Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 09:24:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231873.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_SRR6231873 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231873.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 09:24:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231873.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,076,784
Mapped reads	4,444,067 / 87.54%
Unmapped reads	632,717 / 12.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	31,792 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	394,503 / 7.77%
Duplication rate	6.56%
Clipped reads	2,239,931 / 44.12%

2.2. ACGT Content

Number/percentage of A's	76,672,920 / 26.39%
Number/percentage of C's	53,395,634 / 18.38%
Number/percentage of T's	92,371,838 / 31.79%
Number/percentage of G's	67,985,930 / 23.4%
Number/percentage of N's	112,787 / 0.04%
GC Percentage	41.78%

2.3. Coverage

Mean	0.0939

Standard Deviation	1.2859

2.4. Mapping Quality

Mean Mapping Quality	42.1

2.5. Mismatches and indels

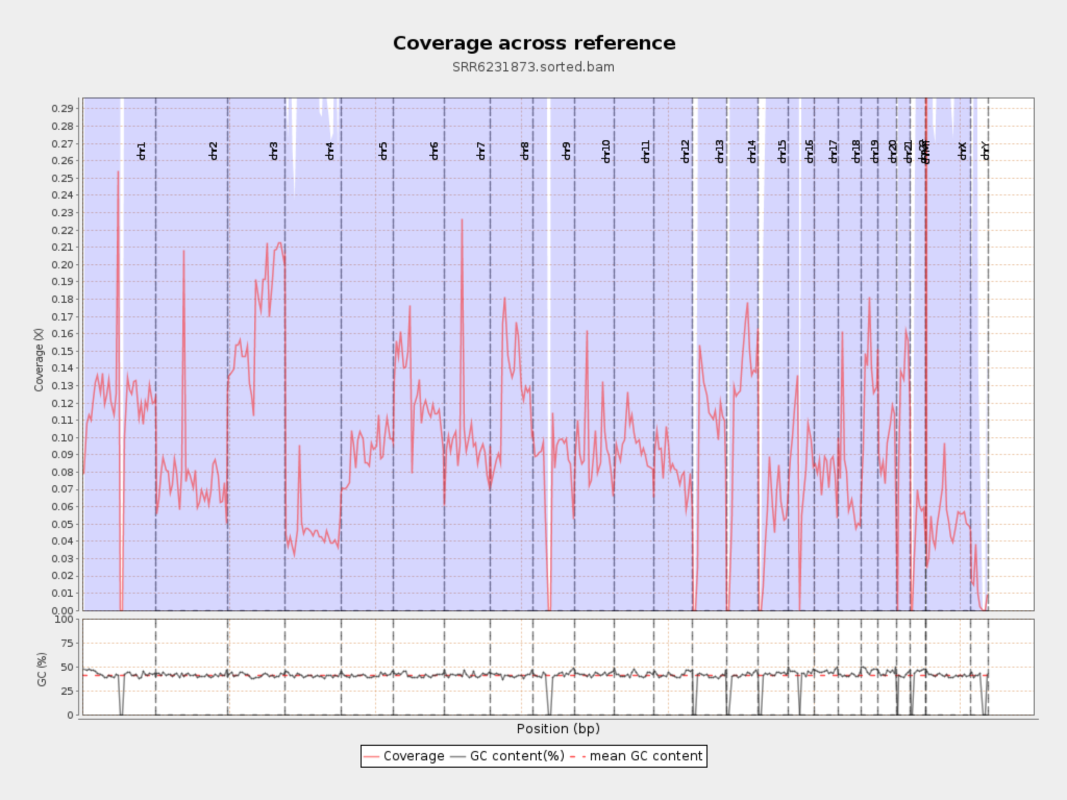
General error rate	0.68%
Mismatches	1,932,508
Insertions	21,309
Mapped reads with at least one insertion	0.48%
Deletions	65,648
Mapped reads with at least one deletion	1.46%
Homopolymer indels	44.53%

2.6. Chromosome stats

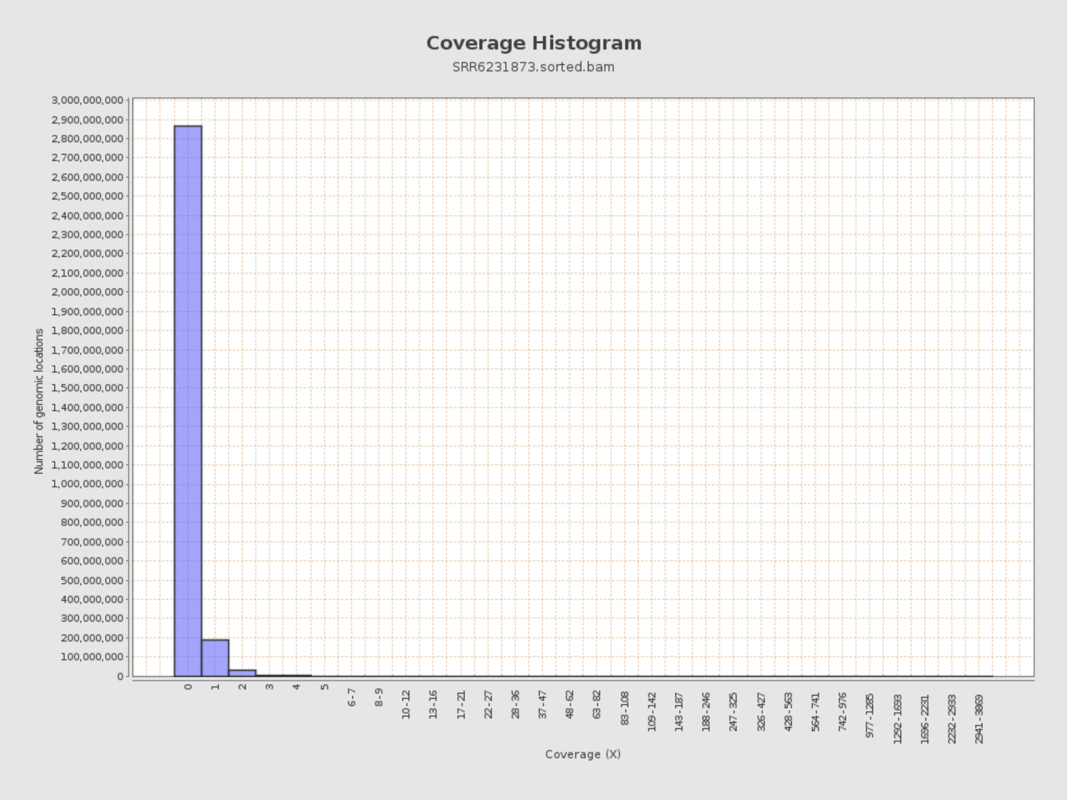
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	29255804	0.1174	3.1446
chr2	243199373	18693565	0.0769	1.4477
chr3	198022430	33493735	0.1691	0.5101
chr4	191154276	8630392	0.0451	0.3927
chr5	180915260	16593809	0.0917	0.3921
chr6	171115067	21621569	0.1264	0.6551
chr7	159138663	15787806	0.0992	1.7066

chr8	146364022	18419552	0.1258	1.4924
chr9	141213431	11187387	0.0792	0.8984
chr10	135534747	12851151	0.0948	0.9866
chr11	135006516	12914332	0.0957	0.9022
chr12	133851895	11143943	0.0833	0.3923
chr13	115169878	11550823	0.1003	0.4069
chr14	107349540	12655401	0.1179	0.5515
chr15	102531392	5021527	0.049	0.3779
chr16	90354753	7592938	0.084	0.5852
chr17	81195210	6532481	0.0805	0.4603
chr18	78077248	5875174	0.0752	2.3396
chr19	59128983	7924080	0.134	1.6944
chr20	63025520	5977723	0.0948	0.5354
chr21	48129895	5769838	0.1199	0.4672
chr22	51304566	2233762	0.0435	0.2456
chrMT	16571	246398	14.8692	8.9485
chrX	155270560	8019897	0.0517	0.5182
chrY	59373566	661648	0.0111	0.2312

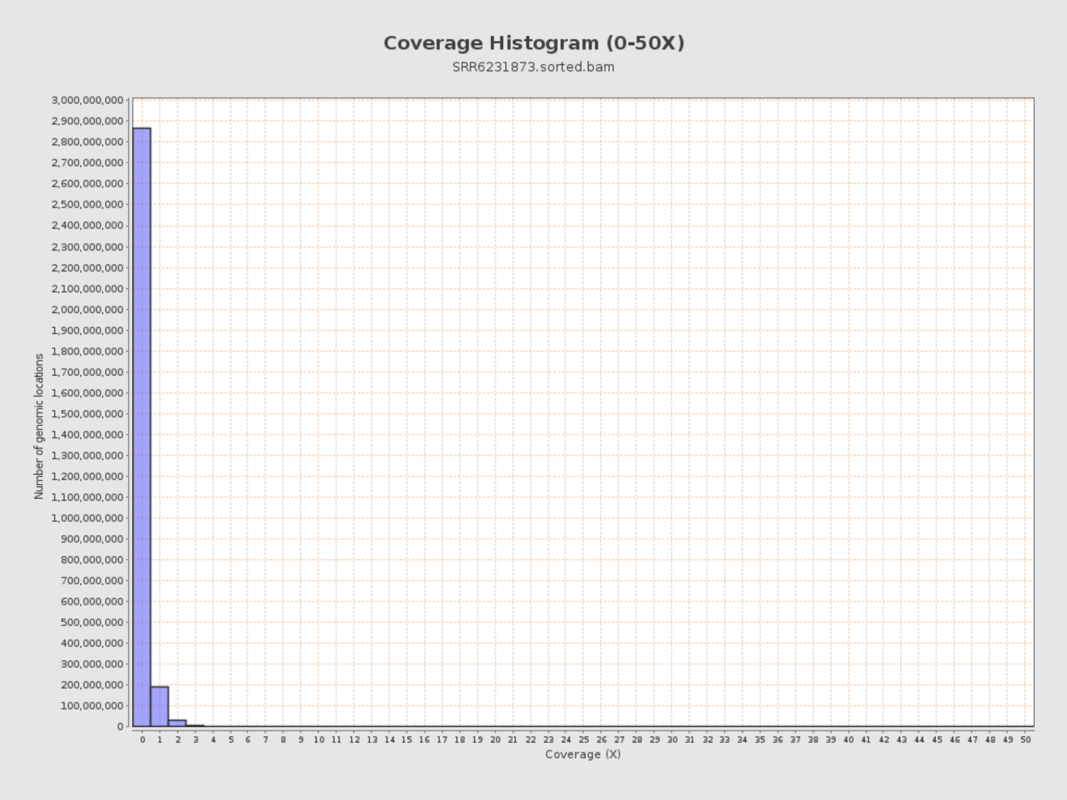
3. Results : Coverage across reference



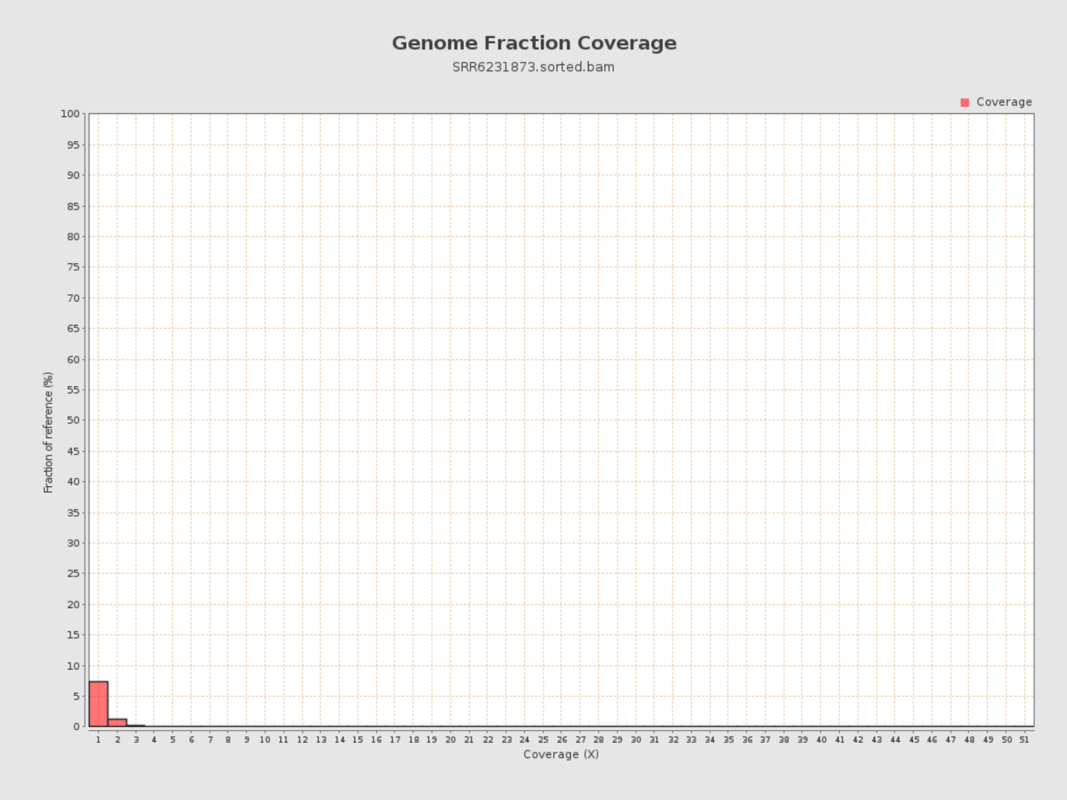
4. Results : Coverage Histogram



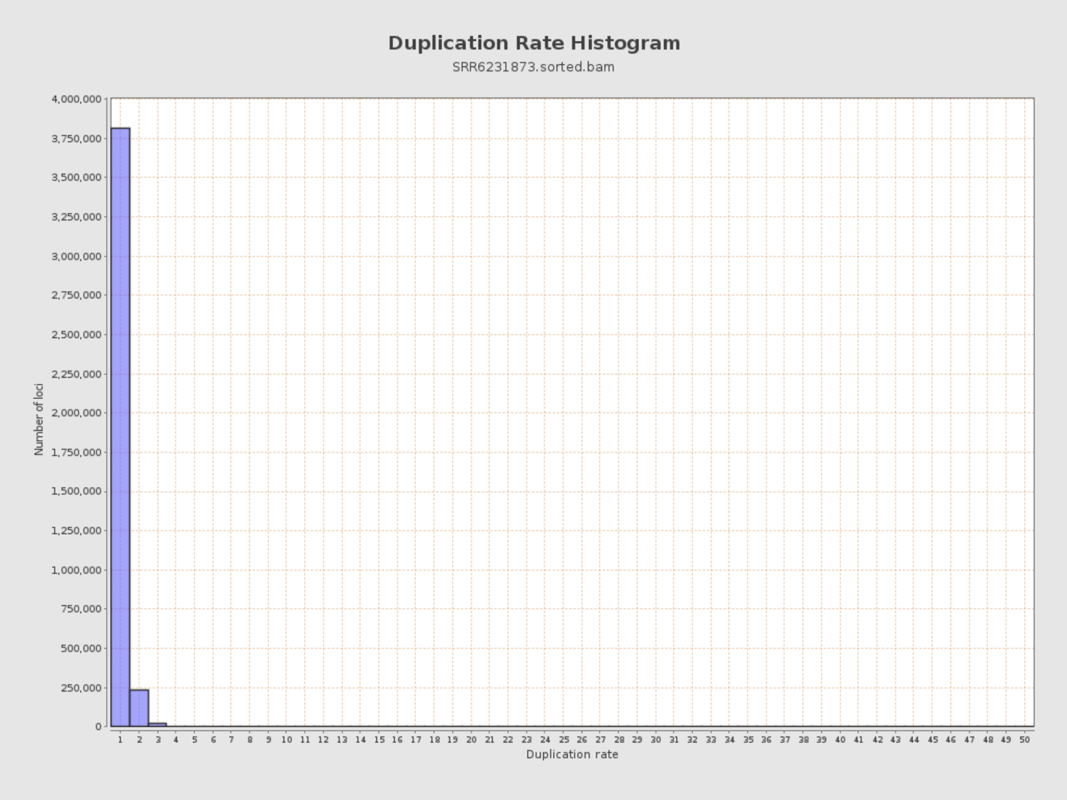
5. Results : Coverage Histogram (0-50X)



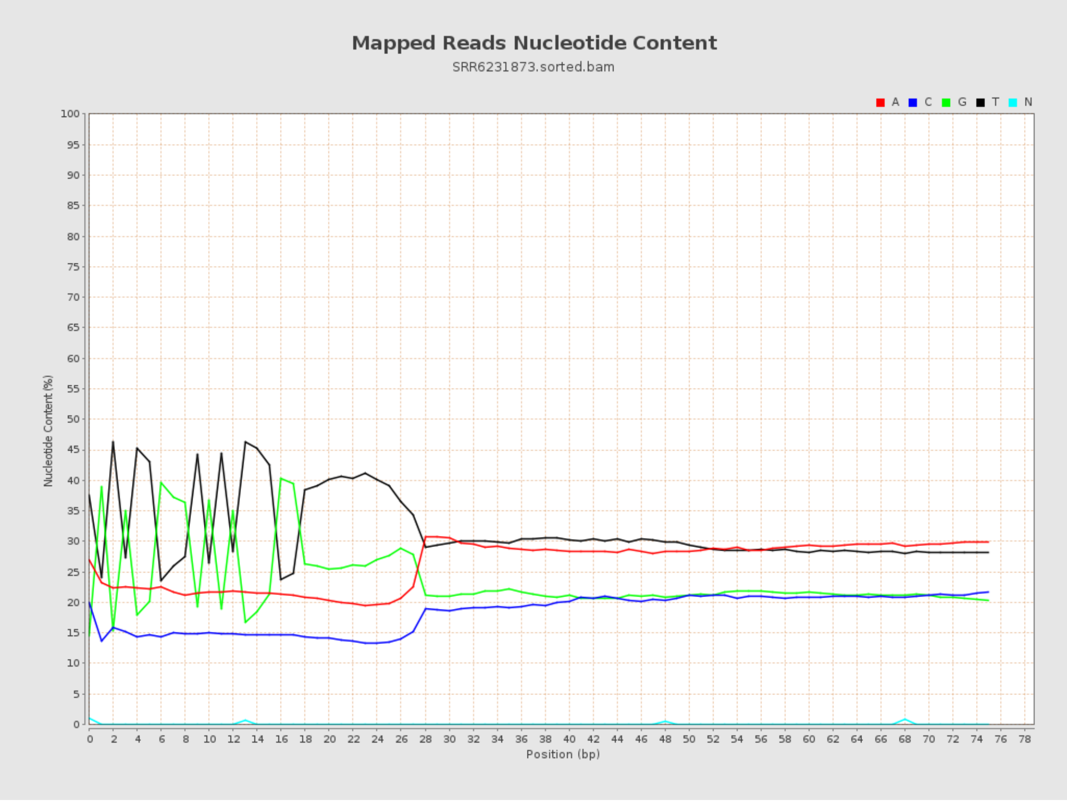
6. Results : Genome Fraction Coverage



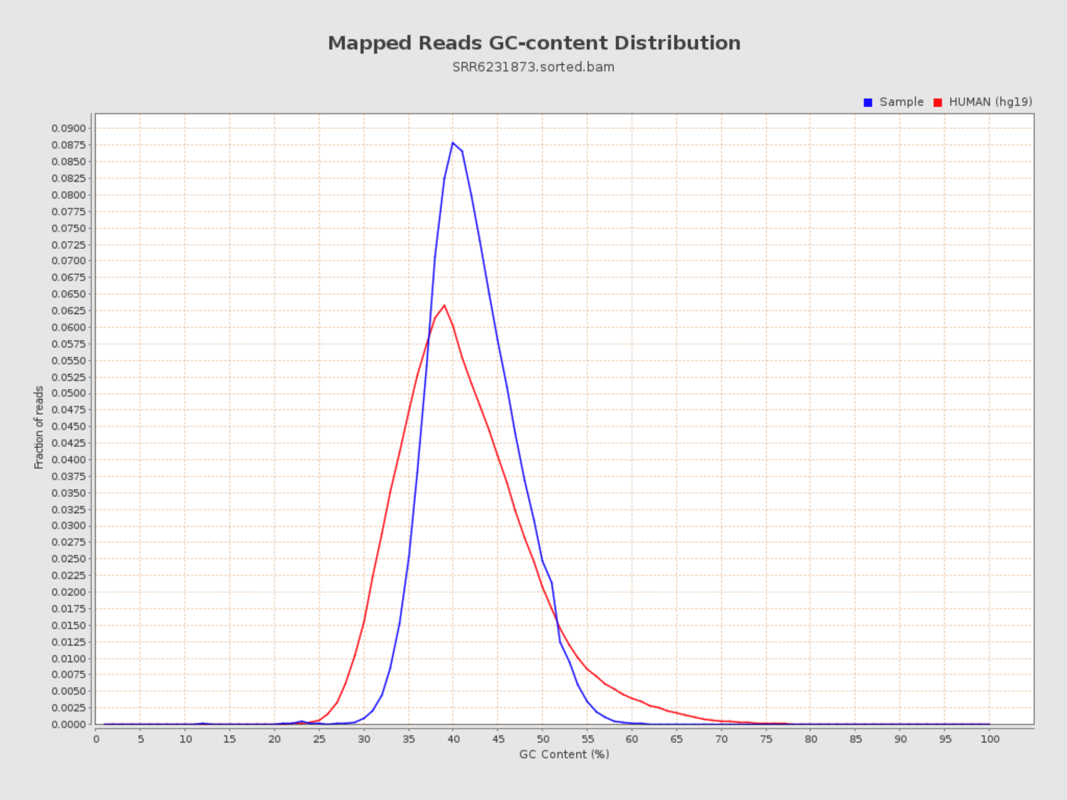
7. Results : Duplication Rate Histogram



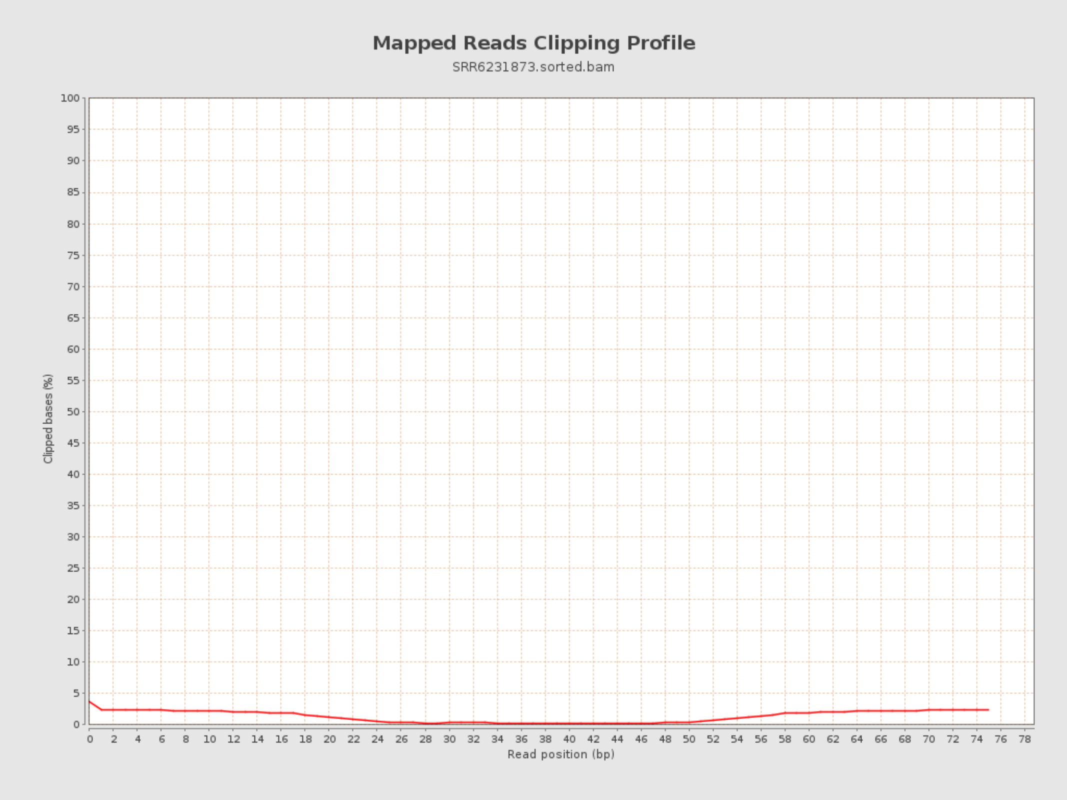
8. Results : Mapped Reads Nucleotide Content



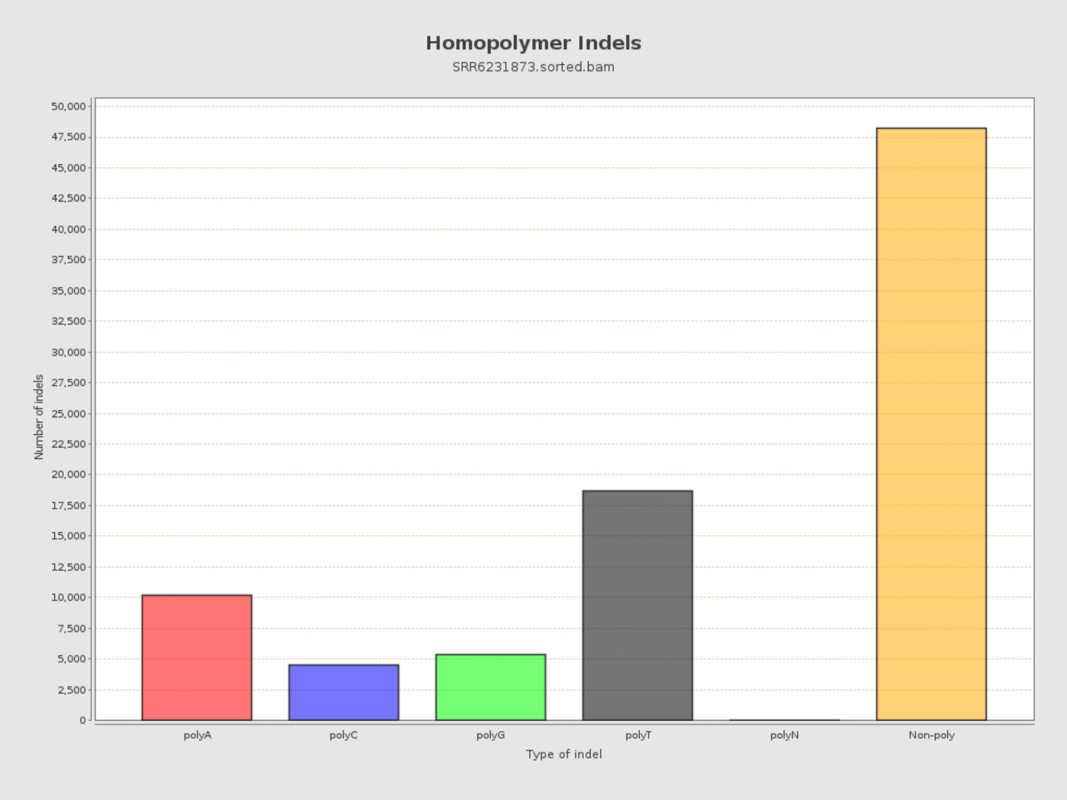
9. Results : Mapped Reads GC-content Distribution



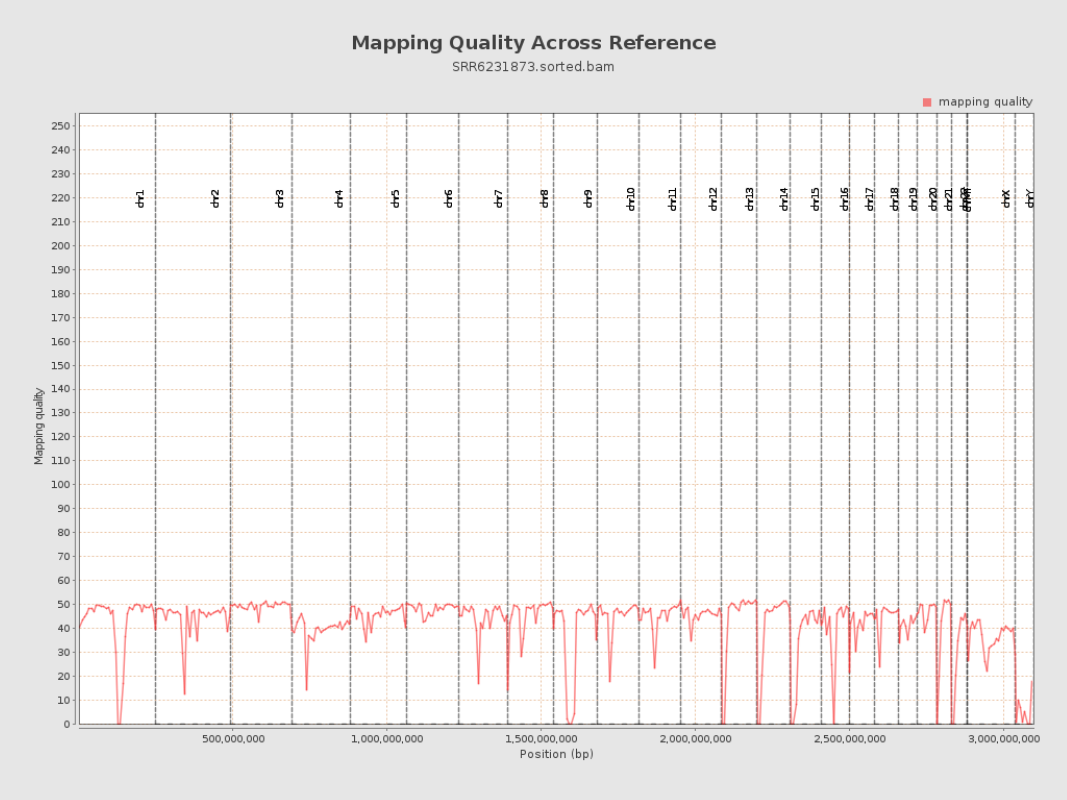
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram