

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:25:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708626.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_SRR1708626 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708626.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:25:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1708626.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,148,117
Mapped reads	2,328,637 / 73.97%
Unmapped reads	819,480 / 26.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	779 / 0.02%
Read min/max/mean length	30 / 51 / 51.01
Duplicated reads (estimated)	82,738 / 2.63%
Duplication rate	2.46%
Clipped reads	358,829 / 11.4%

2.2. ACGT Content

Number/percentage of A's	33,402,480 / 29.44%
Number/percentage of C's	21,384,633 / 18.85%
Number/percentage of T's	35,806,376 / 31.56%
Number/percentage of G's	22,848,525 / 20.14%
Number/percentage of N's	9,750 / 0.01%
GC Percentage	38.99%

2.3. Coverage

Mean	0.0367

Standard Deviation	0.3785
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2.4. Mapping Quality

Mean Mapping Quality	43.76
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2.5. Mismatches and indels

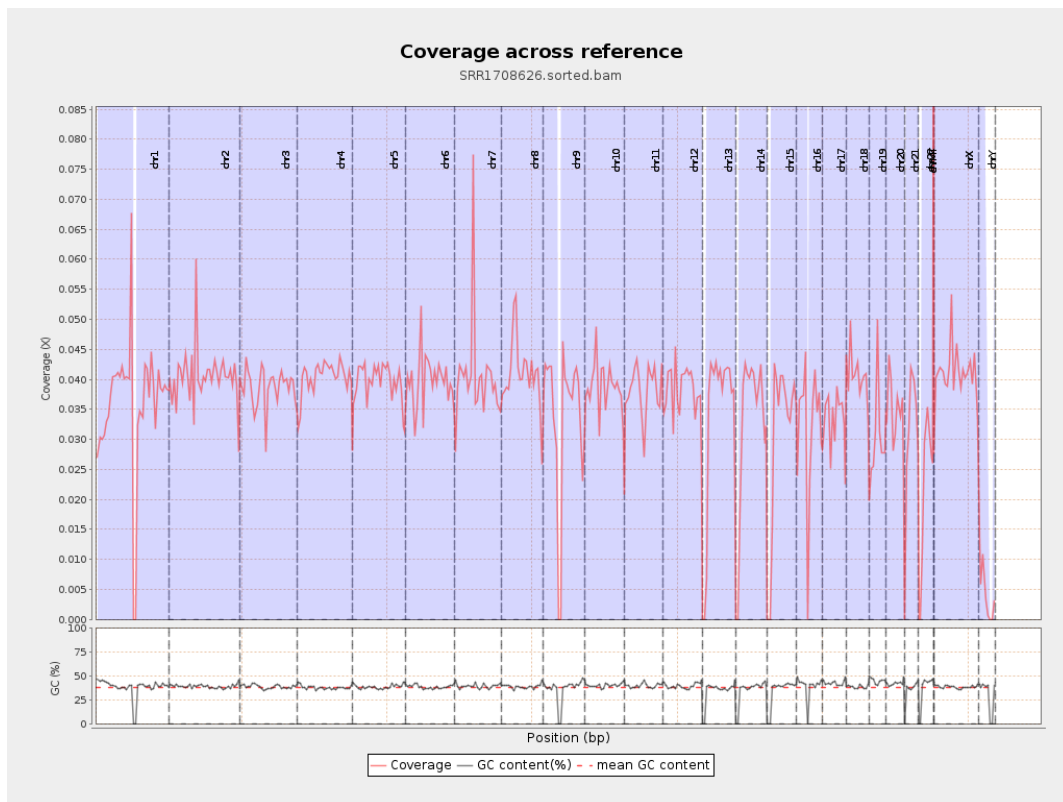
General error rate	0.64%
Mismatches	718,062
Insertions	5,288
Mapped reads with at least one insertion	0.23%
Deletions	13,619
Mapped reads with at least one deletion	0.58%
Homopolymer indels	48.22%

2.6. Chromosome stats

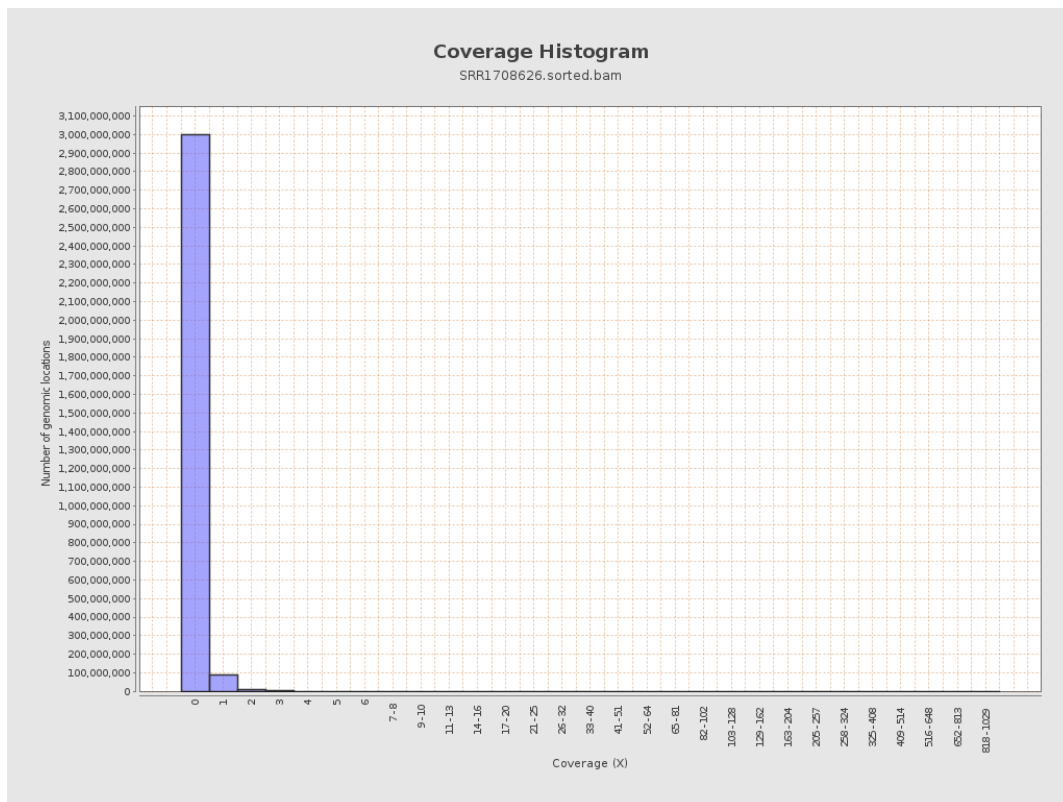
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8958763	0.0359	0.7019
chr2	243199373	9852511	0.0405	0.3713
chr3	198022430	7672391	0.0387	0.2244
chr4	191154276	7730728	0.0404	0.2315
chr5	180915260	7189323	0.0397	0.2292
chr6	171115067	6792431	0.0397	0.2814
chr7	159138663	6487352	0.0408	0.562

chr8	146364022	5986953	0.0409	0.6177
chr9	141213431	4778541	0.0338	0.3134
chr10	135534747	5273308	0.0389	0.2992
chr11	135006516	5130423	0.038	0.3347
chr12	133851895	5104746	0.0381	0.2313
chr13	115169878	3861486	0.0335	0.2089
chr14	107349540	3487490	0.0325	0.2222
chr15	102531392	3159546	0.0308	0.1989
chr16	90354753	2908058	0.0322	0.2211
chr17	81195210	2686400	0.0331	0.2549
chr18	78077248	3183879	0.0408	0.6323
chr19	59128983	1823364	0.0308	0.5207
chr20	63025520	2205016	0.035	0.22
chr21	48129895	1491095	0.031	0.217
chr22	51304566	1090340	0.0213	0.1627
chrMT	16571	2763	0.1667	0.4847
chrX	155270560	6361428	0.041	0.2661
chrY	59373566	254228	0.0043	0.0883

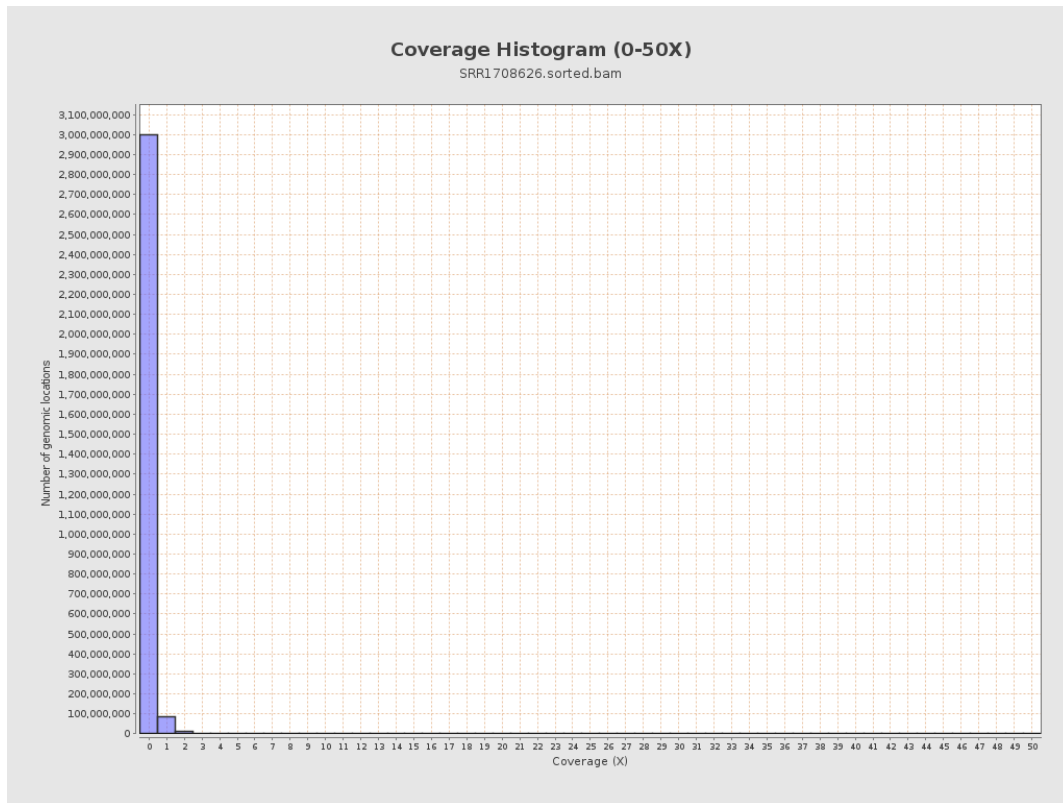
3. Results : Coverage across reference



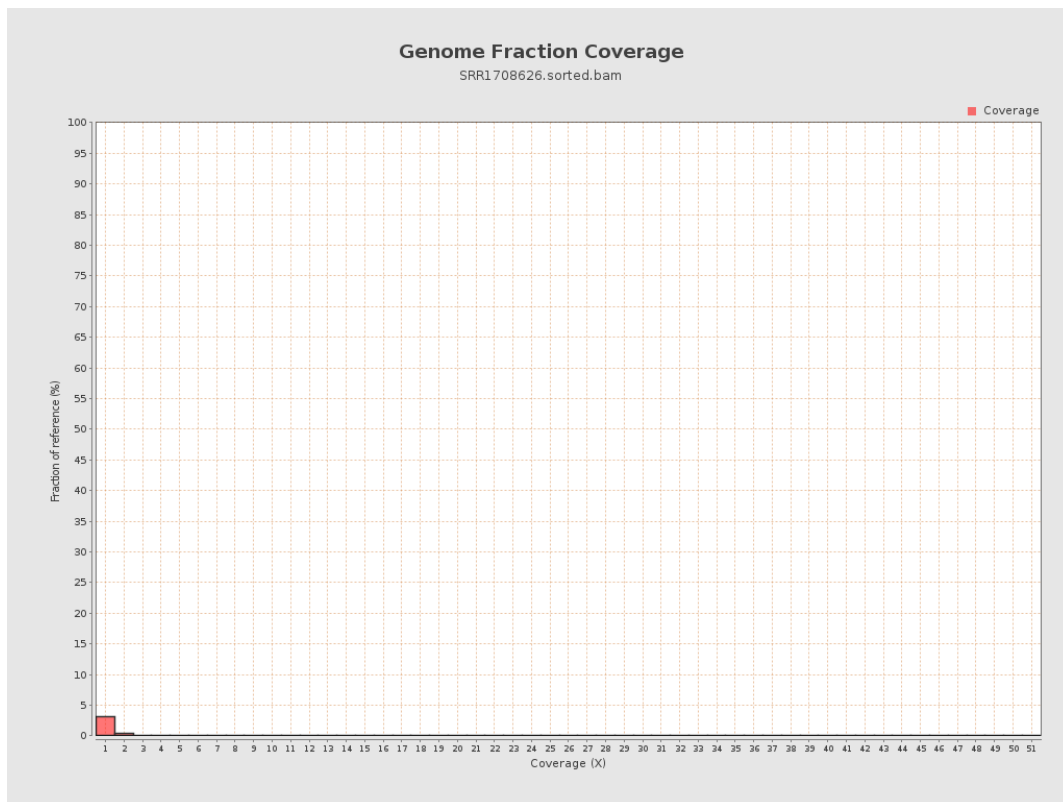
4. Results : Coverage Histogram



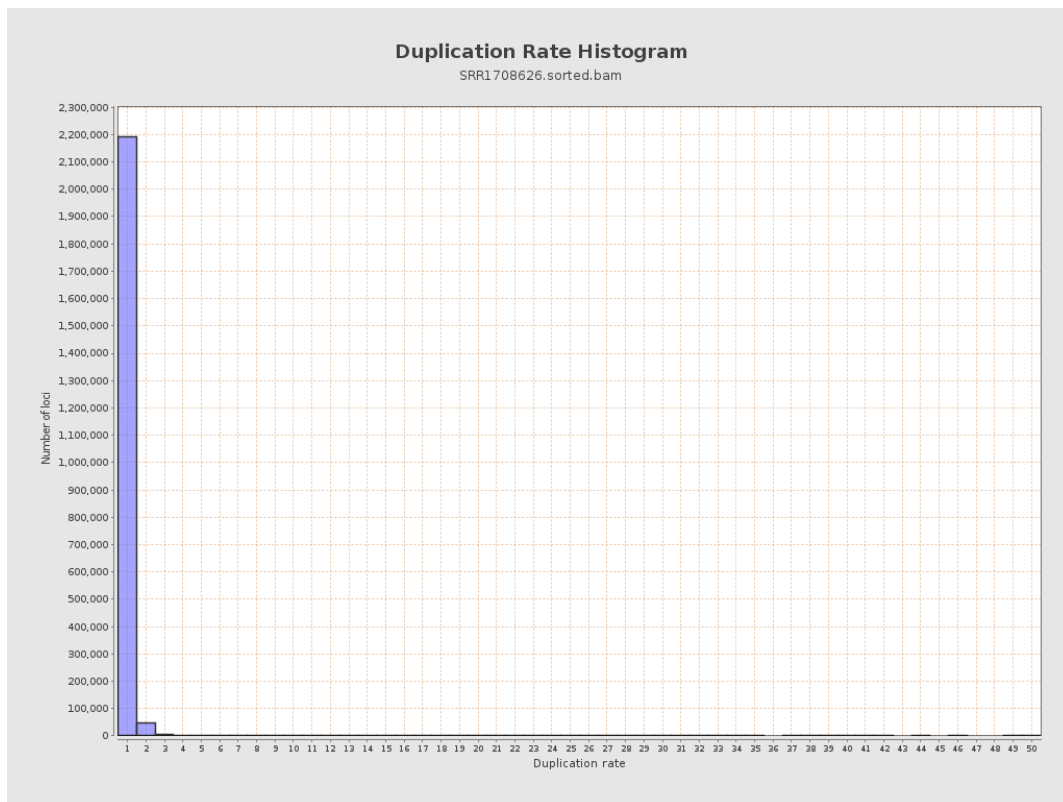
5. Results : Coverage Histogram (0-50X)



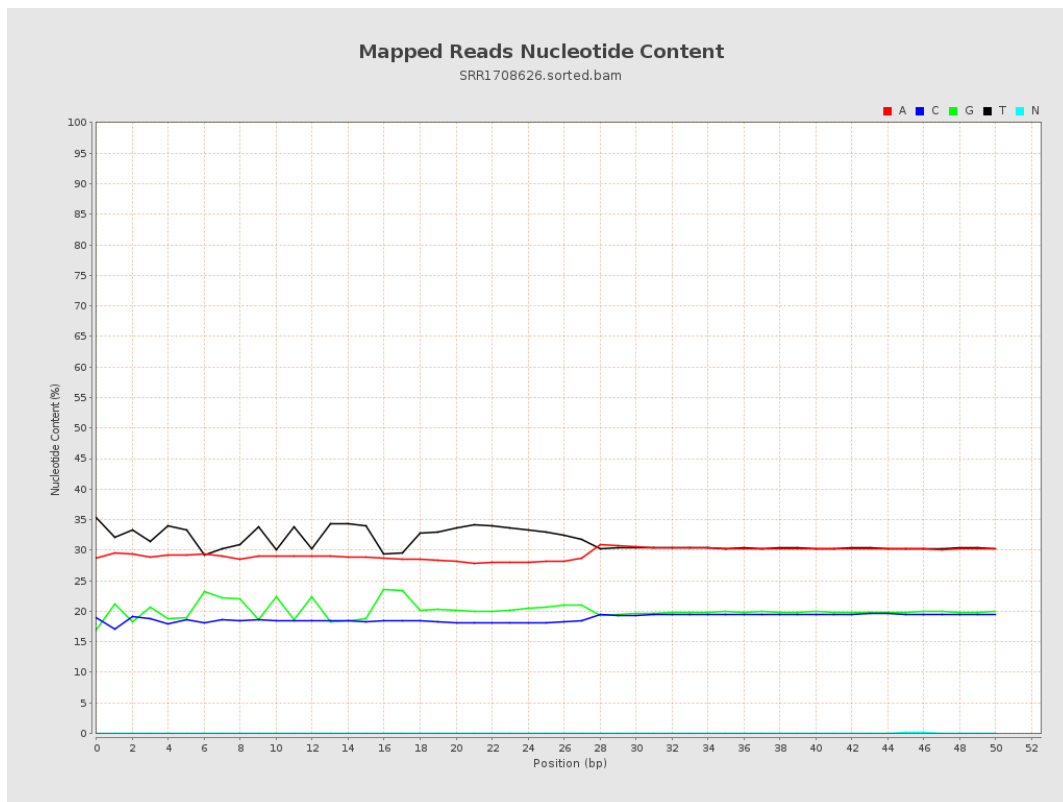
6. Results : Genome Fraction Coverage



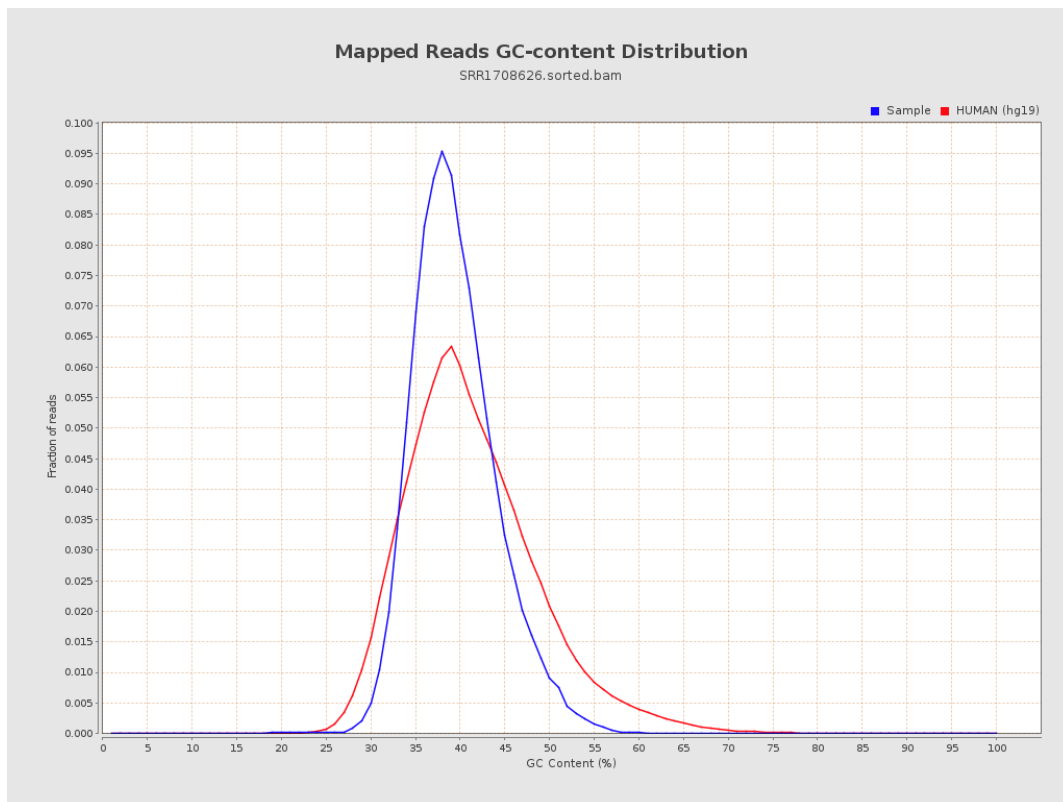
7. Results : Duplication Rate Histogram



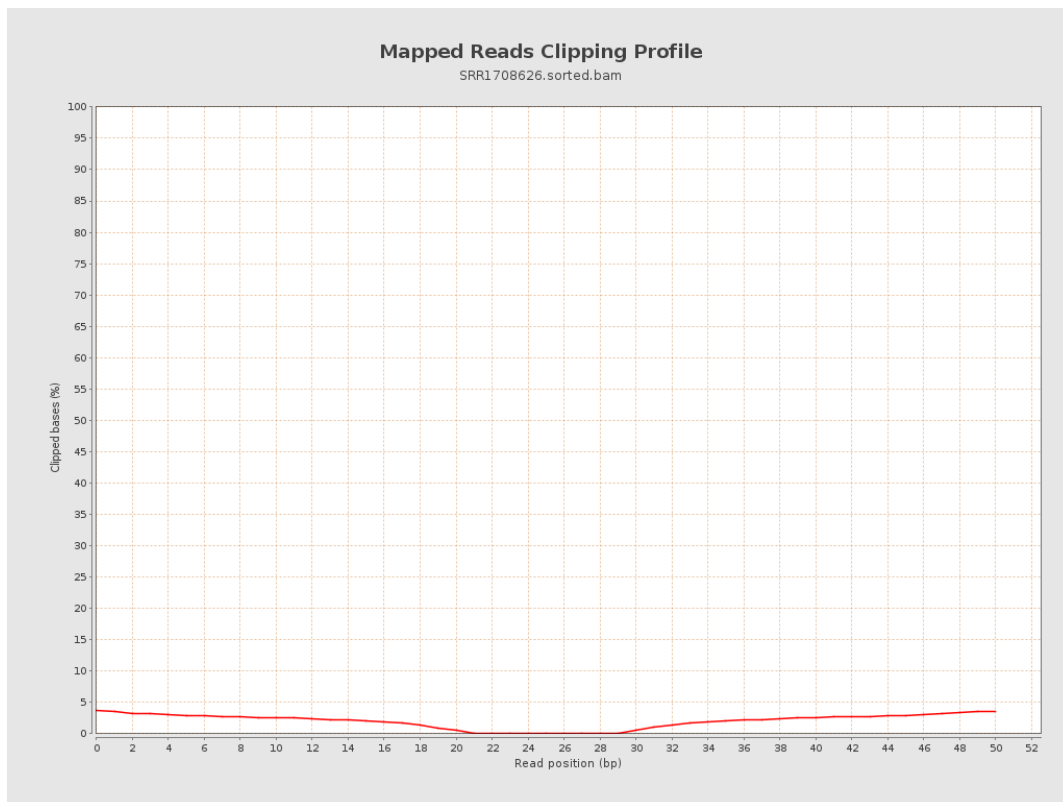
8. Results : Mapped Reads Nucleotide Content



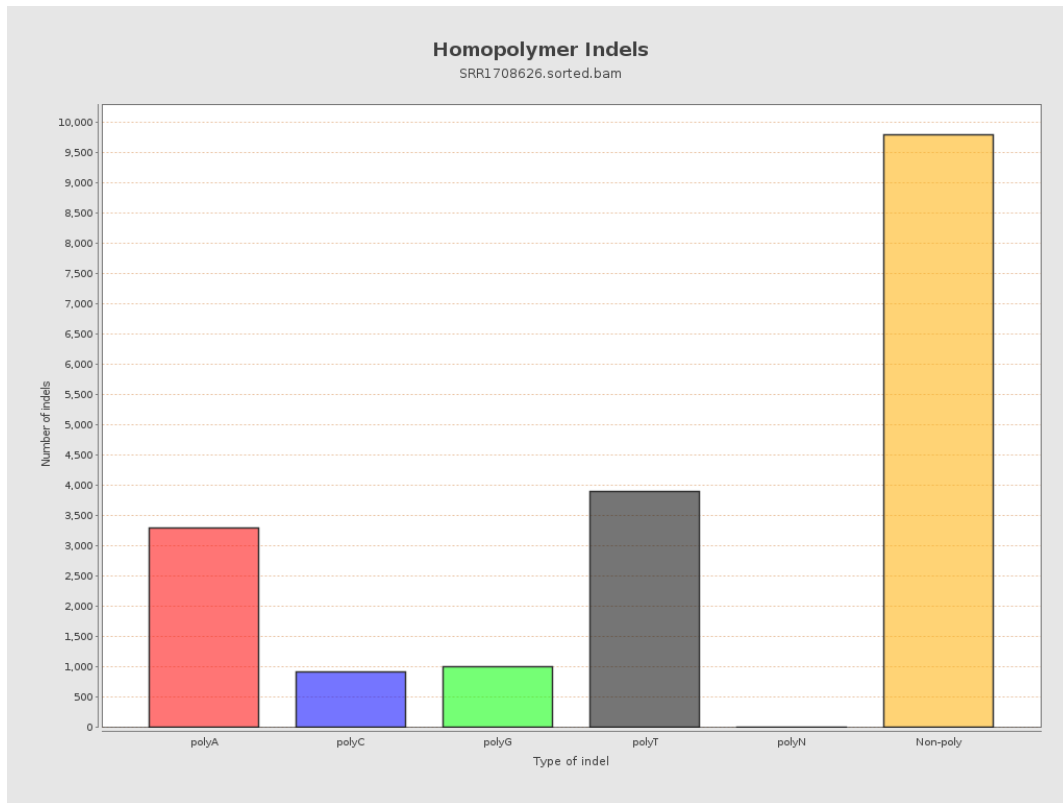
9. Results : Mapped Reads GC-content Distribution



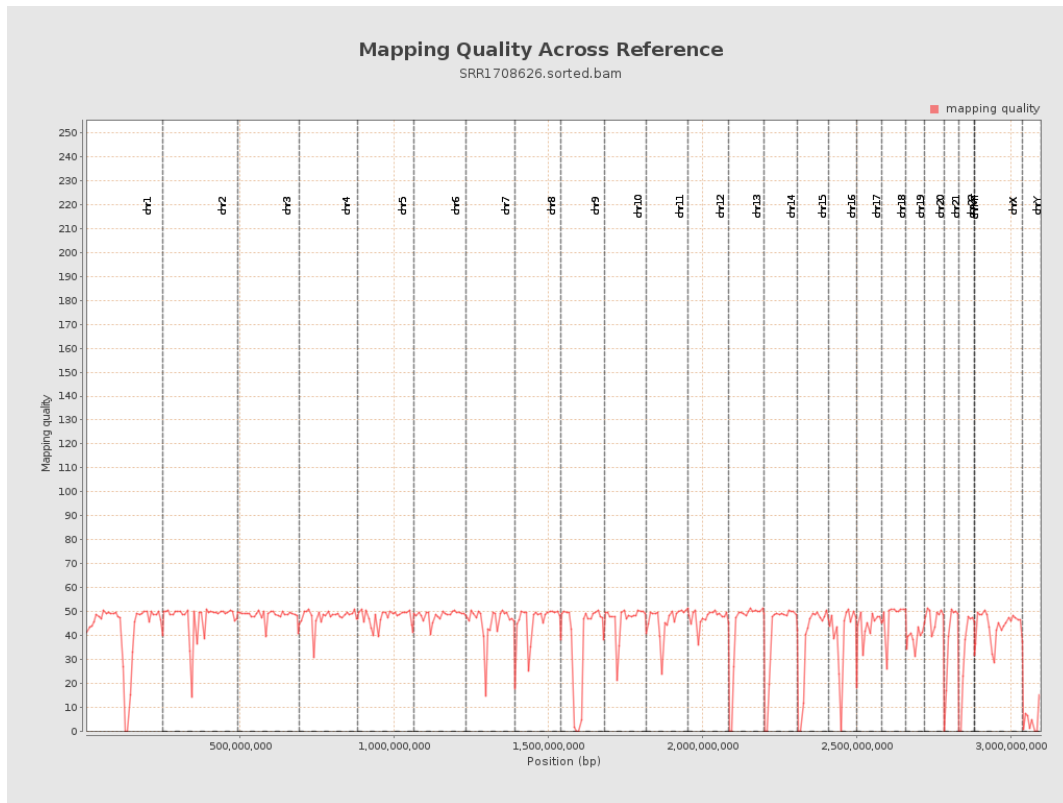
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

