Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 16:36:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084839.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_SRR3084839 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084839.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 16:36:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084839.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,048,912
Mapped reads	1,870,603 / 91.3%
Unmapped reads	178,309 / 8.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,963 / 1.17%
Read min/max/mean length	30 / 76 / 76.41
Duplicated reads (estimated)	83,235 / 4.06%
Duplication rate	3.78%
Clipped reads	812,179 / 39.64%

2.2. ACGT Content

Number/percentage of A's	34,694,777 / 27.63%
Number/percentage of C's	23,322,269 / 18.58%
Number/percentage of T's	39,780,386 / 31.68%
Number/percentage of G's	27,736,785 / 22.09%
Number/percentage of N's	17,536 / 0.01%
GC Percentage	40.67%

2.3. Coverage

Mean	0.0406

Standard Deviation	0.3076

2.4. Mapping Quality

Mean Mapping Quality	45.88

2.5. Mismatches and indels

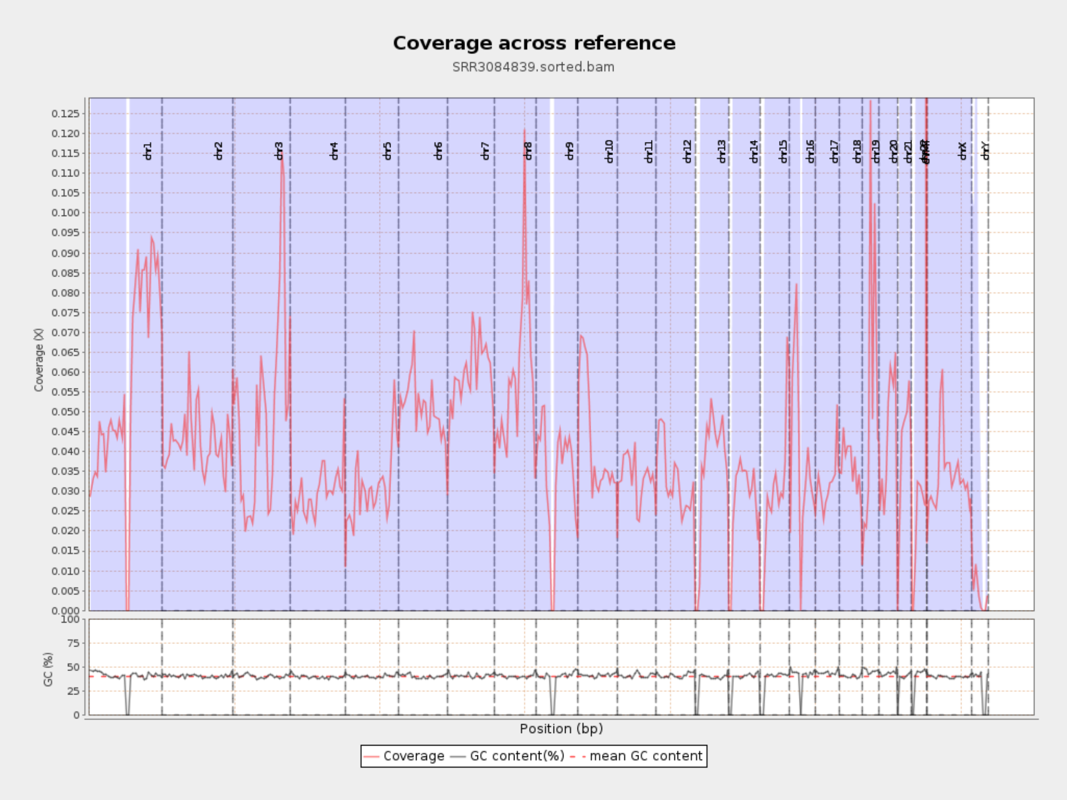
General error rate	0.75%
Mismatches	928,707
Insertions	9,658
Mapped reads with at least one insertion	0.51%
Deletions	29,155
Mapped reads with at least one deletion	1.54%
Homopolymer indels	48.51%

2.6. Chromosome stats

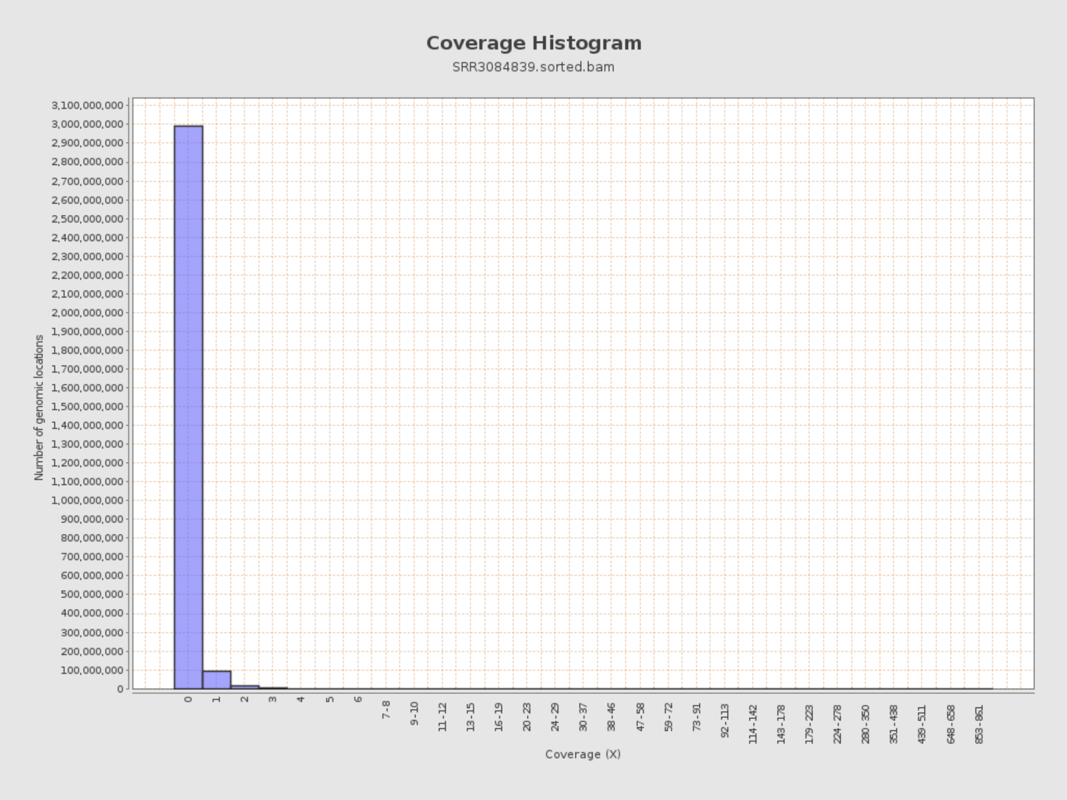
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14204456	0.057	0.518
chr2	243199373	10305285	0.0424	0.4397
chr3	198022430	9668982	0.0488	0.2548
chr4	191154276	5711780	0.0299	0.2021
chr5	180915260	5681470	0.0314	0.2019
chr6	171115067	8708062	0.0509	0.2959
chr7	159138663	9574271	0.0602	0.3989

chr8	146364022	8610558	0.0588	0.3703
chr9	141213431	4869246	0.0345	0.2464
chr10	135534747	5832202	0.043	0.2723
chr11	135006516	4486596	0.0332	0.2334
chr12	133851895	4350583	0.0325	0.207
chr13	115169878	4137799	0.0359	0.217
chr14	107349540	2925451	0.0273	0.1892
chr15	102531392	2901536	0.0283	0.2011
chr16	90354753	3582107	0.0396	0.2341
chr17	81195210	2628247	0.0324	0.2099
chr18	78077248	2860479	0.0366	0.3832
chr19	59128983	3181663	0.0538	0.3833
chr20	63025520	2758823	0.0438	0.2407
chr21	48129895	1934512	0.0402	0.2316
chr22	51304566	1081976	0.0211	0.1635
chrMT	16571	112154	6.7681	4.3814
chrX	155270560	5256162	0.0339	0.2151
chrY	59373566	234443	0.0039	0.0817

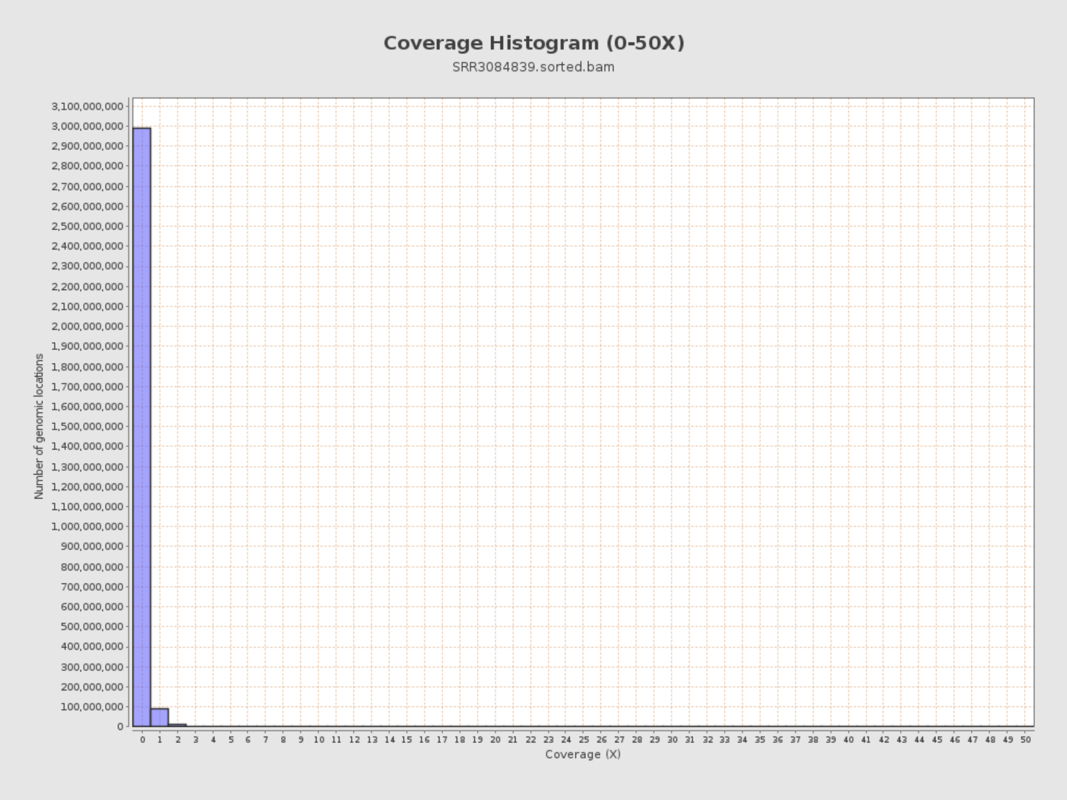
3. Results : Coverage across reference



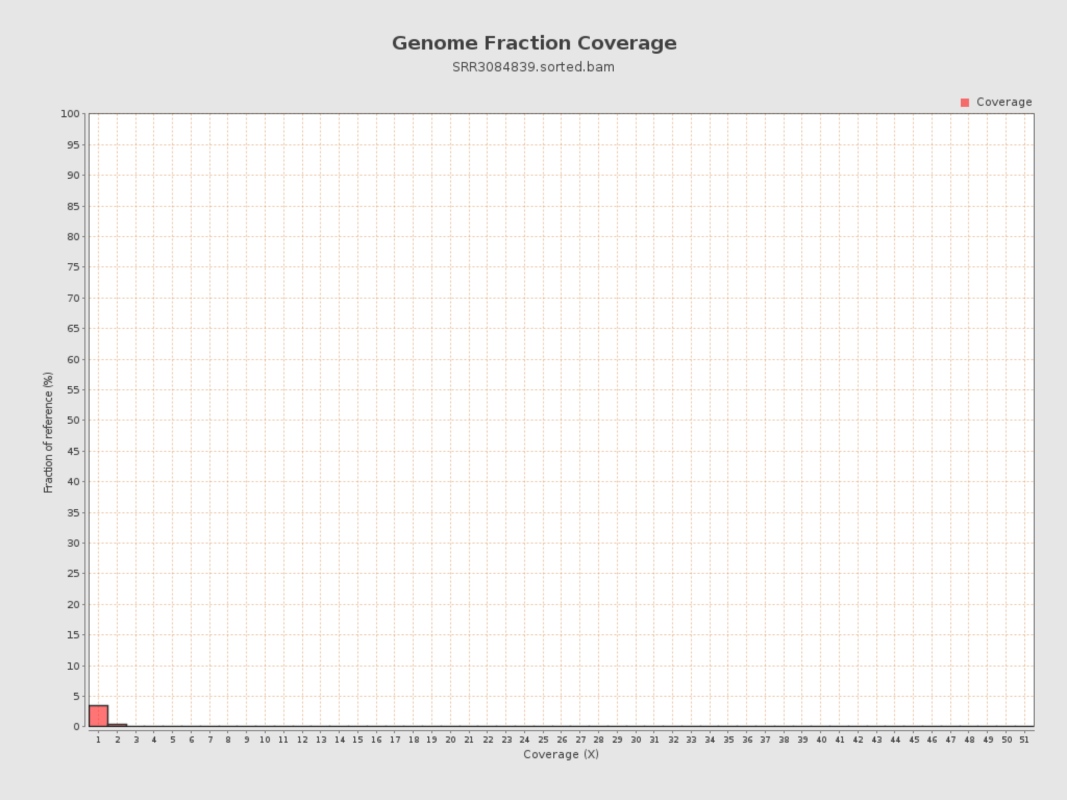
4. Results : Coverage Histogram



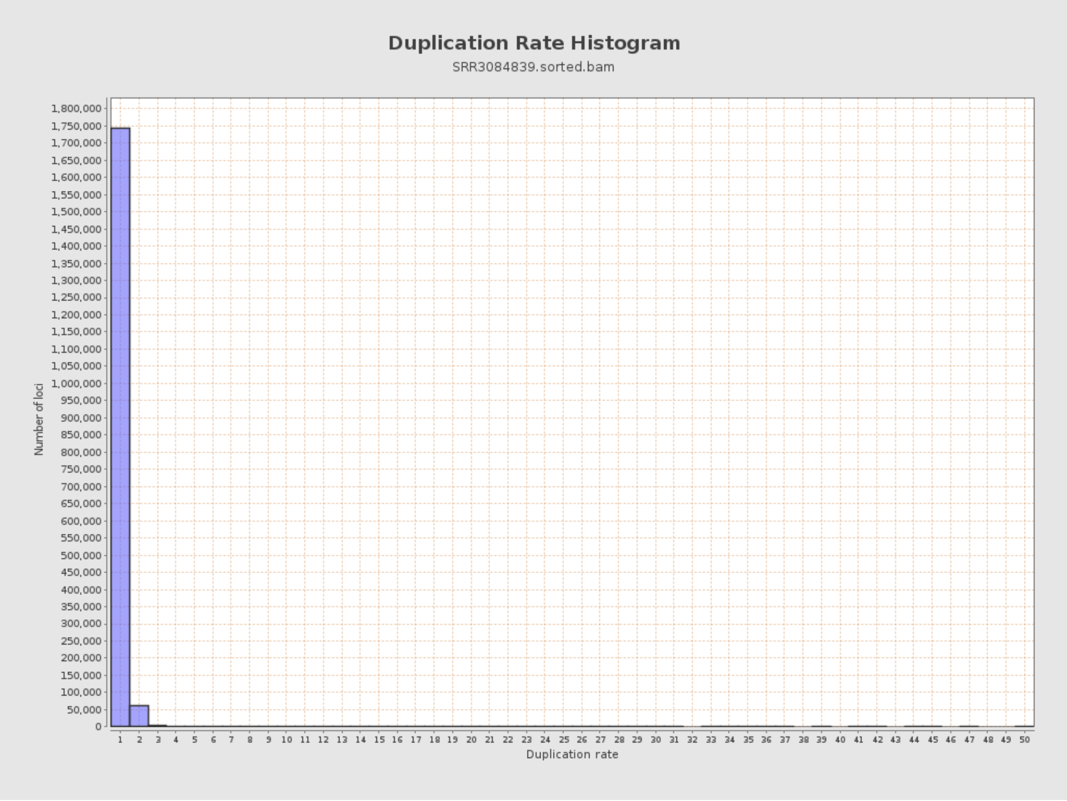
5. Results : Coverage Histogram (0-50X)



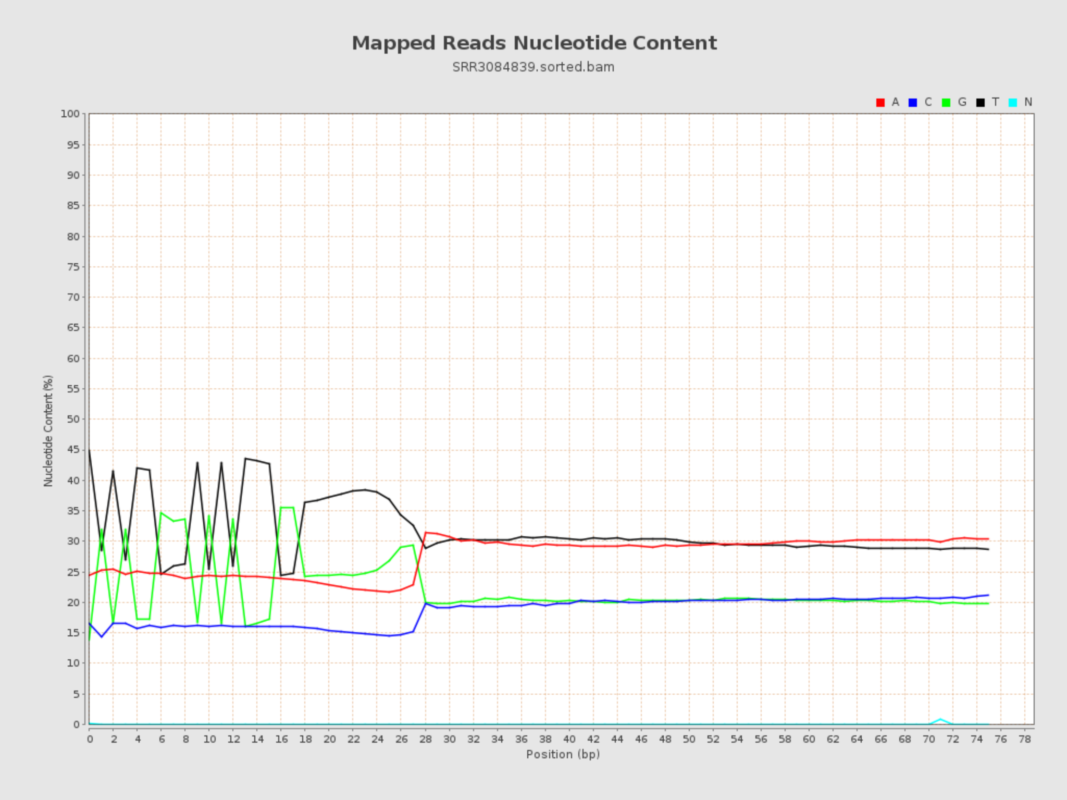
6. Results : Genome Fraction Coverage



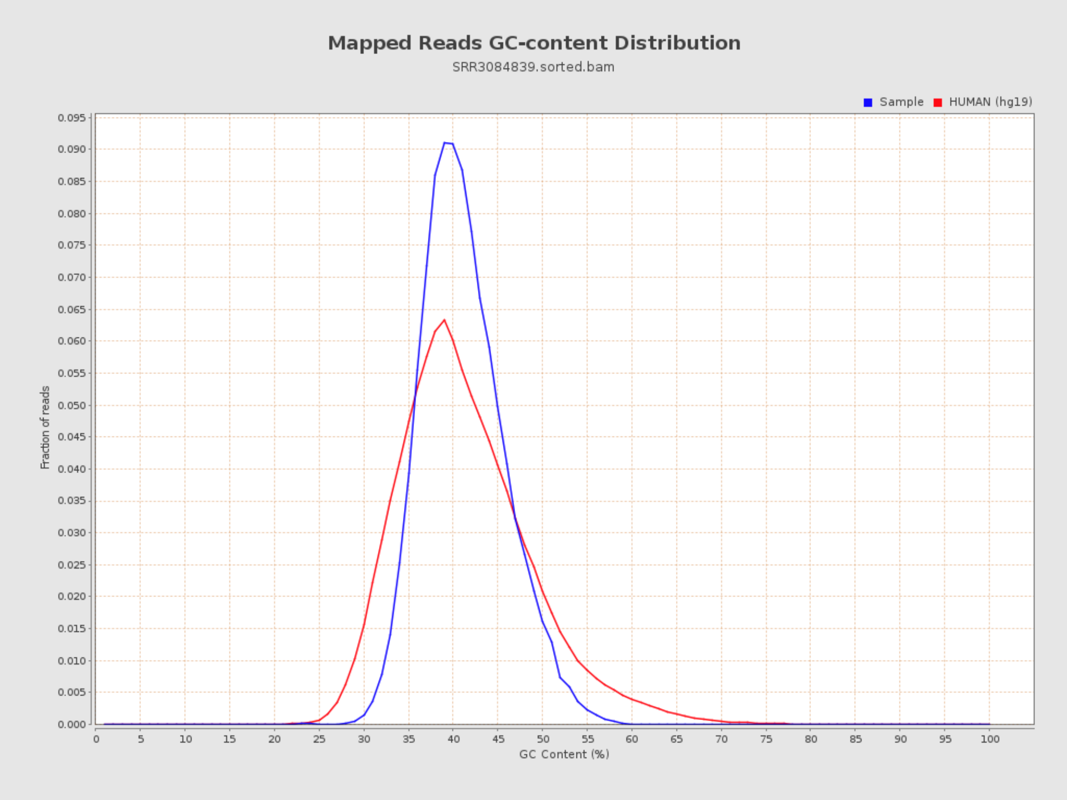
7. Results : Duplication Rate Histogram



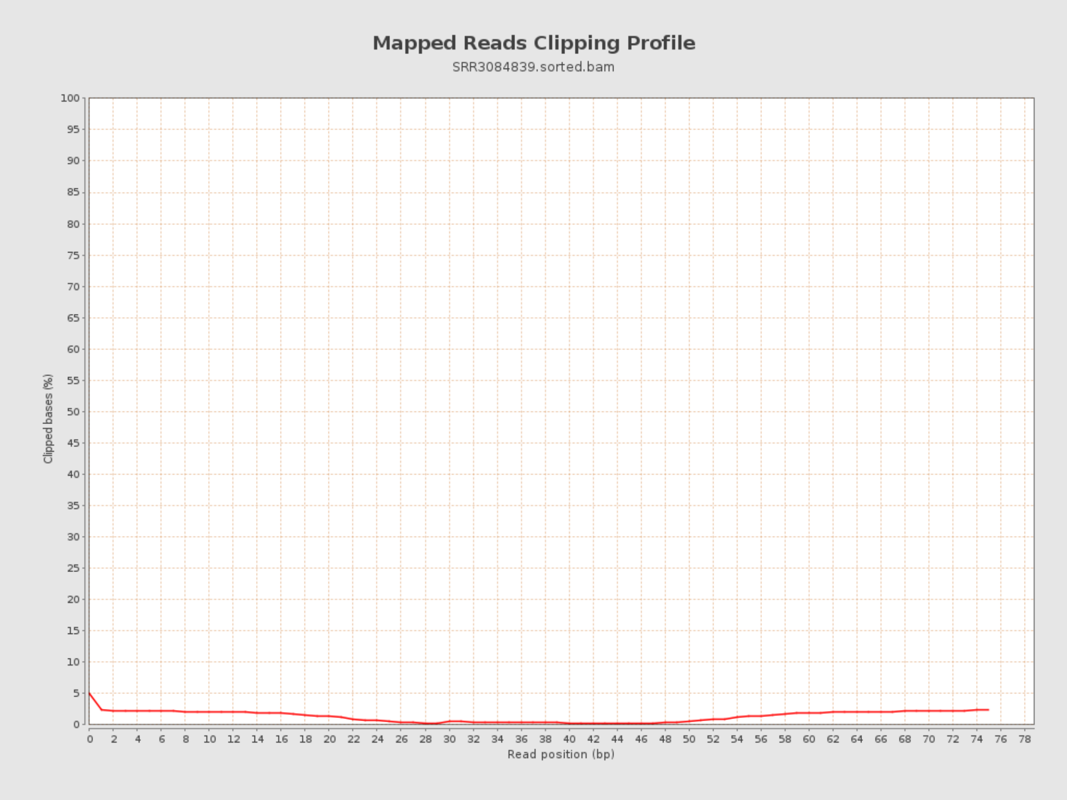
8. Results : Mapped Reads Nucleotide Content



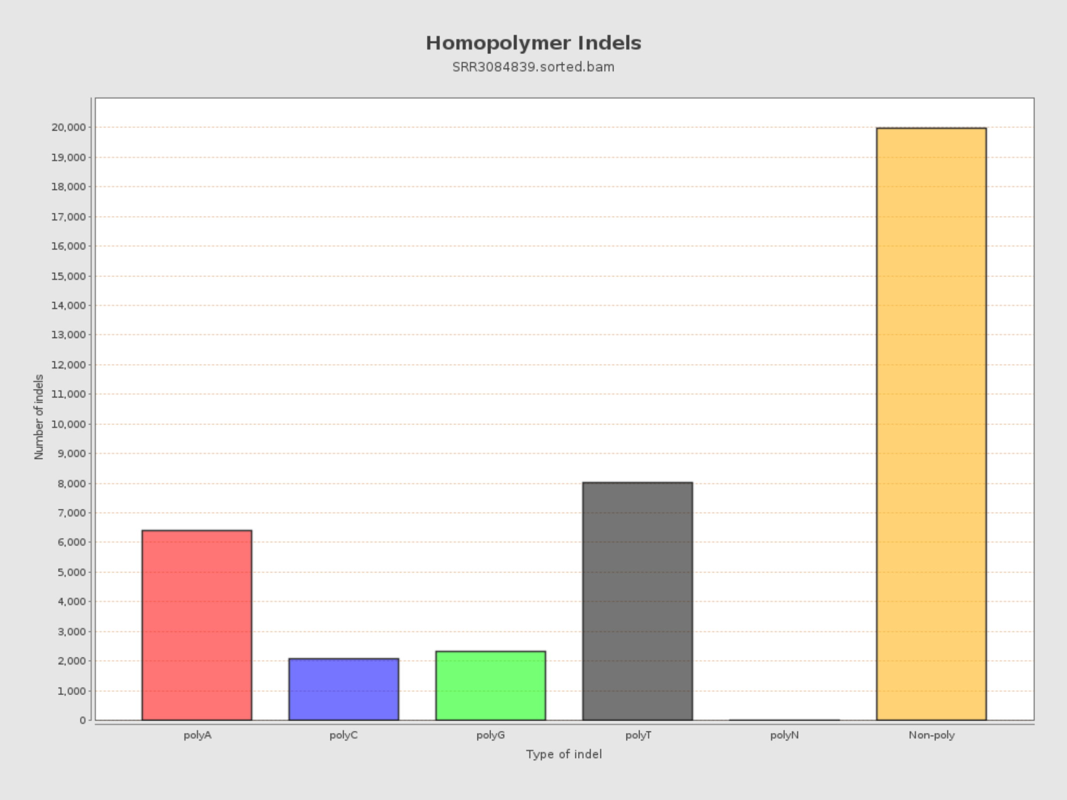
9. Results : Mapped Reads GC-content Distribution



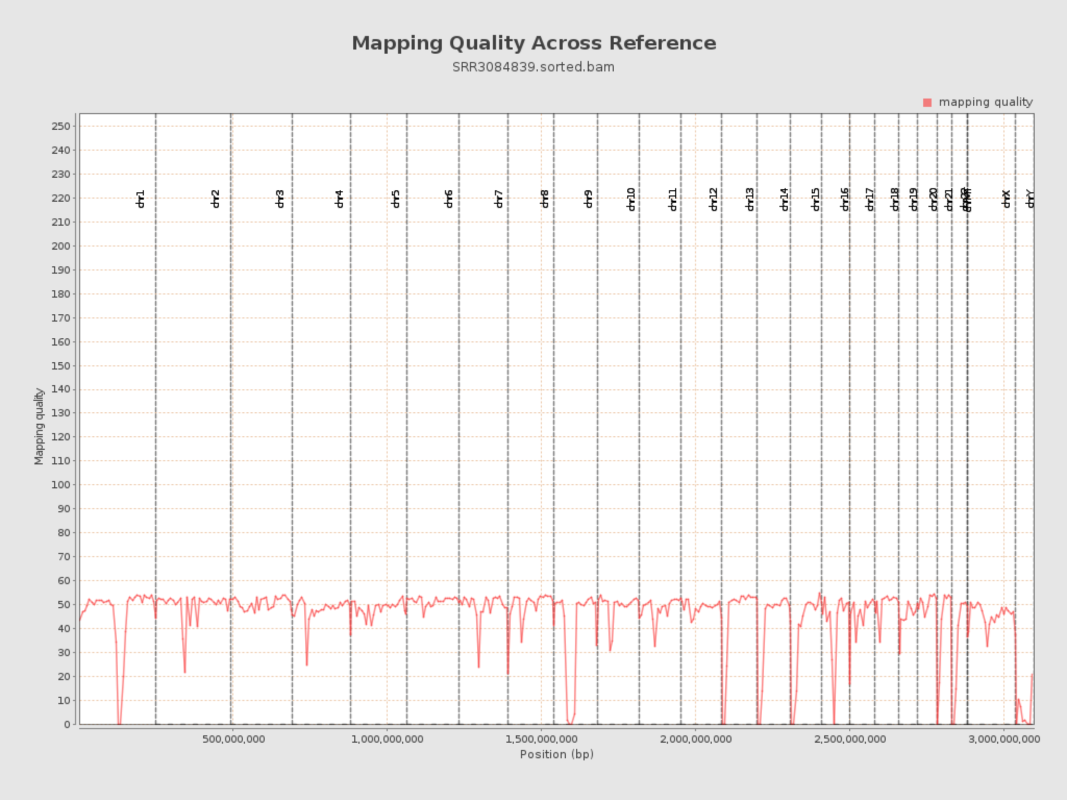
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram