Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 19:01:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716928.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_SRR9716928 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716928.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 19:01:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716928.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,028,948
Mapped reads	926,216 / 90.02%
Unmapped reads	102,732 / 9.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,812 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	23,769 / 2.31%
Duplication rate	1.9%
Clipped reads	928,436 / 90.23%

2.2. ACGT Content

Number/percentage of A's	13,067,004 / 24.3%
Number/percentage of C's	9,695,720 / 18.03%
Number/percentage of T's	17,609,240 / 32.74%
Number/percentage of G's	13,405,357 / 24.93%
Number/percentage of N's	1,400 / 0%
GC Percentage	42.96%

2.3. Coverage

Mean	0.0174

Standard Deviation	0.1863

2.4. Mapping Quality

Mean Mapping Quality	44.66

2.5. Mismatches and indels

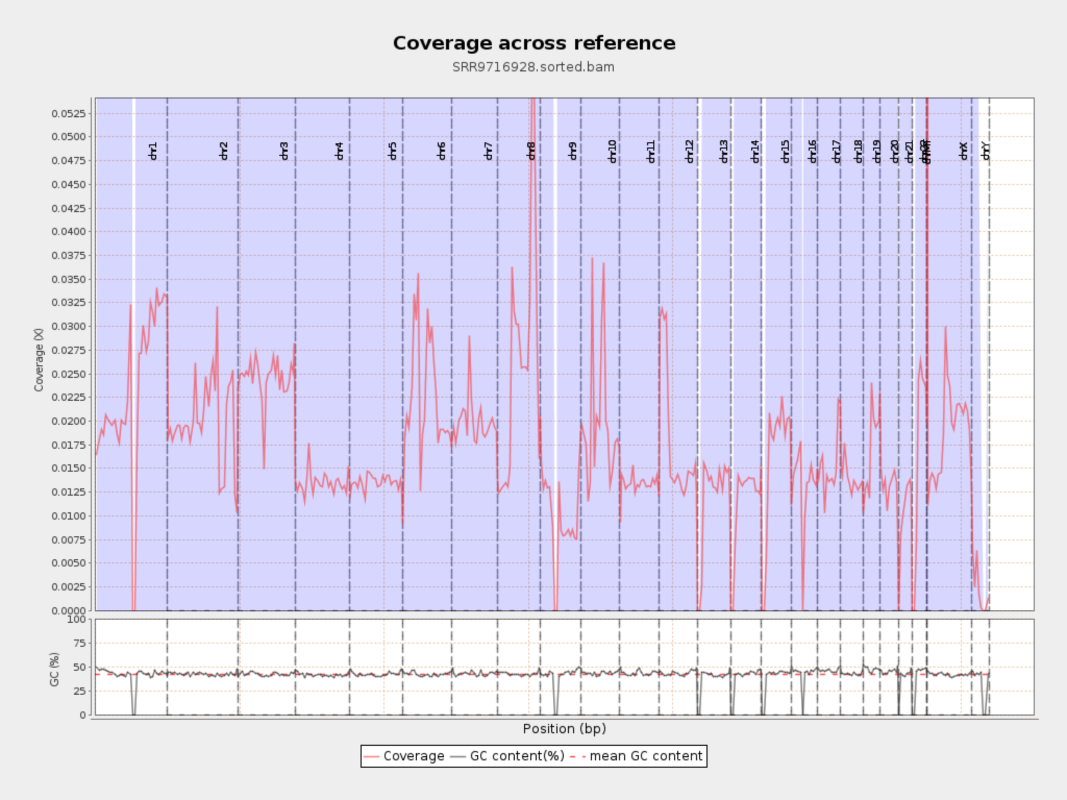
General error rate	0.51%
Mismatches	270,201
Insertions	3,725
Mapped reads with at least one insertion	0.4%
Deletions	9,853
Mapped reads with at least one deletion	1.06%
Homopolymer indels	41.71%

2.6. Chromosome stats

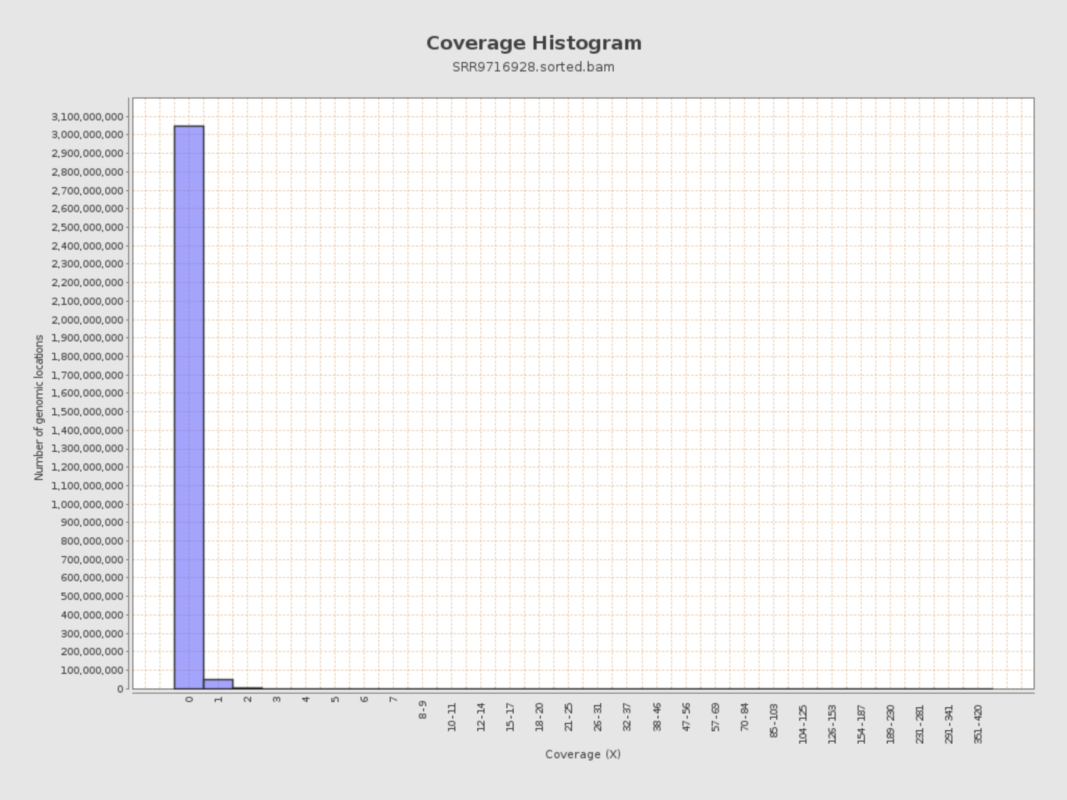
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5777575	0.0232	0.3293
chr2	243199373	4907283	0.0202	0.227
chr3	198022430	4860113	0.0245	0.1665
chr4	191154276	2584071	0.0135	0.126
chr5	180915260	2467551	0.0136	0.1235
chr6	171115067	3854076	0.0225	0.2091
chr7	159138663	3189851	0.02	0.2193

chr8	146364022	3854985	0.0263	0.1877
chr9	141213431	1357288	0.0096	0.13
chr10	135534747	2721033	0.0201	0.2015
chr11	135006516	1816527	0.0135	0.1521
chr12	133851895	2433265	0.0182	0.1431
chr13	115169878	1352850	0.0117	0.1148
chr14	107349540	1212525	0.0113	0.1176
chr15	102531392	1636209	0.016	0.1333
chr16	90354753	1163977	0.0129	0.1317
chr17	81195210	1231950	0.0152	0.1324
chr18	78077248	1083187	0.0139	0.2491
chr19	59128983	1021126	0.0173	0.2287
chr20	63025520	828029	0.0131	0.1215
chr21	48129895	498845	0.0104	0.1129
chr22	51304566	860036	0.0168	0.1365
chrMT	16571	8685	0.5241	0.7866
chrX	155270560	2943720	0.019	0.1594
chrY	59373566	129761	0.0022	0.0595

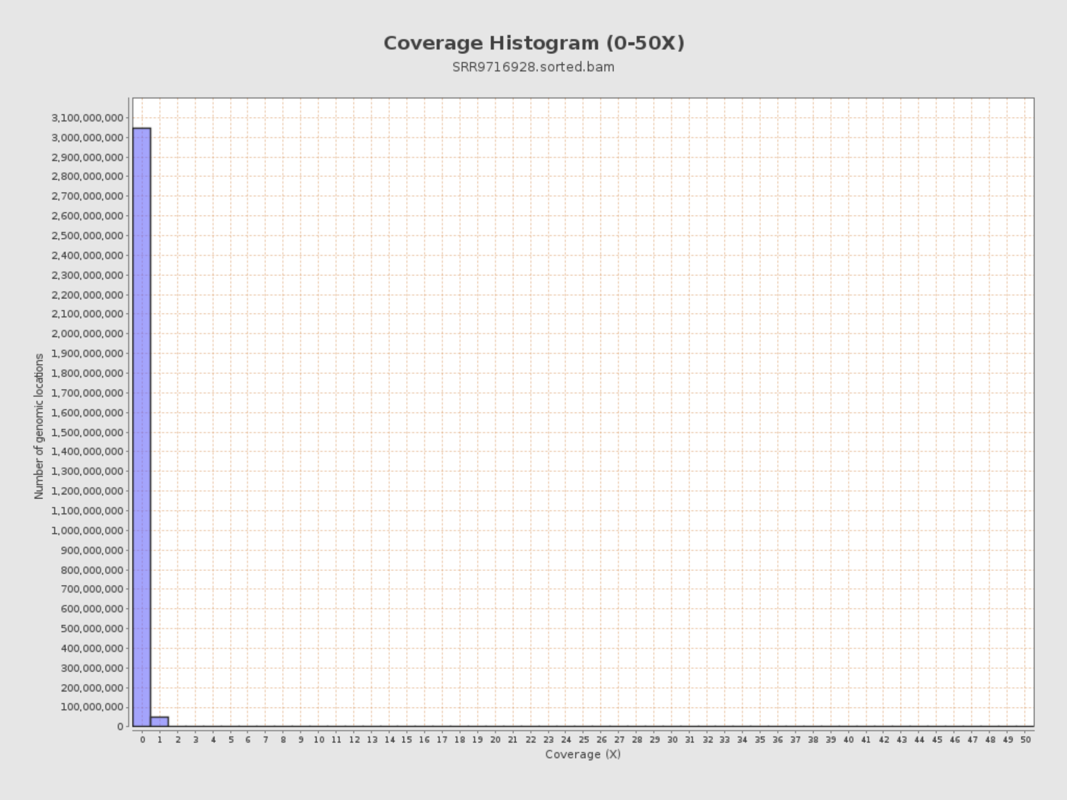
3. Results : Coverage across reference



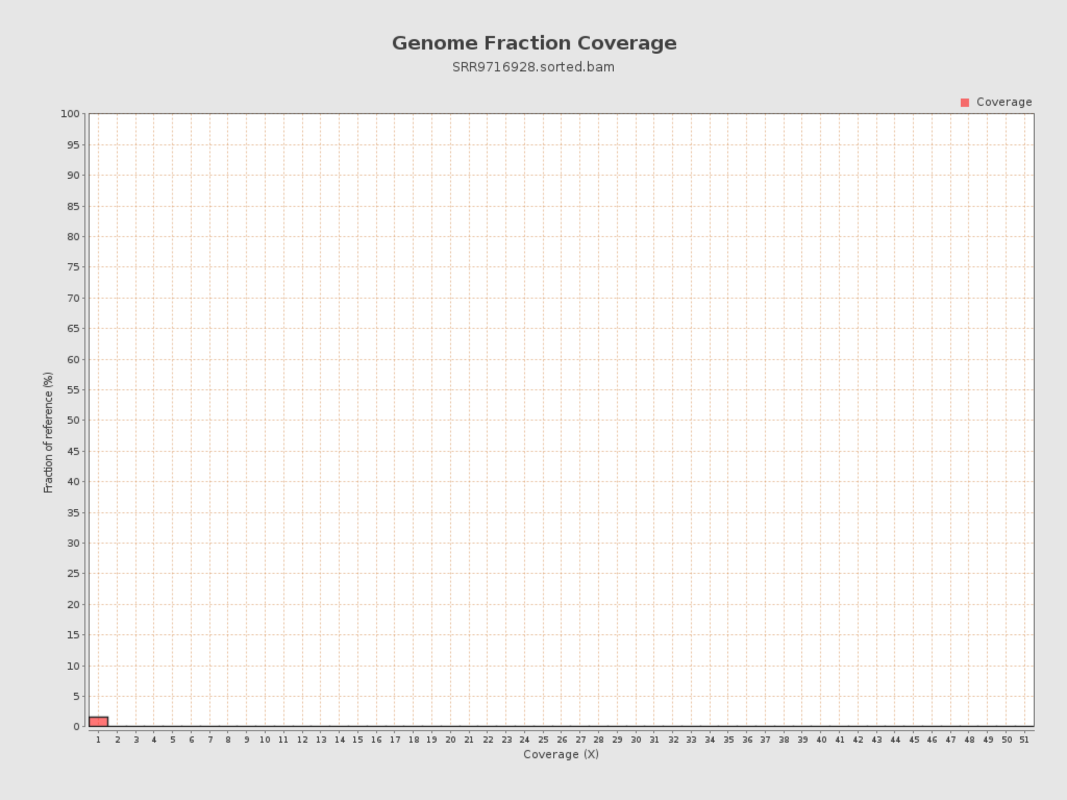
4. Results : Coverage Histogram



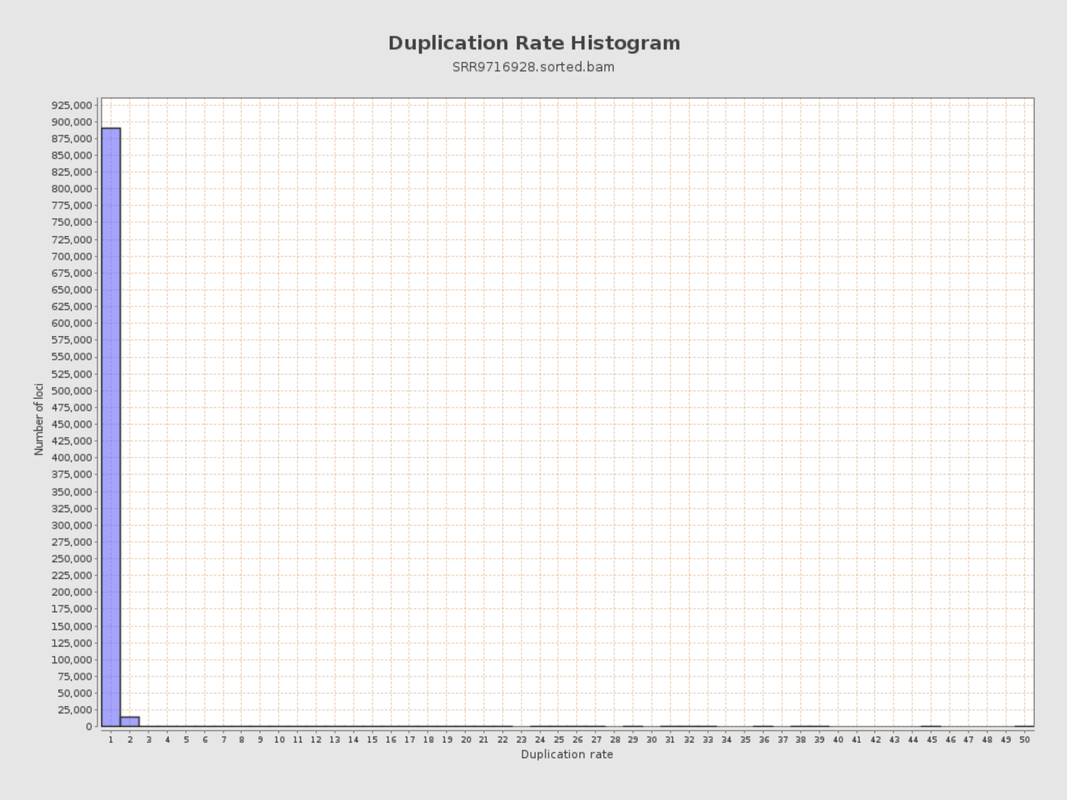
5. Results : Coverage Histogram (0-50X)



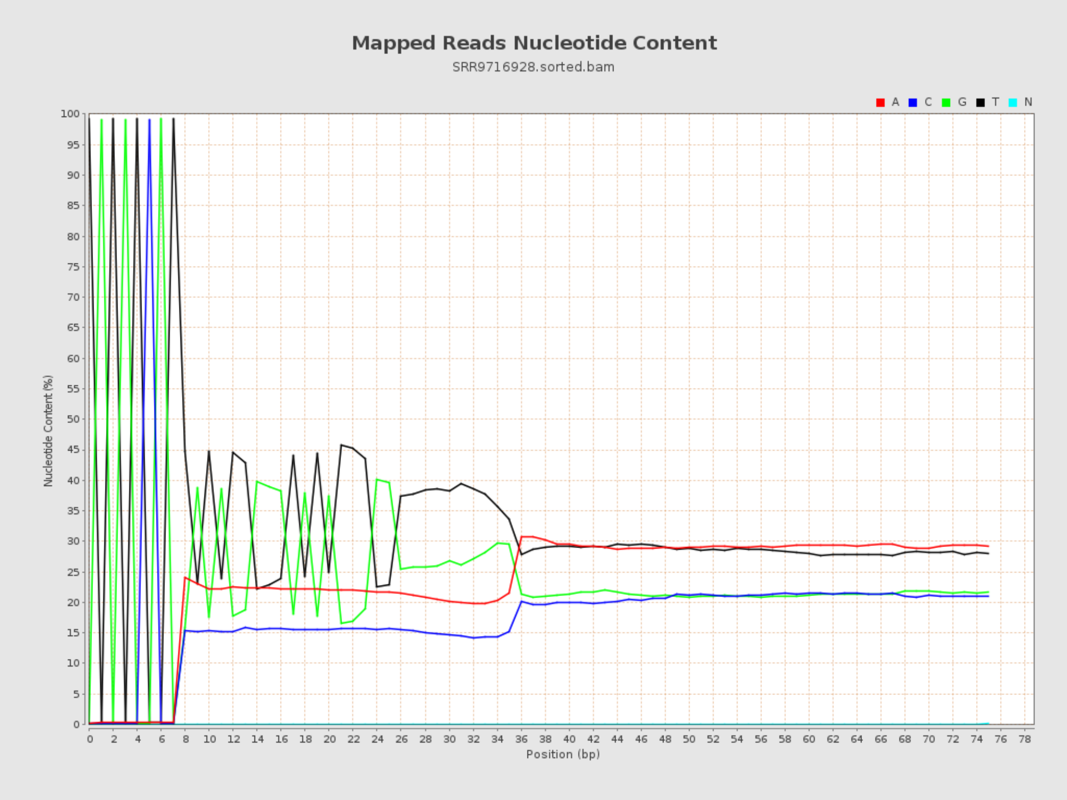
6. Results : Genome Fraction Coverage



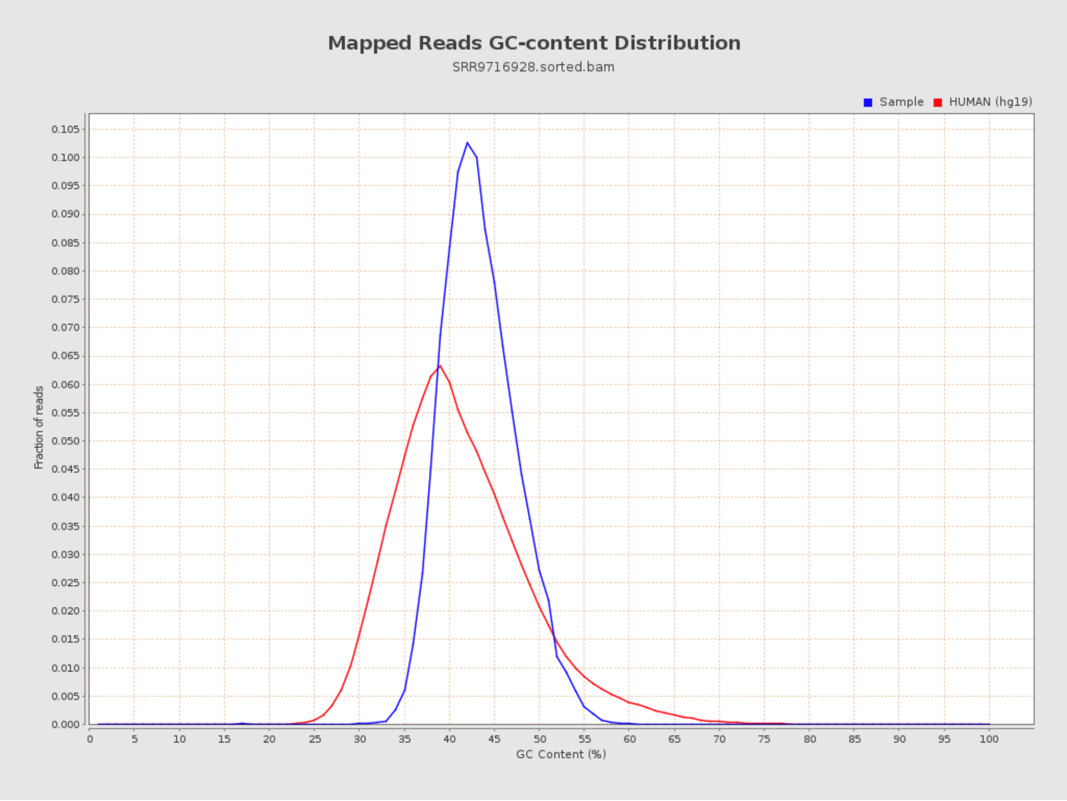
7. Results : Duplication Rate Histogram



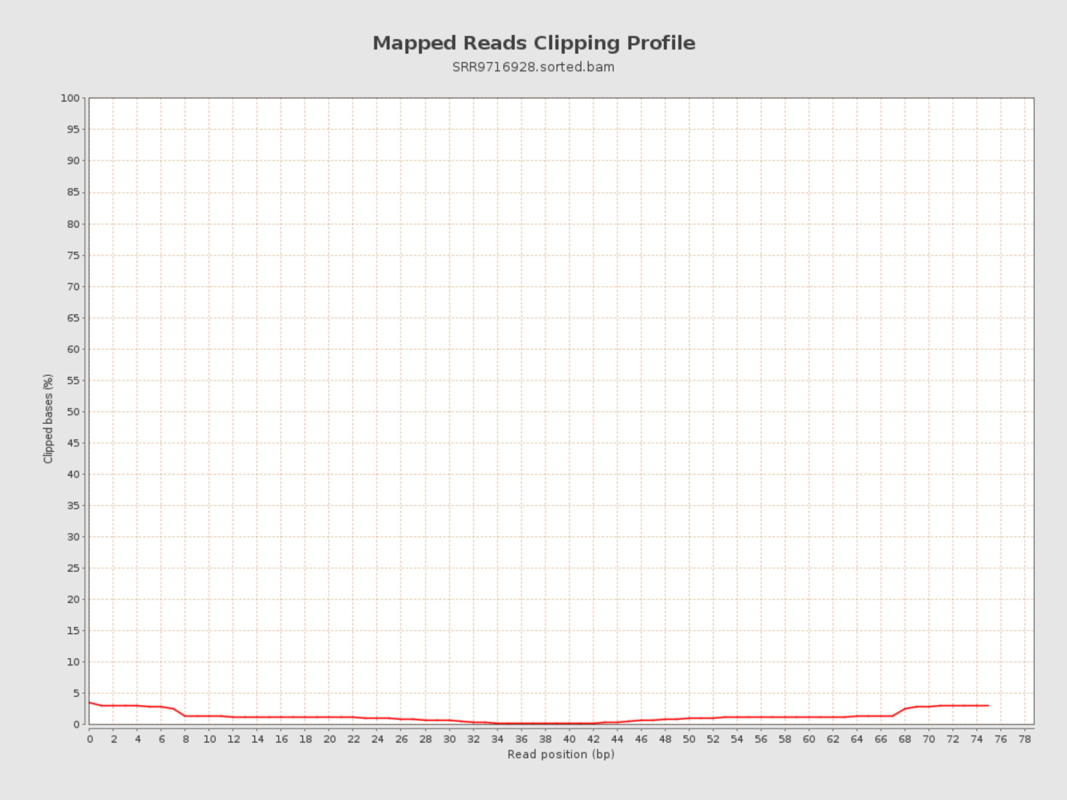
8. Results : Mapped Reads Nucleotide Content



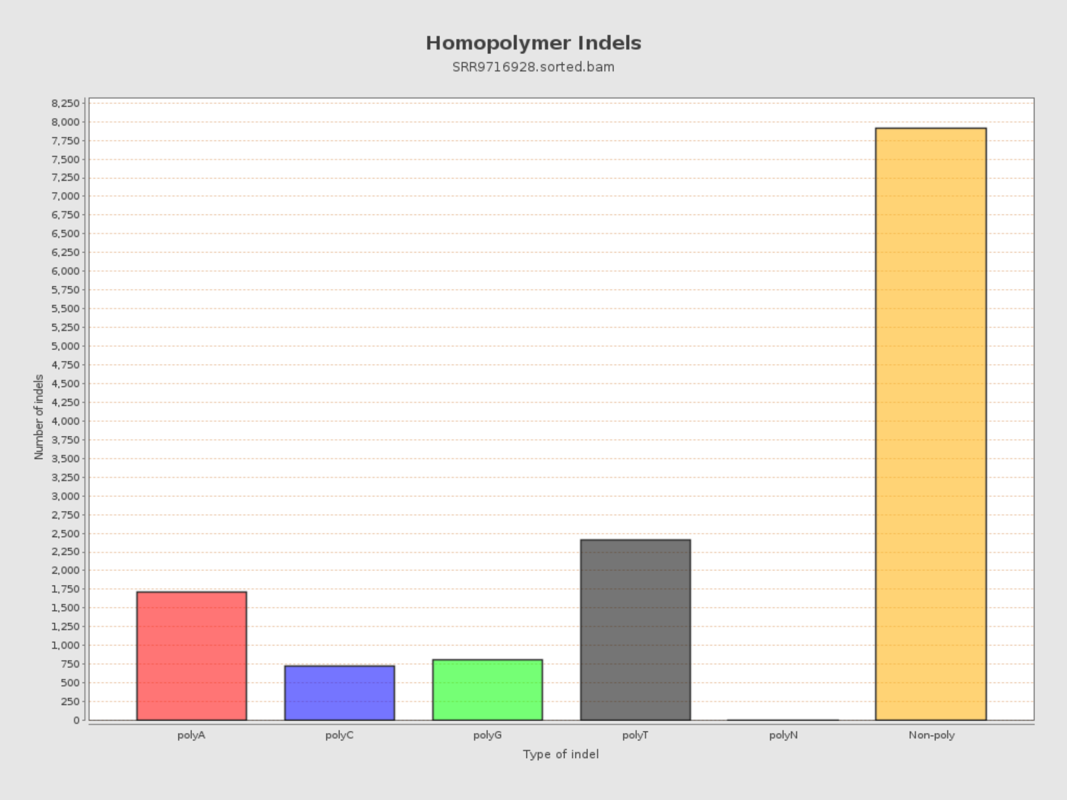
9. Results : Mapped Reads GC-content Distribution



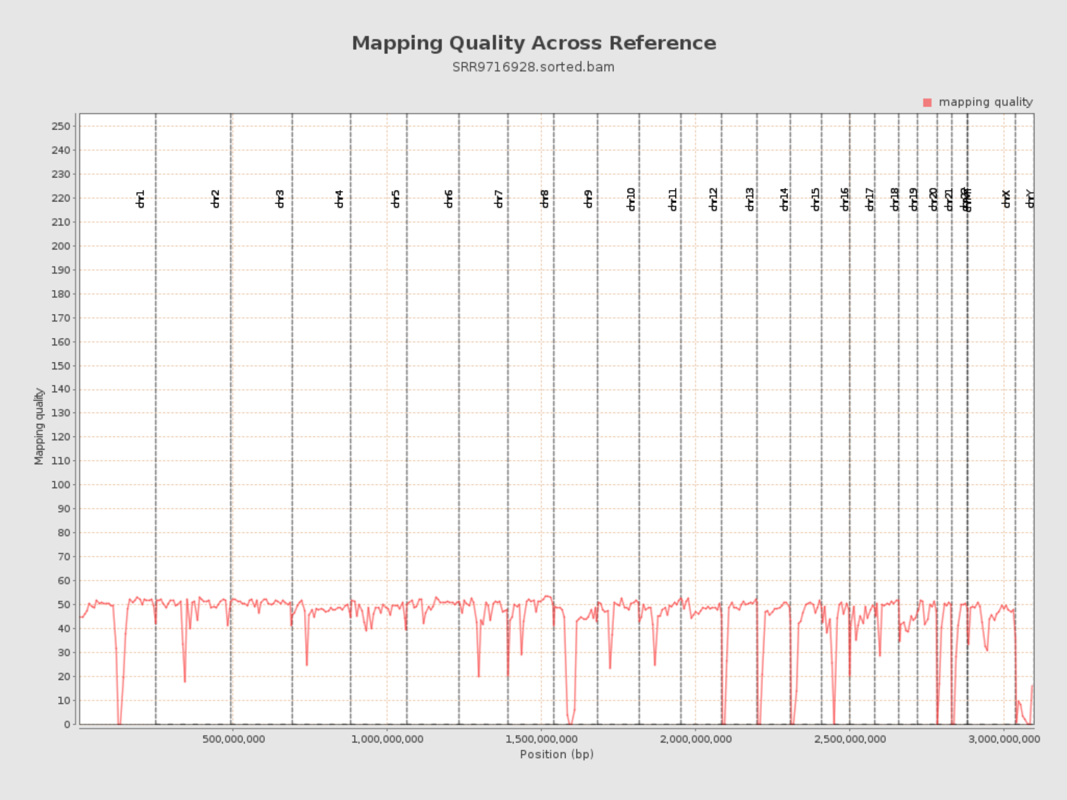
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram