Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 21:54:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524304.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_SRR10524304 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524304.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 21:54:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524304.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	997,411
Mapped reads	905,469 / 90.78%
Unmapped reads	91,942 / 9.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,241 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	21,541 / 2.16%
Duplication rate	1.63%
Clipped reads	906,084 / 90.84%

2.2. ACGT Content

Number/percentage of A's	13,461,295 / 25.77%
Number/percentage of C's	9,781,434 / 18.72%
Number/percentage of T's	15,973,803 / 30.57%
Number/percentage of G's	13,021,588 / 24.92%
Number/percentage of N's	6,865 / 0.01%
GC Percentage	43.65%

2.3. Coverage

Mean	0.0169

Standard Deviation	0.1837

2.4. Mapping Quality

Mean Mapping Quality	43.56

2.5. Mismatches and indels

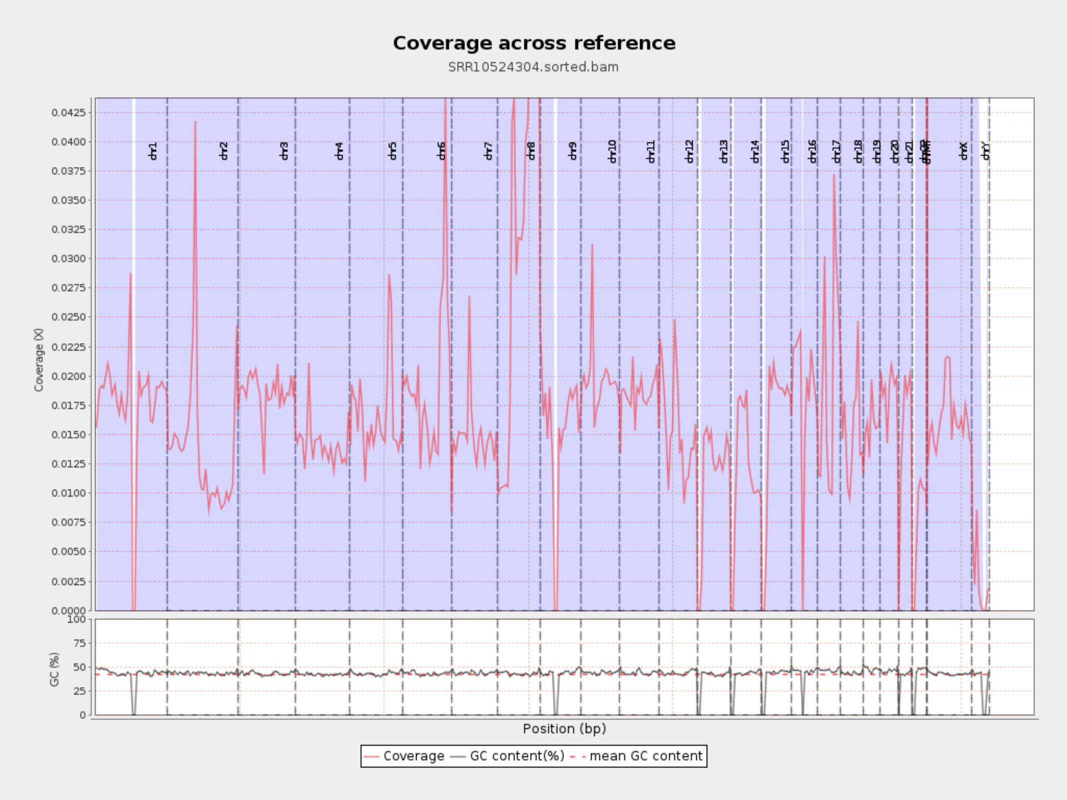
General error rate	0.54%
Mismatches	273,462
Insertions	3,906
Mapped reads with at least one insertion	0.43%
Deletions	9,020
Mapped reads with at least one deletion	0.99%
Homopolymer indels	40.98%

2.6. Chromosome stats

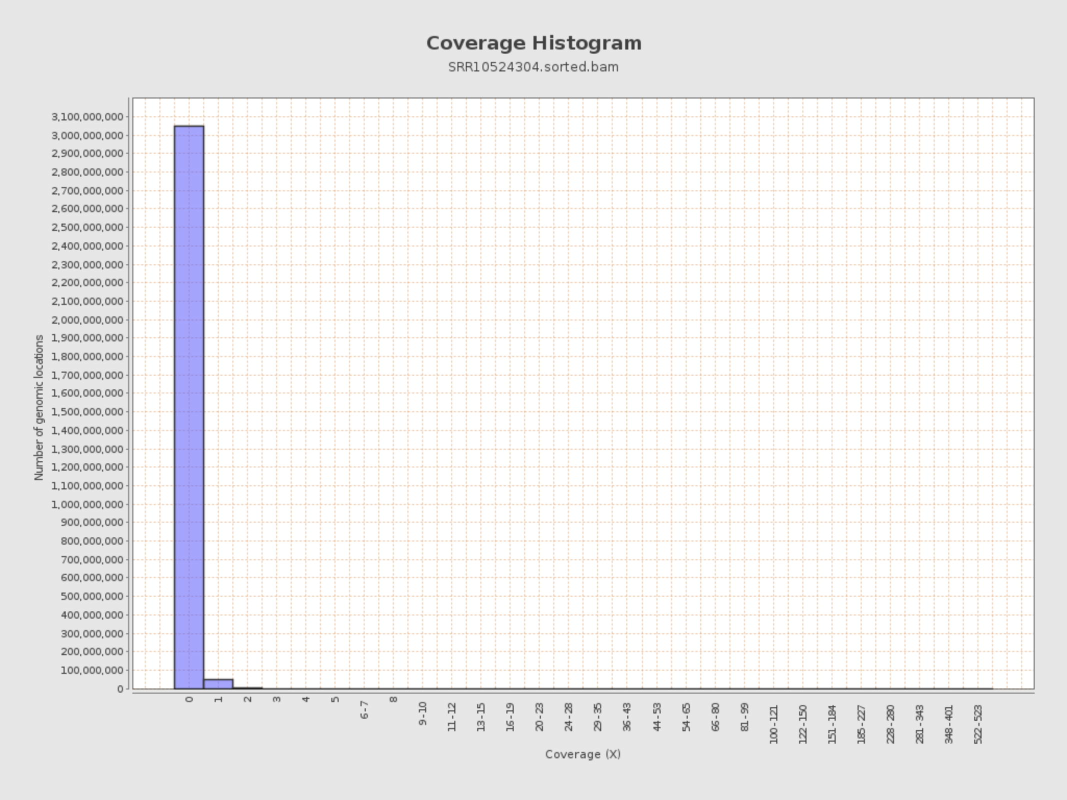
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4369317	0.0175	0.3063
chr2	243199373	3367395	0.0138	0.244
chr3	198022430	3673607	0.0186	0.1431
chr4	191154276	2706837	0.0142	0.1337
chr5	180915260	3035586	0.0168	0.1363
chr6	171115067	3306095	0.0193	0.1543
chr7	159138663	2389359	0.015	0.2149

chr8	146364022	5347421	0.0365	0.2331
chr9	141213431	2142670	0.0152	0.1517
chr10	135534747	2682905	0.0198	0.1785
chr11	135006516	2509220	0.0186	0.165
chr12	133851895	2079362	0.0155	0.1329
chr13	115169878	1313406	0.0114	0.1121
chr14	107349540	1265195	0.0118	0.1179
chr15	102531392	1594255	0.0155	0.133
chr16	90354753	1667765	0.0185	0.1472
chr17	81195210	1648635	0.0203	0.1585
chr18	78077248	1214347	0.0156	0.2433
chr19	59128983	933875	0.0158	0.2239
chr20	63025520	1175478	0.0187	0.1449
chr21	48129895	754204	0.0157	0.1368
chr22	51304566	383930	0.0075	0.0909
chrMT	16571	1413	0.0853	0.2981
chrX	155270560	2550746	0.0164	0.146
chrY	59373566	146297	0.0025	0.0757

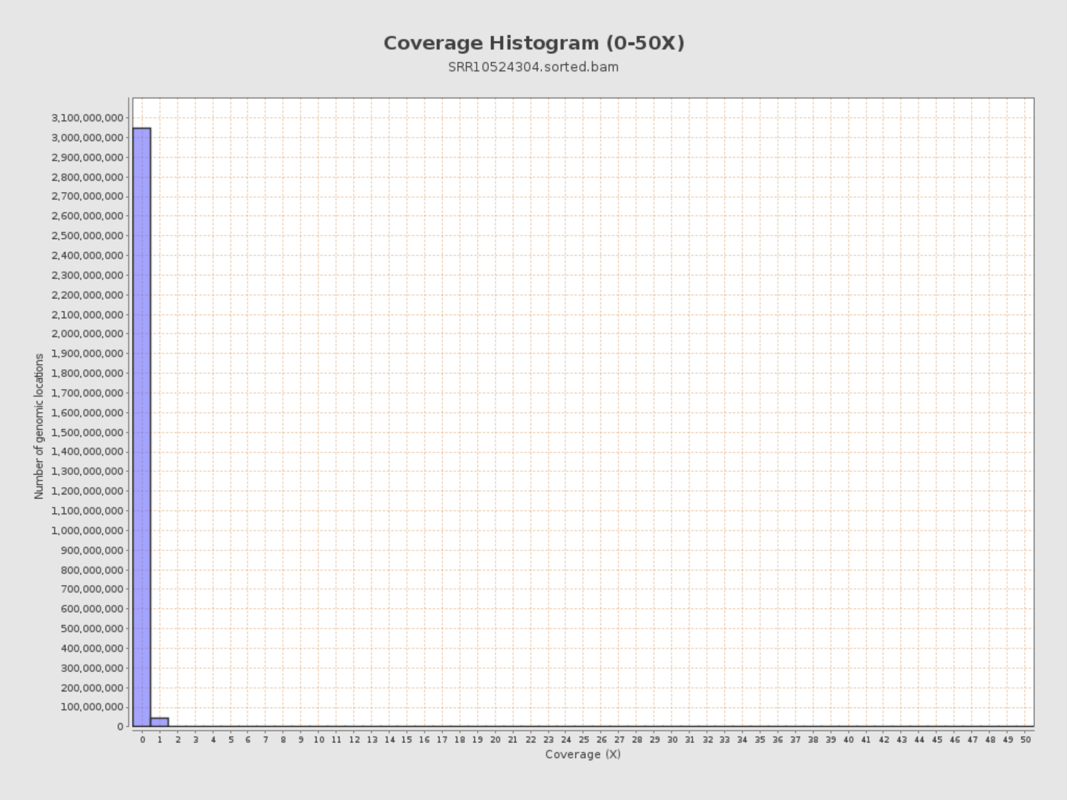
3. Results : Coverage across reference



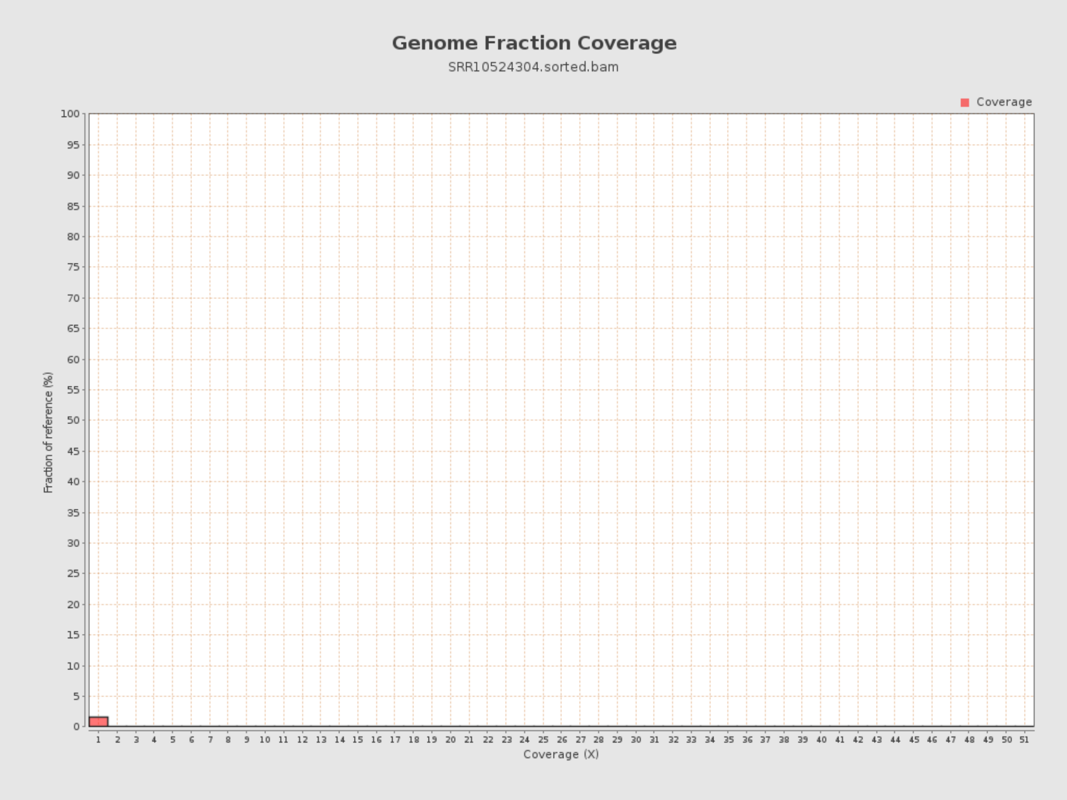
4. Results : Coverage Histogram



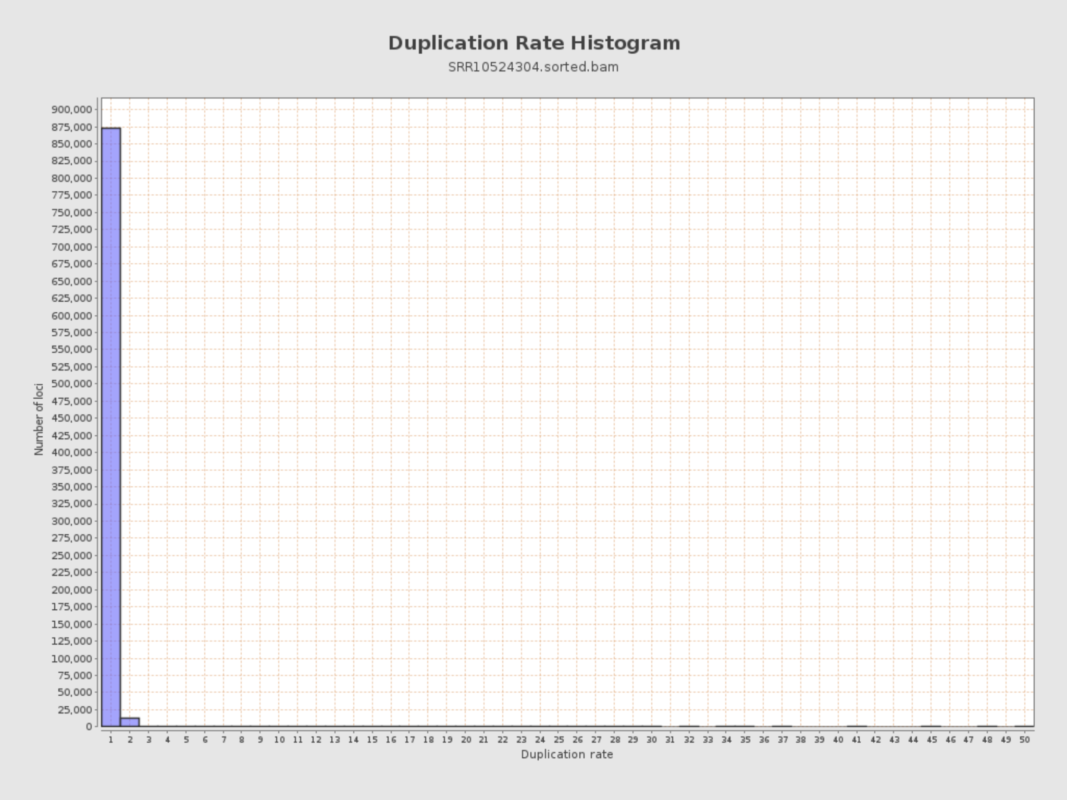
5. Results : Coverage Histogram (0-50X)



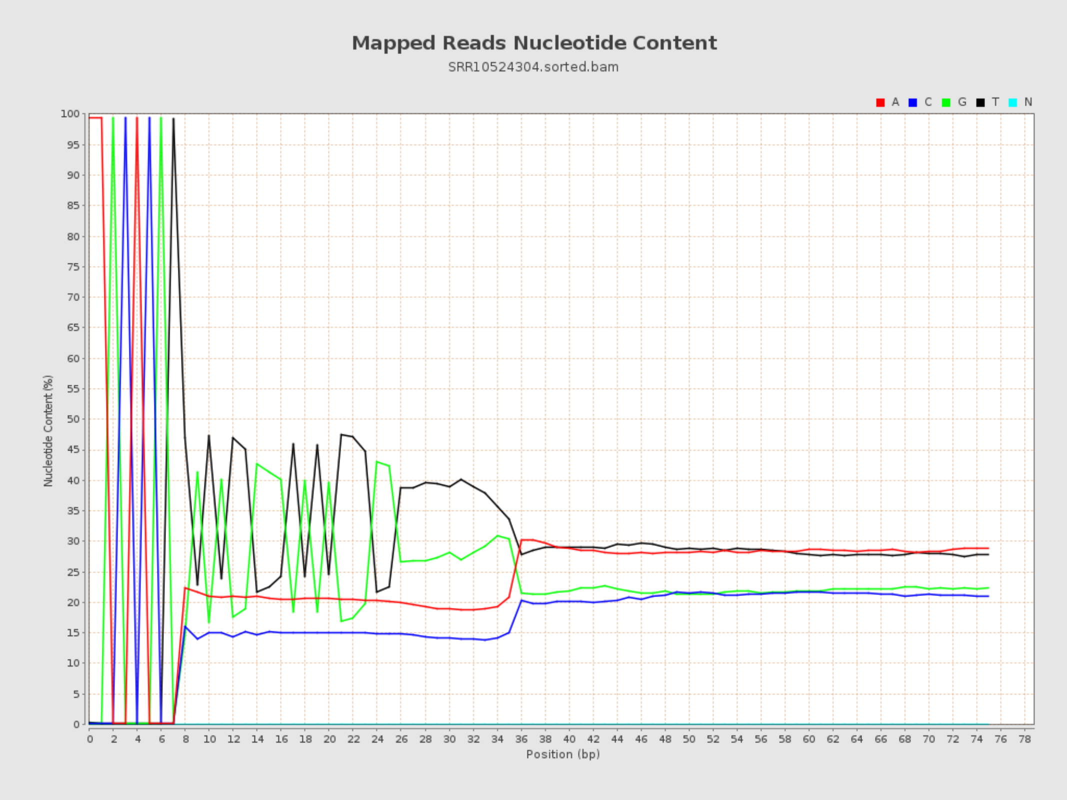
6. Results : Genome Fraction Coverage



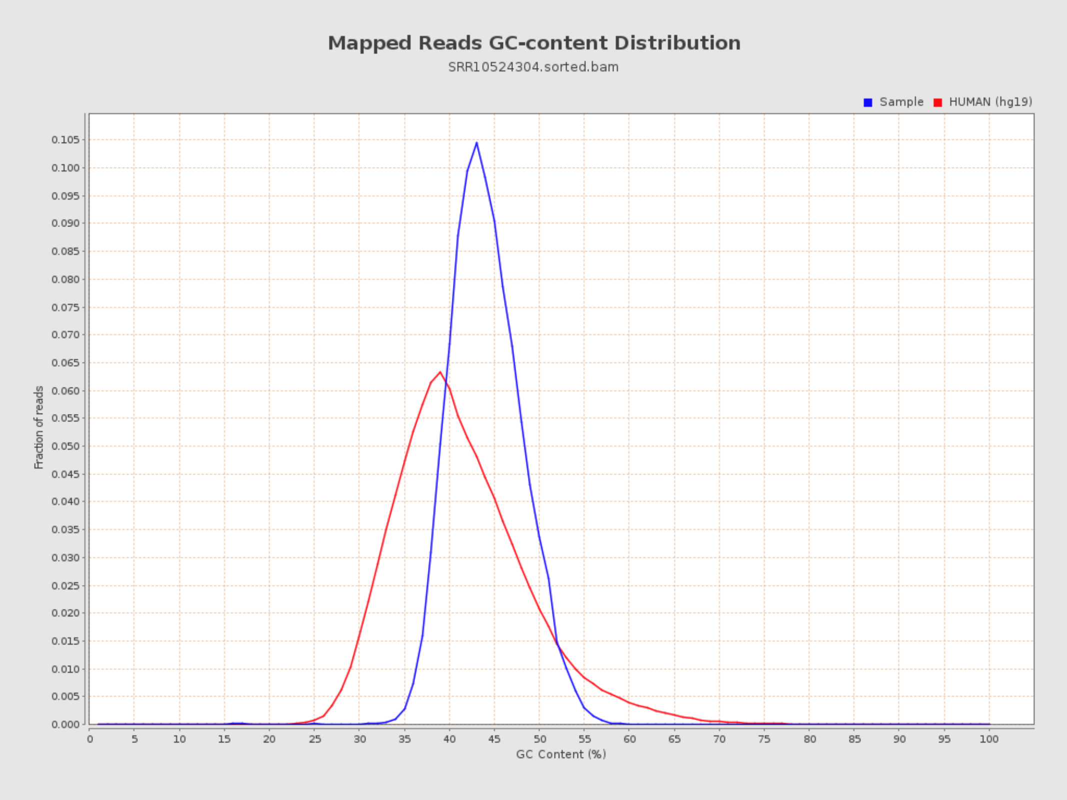
7. Results : Duplication Rate Histogram



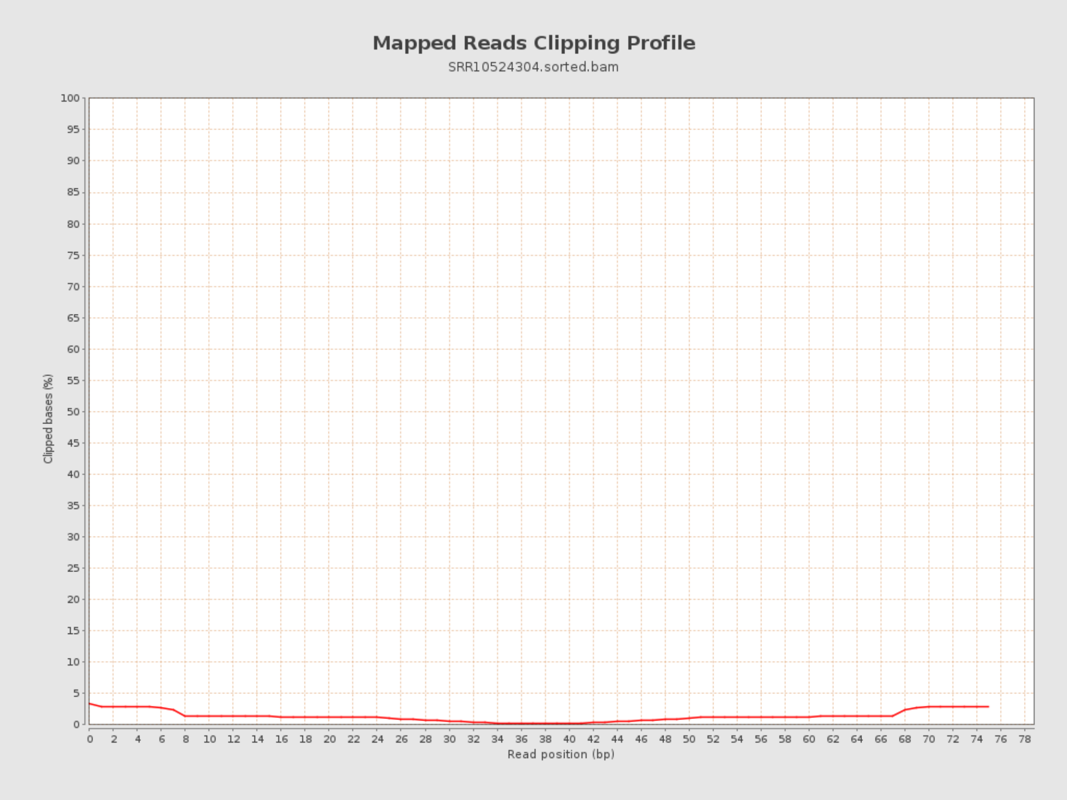
8. Results : Mapped Reads Nucleotide Content



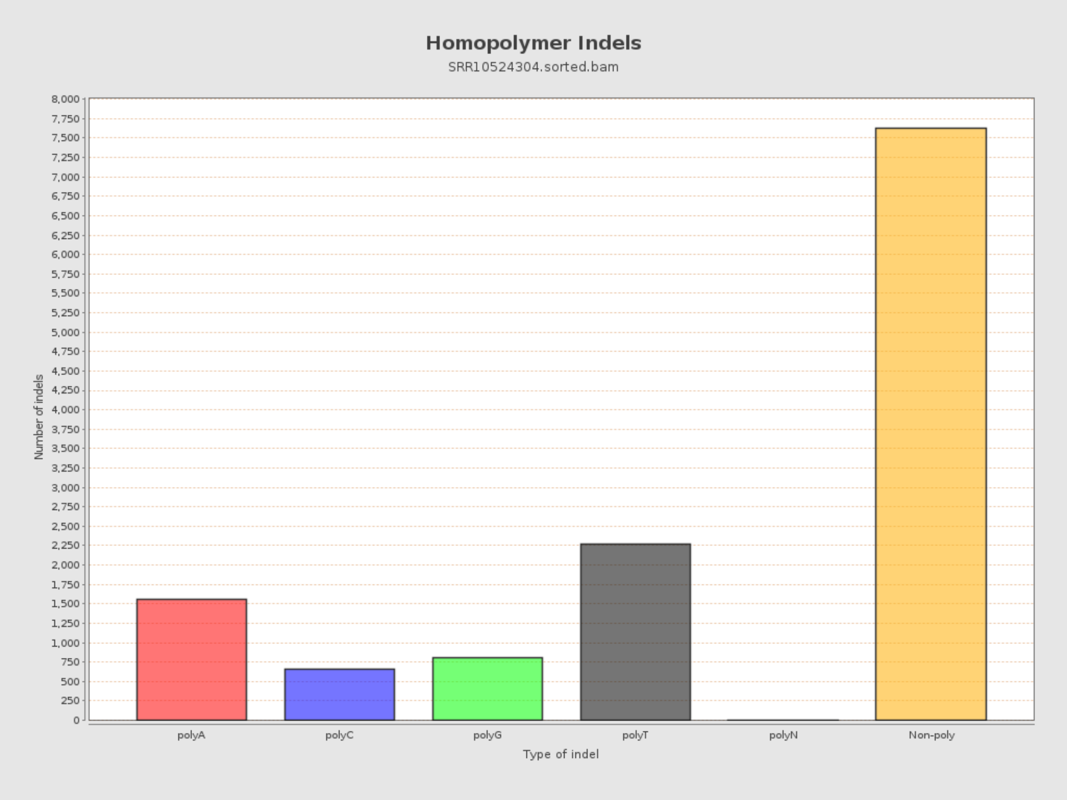
9. Results : Mapped Reads GC-content Distribution



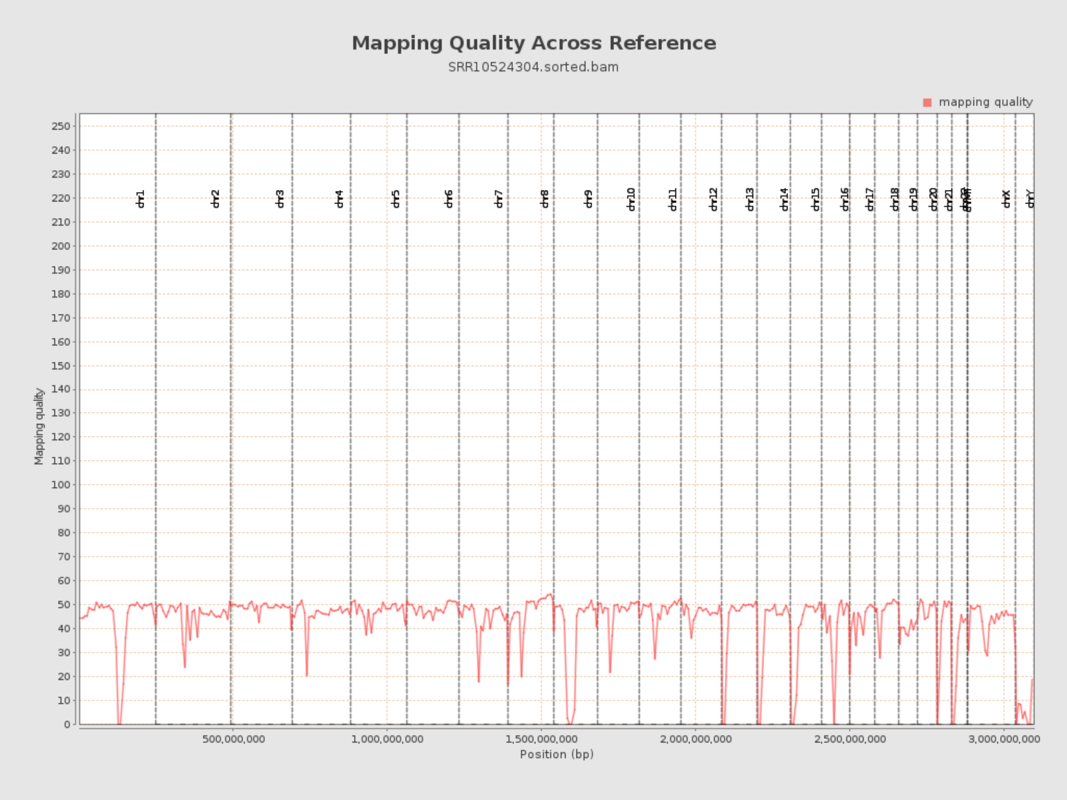
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram