

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 11:09:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173948.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_SRR10173948 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173948_1.fastq.gz SRR10173948_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 11:09:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173948.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,612,588
Mapped reads	9,380,006 / 97.58%
Unmapped reads	232,582 / 2.42%
Mapped paired reads	9,380,006 / 97.58%
Mapped reads, first in pair	4,695,683 / 48.85%
Mapped reads, second in pair	4,684,323 / 48.73%
Mapped reads, both in pair	9,233,324 / 96.05%
Mapped reads, singletons	146,682 / 1.53%
Secondary alignments	0
Supplementary alignments	1,359,792 / 14.15%
Read min/max/mean length	30 / 133 / 126.32
Duplicated reads (estimated)	7,813,623 / 81.29%
Duplication rate	66.75%
Clipped reads	5,152,130 / 53.6%

2.2. ACGT Content

Number/percentage of A's	315,383,650 / 29.75%
Number/percentage of C's	210,923,513 / 19.89%
Number/percentage of T's	313,341,231 / 29.55%
Number/percentage of G's	220,547,808 / 20.8%
Number/percentage of N's	8,050 / 0%

GC Percentage	40.7%
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2.3. Coverage

Mean	0.3427
Standard Deviation	6.5336

2.4. Mapping Quality

Mean Mapping Quality	52.16
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2.5. Insert size

Mean	1,134,119.03
Standard Deviation	10,344,255.49
P25/Median/P75	104 / 155 / 239

2.6. Mismatches and indels

General error rate	0.96%
Mismatches	9,850,244
Insertions	134,615
Mapped reads with at least one insertion	1.38%
Deletions	292,597
Mapped reads with at least one deletion	3.04%
Homopolymer indels	41.19%

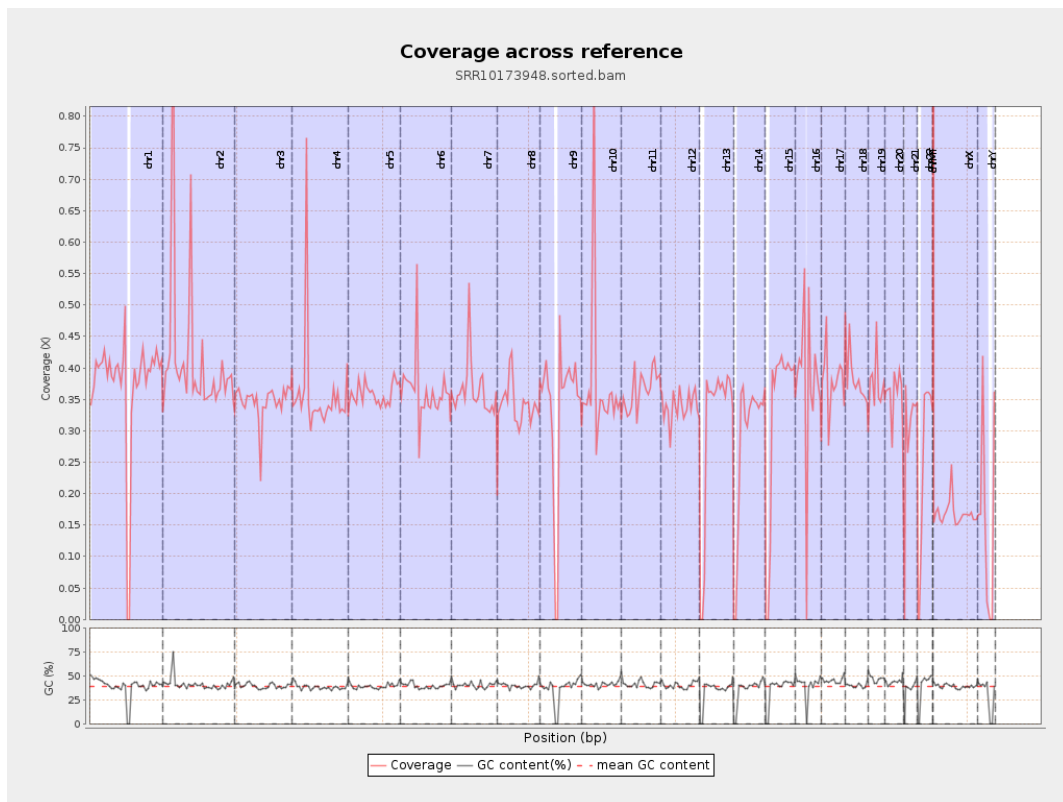
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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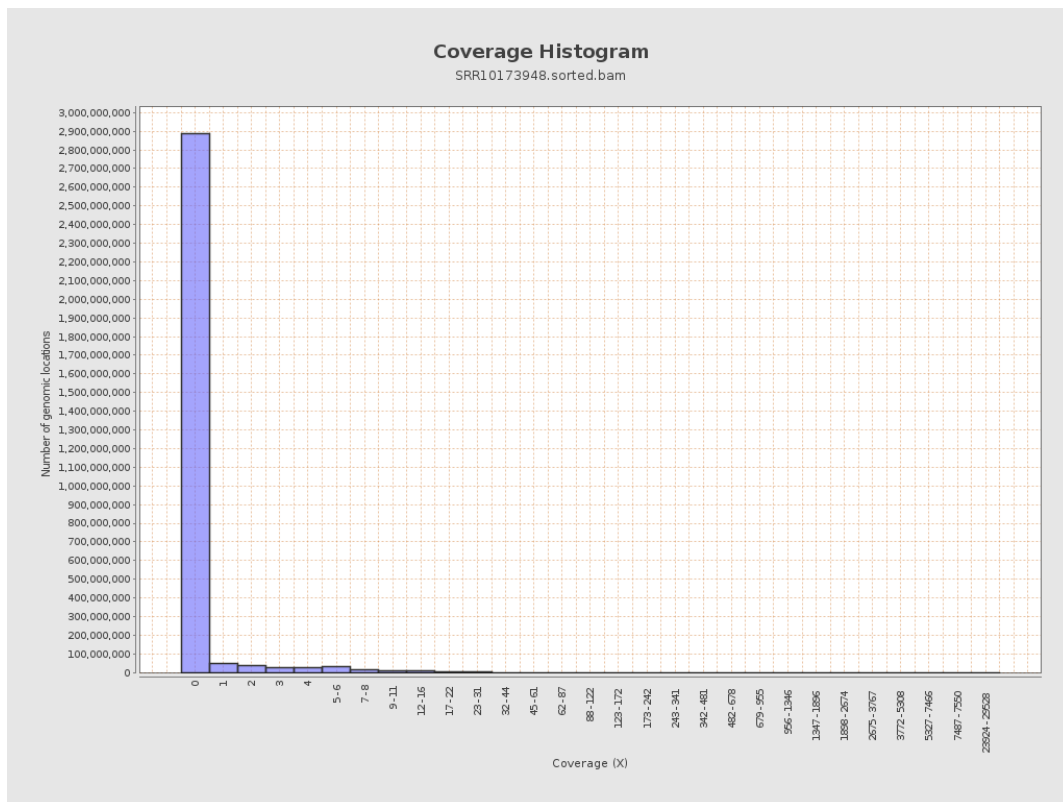
		bases	coverage	deviation
chr1	249250621	93082560	0.3734	3.8067
chr2	243199373	100143560	0.4118	20.7866
chr3	198022430	68584971	0.3463	1.823
chr4	191154276	68521591	0.3585	3.4067
chr5	180915260	64950894	0.359	1.9008
chr6	171115067	62044829	0.3626	3.2578
chr7	159138663	58130900	0.3653	3.5137
chr8	146364022	50072312	0.3421	4.6564
chr9	141213431	47531523	0.3366	3.8173
chr10	135534747	50002875	0.3689	4.7282
chr11	135006516	49190676	0.3644	2.3179
chr12	133851895	45439402	0.3395	1.9596
chr13	115169878	35532757	0.3085	1.7277
chr14	107349540	30905513	0.2879	1.7634
chr15	102531392	32956026	0.3214	1.8516
chr16	90354753	33787221	0.3739	2.8575
chr17	81195210	31093214	0.3829	2.7619
chr18	78077248	30005184	0.3843	5.0334
chr19	59128983	22198924	0.3754	3.1503
chr20	63025520	22652120	0.3594	2.0902
chr21	48129895	14413630	0.2995	2.4557
chr22	51304566	12782800	0.2492	1.7063
chrMT	16571	953438	57.5365	46.0989
chrX	155270560	26176460	0.1686	1.4134

chrY	59373566	9737395	0.164	3.0901
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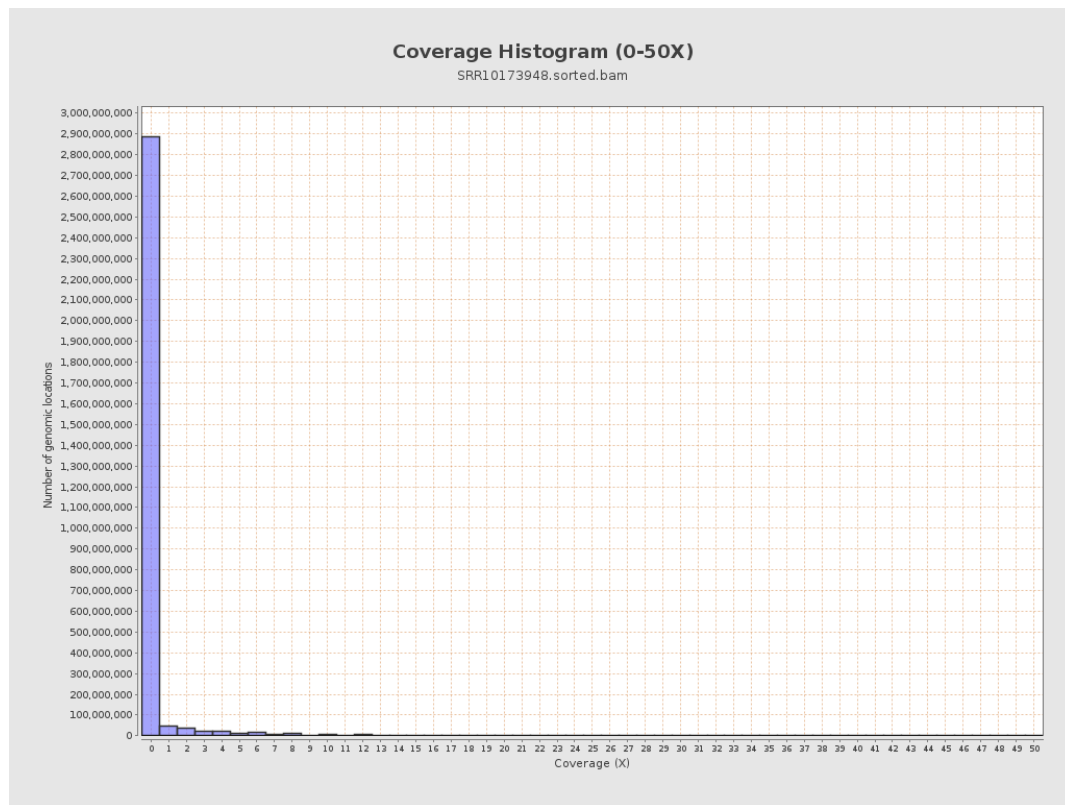
3. Results : Coverage across reference



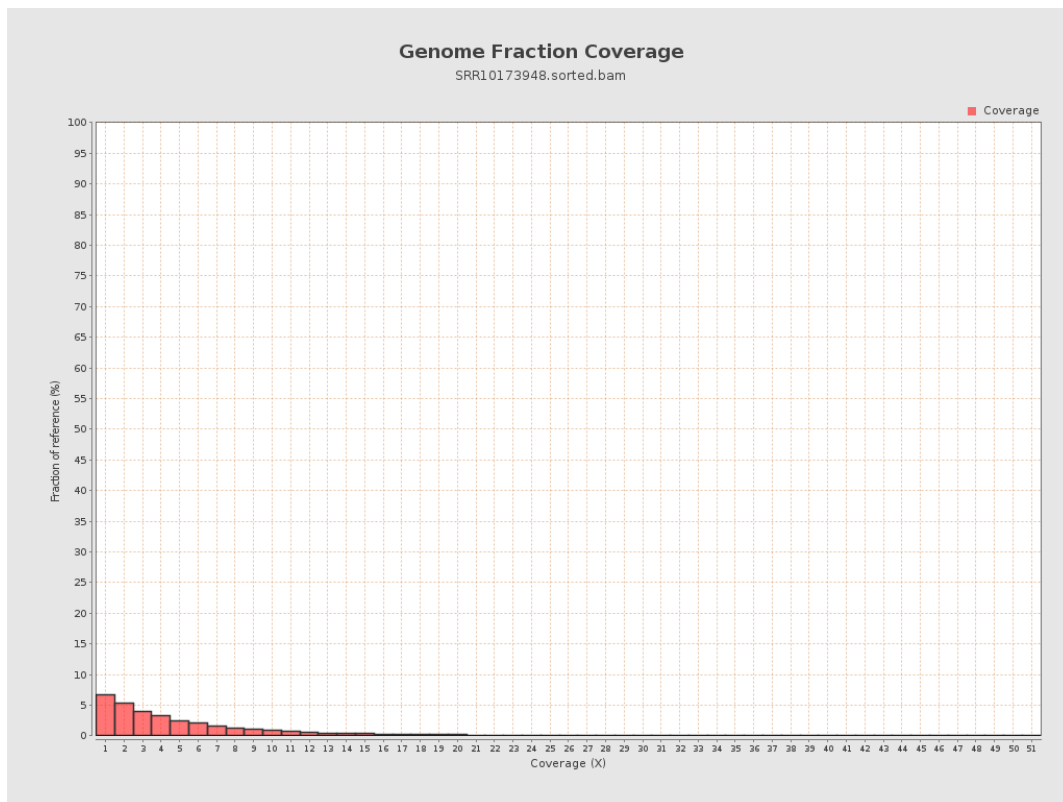
4. Results : Coverage Histogram



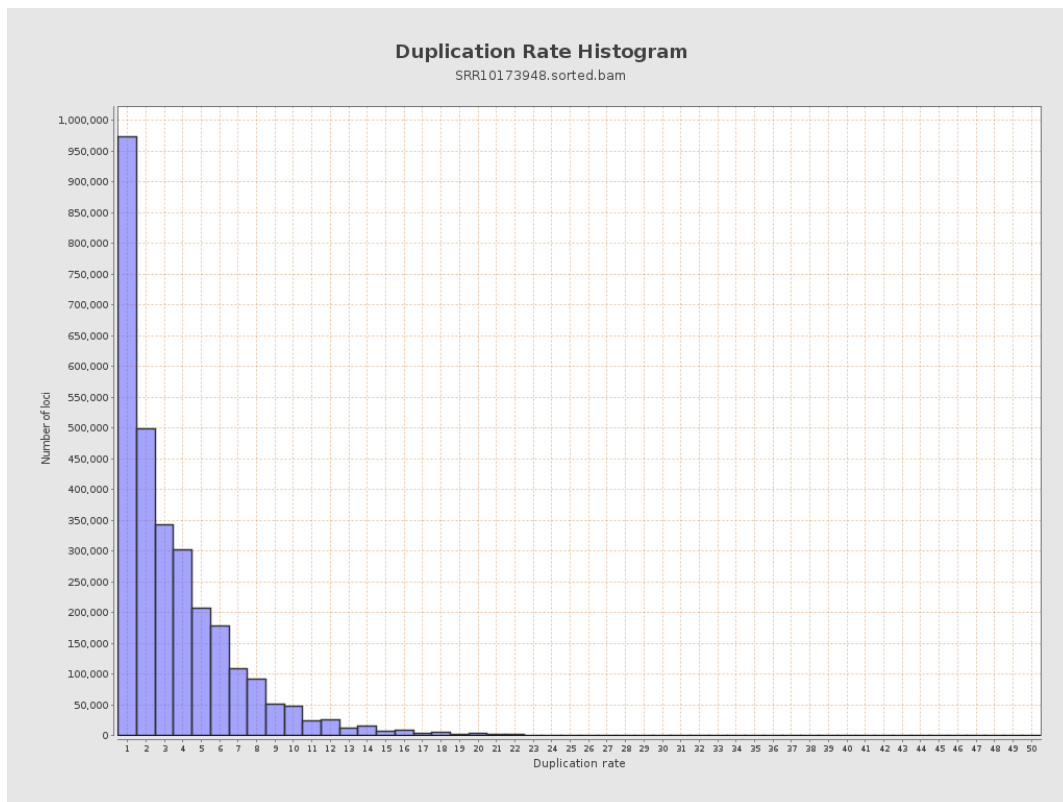
5. Results : Coverage Histogram (0-50X)



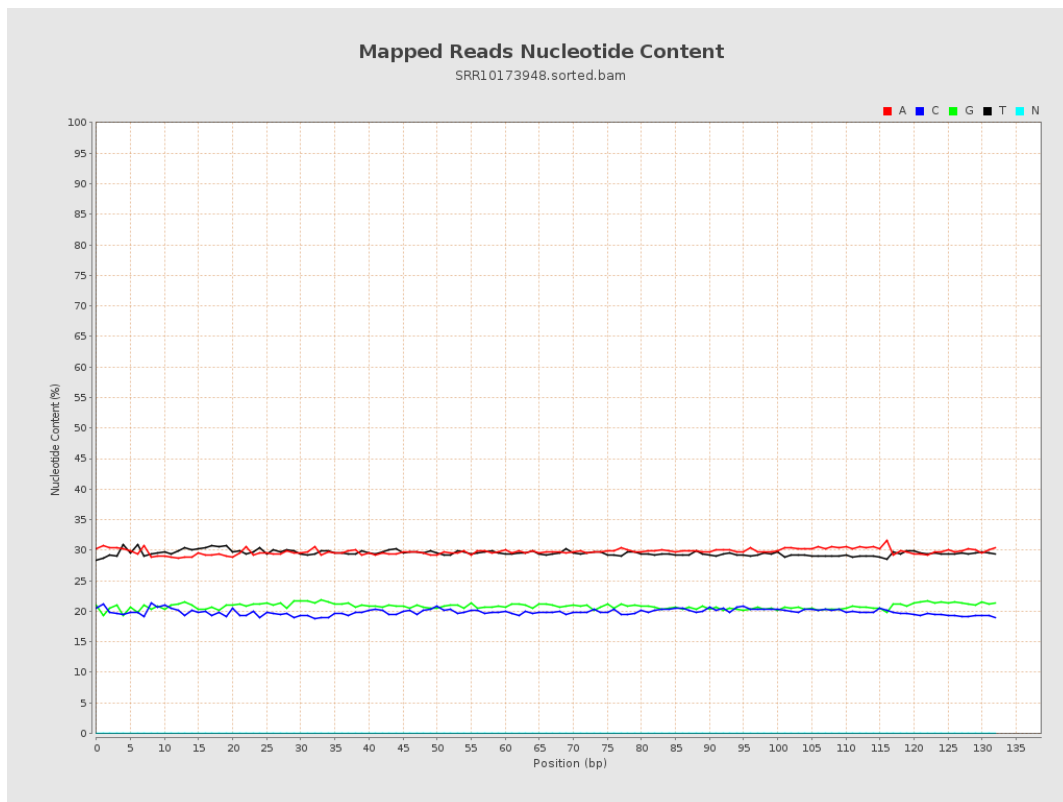
6. Results : Genome Fraction Coverage



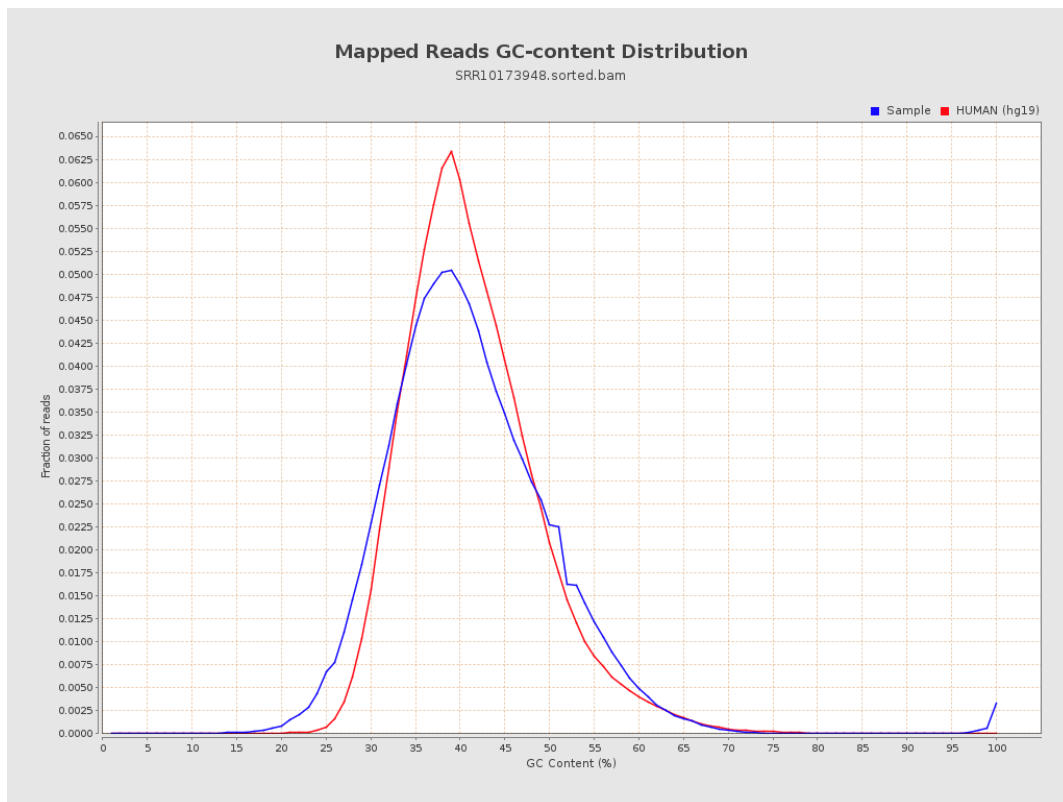
7. Results : Duplication Rate Histogram



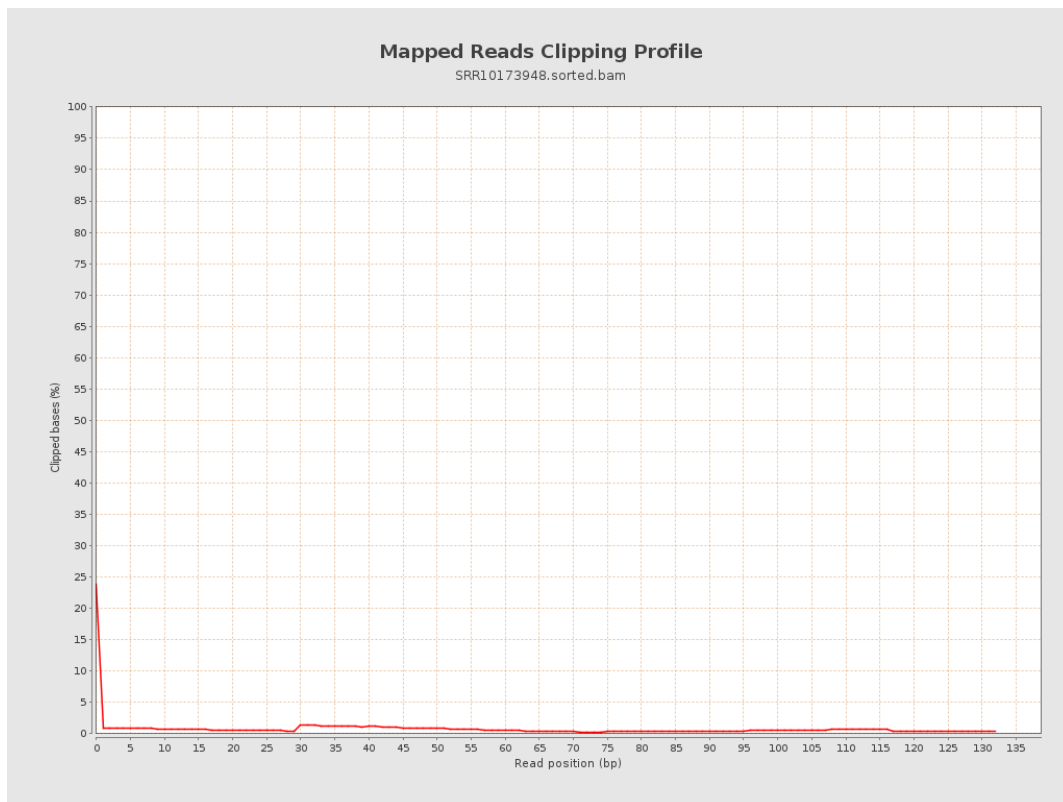
8. Results : Mapped Reads Nucleotide Content



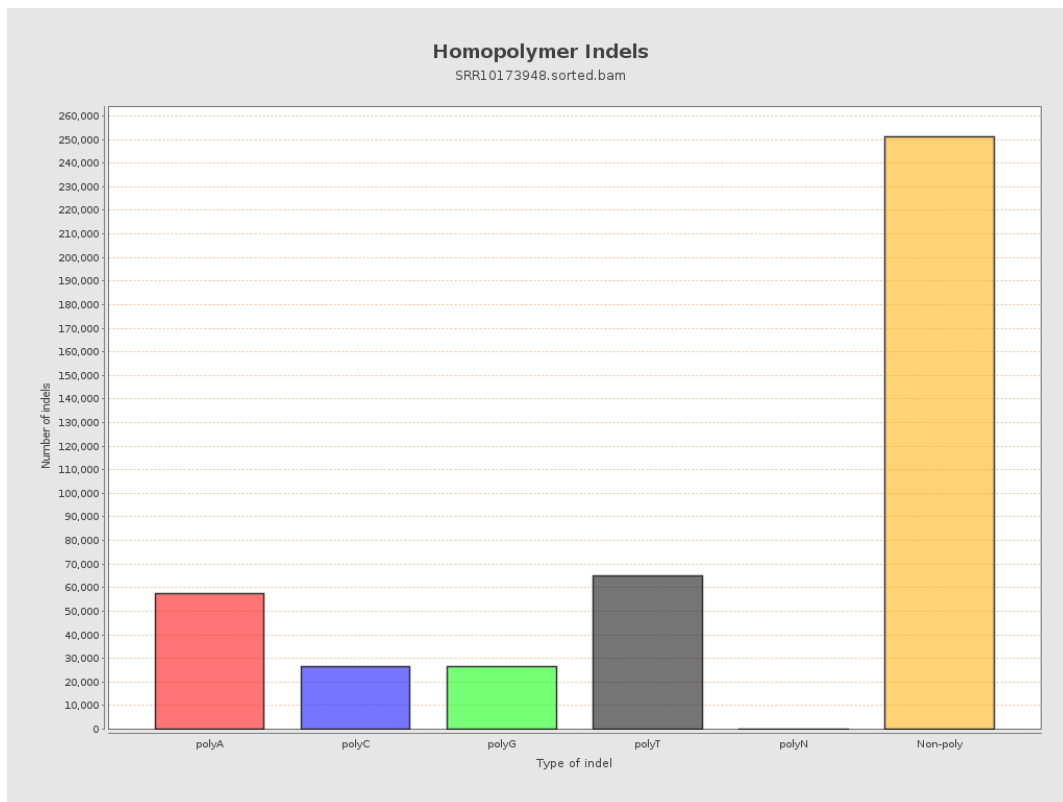
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



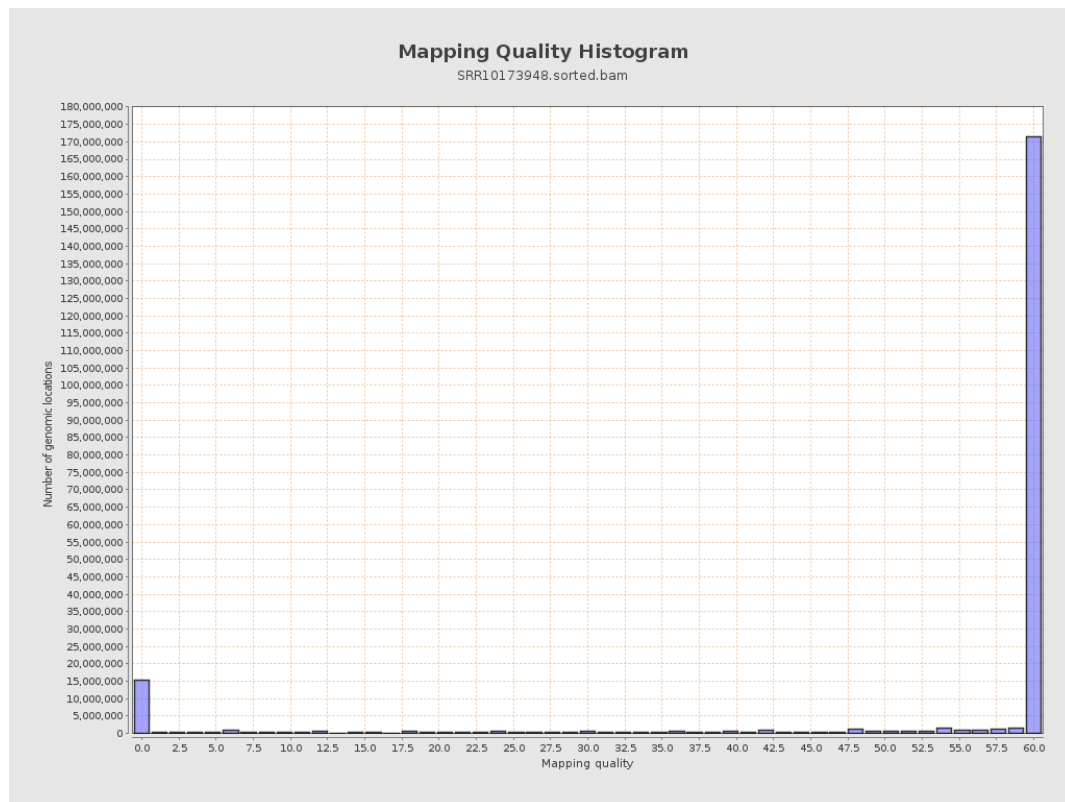
11. Results : Homopolymer Indels



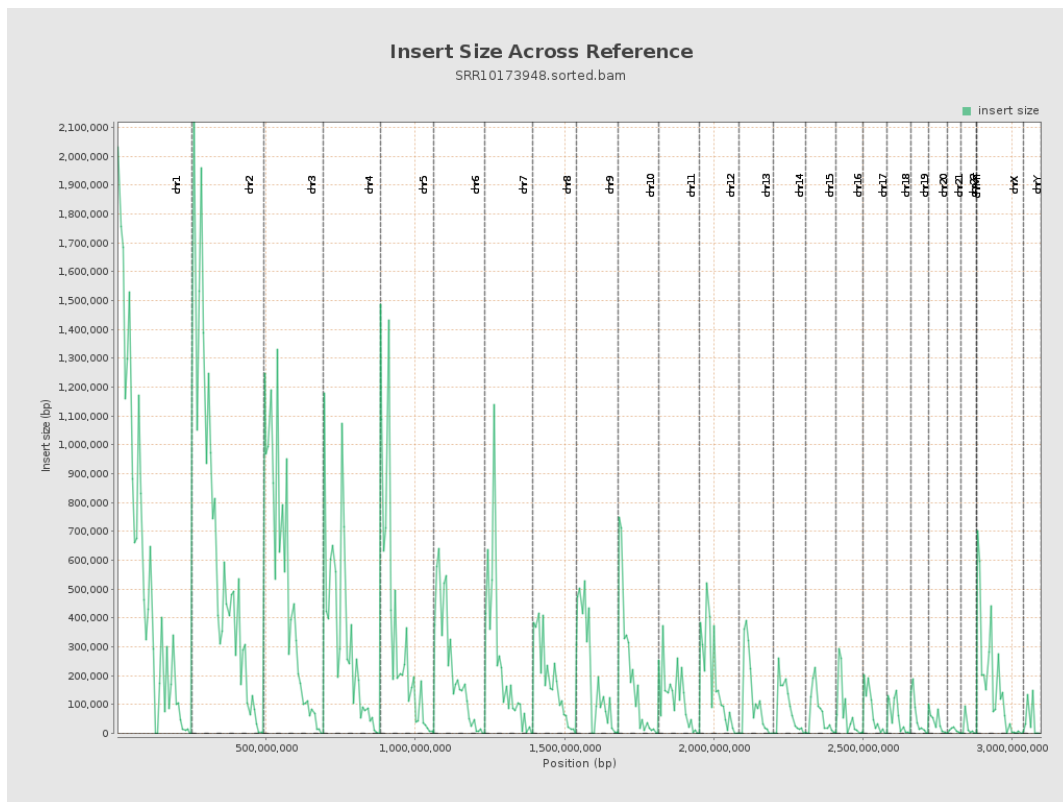
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

