Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 17:25:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082741.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_SRR3082741 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082741.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 17:25:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082741.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,978,347
Mapped reads	2,622,676 / 88.06%
Unmapped reads	355,671 / 11.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,470 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	100,454 / 3.37%
Duplication rate	2.91%
Clipped reads	1,200,414 / 40.3%

2.2. ACGT Content

Number/percentage of A's	48,114,641 / 27.6%
Number/percentage of C's	30,312,746 / 17.39%
Number/percentage of T's	57,602,972 / 33.04%
Number/percentage of G's	38,249,111 / 21.94%
Number/percentage of N's	46,758 / 0.03%
GC Percentage	39.33%

2.3. Coverage

Mean	0.0563

Standard Deviation	0.4371

2.4. Mapping Quality

Mean Mapping Quality	46.89

2.5. Mismatches and indels

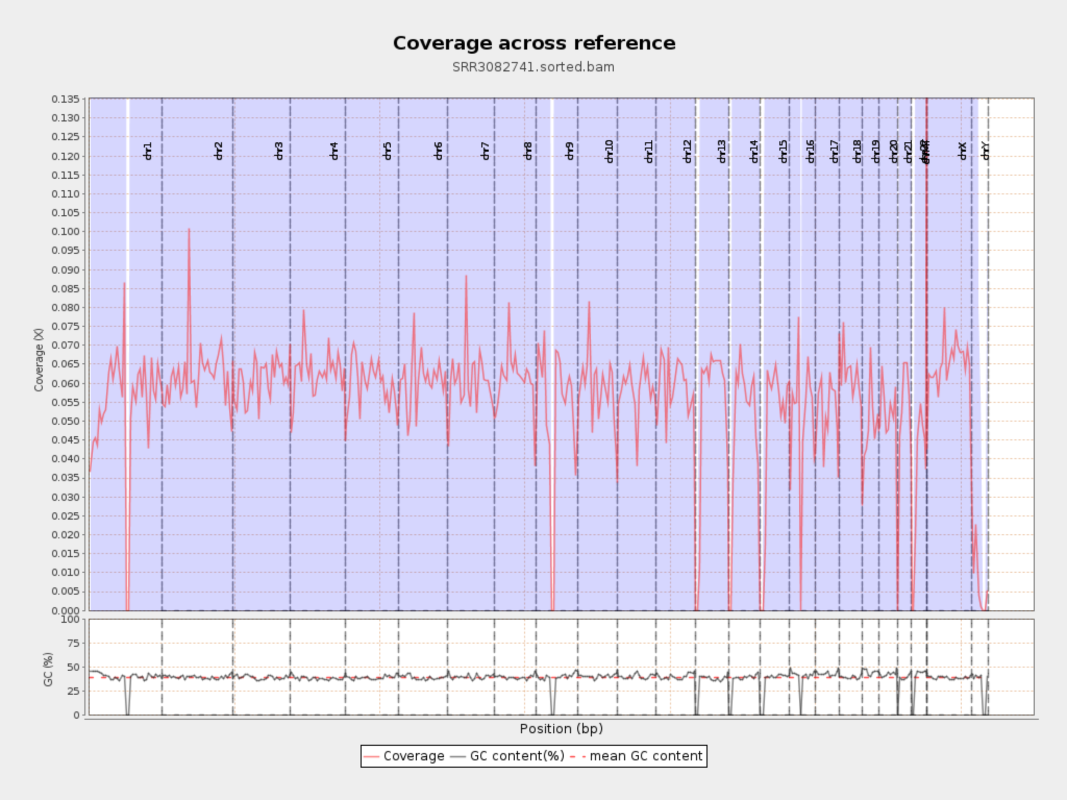
General error rate	0.96%
Mismatches	1,652,420
Insertions	15,970
Mapped reads with at least one insertion	0.6%
Deletions	40,832
Mapped reads with at least one deletion	1.54%
Homopolymer indels	49.18%

2.6. Chromosome stats

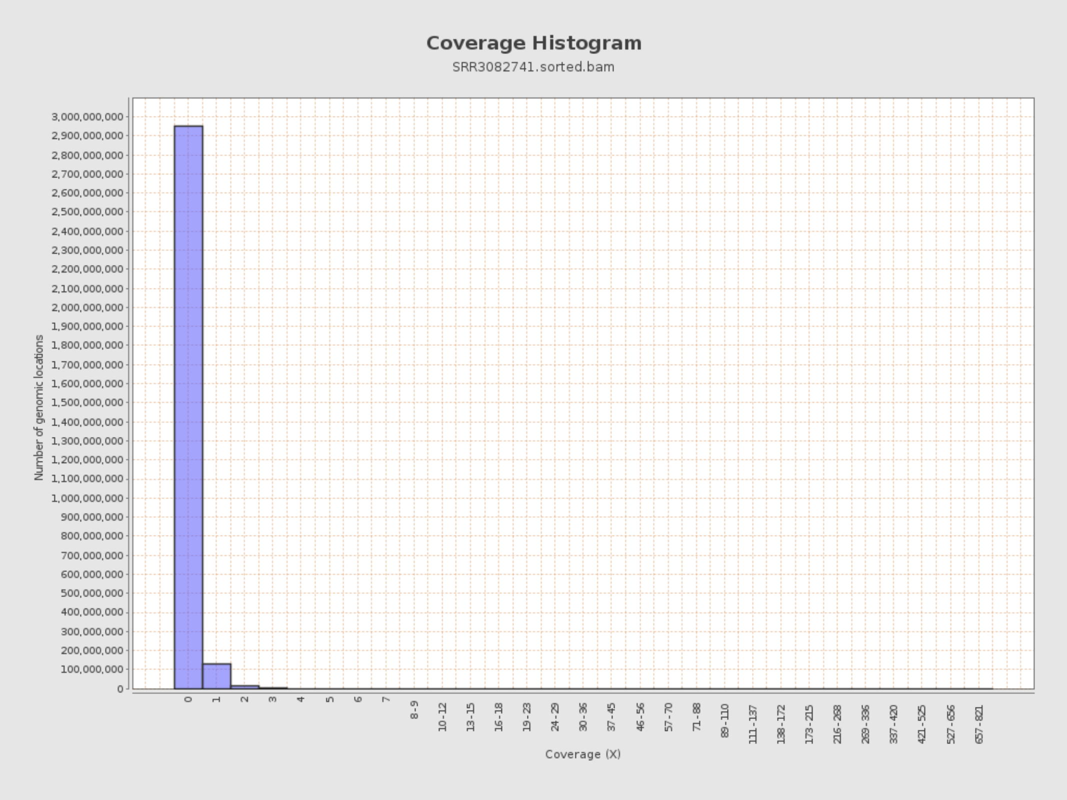
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13494500	0.0541	0.7436
chr2	243199373	15136630	0.0622	0.5258
chr3	198022430	12072783	0.061	0.2823
chr4	191154276	12020732	0.0629	0.3097
chr5	180915260	10885165	0.0602	0.2818
chr6	171115067	10381290	0.0607	0.3634
chr7	159138663	9758121	0.0613	0.5943

chr8	146364022	8947673	0.0611	0.4544
chr9	141213431	7408679	0.0525	0.4909
chr10	135534747	8049456	0.0594	0.378
chr11	135006516	7854276	0.0582	0.3691
chr12	133851895	7874518	0.0588	0.2845
chr13	115169878	5983370	0.052	0.2605
chr14	107349540	5163345	0.0481	0.2808
chr15	102531392	4815638	0.047	0.2471
chr16	90354753	4568761	0.0506	0.3043
chr17	81195210	4233363	0.0521	0.3144
chr18	78077248	4886338	0.0626	0.8822
chr19	59128983	2902279	0.0491	0.5236
chr20	63025520	3309670	0.0525	0.2784
chr21	48129895	2412379	0.0501	0.287
chr22	51304566	1727077	0.0337	0.2076
chrMT	16571	2987	0.1803	0.4511
chrX	155270560	10071722	0.0649	0.3326
chrY	59373566	432096	0.0073	0.1815

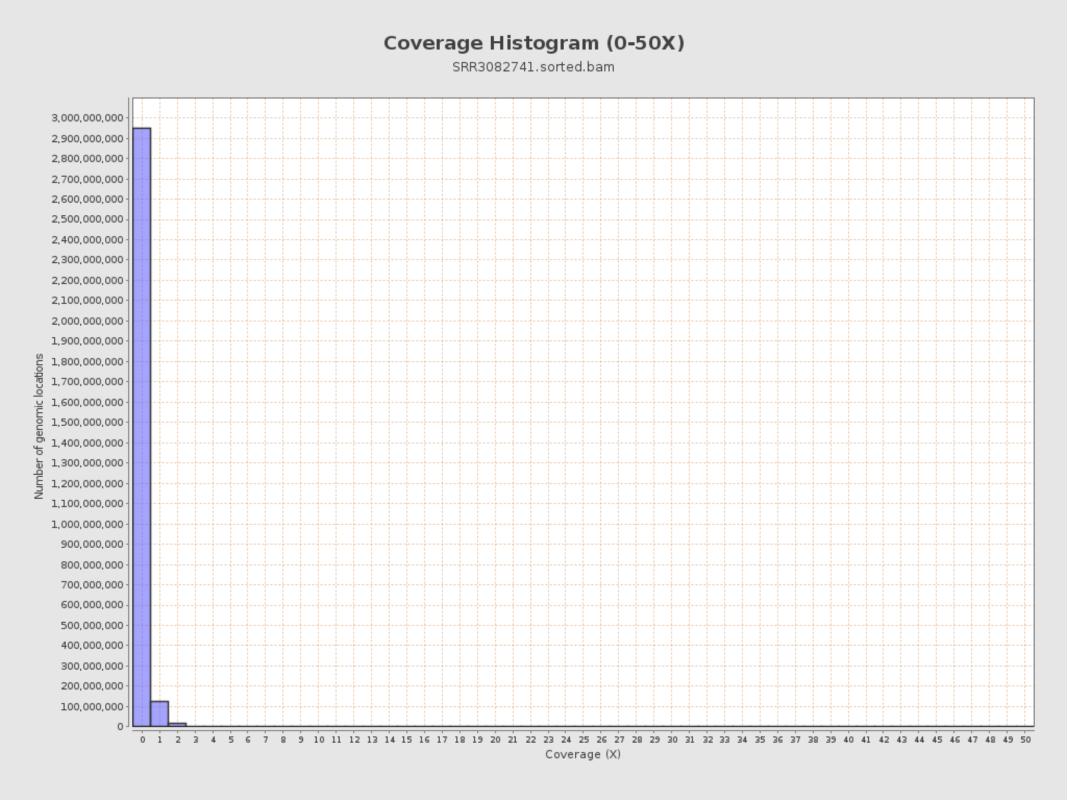
3. Results : Coverage across reference



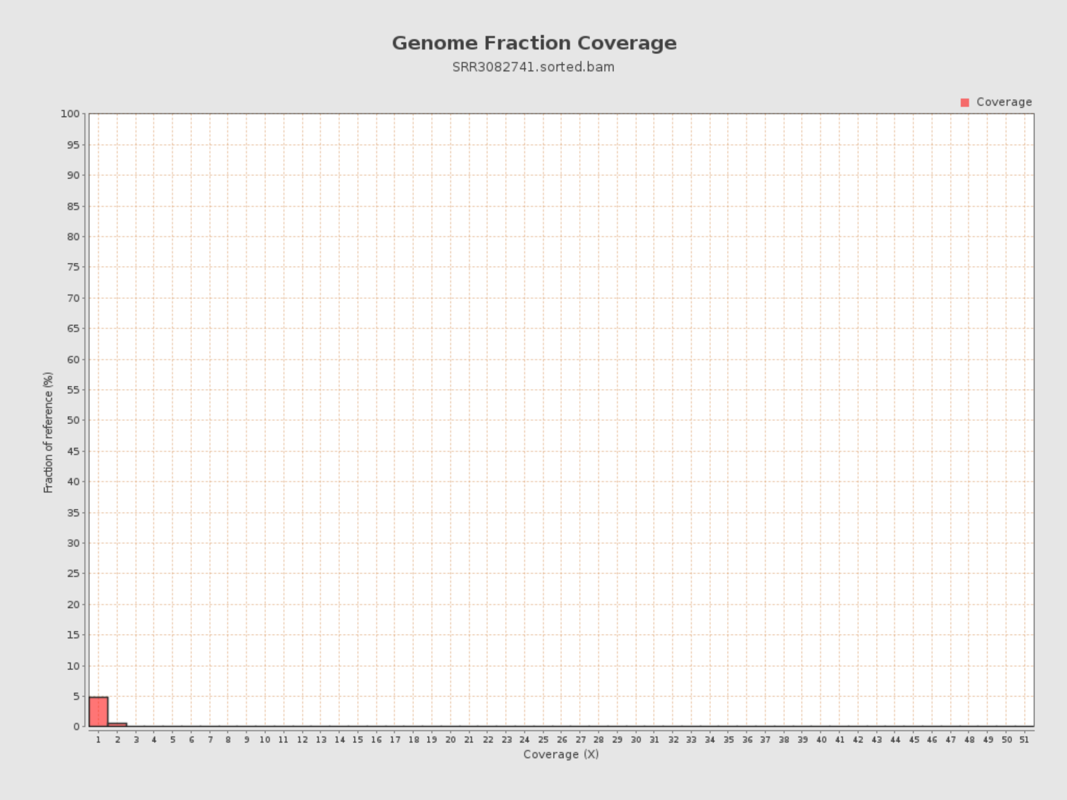
4. Results : Coverage Histogram



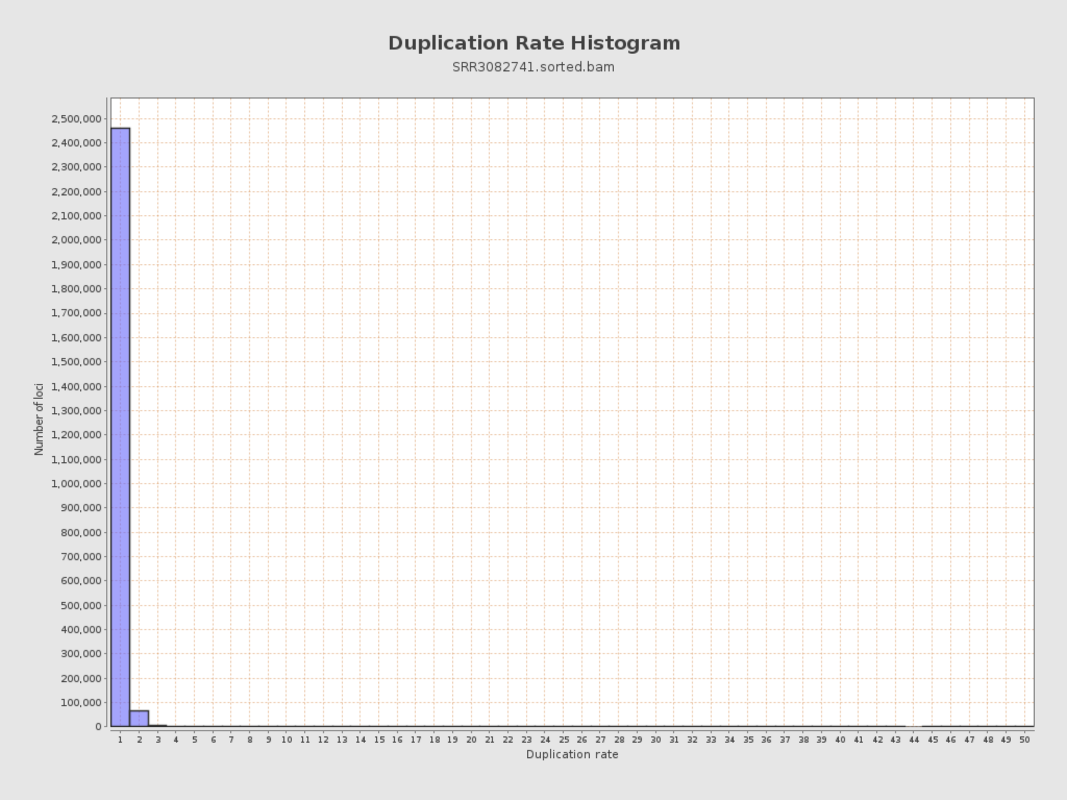
5. Results : Coverage Histogram (0-50X)



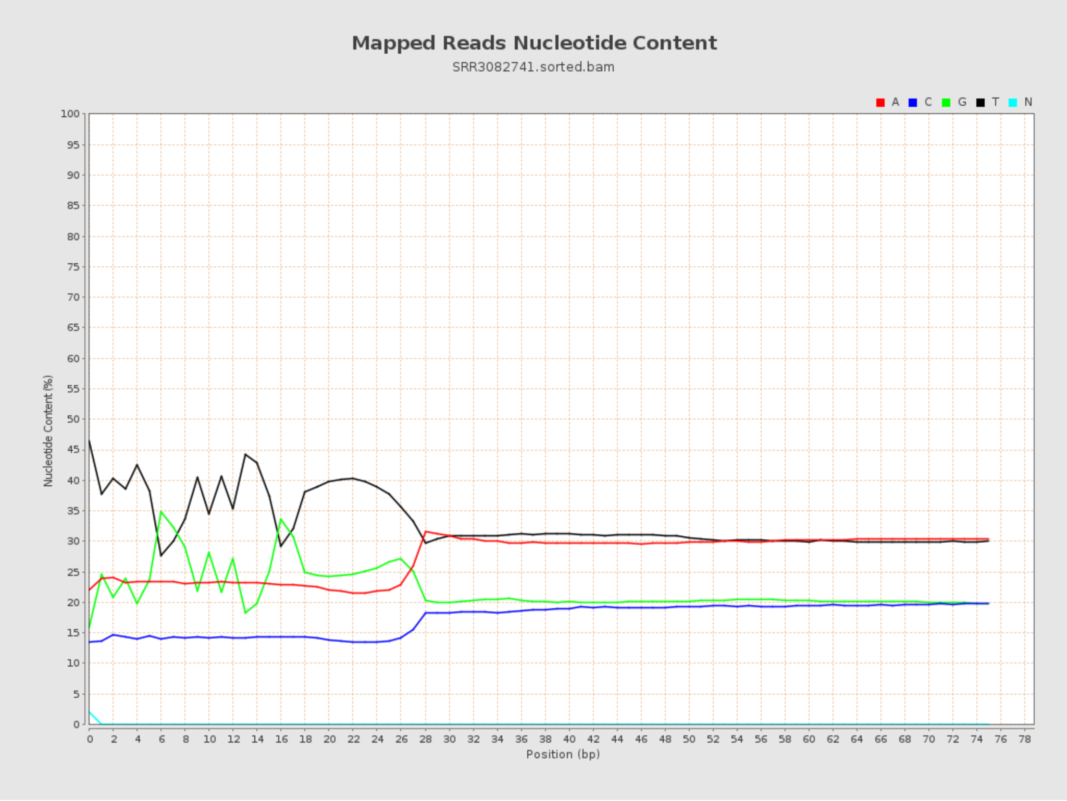
6. Results : Genome Fraction Coverage



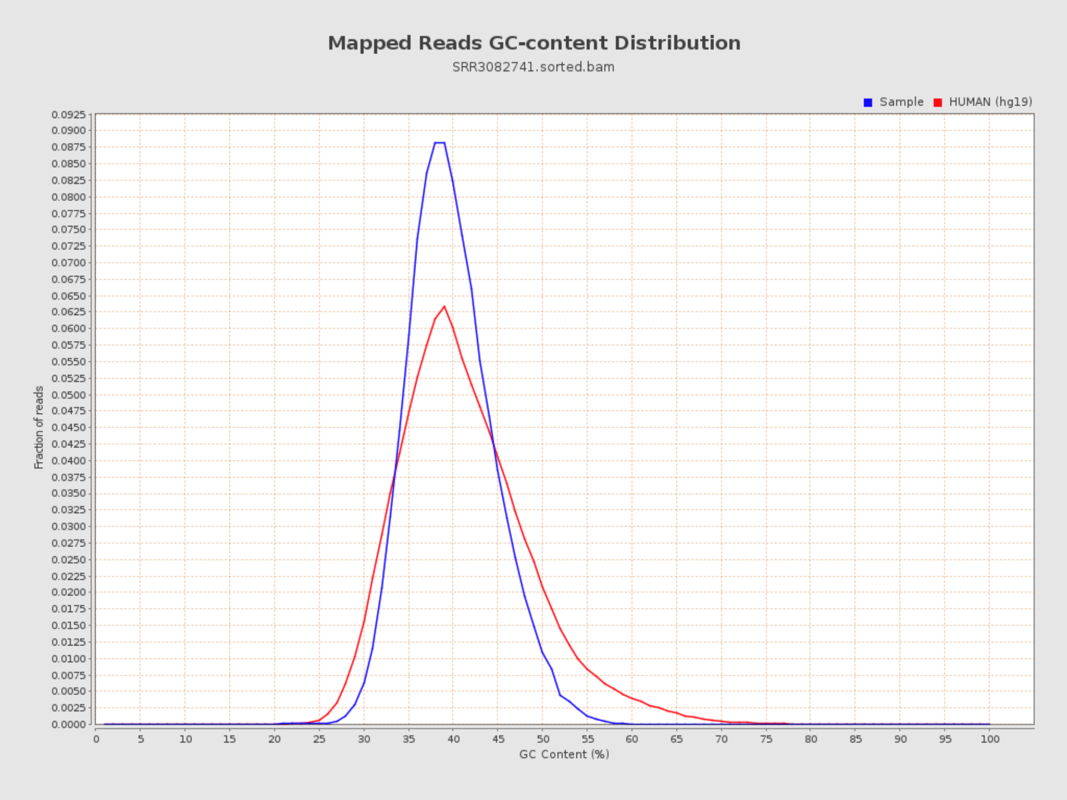
7. Results : Duplication Rate Histogram



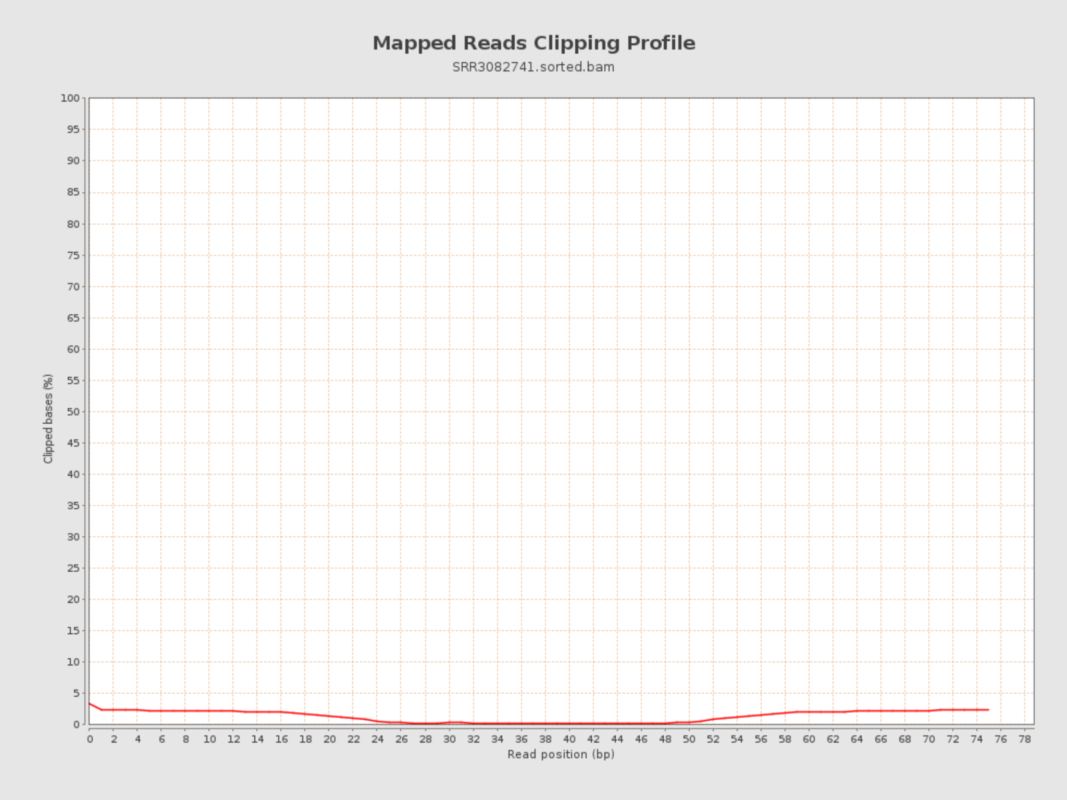
8. Results : Mapped Reads Nucleotide Content



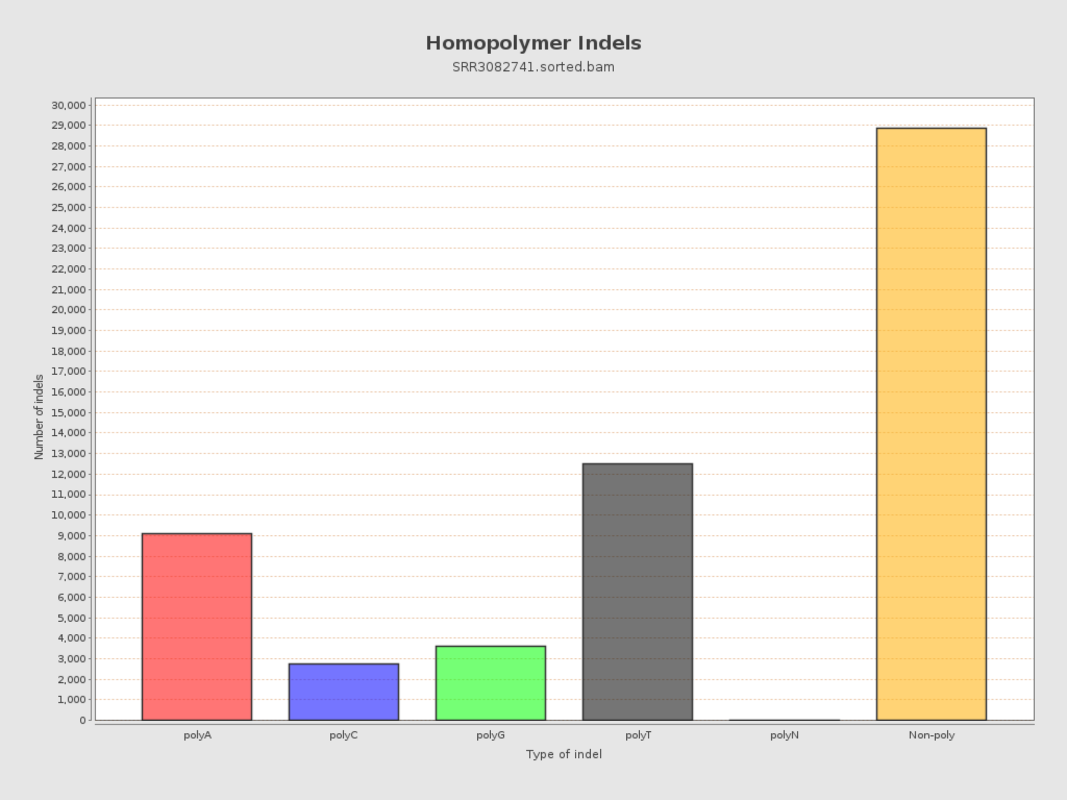
9. Results : Mapped Reads GC-content Distribution



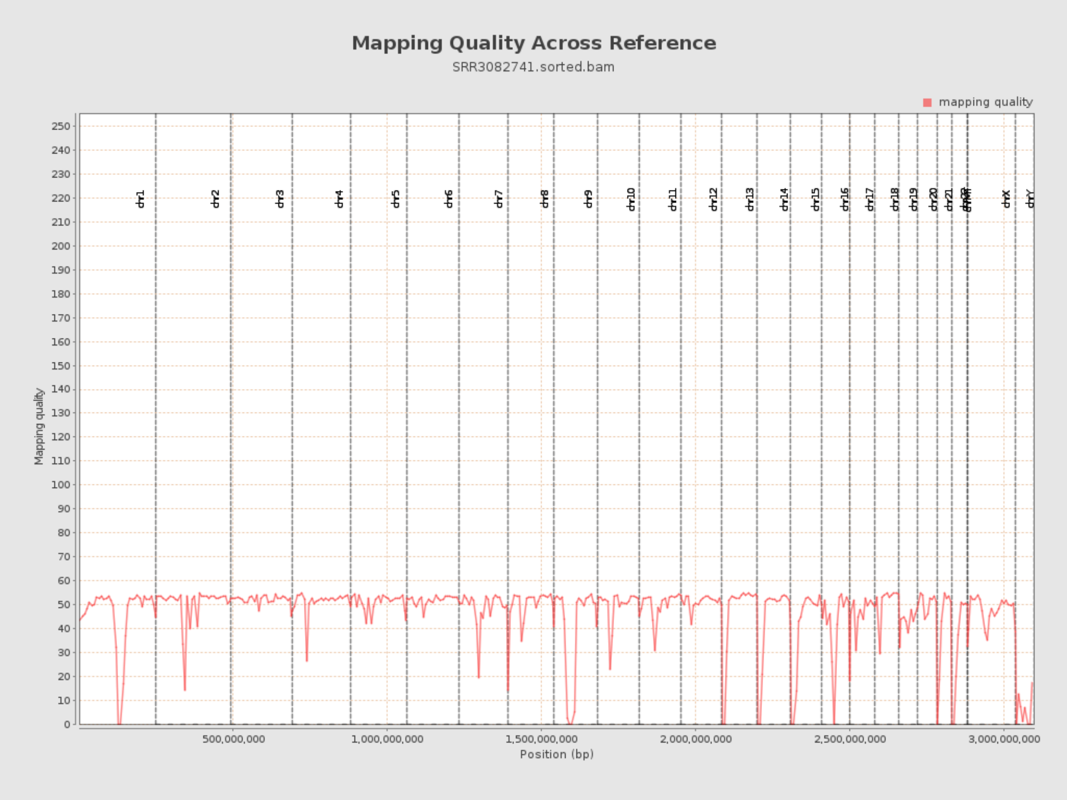
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram