Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 08:21:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524938.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_SRR10524938 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524938.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 08:21:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524938.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	768,316
Mapped reads	711,468 / 92.6%
Unmapped reads	56,848 / 7.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,883 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	23,739 / 3.09%
Duplication rate	2.62%
Clipped reads	712,660 / 92.76%

2.2. ACGT Content

Number/percentage of A's	10,188,436 / 24.69%
Number/percentage of C's	7,706,247 / 18.67%
Number/percentage of T's	13,330,083 / 32.3%
Number/percentage of G's	10,047,906 / 24.34%
Number/percentage of N's	378 / 0%
GC Percentage	43.02%

2.3. Coverage

Mean	0.0133

Standard Deviation	0.1556

2.4. Mapping Quality

Mean Mapping Quality	44.8

2.5. Mismatches and indels

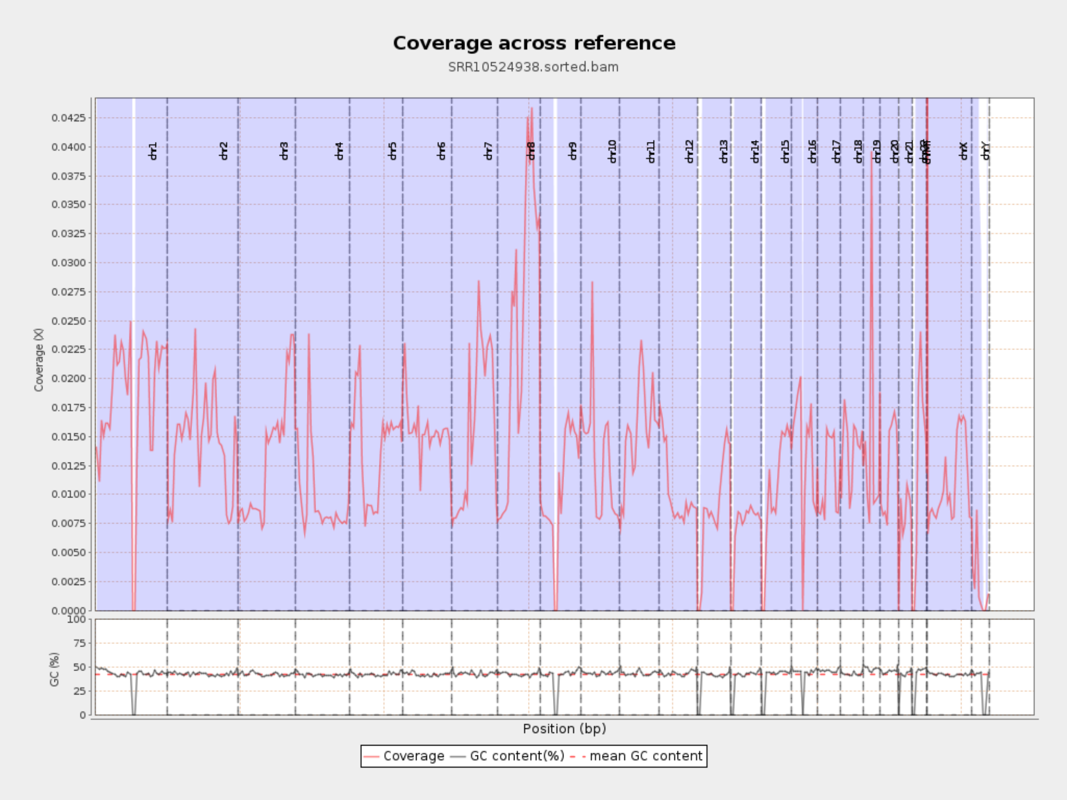
General error rate	0.51%
Mismatches	204,318
Insertions	3,061
Mapped reads with at least one insertion	0.43%
Deletions	8,020
Mapped reads with at least one deletion	1.12%
Homopolymer indels	42.88%

2.6. Chromosome stats

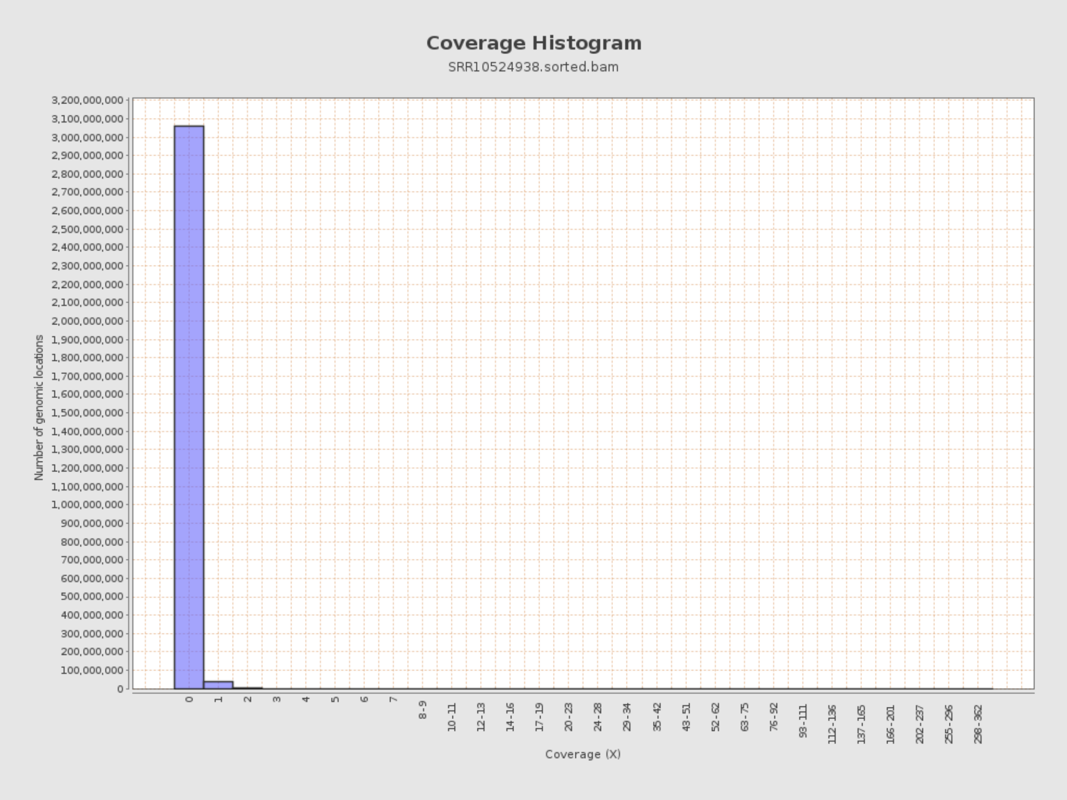
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4568069	0.0183	0.272
chr2	243199373	3518192	0.0145	0.1764
chr3	198022430	2614521	0.0132	0.1217
chr4	191154276	1872193	0.0098	0.1209
chr5	180915260	2552568	0.0141	0.1262
chr6	171115067	2677584	0.0156	0.1373
chr7	159138663	2550552	0.016	0.1827

chr8	146364022	3611145	0.0247	0.1975
chr9	141213431	1485376	0.0105	0.126
chr10	135534747	1796318	0.0133	0.1615
chr11	135006516	2107925	0.0156	0.145
chr12	133851895	1381867	0.0103	0.1101
chr13	115169878	999968	0.0087	0.0995
chr14	107349540	762673	0.0071	0.0913
chr15	102531392	1056658	0.0103	0.1077
chr16	90354753	1226175	0.0136	0.128
chr17	81195210	920237	0.0113	0.1157
chr18	78077248	1085548	0.0139	0.1867
chr19	59128983	849994	0.0144	0.2029
chr20	63025520	780693	0.0124	0.122
chr21	48129895	378865	0.0079	0.1078
chr22	51304566	654919	0.0128	0.1198
chrMT	16571	4266	0.2574	0.5122
chrX	155270560	1704491	0.011	0.1177
chrY	59373566	125834	0.0021	0.0832

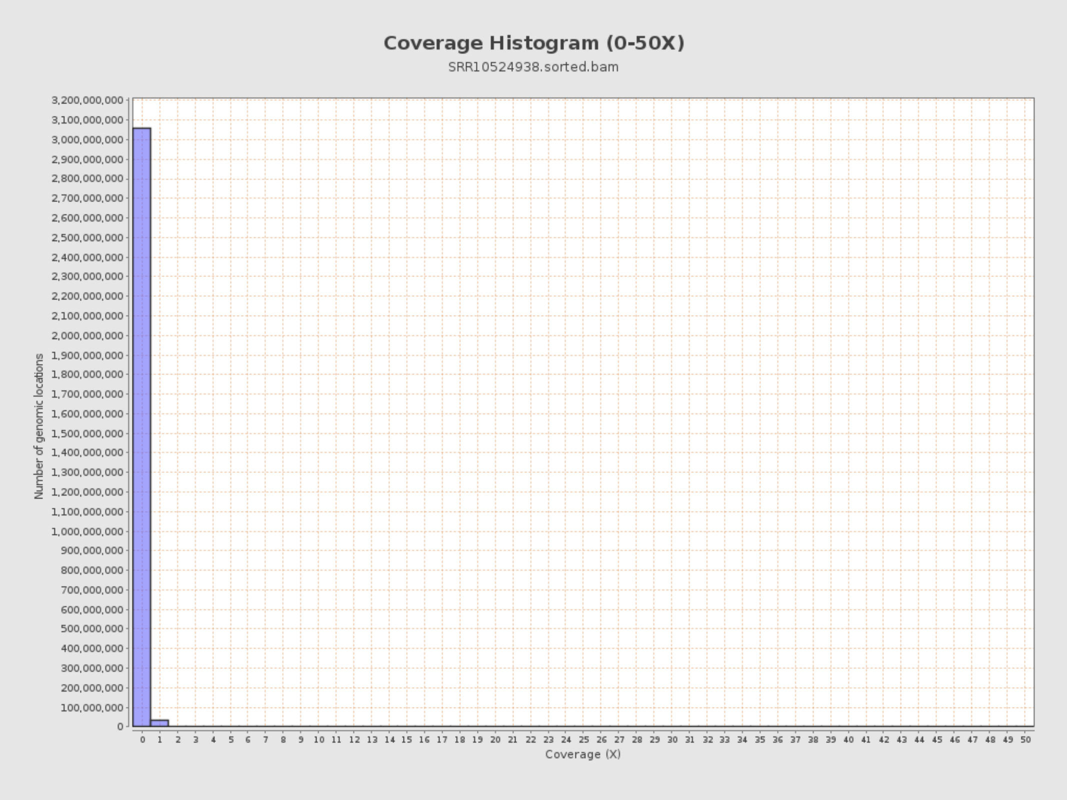
3. Results : Coverage across reference



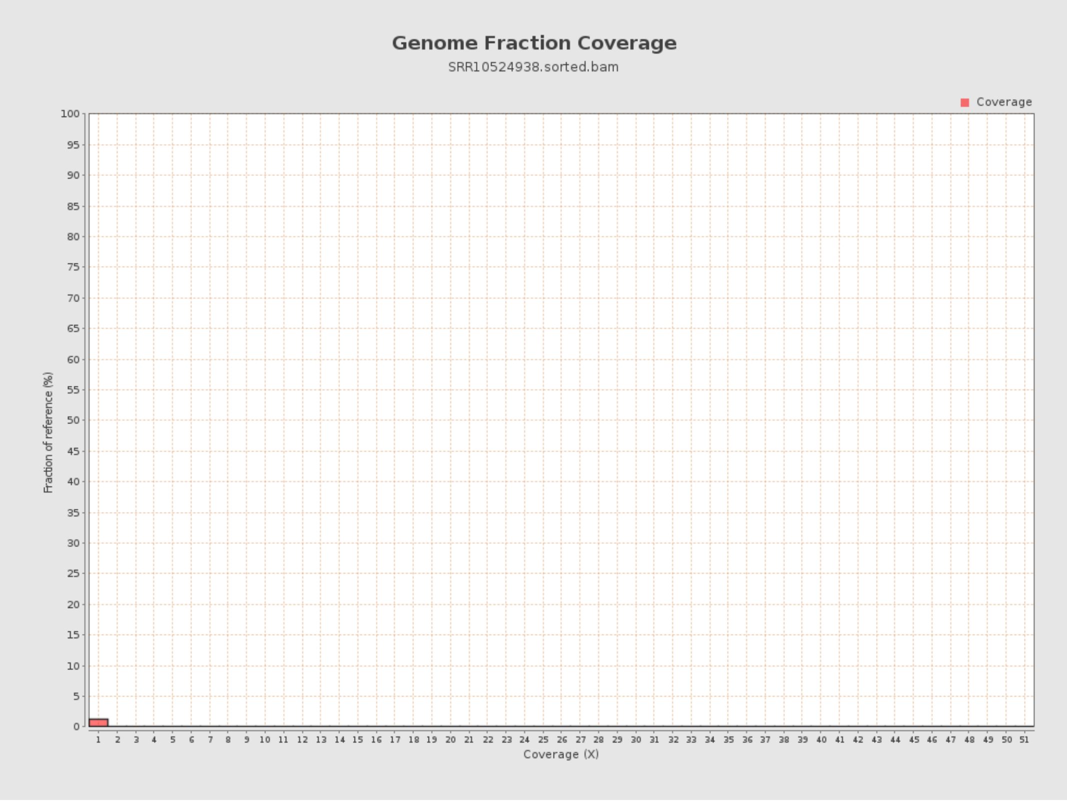
4. Results : Coverage Histogram



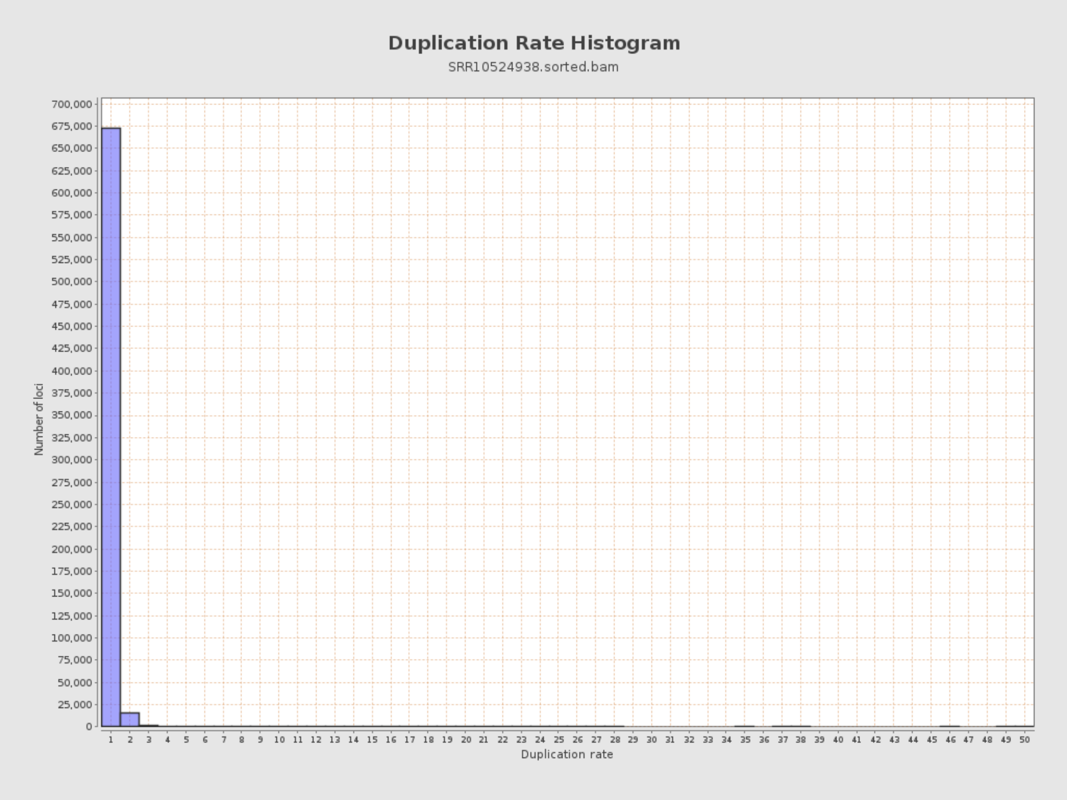
5. Results : Coverage Histogram (0-50X)



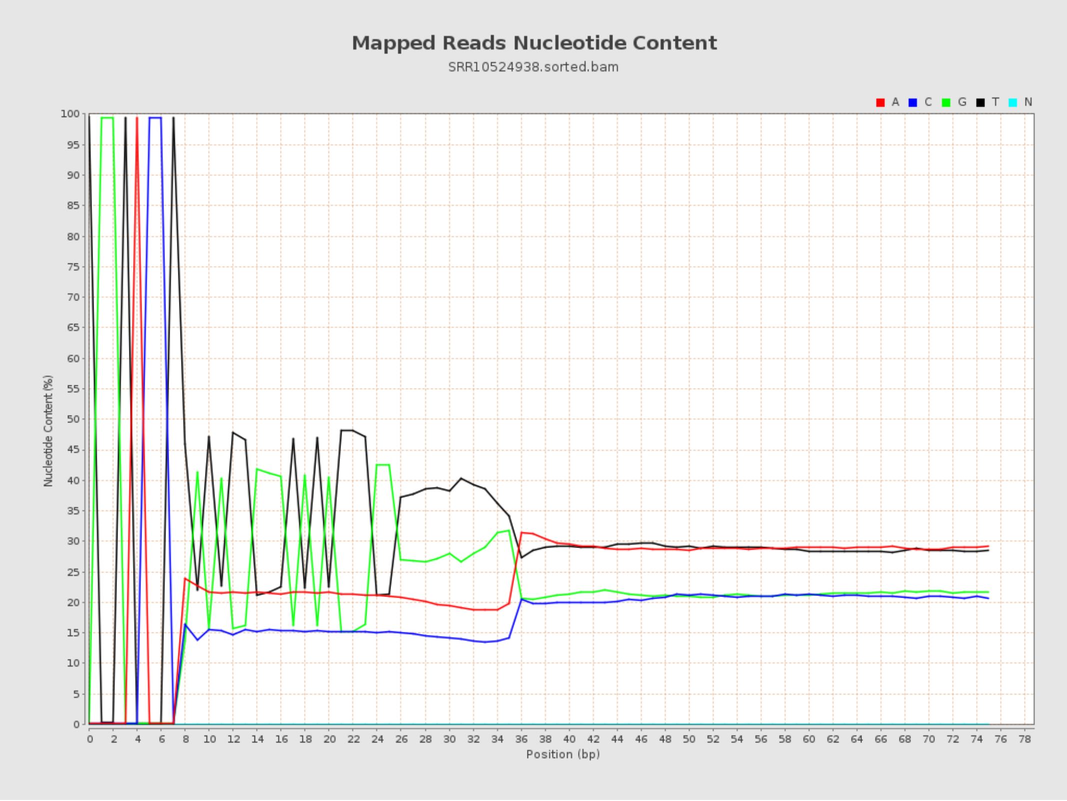
6. Results : Genome Fraction Coverage



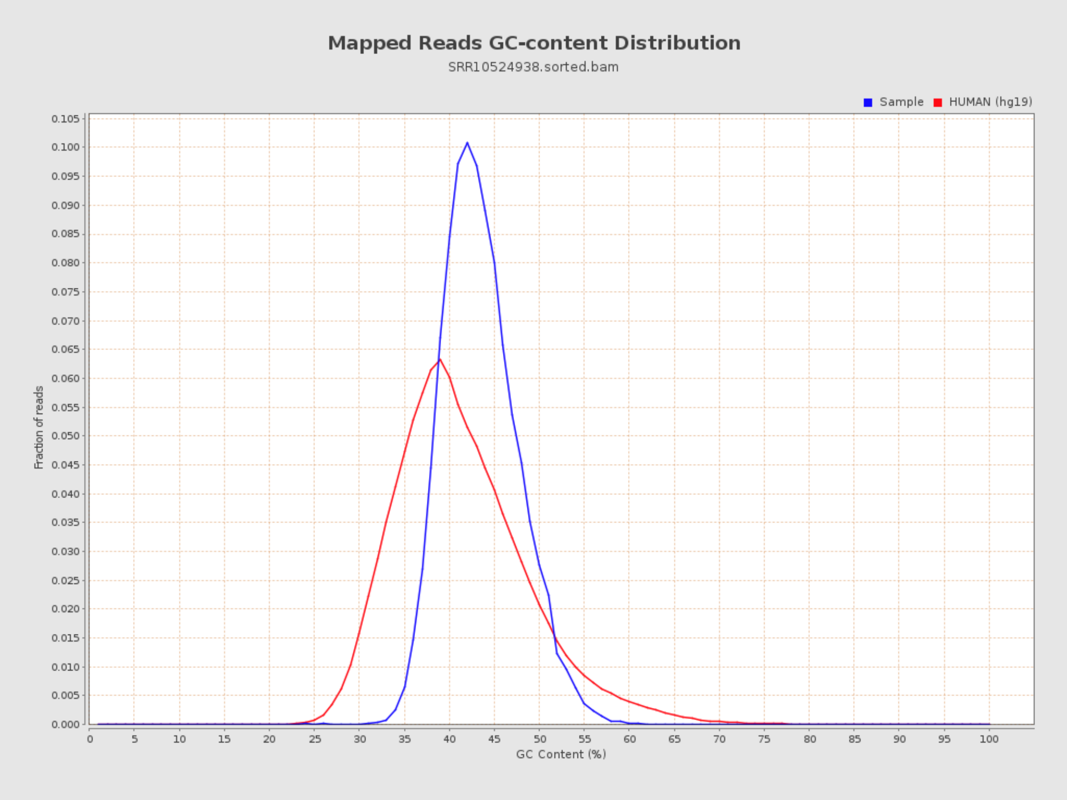
7. Results : Duplication Rate Histogram



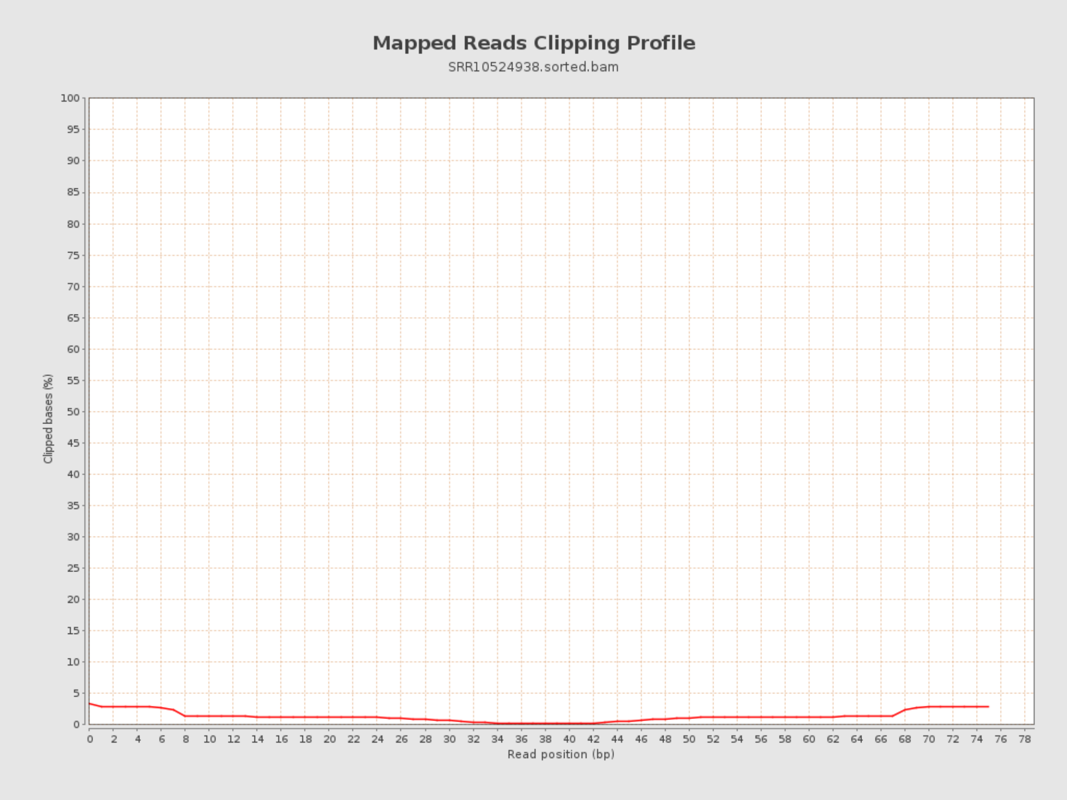
8. Results : Mapped Reads Nucleotide Content



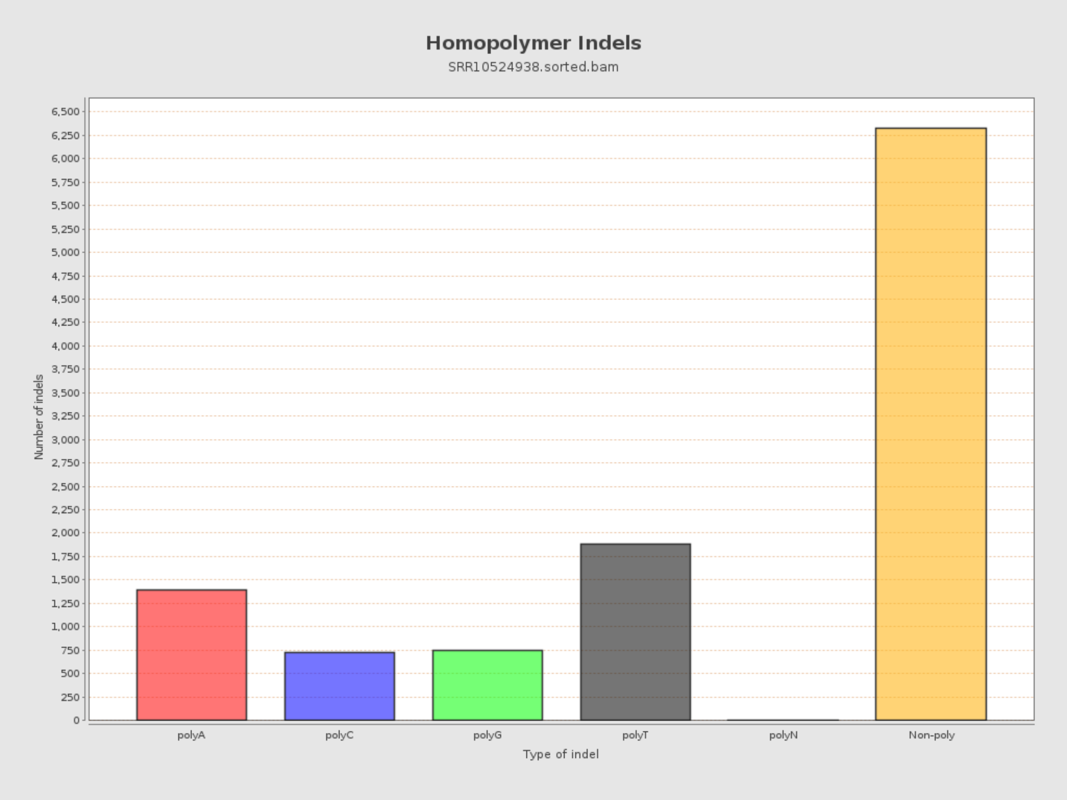
9. Results : Mapped Reads GC-content Distribution



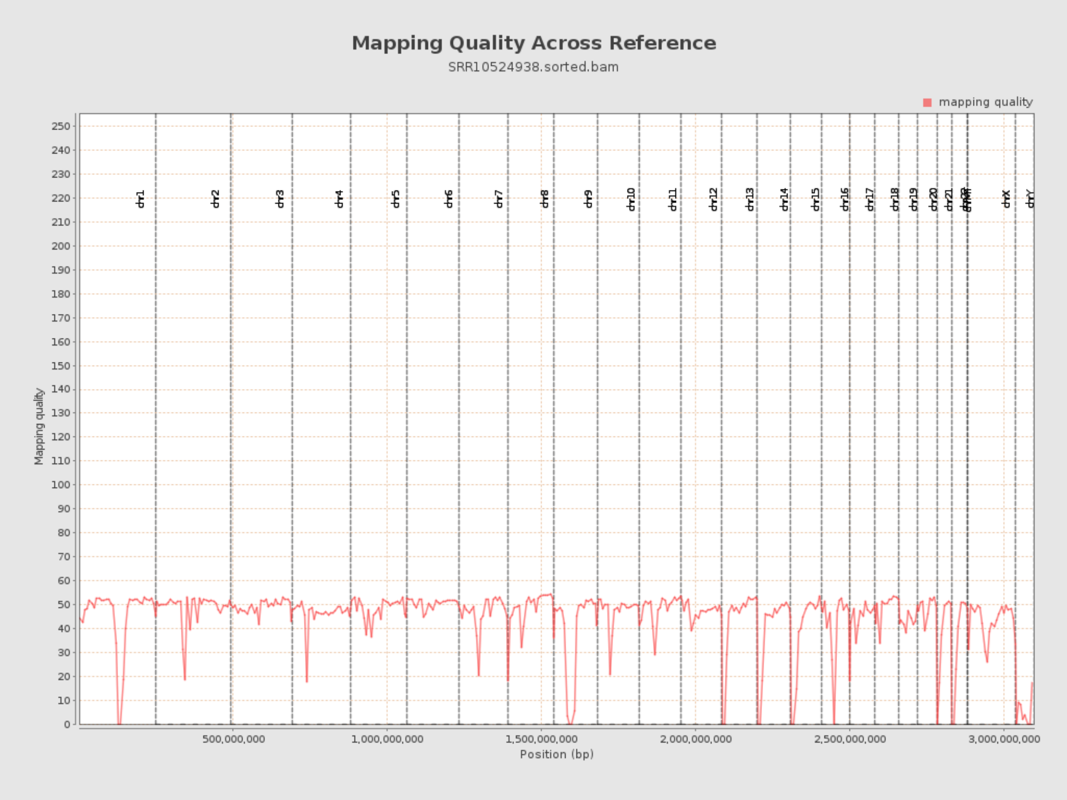
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram