Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 11:17:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084363.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_SRR3084363 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084363.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 11:17:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084363.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,408,283
Mapped reads	2,169,854 / 90.1%
Unmapped reads	238,429 / 9.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,665 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	78,678 / 3.27%
Duplication rate	3.05%
Clipped reads	951,276 / 39.5%

2.2. ACGT Content

Number/percentage of A's	40,070,695 / 27.56%
Number/percentage of C's	27,949,284 / 19.22%
Number/percentage of T's	44,787,320 / 30.8%
Number/percentage of G's	32,405,758 / 22.29%
Number/percentage of N's	188,856 / 0.13%
GC Percentage	41.51%

2.3. Coverage

Mean	0.047

Standard Deviation	0.3233

2.4. Mapping Quality

Mean Mapping Quality	45.85

2.5. Mismatches and indels

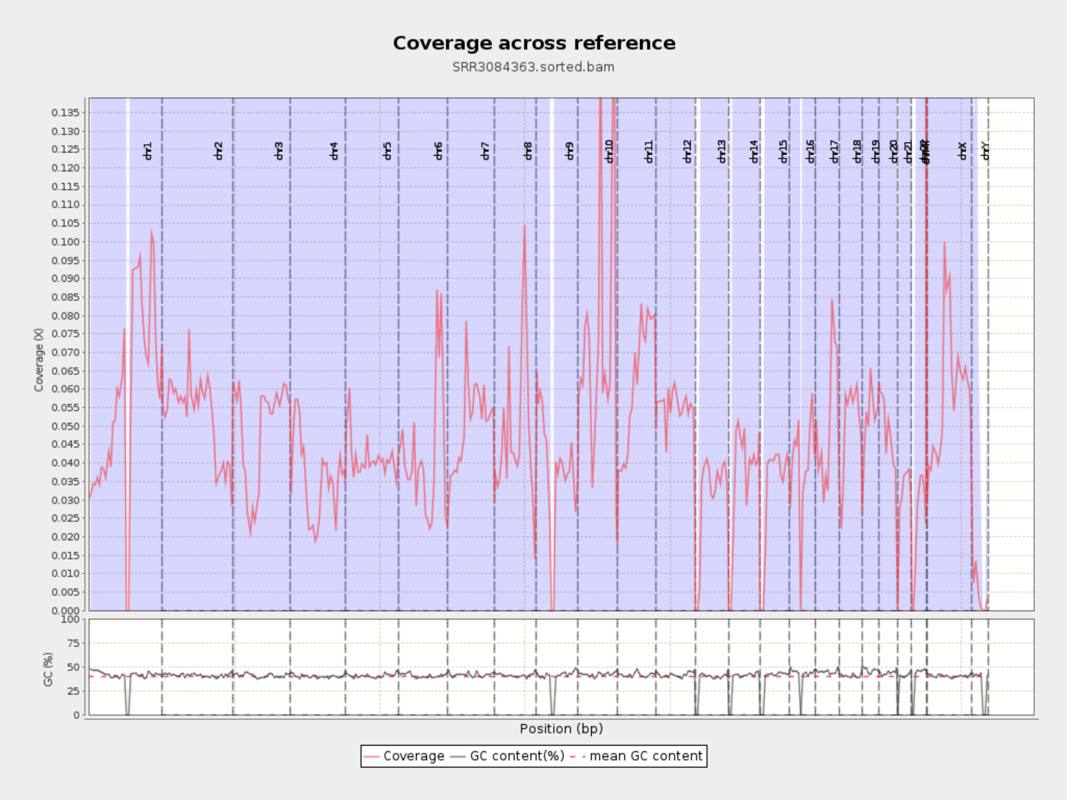
General error rate	1.01%
Mismatches	1,446,342
Insertions	9,868
Mapped reads with at least one insertion	0.45%
Deletions	27,930
Mapped reads with at least one deletion	1.27%
Homopolymer indels	46.69%

2.6. Chromosome stats

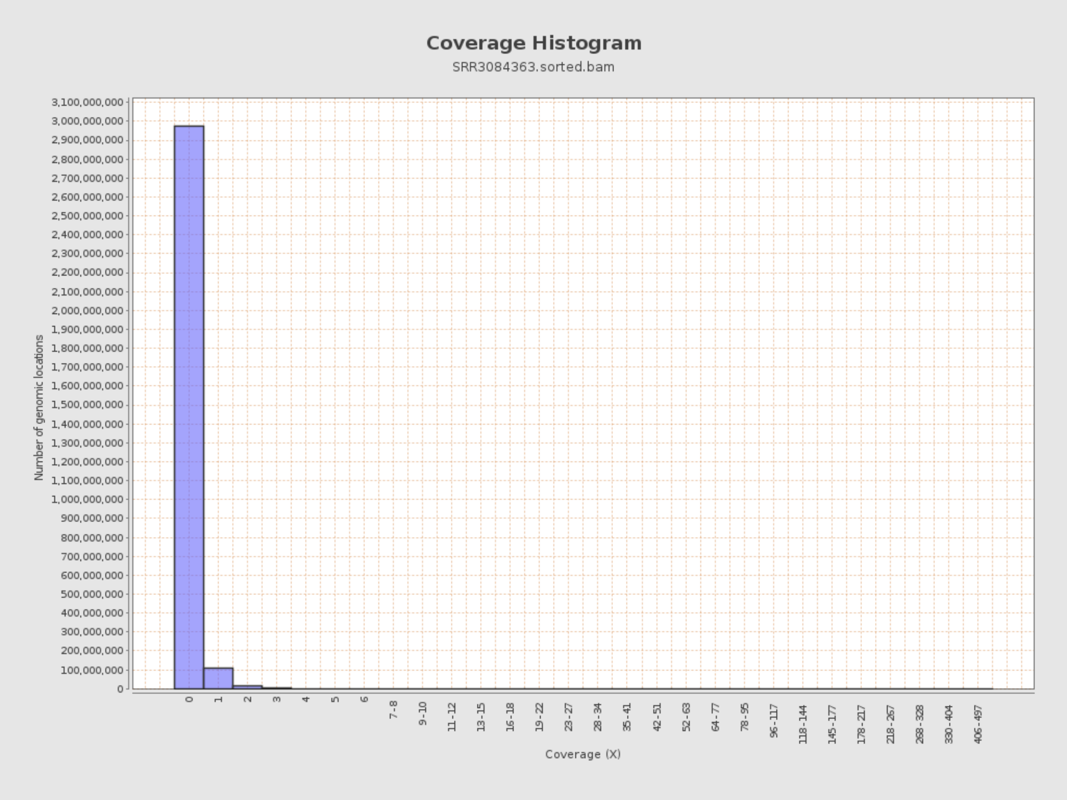
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14354930	0.0576	0.5219
chr2	243199373	12897564	0.053	0.3679
chr3	198022430	9682195	0.0489	0.2545
chr4	191154276	6859254	0.0359	0.2214
chr5	180915260	7463841	0.0413	0.2317
chr6	171115067	7231714	0.0423	0.261
chr7	159138663	8082163	0.0508	0.4478

chr8	146364022	7111582	0.0486	0.2958
chr9	141213431	5283608	0.0374	0.2744
chr10	135534747	10277426	0.0758	0.4368
chr11	135006516	8273319	0.0613	0.3365
chr12	133851895	7402131	0.0553	0.2688
chr13	115169878	3471971	0.0301	0.1977
chr14	107349540	3842861	0.0358	0.2244
chr15	102531392	3321734	0.0324	0.2076
chr16	90354753	3589527	0.0397	0.2409
chr17	81195210	4152909	0.0511	0.2718
chr18	78077248	3928675	0.0503	0.437
chr19	59128983	3132391	0.053	0.4001
chr20	63025520	3003837	0.0477	0.2517
chr21	48129895	1466578	0.0305	0.2066
chr22	51304566	1164111	0.0227	0.1693
chrMT	16571	57170	3.45	2.5921
chrX	155270560	9107832	0.0587	0.303
chrY	59373566	291152	0.0049	0.0996

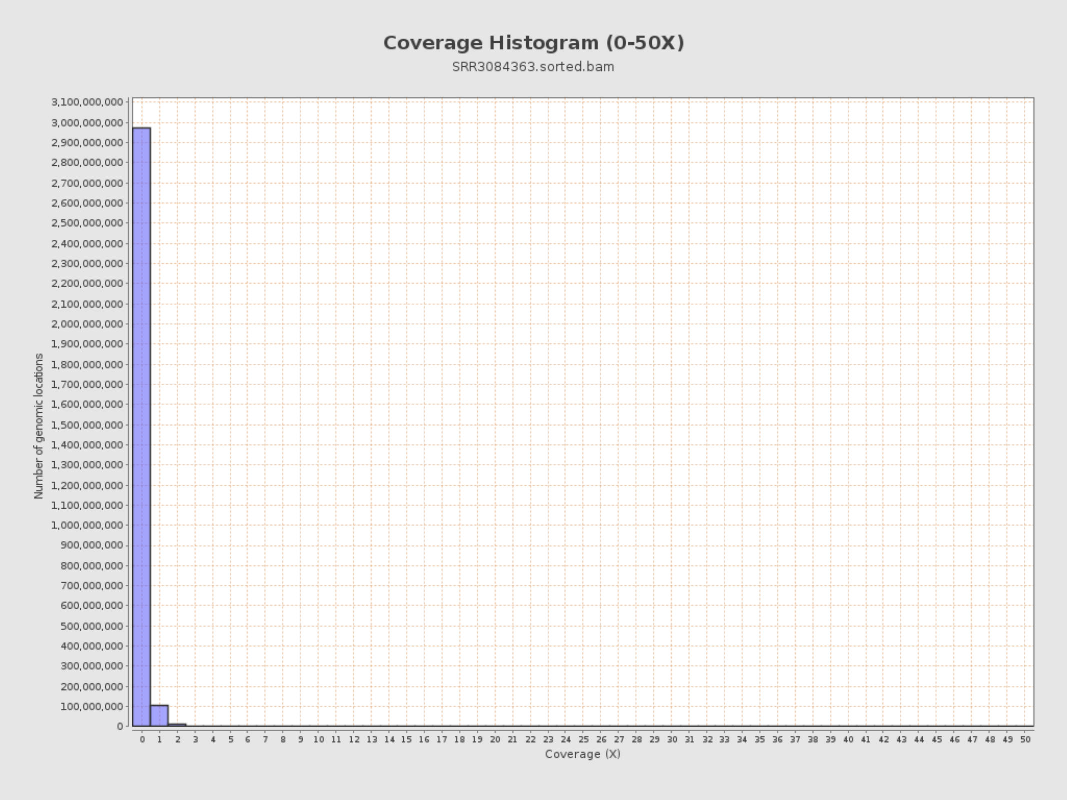
3. Results : Coverage across reference



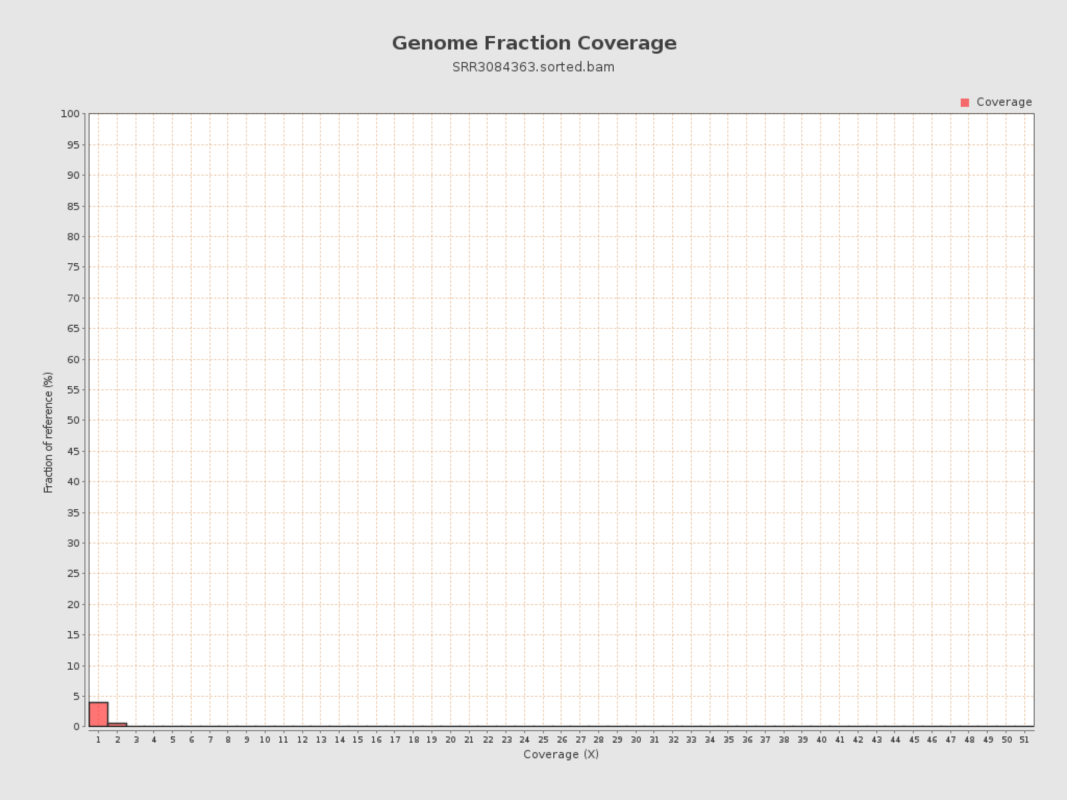
4. Results : Coverage Histogram



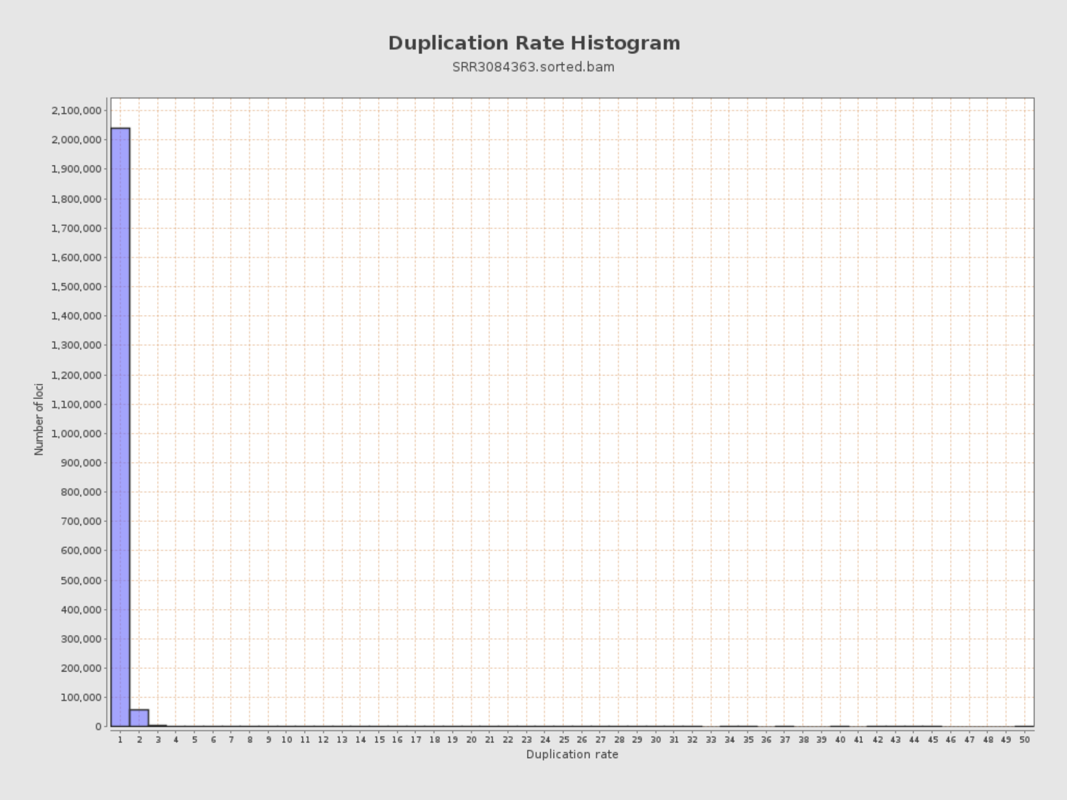
5. Results : Coverage Histogram (0-50X)



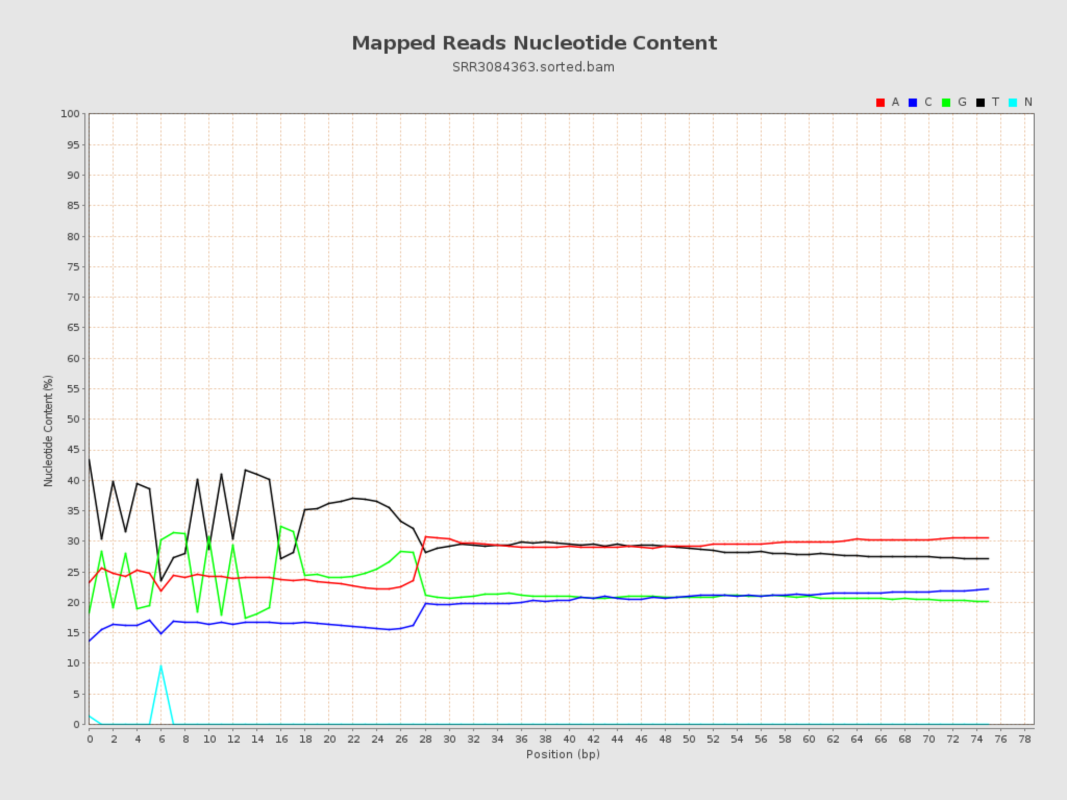
6. Results : Genome Fraction Coverage



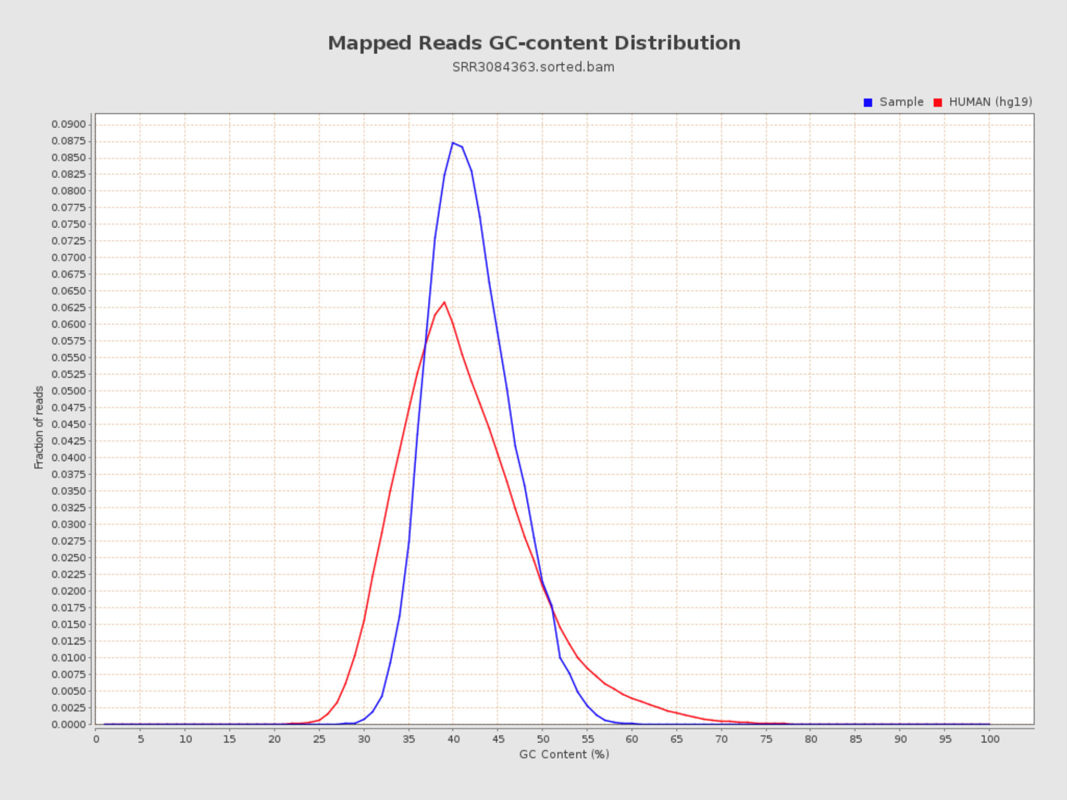
7. Results : Duplication Rate Histogram



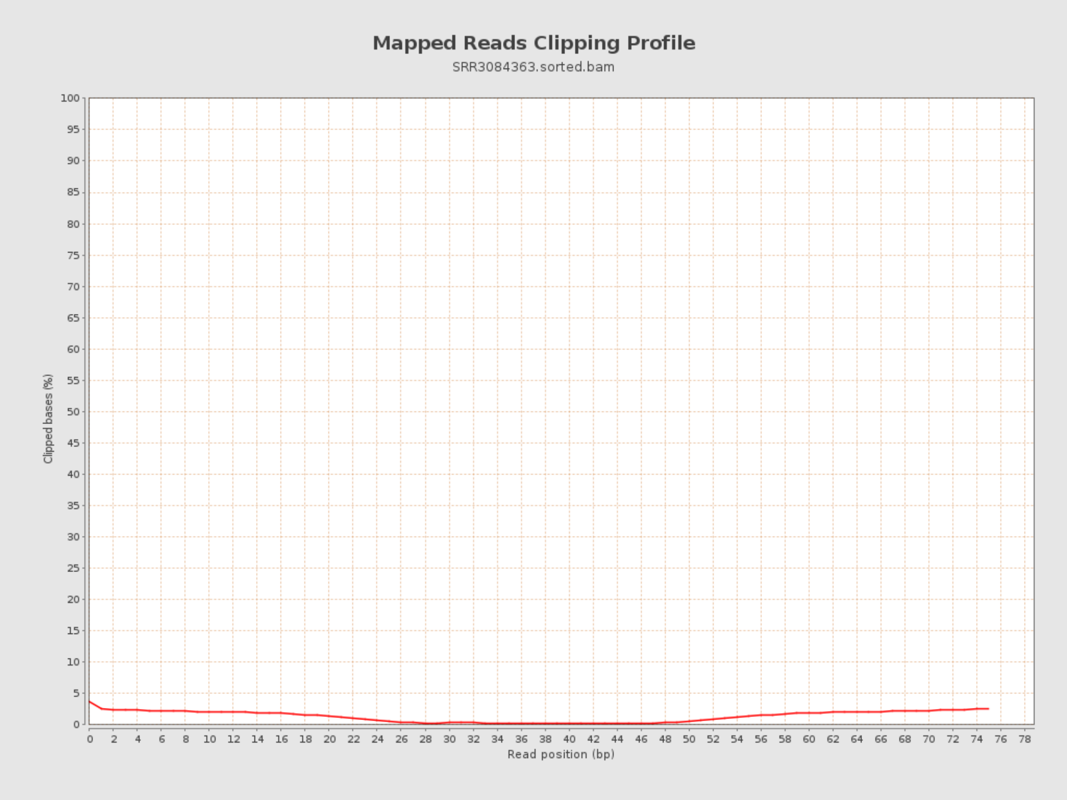
8. Results : Mapped Reads Nucleotide Content



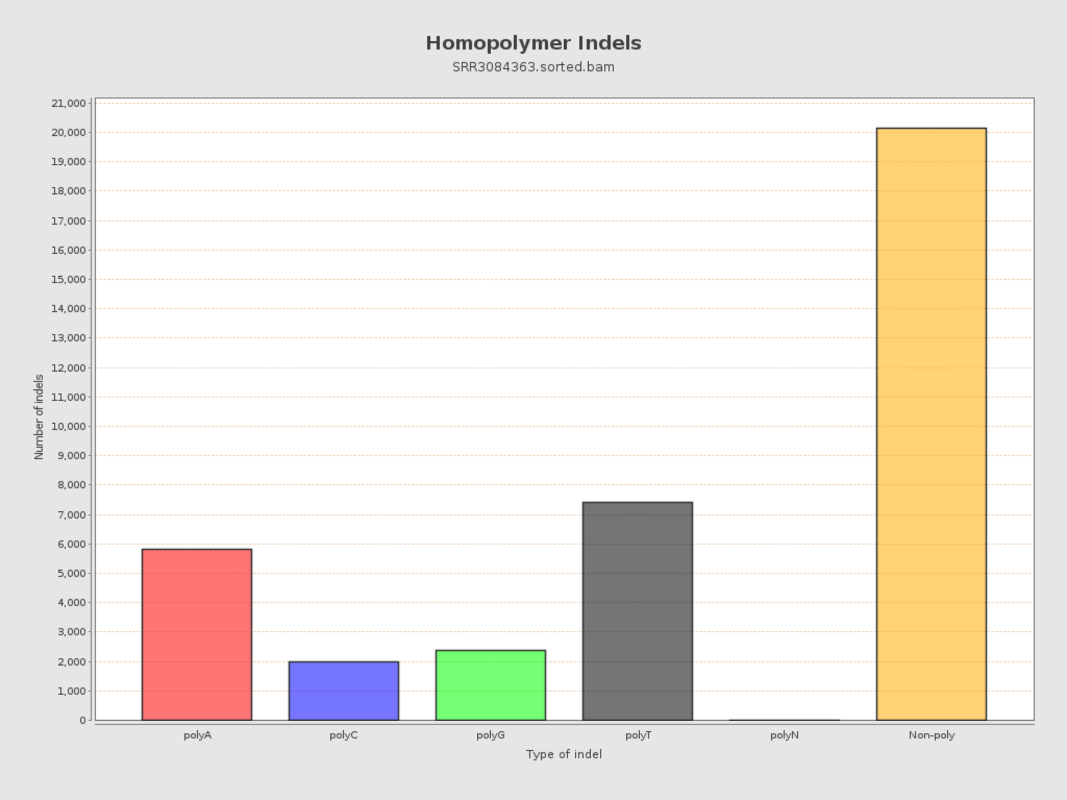
9. Results : Mapped Reads GC-content Distribution



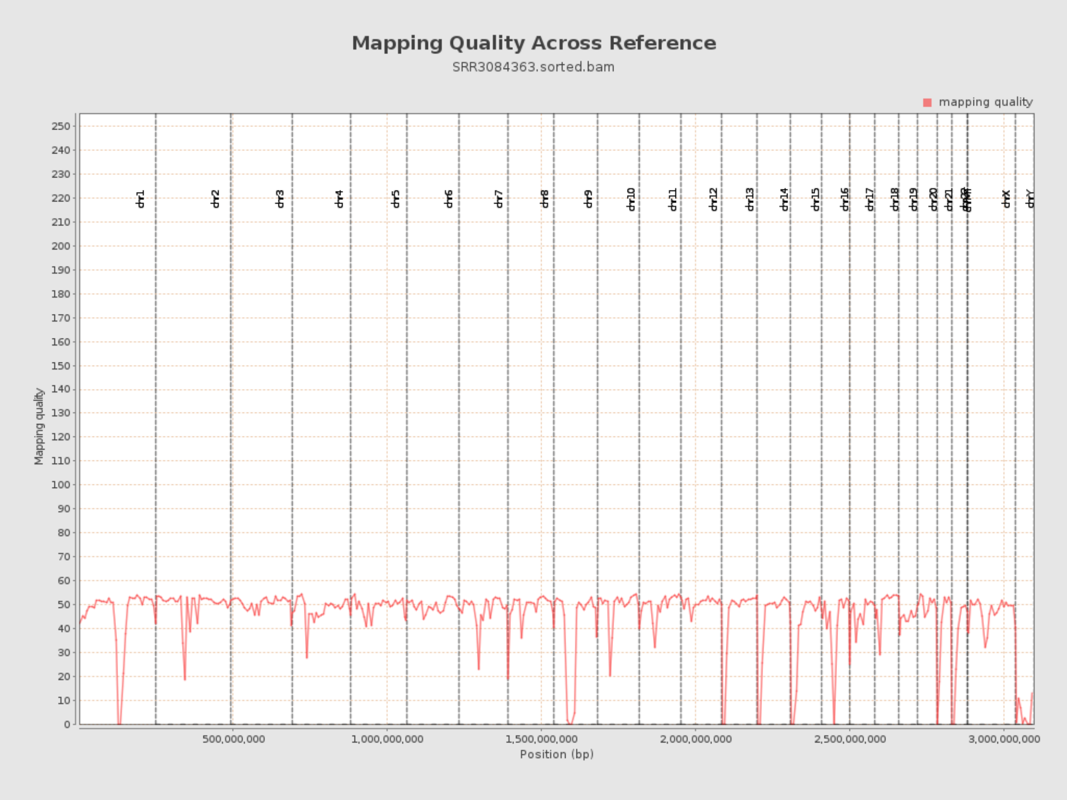
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram