

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 07:09:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR21672005.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_SRR21672005 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR21672005_1.fastq.gz SRR21672005_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 07:09:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR21672005.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	215,837,844
Mapped reads	214,920,994 / 99.58%
Unmapped reads	916,850 / 0.42%
Mapped paired reads	214,920,994 / 99.58%
Mapped reads, first in pair	107,469,316 / 49.79%
Mapped reads, second in pair	107,451,678 / 49.78%
Mapped reads, both in pair	214,601,436 / 99.43%
Mapped reads, singletons	319,558 / 0.15%
Secondary alignments	0
Supplementary alignments	861,478 / 0.4%
Read min/max/mean length	15 / 150 / 149.57
Duplicated reads (estimated)	62,315,134 / 28.87%
Duplication rate	26.57%
Clipped reads	9,765,470 / 4.52%

2.2. ACGT Content

Number/percentage of A's	9,412,856,965 / 29.55%
Number/percentage of C's	6,531,170,191 / 20.5%
Number/percentage of T's	9,357,906,057 / 29.37%
Number/percentage of G's	6,557,097,443 / 20.58%
Number/percentage of N's	137,253 / 0%

GC Percentage	41.08%
---------------	--------

2.3. Coverage

Mean	10.2955
Standard Deviation	116.2834

2.4. Mapping Quality

Mean Mapping Quality	54.46
----------------------	-------

2.5. Insert size

Mean	43,785.38
Standard Deviation	1,978,330.87
P25/Median/P75	326 / 380 / 435

2.6. Mismatches and indels

General error rate	0.61%
Mismatches	184,372,345
Insertions	4,320,396
Mapped reads with at least one insertion	1.91%
Deletions	4,671,337
Mapped reads with at least one deletion	2.09%
Homopolymer indels	45.96%

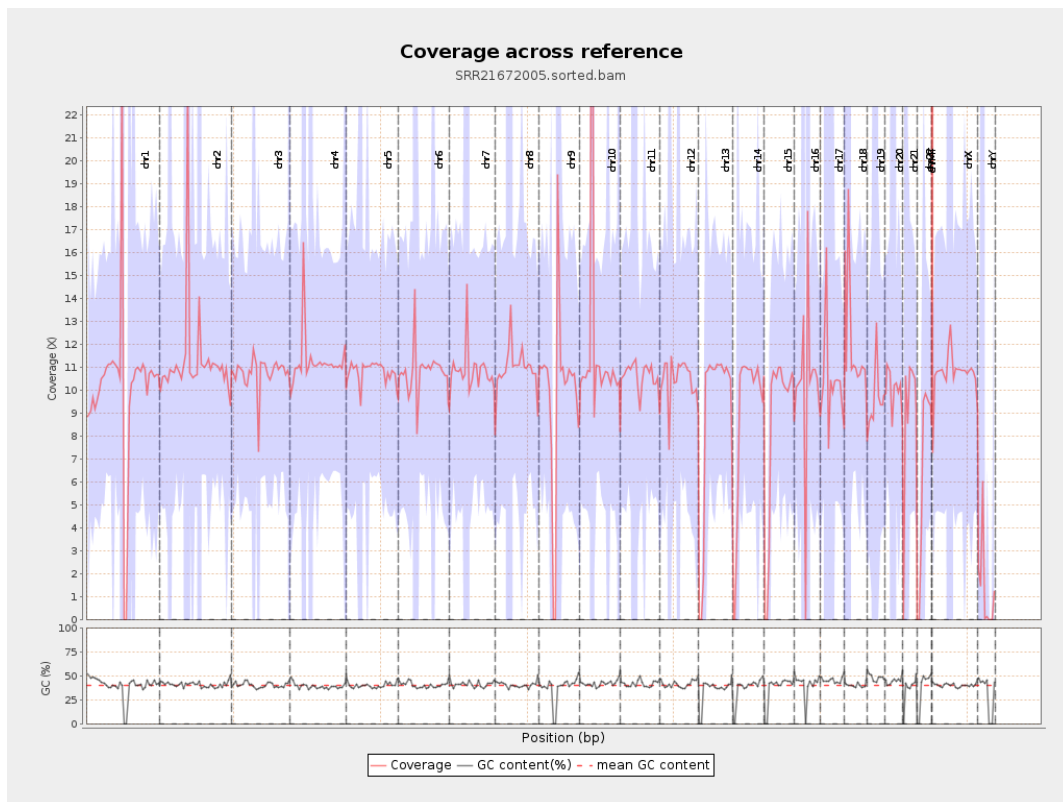
2.7. Chromosome stats

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

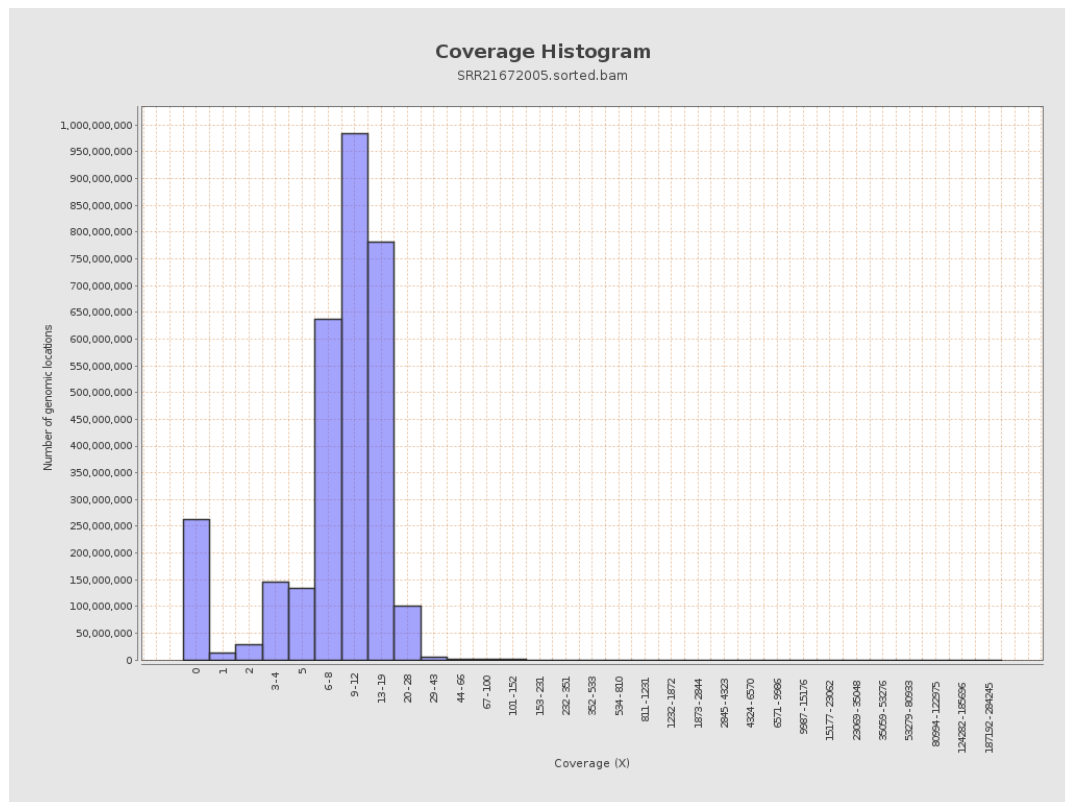
		bases	coverage	deviation
chr1	249250621	2548716608	10.2255	289.5109
chr2	243199373	2752831906	11.3192	74.7291
chr3	198022430	2129010115	10.7514	7.9065
chr4	191154276	2149882515	11.2468	58.5064
chr5	180915260	1949143833	10.7738	9.1417
chr6	171115067	1856012383	10.8466	41.0706
chr7	159138663	1727115004	10.8529	86.6483
chr8	146364022	1614384092	11.0299	95.3376
chr9	141213431	1366367569	9.6759	187.6848
chr10	135534747	1627709418	12.0095	209.3442
chr11	135006516	1430671589	10.5971	51.6526
chr12	133851895	1400661600	10.4643	9.2528
chr13	115169878	1044391921	9.0683	6.4892
chr14	107349540	960306960	8.9456	8.3574
chr15	102531392	867860281	8.4643	6.3207
chr16	90354753	927974296	10.2703	64.8959
chr17	81195210	838000310	10.3208	74.0621
chr18	78077248	925112298	11.8487	184.1468
chr19	59128983	566881699	9.5872	120.3768
chr20	63025520	632549509	10.0364	23.0798
chr21	48129895	444383508	9.233	30.8099
chr22	51304566	341799746	6.6622	8.0362
chrMT	16571	15798510	953.383	129.471
chrX	155270560	1674156617	10.7822	31.8712

chrY	59373566	80011354	1.3476	60.7208
------	----------	----------	--------	---------

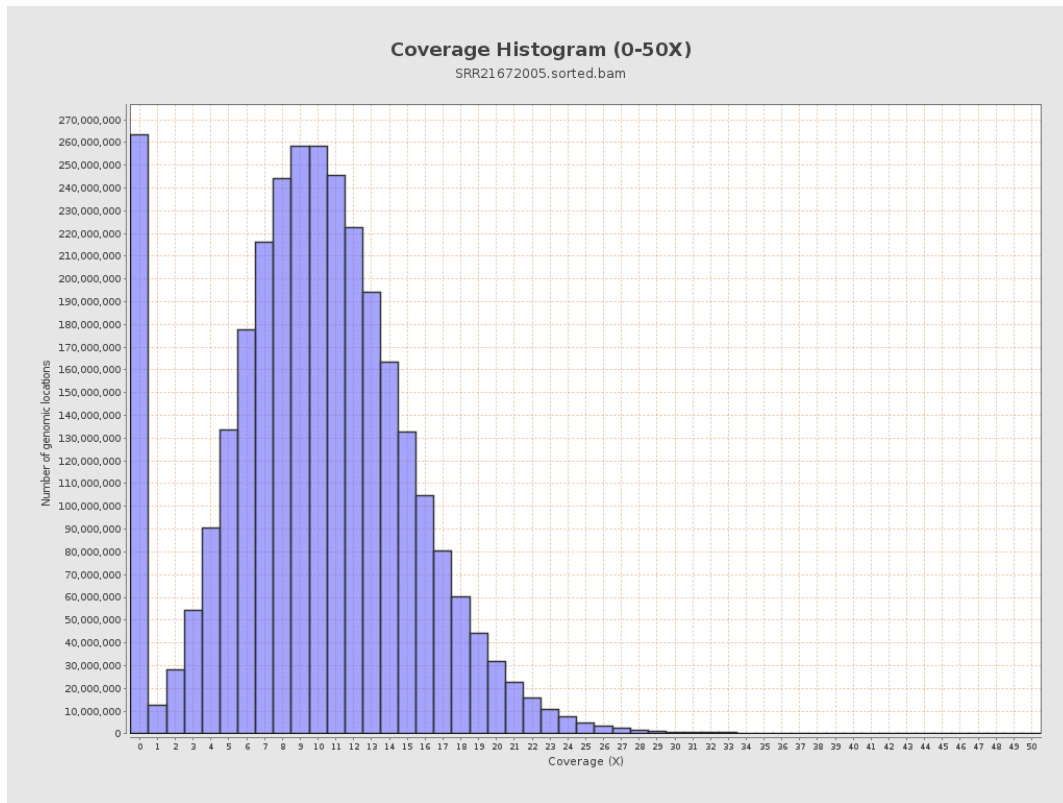
3. Results : Coverage across reference



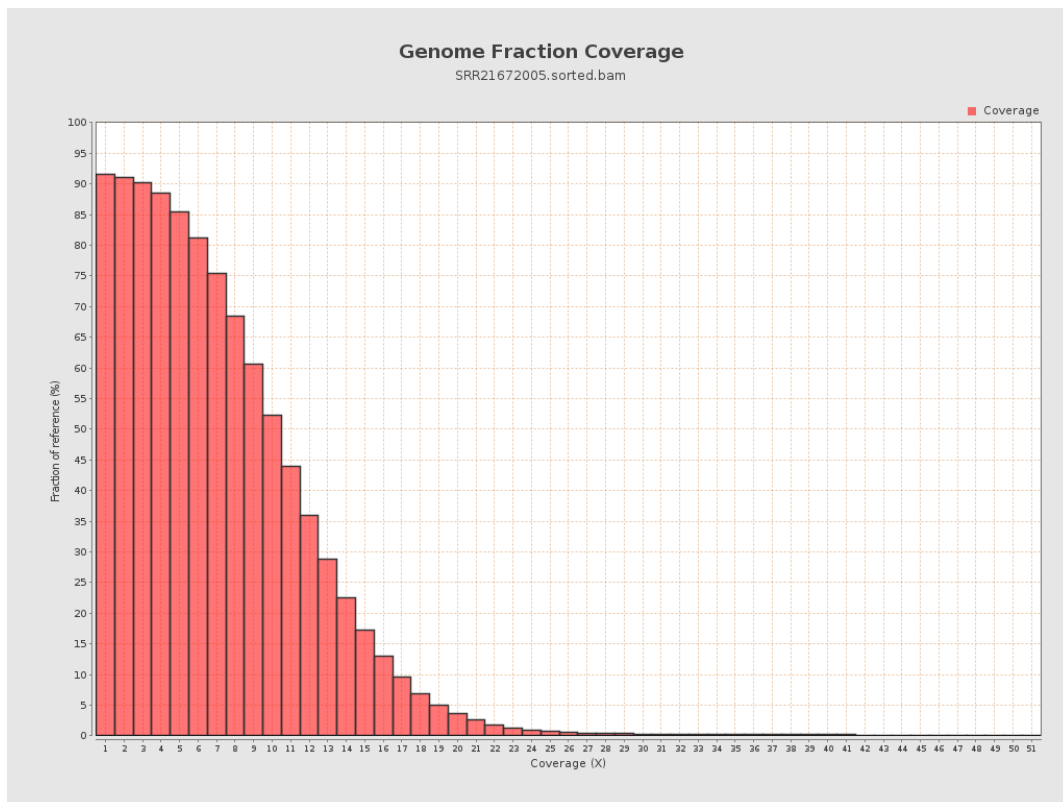
4. Results : Coverage Histogram



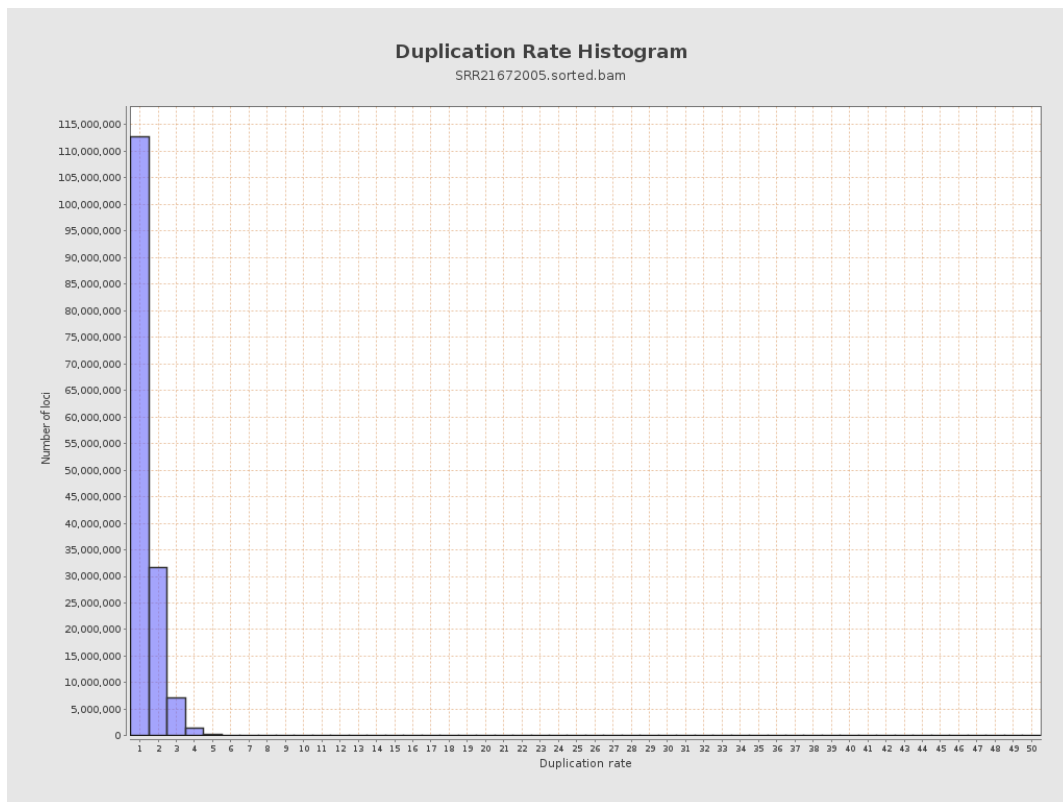
5. Results : Coverage Histogram (0-50X)



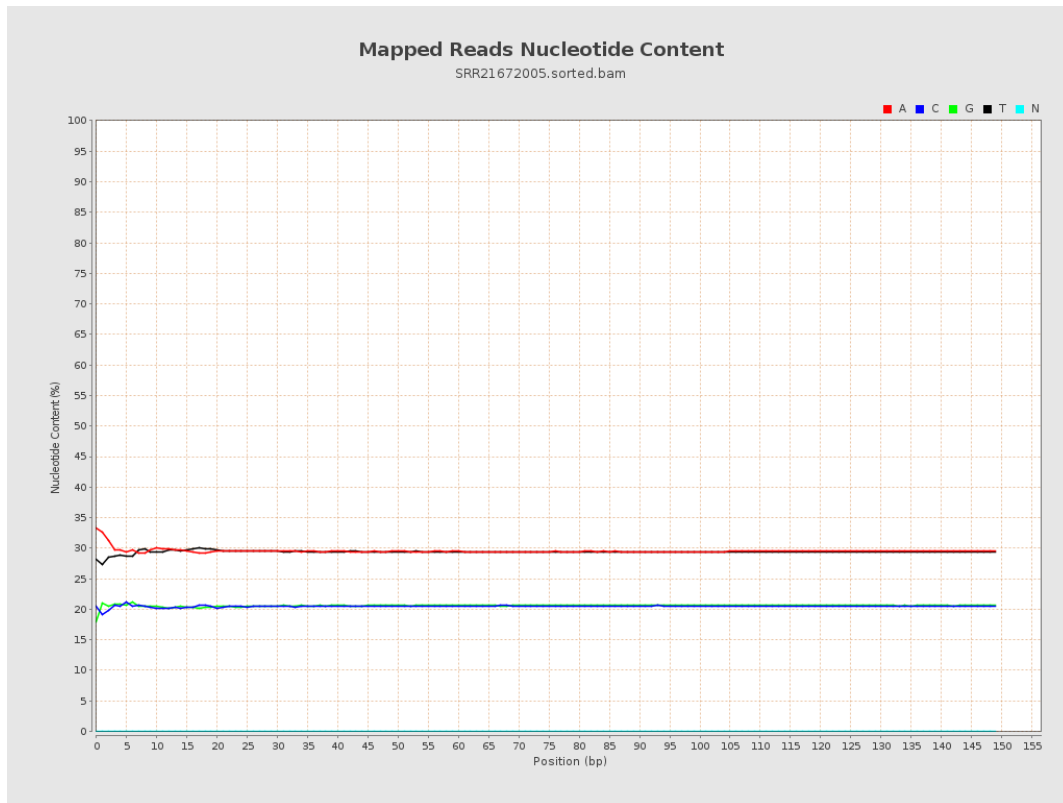
6. Results : Genome Fraction Coverage



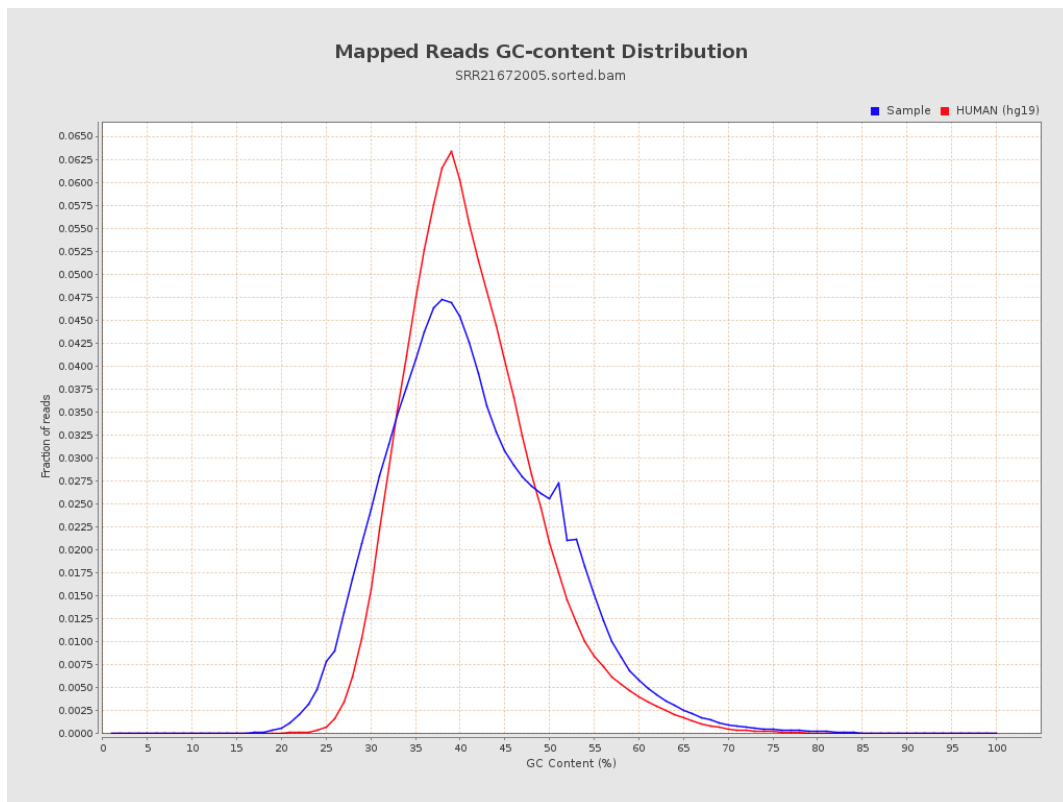
7. Results : Duplication Rate Histogram



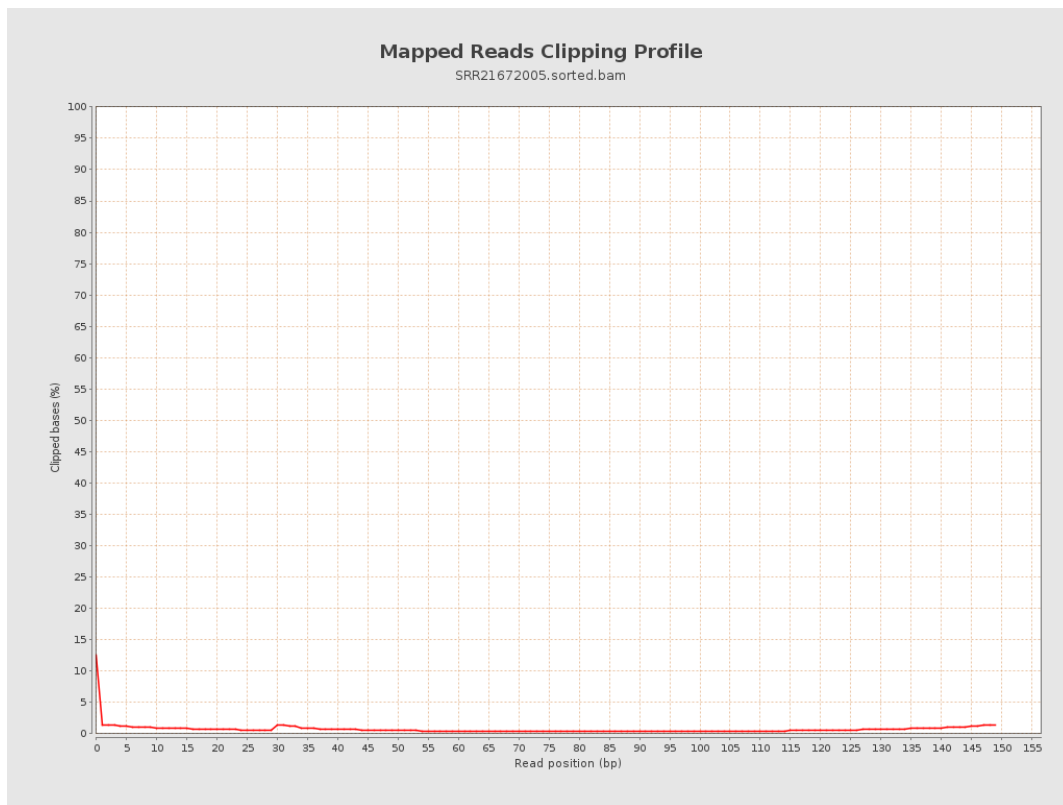
8. Results : Mapped Reads Nucleotide Content



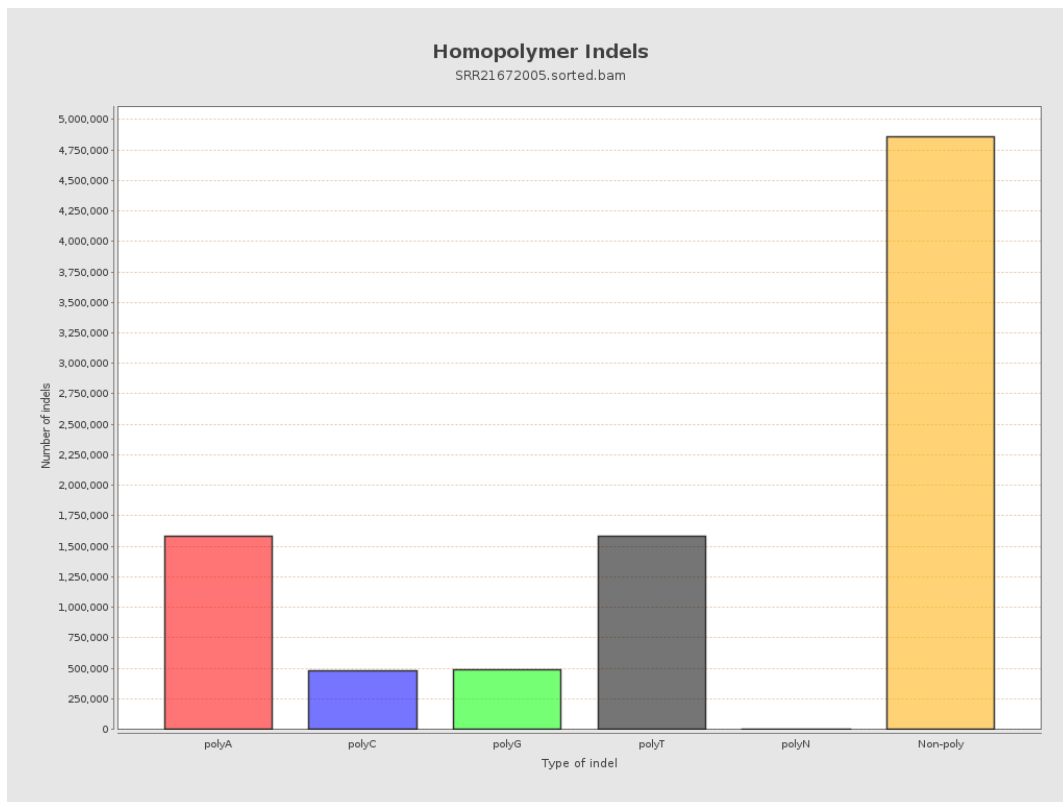
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



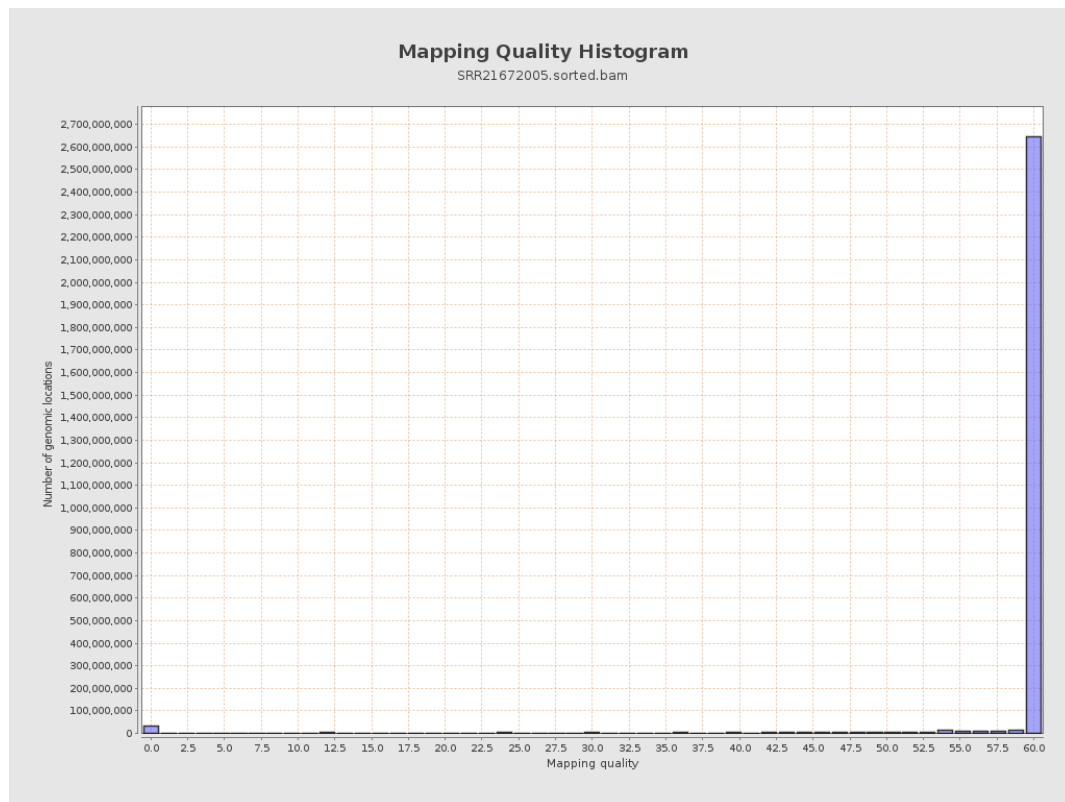
11. Results : Homopolymer Indels



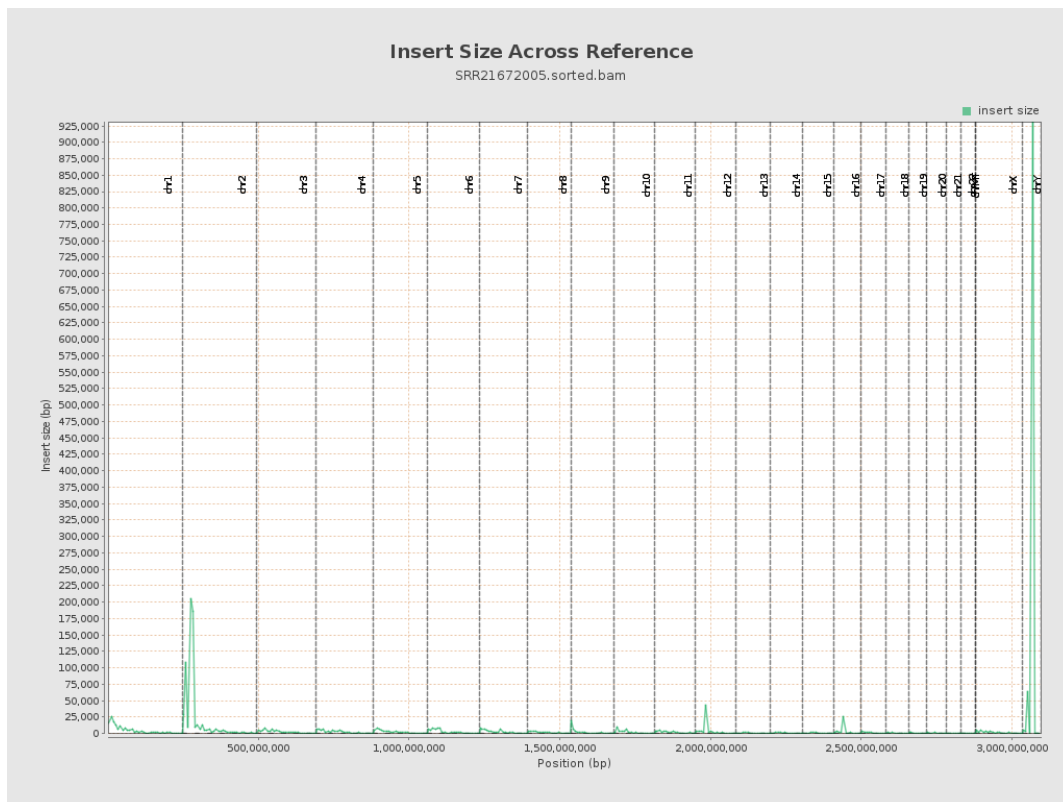
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

