Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:30:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080817.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_SRR3080817 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080817.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:30:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080817.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,473,689
Mapped reads	2,264,655 / 91.55%
Unmapped reads	209,034 / 8.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,753 / 0.68%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	158,737 / 6.42%
Duplication rate	5.91%
Clipped reads	876,016 / 35.41%

2.2. ACGT Content

Number/percentage of A's	43,641,340 / 28.29%
Number/percentage of C's	28,690,437 / 18.6%
Number/percentage of T's	48,820,470 / 31.64%
Number/percentage of G's	33,103,697 / 21.46%
Number/percentage of N's	21,923 / 0.01%
GC Percentage	40.05%

2.3. Coverage

Mean	0.0499

Standard Deviation	0.4168

2.4. Mapping Quality

Mean Mapping Quality	46.41

2.5. Mismatches and indels

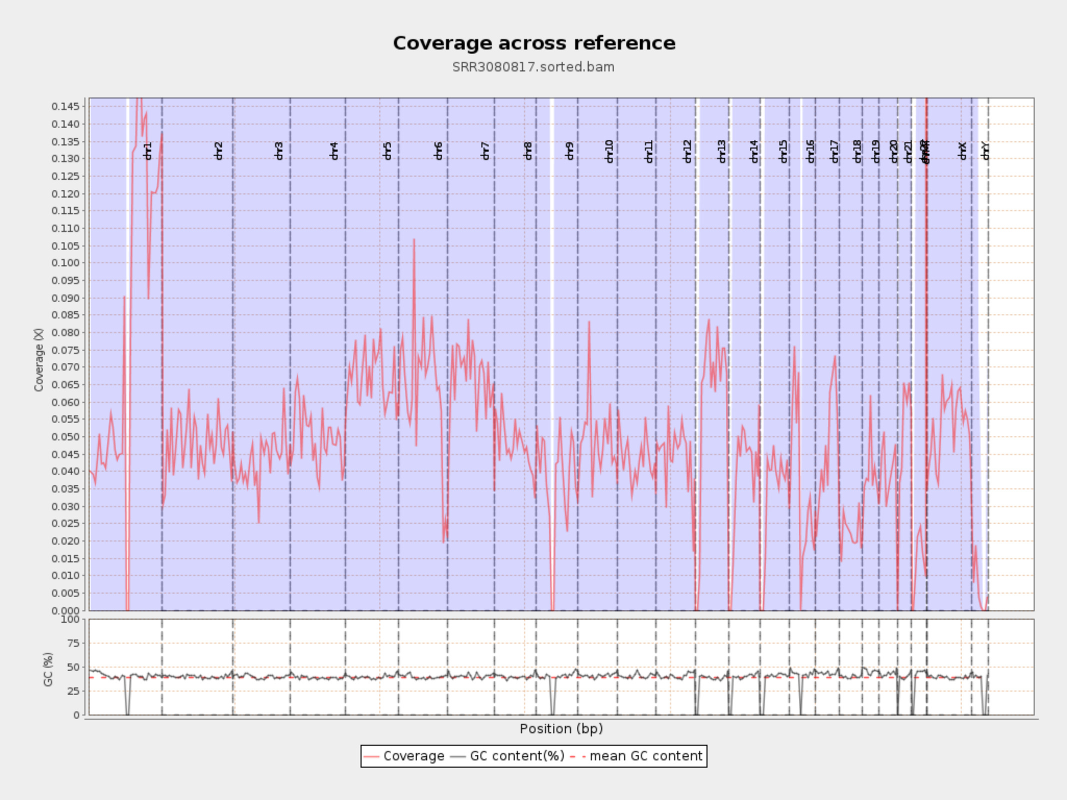
General error rate	0.81%
Mismatches	1,226,064
Insertions	11,160
Mapped reads with at least one insertion	0.49%
Deletions	31,639
Mapped reads with at least one deletion	1.38%
Homopolymer indels	47.7%

2.6. Chromosome stats

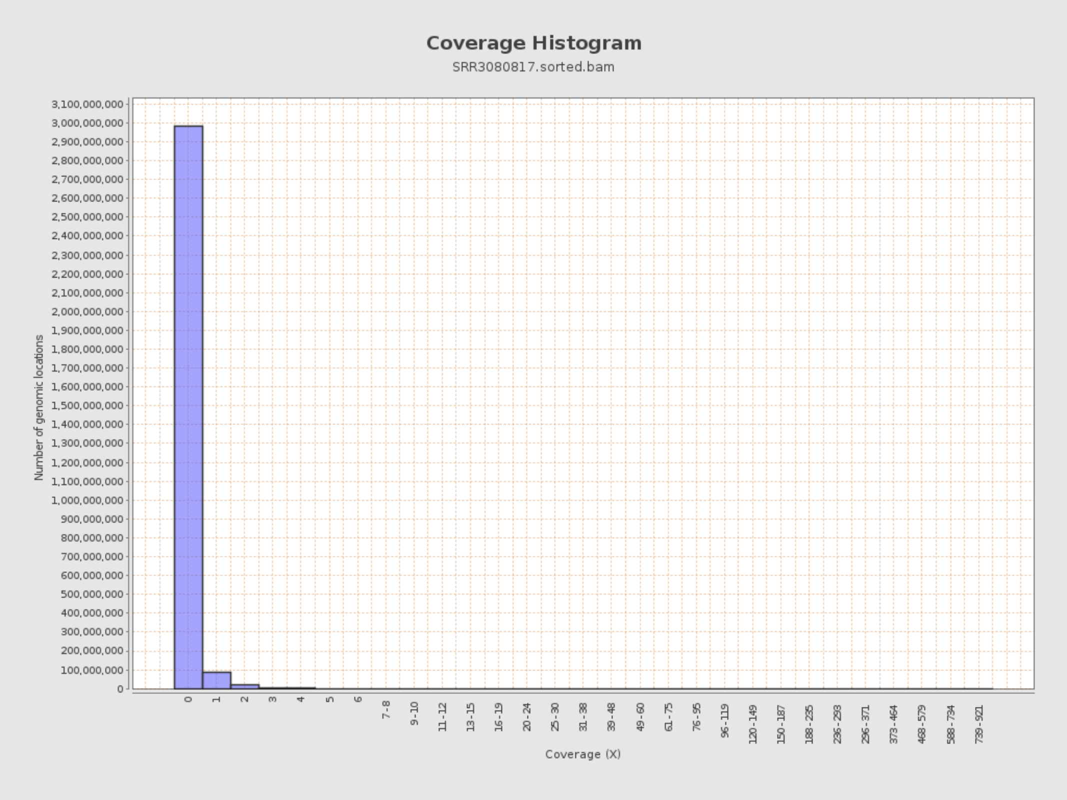
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20059042	0.0805	0.8969
chr2	243199373	11613871	0.0478	0.3926
chr3	198022430	8632551	0.0436	0.2707
chr4	191154276	9537839	0.0499	0.2924
chr5	180915260	12135063	0.0671	0.3292
chr6	171115067	11022620	0.0644	0.4362
chr7	159138663	10809509	0.0679	0.3887

chr8	146364022	6980875	0.0477	0.4713
chr9	141213431	5200014	0.0368	0.2797
chr10	135534747	6690520	0.0494	0.4557
chr11	135006516	5912969	0.0438	0.2802
chr12	133851895	5986505	0.0447	0.2704
chr13	115169878	6818262	0.0592	0.3112
chr14	107349540	3965797	0.0369	0.2525
chr15	102531392	3389451	0.0331	0.2312
chr16	90354753	3228402	0.0357	0.2616
chr17	81195210	3800252	0.0468	0.282
chr18	78077248	1748539	0.0224	0.3744
chr19	59128983	2319066	0.0392	0.5956
chr20	63025520	2516812	0.0399	0.2554
chr21	48129895	2360722	0.049	0.2964
chr22	51304566	667677	0.013	0.1408
chrMT	16571	299757	18.0893	10.1893
chrX	155270560	8265482	0.0532	0.3012
chrY	59373566	371180	0.0063	0.1537

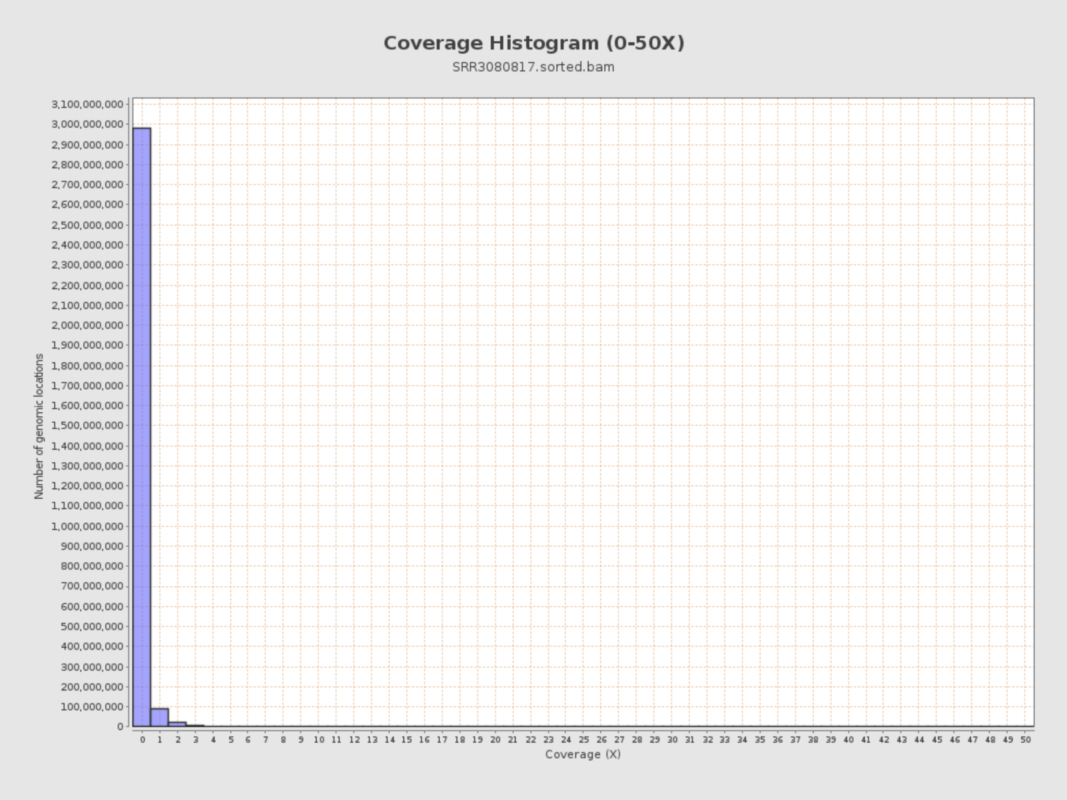
3. Results : Coverage across reference



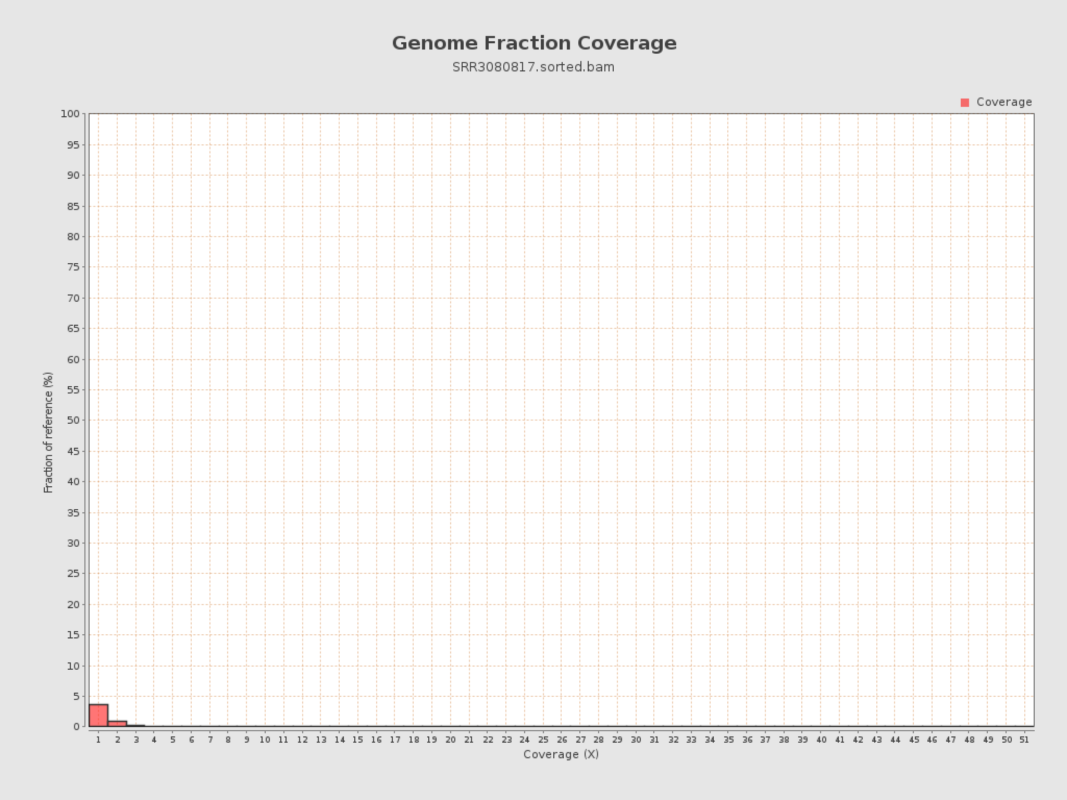
4. Results : Coverage Histogram



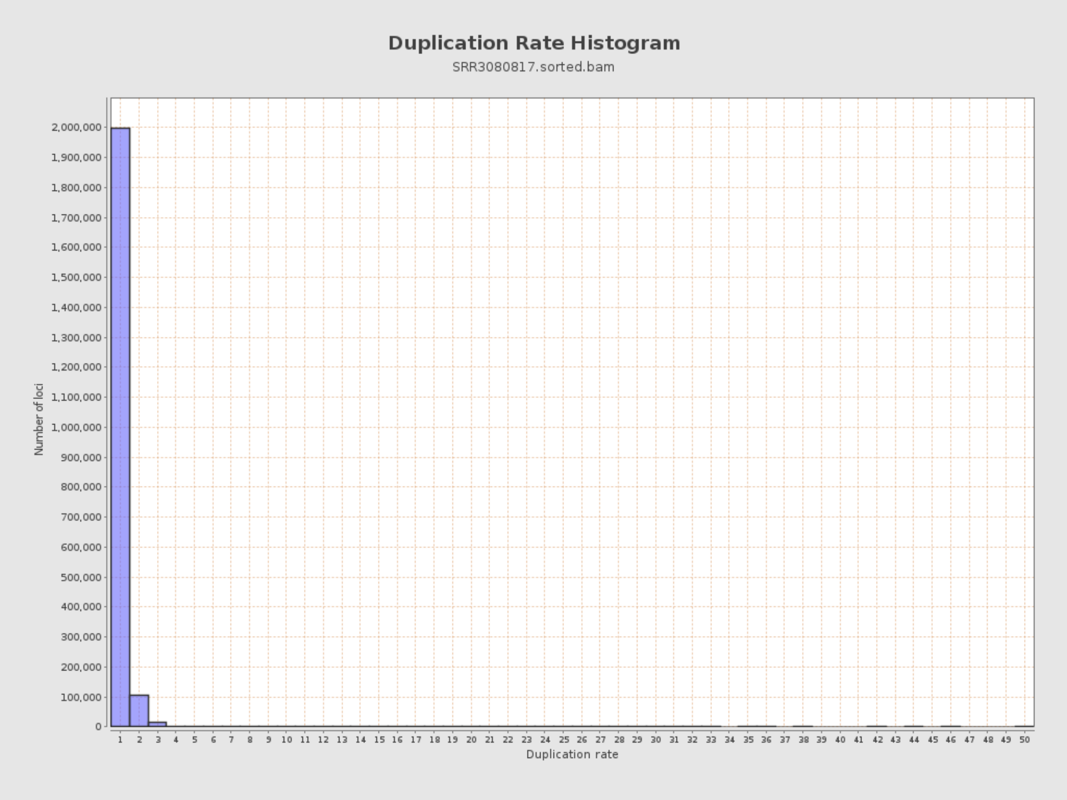
5. Results : Coverage Histogram (0-50X)



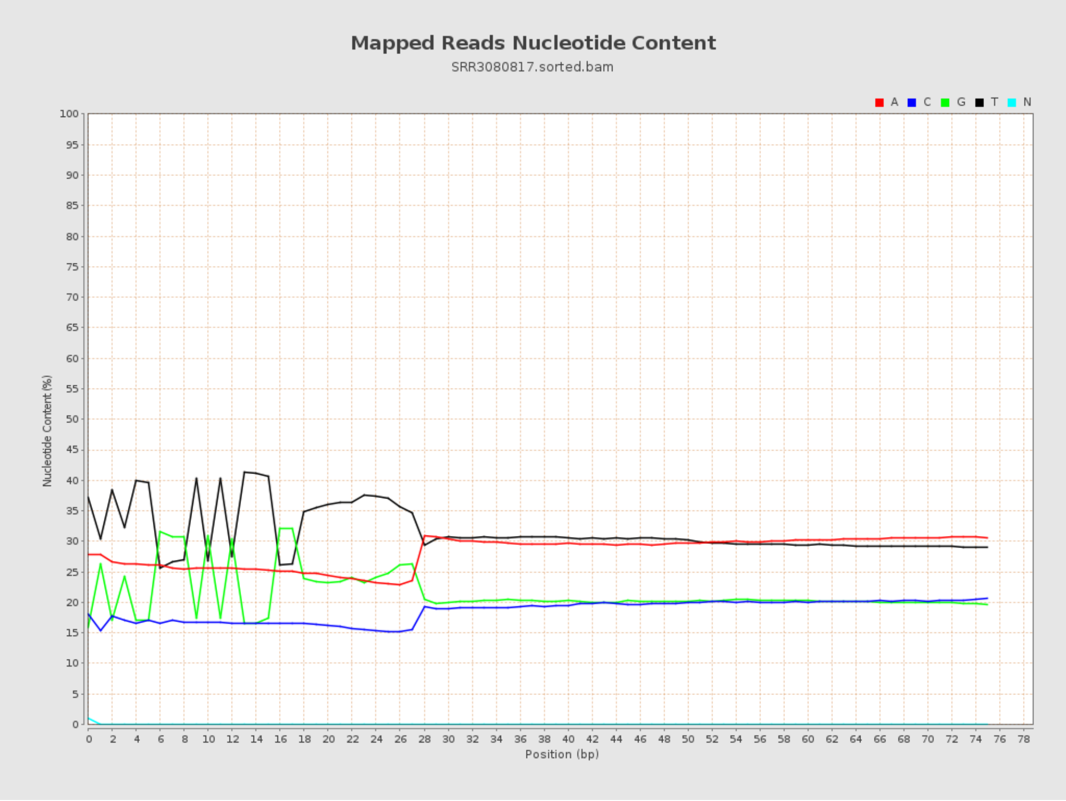
6. Results : Genome Fraction Coverage



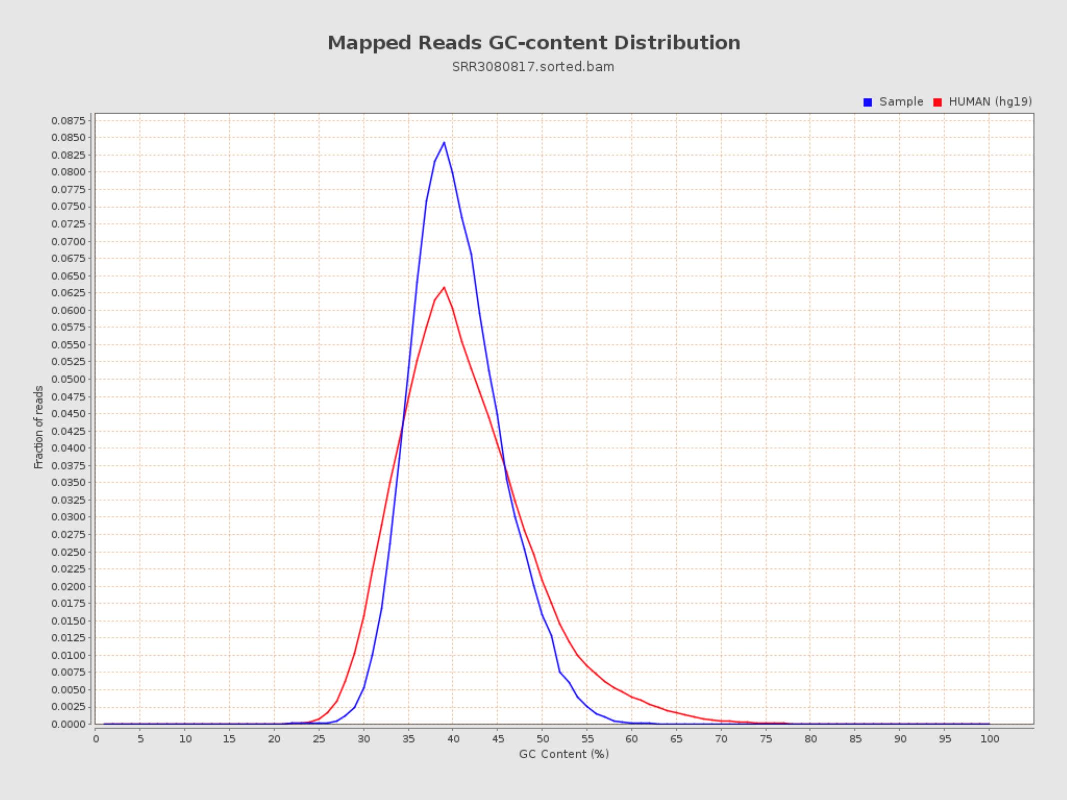
7. Results : Duplication Rate Histogram



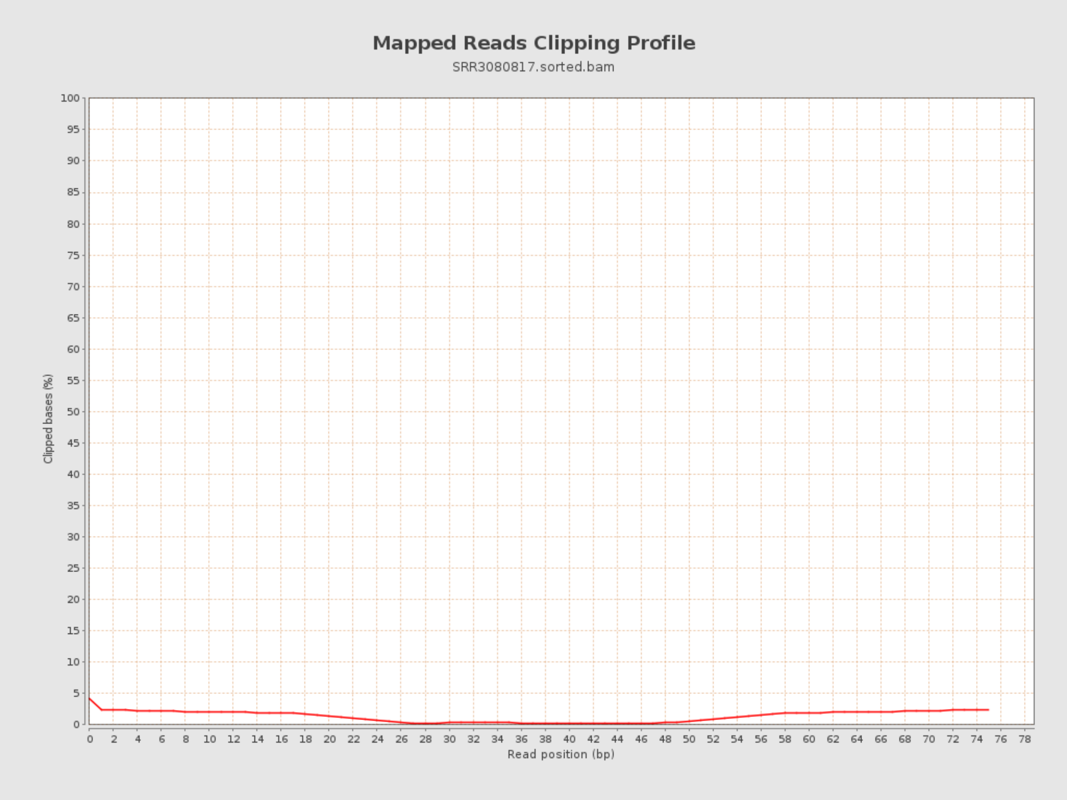
8. Results : Mapped Reads Nucleotide Content



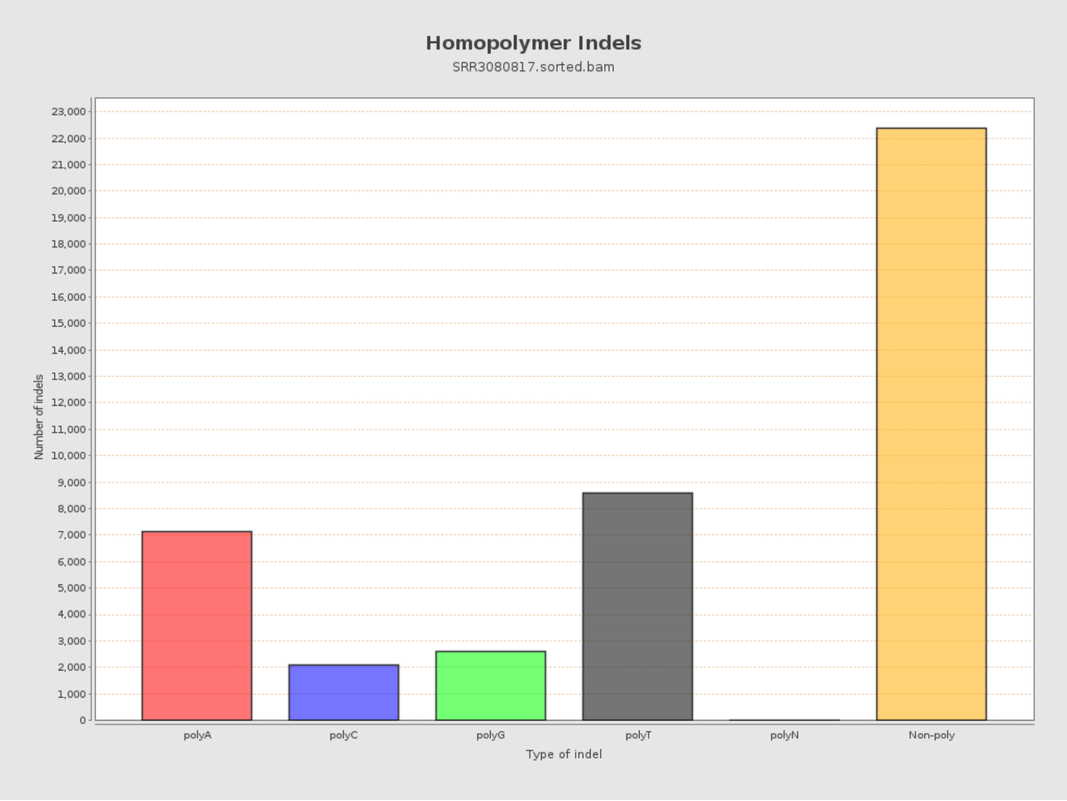
9. Results : Mapped Reads GC-content Distribution



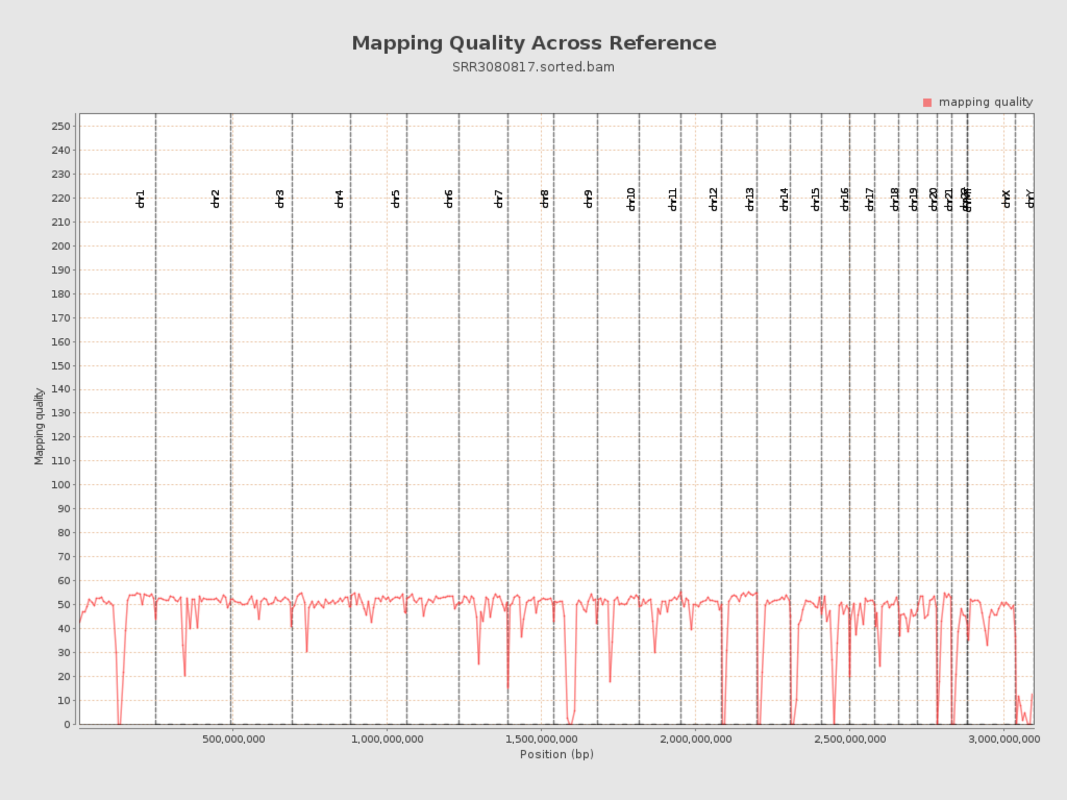
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram