

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 00:26:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173871.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_SRR10173871 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173871_1.fastq.gz SRR10173871_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 00:26:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173871.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,599,832
Mapped reads	2,542,400 / 97.79%
Unmapped reads	57,432 / 2.21%
Mapped paired reads	2,542,400 / 97.79%
Mapped reads, first in pair	1,269,062 / 48.81%
Mapped reads, second in pair	1,273,338 / 48.98%
Mapped reads, both in pair	2,504,246 / 96.32%
Mapped reads, singletons	38,154 / 1.47%
Secondary alignments	0
Supplementary alignments	238,646 / 9.18%
Read min/max/mean length	30 / 133 / 127.66
Duplicated reads (estimated)	1,972,747 / 75.88%
Duplication rate	66.03%
Clipped reads	997,525 / 38.37%

2.2. ACGT Content

Number/percentage of A's	91,103,290 / 30.25%
Number/percentage of C's	58,723,908 / 19.5%
Number/percentage of T's	90,794,531 / 30.15%
Number/percentage of G's	60,526,646 / 20.1%
Number/percentage of N's	3,487 / 0%

GC Percentage	39.6%
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2.3. Coverage

Mean	0.0973
Standard Deviation	1.5593

2.4. Mapping Quality

Mean Mapping Quality	52.87
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2.5. Insert size

Mean	800,803.76
Standard Deviation	7,871,968.2
P25/Median/P75	142 / 197 / 283

2.6. Mismatches and indels

General error rate	1%
Mismatches	2,911,216
Insertions	31,603
Mapped reads with at least one insertion	1.2%
Deletions	60,325
Mapped reads with at least one deletion	2.31%
Homopolymer indels	44.25%

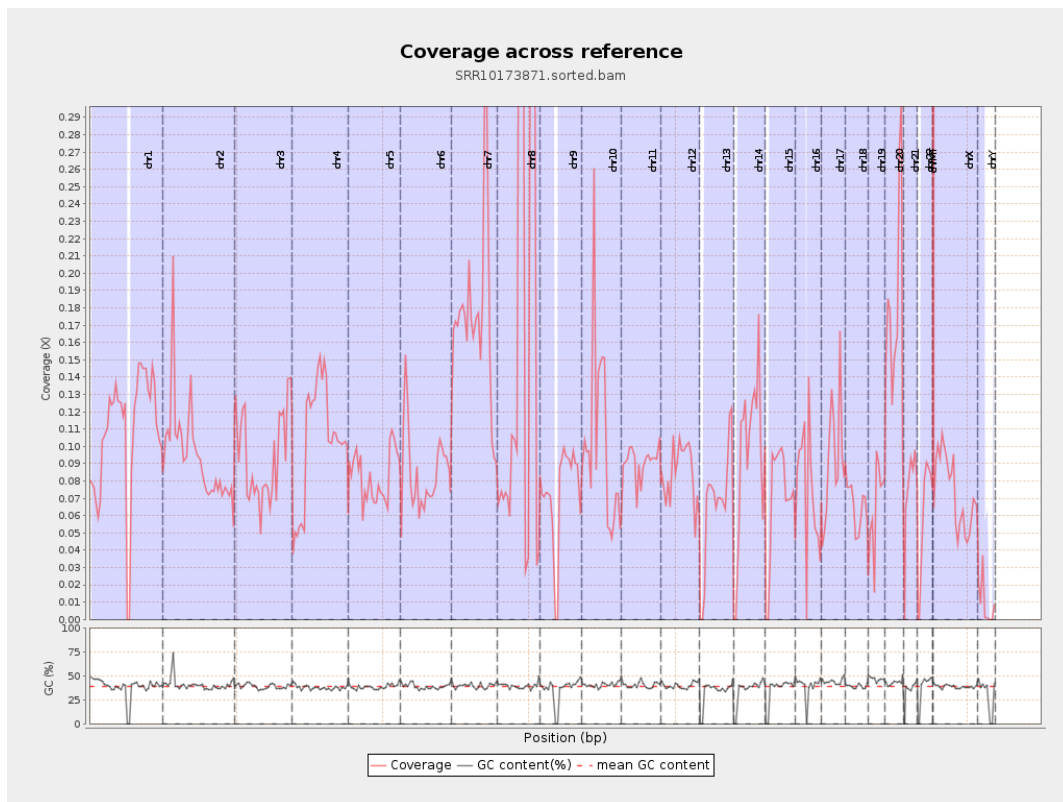
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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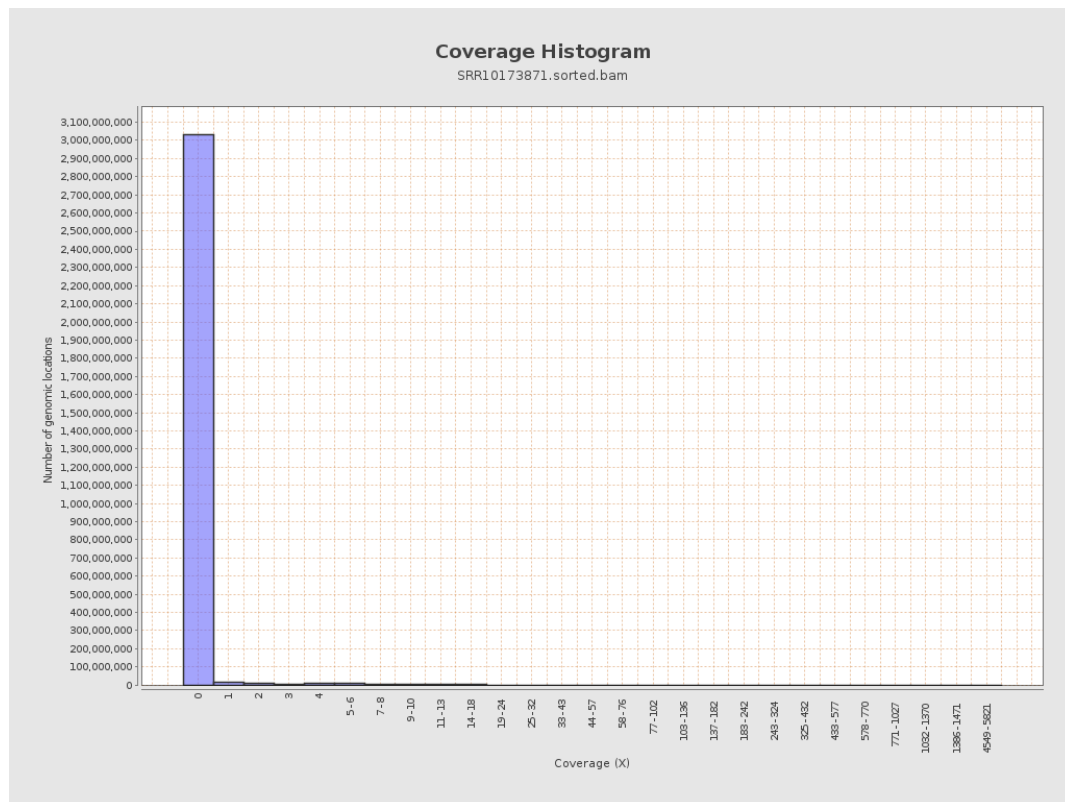
		bases	coverage	deviation
chr1	249250621	26974069	0.1082	1.0255
chr2	243199373	22939961	0.0943	4.1538
chr3	198022430	18681656	0.0943	0.8878
chr4	191154276	19887127	0.104	1.0858
chr5	180915260	14938722	0.0826	0.8222
chr6	171115067	14659239	0.0857	0.862
chr7	159138663	27458849	0.1725	1.8307
chr8	146364022	28951989	0.1978	1.4473
chr9	141213431	10293503	0.0729	0.9129
chr10	135534747	13793314	0.1018	1.9566
chr11	135006516	12179144	0.0902	0.8717
chr12	133851895	11329576	0.0846	0.8362
chr13	115169878	7755777	0.0673	0.7461
chr14	107349540	10268840	0.0957	0.8962
chr15	102531392	7072105	0.069	0.748
chr16	90354753	6681230	0.0739	0.9343
chr17	81195210	7436874	0.0916	0.9021
chr18	78077248	5189324	0.0665	0.952
chr19	59128983	3881210	0.0656	0.8047
chr20	63025520	11806619	0.1873	1.2451
chr21	48129895	3594686	0.0747	0.8283
chr22	51304566	3076140	0.06	0.6693
chrMT	16571	565086	34.1009	35.8615
chrX	155270560	11346679	0.0731	0.7762

chrY	59373566	542442	0.0091	0.4427
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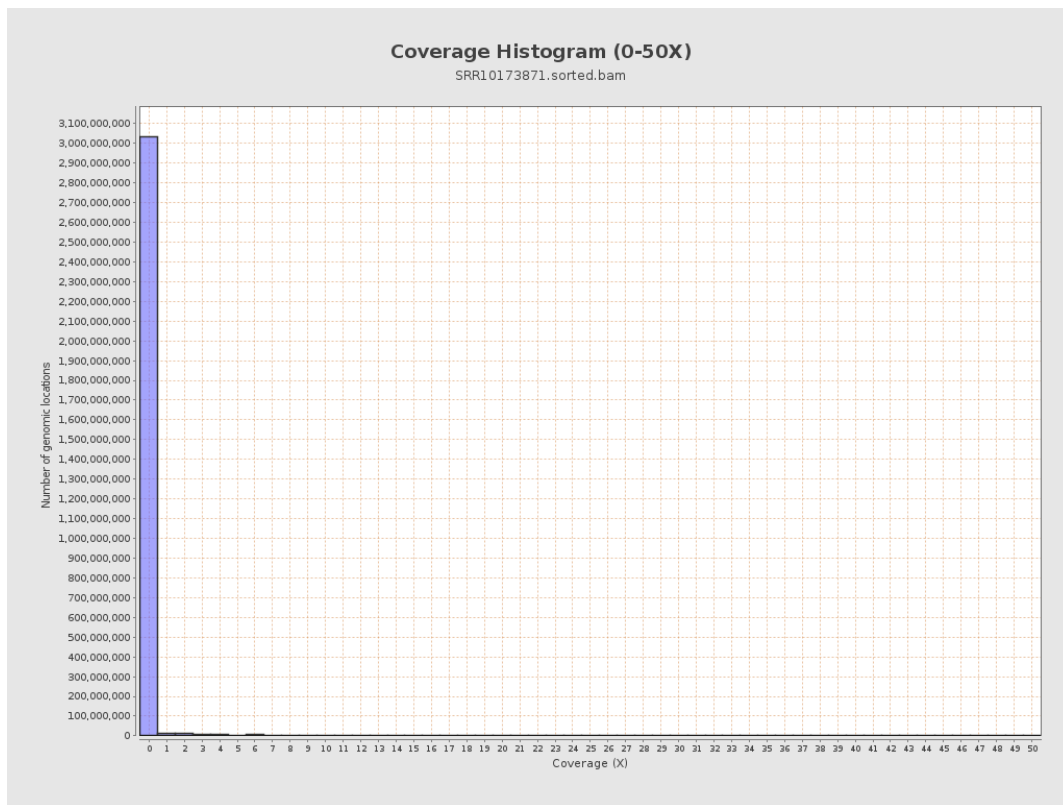
3. Results : Coverage across reference



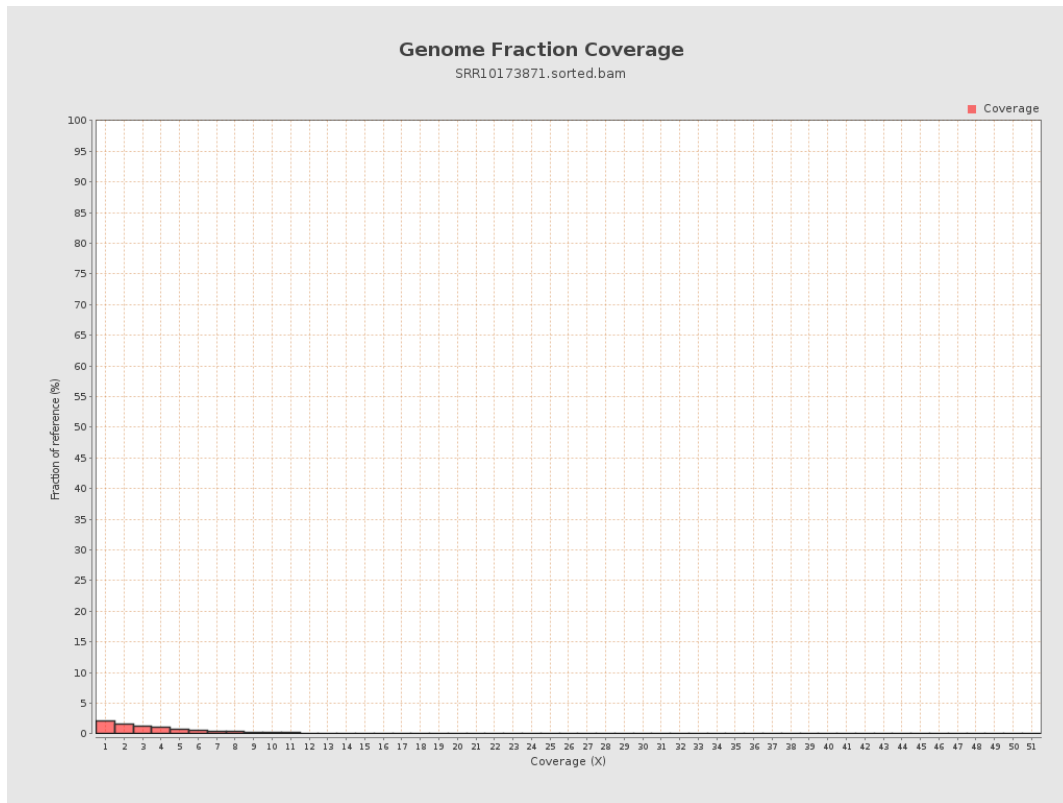
4. Results : Coverage Histogram



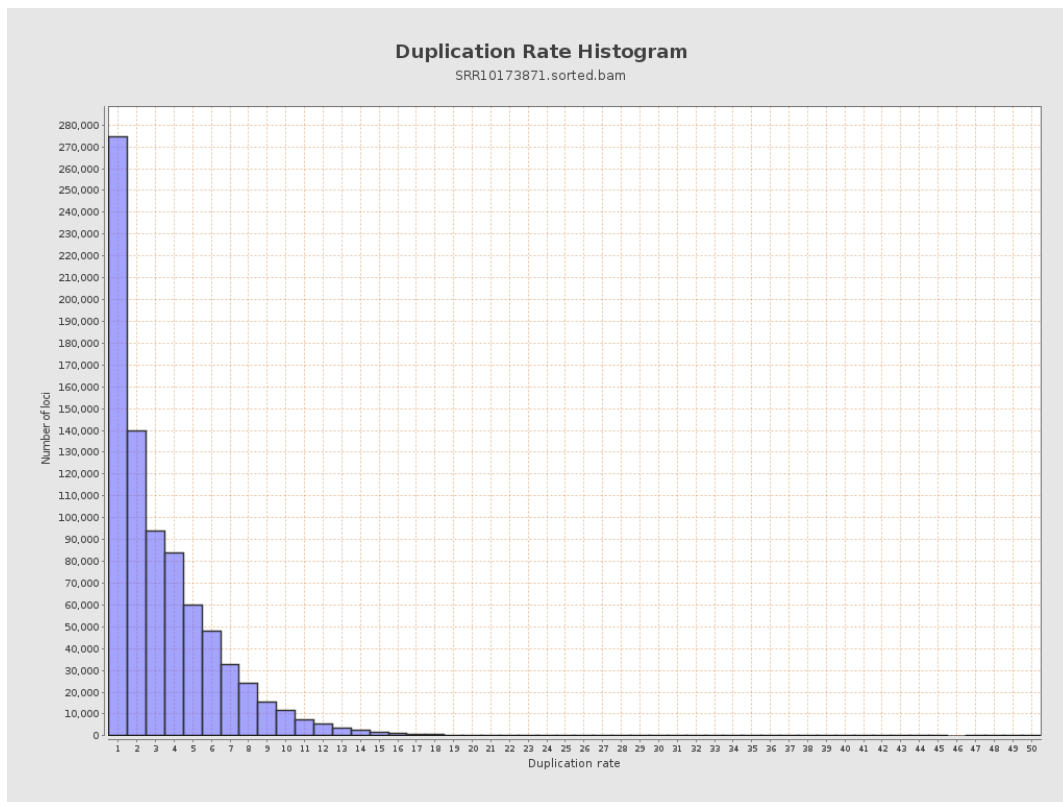
5. Results : Coverage Histogram (0-50X)



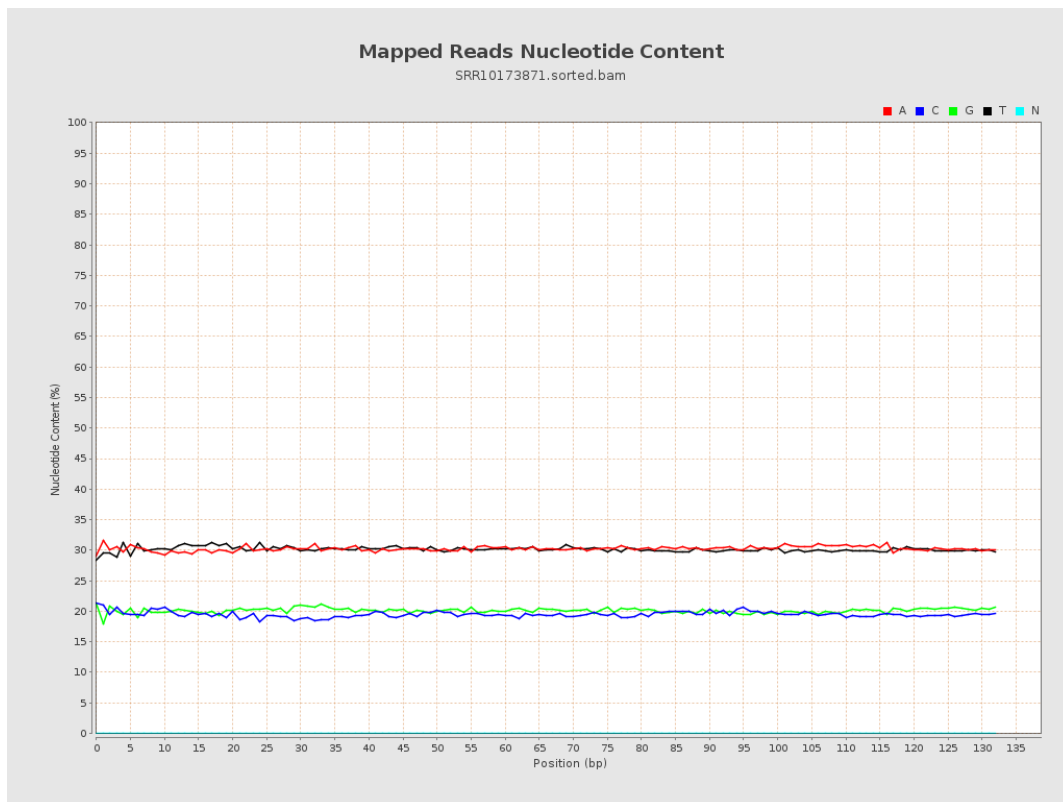
6. Results : Genome Fraction Coverage



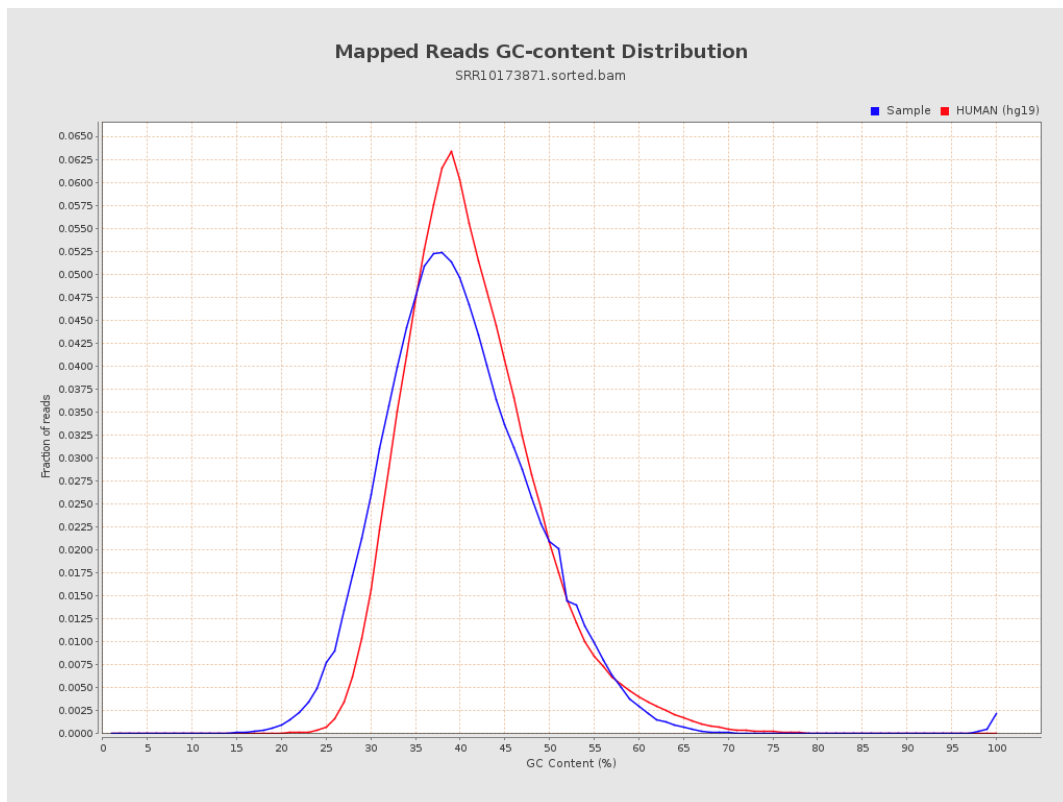
7. Results : Duplication Rate Histogram



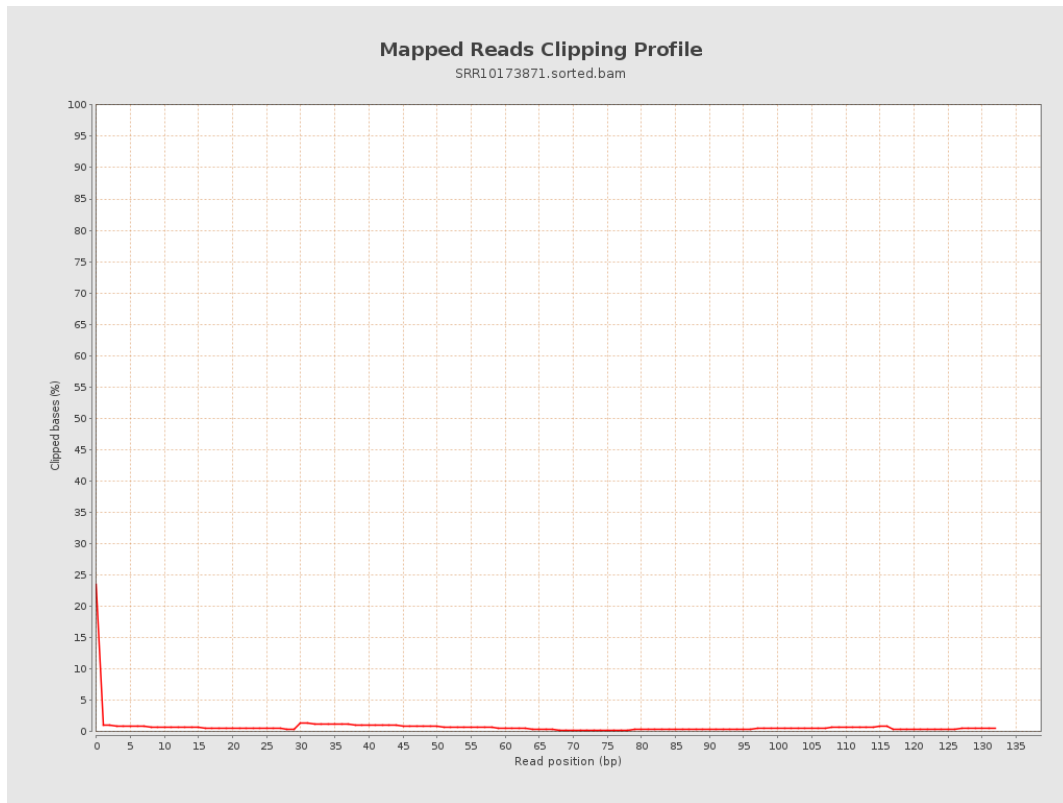
8. Results : Mapped Reads Nucleotide Content



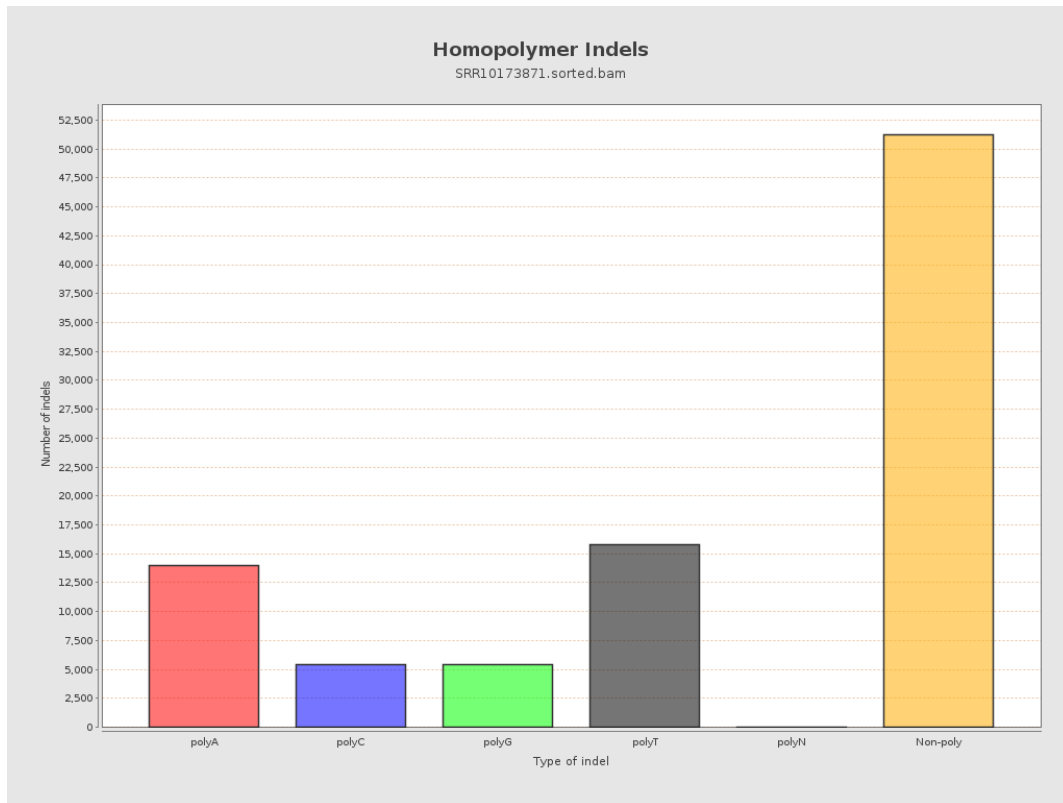
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



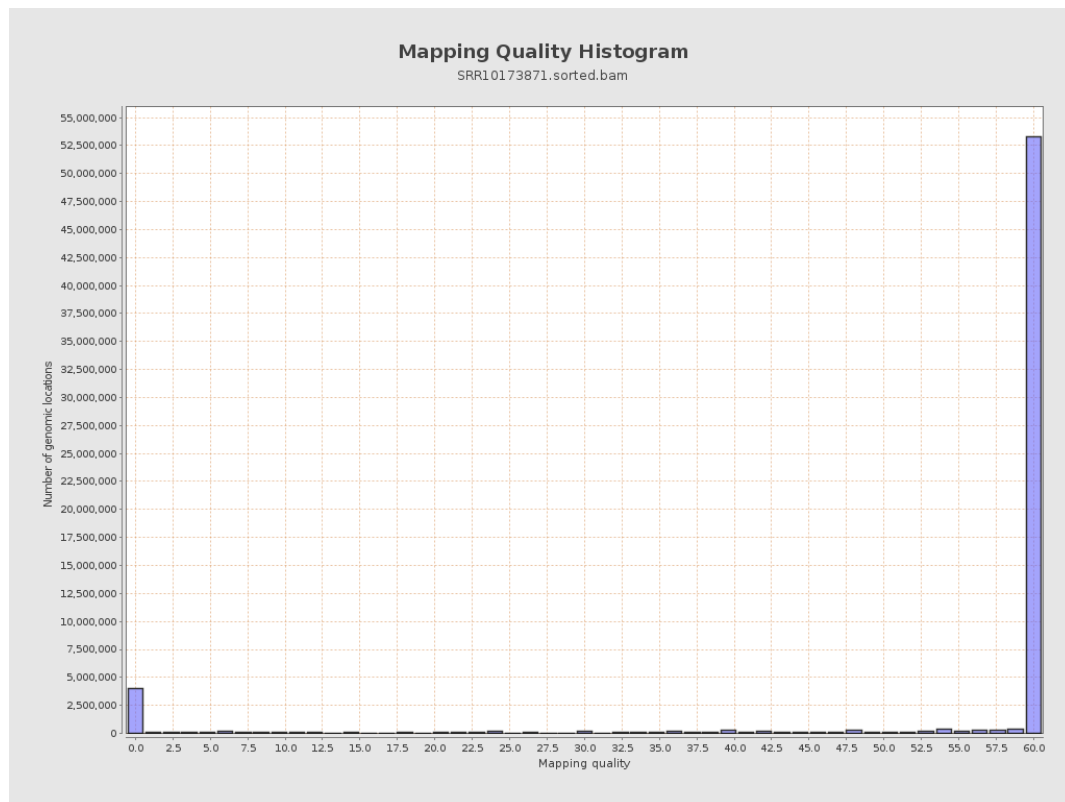
11. Results : Homopolymer Indels



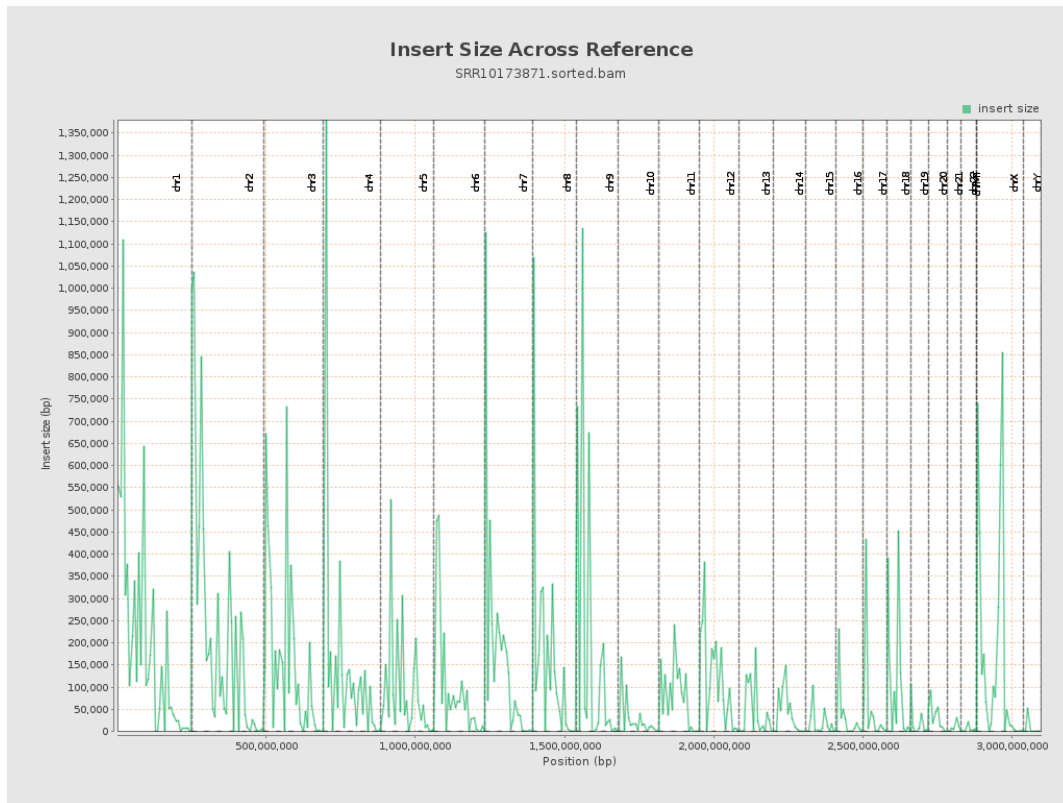
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

