Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 10:06:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008758.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_SRR6008758 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008758.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 10:06:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008758.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,790,519
Mapped reads	1,614,642 / 90.18%
Unmapped reads	175,877 / 9.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,633 / 0.48%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	68,753 / 3.84%
Duplication rate	3.29%
Clipped reads	675,493 / 37.73%

2.2. ACGT Content

Number/percentage of A's	29,065,555 / 26.96%
Number/percentage of C's	20,717,156 / 19.22%
Number/percentage of T's	33,329,886 / 30.92%
Number/percentage of G's	24,541,775 / 22.76%
Number/percentage of N's	152,265 / 0.14%
GC Percentage	41.98%

2.3. Coverage

Mean	0.0348

Standard Deviation	0.3245

2.4. Mapping Quality

Mean Mapping Quality	45.75

2.5. Mismatches and indels

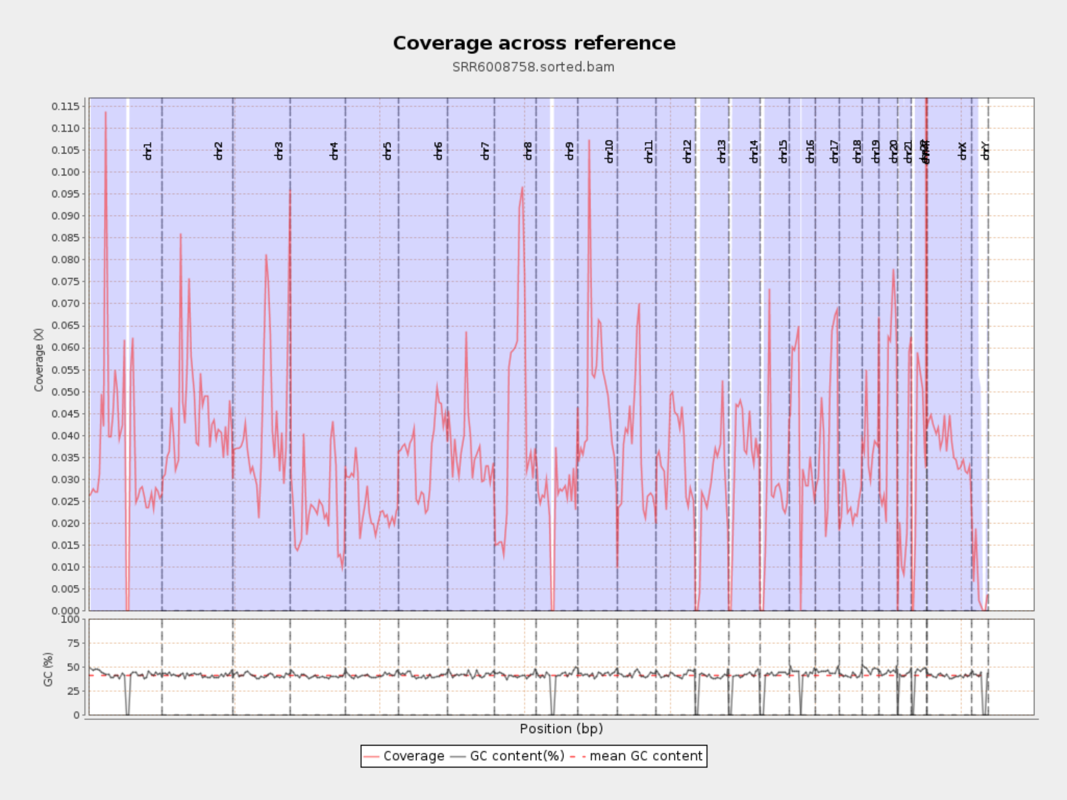
General error rate	0.84%
Mismatches	889,923
Insertions	7,783
Mapped reads with at least one insertion	0.48%
Deletions	29,187
Mapped reads with at least one deletion	1.79%
Homopolymer indels	45.47%

2.6. Chromosome stats

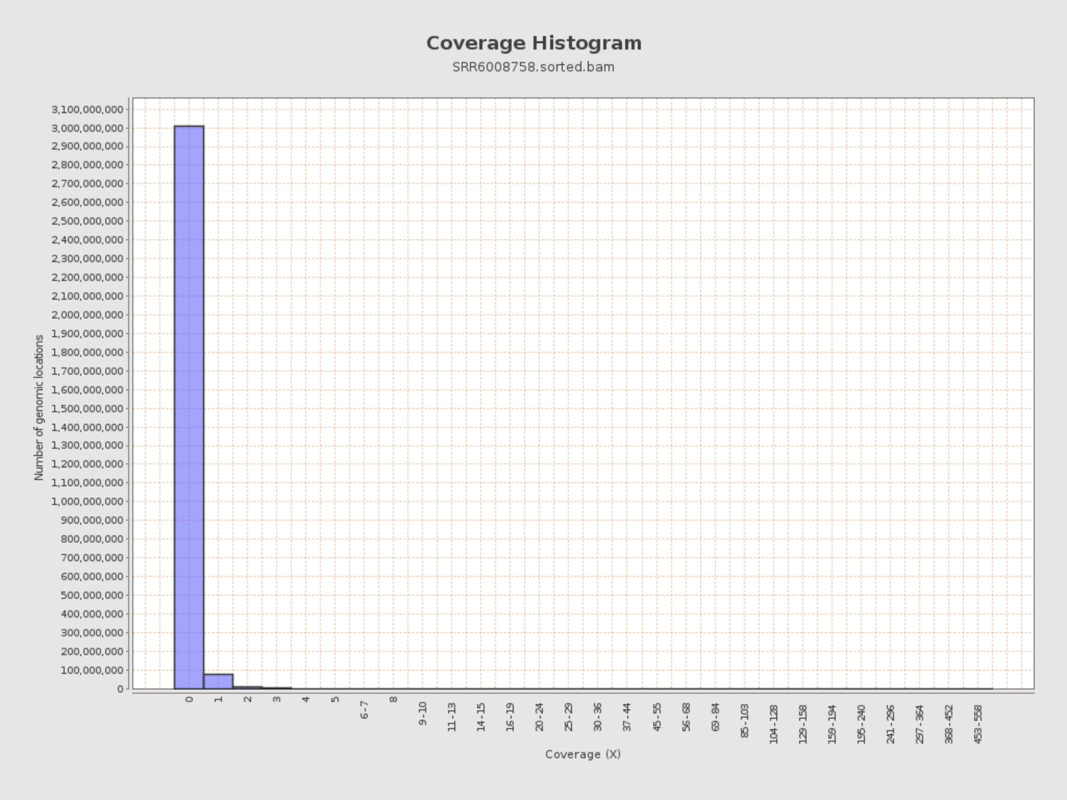
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8905779	0.0357	0.5052
chr2	243199373	10831978	0.0445	0.4017
chr3	198022430	8373711	0.0423	0.2619
chr4	191154276	4293812	0.0225	0.192
chr5	180915260	4345246	0.024	0.1808
chr6	171115067	6159560	0.036	0.2448
chr7	159138663	5808303	0.0365	0.3978

chr8	146364022	6375001	0.0436	0.3241
chr9	141213431	3480866	0.0246	0.2551
chr10	135534747	6764124	0.0499	0.56
chr11	135006516	4838624	0.0358	0.3005
chr12	133851895	4778405	0.0357	0.2213
chr13	115169878	3043147	0.0264	0.1885
chr14	107349540	3664689	0.0341	0.2213
chr15	102531392	2670113	0.026	0.1874
chr16	90354753	3523661	0.039	0.3194
chr17	81195210	3493176	0.043	0.2888
chr18	78077248	1883591	0.0241	0.4416
chr19	59128983	2306697	0.039	0.3785
chr20	63025520	2987725	0.0474	0.2599
chr21	48129895	1199885	0.0249	0.1965
chr22	51304566	1733781	0.0338	0.214
chrMT	16571	199220	12.0222	7.0559
chrX	155270560	5866290	0.0378	0.2391
chrY	59373566	332063	0.0056	0.1794

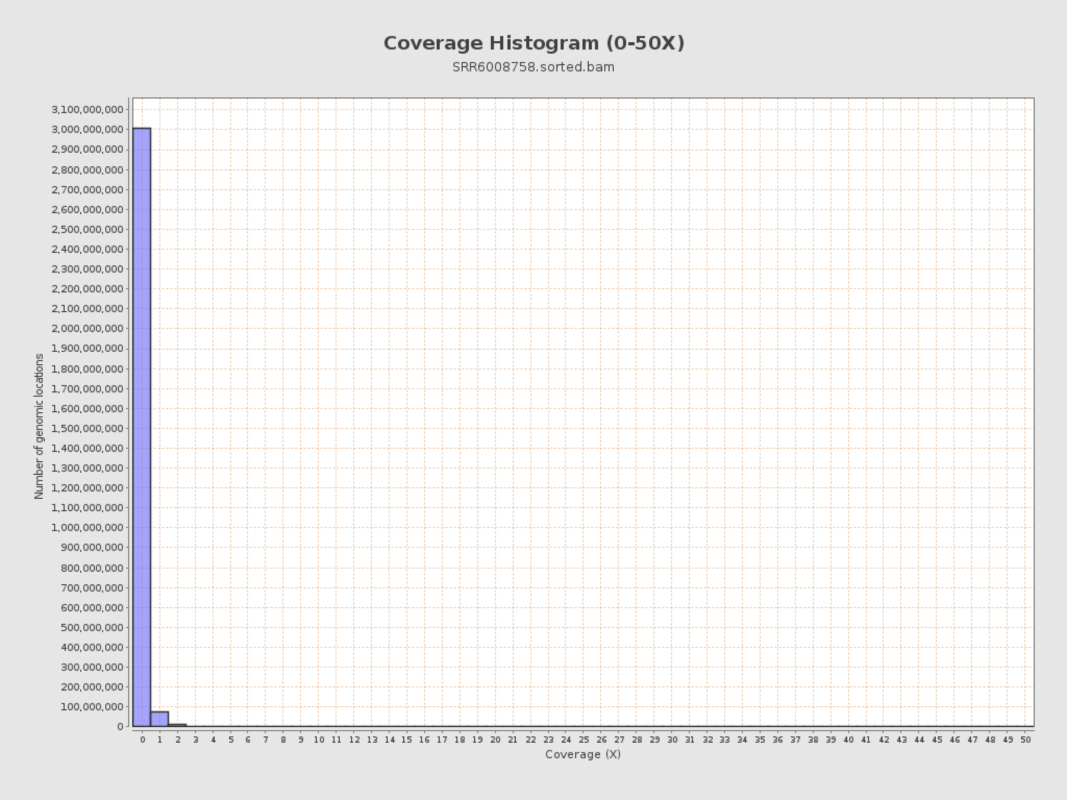
3. Results : Coverage across reference



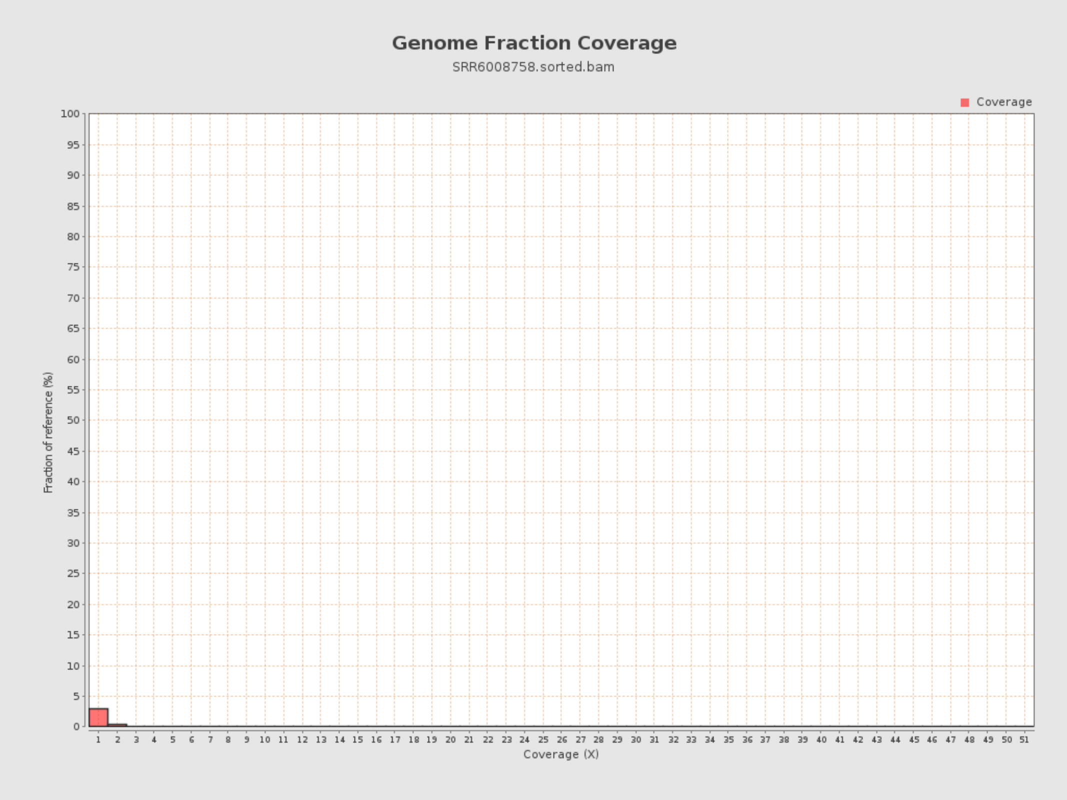
4. Results : Coverage Histogram



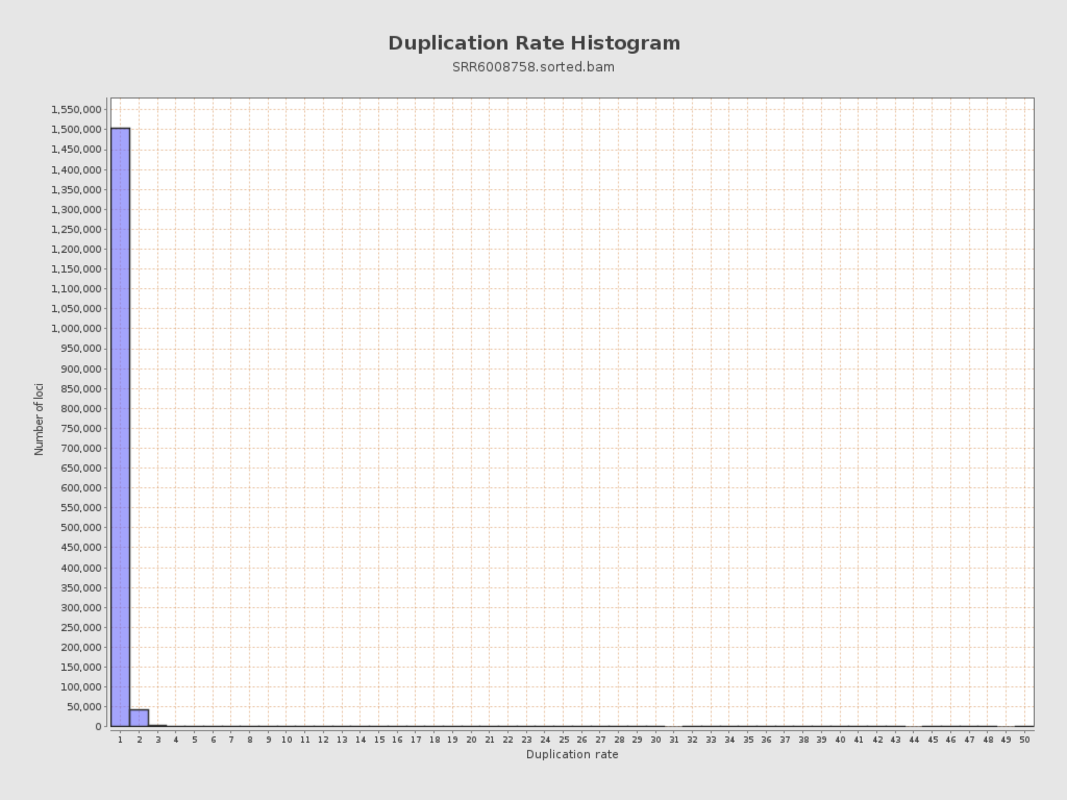
5. Results : Coverage Histogram (0-50X)



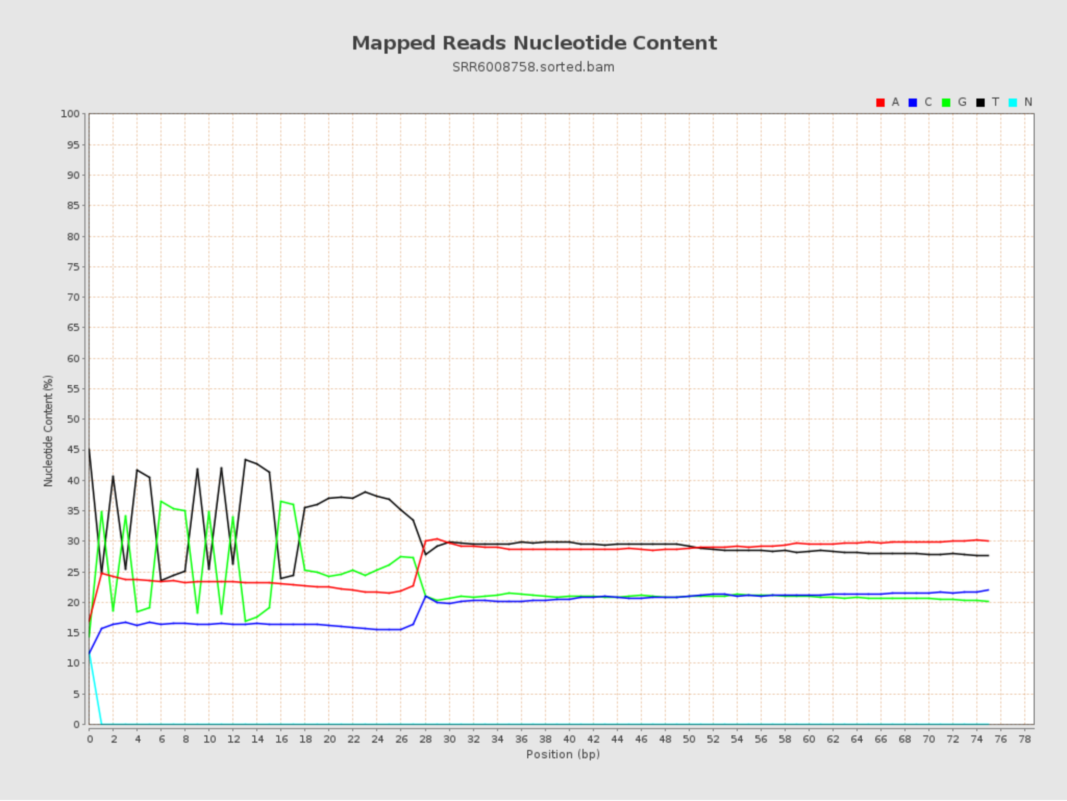
6. Results : Genome Fraction Coverage



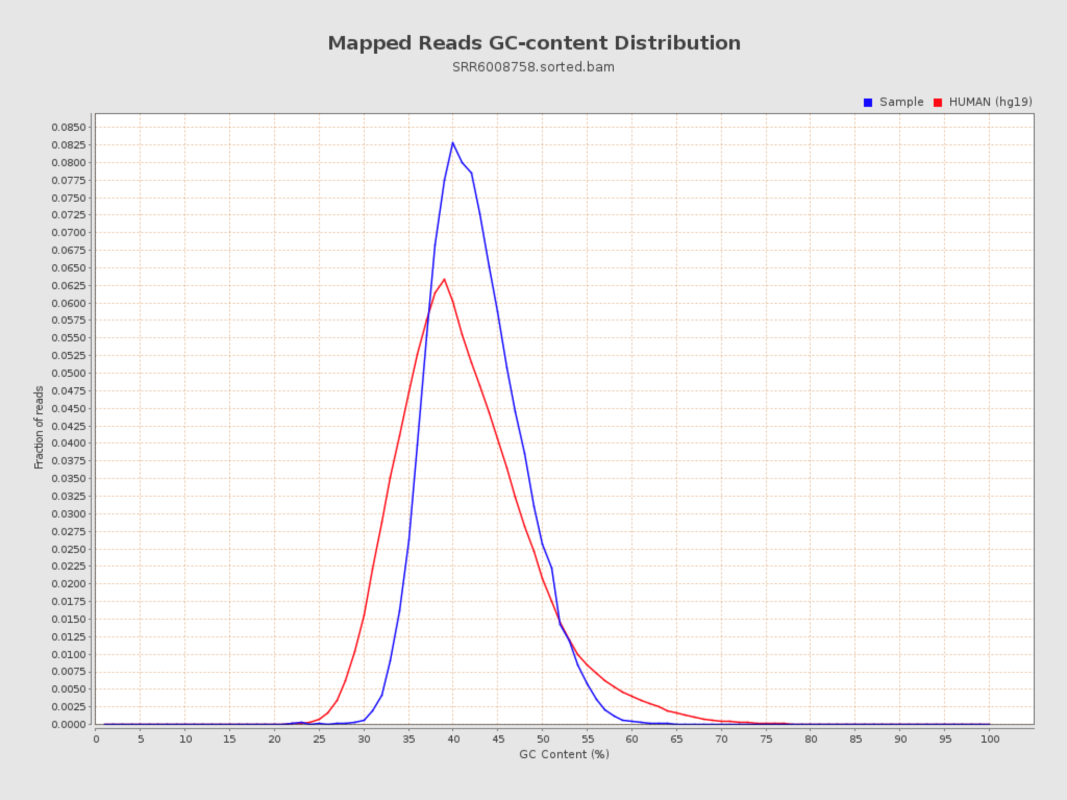
7. Results : Duplication Rate Histogram



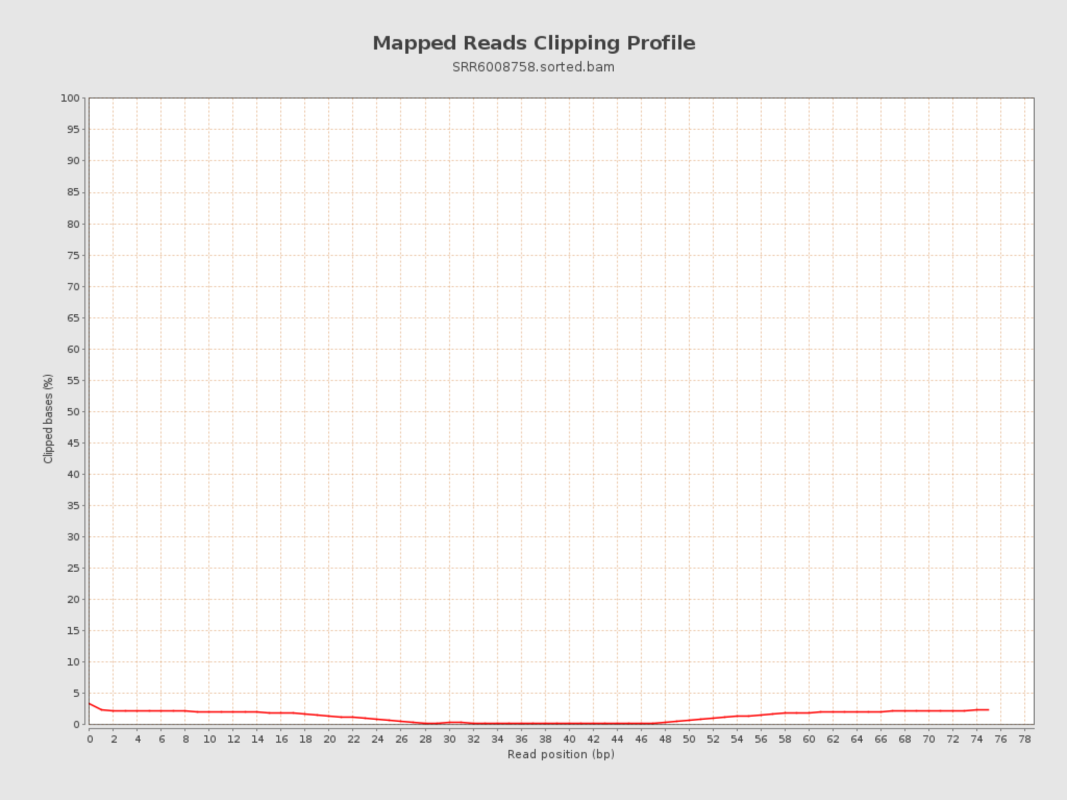
8. Results : Mapped Reads Nucleotide Content



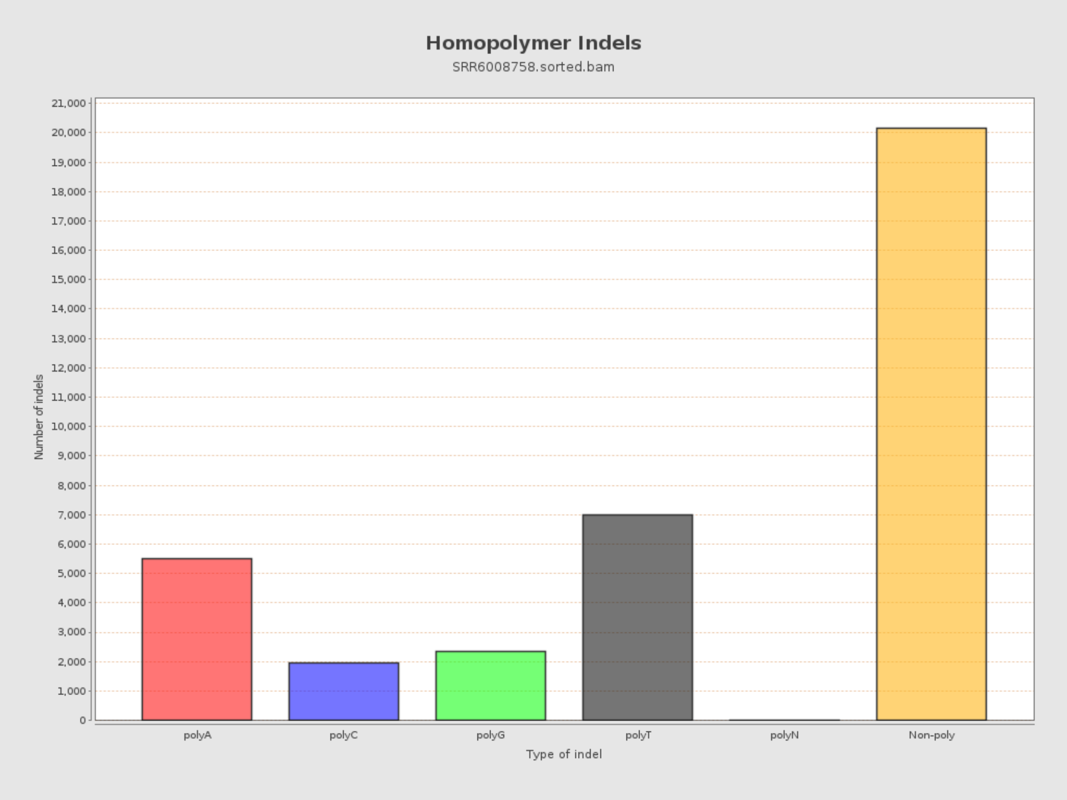
9. Results : Mapped Reads GC-content Distribution



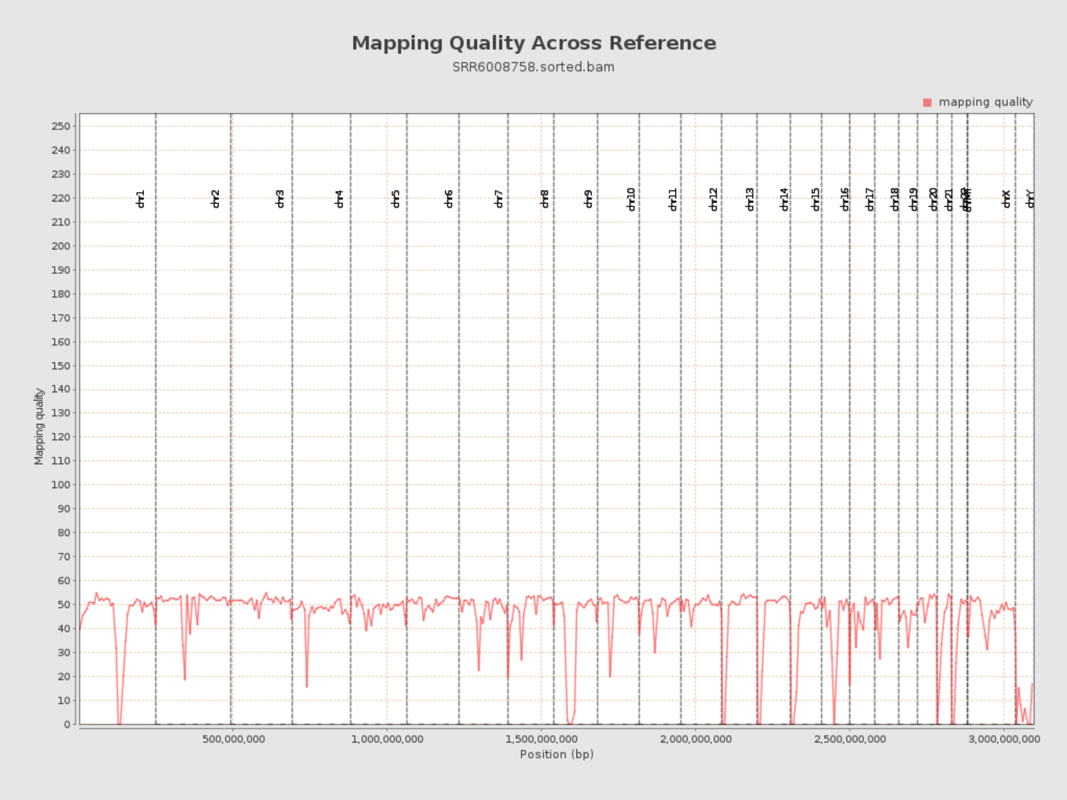
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram