

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 17:52:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173990.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_SRR10173990 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173990_1.fastq.gz SRR10173990_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 17:52:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173990.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,852,242
Mapped reads	6,713,494 / 97.98%
Unmapped reads	138,748 / 2.02%
Mapped paired reads	6,713,494 / 97.98%
Mapped reads, first in pair	3,355,133 / 48.96%
Mapped reads, second in pair	3,358,361 / 49.01%
Mapped reads, both in pair	6,626,990 / 96.71%
Mapped reads, singletons	86,504 / 1.26%
Secondary alignments	0
Supplementary alignments	913,251 / 13.33%
Read min/max/mean length	30 / 133 / 124.55
Duplicated reads (estimated)	5,420,262 / 79.1%
Duplication rate	64.7%
Clipped reads	3,465,678 / 50.58%

2.2. ACGT Content

Number/percentage of A's	226,237,200 / 29.98%
Number/percentage of C's	149,207,514 / 19.77%
Number/percentage of T's	224,291,298 / 29.72%
Number/percentage of G's	154,929,908 / 20.53%
Number/percentage of N's	5,650 / 0%

GC Percentage	40.3%
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2.3. Coverage

Mean	0.244
Standard Deviation	4.2773

2.4. Mapping Quality

Mean Mapping Quality	52.59
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2.5. Insert size

Mean	991,410.49
Standard Deviation	9,143,716.75
P25/Median/P75	101 / 146 / 225

2.6. Mismatches and indels

General error rate	0.86%
Mismatches	6,263,592
Insertions	82,634
Mapped reads with at least one insertion	1.19%
Deletions	230,928
Mapped reads with at least one deletion	3.36%
Homopolymer indels	40.71%

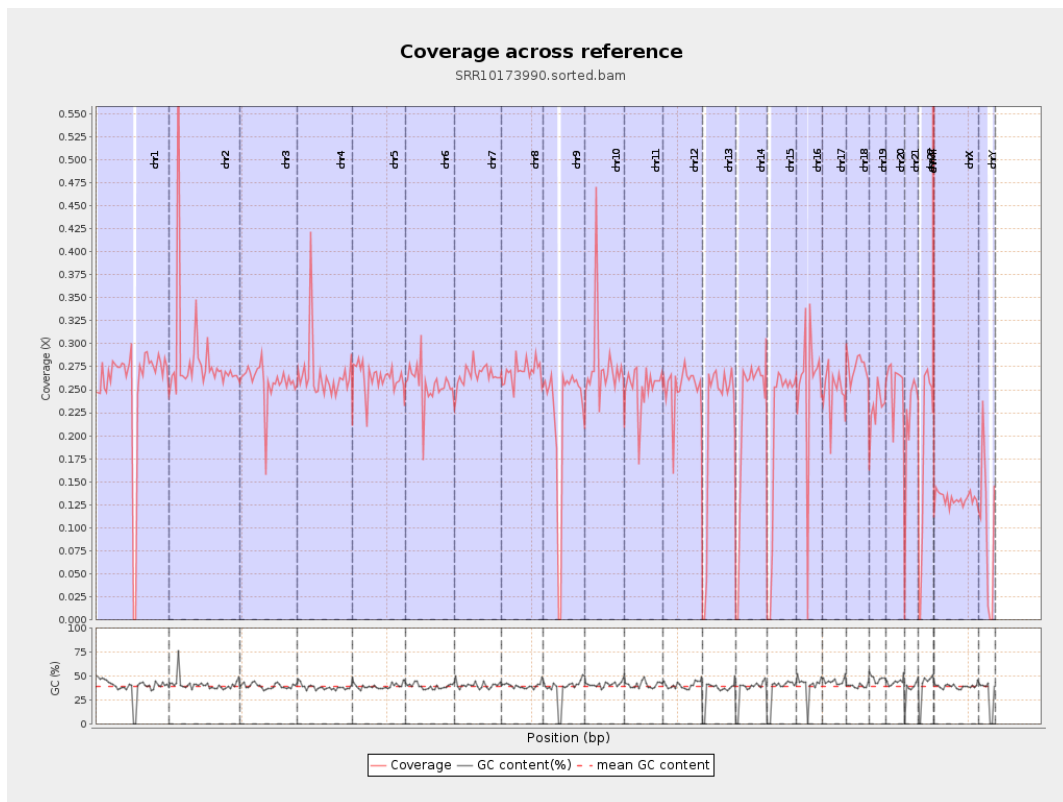
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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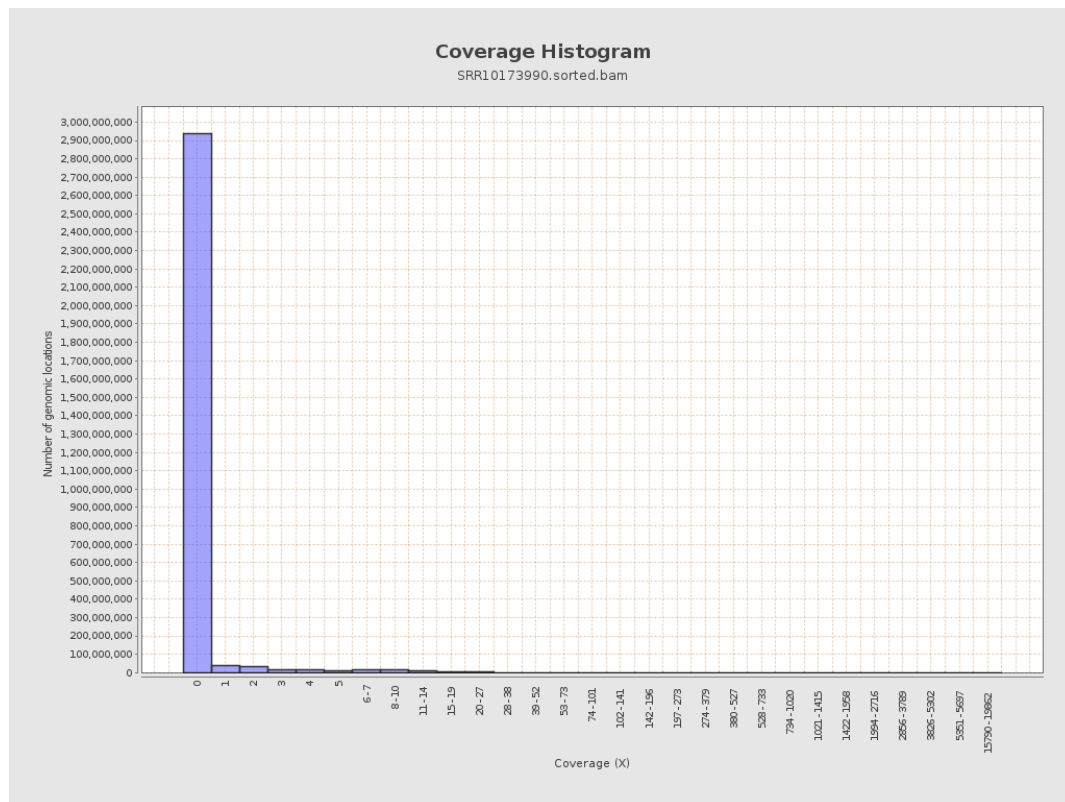
		bases	coverage	deviation
chr1	249250621	63659055	0.2554	2.1433
chr2	243199373	69005249	0.2837	13.9104
chr3	198022430	51236039	0.2587	1.5548
chr4	191154276	50805757	0.2658	2.0421
chr5	180915260	47563645	0.2629	1.577
chr6	171115067	43671870	0.2552	1.7299
chr7	159138663	42431453	0.2666	2.0957
chr8	146364022	39492412	0.2698	2.1981
chr9	141213431	31479538	0.2229	1.8952
chr10	135534747	37419997	0.2761	2.6159
chr11	135006516	34177683	0.2532	1.5754
chr12	133851895	33828823	0.2527	1.599
chr13	115169878	24719782	0.2146	1.4192
chr14	107349540	23798247	0.2217	1.4702
chr15	102531392	21262288	0.2074	1.41
chr16	90354753	22908760	0.2535	1.9446
chr17	81195210	20083273	0.2473	1.6003
chr18	78077248	21486138	0.2752	2.4503
chr19	59128983	13767373	0.2328	1.6879
chr20	63025520	16163883	0.2565	1.6049
chr21	48129895	10339904	0.2148	1.8285
chr22	51304566	9280151	0.1809	1.4943
chrMT	16571	739646	44.635	40.7784
chrX	155270560	20292528	0.1307	1.1096

chrY	59373566	5602576	0.0944	1.4704
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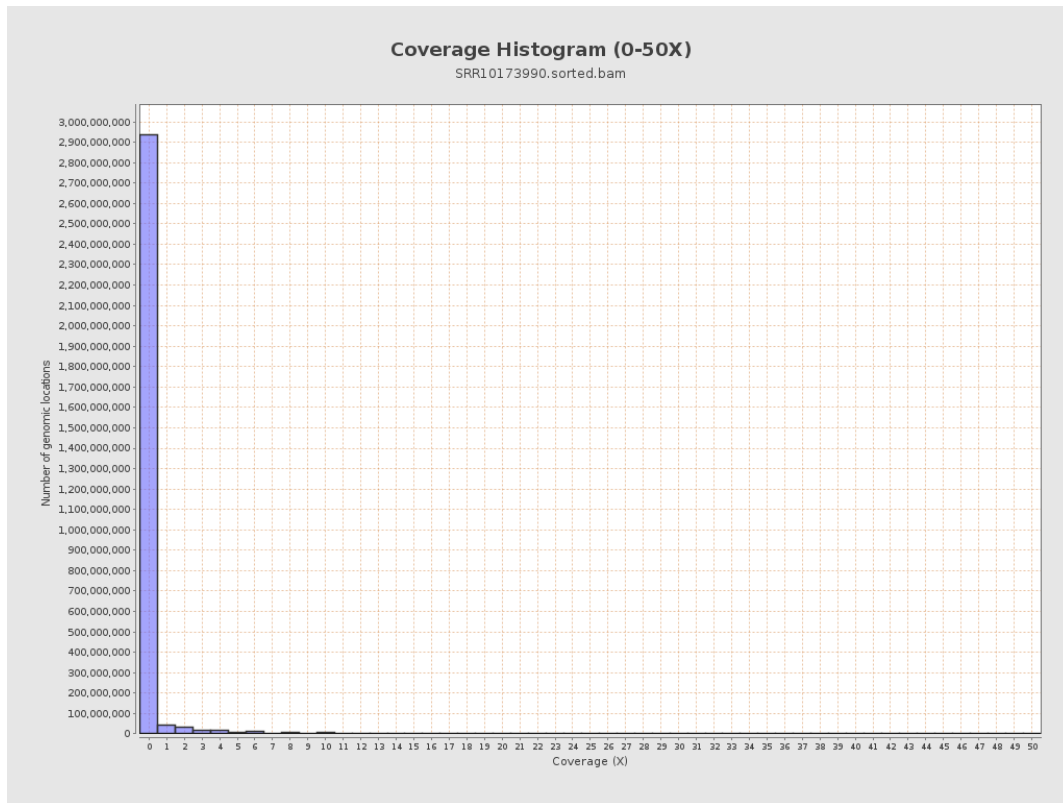
3. Results : Coverage across reference



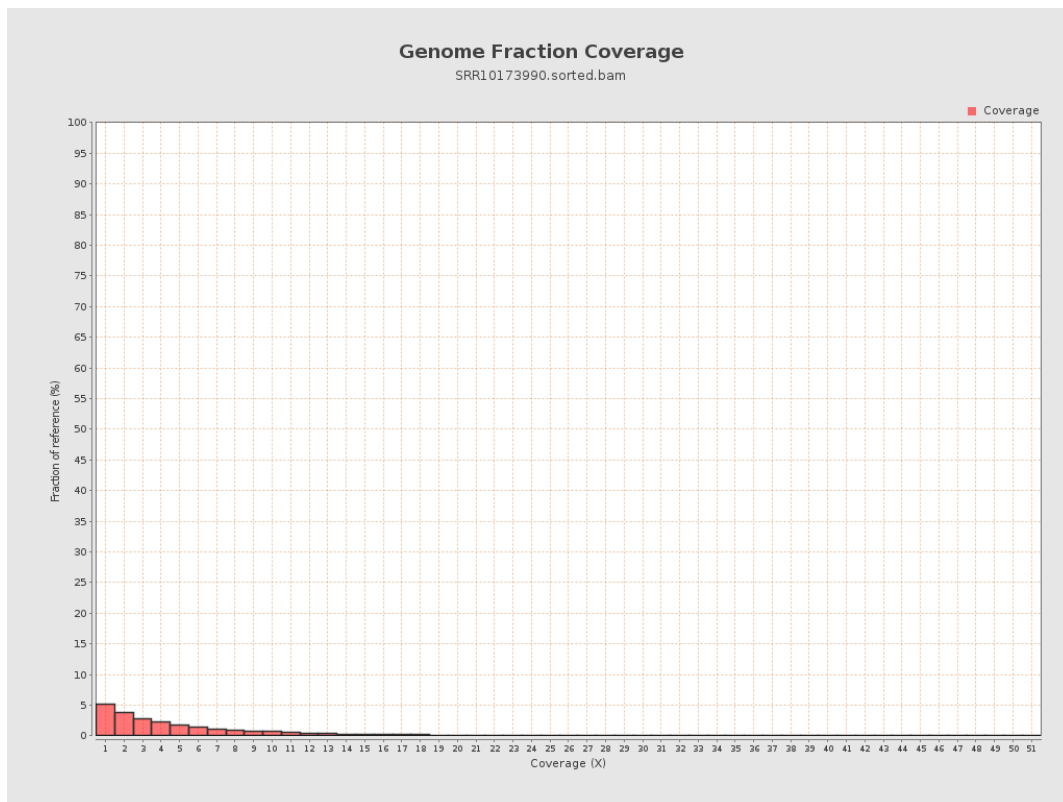
4. Results : Coverage Histogram



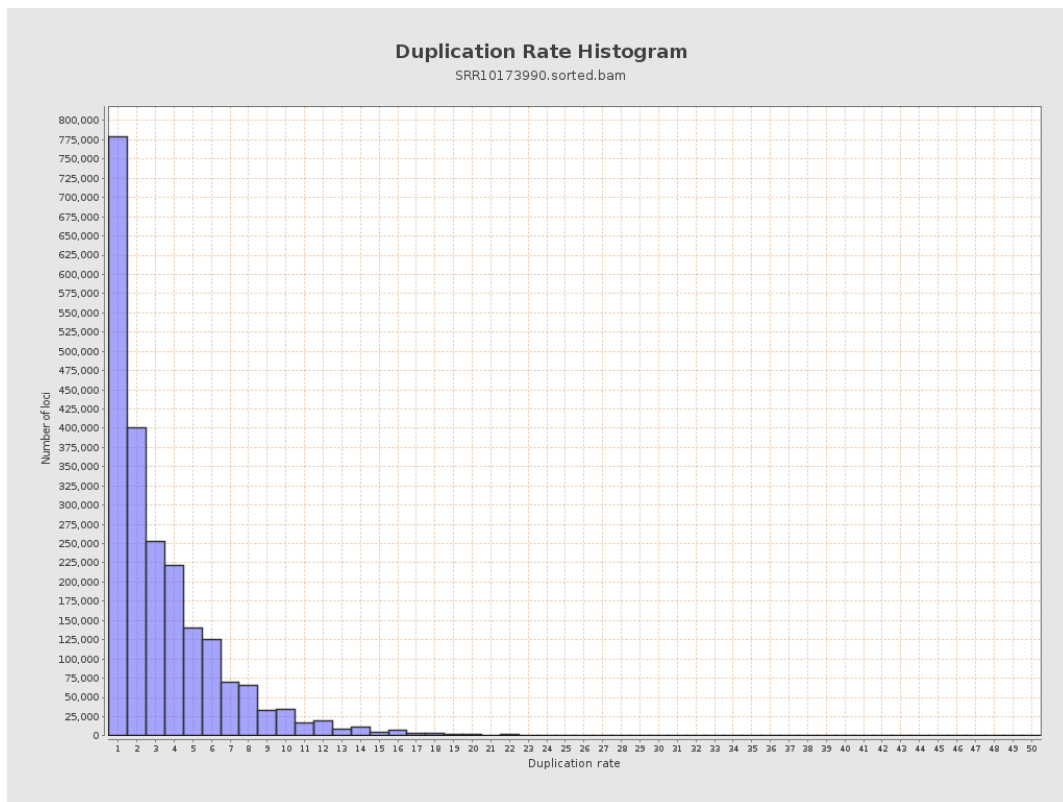
5. Results : Coverage Histogram (0-50X)



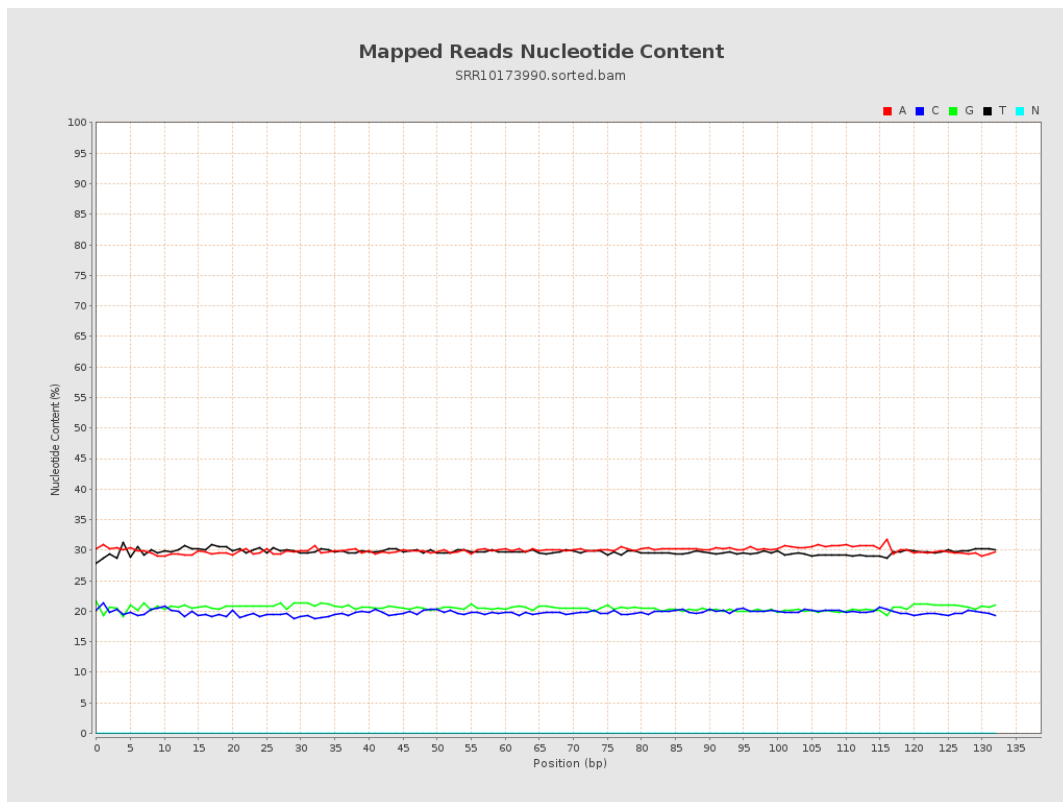
6. Results : Genome Fraction Coverage



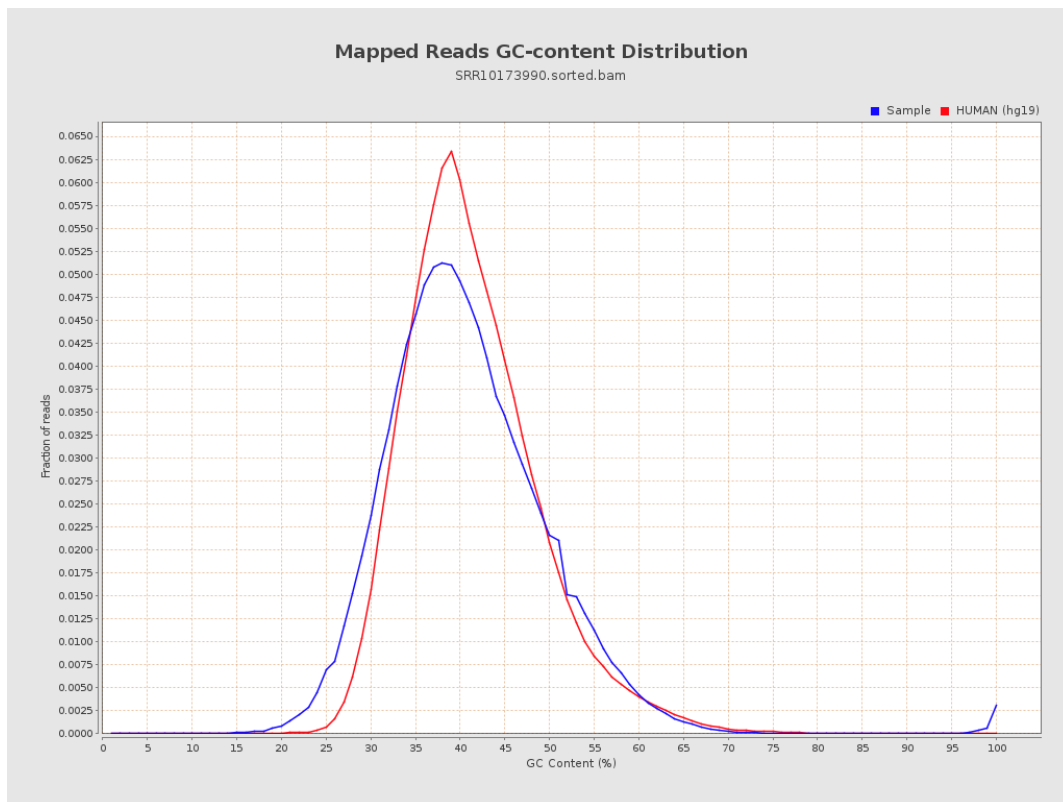
7. Results : Duplication Rate Histogram



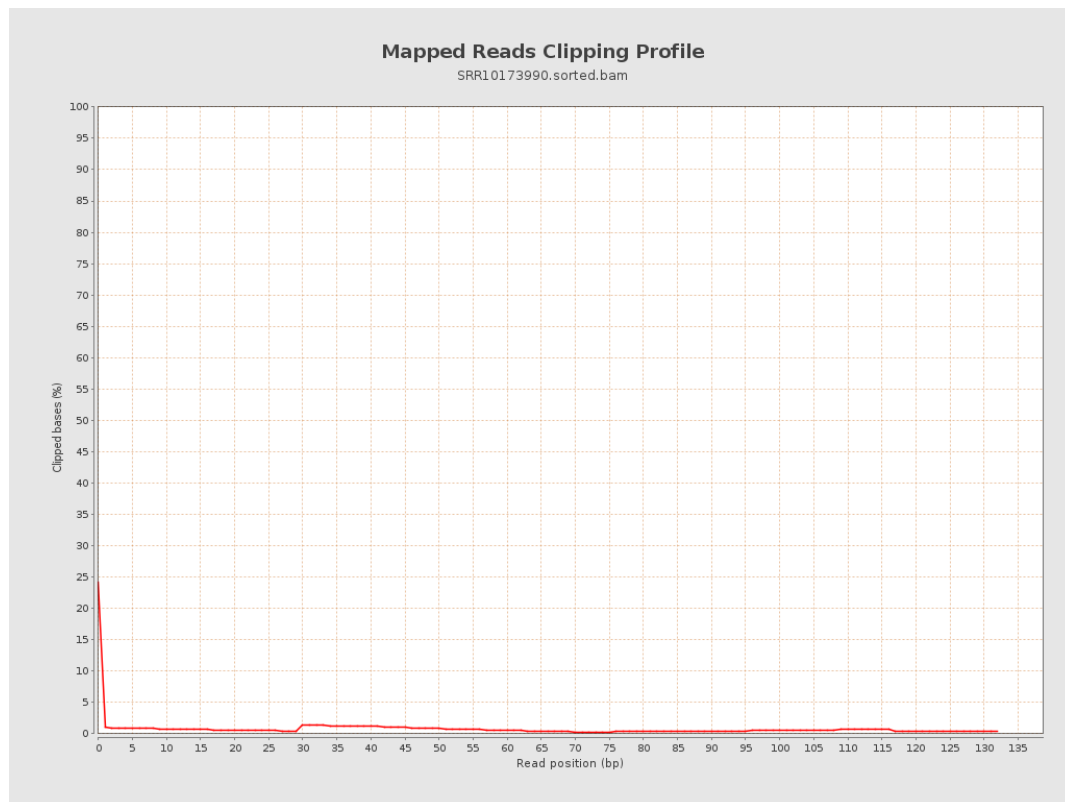
8. Results : Mapped Reads Nucleotide Content



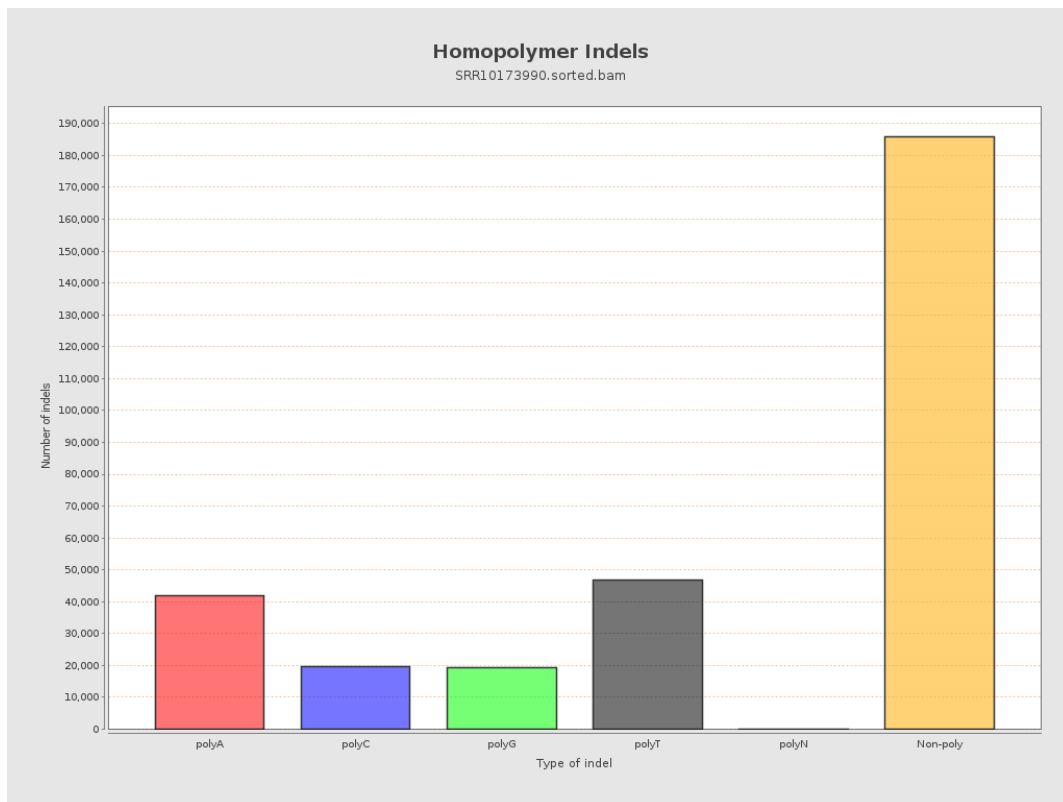
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



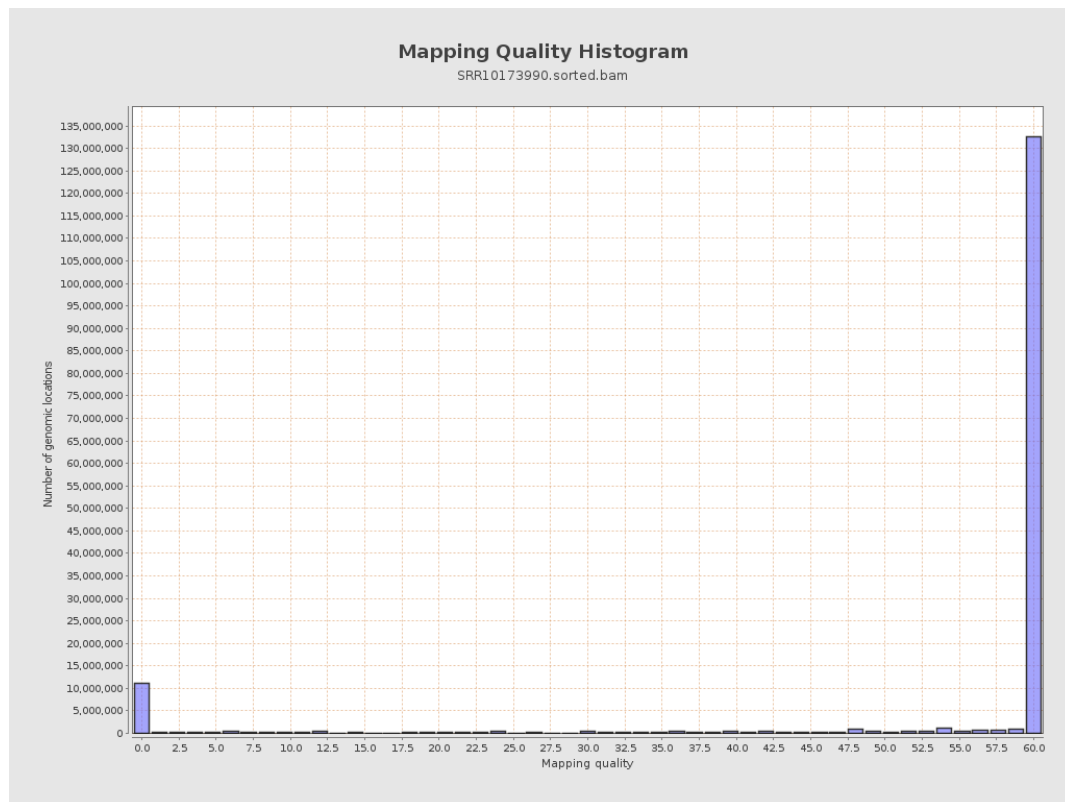
11. Results : Homopolymer Indels



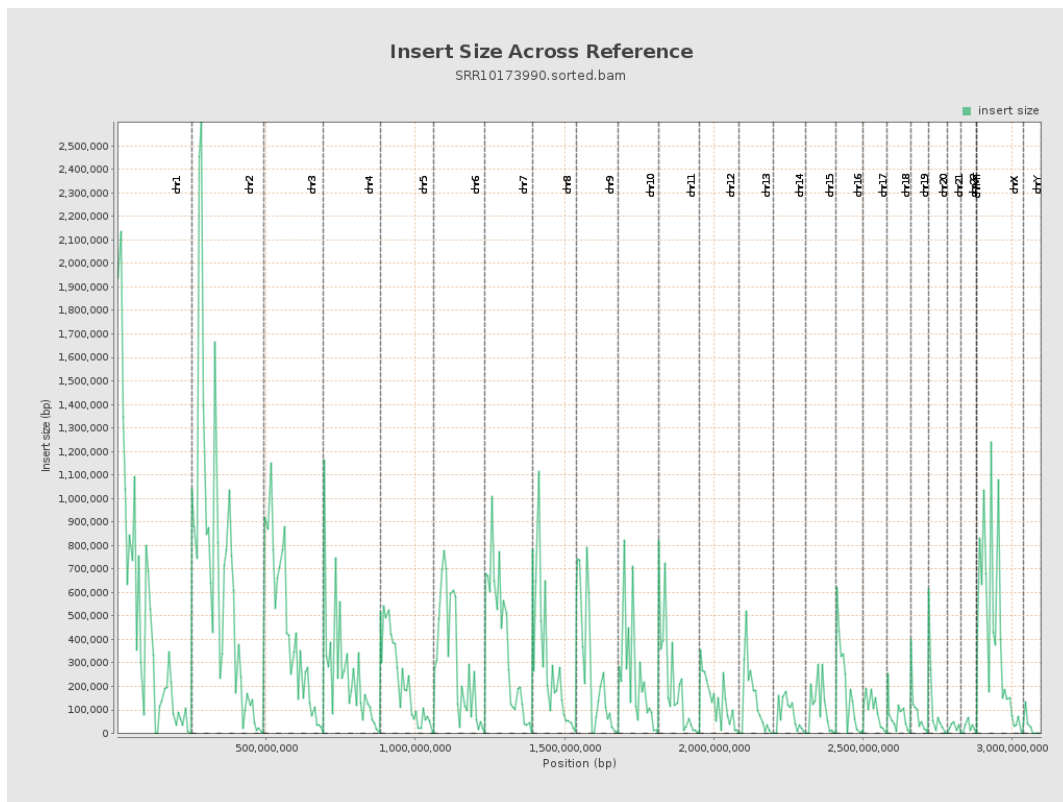
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

