

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 16:17:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006047.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_SRR1006047 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006047_1.fastq.gz SRR1006047_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 16:17:18 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006047.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,165,366
Mapped reads	8,761,644 / 86.19%
Unmapped reads	1,403,722 / 13.81%
Mapped paired reads	8,761,644 / 86.19%
Mapped reads, first in pair	4,470,213 / 43.97%
Mapped reads, second in pair	4,291,431 / 42.22%
Mapped reads, both in pair	7,987,536 / 78.58%
Mapped reads, singletons	774,108 / 7.62%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	592,274 / 5.83%
Duplication rate	6.11%
Clipped reads	676,847 / 6.66%

2.2. ACGT Content

Number/percentage of A's	92,685,272 / 27.38%
Number/percentage of C's	74,110,236 / 21.9%
Number/percentage of T's	95,170,533 / 28.12%
Number/percentage of G's	76,353,286 / 22.56%
Number/percentage of N's	137,085 / 0.04%
GC Percentage	44.46%

2.3. Coverage

Mean	0.1093
Standard Deviation	0.6028

2.4. Mapping Quality

Mean Mapping Quality	46.74
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2.5. Insert size

Mean	58,886.44
Standard Deviation	2,396,082.68
P25/Median/P75	64 / 89 / 127

2.6. Mismatches and indels

General error rate	0.55%
Mismatches	1,860,674
Insertions	10,619
Mapped reads with at least one insertion	0.12%
Deletions	28,595
Mapped reads with at least one deletion	0.33%
Homopolymer indels	46.57%

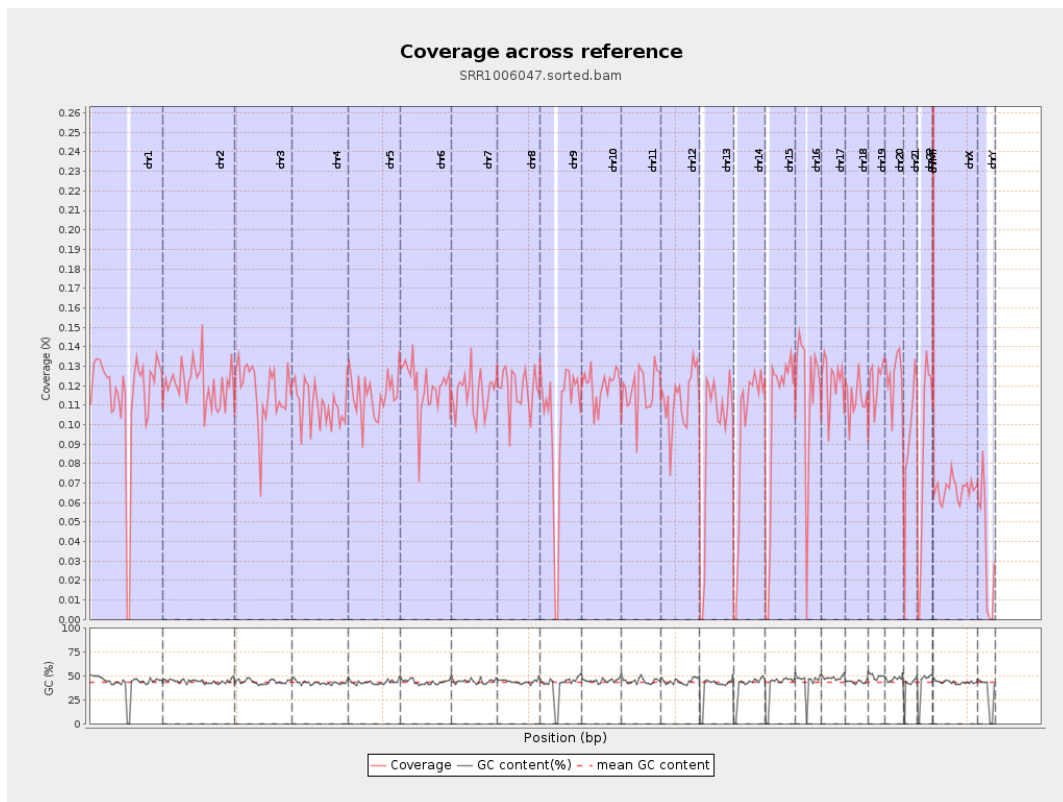
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

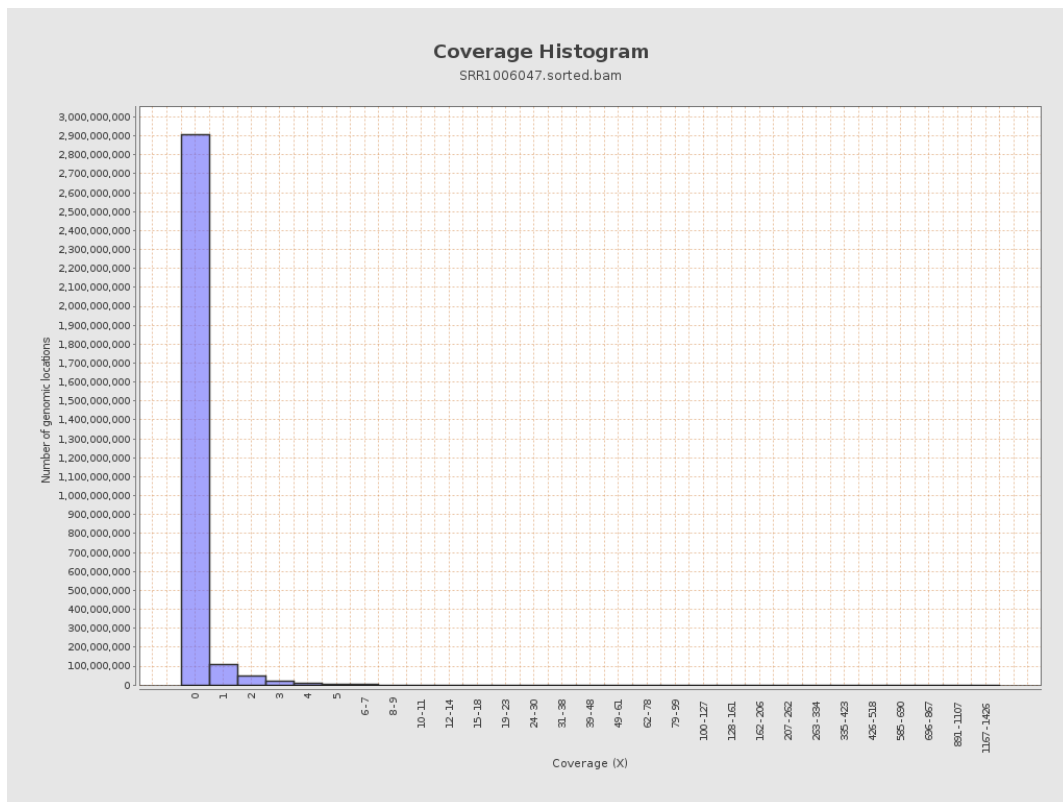
chr1	249250621	28525066	0.1144	0.6471
chr2	243199373	29354229	0.1207	0.667
chr3	198022430	23102313	0.1167	0.5384
chr4	191154276	21074985	0.1103	0.5446
chr5	180915260	20936272	0.1157	0.537
chr6	171115067	20440770	0.1195	0.6274
chr7	159138663	18526182	0.1164	0.7363
chr8	146364022	17252091	0.1179	0.6207
chr9	141213431	14286825	0.1012	0.5554
chr10	135534747	16286880	0.1202	0.5714
chr11	135006516	15869555	0.1175	0.9169
chr12	133851895	15237156	0.1138	0.5374
chr13	115169878	10861058	0.0943	0.4875
chr14	107349540	10463991	0.0975	0.508
chr15	102531392	10444296	0.1019	0.5092
chr16	90354753	10425010	0.1154	0.5882
chr17	81195210	9997466	0.1231	0.6217
chr18	78077248	8838299	0.1132	0.7235
chr19	59128983	7197149	0.1217	0.659
chr20	63025520	7835185	0.1243	0.5685
chr21	48129895	4531974	0.0942	0.5398
chr22	51304566	4425494	0.0863	0.5091
chrMT	16571	32982	1.9903	3.1422
chrX	155270560	10379327	0.0668	0.4368

chrY	59373566	2167924	0.0365	0.3347
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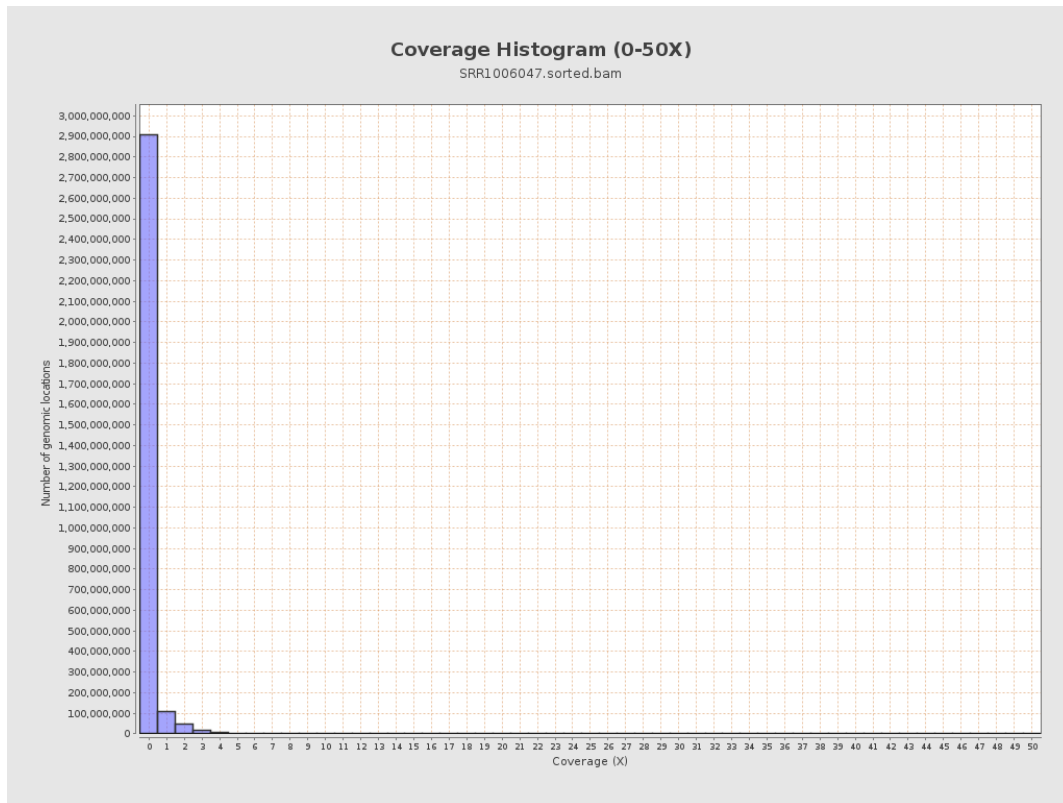
3. Results : Coverage across reference



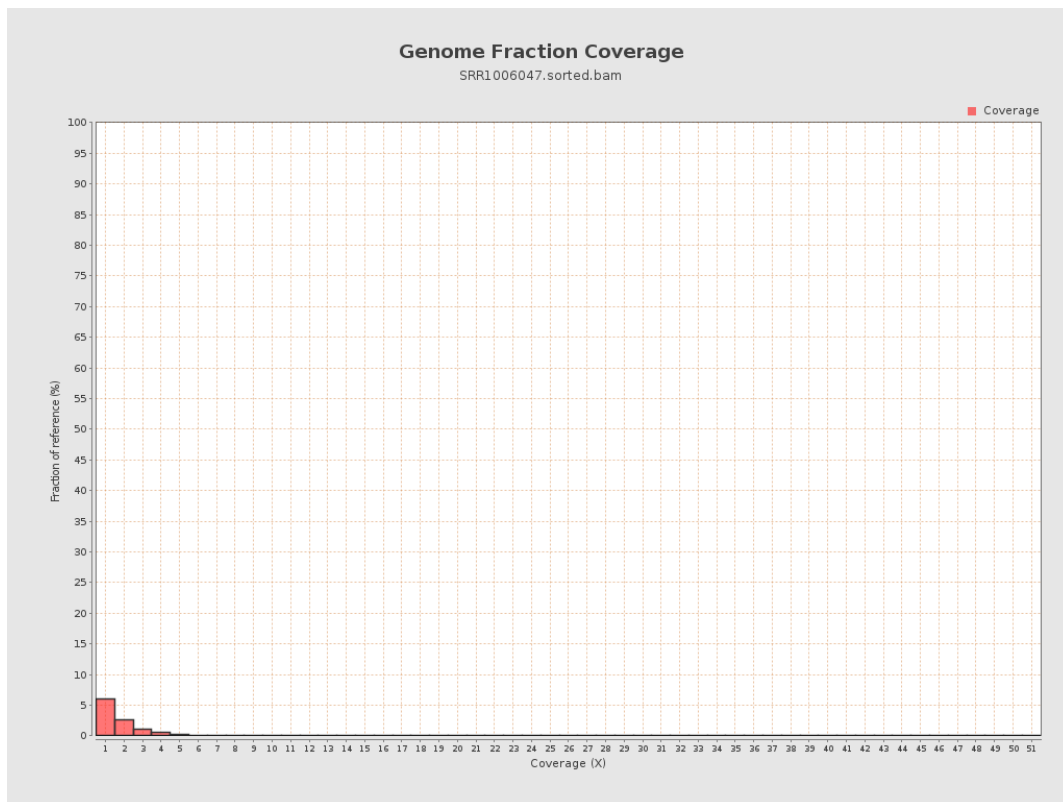
4. Results : Coverage Histogram



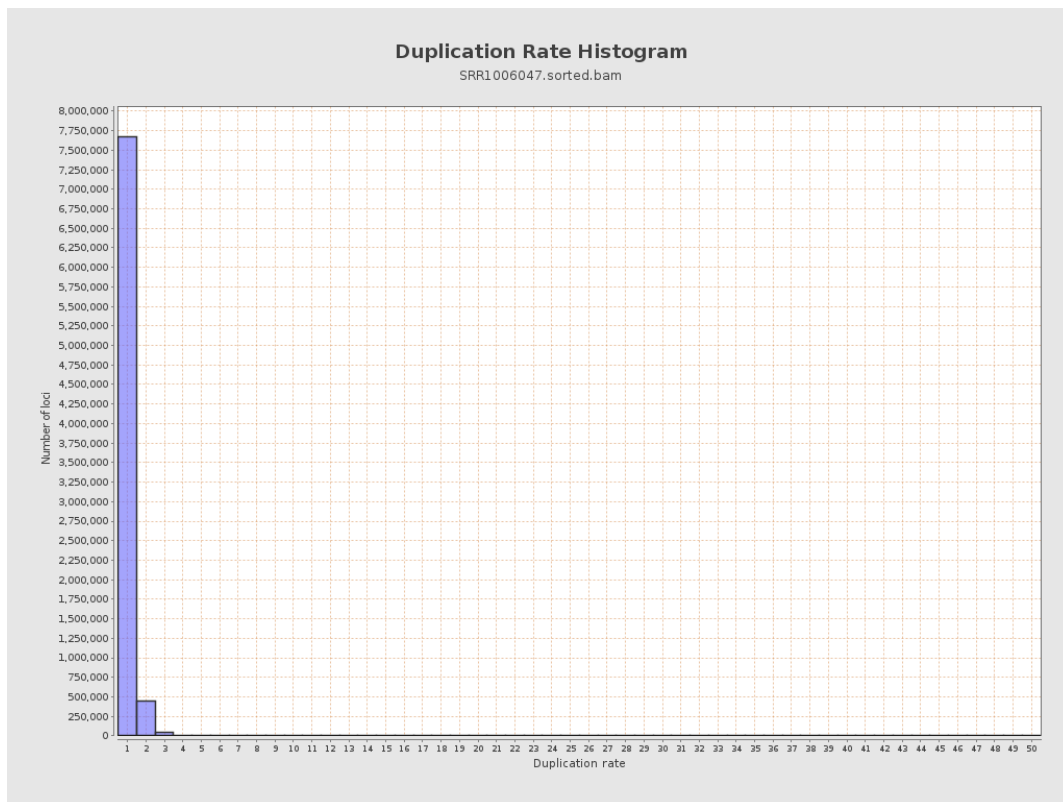
5. Results : Coverage Histogram (0-50X)



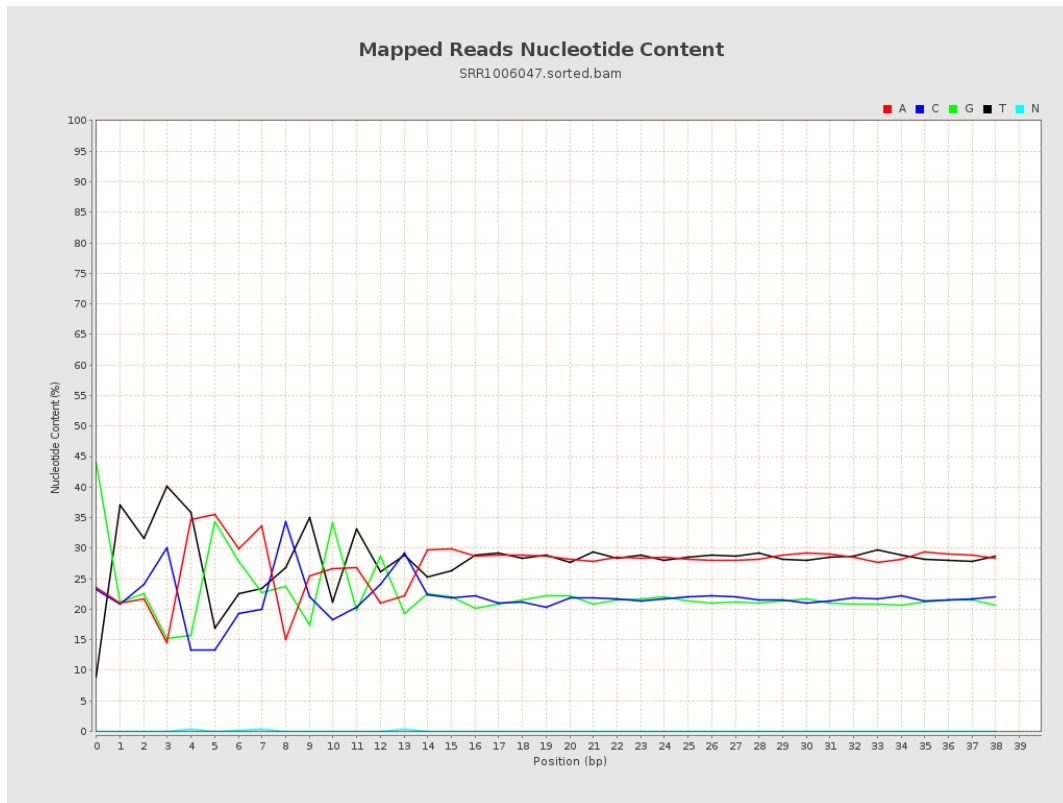
6. Results : Genome Fraction Coverage



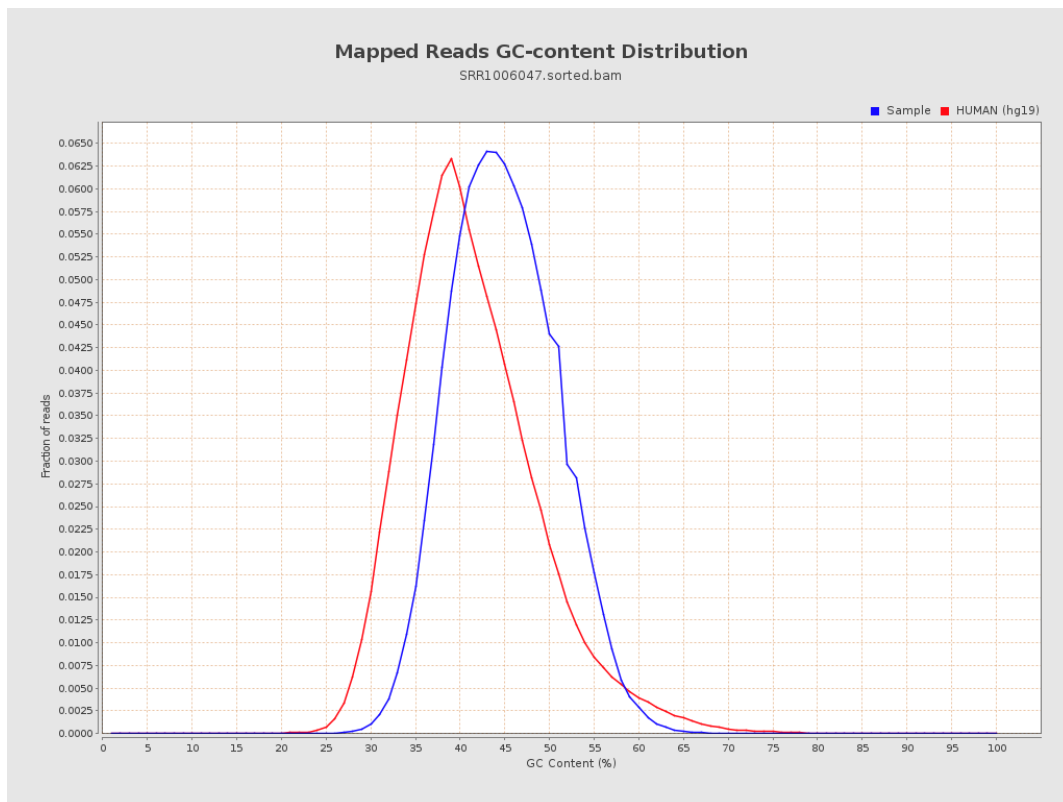
7. Results : Duplication Rate Histogram



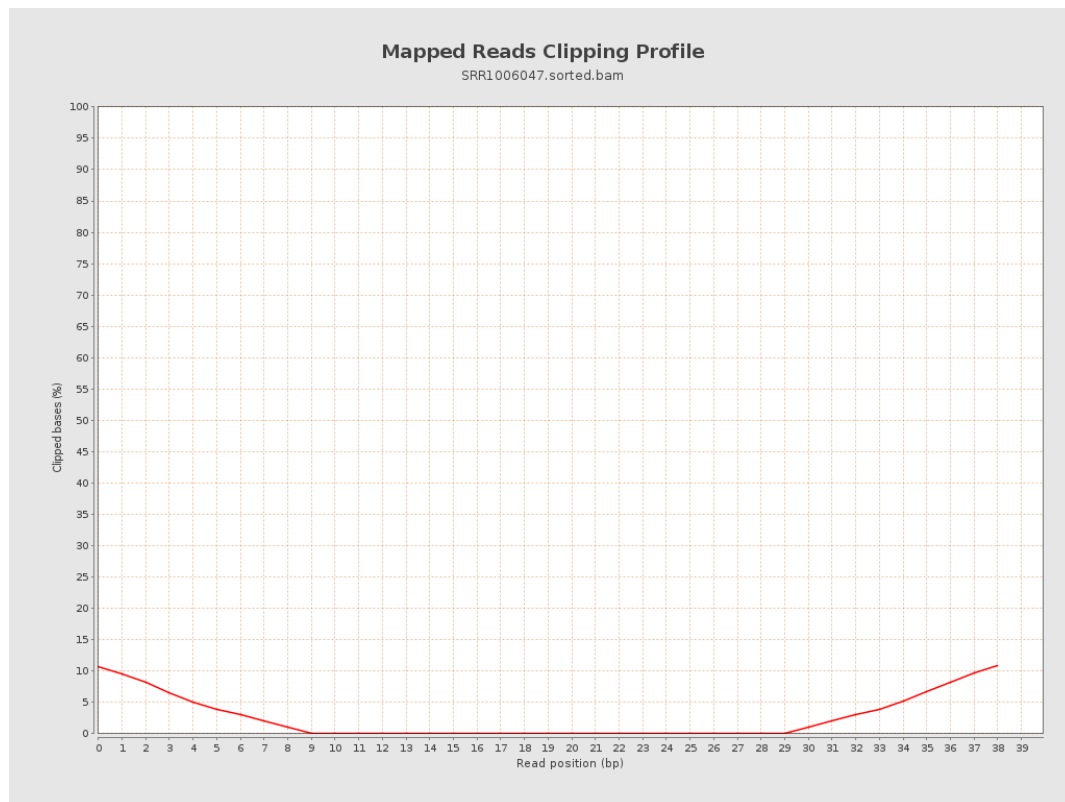
8. Results : Mapped Reads Nucleotide Content



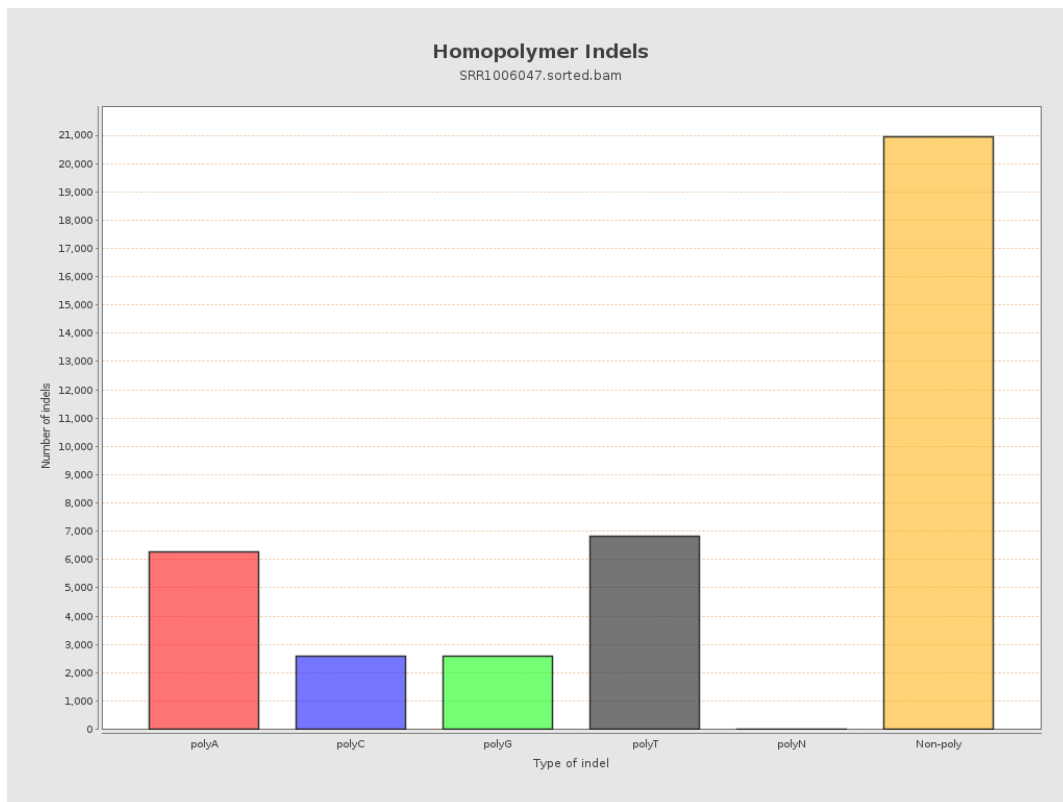
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



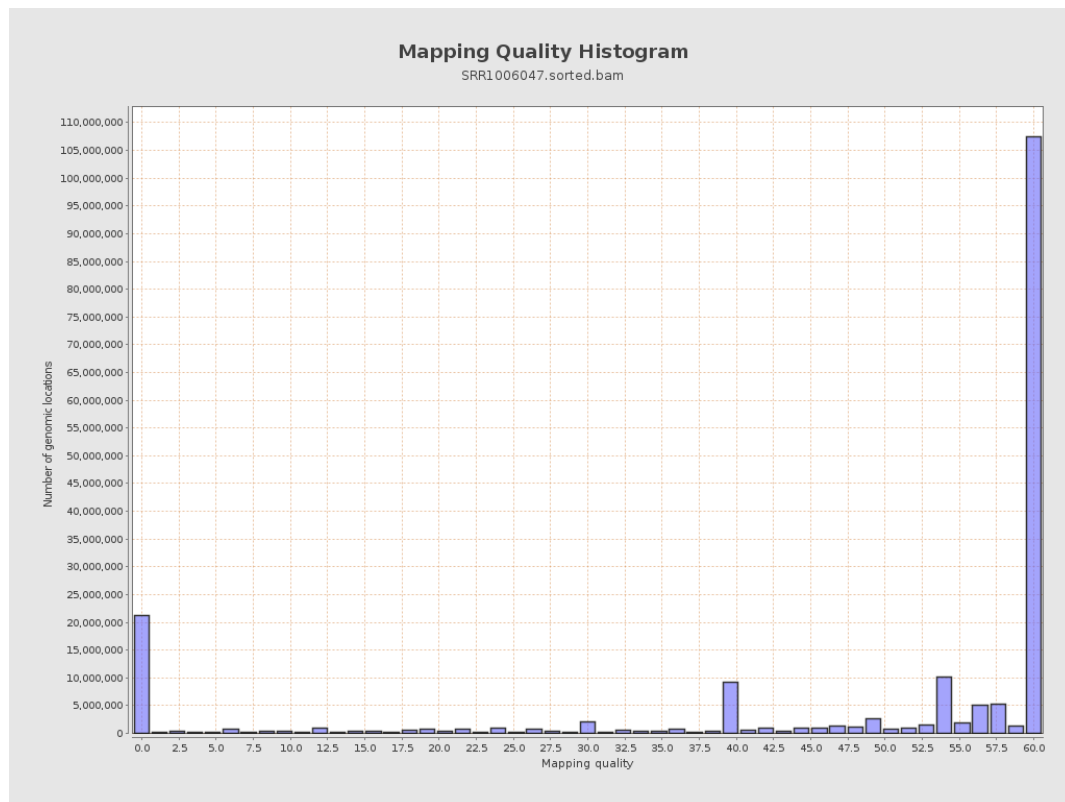
11. Results : Homopolymer Indels



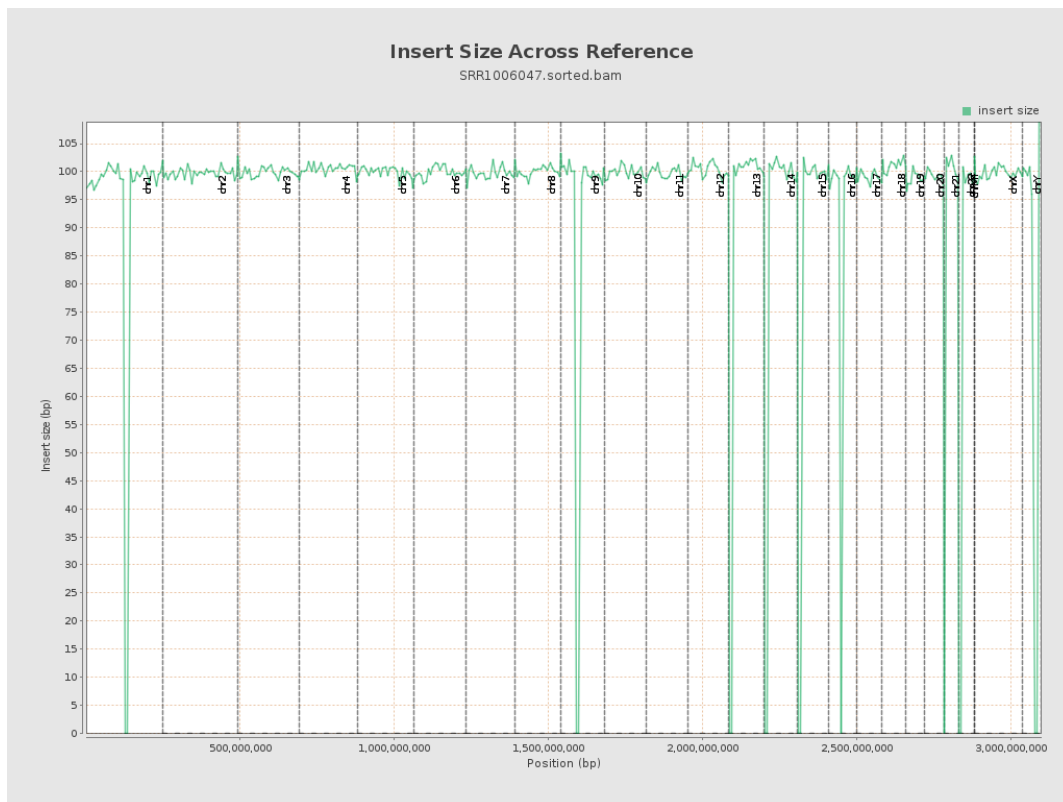
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

