Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 12:20:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524597.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_SRR10524597 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524597.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 12:20:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524597.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,046,447
Mapped reads	2,828,002 / 92.83%
Unmapped reads	218,445 / 7.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,886 / 0.19%
Read min/max/mean length	30 / 76 / 76.06
Duplicated reads (estimated)	214,662 / 7.05%
Duplication rate	5.82%
Clipped reads	2,828,504 / 92.85%

2.2. ACGT Content

Number/percentage of A's	39,139,937 / 23.85%
Number/percentage of C's	30,147,178 / 18.37%
Number/percentage of T's	53,170,608 / 32.4%
Number/percentage of G's	41,665,415 / 25.39%
Number/percentage of N's	1,009 / 0%
GC Percentage	43.76%

2.3. Coverage

Mean	0.053

Standard Deviation	0.4368

2.4. Mapping Quality

Mean Mapping Quality	45.39

2.5. Mismatches and indels

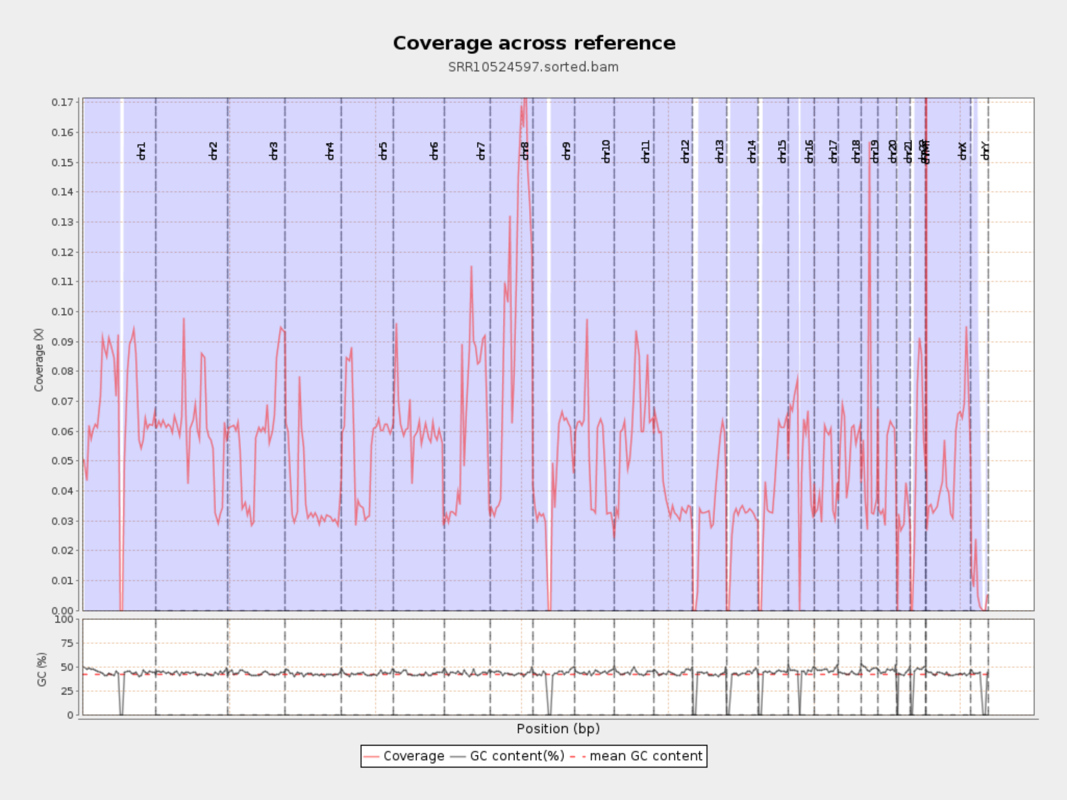
General error rate	0.47%
Mismatches	749,132
Insertions	10,102
Mapped reads with at least one insertion	0.36%
Deletions	28,177
Mapped reads with at least one deletion	0.99%
Homopolymer indels	45.36%

2.6. Chromosome stats

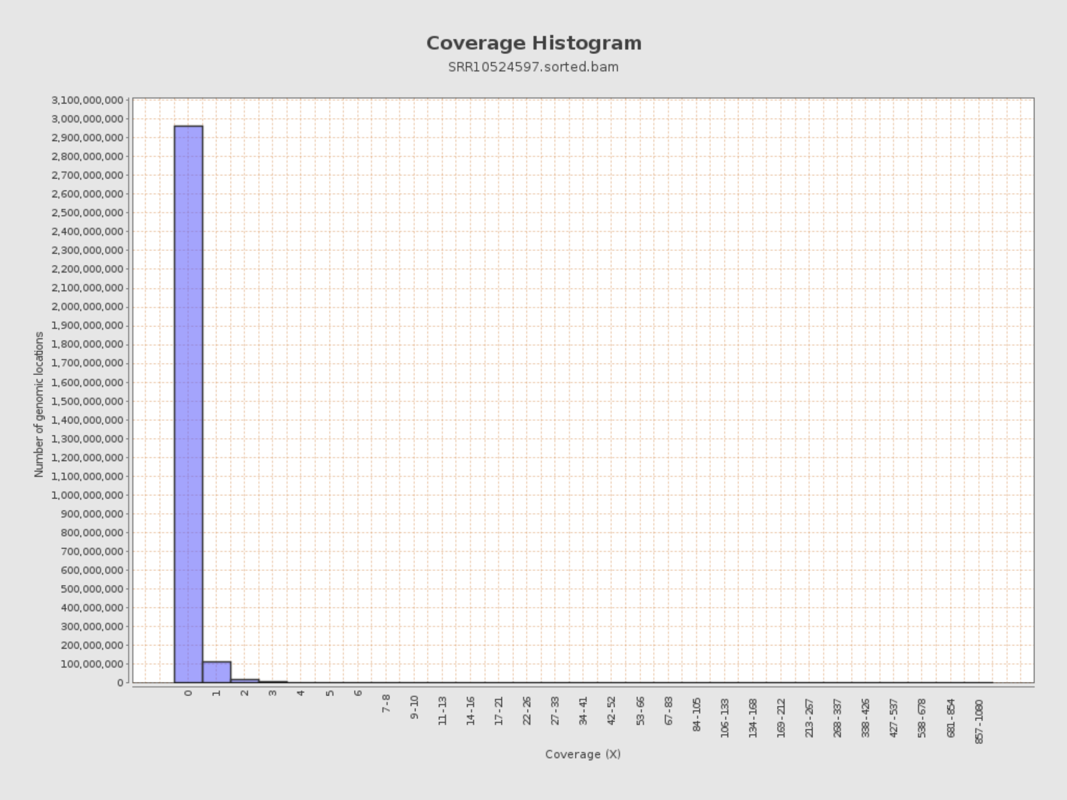
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16650555	0.0668	0.8023
chr2	243199373	14546056	0.0598	0.5279
chr3	198022430	11703902	0.0591	0.2944
chr4	191154276	7328870	0.0383	0.2865
chr5	180915260	10035901	0.0555	0.2835
chr6	171115067	10477547	0.0612	0.334
chr7	159138663	9934365	0.0624	0.6051

chr8	146364022	14647240	0.1001	0.5615
chr9	141213431	5903044	0.0418	0.3782
chr10	135534747	7008759	0.0517	0.4321
chr11	135006516	8336760	0.0618	0.4211
chr12	133851895	5418654	0.0405	0.2568
chr13	115169878	3974527	0.0345	0.2296
chr14	107349540	3040136	0.0283	0.2199
chr15	102531392	4155190	0.0405	0.2563
chr16	90354753	4812783	0.0533	0.3031
chr17	81195210	3582551	0.0441	0.2669
chr18	78077248	4372733	0.056	0.6422
chr19	59128983	3208630	0.0543	0.5641
chr20	63025520	2982511	0.0473	0.2732
chr21	48129895	1430599	0.0297	0.2423
chr22	51304566	2653643	0.0517	0.275
chrMT	16571	16891	1.0193	1.1345
chrX	155270560	7552506	0.0486	0.319
chrY	59373566	397972	0.0067	0.1826

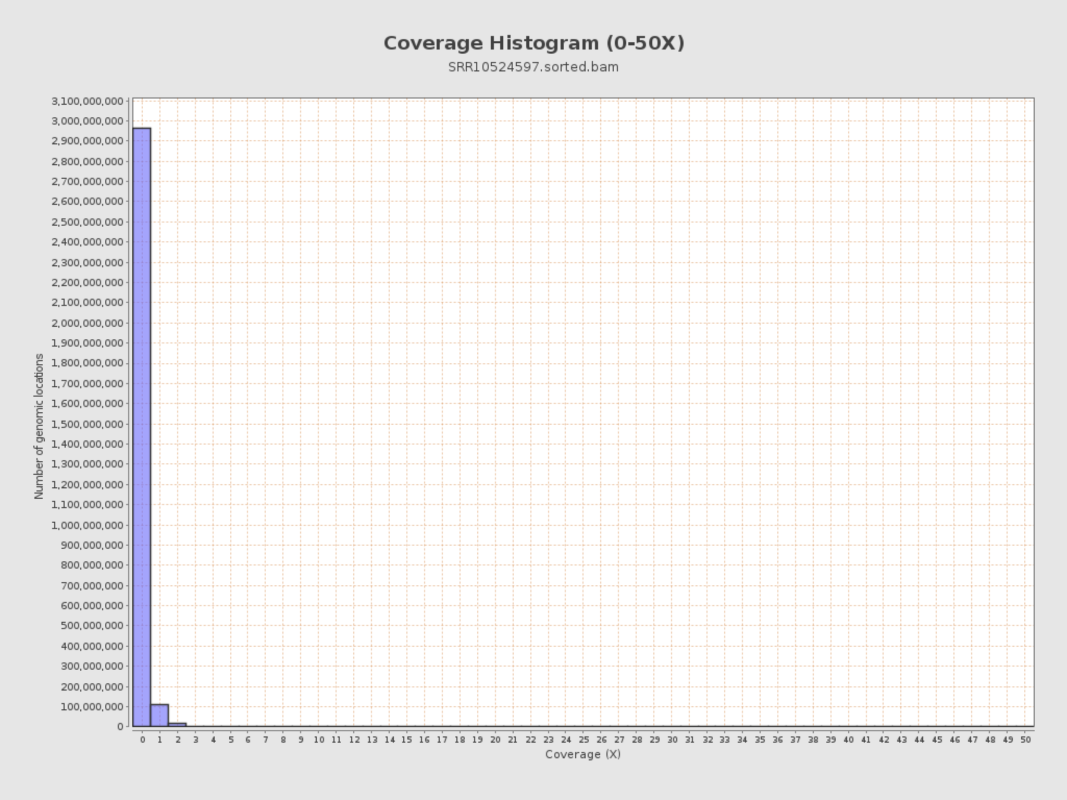
3. Results : Coverage across reference



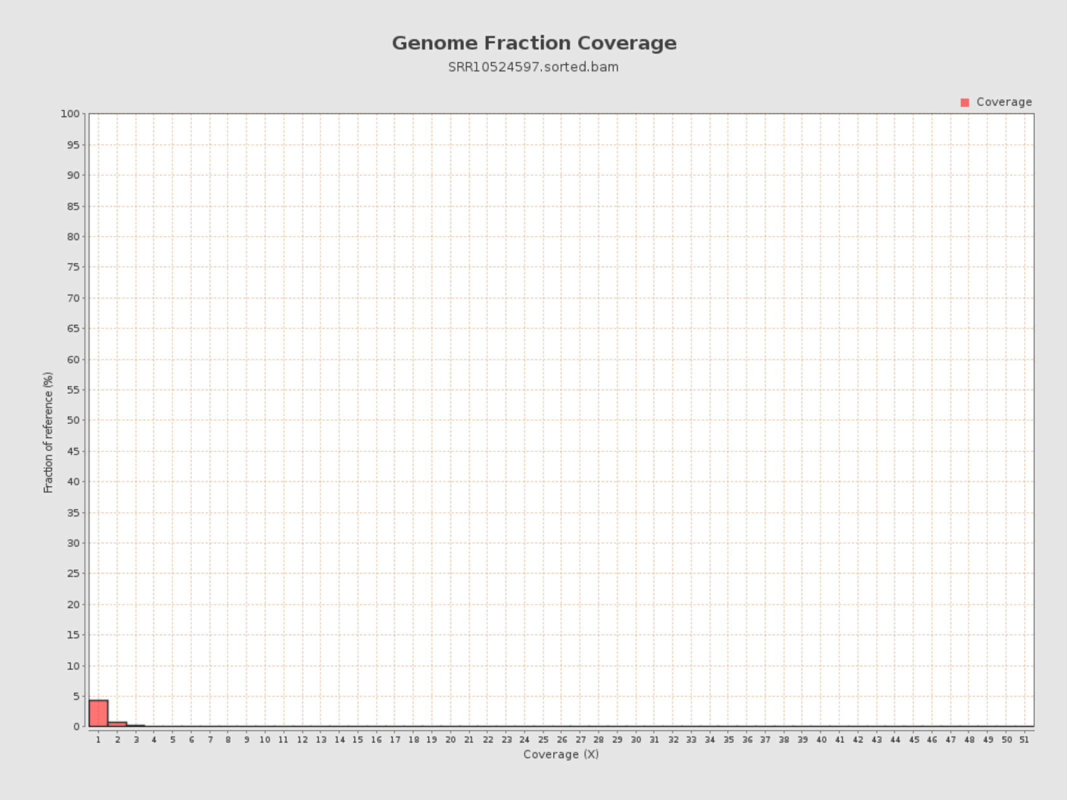
4. Results : Coverage Histogram



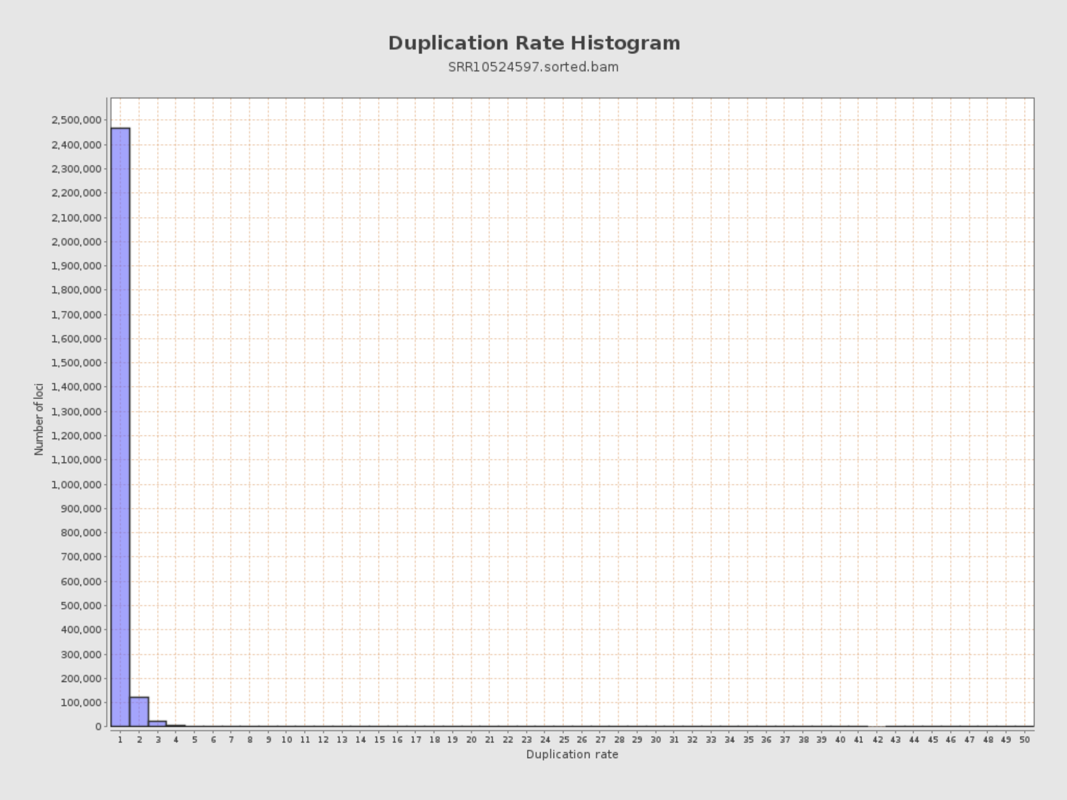
5. Results : Coverage Histogram (0-50X)



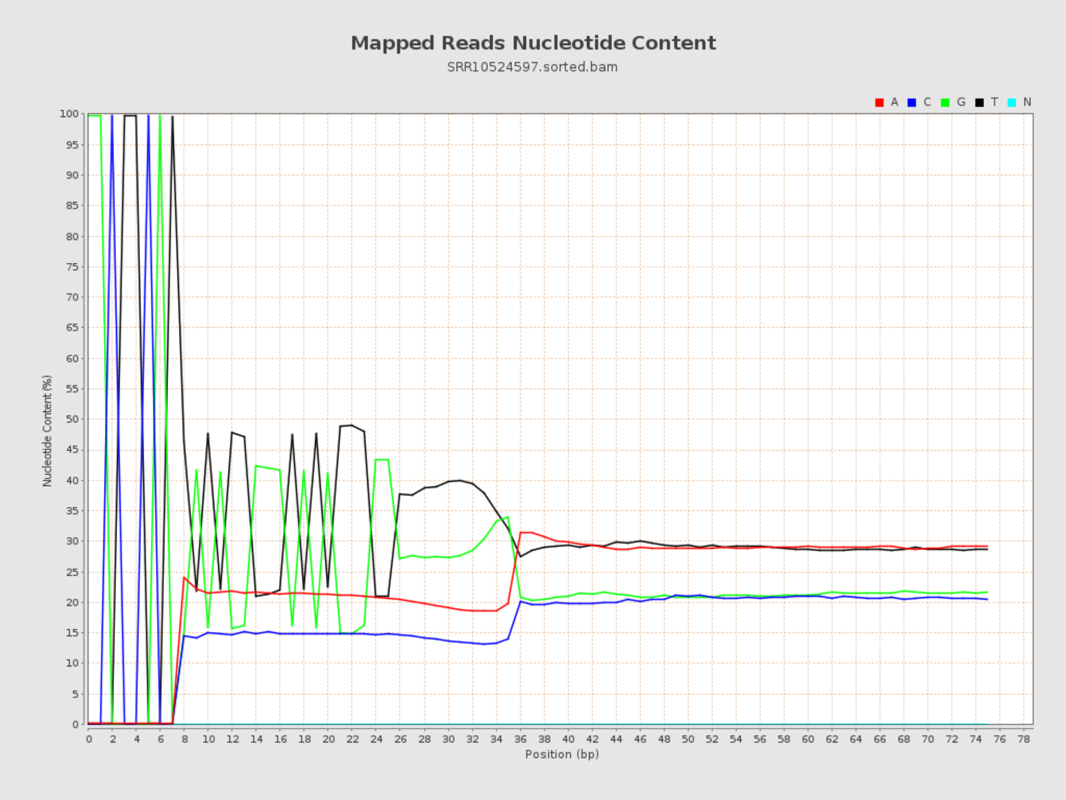
6. Results : Genome Fraction Coverage



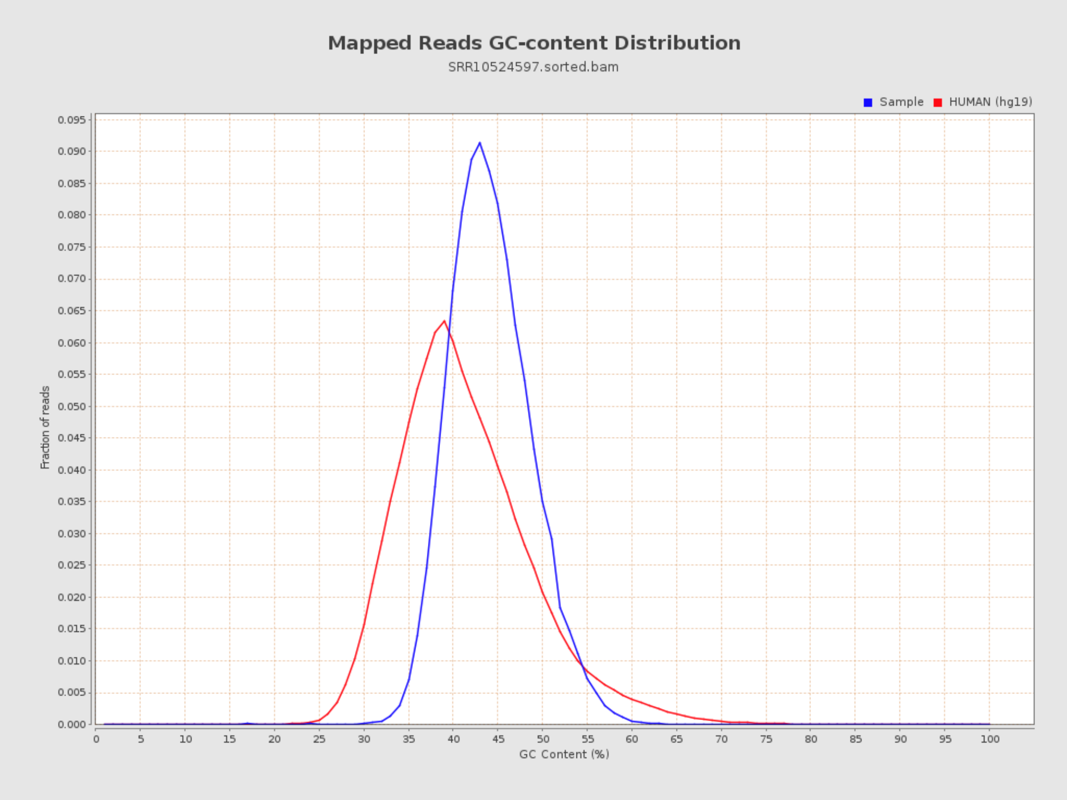
7. Results : Duplication Rate Histogram



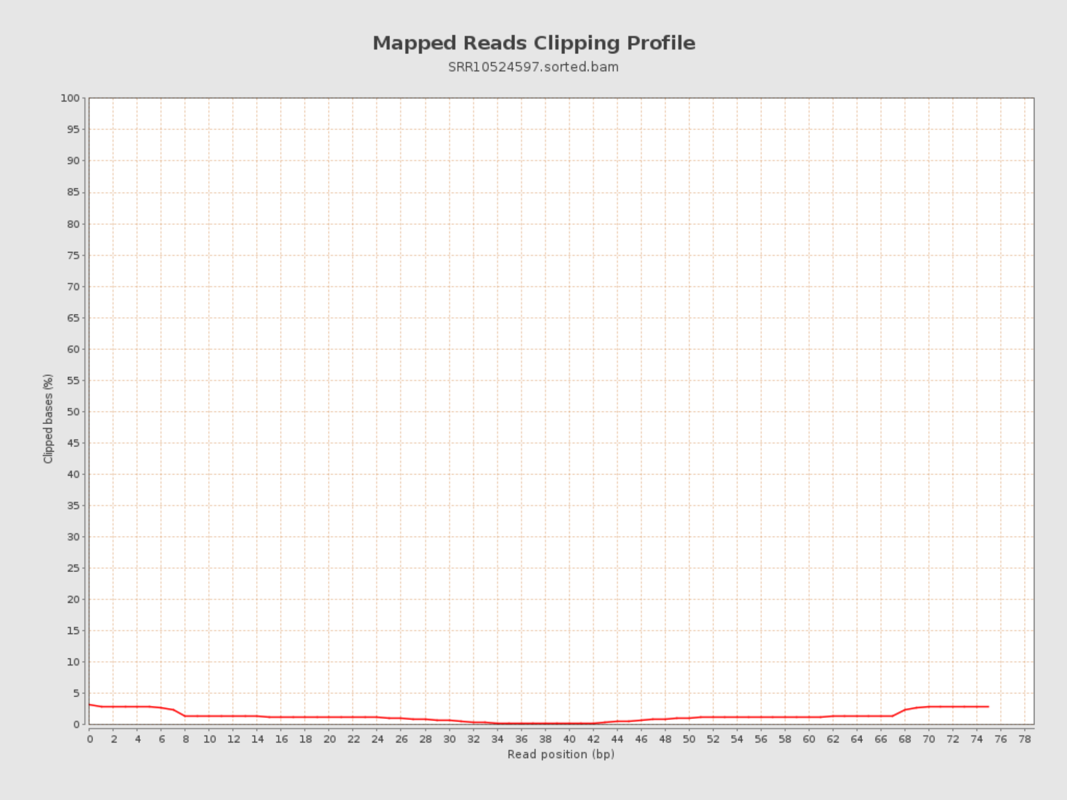
8. Results : Mapped Reads Nucleotide Content



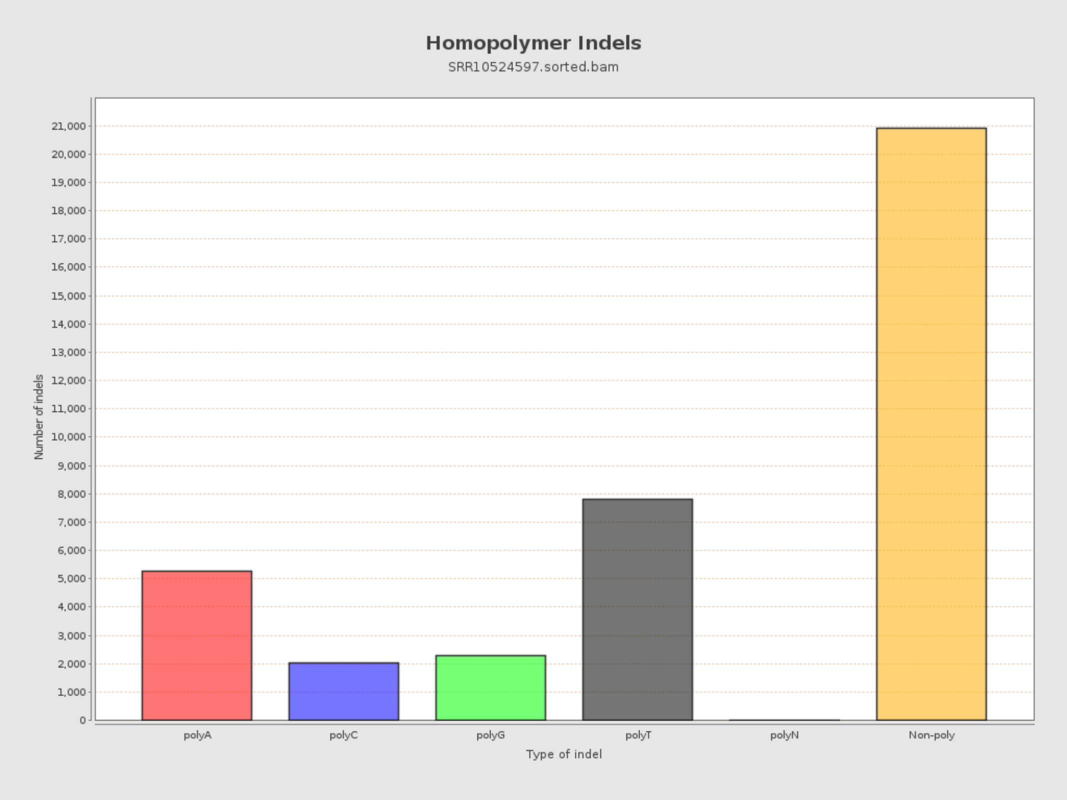
9. Results : Mapped Reads GC-content Distribution



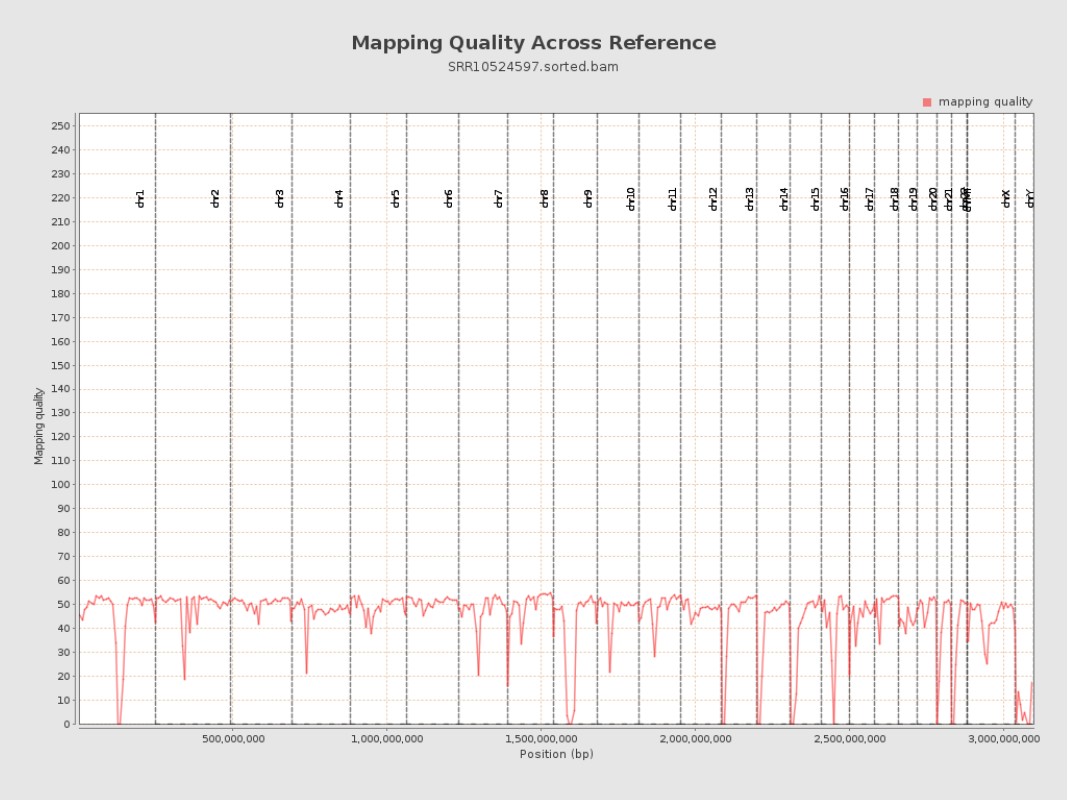
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram