

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 00:22:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173870.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_SRR10173870 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173870_1.fastq.gz SRR10173870_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 00:22:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173870.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,459,988
Mapped reads	1,424,383 / 97.56%
Unmapped reads	35,605 / 2.44%
Mapped paired reads	1,424,383 / 97.56%
Mapped reads, first in pair	712,772 / 48.82%
Mapped reads, second in pair	711,611 / 48.74%
Mapped reads, both in pair	1,400,288 / 95.91%
Mapped reads, singletons	24,095 / 1.65%
Secondary alignments	0
Supplementary alignments	143,906 / 9.86%
Read min/max/mean length	30 / 133 / 128.15
Duplicated reads (estimated)	1,102,388 / 75.51%
Duplication rate	64.58%
Clipped reads	557,459 / 38.18%

2.2. ACGT Content

Number/percentage of A's	50,833,698 / 30.15%
Number/percentage of C's	32,921,748 / 19.52%
Number/percentage of T's	50,725,407 / 30.08%
Number/percentage of G's	34,136,833 / 20.24%
Number/percentage of N's	1,725 / 0%

GC Percentage	39.77%
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2.3. Coverage

Mean	0.0545
Standard Deviation	0.965

2.4. Mapping Quality

Mean Mapping Quality	52.85
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2.5. Insert size

Mean	1,191,632.43
Standard Deviation	9,881,324.86
P25/Median/P75	146 / 204 / 292

2.6. Mismatches and indels

General error rate	1.05%
Mismatches	1,710,582
Insertions	19,124
Mapped reads with at least one insertion	1.29%
Deletions	37,811
Mapped reads with at least one deletion	2.59%
Homopolymer indels	42.96%

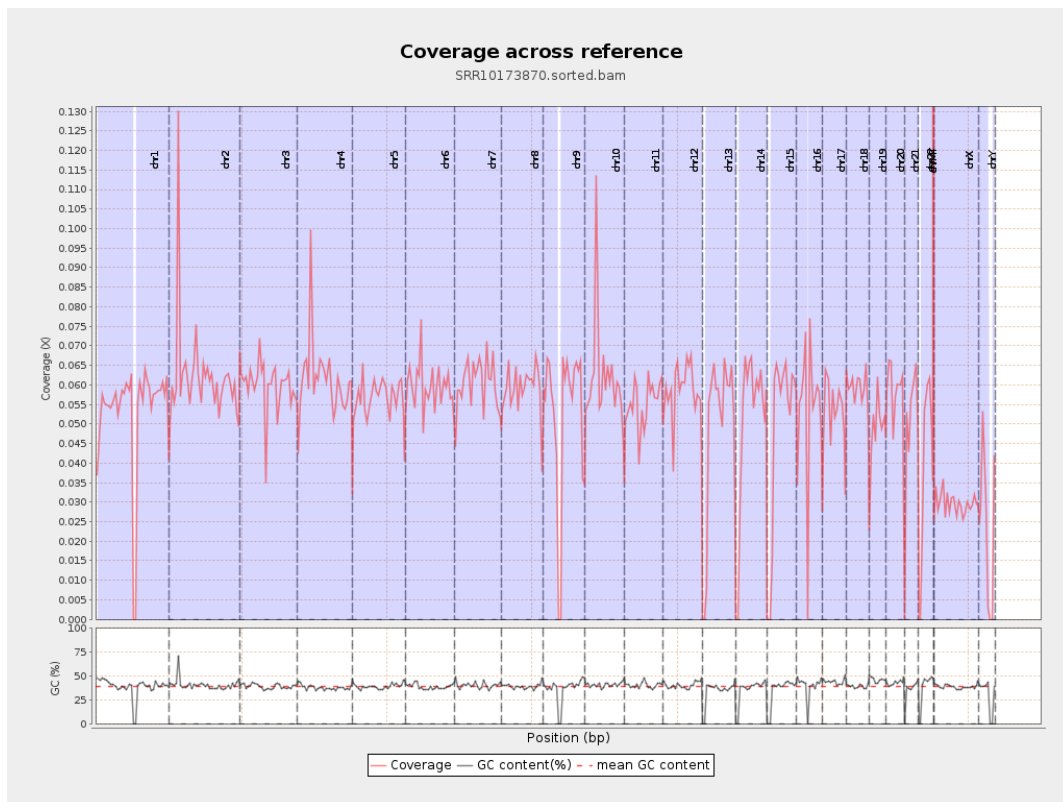
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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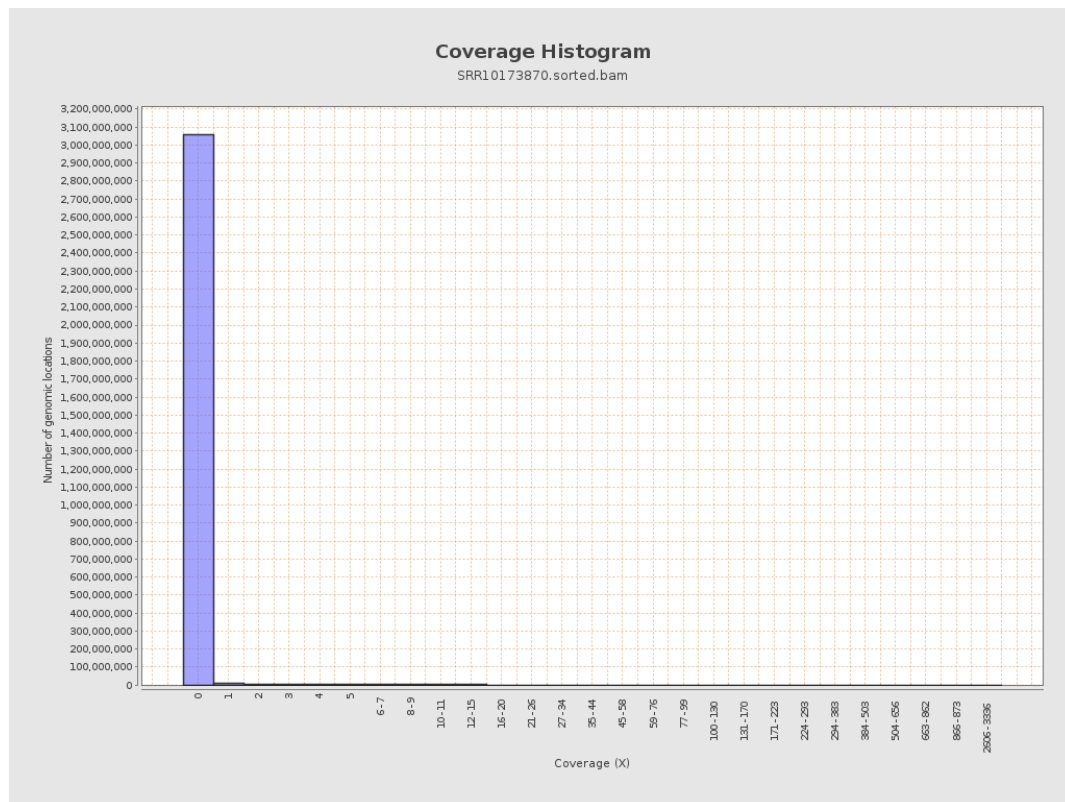
		bases	coverage	deviation
chr1	249250621	13284621	0.0533	0.732
chr2	243199373	15107724	0.0621	2.4231
chr3	198022430	11880567	0.06	0.6948
chr4	191154276	11698615	0.0612	0.7778
chr5	180915260	10280036	0.0568	0.6838
chr6	171115067	10186972	0.0595	0.7259
chr7	159138663	9669641	0.0608	0.7662
chr8	146364022	8650350	0.0591	0.8197
chr9	141213431	7455489	0.0528	0.7963
chr10	135534747	8377781	0.0618	0.8746
chr11	135006516	7441892	0.0551	0.6679
chr12	133851895	7843617	0.0586	0.6971
chr13	115169878	5584514	0.0485	0.6264
chr14	107349540	5412583	0.0504	0.6411
chr15	102531392	4994135	0.0487	0.6188
chr16	90354753	4836510	0.0535	0.7118
chr17	81195210	4300254	0.053	0.655
chr18	78077248	4646353	0.0595	0.9054
chr19	59128983	2919626	0.0494	0.6563
chr20	63025520	3664148	0.0581	0.6992
chr21	48129895	2384168	0.0495	0.6813
chr22	51304566	1979456	0.0386	0.5579
chrMT	16571	169962	10.2566	13.4046
chrX	155270560	4585408	0.0295	0.4897

chrY	59373566	1360480	0.0229	0.5068
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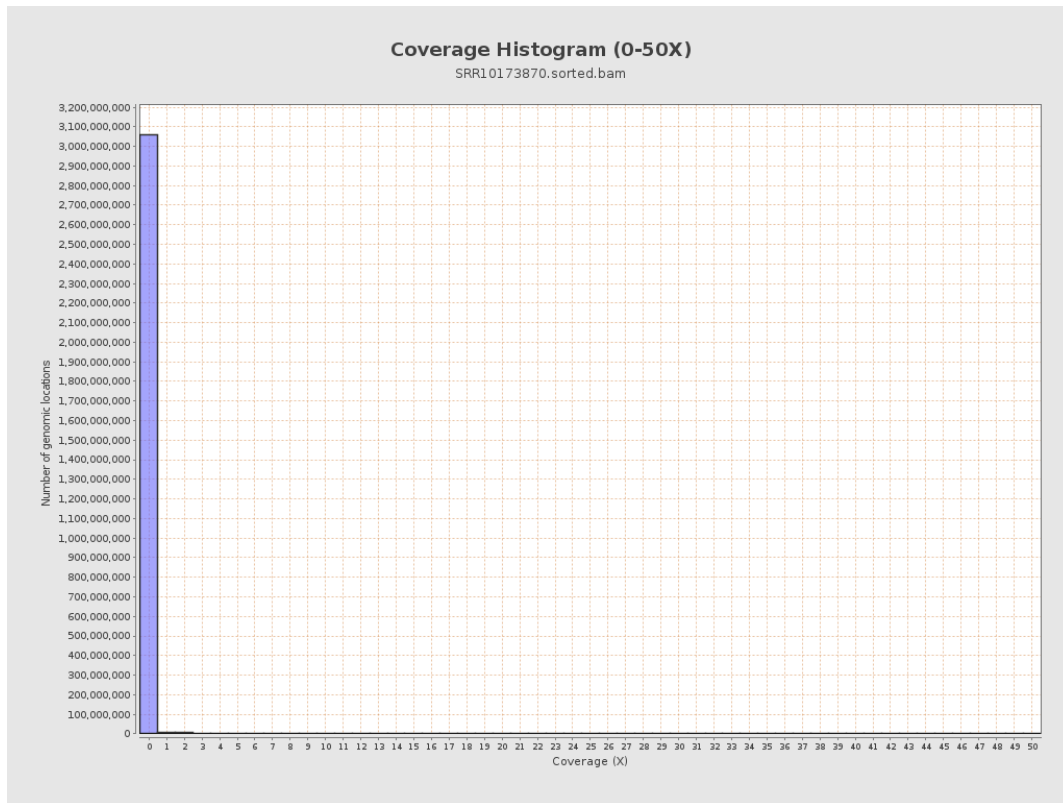
3. Results : Coverage across reference



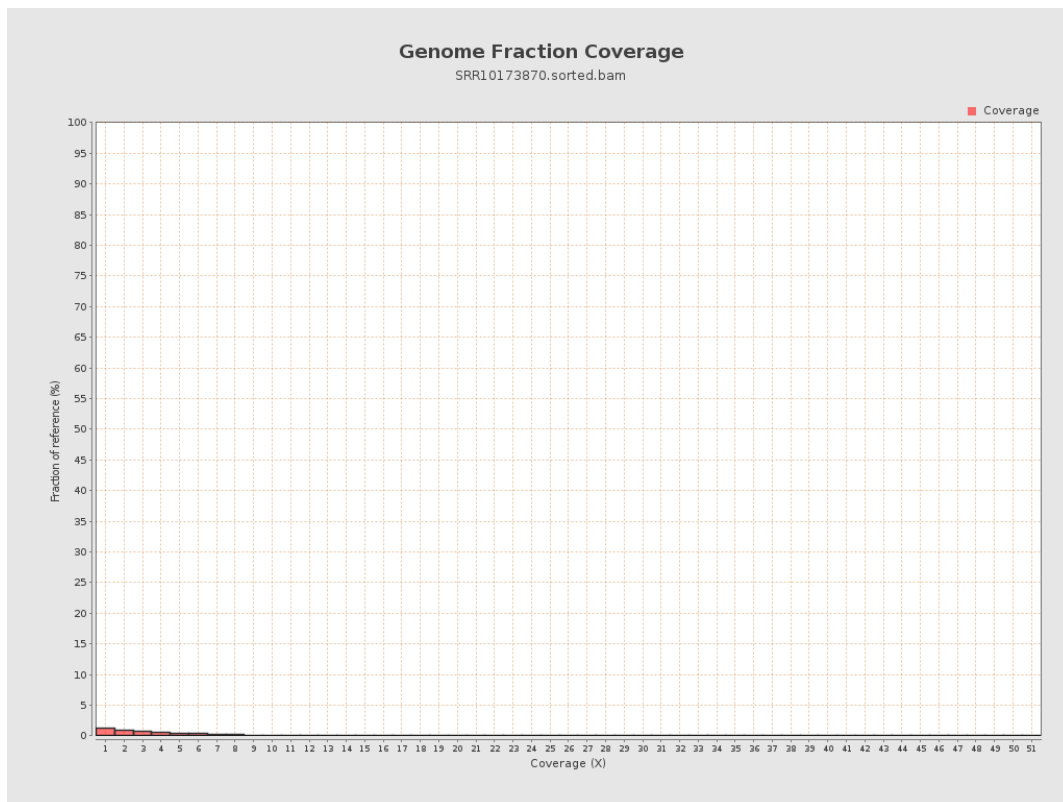
4. Results : Coverage Histogram



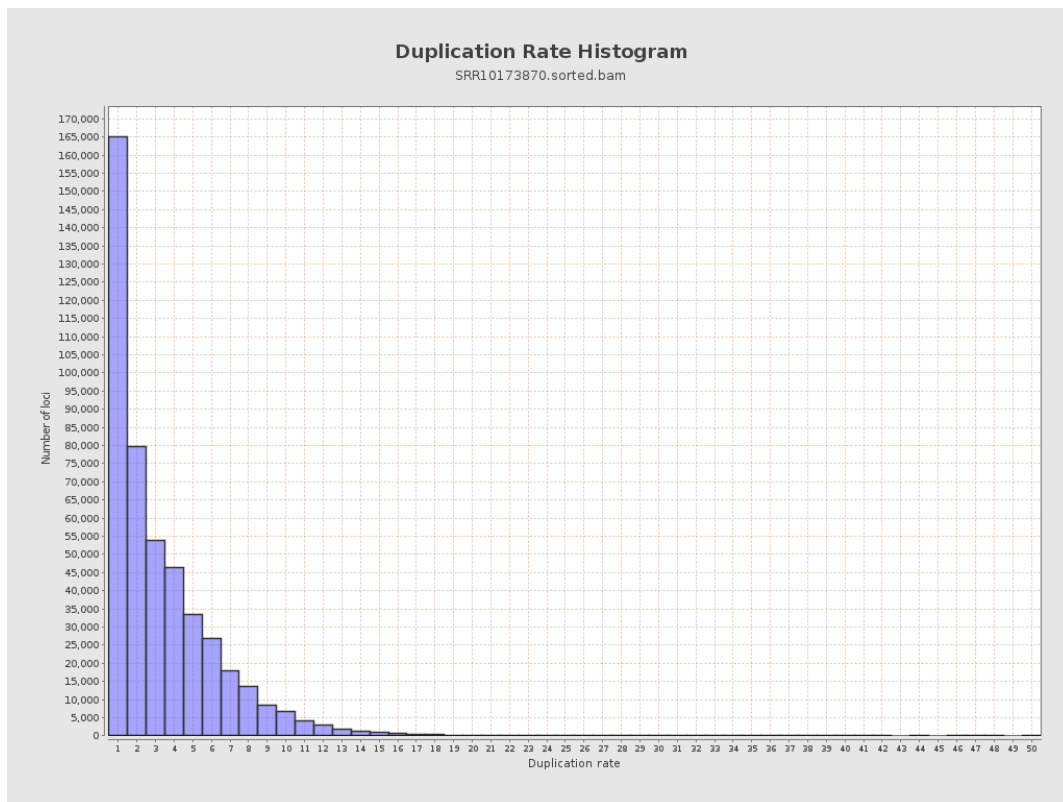
5. Results : Coverage Histogram (0-50X)



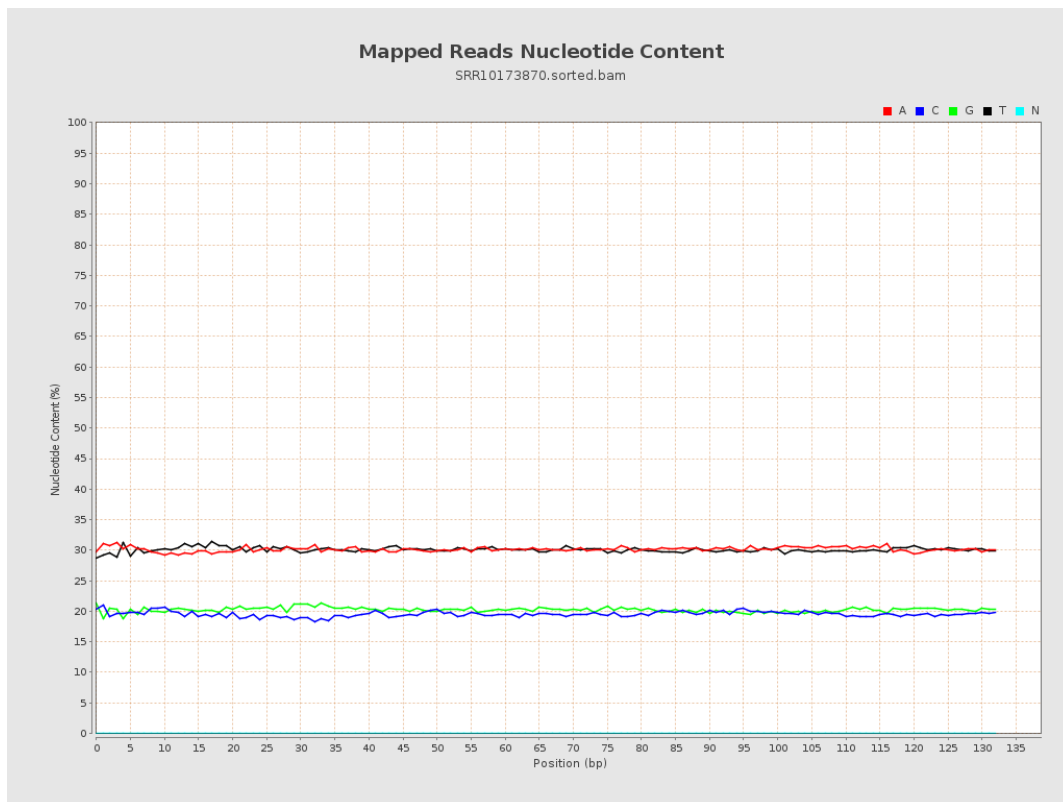
6. Results : Genome Fraction Coverage



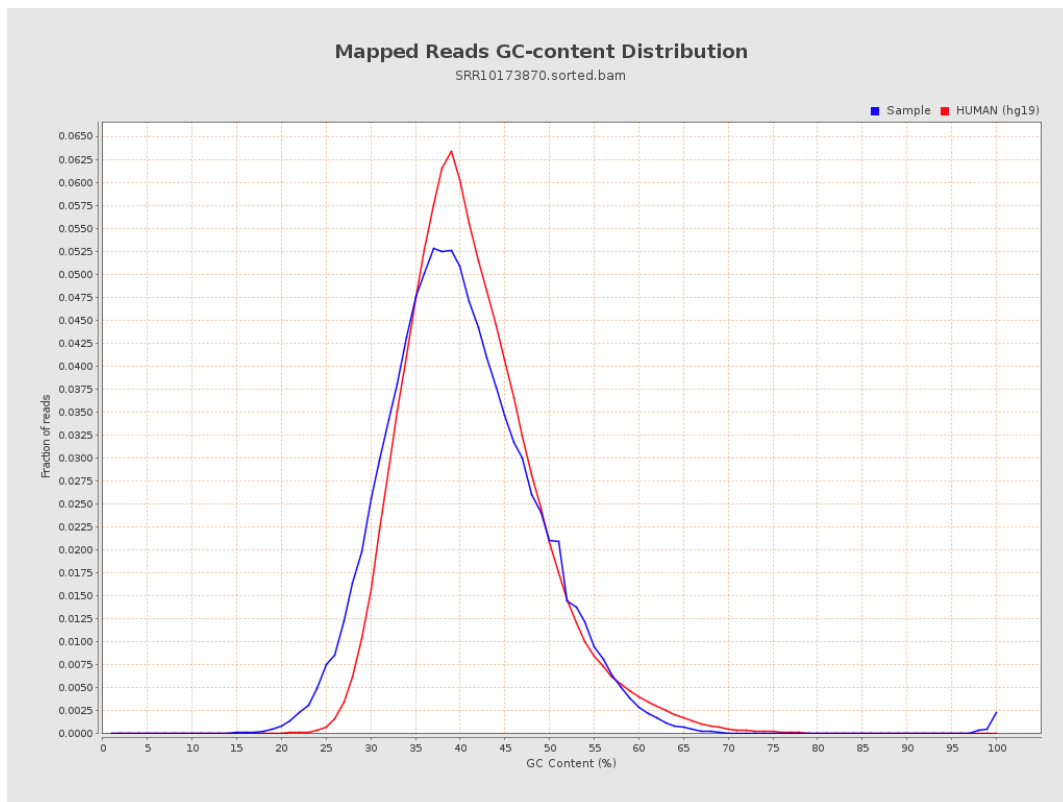
7. Results : Duplication Rate Histogram



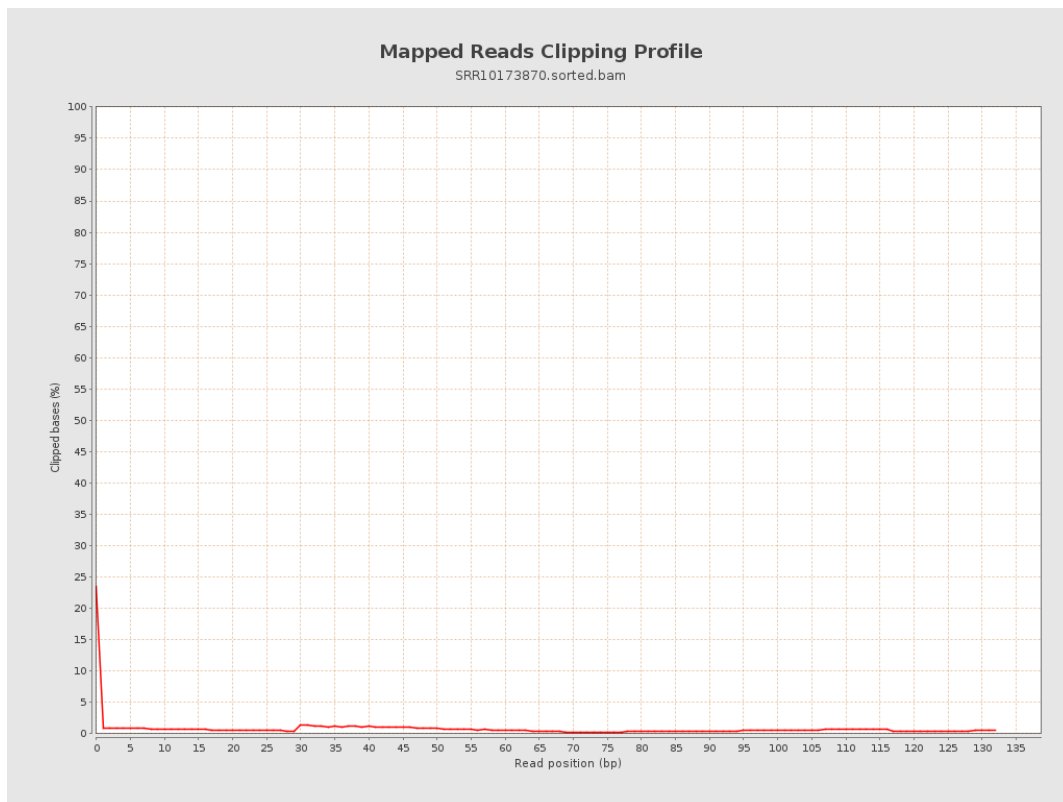
8. Results : Mapped Reads Nucleotide Content



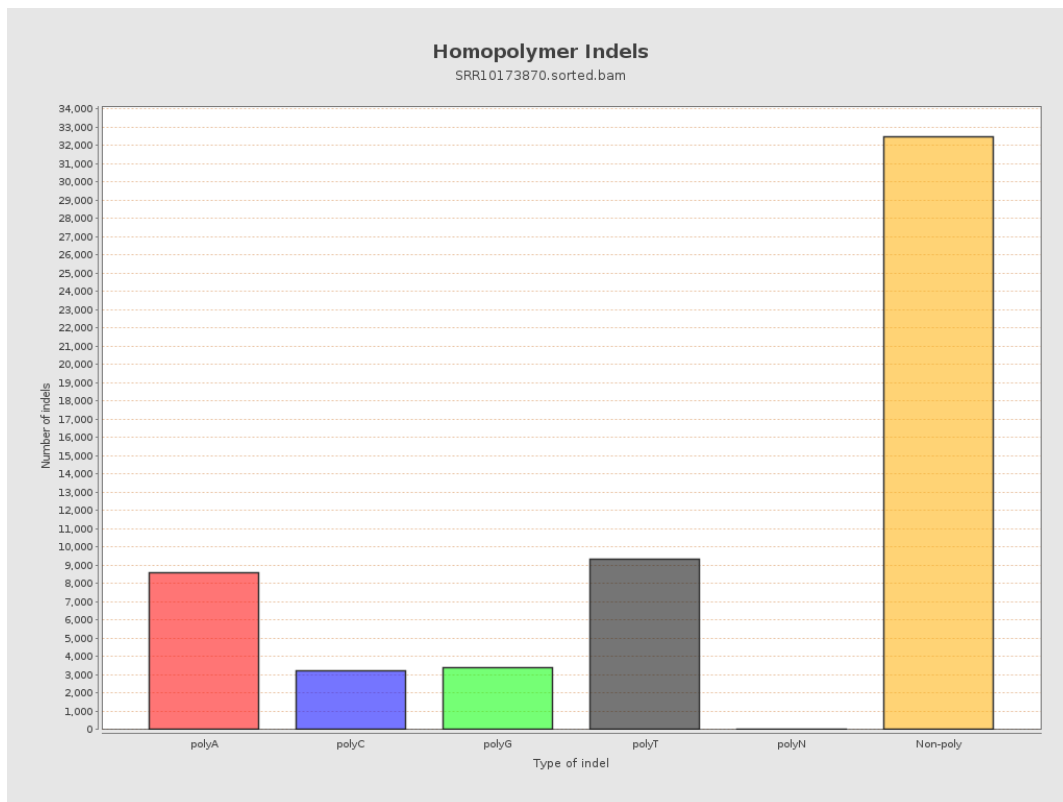
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



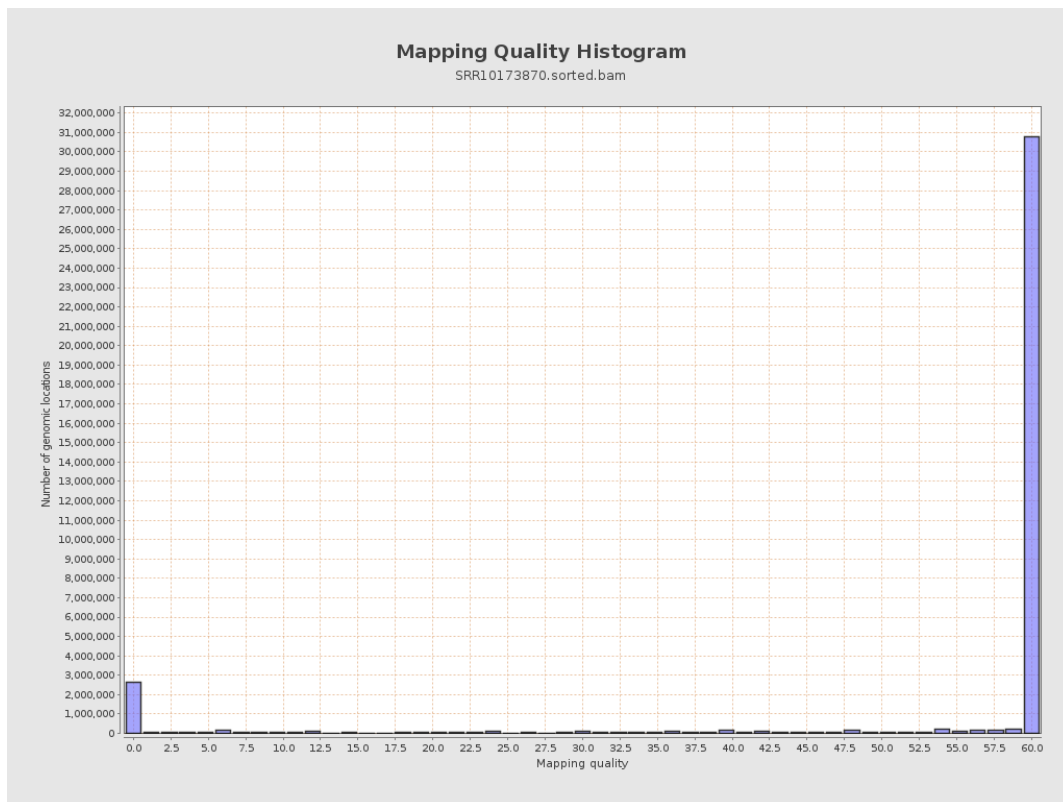
11. Results : Homopolymer Indels



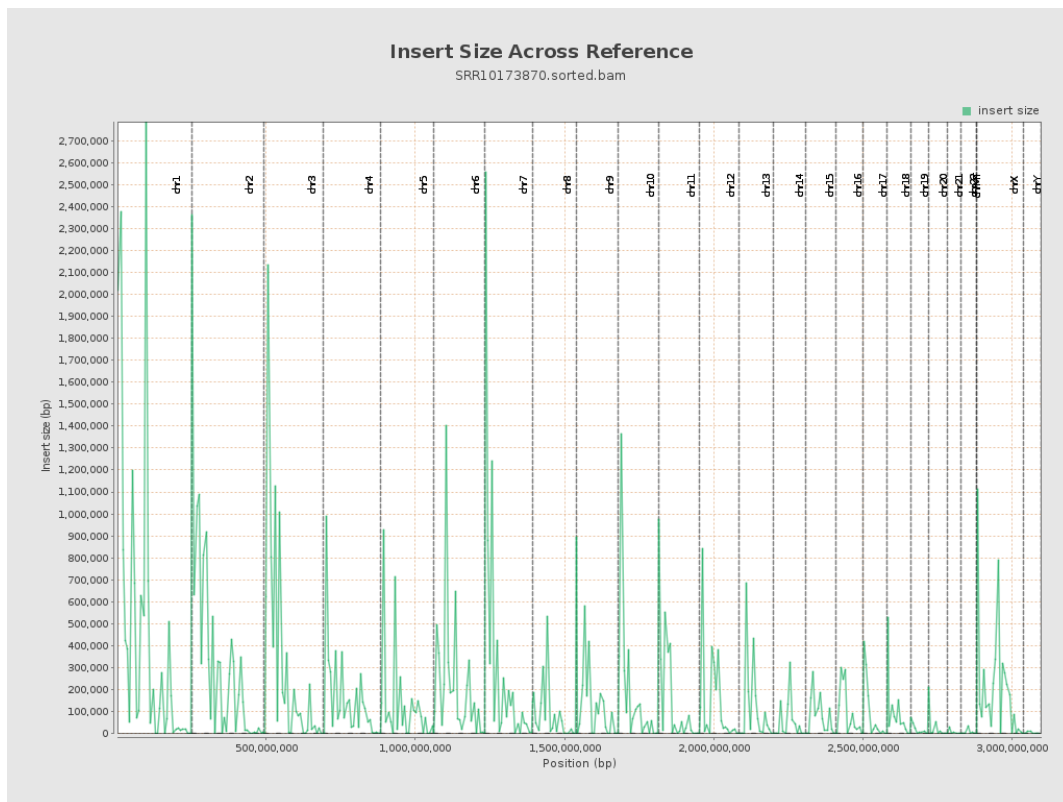
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

