Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 09:57:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231880.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_SRR6231880 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231880.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 09:57:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231880.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,436,695
Mapped reads	1,197,238 / 83.33%
Unmapped reads	239,457 / 16.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,298 / 0.79%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	117,292 / 8.16%
Duplication rate	7.75%
Clipped reads	525,810 / 36.6%

2.2. ACGT Content

Number/percentage of A's	22,219,126 / 27.82%
Number/percentage of C's	14,372,718 / 18%
Number/percentage of T's	25,964,660 / 32.51%
Number/percentage of G's	17,296,764 / 21.66%
Number/percentage of N's	4,126 / 0.01%
GC Percentage	39.66%

2.3. Coverage

Mean	0.0258

Standard Deviation	0.3491

2.4. Mapping Quality

Mean Mapping Quality	42.53

2.5. Mismatches and indels

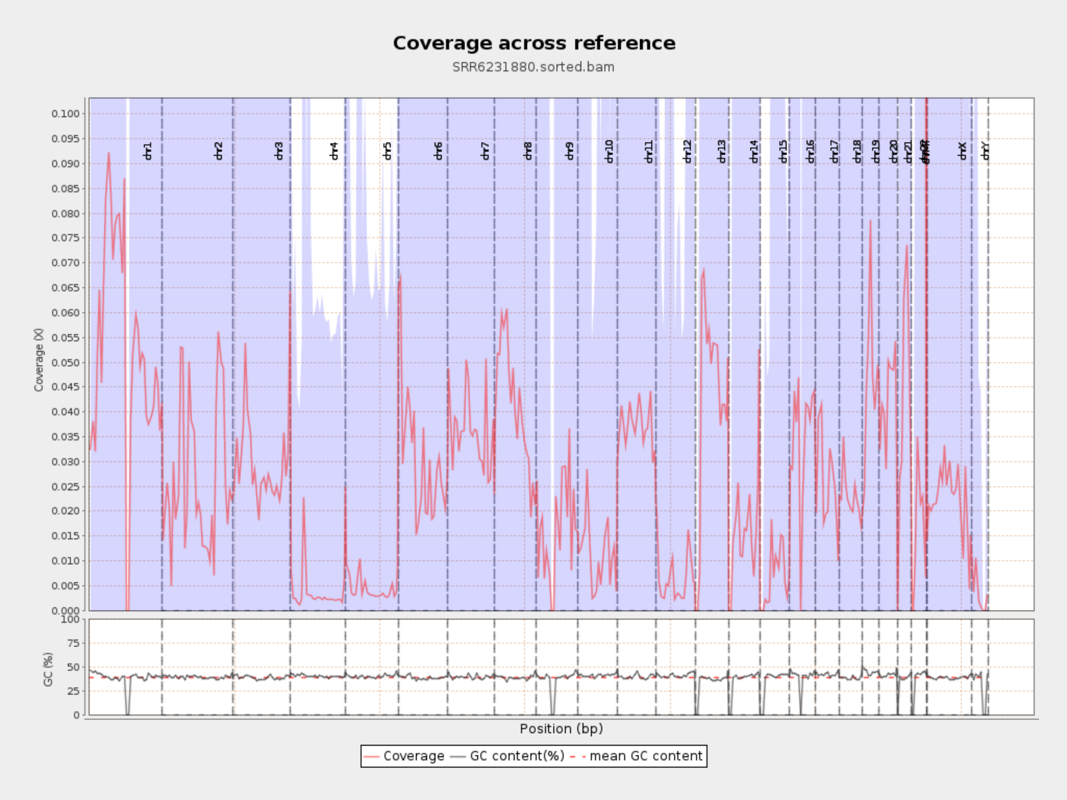
General error rate	0.77%
Mismatches	600,211
Insertions	6,222
Mapped reads with at least one insertion	0.51%
Deletions	23,711
Mapped reads with at least one deletion	1.96%
Homopolymer indels	46.5%

2.6. Chromosome stats

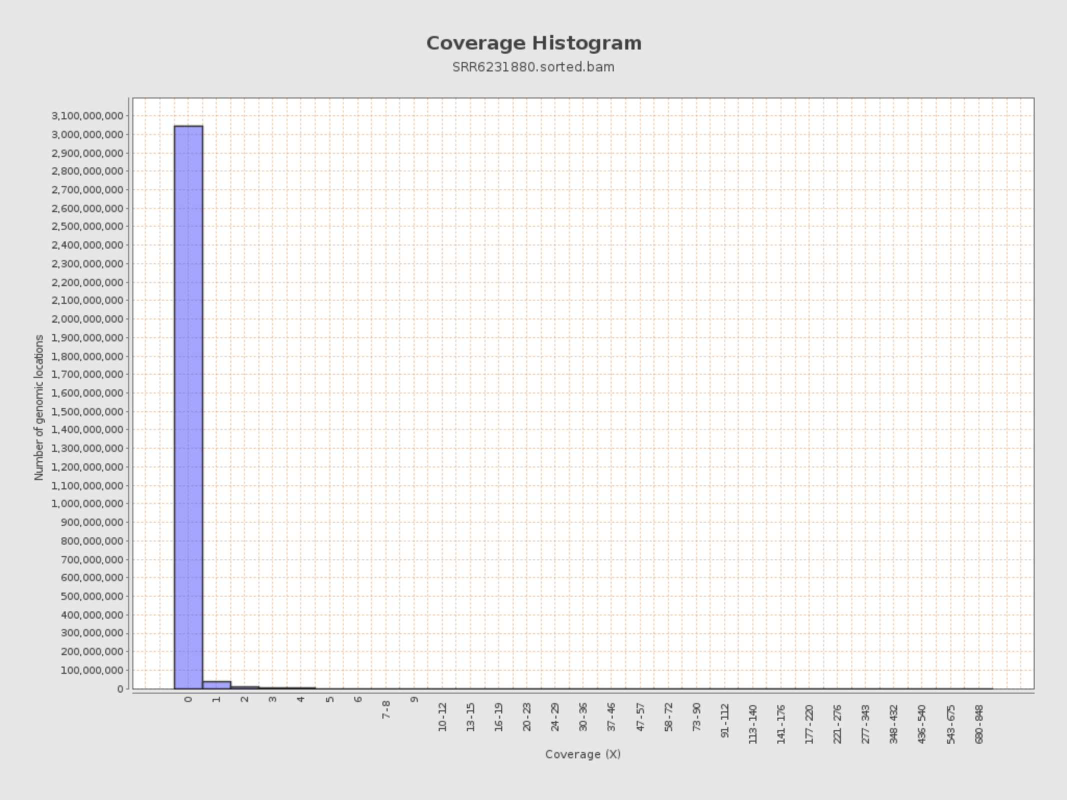
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13216976	0.053	0.768
chr2	243199373	6419135	0.0264	0.3389
chr3	198022430	5771184	0.0291	0.2326
chr4	191154276	666175	0.0035	0.0896
chr5	180915260	804338	0.0044	0.0897
chr6	171115067	5246924	0.0307	0.2599
chr7	159138663	5784605	0.0363	0.3855

chr8	146364022	6007951	0.041	0.5992
chr9	141213431	2235774	0.0158	0.2178
chr10	135534747	1530817	0.0113	0.1562
chr11	135006516	5007608	0.0371	0.3431
chr12	133851895	894030	0.0067	0.1117
chr13	115169878	4916386	0.0427	0.2925
chr14	107349540	1575563	0.0147	0.178
chr15	102531392	705290	0.0069	0.112
chr16	90354753	3168471	0.0351	0.2721
chr17	81195210	2041982	0.0251	0.2321
chr18	78077248	1821848	0.0233	0.446
chr19	59128983	2774271	0.0469	0.4422
chr20	63025520	2700521	0.0428	0.2956
chr21	48129895	2027104	0.0421	0.2902
chr22	51304566	815435	0.0159	0.1683
chrMT	16571	79660	4.8072	4.5927
chrX	155270560	3490351	0.0225	0.2236
chrY	59373566	195866	0.0033	0.0834

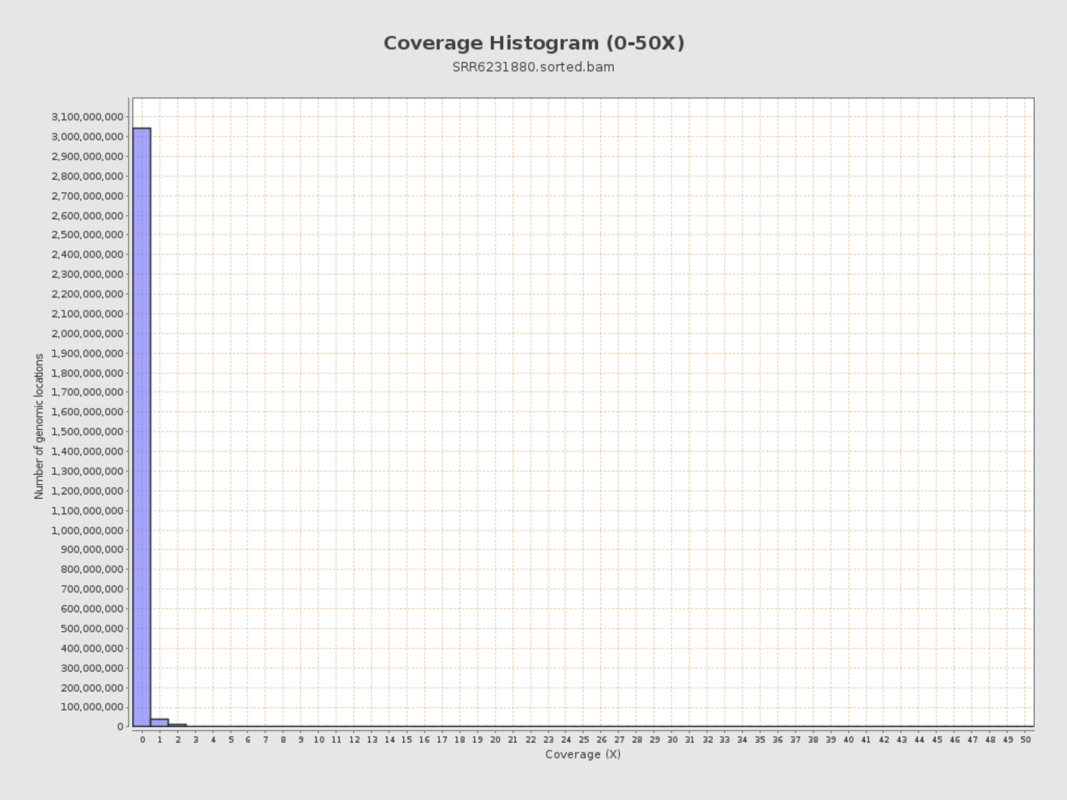
3. Results : Coverage across reference



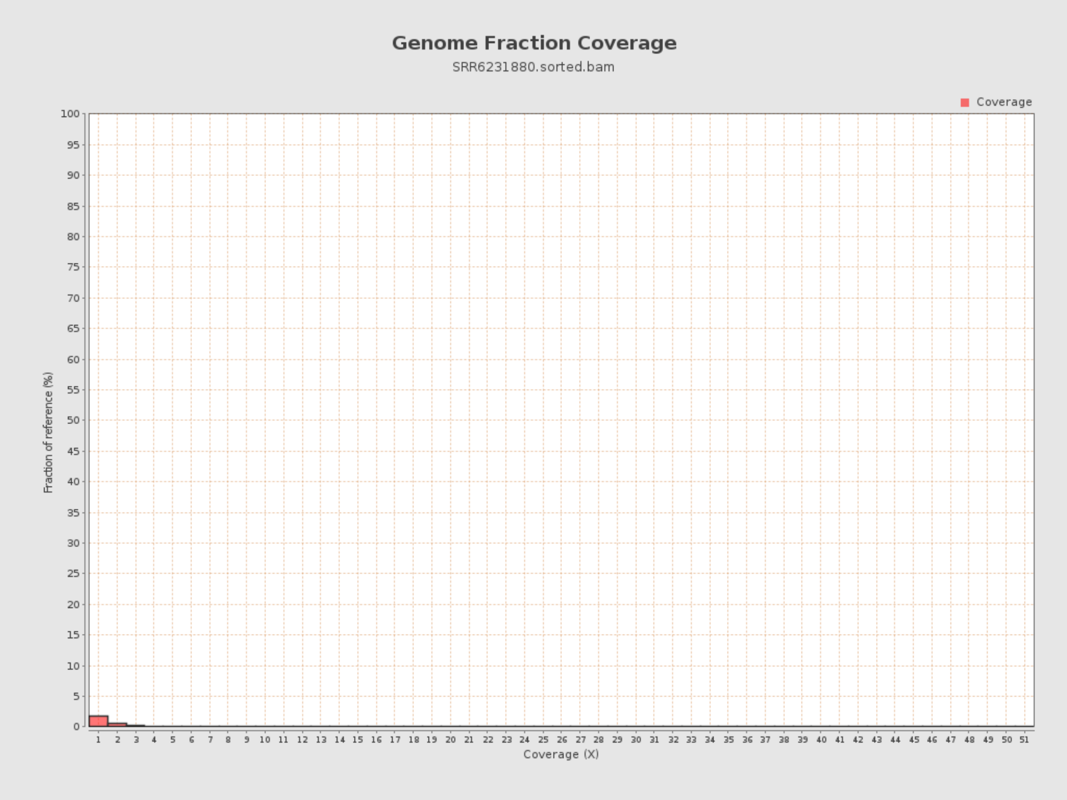
4. Results : Coverage Histogram



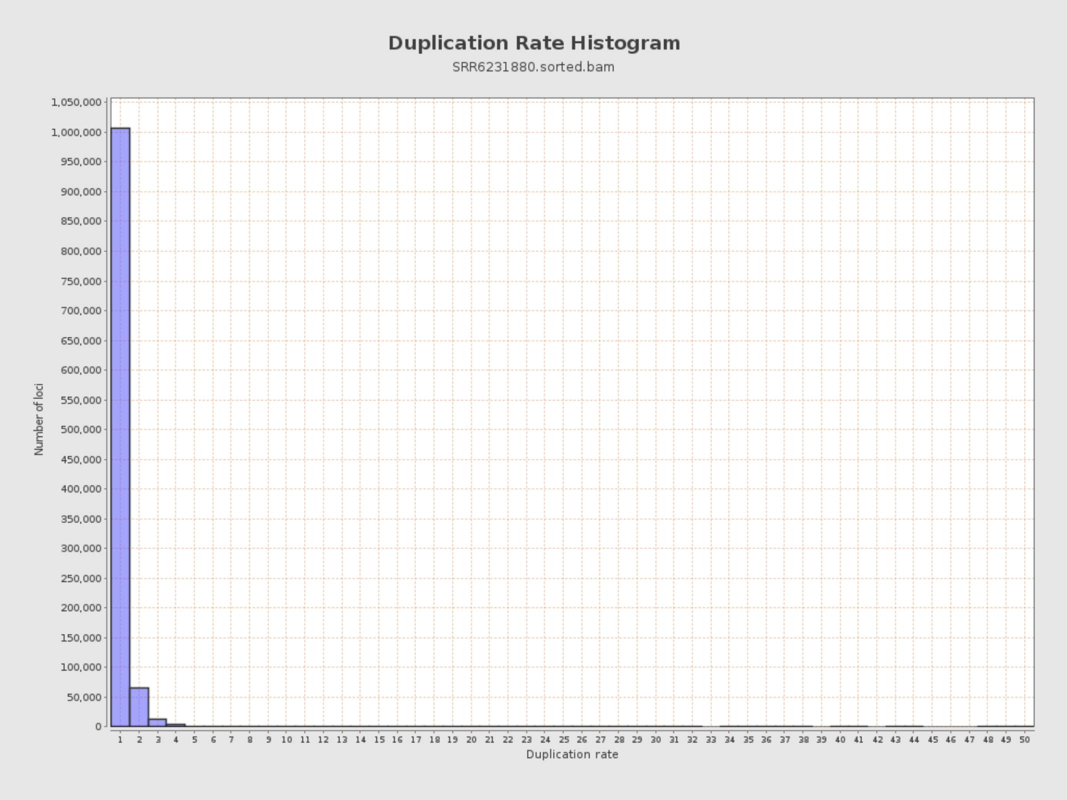
5. Results : Coverage Histogram (0-50X)



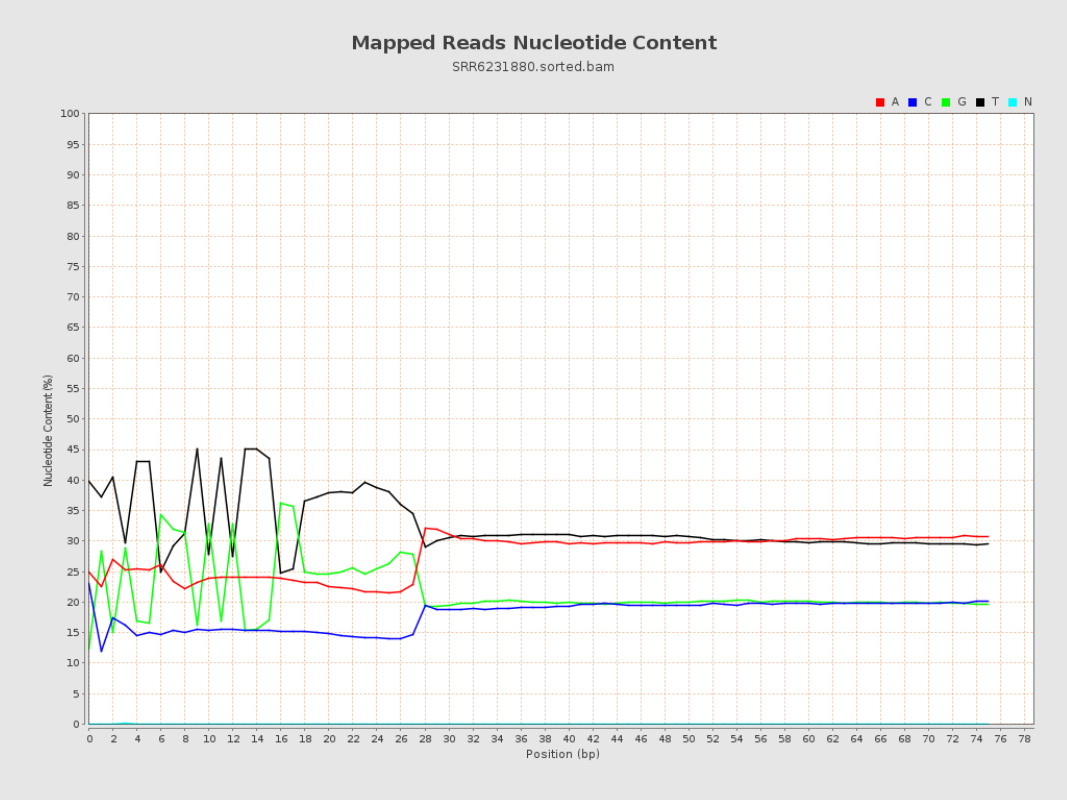
6. Results : Genome Fraction Coverage



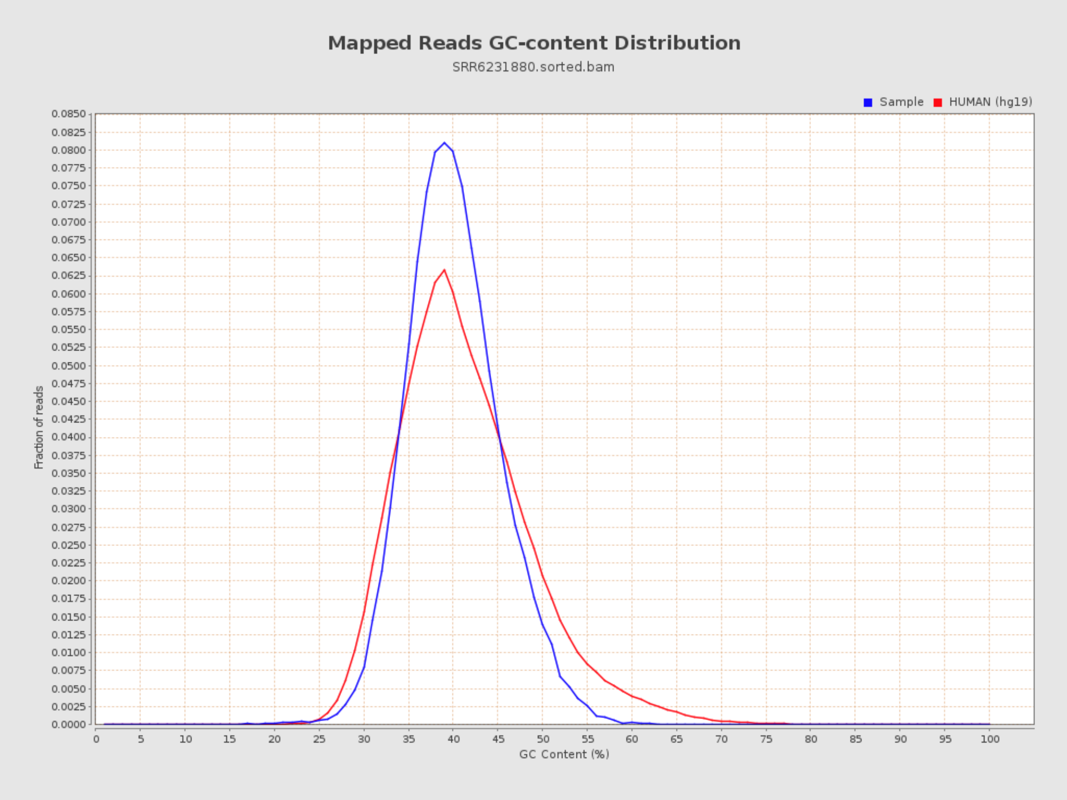
7. Results : Duplication Rate Histogram



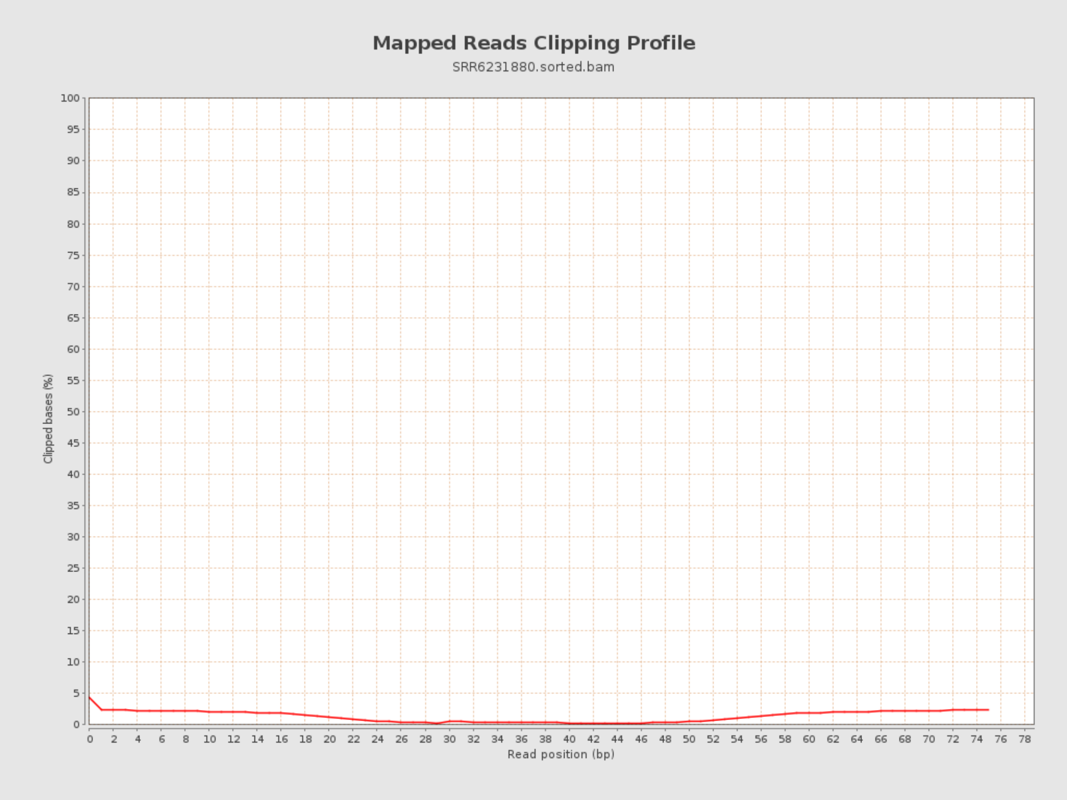
8. Results : Mapped Reads Nucleotide Content



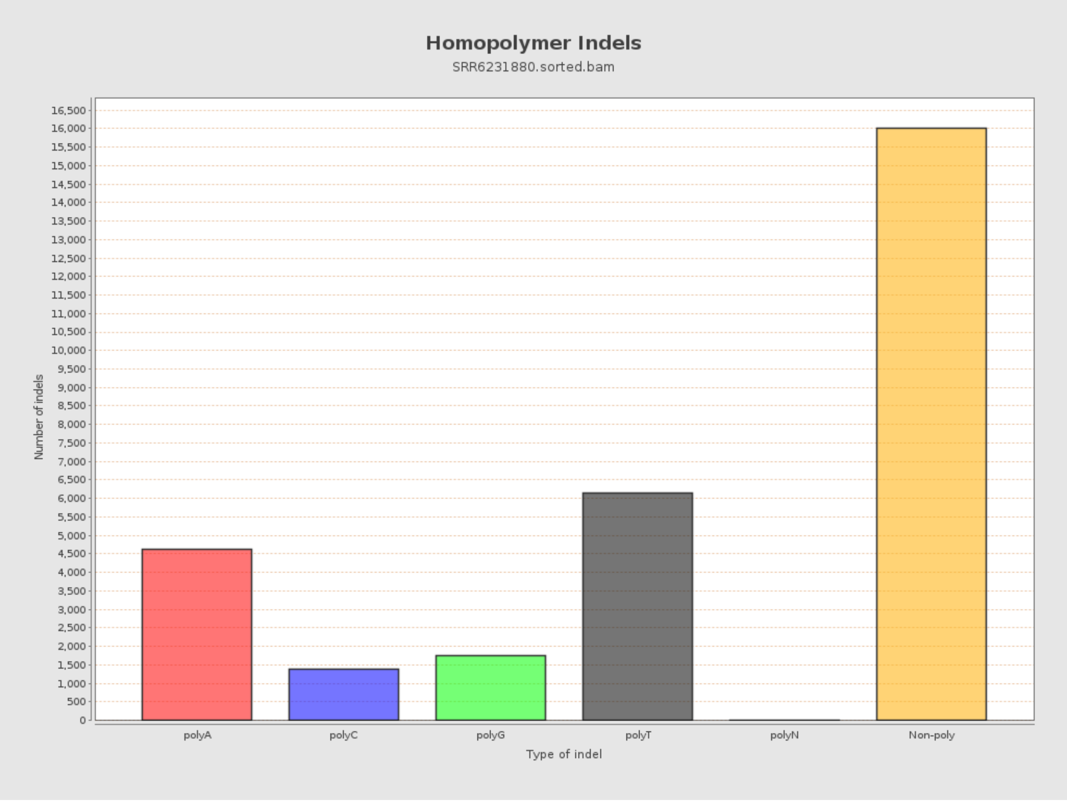
9. Results : Mapped Reads GC-content Distribution



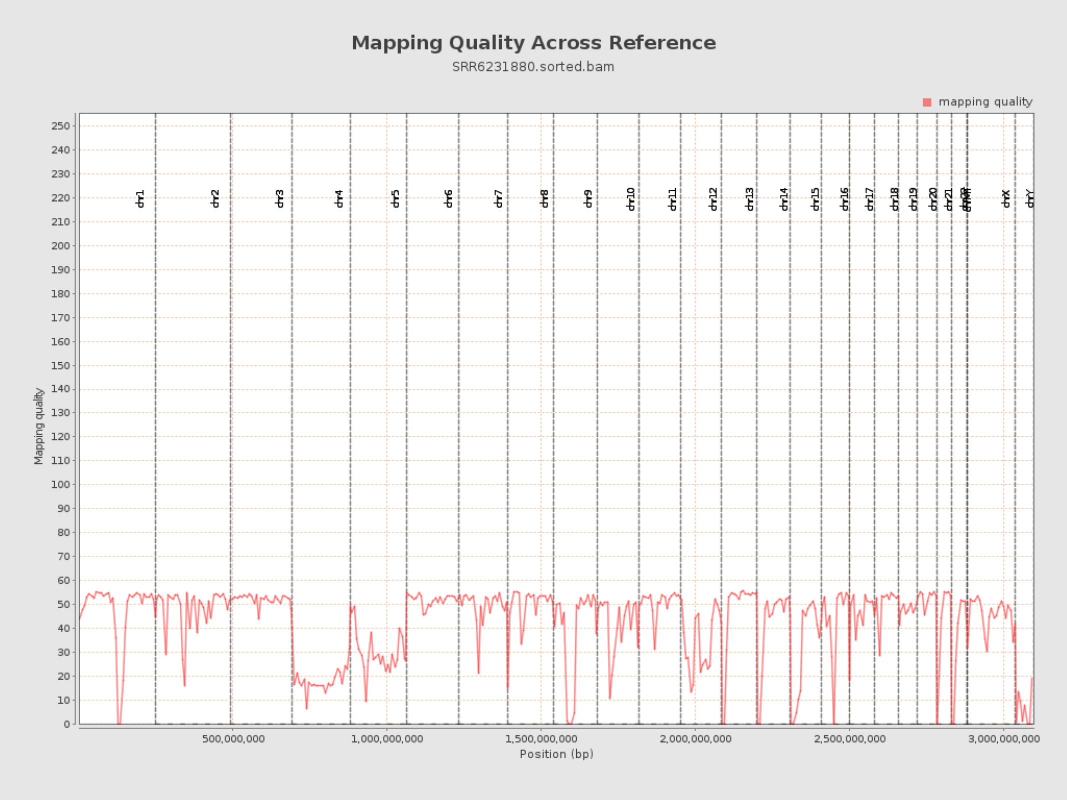
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram