

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 23:31:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006193.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_SRR1006193 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006193_1.fastq.gz SRR1006193_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 23:31:07 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006193.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,531,984
Mapped reads	3,930,283 / 86.72%
Unmapped reads	601,701 / 13.28%
Mapped paired reads	3,930,283 / 86.72%
Mapped reads, first in pair	1,968,231 / 43.43%
Mapped reads, second in pair	1,962,052 / 43.29%
Mapped reads, both in pair	3,645,286 / 80.43%
Mapped reads, singletons	284,997 / 6.29%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	119,326 / 2.63%
Duplication rate	2.57%
Clipped reads	240,527 / 5.31%

2.2. ACGT Content

Number/percentage of A's	41,692,744 / 27.42%
Number/percentage of C's	33,285,218 / 21.89%
Number/percentage of T's	42,594,922 / 28.02%
Number/percentage of G's	34,462,629 / 22.67%
Number/percentage of N's	7,160 / 0%
GC Percentage	44.56%

2.3. Coverage

Mean	0.0491
Standard Deviation	0.3135

2.4. Mapping Quality

Mean Mapping Quality	47.78
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2.5. Insert size

Mean	53,273.6
Standard Deviation	2,205,203.43
P25/Median/P75	71 / 110 / 152

2.6. Mismatches and indels

General error rate	0.3%
Mismatches	444,726
Insertions	4,779
Mapped reads with at least one insertion	0.12%
Deletions	14,829
Mapped reads with at least one deletion	0.38%
Homopolymer indels	44.4%

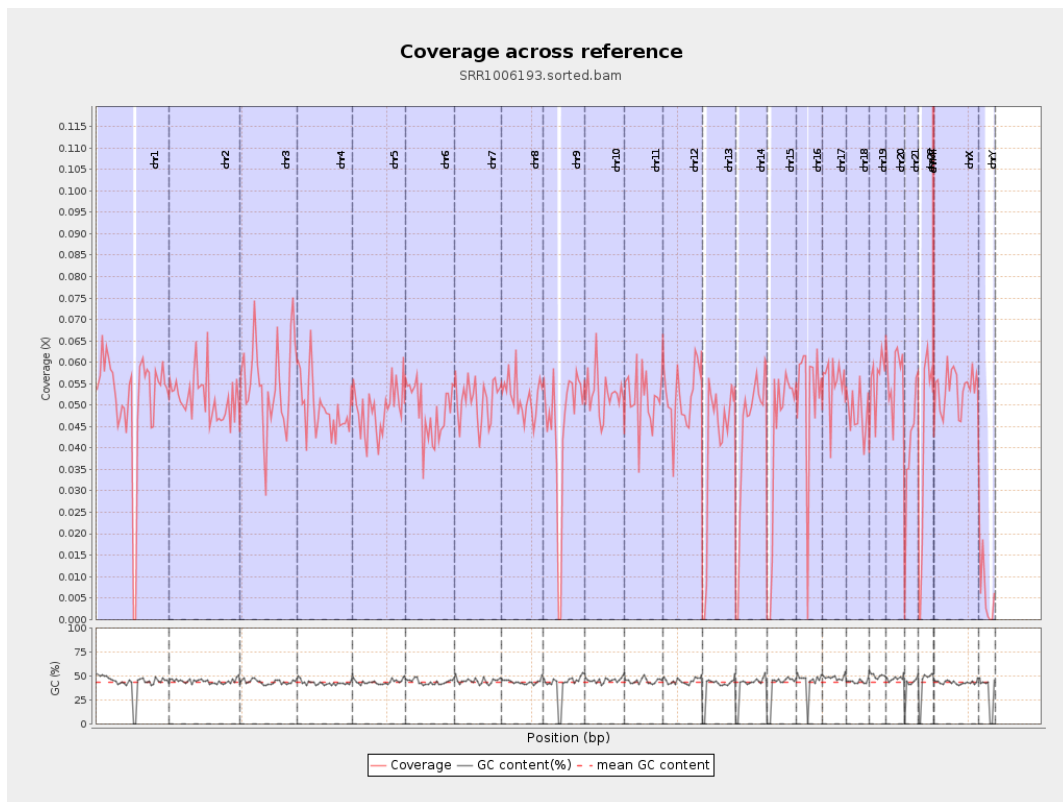
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

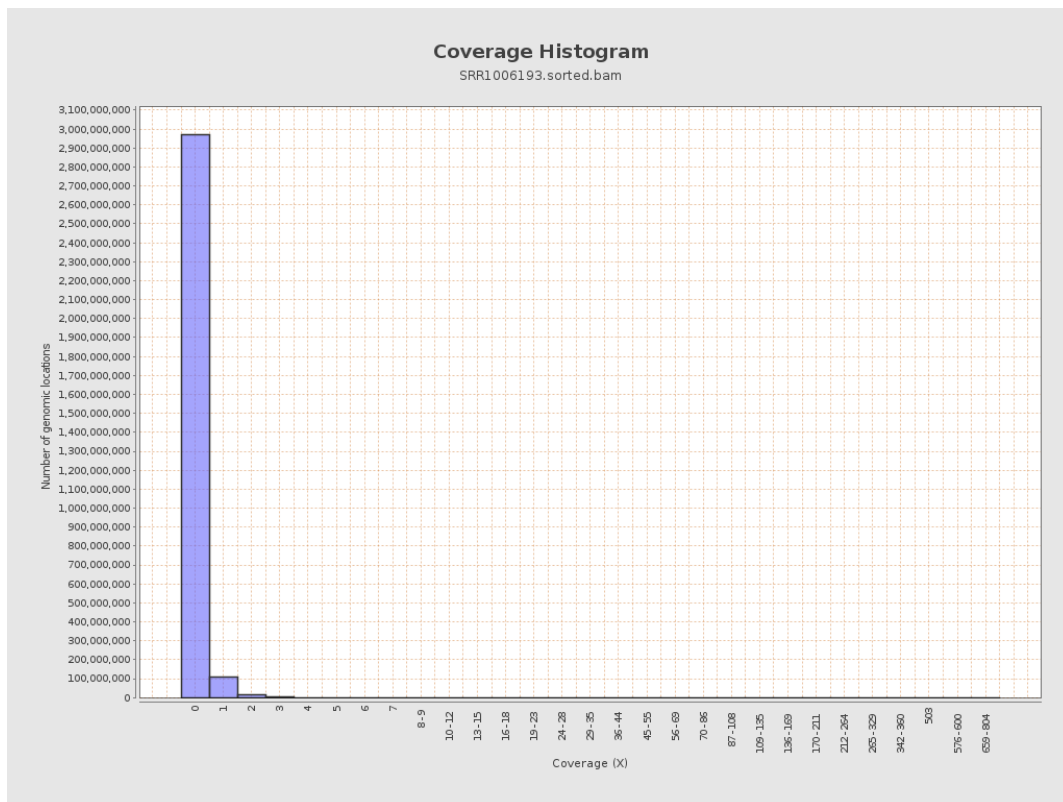
chr1	249250621	12775486	0.0513	0.3909
chr2	243199373	12580079	0.0517	0.3095
chr3	198022430	10850370	0.0548	0.2684
chr4	191154276	9373685	0.049	0.2741
chr5	180915260	8853553	0.0489	0.2543
chr6	171115067	8320227	0.0486	0.2721
chr7	159138663	8098179	0.0509	0.3505
chr8	146364022	7600715	0.0519	0.4752
chr9	141213431	6325543	0.0448	0.2741
chr10	135534747	7096592	0.0524	0.3174
chr11	135006516	6965057	0.0516	0.2905
chr12	133851895	6948089	0.0519	0.2661
chr13	115169878	4697249	0.0408	0.231
chr14	107349540	4646764	0.0433	0.4571
chr15	102531392	4352153	0.0424	0.2369
chr16	90354753	4719625	0.0522	0.2896
chr17	81195210	4487505	0.0553	0.2807
chr18	78077248	3761945	0.0482	0.3858
chr19	59128983	3310911	0.056	0.3448
chr20	63025520	3544182	0.0562	0.2807
chr21	48129895	1955836	0.0406	0.2577
chr22	51304566	2074881	0.0404	0.2566
chrMT	16571	19727	1.1905	1.321
chrX	155270560	8339427	0.0537	0.28

chrY	59373566	364495	0.0061	0.147
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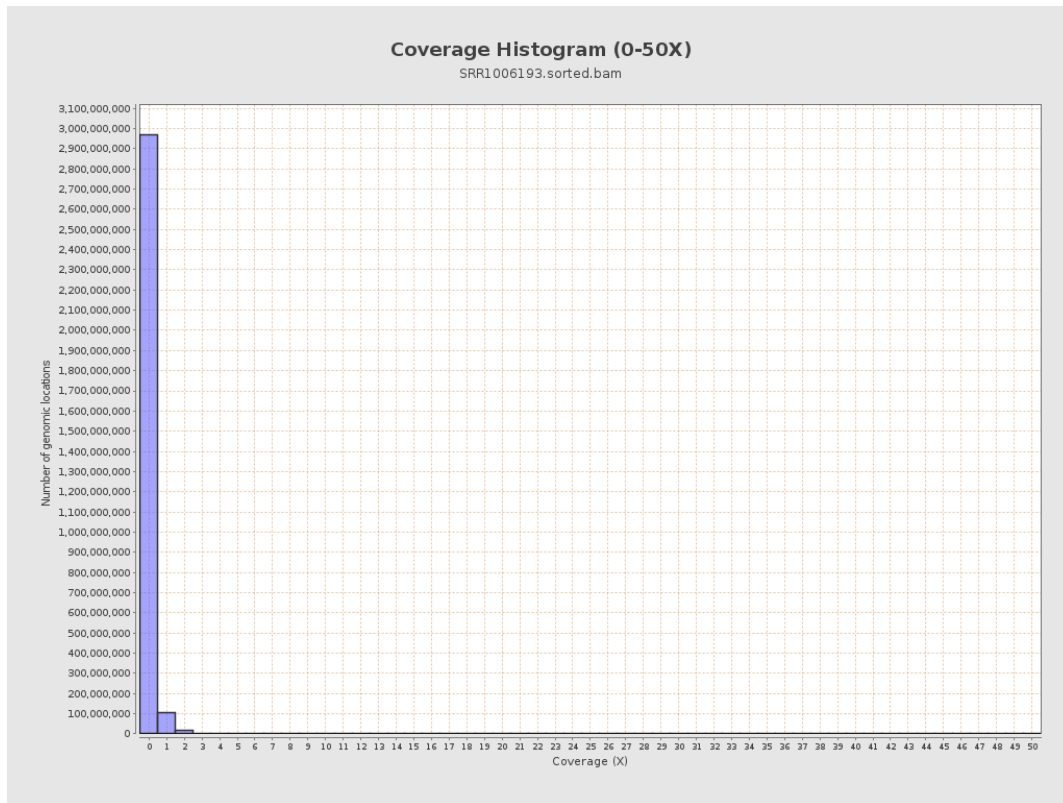
3. Results : Coverage across reference



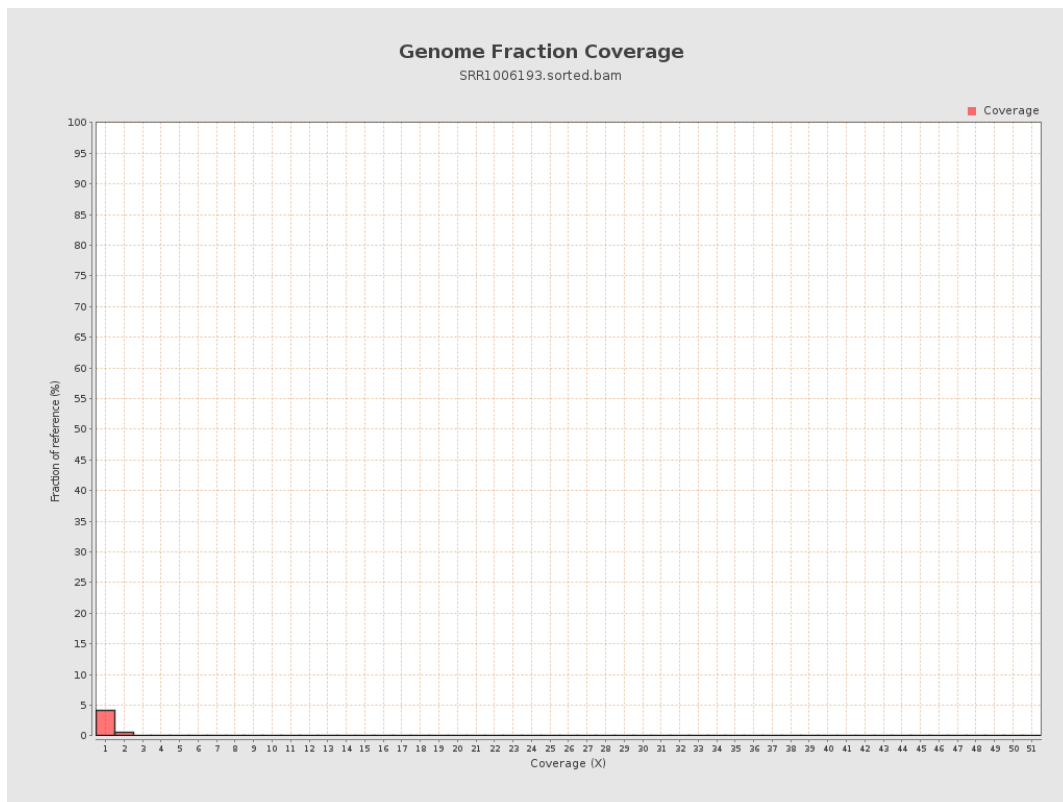
4. Results : Coverage Histogram



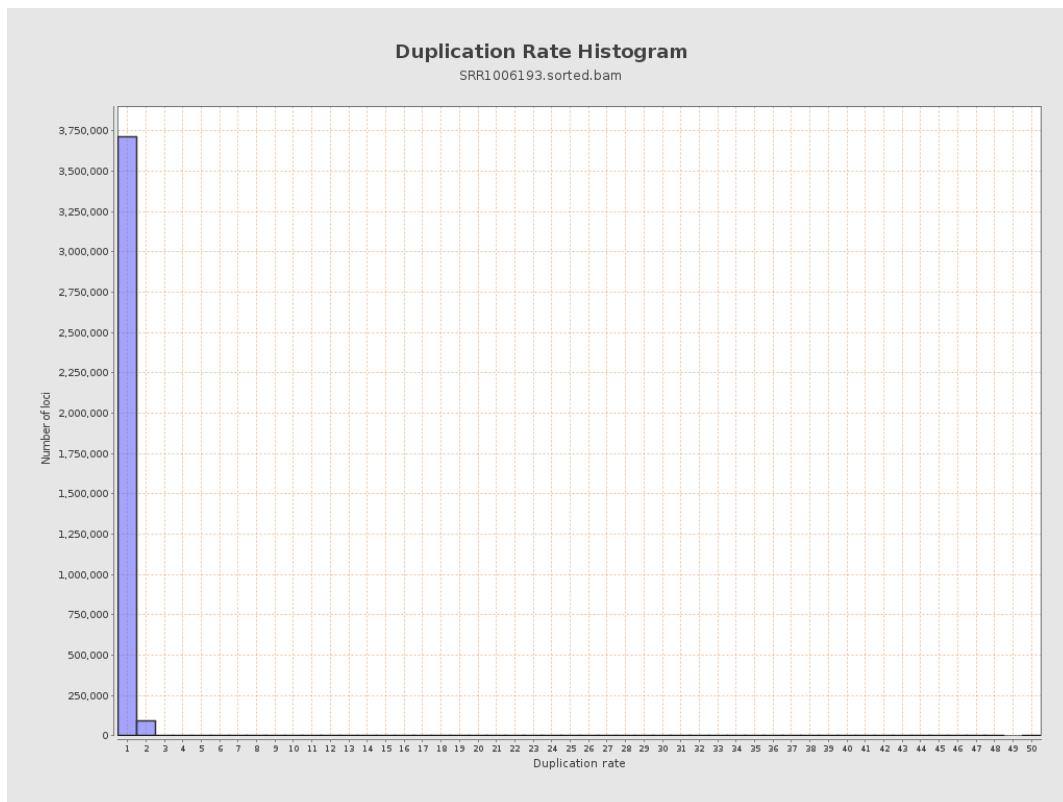
5. Results : Coverage Histogram (0-50X)



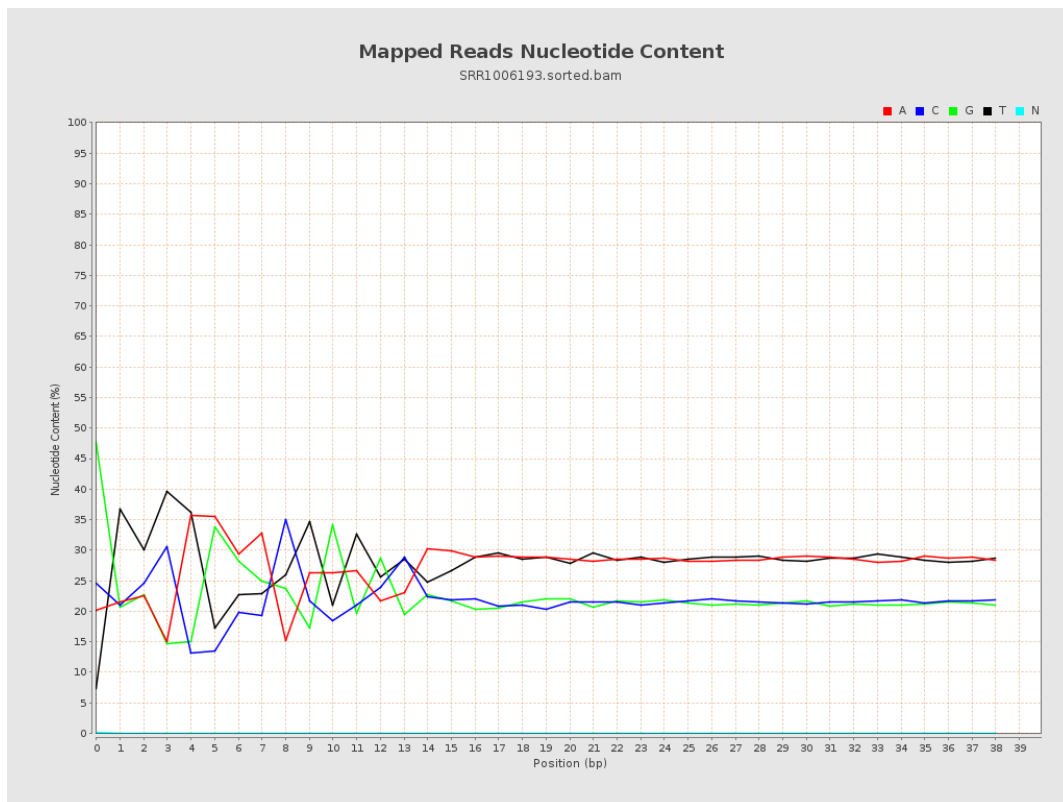
6. Results : Genome Fraction Coverage



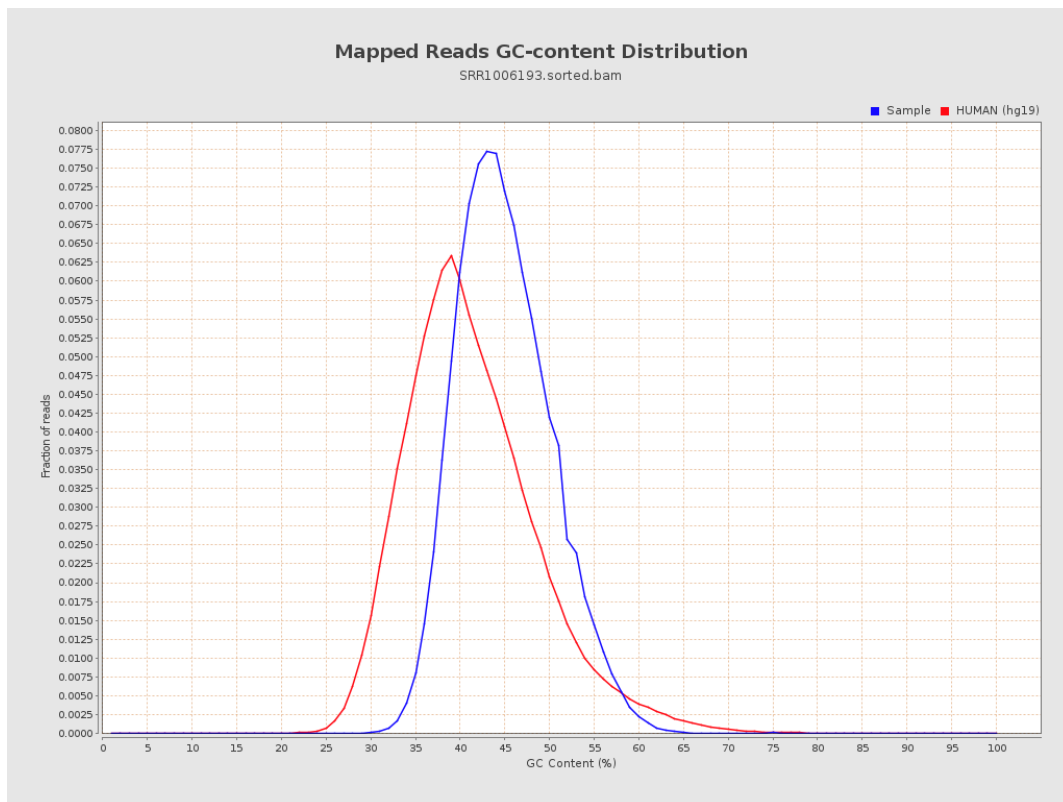
7. Results : Duplication Rate Histogram



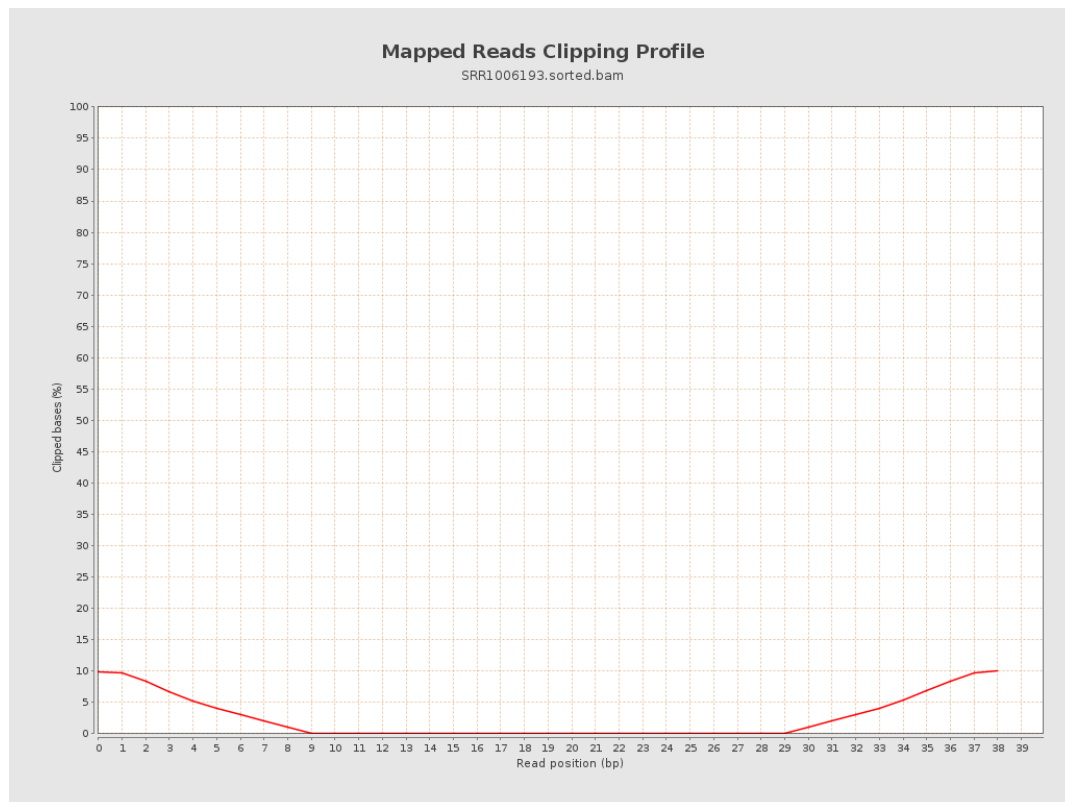
8. Results : Mapped Reads Nucleotide Content



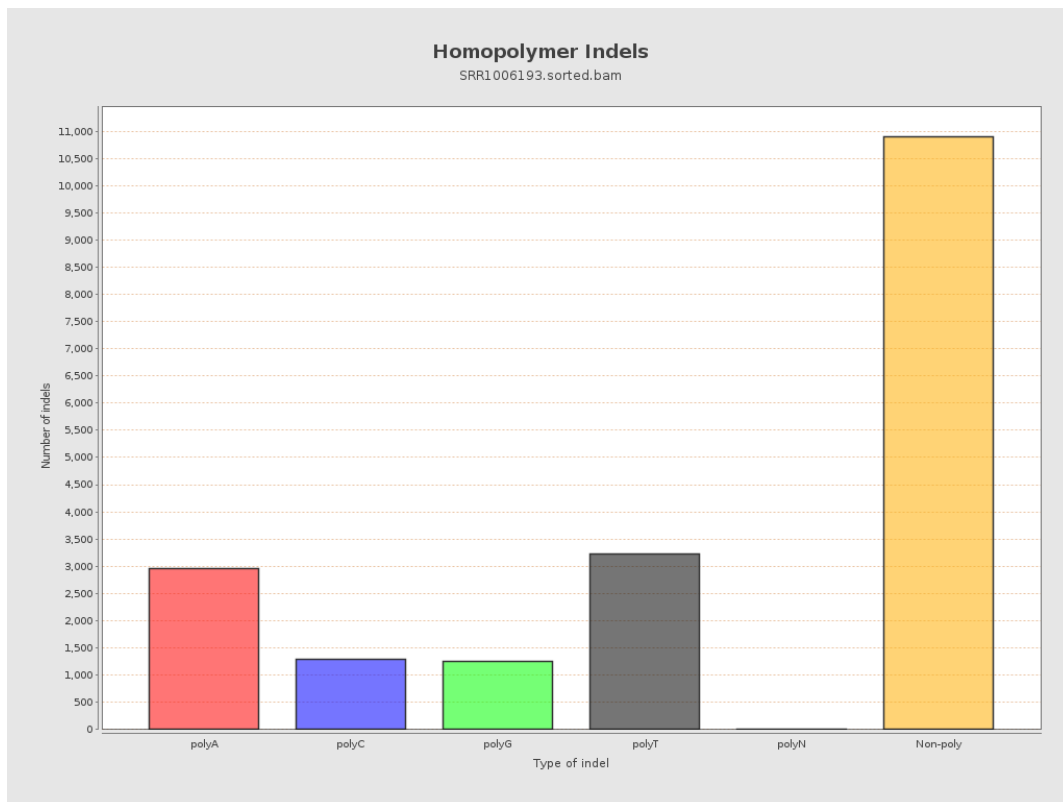
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



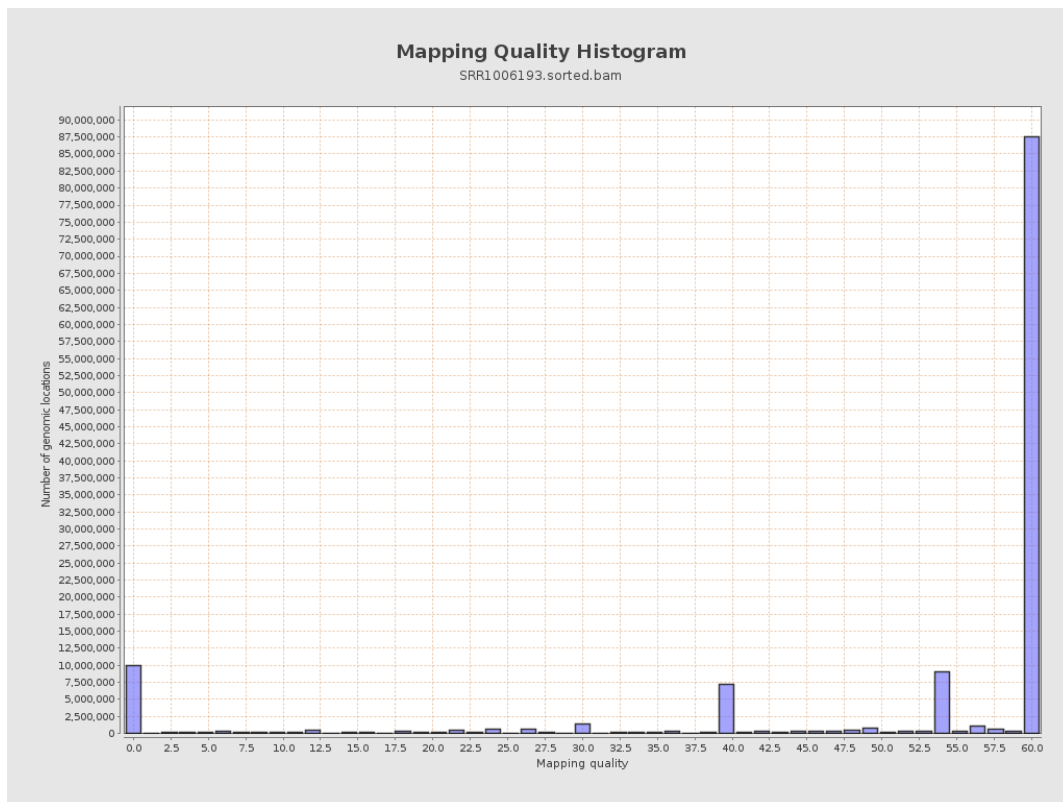
11. Results : Homopolymer Indels



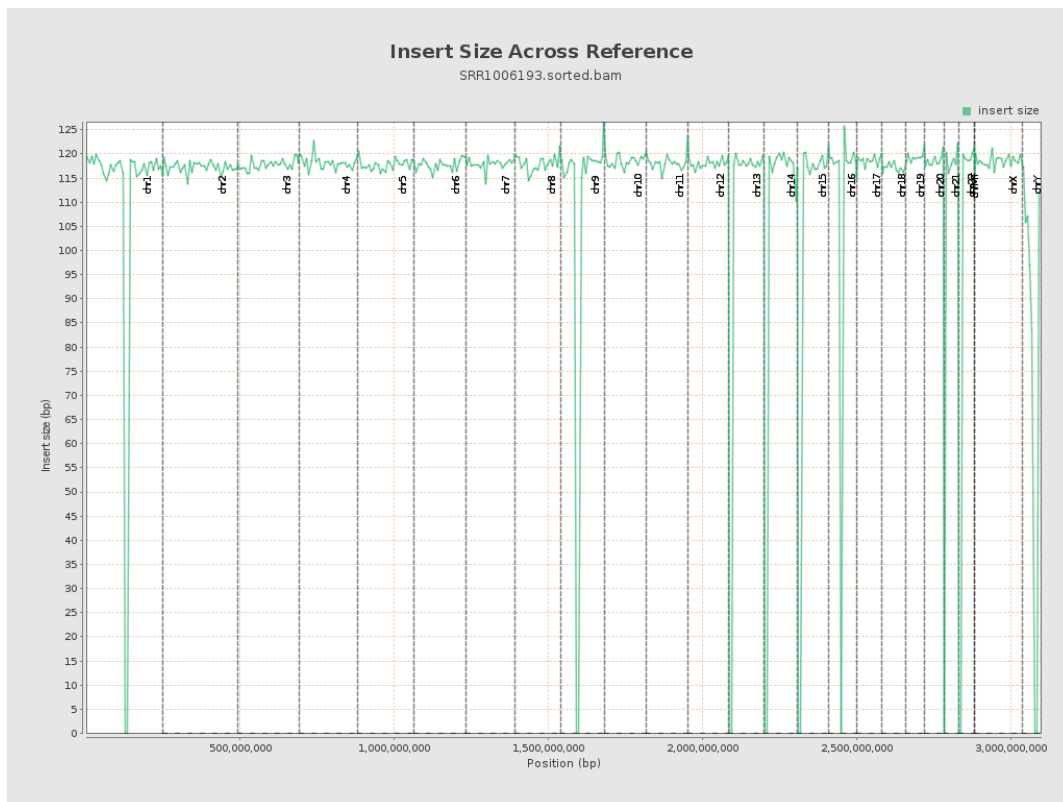
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

