Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 04:00:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524430.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_SRR10524430 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524430.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 04:00:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524430.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,038,311
Mapped reads	911,257 / 87.76%
Unmapped reads	127,054 / 12.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,015 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	37,352 / 3.6%
Duplication rate	3.04%
Clipped reads	911,738 / 87.81%

2.2. ACGT Content

Number/percentage of A's	12,755,203 / 24.03%
Number/percentage of C's	11,075,532 / 20.87%
Number/percentage of T's	16,872,111 / 31.79%
Number/percentage of G's	12,362,886 / 23.29%
Number/percentage of N's	5,725 / 0.01%
GC Percentage	44.16%

2.3. Coverage

Mean	0.0171

Standard Deviation	0.2005

2.4. Mapping Quality

Mean Mapping Quality	44.76

2.5. Mismatches and indels

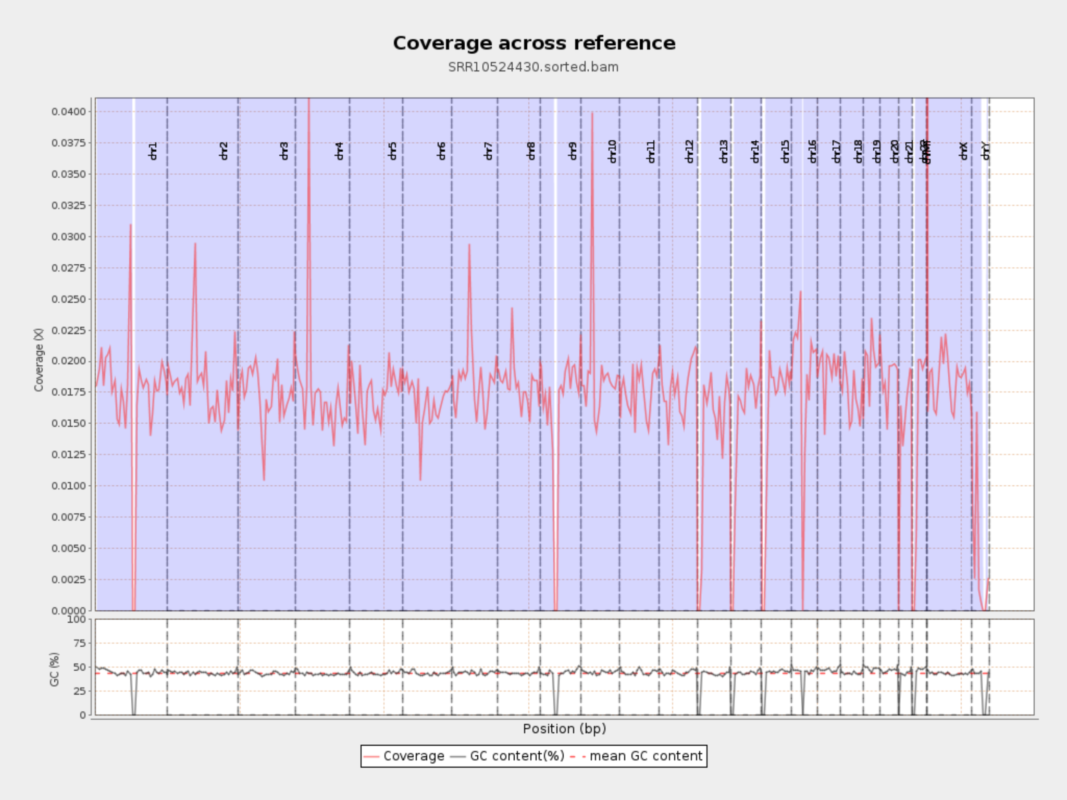
General error rate	0.55%
Mismatches	280,009
Insertions	4,941
Mapped reads with at least one insertion	0.54%
Deletions	9,753
Mapped reads with at least one deletion	1.06%
Homopolymer indels	39.56%

2.6. Chromosome stats

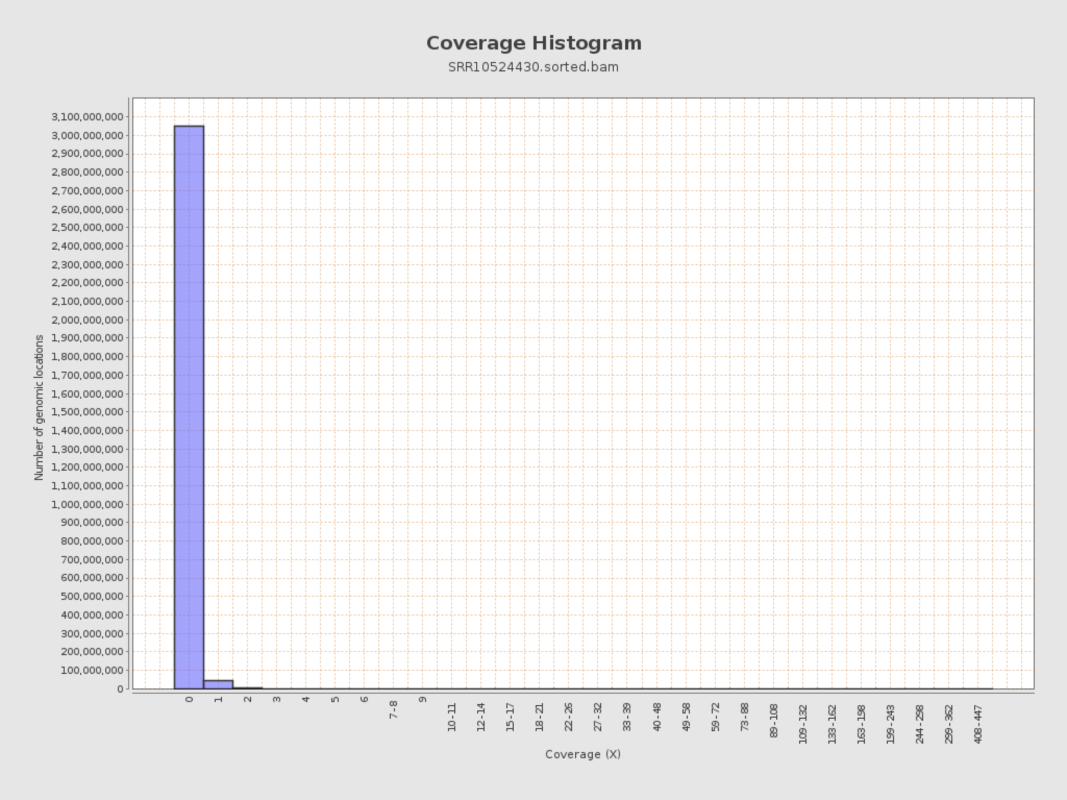
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4309735	0.0173	0.353
chr2	243199373	4450663	0.0183	0.2558
chr3	198022430	3442694	0.0174	0.1423
chr4	191154276	3400856	0.0178	0.1911
chr5	180915260	3149420	0.0174	0.1423
chr6	171115067	2864309	0.0167	0.1464
chr7	159138663	2960732	0.0186	0.2376

chr8	146364022	2662106	0.0182	0.1656
chr9	141213431	2239325	0.0159	0.158
chr10	135534747	2598585	0.0192	0.2436
chr11	135006516	2371328	0.0176	0.1691
chr12	133851895	2397141	0.0179	0.146
chr13	115169878	1602674	0.0139	0.1267
chr14	107349540	1582231	0.0147	0.1329
chr15	102531392	1568555	0.0153	0.1334
chr16	90354753	1669293	0.0185	0.1551
chr17	81195210	1569547	0.0193	0.1606
chr18	78077248	1343206	0.0172	0.2559
chr19	59128983	1184229	0.02	0.2525
chr20	63025520	1177227	0.0187	0.1525
chr21	48129895	725049	0.0151	0.1771
chr22	51304566	708204	0.0138	0.1283
chrMT	16571	17054	1.0291	1.2701
chrX	155270560	2866590	0.0185	0.1567
chrY	59373566	226509	0.0038	0.1553

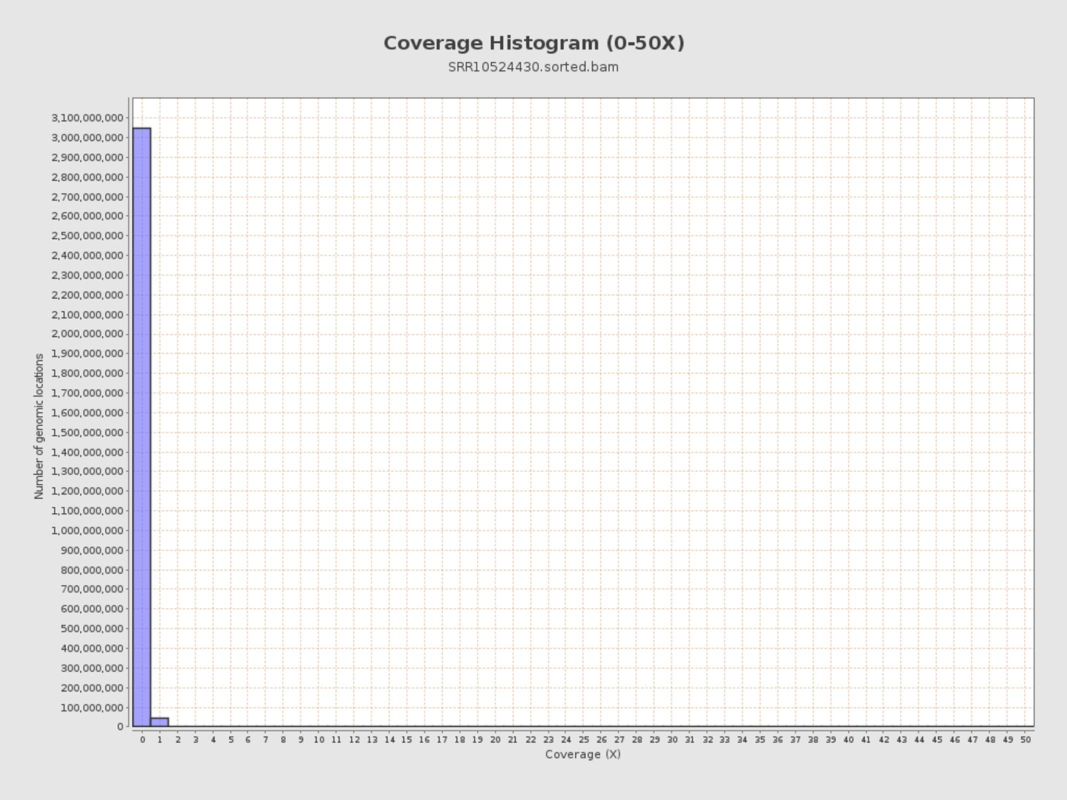
3. Results : Coverage across reference



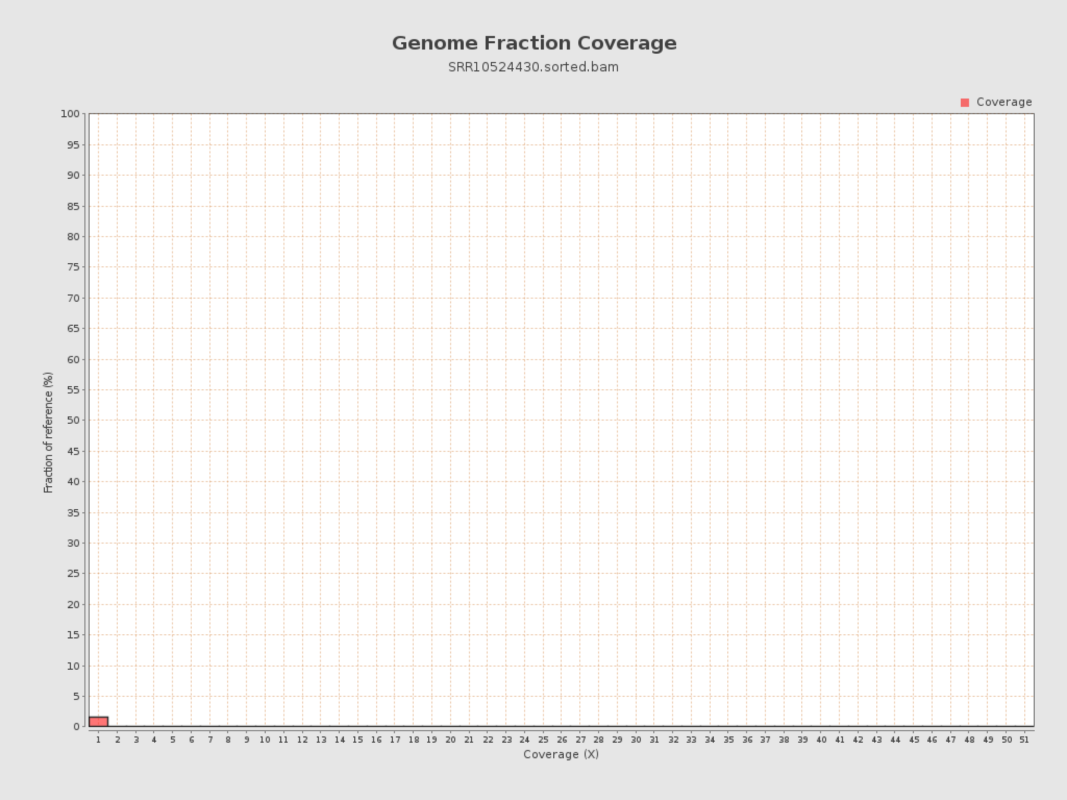
4. Results : Coverage Histogram



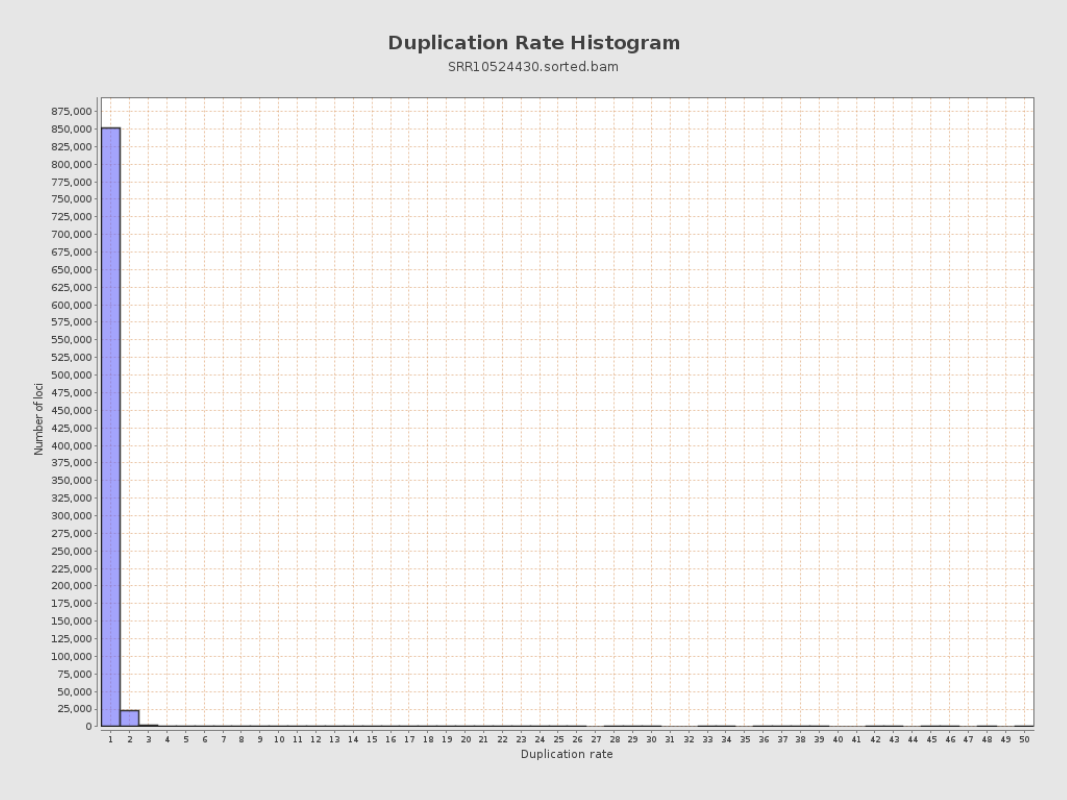
5. Results : Coverage Histogram (0-50X)



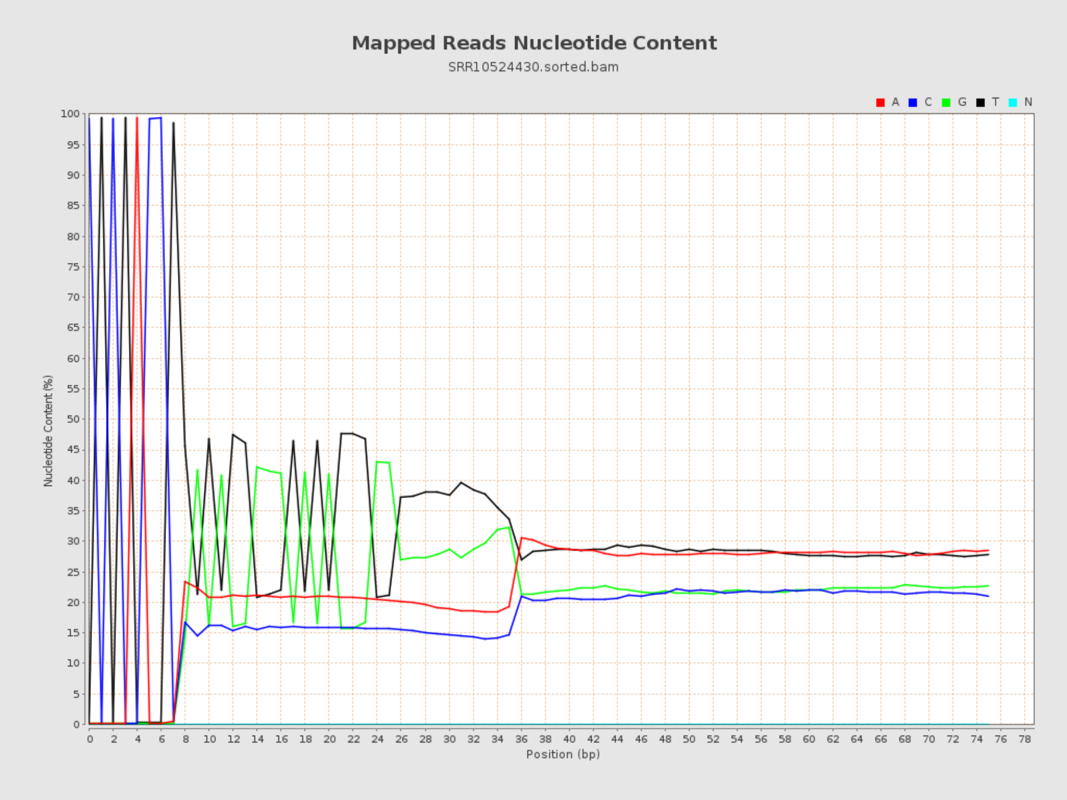
6. Results : Genome Fraction Coverage



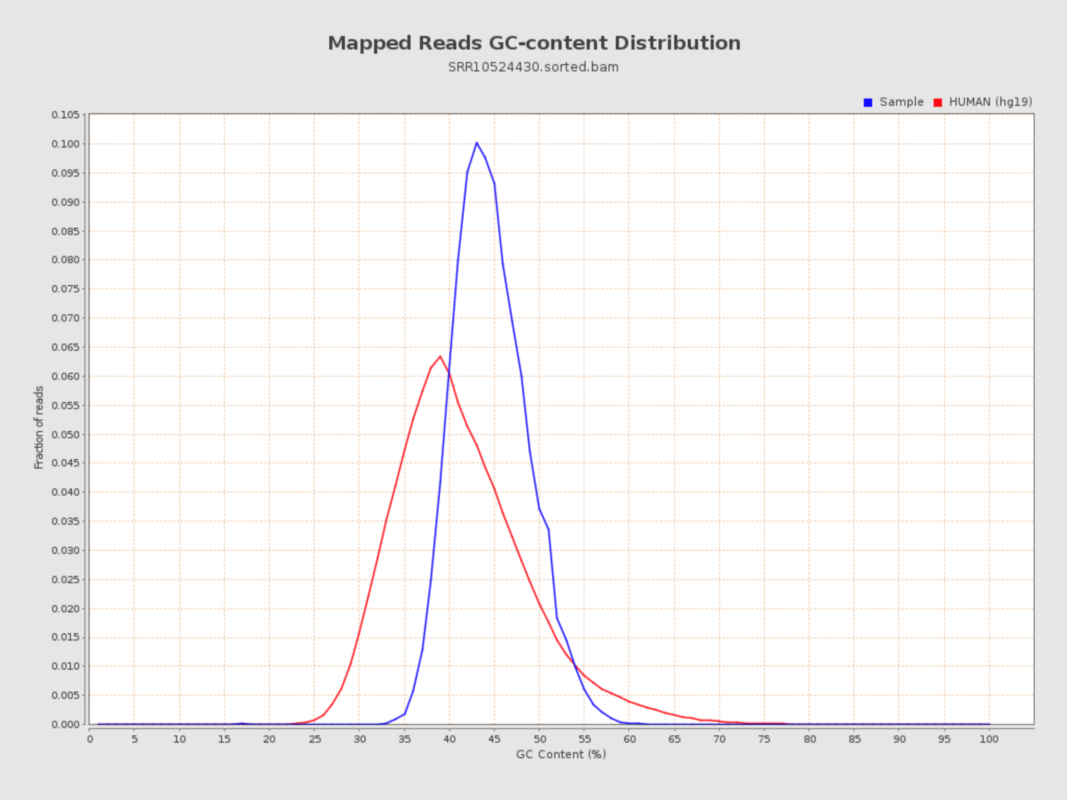
7. Results : Duplication Rate Histogram



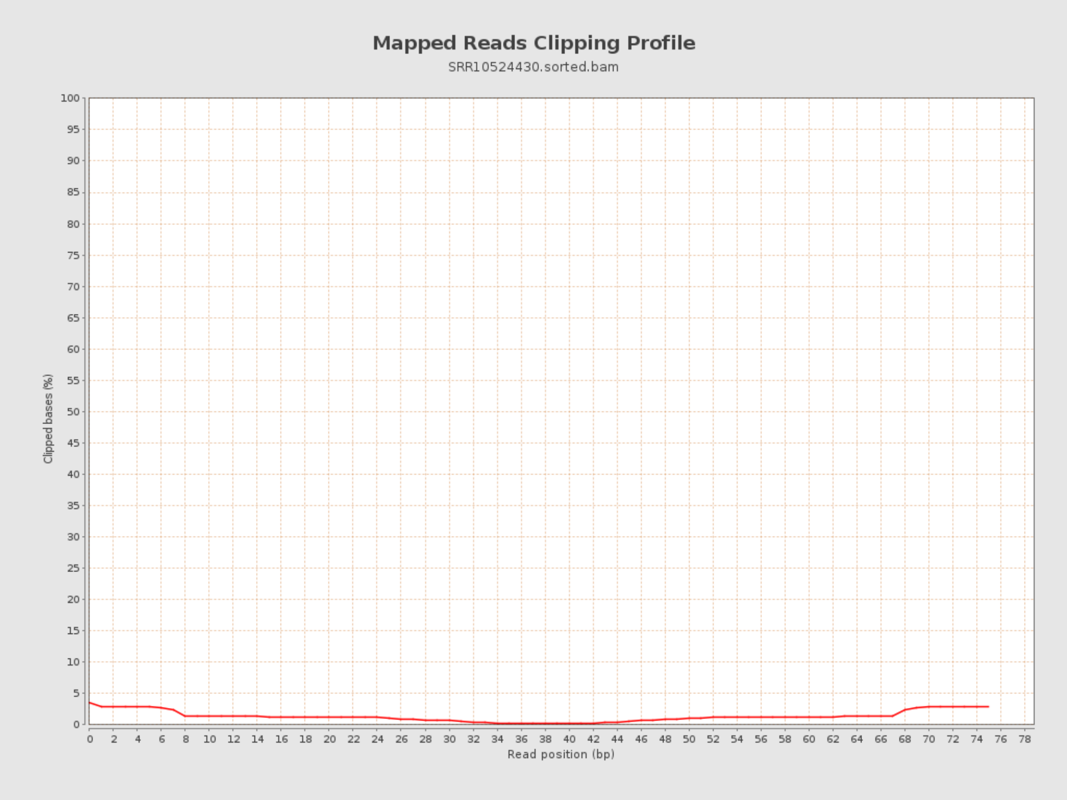
8. Results : Mapped Reads Nucleotide Content



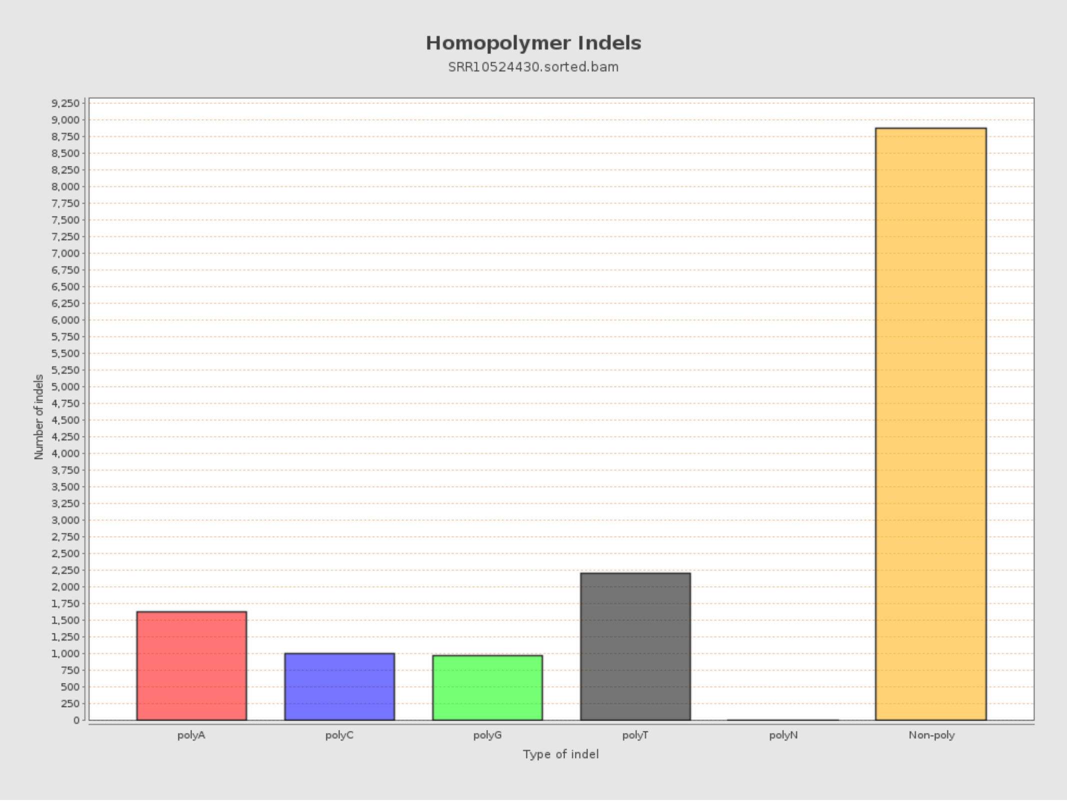
9. Results : Mapped Reads GC-content Distribution



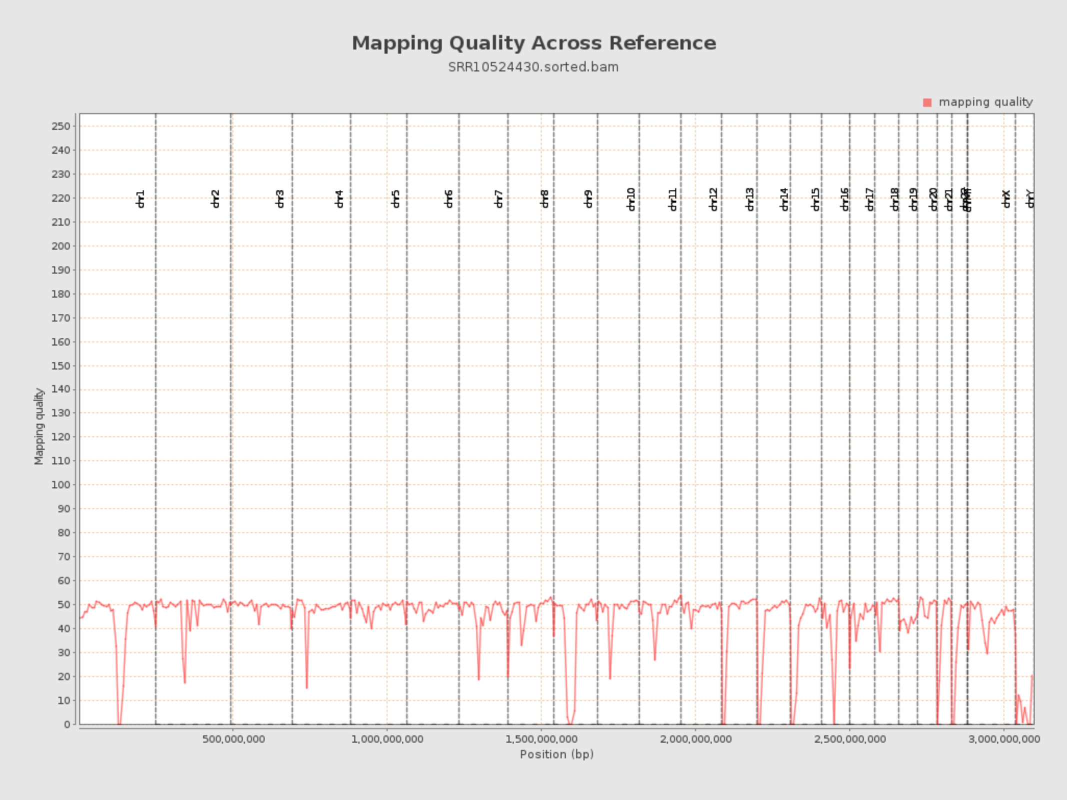
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram