

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 05:06:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173905.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_SRR10173905 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173905_1.fastq.gz SRR10173905_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 05:06:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173905.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,471,152
Mapped reads	4,355,926 / 97.42%
Unmapped reads	115,226 / 2.58%
Mapped paired reads	4,355,926 / 97.42%
Mapped reads, first in pair	2,182,890 / 48.82%
Mapped reads, second in pair	2,173,036 / 48.6%
Mapped reads, both in pair	4,281,412 / 95.76%
Mapped reads, singletons	74,514 / 1.67%
Secondary alignments	0
Supplementary alignments	442,386 / 9.89%
Read min/max/mean length	30 / 133 / 128.46
Duplicated reads (estimated)	3,369,044 / 75.35%
Duplication rate	64.26%
Clipped reads	1,722,189 / 38.52%

2.2. ACGT Content

Number/percentage of A's	154,493,976 / 29.89%
Number/percentage of C's	101,979,521 / 19.73%
Number/percentage of T's	154,268,273 / 29.84%
Number/percentage of G's	106,173,069 / 20.54%
Number/percentage of N's	6,030 / 0%

GC Percentage	40.27%
---------------	--------

2.3. Coverage

Mean	0.1671
Standard Deviation	2.3399

2.4. Mapping Quality

Mean Mapping Quality	52.95
----------------------	-------

2.5. Insert size

Mean	1,375,805.39
Standard Deviation	11,023,510.15
P25/Median/P75	151 / 209 / 299

2.6. Mismatches and indels

General error rate	1.1%
Mismatches	5,545,282
Insertions	58,652
Mapped reads with at least one insertion	1.3%
Deletions	135,505
Mapped reads with at least one deletion	3.03%
Homopolymer indels	42.34%

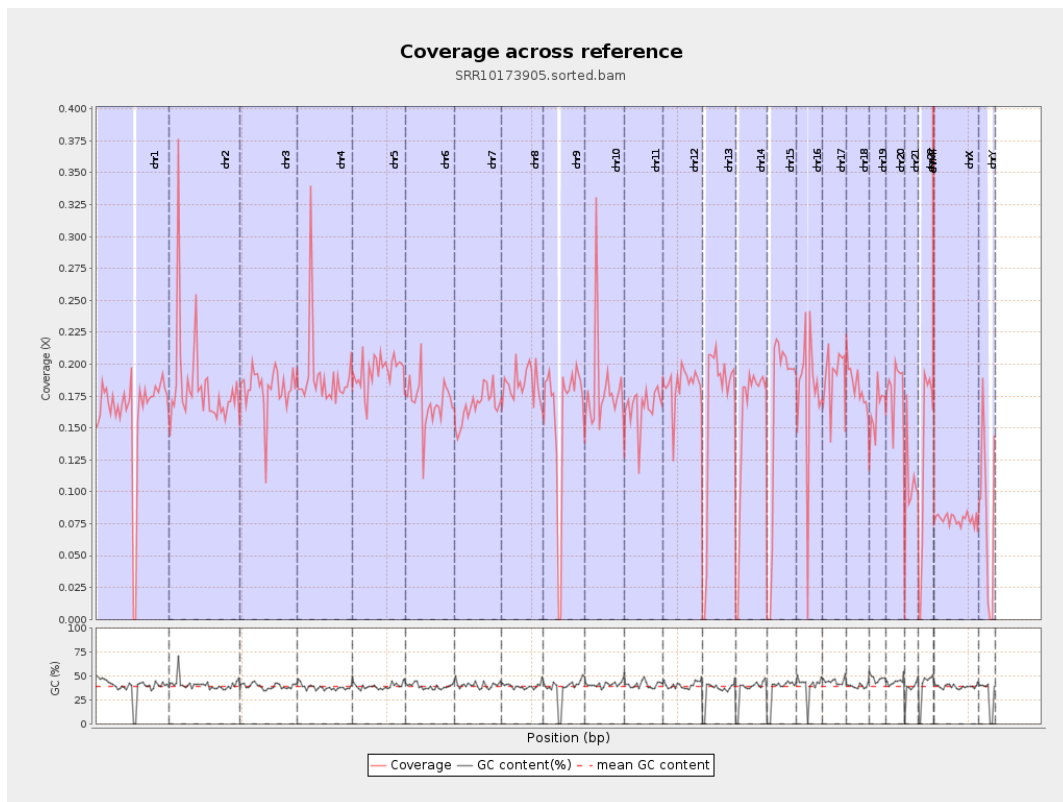
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
------	--------	--------	------	----------

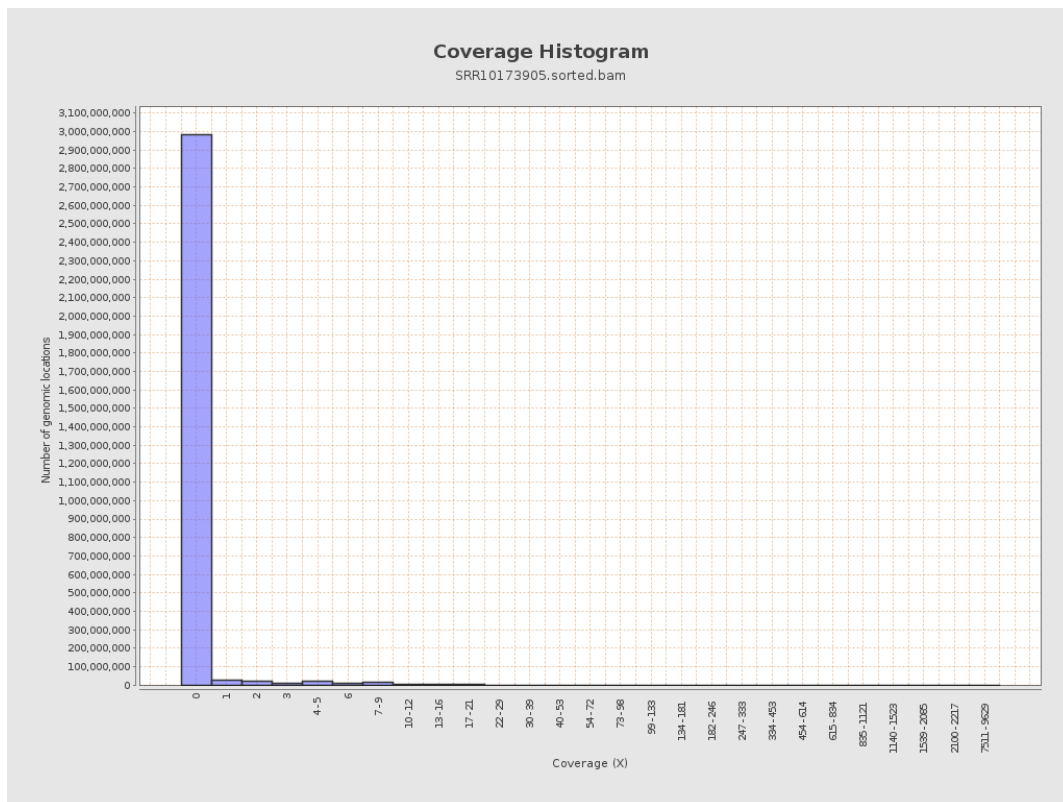
		bases	coverage	deviation
chr1	249250621	40451294	0.1623	1.5703
chr2	243199373	44497970	0.183	6.7928
chr3	198022430	35769656	0.1806	1.2118
chr4	191154276	36263812	0.1897	1.6184
chr5	180915260	35171934	0.1944	1.2585
chr6	171115067	29211533	0.1707	1.3603
chr7	159138663	26620274	0.1673	1.3472
chr8	146364022	26965963	0.1842	1.6934
chr9	141213431	22750635	0.1611	1.4981
chr10	135534747	24387121	0.1799	2.0345
chr11	135006516	22424903	0.1661	1.1695
chr12	133851895	24538743	0.1833	1.2224
chr13	115169878	18802432	0.1633	1.1536
chr14	107349540	16581913	0.1545	1.1165
chr15	102531392	16832741	0.1642	1.132
chr16	90354753	15911025	0.1761	1.4732
chr17	81195210	15375739	0.1894	1.3307
chr18	78077248	14288592	0.183	2.1062
chr19	59128983	9672874	0.1636	1.3913
chr20	63025520	11444732	0.1816	1.25
chr21	48129895	4943426	0.1027	1.3901
chr22	51304566	6572602	0.1281	1.1062
chrMT	16571	872723	52.6657	43.0152
chrX	155270560	12214469	0.0787	0.7884

chrY	59373566	4677910	0.0788	1.2855
------	----------	---------	--------	--------

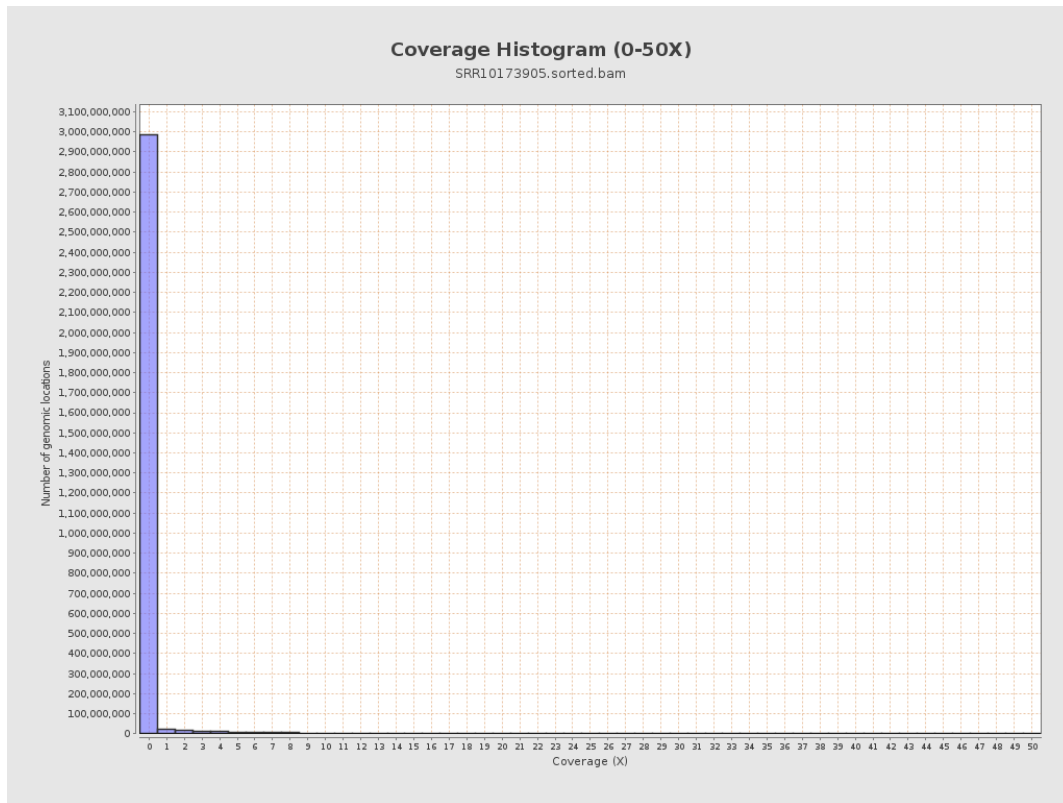
3. Results : Coverage across reference



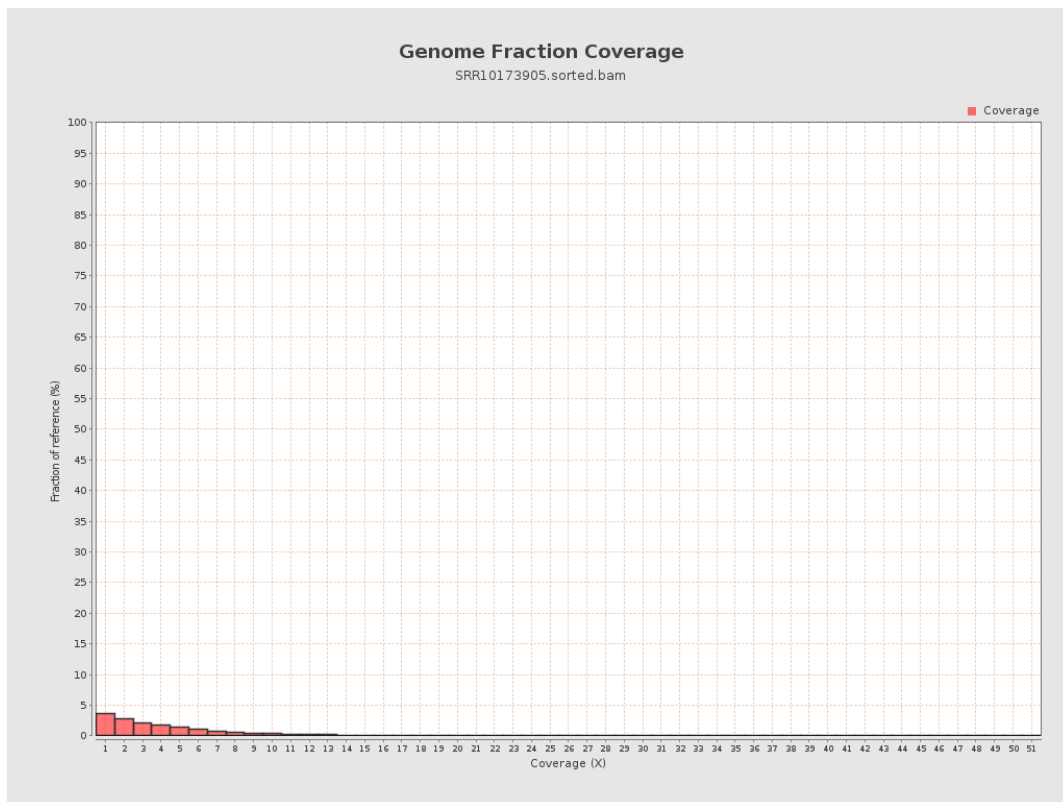
4. Results : Coverage Histogram



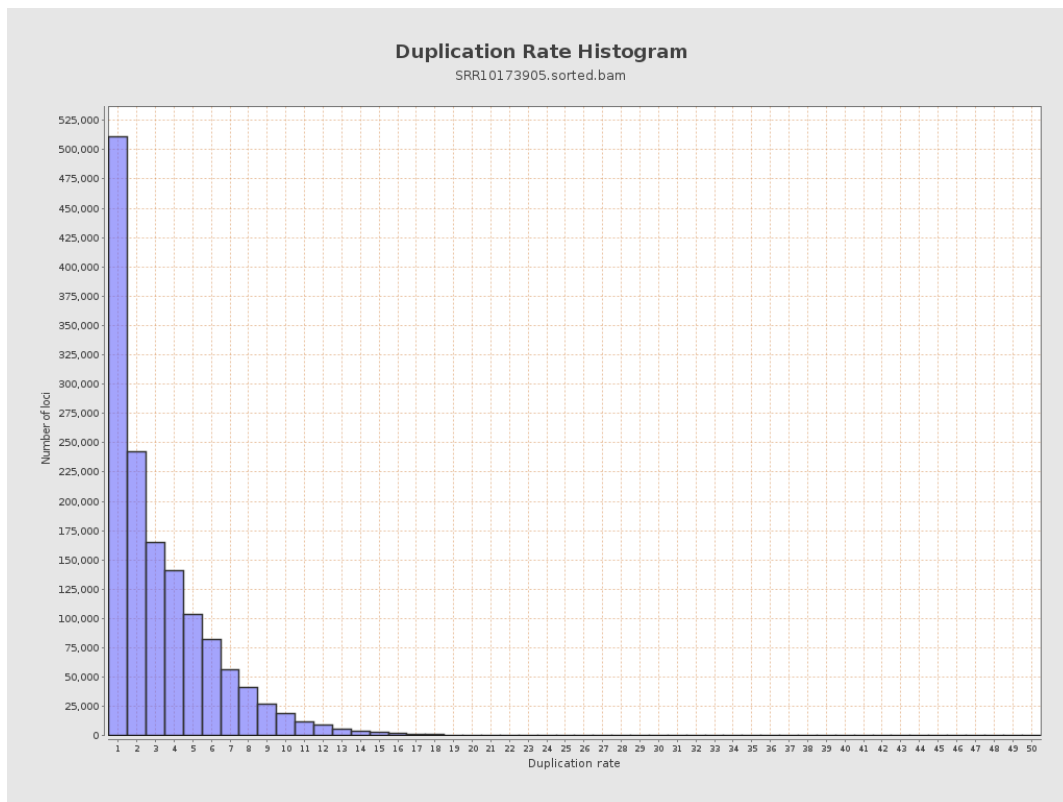
5. Results : Coverage Histogram (0-50X)



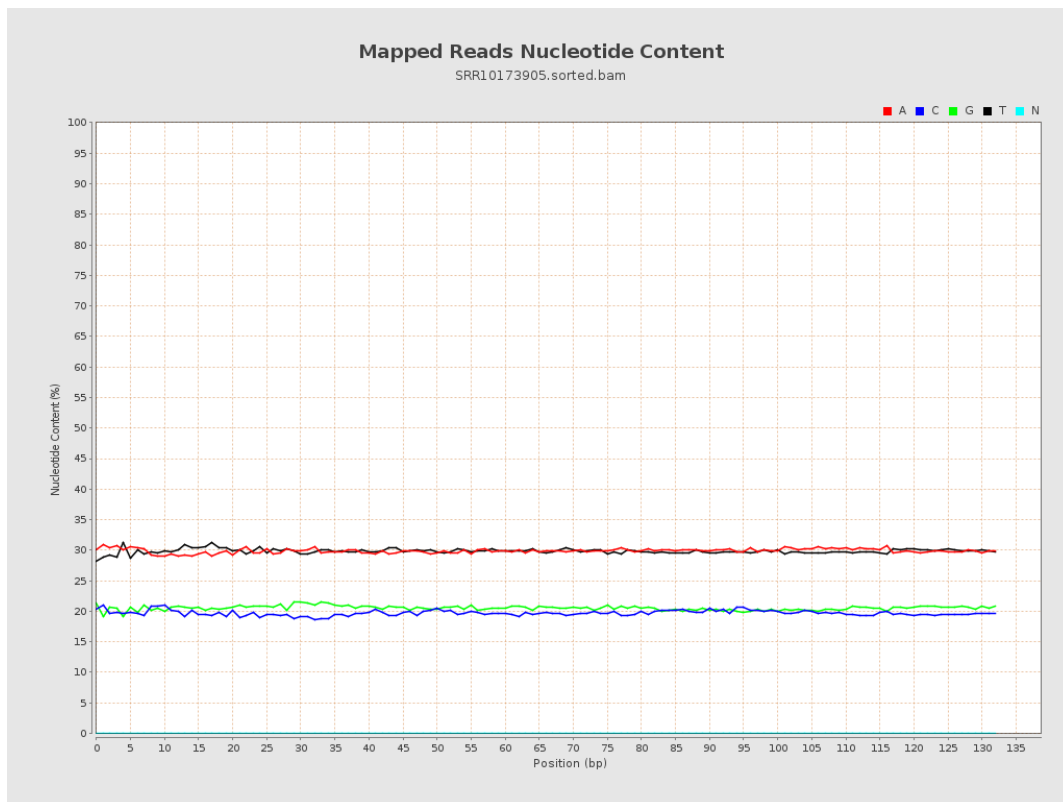
6. Results : Genome Fraction Coverage



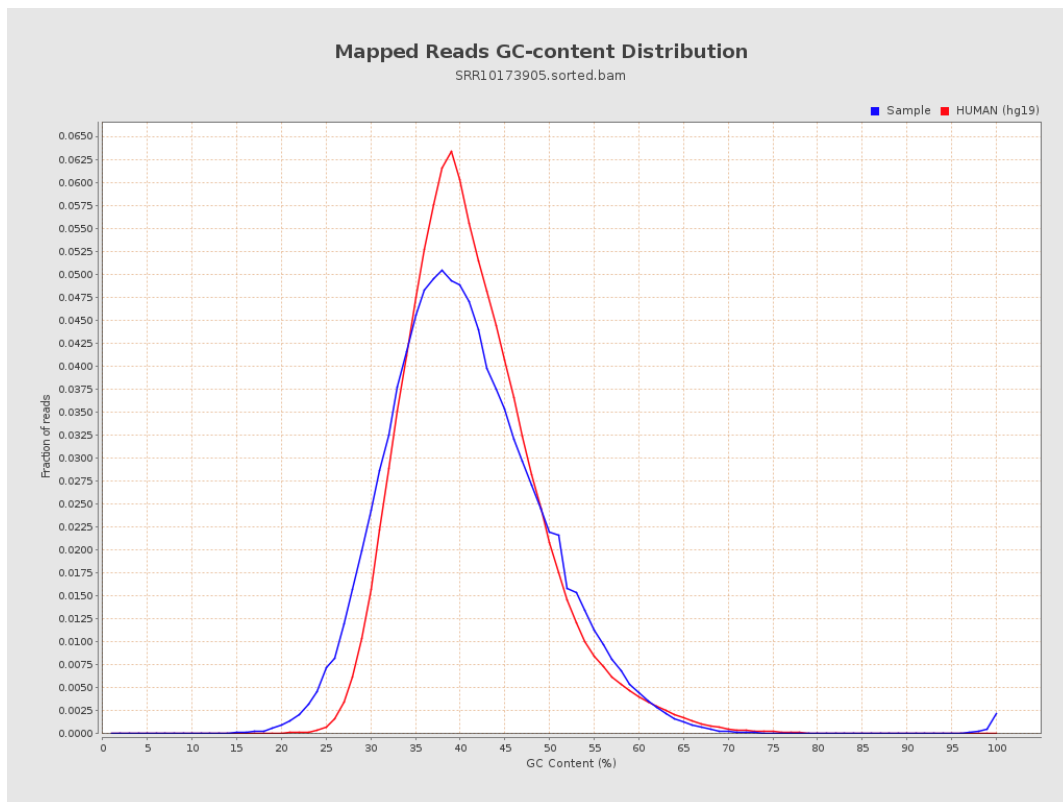
7. Results : Duplication Rate Histogram



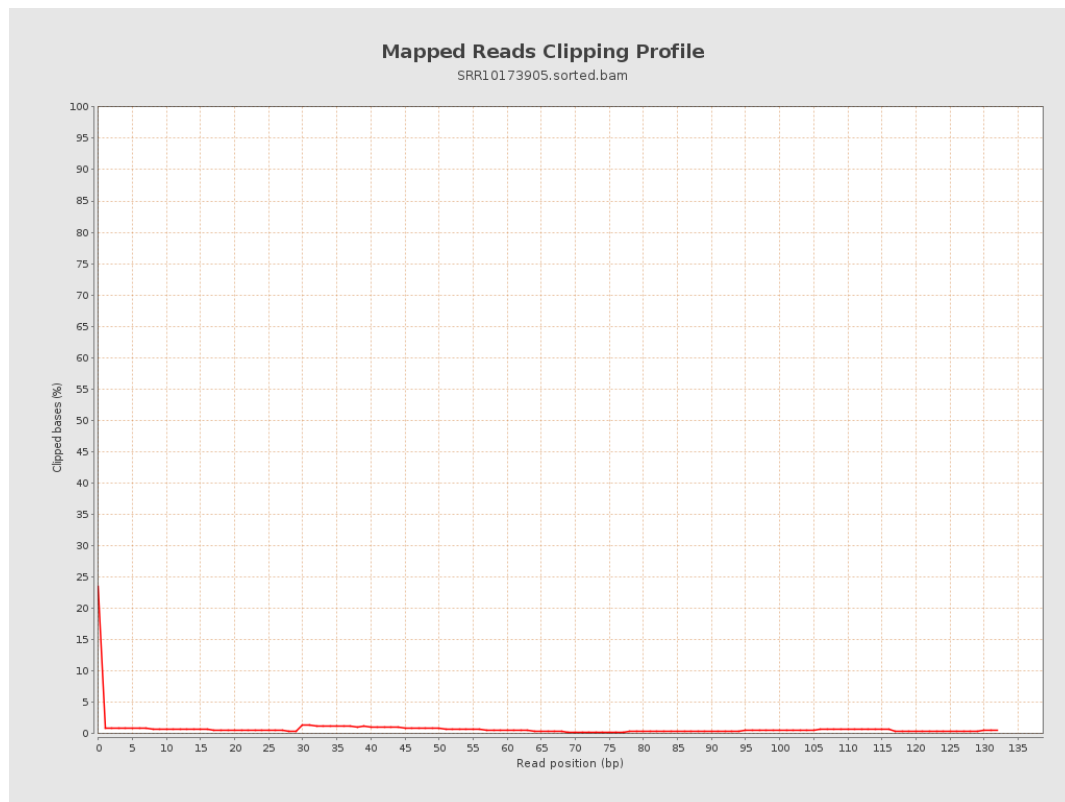
8. Results : Mapped Reads Nucleotide Content



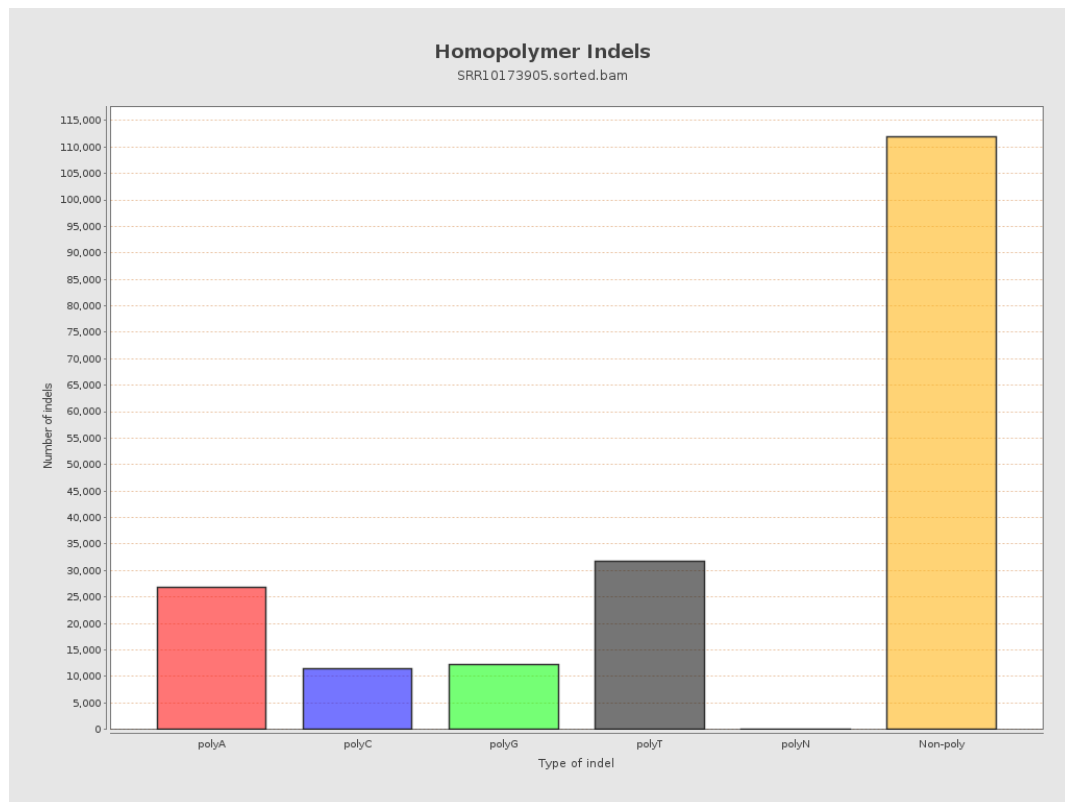
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



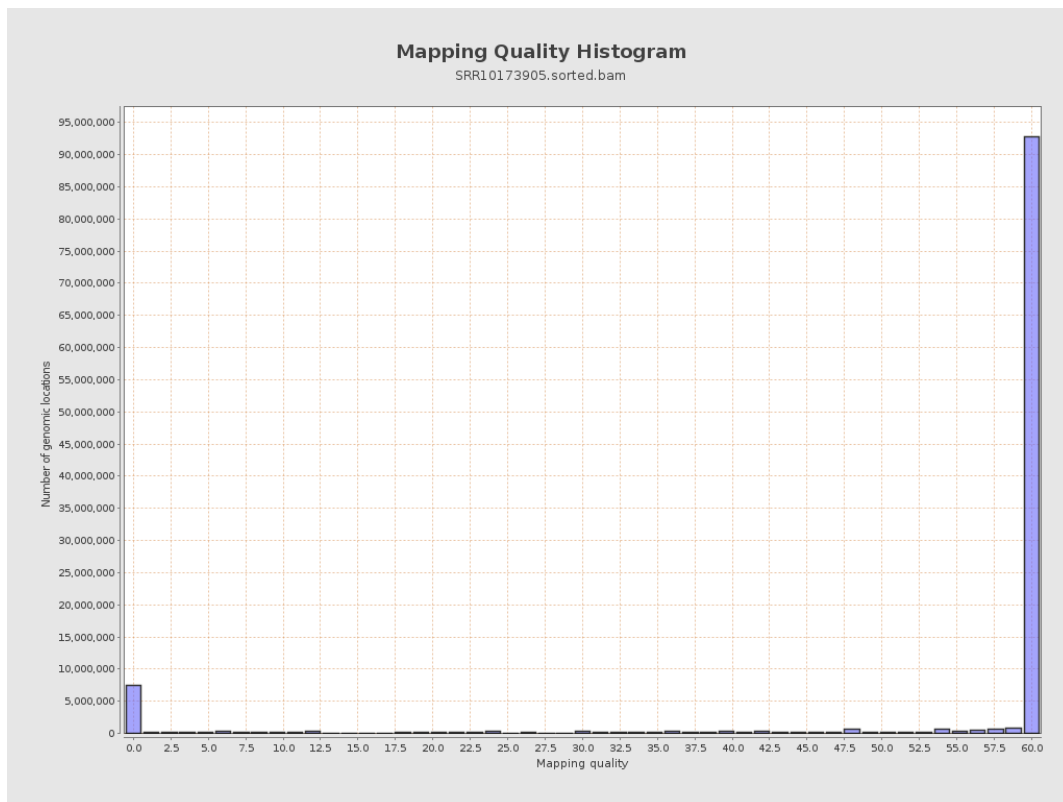
11. Results : Homopolymer Indels



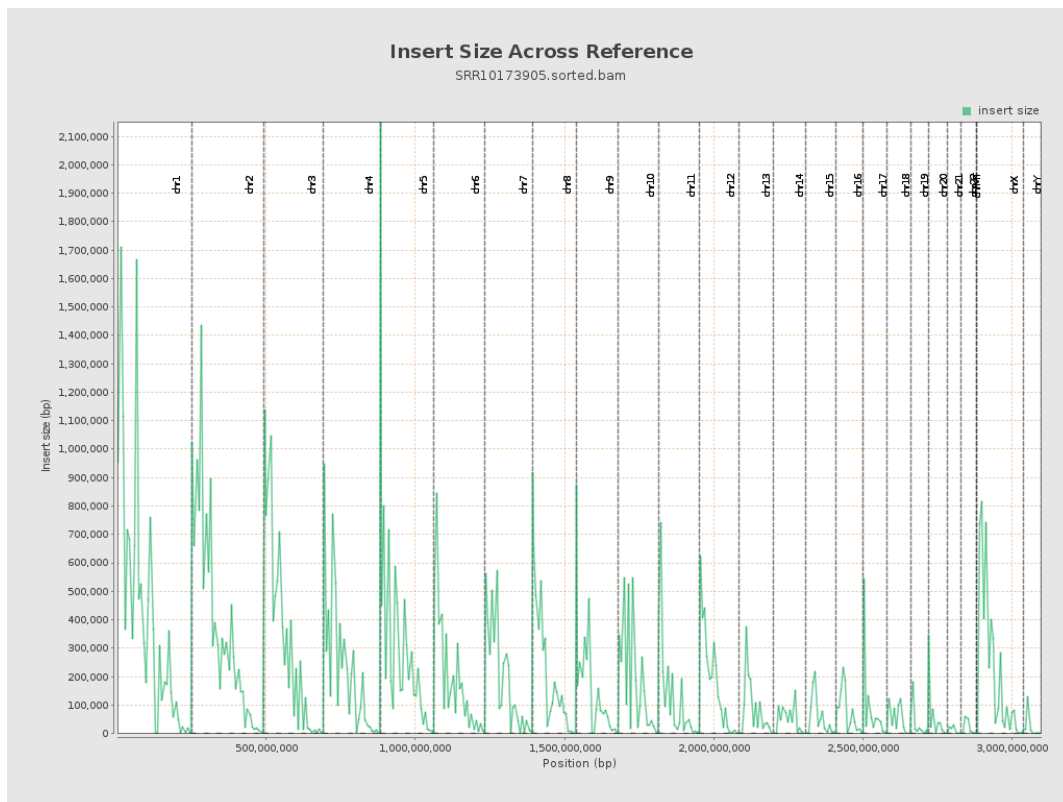
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

