Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 00:55:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524370.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_SRR10524370 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524370.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 00:55:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524370.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	185,534
Mapped reads	171,158 / 92.25%
Unmapped reads	14,376 / 7.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	721 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	2,222 / 1.2%
Duplication rate	1.02%
Clipped reads	171,322 / 92.34%

2.2. ACGT Content

Number/percentage of A's	2,588,454 / 25.64%
Number/percentage of C's	1,940,370 / 19.22%
Number/percentage of T's	3,027,204 / 29.99%
Number/percentage of G's	2,536,290 / 25.13%
Number/percentage of N's	1,763 / 0.02%
GC Percentage	44.35%

2.3. Coverage

Mean	0.0033

Standard Deviation	0.0632

2.4. Mapping Quality

Mean Mapping Quality	45.44

2.5. Mismatches and indels

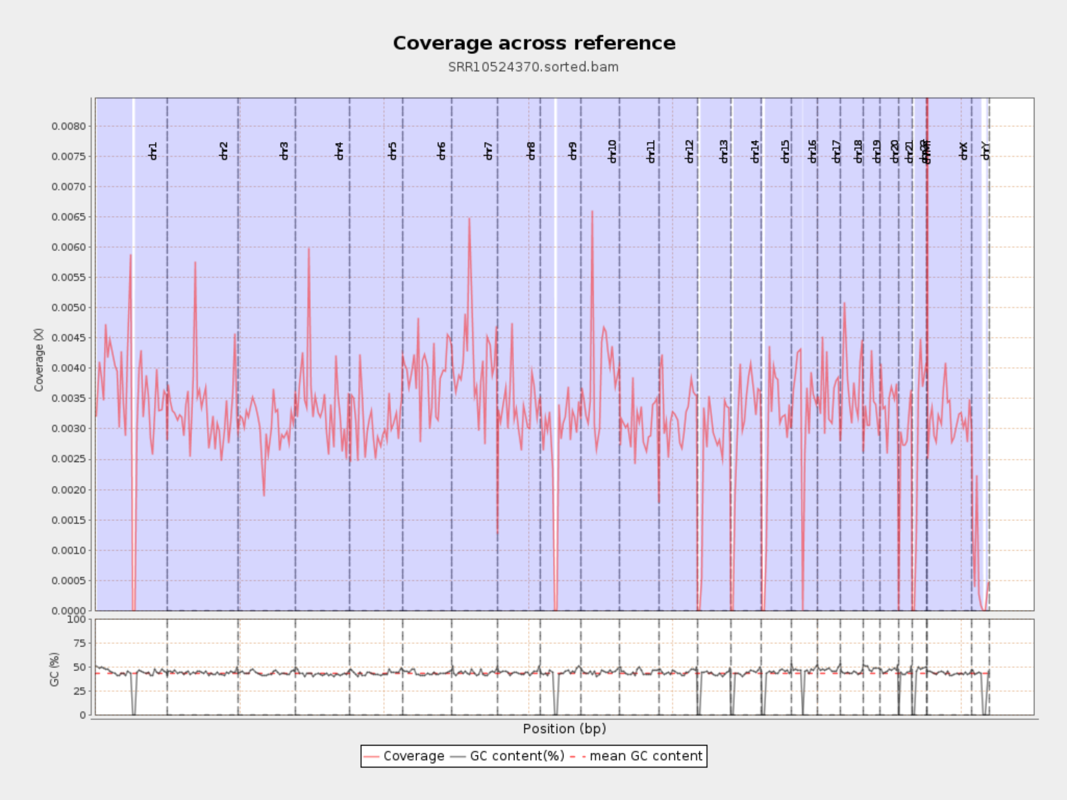
General error rate	0.53%
Mismatches	51,597
Insertions	769
Mapped reads with at least one insertion	0.45%
Deletions	1,782
Mapped reads with at least one deletion	1.03%
Homopolymer indels	40.96%

2.6. Chromosome stats

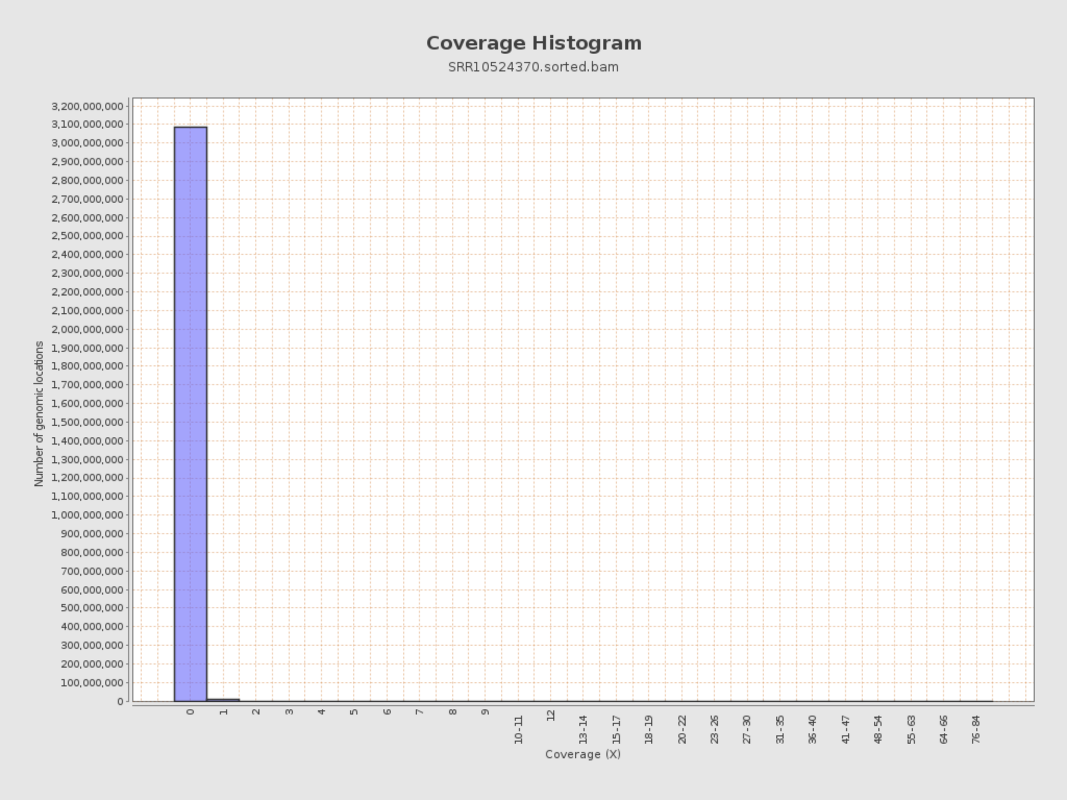
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	874882	0.0035	0.0817
chr2	243199373	811402	0.0033	0.0698
chr3	198022430	602083	0.003	0.0562
chr4	191154276	655314	0.0034	0.0618
chr5	180915260	561015	0.0031	0.0569
chr6	171115067	667856	0.0039	0.0638
chr7	159138663	657722	0.0041	0.0768

chr8	146364022	492434	0.0034	0.0626
chr9	141213431	390081	0.0028	0.0558
chr10	135534747	529280	0.0039	0.0677
chr11	135006516	416066	0.0031	0.0591
chr12	133851895	438420	0.0033	0.0583
chr13	115169878	295091	0.0026	0.0514
chr14	107349540	320916	0.003	0.0557
chr15	102531392	288694	0.0028	0.0538
chr16	90354753	296903	0.0033	0.0589
chr17	81195210	289642	0.0036	0.0612
chr18	78077248	292664	0.0037	0.079
chr19	59128983	196449	0.0033	0.0655
chr20	63025520	217074	0.0034	0.0606
chr21	48129895	131917	0.0027	0.0541
chr22	51304566	140424	0.0027	0.0532
chrMT	16571	4849	0.2926	0.5932
chrX	155270560	492483	0.0032	0.0584
chrY	59373566	33295	0.0006	0.0278

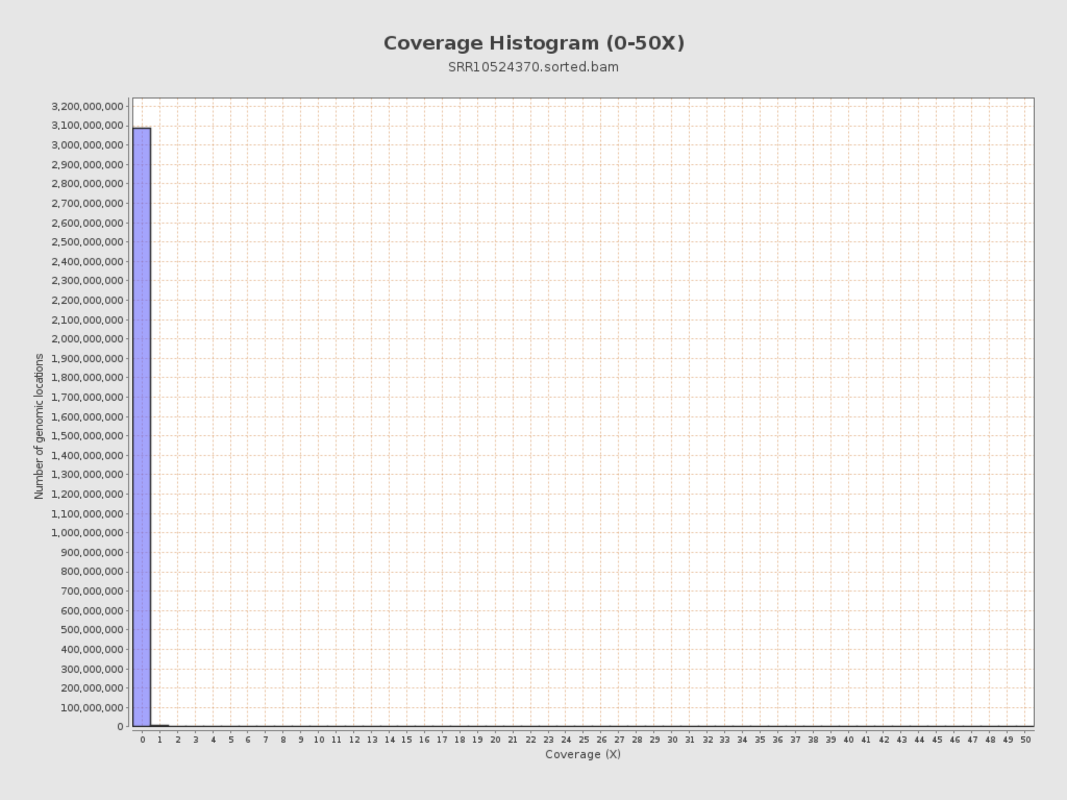
3. Results : Coverage across reference



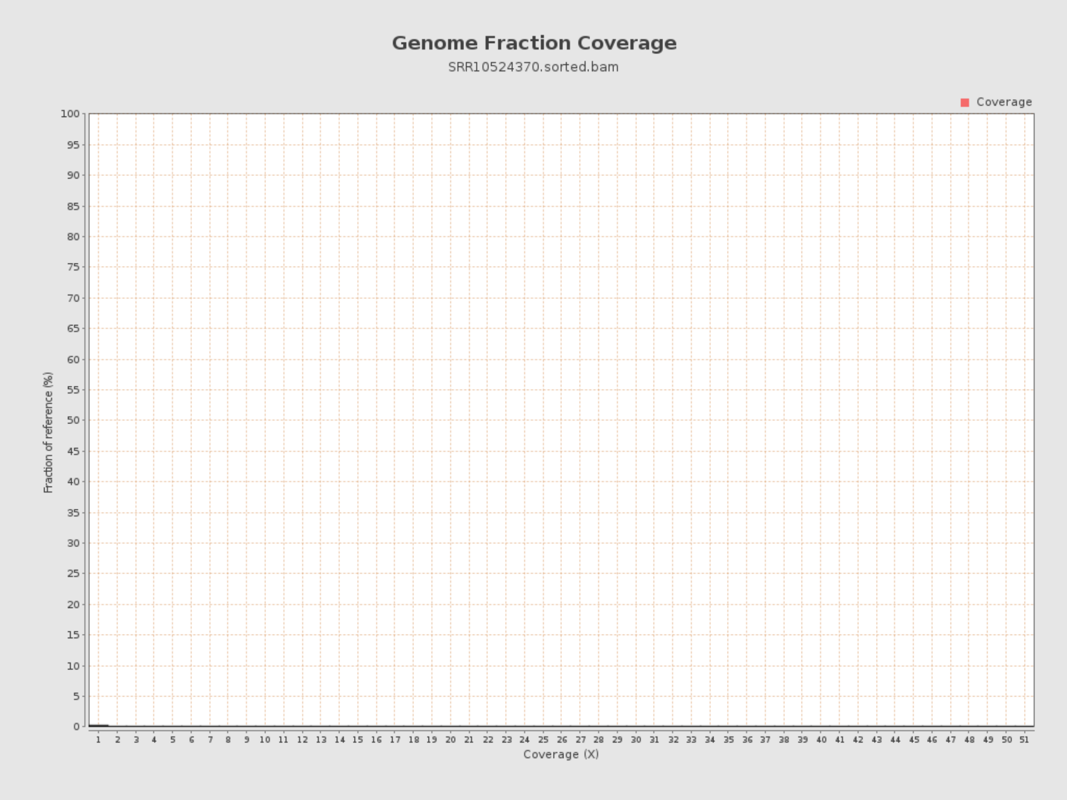
4. Results : Coverage Histogram



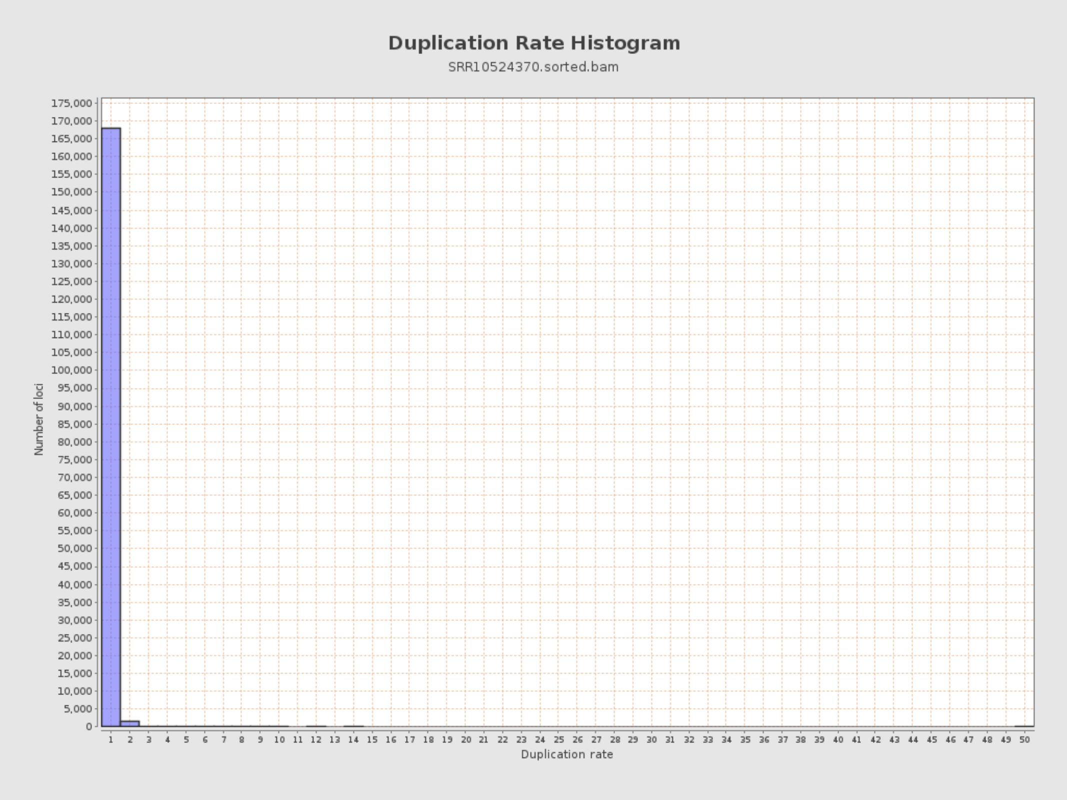
5. Results : Coverage Histogram (0-50X)



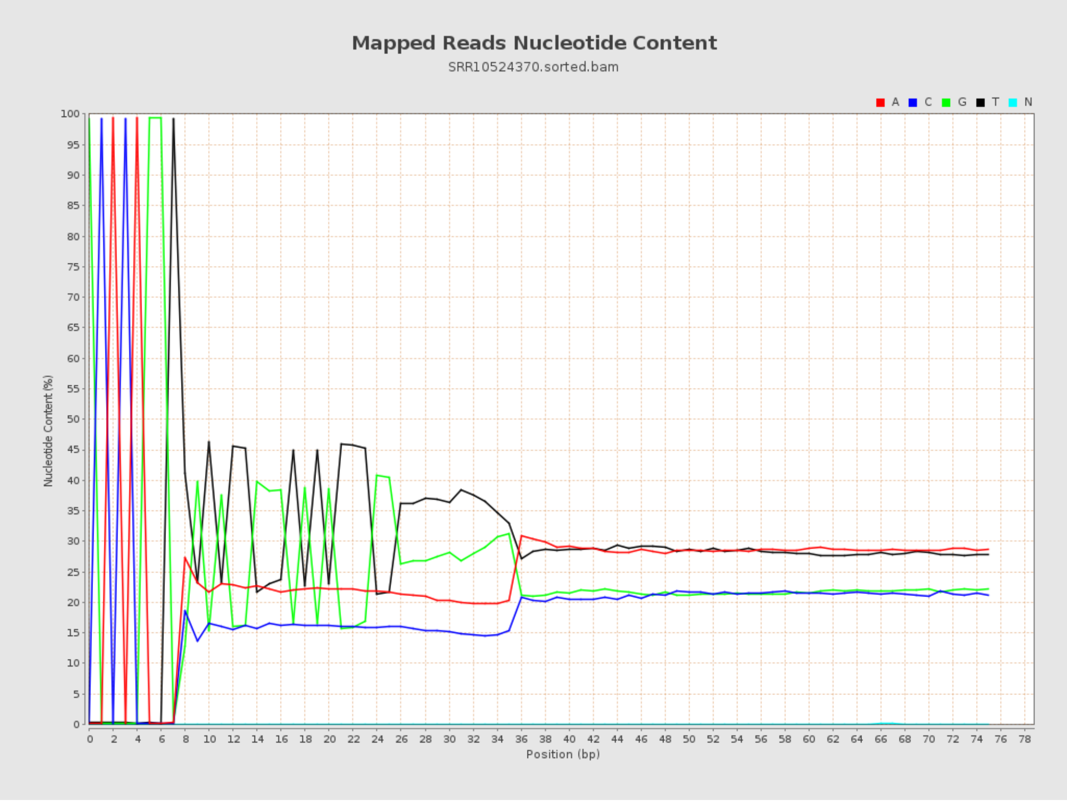
6. Results : Genome Fraction Coverage



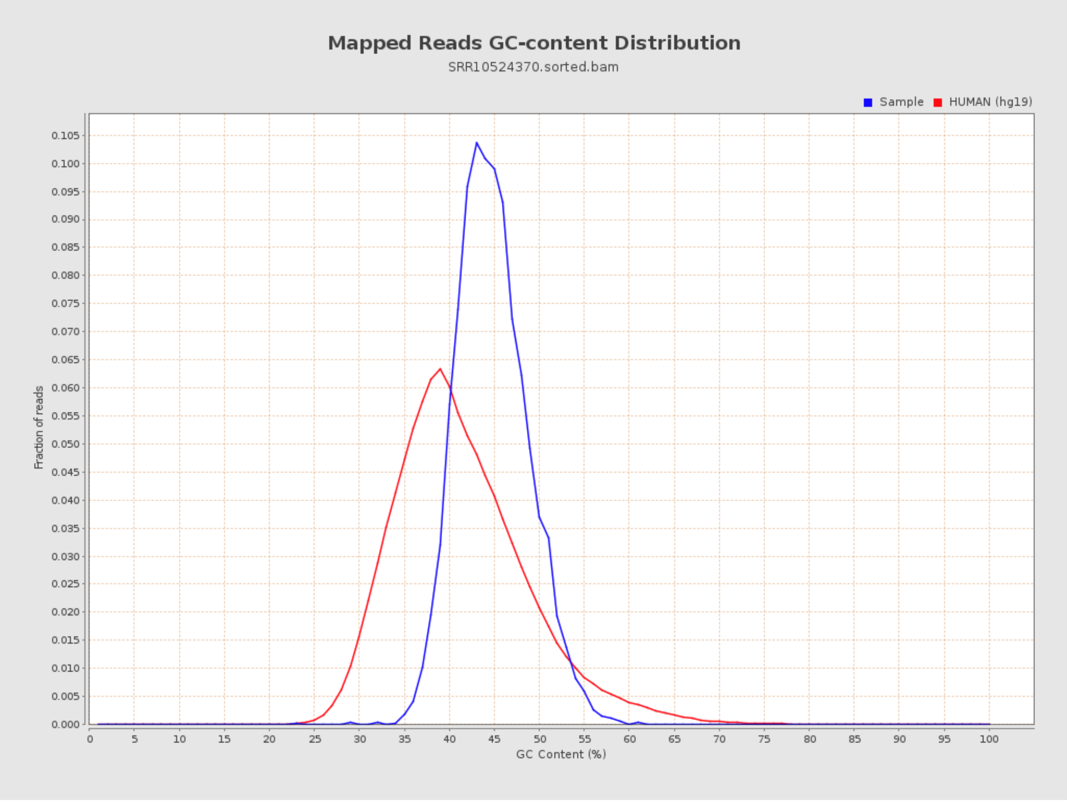
7. Results : Duplication Rate Histogram



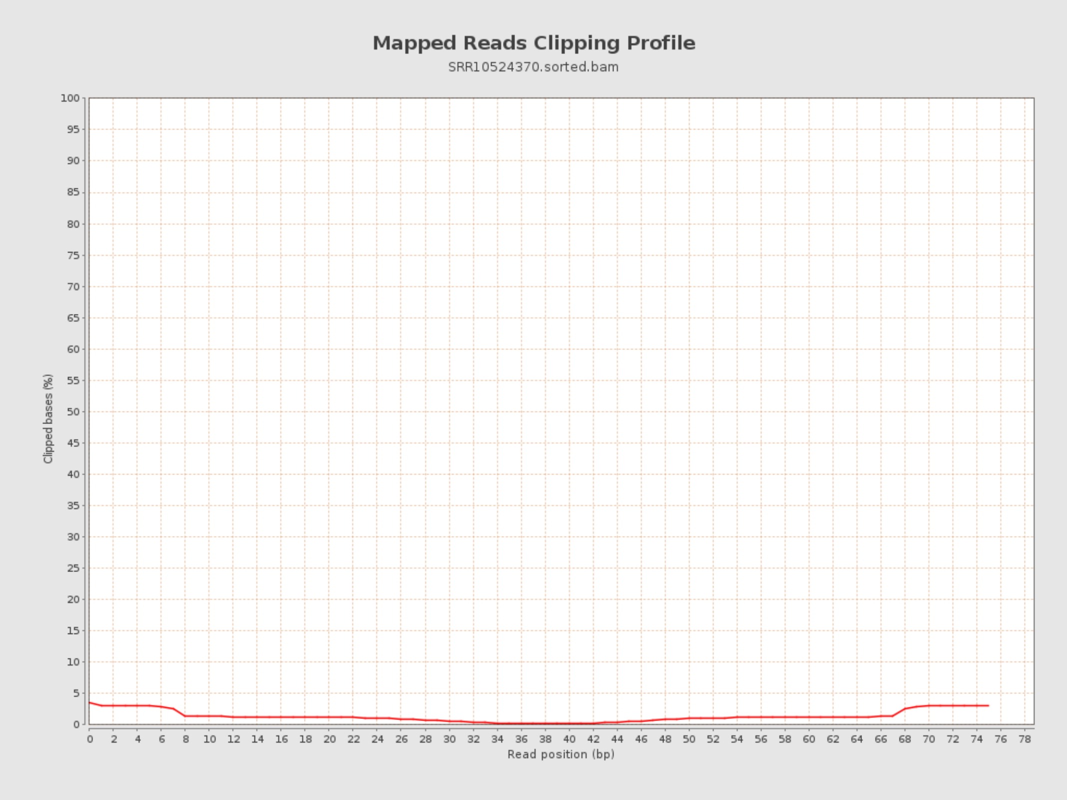
8. Results : Mapped Reads Nucleotide Content



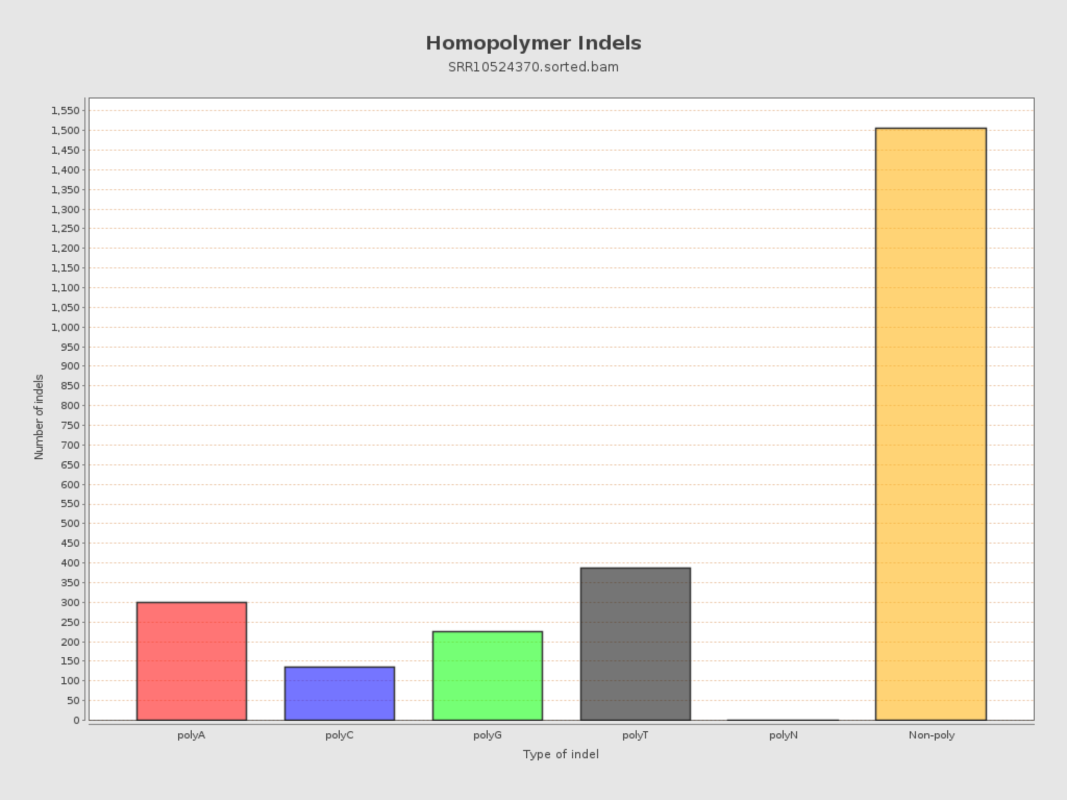
9. Results : Mapped Reads GC-content Distribution



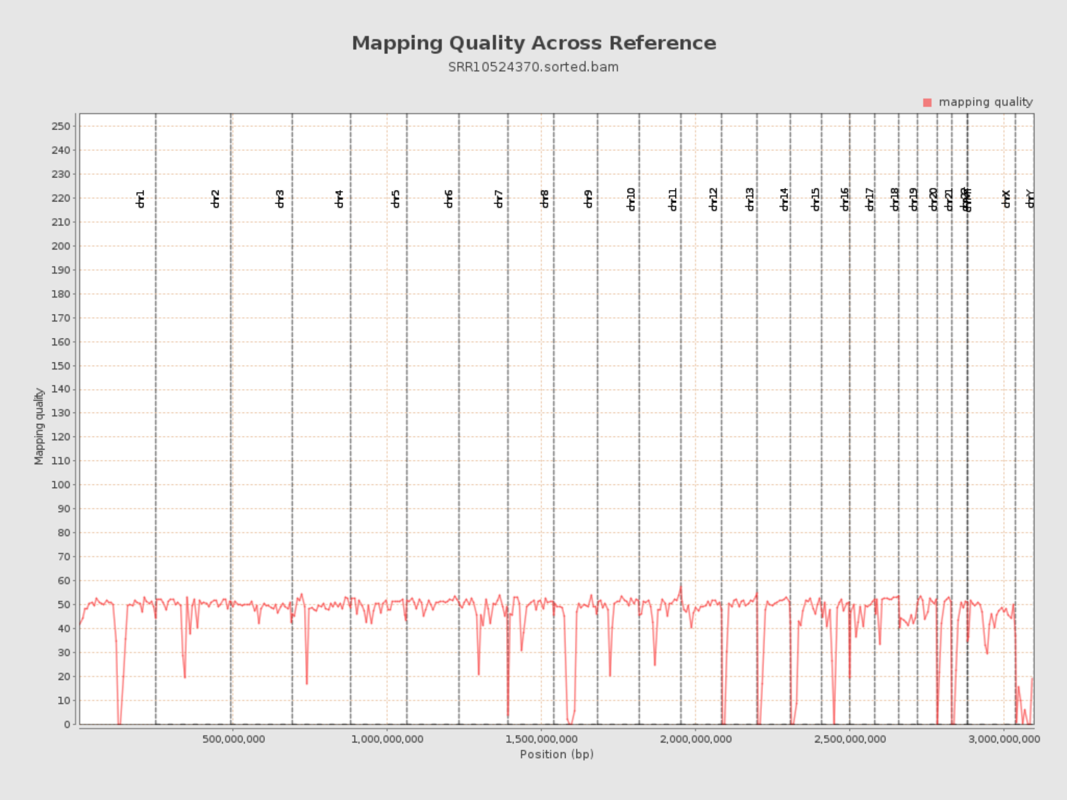
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram