Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 18:29:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716112.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_SRR9716112 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716112.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 18:29:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716112.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	716,883
Mapped reads	640,801 / 89.39%
Unmapped reads	76,082 / 10.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,506 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	9,193 / 1.28%
Duplication rate	1.02%
Clipped reads	640,898 / 89.4%

2.2. ACGT Content

Number/percentage of A's	9,547,083 / 25.75%
Number/percentage of C's	7,590,214 / 20.47%
Number/percentage of T's	11,331,152 / 30.56%
Number/percentage of G's	8,606,094 / 23.21%
Number/percentage of N's	305 / 0%
GC Percentage	43.69%

2.3. Coverage

Mean	0.012

Standard Deviation	0.1317

2.4. Mapping Quality

Mean Mapping Quality	42.94

2.5. Mismatches and indels

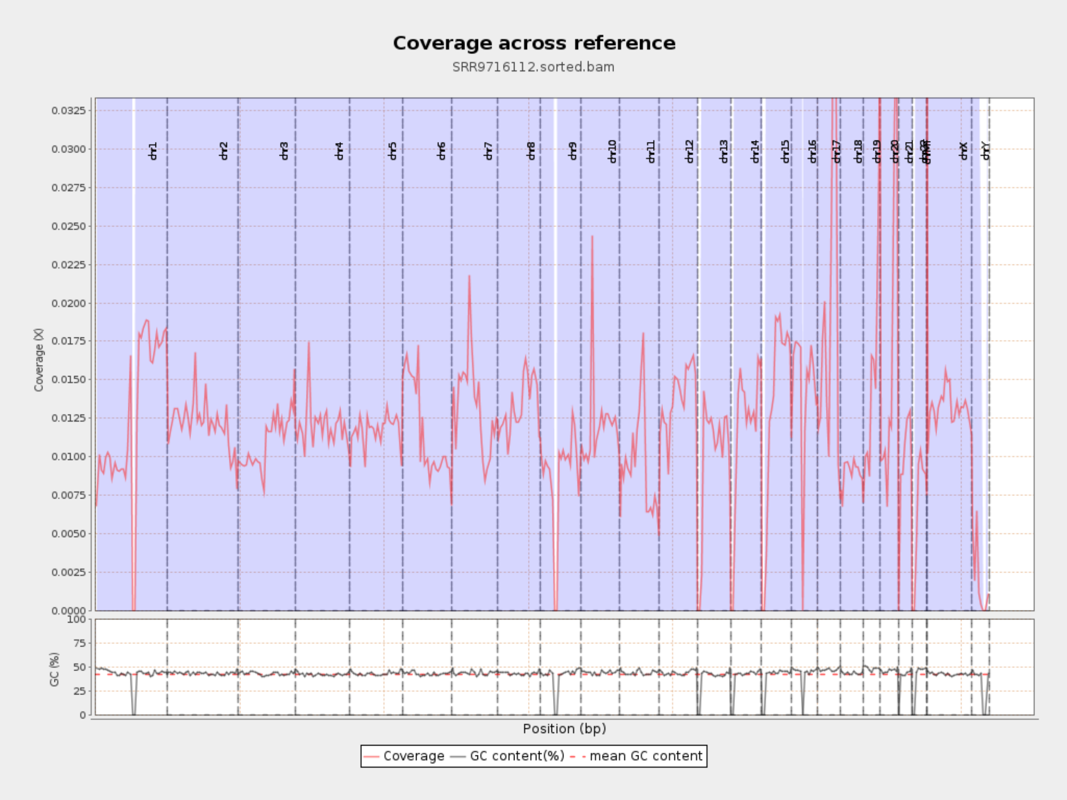
General error rate	0.52%
Mismatches	188,550
Insertions	2,950
Mapped reads with at least one insertion	0.46%
Deletions	7,296
Mapped reads with at least one deletion	1.13%
Homopolymer indels	40.72%

2.6. Chromosome stats

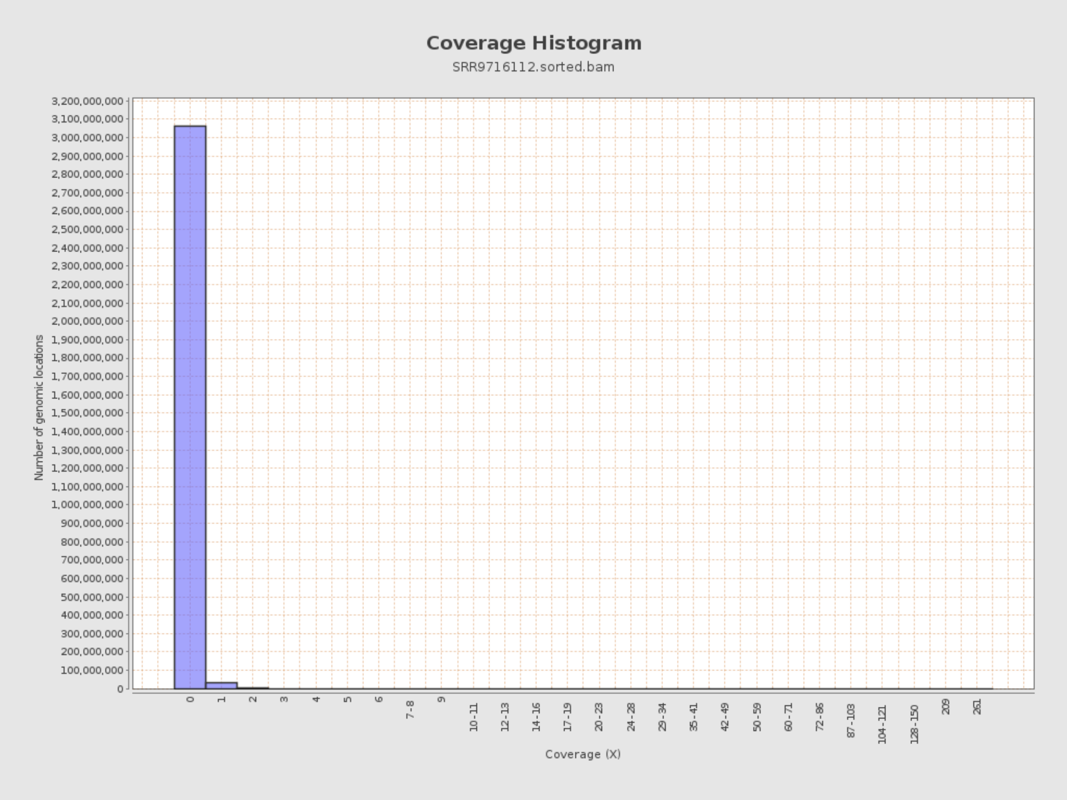
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3107276	0.0125	0.1621
chr2	243199373	2956122	0.0122	0.1593
chr3	198022430	2165947	0.0109	0.1111
chr4	191154276	2303588	0.0121	0.1165
chr5	180915260	2133764	0.0118	0.1121
chr6	171115067	2001253	0.0117	0.1199
chr7	159138663	2131389	0.0134	0.1727

chr8	146364022	1943657	0.0133	0.1343
chr9	141213431	1235785	0.0088	0.1048
chr10	135534747	1641651	0.0121	0.1578
chr11	135006516	1301402	0.0096	0.1132
chr12	133851895	1848432	0.0138	0.1215
chr13	115169878	1136611	0.0099	0.1024
chr14	107349540	1247763	0.0116	0.1134
chr15	102531392	1365215	0.0133	0.1199
chr16	90354753	1280029	0.0142	0.1275
chr17	81195210	1616369	0.0199	0.1489
chr18	78077248	700048	0.009	0.1438
chr19	59128983	921979	0.0156	0.1612
chr20	63025520	1070864	0.017	0.1372
chr21	48129895	468811	0.0097	0.1054
chr22	51304566	340949	0.0066	0.0846
chrMT	16571	1027	0.062	0.2411
chrX	155270560	2052848	0.0132	0.1219
chrY	59373566	113599	0.0019	0.0653

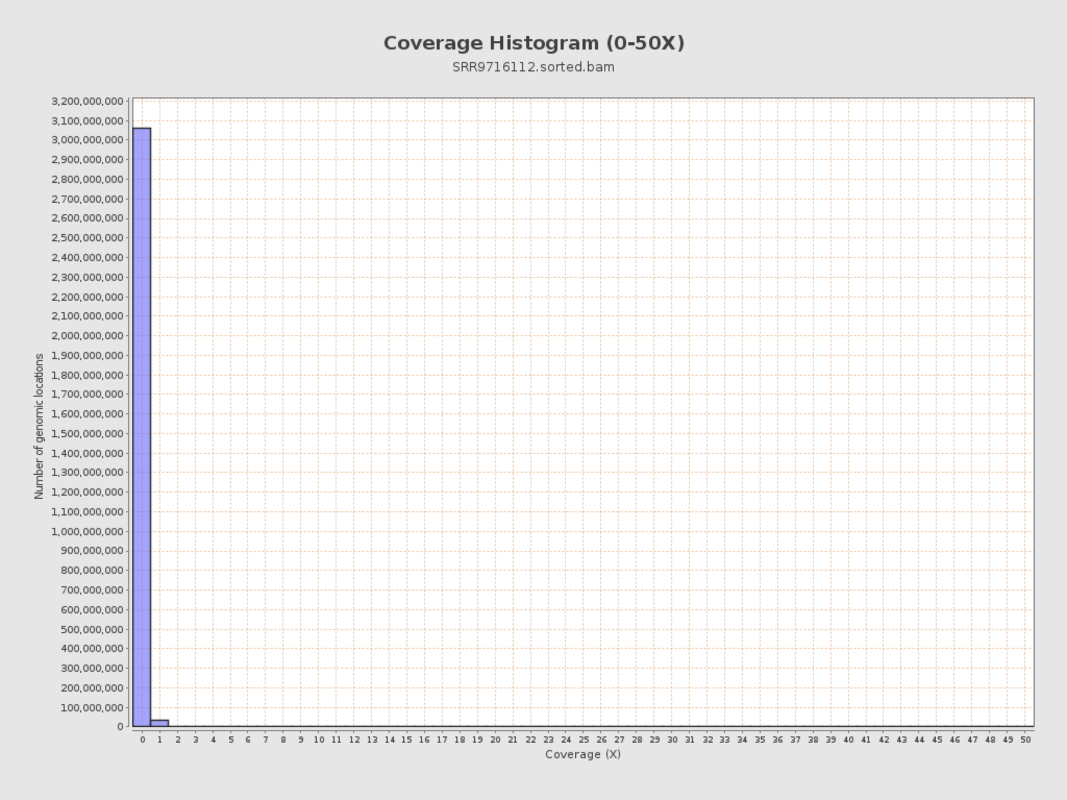
3. Results : Coverage across reference



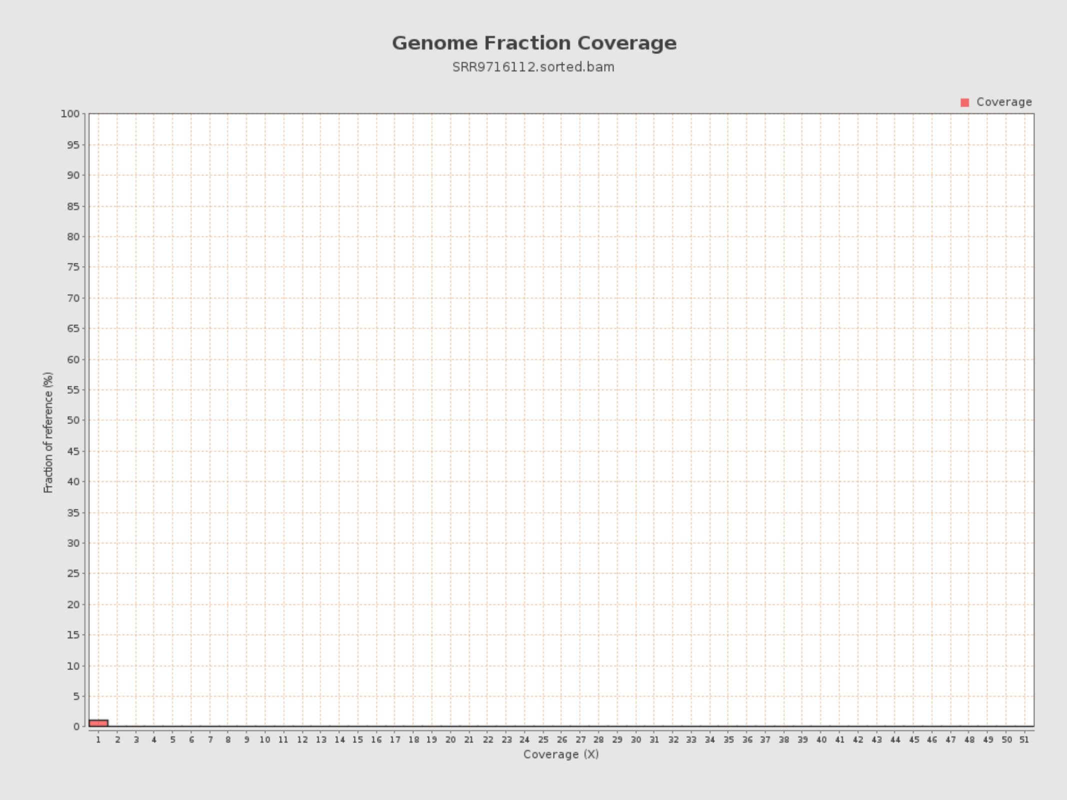
4. Results : Coverage Histogram



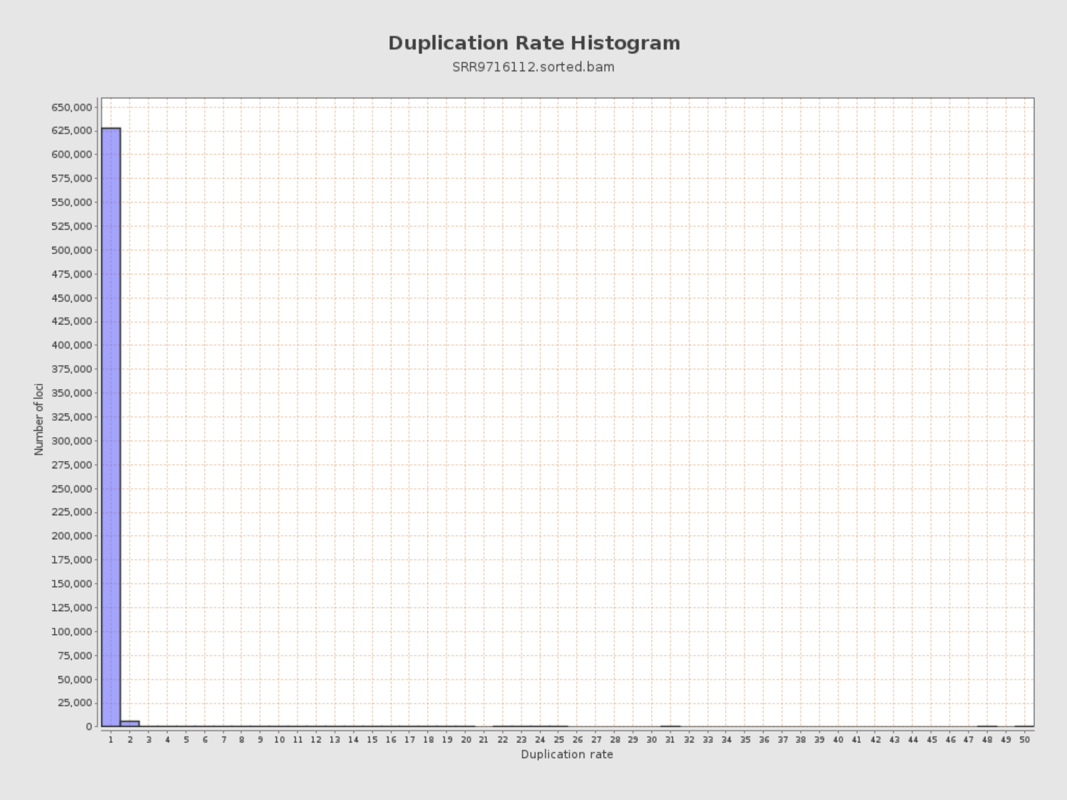
5. Results : Coverage Histogram (0-50X)



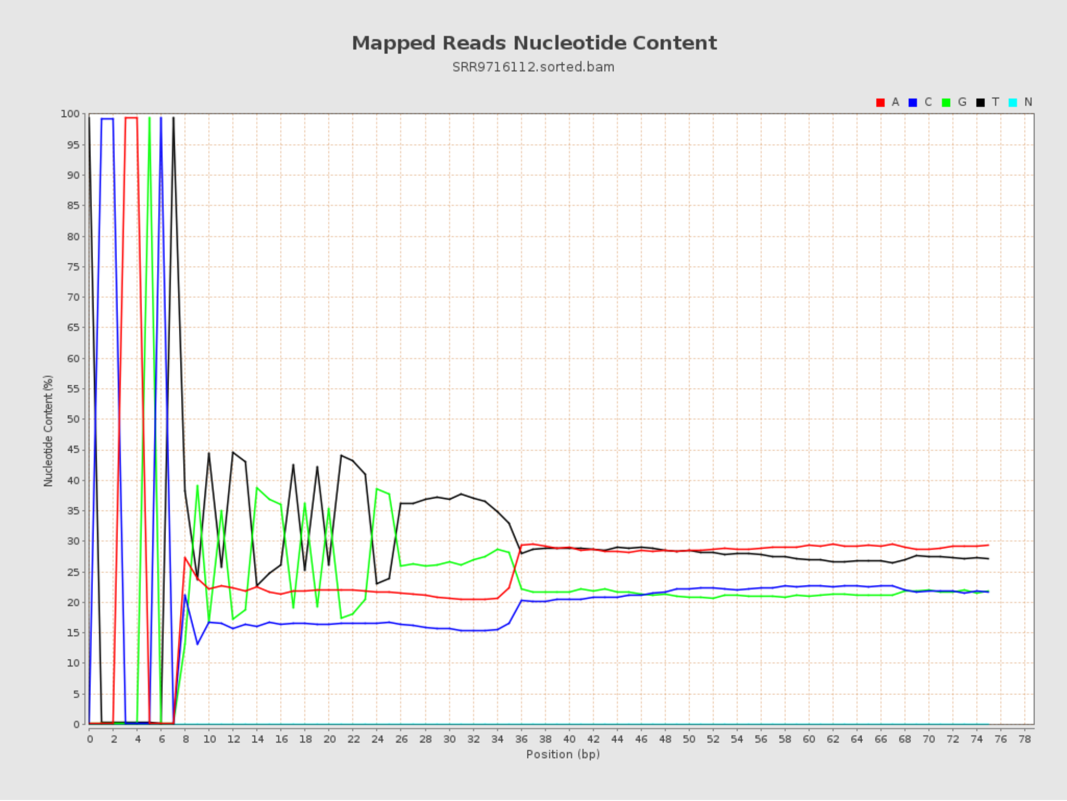
6. Results : Genome Fraction Coverage



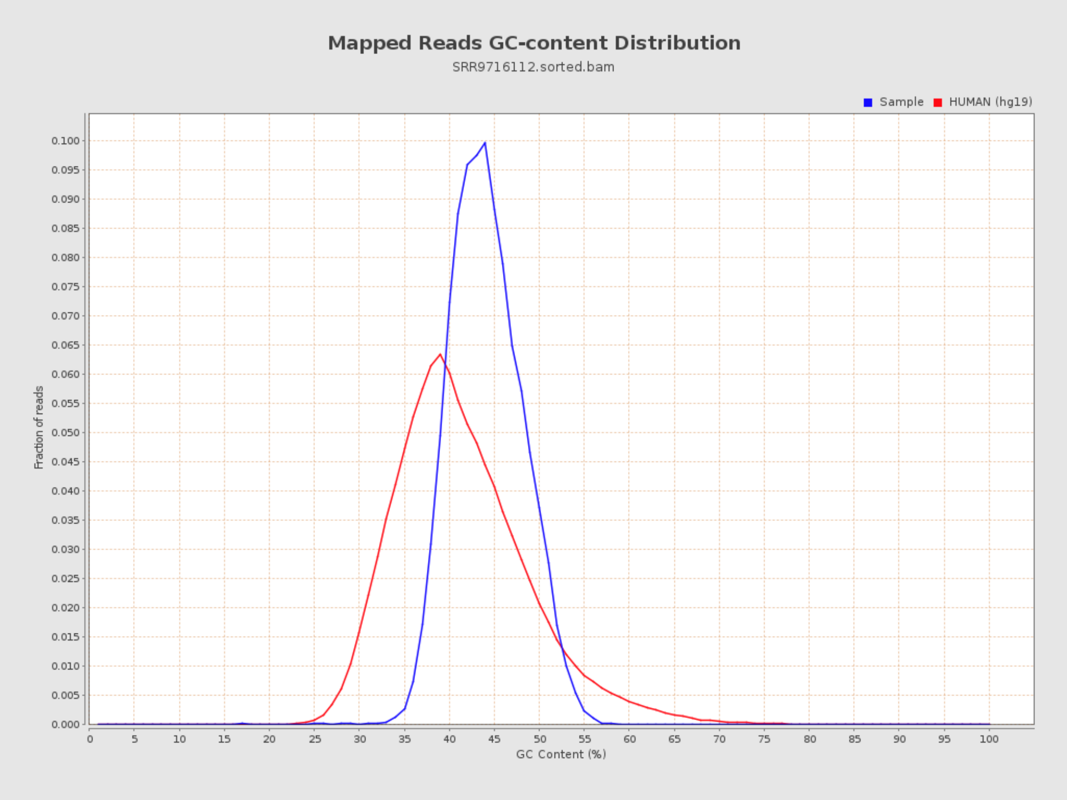
7. Results : Duplication Rate Histogram



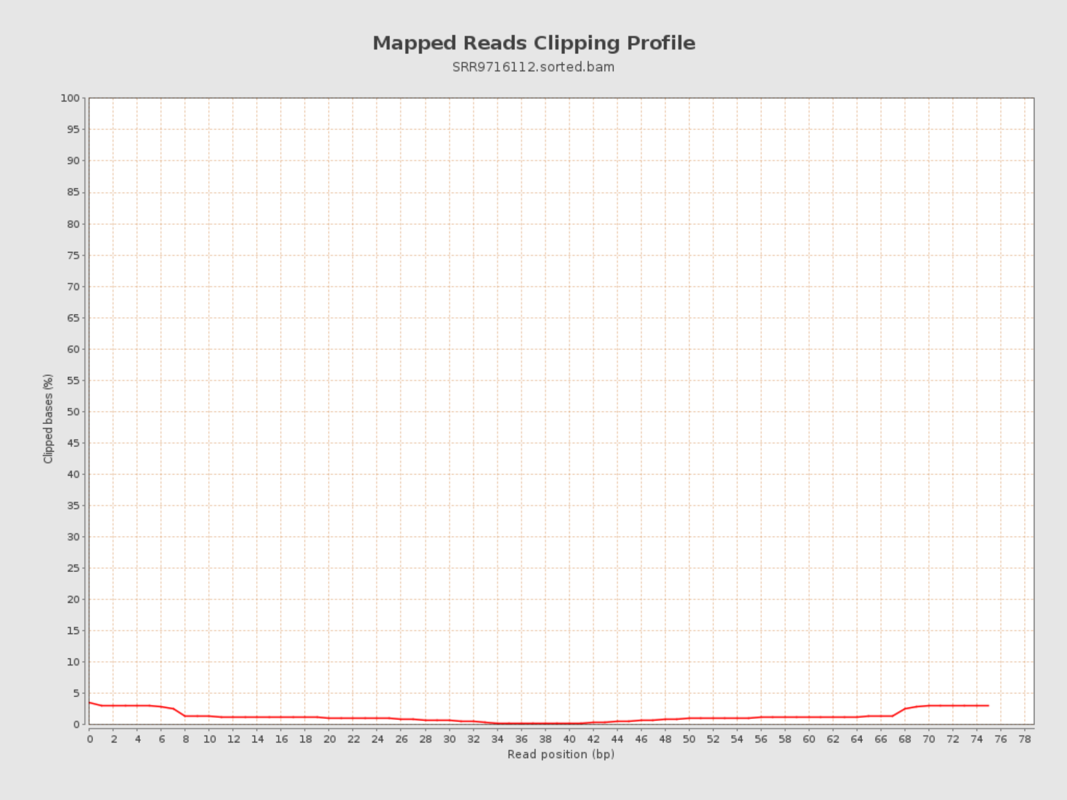
8. Results : Mapped Reads Nucleotide Content



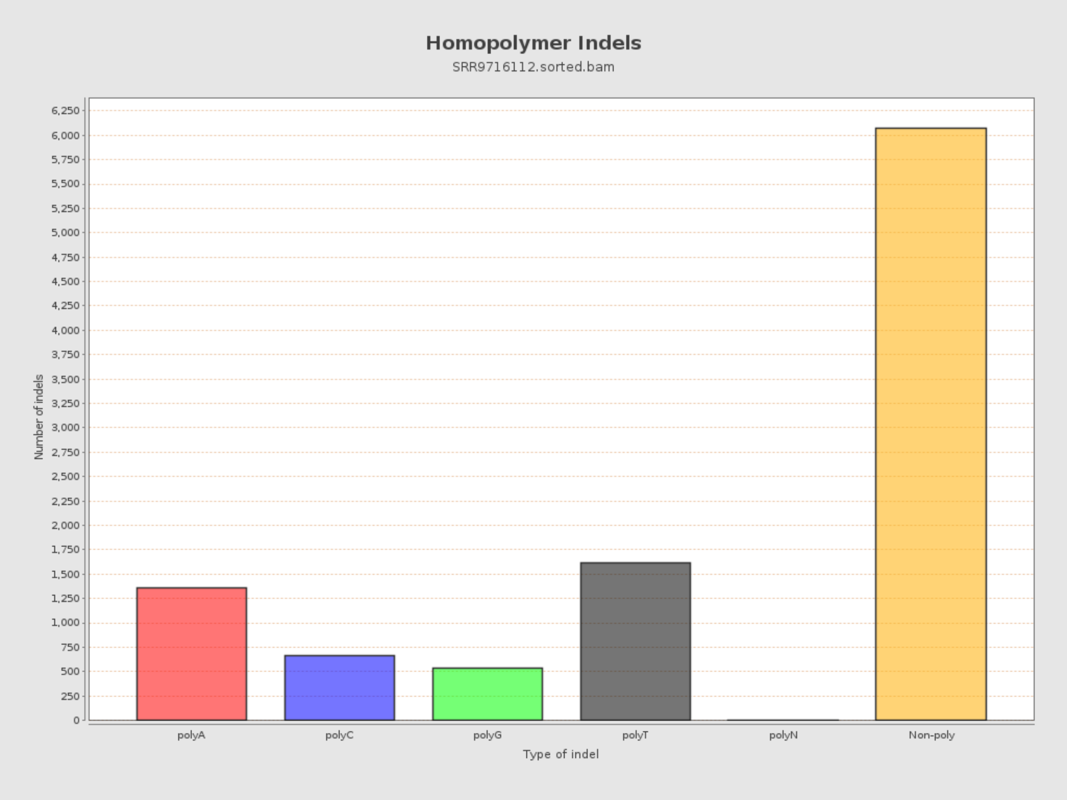
9. Results : Mapped Reads GC-content Distribution



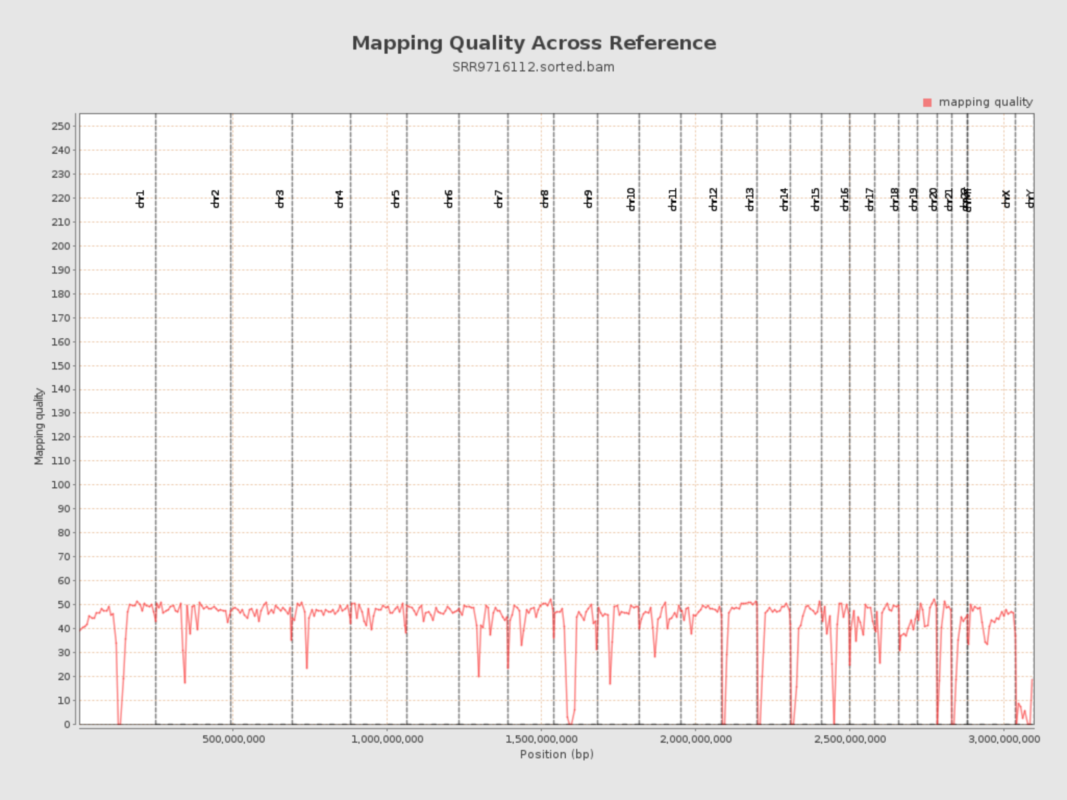
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram