Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 21:27:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082959.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_SRR3082959 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082959.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 21:27:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082959.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,122,048
Mapped reads	2,580,181 / 82.64%
Unmapped reads	541,867 / 17.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,037 / 0.45%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	115,937 / 3.71%
Duplication rate	3.38%
Clipped reads	1,060,869 / 33.98%

2.2. ACGT Content

Number/percentage of A's	48,870,620 / 28.06%
Number/percentage of C's	31,530,919 / 18.1%
Number/percentage of T's	56,371,362 / 32.37%
Number/percentage of G's	37,382,634 / 21.46%
Number/percentage of N's	17,317 / 0.01%
GC Percentage	39.57%

2.3. Coverage

Mean	0.0563

Standard Deviation	0.5003

2.4. Mapping Quality

Mean Mapping Quality	46.31

2.5. Mismatches and indels

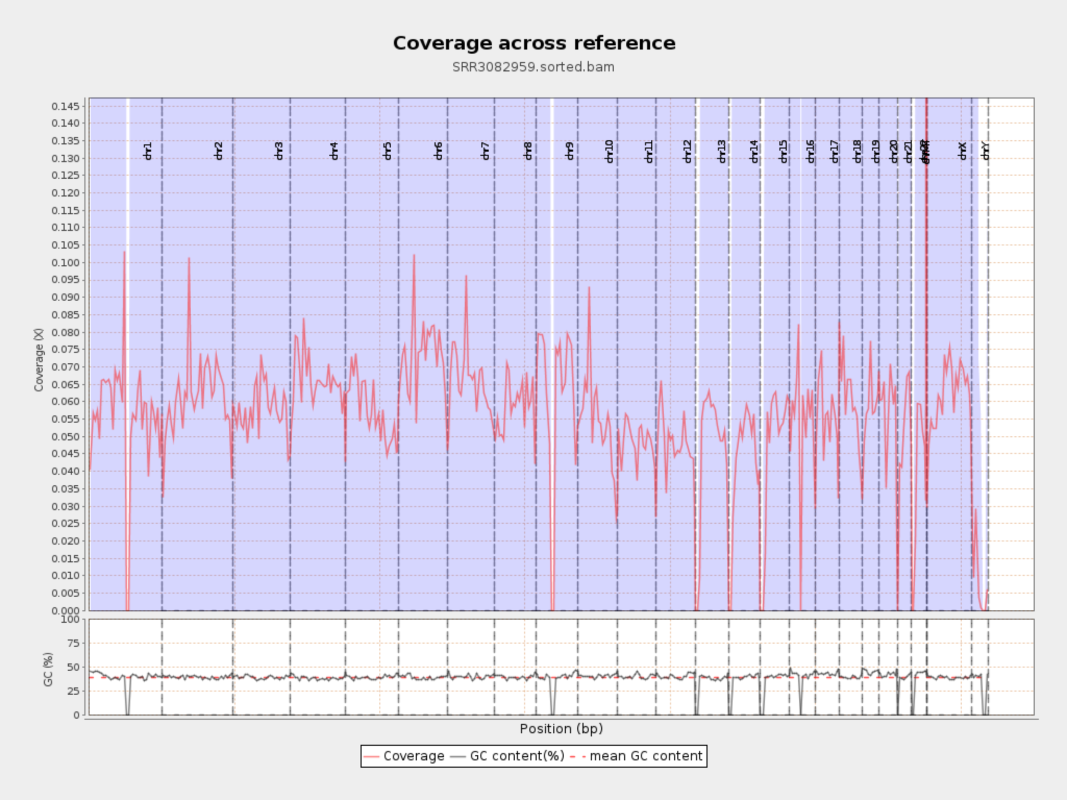
General error rate	0.95%
Mismatches	1,618,485
Insertions	16,441
Mapped reads with at least one insertion	0.63%
Deletions	43,748
Mapped reads with at least one deletion	1.68%
Homopolymer indels	47.62%

2.6. Chromosome stats

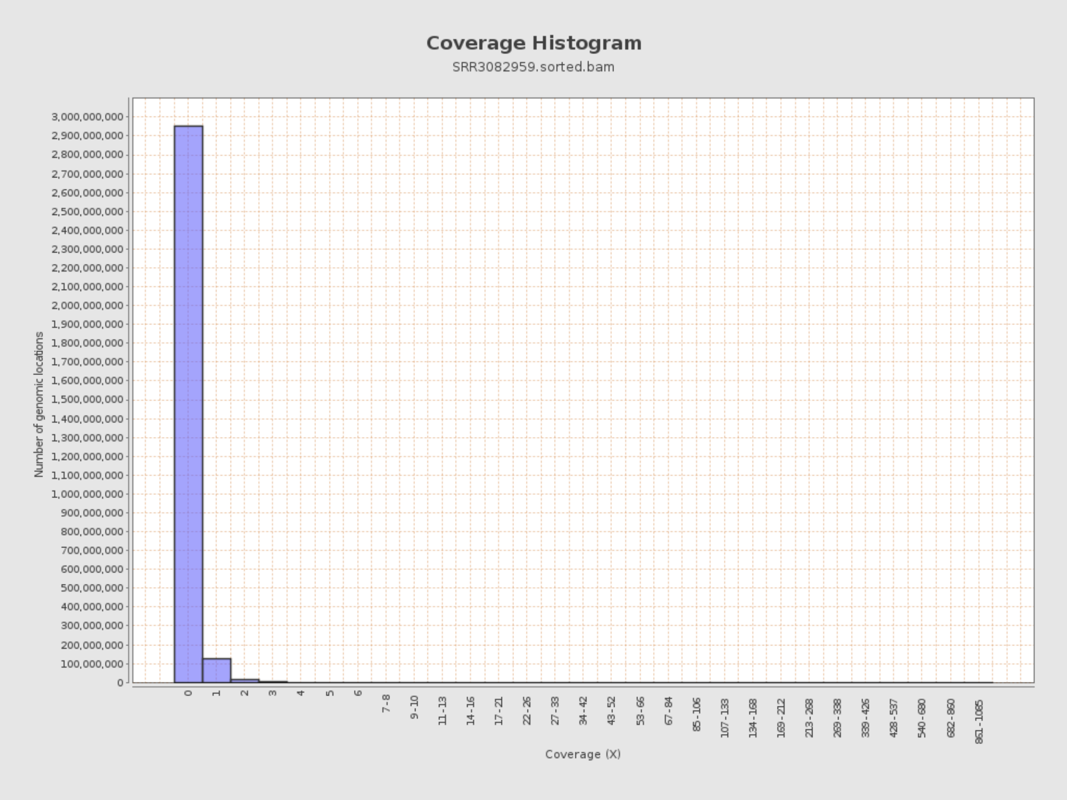
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13875552	0.0557	0.9588
chr2	243199373	14958694	0.0615	0.5568
chr3	198022430	11504488	0.0581	0.2842
chr4	191154276	12681261	0.0663	0.3289
chr5	180915260	10422605	0.0576	0.2839
chr6	171115067	12552686	0.0734	0.4063
chr7	159138663	10644858	0.0669	0.6231

chr8	146364022	8547213	0.0584	0.7175
chr9	141213431	8760976	0.062	0.5053
chr10	135534747	7468205	0.0551	0.4176
chr11	135006516	6493166	0.0481	0.3438
chr12	133851895	6462081	0.0483	0.2704
chr13	115169878	5214680	0.0453	0.2478
chr14	107349540	4516393	0.0421	0.2901
chr15	102531392	4680875	0.0457	0.2486
chr16	90354753	4862330	0.0538	0.3716
chr17	81195210	4473490	0.0551	0.3138
chr18	78077248	4738272	0.0607	0.9257
chr19	59128983	3459629	0.0585	0.6579
chr20	63025520	3612895	0.0573	0.2966
chr21	48129895	2340411	0.0486	0.302
chr22	51304566	1896925	0.037	0.2239
chrMT	16571	13640	0.8231	1.0234
chrX	155270560	9580644	0.0617	0.3204
chrY	59373566	488212	0.0082	0.2623

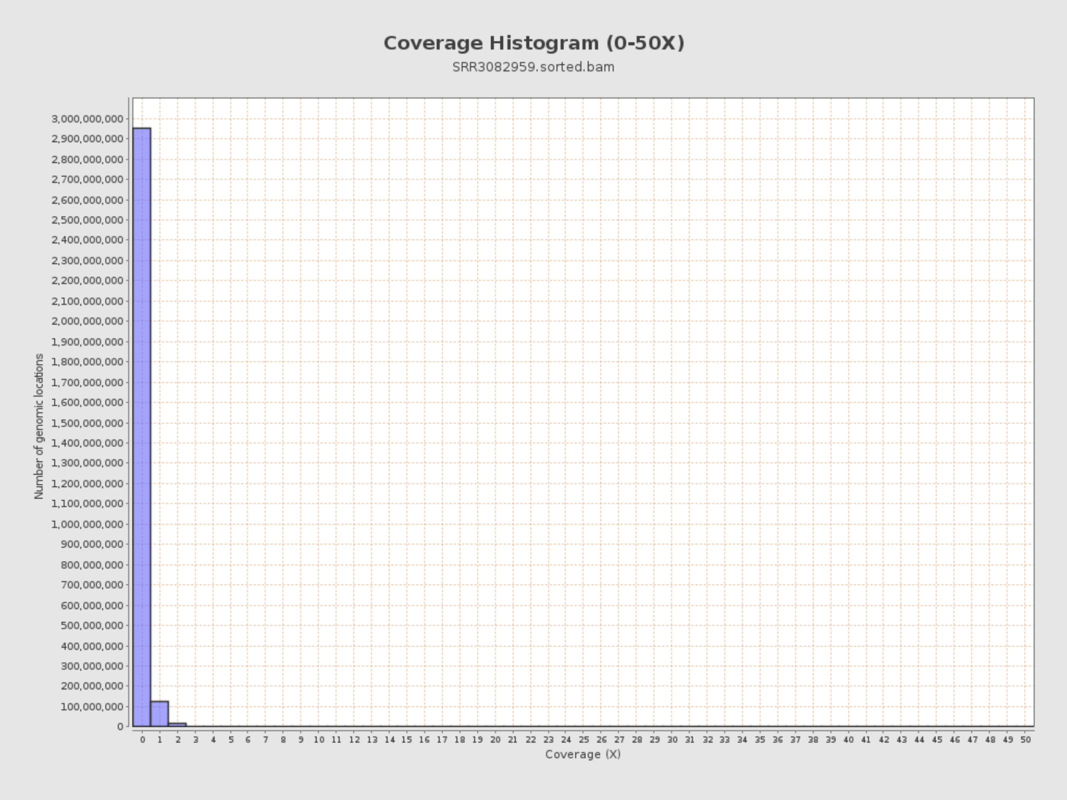
3. Results : Coverage across reference



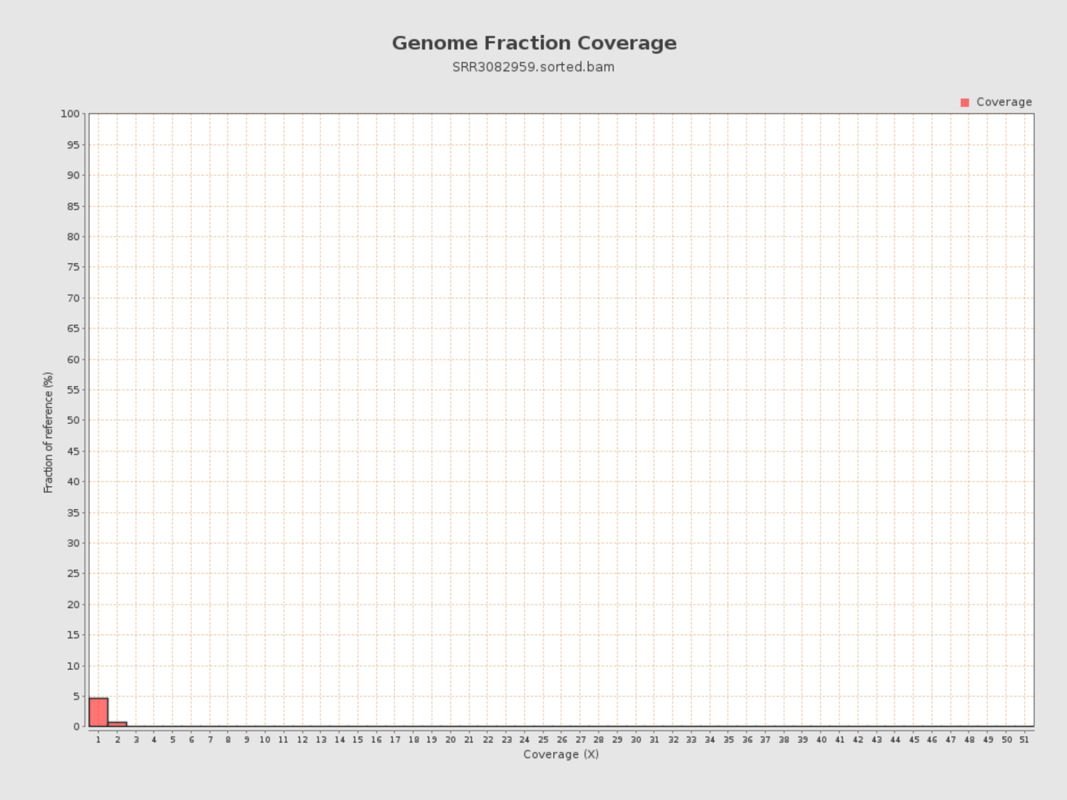
4. Results : Coverage Histogram



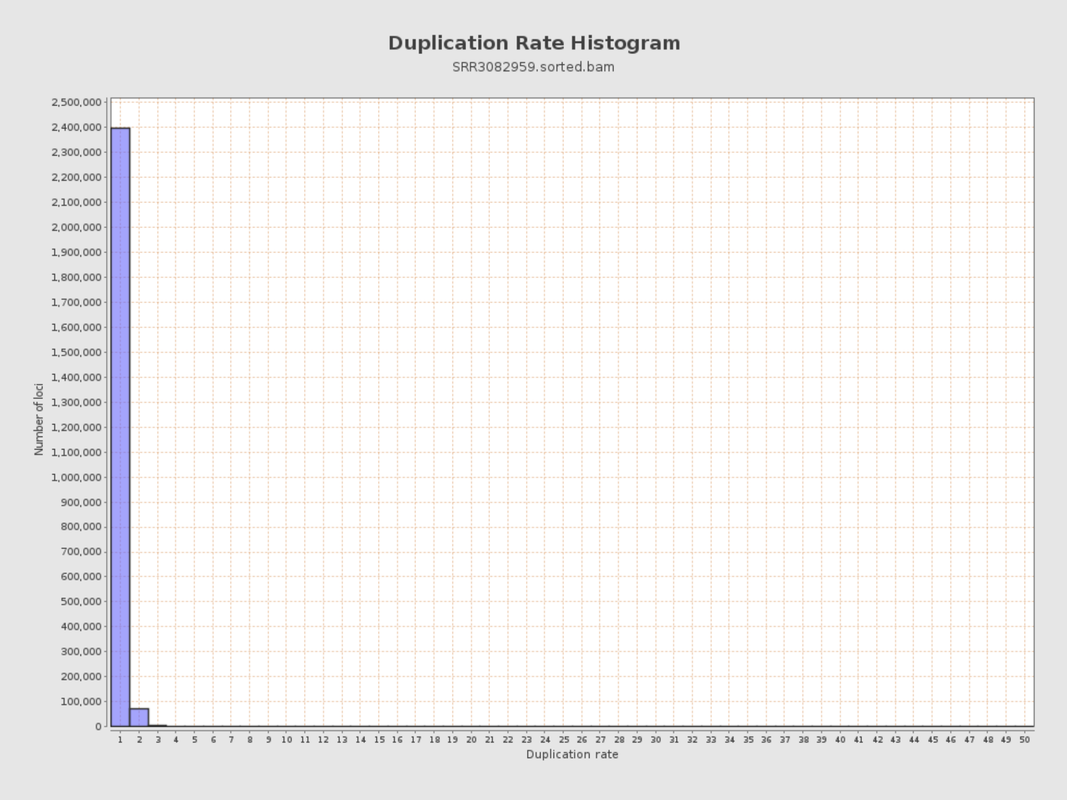
5. Results : Coverage Histogram (0-50X)



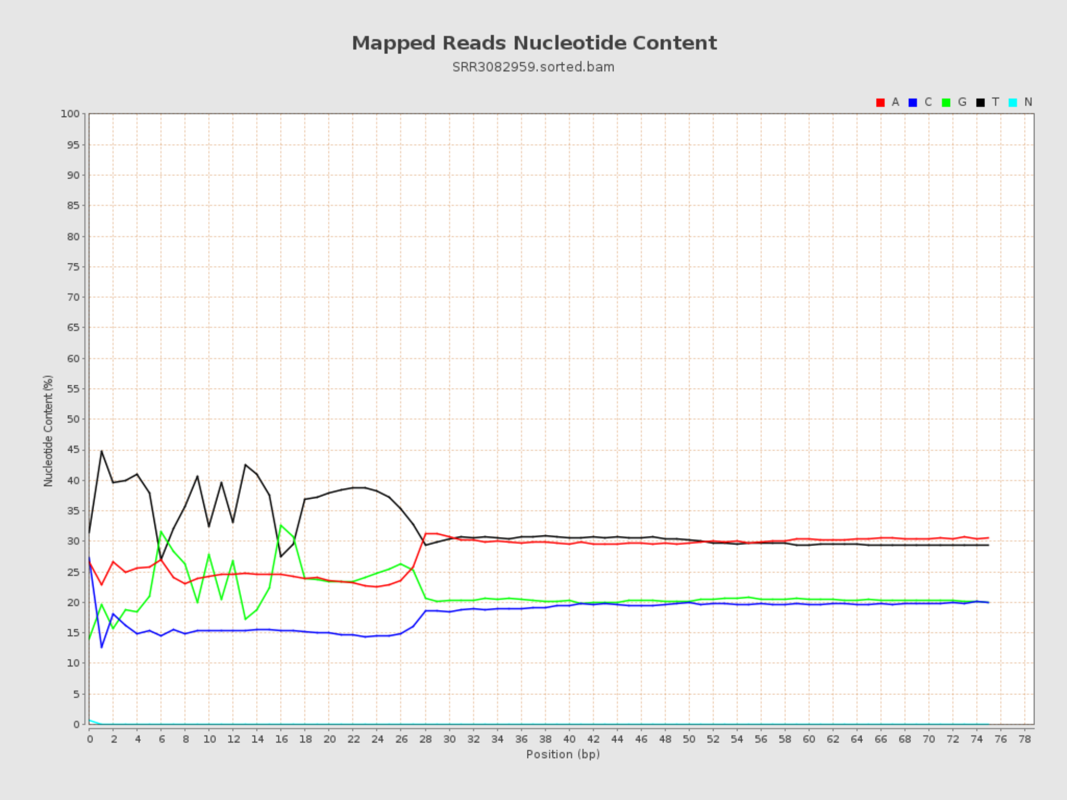
6. Results : Genome Fraction Coverage



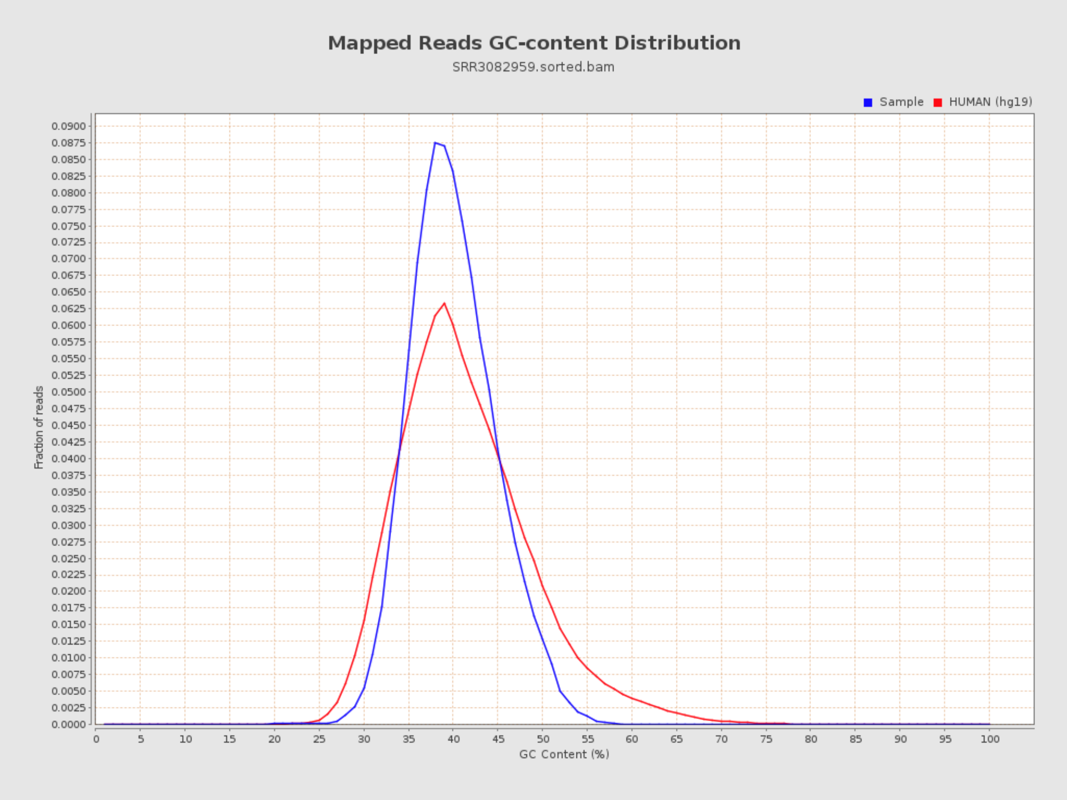
7. Results : Duplication Rate Histogram



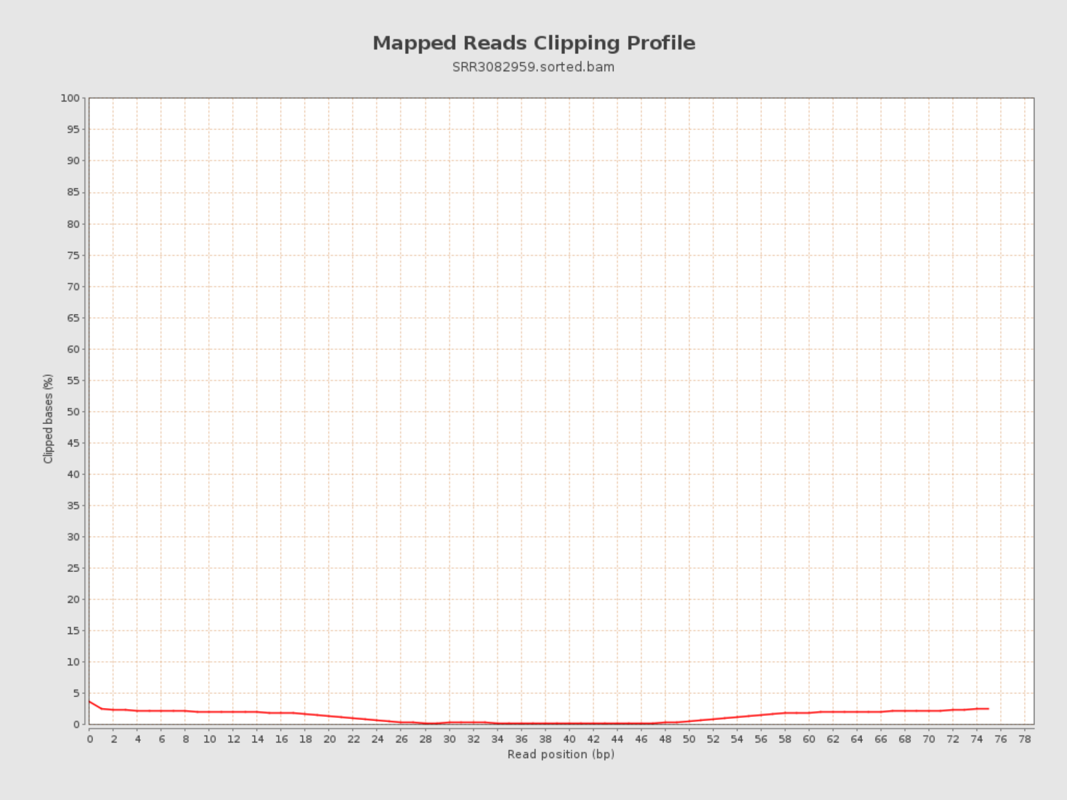
8. Results : Mapped Reads Nucleotide Content



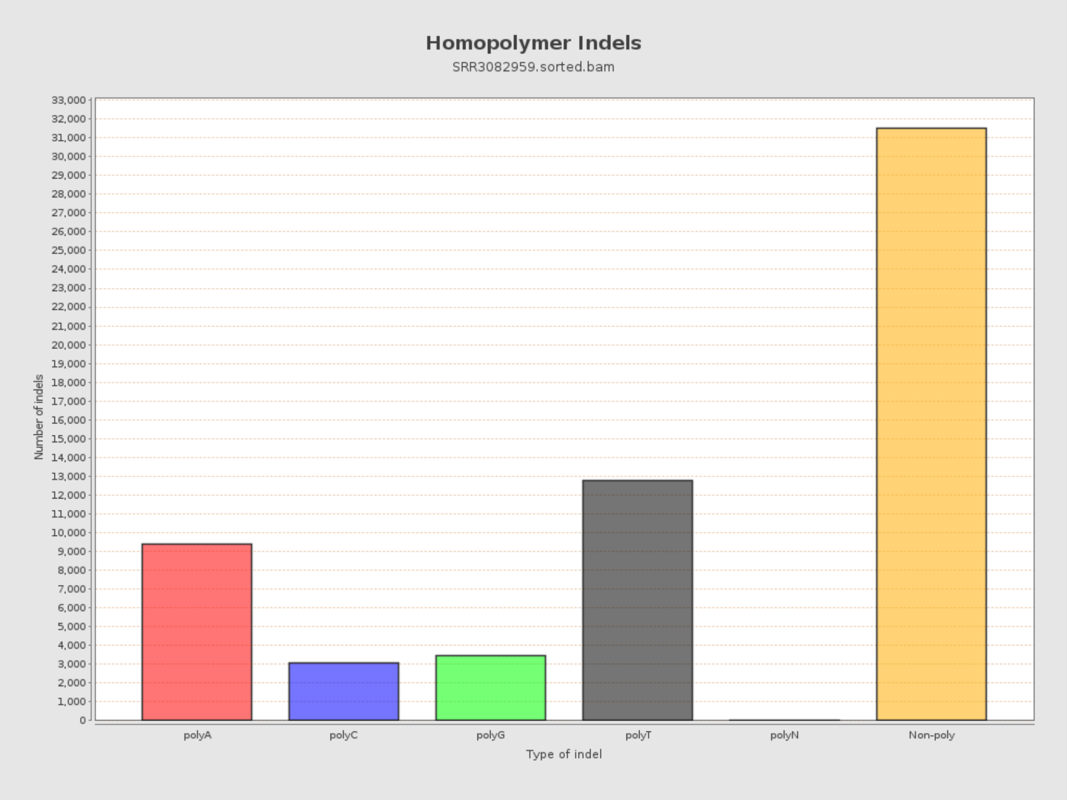
9. Results : Mapped Reads GC-content Distribution



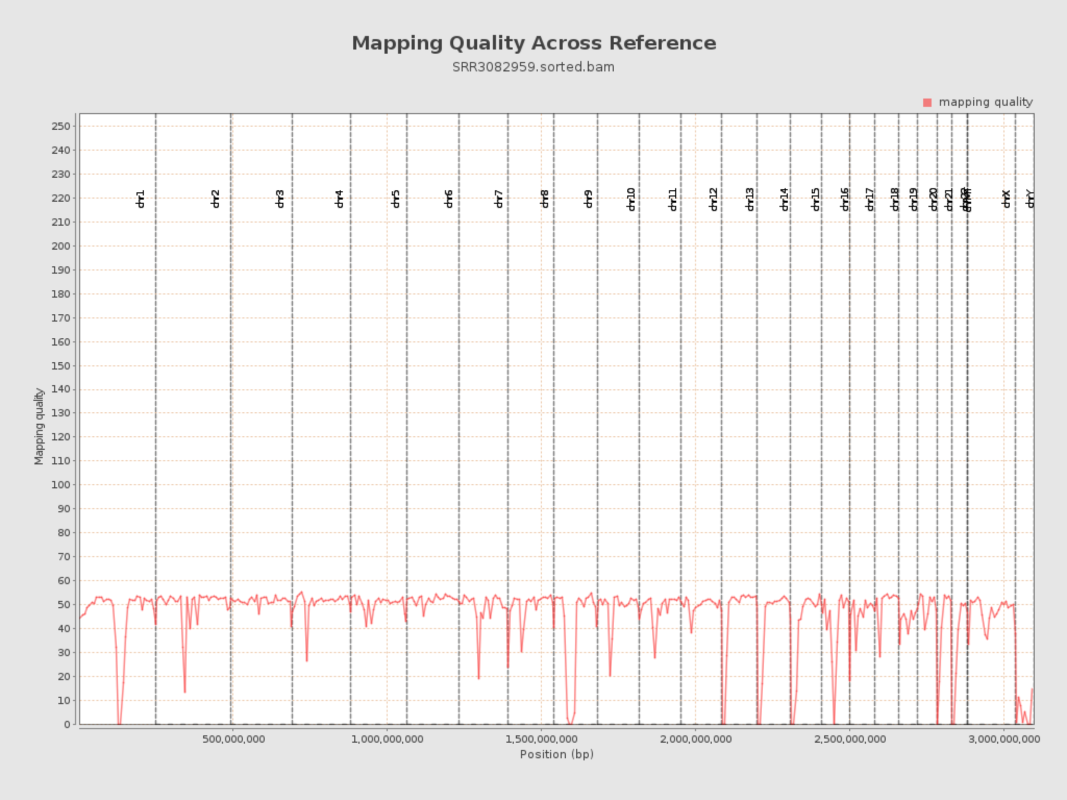
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram