Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 06:21:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524495.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_SRR10524495 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524495.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 06:21:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524495.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,770,042
Mapped reads	2,563,071 / 92.53%
Unmapped reads	206,971 / 7.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,117 / 0.22%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	161,478 / 5.83%
Duplication rate	4.82%
Clipped reads	2,561,816 / 92.48%

2.2. ACGT Content

Number/percentage of A's	36,980,255 / 24.77%
Number/percentage of C's	26,453,101 / 17.72%
Number/percentage of T's	49,161,428 / 32.92%
Number/percentage of G's	36,719,276 / 24.59%
Number/percentage of N's	3,203 / 0%
GC Percentage	42.31%

2.3. Coverage

Mean	0.0482

Standard Deviation	0.4124

2.4. Mapping Quality

Mean Mapping Quality	45.47

2.5. Mismatches and indels

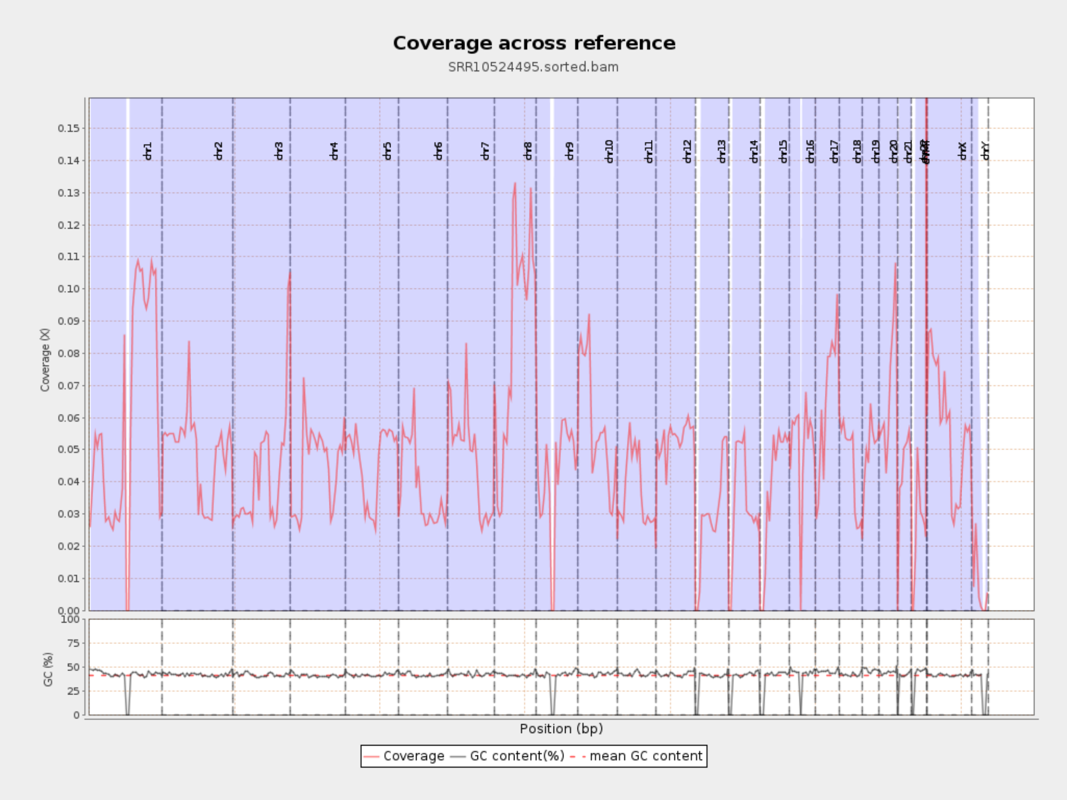
General error rate	0.48%
Mismatches	693,636
Insertions	10,777
Mapped reads with at least one insertion	0.42%
Deletions	27,555
Mapped reads with at least one deletion	1.07%
Homopolymer indels	42.39%

2.6. Chromosome stats

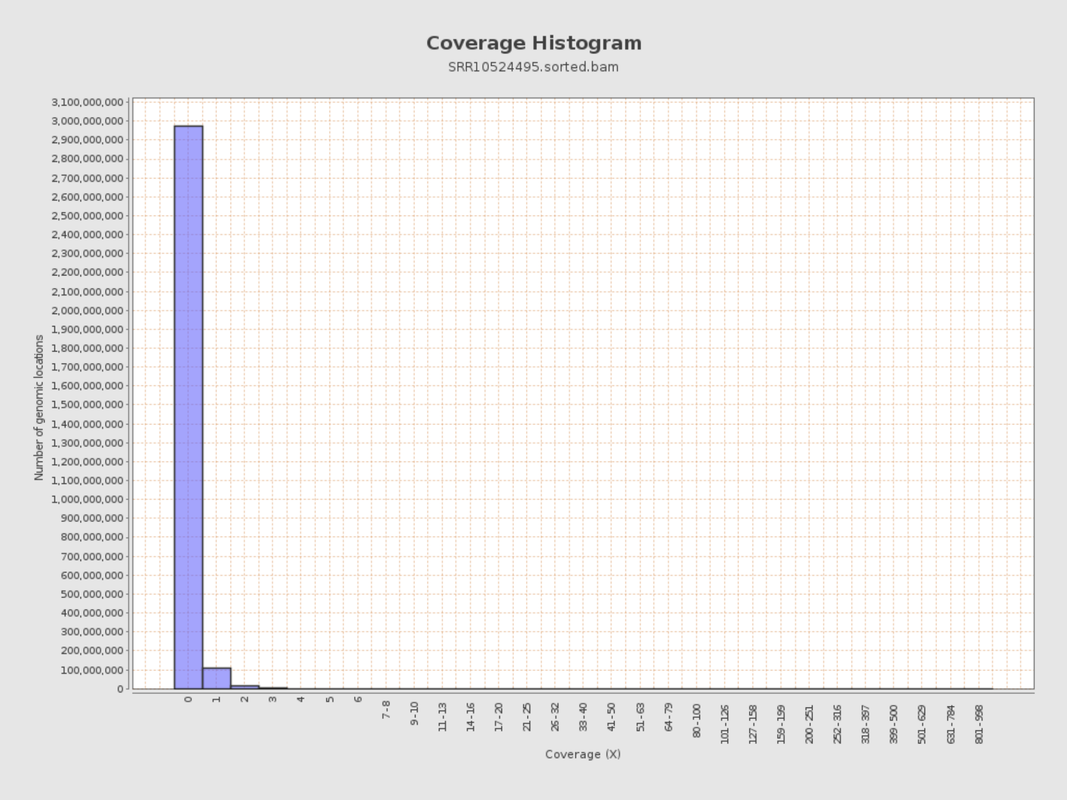
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14916385	0.0598	0.7862
chr2	243199373	11994883	0.0493	0.4769
chr3	198022430	8297768	0.0419	0.2407
chr4	191154276	8586652	0.0449	0.297
chr5	180915260	8433125	0.0466	0.2538
chr6	171115067	6532376	0.0382	0.312
chr7	159138663	7540787	0.0474	0.5732

chr8	146364022	12524114	0.0856	0.4149
chr9	141213431	5864856	0.0415	0.3412
chr10	135534747	7940598	0.0586	0.422
chr11	135006516	5053335	0.0374	0.376
chr12	133851895	7177729	0.0536	0.2717
chr13	115169878	3398363	0.0295	0.202
chr14	107349540	3577349	0.0333	0.2189
chr15	102531392	3936551	0.0384	0.245
chr16	90354753	4611570	0.051	0.2897
chr17	81195210	5374238	0.0662	0.3309
chr18	78077248	3539325	0.0453	0.651
chr19	59128983	2984212	0.0505	0.5239
chr20	63025520	4351492	0.069	0.3165
chr21	48129895	2057257	0.0427	0.2765
chr22	51304566	1232983	0.024	0.1809
chrMT	16571	9991	0.6029	1.0201
chrX	155270560	8961646	0.0577	0.3282
chrY	59373566	467188	0.0079	0.2086

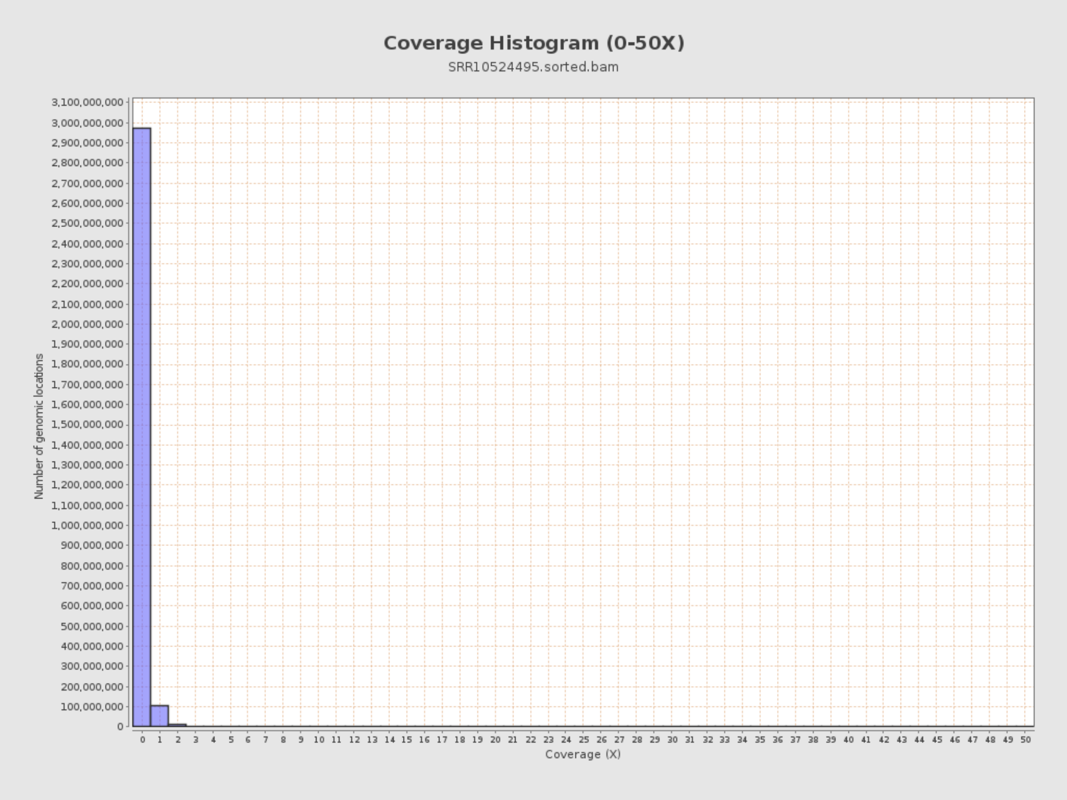
3. Results : Coverage across reference



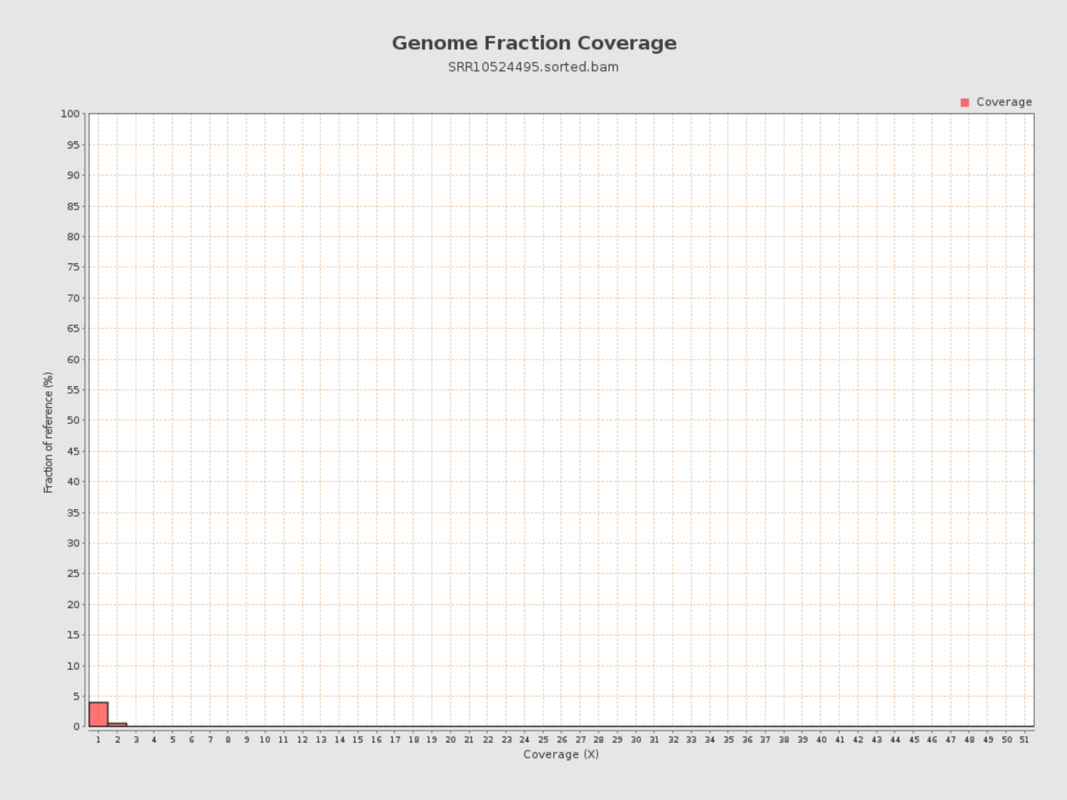
4. Results : Coverage Histogram



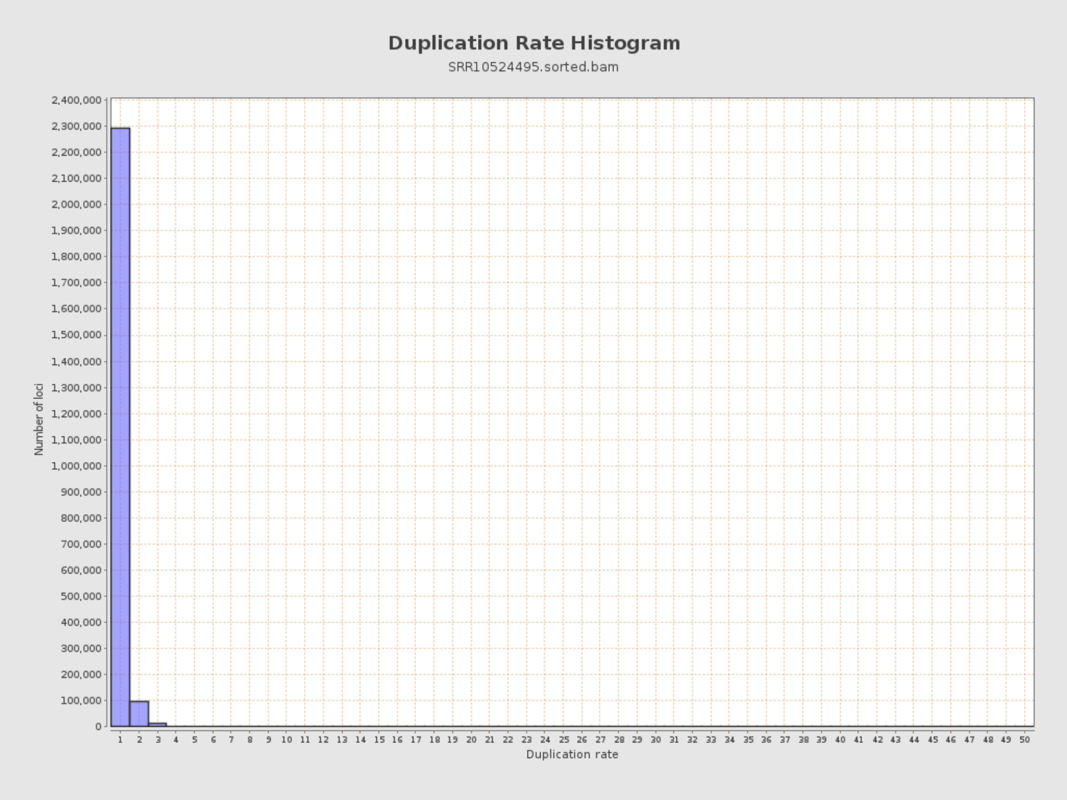
5. Results : Coverage Histogram (0-50X)



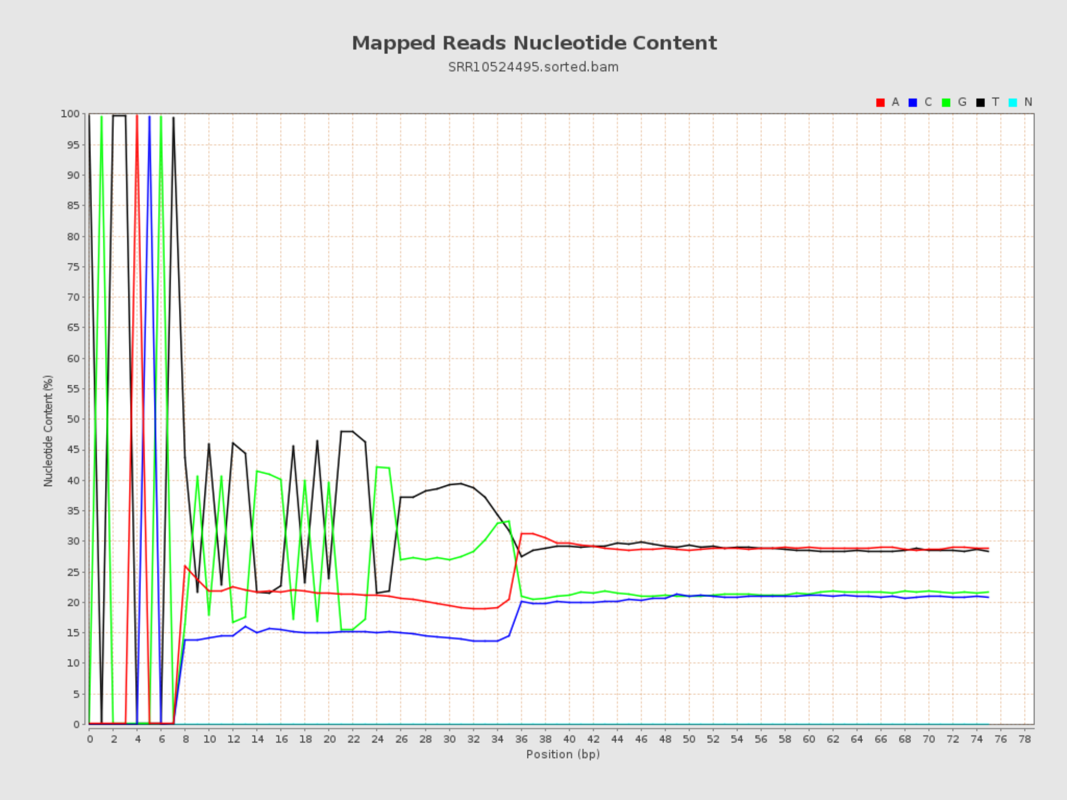
6. Results : Genome Fraction Coverage



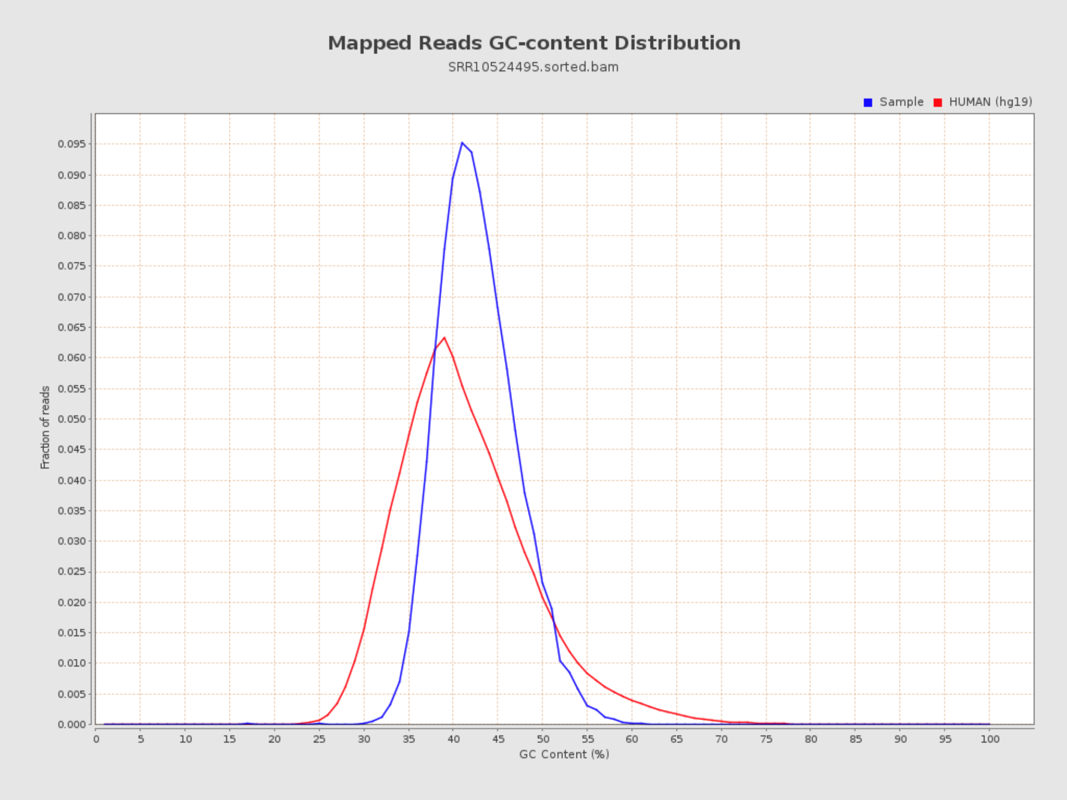
7. Results : Duplication Rate Histogram



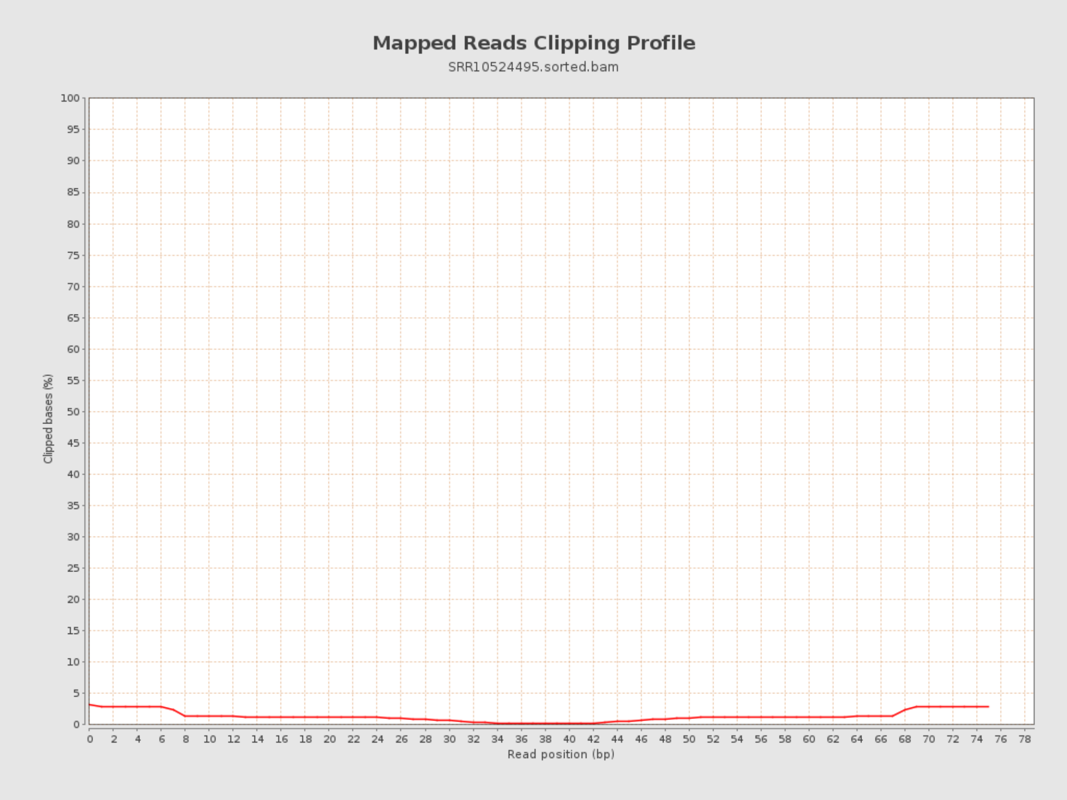
8. Results : Mapped Reads Nucleotide Content



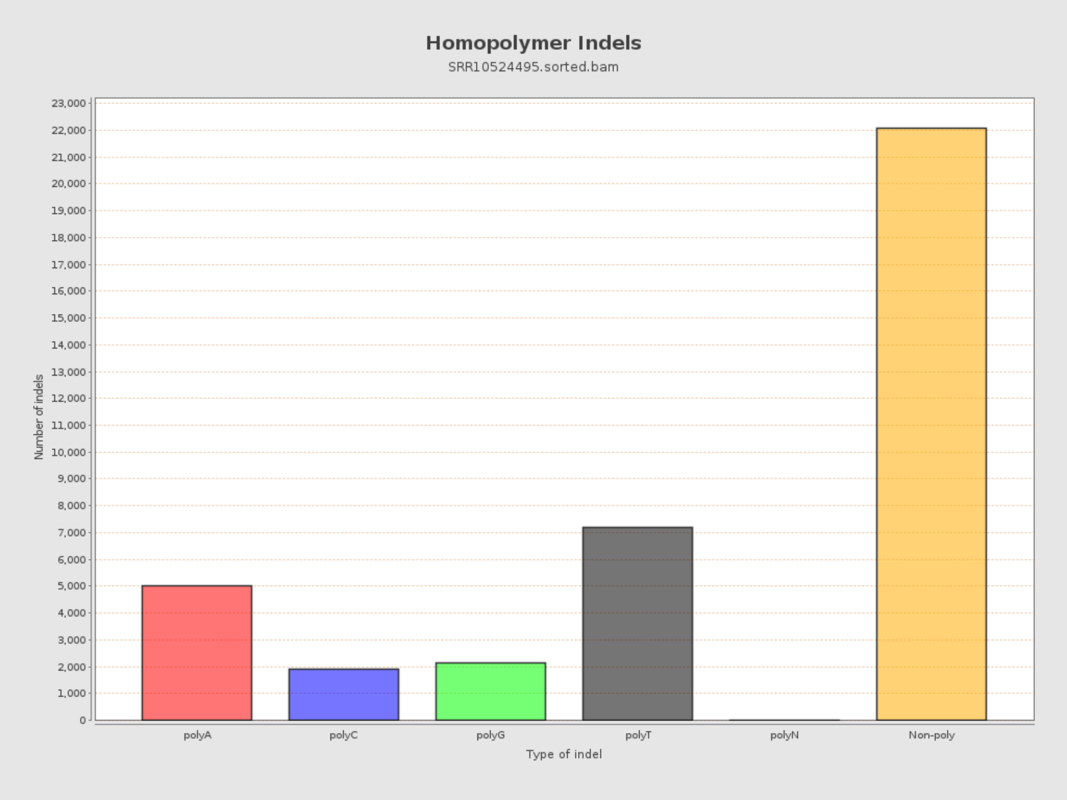
9. Results : Mapped Reads GC-content Distribution



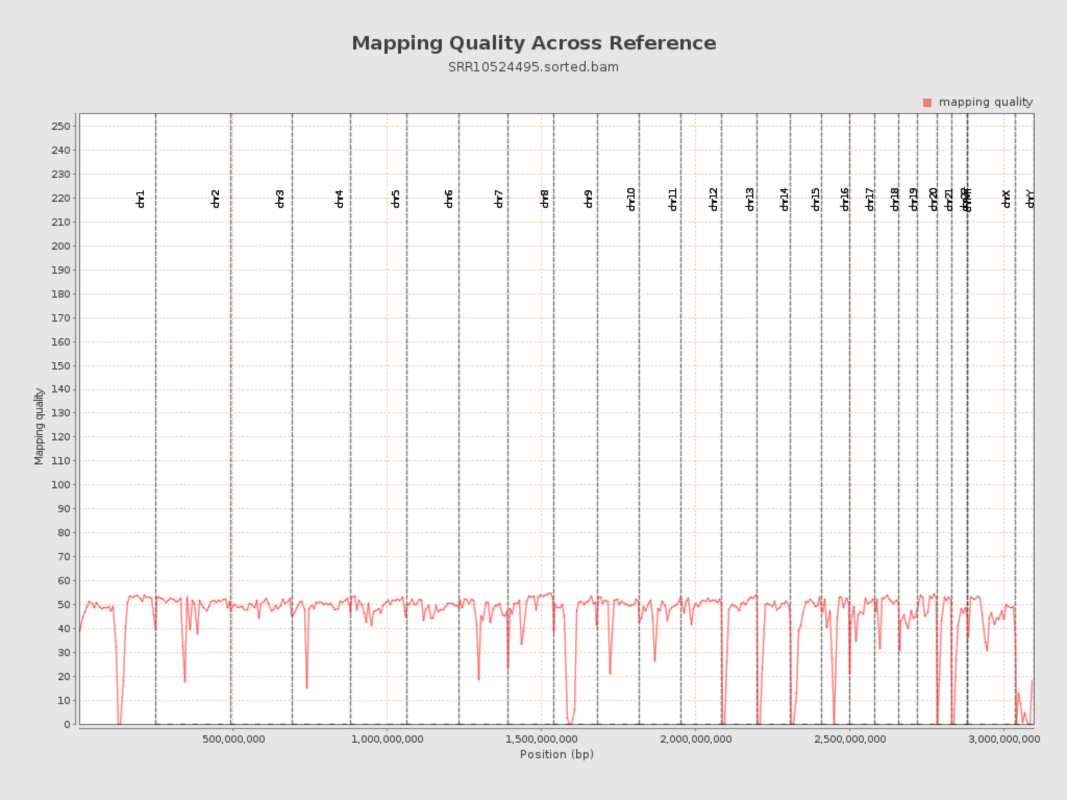
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram