Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 04:19:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081237.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_SRR3081237 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081237.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 04:19:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081237.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,420,814
Mapped reads	2,109,111 / 87.12%
Unmapped reads	311,703 / 12.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,851 / 1.19%
Read min/max/mean length	30 / 76 / 76.42
Duplicated reads (estimated)	107,920 / 4.46%
Duplication rate	4.32%
Clipped reads	1,232,747 / 50.92%

2.2. ACGT Content

Number/percentage of A's	38,982,285 / 28.92%
Number/percentage of C's	26,190,492 / 19.43%
Number/percentage of T's	41,021,598 / 30.43%
Number/percentage of G's	28,598,335 / 21.22%
Number/percentage of N's	8,648 / 0.01%
GC Percentage	40.64%

2.3. Coverage

Mean	0.0436

Standard Deviation	0.3198

2.4. Mapping Quality

Mean Mapping Quality	45.06

2.5. Mismatches and indels

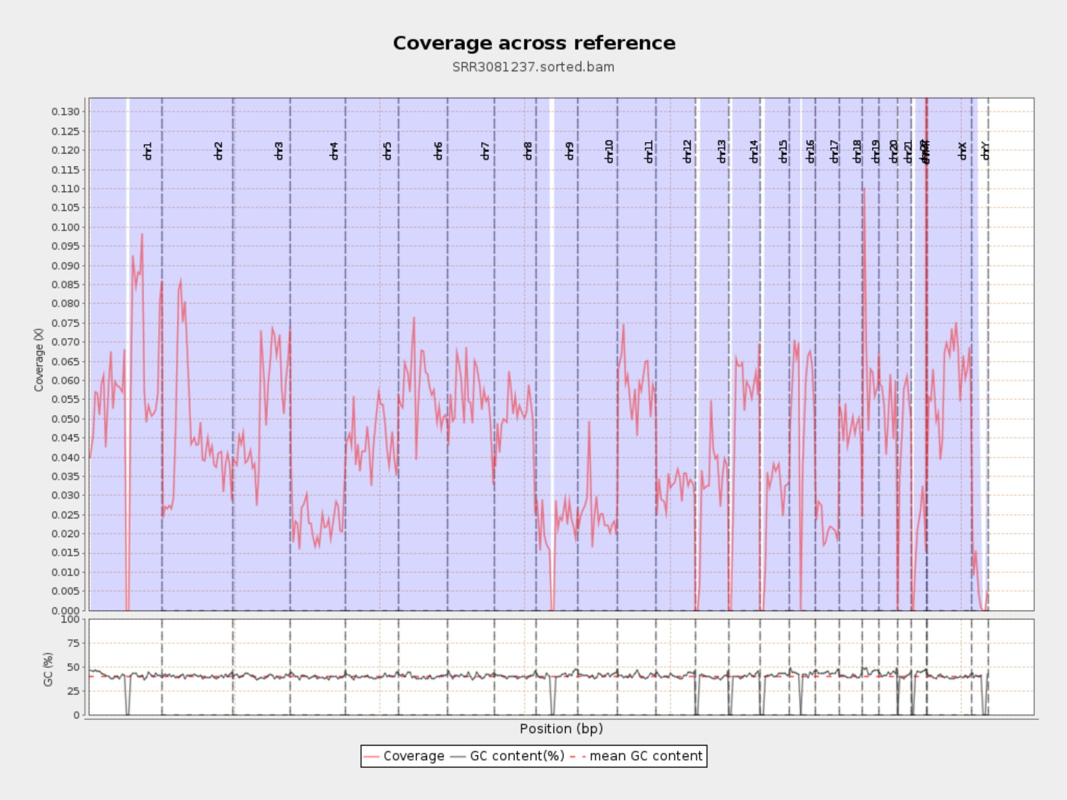
General error rate	0.9%
Mismatches	1,196,957
Insertions	9,726
Mapped reads with at least one insertion	0.46%
Deletions	30,023
Mapped reads with at least one deletion	1.41%
Homopolymer indels	47.98%

2.6. Chromosome stats

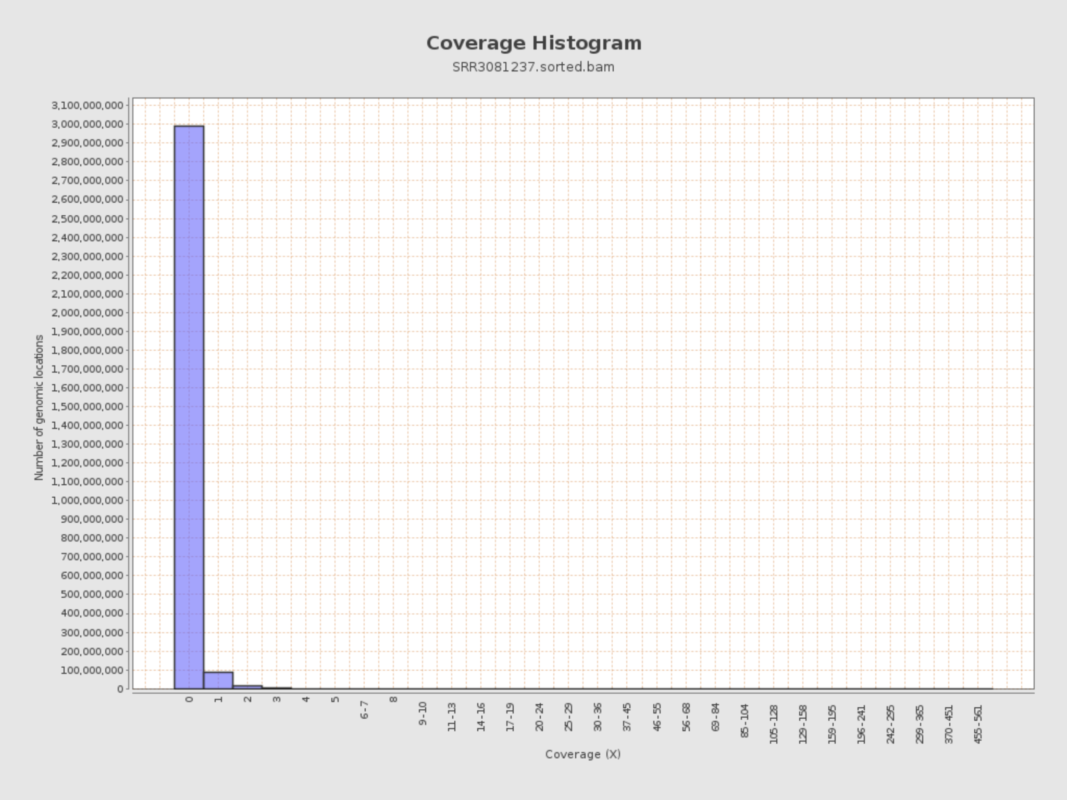
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14487962	0.0581	0.5278
chr2	243199373	10906461	0.0448	0.3506
chr3	198022430	10265616	0.0518	0.2776
chr4	191154276	4428077	0.0232	0.189
chr5	180915260	7993280	0.0442	0.255
chr6	171115067	9830274	0.0574	0.3268
chr7	159138663	8824111	0.0554	0.4085

chr8	146364022	7324114	0.05	0.4004
chr9	141213431	2876122	0.0204	0.2001
chr10	135534747	3436689	0.0254	0.2881
chr11	135006516	7916580	0.0586	0.3461
chr12	133851895	4310921	0.0322	0.2183
chr13	115169878	3603583	0.0313	0.215
chr14	107349540	5357774	0.0499	0.2745
chr15	102531392	2788248	0.0272	0.2065
chr16	90354753	4996304	0.0553	0.2918
chr17	81195210	1764839	0.0217	0.1926
chr18	78077248	3773277	0.0483	0.3704
chr19	59128983	3805698	0.0644	0.4187
chr20	63025520	3313620	0.0526	0.2804
chr21	48129895	2201197	0.0457	0.2651
chr22	51304566	920320	0.0179	0.1595
chrMT	16571	39720	2.397	2.5725
chrX	155270560	9319988	0.06	0.309
chrY	59373566	365454	0.0062	0.1091

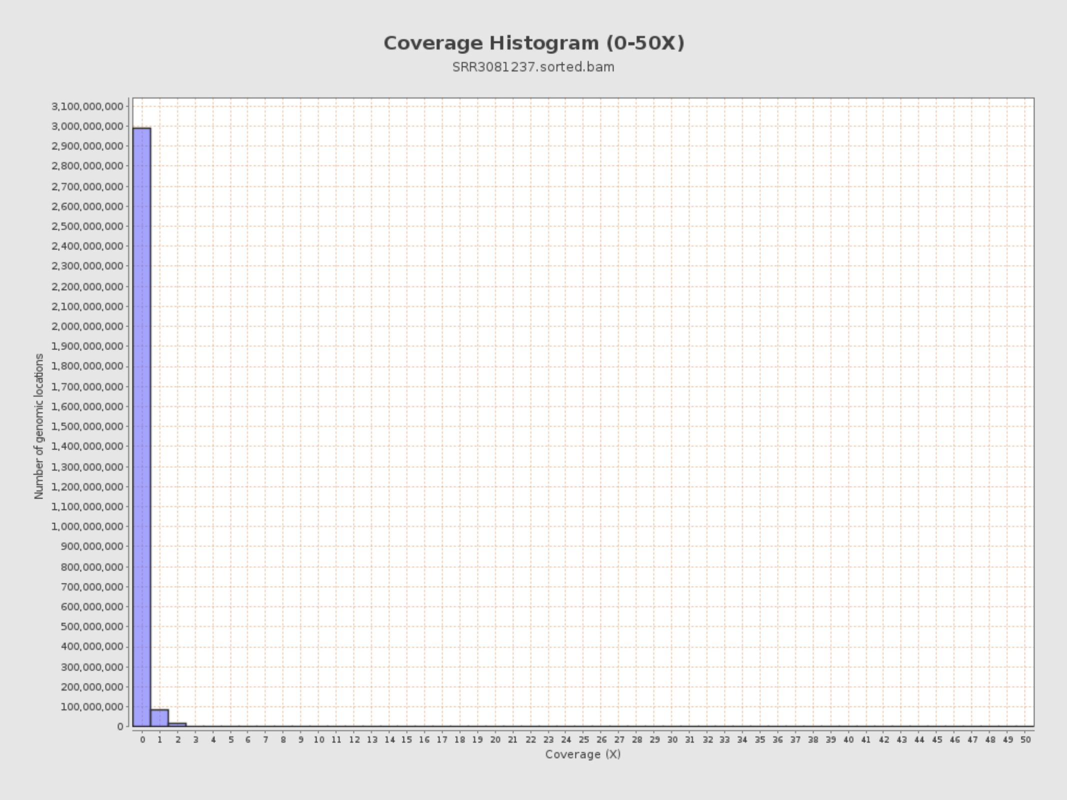
3. Results : Coverage across reference



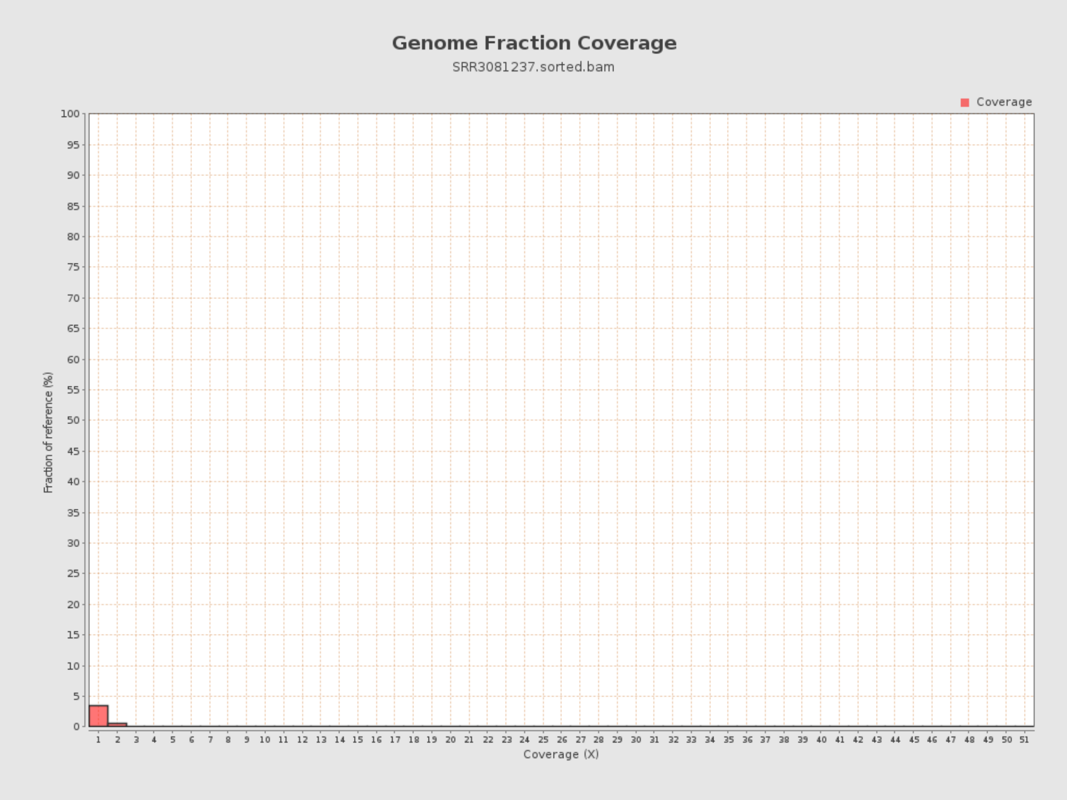
4. Results : Coverage Histogram



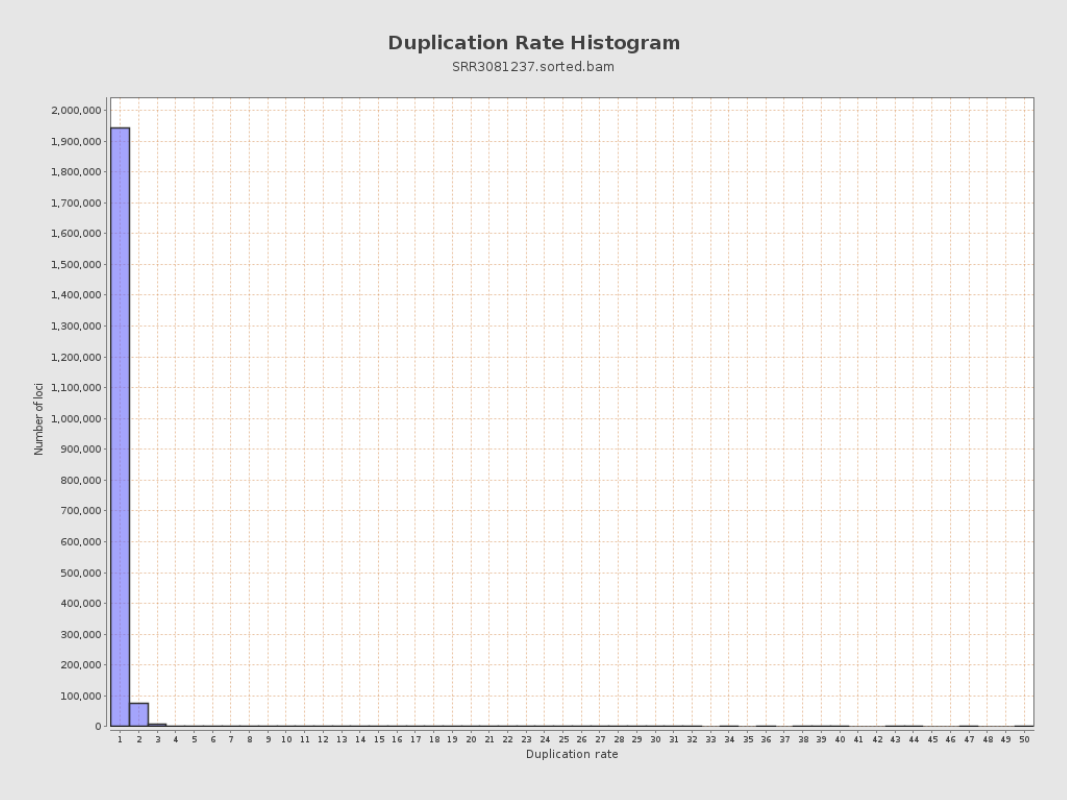
5. Results : Coverage Histogram (0-50X)



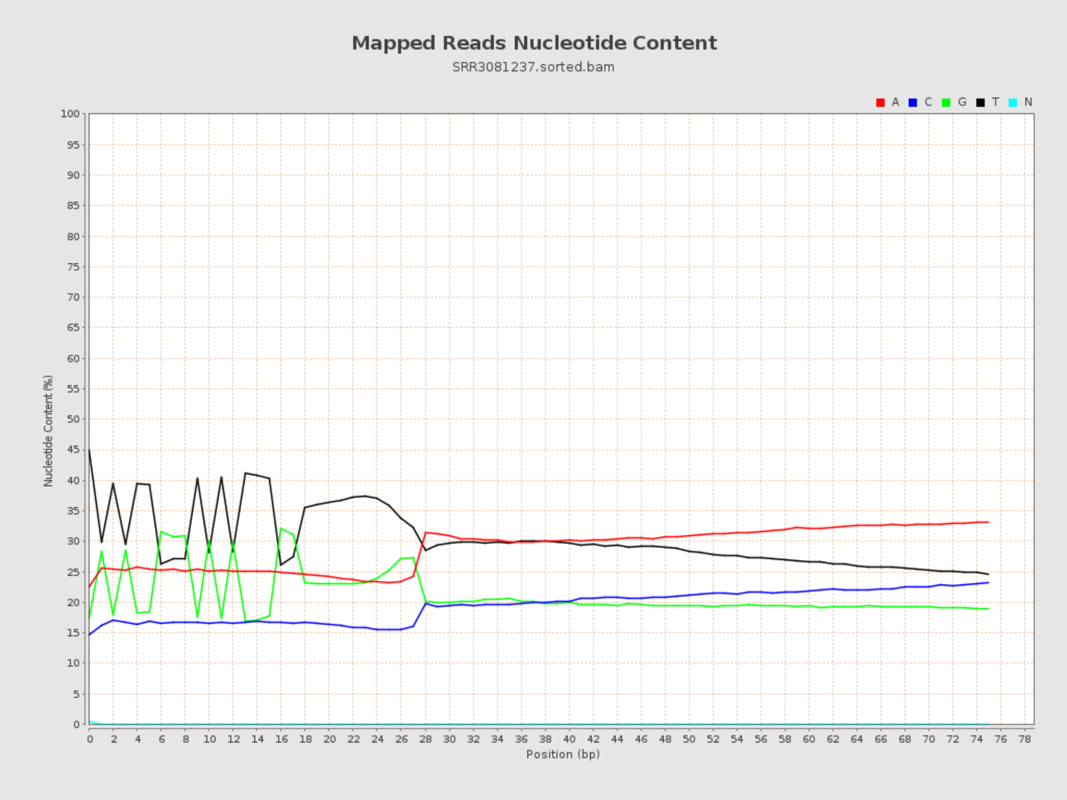
6. Results : Genome Fraction Coverage



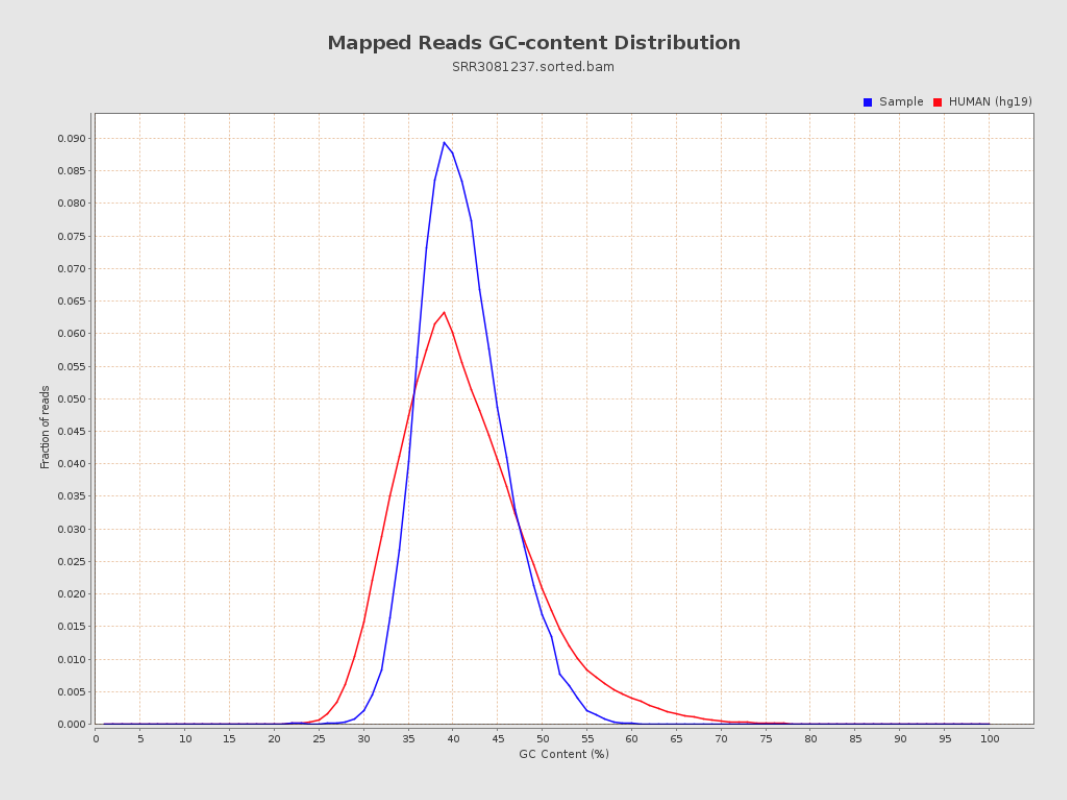
7. Results : Duplication Rate Histogram



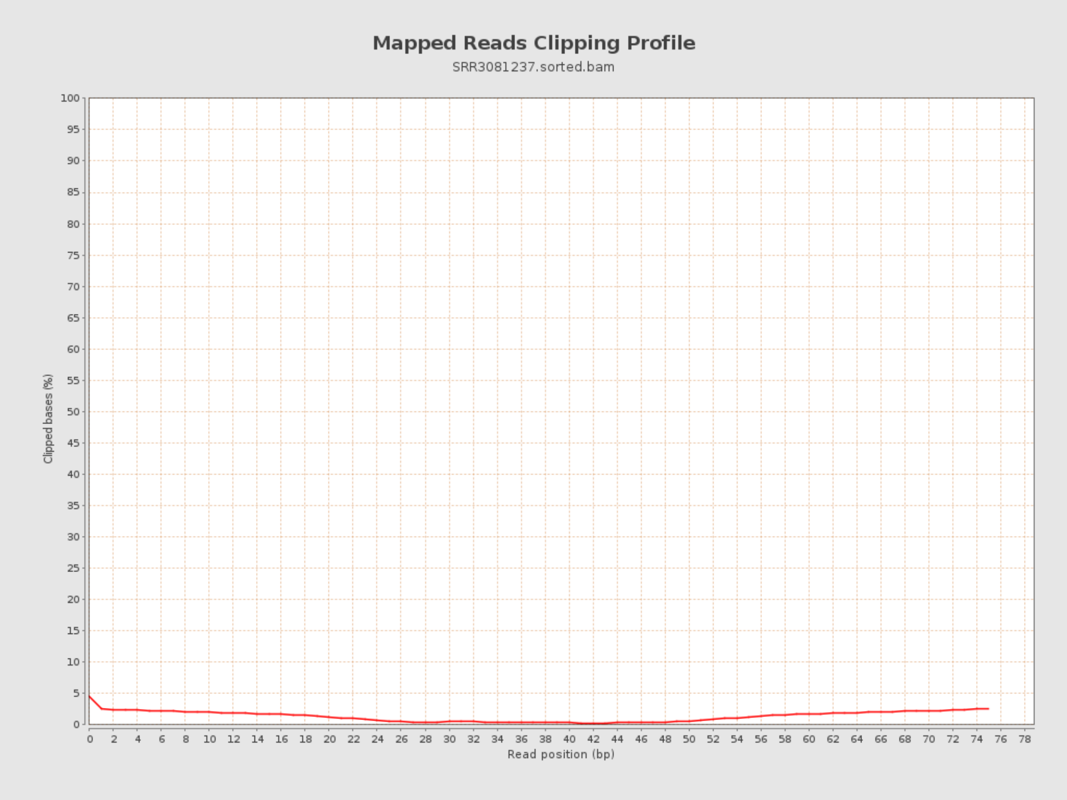
8. Results : Mapped Reads Nucleotide Content



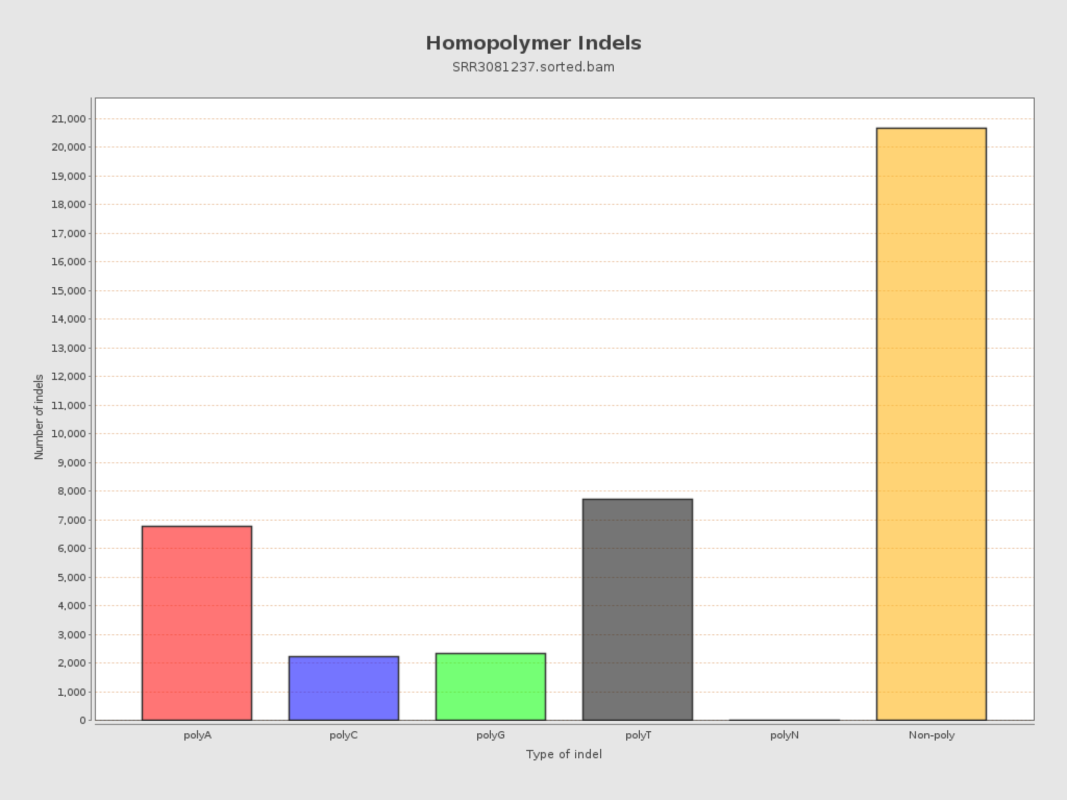
9. Results : Mapped Reads GC-content Distribution



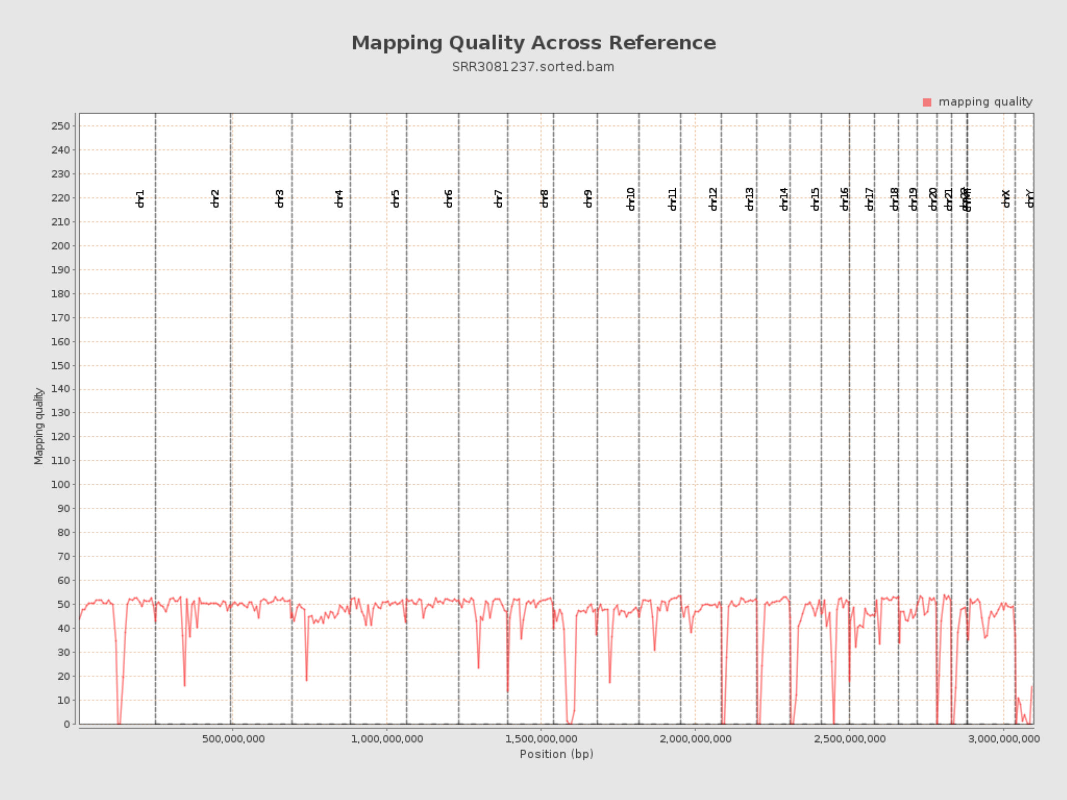
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram