Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 17:49:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084854.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_SRR3084854 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084854.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 17:49:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084854.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,235,072
Mapped reads	1,771,882 / 79.28%
Unmapped reads	463,190 / 20.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,410 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	110,158 / 4.93%
Duplication rate	5.45%
Clipped reads	777,102 / 34.77%

2.2. ACGT Content

Number/percentage of A's	32,369,492 / 27.29%
Number/percentage of C's	22,394,265 / 18.88%
Number/percentage of T's	37,115,431 / 31.3%
Number/percentage of G's	26,698,564 / 22.51%
Number/percentage of N's	17,442 / 0.01%
GC Percentage	41.4%

2.3. Coverage

Mean	0.0383

Standard Deviation	0.2895

2.4. Mapping Quality

Mean Mapping Quality	46.83

2.5. Mismatches and indels

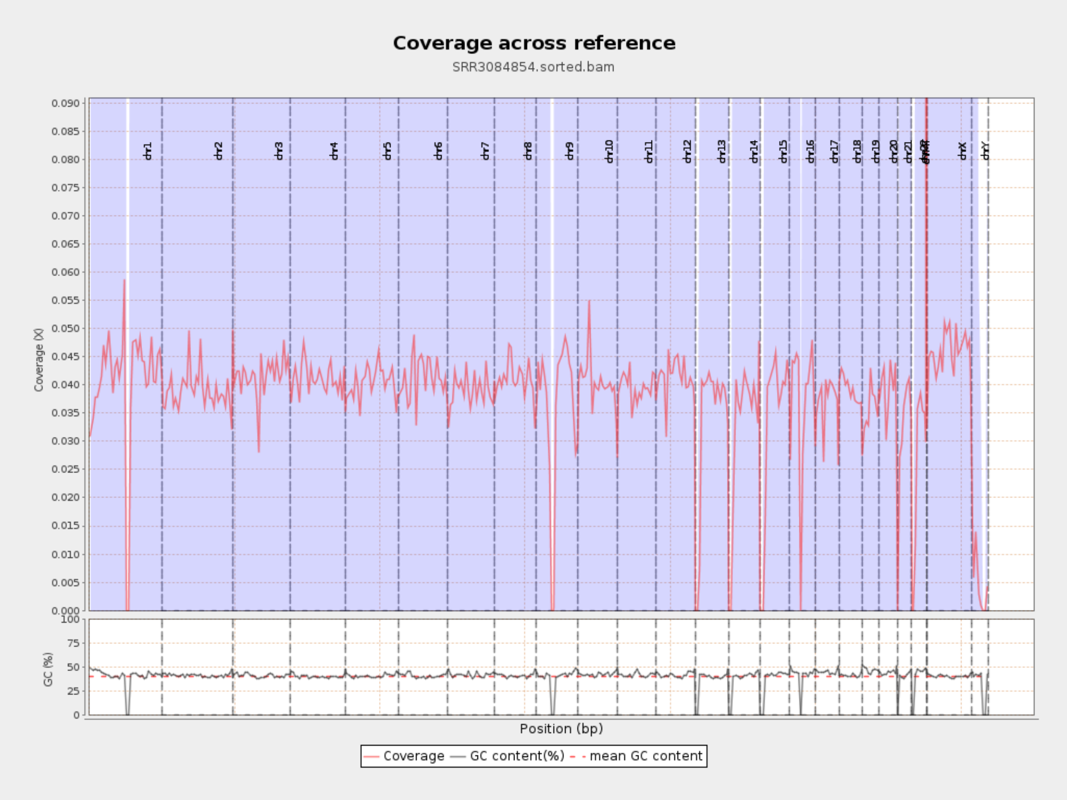
General error rate	0.87%
Mismatches	1,010,028
Insertions	8,862
Mapped reads with at least one insertion	0.5%
Deletions	23,837
Mapped reads with at least one deletion	1.33%
Homopolymer indels	46.87%

2.6. Chromosome stats

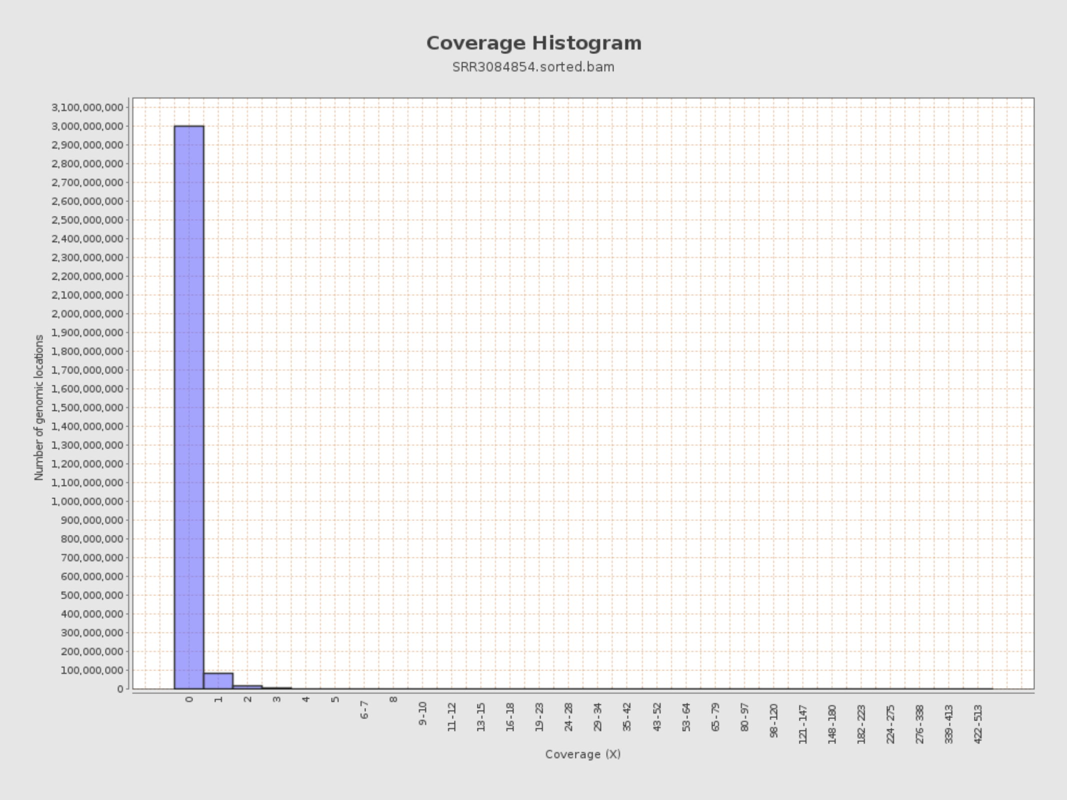
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10070873	0.0404	0.465
chr2	243199373	9502709	0.0391	0.2955
chr3	198022430	8251006	0.0417	0.2395
chr4	191154276	7858369	0.0411	0.2474
chr5	180915260	7310247	0.0404	0.2369
chr6	171115067	7054240	0.0412	0.2488
chr7	159138663	6224527	0.0391	0.2758

chr8	146364022	5994606	0.041	0.3874
chr9	141213431	5081637	0.036	0.2722
chr10	135534747	5530584	0.0408	0.3057
chr11	135006516	5323696	0.0394	0.2635
chr12	133851895	5530580	0.0413	0.2403
chr13	115169878	3802065	0.033	0.2137
chr14	107349540	3424371	0.0319	0.2163
chr15	102531392	3428703	0.0334	0.2149
chr16	90354753	3342849	0.037	0.2359
chr17	81195210	2993049	0.0369	0.2359
chr18	78077248	3064256	0.0392	0.4436
chr19	59128983	2113897	0.0358	0.3358
chr20	63025520	2456823	0.039	0.2373
chr21	48129895	1517875	0.0315	0.2193
chr22	51304566	1269229	0.0247	0.1844
chrMT	16571	91695	5.5335	3.6121
chrX	155270560	7111891	0.0458	0.2597
chrY	59373566	287499	0.0048	0.1031

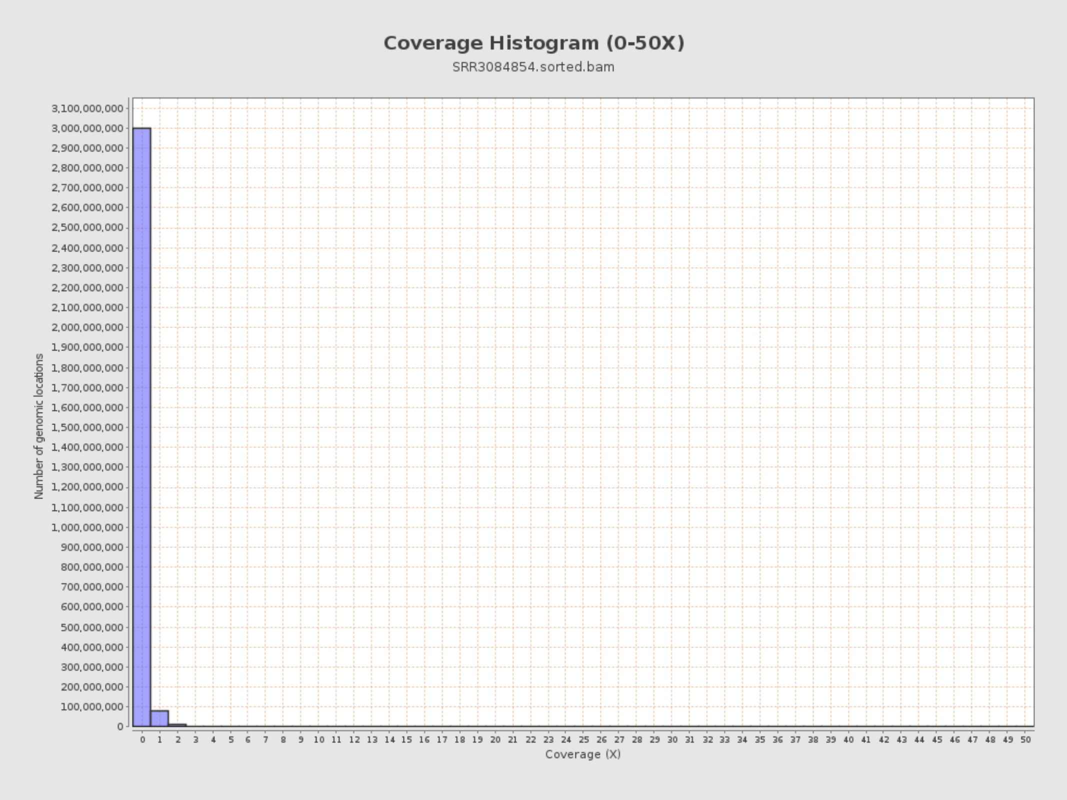
3. Results : Coverage across reference



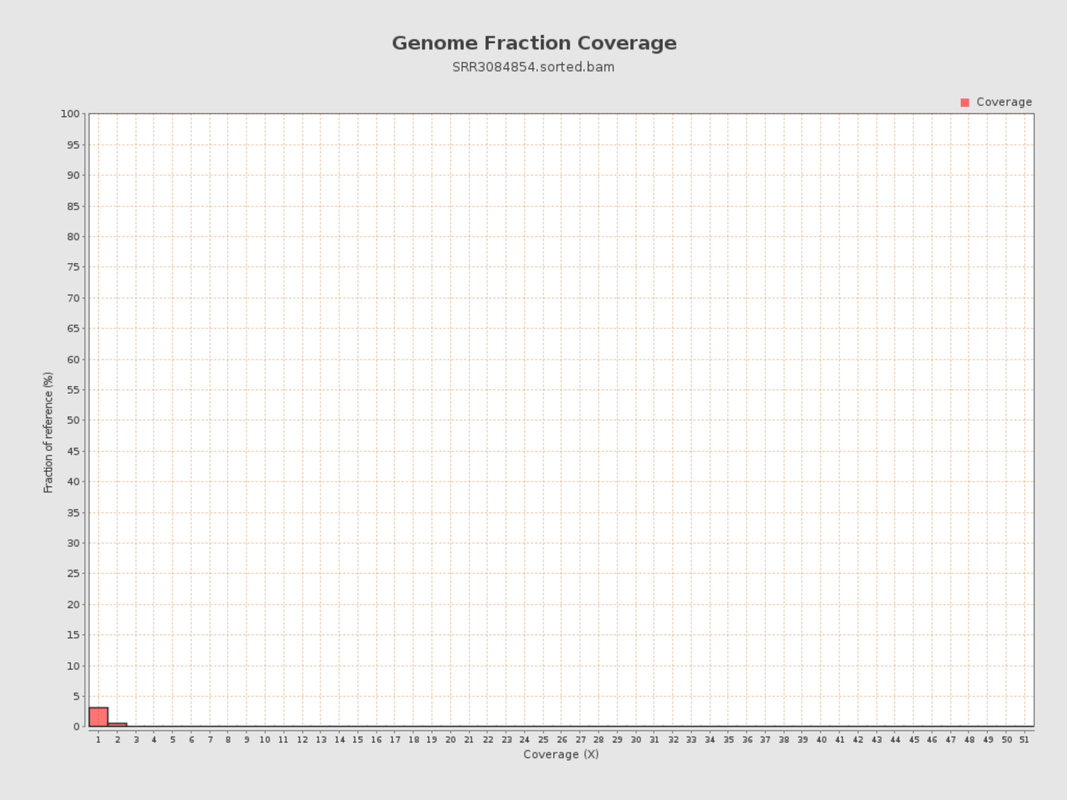
4. Results : Coverage Histogram



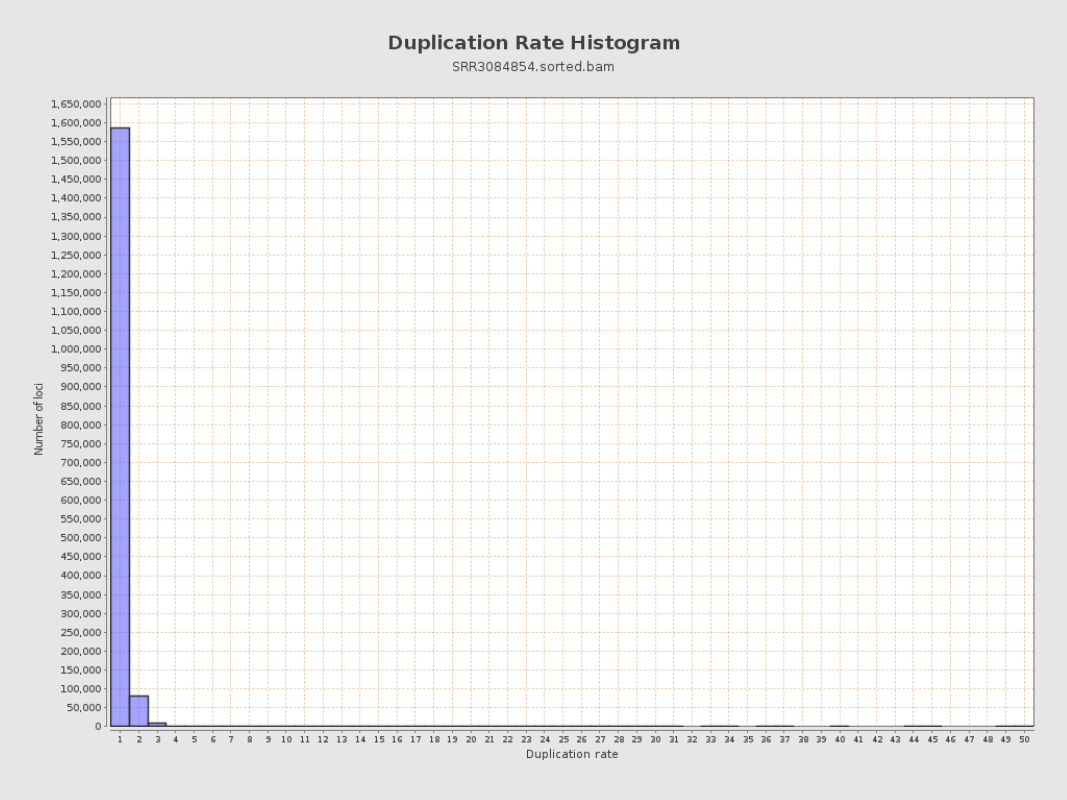
5. Results : Coverage Histogram (0-50X)



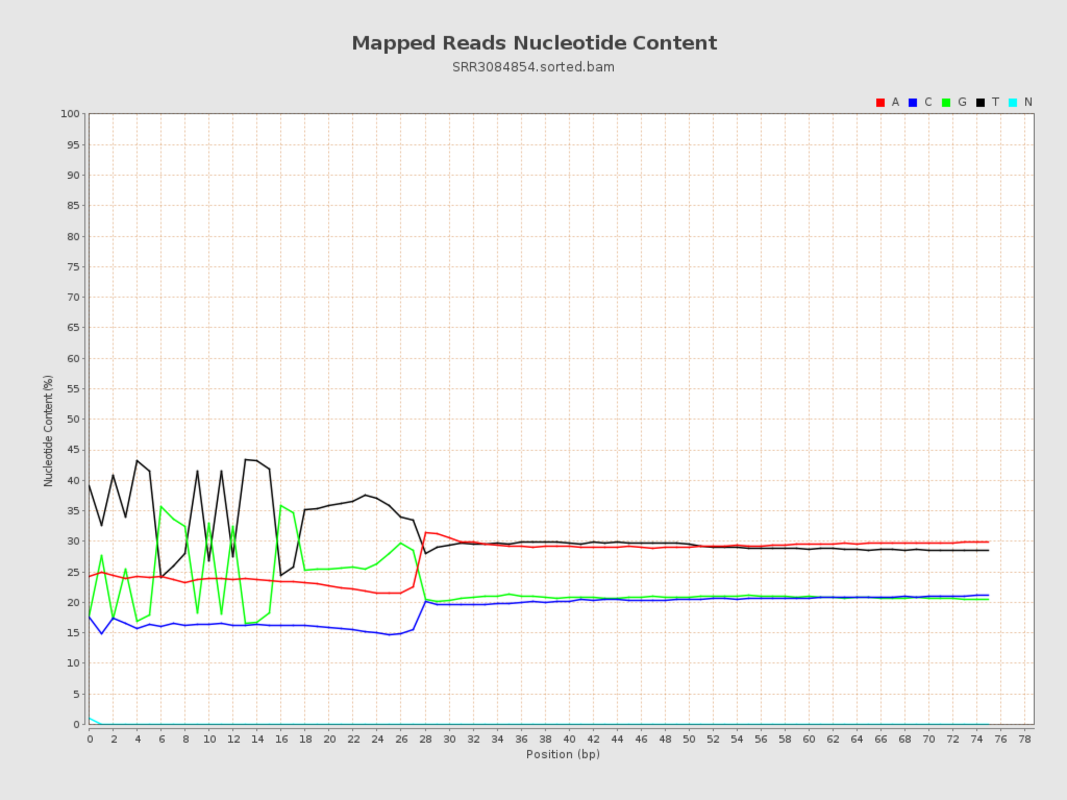
6. Results : Genome Fraction Coverage



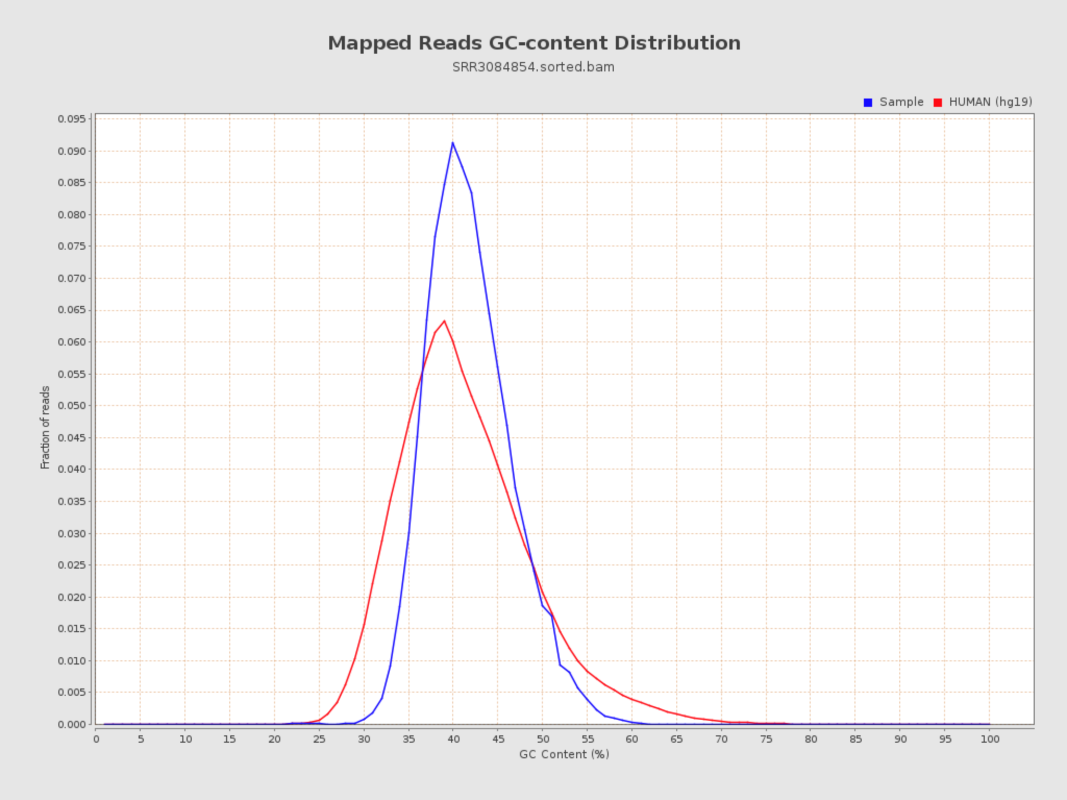
7. Results : Duplication Rate Histogram



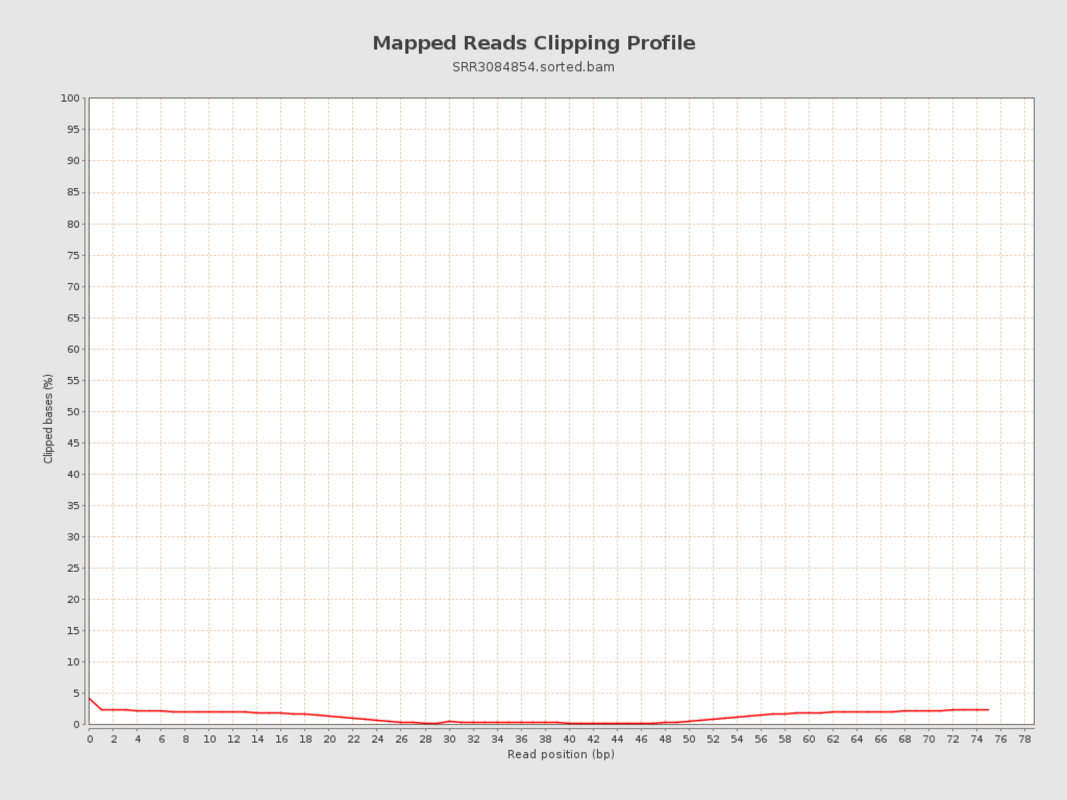
8. Results : Mapped Reads Nucleotide Content



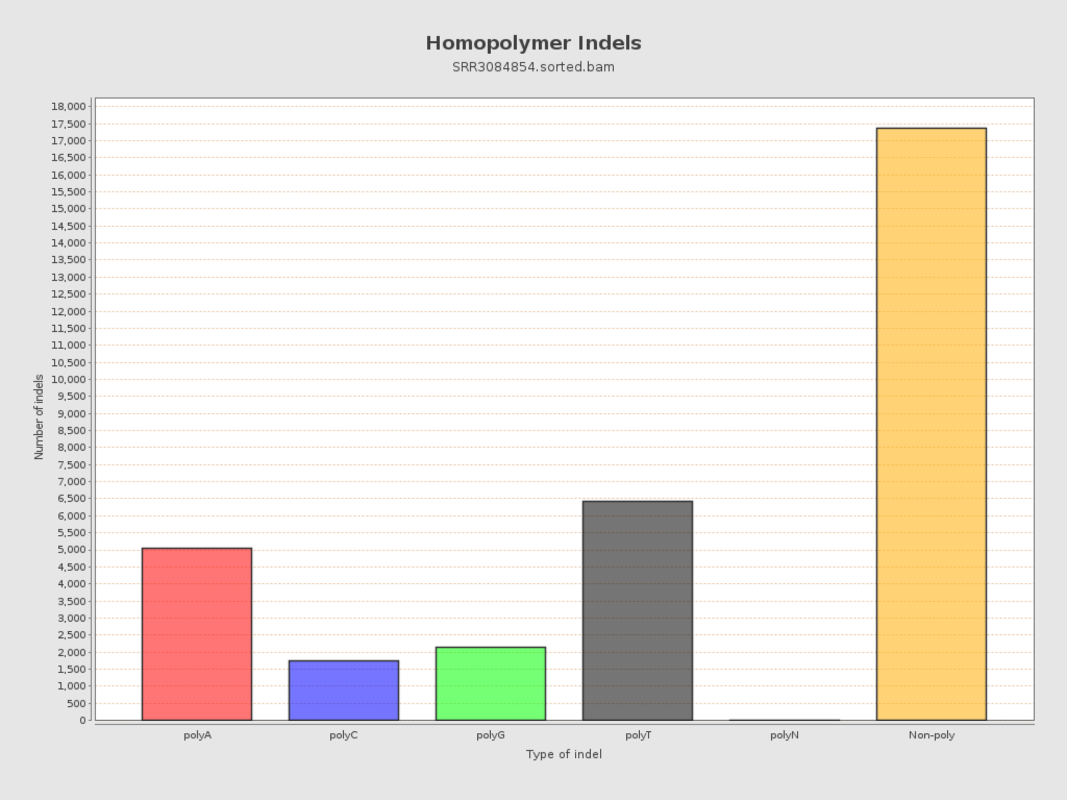
9. Results : Mapped Reads GC-content Distribution



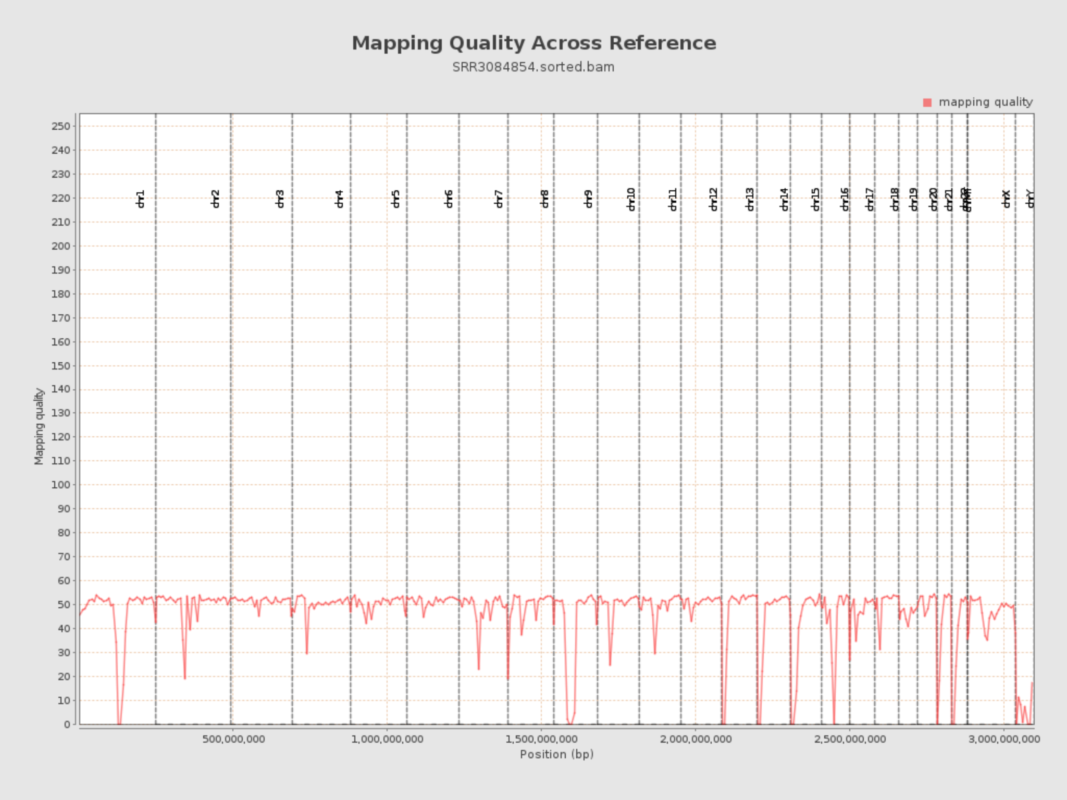
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram