Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 06:07:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524490.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_SRR10524490 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524490.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 06:07:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524490.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,282,838
Mapped reads	1,178,727 / 91.88%
Unmapped reads	104,111 / 8.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,736 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	44,325 / 3.46%
Duplication rate	2.92%
Clipped reads	1,177,897 / 91.82%

2.2. ACGT Content

Number/percentage of A's	17,507,508 / 25.59%
Number/percentage of C's	11,450,632 / 16.74%
Number/percentage of T's	22,000,693 / 32.16%
Number/percentage of G's	17,445,698 / 25.5%
Number/percentage of N's	1,423 / 0%
GC Percentage	42.24%

2.3. Coverage

Mean	0.0221

Standard Deviation	0.2169

2.4. Mapping Quality

Mean Mapping Quality	45.39

2.5. Mismatches and indels

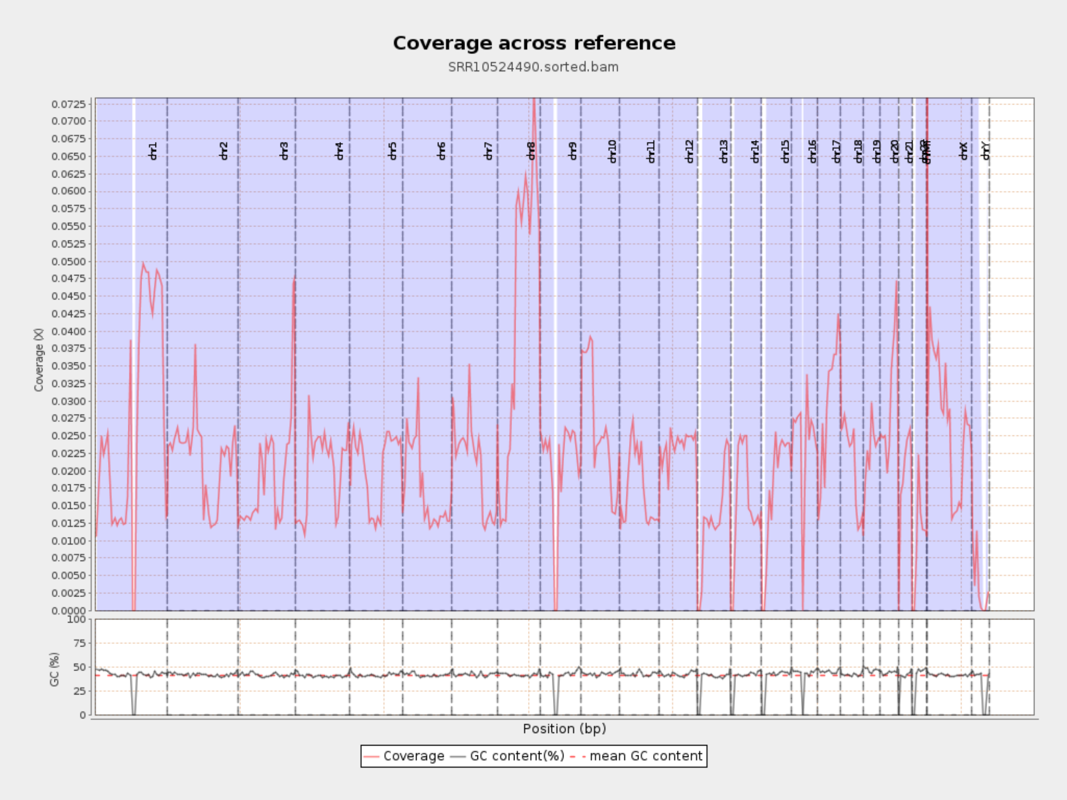
General error rate	0.48%
Mismatches	318,701
Insertions	4,510
Mapped reads with at least one insertion	0.38%
Deletions	13,043
Mapped reads with at least one deletion	1.1%
Homopolymer indels	43.33%

2.6. Chromosome stats

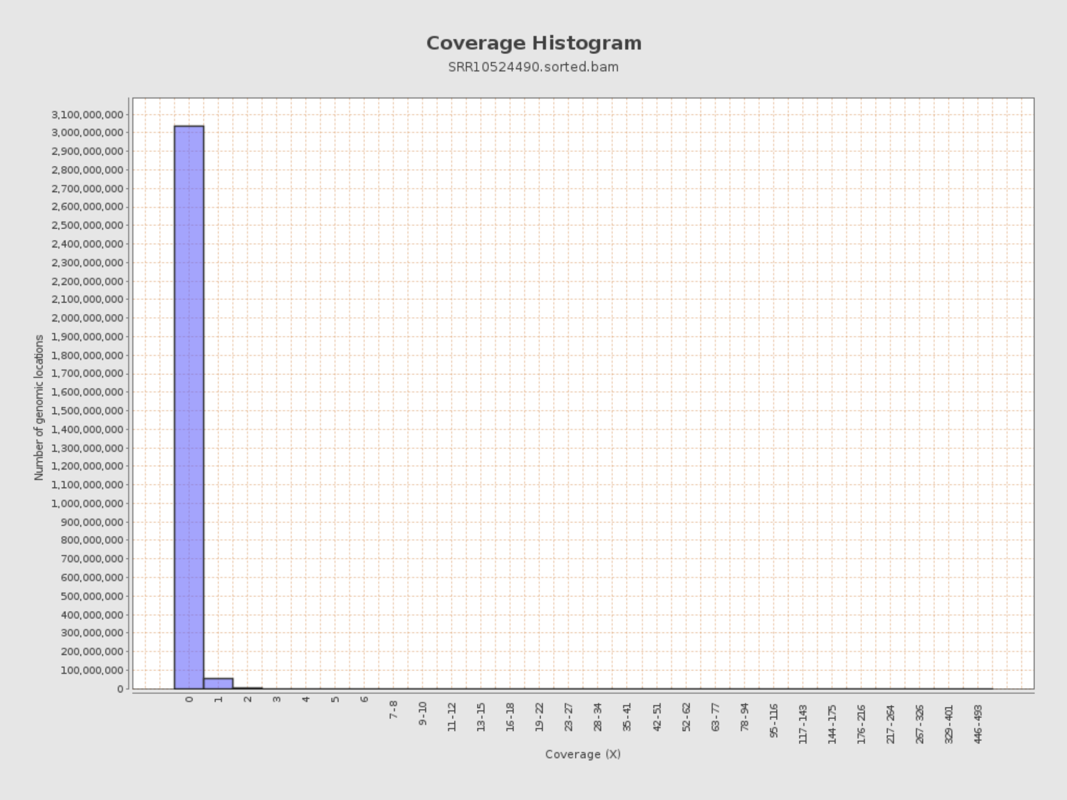
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6710156	0.0269	0.3794
chr2	243199373	5321333	0.0219	0.2448
chr3	198022430	3780353	0.0191	0.1503
chr4	191154276	3873073	0.0203	0.1694
chr5	180915260	3763440	0.0208	0.1575
chr6	171115067	2979133	0.0174	0.1729
chr7	159138663	3334113	0.021	0.2559

chr8	146364022	6313161	0.0431	0.2522
chr9	141213431	2901262	0.0205	0.1892
chr10	135534747	3628025	0.0268	0.2197
chr11	135006516	2341955	0.0173	0.1999
chr12	133851895	3160534	0.0236	0.167
chr13	115169878	1507795	0.0131	0.1253
chr14	107349540	1651987	0.0154	0.1365
chr15	102531392	1779661	0.0174	0.1499
chr16	90354753	2150522	0.0238	0.1735
chr17	81195210	2375482	0.0293	0.1943
chr18	78077248	1643766	0.0211	0.3192
chr19	59128983	1358994	0.023	0.2792
chr20	63025520	1919833	0.0305	0.1922
chr21	48129895	941877	0.0196	0.1588
chr22	51304566	539443	0.0105	0.1107
chrMT	16571	4955	0.299	0.6255
chrX	155270560	4234720	0.0273	0.1943
chrY	59373566	212811	0.0036	0.0991

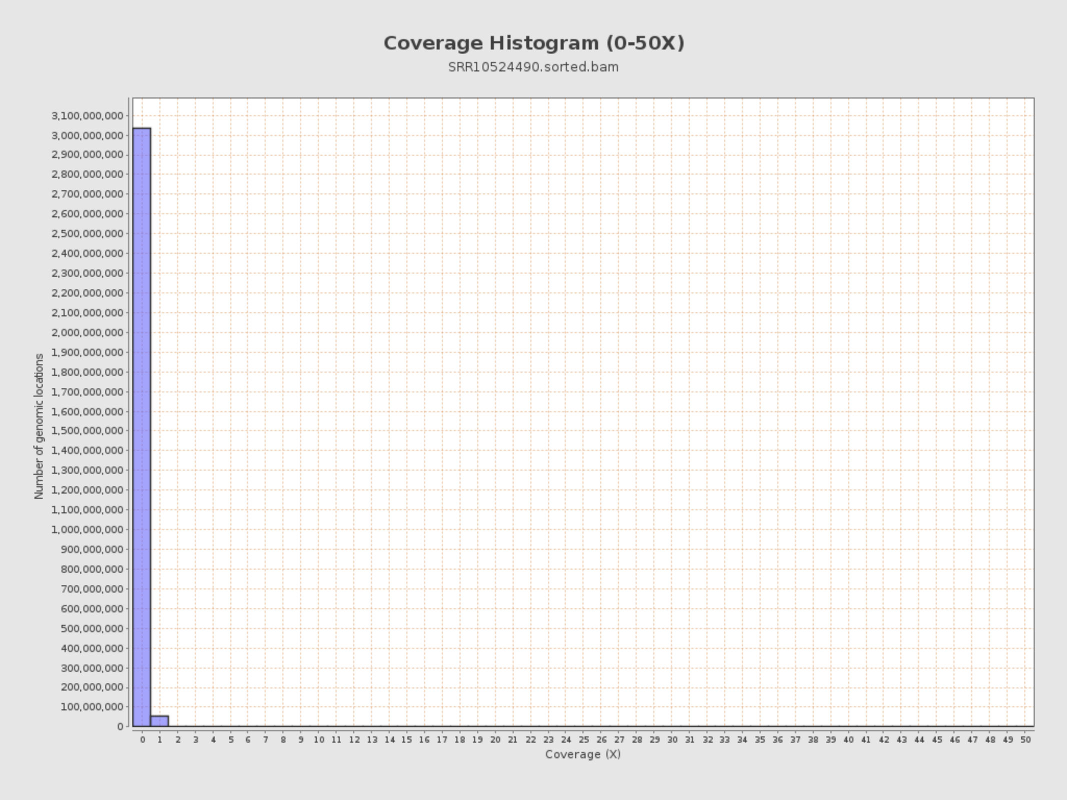
3. Results : Coverage across reference



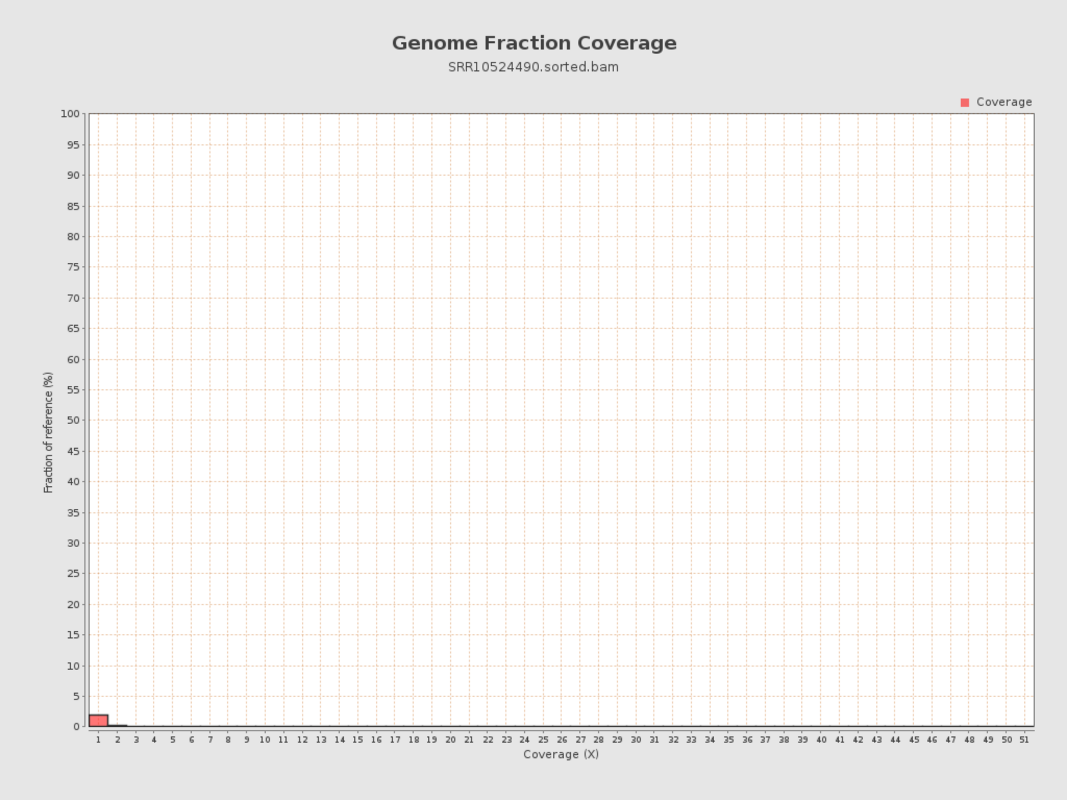
4. Results : Coverage Histogram



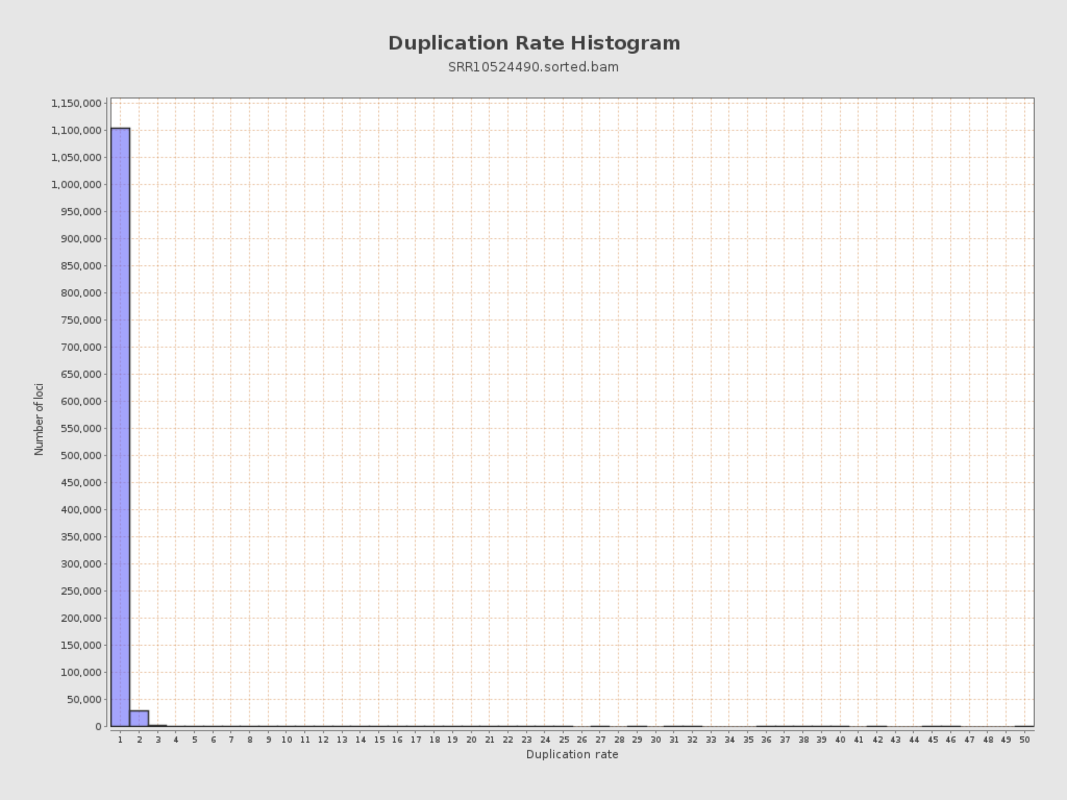
5. Results : Coverage Histogram (0-50X)



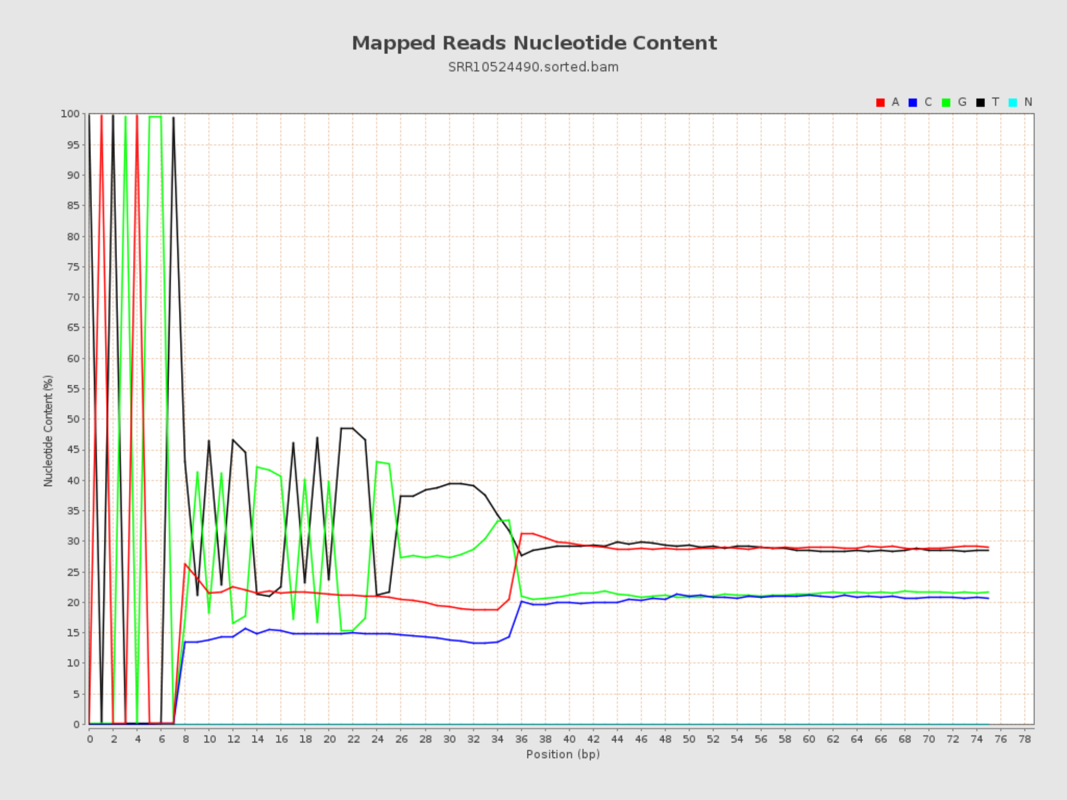
6. Results : Genome Fraction Coverage



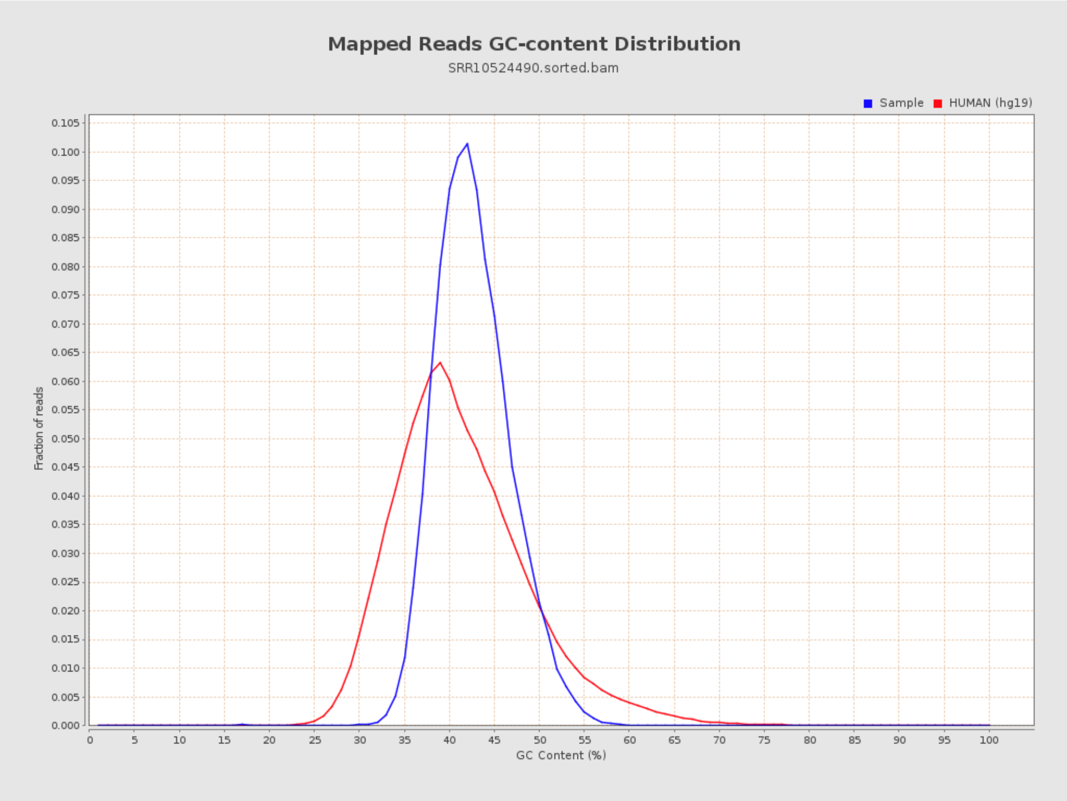
7. Results : Duplication Rate Histogram



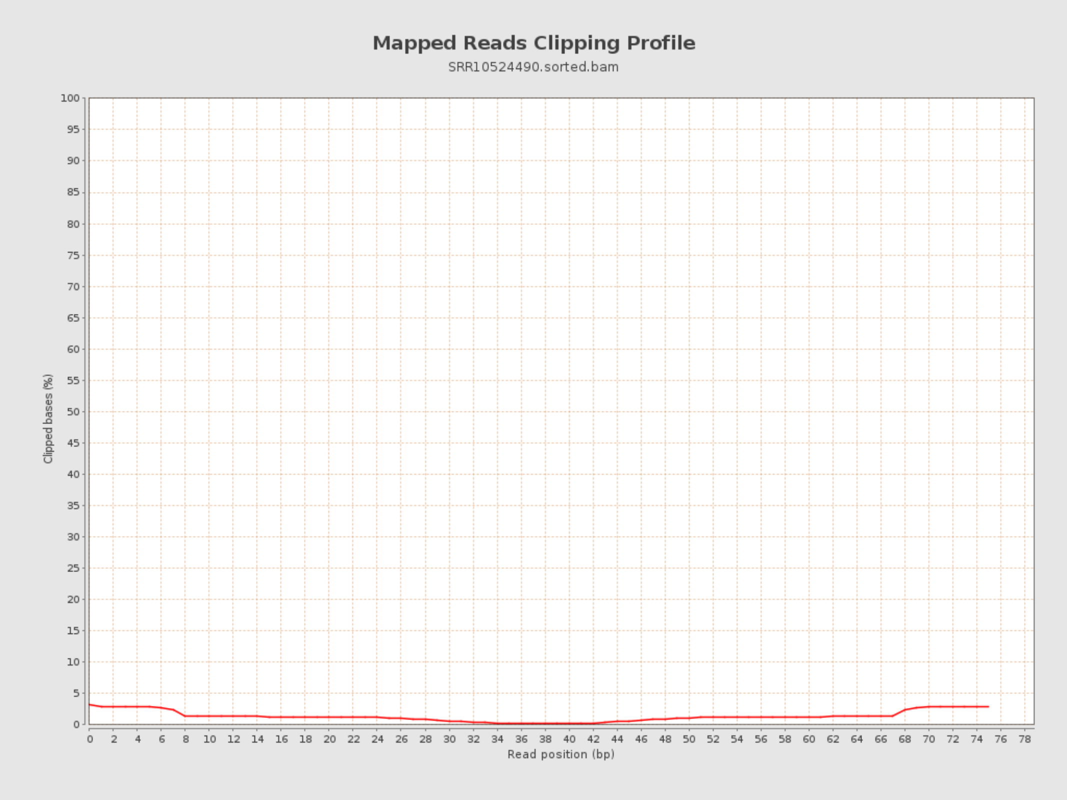
8. Results : Mapped Reads Nucleotide Content



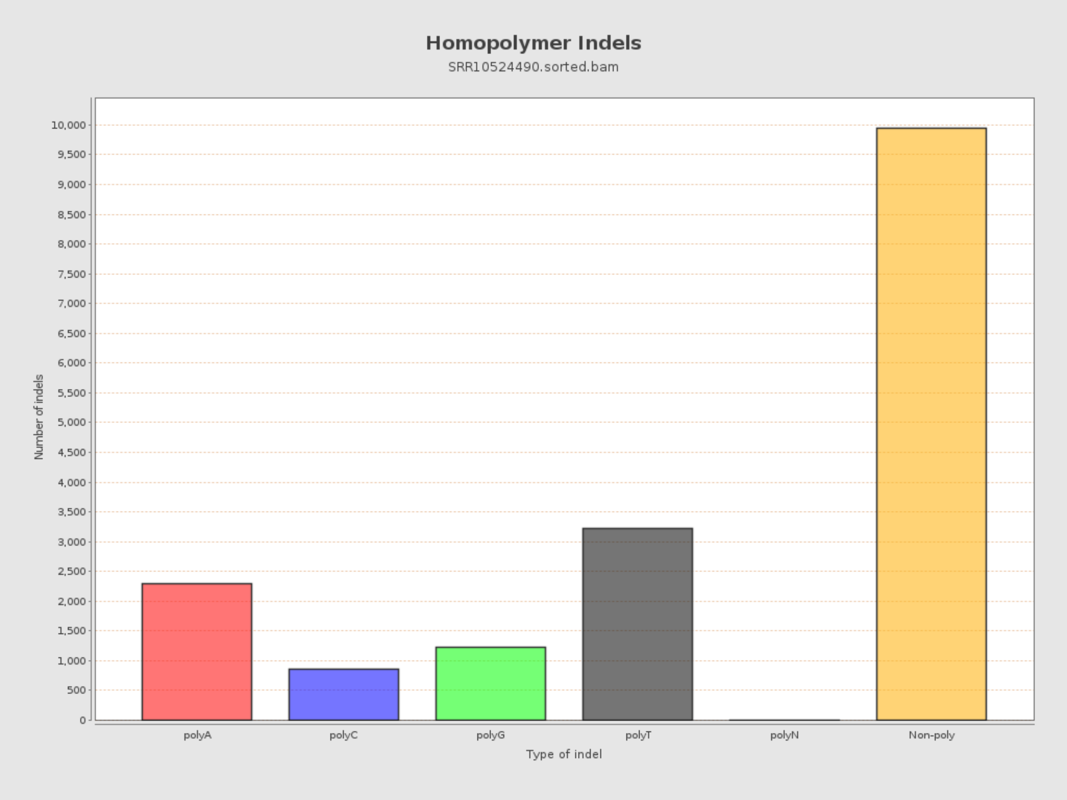
9. Results : Mapped Reads GC-content Distribution



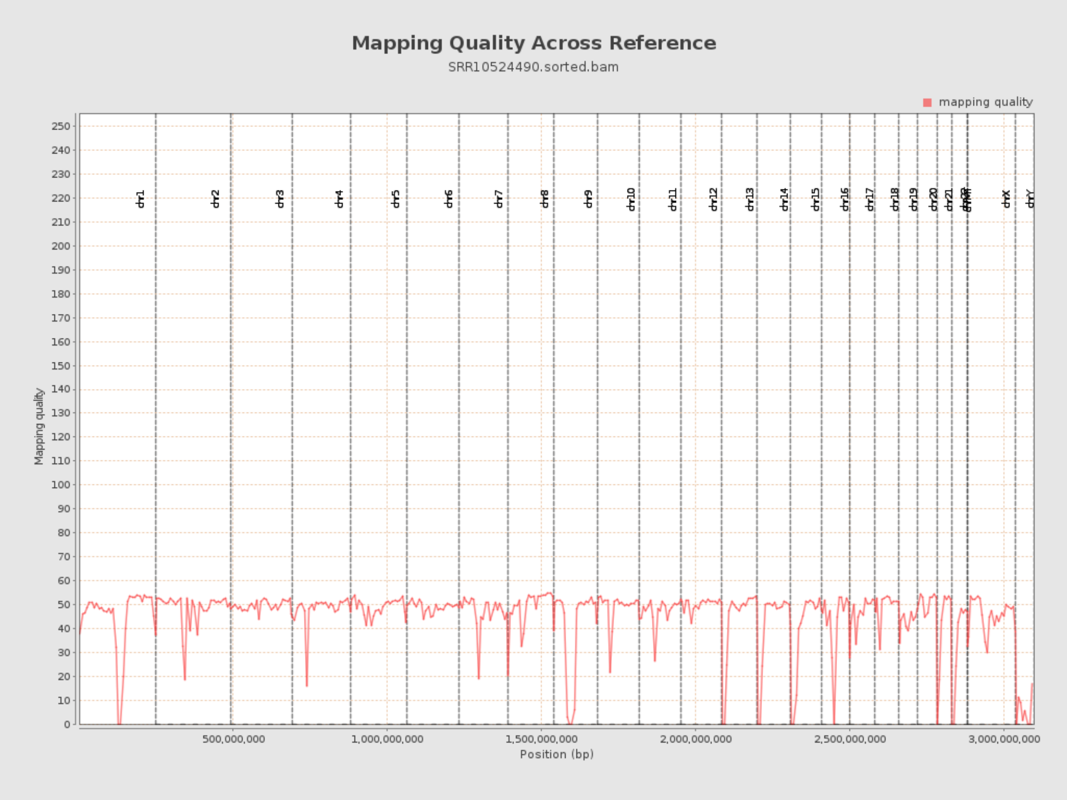
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram