Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 13:54:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084790.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_SRR3084790 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084790.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 13:54:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084790.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,377,270
Mapped reads	2,131,110 / 89.65%
Unmapped reads	246,160 / 10.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,832 / 0.92%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	96,363 / 4.05%
Duplication rate	3.56%
Clipped reads	892,970 / 37.56%

2.2. ACGT Content

Number/percentage of A's	39,758,990 / 27.64%
Number/percentage of C's	27,379,073 / 19.03%
Number/percentage of T's	44,741,373 / 31.1%
Number/percentage of G's	31,922,671 / 22.19%
Number/percentage of N's	41,316 / 0.03%
GC Percentage	41.23%

2.3. Coverage

Mean	0.0465

Standard Deviation	0.377

2.4. Mapping Quality

Mean Mapping Quality	46.85

2.5. Mismatches and indels

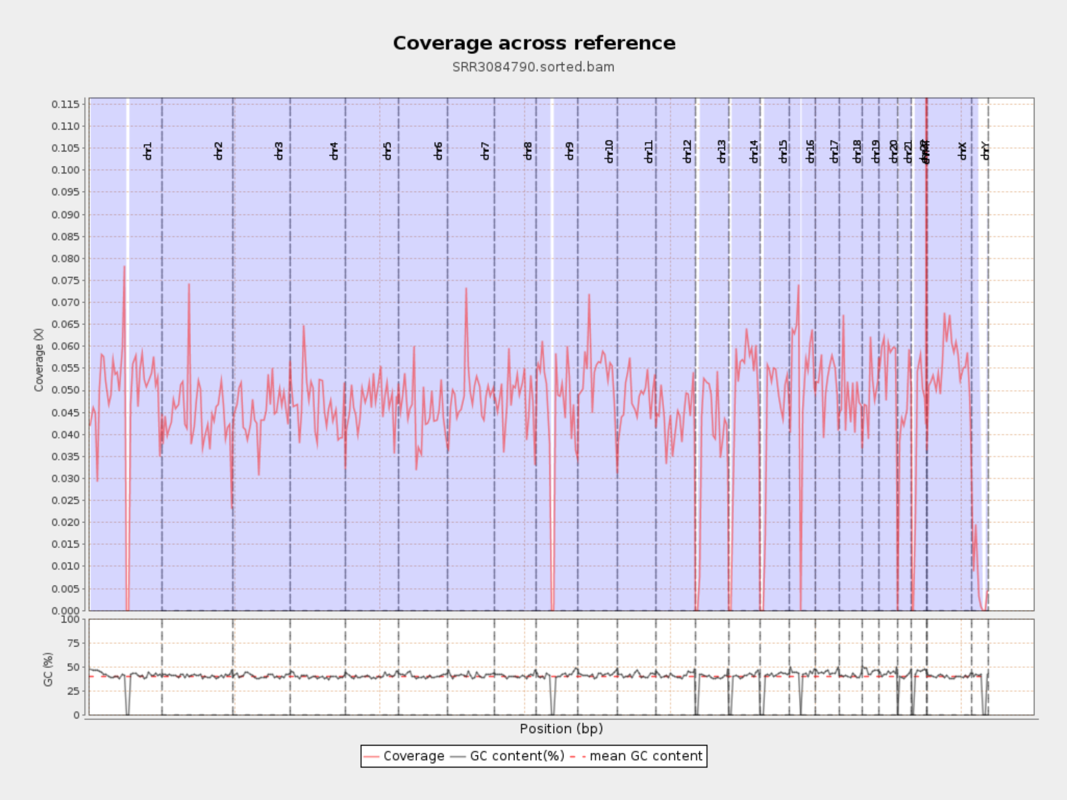
General error rate	0.88%
Mismatches	1,239,066
Insertions	11,250
Mapped reads with at least one insertion	0.52%
Deletions	35,332
Mapped reads with at least one deletion	1.64%
Homopolymer indels	47.05%

2.6. Chromosome stats

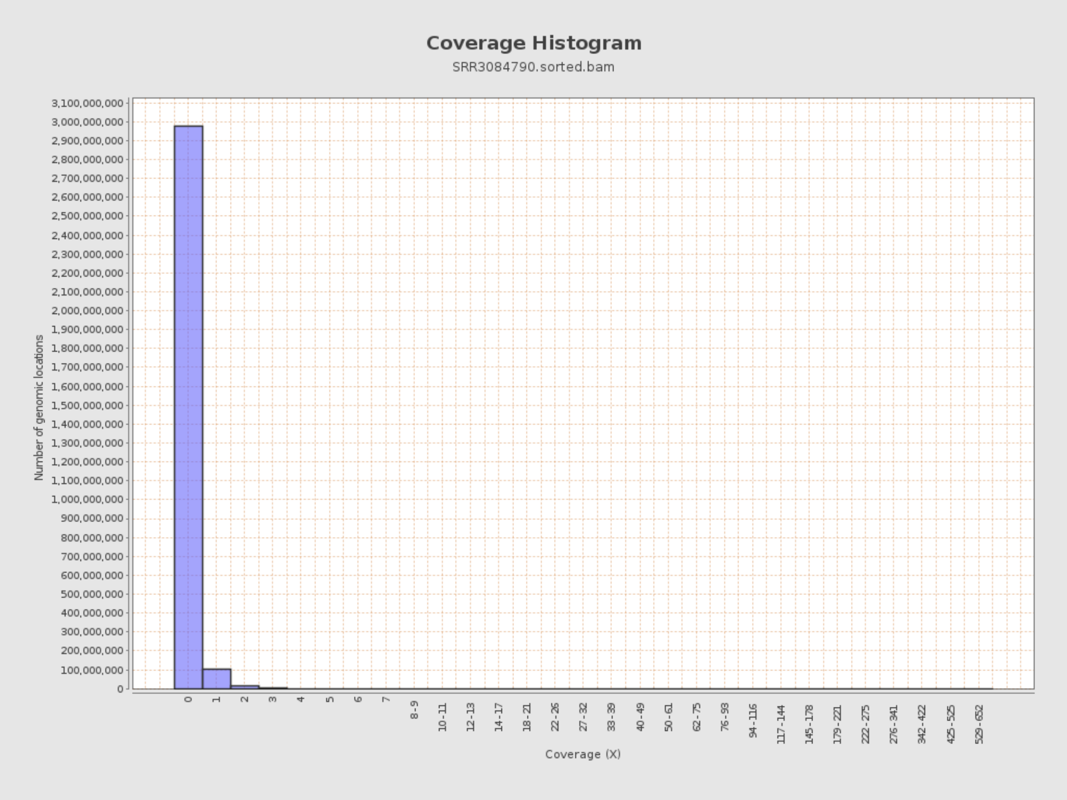
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12115645	0.0486	0.6051
chr2	243199373	10853087	0.0446	0.4415
chr3	198022430	8989613	0.0454	0.2445
chr4	191154276	8879737	0.0465	0.2668
chr5	180915260	8554821	0.0473	0.2509
chr6	171115067	7721741	0.0451	0.2966
chr7	159138663	7859305	0.0494	0.4479

chr8	146364022	7024216	0.048	0.4093
chr9	141213431	6294511	0.0446	0.3858
chr10	135534747	7341648	0.0542	0.3613
chr11	135006516	6515742	0.0483	0.374
chr12	133851895	5864695	0.0438	0.2453
chr13	115169878	4312459	0.0374	0.2248
chr14	107349540	5096458	0.0475	0.2729
chr15	102531392	4256871	0.0415	0.2424
chr16	90354753	4842316	0.0536	0.2994
chr17	81195210	4190340	0.0516	0.3023
chr18	78077248	3789829	0.0485	0.8303
chr19	59128983	2907304	0.0492	0.4652
chr20	63025520	3600567	0.0571	0.2882
chr21	48129895	2024919	0.0421	0.253
chr22	51304566	1871687	0.0365	0.2173
chrMT	16571	6232	0.3761	0.6846
chrX	155270560	8606767	0.0554	0.2913
chrY	59373566	380296	0.0064	0.1439

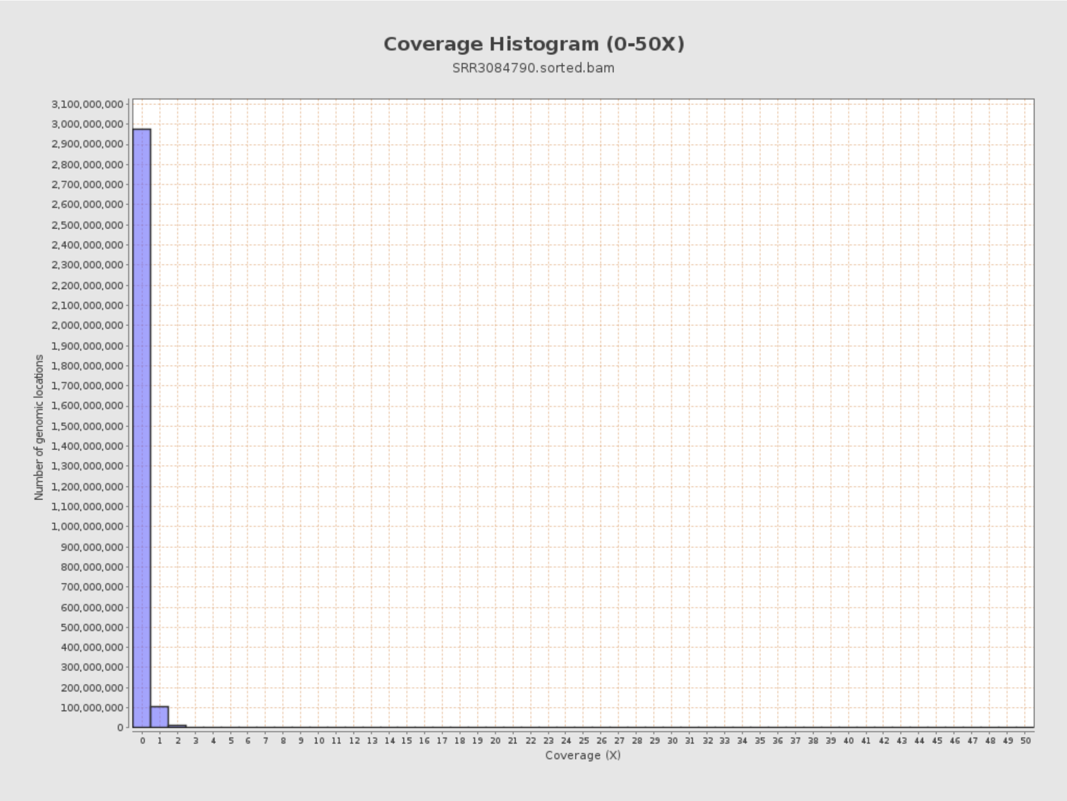
3. Results : Coverage across reference



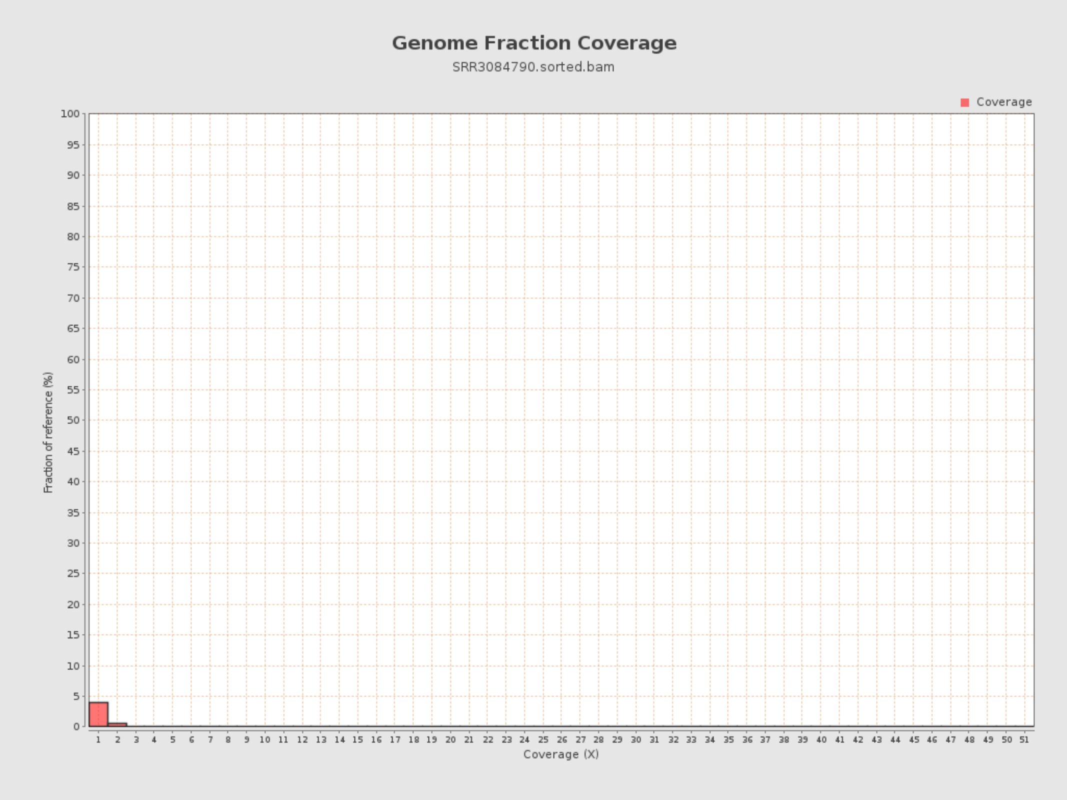
4. Results : Coverage Histogram



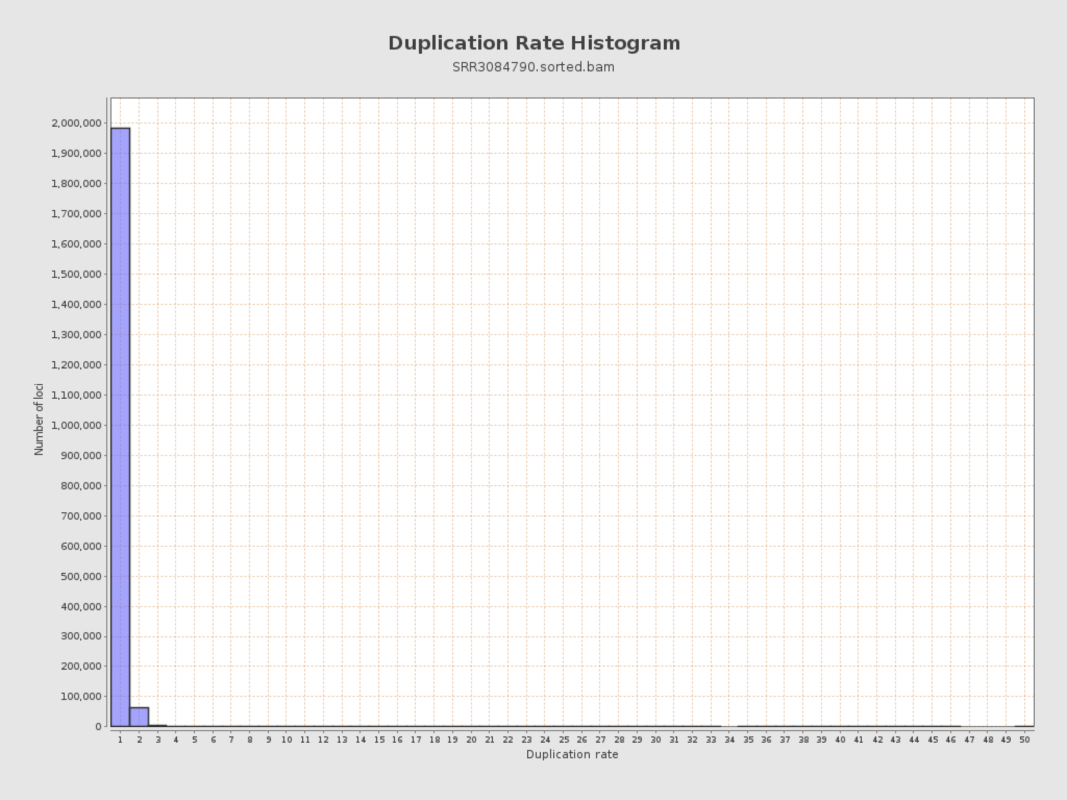
5. Results : Coverage Histogram (0-50X)



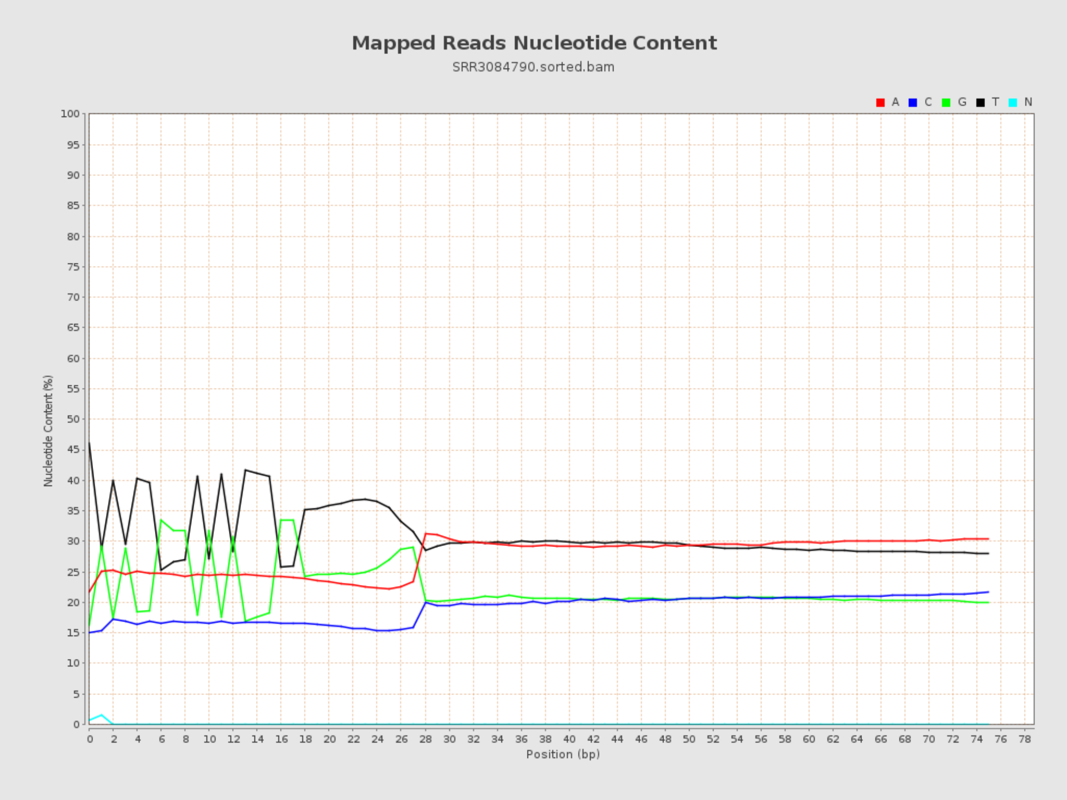
6. Results : Genome Fraction Coverage



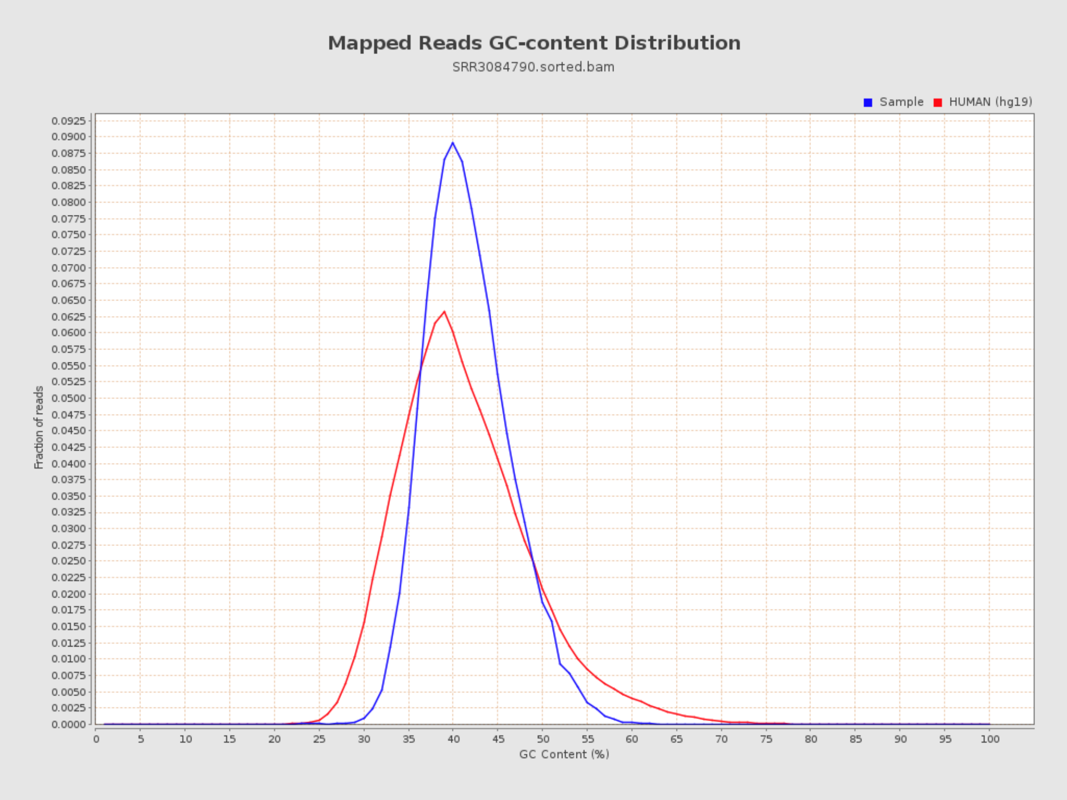
7. Results : Duplication Rate Histogram



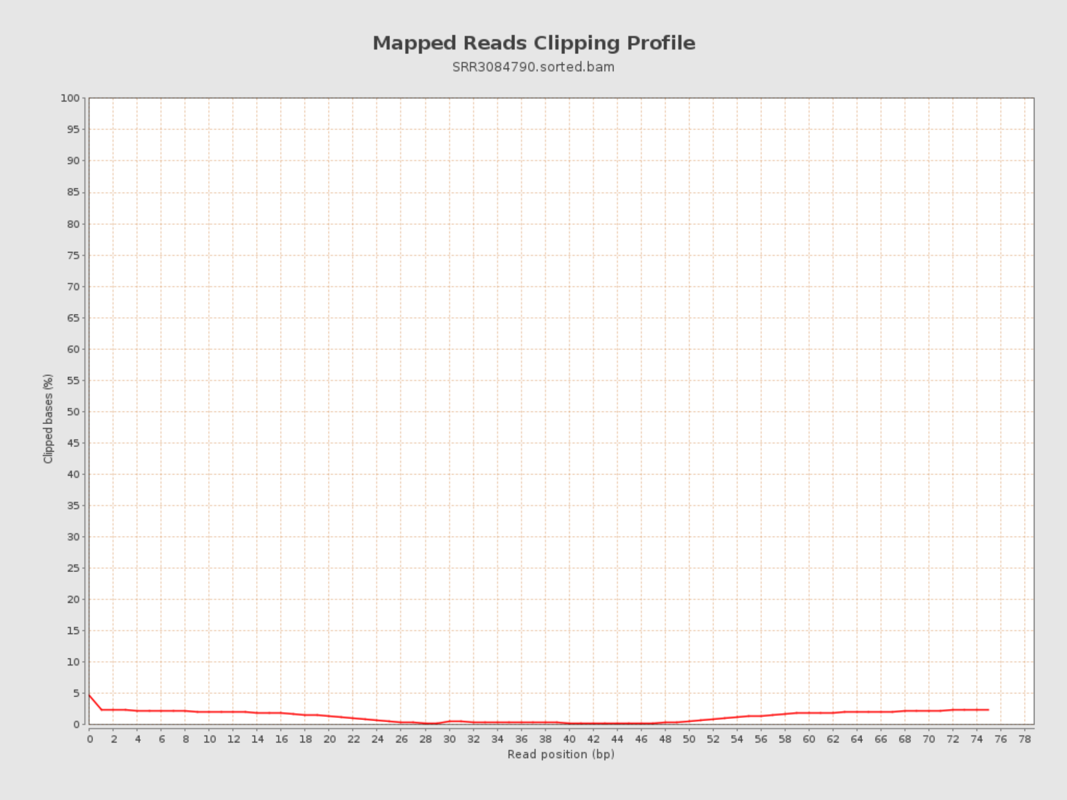
8. Results : Mapped Reads Nucleotide Content



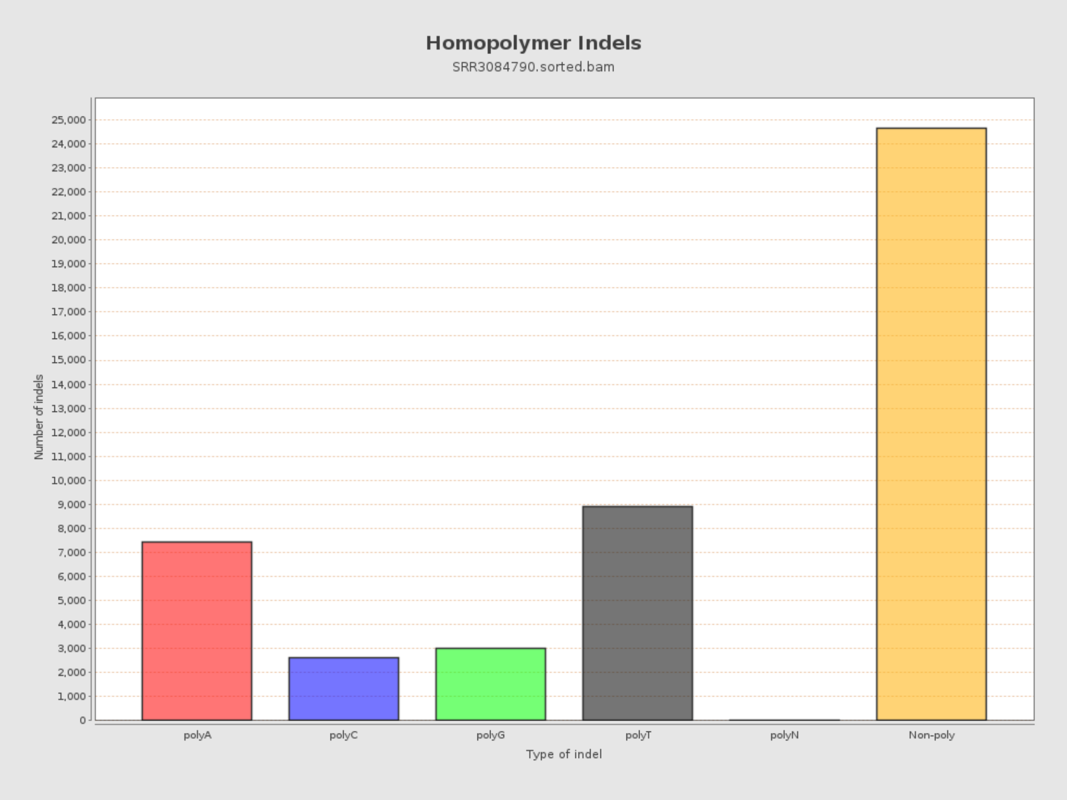
9. Results : Mapped Reads GC-content Distribution



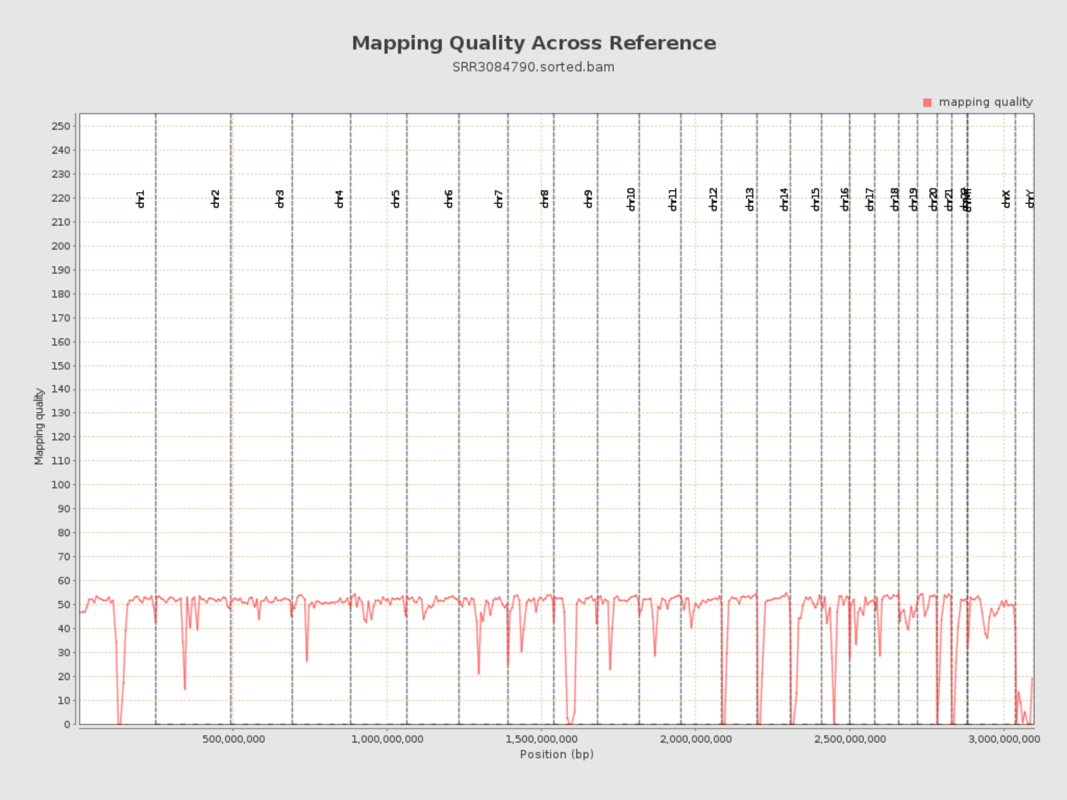
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram