Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 00:57:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081179.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_SRR3081179 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081179.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 00:57:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081179.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,732,776
Mapped reads	2,481,785 / 90.82%
Unmapped reads	250,991 / 9.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,762 / 1.02%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	107,398 / 3.93%
Duplication rate	3.49%
Clipped reads	1,074,160 / 39.31%

2.2. ACGT Content

Number/percentage of A's	47,784,525 / 28.57%
Number/percentage of C's	30,765,363 / 18.39%
Number/percentage of T's	52,875,906 / 31.61%
Number/percentage of G's	35,804,295 / 21.4%
Number/percentage of N's	49,341 / 0.03%
GC Percentage	39.8%

2.3. Coverage

Mean	0.0541

Standard Deviation	0.4191

2.4. Mapping Quality

Mean Mapping Quality	47.21

2.5. Mismatches and indels

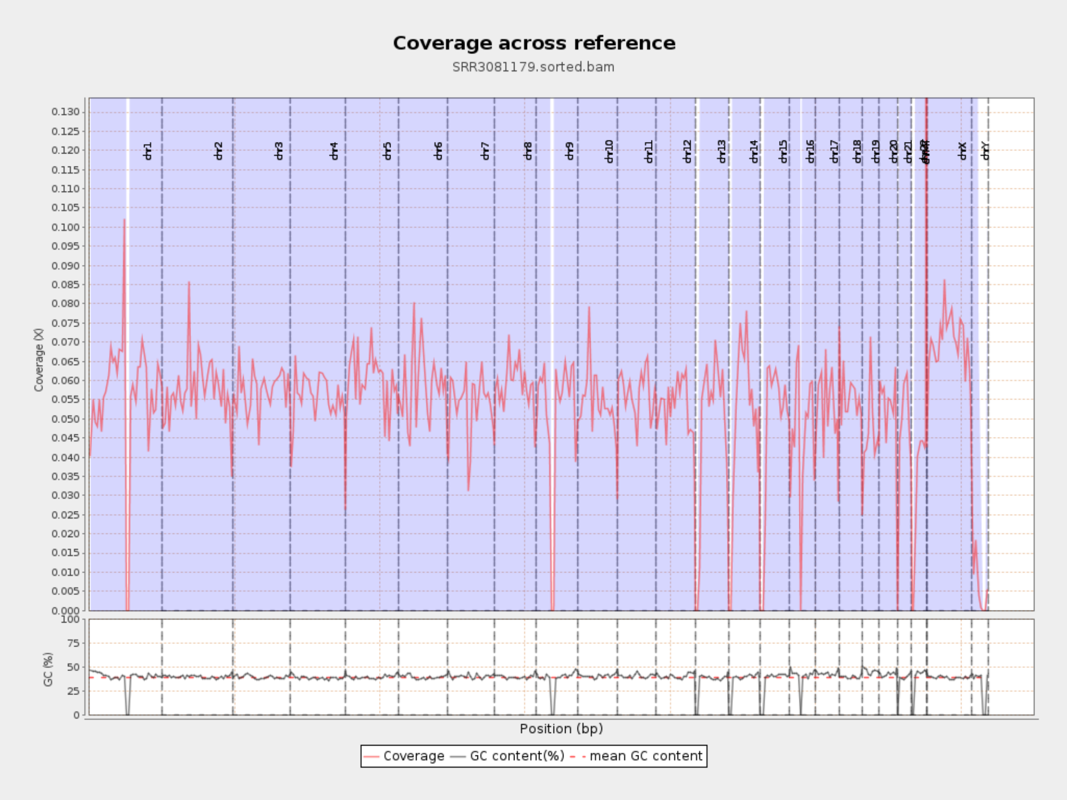
General error rate	0.83%
Mismatches	1,362,886
Insertions	13,228
Mapped reads with at least one insertion	0.53%
Deletions	38,341
Mapped reads with at least one deletion	1.53%
Homopolymer indels	47.33%

2.6. Chromosome stats

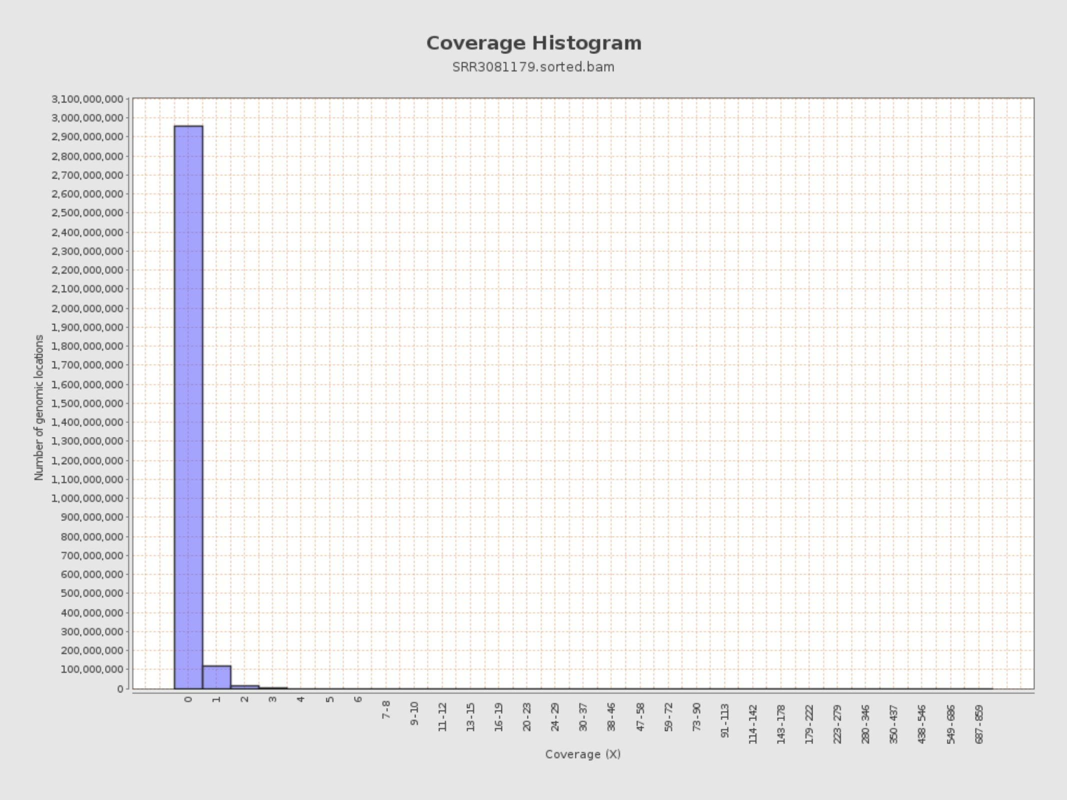
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13992664	0.0561	0.797
chr2	243199373	14011705	0.0576	0.4688
chr3	198022430	11430918	0.0577	0.2745
chr4	191154276	10671983	0.0558	0.2788
chr5	180915260	10927521	0.0604	0.2828
chr6	171115067	10017092	0.0585	0.3369
chr7	159138663	8623539	0.0542	0.4633

chr8	146364022	8660272	0.0592	0.5747
chr9	141213431	7199740	0.051	0.3618
chr10	135534747	7443292	0.0549	0.3638
chr11	135006516	7602592	0.0563	0.3812
chr12	133851895	7157609	0.0535	0.2667
chr13	115169878	5448888	0.0473	0.2486
chr14	107349540	5329983	0.0497	0.2642
chr15	102531392	4832948	0.0471	0.2525
chr16	90354753	4141646	0.0458	0.277
chr17	81195210	4297235	0.0529	0.2962
chr18	78077248	4374477	0.056	0.709
chr19	59128983	2779128	0.047	0.5546
chr20	63025520	3395908	0.0539	0.2698
chr21	48129895	2215560	0.046	0.2573
chr22	51304566	1560845	0.0304	0.1969
chrMT	16571	16506	0.9961	1.2374
chrX	155270560	10811433	0.0696	0.3262
chrY	59373566	397972	0.0067	0.1278

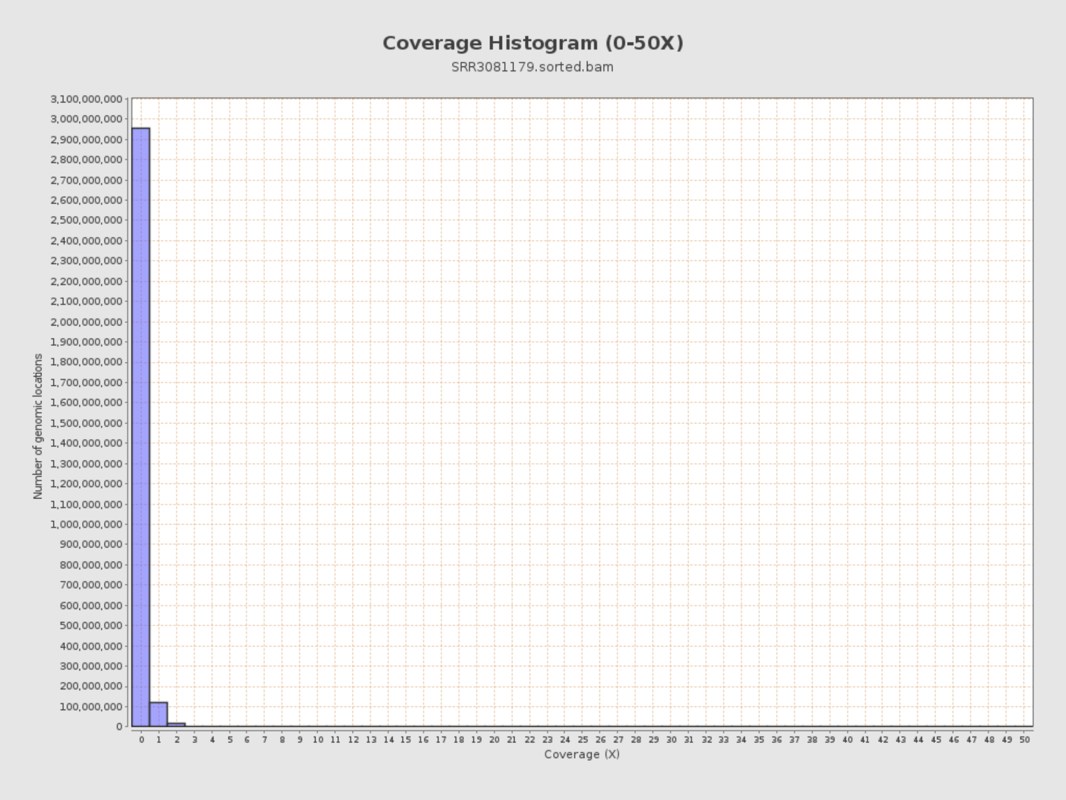
3. Results : Coverage across reference



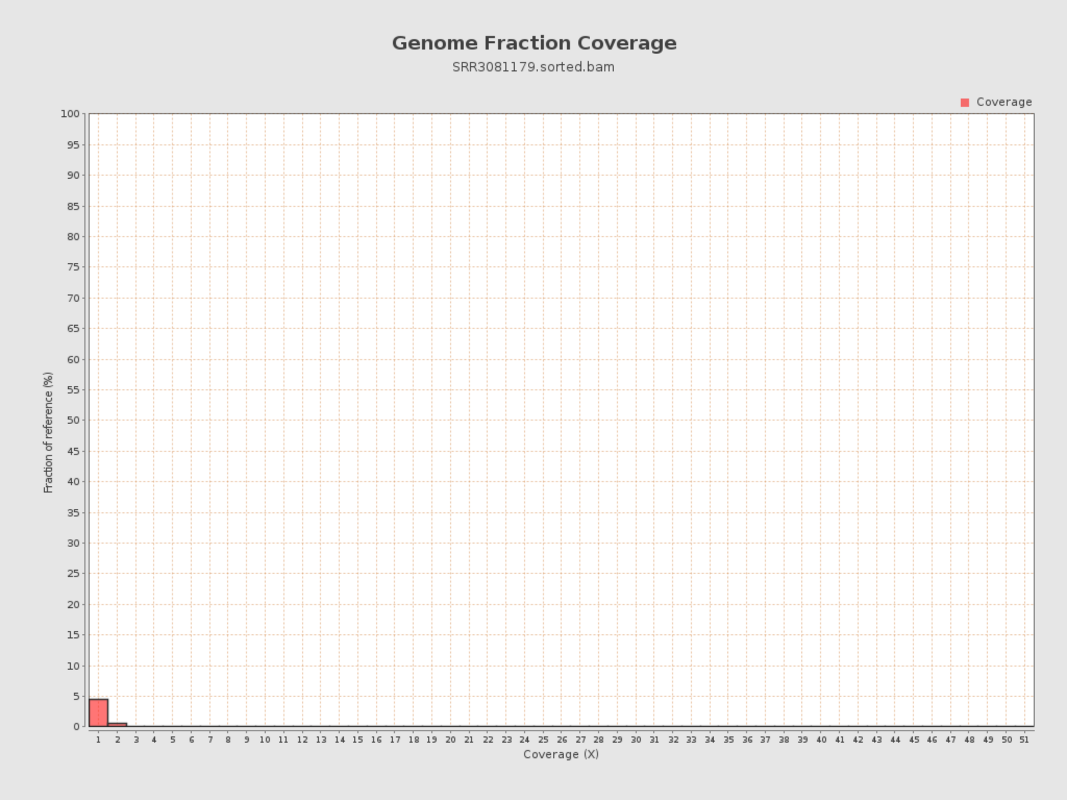
4. Results : Coverage Histogram



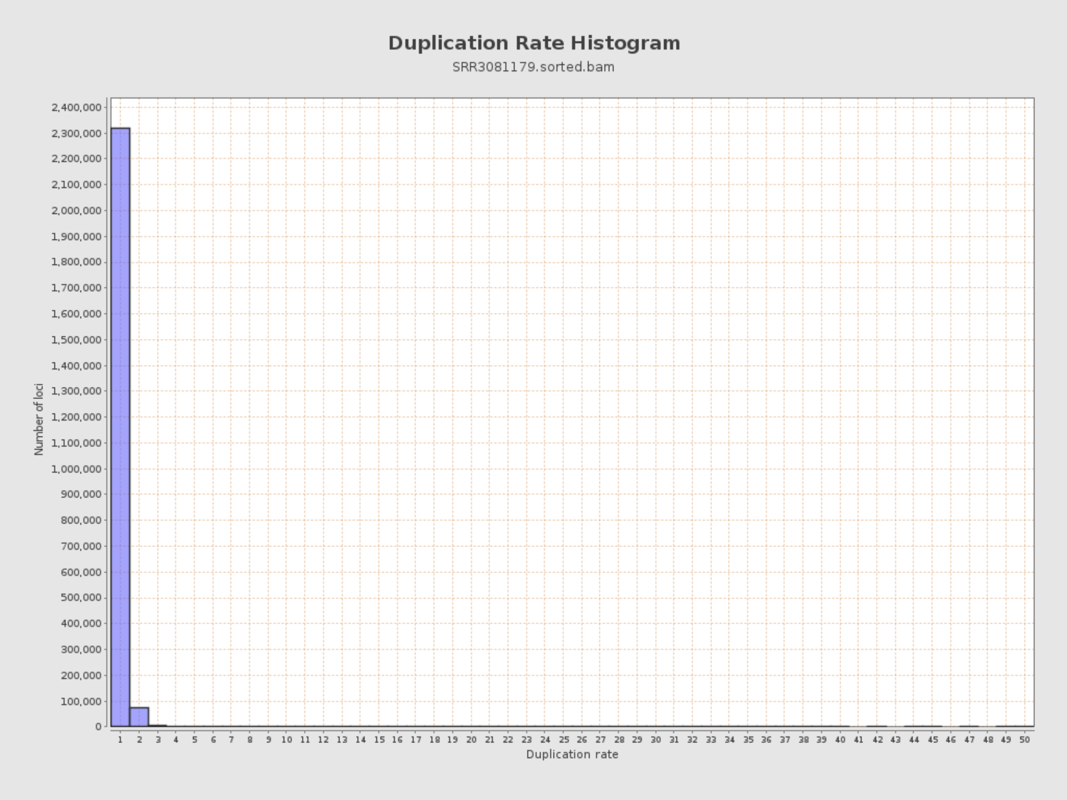
5. Results : Coverage Histogram (0-50X)



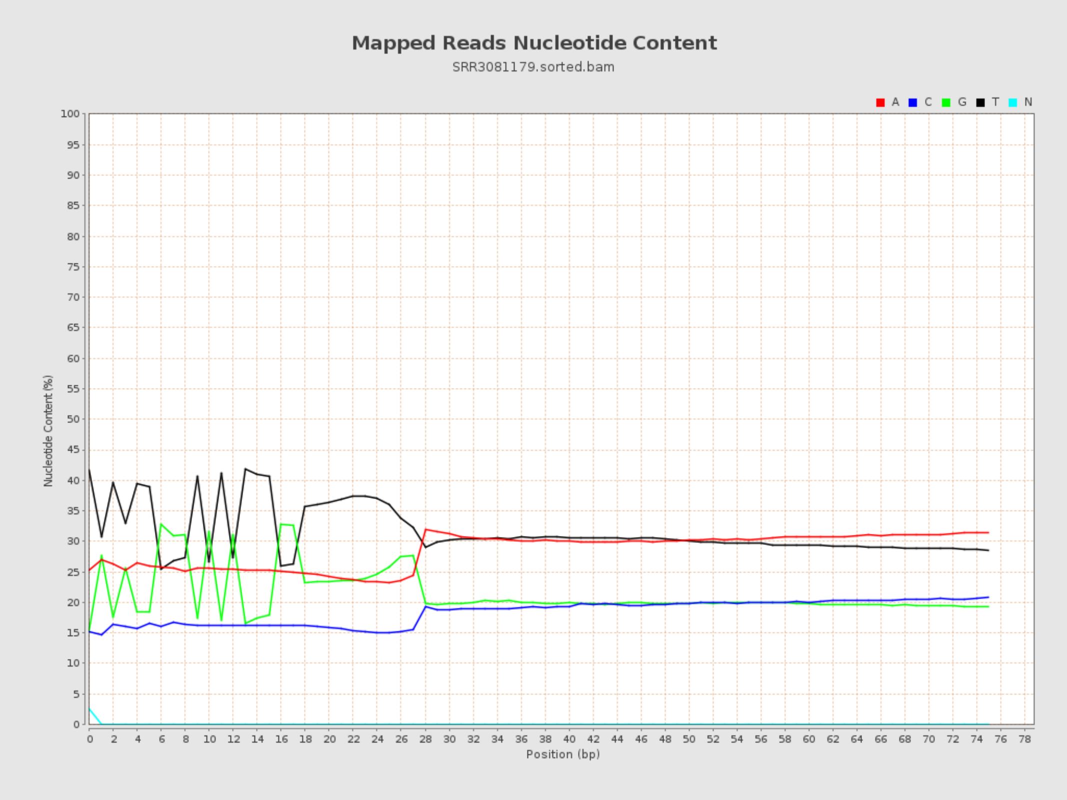
6. Results : Genome Fraction Coverage



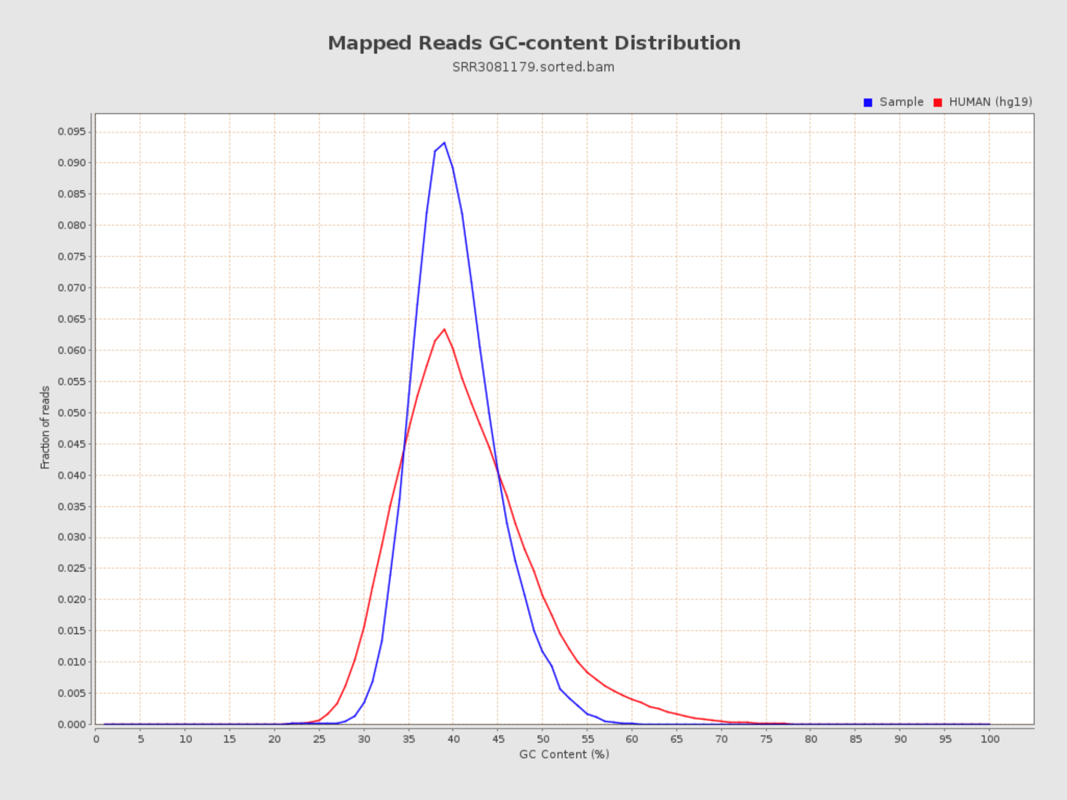
7. Results : Duplication Rate Histogram



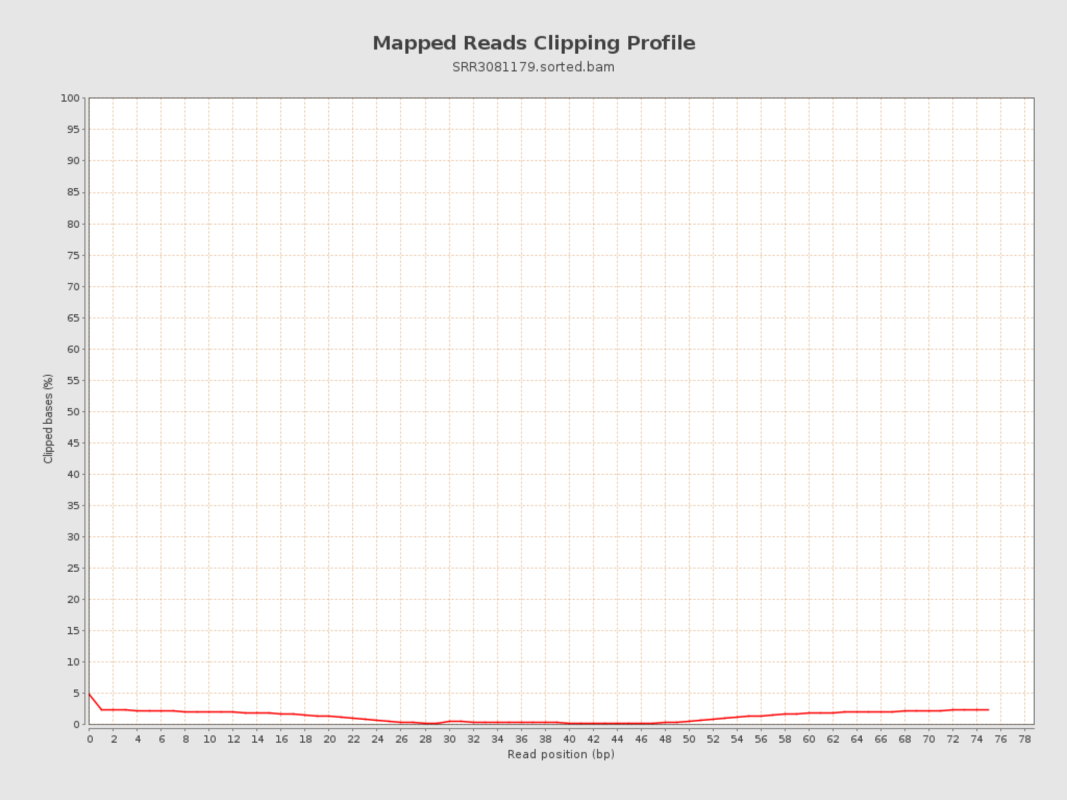
8. Results : Mapped Reads Nucleotide Content



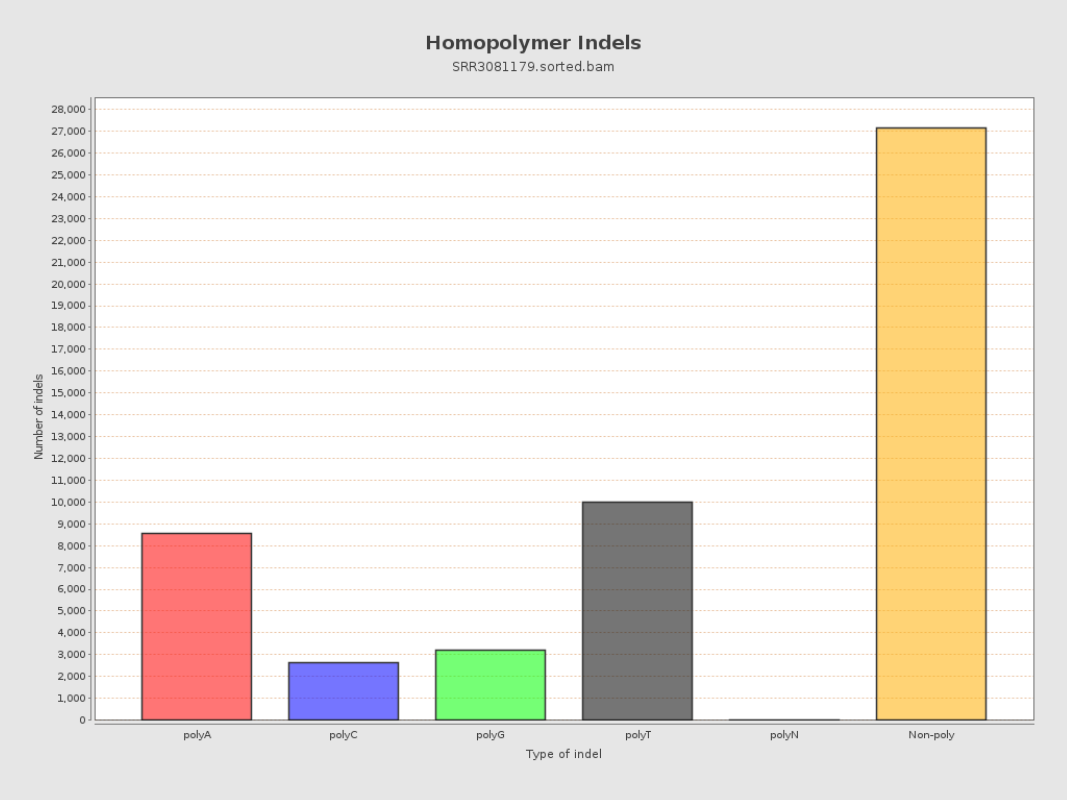
9. Results : Mapped Reads GC-content Distribution



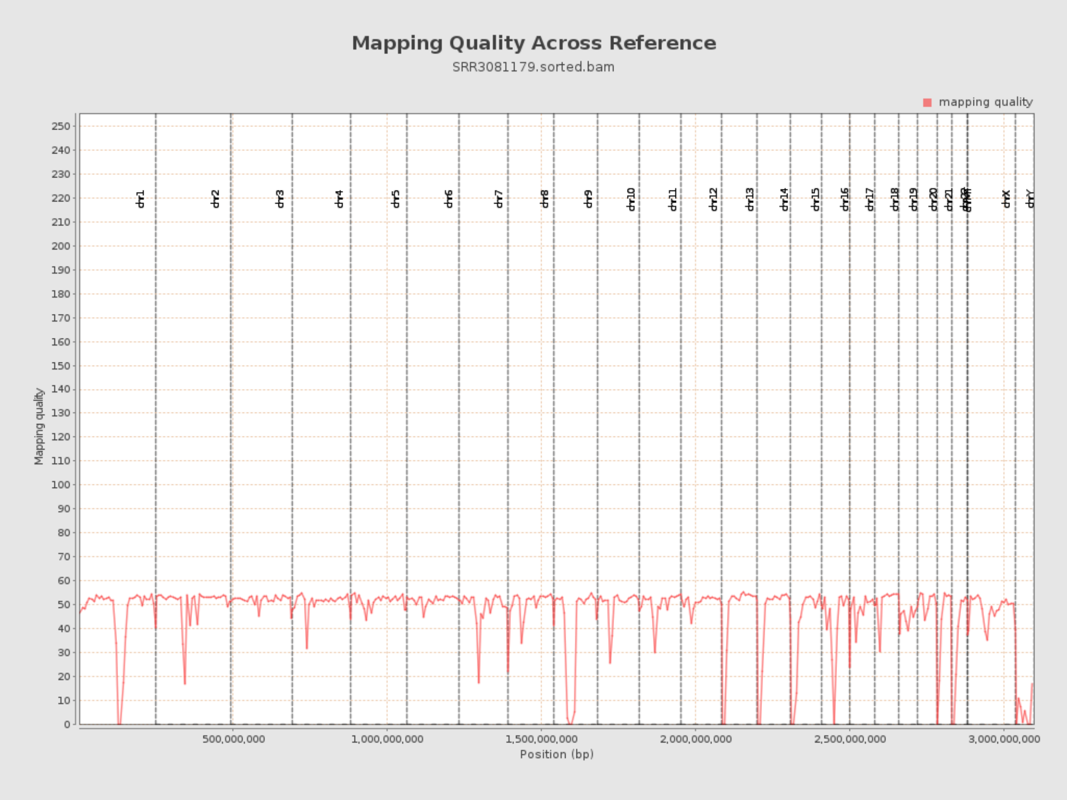
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram