Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 18:14:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716105.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_SRR9716105 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716105.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 18:14:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716105.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	767,801
Mapped reads	695,608 / 90.6%
Unmapped reads	72,193 / 9.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,293 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	15,238 / 1.98%
Duplication rate	1.45%
Clipped reads	696,159 / 90.67%

2.2. ACGT Content

Number/percentage of A's	9,359,792 / 23.56%
Number/percentage of C's	6,880,128 / 17.32%
Number/percentage of T's	13,337,173 / 33.57%
Number/percentage of G's	10,153,934 / 25.56%
Number/percentage of N's	787 / 0%
GC Percentage	42.87%

2.3. Coverage

Mean	0.0128

Standard Deviation	0.1528

2.4. Mapping Quality

Mean Mapping Quality	43

2.5. Mismatches and indels

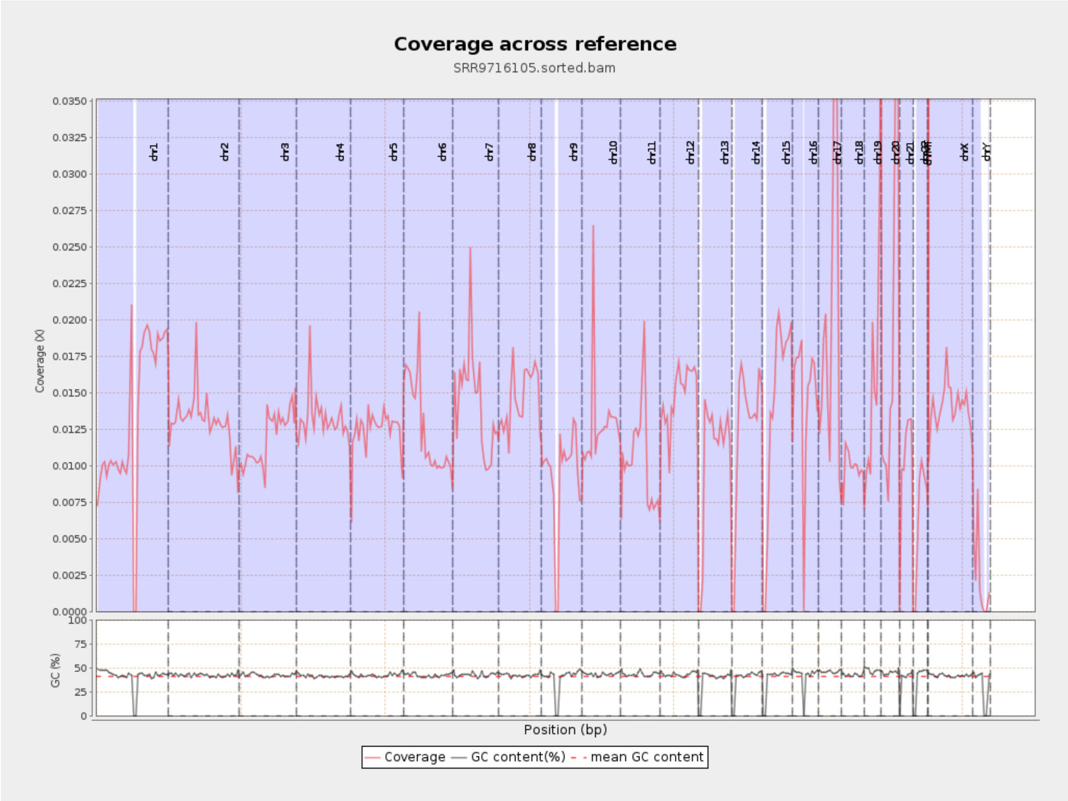
General error rate	0.54%
Mismatches	208,456
Insertions	2,756
Mapped reads with at least one insertion	0.39%
Deletions	7,611
Mapped reads with at least one deletion	1.09%
Homopolymer indels	43.19%

2.6. Chromosome stats

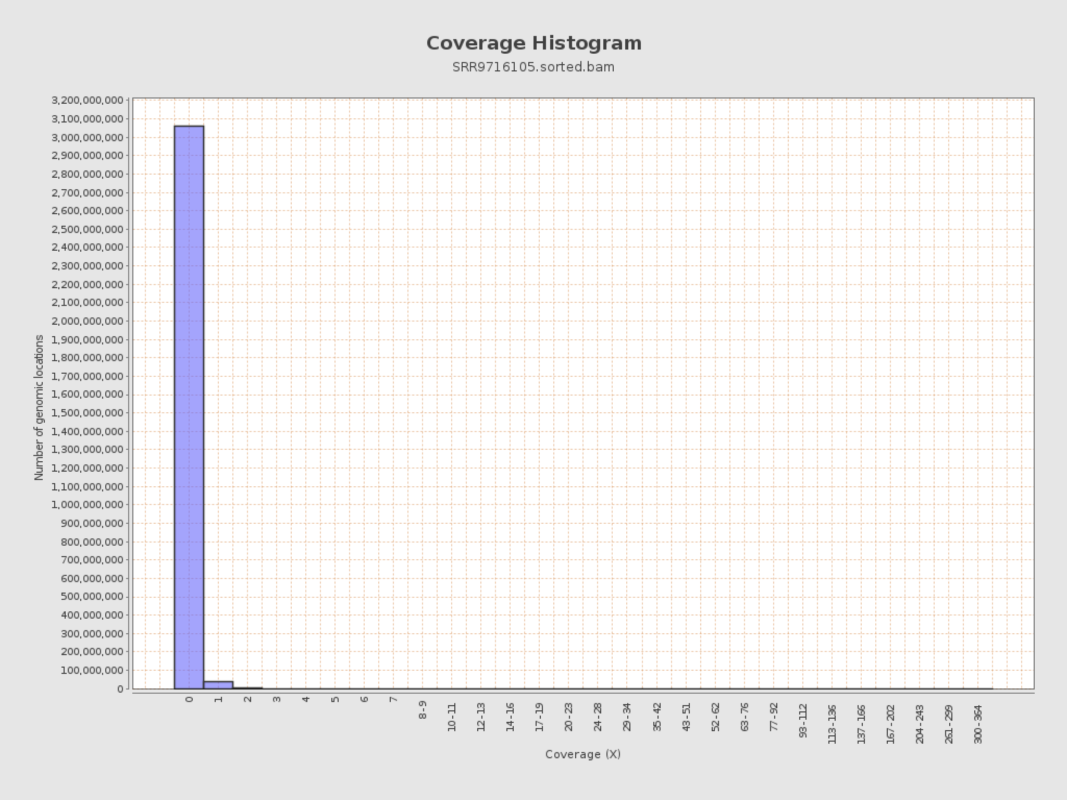
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3300184	0.0132	0.2315
chr2	243199373	3170969	0.013	0.1934
chr3	198022430	2343030	0.0118	0.1146
chr4	191154276	2520924	0.0132	0.1251
chr5	180915260	2279005	0.0126	0.1171
chr6	171115067	2150455	0.0126	0.1306
chr7	159138663	2282208	0.0143	0.2

chr8	146364022	2148930	0.0147	0.1839
chr9	141213431	1314132	0.0093	0.1142
chr10	135534747	1745088	0.0129	0.162
chr11	135006516	1420910	0.0105	0.1236
chr12	133851895	1978430	0.0148	0.127
chr13	115169878	1210278	0.0105	0.107
chr14	107349540	1335344	0.0124	0.1173
chr15	102531392	1448186	0.0141	0.1246
chr16	90354753	1312368	0.0145	0.1307
chr17	81195210	1661953	0.0205	0.1514
chr18	78077248	765931	0.0098	0.1716
chr19	59128983	966733	0.0163	0.1978
chr20	63025520	1225721	0.0194	0.148
chr21	48129895	499086	0.0104	0.1118
chr22	51304566	338603	0.0066	0.0845
chrMT	16571	6997	0.4222	0.712
chrX	155270560	2186157	0.0141	0.1309
chrY	59373566	132293	0.0022	0.0861

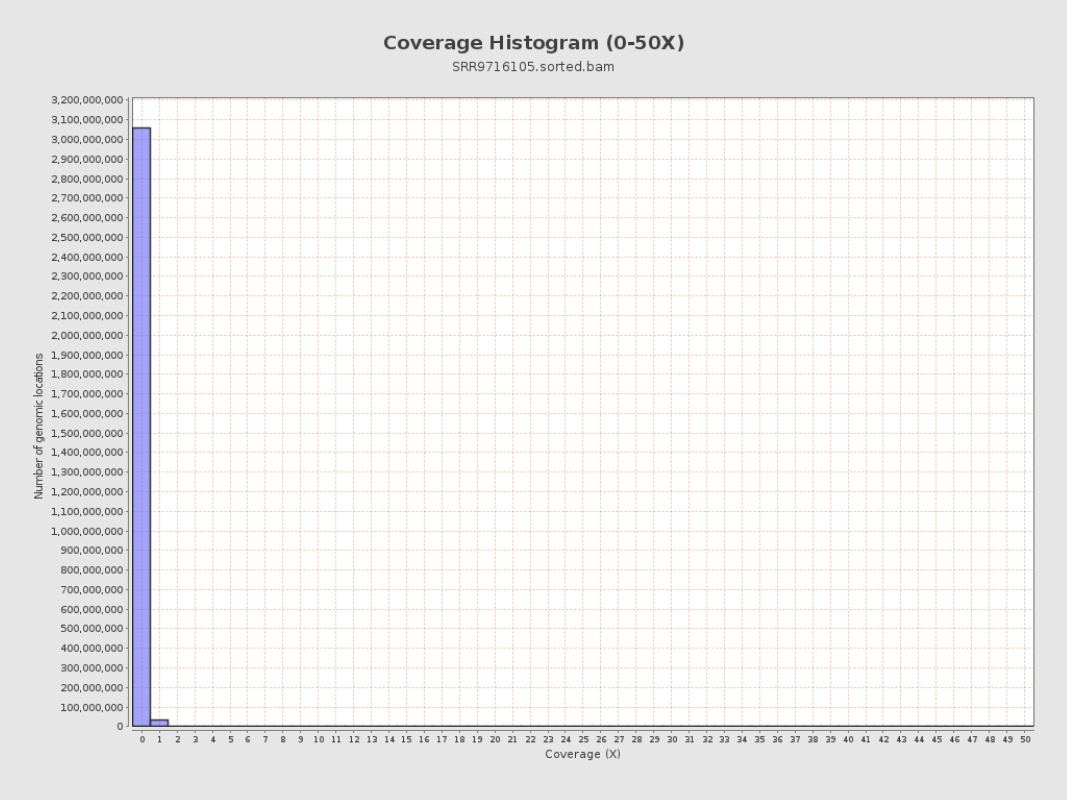
3. Results : Coverage across reference



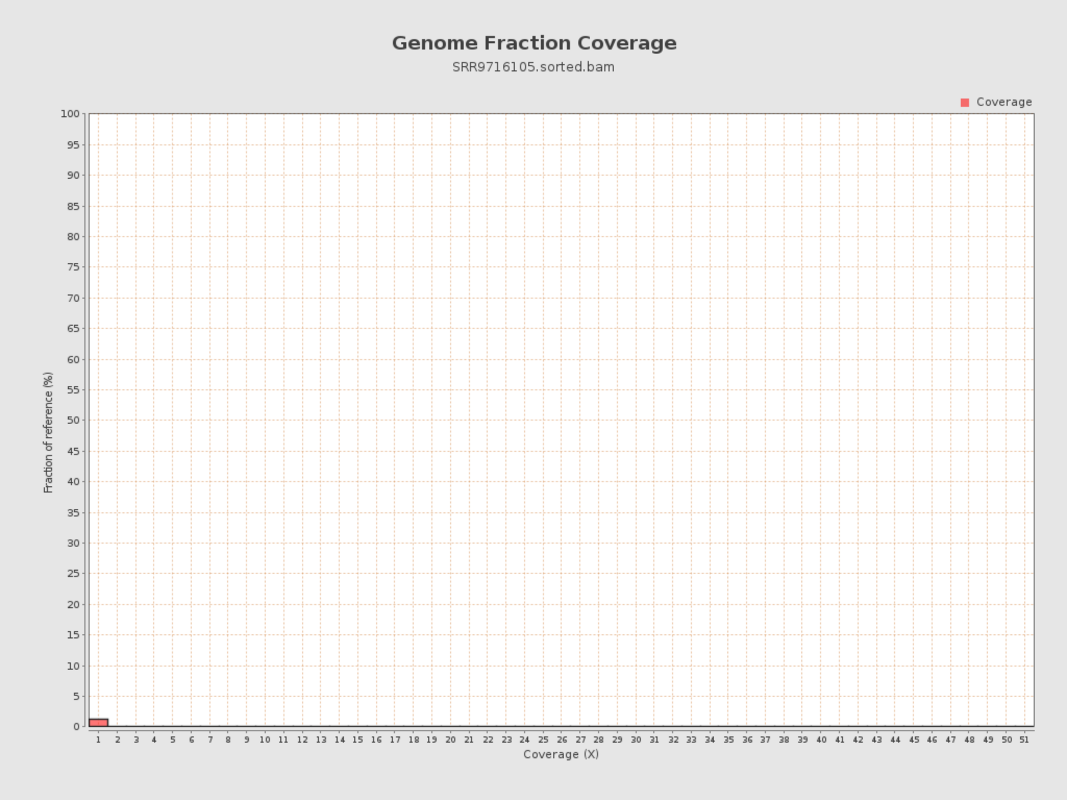
4. Results : Coverage Histogram



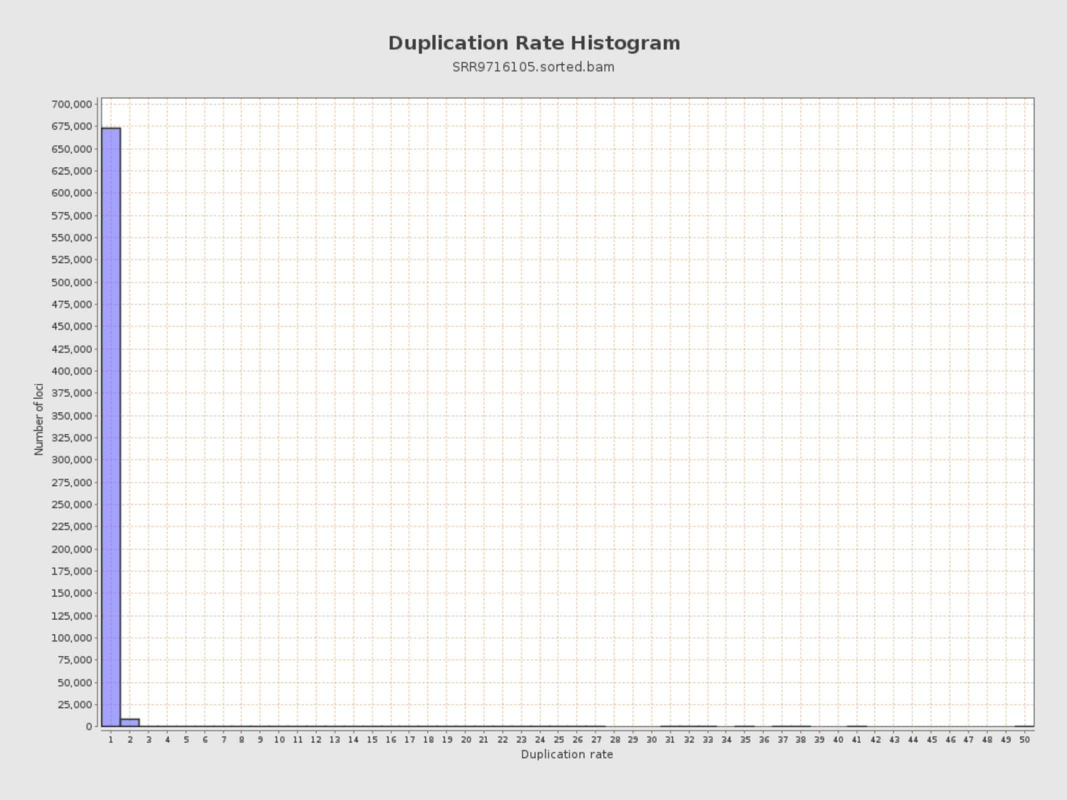
5. Results : Coverage Histogram (0-50X)



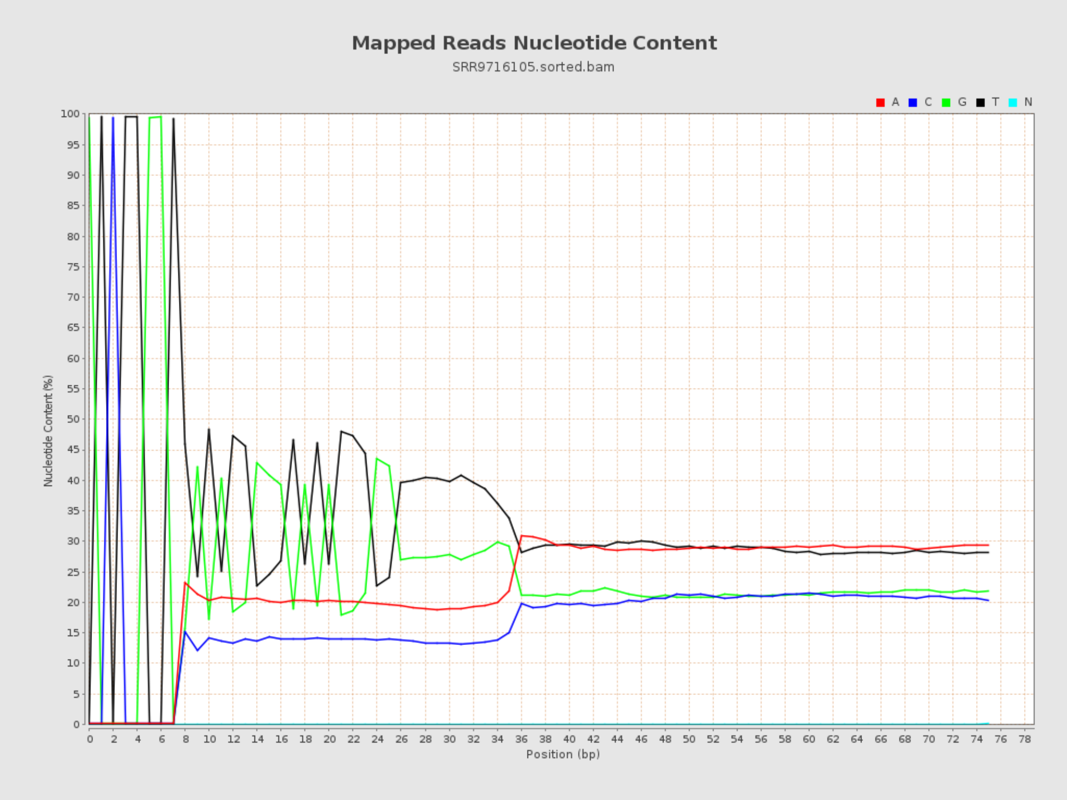
6. Results : Genome Fraction Coverage



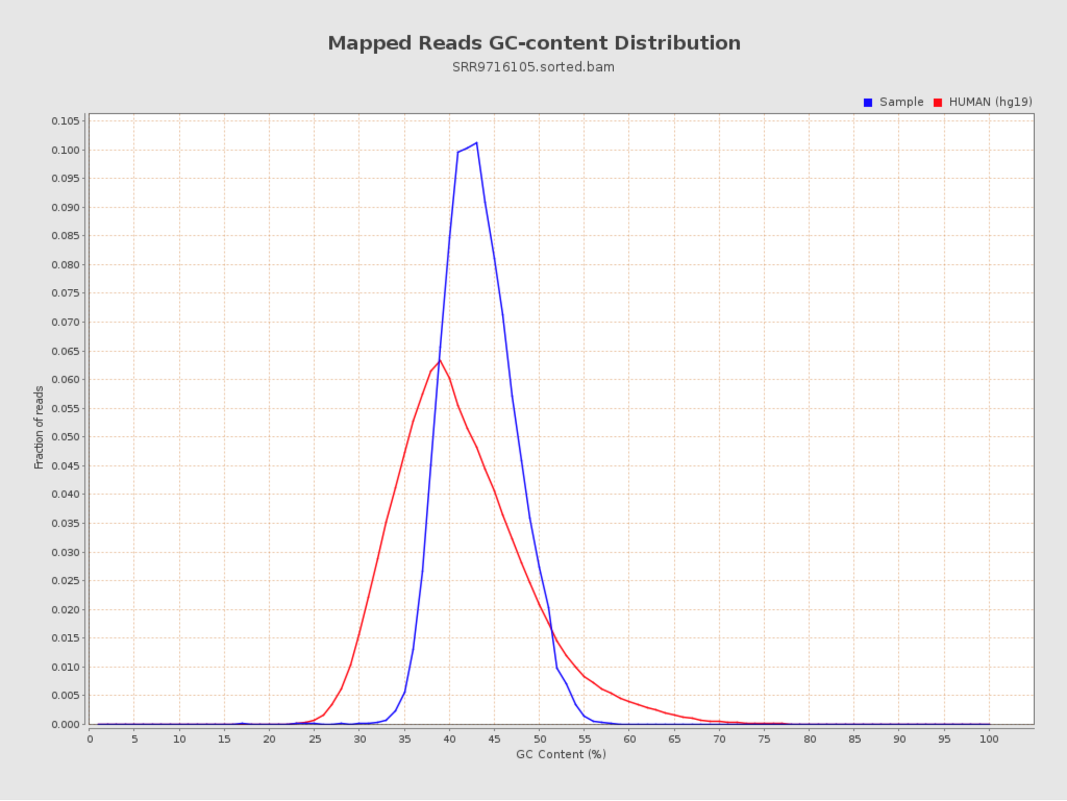
7. Results : Duplication Rate Histogram



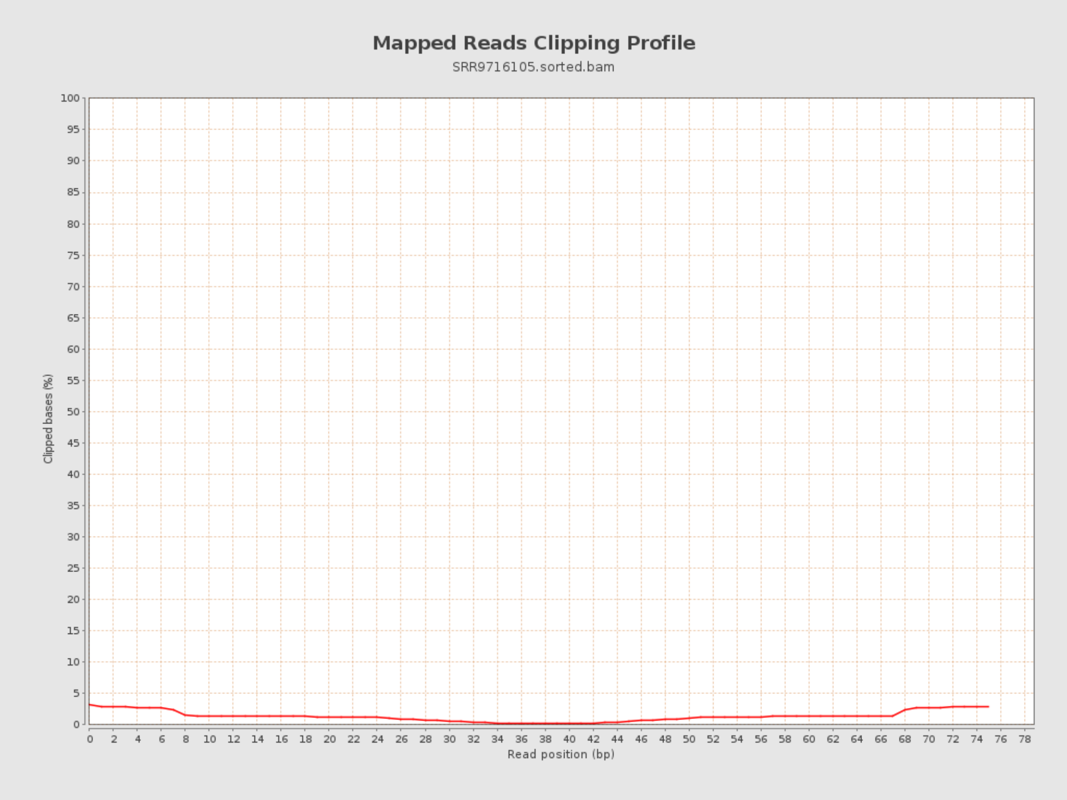
8. Results : Mapped Reads Nucleotide Content



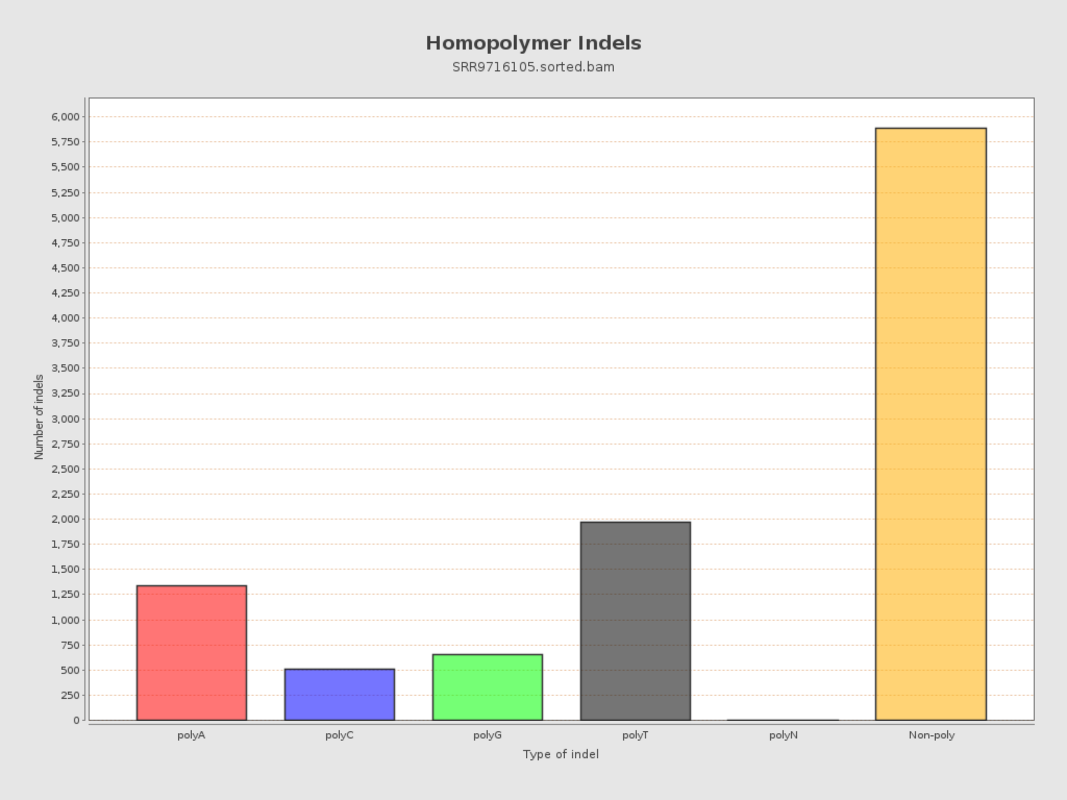
9. Results : Mapped Reads GC-content Distribution



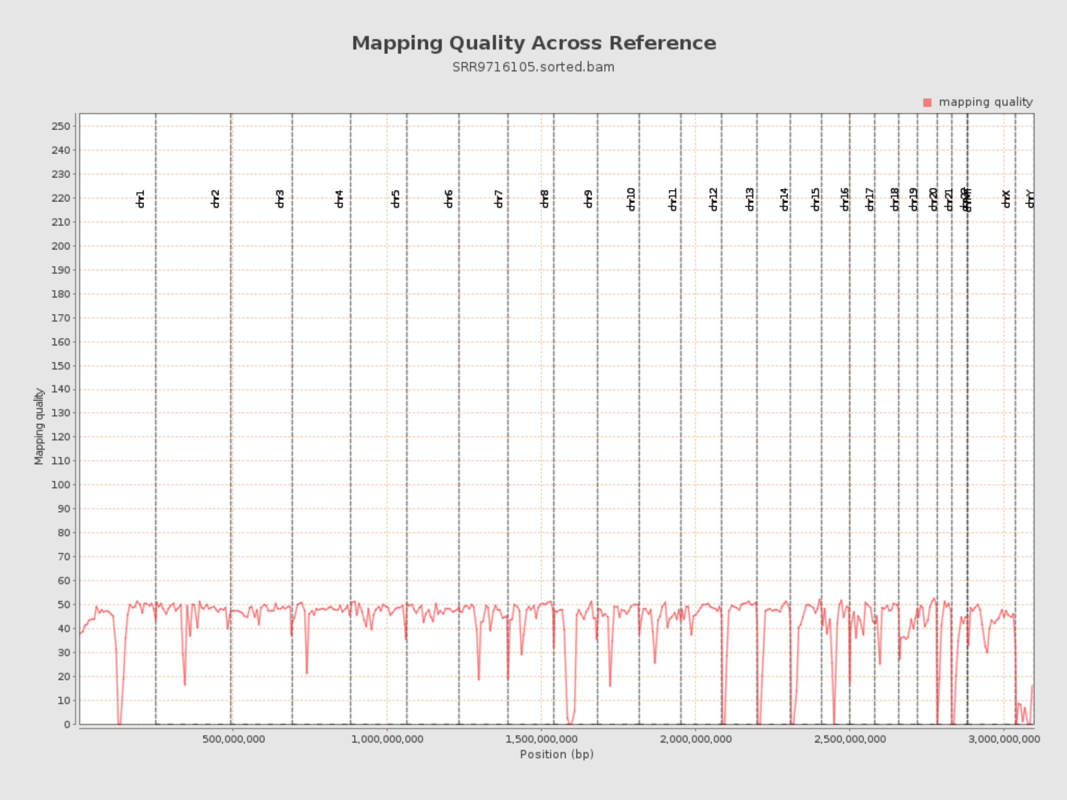
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram