Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 01:51:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524892.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_SRR10524892 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524892.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 01:51:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524892.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,905,453
Mapped reads	1,760,325 / 92.38%
Unmapped reads	145,128 / 7.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,957 / 0.31%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	81,957 / 4.3%
Duplication rate	3.45%
Clipped reads	1,761,238 / 92.43%

2.2. ACGT Content

Number/percentage of A's	26,672,842 / 25.93%
Number/percentage of C's	18,916,576 / 18.39%
Number/percentage of T's	33,276,200 / 32.35%
Number/percentage of G's	23,998,806 / 23.33%
Number/percentage of N's	14,086 / 0.01%
GC Percentage	41.71%

2.3. Coverage

Mean	0.0332

Standard Deviation	0.3335

2.4. Mapping Quality

Mean Mapping Quality	46.38

2.5. Mismatches and indels

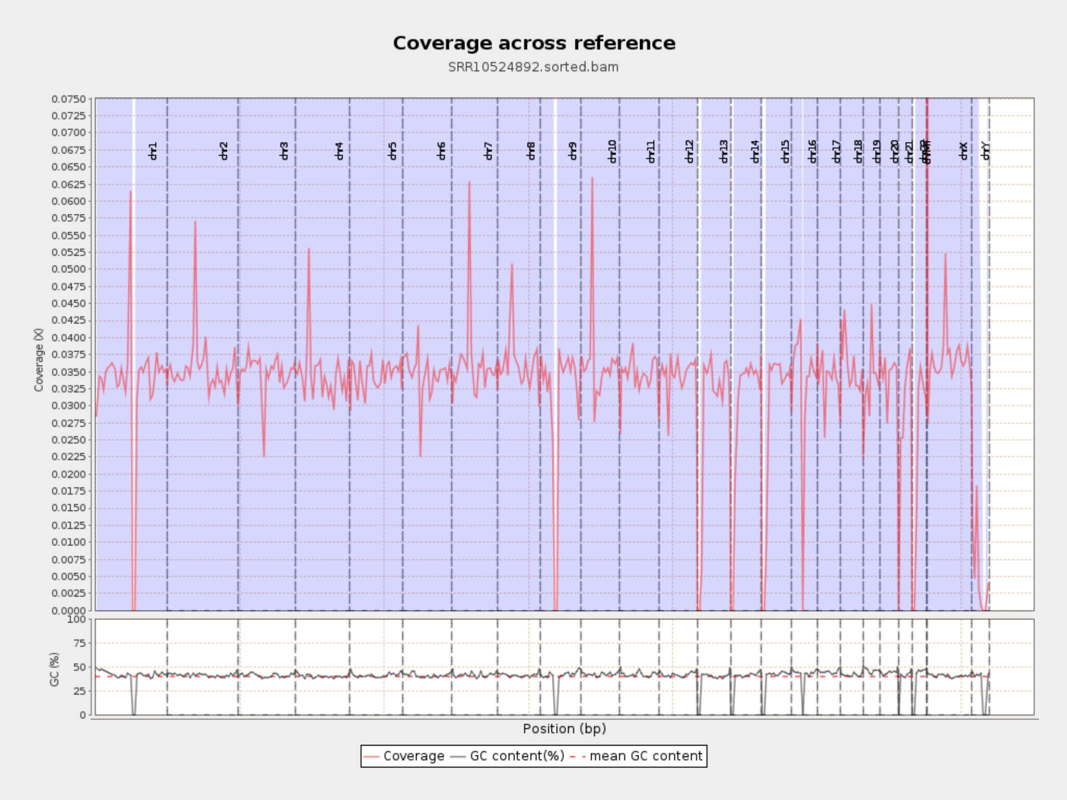
General error rate	0.5%
Mismatches	500,501
Insertions	7,908
Mapped reads with at least one insertion	0.45%
Deletions	18,747
Mapped reads with at least one deletion	1.06%
Homopolymer indels	43.33%

2.6. Chromosome stats

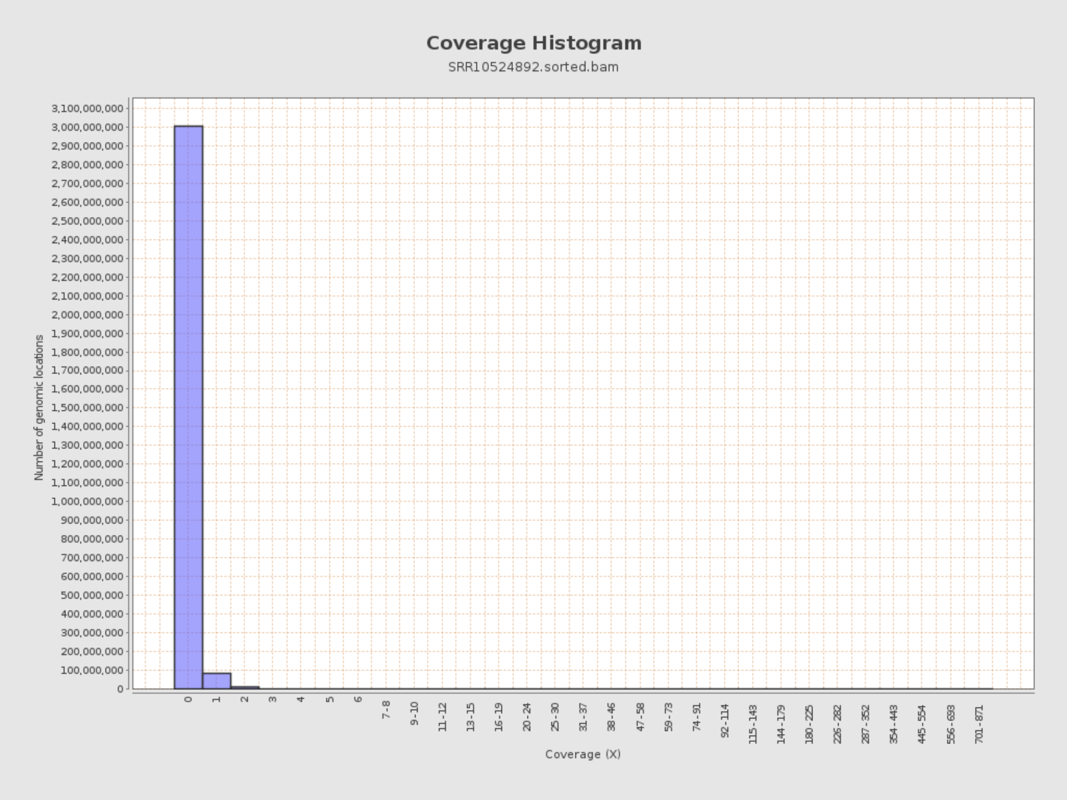
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8244255	0.0331	0.6654
chr2	243199373	8659849	0.0356	0.3546
chr3	198022430	6878834	0.0347	0.2044
chr4	191154276	6632869	0.0347	0.2276
chr5	180915260	6276402	0.0347	0.2062
chr6	171115067	5924521	0.0346	0.2305
chr7	159138663	5794759	0.0364	0.4641

chr8	146364022	5353899	0.0366	0.3173
chr9	141213431	4324456	0.0306	0.3022
chr10	135534747	4926797	0.0364	0.3039
chr11	135006516	4710531	0.0349	0.3045
chr12	133851895	4632018	0.0346	0.2126
chr13	115169878	3286694	0.0285	0.1865
chr14	107349540	3108933	0.029	0.1971
chr15	102531392	2900666	0.0283	0.1851
chr16	90354753	2950227	0.0327	0.2209
chr17	81195210	2736046	0.0337	0.2179
chr18	78077248	2792648	0.0358	0.5855
chr19	59128983	2006921	0.0339	0.4415
chr20	63025520	2148751	0.0341	0.2055
chr21	48129895	1368582	0.0284	0.2058
chr22	51304566	1183311	0.0231	0.166
chrMT	16571	17624	1.0635	1.3063
chrX	155270560	5745634	0.037	0.2527
chrY	59373566	302674	0.0051	0.1348

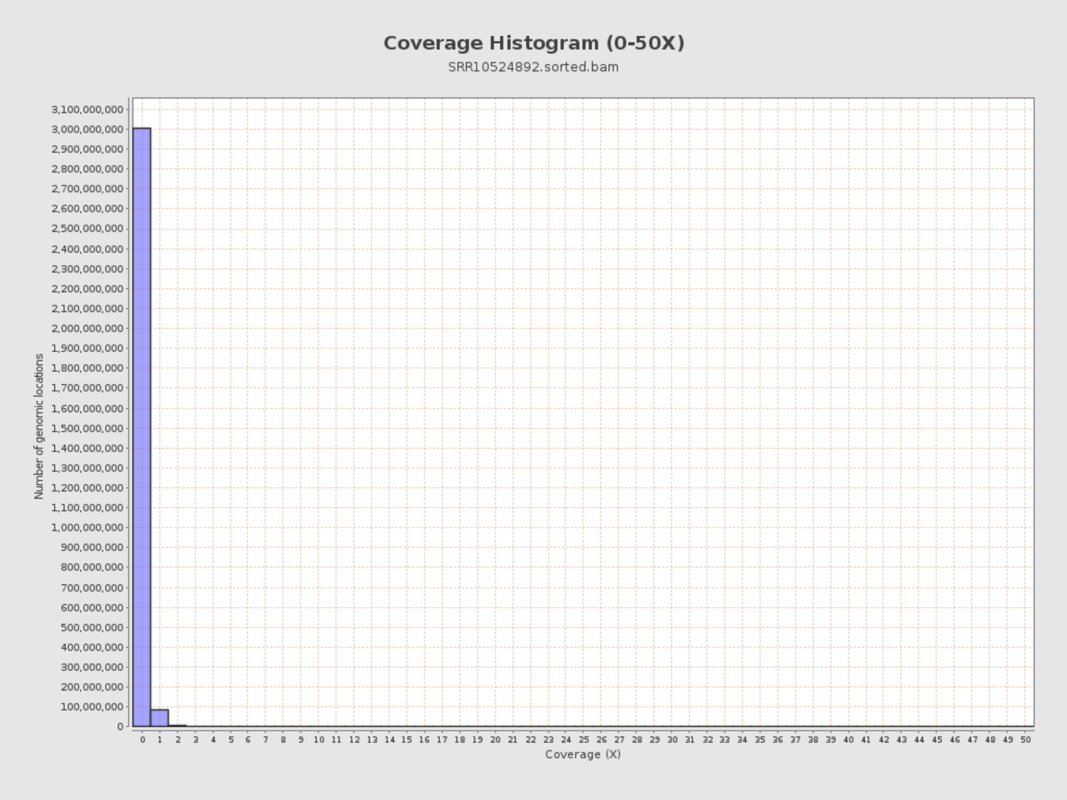
3. Results : Coverage across reference



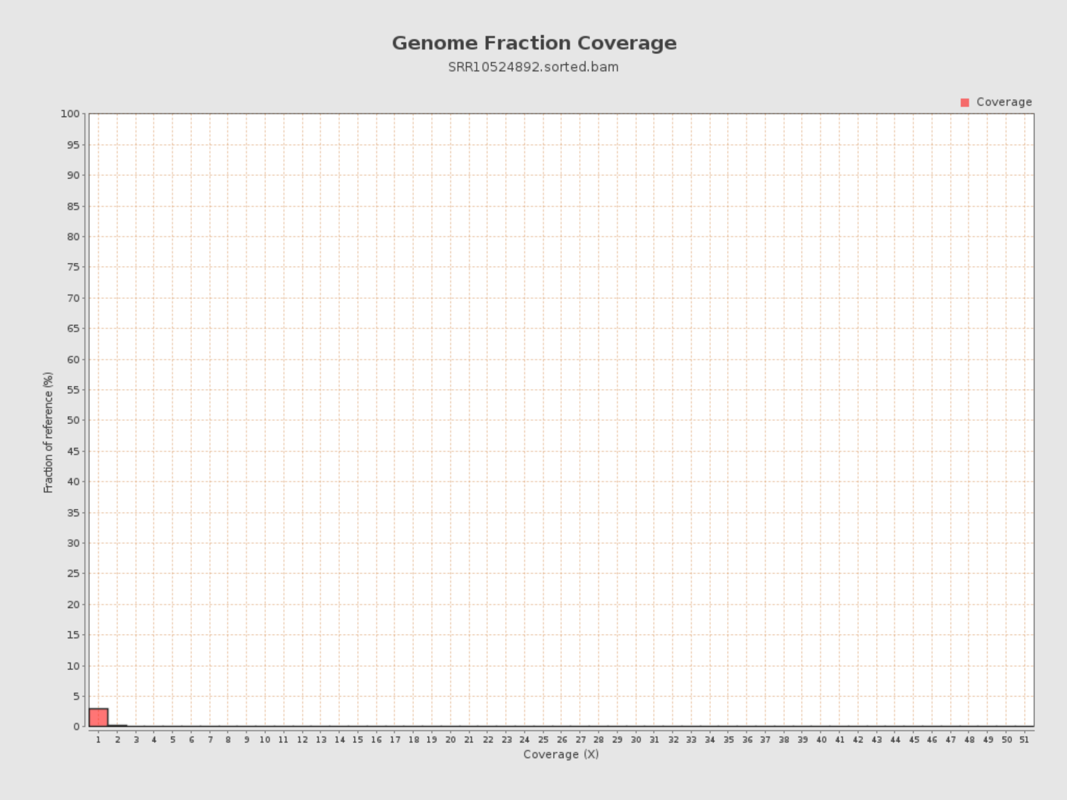
4. Results : Coverage Histogram



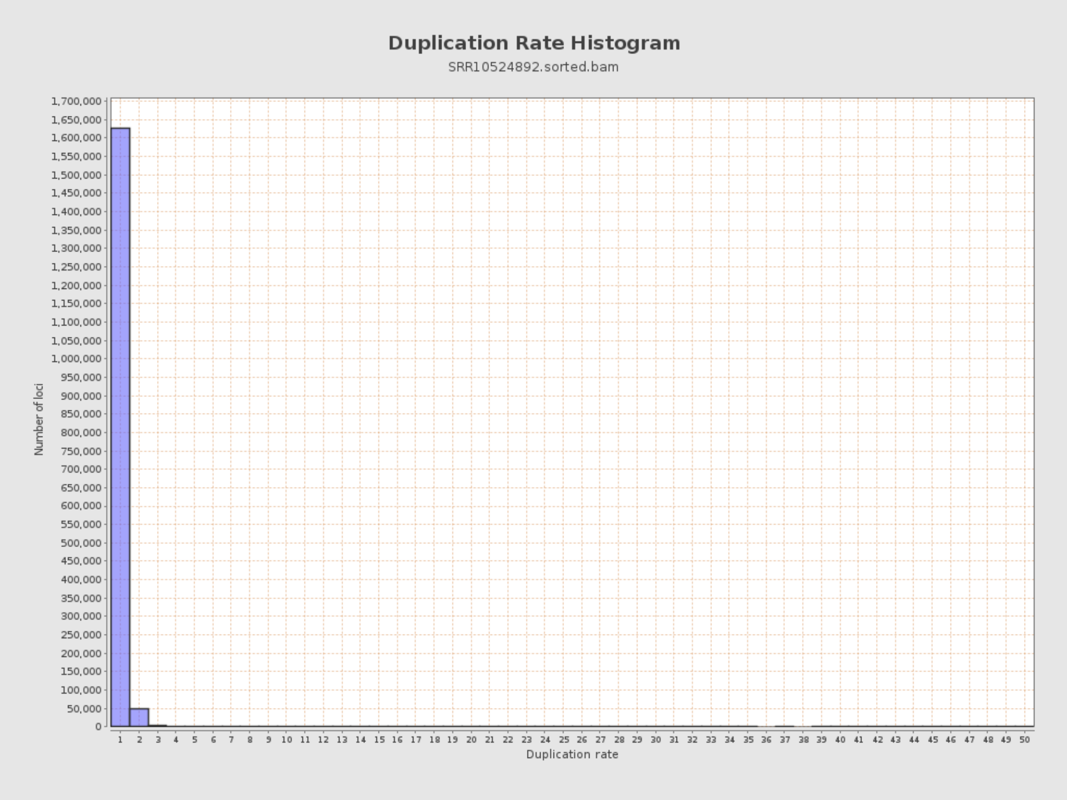
5. Results : Coverage Histogram (0-50X)



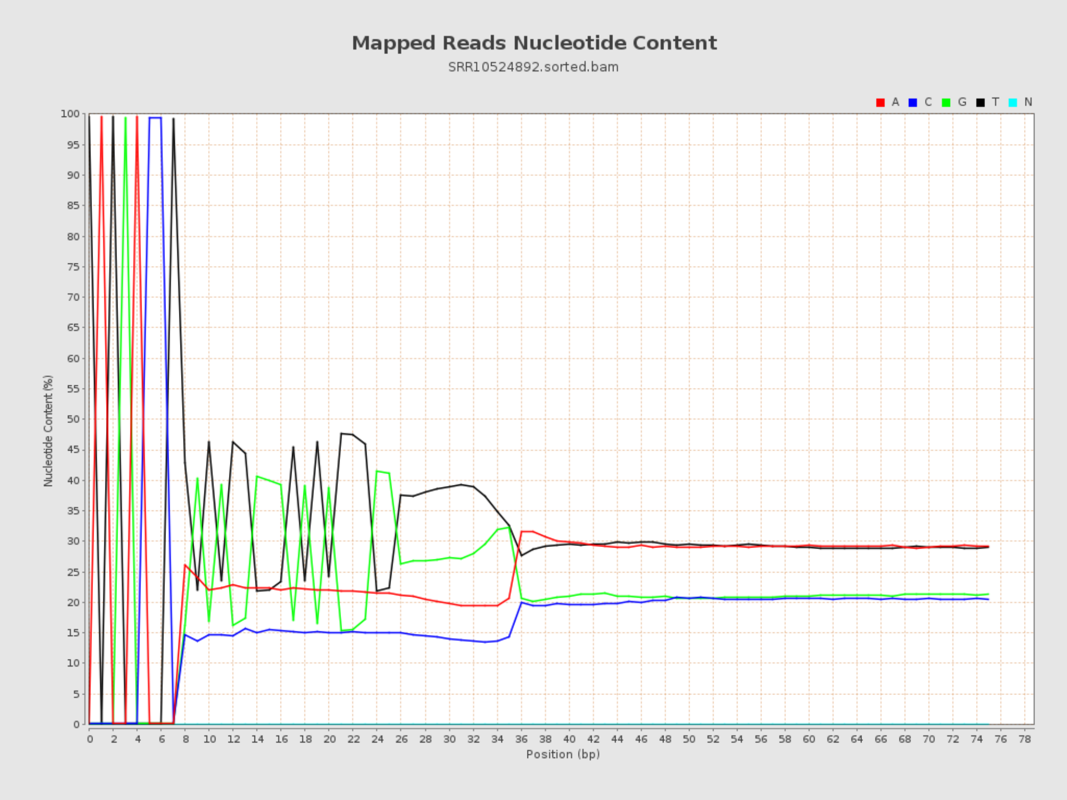
6. Results : Genome Fraction Coverage



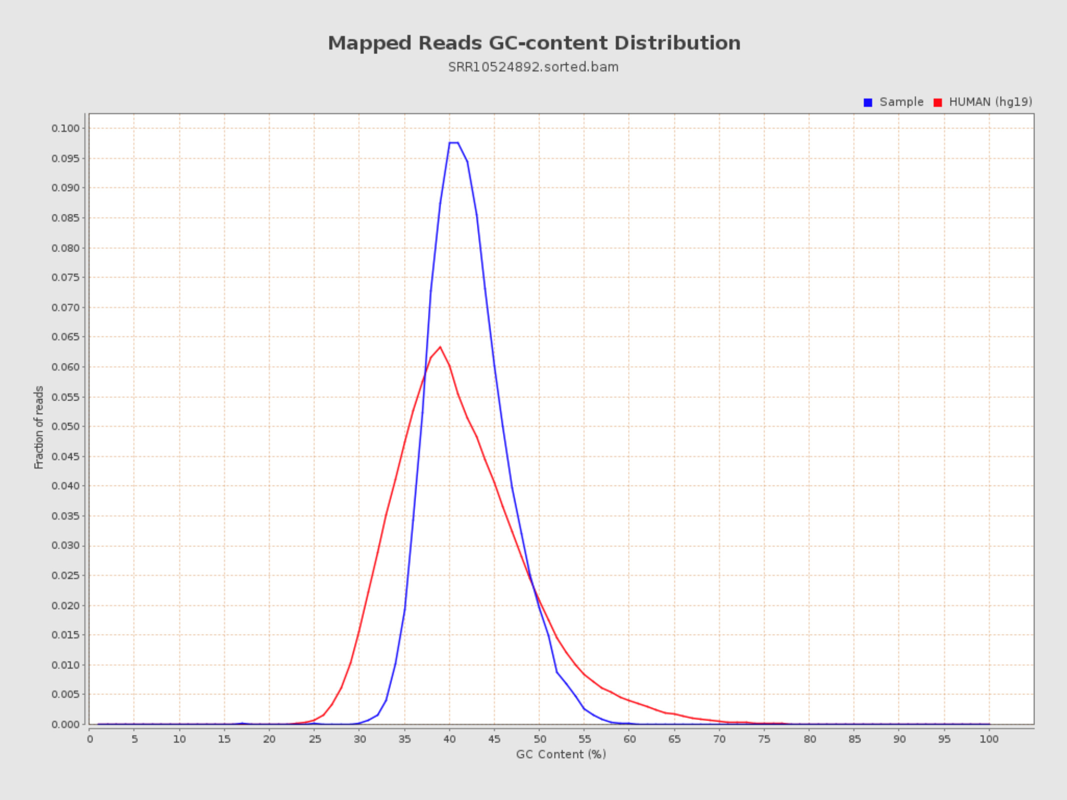
7. Results : Duplication Rate Histogram



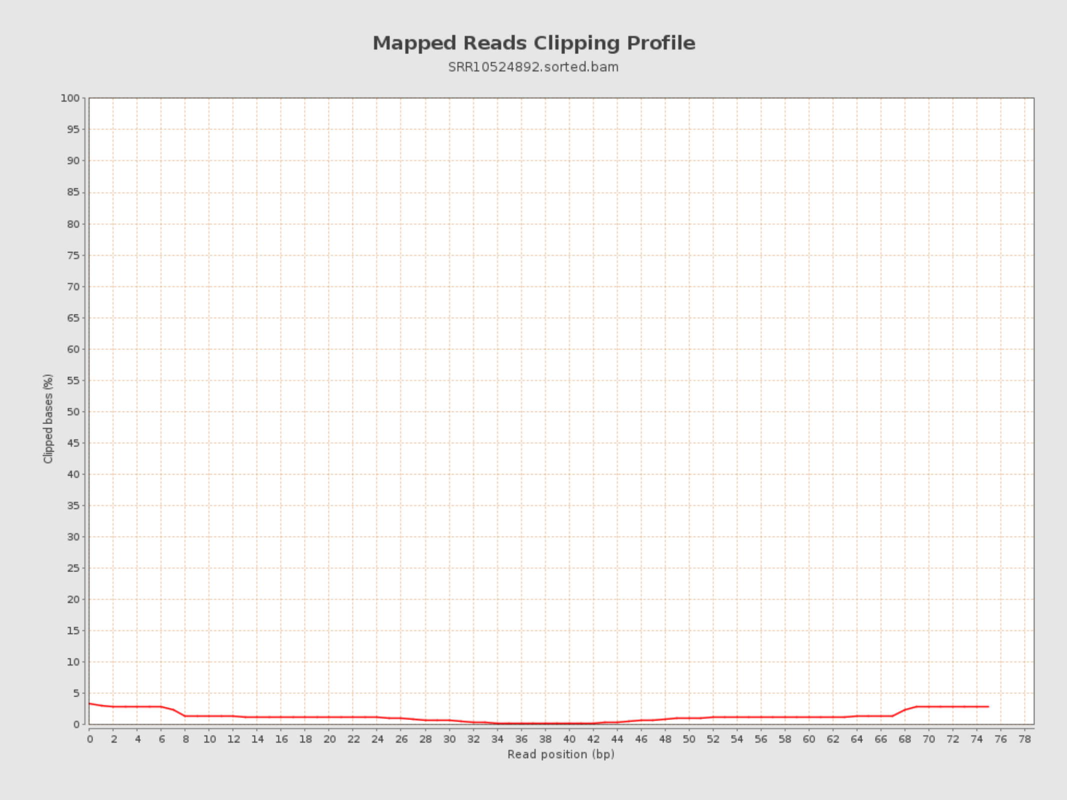
8. Results : Mapped Reads Nucleotide Content



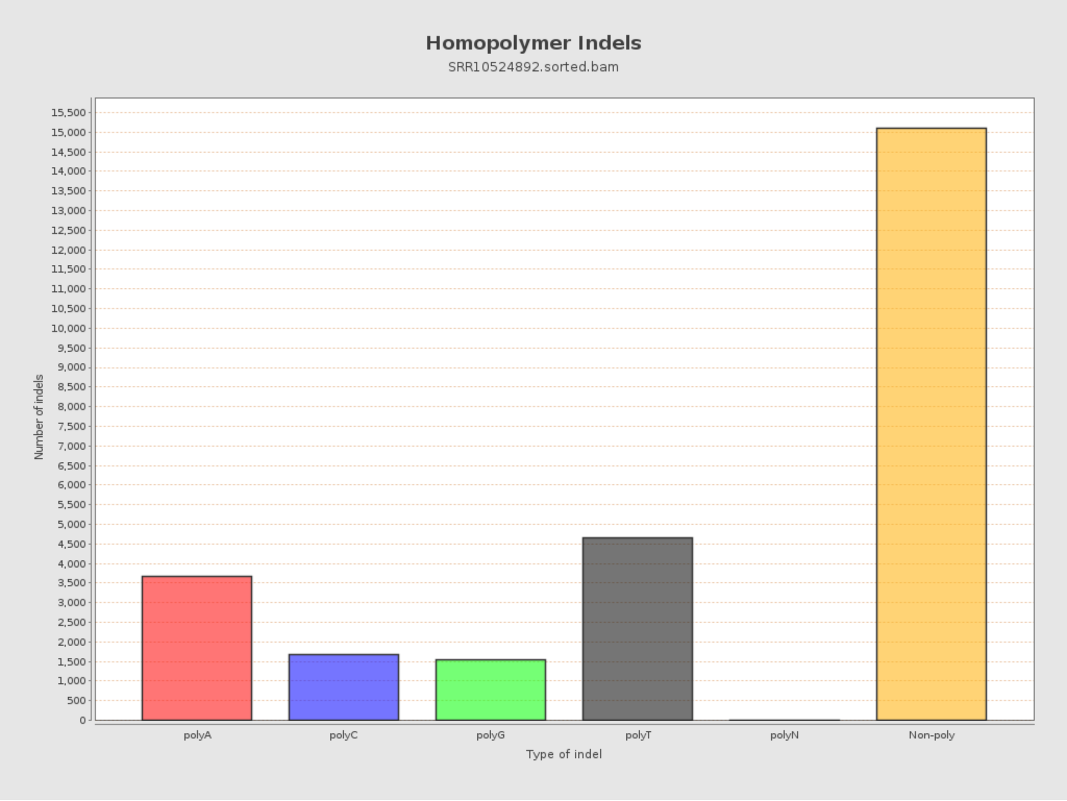
9. Results : Mapped Reads GC-content Distribution



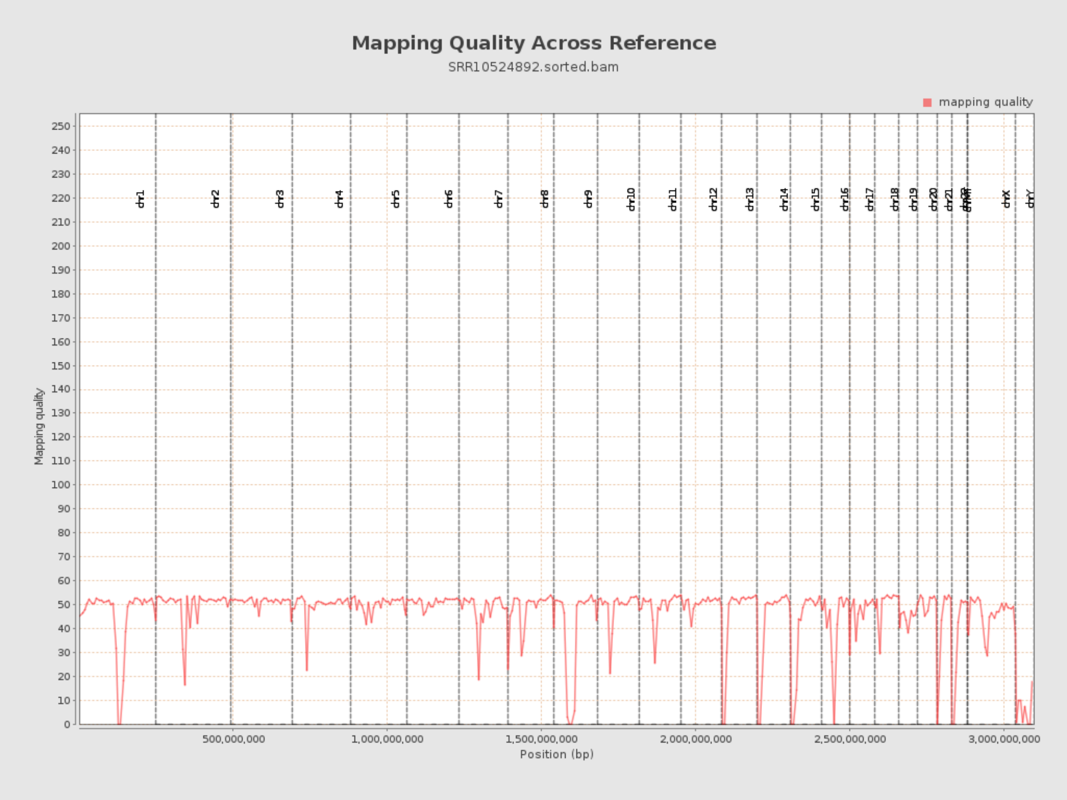
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram