Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 07:47:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231849.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_SRR6231849 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231849.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 07:47:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231849.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,051,677
Mapped reads	1,907,580 / 62.51%
Unmapped reads	1,144,097 / 37.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,049 / 0.46%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	104,900 / 3.44%
Duplication rate	2.45%
Clipped reads	1,215,272 / 39.82%

2.2. ACGT Content

Number/percentage of A's	33,536,832 / 28.47%
Number/percentage of C's	24,367,485 / 20.69%
Number/percentage of T's	31,794,648 / 26.99%
Number/percentage of G's	28,072,420 / 23.83%
Number/percentage of N's	8,731 / 0.01%
GC Percentage	44.52%

2.3. Coverage

Mean	0.0381

Standard Deviation	5.3563

2.4. Mapping Quality

Mean Mapping Quality	41.77

2.5. Mismatches and indels

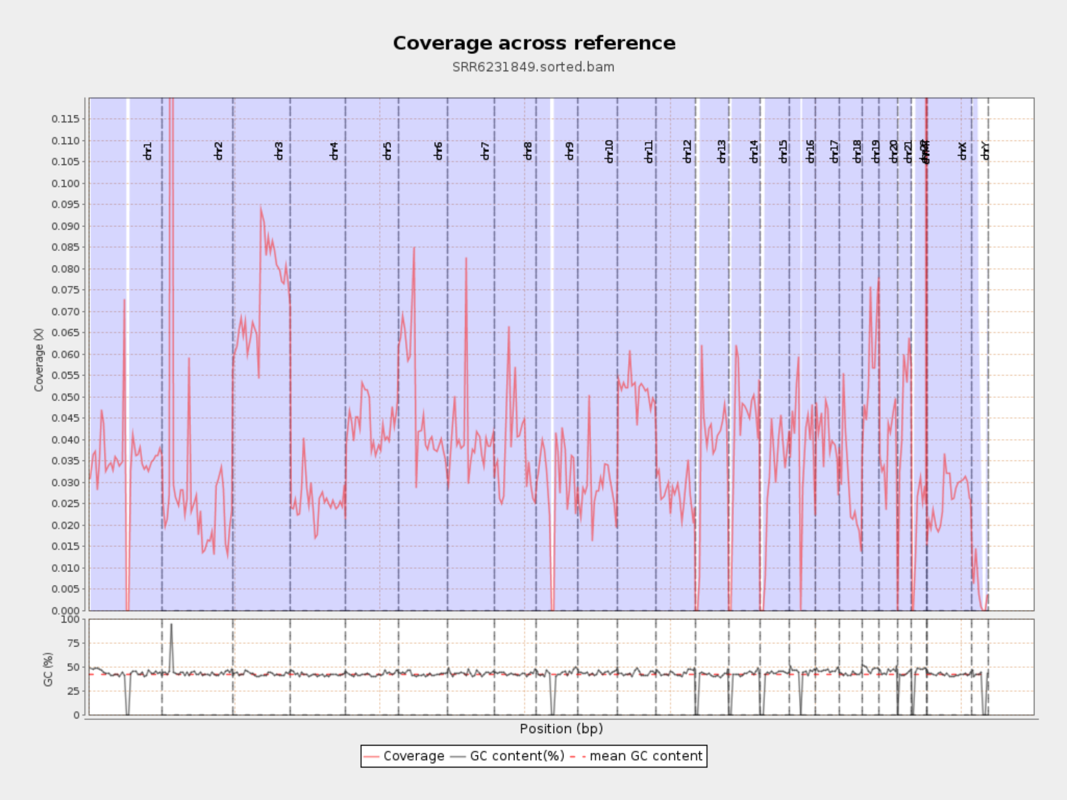
General error rate	0.65%
Mismatches	755,344
Insertions	8,235
Mapped reads with at least one insertion	0.43%
Deletions	25,323
Mapped reads with at least one deletion	1.31%
Homopolymer indels	42.33%

2.6. Chromosome stats

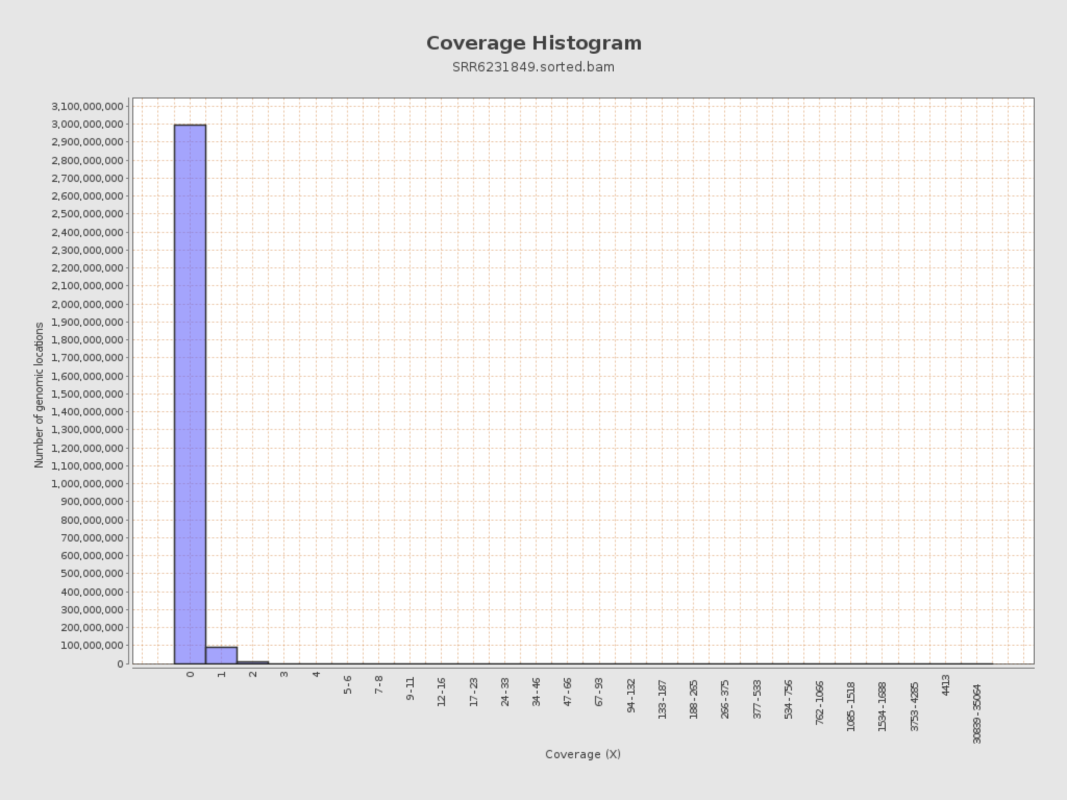
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8607231	0.0345	0.8698
chr2	243199373	8684735	0.0357	19.0583
chr3	198022430	14565838	0.0736	0.2984
chr4	191154276	4876910	0.0255	0.1867
chr5	180915260	7863137	0.0435	0.2314
chr6	171115067	8296223	0.0485	0.3113
chr7	159138663	6465280	0.0406	0.588

chr8	146364022	5567003	0.038	0.3526
chr9	141213431	4189965	0.0297	0.3137
chr10	135534747	3884772	0.0287	0.3209
chr11	135006516	6926126	0.0513	0.4069
chr12	133851895	3689079	0.0276	0.196
chr13	115169878	4191320	0.0364	0.2082
chr14	107349540	4408163	0.0411	0.2947
chr15	102531392	3029246	0.0295	0.1918
chr16	90354753	3549883	0.0393	0.2629
chr17	81195210	3321139	0.0409	0.2595
chr18	78077248	2263266	0.029	0.7525
chr19	59128983	3432811	0.0581	0.5807
chr20	63025520	2411168	0.0383	0.2319
chr21	48129895	2210149	0.0459	0.2478
chr22	51304566	1008499	0.0197	0.1512
chrMT	16571	44220	2.6685	2.0818
chrX	155270560	4062808	0.0262	0.2364
chrY	59373566	272483	0.0046	0.0959

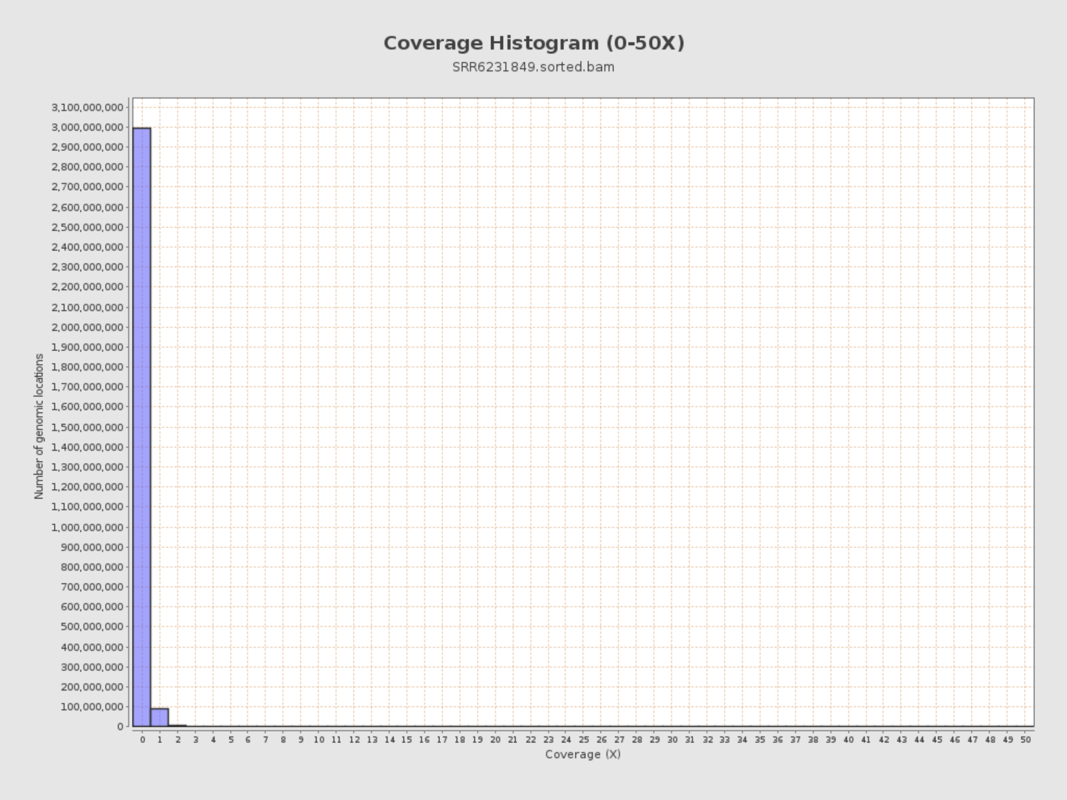
3. Results : Coverage across reference



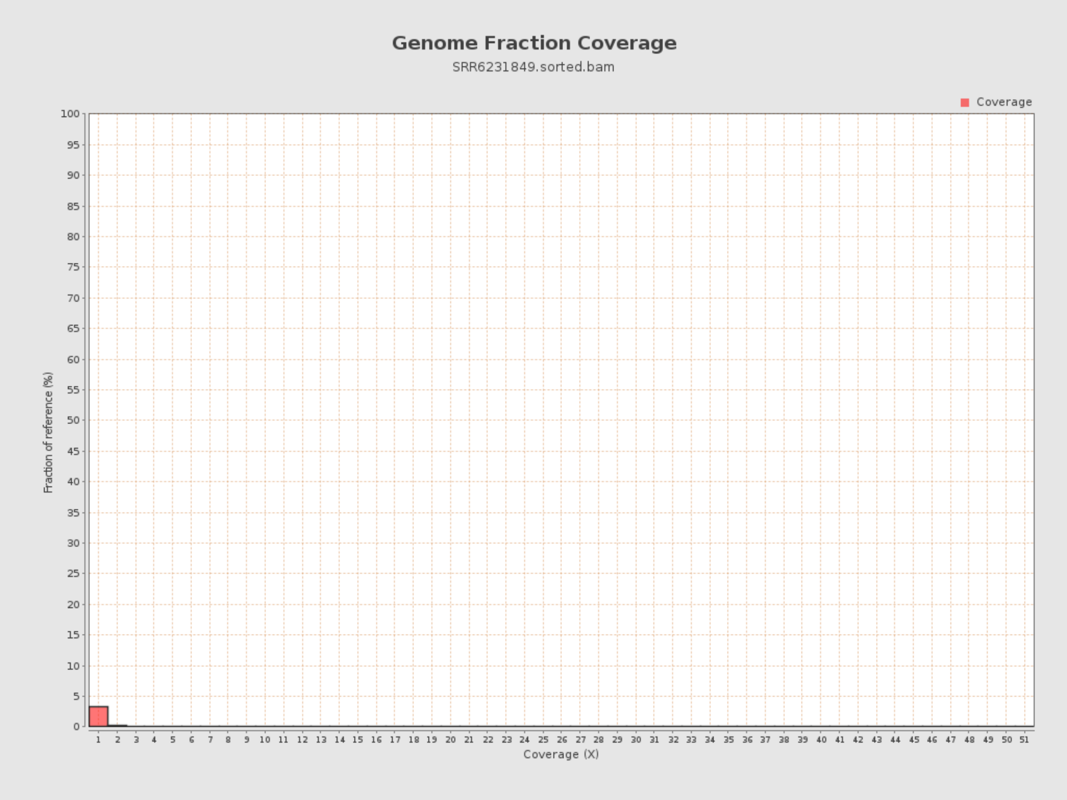
4. Results : Coverage Histogram



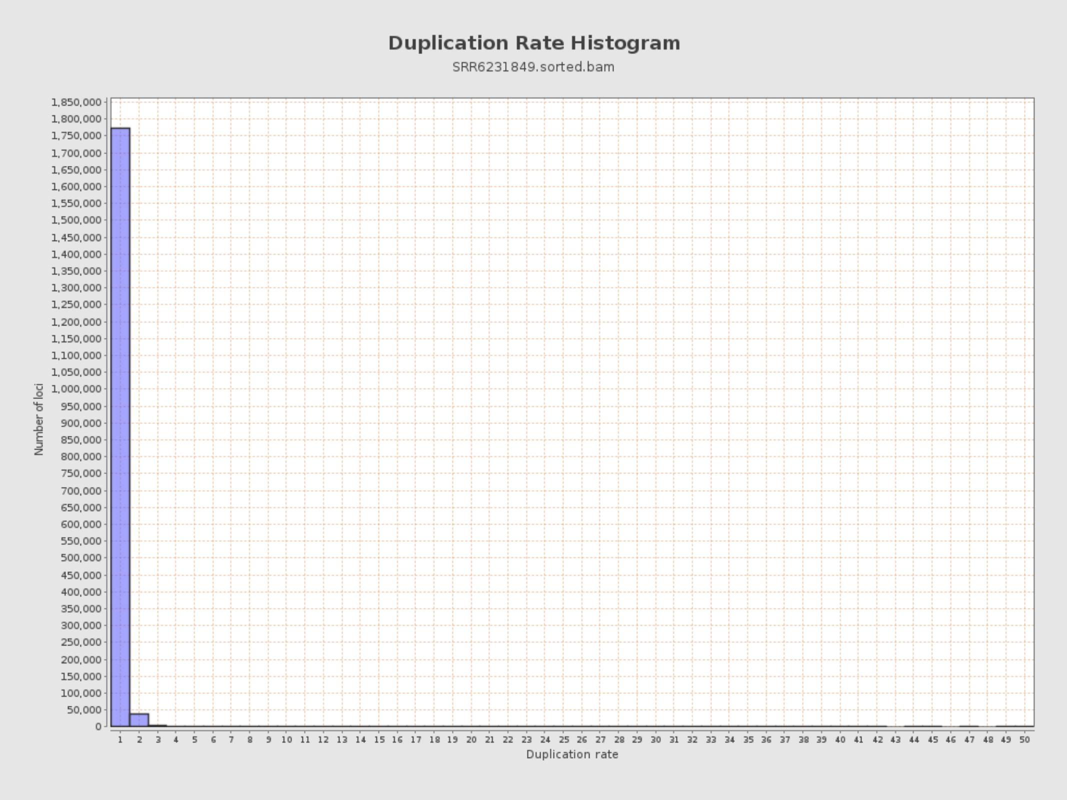
5. Results : Coverage Histogram (0-50X)



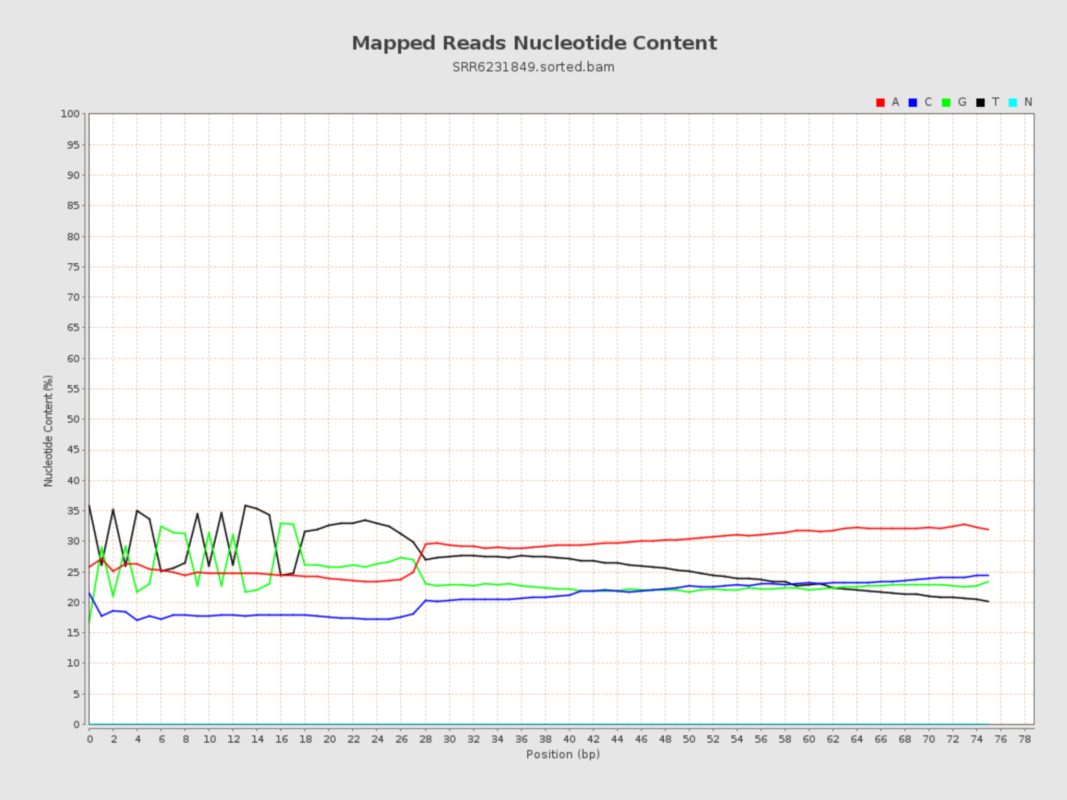
6. Results : Genome Fraction Coverage



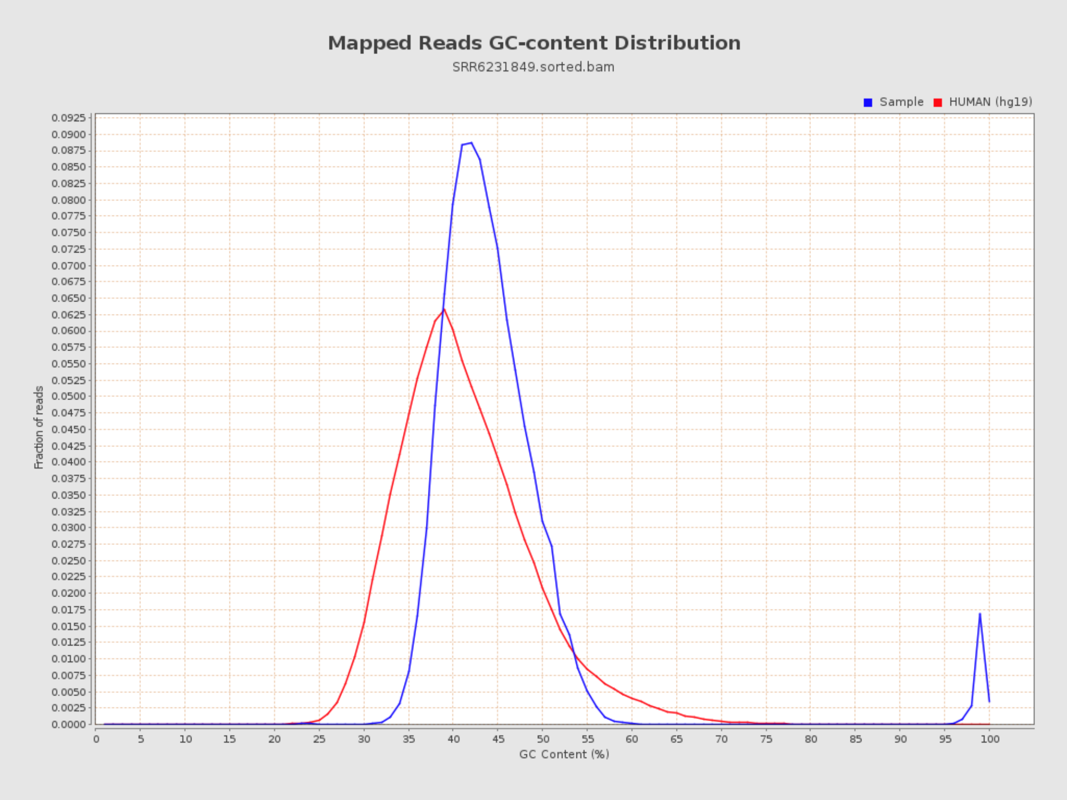
7. Results : Duplication Rate Histogram



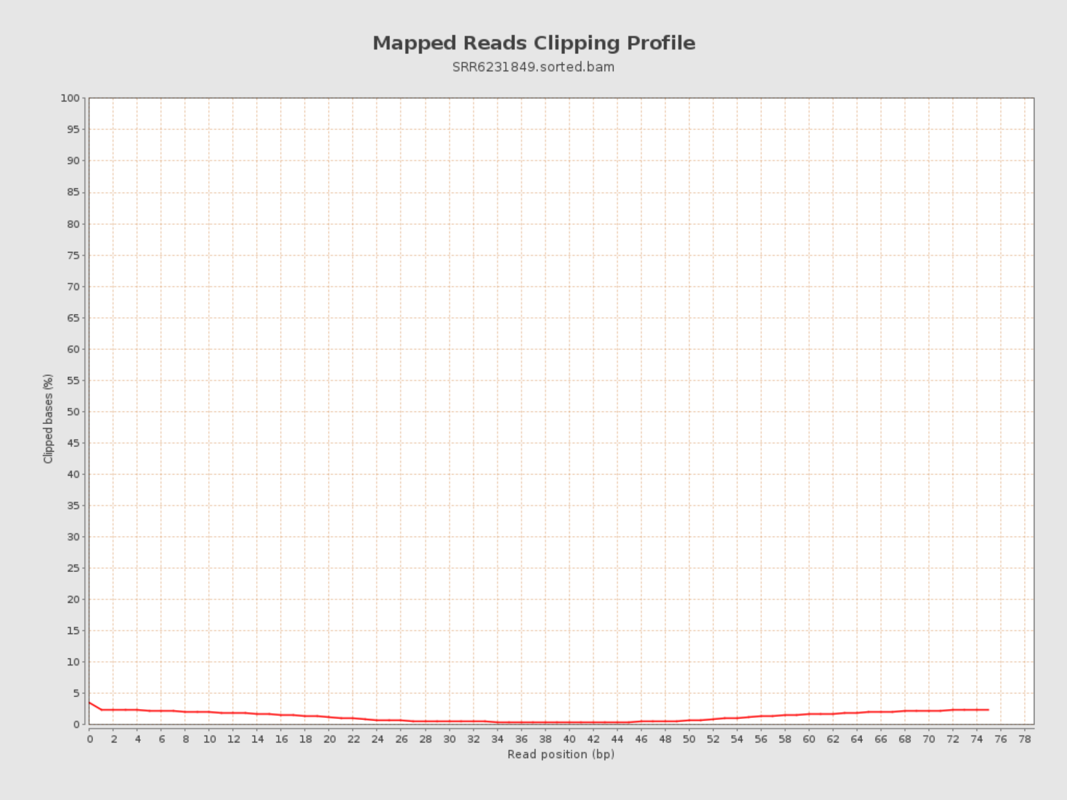
8. Results : Mapped Reads Nucleotide Content



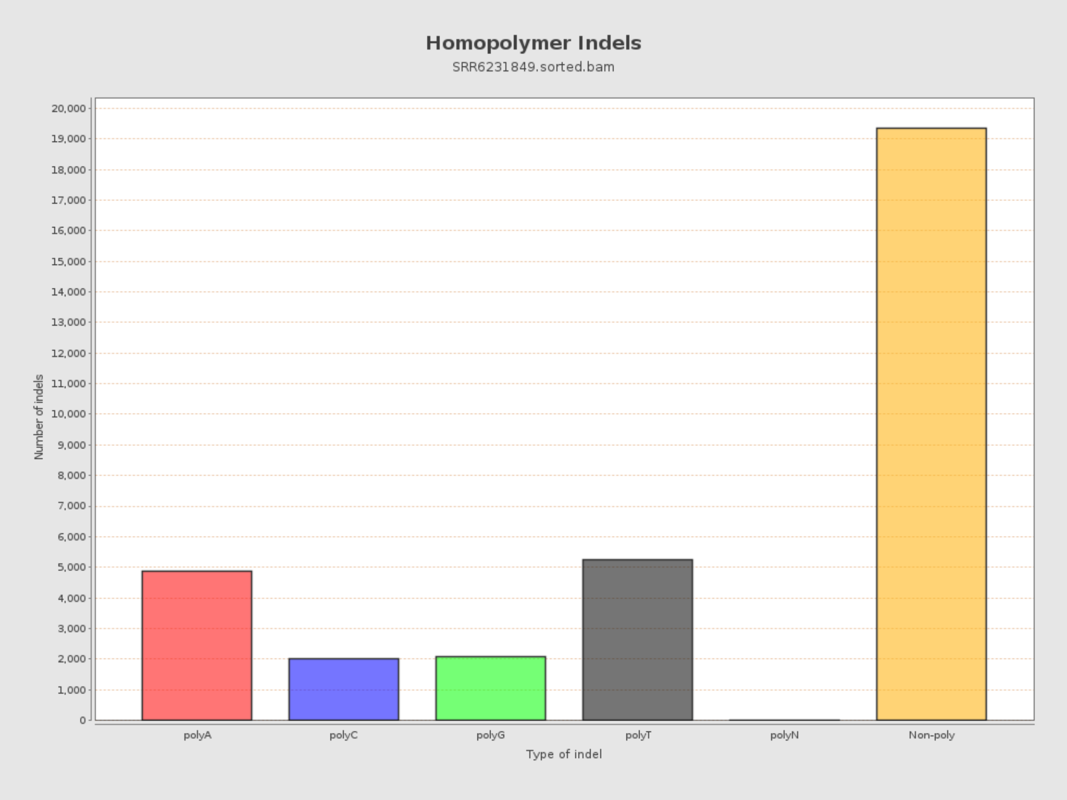
9. Results : Mapped Reads GC-content Distribution



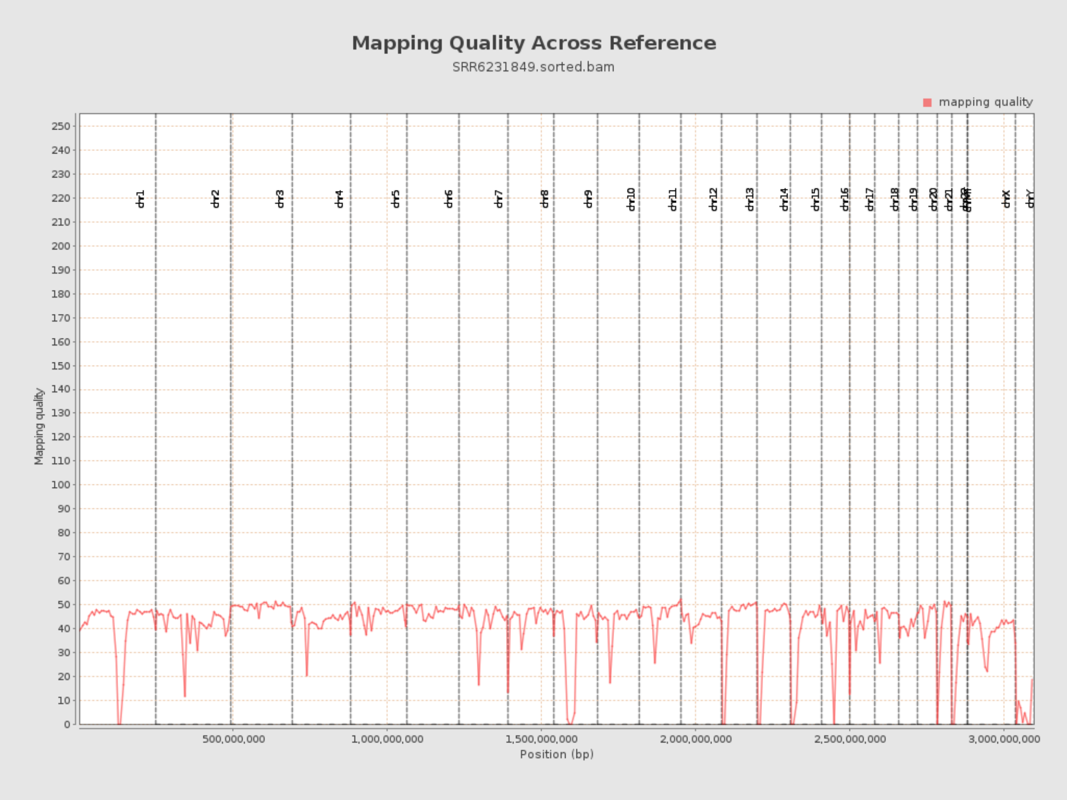
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram