

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 02:18:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173890.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_SRR10173890 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173890_1.fastq.gz SRR10173890_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 02:18:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173890.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,122,824
Mapped reads	5,947,930 / 97.14%
Unmapped reads	174,894 / 2.86%
Mapped paired reads	5,947,930 / 97.14%
Mapped reads, first in pair	2,977,306 / 48.63%
Mapped reads, second in pair	2,970,624 / 48.52%
Mapped reads, both in pair	5,837,204 / 95.34%
Mapped reads, singletons	110,726 / 1.81%
Secondary alignments	0
Supplementary alignments	604,392 / 9.87%
Read min/max/mean length	30 / 133 / 128.25
Duplicated reads (estimated)	4,808,975 / 78.54%
Duplication rate	66.18%
Clipped reads	2,438,010 / 39.82%

2.2. ACGT Content

Number/percentage of A's	210,917,535 / 30.02%
Number/percentage of C's	138,388,770 / 19.7%
Number/percentage of T's	210,229,562 / 29.92%
Number/percentage of G's	143,107,187 / 20.37%
Number/percentage of N's	9,028 / 0%

GC Percentage	40.06%
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2.3. Coverage

Mean	0.2271
Standard Deviation	3.1943

2.4. Mapping Quality

Mean Mapping Quality	52.63
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2.5. Insert size

Mean	852,744.46
Standard Deviation	8,507,629.12
P25/Median/P75	146 / 204 / 295

2.6. Mismatches and indels

General error rate	1.07%
Mismatches	7,326,951
Insertions	73,512
Mapped reads with at least one insertion	1.19%
Deletions	163,128
Mapped reads with at least one deletion	2.68%
Homopolymer indels	43.05%

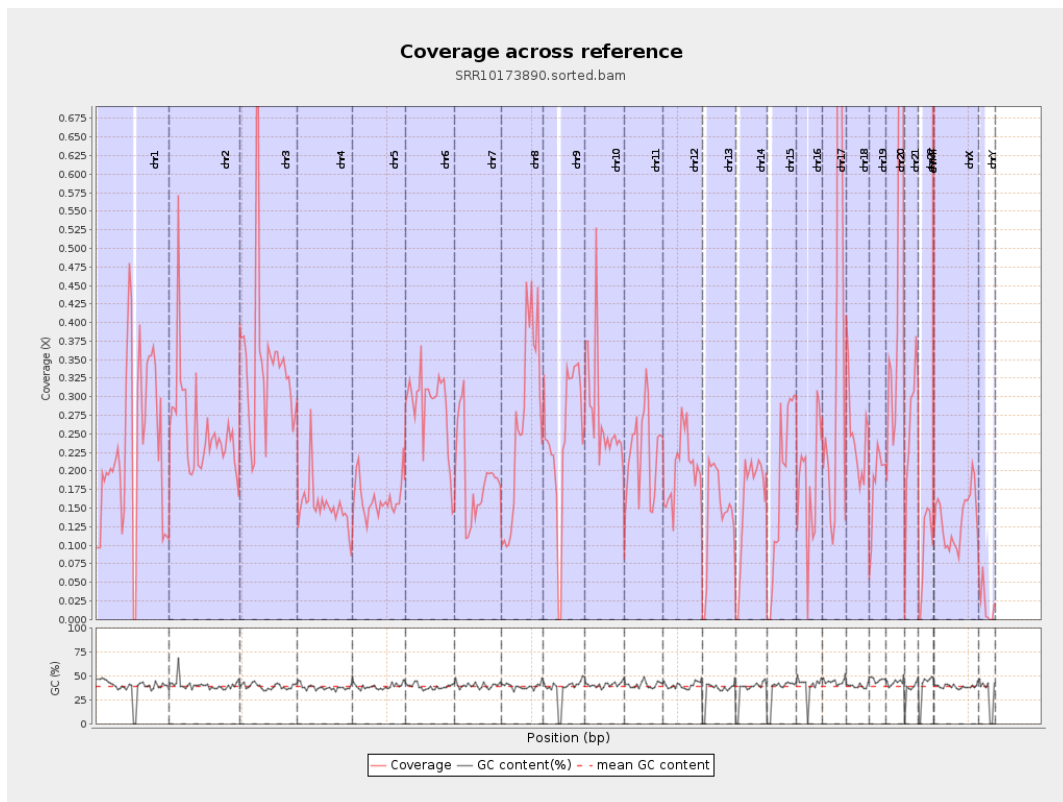
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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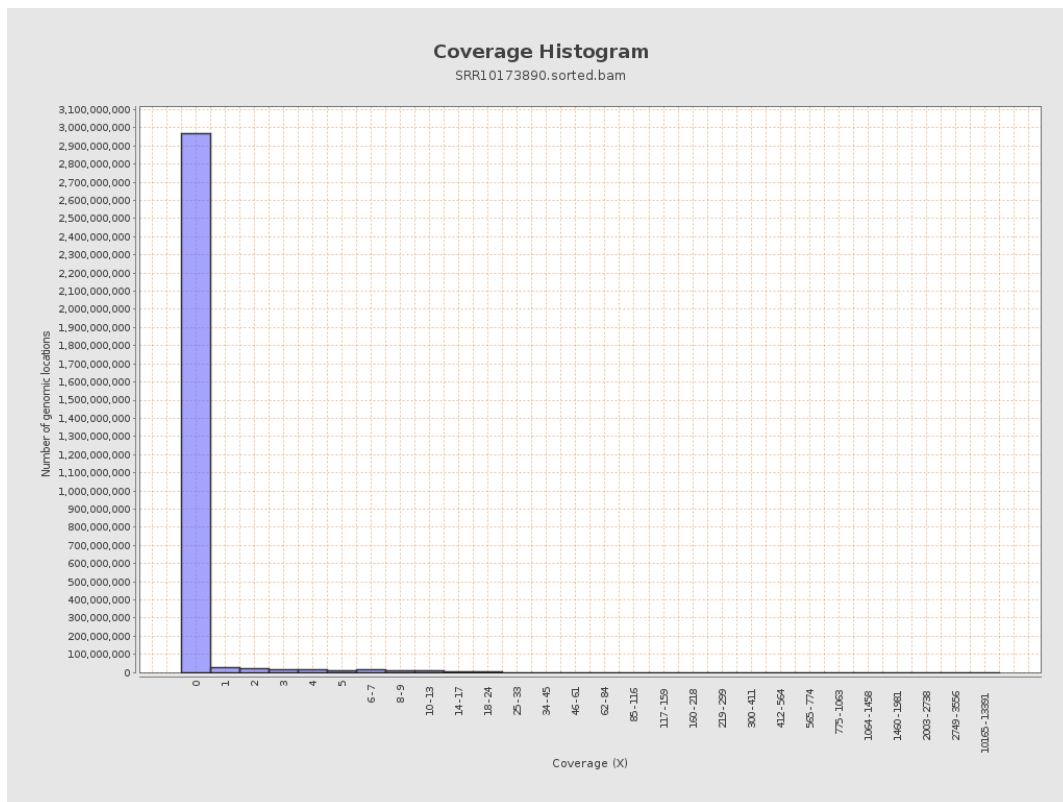
		bases	coverage	deviation
chr1	249250621	57014321	0.2287	2.3353
chr2	243199373	61947641	0.2547	9.4111
chr3	198022430	67679231	0.3418	1.8223
chr4	191154276	29012925	0.1518	1.5436
chr5	180915260	29444253	0.1628	1.2261
chr6	171115067	48782974	0.2851	2.0292
chr7	159138663	30587388	0.1922	1.6126
chr8	146364022	38593548	0.2637	2.2247
chr9	141213431	34375403	0.2434	1.8791
chr10	135534747	37170132	0.2742	3.2031
chr11	135006516	30531098	0.2261	1.4822
chr12	133851895	27055643	0.2021	1.3832
chr13	115169878	16376032	0.1422	1.1455
chr14	107349540	17190263	0.1601	1.2183
chr15	102531392	18264573	0.1781	1.2831
chr16	90354753	16894114	0.187	1.5319
chr17	81195210	32864790	0.4048	2.1782
chr18	78077248	19167885	0.2455	2.2691
chr19	59128983	11033207	0.1866	1.6101
chr20	63025520	37338499	0.5924	2.6229
chr21	48129895	12421211	0.2581	1.6346
chr22	51304566	4833759	0.0942	0.8842
chrMT	16571	2438022	147.1258	103.071
chrX	155270560	20908520	0.1347	1.1081

chrY	59373566	1131292	0.0191	0.781
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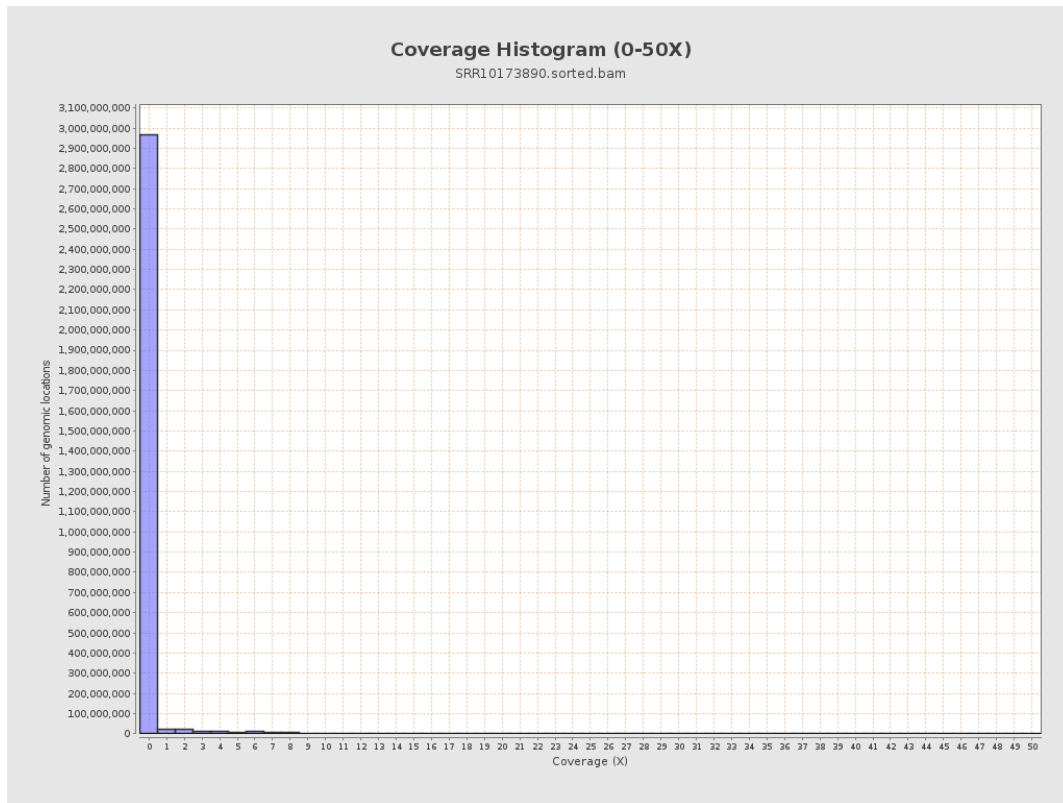
3. Results : Coverage across reference



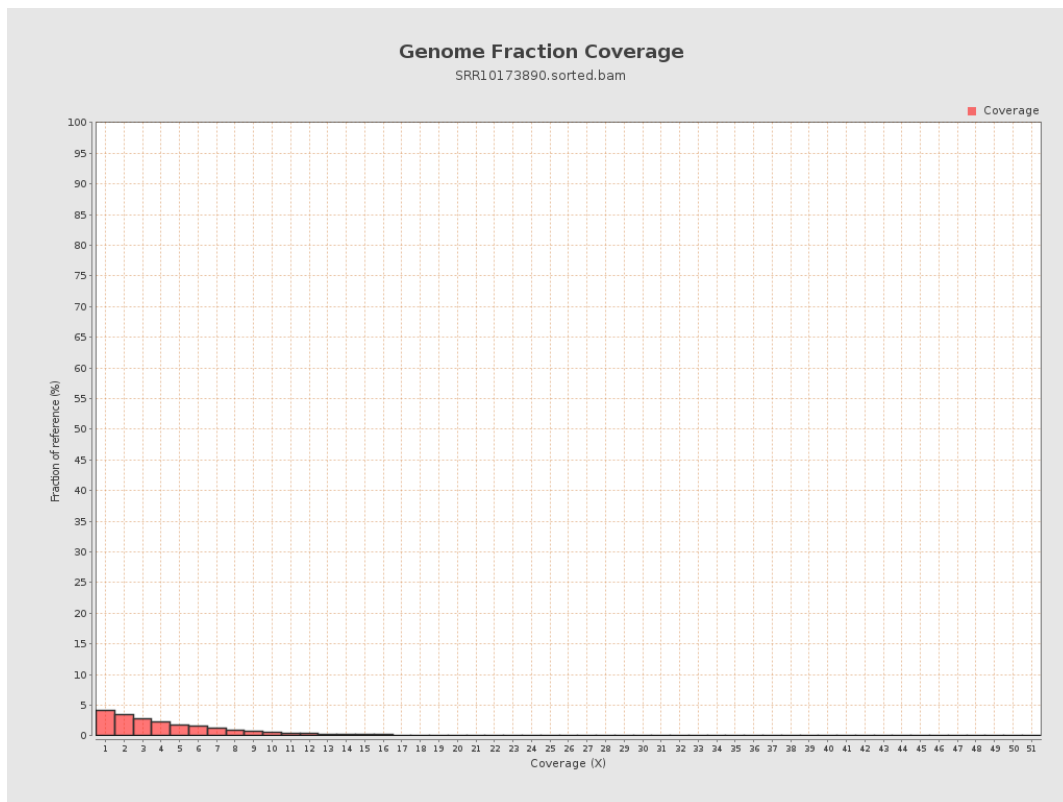
4. Results : Coverage Histogram



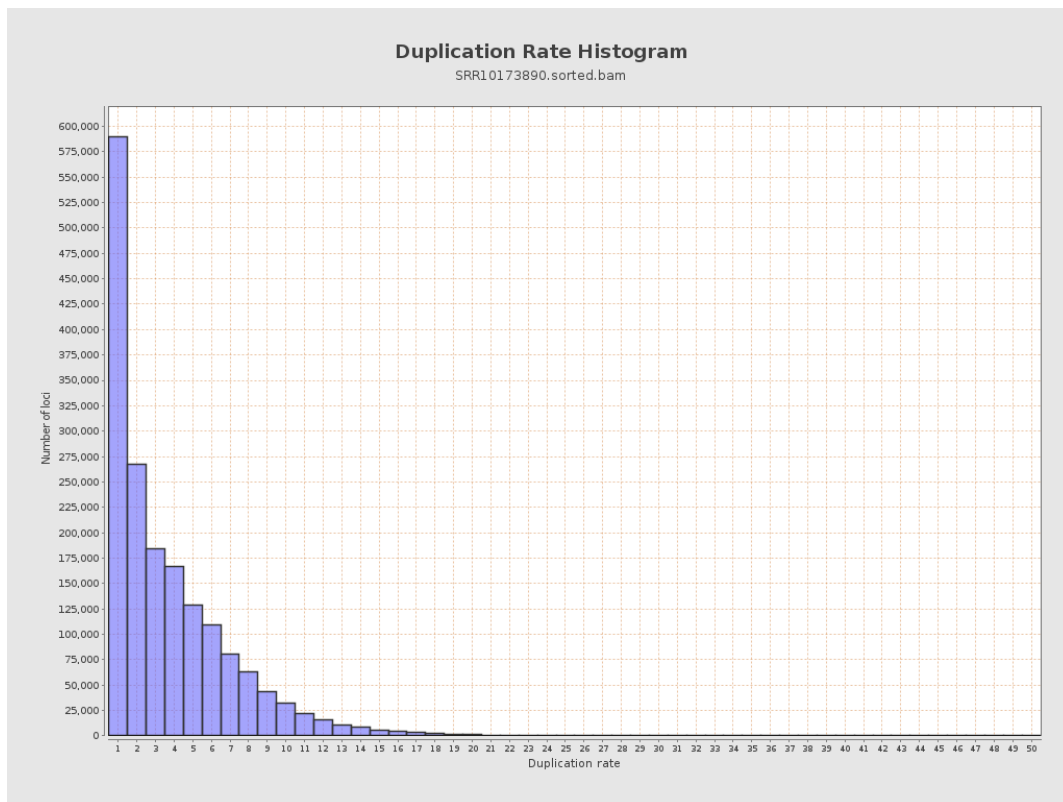
5. Results : Coverage Histogram (0-50X)



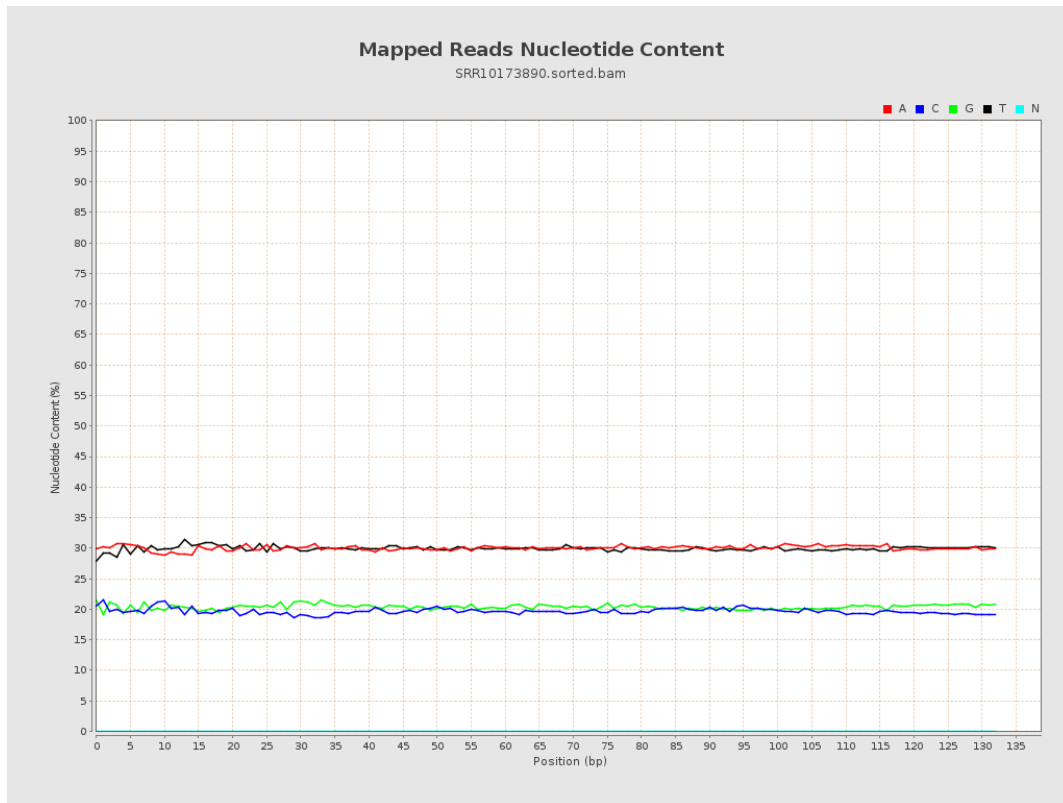
6. Results : Genome Fraction Coverage



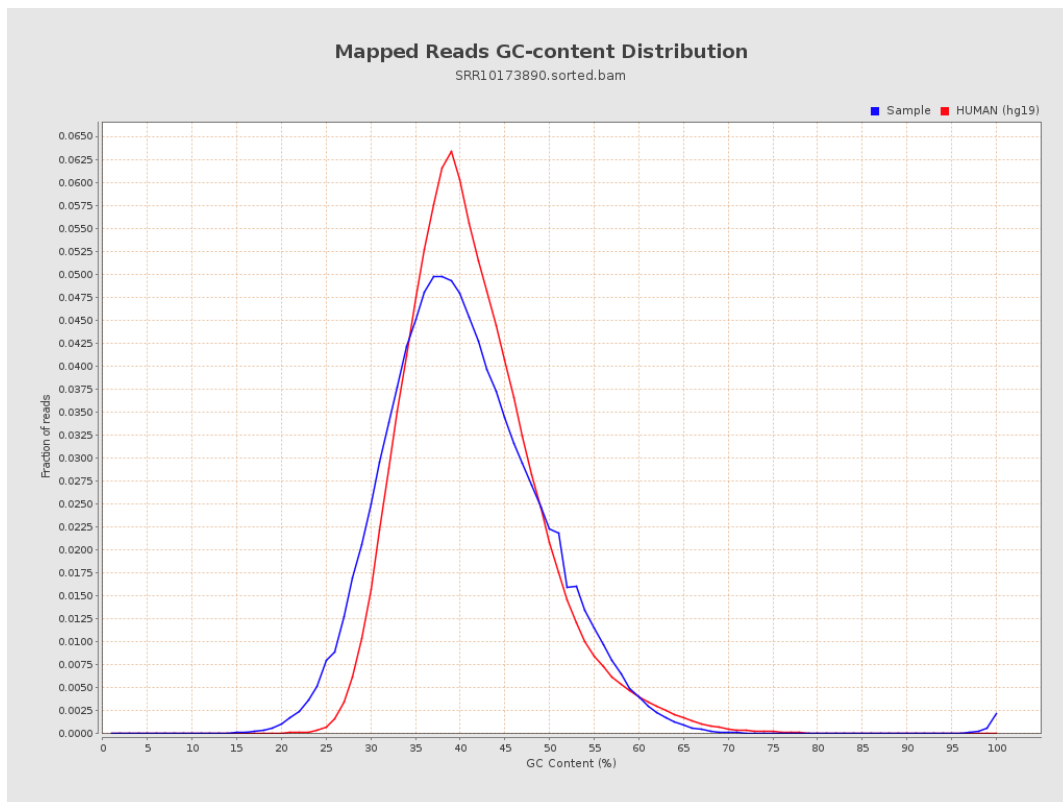
7. Results : Duplication Rate Histogram



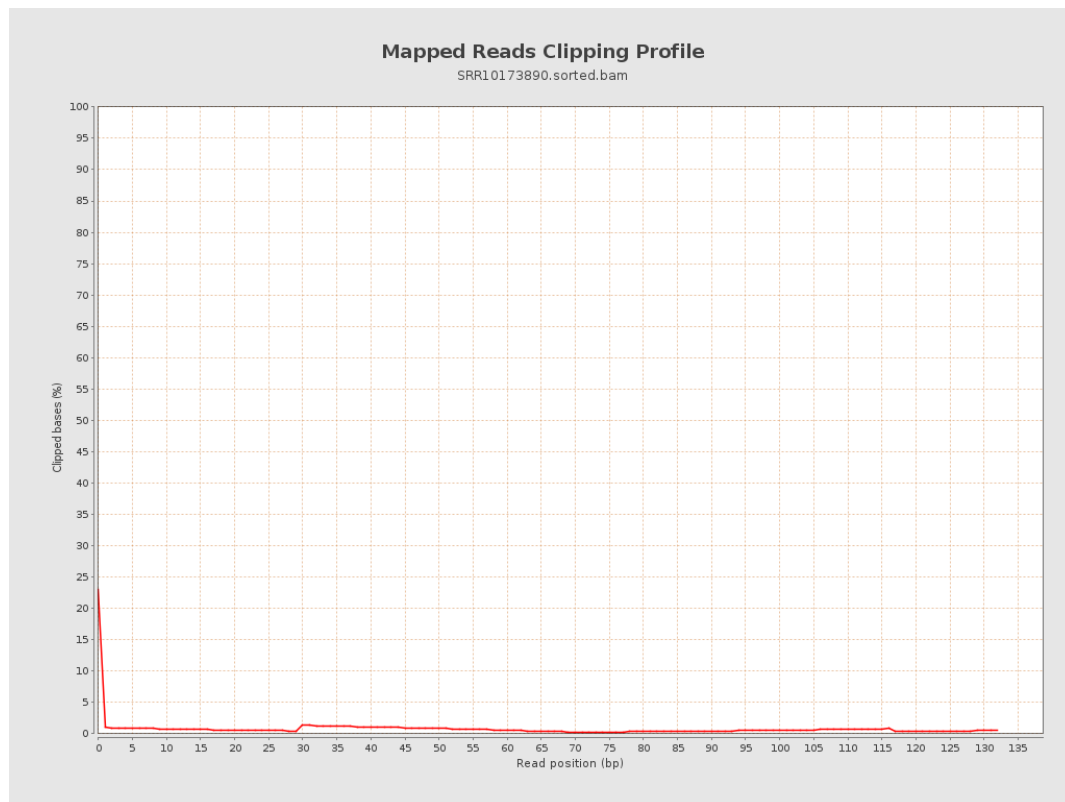
8. Results : Mapped Reads Nucleotide Content



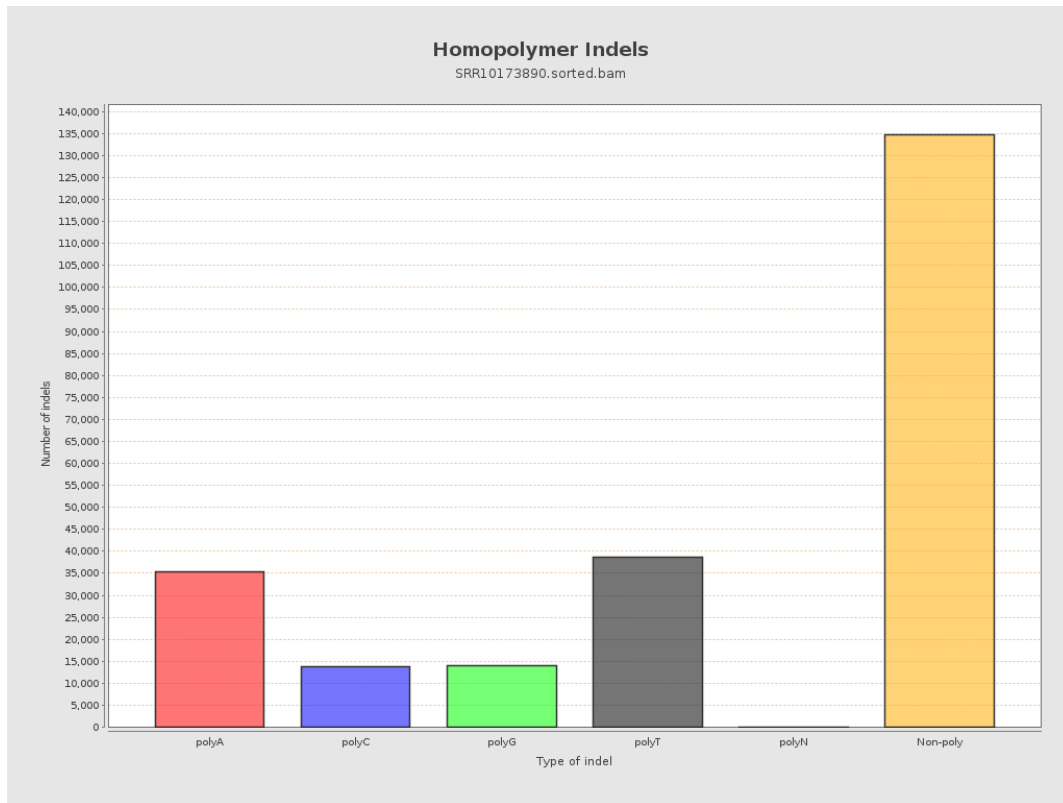
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



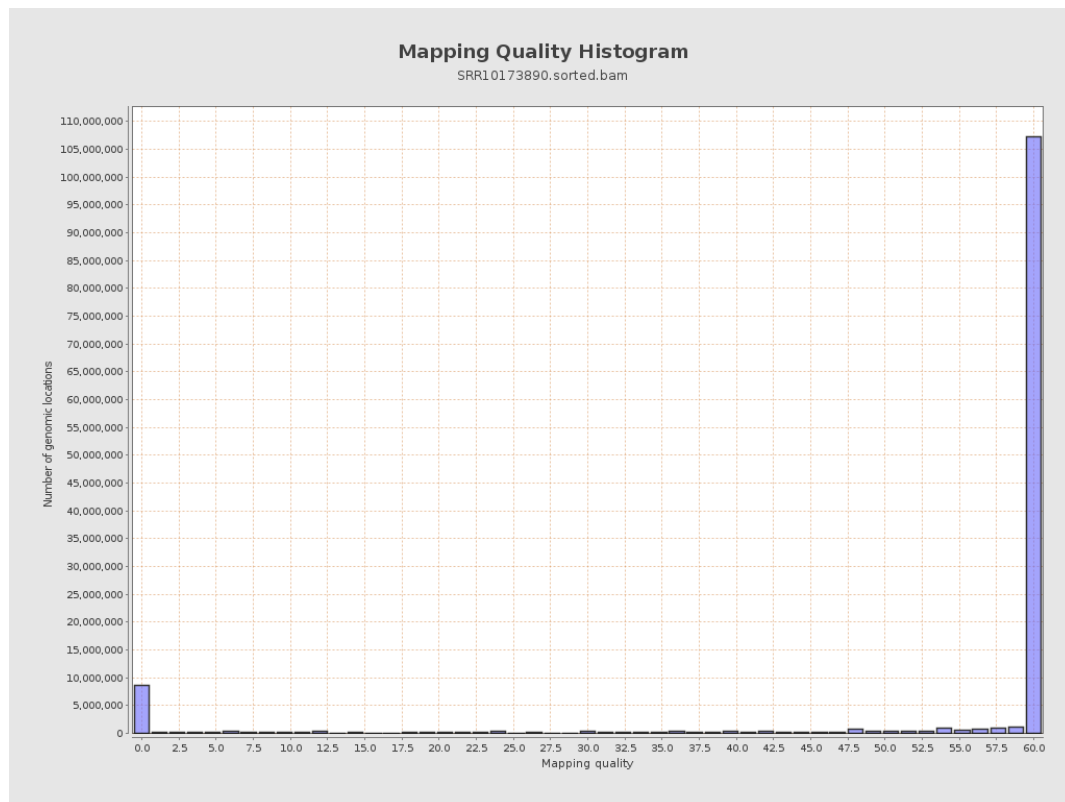
11. Results : Homopolymer Indels



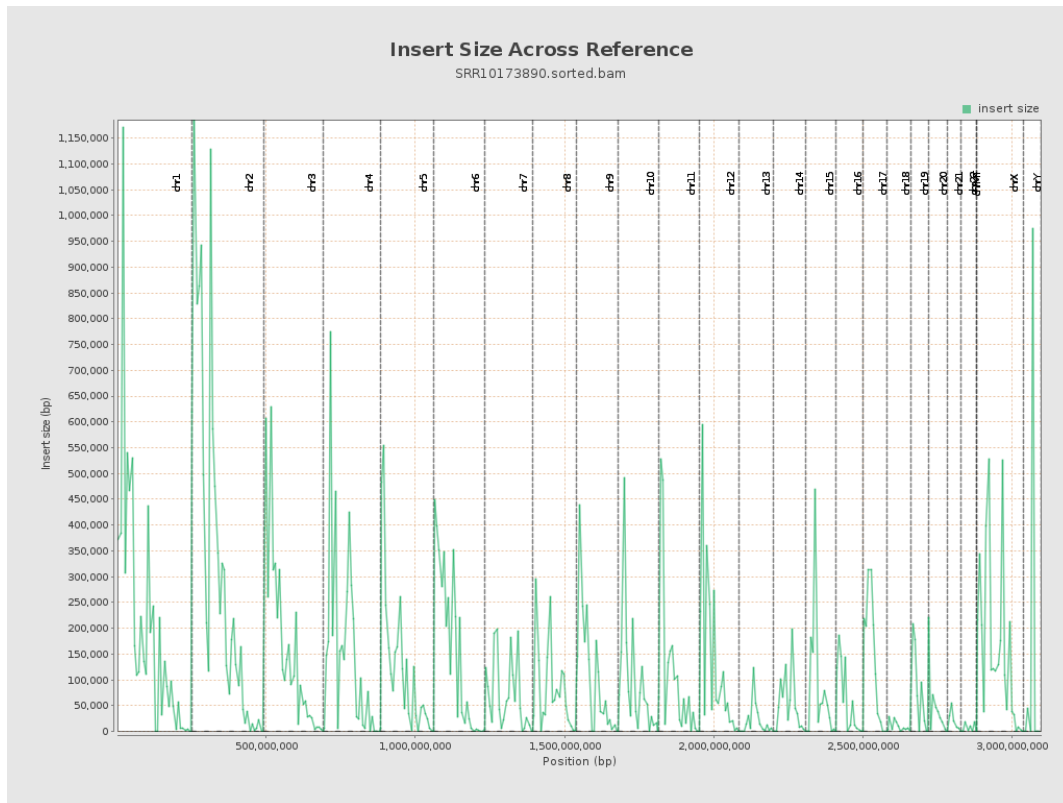
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

