Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 23:55:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716602.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_SRR9716602 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716602.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 23:55:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716602.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,095,979
Mapped reads	965,925 / 88.13%
Unmapped reads	130,054 / 11.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,721 / 0.43%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	22,524 / 2.06%
Duplication rate	1.58%
Clipped reads	969,518 / 88.46%

2.2. ACGT Content

Number/percentage of A's	14,342,696 / 26.04%
Number/percentage of C's	11,293,101 / 20.5%
Number/percentage of T's	16,744,132 / 30.4%
Number/percentage of G's	12,703,182 / 23.06%
Number/percentage of N's	853 / 0%
GC Percentage	43.56%

2.3. Coverage

Mean	0.0178

Standard Deviation	0.1991

2.4. Mapping Quality

Mean Mapping Quality	42.91

2.5. Mismatches and indels

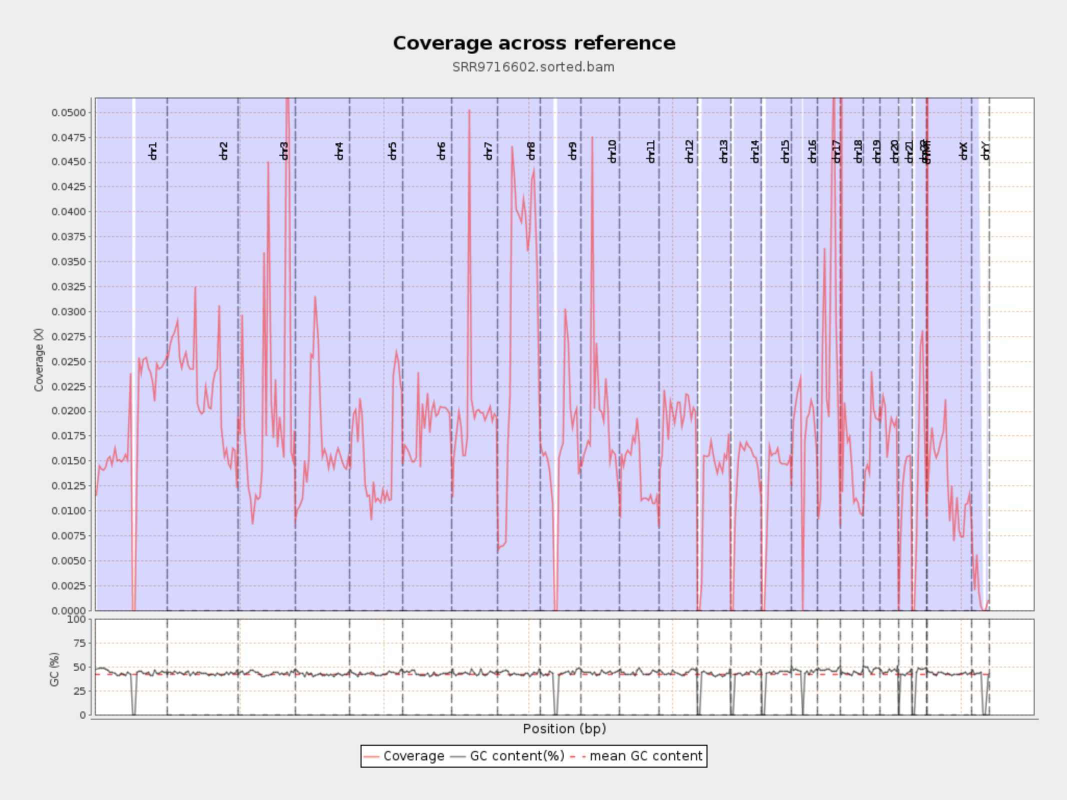
General error rate	0.52%
Mismatches	280,879
Insertions	3,581
Mapped reads with at least one insertion	0.37%
Deletions	10,693
Mapped reads with at least one deletion	1.1%
Homopolymer indels	41.64%

2.6. Chromosome stats

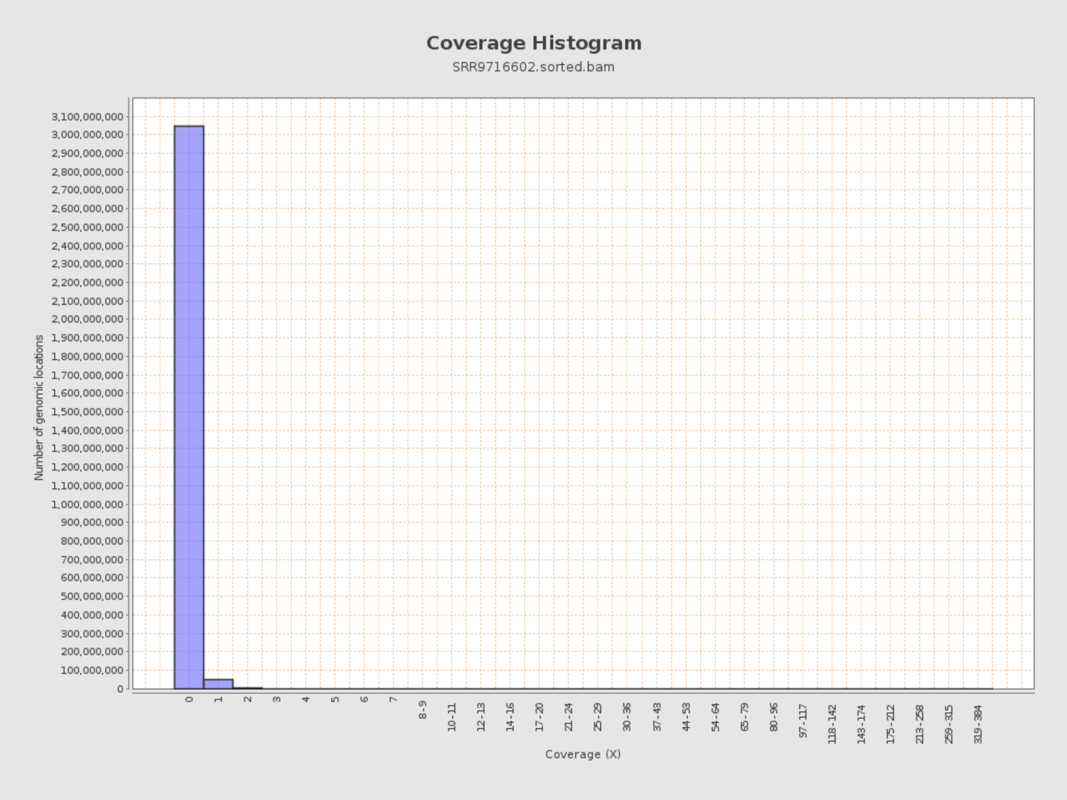
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4491285	0.018	0.2389
chr2	243199373	5434427	0.0223	0.2316
chr3	198022430	4157528	0.021	0.1602
chr4	191154276	3163196	0.0165	0.1379
chr5	180915260	2847452	0.0157	0.1322
chr6	171115067	3164716	0.0185	0.1544
chr7	159138663	3200002	0.0201	0.4496

chr8	146364022	4412309	0.0301	0.2092
chr9	141213431	2240445	0.0159	0.1517
chr10	135534747	2652946	0.0196	0.2597
chr11	135006516	1868513	0.0138	0.1497
chr12	133851895	2596096	0.0194	0.1529
chr13	115169878	1477912	0.0128	0.1188
chr14	107349540	1406178	0.0131	0.1246
chr15	102531392	1282376	0.0125	0.1199
chr16	90354753	1605211	0.0178	0.1475
chr17	81195210	2139679	0.0264	0.1759
chr18	78077248	1275593	0.0163	0.2099
chr19	59128983	1039192	0.0176	0.2274
chr20	63025520	1164988	0.0185	0.1456
chr21	48129895	565896	0.0118	0.1167
chr22	51304566	716258	0.014	0.125
chrMT	16571	83915	5.064	4.2467
chrX	155270560	1999128	0.0129	0.135
chrY	59373566	115350	0.0019	0.0543

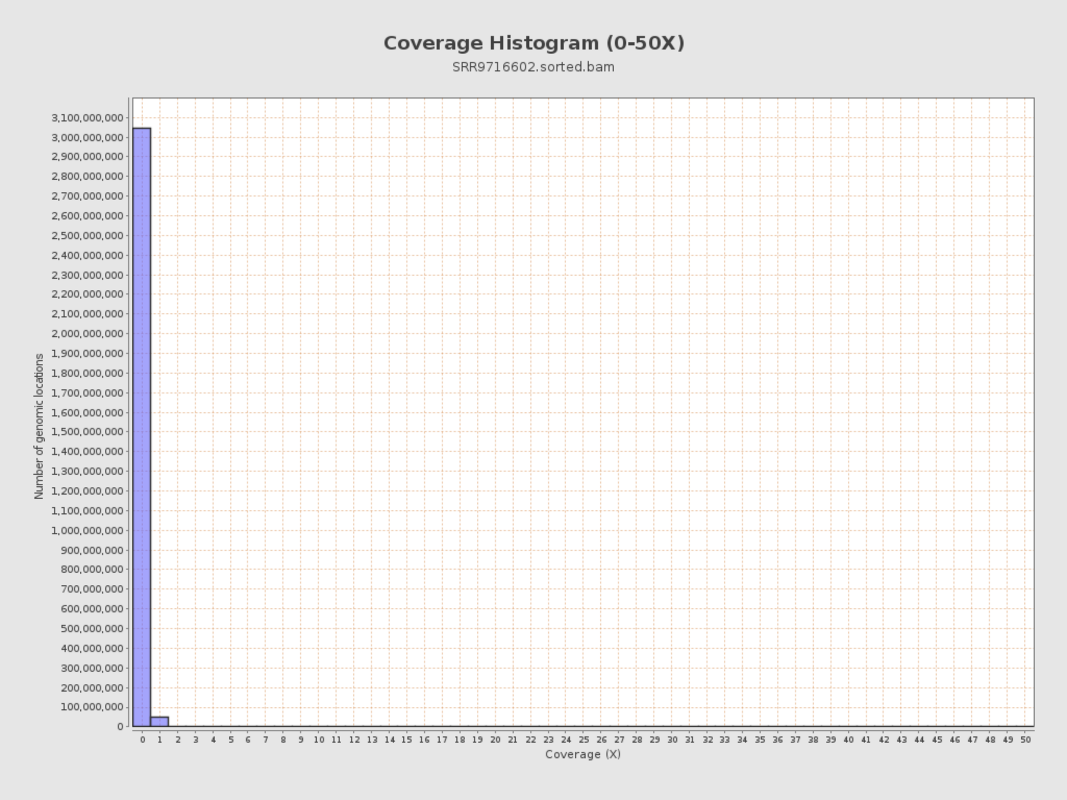
3. Results : Coverage across reference



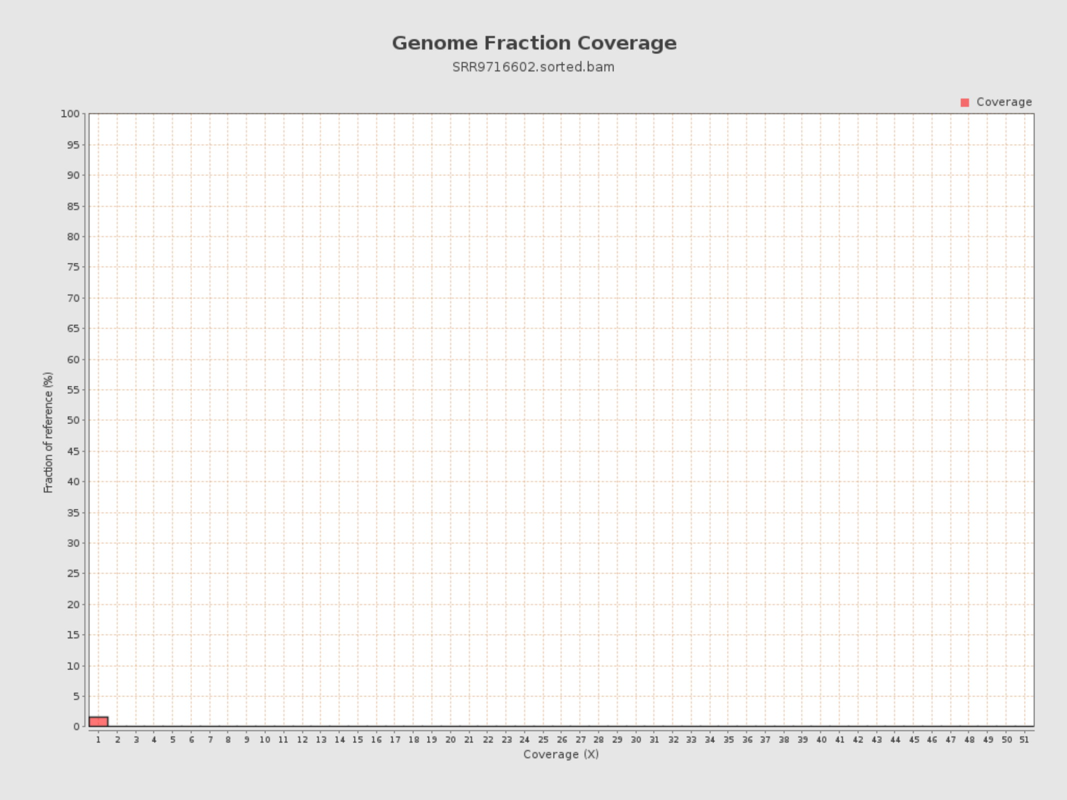
4. Results : Coverage Histogram



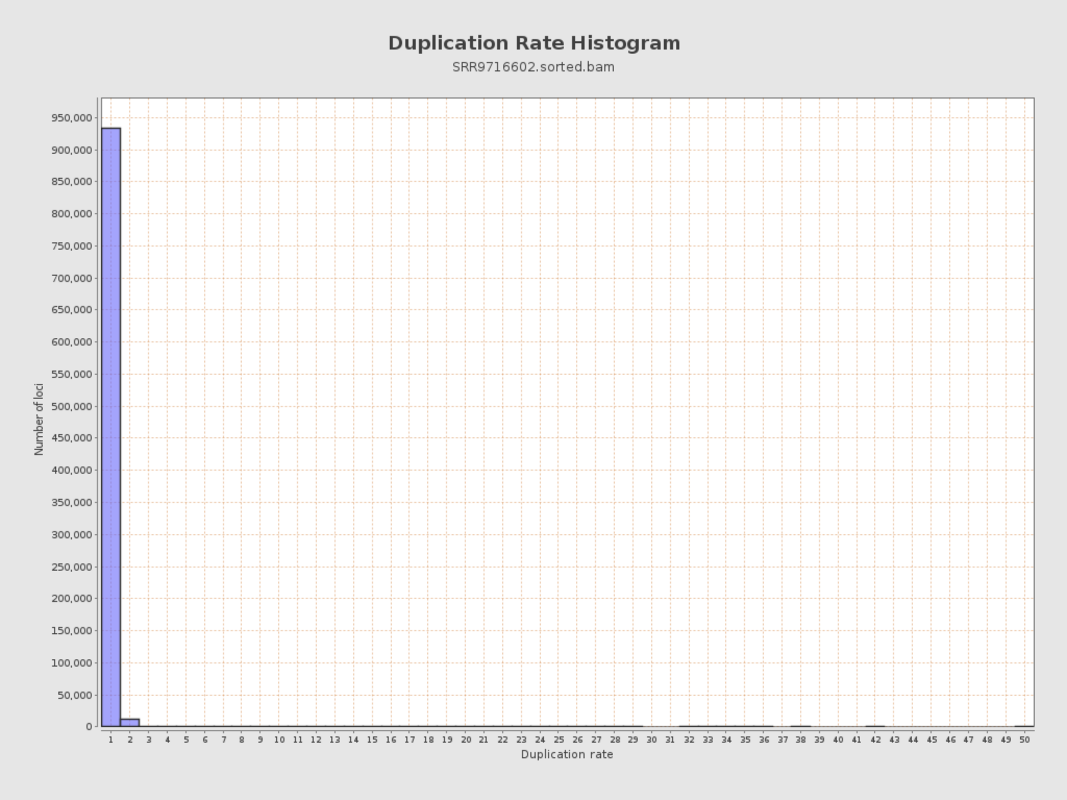
5. Results : Coverage Histogram (0-50X)



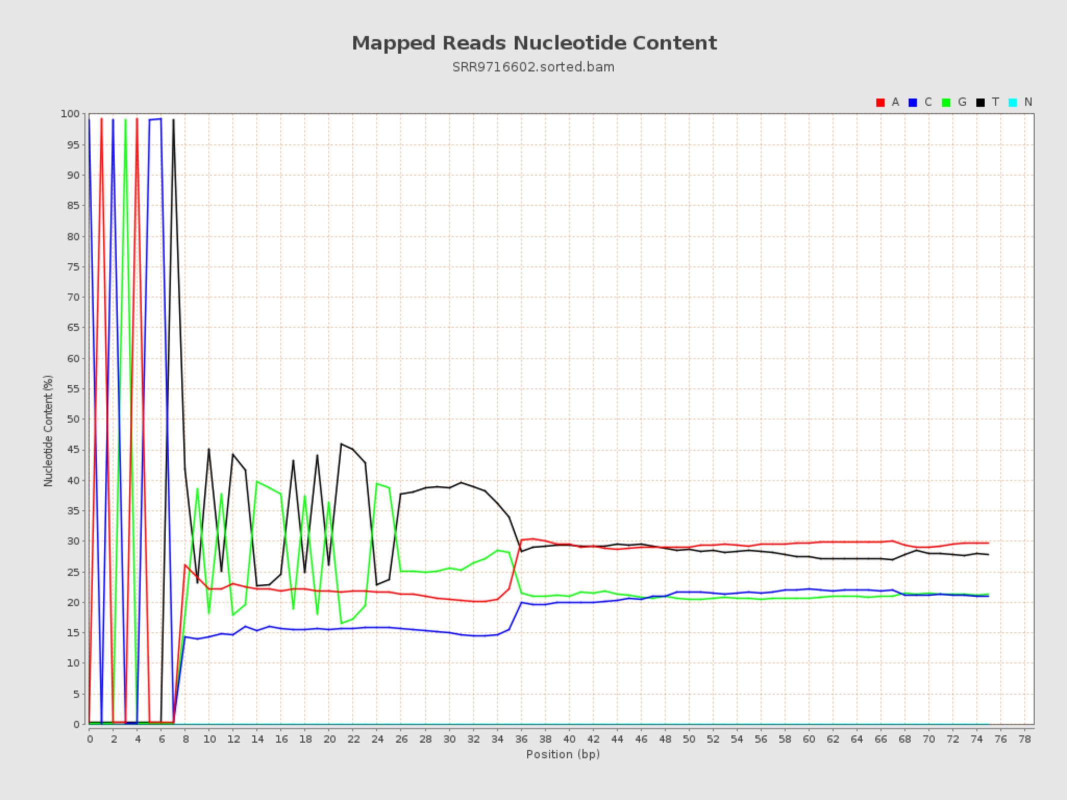
6. Results : Genome Fraction Coverage



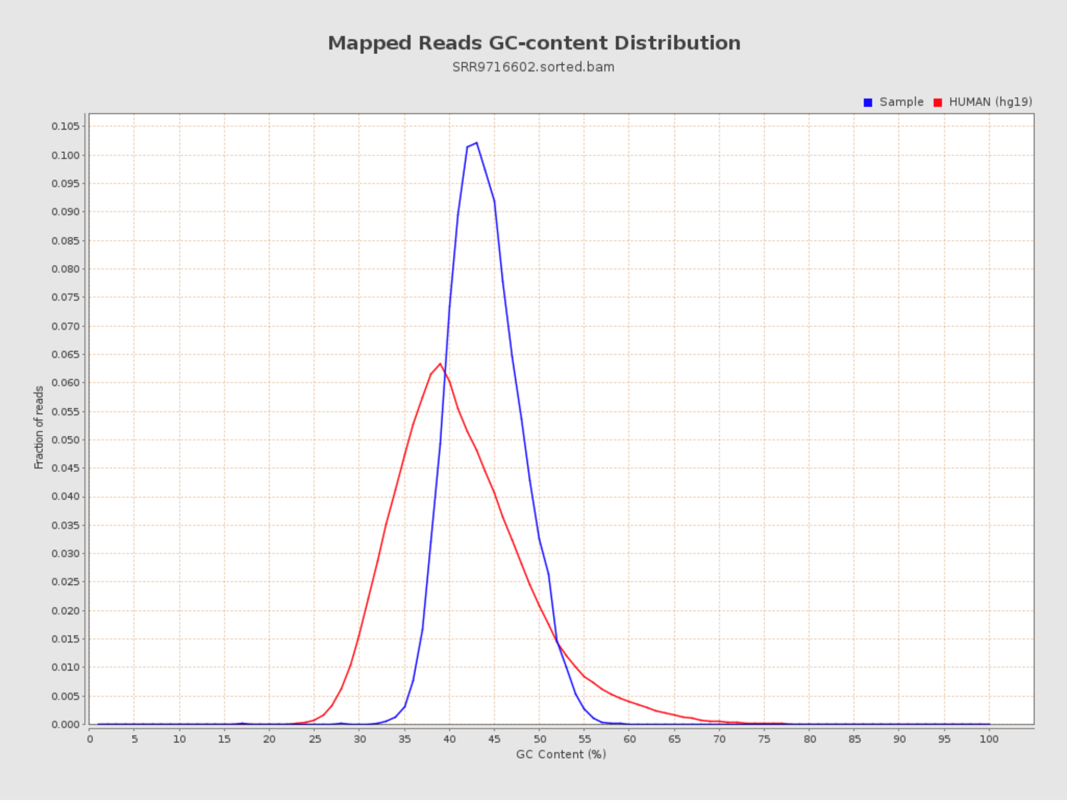
7. Results : Duplication Rate Histogram



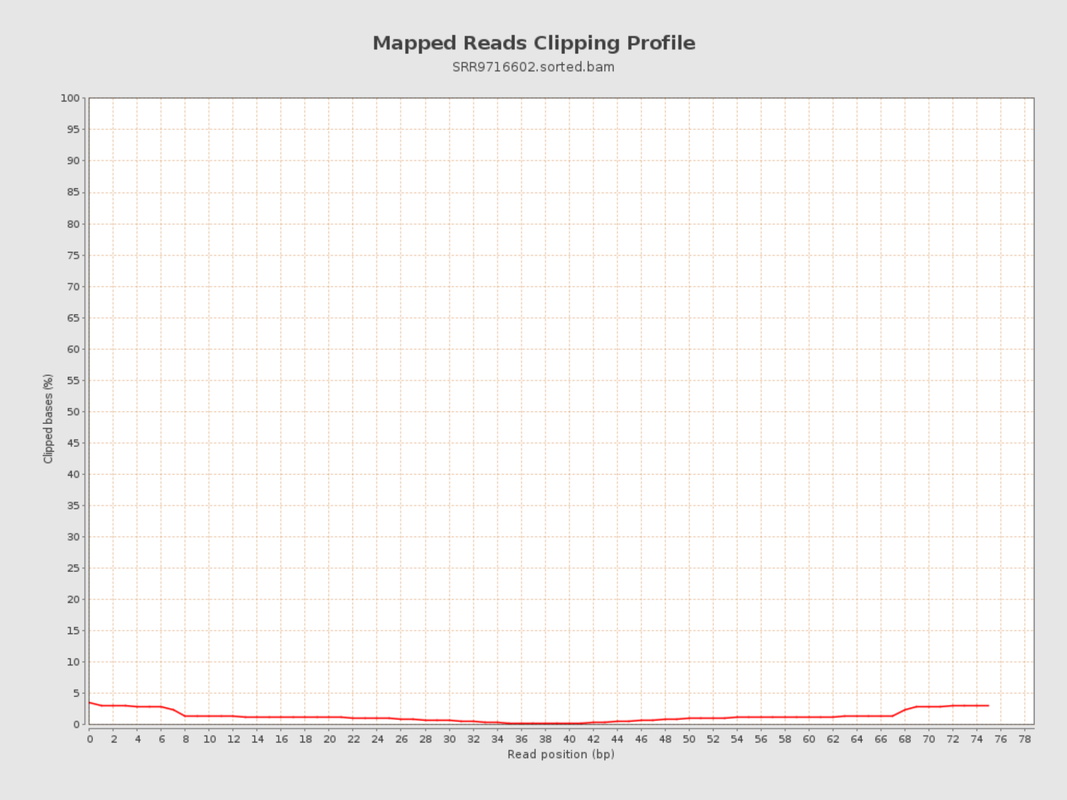
8. Results : Mapped Reads Nucleotide Content



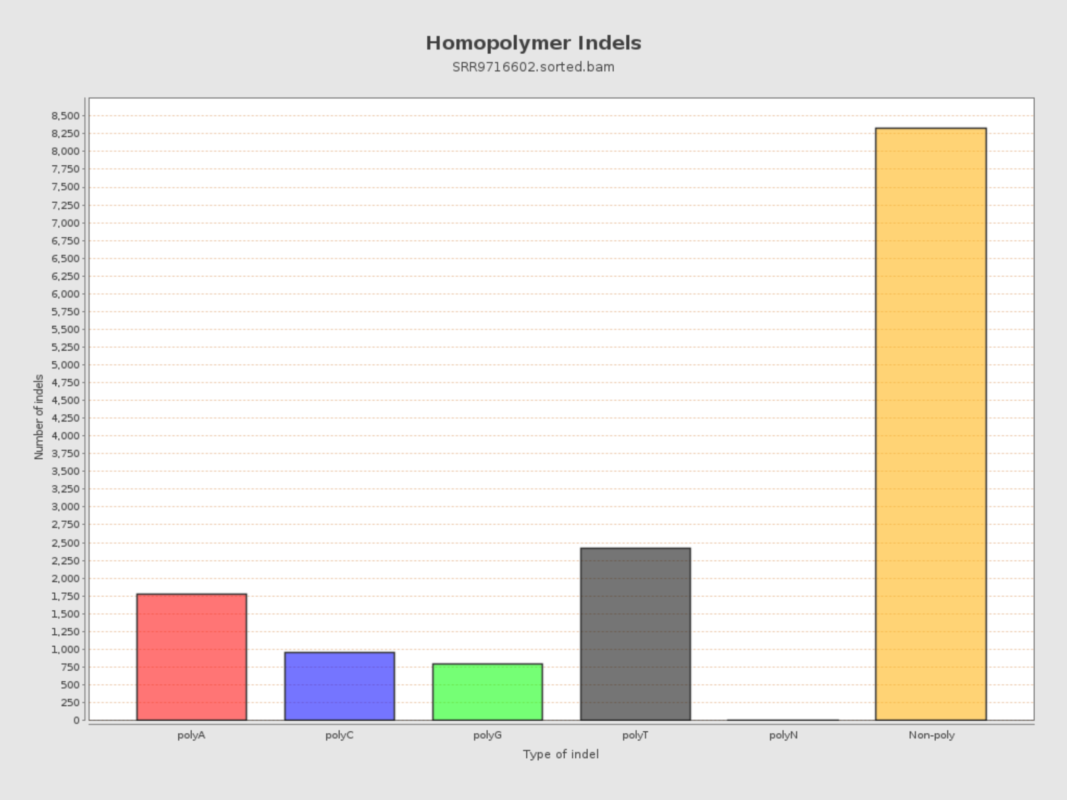
9. Results : Mapped Reads GC-content Distribution



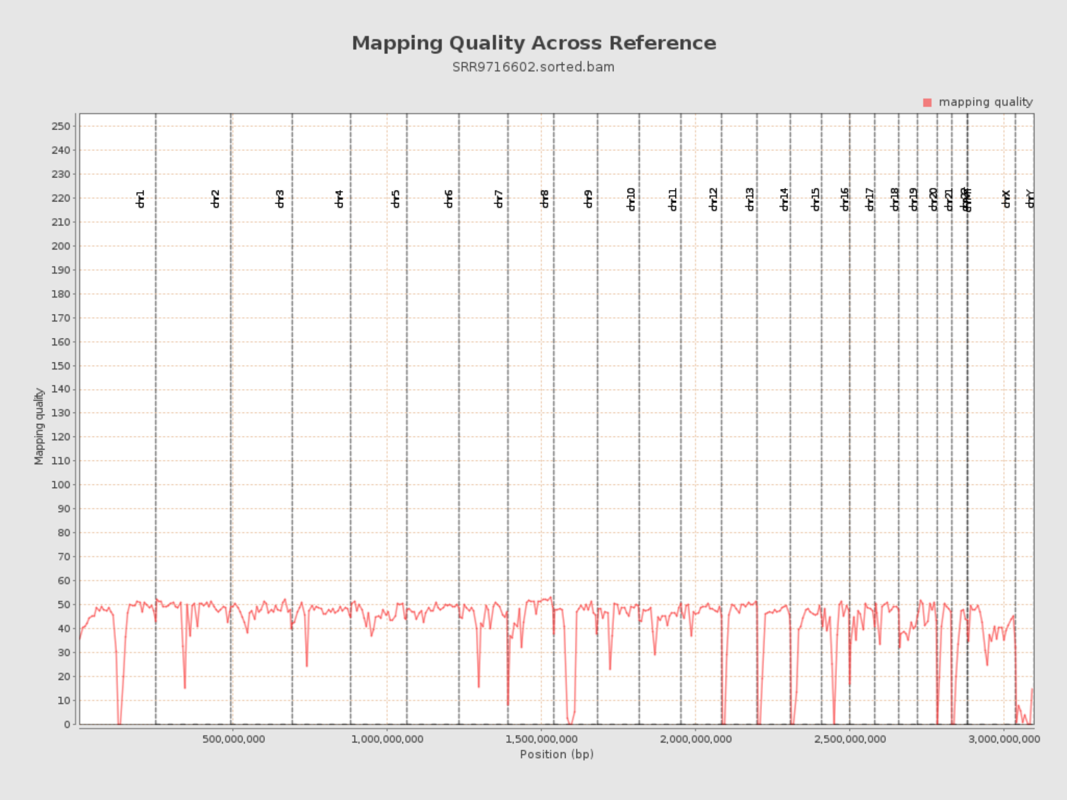
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram