Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 21:11:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230391.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_SRR6230391 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230391.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 21:11:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230391.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,643,279
Mapped reads	1,020,309 / 62.09%
Unmapped reads	622,970 / 37.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,225 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	81,809 / 4.98%
Duplication rate	6.9%
Clipped reads	636,698 / 38.75%

2.2. ACGT Content

Number/percentage of A's	16,337,260 / 25.8%
Number/percentage of C's	10,482,811 / 16.56%
Number/percentage of T's	21,747,326 / 34.35%
Number/percentage of G's	14,644,715 / 23.13%
Number/percentage of N's	105,601 / 0.17%
GC Percentage	39.68%

2.3. Coverage

Mean	0.0205

Standard Deviation	0.2243

2.4. Mapping Quality

Mean Mapping Quality	45.97

2.5. Mismatches and indels

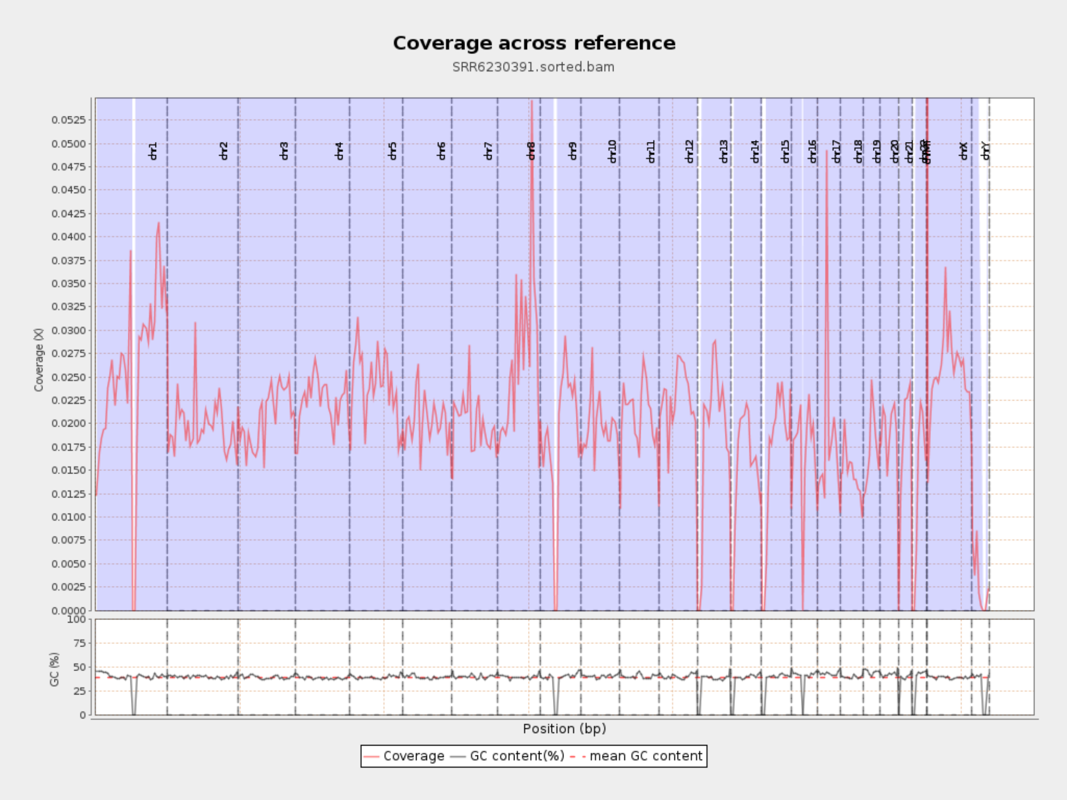
General error rate	1.09%
Mismatches	680,503
Insertions	5,371
Mapped reads with at least one insertion	0.52%
Deletions	20,331
Mapped reads with at least one deletion	1.97%
Homopolymer indels	49.67%

2.6. Chromosome stats

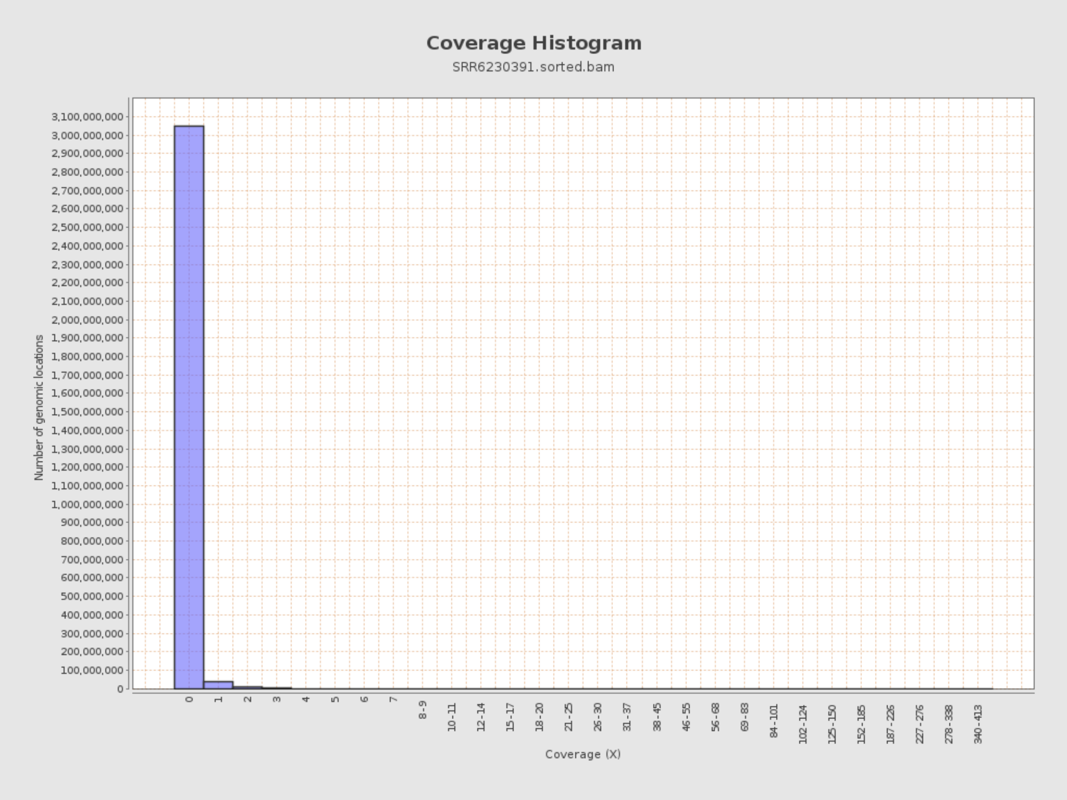
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6379104	0.0256	0.3805
chr2	243199373	4803559	0.0198	0.2274
chr3	198022430	4112456	0.0208	0.182
chr4	191154276	4284900	0.0224	0.1923
chr5	180915260	4391512	0.0243	0.1973
chr6	171115067	3452100	0.0202	0.2041
chr7	159138663	3204179	0.0201	0.2374

chr8	146364022	3958145	0.027	0.288
chr9	141213431	2636805	0.0187	0.2043
chr10	135534747	2647077	0.0195	0.2076
chr11	135006516	2835939	0.021	0.2057
chr12	133851895	3034161	0.0227	0.1915
chr13	115169878	2133067	0.0185	0.1732
chr14	107349540	1619074	0.0151	0.1595
chr15	102531392	1688322	0.0165	0.1626
chr16	90354753	1509262	0.0167	0.165
chr17	81195210	1514379	0.0187	0.1778
chr18	78077248	1148631	0.0147	0.2802
chr19	59128983	1028196	0.0174	0.2491
chr20	63025520	1203505	0.0191	0.1747
chr21	48129895	858932	0.0178	0.1718
chr22	51304566	686477	0.0134	0.1441
chrMT	16571	49854	3.0085	2.9114
chrX	155270560	4000727	0.0258	0.2122
chrY	59373566	169833	0.0029	0.076

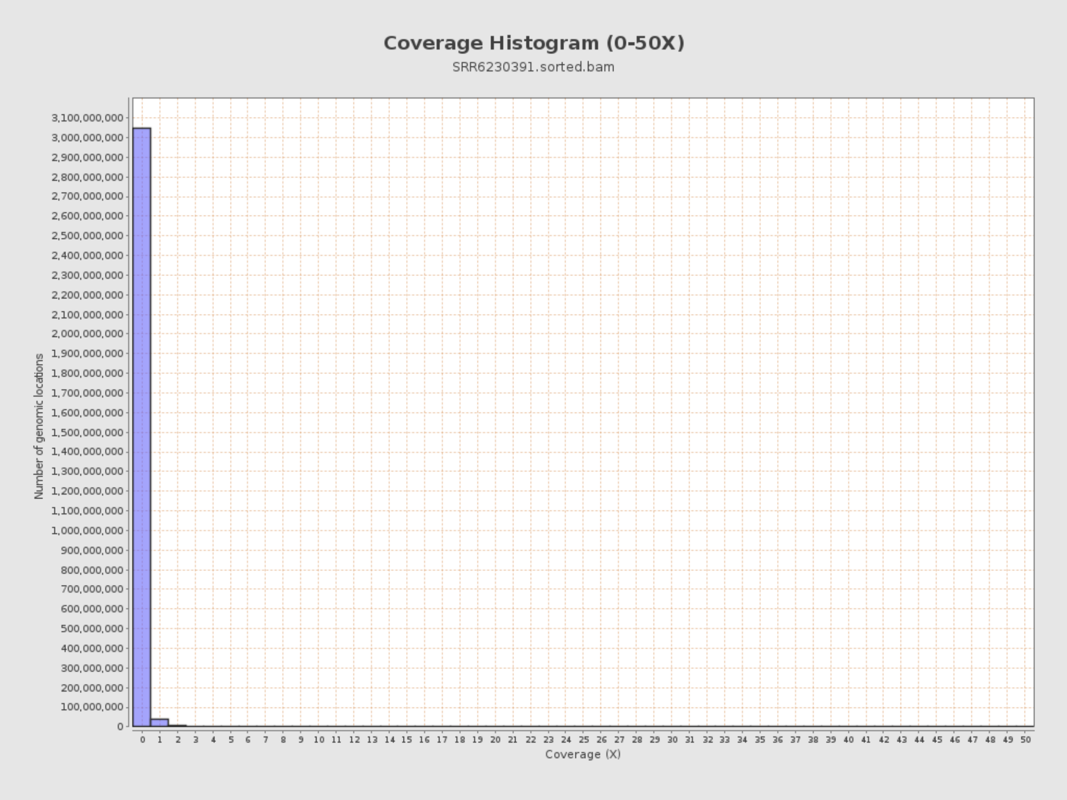
3. Results : Coverage across reference



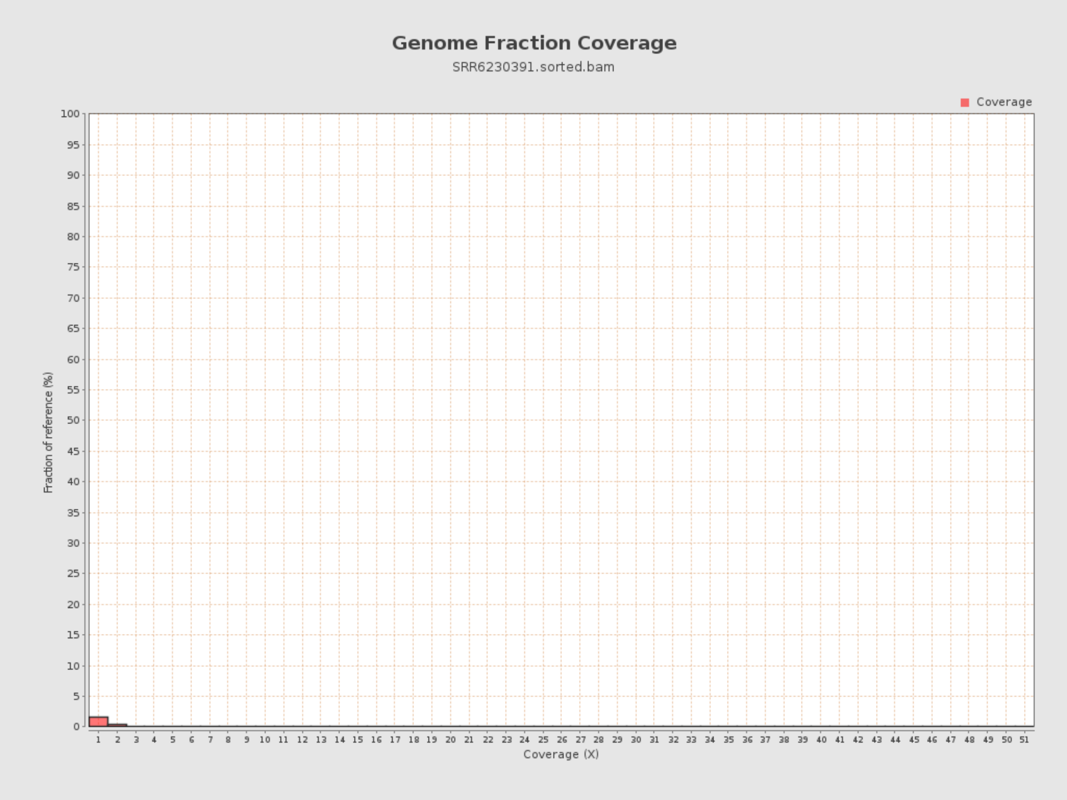
4. Results : Coverage Histogram



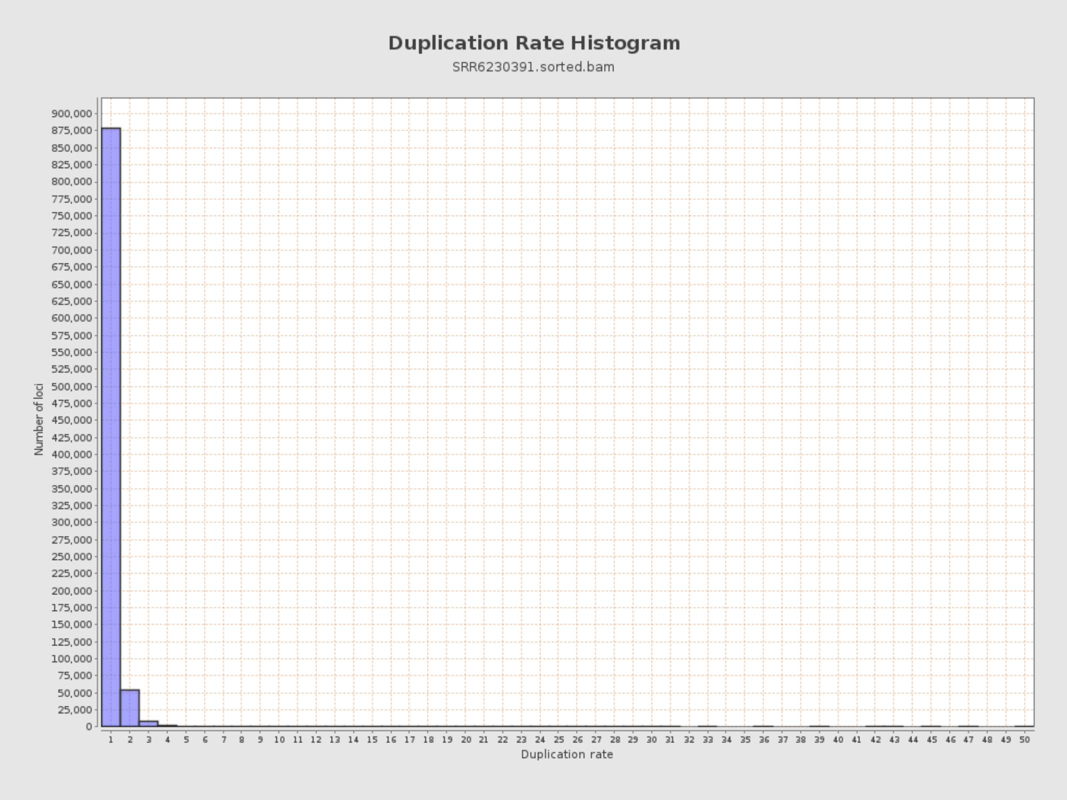
5. Results : Coverage Histogram (0-50X)



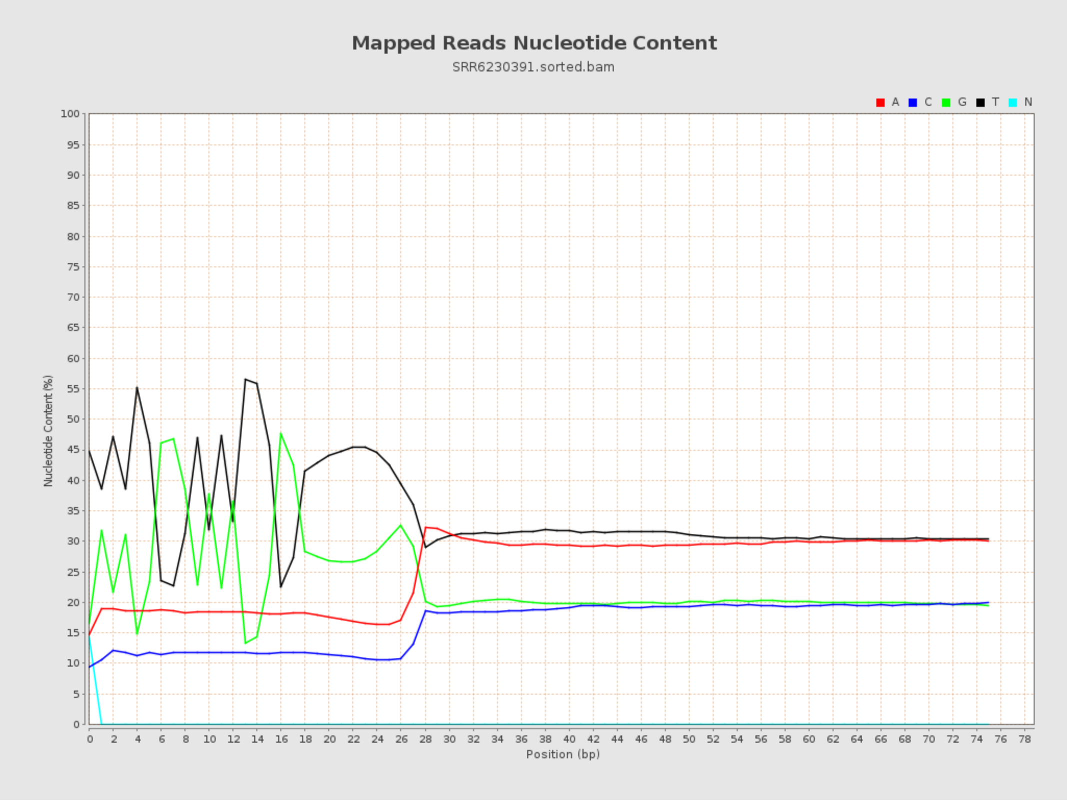
6. Results : Genome Fraction Coverage



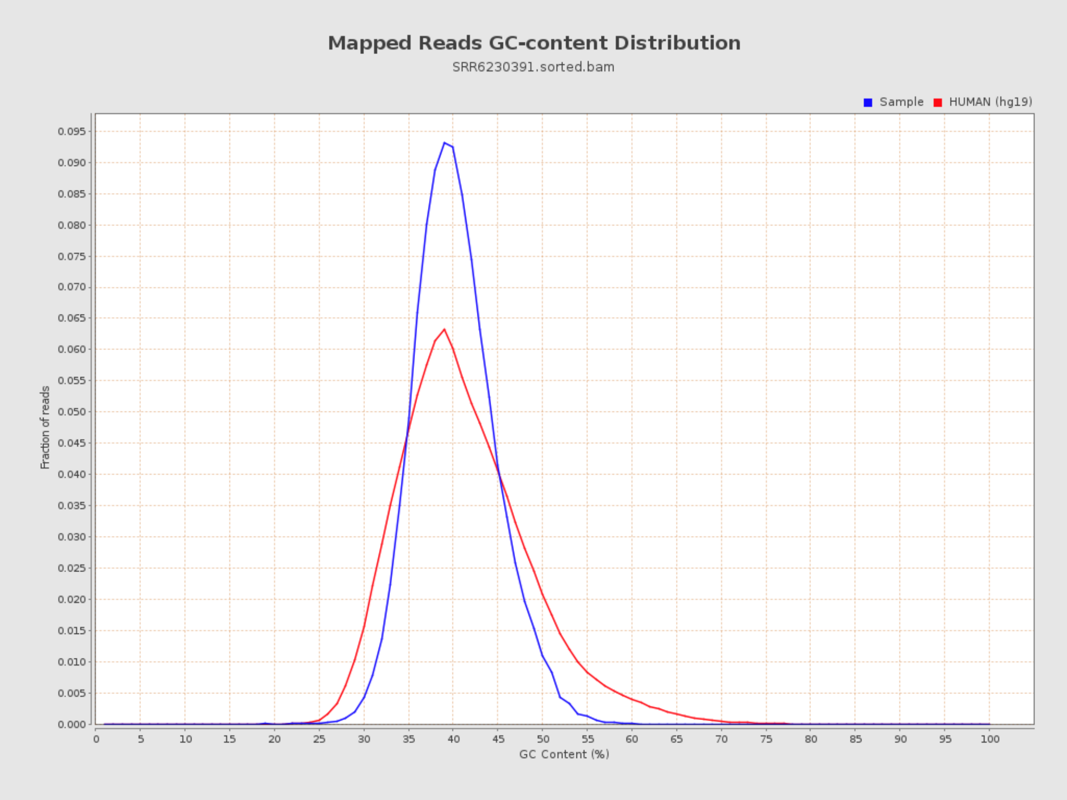
7. Results : Duplication Rate Histogram



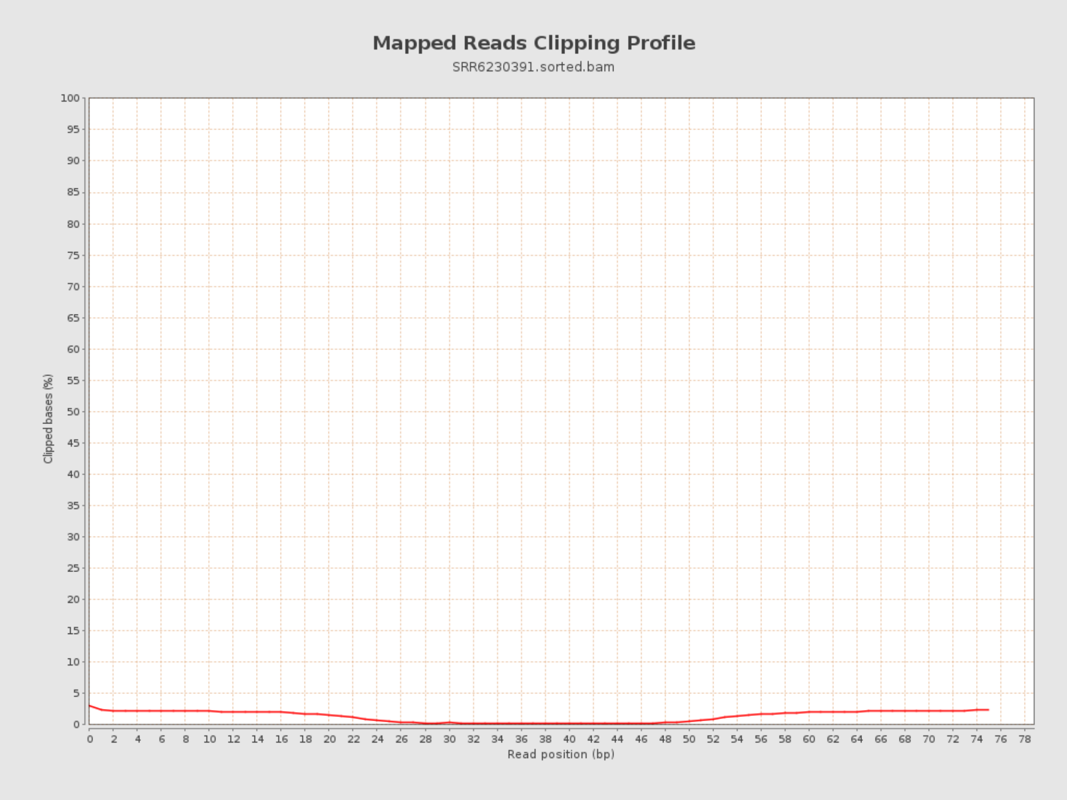
8. Results : Mapped Reads Nucleotide Content



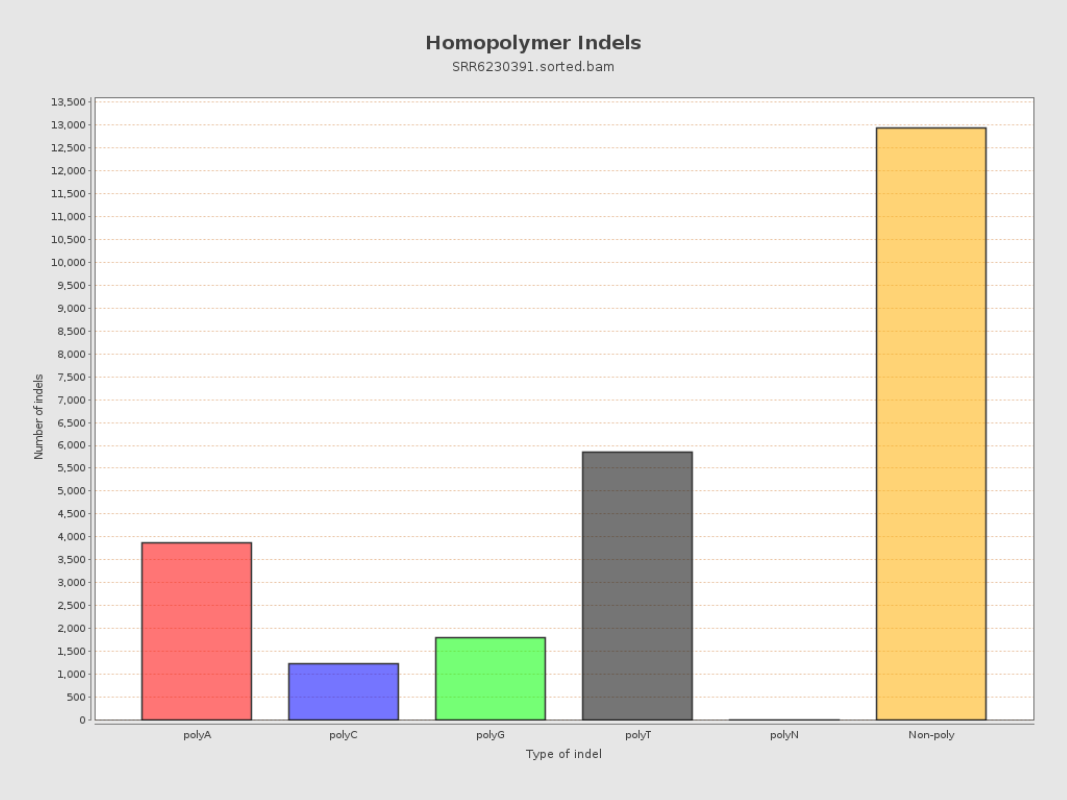
9. Results : Mapped Reads GC-content Distribution



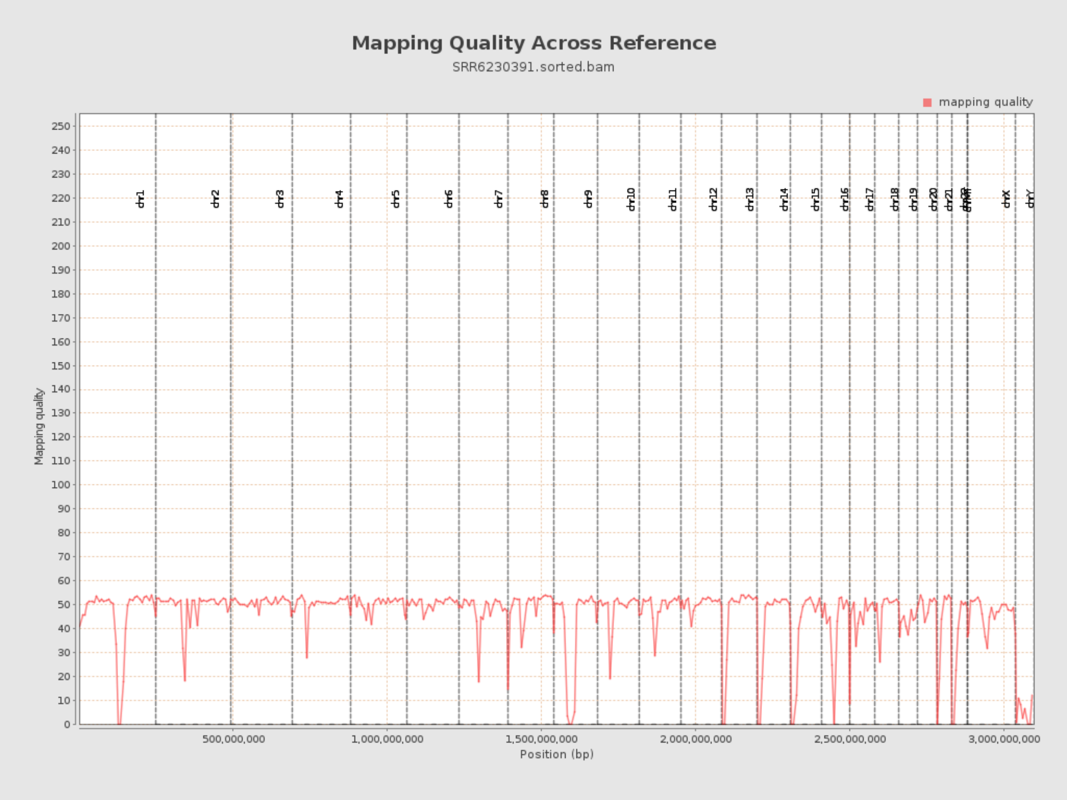
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram