Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 21:57:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524306.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_SRR10524306 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524306.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 21:57:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524306.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,098,922
Mapped reads	1,009,006 / 91.82%
Unmapped reads	89,916 / 8.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,129 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	24,984 / 2.27%
Duplication rate	1.76%
Clipped reads	1,011,062 / 92%

2.2. ACGT Content

Number/percentage of A's	14,335,017 / 24.32%
Number/percentage of C's	11,795,479 / 20.01%
Number/percentage of T's	18,146,893 / 30.79%
Number/percentage of G's	14,651,412 / 24.86%
Number/percentage of N's	8,046 / 0.01%
GC Percentage	44.87%

2.3. Coverage

Mean	0.019

Standard Deviation	0.1983

2.4. Mapping Quality

Mean Mapping Quality	44.25

2.5. Mismatches and indels

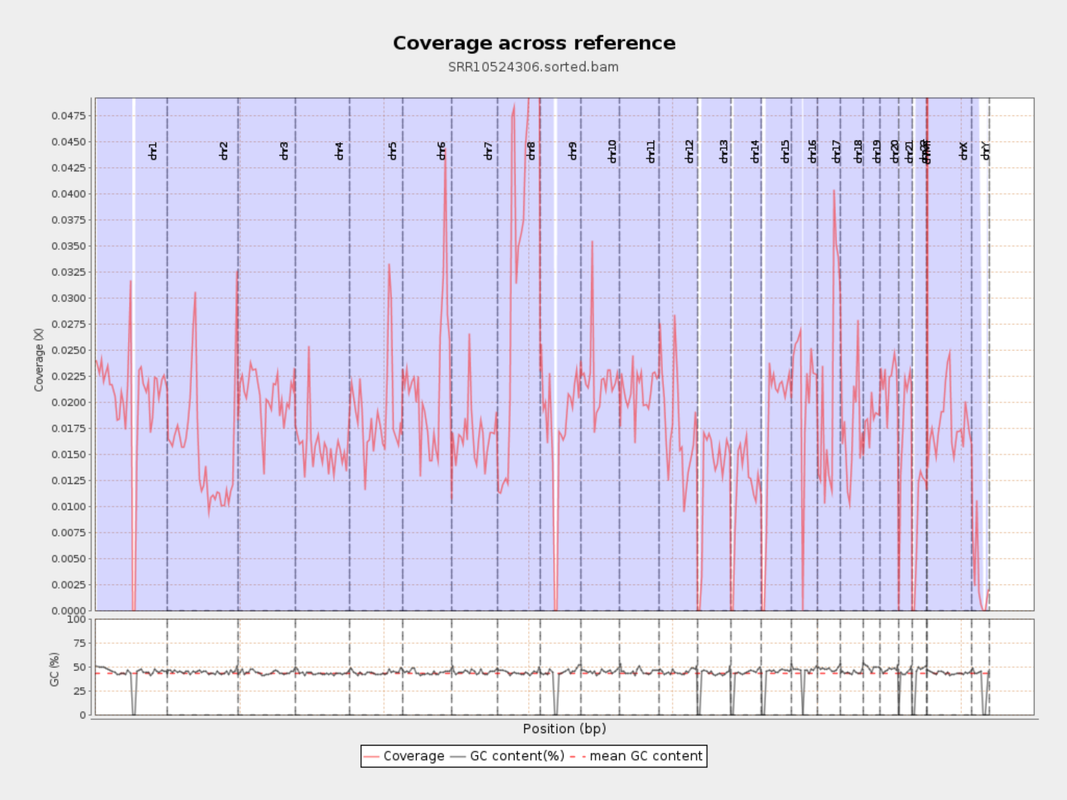
General error rate	0.51%
Mismatches	293,627
Insertions	3,688
Mapped reads with at least one insertion	0.36%
Deletions	9,397
Mapped reads with at least one deletion	0.93%
Homopolymer indels	43.03%

2.6. Chromosome stats

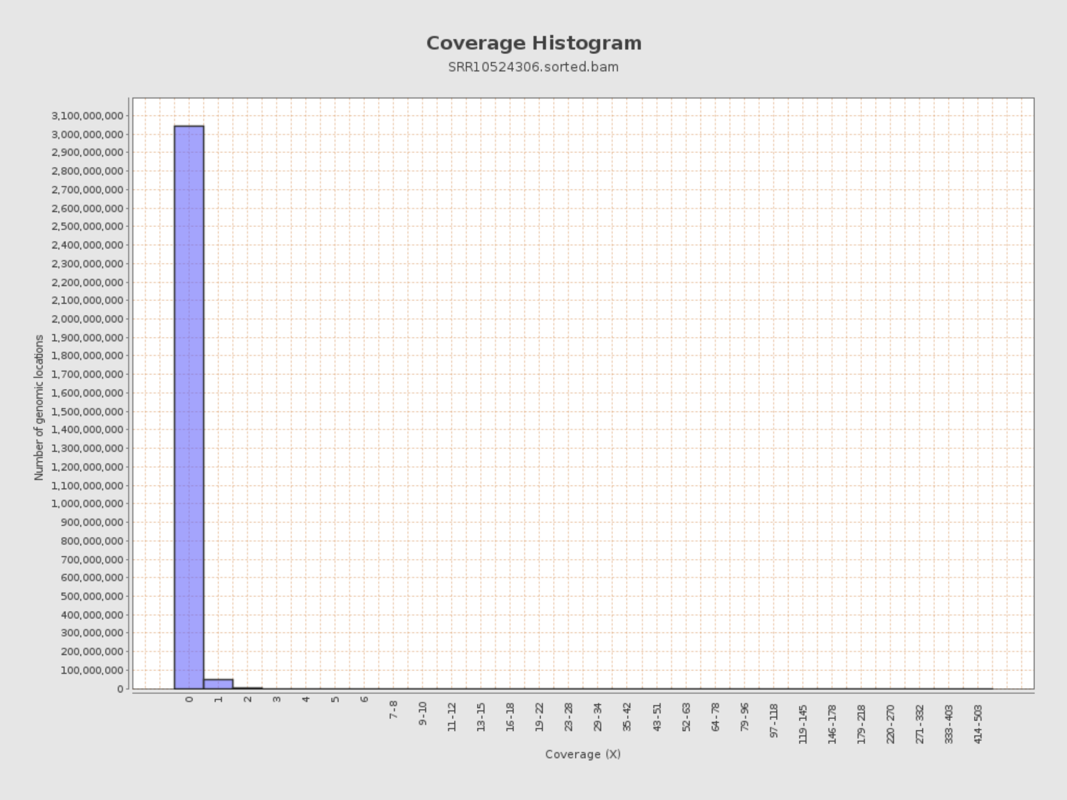
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5028761	0.0202	0.3466
chr2	243199373	3729177	0.0153	0.2386
chr3	198022430	4077187	0.0206	0.151
chr4	191154276	3011990	0.0158	0.1435
chr5	180915260	3438081	0.019	0.1457
chr6	171115067	3679293	0.0215	0.1631
chr7	159138663	2701921	0.017	0.2112

chr8	146364022	6100222	0.0417	0.2581
chr9	141213431	2455112	0.0174	0.1572
chr10	135534747	3025452	0.0223	0.1961
chr11	135006516	2856812	0.0212	0.1703
chr12	133851895	2344544	0.0175	0.1403
chr13	115169878	1481478	0.0129	0.1188
chr14	107349540	1229784	0.0115	0.1182
chr15	102531392	1813715	0.0177	0.1417
chr16	90354753	1912869	0.0212	0.1578
chr17	81195210	1739383	0.0214	0.1634
chr18	78077248	1358950	0.0174	0.2459
chr19	59128983	1086059	0.0184	0.2392
chr20	63025520	1390076	0.0221	0.1577
chr21	48129895	855173	0.0178	0.1495
chr22	51304566	455603	0.0089	0.0988
chrMT	16571	222124	13.4044	7.7656
chrX	155270560	2785885	0.0179	0.1502
chrY	59373566	172326	0.0029	0.0952

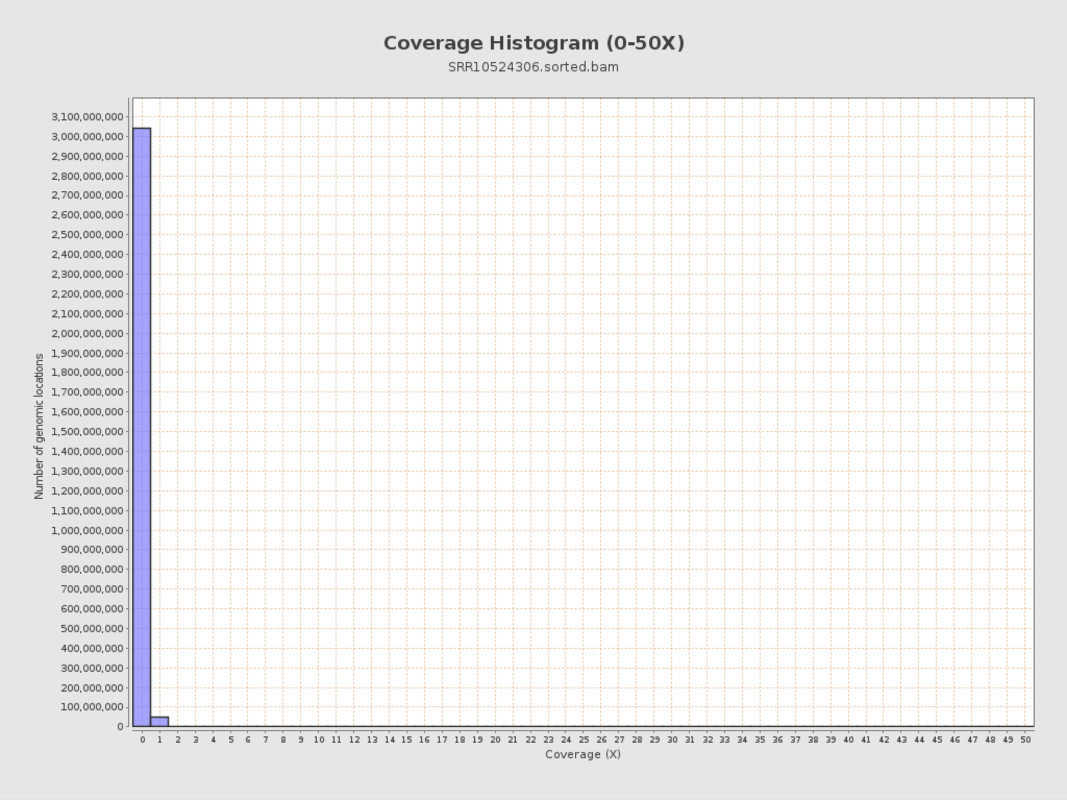
3. Results : Coverage across reference



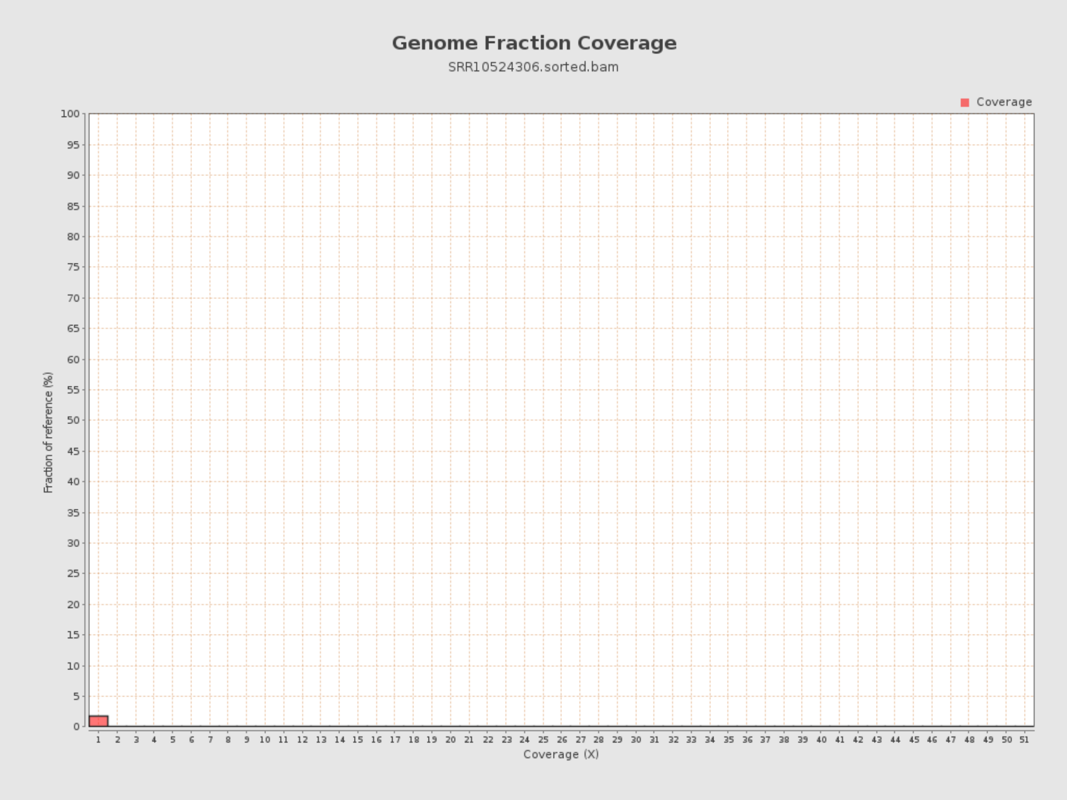
4. Results : Coverage Histogram



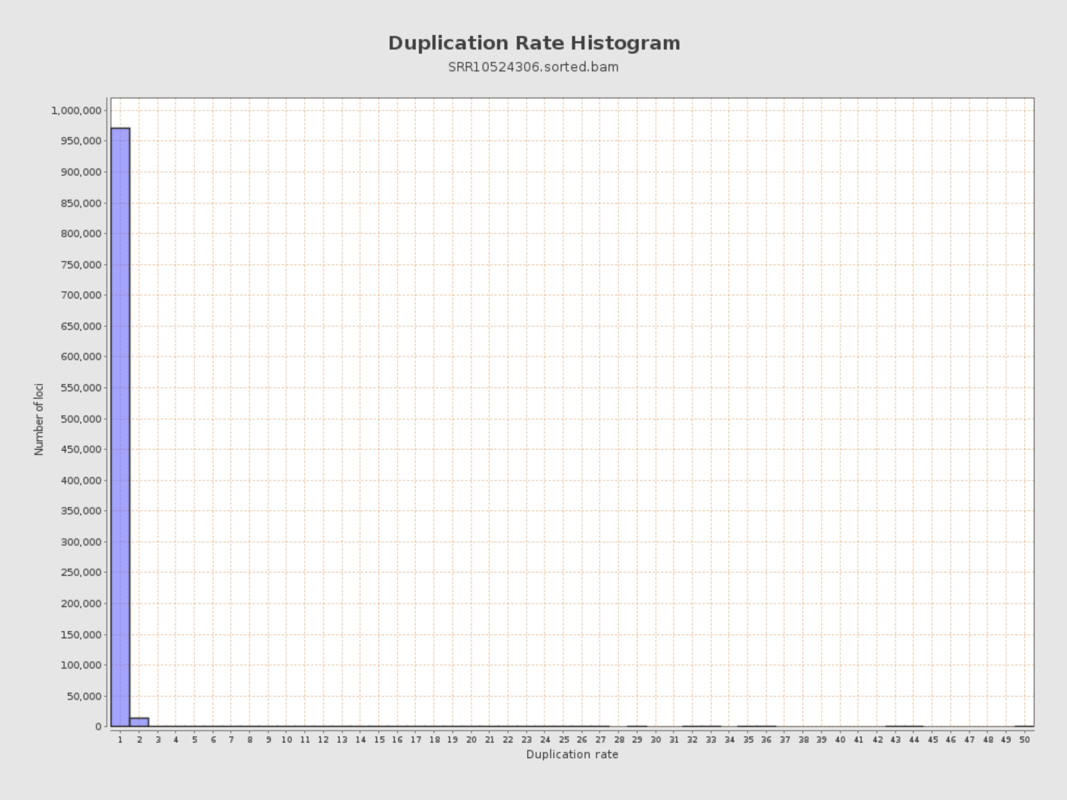
5. Results : Coverage Histogram (0-50X)



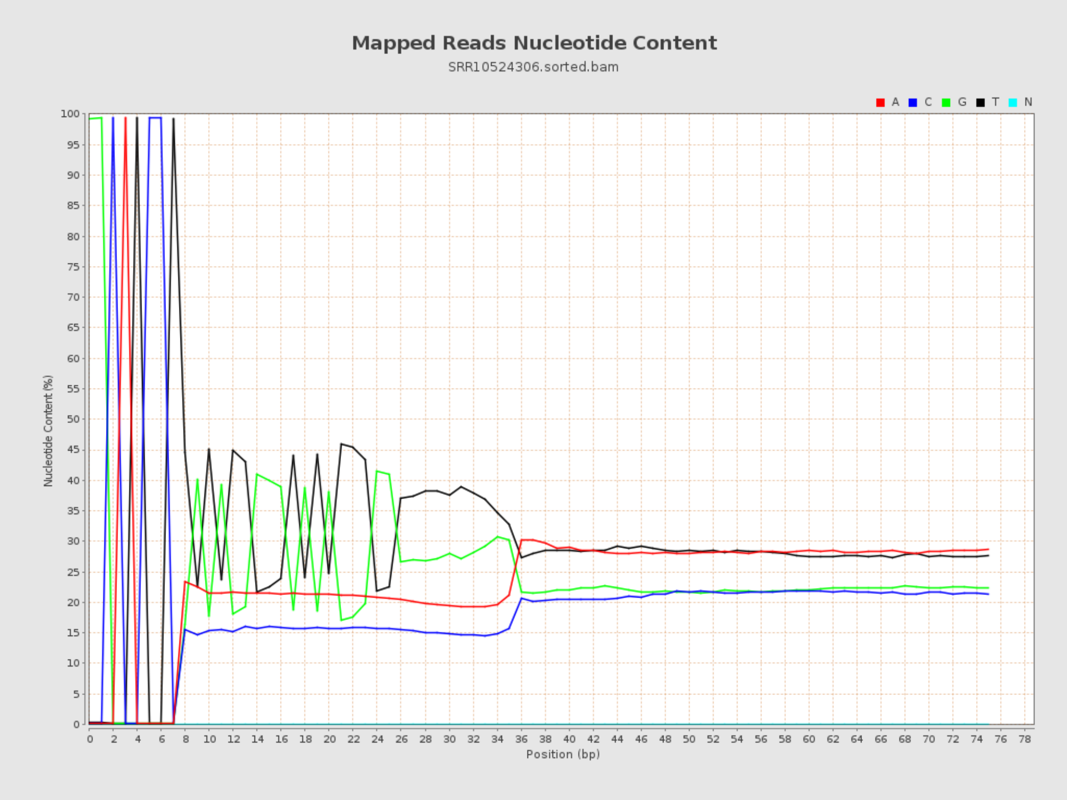
6. Results : Genome Fraction Coverage



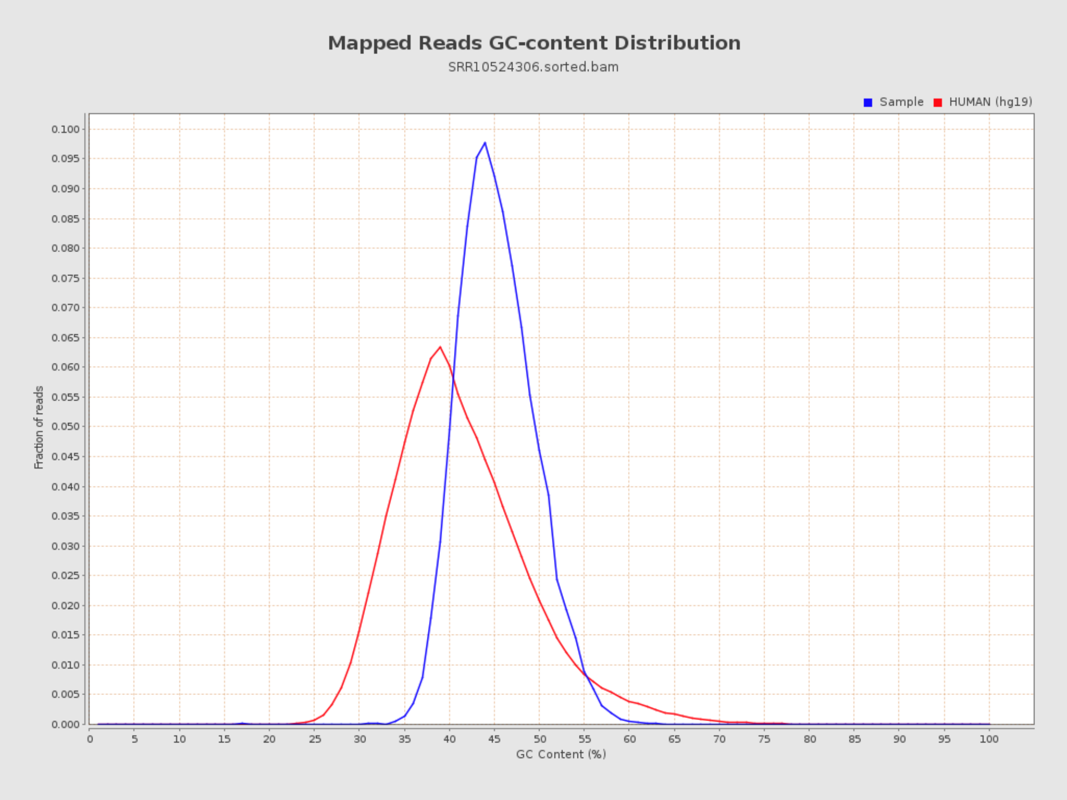
7. Results : Duplication Rate Histogram



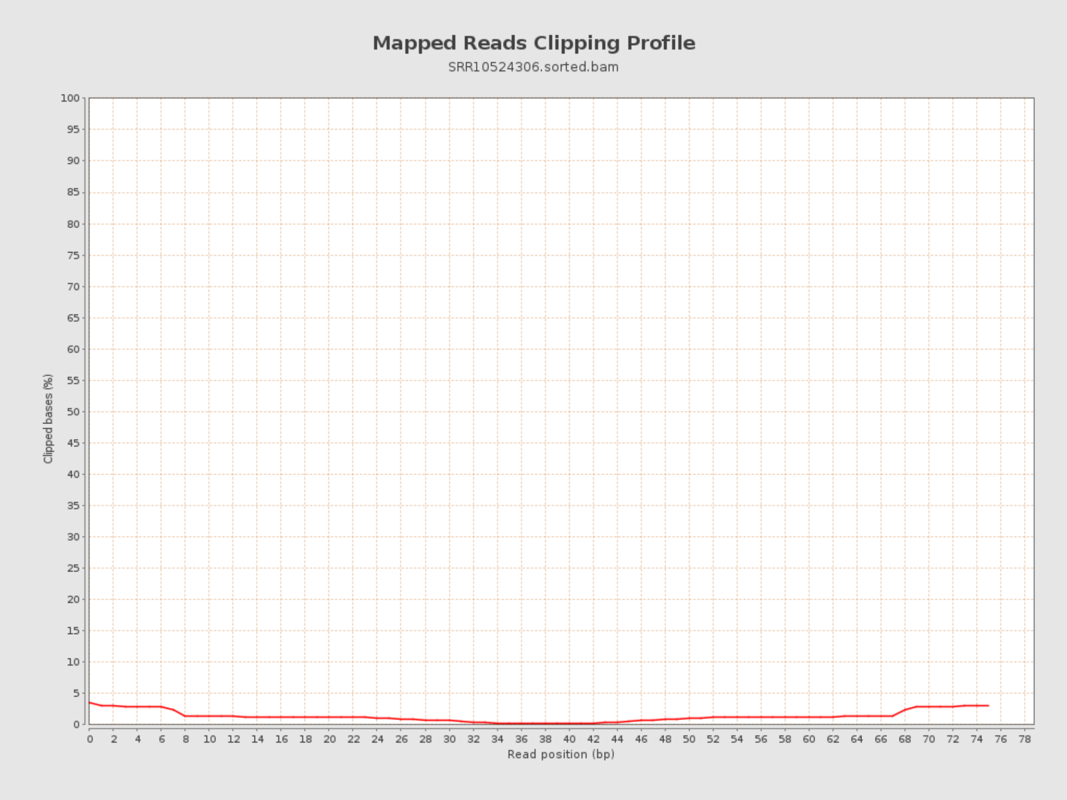
8. Results : Mapped Reads Nucleotide Content



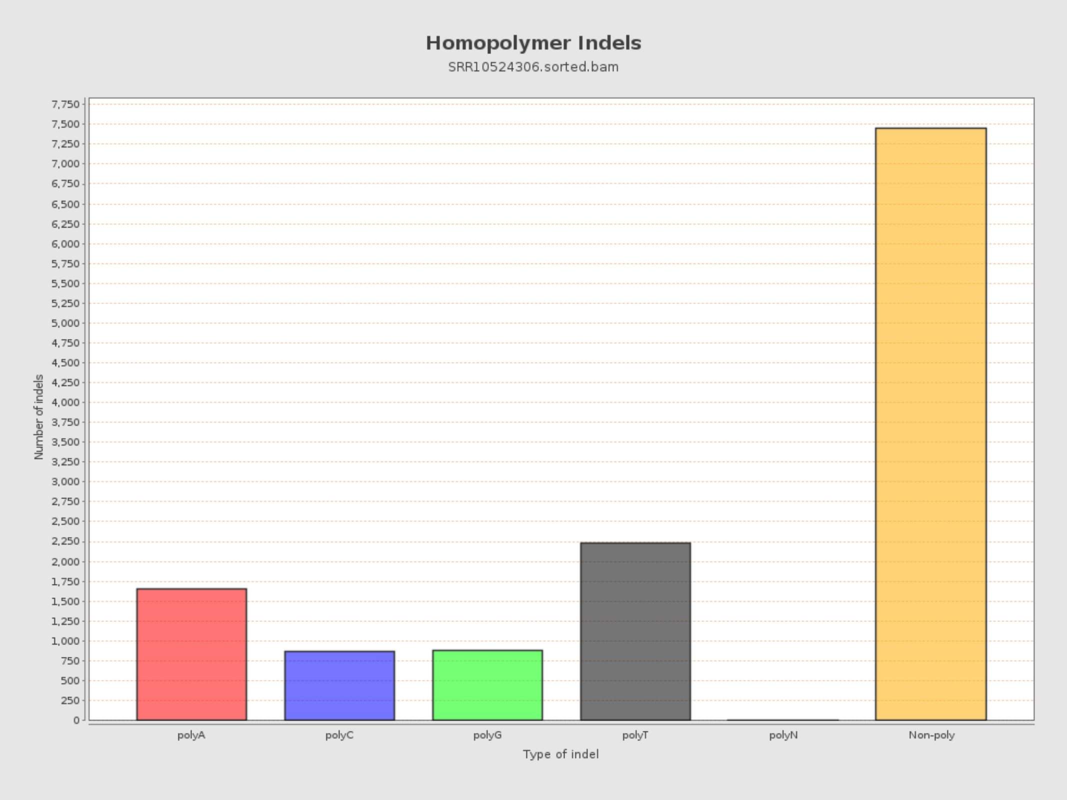
9. Results : Mapped Reads GC-content Distribution



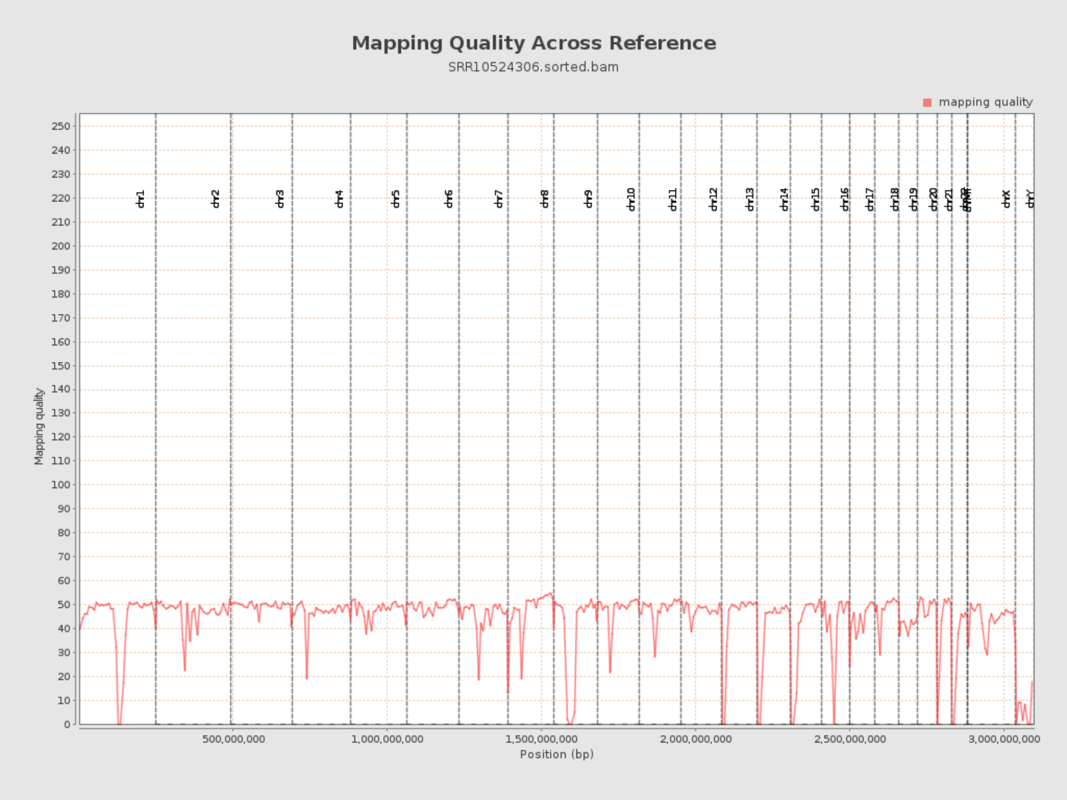
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram