Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 11:00:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524563.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_SRR10524563 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524563.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 11:00:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524563.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,047,034
Mapped reads	1,882,648 / 91.97%
Unmapped reads	164,386 / 8.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,604 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	94,031 / 4.59%
Duplication rate	3.8%
Clipped reads	1,884,750 / 92.07%

2.2. ACGT Content

Number/percentage of A's	28,036,771 / 25.48%
Number/percentage of C's	22,698,376 / 20.63%
Number/percentage of T's	33,237,247 / 30.21%
Number/percentage of G's	26,063,961 / 23.69%
Number/percentage of N's	1,536 / 0%
GC Percentage	44.31%

2.3. Coverage

Mean	0.0356

Standard Deviation	0.3182

2.4. Mapping Quality

Mean Mapping Quality	45.04

2.5. Mismatches and indels

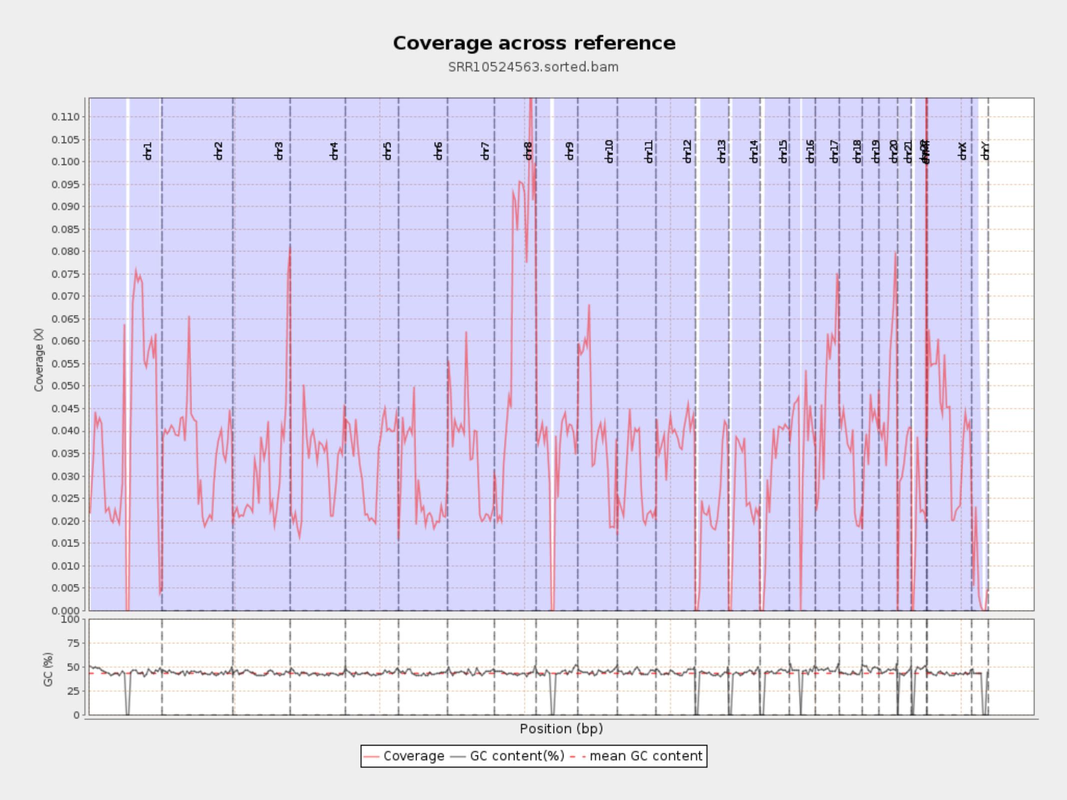
General error rate	0.52%
Mismatches	557,772
Insertions	7,596
Mapped reads with at least one insertion	0.4%
Deletions	20,682
Mapped reads with at least one deletion	1.09%
Homopolymer indels	42.18%

2.6. Chromosome stats

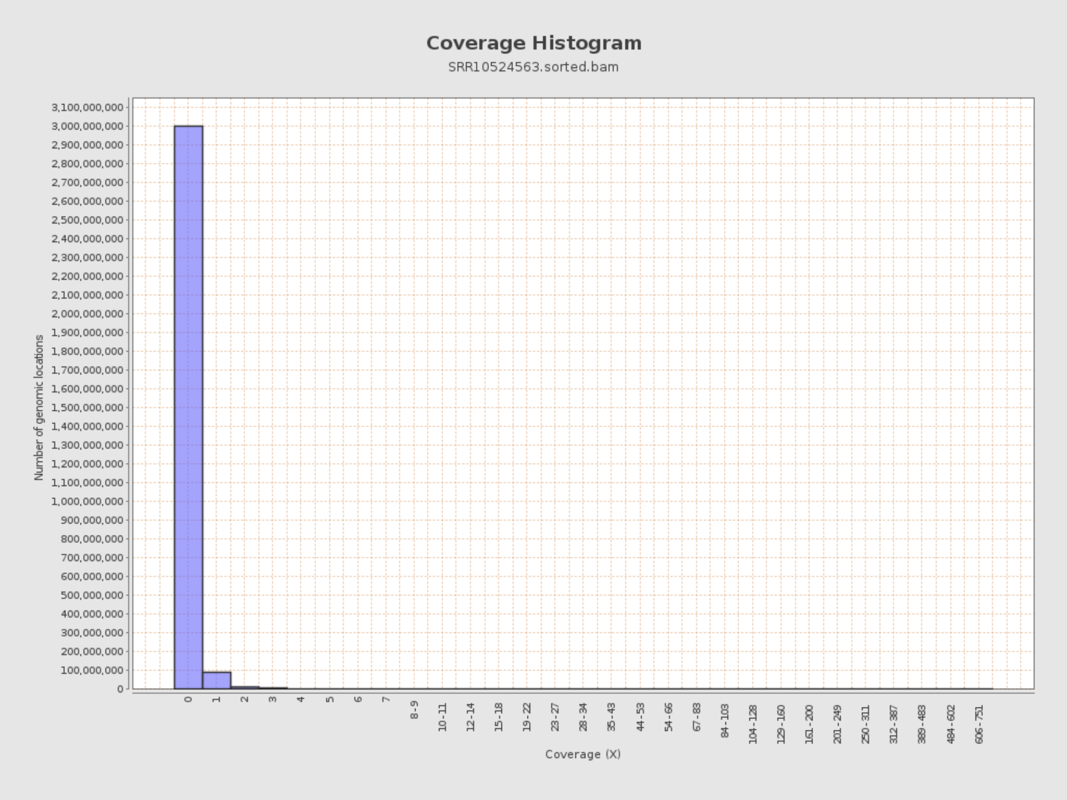
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9903739	0.0397	0.5865
chr2	243199373	8869421	0.0365	0.3574
chr3	198022430	6037290	0.0305	0.1956
chr4	191154276	6043695	0.0316	0.2348
chr5	180915260	6215568	0.0344	0.2077
chr6	171115067	4642080	0.0271	0.235
chr7	159138663	5616002	0.0353	0.4051

chr8	146364022	9967242	0.0681	0.3544
chr9	141213431	4795757	0.034	0.2748
chr10	135534747	5653075	0.0417	0.3295
chr11	135006516	3841121	0.0285	0.29
chr12	133851895	5266518	0.0393	0.2258
chr13	115169878	2543389	0.0221	0.1671
chr14	107349540	2622532	0.0244	0.1789
chr15	102531392	2985552	0.0291	0.1954
chr16	90354753	3518885	0.0389	0.2383
chr17	81195210	4060916	0.05	0.2669
chr18	78077248	2579293	0.033	0.5162
chr19	59128983	2339490	0.0396	0.4195
chr20	63025520	3233388	0.0513	0.2585
chr21	48129895	1519238	0.0316	0.2273
chr22	51304566	948315	0.0185	0.1514
chrMT	16571	4920	0.2969	0.5699
chrX	155270560	6494869	0.0418	0.2544
chrY	59373566	369544	0.0062	0.1982

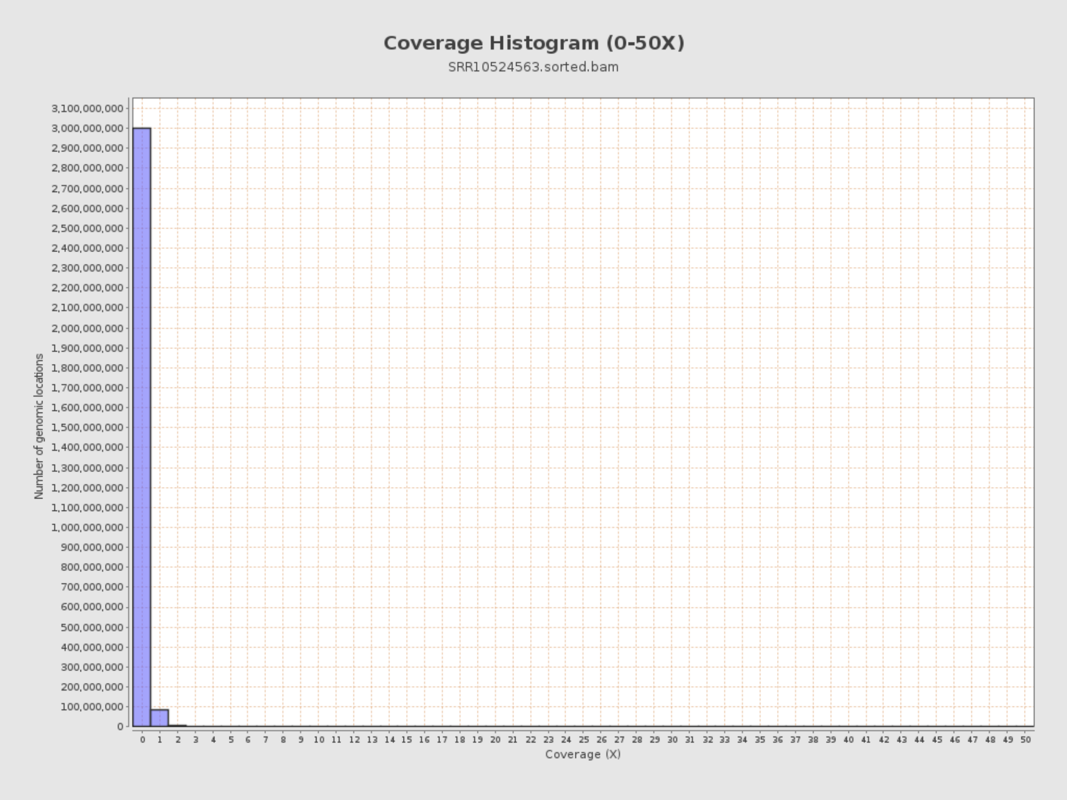
3. Results : Coverage across reference



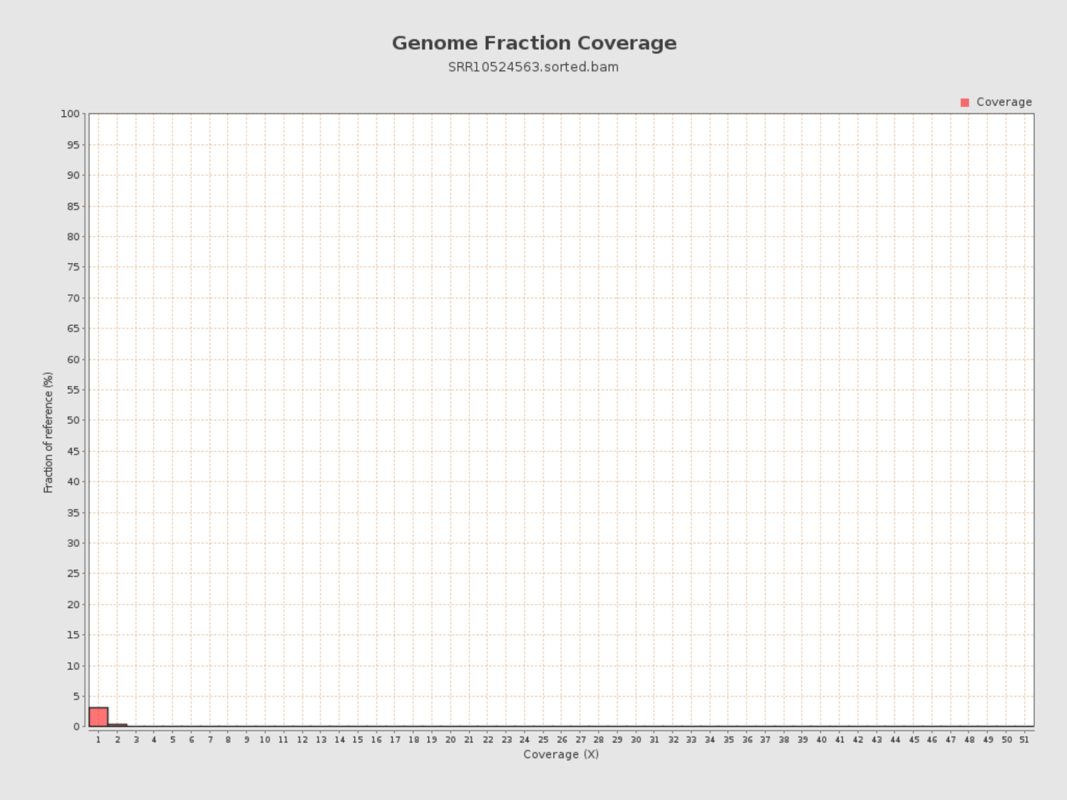
4. Results : Coverage Histogram



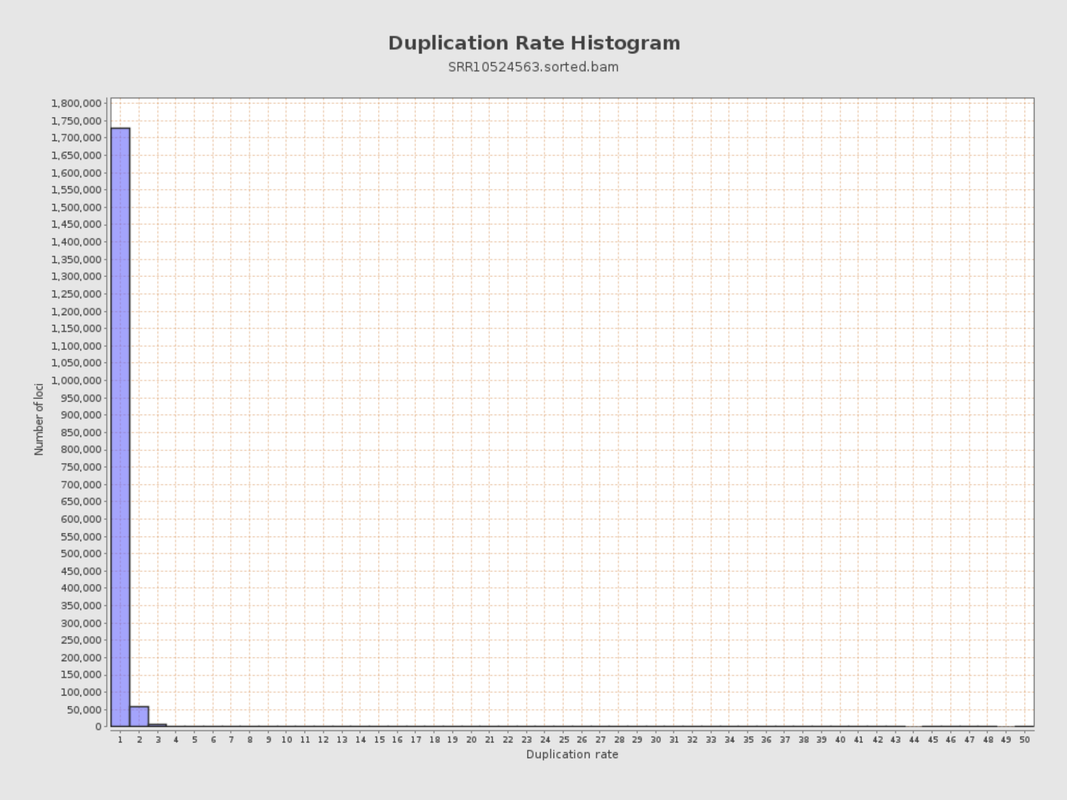
5. Results : Coverage Histogram (0-50X)



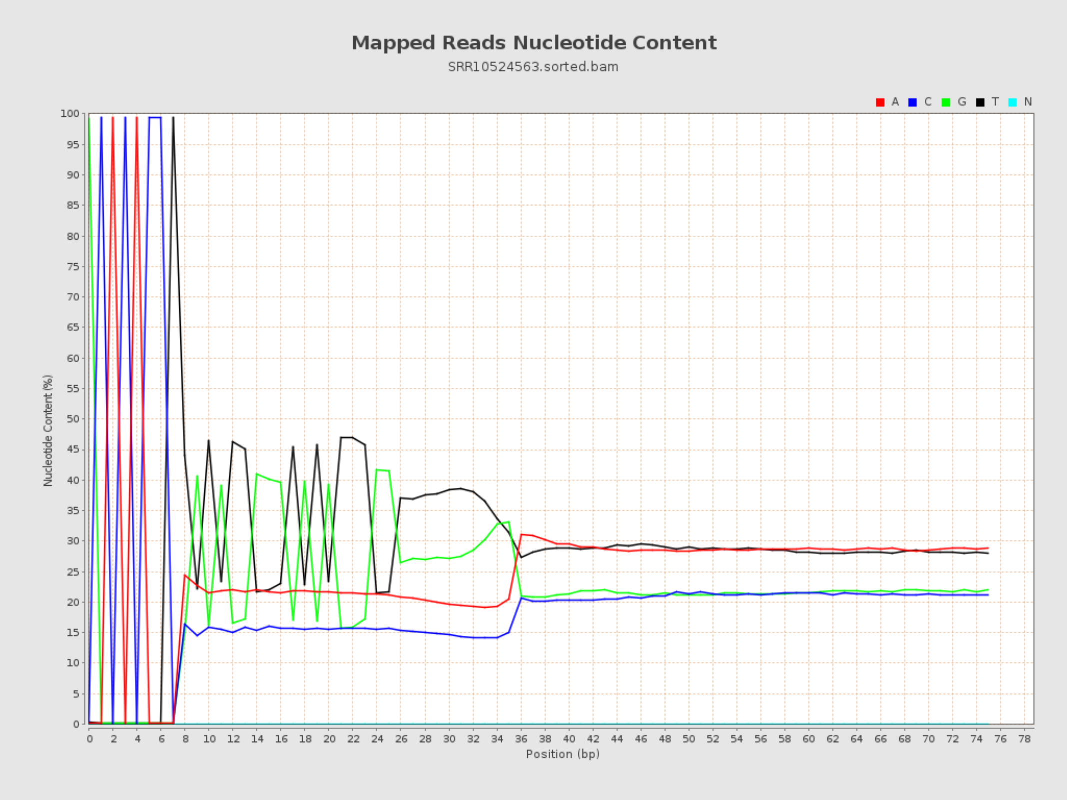
6. Results : Genome Fraction Coverage



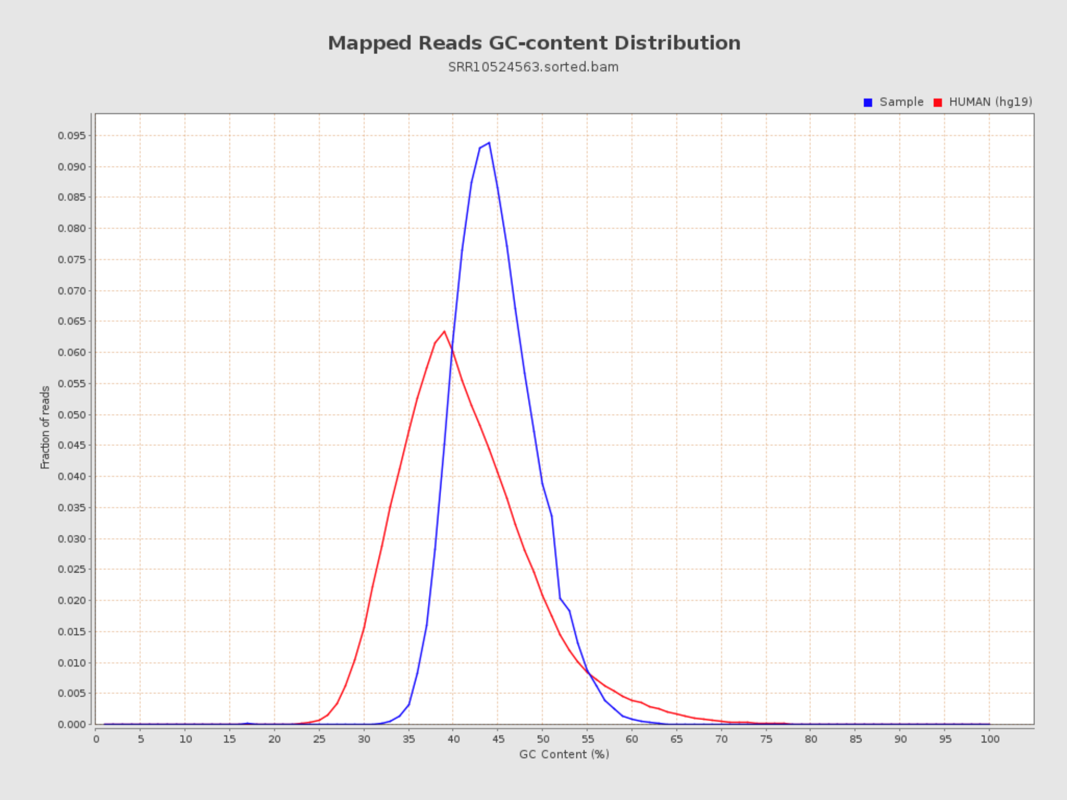
7. Results : Duplication Rate Histogram



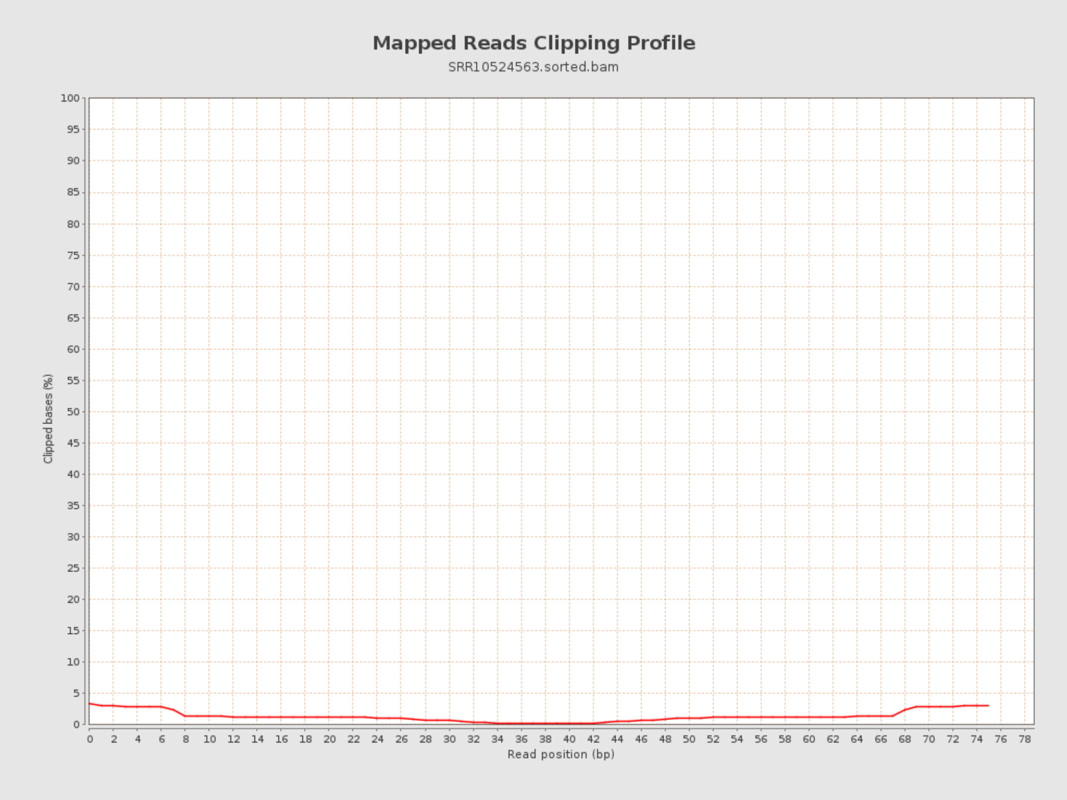
8. Results : Mapped Reads Nucleotide Content



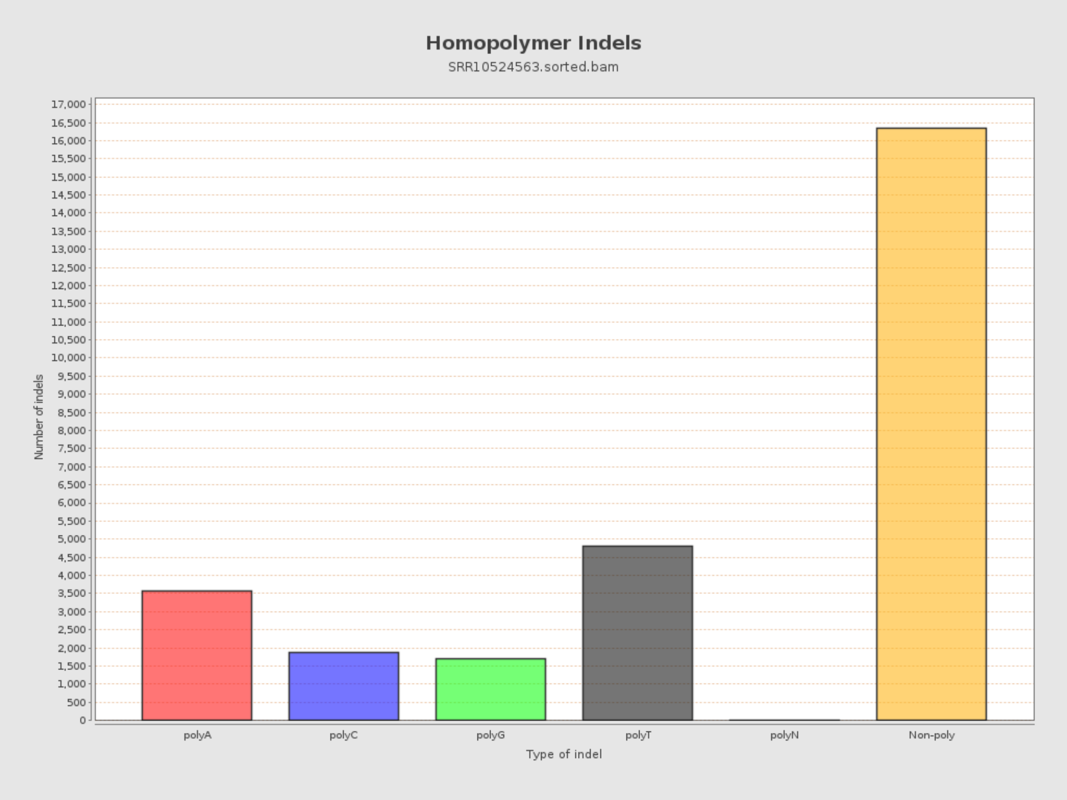
9. Results : Mapped Reads GC-content Distribution



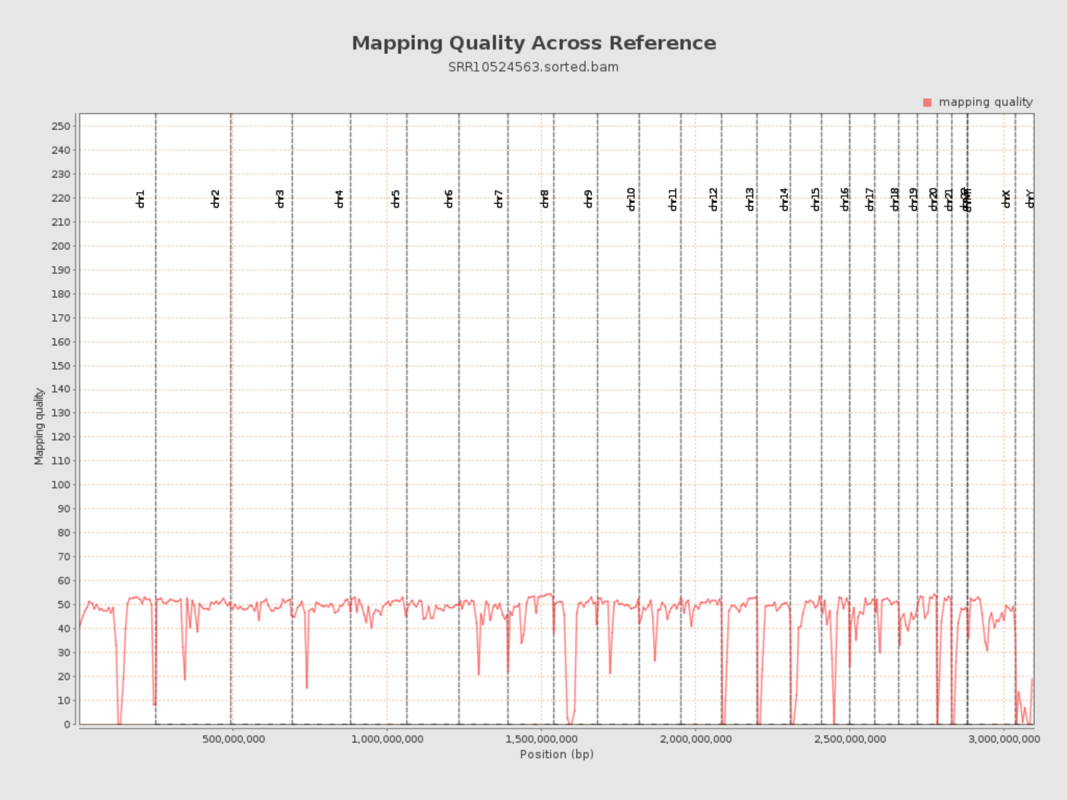
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram