Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 03:51:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085138.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_SRR3085138 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085138.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 03:51:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085138.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,545,873
Mapped reads	2,315,092 / 90.94%
Unmapped reads	230,781 / 9.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,350 / 0.92%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	84,891 / 3.33%
Duplication rate	2.85%
Clipped reads	960,527 / 37.73%

2.2. ACGT Content

Number/percentage of A's	44,539,042 / 28.39%
Number/percentage of C's	29,039,747 / 18.51%
Number/percentage of T's	49,325,786 / 31.44%
Number/percentage of G's	33,944,602 / 21.64%
Number/percentage of N's	34,946 / 0.02%
GC Percentage	40.15%

2.3. Coverage

Mean	0.0507

Standard Deviation	0.3967

2.4. Mapping Quality

Mean Mapping Quality	46.77

2.5. Mismatches and indels

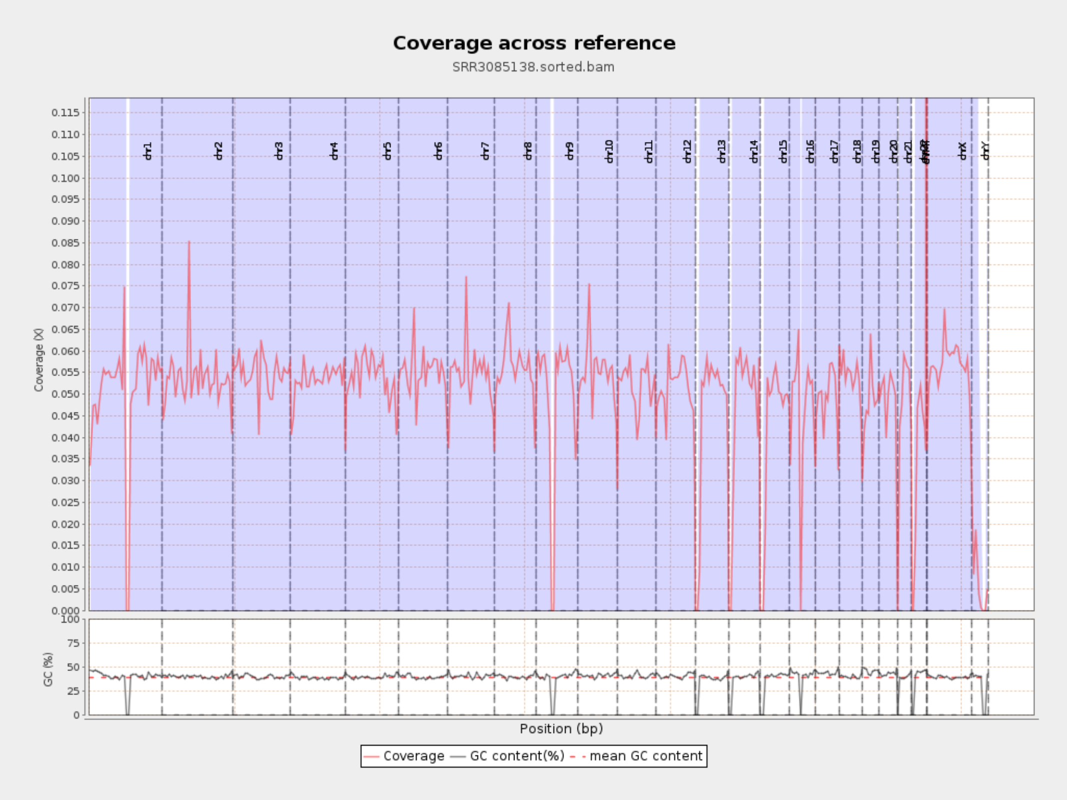
General error rate	0.89%
Mismatches	1,379,078
Insertions	12,487
Mapped reads with at least one insertion	0.53%
Deletions	35,915
Mapped reads with at least one deletion	1.54%
Homopolymer indels	47.25%

2.6. Chromosome stats

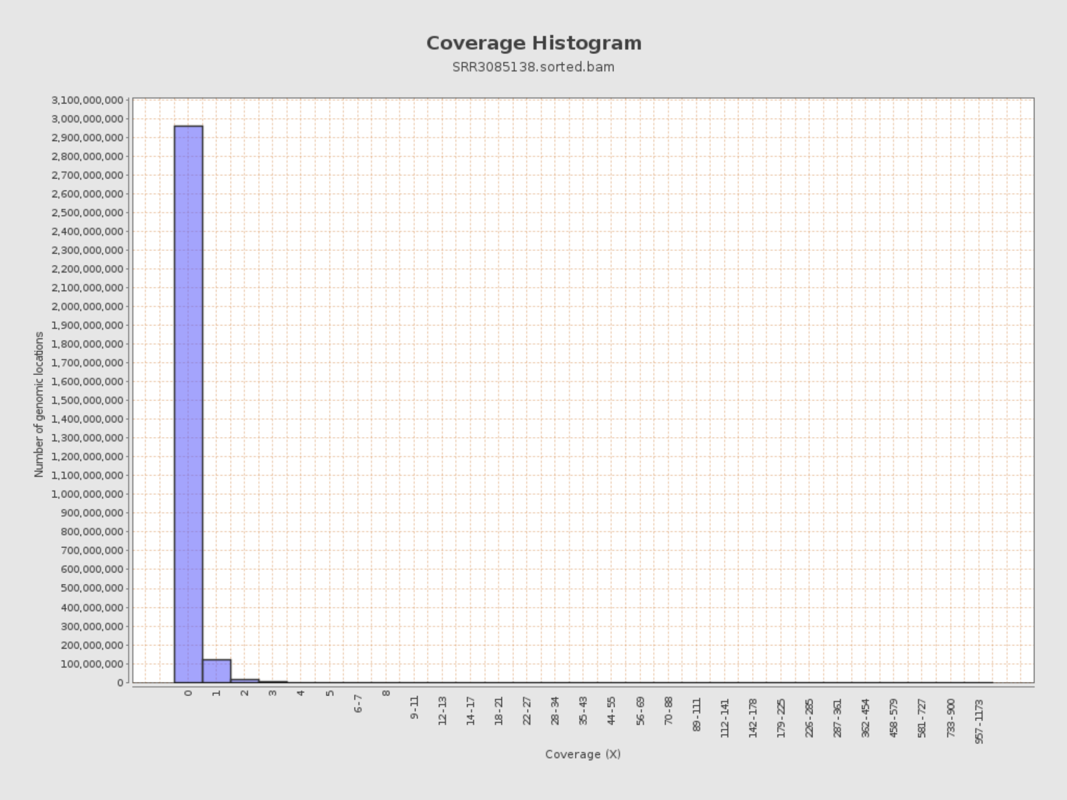
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12612566	0.0506	0.6306
chr2	243199373	13094585	0.0538	0.4671
chr3	198022430	10862331	0.0549	0.2591
chr4	191154276	10215594	0.0534	0.2679
chr5	180915260	9762002	0.054	0.2589
chr6	171115067	9448697	0.0552	0.3054
chr7	159138663	8758127	0.055	0.4654

chr8	146364022	8176789	0.0559	0.7482
chr9	141213431	6900515	0.0489	0.3569
chr10	135534747	7495497	0.0553	0.3655
chr11	135006516	7014536	0.052	0.3368
chr12	133851895	6935279	0.0518	0.2545
chr13	115169878	5119206	0.0444	0.2361
chr14	107349540	4867968	0.0453	0.2499
chr15	102531392	4261747	0.0416	0.2309
chr16	90354753	4185273	0.0463	0.2653
chr17	81195210	3969215	0.0489	0.2656
chr18	78077248	4254385	0.0545	0.6449
chr19	59128983	2873749	0.0486	0.5309
chr20	63025520	3099689	0.0492	0.2499
chr21	48129895	2230054	0.0463	0.2524
chr22	51304566	1645305	0.0321	0.1962
chrMT	16571	14014	0.8457	0.9226
chrX	155270560	8767910	0.0565	0.2913
chrY	59373566	377539	0.0064	0.1384

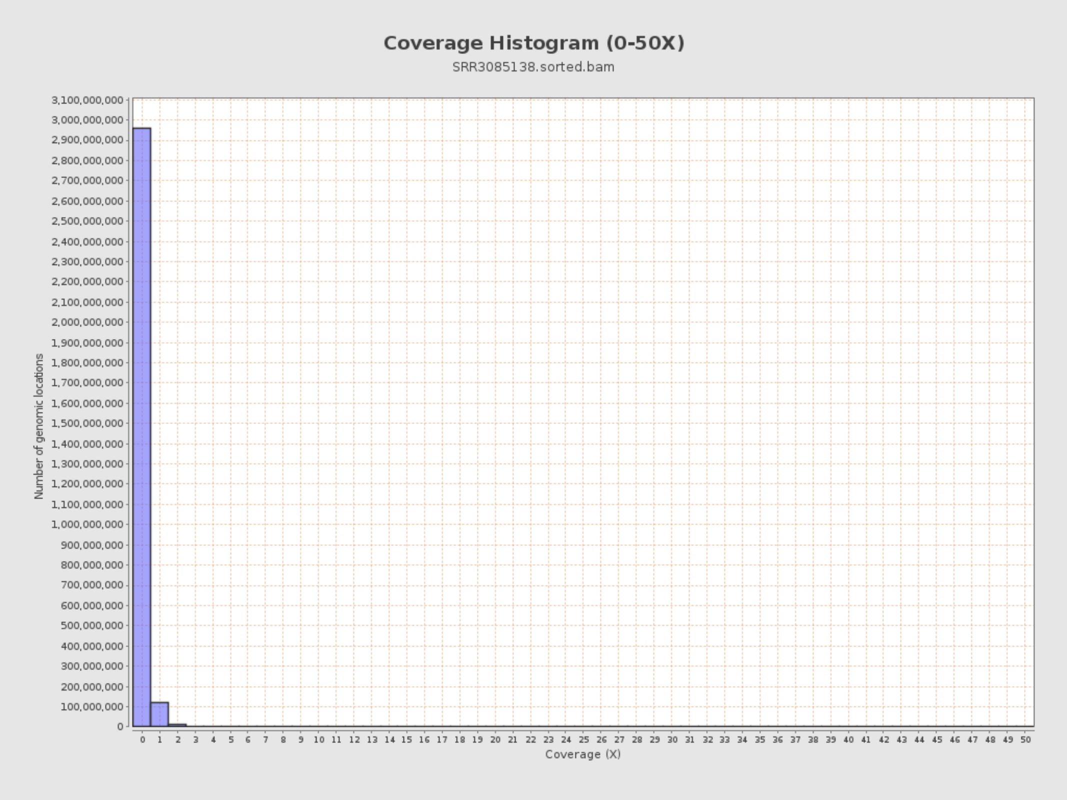
3. Results : Coverage across reference



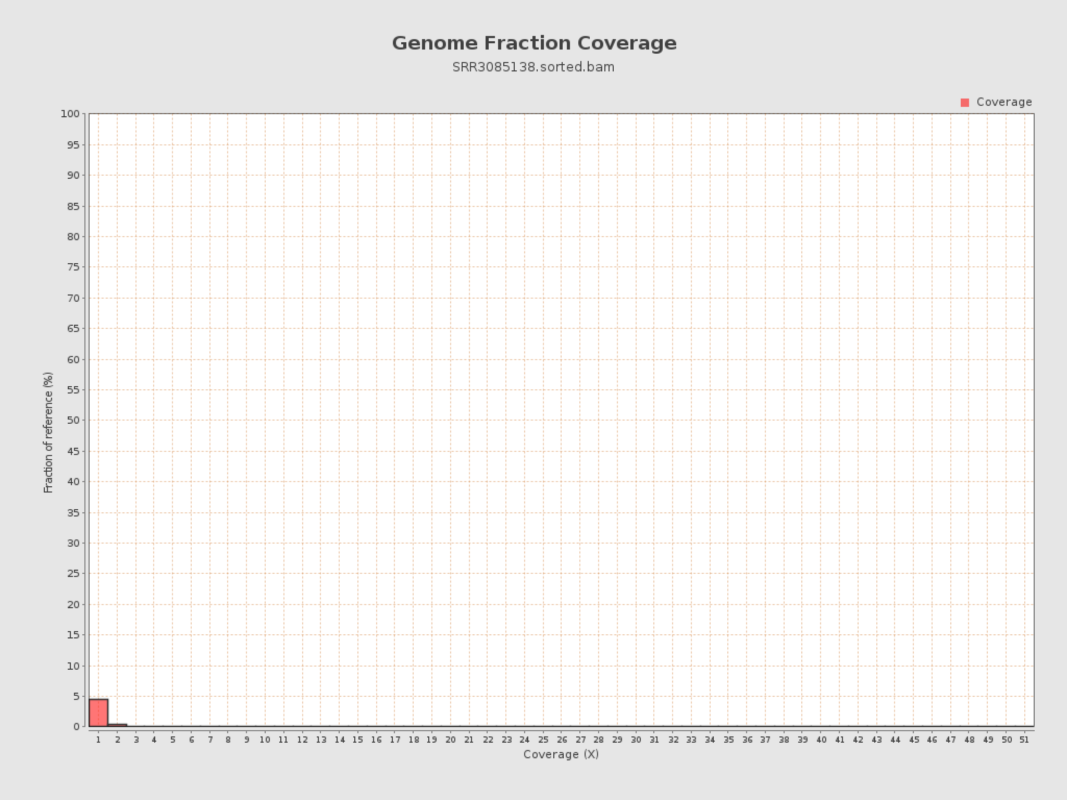
4. Results : Coverage Histogram



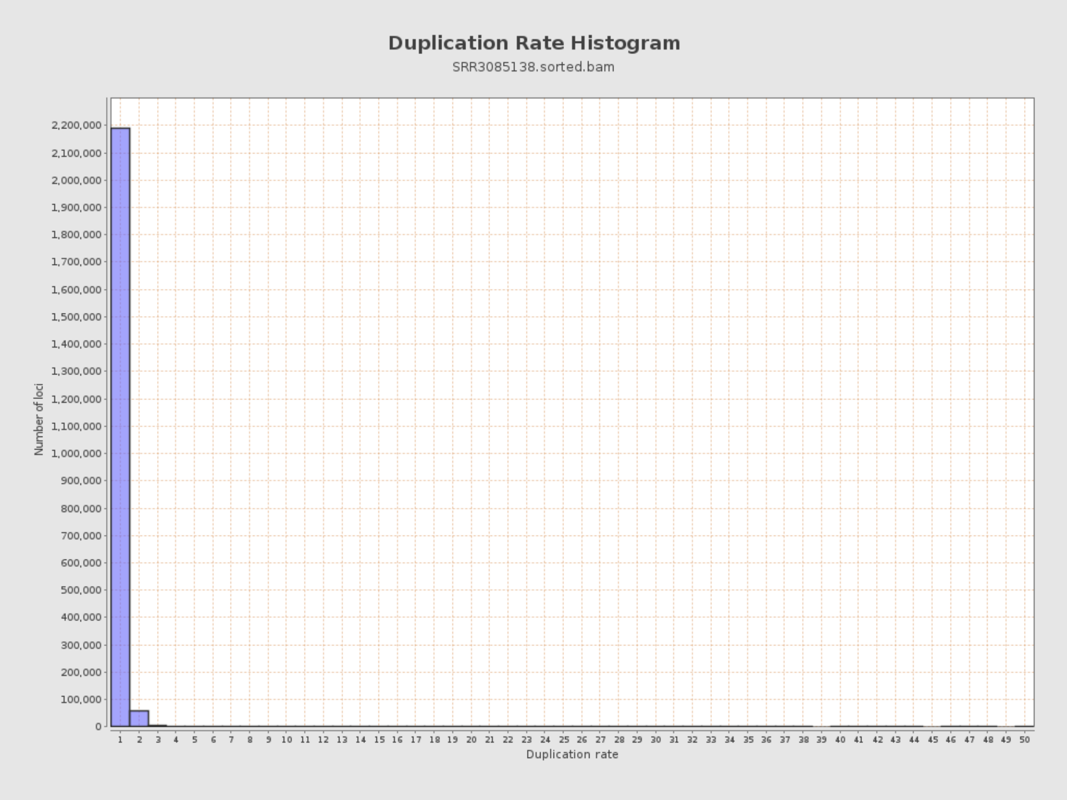
5. Results : Coverage Histogram (0-50X)



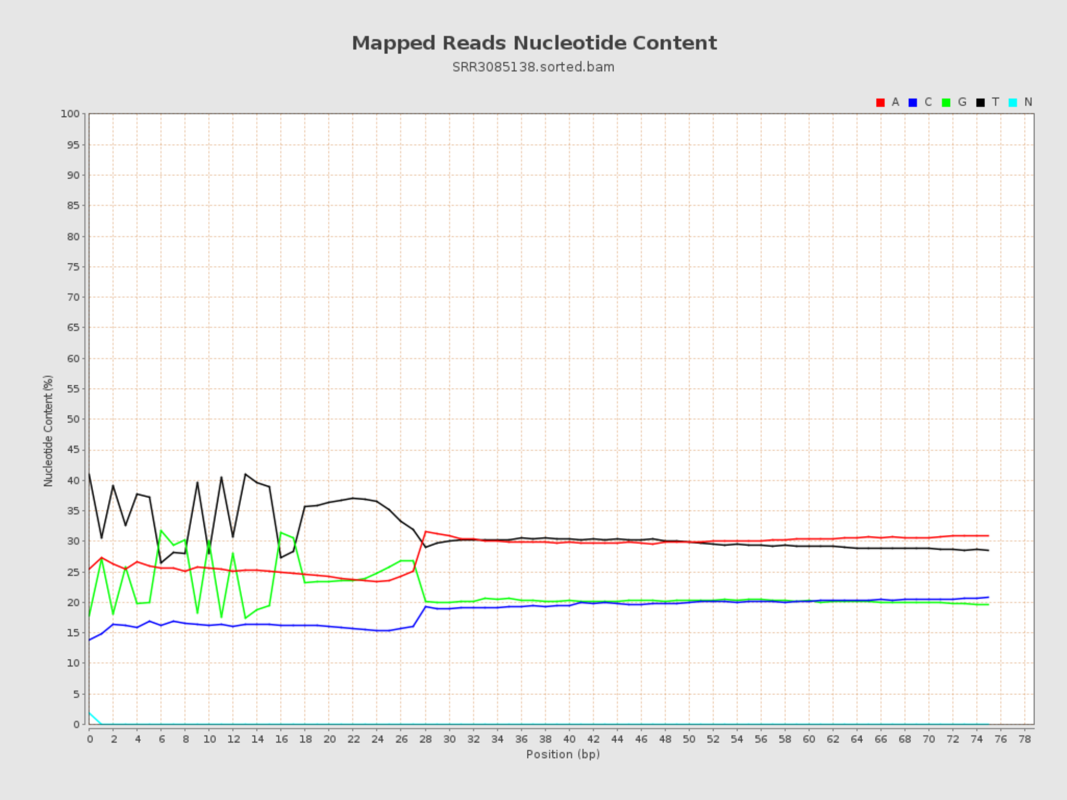
6. Results : Genome Fraction Coverage



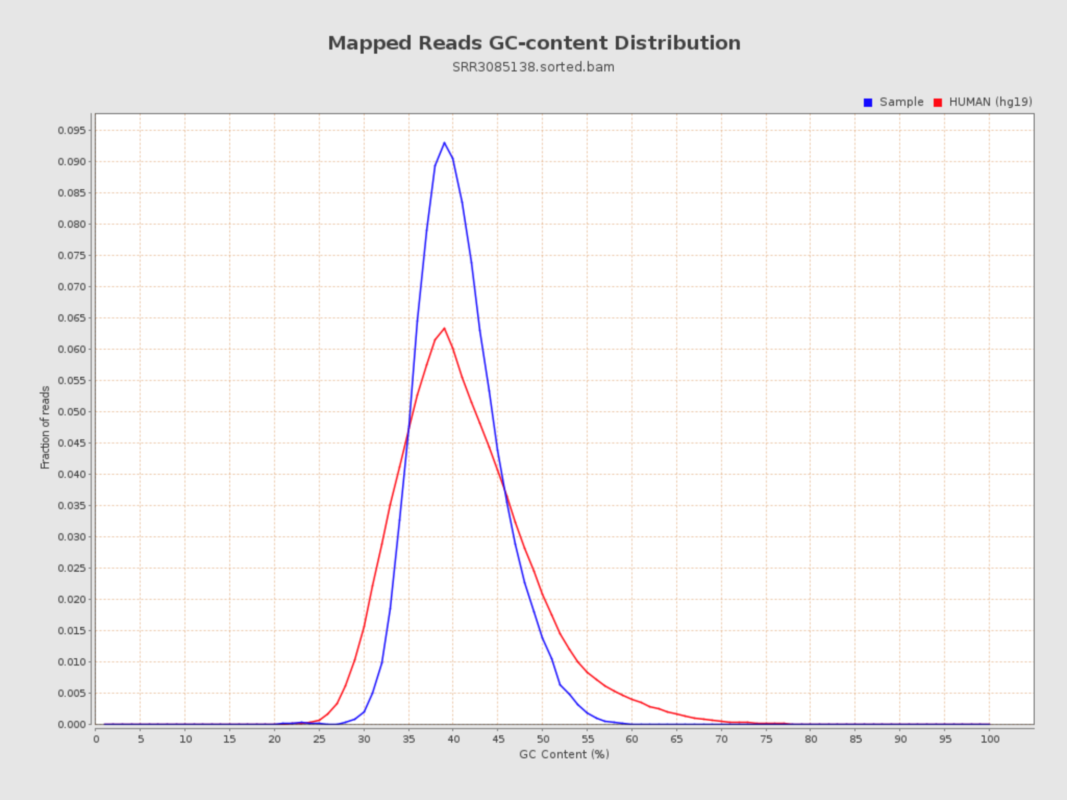
7. Results : Duplication Rate Histogram



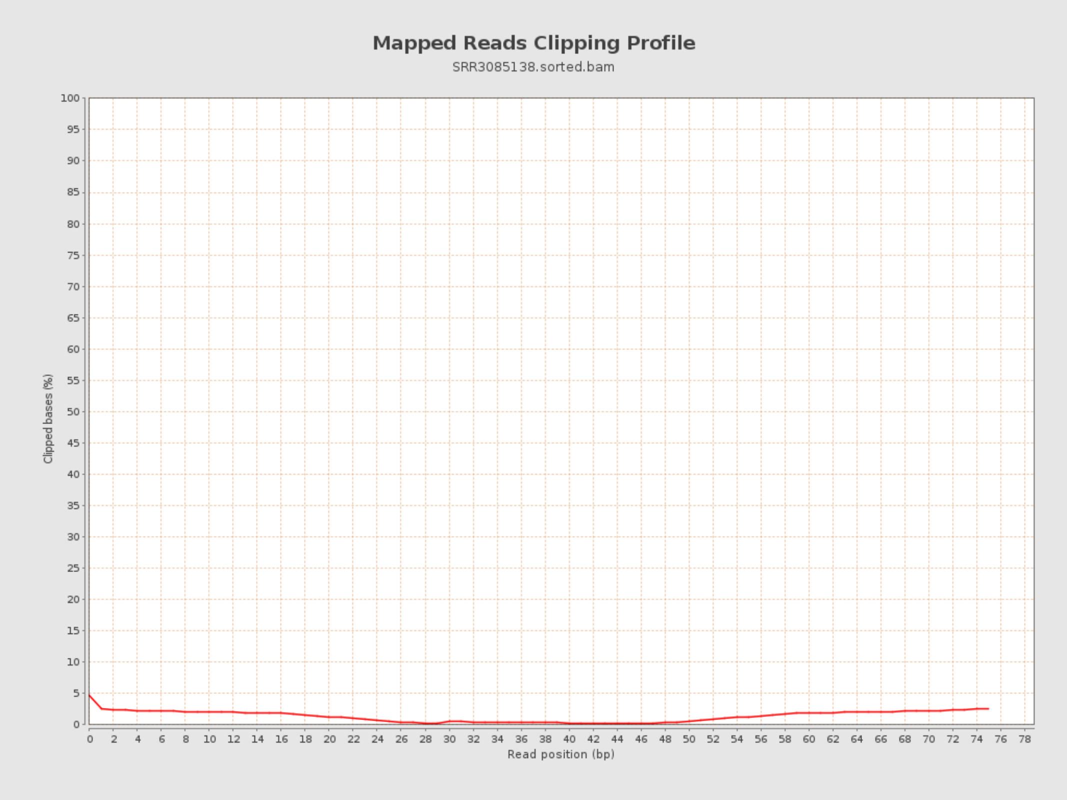
8. Results : Mapped Reads Nucleotide Content



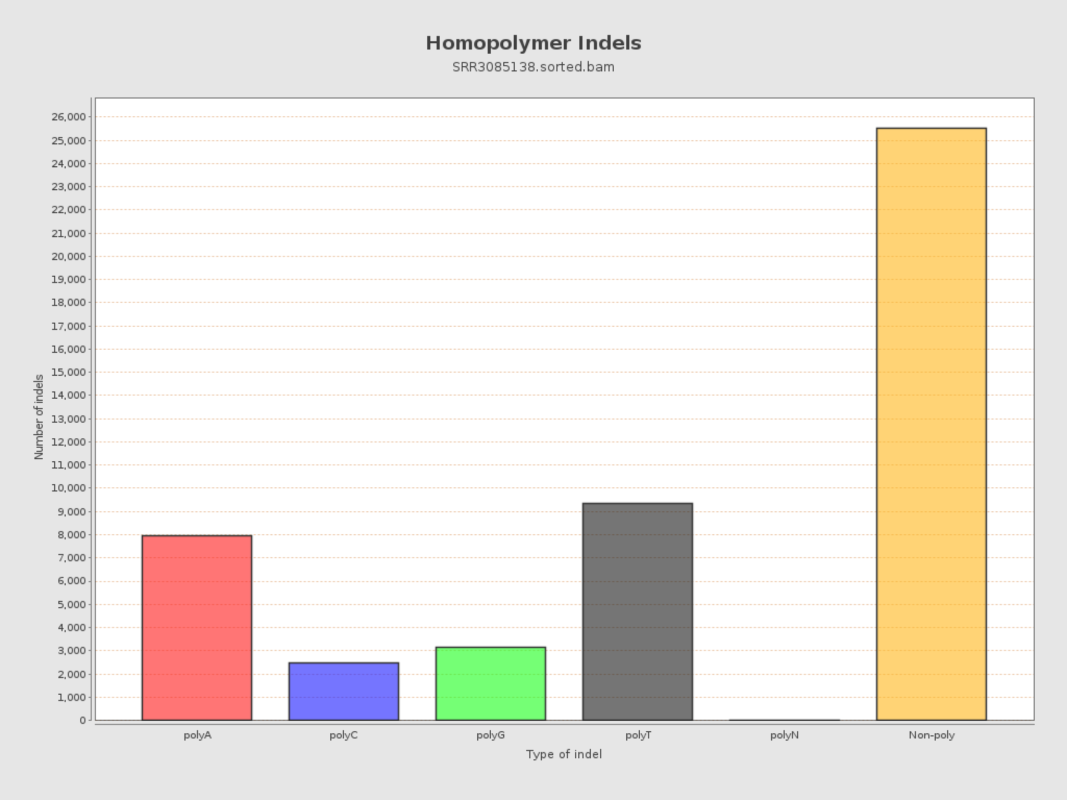
9. Results : Mapped Reads GC-content Distribution



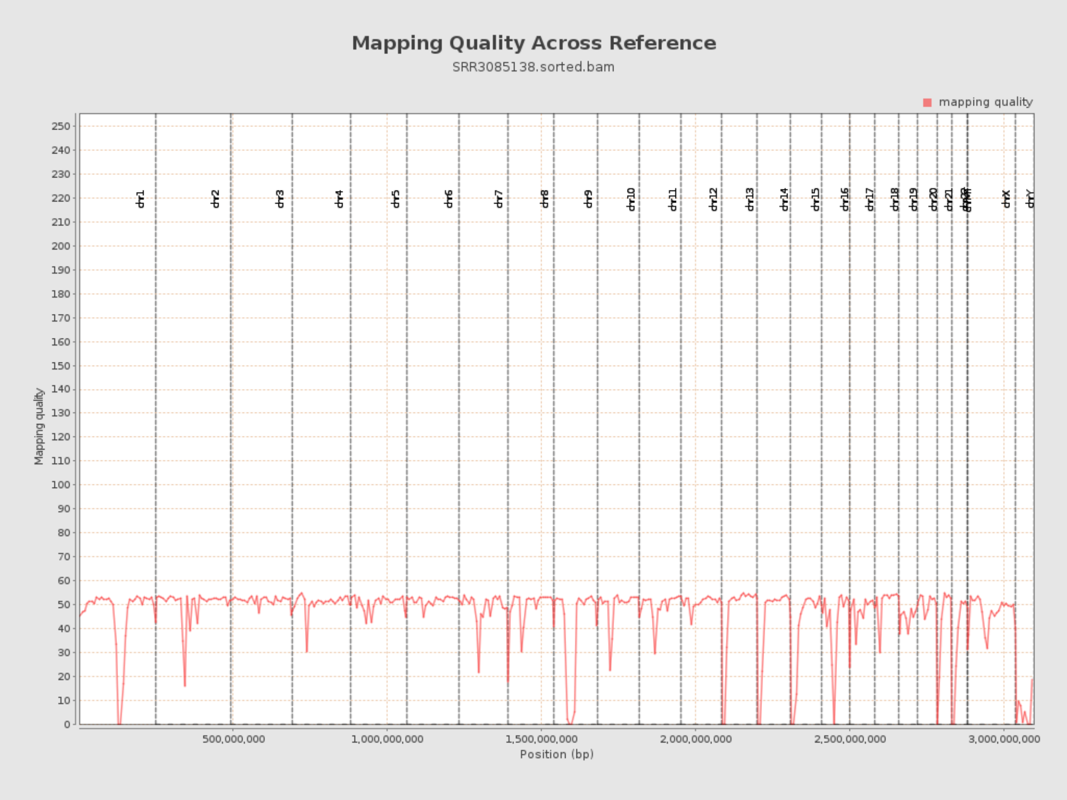
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram