Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 21:17:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084998.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_SRR3084998 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084998.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 21:17:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084998.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,531,714
Mapped reads	2,363,613 / 93.36%
Unmapped reads	168,101 / 6.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,744 / 1.02%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	99,795 / 3.94%
Duplication rate	3.38%
Clipped reads	839,226 / 33.15%

2.2. ACGT Content

Number/percentage of A's	47,568,458 / 29.14%
Number/percentage of C's	30,210,784 / 18.5%
Number/percentage of T's	51,736,120 / 31.69%
Number/percentage of G's	33,721,357 / 20.65%
Number/percentage of N's	24,291 / 0.01%
GC Percentage	39.16%

2.3. Coverage

Mean	0.0528

Standard Deviation	0.4539

2.4. Mapping Quality

Mean Mapping Quality	47.47

2.5. Mismatches and indels

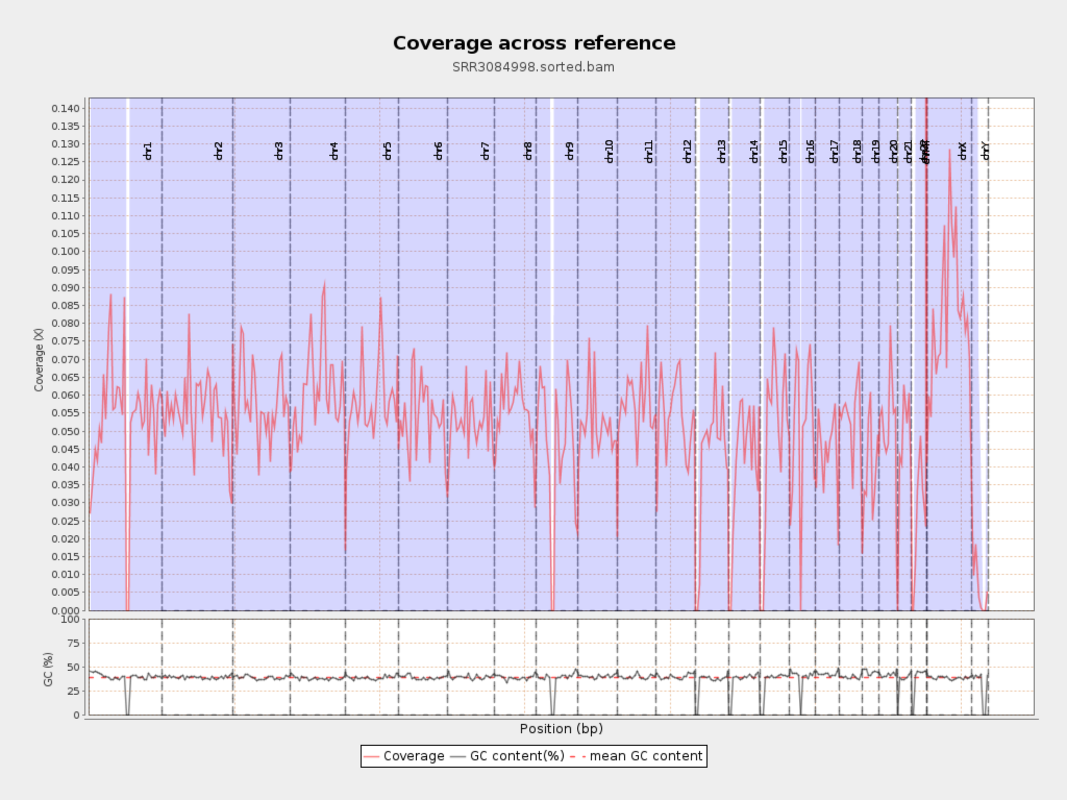
General error rate	0.81%
Mismatches	1,294,102
Insertions	13,200
Mapped reads with at least one insertion	0.55%
Deletions	37,633
Mapped reads with at least one deletion	1.58%
Homopolymer indels	48.02%

2.6. Chromosome stats

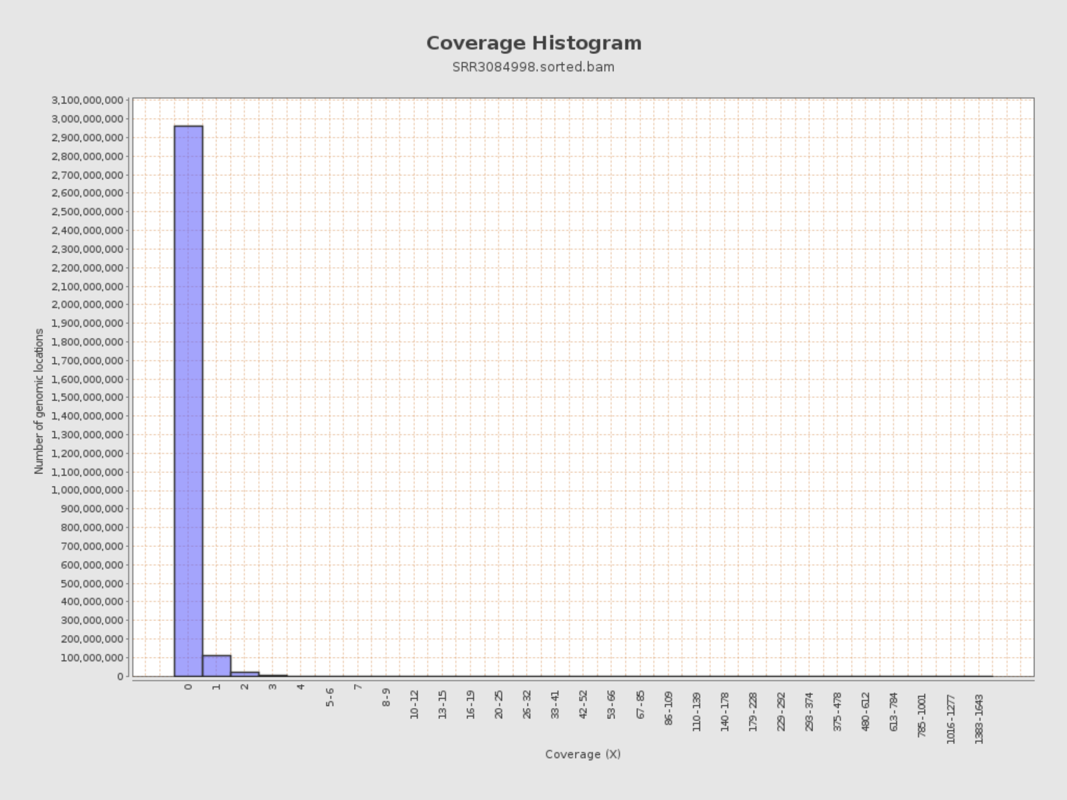
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13171126	0.0528	0.8098
chr2	243199373	13480512	0.0554	0.4235
chr3	198022430	11482686	0.058	0.2845
chr4	191154276	11711447	0.0613	0.3011
chr5	180915260	10540961	0.0583	0.2849
chr6	171115067	9162960	0.0535	0.3293
chr7	159138663	8437417	0.053	0.3576

chr8	146364022	8132372	0.0556	1.0171
chr9	141213431	6513371	0.0461	0.3655
chr10	135534747	7029928	0.0519	0.4003
chr11	135006516	7710286	0.0571	0.3643
chr12	133851895	7140042	0.0533	0.2748
chr13	115169878	4881136	0.0424	0.2419
chr14	107349540	4287791	0.0399	0.2558
chr15	102531392	4984363	0.0486	0.2585
chr16	90354753	4580182	0.0507	0.3061
chr17	81195210	3514515	0.0433	0.2656
chr18	78077248	4254788	0.0545	0.7237
chr19	59128983	2356086	0.0398	0.5164
chr20	63025520	3324034	0.0527	0.2802
chr21	48129895	2180439	0.0453	0.2671
chr22	51304566	1258929	0.0245	0.1801
chrMT	16571	24190	1.4598	1.4855
chrX	155270560	12761276	0.0822	0.3664
chrY	59373566	401326	0.0068	0.1284

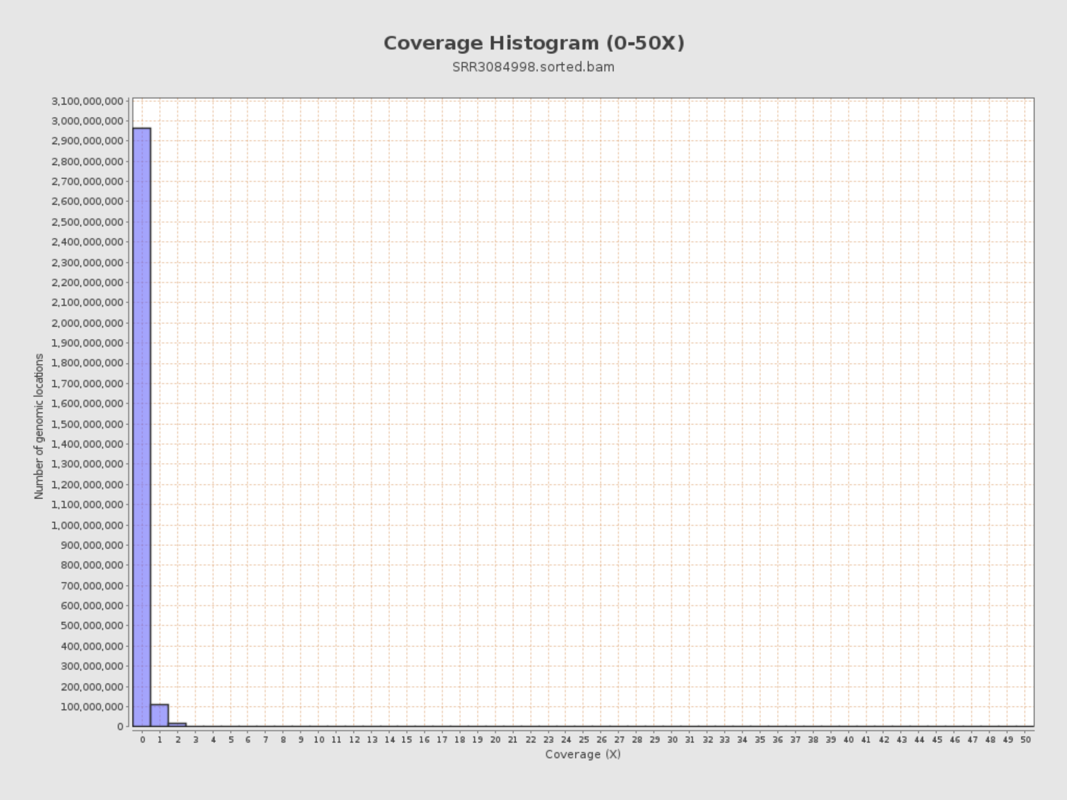
3. Results : Coverage across reference



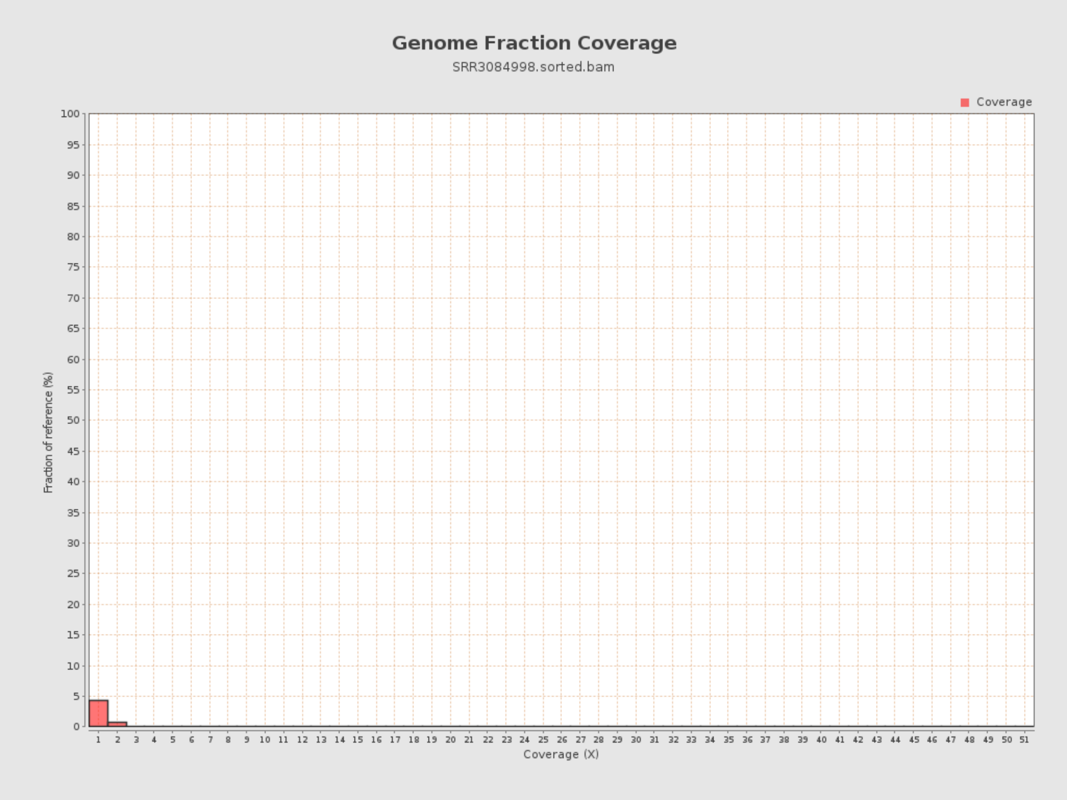
4. Results : Coverage Histogram



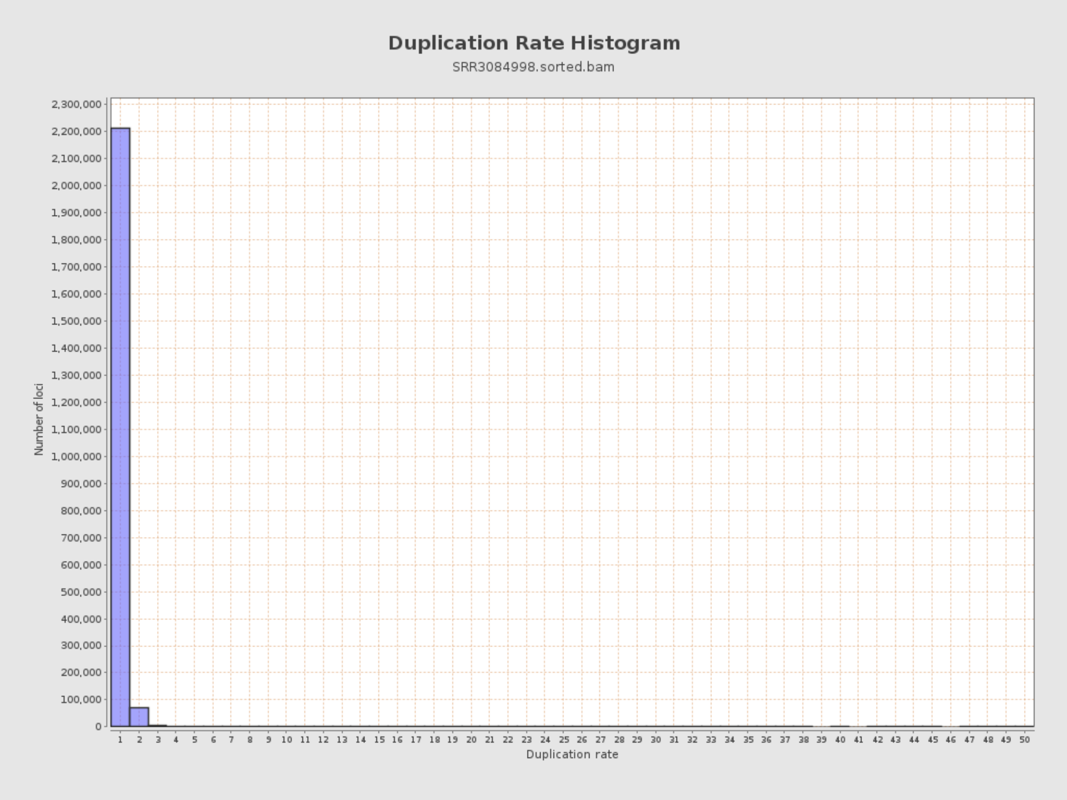
5. Results : Coverage Histogram (0-50X)



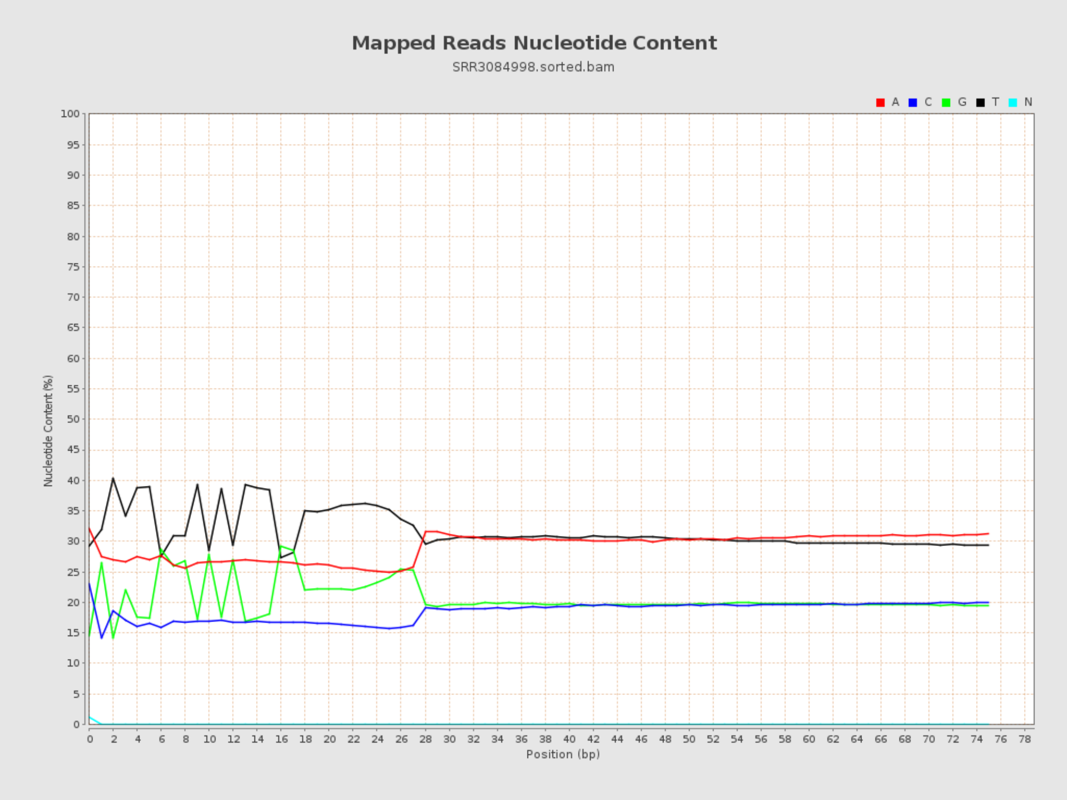
6. Results : Genome Fraction Coverage



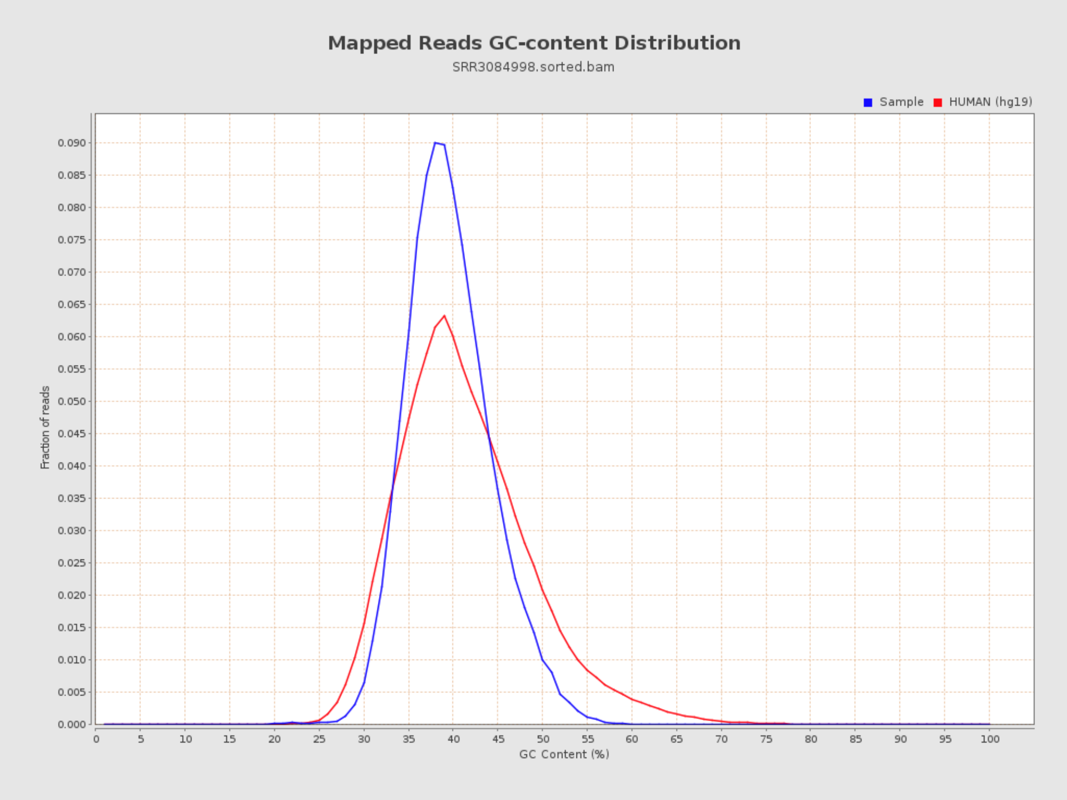
7. Results : Duplication Rate Histogram



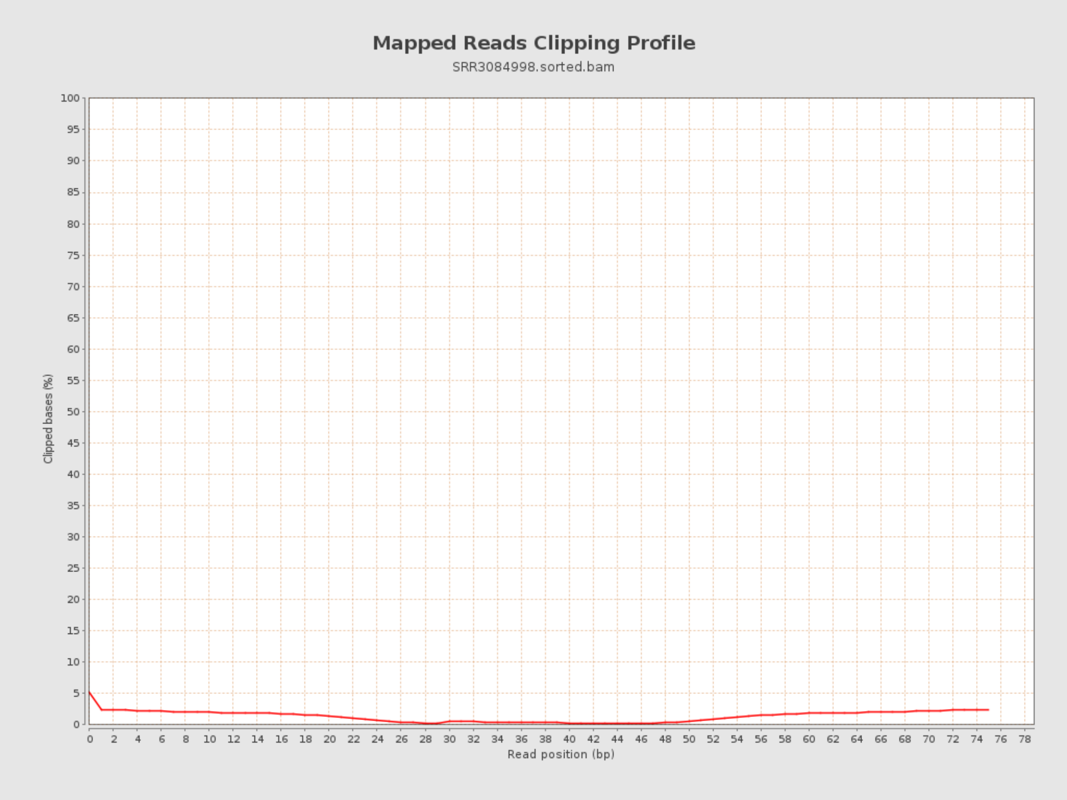
8. Results : Mapped Reads Nucleotide Content



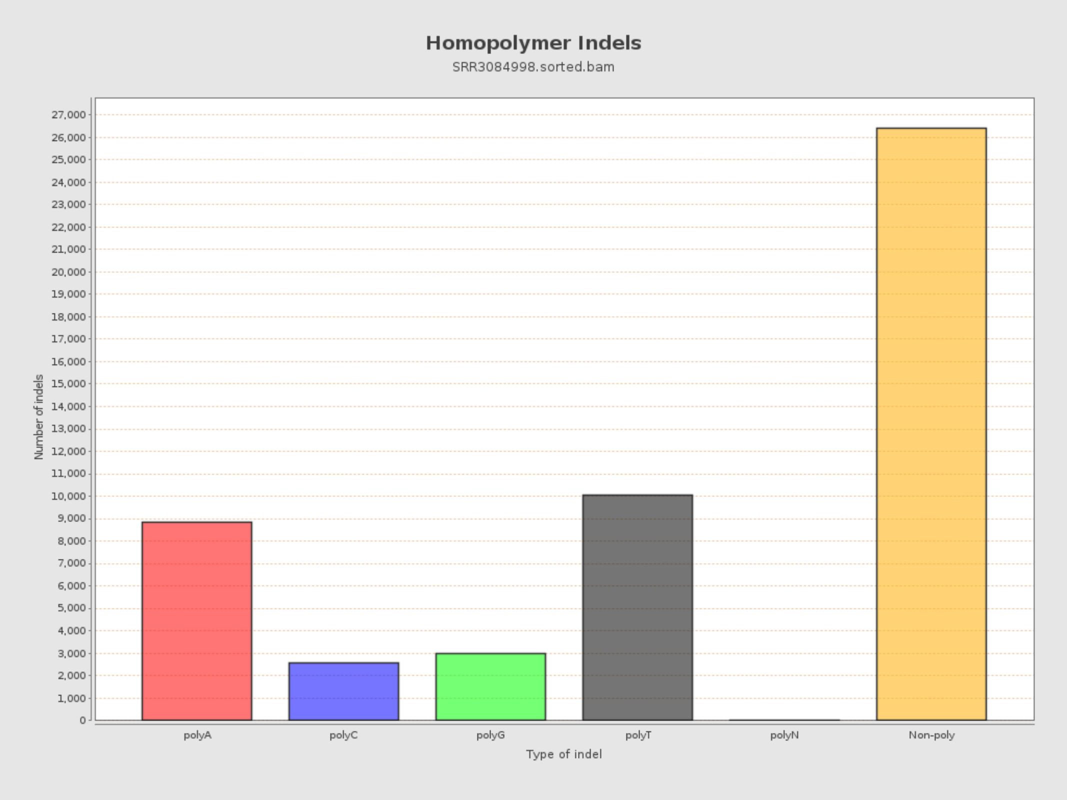
9. Results : Mapped Reads GC-content Distribution



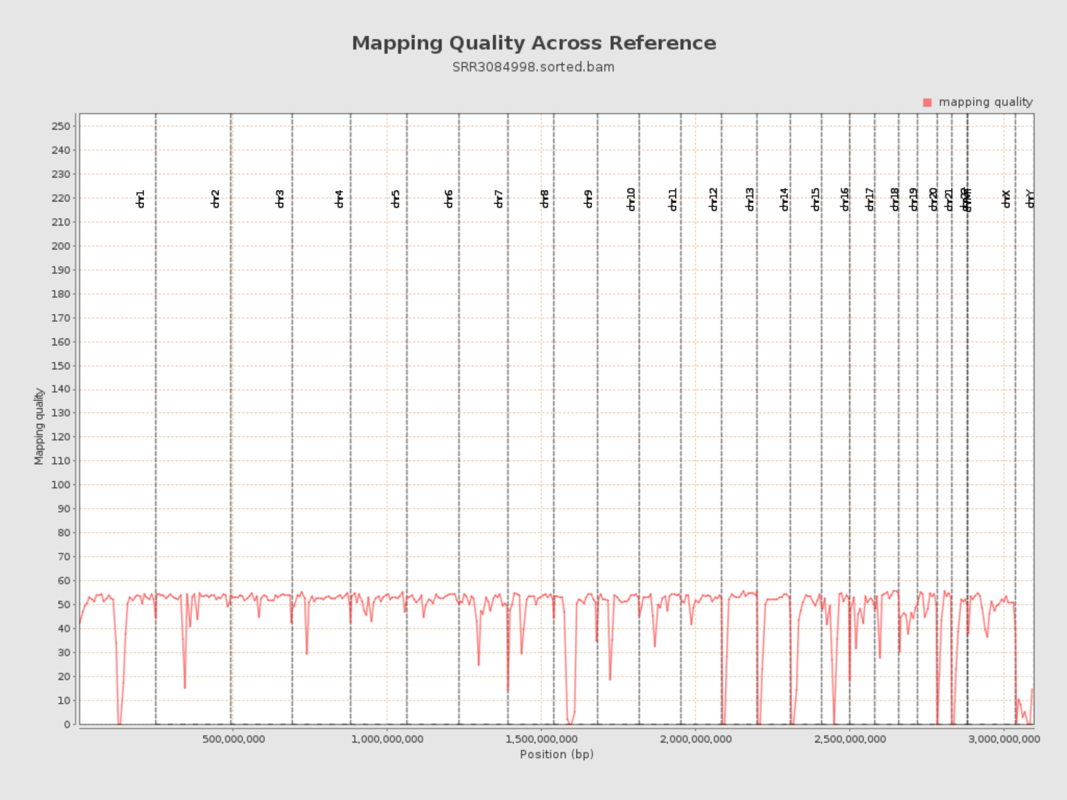
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram