

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 21:05:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006145.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_SRR1006145 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006145_1.fastq.gz SRR1006145_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 21:05:49 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006145.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,167,146
Mapped reads	7,908,475 / 86.27%
Unmapped reads	1,258,671 / 13.73%
Mapped paired reads	7,908,475 / 86.27%
Mapped reads, first in pair	4,016,547 / 43.81%
Mapped reads, second in pair	3,891,928 / 42.46%
Mapped reads, both in pair	7,247,342 / 79.06%
Mapped reads, singletons	661,133 / 7.21%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	279,332 / 3.05%
Duplication rate	2.82%
Clipped reads	517,079 / 5.64%

2.2. ACGT Content

Number/percentage of A's	85,166,354 / 27.84%
Number/percentage of C's	65,974,822 / 21.57%
Number/percentage of T's	86,504,184 / 28.28%
Number/percentage of G's	68,239,513 / 22.31%
Number/percentage of N's	13,766 / 0%
GC Percentage	43.88%

2.3. Coverage

Mean	0.0988
Standard Deviation	0.5585

2.4. Mapping Quality

Mean Mapping Quality	47.72
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2.5. Insert size

Mean	61,825.29
Standard Deviation	2,392,912.5
P25/Median/P75	83 / 124 / 165

2.6. Mismatches and indels

General error rate	0.43%
Mismatches	1,313,845
Insertions	8,588
Mapped reads with at least one insertion	0.11%
Deletions	24,864
Mapped reads with at least one deletion	0.31%
Homopolymer indels	45.92%

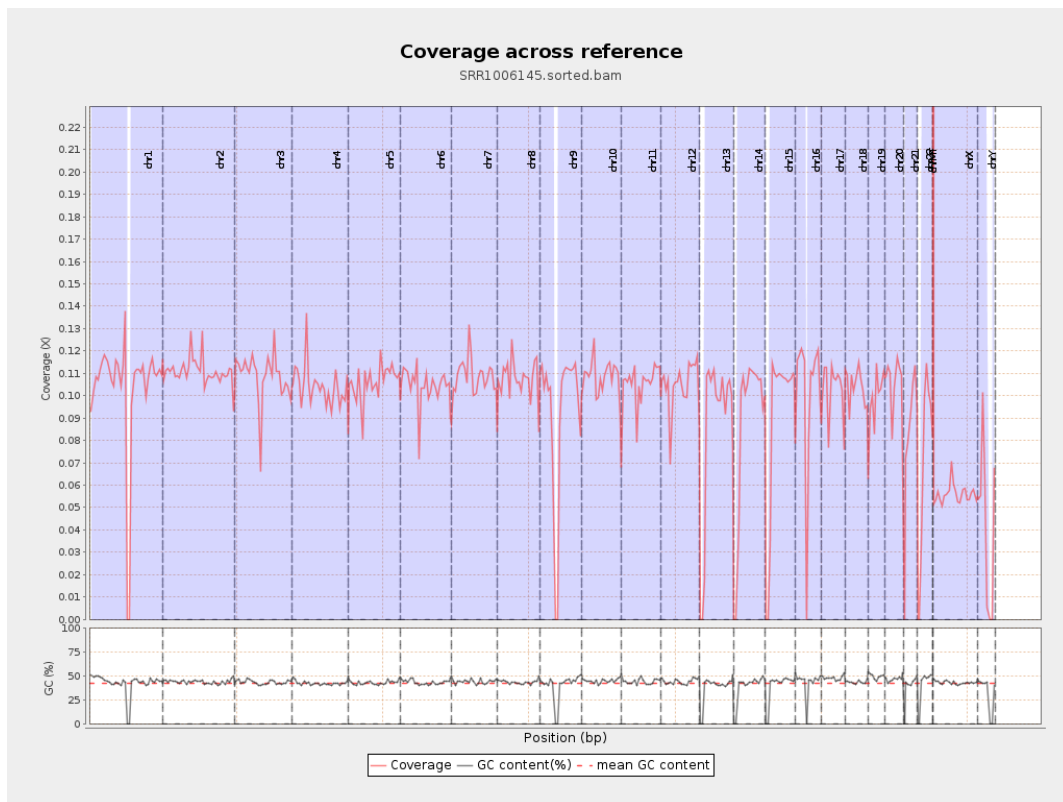
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

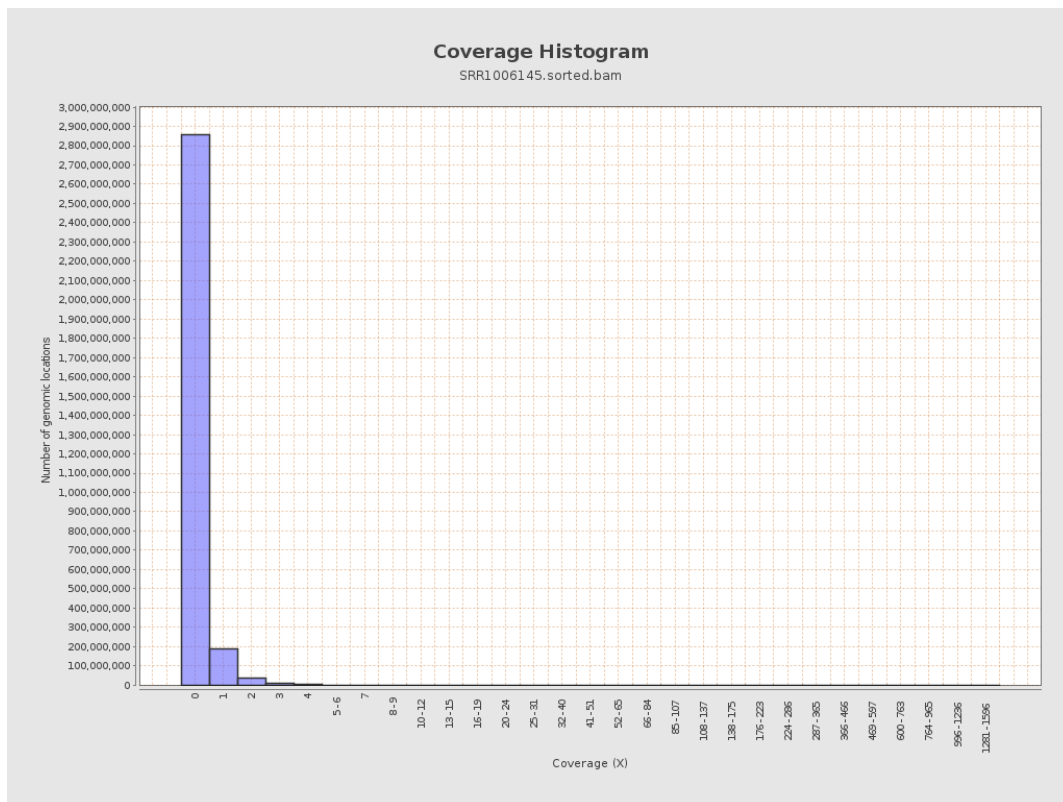
chr1	249250621	25818769	0.1036	0.958
chr2	243199373	27001425	0.111	0.5343
chr3	198022430	21474762	0.1084	0.4007
chr4	191154276	19969384	0.1045	0.4336
chr5	180915260	19188275	0.1061	0.398
chr6	171115067	17895381	0.1046	0.4296
chr7	159138663	17289452	0.1086	0.754
chr8	146364022	15743489	0.1076	0.9034
chr9	141213431	13027537	0.0923	0.4578
chr10	135534747	14729940	0.1087	0.5086
chr11	135006516	14212896	0.1053	0.5585
chr12	133851895	14107129	0.1054	0.4003
chr13	115169878	9931500	0.0862	0.3555
chr14	107349540	9459071	0.0881	0.3826
chr15	102531392	9032476	0.0881	0.3631
chr16	90354753	8977261	0.0994	0.4232
chr17	81195210	8408492	0.1036	0.4558
chr18	78077248	8112692	0.1039	0.6908
chr19	59128983	5879745	0.0994	0.7347
chr20	63025520	6623850	0.1051	0.4086
chr21	48129895	4053311	0.0842	0.4047
chr22	51304566	3609302	0.0704	0.3702
chrMT	16571	146854	8.8621	5.5229
chrX	155270560	8696104	0.056	0.3338

chrY	59373566	2541811	0.0428	0.4105
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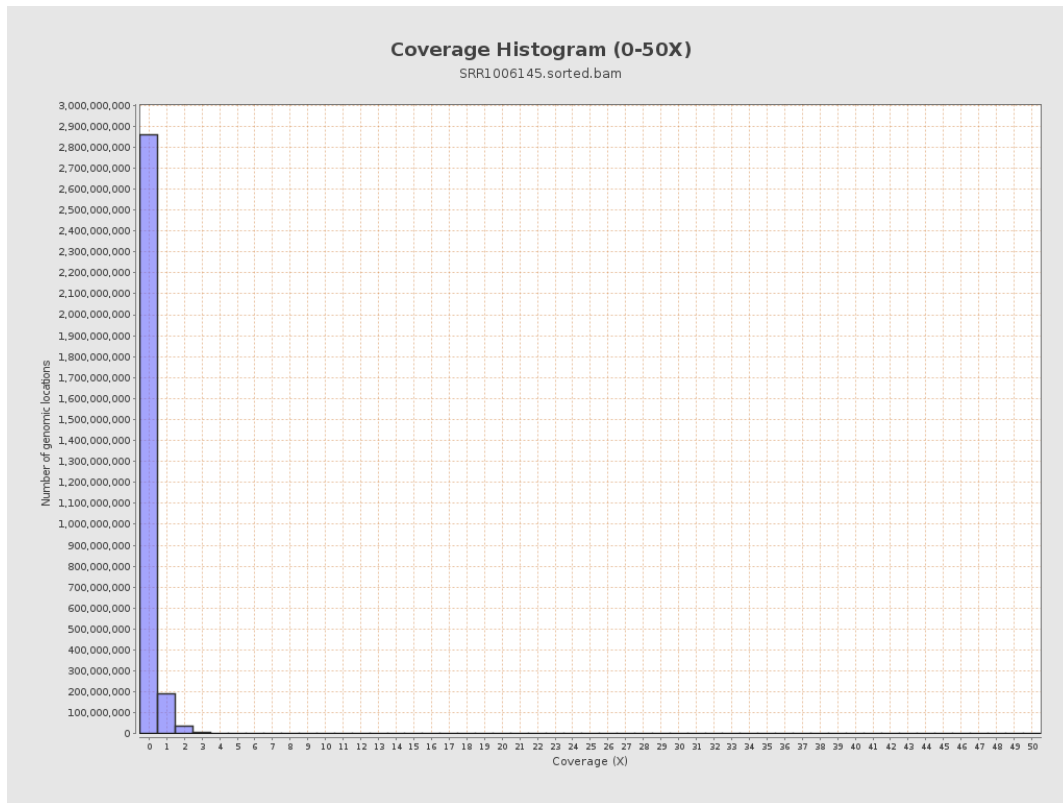
3. Results : Coverage across reference



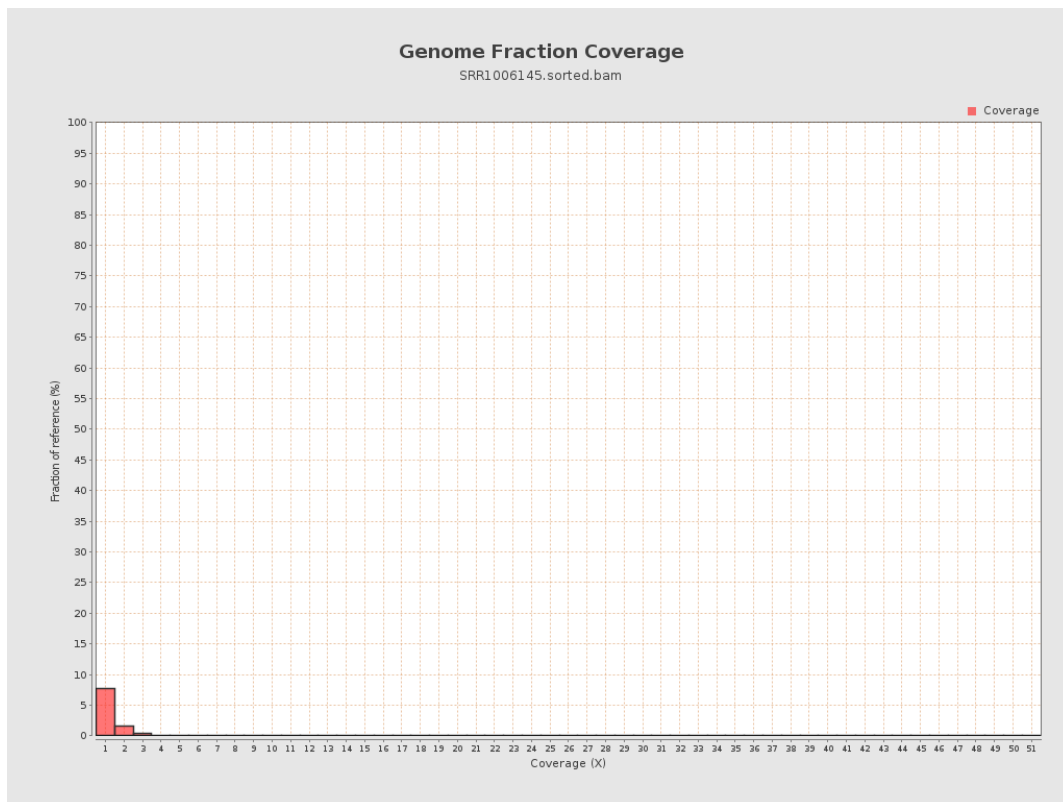
4. Results : Coverage Histogram



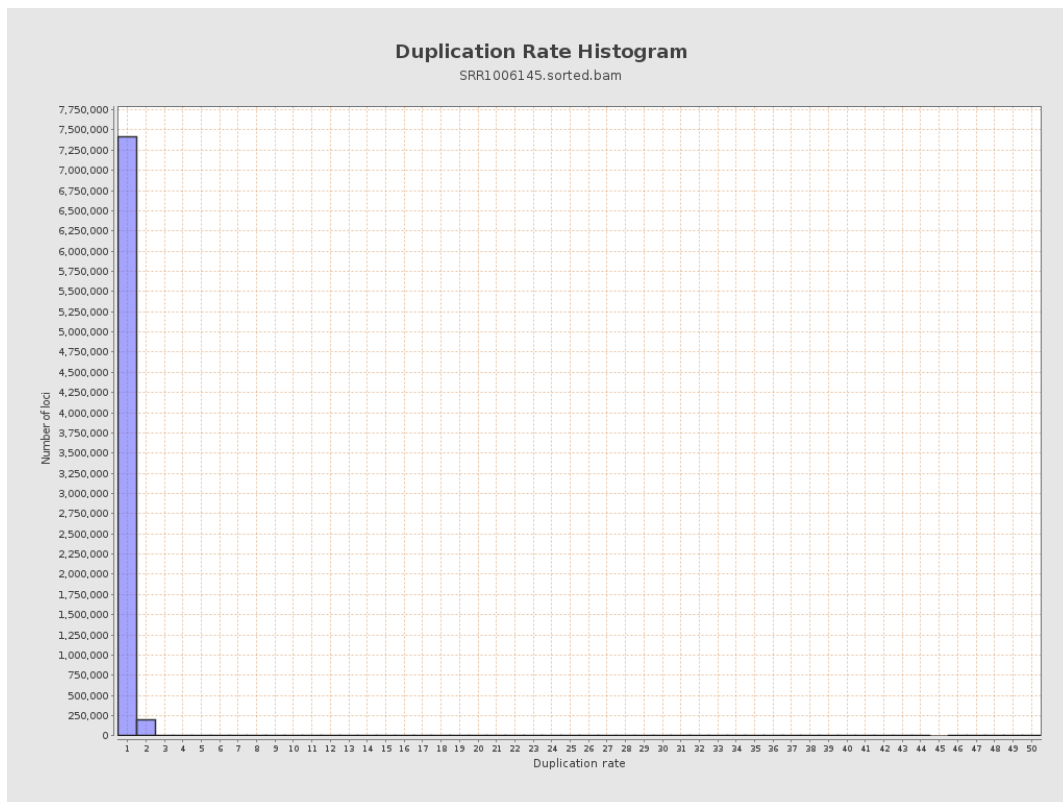
5. Results : Coverage Histogram (0-50X)



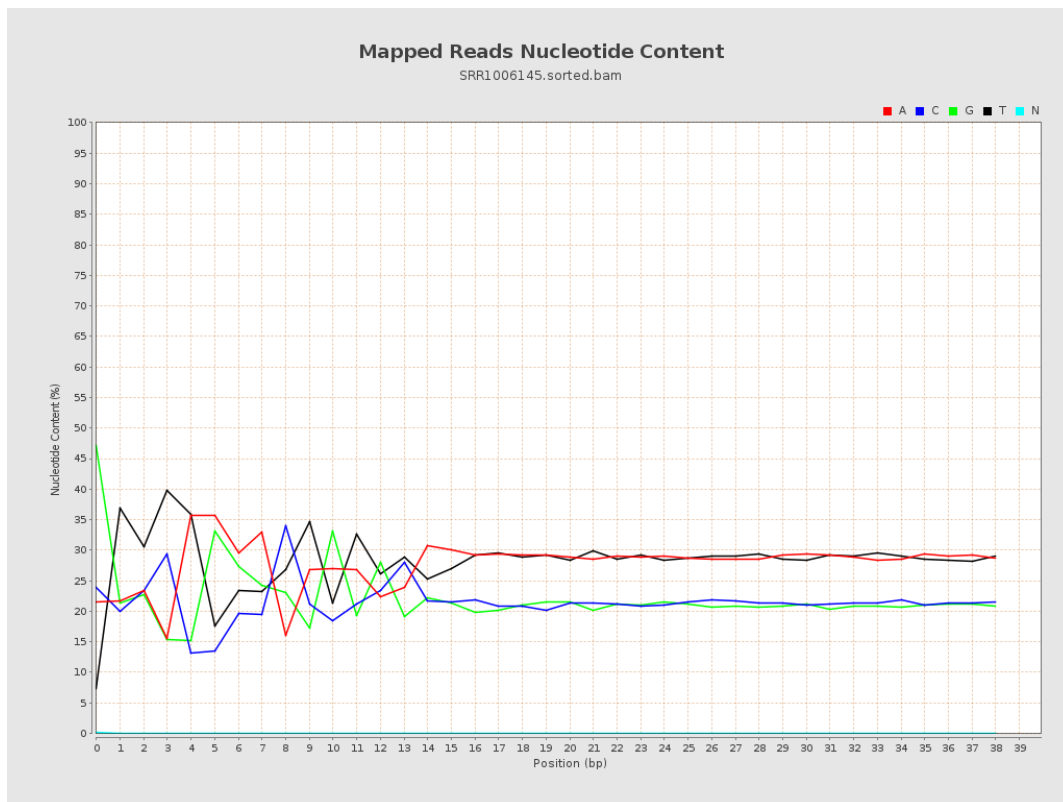
6. Results : Genome Fraction Coverage



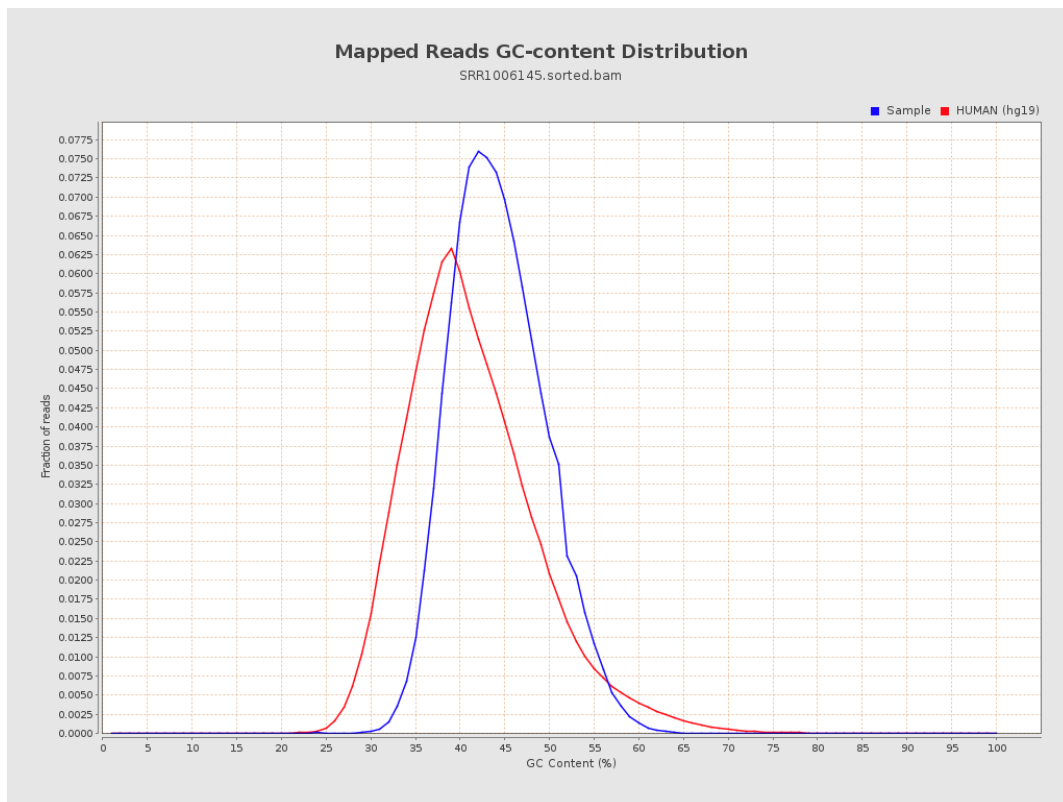
7. Results : Duplication Rate Histogram



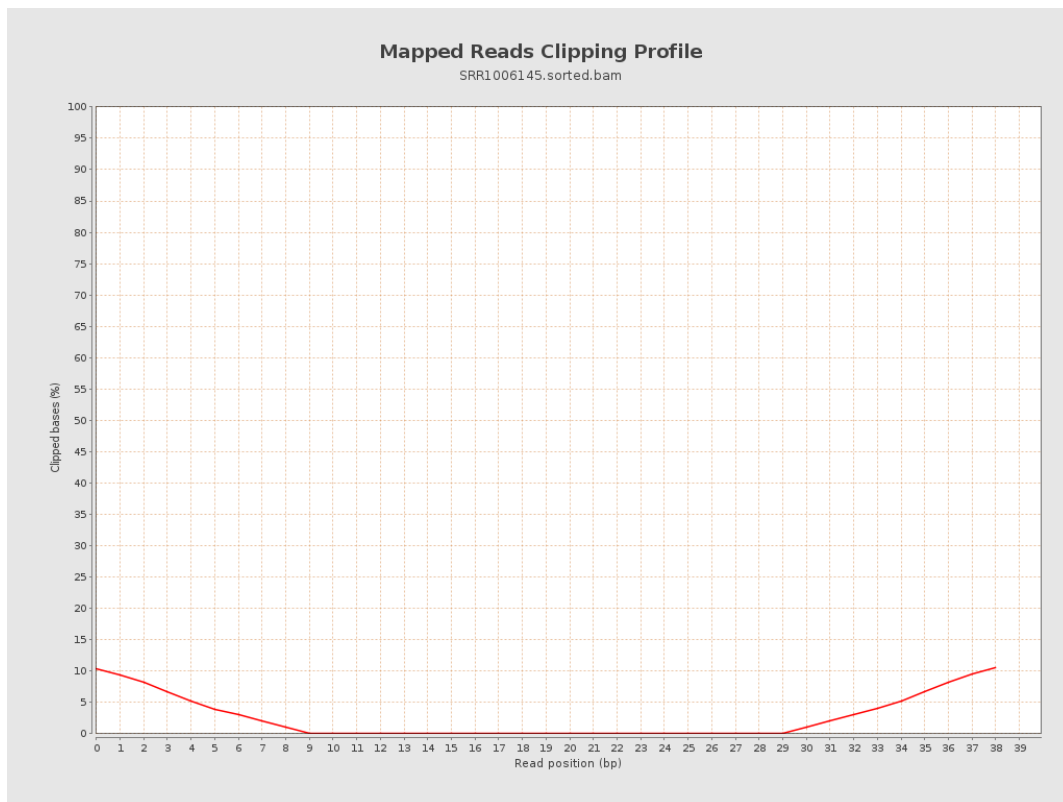
8. Results : Mapped Reads Nucleotide Content



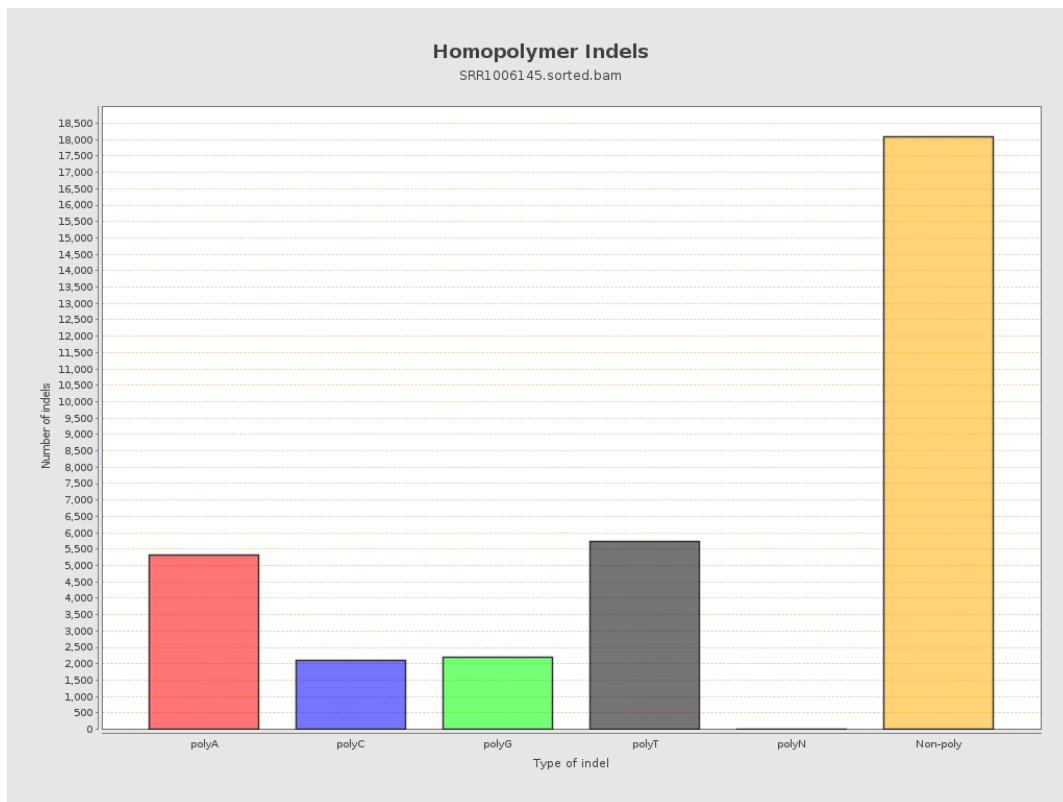
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



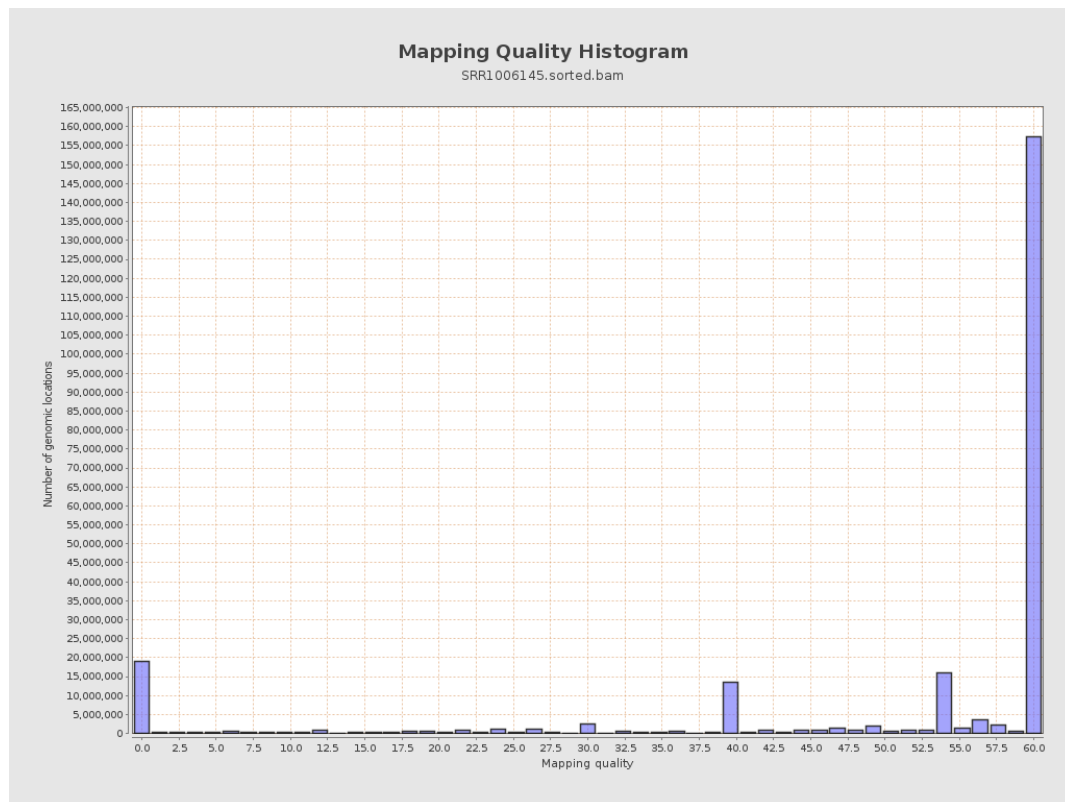
11. Results : Homopolymer Indels



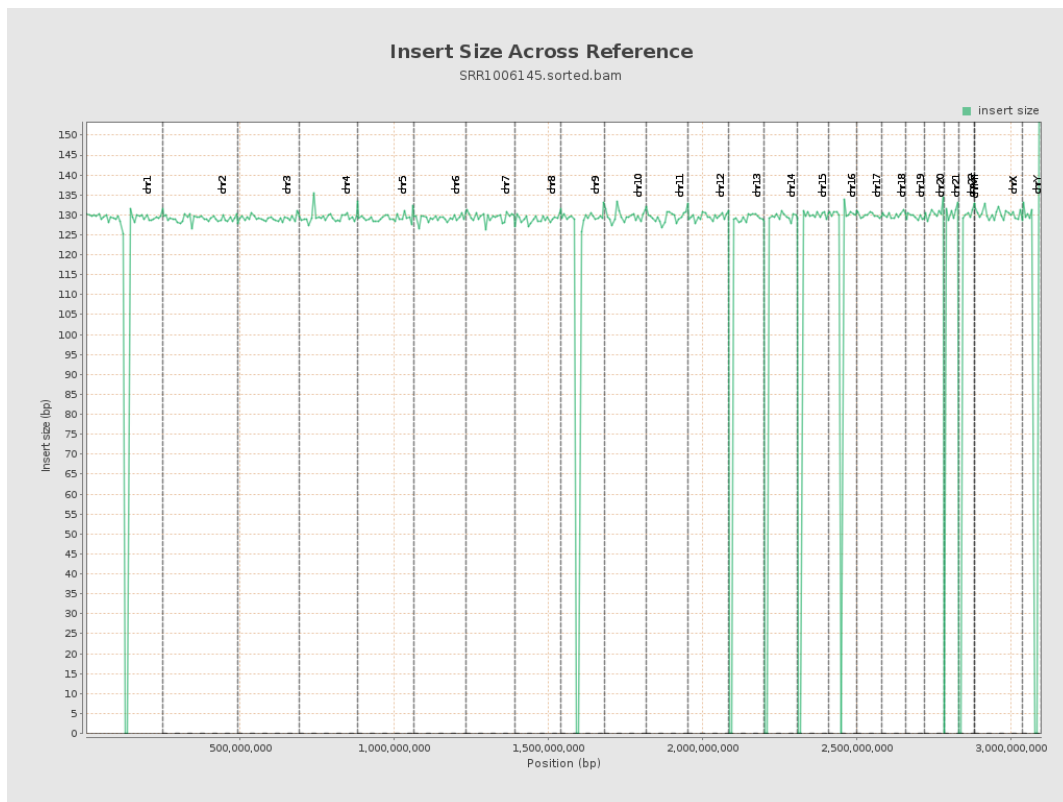
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

