Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 14:59:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524652.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_SRR10524652 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524652.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 14:59:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524652.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,196,333
Mapped reads	3,867,882 / 92.17%
Unmapped reads	328,451 / 7.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,310 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	445,274 / 10.61%
Duplication rate	8.4%
Clipped reads	3,874,779 / 92.34%

2.2. ACGT Content

Number/percentage of A's	56,971,585 / 25.33%
Number/percentage of C's	41,915,667 / 18.64%
Number/percentage of T's	72,746,570 / 32.35%
Number/percentage of G's	53,255,534 / 23.68%
Number/percentage of N's	1,814 / 0%
GC Percentage	42.32%

2.3. Coverage

Mean	0.0727

Standard Deviation	0.6023

2.4. Mapping Quality

Mean Mapping Quality	44.78

2.5. Mismatches and indels

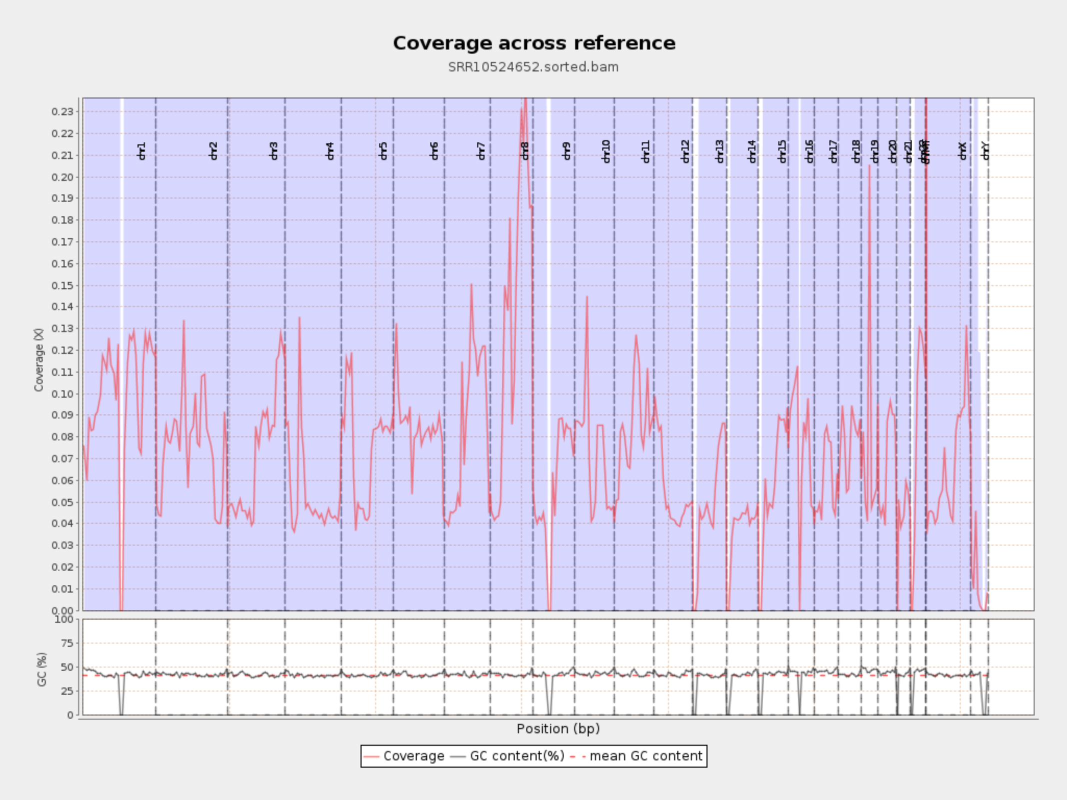
General error rate	0.52%
Mismatches	1,150,002
Insertions	14,381
Mapped reads with at least one insertion	0.37%
Deletions	43,138
Mapped reads with at least one deletion	1.11%
Homopolymer indels	43.51%

2.6. Chromosome stats

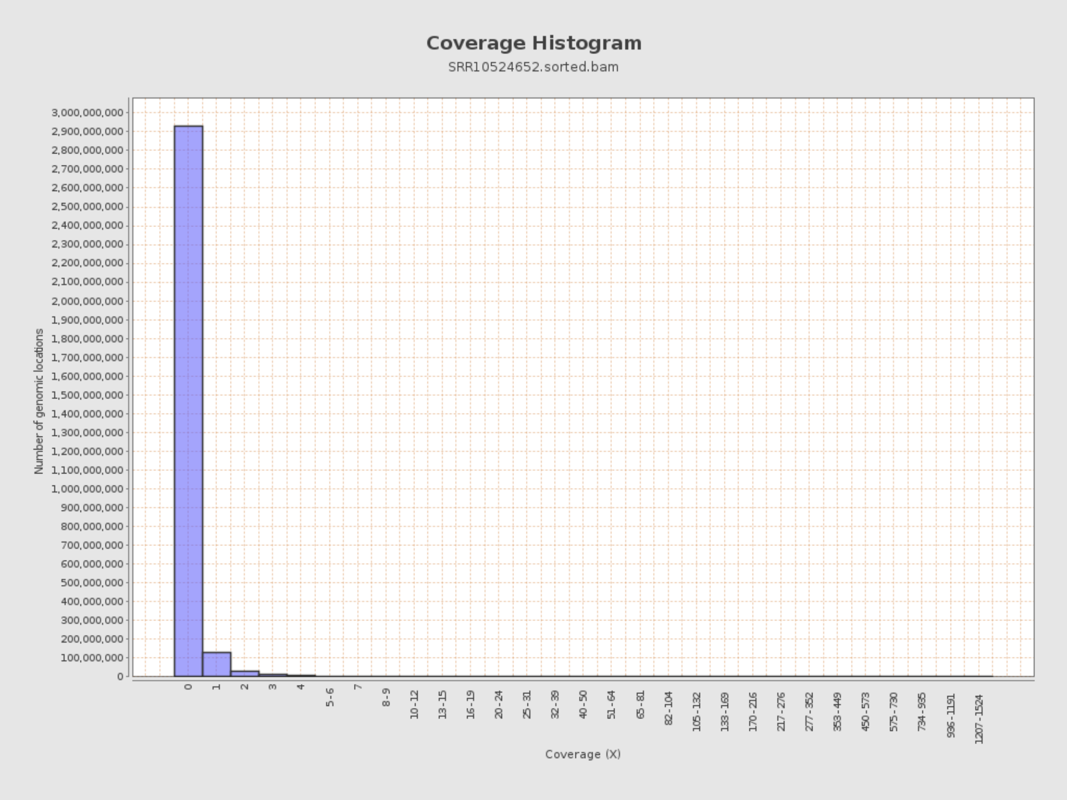
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	24540481	0.0985	1.1455
chr2	243199373	18553261	0.0763	0.8026
chr3	198022430	14230455	0.0719	0.354
chr4	191154276	10359357	0.0542	0.4538
chr5	180915260	13589547	0.0751	0.3612
chr6	171115067	14658633	0.0857	0.4194
chr7	159138663	13335937	0.0838	0.7008

chr8	146364022	19958556	0.1364	0.8325
chr9	141213431	7933757	0.0562	0.4735
chr10	135534747	9788218	0.0722	0.6698
chr11	135006516	11366554	0.0842	0.501
chr12	133851895	7454722	0.0557	0.3304
chr13	115169878	5578119	0.0484	0.2916
chr14	107349540	3988383	0.0372	0.2735
chr15	102531392	5795828	0.0565	0.313
chr16	90354753	6806505	0.0753	0.3927
chr17	81195210	4865968	0.0599	0.3486
chr18	78077248	6094170	0.0781	0.8175
chr19	59128983	4511981	0.0763	0.8001
chr20	63025520	4363253	0.0692	0.3672
chr21	48129895	2138209	0.0444	0.3924
chr22	51304566	4196191	0.0818	0.3825
chrMT	16571	24247	1.4632	1.837
chrX	155270560	10163552	0.0655	0.401
chrY	59373566	667492	0.0112	0.3933

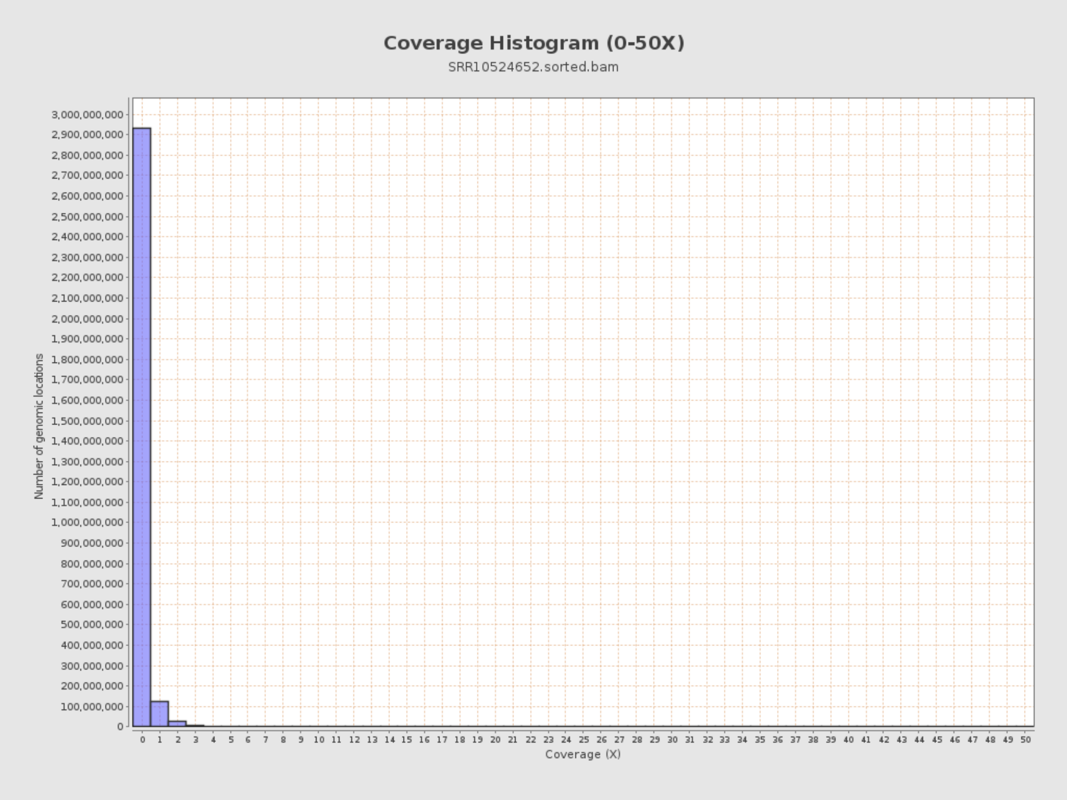
3. Results : Coverage across reference



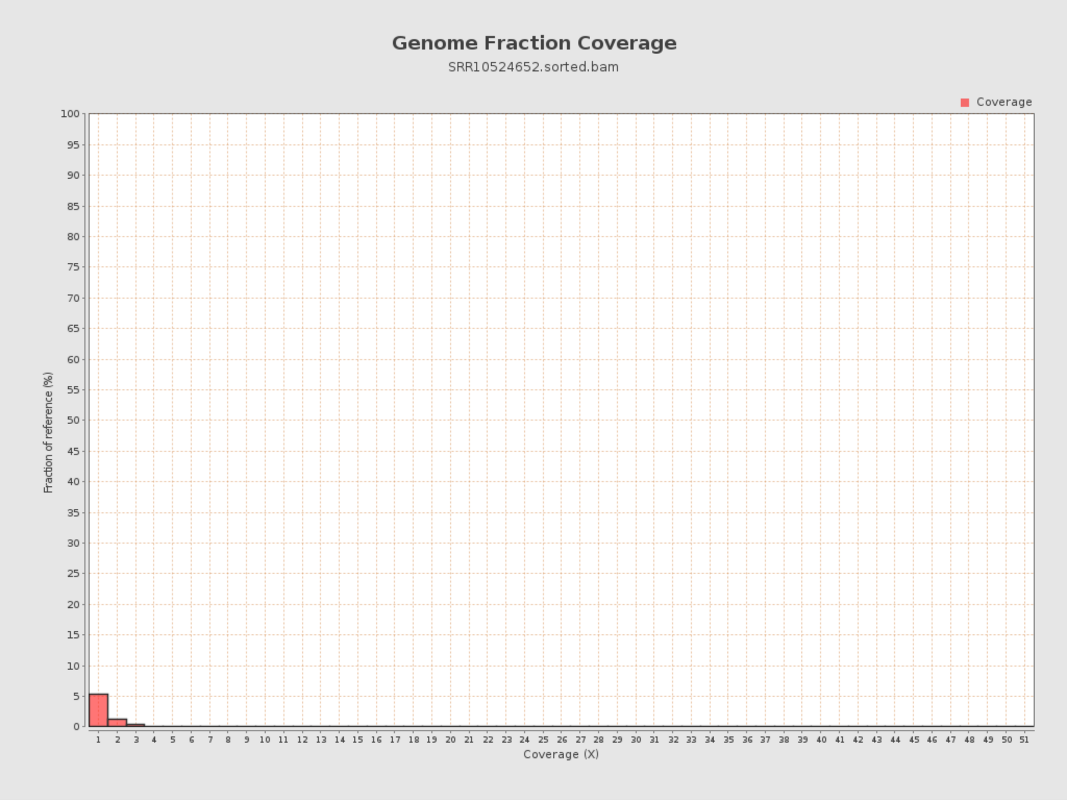
4. Results : Coverage Histogram



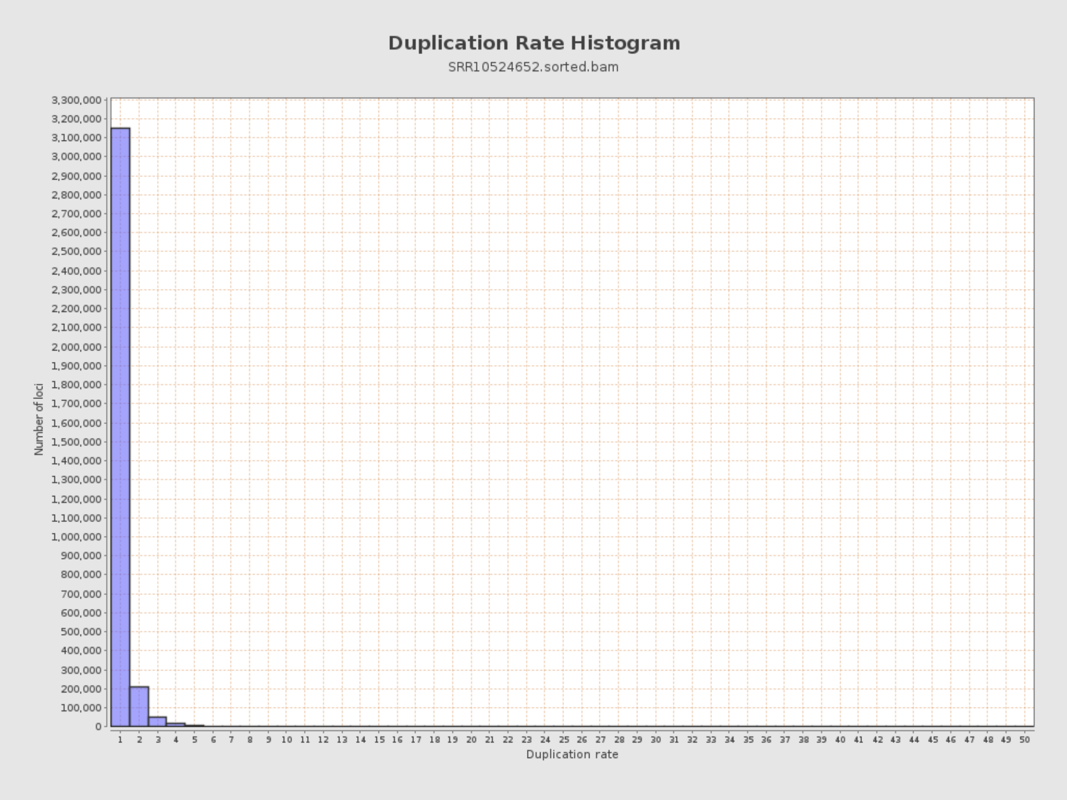
5. Results : Coverage Histogram (0-50X)



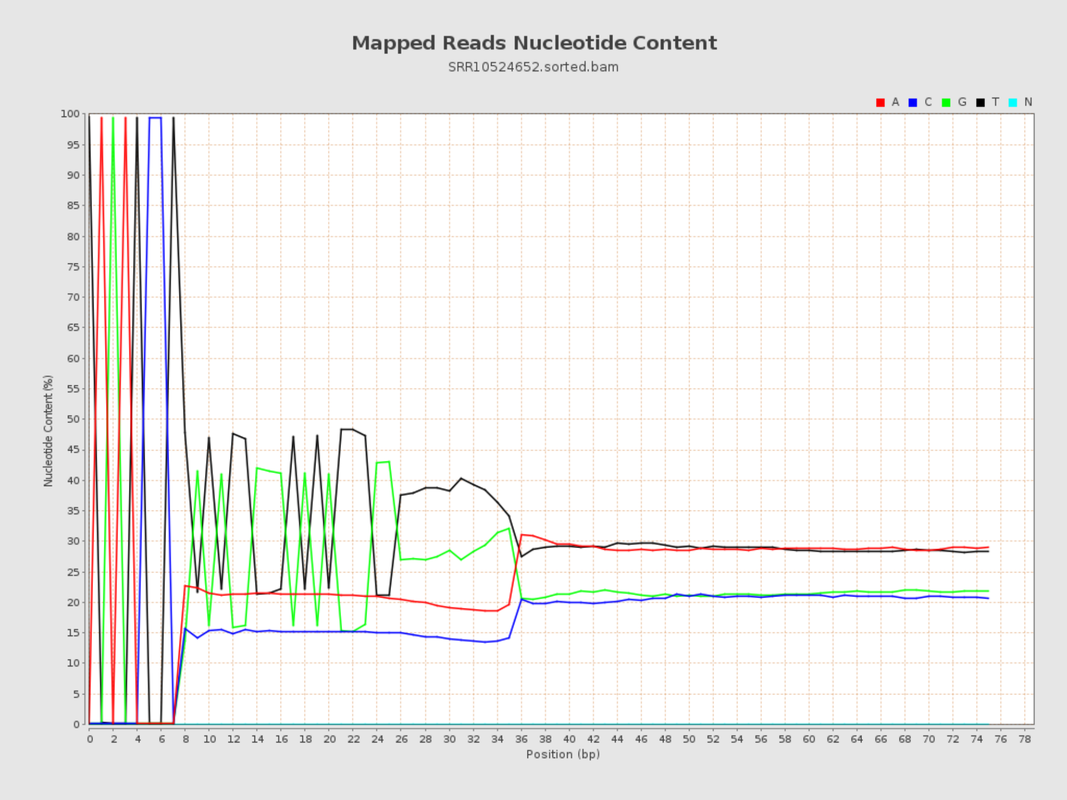
6. Results : Genome Fraction Coverage



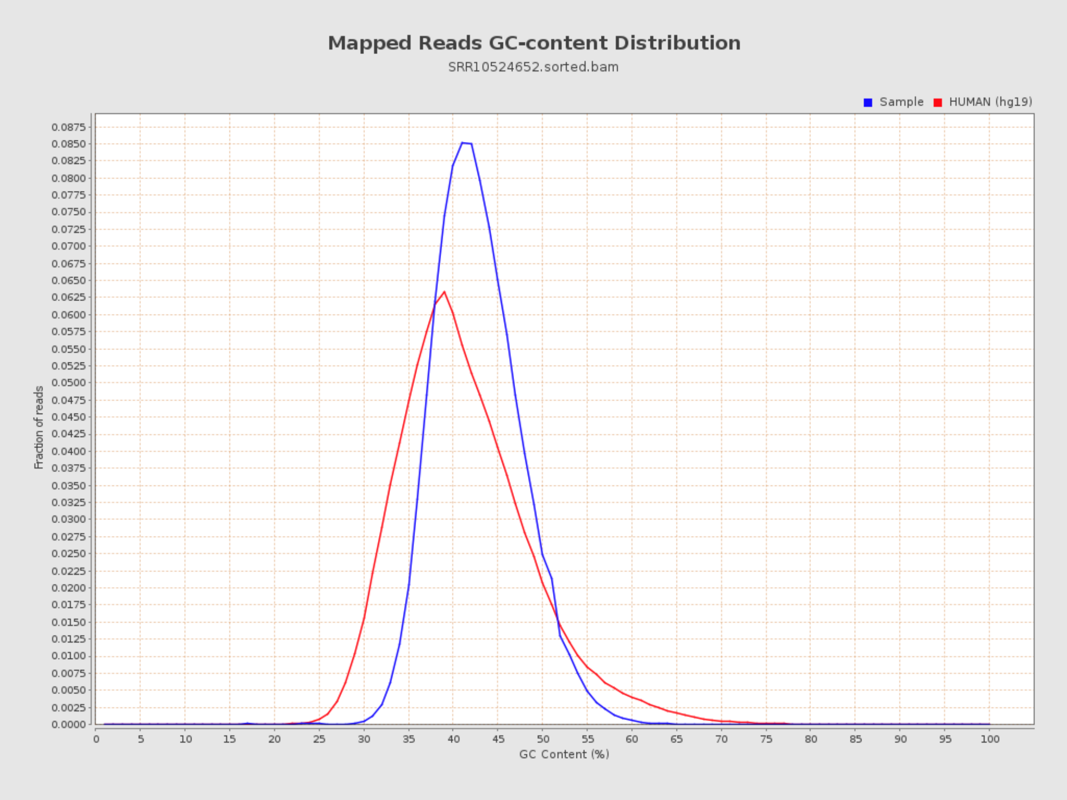
7. Results : Duplication Rate Histogram



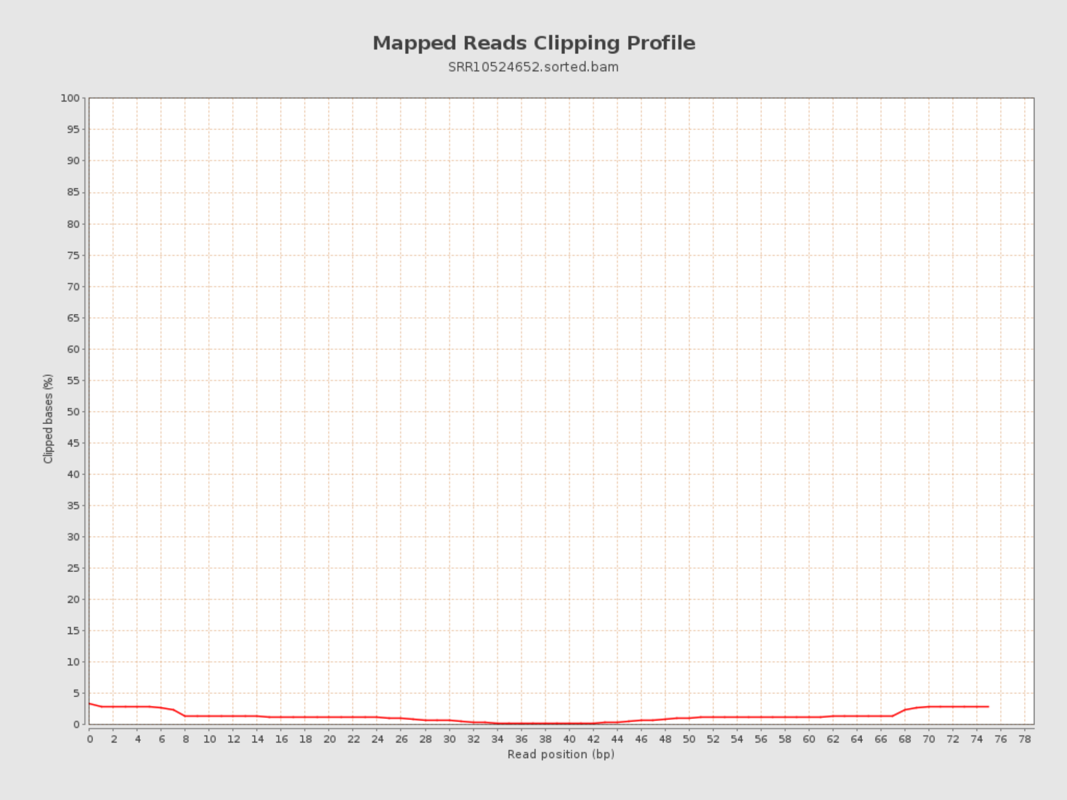
8. Results : Mapped Reads Nucleotide Content



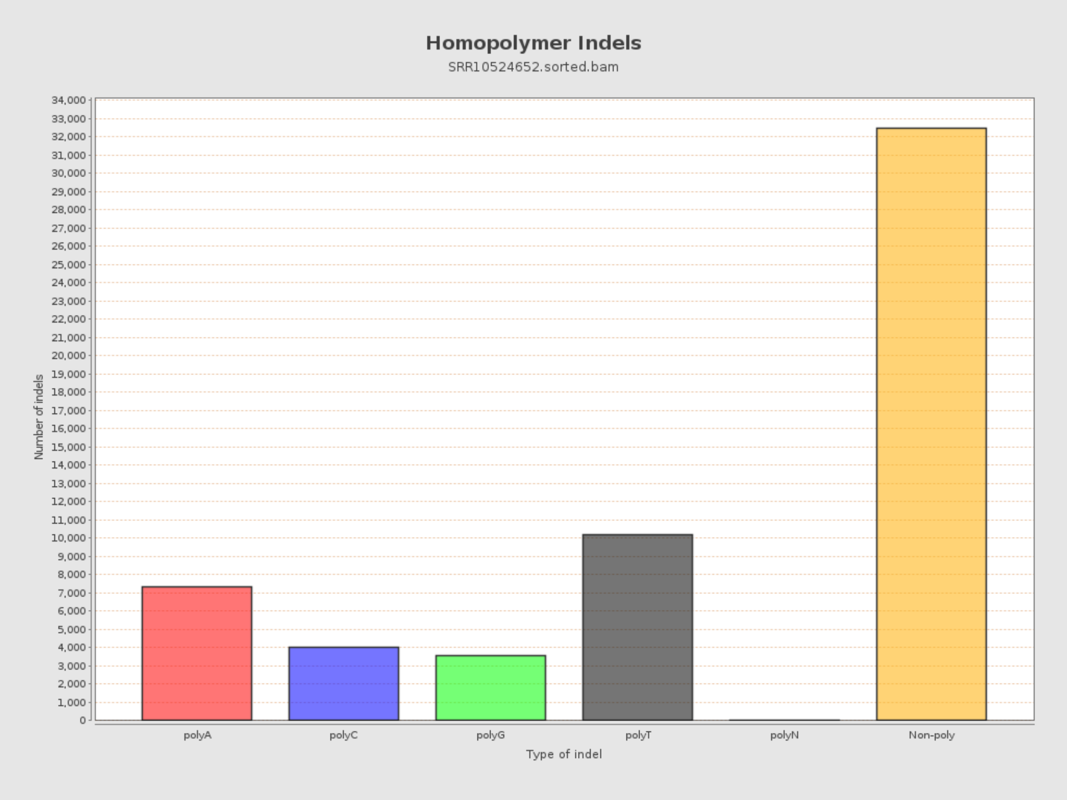
9. Results : Mapped Reads GC-content Distribution



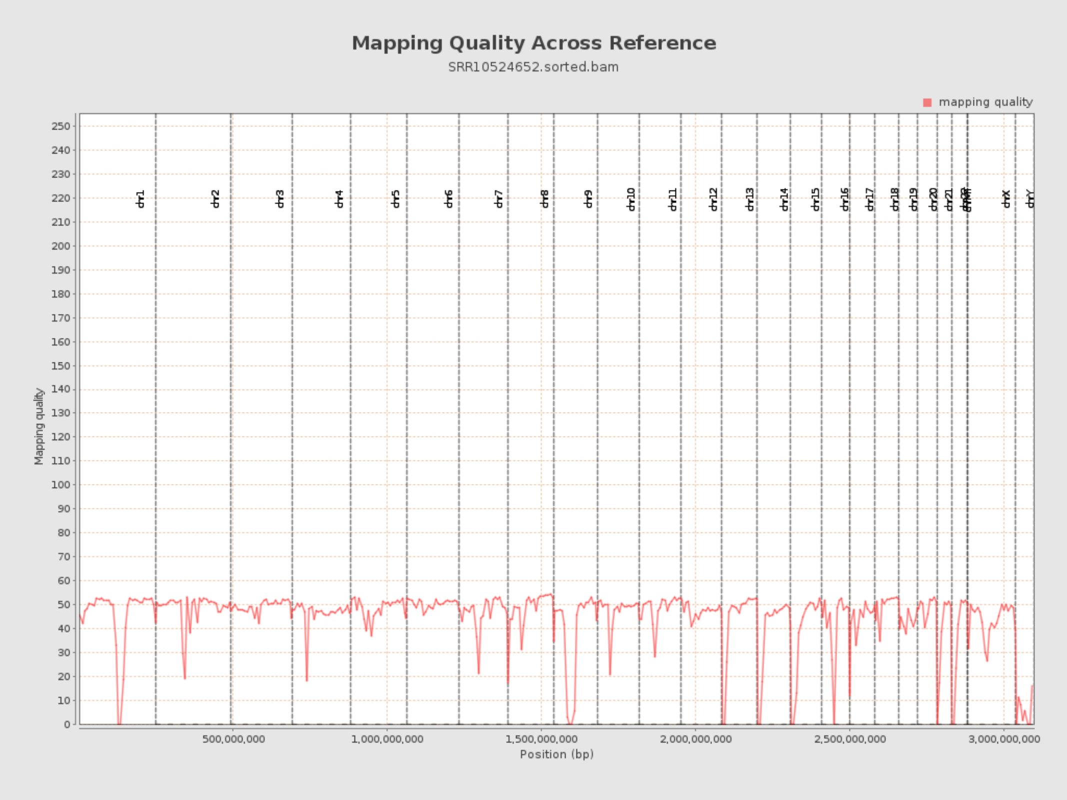
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram