Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 09:47:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231877.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_SRR6231877 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231877.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 09:47:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231877.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,140,253
Mapped reads	8,080,600 / 40.12%
Unmapped reads	12,059,653 / 59.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	47,962 / 0.24%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	609,318 / 3.03%
Duplication rate	4.28%
Clipped reads	4,529,159 / 22.49%

2.2. ACGT Content

Number/percentage of A's	141,247,764 / 27.42%
Number/percentage of C's	104,407,227 / 20.27%
Number/percentage of T's	144,343,812 / 28.02%
Number/percentage of G's	125,083,051 / 24.28%
Number/percentage of N's	34,501 / 0.01%
GC Percentage	44.55%

2.3. Coverage

Mean	0.1665

Standard Deviation	18.1509

2.4. Mapping Quality

Mean Mapping Quality	42.43

2.5. Mismatches and indels

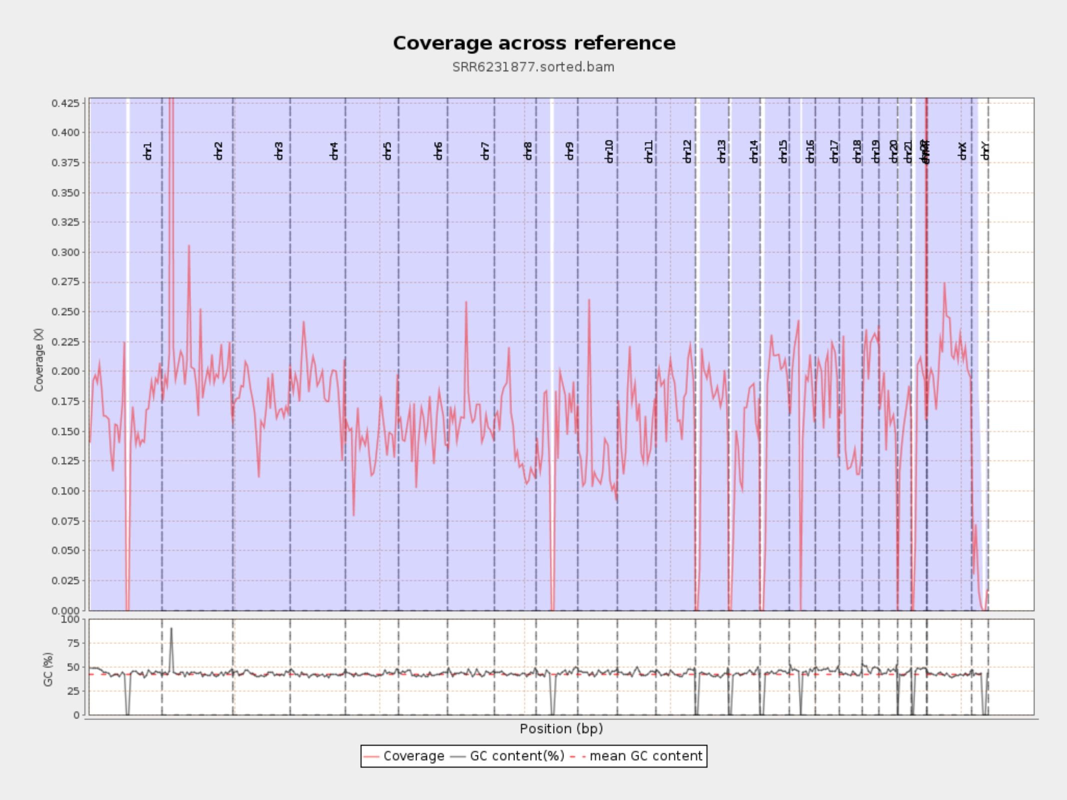
General error rate	0.7%
Mismatches	3,541,018
Insertions	39,897
Mapped reads with at least one insertion	0.49%
Deletions	125,210
Mapped reads with at least one deletion	1.53%
Homopolymer indels	43.43%

2.6. Chromosome stats

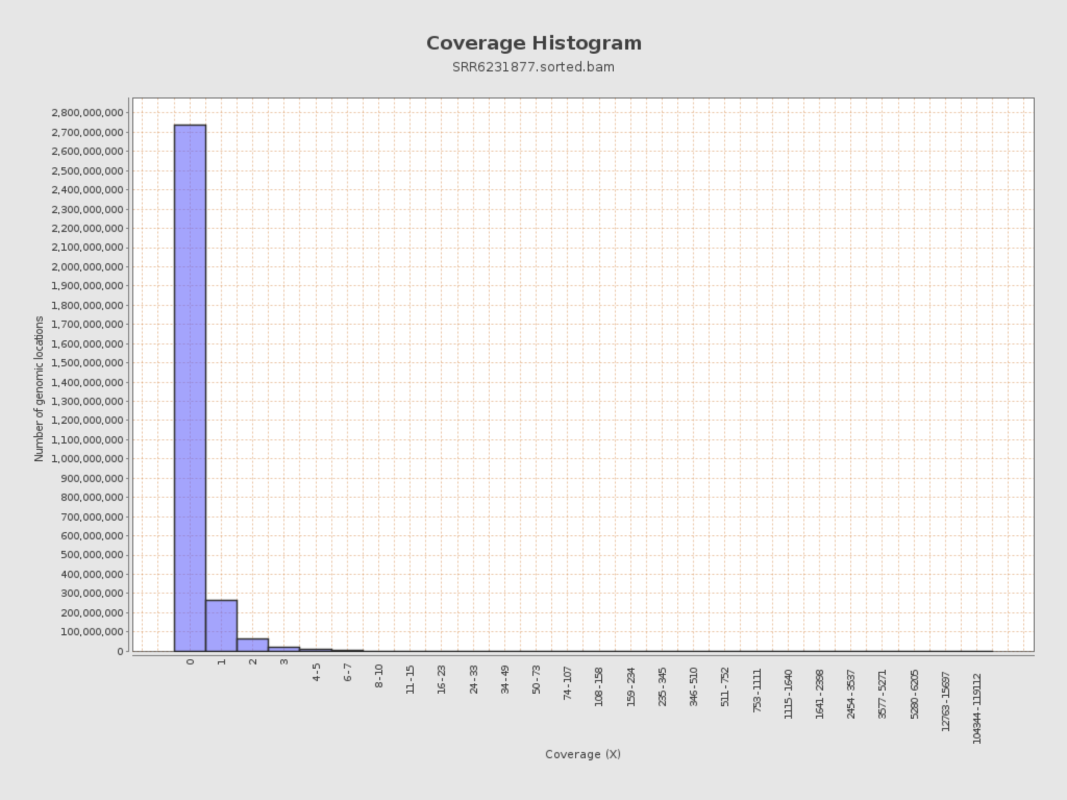
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	39143031	0.157	2.0225
chr2	243199373	59478711	0.2446	64.6433
chr3	198022430	34189432	0.1727	0.5535
chr4	191154276	36636653	0.1917	0.6744
chr5	180915260	25839794	0.1428	0.515
chr6	171115067	26203670	0.1531	0.7231
chr7	159138663	26001493	0.1634	1.7

chr8	146364022	21267929	0.1453	1.104
chr9	141213431	20306640	0.1438	1.0829
chr10	135534747	16752669	0.1236	1.2041
chr11	135006516	21127292	0.1565	1.2581
chr12	133851895	24735731	0.1848	0.5941
chr13	115169878	18226272	0.1583	0.5296
chr14	107349540	13777200	0.1283	0.8181
chr15	102531392	17012276	0.1659	0.5678
chr16	90354753	16254339	0.1799	0.7844
chr17	81195210	15727545	0.1937	0.7533
chr18	78077248	10934466	0.14	2.5013
chr19	59128983	12969415	0.2193	1.5518
chr20	63025520	10317658	0.1637	0.6284
chr21	48129895	6767749	0.1406	0.6079
chr22	51304566	7019621	0.1368	0.5034
chrMT	16571	132220	7.979	10.071
chrX	155270560	32987200	0.2124	0.8389
chrY	59373566	1508046	0.0254	0.4623

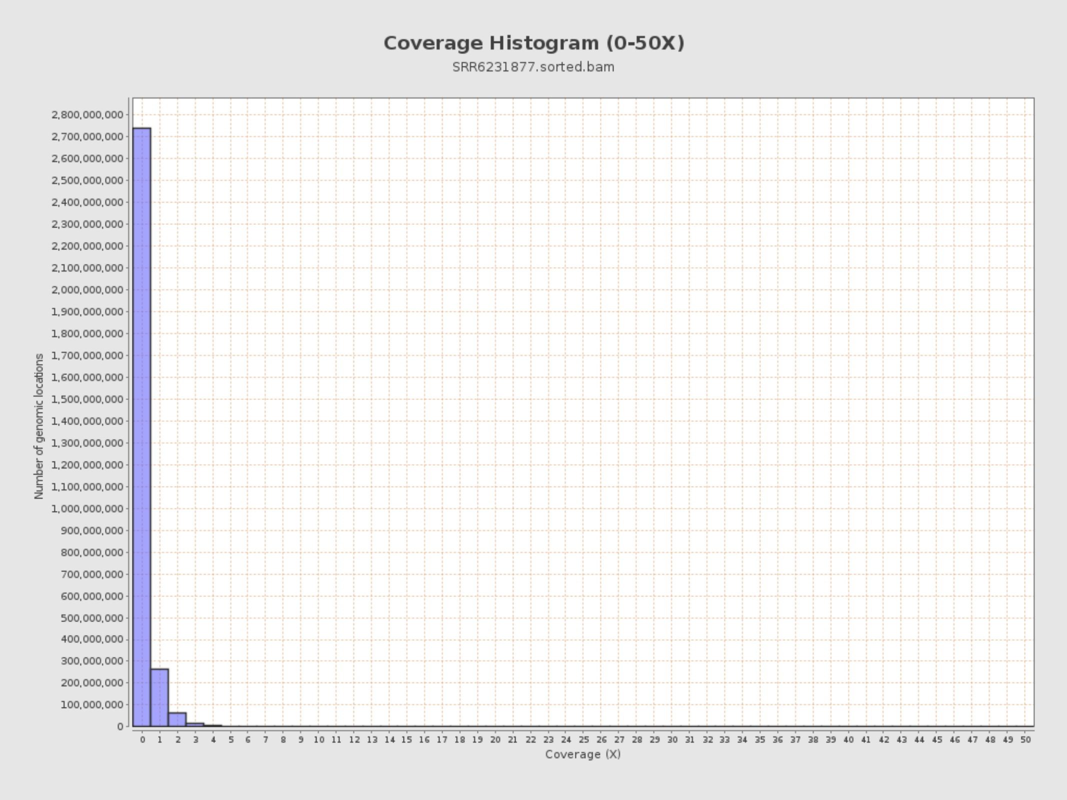
3. Results : Coverage across reference



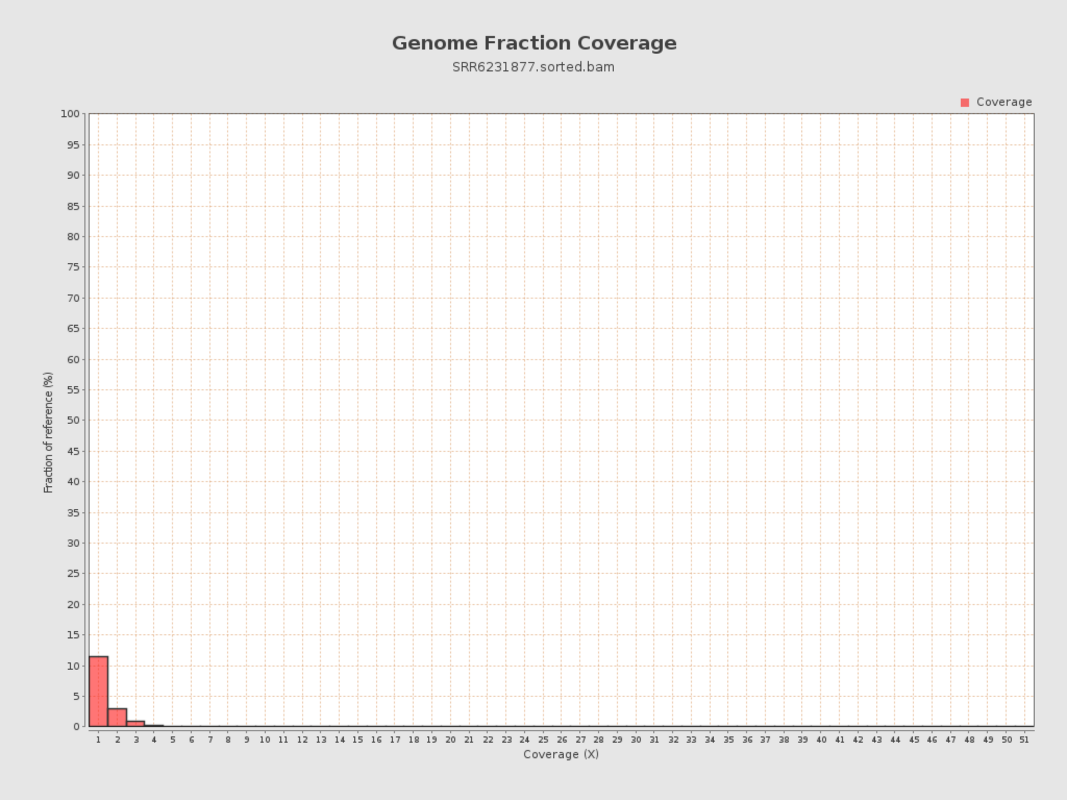
4. Results : Coverage Histogram



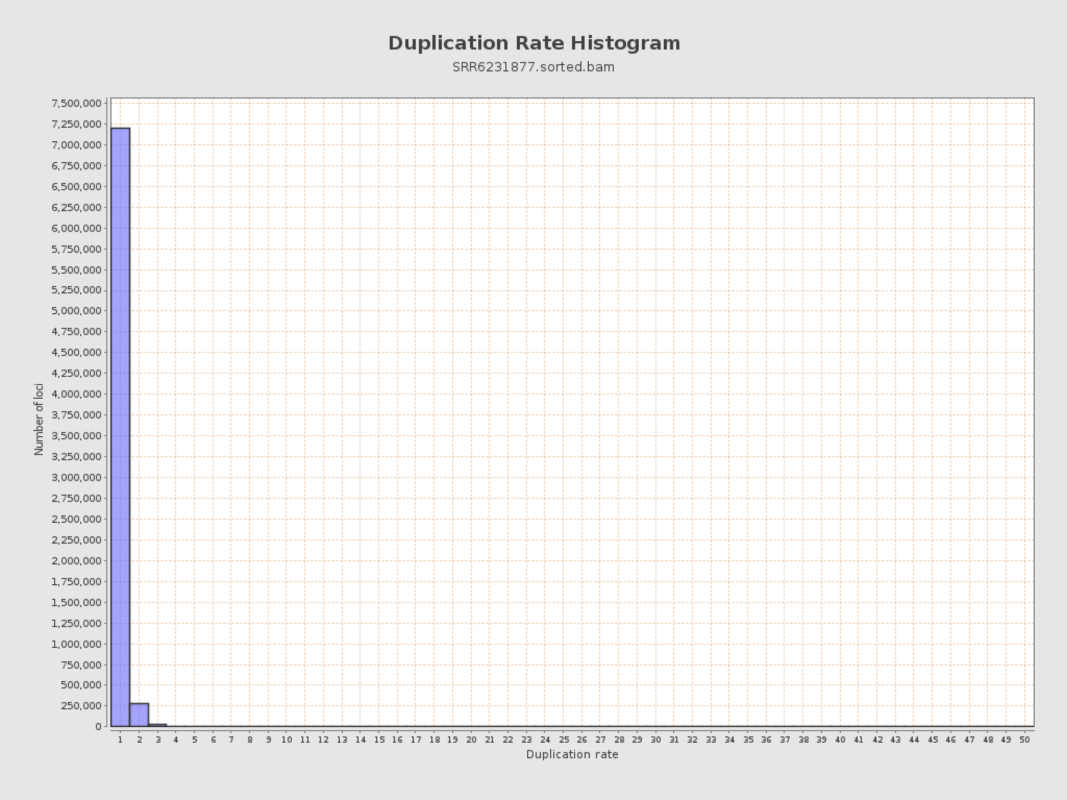
5. Results : Coverage Histogram (0-50X)



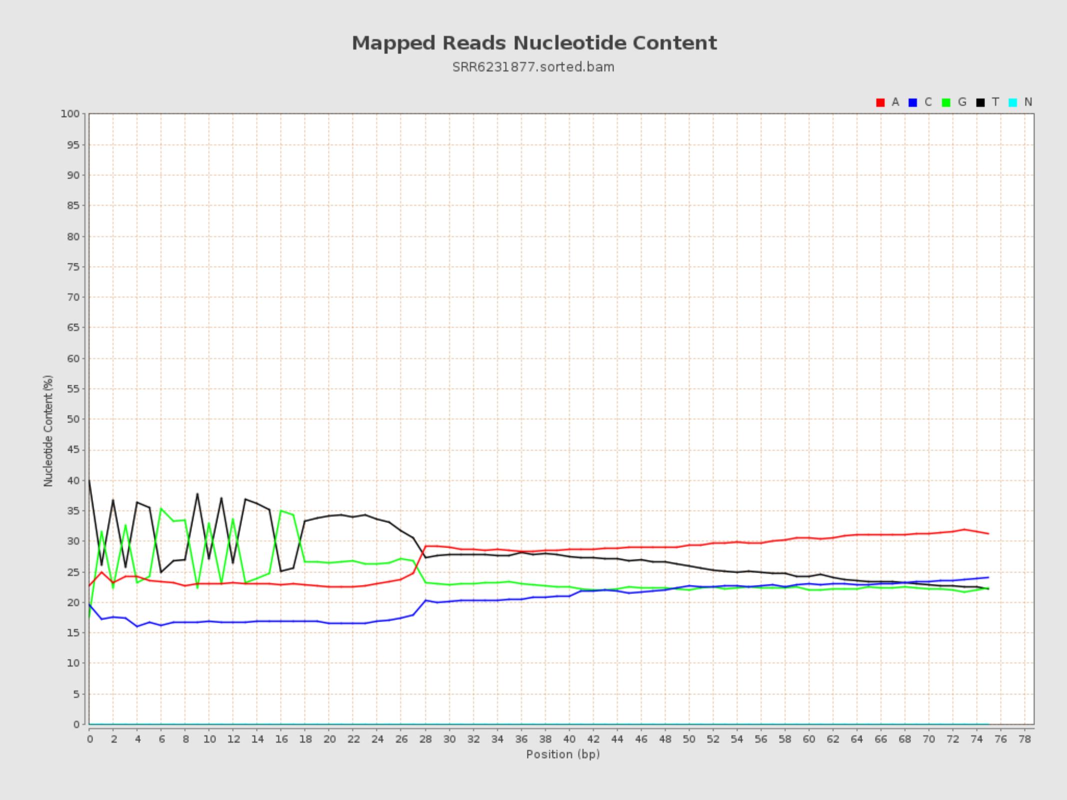
6. Results : Genome Fraction Coverage



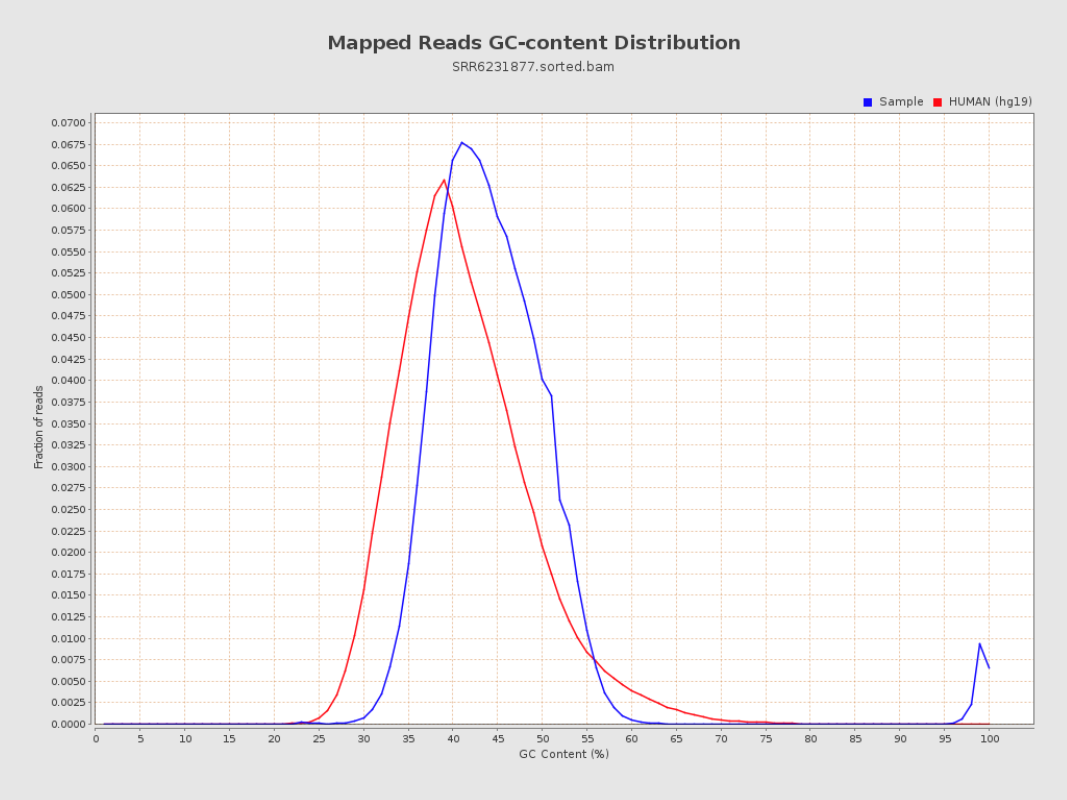
7. Results : Duplication Rate Histogram



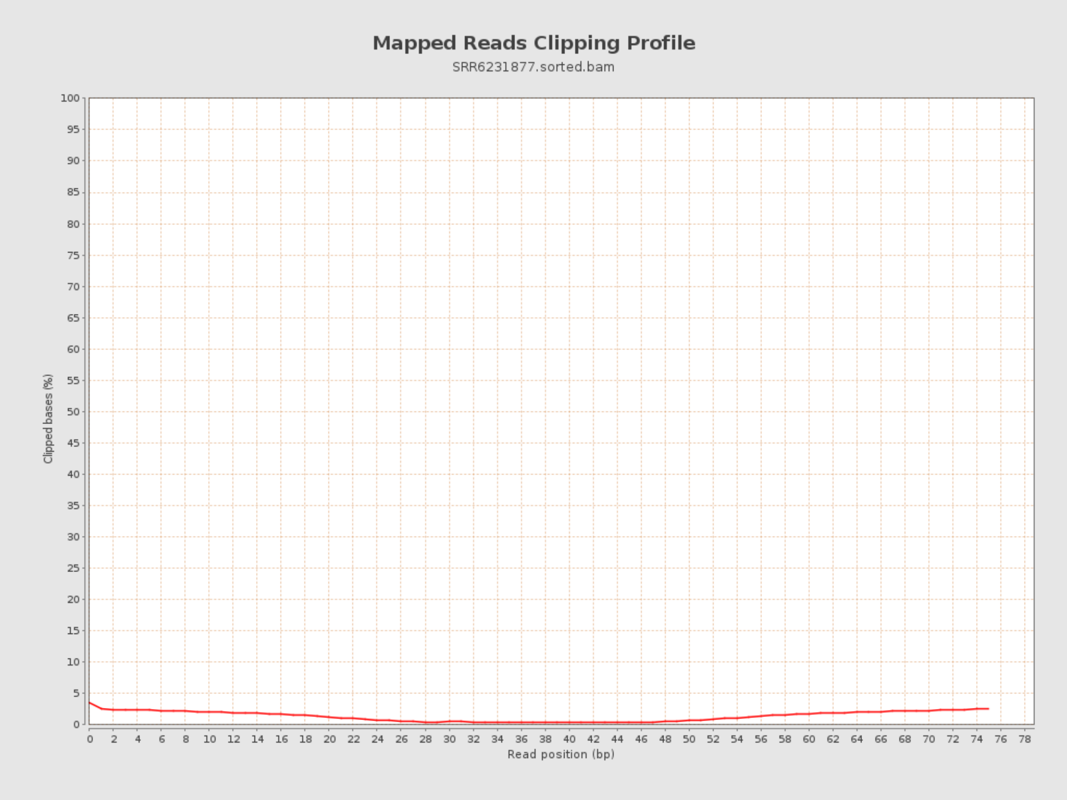
8. Results : Mapped Reads Nucleotide Content



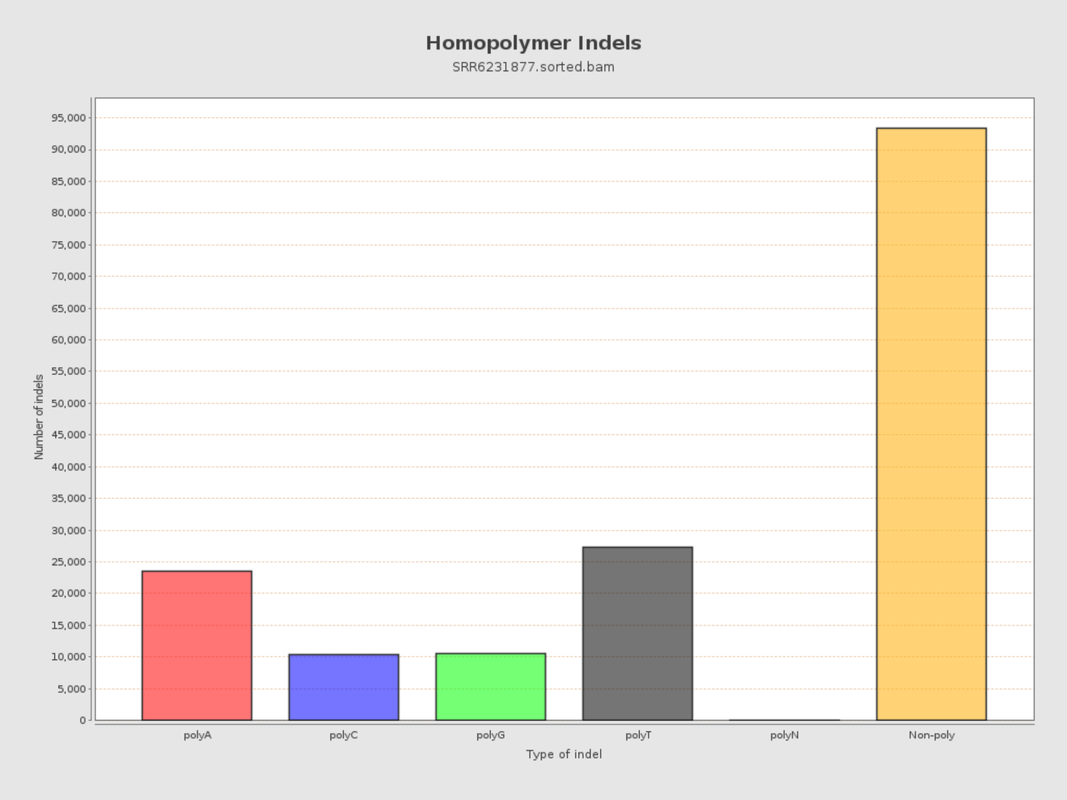
9. Results : Mapped Reads GC-content Distribution



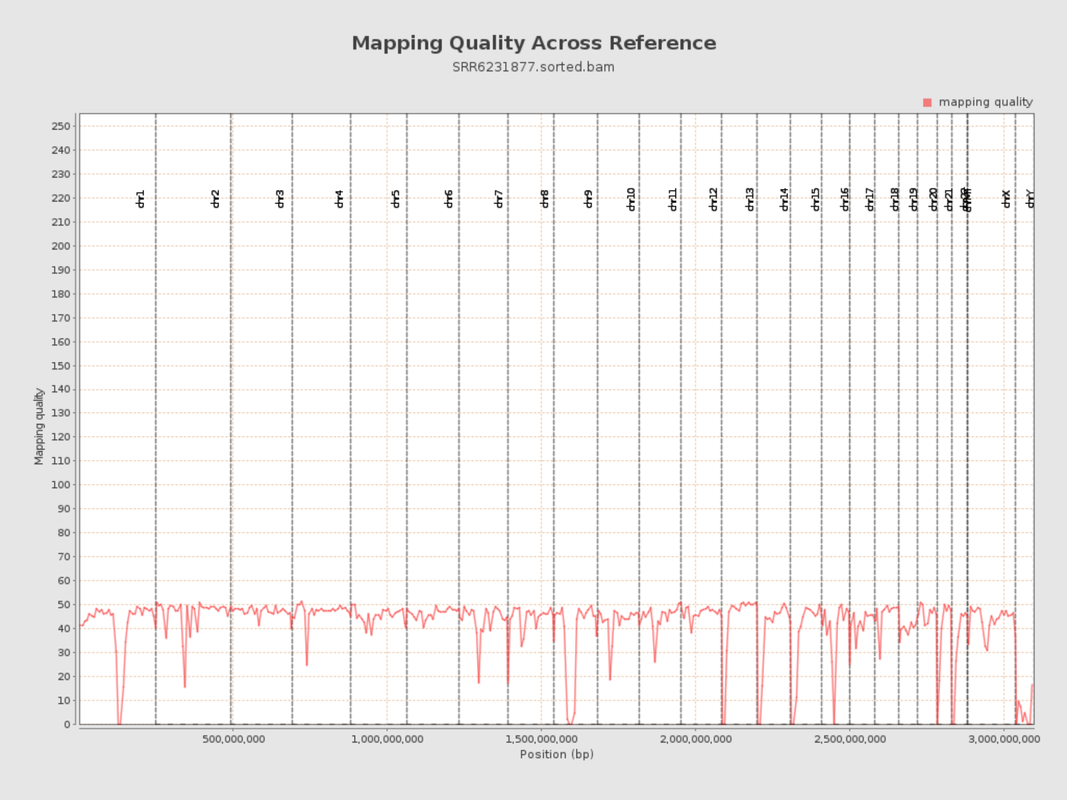
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram