Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 20:53:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524281.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_SRR10524281 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524281.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 20:53:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524281.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,276,236
Mapped reads	1,186,993 / 93.01%
Unmapped reads	89,243 / 6.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,696 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	37,219 / 2.92%
Duplication rate	2.26%
Clipped reads	1,188,359 / 93.11%

2.2. ACGT Content

Number/percentage of A's	18,513,150 / 26.38%
Number/percentage of C's	13,600,430 / 19.38%
Number/percentage of T's	22,024,764 / 31.38%
Number/percentage of G's	16,030,764 / 22.84%
Number/percentage of N's	9,720 / 0.01%
GC Percentage	42.22%

2.3. Coverage

Mean	0.0227

Standard Deviation	0.236

2.4. Mapping Quality

Mean Mapping Quality	46.51

2.5. Mismatches and indels

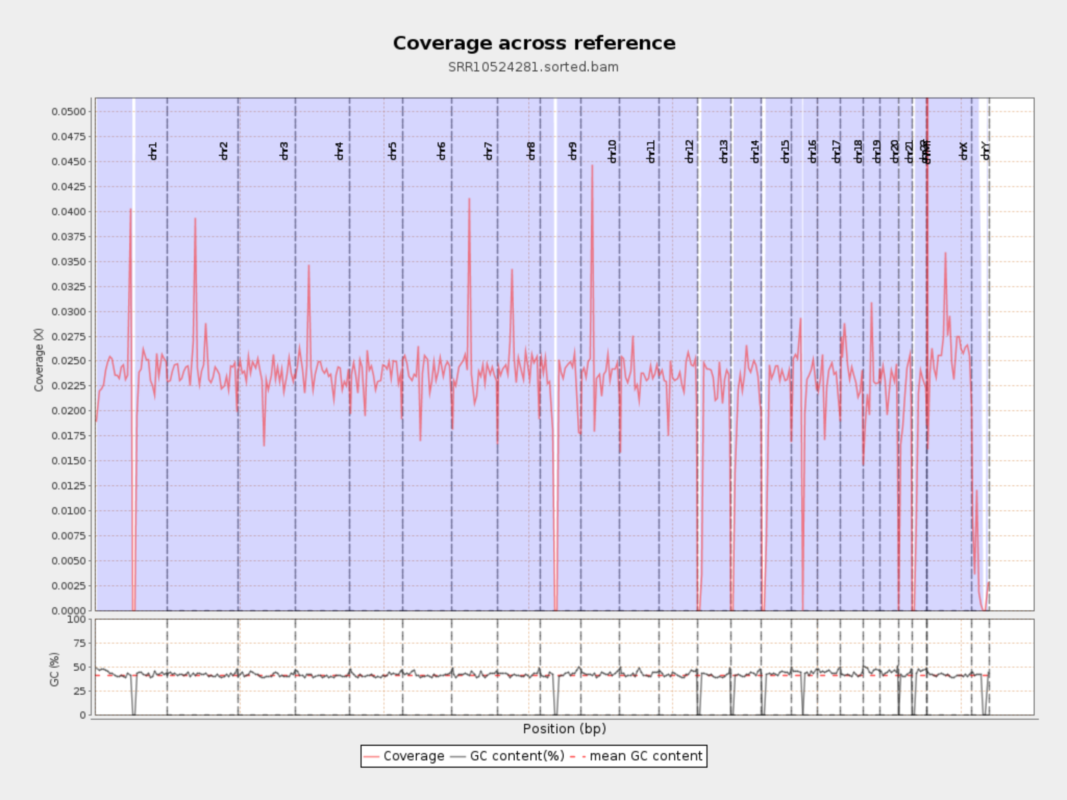
General error rate	0.49%
Mismatches	336,089
Insertions	5,318
Mapped reads with at least one insertion	0.45%
Deletions	13,335
Mapped reads with at least one deletion	1.12%
Homopolymer indels	44.44%

2.6. Chromosome stats

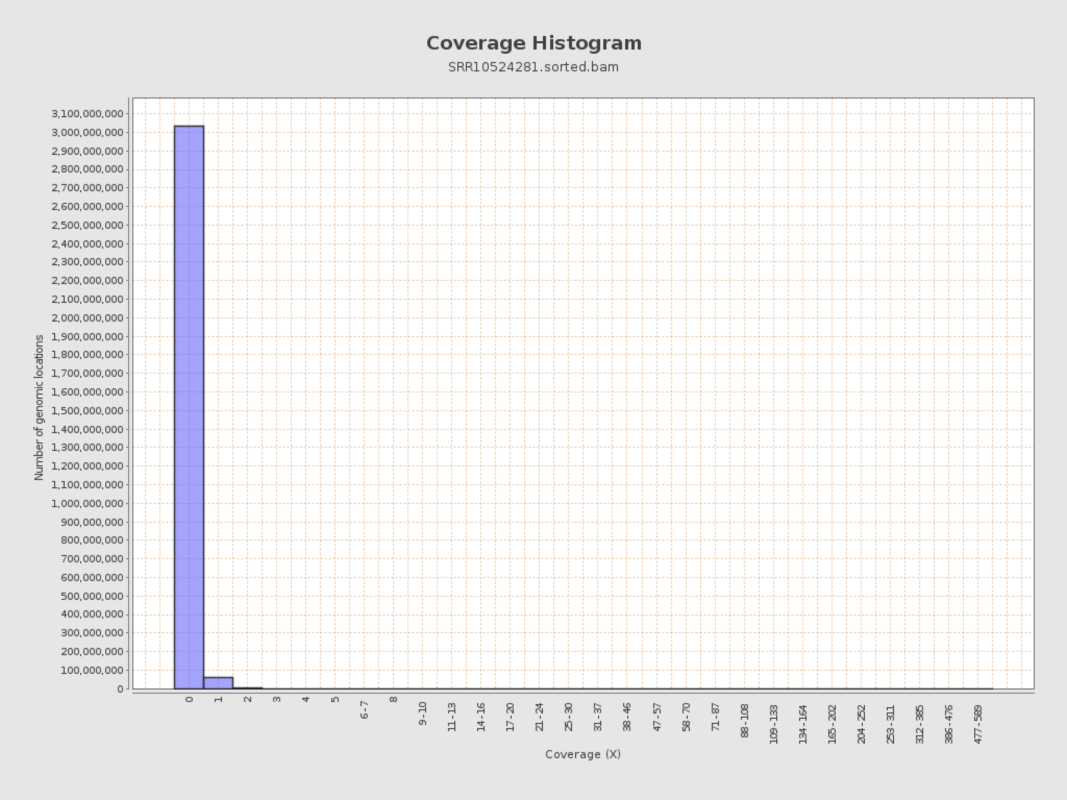
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5677179	0.0228	0.4394
chr2	243199373	5924364	0.0244	0.244
chr3	198022430	4675522	0.0236	0.1636
chr4	191154276	4618343	0.0242	0.1778
chr5	180915260	4296597	0.0237	0.1647
chr6	171115067	4084769	0.0239	0.1764
chr7	159138663	3879604	0.0244	0.3105

chr8	146364022	3633721	0.0248	0.2407
chr9	141213431	2939312	0.0208	0.2136
chr10	135534747	3353374	0.0247	0.2318
chr11	135006516	3190239	0.0236	0.2137
chr12	133851895	3140568	0.0235	0.1654
chr13	115169878	2228338	0.0193	0.1467
chr14	107349540	2140166	0.0199	0.1591
chr15	102531392	1963091	0.0191	0.1473
chr16	90354753	1977440	0.0219	0.1697
chr17	81195210	1838495	0.0226	0.1689
chr18	78077248	1886369	0.0242	0.4038
chr19	59128983	1327854	0.0225	0.3101
chr20	63025520	1426007	0.0226	0.1622
chr21	48129895	928803	0.0193	0.1611
chr22	51304566	816601	0.0159	0.1335
chrMT	16571	8868	0.5352	0.7657
chrX	155270560	4035672	0.026	0.1913
chrY	59373566	208500	0.0035	0.1018

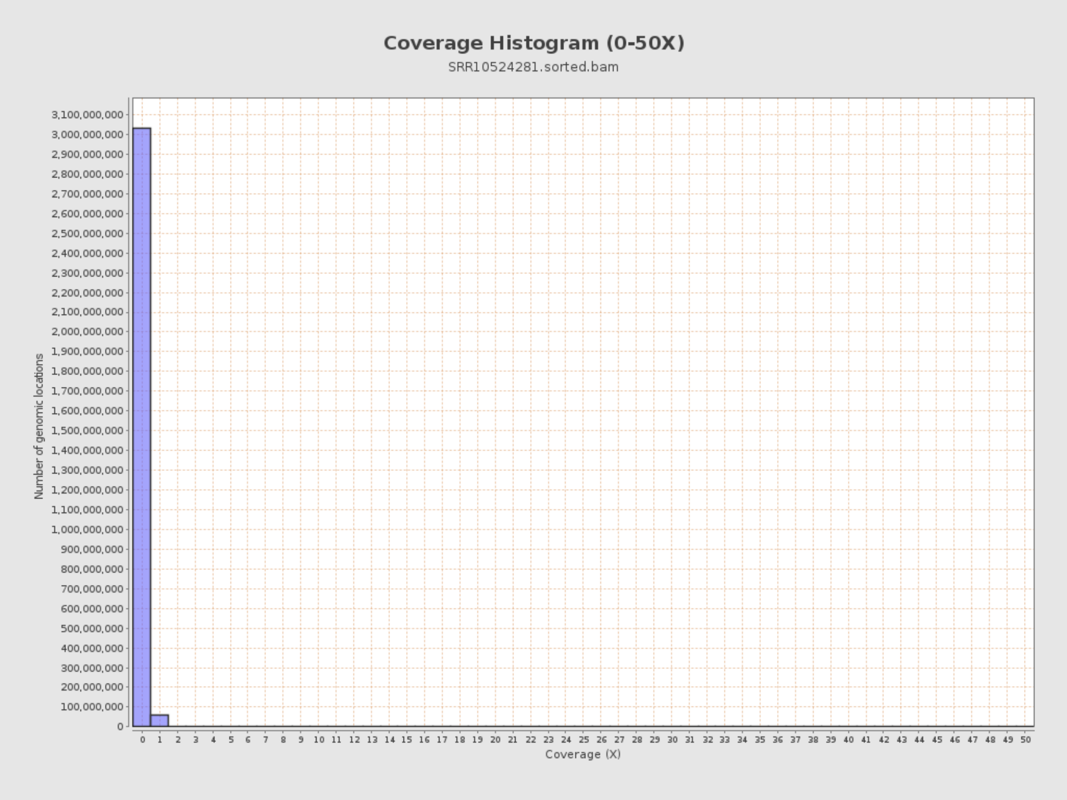
3. Results : Coverage across reference



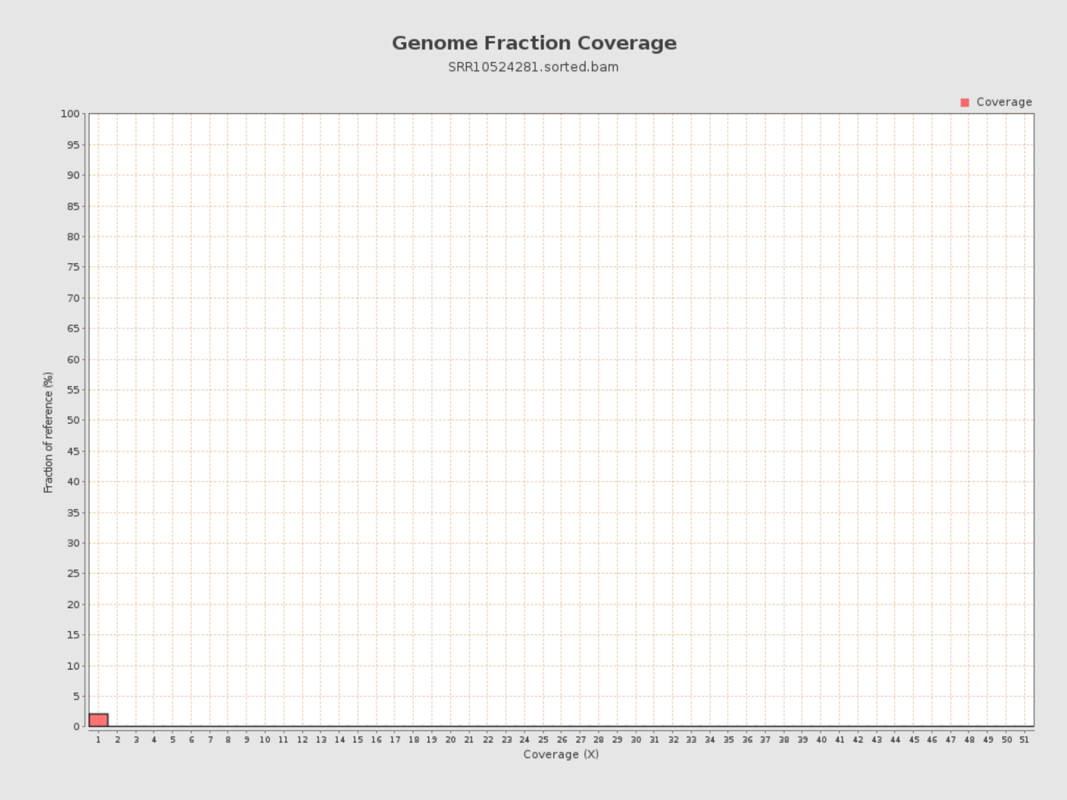
4. Results : Coverage Histogram



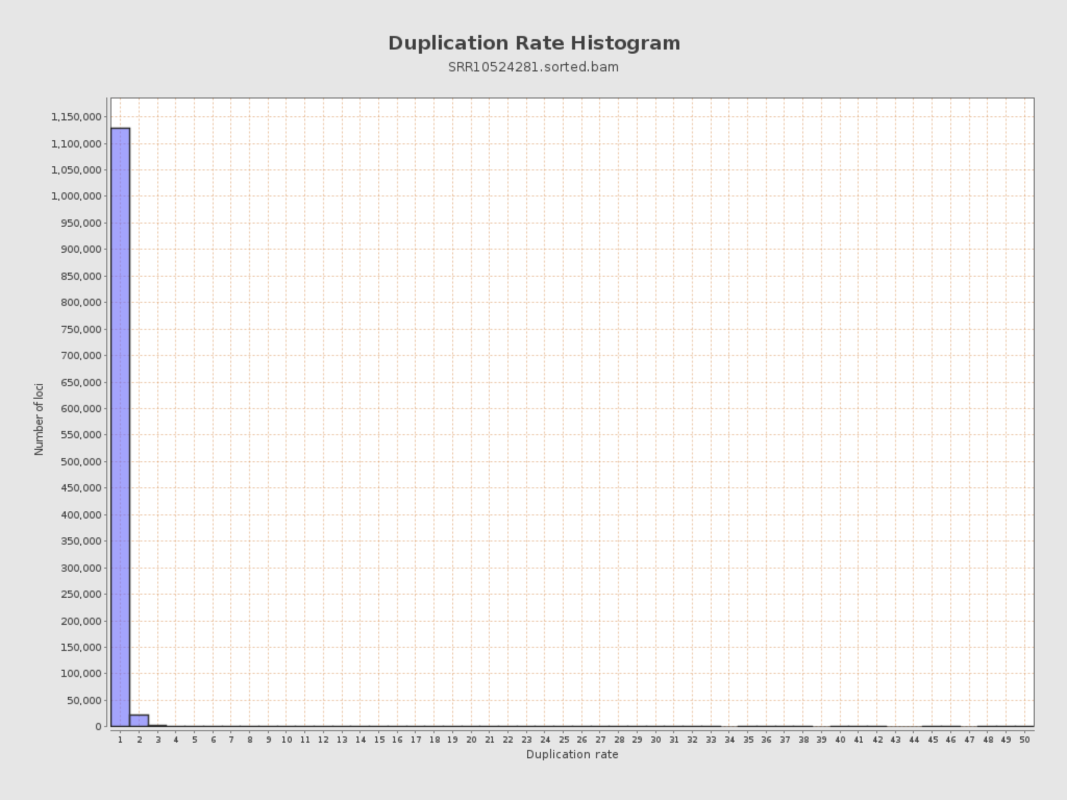
5. Results : Coverage Histogram (0-50X)



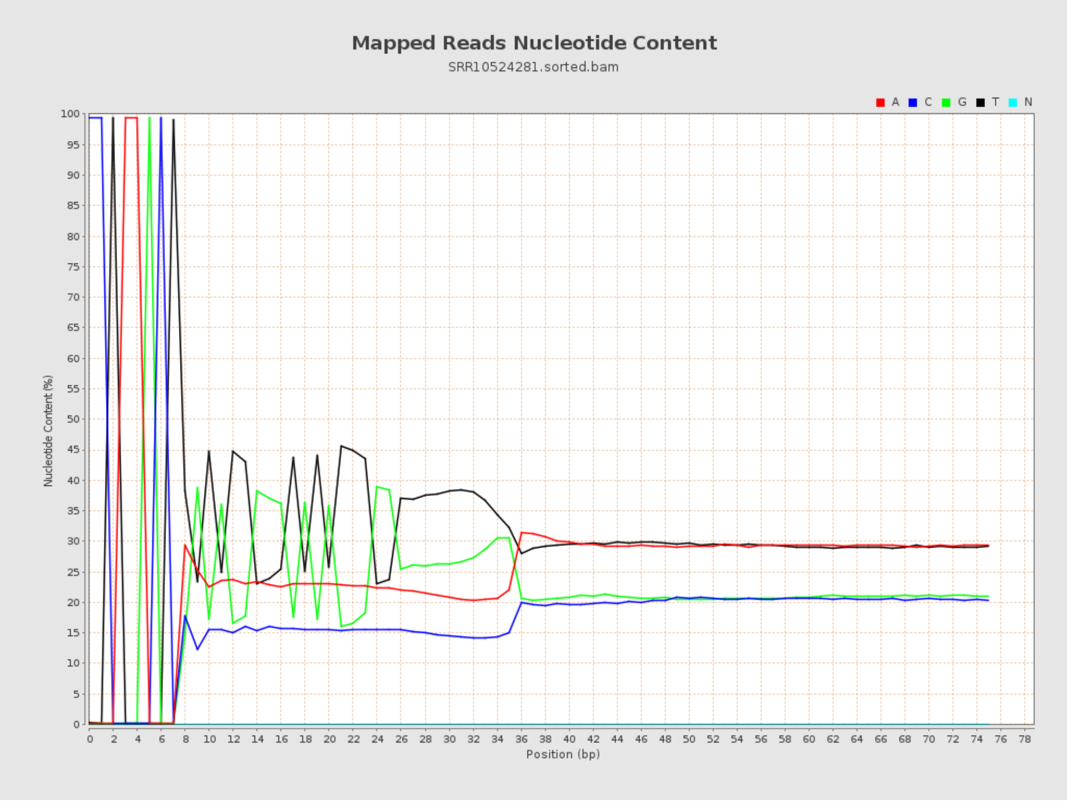
6. Results : Genome Fraction Coverage



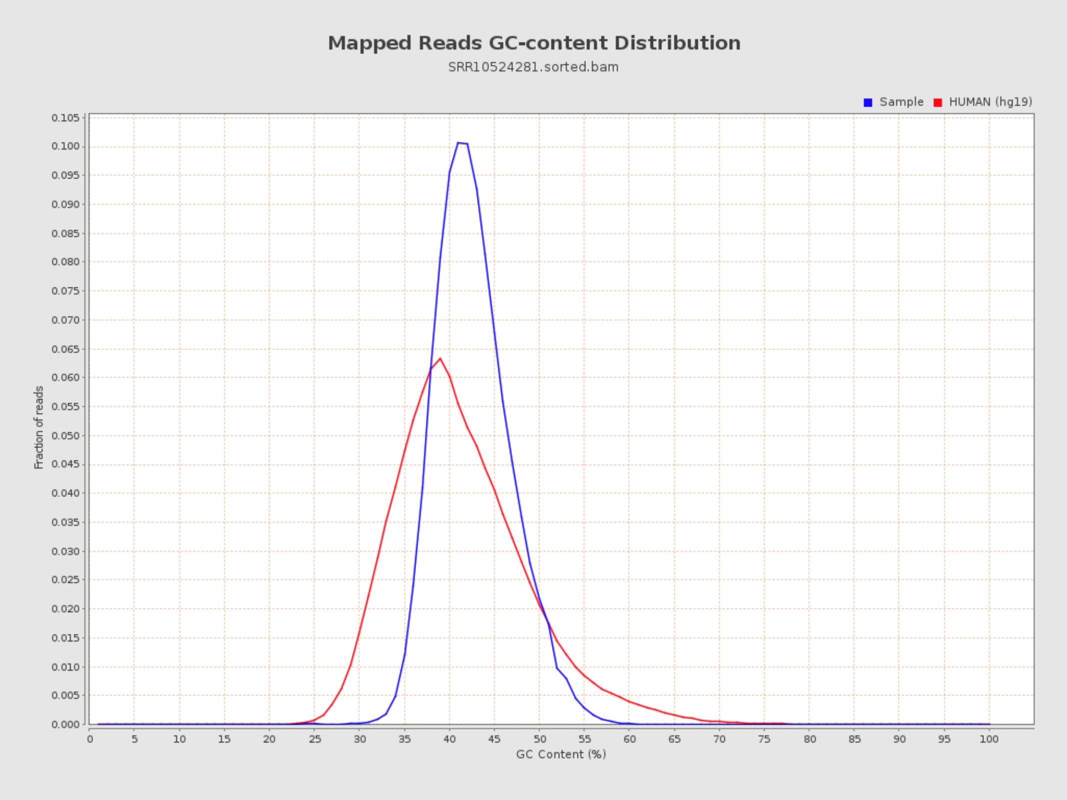
7. Results : Duplication Rate Histogram



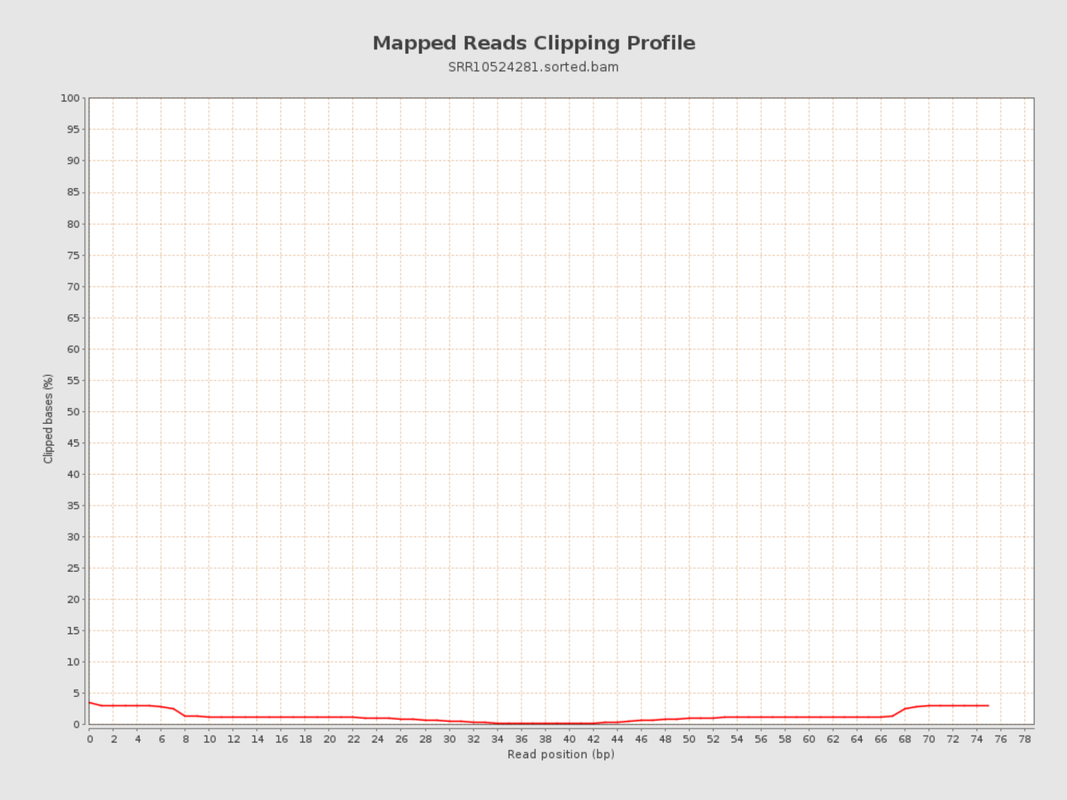
8. Results : Mapped Reads Nucleotide Content



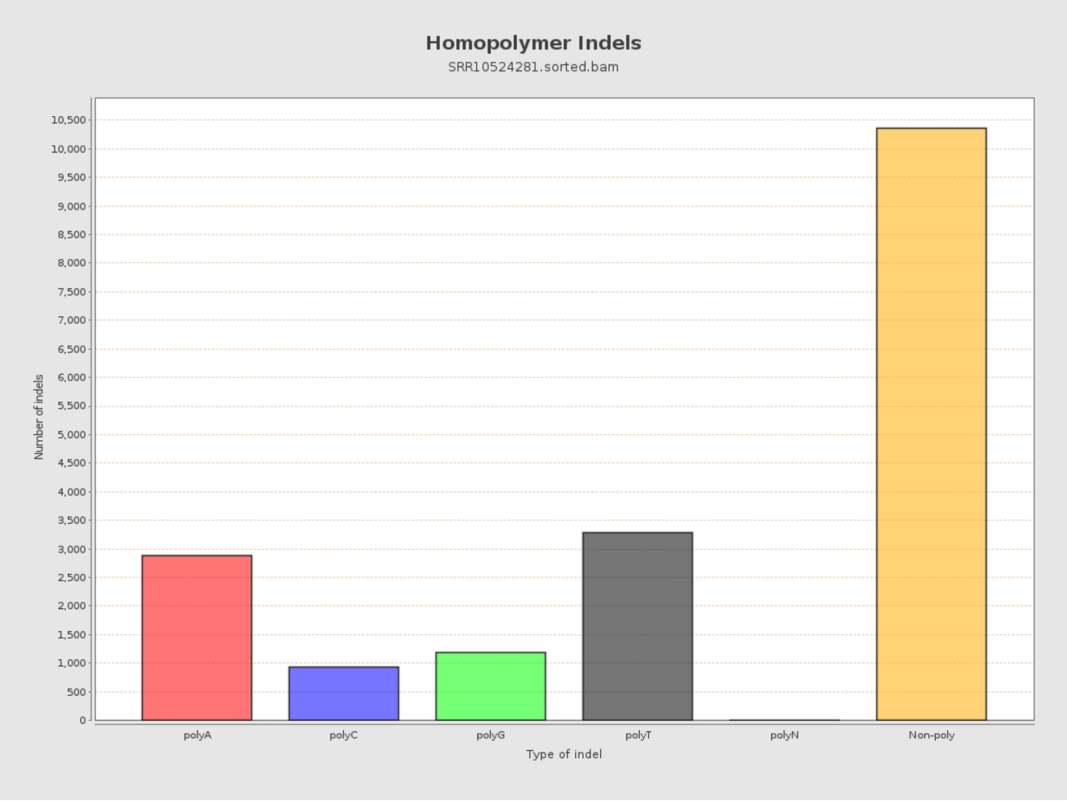
9. Results : Mapped Reads GC-content Distribution



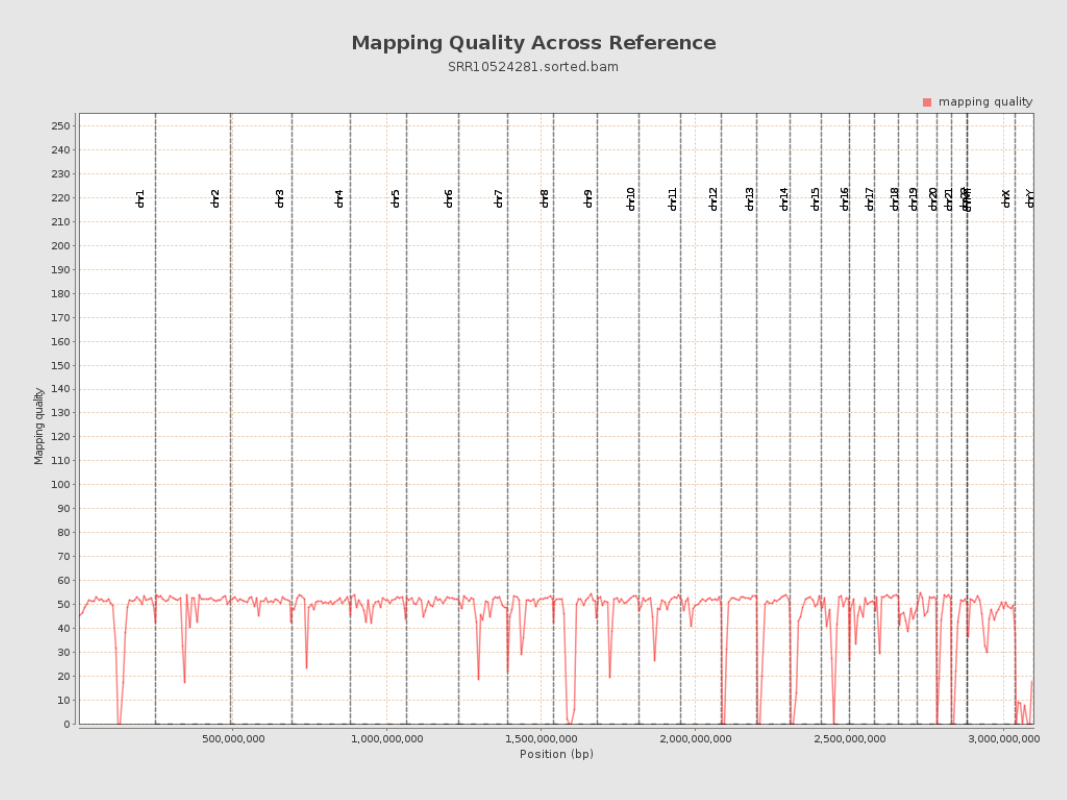
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram