

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 06:58:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173918.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_SRR10173918 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173918_1.fastq.gz SRR10173918_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 06:58:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173918.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,974,178
Mapped reads	2,890,433 / 97.18%
Unmapped reads	83,745 / 2.82%
Mapped paired reads	2,890,433 / 97.18%
Mapped reads, first in pair	1,447,757 / 48.68%
Mapped reads, second in pair	1,442,676 / 48.51%
Mapped reads, both in pair	2,833,782 / 95.28%
Mapped reads, singletons	56,651 / 1.9%
Secondary alignments	0
Supplementary alignments	293,463 / 9.87%
Read min/max/mean length	30 / 133 / 128.27
Duplicated reads (estimated)	2,248,695 / 75.61%
Duplication rate	64.51%
Clipped reads	1,220,032 / 41.02%

2.2. ACGT Content

Number/percentage of A's	102,165,081 / 30.01%
Number/percentage of C's	66,940,932 / 19.66%
Number/percentage of T's	101,988,563 / 29.96%
Number/percentage of G's	69,348,210 / 20.37%
Number/percentage of N's	4,436 / 0%

GC Percentage	40.03%
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2.3. Coverage

Mean	0.11
Standard Deviation	1.7633

2.4. Mapping Quality

Mean Mapping Quality	52.76
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2.5. Insert size

Mean	1,000,094.23
Standard Deviation	9,393,828.32
P25/Median/P75	144 / 201 / 289

2.6. Mismatches and indels

General error rate	1.08%
Mismatches	3,579,565
Insertions	35,710
Mapped reads with at least one insertion	1.19%
Deletions	79,321
Mapped reads with at least one deletion	2.68%
Homopolymer indels	42.49%

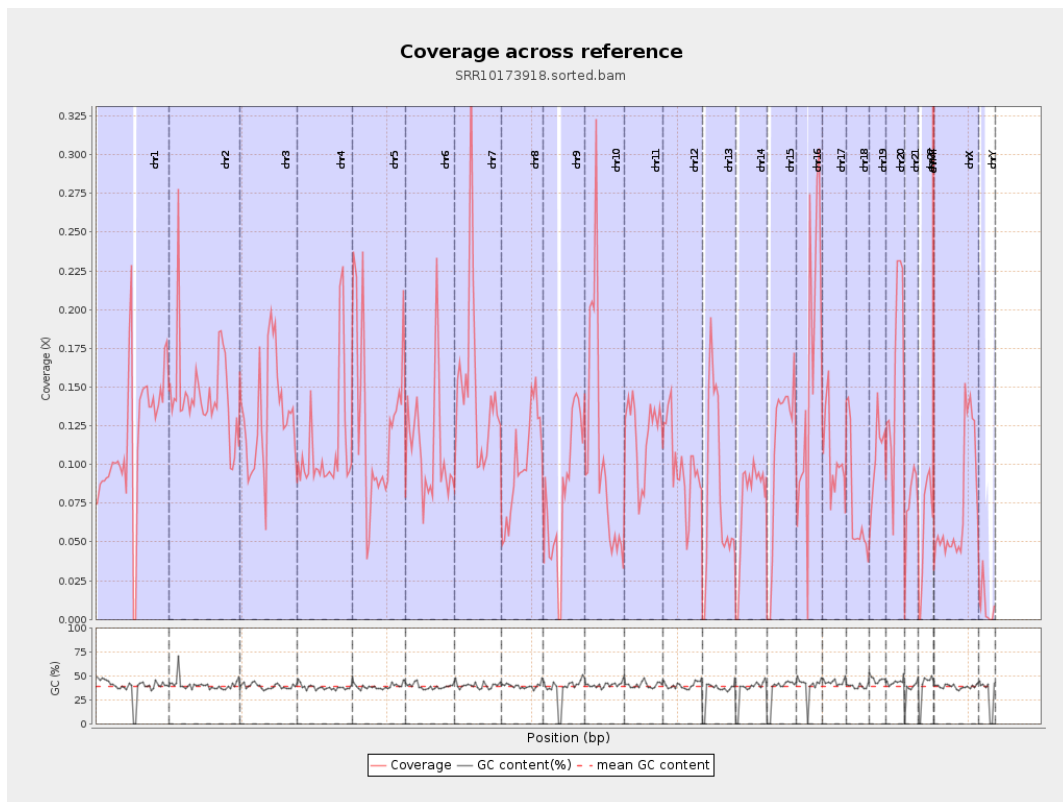
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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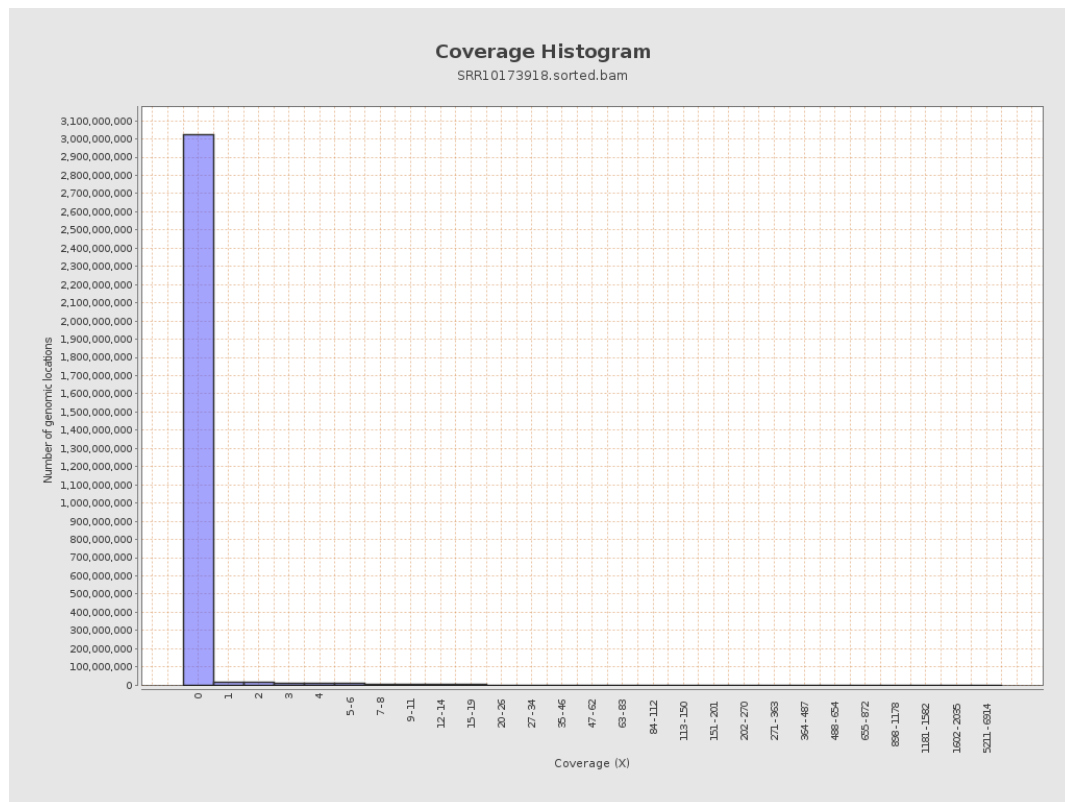
		bases	coverage	deviation
chr1	249250621	29246840	0.1173	1.3063
chr2	243199373	35290540	0.1451	4.8996
chr3	198022430	26128803	0.1319	1.0579
chr4	191154276	20914088	0.1094	1.0583
chr5	180915260	23115733	0.1278	1.0348
chr6	171115067	19052523	0.1113	0.995
chr7	159138663	23432968	0.1472	1.6304
chr8	146364022	14759911	0.1008	1.033
chr9	141213431	11884336	0.0842	0.9279
chr10	135534747	14440257	0.1065	1.9629
chr11	135006516	16168840	0.1198	1.0195
chr12	133851895	13266632	0.0991	0.9132
chr13	115169878	9374823	0.0814	0.831
chr14	107349540	8146663	0.0759	0.7922
chr15	102531392	11307319	0.1103	0.9448
chr16	90354753	14407595	0.1595	1.4465
chr17	81195210	8312706	0.1024	0.9671
chr18	78077248	5640912	0.0722	1.2778
chr19	59128983	6215422	0.1051	1.4598
chr20	63025520	10180363	0.1615	1.1479
chr21	48129895	3585819	0.0745	0.7998
chr22	51304566	3034026	0.0591	0.6509
chrMT	16571	946839	57.1383	47.6389
chrX	155270560	11291002	0.0727	0.7721

chrY	59373566	495391	0.0083	0.3815
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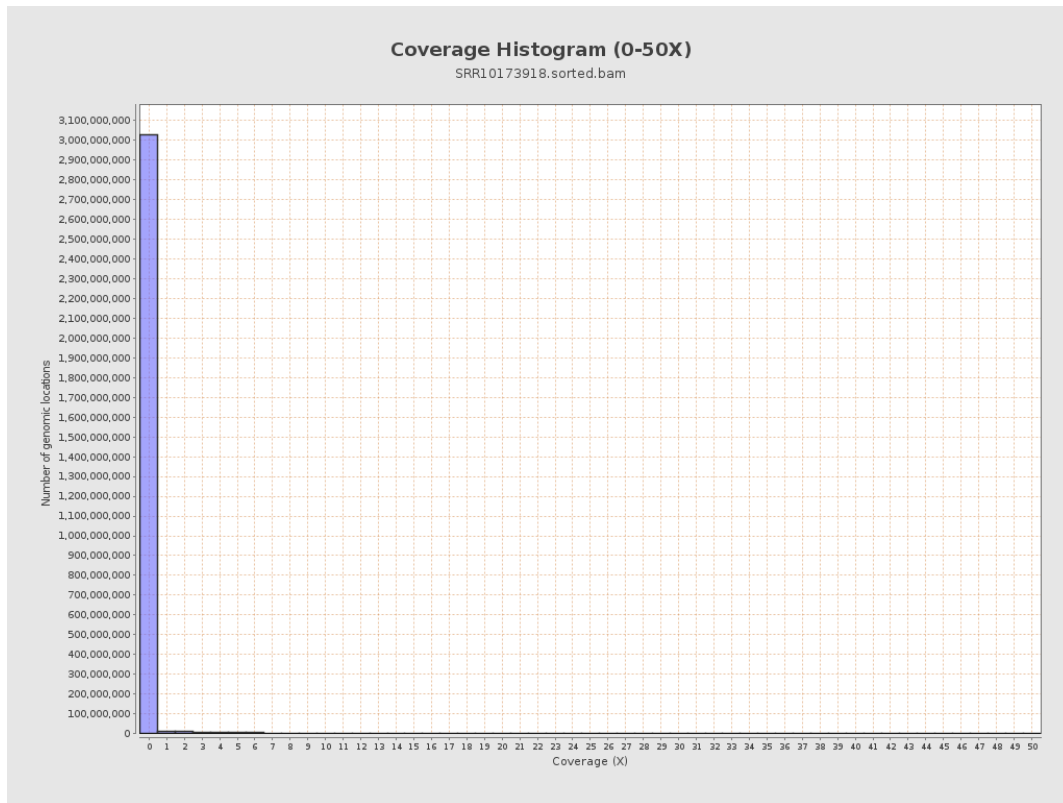
3. Results : Coverage across reference



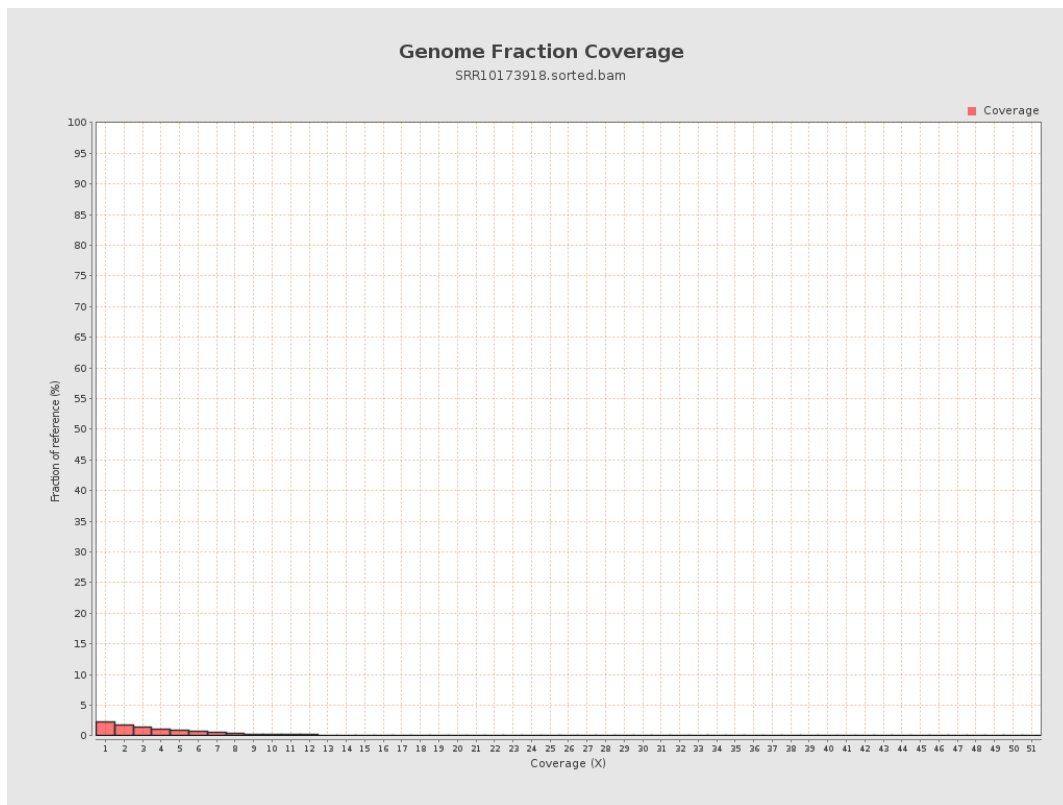
4. Results : Coverage Histogram



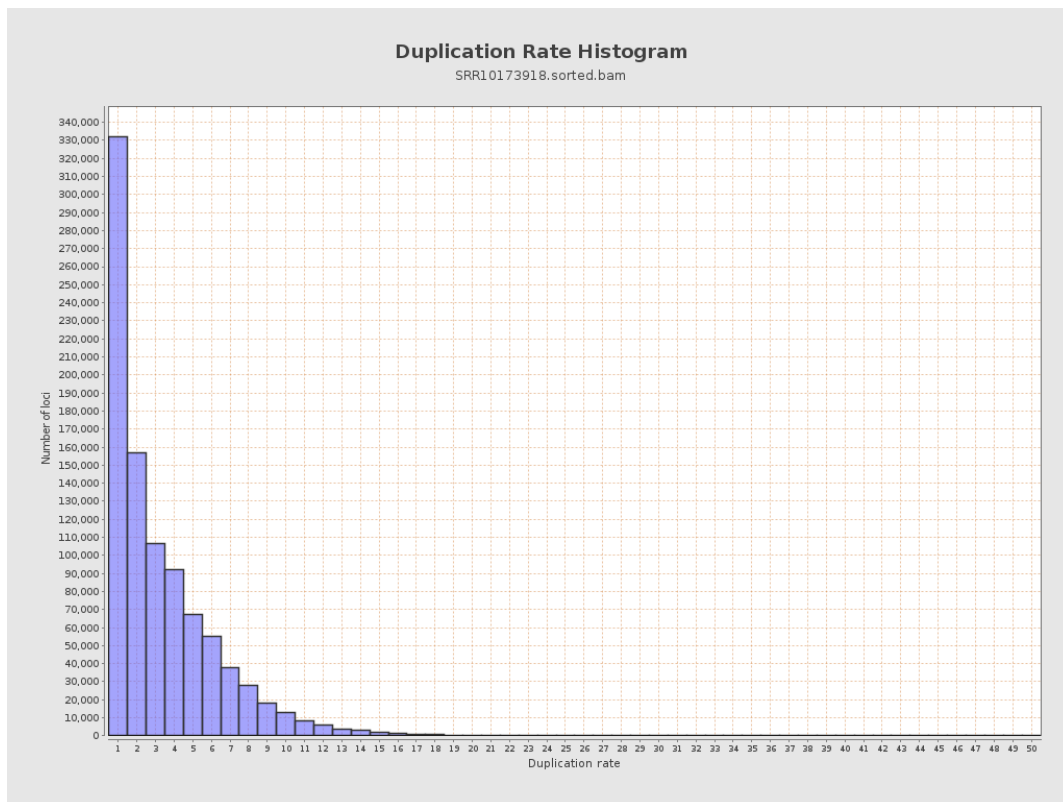
5. Results : Coverage Histogram (0-50X)



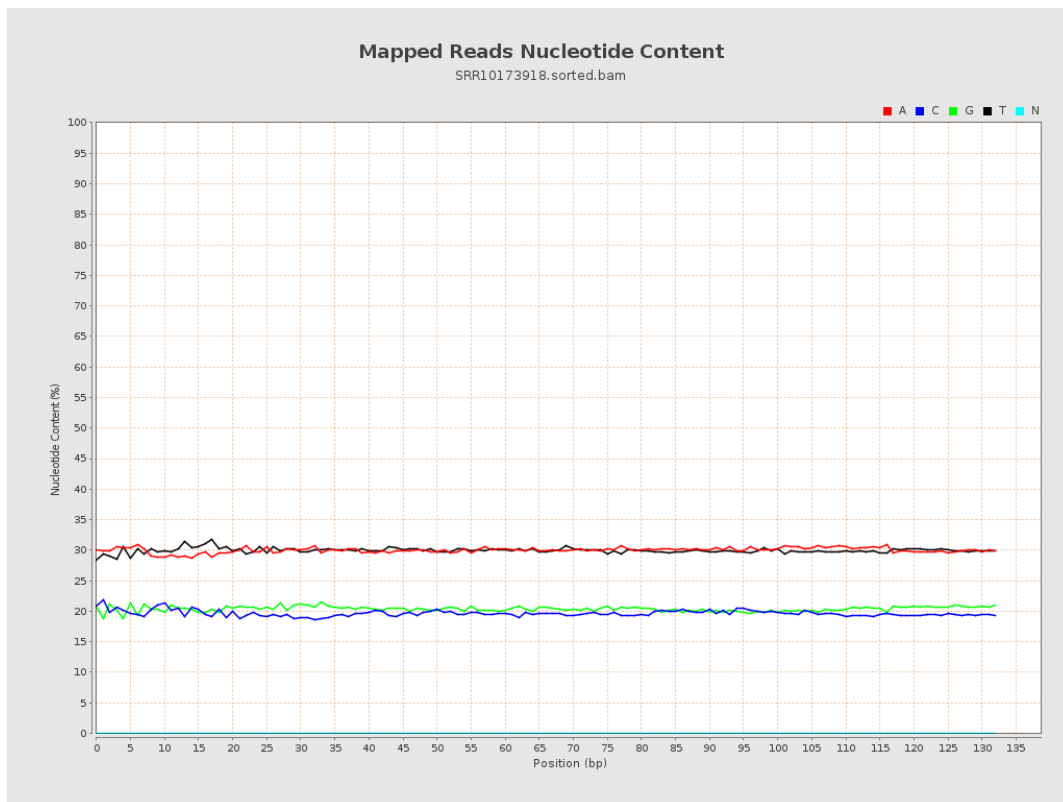
6. Results : Genome Fraction Coverage



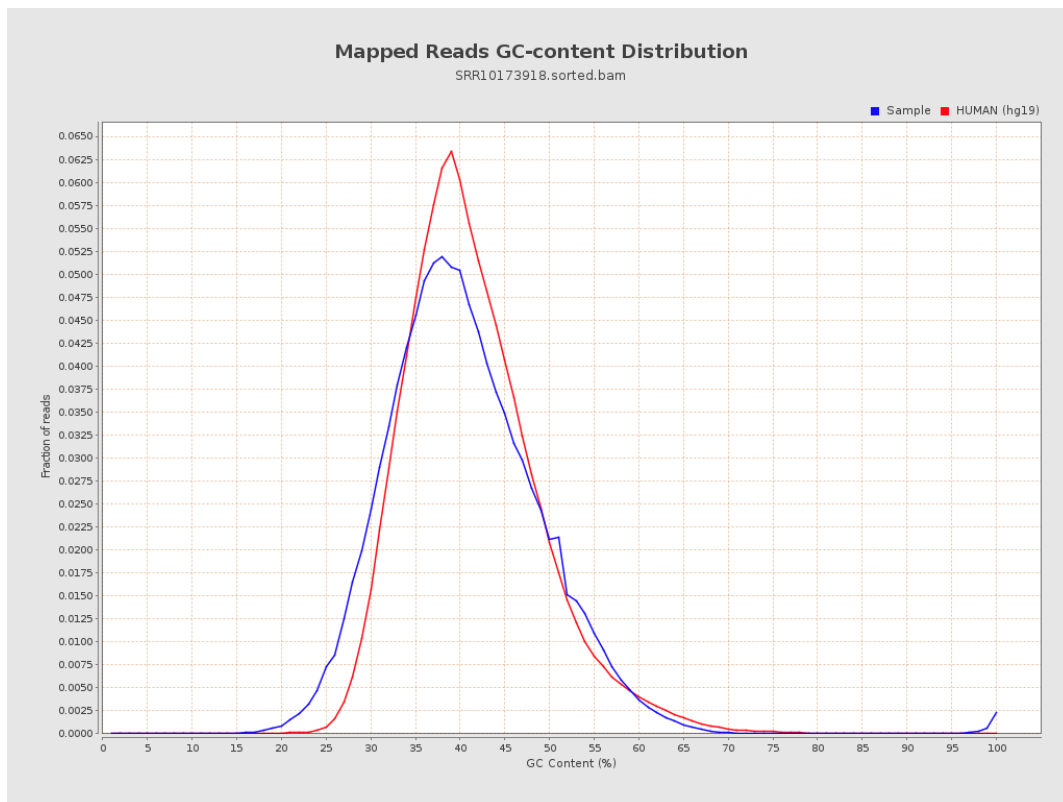
7. Results : Duplication Rate Histogram



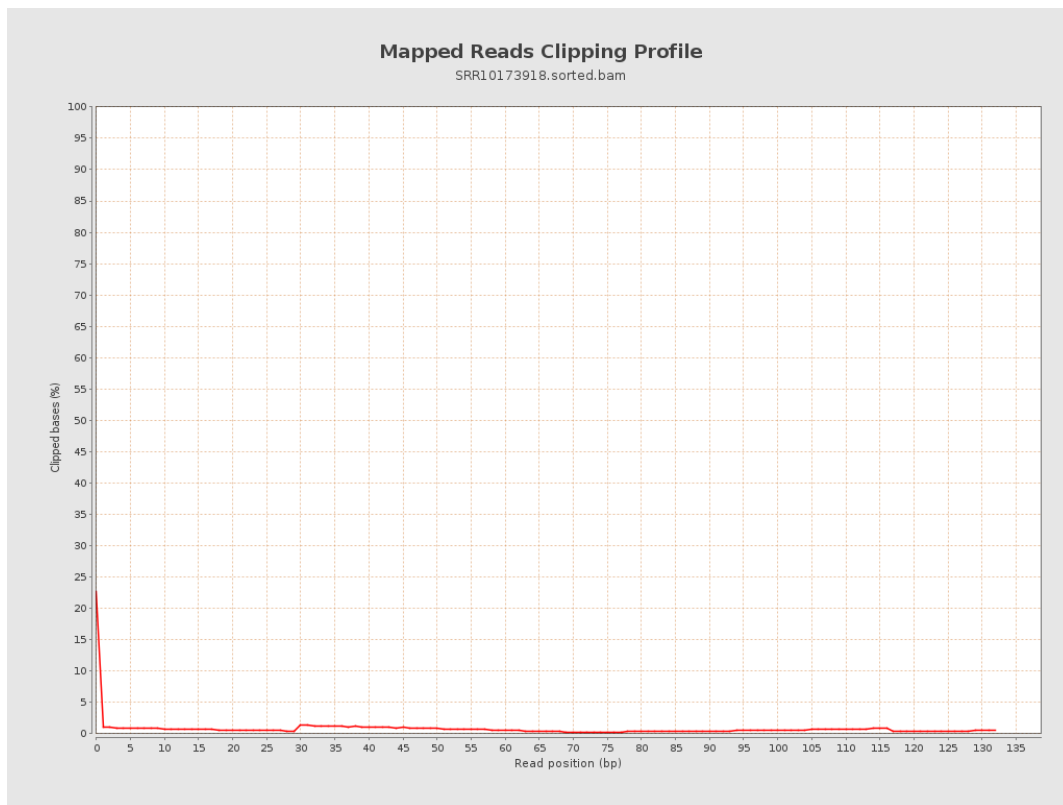
8. Results : Mapped Reads Nucleotide Content



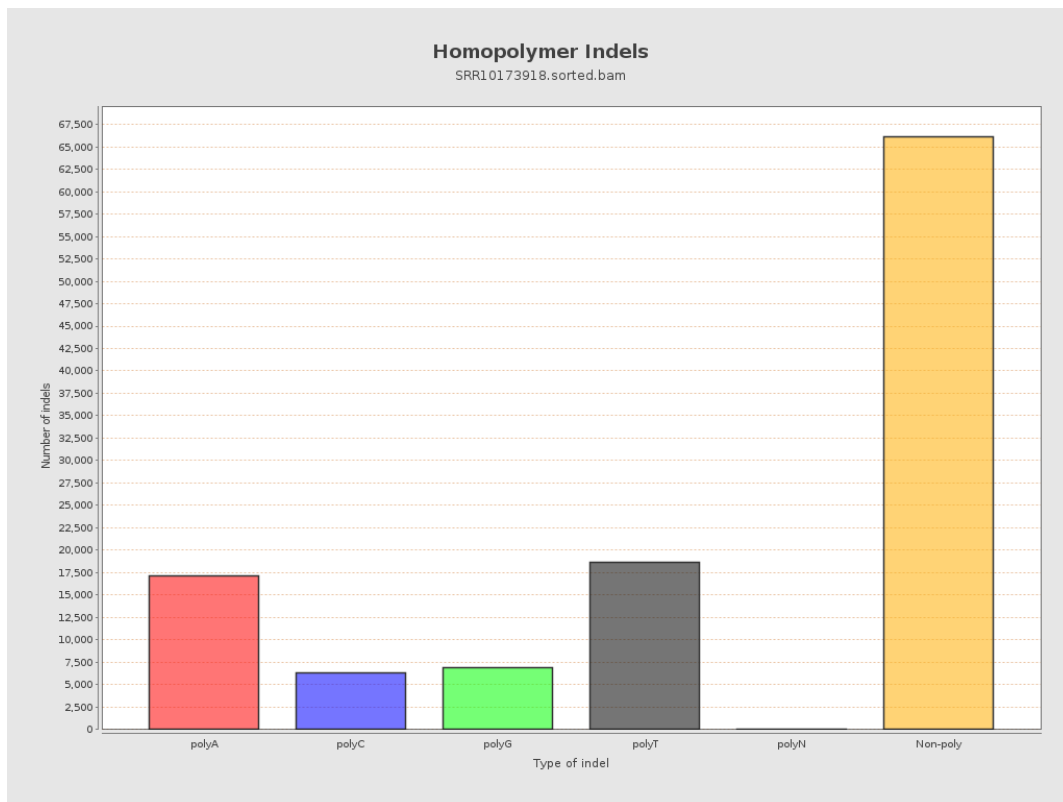
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



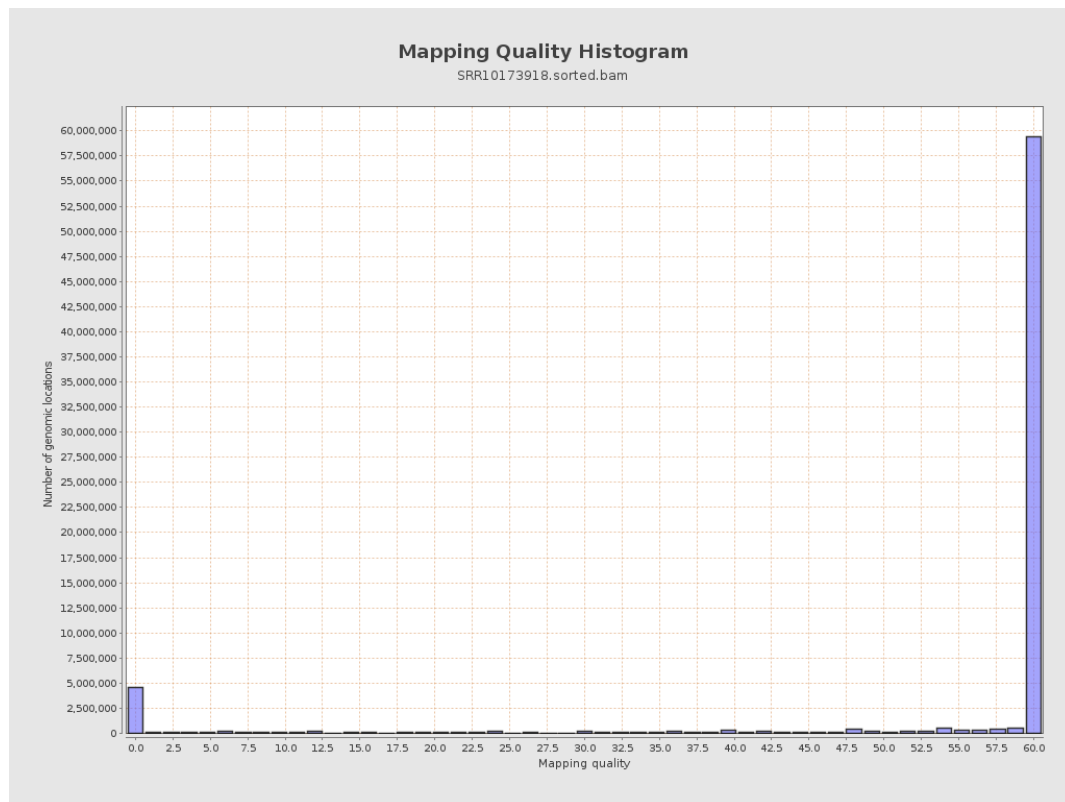
11. Results : Homopolymer Indels



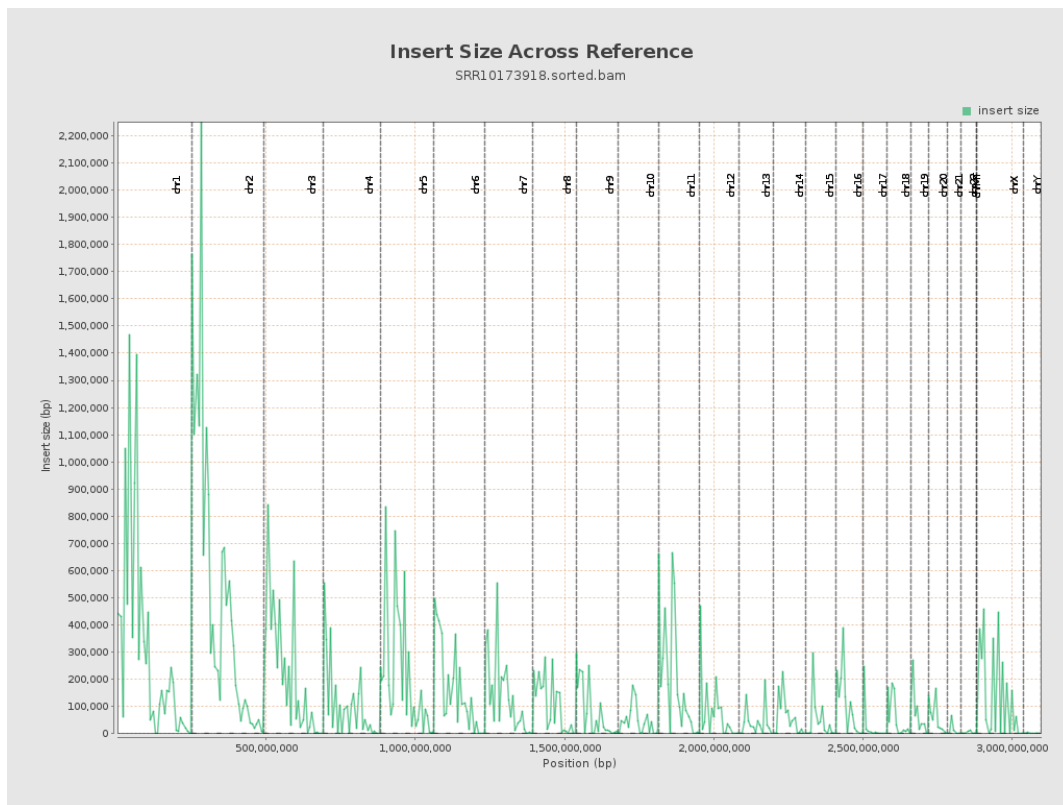
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

