Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 11:21:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081948.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_SRR3081948 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081948.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 11:21:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081948.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,143,042
Mapped reads	2,887,293 / 91.86%
Unmapped reads	255,749 / 8.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,777 / 0.53%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	153,818 / 4.89%
Duplication rate	4.05%
Clipped reads	1,106,487 / 35.2%

2.2. ACGT Content

Number/percentage of A's	55,219,107 / 28.2%
Number/percentage of C's	35,828,475 / 18.3%
Number/percentage of T's	62,393,192 / 31.86%
Number/percentage of G's	42,352,668 / 21.63%
Number/percentage of N's	24,849 / 0.01%
GC Percentage	39.93%

2.3. Coverage

Mean	0.0633

Standard Deviation	0.5575

2.4. Mapping Quality

Mean Mapping Quality	46.67

2.5. Mismatches and indels

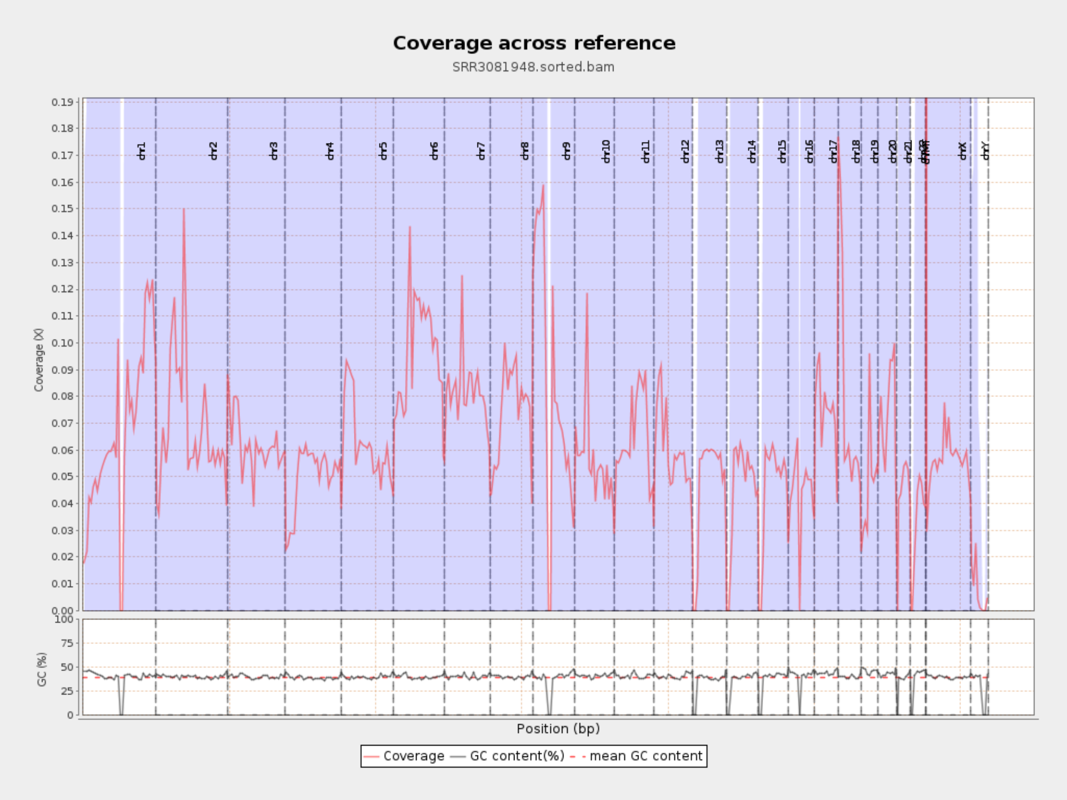
General error rate	0.78%
Mismatches	1,502,702
Insertions	13,737
Mapped reads with at least one insertion	0.47%
Deletions	44,956
Mapped reads with at least one deletion	1.54%
Homopolymer indels	47.16%

2.6. Chromosome stats

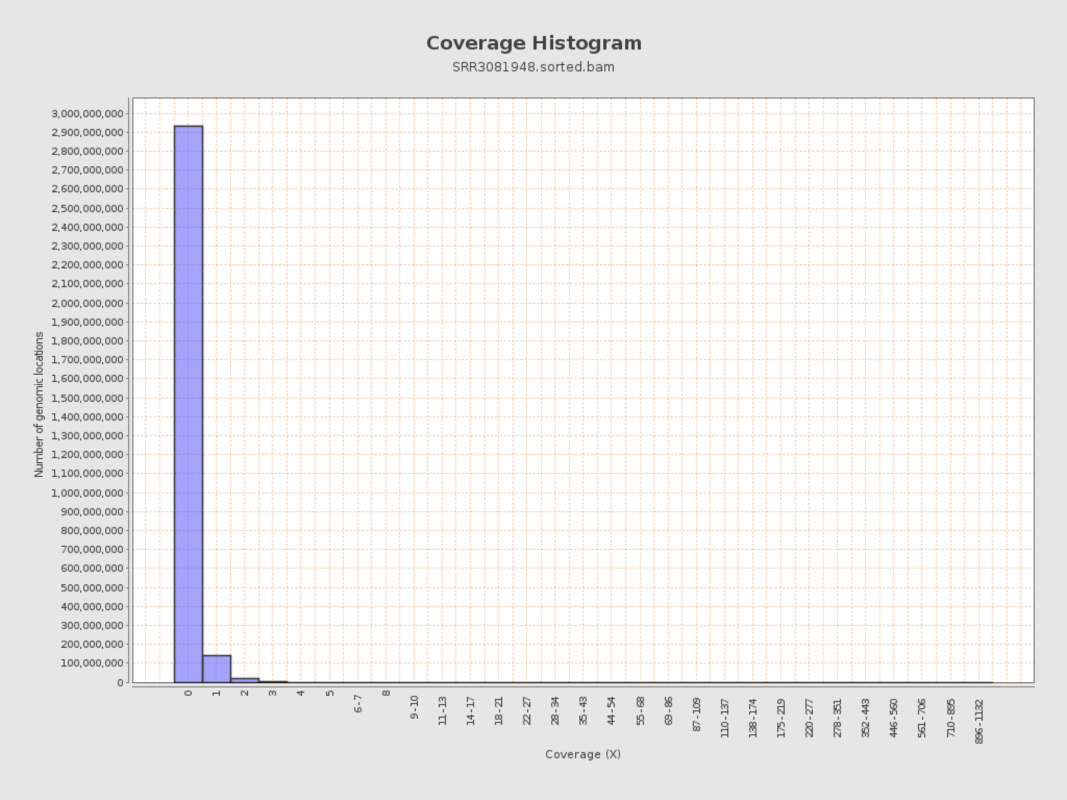
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16595714	0.0666	1.0105
chr2	243199373	17040325	0.0701	0.7459
chr3	198022430	12319201	0.0622	0.2846
chr4	191154276	9526977	0.0498	0.2966
chr5	180915260	11301727	0.0625	0.288
chr6	171115067	16823603	0.0983	0.4946
chr7	159138663	12961006	0.0814	0.7975

chr8	146364022	10937263	0.0747	0.6865
chr9	141213431	11943522	0.0846	0.6066
chr10	135534747	7656672	0.0565	0.5492
chr11	135006516	8841554	0.0655	0.4196
chr12	133851895	8089950	0.0604	0.3006
chr13	115169878	5476631	0.0476	0.2464
chr14	107349540	4953515	0.0461	0.2811
chr15	102531392	4619014	0.045	0.2441
chr16	90354753	3879877	0.0429	0.2997
chr17	81195210	6201267	0.0764	0.3679
chr18	78077248	6180054	0.0792	0.9758
chr19	59128983	2810750	0.0475	0.7617
chr20	63025520	4821534	0.0765	0.3252
chr21	48129895	2114044	0.0439	0.2844
chr22	51304566	1633969	0.0318	0.1992
chrMT	16571	27133	1.6374	1.7349
chrX	155270560	8710722	0.0561	0.346
chrY	59373566	431682	0.0073	0.202

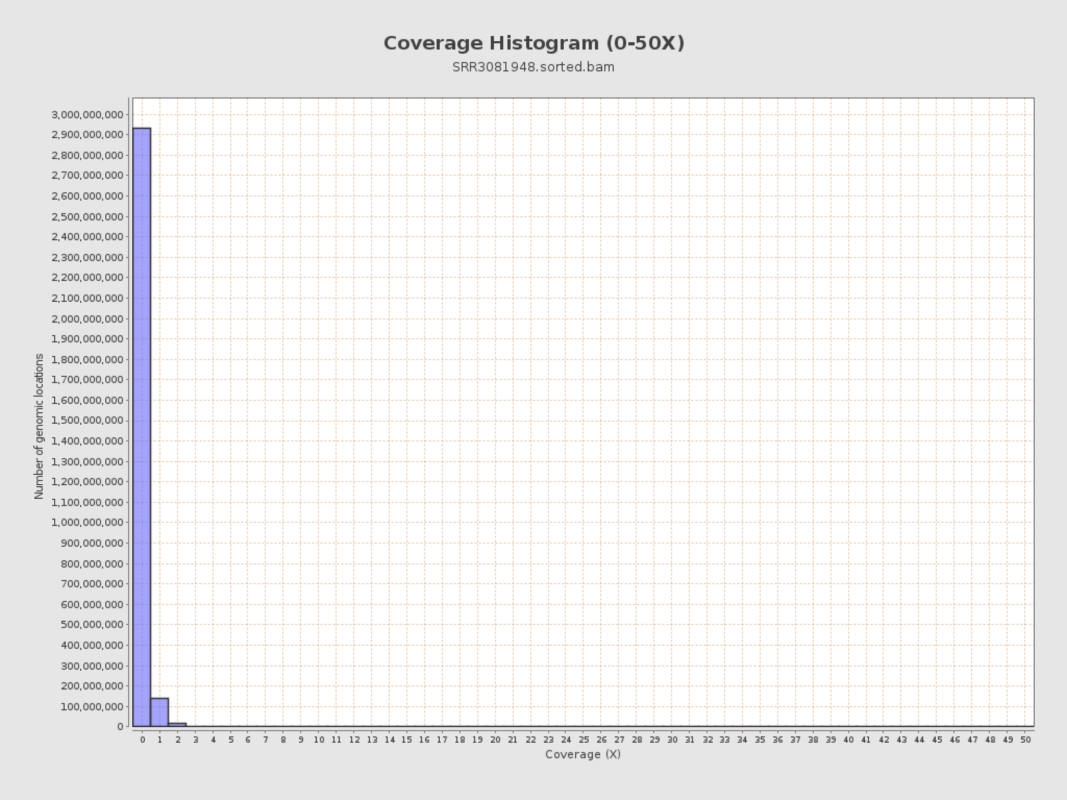
3. Results : Coverage across reference



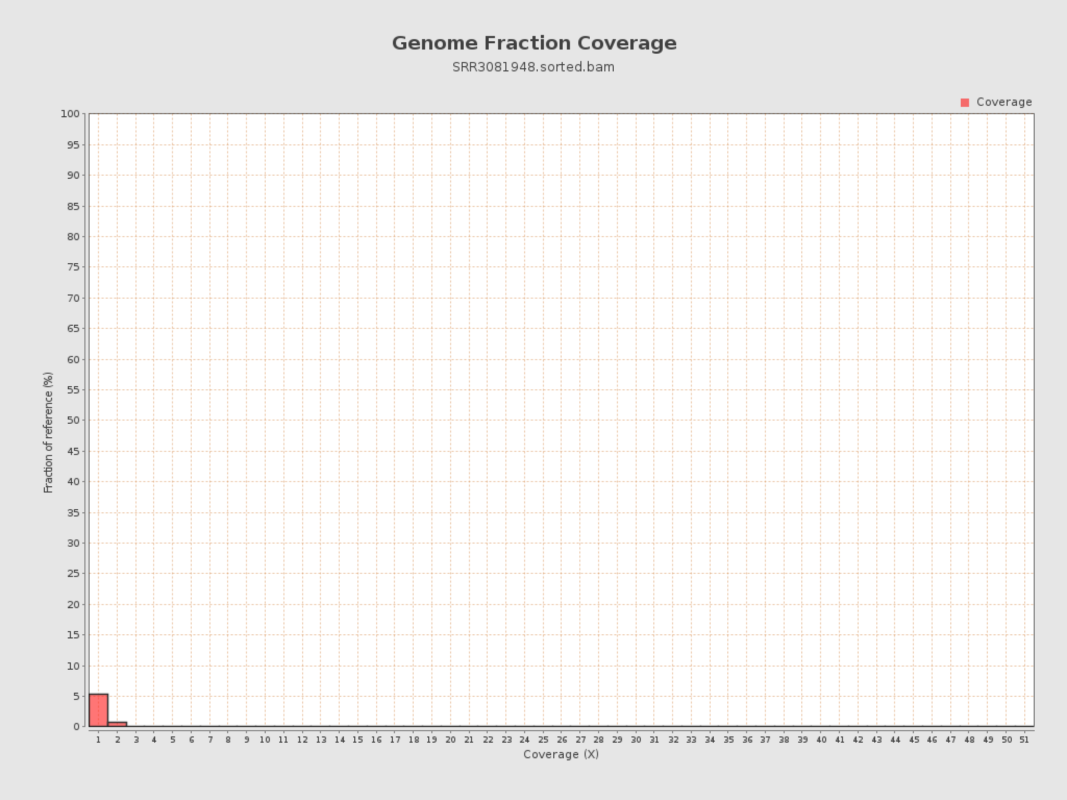
4. Results : Coverage Histogram



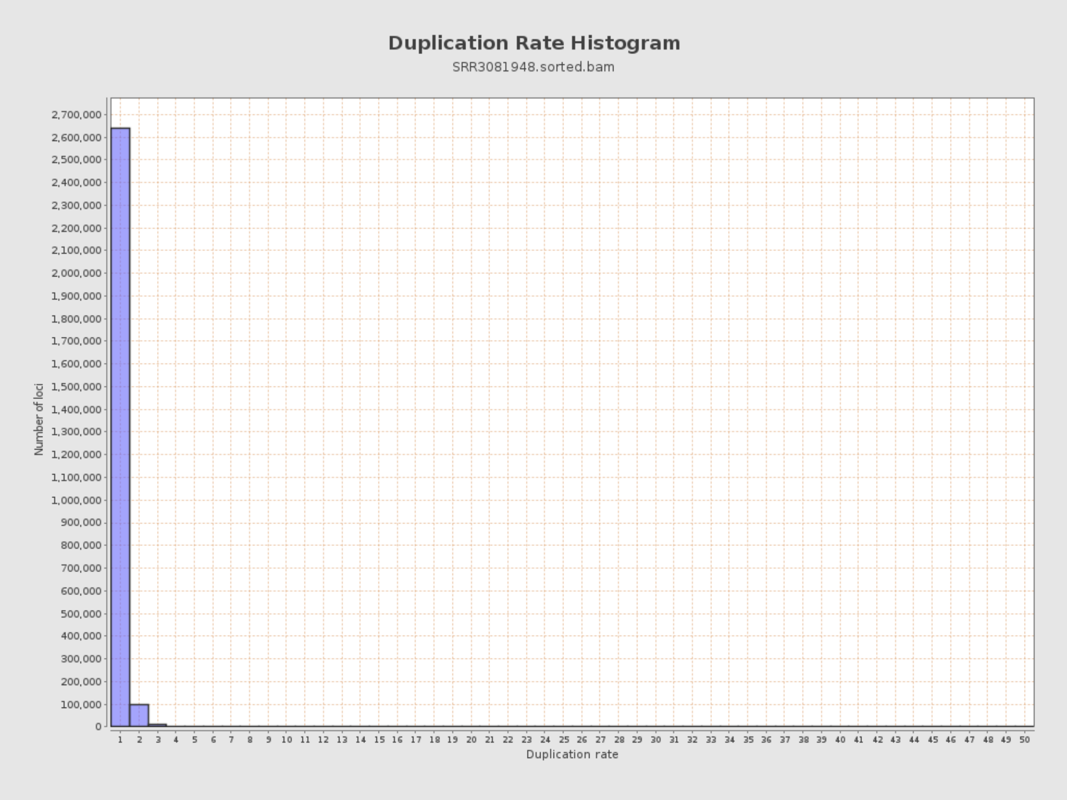
5. Results : Coverage Histogram (0-50X)



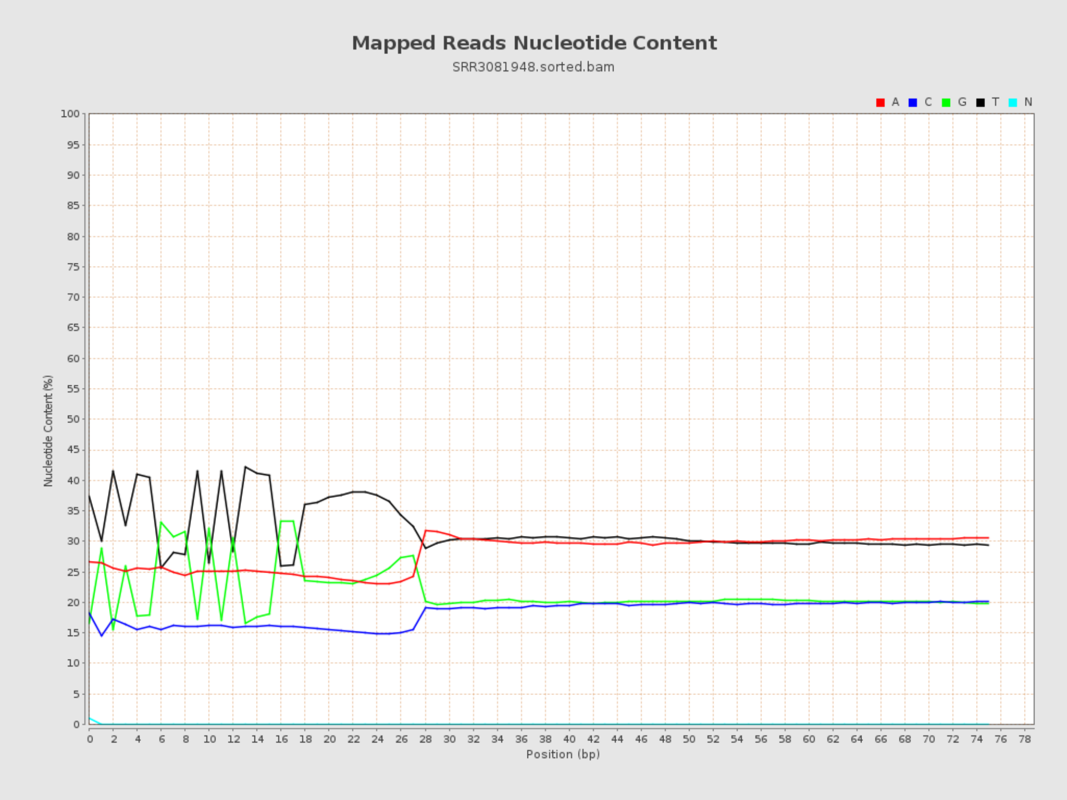
6. Results : Genome Fraction Coverage



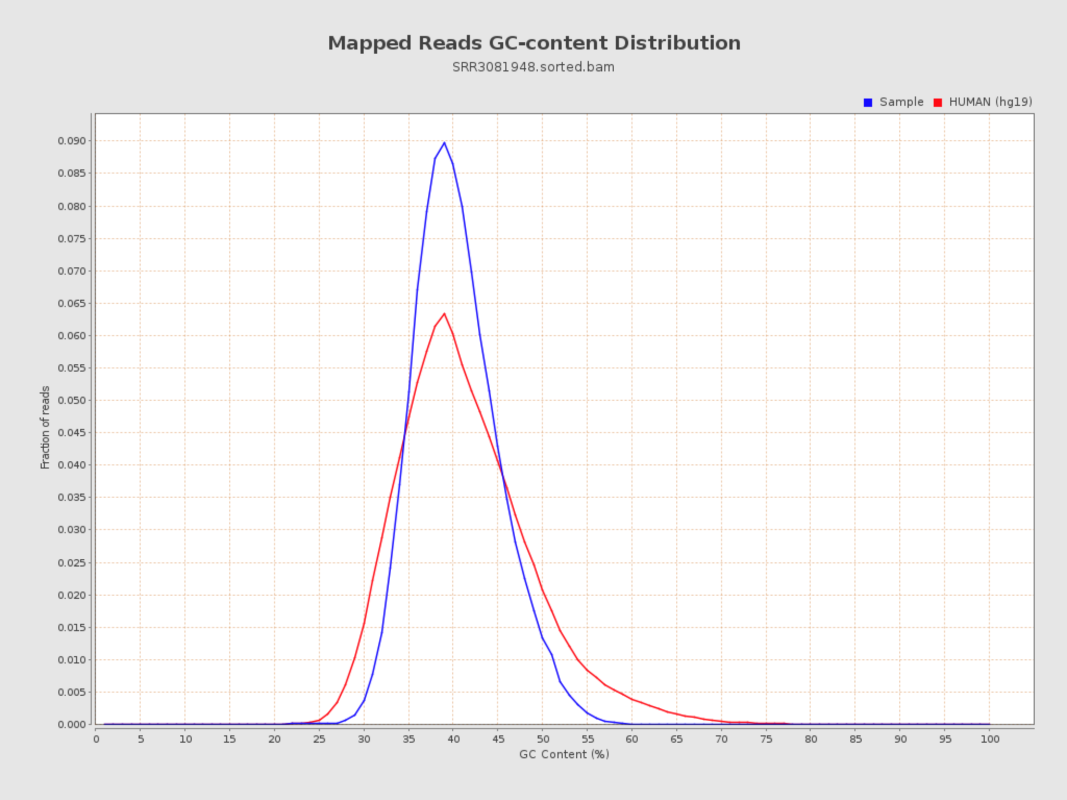
7. Results : Duplication Rate Histogram



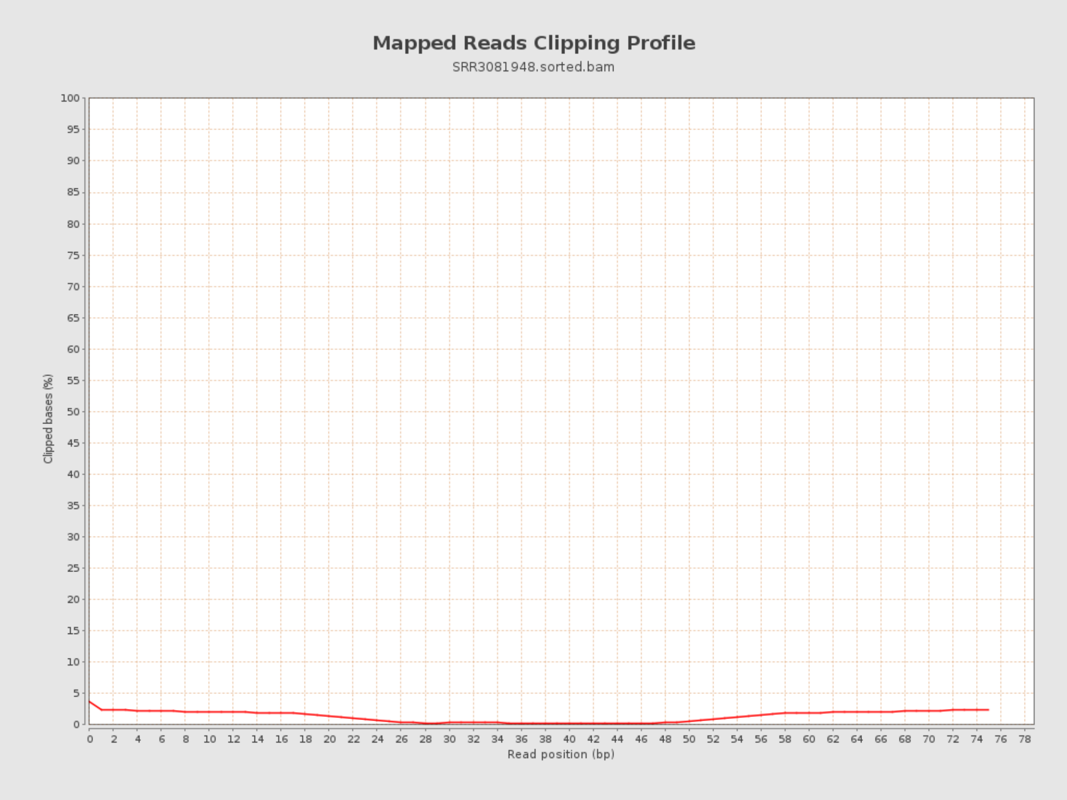
8. Results : Mapped Reads Nucleotide Content



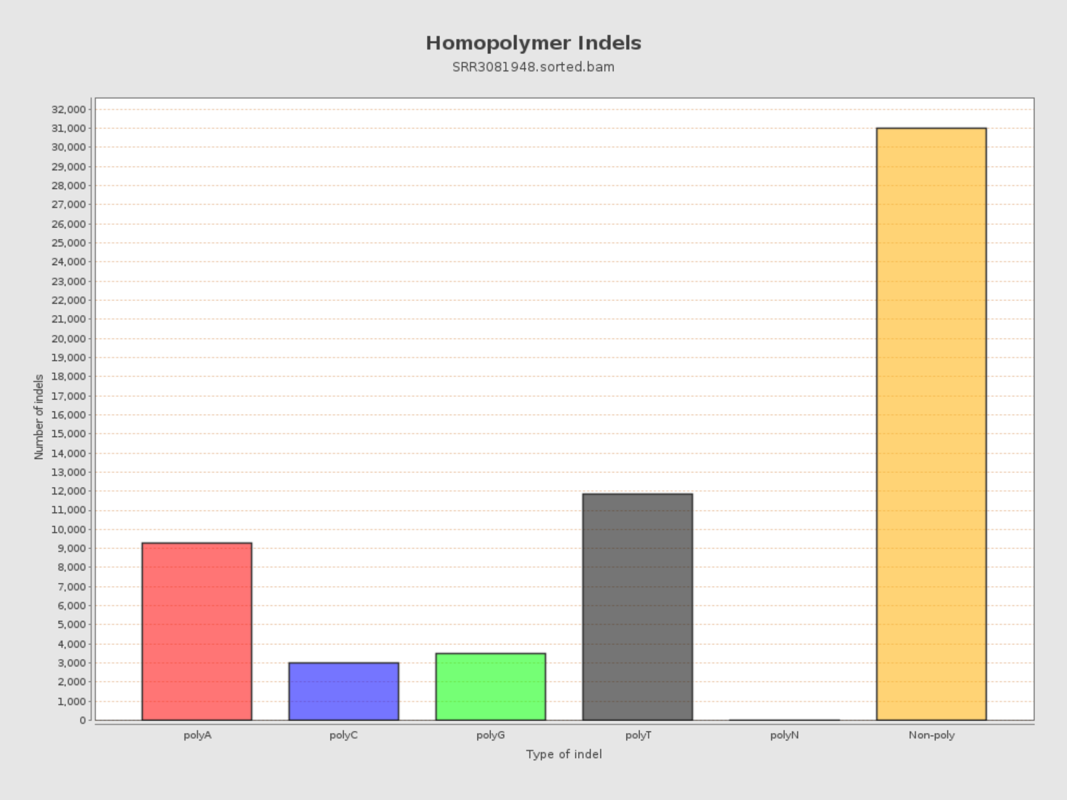
9. Results : Mapped Reads GC-content Distribution



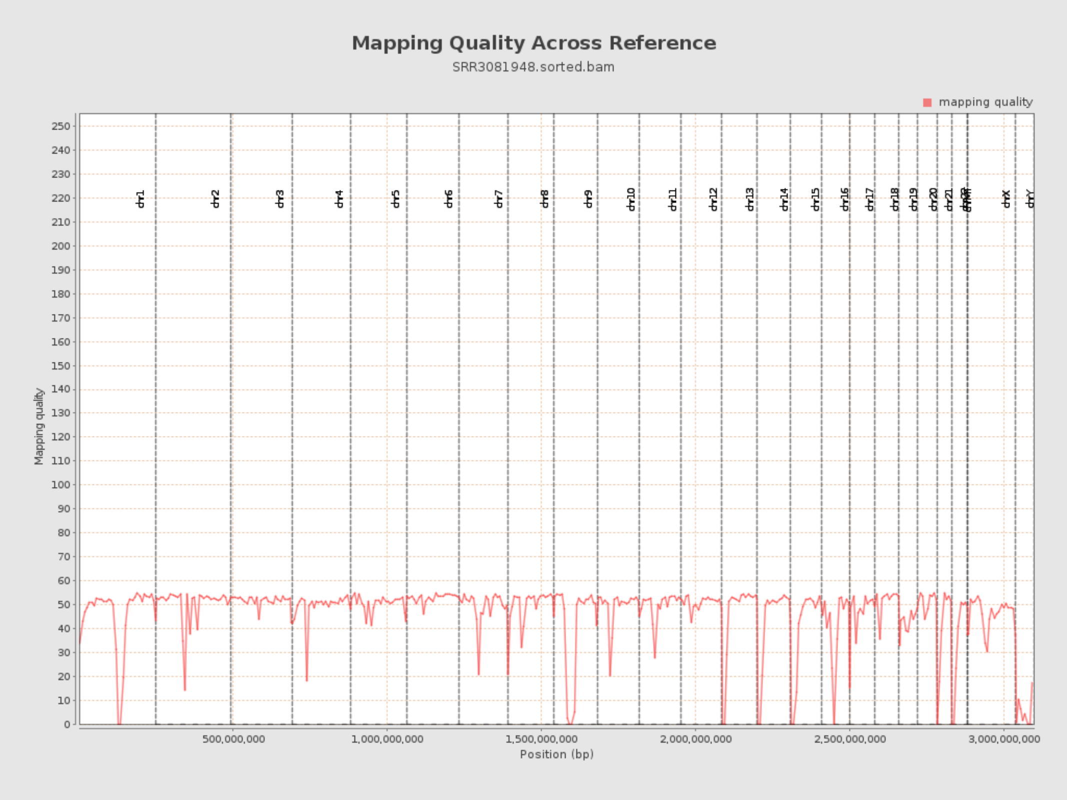
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram