Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 08:35:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716717.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_SRR9716717 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716717.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 08:35:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716717.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	552,830
Mapped reads	521,772 / 94.38%
Unmapped reads	31,058 / 5.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,963 / 1.98%
Read min/max/mean length	30 / 101 / 101.72
Duplicated reads (estimated)	12,875 / 2.33%
Duplication rate	1.93%
Clipped reads	532,313 / 96.29%

2.2. ACGT Content

Number/percentage of A's	9,824,514 / 24.23%
Number/percentage of C's	8,089,139 / 19.95%
Number/percentage of T's	12,332,154 / 30.41%
Number/percentage of G's	10,301,367 / 25.4%
Number/percentage of N's	1,481 / 0%
GC Percentage	45.35%

2.3. Coverage

Mean	0.0131

Standard Deviation	0.1493

2.4. Mapping Quality

Mean Mapping Quality	46.03

2.5. Mismatches and indels

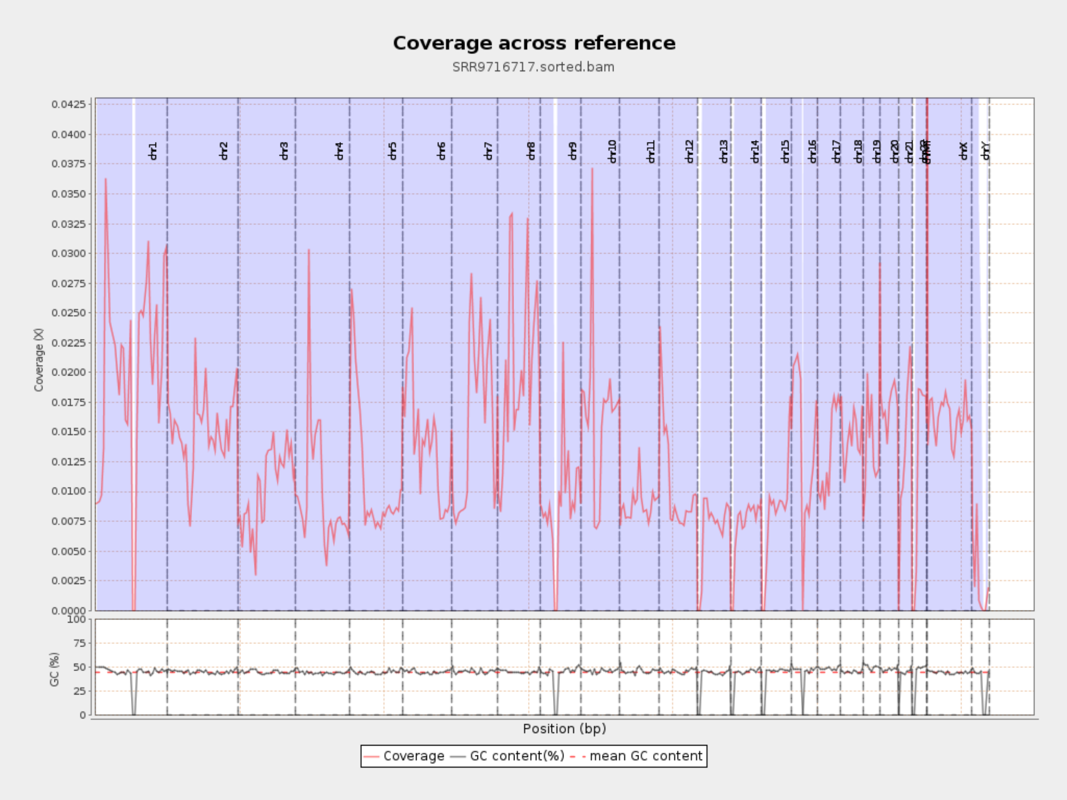
General error rate	0.67%
Mismatches	264,879
Insertions	3,205
Mapped reads with at least one insertion	0.6%
Deletions	7,442
Mapped reads with at least one deletion	1.4%
Homopolymer indels	39.16%

2.6. Chromosome stats

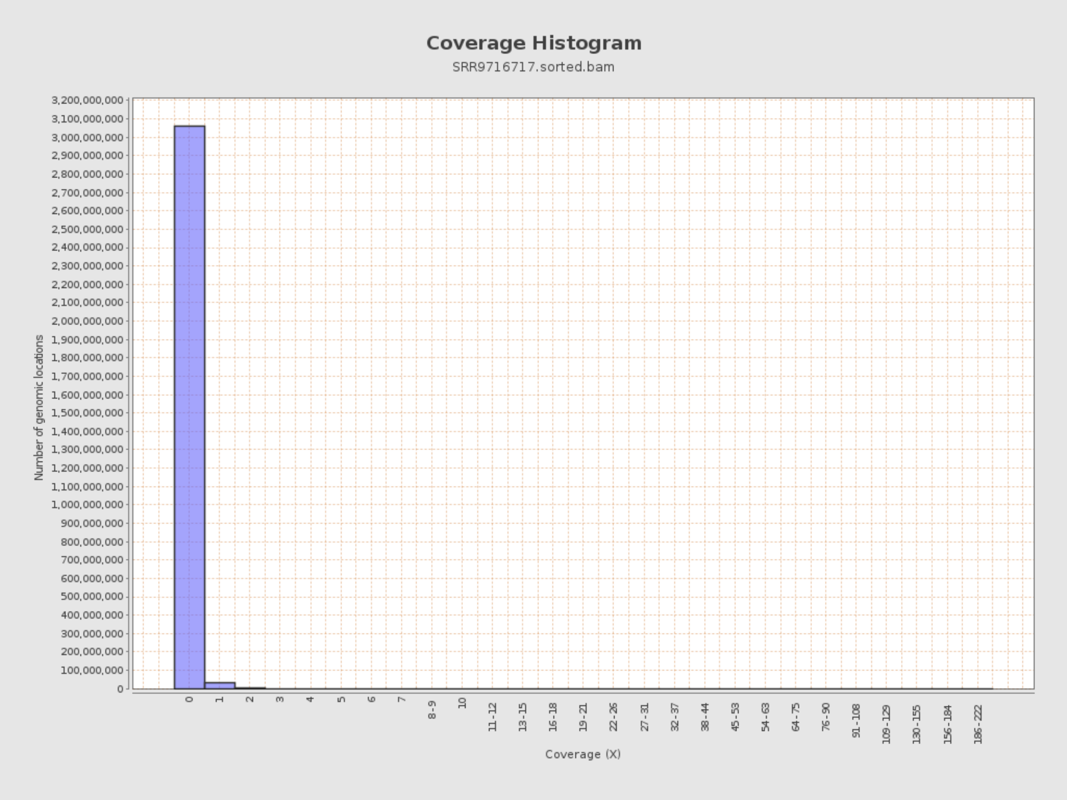
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5098350	0.0205	0.2455
chr2	243199373	3696602	0.0152	0.1603
chr3	198022430	2046947	0.0103	0.1081
chr4	191154276	1878705	0.0098	0.1324
chr5	180915260	2050586	0.0113	0.1138
chr6	171115067	2422321	0.0142	0.1302
chr7	159138663	2509479	0.0158	0.1788

chr8	146364022	2971802	0.0203	0.1869
chr9	141213431	1262434	0.0089	0.1121
chr10	135534747	2284618	0.0169	0.2006
chr11	135006516	1212255	0.009	0.1177
chr12	133851895	1450399	0.0108	0.1104
chr13	115169878	776142	0.0067	0.0865
chr14	107349540	744083	0.0069	0.0905
chr15	102531392	831372	0.0081	0.0951
chr16	90354753	1223861	0.0135	0.1273
chr17	81195210	1072890	0.0132	0.1294
chr18	78077248	1142169	0.0146	0.1621
chr19	59128983	844398	0.0143	0.179
chr20	63025520	1086309	0.0172	0.1445
chr21	48129895	665827	0.0138	0.1338
chr22	51304566	626216	0.0122	0.1195
chrMT	16571	3401	0.2052	0.5158
chrX	155270560	2520351	0.0162	0.1379
chrY	59373566	142893	0.0024	0.0929

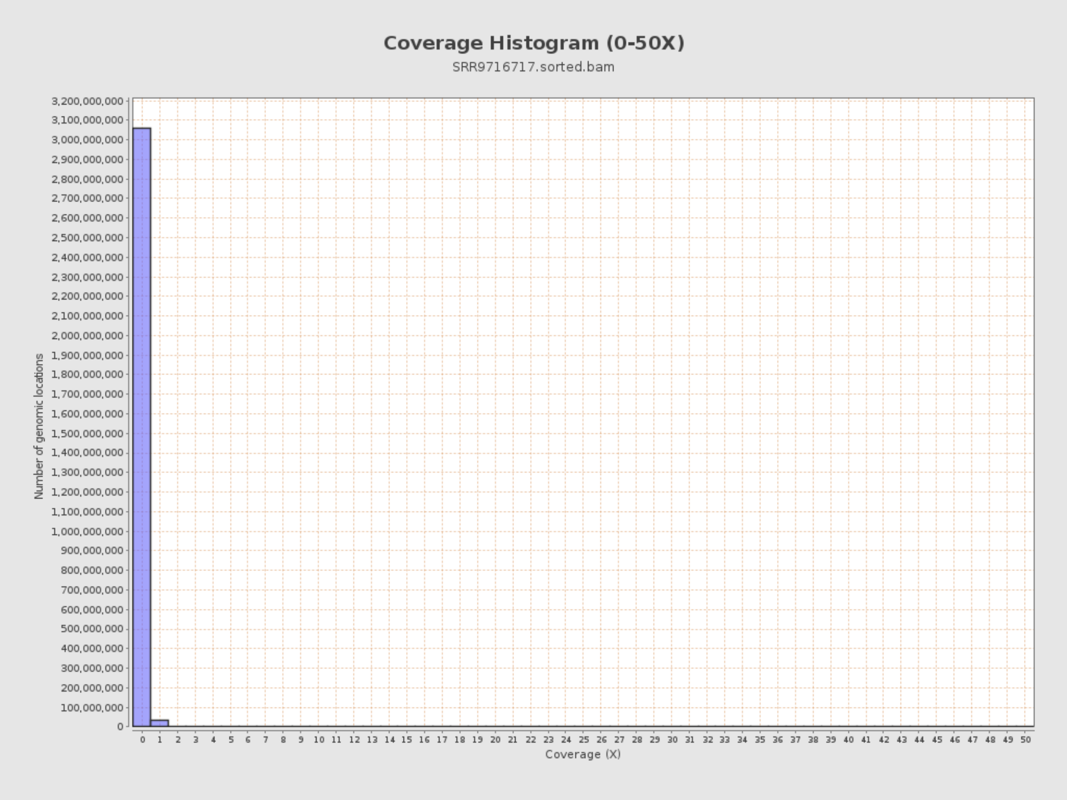
3. Results : Coverage across reference



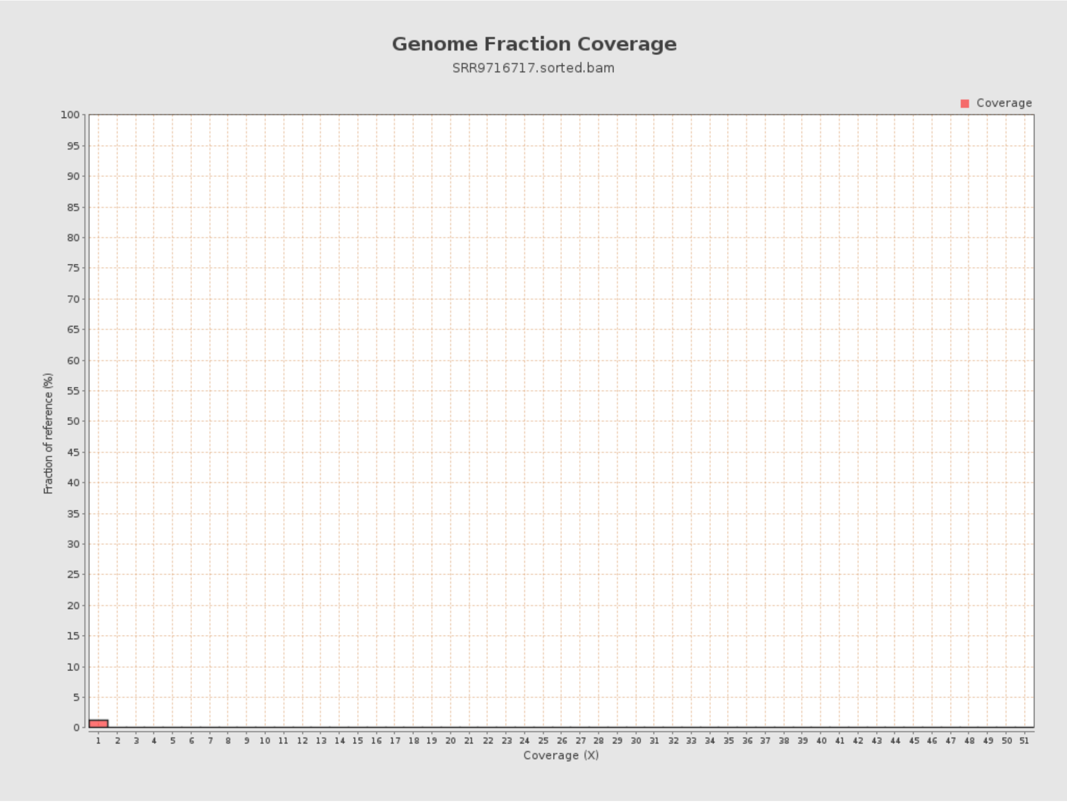
4. Results : Coverage Histogram



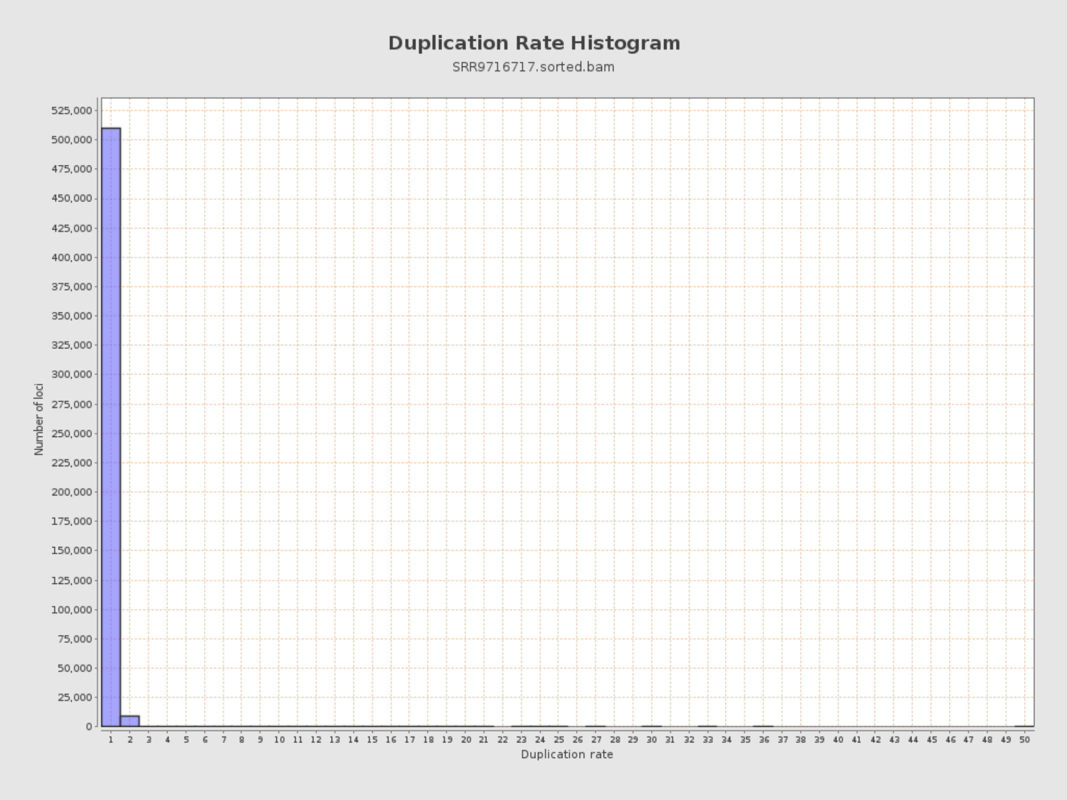
5. Results : Coverage Histogram (0-50X)



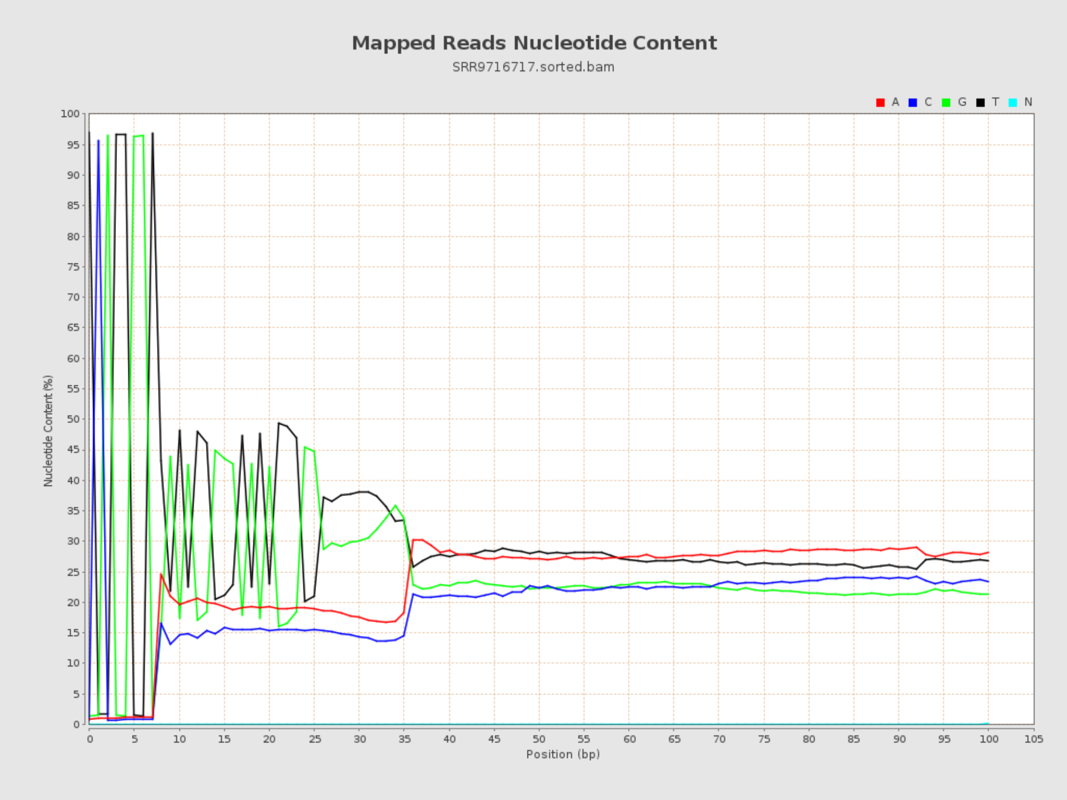
6. Results : Genome Fraction Coverage



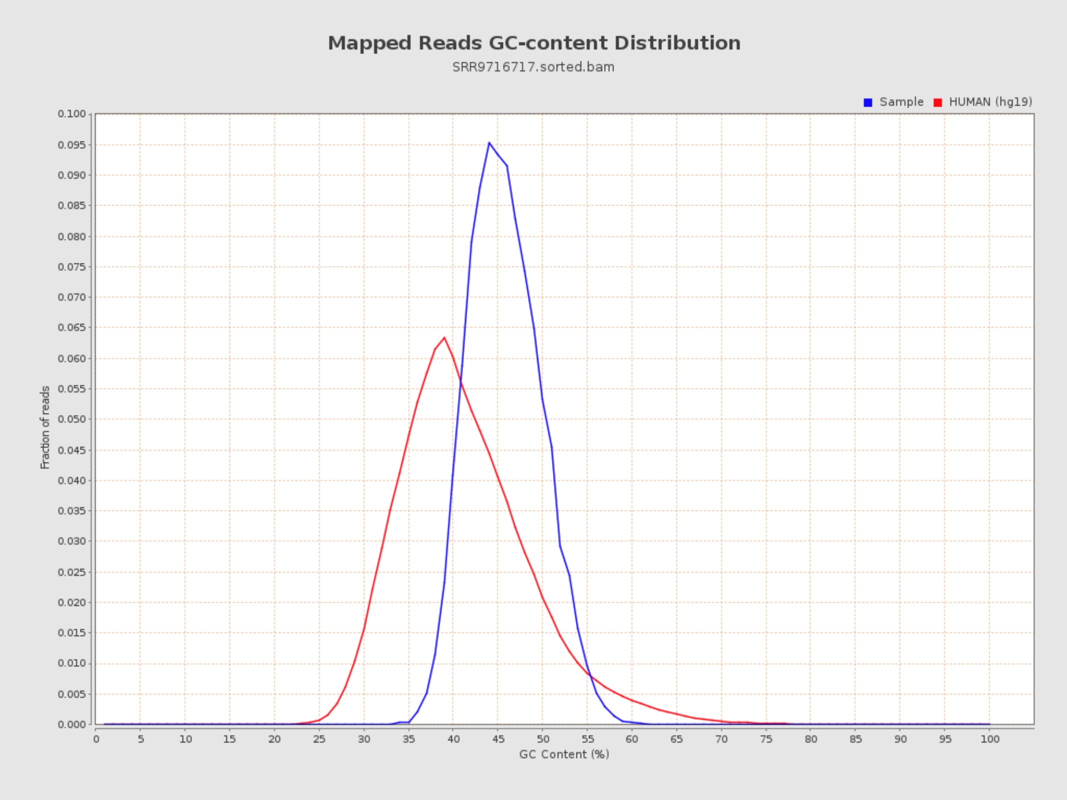
7. Results : Duplication Rate Histogram



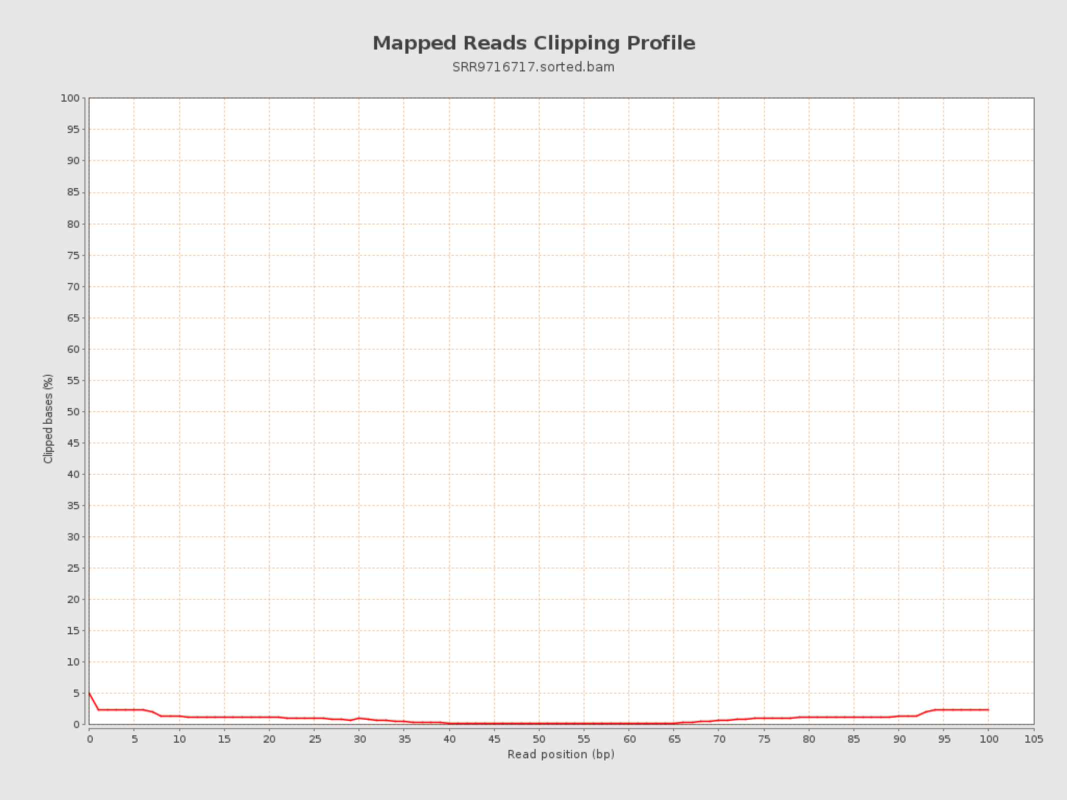
8. Results : Mapped Reads Nucleotide Content



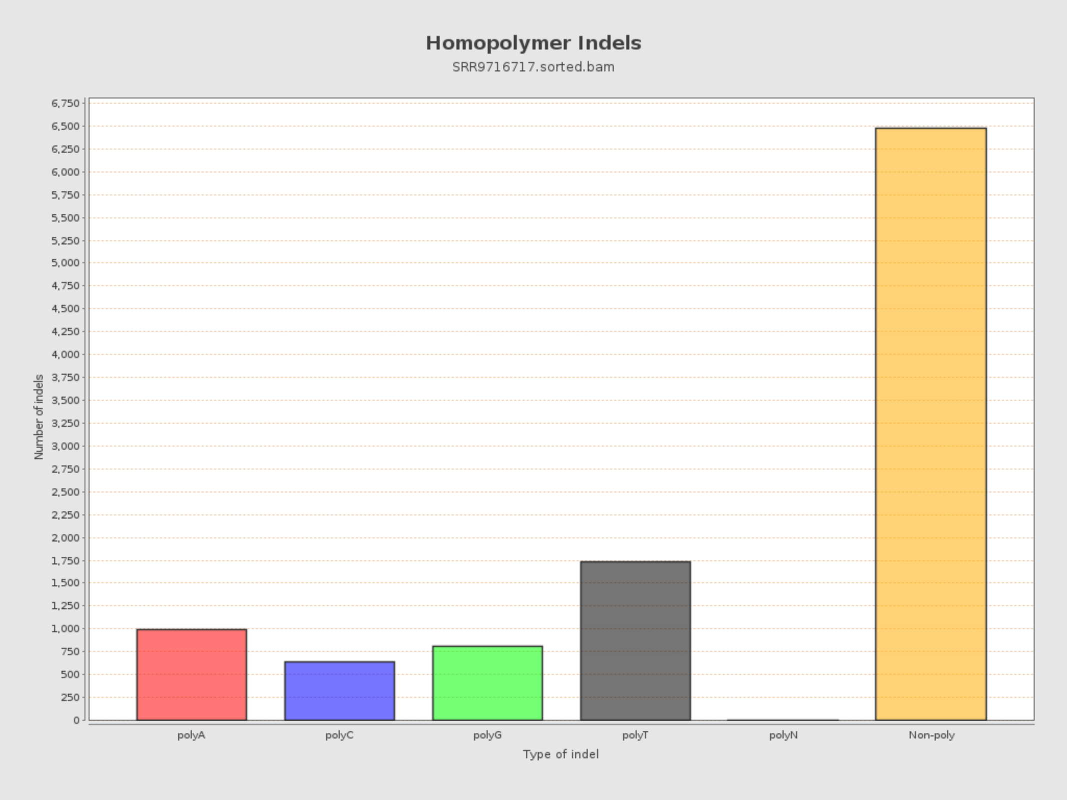
9. Results : Mapped Reads GC-content Distribution



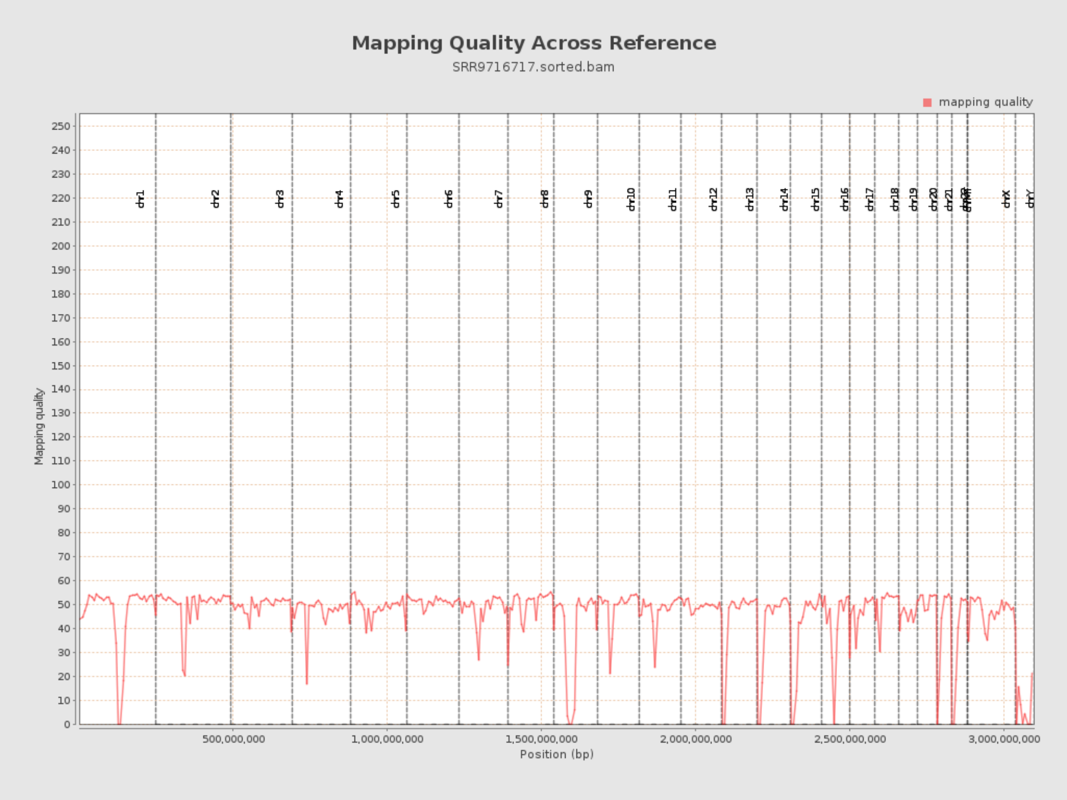
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram