Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 22:06:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082973.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_SRR3082973 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082973.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 22:06:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082973.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,032,312
Mapped reads	2,525,387 / 83.28%
Unmapped reads	506,925 / 16.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,802 / 0.78%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	91,430 / 3.02%
Duplication rate	2.75%
Clipped reads	1,130,727 / 37.29%

2.2. ACGT Content

Number/percentage of A's	49,107,686 / 29%
Number/percentage of C's	30,935,306 / 18.27%
Number/percentage of T's	52,859,933 / 31.22%
Number/percentage of G's	36,420,866 / 21.51%
Number/percentage of N's	16,010 / 0.01%
GC Percentage	39.78%

2.3. Coverage

Mean	0.0547

Standard Deviation	0.4325

2.4. Mapping Quality

Mean Mapping Quality	46.1

2.5. Mismatches and indels

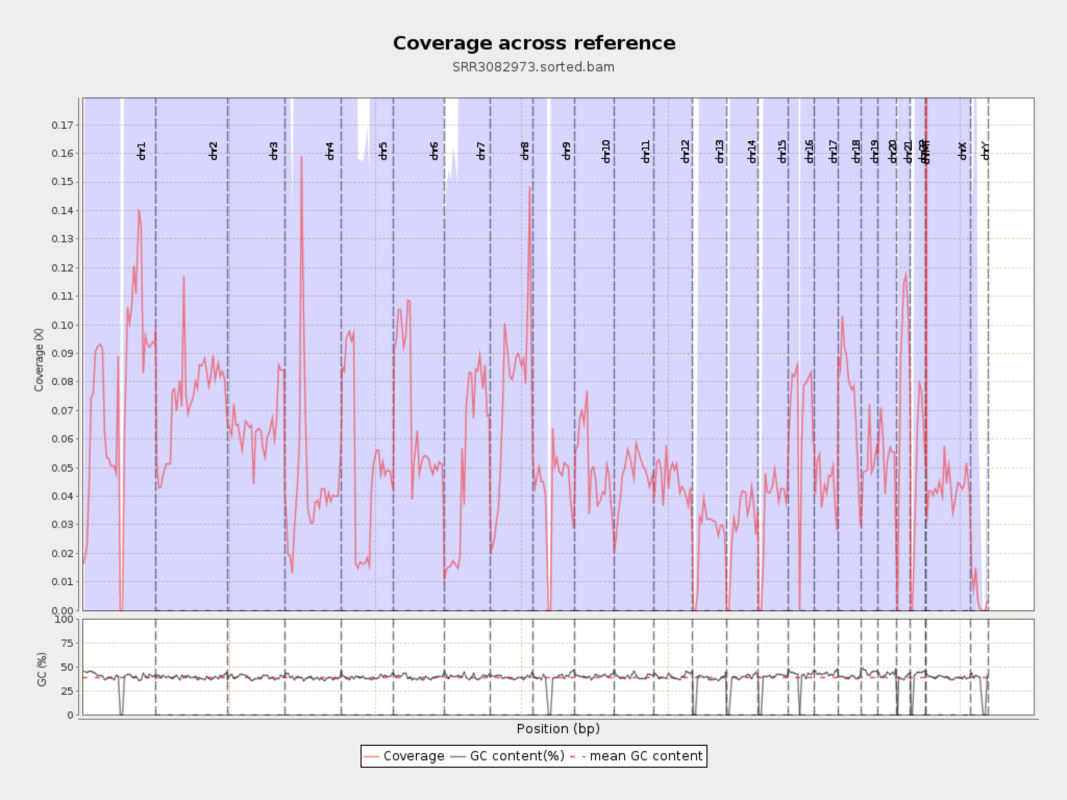
General error rate	0.94%
Mismatches	1,572,340
Insertions	14,295
Mapped reads with at least one insertion	0.56%
Deletions	38,993
Mapped reads with at least one deletion	1.53%
Homopolymer indels	47.44%

2.6. Chromosome stats

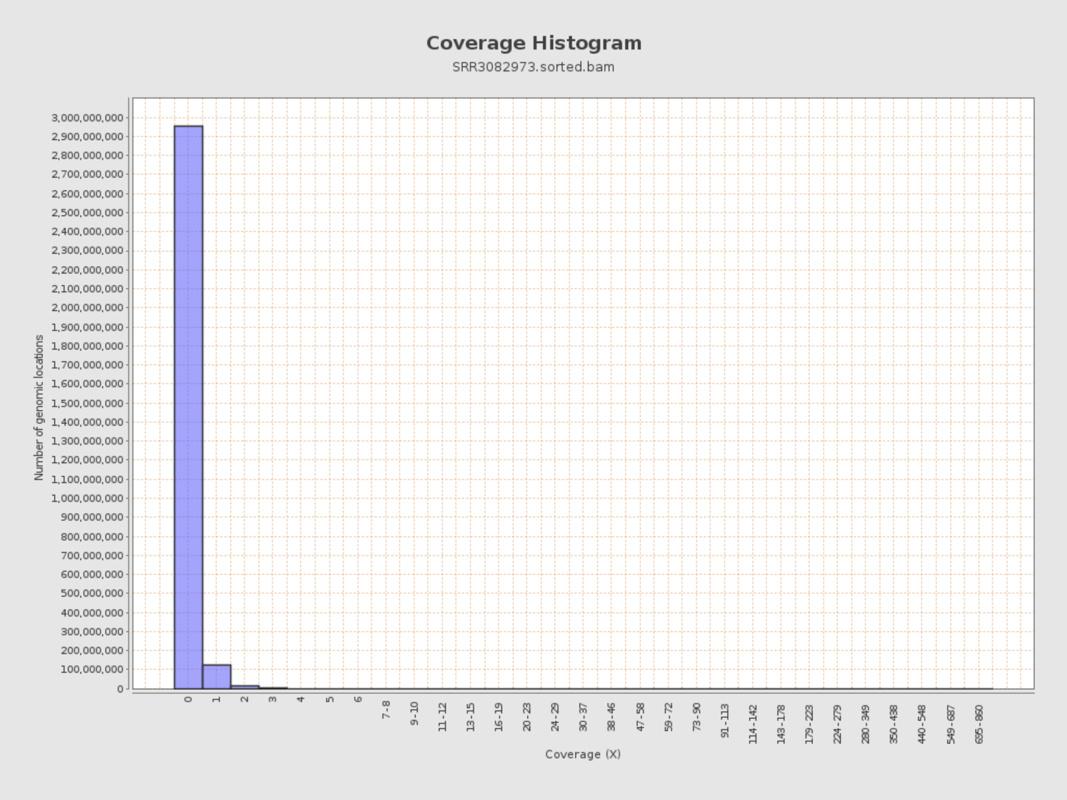
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19021164	0.0763	0.7985
chr2	243199373	17980665	0.0739	0.5421
chr3	198022430	12796325	0.0646	0.2895
chr4	191154276	8637002	0.0452	0.253
chr5	180915260	9139427	0.0505	0.2604
chr6	171115067	11656462	0.0681	0.3656
chr7	159138663	8311213	0.0522	0.3764

chr8	146364022	11010534	0.0752	0.5111
chr9	141213431	5941959	0.0421	0.4153
chr10	135534747	6791513	0.0501	0.3736
chr11	135006516	6324138	0.0468	0.3452
chr12	133851895	6088604	0.0455	0.25
chr13	115169878	2976961	0.0258	0.1807
chr14	107349540	3239455	0.0302	0.2623
chr15	102531392	3560246	0.0347	0.2099
chr16	90354753	6200534	0.0686	0.3426
chr17	81195210	3585929	0.0442	0.2775
chr18	78077248	6029632	0.0772	0.9966
chr19	59128983	3100194	0.0524	0.5407
chr20	63025520	3475764	0.0551	0.2843
chr21	48129895	3957346	0.0822	0.3424
chr22	51304566	2468287	0.0481	0.2498
chrMT	16571	117299	7.0786	6.2921
chrX	155270560	6692166	0.0431	0.2754
chrY	59373566	304956	0.0051	0.1139

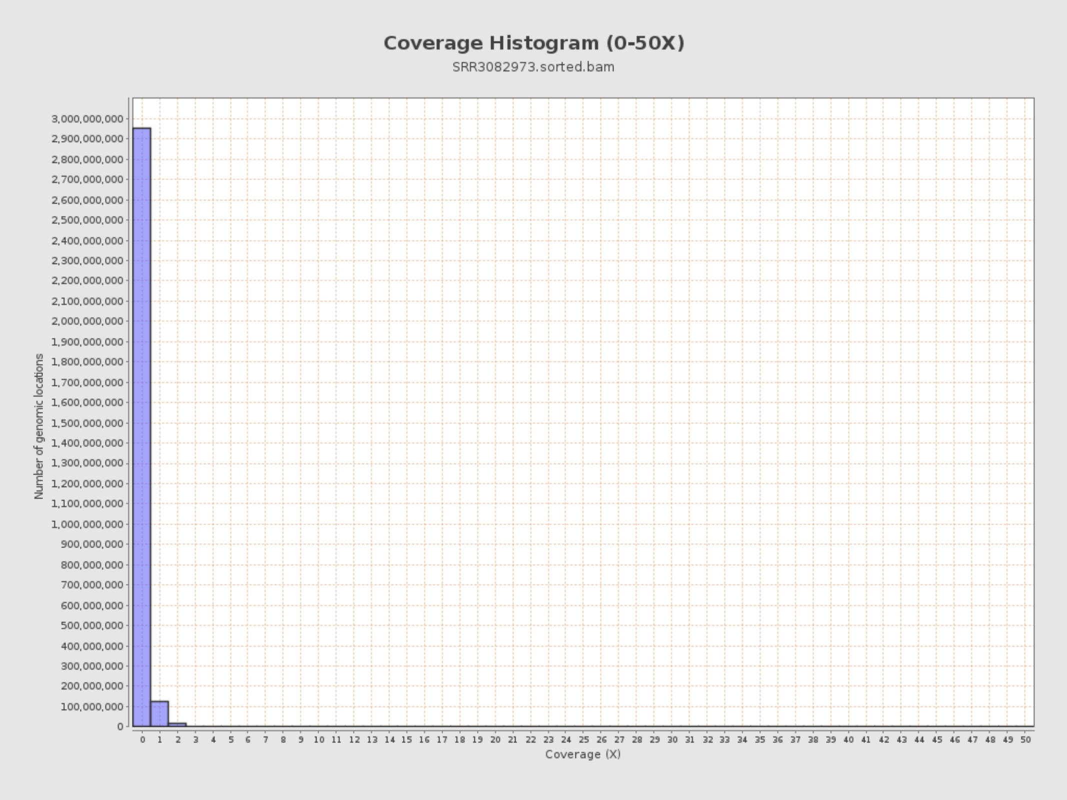
3. Results : Coverage across reference



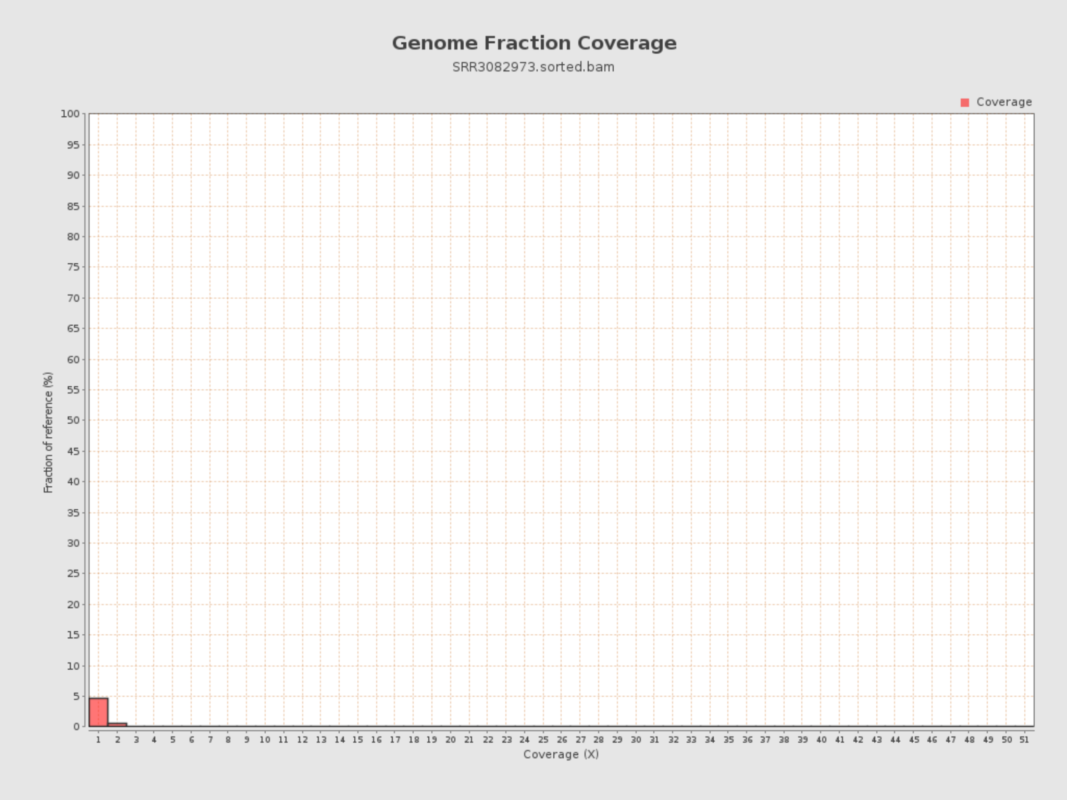
4. Results : Coverage Histogram



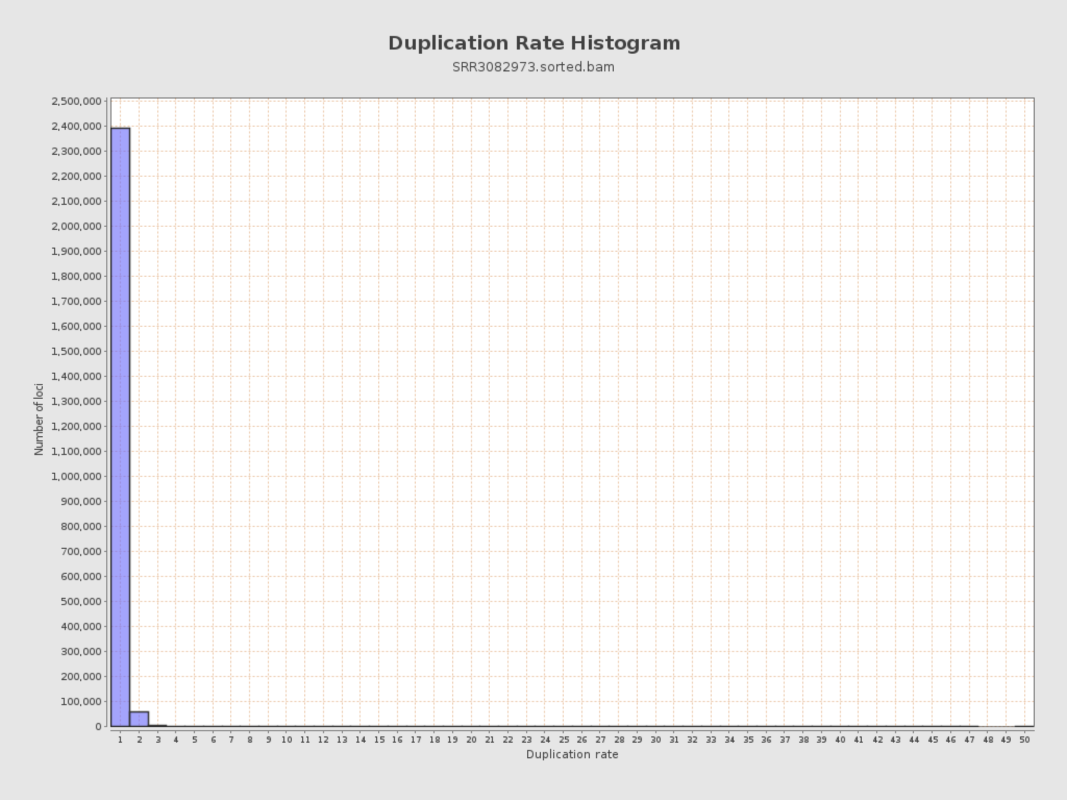
5. Results : Coverage Histogram (0-50X)



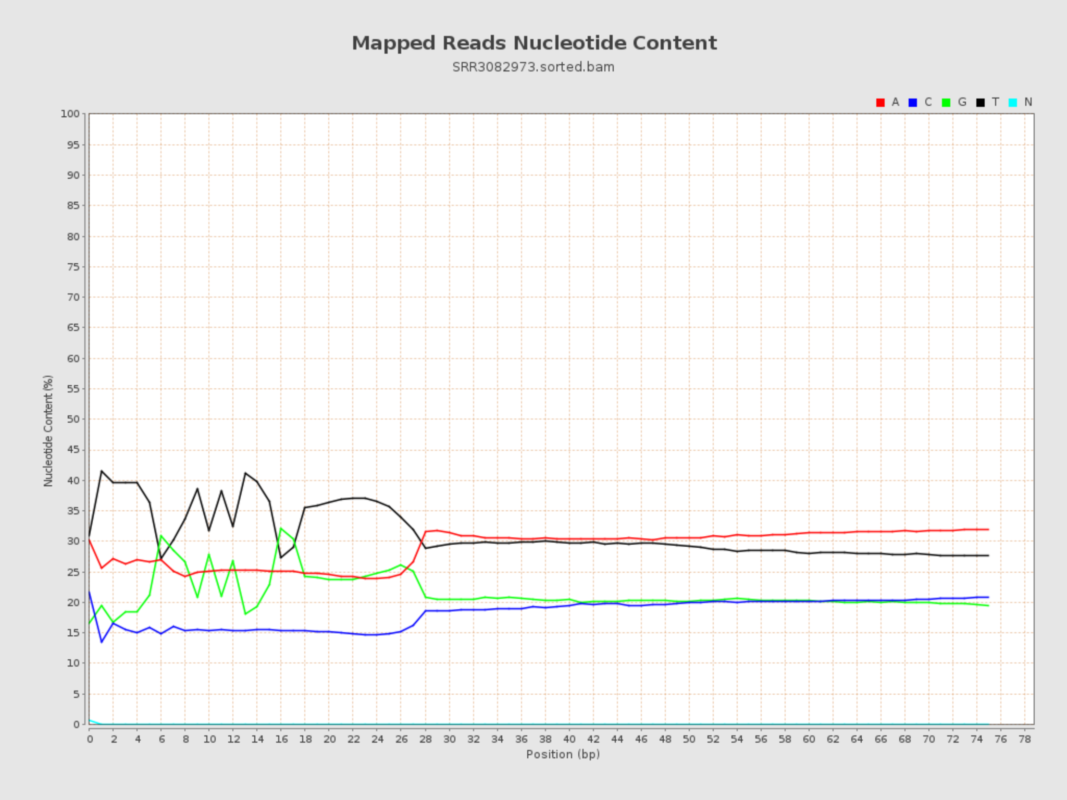
6. Results : Genome Fraction Coverage



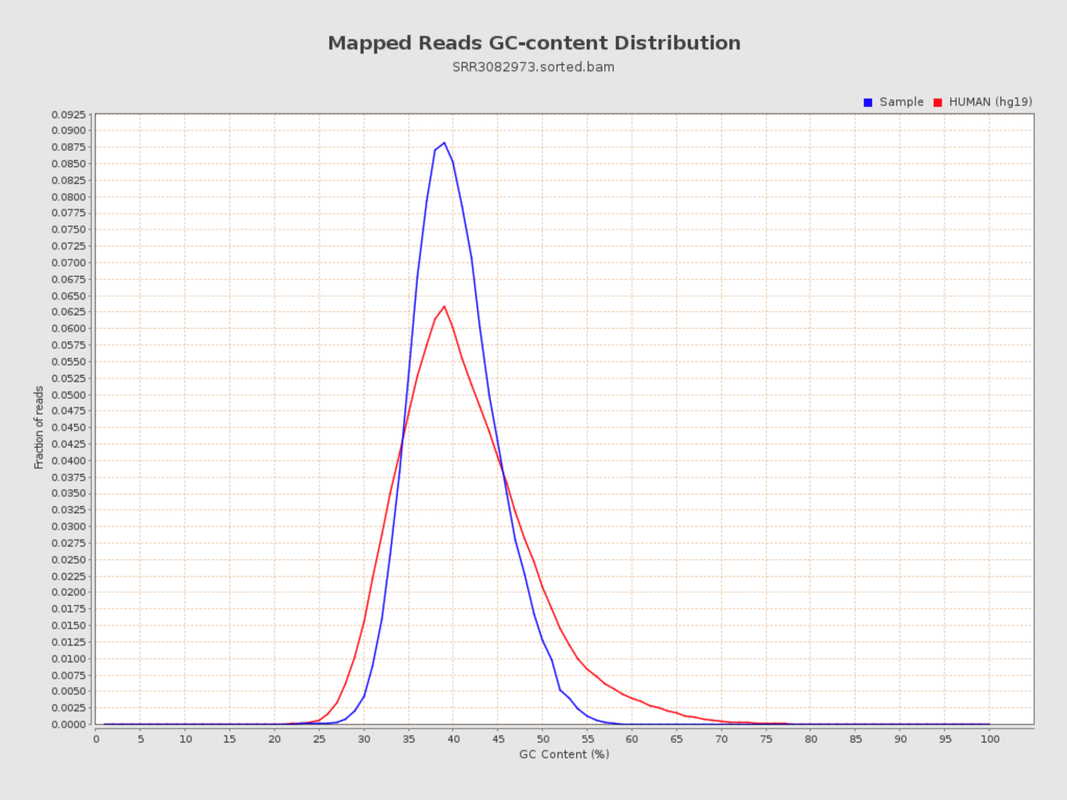
7. Results : Duplication Rate Histogram



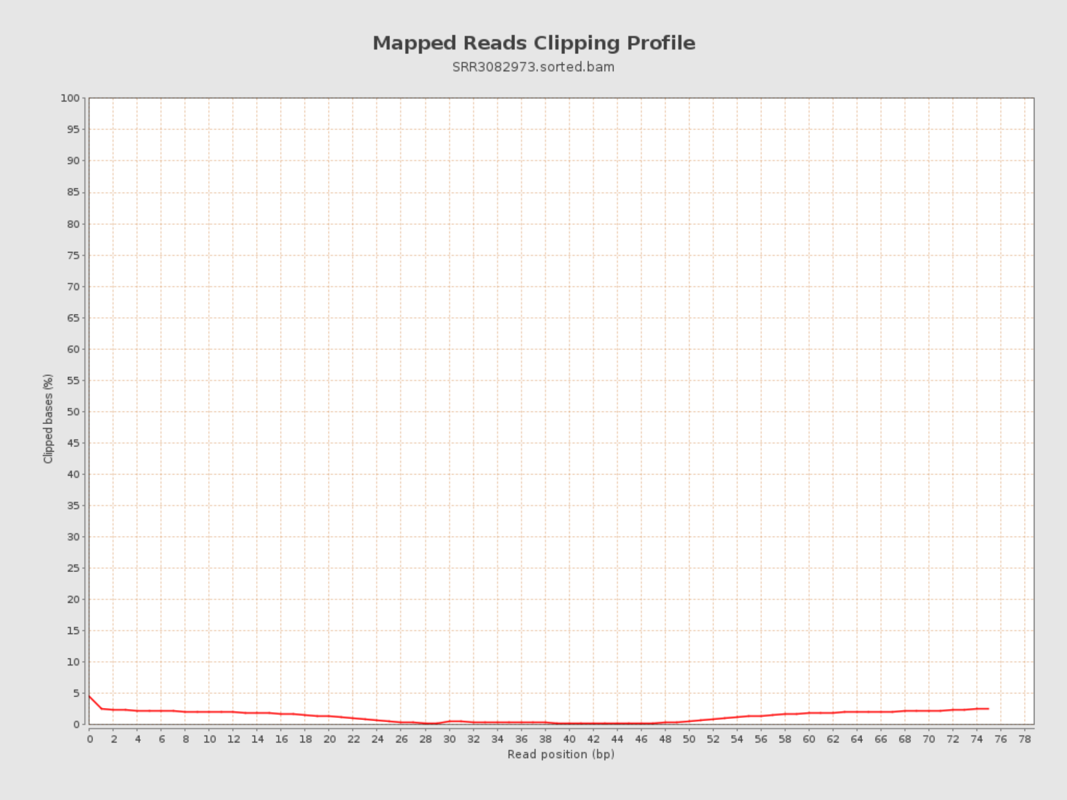
8. Results : Mapped Reads Nucleotide Content



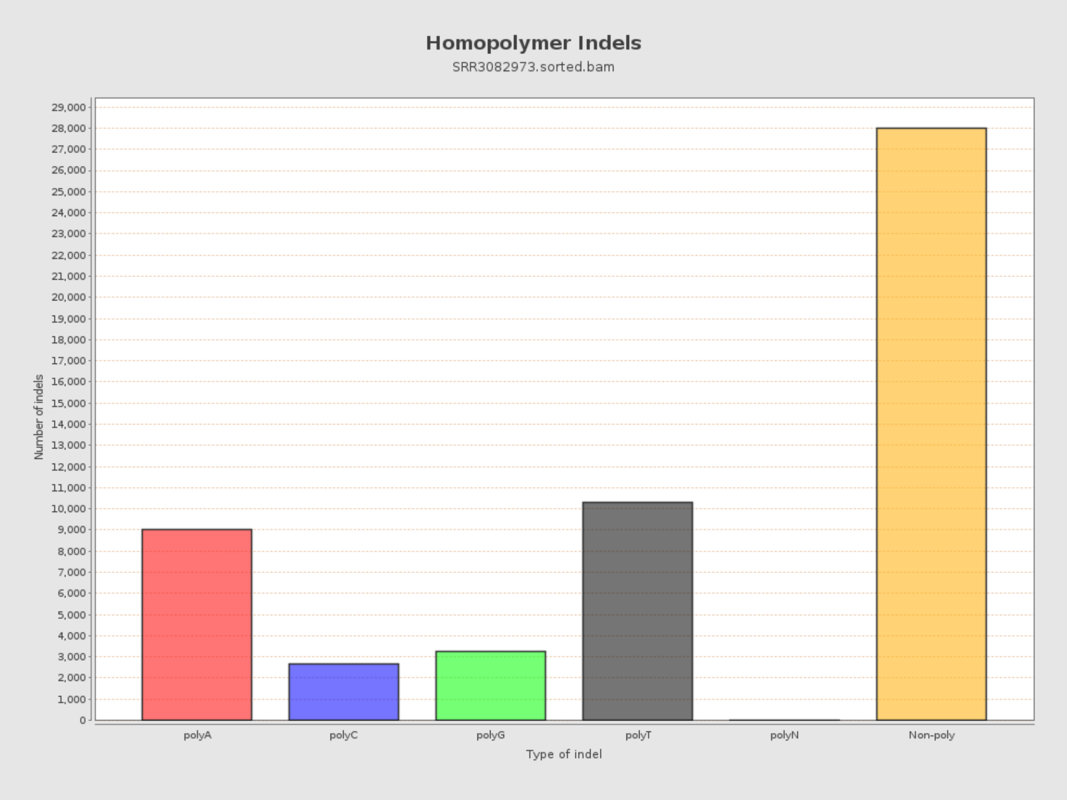
9. Results : Mapped Reads GC-content Distribution



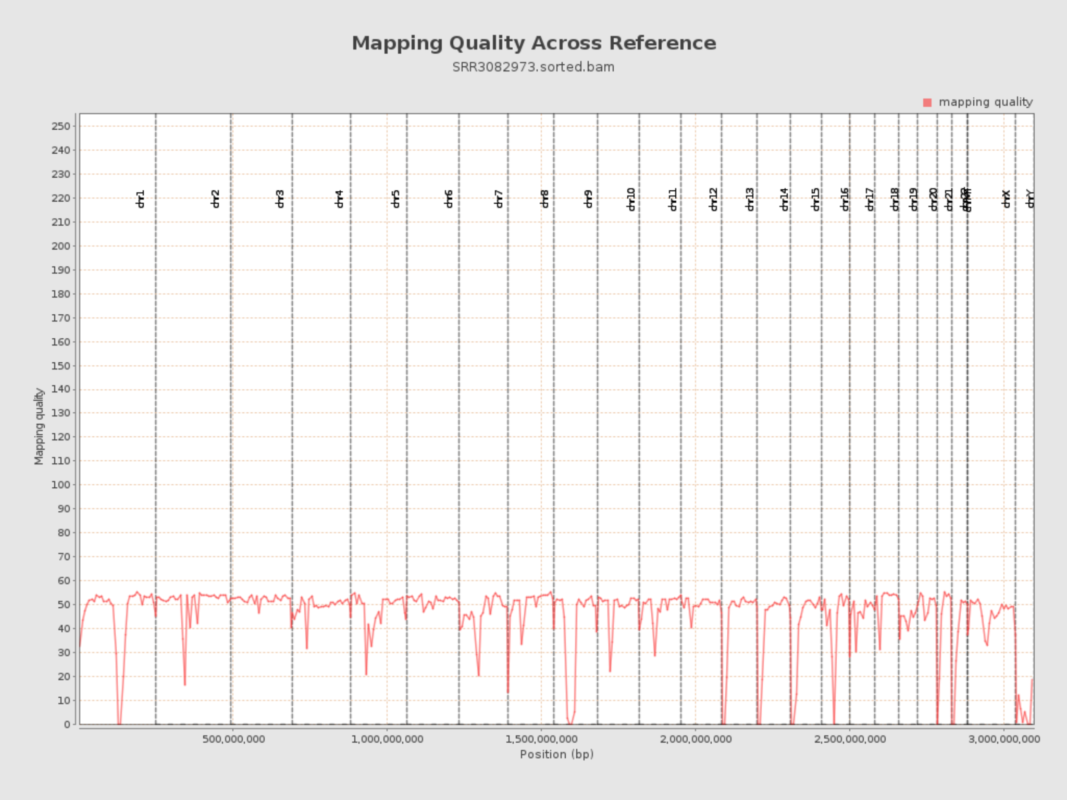
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram