Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 06:42:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231838.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_SRR6231838 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231838.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 06:42:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231838.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,580,835
Mapped reads	4,620,700 / 39.9%
Unmapped reads	6,960,135 / 60.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	36,961 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	320,007 / 2.76%
Duplication rate	2.37%
Clipped reads	2,349,677 / 20.29%

2.2. ACGT Content

Number/percentage of A's	85,540,987 / 28.36%
Number/percentage of C's	61,121,162 / 20.27%
Number/percentage of T's	80,012,380 / 26.53%
Number/percentage of G's	74,905,937 / 24.84%
Number/percentage of N's	22,990 / 0.01%
GC Percentage	45.1%

2.3. Coverage

Mean	0.0975

Standard Deviation	17.9616

2.4. Mapping Quality

Mean Mapping Quality	41.04

2.5. Mismatches and indels

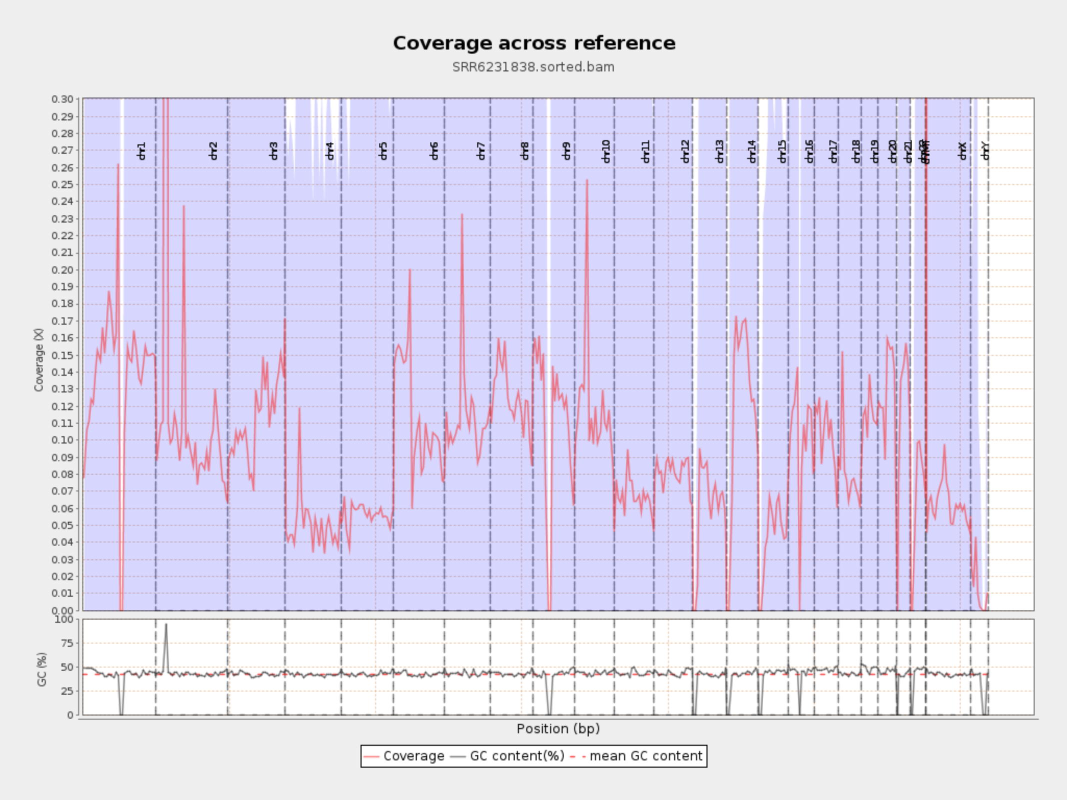
General error rate	0.69%
Mismatches	2,034,075
Insertions	25,480
Mapped reads with at least one insertion	0.54%
Deletions	63,232
Mapped reads with at least one deletion	1.35%
Homopolymer indels	42.51%

2.6. Chromosome stats

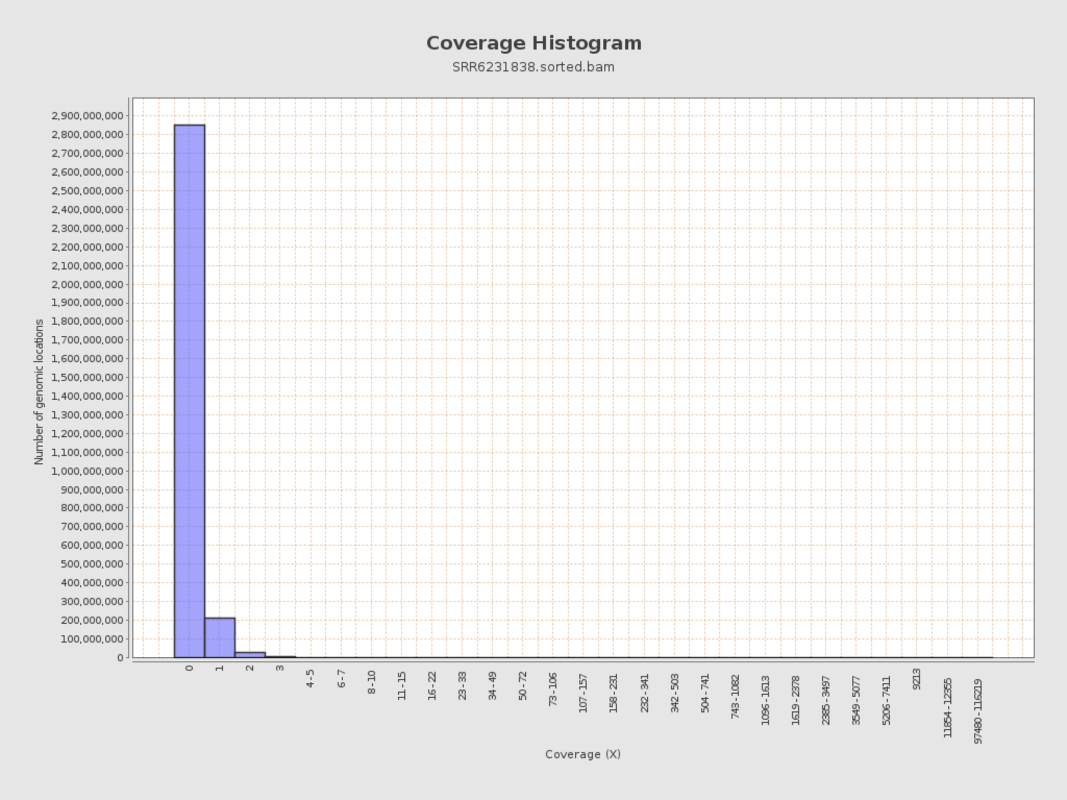
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	34650934	0.139	2.53
chr2	243199373	34149878	0.1404	63.9752
chr3	198022430	22250522	0.1124	0.4106
chr4	191154276	9729741	0.0509	0.3564
chr5	180915260	10191496	0.0563	0.2951
chr6	171115067	19819915	0.1158	0.6762
chr7	159138663	18132245	0.1139	1.5525

chr8	146364022	18234158	0.1246	0.8544
chr9	141213431	15588537	0.1104	0.9335
chr10	135534747	16215496	0.1196	1.1763
chr11	135006516	9074153	0.0672	0.7648
chr12	133851895	10933633	0.0817	0.3557
chr13	115169878	6928550	0.0602	0.2711
chr14	107349540	13166628	0.1227	0.6769
chr15	102531392	4290458	0.0418	0.2331
chr16	90354753	8855200	0.098	0.6194
chr17	81195210	8527742	0.105	0.5314
chr18	78077248	6430874	0.0824	2.1752
chr19	59128983	6794229	0.1149	1.5952
chr20	63025520	8179385	0.1298	0.4543
chr21	48129895	5592289	0.1162	0.4836
chr22	51304566	3251119	0.0634	0.2864
chrMT	16571	238801	14.4108	7.7801
chrX	155270560	9744886	0.0628	0.4201
chrY	59373566	739965	0.0125	0.2767

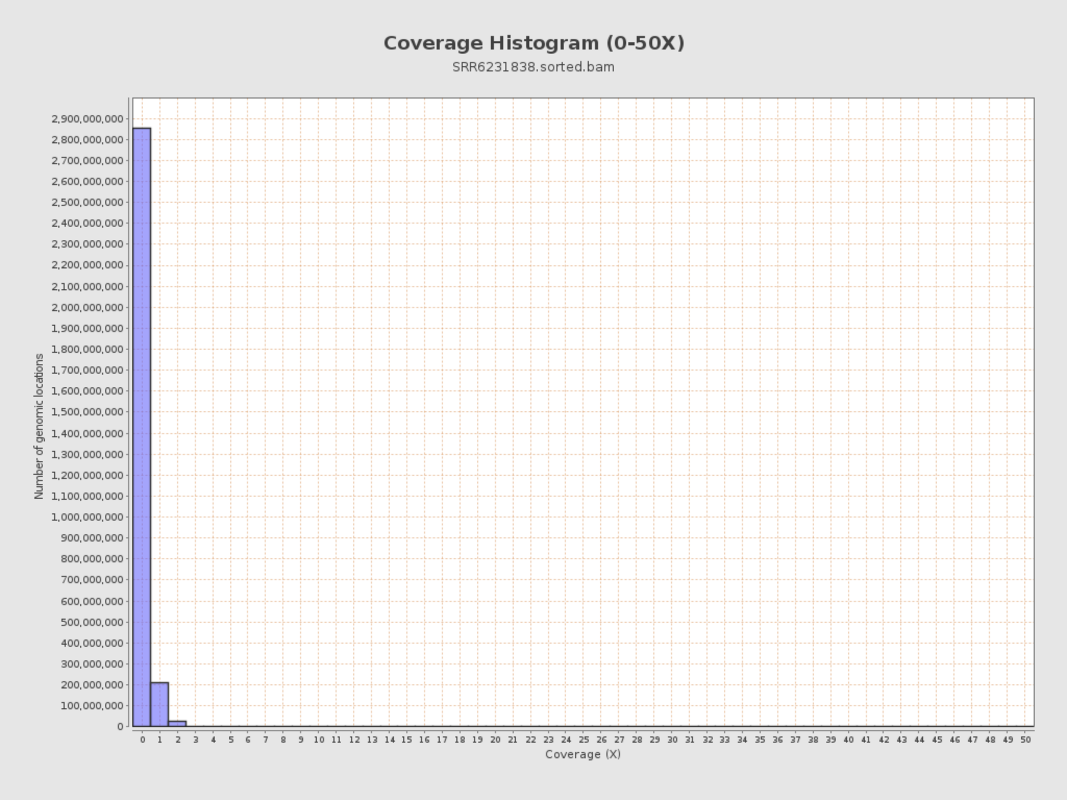
3. Results : Coverage across reference



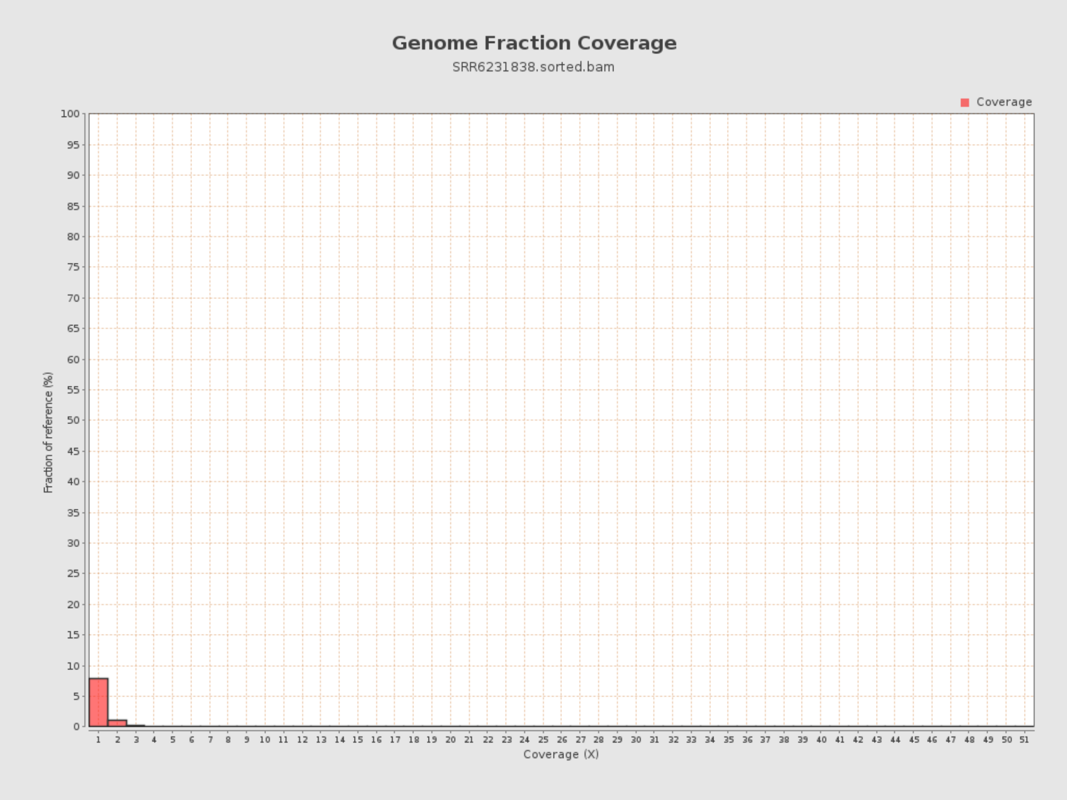
4. Results : Coverage Histogram



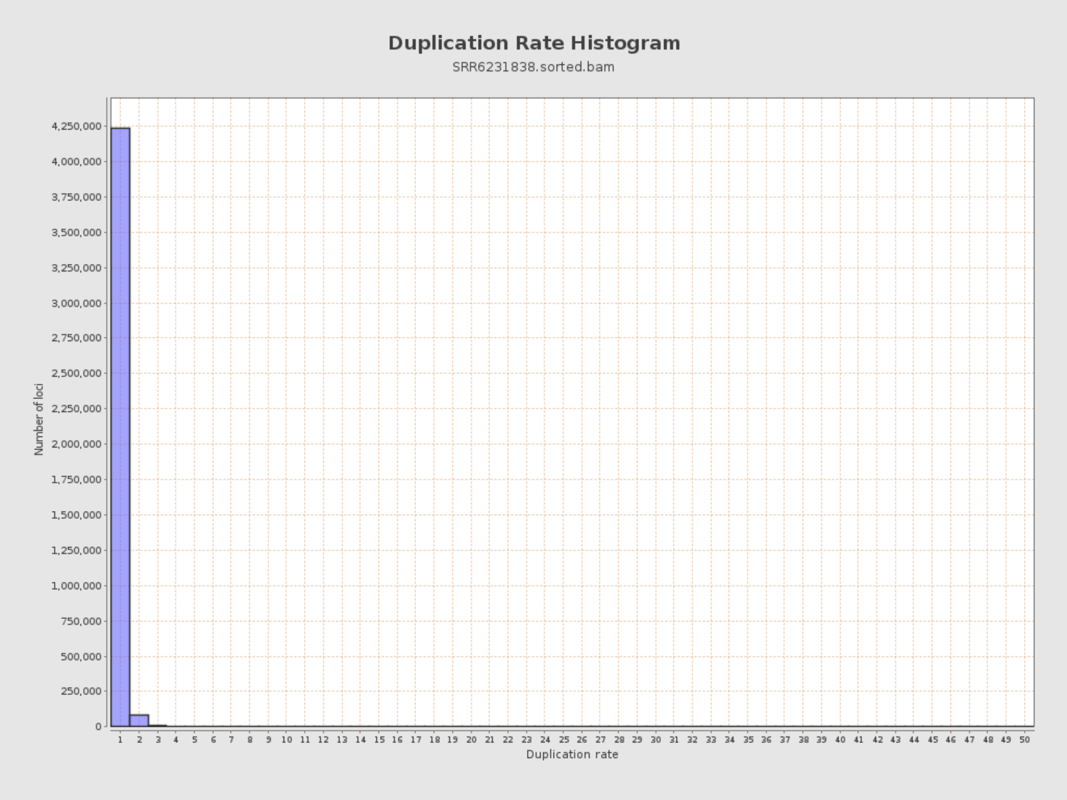
5. Results : Coverage Histogram (0-50X)



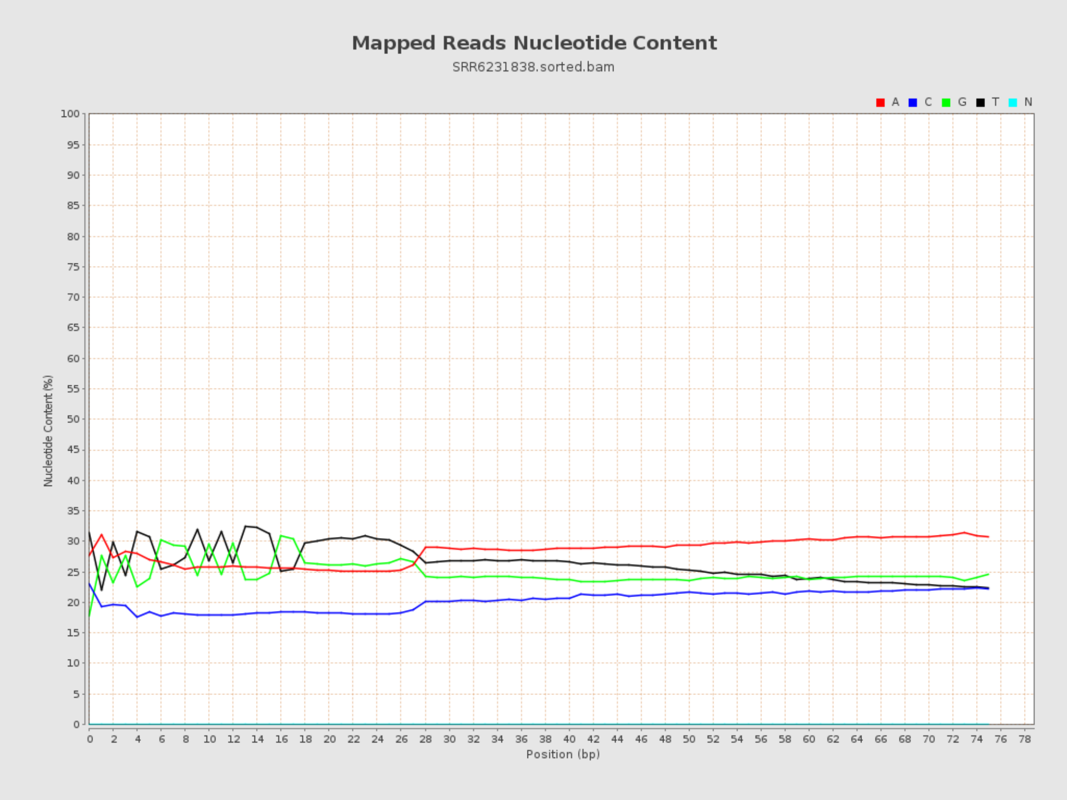
6. Results : Genome Fraction Coverage



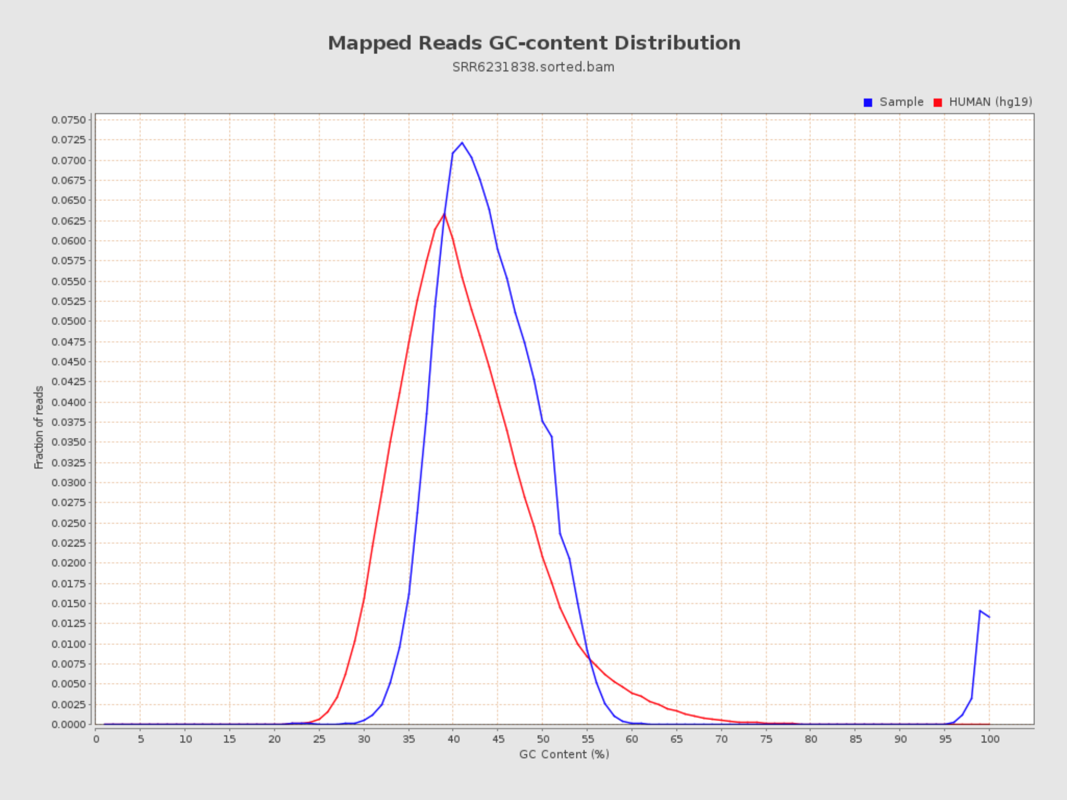
7. Results : Duplication Rate Histogram



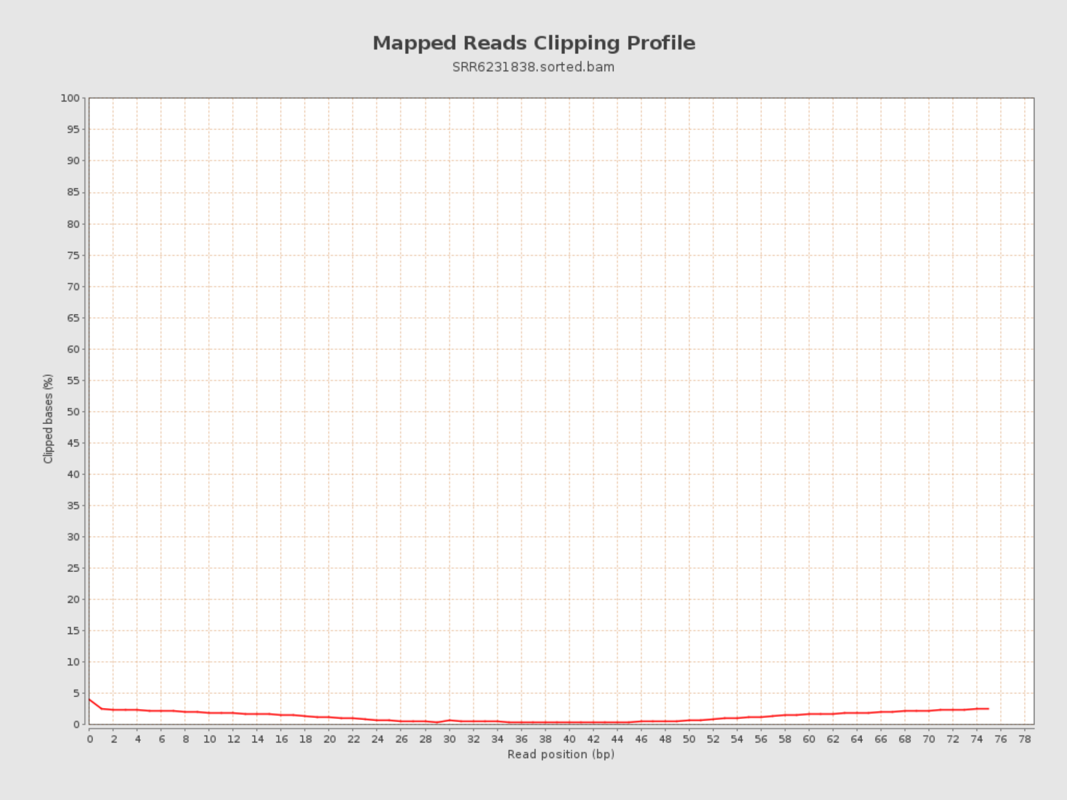
8. Results : Mapped Reads Nucleotide Content



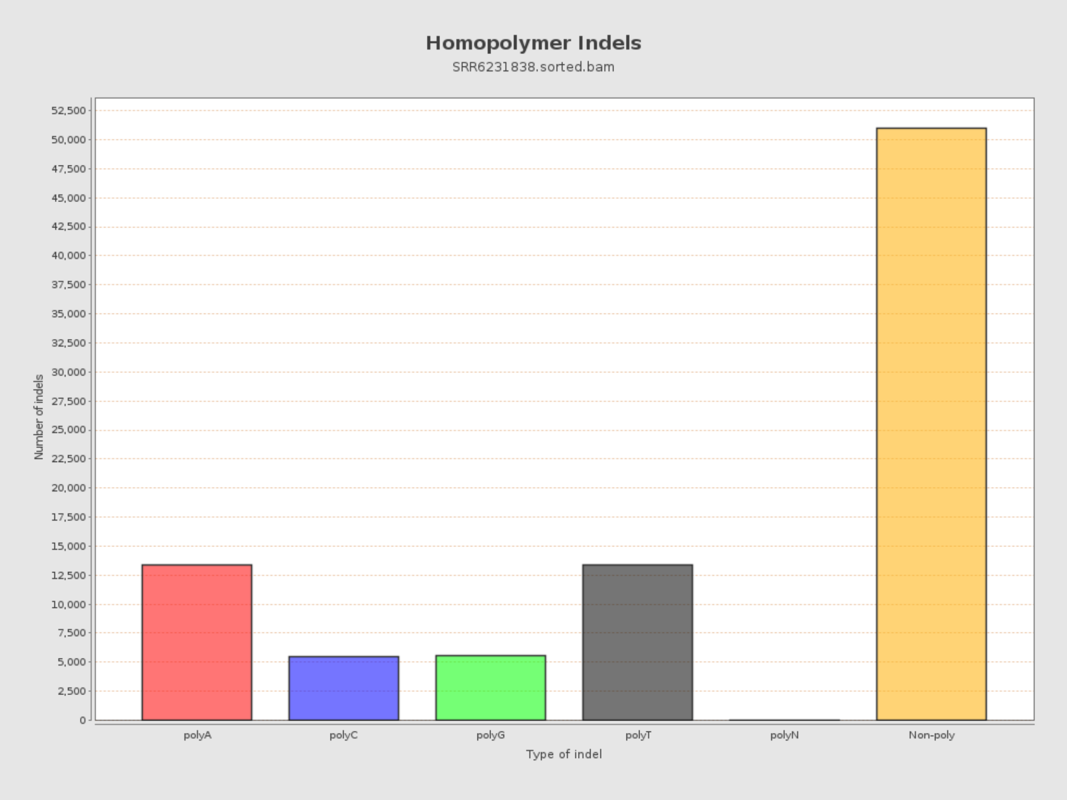
9. Results : Mapped Reads GC-content Distribution



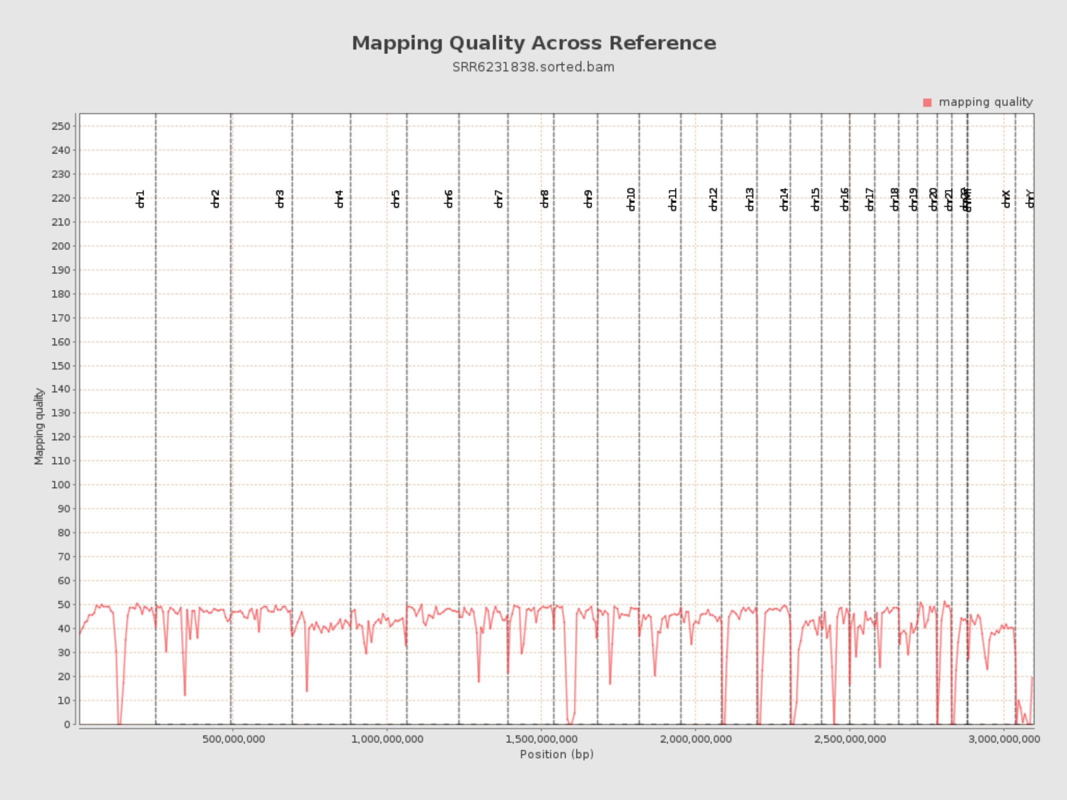
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram