Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 22:52:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013352.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_SRR6013352 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013352.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 22:52:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013352.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,604,791
Mapped reads	2,372,730 / 91.09%
Unmapped reads	232,061 / 8.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,863 / 0.88%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	153,007 / 5.87%
Duplication rate	5.14%
Clipped reads	1,107,534 / 42.52%

2.2. ACGT Content

Number/percentage of A's	42,919,550 / 27.36%
Number/percentage of C's	29,365,217 / 18.72%
Number/percentage of T's	49,331,393 / 31.45%
Number/percentage of G's	35,232,750 / 22.46%
Number/percentage of N's	17,241 / 0.01%
GC Percentage	41.18%

2.3. Coverage

Mean	0.0507

Standard Deviation	0.4597

2.4. Mapping Quality

Mean Mapping Quality	45.67

2.5. Mismatches and indels

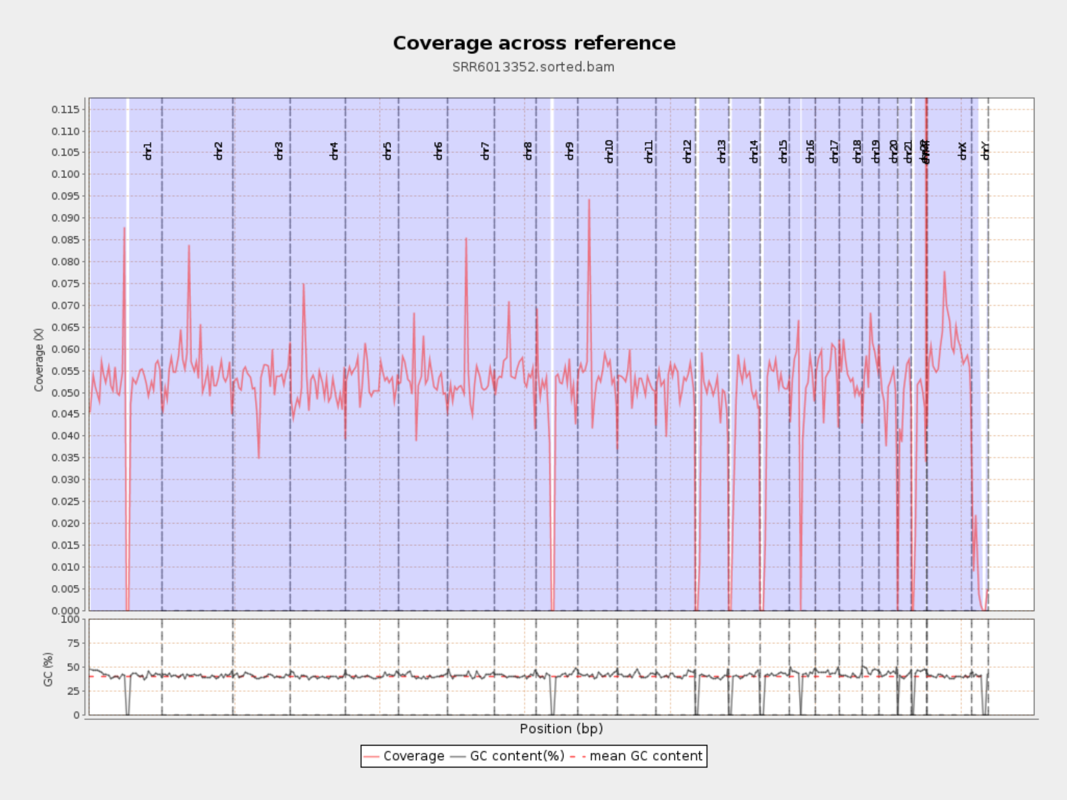
General error rate	0.75%
Mismatches	1,147,979
Insertions	11,801
Mapped reads with at least one insertion	0.49%
Deletions	36,885
Mapped reads with at least one deletion	1.54%
Homopolymer indels	46.91%

2.6. Chromosome stats

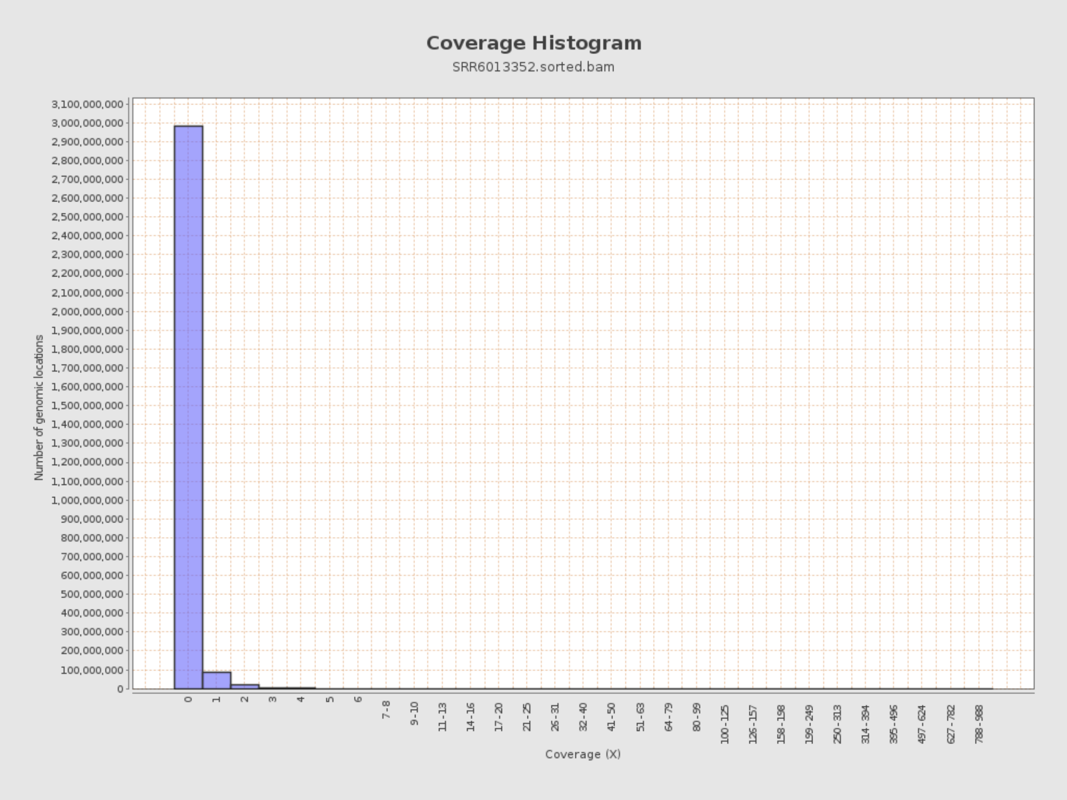
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12546752	0.0503	0.8918
chr2	243199373	13520544	0.0556	0.557
chr3	198022430	10424080	0.0526	0.2972
chr4	191154276	9753158	0.051	0.3178
chr5	180915260	9599336	0.0531	0.2976
chr6	171115067	9132167	0.0534	0.3644
chr7	159138663	8409177	0.0528	0.5909

chr8	146364022	7991201	0.0546	0.4512
chr9	141213431	6471951	0.0458	0.3618
chr10	135534747	7558445	0.0558	0.4983
chr11	135006516	7031280	0.0521	0.3583
chr12	133851895	7015676	0.0524	0.2983
chr13	115169878	4873089	0.0423	0.266
chr14	107349540	4660888	0.0434	0.2829
chr15	102531392	4427362	0.0432	0.2691
chr16	90354753	4414363	0.0489	0.3227
chr17	81195210	4423834	0.0545	0.3246
chr18	78077248	4219673	0.054	0.6663
chr19	59128983	3404997	0.0576	0.612
chr20	63025520	3106589	0.0493	0.2919
chr21	48129895	2129813	0.0443	0.2954
chr22	51304566	1759639	0.0343	0.2374
chrMT	16571	299006	18.0439	10.6148
chrX	155270560	9332019	0.0601	0.3376
chrY	59373566	425660	0.0072	0.1744

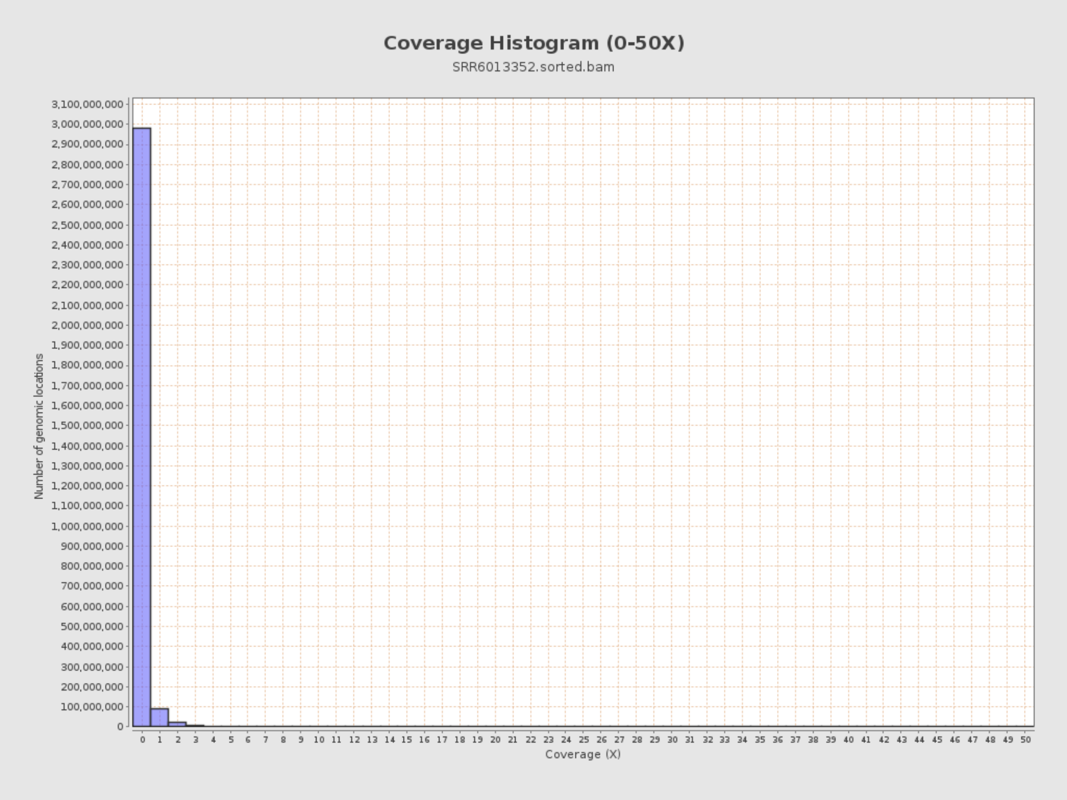
3. Results : Coverage across reference



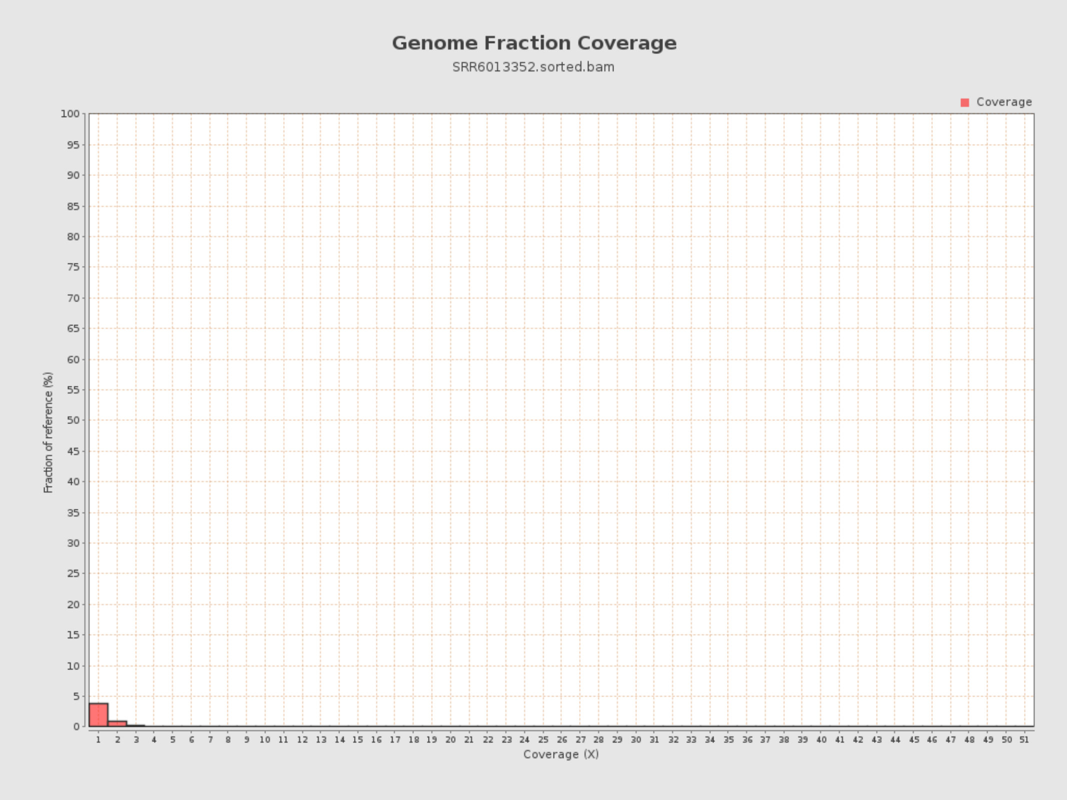
4. Results : Coverage Histogram



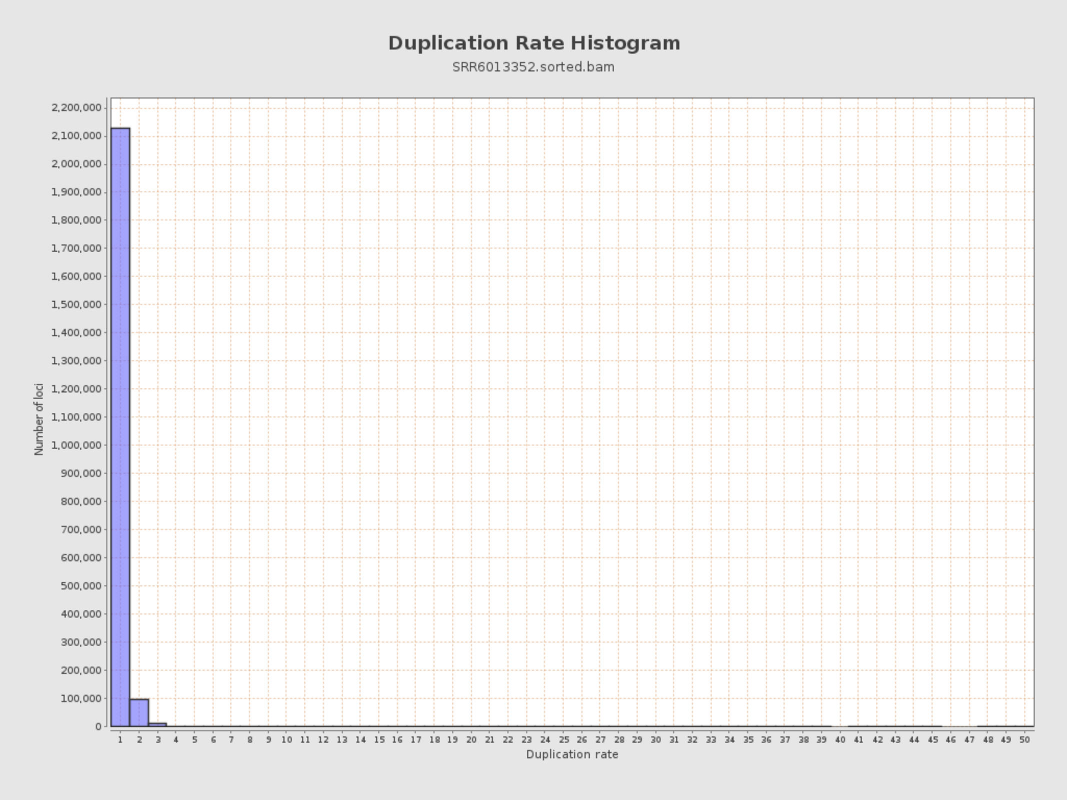
5. Results : Coverage Histogram (0-50X)



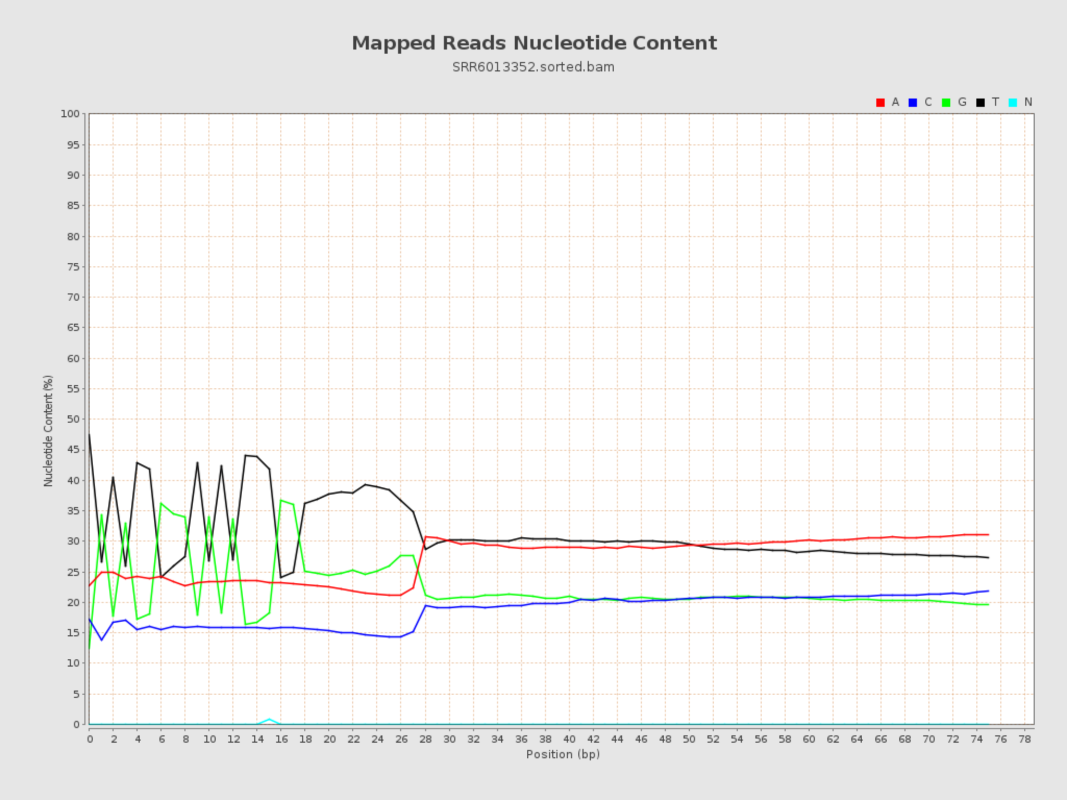
6. Results : Genome Fraction Coverage



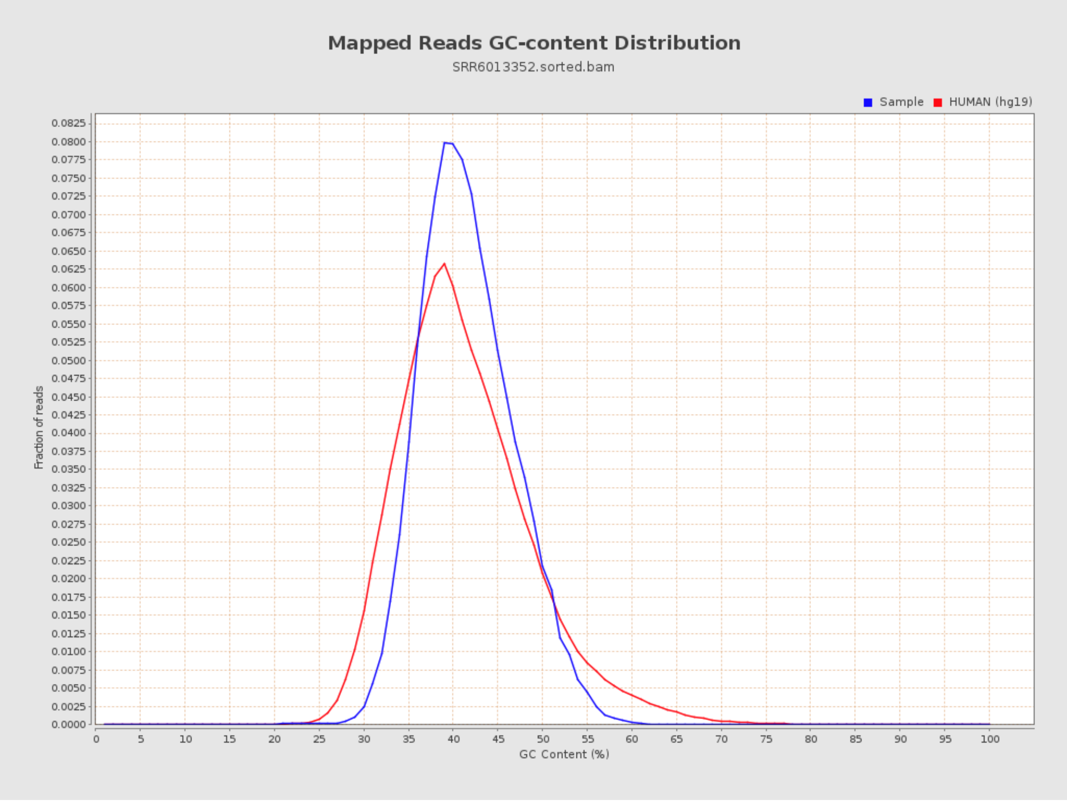
7. Results : Duplication Rate Histogram



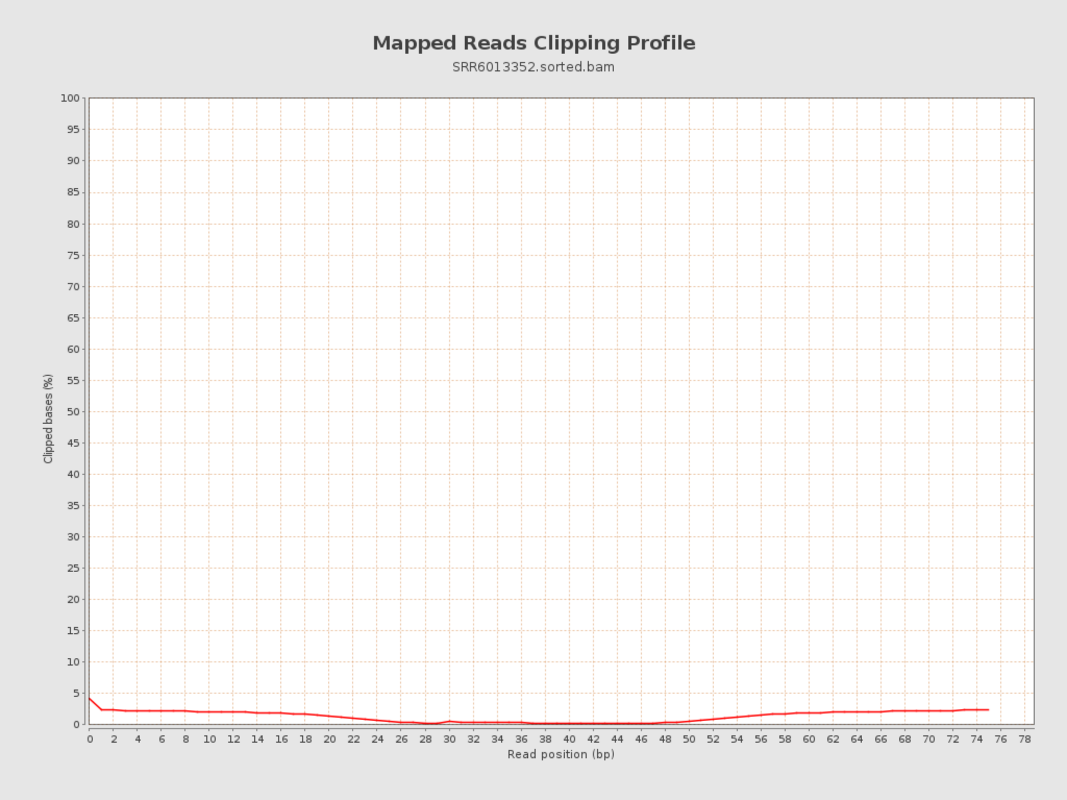
8. Results : Mapped Reads Nucleotide Content



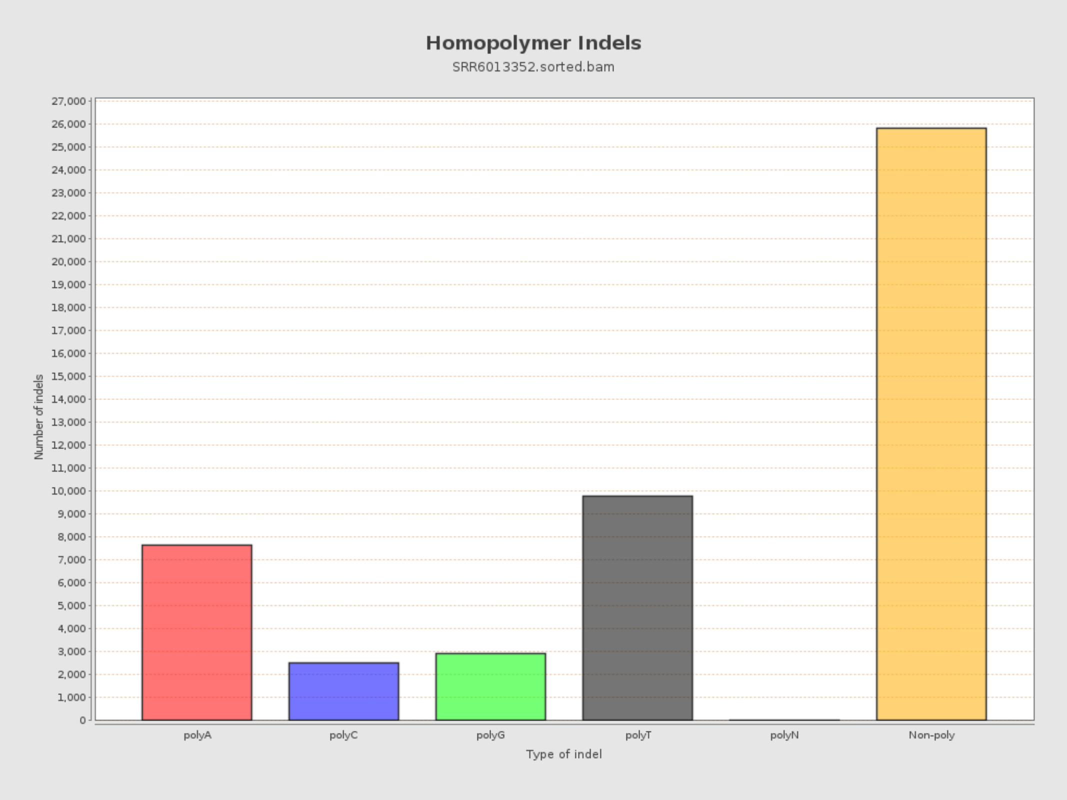
9. Results : Mapped Reads GC-content Distribution



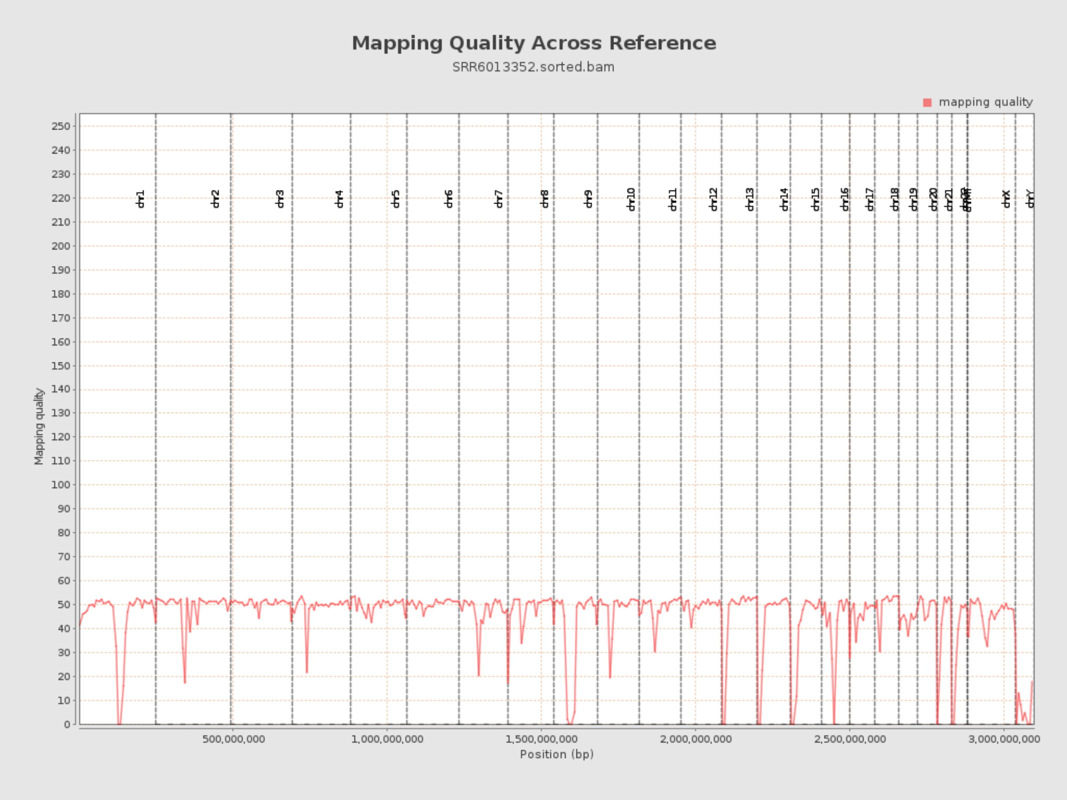
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram