Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 00:11:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716606.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_SRR9716606 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716606.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 00:11:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716606.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	920,273
Mapped reads	715,255 / 77.72%
Unmapped reads	205,018 / 22.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,474 / 2.44%
Read min/max/mean length	30 / 101 / 101.88
Duplicated reads (estimated)	11,648 / 1.27%
Duplication rate	1.03%
Clipped reads	736,766 / 80.06%

2.2. ACGT Content

Number/percentage of A's	13,955,201 / 25.9%
Number/percentage of C's	10,699,387 / 19.86%
Number/percentage of T's	16,604,581 / 30.81%
Number/percentage of G's	12,620,166 / 23.42%
Number/percentage of N's	6,639 / 0.01%
GC Percentage	43.28%

2.3. Coverage

Mean	0.0174

Standard Deviation	0.1707

2.4. Mapping Quality

Mean Mapping Quality	44.68

2.5. Mismatches and indels

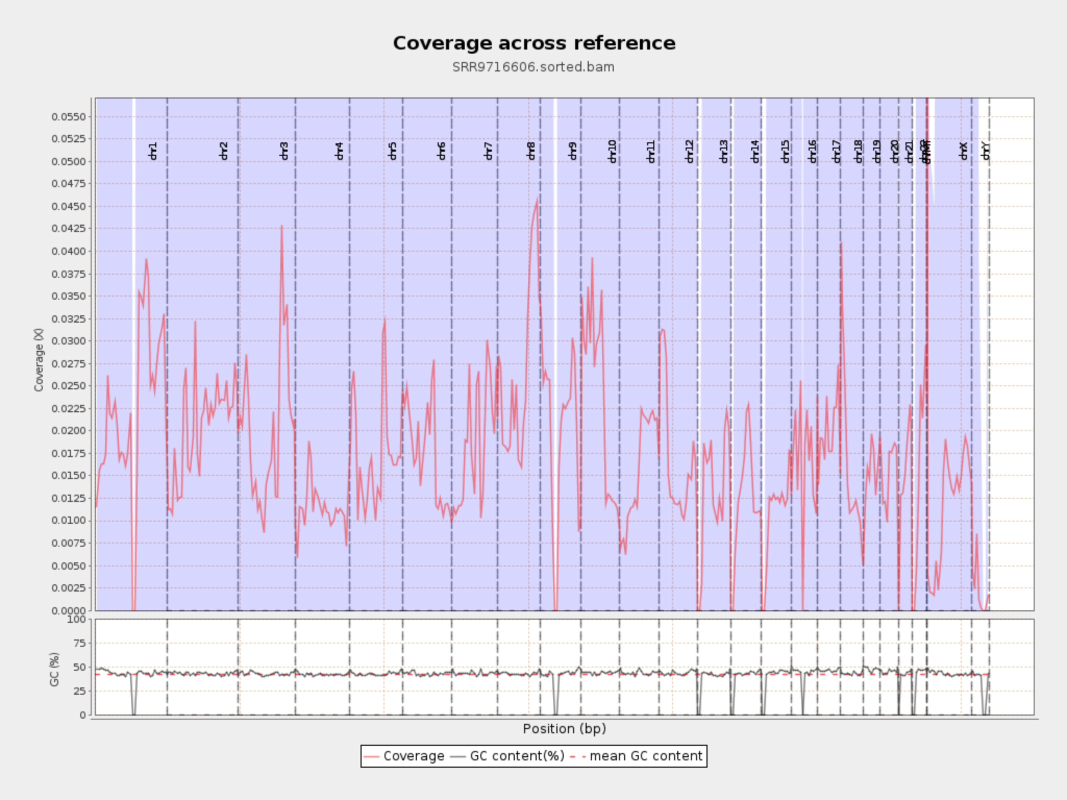
General error rate	0.81%
Mismatches	424,962
Insertions	5,002
Mapped reads with at least one insertion	0.69%
Deletions	12,050
Mapped reads with at least one deletion	1.66%
Homopolymer indels	40.37%

2.6. Chromosome stats

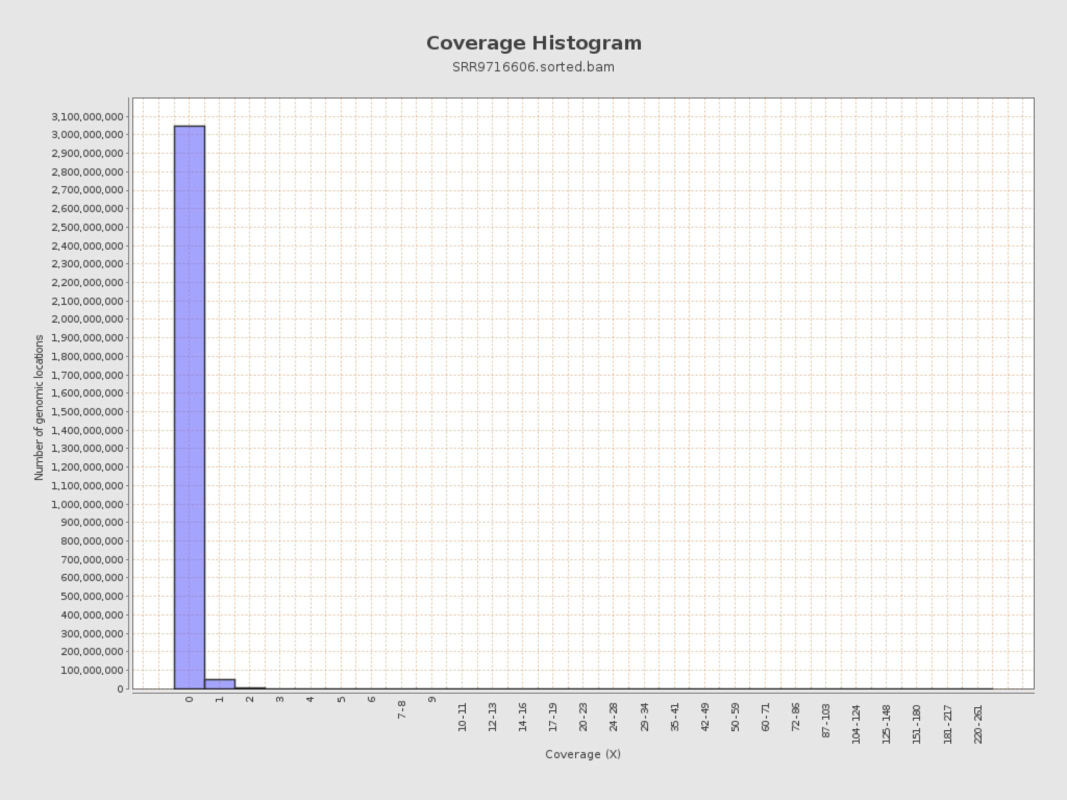
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5530552	0.0222	0.213
chr2	243199373	4968318	0.0204	0.2366
chr3	198022430	3975169	0.0201	0.1482
chr4	191154276	2183115	0.0114	0.1195
chr5	180915260	3170546	0.0175	0.1381
chr6	171115067	3025604	0.0177	0.147
chr7	159138663	2950987	0.0185	0.2278

chr8	146364022	3954594	0.027	0.2133
chr9	141213431	2845918	0.0202	0.1711
chr10	135534747	3262602	0.0241	0.214
chr11	135006516	2112707	0.0156	0.1513
chr12	133851895	2303856	0.0172	0.1367
chr13	115169878	1515303	0.0132	0.1192
chr14	107349540	1338676	0.0125	0.122
chr15	102531392	1085558	0.0106	0.1072
chr16	90354753	1476135	0.0163	0.1395
chr17	81195210	1613038	0.0199	0.1563
chr18	78077248	1272028	0.0163	0.2248
chr19	59128983	912813	0.0154	0.1961
chr20	63025520	954582	0.0151	0.1321
chr21	48129895	734040	0.0153	0.1342
chr22	51304566	766658	0.0149	0.1279
chrMT	16571	3094	0.1867	0.5009
chrX	155270560	1818672	0.0117	0.1243
chrY	59373566	132477	0.0022	0.095

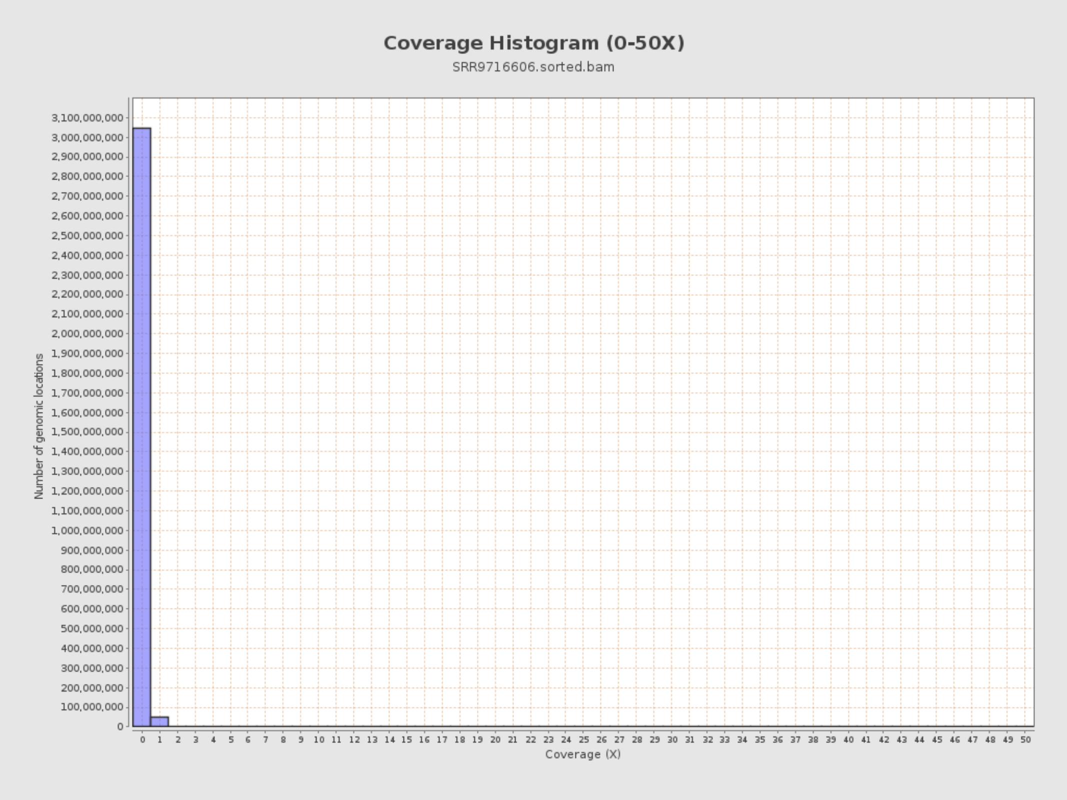
3. Results : Coverage across reference



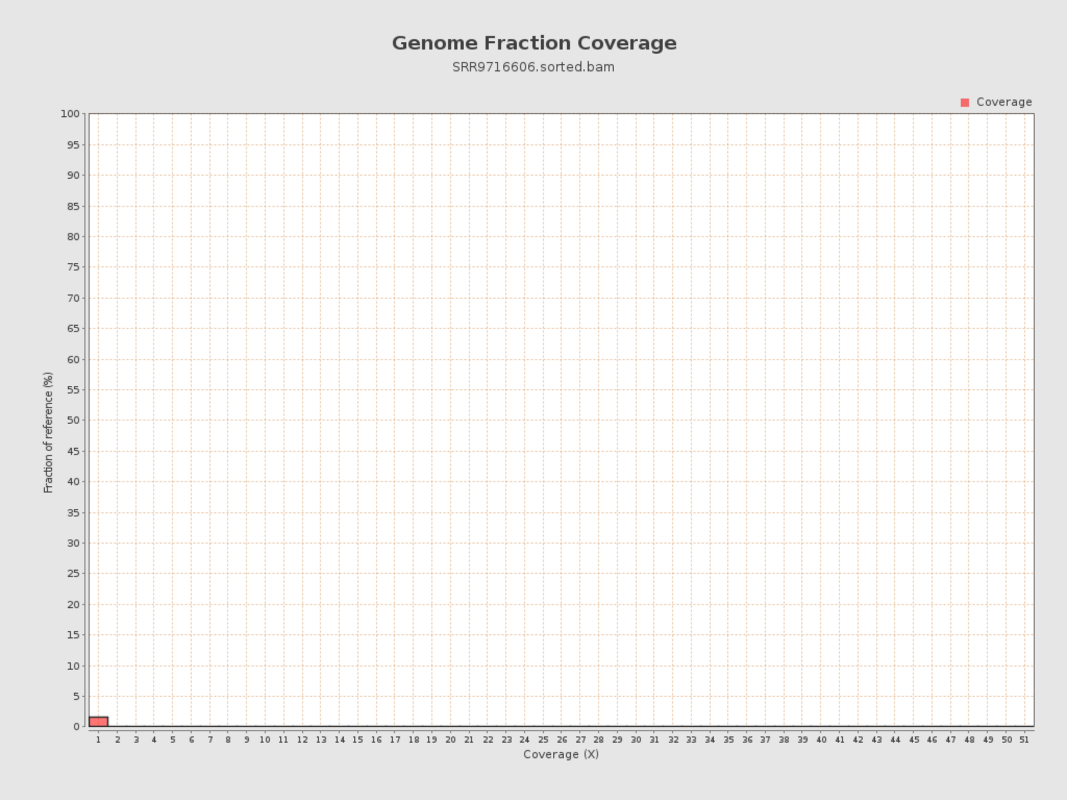
4. Results : Coverage Histogram



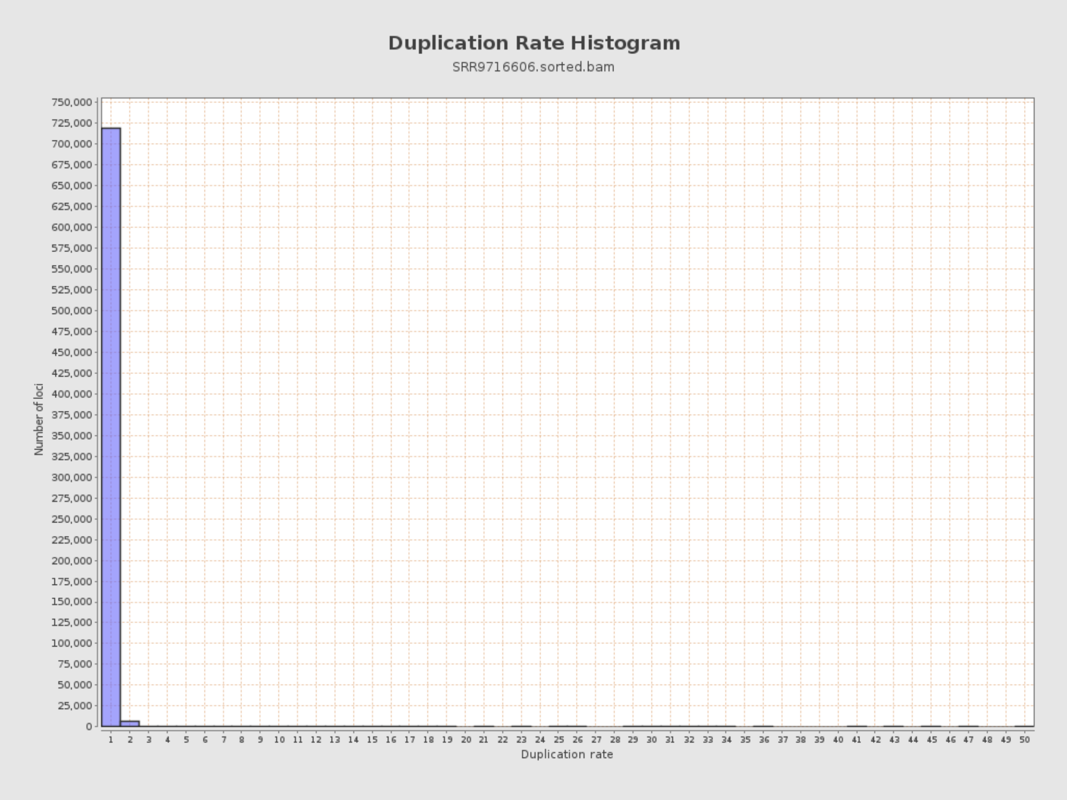
5. Results : Coverage Histogram (0-50X)



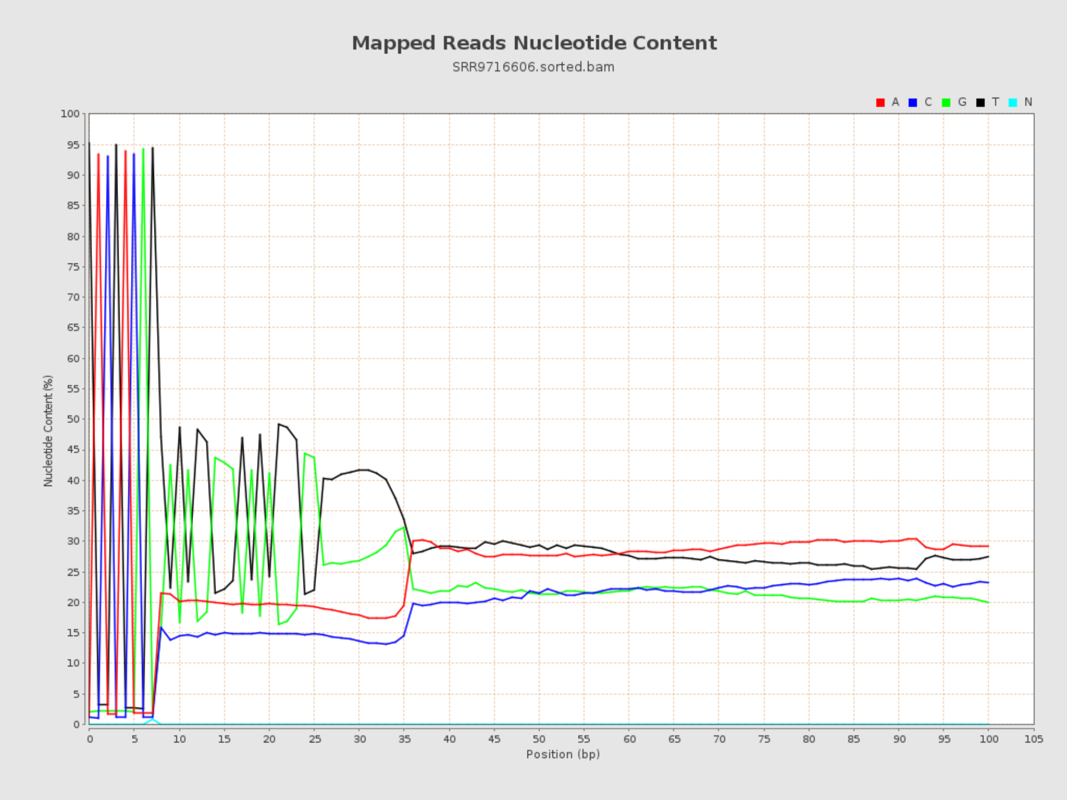
6. Results : Genome Fraction Coverage



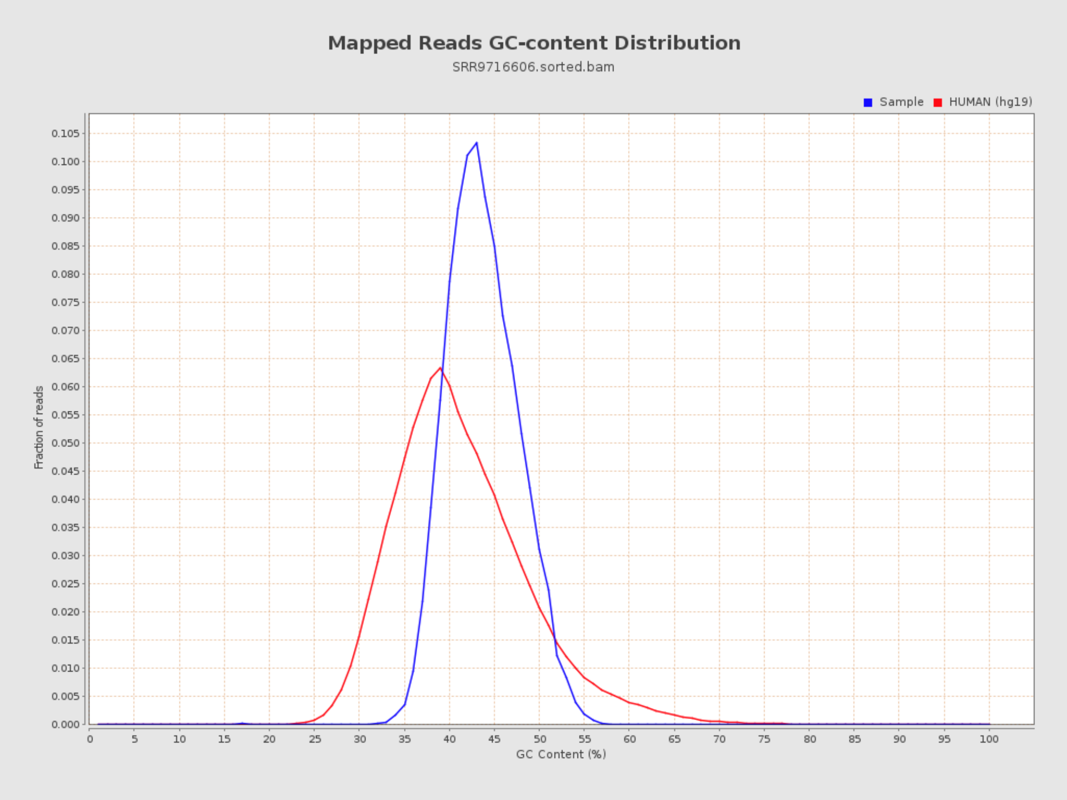
7. Results : Duplication Rate Histogram



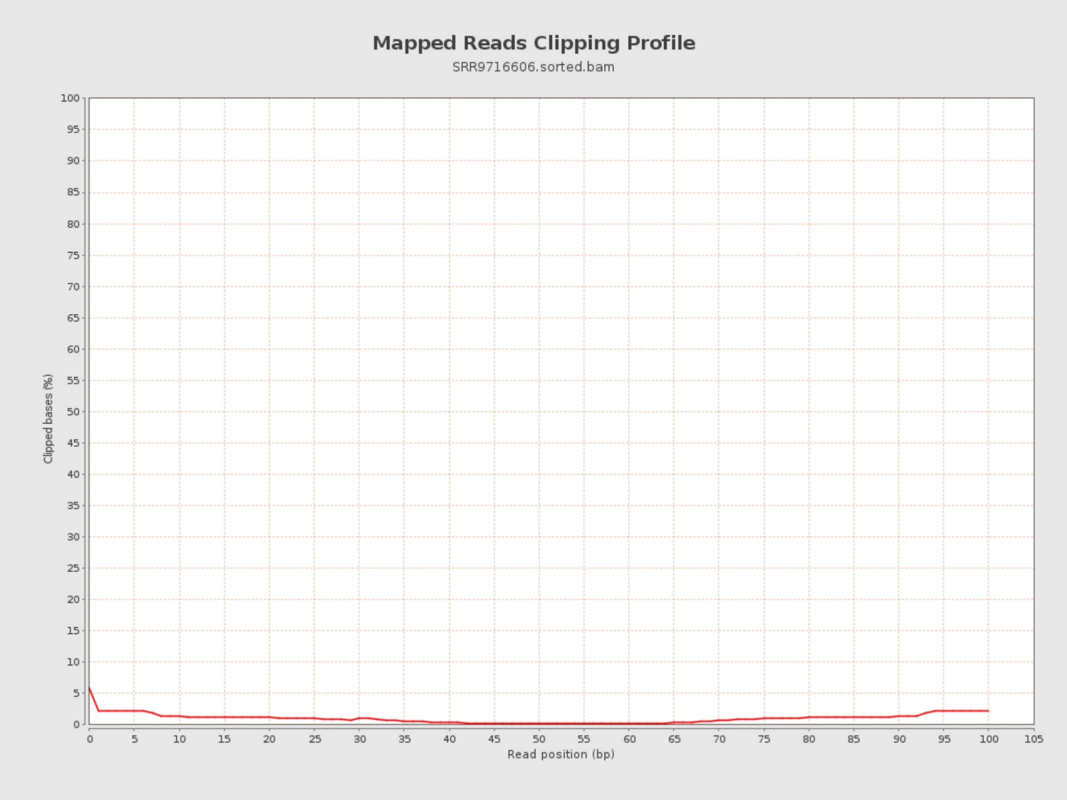
8. Results : Mapped Reads Nucleotide Content



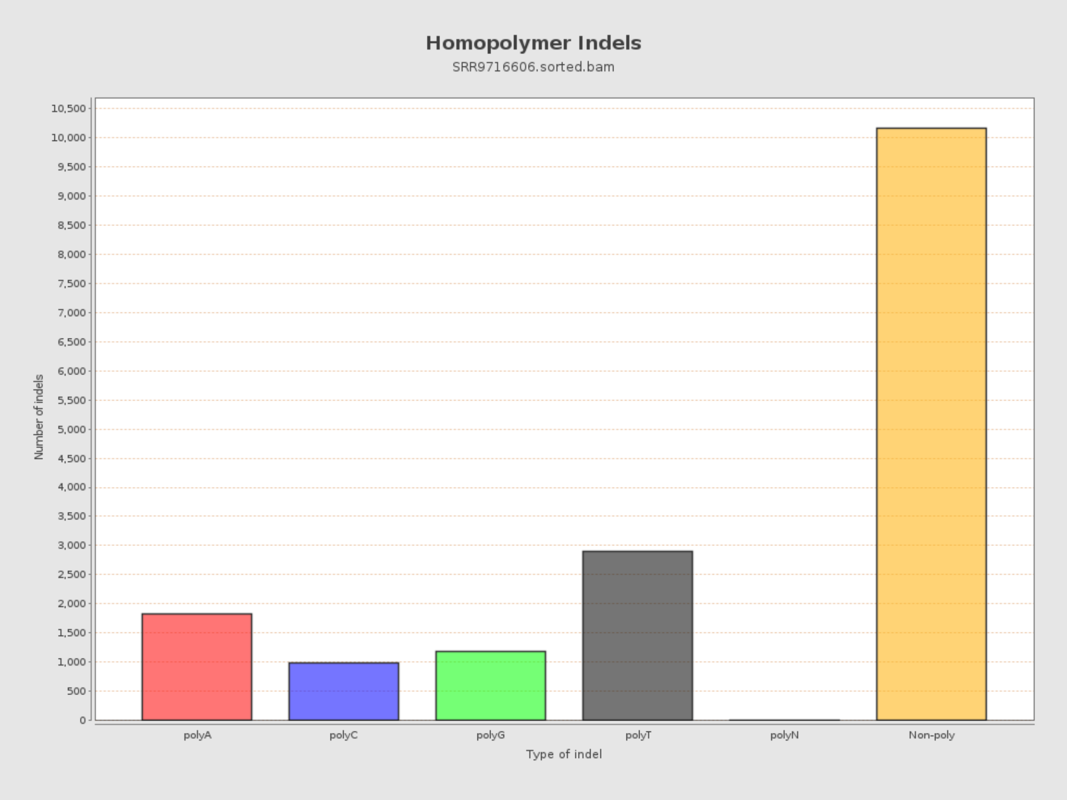
9. Results : Mapped Reads GC-content Distribution



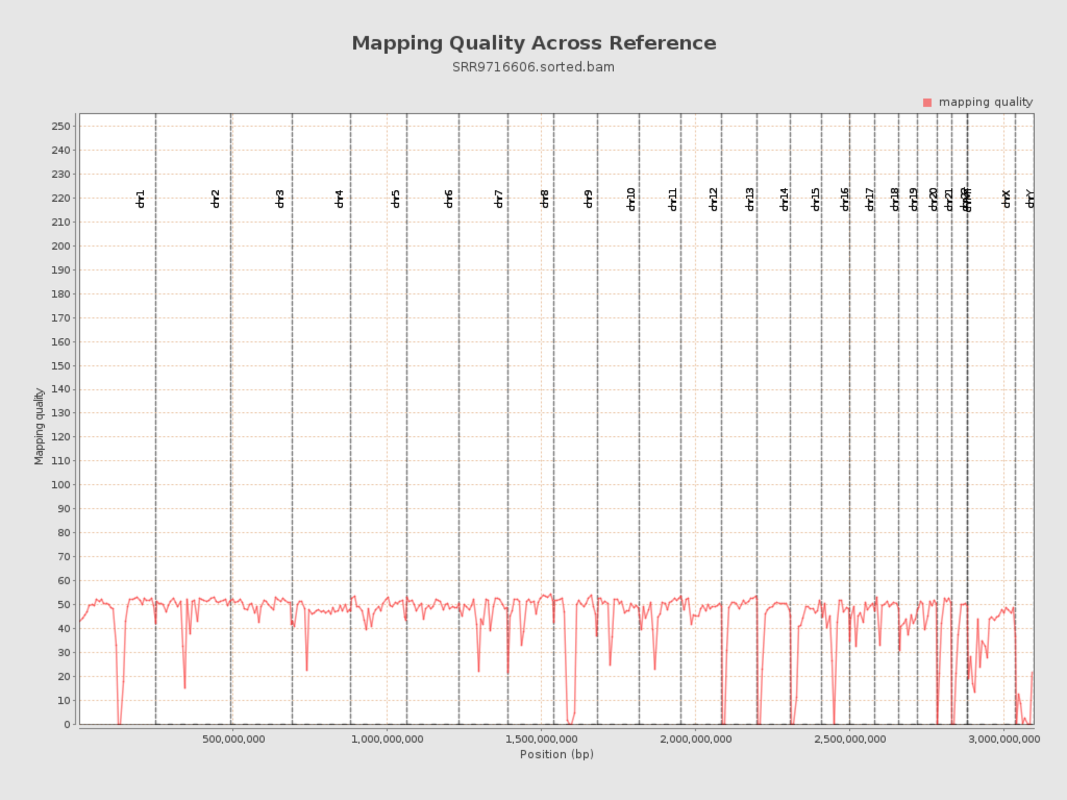
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram