Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 22:16:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524828.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_SRR10524828 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524828.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 22:16:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524828.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,501,959
Mapped reads	1,364,042 / 90.82%
Unmapped reads	137,917 / 9.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,641 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	43,471 / 2.89%
Duplication rate	2.44%
Clipped reads	1,365,424 / 90.91%

2.2. ACGT Content

Number/percentage of A's	19,667,972 / 25.07%
Number/percentage of C's	14,017,349 / 17.86%
Number/percentage of T's	24,515,608 / 31.24%
Number/percentage of G's	20,254,492 / 25.81%
Number/percentage of N's	10,442 / 0.01%
GC Percentage	43.68%

2.3. Coverage

Mean	0.0254

Standard Deviation	0.22

2.4. Mapping Quality

Mean Mapping Quality	44.78

2.5. Mismatches and indels

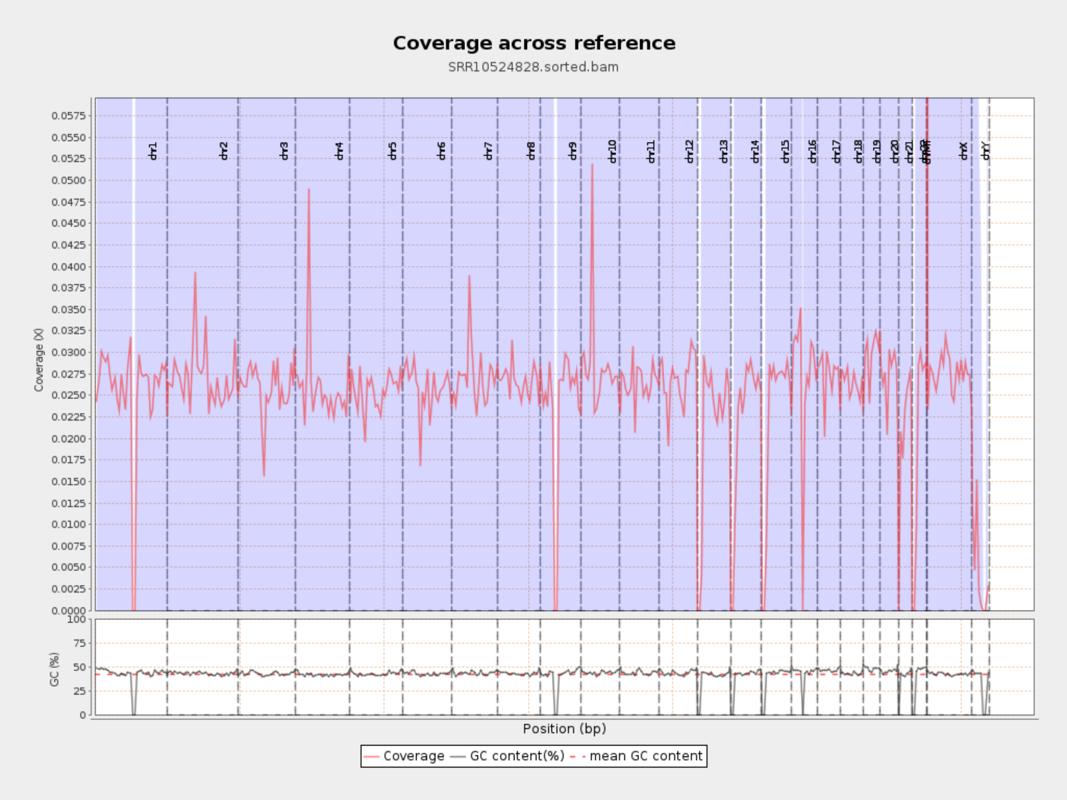
General error rate	0.51%
Mismatches	390,474
Insertions	5,666
Mapped reads with at least one insertion	0.41%
Deletions	15,205
Mapped reads with at least one deletion	1.11%
Homopolymer indels	41.63%

2.6. Chromosome stats

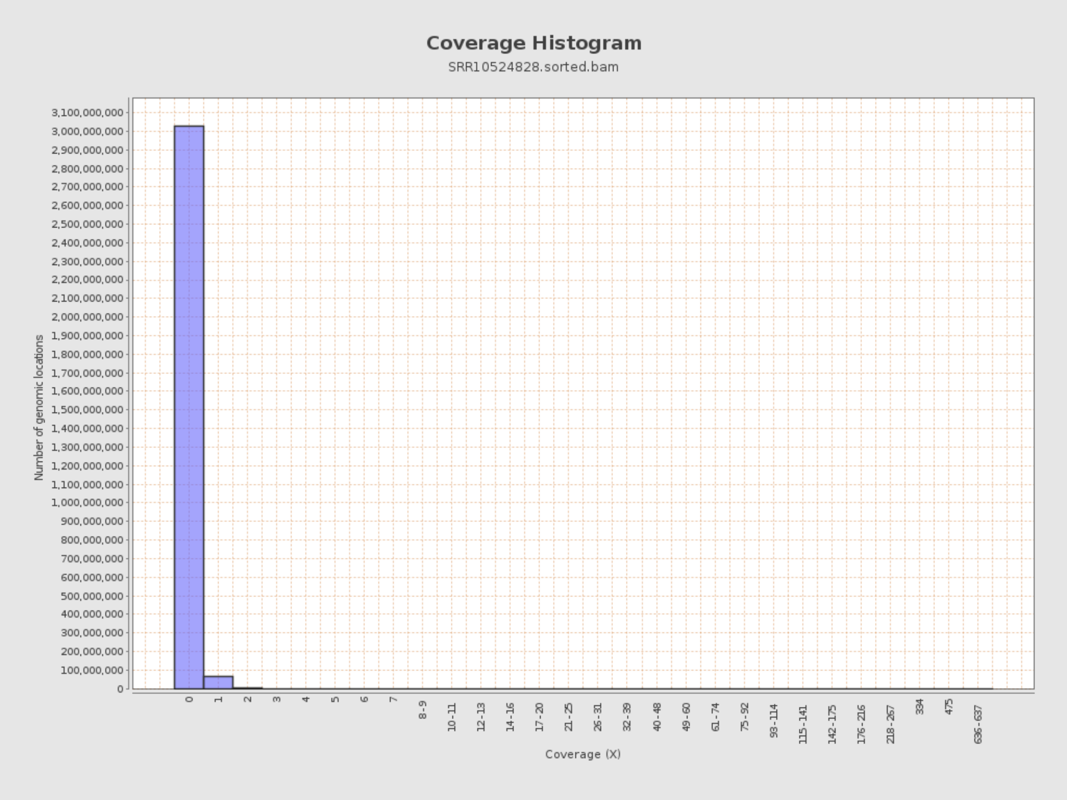
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6298437	0.0253	0.2629
chr2	243199373	6609195	0.0272	0.3352
chr3	198022430	5112201	0.0258	0.1766
chr4	191154276	4989742	0.0261	0.2033
chr5	180915260	4641098	0.0257	0.1744
chr6	171115067	4423886	0.0259	0.189
chr7	159138663	4314830	0.0271	0.2667

chr8	146364022	3895385	0.0266	0.1995
chr9	141213431	3319341	0.0235	0.1997
chr10	135534747	3862230	0.0285	0.2724
chr11	135006516	3582040	0.0265	0.2033
chr12	133851895	3594021	0.0269	0.1803
chr13	115169878	2440412	0.0212	0.1589
chr14	107349540	2345753	0.0219	0.1648
chr15	102531392	2277201	0.0222	0.1657
chr16	90354753	2410224	0.0267	0.1941
chr17	81195210	2225807	0.0274	0.1876
chr18	78077248	2067604	0.0265	0.2893
chr19	59128983	1757530	0.0297	0.2422
chr20	63025520	1712291	0.0272	0.1894
chr21	48129895	1015182	0.0211	0.1781
chr22	51304566	1014748	0.0198	0.1553
chrMT	16571	18831	1.1364	1.2187
chrX	155270560	4300348	0.0277	0.1934
chrY	59373566	261966	0.0044	0.1287

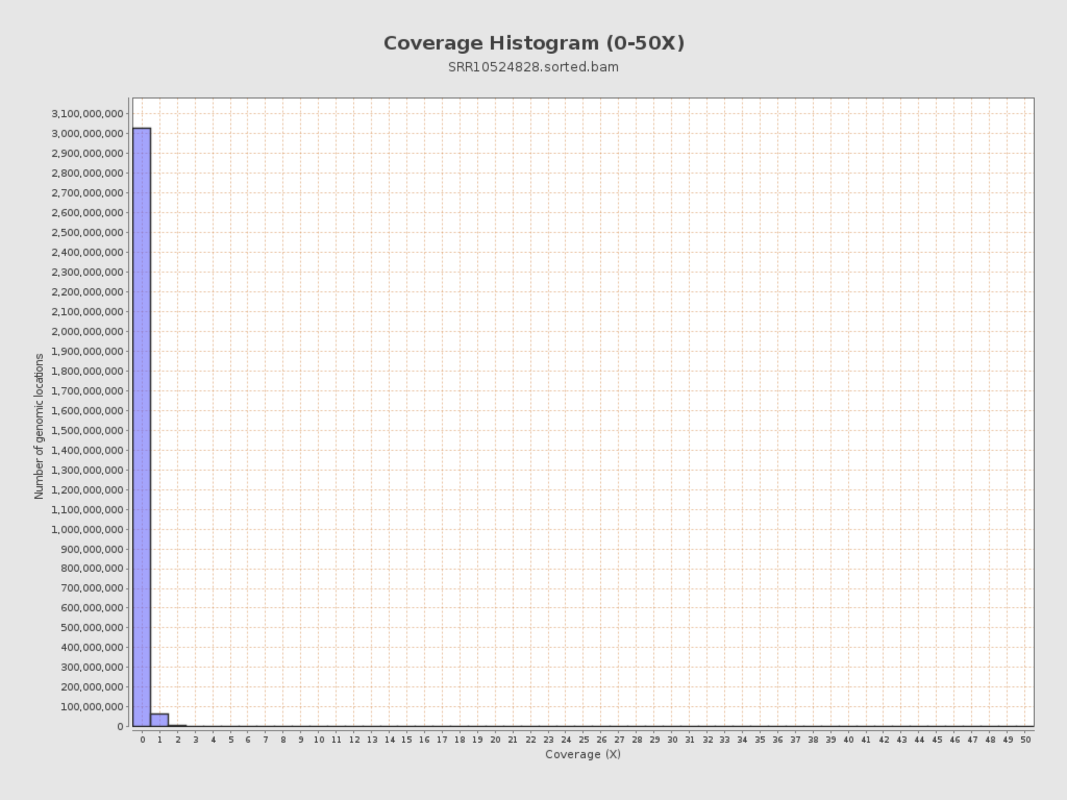
3. Results : Coverage across reference



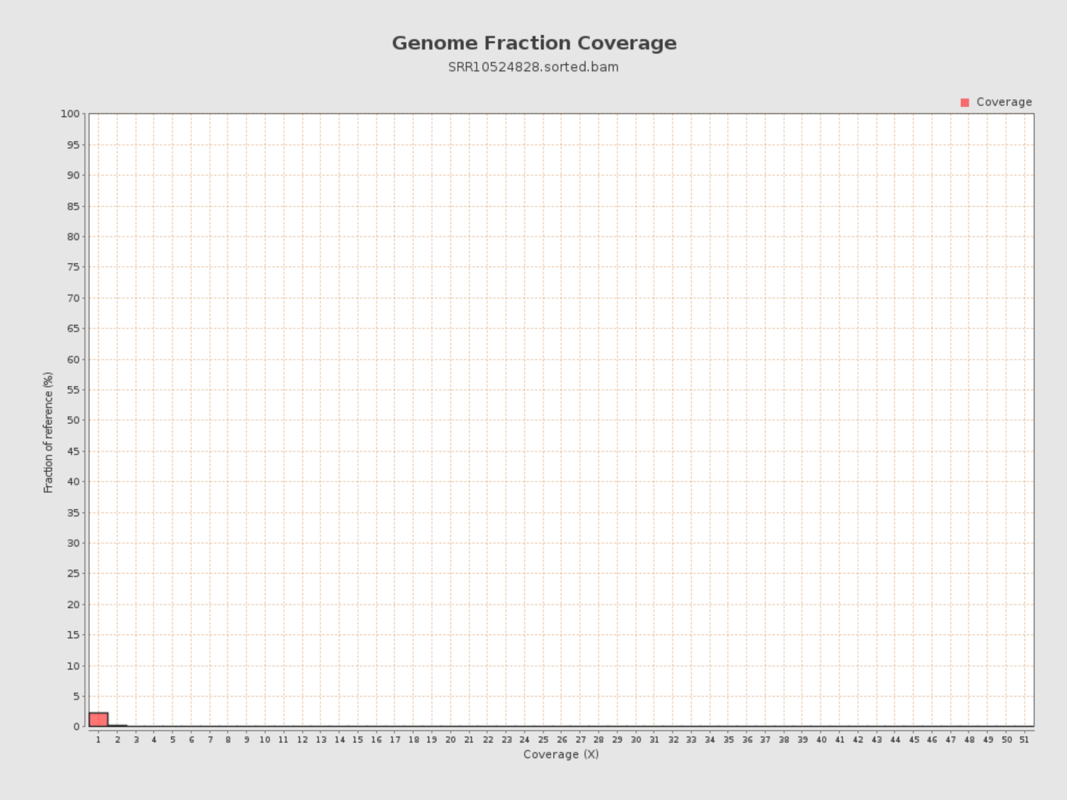
4. Results : Coverage Histogram



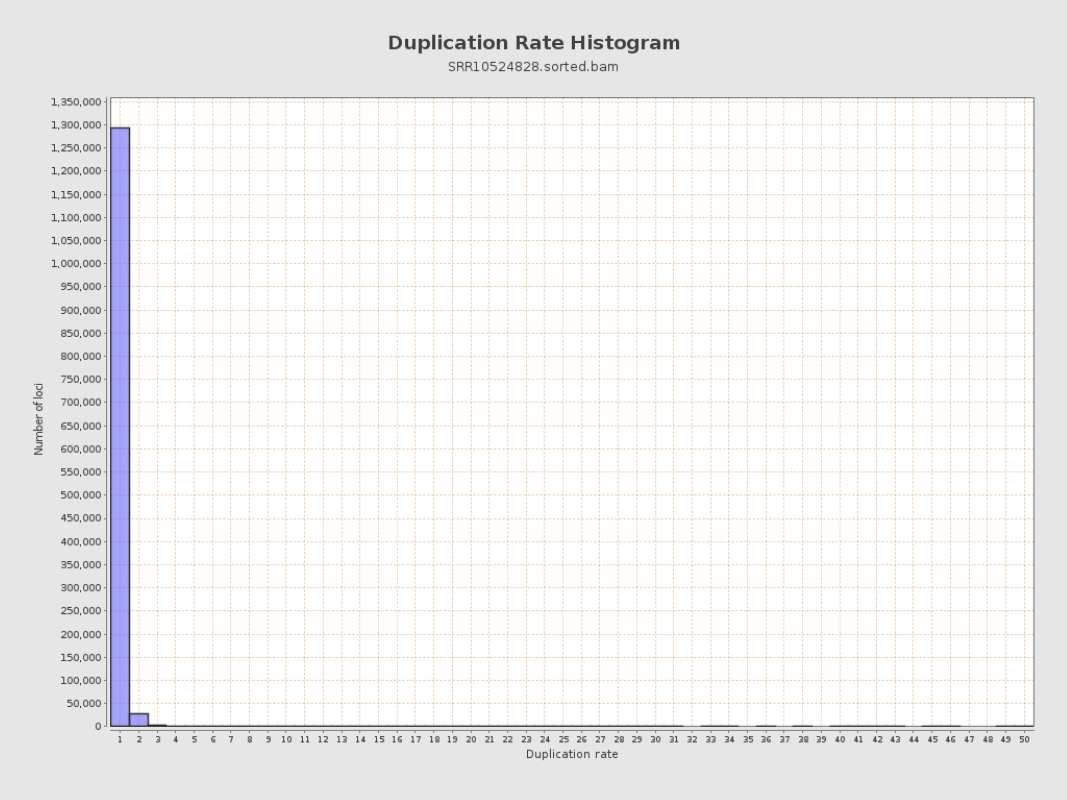
5. Results : Coverage Histogram (0-50X)



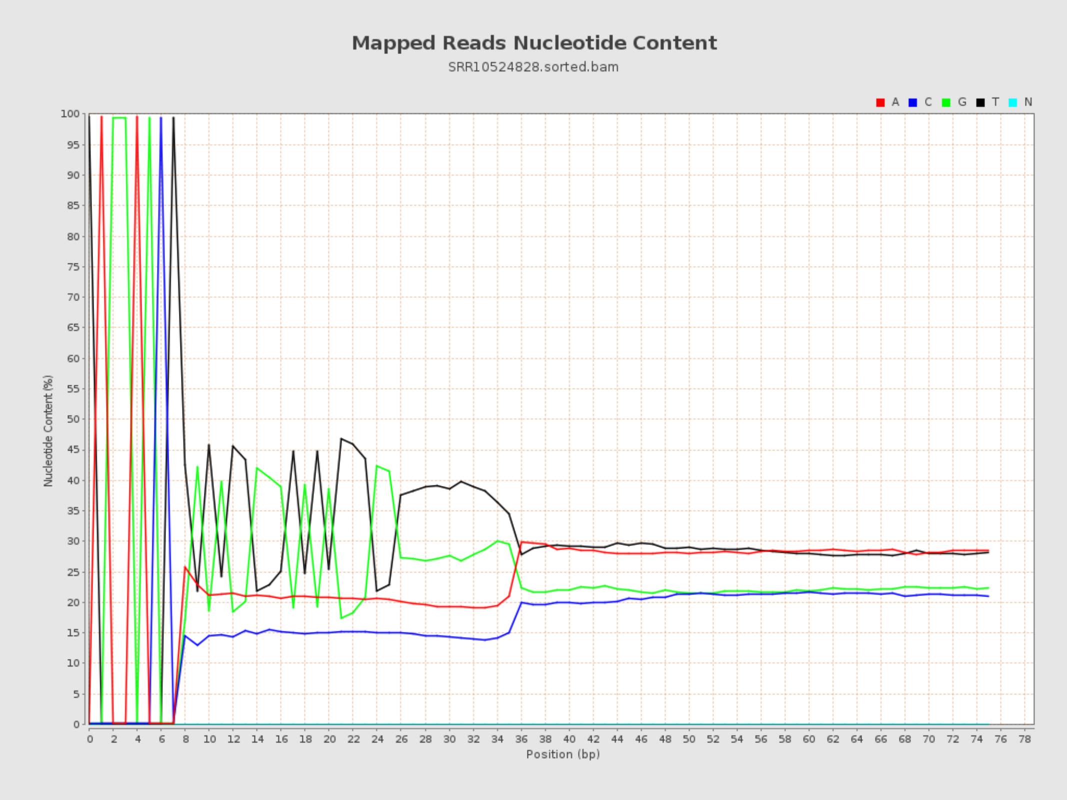
6. Results : Genome Fraction Coverage



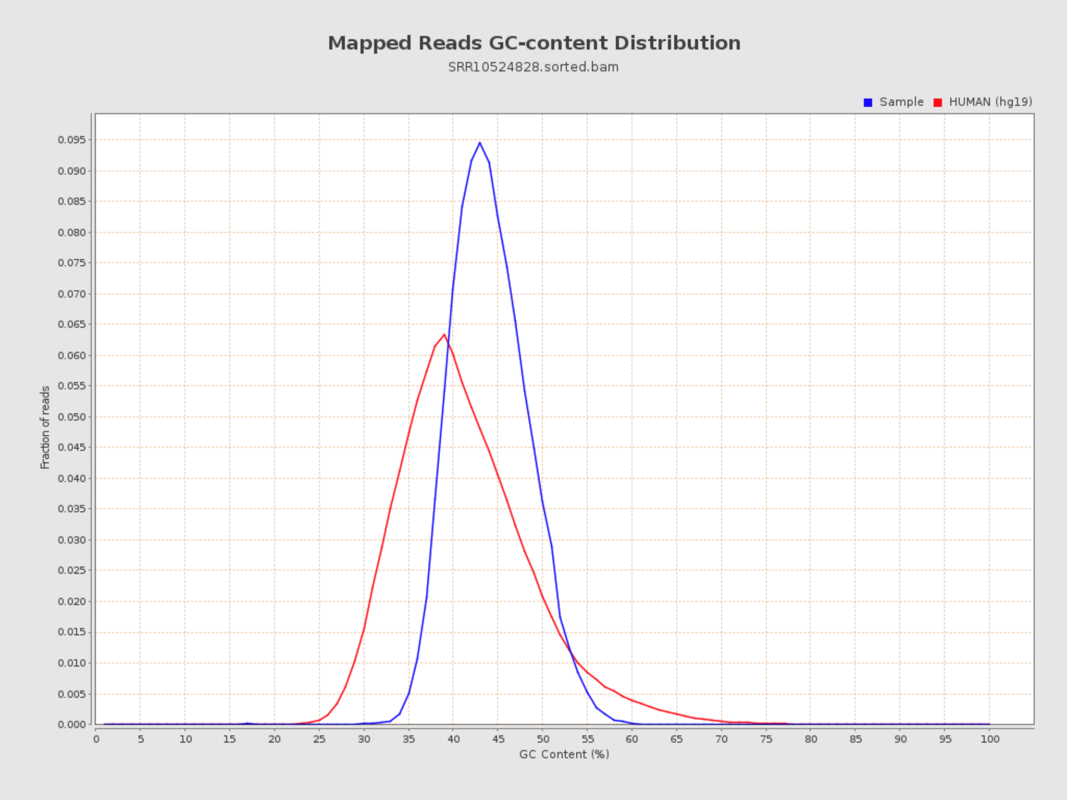
7. Results : Duplication Rate Histogram



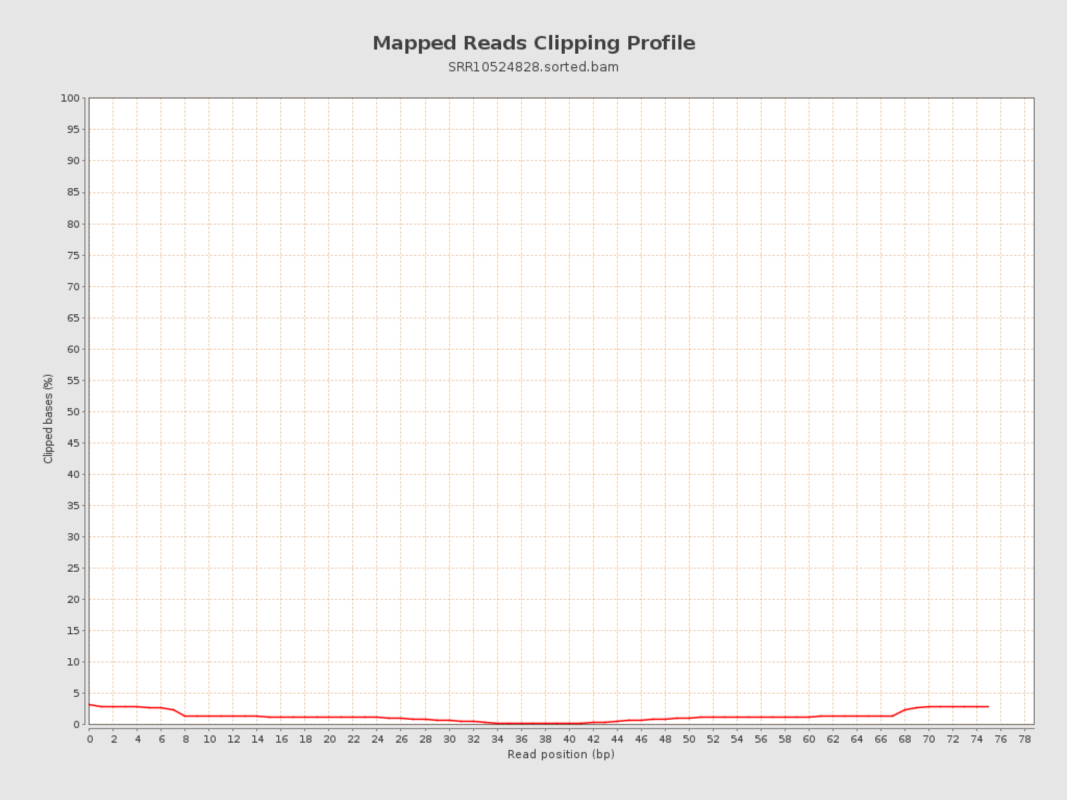
8. Results : Mapped Reads Nucleotide Content



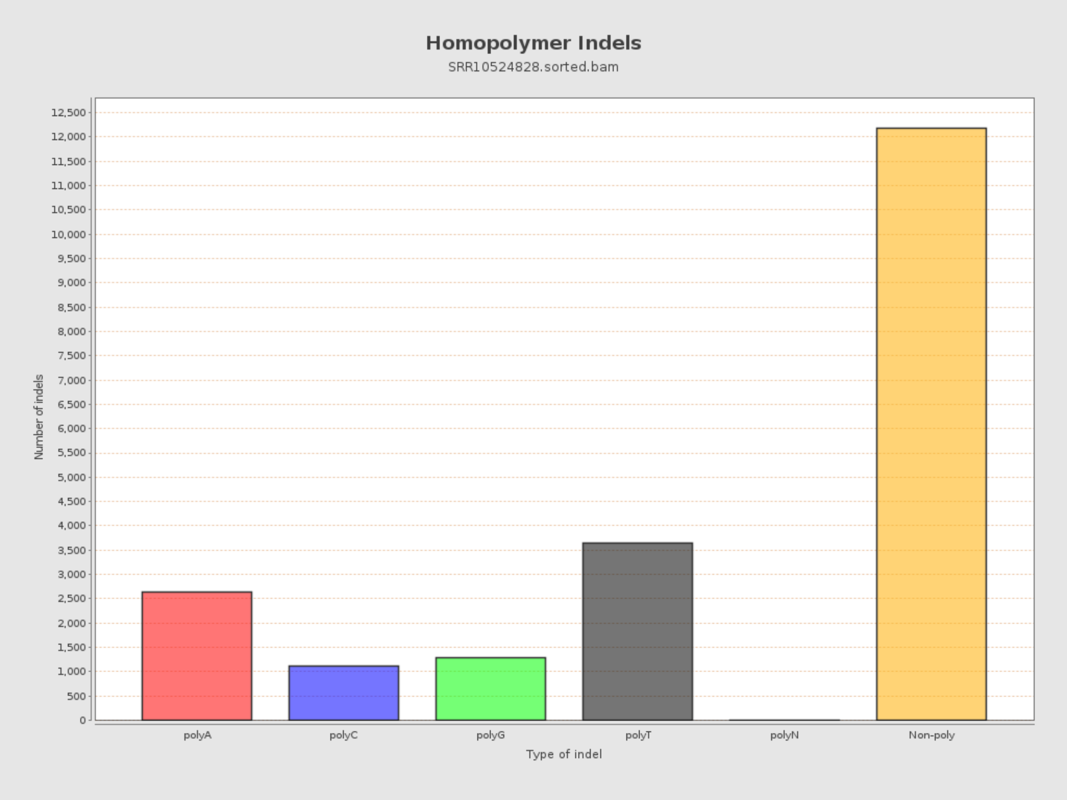
9. Results : Mapped Reads GC-content Distribution



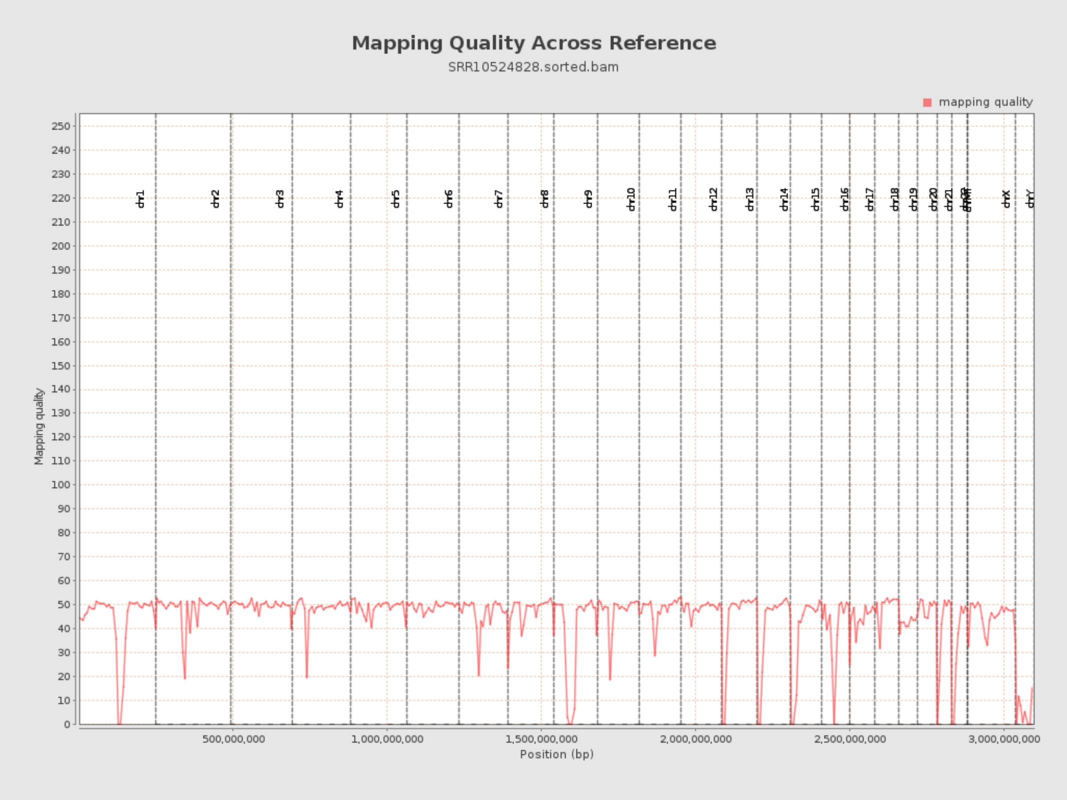
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram