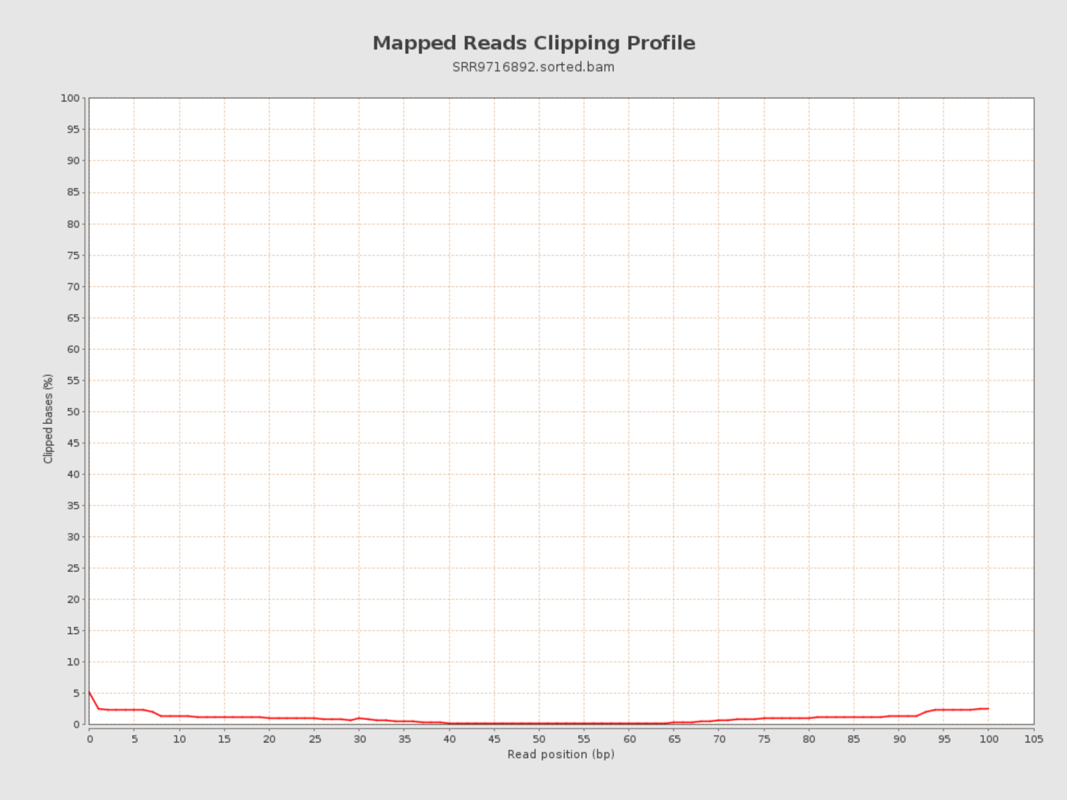
8. Results : Mapped Reads Nucleotide Content



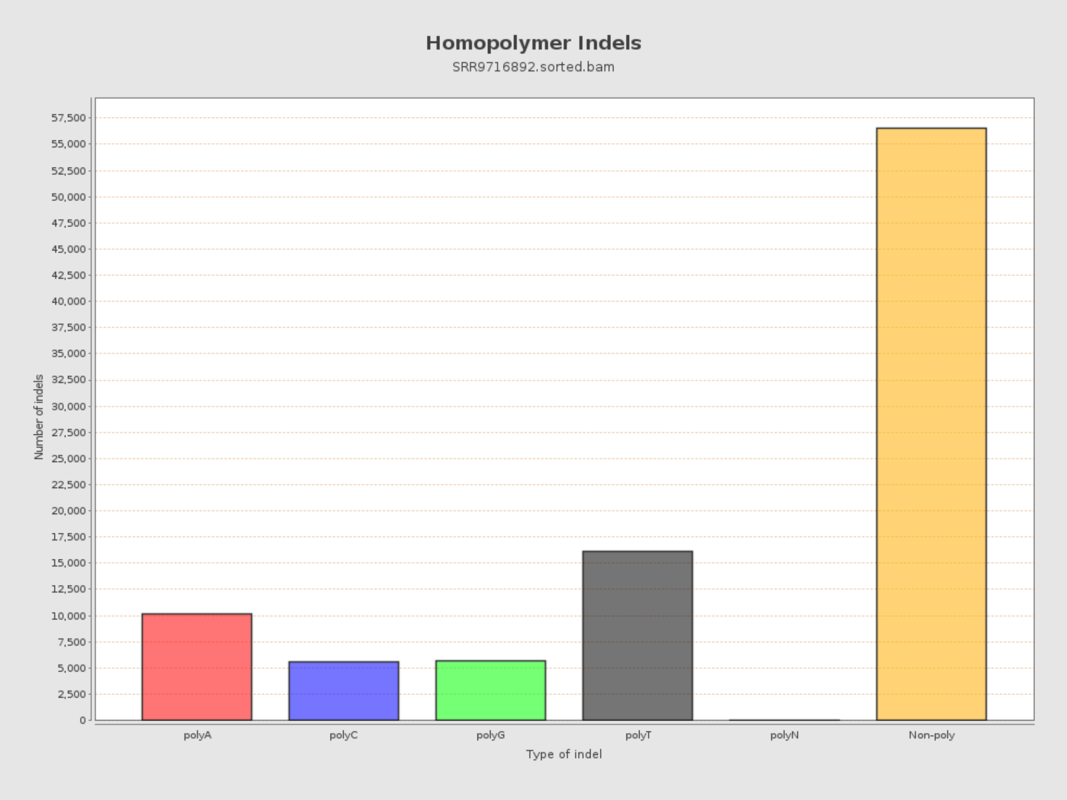
9. Results : Mapped Reads GC-content Distribution



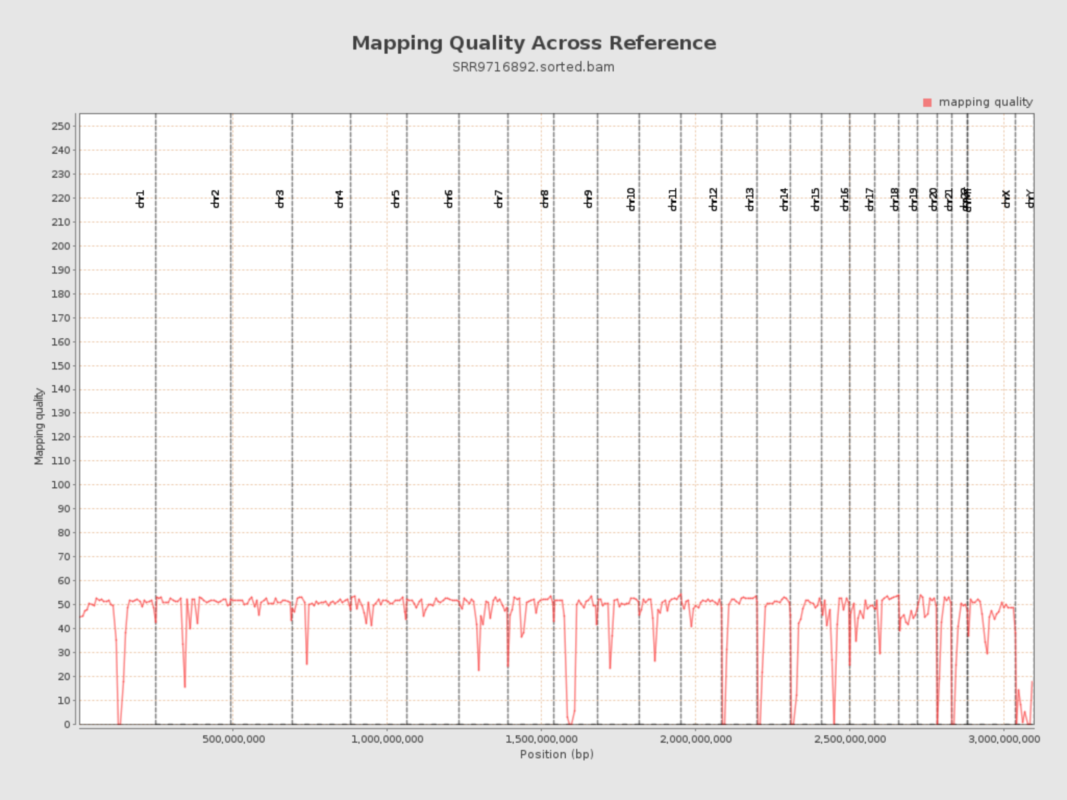
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram