Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 16:28:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524686.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_SRR10524686 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524686.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 16:28:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524686.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,026,902
Mapped reads	1,884,360 / 92.97%
Unmapped reads	142,542 / 7.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,287 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	80,293 / 3.96%
Duplication rate	3.09%
Clipped reads	1,886,685 / 93.08%

2.2. ACGT Content

Number/percentage of A's	29,713,095 / 26.39%
Number/percentage of C's	23,194,159 / 20.6%
Number/percentage of T's	33,920,505 / 30.12%
Number/percentage of G's	25,757,752 / 22.88%
Number/percentage of N's	15,945 / 0.01%
GC Percentage	43.47%

2.3. Coverage

Mean	0.0364

Standard Deviation	0.3336

2.4. Mapping Quality

Mean Mapping Quality	46.09

2.5. Mismatches and indels

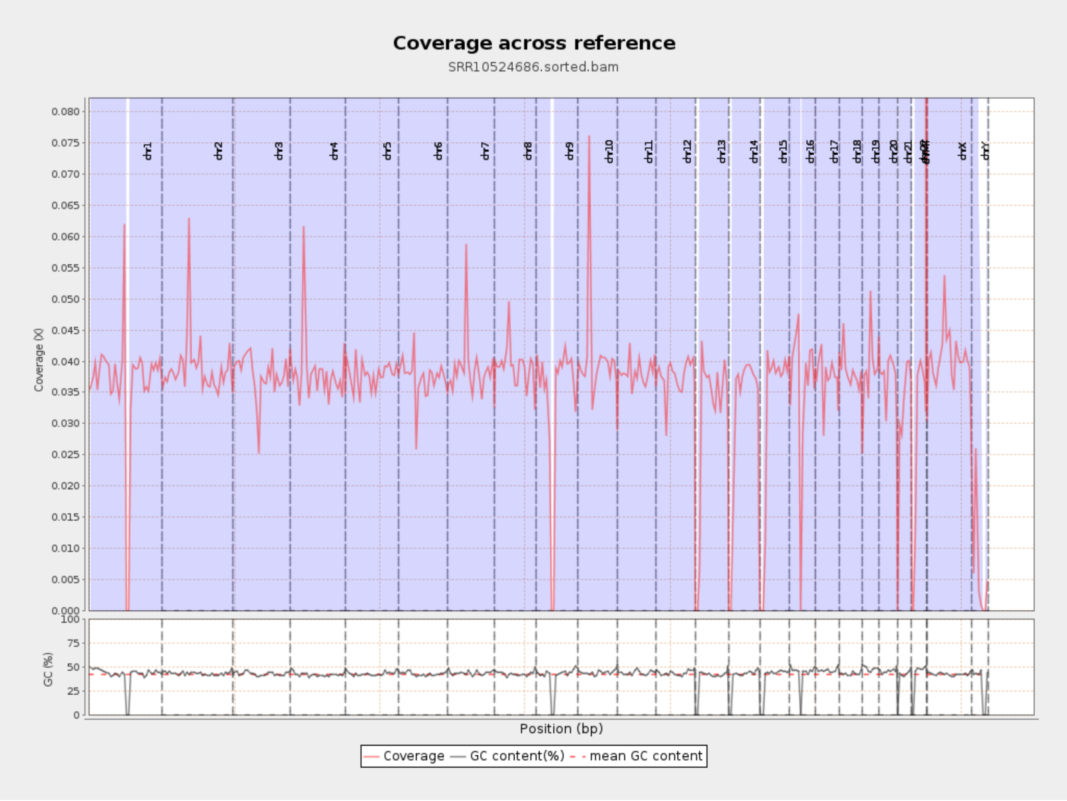
General error rate	0.51%
Mismatches	553,664
Insertions	8,769
Mapped reads with at least one insertion	0.46%
Deletions	21,676
Mapped reads with at least one deletion	1.14%
Homopolymer indels	42.89%

2.6. Chromosome stats

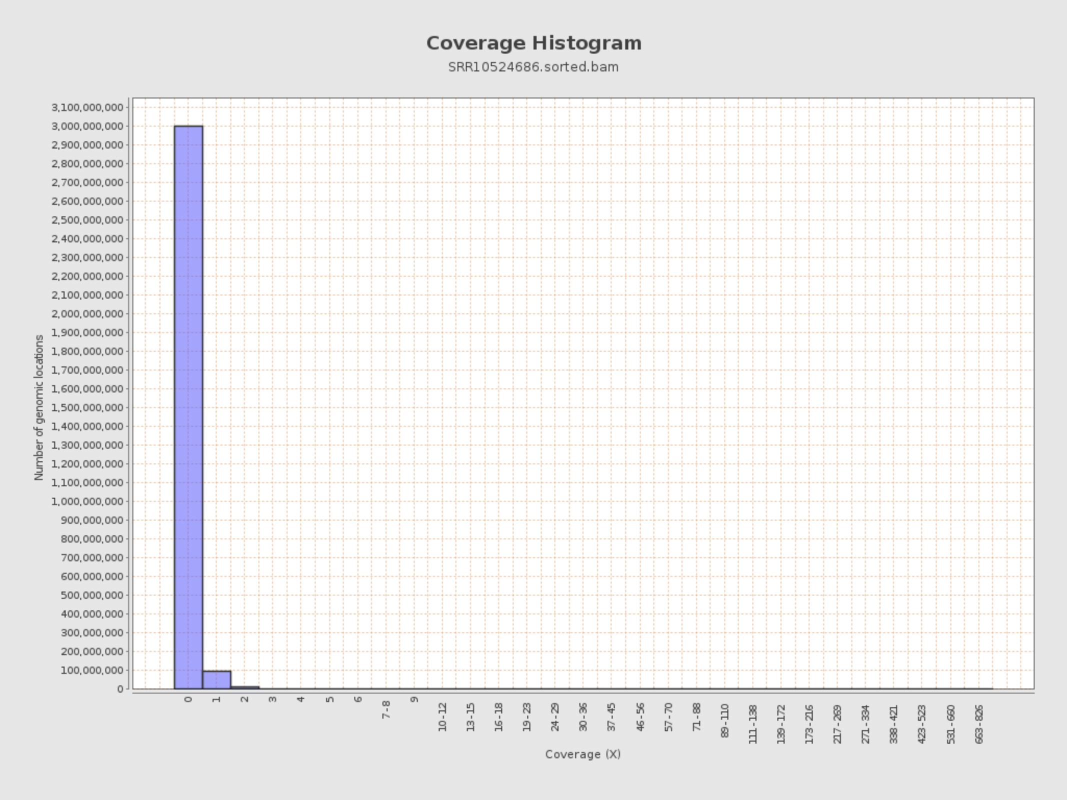
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9066565	0.0364	0.6133
chr2	243199373	9511829	0.0391	0.4385
chr3	198022430	7475311	0.0377	0.2134
chr4	191154276	7299945	0.0382	0.2497
chr5	180915260	6841952	0.0378	0.2147
chr6	171115067	6402674	0.0374	0.2417
chr7	159138663	6194673	0.0389	0.3812

chr8	146364022	5732986	0.0392	0.372
chr9	141213431	4737287	0.0335	0.2763
chr10	135534747	5529269	0.0408	0.3571
chr11	135006516	5141930	0.0381	0.2865
chr12	133851895	5036172	0.0376	0.2154
chr13	115169878	3525658	0.0306	0.192
chr14	107349540	3337215	0.0311	0.2015
chr15	102531392	3227146	0.0315	0.1947
chr16	90354753	3265981	0.0361	0.2284
chr17	81195210	3024301	0.0372	0.2277
chr18	78077248	3012100	0.0386	0.5236
chr19	59128983	2322428	0.0393	0.459
chr20	63025520	2370085	0.0376	0.2176
chr21	48129895	1514053	0.0315	0.232
chr22	51304566	1345415	0.0262	0.1781
chrMT	16571	50269	3.0336	2.3411
chrX	155270560	6279497	0.0404	0.2436
chrY	59373566	391337	0.0066	0.2595

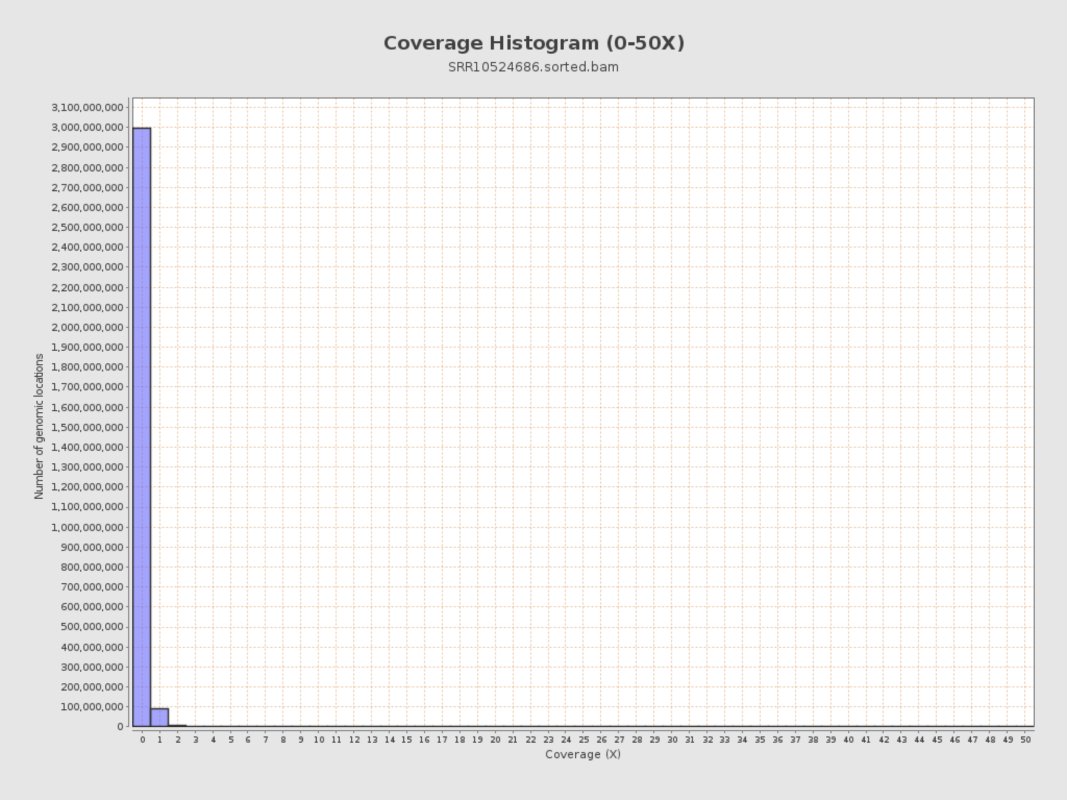
3. Results : Coverage across reference



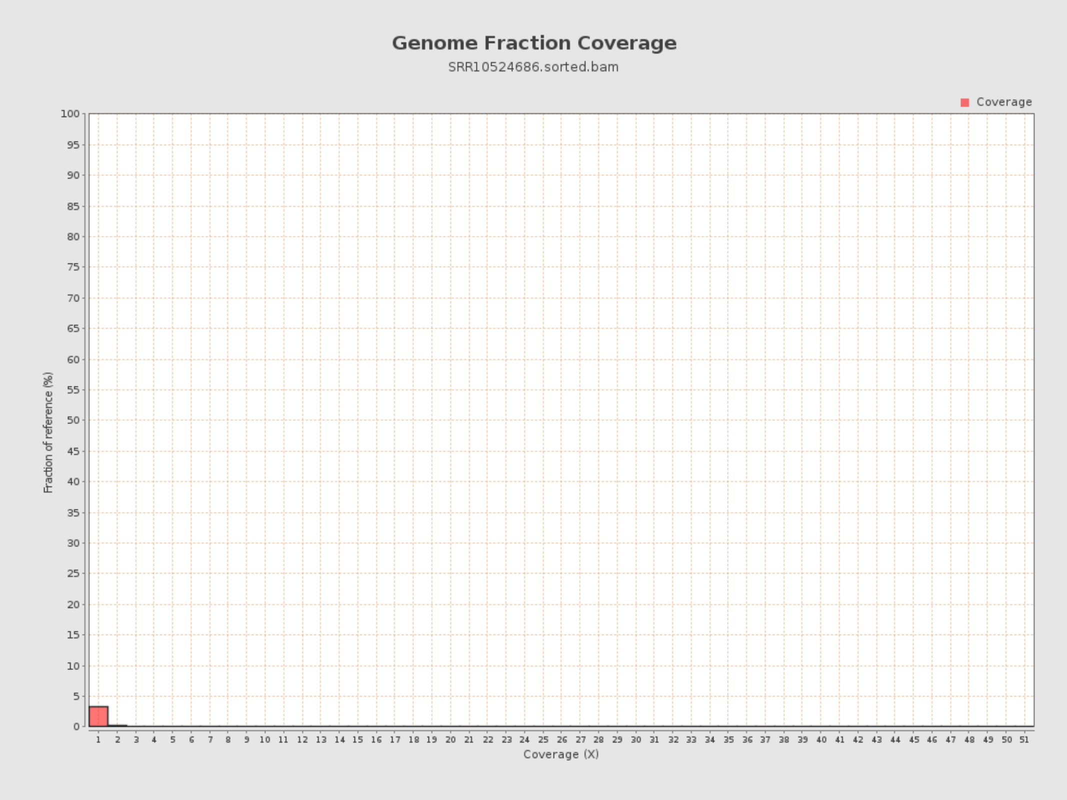
4. Results : Coverage Histogram



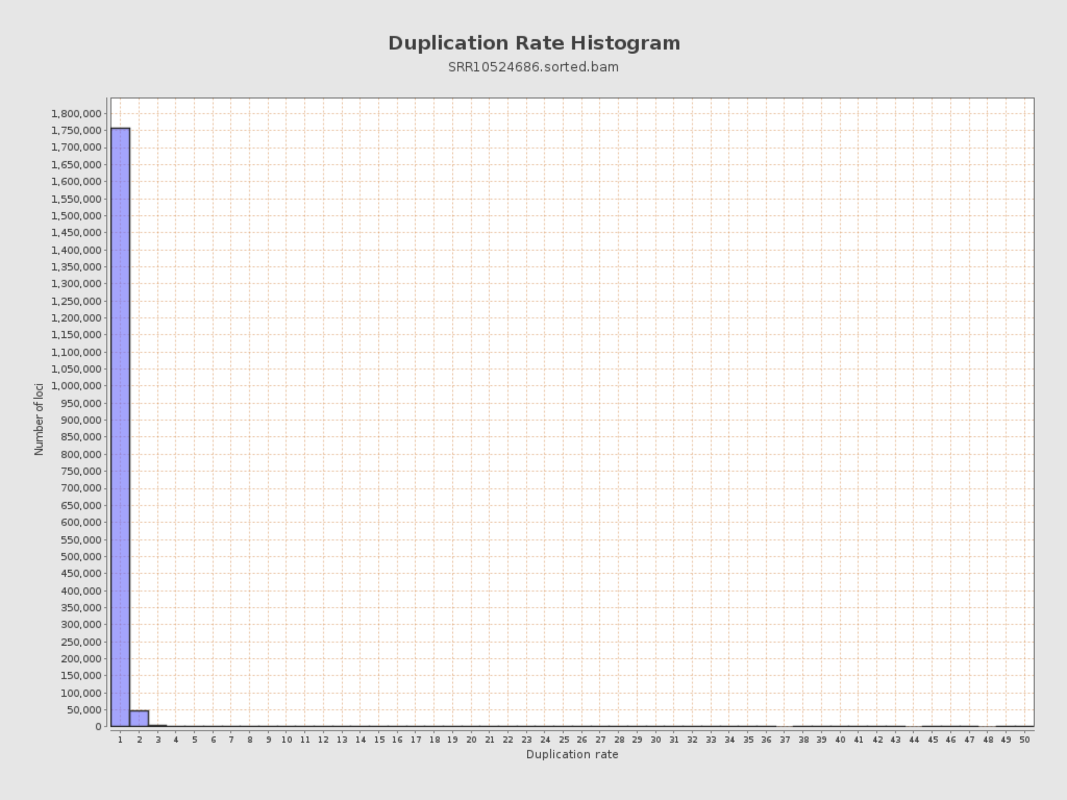
5. Results : Coverage Histogram (0-50X)



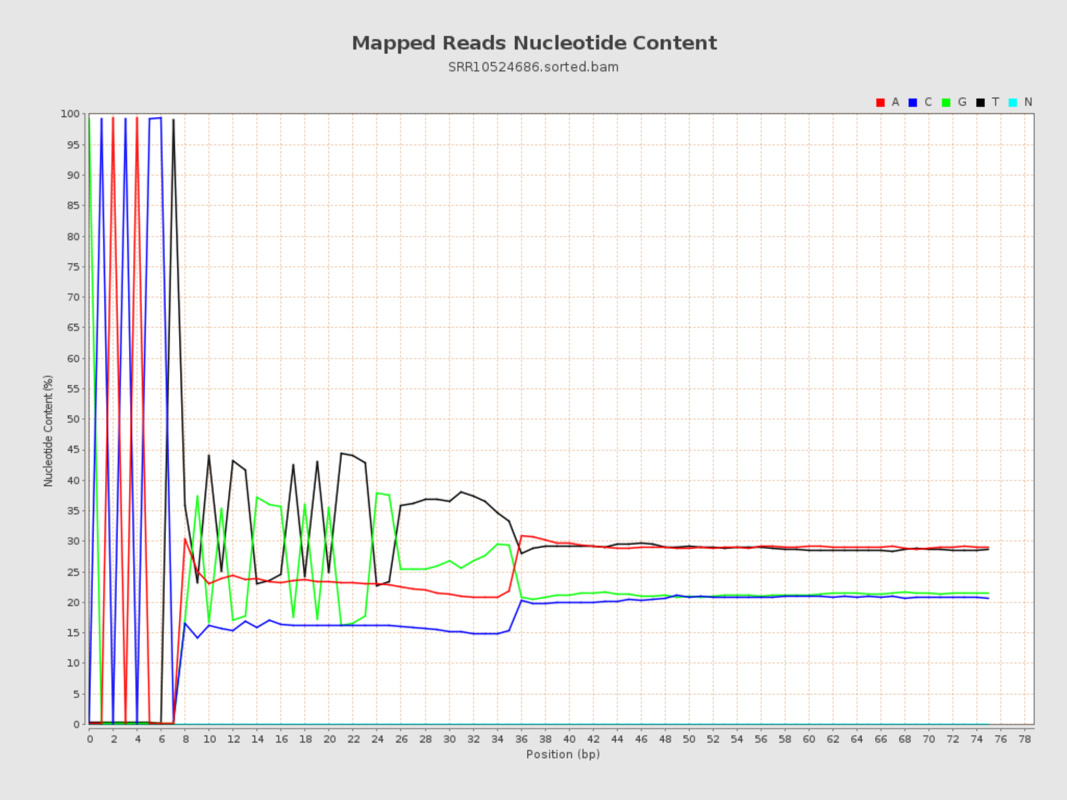
6. Results : Genome Fraction Coverage



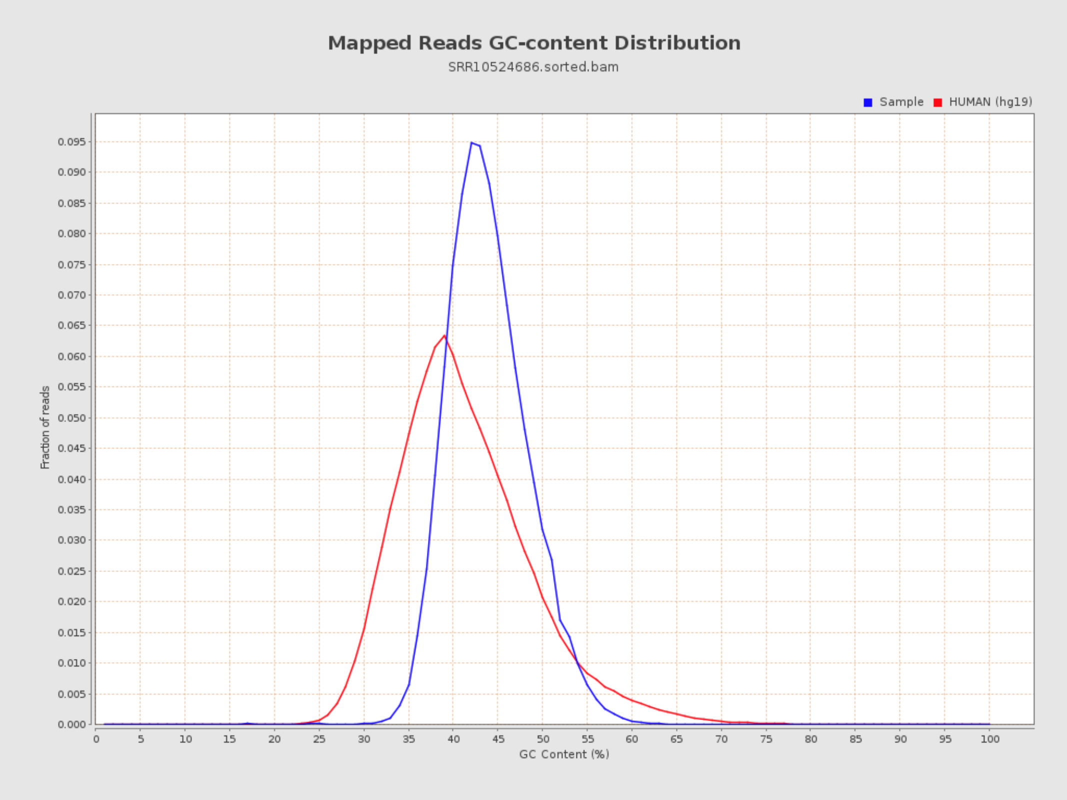
7. Results : Duplication Rate Histogram



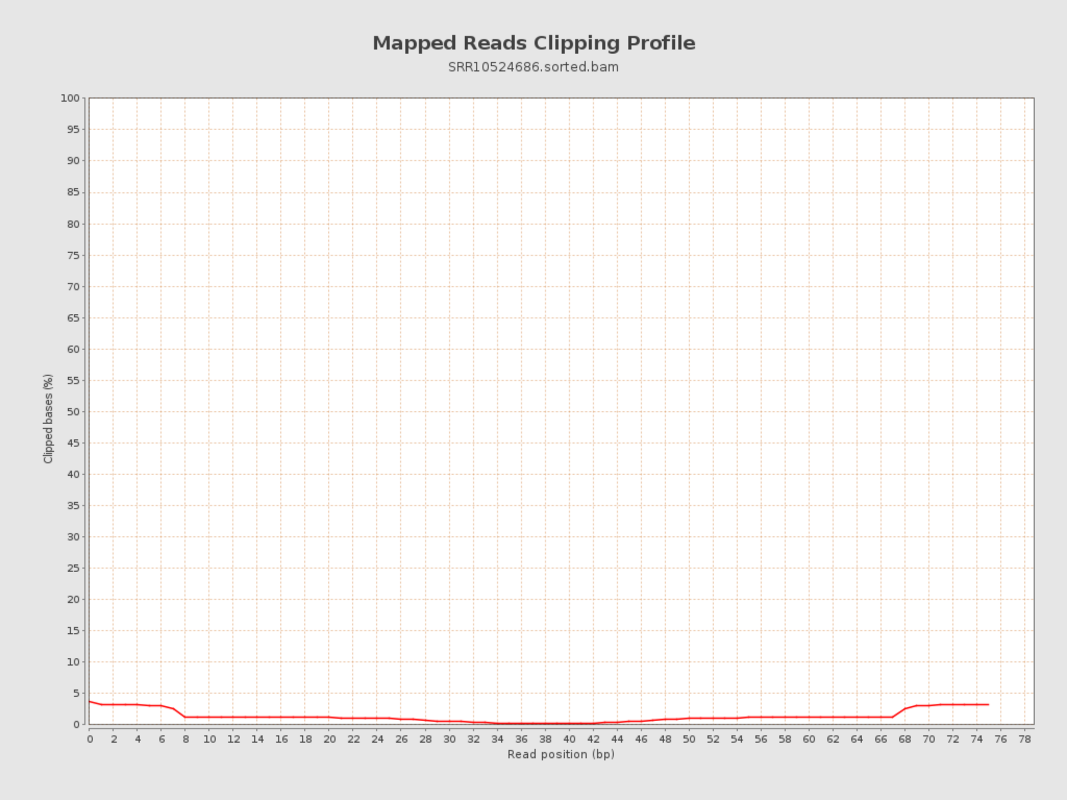
8. Results : Mapped Reads Nucleotide Content



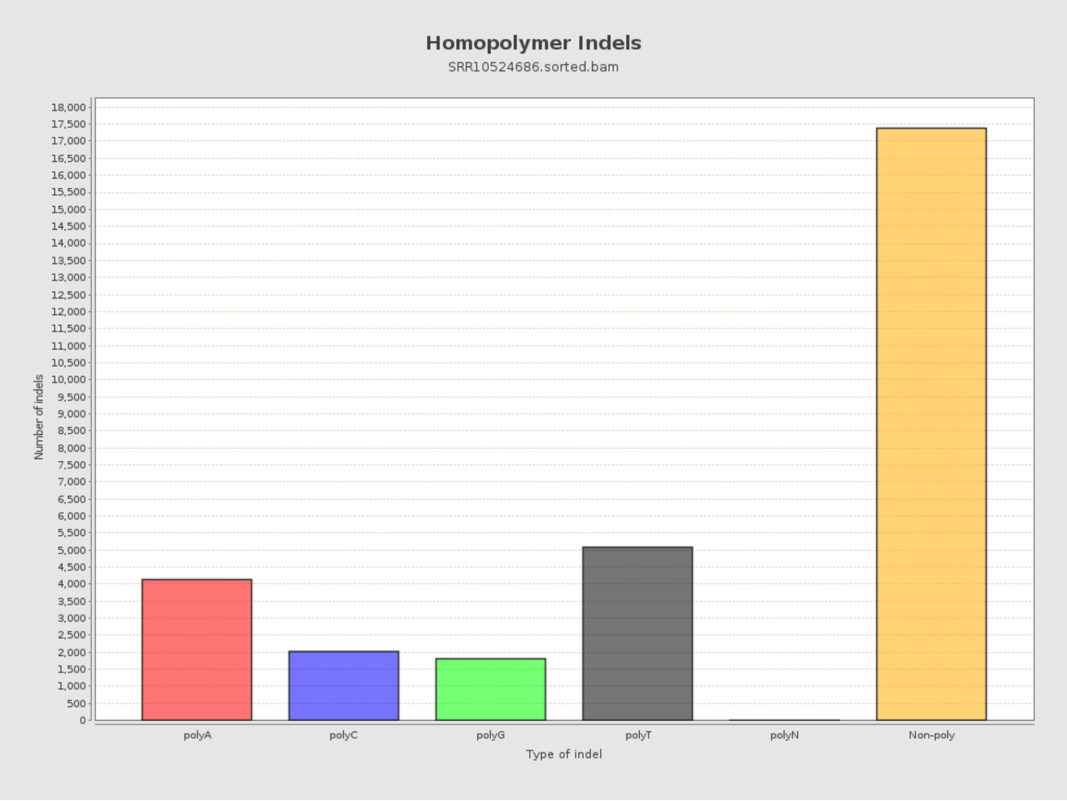
9. Results : Mapped Reads GC-content Distribution



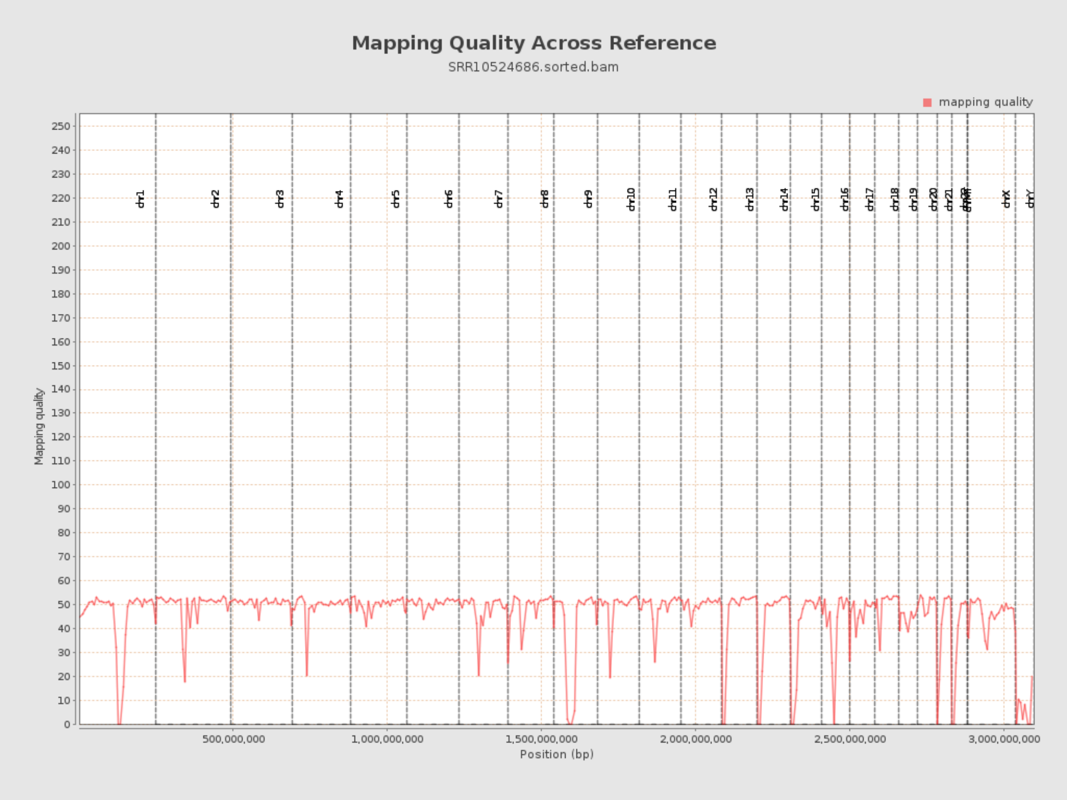
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram