Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 10:45:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716384.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_SRR9716384 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716384.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 10:44:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716384.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	749,396
Mapped reads	664,567 / 88.68%
Unmapped reads	84,829 / 11.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,840 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	10,109 / 1.35%
Duplication rate	1.08%
Clipped reads	665,891 / 88.86%

2.2. ACGT Content

Number/percentage of A's	9,870,826 / 25.71%
Number/percentage of C's	7,874,165 / 20.51%
Number/percentage of T's	11,673,235 / 30.4%
Number/percentage of G's	8,975,439 / 23.38%
Number/percentage of N's	259 / 0%
GC Percentage	43.89%

2.3. Coverage

Mean	0.0124

Standard Deviation	0.1356

2.4. Mapping Quality

Mean Mapping Quality	42.56

2.5. Mismatches and indels

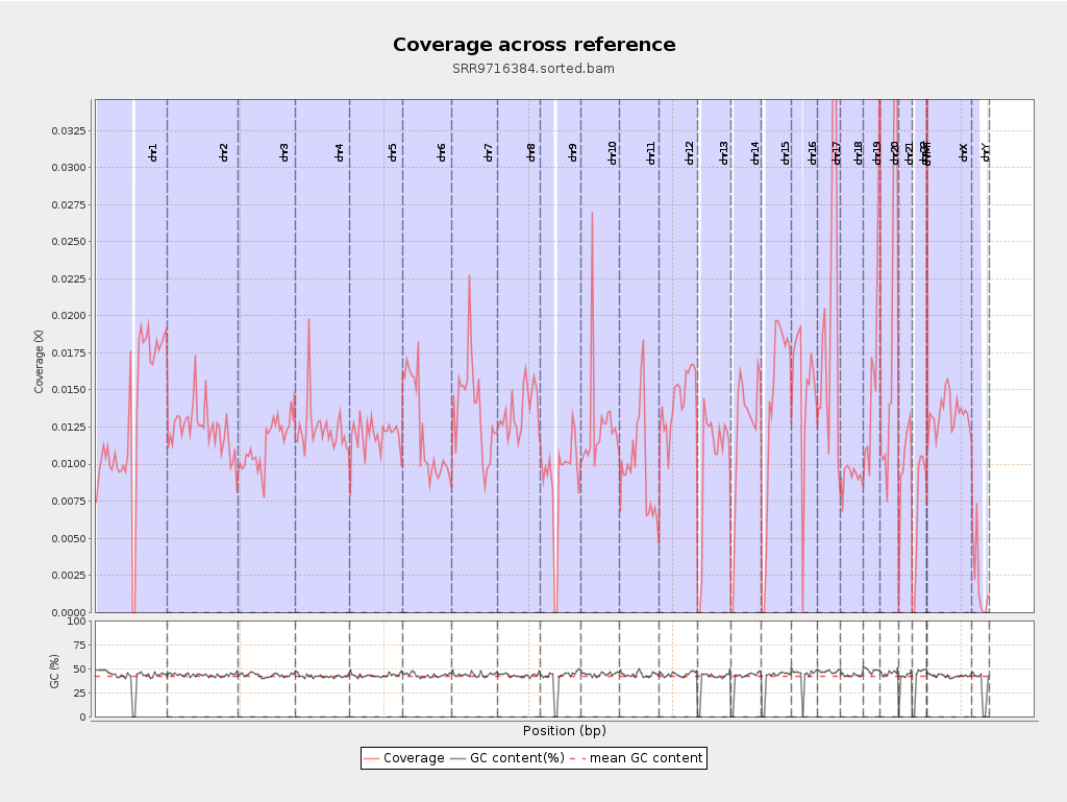
General error rate	0.52%
Mismatches	195,818
Insertions	2,974
Mapped reads with at least one insertion	0.45%
Deletions	7,156
Mapped reads with at least one deletion	1.07%
Homopolymer indels	38.93%

2.6. Chromosome stats

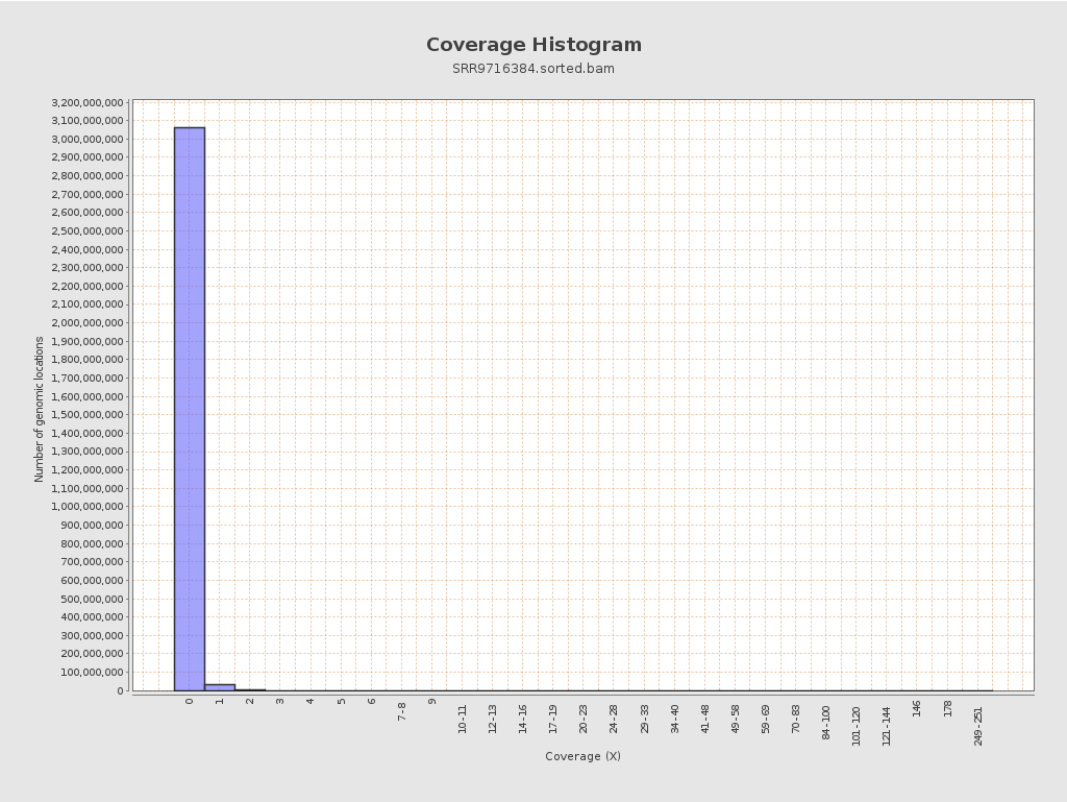
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3255109	0.0131	0.1731
chr2	243199373	3008348	0.0124	0.158
chr3	198022430	2245725	0.0113	0.1124
chr4	191154276	2369205	0.0124	0.1215
chr5	180915260	2175531	0.012	0.1133
chr6	171115067	2072908	0.0121	0.1233
chr7	159138663	2177187	0.0137	0.1722

chr8	146364022	1990779	0.0136	0.1367
chr9	141213431	1276142	0.009	0.1074
chr10	135534747	1705925	0.0126	0.1713
chr11	135006516	1346306	0.01	0.1153
chr12	133851895	1907310	0.0142	0.1242
chr13	115169878	1161397	0.0101	0.1042
chr14	107349540	1294747	0.0121	0.1163
chr15	102531392	1434658	0.014	0.1247
chr16	90354753	1345589	0.0149	0.1329
chr17	81195210	1668054	0.0205	0.1528
chr18	78077248	714004	0.0091	0.1465
chr19	59128983	994434	0.0168	0.1738
chr20	63025520	1215819	0.0193	0.147
chr21	48129895	482130	0.01	0.1081
chr22	51304566	356333	0.0069	0.0863
chrMT	16571	1450	0.0875	0.3162
chrX	155270560	2082844	0.0134	0.1231
chrY	59373566	123534	0.0021	0.0734

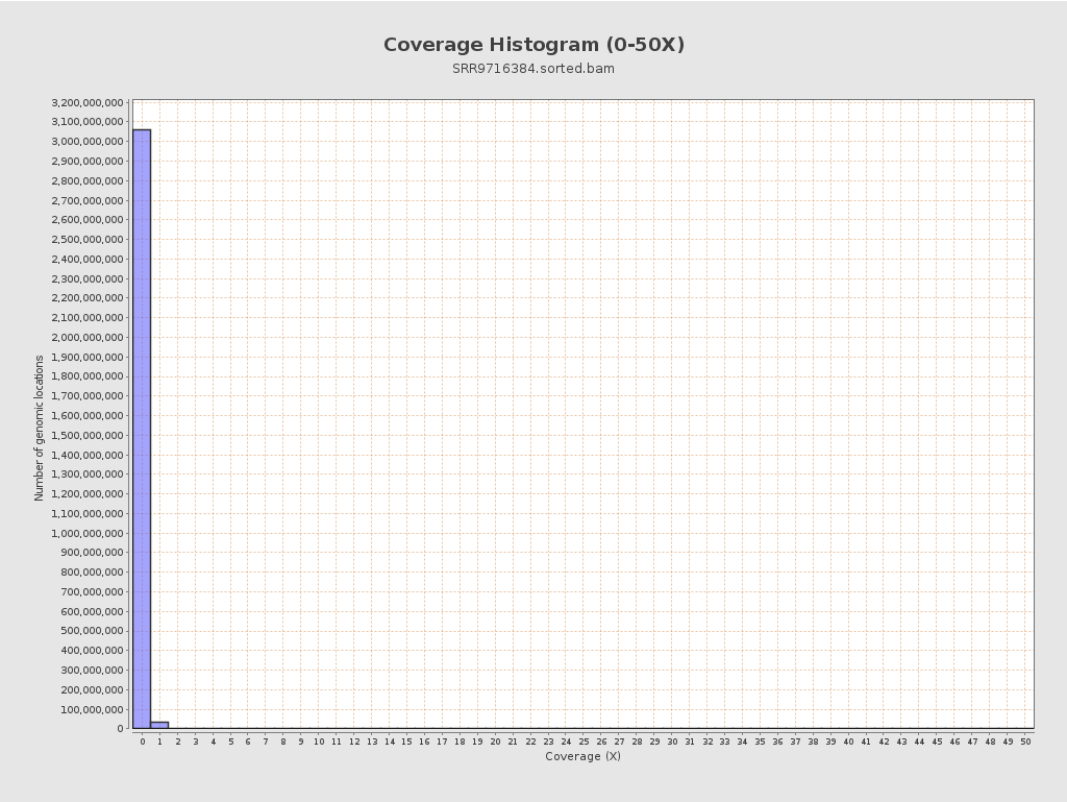
3. Results : Coverage across reference



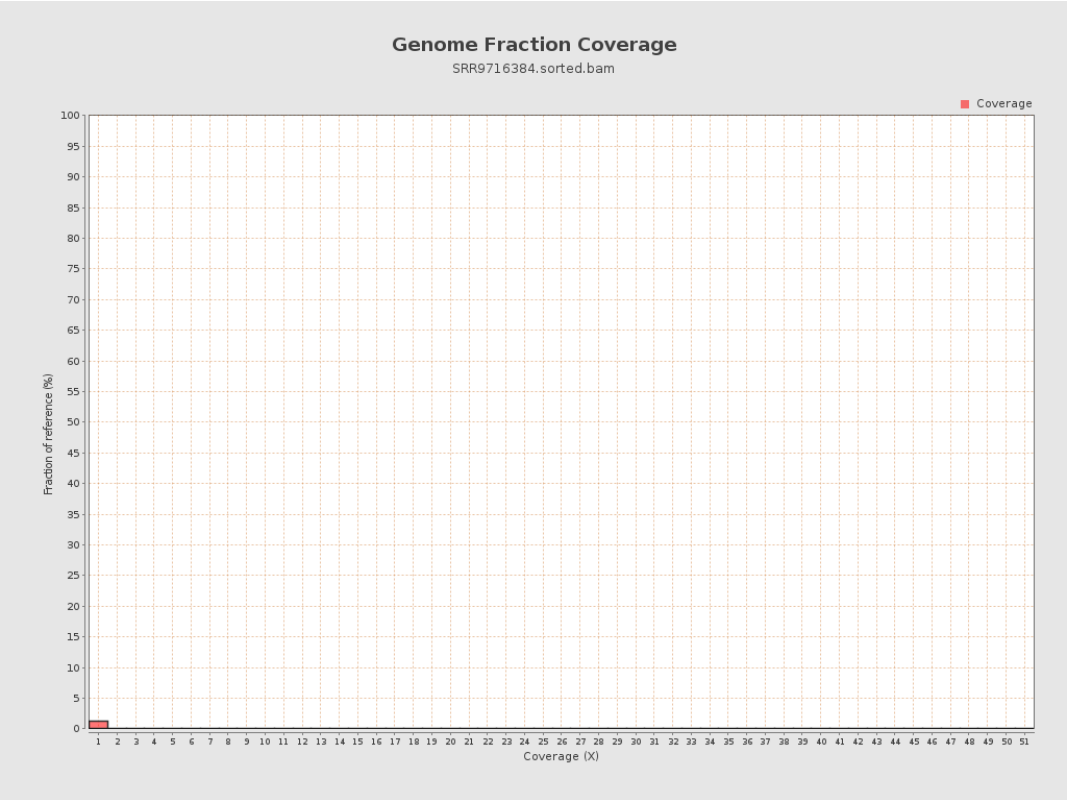
4. Results : Coverage Histogram



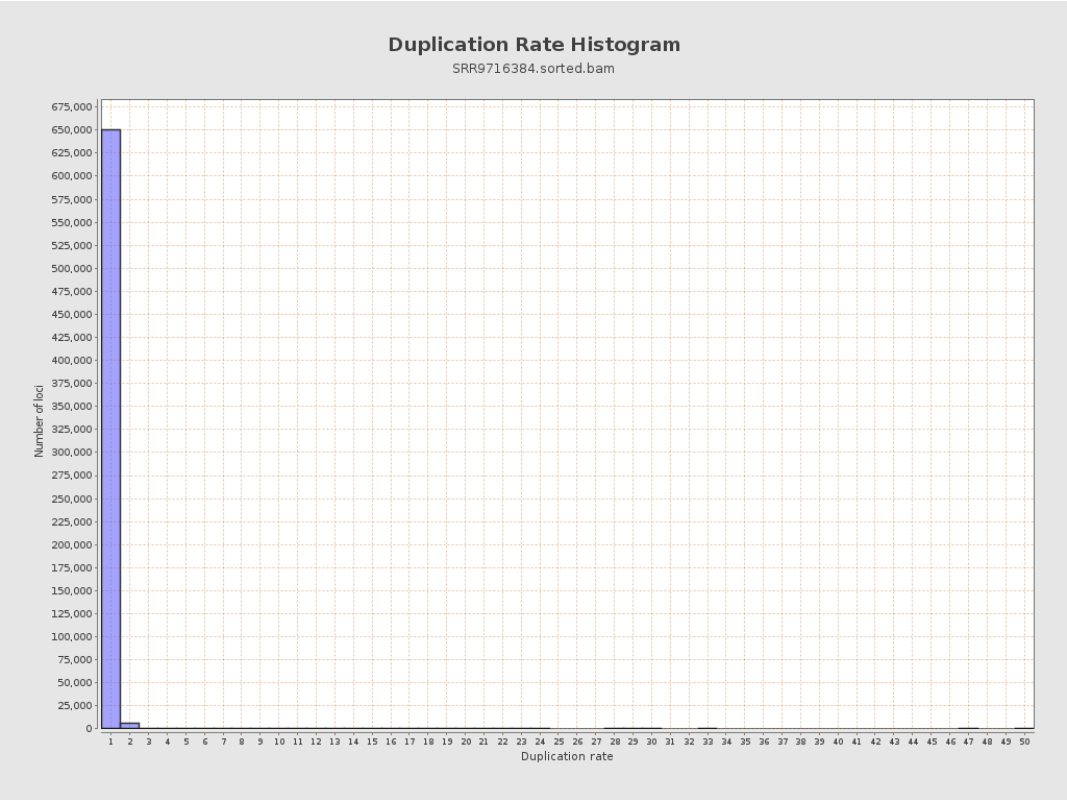
5. Results : Coverage Histogram (0-50X)



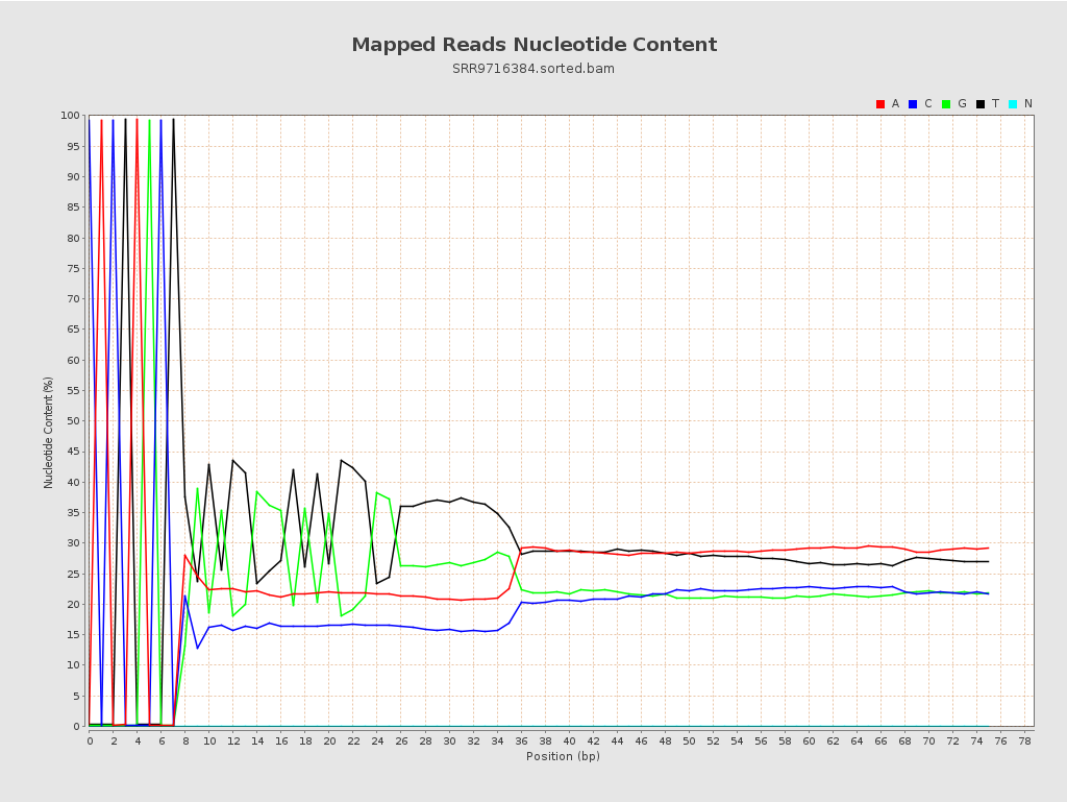
6. Results : Genome Fraction Coverage



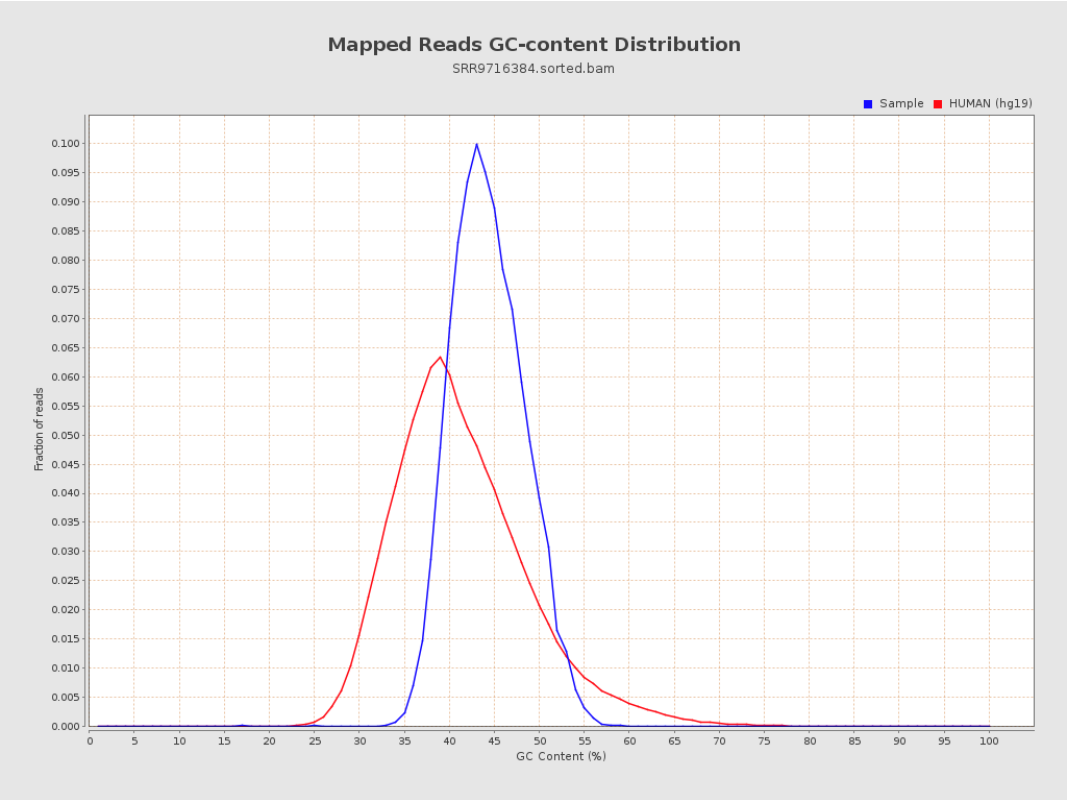
7. Results : Duplication Rate Histogram



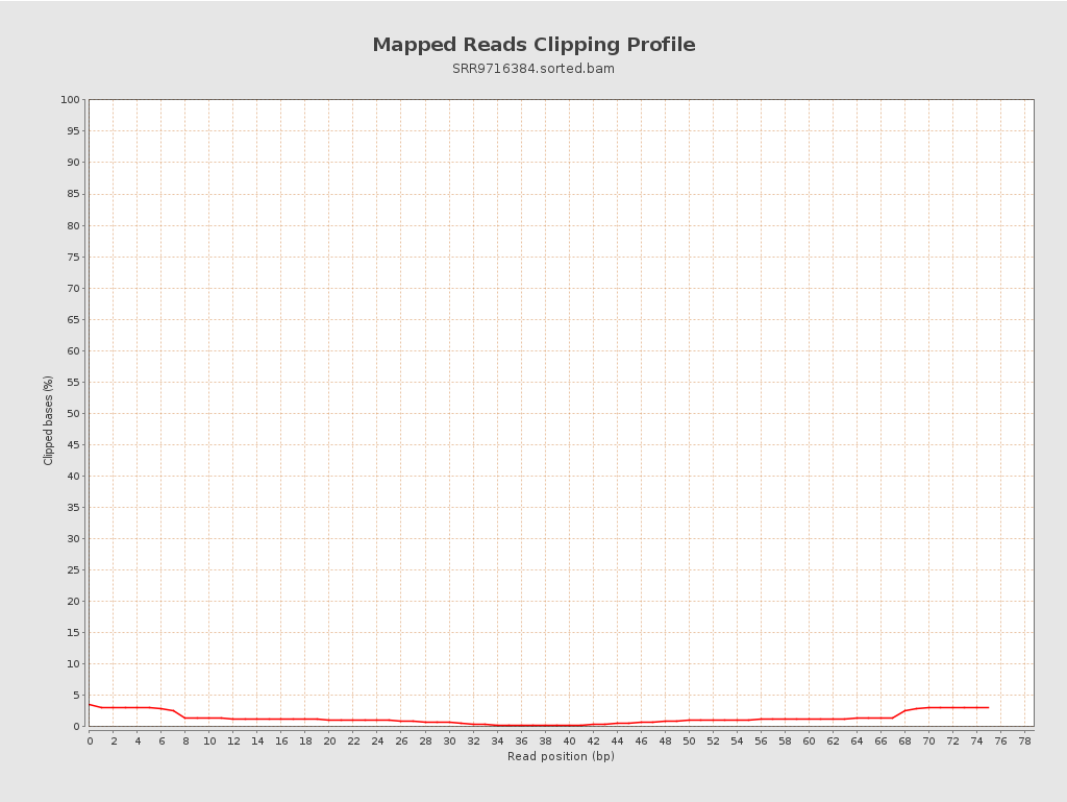
8. Results : Mapped Reads Nucleotide Content



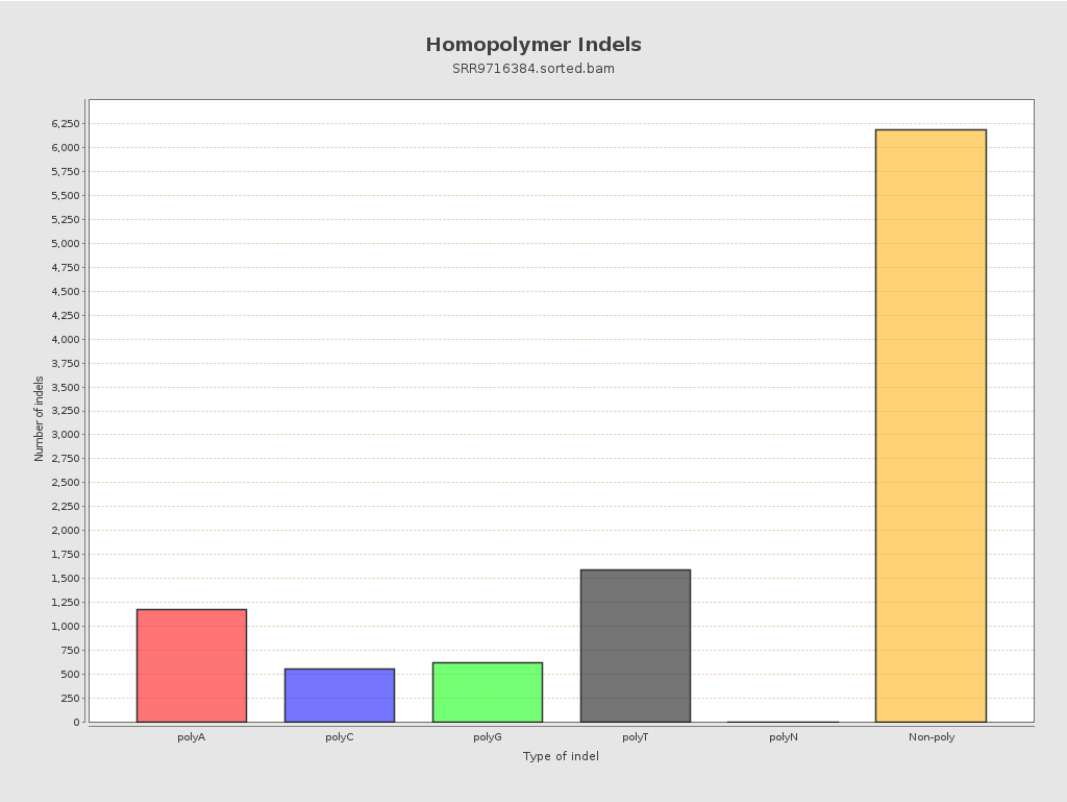
9. Results : Mapped Reads GC-content Distribution



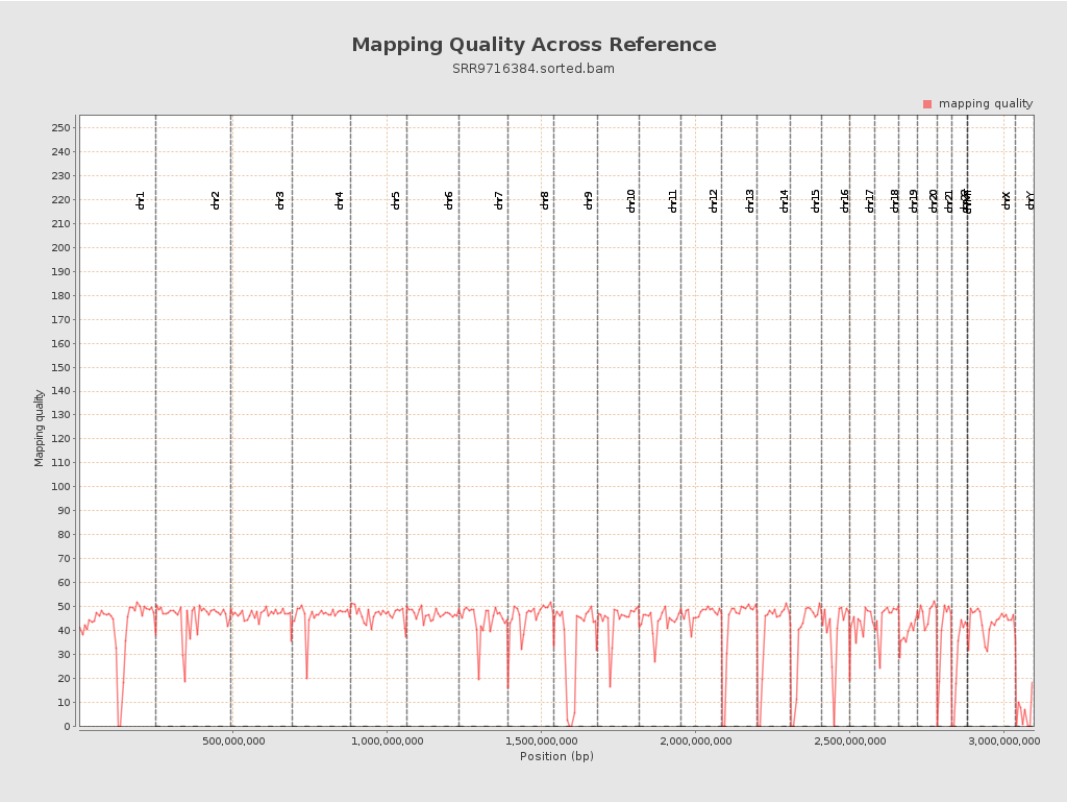
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram