Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 20:11:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818837.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_SRR1818837 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818837.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 20:11:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818837.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,576,195
Mapped reads	1,522,700 / 96.61%
Unmapped reads	53,495 / 3.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,413 / 1.68%
Read min/max/mean length	30 / 101 / 101.65
Duplicated reads (estimated)	382,733 / 24.28%
Duplication rate	21.61%
Clipped reads	1,535,331 / 97.41%

2.2. ACGT Content

Number/percentage of A's	41,557,499 / 29.52%
Number/percentage of C's	29,032,187 / 20.63%
Number/percentage of T's	40,352,962 / 28.67%
Number/percentage of G's	29,816,773 / 21.18%
Number/percentage of N's	2,310 / 0%
GC Percentage	41.81%

2.3. Coverage

Mean	0.0455

Standard Deviation	0.4927

2.4. Mapping Quality

Mean Mapping Quality	49.3

2.5. Mismatches and indels

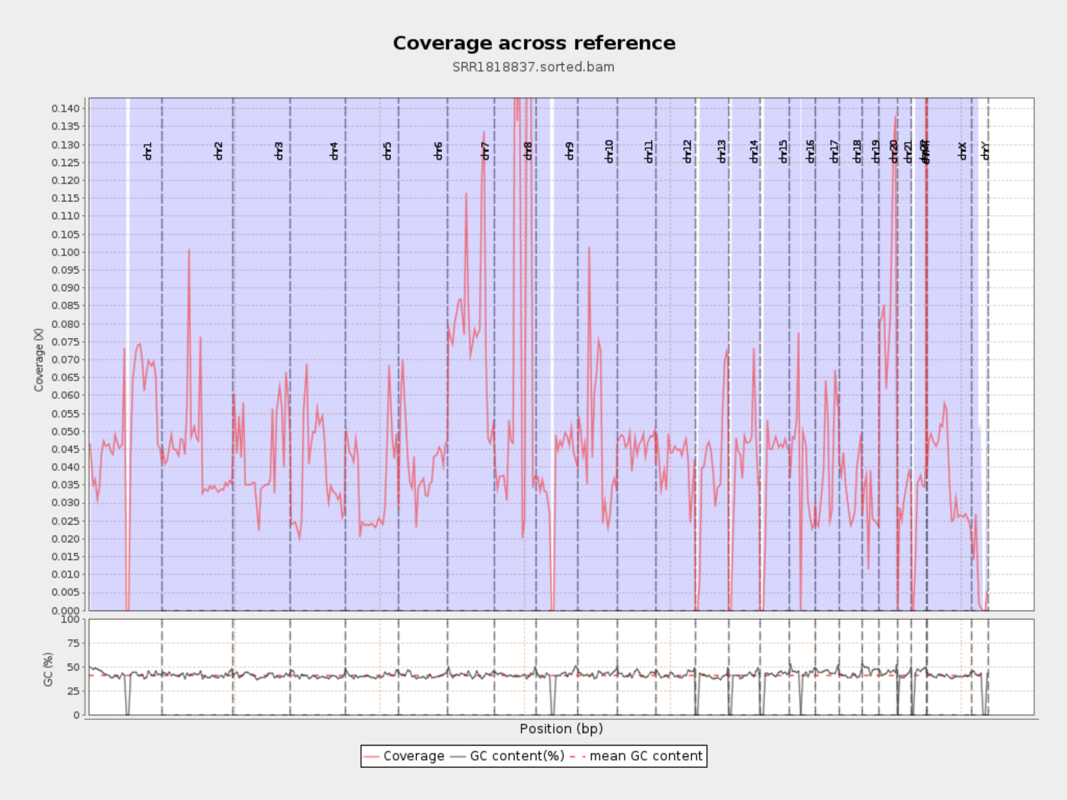
General error rate	0.63%
Mismatches	832,767
Insertions	24,111
Mapped reads with at least one insertion	1.54%
Deletions	45,581
Mapped reads with at least one deletion	2.93%
Homopolymer indels	39.03%

2.6. Chromosome stats

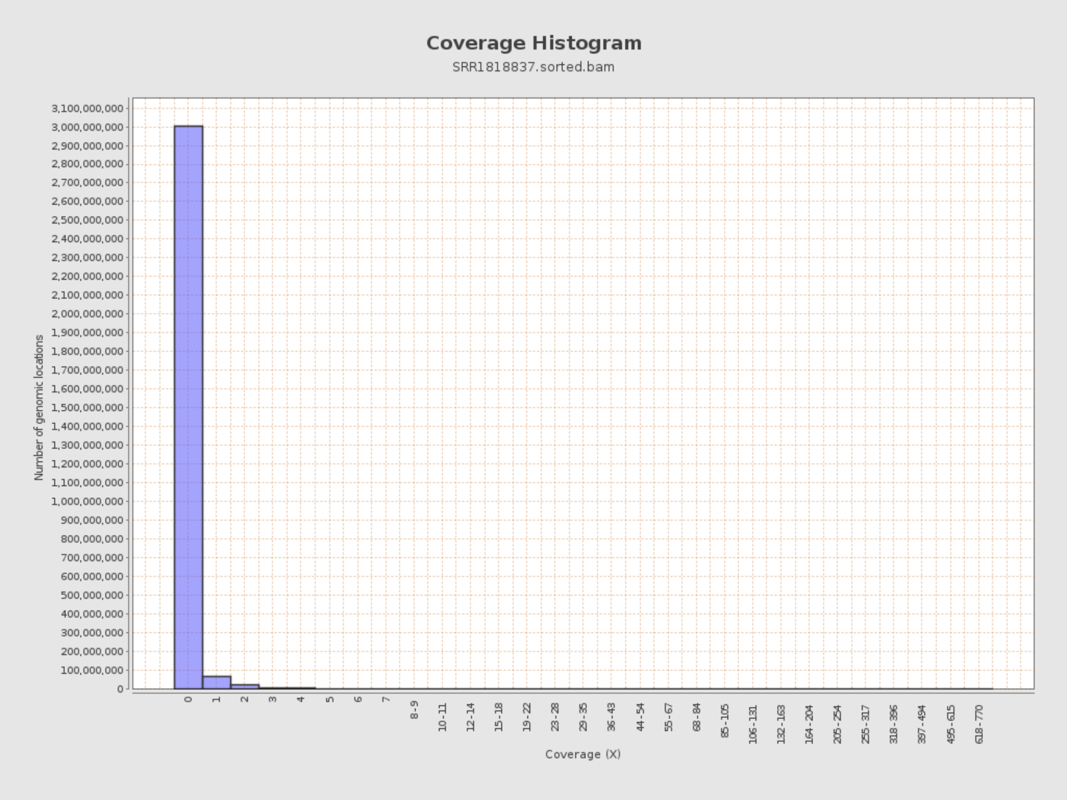
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12503845	0.0502	0.6736
chr2	243199373	10696510	0.044	0.7181
chr3	198022430	8669377	0.0438	0.2916
chr4	191154276	7262754	0.038	0.3209
chr5	180915260	6441905	0.0356	0.2739
chr6	171115067	7035826	0.0411	0.301
chr7	159138663	12853367	0.0808	0.9573

chr8	146364022	12739307	0.087	0.5012
chr9	141213431	5254586	0.0372	0.4324
chr10	135534747	6496121	0.0479	0.6489
chr11	135006516	6330039	0.0469	0.3473
chr12	133851895	5604458	0.0419	0.2878
chr13	115169878	4468578	0.0388	0.2724
chr14	107349540	4232304	0.0394	0.3081
chr15	102531392	3906608	0.0381	0.2697
chr16	90354753	3493753	0.0387	0.5135
chr17	81195210	3468547	0.0427	0.3476
chr18	78077248	2783998	0.0357	0.4868
chr19	59128983	1654424	0.028	0.5748
chr20	63025520	5691841	0.0903	0.4415
chr21	48129895	1410072	0.0293	0.2736
chr22	51304566	1288624	0.0251	0.2412
chrMT	16571	192990	11.6462	7.9656
chrX	155270560	5894526	0.038	0.3065
chrY	59373566	472666	0.008	0.5583

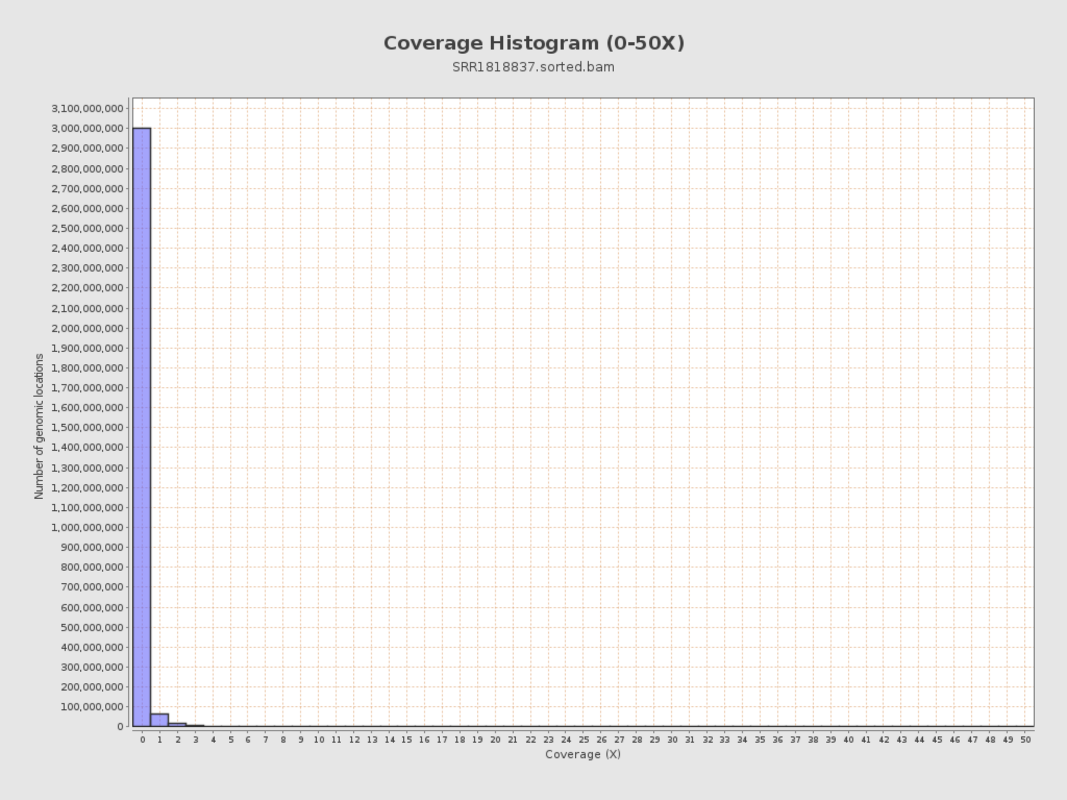
3. Results : Coverage across reference



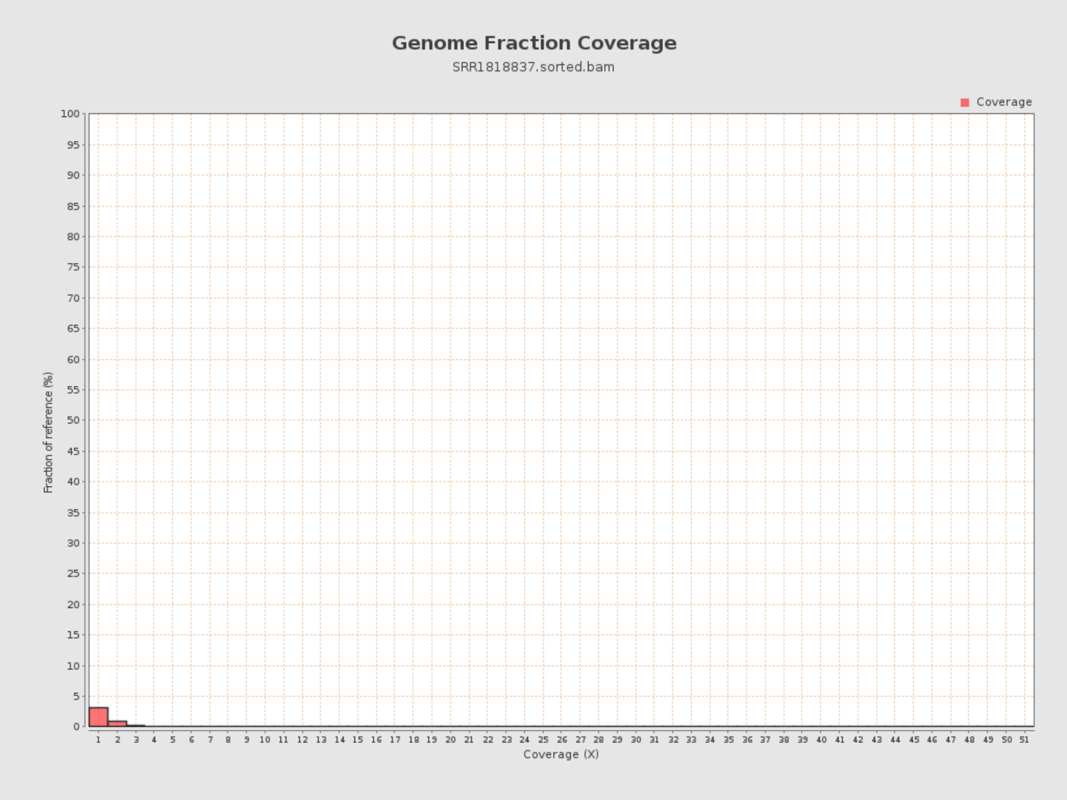
4. Results : Coverage Histogram



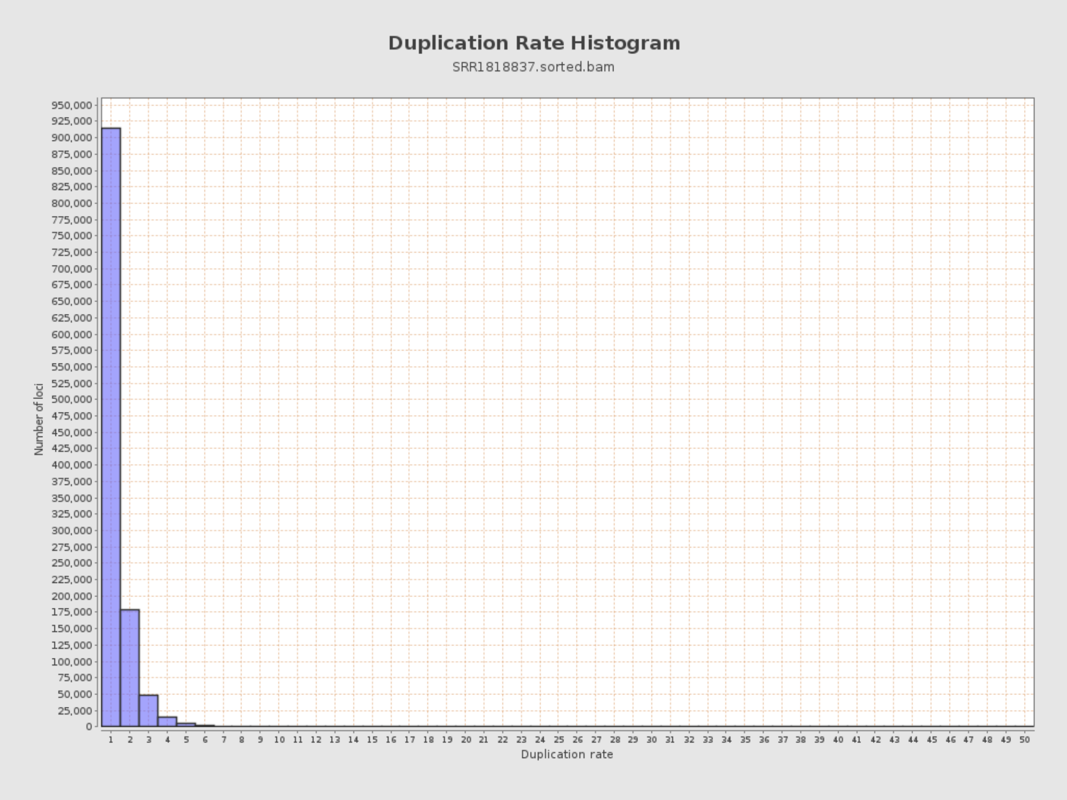
5. Results : Coverage Histogram (0-50X)



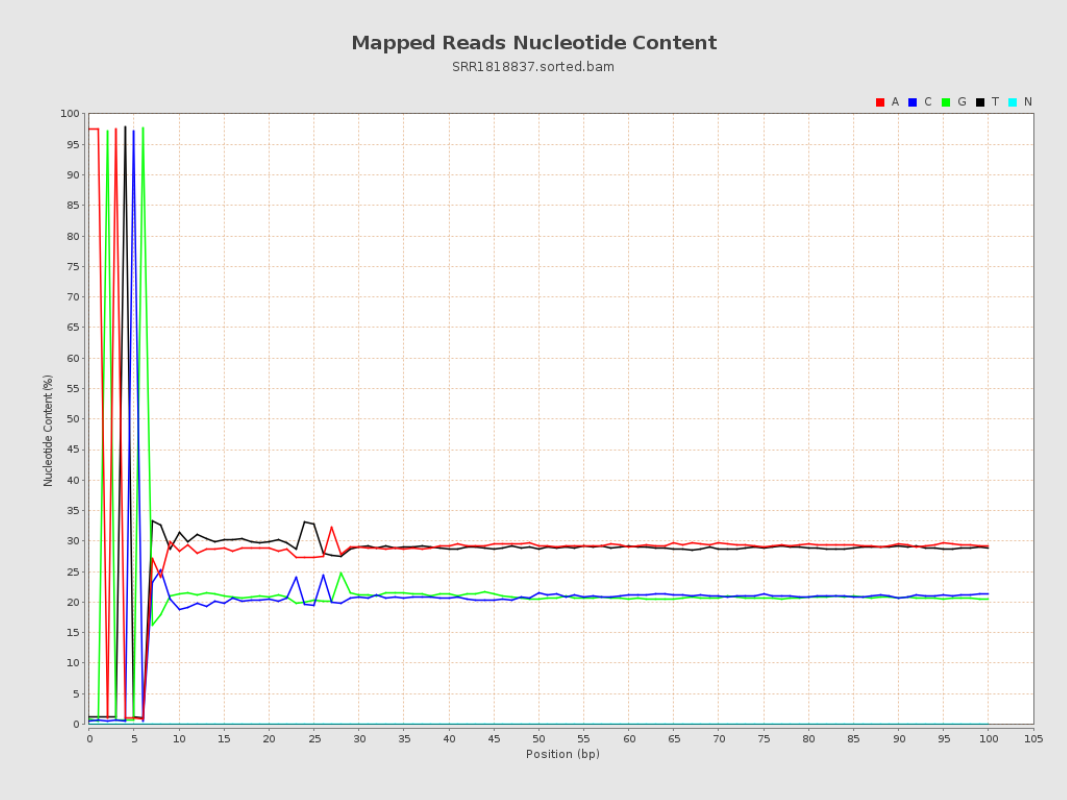
6. Results : Genome Fraction Coverage



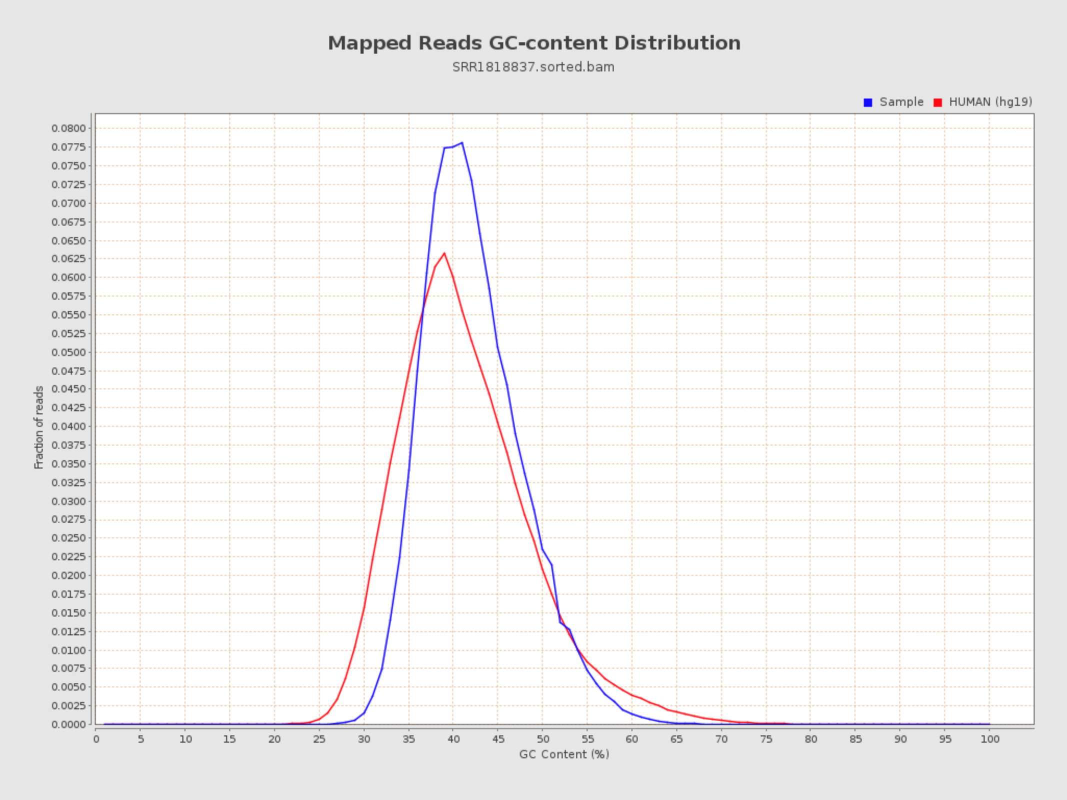
7. Results : Duplication Rate Histogram



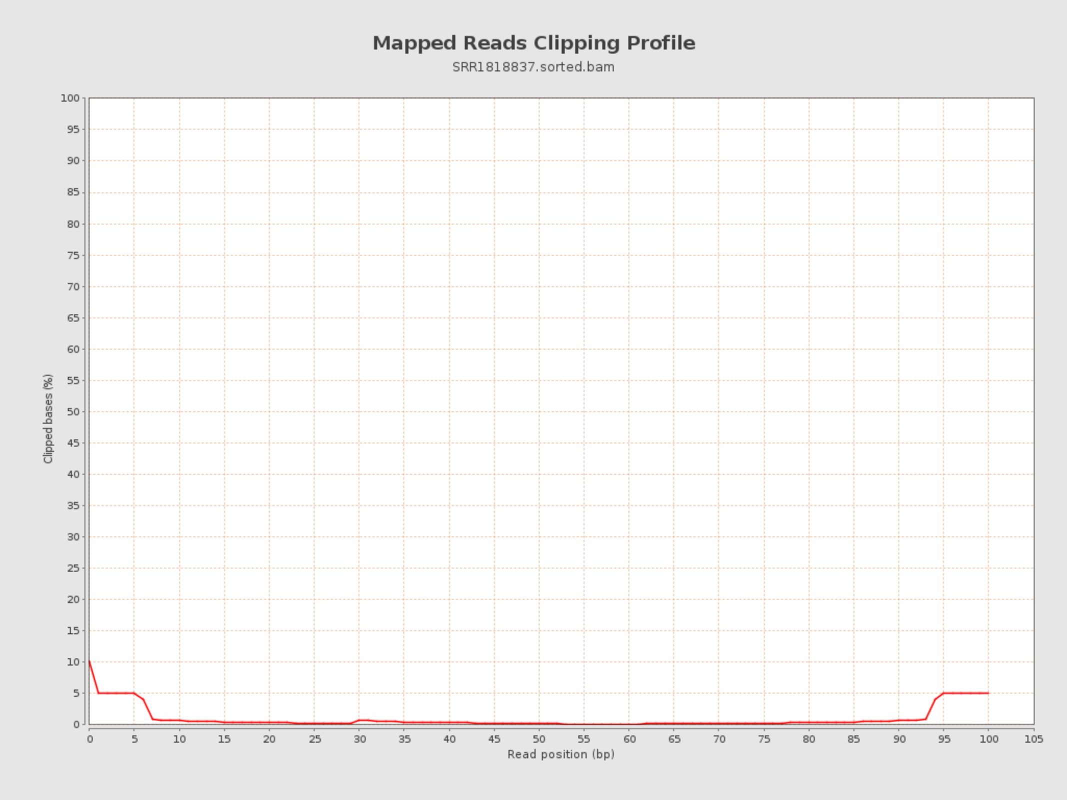
8. Results : Mapped Reads Nucleotide Content



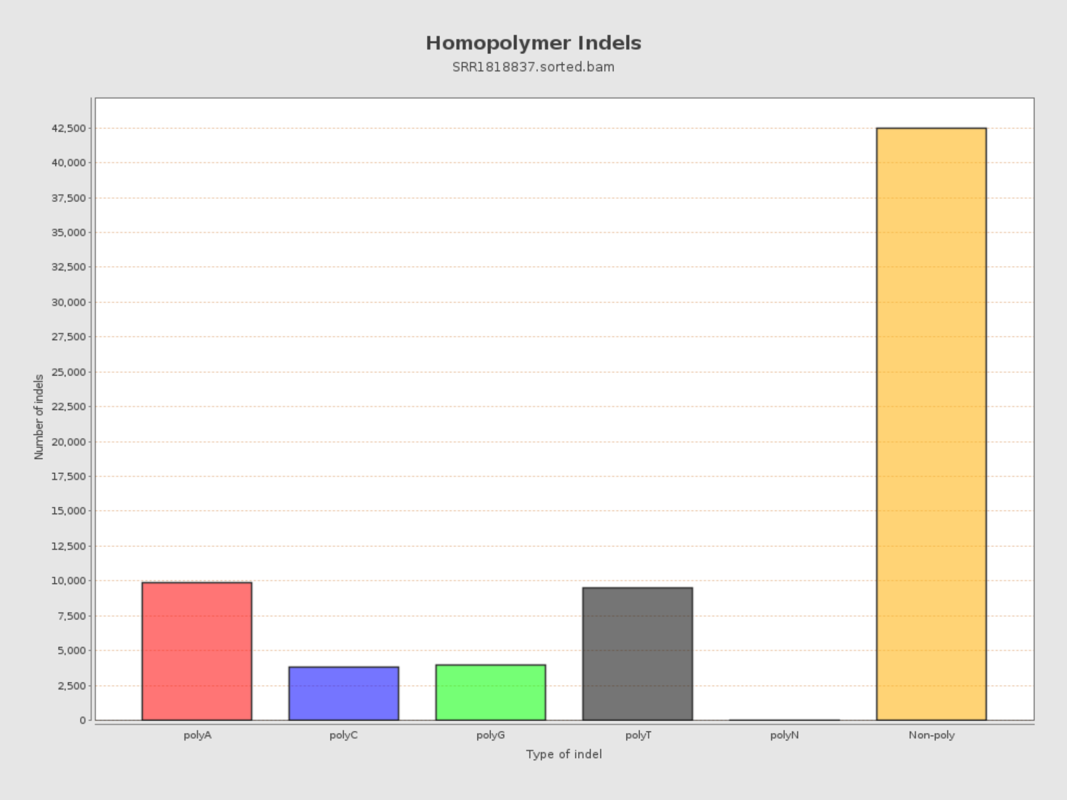
9. Results : Mapped Reads GC-content Distribution



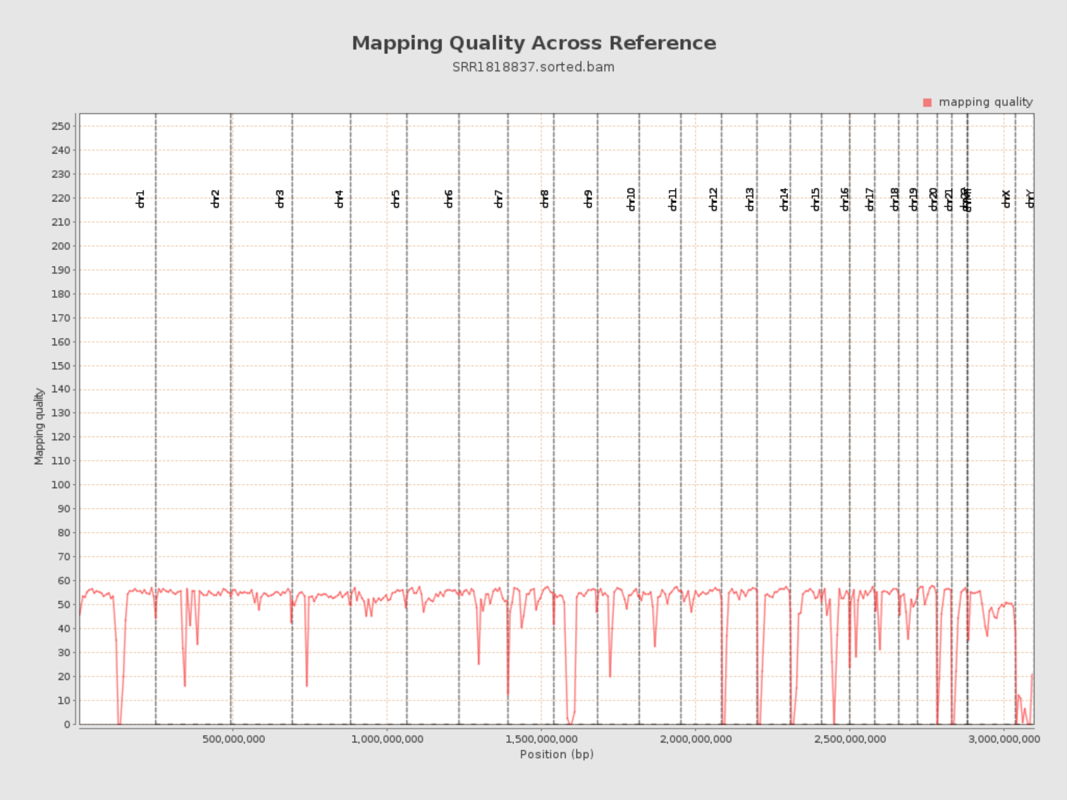
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram