

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 19:18:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006099.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_SRR1006099 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006099_1.fastq.gz SRR1006099_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 19:18:47 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006099.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,364,604
Mapped reads	12,303,695 / 85.65%
Unmapped reads	2,060,909 / 14.35%
Mapped paired reads	12,303,695 / 85.65%
Mapped reads, first in pair	6,267,551 / 43.63%
Mapped reads, second in pair	6,036,144 / 42.02%
Mapped reads, both in pair	11,011,148 / 76.65%
Mapped reads, singletons	1,292,547 / 9%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	2,162,695 / 15.06%
Duplication rate	15.58%
Clipped reads	1,144,224 / 7.97%

2.2. ACGT Content

Number/percentage of A's	126,551,650 / 26.69%
Number/percentage of C's	103,815,472 / 21.9%
Number/percentage of T's	131,666,795 / 27.77%
Number/percentage of G's	112,087,171 / 23.64%
Number/percentage of N's	19,409 / 0%
GC Percentage	45.54%

2.3. Coverage

Mean	0.1532
Standard Deviation	1.0285

2.4. Mapping Quality

Mean Mapping Quality	46.48
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2.5. Insert size

Mean	84,632.24
Standard Deviation	2,851,300.31
P25/Median/P75	80 / 110 / 146

2.6. Mismatches and indels

General error rate	0.53%
Mismatches	2,514,515
Insertions	16,023
Mapped reads with at least one insertion	0.13%
Deletions	41,082
Mapped reads with at least one deletion	0.33%
Homopolymer indels	45.47%

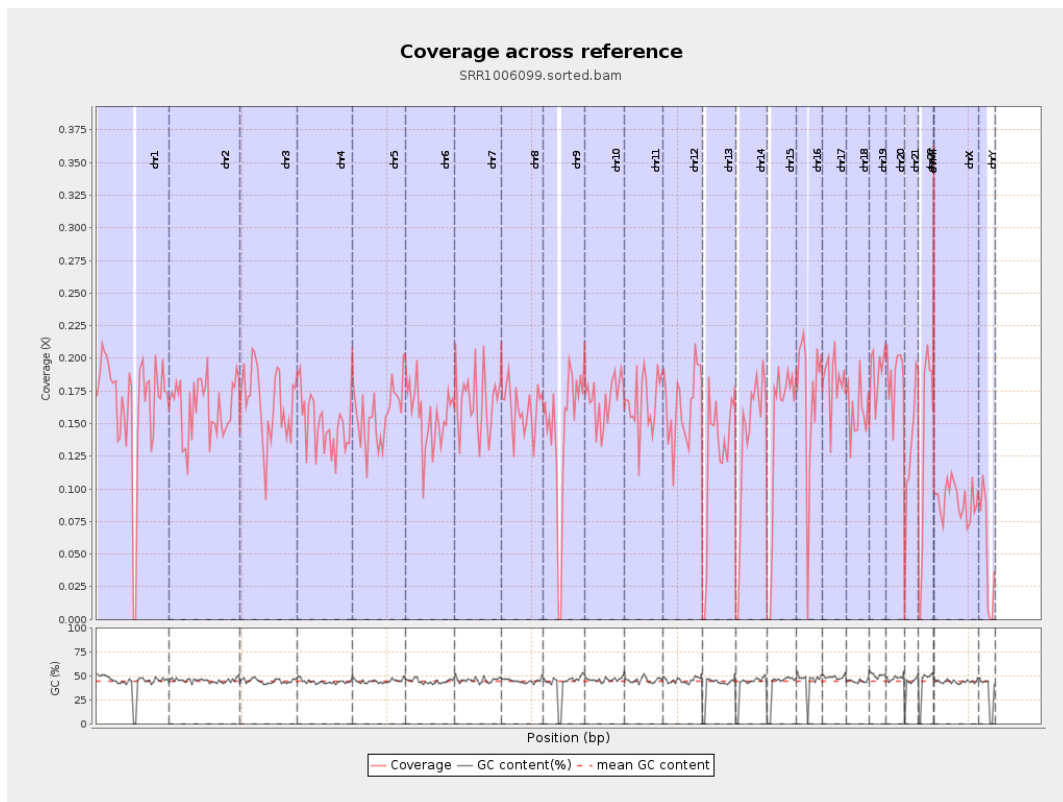
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

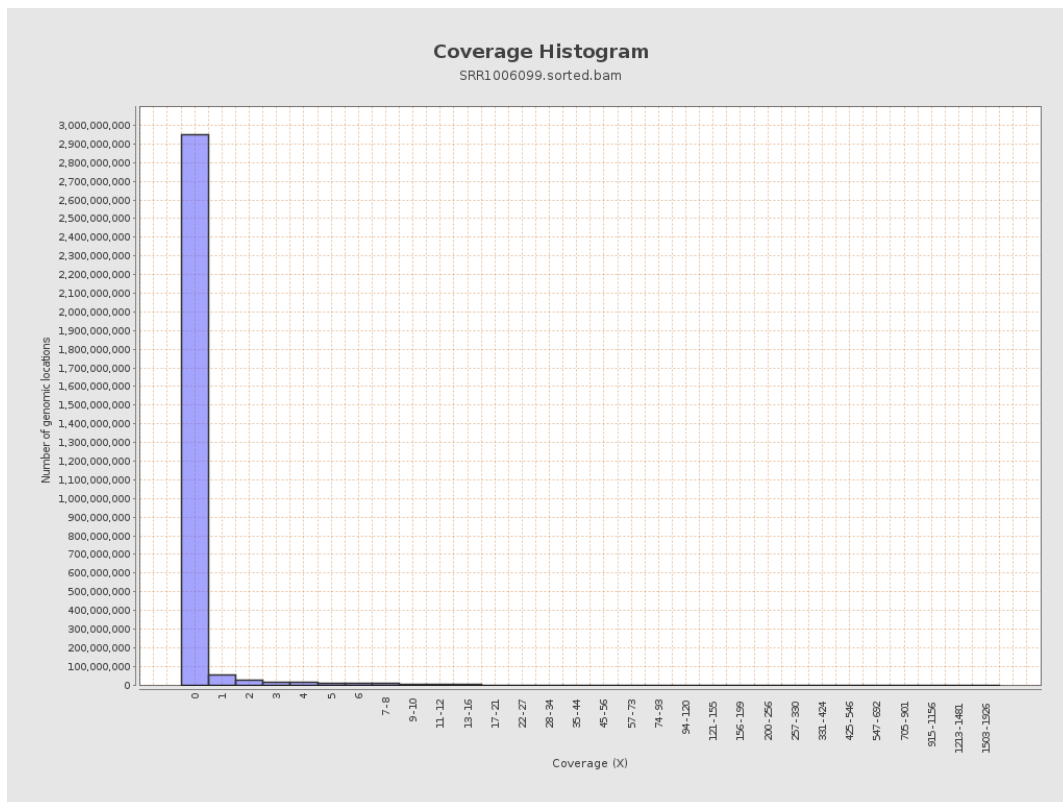
chr1	249250621	40904769	0.1641	1.1773
chr2	243199373	39563541	0.1627	1.0439
chr3	198022430	32604301	0.1646	0.9784
chr4	191154276	28453067	0.1488	0.9547
chr5	180915260	28433449	0.1572	0.9502
chr6	171115067	26777512	0.1565	1.0528
chr7	159138663	26356701	0.1656	1.1542
chr8	146364022	23678568	0.1618	1.1129
chr9	141213431	20317629	0.1439	0.9356
chr10	135534747	22779522	0.1681	1.0055
chr11	135006516	22501893	0.1667	1.4393
chr12	133851895	21791420	0.1628	0.9718
chr13	115169878	14323033	0.1244	0.857
chr14	107349540	14705780	0.137	0.9
chr15	102531392	14748209	0.1438	0.9246
chr16	90354753	15596892	0.1726	1.0233
chr17	81195210	14886091	0.1833	1.1157
chr18	78077248	12473637	0.1598	1.0925
chr19	59128983	11189770	0.1892	1.2014
chr20	63025520	11728488	0.1861	1.0705
chr21	48129895	6338276	0.1317	0.9279
chr22	51304566	6786450	0.1323	0.8947
chrMT	16571	6017	0.3631	1.4836
chrX	155270560	14240093	0.0917	0.7266

chrY	59373566	3007095	0.0506	0.5101
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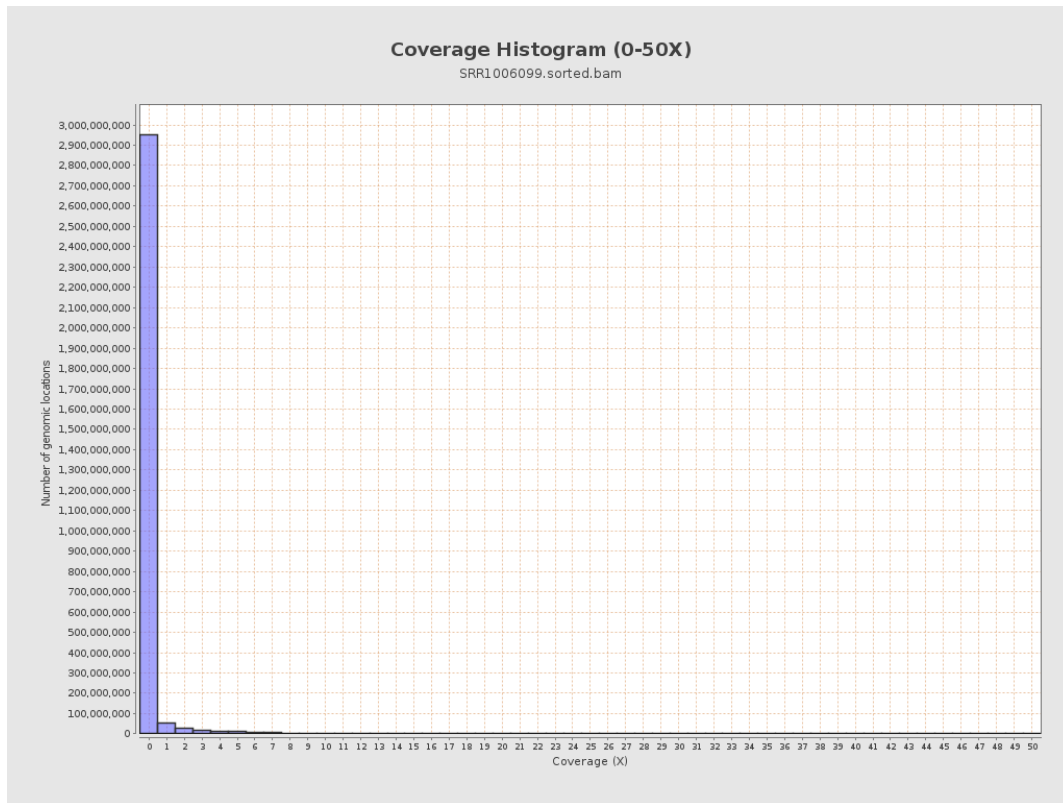
3. Results : Coverage across reference



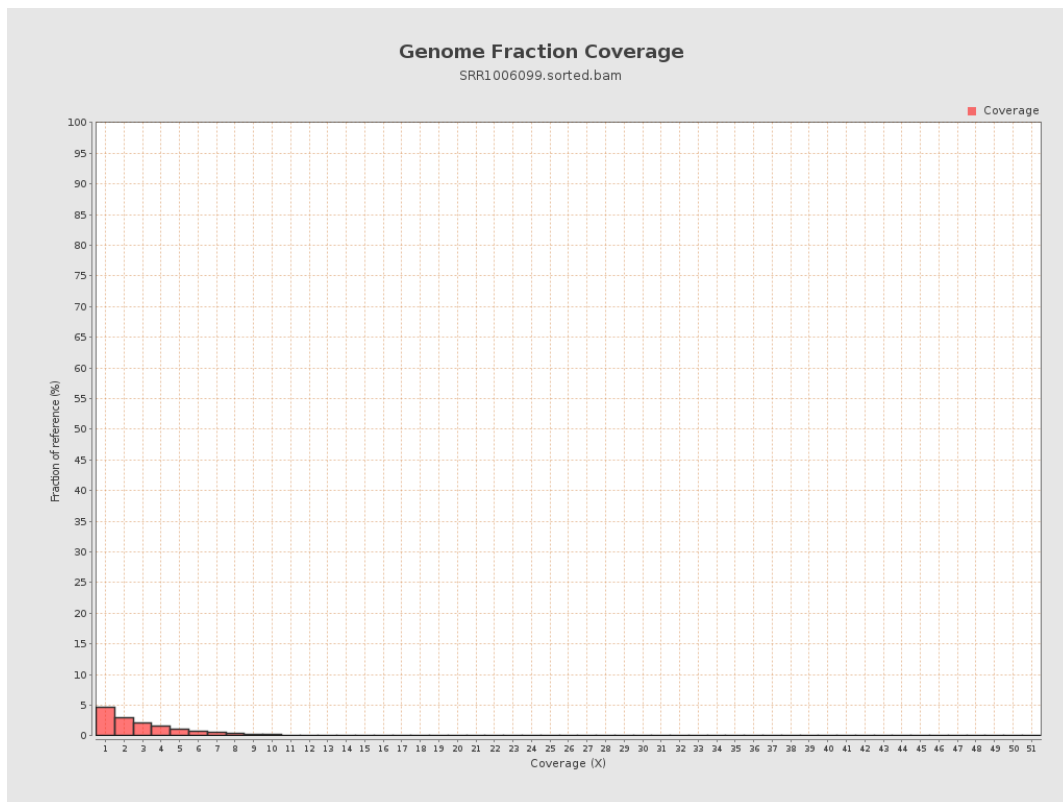
4. Results : Coverage Histogram



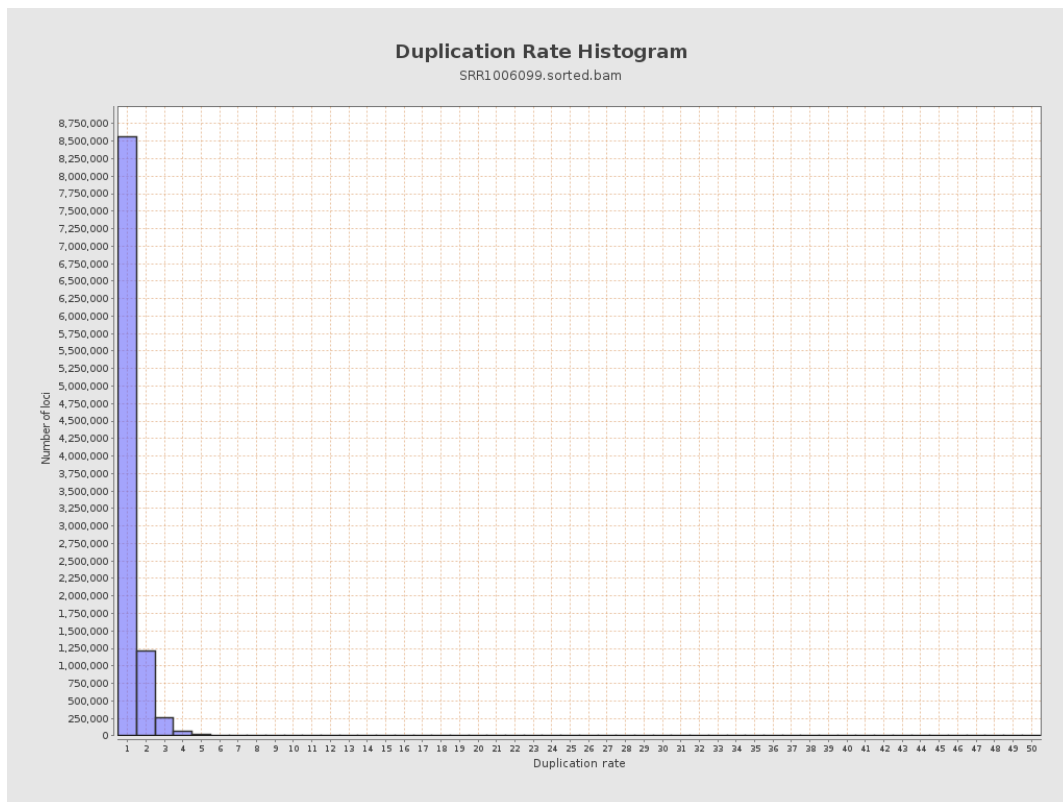
5. Results : Coverage Histogram (0-50X)



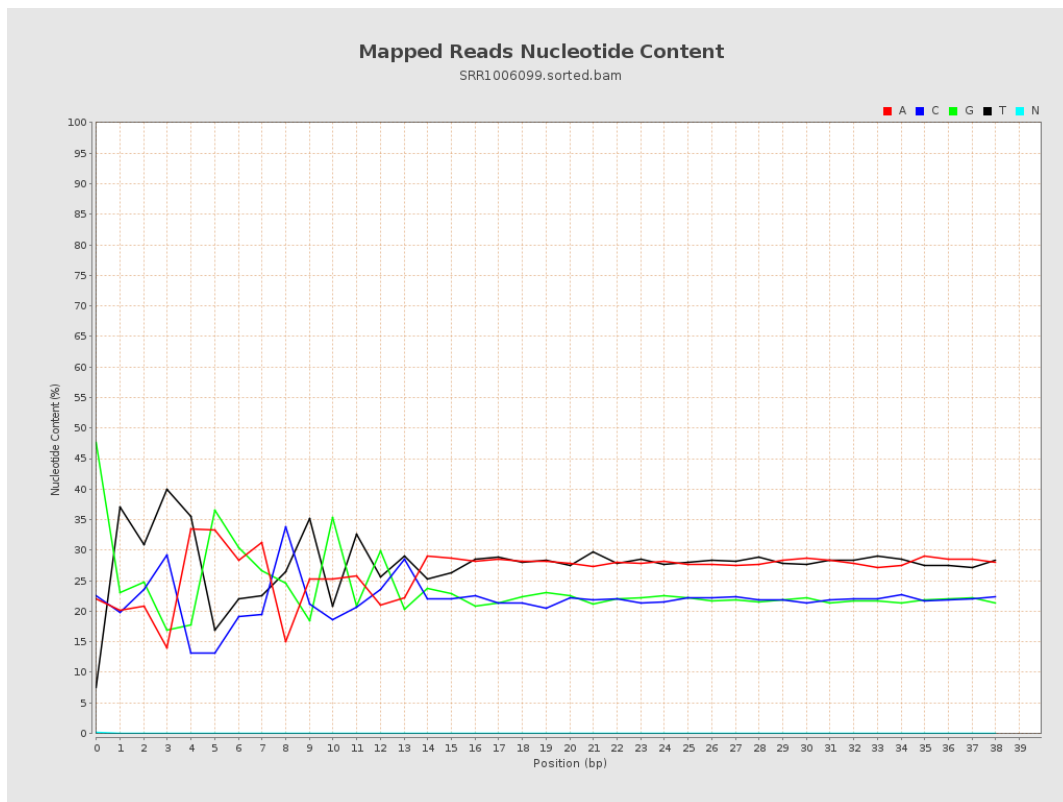
6. Results : Genome Fraction Coverage



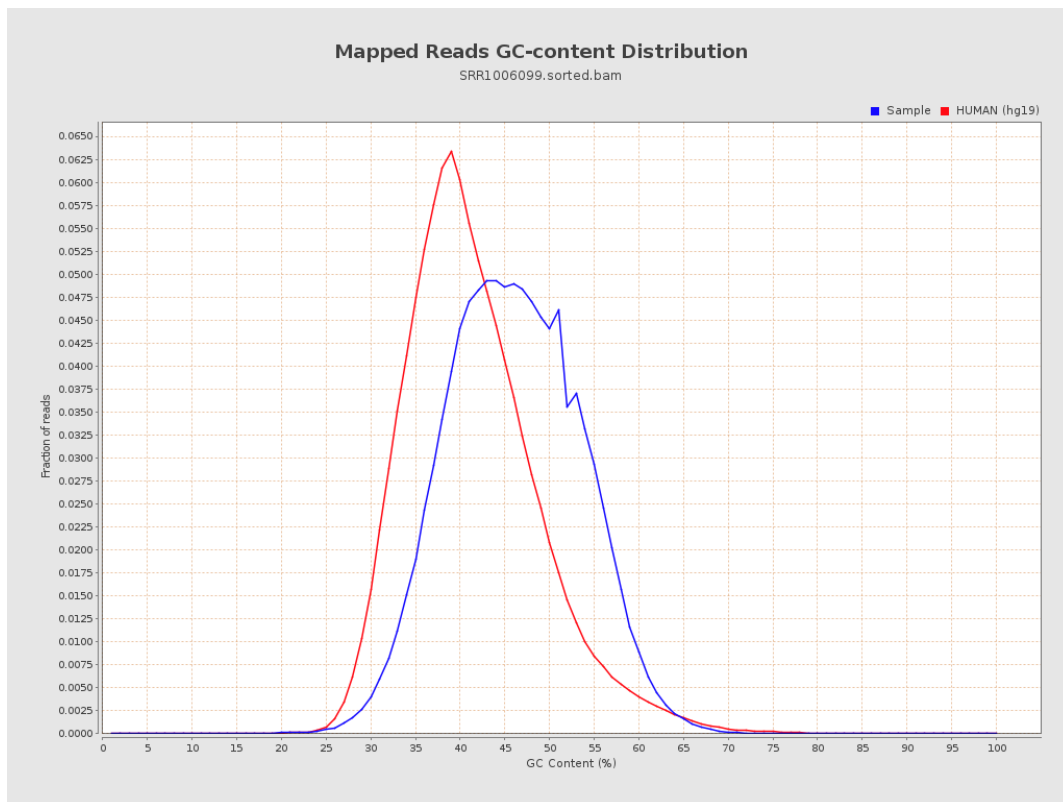
7. Results : Duplication Rate Histogram



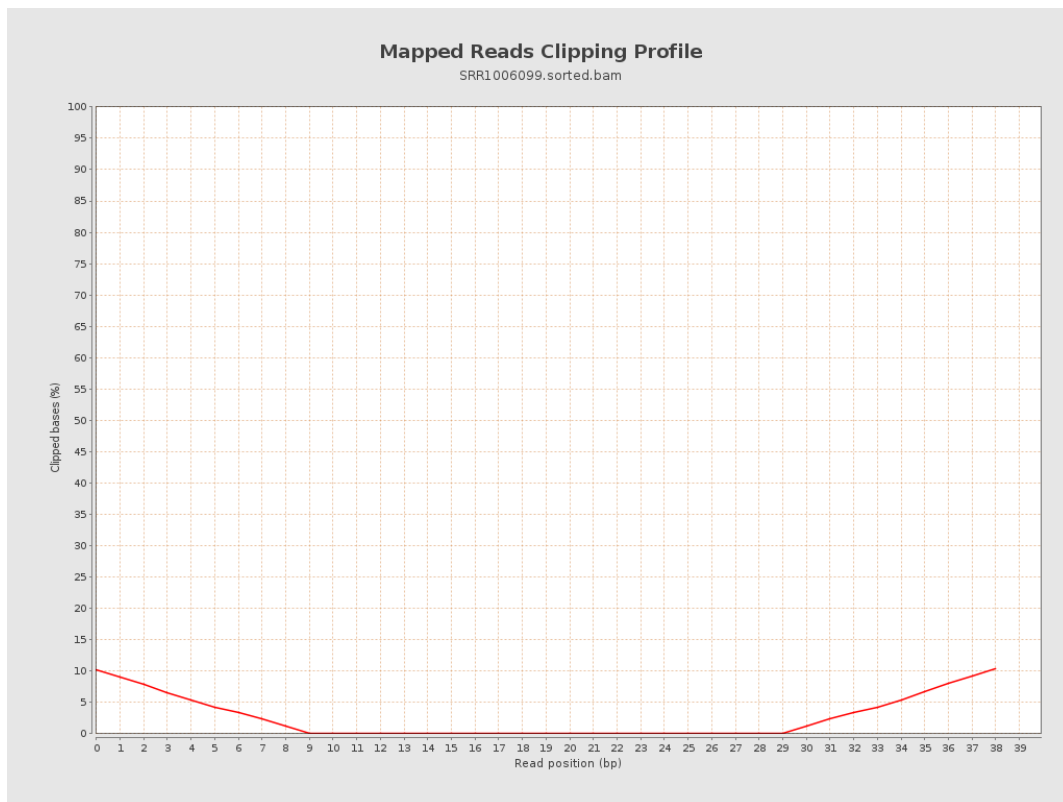
8. Results : Mapped Reads Nucleotide Content



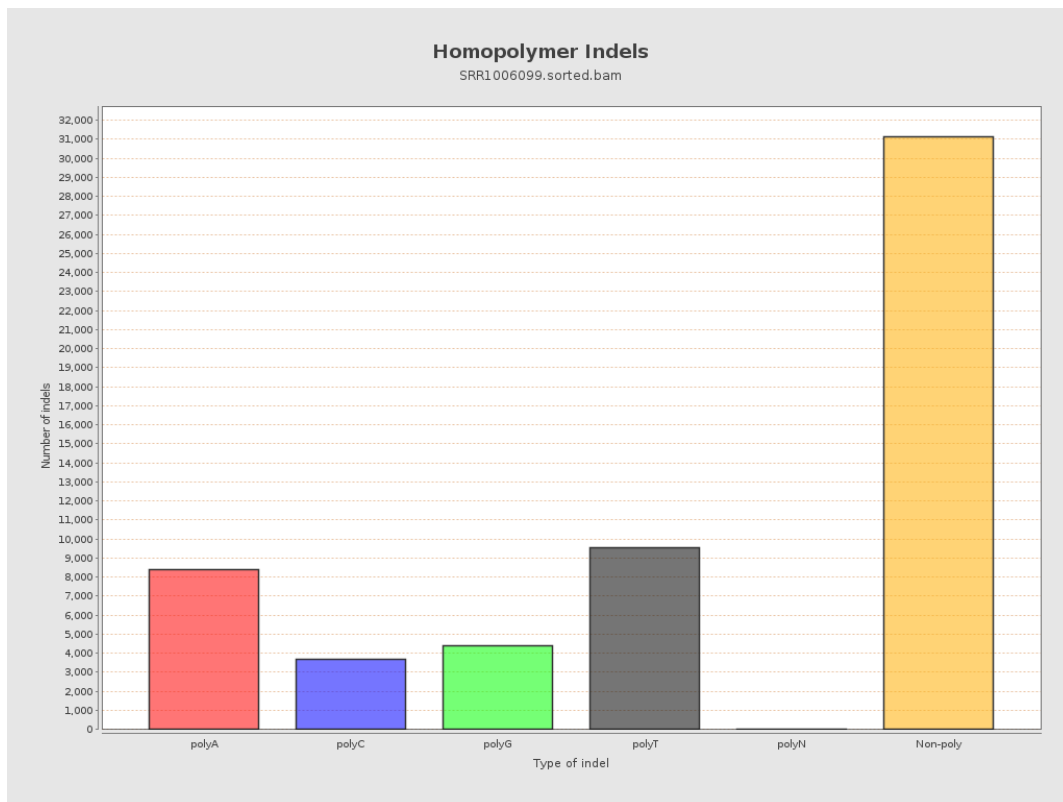
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



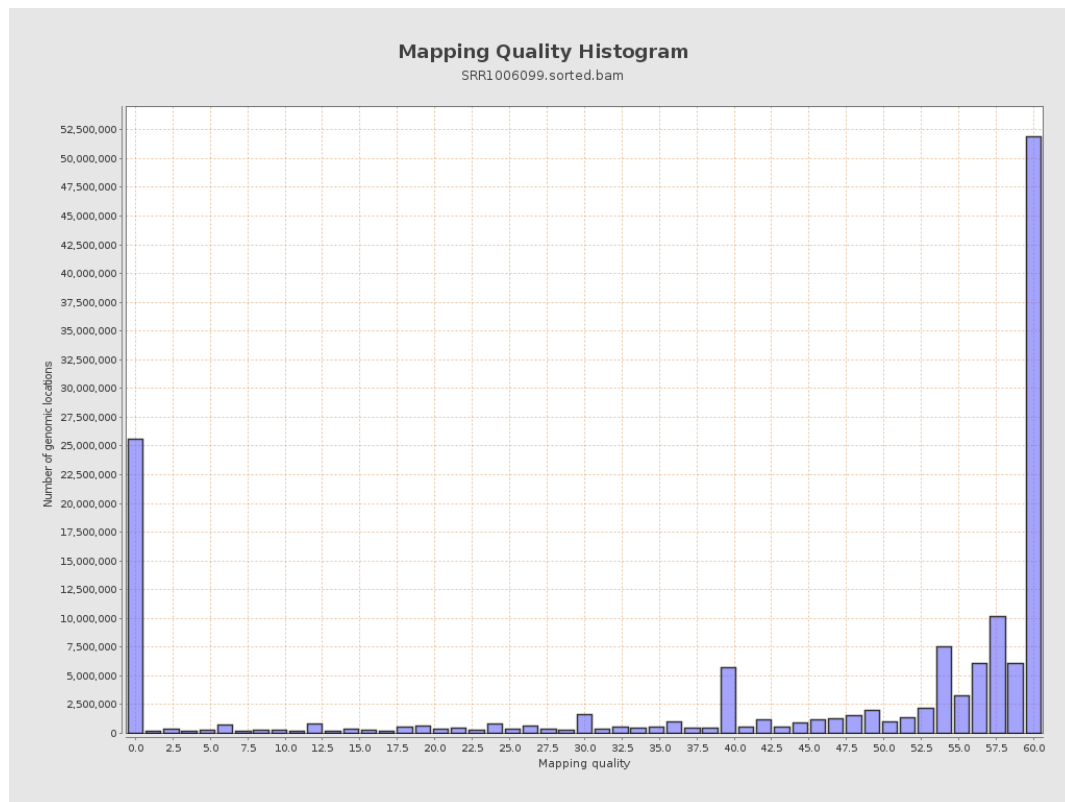
11. Results : Homopolymer Indels



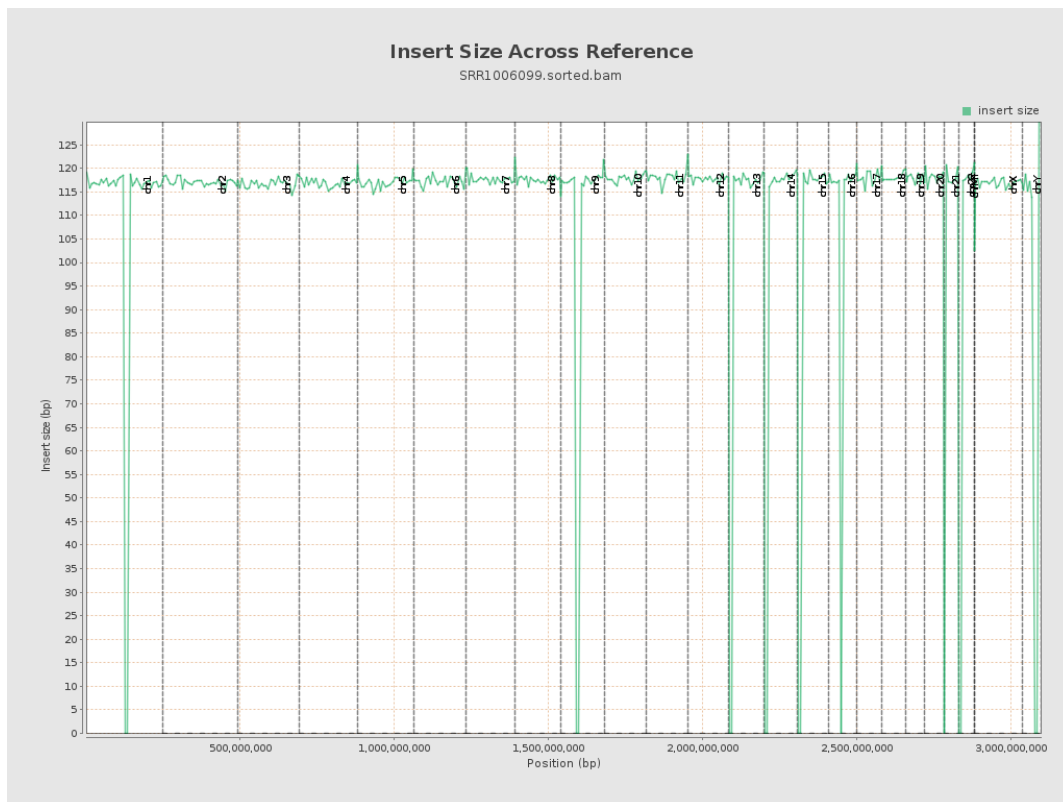
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

