

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/24 09:07:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8617705.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_SRR8617705 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8617705_1.fastq.gz SRR8617705_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 24 09:07:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8617705.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,640,674
Mapped reads	31,830,275 / 97.52%
Unmapped reads	810,399 / 2.48%
Mapped paired reads	31,830,275 / 97.52%
Mapped reads, first in pair	16,097,895 / 49.32%
Mapped reads, second in pair	15,732,380 / 48.2%
Mapped reads, both in pair	31,317,238 / 95.95%
Mapped reads, singletons	513,037 / 1.57%
Secondary alignments	0
Supplementary alignments	2,380,856 / 7.29%
Read min/max/mean length	30 / 150 / 153.76
Duplicated reads (estimated)	9,538,444 / 29.22%
Duplication rate	21.97%
Clipped reads	20,951,540 / 64.19%

2.2. ACGT Content

Number/percentage of A's	1,241,418,847 / 29.38%
Number/percentage of C's	788,315,424 / 18.66%
Number/percentage of T's	1,288,594,172 / 30.49%
Number/percentage of G's	907,184,040 / 21.47%
Number/percentage of N's	158,118 / 0%

GC Percentage	40.12%
---------------	--------

2.3. Coverage

Mean	1.366
Standard Deviation	15.9194

2.4. Mapping Quality

Mean Mapping Quality	52.39
----------------------	-------

2.5. Insert size

Mean	565,869.42
Standard Deviation	7,414,228.59
P25/Median/P75	198 / 252 / 317

2.6. Mismatches and indels

General error rate	1.21%
Mismatches	49,185,964
Insertions	739,705
Mapped reads with at least one insertion	2.2%
Deletions	1,521,834
Mapped reads with at least one deletion	4.6%
Homopolymer indels	46.5%

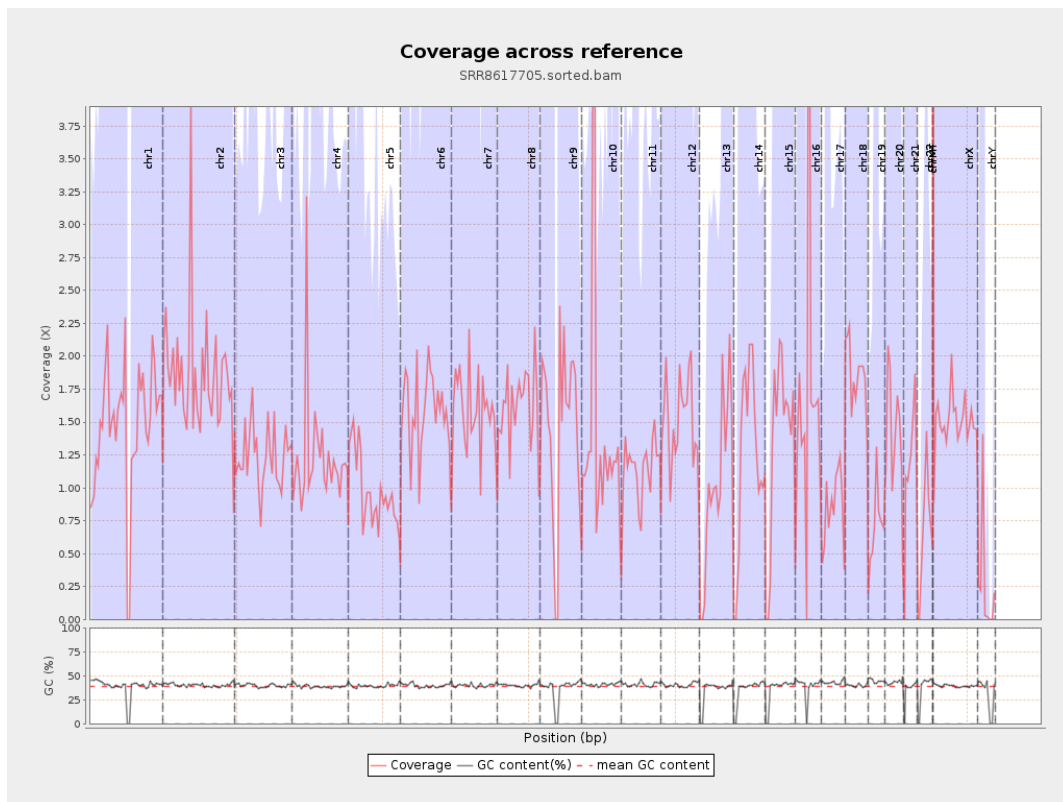
2.7. Chromosome stats

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

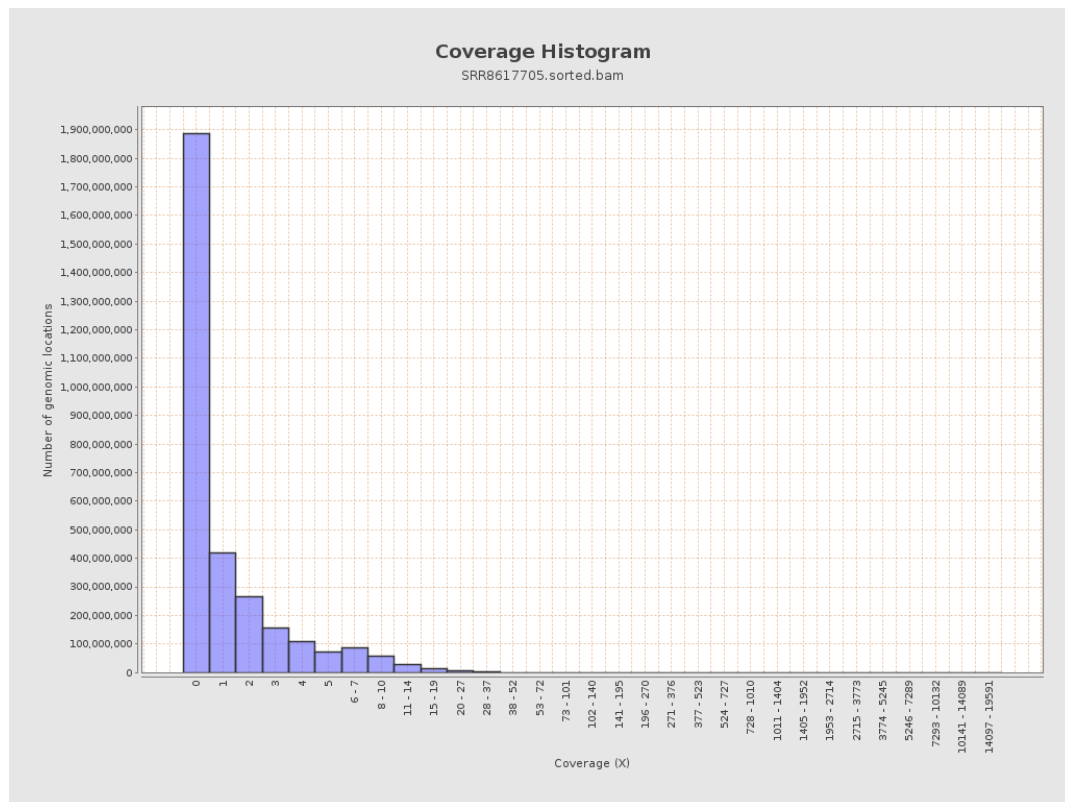
		bases	coverage	deviation
chr1	249250621	365842278	1.4678	15.8166
chr2	243199373	455669454	1.8736	16.5118
chr3	198022430	245092516	1.2377	2.9418
chr4	191154276	234041896	1.2244	14.7132
chr5	180915260	173441092	0.9587	2.3453
chr6	171115067	272651313	1.5934	6.657
chr7	159138663	250724680	1.5755	15.8619
chr8	146364022	237211316	1.6207	5.2512
chr9	141213431	206864252	1.4649	28.8594
chr10	135534747	190575159	1.4061	42.2632
chr11	135006516	154059683	1.1411	6.0445
chr12	133851895	203056900	1.517	7.1451
chr13	115169878	118879118	1.0322	2.3679
chr14	107349540	134546588	1.2534	2.9982
chr15	102531392	137211723	1.3382	4.006
chr16	90354753	158604792	1.7554	34.1244
chr17	81195210	70086052	0.8632	7.2251
chr18	78077248	145632458	1.8652	22.3641
chr19	59128983	43400001	0.734	8.1545
chr20	63025520	90339353	1.4334	5.1771
chr21	48129895	55993344	1.1634	7.4504
chr22	51304566	35155241	0.6852	2.0993
chrMT	16571	203651	12.2896	8.1518
chrX	155270560	233508715	1.5039	5.2723

chrY	59373566	15884240	0.2675	19.9929
------	----------	----------	--------	---------

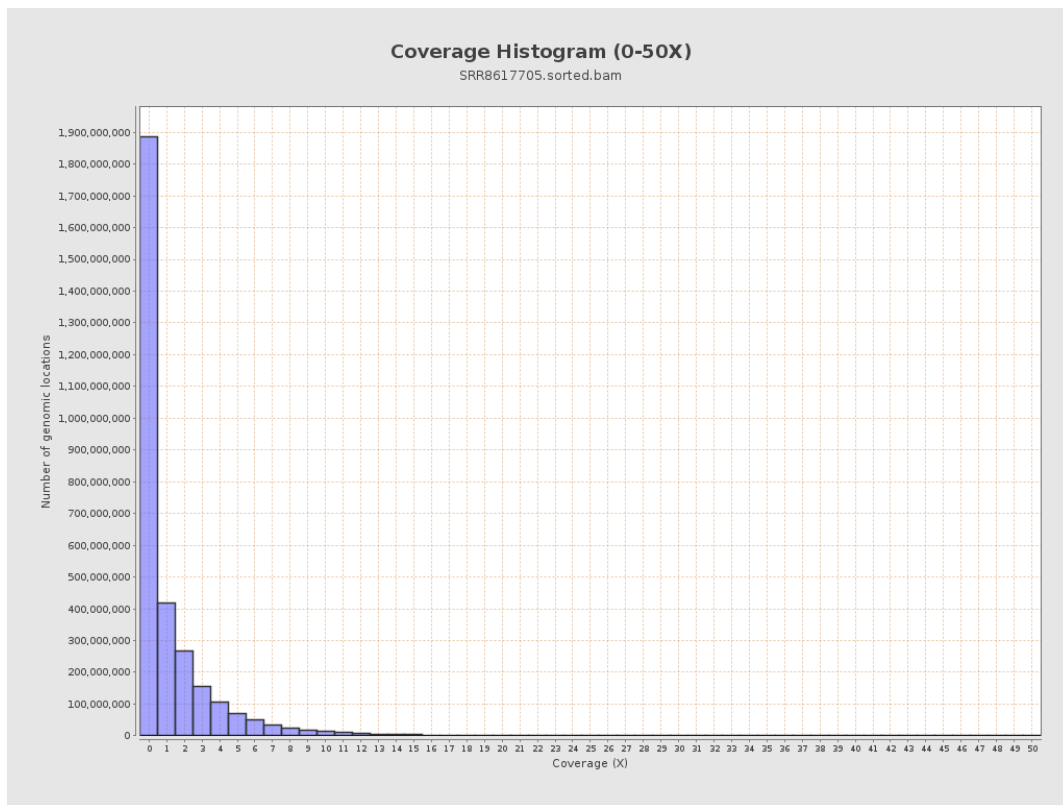
3. Results : Coverage across reference



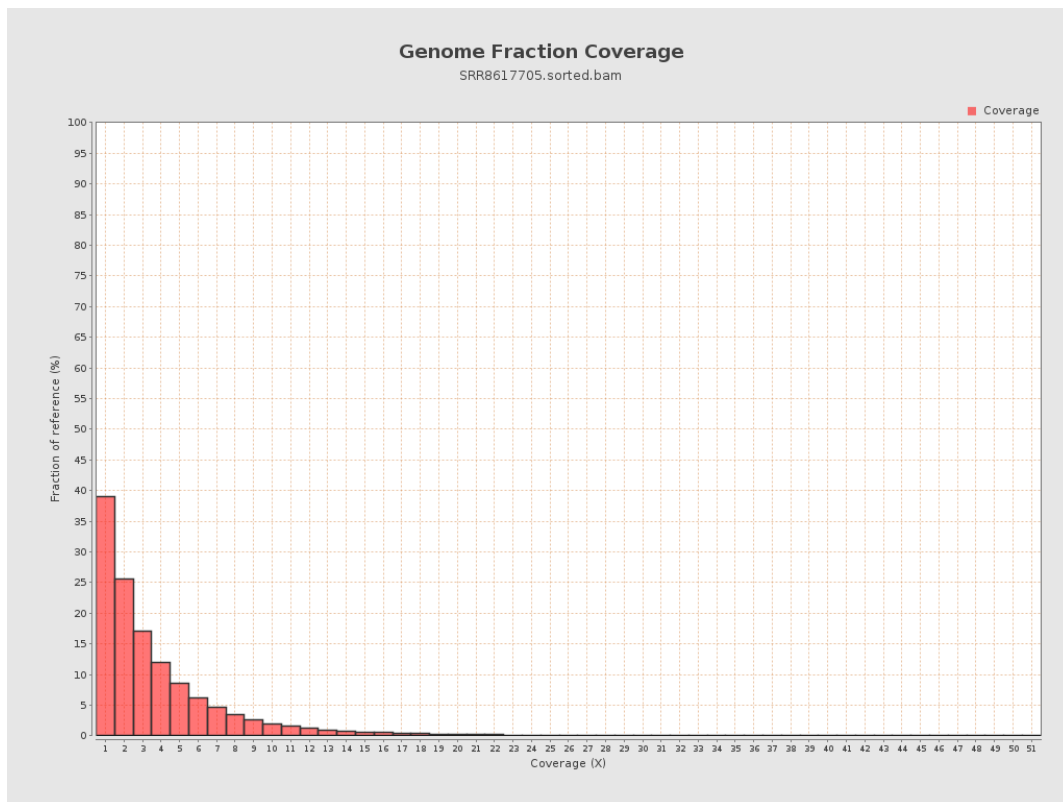
4. Results : Coverage Histogram



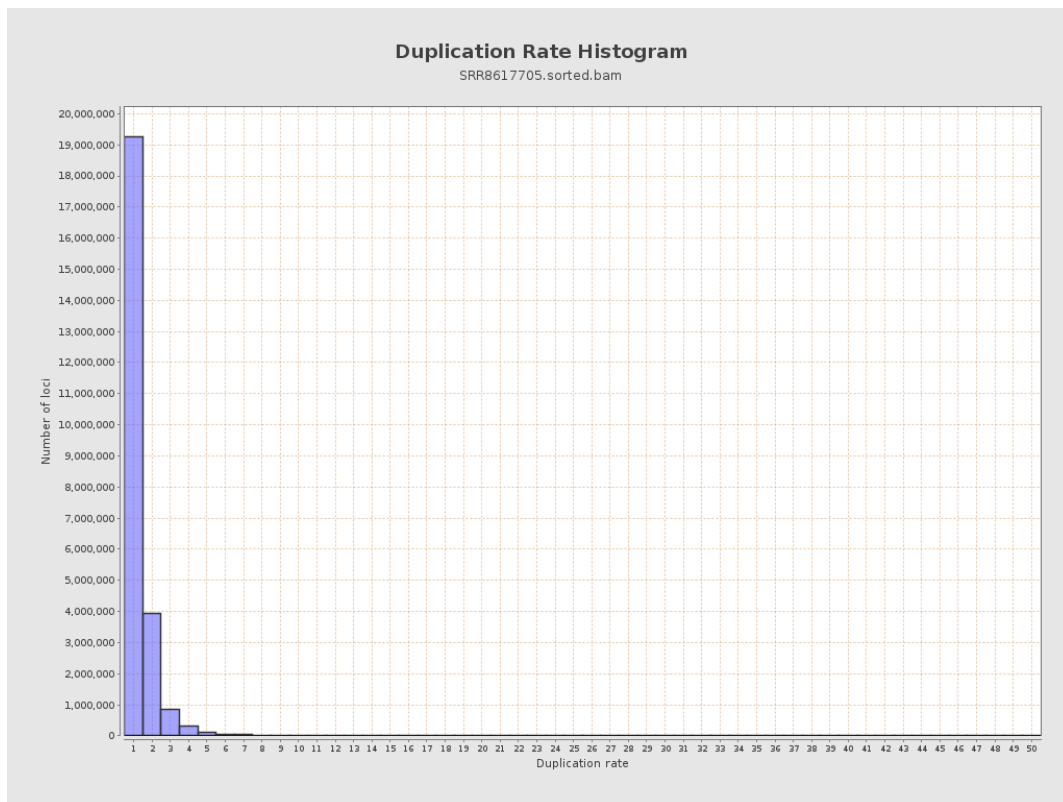
5. Results : Coverage Histogram (0-50X)



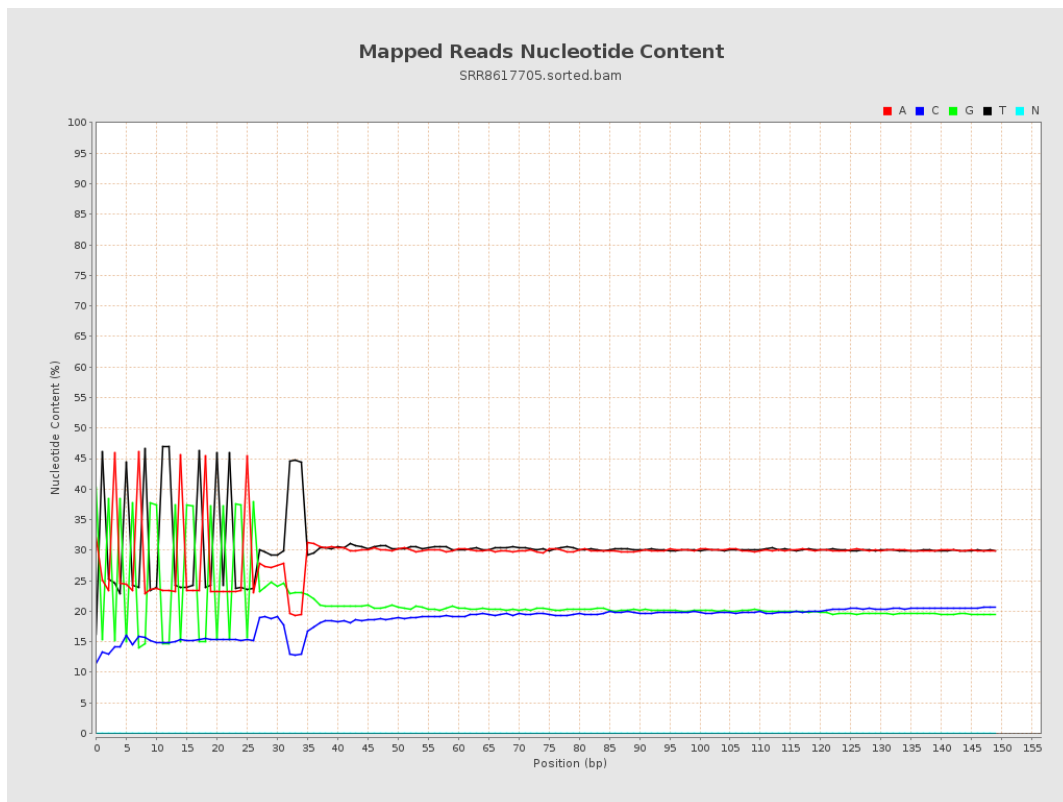
6. Results : Genome Fraction Coverage



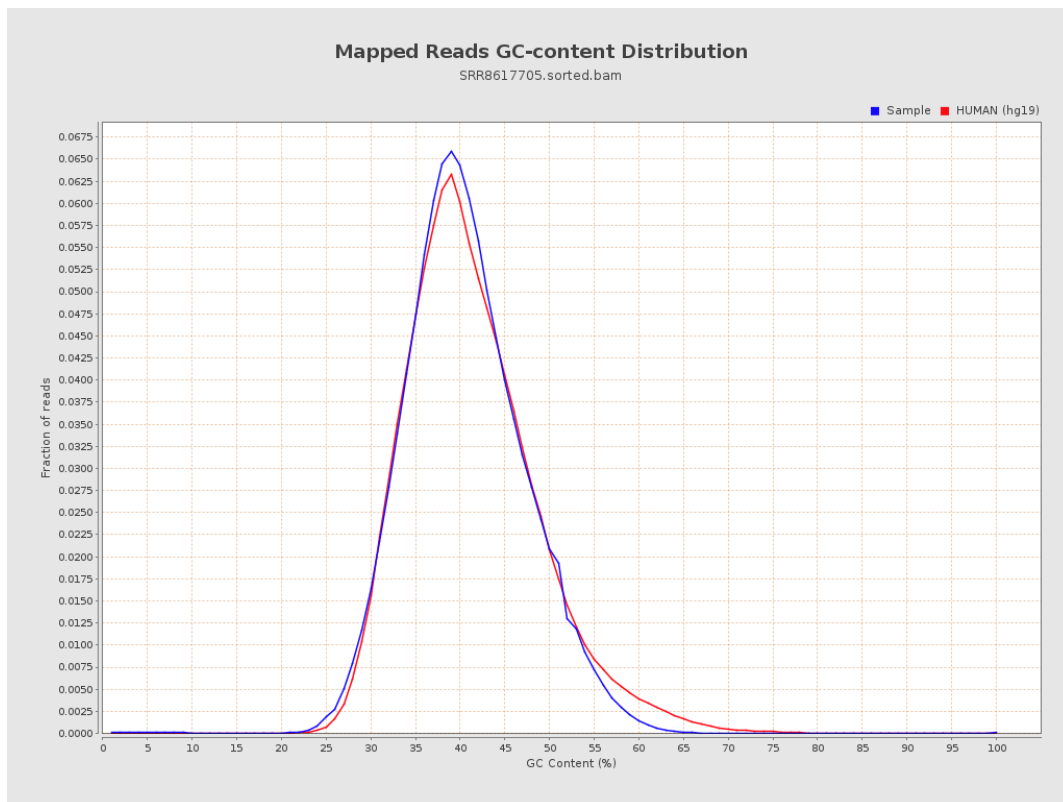
7. Results : Duplication Rate Histogram



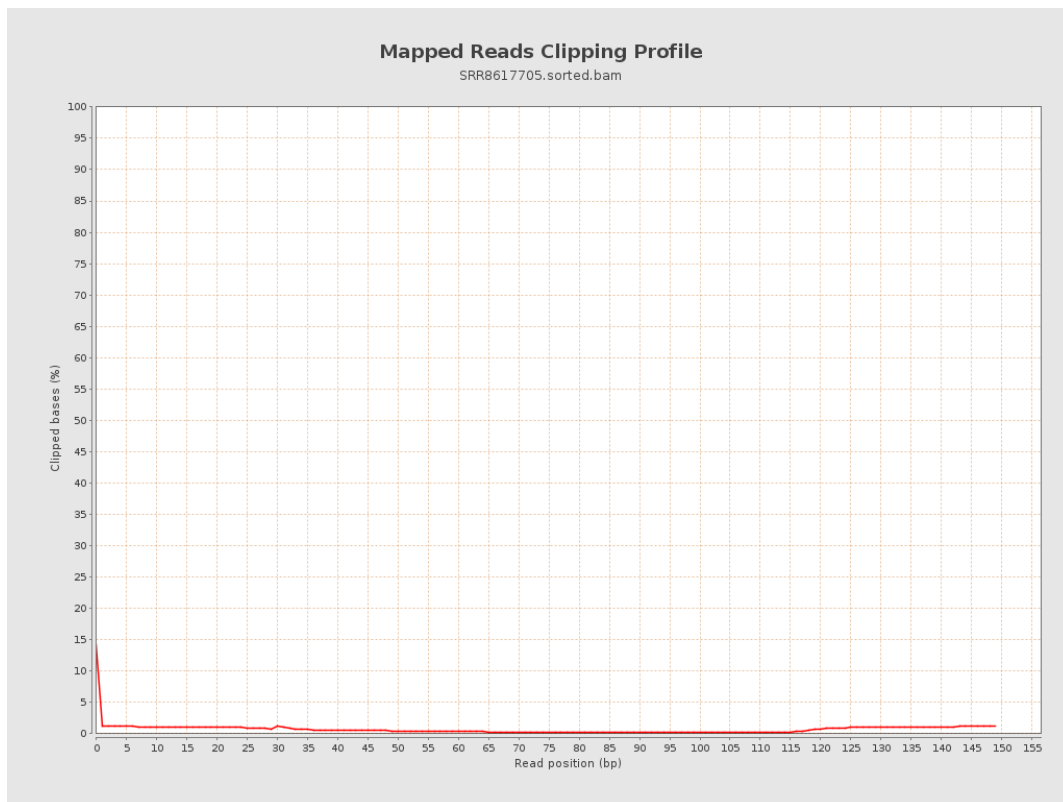
8. Results : Mapped Reads Nucleotide Content



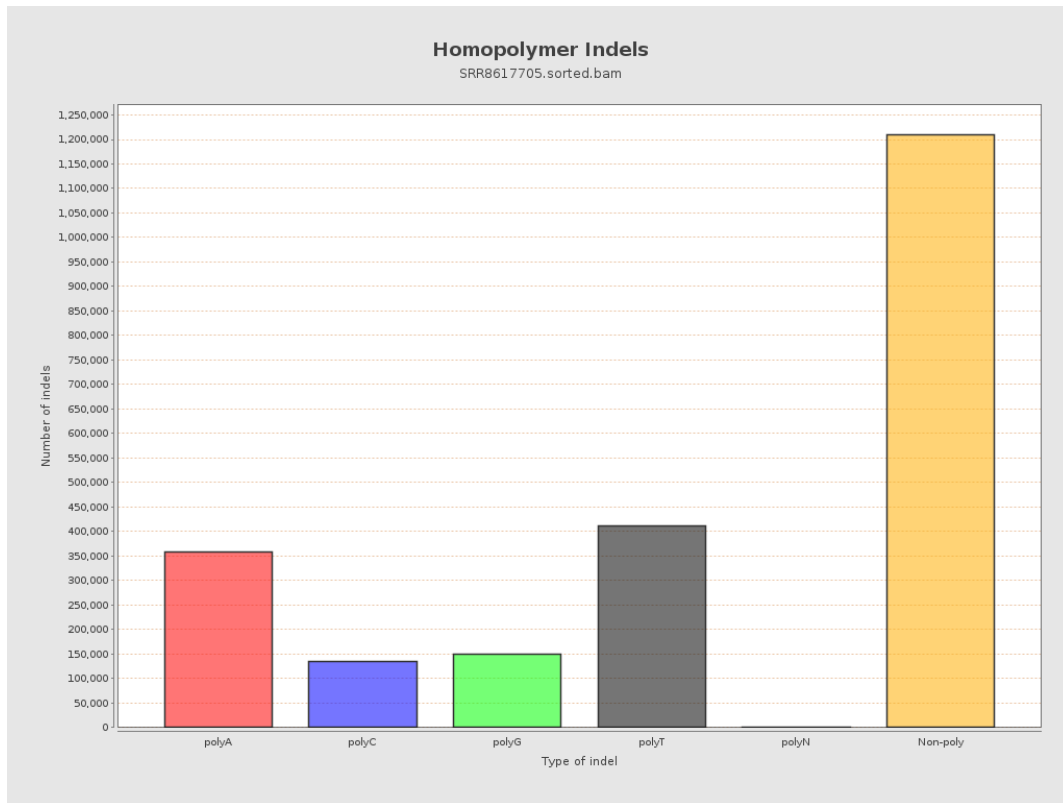
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



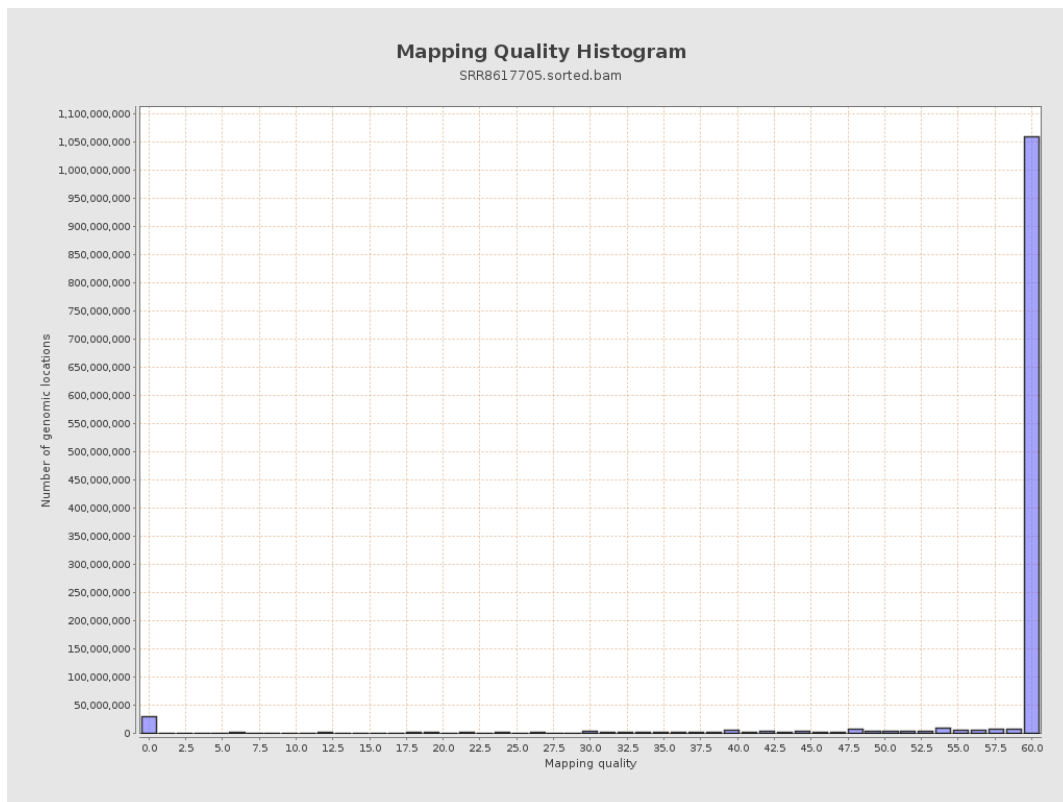
11. Results : Homopolymer Indels



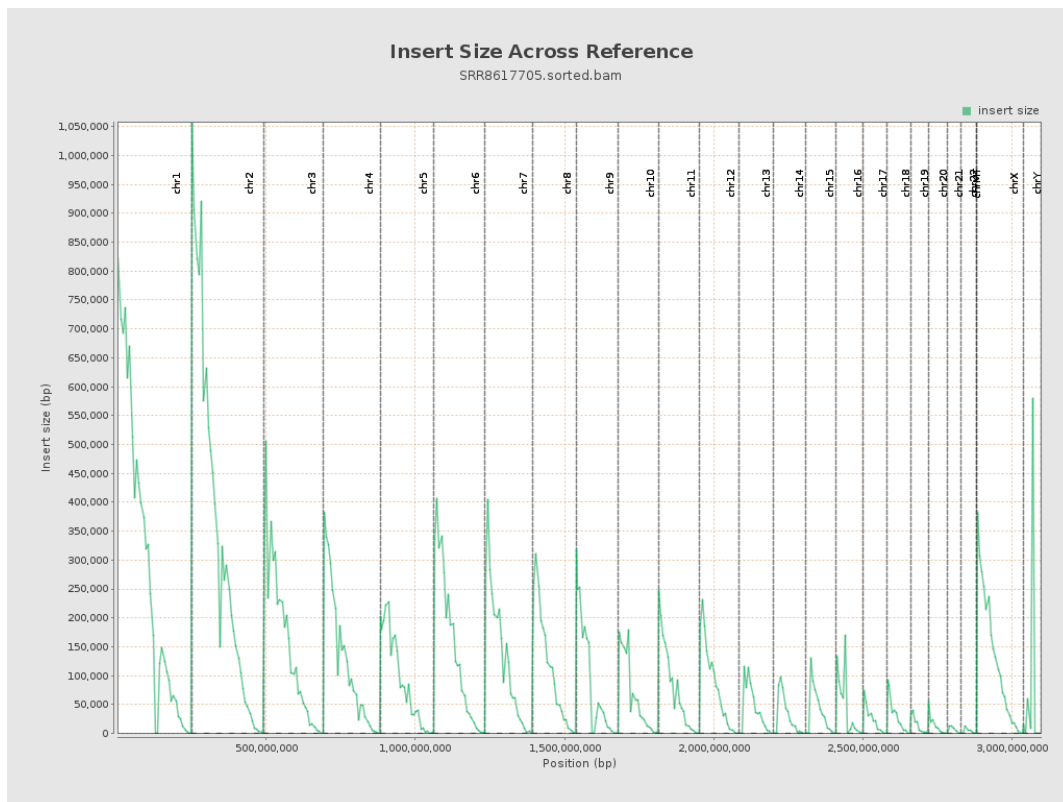
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

