Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 20:48:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524792.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_SRR10524792 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524792.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 20:48:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524792.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,246,183
Mapped reads	1,133,718 / 90.98%
Unmapped reads	112,465 / 9.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,701 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	41,684 / 3.34%
Duplication rate	2.85%
Clipped reads	1,135,256 / 91.1%

2.2. ACGT Content

Number/percentage of A's	16,192,276 / 24.96%
Number/percentage of C's	11,440,519 / 17.64%
Number/percentage of T's	20,464,436 / 31.55%
Number/percentage of G's	16,763,272 / 25.84%
Number/percentage of N's	7,513 / 0.01%
GC Percentage	43.48%

2.3. Coverage

Mean	0.021

Standard Deviation	0.2018

2.4. Mapping Quality

Mean Mapping Quality	44.34

2.5. Mismatches and indels

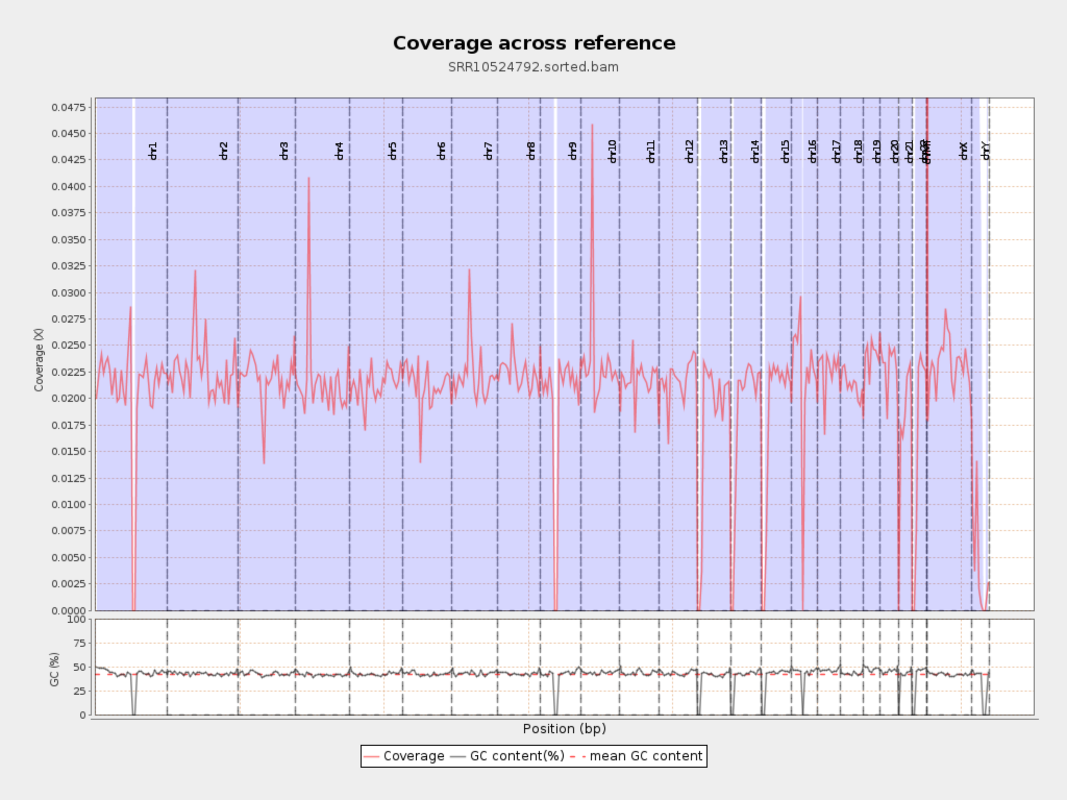
General error rate	0.52%
Mismatches	332,276
Insertions	4,249
Mapped reads with at least one insertion	0.37%
Deletions	13,141
Mapped reads with at least one deletion	1.15%
Homopolymer indels	42.7%

2.6. Chromosome stats

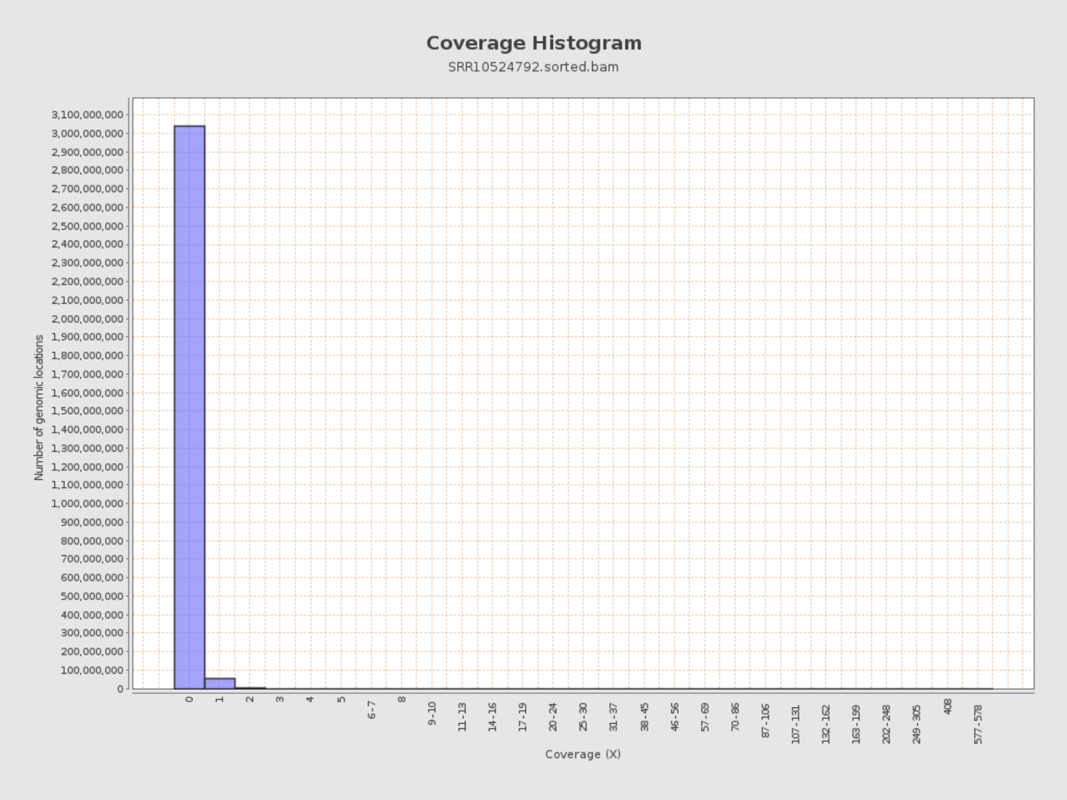
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5146083	0.0206	0.2746
chr2	243199373	5501044	0.0226	0.3003
chr3	198022430	4313073	0.0218	0.1619
chr4	191154276	4152029	0.0217	0.1809
chr5	180915260	3874977	0.0214	0.1588
chr6	171115067	3624863	0.0212	0.1696
chr7	159138663	3541609	0.0223	0.236

chr8	146364022	3273481	0.0224	0.1926
chr9	141213431	2737506	0.0194	0.1741
chr10	135534747	3189193	0.0235	0.2474
chr11	135006516	2945802	0.0218	0.1807
chr12	133851895	2915051	0.0218	0.1621
chr13	115169878	2024779	0.0176	0.1441
chr14	107349540	1955369	0.0182	0.1499
chr15	102531392	1845188	0.018	0.1477
chr16	90354753	1960746	0.0217	0.1724
chr17	81195210	1840664	0.0227	0.169
chr18	78077248	1661903	0.0213	0.2507
chr19	59128983	1414867	0.0239	0.224
chr20	63025520	1448601	0.023	0.1707
chr21	48129895	852052	0.0177	0.157
chr22	51304566	815484	0.0159	0.1384
chrMT	16571	16433	0.9917	1.1499
chrX	155270560	3608426	0.0232	0.176
chrY	59373566	230179	0.0039	0.1176

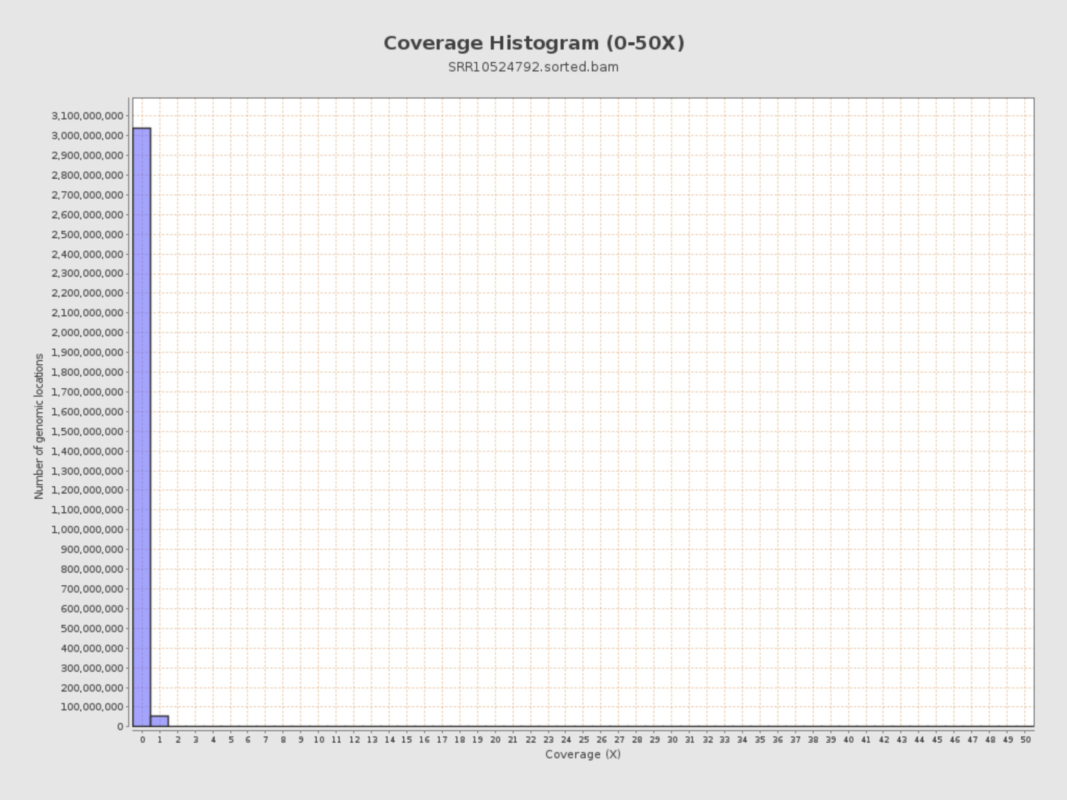
3. Results : Coverage across reference



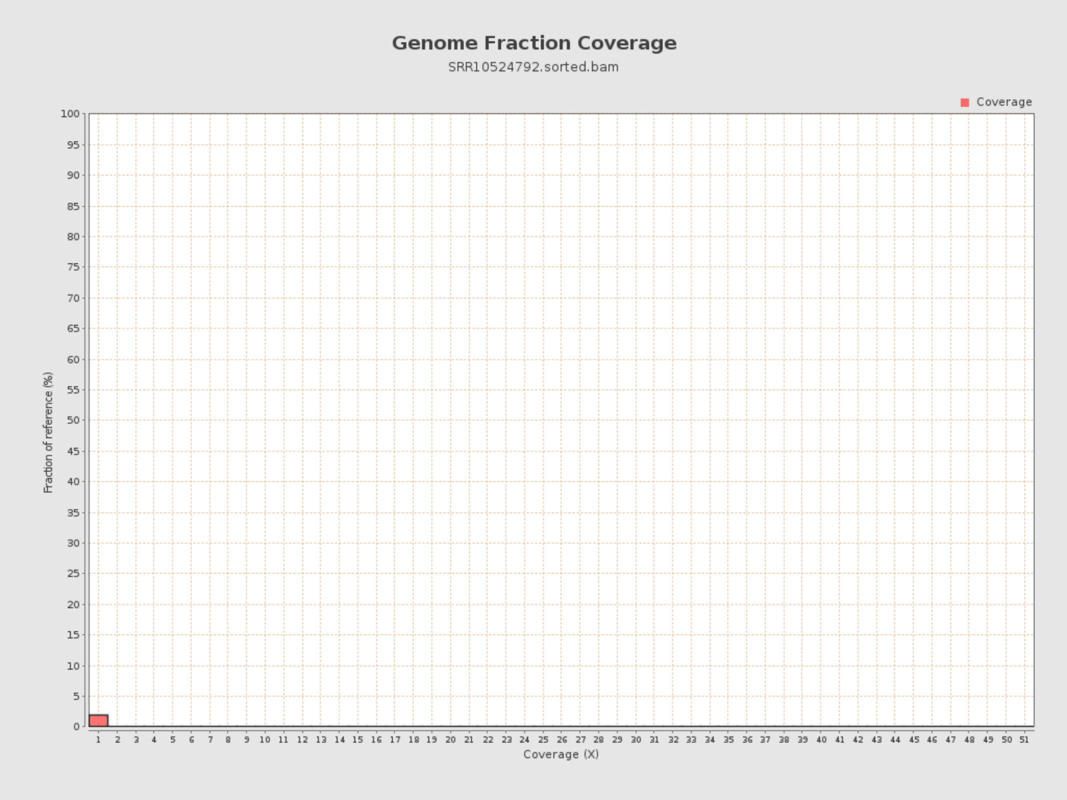
4. Results : Coverage Histogram



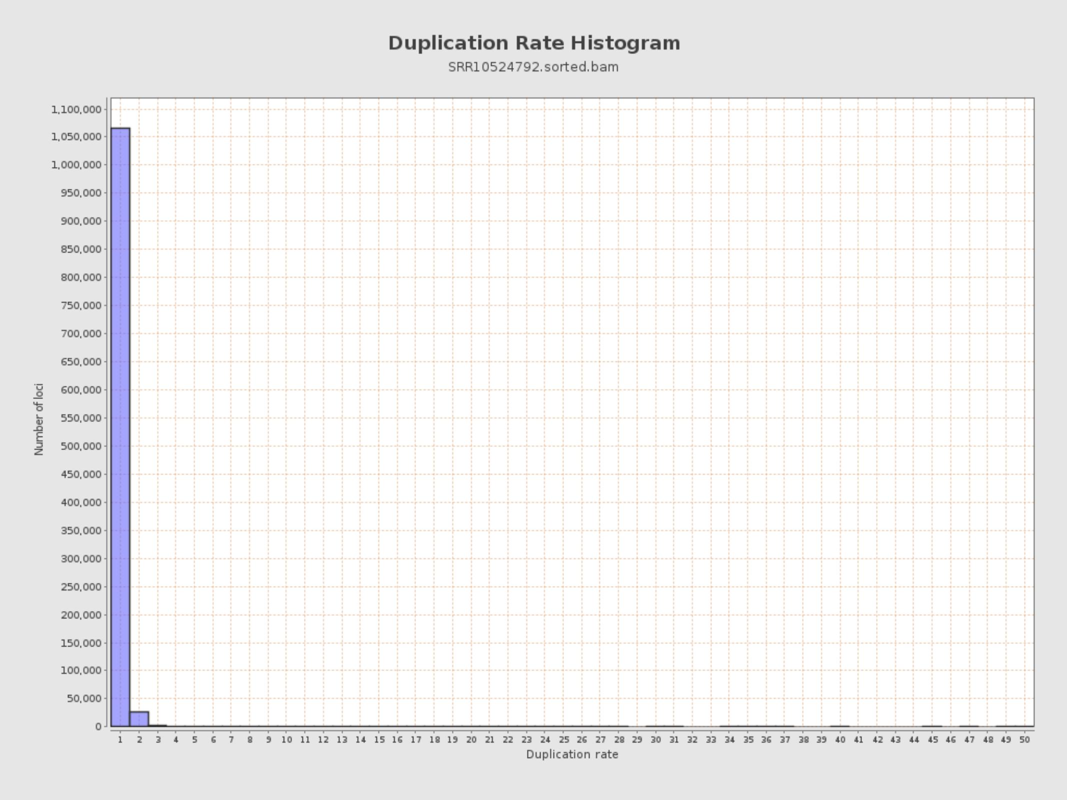
5. Results : Coverage Histogram (0-50X)



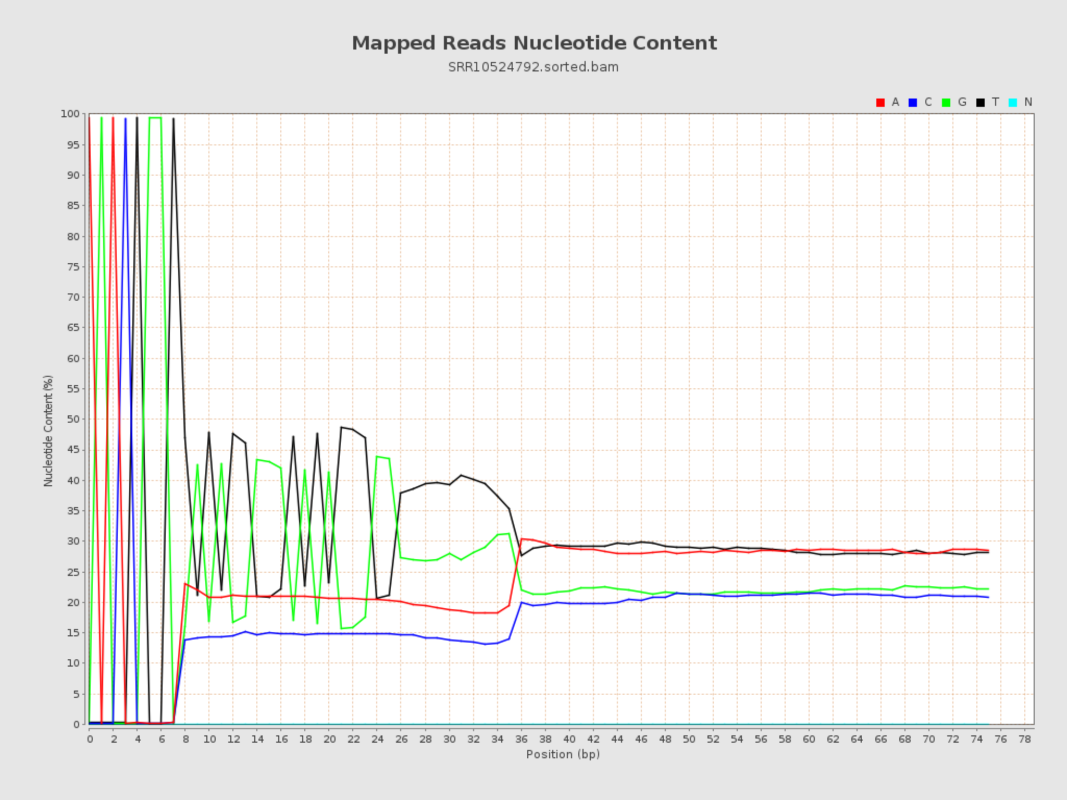
6. Results : Genome Fraction Coverage



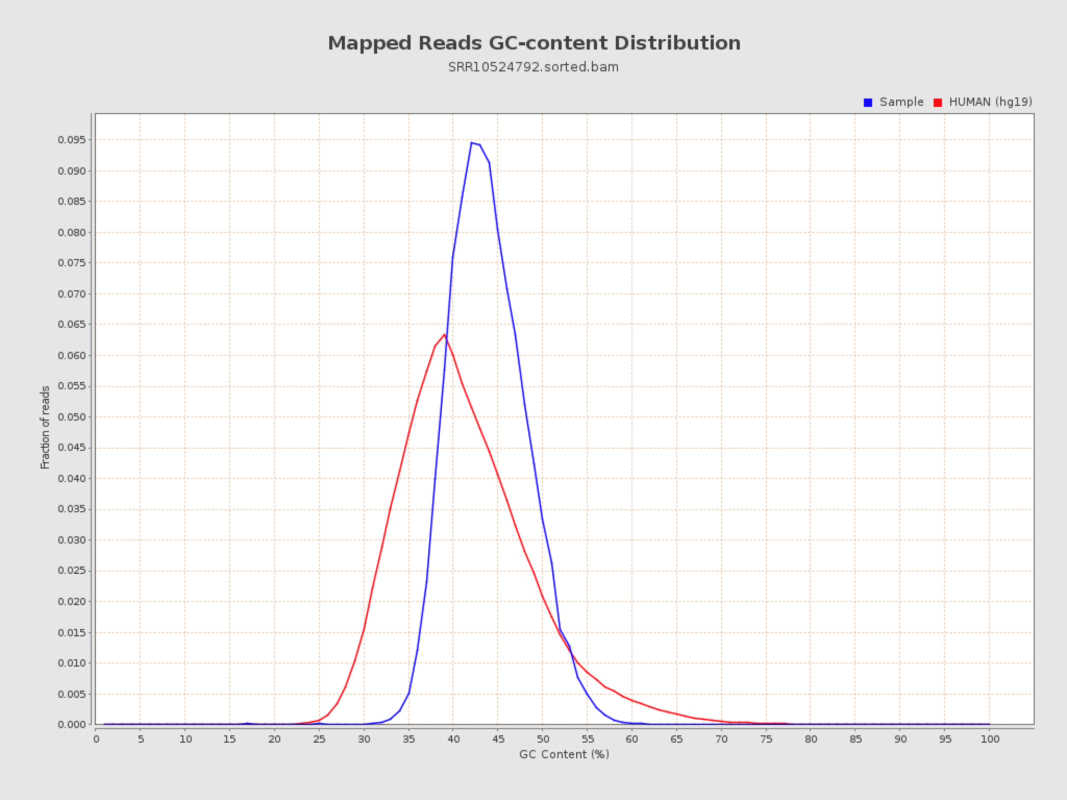
7. Results : Duplication Rate Histogram



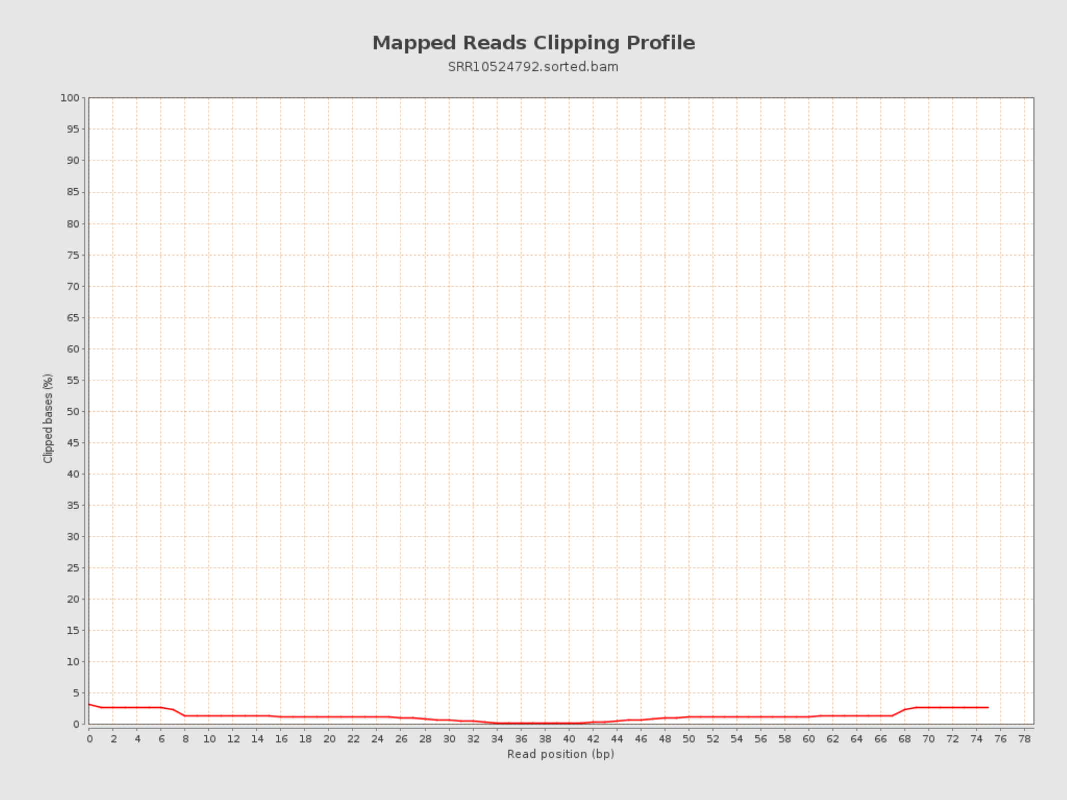
8. Results : Mapped Reads Nucleotide Content



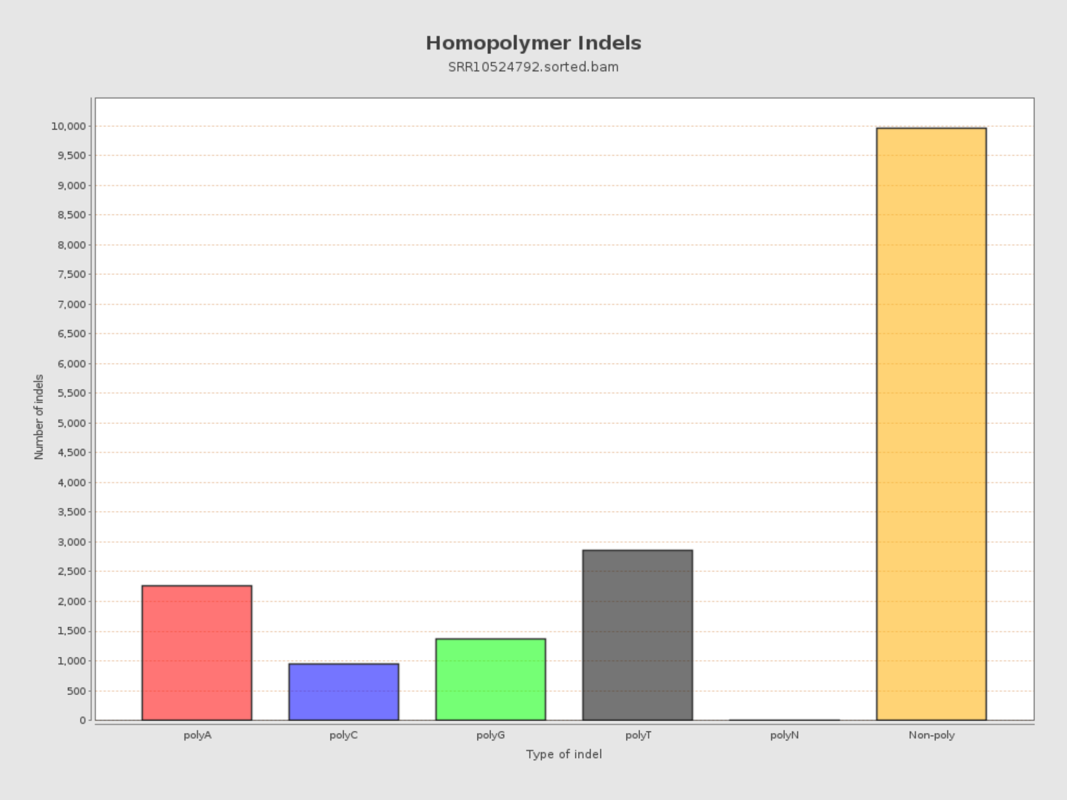
9. Results : Mapped Reads GC-content Distribution



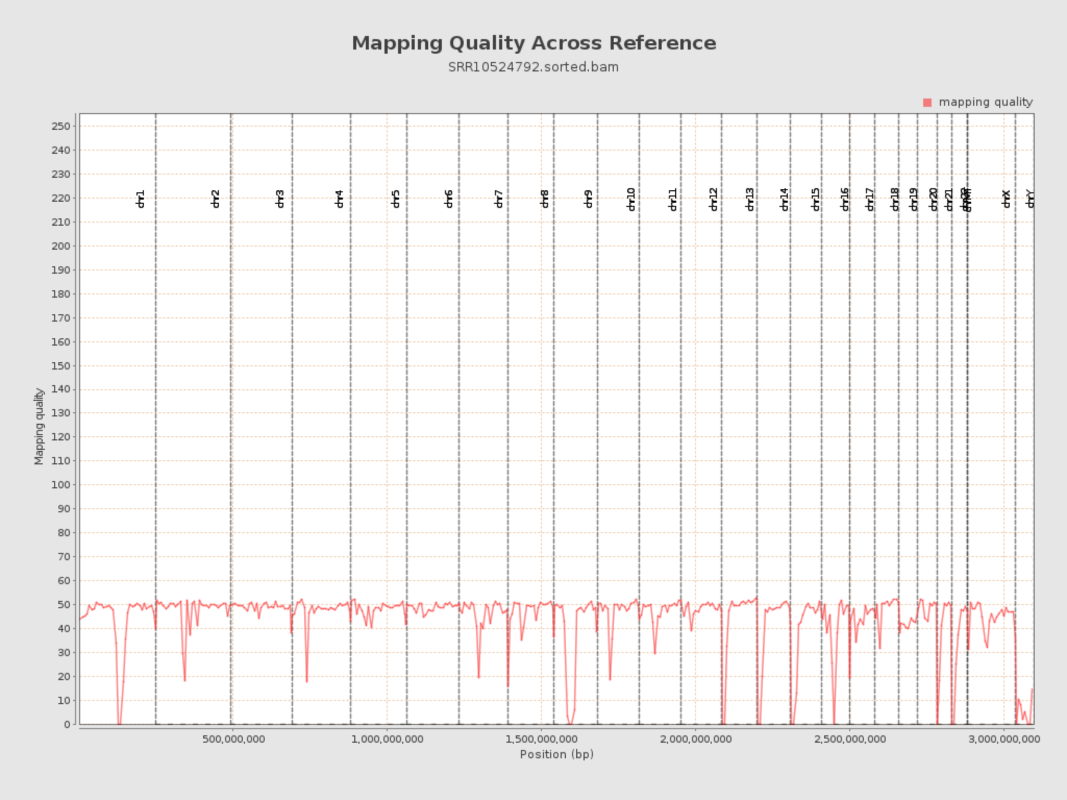
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram