Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 14:17:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524636.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_SRR10524636 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524636.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 14:17:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524636.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	939,852
Mapped reads	856,758 / 91.16%
Unmapped reads	83,094 / 8.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,653 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	34,756 / 3.7%
Duplication rate	3.22%
Clipped reads	858,048 / 91.3%

2.2. ACGT Content

Number/percentage of A's	12,398,755 / 24.74%
Number/percentage of C's	9,386,594 / 18.73%
Number/percentage of T's	16,155,324 / 32.23%
Number/percentage of G's	12,184,340 / 24.31%
Number/percentage of N's	434 / 0%
GC Percentage	43.03%

2.3. Coverage

Mean	0.0162

Standard Deviation	0.1785

2.4. Mapping Quality

Mean Mapping Quality	45.09

2.5. Mismatches and indels

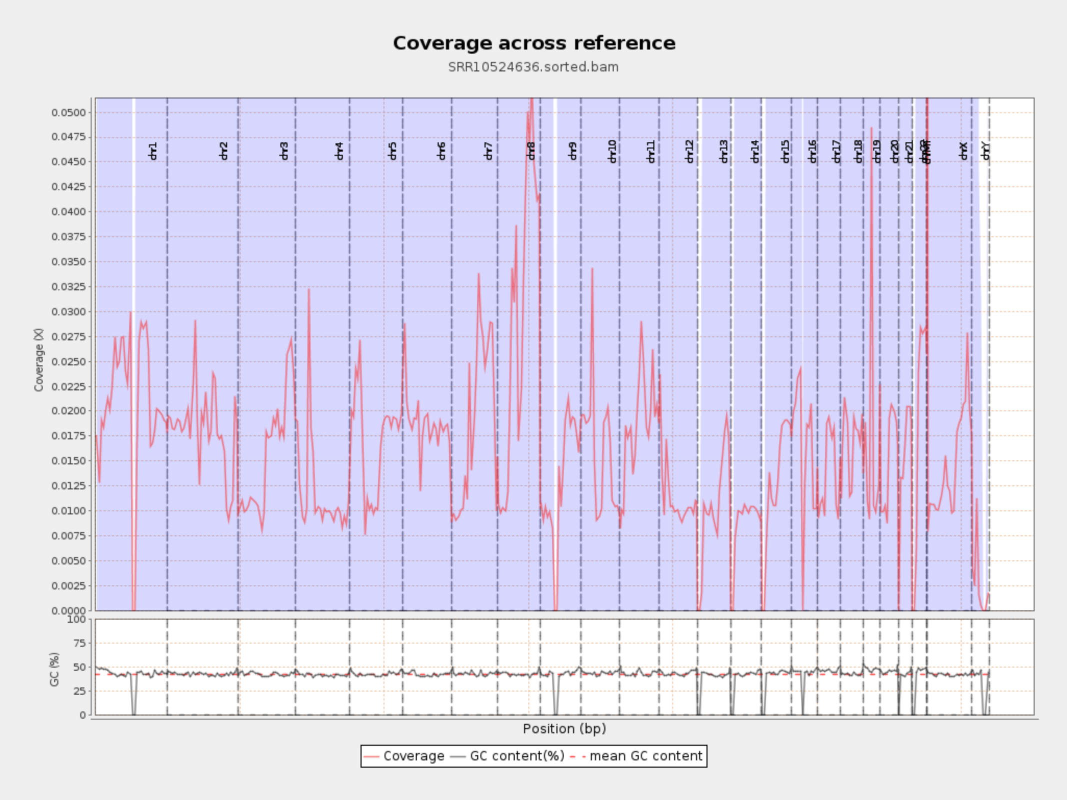
General error rate	0.52%
Mismatches	252,220
Insertions	3,961
Mapped reads with at least one insertion	0.46%
Deletions	9,542
Mapped reads with at least one deletion	1.11%
Homopolymer indels	40.54%

2.6. Chromosome stats

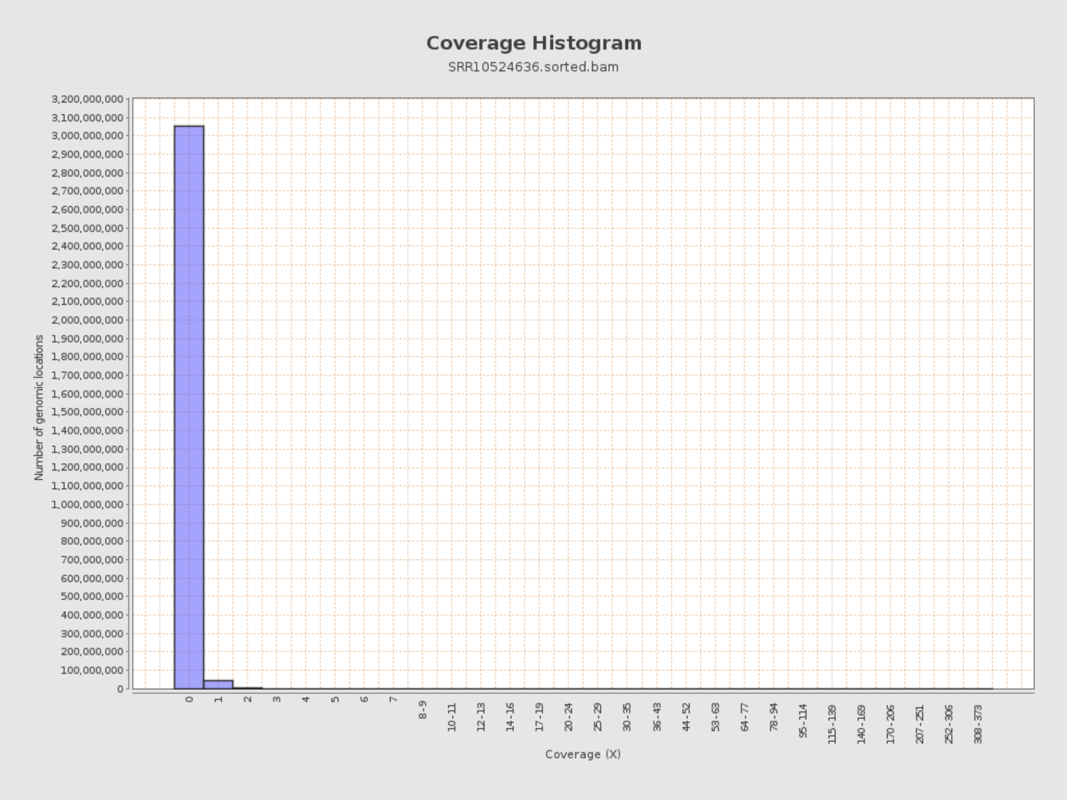
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5175181	0.0208	0.3099
chr2	243199373	4421068	0.0182	0.2055
chr3	198022430	3092503	0.0156	0.135
chr4	191154276	2294057	0.012	0.1444
chr5	180915260	3083053	0.017	0.141
chr6	171115067	3210509	0.0188	0.1536
chr7	159138663	3023993	0.019	0.1941

chr8	146364022	4386734	0.03	0.2398
chr9	141213431	1793815	0.0127	0.145
chr10	135534747	2216615	0.0164	0.1982
chr11	135006516	2538666	0.0188	0.1643
chr12	133851895	1542053	0.0115	0.1176
chr13	115169878	1187302	0.0103	0.1099
chr14	107349540	920402	0.0086	0.1027
chr15	102531392	1275231	0.0124	0.1207
chr16	90354753	1478254	0.0164	0.1431
chr17	81195210	1101365	0.0136	0.1289
chr18	78077248	1315464	0.0168	0.2249
chr19	59128983	1019443	0.0172	0.2194
chr20	63025520	944741	0.015	0.1368
chr21	48129895	744039	0.0155	0.1492
chr22	51304566	938535	0.0183	0.147
chrMT	16571	6364	0.384	0.6543
chrX	155270560	2274336	0.0146	0.1362
chrY	59373566	158272	0.0027	0.1087

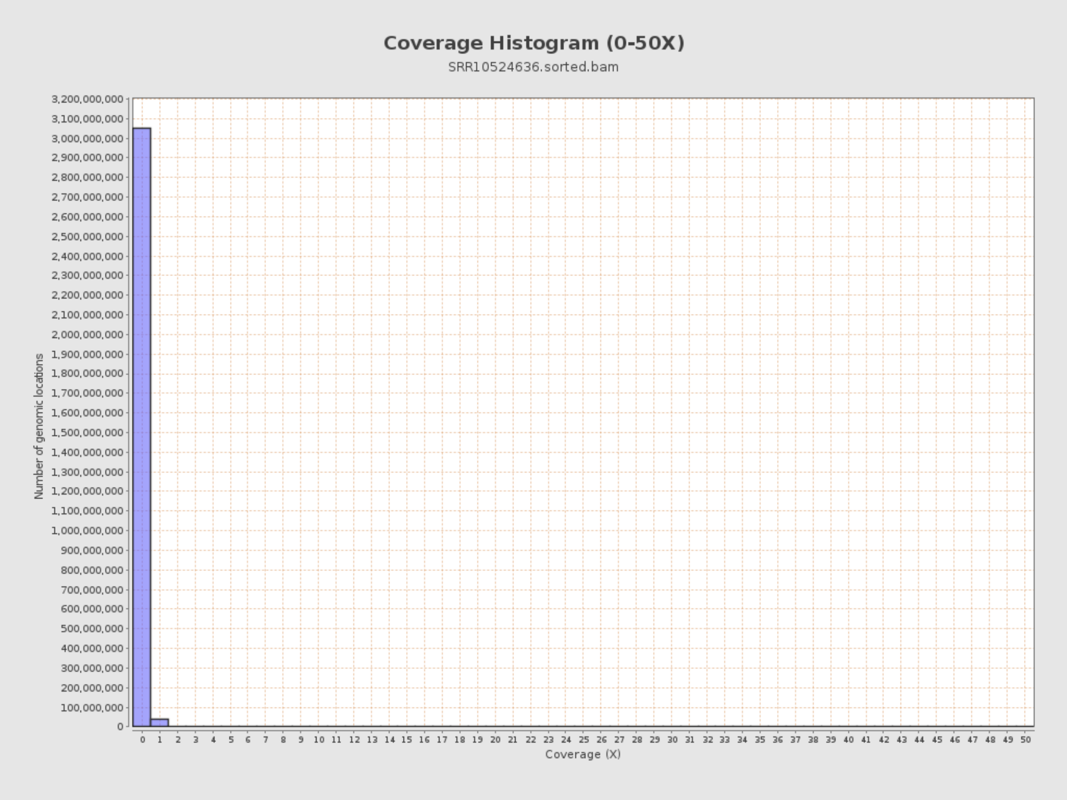
3. Results : Coverage across reference



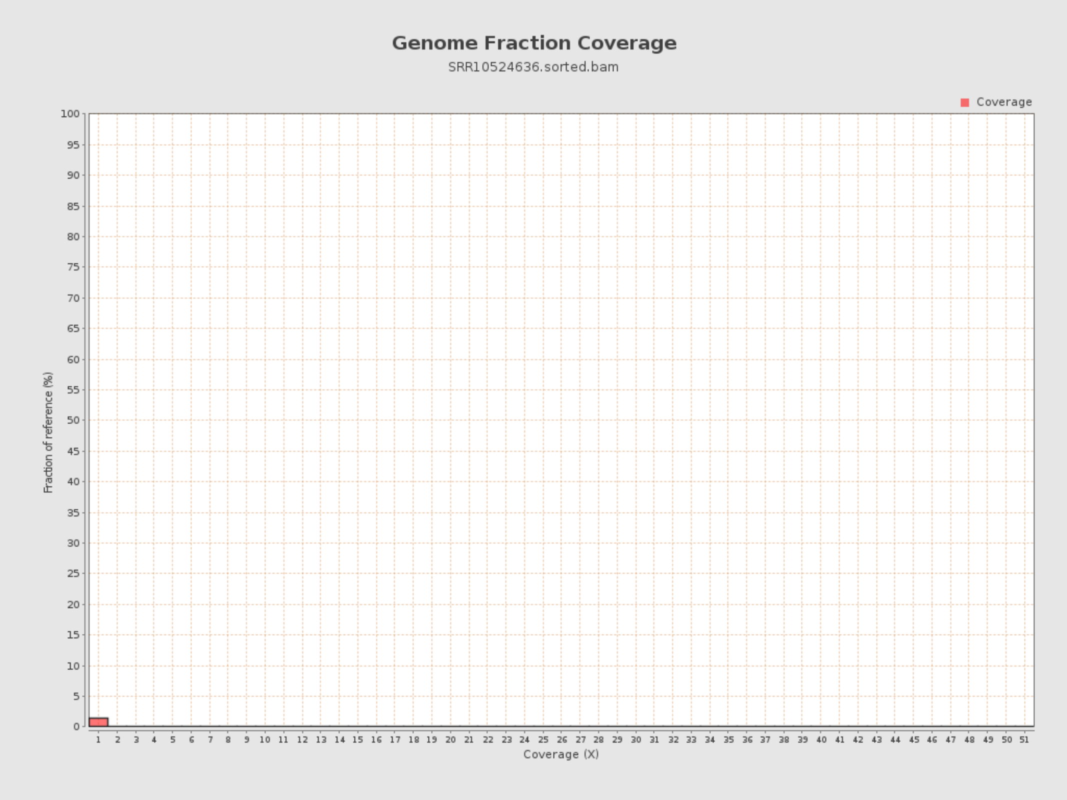
4. Results : Coverage Histogram



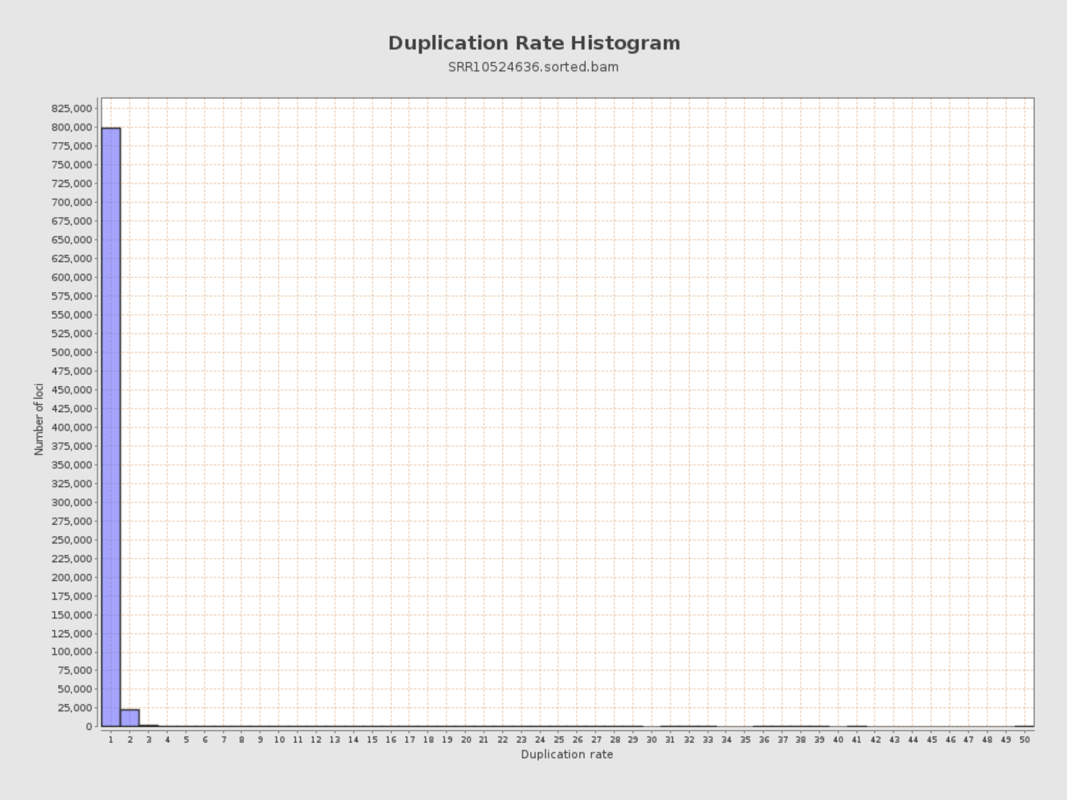
5. Results : Coverage Histogram (0-50X)



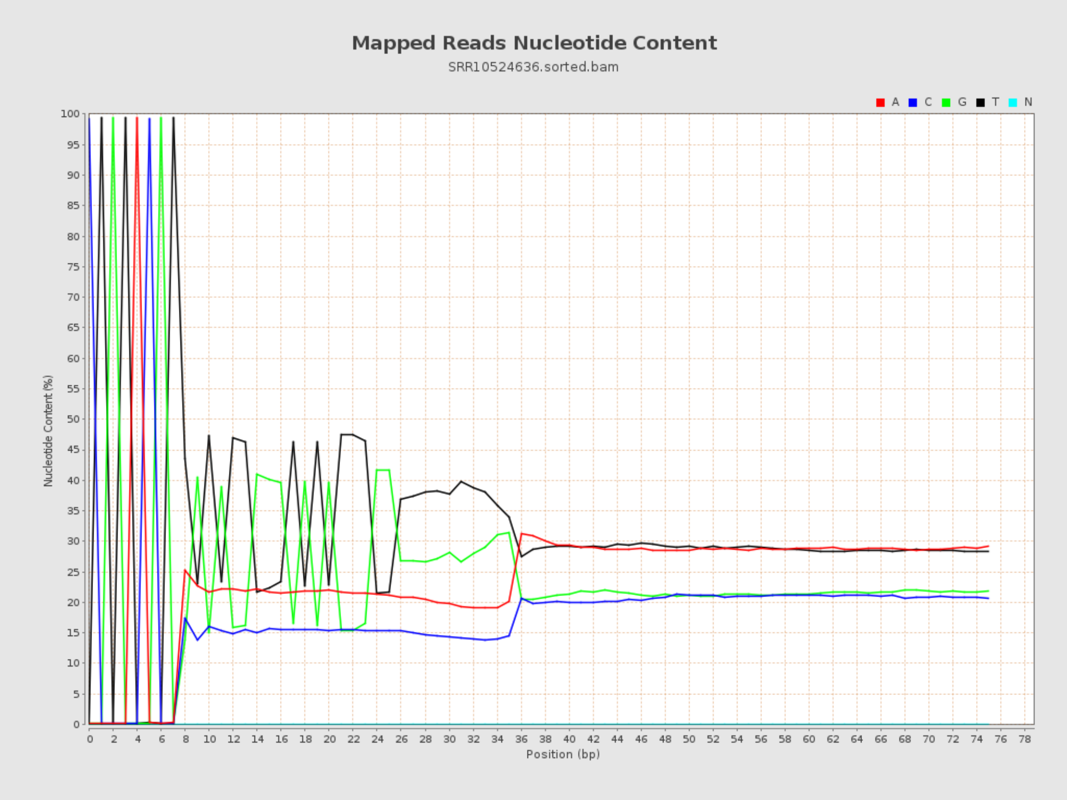
6. Results : Genome Fraction Coverage



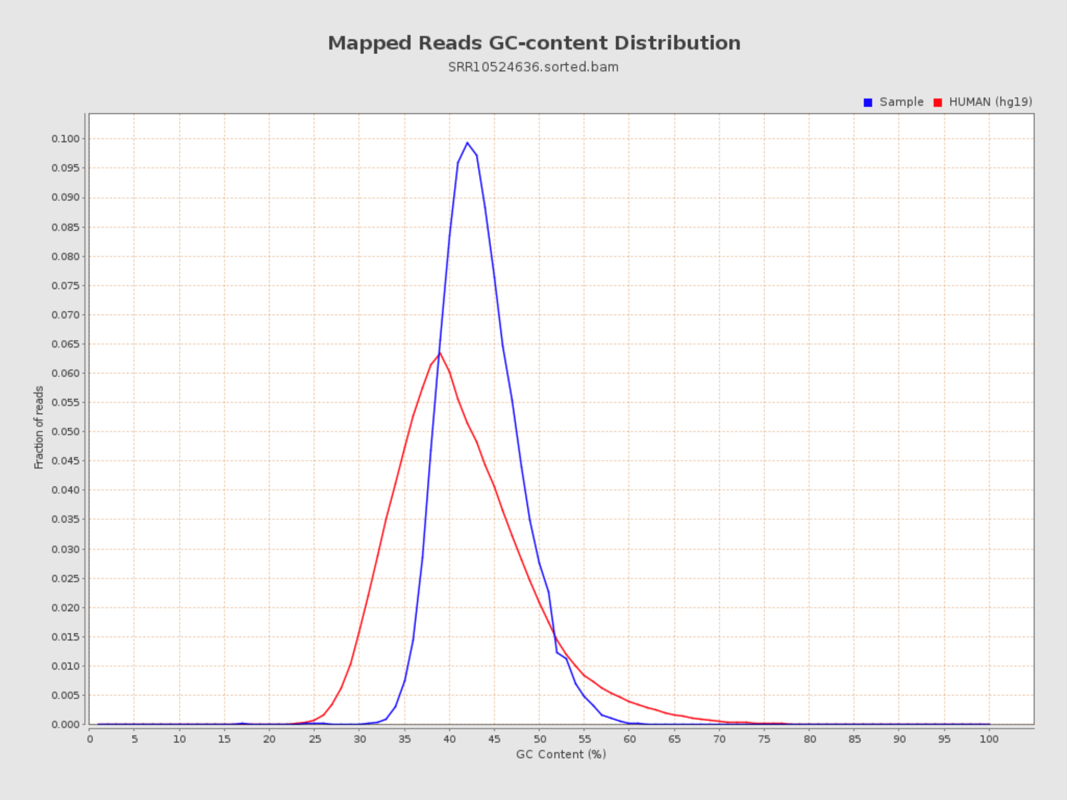
7. Results : Duplication Rate Histogram



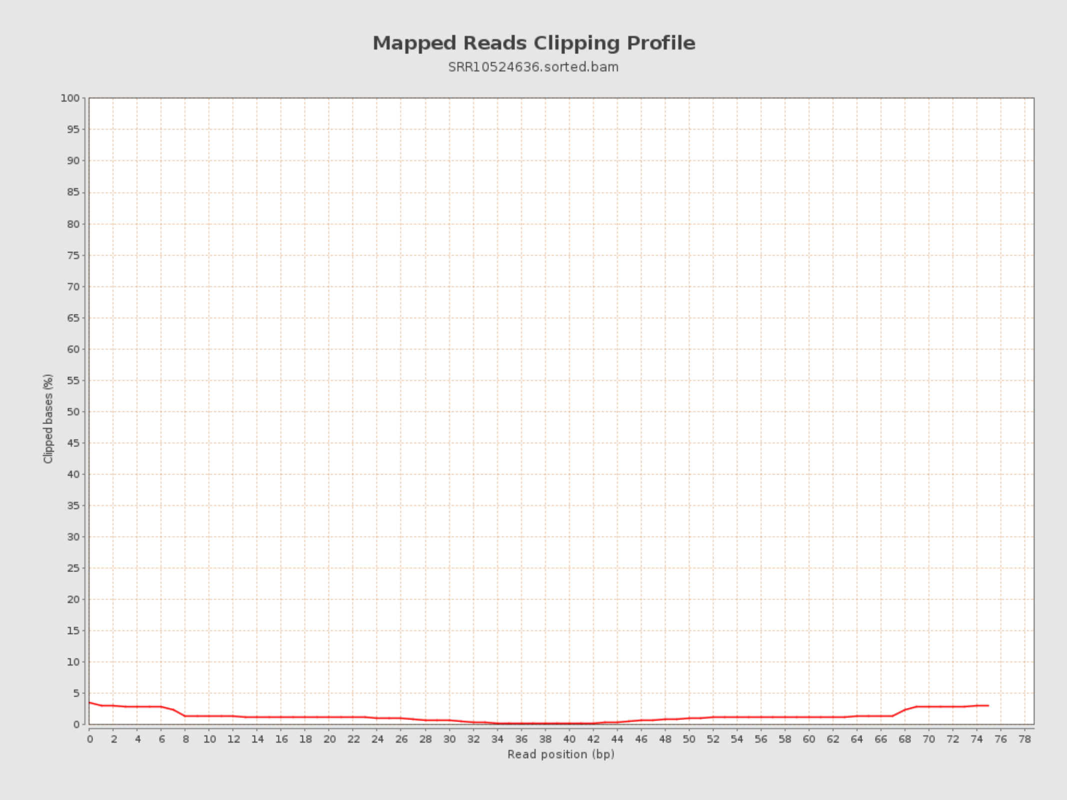
8. Results : Mapped Reads Nucleotide Content



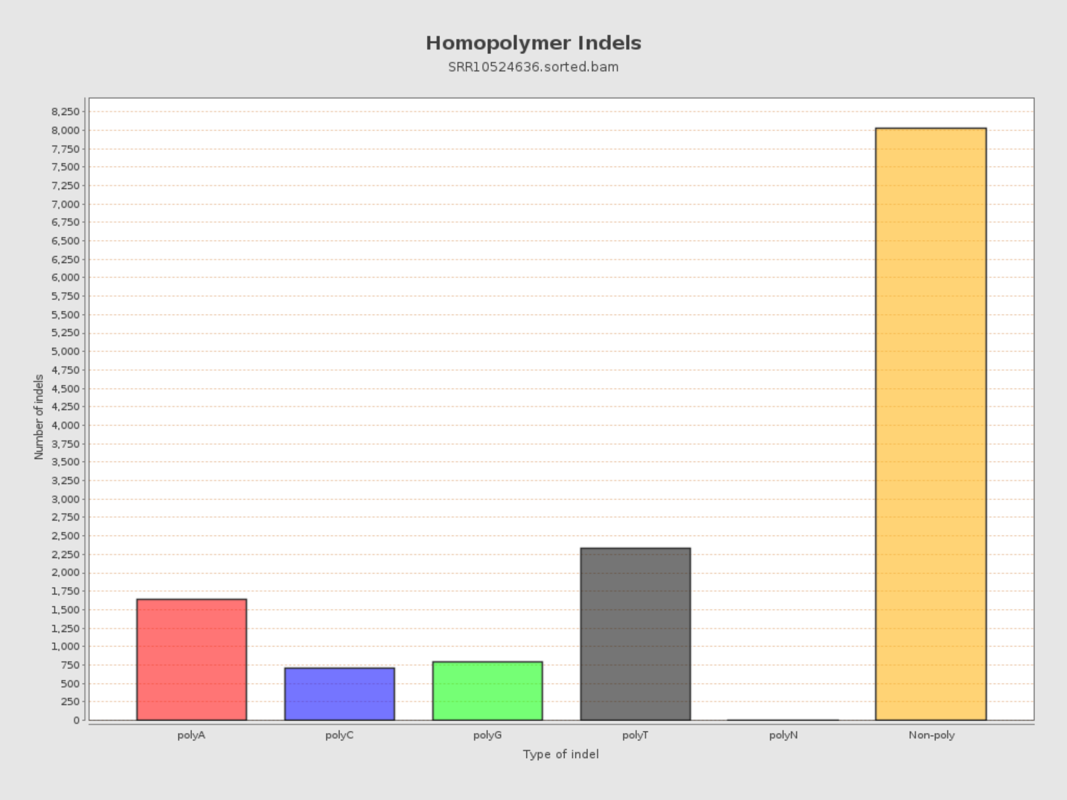
9. Results : Mapped Reads GC-content Distribution



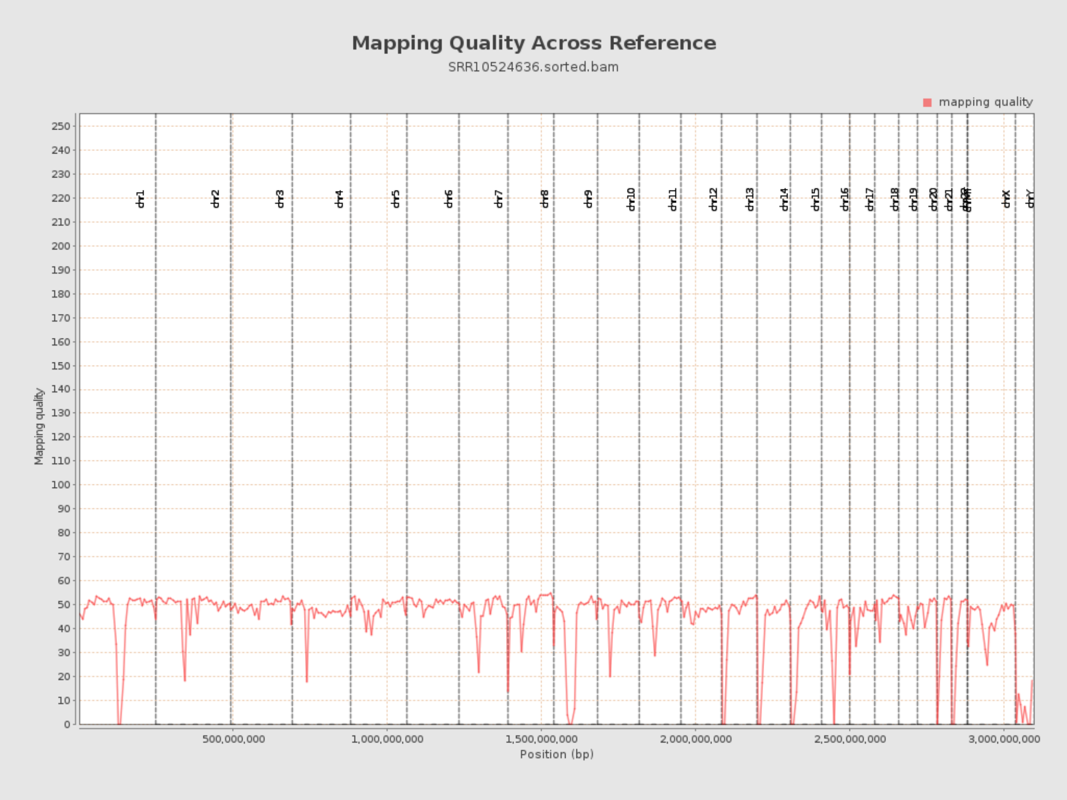
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram