Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 01:57:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231780.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_SRR6231780 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231780.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 01:57:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231780.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,352,198
Mapped reads	1,162,598 / 85.98%
Unmapped reads	189,600 / 14.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,253 / 0.68%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	73,456 / 5.43%
Duplication rate	1.96%
Clipped reads	587,722 / 43.46%

2.2. ACGT Content

Number/percentage of A's	22,193,505 / 29.15%
Number/percentage of C's	14,339,318 / 18.83%
Number/percentage of T's	21,031,390 / 27.62%
Number/percentage of G's	18,567,526 / 24.39%
Number/percentage of N's	5,336 / 0.01%
GC Percentage	43.22%

2.3. Coverage

Mean	0.0246

Standard Deviation	5.6213

2.4. Mapping Quality

Mean Mapping Quality	43.86

2.5. Mismatches and indels

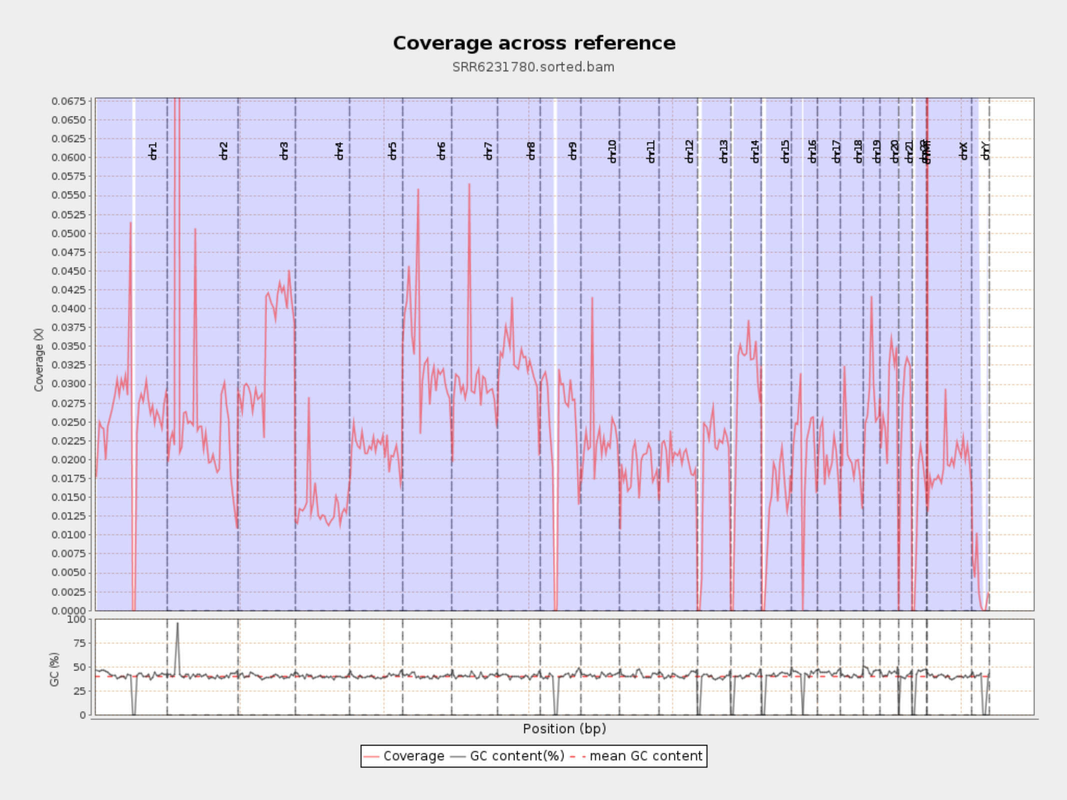
General error rate	0.72%
Mismatches	538,040
Insertions	6,373
Mapped reads with at least one insertion	0.54%
Deletions	17,847
Mapped reads with at least one deletion	1.52%
Homopolymer indels	42.71%

2.6. Chromosome stats

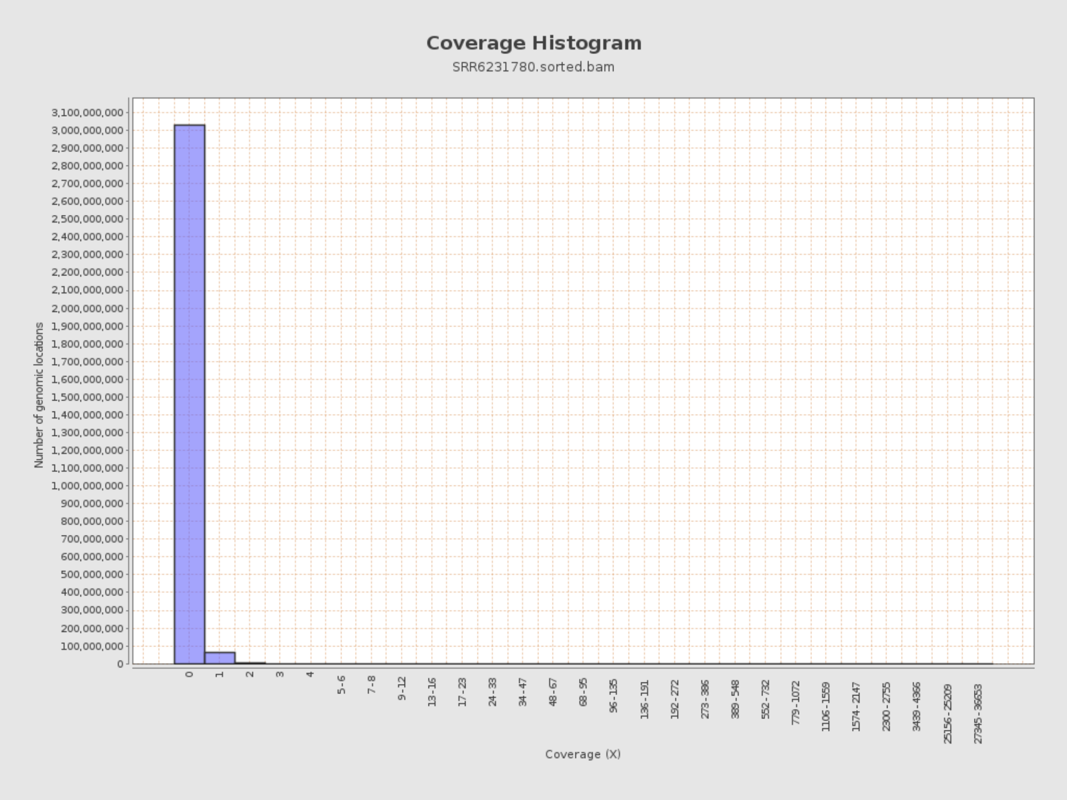
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6419618	0.0258	0.5865
chr2	243199373	8676515	0.0357	20.032
chr3	198022430	6929711	0.035	0.1956
chr4	191154276	2630260	0.0138	0.1336
chr5	180915260	3877829	0.0214	0.1554
chr6	171115067	5820721	0.034	0.2496
chr7	159138663	4835462	0.0304	0.4224

chr8	146364022	4831962	0.033	0.3578
chr9	141213431	3418286	0.0242	0.2284
chr10	135534747	3094651	0.0228	0.243
chr11	135006516	2549787	0.0189	0.2283
chr12	133851895	2681701	0.02	0.1502
chr13	115169878	2230261	0.0194	0.1445
chr14	107349540	3006260	0.028	0.2201
chr15	102531392	1385885	0.0135	0.1222
chr16	90354753	1879353	0.0208	0.1732
chr17	81195210	1642755	0.0202	0.1623
chr18	78077248	1592002	0.0204	0.4426
chr19	59128983	1672436	0.0283	0.3687
chr20	63025520	1768515	0.0281	0.1795
chr21	48129895	1243558	0.0258	0.179
chr22	51304566	690955	0.0135	0.1204
chrMT	16571	59943	3.6173	2.6683
chrX	155270560	3041323	0.0196	0.1618
chrY	59373566	187648	0.0032	0.083

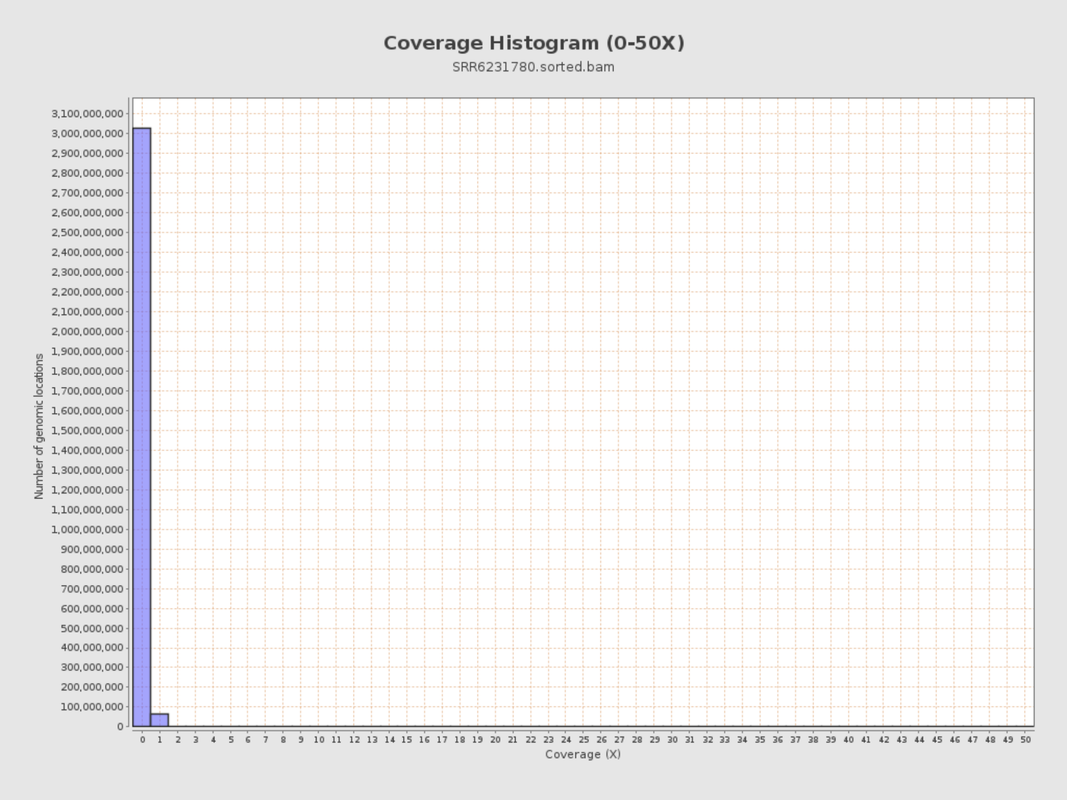
3. Results : Coverage across reference



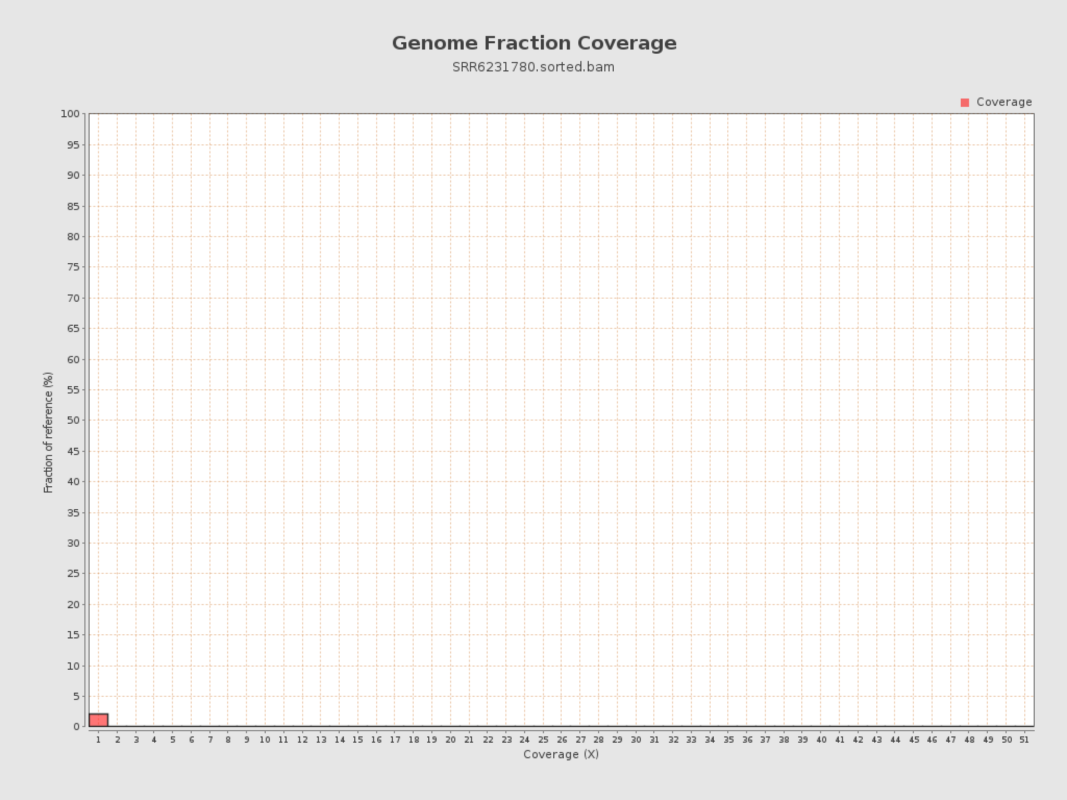
4. Results : Coverage Histogram



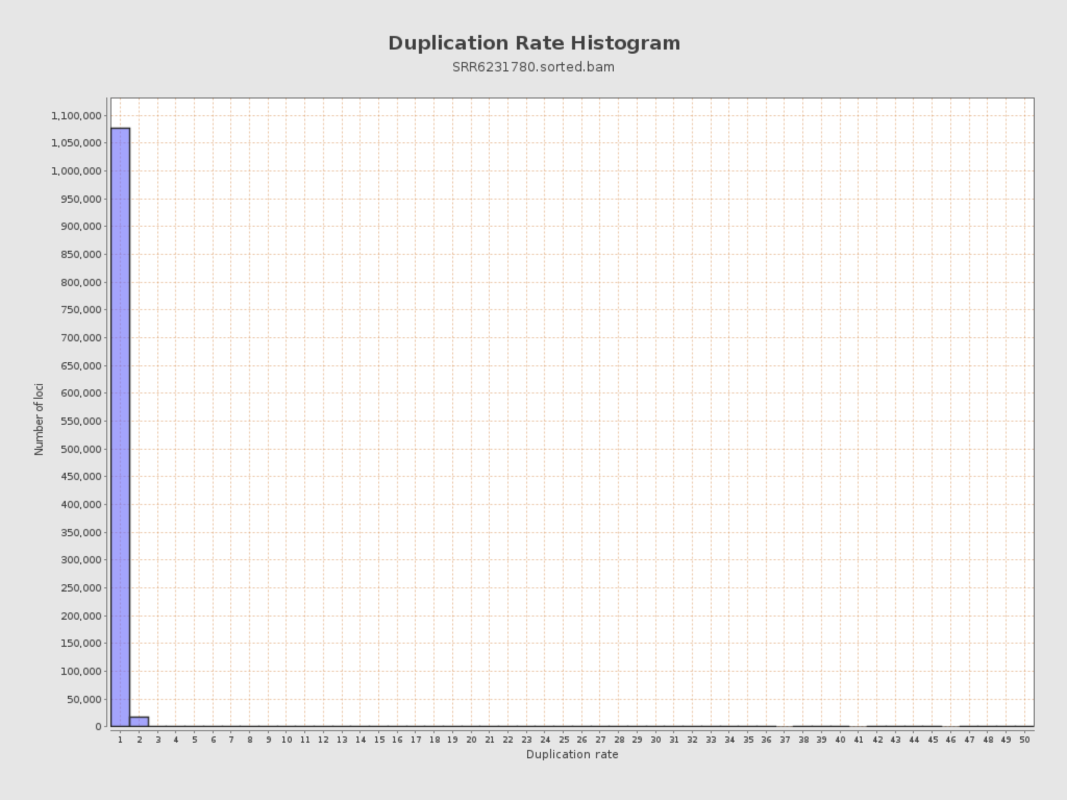
5. Results : Coverage Histogram (0-50X)



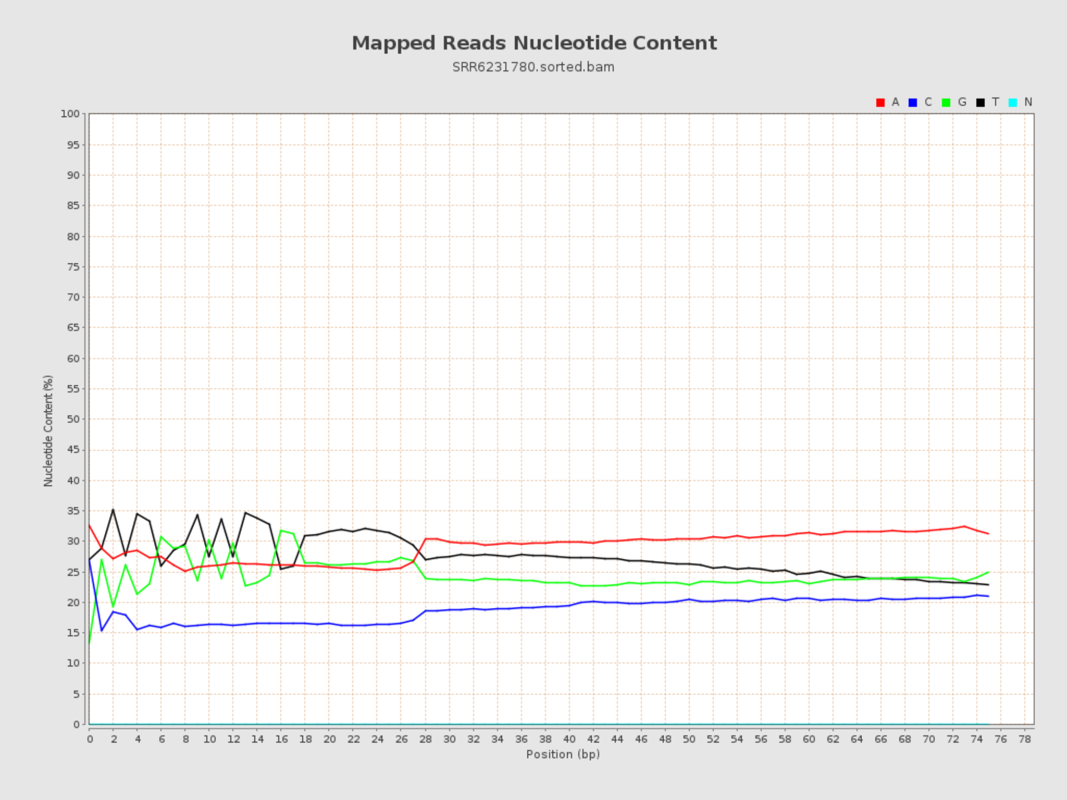
6. Results : Genome Fraction Coverage



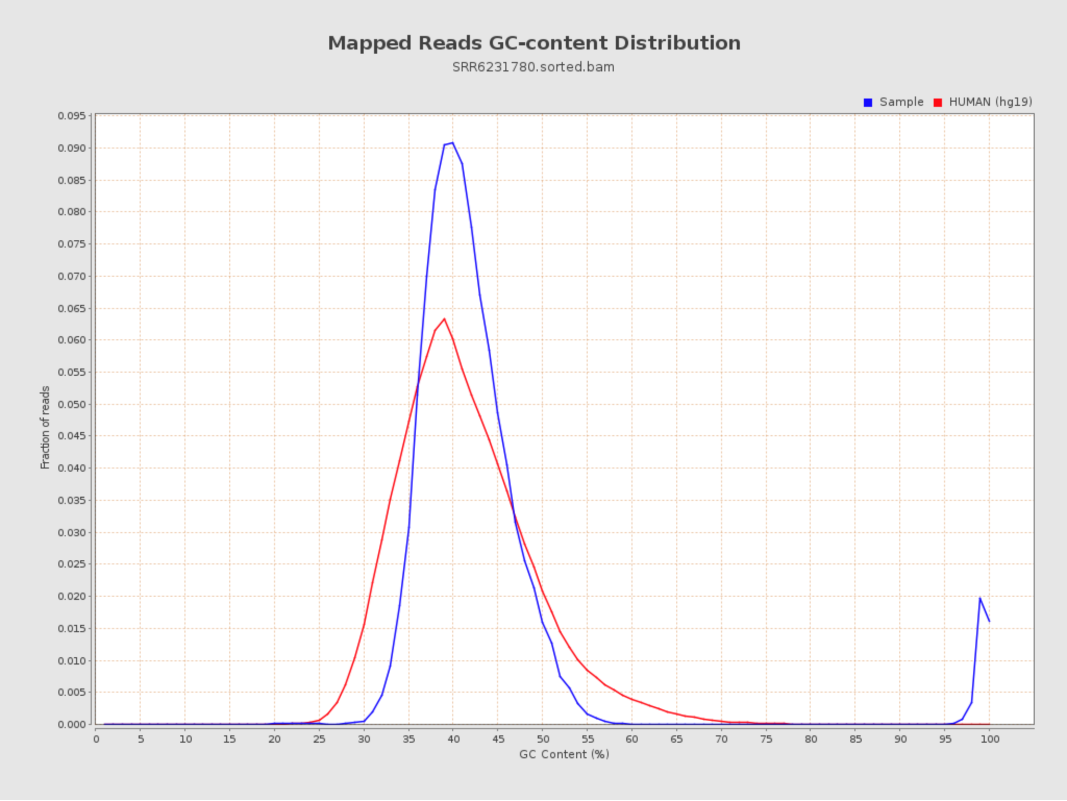
7. Results : Duplication Rate Histogram



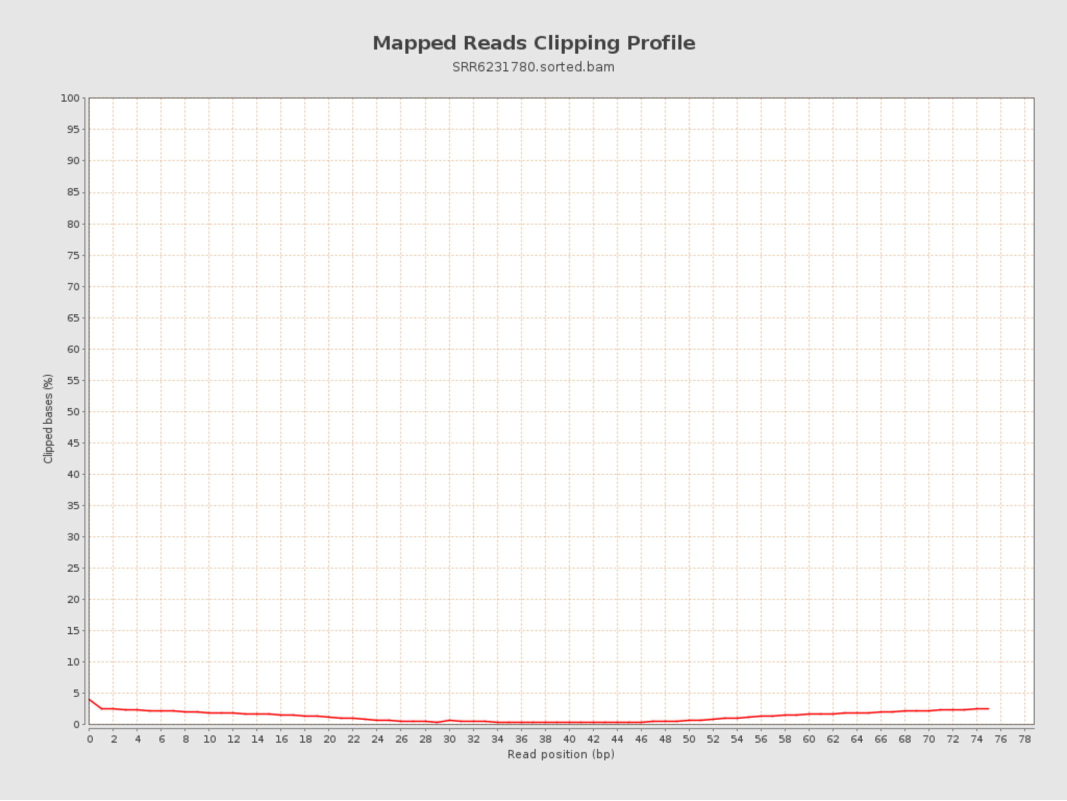
8. Results : Mapped Reads Nucleotide Content



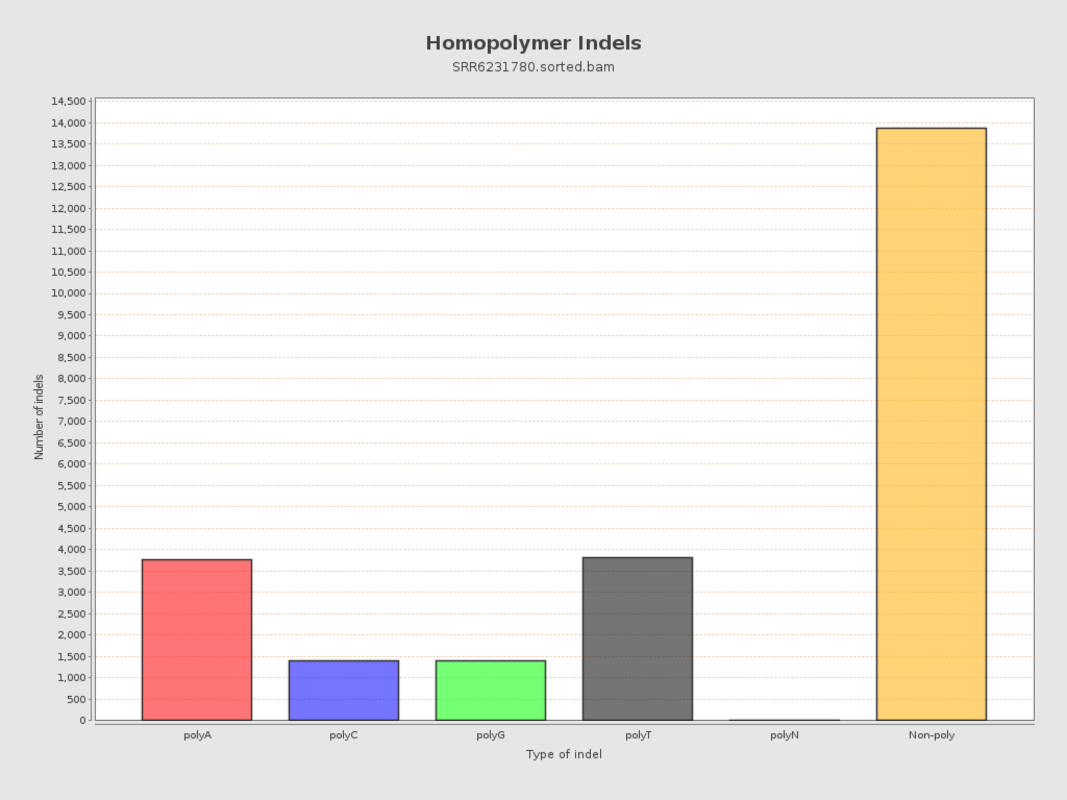
9. Results : Mapped Reads GC-content Distribution



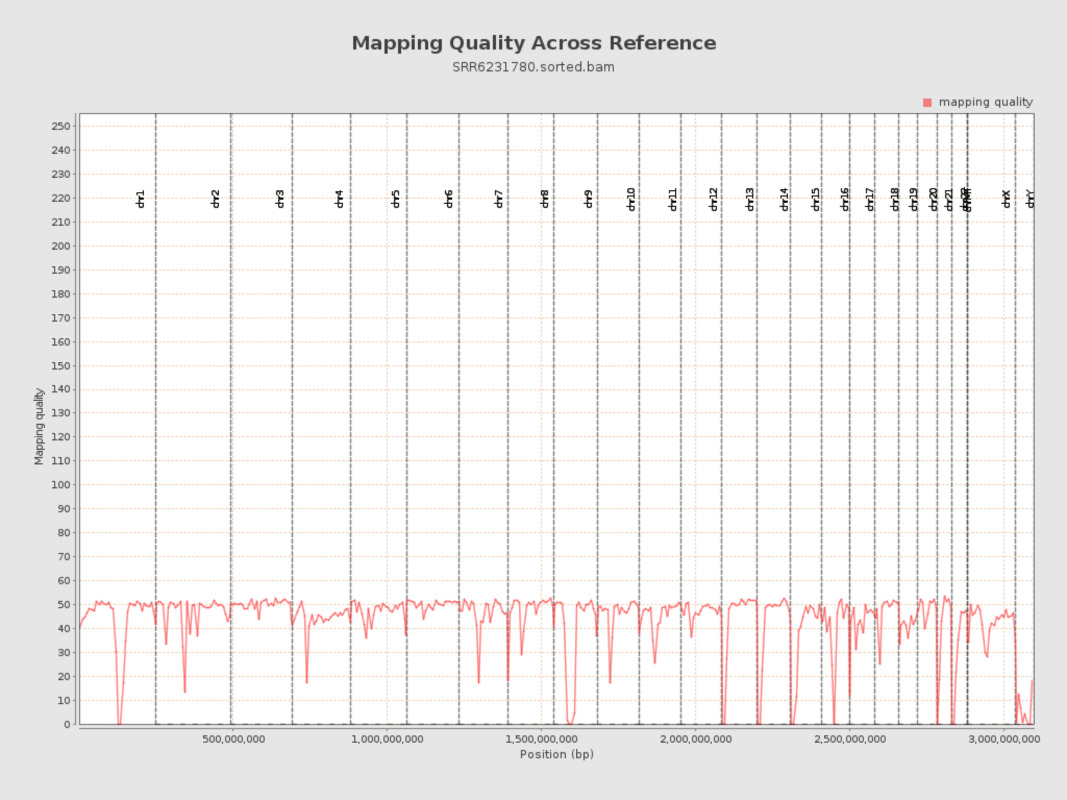
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram