

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 16:08:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006045.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_SRR1006045 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006045_1.fastq.gz SRR1006045_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 16:08:53 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006045.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,485,278
Mapped reads	5,674,059 / 87.49%
Unmapped reads	811,219 / 12.51%
Mapped paired reads	5,674,059 / 87.49%
Mapped reads, first in pair	2,881,663 / 44.43%
Mapped reads, second in pair	2,792,396 / 43.06%
Mapped reads, both in pair	5,248,804 / 80.93%
Mapped reads, singletons	425,255 / 6.56%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	168,242 / 2.59%
Duplication rate	2.48%
Clipped reads	384,898 / 5.93%

2.2. ACGT Content

Number/percentage of A's	60,206,792 / 27.43%
Number/percentage of C's	48,172,572 / 21.95%
Number/percentage of T's	61,495,999 / 28.02%
Number/percentage of G's	49,542,809 / 22.57%
Number/percentage of N's	89,452 / 0.04%
GC Percentage	44.52%

2.3. Coverage

Mean	0.0709
Standard Deviation	0.3825

2.4. Mapping Quality

Mean Mapping Quality	47.6
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2.5. Insert size

Mean	50,319.81
Standard Deviation	2,190,680.69
P25/Median/P75	71 / 105 / 156

2.6. Mismatches and indels

General error rate	0.55%
Mismatches	1,201,431
Insertions	6,537
Mapped reads with at least one insertion	0.12%
Deletions	18,536
Mapped reads with at least one deletion	0.33%
Homopolymer indels	45.46%

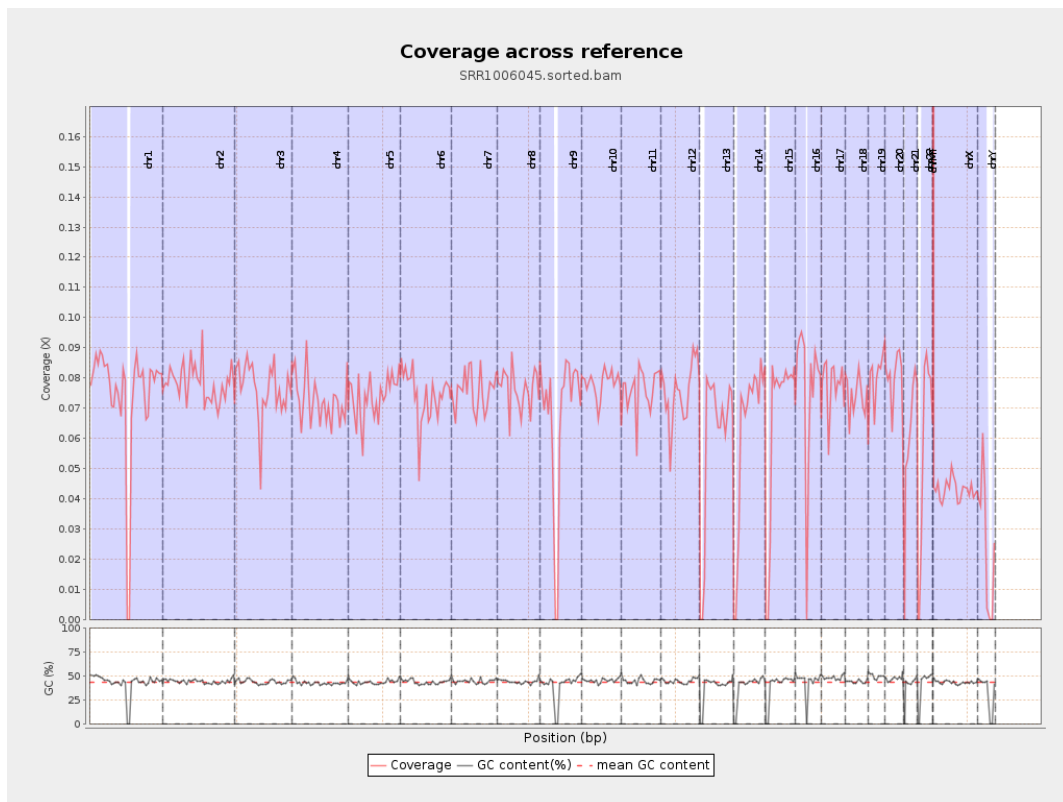
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

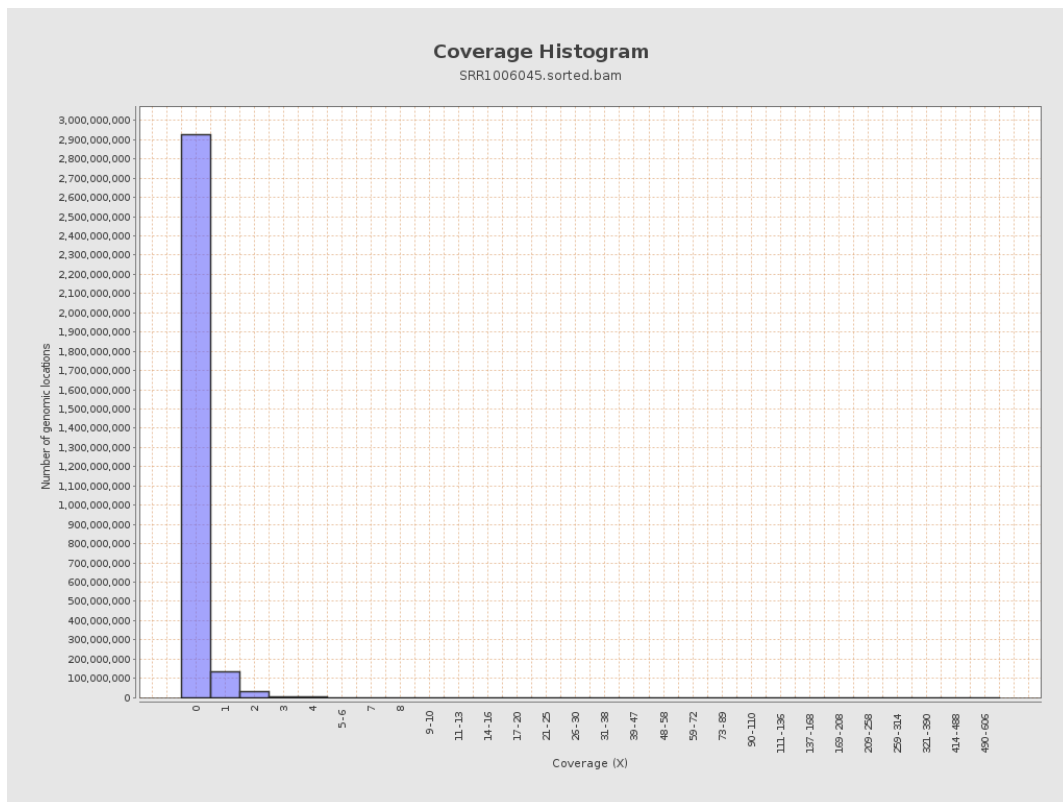
chr1	249250621	18585247	0.0746	0.4288
chr2	243199373	19062830	0.0784	0.4406
chr3	198022430	15126688	0.0764	0.3354
chr4	191154276	13911844	0.0728	0.3513
chr5	180915260	13380768	0.074	0.3313
chr6	171115067	12683012	0.0741	0.3509
chr7	159138663	12051166	0.0757	0.5126
chr8	146364022	11138418	0.0761	0.4072
chr9	141213431	9444219	0.0669	0.3703
chr10	135534747	10597316	0.0782	0.3803
chr11	135006516	10243066	0.0759	0.4749
chr12	133851895	10134347	0.0757	0.338
chr13	115169878	6908124	0.06	0.2978
chr14	107349540	6776643	0.0631	0.3215
chr15	102531392	6623221	0.0646	0.3105
chr16	90354753	6835491	0.0757	0.3876
chr17	81195210	6350053	0.0782	0.3753
chr18	78077248	5769146	0.0739	0.5029
chr19	59128983	4755554	0.0804	0.4408
chr20	63025520	5049797	0.0801	0.3555
chr21	48129895	2936133	0.061	0.3451
chr22	51304566	2916221	0.0568	0.3151
chrMT	16571	45786	2.763	3.7401
chrX	155270560	6672845	0.043	0.271

chrY	59373566	1533676	0.0258	0.2566
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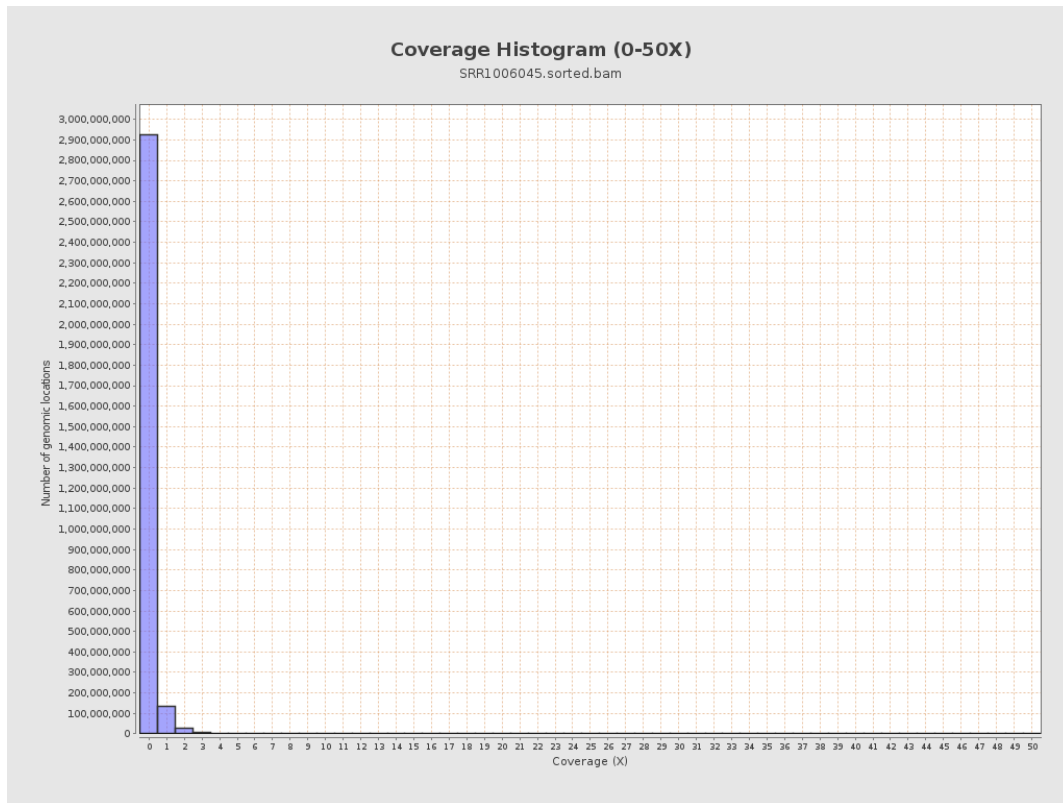
3. Results : Coverage across reference



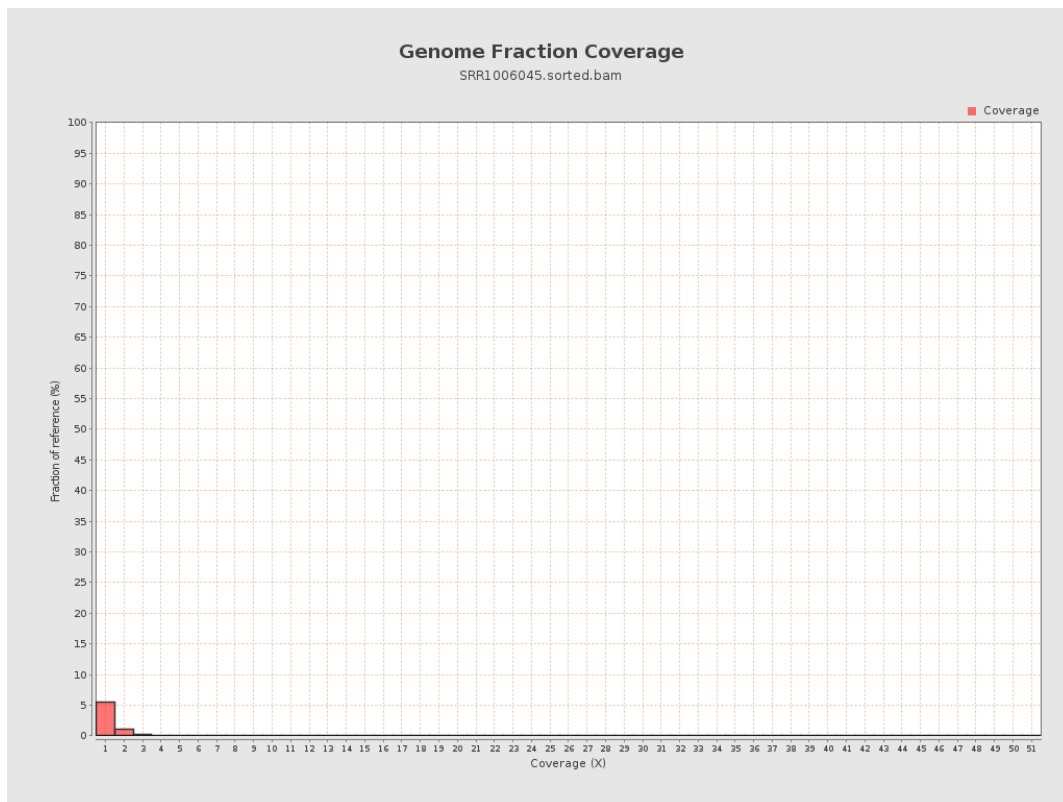
4. Results : Coverage Histogram



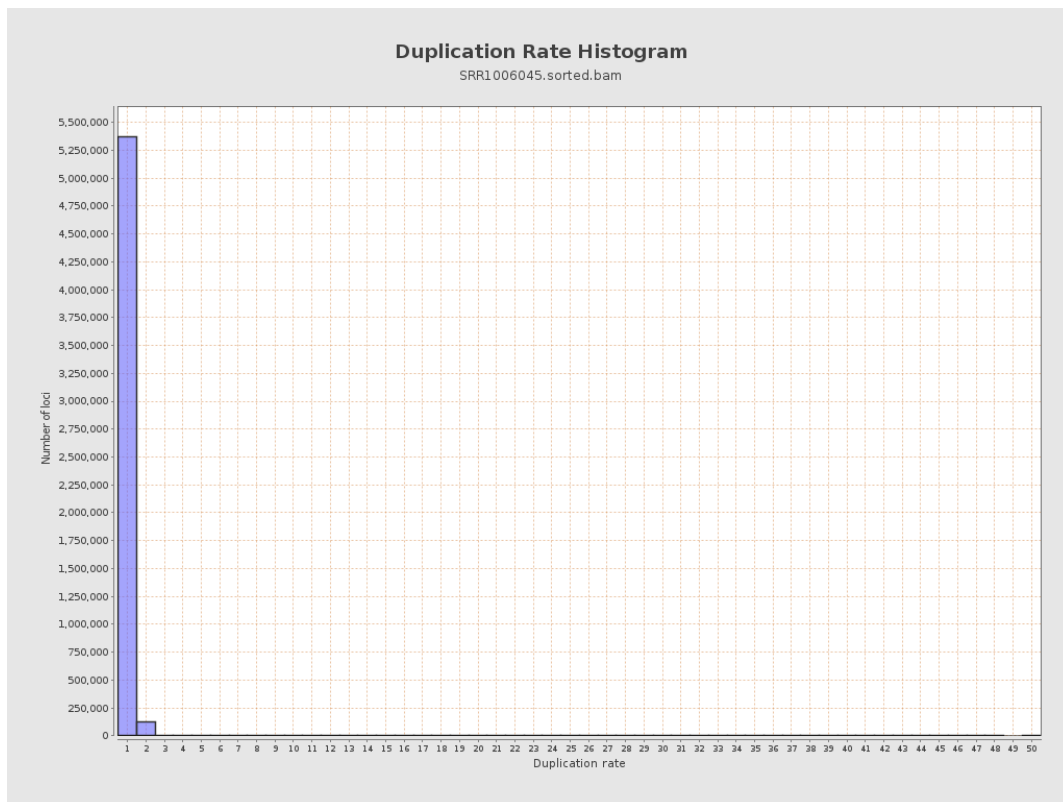
5. Results : Coverage Histogram (0-50X)



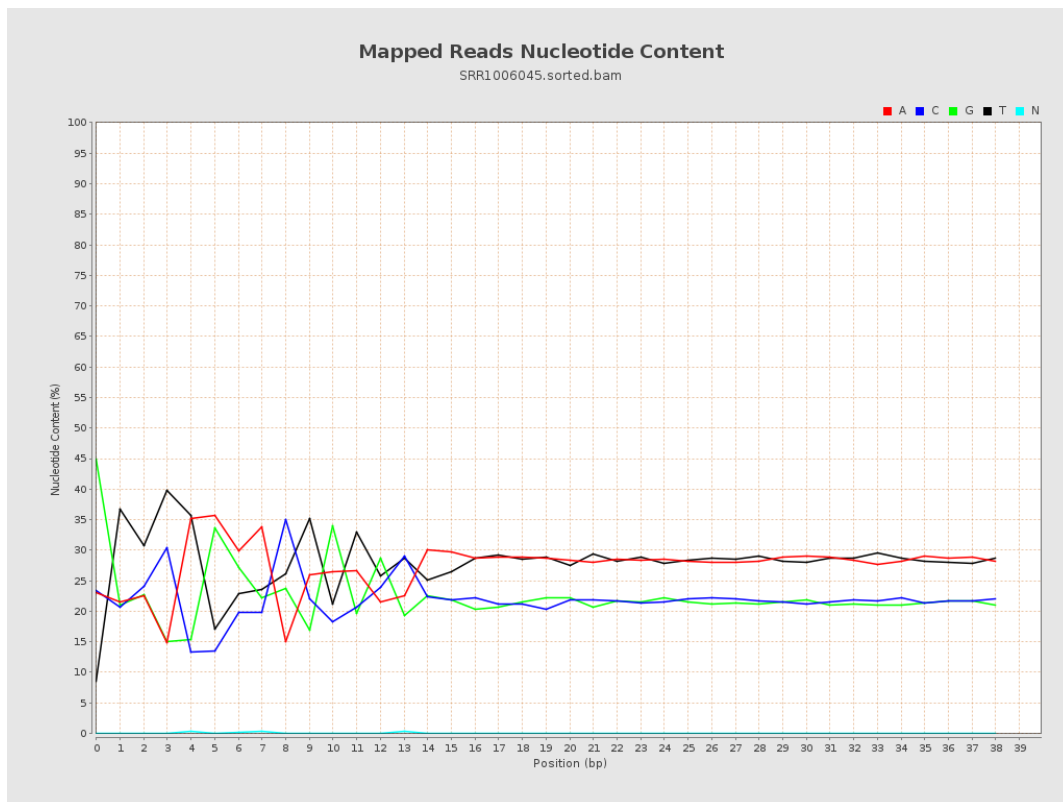
6. Results : Genome Fraction Coverage



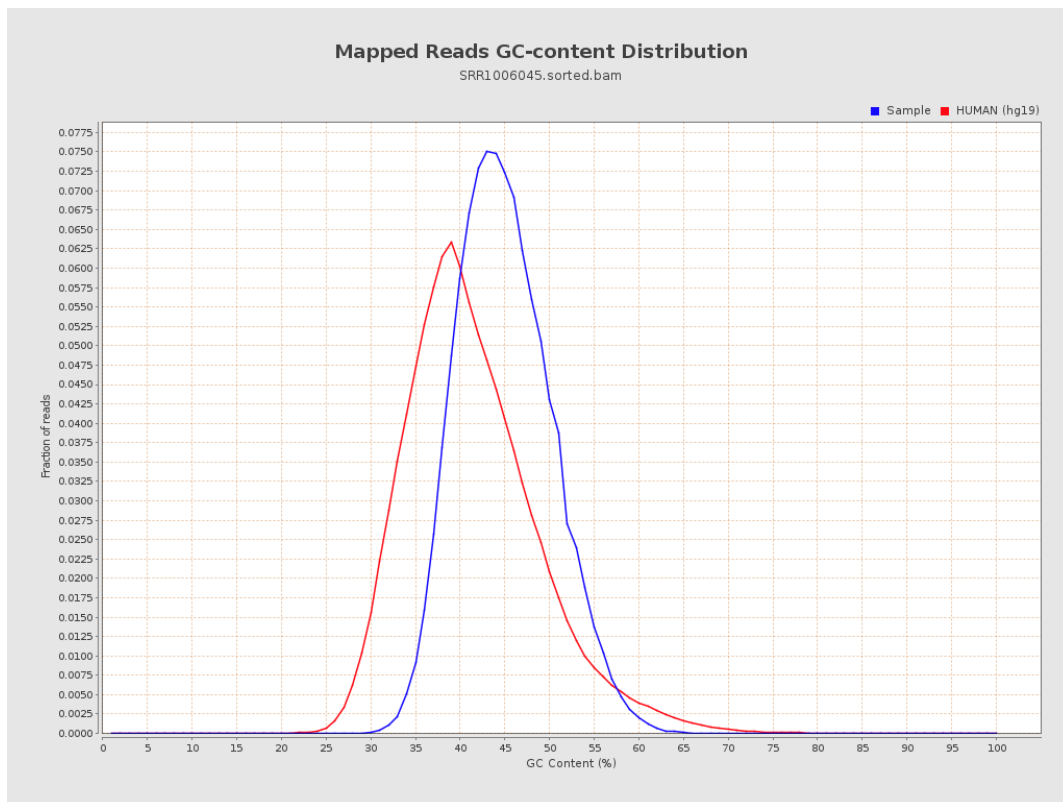
7. Results : Duplication Rate Histogram



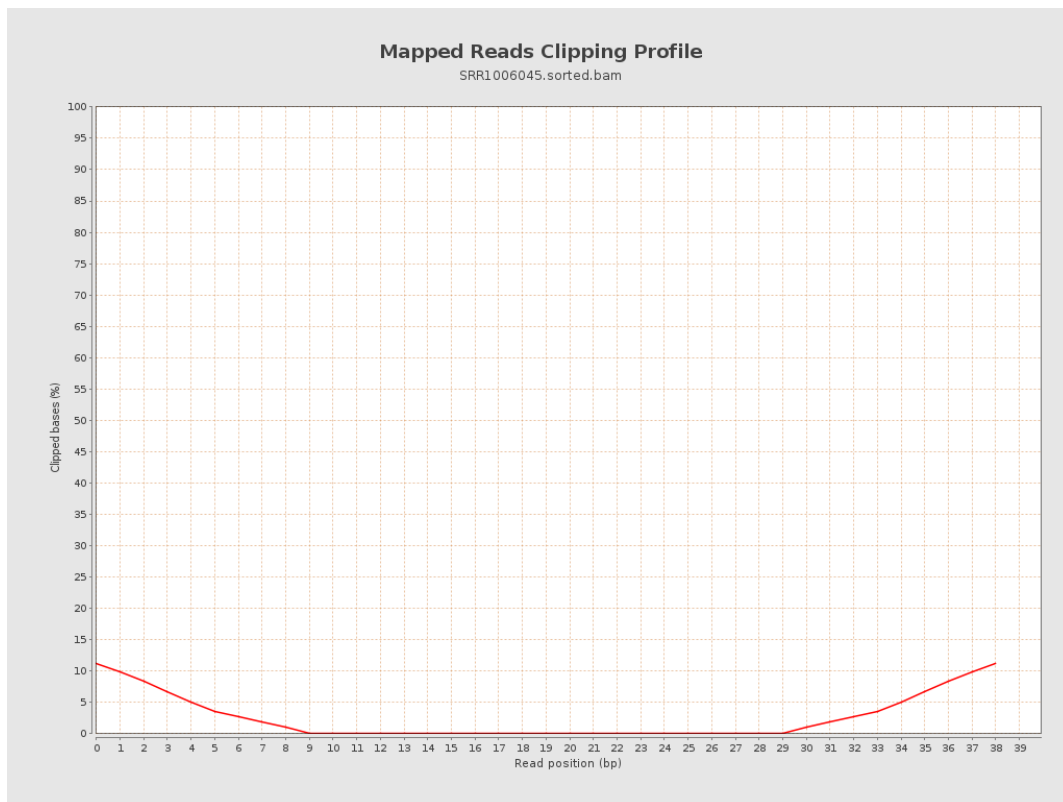
8. Results : Mapped Reads Nucleotide Content



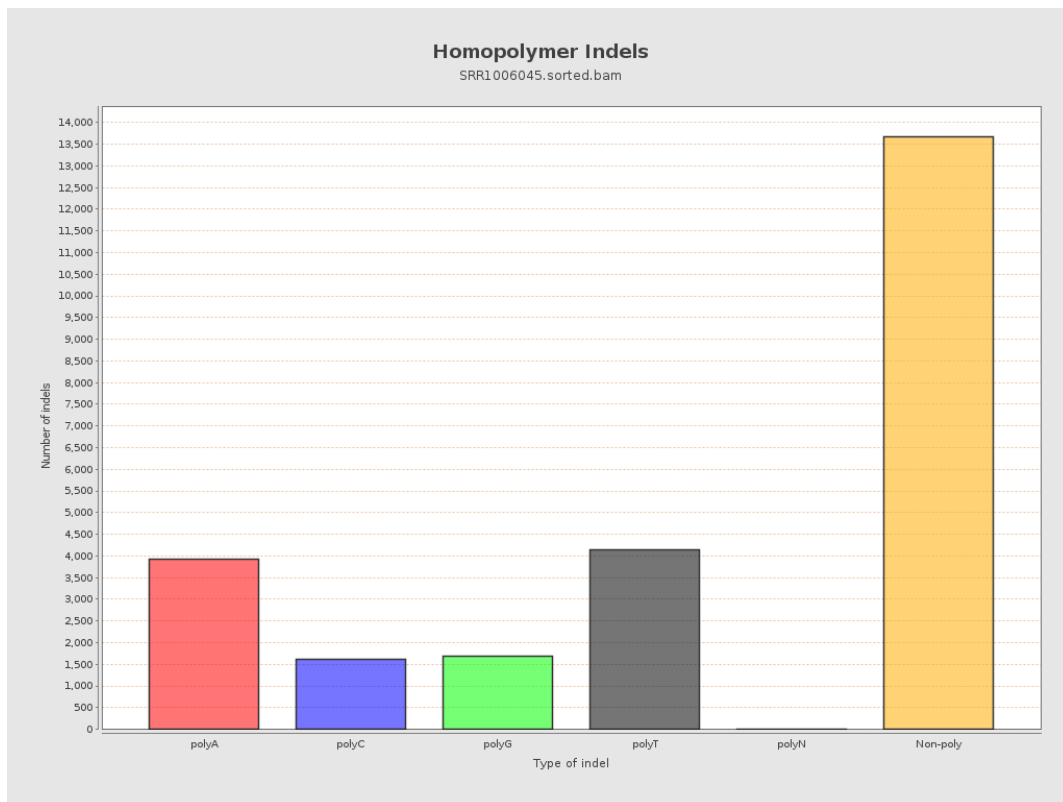
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



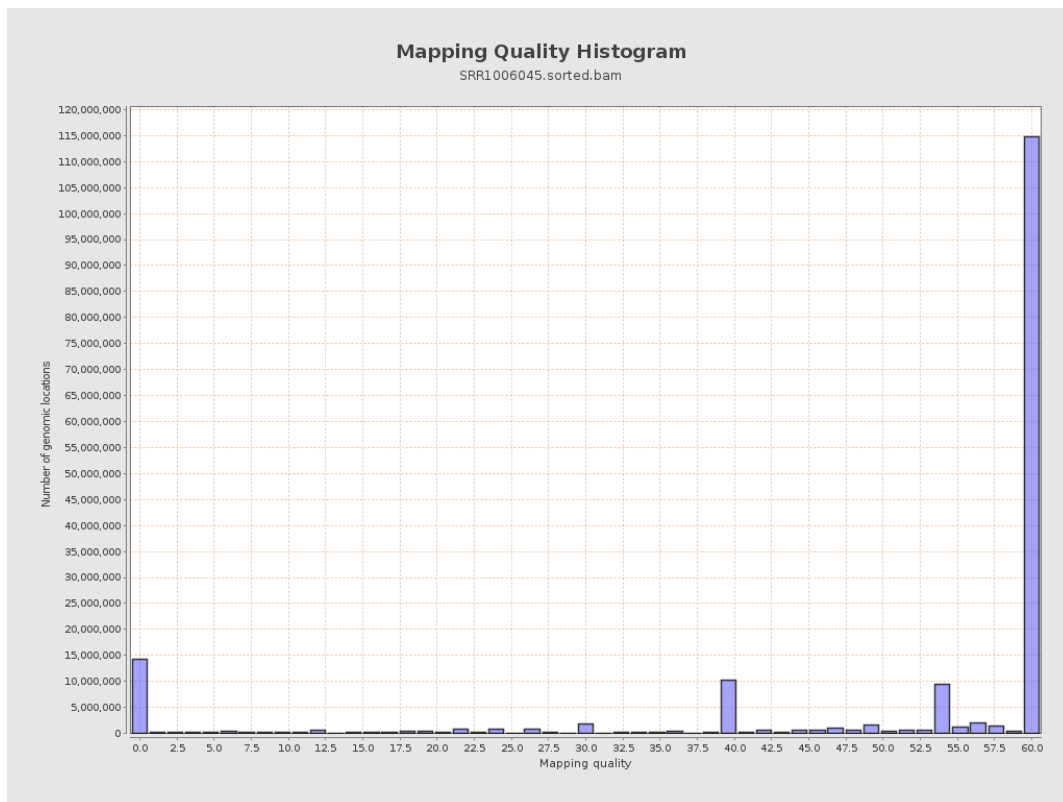
11. Results : Homopolymer Indels



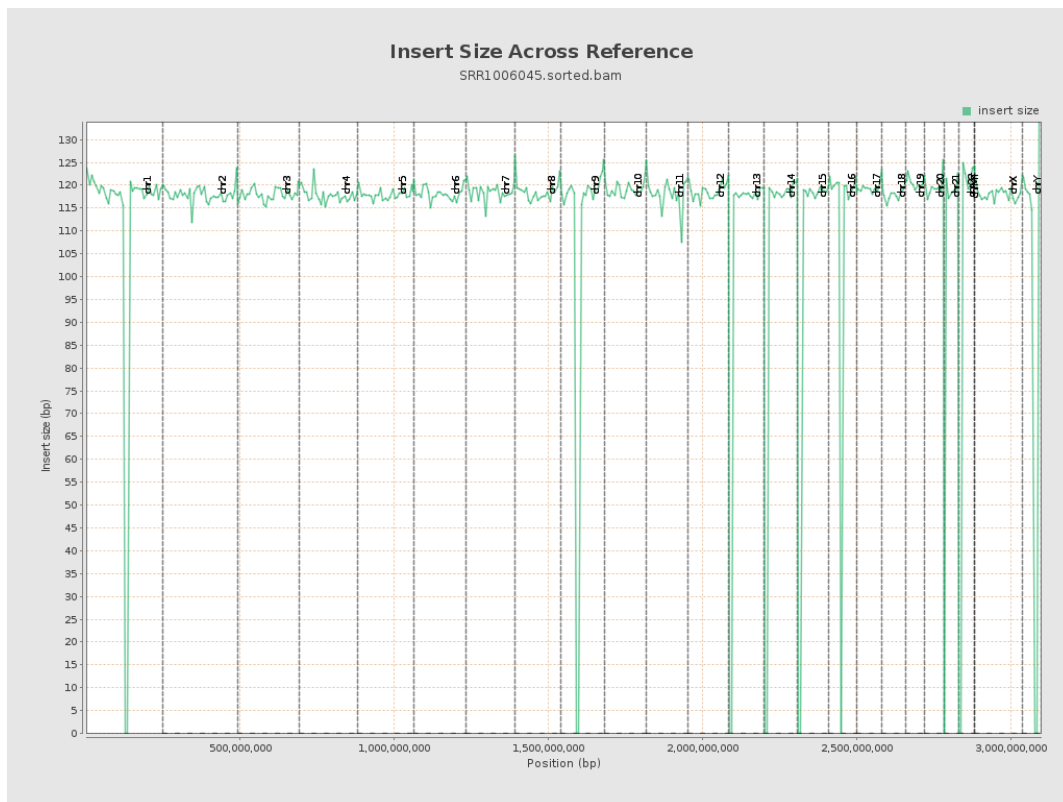
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

