Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 21:38:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230401.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_SRR6230401 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230401.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 21:38:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230401.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,674,596
Mapped reads	2,324,490 / 86.91%
Unmapped reads	350,106 / 13.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,396 / 0.99%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	202,211 / 7.56%
Duplication rate	6.93%
Clipped reads	1,240,445 / 46.38%

2.2. ACGT Content

Number/percentage of A's	41,636,466 / 27.63%
Number/percentage of C's	27,332,588 / 18.14%
Number/percentage of T's	48,019,052 / 31.86%
Number/percentage of G's	33,647,977 / 22.33%
Number/percentage of N's	77,973 / 0.05%
GC Percentage	40.46%

2.3. Coverage

Mean	0.0487

Standard Deviation	0.4682

2.4. Mapping Quality

Mean Mapping Quality	45.73

2.5. Mismatches and indels

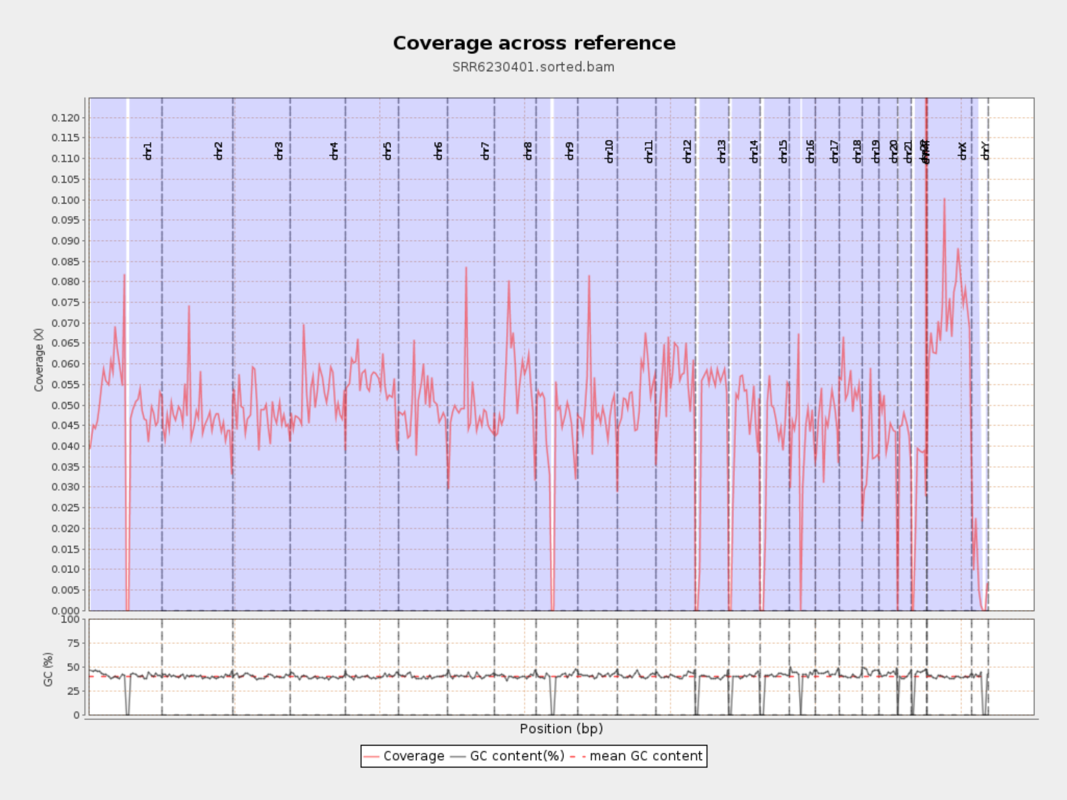
General error rate	0.9%
Mismatches	1,332,472
Insertions	12,480
Mapped reads with at least one insertion	0.53%
Deletions	37,115
Mapped reads with at least one deletion	1.58%
Homopolymer indels	46.74%

2.6. Chromosome stats

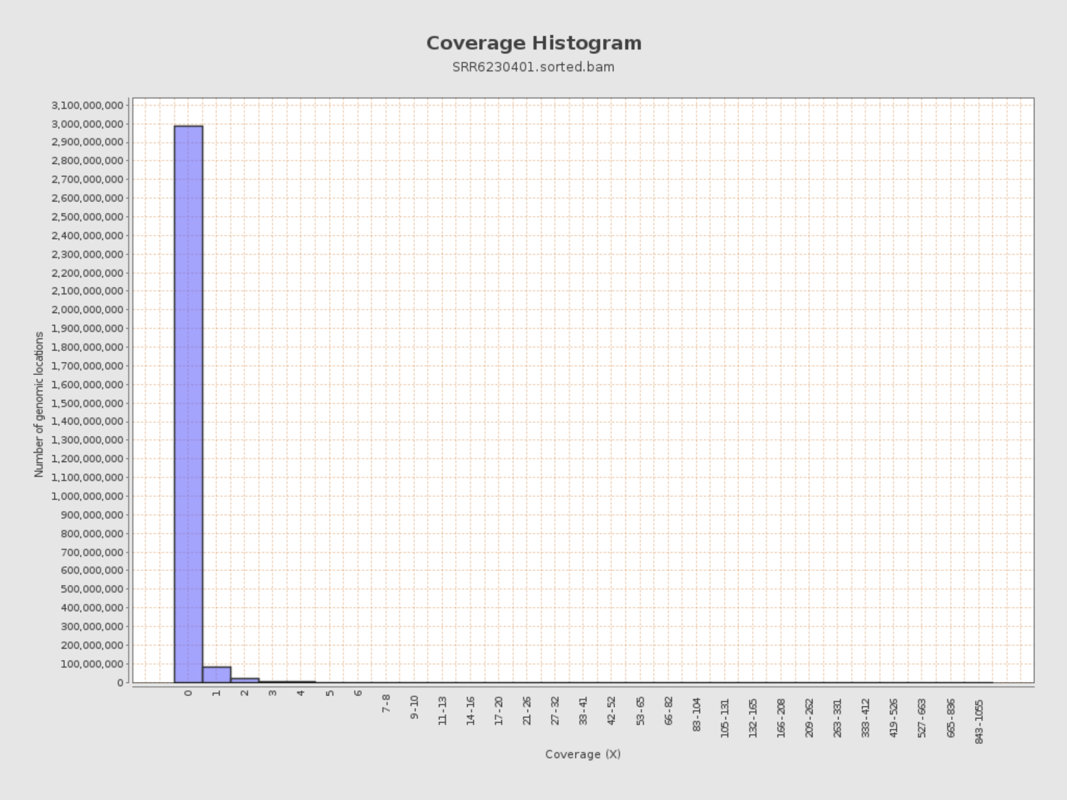
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12274083	0.0492	0.8403
chr2	243199373	11478736	0.0472	0.5107
chr3	198022430	9585968	0.0484	0.2865
chr4	191154276	9926203	0.0519	0.325
chr5	180915260	10099802	0.0558	0.3101
chr6	171115067	8519035	0.0498	0.3393
chr7	159138663	7742681	0.0487	0.5313

chr8	146364022	8023502	0.0548	0.7187
chr9	141213431	5868456	0.0416	0.406
chr10	135534747	6726949	0.0496	0.4451
chr11	135006516	7066226	0.0523	0.4134
chr12	133851895	7540040	0.0563	0.3175
chr13	115169878	5403210	0.0469	0.2863
chr14	107349540	4546404	0.0424	0.2847
chr15	102531392	4012789	0.0391	0.2578
chr16	90354753	3739592	0.0414	0.2982
chr17	81195210	3673006	0.0452	0.3012
chr18	78077248	4257169	0.0545	0.8064
chr19	59128983	2229389	0.0377	0.5519
chr20	63025520	2812086	0.0446	0.2944
chr21	48129895	1915596	0.0398	0.2797
chr22	51304566	1396145	0.0272	0.2083
chrMT	16571	338087	20.4023	16.6767
chrX	155270560	11144985	0.0718	0.3971
chrY	59373566	454102	0.0076	0.1663

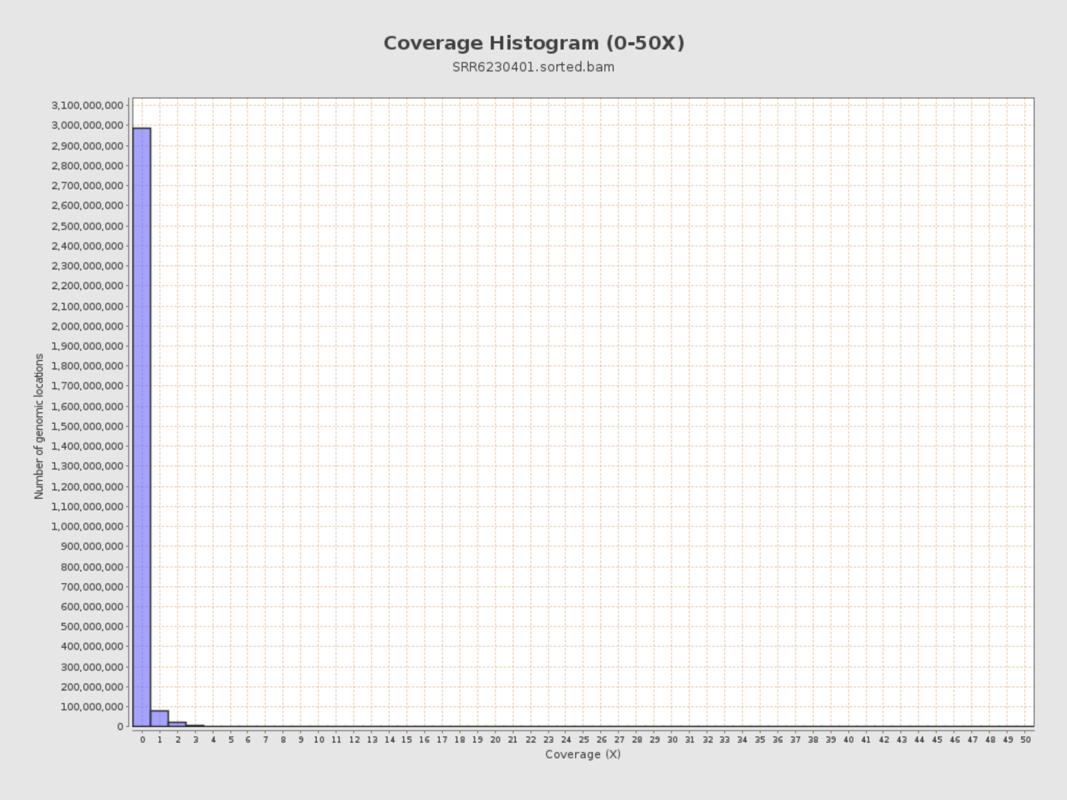
3. Results : Coverage across reference



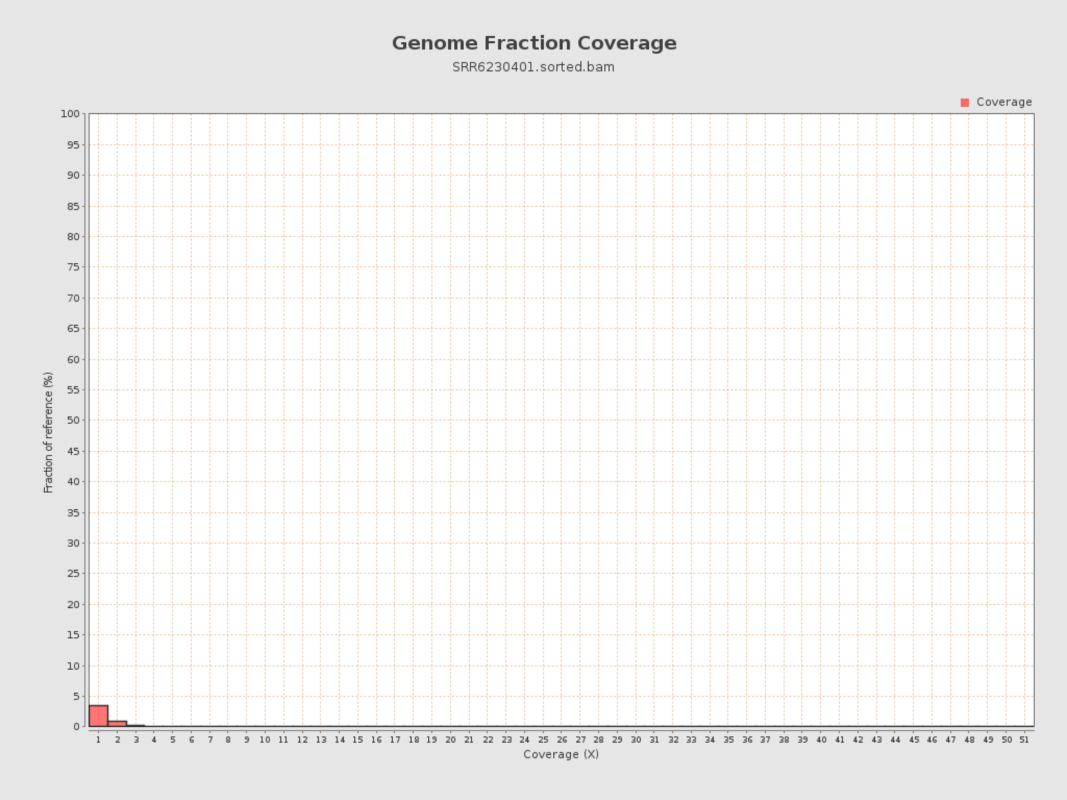
4. Results : Coverage Histogram



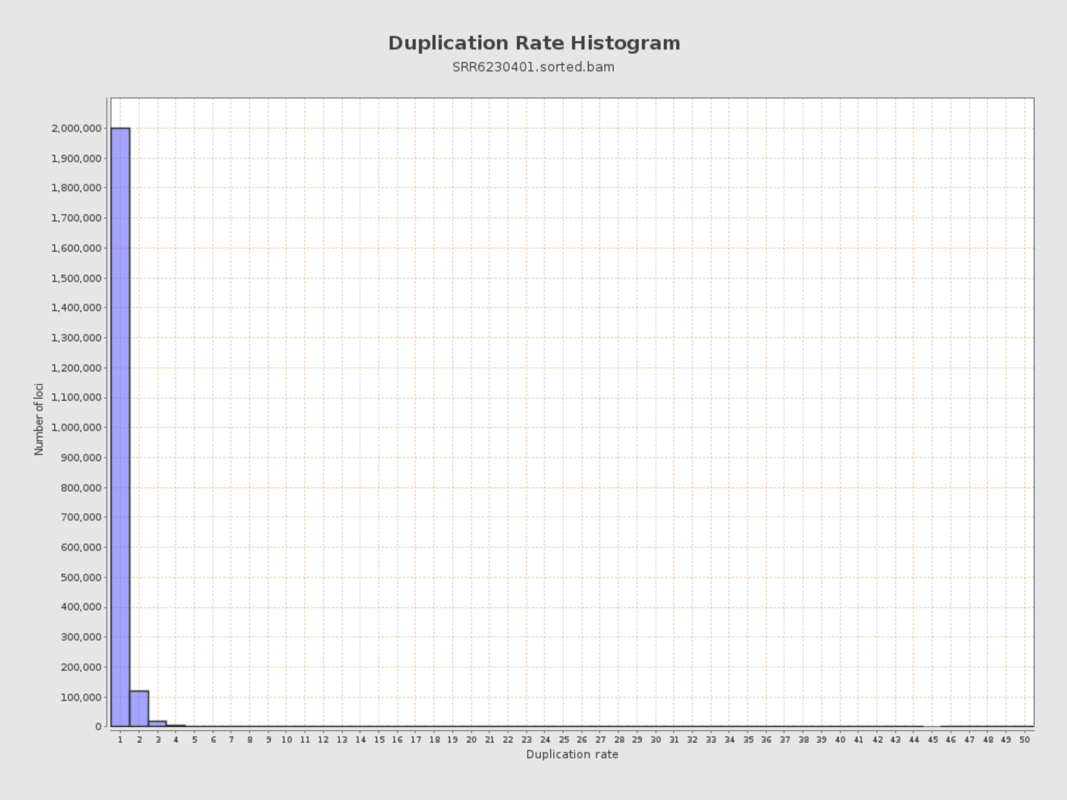
5. Results : Coverage Histogram (0-50X)



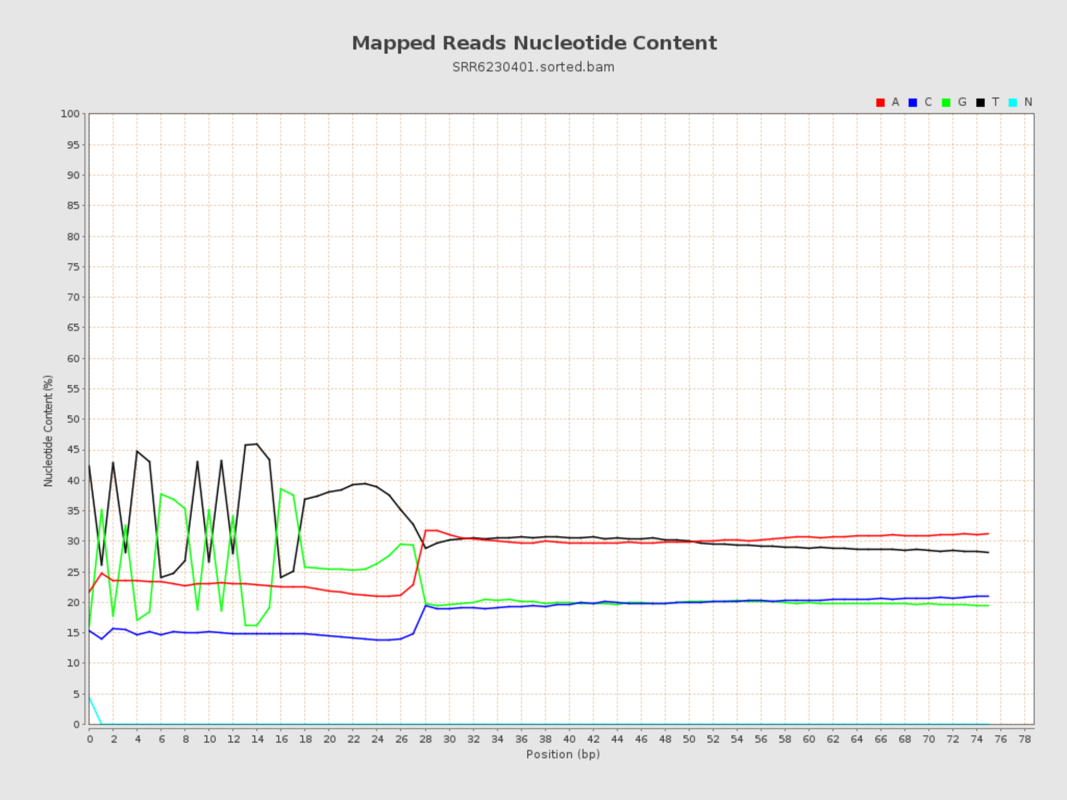
6. Results : Genome Fraction Coverage



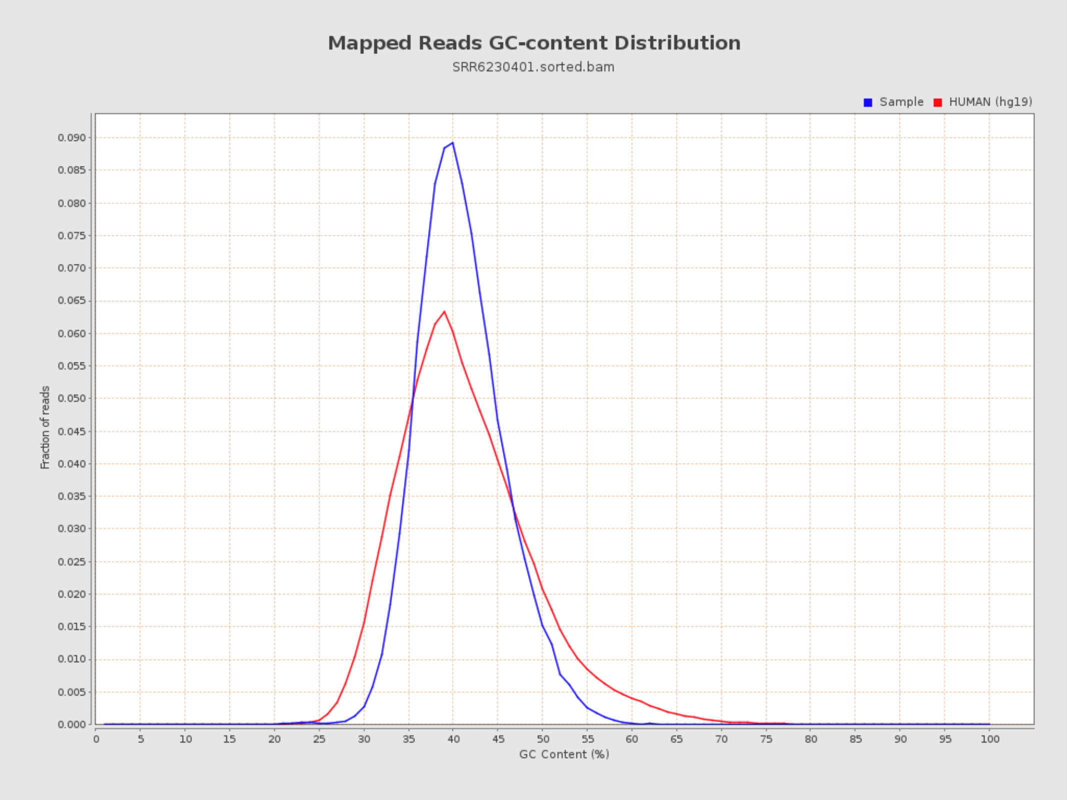
7. Results : Duplication Rate Histogram



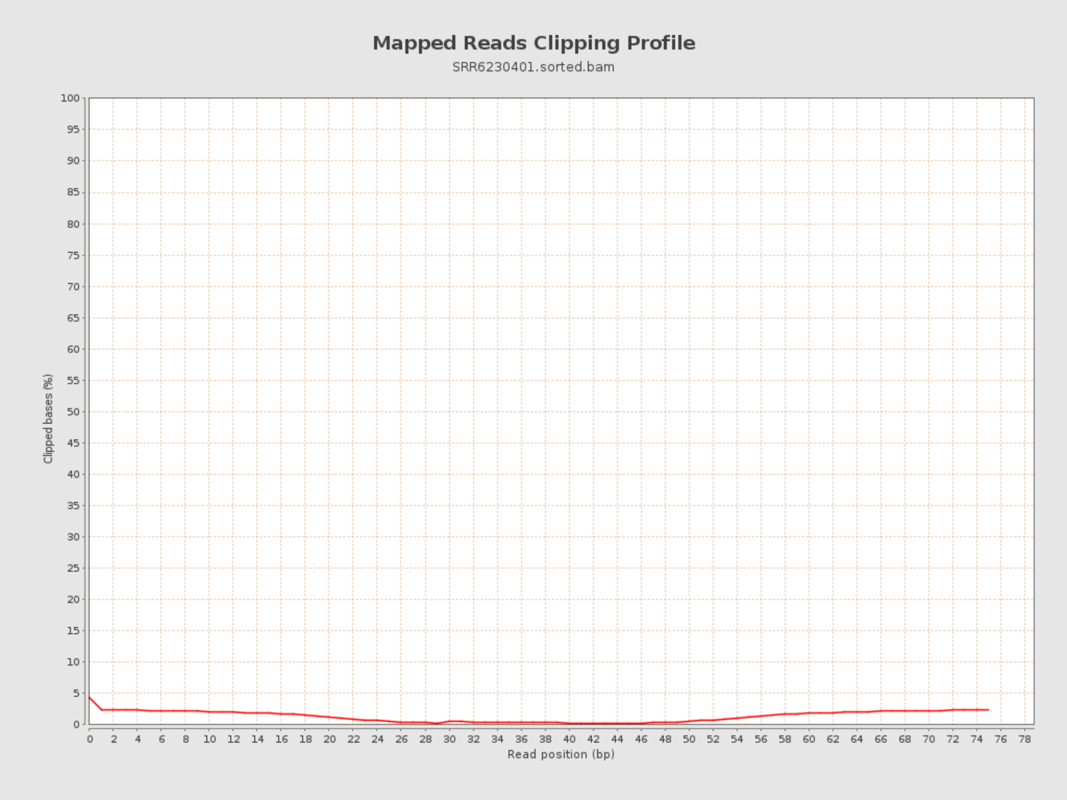
8. Results : Mapped Reads Nucleotide Content



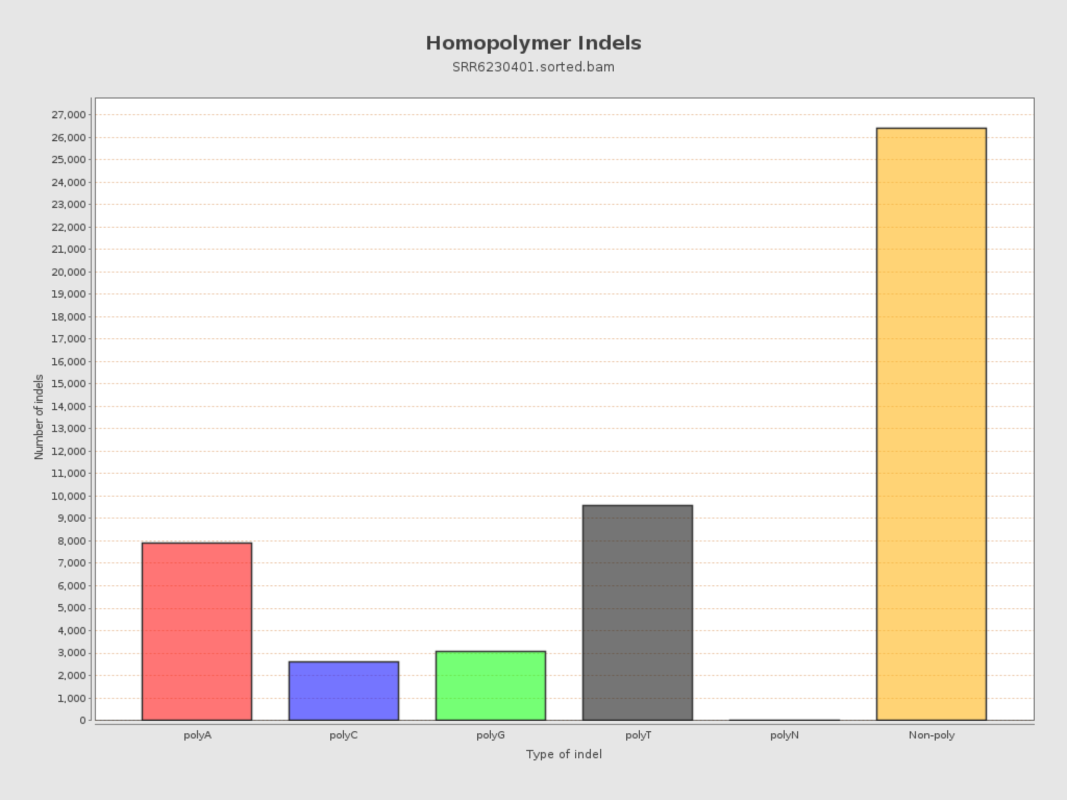
9. Results : Mapped Reads GC-content Distribution



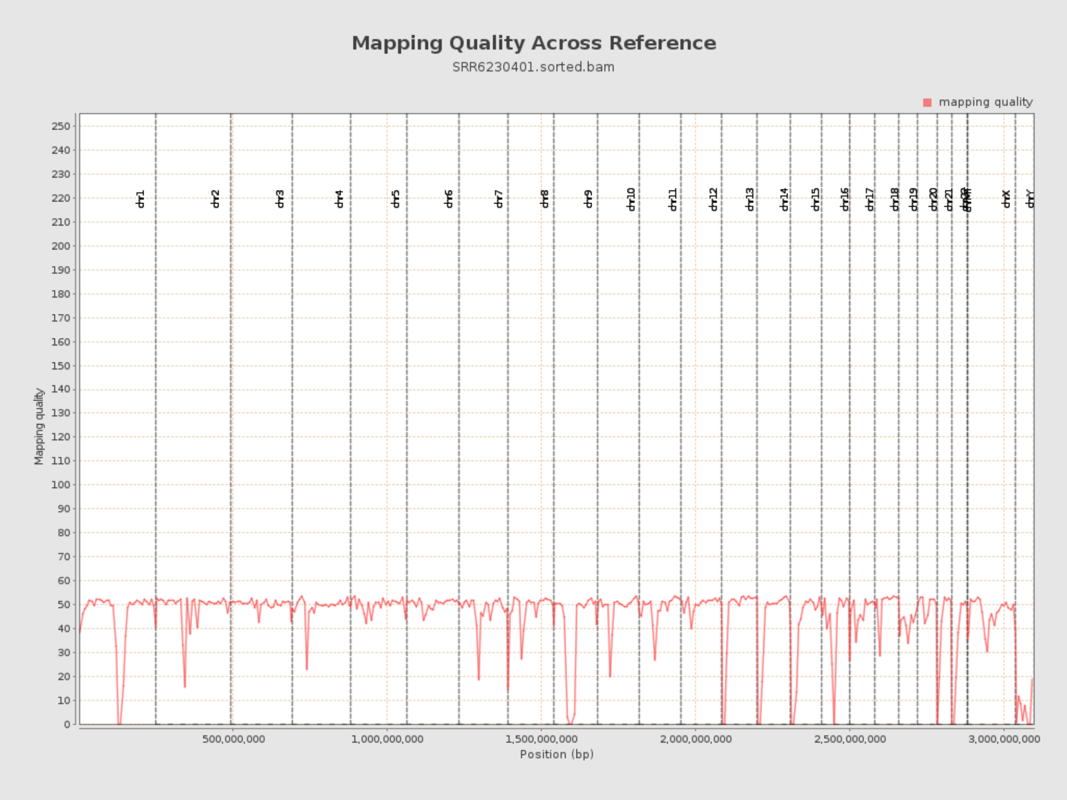
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram