Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 16:05:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716874.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_SRR9716874 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716874.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 16:05:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716874.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	795,510
Mapped reads	728,188 / 91.54%
Unmapped reads	67,322 / 8.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,317 / 0.17%
Read min/max/mean length	30 / 76 / 76.06
Duplicated reads (estimated)	17,837 / 2.24%
Duplication rate	1.85%
Clipped reads	727,338 / 91.43%

2.2. ACGT Content

Number/percentage of A's	10,954,656 / 26.07%
Number/percentage of C's	7,742,744 / 18.42%
Number/percentage of T's	12,975,091 / 30.88%
Number/percentage of G's	10,350,262 / 24.63%
Number/percentage of N's	362 / 0%
GC Percentage	43.05%

2.3. Coverage

Mean	0.0136

Standard Deviation	0.1491

2.4. Mapping Quality

Mean Mapping Quality	44.34

2.5. Mismatches and indels

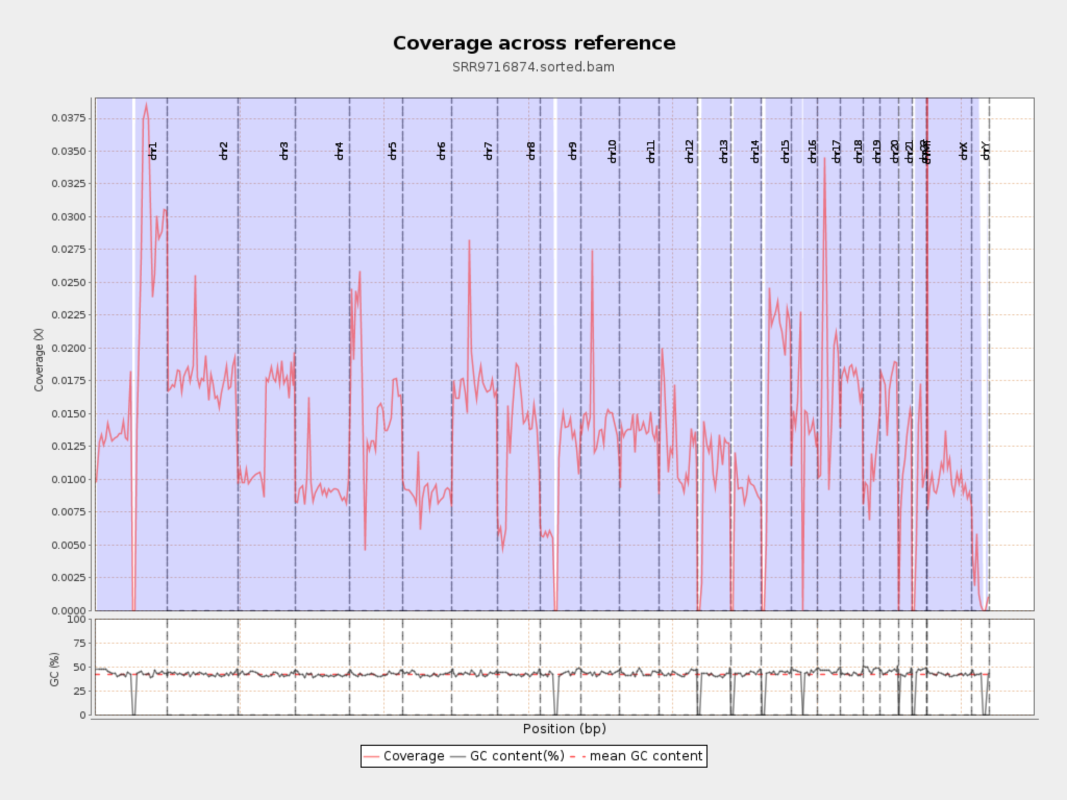
General error rate	0.5%
Mismatches	204,276
Insertions	3,173
Mapped reads with at least one insertion	0.43%
Deletions	8,391
Mapped reads with at least one deletion	1.14%
Homopolymer indels	41.17%

2.6. Chromosome stats

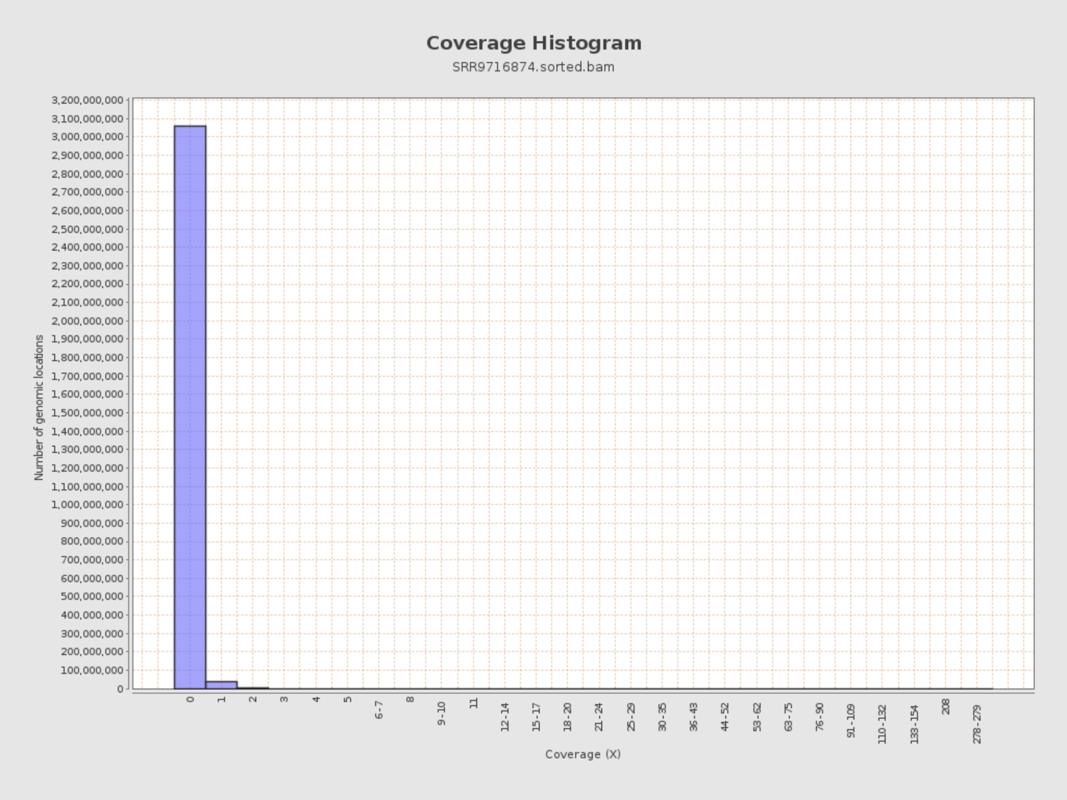
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4822023	0.0193	0.1936
chr2	243199373	4299057	0.0177	0.1953
chr3	198022430	2781341	0.014	0.1251
chr4	191154276	1778403	0.0093	0.1066
chr5	180915260	2940335	0.0163	0.1339
chr6	171115067	1533855	0.009	0.1092
chr7	159138663	2792688	0.0175	0.2329

chr8	146364022	1908709	0.013	0.1316
chr9	141213431	1313527	0.0093	0.1228
chr10	135534747	1991296	0.0147	0.176
chr11	135006516	1852109	0.0137	0.1444
chr12	133851895	1696941	0.0127	0.1183
chr13	115169878	1162450	0.0101	0.1056
chr14	107349540	879054	0.0082	0.098
chr15	102531392	1826531	0.0178	0.1411
chr16	90354753	1238530	0.0137	0.1306
chr17	81195210	1497759	0.0184	0.1474
chr18	78077248	1392193	0.0178	0.2241
chr19	59128983	627440	0.0106	0.1485
chr20	63025520	1076109	0.0171	0.1374
chr21	48129895	522753	0.0109	0.1118
chr22	51304566	461822	0.009	0.0992
chrMT	16571	1864	0.1125	0.3602
chrX	155270560	1539379	0.0099	0.1147
chrY	59373566	100163	0.0017	0.0575

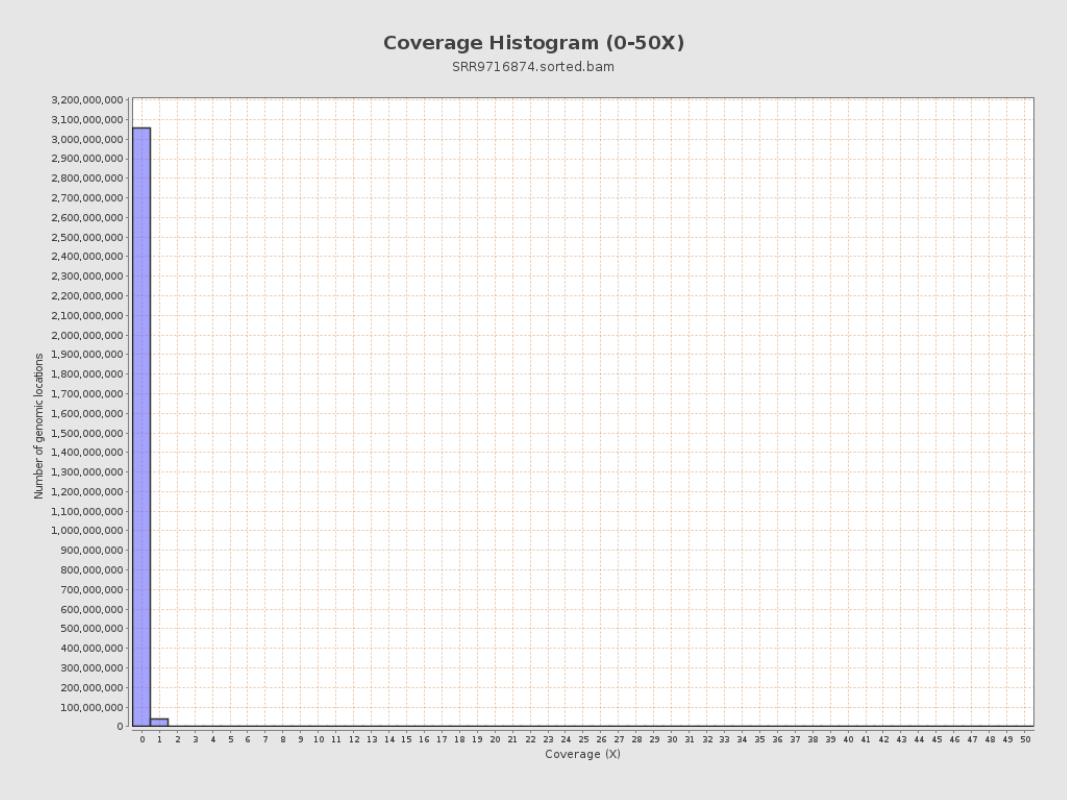
3. Results : Coverage across reference



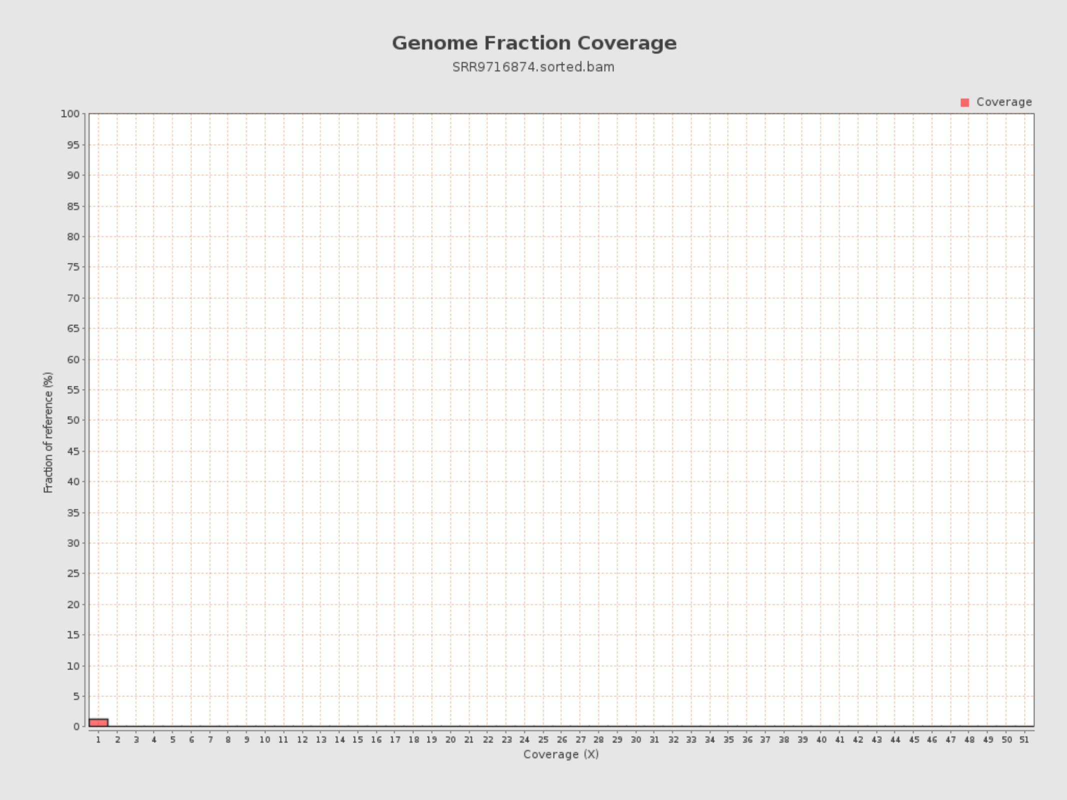
4. Results : Coverage Histogram



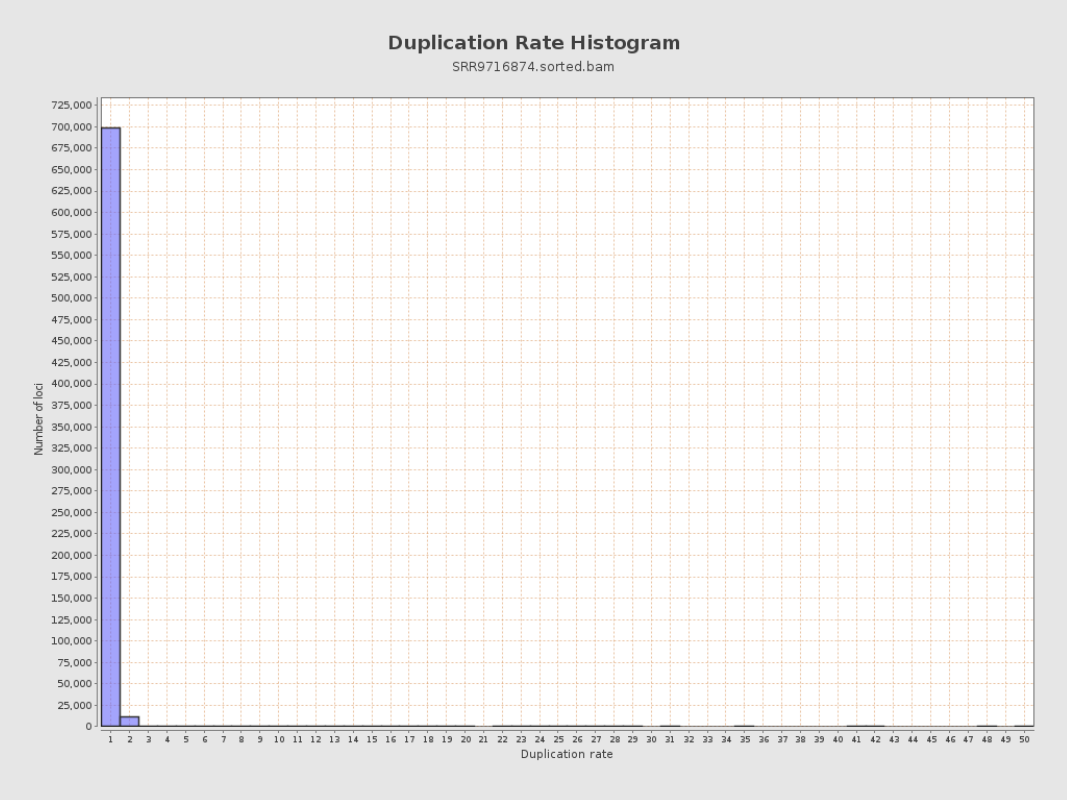
5. Results : Coverage Histogram (0-50X)



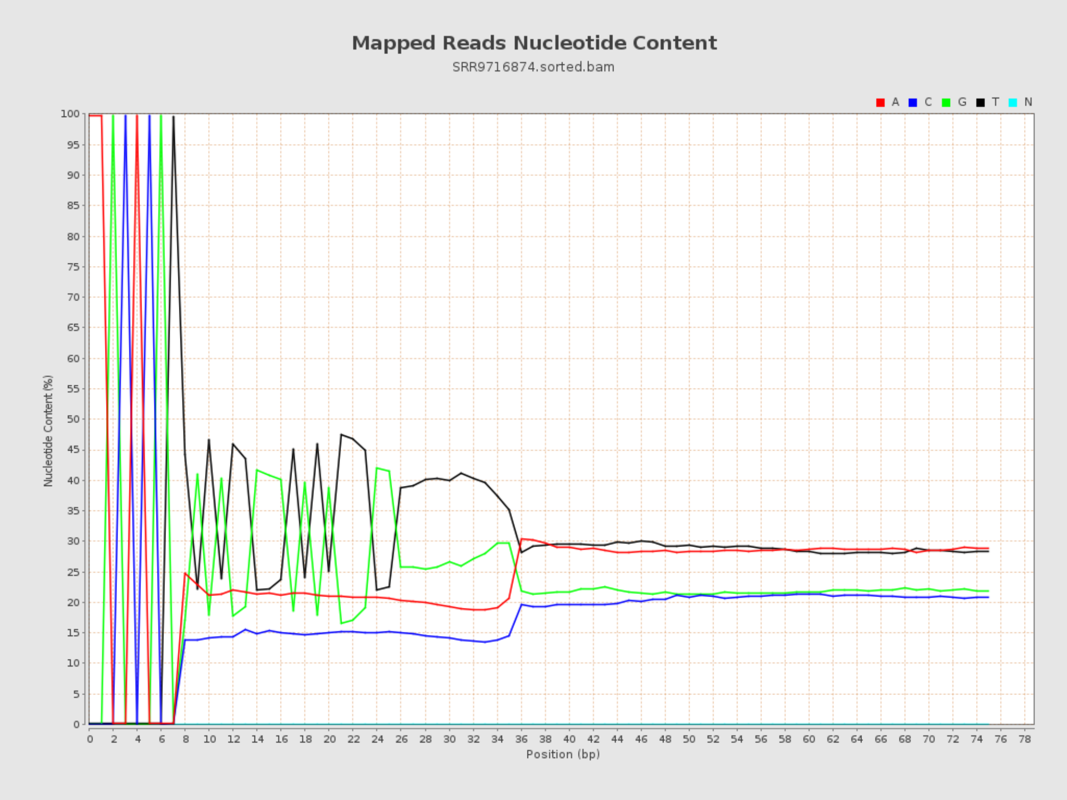
6. Results : Genome Fraction Coverage



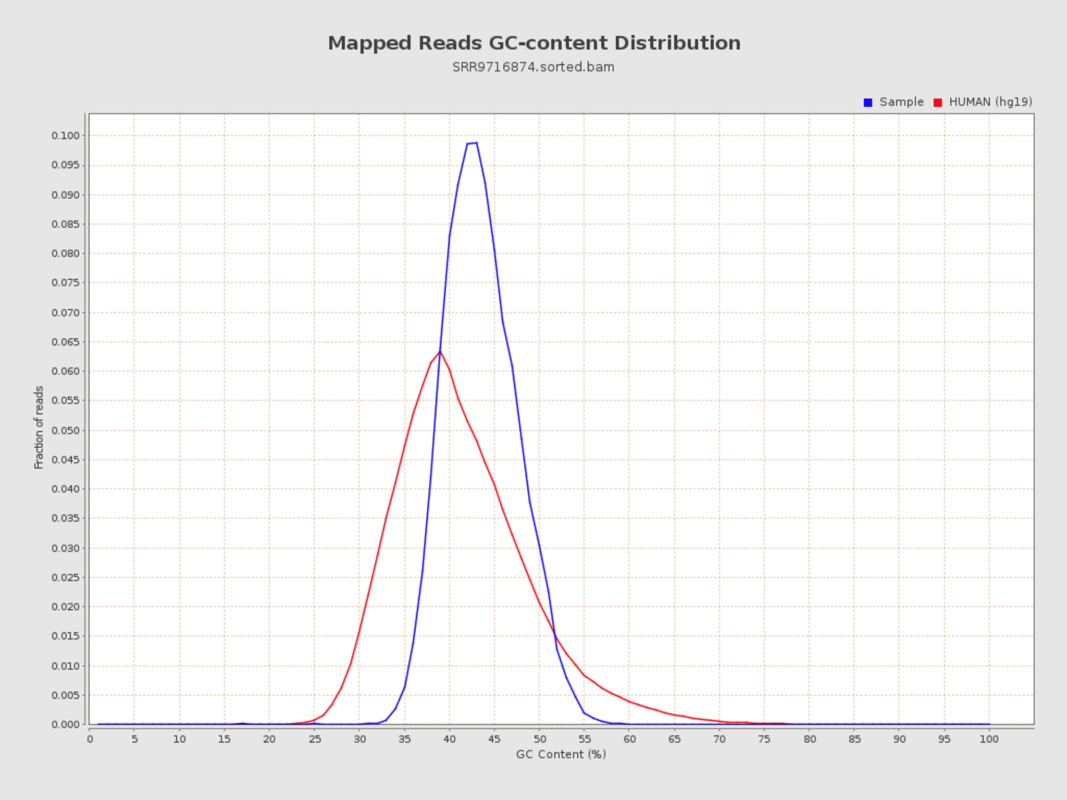
7. Results : Duplication Rate Histogram



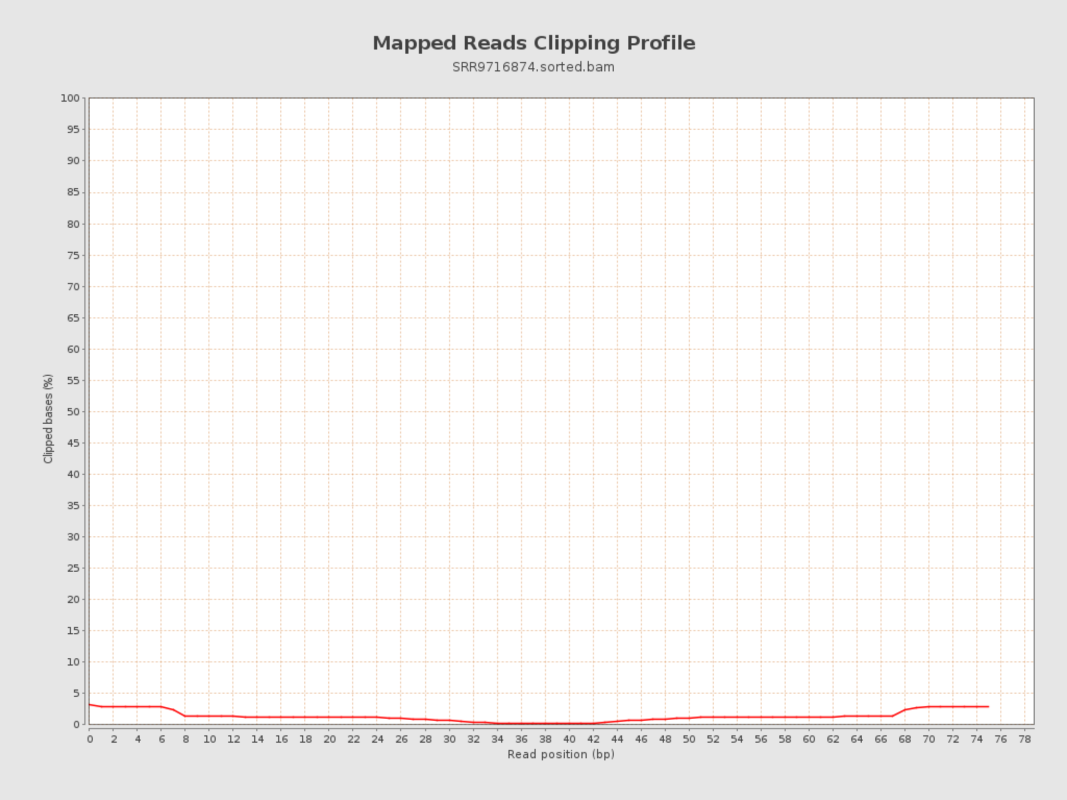
8. Results : Mapped Reads Nucleotide Content



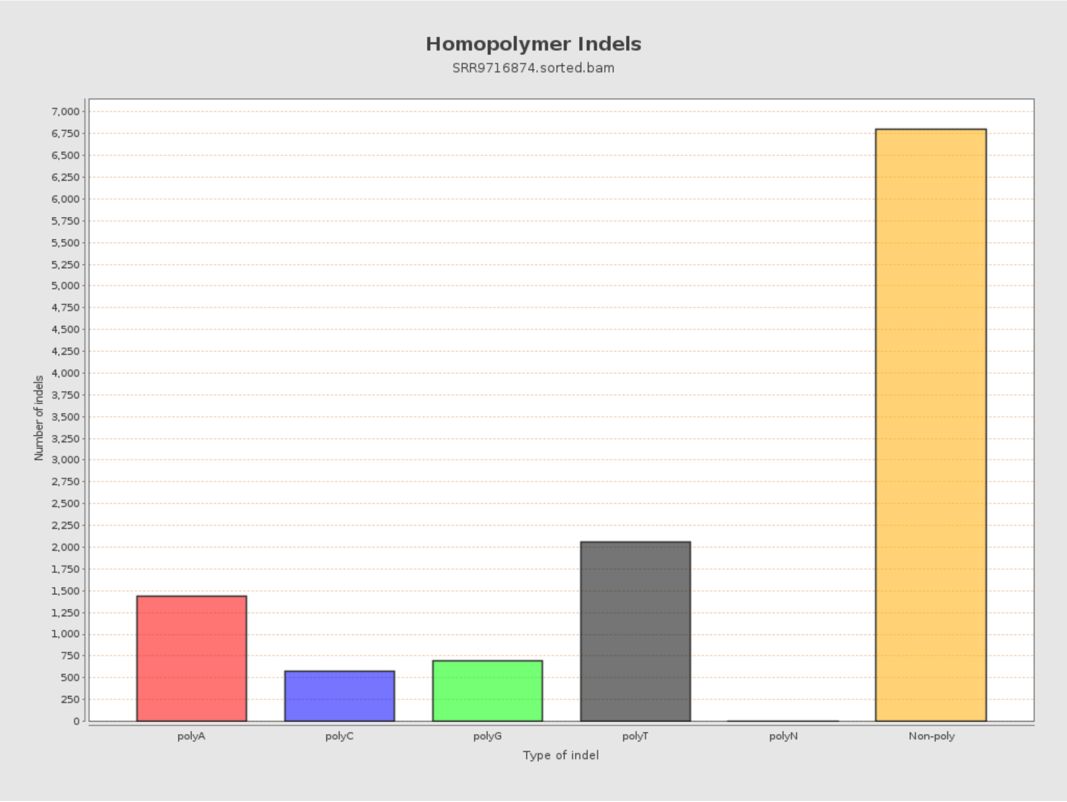
9. Results : Mapped Reads GC-content Distribution



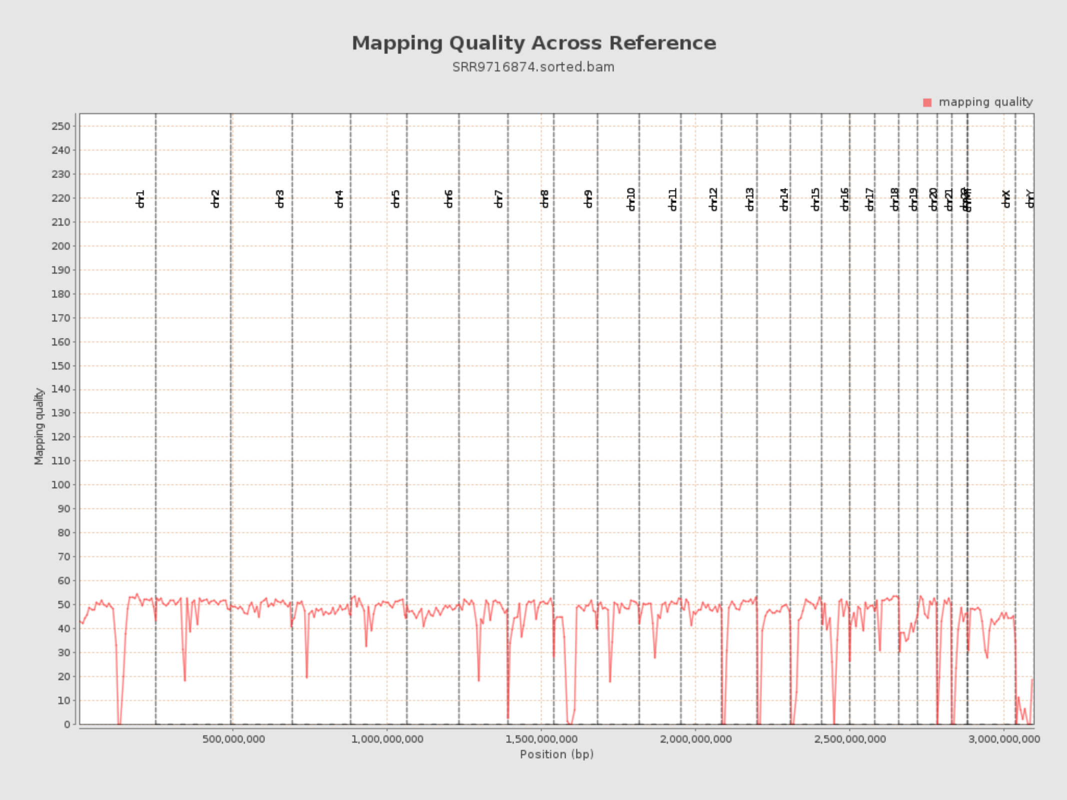
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram