Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 23:56:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524870.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_SRR10524870 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524870.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 23:56:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524870.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,075,430
Mapped reads	989,032 / 91.97%
Unmapped reads	86,398 / 8.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,575 / 0.43%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	24,196 / 2.25%
Duplication rate	1.67%
Clipped reads	990,297 / 92.08%

2.2. ACGT Content

Number/percentage of A's	14,805,211 / 25.62%
Number/percentage of C's	11,413,530 / 19.75%
Number/percentage of T's	18,814,175 / 32.56%
Number/percentage of G's	12,740,900 / 22.05%
Number/percentage of N's	7,771 / 0.01%
GC Percentage	41.8%

2.3. Coverage

Mean	0.0187

Standard Deviation	0.2069

2.4. Mapping Quality

Mean Mapping Quality	45.4

2.5. Mismatches and indels

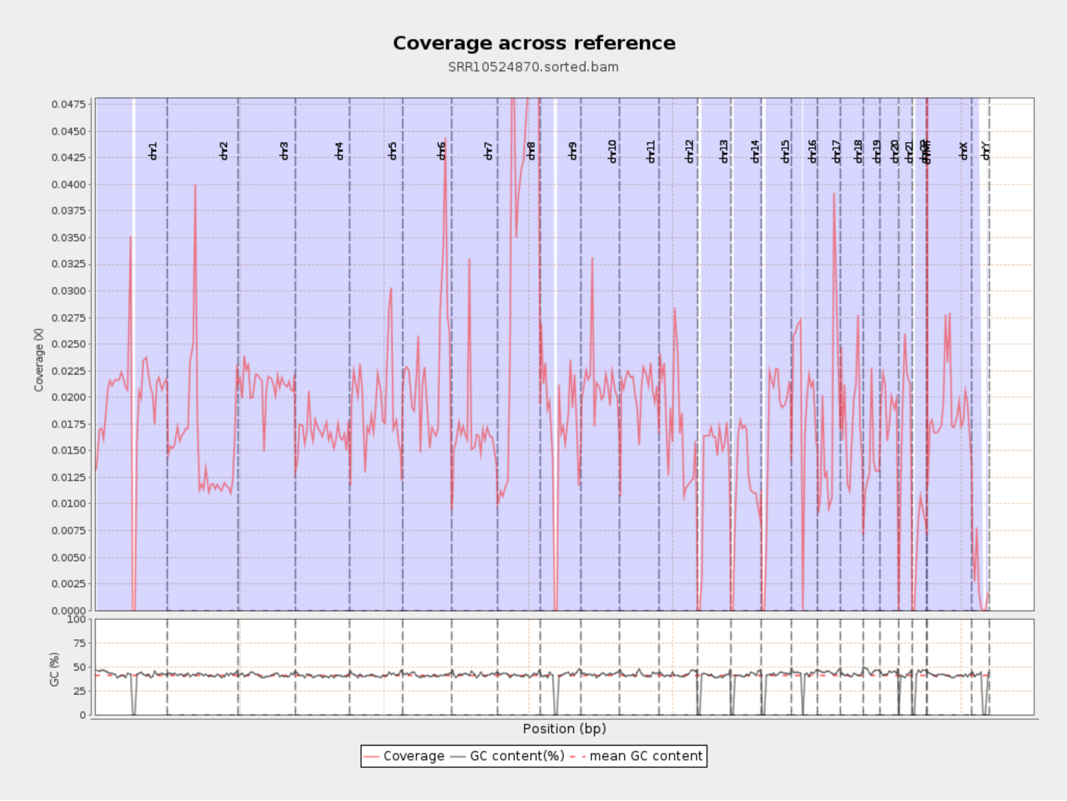
General error rate	0.49%
Mismatches	276,431
Insertions	4,597
Mapped reads with at least one insertion	0.46%
Deletions	10,652
Mapped reads with at least one deletion	1.07%
Homopolymer indels	43.62%

2.6. Chromosome stats

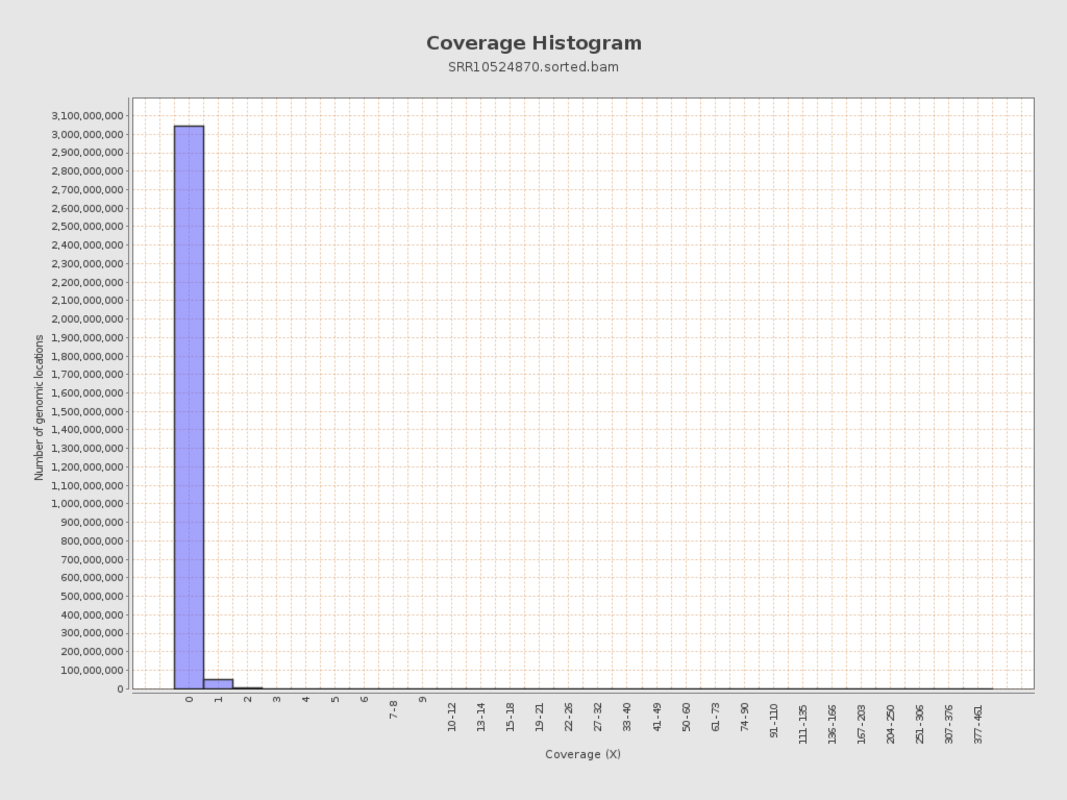
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4854167	0.0195	0.38
chr2	243199373	3741517	0.0154	0.2035
chr3	198022430	4196845	0.0212	0.1518
chr4	191154276	3169395	0.0166	0.1405
chr5	180915260	3551128	0.0196	0.1465
chr6	171115067	3810571	0.0223	0.1674
chr7	159138663	2659771	0.0167	0.2804

chr8	146364022	5942996	0.0406	0.2785
chr9	141213431	2412812	0.0171	0.1788
chr10	135534747	2892920	0.0213	0.192
chr11	135006516	2802103	0.0208	0.1944
chr12	133851895	2310877	0.0173	0.1398
chr13	115169878	1541870	0.0134	0.121
chr14	107349540	1240048	0.0116	0.1177
chr15	102531392	1732226	0.0169	0.1368
chr16	90354753	1798403	0.0199	0.156
chr17	81195210	1453630	0.0179	0.1545
chr18	78077248	1410370	0.0181	0.3105
chr19	59128983	819867	0.0139	0.2745
chr20	63025520	1190778	0.0189	0.1446
chr21	48129895	852435	0.0177	0.1444
chr22	51304566	338568	0.0066	0.0845
chrMT	16571	1246	0.0752	0.2863
chrX	155270560	2930207	0.0189	0.1606
chrY	59373566	143625	0.0024	0.0678

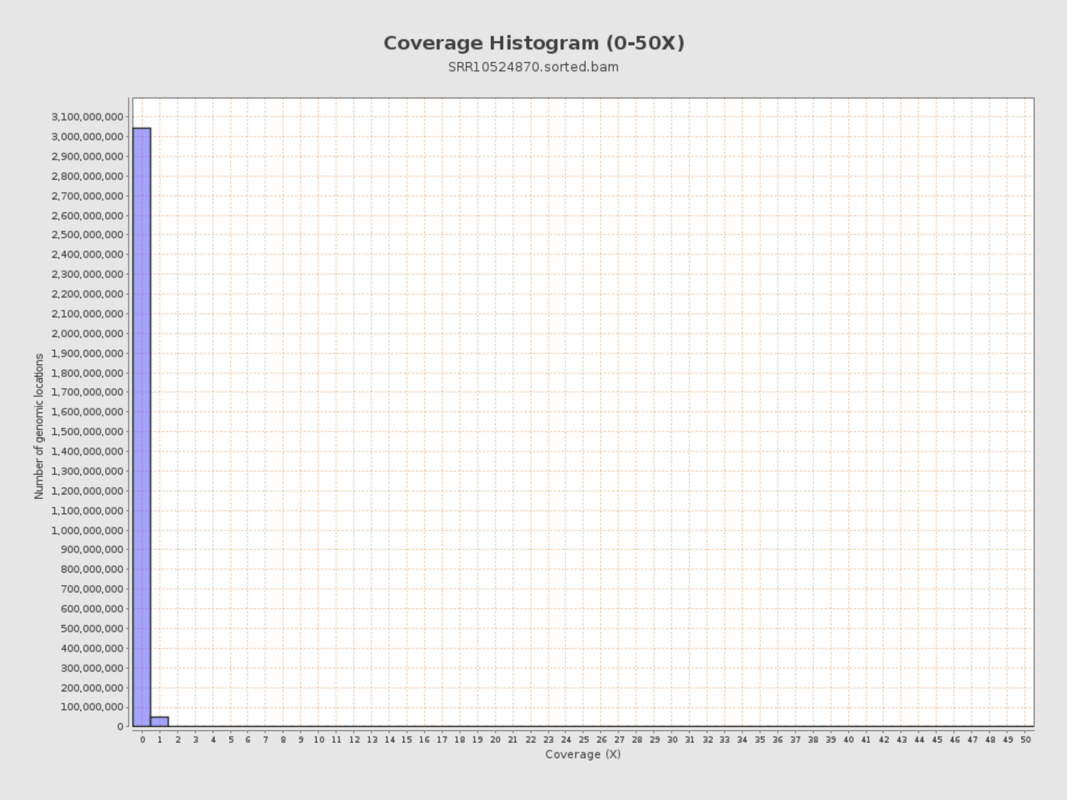
3. Results : Coverage across reference



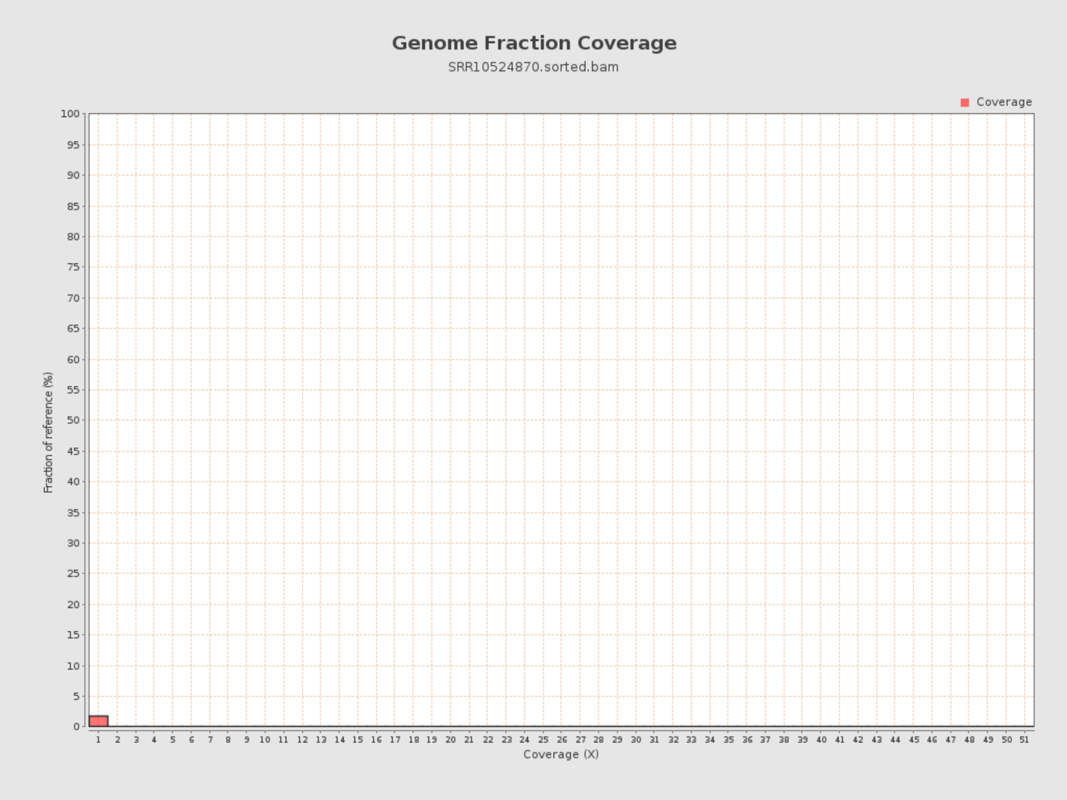
4. Results : Coverage Histogram



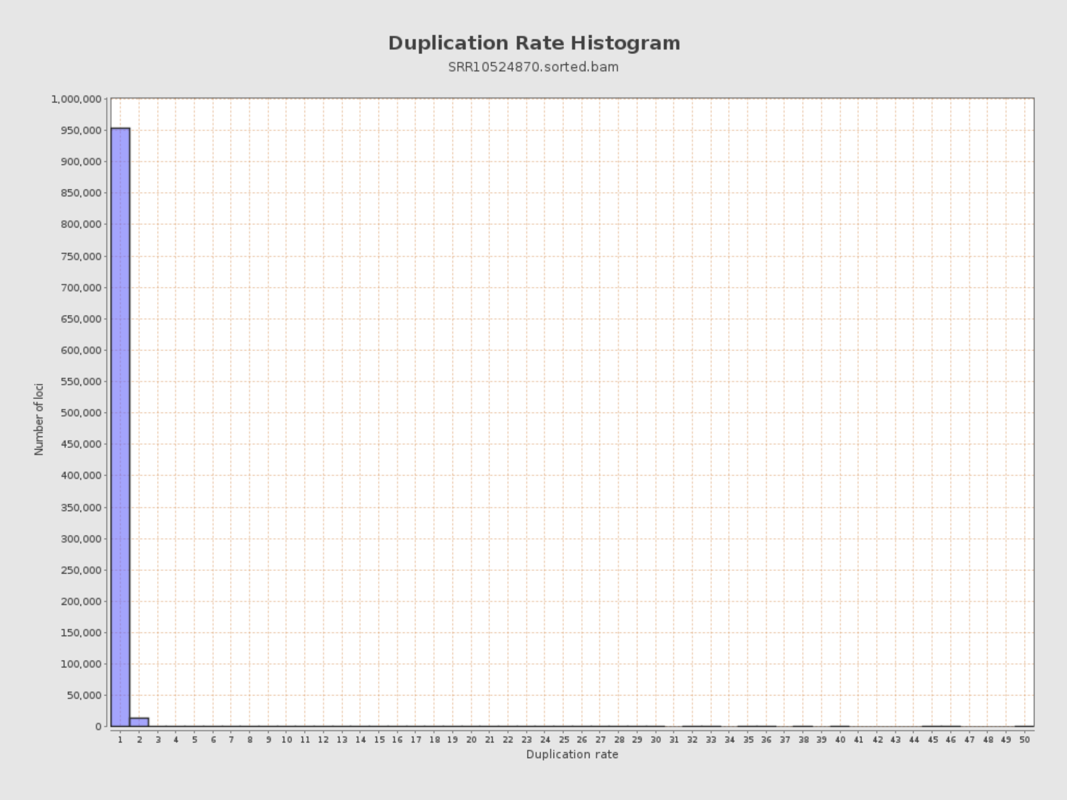
5. Results : Coverage Histogram (0-50X)



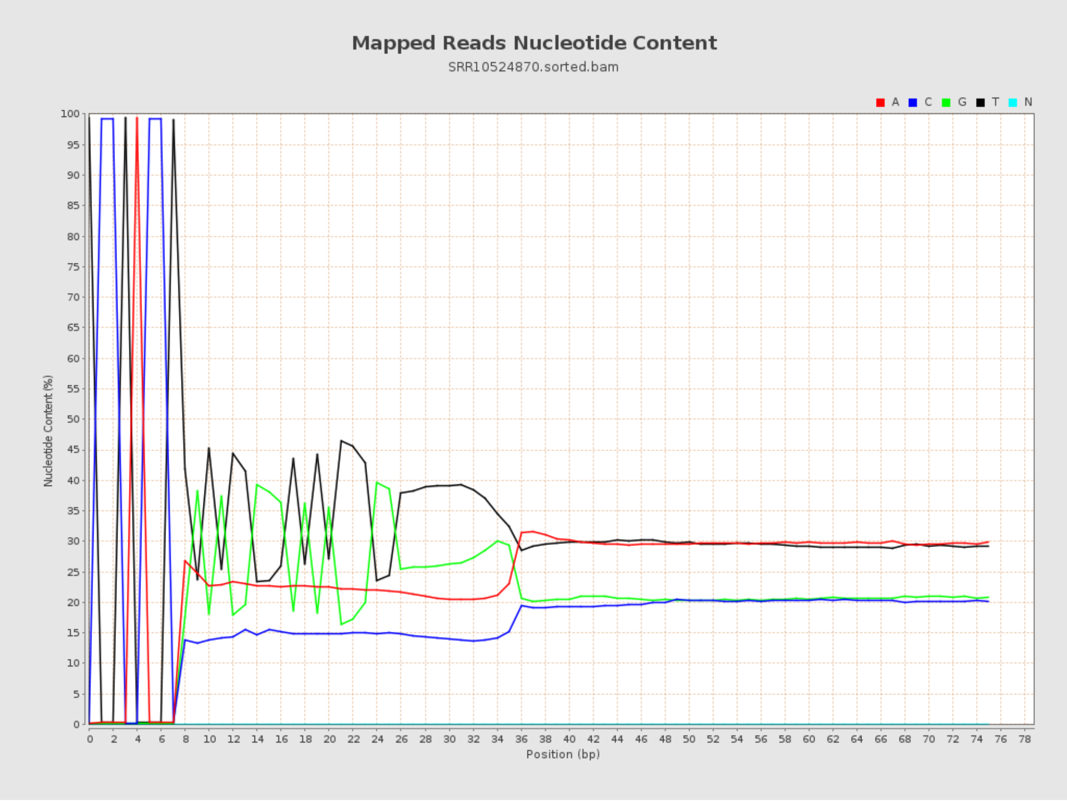
6. Results : Genome Fraction Coverage



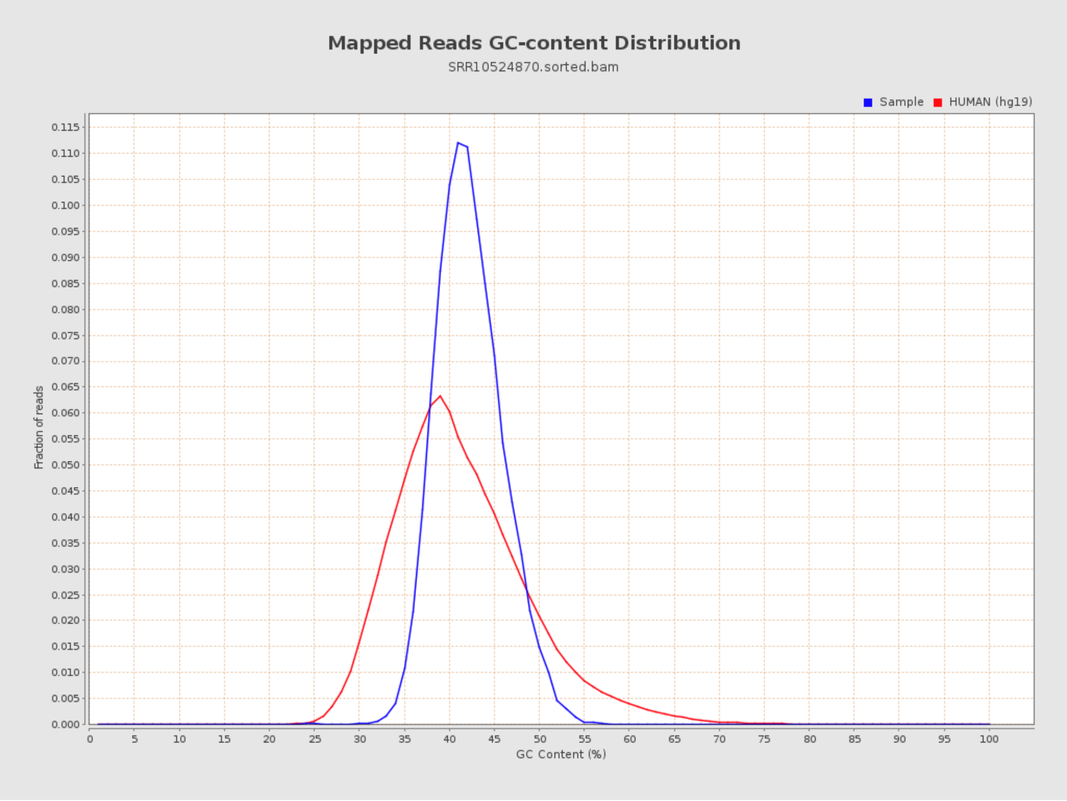
7. Results : Duplication Rate Histogram



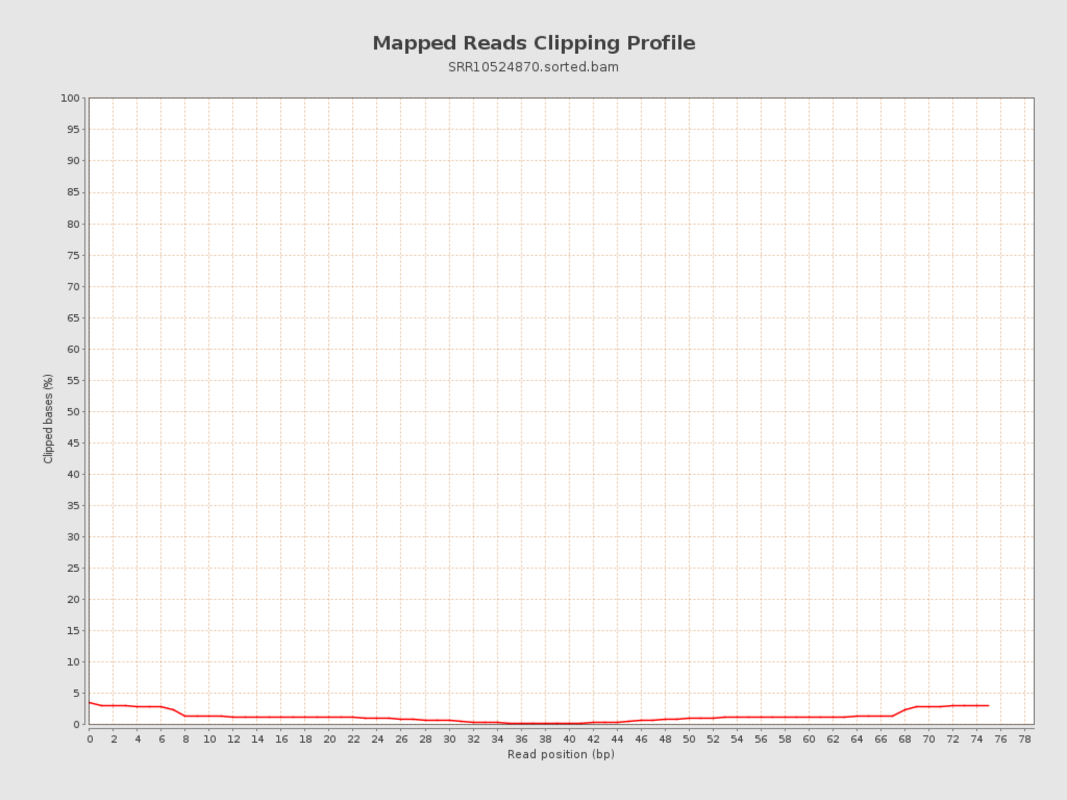
8. Results : Mapped Reads Nucleotide Content



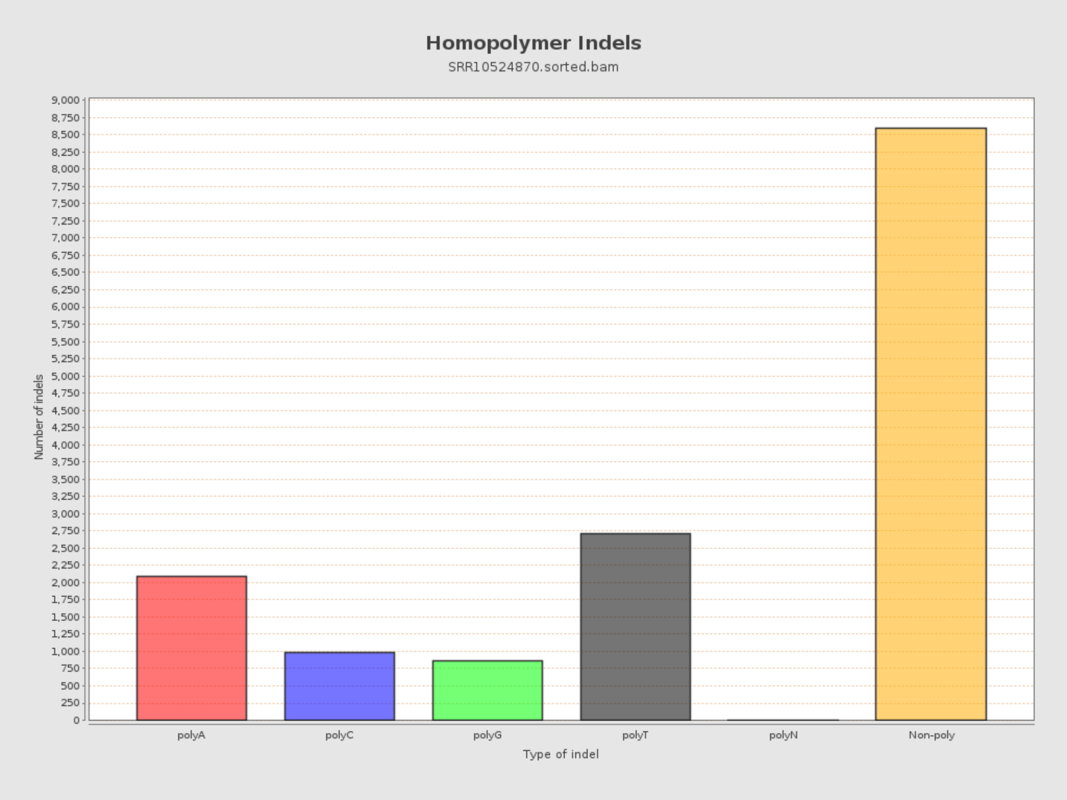
9. Results : Mapped Reads GC-content Distribution



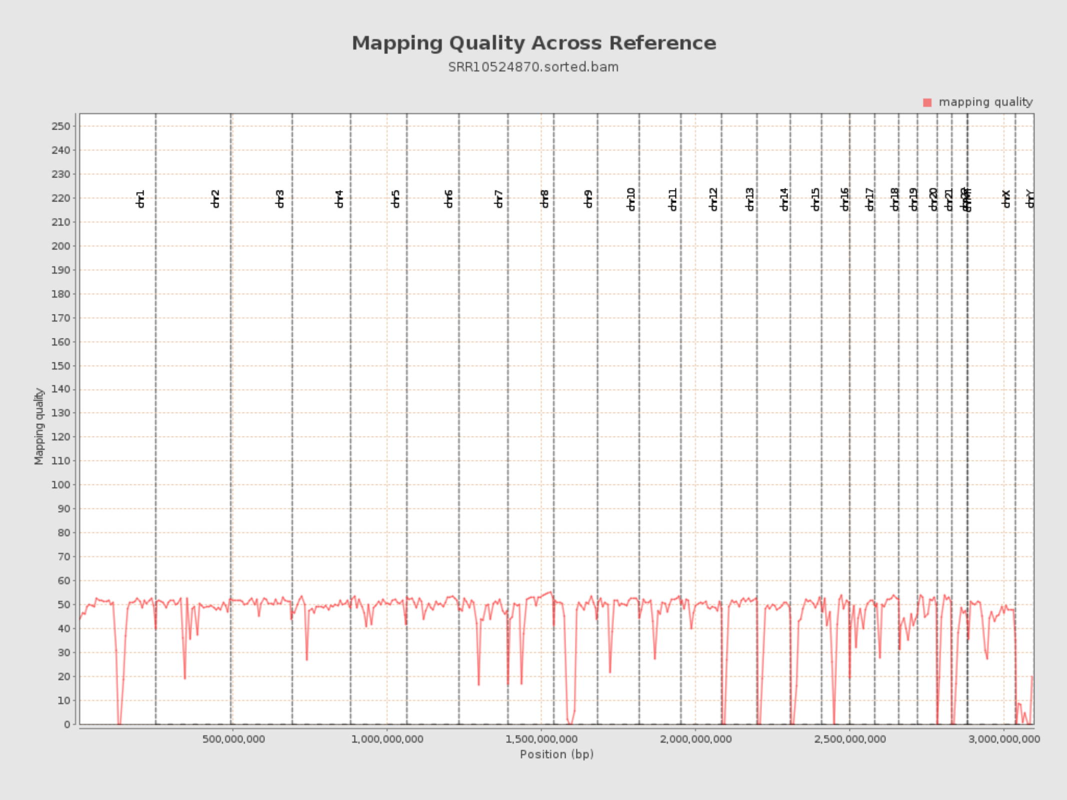
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram