Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 10:31:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231888.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_SRR6231888 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231888.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 10:31:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231888.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,999,144
Mapped reads	3,755,579 / 93.91%
Unmapped reads	243,565 / 6.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	41,665 / 1.04%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	829,859 / 20.75%
Duplication rate	9.76%
Clipped reads	1,246,833 / 31.18%

2.2. ACGT Content

Number/percentage of A's	64,725,515 / 24.85%
Number/percentage of C's	45,713,926 / 17.55%
Number/percentage of T's	70,415,415 / 27.03%
Number/percentage of G's	79,563,946 / 30.55%
Number/percentage of N's	56,031 / 0.02%
GC Percentage	48.1%

2.3. Coverage

Mean	0.0842

Standard Deviation	56.1009

2.4. Mapping Quality

Mean Mapping Quality	39.9

2.5. Mismatches and indels

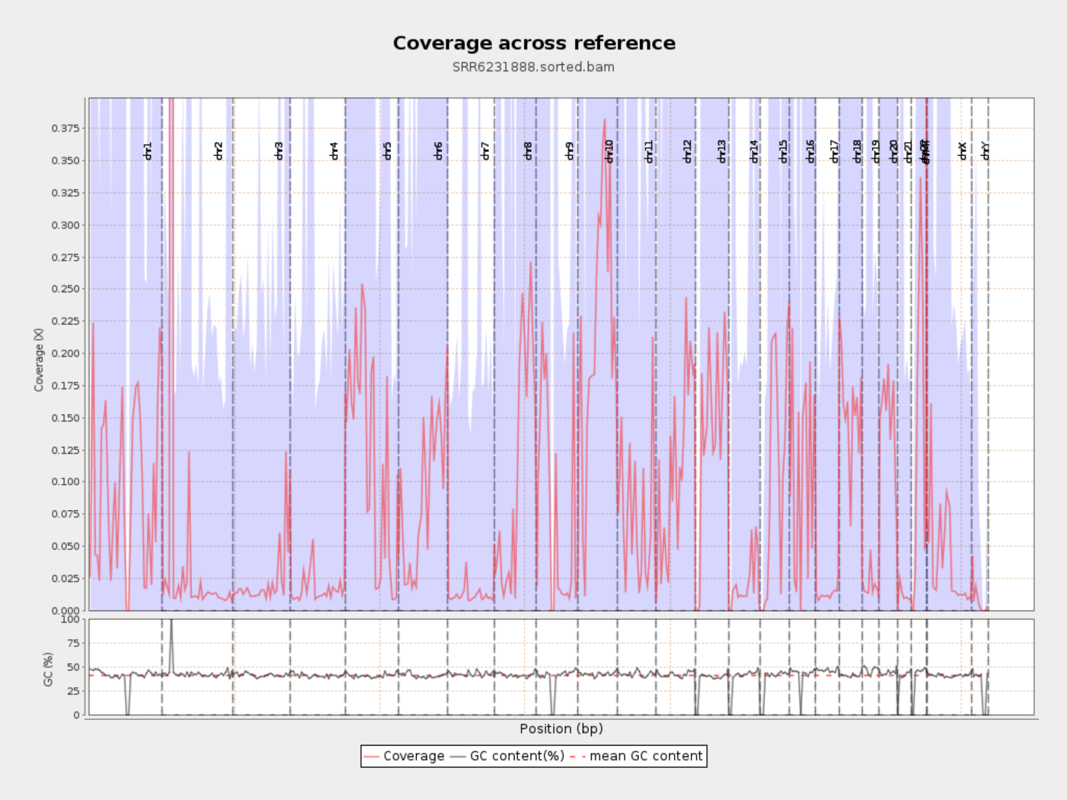
General error rate	0.6%
Mismatches	1,539,506
Insertions	16,234
Mapped reads with at least one insertion	0.43%
Deletions	52,676
Mapped reads with at least one deletion	1.39%
Homopolymer indels	47.76%

2.6. Chromosome stats

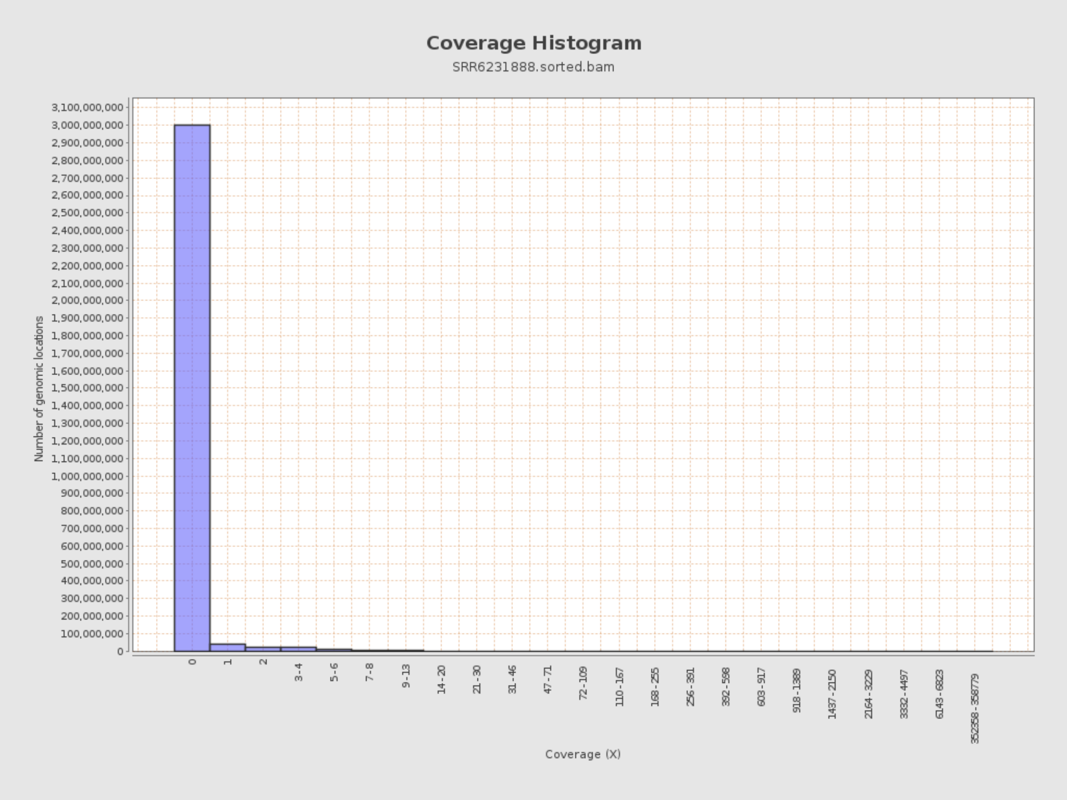
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23152752	0.0929	0.8445
chr2	243199373	31970280	0.1315	200.1407
chr3	198022430	4473964	0.0226	0.2956
chr4	191154276	3288500	0.0172	0.2577
chr5	180915260	21544273	0.1191	0.7111
chr6	171115067	15256290	0.0892	0.6062
chr7	159138663	1886090	0.0119	0.3506

chr8	146364022	16219045	0.1108	0.8165
chr9	141213431	10982277	0.0778	0.959
chr10	135534747	29934891	0.2209	1.0668
chr11	135006516	9838671	0.0729	0.6986
chr12	133851895	15056070	0.1125	0.7269
chr13	115169878	16010551	0.139	0.754
chr14	107349540	2410079	0.0225	0.5693
chr15	102531392	10836330	0.1057	0.6559
chr16	90354753	9569123	0.1059	0.7178
chr17	81195210	1047781	0.0129	0.2298
chr18	78077248	12245217	0.1568	1.4808
chr19	59128983	1185702	0.0201	0.8933
chr20	63025520	9566109	0.1518	0.8009
chr21	48129895	569985	0.0118	0.3859
chr22	51304566	6711407	0.1308	0.7481
chrMT	16571	10304	0.6218	1.8288
chrX	155270560	6301257	0.0406	0.4668
chrY	59373566	495489	0.0083	0.1891

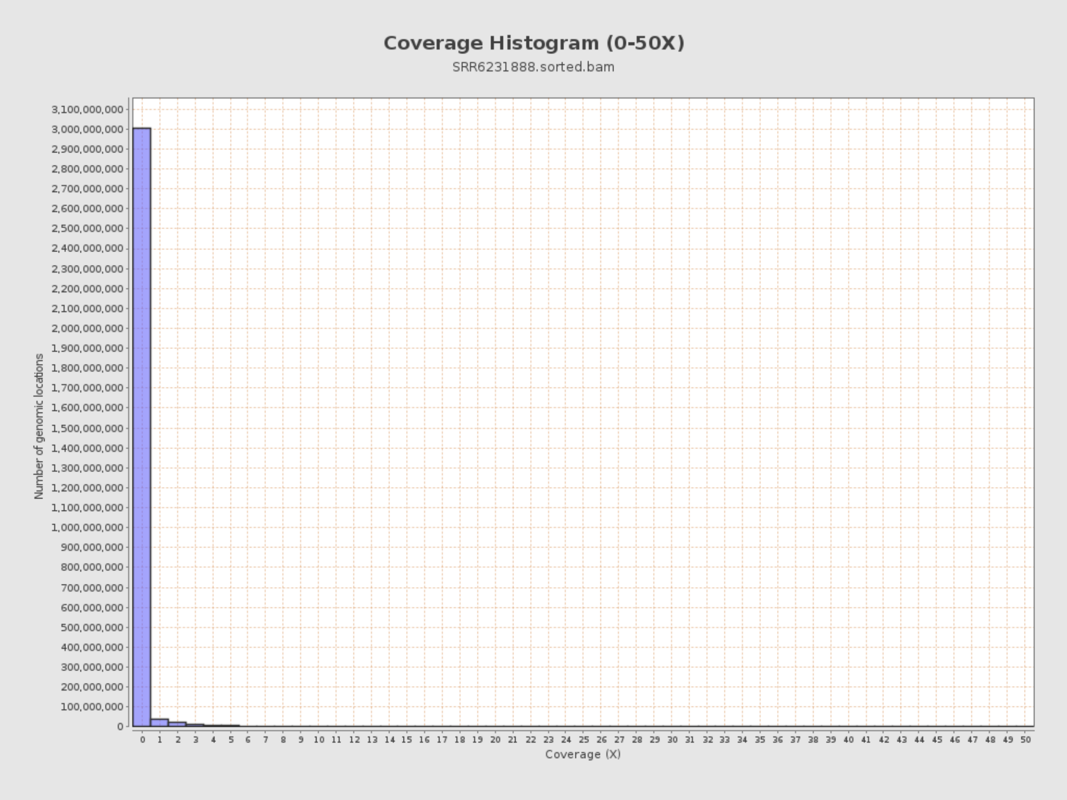
3. Results : Coverage across reference



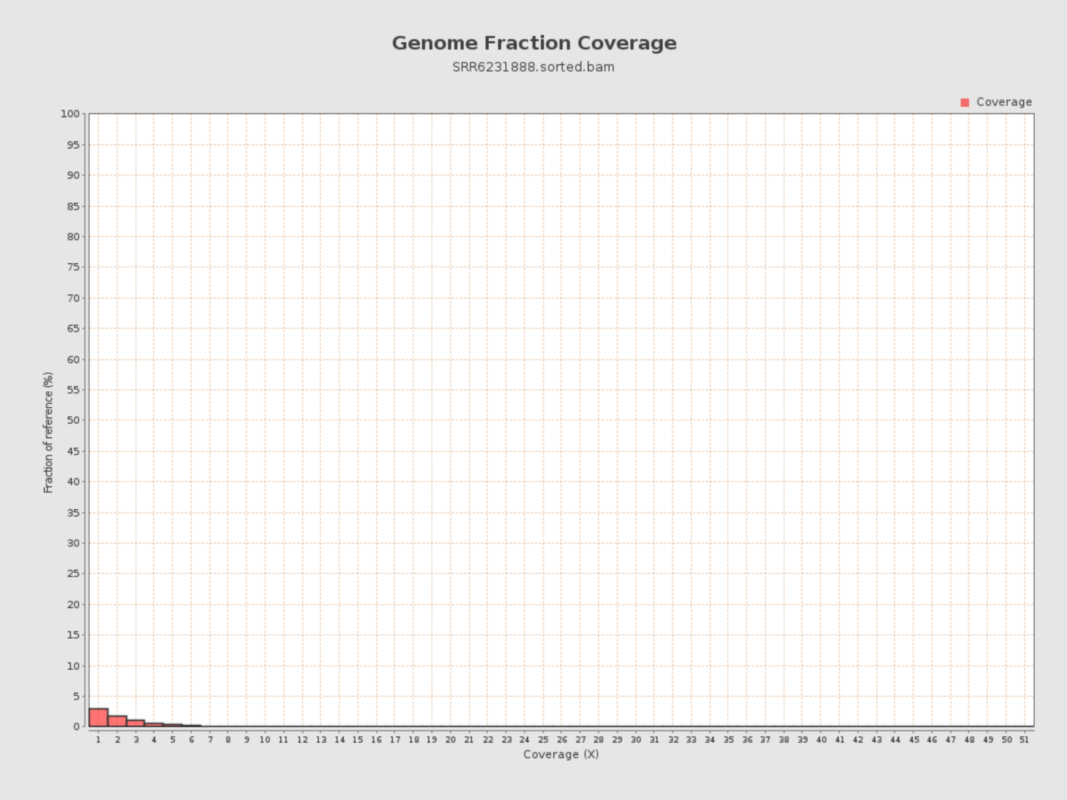
4. Results : Coverage Histogram



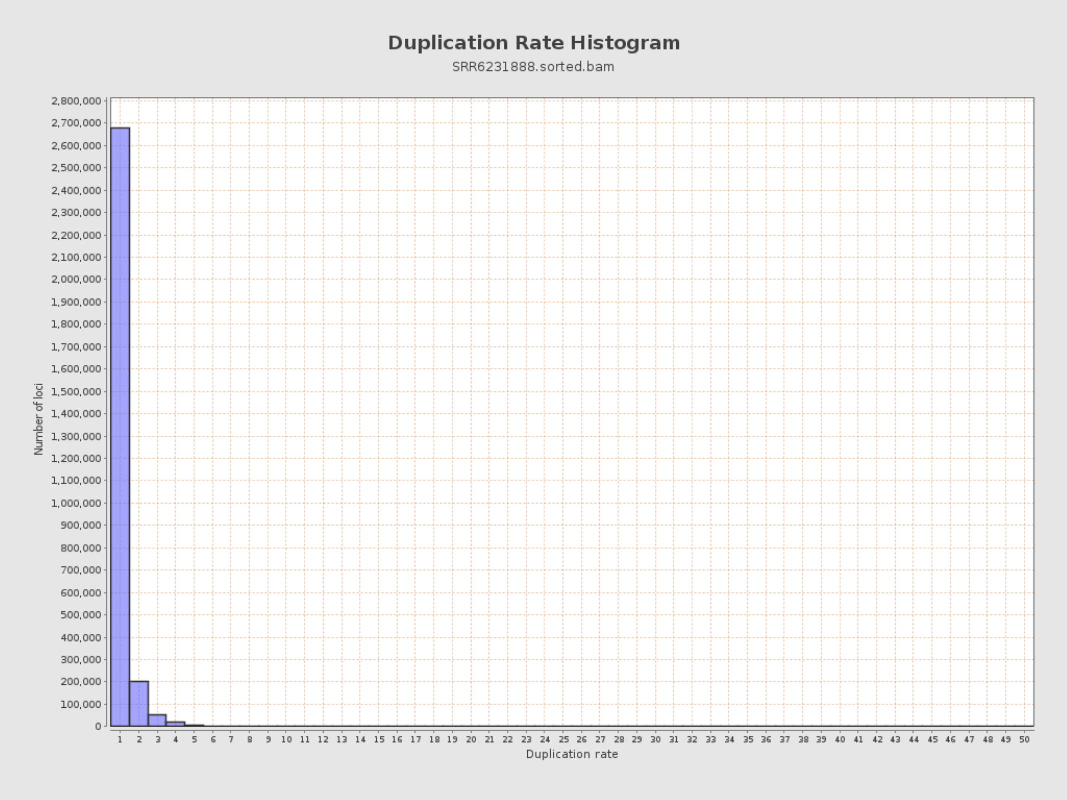
5. Results : Coverage Histogram (0-50X)



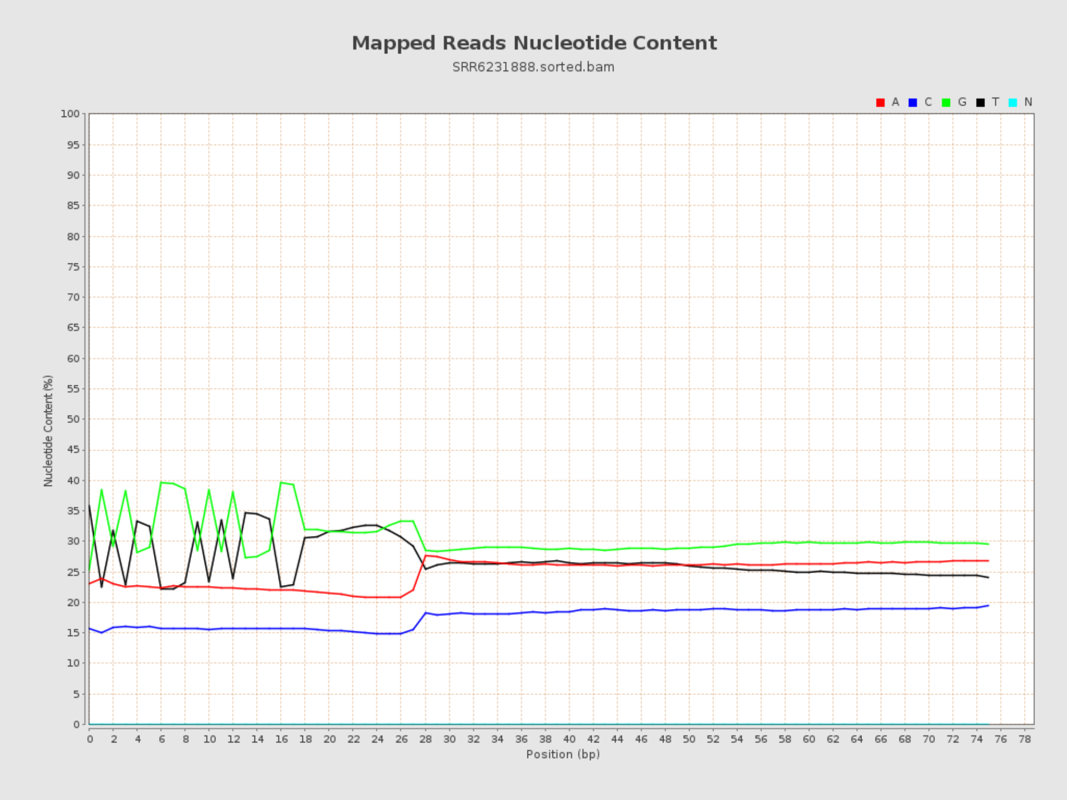
6. Results : Genome Fraction Coverage



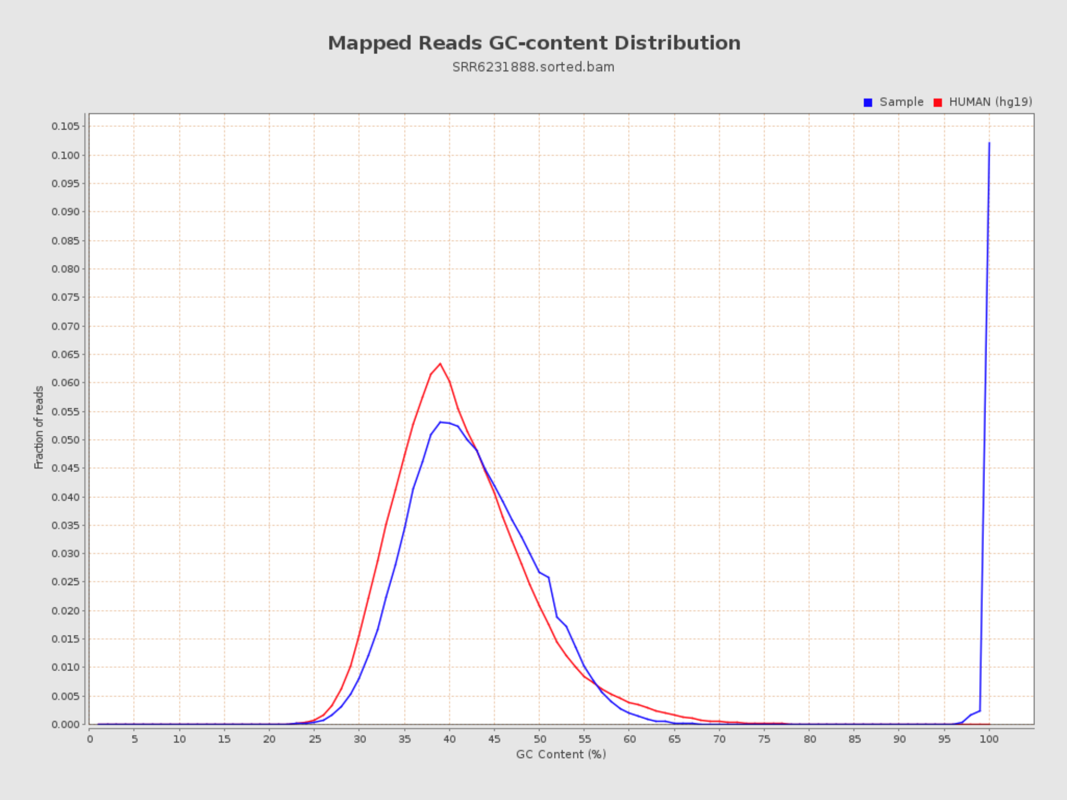
7. Results : Duplication Rate Histogram



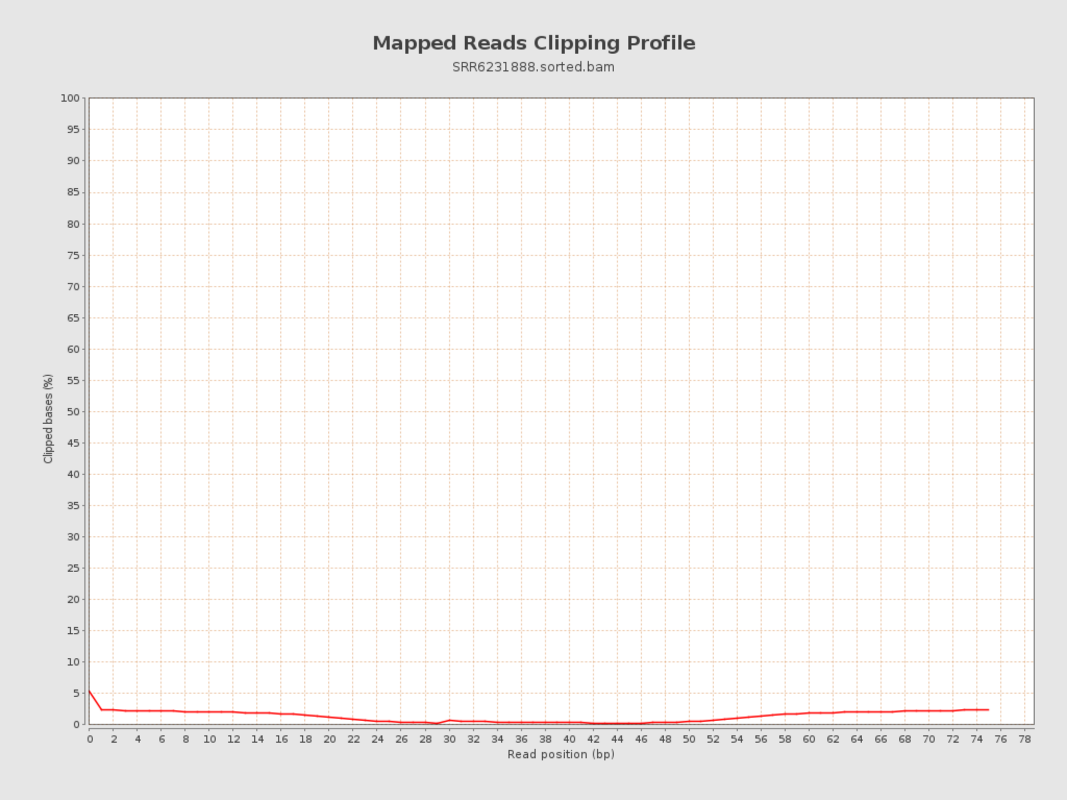
8. Results : Mapped Reads Nucleotide Content



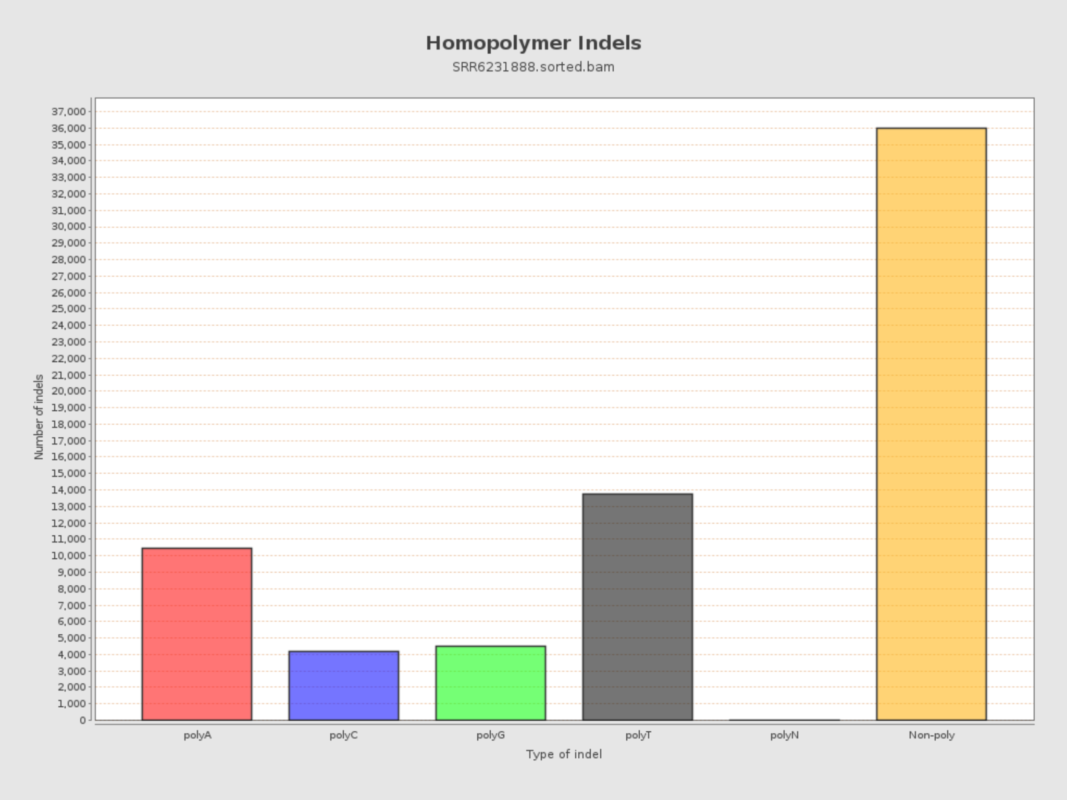
9. Results : Mapped Reads GC-content Distribution



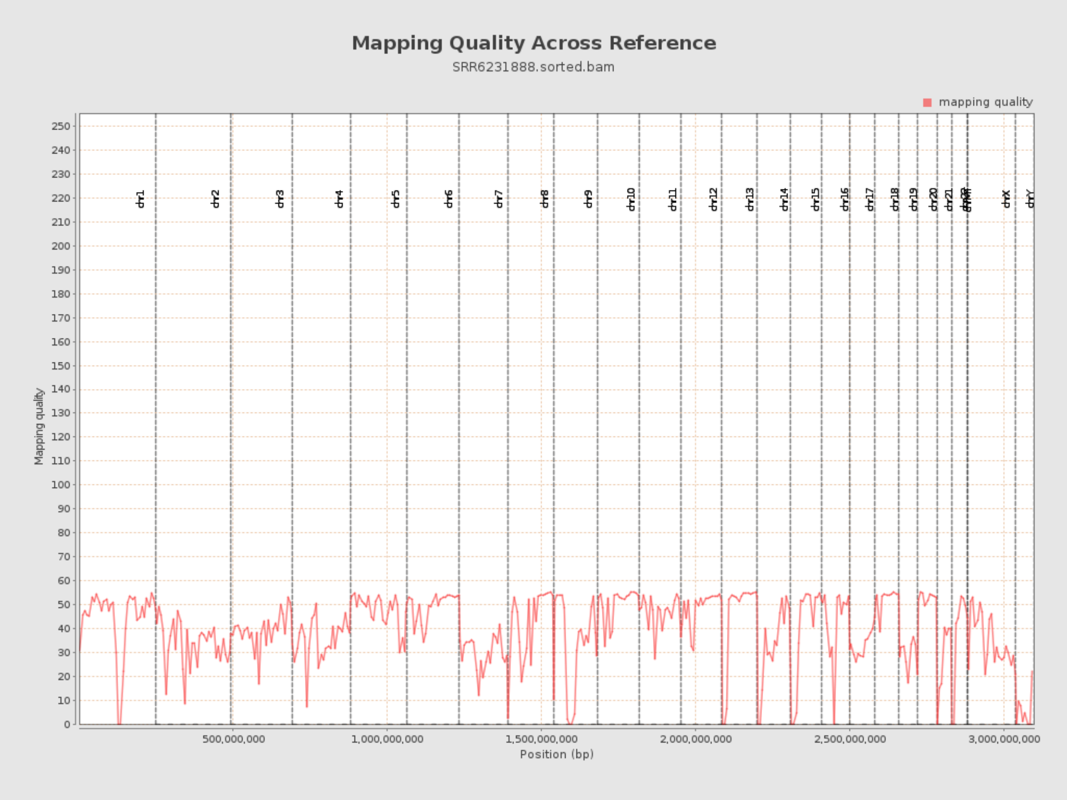
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram