Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 08:23:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716713.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_SRR9716713 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716713.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 08:23:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716713.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,171,358
Mapped reads	1,089,730 / 93.03%
Unmapped reads	81,628 / 6.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,049 / 2.57%
Read min/max/mean length	30 / 101 / 101.93
Duplicated reads (estimated)	36,688 / 3.13%
Duplication rate	2.59%
Clipped reads	1,117,689 / 95.42%

2.2. ACGT Content

Number/percentage of A's	19,955,024 / 24.01%
Number/percentage of C's	16,687,365 / 20.08%
Number/percentage of T's	25,129,706 / 30.23%
Number/percentage of G's	21,349,732 / 25.68%
Number/percentage of N's	3,097 / 0%
GC Percentage	45.76%

2.3. Coverage

Mean	0.0269

Standard Deviation	0.2421

2.4. Mapping Quality

Mean Mapping Quality	45.28

2.5. Mismatches and indels

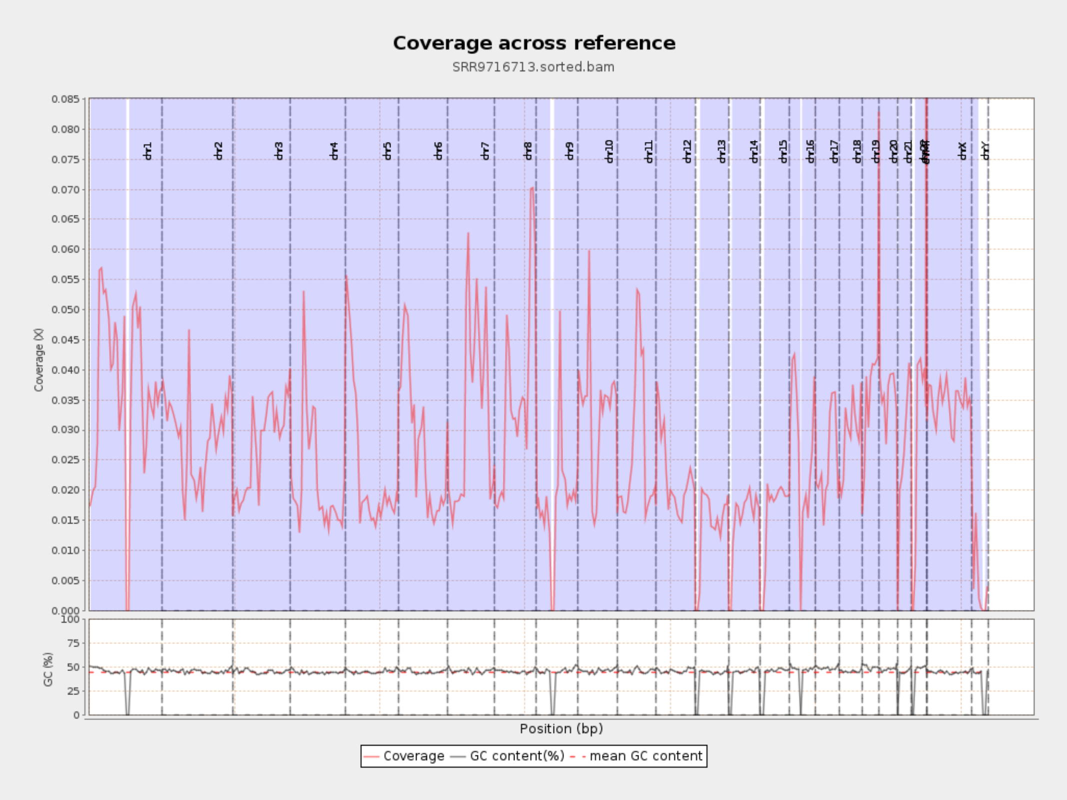
General error rate	0.68%
Mismatches	548,590
Insertions	7,246
Mapped reads with at least one insertion	0.65%
Deletions	15,295
Mapped reads with at least one deletion	1.38%
Homopolymer indels	39.47%

2.6. Chromosome stats

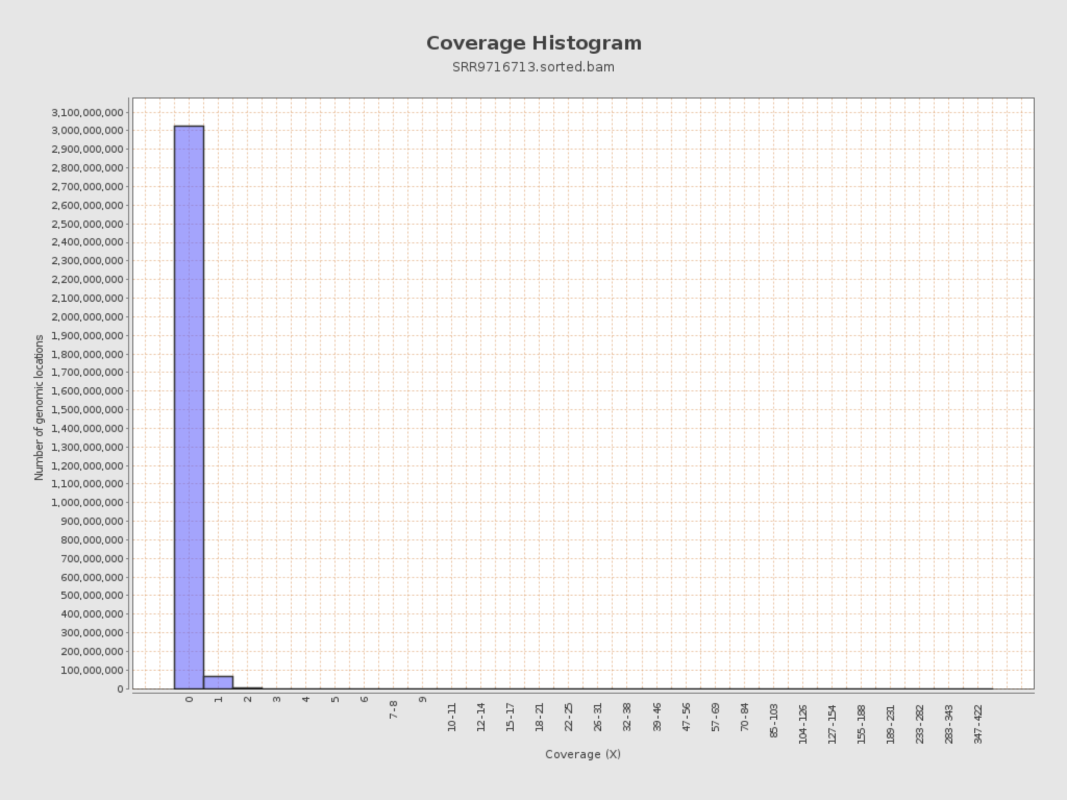
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9150279	0.0367	0.4129
chr2	243199373	7063518	0.029	0.2595
chr3	198022430	5414652	0.0273	0.1859
chr4	191154276	4083307	0.0214	0.2152
chr5	180915260	4280471	0.0237	0.1723
chr6	171115067	4736797	0.0277	0.1944
chr7	159138663	5273662	0.0331	0.3291

chr8	146364022	5261750	0.0359	0.2676
chr9	141213431	2550821	0.0181	0.174
chr10	135534747	4513185	0.0333	0.3158
chr11	135006516	3573285	0.0265	0.2146
chr12	133851895	2993271	0.0224	0.1662
chr13	115169878	1584770	0.0138	0.128
chr14	107349540	1589190	0.0148	0.142
chr15	102531392	1605254	0.0157	0.1375
chr16	90354753	2392533	0.0265	0.1907
chr17	81195210	2000867	0.0246	0.1884
chr18	78077248	2288986	0.0293	0.2625
chr19	59128983	2189243	0.037	0.3253
chr20	63025520	2261203	0.0359	0.219
chr21	48129895	1298320	0.027	0.2142
chr22	51304566	1375422	0.0268	0.1912
chrMT	16571	12190	0.7356	0.9852
chrX	155270560	5387678	0.0347	0.2139
chrY	59373566	275831	0.0046	0.1569

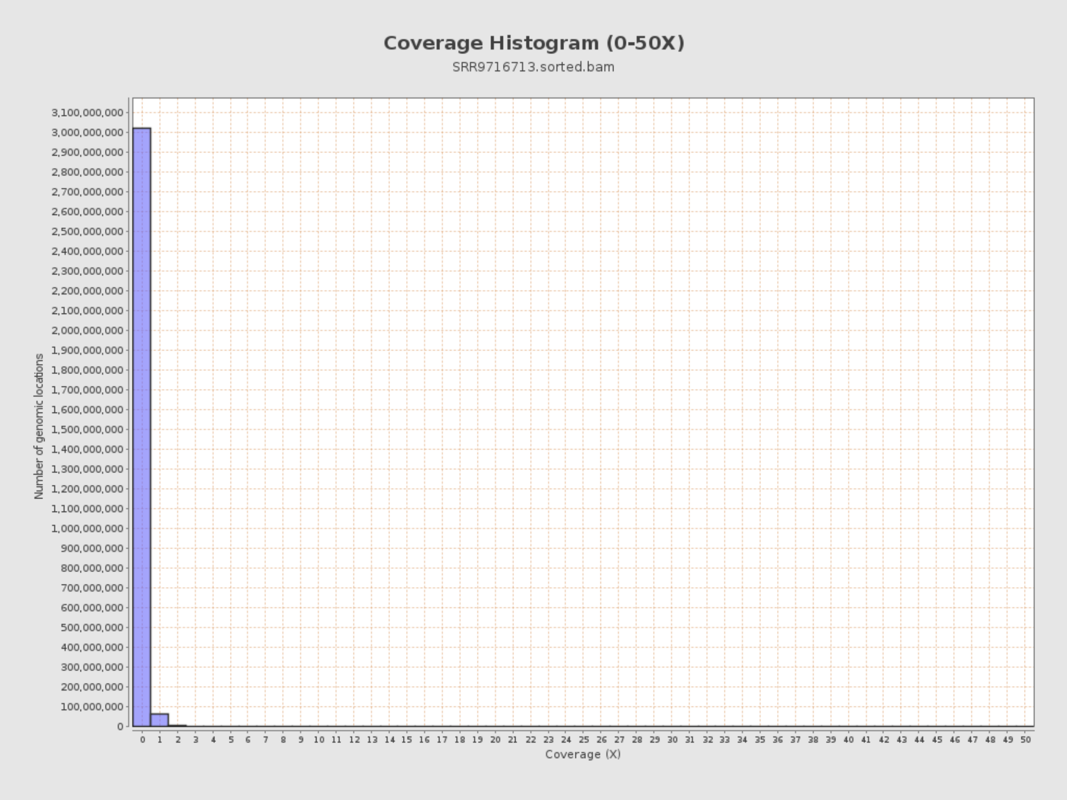
3. Results : Coverage across reference



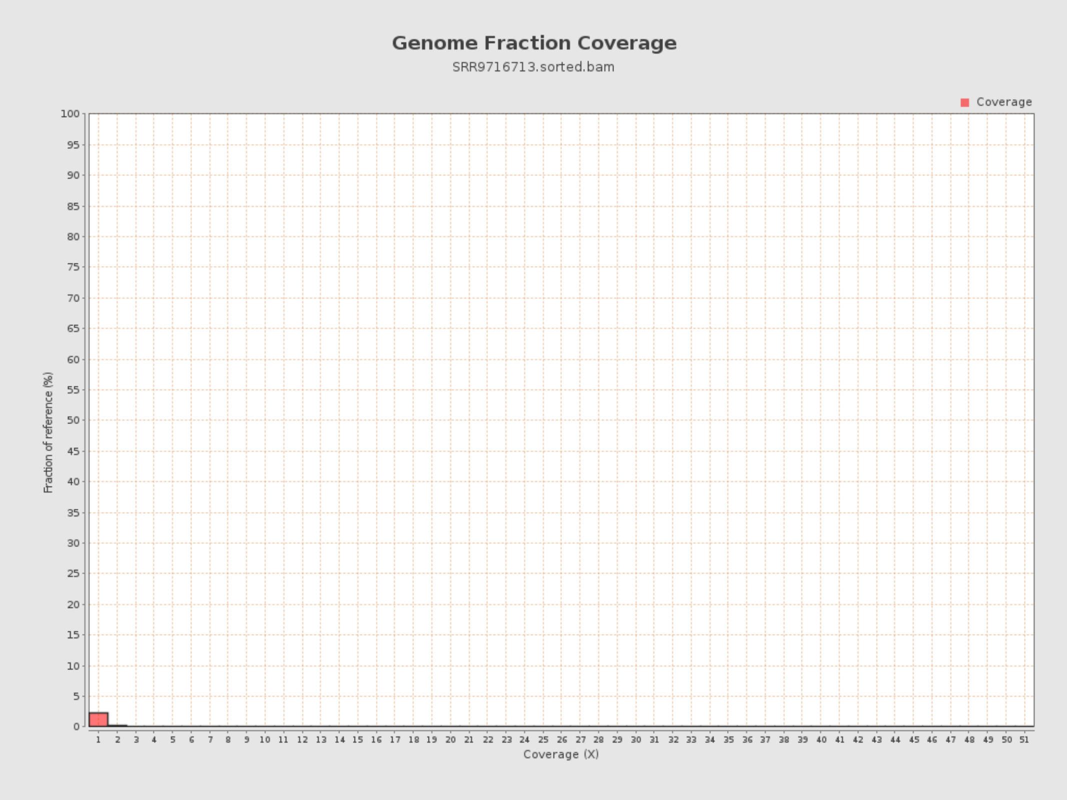
4. Results : Coverage Histogram



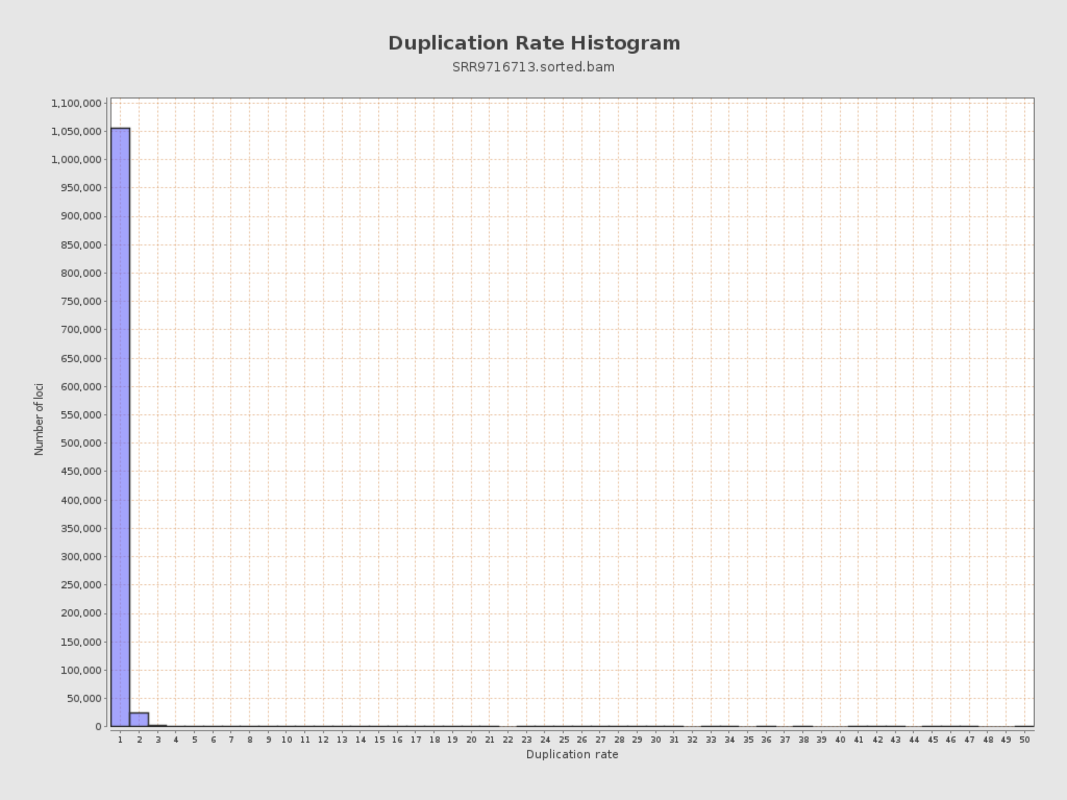
5. Results : Coverage Histogram (0-50X)



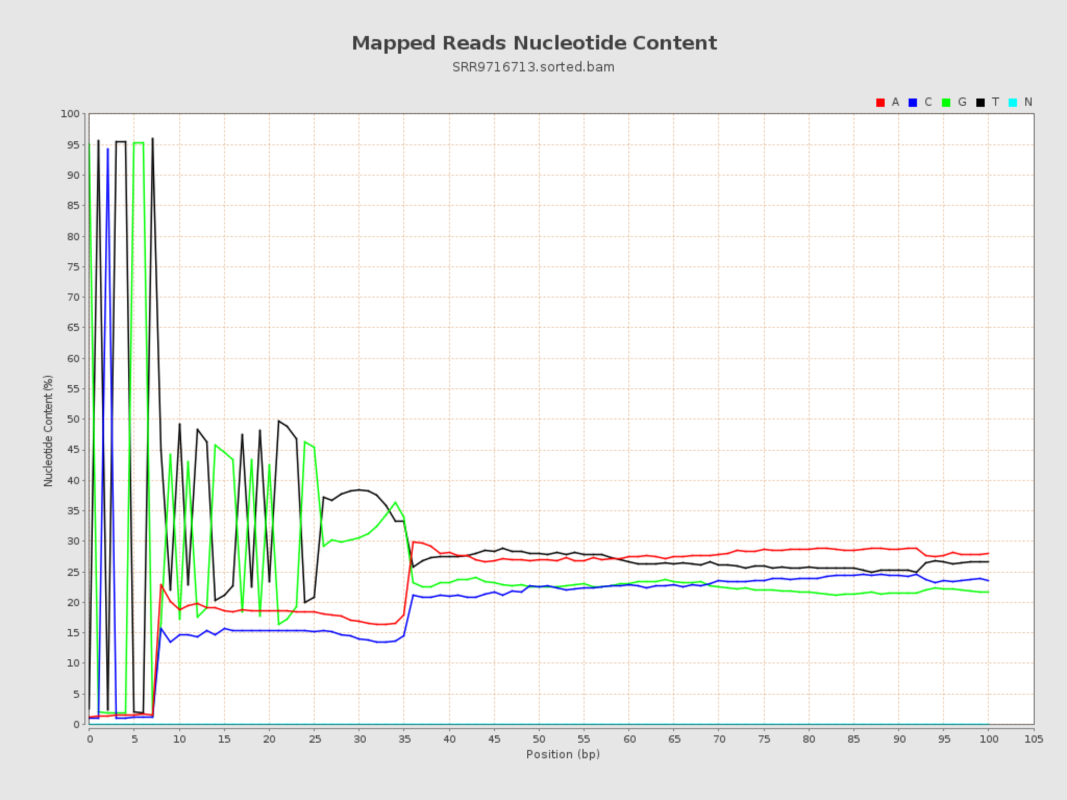
6. Results : Genome Fraction Coverage



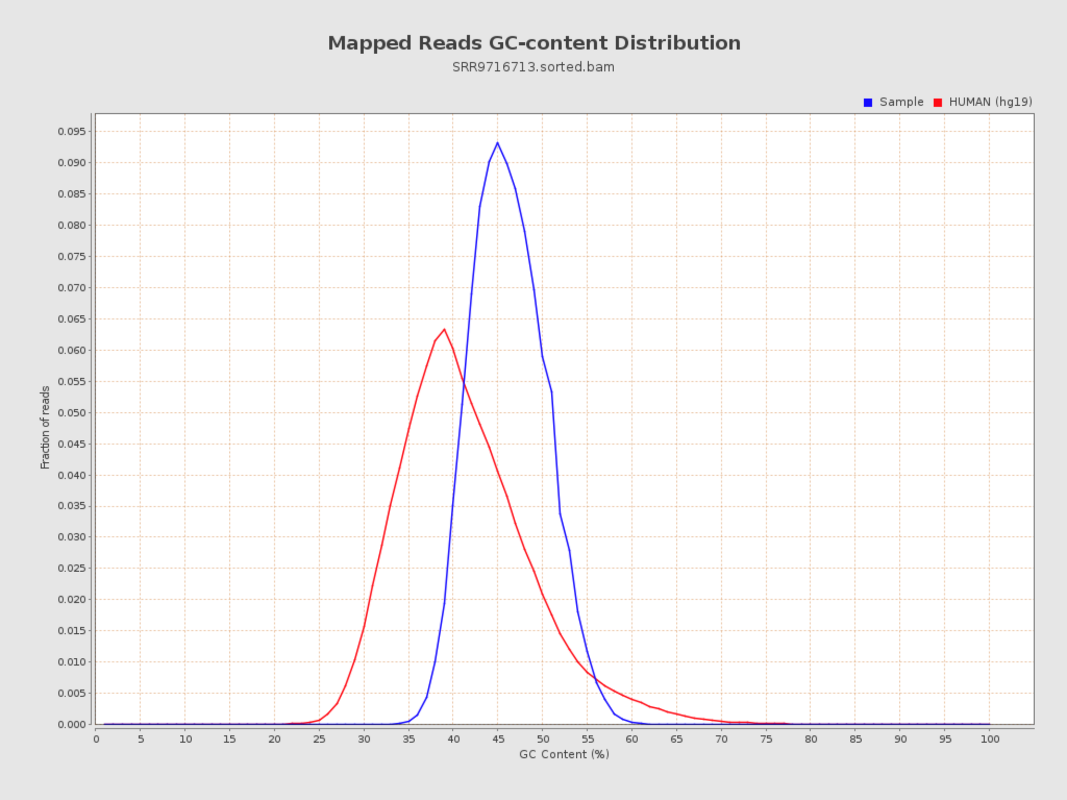
7. Results : Duplication Rate Histogram



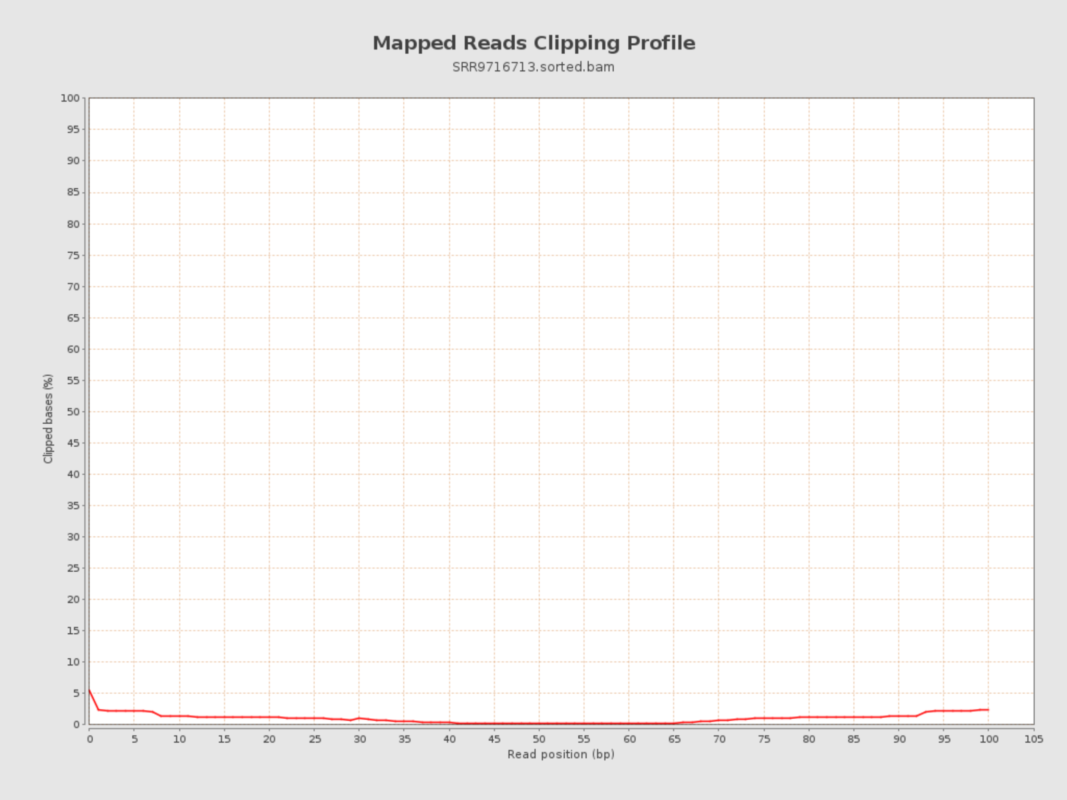
8. Results : Mapped Reads Nucleotide Content



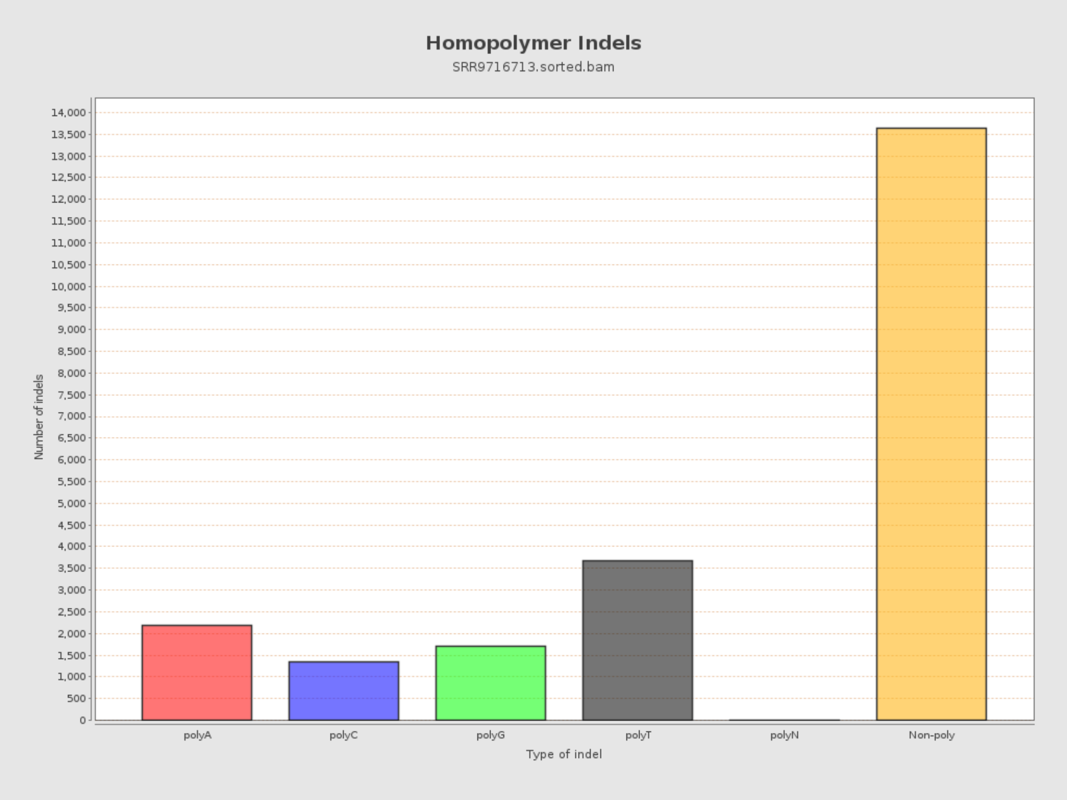
9. Results : Mapped Reads GC-content Distribution



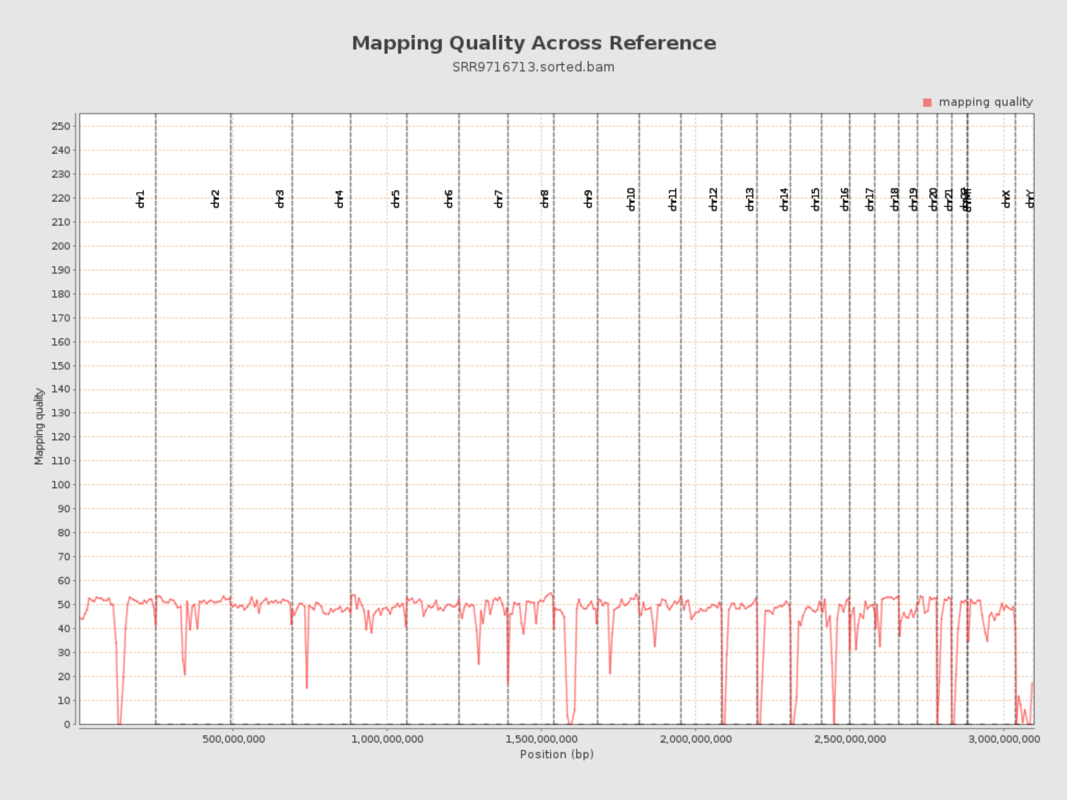
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram