Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 14:00:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716832.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_SRR9716832 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716832.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 14:00:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716832.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,084,902
Mapped reads	886,323 / 81.7%
Unmapped reads	198,579 / 18.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	938 / 0.09%
Read min/max/mean length	30 / 76 / 76.03
Duplicated reads (estimated)	52,661 / 4.85%
Duplication rate	5.3%
Clipped reads	886,904 / 81.75%

2.2. ACGT Content

Number/percentage of A's	9,754,370 / 20.48%
Number/percentage of C's	8,613,067 / 18.09%
Number/percentage of T's	15,695,411 / 32.96%
Number/percentage of G's	13,554,610 / 28.47%
Number/percentage of N's	799 / 0%
GC Percentage	46.55%

2.3. Coverage

Mean	0.0154

Standard Deviation	0.1547

2.4. Mapping Quality

Mean Mapping Quality	43.68

2.5. Mismatches and indels

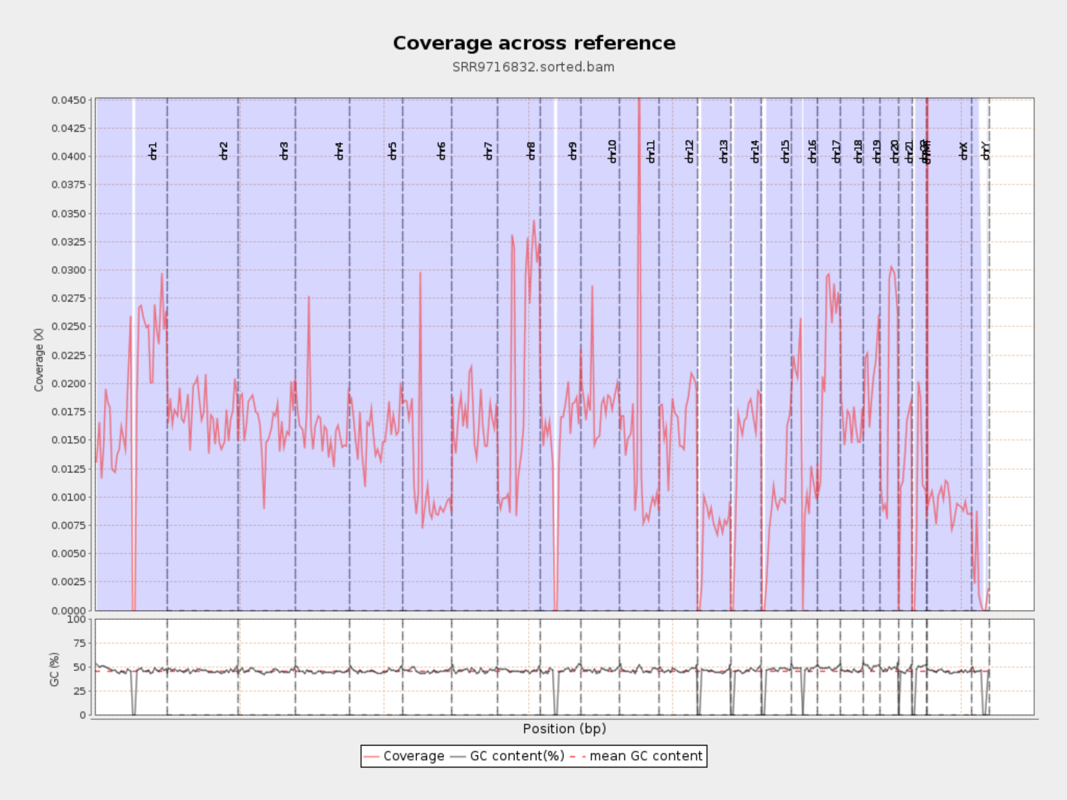
General error rate	0.64%
Mismatches	300,235
Insertions	2,394
Mapped reads with at least one insertion	0.27%
Deletions	7,503
Mapped reads with at least one deletion	0.84%
Homopolymer indels	44.01%

2.6. Chromosome stats

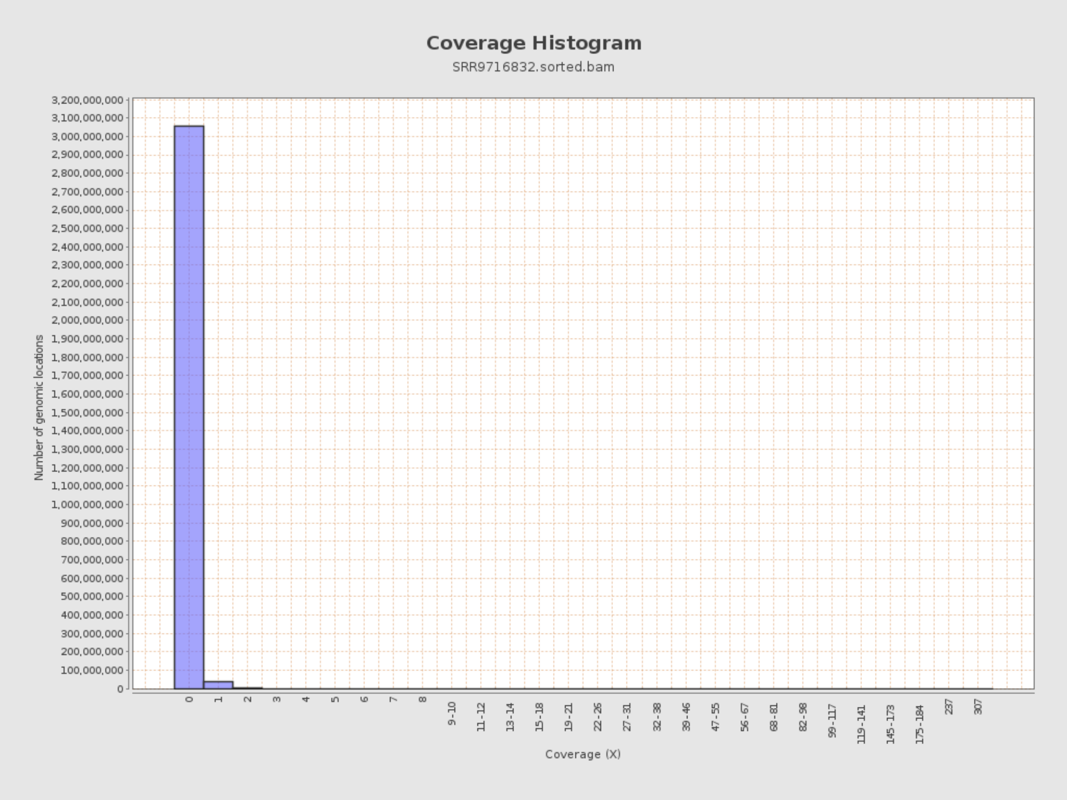
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4678216	0.0188	0.1954
chr2	243199373	4210996	0.0173	0.1992
chr3	198022430	3266168	0.0165	0.1435
chr4	191154276	3115226	0.0163	0.1496
chr5	180915260	2852492	0.0158	0.1394
chr6	171115067	2053551	0.012	0.1316
chr7	159138663	2688111	0.0169	0.1695

chr8	146364022	3004341	0.0205	0.1653
chr9	141213431	2109439	0.0149	0.144
chr10	135534747	2505220	0.0185	0.1824
chr11	135006516	1956346	0.0145	0.1459
chr12	133851895	2274654	0.017	0.1465
chr13	115169878	787173	0.0068	0.0925
chr14	107349540	1539158	0.0143	0.1339
chr15	102531392	905858	0.0088	0.1048
chr16	90354753	1268073	0.014	0.1404
chr17	81195210	1874981	0.0231	0.1752
chr18	78077248	1279167	0.0164	0.1701
chr19	59128983	1234535	0.0209	0.1929
chr20	63025520	1252658	0.0199	0.1608
chr21	48129895	637868	0.0133	0.1349
chr22	51304566	529346	0.0103	0.1156
chrMT	16571	8842	0.5336	0.8694
chrX	155270560	1459122	0.0094	0.1128
chrY	59373566	139481	0.0023	0.0777

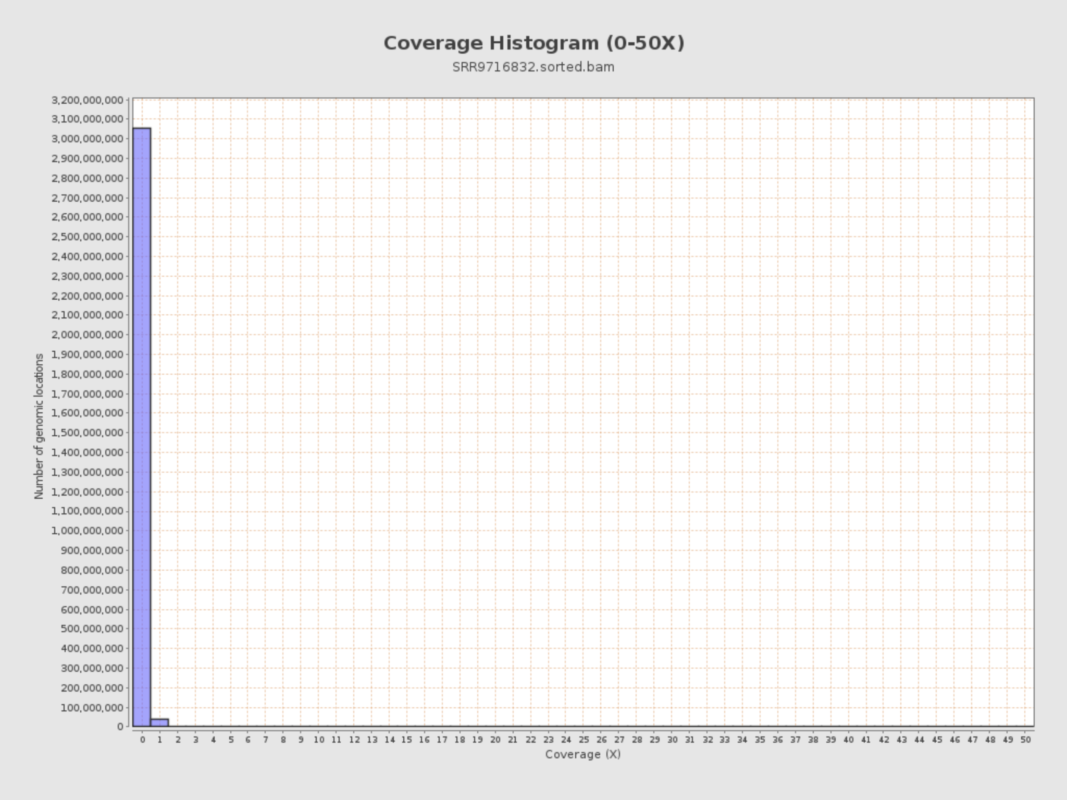
3. Results : Coverage across reference



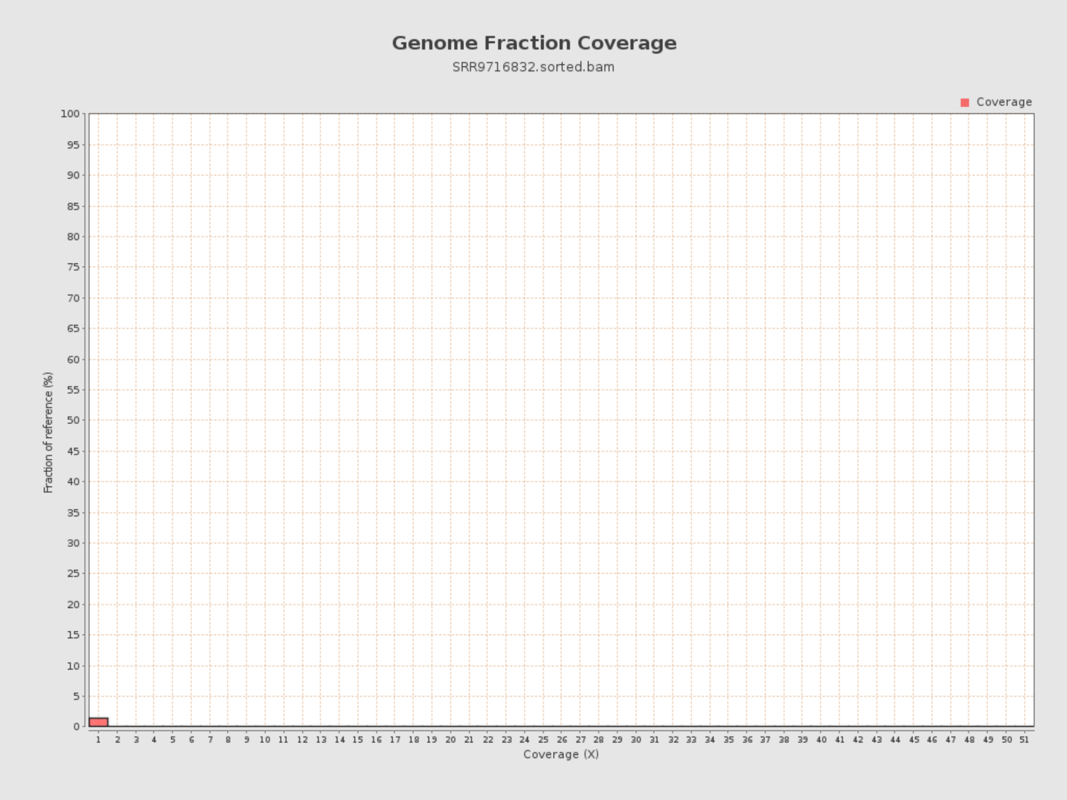
4. Results : Coverage Histogram



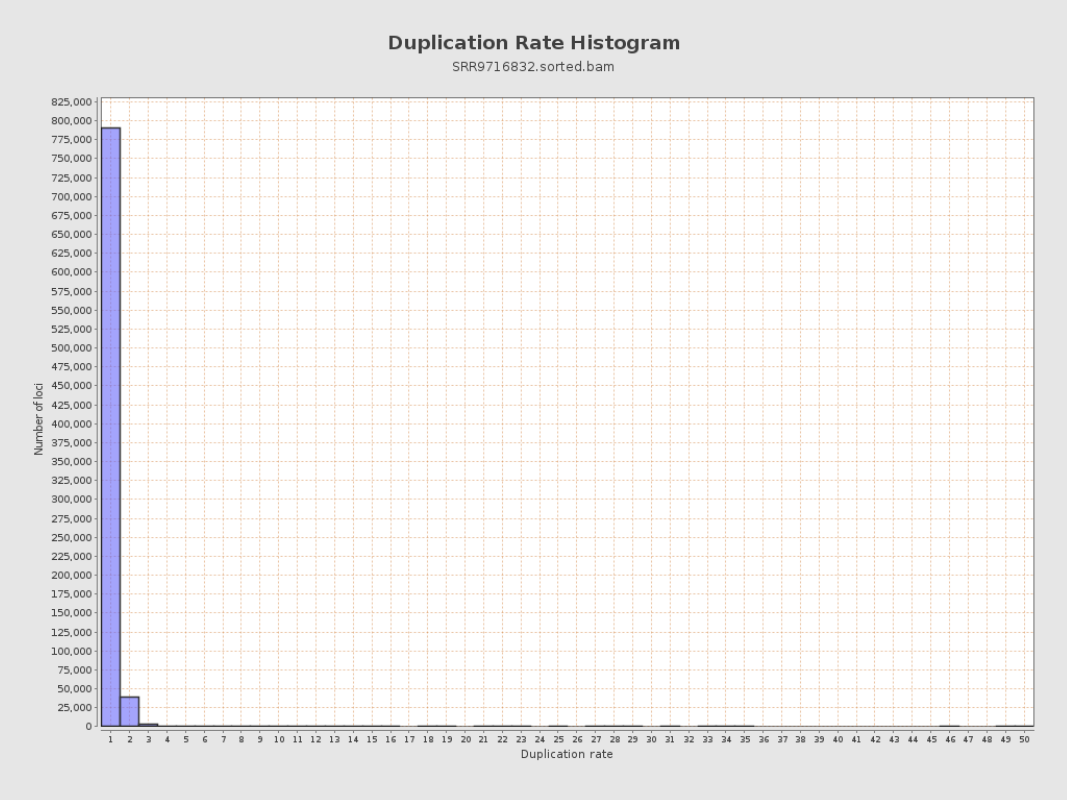
5. Results : Coverage Histogram (0-50X)



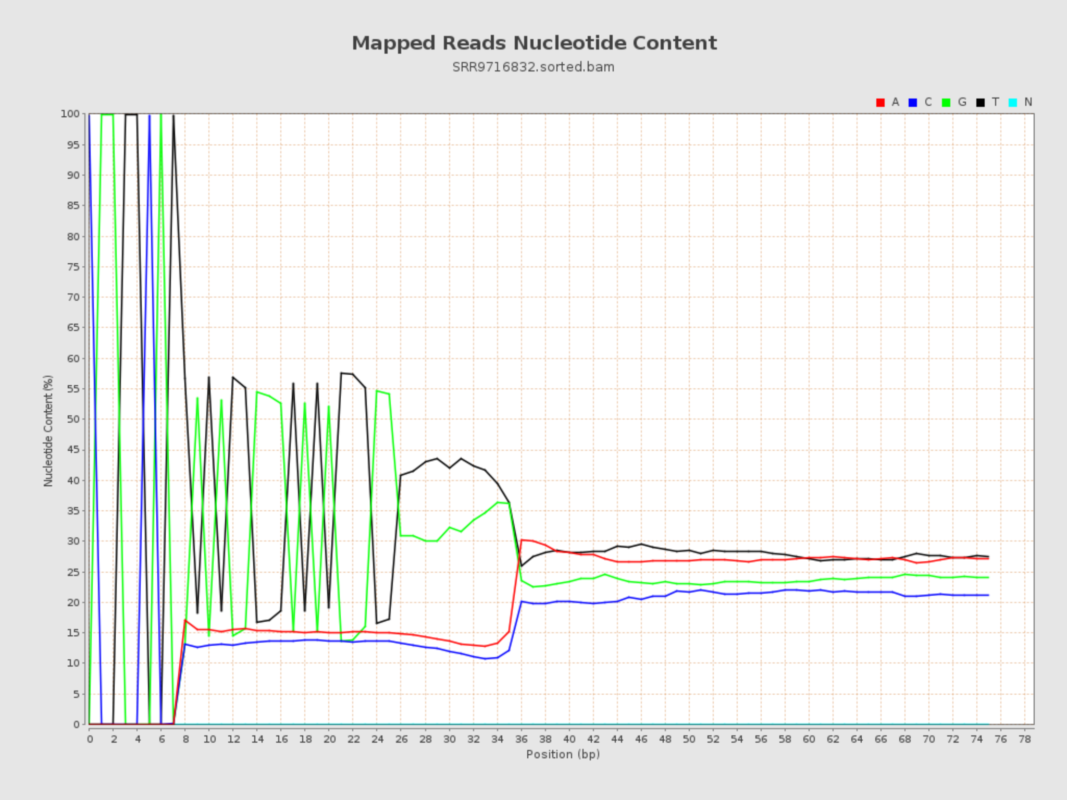
6. Results : Genome Fraction Coverage



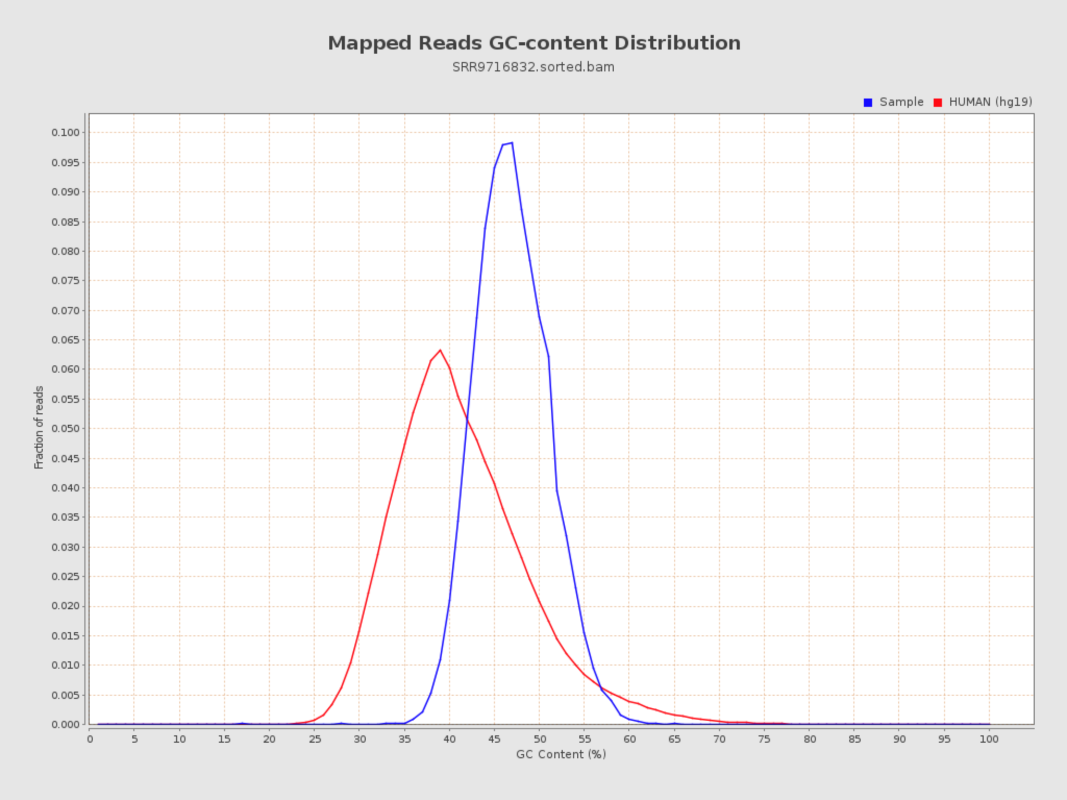
7. Results : Duplication Rate Histogram



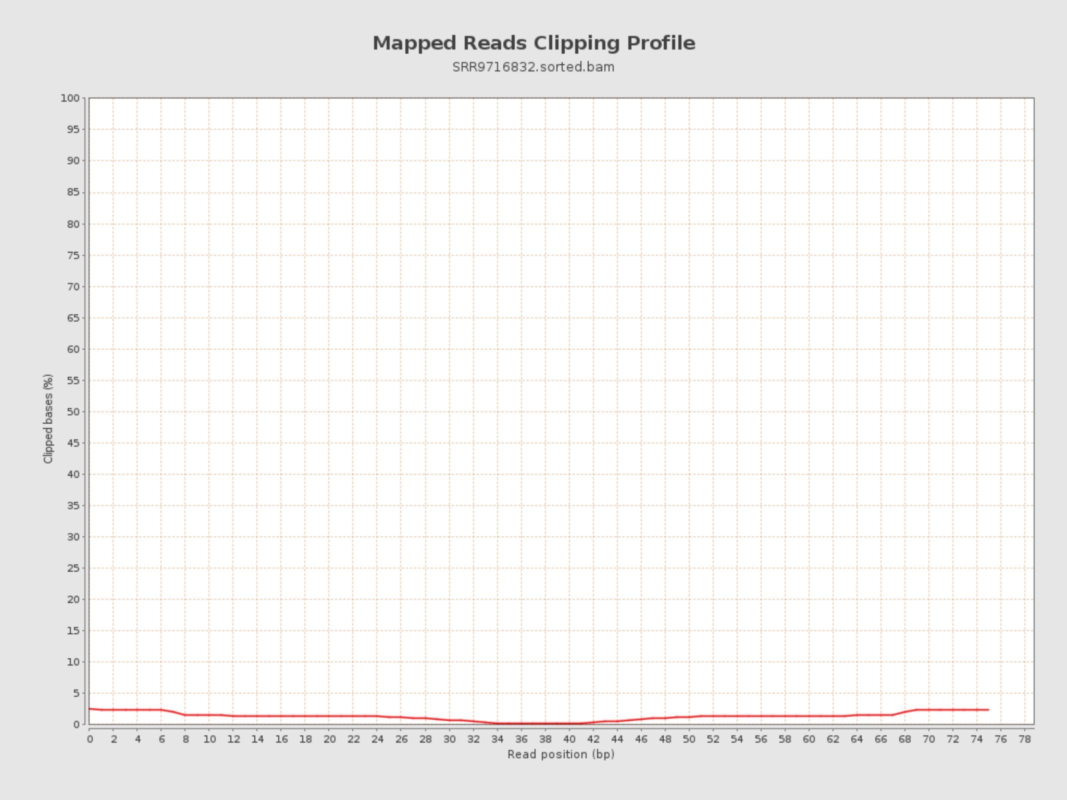
8. Results : Mapped Reads Nucleotide Content



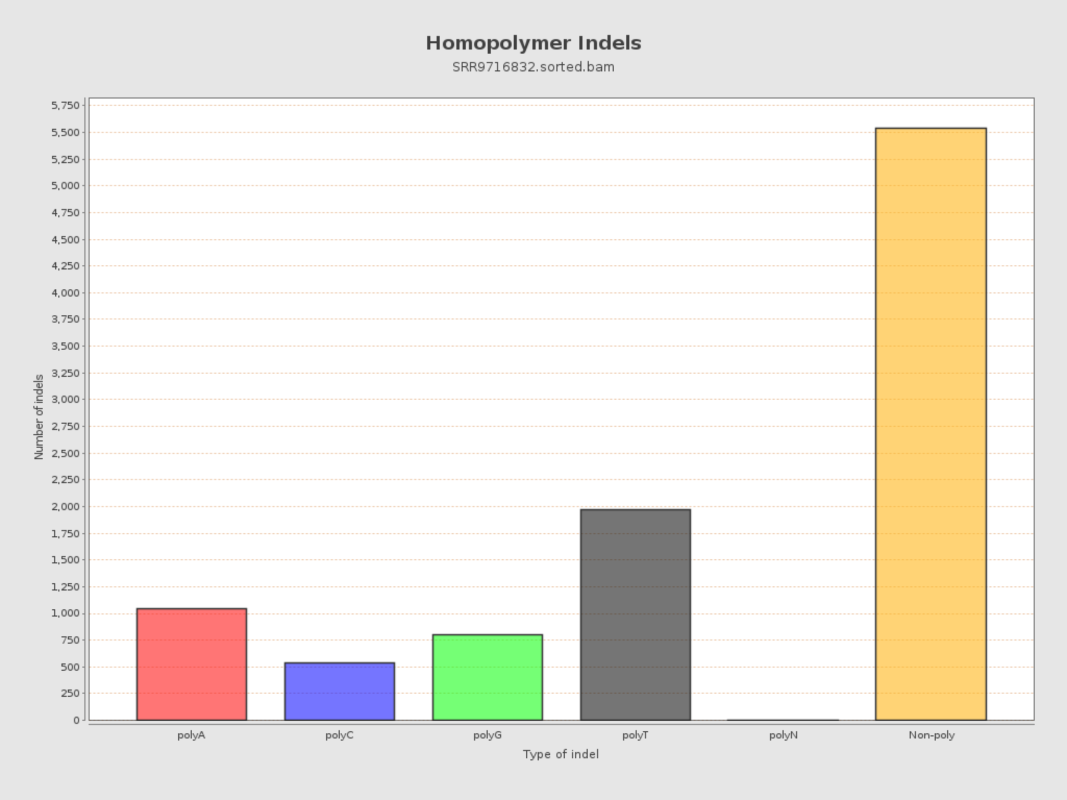
9. Results : Mapped Reads GC-content Distribution



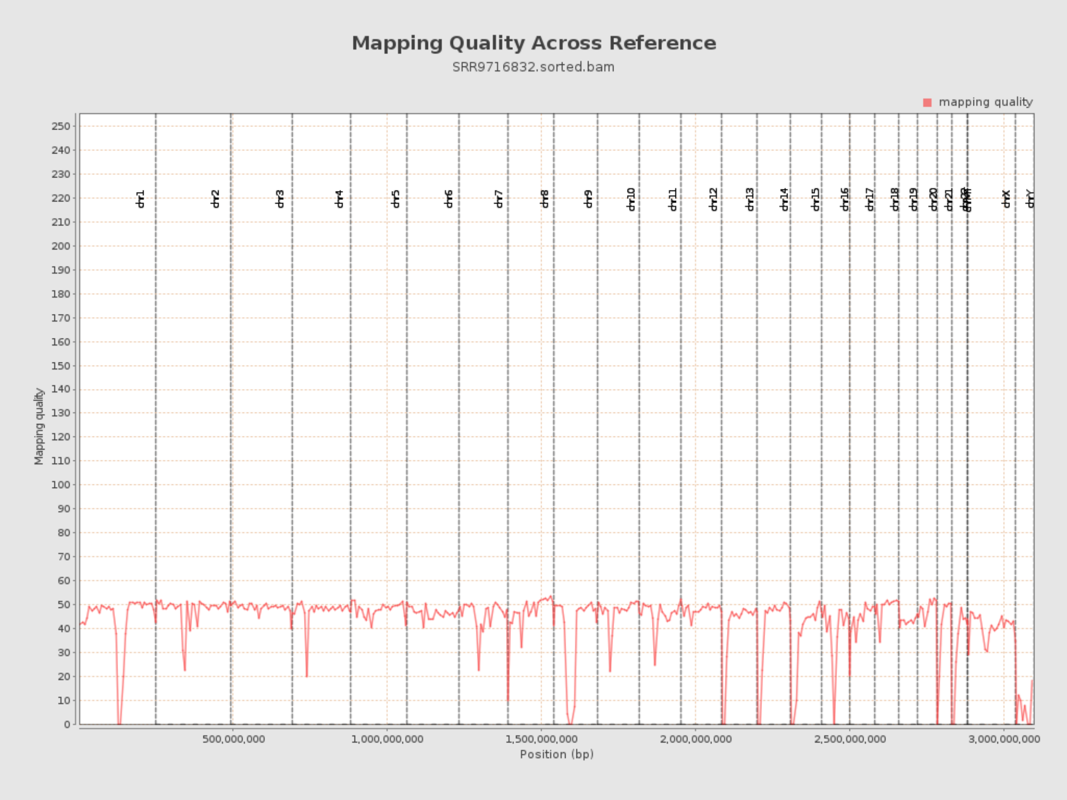
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram