

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 16:56:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006057.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_SRR1006057 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006057_1.fastq.gz SRR1006057_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 16:56:38 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006057.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,626,734
Mapped reads	3,058,584 / 84.33%
Unmapped reads	568,150 / 15.67%
Mapped paired reads	3,058,584 / 84.33%
Mapped reads, first in pair	1,555,356 / 42.89%
Mapped reads, second in pair	1,503,228 / 41.45%
Mapped reads, both in pair	2,812,202 / 77.54%
Mapped reads, singletons	246,382 / 6.79%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	122,227 / 3.37%
Duplication rate	3.71%
Clipped reads	269,820 / 7.44%

2.2. ACGT Content

Number/percentage of A's	30,269,634 / 25.66%
Number/percentage of C's	27,396,701 / 23.22%
Number/percentage of T's	31,369,272 / 26.59%
Number/percentage of G's	28,938,492 / 24.53%
Number/percentage of N's	5,803 / 0%
GC Percentage	47.75%

2.3. Coverage

Mean	0.0381
Standard Deviation	0.2741

2.4. Mapping Quality

Mean Mapping Quality	45.8
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2.5. Insert size

Mean	63,210.7
Standard Deviation	2,428,110.07
P25/Median/P75	64 / 90 / 119

2.6. Mismatches and indels

General error rate	0.47%
Mismatches	552,566
Insertions	4,151
Mapped reads with at least one insertion	0.14%
Deletions	9,898
Mapped reads with at least one deletion	0.32%
Homopolymer indels	43.12%

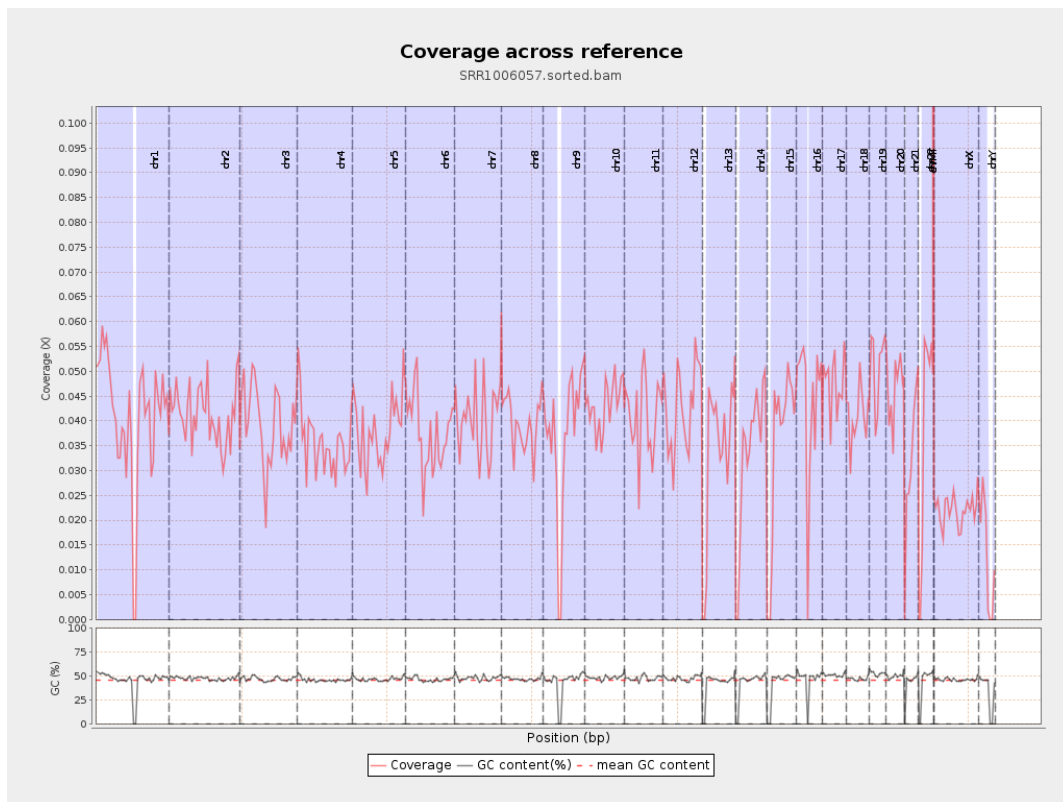
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

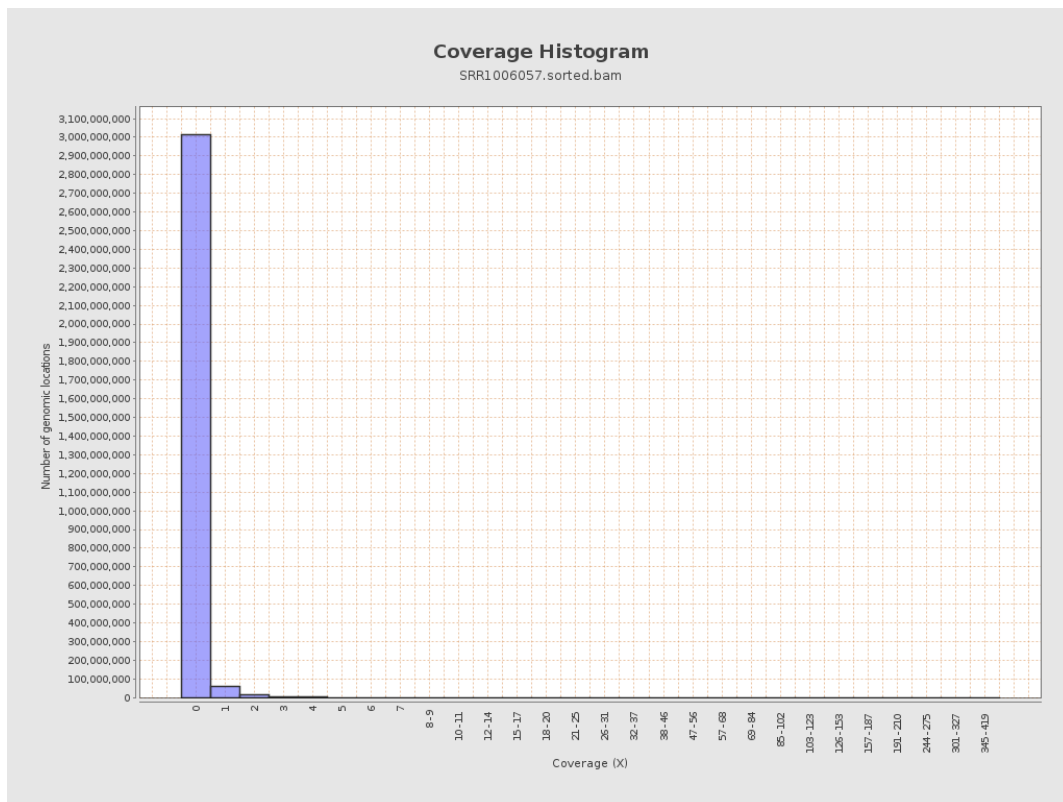
chr1	249250621	10136835	0.0407	0.2813
chr2	243199373	10034490	0.0413	0.3054
chr3	198022430	7758940	0.0392	0.2615
chr4	191154276	6768845	0.0354	0.2558
chr5	180915260	6853099	0.0379	0.258
chr6	171115067	6453368	0.0377	0.2699
chr7	159138663	6343980	0.0399	0.2879
chr8	146364022	5775552	0.0395	0.2785
chr9	141213431	5093802	0.0361	0.2589
chr10	135534747	5835928	0.0431	0.2833
chr11	135006516	5546085	0.0411	0.3407
chr12	133851895	5709910	0.0427	0.2768
chr13	115169878	3846707	0.0334	0.2479
chr14	107349540	3565998	0.0332	0.2462
chr15	102531392	3677621	0.0359	0.2554
chr16	90354753	3958006	0.0438	0.301
chr17	81195210	3897096	0.048	0.3023
chr18	78077248	3194348	0.0409	0.2827
chr19	59128983	2992203	0.0506	0.335
chr20	63025520	2913133	0.0462	0.2913
chr21	48129895	1559222	0.0324	0.255
chr22	51304566	1898720	0.037	0.2812
chrMT	16571	16131	0.9734	1.7855
chrX	155270560	3417797	0.022	0.1949

chrY	59373566	744839	0.0125	0.158
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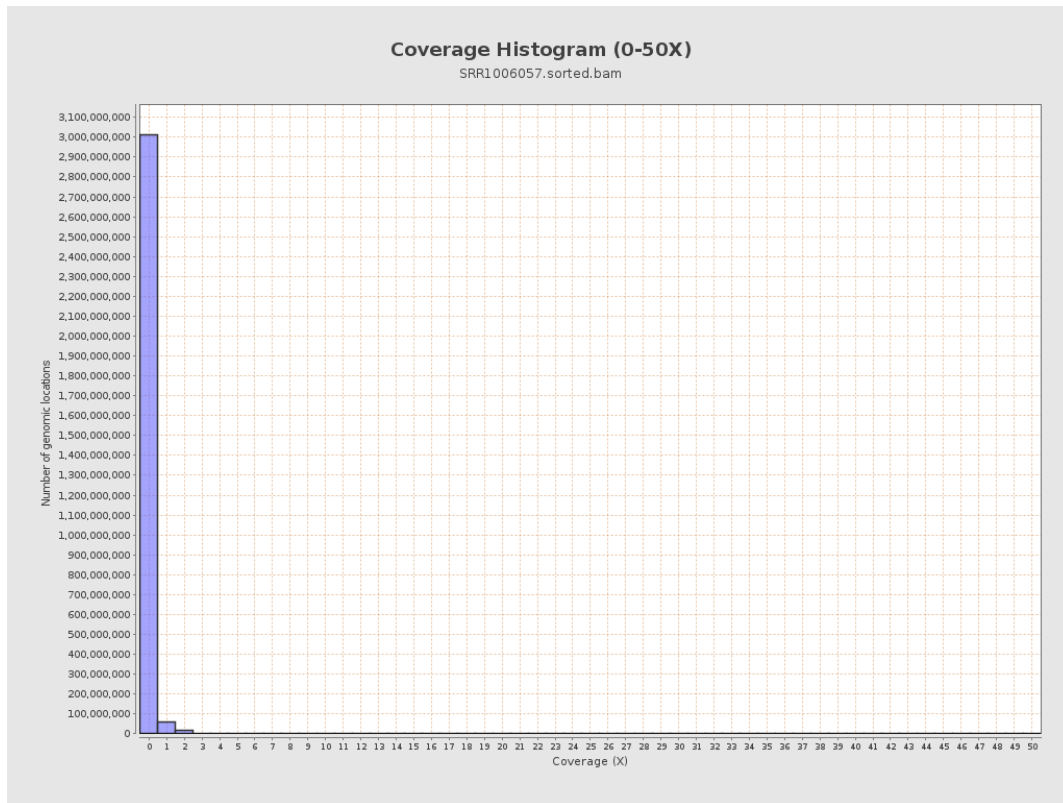
3. Results : Coverage across reference



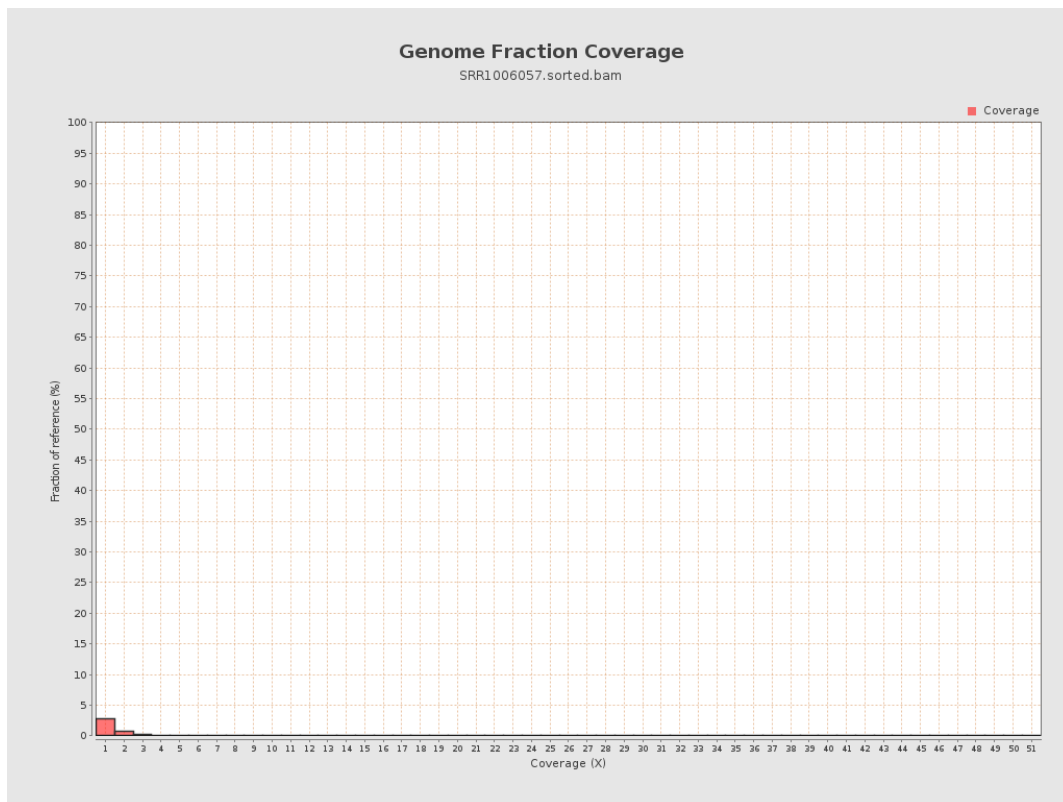
4. Results : Coverage Histogram



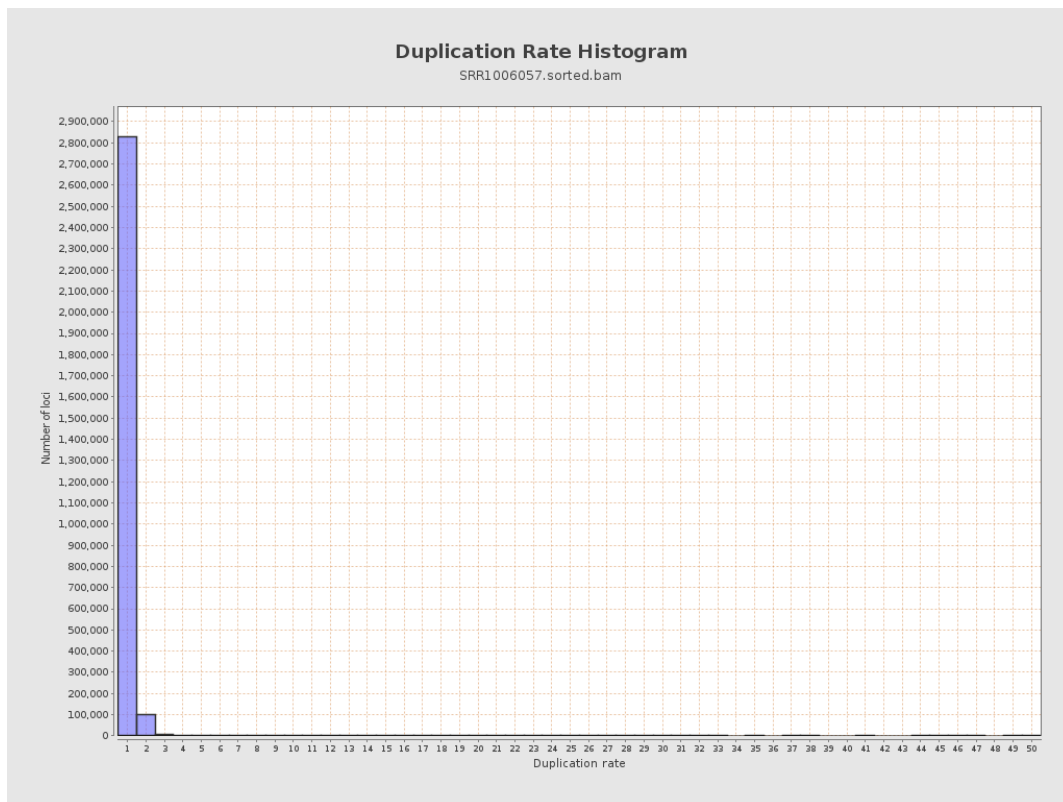
5. Results : Coverage Histogram (0-50X)



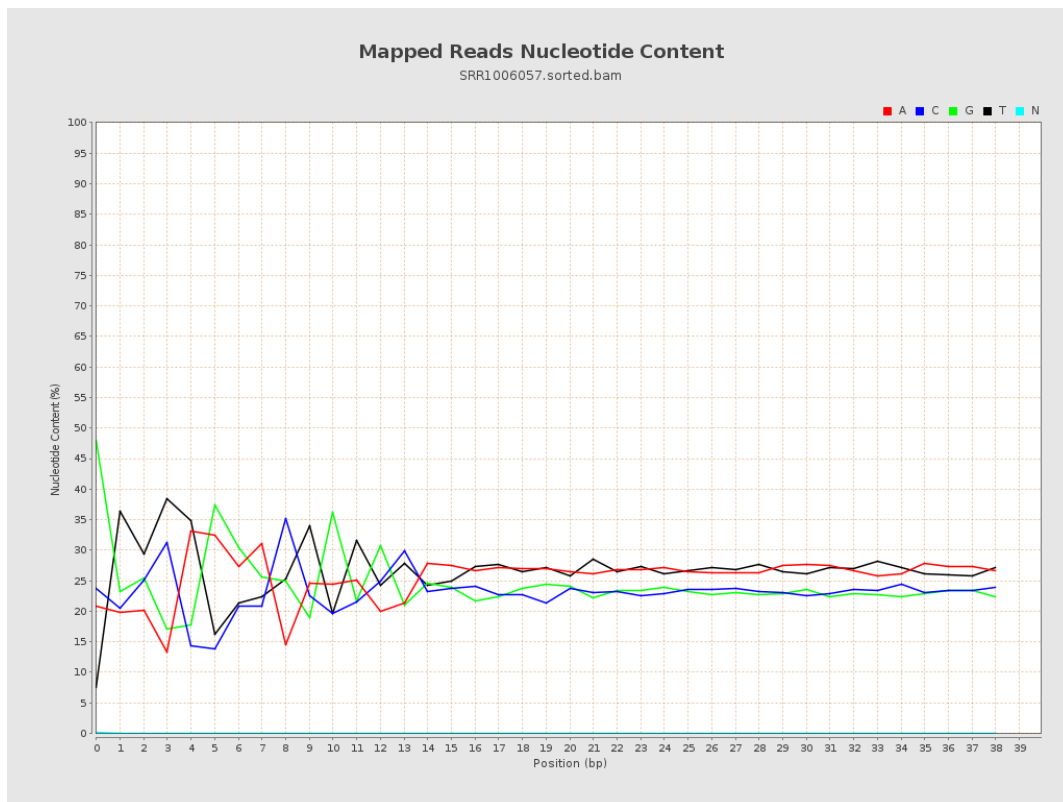
6. Results : Genome Fraction Coverage



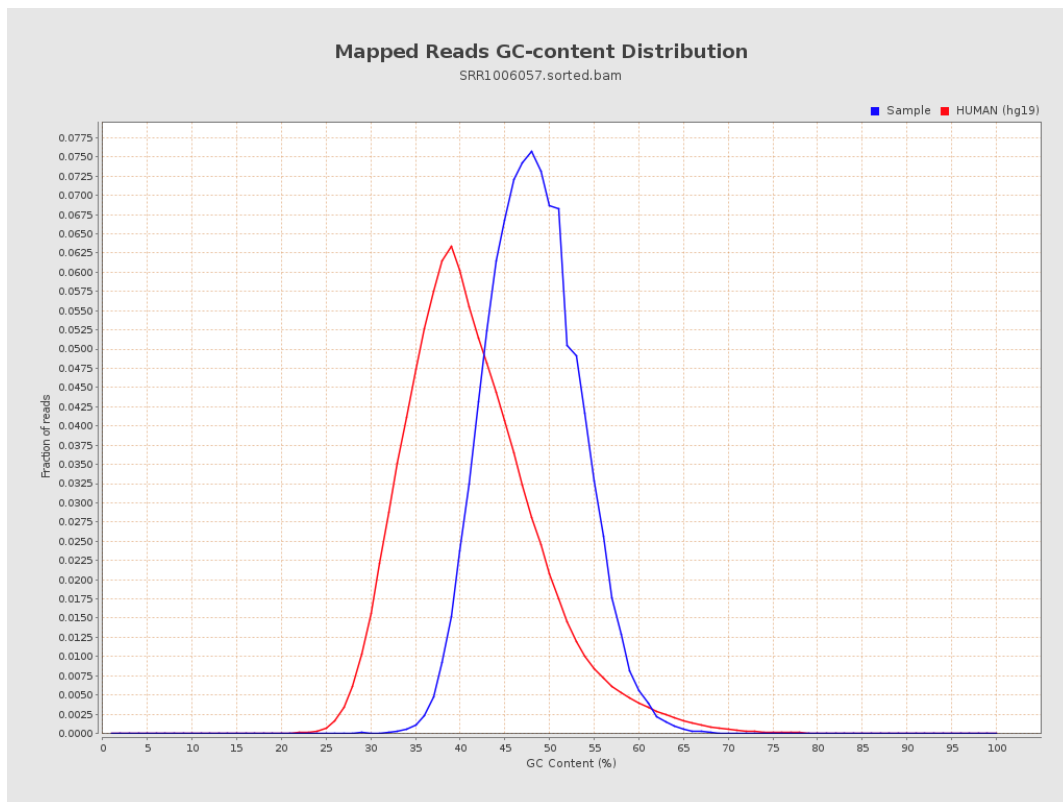
7. Results : Duplication Rate Histogram



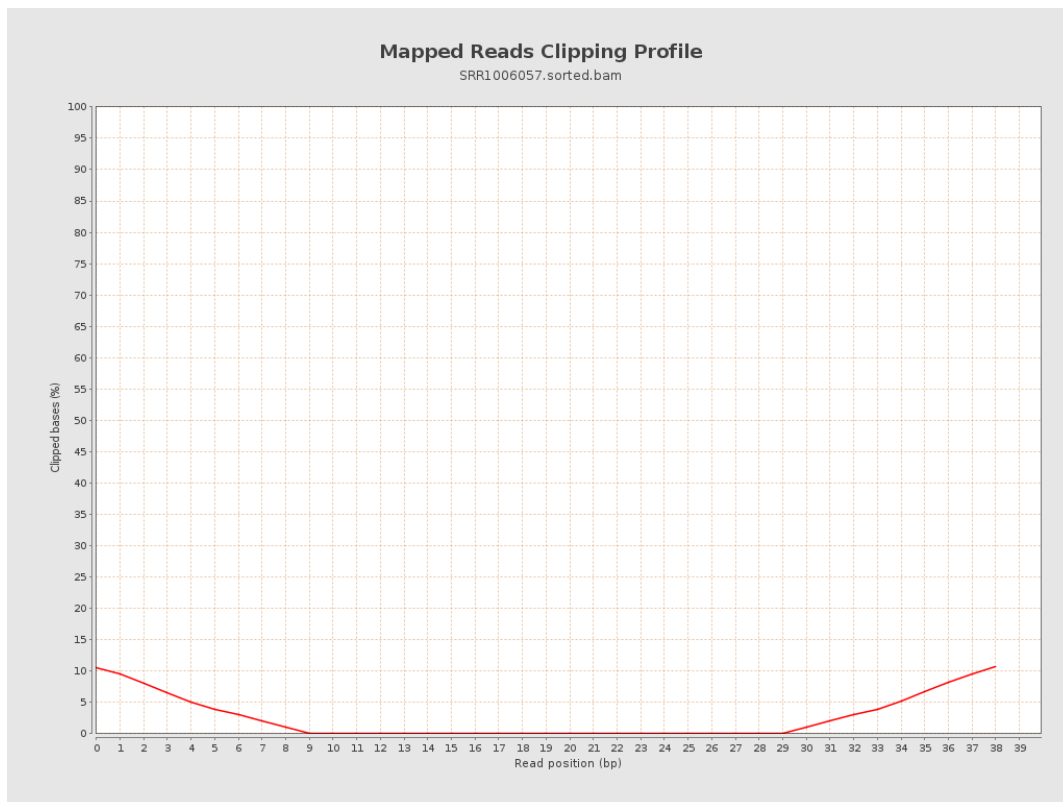
8. Results : Mapped Reads Nucleotide Content



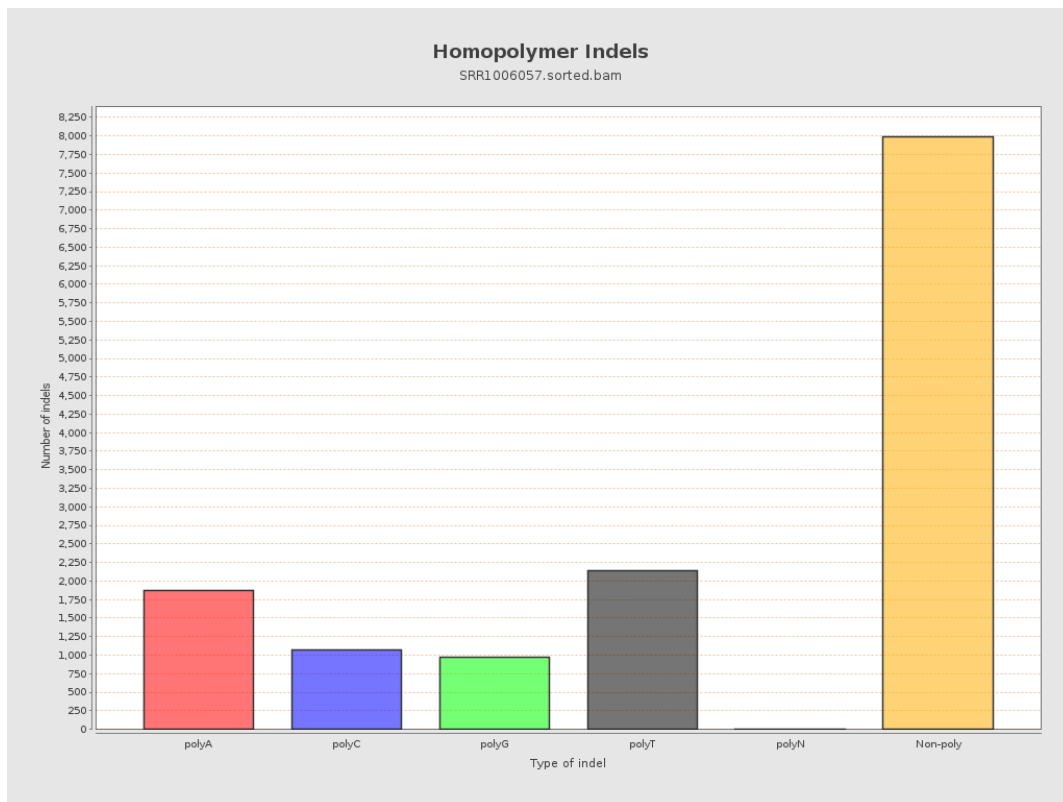
9. Results : Mapped Reads GC-content Distribution



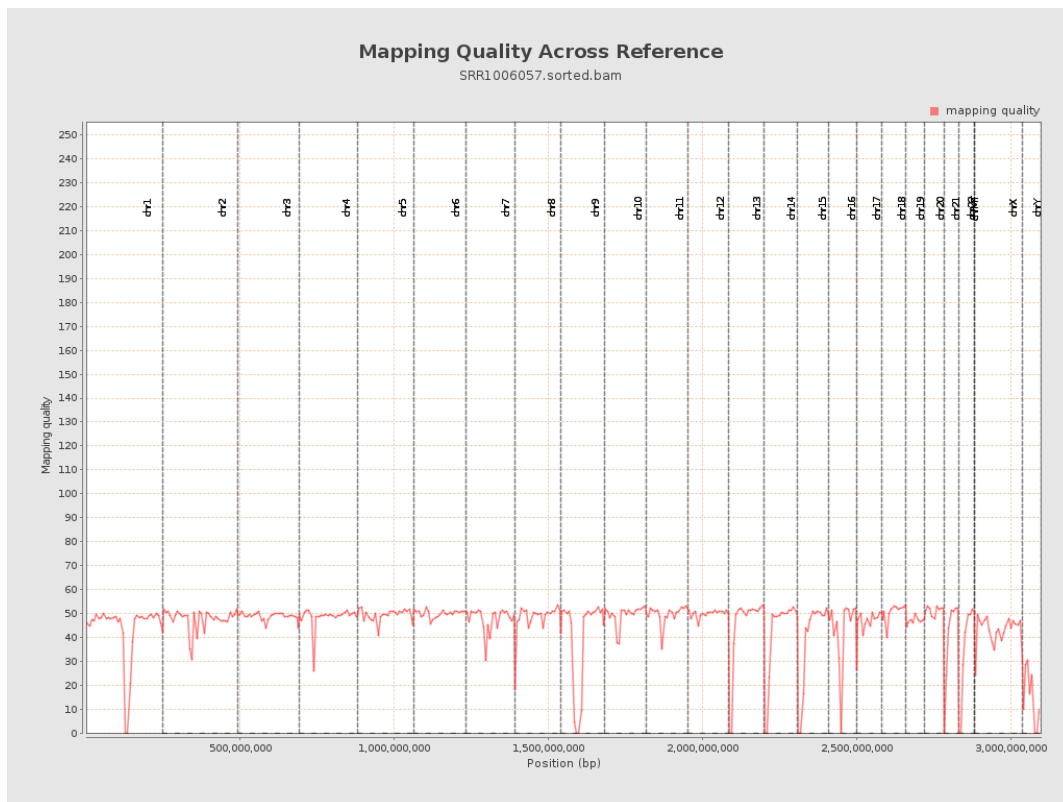
10. Results : Mapped Reads Clipping Profile



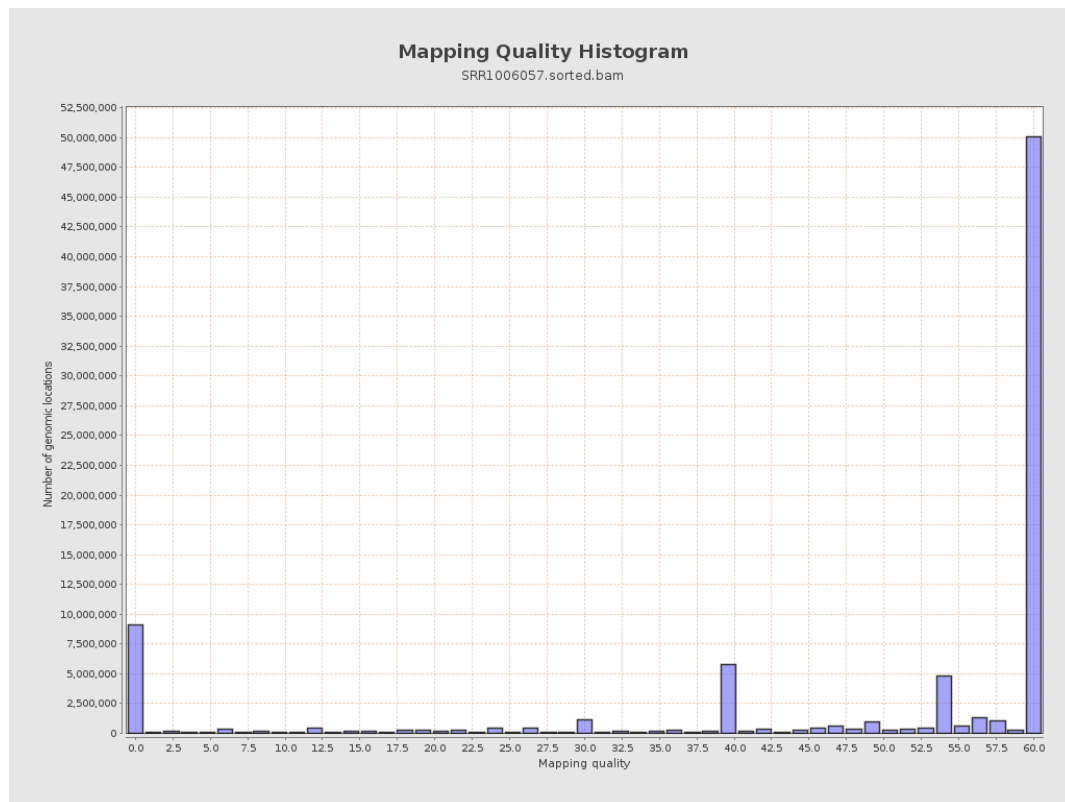
11. Results : Homopolymer Indels



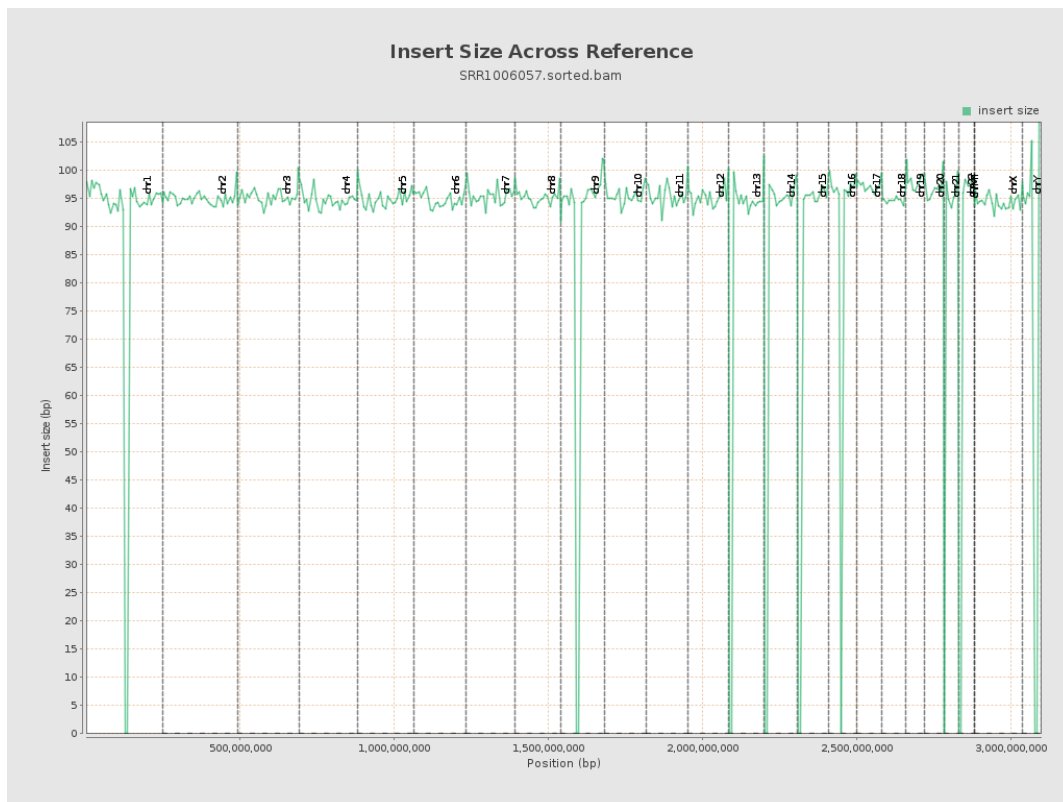
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

