Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 10:25:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231887.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_SRR6231887 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231887.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 10:25:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231887.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,842,121
Mapped reads	5,416,718 / 92.72%
Unmapped reads	425,403 / 7.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	38,617 / 0.66%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	501,874 / 8.59%
Duplication rate	4.39%
Clipped reads	2,121,595 / 36.32%

2.2. ACGT Content

Number/percentage of A's	98,255,248 / 26.67%
Number/percentage of C's	67,978,647 / 18.46%
Number/percentage of T's	108,096,038 / 29.35%
Number/percentage of G's	93,937,066 / 25.5%
Number/percentage of N's	79,443 / 0.02%
GC Percentage	43.96%

2.3. Coverage

Mean	0.119

Standard Deviation	28.1802

2.4. Mapping Quality

Mean Mapping Quality	45.1

2.5. Mismatches and indels

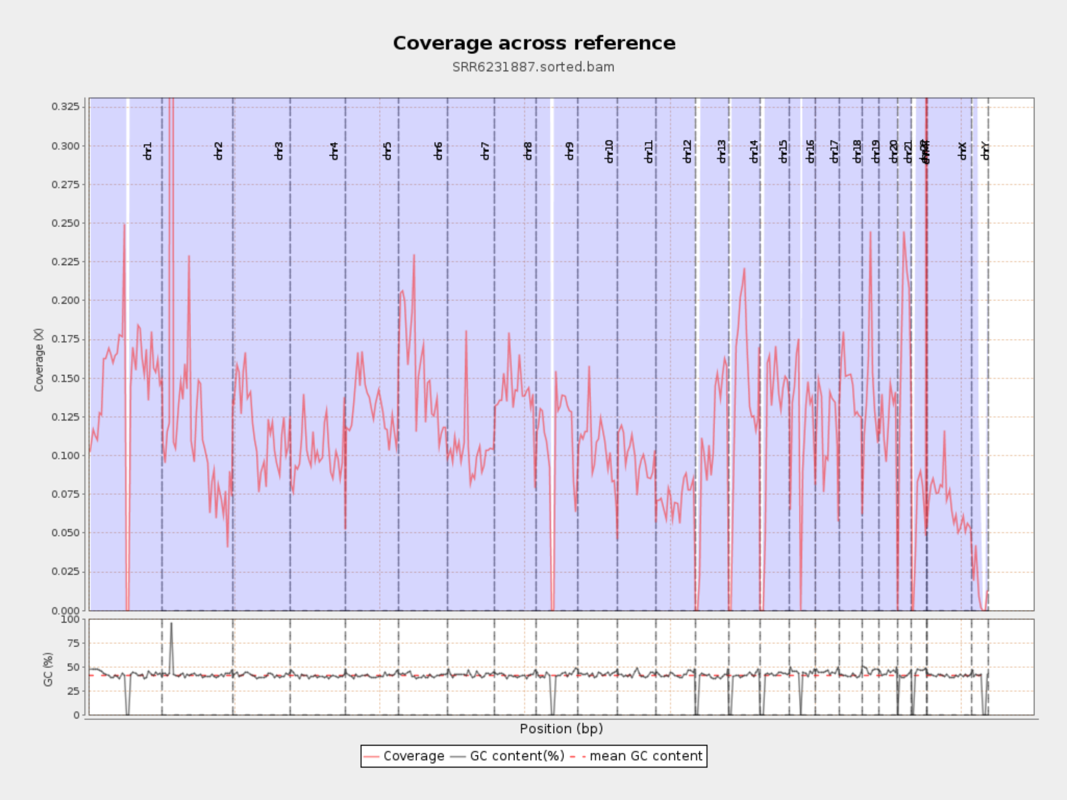
General error rate	0.68%
Mismatches	2,454,206
Insertions	25,475
Mapped reads with at least one insertion	0.47%
Deletions	83,992
Mapped reads with at least one deletion	1.54%
Homopolymer indels	46.52%

2.6. Chromosome stats

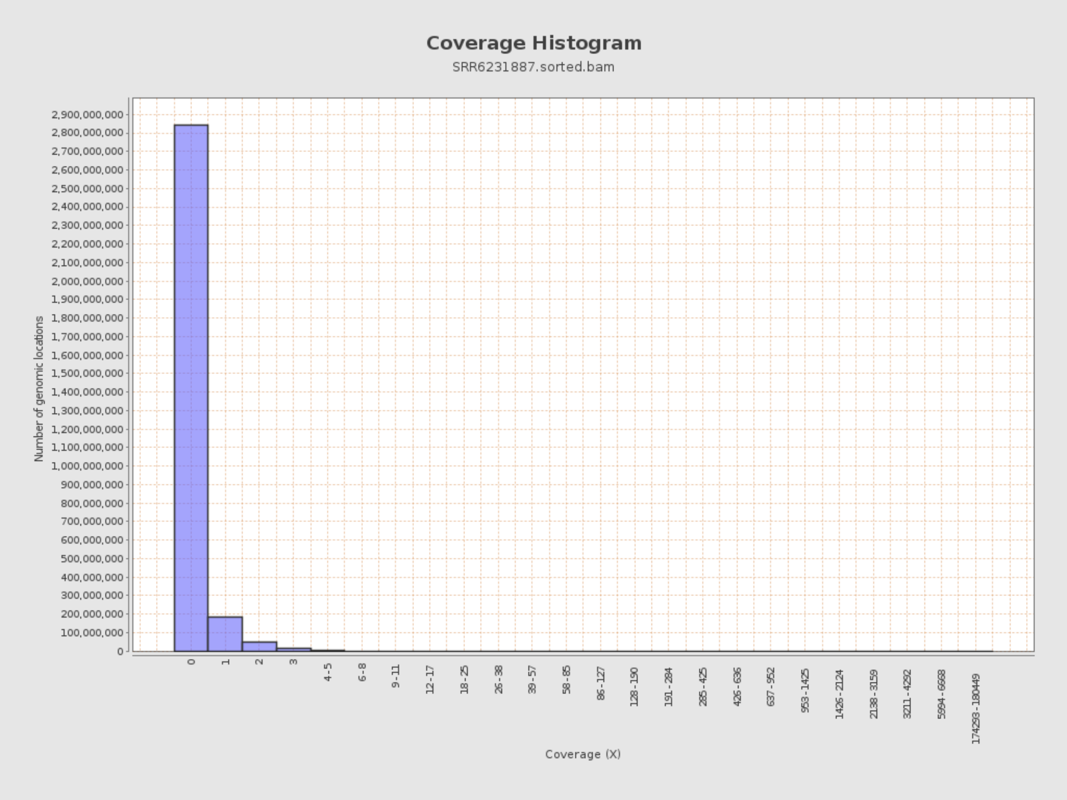
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	36634985	0.147	2.2805
chr2	243199373	40595099	0.1669	100.4823
chr3	198022430	23327240	0.1178	0.4556
chr4	191154276	19426819	0.1016	0.4558
chr5	180915260	23649258	0.1307	0.4965
chr6	171115067	26214614	0.1532	0.6725
chr7	159138663	16466738	0.1035	1.2195

chr8	146364022	20498279	0.14	1.0516
chr9	141213431	15073819	0.1067	0.9152
chr10	135534747	14411560	0.1063	0.6909
chr11	135006516	13221249	0.0979	0.8602
chr12	133851895	9688891	0.0724	0.3976
chr13	115169878	11945455	0.1037	0.4262
chr14	107349540	14540089	0.1354	0.701
chr15	102531392	12296993	0.1199	0.4676
chr16	90354753	10902653	0.1207	0.5784
chr17	81195210	9427134	0.1161	0.5832
chr18	78077248	11337588	0.1452	1.9106
chr19	59128983	8528406	0.1442	1.514
chr20	63025520	7751959	0.123	0.5171
chr21	48129895	8222714	0.1708	0.6288
chr22	51304566	2805832	0.0547	0.3048
chrMT	16571	35052	2.1153	2.284
chrX	155270560	10674343	0.0687	0.4936
chrY	59373566	806416	0.0136	0.2584

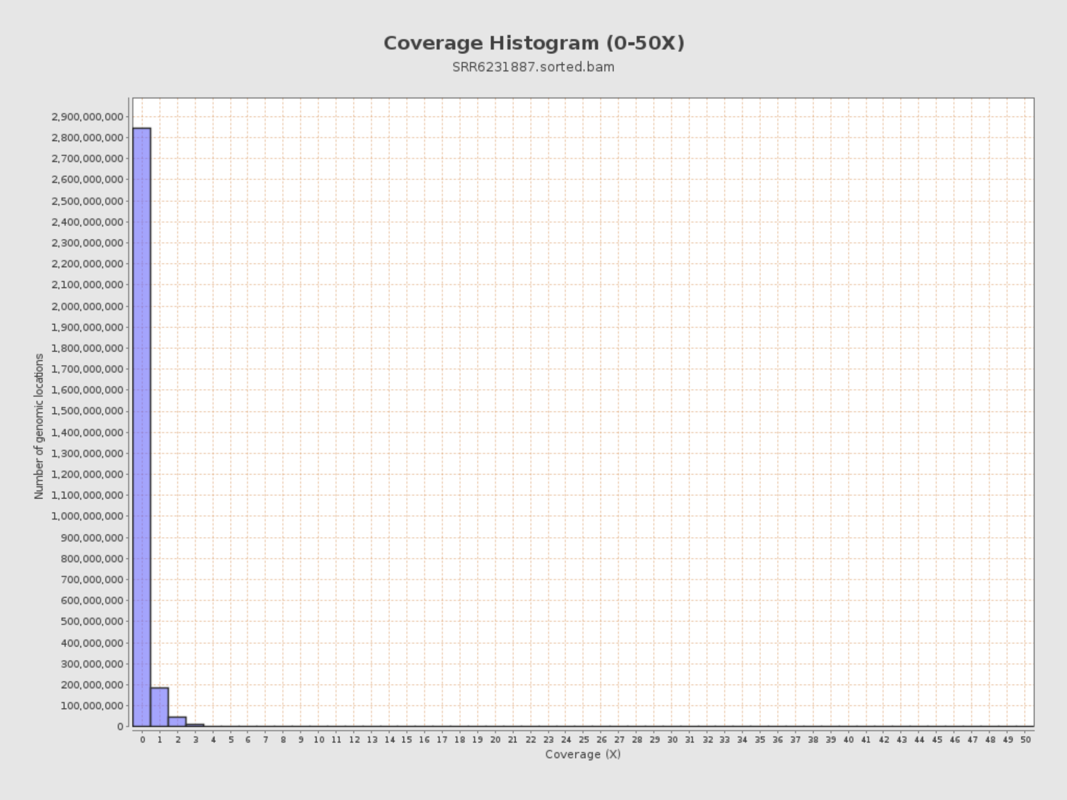
3. Results : Coverage across reference



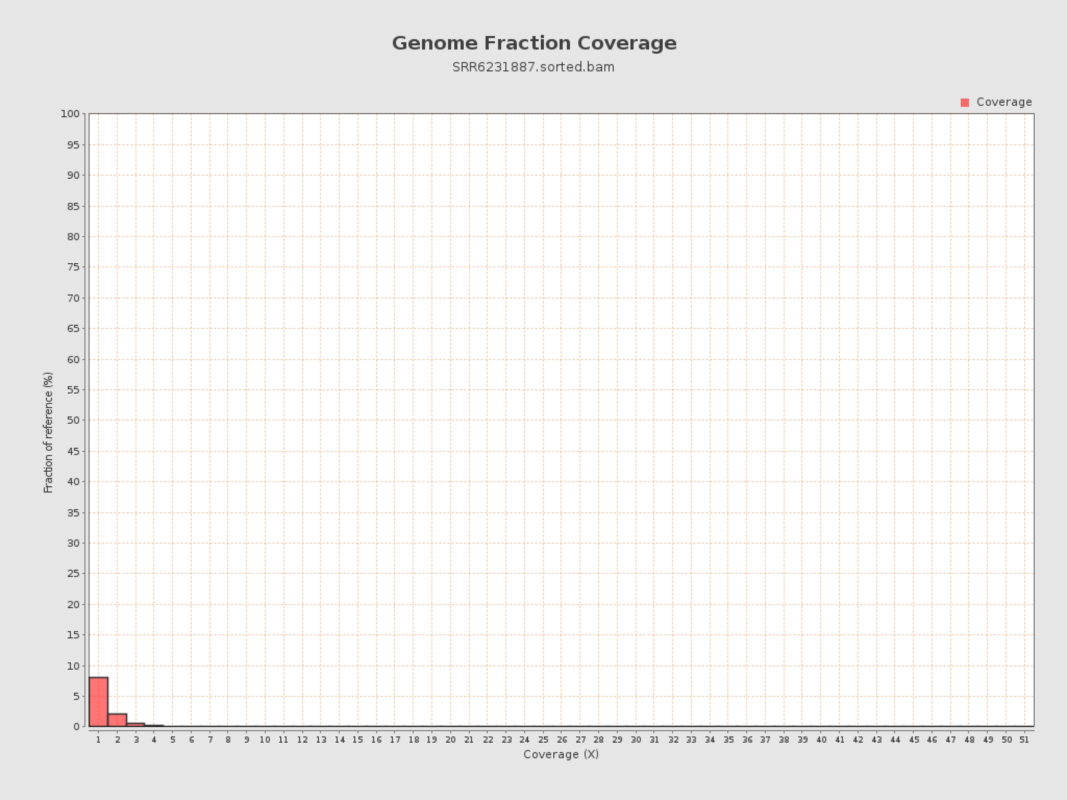
4. Results : Coverage Histogram



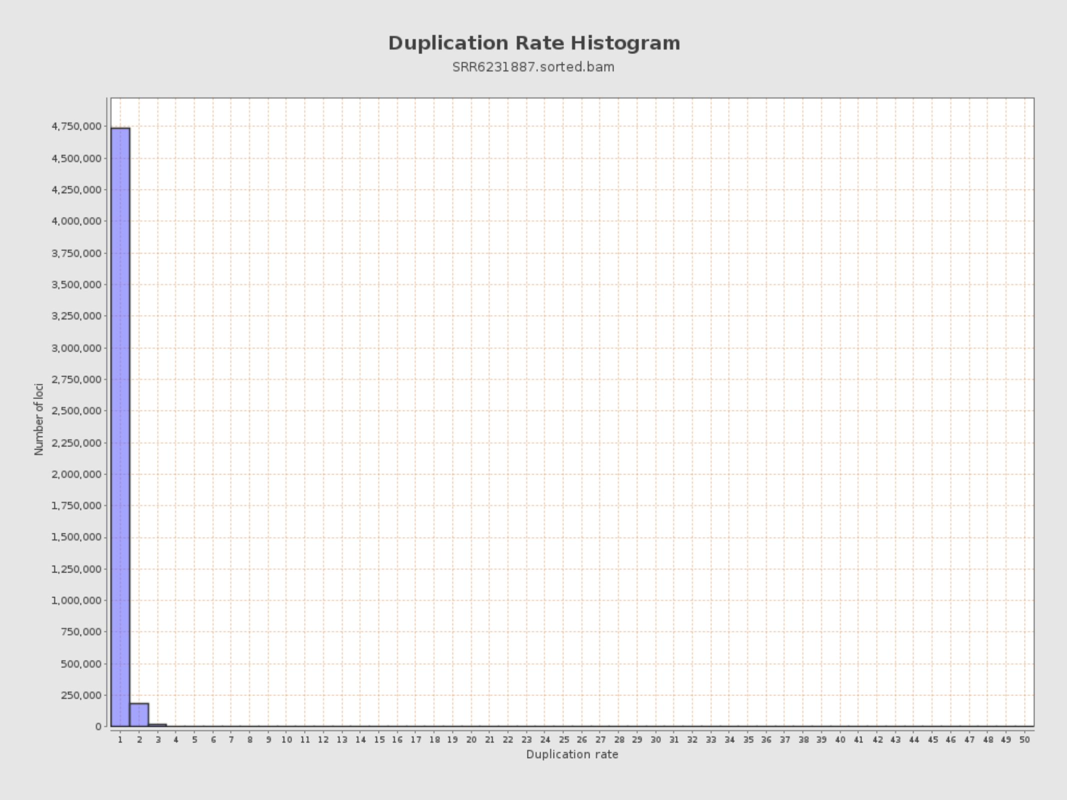
5. Results : Coverage Histogram (0-50X)



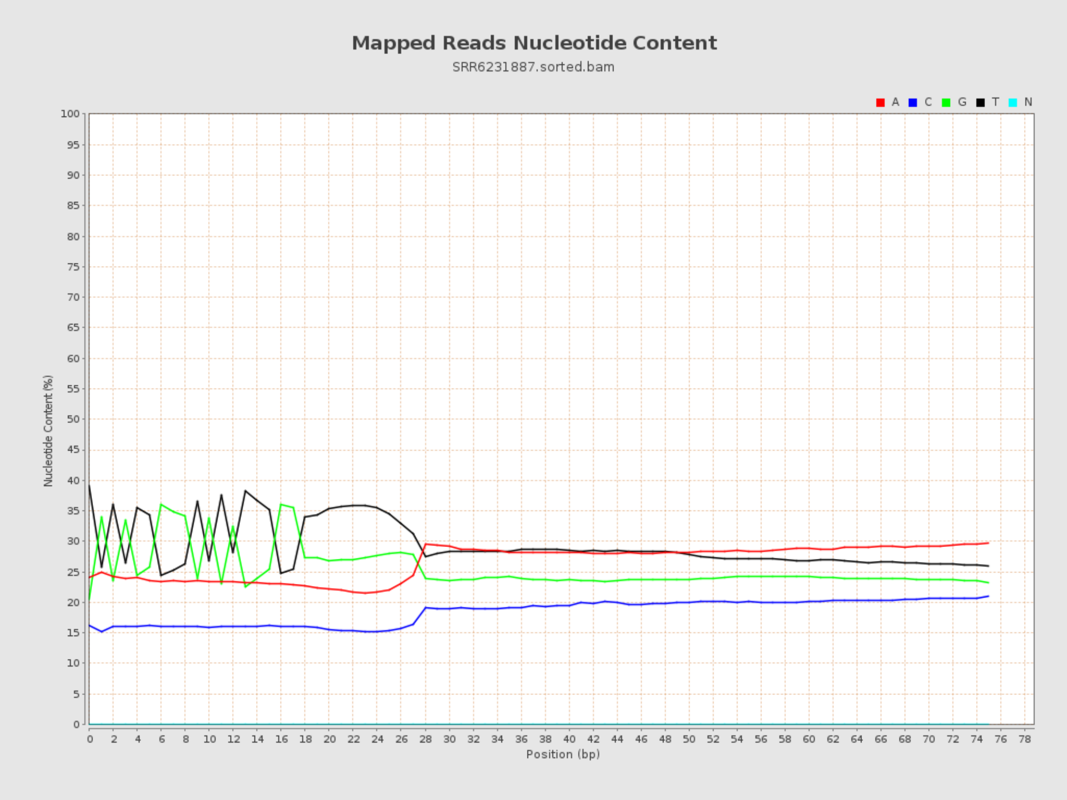
6. Results : Genome Fraction Coverage



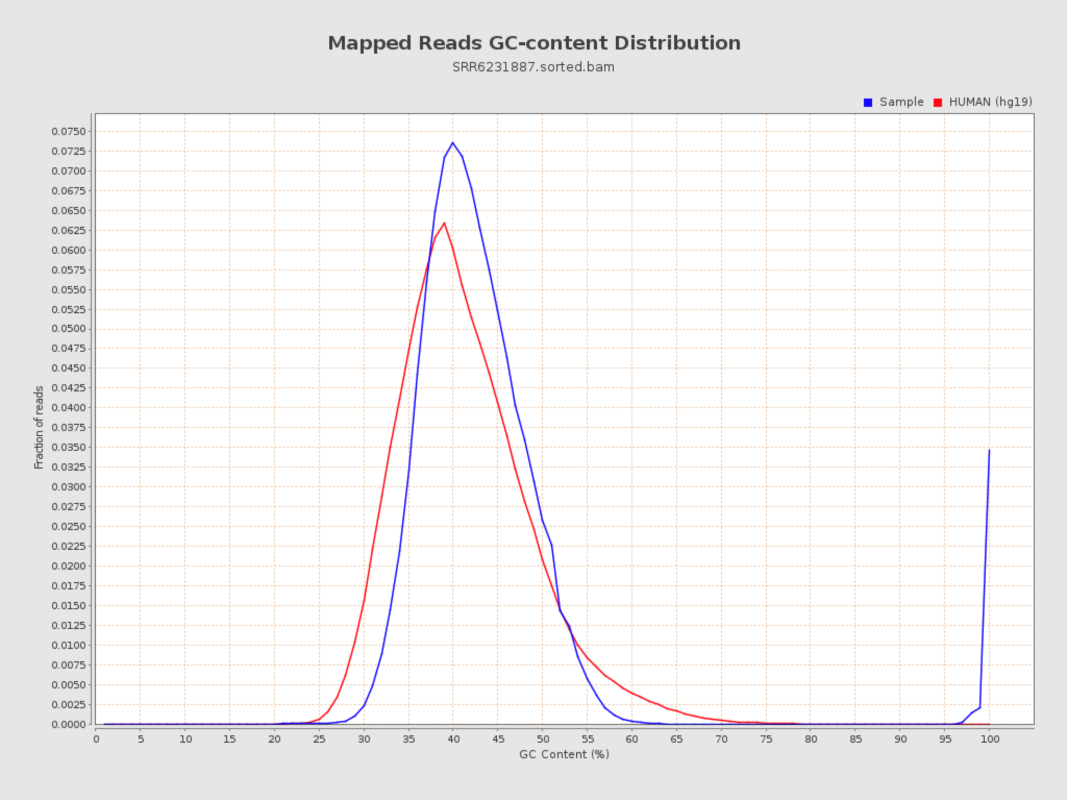
7. Results : Duplication Rate Histogram



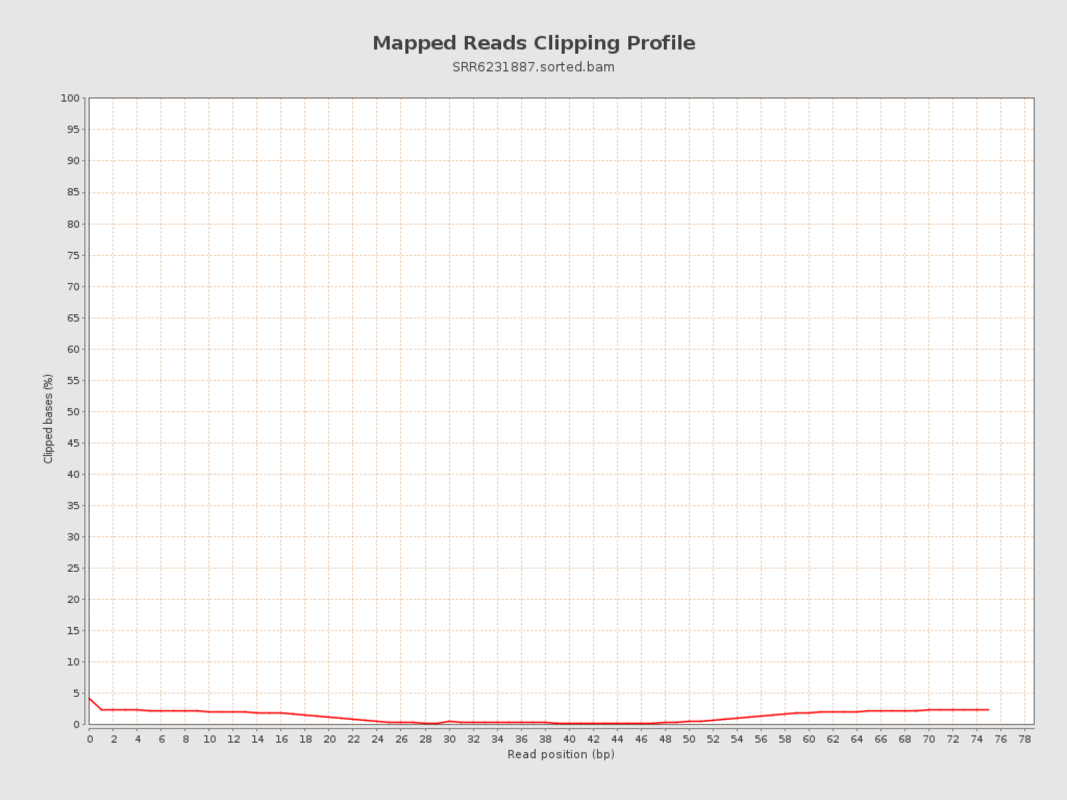
8. Results : Mapped Reads Nucleotide Content



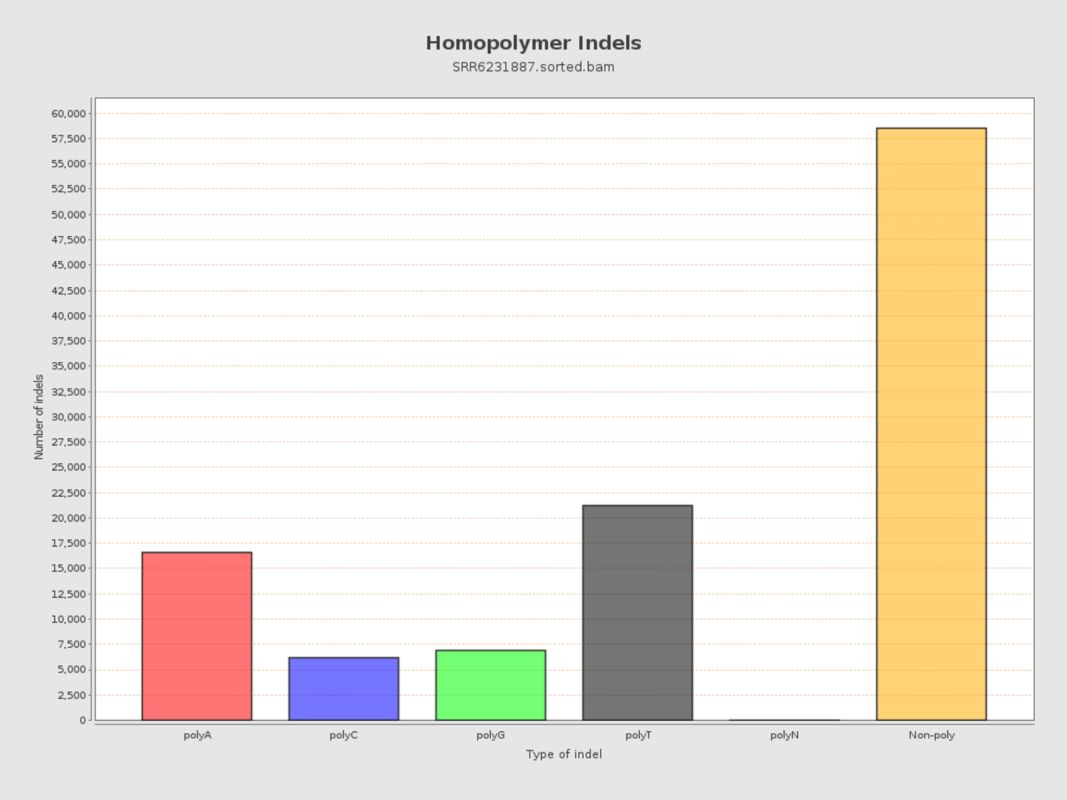
9. Results : Mapped Reads GC-content Distribution



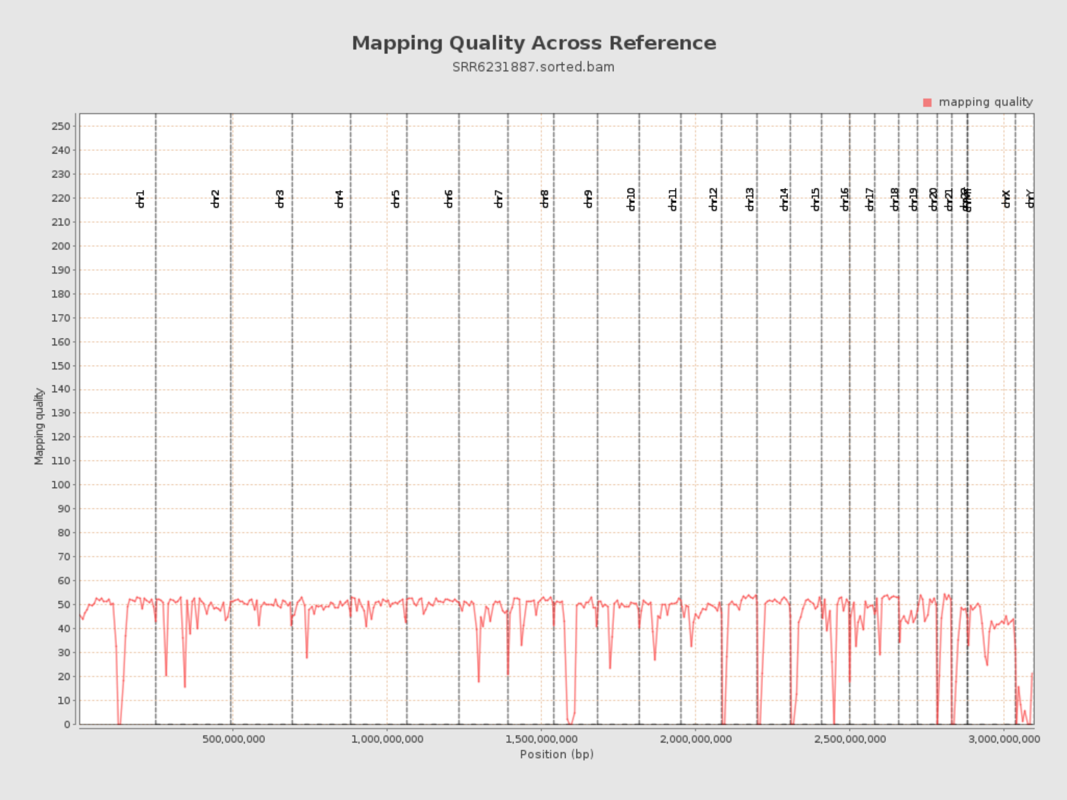
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram