Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 19:03:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084878.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_SRR3084878 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084878.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 19:03:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084878.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,347,753
Mapped reads	2,115,392 / 90.1%
Unmapped reads	232,361 / 9.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,700 / 0.67%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	98,216 / 4.18%
Duplication rate	3.96%
Clipped reads	735,981 / 31.35%

2.2. ACGT Content

Number/percentage of A's	42,341,557 / 29.02%
Number/percentage of C's	26,512,966 / 18.17%
Number/percentage of T's	47,040,791 / 32.24%
Number/percentage of G's	29,985,936 / 20.55%
Number/percentage of N's	23,481 / 0.02%
GC Percentage	38.72%

2.3. Coverage

Mean	0.0471

Standard Deviation	0.35

2.4. Mapping Quality

Mean Mapping Quality	47.65

2.5. Mismatches and indels

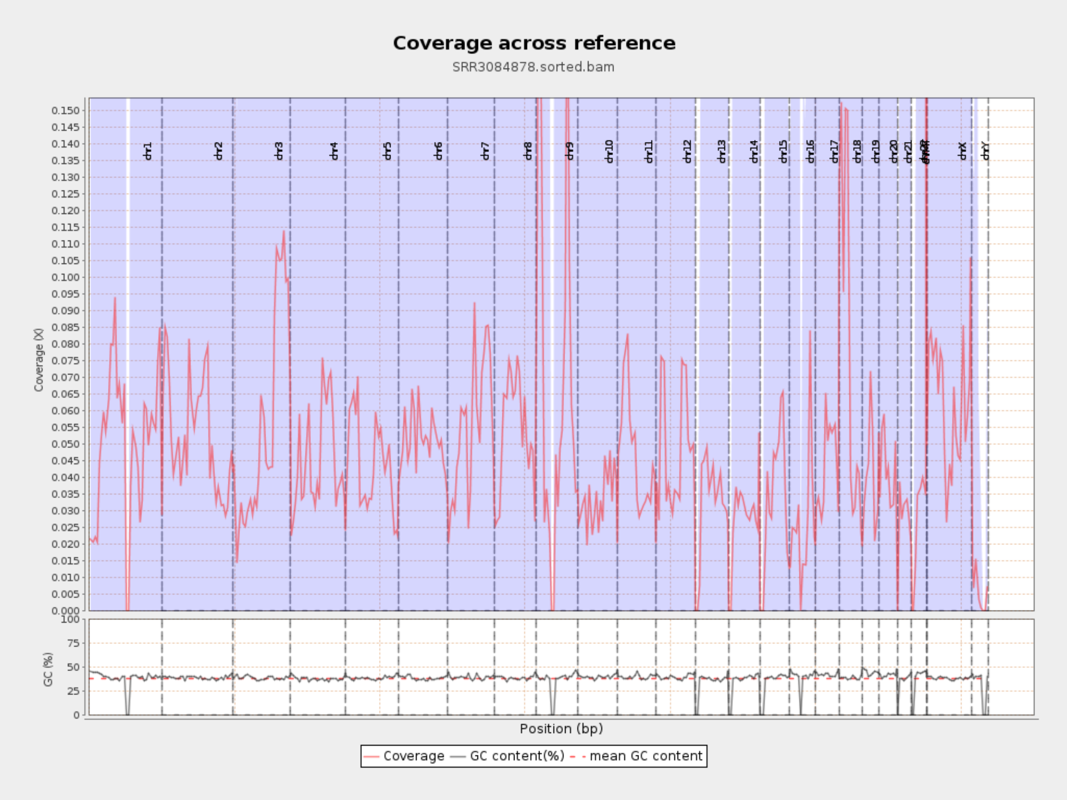
General error rate	0.83%
Mismatches	1,186,545
Insertions	11,563
Mapped reads with at least one insertion	0.54%
Deletions	32,533
Mapped reads with at least one deletion	1.52%
Homopolymer indels	49.29%

2.6. Chromosome stats

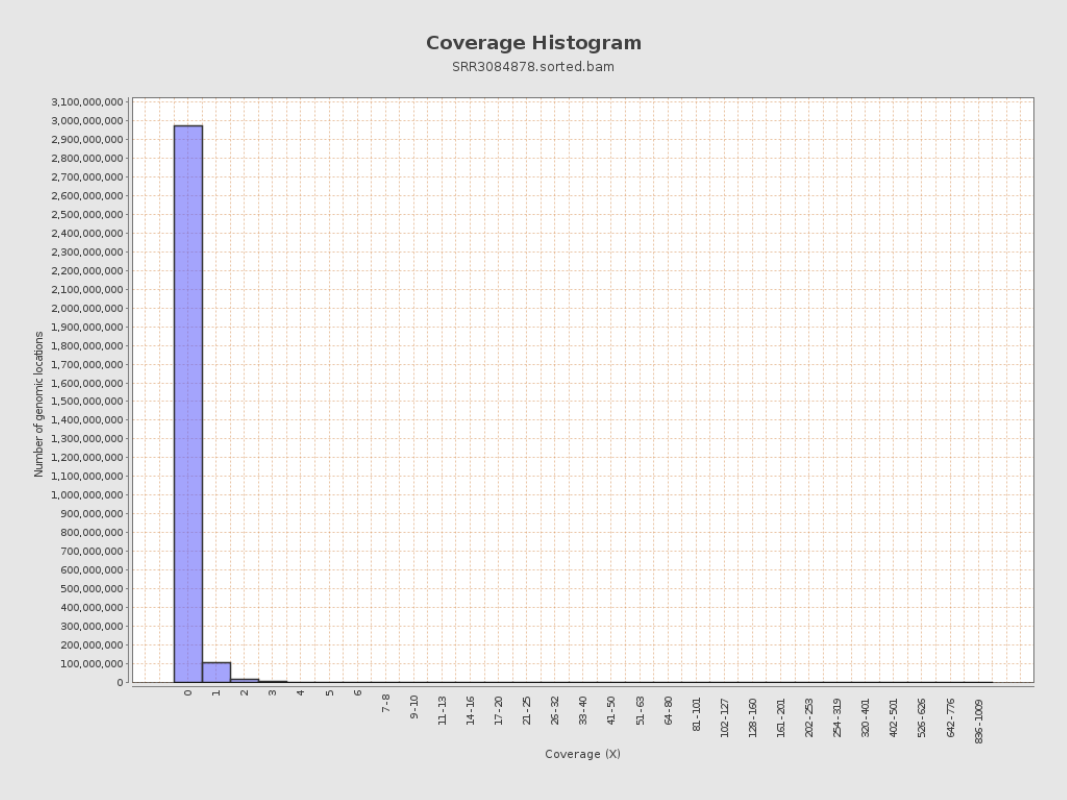
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12537615	0.0503	0.4948
chr2	243199373	12834921	0.0528	0.3907
chr3	198022430	10937439	0.0552	0.2709
chr4	191154276	8628191	0.0451	0.2455
chr5	180915260	7966666	0.044	0.2416
chr6	171115067	8726396	0.051	0.2628
chr7	159138663	8882513	0.0558	0.3509

chr8	146364022	7828655	0.0535	0.6989
chr9	141213431	10281502	0.0728	0.4128
chr10	135534747	4508969	0.0333	0.2513
chr11	135006516	6326413	0.0469	0.3167
chr12	133851895	6462278	0.0483	0.2554
chr13	115169878	3665618	0.0318	0.2031
chr14	107349540	2856911	0.0266	0.2034
chr15	102531392	3485757	0.034	0.2107
chr16	90354753	2465612	0.0273	0.2032
chr17	81195210	3569161	0.044	0.2523
chr18	78077248	6248509	0.08	0.6554
chr19	59128983	2444555	0.0413	0.3381
chr20	63025520	2668449	0.0423	0.2444
chr21	48129895	1325114	0.0275	0.2021
chr22	51304566	1316663	0.0257	0.1802
chrMT	16571	48855	2.9482	2.1613
chrX	155270560	9614955	0.0619	0.307
chrY	59373566	329835	0.0056	0.1265

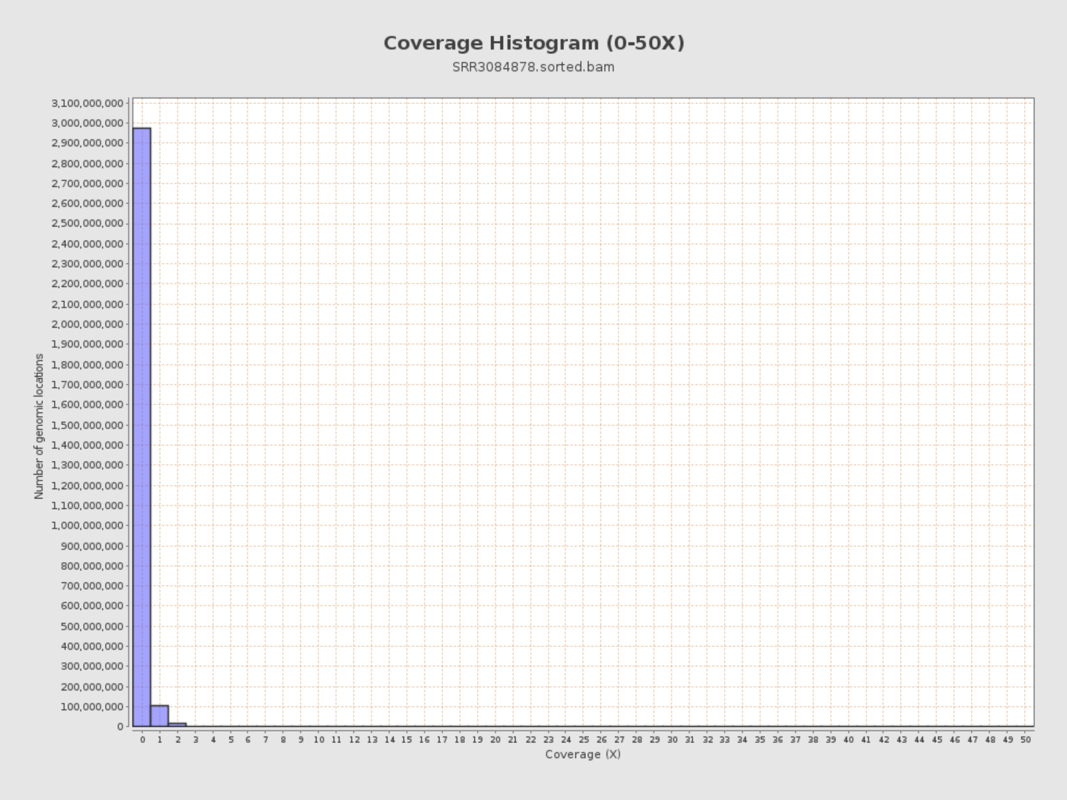
3. Results : Coverage across reference



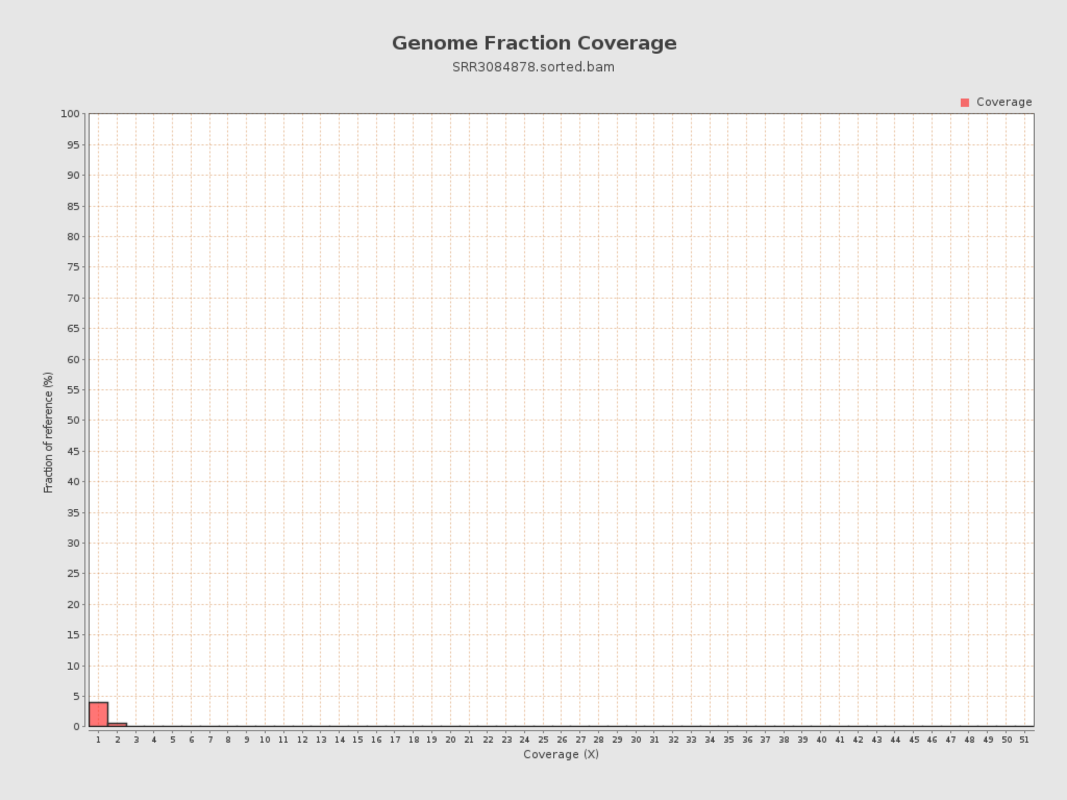
4. Results : Coverage Histogram



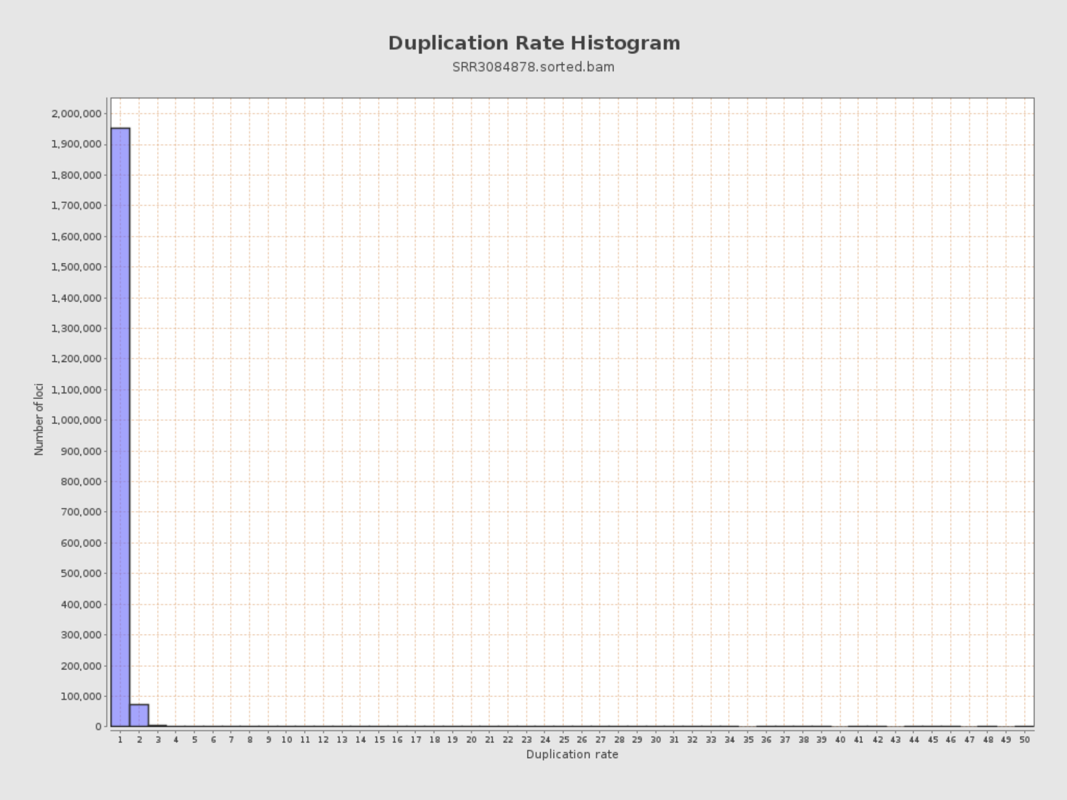
5. Results : Coverage Histogram (0-50X)



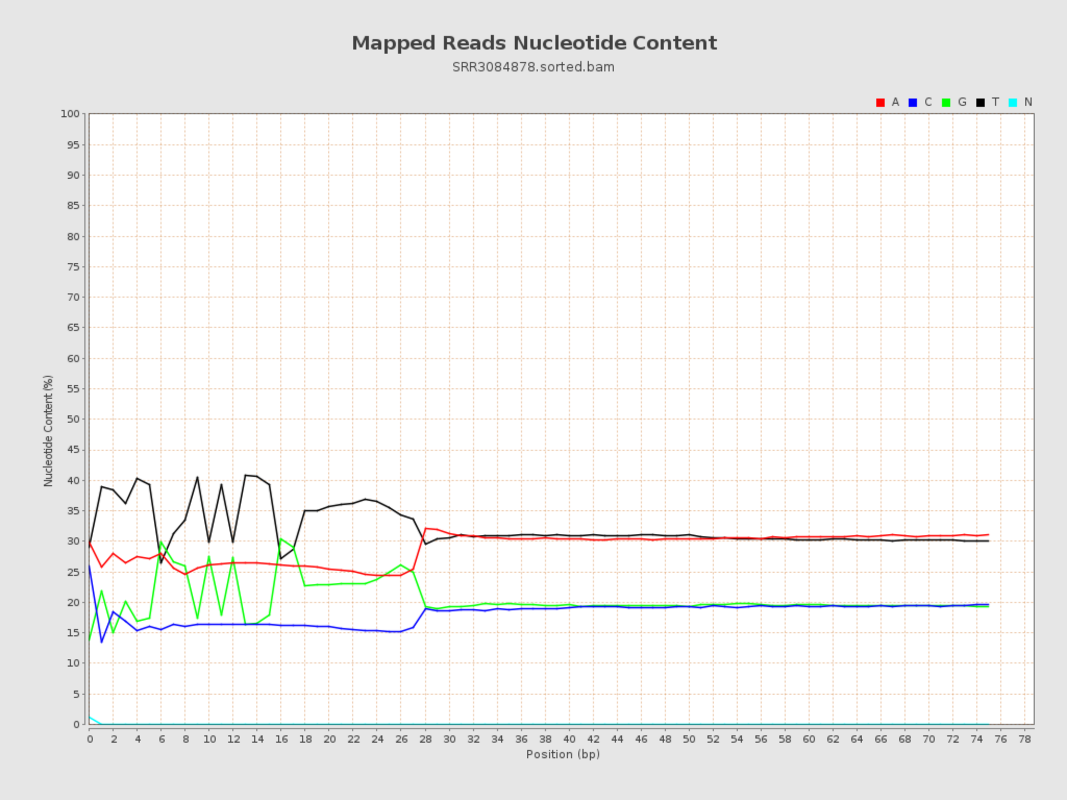
6. Results : Genome Fraction Coverage



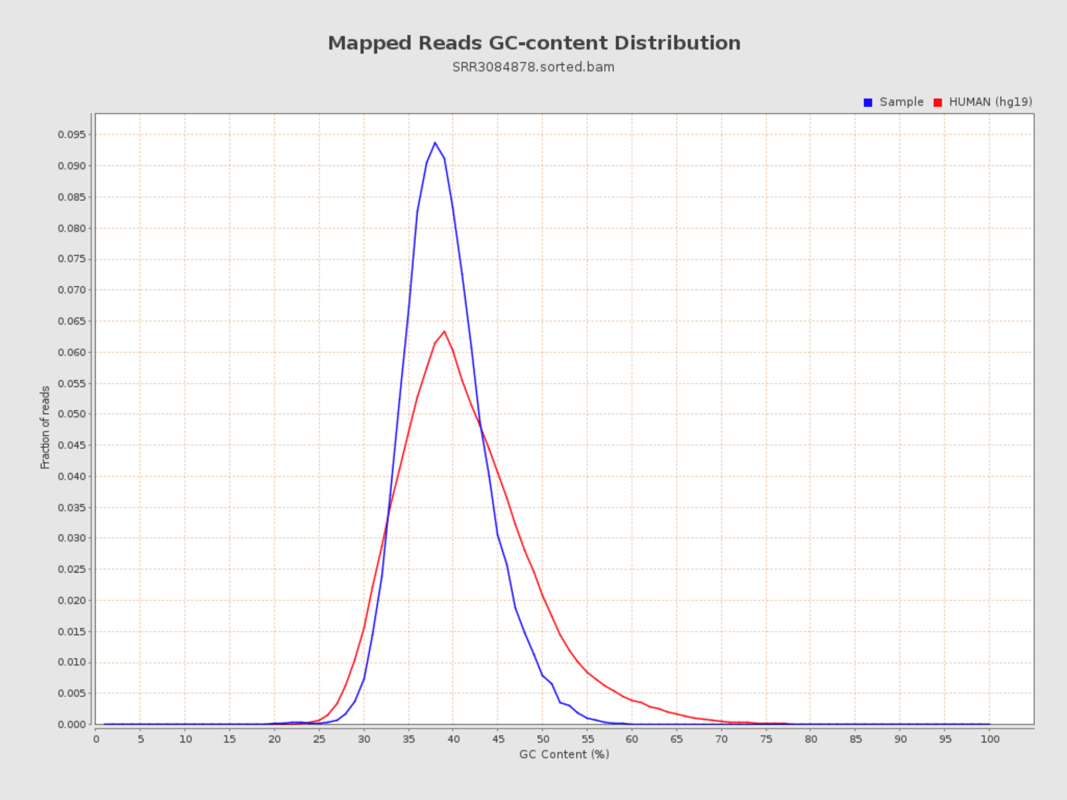
7. Results : Duplication Rate Histogram



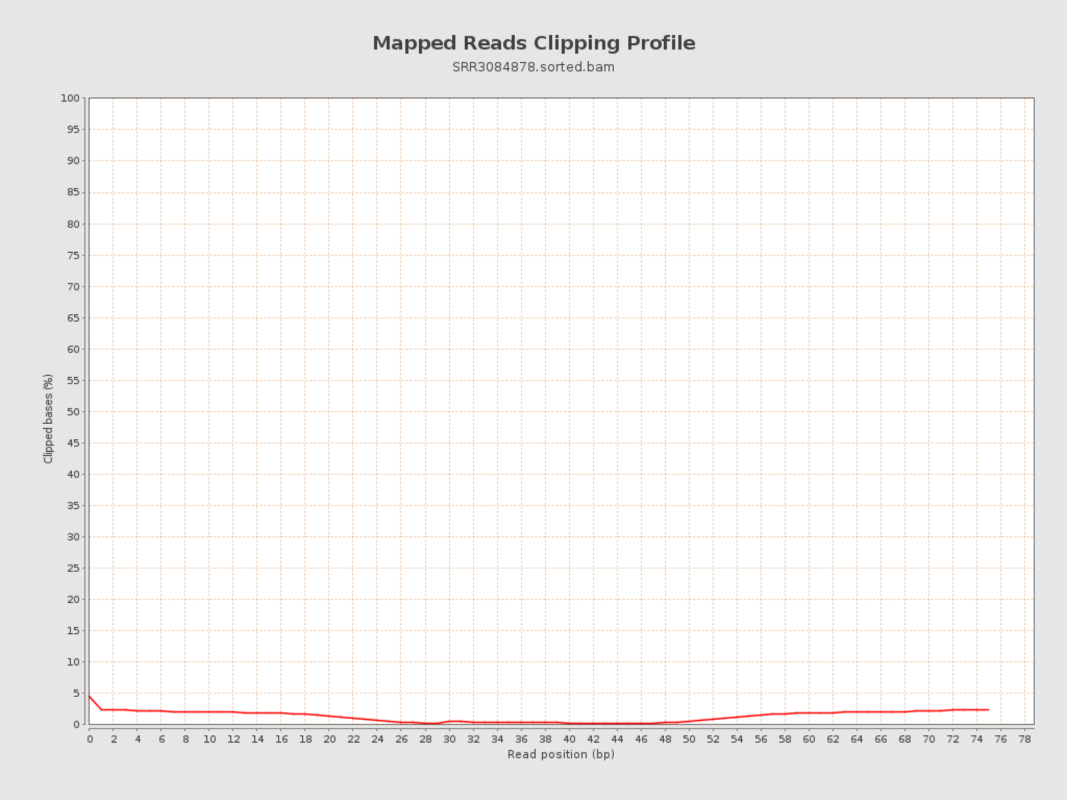
8. Results : Mapped Reads Nucleotide Content



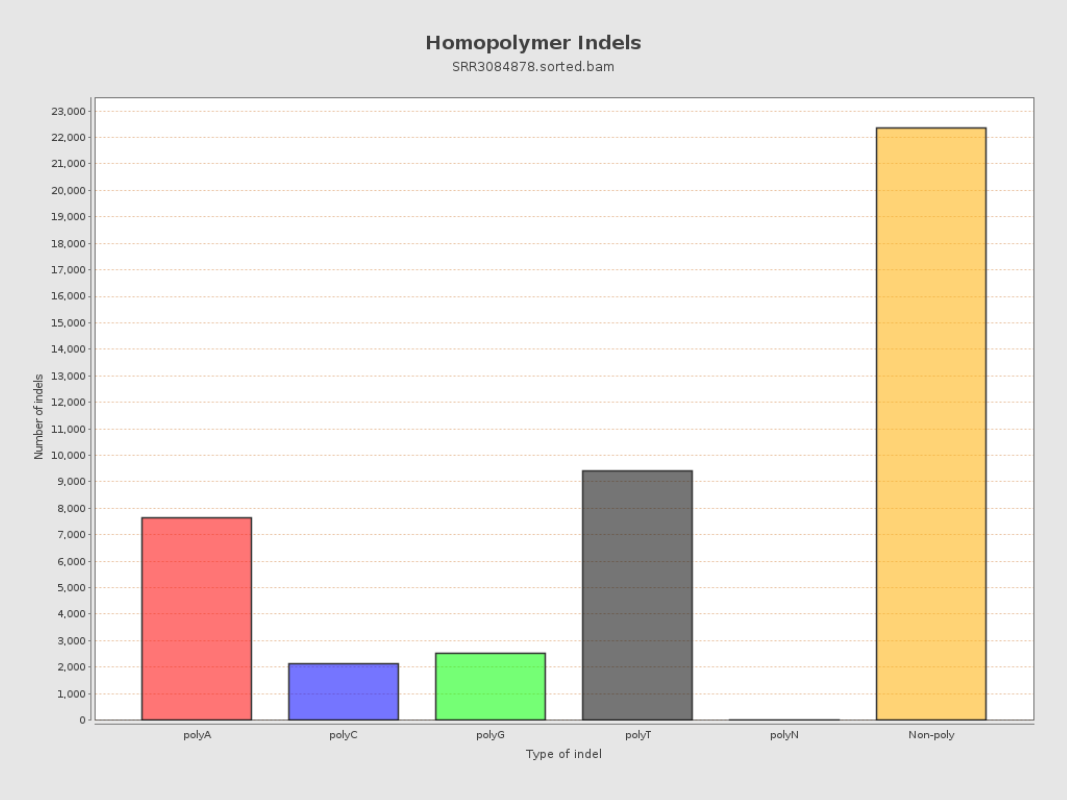
9. Results : Mapped Reads GC-content Distribution



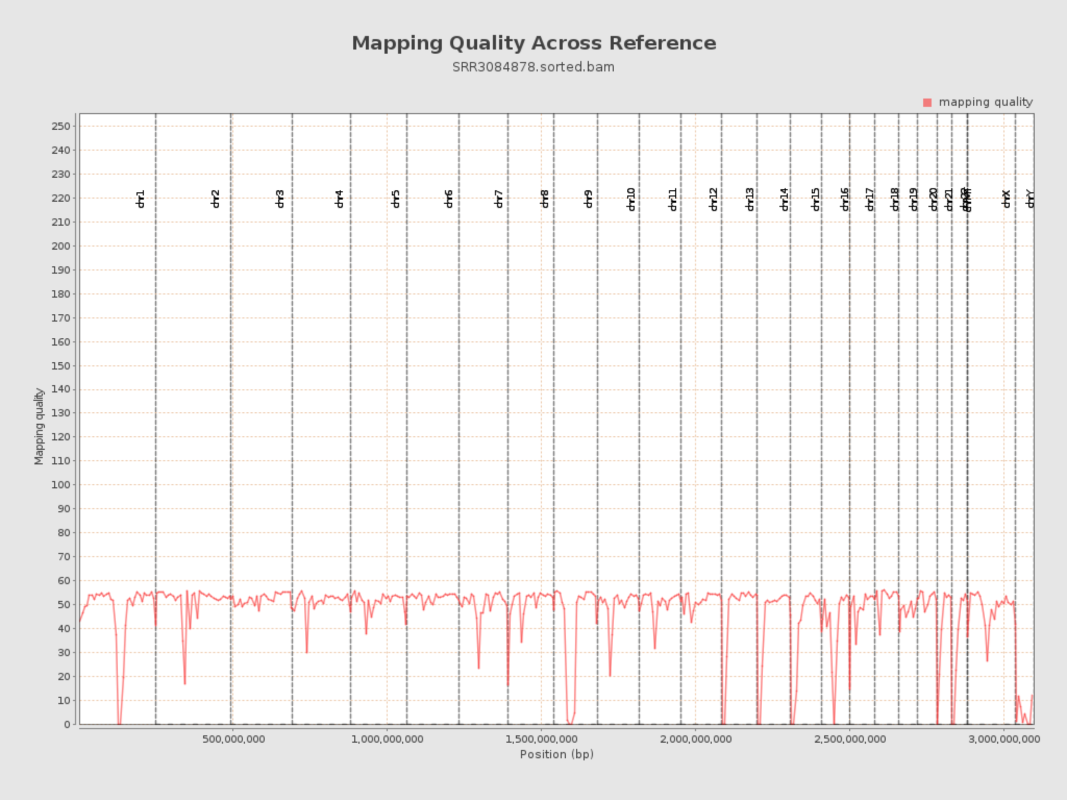
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram