Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 08:34:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716346.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_SRR9716346 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716346.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 08:34:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716346.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,086,091
Mapped reads	1,028,685 / 94.71%
Unmapped reads	57,406 / 5.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,128 / 1.85%
Read min/max/mean length	30 / 101 / 101.67
Duplicated reads (estimated)	30,652 / 2.82%
Duplication rate	2.05%
Clipped reads	1,048,617 / 96.55%

2.2. ACGT Content

Number/percentage of A's	20,609,551 / 25.23%
Number/percentage of C's	16,321,181 / 19.98%
Number/percentage of T's	24,712,161 / 30.25%
Number/percentage of G's	20,032,867 / 24.53%
Number/percentage of N's	5,731 / 0.01%
GC Percentage	44.51%

2.3. Coverage

Mean	0.0264

Standard Deviation	0.2769

2.4. Mapping Quality

Mean Mapping Quality	47.51

2.5. Mismatches and indels

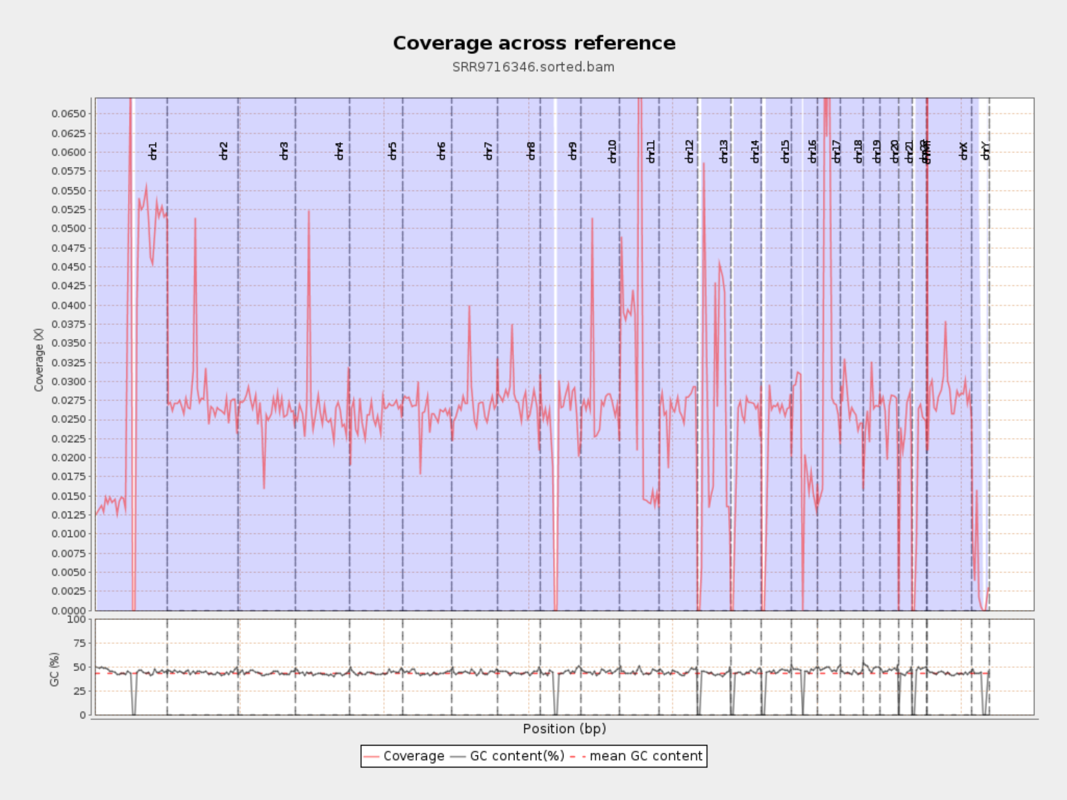
General error rate	0.65%
Mismatches	514,736
Insertions	6,316
Mapped reads with at least one insertion	0.6%
Deletions	20,330
Mapped reads with at least one deletion	1.95%
Homopolymer indels	43.27%

2.6. Chromosome stats

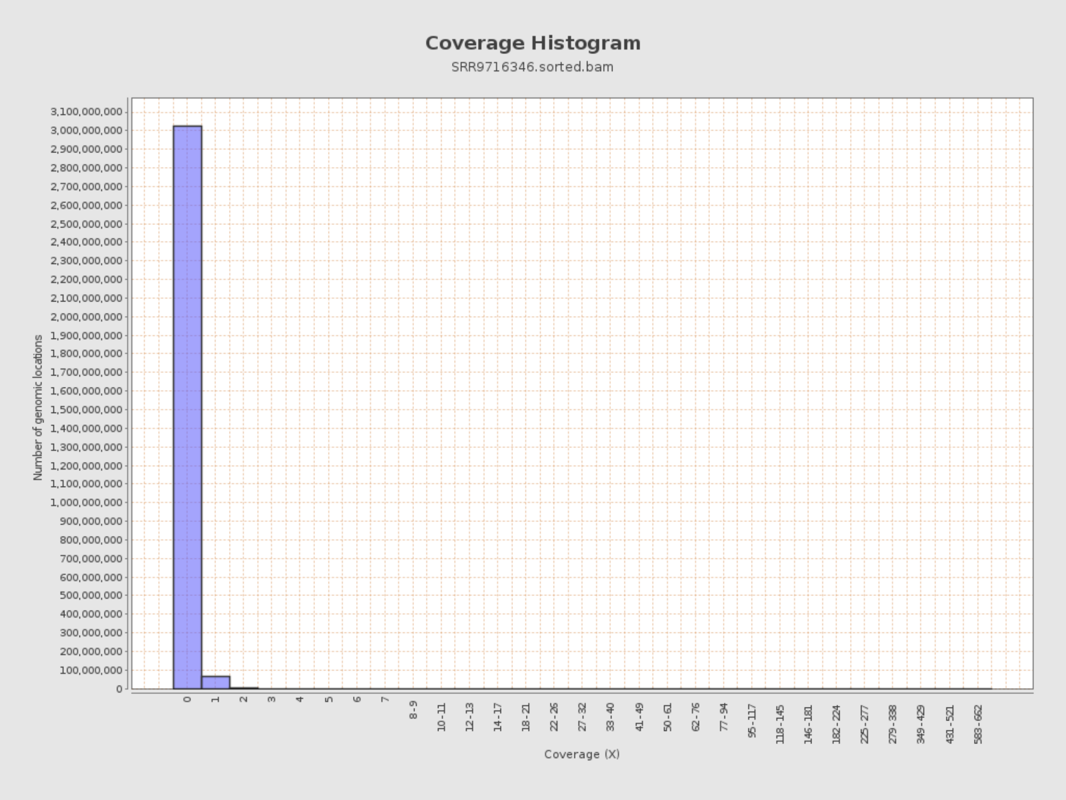
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7940077	0.0319	0.5615
chr2	243199373	6761289	0.0278	0.2901
chr3	198022430	5196253	0.0262	0.1732
chr4	191154276	5094847	0.0267	0.2064
chr5	180915260	4674613	0.0258	0.1728
chr6	171115067	4457868	0.0261	0.1822
chr7	159138663	4304742	0.0271	0.3195

chr8	146364022	4057700	0.0277	0.297
chr9	141213431	3299865	0.0234	0.2295
chr10	135534747	3749567	0.0277	0.2787
chr11	135006516	4492353	0.0333	0.3029
chr12	133851895	3542632	0.0265	0.1752
chr13	115169878	2864877	0.0249	0.1691
chr14	107349540	2363587	0.022	0.1699
chr15	102531392	2238196	0.0218	0.1576
chr16	90354753	1823283	0.0202	0.1625
chr17	81195210	2948401	0.0363	0.2397
chr18	78077248	2082043	0.0267	0.3811
chr19	59128983	1530885	0.0259	0.4087
chr20	63025520	1650573	0.0262	0.1783
chr21	48129895	1068965	0.0222	0.1816
chr22	51304566	912213	0.0178	0.1429
chrMT	16571	3788	0.2286	0.5902
chrX	155270560	4421489	0.0285	0.2029
chrY	59373566	240298	0.004	0.1445

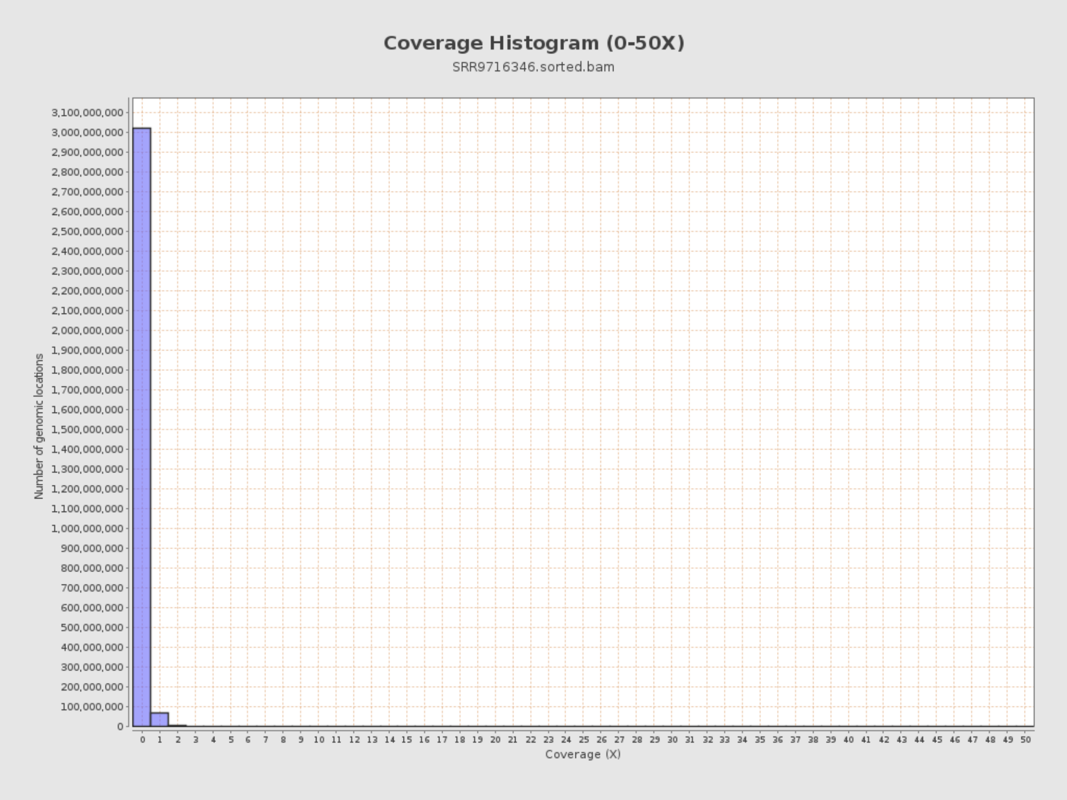
3. Results : Coverage across reference



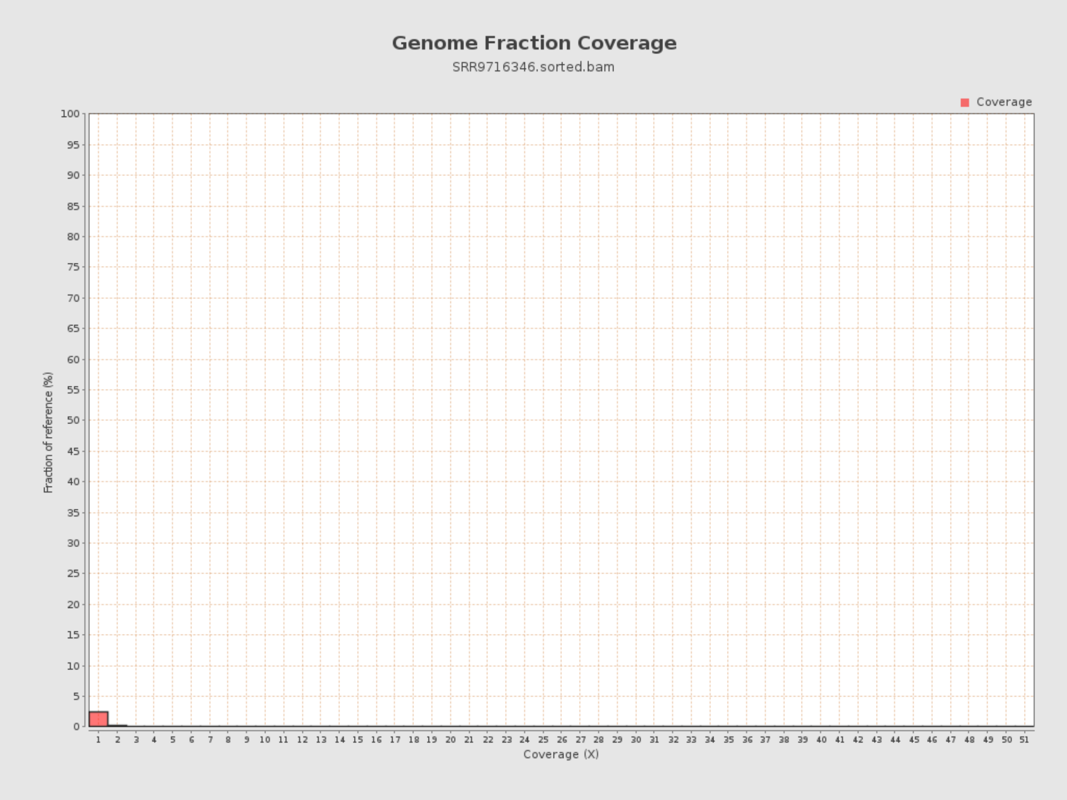
4. Results : Coverage Histogram



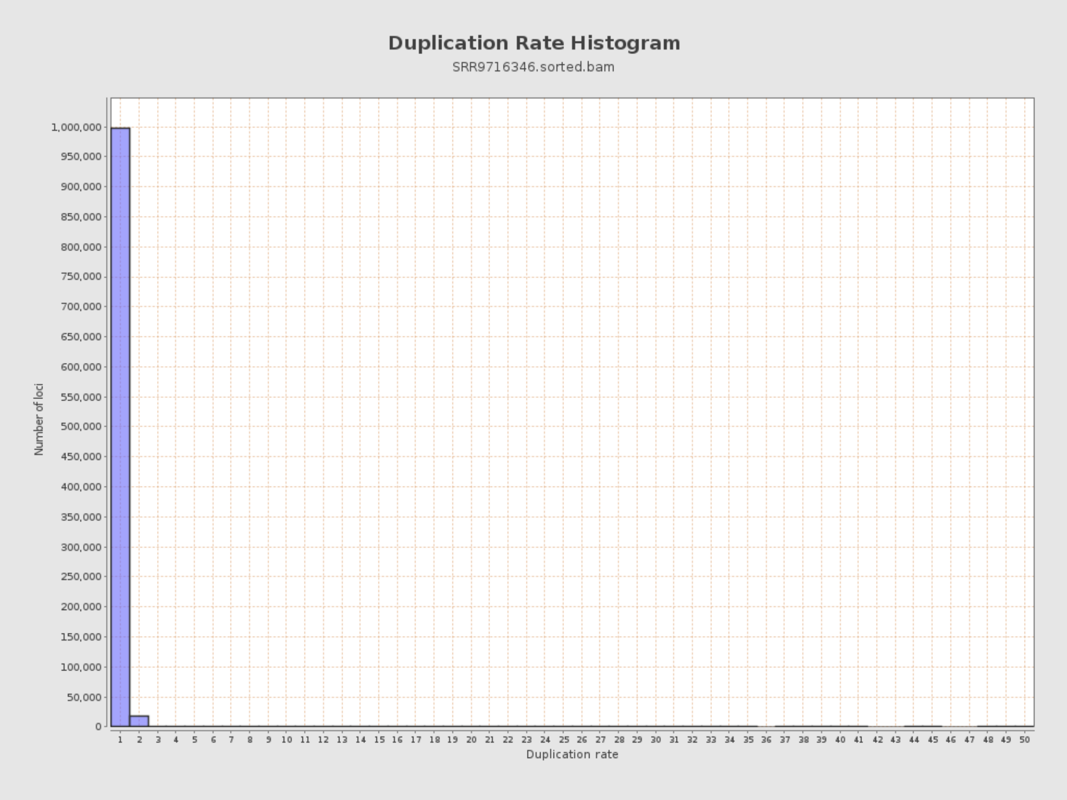
5. Results : Coverage Histogram (0-50X)



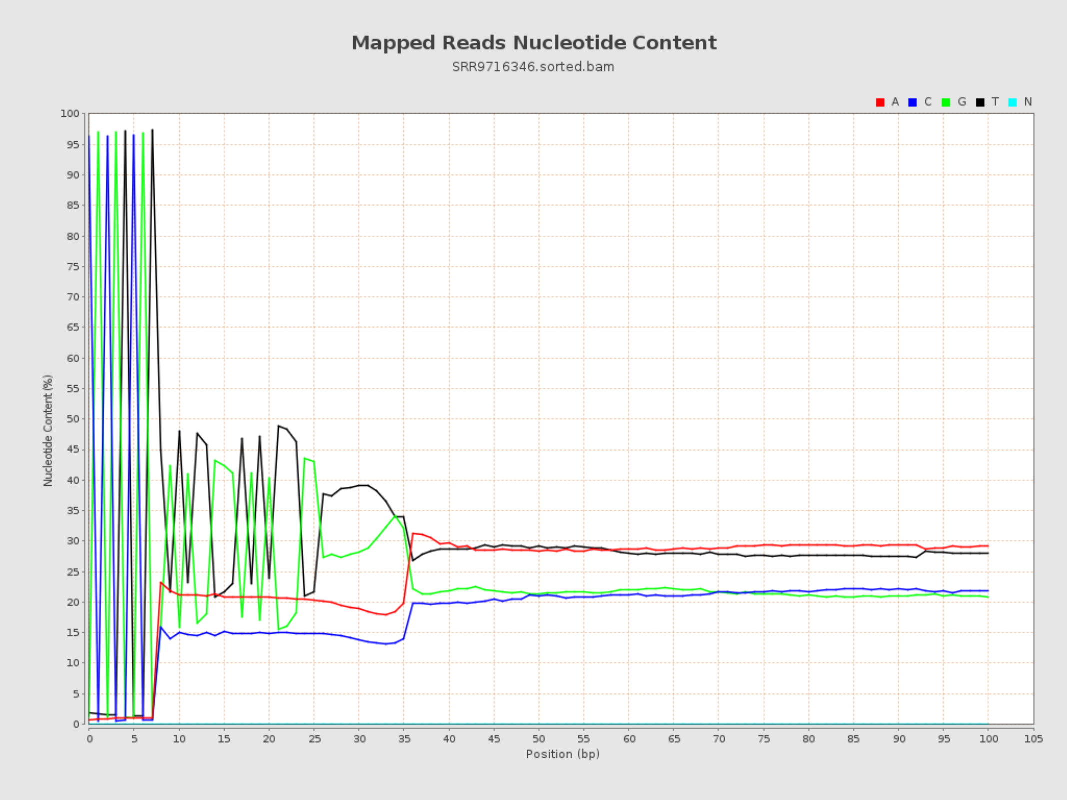
6. Results : Genome Fraction Coverage



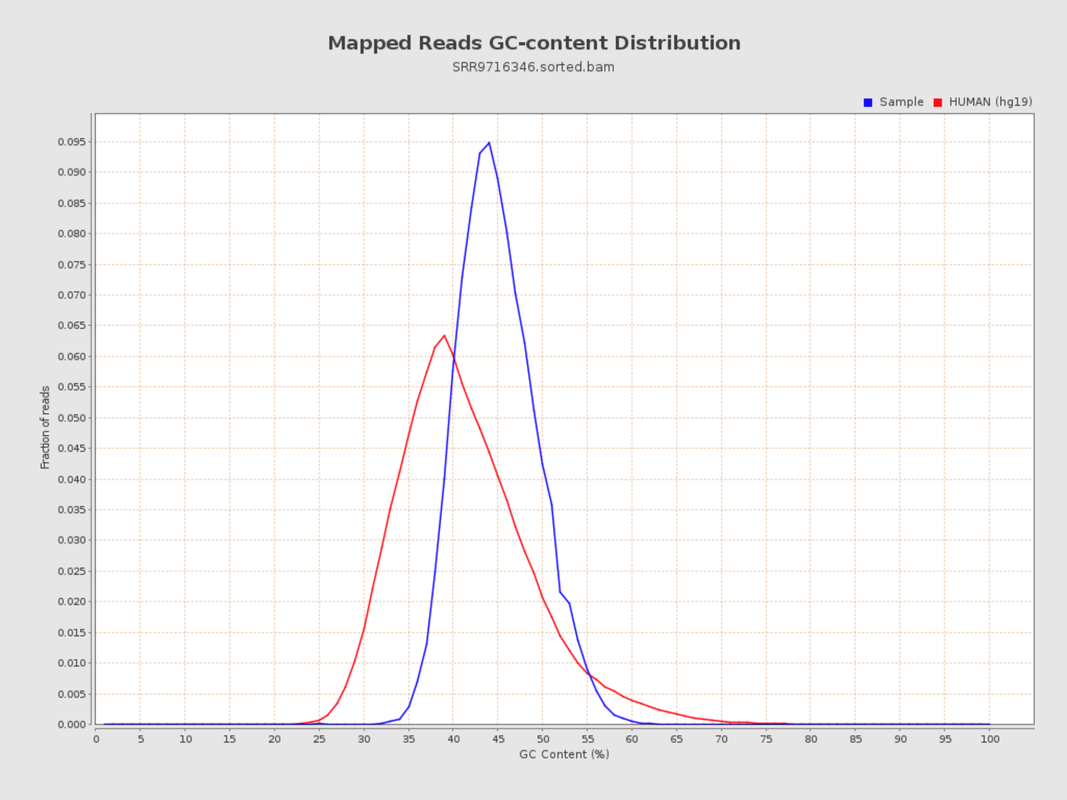
7. Results : Duplication Rate Histogram



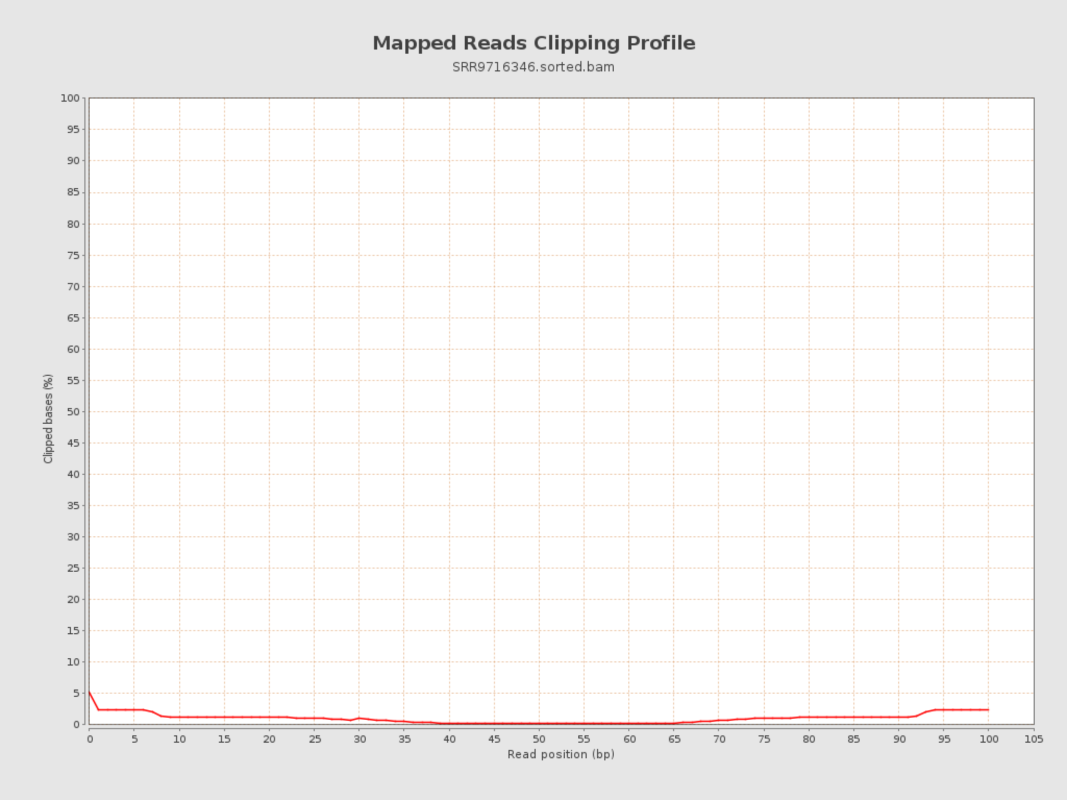
8. Results : Mapped Reads Nucleotide Content



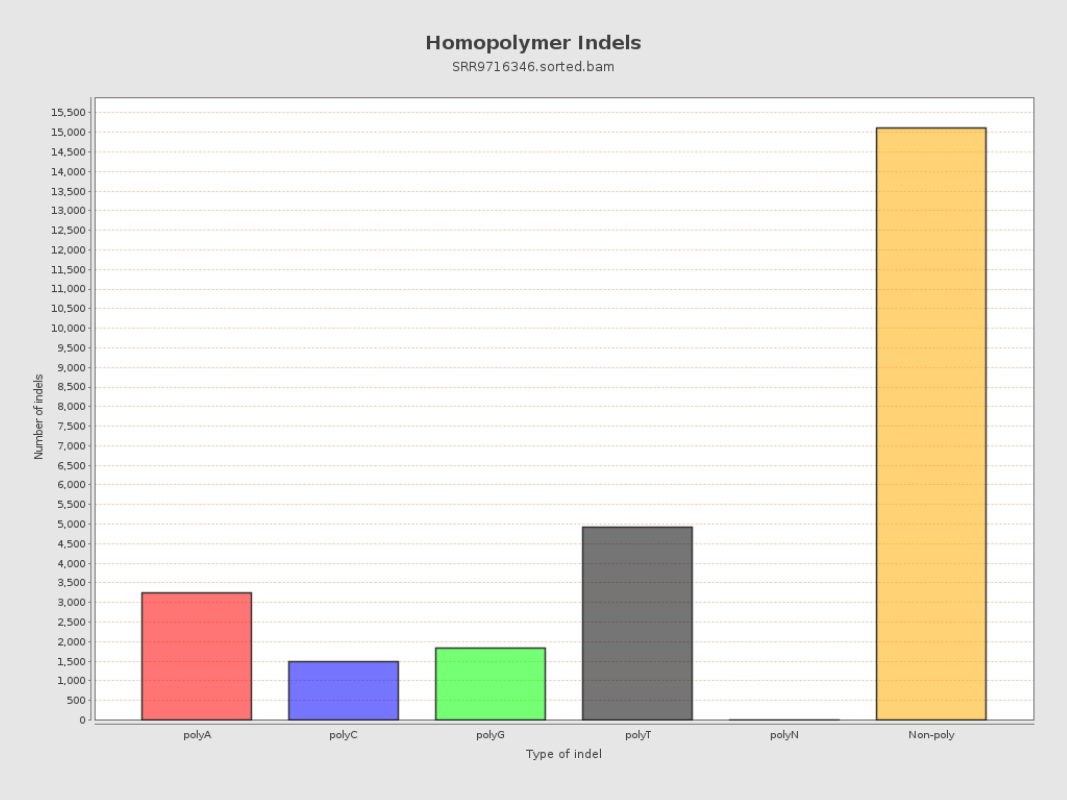
9. Results : Mapped Reads GC-content Distribution



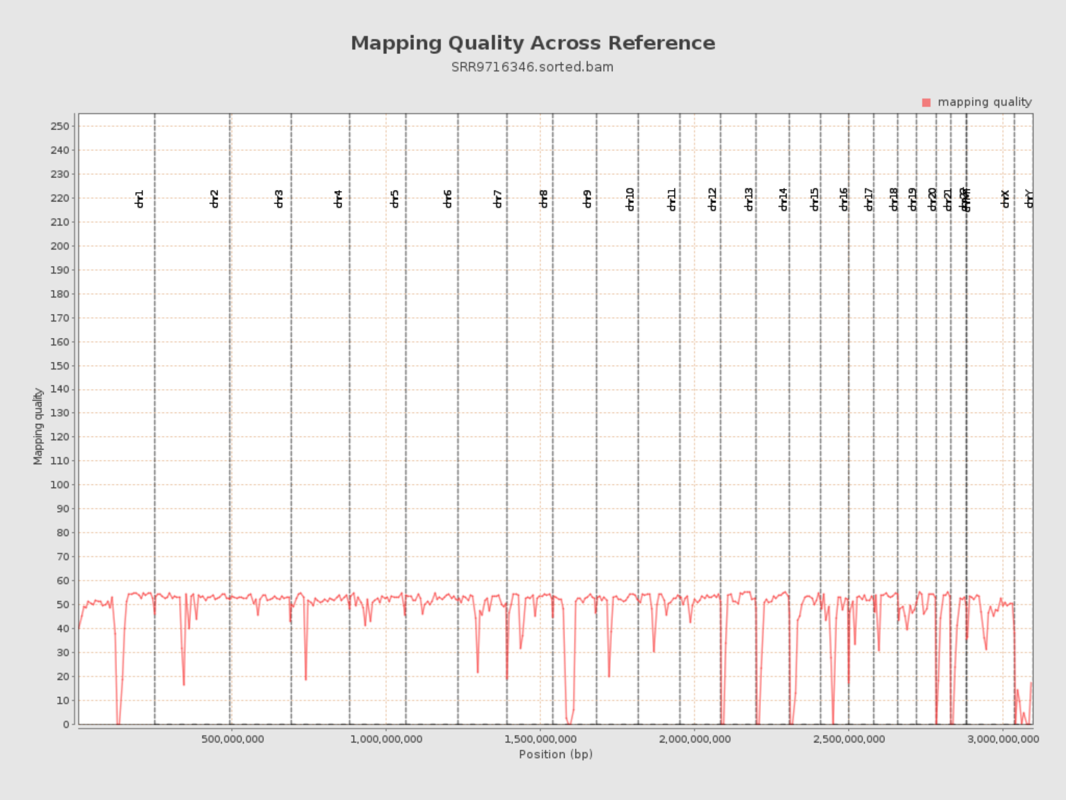
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram