Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 00:27:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081170.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_SRR3081170 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081170.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 00:27:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081170.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,432,317
Mapped reads	2,132,840 / 87.69%
Unmapped reads	299,477 / 12.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,714 / 0.85%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	92,726 / 3.81%
Duplication rate	3.54%
Clipped reads	995,514 / 40.93%

2.2. ACGT Content

Number/percentage of A's	39,521,516 / 27.87%
Number/percentage of C's	26,248,259 / 18.51%
Number/percentage of T's	44,673,631 / 31.51%
Number/percentage of G's	31,304,496 / 22.08%
Number/percentage of N's	41,812 / 0.03%
GC Percentage	40.59%

2.3. Coverage

Mean	0.0458

Standard Deviation	0.3572

2.4. Mapping Quality

Mean Mapping Quality	46.62

2.5. Mismatches and indels

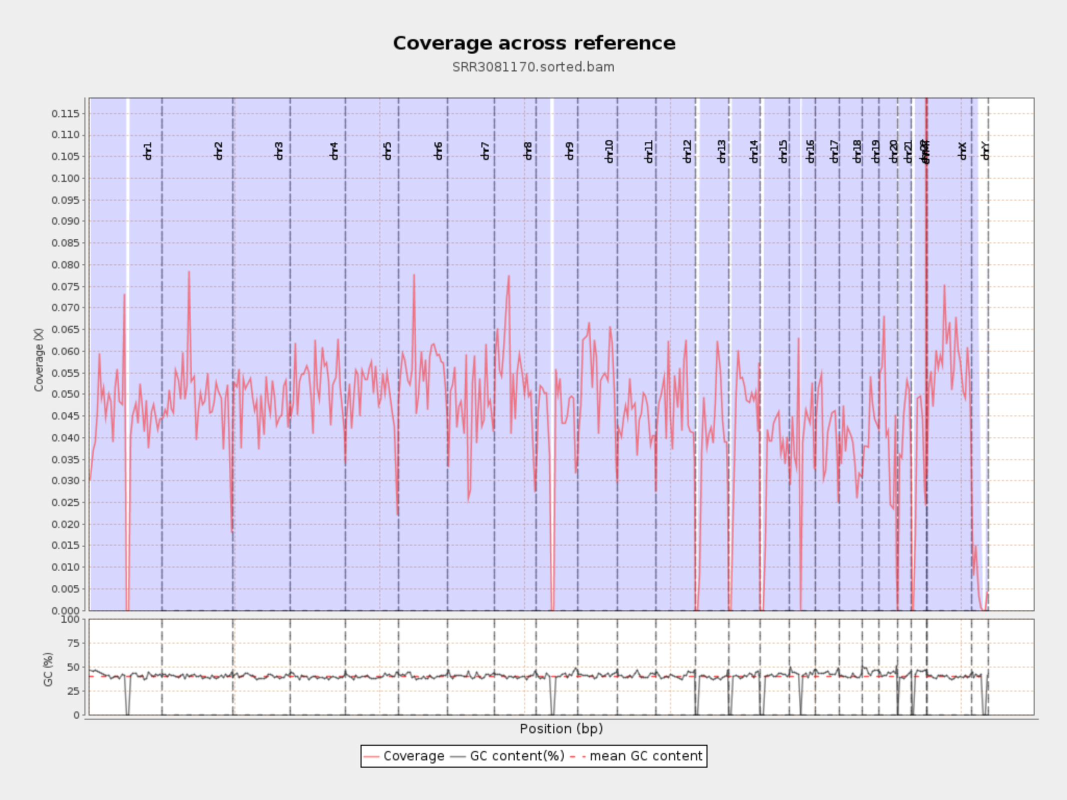
General error rate	0.85%
Mismatches	1,180,932
Insertions	10,767
Mapped reads with at least one insertion	0.5%
Deletions	30,896
Mapped reads with at least one deletion	1.43%
Homopolymer indels	47.09%

2.6. Chromosome stats

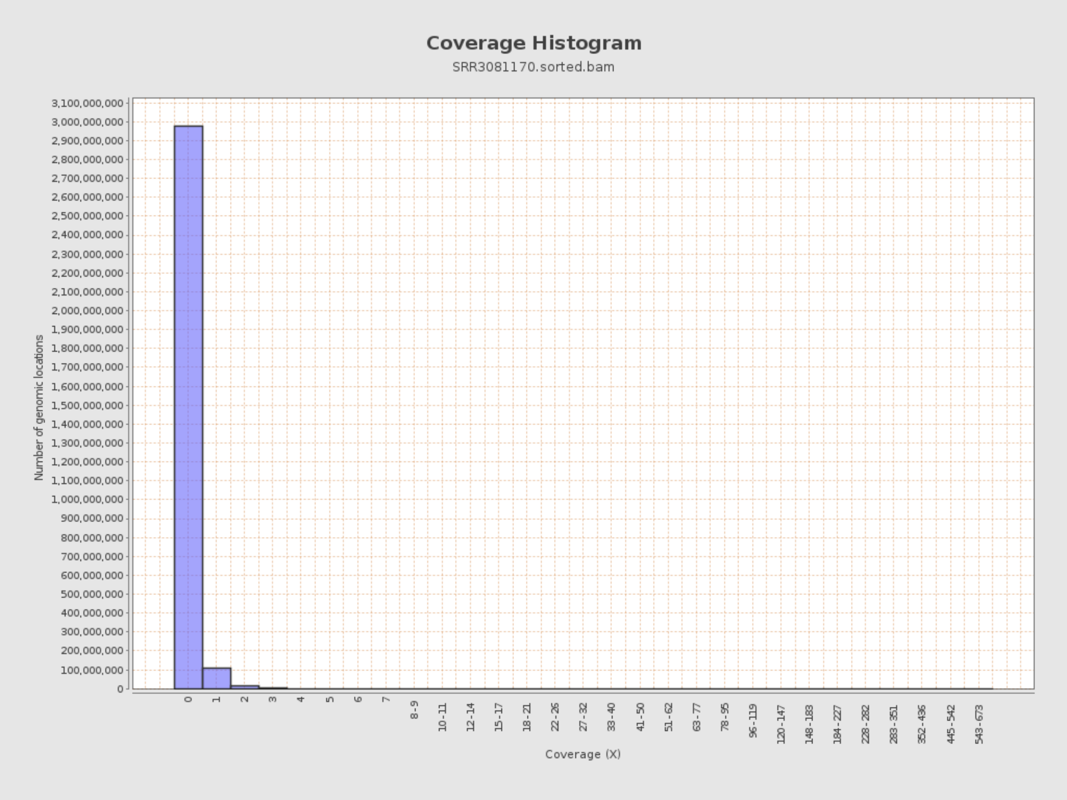
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10904124	0.0437	0.599
chr2	243199373	11923381	0.049	0.4381
chr3	198022430	9581143	0.0484	0.2475
chr4	191154276	10019969	0.0524	0.2656
chr5	180915260	8981101	0.0496	0.2529
chr6	171115067	9610921	0.0562	0.3531
chr7	159138663	7429536	0.0467	0.4273

chr8	146364022	7918113	0.0541	0.4827
chr9	141213431	5927159	0.042	0.3268
chr10	135534747	7504392	0.0554	0.3344
chr11	135006516	5978025	0.0443	0.3048
chr12	133851895	6451629	0.0482	0.2528
chr13	115169878	4248497	0.0369	0.217
chr14	107349540	4539259	0.0423	0.2487
chr15	102531392	3331453	0.0325	0.2096
chr16	90354753	3528364	0.0391	0.2432
chr17	81195210	3382330	0.0417	0.3042
chr18	78077248	2865952	0.0367	0.5419
chr19	59128983	2522127	0.0427	0.4281
chr20	63025520	2658652	0.0422	0.2396
chr21	48129895	1881149	0.0391	0.2363
chr22	51304566	1503759	0.0293	0.1909
chrMT	16571	41669	2.5146	2.2949
chrX	155270560	8780890	0.0566	0.2944
chrY	59373566	325772	0.0055	0.1094

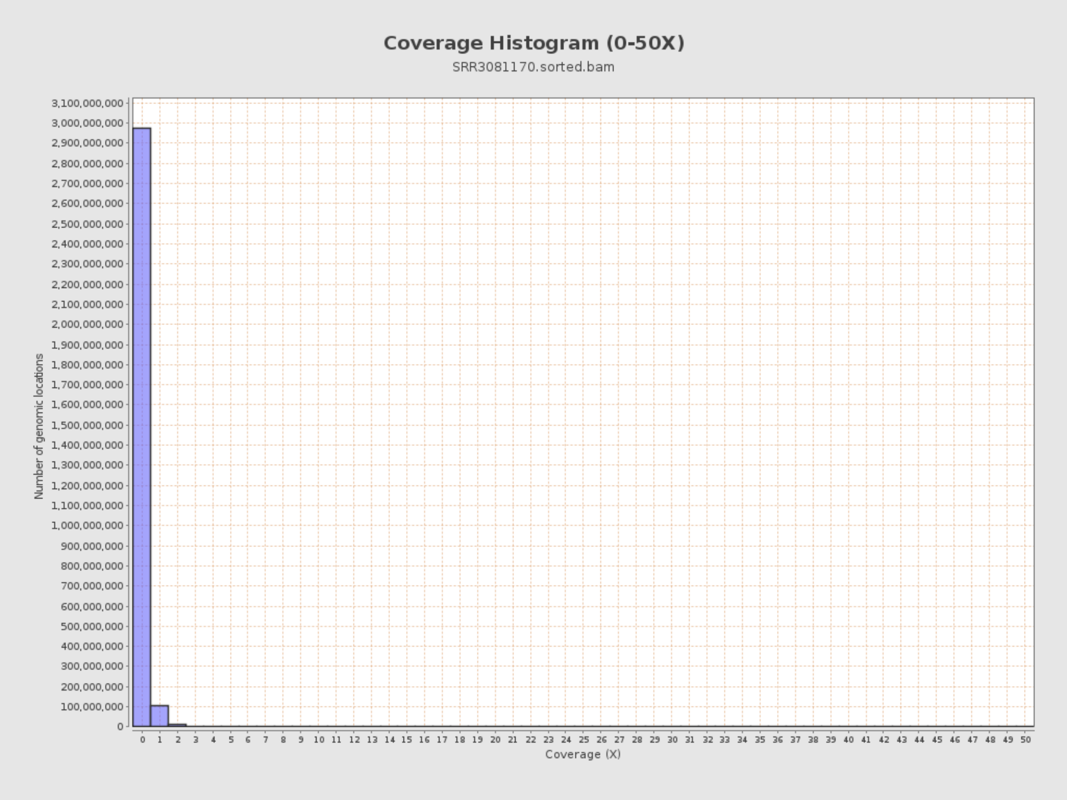
3. Results : Coverage across reference



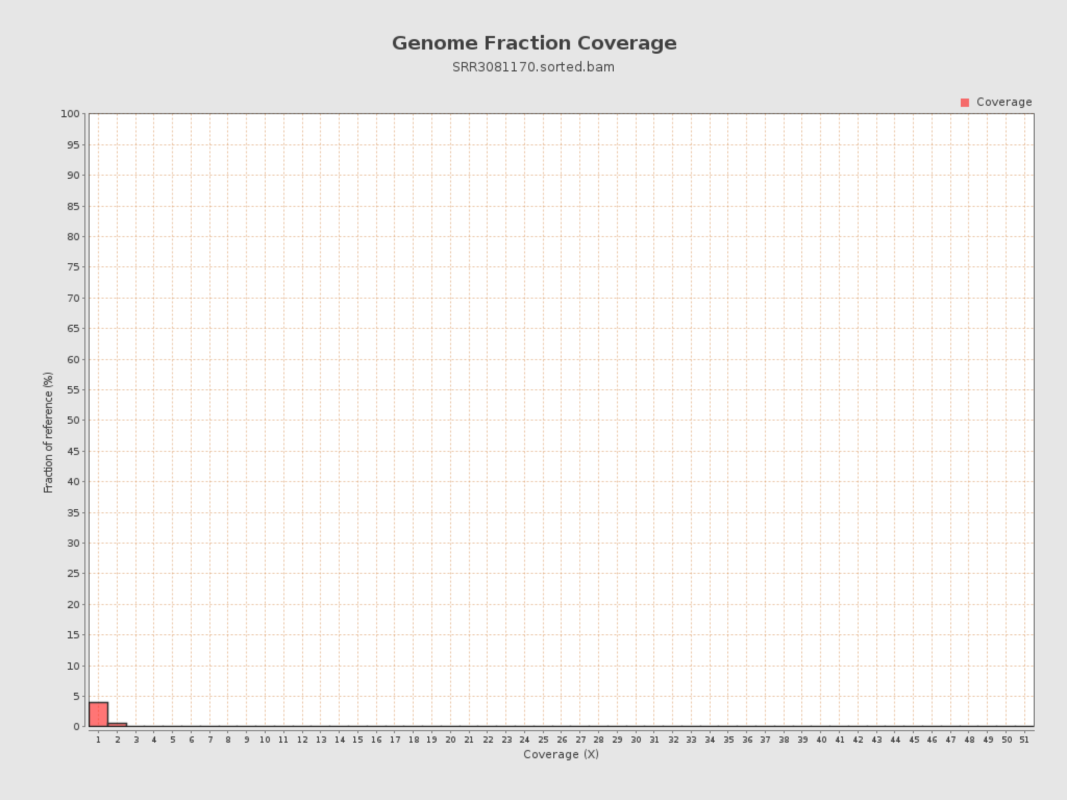
4. Results : Coverage Histogram



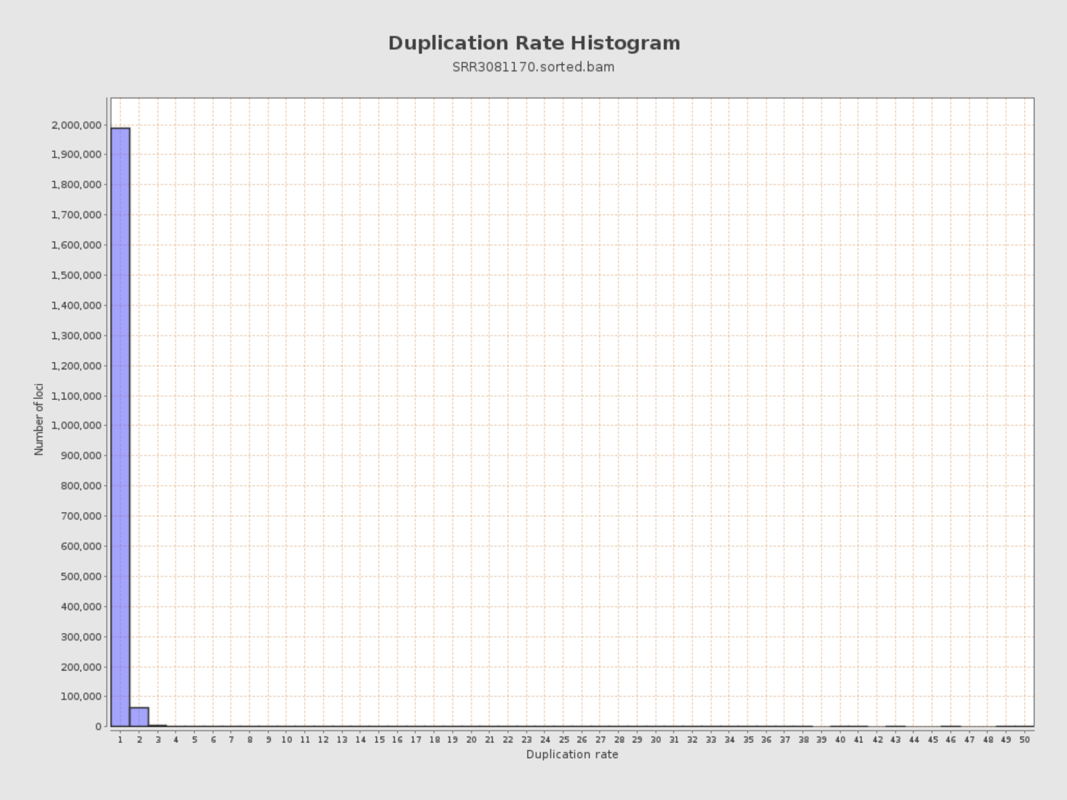
5. Results : Coverage Histogram (0-50X)



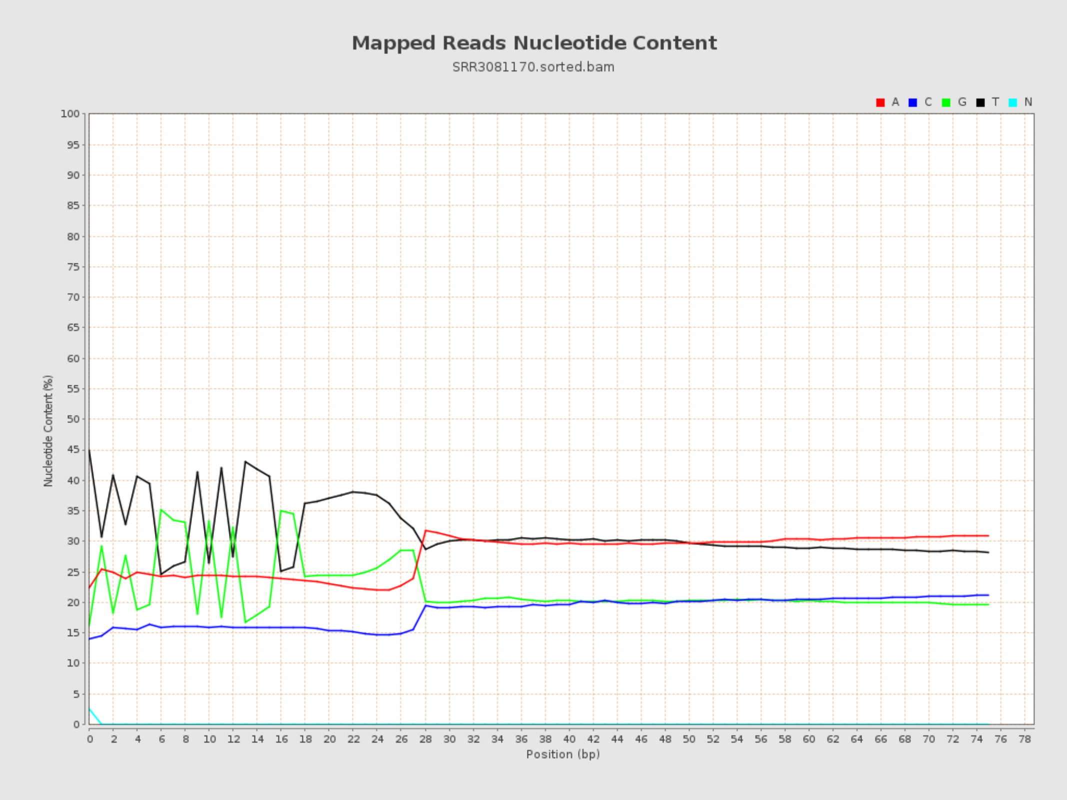
6. Results : Genome Fraction Coverage



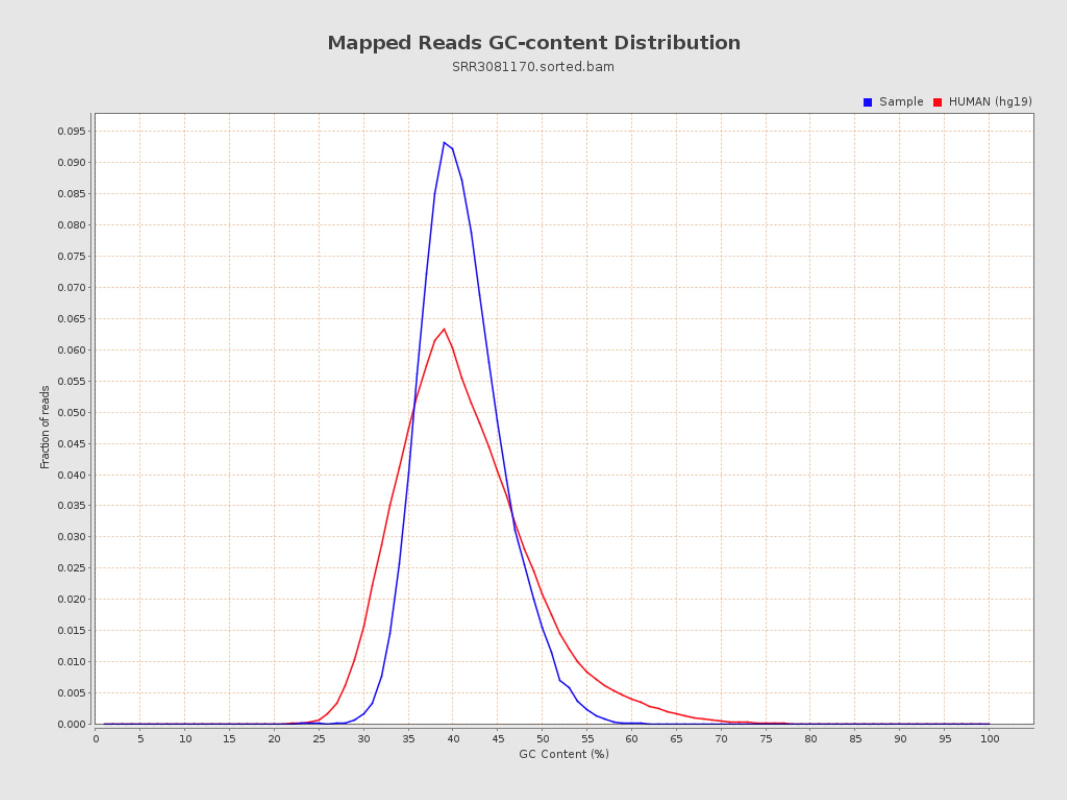
7. Results : Duplication Rate Histogram



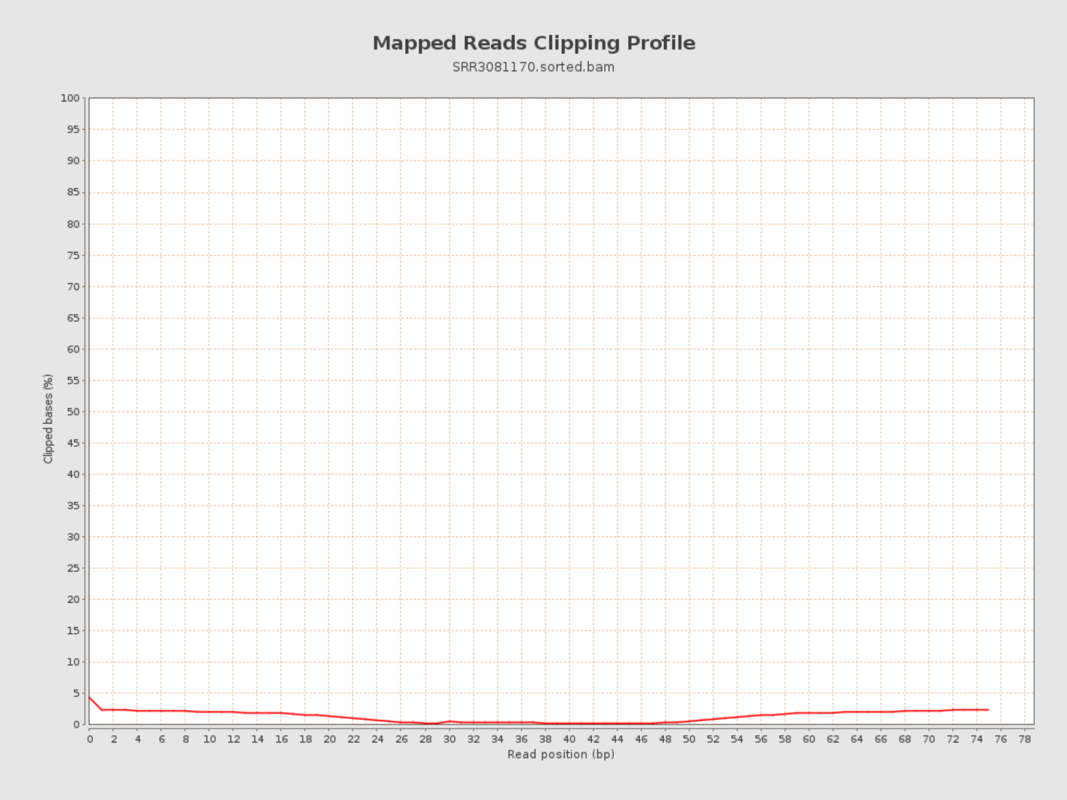
8. Results : Mapped Reads Nucleotide Content



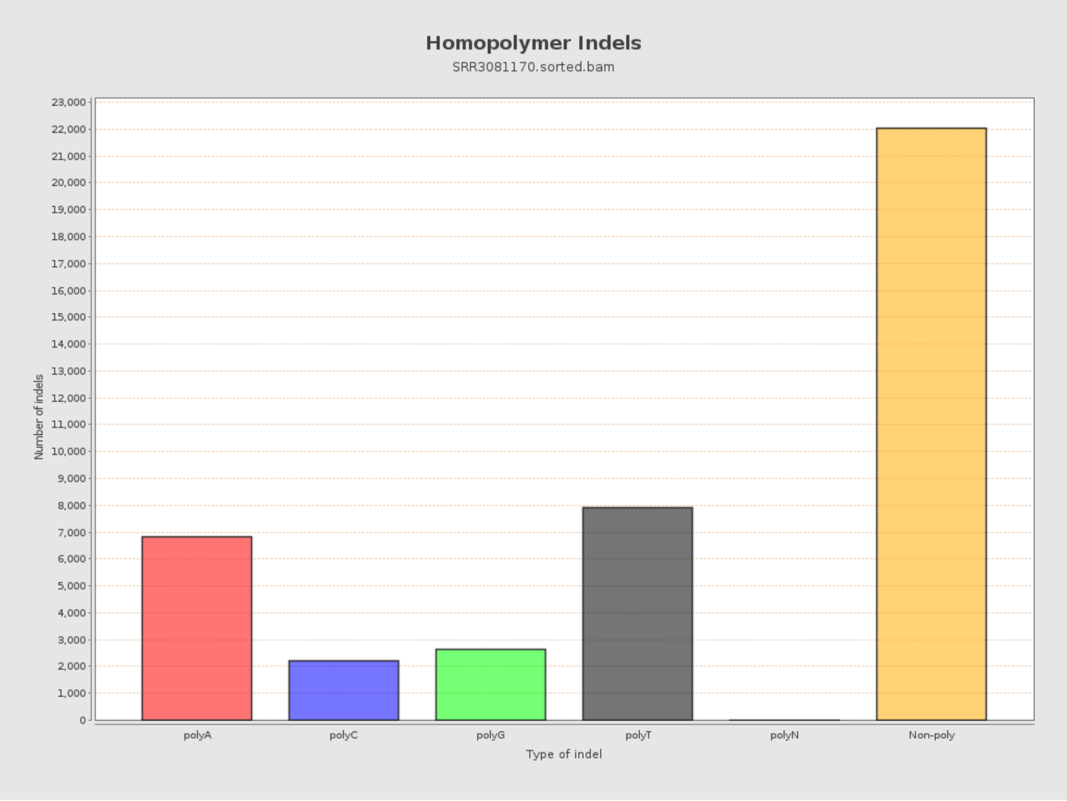
9. Results : Mapped Reads GC-content Distribution



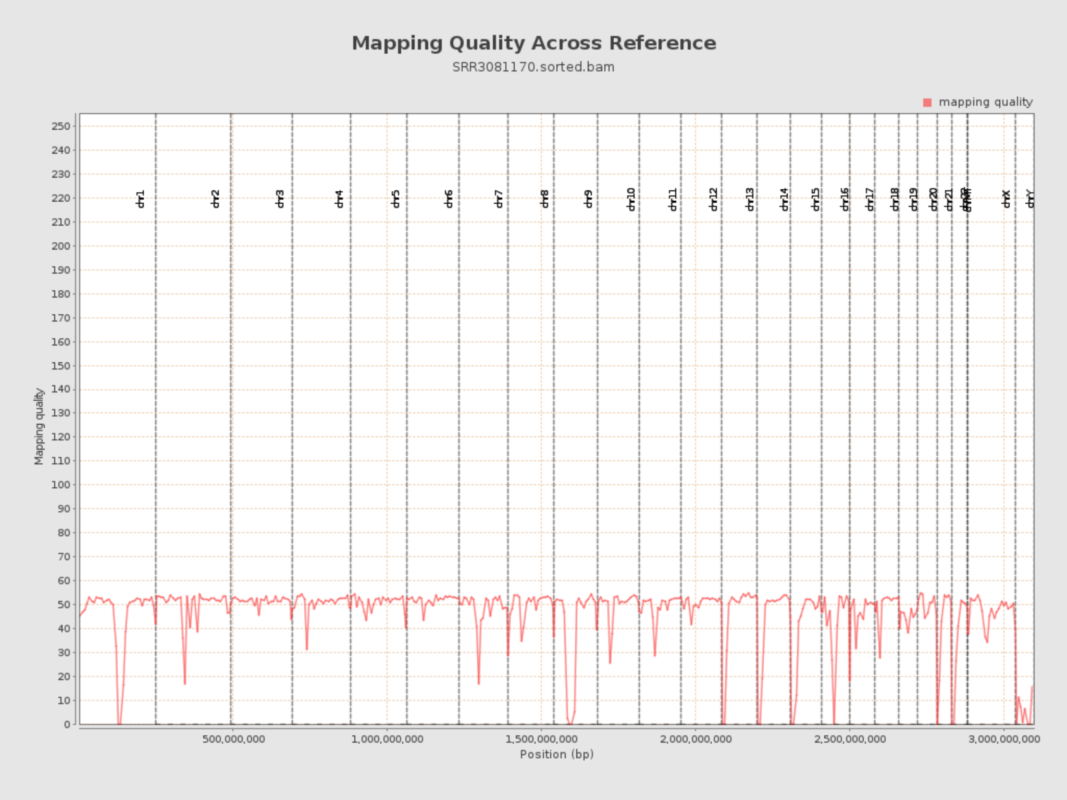
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram