Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 02:04:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524401.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_SRR10524401 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524401.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 02:04:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524401.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,366,714
Mapped reads	1,255,655 / 91.87%
Unmapped reads	111,059 / 8.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,763 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	41,800 / 3.06%
Duplication rate	2.45%
Clipped reads	1,256,928 / 91.97%

2.2. ACGT Content

Number/percentage of A's	18,810,701 / 25.7%
Number/percentage of C's	13,578,244 / 18.55%
Number/percentage of T's	23,506,767 / 32.11%
Number/percentage of G's	17,299,519 / 23.63%
Number/percentage of N's	8,693 / 0.01%
GC Percentage	42.18%

2.3. Coverage

Mean	0.0237

Standard Deviation	0.241

2.4. Mapping Quality

Mean Mapping Quality	45.86

2.5. Mismatches and indels

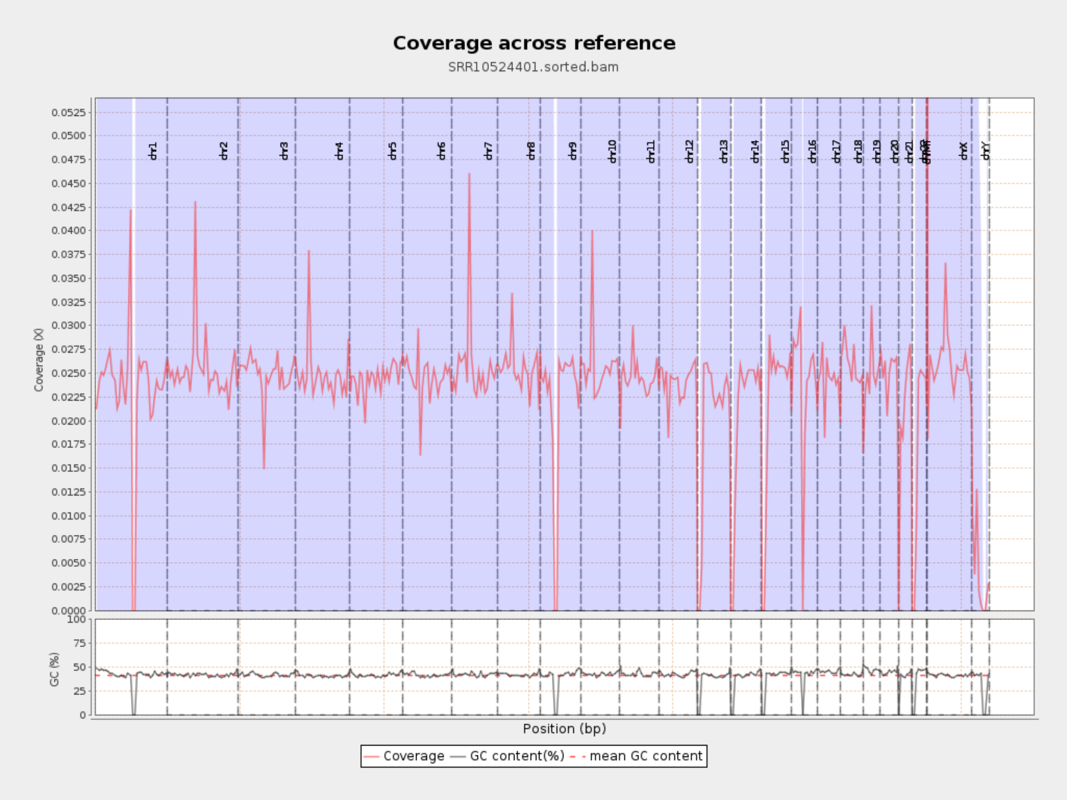
General error rate	0.51%
Mismatches	361,038
Insertions	4,874
Mapped reads with at least one insertion	0.39%
Deletions	13,272
Mapped reads with at least one deletion	1.05%
Homopolymer indels	42.31%

2.6. Chromosome stats

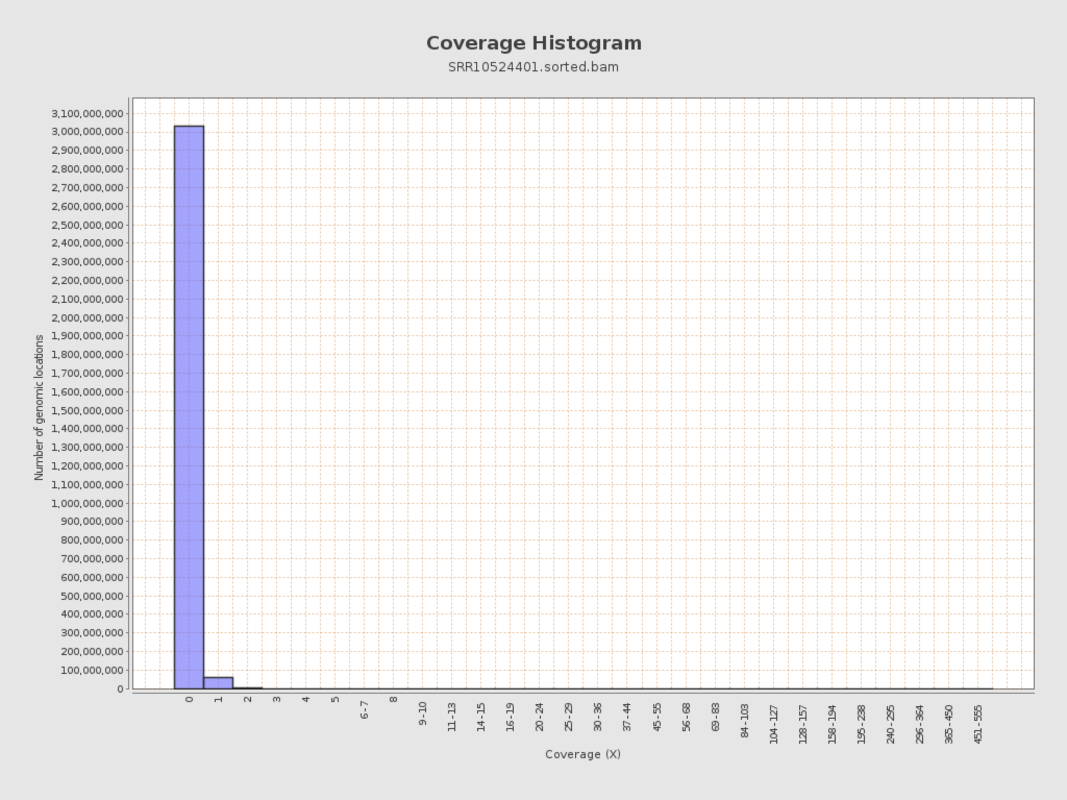
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5782867	0.0232	0.4505
chr2	243199373	6186734	0.0254	0.2684
chr3	198022430	4919498	0.0248	0.1686
chr4	191154276	4764607	0.0249	0.1861
chr5	180915260	4428194	0.0245	0.1673
chr6	171115067	4200405	0.0245	0.1859
chr7	159138663	4114156	0.0259	0.3465

chr8	146364022	3727323	0.0255	0.2226
chr9	141213431	3074019	0.0218	0.2044
chr10	135534747	3490586	0.0258	0.2277
chr11	135006516	3327134	0.0246	0.216
chr12	133851895	3218800	0.024	0.1707
chr13	115169878	2276813	0.0198	0.15
chr14	107349540	2203795	0.0205	0.1602
chr15	102531392	2181025	0.0213	0.1563
chr16	90354753	2126208	0.0235	0.1732
chr17	81195210	1967130	0.0242	0.1779
chr18	78077248	2032887	0.026	0.3545
chr19	59128983	1475389	0.025	0.3021
chr20	63025520	1575811	0.025	0.1717
chr21	48129895	998849	0.0208	0.1679
chr22	51304566	876972	0.0171	0.1403
chrMT	16571	10999	0.6637	0.9396
chrX	155270560	4042873	0.026	0.1921
chrY	59373566	222031	0.0037	0.1046

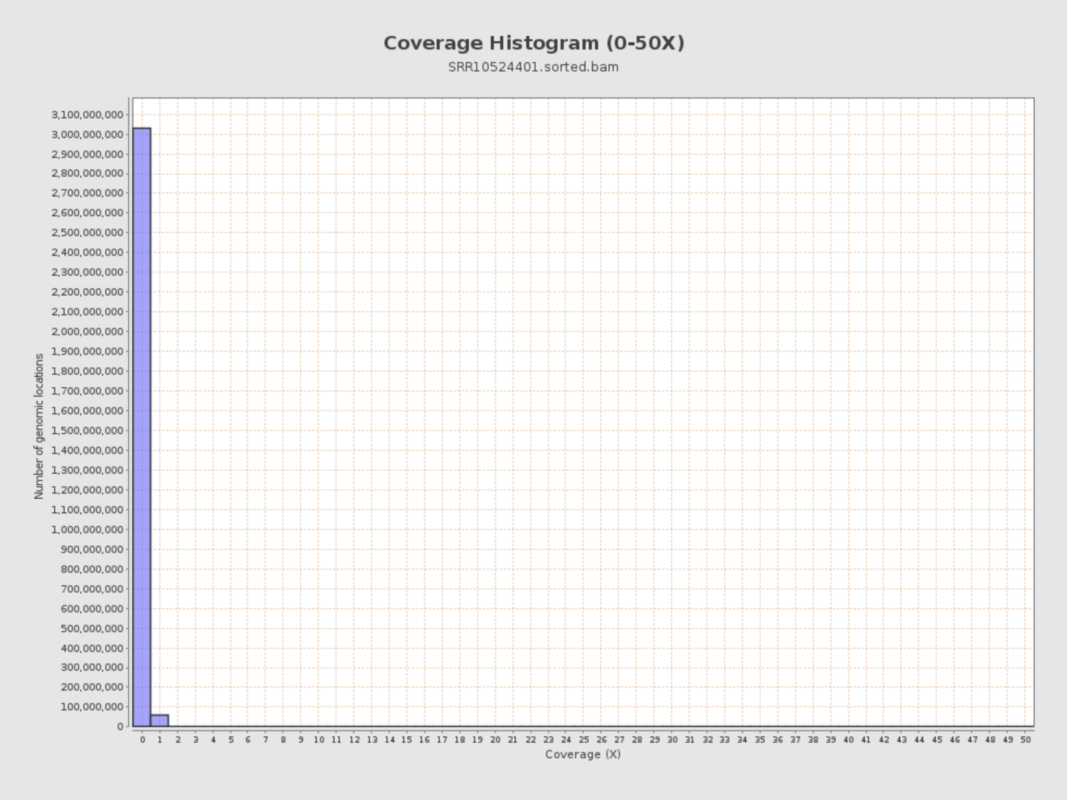
3. Results : Coverage across reference



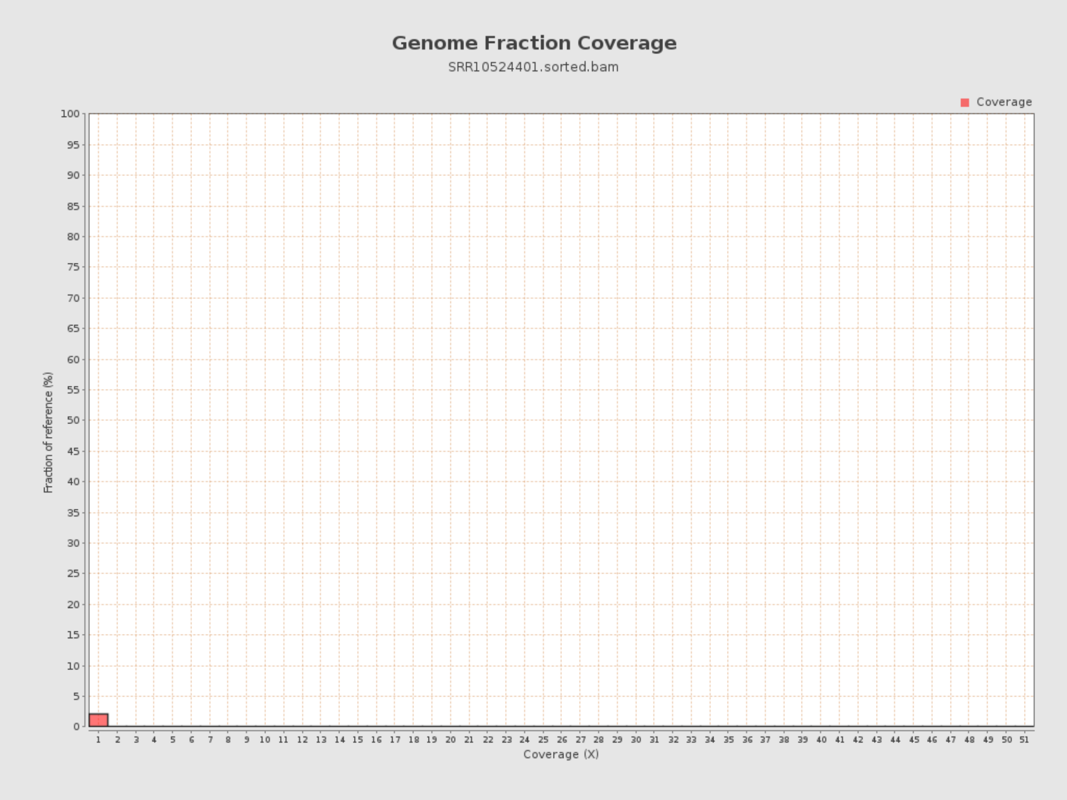
4. Results : Coverage Histogram



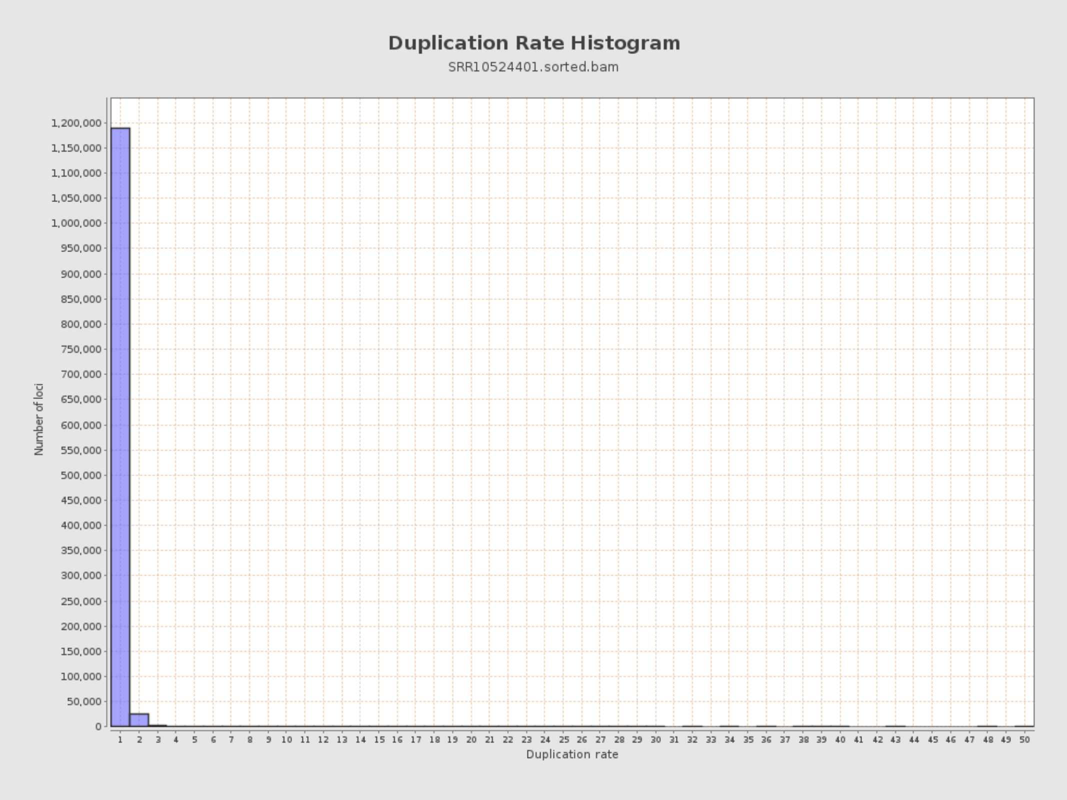
5. Results : Coverage Histogram (0-50X)



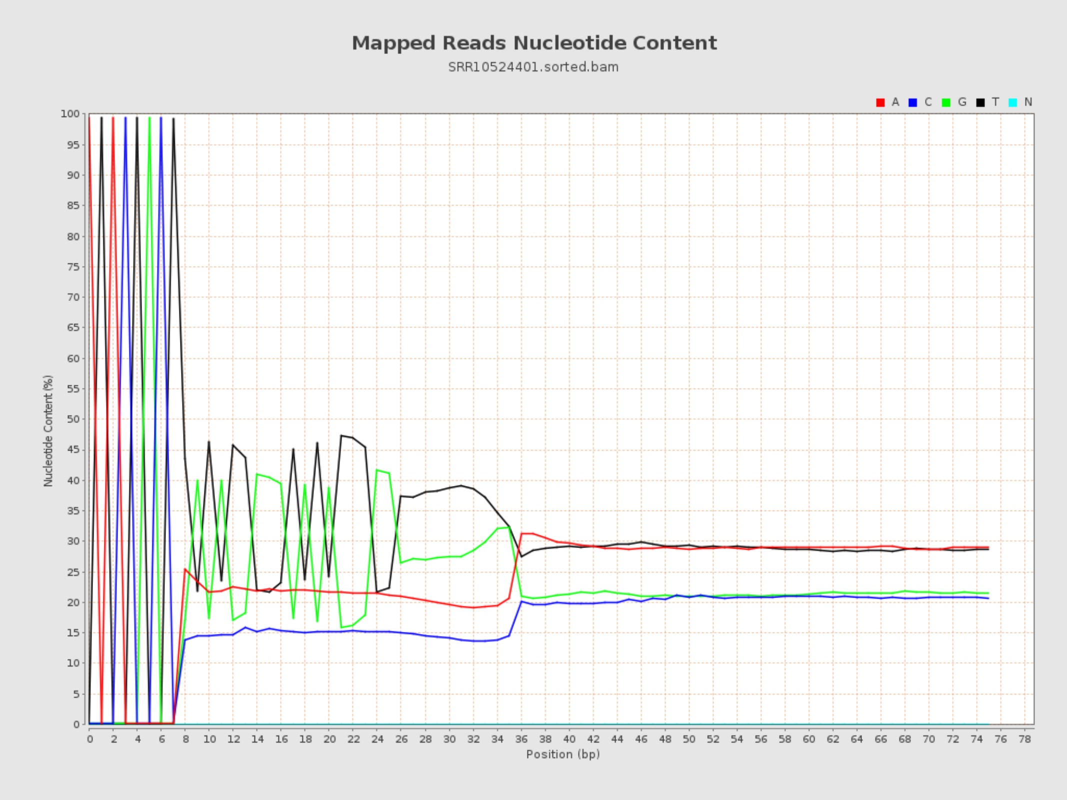
6. Results : Genome Fraction Coverage



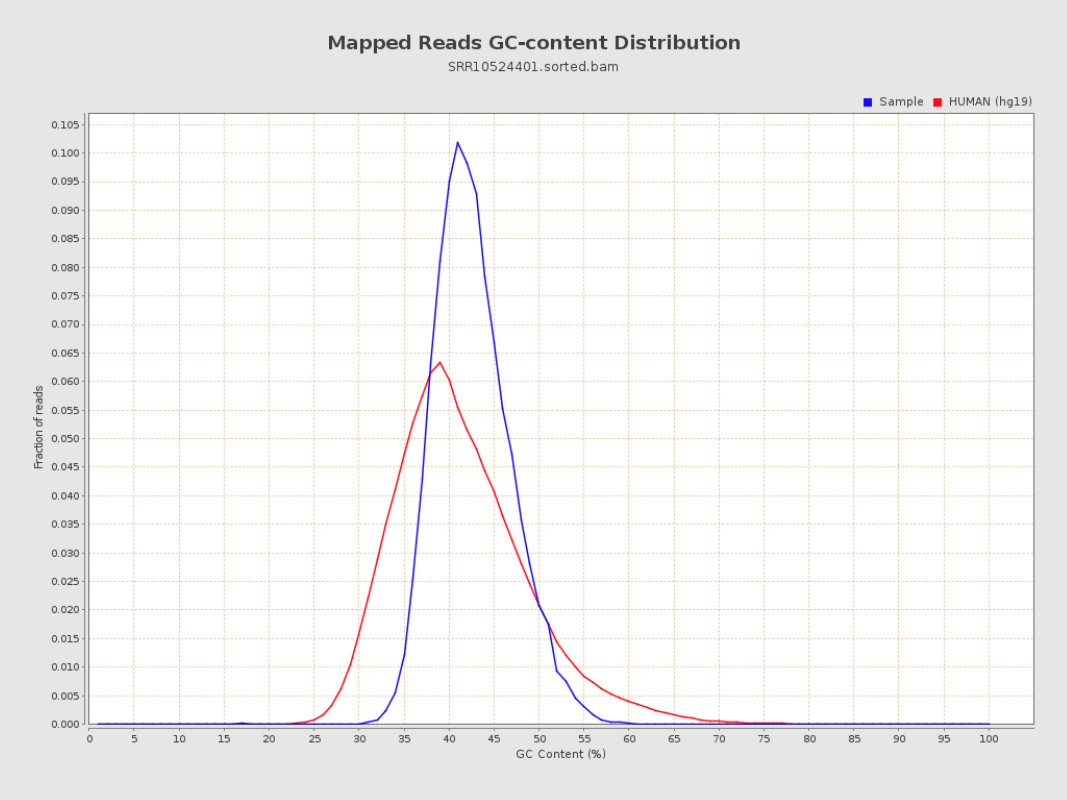
7. Results : Duplication Rate Histogram



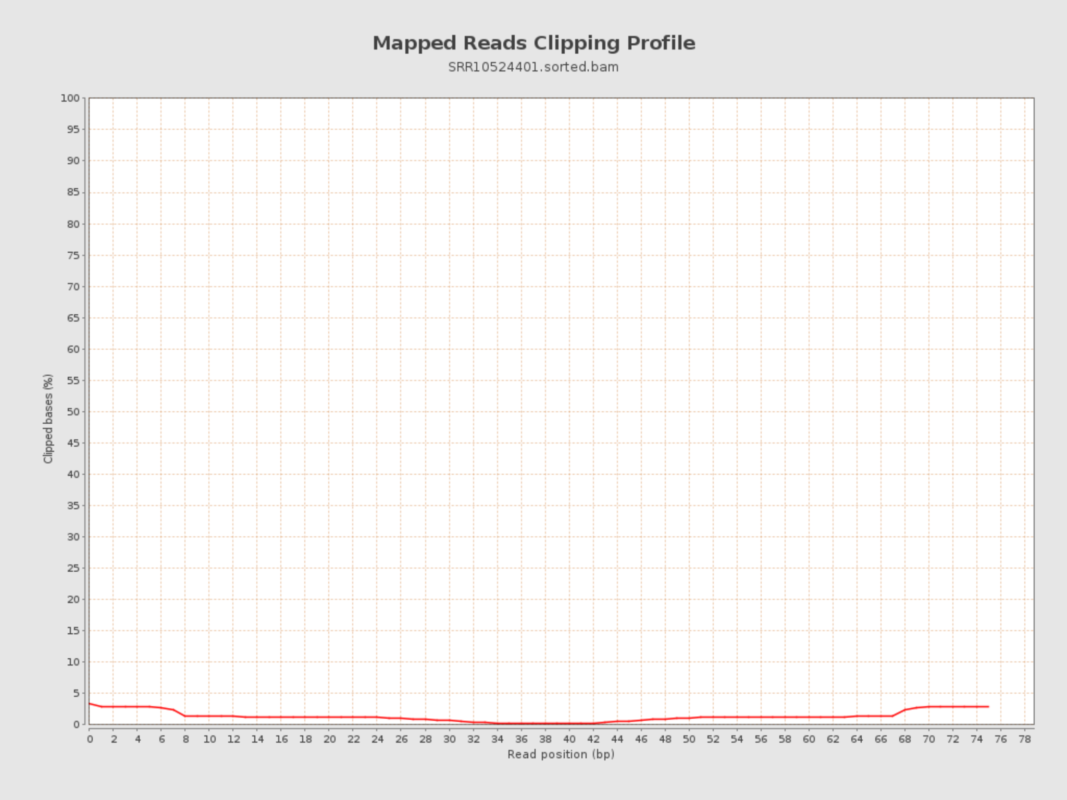
8. Results : Mapped Reads Nucleotide Content



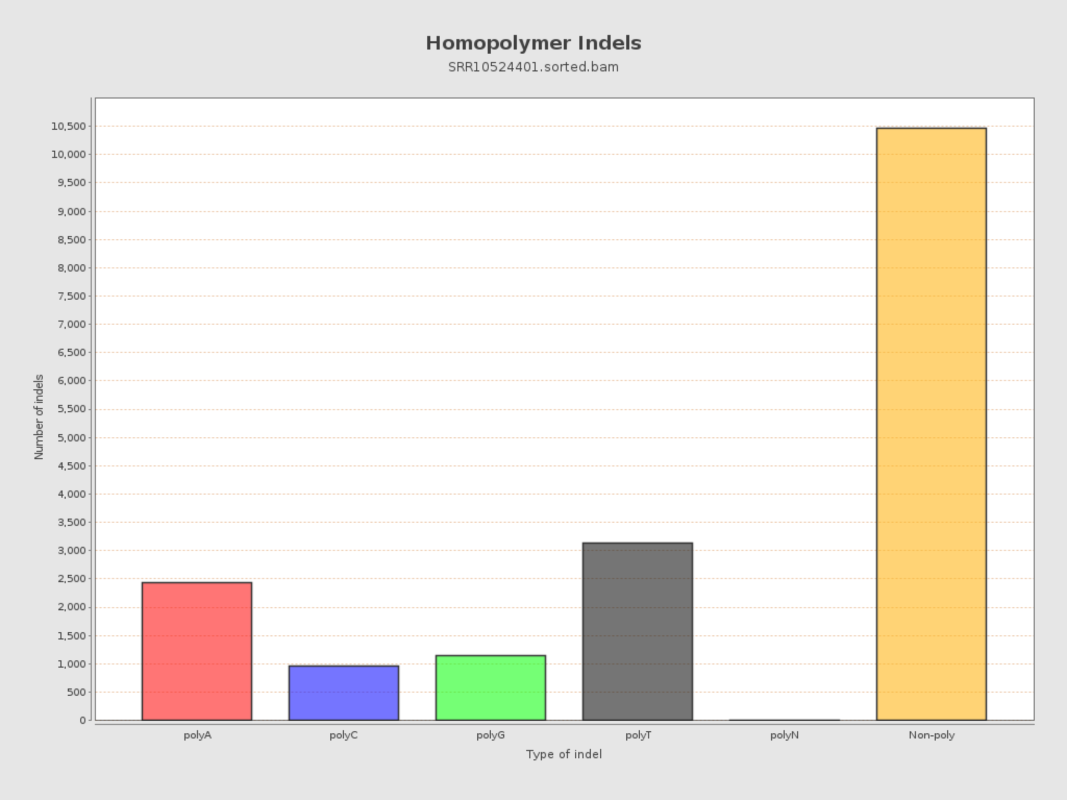
9. Results : Mapped Reads GC-content Distribution



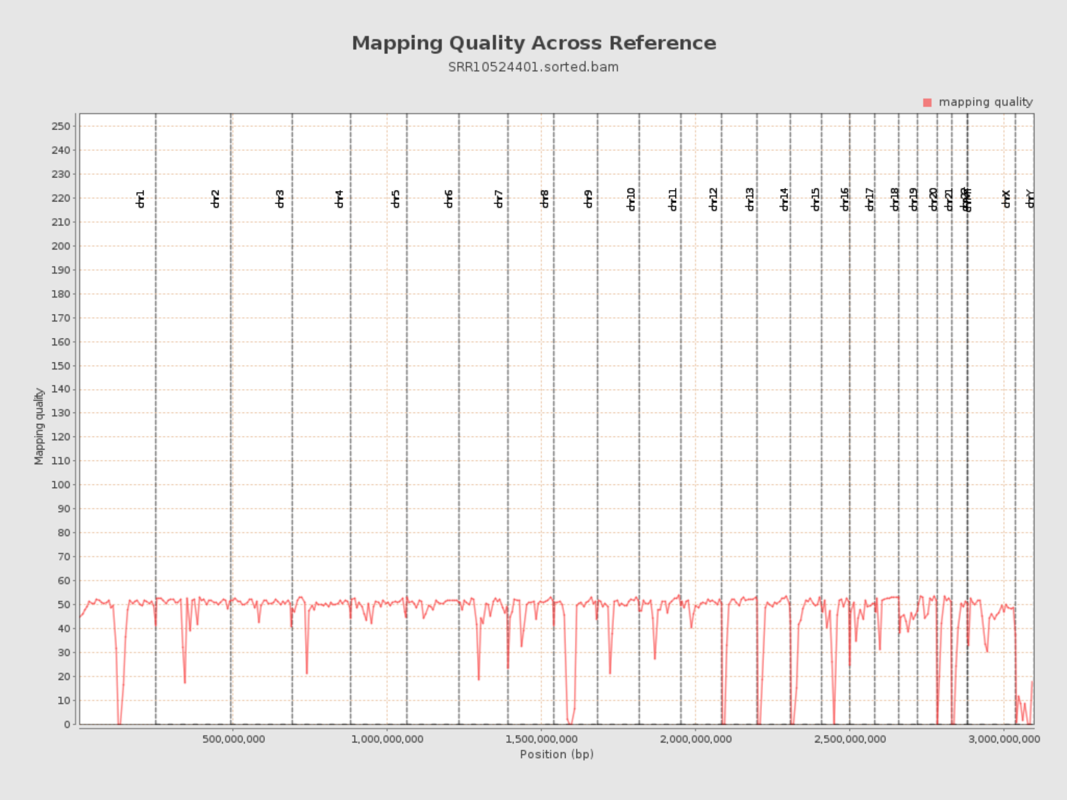
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram