Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 13:44:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716824.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_SRR9716824 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716824.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 13:44:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716824.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	892,990
Mapped reads	771,845 / 86.43%
Unmapped reads	121,145 / 13.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,230 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	32,240 / 3.61%
Duplication rate	3.4%
Clipped reads	774,102 / 86.69%

2.2. ACGT Content

Number/percentage of A's	11,550,305 / 25.73%
Number/percentage of C's	8,727,916 / 19.44%
Number/percentage of T's	14,048,403 / 31.29%
Number/percentage of G's	10,567,825 / 23.54%
Number/percentage of N's	314 / 0%
GC Percentage	42.98%

2.3. Coverage

Mean	0.0145

Standard Deviation	0.1601

2.4. Mapping Quality

Mean Mapping Quality	45.12

2.5. Mismatches and indels

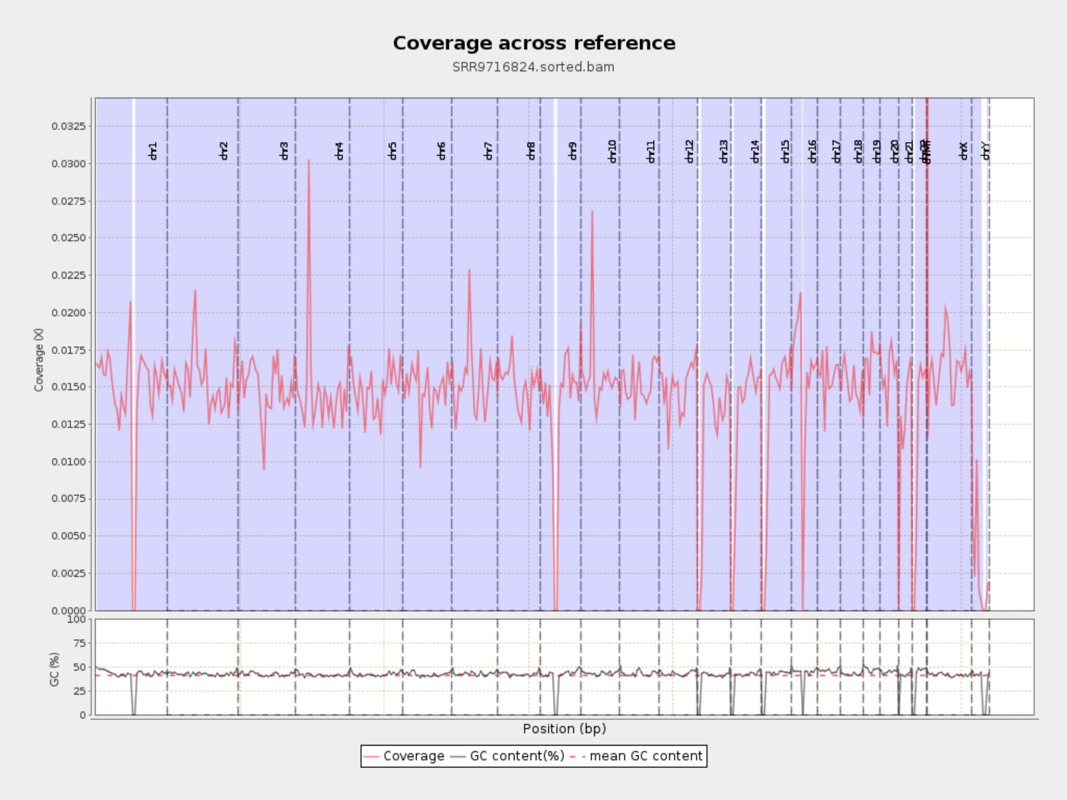
General error rate	0.52%
Mismatches	226,847
Insertions	3,576
Mapped reads with at least one insertion	0.46%
Deletions	8,319
Mapped reads with at least one deletion	1.07%
Homopolymer indels	41.33%

2.6. Chromosome stats

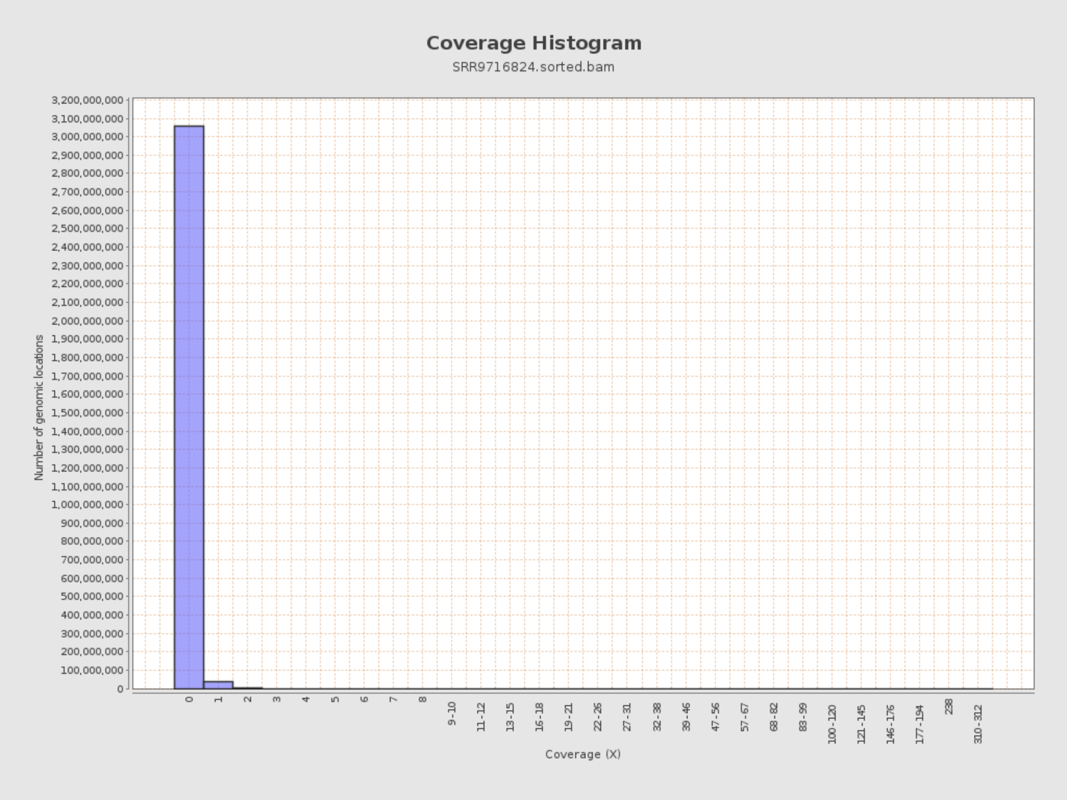
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3641503	0.0146	0.2059
chr2	243199373	3738394	0.0154	0.2009
chr3	198022430	2948210	0.0149	0.1334
chr4	191154276	2839213	0.0149	0.155
chr5	180915260	2694615	0.0149	0.1339
chr6	171115067	2543975	0.0149	0.1415
chr7	159138663	2460598	0.0155	0.1931

chr8	146364022	2229571	0.0152	0.1804
chr9	141213431	1859663	0.0132	0.138
chr10	135534747	2149660	0.0159	0.1827
chr11	135006516	2062005	0.0153	0.1527
chr12	133851895	2001493	0.015	0.1341
chr13	115169878	1373084	0.0119	0.1198
chr14	107349540	1359579	0.0127	0.1248
chr15	102531392	1312139	0.0128	0.1247
chr16	90354753	1384863	0.0153	0.1398
chr17	81195210	1278275	0.0157	0.1428
chr18	78077248	1179944	0.0151	0.2189
chr19	59128983	994737	0.0168	0.1797
chr20	63025520	998347	0.0158	0.1427
chr21	48129895	607803	0.0126	0.1339
chr22	51304566	560851	0.0109	0.1135
chrMT	16571	17086	1.0311	1.3414
chrX	155270560	2513727	0.0162	0.145
chrY	59373566	158743	0.0027	0.0953

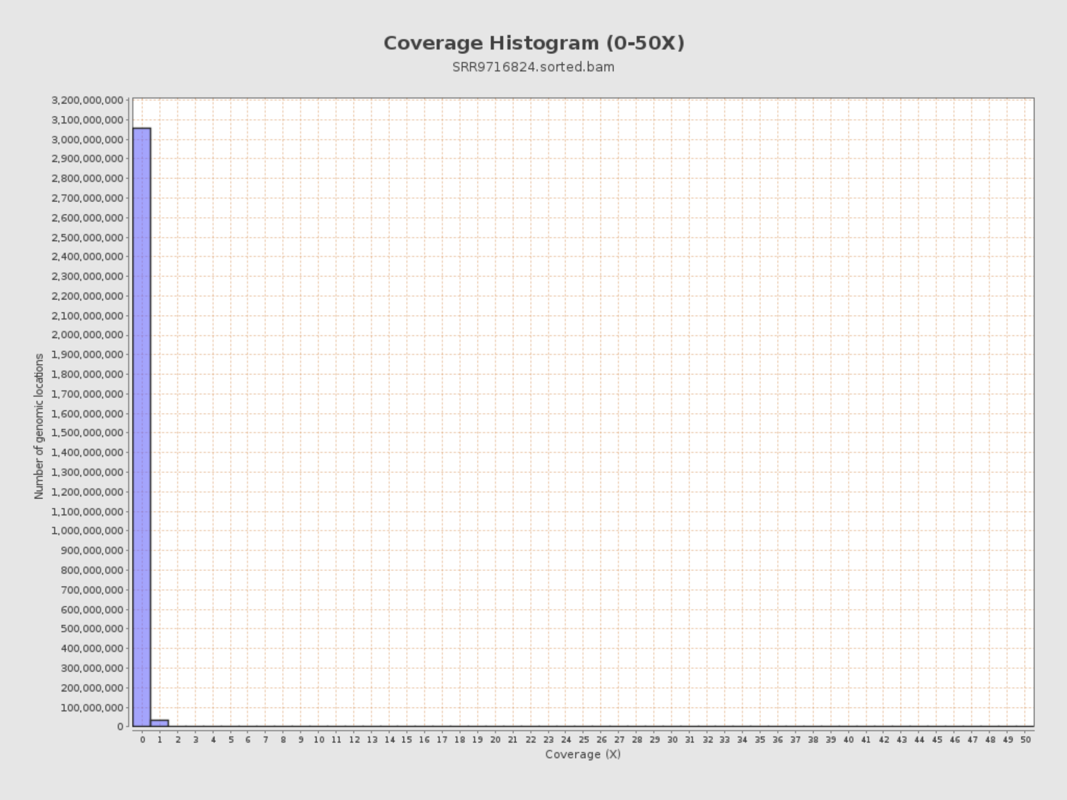
3. Results : Coverage across reference



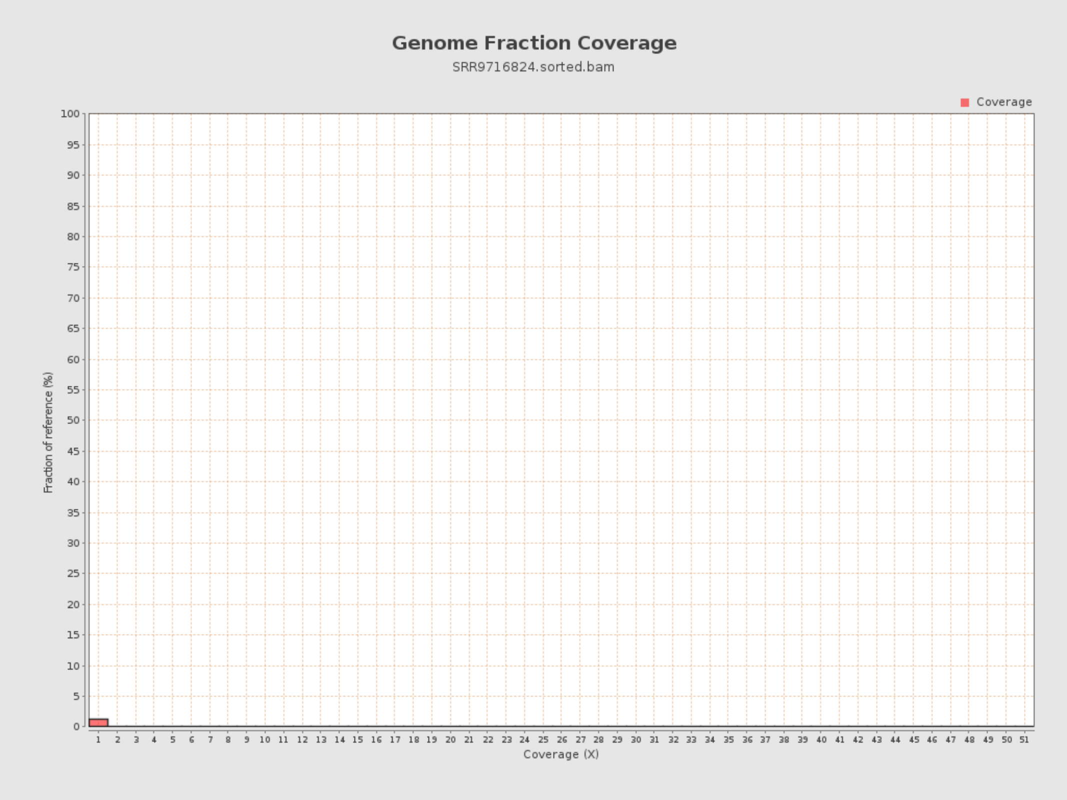
4. Results : Coverage Histogram



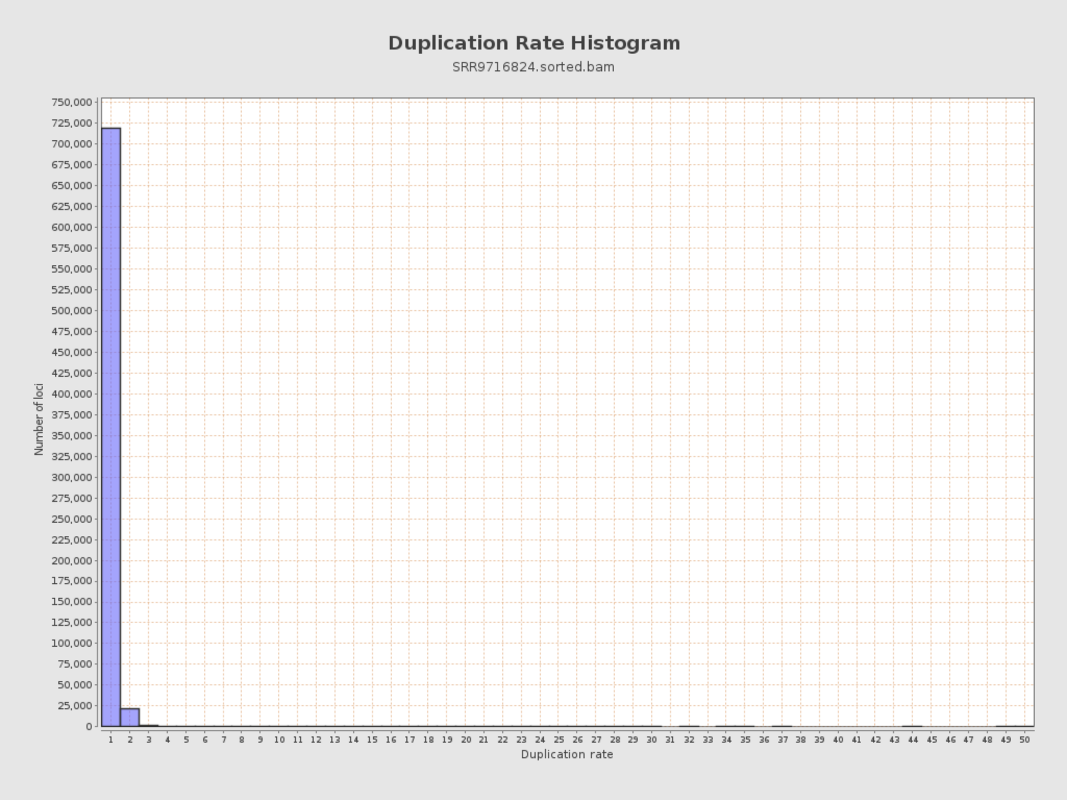
5. Results : Coverage Histogram (0-50X)



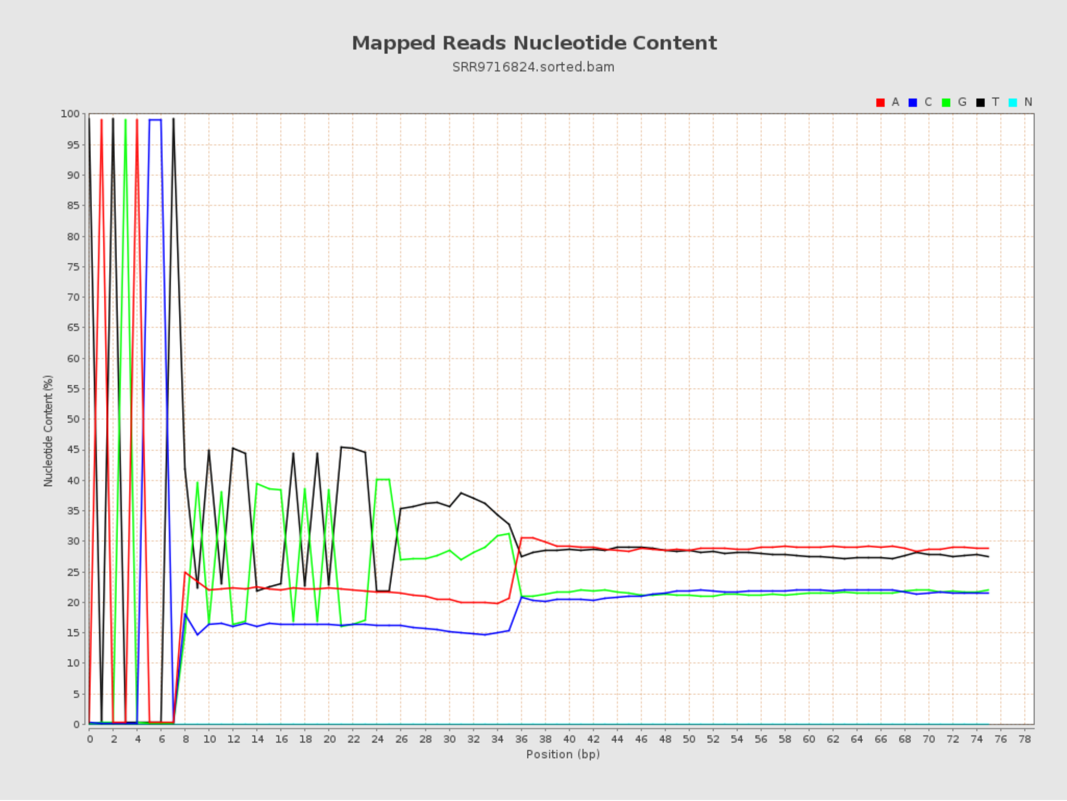
6. Results : Genome Fraction Coverage



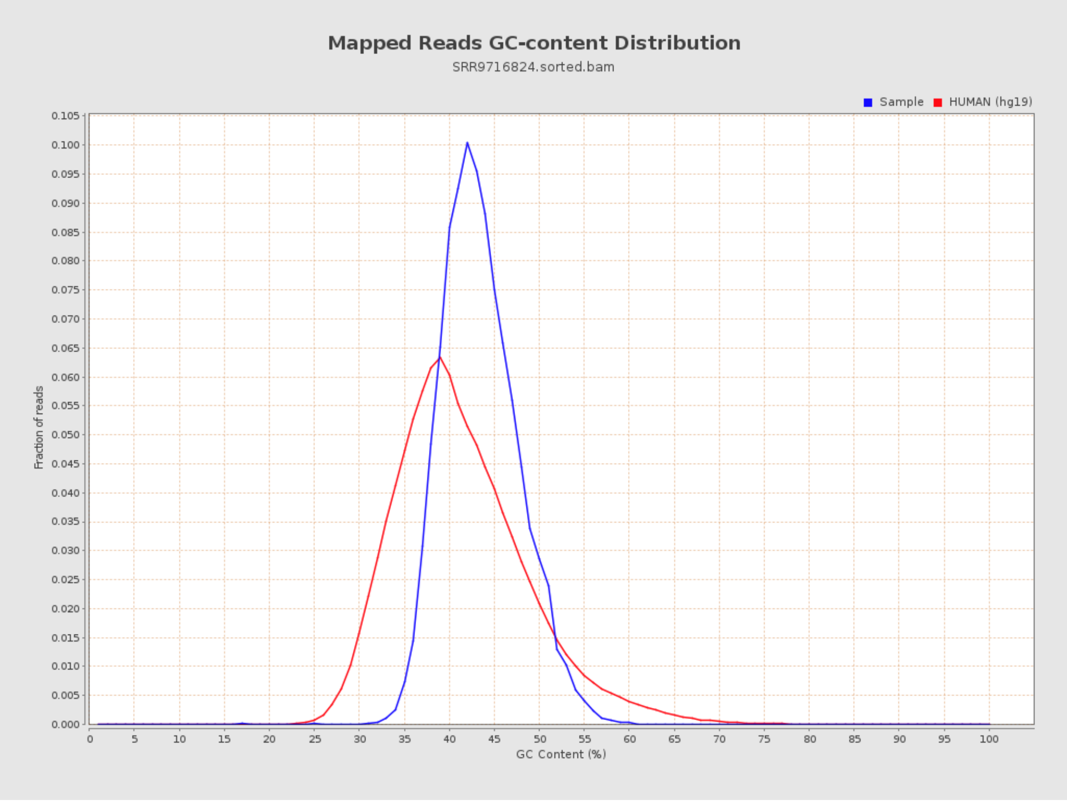
7. Results : Duplication Rate Histogram



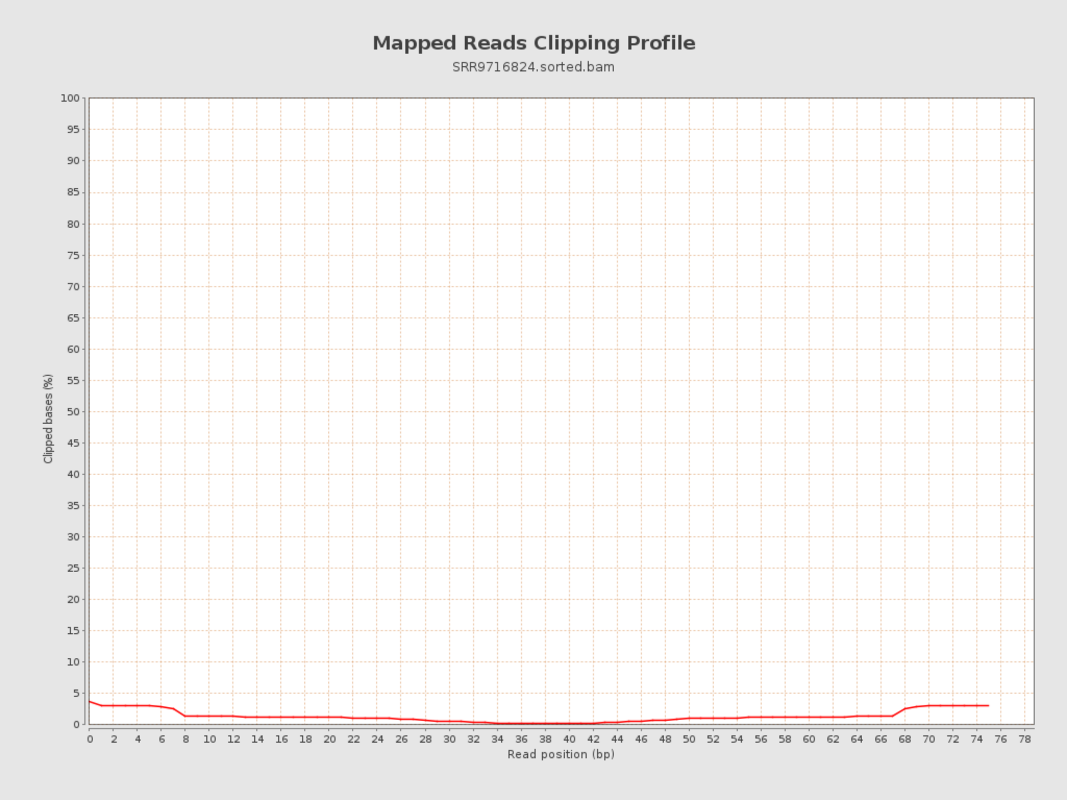
8. Results : Mapped Reads Nucleotide Content



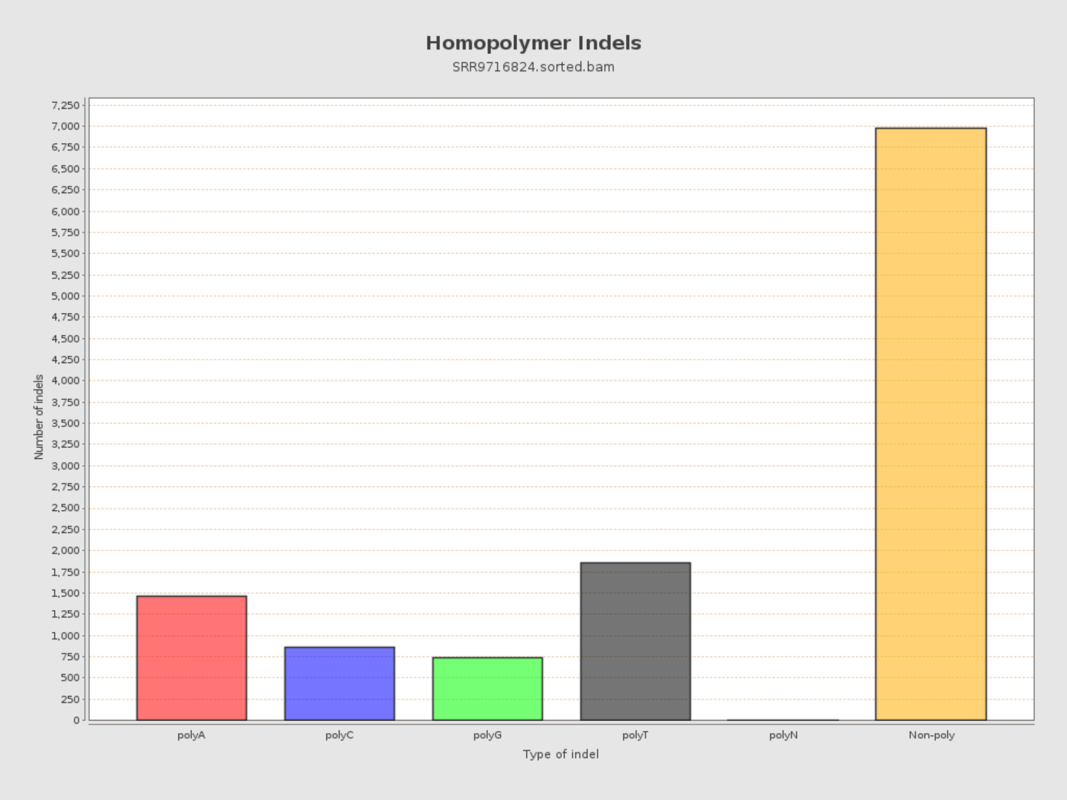
9. Results : Mapped Reads GC-content Distribution



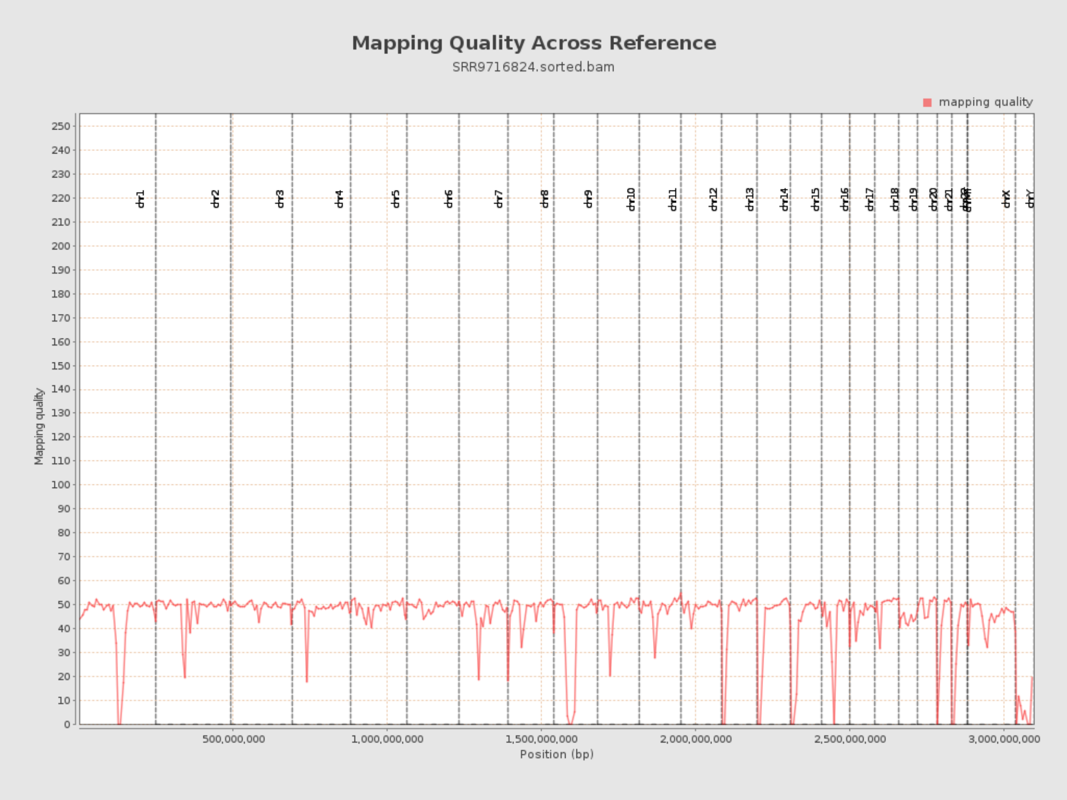
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram