Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 05:23:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080634.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_SRR3080634 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080634.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 05:23:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080634.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,197,868
Mapped reads	2,706,423 / 84.63%
Unmapped reads	491,445 / 15.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,342 / 0.67%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	139,723 / 4.37%
Duplication rate	4.39%
Clipped reads	1,321,967 / 41.34%

2.2. ACGT Content

Number/percentage of A's	48,887,907 / 27.38%
Number/percentage of C's	31,178,528 / 17.46%
Number/percentage of T's	58,815,259 / 32.94%
Number/percentage of G's	39,546,087 / 22.15%
Number/percentage of N's	145,837 / 0.08%
GC Percentage	39.61%

2.3. Coverage

Mean	0.0577

Standard Deviation	0.4247

2.4. Mapping Quality

Mean Mapping Quality	46.89

2.5. Mismatches and indels

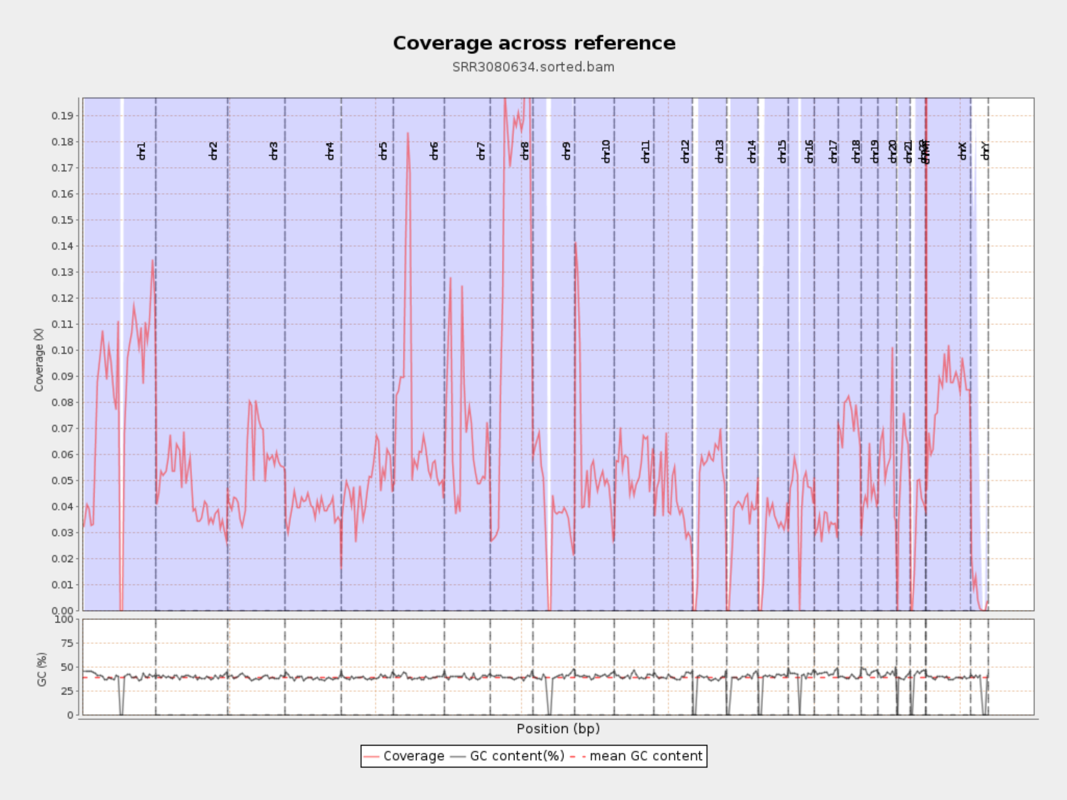
General error rate	0.89%
Mismatches	1,569,572
Insertions	14,358
Mapped reads with at least one insertion	0.53%
Deletions	43,739
Mapped reads with at least one deletion	1.6%
Homopolymer indels	48.76%

2.6. Chromosome stats

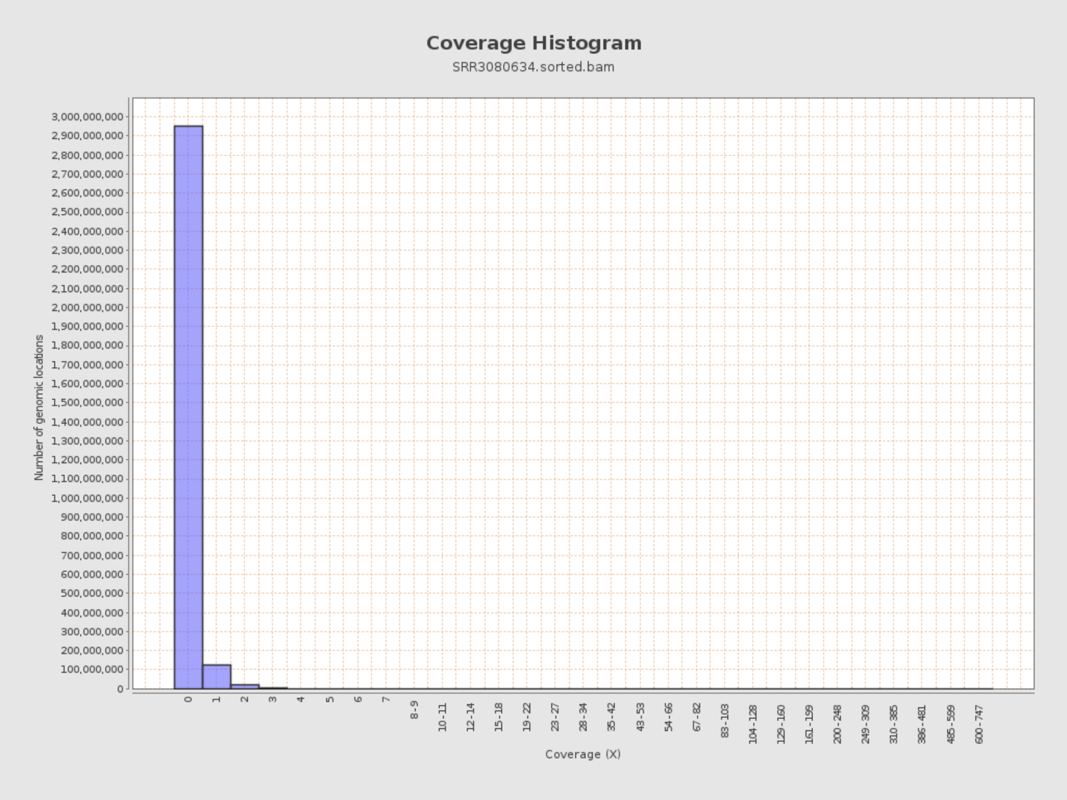
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20787798	0.0834	0.7109
chr2	243199373	11042181	0.0454	0.3641
chr3	198022430	11002776	0.0556	0.2742
chr4	191154276	7519193	0.0393	0.2335
chr5	180915260	8668495	0.0479	0.2538
chr6	171115067	12958980	0.0757	0.4175
chr7	159138663	10778290	0.0677	0.9348

chr8	146364022	20948072	0.1431	0.6259
chr9	141213431	5448866	0.0386	0.3029
chr10	135534747	8099620	0.0598	0.3169
chr11	135006516	7535040	0.0558	0.2933
chr12	133851895	5602729	0.0419	0.2413
chr13	115169878	5553522	0.0482	0.2561
chr14	107349540	3636560	0.0339	0.2262
chr15	102531392	2933142	0.0286	0.1961
chr16	90354753	3929896	0.0435	0.253
chr17	81195210	2663700	0.0328	0.2122
chr18	78077248	5739997	0.0735	0.4864
chr19	59128983	2651541	0.0448	0.4454
chr20	63025520	3788819	0.0601	0.2893
chr21	48129895	2503743	0.052	0.2729
chr22	51304566	1614826	0.0315	0.2037
chrMT	16571	81188	4.8994	3.8068
chrX	155270560	12818085	0.0826	0.3594
chrY	59373566	337822	0.0057	0.1007

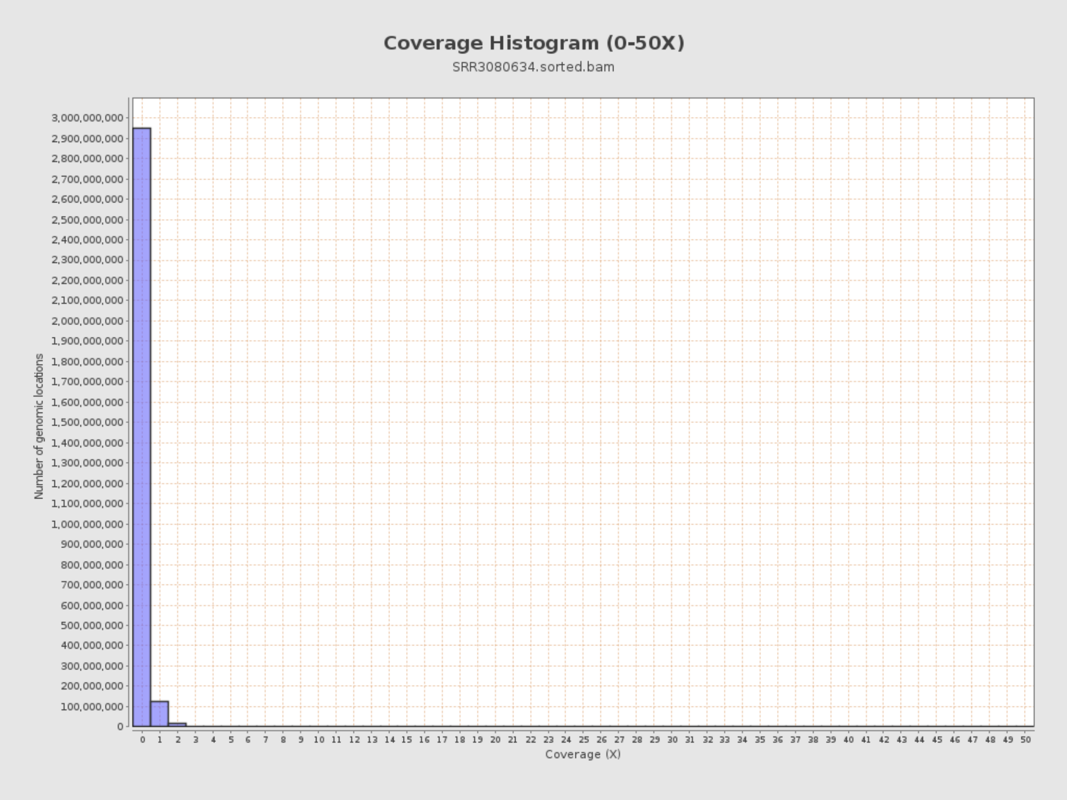
3. Results : Coverage across reference



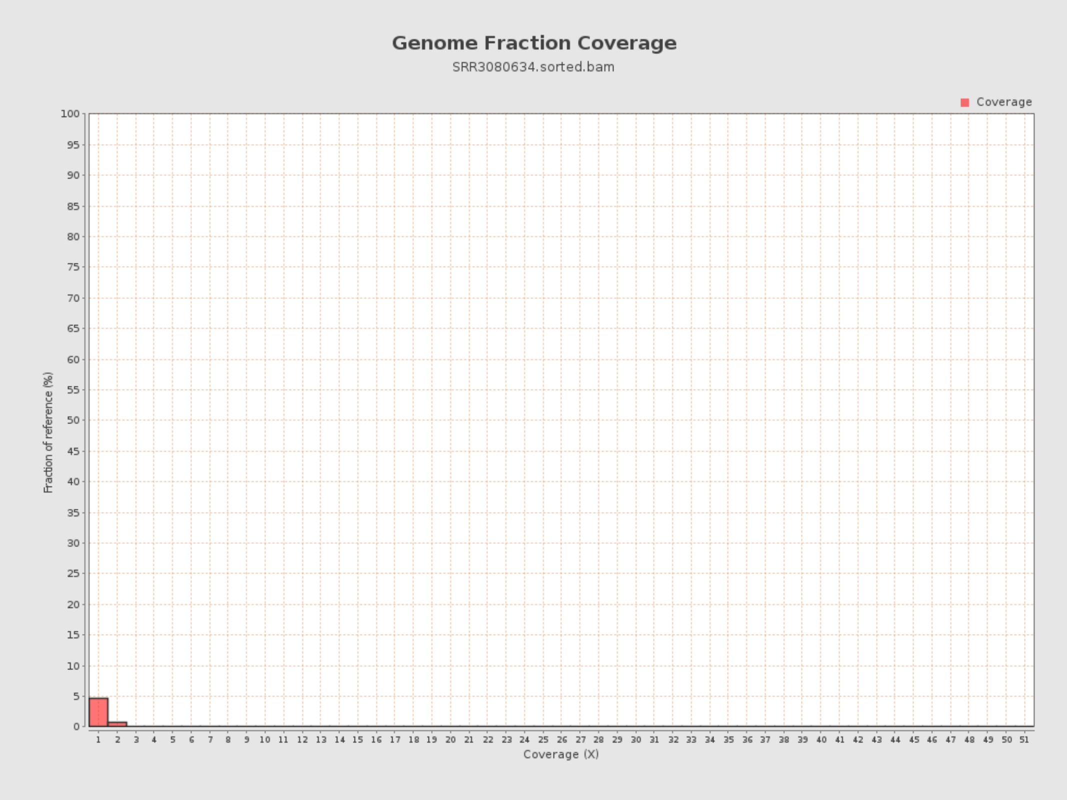
4. Results : Coverage Histogram



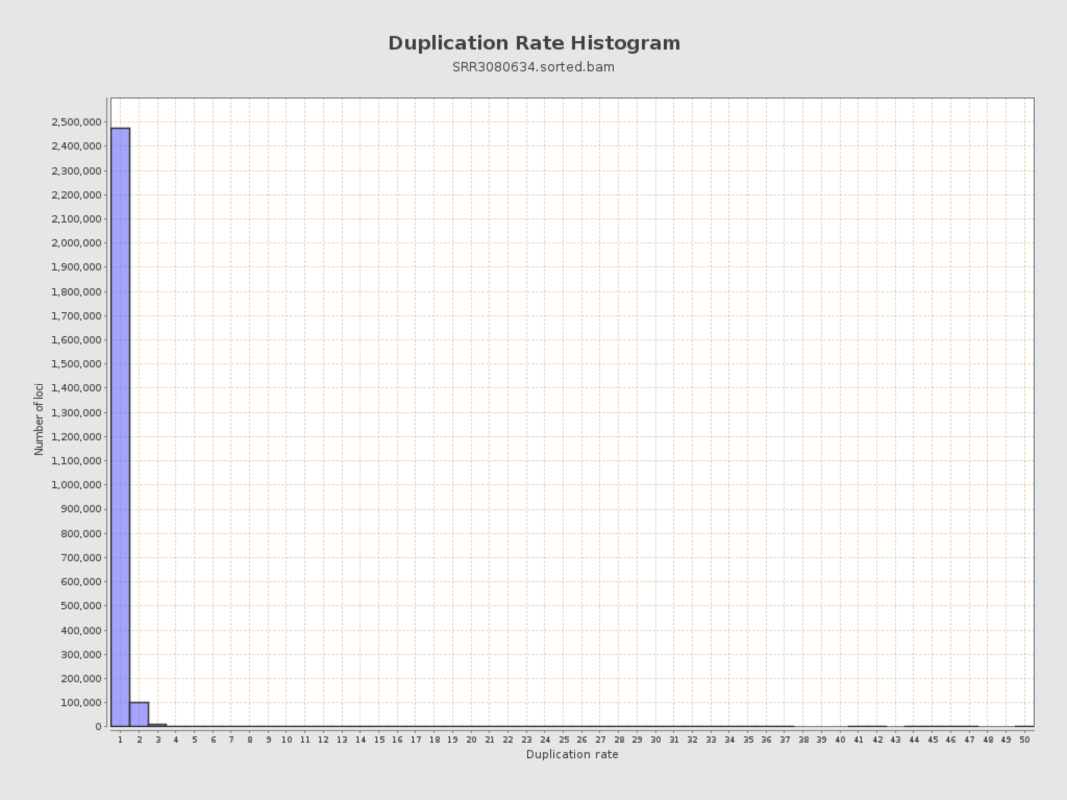
5. Results : Coverage Histogram (0-50X)



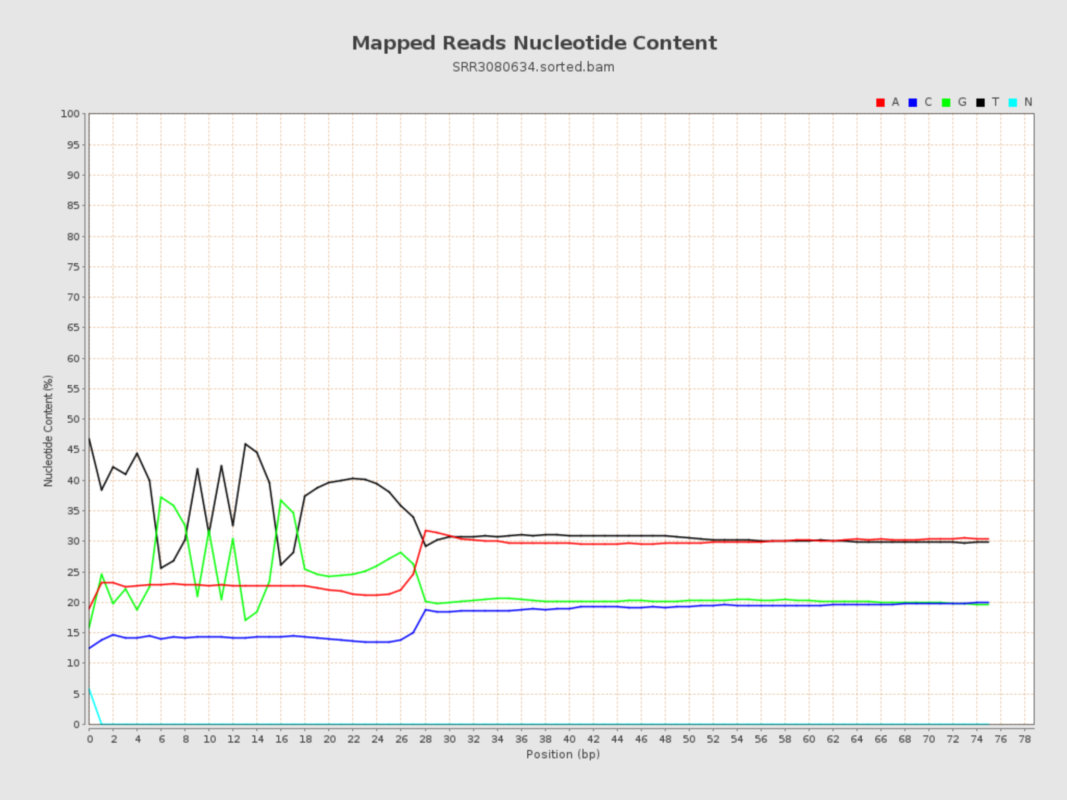
6. Results : Genome Fraction Coverage



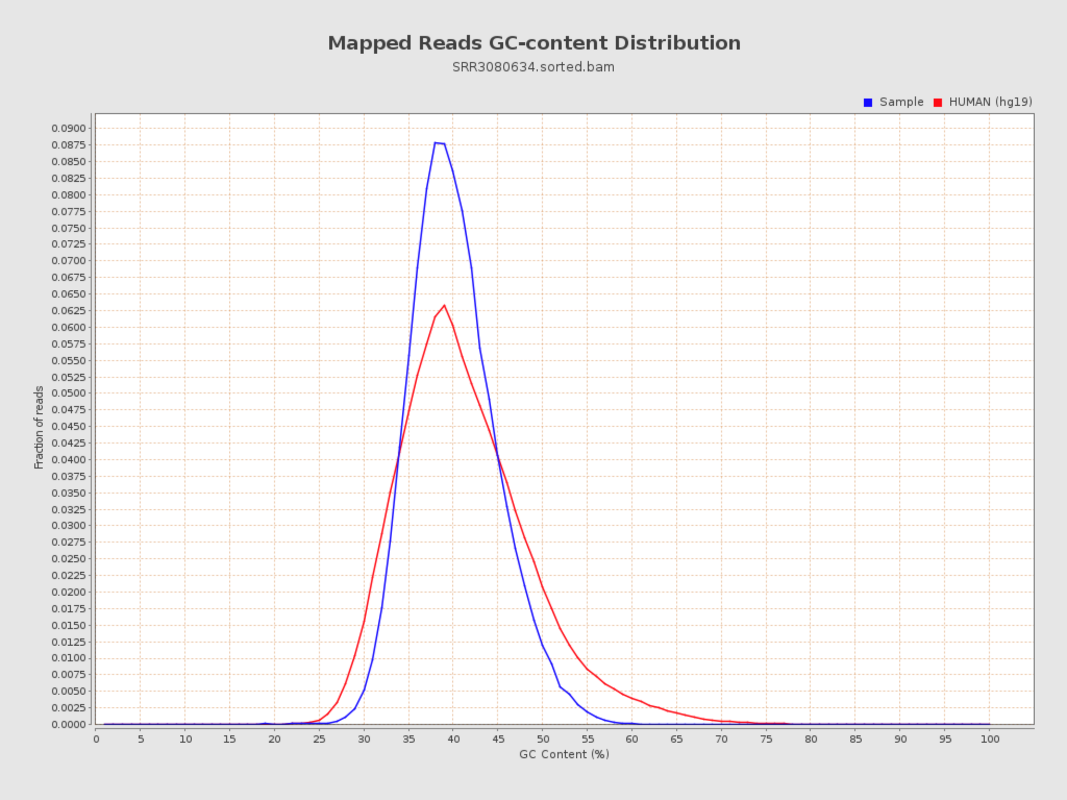
7. Results : Duplication Rate Histogram



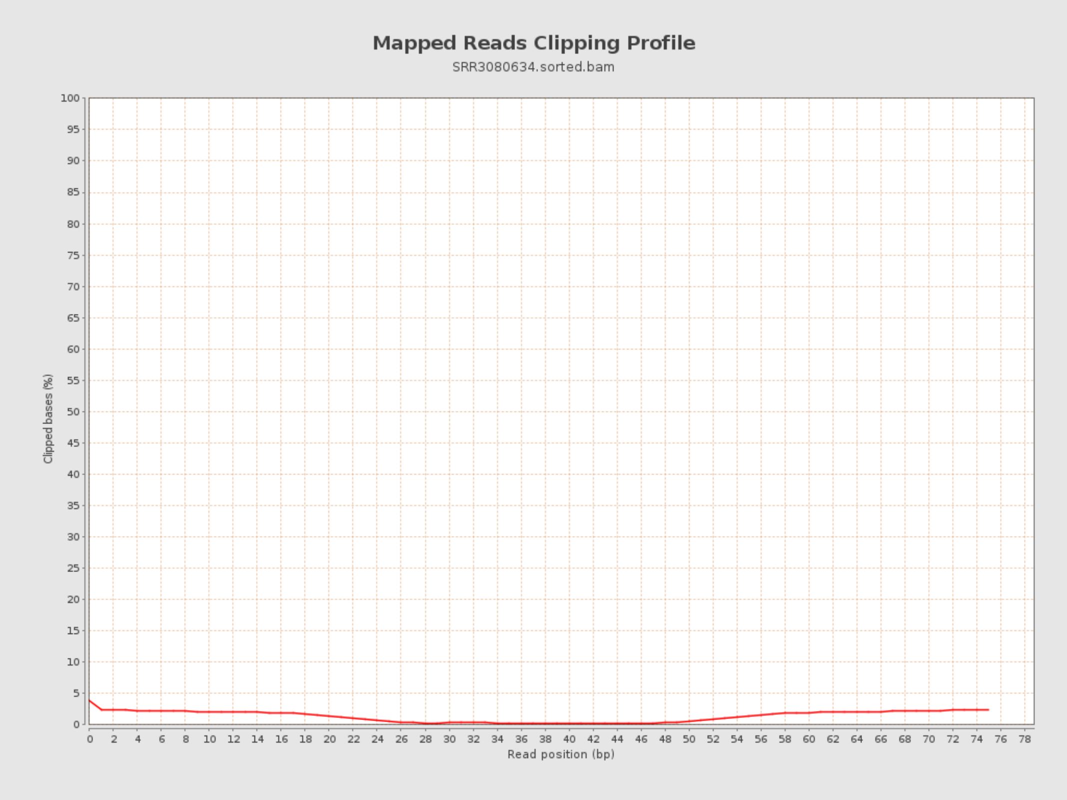
8. Results : Mapped Reads Nucleotide Content



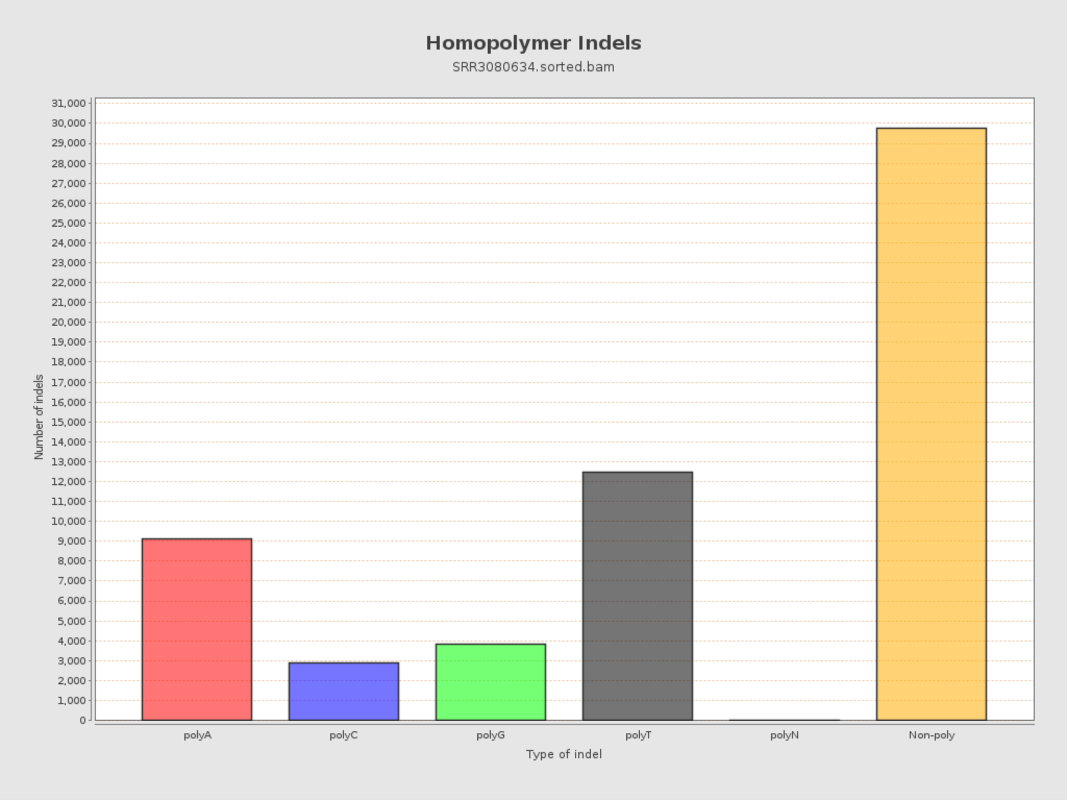
9. Results : Mapped Reads GC-content Distribution



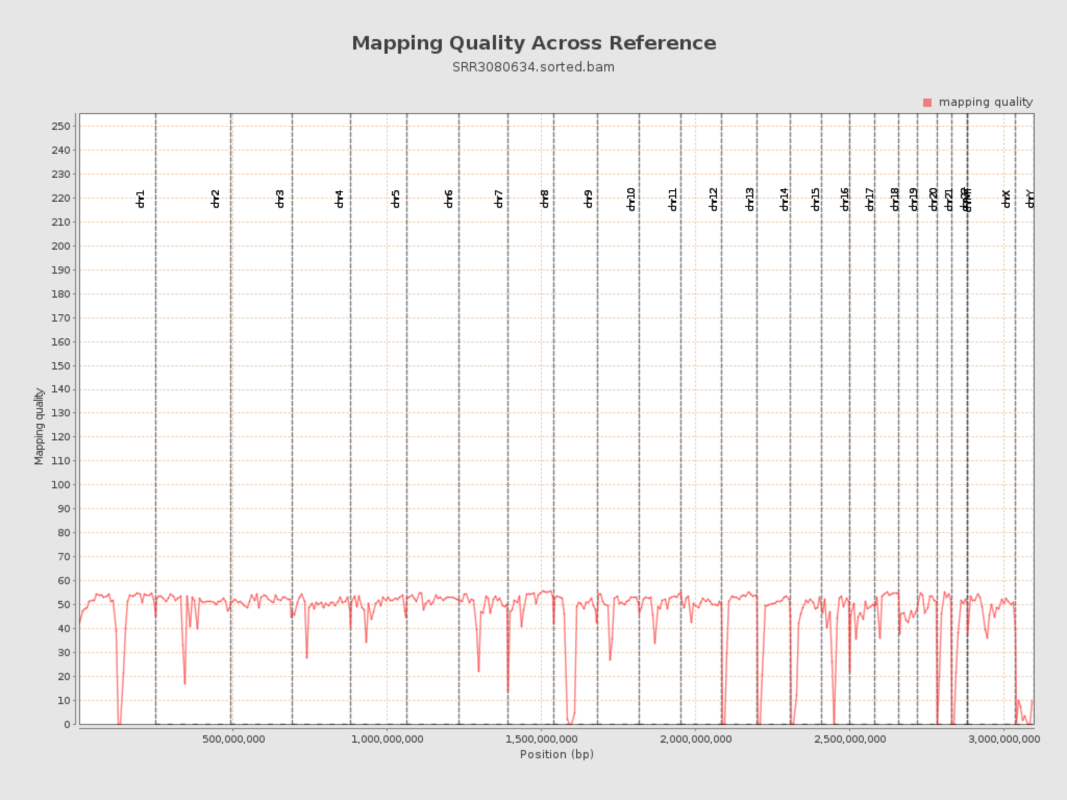
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram