

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 14:28:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173966.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_SRR10173966 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173966_1.fastq.gz SRR10173966_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 14:28:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173966.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,754,794
Mapped reads	4,647,297 / 97.74%
Unmapped reads	107,497 / 2.26%
Mapped paired reads	4,647,297 / 97.74%
Mapped reads, first in pair	2,322,547 / 48.85%
Mapped reads, second in pair	2,324,750 / 48.89%
Mapped reads, both in pair	4,577,324 / 96.27%
Mapped reads, singletons	69,973 / 1.47%
Secondary alignments	0
Supplementary alignments	638,584 / 13.43%
Read min/max/mean length	30 / 133 / 126.1
Duplicated reads (estimated)	3,620,302 / 76.14%
Duplication rate	63.5%
Clipped reads	2,408,647 / 50.66%

2.2. ACGT Content

Number/percentage of A's	157,244,432 / 29.76%
Number/percentage of C's	105,418,358 / 19.95%
Number/percentage of T's	155,882,937 / 29.51%
Number/percentage of G's	109,773,925 / 20.78%
Number/percentage of N's	4,337 / 0%

GC Percentage	40.73%
---------------	--------

2.3. Coverage

Mean	0.1708
Standard Deviation	3.0551

2.4. Mapping Quality

Mean Mapping Quality	52.43
----------------------	-------

2.5. Insert size

Mean	1,128,247.94
Standard Deviation	9,538,872.29
P25/Median/P75	108 / 161 / 255

2.6. Mismatches and indels

General error rate	0.9%
Mismatches	4,570,144
Insertions	59,375
Mapped reads with at least one insertion	1.23%
Deletions	148,816
Mapped reads with at least one deletion	3.12%
Homopolymer indels	40.81%

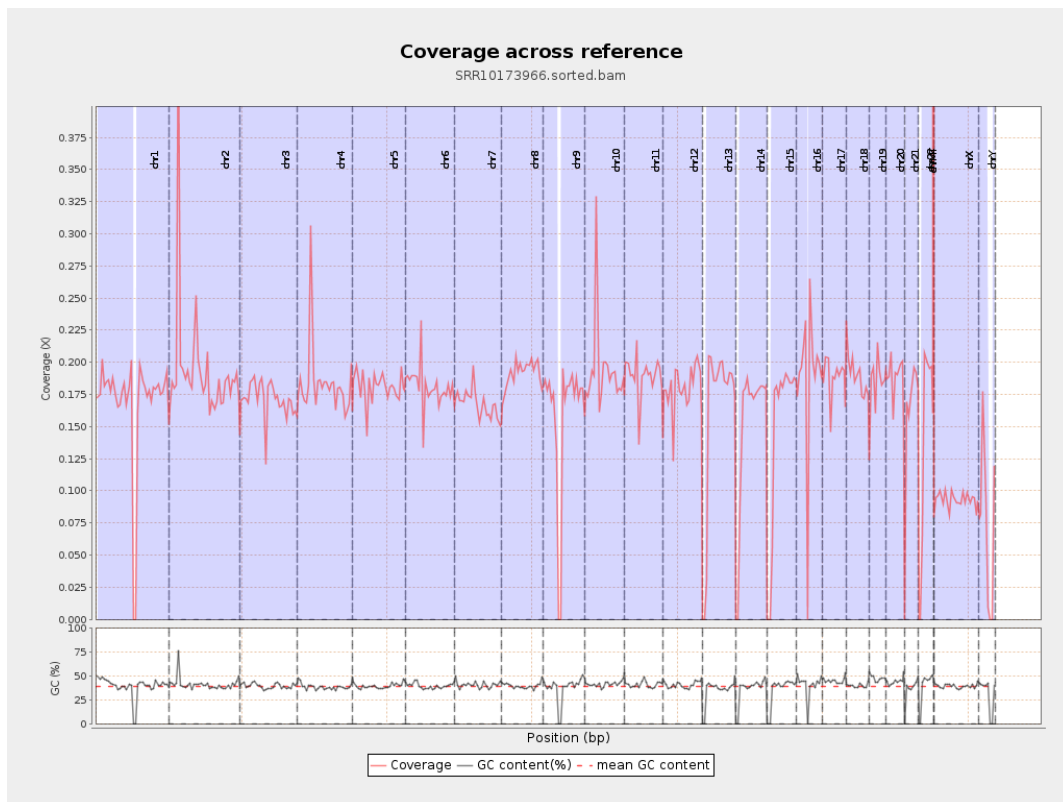
2.7. Chromosome stats

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

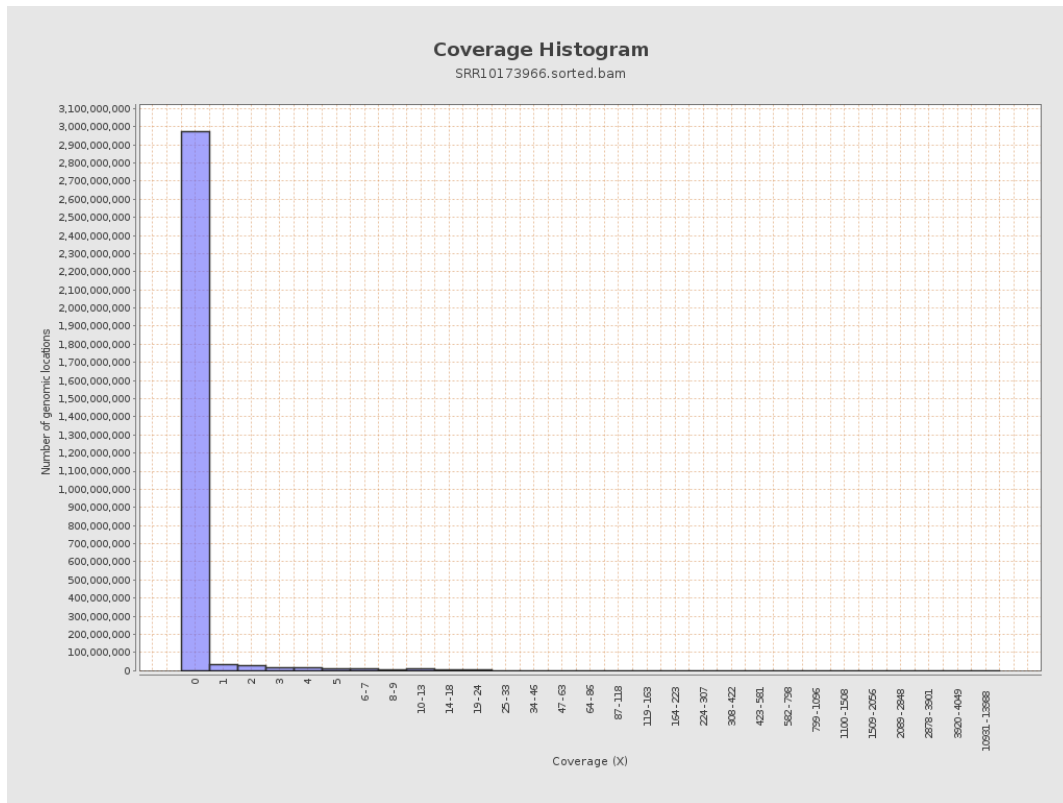
		bases	coverage	deviation
chr1	249250621	42088117	0.1689	1.6823
chr2	243199373	47376616	0.1948	9.7708
chr3	198022430	33906519	0.1712	1.176
chr4	191154276	34961437	0.1829	1.5571
chr5	180915260	32764998	0.1811	1.2087
chr6	171115067	30929713	0.1808	1.3229
chr7	159138663	26716352	0.1679	1.3606
chr8	146364022	28021264	0.1914	1.7693
chr9	141213431	22323061	0.1581	1.4838
chr10	135534747	26181600	0.1932	1.8188
chr11	135006516	25563119	0.1893	1.2727
chr12	133851895	24142090	0.1804	1.2536
chr13	115169878	18444871	0.1602	1.1522
chr14	107349540	16093005	0.1499	1.1109
chr15	102531392	15156933	0.1478	1.1065
chr16	90354753	17021712	0.1884	1.5343
chr17	81195210	15236620	0.1877	1.2927
chr18	78077248	14815716	0.1898	1.9775
chr19	59128983	11003766	0.1861	1.4814
chr20	63025520	11875795	0.1884	1.2681
chr21	48129895	7778687	0.1616	1.4239
chr22	51304566	7010821	0.1367	1.2875
chrMT	16571	713993	43.0869	36.7096
chrX	155270560	14391686	0.0927	0.8728

chrY	59373566	4161922	0.0701	1.1351
------	----------	---------	--------	--------

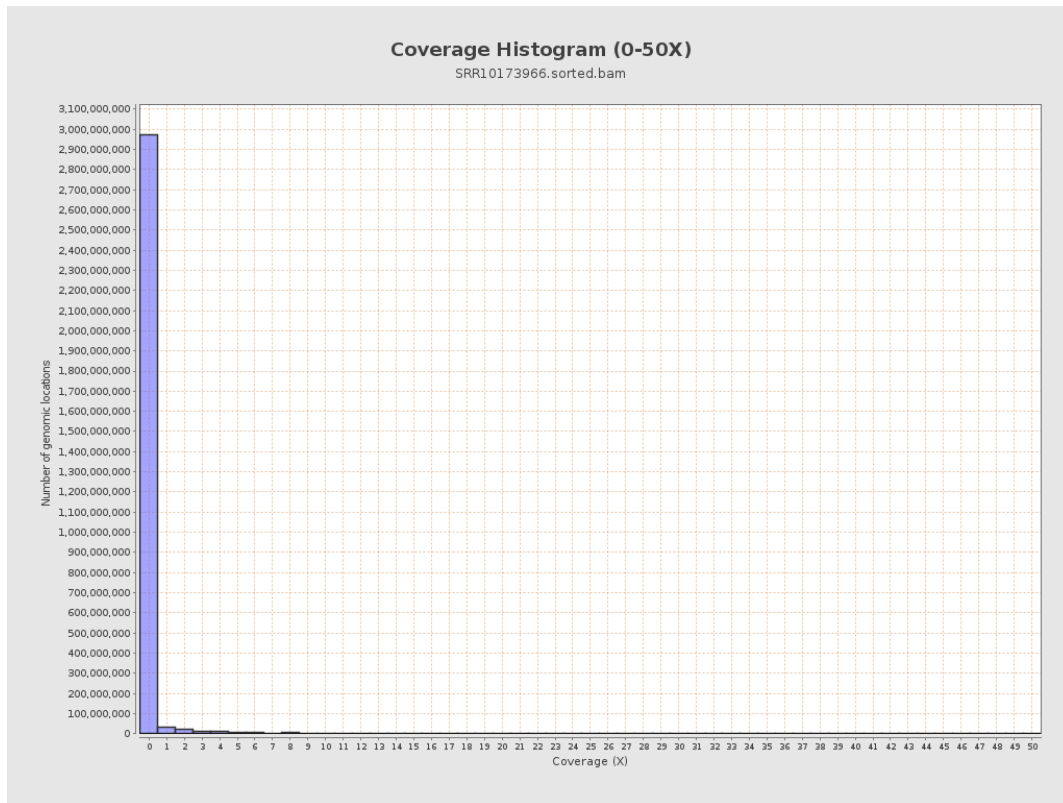
3. Results : Coverage across reference



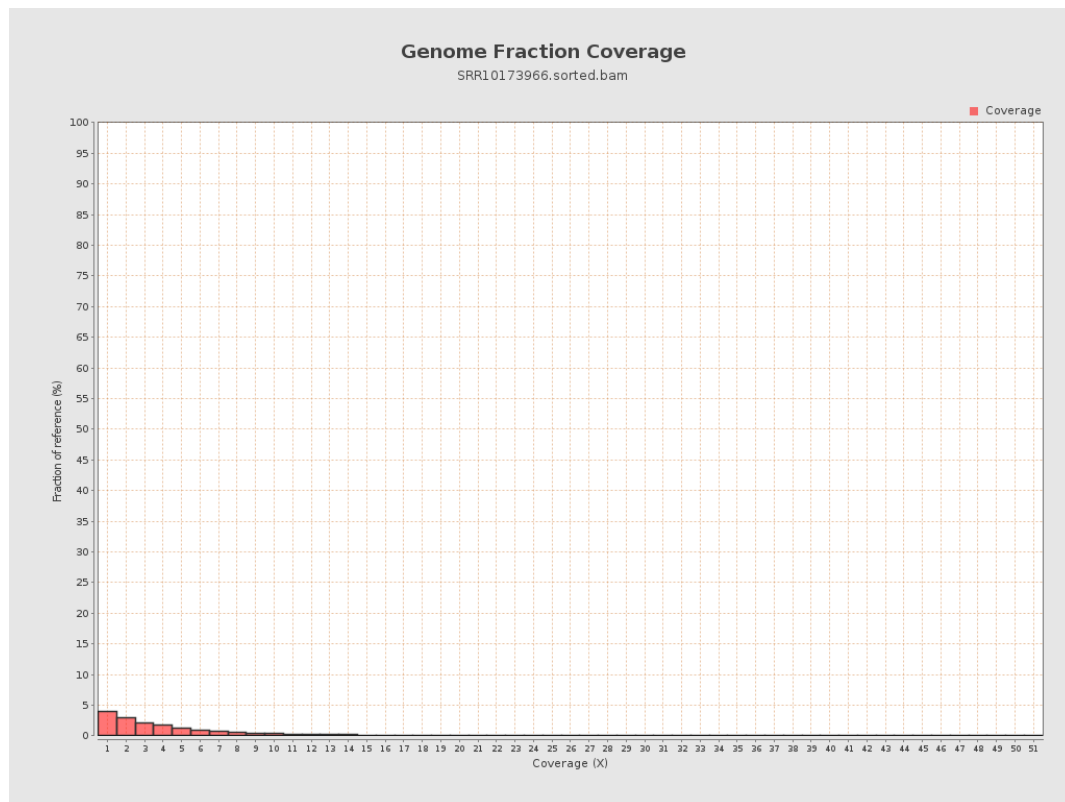
4. Results : Coverage Histogram



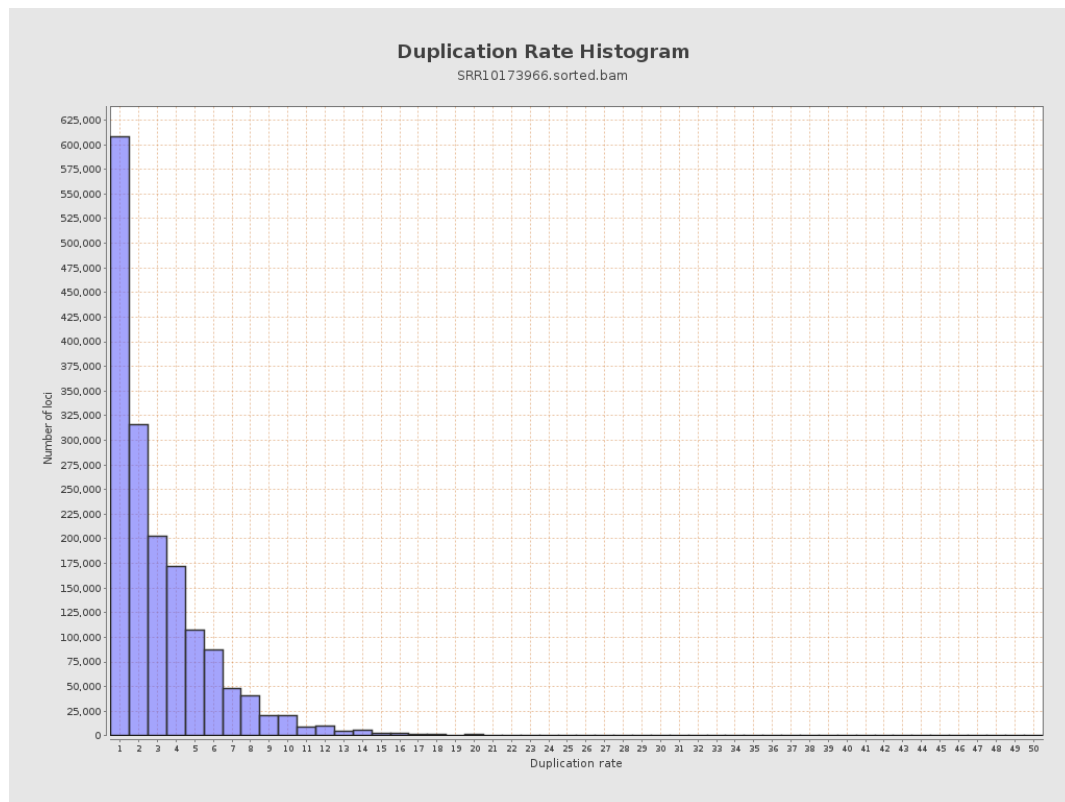
5. Results : Coverage Histogram (0-50X)



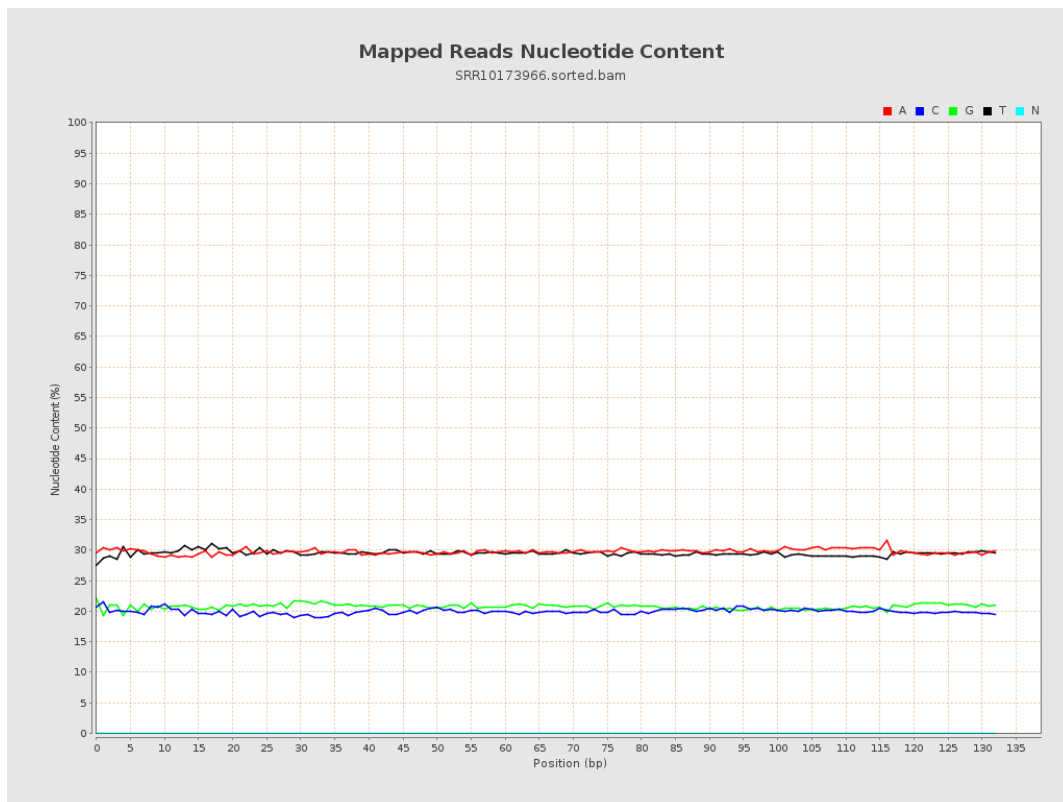
6. Results : Genome Fraction Coverage



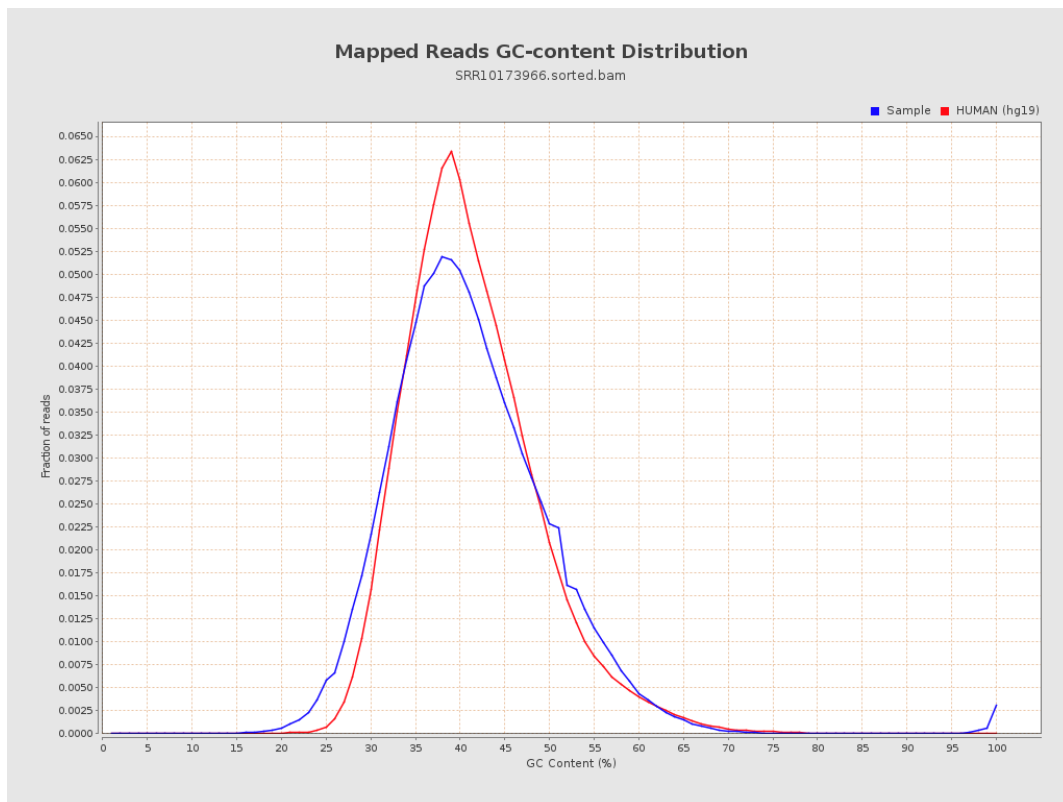
7. Results : Duplication Rate Histogram



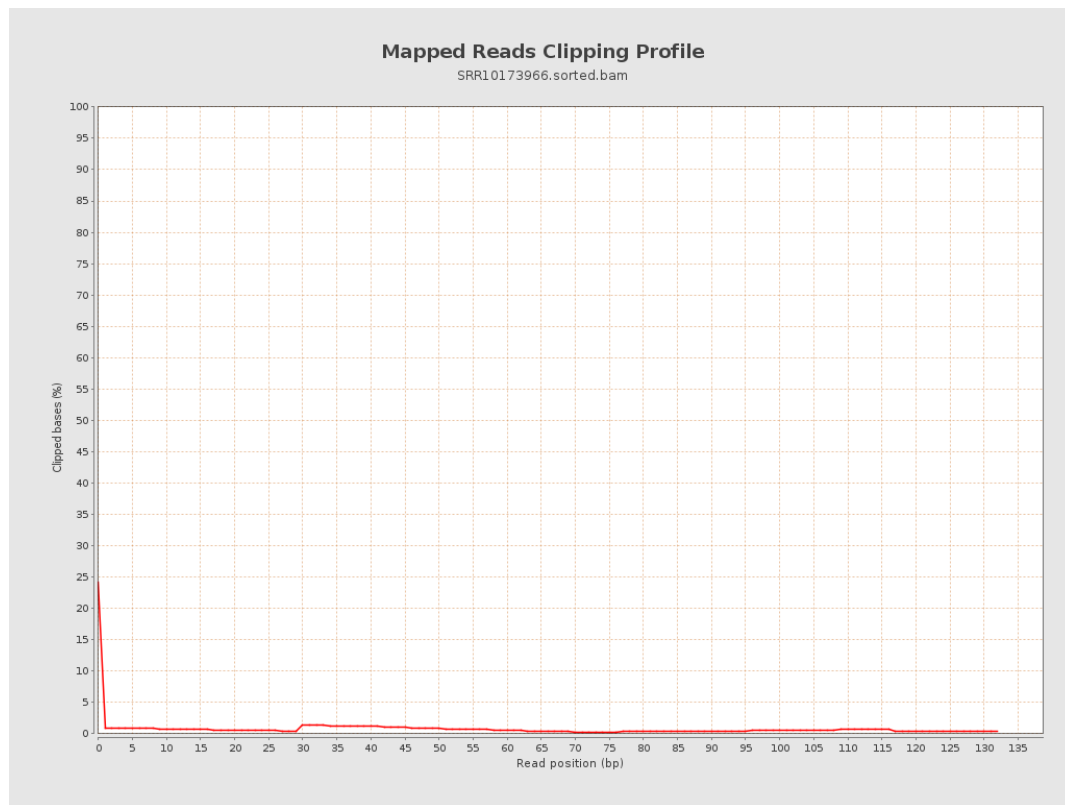
8. Results : Mapped Reads Nucleotide Content



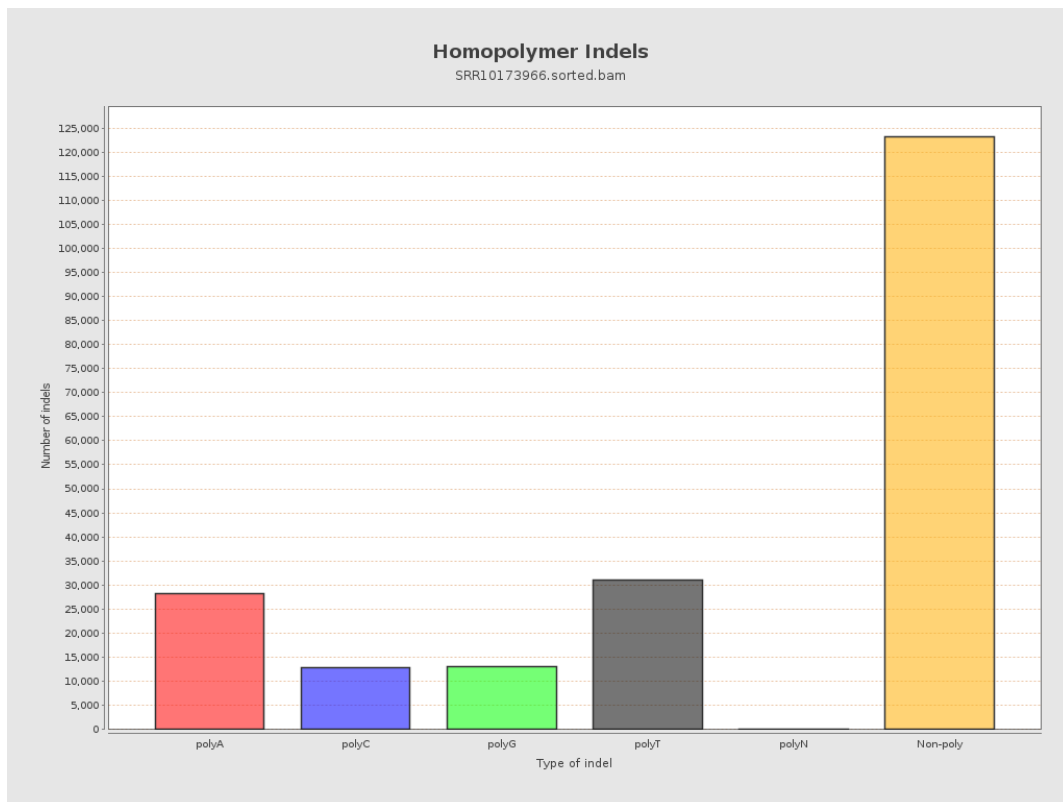
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



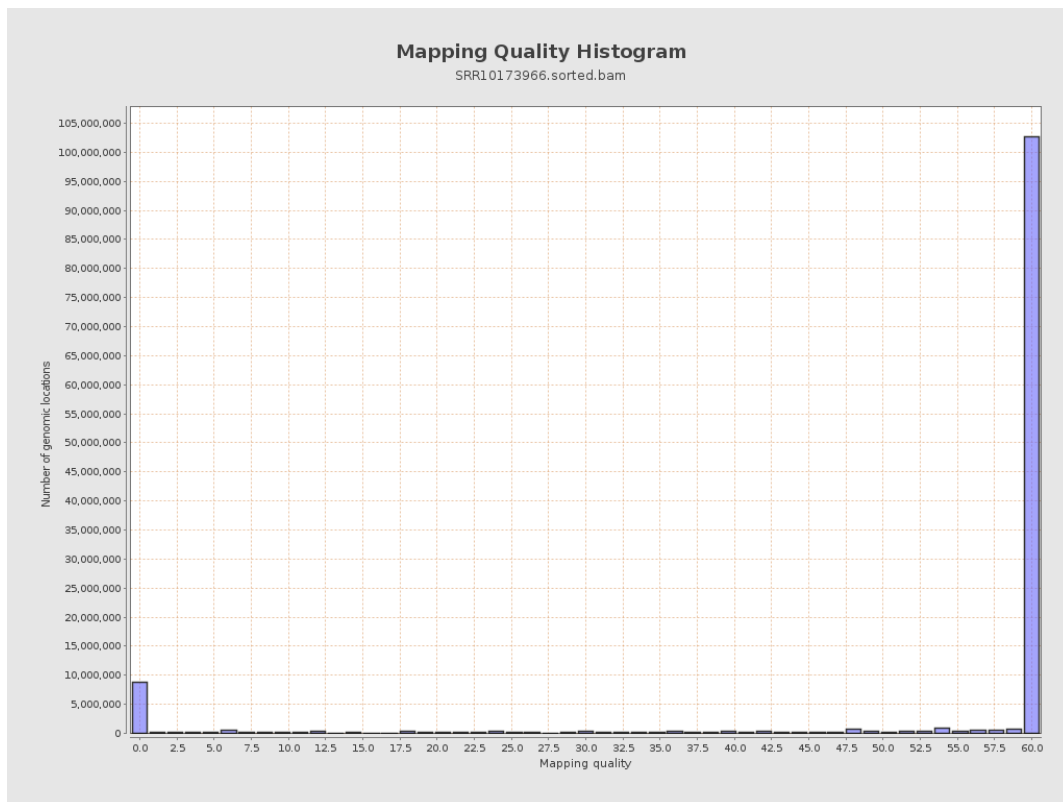
11. Results : Homopolymer Indels



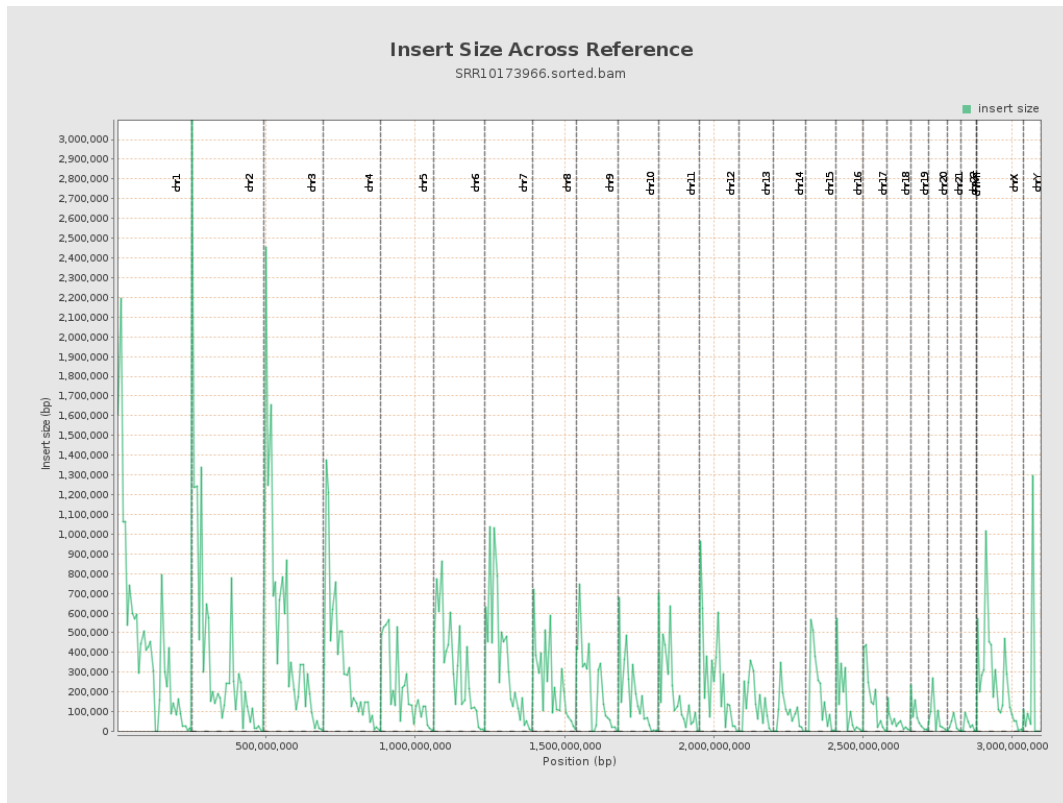
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

