Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 01:53:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716642.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_SRR9716642 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716642.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 01:53:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716642.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	940,026
Mapped reads	860,687 / 91.56%
Unmapped reads	79,339 / 8.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,869 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	27,278 / 2.9%
Duplication rate	2.29%
Clipped reads	861,436 / 91.64%

2.2. ACGT Content

Number/percentage of A's	12,470,416 / 25.13%
Number/percentage of C's	9,594,886 / 19.34%
Number/percentage of T's	15,714,695 / 31.67%
Number/percentage of G's	11,839,132 / 23.86%
Number/percentage of N's	922 / 0%
GC Percentage	43.2%

2.3. Coverage

Mean	0.016

Standard Deviation	0.1794

2.4. Mapping Quality

Mean Mapping Quality	44.37

2.5. Mismatches and indels

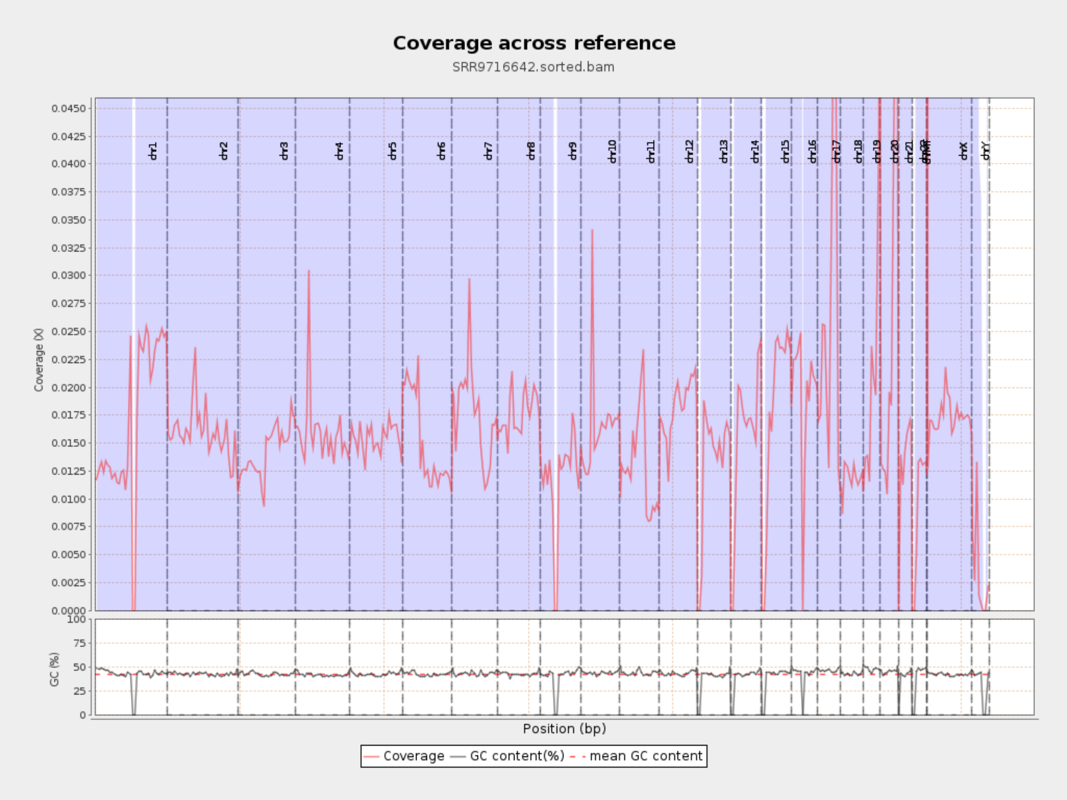
General error rate	0.53%
Mismatches	254,493
Insertions	3,406
Mapped reads with at least one insertion	0.39%
Deletions	9,737
Mapped reads with at least one deletion	1.12%
Homopolymer indels	42.17%

2.6. Chromosome stats

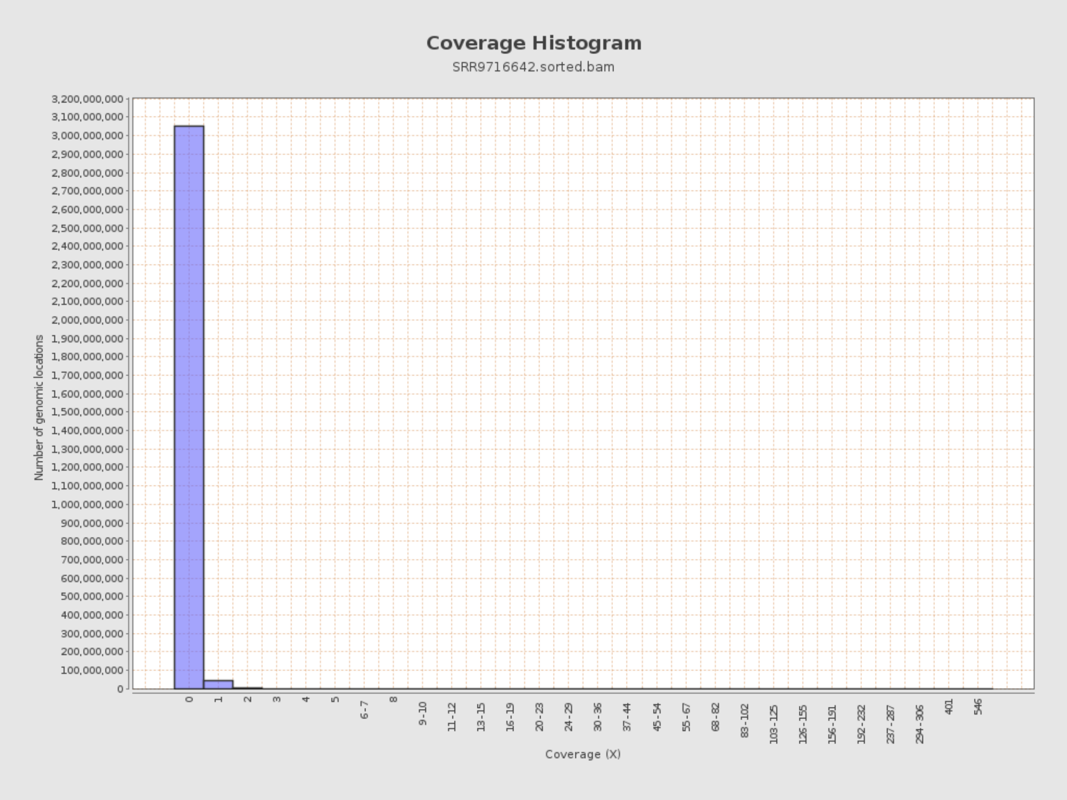
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4191625	0.0168	0.2519
chr2	243199373	3880253	0.016	0.2578
chr3	198022430	2820033	0.0142	0.1269
chr4	191154276	3051374	0.016	0.1549
chr5	180915260	2810728	0.0155	0.1319
chr6	171115067	2596065	0.0152	0.1452
chr7	159138663	2821891	0.0177	0.2147

chr8	146364022	2590987	0.0177	0.2317
chr9	141213431	1645313	0.0117	0.1318
chr10	135534747	2235529	0.0165	0.1961
chr11	135006516	1769557	0.0131	0.1437
chr12	133851895	2433406	0.0182	0.1438
chr13	115169878	1502927	0.013	0.124
chr14	107349540	1666471	0.0155	0.134
chr15	102531392	1824994	0.0178	0.1407
chr16	90354753	1719322	0.019	0.1511
chr17	81195210	2177542	0.0268	0.1775
chr18	78077248	919658	0.0118	0.201
chr19	59128983	1301350	0.022	0.2233
chr20	63025520	1626846	0.0258	0.1744
chr21	48129895	639997	0.0133	0.1444
chr22	51304566	475609	0.0093	0.1018
chrMT	16571	45593	2.7514	2.3142
chrX	155270560	2697616	0.0174	0.1464
chrY	59373566	191122	0.0032	0.1427

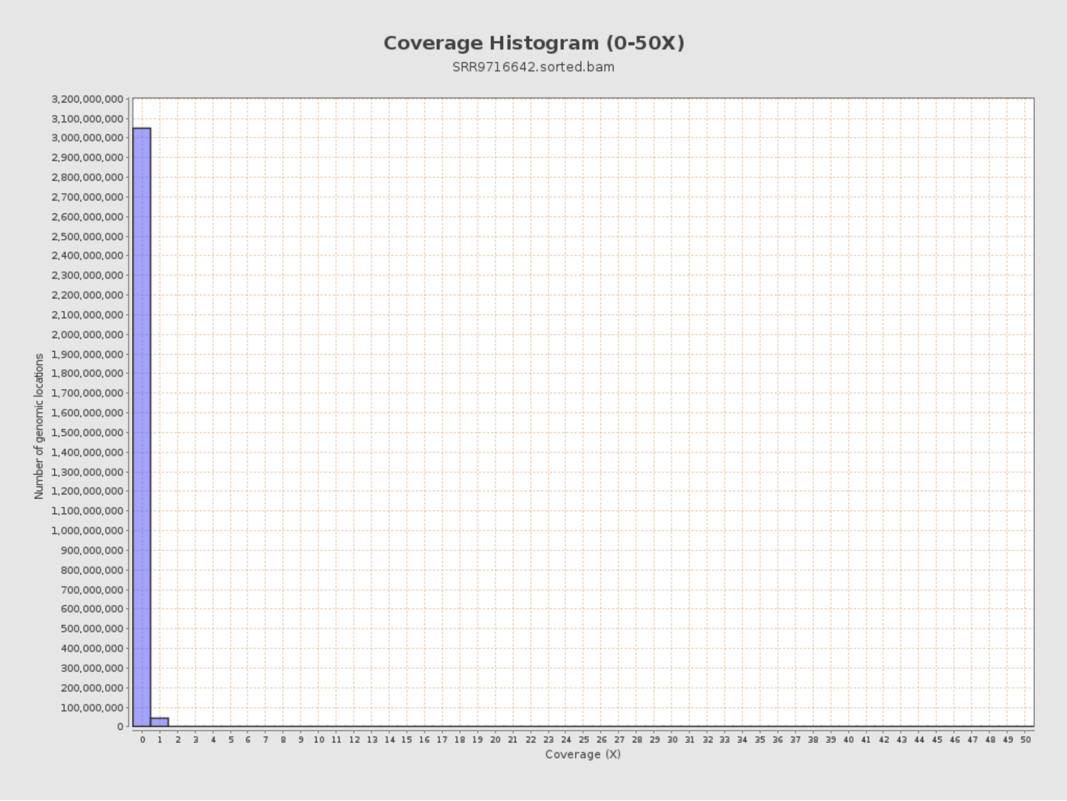
3. Results : Coverage across reference



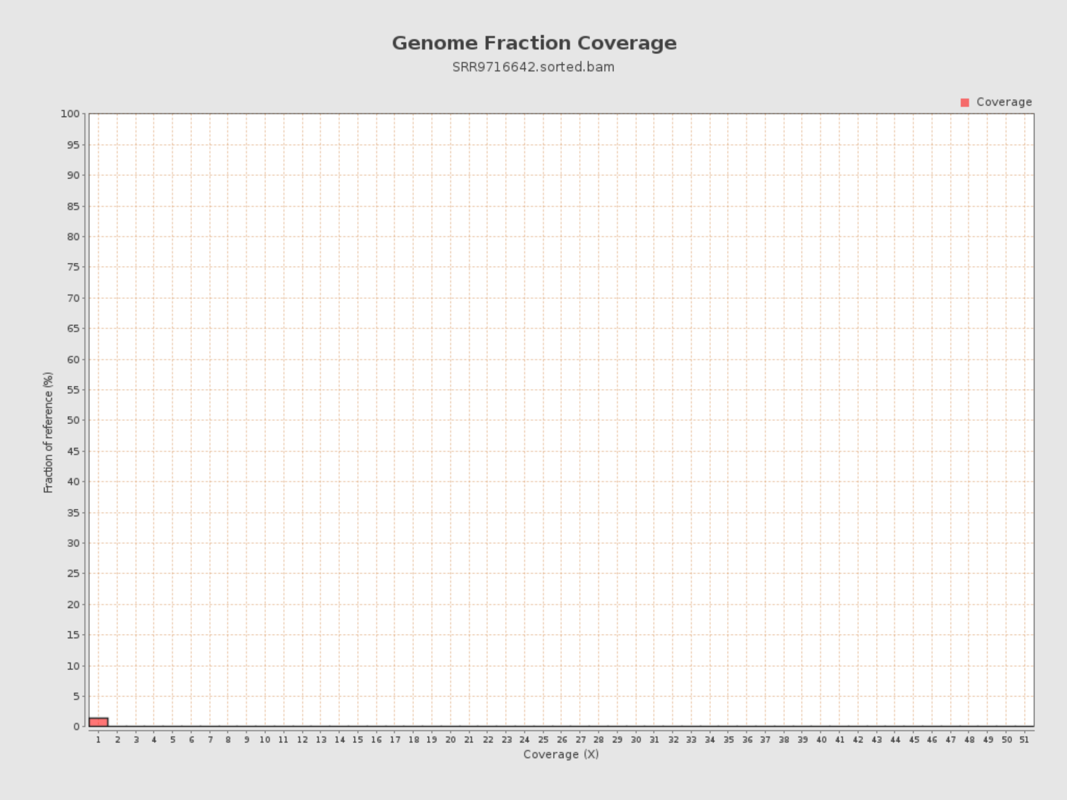
4. Results : Coverage Histogram



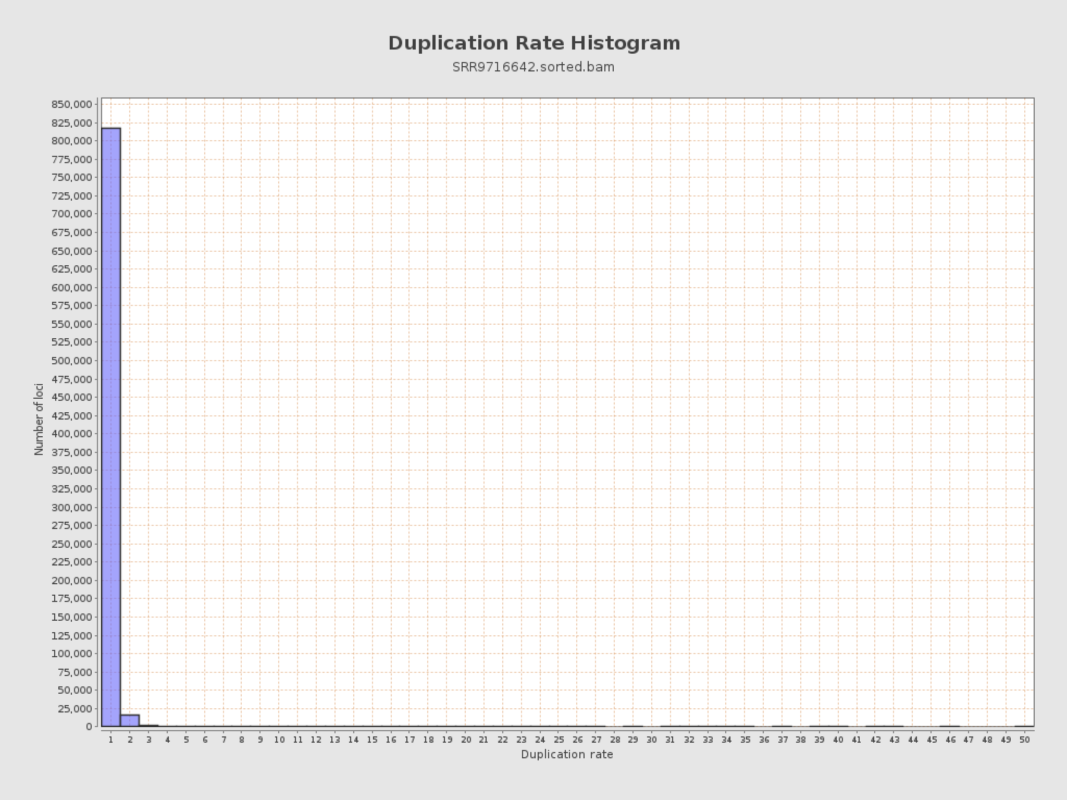
5. Results : Coverage Histogram (0-50X)



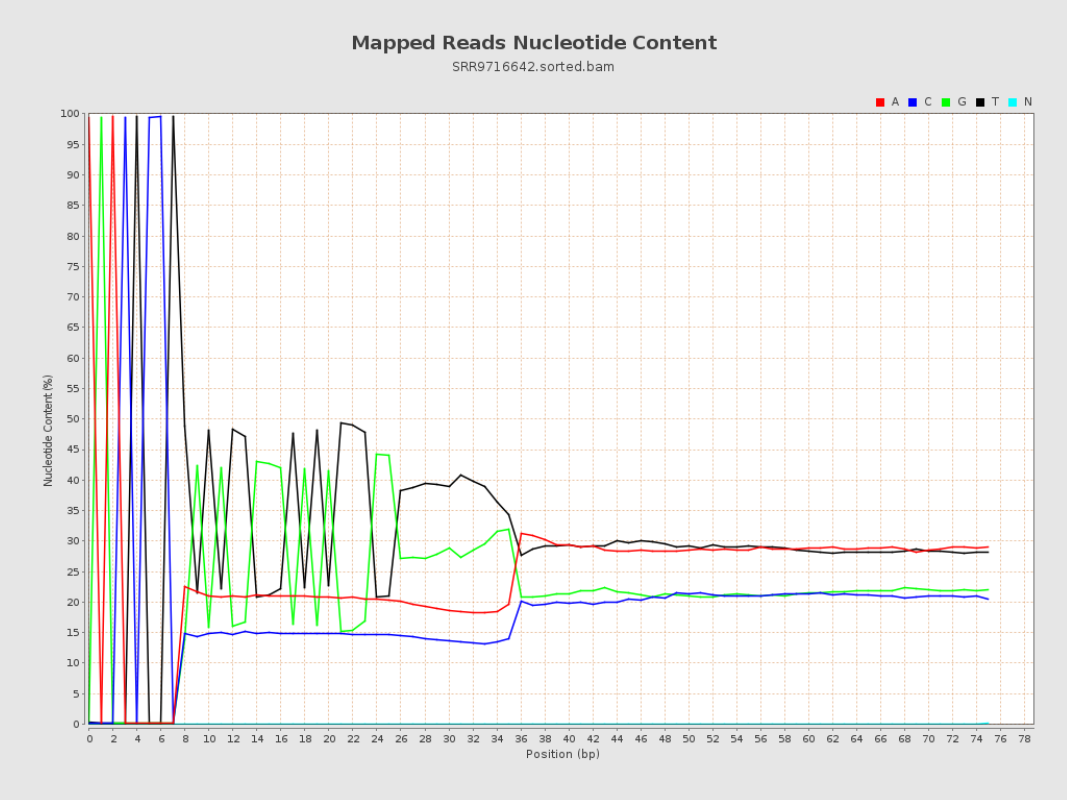
6. Results : Genome Fraction Coverage



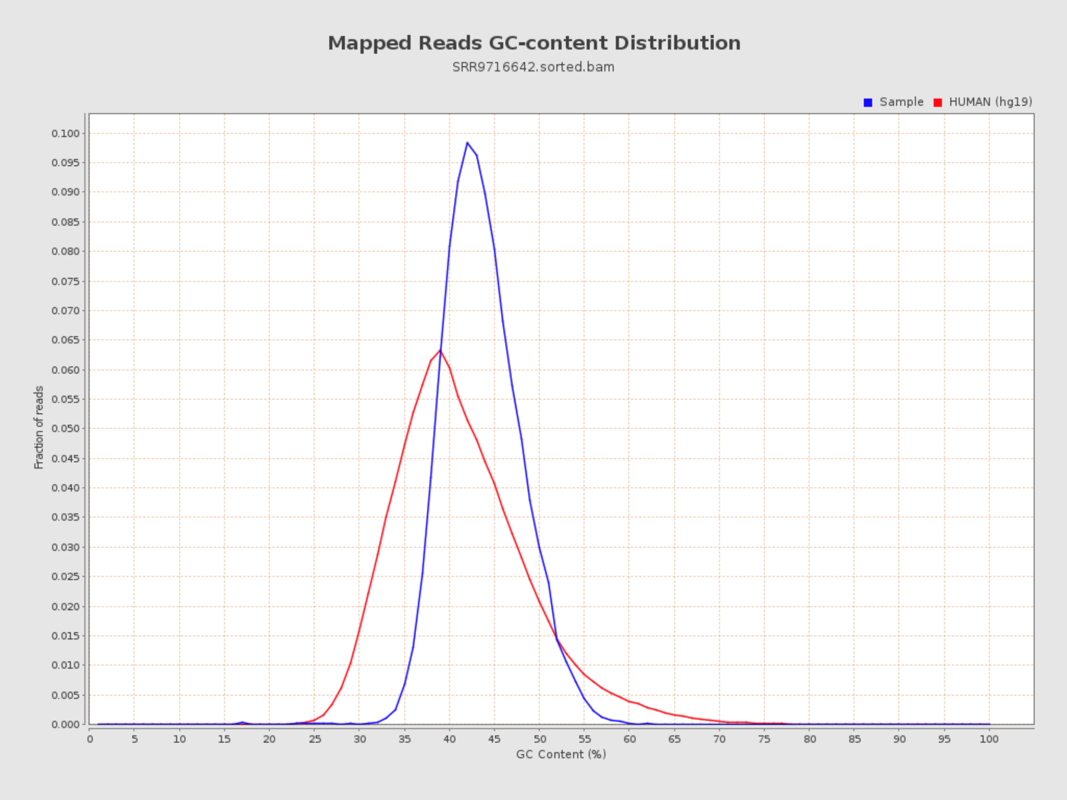
7. Results : Duplication Rate Histogram



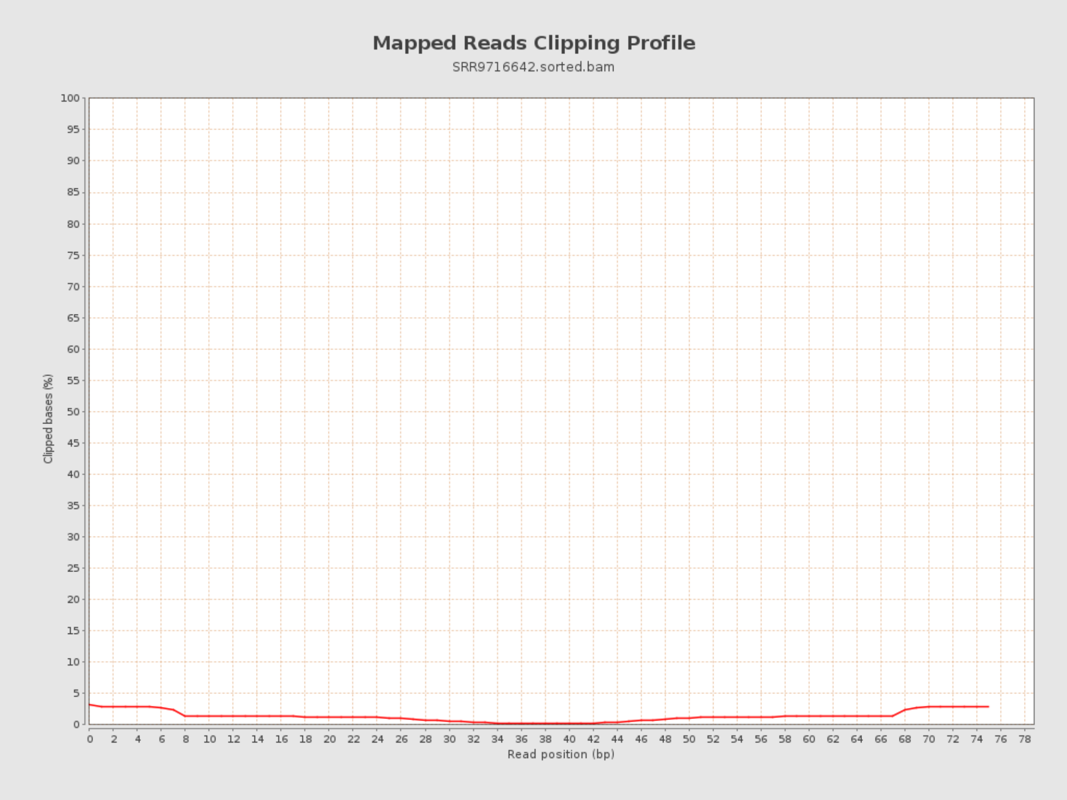
8. Results : Mapped Reads Nucleotide Content



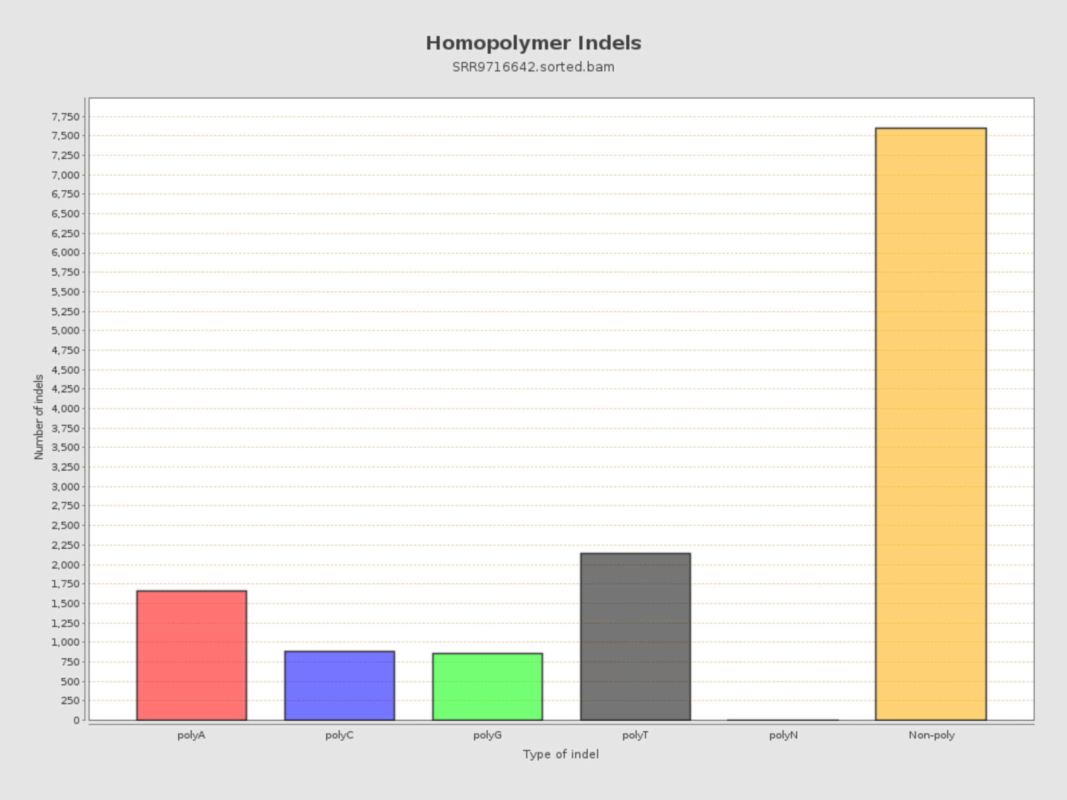
9. Results : Mapped Reads GC-content Distribution



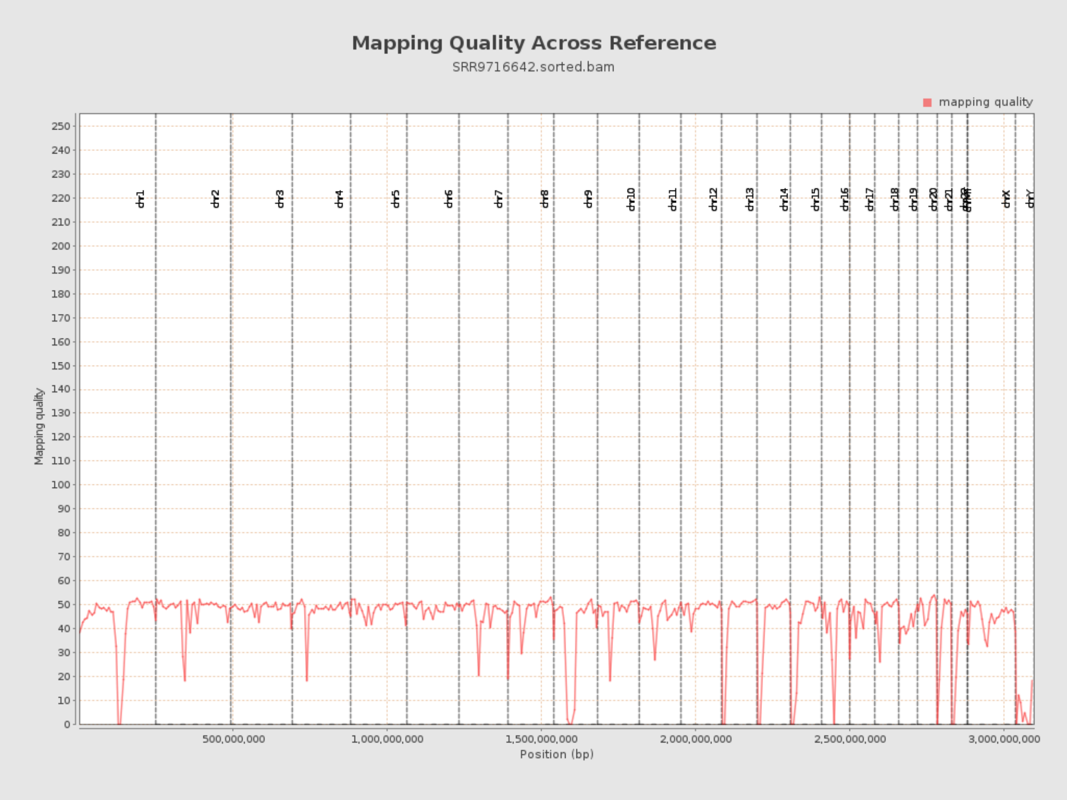
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram