Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 02:05:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524898.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_SRR10524898 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524898.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 02:05:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524898.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,512,908
Mapped reads	2,302,762 / 91.64%
Unmapped reads	210,146 / 8.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,951 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	131,168 / 5.22%
Duplication rate	4.27%
Clipped reads	2,303,712 / 91.68%

2.2. ACGT Content

Number/percentage of A's	33,356,972 / 24.93%
Number/percentage of C's	25,611,010 / 19.14%
Number/percentage of T's	44,535,079 / 33.29%
Number/percentage of G's	30,259,237 / 22.62%
Number/percentage of N's	17,392 / 0.01%
GC Percentage	41.76%

2.3. Coverage

Mean	0.0432

Standard Deviation	0.4185

2.4. Mapping Quality

Mean Mapping Quality	46.12

2.5. Mismatches and indels

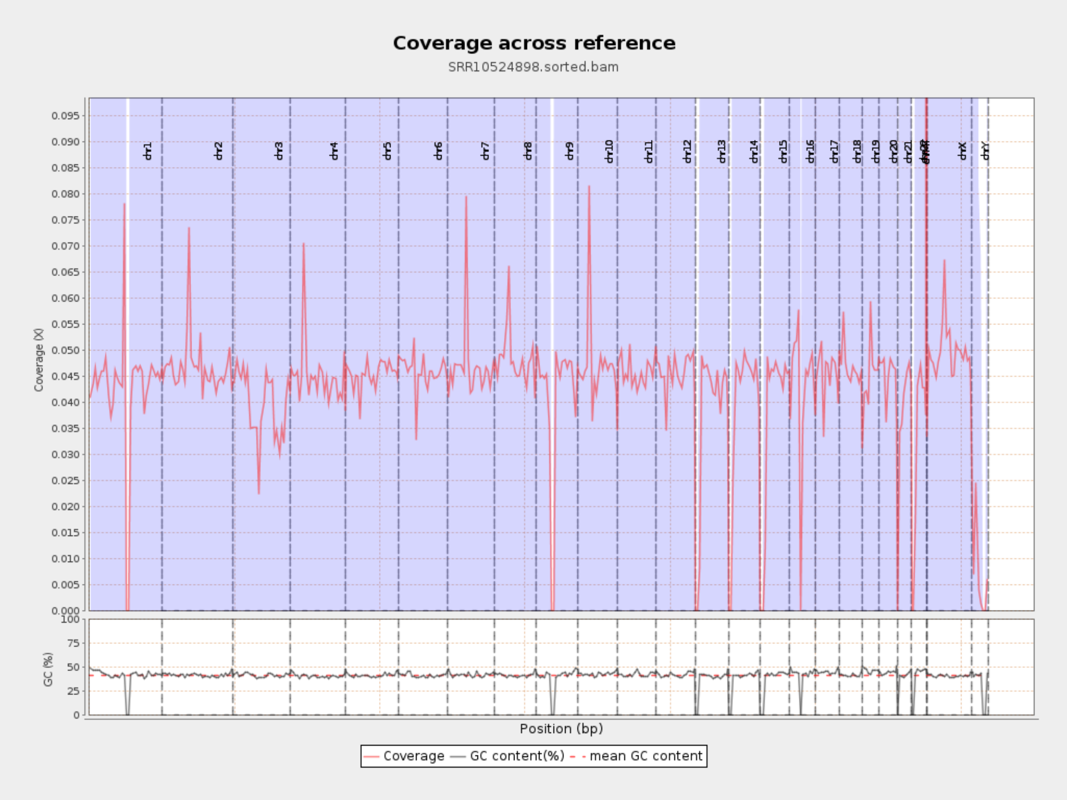
General error rate	0.52%
Mismatches	674,511
Insertions	9,395
Mapped reads with at least one insertion	0.41%
Deletions	25,742
Mapped reads with at least one deletion	1.11%
Homopolymer indels	43.77%

2.6. Chromosome stats

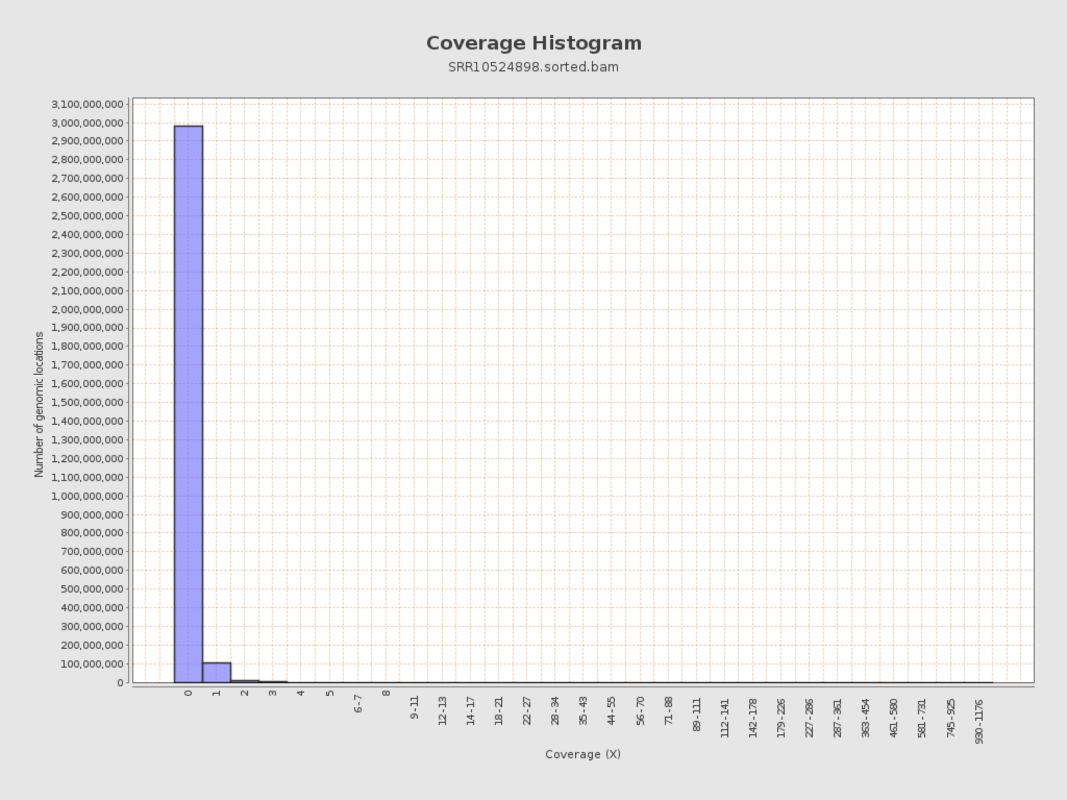
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10547863	0.0423	0.8699
chr2	243199373	11414531	0.0469	0.4481
chr3	198022430	7823602	0.0395	0.2251
chr4	191154276	8592917	0.045	0.2807
chr5	180915260	8201648	0.0453	0.2444
chr6	171115067	7859135	0.0459	0.2735
chr7	159138663	7484833	0.047	0.5613

chr8	146364022	7061305	0.0482	0.4094
chr9	141213431	5684065	0.0403	0.3597
chr10	135534747	6411001	0.0473	0.3809
chr11	135006516	6133857	0.0454	0.3678
chr12	133851895	6123819	0.0458	0.2499
chr13	115169878	4268416	0.0371	0.219
chr14	107349540	4173171	0.0389	0.2364
chr15	102531392	3783334	0.0369	0.2162
chr16	90354753	3872710	0.0429	0.2671
chr17	81195210	3671700	0.0452	0.2628
chr18	78077248	3672369	0.047	0.7464
chr19	59128983	2683101	0.0454	0.5744
chr20	63025520	2847899	0.0452	0.2473
chr21	48129895	1803553	0.0375	0.254
chr22	51304566	1565892	0.0305	0.196
chrMT	16571	40270	2.4301	2.0694
chrX	155270560	7681614	0.0495	0.3024
chrY	59373566	417619	0.007	0.1866

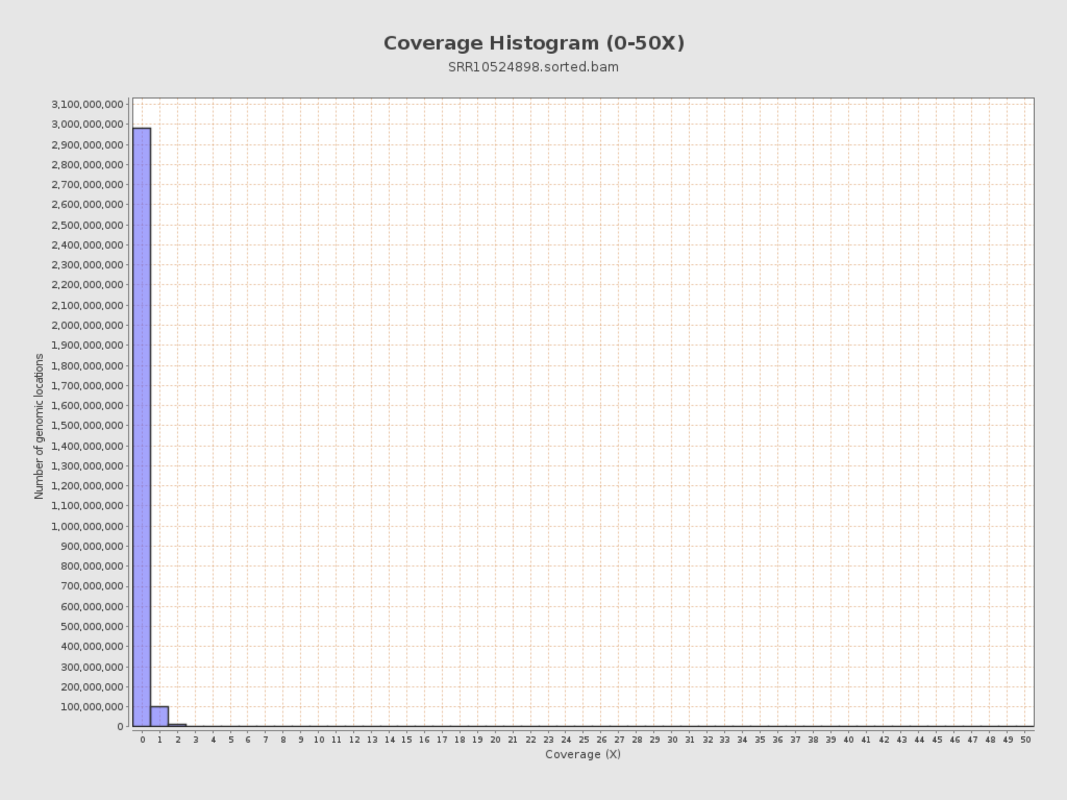
3. Results : Coverage across reference



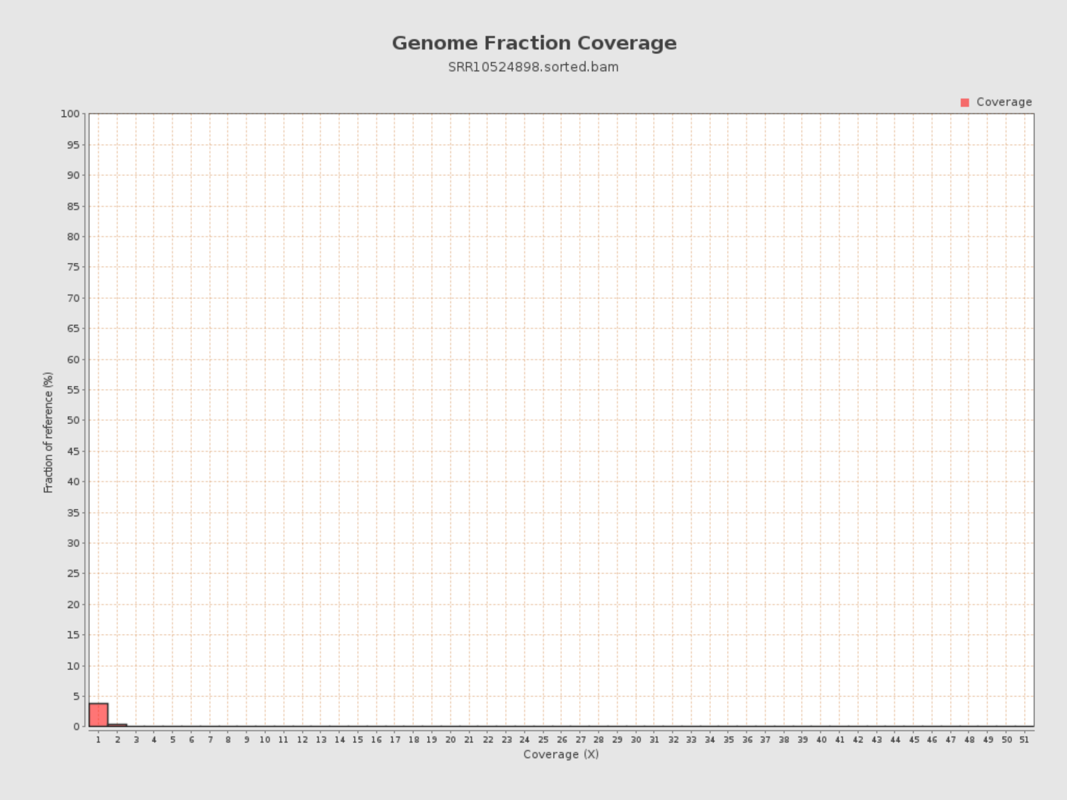
4. Results : Coverage Histogram



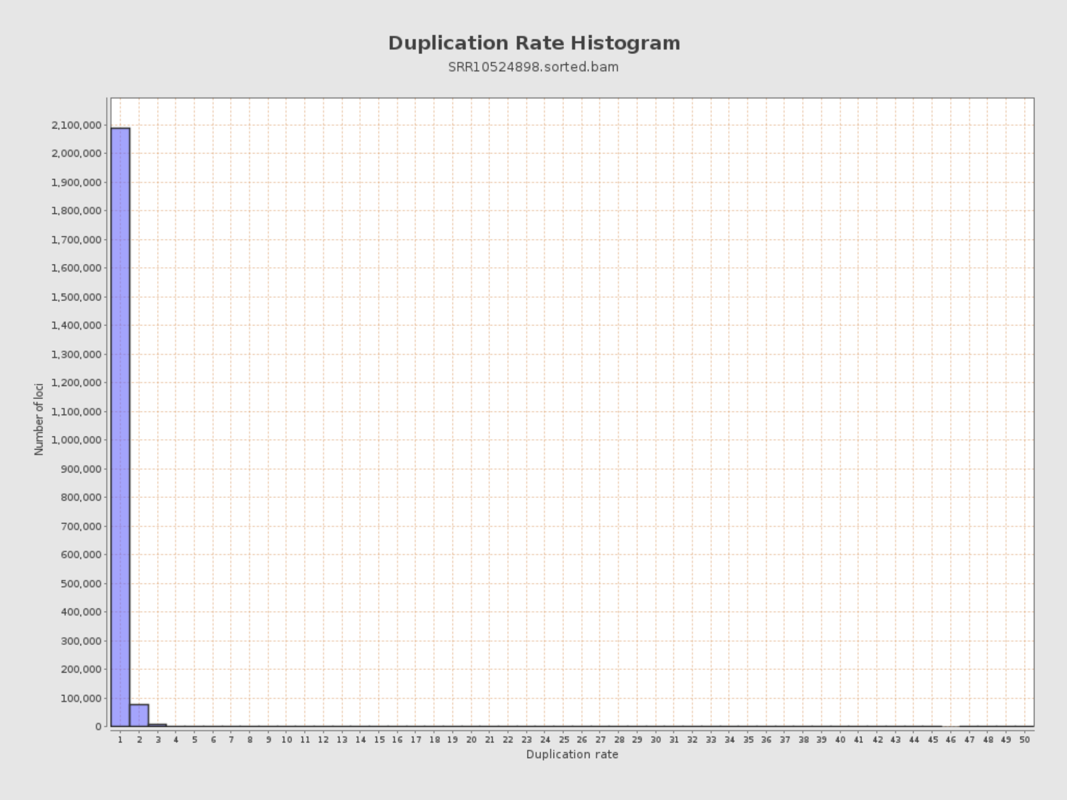
5. Results : Coverage Histogram (0-50X)



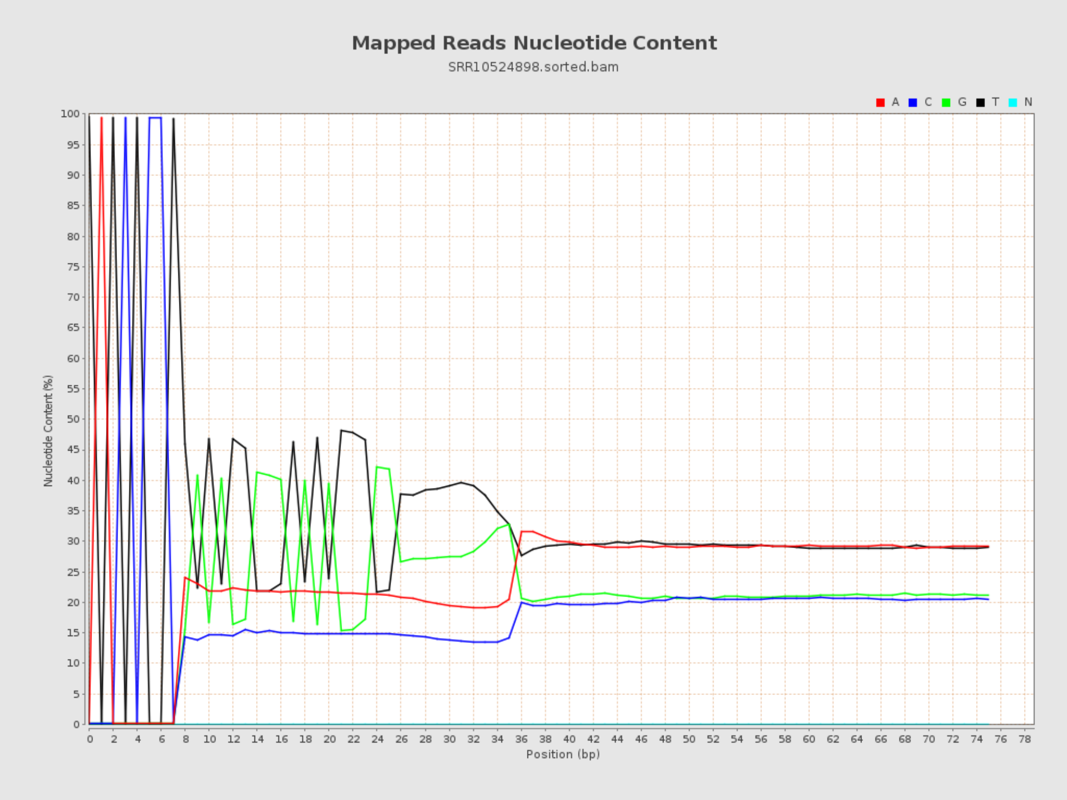
6. Results : Genome Fraction Coverage



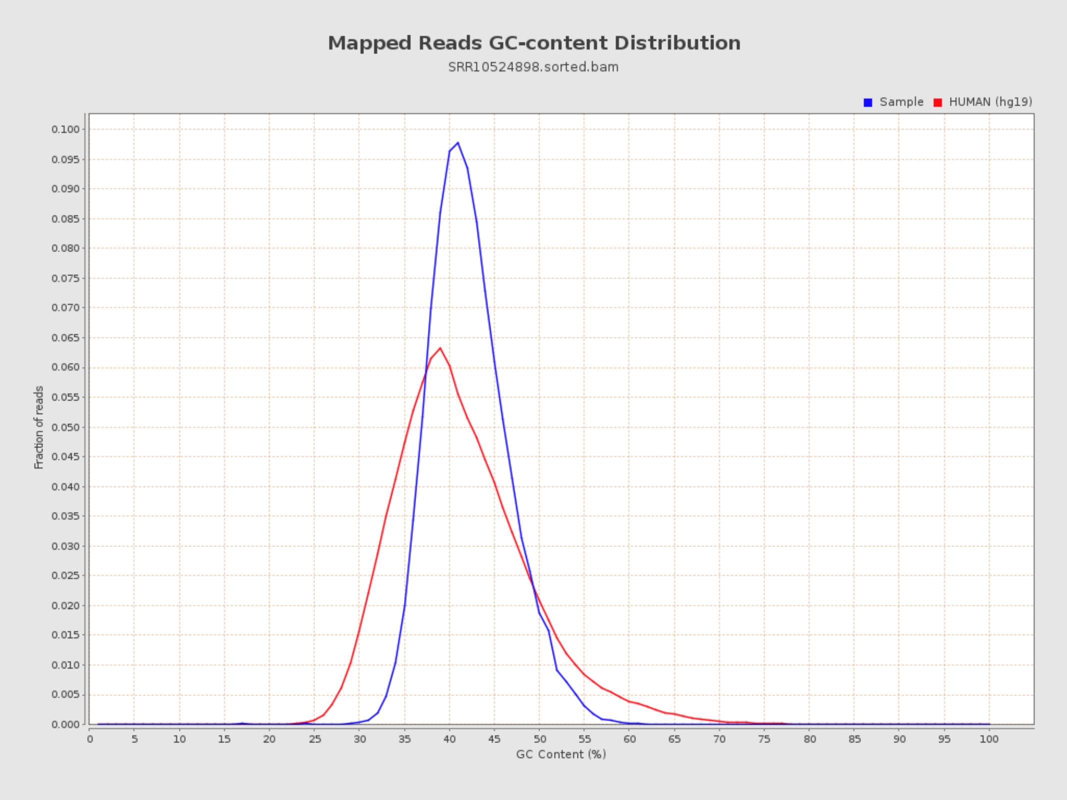
7. Results : Duplication Rate Histogram



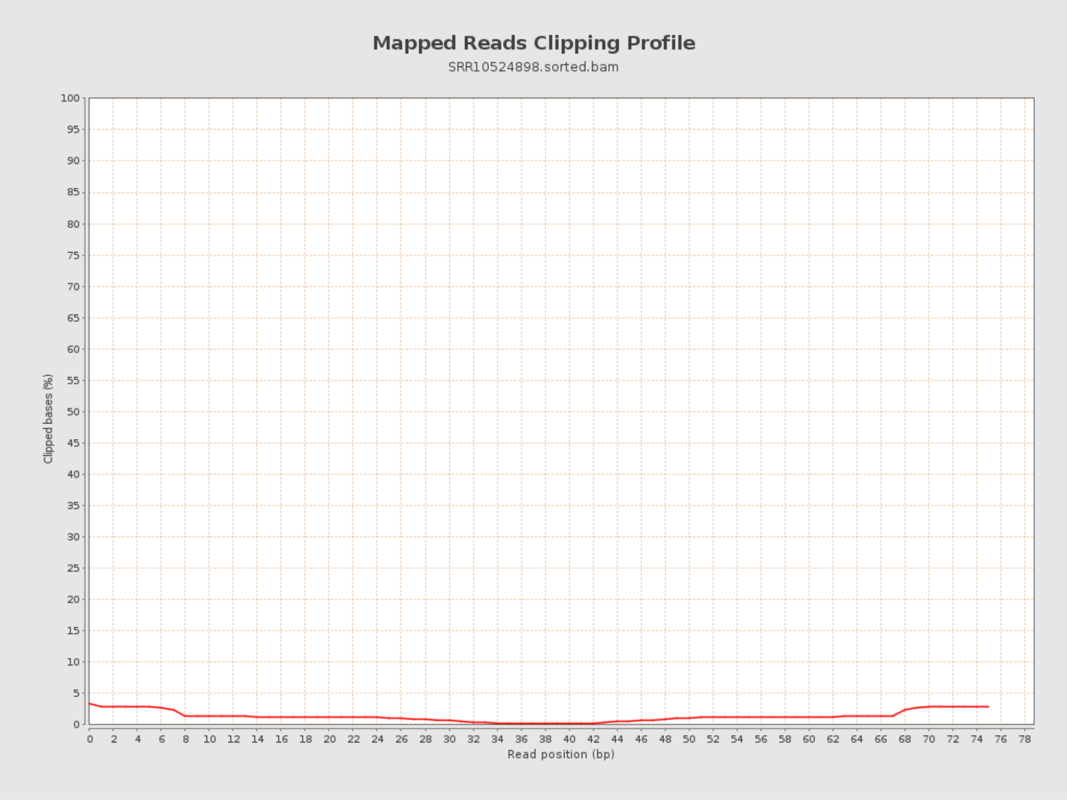
8. Results : Mapped Reads Nucleotide Content



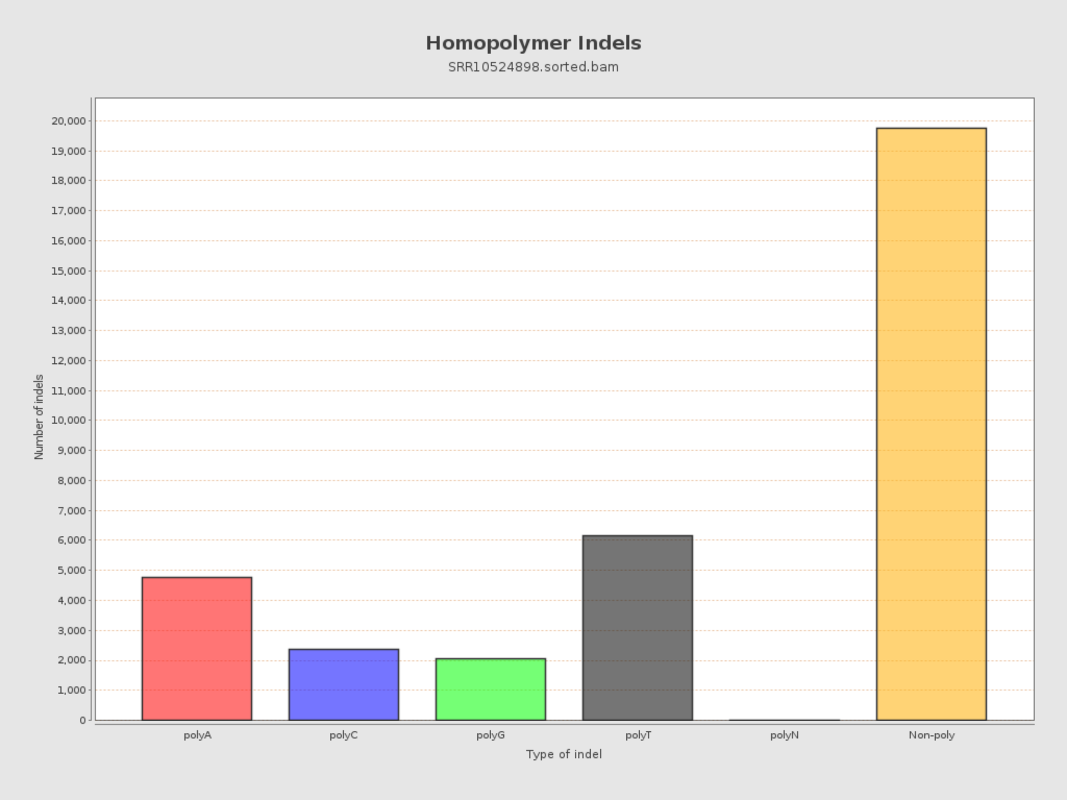
9. Results : Mapped Reads GC-content Distribution



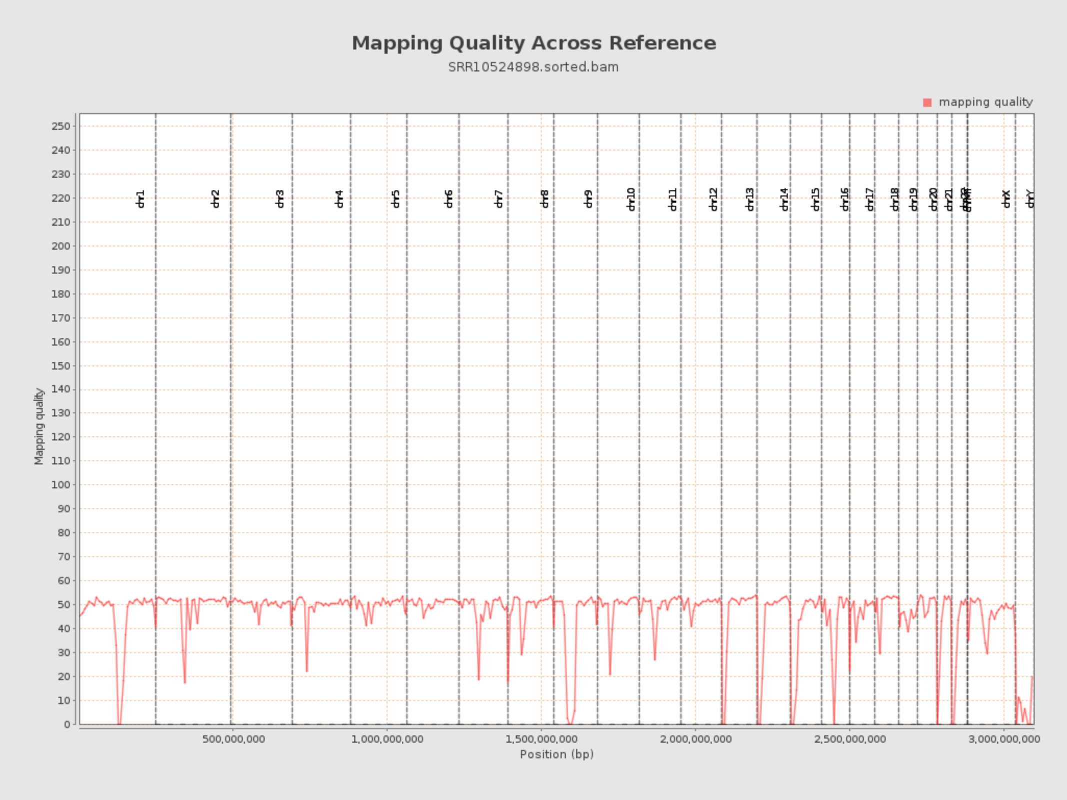
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram