

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/27 15:12:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472570.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_SRR3472570 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472570_1.fastq.gz SRR3472570_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 27 15:12:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472570.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	242,144,252
Mapped reads	238,375,939 / 98.44%
Unmapped reads	3,768,313 / 1.56%
Mapped paired reads	238,375,939 / 98.44%
Mapped reads, first in pair	119,684,233 / 49.43%
Mapped reads, second in pair	118,691,706 / 49.02%
Mapped reads, both in pair	236,961,460 / 97.86%
Mapped reads, singletons	1,414,479 / 0.58%
Secondary alignments	0
Supplementary alignments	217,862 / 0.09%
Read min/max/mean length	30 / 100 / 100.04
Duplicated reads (estimated)	146,411,492 / 60.46%
Duplication rate	49.97%
Clipped reads	39,179,959 / 16.18%

2.2. ACGT Content

Number/percentage of A's	5,919,168,150 / 25.8%
Number/percentage of C's	5,548,303,102 / 24.19%
Number/percentage of T's	5,971,673,805 / 26.03%
Number/percentage of G's	5,495,914,445 / 23.96%
Number/percentage of N's	4,591,822 / 0.02%

GC Percentage	48.14%
---------------	--------

2.3. Coverage

Mean	7.4117
Standard Deviation	64.062

2.4. Mapping Quality

Mean Mapping Quality	51.94
----------------------	-------

2.5. Insert size

Mean	9,864.18
Standard Deviation	931,228.87
P25/Median/P75	129 / 190 / 274

2.6. Mismatches and indels

General error rate	1.04%
Mismatches	233,722,140
Insertions	1,753,971
Mapped reads with at least one insertion	0.71%
Deletions	1,959,979
Mapped reads with at least one deletion	0.8%
Homopolymer indels	40.63%

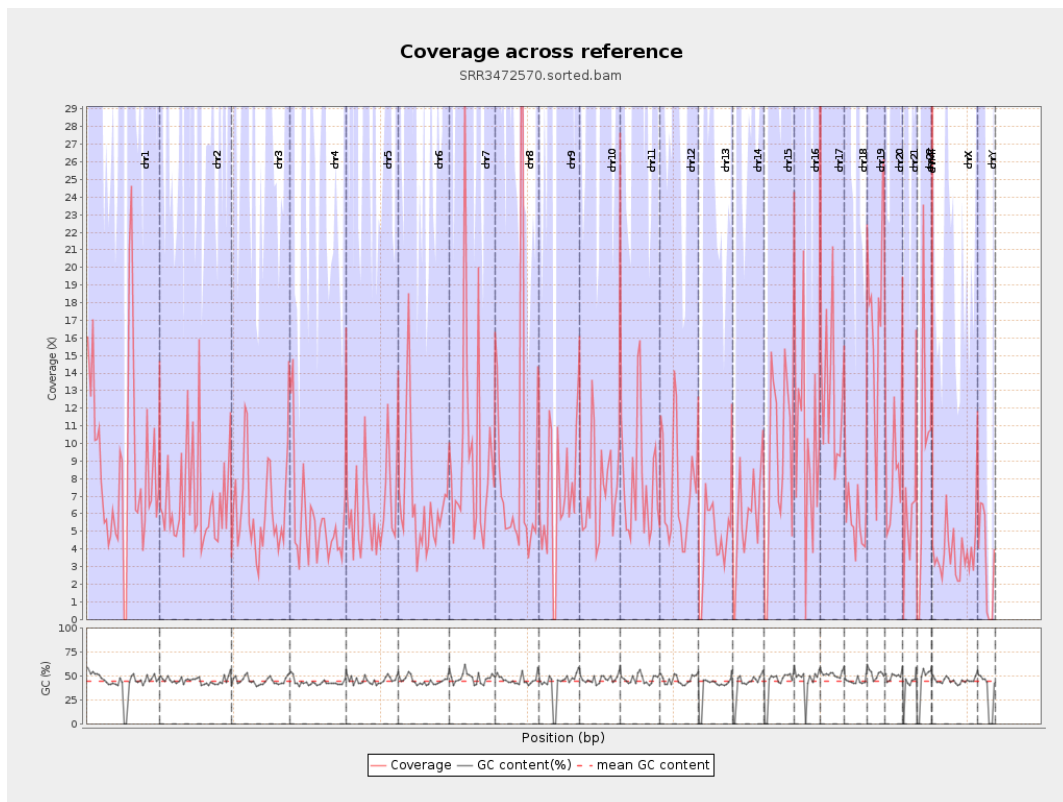
2.7. Chromosome stats

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

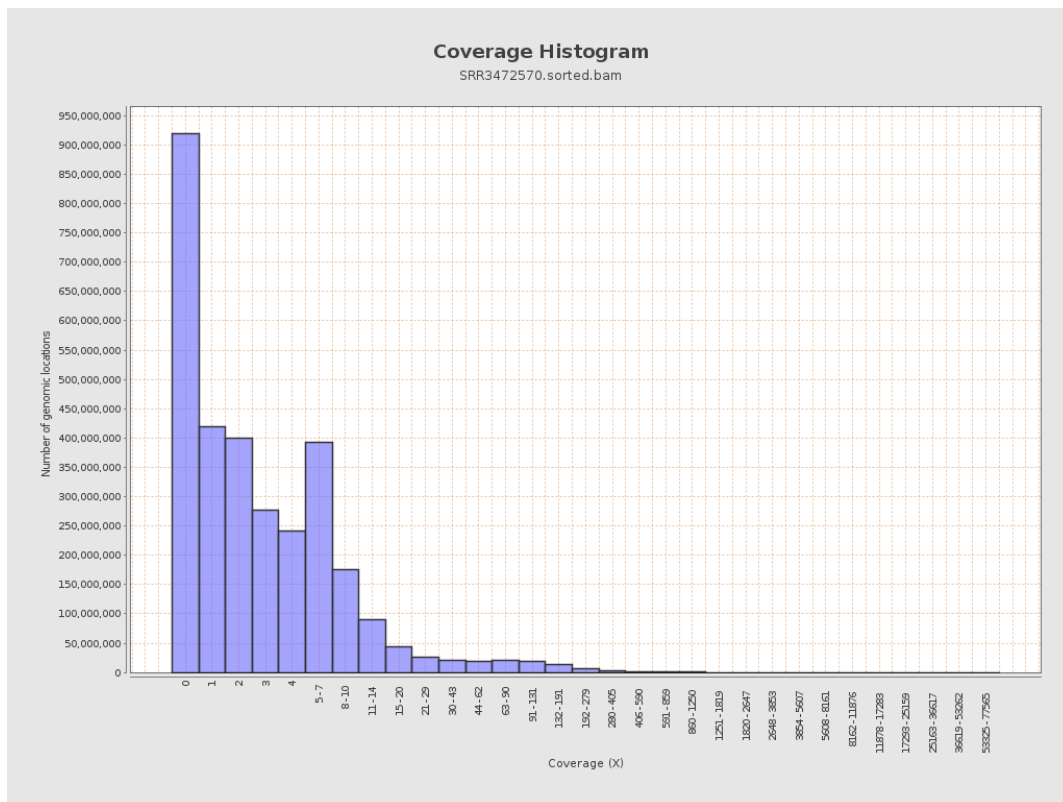
		bases	coverage	deviation
chr1	249250621	2174179293	8.7229	65.6009
chr2	243199373	1653882001	6.8005	51.5284
chr3	198022430	1247096205	6.2978	31.6399
chr4	191154276	1059960935	5.5451	41.2788
chr5	180915260	1174223871	6.4905	45.4872
chr6	171115067	1120425878	6.5478	30.8844
chr7	159138663	1501295138	9.4339	180.6098
chr8	146364022	1217647878	8.3193	116.219
chr9	141213431	999532863	7.0782	36.9819
chr10	135534747	1004549210	7.4117	52.517
chr11	135006516	1123712957	8.3234	35.0708
chr12	133851895	1001852202	7.4848	28.2407
chr13	115169878	527035831	4.5762	20.0259
chr14	107349540	617409978	5.7514	25.5142
chr15	102531392	921174963	8.9843	45.881
chr16	90354753	953766646	10.5558	52.1624
chr17	81195210	1041484299	12.8269	66.1479
chr18	78077248	440543955	5.6424	41.6014
chr19	59128983	1030685661	17.4311	68.4444
chr20	63025520	537826634	8.5335	36.43
chr21	48129895	307454718	6.388	45.3249
chr22	51304566	494736391	9.6431	50.1434
chrMT	16571	5920402	357.2749	88.0311
chrX	155270560	585040092	3.7679	17.3234

chrY	59373566	202771521	3.4152	57.2412
------	----------	-----------	--------	---------

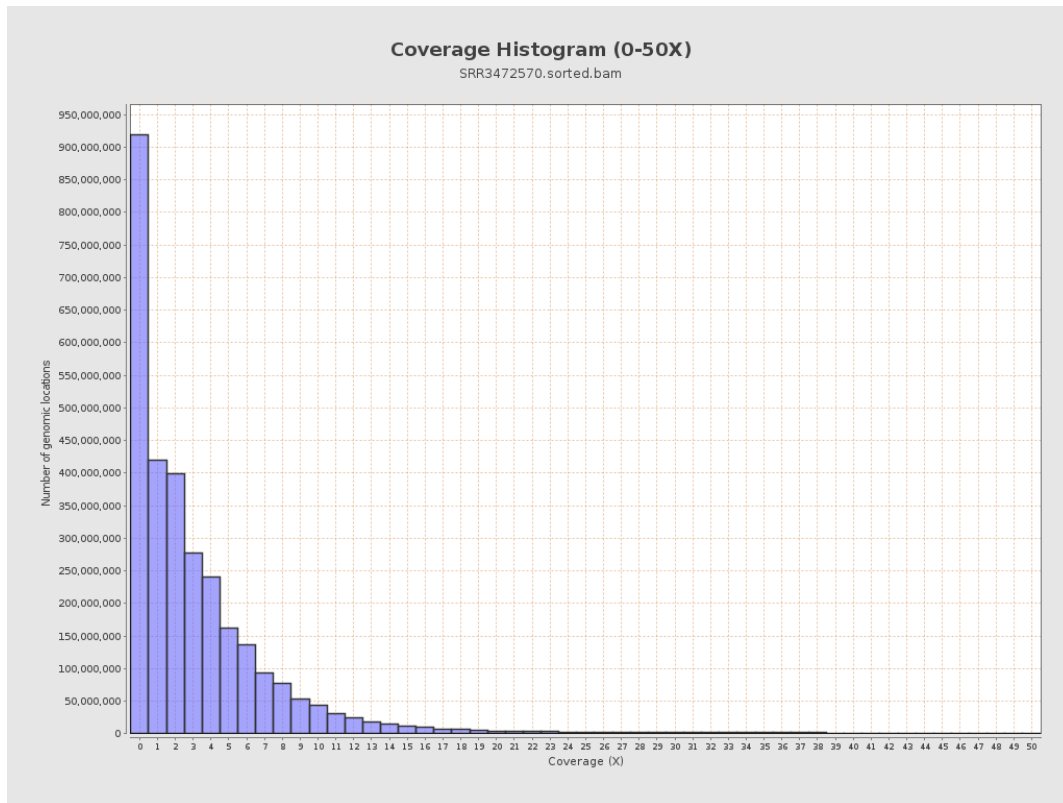
3. Results : Coverage across reference



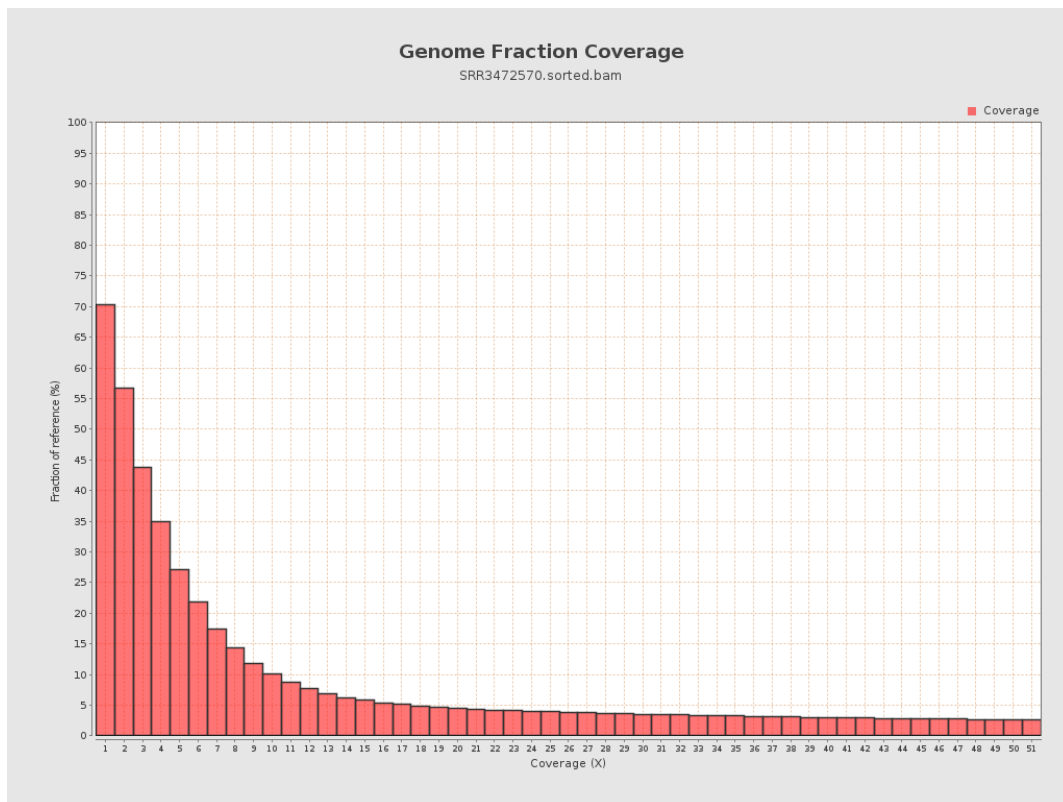
4. Results : Coverage Histogram



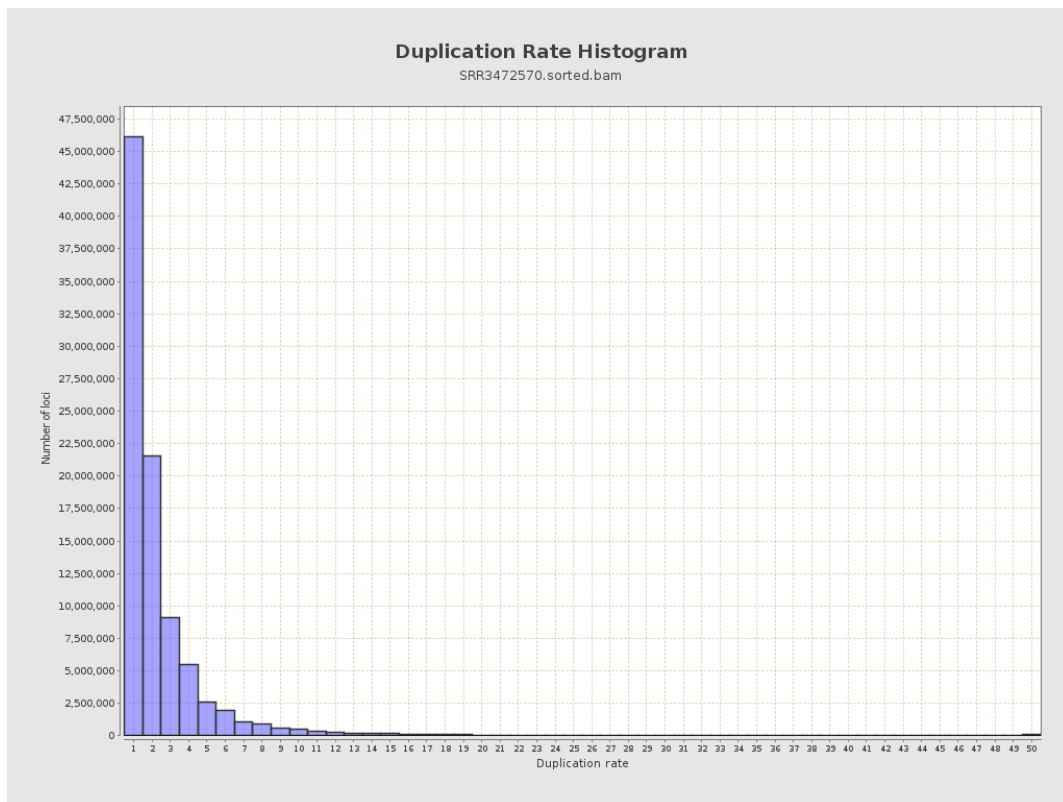
5. Results : Coverage Histogram (0-50X)



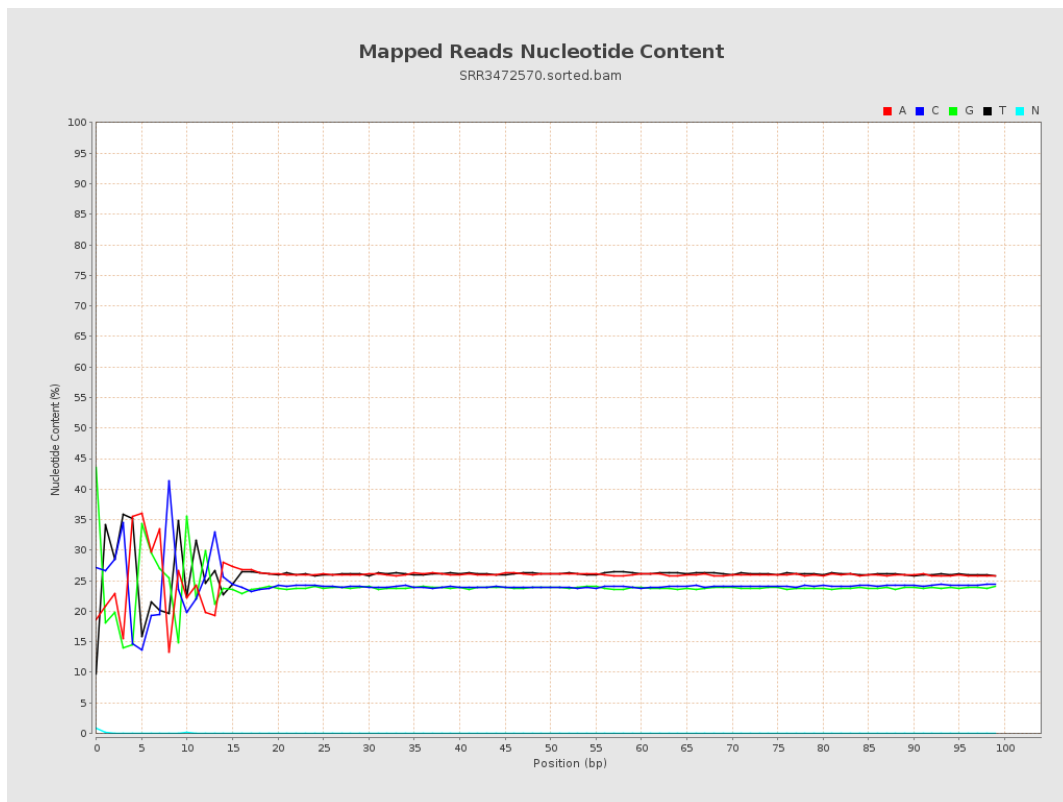
6. Results : Genome Fraction Coverage



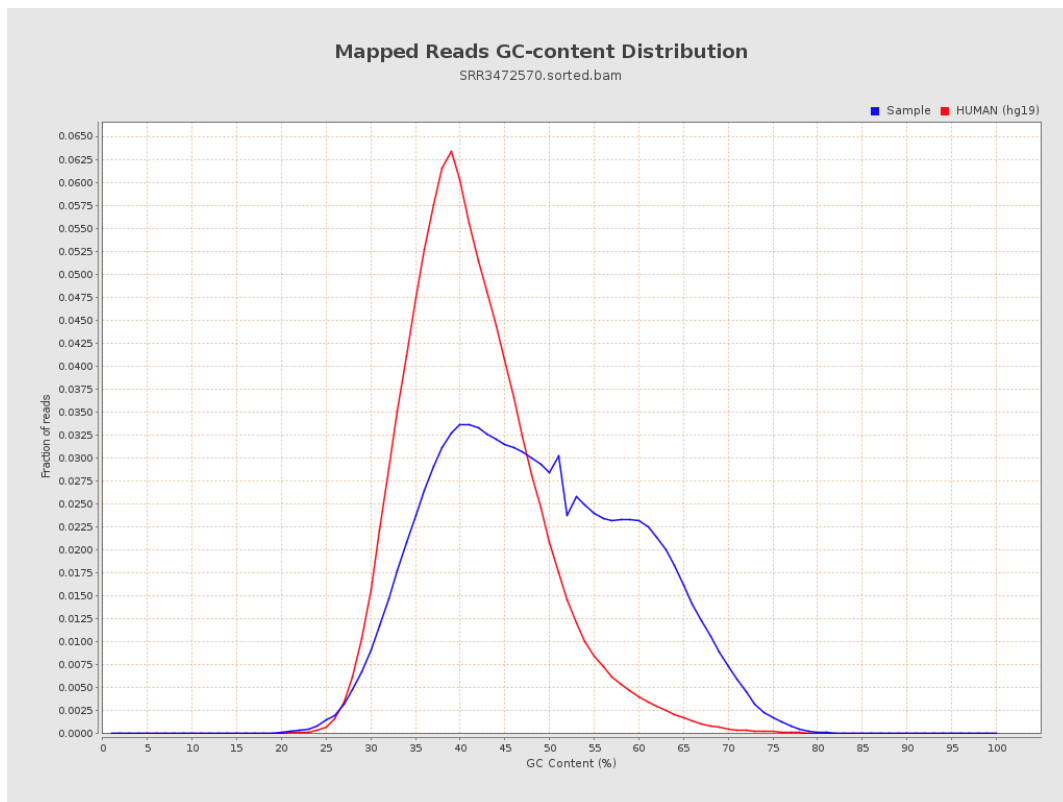
7. Results : Duplication Rate Histogram



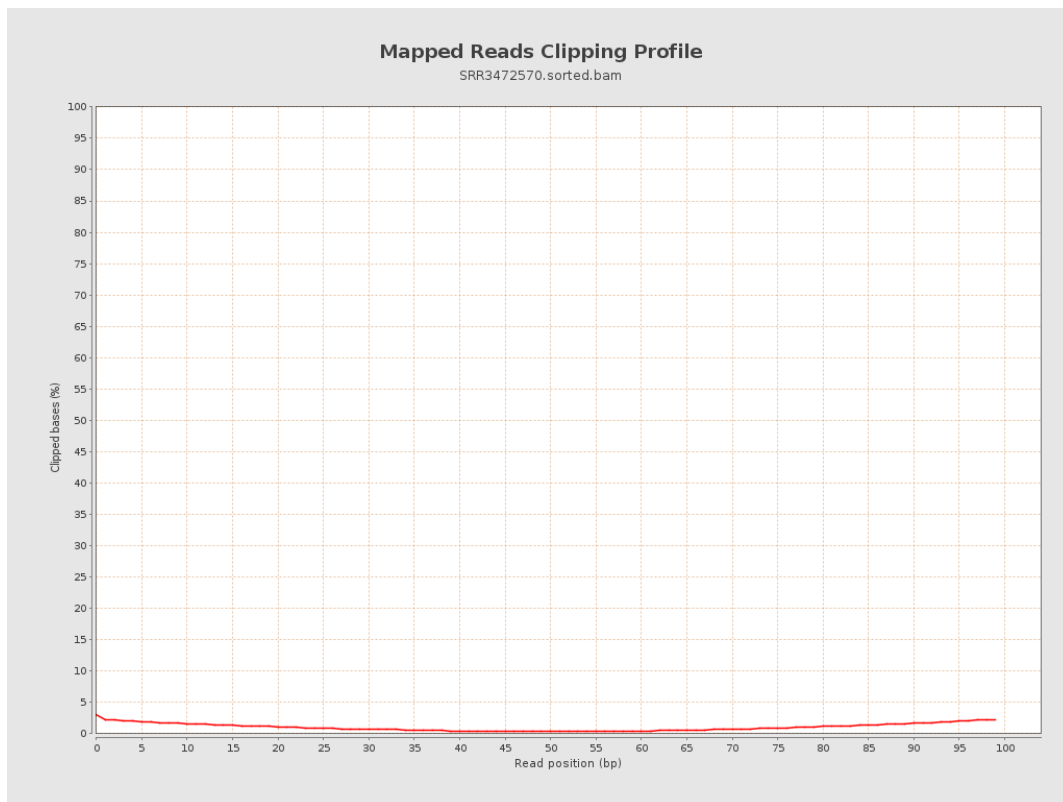
8. Results : Mapped Reads Nucleotide Content



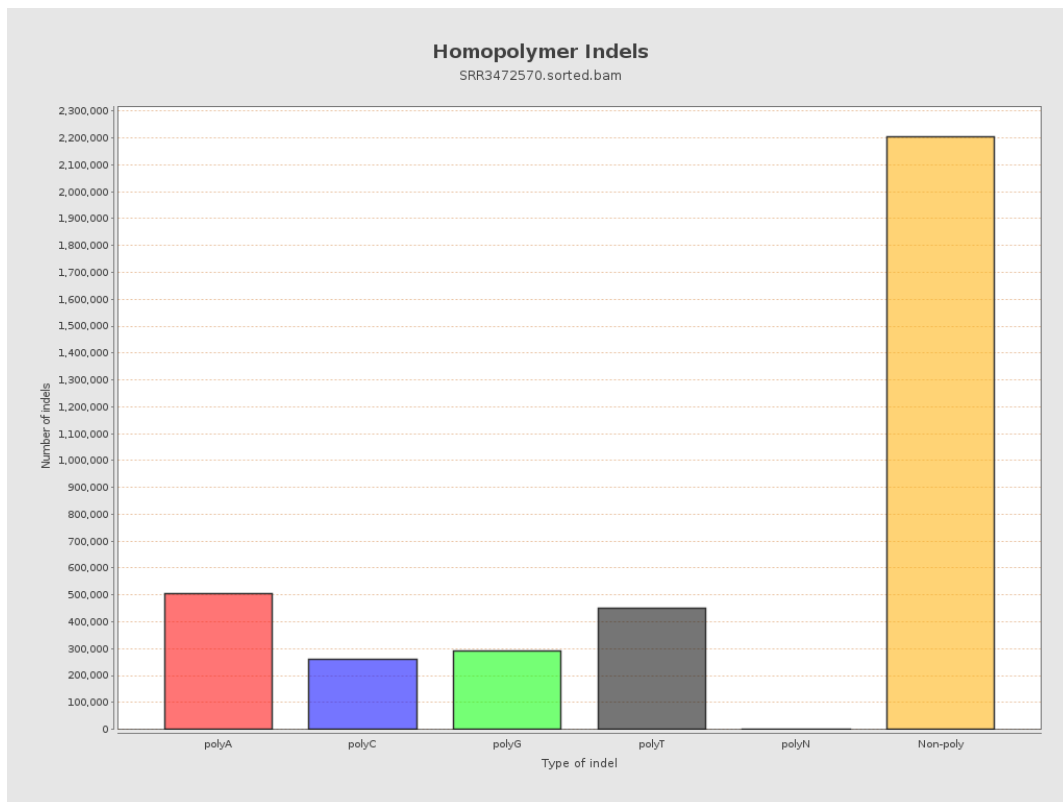
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



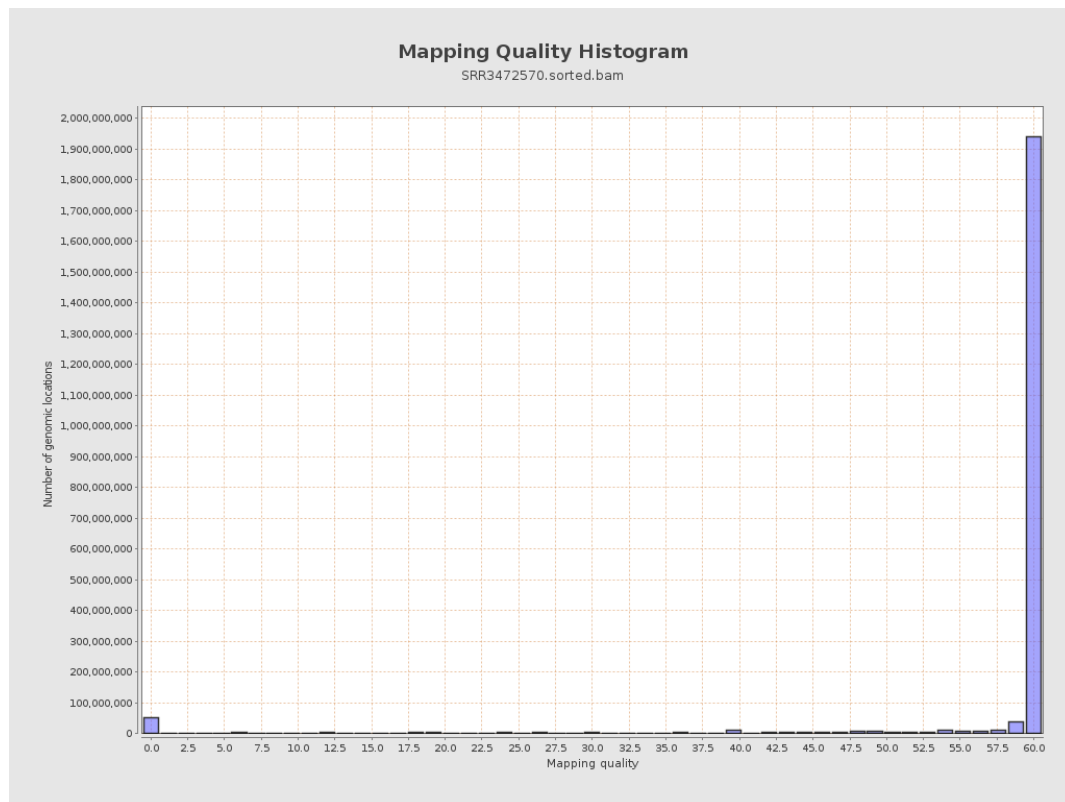
11. Results : Homopolymer Indels



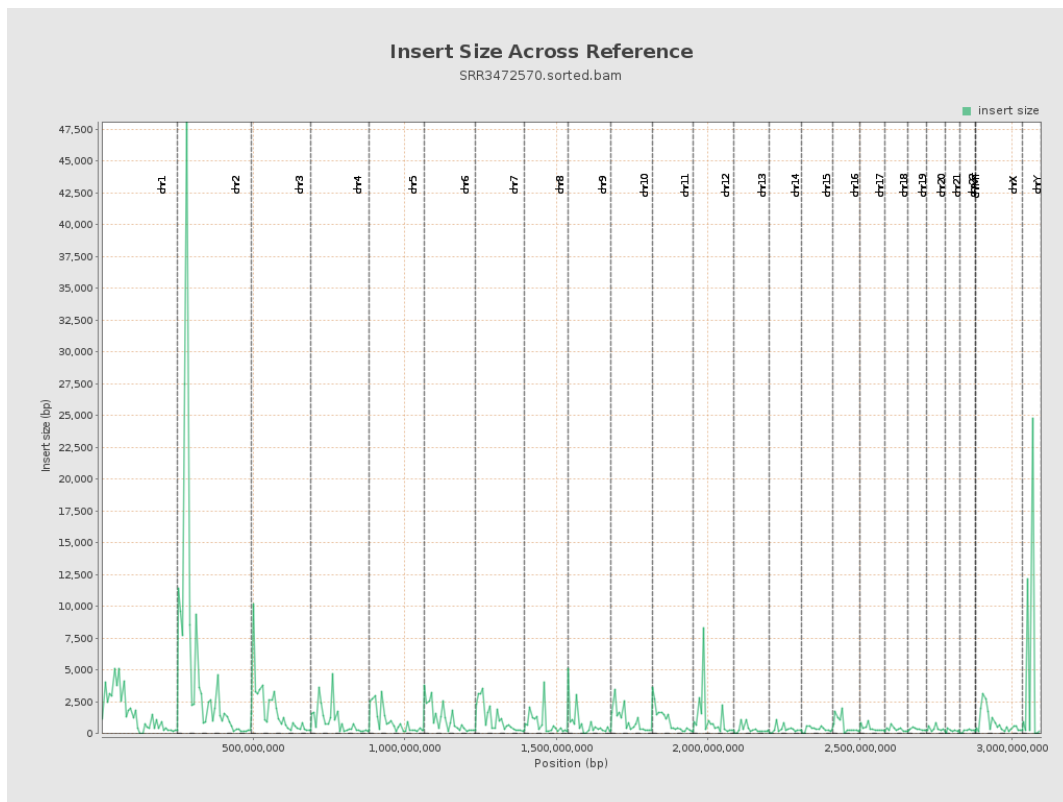
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

