Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 00:26:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231755.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_SRR6231755 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231755.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 00:26:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231755.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,251,616
Mapped reads	3,361,979 / 79.08%
Unmapped reads	889,637 / 20.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	36,427 / 0.86%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	932,918 / 21.94%
Duplication rate	11.78%
Clipped reads	1,217,997 / 28.65%

2.2. ACGT Content

Number/percentage of A's	55,948,367 / 24.24%
Number/percentage of C's	38,437,616 / 16.66%
Number/percentage of T's	59,975,714 / 25.99%
Number/percentage of G's	76,370,336 / 33.09%
Number/percentage of N's	48,460 / 0.02%
GC Percentage	49.75%

2.3. Coverage

Mean	0.0746

Standard Deviation	67.5019

2.4. Mapping Quality

Mean Mapping Quality	40.31

2.5. Mismatches and indels

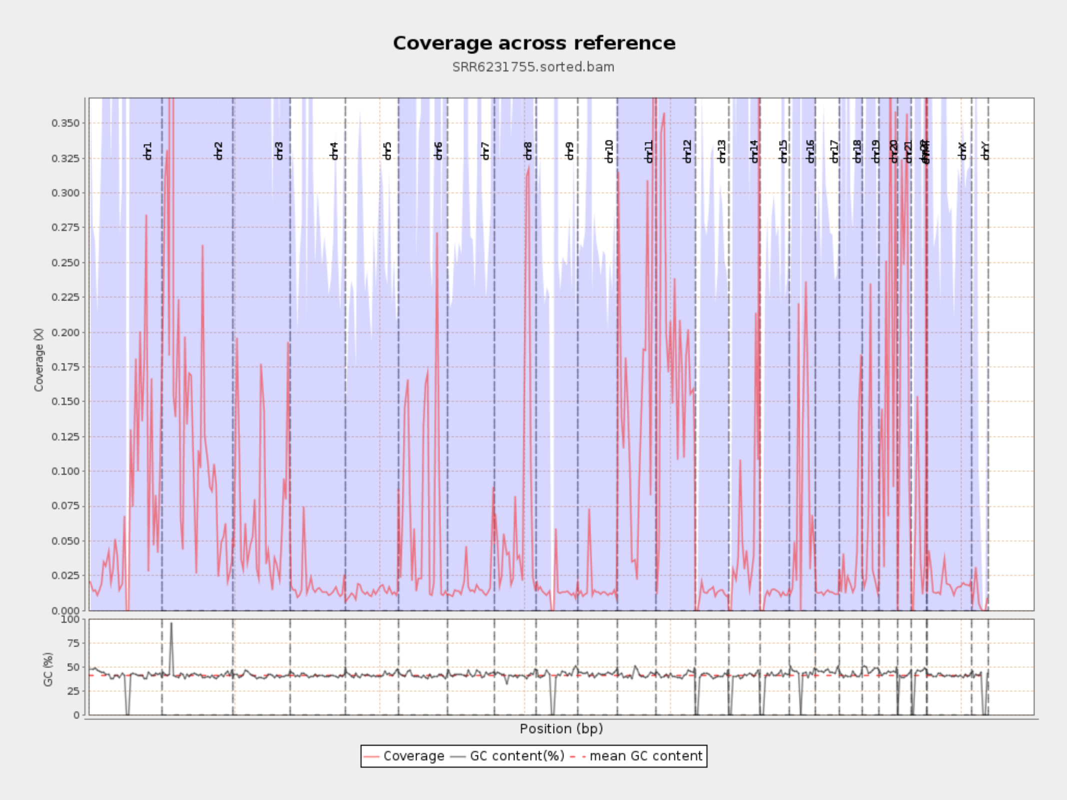
General error rate	0.62%
Mismatches	1,401,314
Insertions	14,735
Mapped reads with at least one insertion	0.43%
Deletions	43,811
Mapped reads with at least one deletion	1.29%
Homopolymer indels	46.55%

2.6. Chromosome stats

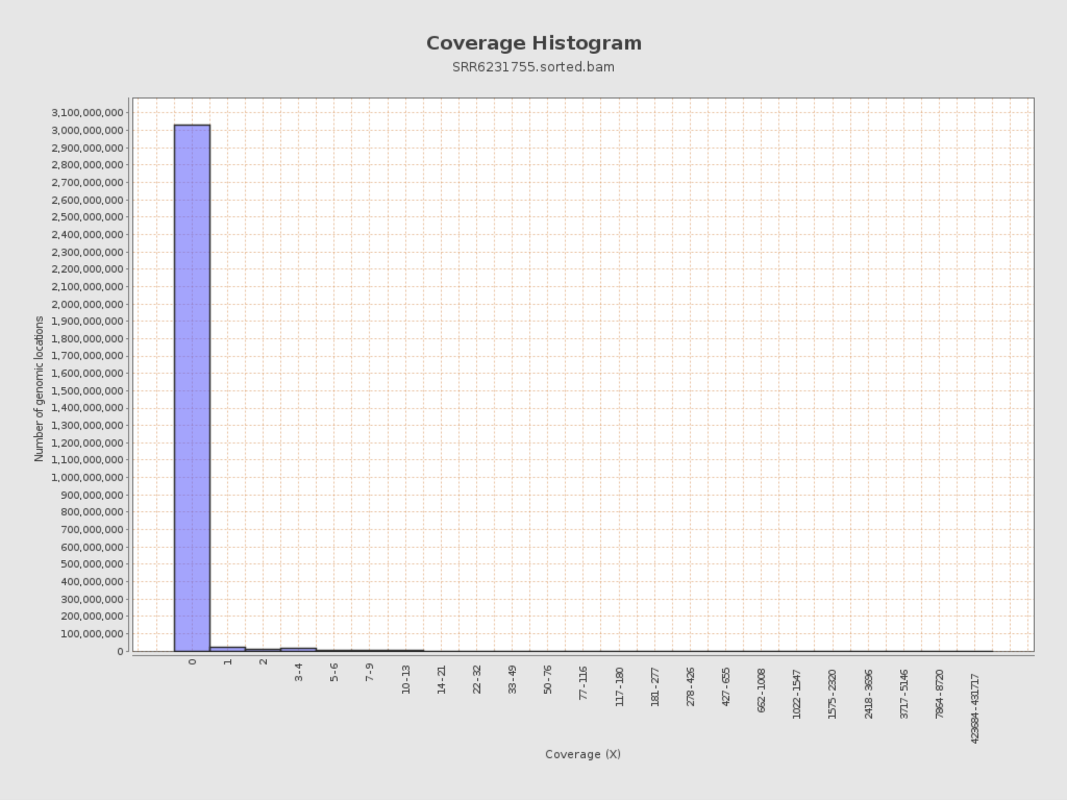
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17266339	0.0693	0.7745
chr2	243199373	65226085	0.2682	240.8206
chr3	198022430	13515970	0.0683	0.6206
chr4	191154276	3226624	0.0169	0.3381
chr5	180915260	2393851	0.0132	0.242
chr6	171115067	12438850	0.0727	0.7213
chr7	159138663	3058473	0.0192	0.43

chr8	146364022	11335049	0.0774	0.9536
chr9	141213431	2005454	0.0142	0.4077
chr10	135534747	2153509	0.0159	0.835
chr11	135006516	23589960	0.1747	1.0683
chr12	133851895	23749684	0.1774	1.0321
chr13	115169878	1388361	0.0121	0.2517
chr14	107349540	6014739	0.056	0.6617
chr15	102531392	1121035	0.0109	0.2686
chr16	90354753	7620663	0.0843	0.7166
chr17	81195210	1037274	0.0128	0.2683
chr18	78077248	3571971	0.0457	0.6635
chr19	59128983	3296578	0.0558	0.8352
chr20	63025520	11774290	0.1868	1.1103
chr21	48129895	8978130	0.1865	1.0875
chr22	51304566	2458081	0.0479	0.5072
chrMT	16571	120595	7.2775	8.0745
chrX	155270560	3032992	0.0195	0.3262
chrY	59373566	477771	0.008	0.2044

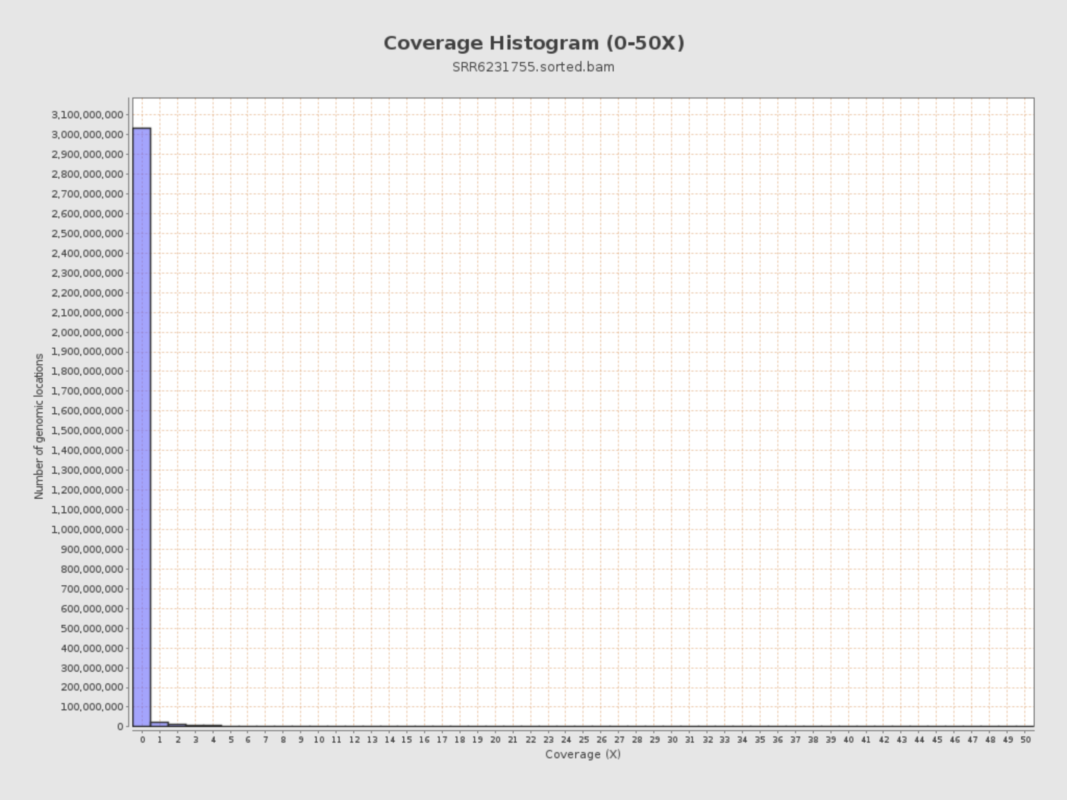
3. Results : Coverage across reference



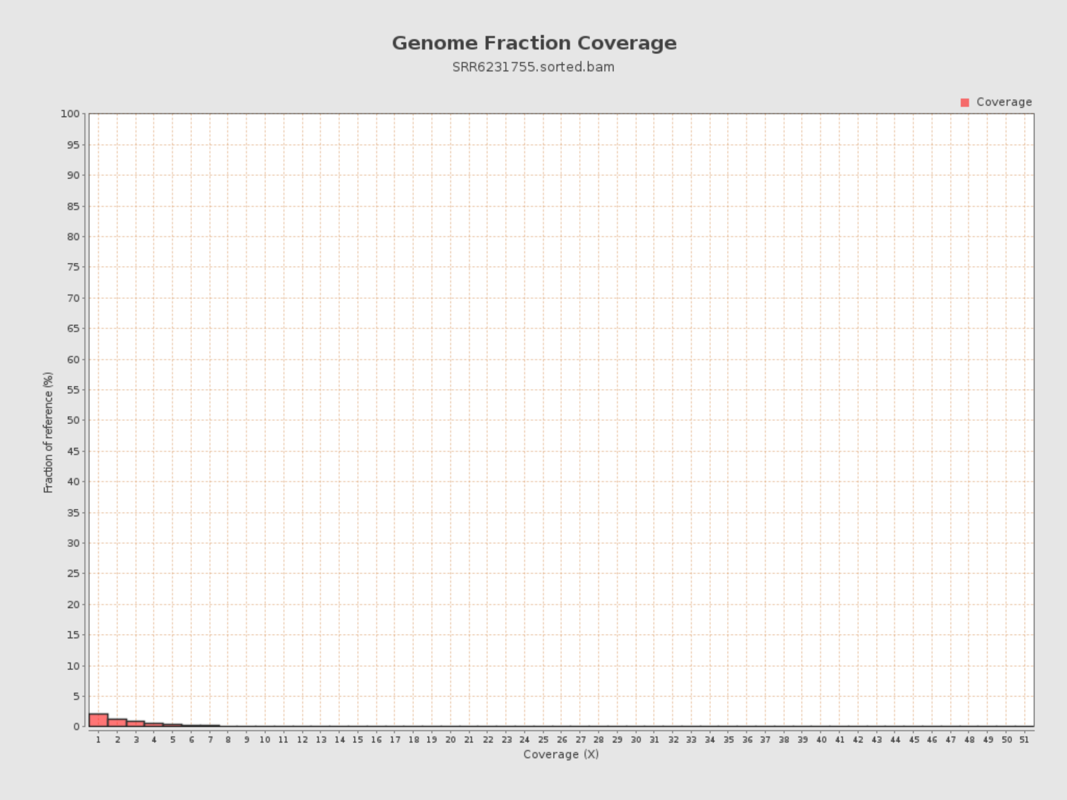
4. Results : Coverage Histogram



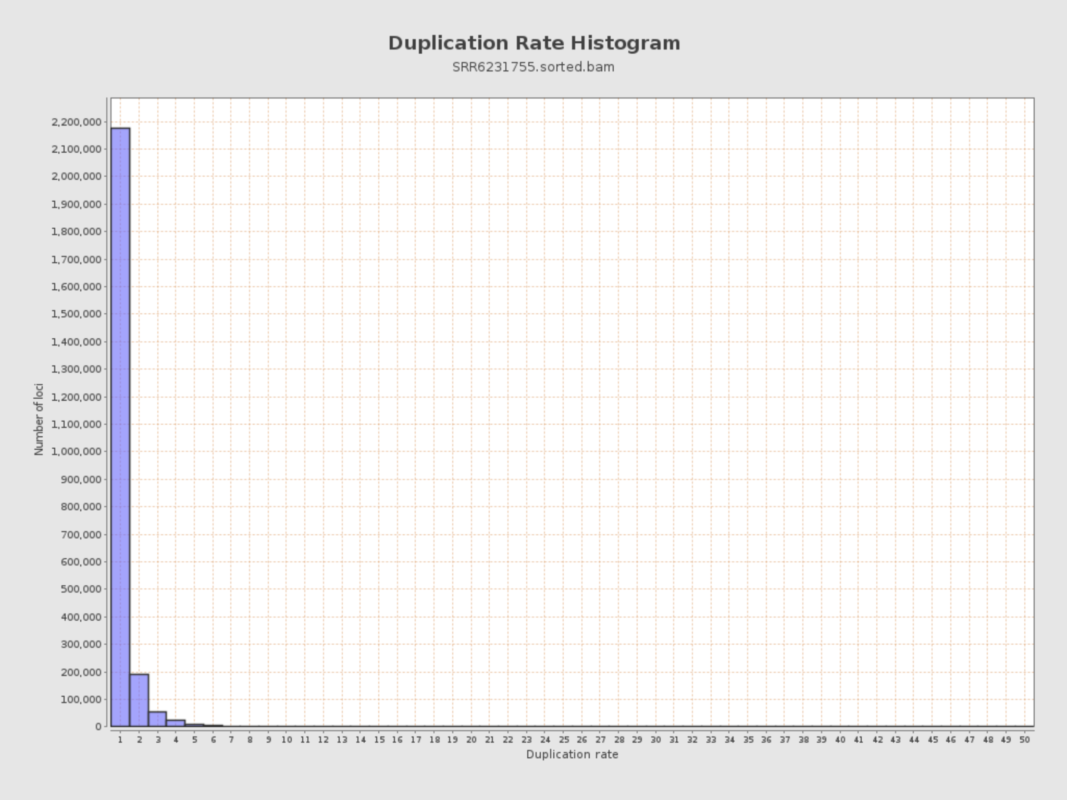
5. Results : Coverage Histogram (0-50X)



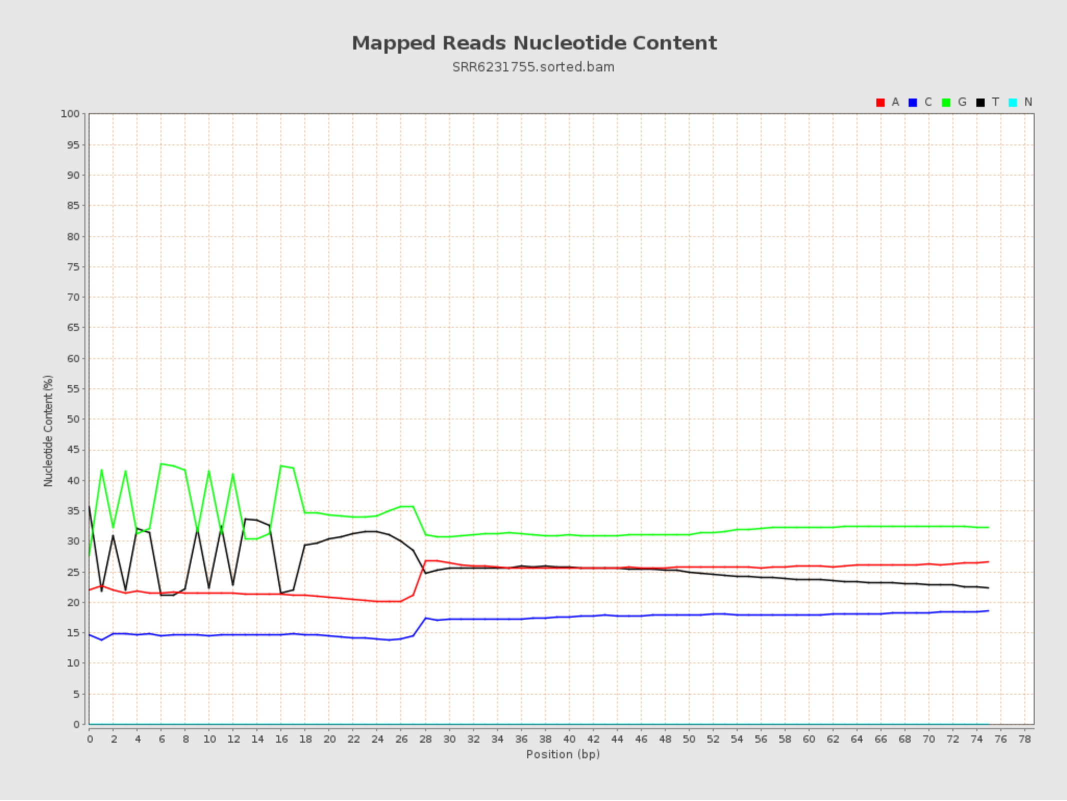
6. Results : Genome Fraction Coverage



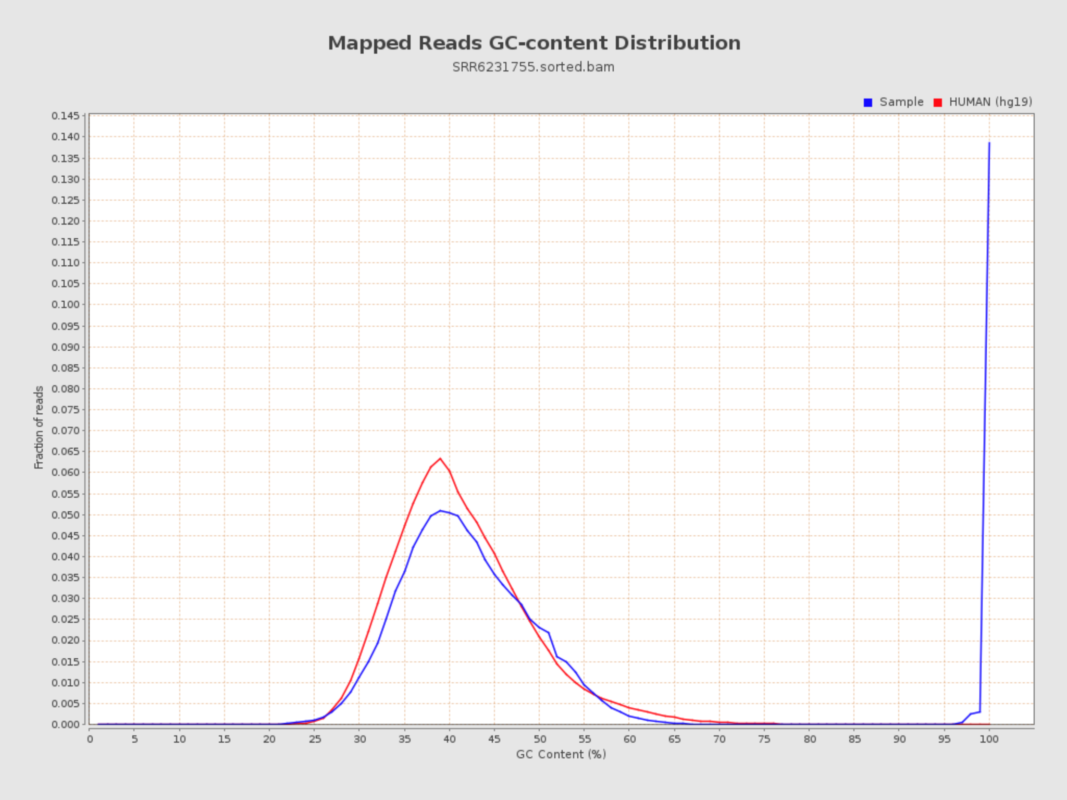
7. Results : Duplication Rate Histogram



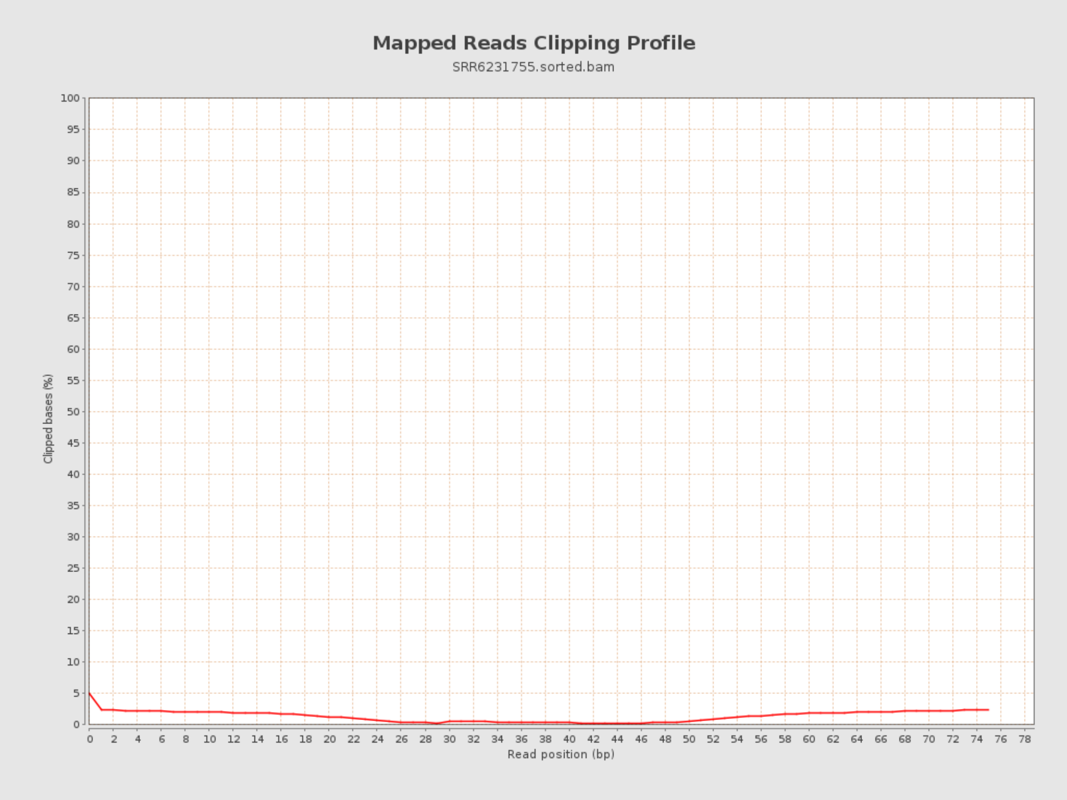
8. Results : Mapped Reads Nucleotide Content



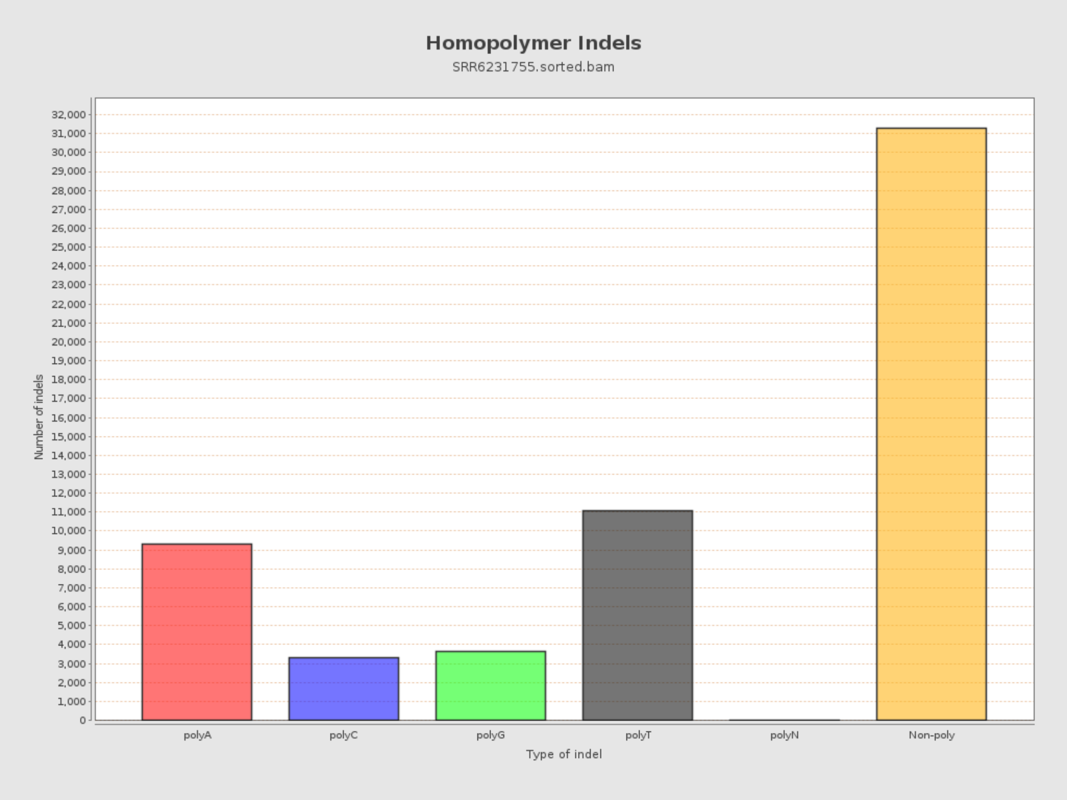
9. Results : Mapped Reads GC-content Distribution



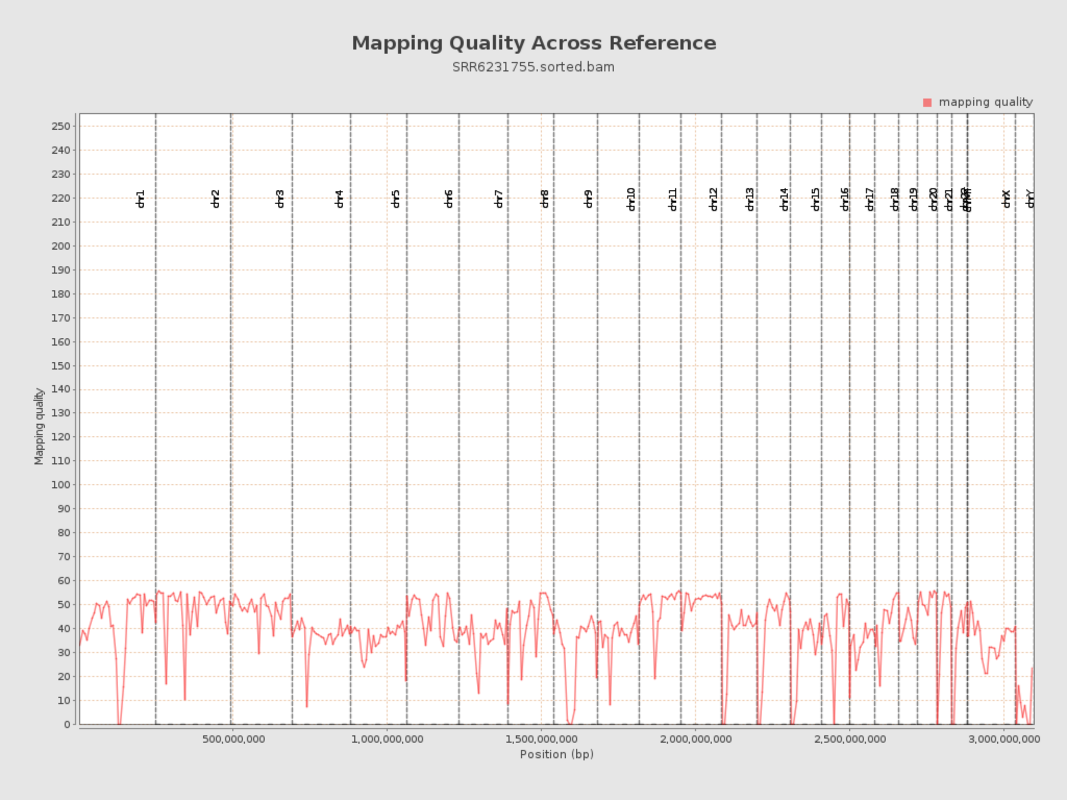
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram