Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 06:52:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716698.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_SRR9716698 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716698.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 06:52:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716698.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,325,875
Mapped reads	1,198,742 / 90.41%
Unmapped reads	127,133 / 9.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,355 / 1.46%
Read min/max/mean length	30 / 101 / 101.54
Duplicated reads (estimated)	45,866 / 3.46%
Duplication rate	2.02%
Clipped reads	1,215,837 / 91.7%

2.2. ACGT Content

Number/percentage of A's	23,342,346 / 24.83%
Number/percentage of C's	17,672,301 / 18.8%
Number/percentage of T's	28,734,455 / 30.56%
Number/percentage of G's	24,264,766 / 25.81%
Number/percentage of N's	5,622 / 0.01%
GC Percentage	44.6%

2.3. Coverage

Mean	0.0304

Standard Deviation	0.3953

2.4. Mapping Quality

Mean Mapping Quality	43.37

2.5. Mismatches and indels

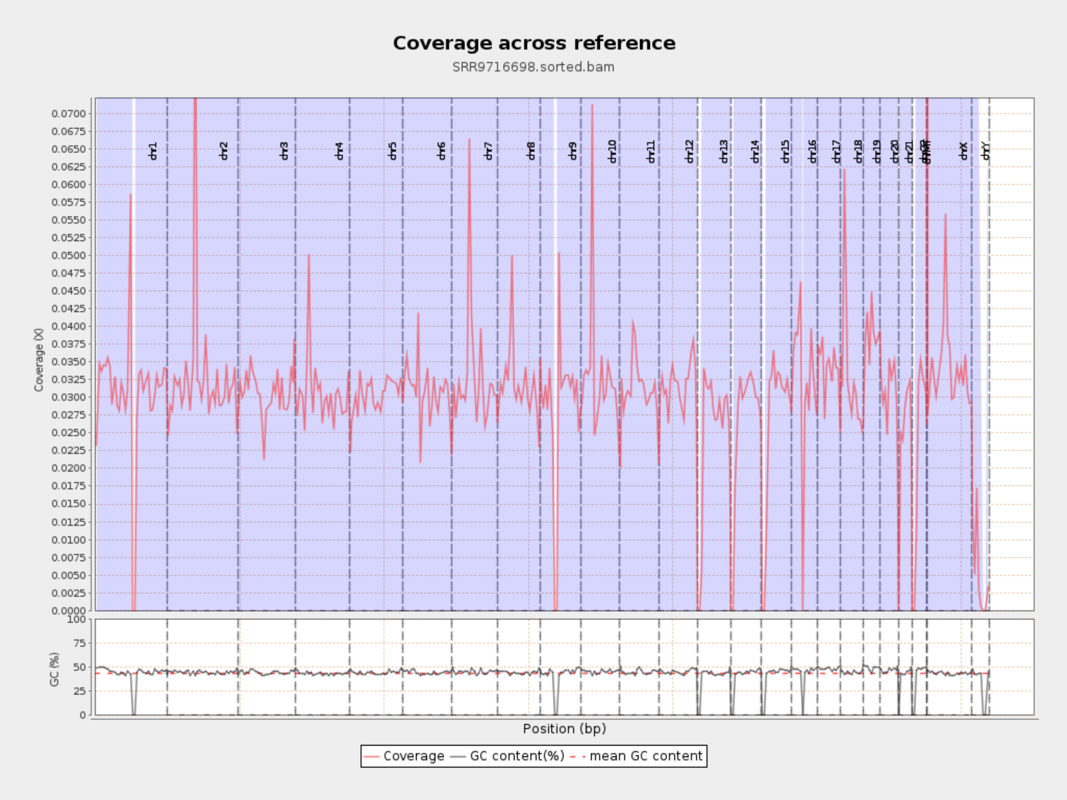
General error rate	0.87%
Mismatches	802,509
Insertions	9,424
Mapped reads with at least one insertion	0.77%
Deletions	23,875
Mapped reads with at least one deletion	1.96%
Homopolymer indels	43.24%

2.6. Chromosome stats

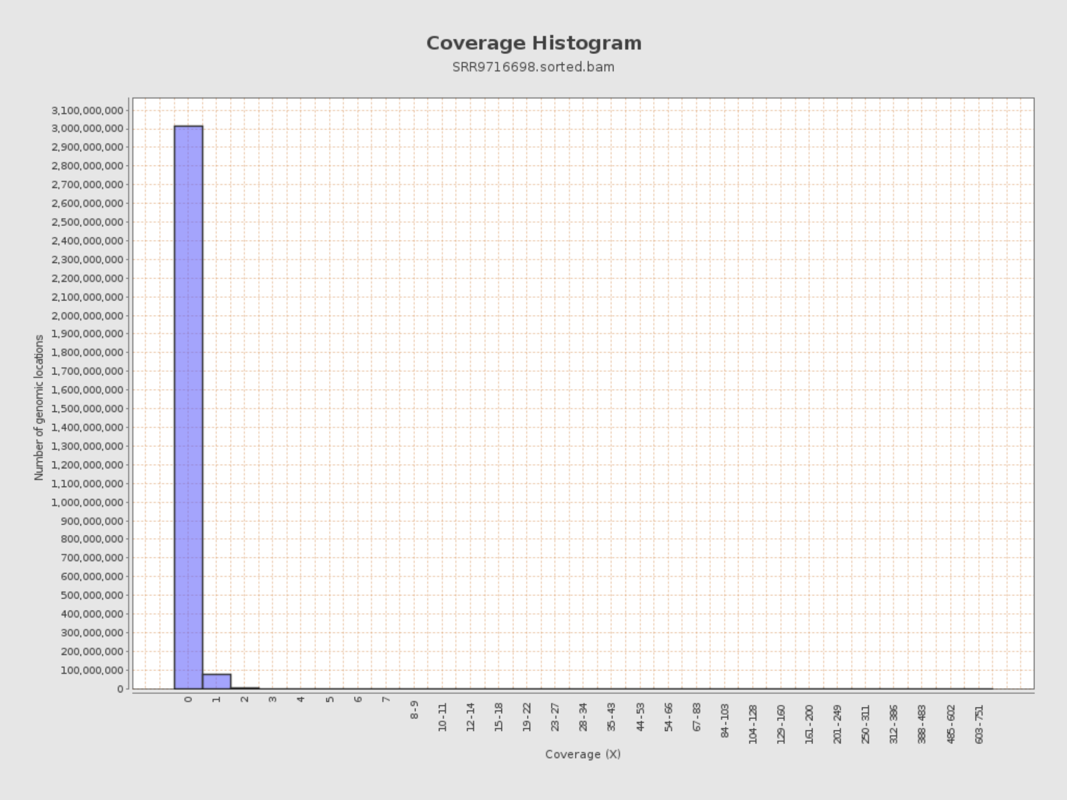
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7578319	0.0304	0.6312
chr2	243199373	8055092	0.0331	0.5823
chr3	198022430	6067666	0.0306	0.1923
chr4	191154276	5851462	0.0306	0.2236
chr5	180915260	5535985	0.0306	0.196
chr6	171115067	5277697	0.0308	0.2441
chr7	159138663	5234555	0.0329	0.5264

chr8	146364022	4673928	0.0319	0.507
chr9	141213431	4019750	0.0285	0.43
chr10	135534747	4494413	0.0332	0.413
chr11	135006516	4273149	0.0317	0.3787
chr12	133851895	4251511	0.0318	0.2002
chr13	115169878	2821030	0.0245	0.1686
chr14	107349540	2797922	0.0261	0.255
chr15	102531392	2682134	0.0262	0.1771
chr16	90354753	2865600	0.0317	0.2321
chr17	81195210	2775430	0.0342	0.2227
chr18	78077248	2570834	0.0329	0.8331
chr19	59128983	2288699	0.0387	0.5069
chr20	63025520	1935415	0.0307	0.2042
chr21	48129895	1214355	0.0252	0.2018
chr22	51304566	1149107	0.0224	0.1624
chrMT	16571	14601	0.8811	1.1325
chrX	155270560	5339508	0.0344	0.2883
chrY	59373566	293176	0.0049	0.1618

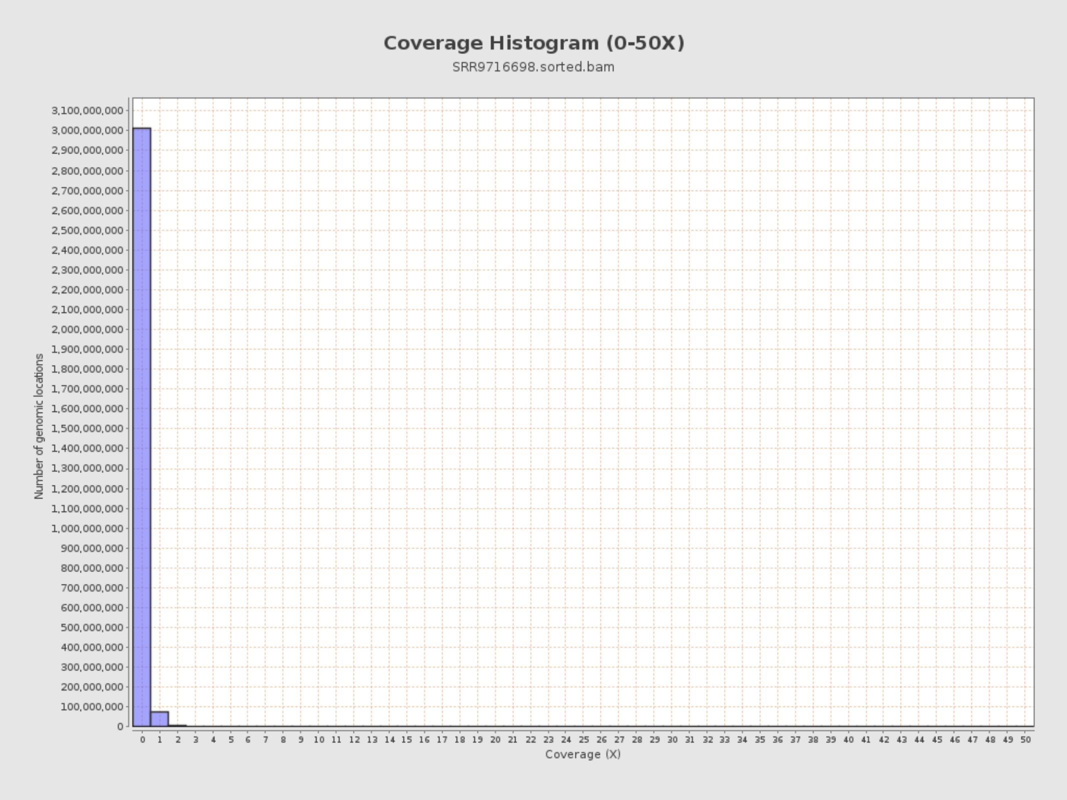
3. Results : Coverage across reference



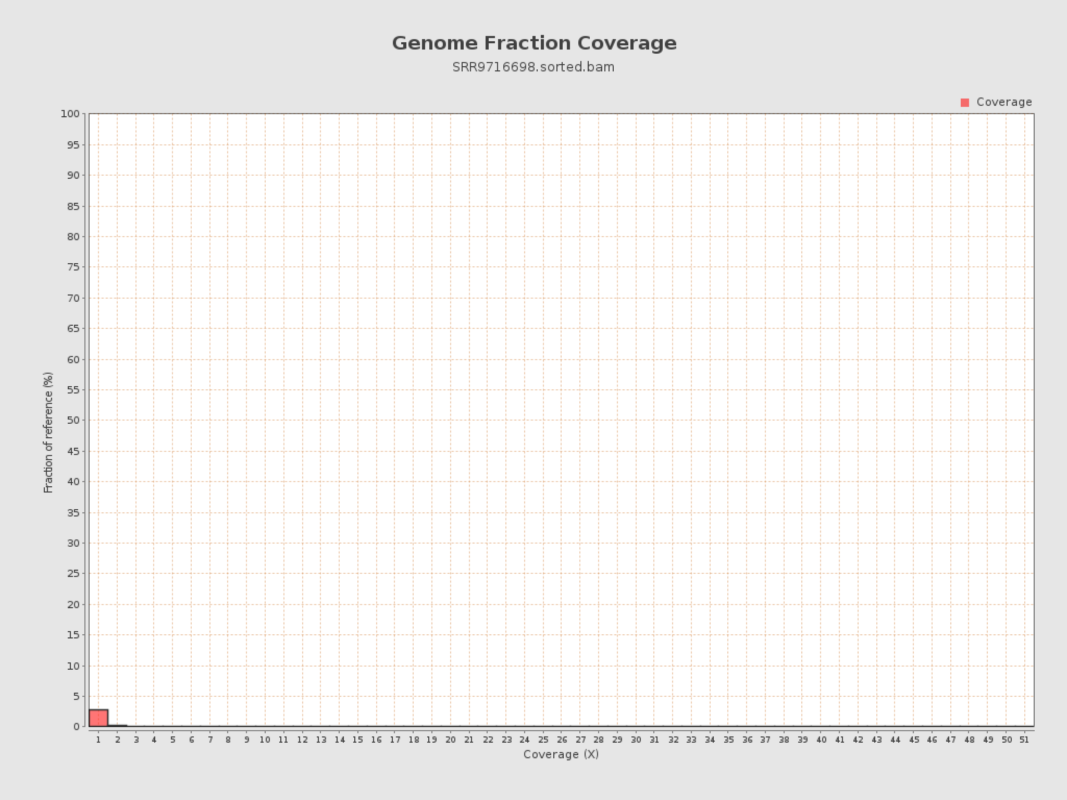
4. Results : Coverage Histogram



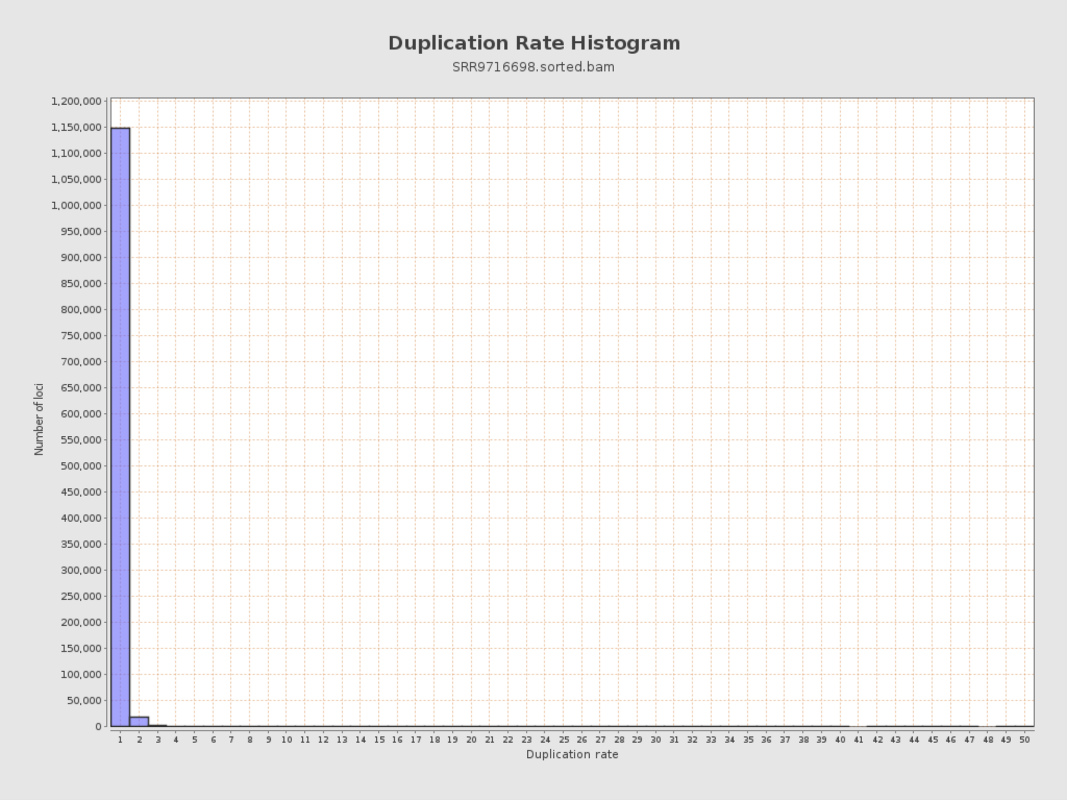
5. Results : Coverage Histogram (0-50X)



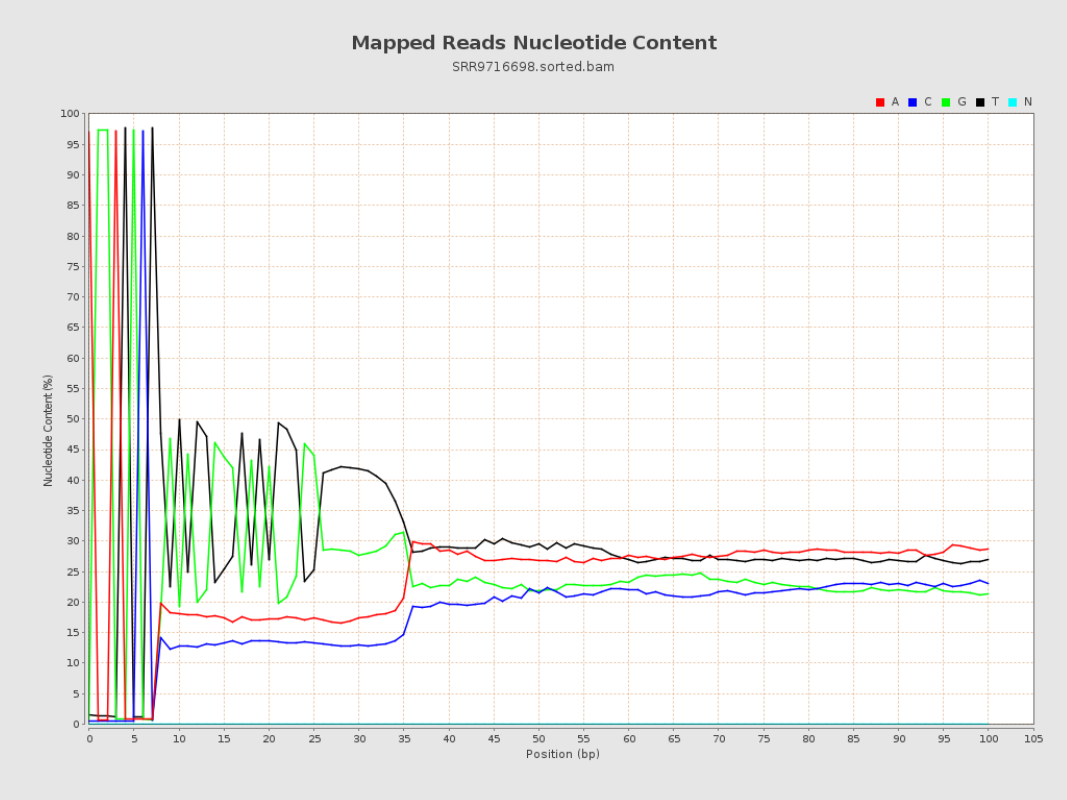
6. Results : Genome Fraction Coverage



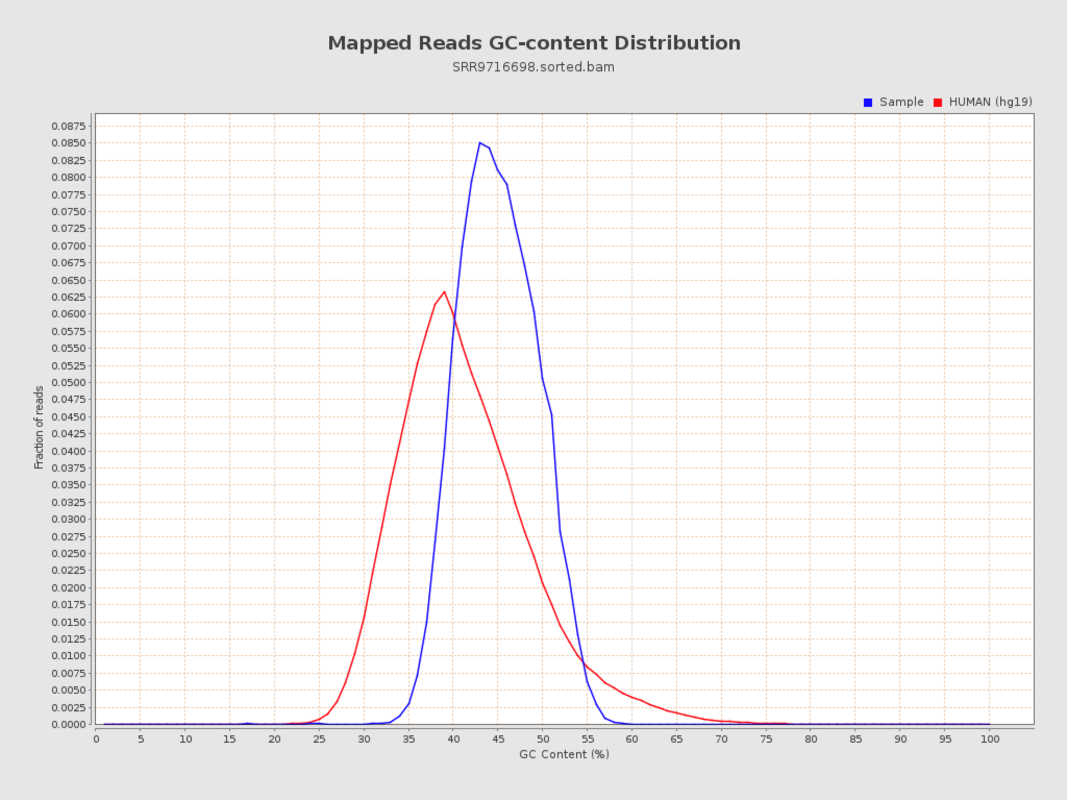
7. Results : Duplication Rate Histogram



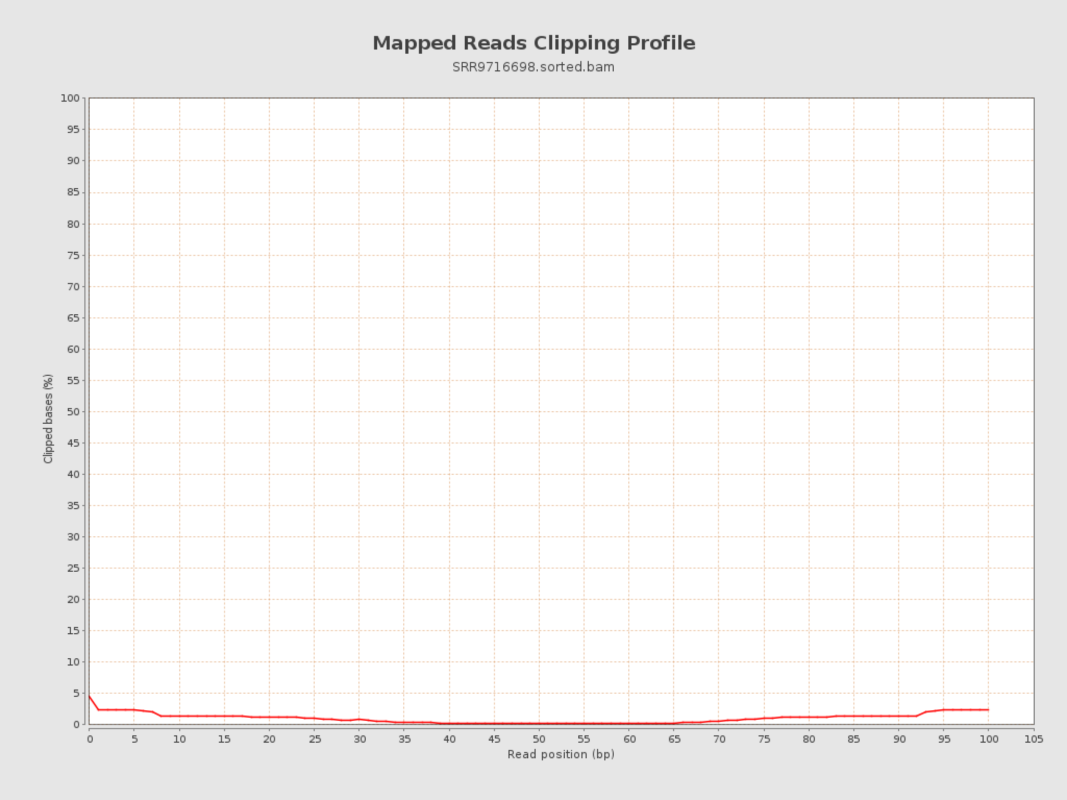
8. Results : Mapped Reads Nucleotide Content



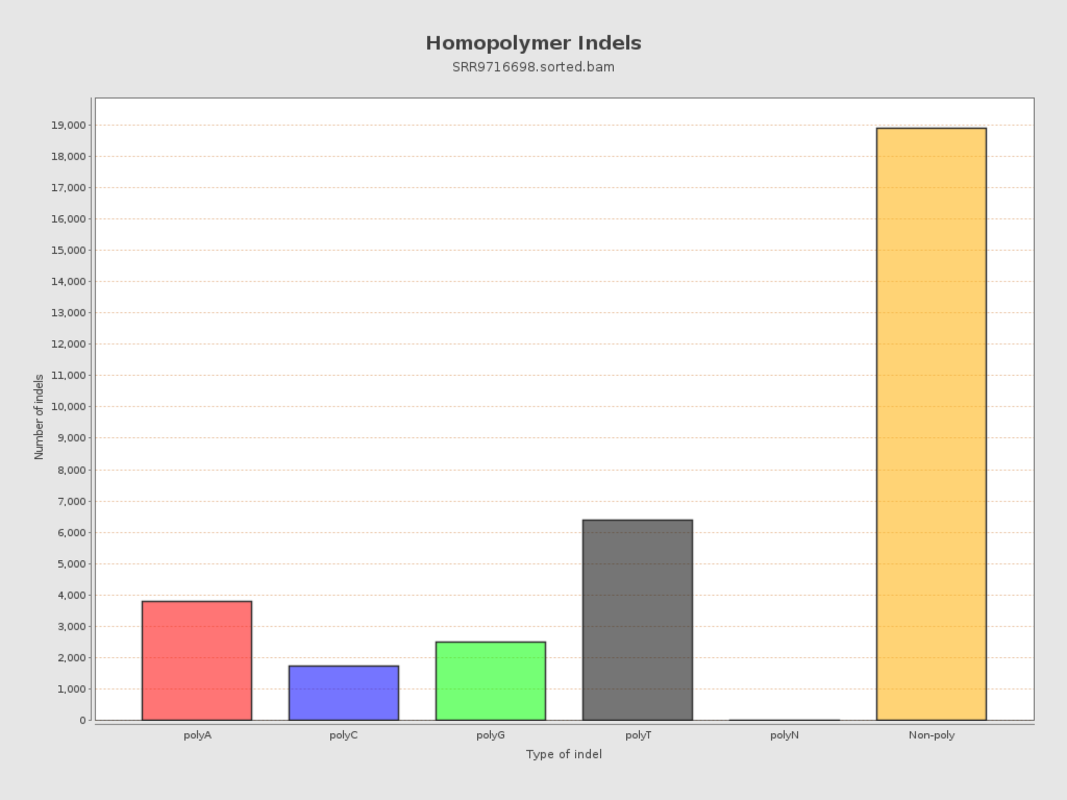
9. Results : Mapped Reads GC-content Distribution



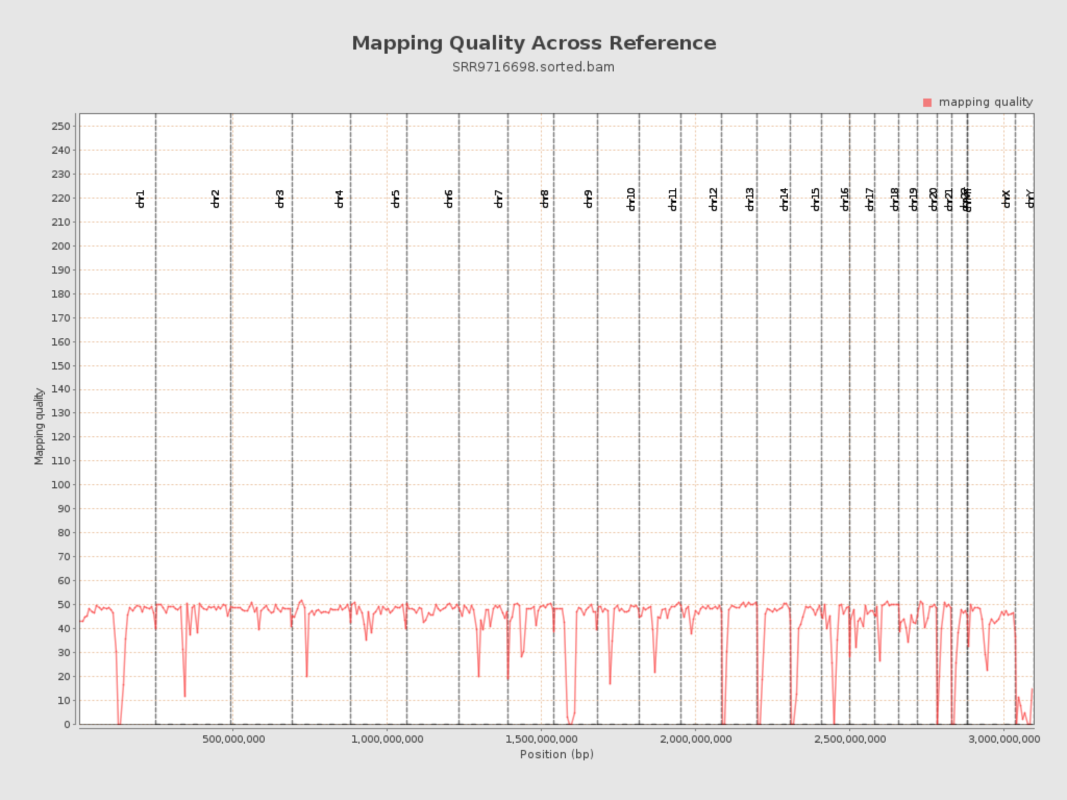
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram