Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 00:48:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231759.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_SRR6231759 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231759.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 00:48:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231759.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,148,898
Mapped reads	5,773,687 / 93.9%
Unmapped reads	375,211 / 6.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,295 / 0.48%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	531,325 / 8.64%
Duplication rate	3.68%
Clipped reads	2,252,998 / 36.64%

2.2. ACGT Content

Number/percentage of A's	102,319,216 / 26.09%
Number/percentage of C's	73,780,400 / 18.81%
Number/percentage of T's	111,261,965 / 28.37%
Number/percentage of G's	104,717,878 / 26.7%
Number/percentage of N's	83,269 / 0.02%
GC Percentage	45.52%

2.3. Coverage

Mean	0.1267

Standard Deviation	35.9243

2.4. Mapping Quality

Mean Mapping Quality	42.88

2.5. Mismatches and indels

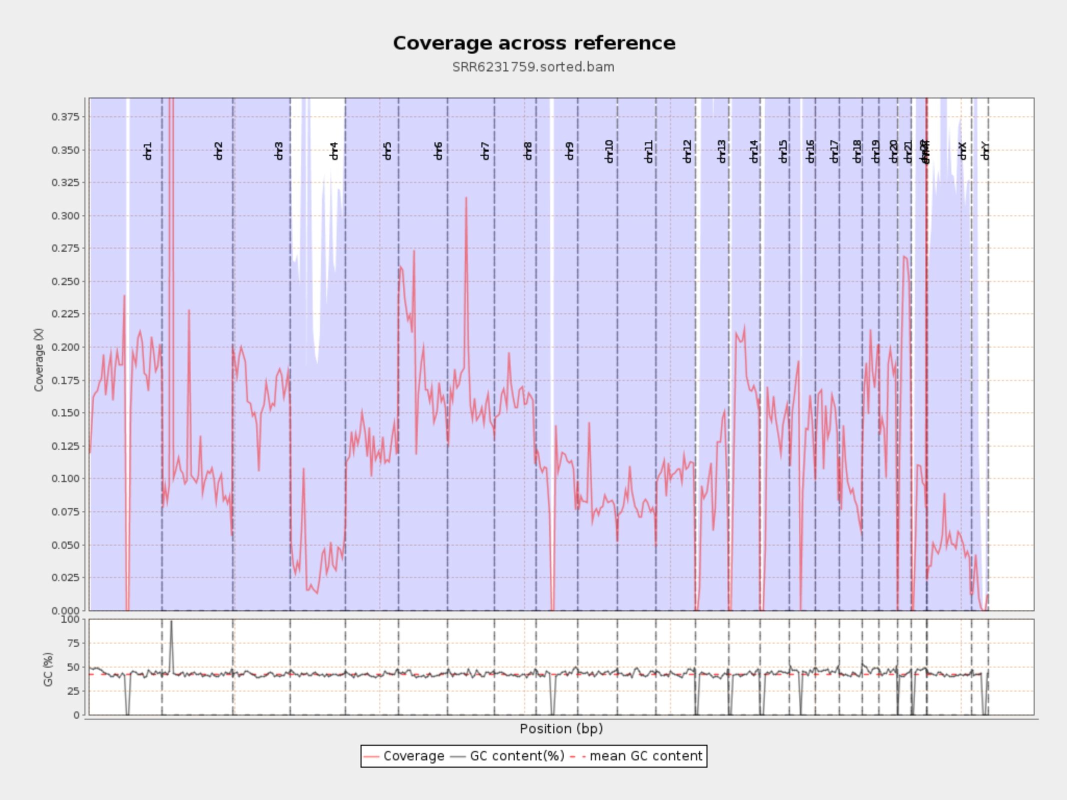
General error rate	0.68%
Mismatches	2,635,502
Insertions	27,885
Mapped reads with at least one insertion	0.48%
Deletions	88,202
Mapped reads with at least one deletion	1.51%
Homopolymer indels	46%

2.6. Chromosome stats

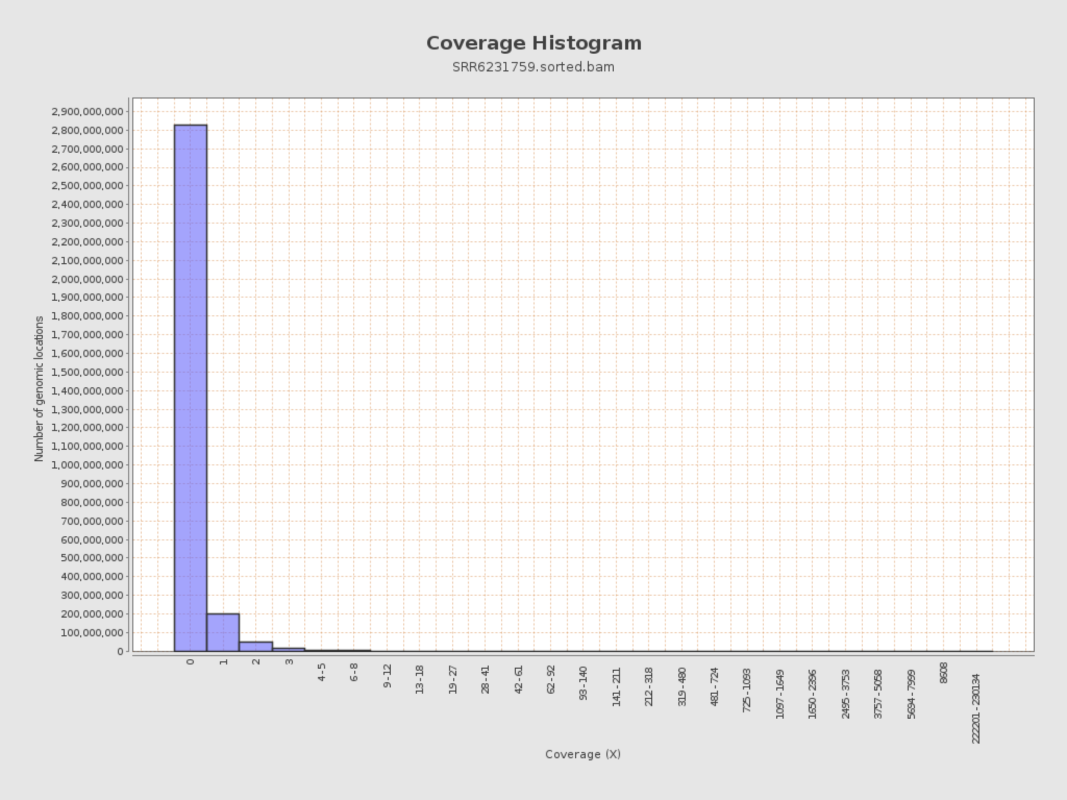
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	42959450	0.1724	1.7019
chr2	243199373	42788550	0.1759	128.1236
chr3	198022430	33128598	0.1673	0.5425
chr4	191154276	7049274	0.0369	0.32
chr5	180915260	22546026	0.1246	0.4787
chr6	171115067	32386655	0.1893	0.8317
chr7	159138663	26757285	0.1681	2.3214

chr8	146364022	23299632	0.1592	0.8629
chr9	141213431	13718417	0.0971	0.9072
chr10	135534747	11250342	0.083	0.7235
chr11	135006516	10821489	0.0802	0.8217
chr12	133851895	14070819	0.1051	0.4419
chr13	115169878	10181638	0.0884	0.3858
chr14	107349540	16629740	0.1549	0.7226
chr15	102531392	12127821	0.1183	0.47
chr16	90354753	11952345	0.1323	0.647
chr17	81195210	11520816	0.1419	0.6216
chr18	78077248	7233957	0.0927	1.9559
chr19	59128983	10618370	0.1796	1.2602
chr20	63025520	9870466	0.1566	0.5598
chr21	48129895	9387199	0.195	0.6825
chr22	51304566	3720353	0.0725	0.3532
chrMT	16571	13279	0.8013	1.1163
chrX	155270560	7543505	0.0486	0.4672
chrY	59373566	731897	0.0123	0.2575

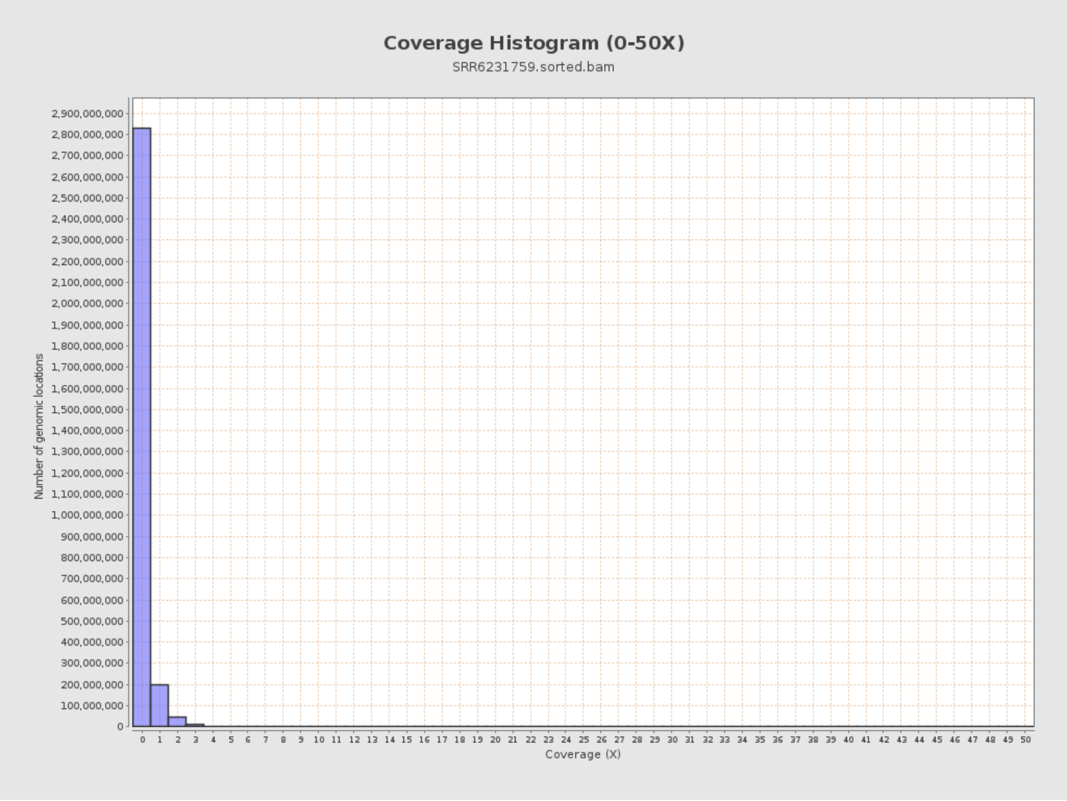
3. Results : Coverage across reference



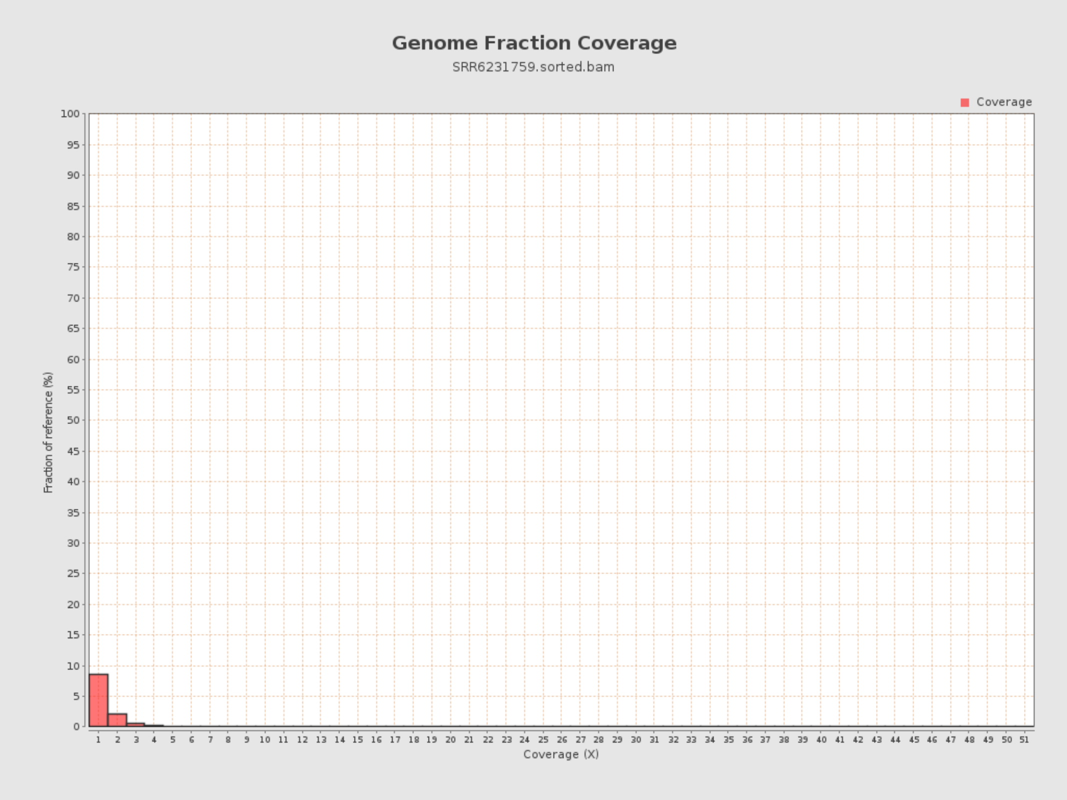
4. Results : Coverage Histogram



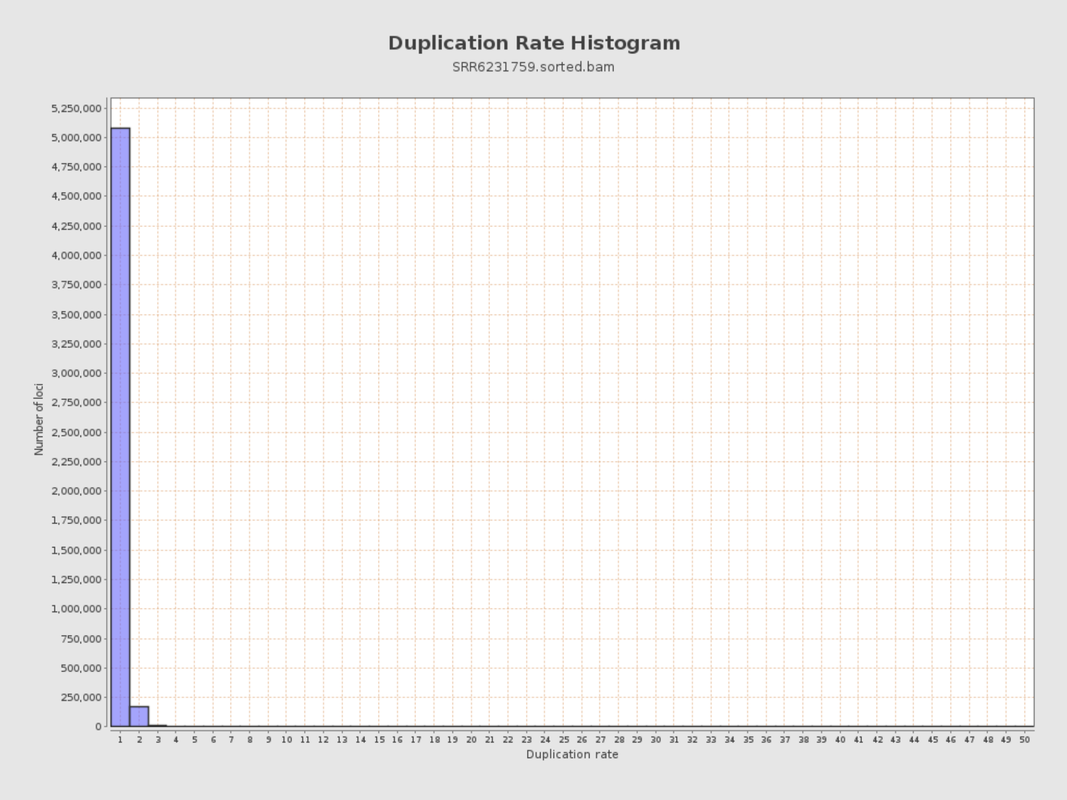
5. Results : Coverage Histogram (0-50X)



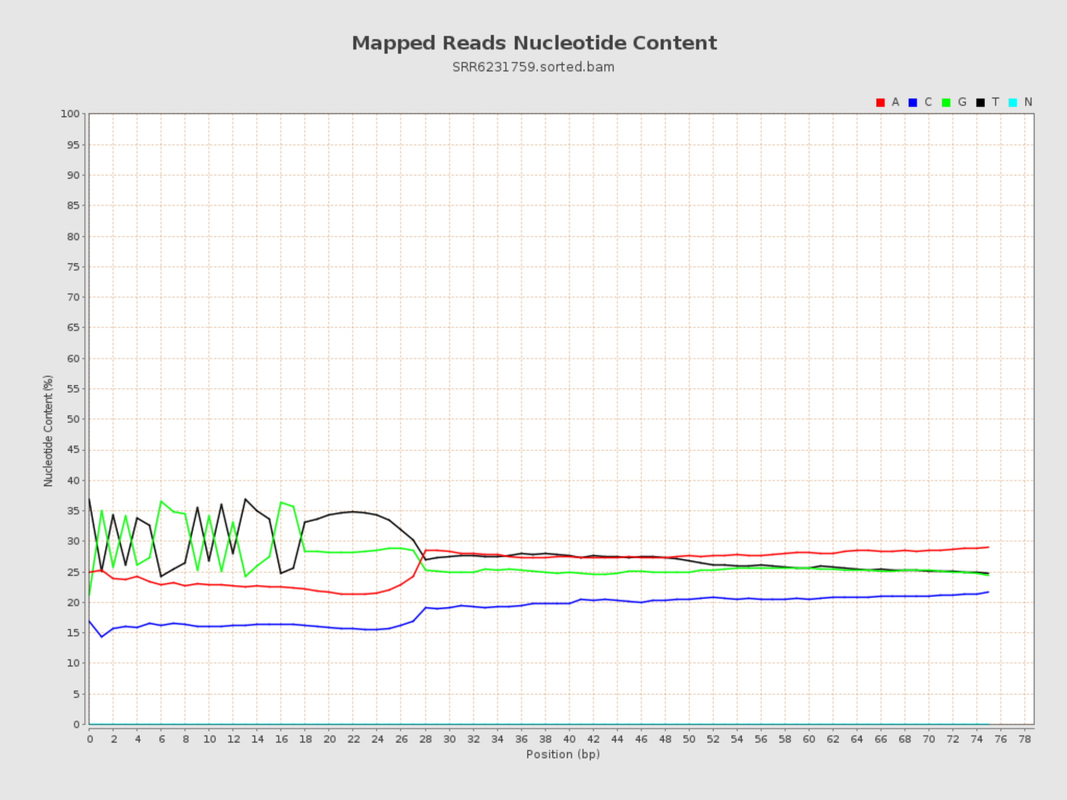
6. Results : Genome Fraction Coverage



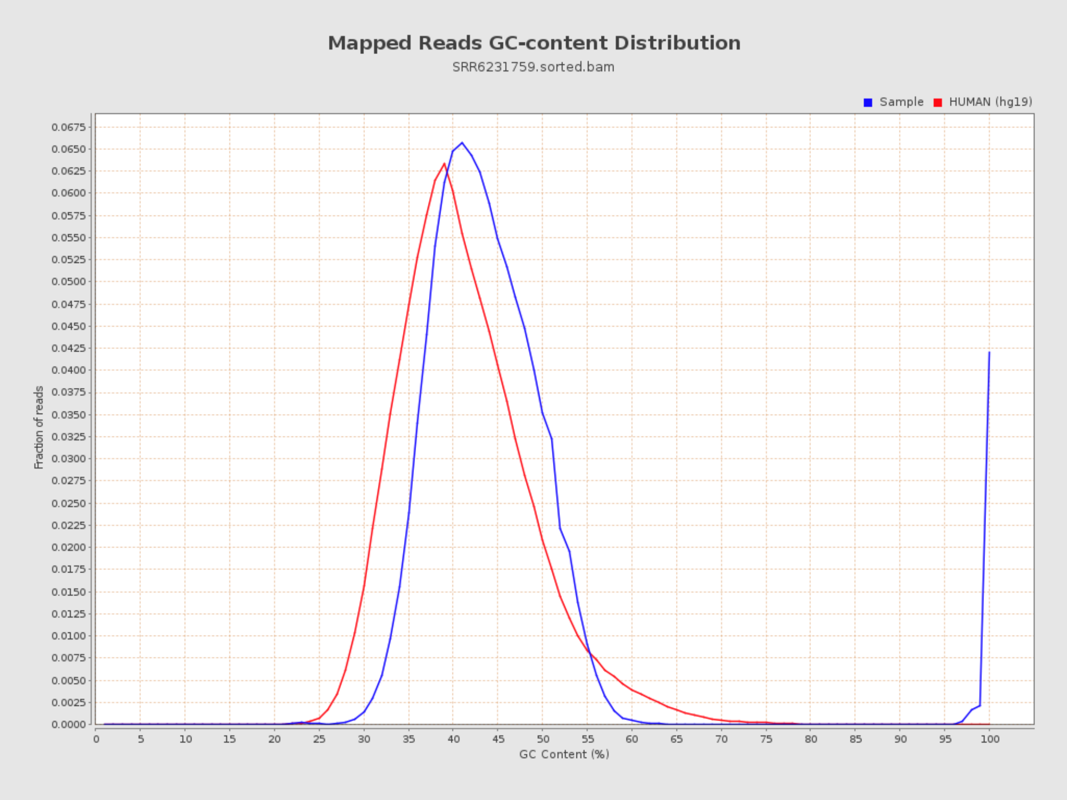
7. Results : Duplication Rate Histogram



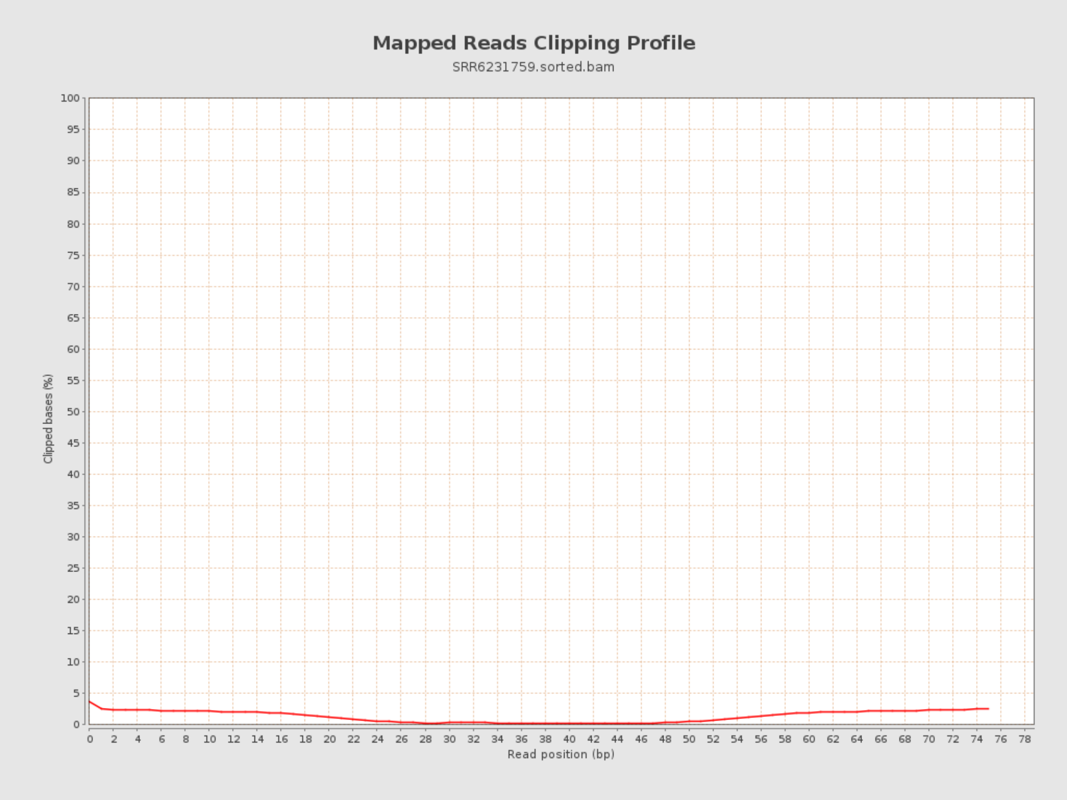
8. Results : Mapped Reads Nucleotide Content



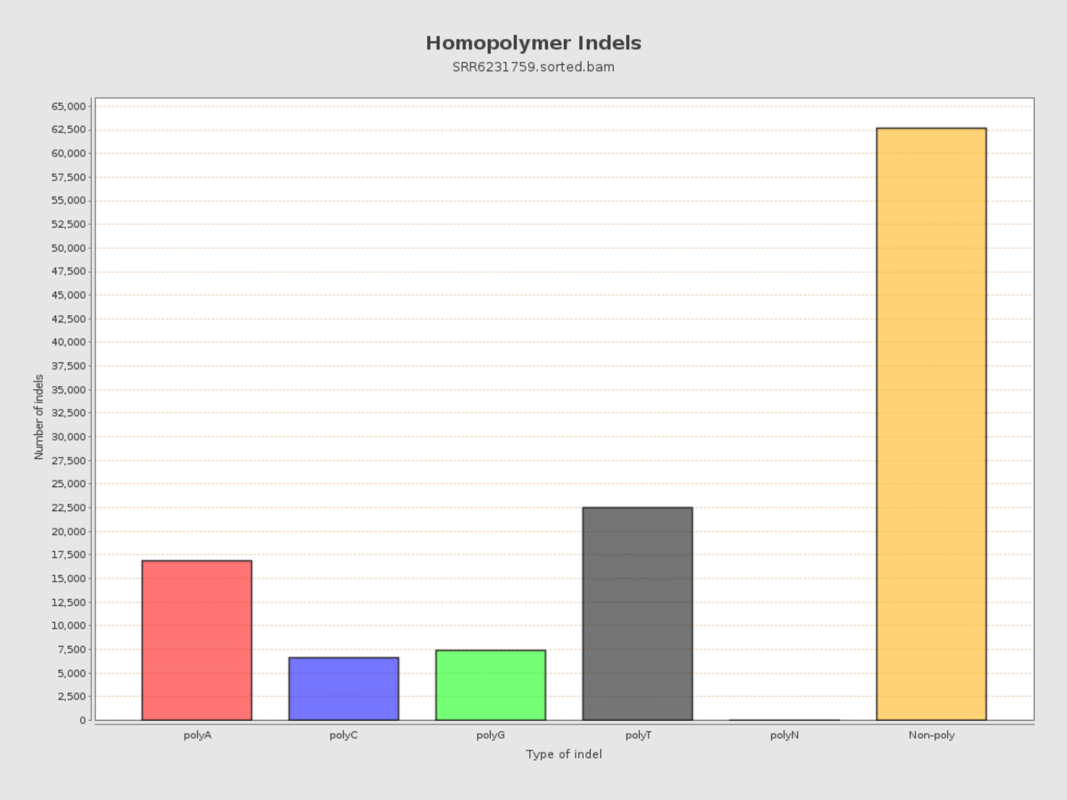
9. Results : Mapped Reads GC-content Distribution



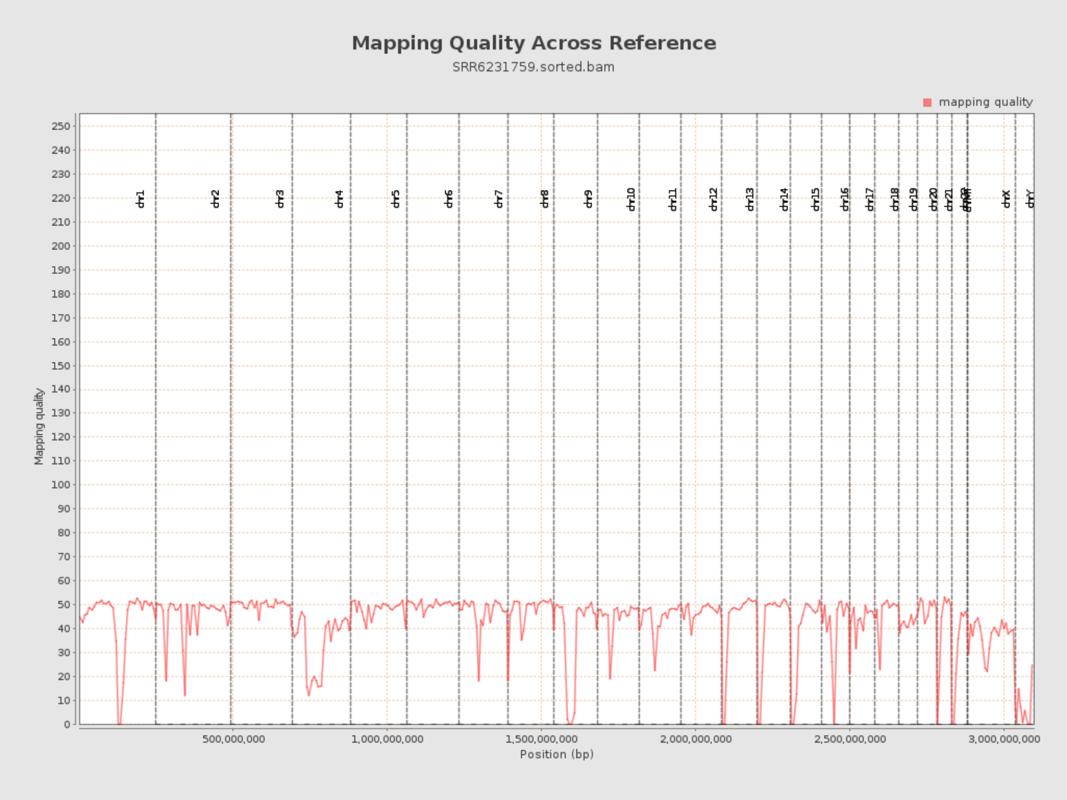
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram