Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 23:32:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524340.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_SRR10524340 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524340.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 23:32:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524340.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,851,865
Mapped reads	1,670,842 / 90.22%
Unmapped reads	181,023 / 9.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,691 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	56,477 / 3.05%
Duplication rate	2.31%
Clipped reads	1,674,381 / 90.42%

2.2. ACGT Content

Number/percentage of A's	23,807,043 / 25.02%
Number/percentage of C's	17,463,182 / 18.36%
Number/percentage of T's	30,990,677 / 32.58%
Number/percentage of G's	22,862,673 / 24.03%
Number/percentage of N's	12,397 / 0.01%
GC Percentage	42.39%

2.3. Coverage

Mean	0.0307

Standard Deviation	0.3027

2.4. Mapping Quality

Mean Mapping Quality	43.05

2.5. Mismatches and indels

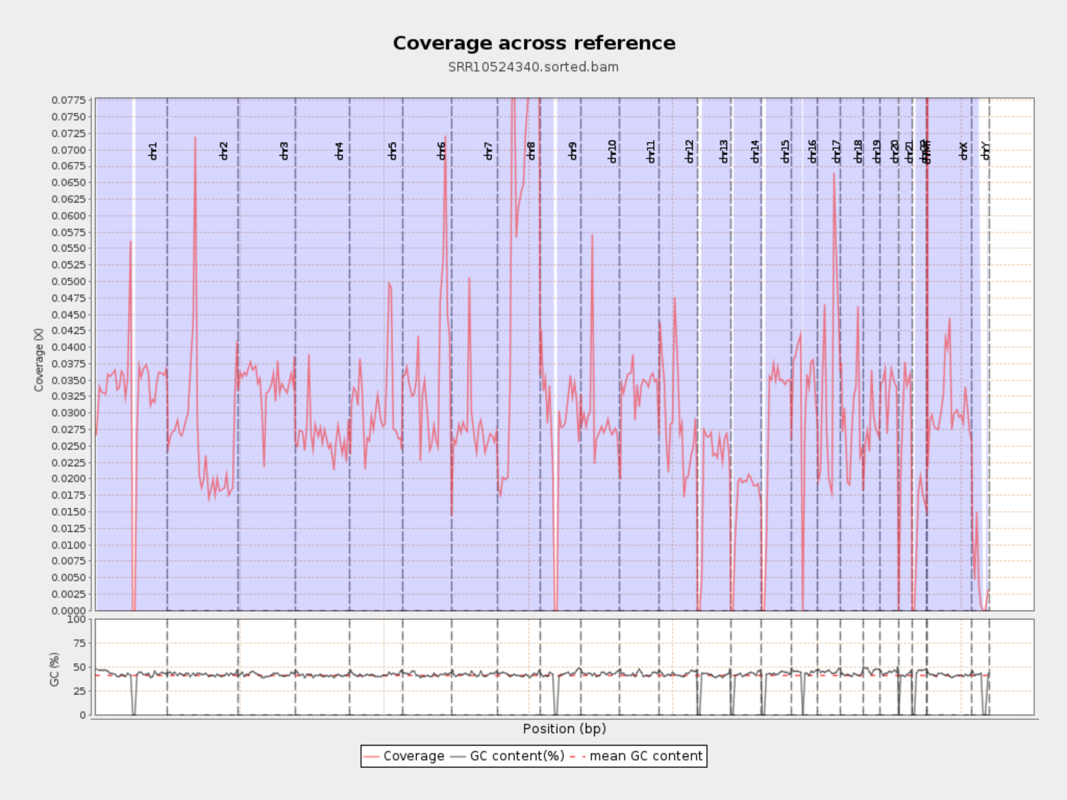
General error rate	0.53%
Mismatches	494,959
Insertions	7,092
Mapped reads with at least one insertion	0.42%
Deletions	15,704
Mapped reads with at least one deletion	0.93%
Homopolymer indels	41.42%

2.6. Chromosome stats

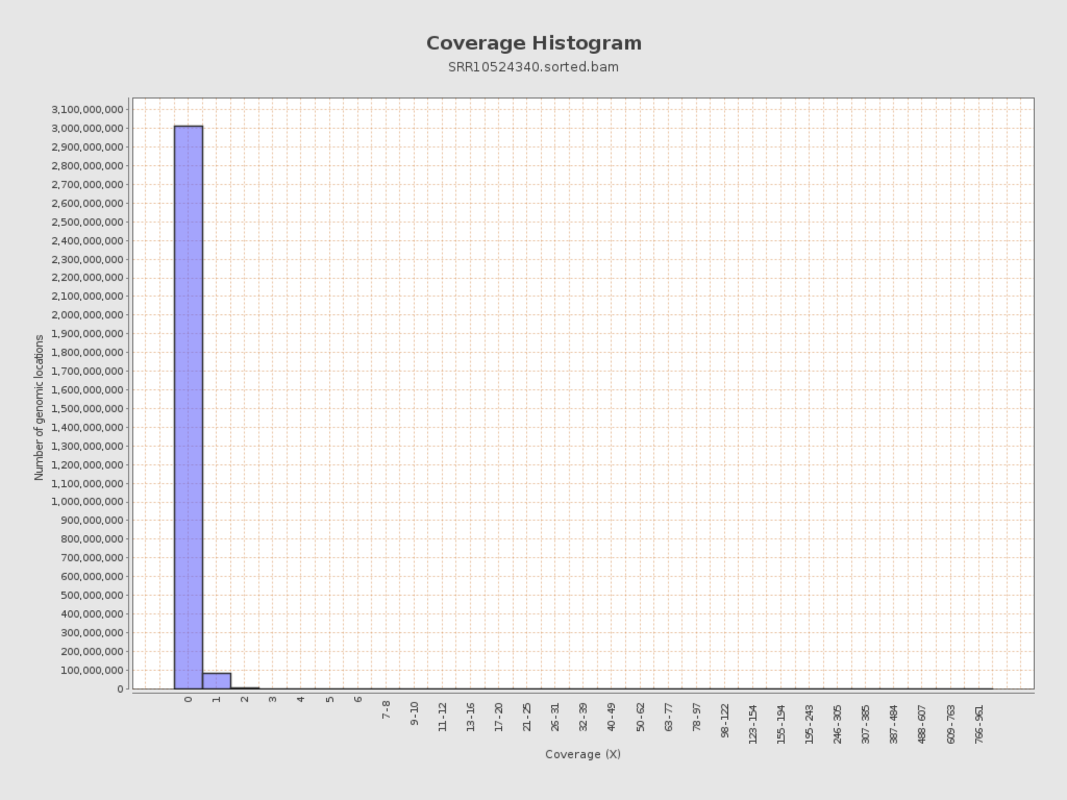
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8192969	0.0329	0.5737
chr2	243199373	6303120	0.0259	0.4231
chr3	198022430	6812708	0.0344	0.2024
chr4	191154276	5058418	0.0265	0.1936
chr5	180915260	5674094	0.0314	0.1946
chr6	171115067	6104972	0.0357	0.2256
chr7	159138663	4428343	0.0278	0.3932

chr8	146364022	10104836	0.069	0.369
chr9	141213431	3965974	0.0281	0.2333
chr10	135534747	3943351	0.0291	0.2861
chr11	135006516	4612716	0.0342	0.2386
chr12	133851895	3889316	0.0291	0.1898
chr13	115169878	2432720	0.0211	0.1597
chr14	107349540	1751734	0.0163	0.154
chr15	102531392	2918518	0.0285	0.1946
chr16	90354753	2944768	0.0326	0.2122
chr17	81195210	2890795	0.0356	0.2302
chr18	78077248	2263550	0.029	0.3783
chr19	59128983	1642543	0.0278	0.3847
chr20	63025520	2105920	0.0334	0.2031
chr21	48129895	1365582	0.0284	0.1957
chr22	51304566	654034	0.0127	0.1224
chrMT	16571	7994	0.4824	0.7955
chrX	155270560	4823712	0.0311	0.2199
chrY	59373566	268092	0.0045	0.1106

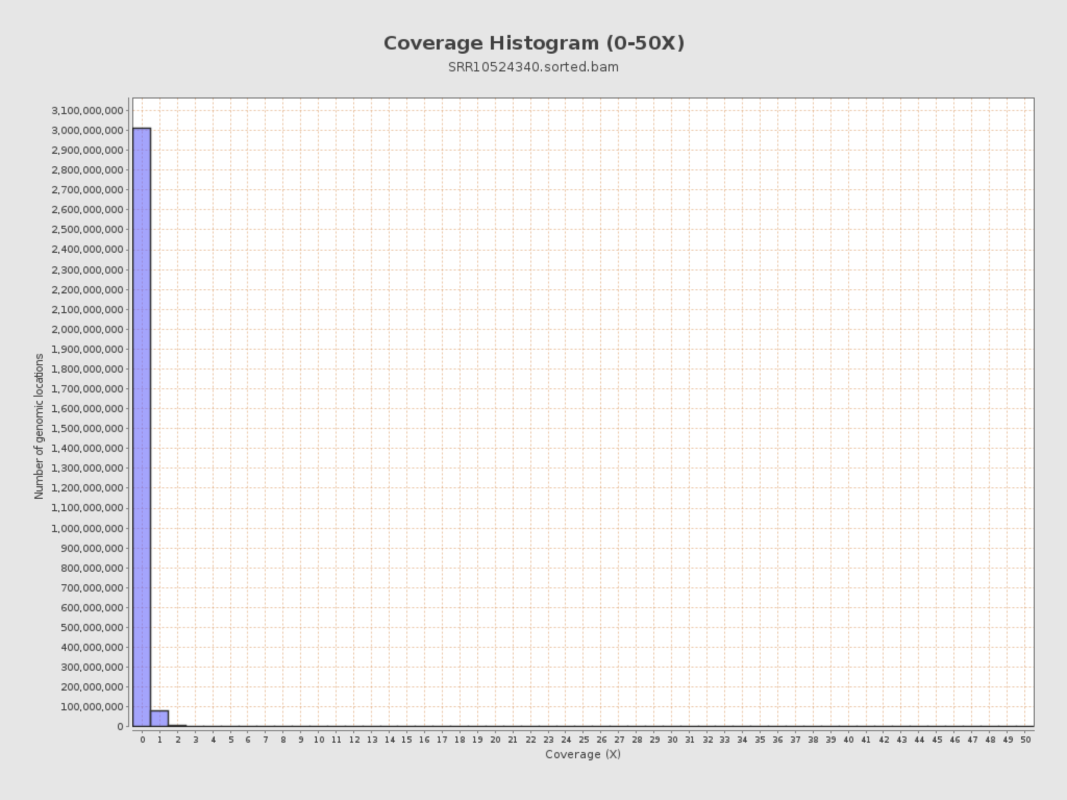
3. Results : Coverage across reference



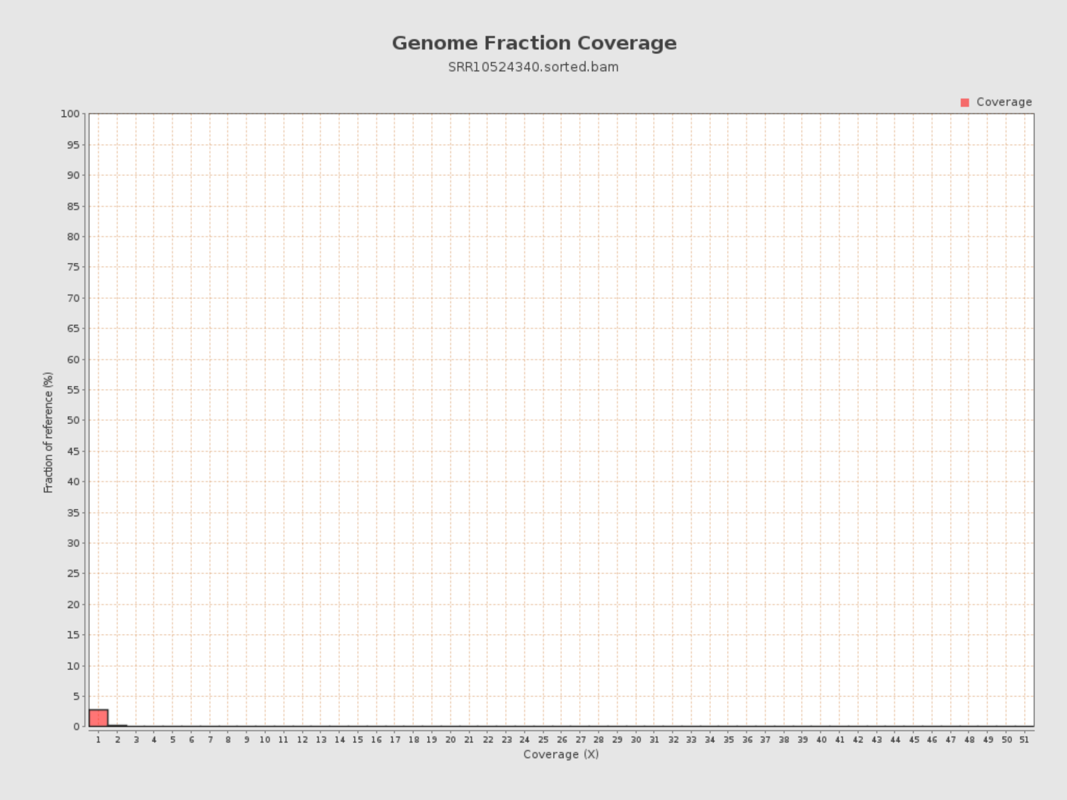
4. Results : Coverage Histogram



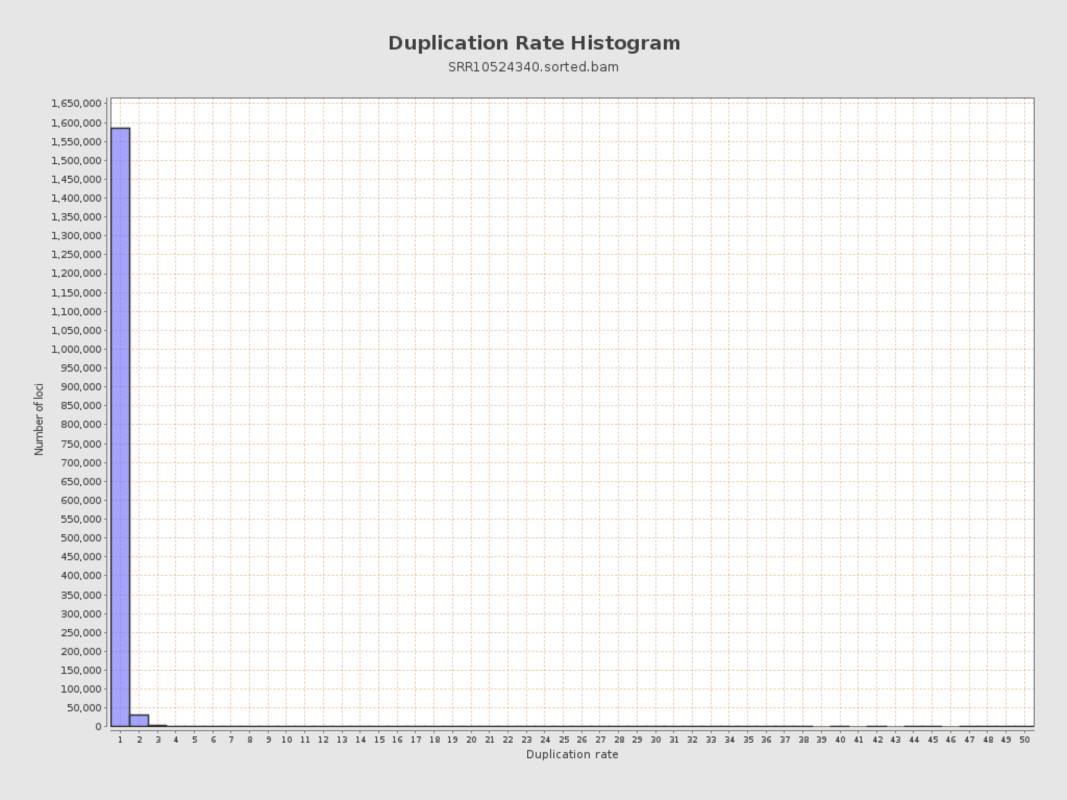
5. Results : Coverage Histogram (0-50X)



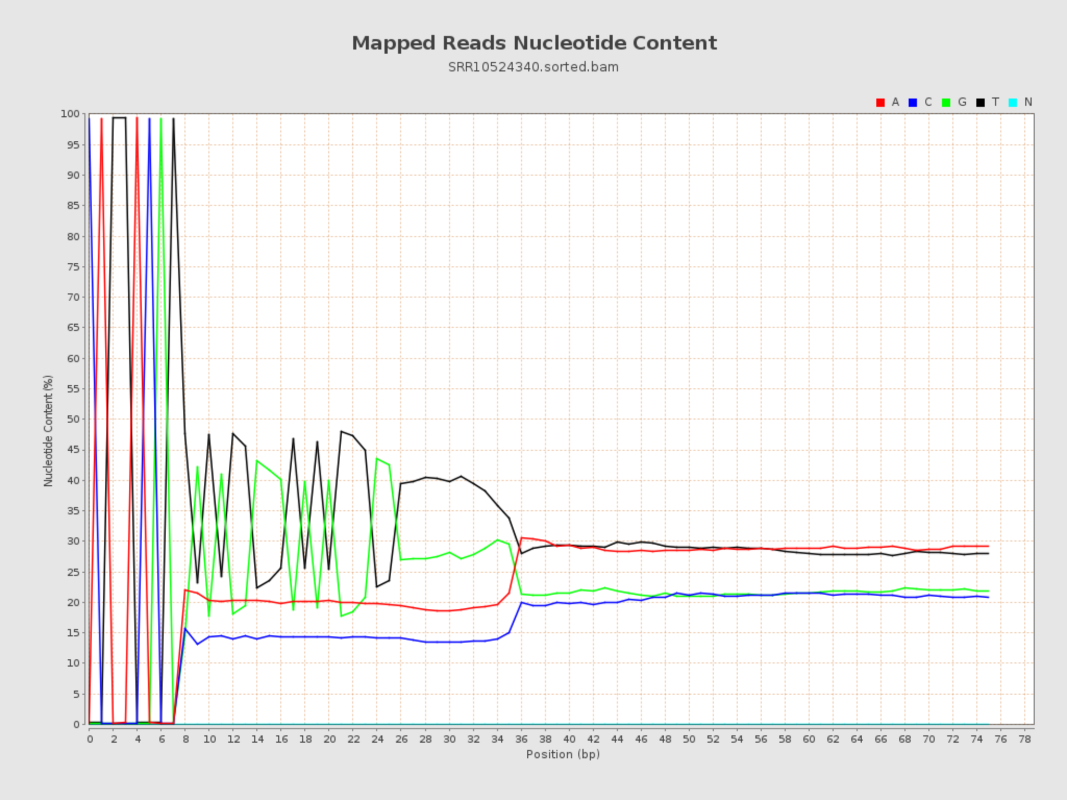
6. Results : Genome Fraction Coverage



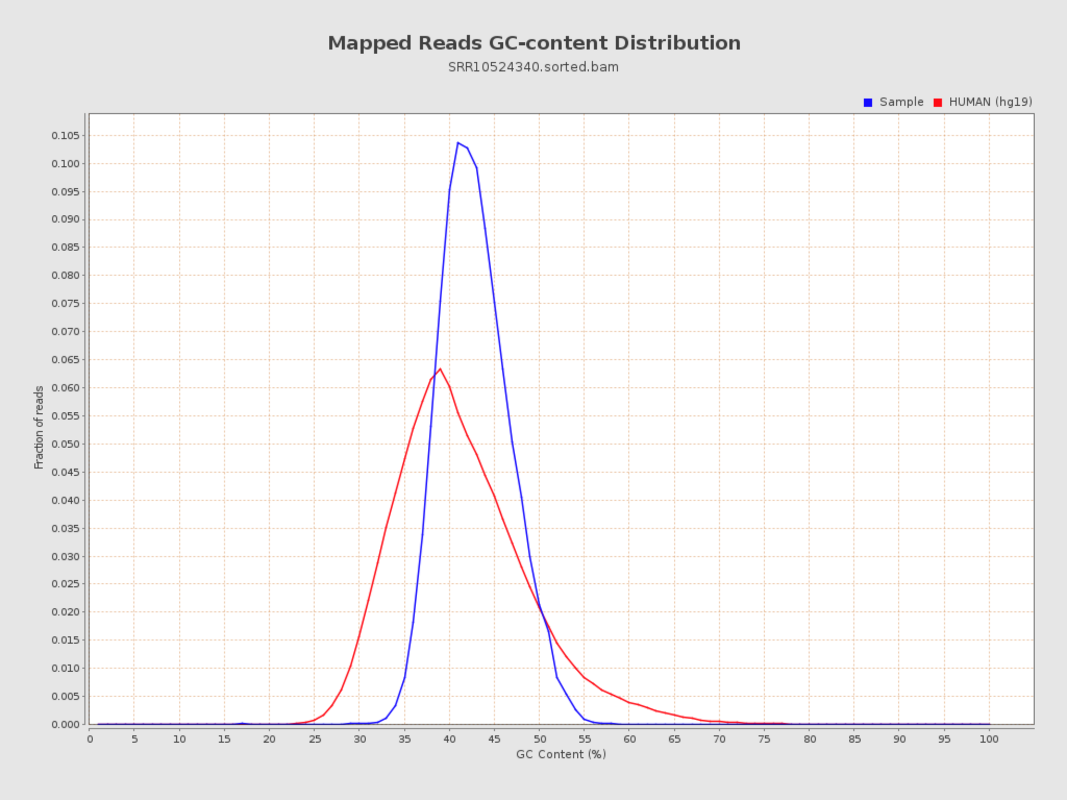
7. Results : Duplication Rate Histogram



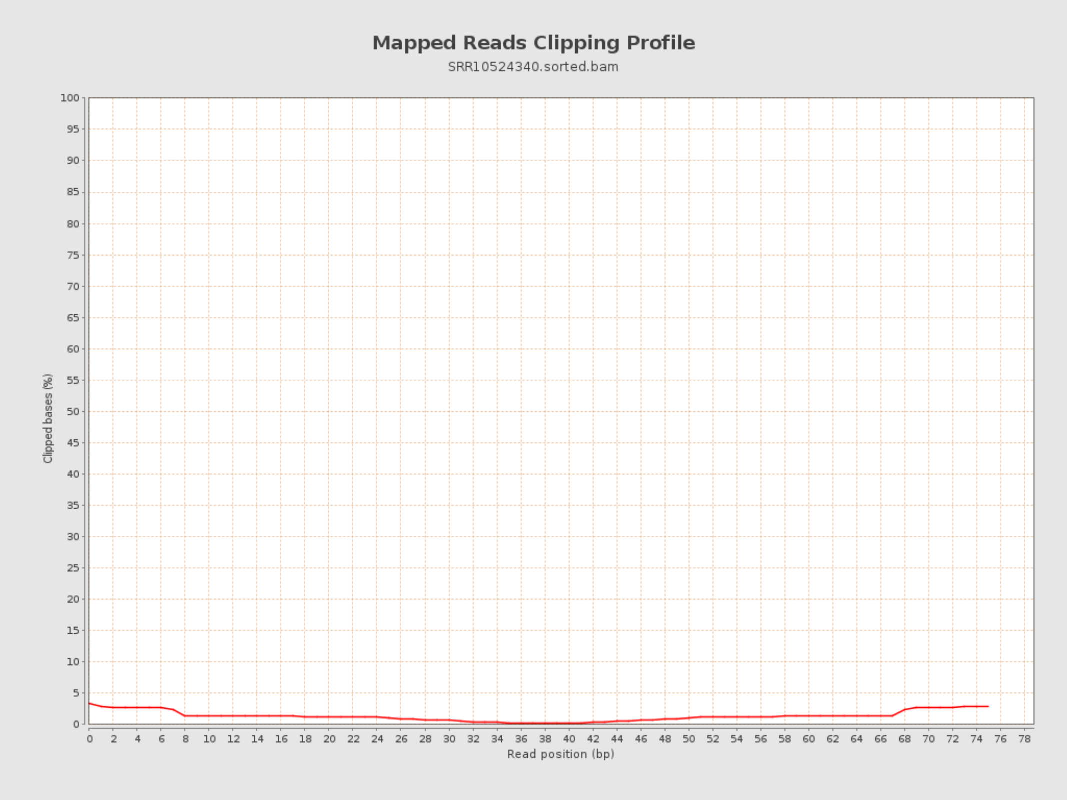
8. Results : Mapped Reads Nucleotide Content



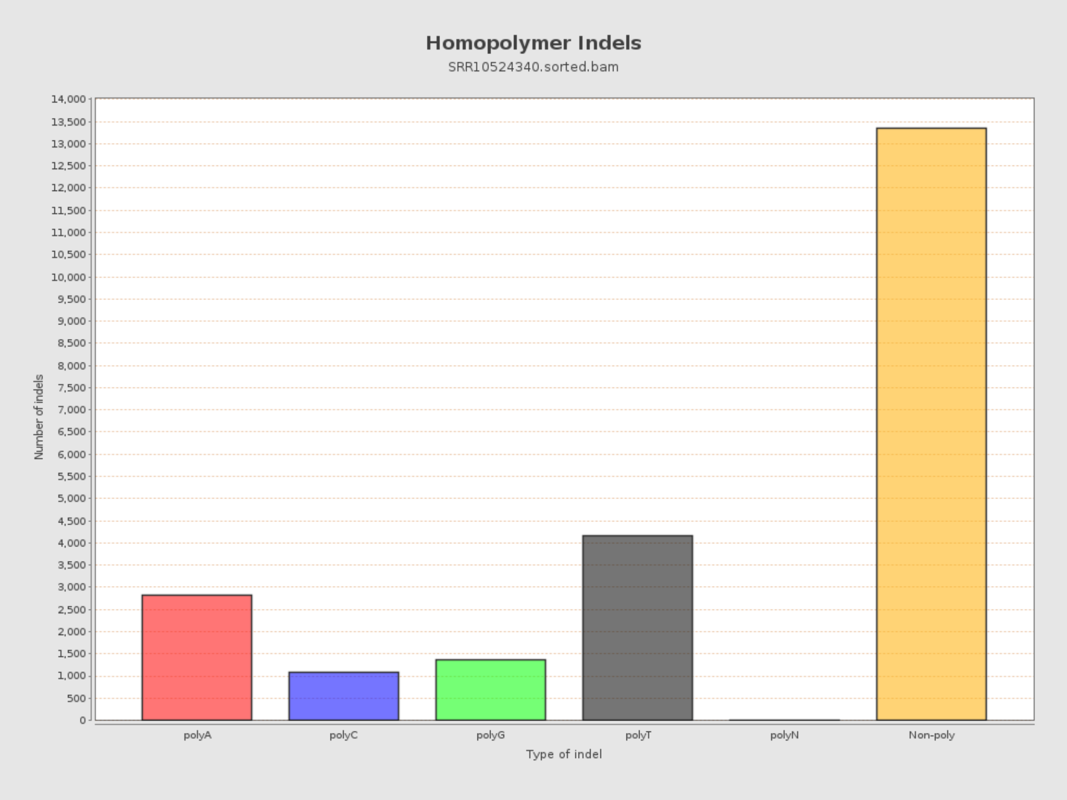
9. Results : Mapped Reads GC-content Distribution



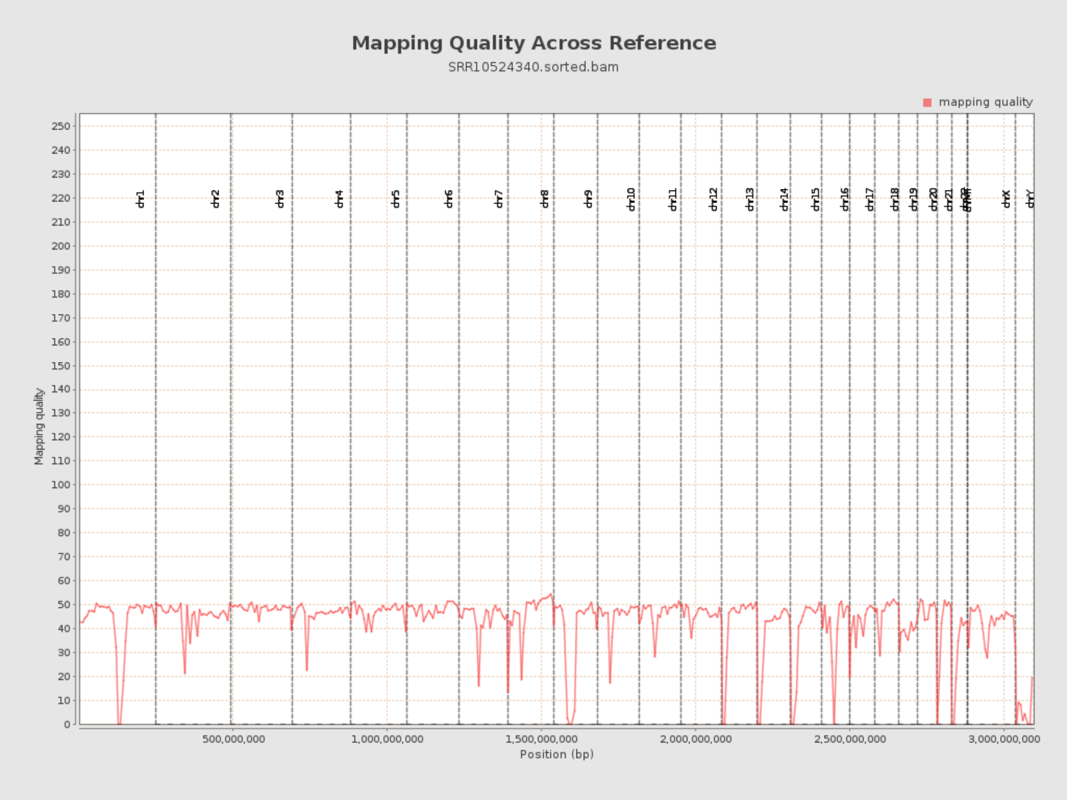
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram