

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 19:00:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173999.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_SRR10173999 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173999_1.fastq.gz SRR10173999_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 19:00:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173999.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,436,248
Mapped reads	2,393,866 / 98.26%
Unmapped reads	42,382 / 1.74%
Mapped paired reads	2,393,866 / 98.26%
Mapped reads, first in pair	1,195,711 / 49.08%
Mapped reads, second in pair	1,198,155 / 49.18%
Mapped reads, both in pair	2,365,222 / 97.08%
Mapped reads, singletons	28,644 / 1.18%
Secondary alignments	0
Supplementary alignments	304,252 / 12.49%
Read min/max/mean length	30 / 133 / 128.76
Duplicated reads (estimated)	1,990,571 / 81.71%
Duplication rate	70.08%
Clipped reads	1,171,652 / 48.09%

2.2. ACGT Content

Number/percentage of A's	84,717,426 / 29.99%
Number/percentage of C's	56,195,325 / 19.9%
Number/percentage of T's	84,219,559 / 29.82%
Number/percentage of G's	57,321,877 / 20.29%
Number/percentage of N's	3,540 / 0%

GC Percentage	40.19%
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2.3. Coverage

Mean	0.0913
Standard Deviation	1.4572

2.4. Mapping Quality

Mean Mapping Quality	53.07
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2.5. Insert size

Mean	1,126,085.02
Standard Deviation	10,375,144.76
P25/Median/P75	122 / 155 / 202

2.6. Mismatches and indels

General error rate	0.77%
Mismatches	2,124,668
Insertions	22,739
Mapped reads with at least one insertion	0.93%
Deletions	38,072
Mapped reads with at least one deletion	1.56%
Homopolymer indels	45.96%

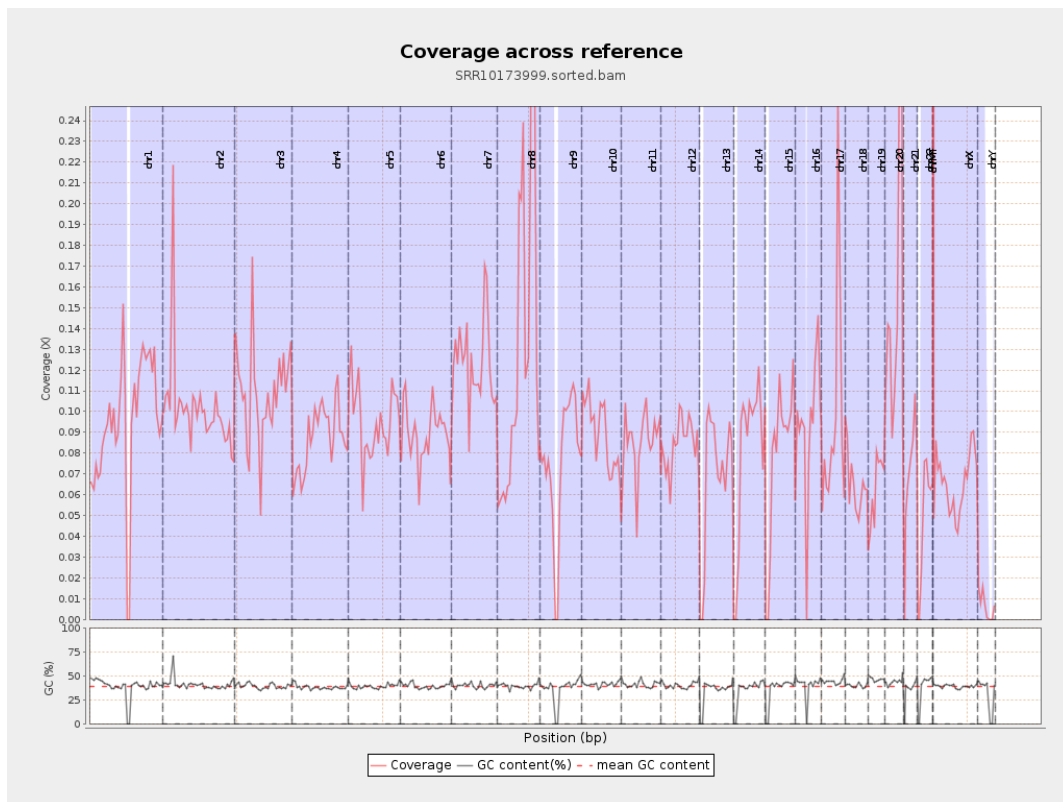
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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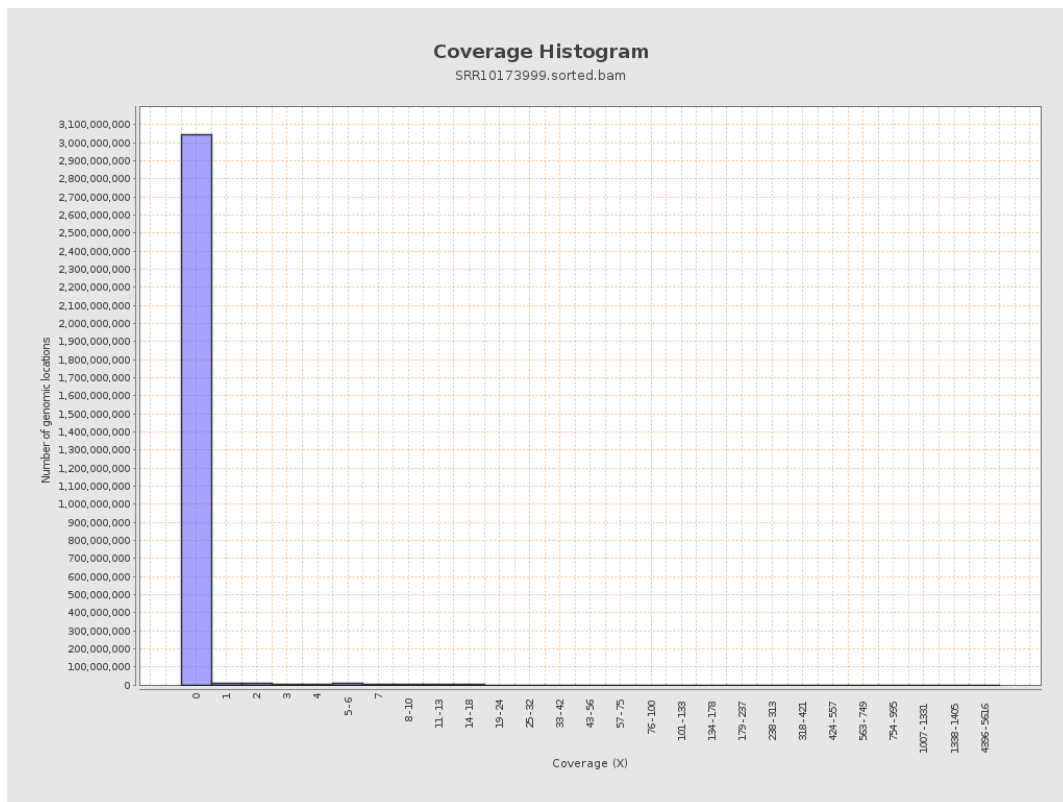
		bases	coverage	deviation
chr1	249250621	23742487	0.0953	0.9483
chr2	243199373	24610609	0.1012	4.0123
chr3	198022430	21556696	0.1089	1.0258
chr4	191154276	16757628	0.0877	0.9317
chr5	180915260	17200789	0.0951	0.9541
chr6	171115067	15332741	0.0896	0.947
chr7	159138663	19525512	0.1227	1.1077
chr8	146364022	20477788	0.1399	1.4751
chr9	141213431	10707802	0.0758	0.8338
chr10	135534747	12151386	0.0897	0.9758
chr11	135006516	11484063	0.0851	0.895
chr12	133851895	11334216	0.0847	0.8935
chr13	115169878	7997765	0.0694	0.8186
chr14	107349540	8796328	0.0819	0.8839
chr15	102531392	8057916	0.0786	0.855
chr16	90354753	8249684	0.0913	0.938
chr17	81195210	8053157	0.0992	0.9698
chr18	78077248	5081747	0.0651	0.7944
chr19	59128983	3771318	0.0638	0.7436
chr20	63025520	10747553	0.1705	1.2817
chr21	48129895	3370081	0.07	0.8247
chr22	51304566	2475973	0.0483	0.6609
chrMT	16571	487304	29.407	46.5896
chrX	155270560	10191286	0.0656	0.7936

chrY	59373566	383372	0.0065	0.2248
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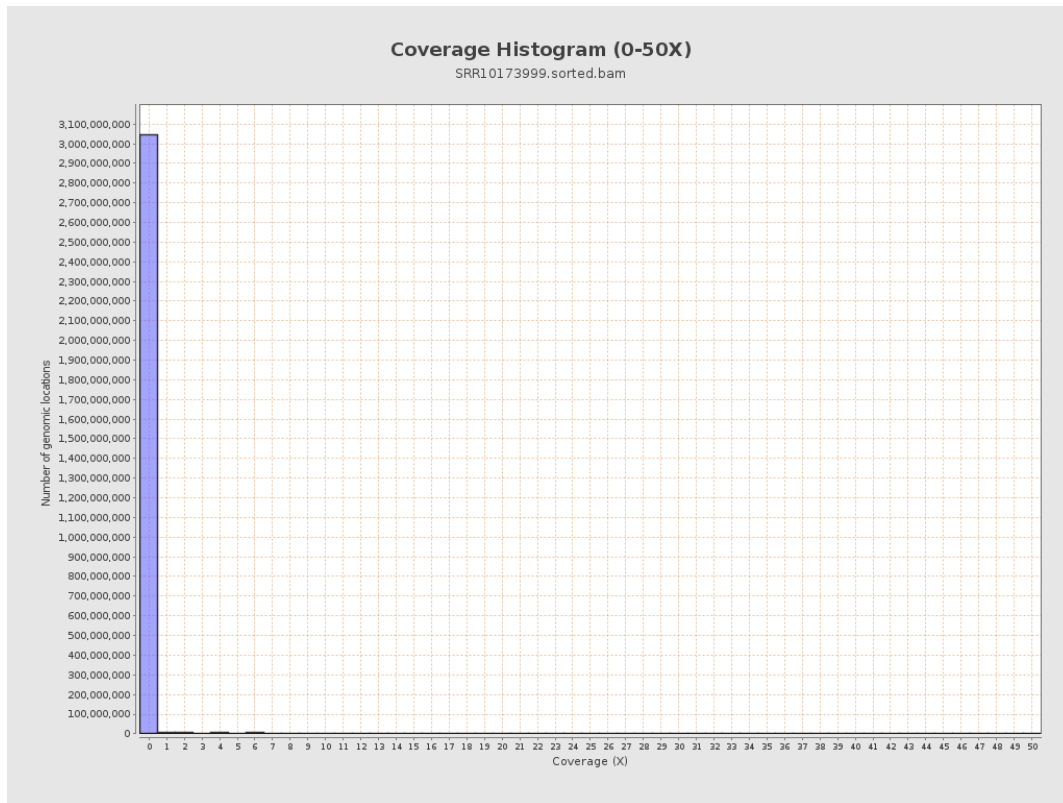
3. Results : Coverage across reference



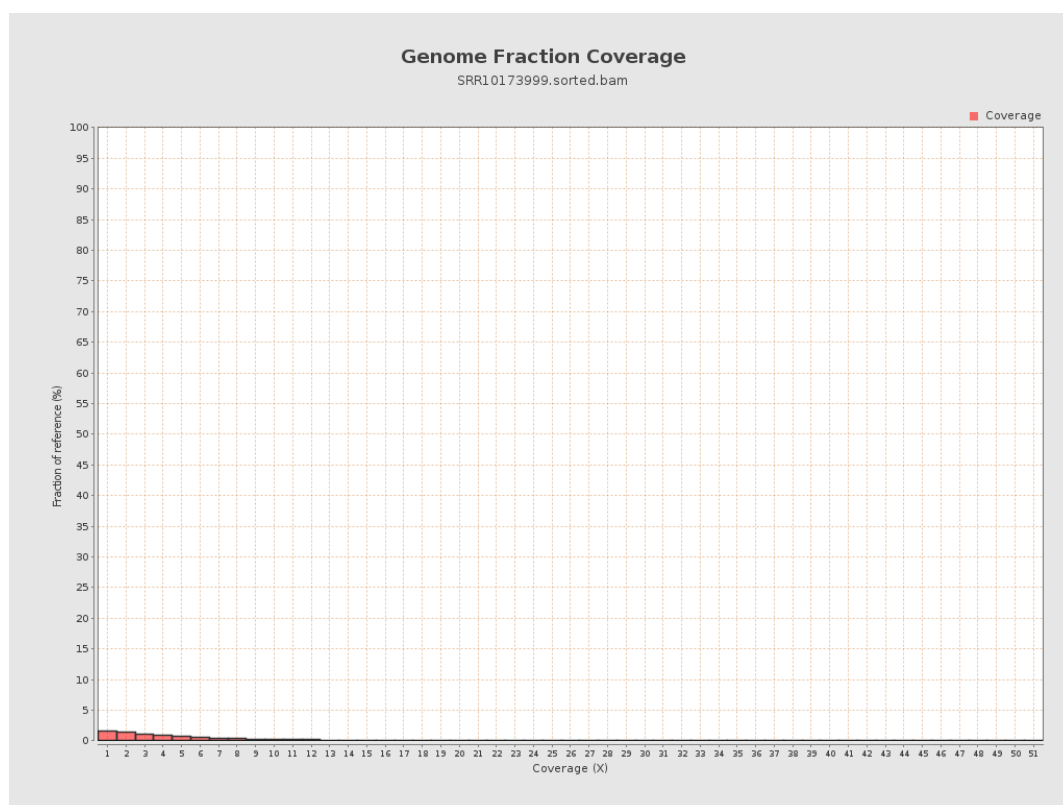
4. Results : Coverage Histogram



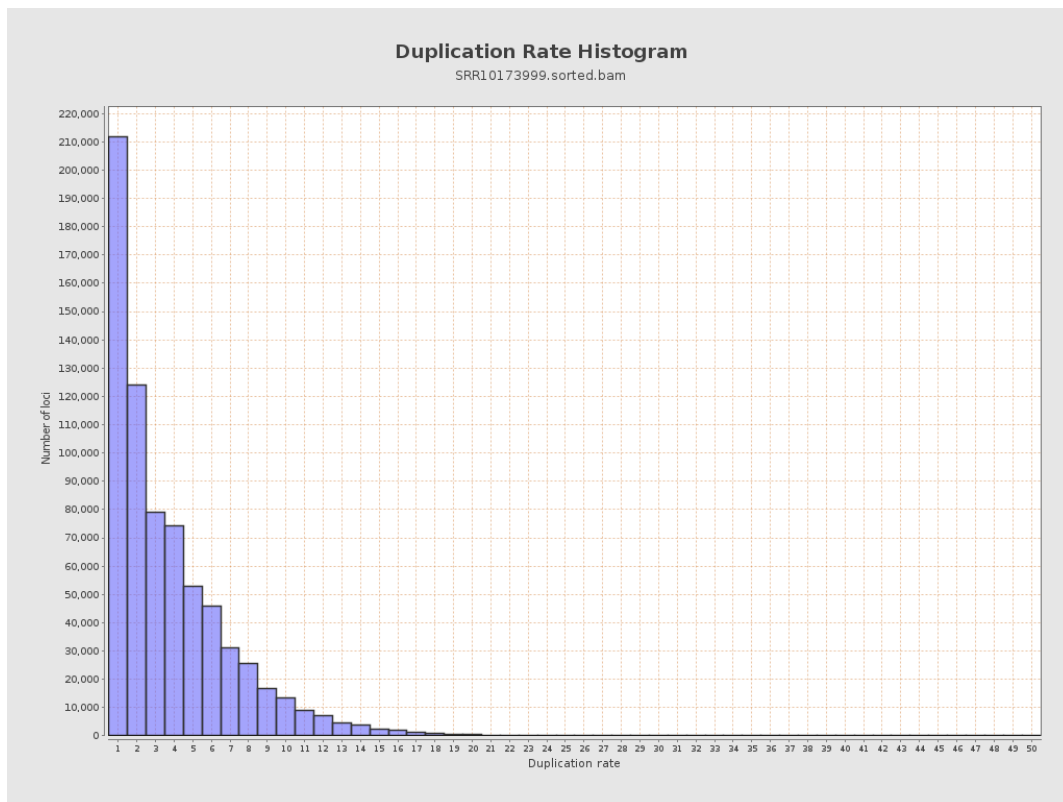
5. Results : Coverage Histogram (0-50X)



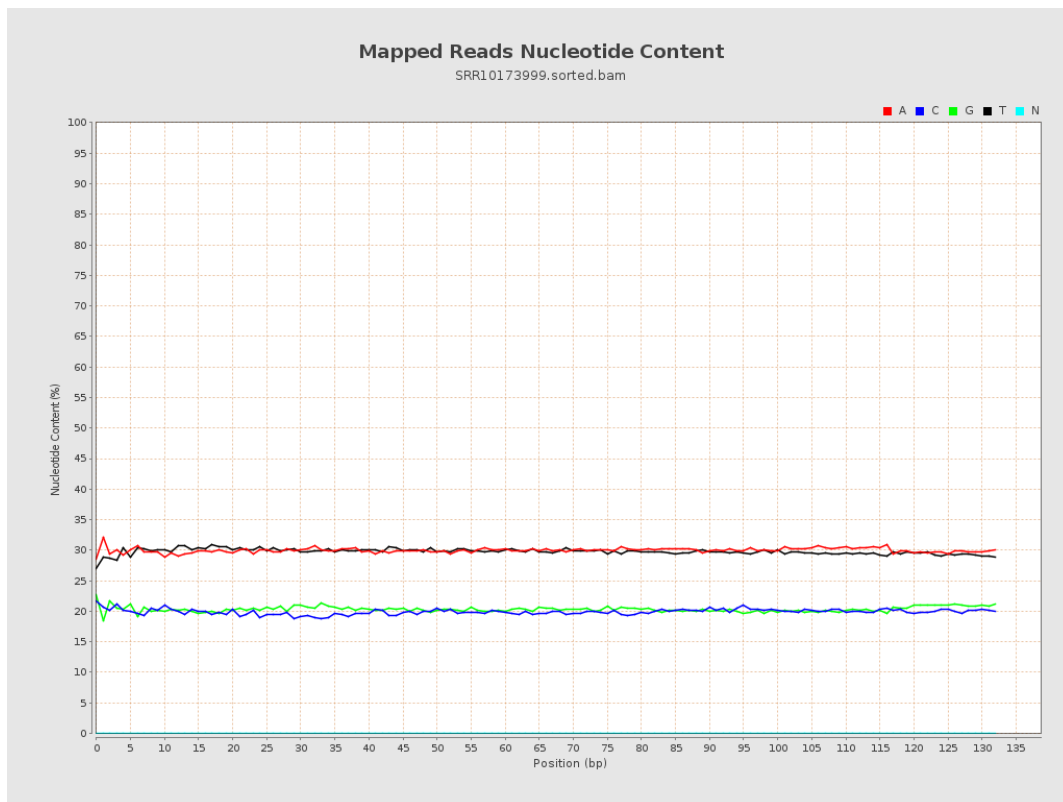
6. Results : Genome Fraction Coverage



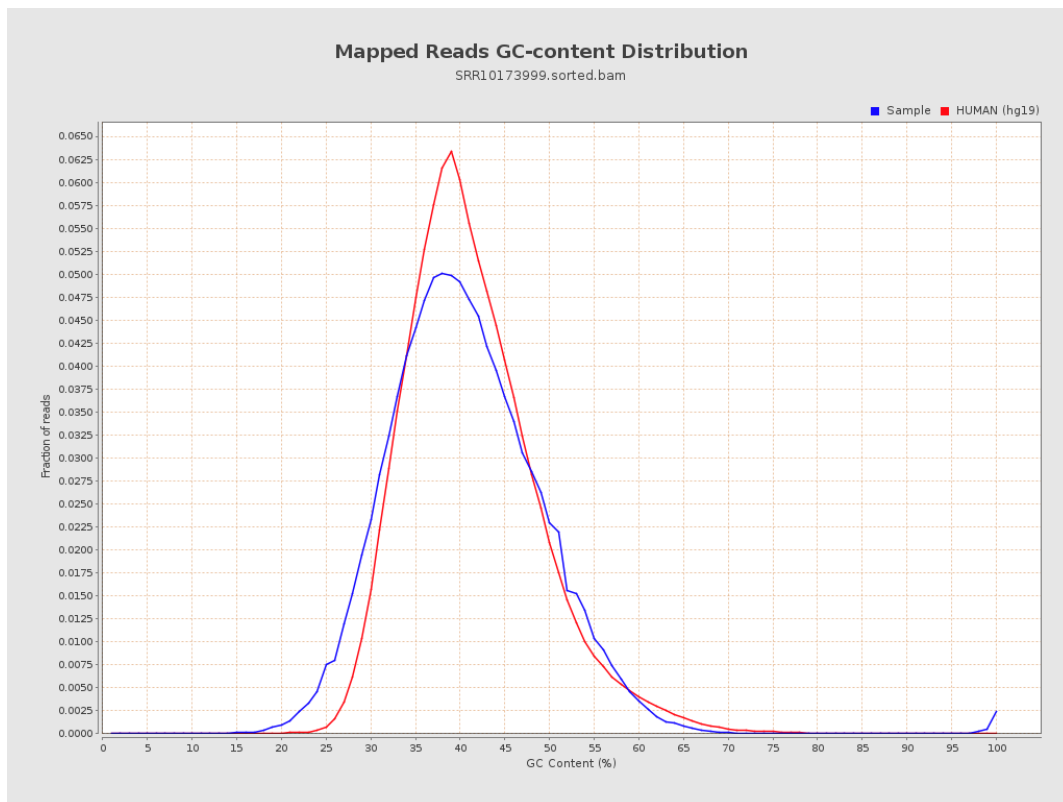
7. Results : Duplication Rate Histogram



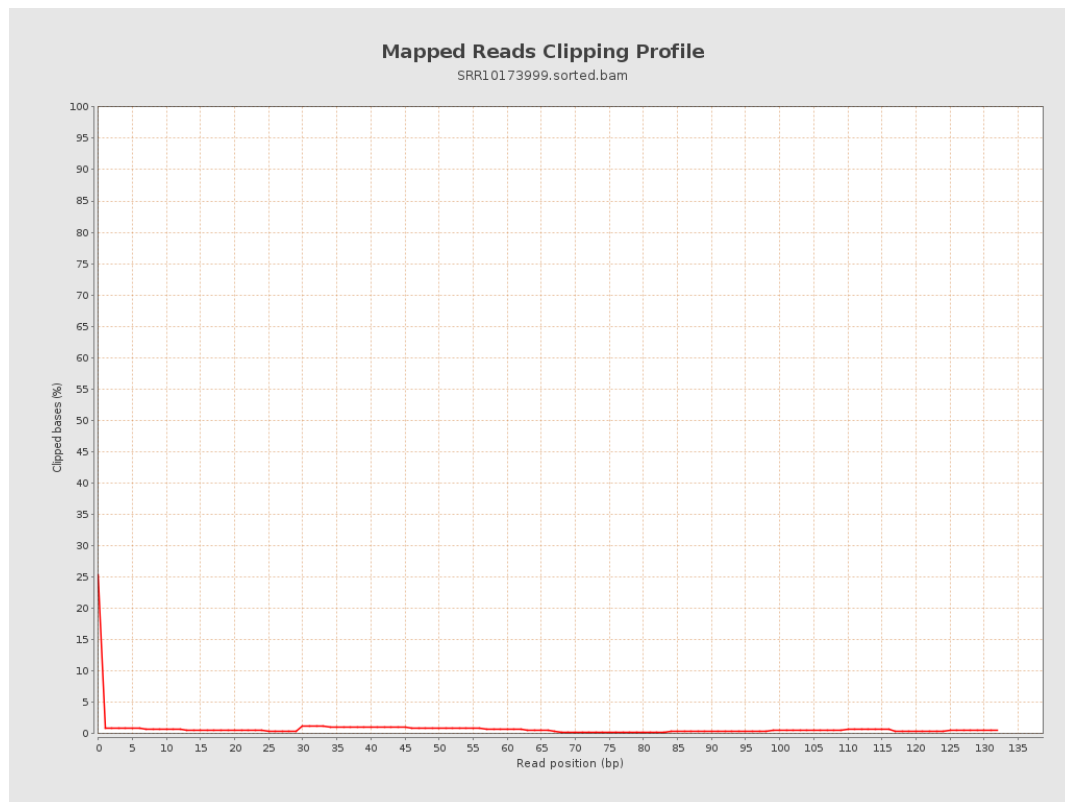
8. Results : Mapped Reads Nucleotide Content



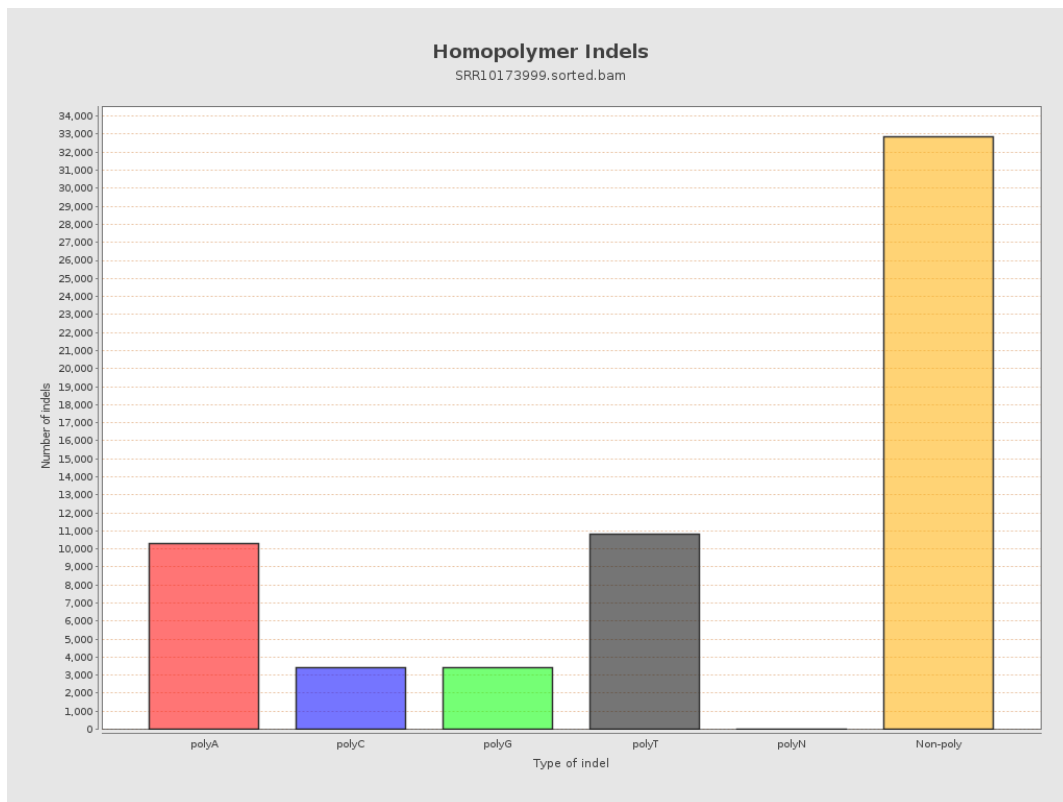
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



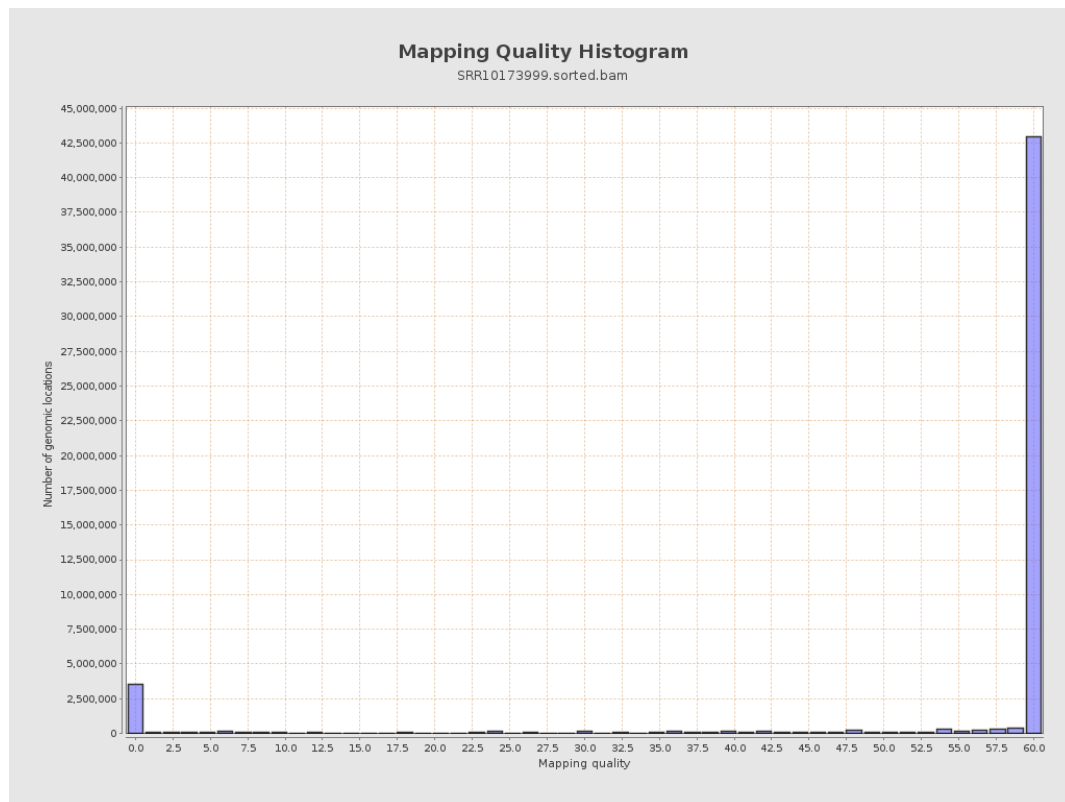
11. Results : Homopolymer Indels



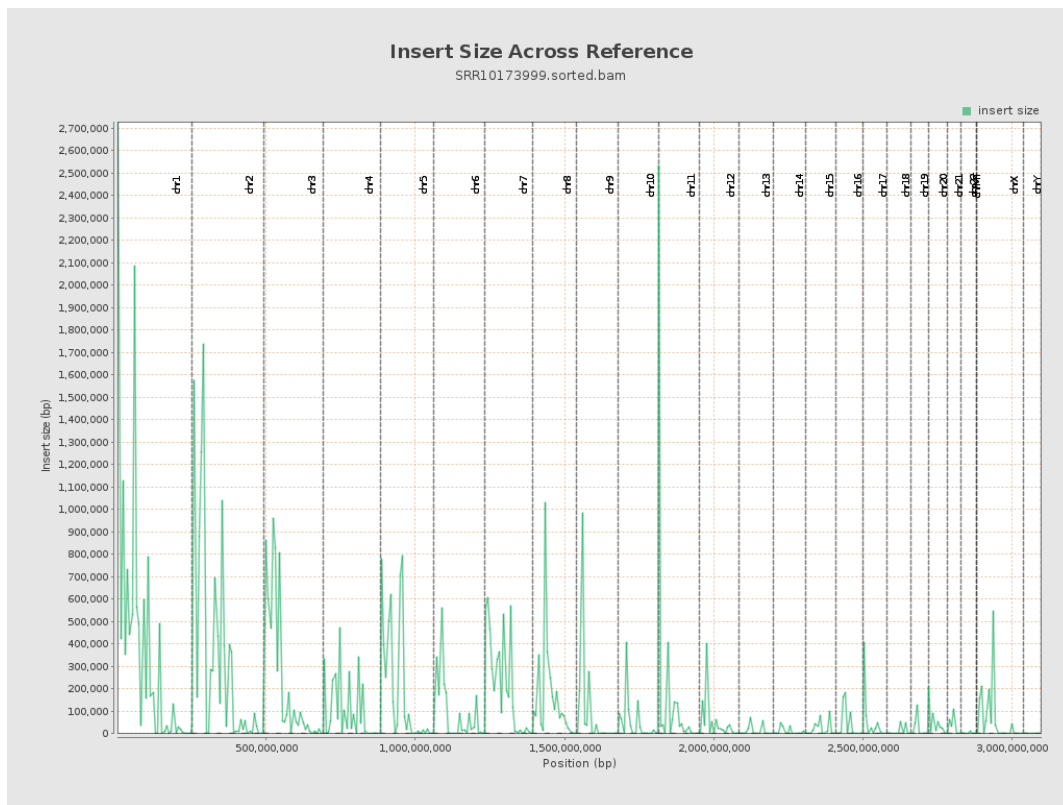
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

