Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 01:38:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083638.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_SRR3083638 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083638.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 01:38:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083638.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,867,413
Mapped reads	2,102,148 / 73.31%
Unmapped reads	765,265 / 26.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,876 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	84,675 / 2.95%
Duplication rate	3.46%
Clipped reads	1,472,219 / 51.34%

2.2. ACGT Content

Number/percentage of A's	35,671,729 / 28.45%
Number/percentage of C's	25,046,034 / 19.98%
Number/percentage of T's	36,371,987 / 29.01%
Number/percentage of G's	28,269,090 / 22.55%
Number/percentage of N's	17,267 / 0.01%
GC Percentage	42.52%

2.3. Coverage

Mean	0.0405

Standard Deviation	0.2797

2.4. Mapping Quality

Mean Mapping Quality	44.75

2.5. Mismatches and indels

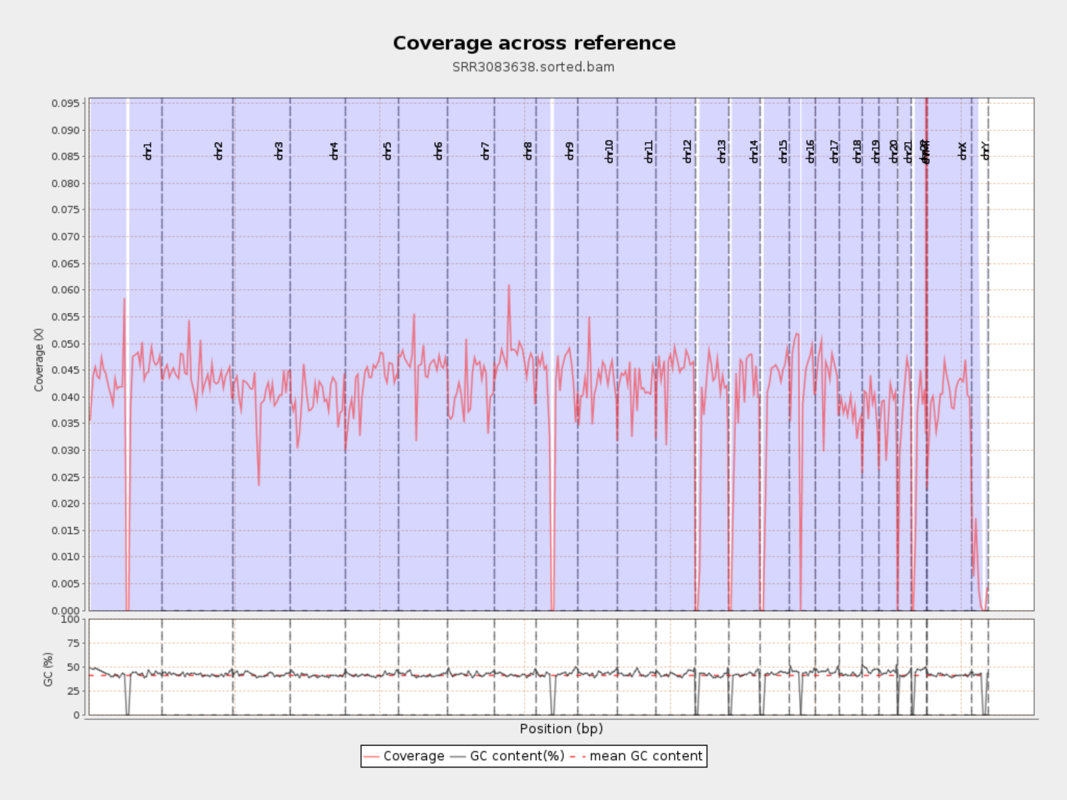
General error rate	0.83%
Mismatches	1,027,179
Insertions	8,530
Mapped reads with at least one insertion	0.4%
Deletions	24,385
Mapped reads with at least one deletion	1.15%
Homopolymer indels	45.21%

2.6. Chromosome stats

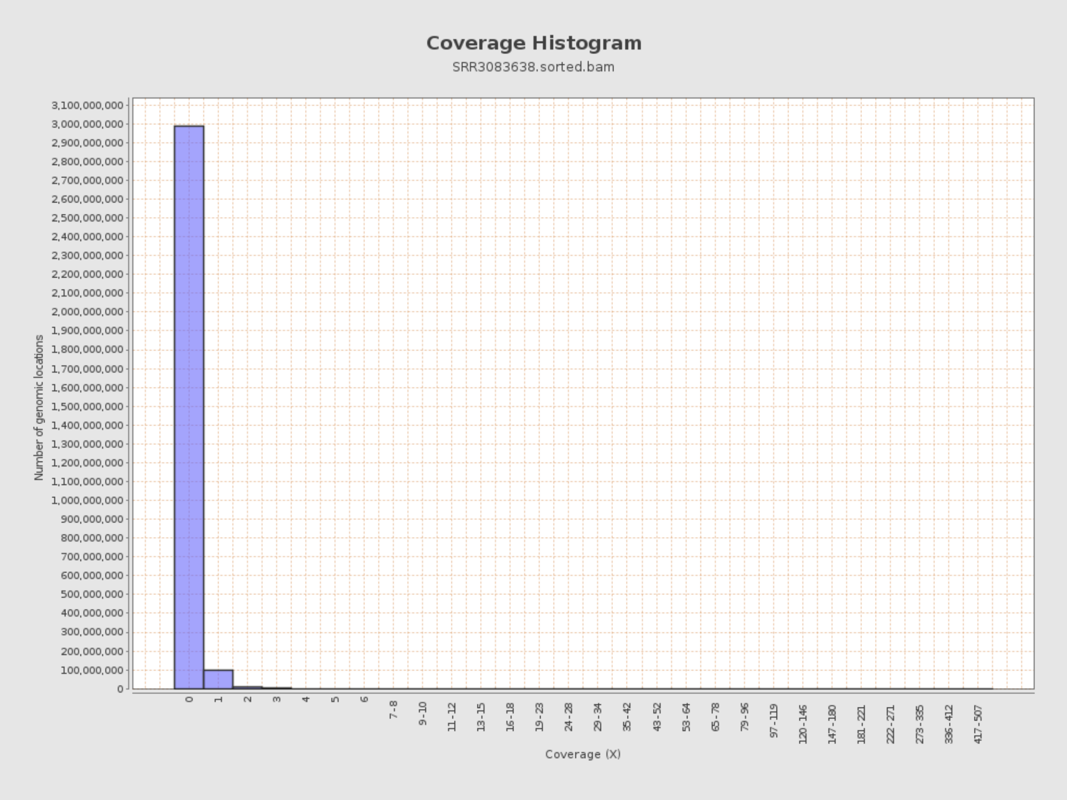
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10481877	0.0421	0.4335
chr2	243199373	10775763	0.0443	0.2964
chr3	198022430	8003745	0.0404	0.2219
chr4	191154276	7510093	0.0393	0.2321
chr5	180915260	7737383	0.0428	0.2298
chr6	171115067	7916451	0.0463	0.2726
chr7	159138663	6578636	0.0413	0.3263

chr8	146364022	6966860	0.0476	0.3233
chr9	141213431	5593217	0.0396	0.2691
chr10	135534747	5801566	0.0428	0.2903
chr11	135006516	5681165	0.0421	0.2489
chr12	133851895	6053973	0.0452	0.2378
chr13	115169878	4152411	0.0361	0.2098
chr14	107349540	3902400	0.0364	0.2194
chr15	102531392	3751343	0.0366	0.2118
chr16	90354753	3833320	0.0424	0.2423
chr17	81195210	3571000	0.044	0.2546
chr18	78077248	2891383	0.037	0.4013
chr19	59128983	2246104	0.038	0.3412
chr20	63025520	2350685	0.0373	0.2229
chr21	48129895	1713096	0.0356	0.2224
chr22	51304566	1425111	0.0278	0.1839
chrMT	16571	14877	0.8978	1.0727
chrX	155270560	6158565	0.0397	0.2358
chrY	59373566	303657	0.0051	0.1239

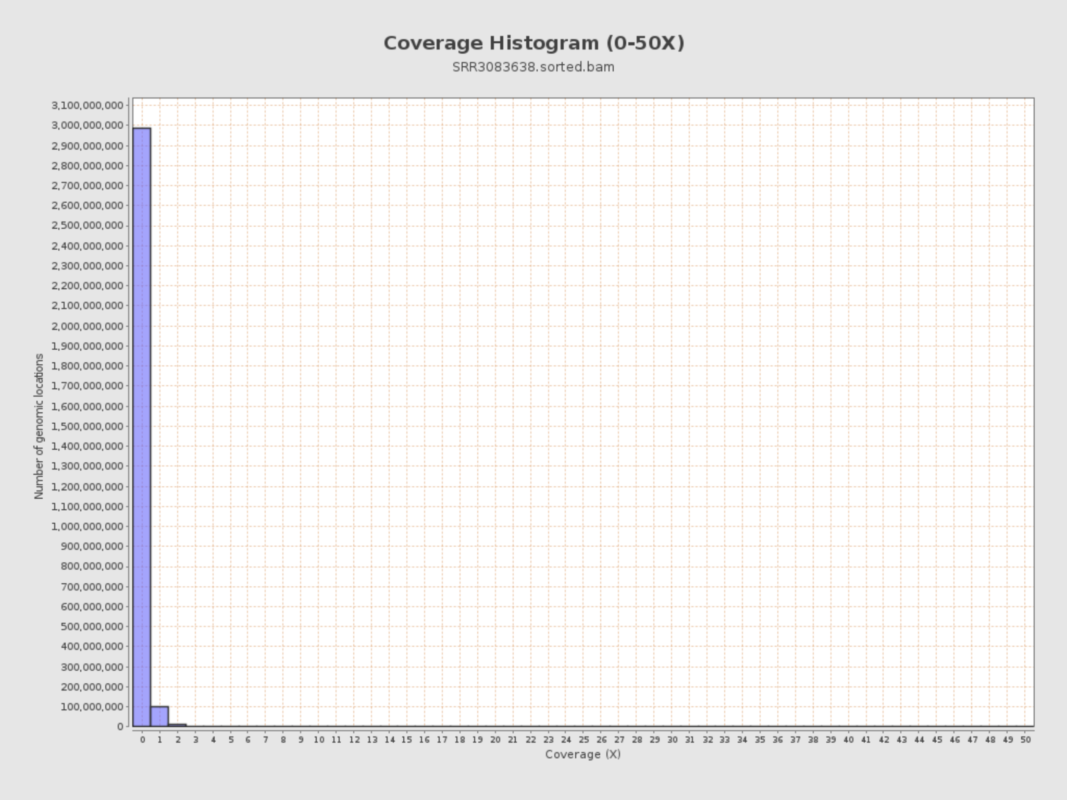
3. Results : Coverage across reference



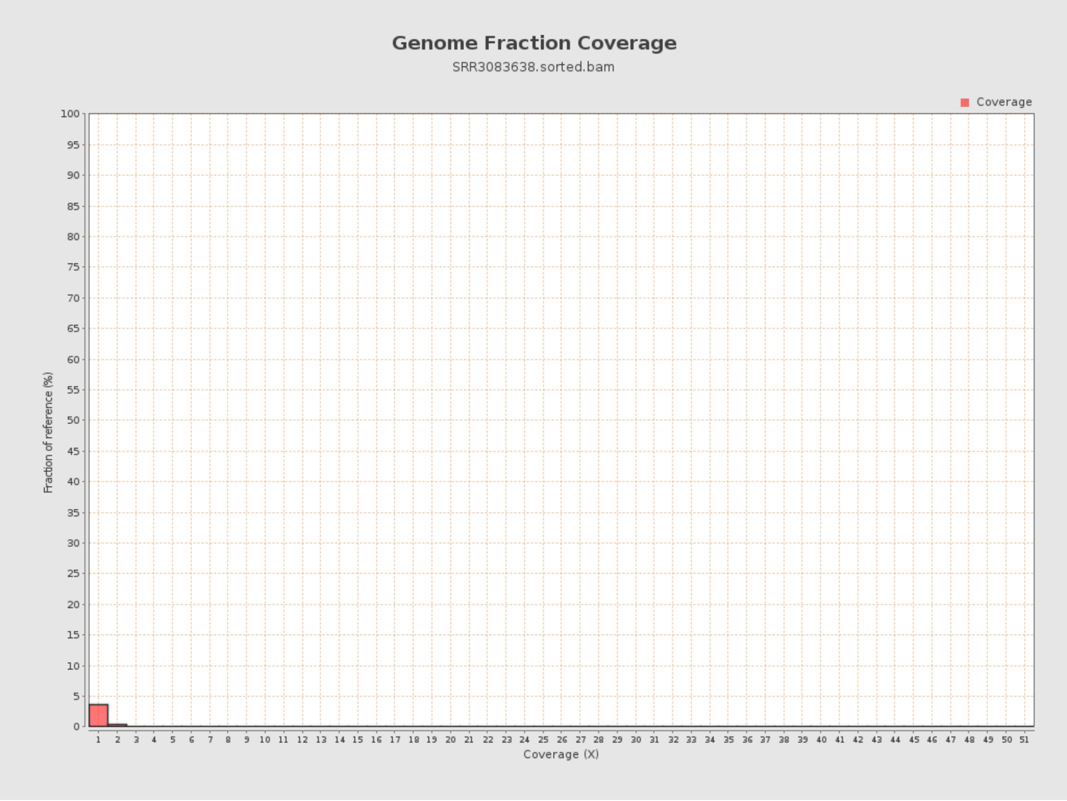
4. Results : Coverage Histogram



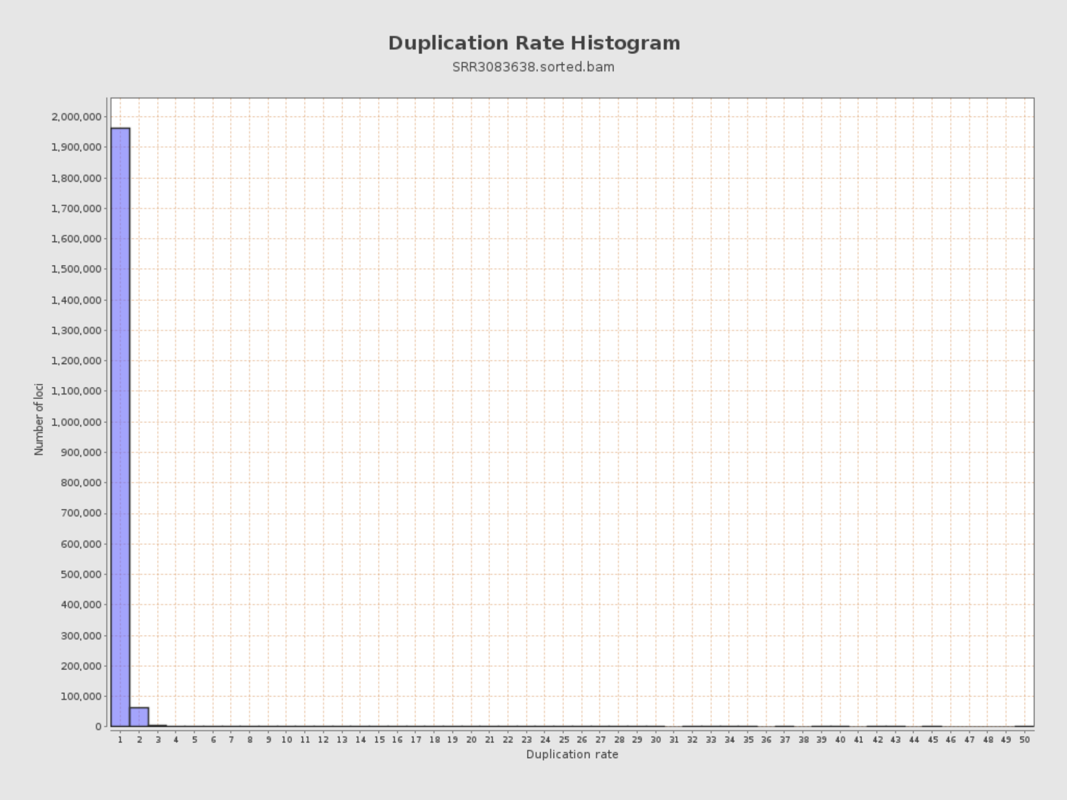
5. Results : Coverage Histogram (0-50X)



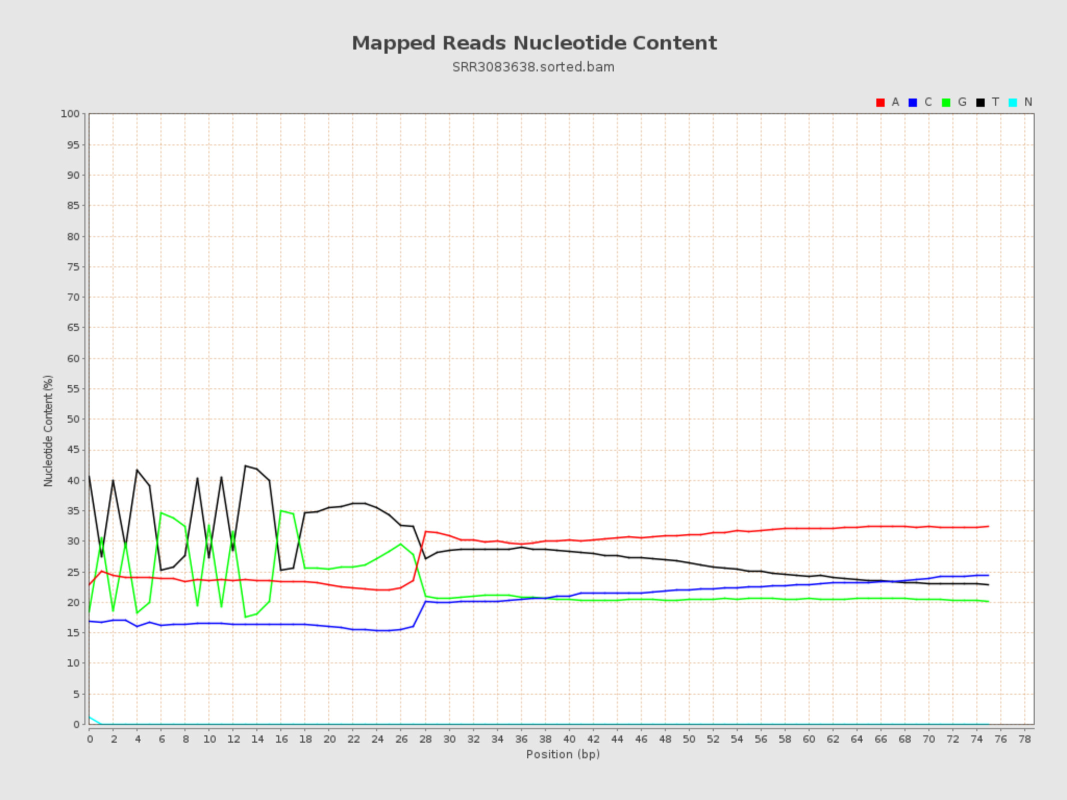
6. Results : Genome Fraction Coverage



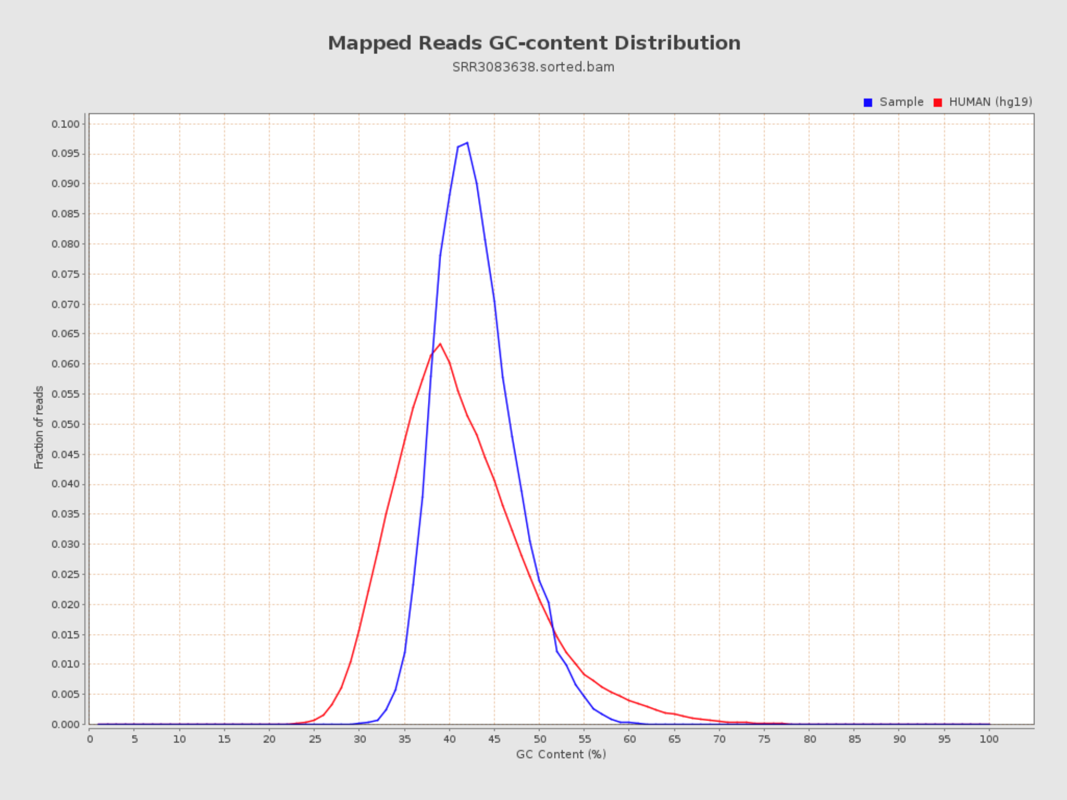
7. Results : Duplication Rate Histogram



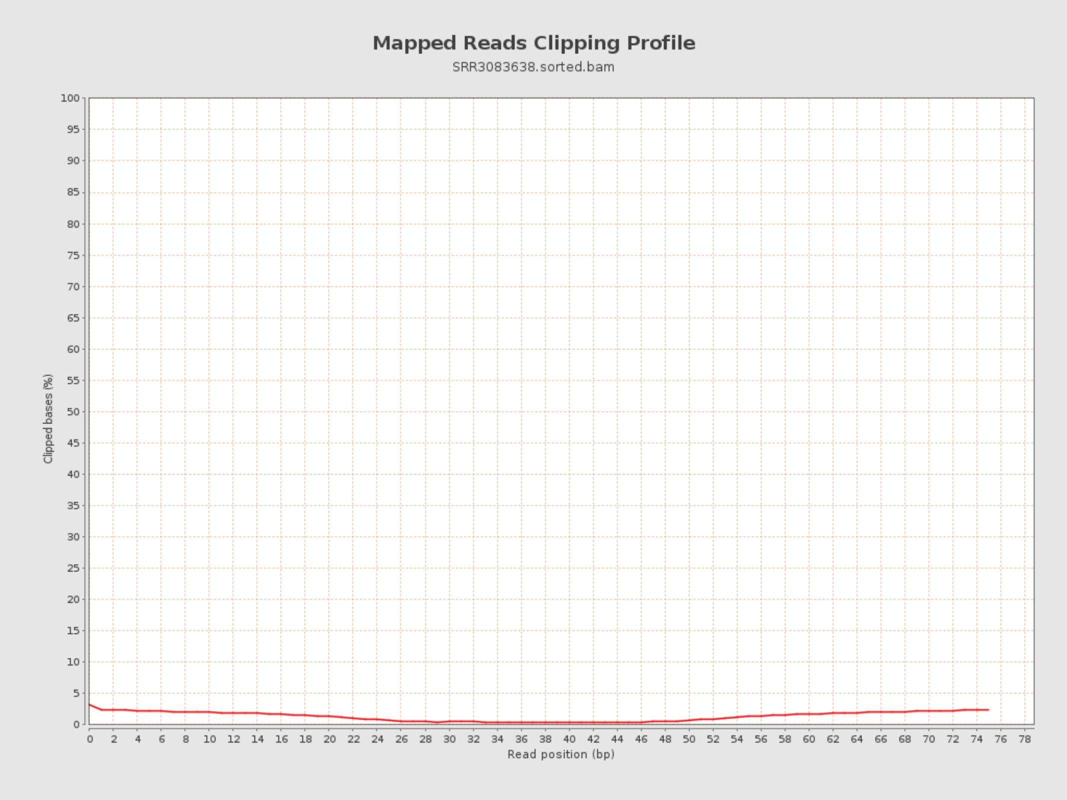
8. Results : Mapped Reads Nucleotide Content



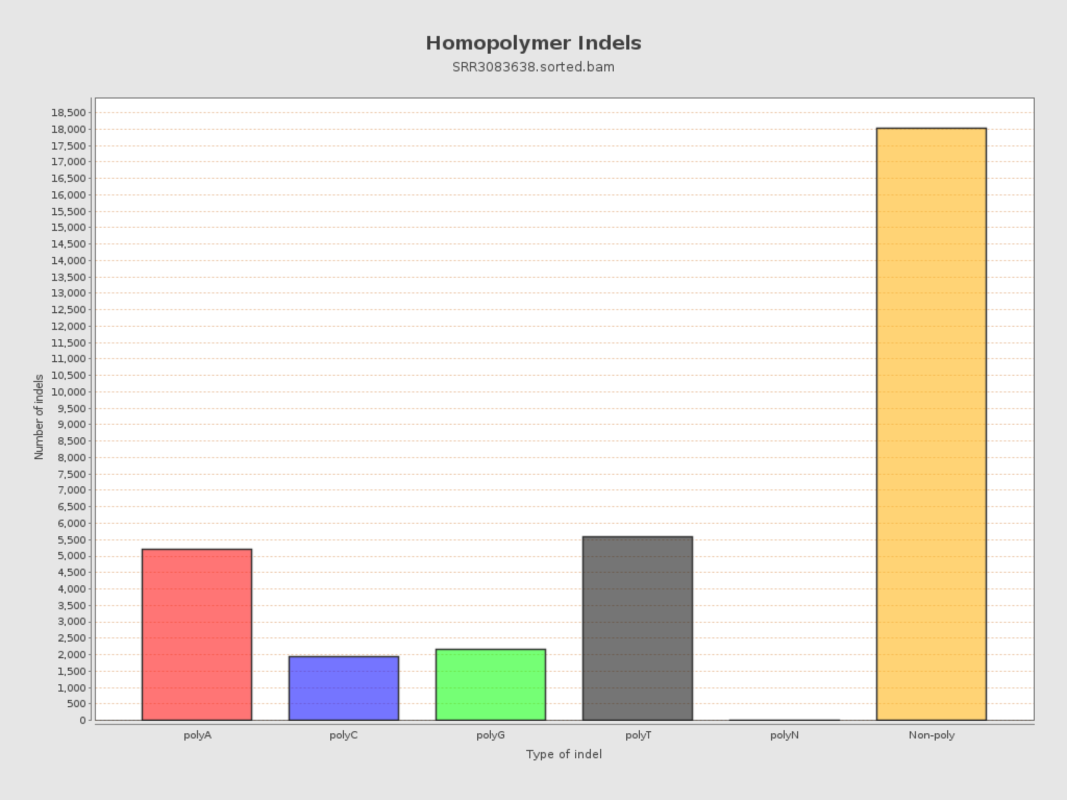
9. Results : Mapped Reads GC-content Distribution



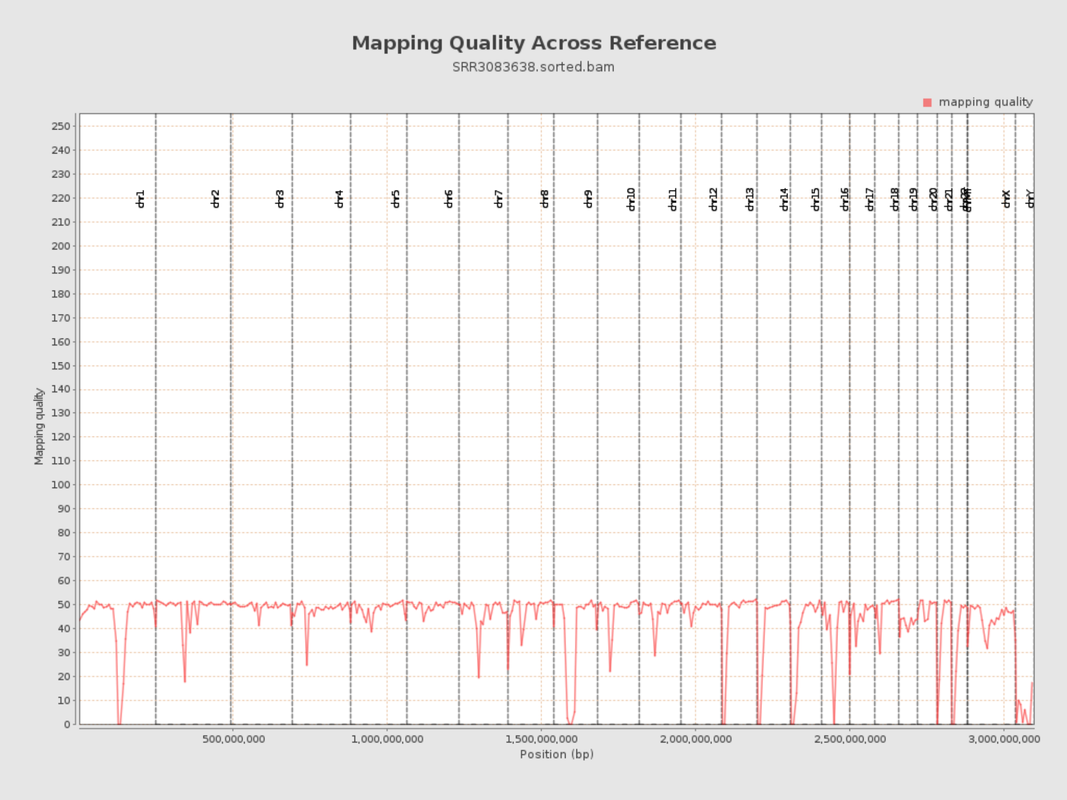
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram