Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 14:50:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084806.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_SRR3084806 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084806.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 14:50:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084806.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,006,846
Mapped reads	1,810,592 / 90.22%
Unmapped reads	196,254 / 9.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,670 / 0.88%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	81,246 / 4.05%
Duplication rate	3.94%
Clipped reads	802,122 / 39.97%

2.2. ACGT Content

Number/percentage of A's	32,611,204 / 26.99%
Number/percentage of C's	22,752,561 / 18.83%
Number/percentage of T's	37,792,174 / 31.28%
Number/percentage of G's	27,655,124 / 22.89%
Number/percentage of N's	17,021 / 0.01%
GC Percentage	41.72%

2.3. Coverage

Mean	0.039

Standard Deviation	0.2699

2.4. Mapping Quality

Mean Mapping Quality	45.35

2.5. Mismatches and indels

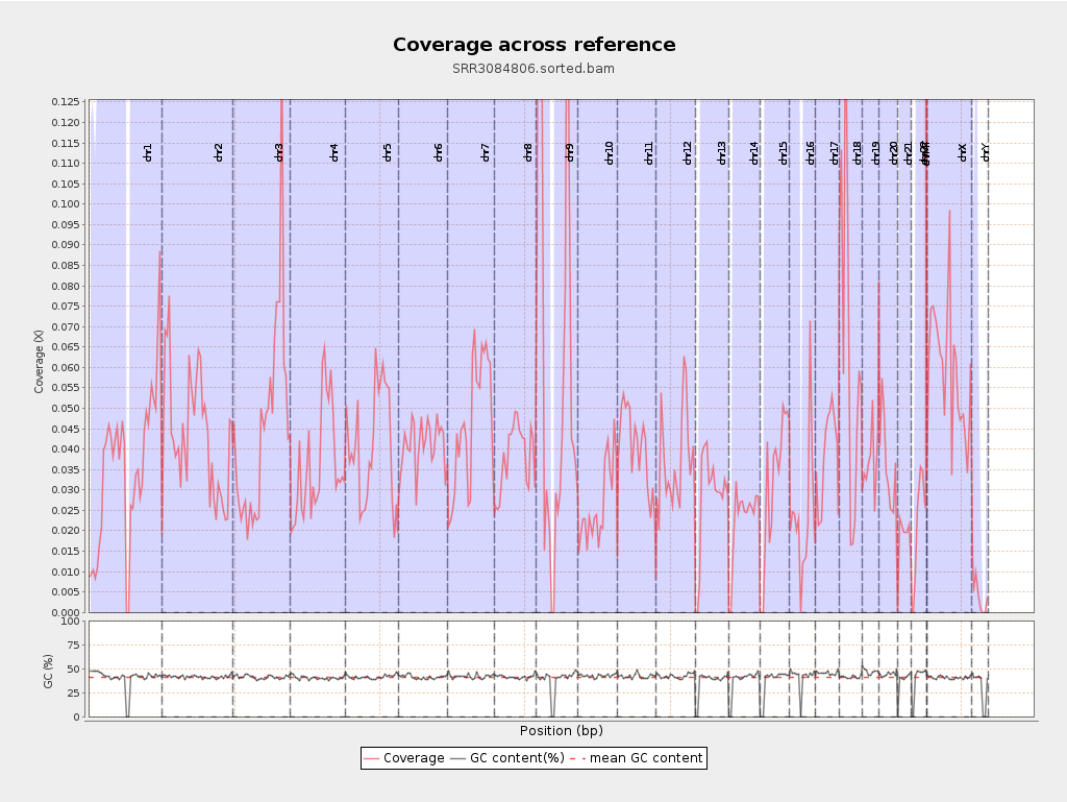
General error rate	0.76%
Mismatches	901,644
Insertions	9,214
Mapped reads with at least one insertion	0.5%
Deletions	27,563
Mapped reads with at least one deletion	1.51%
Homopolymer indels	47.81%

2.6. Chromosome stats

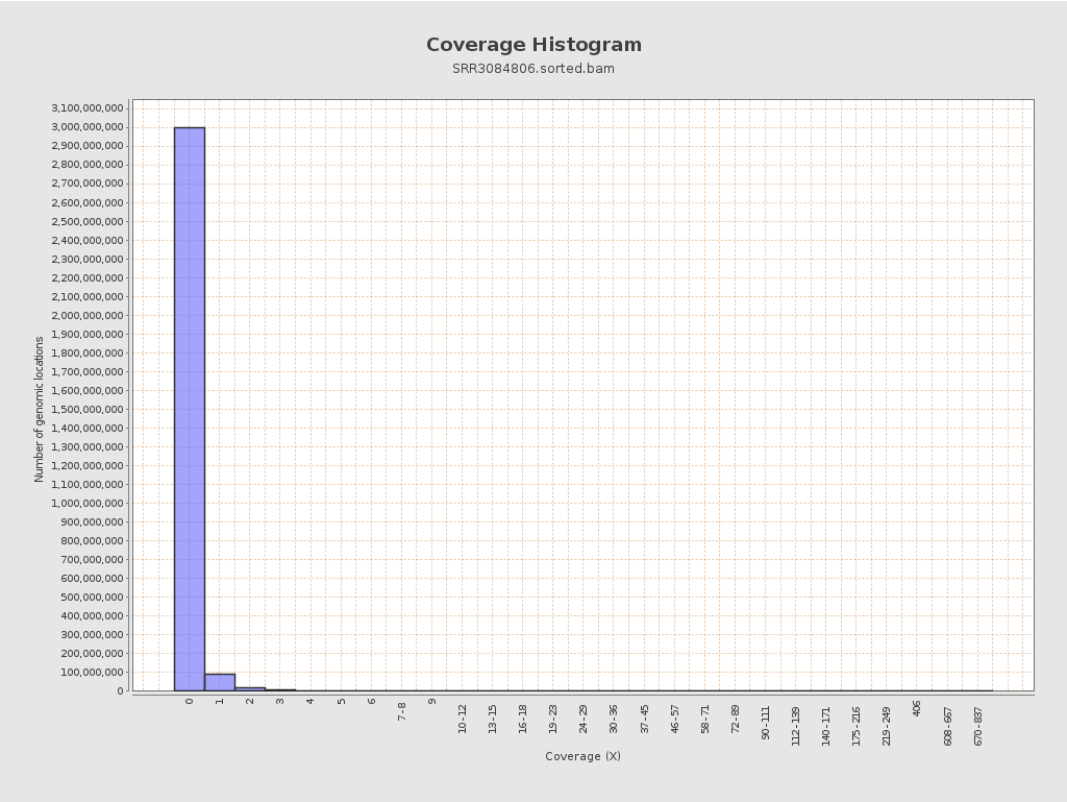
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8806489	0.0353	0.2645
chr2	243199373	10622502	0.0437	0.4474
chr3	198022430	9003697	0.0455	0.2514
chr4	191154276	6918381	0.0362	0.2268
chr5	180915260	7417576	0.041	0.2363
chr6	171115067	6976236	0.0408	0.2496
chr7	159138663	7362268	0.0463	0.306

chr8	146364022	5577003	0.0381	0.2552
chr9	141213431	9188179	0.0651	0.336
chr10	135534747	3529972	0.026	0.1989
chr11	135006516	5373444	0.0398	0.2525
chr12	133851895	4967023	0.0371	0.2248
chr13	115169878	3216967	0.0279	0.1945
chr14	107349540	2409967	0.0224	0.1749
chr15	102531392	3238150	0.0316	0.2159
chr16	90354753	2185736	0.0242	0.1879
chr17	81195210	3161971	0.0389	0.2347
chr18	78077248	5105920	0.0654	0.3894
chr19	59128983	2290050	0.0387	0.2496
chr20	63025520	2285208	0.0363	0.2236
chr21	48129895	872822	0.0181	0.1611
chr22	51304566	1076543	0.021	0.1668
chrMT	16571	22988	1.3872	1.5022
chrX	155270560	9022295	0.0581	0.2881
chrY	59373566	242322	0.0041	0.0832

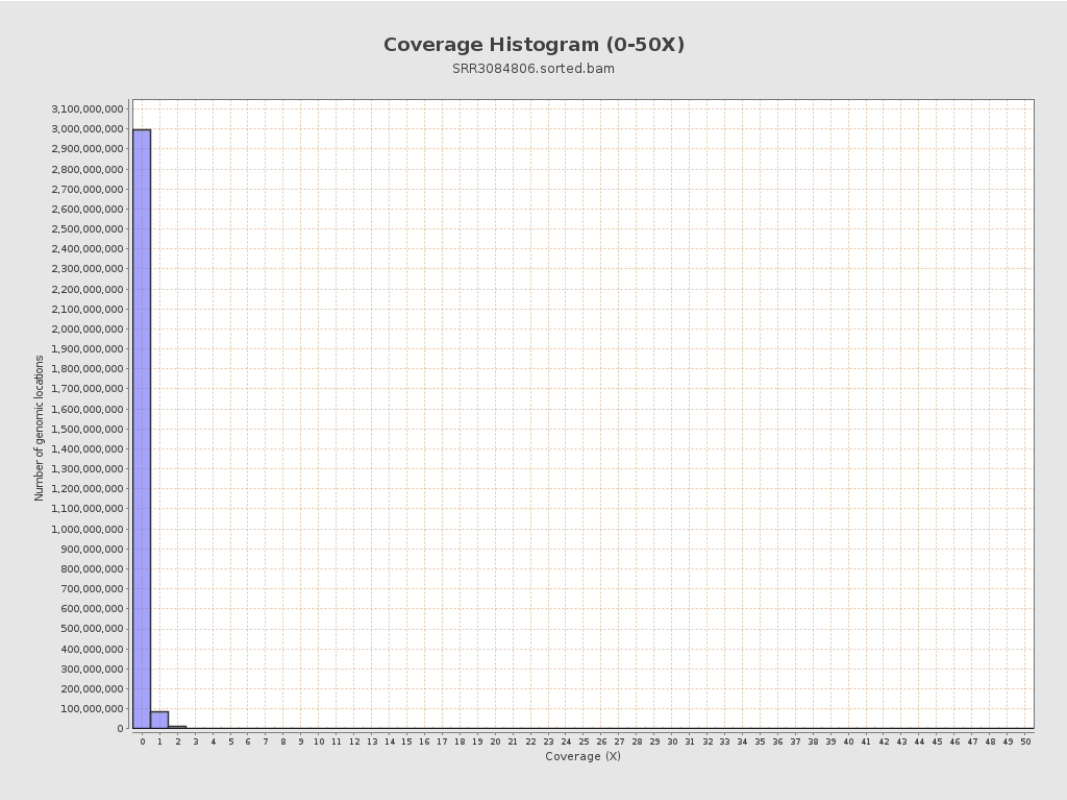
3. Results : Coverage across reference



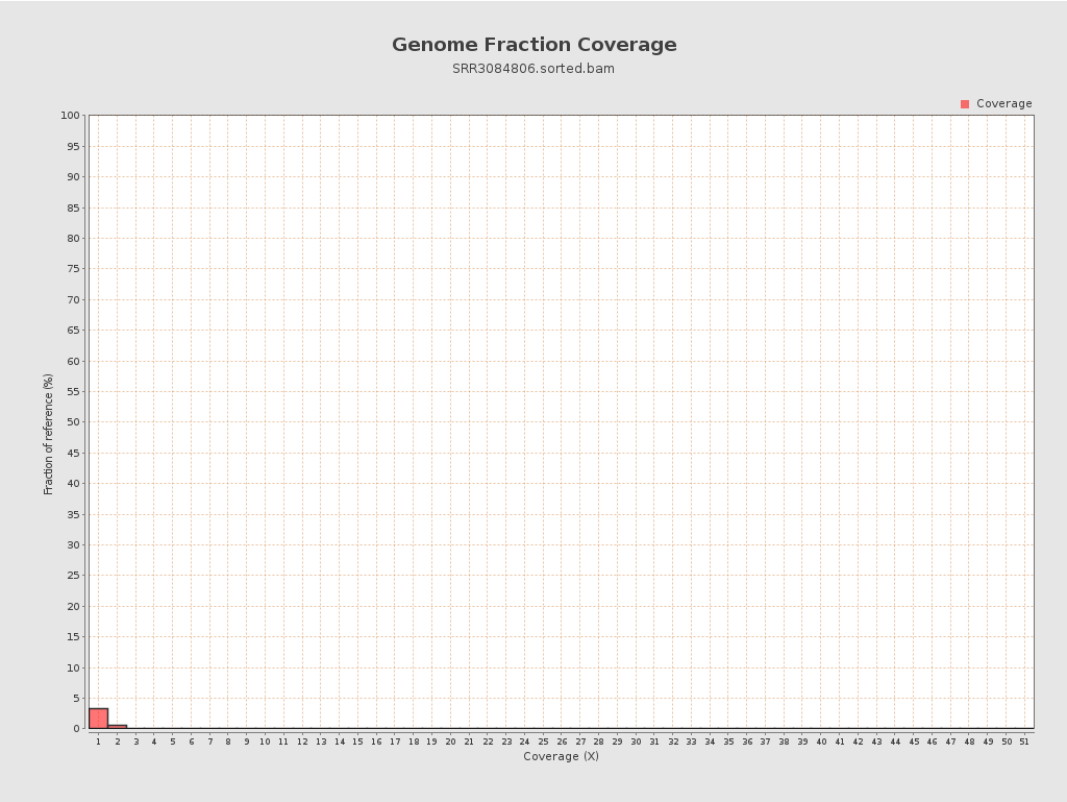
4. Results : Coverage Histogram



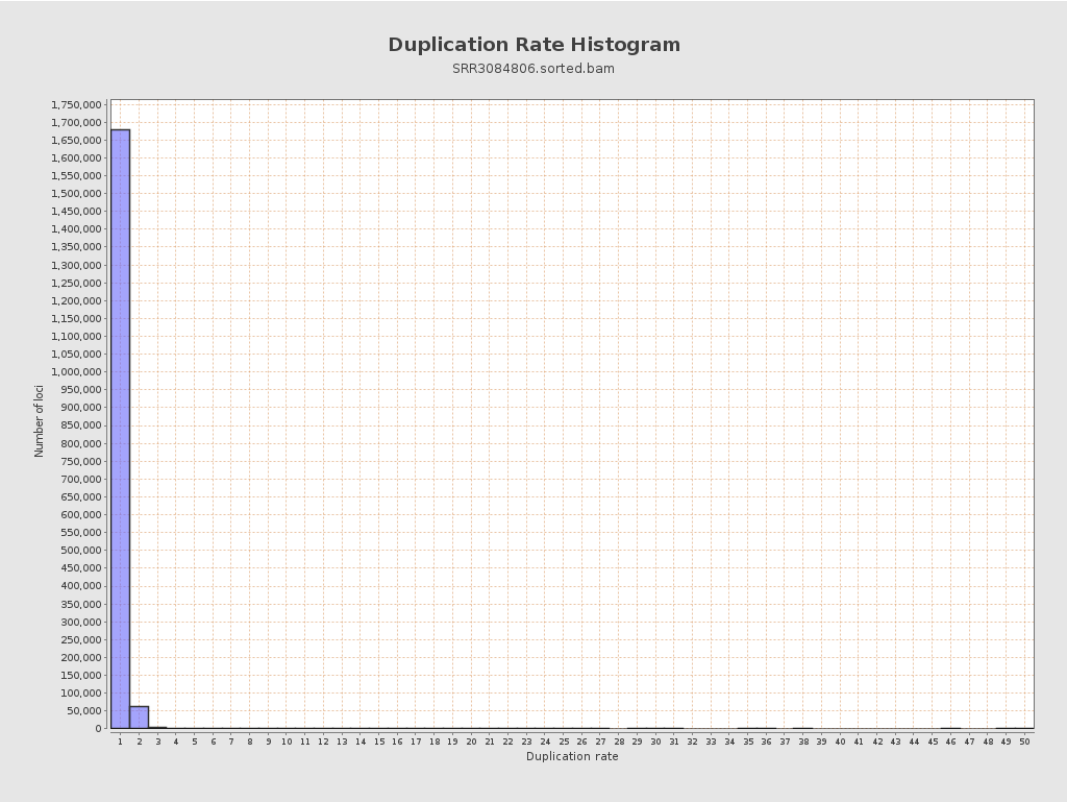
5. Results : Coverage Histogram (0-50X)



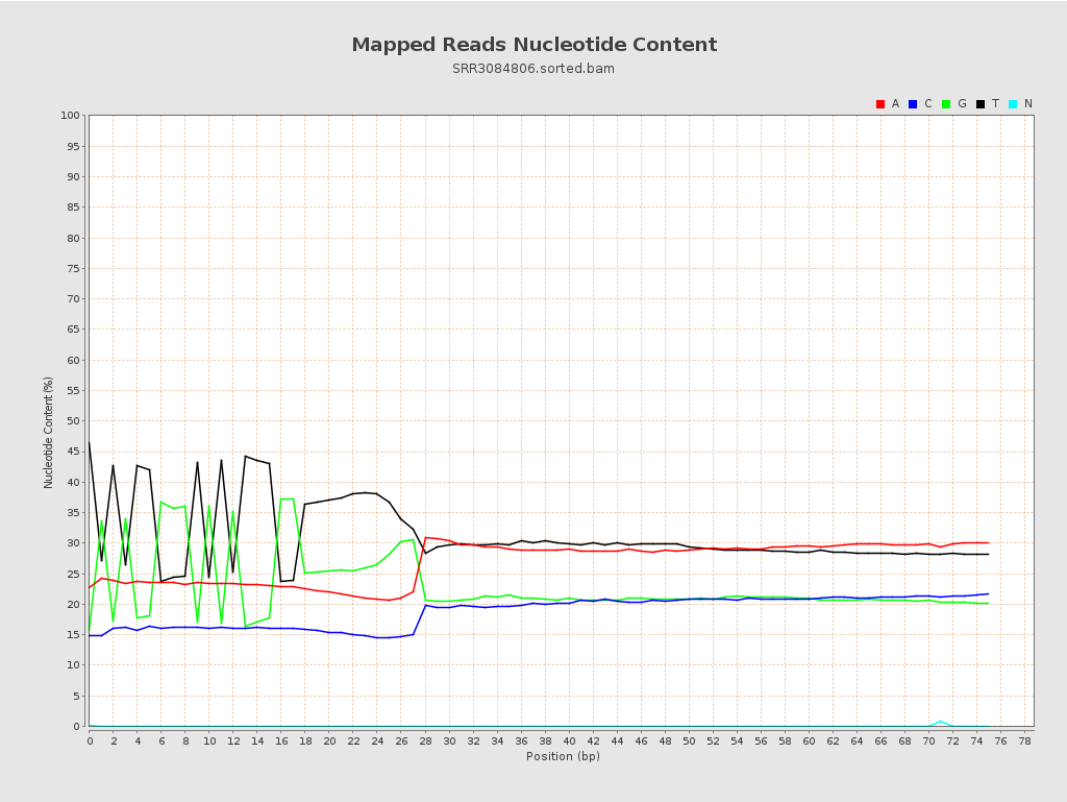
6. Results : Genome Fraction Coverage



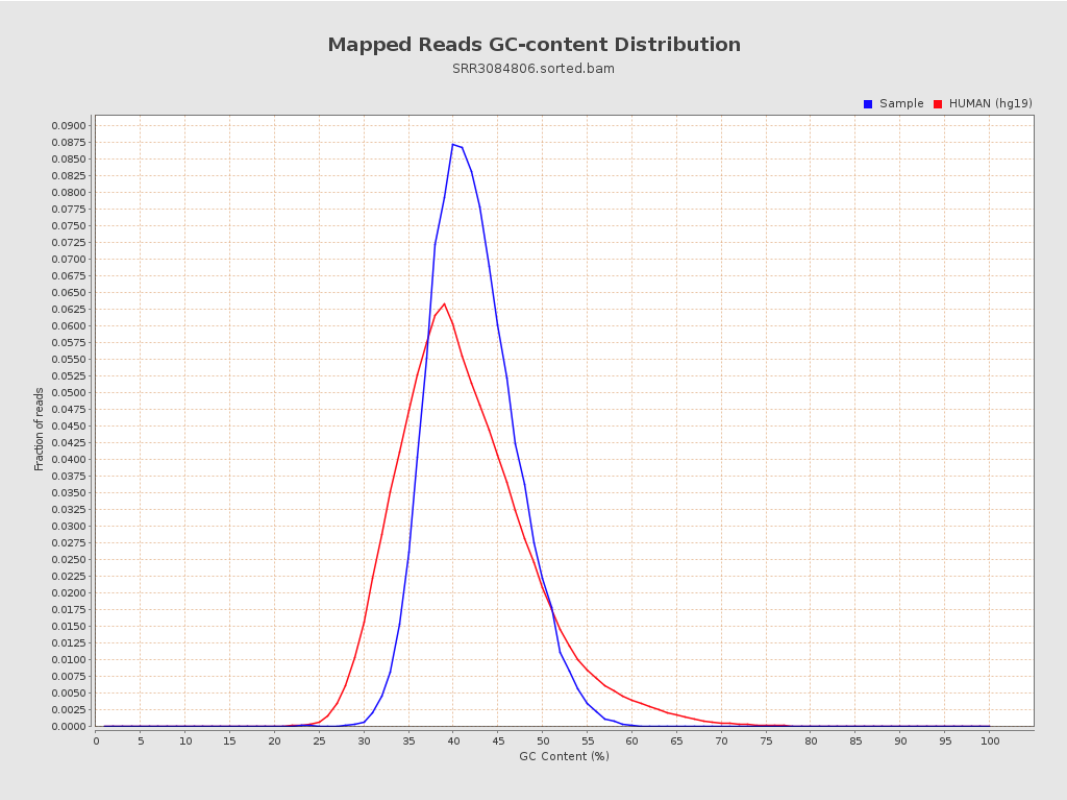
7. Results : Duplication Rate Histogram



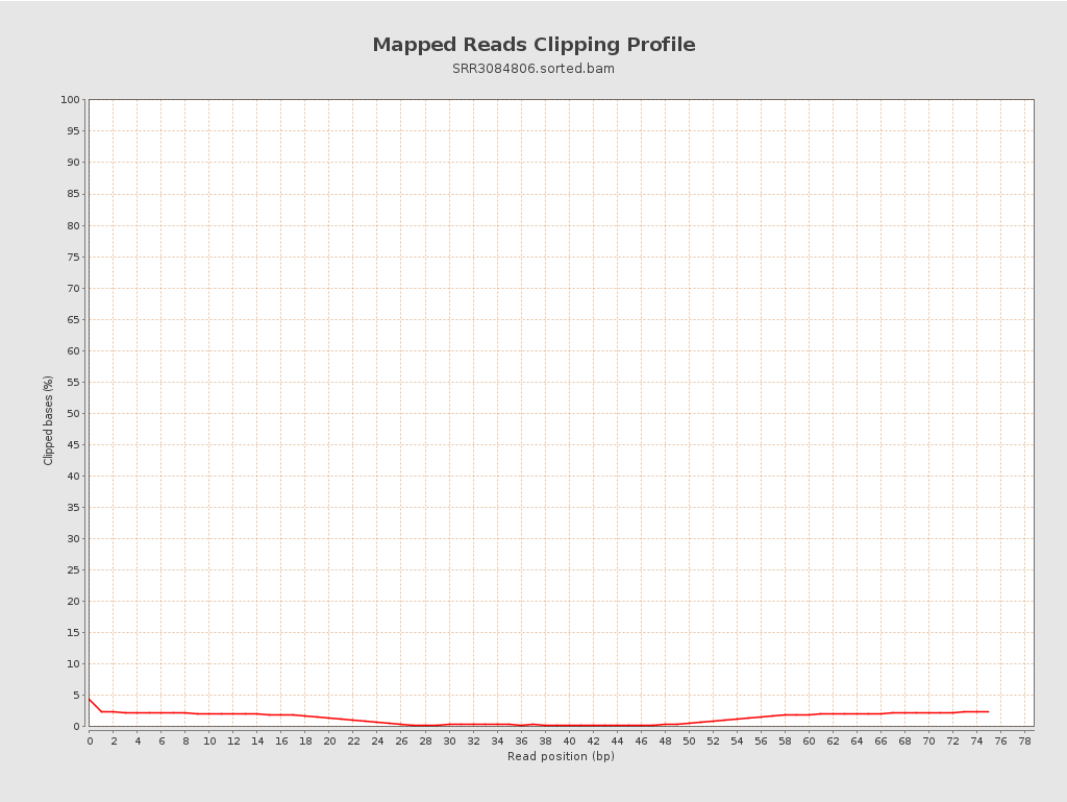
8. Results : Mapped Reads Nucleotide Content



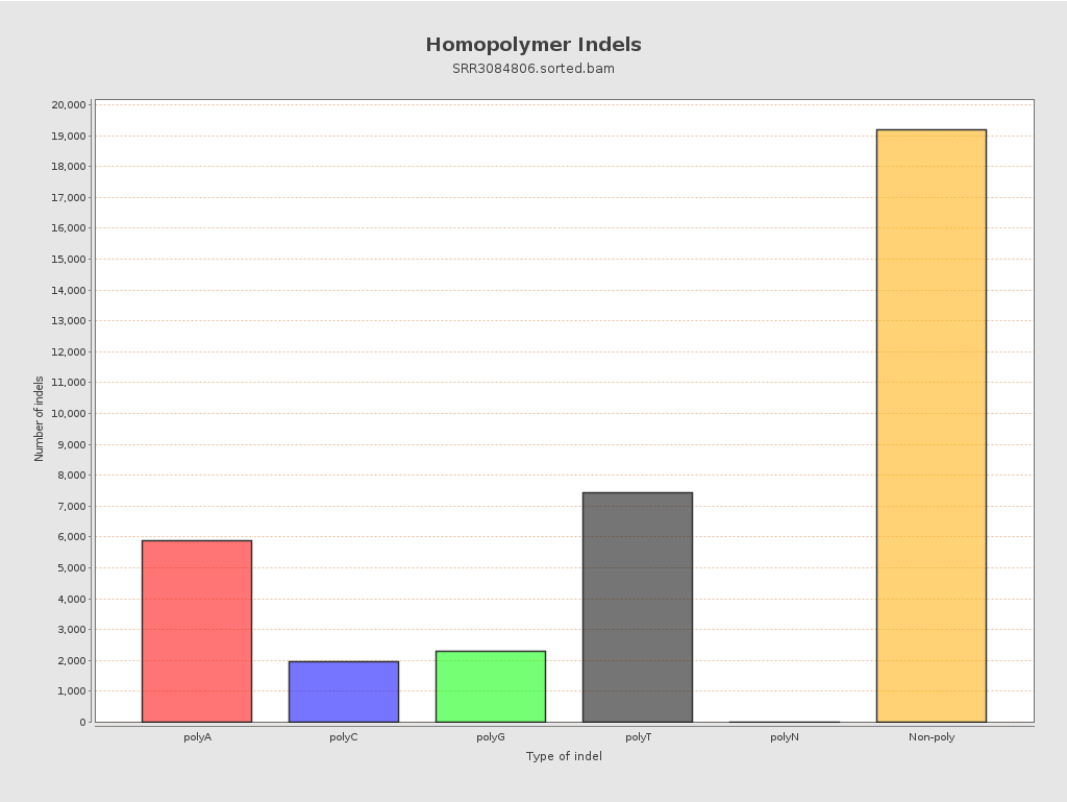
9. Results : Mapped Reads GC-content Distribution



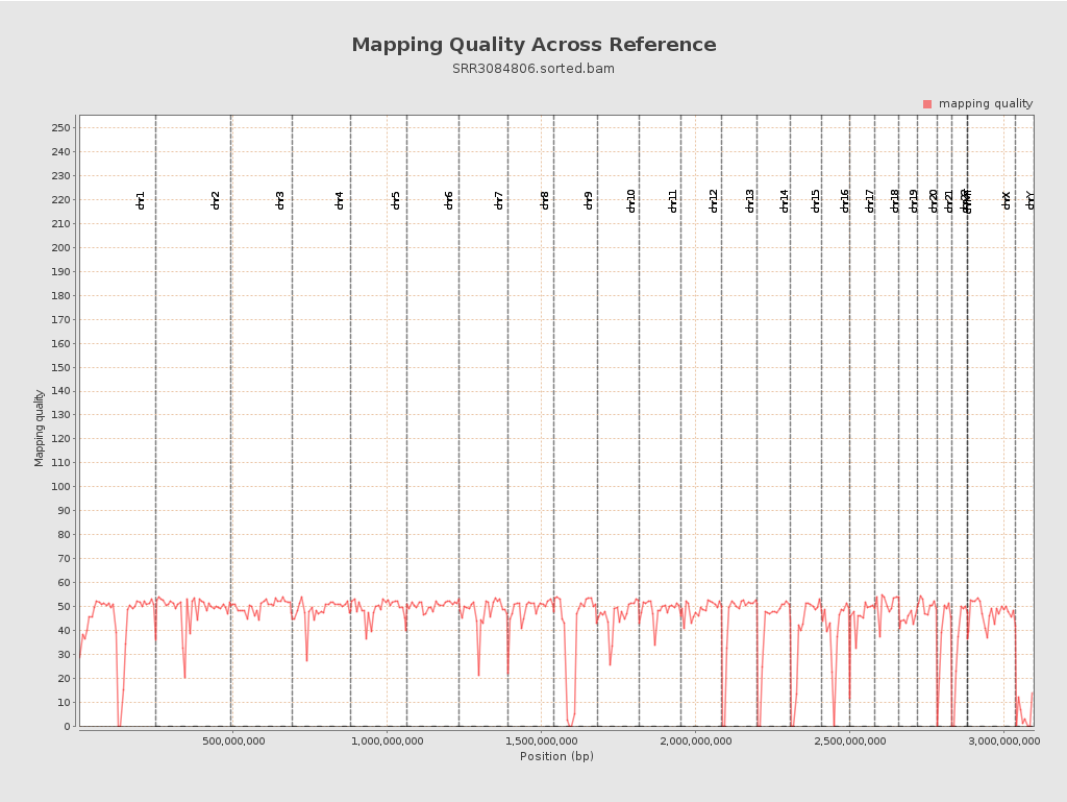
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram