

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 07:50:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173926.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_SRR10173926 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173926_1.fastq.gz SRR10173926_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 07:50:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173926.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,195,206
Mapped reads	3,123,841 / 97.77%
Unmapped reads	71,365 / 2.23%
Mapped paired reads	3,123,841 / 97.77%
Mapped reads, first in pair	1,562,907 / 48.91%
Mapped reads, second in pair	1,560,934 / 48.85%
Mapped reads, both in pair	3,080,908 / 96.42%
Mapped reads, singletons	42,933 / 1.34%
Secondary alignments	0
Supplementary alignments	400,521 / 12.54%
Read min/max/mean length	30 / 133 / 124.11
Duplicated reads (estimated)	2,442,686 / 76.45%
Duplication rate	61.6%
Clipped reads	1,611,986 / 50.45%

2.2. ACGT Content

Number/percentage of A's	105,235,866 / 30.05%
Number/percentage of C's	69,070,612 / 19.72%
Number/percentage of T's	104,205,887 / 29.76%
Number/percentage of G's	71,679,011 / 20.47%
Number/percentage of N's	2,536 / 0%

GC Percentage	40.19%
---------------	--------

2.3. Coverage

Mean	0.1132
Standard Deviation	2.2417

2.4. Mapping Quality

Mean Mapping Quality	52.56
----------------------	-------

2.5. Insert size

Mean	812,970.44
Standard Deviation	8,343,962.92
P25/Median/P75	100 / 144 / 219

2.6. Mismatches and indels

General error rate	0.88%
Mismatches	2,976,598
Insertions	39,297
Mapped reads with at least one insertion	1.21%
Deletions	107,784
Mapped reads with at least one deletion	3.36%
Homopolymer indels	40.58%

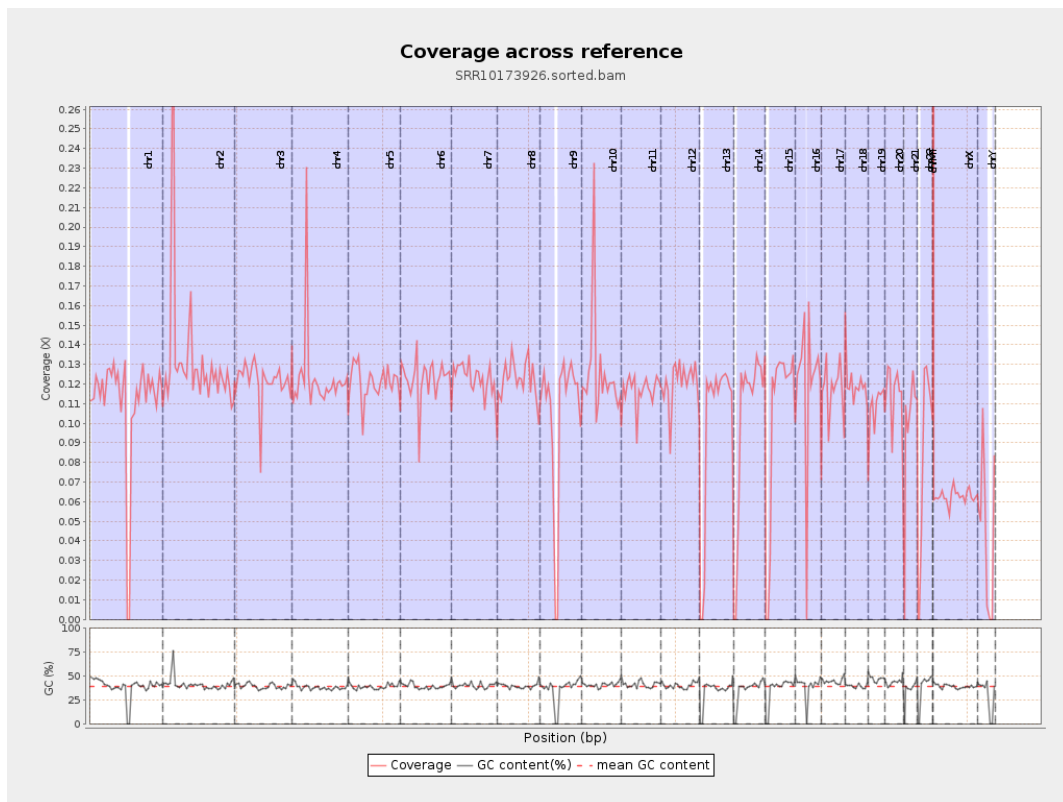
2.7. Chromosome stats

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

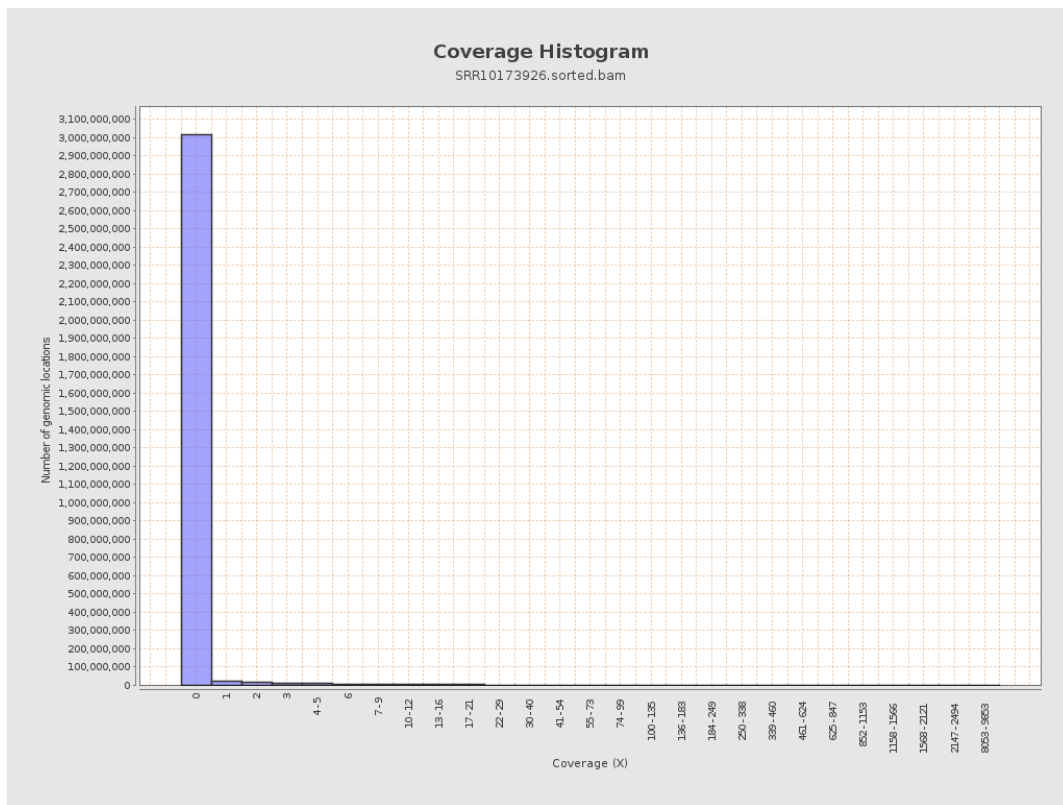
		bases	coverage	deviation
chr1	249250621	27724510	0.1112	1.1571
chr2	243199373	31890763	0.1311	6.9528
chr3	198022430	24089739	0.1217	1.0547
chr4	191154276	23505148	0.123	1.299
chr5	180915260	21777186	0.1204	1.0508
chr6	171115067	20969555	0.1225	1.1416
chr7	159138663	19464815	0.1223	1.2032
chr8	146364022	17895215	0.1223	1.4528
chr9	141213431	14856885	0.1052	1.1198
chr10	135534747	16929364	0.1249	1.4536
chr11	135006516	15752467	0.1167	1.0344
chr12	133851895	16163978	0.1208	1.0675
chr13	115169878	11444349	0.0994	0.9542
chr14	107349540	11133657	0.1037	0.975
chr15	102531392	10395457	0.1014	0.9616
chr16	90354753	10824316	0.1198	1.1525
chr17	81195210	9600912	0.1182	1.0961
chr18	78077248	9342306	0.1197	1.3048
chr19	59128983	6411976	0.1084	1.0309
chr20	63025520	7249014	0.115	1.03
chr21	48129895	4853895	0.1008	1.0468
chr22	51304566	4323615	0.0843	0.9379
chrMT	16571	1358188	81.9617	69.6202
chrX	155270560	9771083	0.0629	0.7543

chrY	59373566	2722375	0.0459	0.8339
------	----------	---------	--------	--------

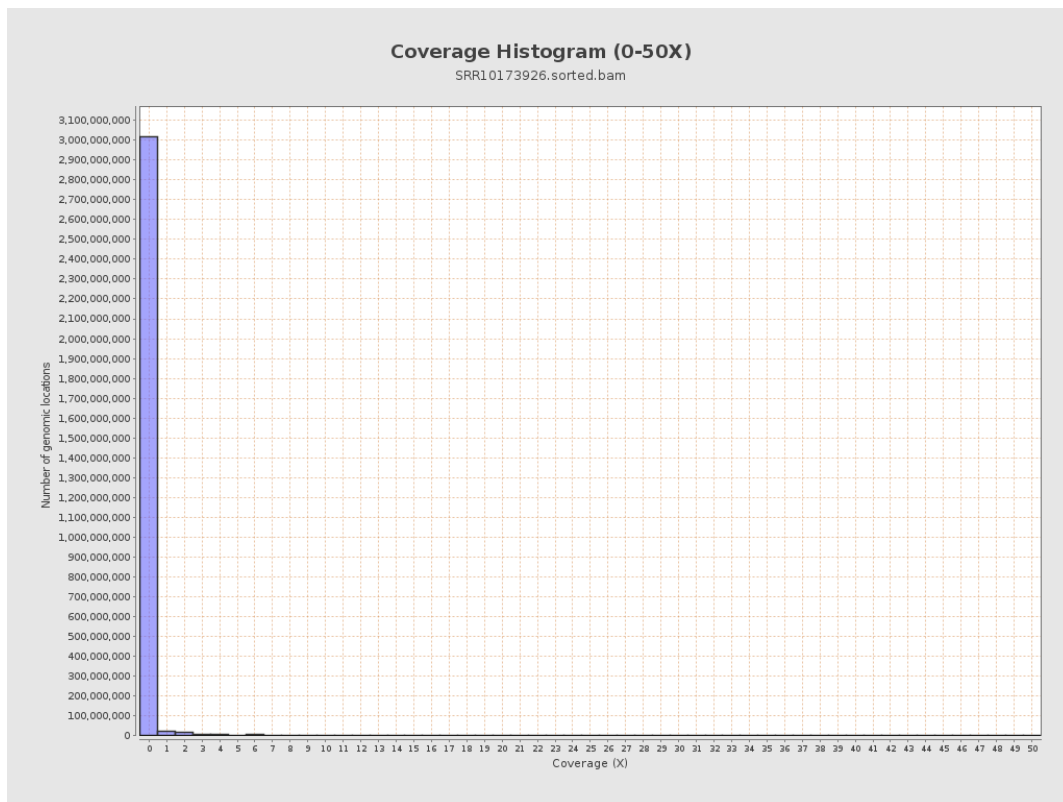
3. Results : Coverage across reference



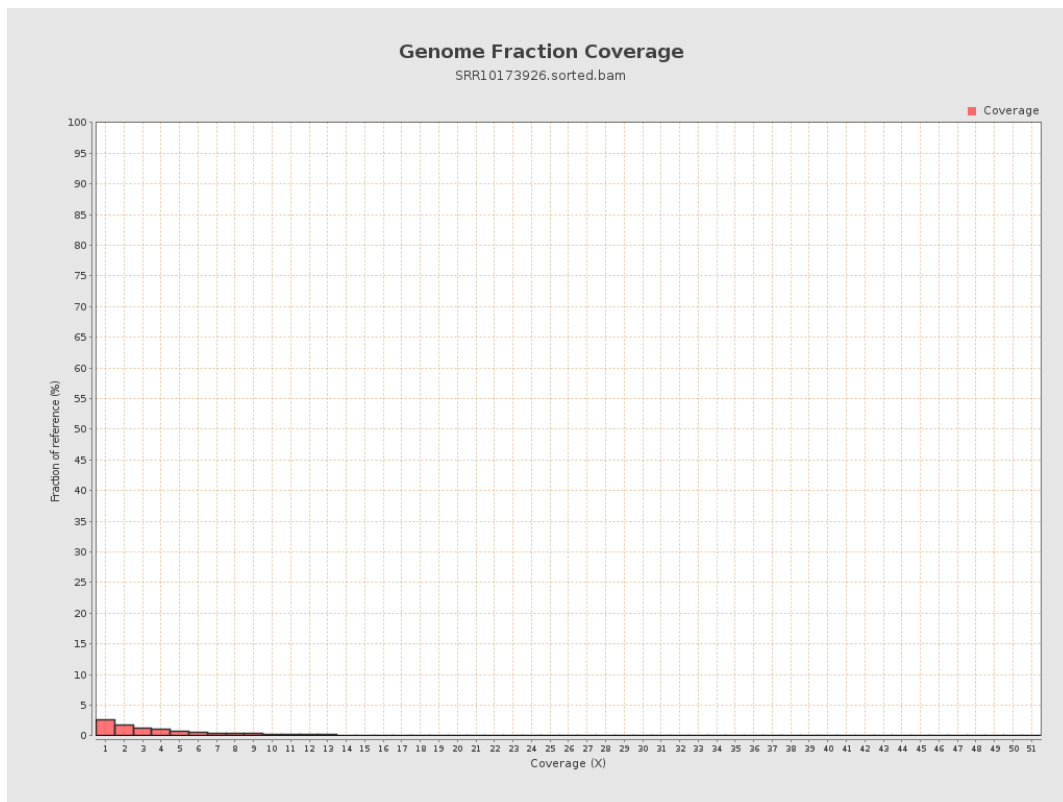
4. Results : Coverage Histogram



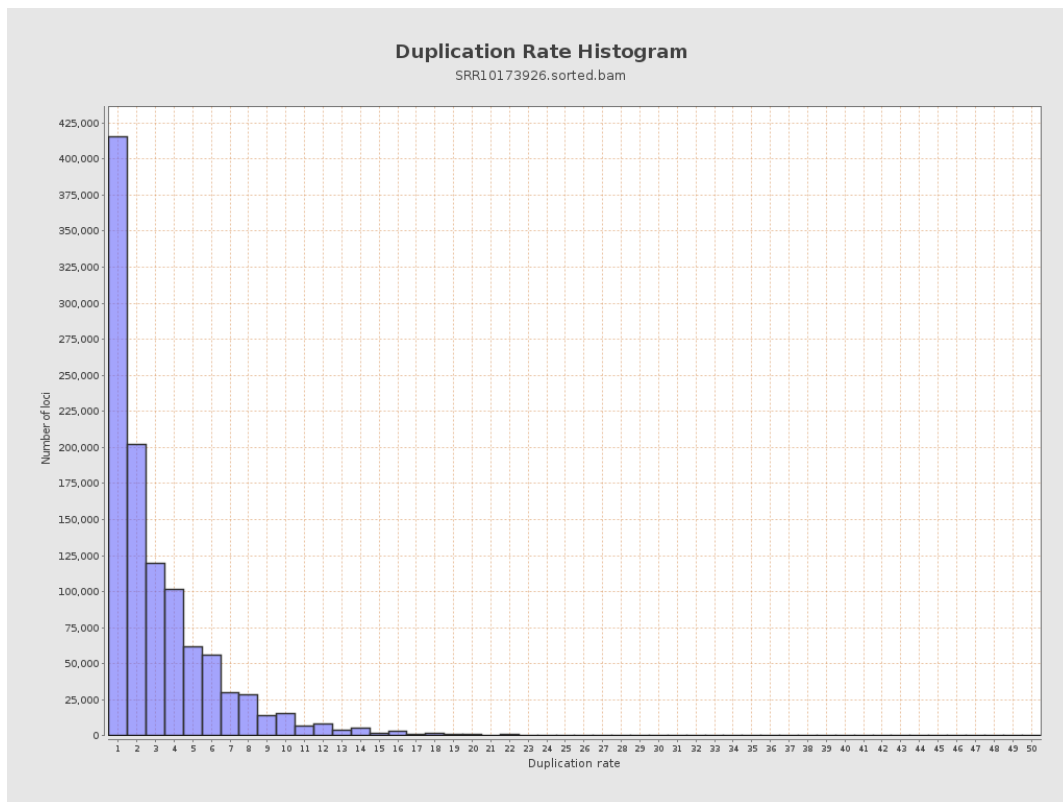
5. Results : Coverage Histogram (0-50X)



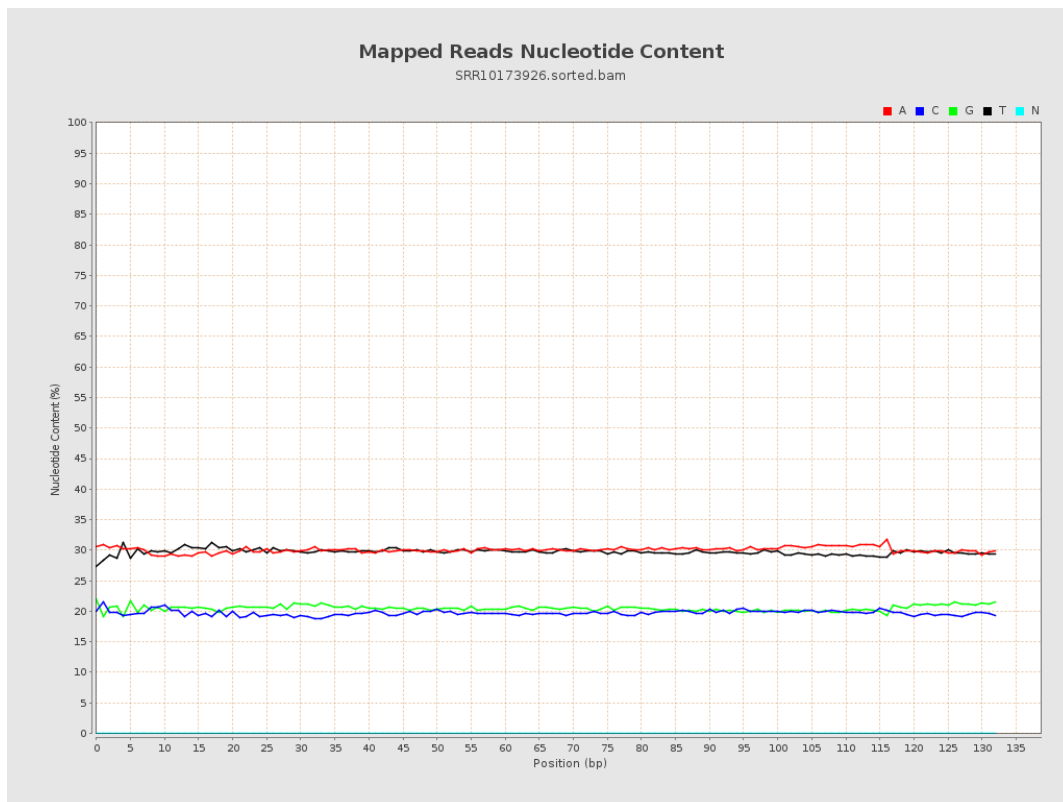
6. Results : Genome Fraction Coverage



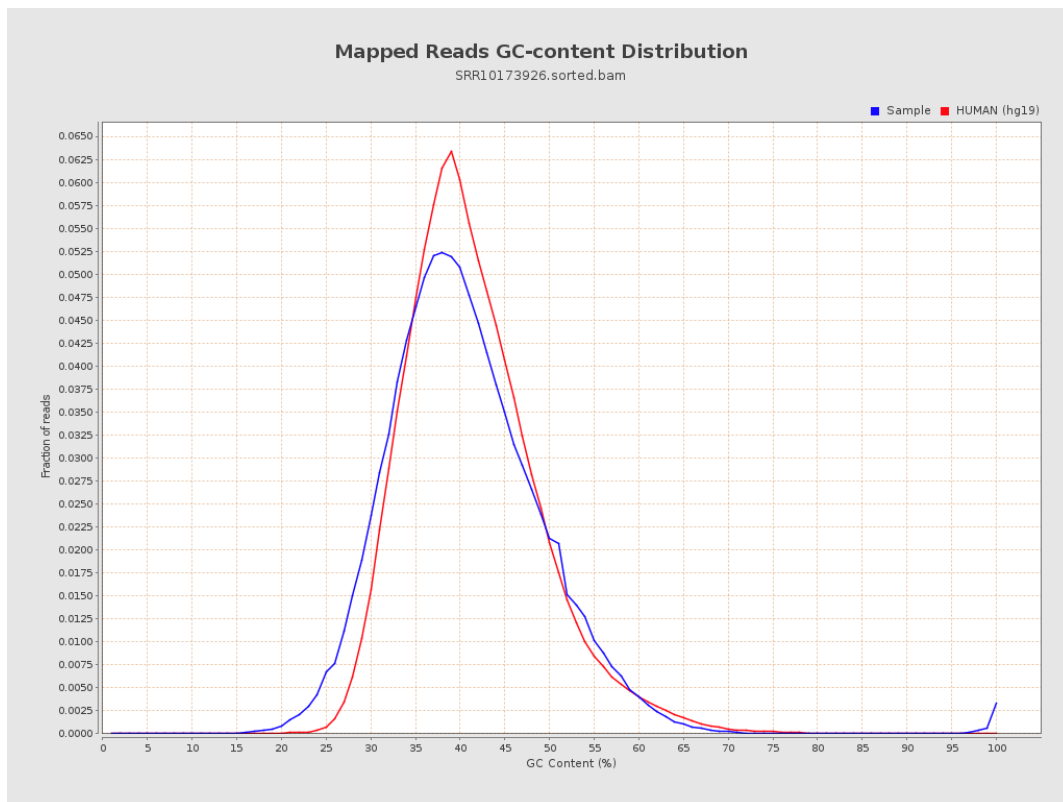
7. Results : Duplication Rate Histogram



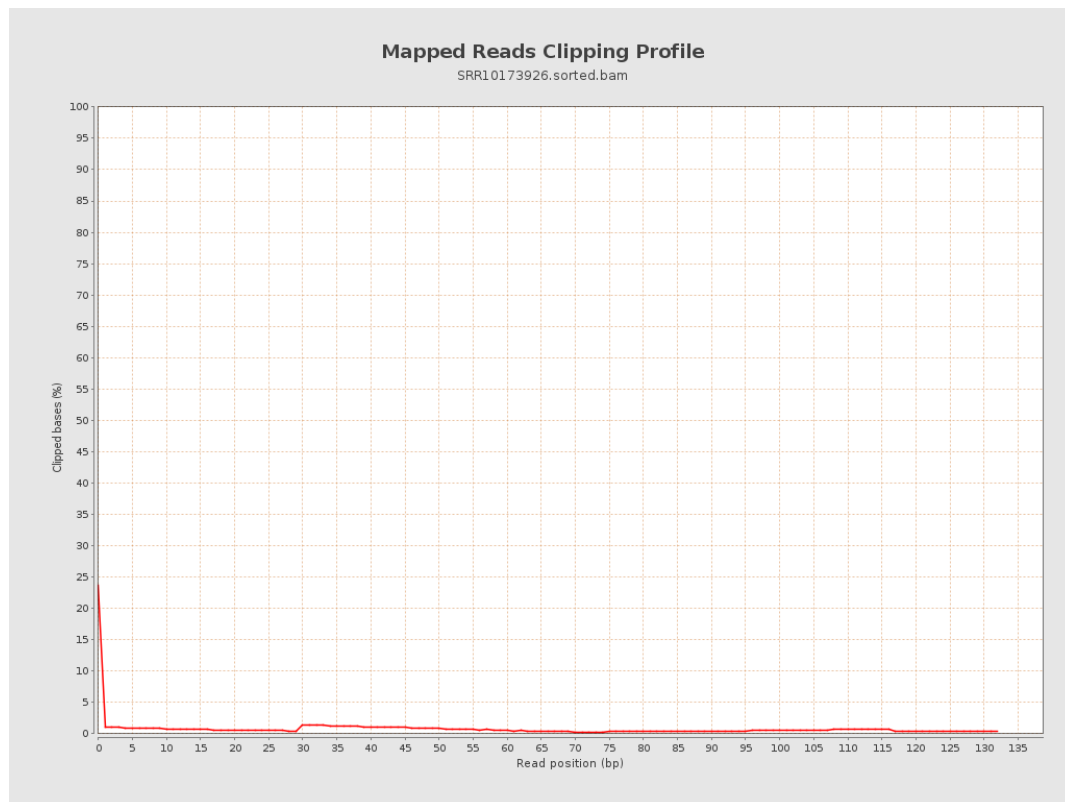
8. Results : Mapped Reads Nucleotide Content



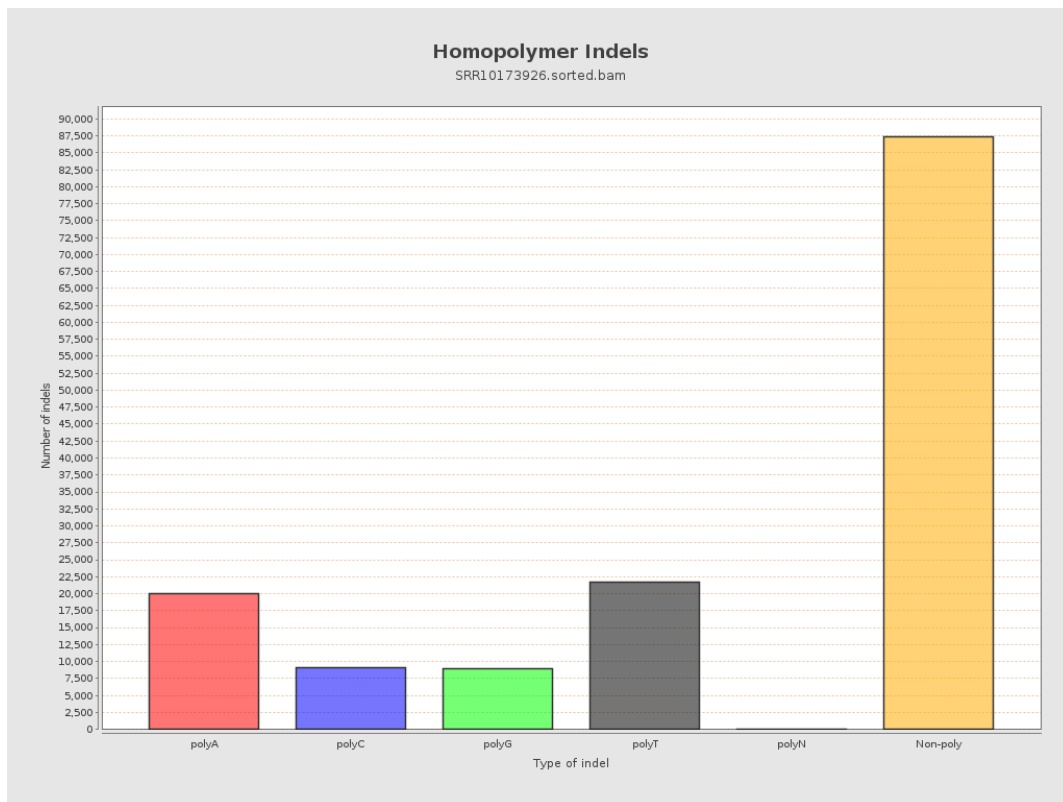
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



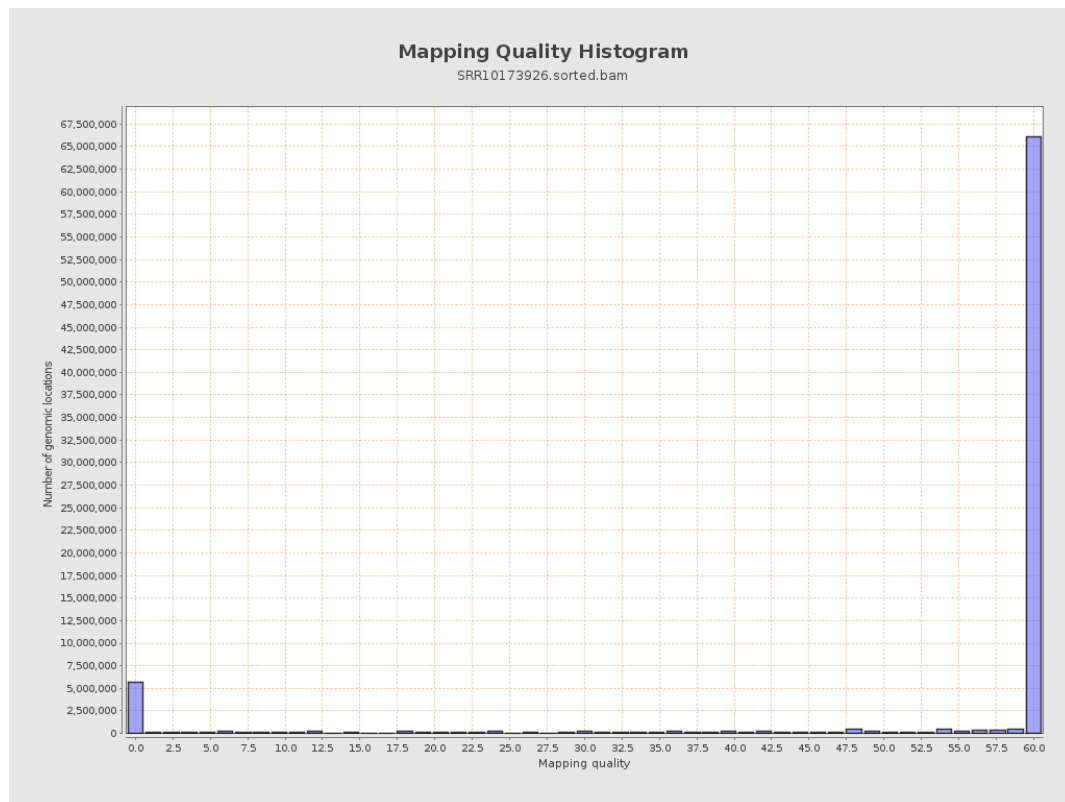
11. Results : Homopolymer Indels



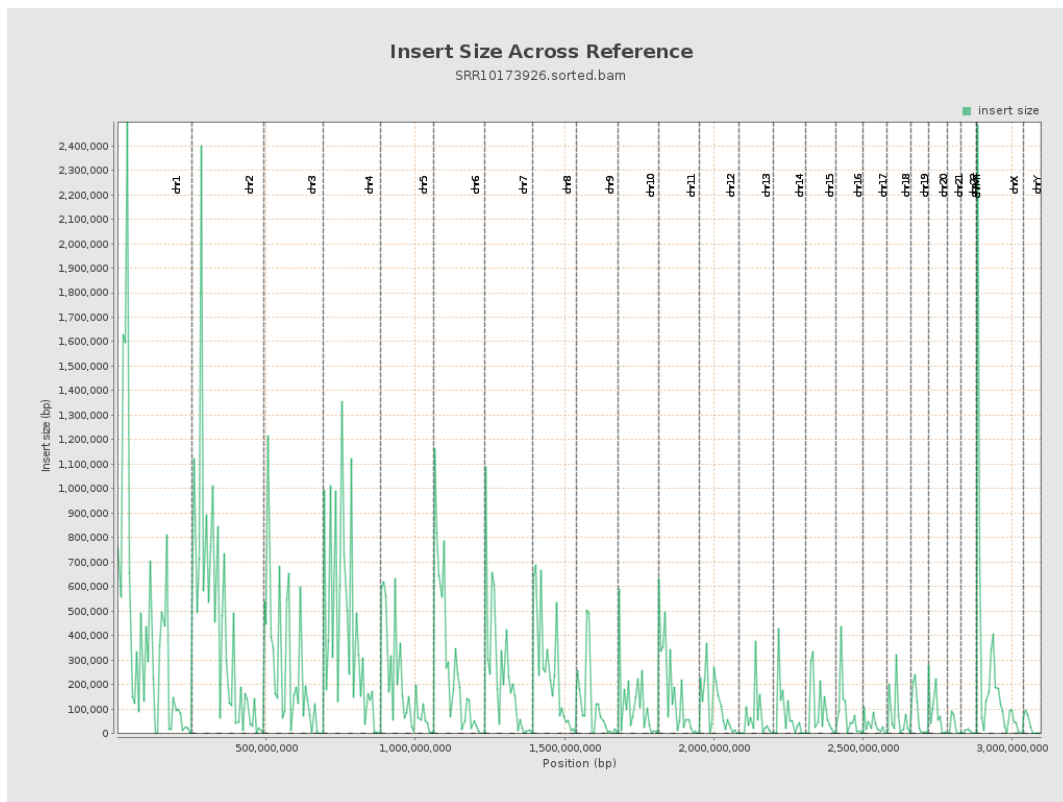
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

