Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 08:24:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231857.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_SRR6231857 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231857.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 08:24:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231857.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,653,087
Mapped reads	1,301,470 / 27.97%
Unmapped reads	3,351,617 / 72.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,558 / 0.23%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	184,778 / 3.97%
Duplication rate	10.49%
Clipped reads	669,660 / 14.39%

2.2. ACGT Content

Number/percentage of A's	23,290,652 / 27.8%
Number/percentage of C's	15,101,456 / 18.02%
Number/percentage of T's	27,209,600 / 32.47%
Number/percentage of G's	18,187,304 / 21.71%
Number/percentage of N's	2,355 / 0%
GC Percentage	39.73%

2.3. Coverage

Mean	0.0271

Standard Deviation	0.3892

2.4. Mapping Quality

Mean Mapping Quality	43.89

2.5. Mismatches and indels

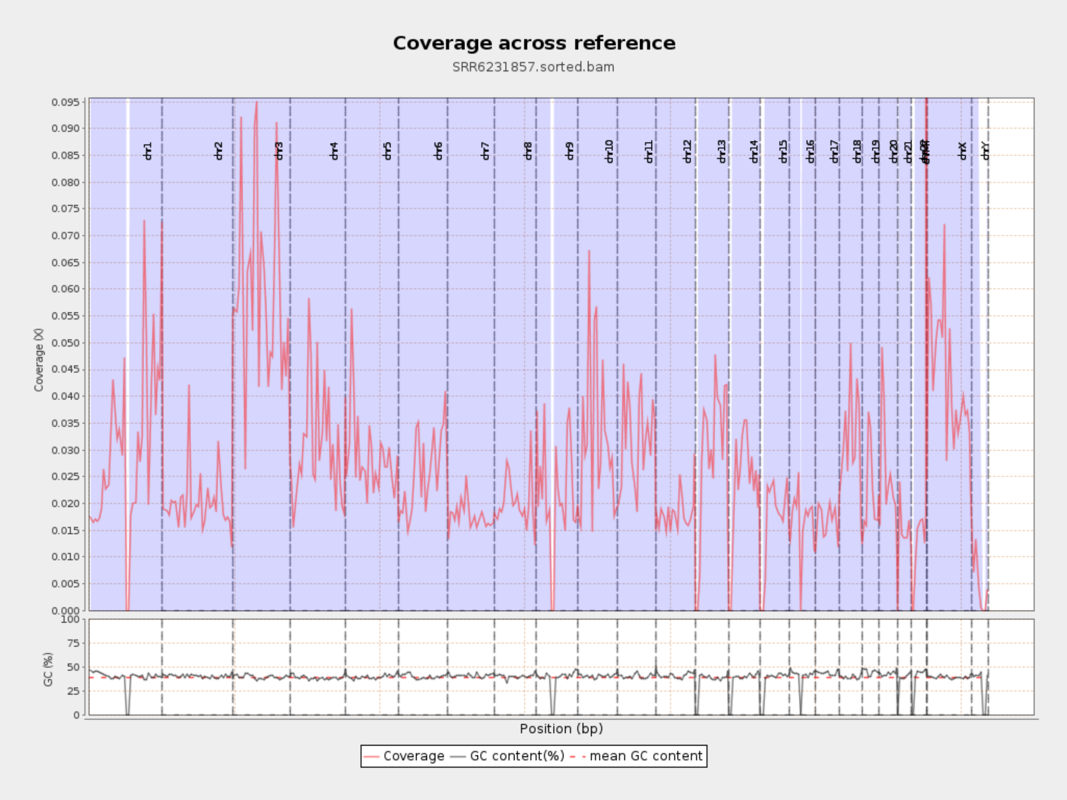
General error rate	0.78%
Mismatches	634,357
Insertions	8,442
Mapped reads with at least one insertion	0.64%
Deletions	20,620
Mapped reads with at least one deletion	1.56%
Homopolymer indels	43.64%

2.6. Chromosome stats

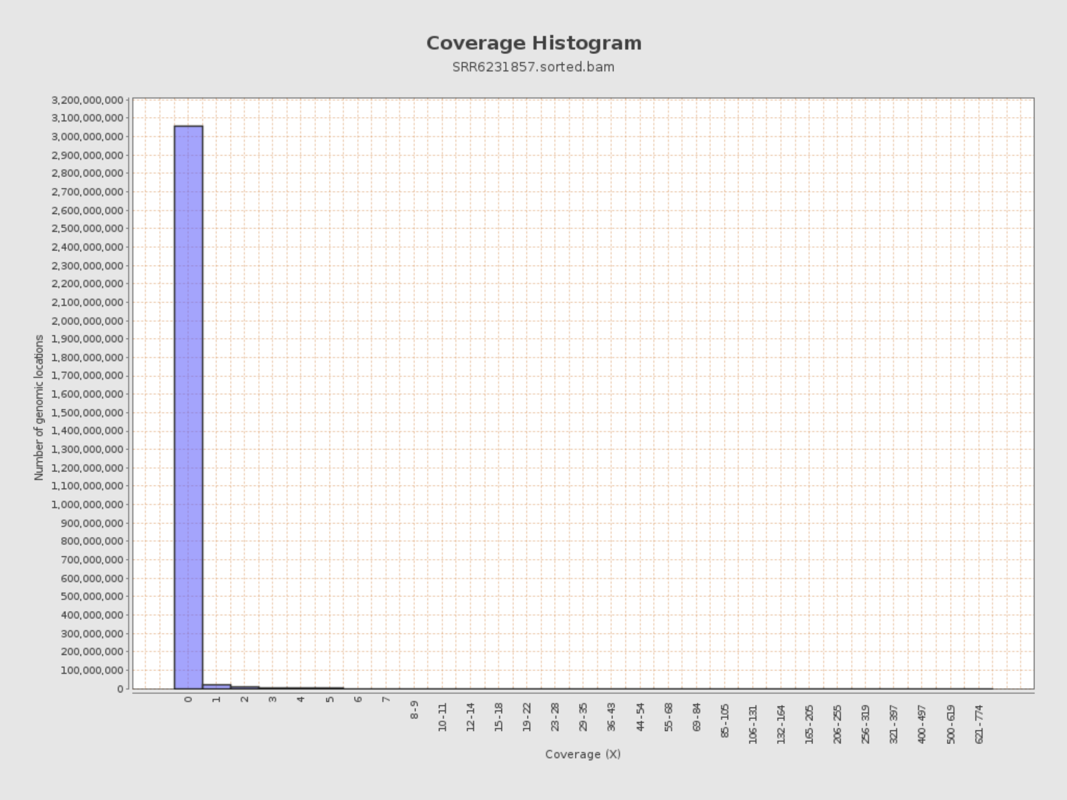
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7483932	0.03	0.7011
chr2	243199373	4905759	0.0202	0.4032
chr3	198022430	11769285	0.0594	0.4645
chr4	191154276	5819062	0.0304	0.3296
chr5	180915260	5246451	0.029	0.3182
chr6	171115067	4399671	0.0257	0.2991
chr7	159138663	2818547	0.0177	0.265

chr8	146364022	2972361	0.0203	0.4464
chr9	141213431	3032169	0.0215	0.2995
chr10	135534747	4414371	0.0326	0.472
chr11	135006516	4324157	0.032	0.3443
chr12	133851895	2422884	0.0181	0.2453
chr13	115169878	3327695	0.0289	0.3467
chr14	107349540	2492032	0.0232	0.2892
chr15	102531392	1714736	0.0167	0.2356
chr16	90354753	1506058	0.0167	0.2363
chr17	81195210	1351487	0.0166	0.2337
chr18	78077248	2528898	0.0324	0.4604
chr19	59128983	1323628	0.0224	0.438
chr20	63025520	1665602	0.0264	0.2997
chr21	48129895	693889	0.0144	0.2175
chr22	51304566	579362	0.0113	0.1814
chrMT	16571	20474	1.2355	1.835
chrX	155270560	6732241	0.0434	0.4064
chrY	59373566	283080	0.0048	0.1183

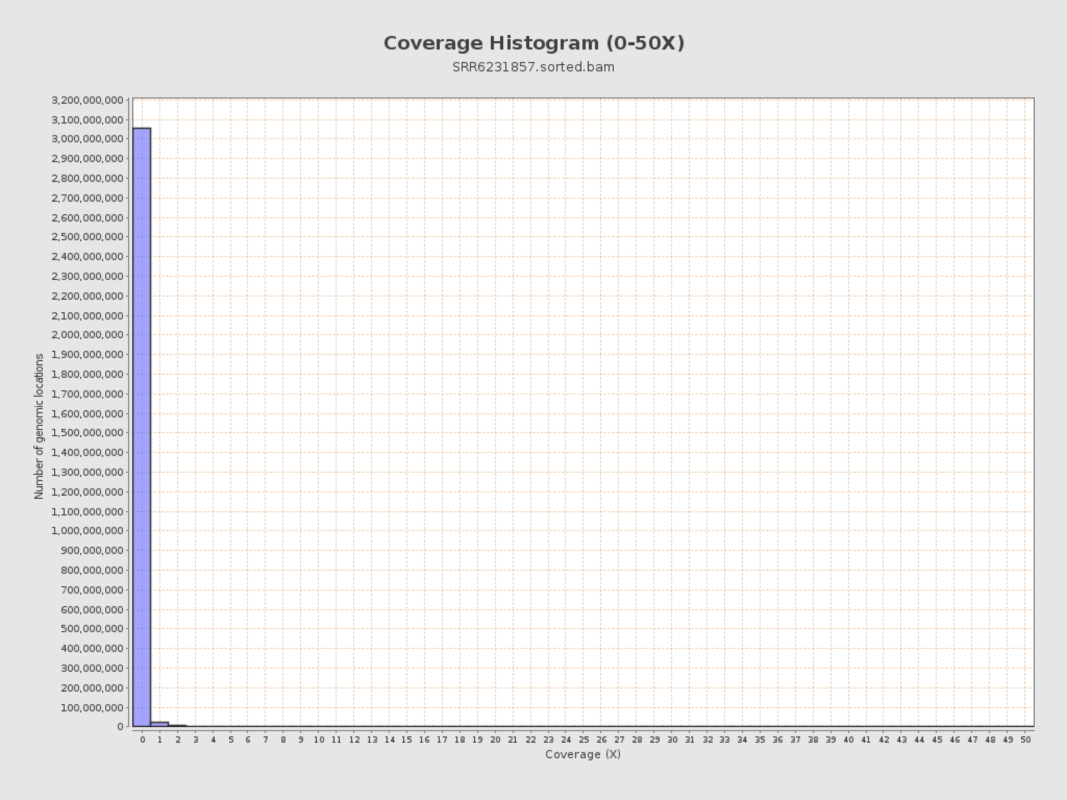
3. Results : Coverage across reference



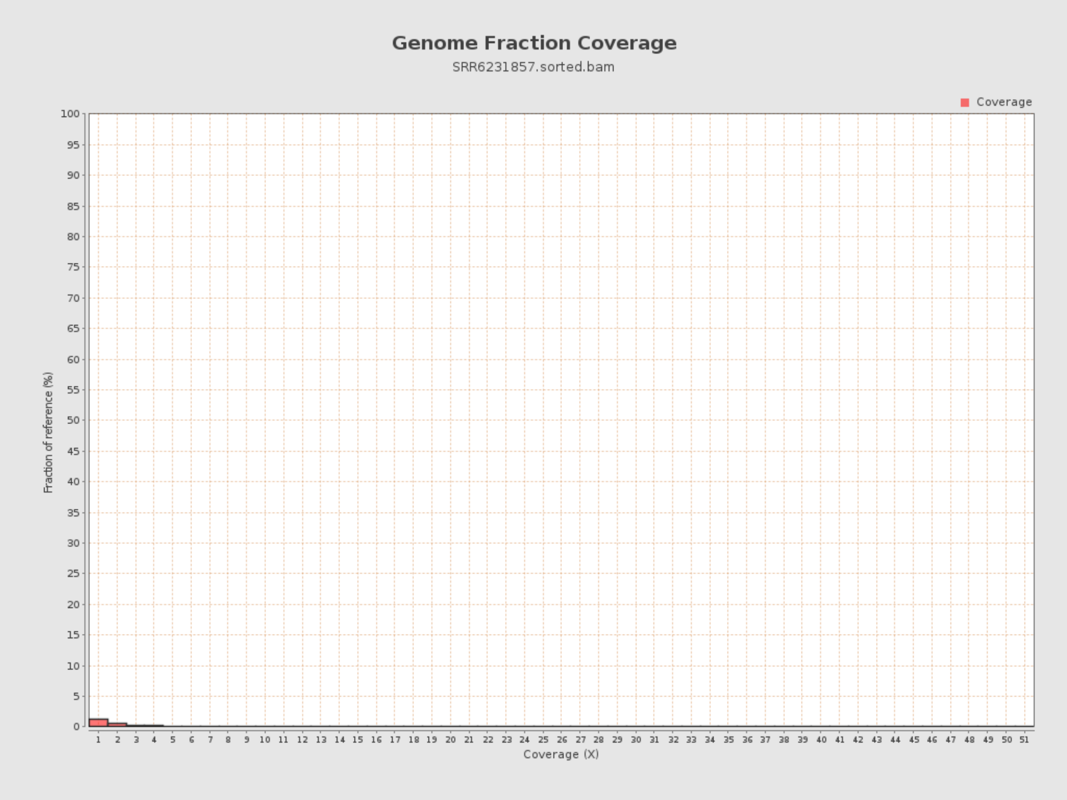
4. Results : Coverage Histogram



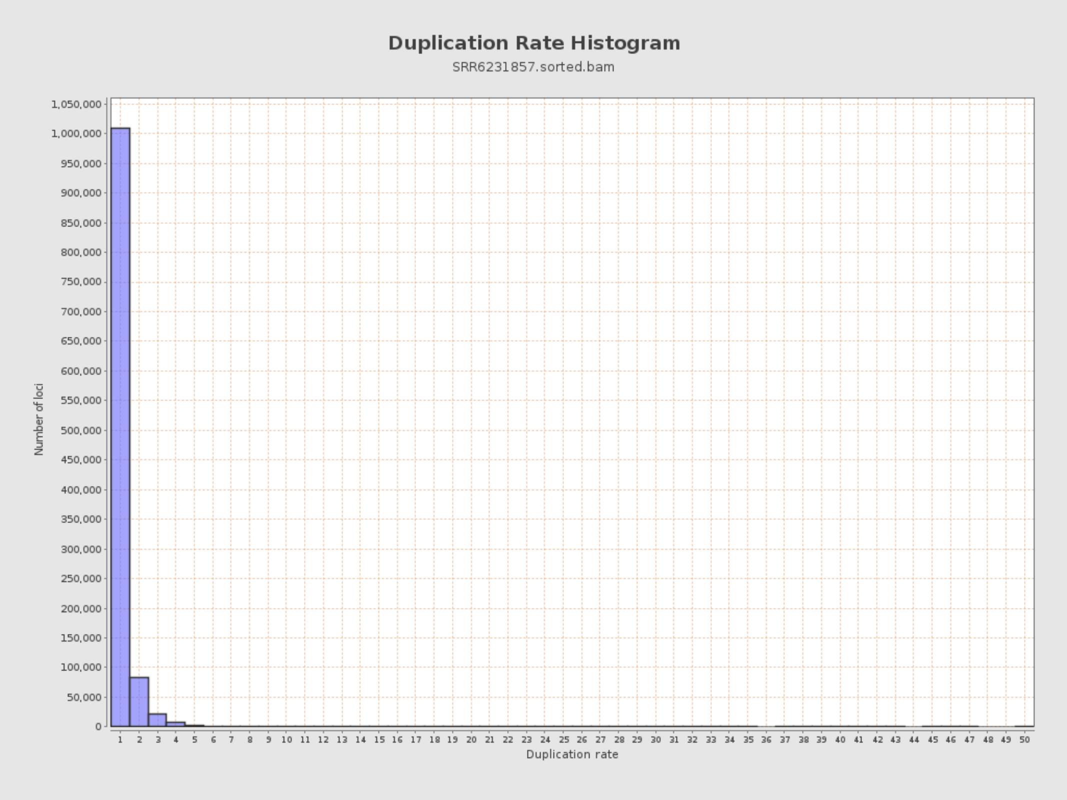
5. Results : Coverage Histogram (0-50X)



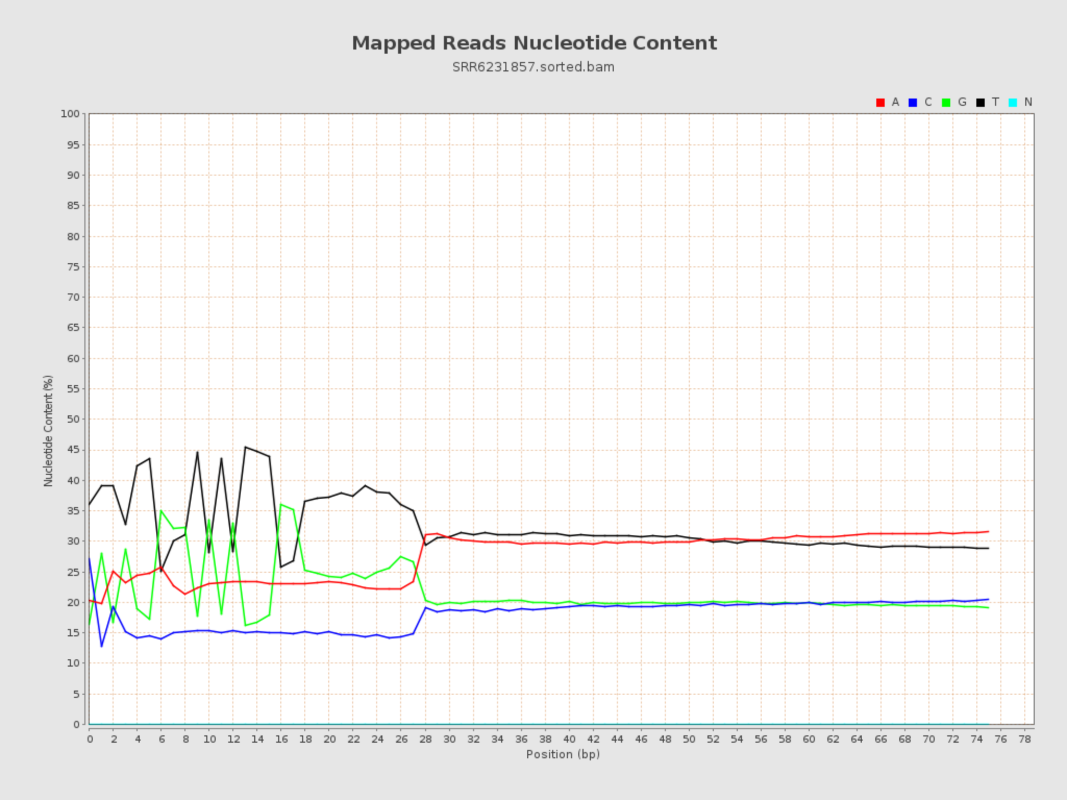
6. Results : Genome Fraction Coverage



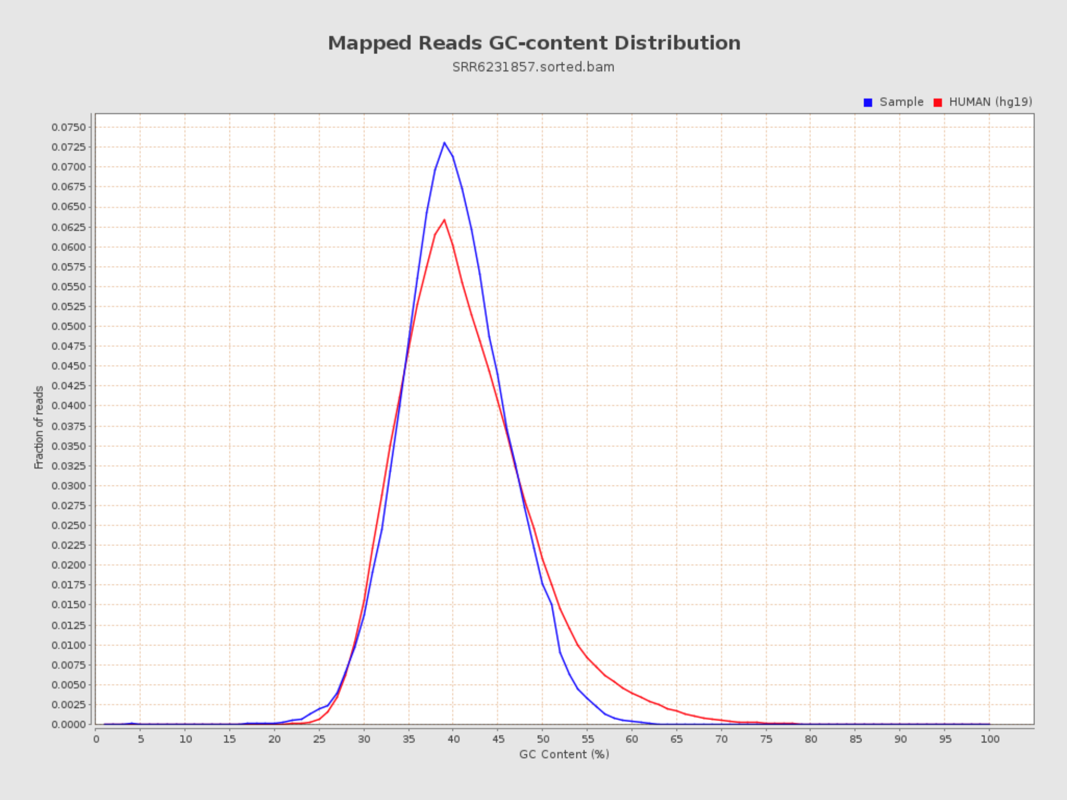
7. Results : Duplication Rate Histogram



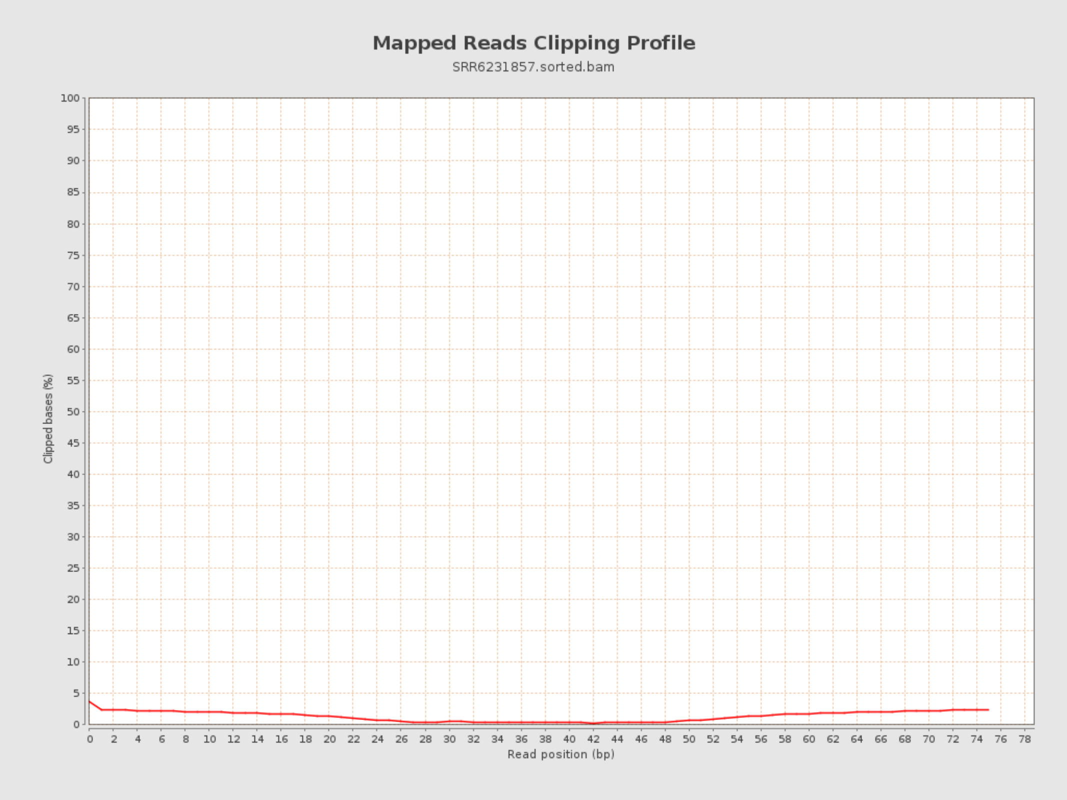
8. Results : Mapped Reads Nucleotide Content



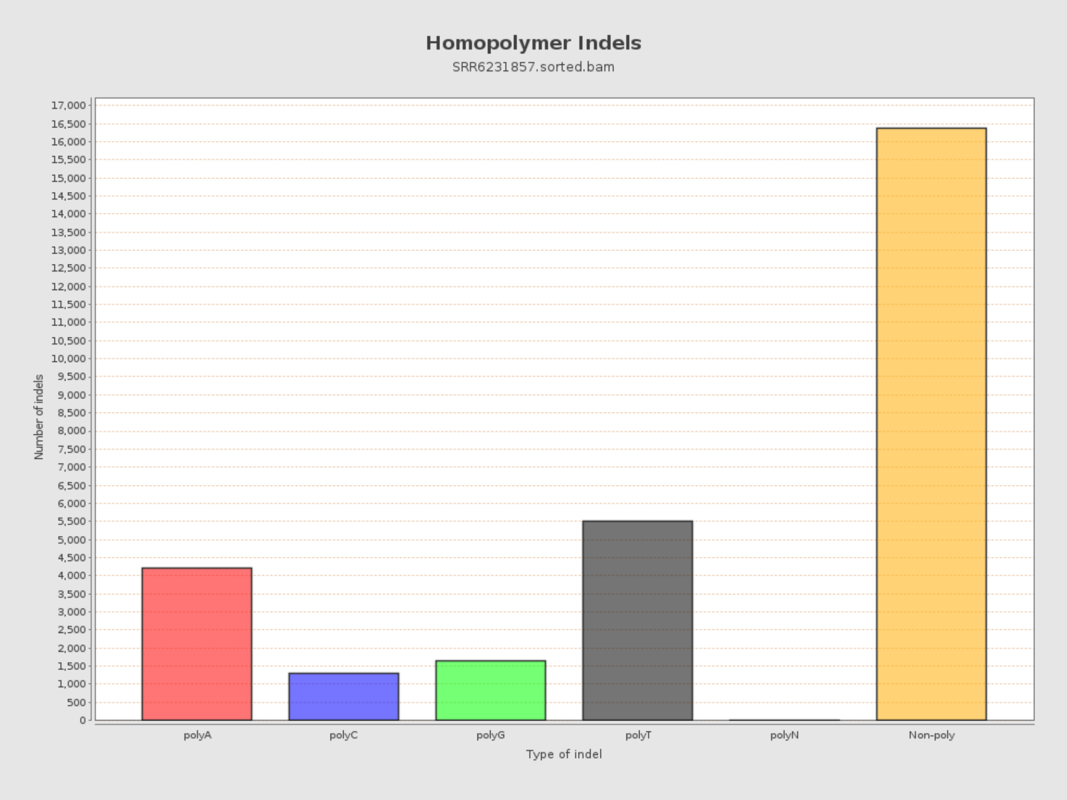
9. Results : Mapped Reads GC-content Distribution



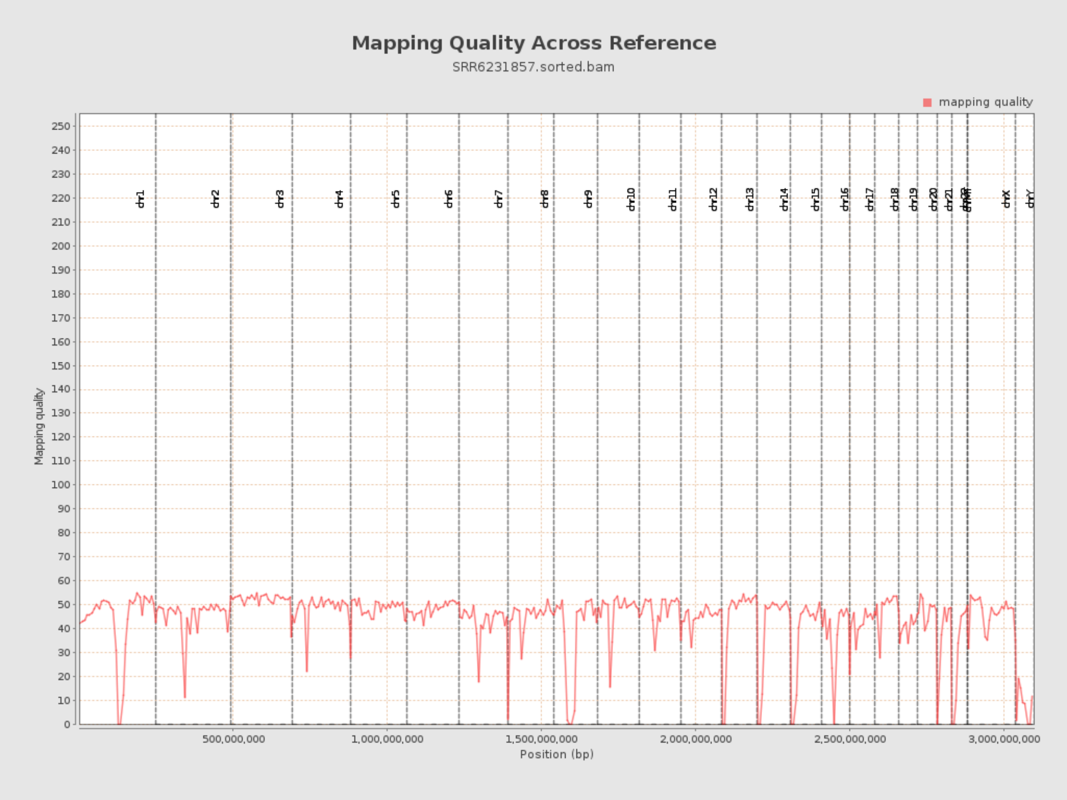
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram