Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 23:47:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081159.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_SRR3081159 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081159.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 23:47:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081159.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,534,492
Mapped reads	2,285,006 / 90.16%
Unmapped reads	249,486 / 9.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,585 / 0.93%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	90,872 / 3.59%
Duplication rate	3.05%
Clipped reads	965,931 / 38.11%

2.2. ACGT Content

Number/percentage of A's	44,169,397 / 28.6%
Number/percentage of C's	28,527,381 / 18.47%
Number/percentage of T's	48,640,463 / 31.49%
Number/percentage of G's	33,078,809 / 21.42%
Number/percentage of N's	45,989 / 0.03%
GC Percentage	39.88%

2.3. Coverage

Mean	0.0499

Standard Deviation	0.4156

2.4. Mapping Quality

Mean Mapping Quality	47.22

2.5. Mismatches and indels

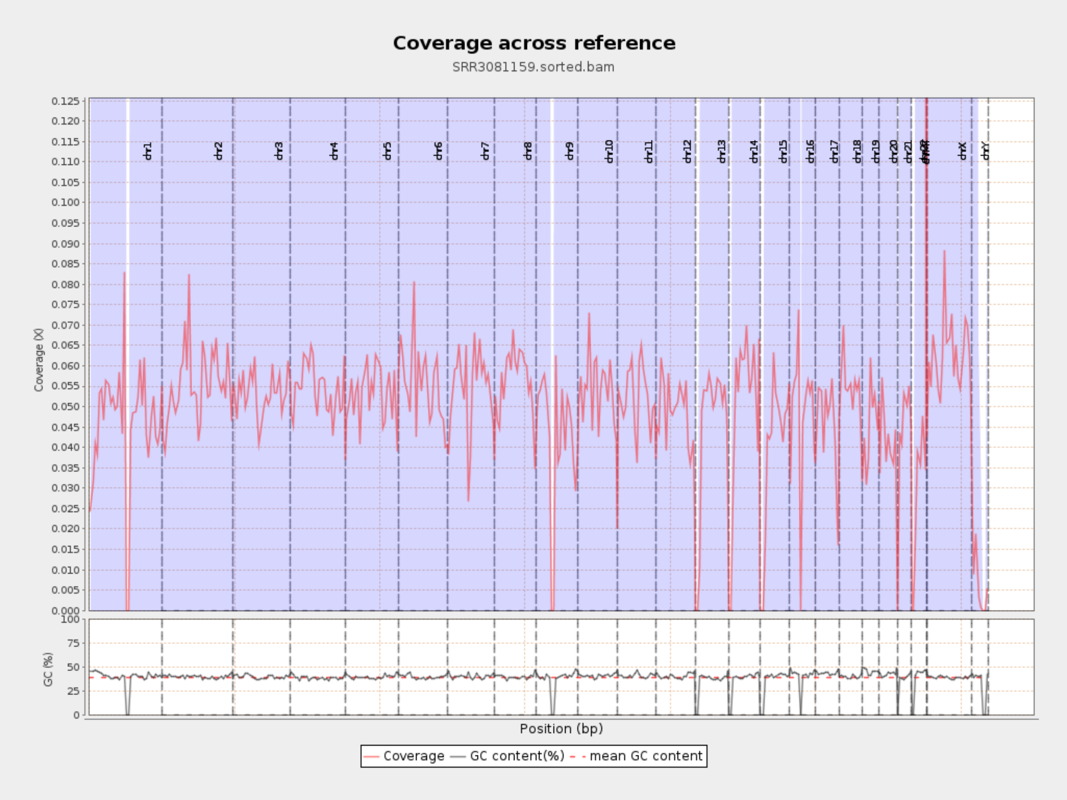
General error rate	0.86%
Mismatches	1,302,635
Insertions	11,969
Mapped reads with at least one insertion	0.52%
Deletions	37,789
Mapped reads with at least one deletion	1.64%
Homopolymer indels	47.12%

2.6. Chromosome stats

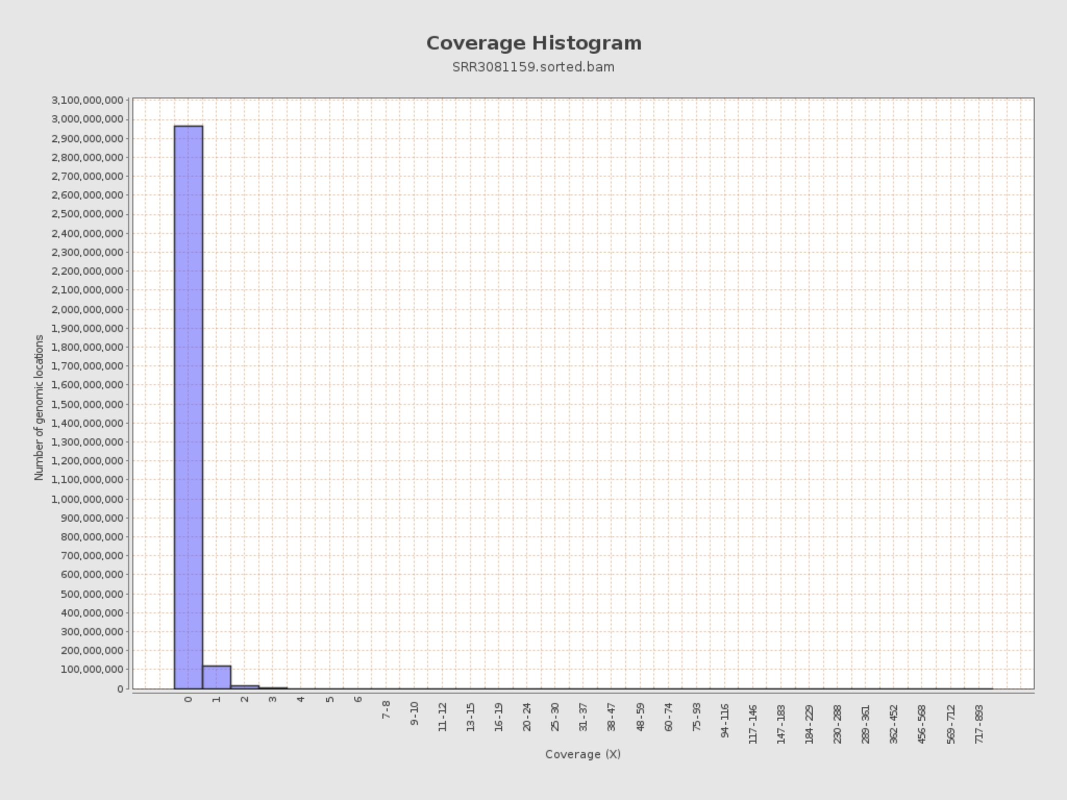
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11426310	0.0458	0.7371
chr2	243199373	13547567	0.0557	0.4669
chr3	198022430	10551581	0.0533	0.2571
chr4	191154276	10424162	0.0545	0.2706
chr5	180915260	9613837	0.0531	0.2578
chr6	171115067	9499841	0.0555	0.3532
chr7	159138663	8720649	0.0548	0.4831

chr8	146364022	8234162	0.0563	0.6034
chr9	141213431	5978862	0.0423	0.3606
chr10	135534747	7368750	0.0544	0.354
chr11	135006516	7020933	0.052	0.4276
chr12	133851895	6511518	0.0486	0.2513
chr13	115169878	5077552	0.0441	0.2343
chr14	107349540	5242060	0.0488	0.2694
chr15	102531392	4008363	0.0391	0.2225
chr16	90354753	4383510	0.0485	0.2813
chr17	81195210	3632679	0.0447	0.2992
chr18	78077248	4312600	0.0552	0.7757
chr19	59128983	2665793	0.0451	0.5771
chr20	63025520	2616264	0.0415	0.236
chr21	48129895	2103865	0.0437	0.2578
chr22	51304566	1450798	0.0283	0.1854
chrMT	16571	27897	1.6835	1.5486
chrX	155270560	9713909	0.0626	0.3283
chrY	59373566	389410	0.0066	0.1412

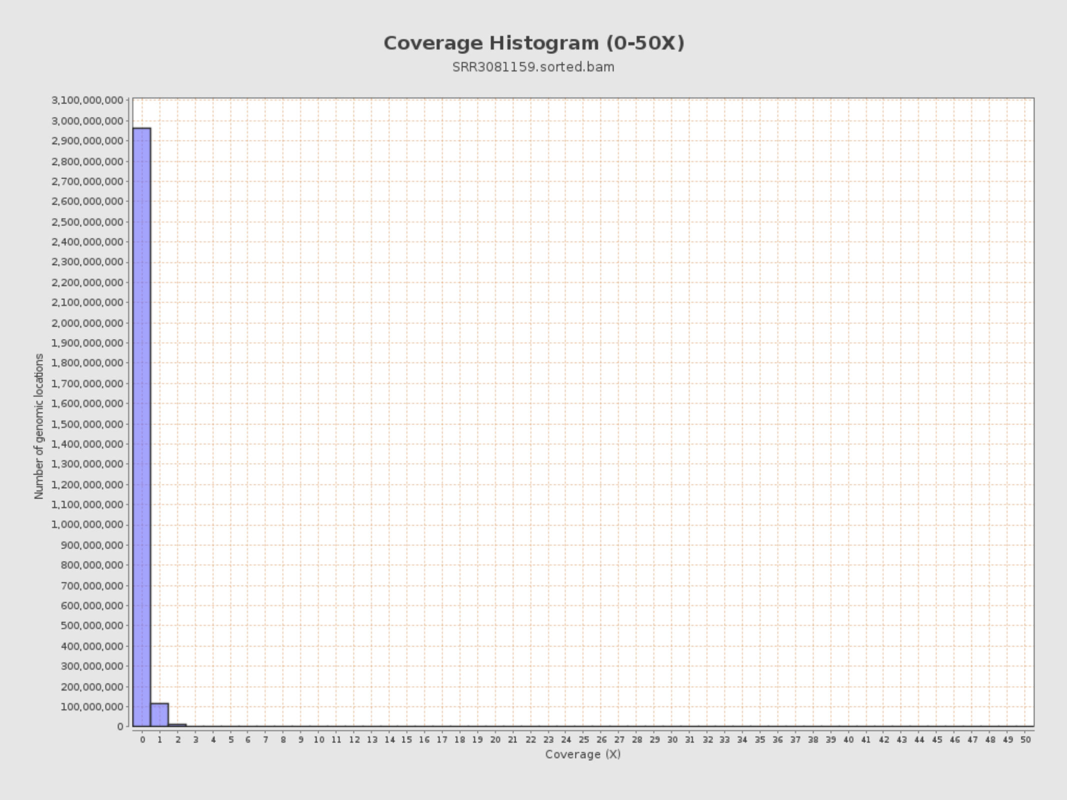
3. Results : Coverage across reference



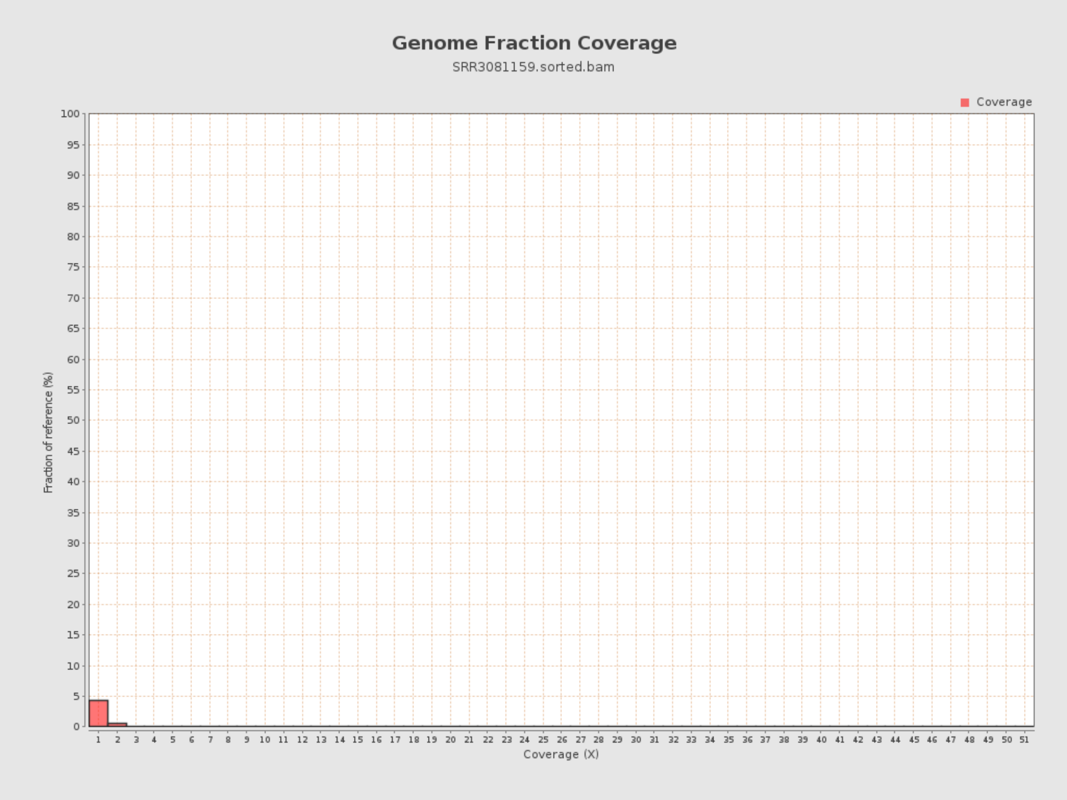
4. Results : Coverage Histogram



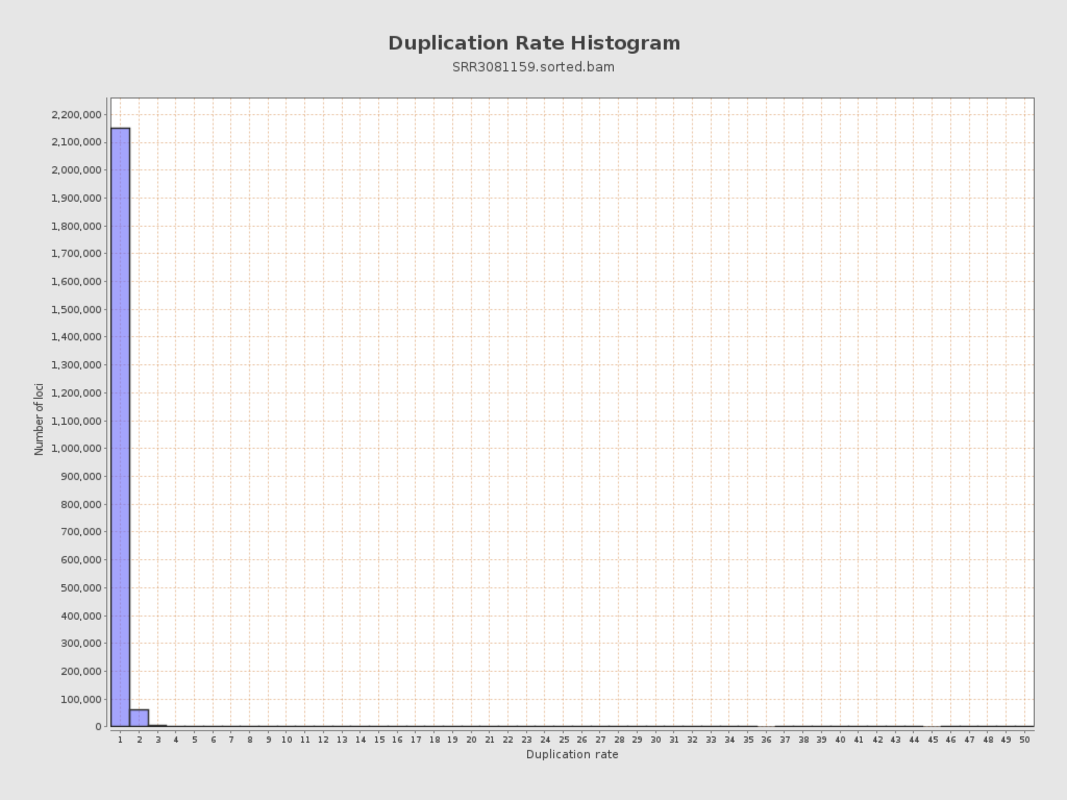
5. Results : Coverage Histogram (0-50X)



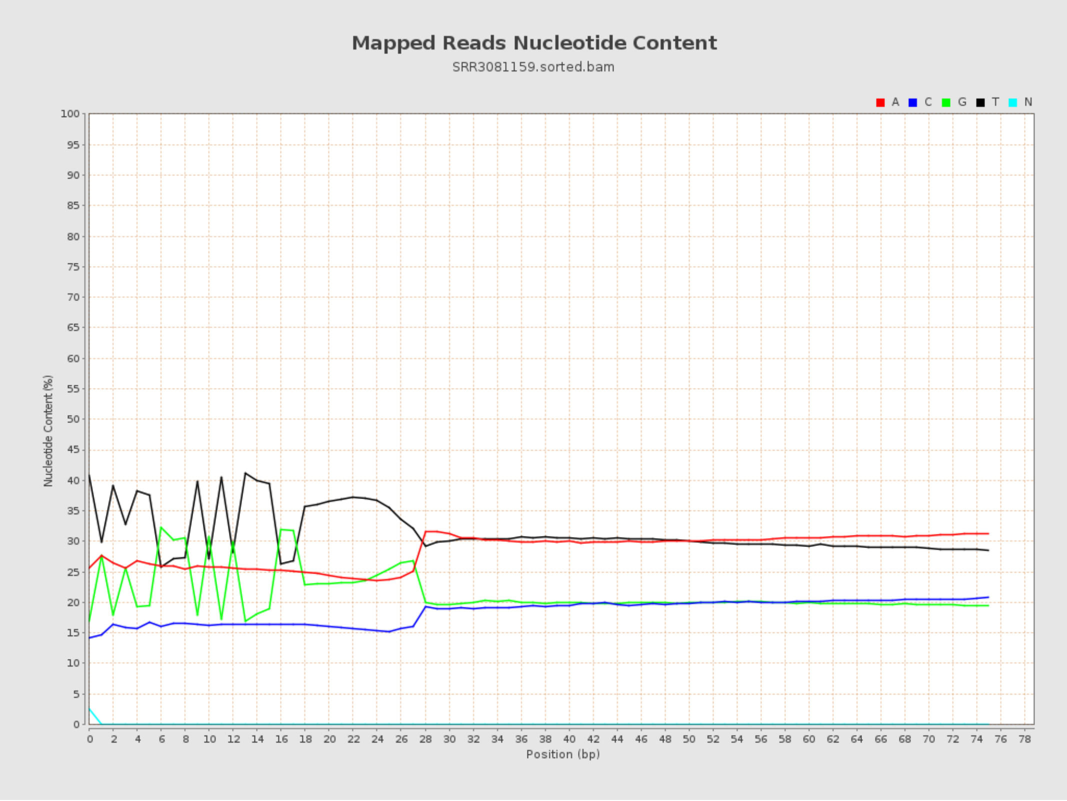
6. Results : Genome Fraction Coverage



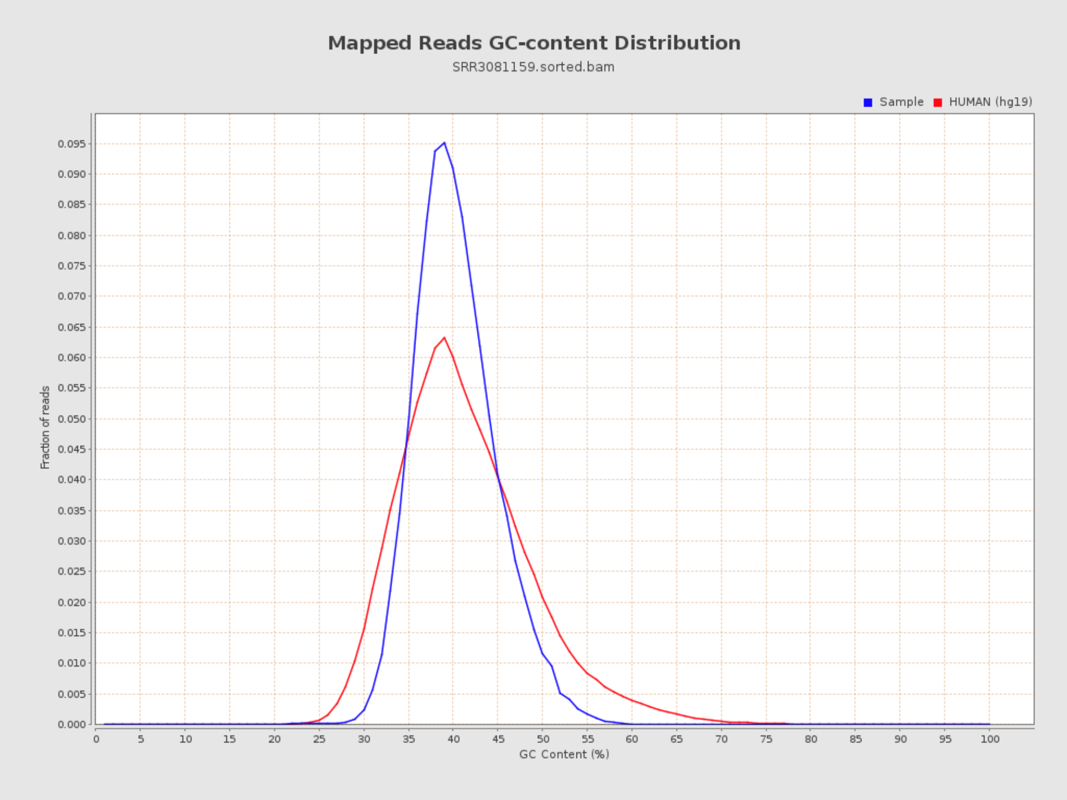
7. Results : Duplication Rate Histogram



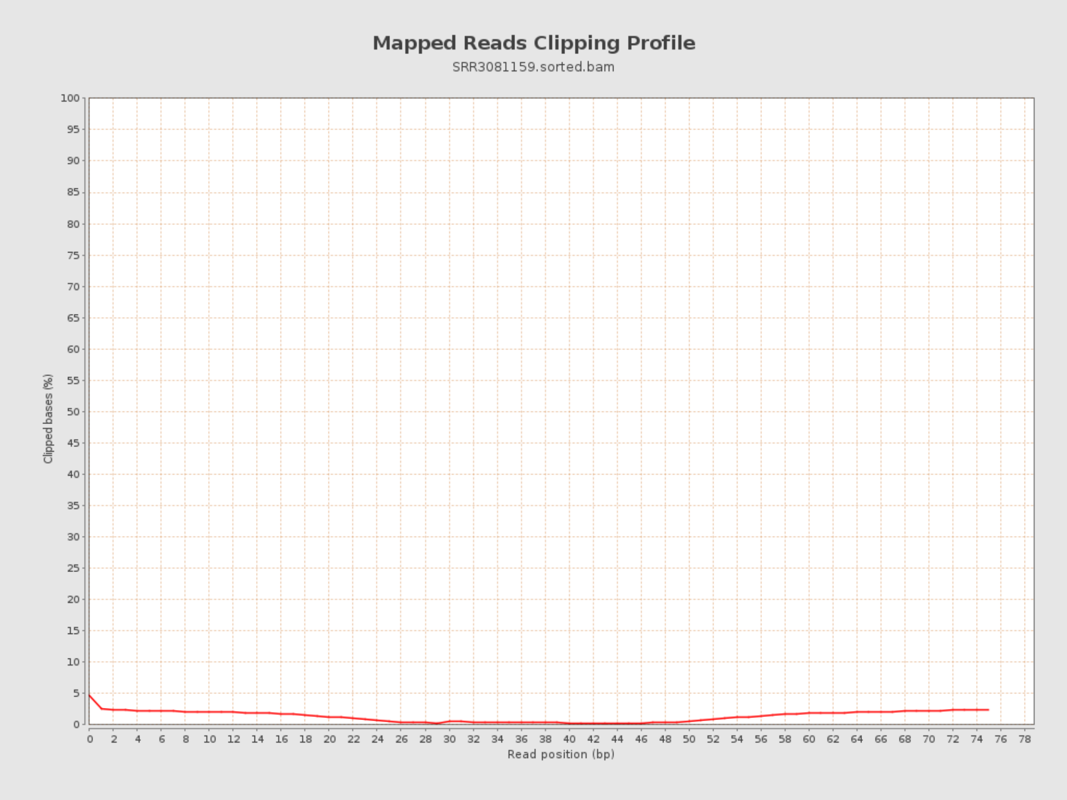
8. Results : Mapped Reads Nucleotide Content



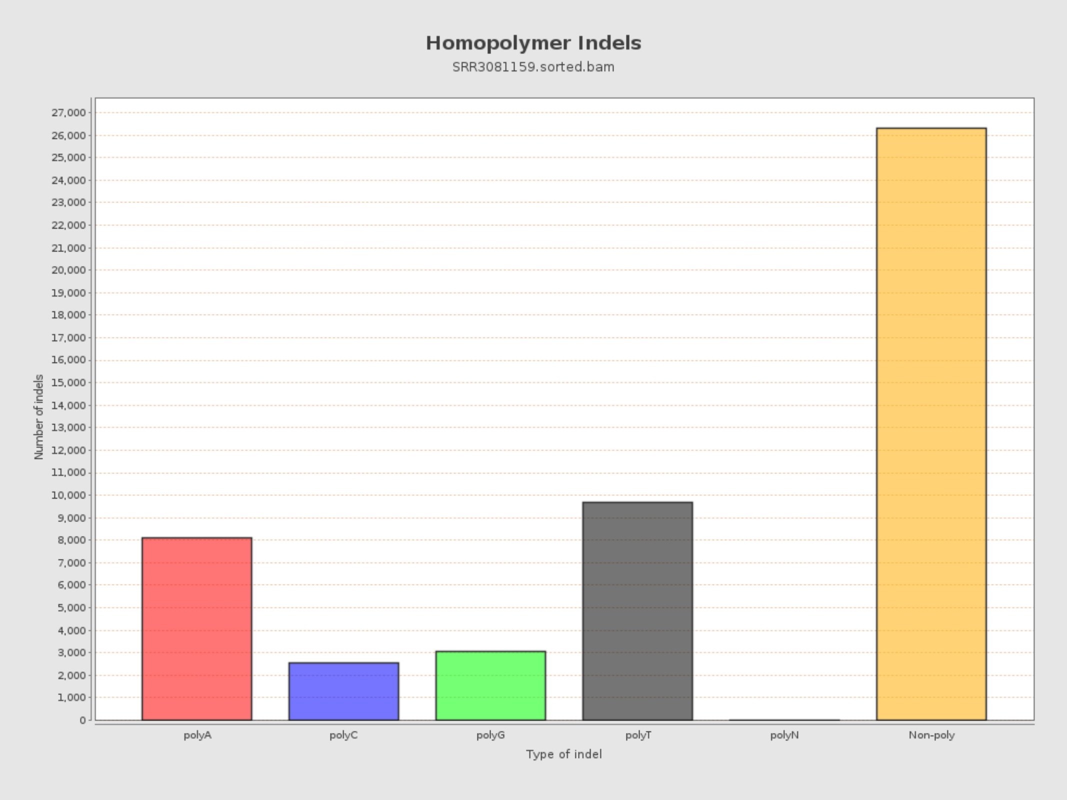
9. Results : Mapped Reads GC-content Distribution



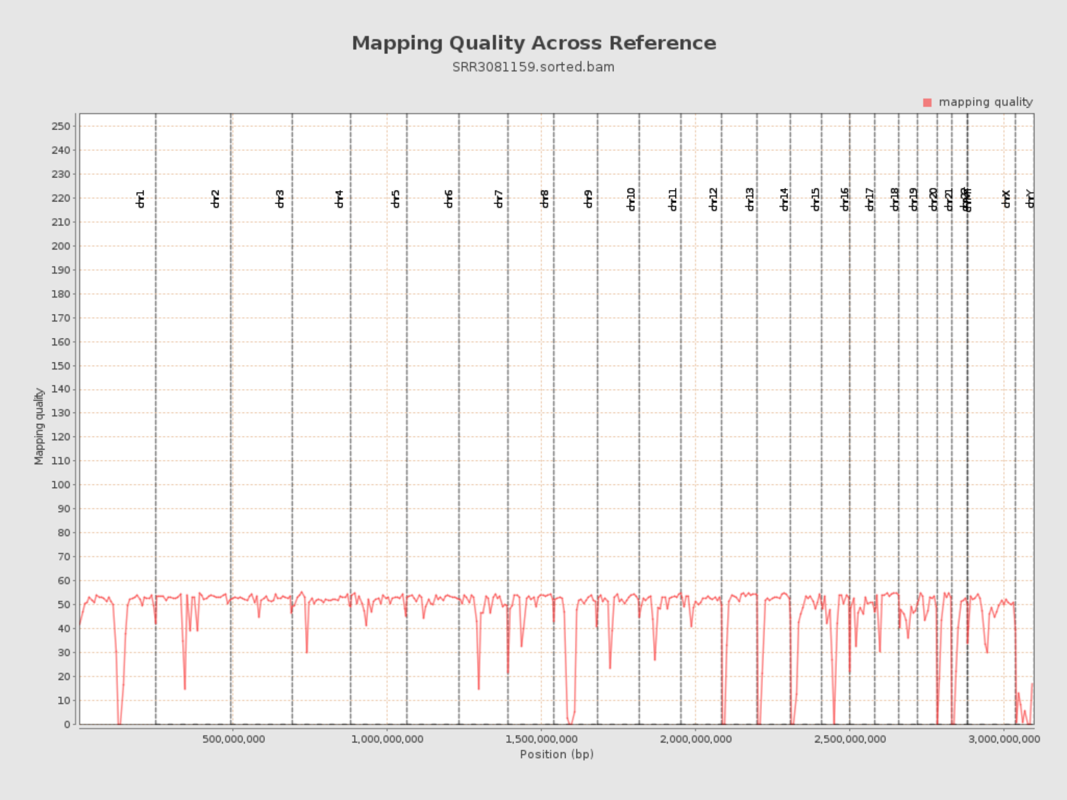
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram