Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 19:34:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084893.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_SRR3084893 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084893.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 19:34:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084893.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,307,774
Mapped reads	2,064,768 / 89.47%
Unmapped reads	243,006 / 10.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,879 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	108,782 / 4.71%
Duplication rate	4.63%
Clipped reads	824,457 / 35.73%

2.2. ACGT Content

Number/percentage of A's	39,712,471 / 28.41%
Number/percentage of C's	25,197,827 / 18.02%
Number/percentage of T's	45,108,773 / 32.27%
Number/percentage of G's	29,760,713 / 21.29%
Number/percentage of N's	21,625 / 0.02%
GC Percentage	39.31%

2.3. Coverage

Mean	0.0452

Standard Deviation	0.3138

2.4. Mapping Quality

Mean Mapping Quality	47.33

2.5. Mismatches and indels

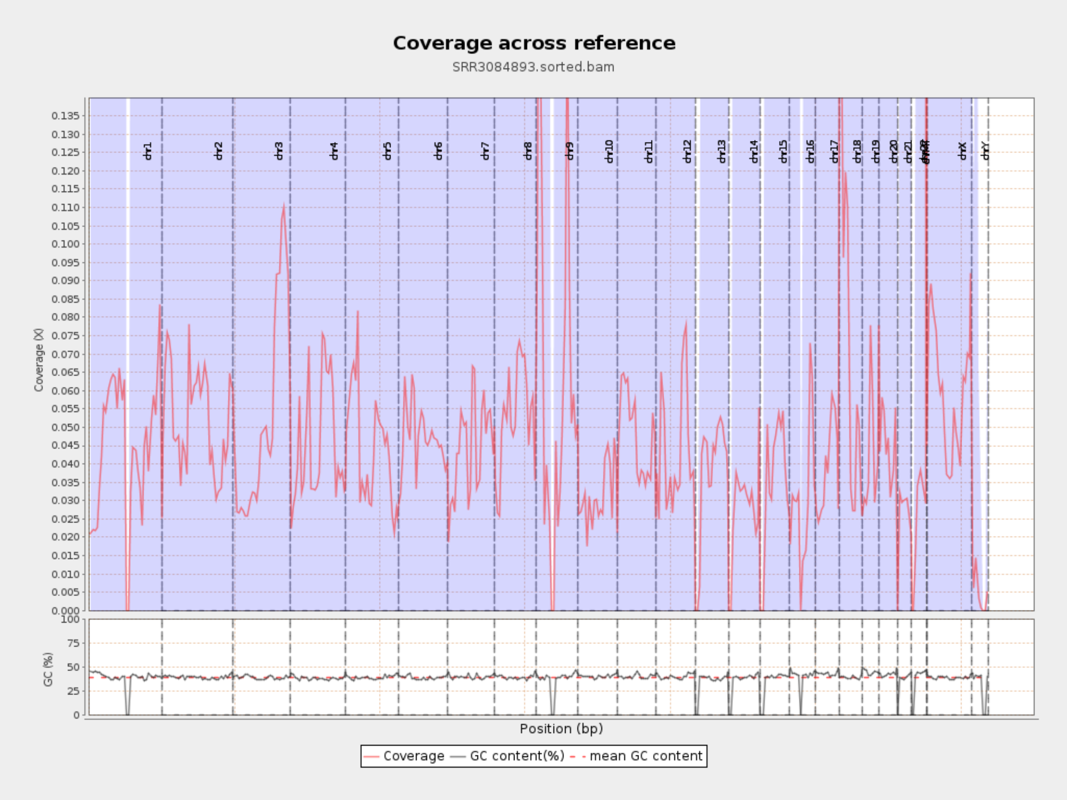
General error rate	0.81%
Mismatches	1,117,839
Insertions	10,592
Mapped reads with at least one insertion	0.51%
Deletions	29,574
Mapped reads with at least one deletion	1.42%
Homopolymer indels	48.82%

2.6. Chromosome stats

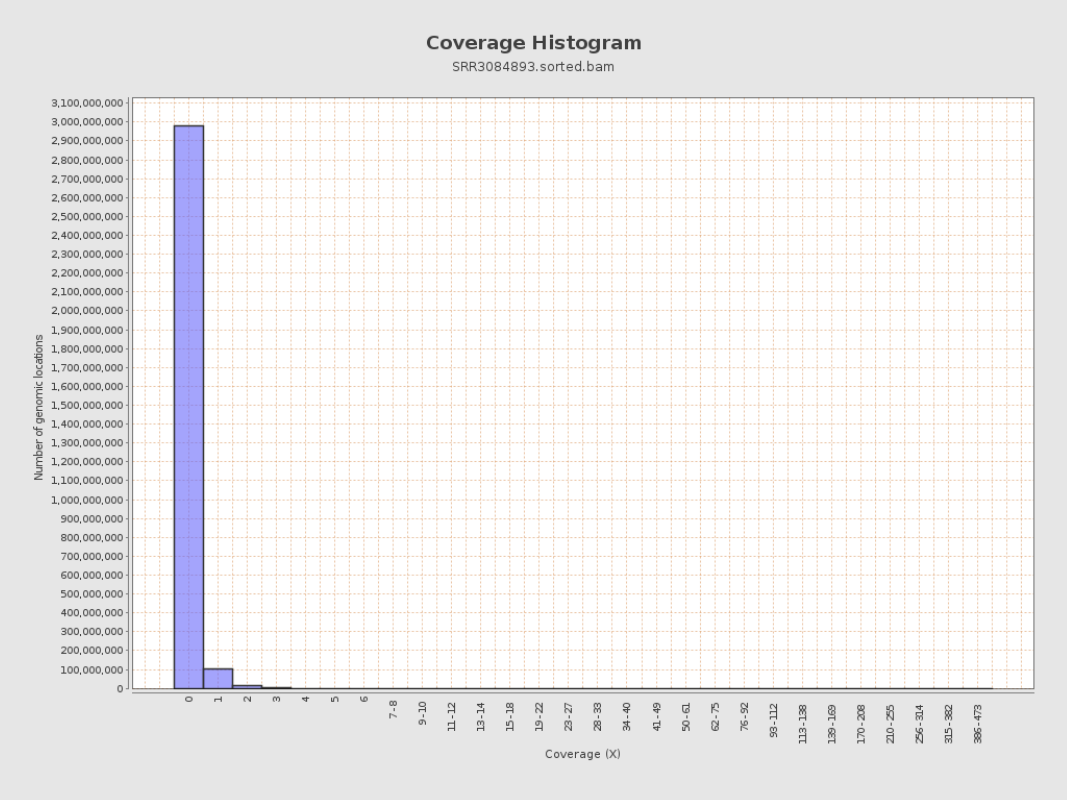
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11118657	0.0446	0.4651
chr2	243199373	12765565	0.0525	0.4019
chr3	198022430	10509983	0.0531	0.264
chr4	191154276	8692983	0.0455	0.2447
chr5	180915260	8087327	0.0447	0.243
chr6	171115067	8009727	0.0468	0.254
chr7	159138663	7086347	0.0445	0.2967

chr8	146364022	7714777	0.0527	0.418
chr9	141213431	9083364	0.0643	0.3885
chr10	135534747	4241224	0.0313	0.2276
chr11	135006516	6410520	0.0475	0.3042
chr12	133851895	5855944	0.0437	0.2433
chr13	115169878	4263502	0.037	0.2185
chr14	107349540	2843593	0.0265	0.1922
chr15	102531392	3615265	0.0353	0.2138
chr16	90354753	2831961	0.0313	0.2144
chr17	81195210	3189023	0.0393	0.2326
chr18	78077248	5959708	0.0763	0.5536
chr19	59128983	2567188	0.0434	0.331
chr20	63025520	2860965	0.0454	0.248
chr21	48129895	1254077	0.0261	0.194
chr22	51304566	1239379	0.0242	0.1748
chrMT	16571	110241	6.6526	3.9563
chrX	155270560	9240781	0.0595	0.2966
chrY	59373566	300439	0.0051	0.1256

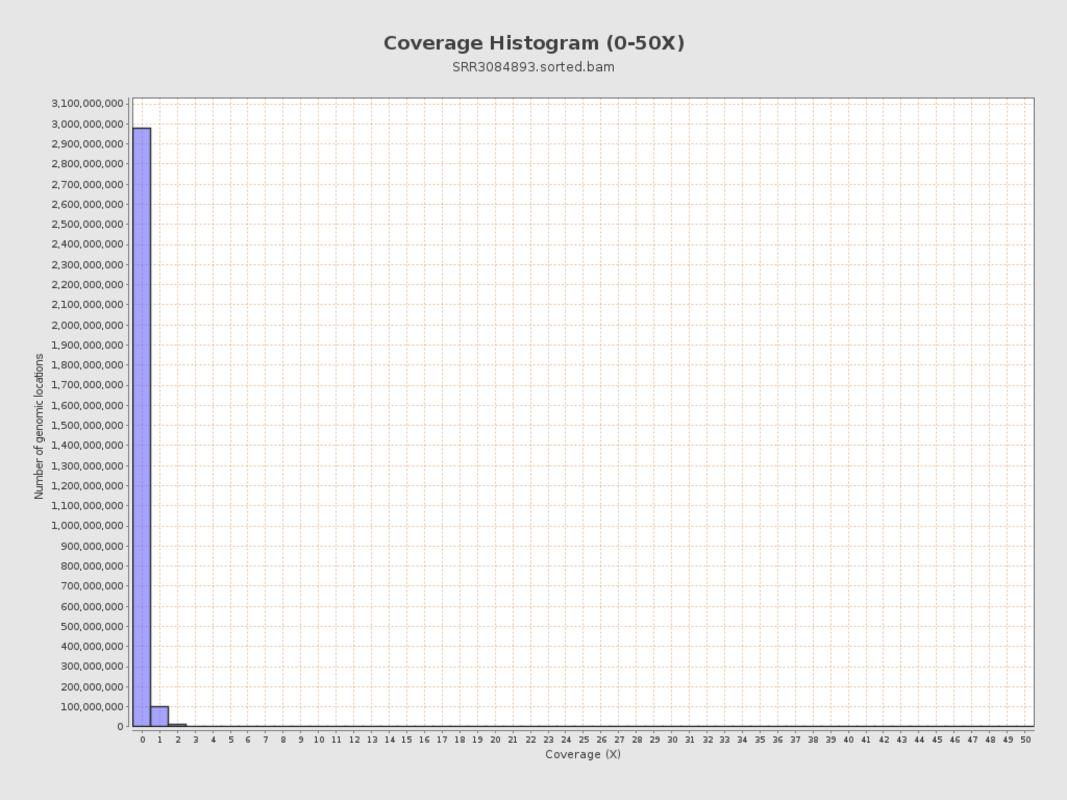
3. Results : Coverage across reference



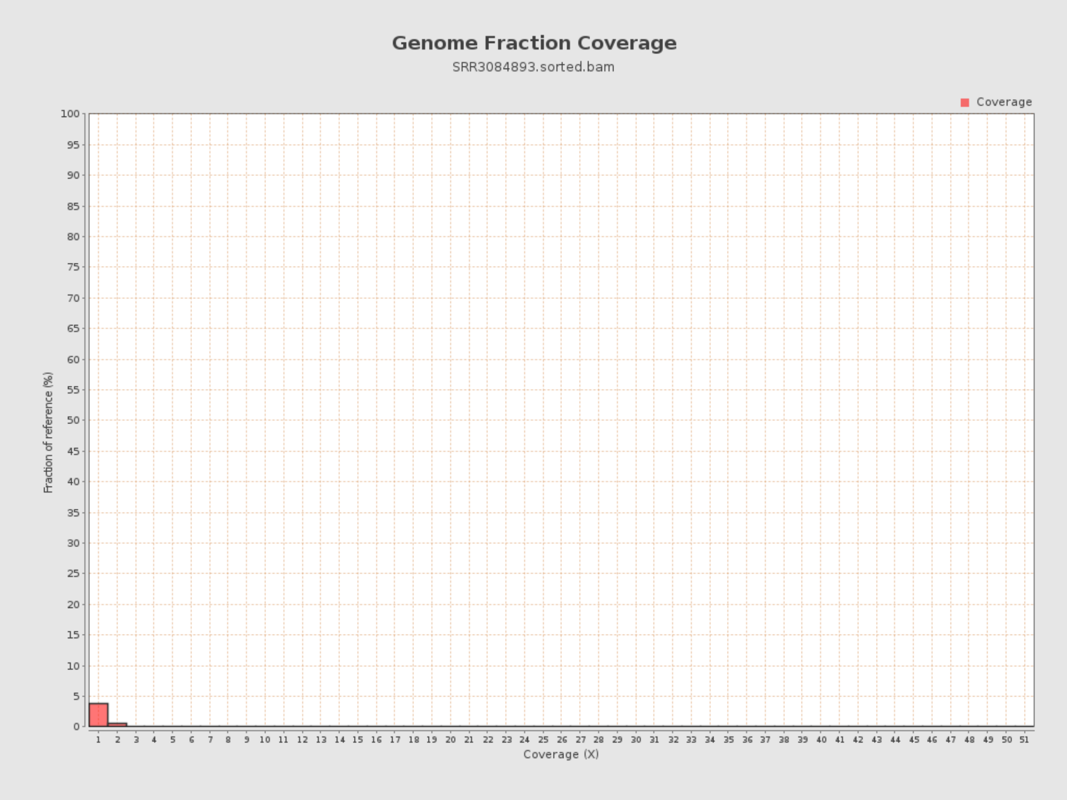
4. Results : Coverage Histogram



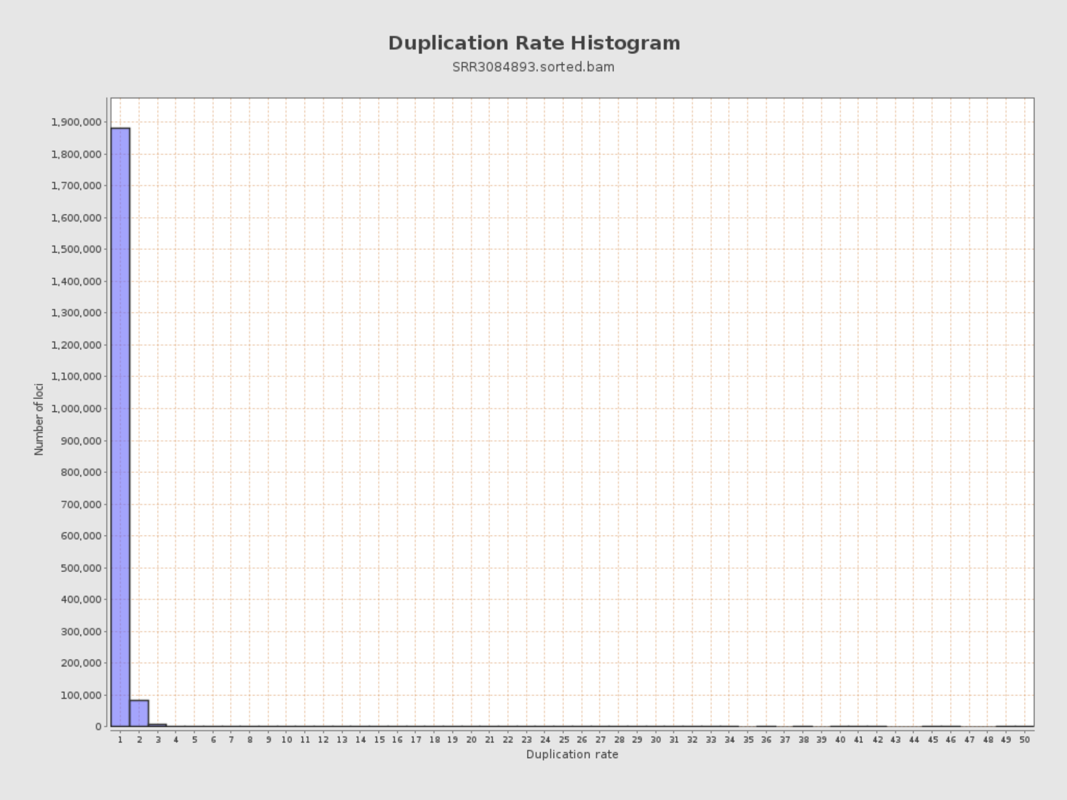
5. Results : Coverage Histogram (0-50X)



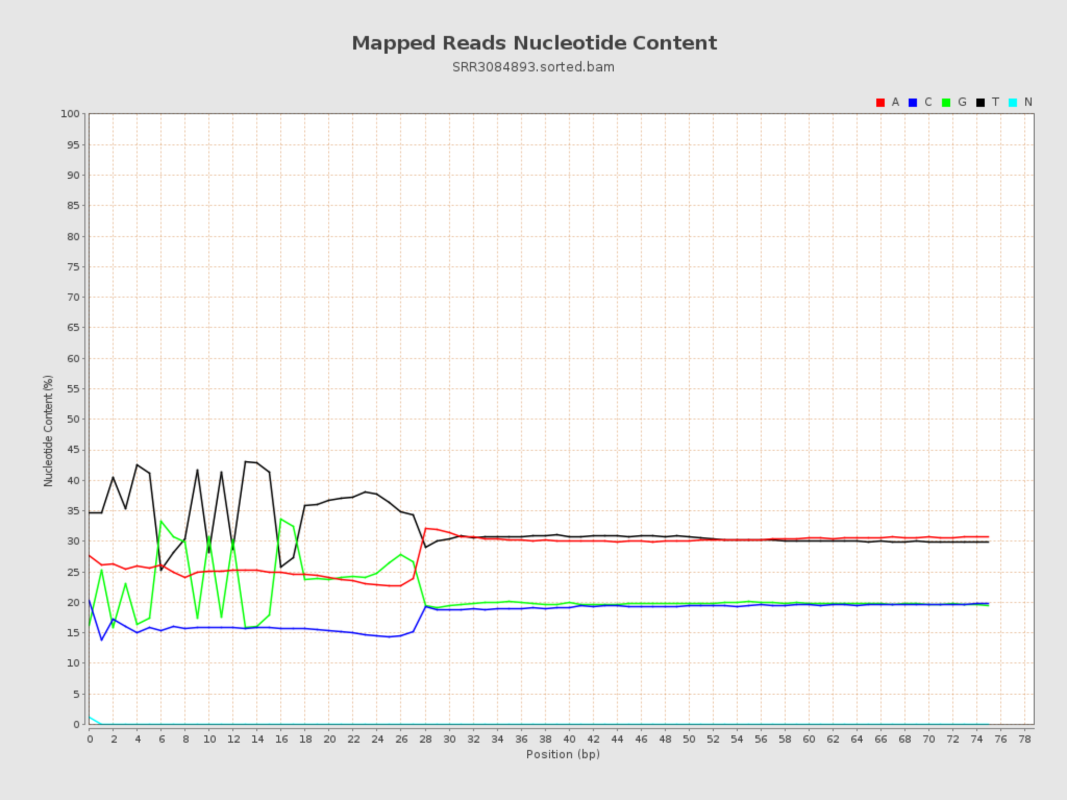
6. Results : Genome Fraction Coverage



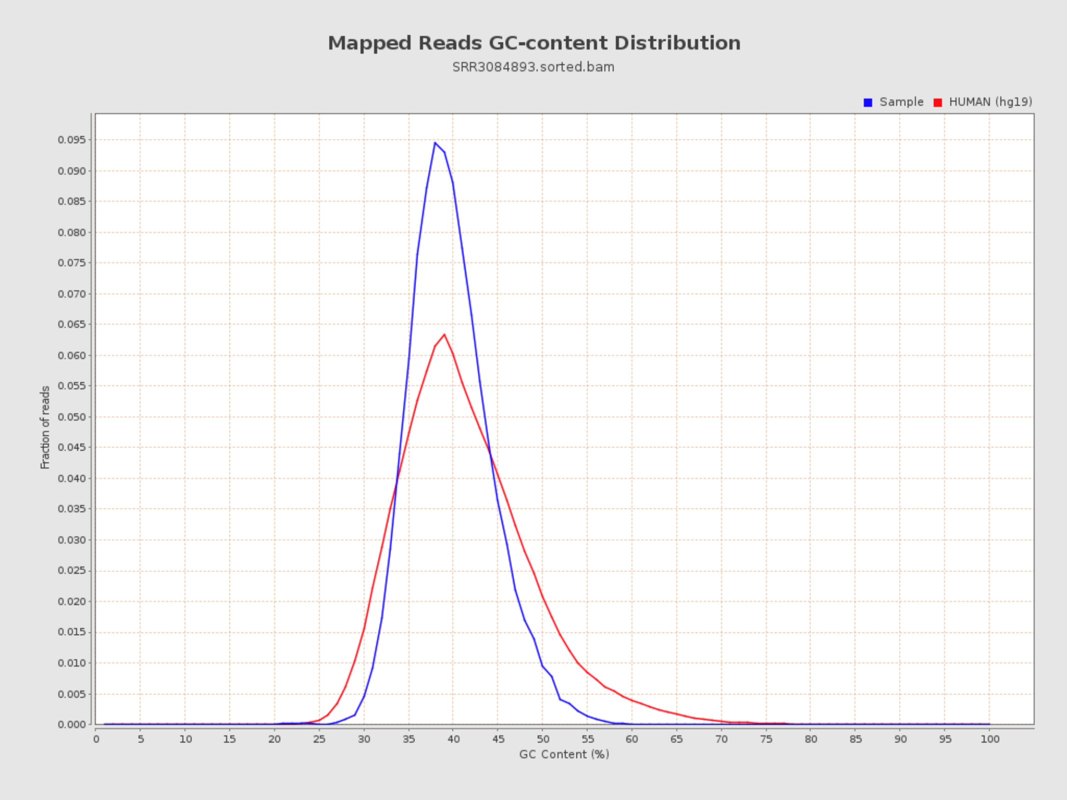
7. Results : Duplication Rate Histogram



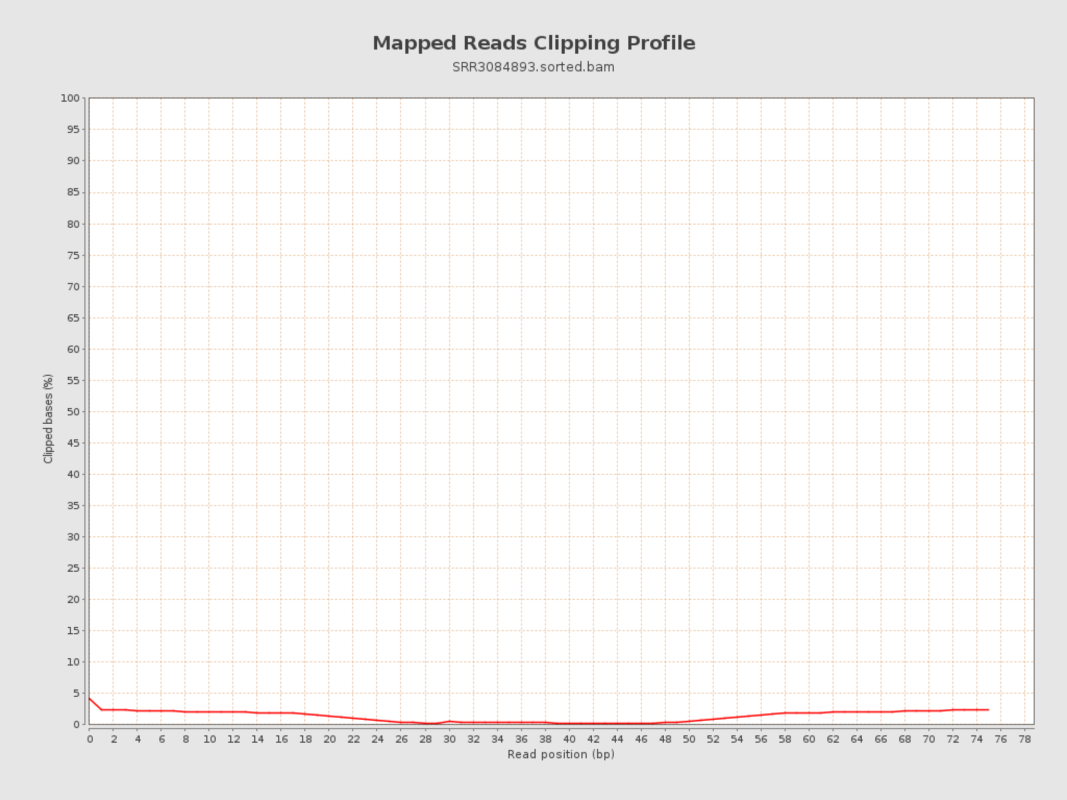
8. Results : Mapped Reads Nucleotide Content



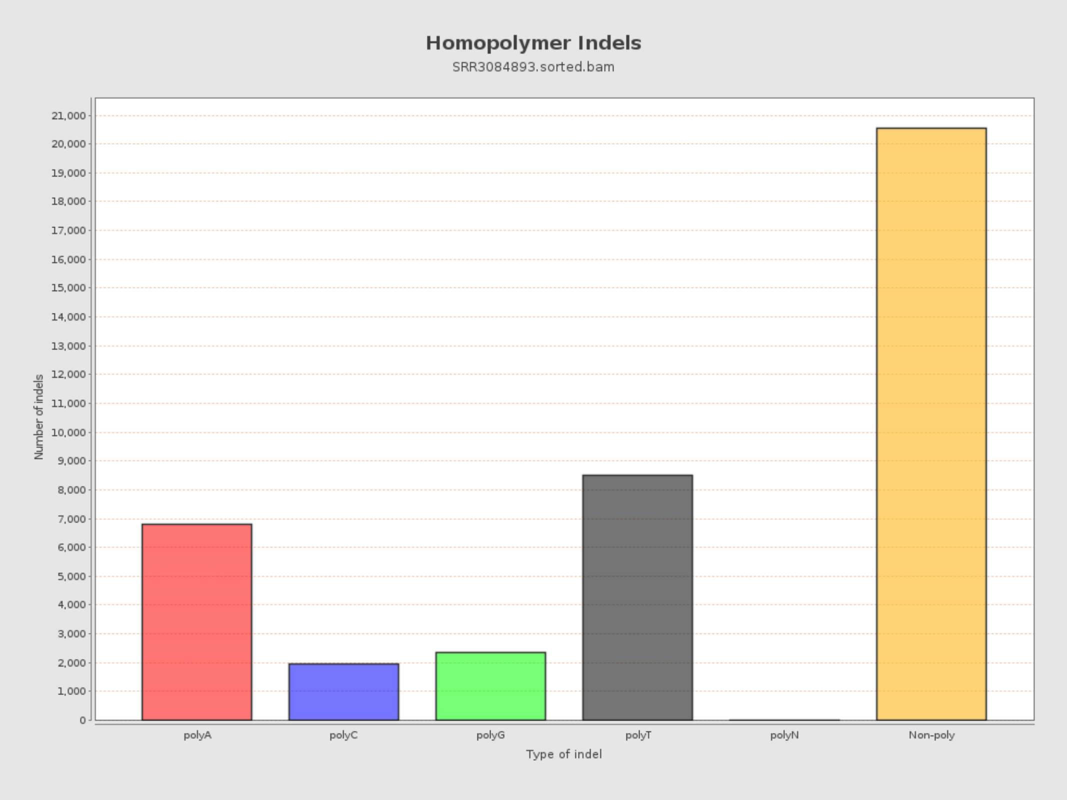
9. Results : Mapped Reads GC-content Distribution



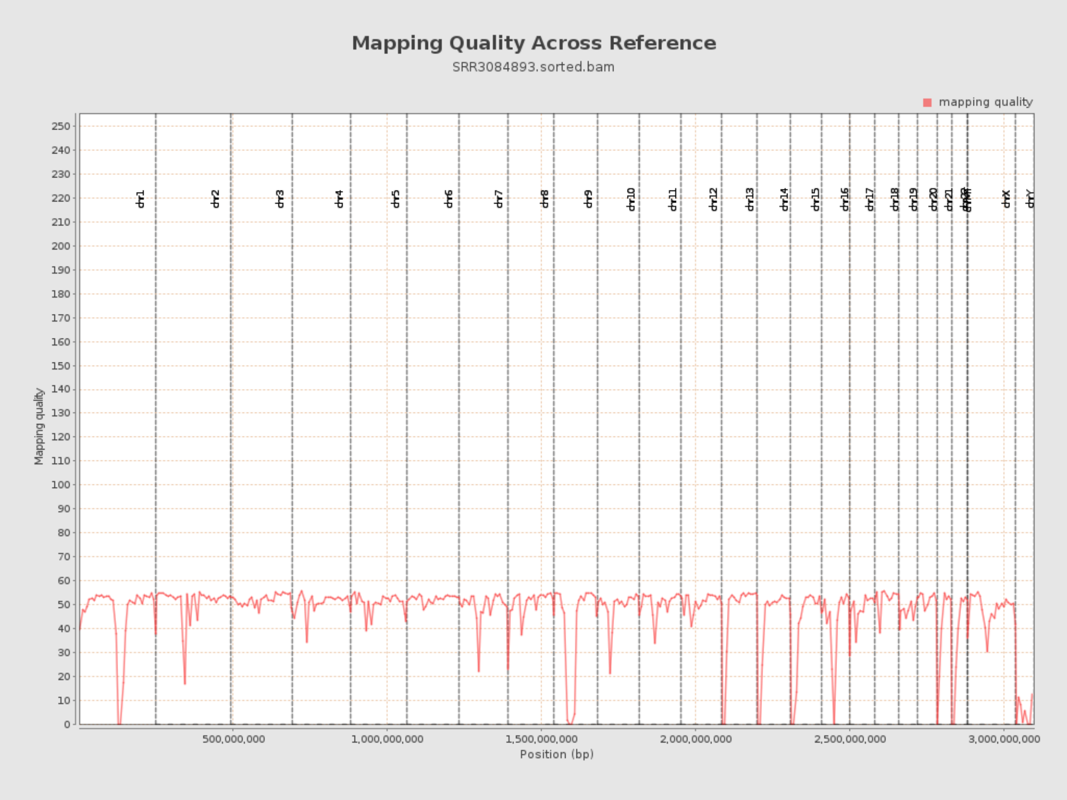
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram