Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 21:14:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230392.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_SRR6230392 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230392.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 21:14:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230392.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,583,035
Mapped reads	2,076,112 / 80.37%
Unmapped reads	506,923 / 19.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,523 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	95,518 / 3.7%
Duplication rate	3.26%
Clipped reads	1,128,071 / 43.67%

2.2. ACGT Content

Number/percentage of A's	35,554,893 / 26.7%
Number/percentage of C's	22,528,161 / 16.91%
Number/percentage of T's	44,564,647 / 33.46%
Number/percentage of G's	30,293,139 / 22.74%
Number/percentage of N's	248,397 / 0.19%
GC Percentage	39.66%

2.3. Coverage

Mean	0.043

Standard Deviation	0.463

2.4. Mapping Quality

Mean Mapping Quality	45.76

2.5. Mismatches and indels

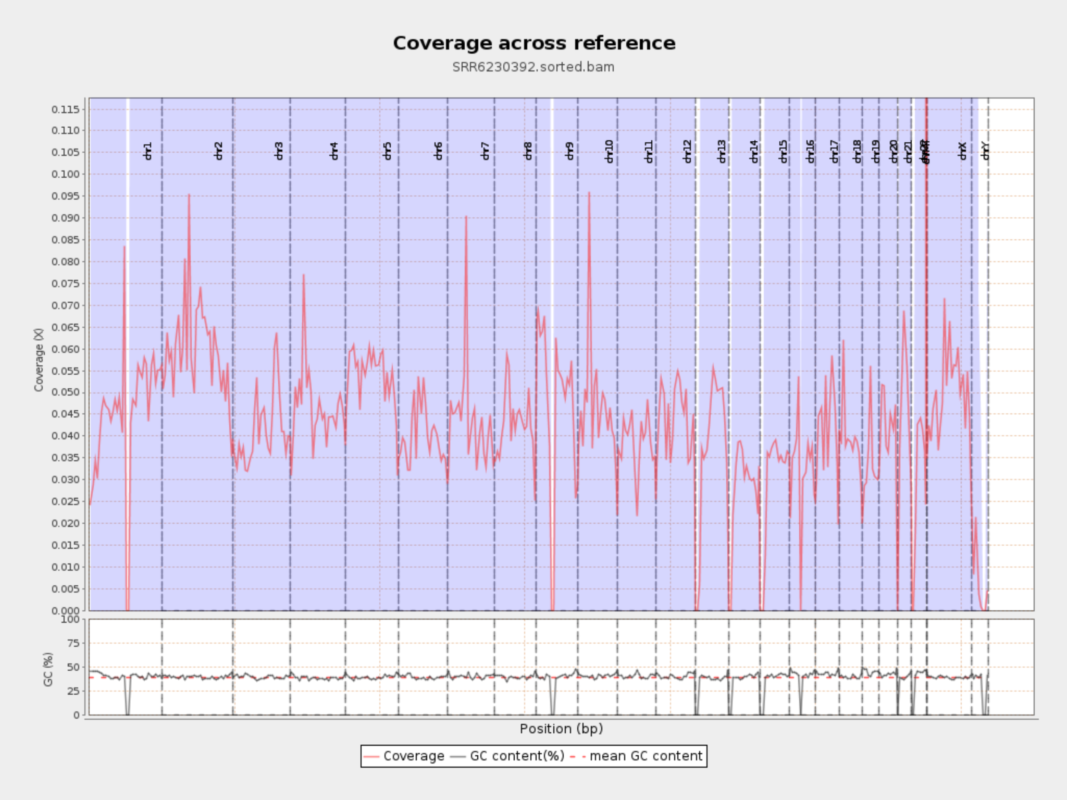
General error rate	0.94%
Mismatches	1,228,978
Insertions	12,259
Mapped reads with at least one insertion	0.58%
Deletions	37,816
Mapped reads with at least one deletion	1.8%
Homopolymer indels	47.88%

2.6. Chromosome stats

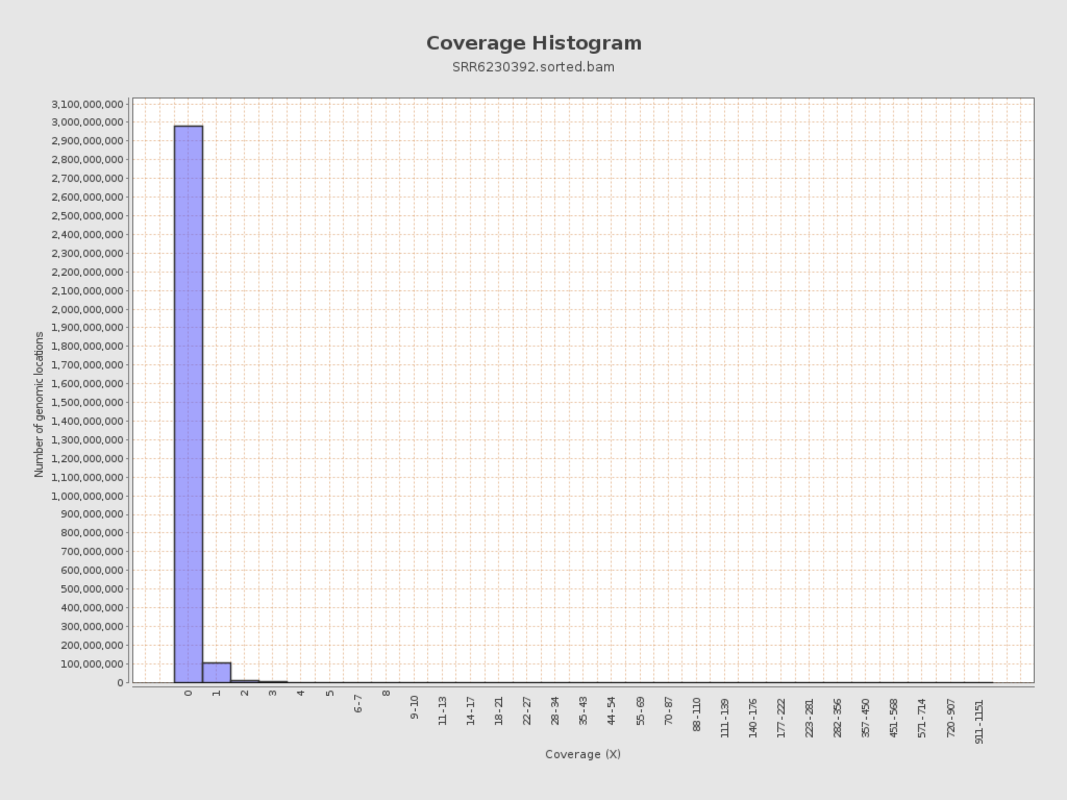
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11234341	0.0451	0.913
chr2	243199373	14660090	0.0603	0.4819
chr3	198022430	8198277	0.0414	0.2306
chr4	191154276	8906223	0.0466	0.2684
chr5	180915260	9838457	0.0544	0.2601
chr6	171115067	6861630	0.0401	0.2936
chr7	159138663	7034388	0.0442	0.6246

chr8	146364022	6221935	0.0425	0.6983
chr9	141213431	6745893	0.0478	0.4872
chr10	135534747	6394543	0.0472	0.486
chr11	135006516	5136867	0.038	0.3289
chr12	133851895	5906159	0.0441	0.2436
chr13	115169878	4264299	0.037	0.2114
chr14	107349540	2928364	0.0273	0.2177
chr15	102531392	2994735	0.0292	0.1888
chr16	90354753	2929546	0.0324	0.2507
chr17	81195210	3364987	0.0414	0.254
chr18	78077248	3132384	0.0401	0.8133
chr19	59128983	2011832	0.034	0.6429
chr20	63025520	2689159	0.0427	0.2439
chr21	48129895	2120663	0.0441	0.2586
chr22	51304566	1461370	0.0285	0.185
chrMT	16571	76247	4.6012	3.269
chrX	155270560	7758186	0.05	0.3045
chrY	59373566	381124	0.0064	0.1664

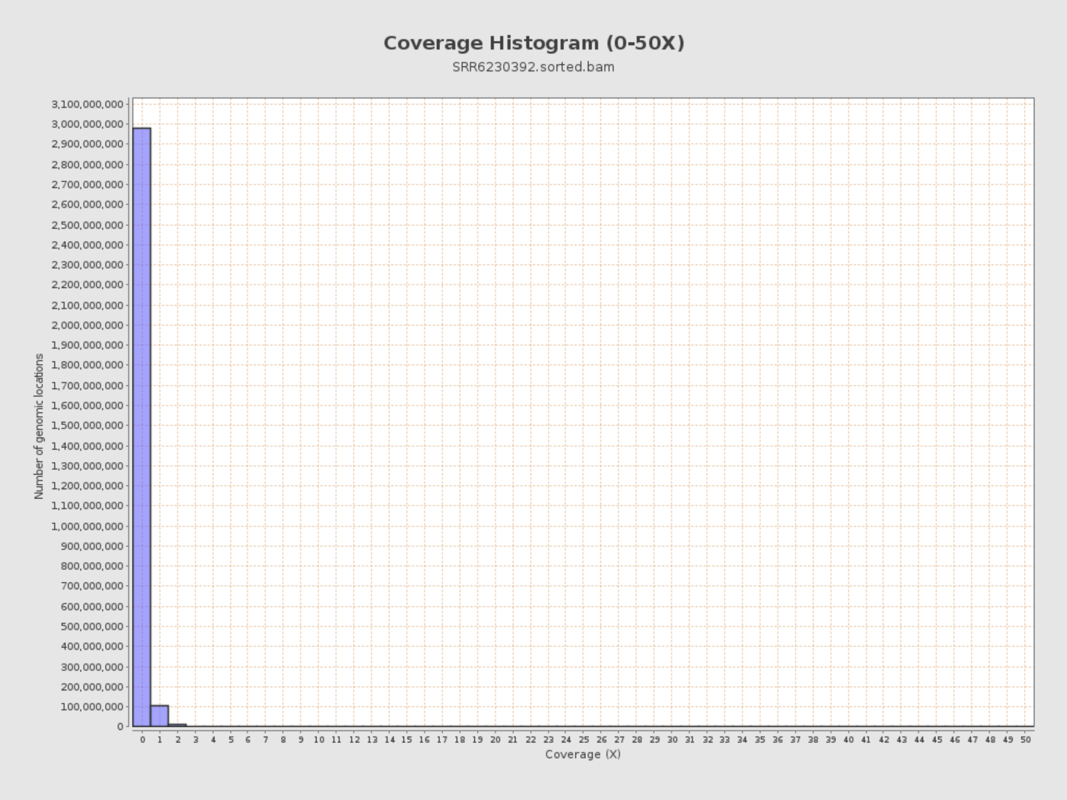
3. Results : Coverage across reference



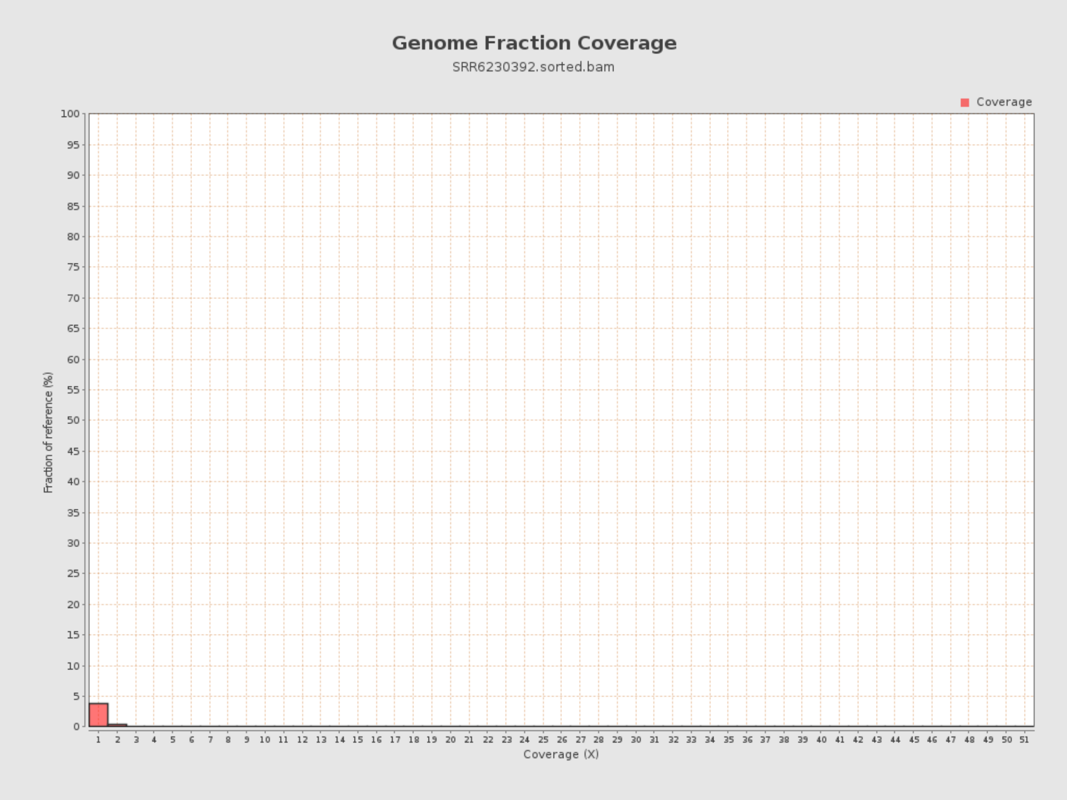
4. Results : Coverage Histogram



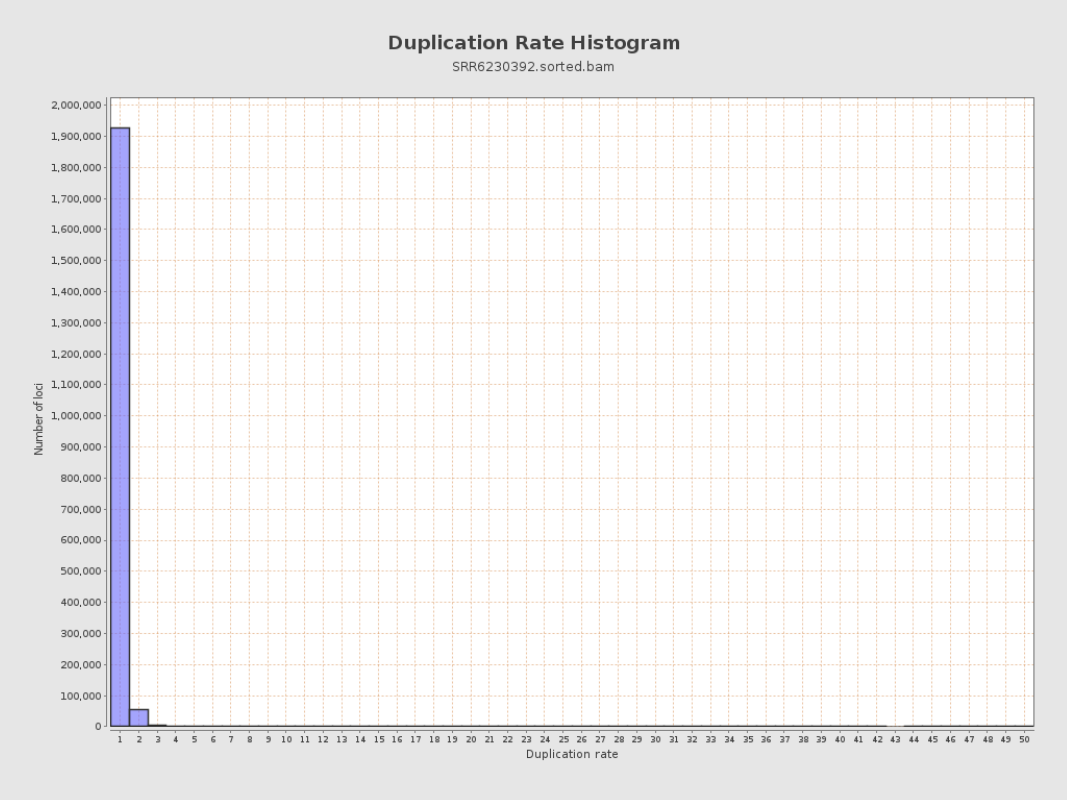
5. Results : Coverage Histogram (0-50X)



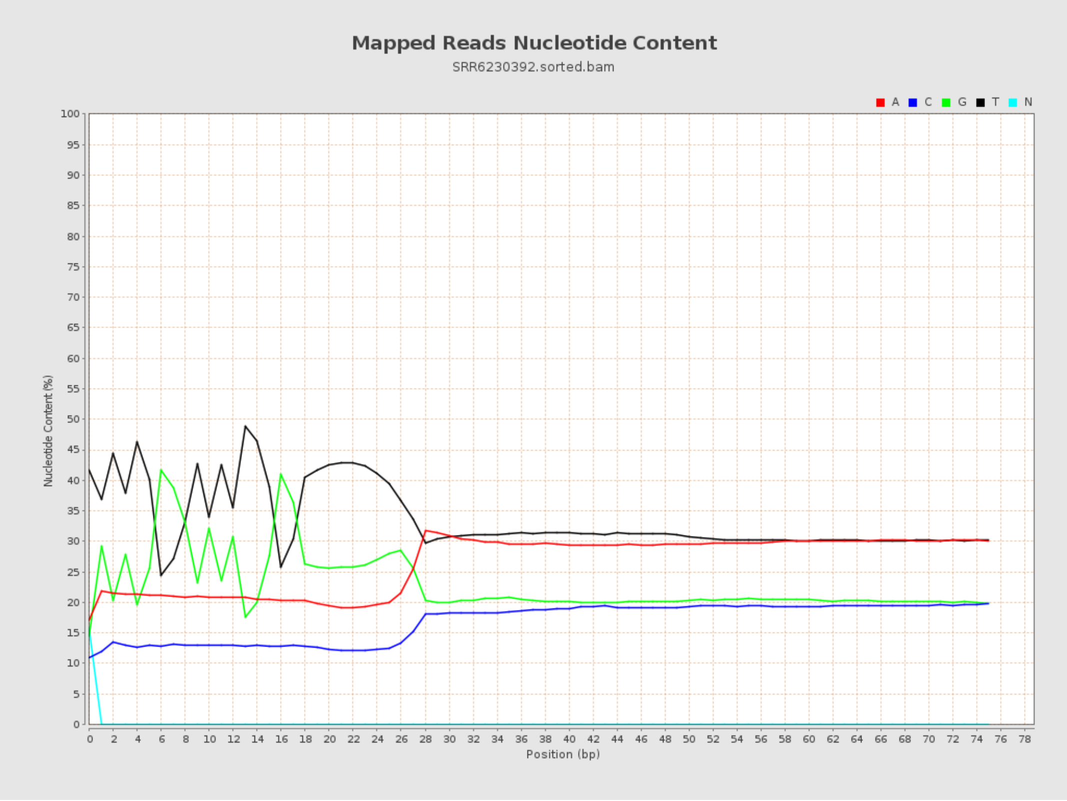
6. Results : Genome Fraction Coverage



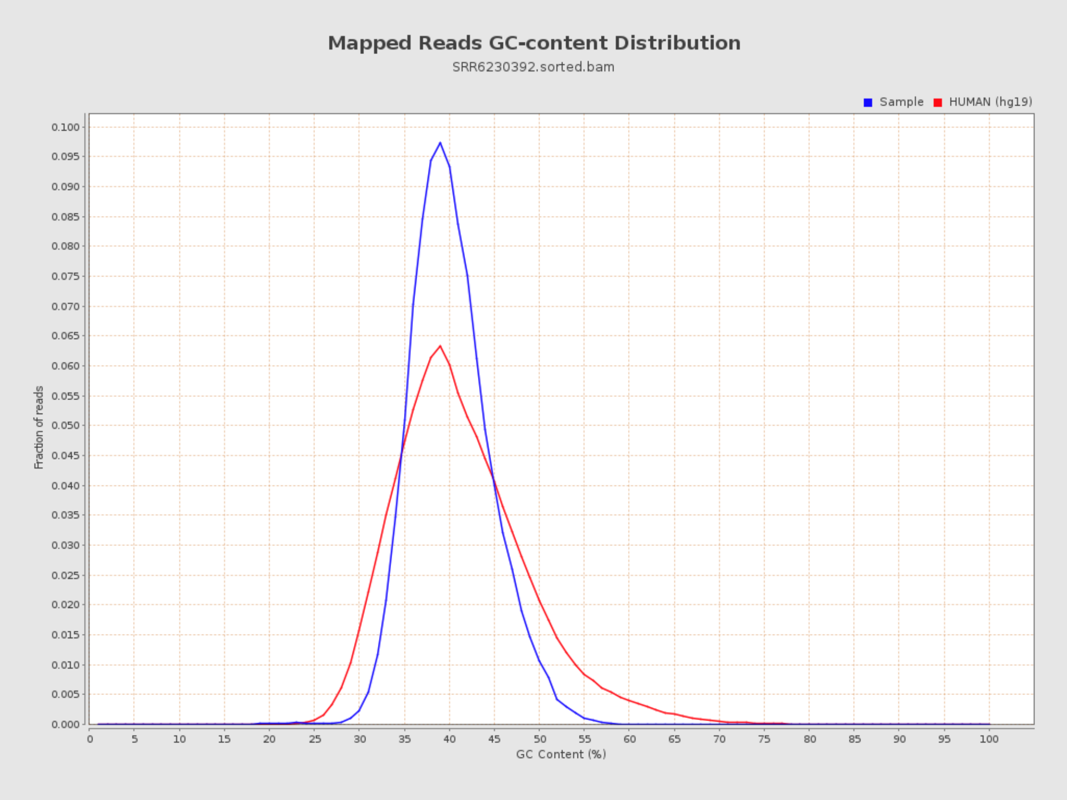
7. Results : Duplication Rate Histogram



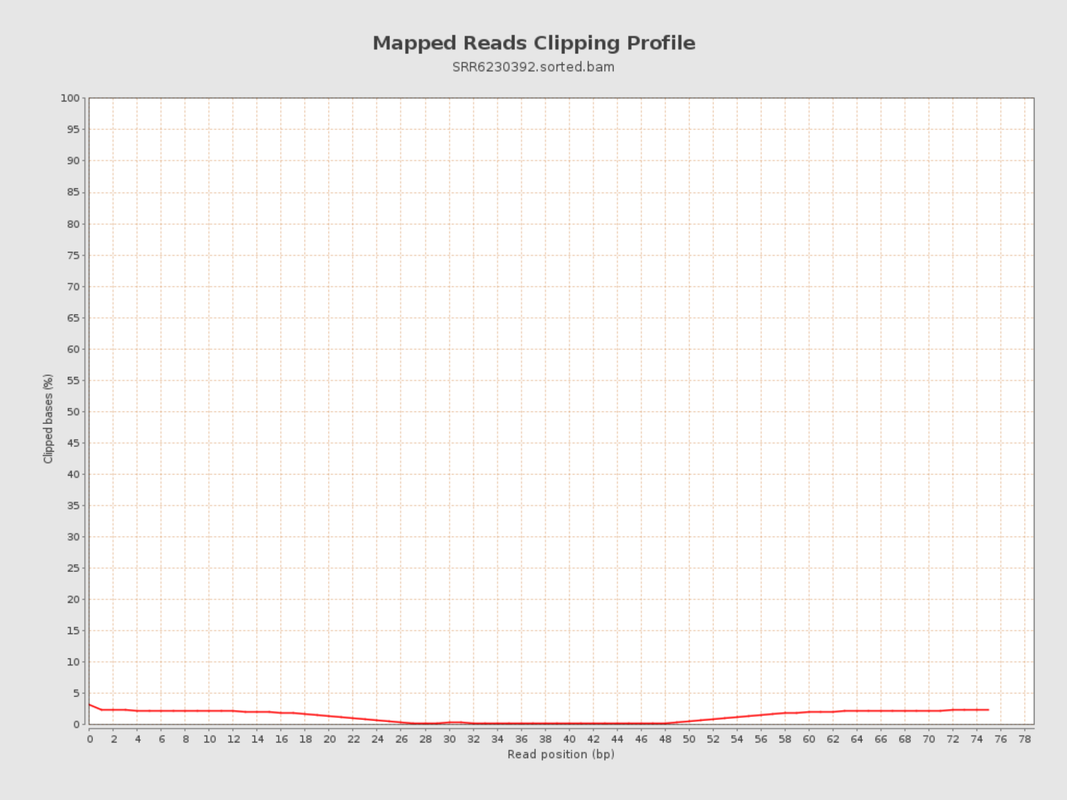
8. Results : Mapped Reads Nucleotide Content



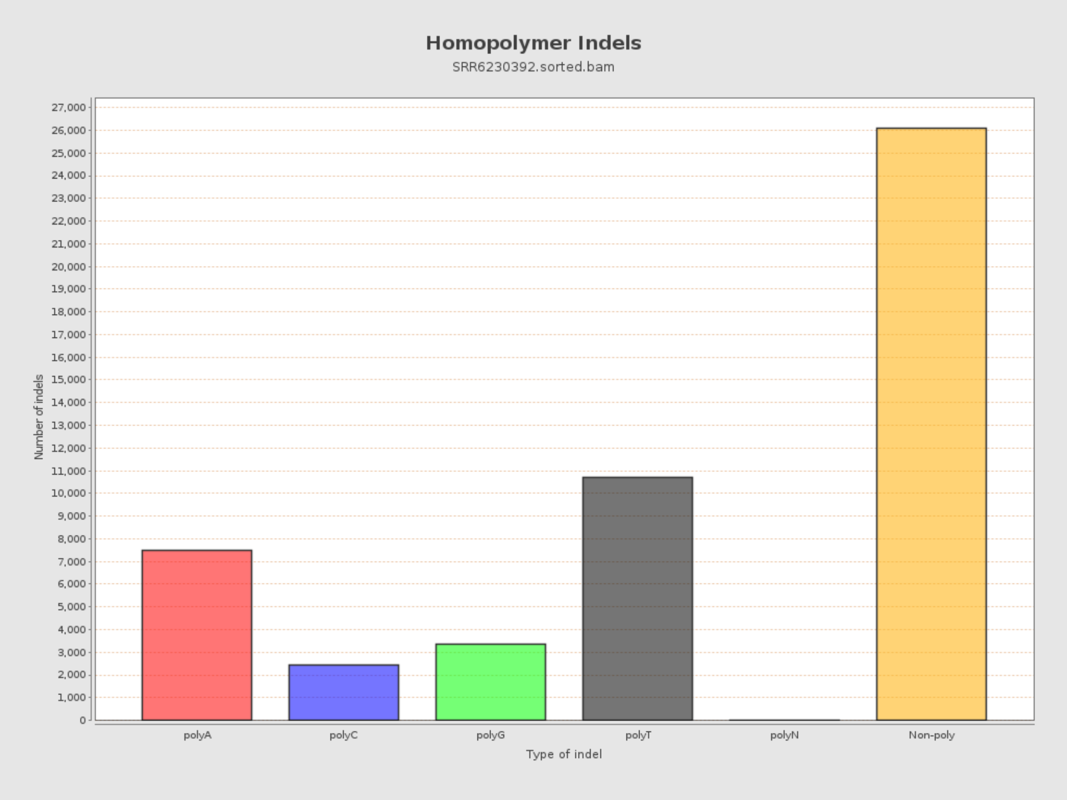
9. Results : Mapped Reads GC-content Distribution



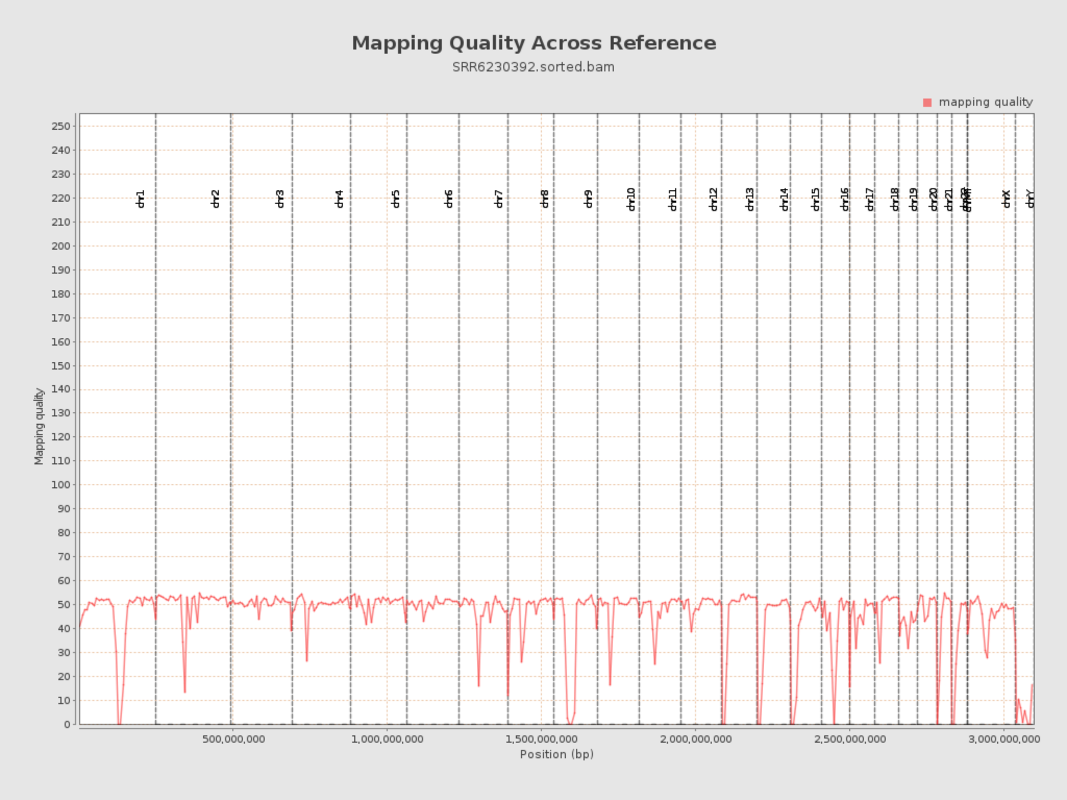
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram