

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 20:04:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080706.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_SRR3080706 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080706.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 20:04:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080706.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,982,222
Mapped reads	1,707,050 / 86.12%
Unmapped reads	275,172 / 13.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,739 / 0.79%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	96,938 / 4.89%
Duplication rate	4.78%
Clipped reads	681,918 / 34.4%

2.2. ACGT Content

Number/percentage of A's	33,591,811 / 28.96%
Number/percentage of C's	21,383,616 / 18.44%
Number/percentage of T's	36,388,410 / 31.37%
Number/percentage of G's	24,624,471 / 21.23%
Number/percentage of N's	1,631 / 0%
GC Percentage	39.67%

2.3. Coverage

Mean	0.0375

Standard Deviation	0.3423
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2.4. Mapping Quality

Mean Mapping Quality	47.04
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2.5. Mismatches and indels

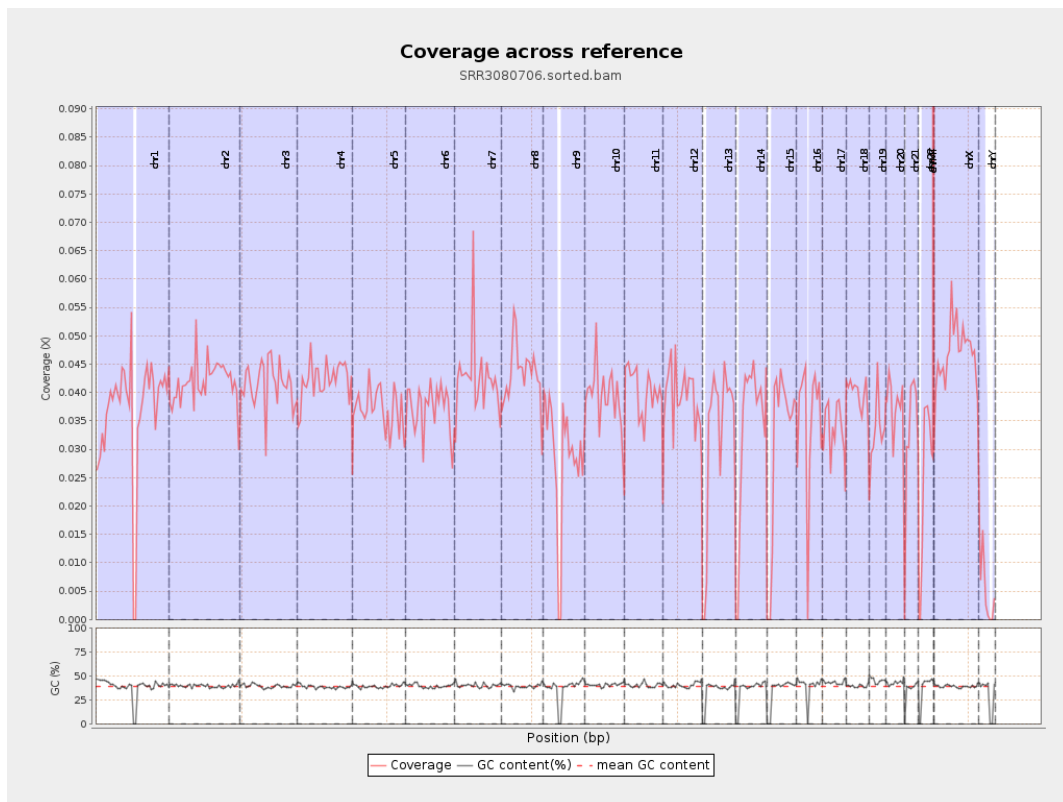
General error rate	0.83%
Mismatches	948,758
Insertions	9,001
Mapped reads with at least one insertion	0.52%
Deletions	24,448
Mapped reads with at least one deletion	1.42%
Homopolymer indels	47.25%

2.6. Chromosome stats

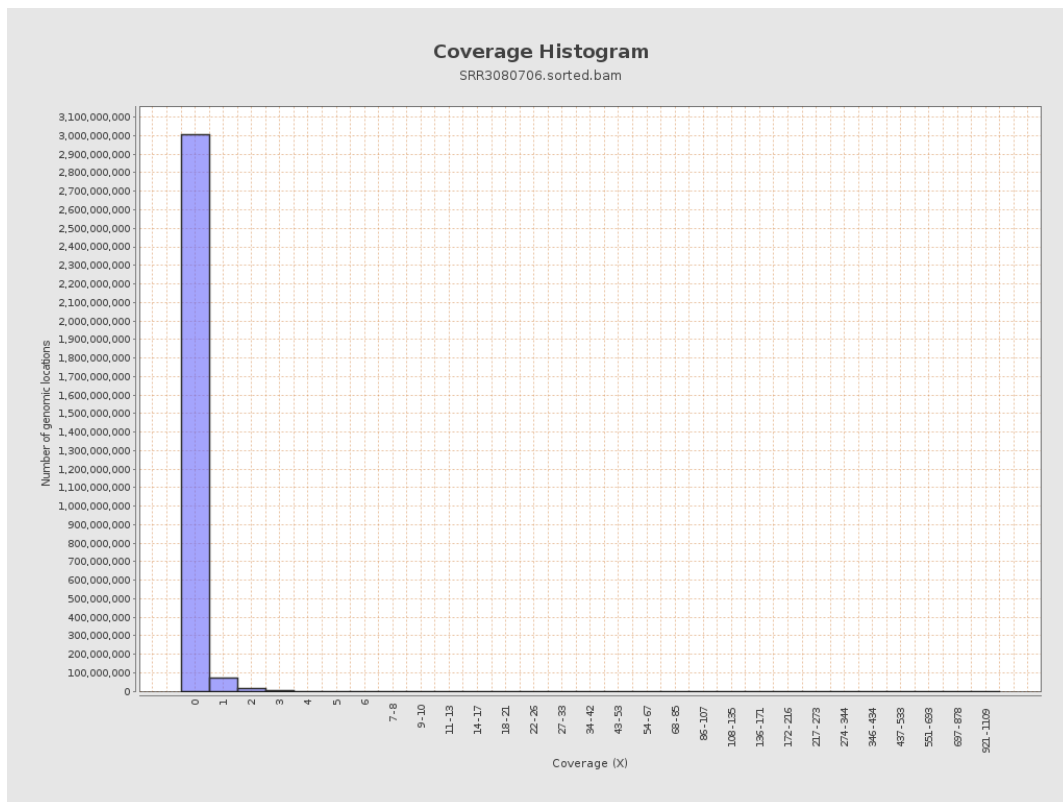
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9165023	0.0368	0.508
chr2	243199373	10190227	0.0419	0.3485
chr3	198022430	8193107	0.0414	0.2492
chr4	191154276	8070434	0.0422	0.2635
chr5	180915260	6709705	0.0371	0.2372
chr6	171115067	6334737	0.037	0.2464
chr7	159138663	6794157	0.0427	0.4968

chr8	146364022	6317012	0.0432	0.7073
chr9	141213431	4003464	0.0284	0.2657
chr10	135534747	5346508	0.0394	0.2985
chr11	135006516	5393612	0.04	0.2816
chr12	133851895	5263976	0.0393	0.2448
chr13	115169878	3684905	0.032	0.2198
chr14	107349540	3597972	0.0335	0.2347
chr15	102531392	3237643	0.0316	0.2192
chr16	90354753	3178694	0.0352	0.2398
chr17	81195210	2686523	0.0331	0.2331
chr18	78077248	3109603	0.0398	0.4295
chr19	59128983	1989406	0.0336	0.3583
chr20	63025520	2363234	0.0375	0.2395
chr21	48129895	1571277	0.0326	0.2323
chr22	51304566	1237884	0.0241	0.1871
chrMT	16571	44474	2.6838	2.327
chrX	155270560	7243725	0.0467	0.278
chrY	59373566	305608	0.0051	0.13

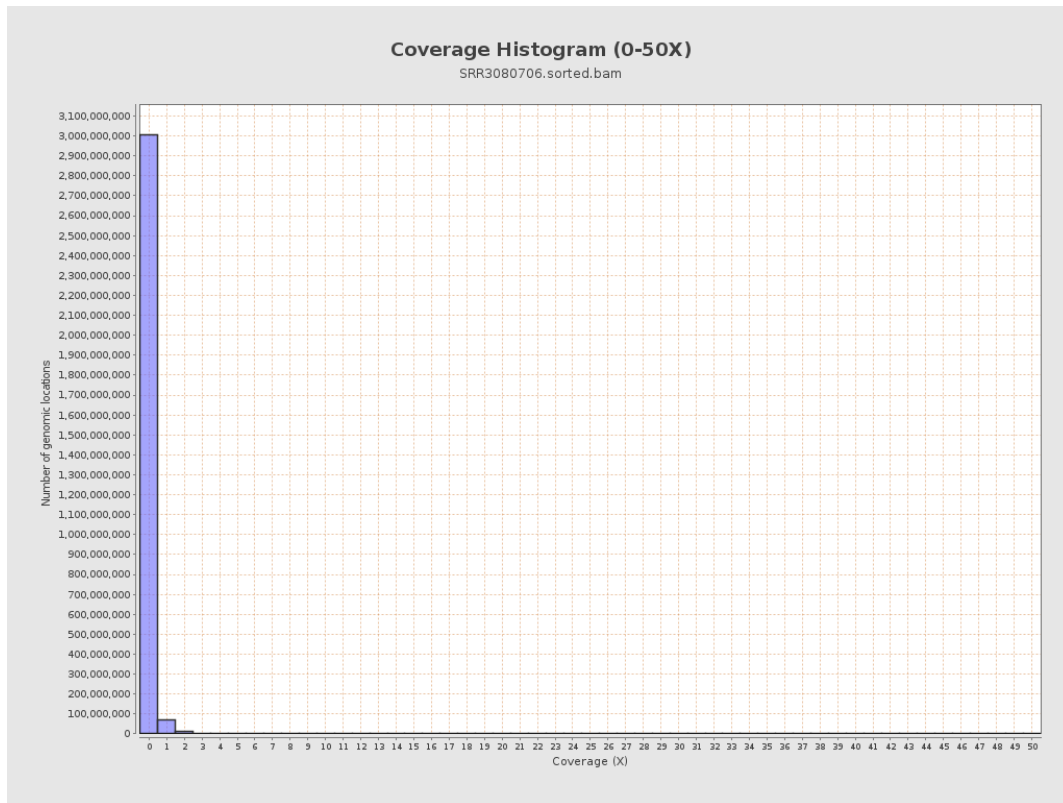
3. Results : Coverage across reference



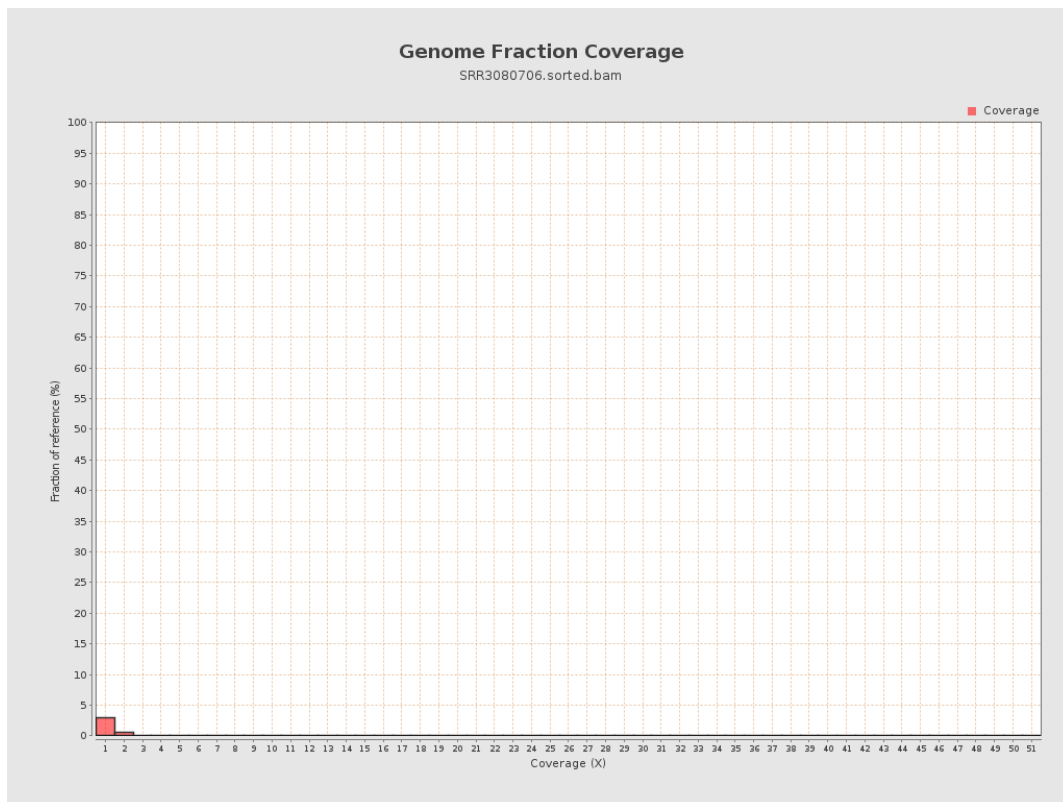
4. Results : Coverage Histogram



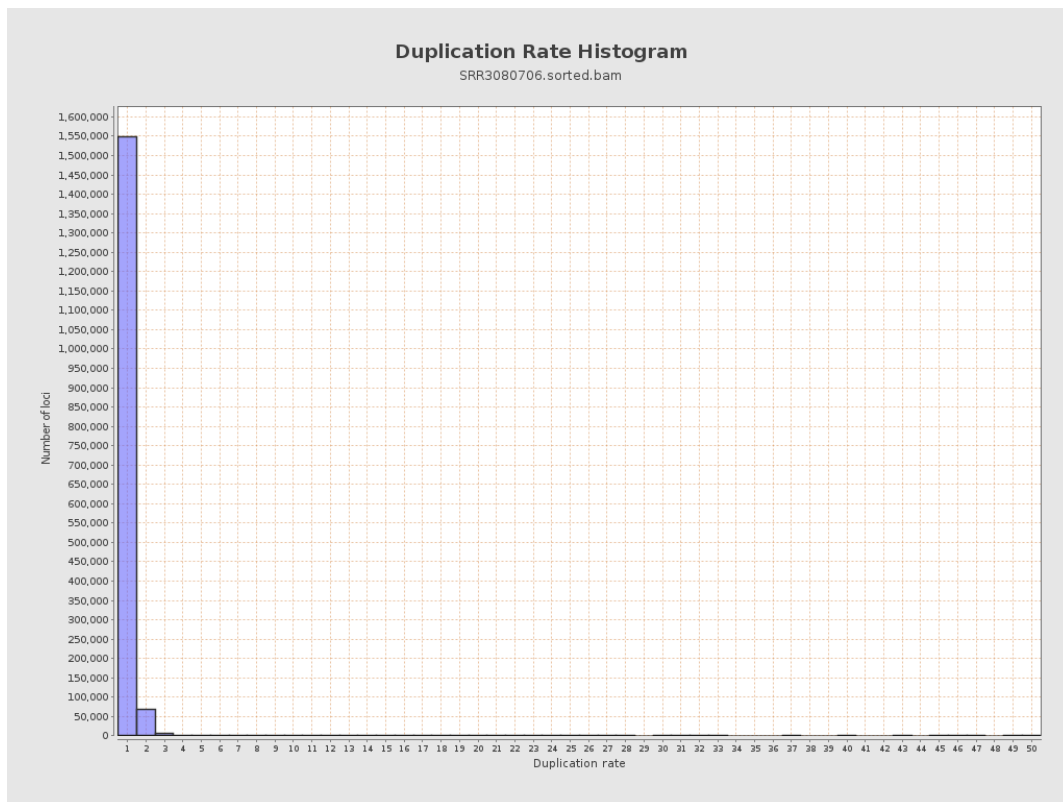
5. Results : Coverage Histogram (0-50X)



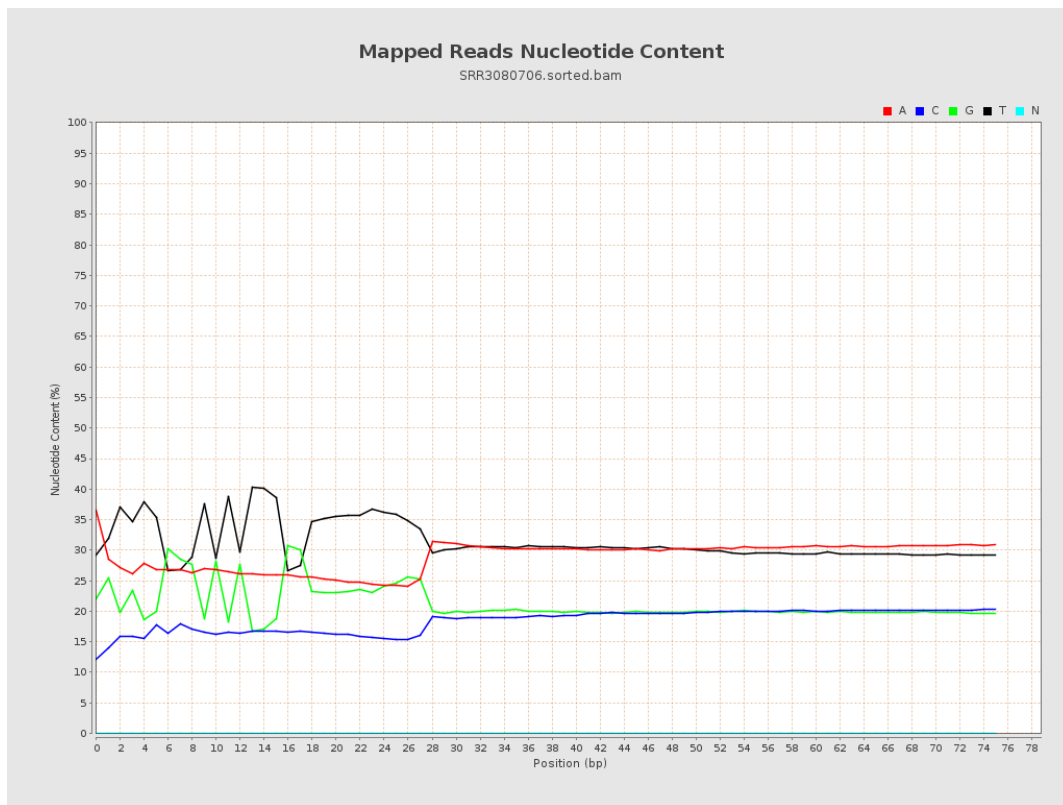
6. Results : Genome Fraction Coverage



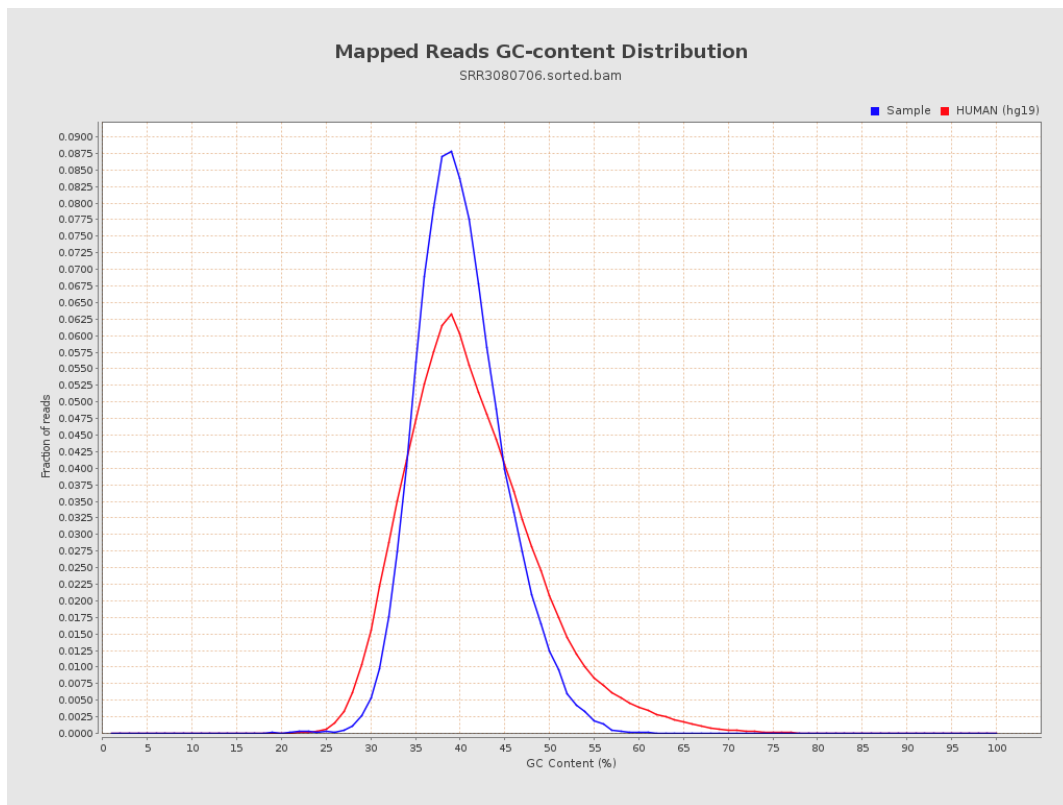
7. Results : Duplication Rate Histogram



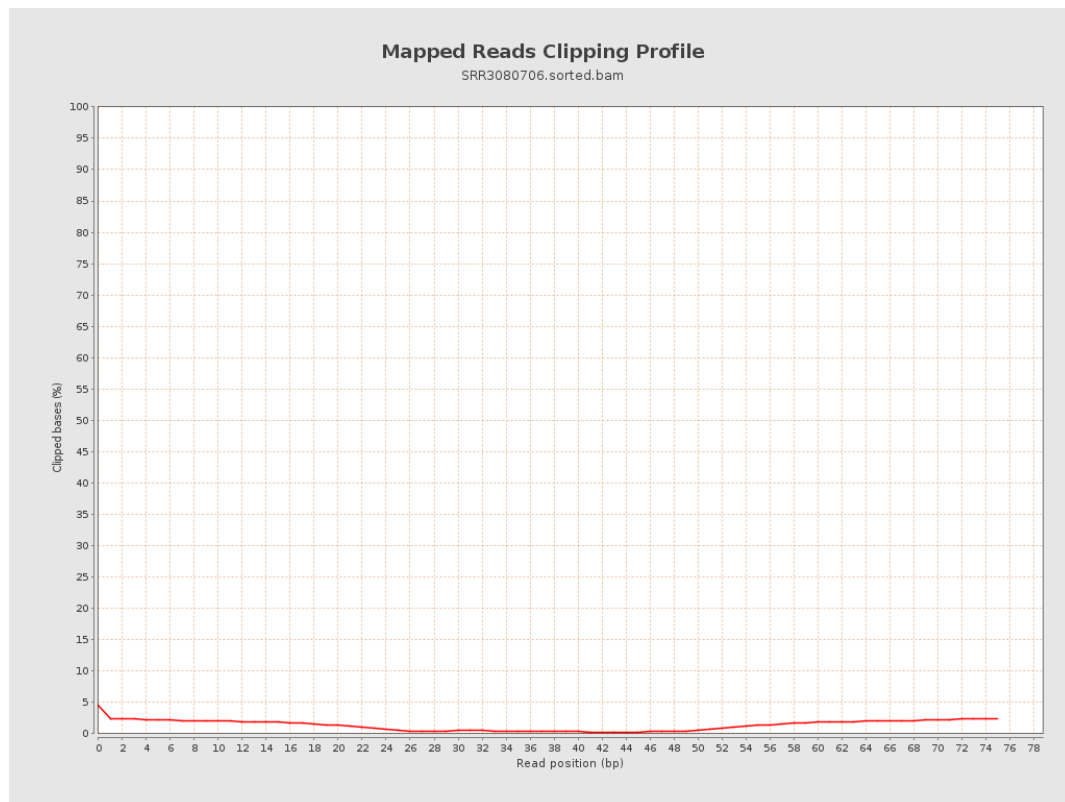
8. Results : Mapped Reads Nucleotide Content



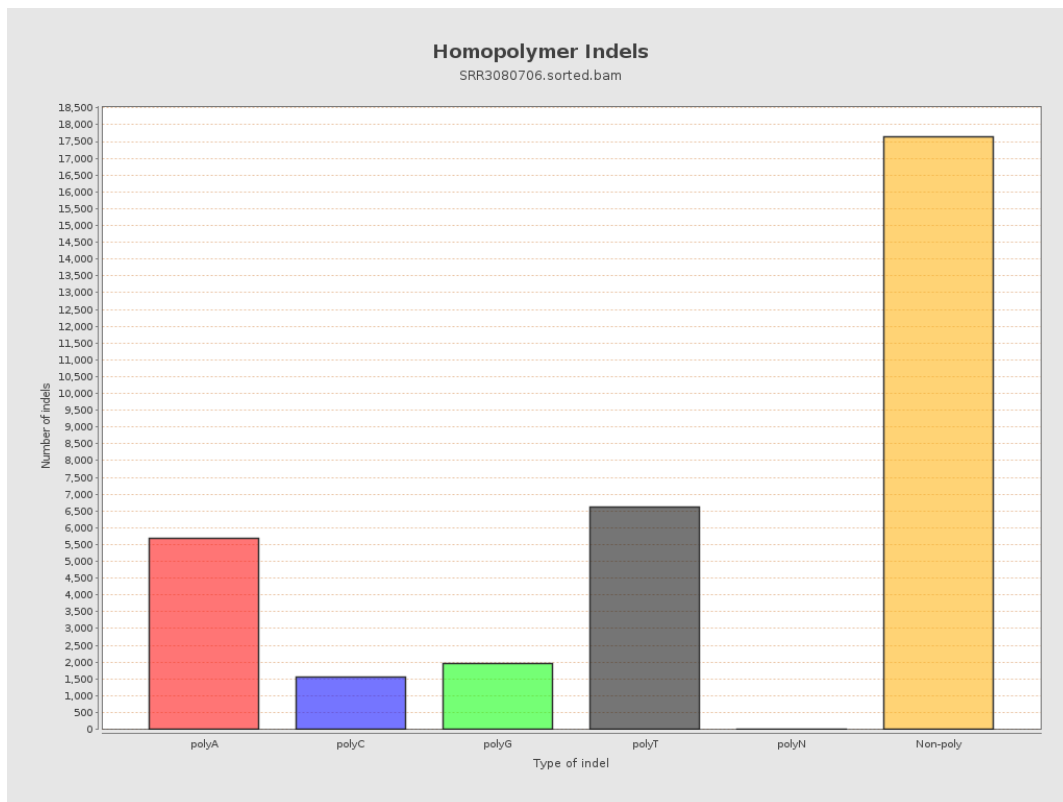
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

