

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 11:33:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10251066.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_SRR10251066 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10251066.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 11:33:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10251066.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,361,170
Mapped reads	4,208,747 / 96.5%
Unmapped reads	152,423 / 3.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	35,435 / 0.81%
Read min/max/mean length	30 / 80 / 80.29
Duplicated reads (estimated)	907,025 / 20.8%
Duplication rate	19.12%
Clipped reads	594,971 / 13.64%

2.2. ACGT Content

Number/percentage of A's	94,678,721 / 29.03%
Number/percentage of C's	65,535,996 / 20.09%
Number/percentage of T's	96,098,176 / 29.46%
Number/percentage of G's	69,857,446 / 21.42%
Number/percentage of N's	2,977 / 0%
GC Percentage	41.51%

2.3. Coverage

Mean	0.1054

Standard Deviation	0.9879
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2.4. Mapping Quality

Mean Mapping Quality	48.15
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2.5. Mismatches and indels

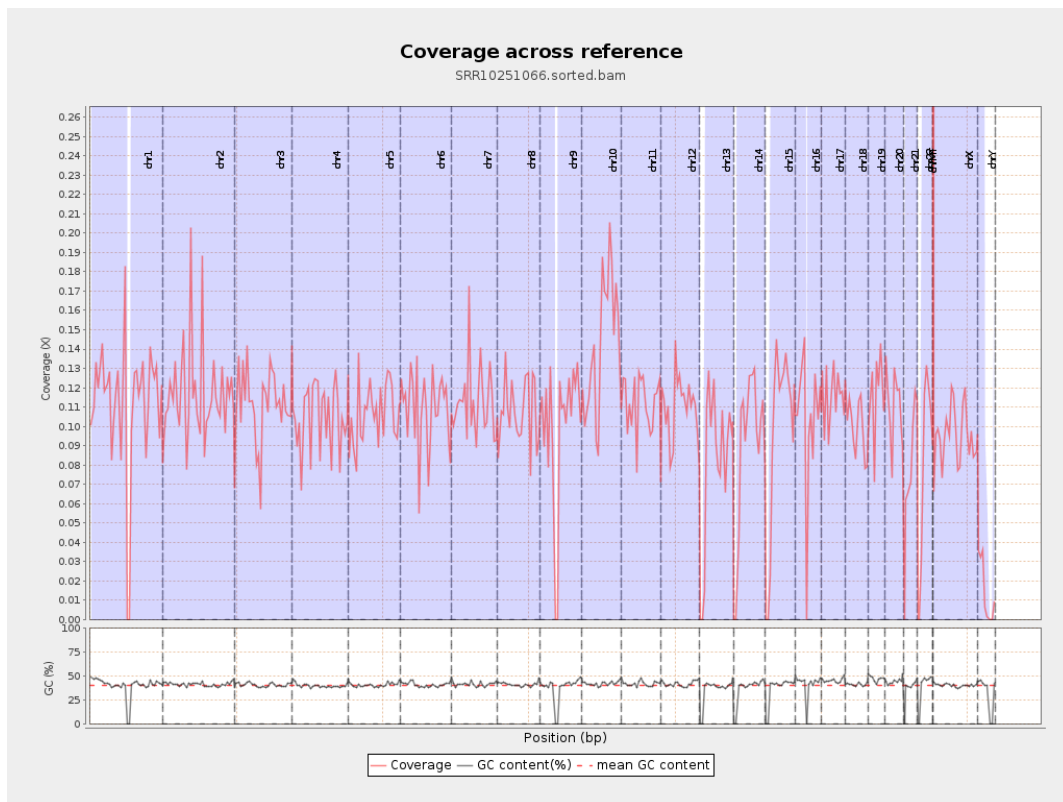
General error rate	0.61%
Mismatches	1,902,608
Insertions	39,584
Mapped reads with at least one insertion	0.92%
Deletions	121,810
Mapped reads with at least one deletion	2.85%
Homopolymer indels	44.82%

2.6. Chromosome stats

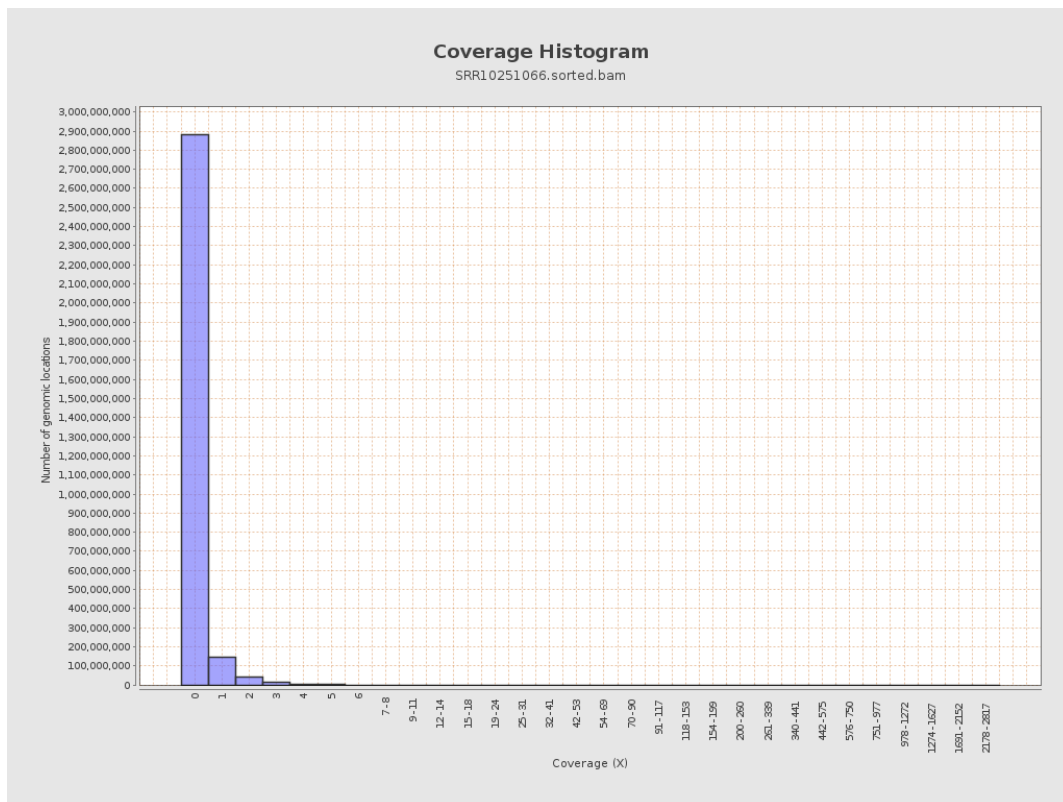
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	27944399	0.1121	1.9839
chr2	243199373	28581786	0.1175	1.3302
chr3	198022430	22006535	0.1111	0.471
chr4	191154276	19948870	0.1044	0.5248
chr5	180915260	19341397	0.1069	0.4777
chr6	171115067	18582738	0.1086	0.5923
chr7	159138663	17907766	0.1125	1.422

chr8	146364022	15673865	0.1071	0.6736
chr9	141213431	14040271	0.0994	1.0777
chr10	135534747	19280800	0.1423	1.0472
chr11	135006516	15065886	0.1116	0.6418
chr12	133851895	14877979	0.1112	0.486
chr13	115169878	9427248	0.0819	0.4017
chr14	107349540	9748718	0.0908	0.6261
chr15	102531392	9761924	0.0952	0.4366
chr16	90354753	9337839	0.1033	0.8623
chr17	81195210	9431480	0.1162	0.5768
chr18	78077248	7822441	0.1002	1.1889
chr19	59128983	6846276	0.1158	1.8588
chr20	63025520	6926779	0.1099	0.5148
chr21	48129895	3792899	0.0788	0.4322
chr22	51304566	4124001	0.0804	0.4421
chrMT	16571	303943	18.3419	10.8792
chrX	155270560	14777186	0.0952	0.5063
chrY	59373566	837295	0.0141	0.9262

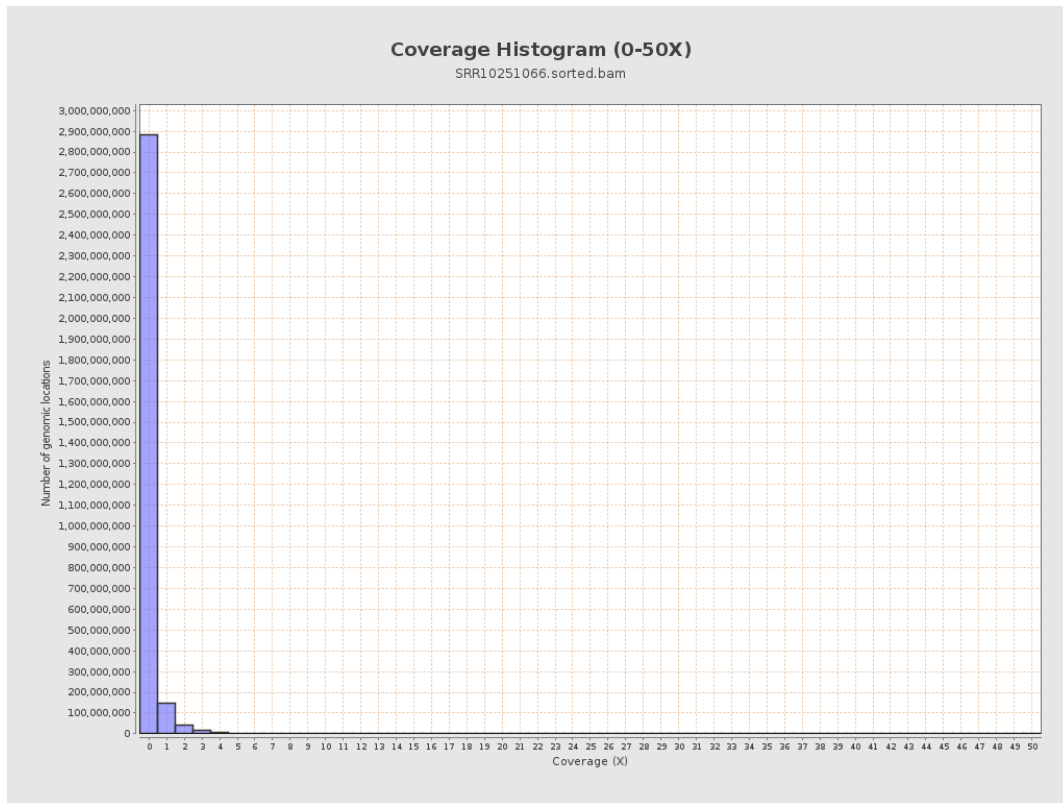
3. Results : Coverage across reference



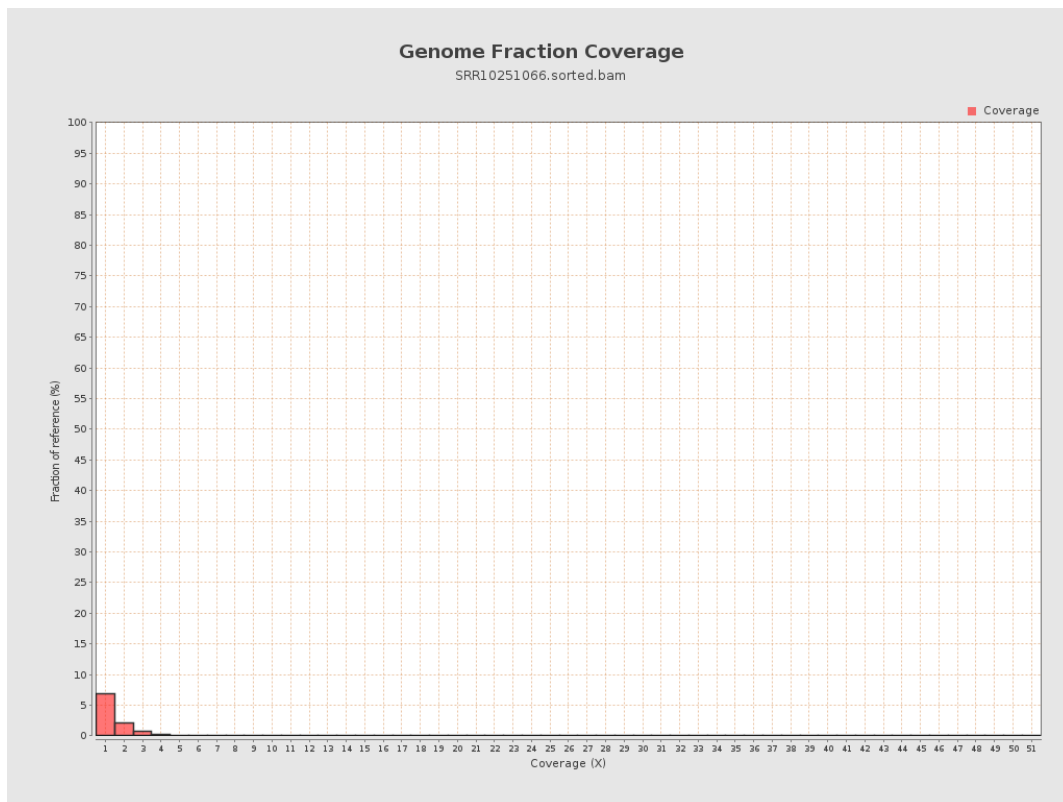
4. Results : Coverage Histogram



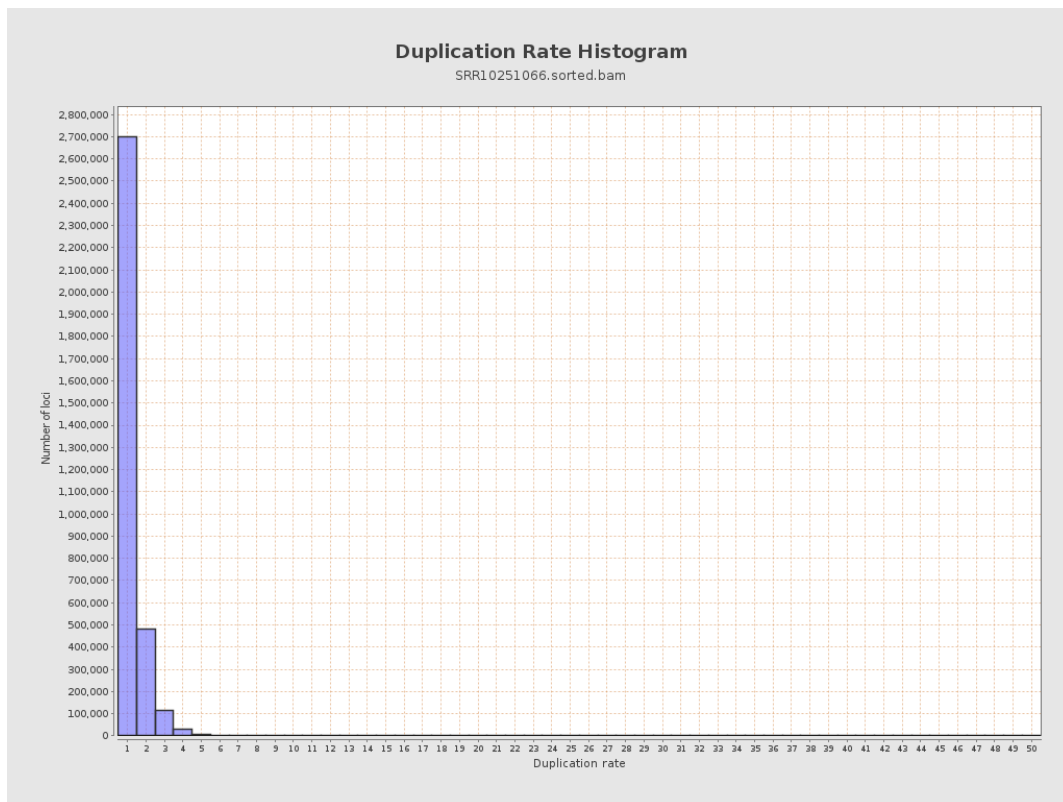
5. Results : Coverage Histogram (0-50X)



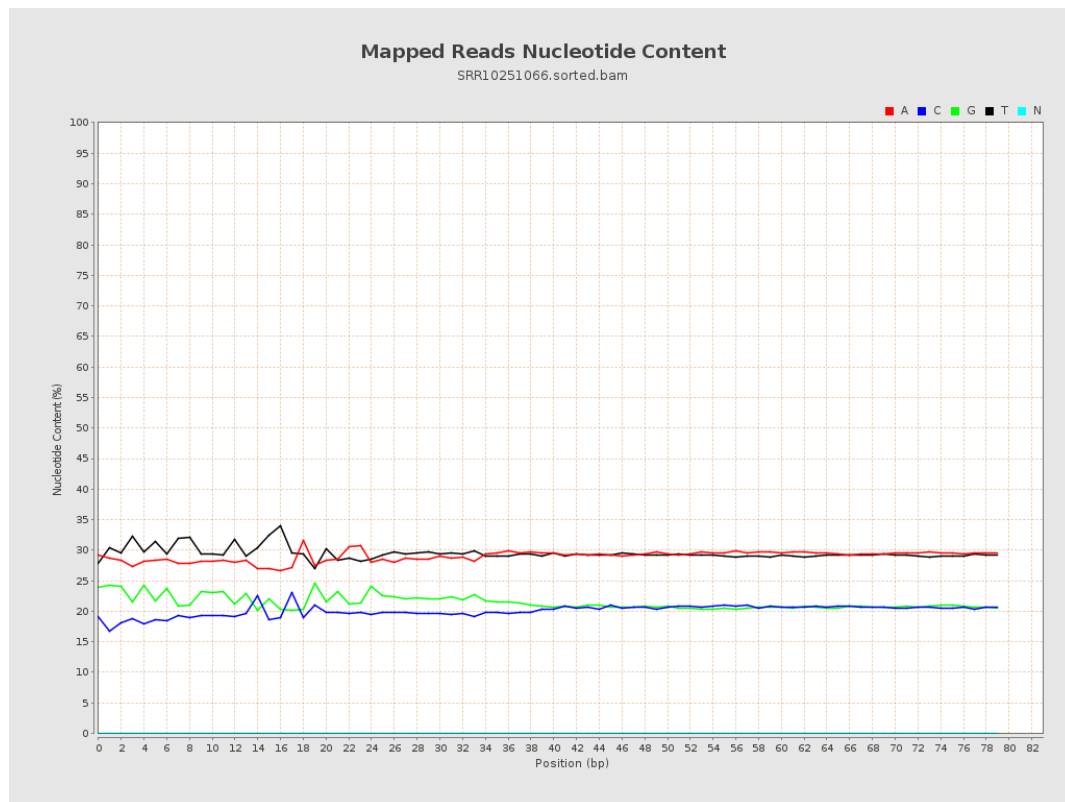
6. Results : Genome Fraction Coverage



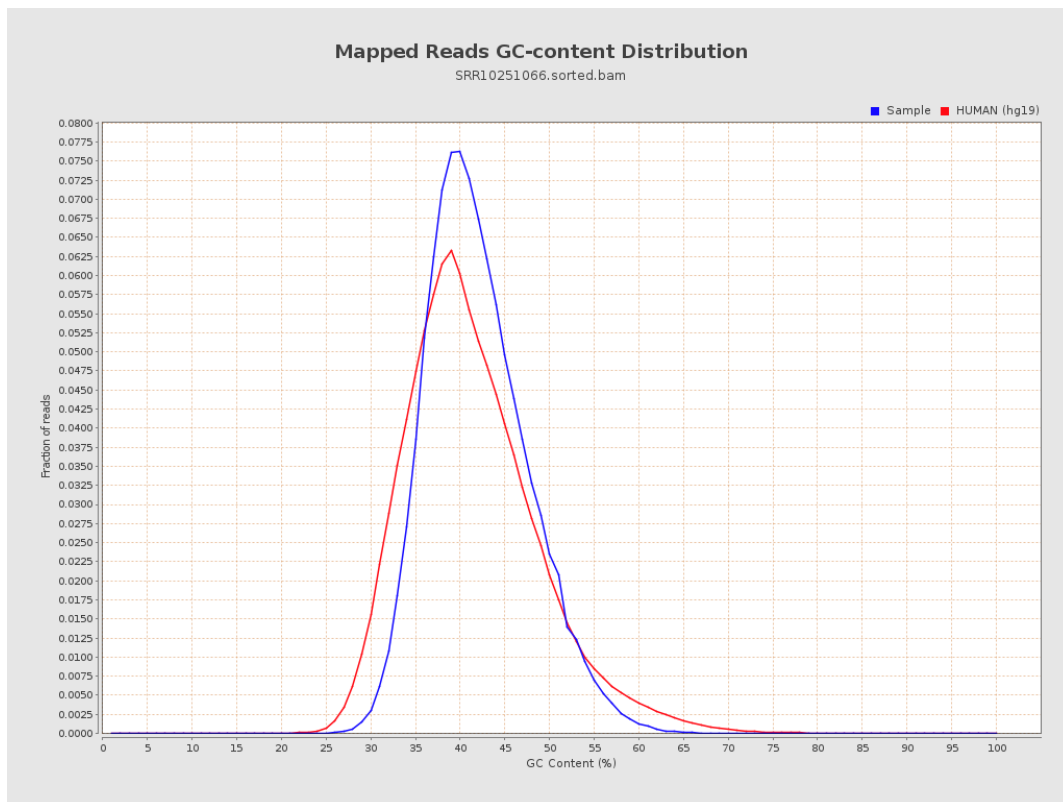
7. Results : Duplication Rate Histogram



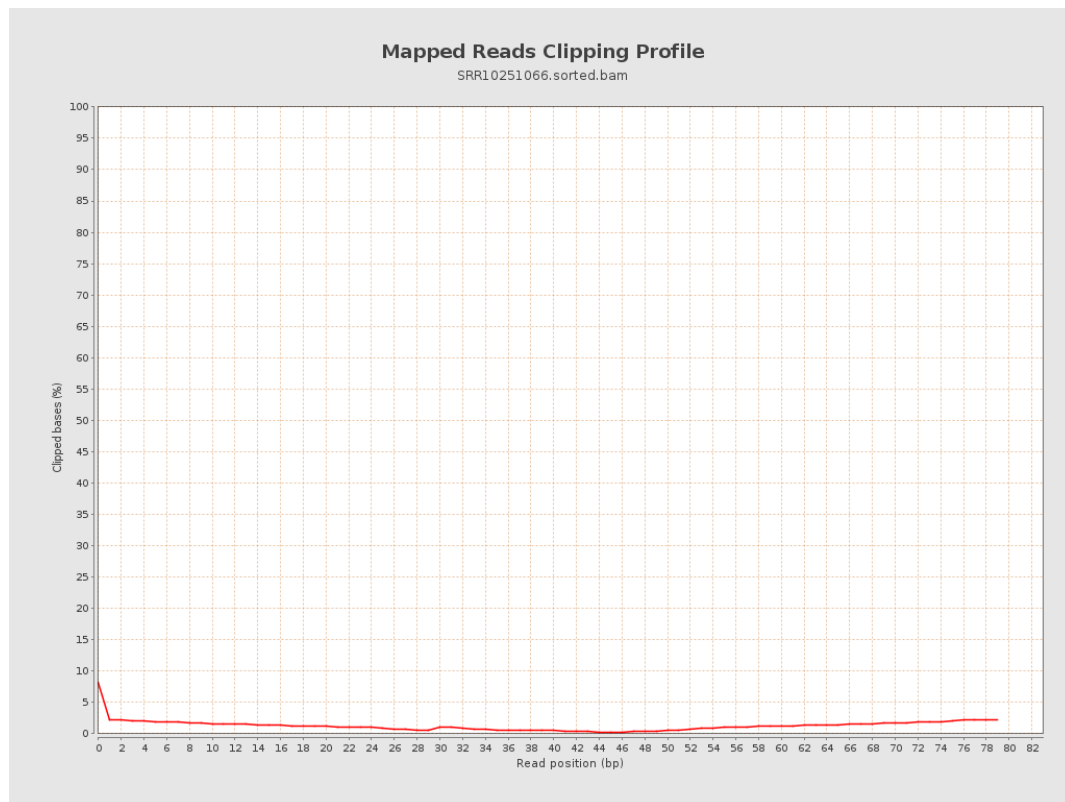
8. Results : Mapped Reads Nucleotide Content



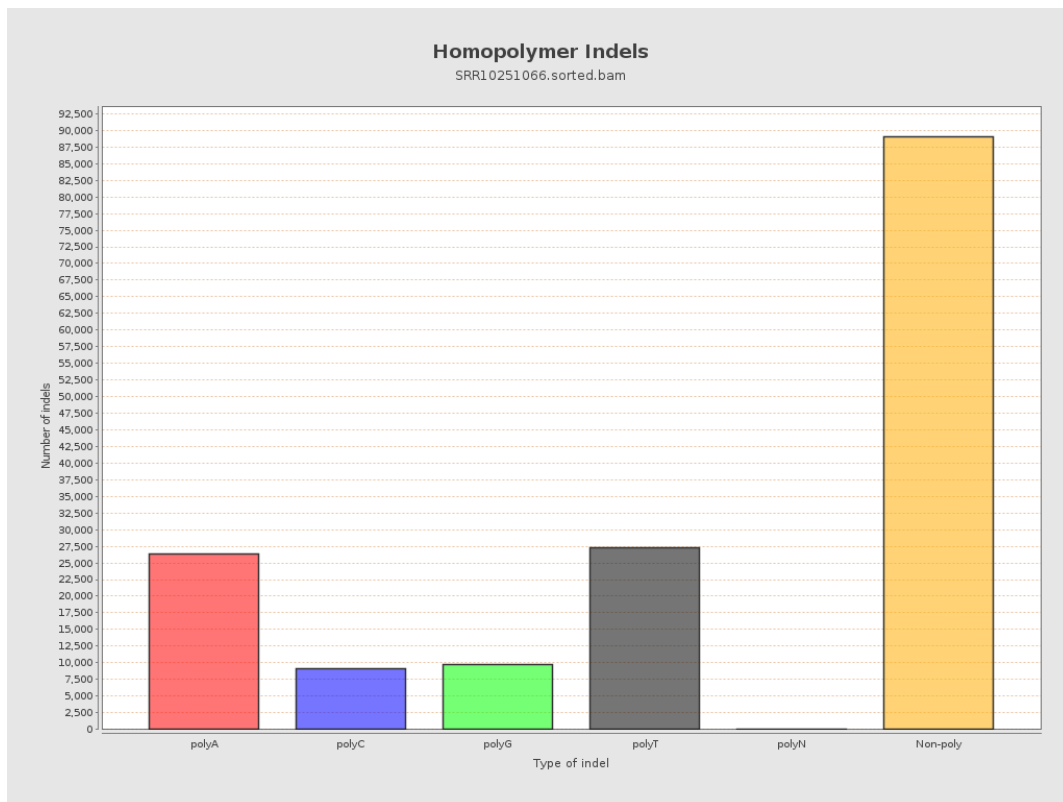
9. Results : Mapped Reads GC-content Distribution



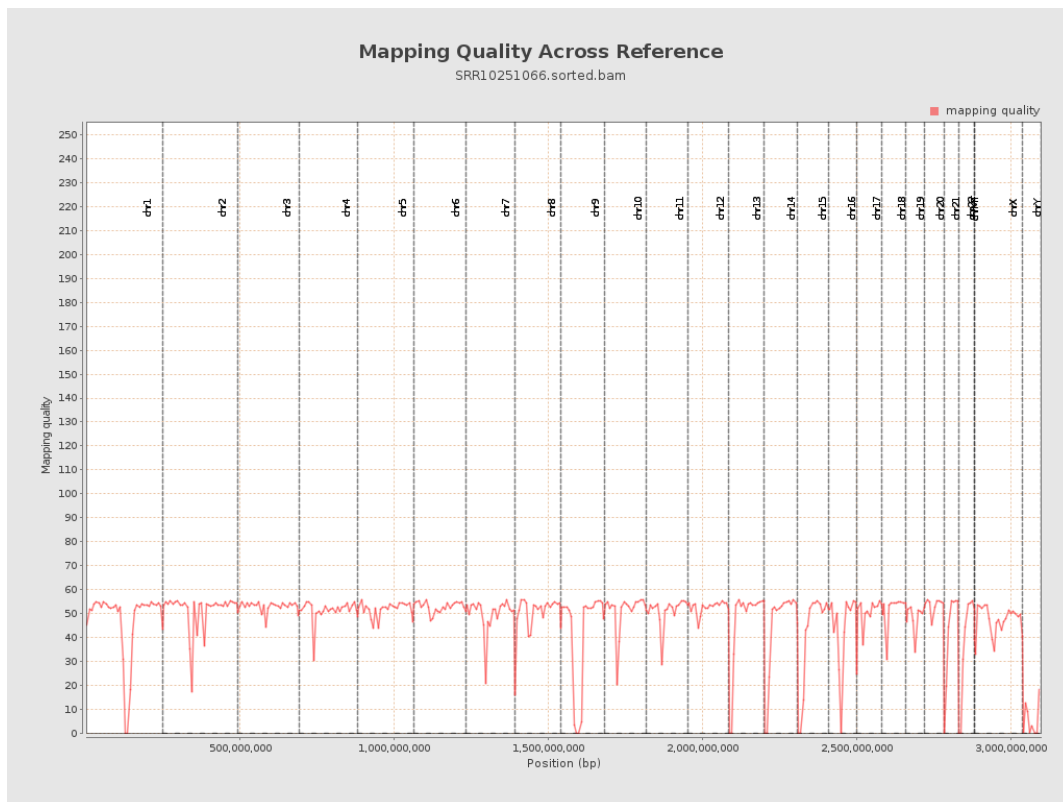
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

