Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 00:38:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716212.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_SRR9716212 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716212.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 00:38:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716212.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,596,767
Mapped reads	1,397,626 / 87.53%
Unmapped reads	199,141 / 12.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,599 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	34,524 / 2.16%
Duplication rate	1.7%
Clipped reads	1,399,265 / 87.63%

2.2. ACGT Content

Number/percentage of A's	19,659,592 / 24.98%
Number/percentage of C's	15,622,050 / 19.85%
Number/percentage of T's	24,544,902 / 31.18%
Number/percentage of G's	18,880,598 / 23.99%
Number/percentage of N's	598 / 0%
GC Percentage	43.84%

2.3. Coverage

Mean	0.0254

Standard Deviation	0.2287

2.4. Mapping Quality

Mean Mapping Quality	42.04

2.5. Mismatches and indels

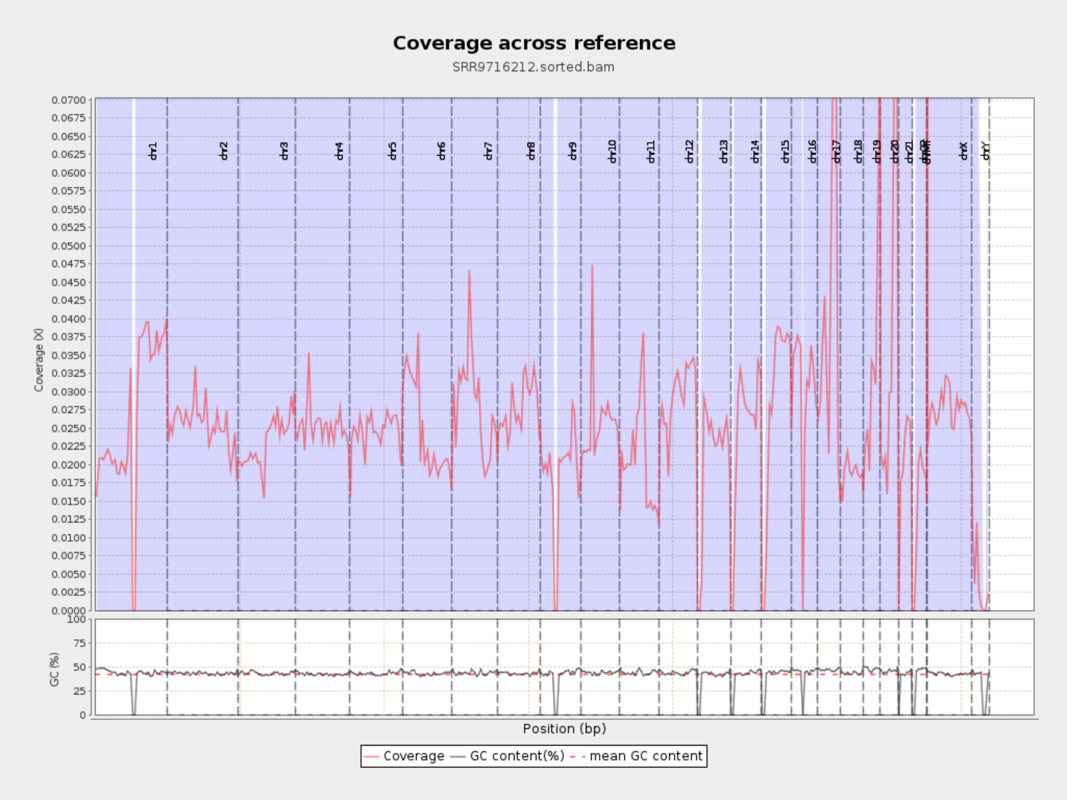
General error rate	0.54%
Mismatches	414,658
Insertions	5,065
Mapped reads with at least one insertion	0.36%
Deletions	14,786
Mapped reads with at least one deletion	1.05%
Homopolymer indels	41.63%

2.6. Chromosome stats

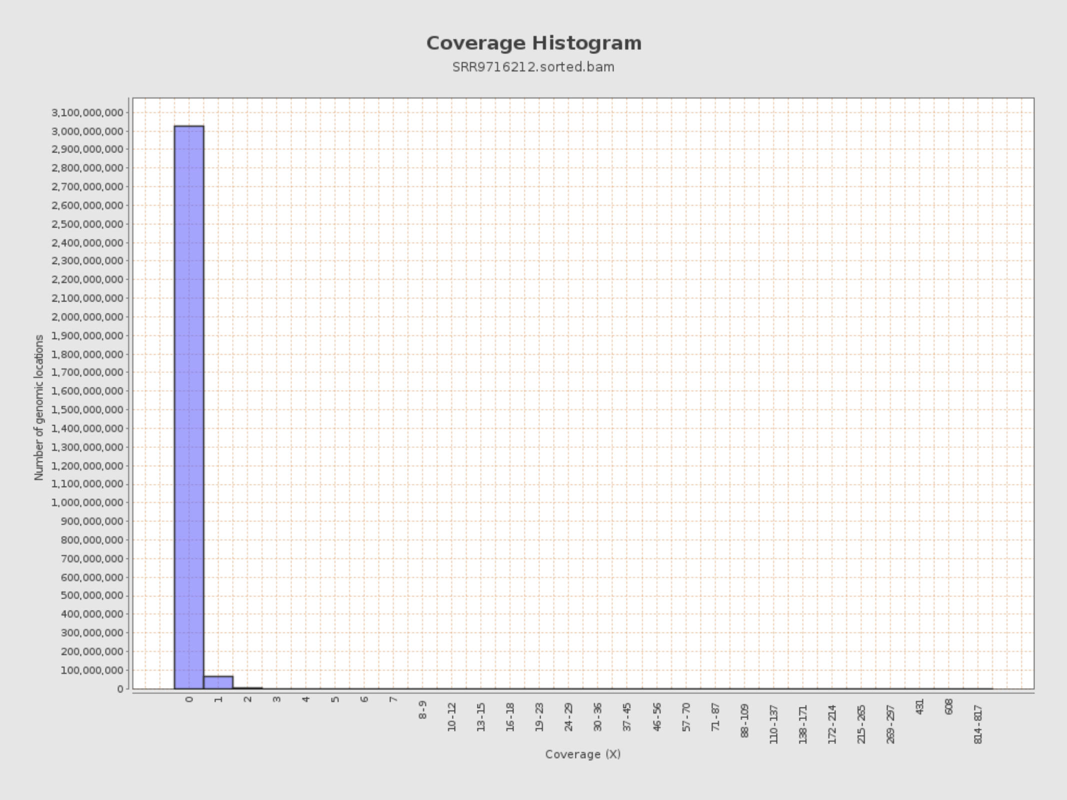
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6616194	0.0265	0.2883
chr2	243199373	6192177	0.0255	0.3637
chr3	198022430	4560558	0.023	0.1655
chr4	191154276	4839815	0.0253	0.1795
chr5	180915260	4491788	0.0248	0.169
chr6	171115067	4245852	0.0248	0.2065
chr7	159138663	4514000	0.0284	0.3261

chr8	146364022	4085313	0.0279	0.217
chr9	141213431	2630487	0.0186	0.1718
chr10	135534747	3490101	0.0258	0.2564
chr11	135006516	2813816	0.0208	0.1895
chr12	133851895	3927917	0.0293	0.1854
chr13	115169878	2361691	0.0205	0.1547
chr14	107349540	2640514	0.0246	0.1749
chr15	102531392	2883923	0.0281	0.1883
chr16	90354753	2681662	0.0297	0.1953
chr17	81195210	3483465	0.0429	0.2348
chr18	78077248	1467786	0.0188	0.2545
chr19	59128983	2047374	0.0346	0.2695
chr20	63025520	2492524	0.0395	0.2224
chr21	48129895	981167	0.0204	0.1602
chr22	51304566	716100	0.014	0.1284
chrMT	16571	23582	1.4231	1.461
chrX	155270560	4316875	0.0278	0.1923
chrY	59373566	226232	0.0038	0.1025

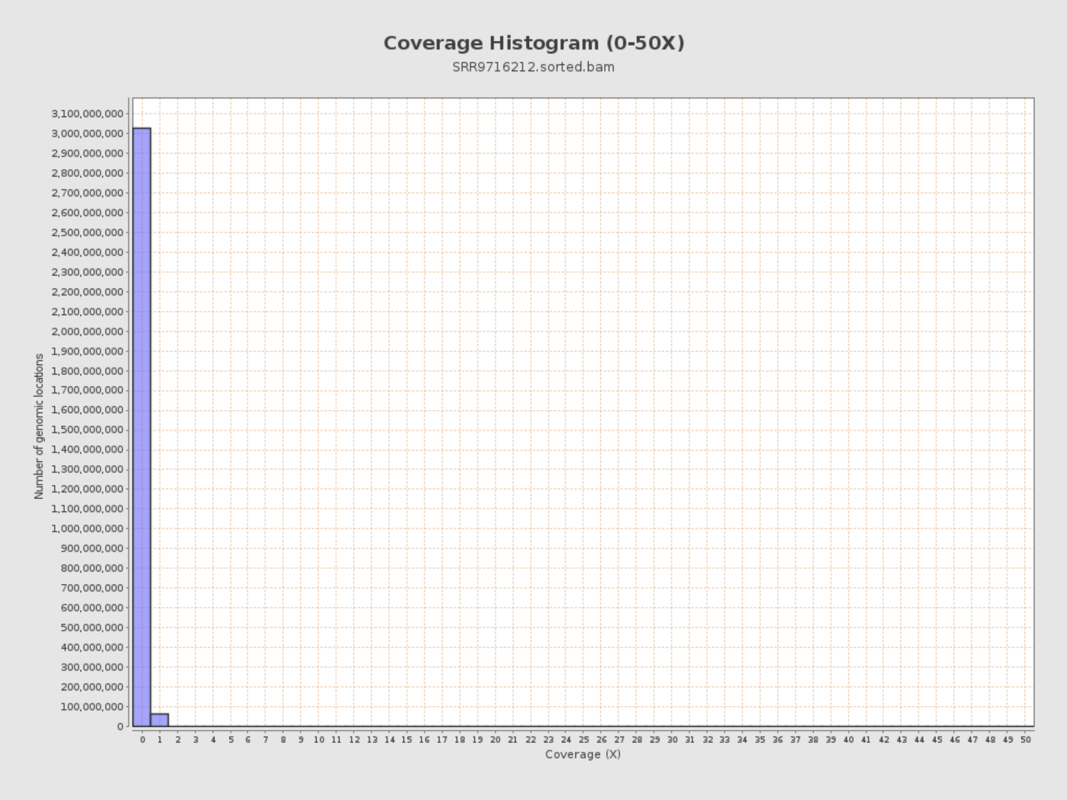
3. Results : Coverage across reference



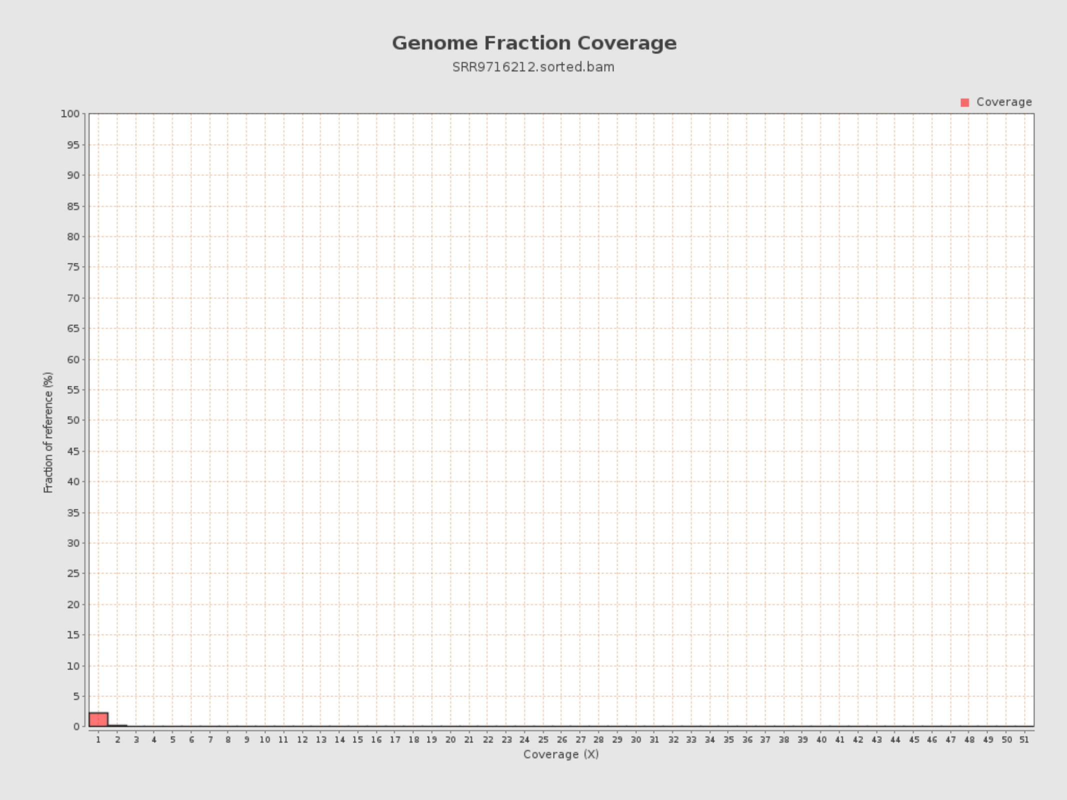
4. Results : Coverage Histogram



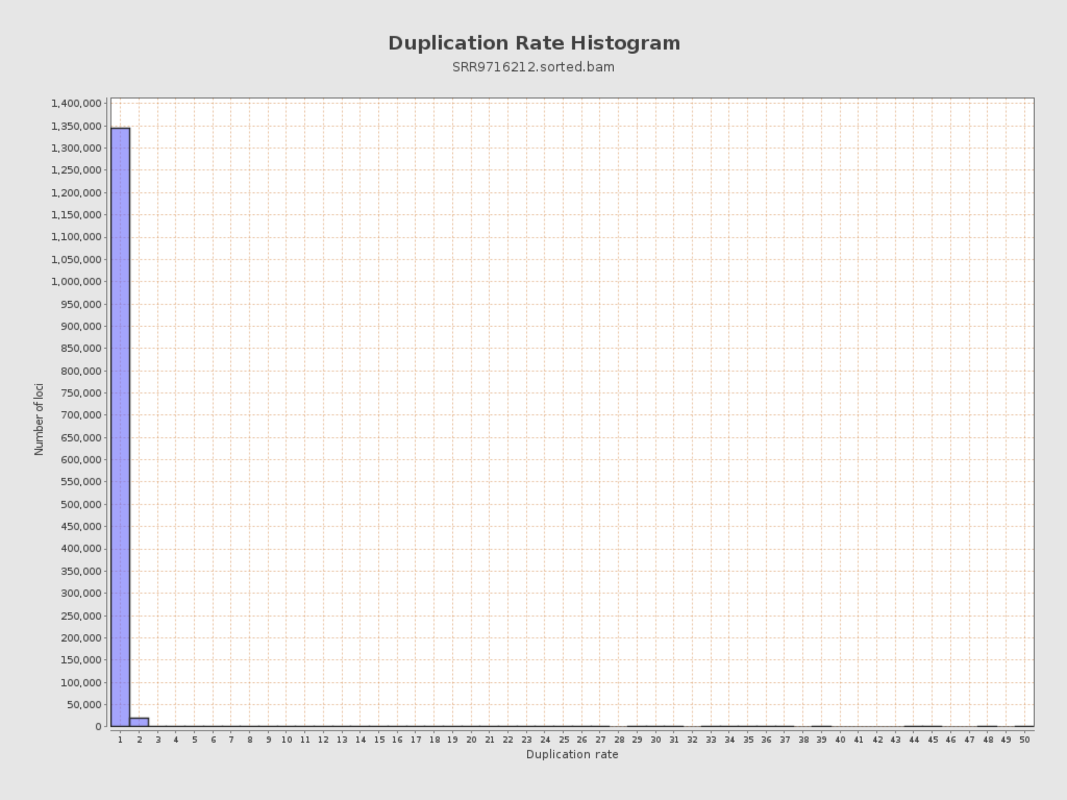
5. Results : Coverage Histogram (0-50X)



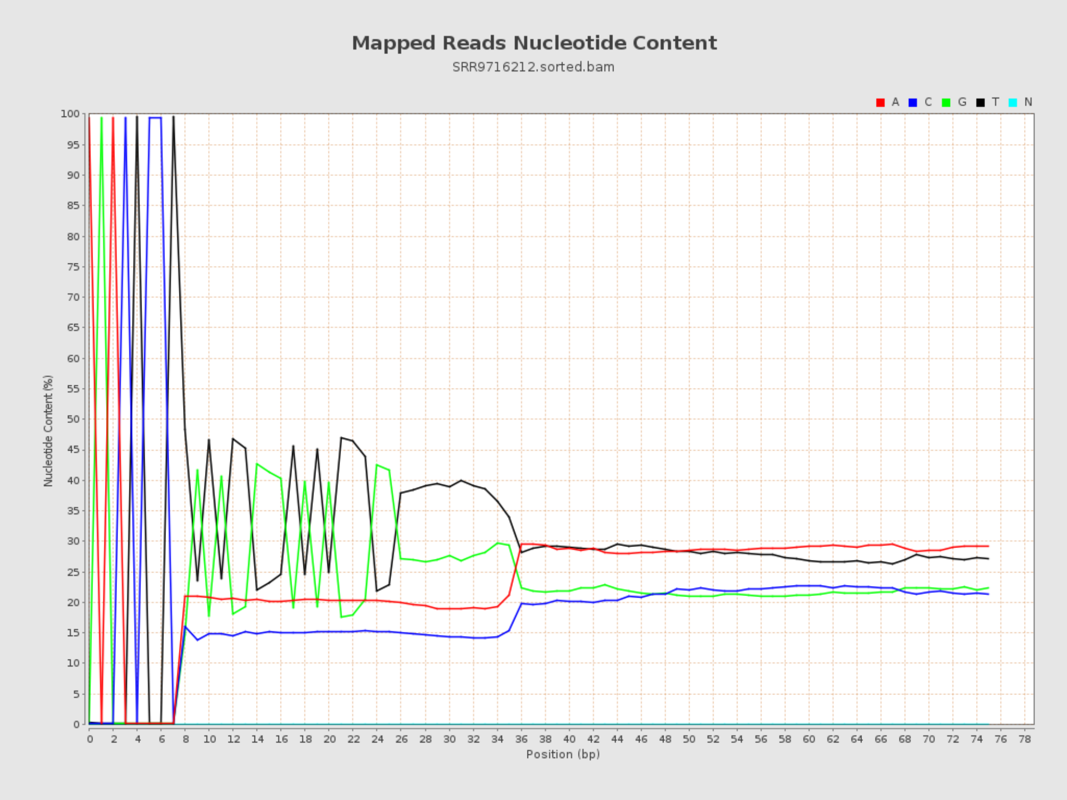
6. Results : Genome Fraction Coverage



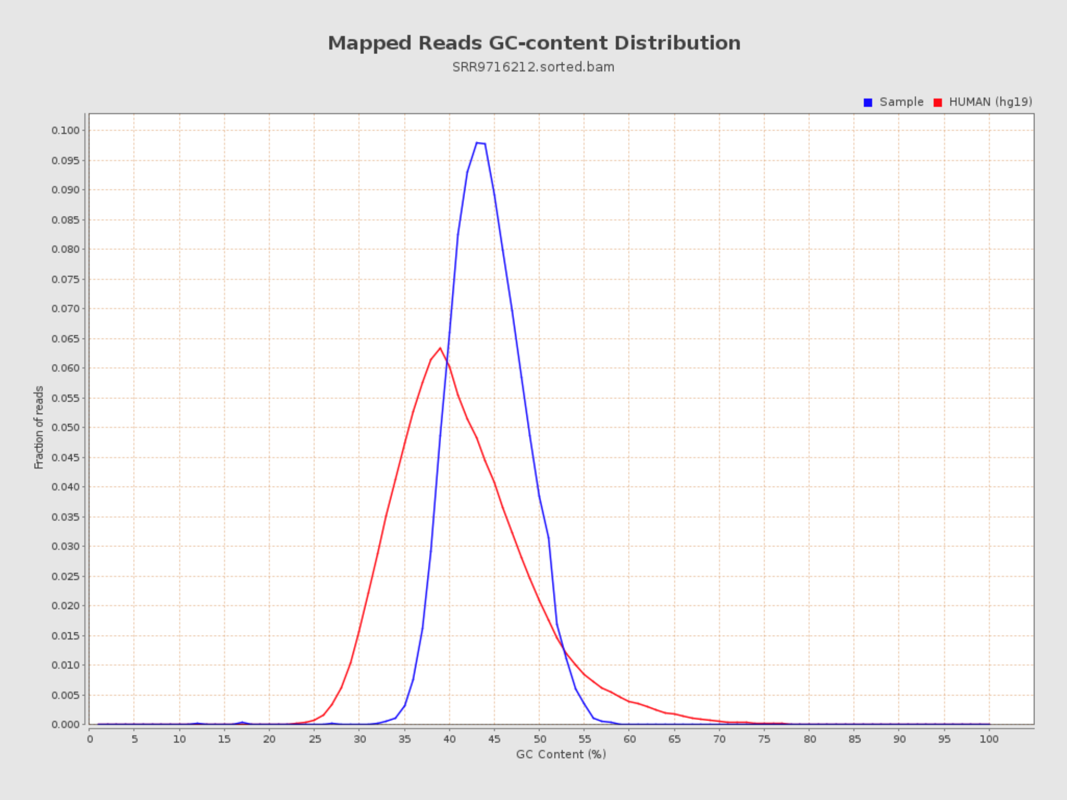
7. Results : Duplication Rate Histogram



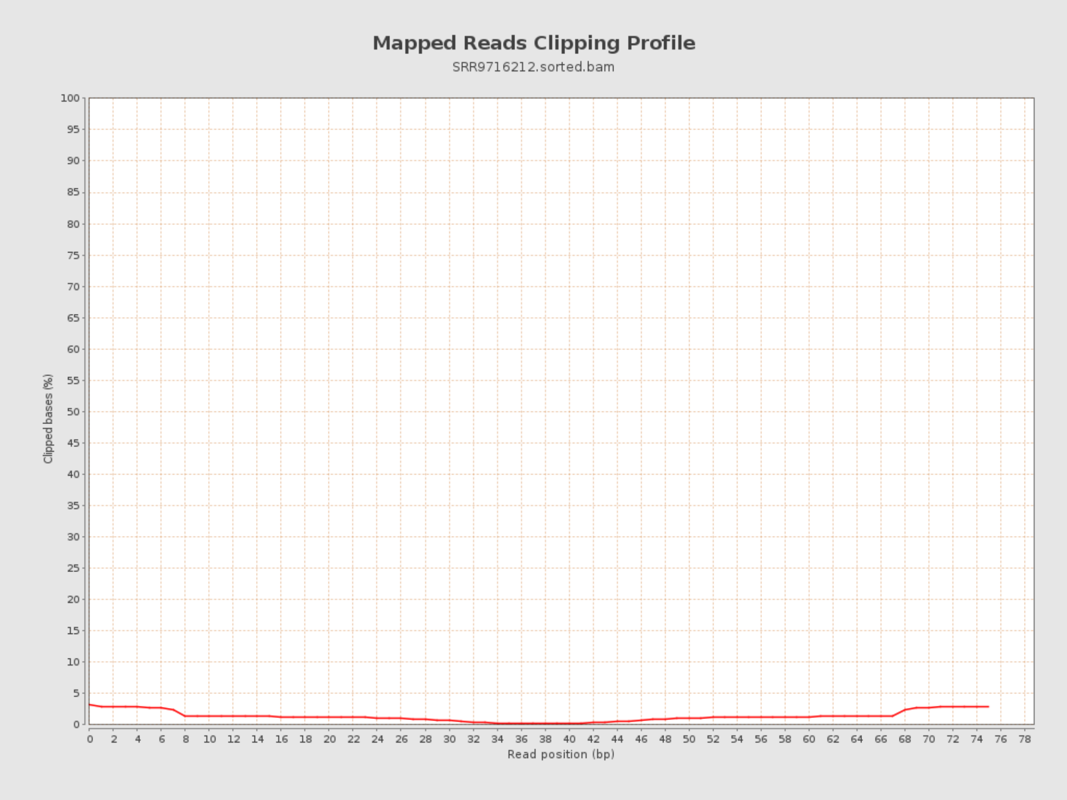
8. Results : Mapped Reads Nucleotide Content



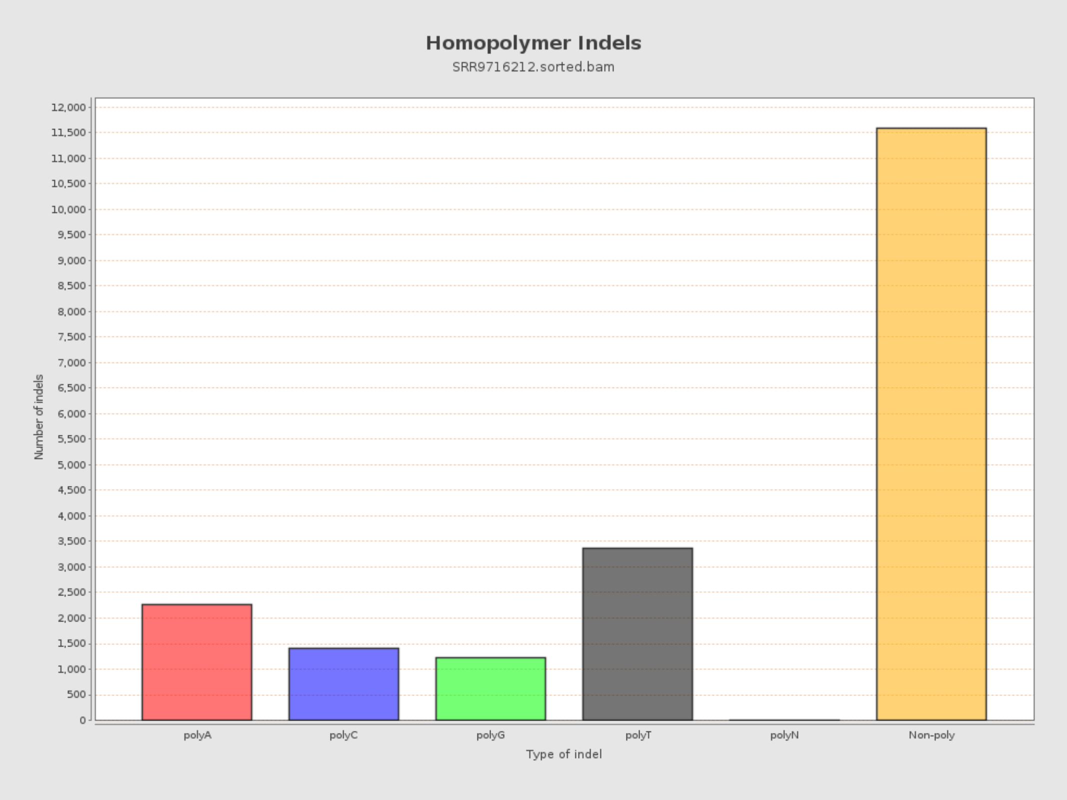
9. Results : Mapped Reads GC-content Distribution



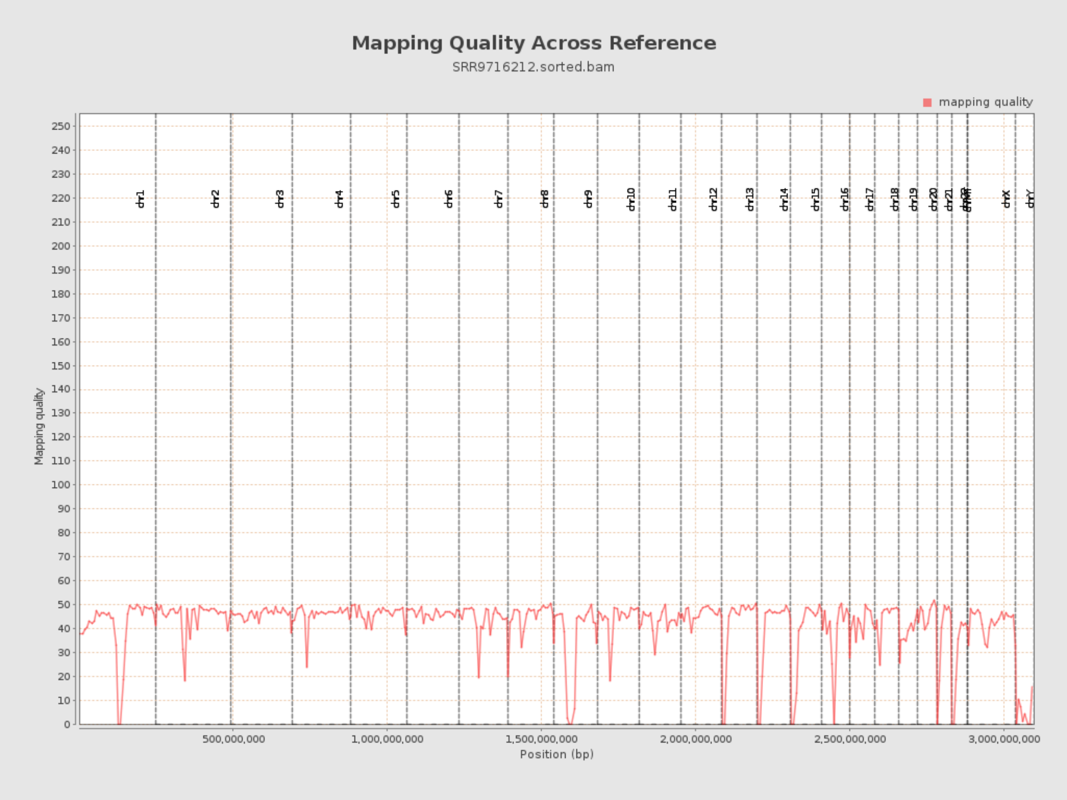
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram