Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 16:17:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524682.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_SRR10524682 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524682.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 16:17:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524682.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,254,908
Mapped reads	2,091,475 / 92.75%
Unmapped reads	163,433 / 7.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,523 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	98,609 / 4.37%
Duplication rate	3.5%
Clipped reads	2,094,854 / 92.9%

2.2. ACGT Content

Number/percentage of A's	32,164,685 / 26.03%
Number/percentage of C's	24,178,367 / 19.56%
Number/percentage of T's	38,531,132 / 31.18%
Number/percentage of G's	28,694,538 / 23.22%
Number/percentage of N's	17,006 / 0.01%
GC Percentage	42.78%

2.3. Coverage

Mean	0.0399

Standard Deviation	0.3509

2.4. Mapping Quality

Mean Mapping Quality	45.74

2.5. Mismatches and indels

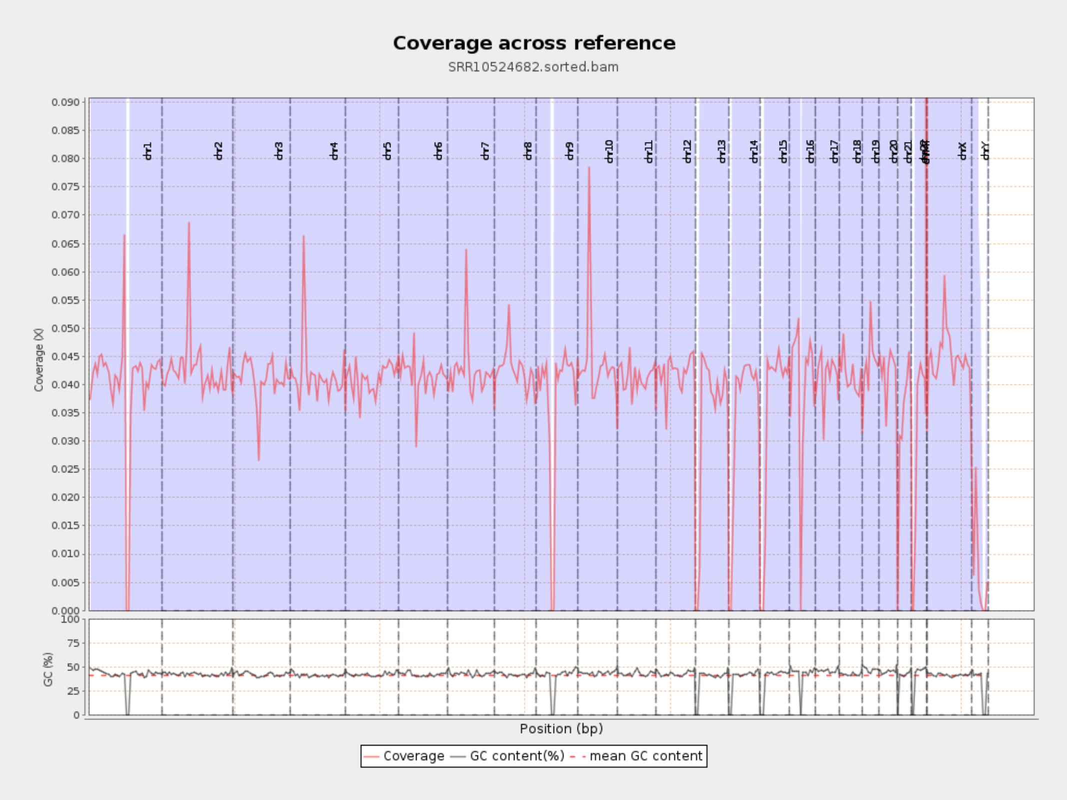
General error rate	0.51%
Mismatches	613,149
Insertions	8,647
Mapped reads with at least one insertion	0.41%
Deletions	23,493
Mapped reads with at least one deletion	1.11%
Homopolymer indels	43.34%

2.6. Chromosome stats

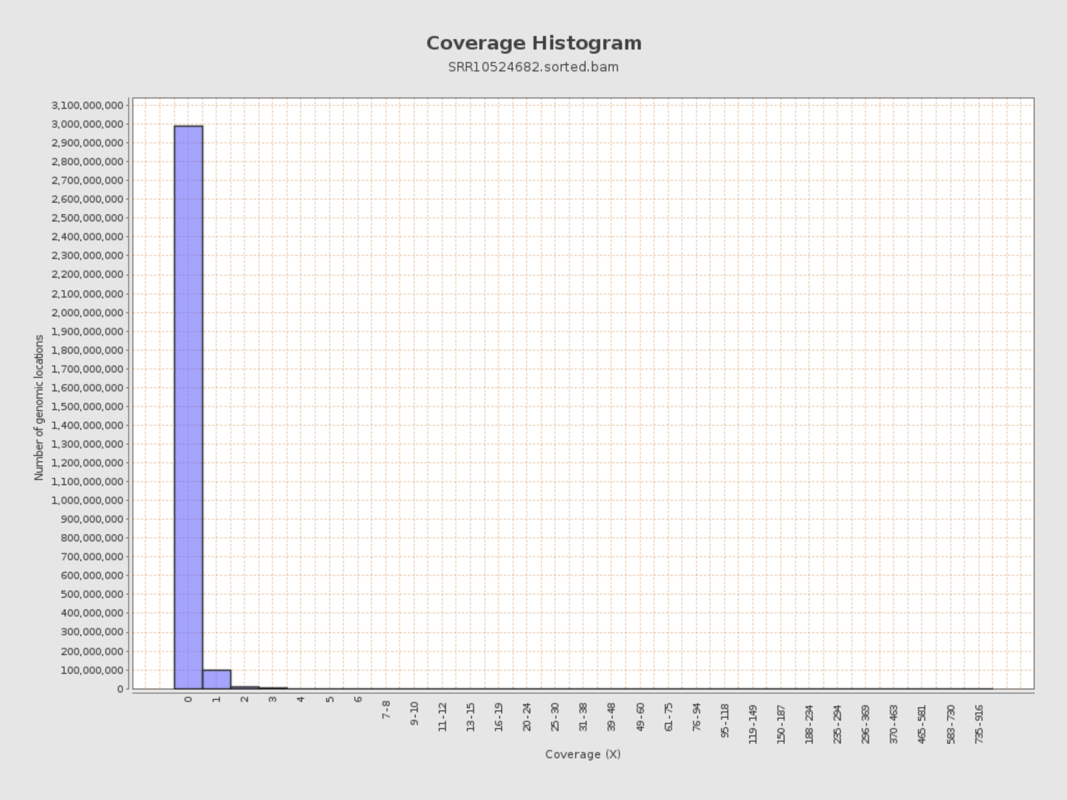
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9952285	0.0399	0.6177
chr2	243199373	10452194	0.043	0.4802
chr3	198022430	8127672	0.041	0.2265
chr4	191154276	7947431	0.0416	0.2688
chr5	180915260	7426387	0.041	0.227
chr6	171115067	7127344	0.0417	0.2582
chr7	159138663	6778809	0.0426	0.4126

chr8	146364022	6248886	0.0427	0.3938
chr9	141213431	5235059	0.0371	0.294
chr10	135534747	5955342	0.0439	0.3713
chr11	135006516	5561520	0.0412	0.3038
chr12	133851895	5647063	0.0422	0.2314
chr13	115169878	3896764	0.0338	0.2049
chr14	107349540	3700906	0.0345	0.2174
chr15	102531392	3568006	0.0348	0.2104
chr16	90354753	3598992	0.0398	0.2408
chr17	81195210	3358552	0.0414	0.245
chr18	78077248	3256720	0.0417	0.542
chr19	59128983	2607839	0.0441	0.4897
chr20	63025520	2652404	0.0421	0.2352
chr21	48129895	1617750	0.0336	0.2379
chr22	51304566	1464338	0.0285	0.1895
chrMT	16571	102659	6.1951	4.1019
chrX	155270560	6936346	0.0447	0.264
chrY	59373566	402154	0.0068	0.2391

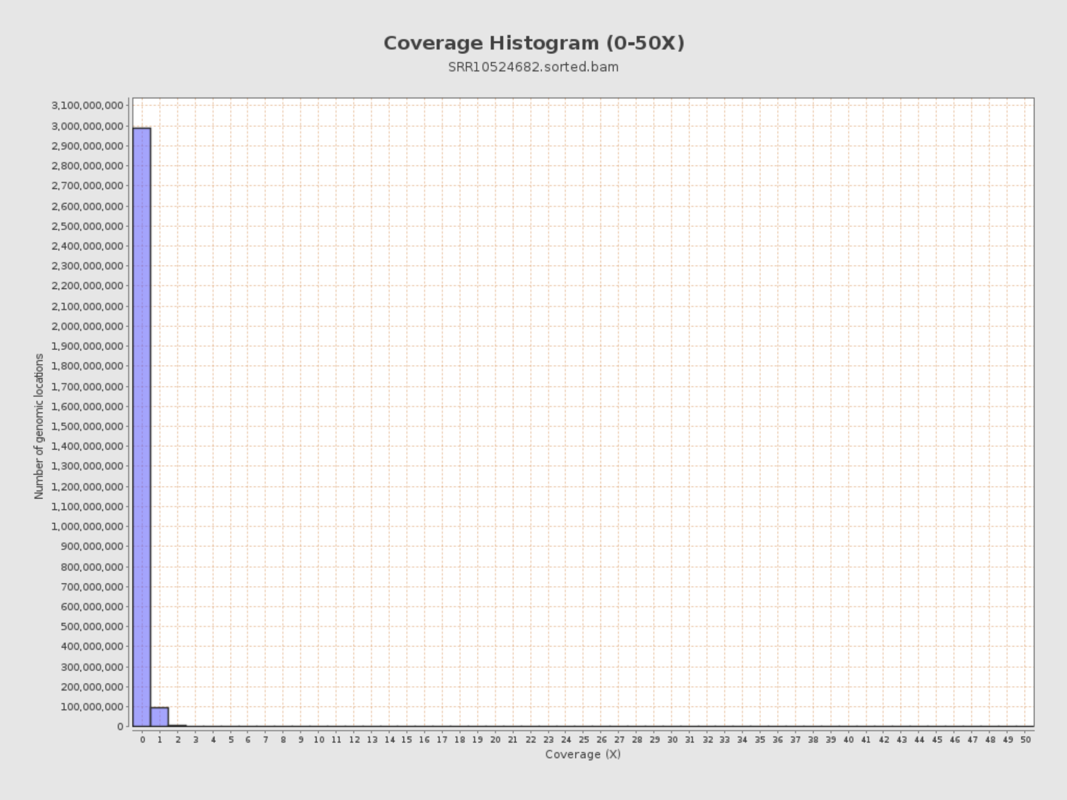
3. Results : Coverage across reference



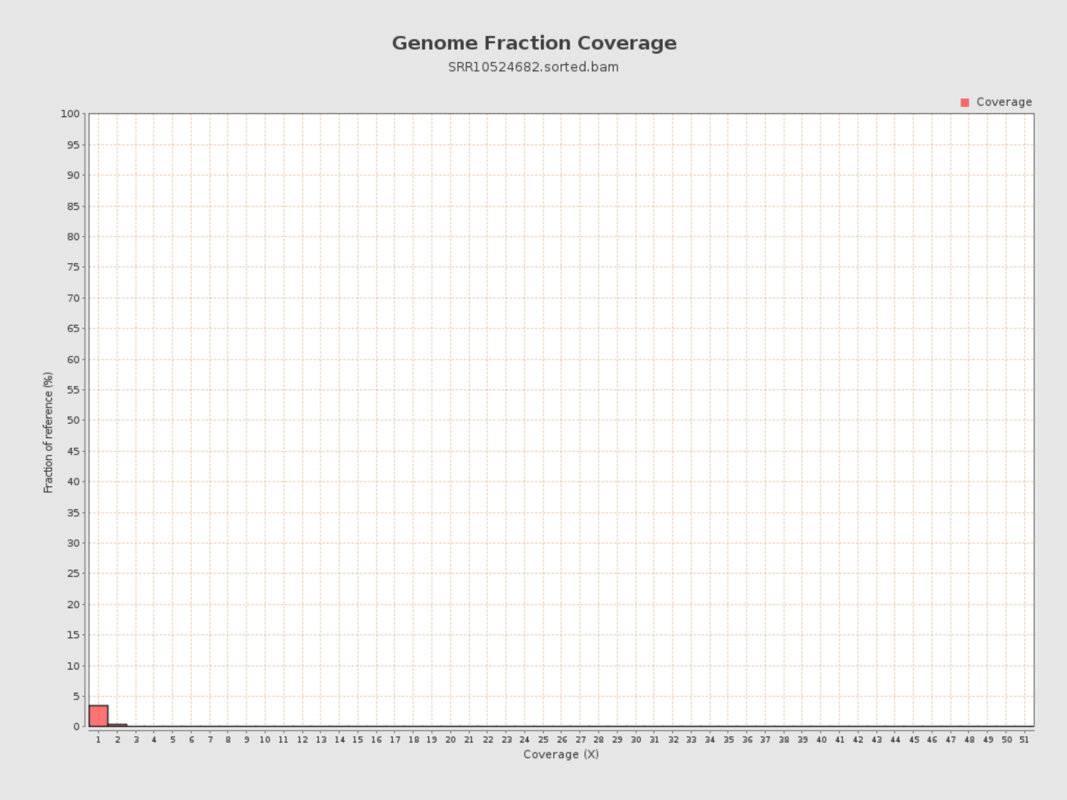
4. Results : Coverage Histogram



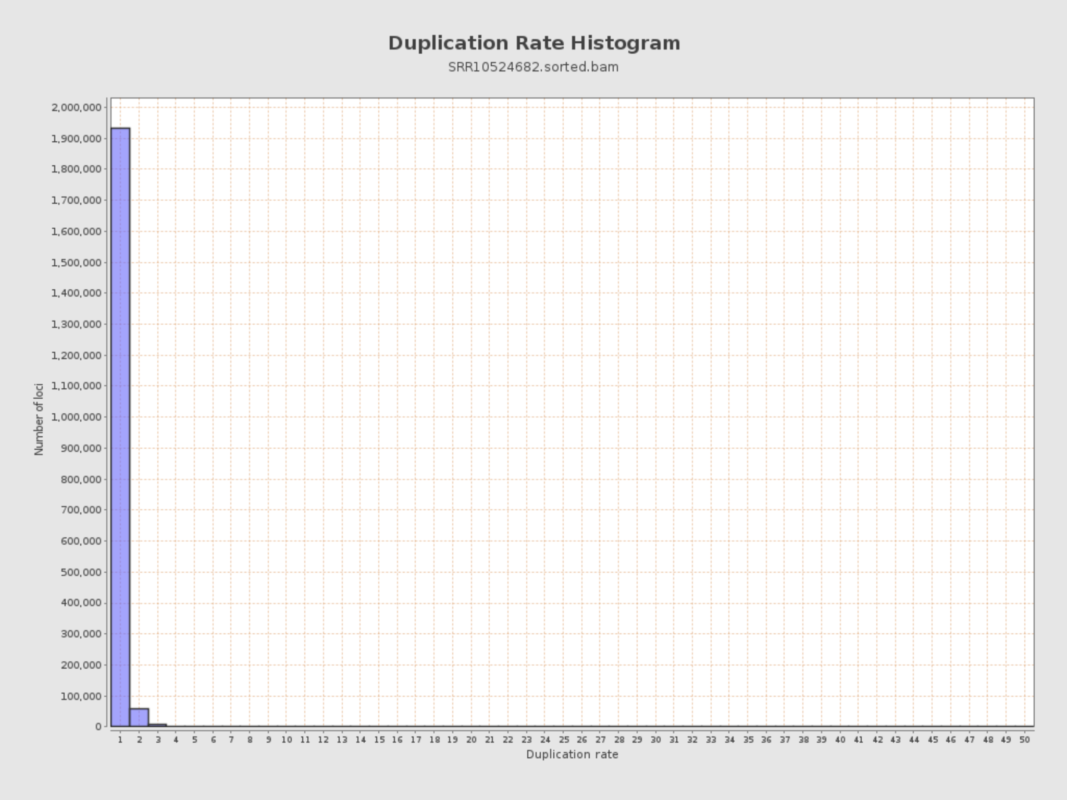
5. Results : Coverage Histogram (0-50X)



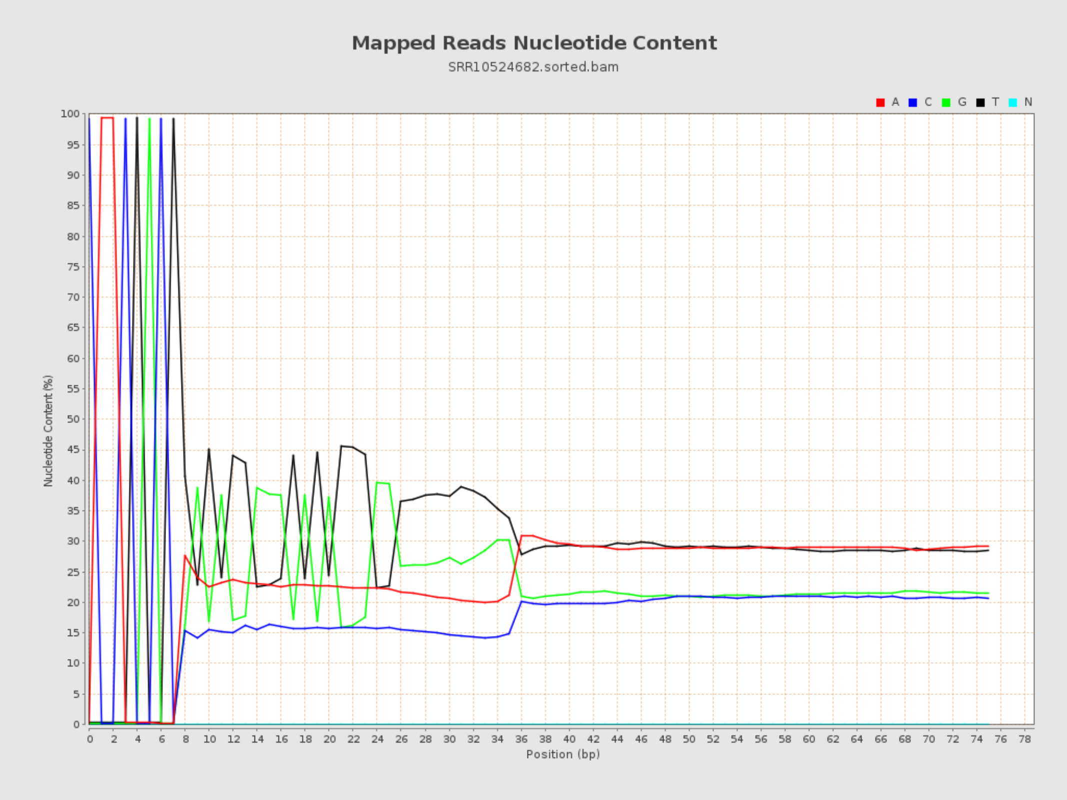
6. Results : Genome Fraction Coverage



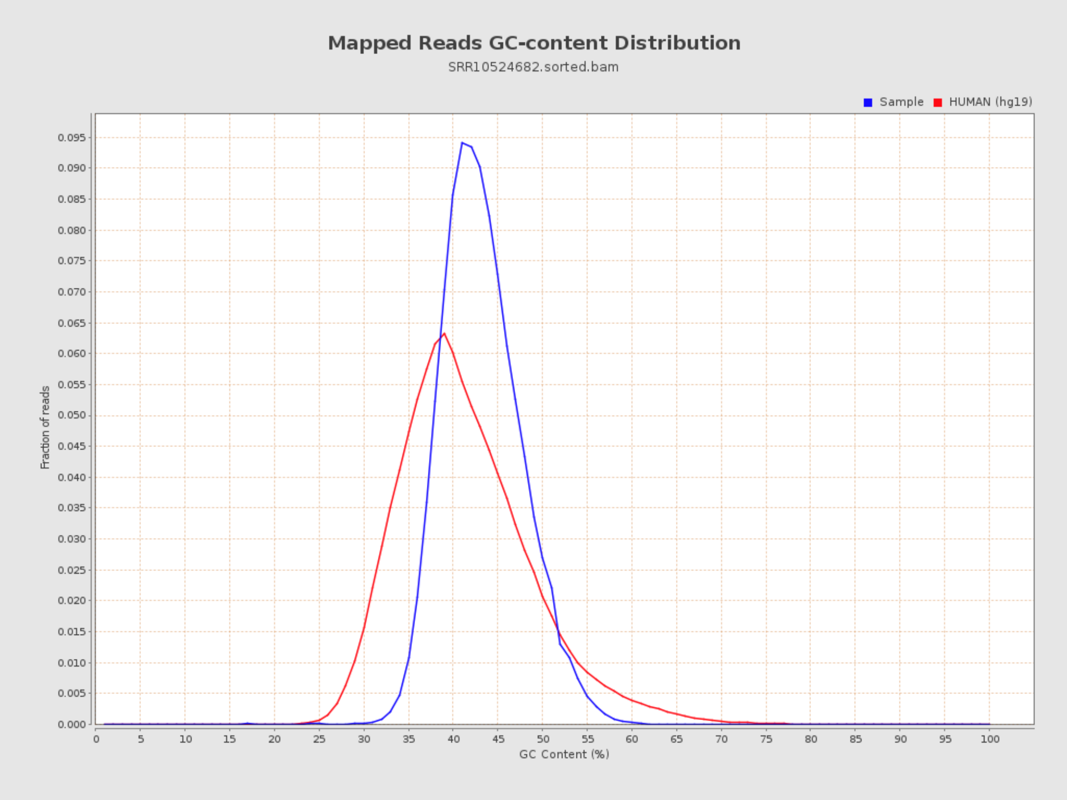
7. Results : Duplication Rate Histogram



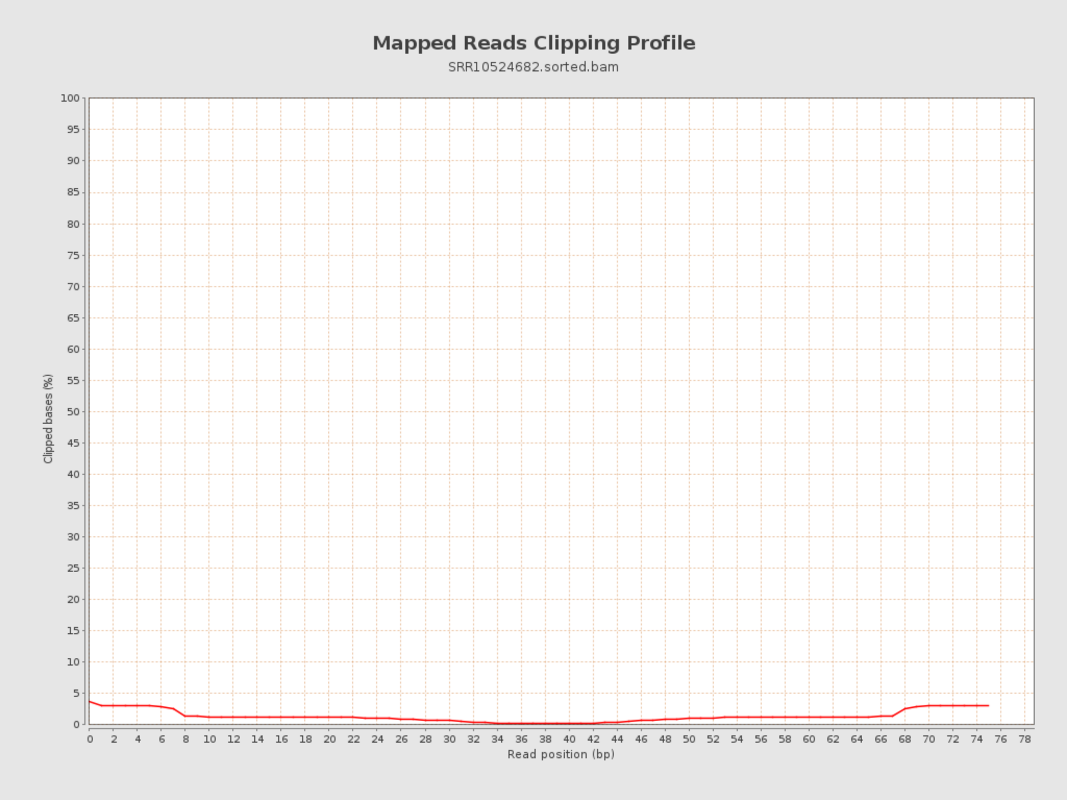
8. Results : Mapped Reads Nucleotide Content



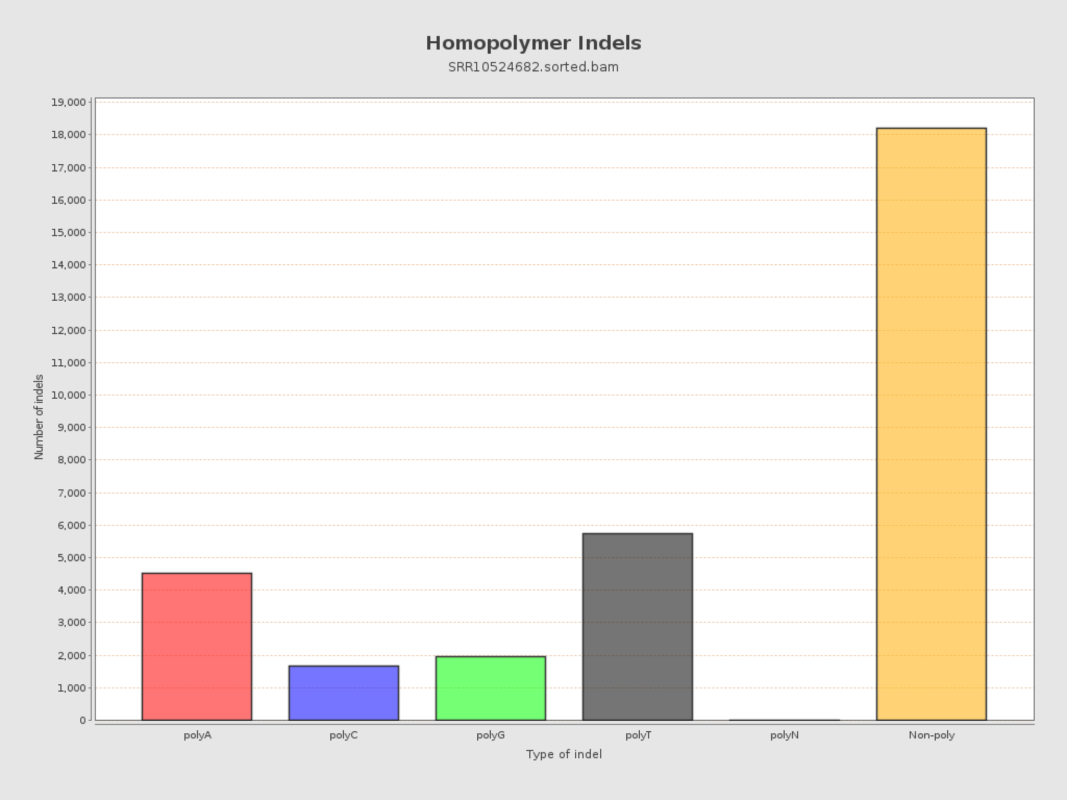
9. Results : Mapped Reads GC-content Distribution



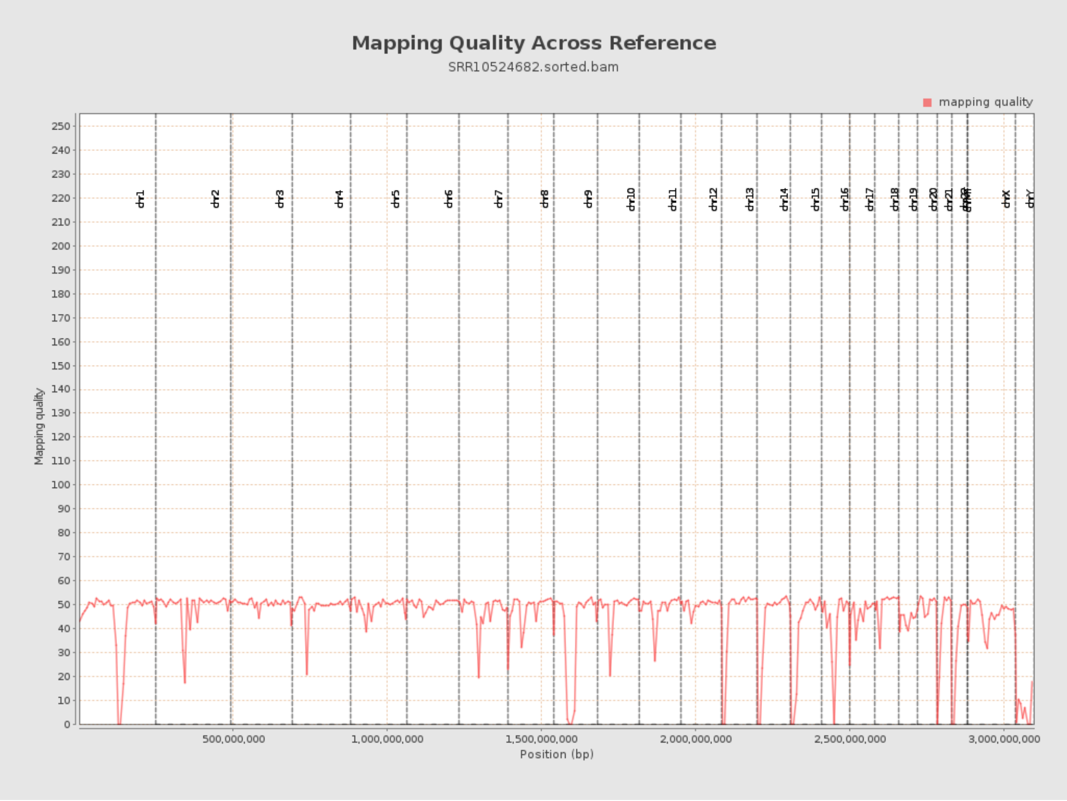
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram