Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 07:09:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524936.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_SRR10524936 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524936.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 07:08:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524936.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,035,215
Mapped reads	952,434 / 92%
Unmapped reads	82,781 / 8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,895 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	32,431 / 3.13%
Duplication rate	2.64%
Clipped reads	953,825 / 92.14%

2.2. ACGT Content

Number/percentage of A's	14,318,282 / 25.71%
Number/percentage of C's	10,966,053 / 19.69%
Number/percentage of T's	17,397,223 / 31.24%
Number/percentage of G's	13,015,703 / 23.37%
Number/percentage of N's	422 / 0%
GC Percentage	43.06%

2.3. Coverage

Mean	0.018

Standard Deviation	0.189

2.4. Mapping Quality

Mean Mapping Quality	45.03

2.5. Mismatches and indels

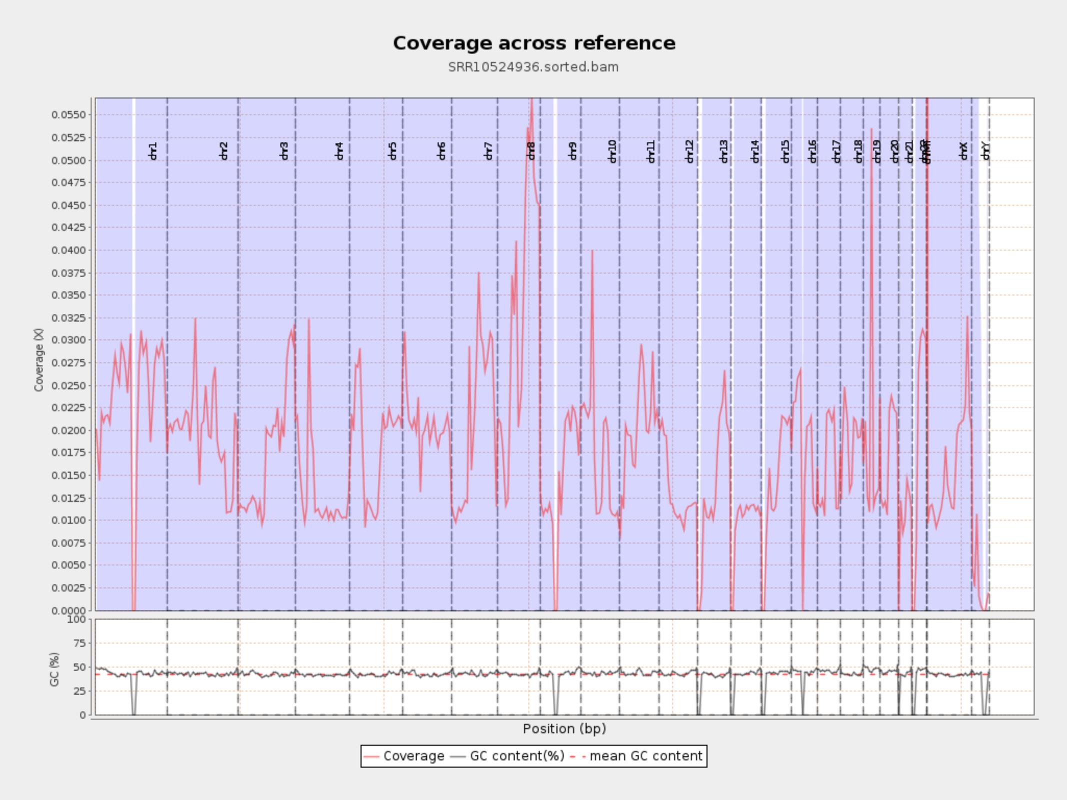
General error rate	0.52%
Mismatches	282,319
Insertions	3,989
Mapped reads with at least one insertion	0.42%
Deletions	10,862
Mapped reads with at least one deletion	1.13%
Homopolymer indels	43.53%

2.6. Chromosome stats

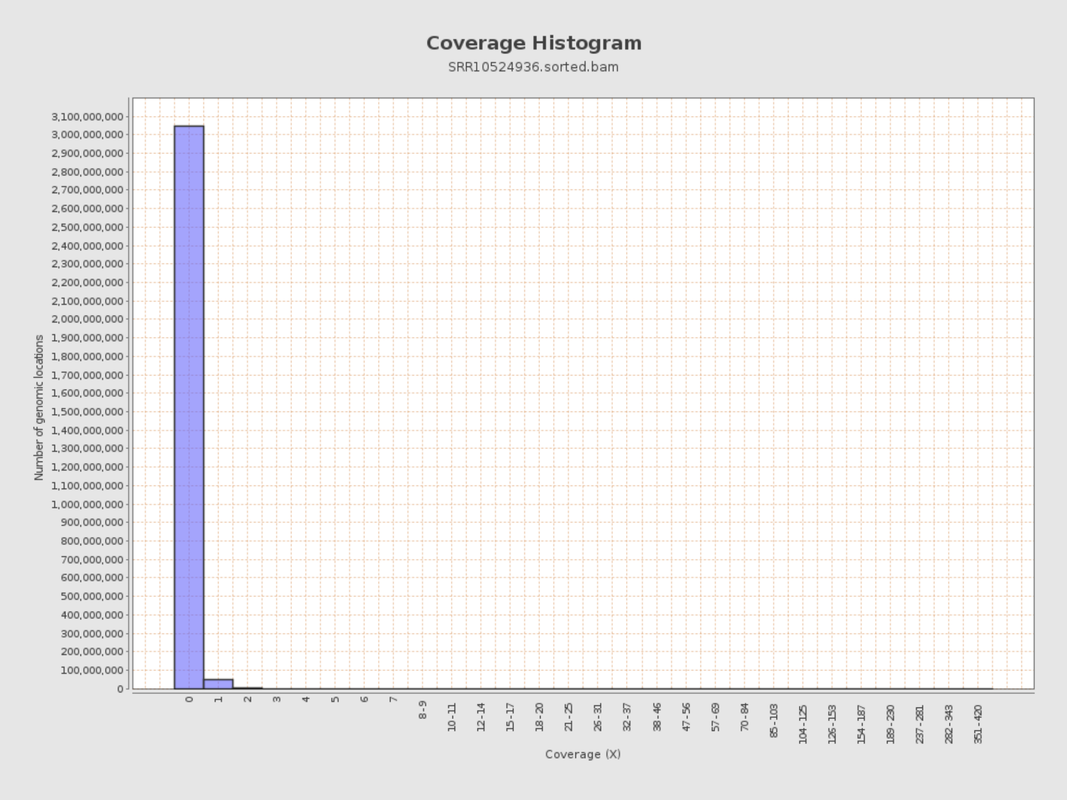
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5841596	0.0234	0.3304
chr2	243199373	4821837	0.0198	0.2137
chr3	198022430	3458346	0.0175	0.1426
chr4	191154276	2555362	0.0134	0.1425
chr5	180915260	3382160	0.0187	0.1458
chr6	171115067	3547912	0.0207	0.162
chr7	159138663	3296278	0.0207	0.2234

chr8	146364022	4962676	0.0339	0.243
chr9	141213431	1998826	0.0142	0.1518
chr10	135534747	2408120	0.0178	0.2086
chr11	135006516	2772548	0.0205	0.1764
chr12	133851895	1777259	0.0133	0.1265
chr13	115169878	1570362	0.0136	0.1256
chr14	107349540	1034194	0.0096	0.1098
chr15	102531392	1420686	0.0139	0.1251
chr16	90354753	1633882	0.0181	0.1498
chr17	81195210	1277910	0.0157	0.138
chr18	78077248	1481935	0.019	0.2365
chr19	59128983	1150856	0.0195	0.2386
chr20	63025520	1091722	0.0173	0.1455
chr21	48129895	501827	0.0104	0.1297
chr22	51304566	1024736	0.02	0.1521
chrMT	16571	80111	4.8344	3.2742
chrX	155270560	2465915	0.0159	0.1443
chrY	59373566	158894	0.0027	0.1088

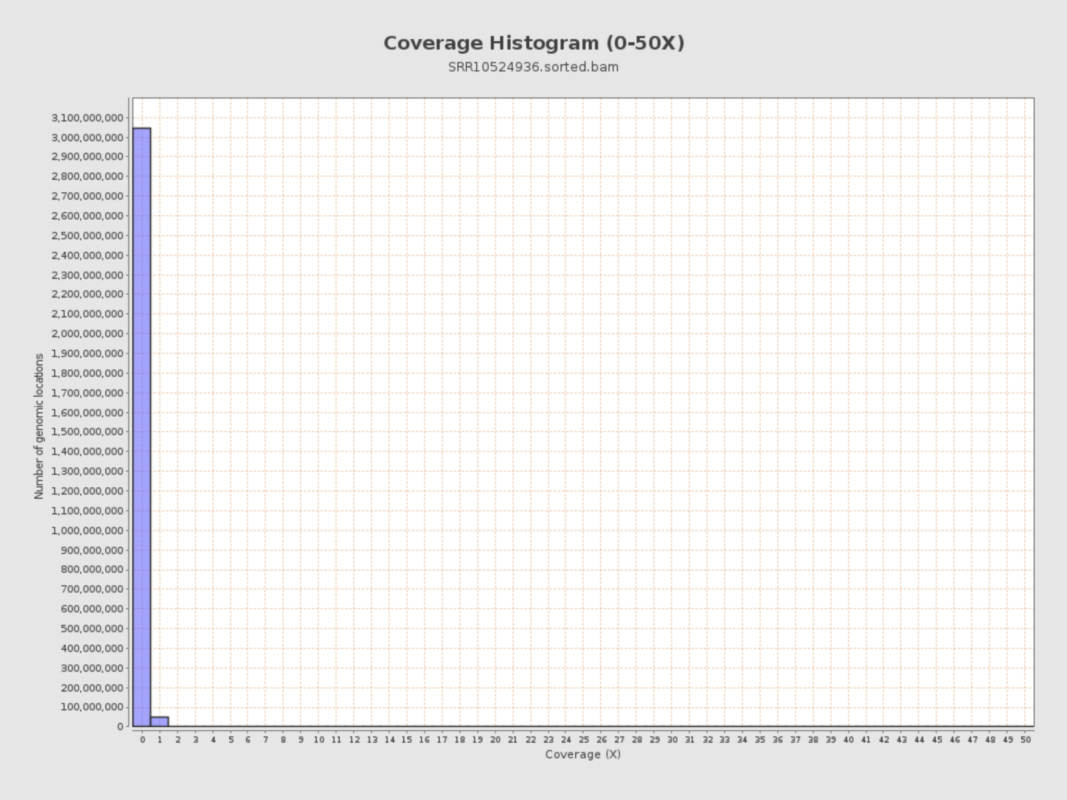
3. Results : Coverage across reference



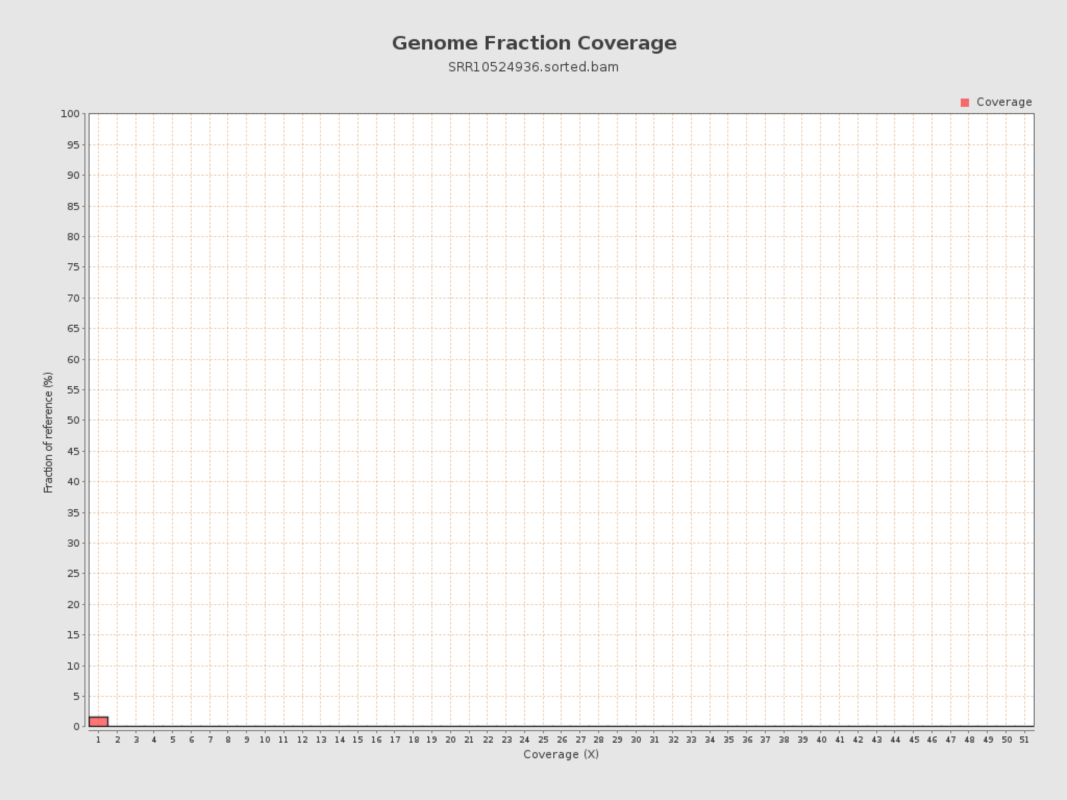
4. Results : Coverage Histogram



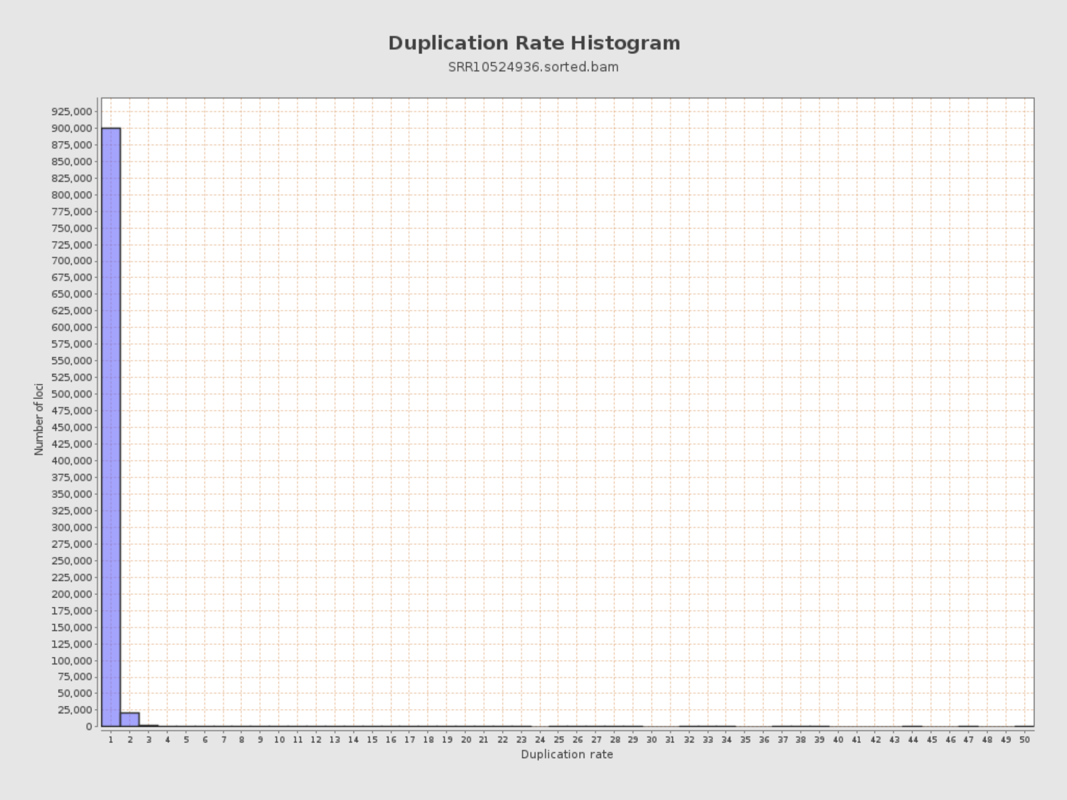
5. Results : Coverage Histogram (0-50X)



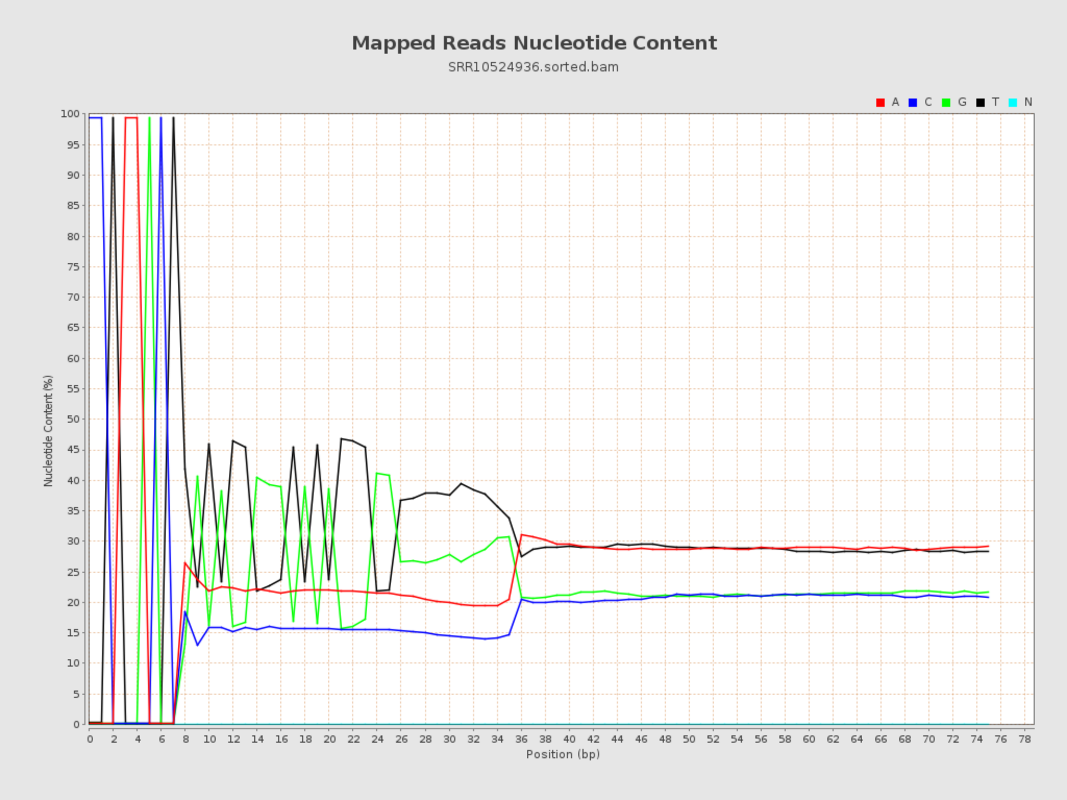
6. Results : Genome Fraction Coverage



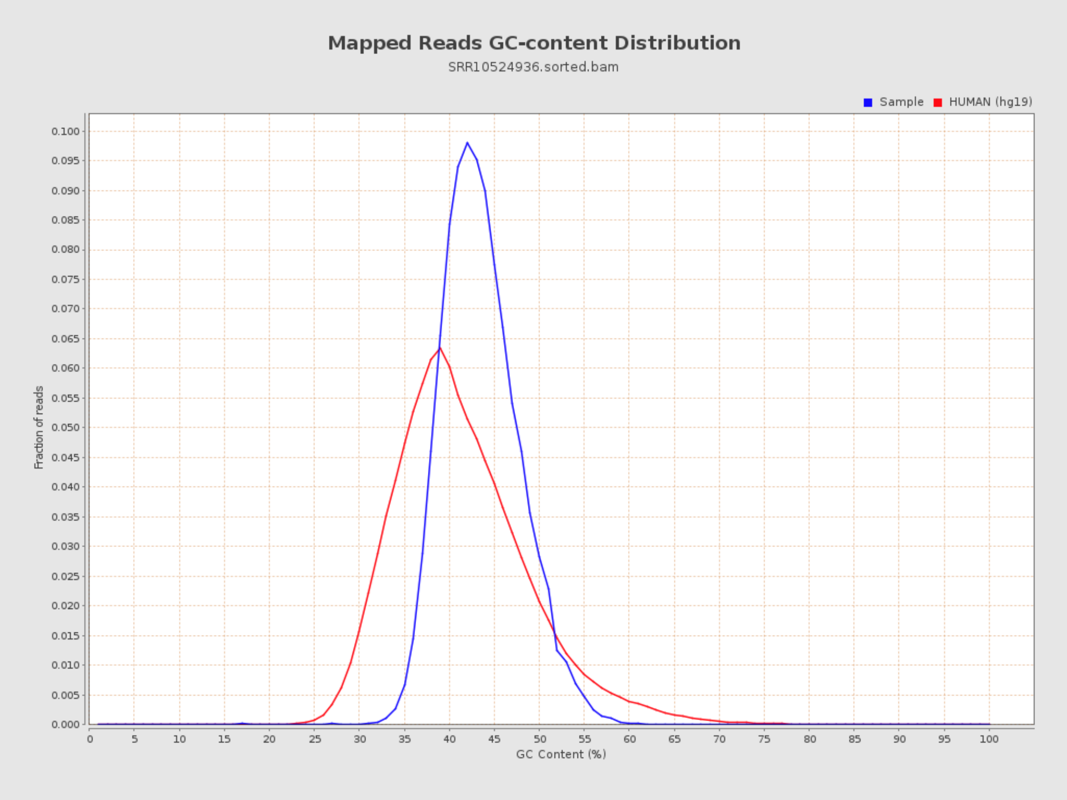
7. Results : Duplication Rate Histogram



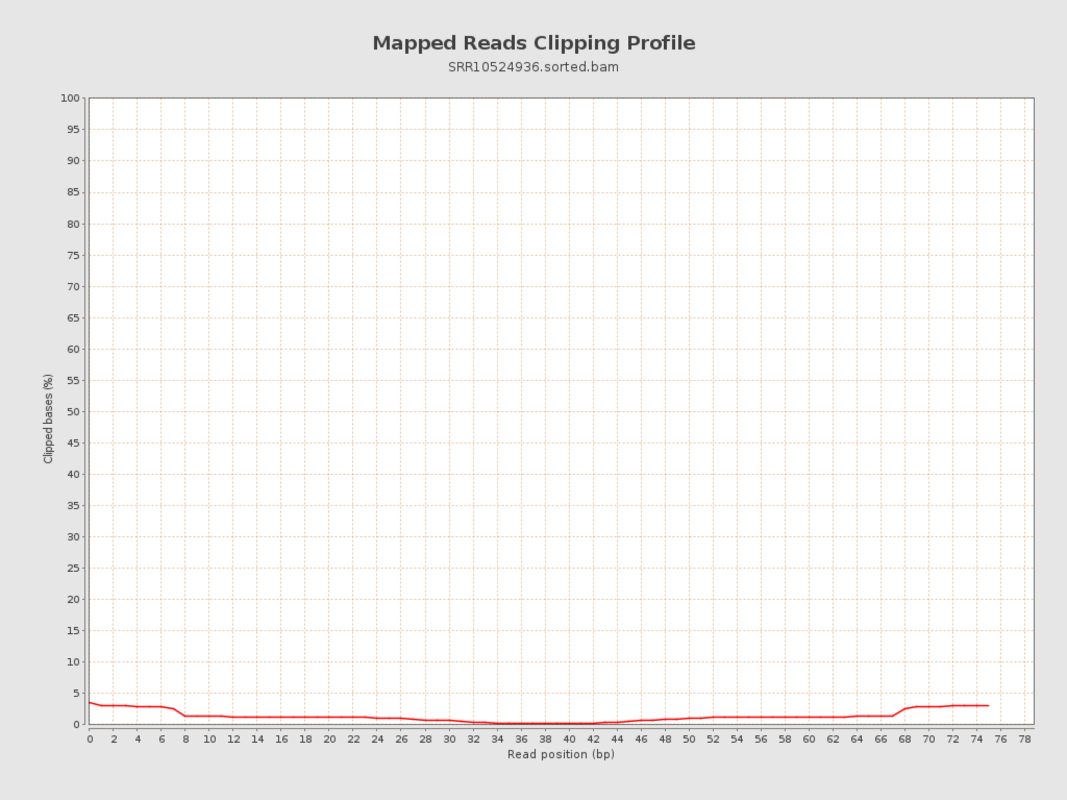
8. Results : Mapped Reads Nucleotide Content



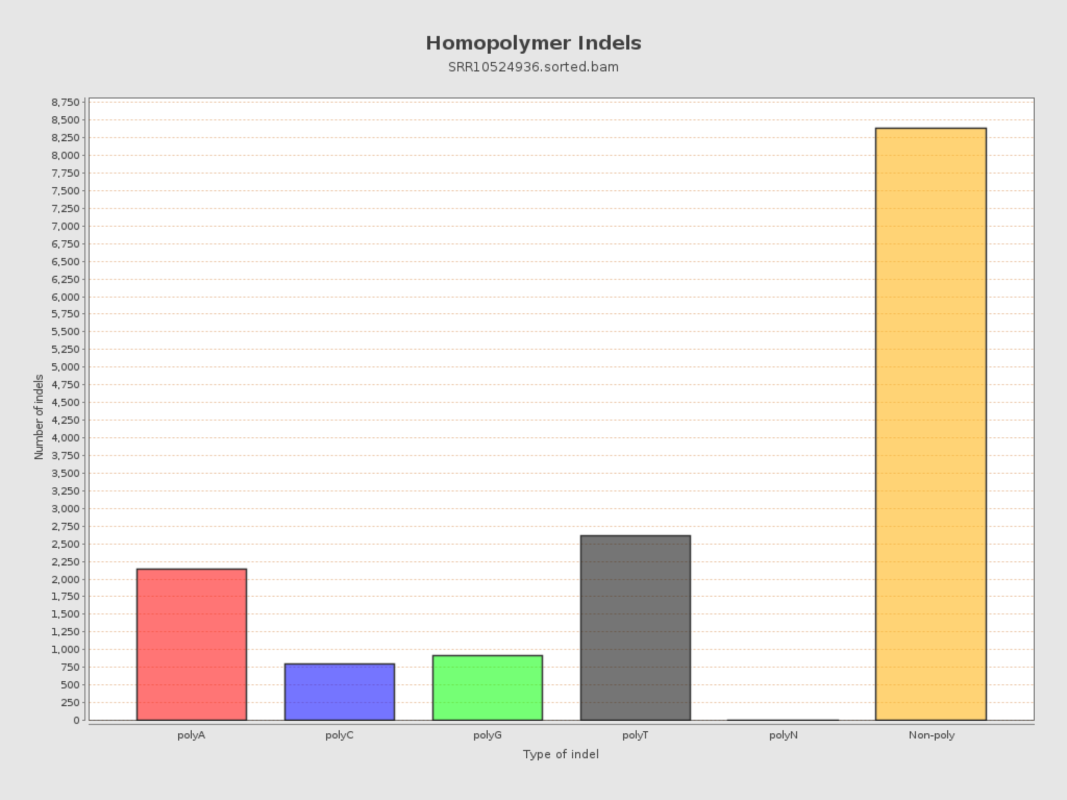
9. Results : Mapped Reads GC-content Distribution



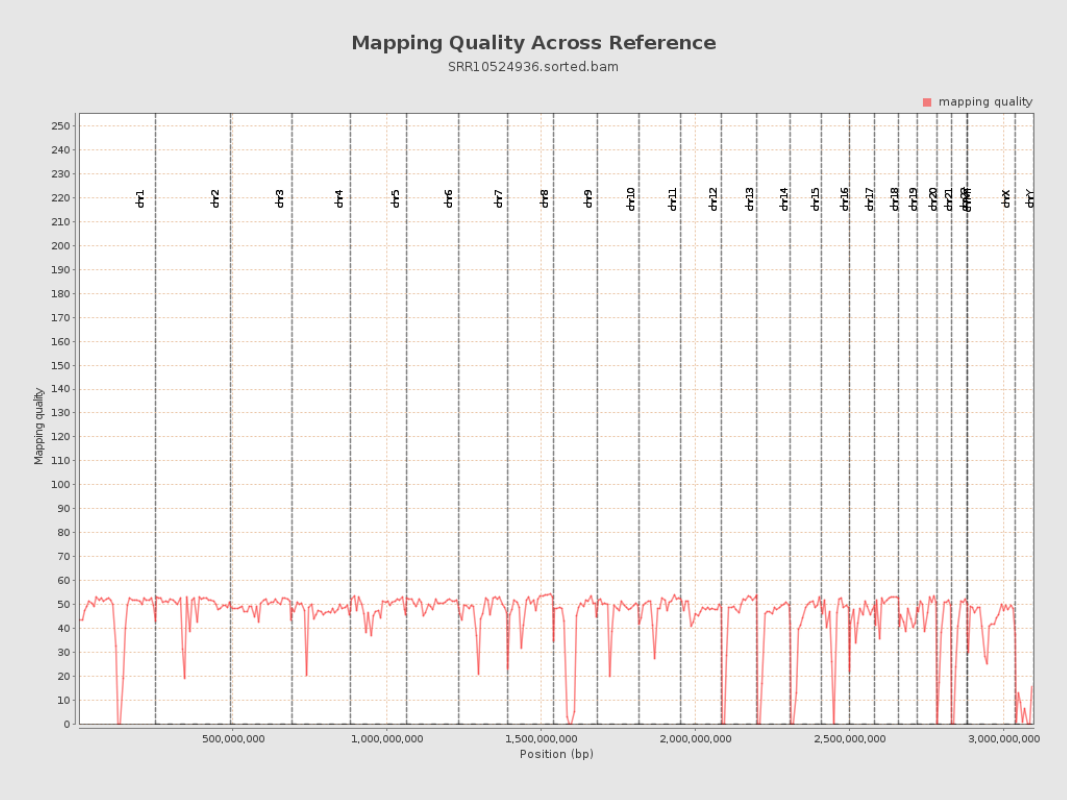
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram