Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 13:22:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008831.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_SRR6008831 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008831.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 13:22:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008831.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,762,421
Mapped reads	1,602,178 / 90.91%
Unmapped reads	160,243 / 9.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,957 / 0.39%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	58,778 / 3.34%
Duplication rate	2.21%
Clipped reads	720,974 / 40.91%

2.2. ACGT Content

Number/percentage of A's	28,959,113 / 27.4%
Number/percentage of C's	19,915,718 / 18.84%
Number/percentage of T's	32,649,296 / 30.89%
Number/percentage of G's	24,028,677 / 22.73%
Number/percentage of N's	152,726 / 0.14%
GC Percentage	41.57%

2.3. Coverage

Mean	0.0342

Standard Deviation	0.4212

2.4. Mapping Quality

Mean Mapping Quality	44.64

2.5. Mismatches and indels

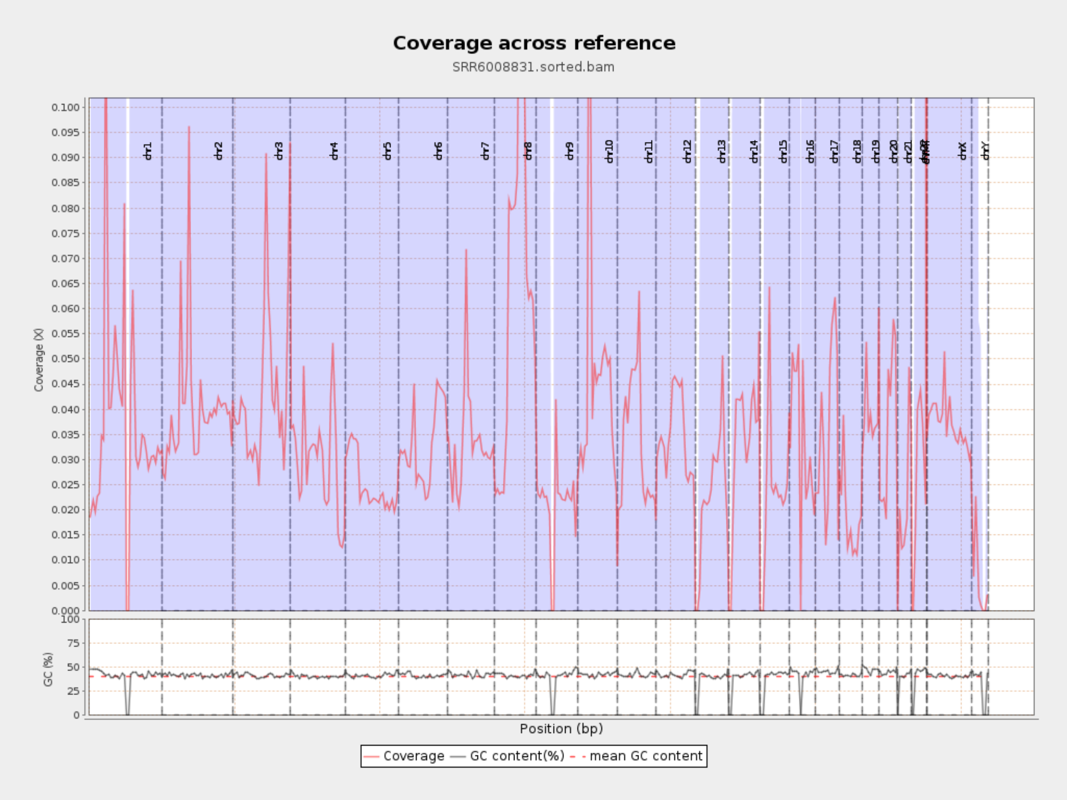
General error rate	0.9%
Mismatches	940,239
Insertions	7,959
Mapped reads with at least one insertion	0.49%
Deletions	33,228
Mapped reads with at least one deletion	2.05%
Homopolymer indels	44.8%

2.6. Chromosome stats

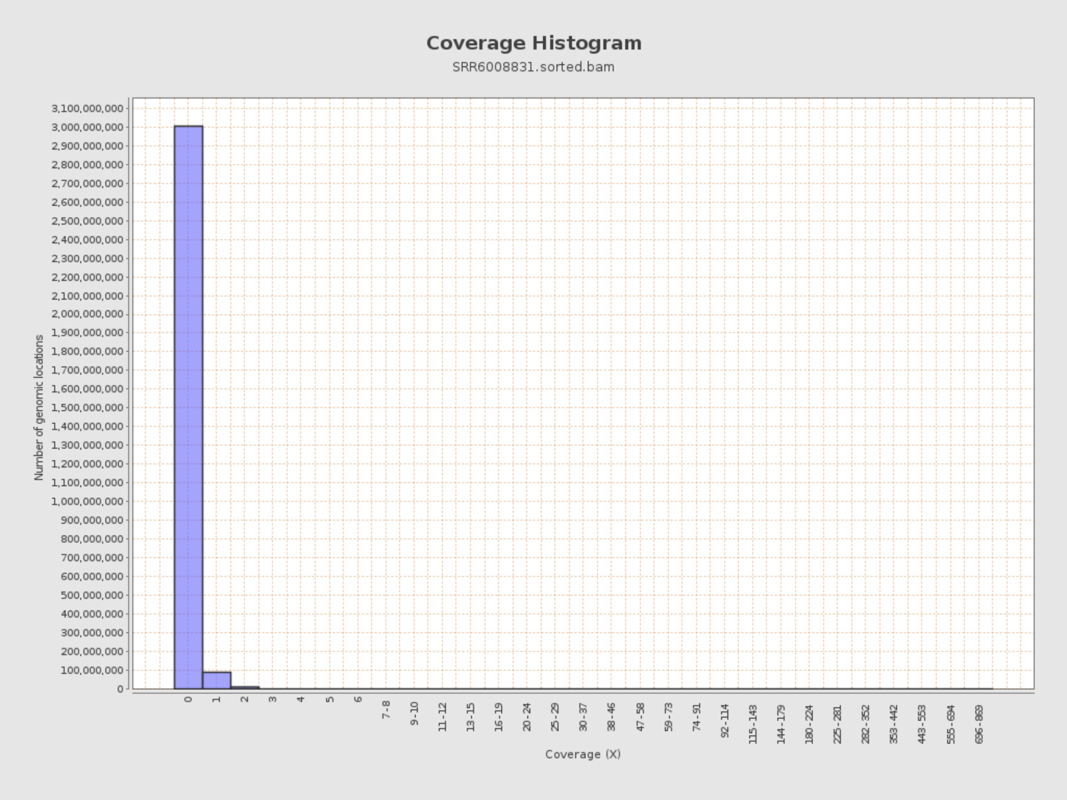
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9189689	0.0369	0.7497
chr2	243199373	9811599	0.0403	0.4373
chr3	198022430	8464910	0.0427	0.2966
chr4	191154276	5621863	0.0294	0.2167
chr5	180915260	4520847	0.025	0.1739
chr6	171115067	5654294	0.033	0.2311
chr7	159138663	5345297	0.0336	0.4577

chr8	146364022	9474008	0.0647	0.4259
chr9	141213431	2955193	0.0209	0.2956
chr10	135534747	6335279	0.0467	1.0276
chr11	135006516	4526726	0.0335	0.3207
chr12	133851895	4657465	0.0348	0.2047
chr13	115169878	2653162	0.023	0.1637
chr14	107349540	3525495	0.0328	0.206
chr15	102531392	2434149	0.0237	0.1689
chr16	90354753	3029265	0.0335	0.3291
chr17	81195210	2943903	0.0363	0.2881
chr18	78077248	1460700	0.0187	0.58
chr19	59128983	2327919	0.0394	0.4961
chr20	63025520	2286874	0.0363	0.2142
chr21	48129895	1047101	0.0218	0.1873
chr22	51304566	1301101	0.0254	0.1744
chrMT	16571	68839	4.1542	3.3033
chrX	155270560	5770421	0.0372	0.2415
chrY	59373566	358347	0.006	0.224

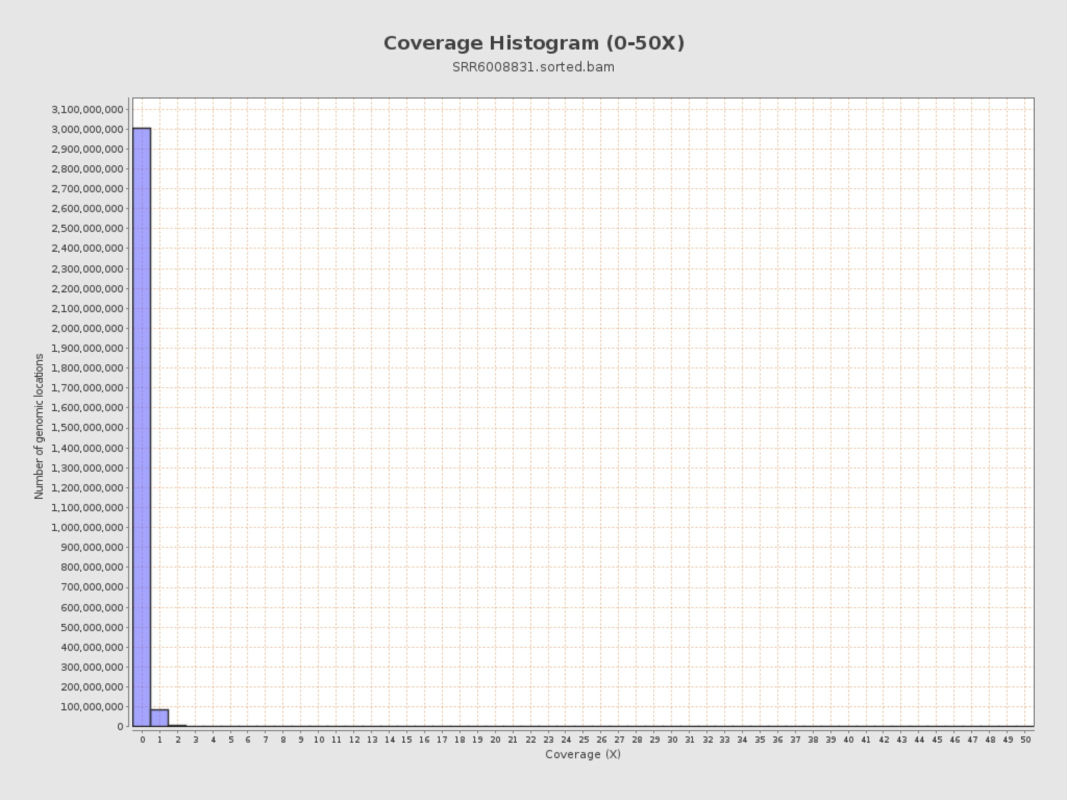
3. Results : Coverage across reference



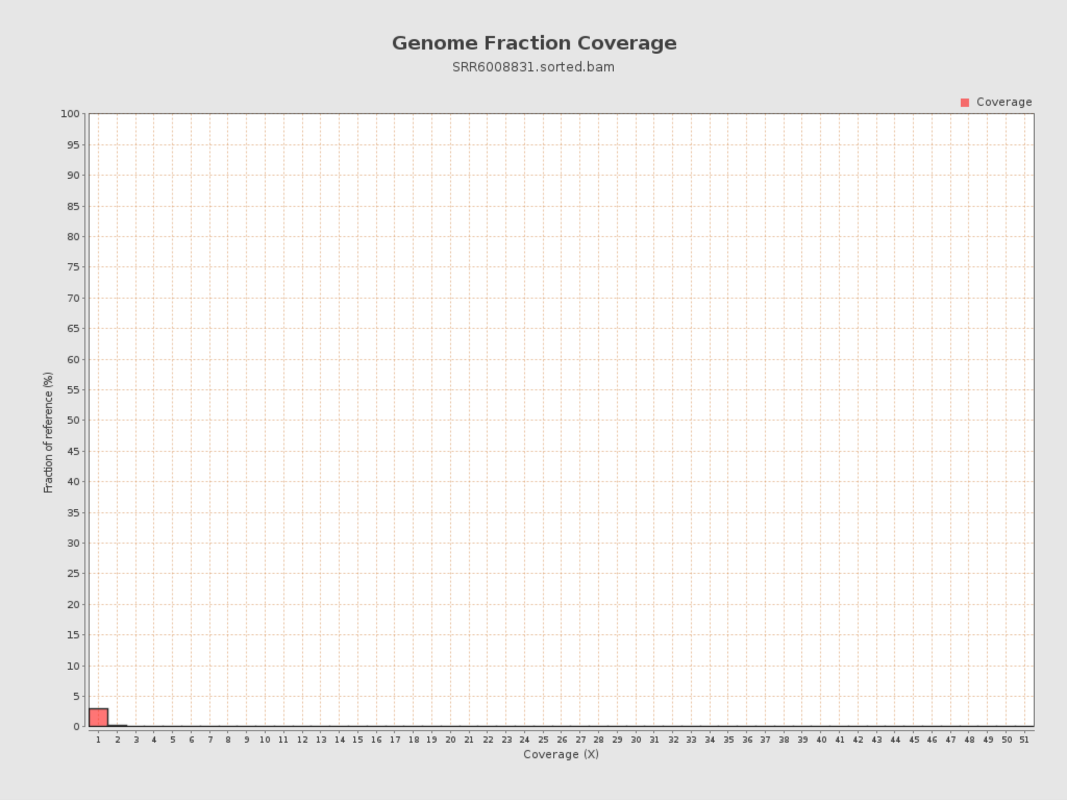
4. Results : Coverage Histogram



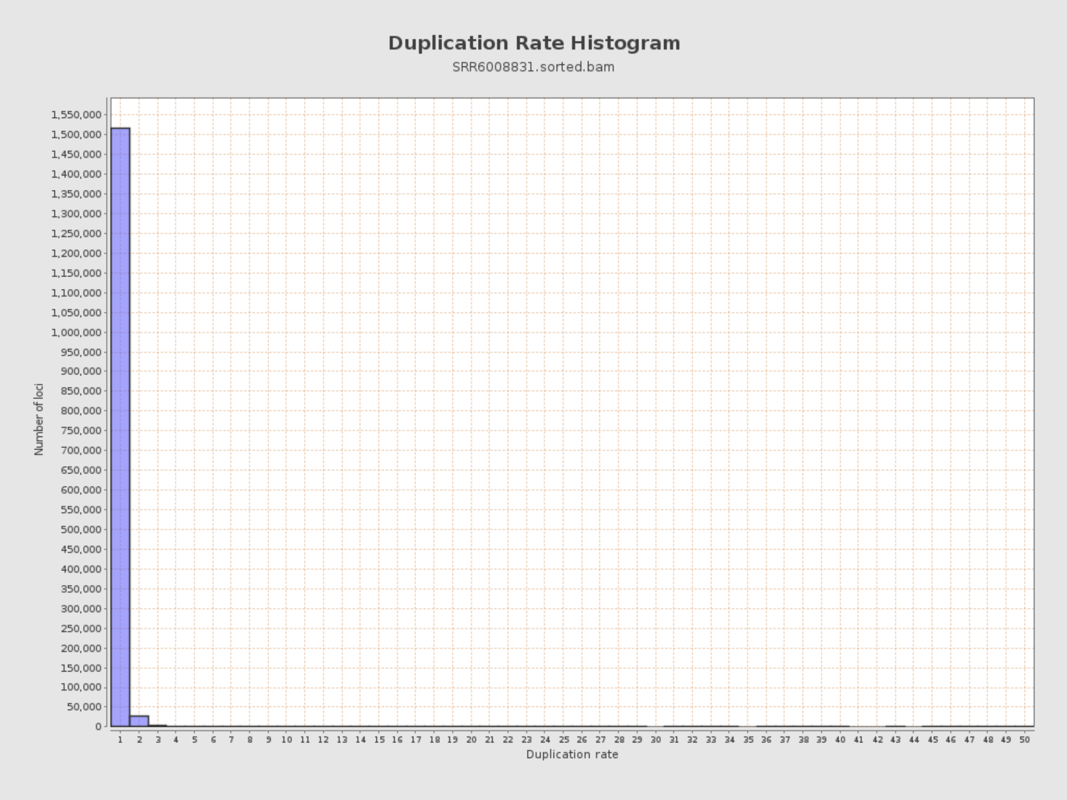
5. Results : Coverage Histogram (0-50X)



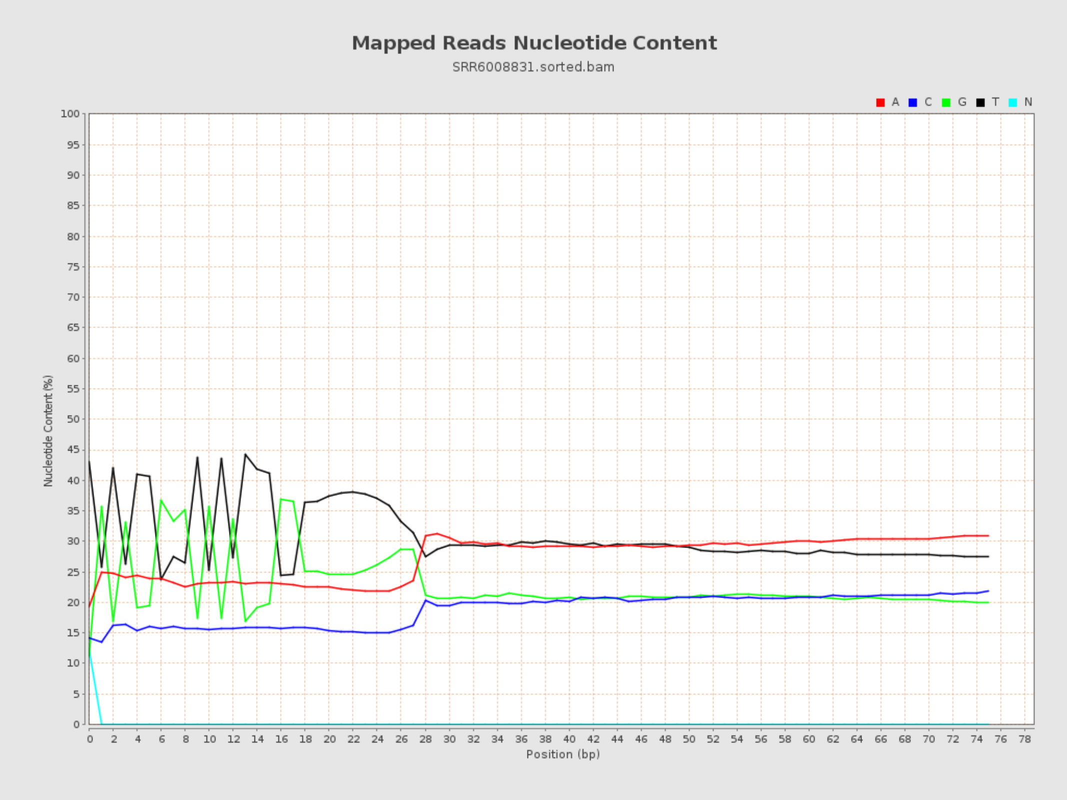
6. Results : Genome Fraction Coverage



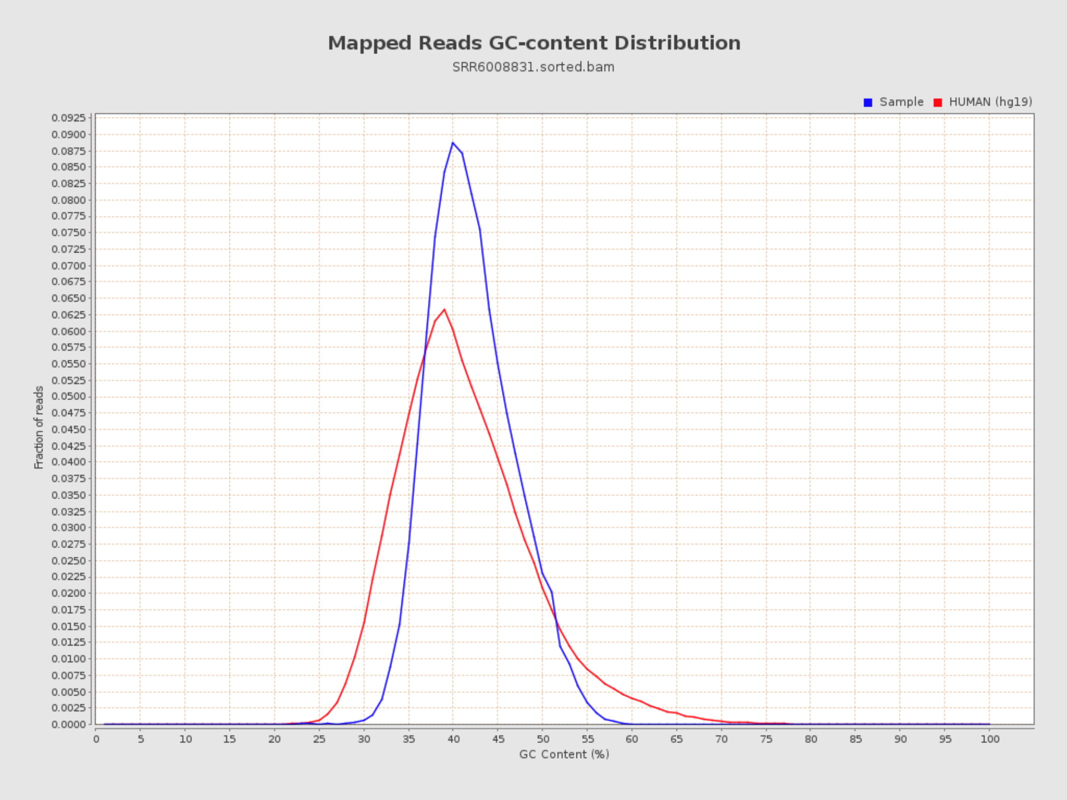
7. Results : Duplication Rate Histogram



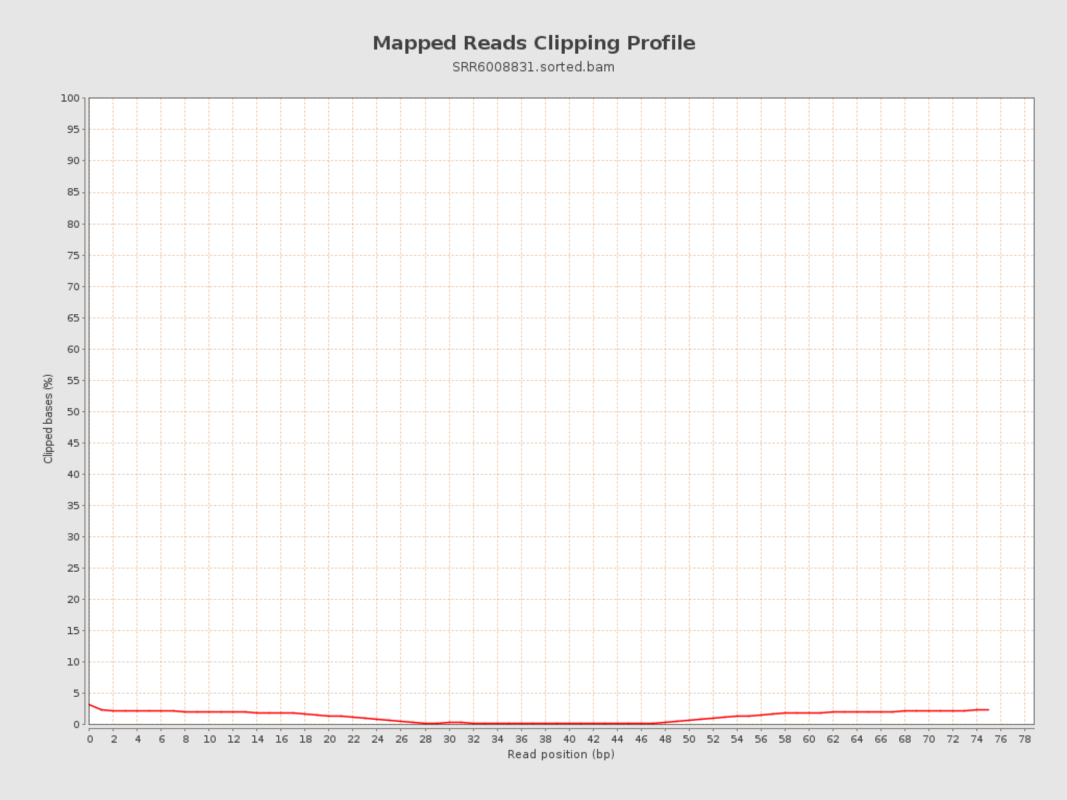
8. Results : Mapped Reads Nucleotide Content



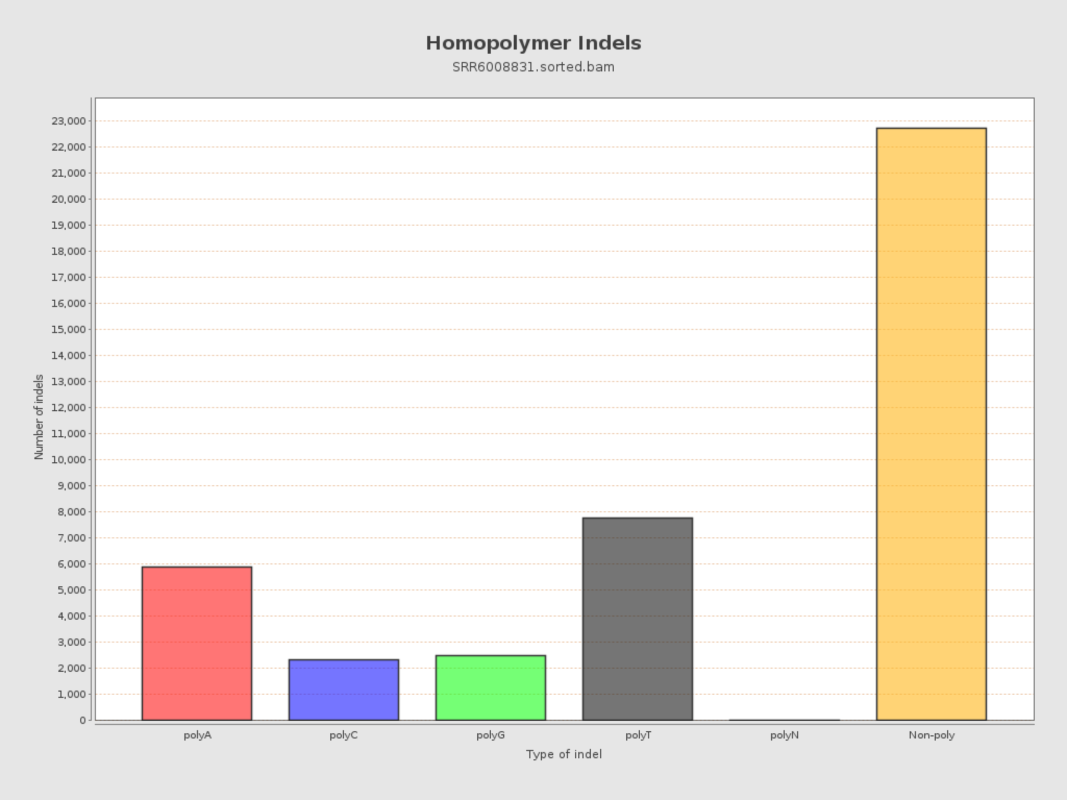
9. Results : Mapped Reads GC-content Distribution



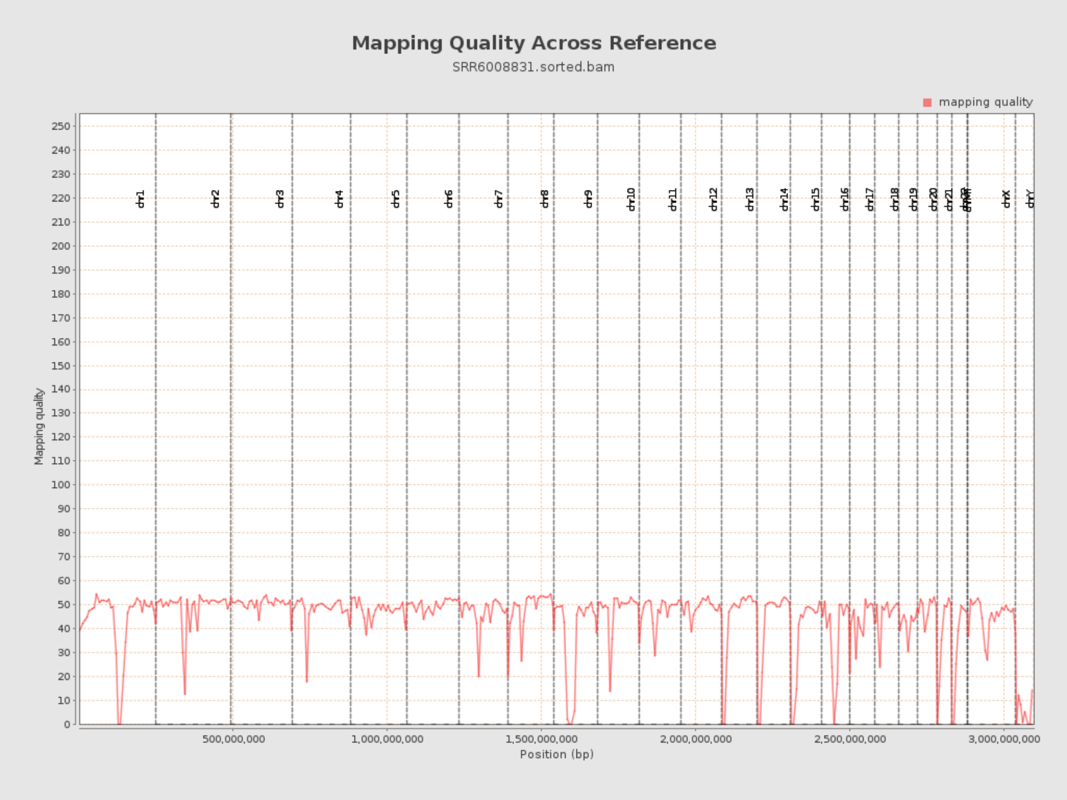
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram