Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 04:24:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081238.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_SRR3081238 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081238.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 04:23:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081238.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,421,947
Mapped reads	2,124,532 / 87.72%
Unmapped reads	297,415 / 12.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,522 / 1.1%
Read min/max/mean length	30 / 76 / 76.38
Duplicated reads (estimated)	98,783 / 4.08%
Duplication rate	3.83%
Clipped reads	1,128,354 / 46.59%

2.2. ACGT Content

Number/percentage of A's	39,322,939 / 28.45%
Number/percentage of C's	26,572,596 / 19.22%
Number/percentage of T's	42,515,953 / 30.76%
Number/percentage of G's	29,790,548 / 21.55%
Number/percentage of N's	17,782 / 0.01%
GC Percentage	40.78%

2.3. Coverage

Mean	0.0447

Standard Deviation	0.3532

2.4. Mapping Quality

Mean Mapping Quality	45.3

2.5. Mismatches and indels

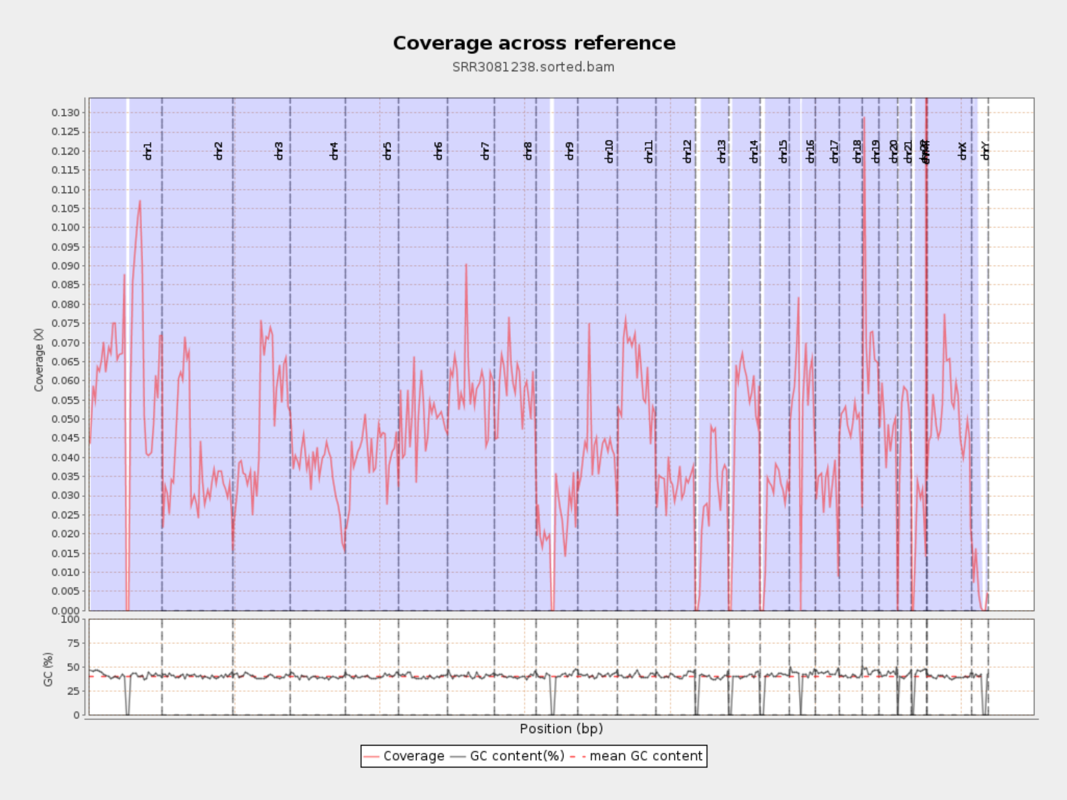
General error rate	0.93%
Mismatches	1,262,381
Insertions	10,257
Mapped reads with at least one insertion	0.48%
Deletions	31,326
Mapped reads with at least one deletion	1.46%
Homopolymer indels	47.96%

2.6. Chromosome stats

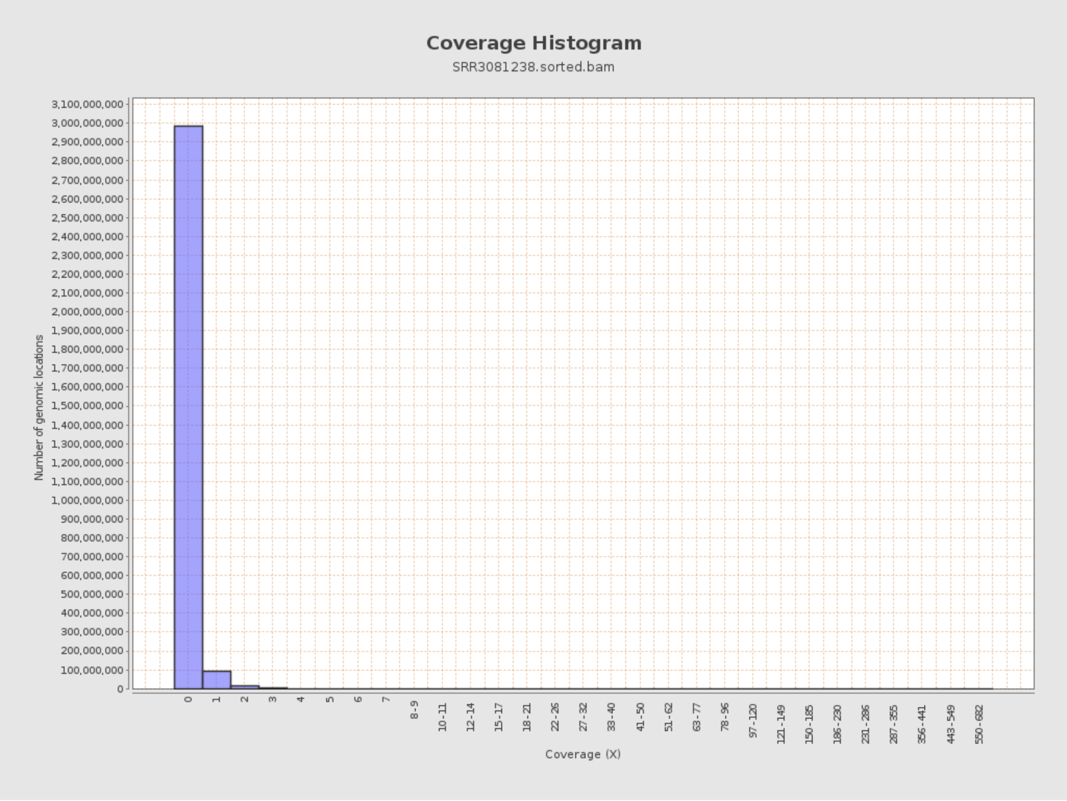
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15666337	0.0629	0.6376
chr2	243199373	9300434	0.0382	0.3537
chr3	198022430	9742153	0.0492	0.2675
chr4	191154276	6960573	0.0364	0.2299
chr5	180915260	7299470	0.0403	0.2378
chr6	171115067	8477505	0.0495	0.2944
chr7	159138663	9416601	0.0592	0.4682

chr8	146364022	8511052	0.0581	0.3938
chr9	141213431	3081355	0.0218	0.2317
chr10	135534747	5733264	0.0423	0.4035
chr11	135006516	8202753	0.0608	0.4783
chr12	133851895	4403194	0.0329	0.2164
chr13	115169878	3259535	0.0283	0.1998
chr14	107349540	5277151	0.0492	0.2716
chr15	102531392	2734650	0.0267	0.1962
chr16	90354753	5032550	0.0557	0.2891
chr17	81195210	2491939	0.0307	0.2464
chr18	78077248	3880855	0.0497	0.4121
chr19	59128983	4289007	0.0725	0.4974
chr20	63025520	2962082	0.047	0.2592
chr21	48129895	2197745	0.0457	0.2606
chr22	51304566	1035085	0.0202	0.1647
chrMT	16571	14770	0.8913	1.153
chrX	155270560	7966983	0.0513	0.2971
chrY	59373566	334001	0.0056	0.1065

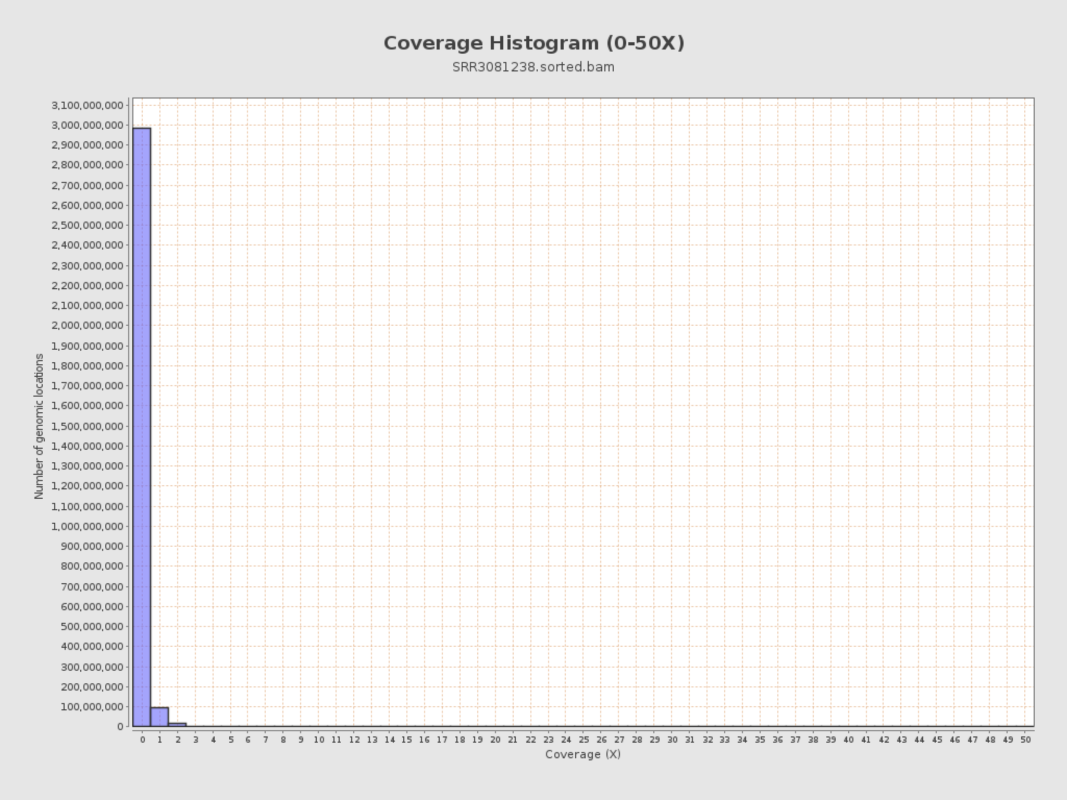
3. Results : Coverage across reference



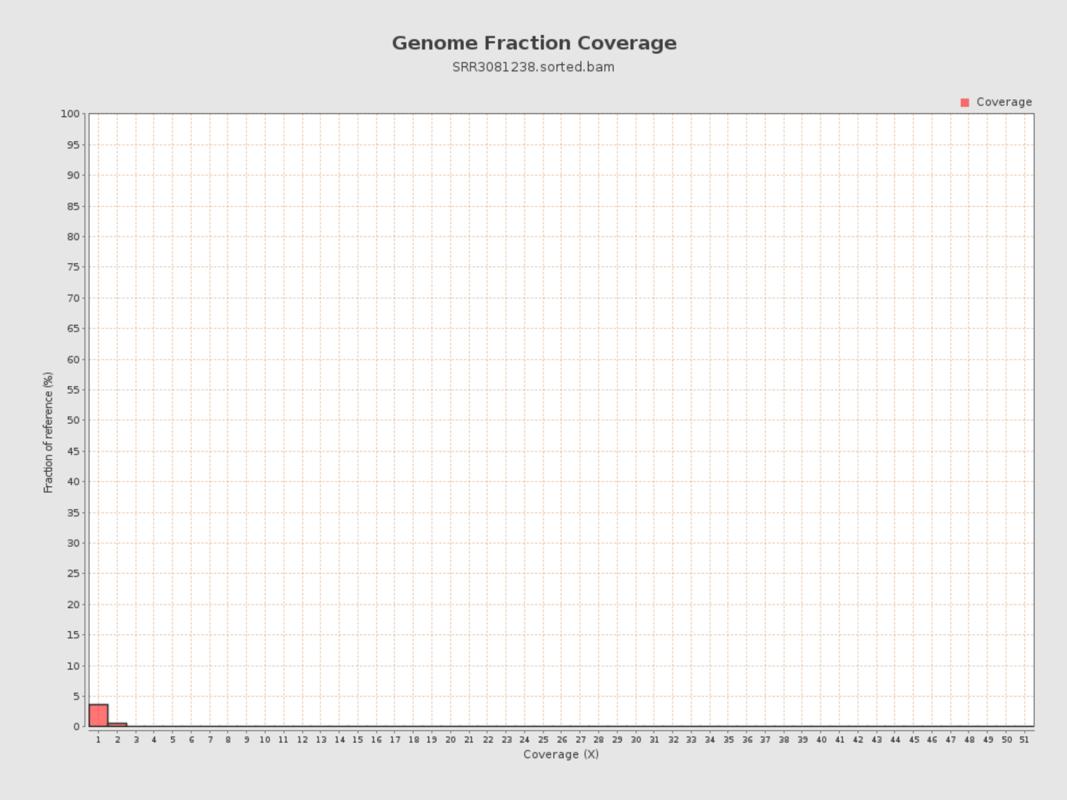
4. Results : Coverage Histogram



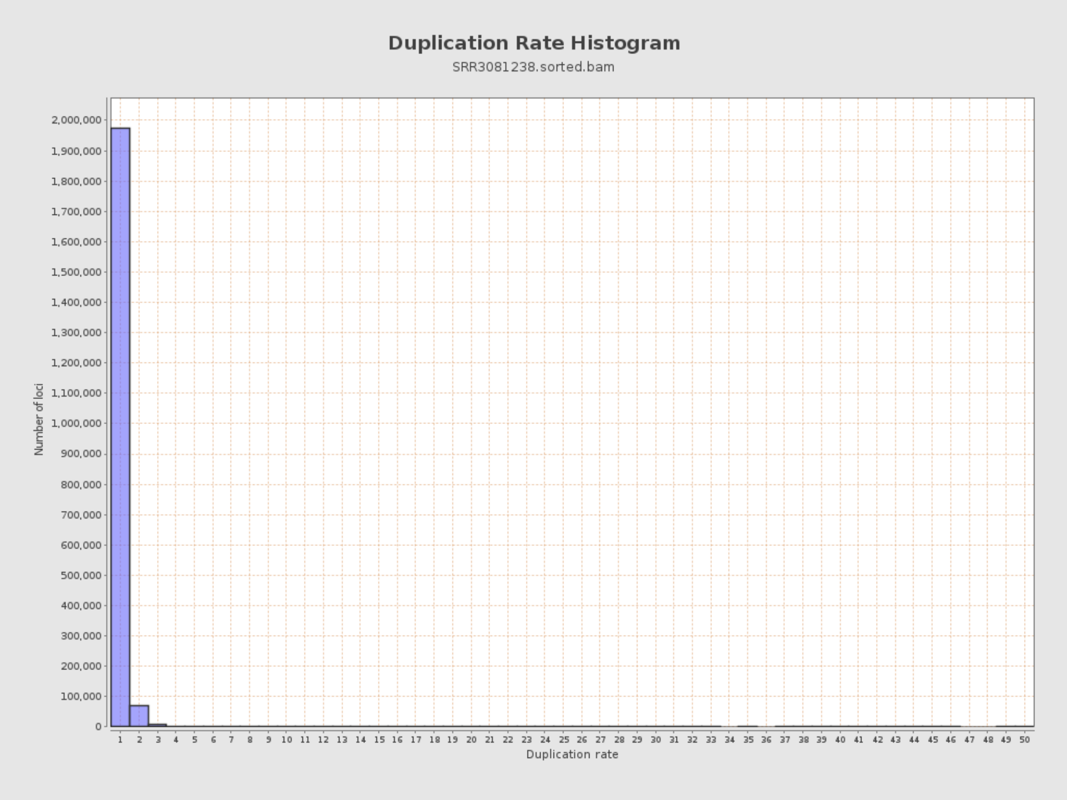
5. Results : Coverage Histogram (0-50X)



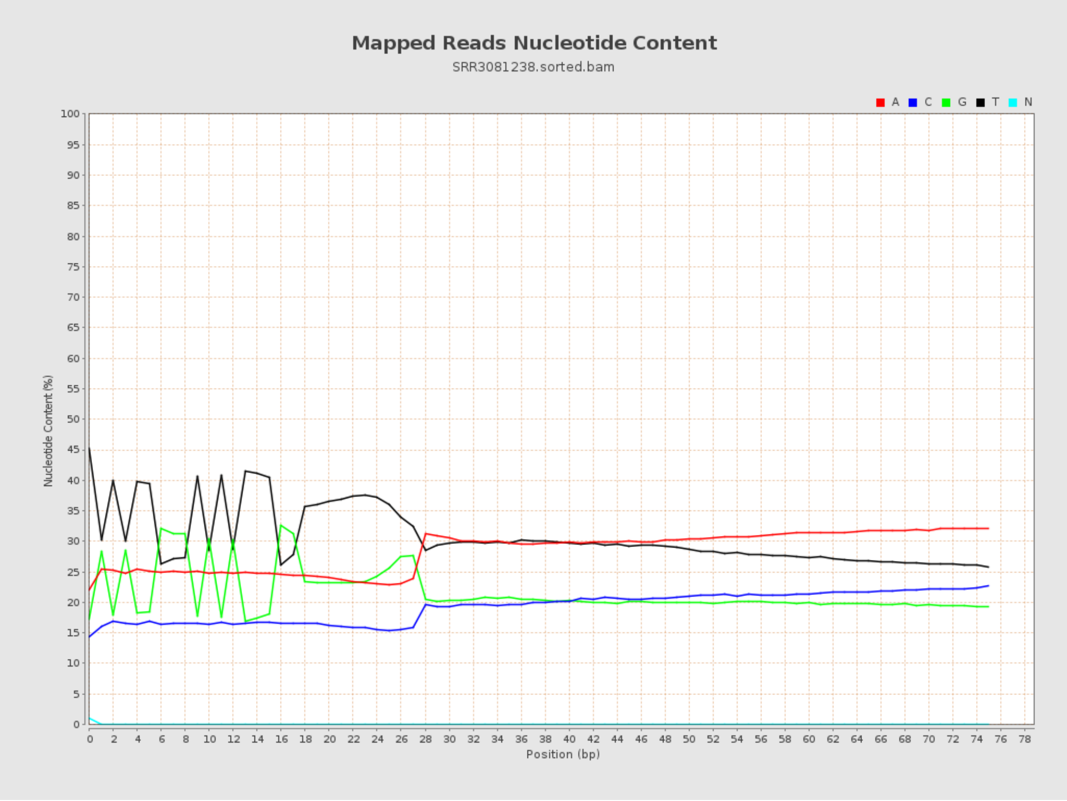
6. Results : Genome Fraction Coverage



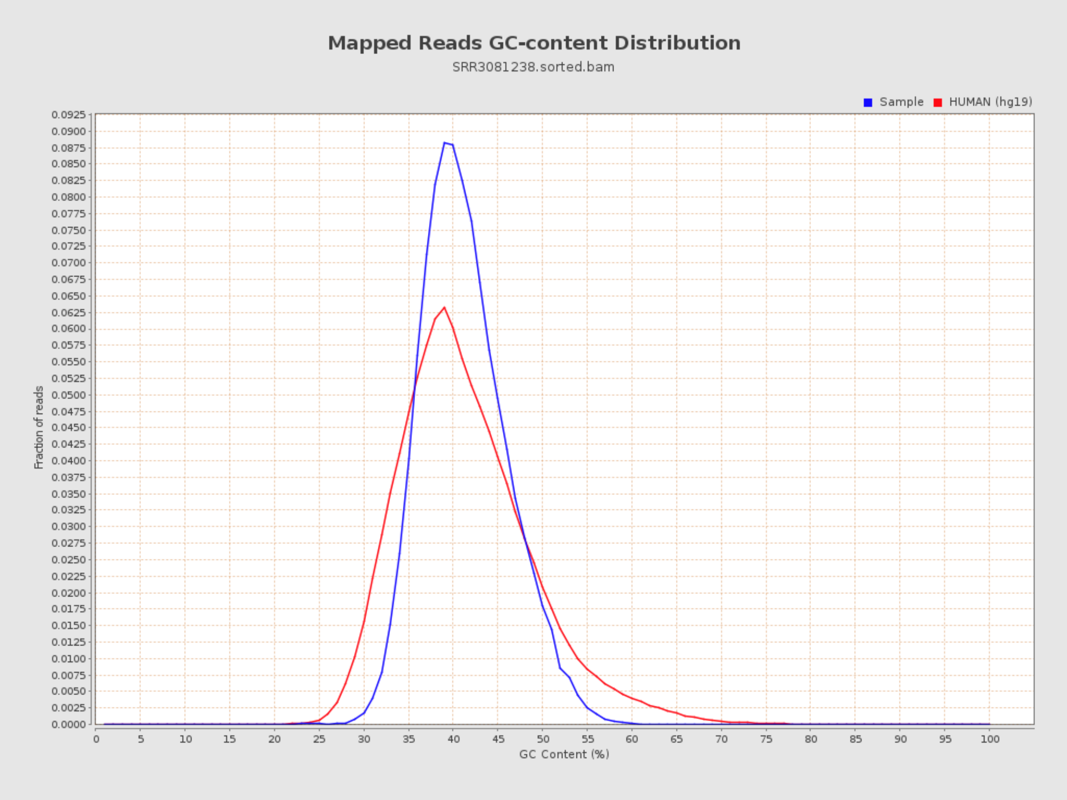
7. Results : Duplication Rate Histogram



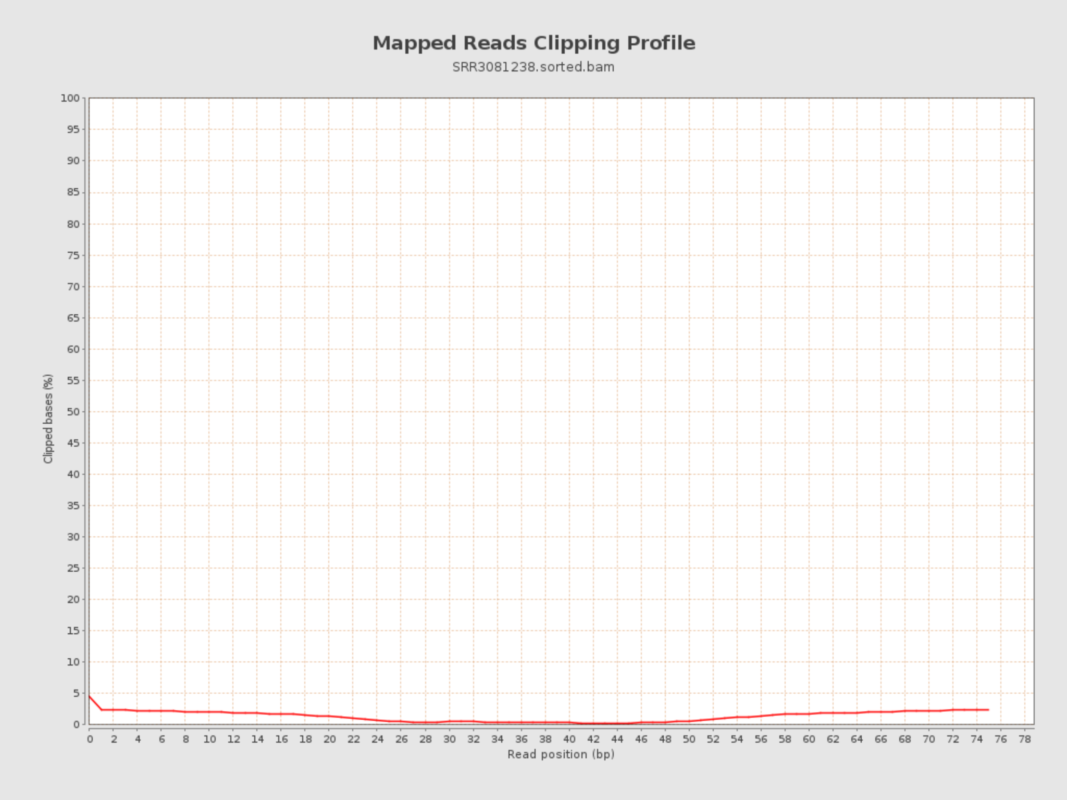
8. Results : Mapped Reads Nucleotide Content



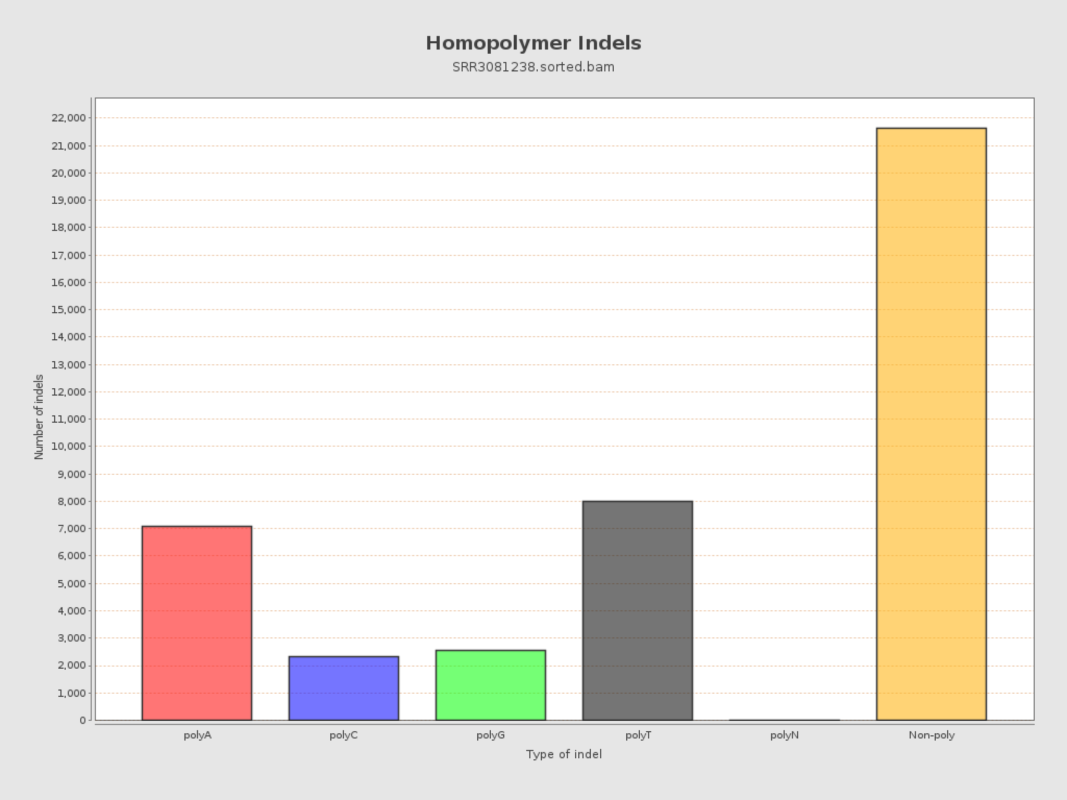
9. Results : Mapped Reads GC-content Distribution



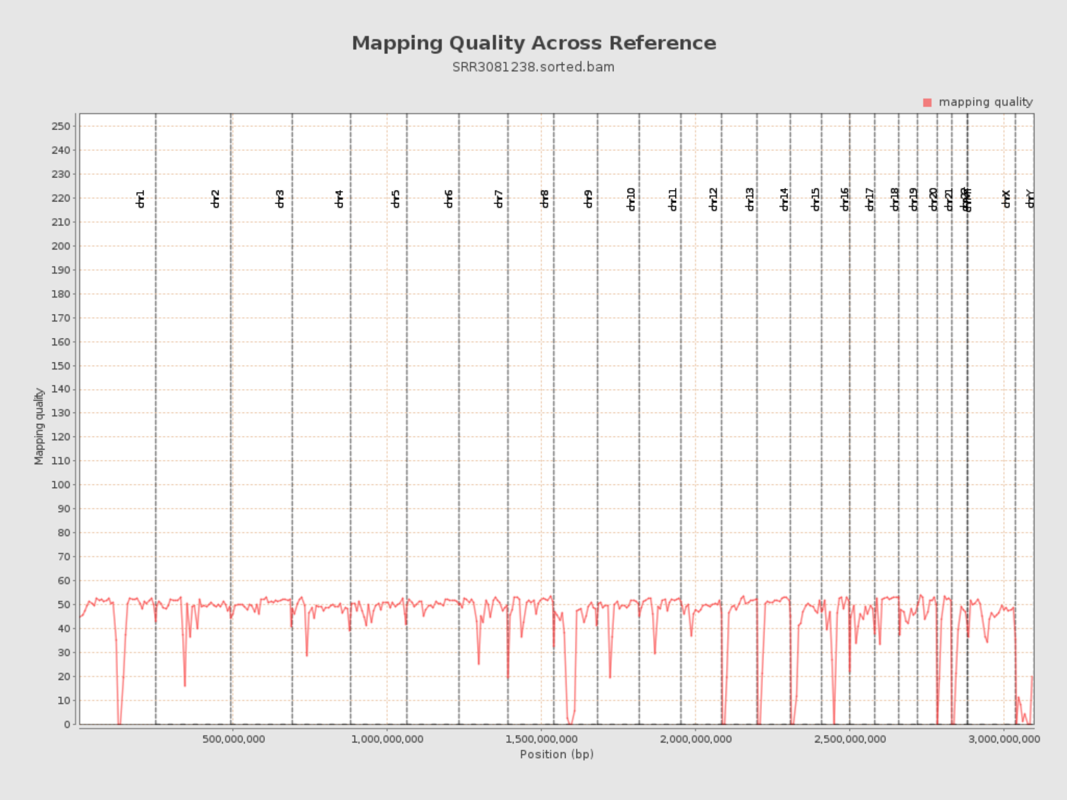
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram