

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 18:54:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006092.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_SRR1006092 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006092_1.fastq.gz SRR1006092_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 18:54:21 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006092.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,862,722
Mapped reads	6,951,196 / 88.41%
Unmapped reads	911,526 / 11.59%
Mapped paired reads	6,951,196 / 88.41%
Mapped reads, first in pair	3,510,371 / 44.65%
Mapped reads, second in pair	3,440,825 / 43.76%
Mapped reads, both in pair	6,390,560 / 81.28%
Mapped reads, singletons	560,636 / 7.13%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	473,941 / 6.03%
Duplication rate	6.19%
Clipped reads	553,137 / 7.03%

2.2. ACGT Content

Number/percentage of A's	69,566,978 / 25.93%
Number/percentage of C's	61,159,953 / 22.8%
Number/percentage of T's	72,208,669 / 26.92%
Number/percentage of G's	65,322,804 / 24.35%
Number/percentage of N's	11,199 / 0%
GC Percentage	47.15%

2.3. Coverage

Mean	0.0867
Standard Deviation	0.5079

2.4. Mapping Quality

Mean Mapping Quality	46.5
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2.5. Insert size

Mean	65,312.74
Standard Deviation	2,522,275.06
P25/Median/P75	66 / 93 / 127

2.6. Mismatches and indels

General error rate	0.38%
Mismatches	1,005,729
Insertions	8,347
Mapped reads with at least one insertion	0.12%
Deletions	21,350
Mapped reads with at least one deletion	0.31%
Homopolymer indels	43.12%

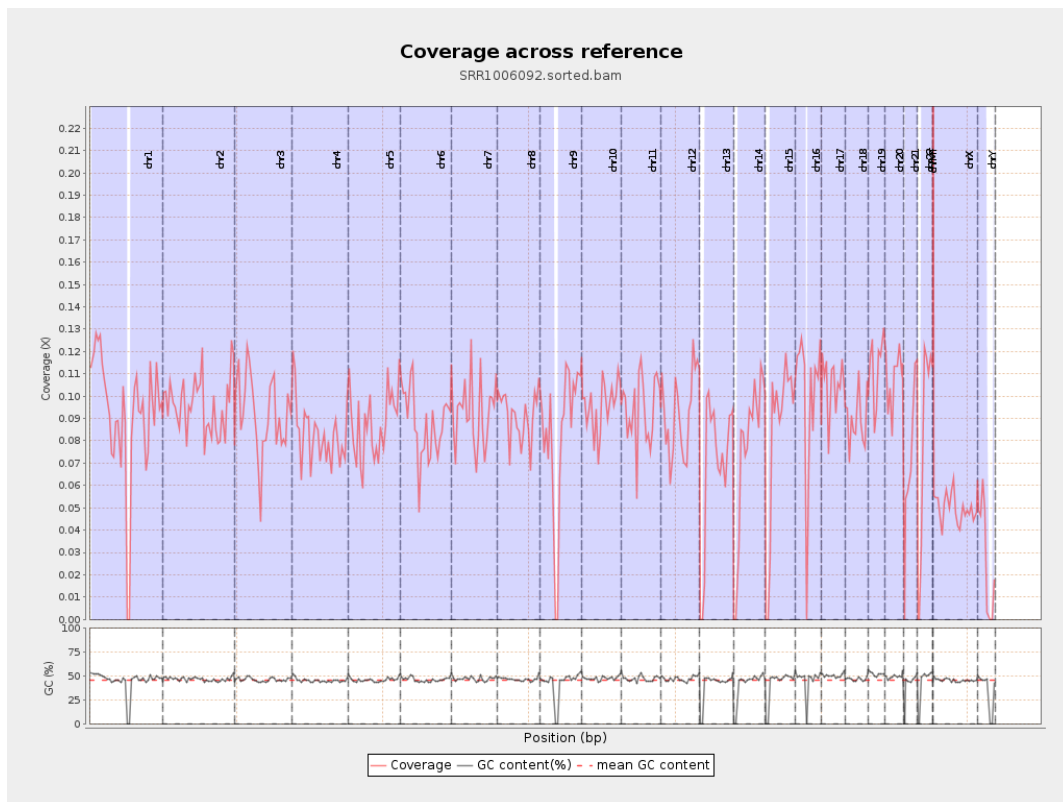
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

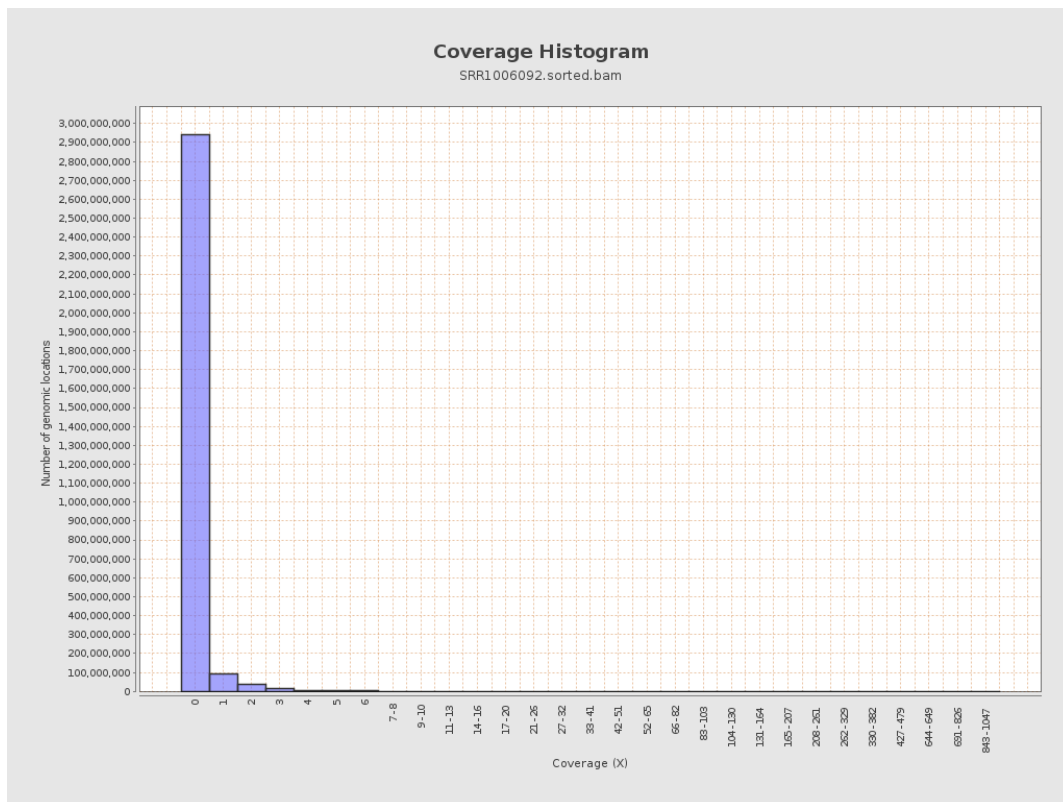
chr1	249250621	22884555	0.0918	0.5349
chr2	243199373	23319478	0.0959	0.5395
chr3	198022430	18152395	0.0917	0.4716
chr4	191154276	15793883	0.0826	0.4673
chr5	180915260	15919798	0.088	0.4649
chr6	171115067	14936211	0.0873	0.5089
chr7	159138663	14772414	0.0928	0.6056
chr8	146364022	13263358	0.0906	0.5128
chr9	141213431	11639934	0.0824	0.474
chr10	135534747	12960393	0.0956	0.4988
chr11	135006516	12673854	0.0939	0.7222
chr12	133851895	12402339	0.0927	0.481
chr13	115169878	7966330	0.0692	0.4145
chr14	107349540	8220331	0.0766	0.4396
chr15	102531392	8411653	0.082	0.4563
chr16	90354753	8981028	0.0994	0.5289
chr17	81195210	8611781	0.1061	0.5537
chr18	78077248	6894596	0.0883	0.537
chr19	59128983	6653389	0.1125	0.6259
chr20	63025520	6770832	0.1074	0.5322
chr21	48129895	3552664	0.0738	0.4771
chr22	51304566	4105548	0.08	0.5053
chrMT	16571	9930	0.5992	1.225
chrX	155270560	7757735	0.05	0.348

chrY	59373566	1642610	0.0277	0.2724
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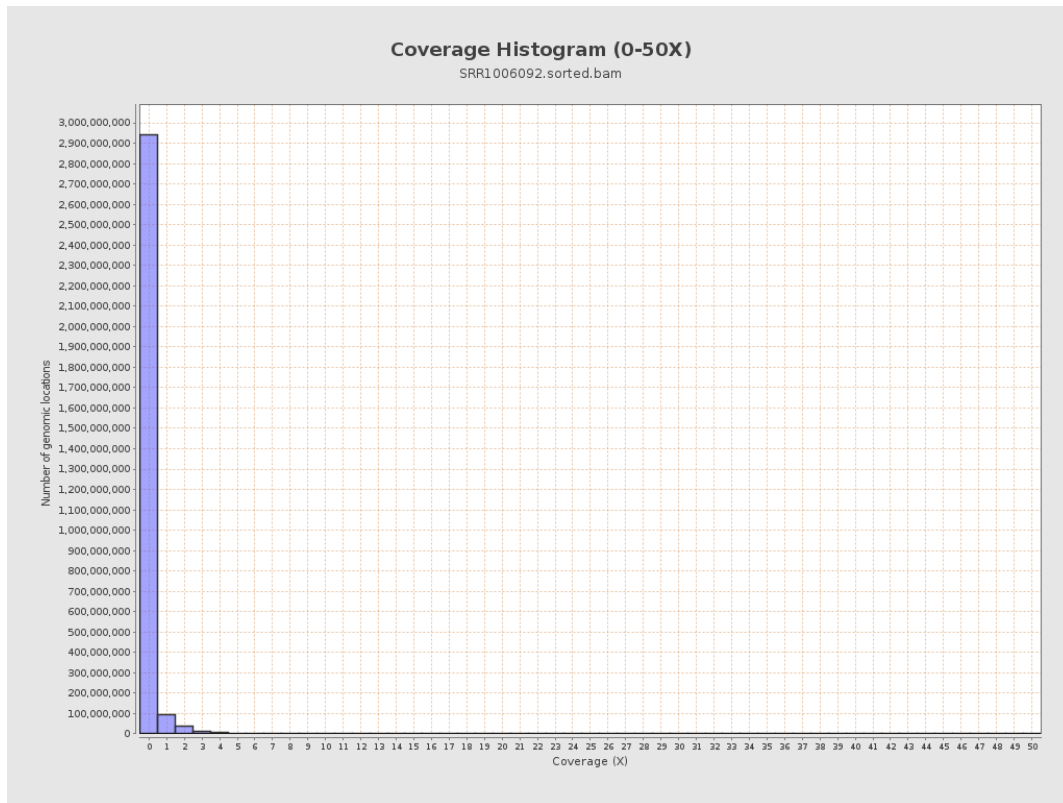
3. Results : Coverage across reference



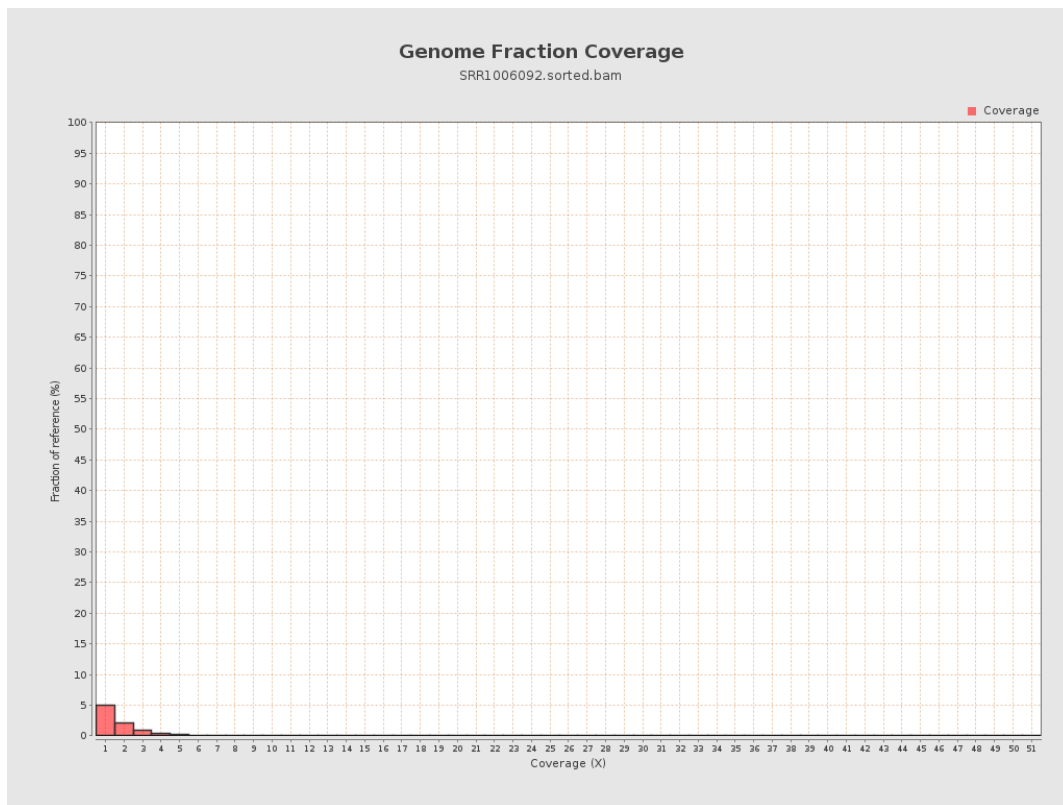
4. Results : Coverage Histogram



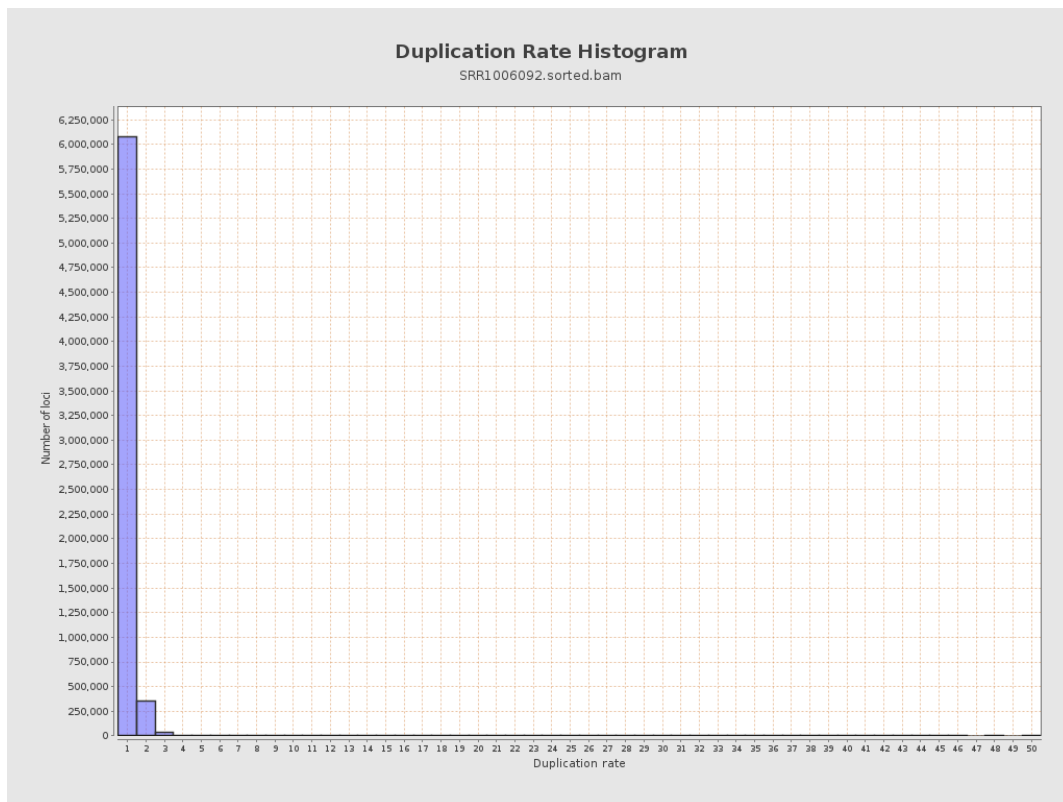
5. Results : Coverage Histogram (0-50X)



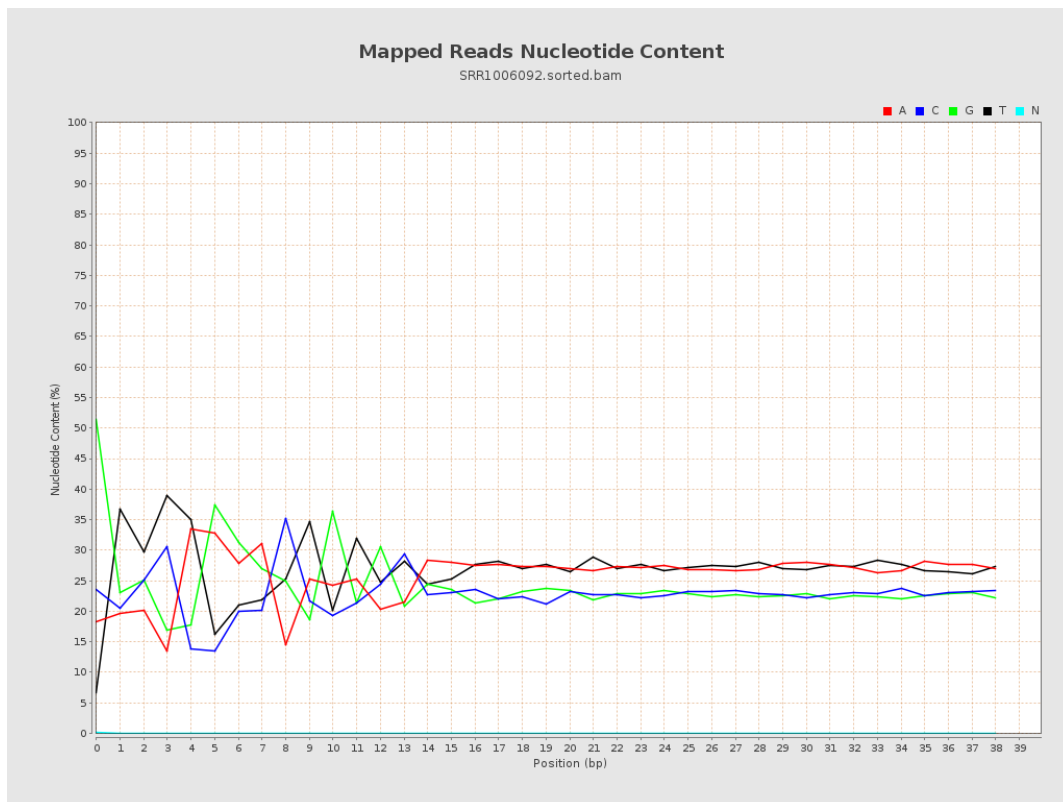
6. Results : Genome Fraction Coverage



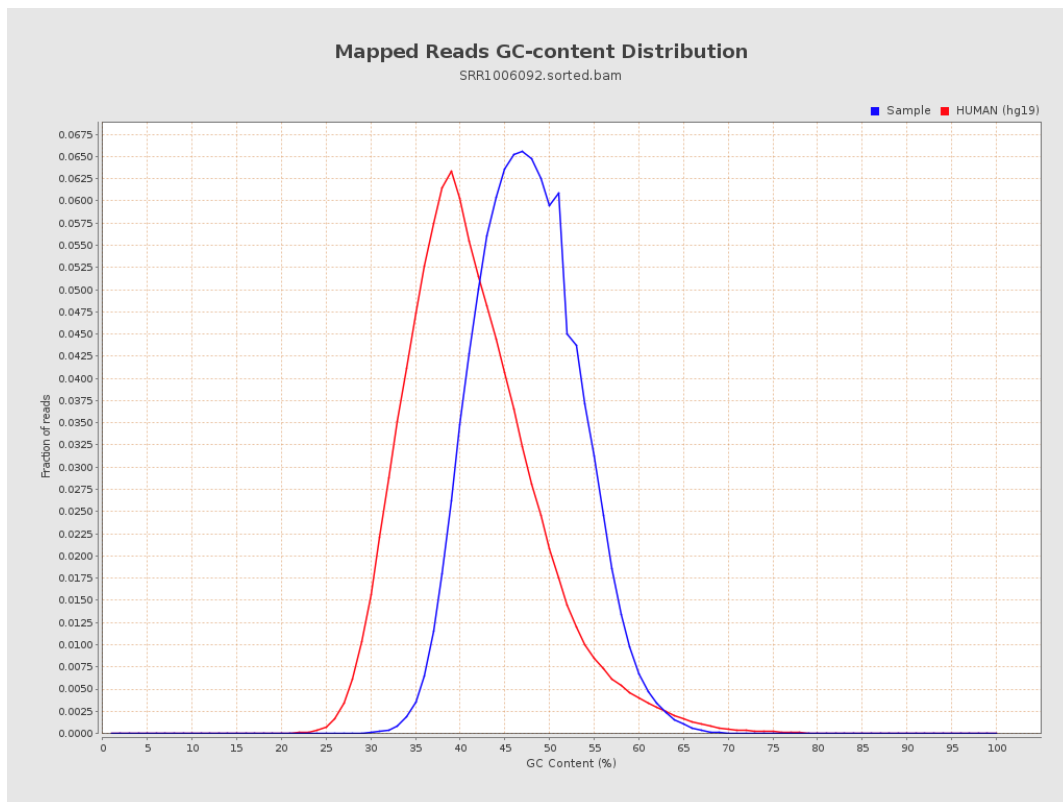
7. Results : Duplication Rate Histogram



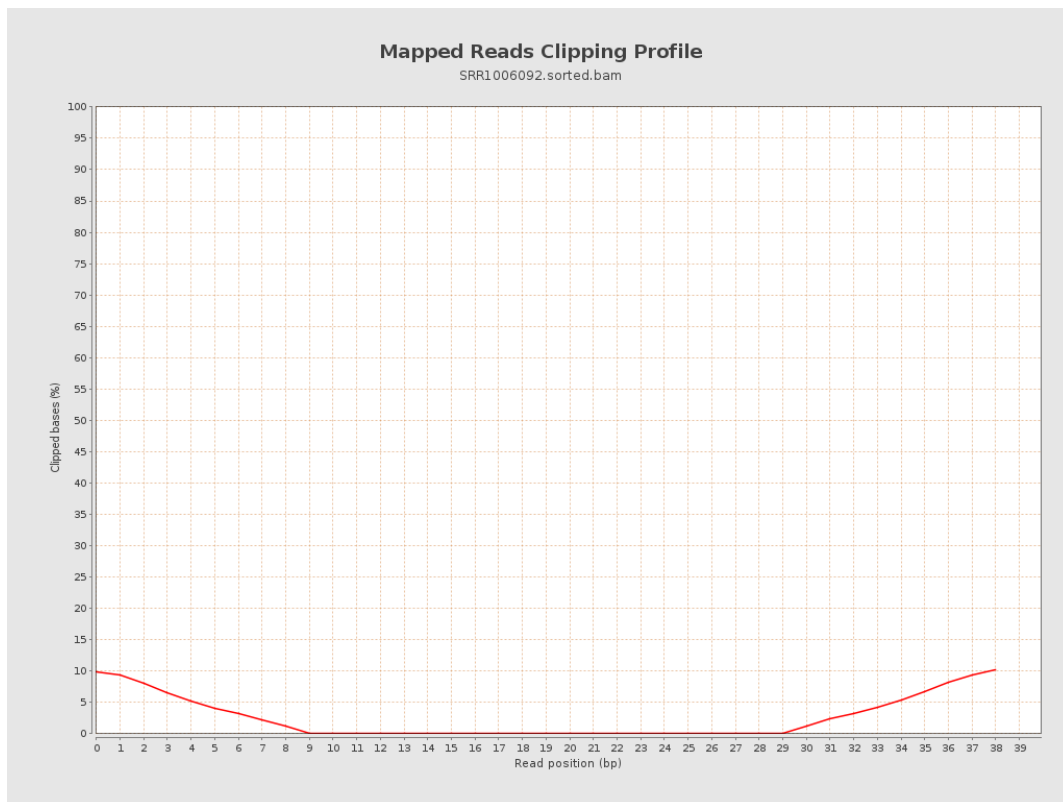
8. Results : Mapped Reads Nucleotide Content



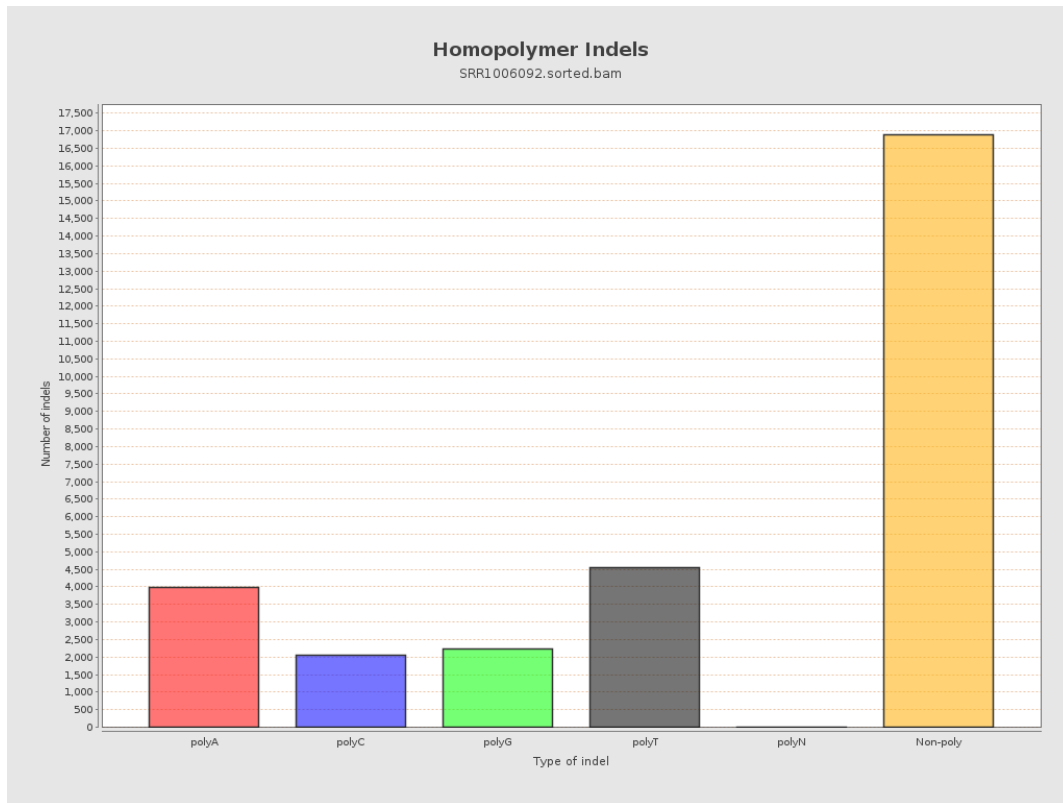
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



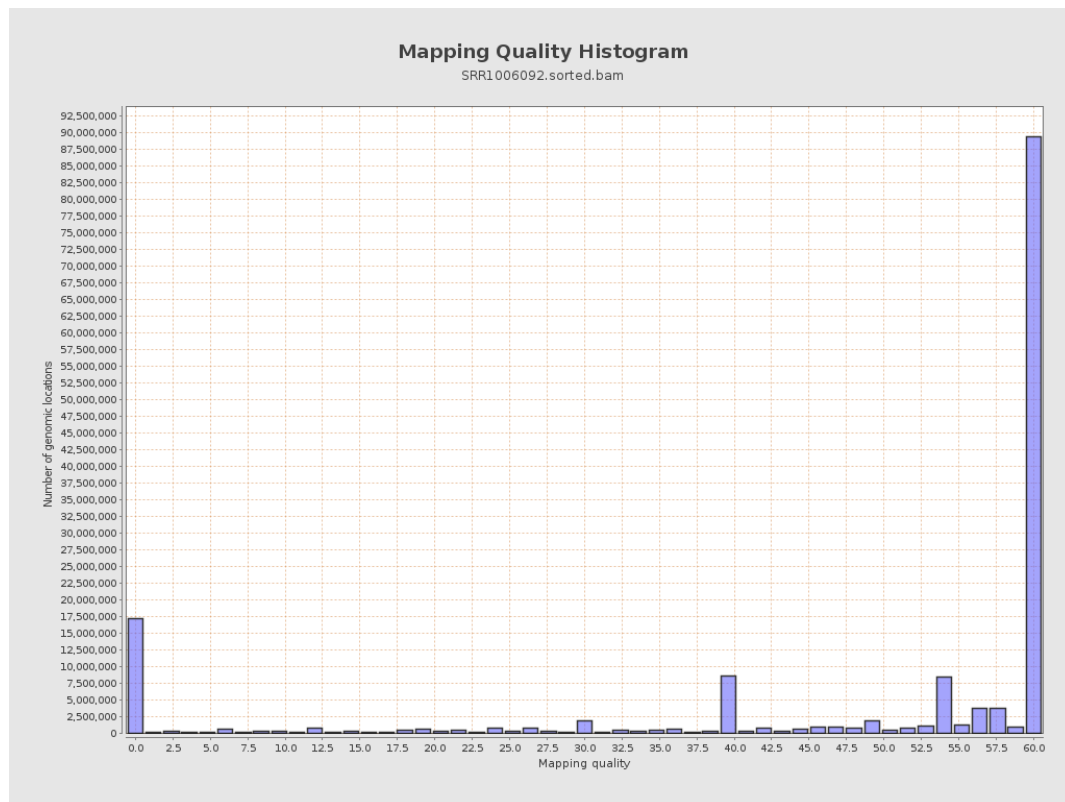
11. Results : Homopolymer Indels



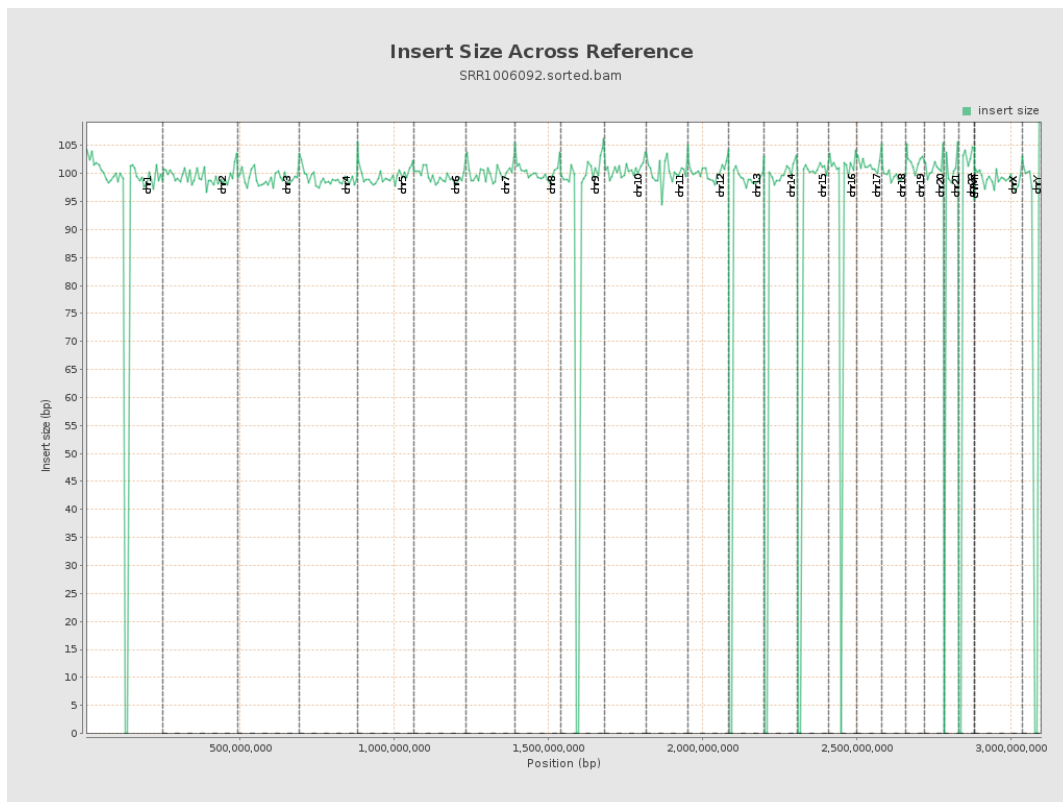
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

