Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 18:28:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524738.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_SRR10524738 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524738.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 18:28:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524738.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,702,349
Mapped reads	1,543,196 / 90.65%
Unmapped reads	159,153 / 9.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,023 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	61,402 / 3.61%
Duplication rate	3.02%
Clipped reads	1,545,823 / 90.81%

2.2. ACGT Content

Number/percentage of A's	22,711,883 / 25.69%
Number/percentage of C's	16,421,791 / 18.58%
Number/percentage of T's	27,155,991 / 30.72%
Number/percentage of G's	22,093,184 / 24.99%
Number/percentage of N's	10,630 / 0.01%
GC Percentage	43.57%

2.3. Coverage

Mean	0.0286

Standard Deviation	0.2536

2.4. Mapping Quality

Mean Mapping Quality	44.39

2.5. Mismatches and indels

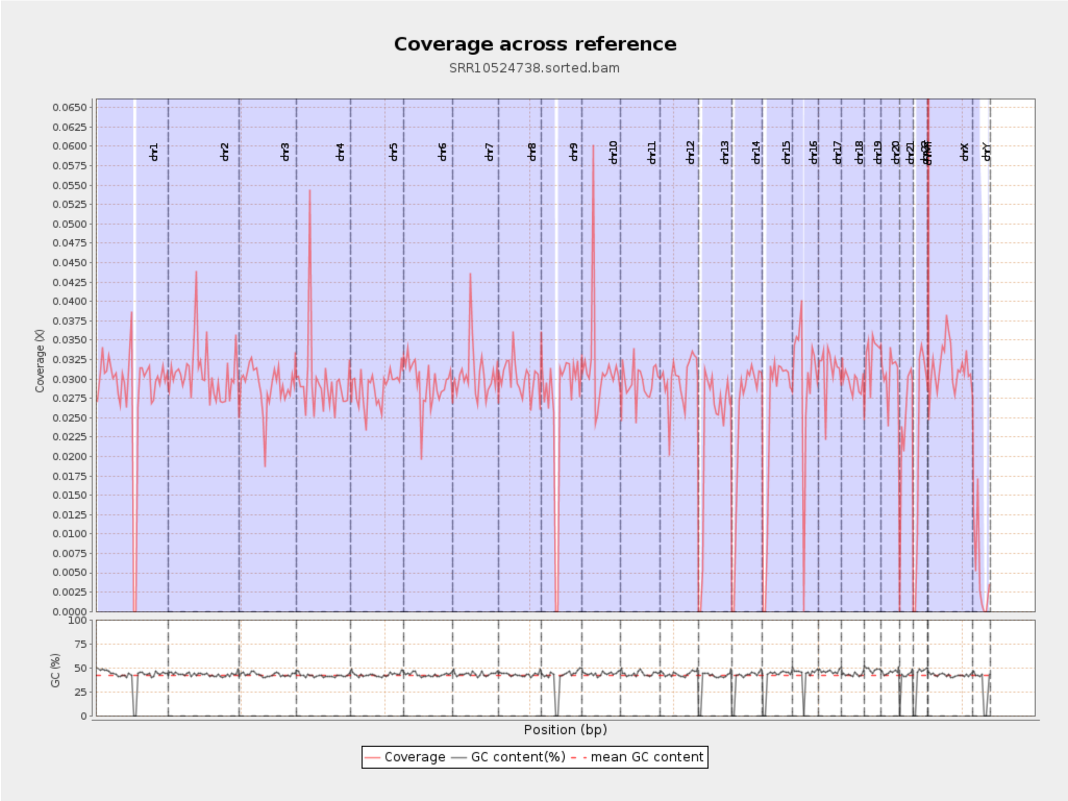
General error rate	0.53%
Mismatches	457,301
Insertions	6,955
Mapped reads with at least one insertion	0.45%
Deletions	17,798
Mapped reads with at least one deletion	1.14%
Homopolymer indels	40.32%

2.6. Chromosome stats

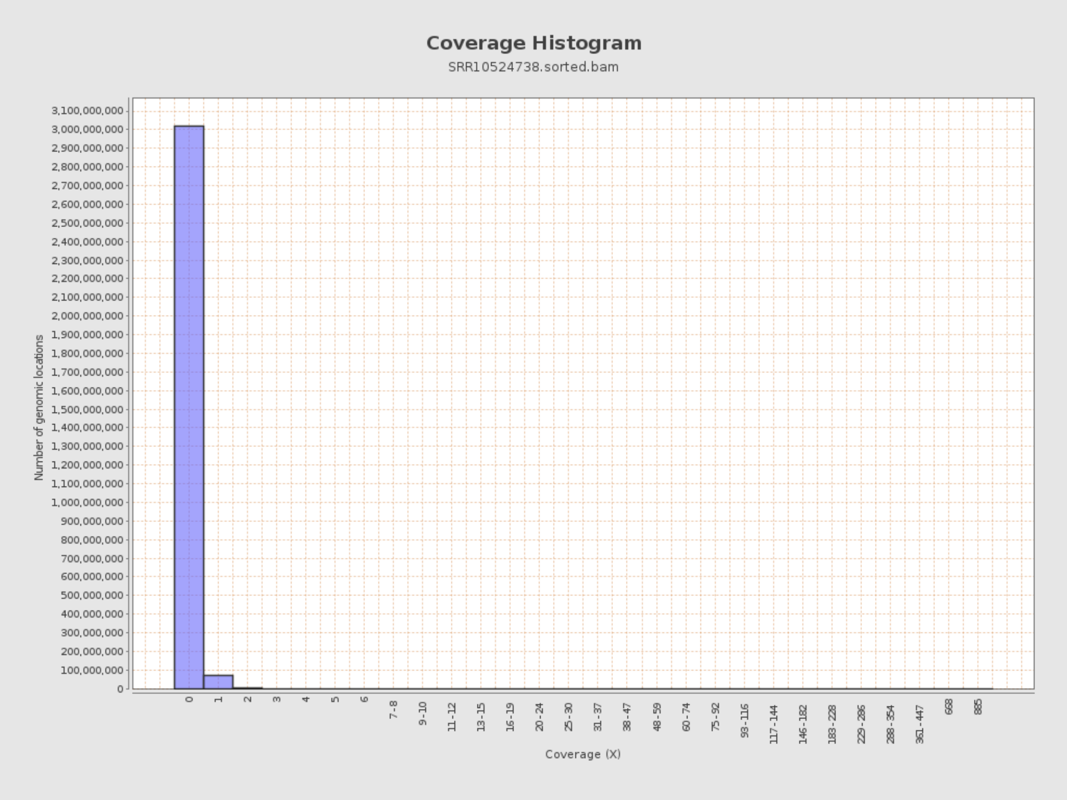
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7074457	0.0284	0.3425
chr2	243199373	7452249	0.0306	0.4141
chr3	198022430	5767817	0.0291	0.1927
chr4	191154276	5669693	0.0297	0.2174
chr5	180915260	5250682	0.029	0.1874
chr6	171115067	5026696	0.0294	0.2096
chr7	159138663	4892701	0.0307	0.3011

chr8	146364022	4413048	0.0302	0.2375
chr9	141213431	3765963	0.0267	0.2183
chr10	135534747	4303056	0.0317	0.3057
chr11	135006516	4000424	0.0296	0.2282
chr12	133851895	3991790	0.0298	0.1924
chr13	115169878	2679141	0.0233	0.169
chr14	107349540	2666134	0.0248	0.178
chr15	102531392	2540156	0.0248	0.1739
chr16	90354753	2671880	0.0296	0.2094
chr17	81195210	2538238	0.0313	0.2035
chr18	78077248	2312774	0.0296	0.315
chr19	59128983	1958193	0.0331	0.2914
chr20	63025520	1914121	0.0304	0.2005
chr21	48129895	1167233	0.0243	0.1959
chr22	51304566	1139420	0.0222	0.1657
chrMT	16571	33613	2.0284	1.85
chrX	155270560	4899180	0.0316	0.2103
chrY	59373566	294125	0.005	0.1387

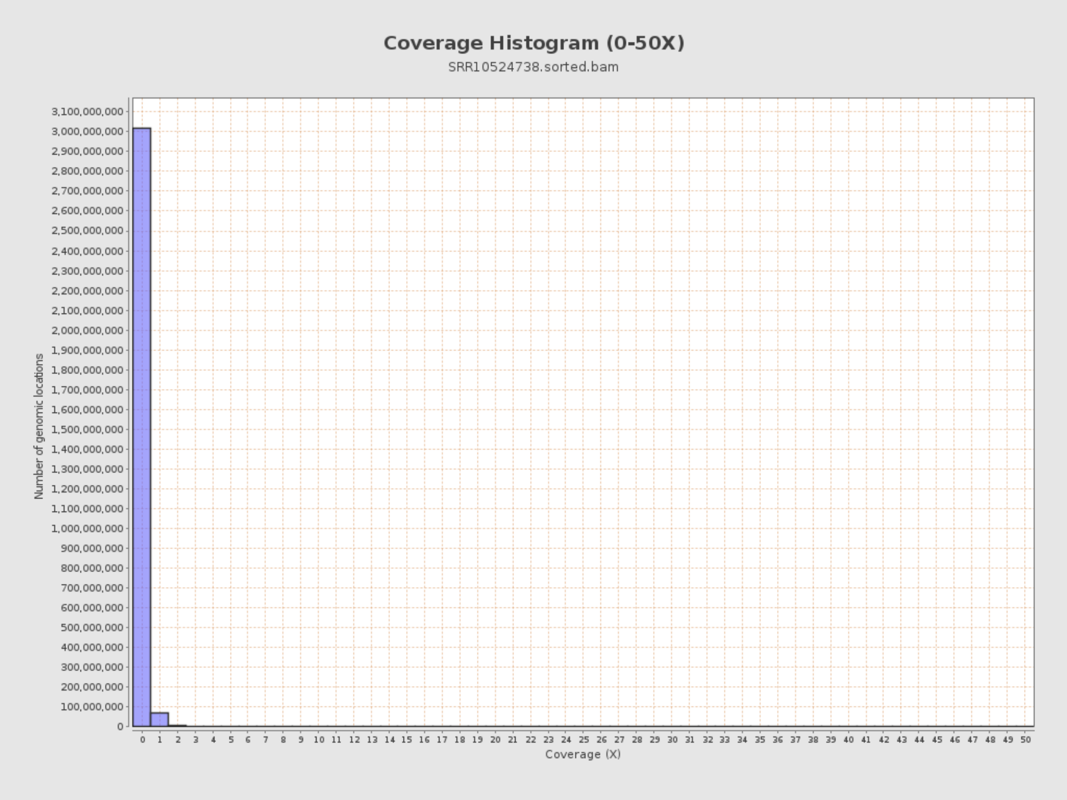
3. Results : Coverage across reference



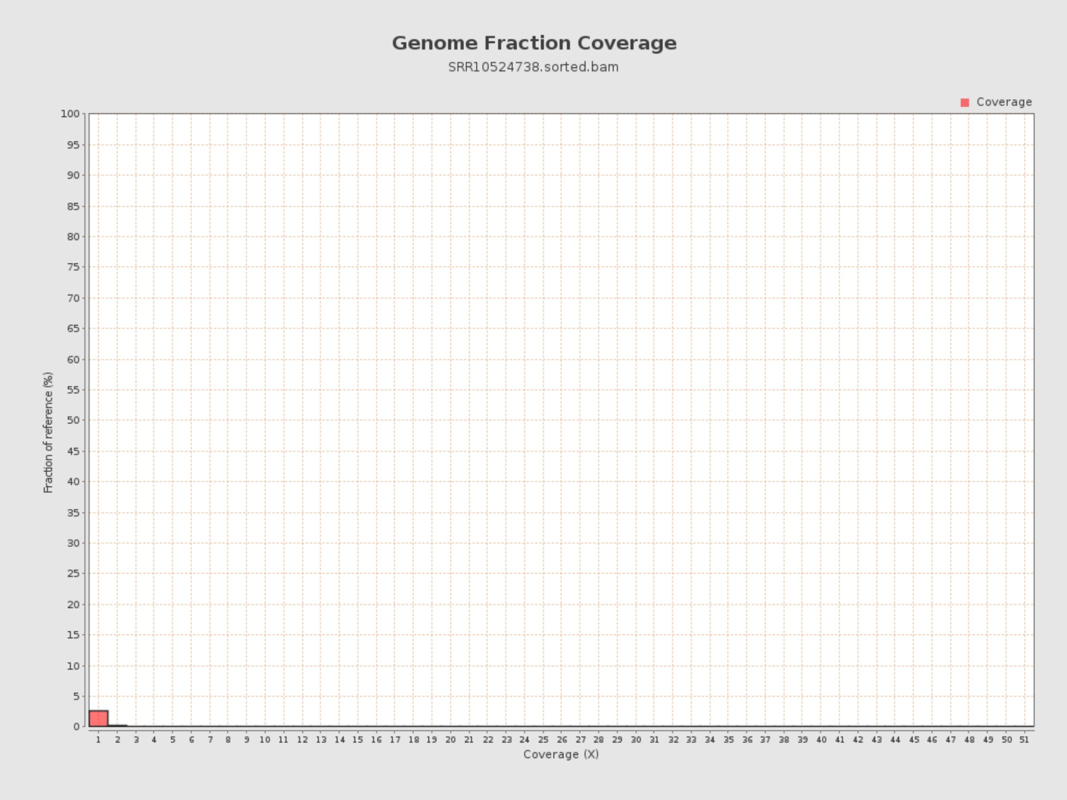
4. Results : Coverage Histogram



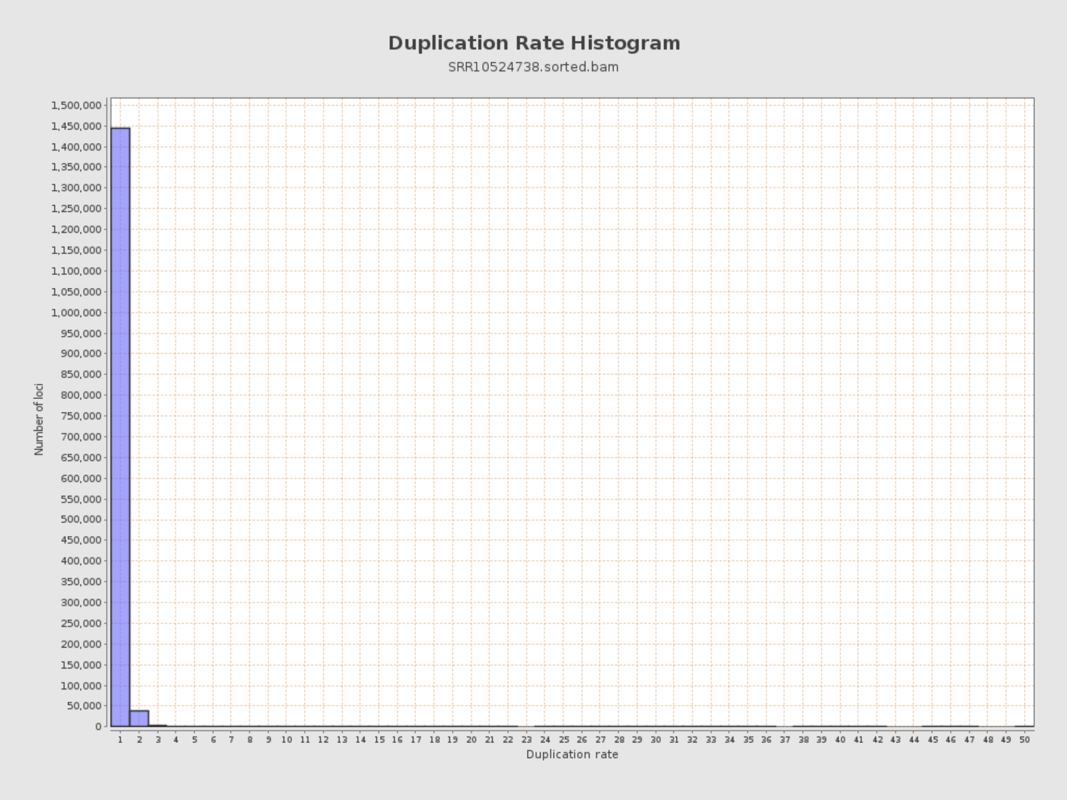
5. Results : Coverage Histogram (0-50X)



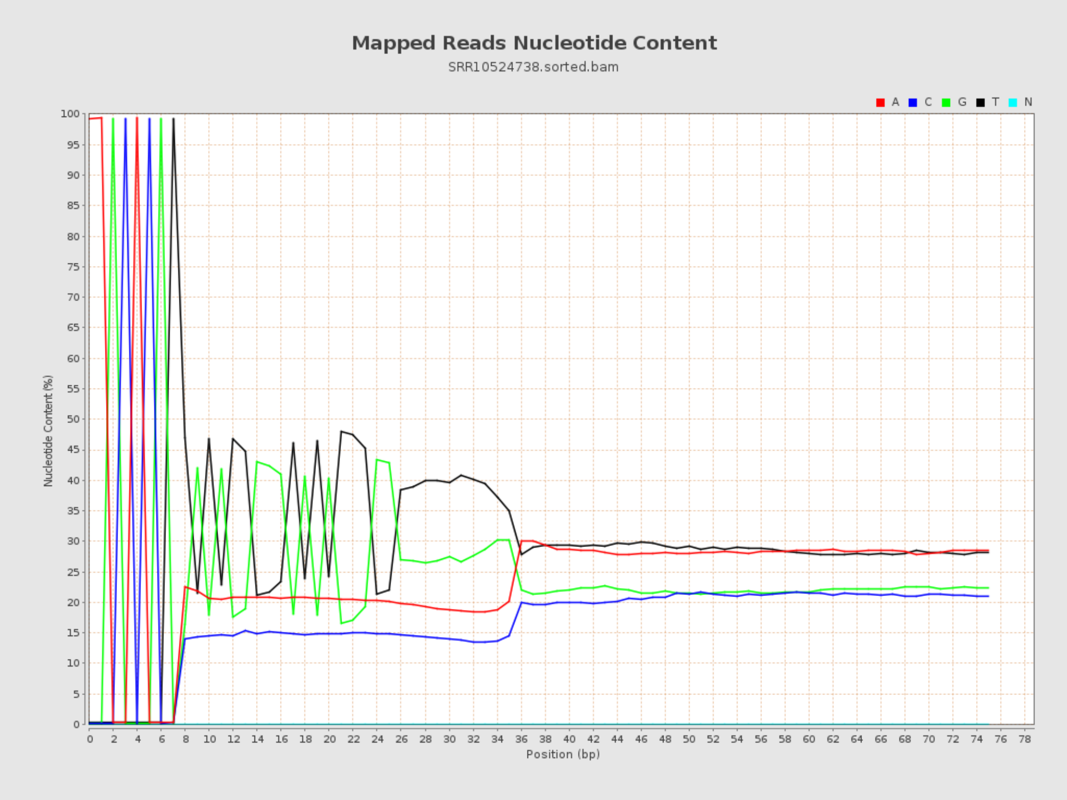
6. Results : Genome Fraction Coverage



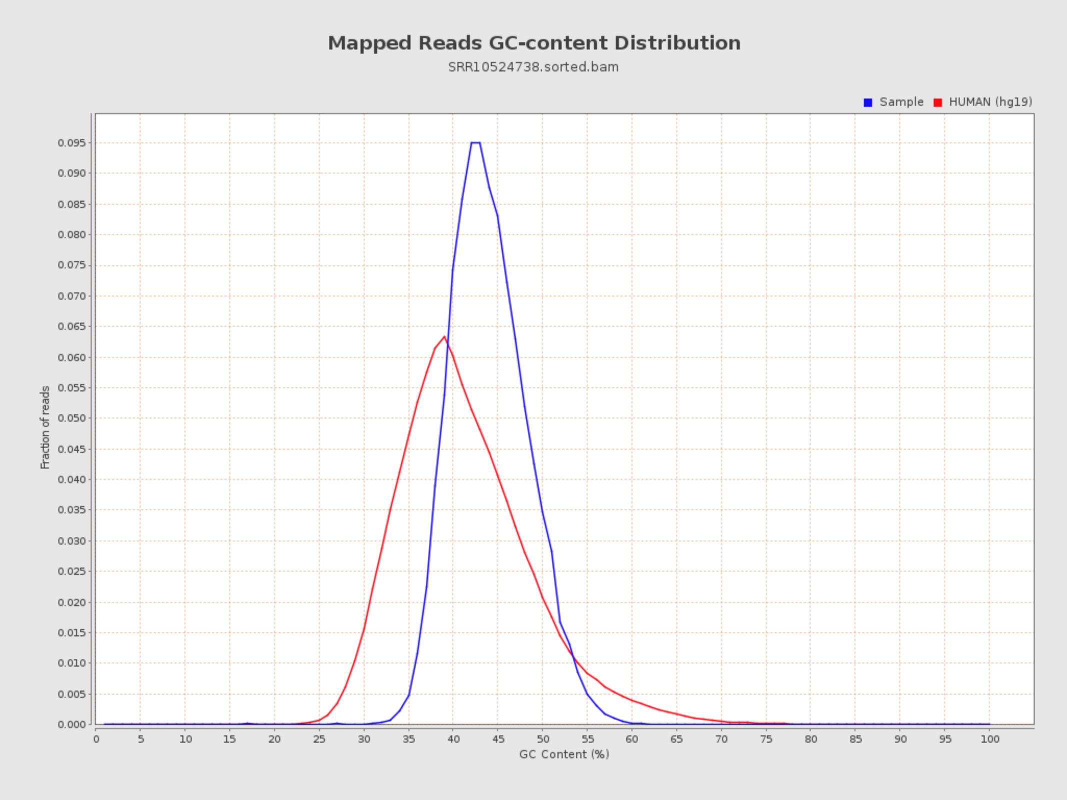
7. Results : Duplication Rate Histogram



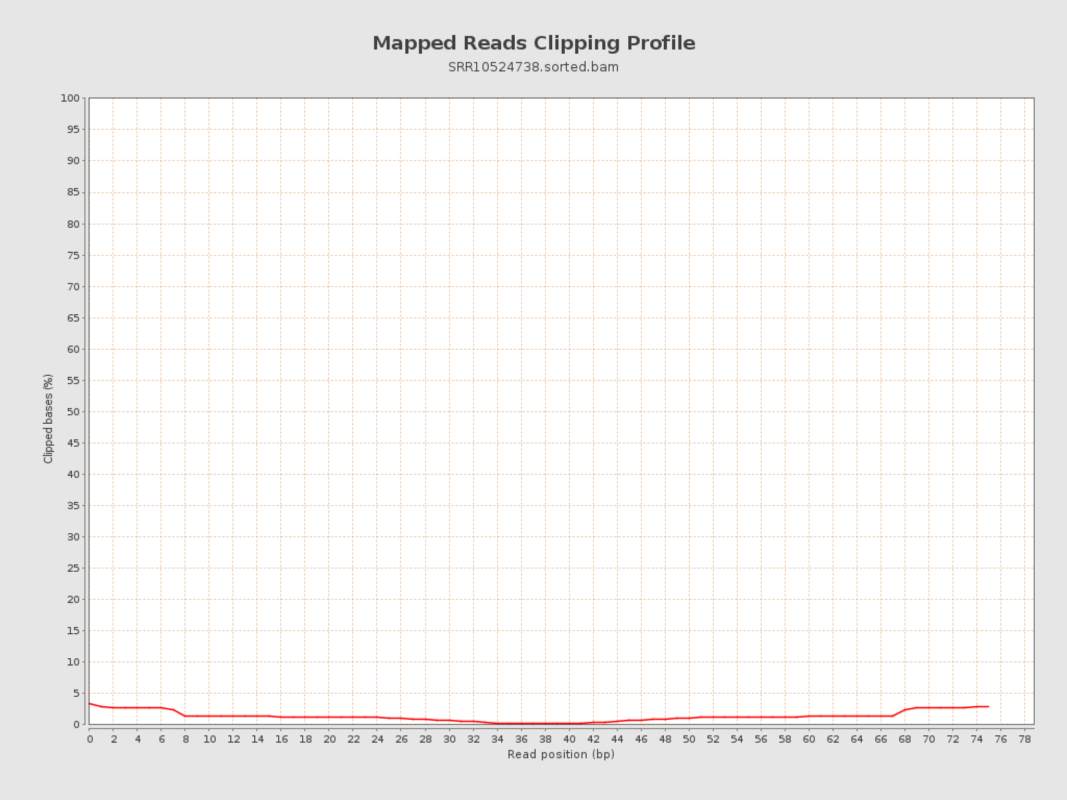
8. Results : Mapped Reads Nucleotide Content



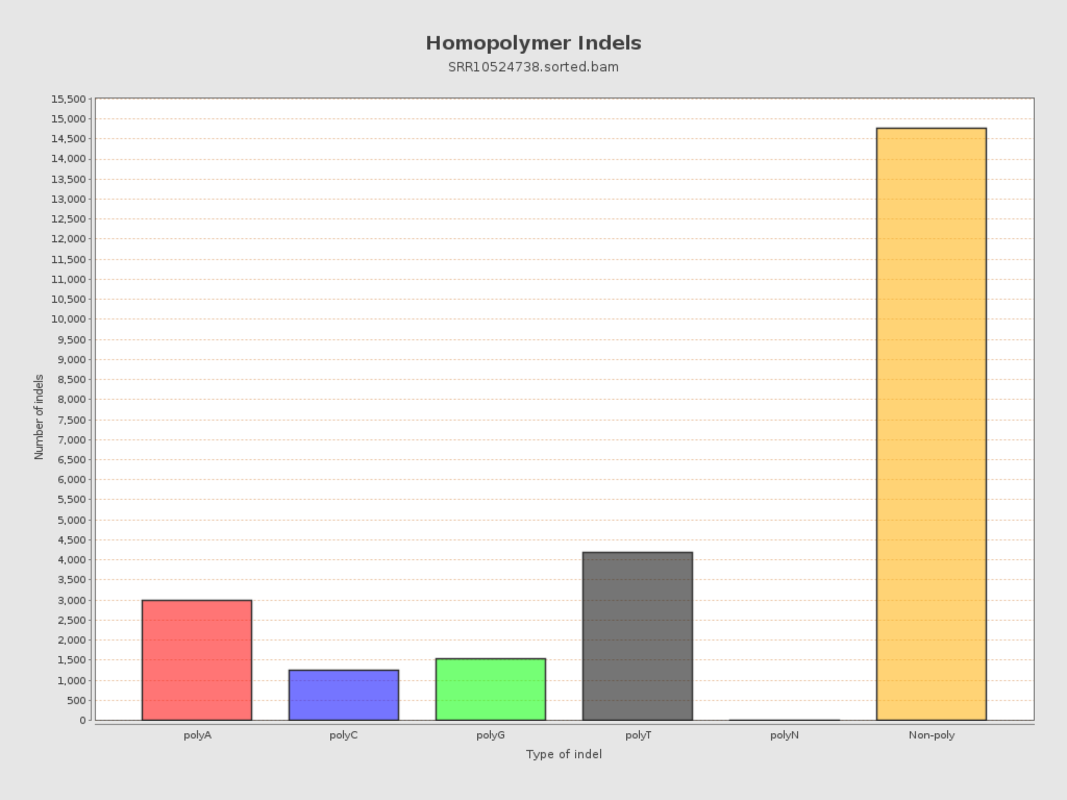
9. Results : Mapped Reads GC-content Distribution



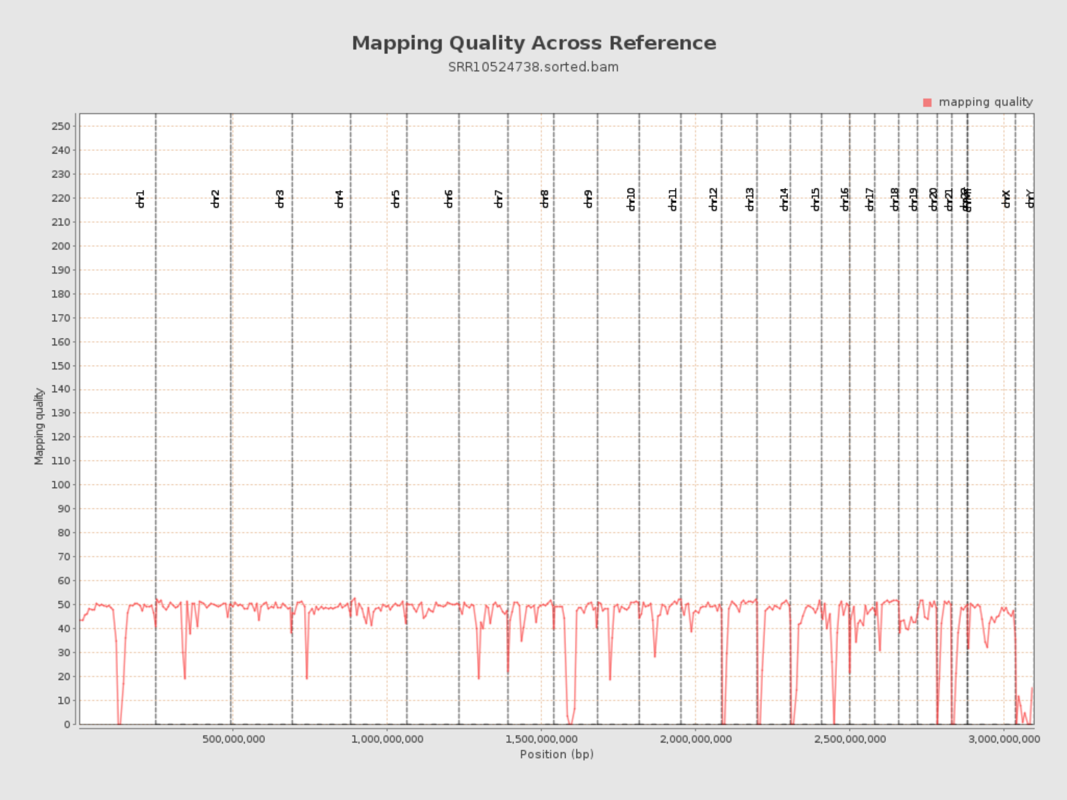
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram