Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 13:15:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084780.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_SRR3084780 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084780.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 13:15:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084780.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,142,972
Mapped reads	1,936,217 / 90.35%
Unmapped reads	206,755 / 9.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,175 / 0.8%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	79,895 / 3.73%
Duplication rate	3.22%
Clipped reads	837,014 / 39.06%

2.2. ACGT Content

Number/percentage of A's	36,231,643 / 27.86%
Number/percentage of C's	24,313,677 / 18.7%
Number/percentage of T's	40,730,583 / 31.32%
Number/percentage of G's	28,724,530 / 22.09%
Number/percentage of N's	39,326 / 0.03%
GC Percentage	40.79%

2.3. Coverage

Mean	0.042

Standard Deviation	0.3525

2.4. Mapping Quality

Mean Mapping Quality	46.94

2.5. Mismatches and indels

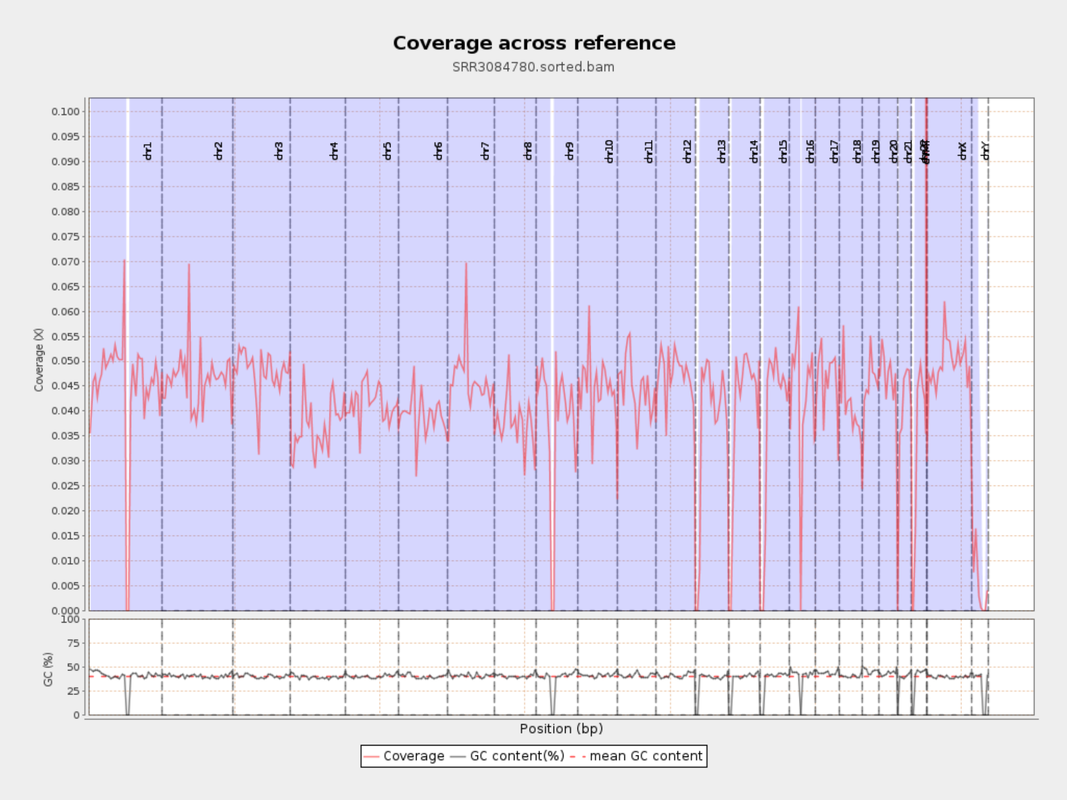
General error rate	0.86%
Mismatches	1,104,326
Insertions	10,228
Mapped reads with at least one insertion	0.52%
Deletions	32,068
Mapped reads with at least one deletion	1.64%
Homopolymer indels	47.28%

2.6. Chromosome stats

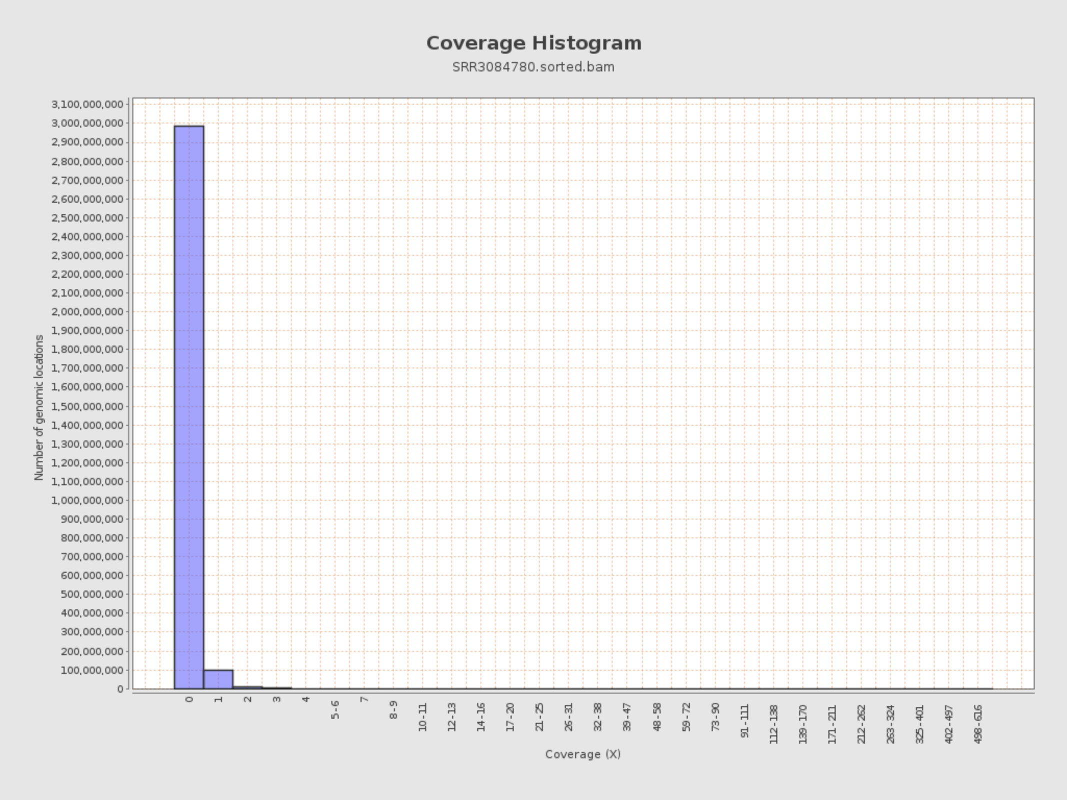
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11167694	0.0448	0.5557
chr2	243199373	11331521	0.0466	0.4311
chr3	198022430	9488400	0.0479	0.2458
chr4	191154276	7015613	0.0367	0.2319
chr5	180915260	7516800	0.0415	0.2306
chr6	171115067	6687563	0.0391	0.2576
chr7	159138663	7394681	0.0465	0.4571

chr8	146364022	5492958	0.0375	0.3541
chr9	141213431	5337910	0.0378	0.3412
chr10	135534747	6105821	0.045	0.3192
chr11	135006516	5981713	0.0443	0.3406
chr12	133851895	6322666	0.0472	0.2477
chr13	115169878	4235081	0.0368	0.2173
chr14	107349540	4204268	0.0392	0.2491
chr15	102531392	3888980	0.0379	0.2252
chr16	90354753	3885426	0.043	0.2739
chr17	81195210	3720736	0.0458	0.291
chr18	78077248	3222195	0.0413	0.7971
chr19	59128983	2689586	0.0455	0.4232
chr20	63025520	2963482	0.047	0.262
chr21	48129895	1863636	0.0387	0.2326
chr22	51304566	1594677	0.0311	0.1969
chrMT	16571	31930	1.9269	1.7317
chrX	155270560	7630312	0.0491	0.2812
chrY	59373566	318262	0.0054	0.1209

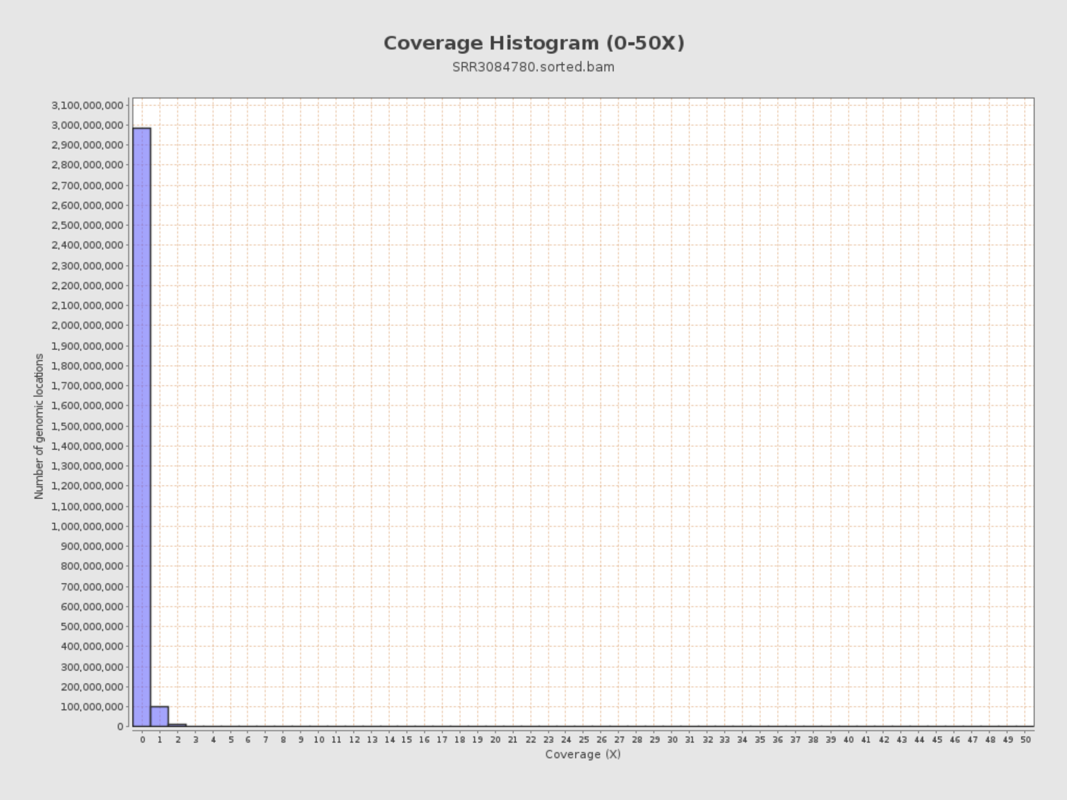
3. Results : Coverage across reference



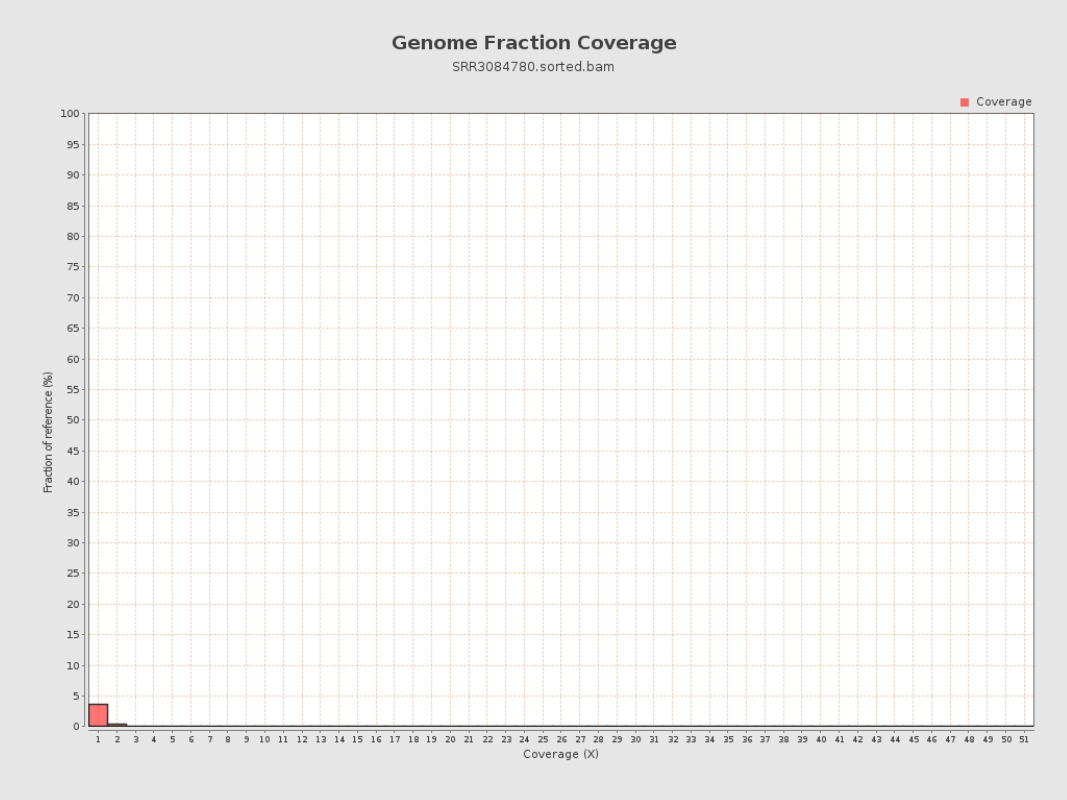
4. Results : Coverage Histogram



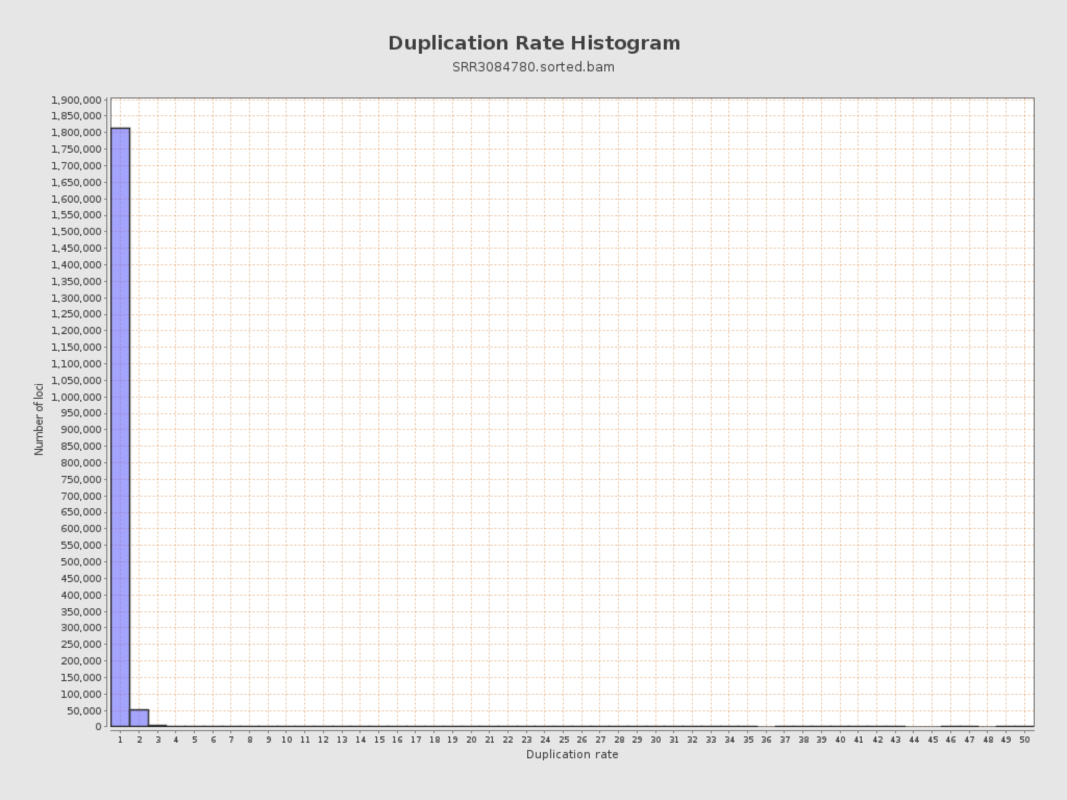
5. Results : Coverage Histogram (0-50X)



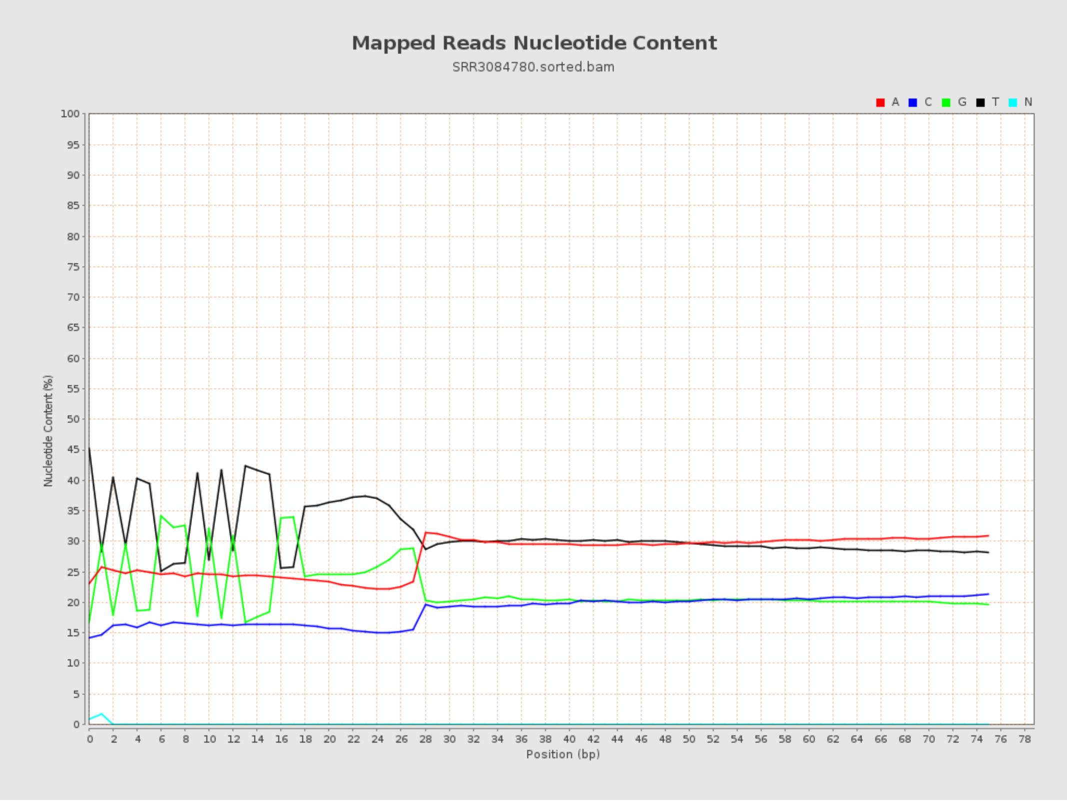
6. Results : Genome Fraction Coverage



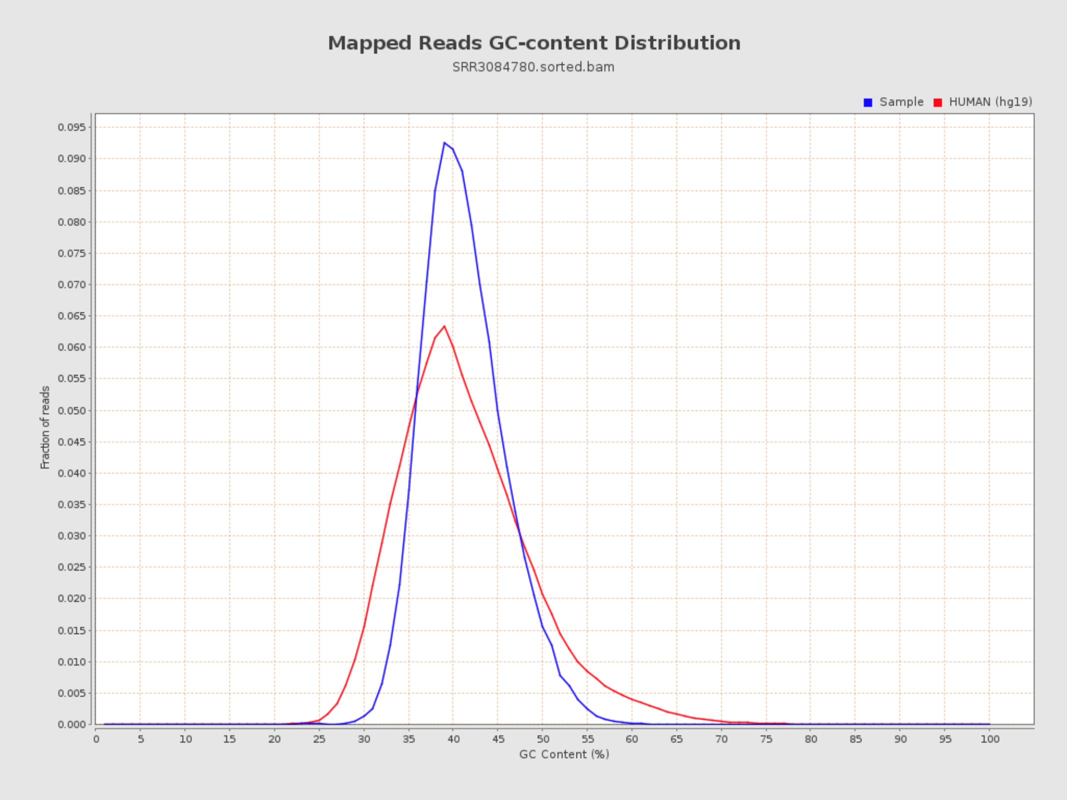
7. Results : Duplication Rate Histogram



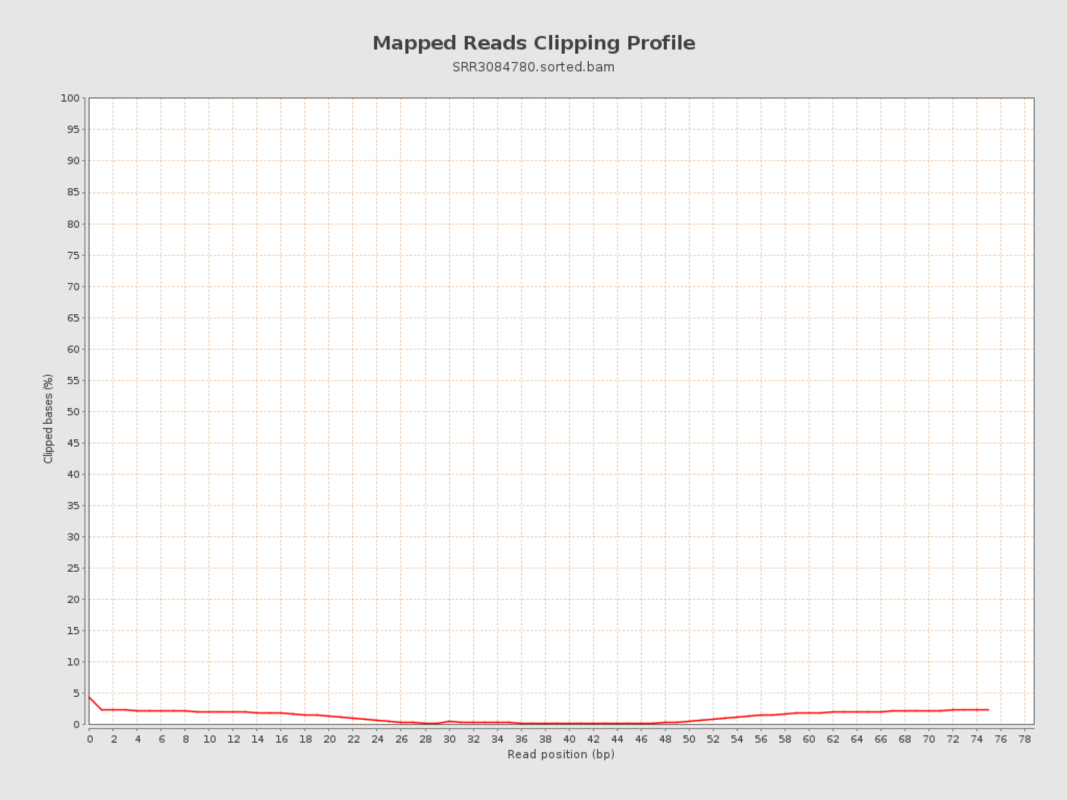
8. Results : Mapped Reads Nucleotide Content



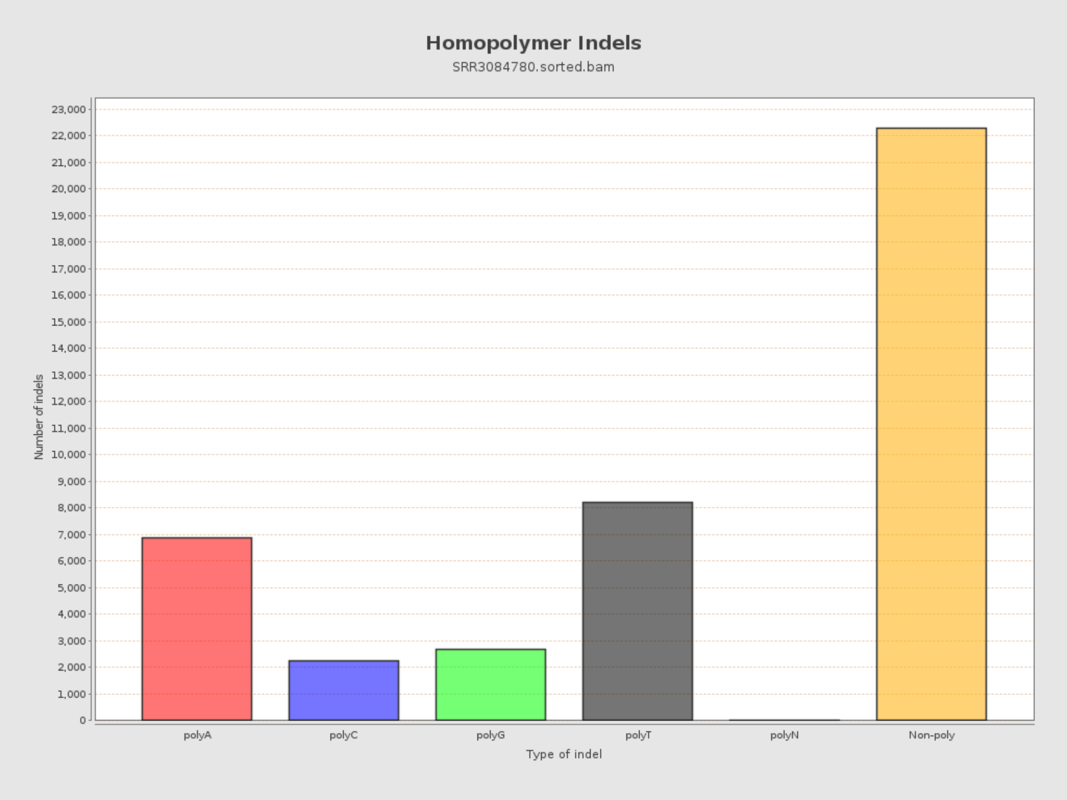
9. Results : Mapped Reads GC-content Distribution



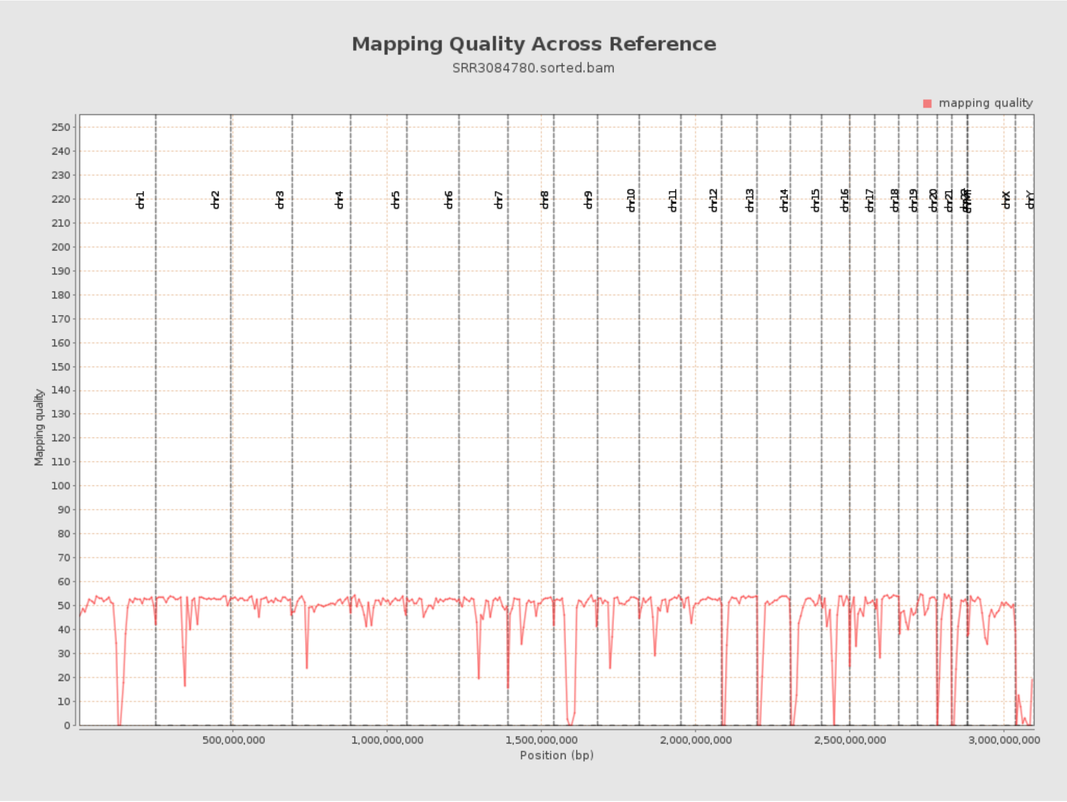
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram