

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/18 17:50:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618593.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_SRR618593 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618593_1.fastq.gz SRR618593_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jan 18 17:50:28 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618593.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	58,099,888
Mapped reads	53,850,682 / 92.69%
Unmapped reads	4,249,206 / 7.31%
Mapped paired reads	53,850,682 / 92.69%
Mapped reads, first in pair	27,261,368 / 46.92%
Mapped reads, second in pair	26,589,314 / 45.76%
Mapped reads, both in pair	52,524,080 / 90.4%
Mapped reads, singletons	1,326,602 / 2.28%
Secondary alignments	0
Supplementary alignments	341,085 / 0.59%
Read min/max/mean length	30 / 101 / 100.24
Duplicated reads (estimated)	16,084,319 / 27.68%
Duplication rate	25.45%
Clipped reads	14,485,369 / 24.93%

2.2. ACGT Content

Number/percentage of A's	1,377,380,633 / 27.24%
Number/percentage of C's	1,095,058,411 / 21.66%
Number/percentage of T's	1,394,483,029 / 27.58%
Number/percentage of G's	1,188,592,734 / 23.51%
Number/percentage of N's	239,328 / 0%

GC Percentage	45.17%
---------------	--------

2.3. Coverage

Mean	1.6344
Standard Deviation	6.2476

2.4. Mapping Quality

Mean Mapping Quality	53.32
----------------------	-------

2.5. Insert size

Mean	135,163.7
Standard Deviation	3,666,588.02
P25/Median/P75	182 / 211 / 252

2.6. Mismatches and indels

General error rate	1.62%
Mismatches	80,401,237
Insertions	966,563
Mapped reads with at least one insertion	1.77%
Deletions	2,958,760
Mapped reads with at least one deletion	5.34%
Homopolymer indels	53.23%

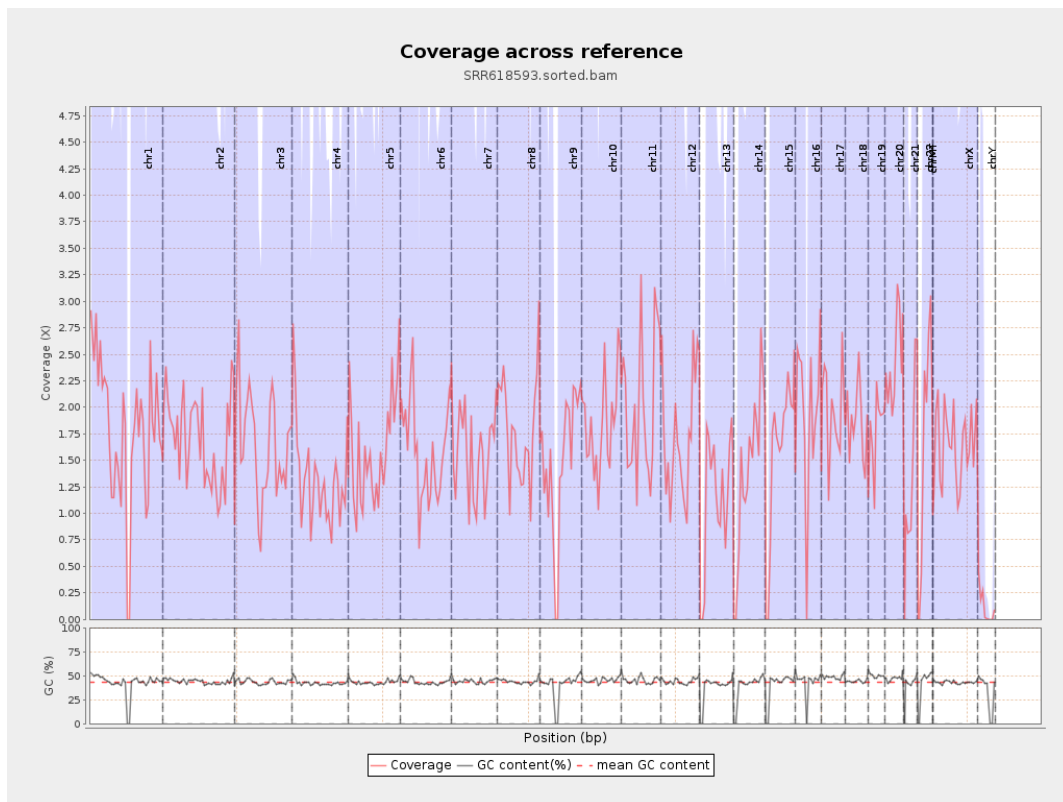
2.7. Chromosome stats

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

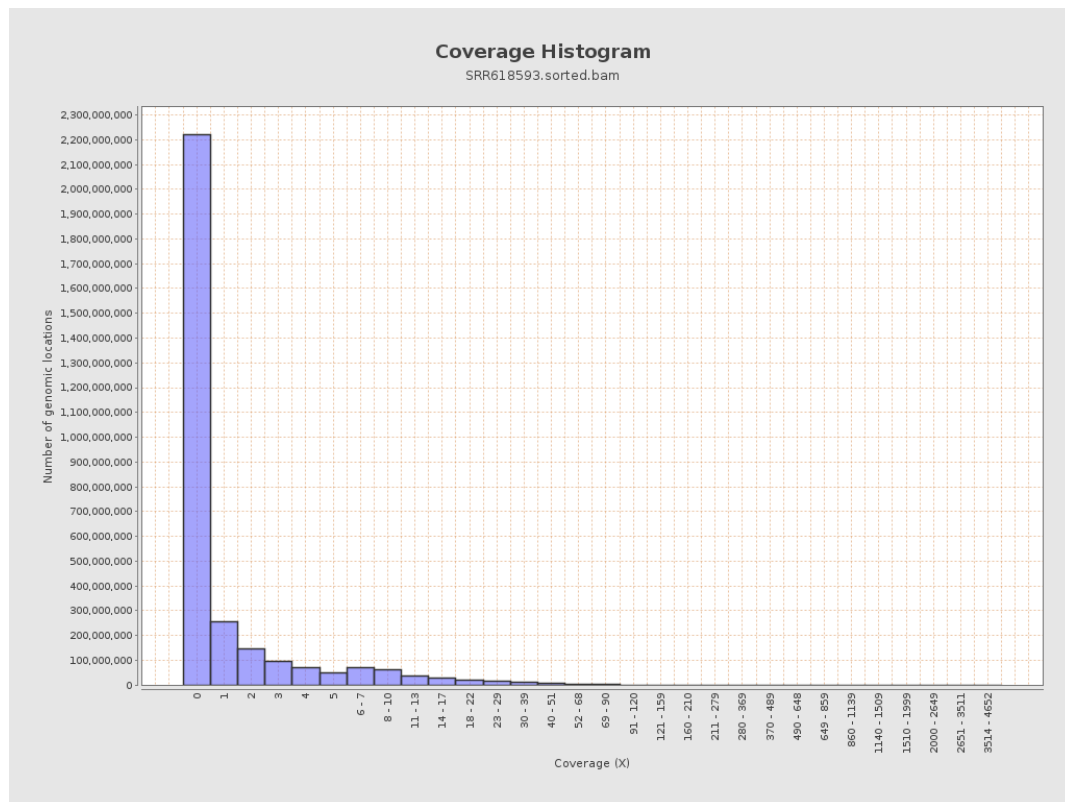
		bases	coverage	deviation
chr1	249250621	441633310	1.7718	7.9797
chr2	243199373	414526770	1.7045	6.3985
chr3	198022430	322467052	1.6284	5.0948
chr4	191154276	252623390	1.3216	4.9826
chr5	180915260	291096193	1.609	5.036
chr6	171115067	270639712	1.5816	6.1611
chr7	159138663	251482259	1.5803	5.2409
chr8	146364022	259576689	1.7735	5.5355
chr9	141213431	207795081	1.4715	7.4798
chr10	135534747	247558250	1.8265	5.8836
chr11	135006516	271876847	2.0138	7.8545
chr12	133851895	231900653	1.7325	6.2217
chr13	115169878	131198134	1.1392	4.0501
chr14	107349540	153572779	1.4306	4.9702
chr15	102531392	159677801	1.5574	5.5596
chr16	90354753	174299670	1.9291	7.6993
chr17	81195210	160636358	1.9784	7.0266
chr18	78077248	144459875	1.8502	8.3576
chr19	59128983	105379549	1.7822	6.8272
chr20	63025520	153050870	2.4284	7.3657
chr21	48129895	66221448	1.3759	8.2971
chr22	51304566	85020644	1.6572	6.3547
chrMT	16571	16202	0.9777	3.9965
chrX	155270560	256240011	1.6503	5.2822

chrY	59373566	6761301	0.1139	2.4703
------	----------	---------	--------	--------

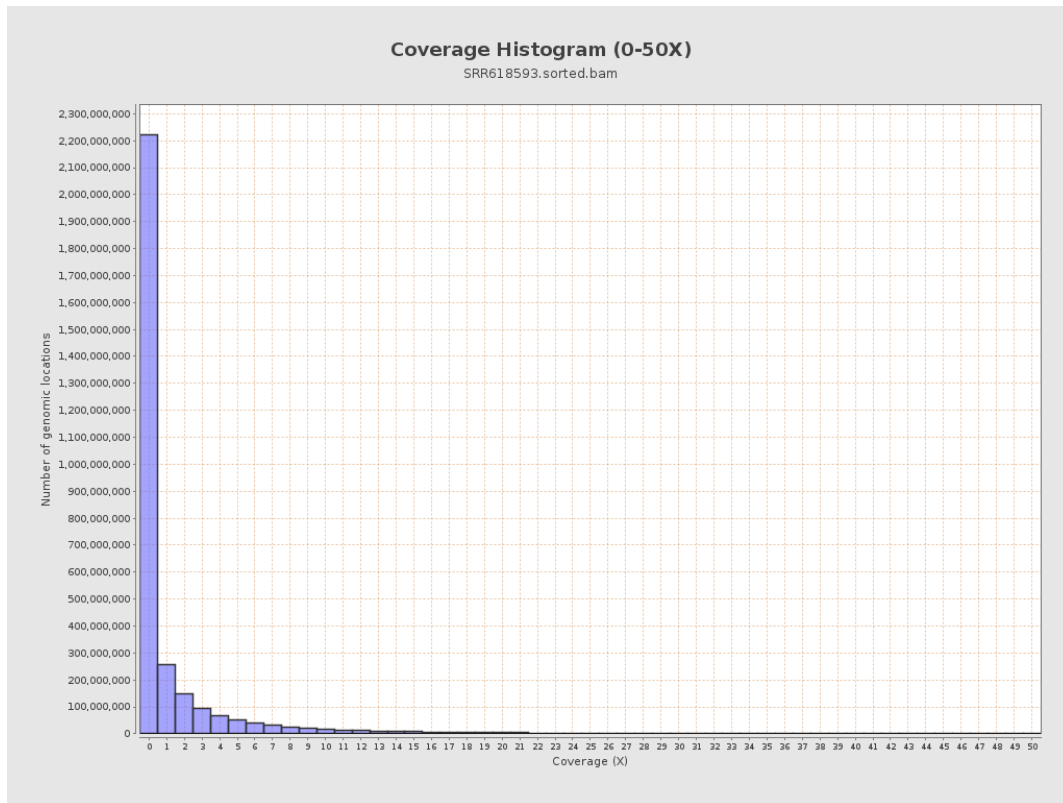
3. Results : Coverage across reference



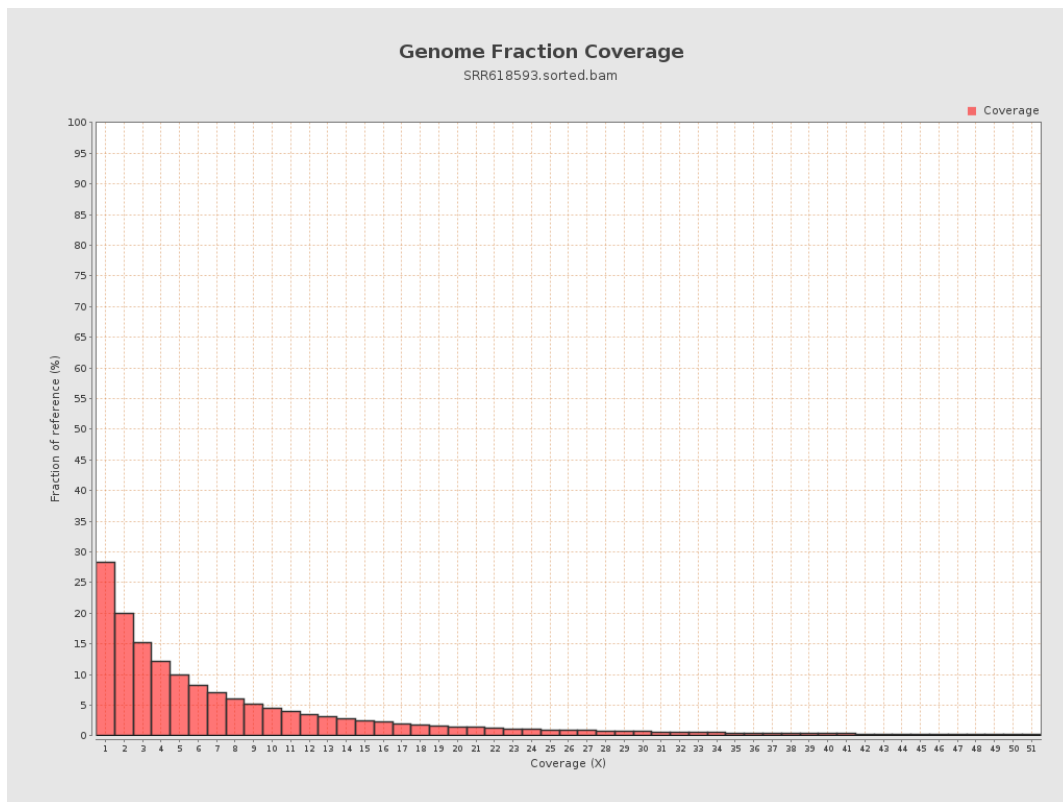
4. Results : Coverage Histogram



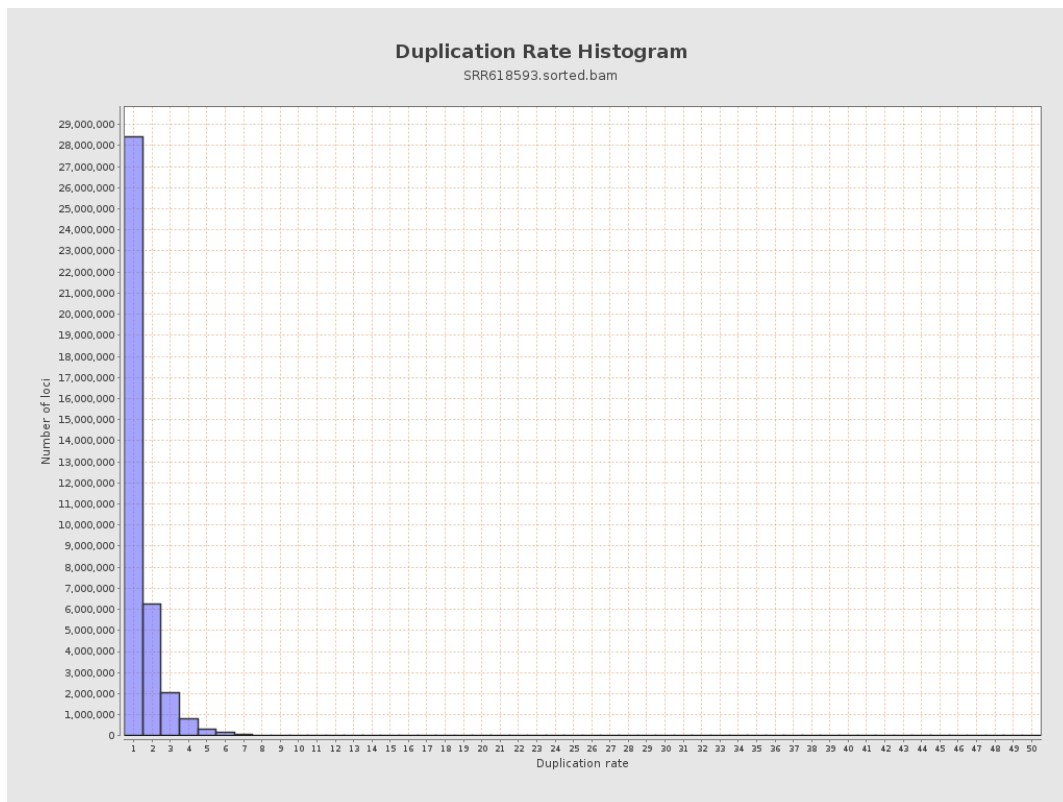
5. Results : Coverage Histogram (0-50X)



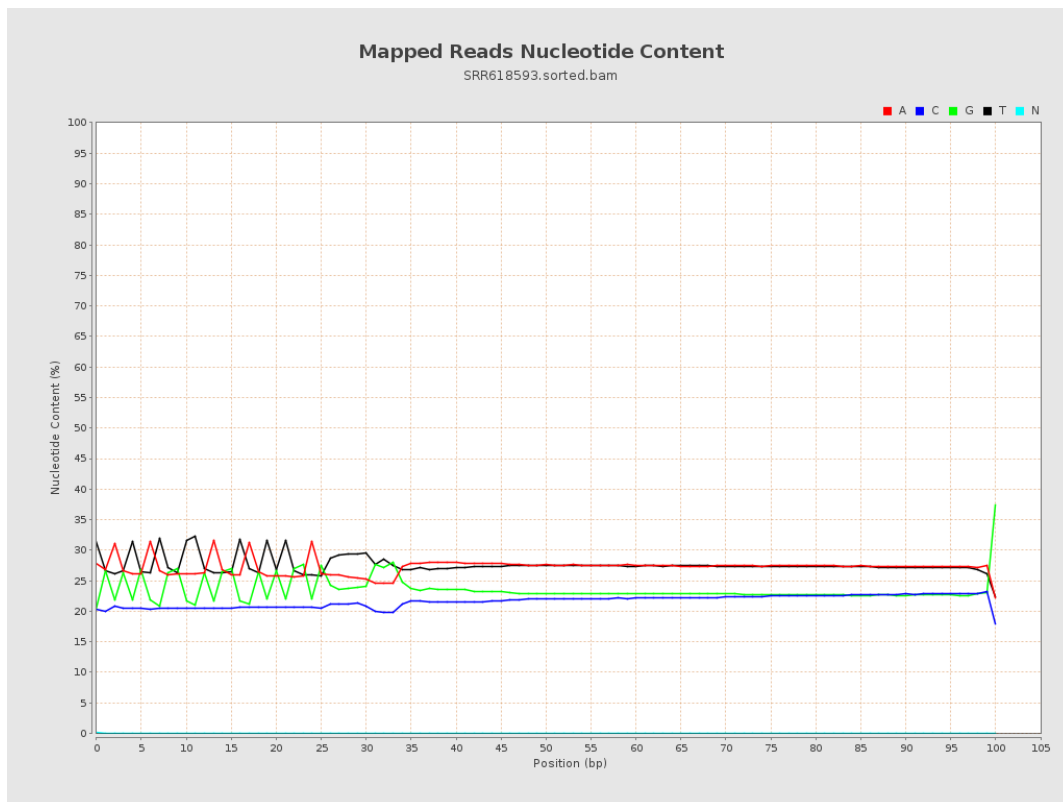
6. Results : Genome Fraction Coverage



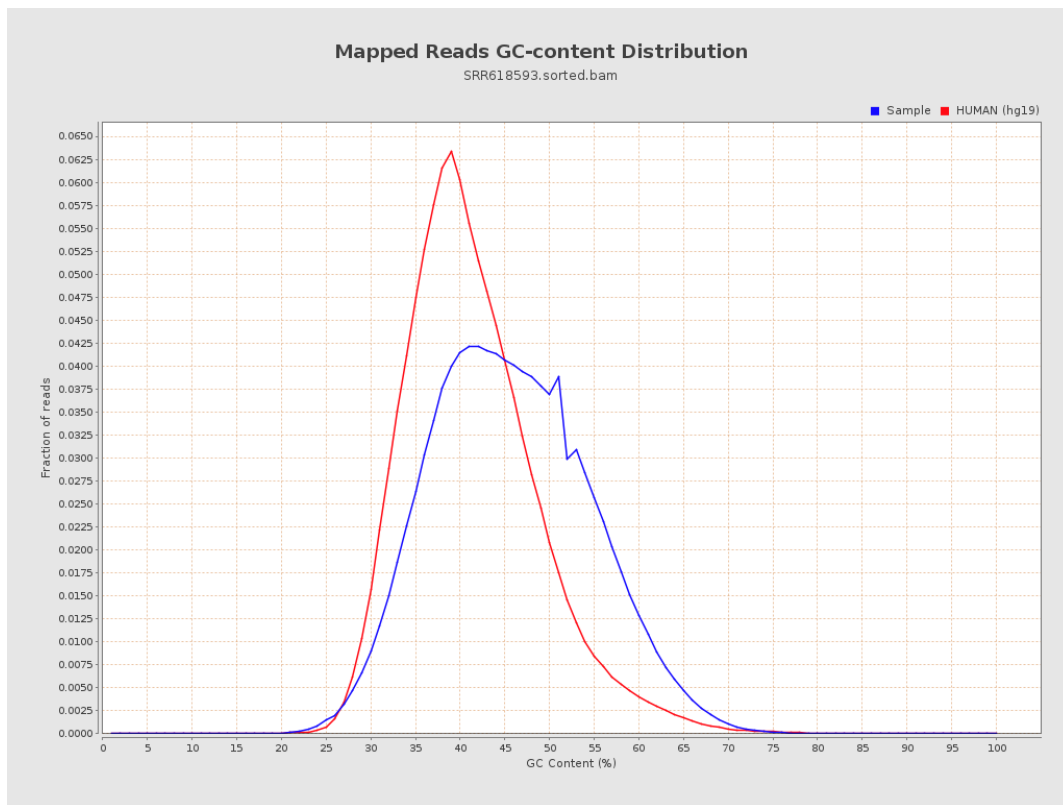
7. Results : Duplication Rate Histogram



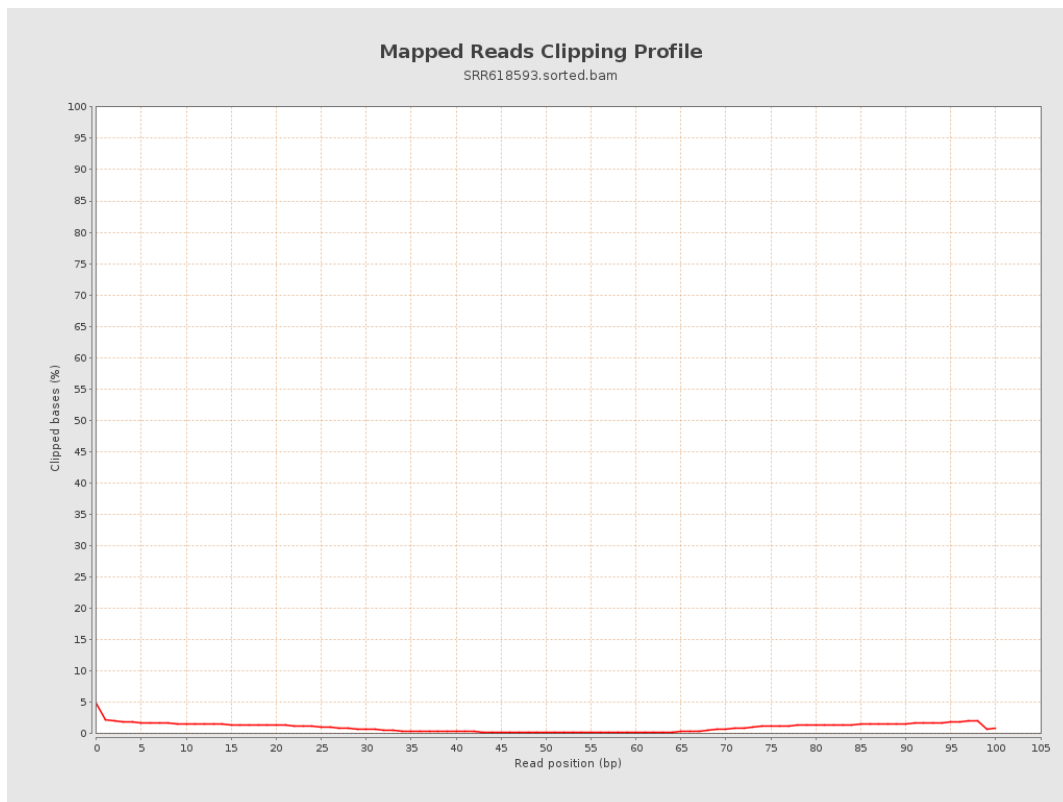
8. Results : Mapped Reads Nucleotide Content



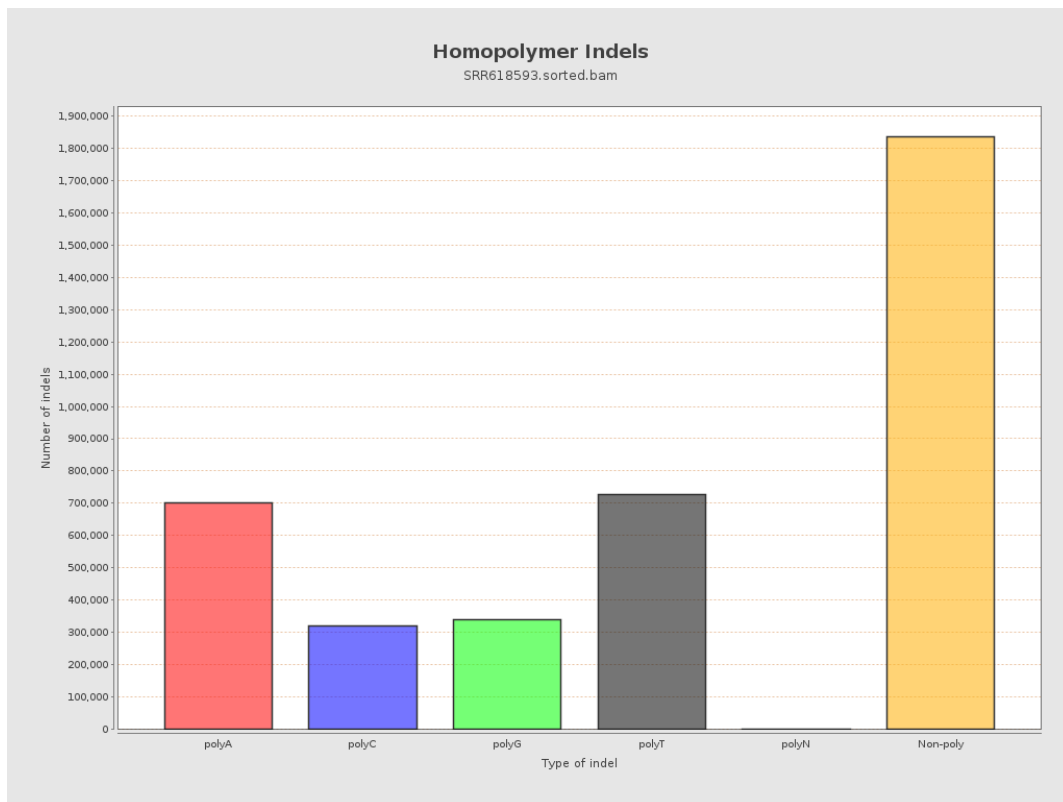
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



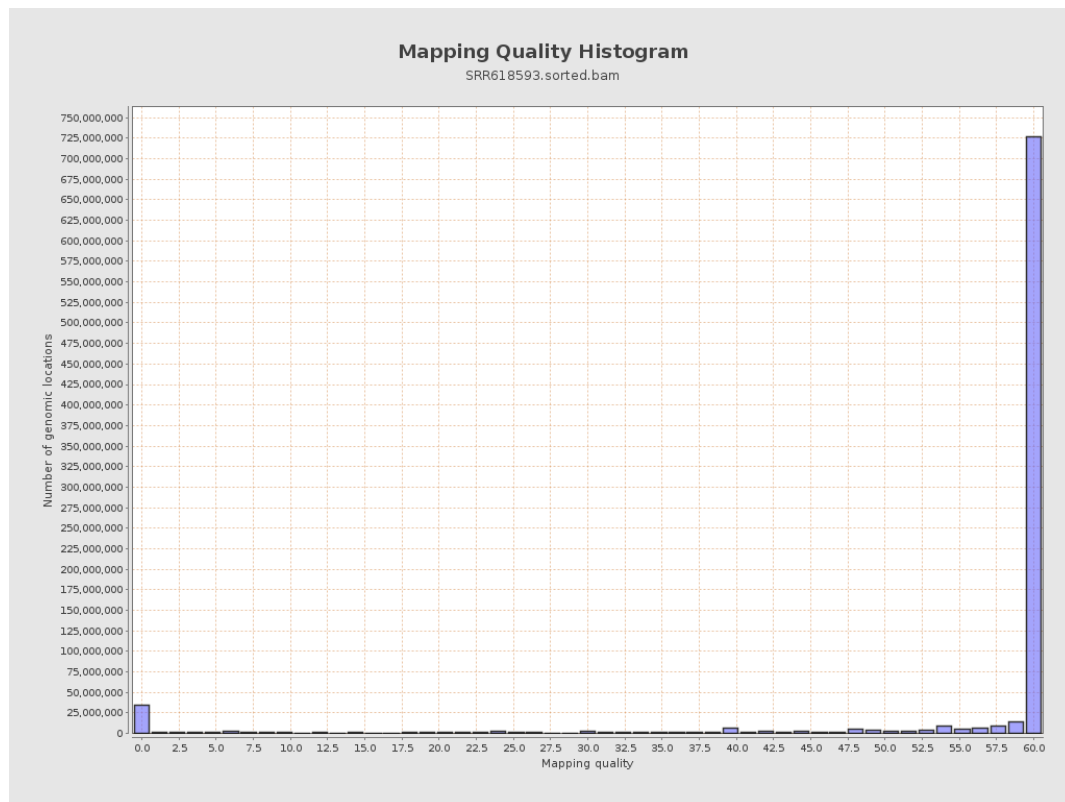
11. Results : Homopolymer Indels



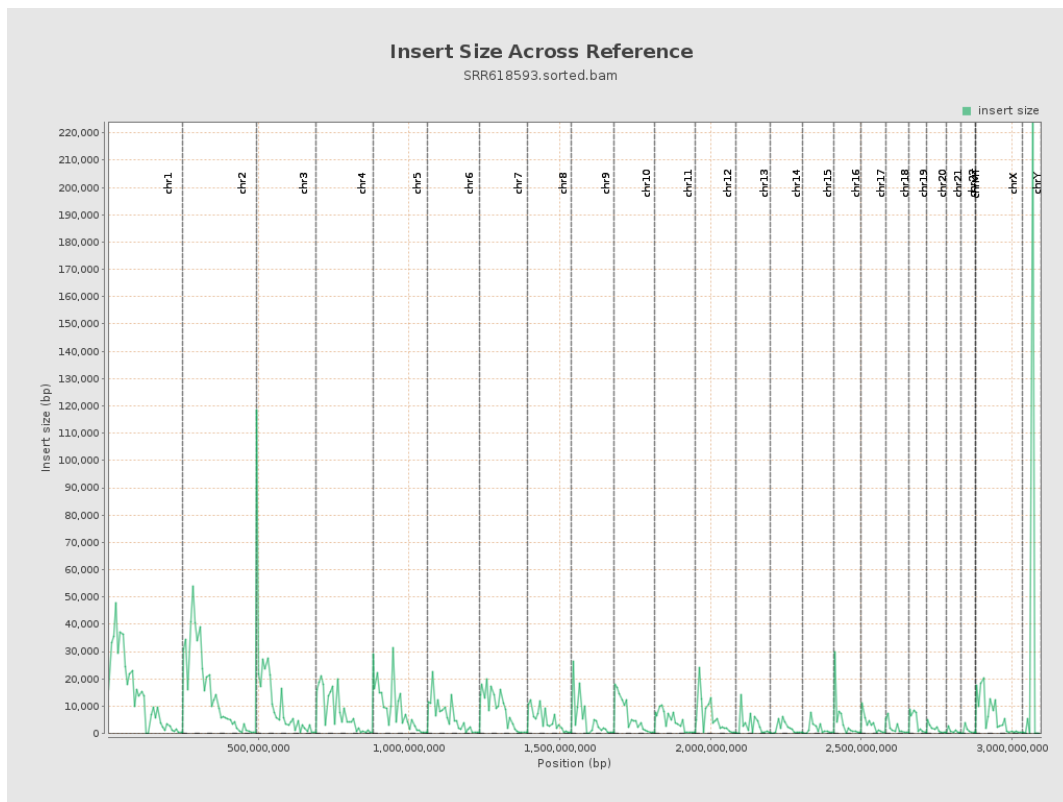
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

