Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 18:50:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080696.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_SRR3080696 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080696.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 18:50:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080696.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,045,546
Mapped reads	1,644,107 / 80.37%
Unmapped reads	401,439 / 19.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,388 / 0.75%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	103,934 / 5.08%
Duplication rate	5.27%
Clipped reads	660,940 / 32.31%

2.2. ACGT Content

Number/percentage of A's	31,912,669 / 28.61%
Number/percentage of C's	20,275,036 / 18.18%
Number/percentage of T's	35,822,732 / 32.12%
Number/percentage of G's	23,522,038 / 21.09%
Number/percentage of N's	1,655 / 0%
GC Percentage	39.27%

2.3. Coverage

Mean	0.036

Standard Deviation	0.3561

2.4. Mapping Quality

Mean Mapping Quality	47.14

2.5. Mismatches and indels

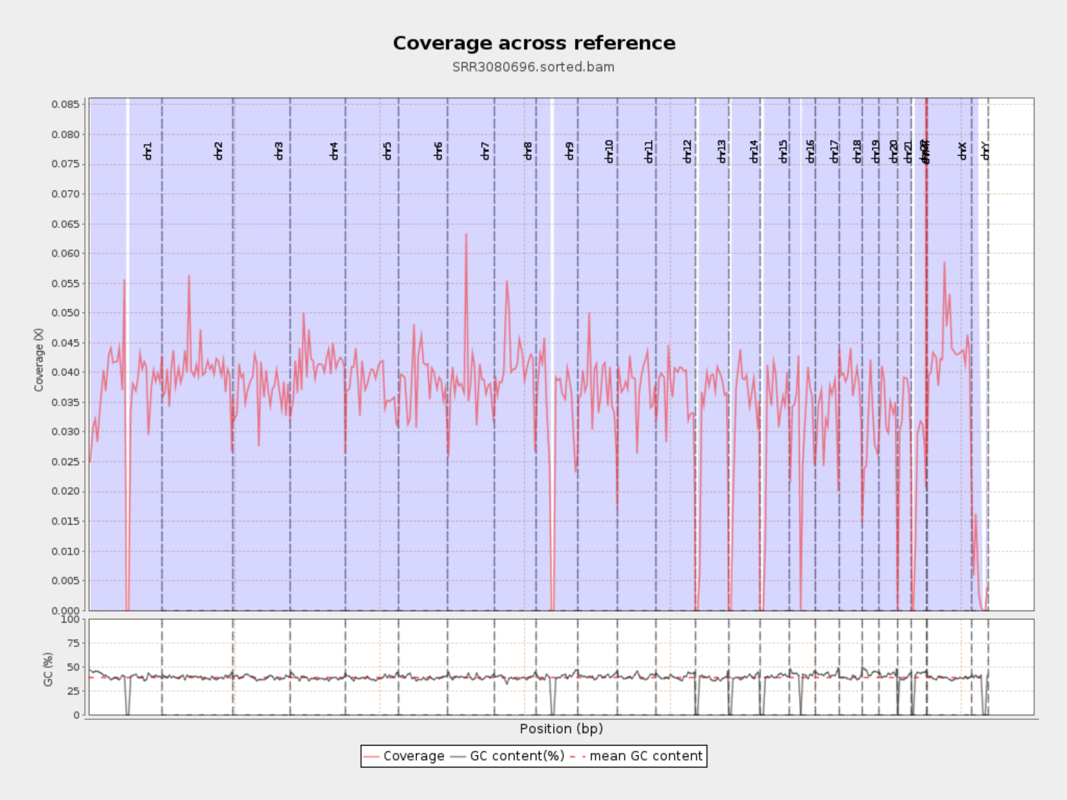
General error rate	0.81%
Mismatches	884,110
Insertions	8,832
Mapped reads with at least one insertion	0.53%
Deletions	23,805
Mapped reads with at least one deletion	1.43%
Homopolymer indels	47.86%

2.6. Chromosome stats

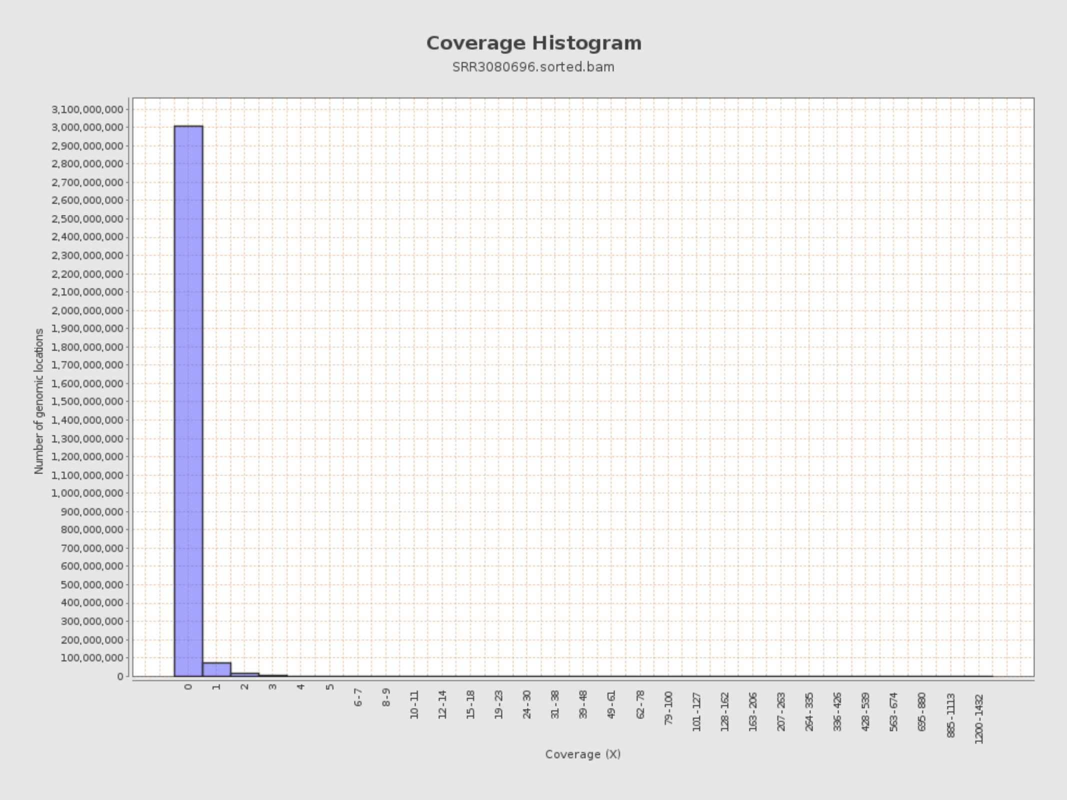
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8980533	0.036	0.4911
chr2	243199373	9842656	0.0405	0.352
chr3	198022430	7368573	0.0372	0.2355
chr4	191154276	7901950	0.0413	0.259
chr5	180915260	6905179	0.0382	0.2392
chr6	171115067	6605808	0.0386	0.2657
chr7	159138663	6158579	0.0387	0.482

chr8	146364022	6045779	0.0413	0.8799
chr9	141213431	4597936	0.0326	0.2731
chr10	135534747	5082761	0.0375	0.2866
chr11	135006516	5078018	0.0376	0.2849
chr12	133851895	5001458	0.0374	0.2384
chr13	115169878	3631794	0.0315	0.2198
chr14	107349540	3378713	0.0315	0.2289
chr15	102531392	3040521	0.0297	0.2097
chr16	90354753	2798271	0.031	0.2254
chr17	81195210	2615111	0.0322	0.2344
chr18	78077248	3056062	0.0391	0.4323
chr19	59128983	1743799	0.0295	0.3224
chr20	63025520	2131347	0.0338	0.2307
chr21	48129895	1493346	0.031	0.2264
chr22	51304566	1052075	0.0205	0.1716
chrMT	16571	61665	3.7213	2.7211
chrX	155270560	6716832	0.0433	0.2694
chrY	59373566	287303	0.0048	0.1287

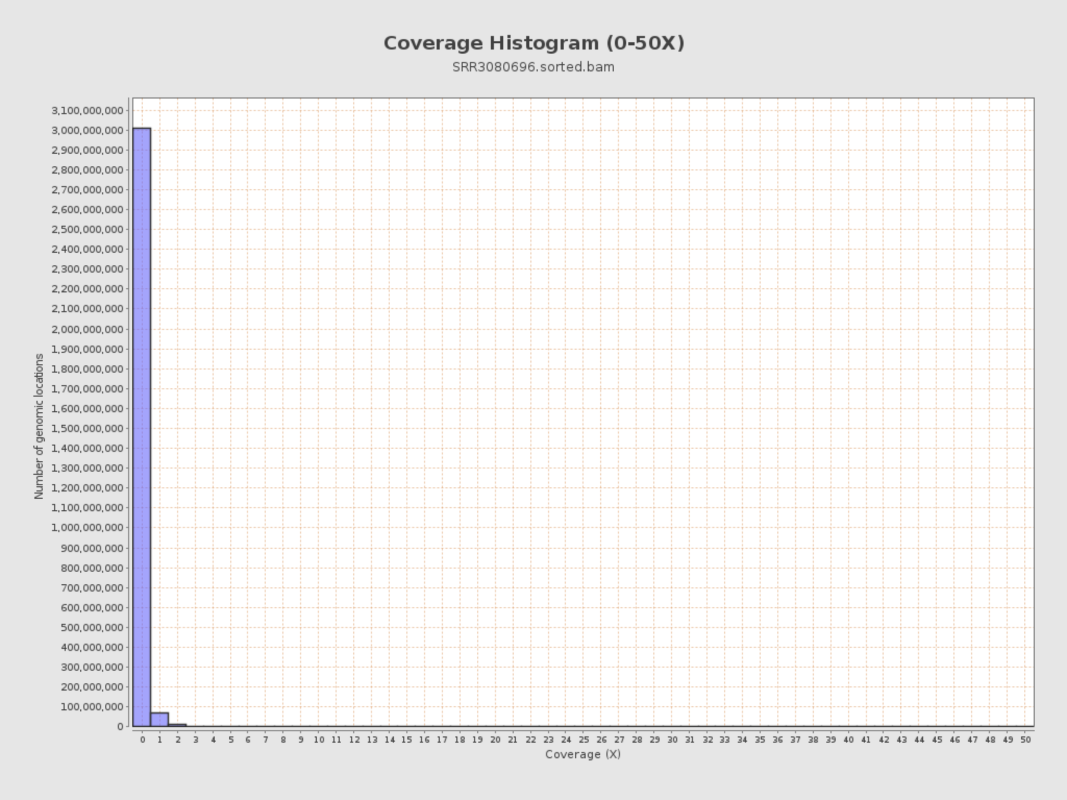
3. Results : Coverage across reference



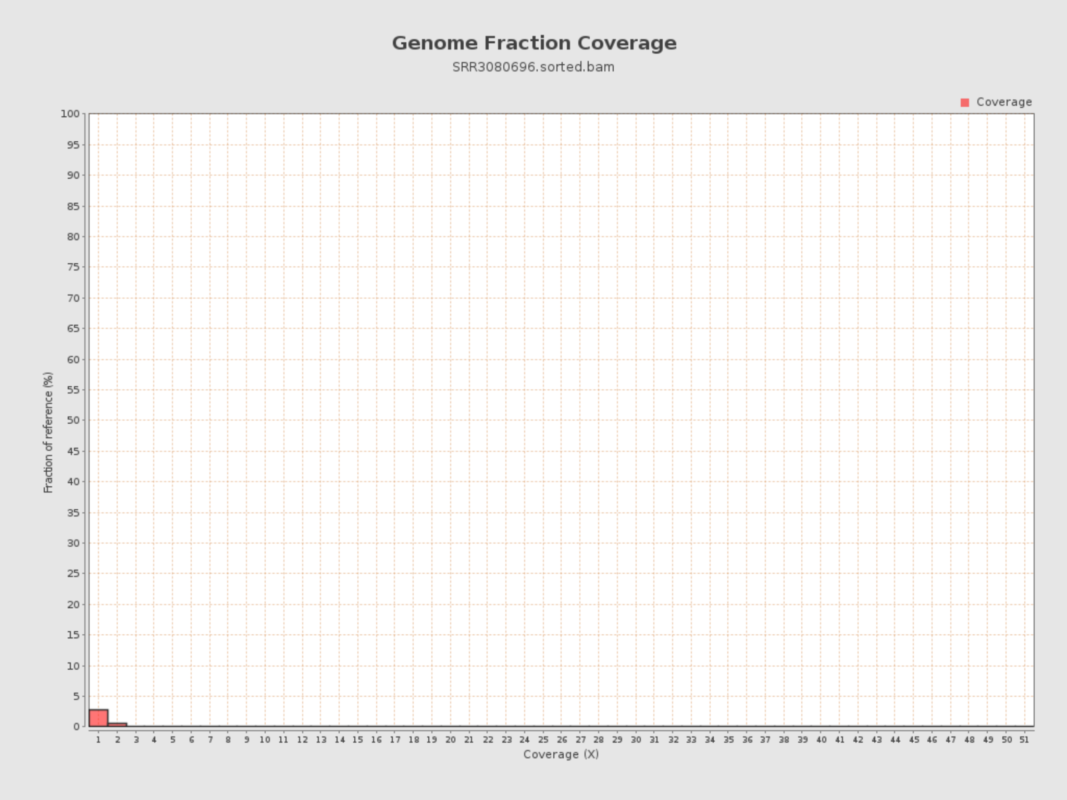
4. Results : Coverage Histogram



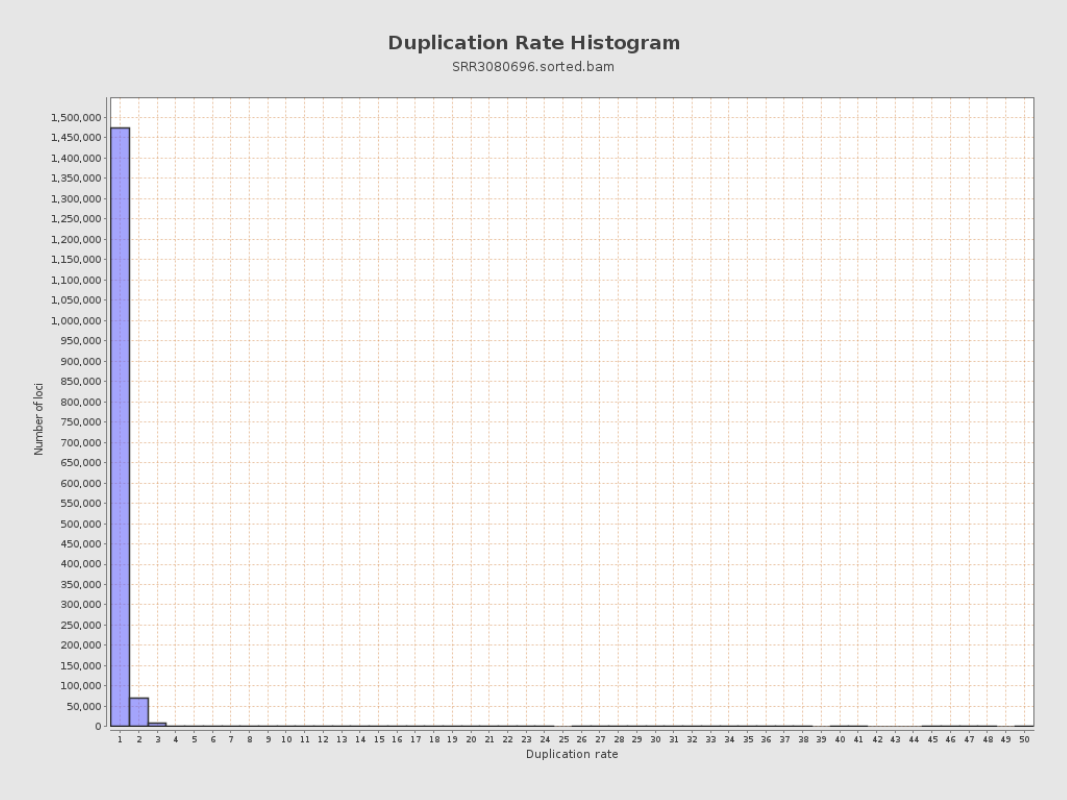
5. Results : Coverage Histogram (0-50X)



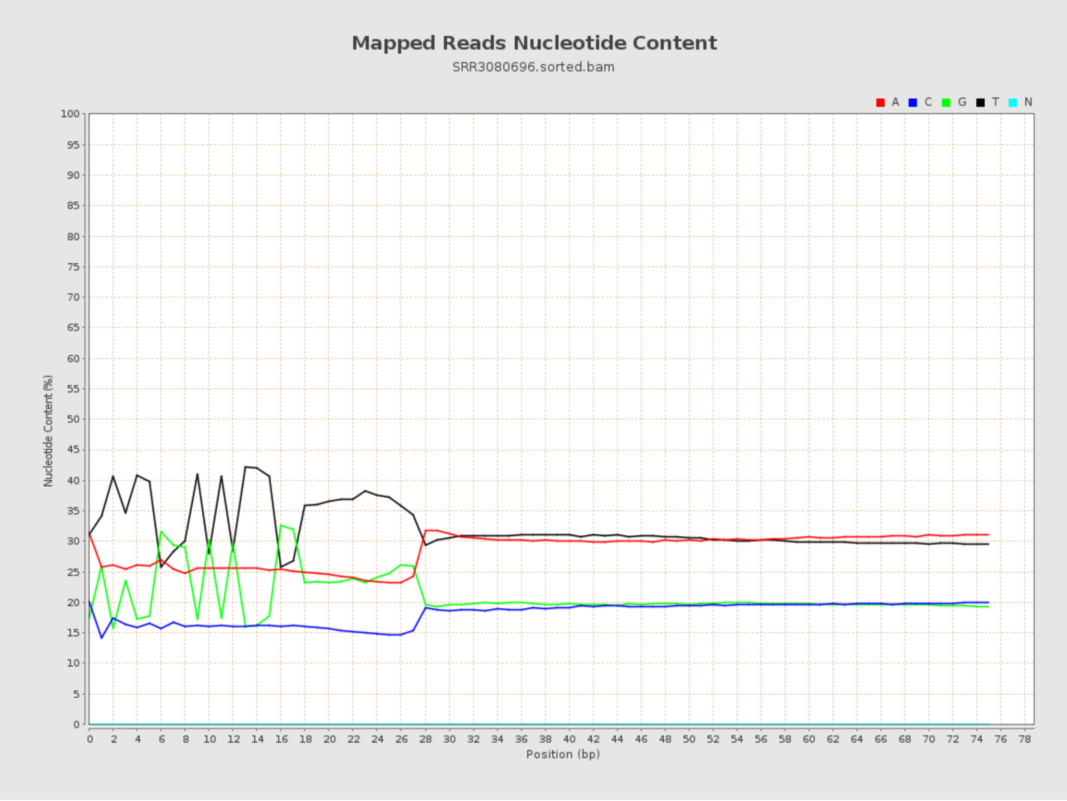
6. Results : Genome Fraction Coverage



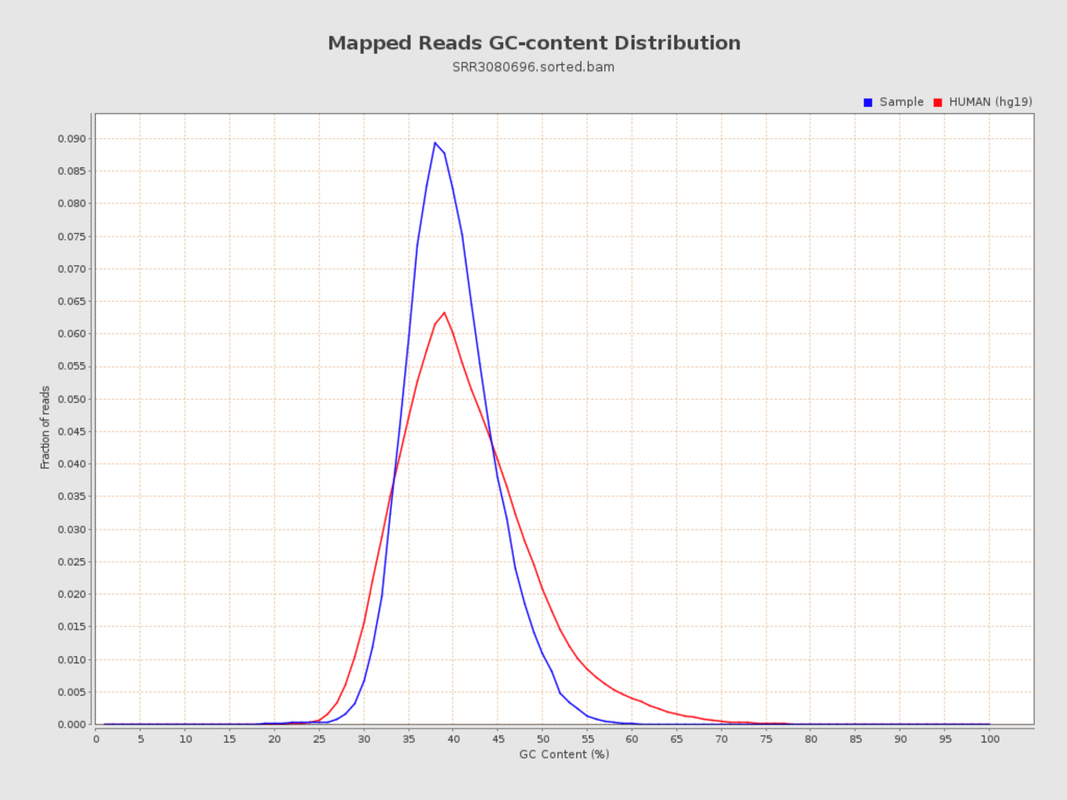
7. Results : Duplication Rate Histogram



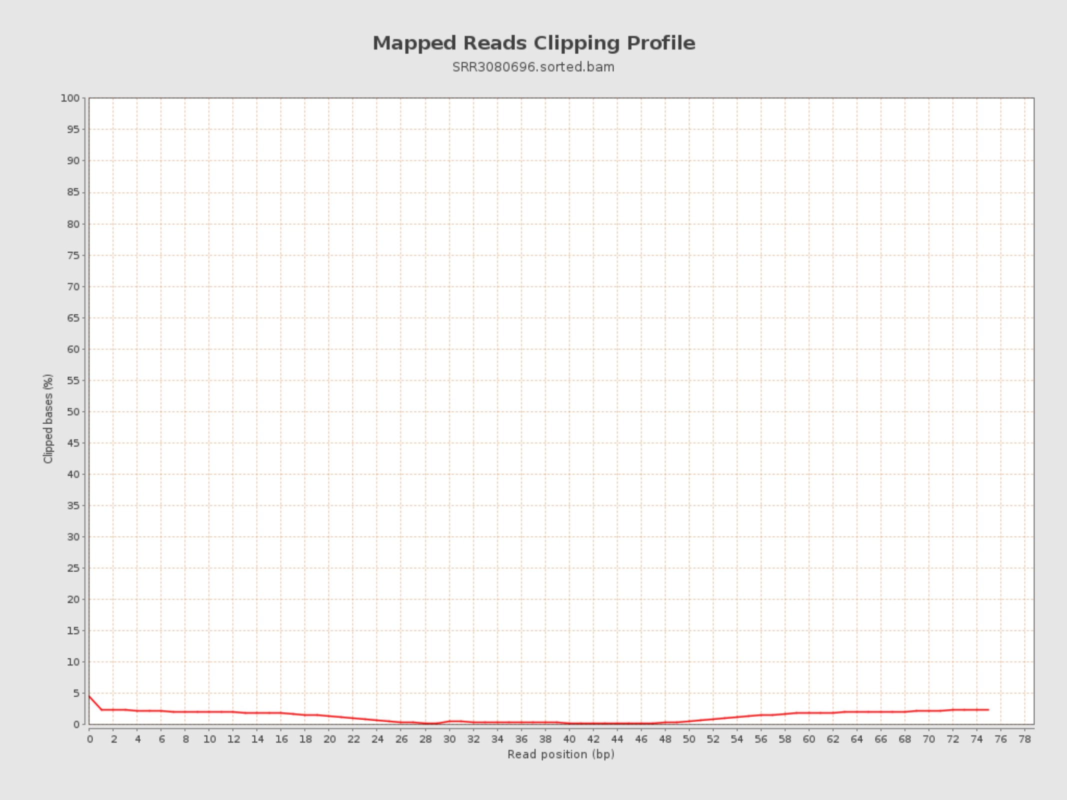
8. Results : Mapped Reads Nucleotide Content



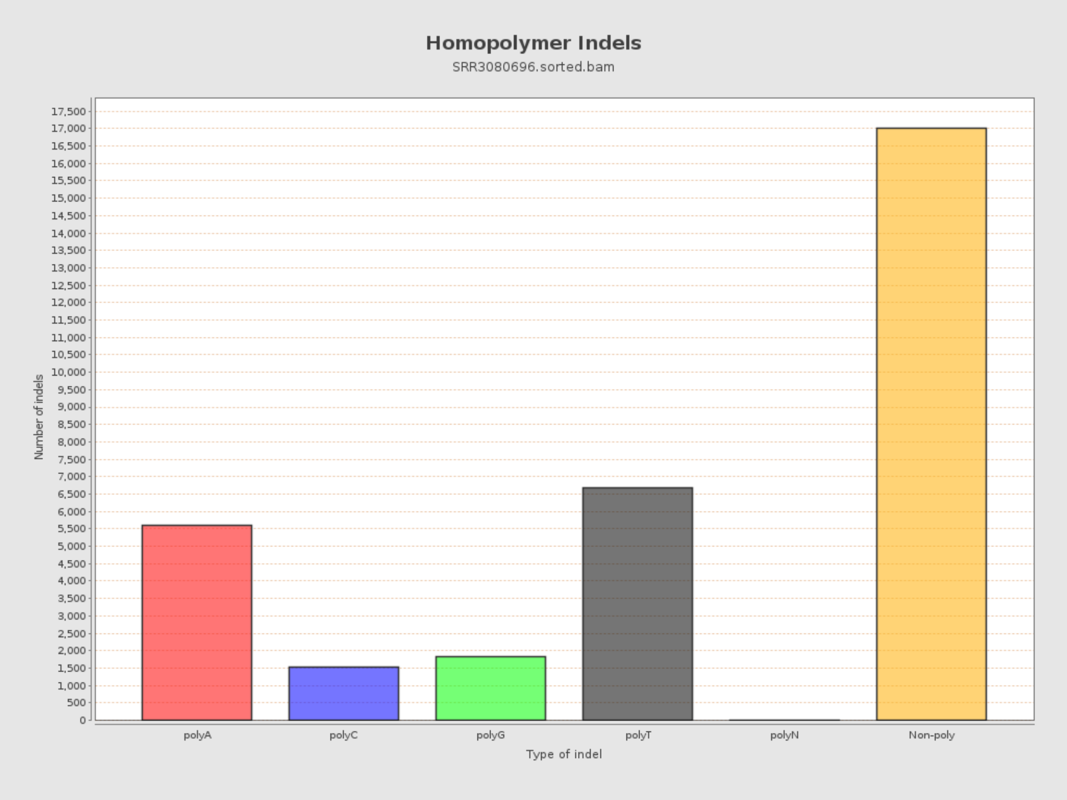
9. Results : Mapped Reads GC-content Distribution



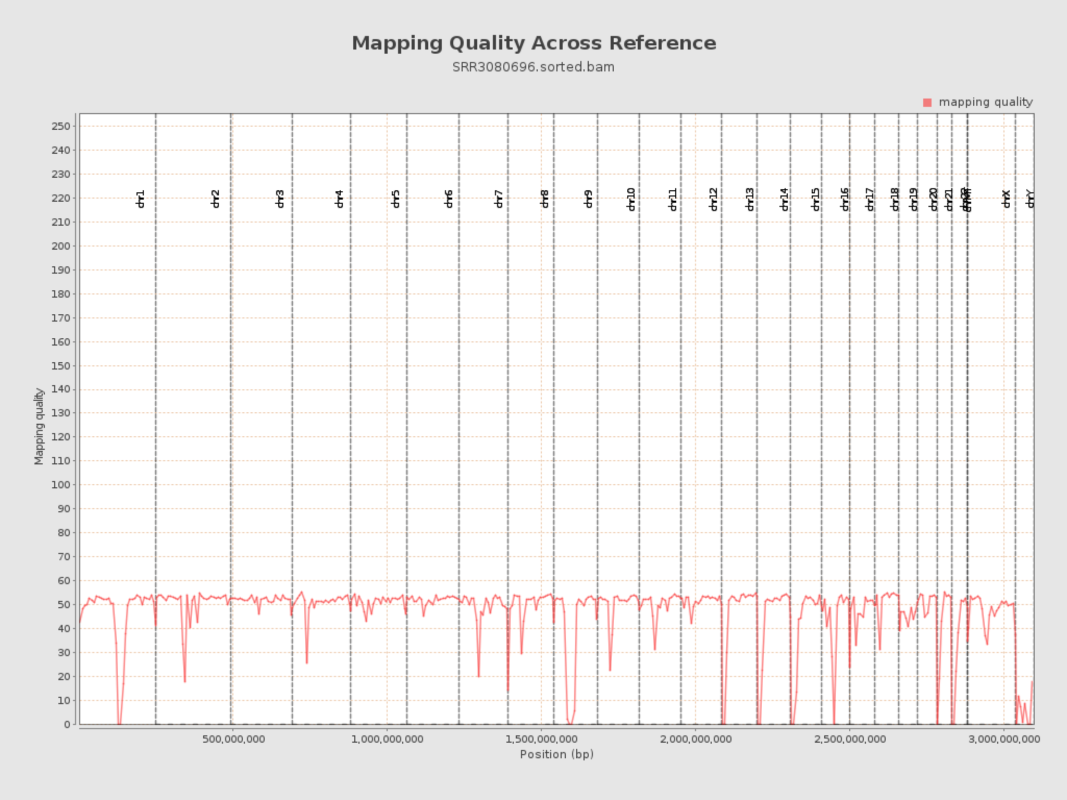
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram