

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/22 23:43:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR630584.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_SRR630584 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR630584_1.fastq.gz SRR630584_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Jan 22 23:43:42 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR630584.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	34,132,770
Mapped reads	33,809,245 / 99.05%
Unmapped reads	323,525 / 0.95%
Mapped paired reads	33,809,245 / 99.05%
Mapped reads, first in pair	16,961,770 / 49.69%
Mapped reads, second in pair	16,847,475 / 49.36%
Mapped reads, both in pair	33,628,928 / 98.52%
Mapped reads, singletons	180,317 / 0.53%
Secondary alignments	0
Supplementary alignments	72,258 / 0.21%
Read min/max/mean length	30 / 101 / 101.08
Duplicated reads (estimated)	3,479,497 / 10.19%
Duplication rate	8.21%
Clipped reads	5,033,807 / 14.75%

2.2. ACGT Content

Number/percentage of A's	958,520,153 / 29.29%
Number/percentage of C's	645,940,078 / 19.74%
Number/percentage of T's	971,724,432 / 29.7%
Number/percentage of G's	695,745,850 / 21.26%
Number/percentage of N's	371,691 / 0.01%

GC Percentage	41%
---------------	-----

2.3. Coverage

Mean	1.0578
Standard Deviation	4.2684

2.4. Mapping Quality

Mean Mapping Quality	54.06
----------------------	-------

2.5. Insert size

Mean	33,040.39
Standard Deviation	1,790,946.42
P25/Median/P75	185 / 231 / 295

2.6. Mismatches and indels

General error rate	0.9%
Mismatches	28,616,100
Insertions	592,920
Mapped reads with at least one insertion	1.72%
Deletions	1,732,409
Mapped reads with at least one deletion	4.99%
Homopolymer indels	54.23%

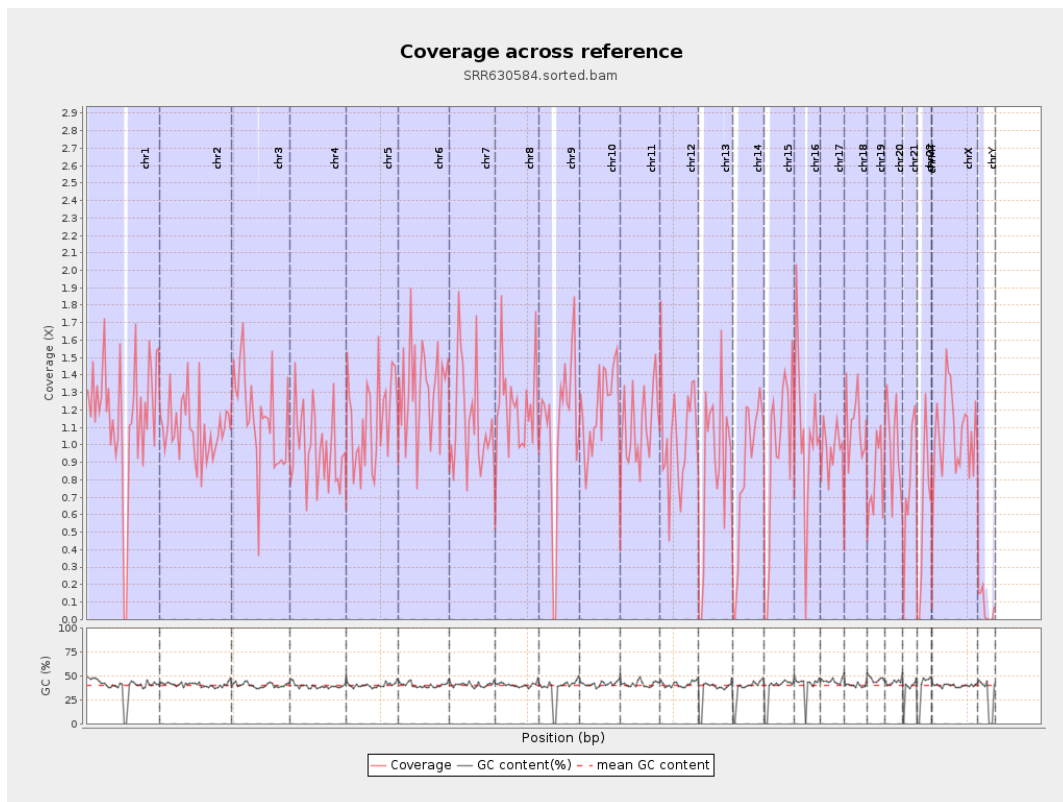
2.7. Chromosome stats

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

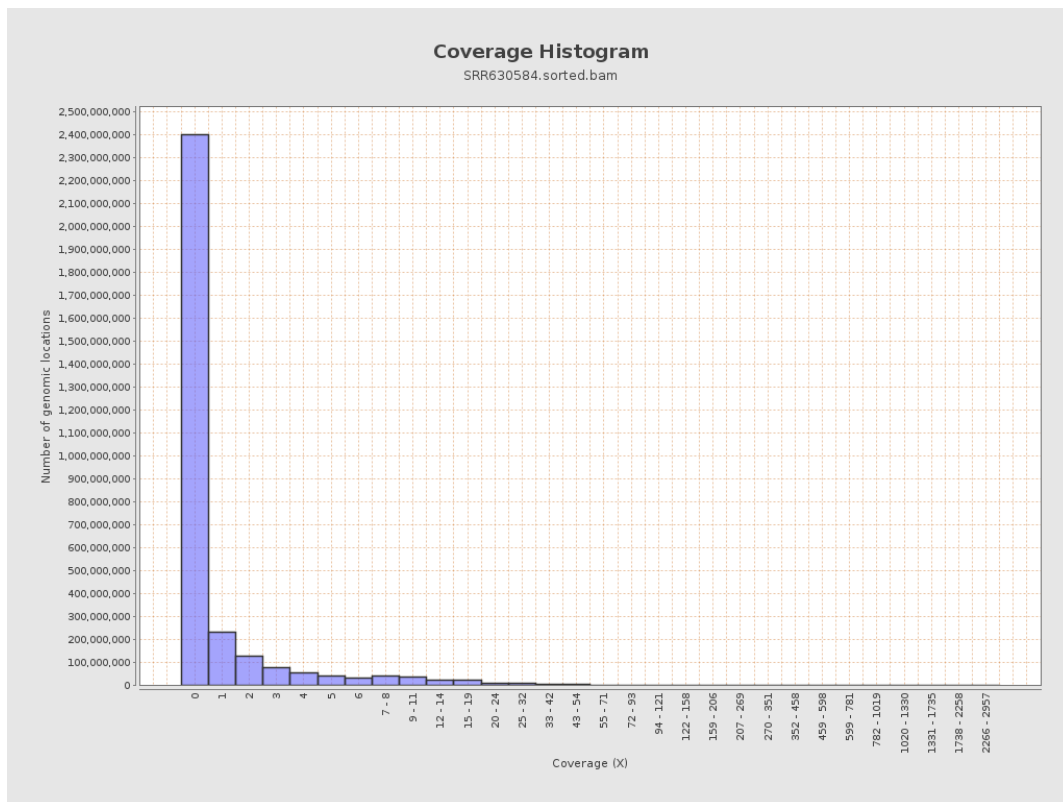
		bases	coverage	deviation
chr1	249250621	292211946	1.1724	5.0384
chr2	243199373	265243635	1.0906	5.1095
chr3	198022430	227597611	1.1494	3.6464
chr4	191154276	188229186	0.9847	4.0815
chr5	180915260	205296373	1.1348	3.6556
chr6	171115067	229099210	1.3389	4.8622
chr7	159138663	179096152	1.1254	3.8228
chr8	146364022	180156736	1.2309	3.9198
chr9	141213431	153861036	1.0896	5.5357
chr10	135534747	164427253	1.2132	4.2505
chr11	135006516	148531397	1.1002	5.3614
chr12	133851895	139640620	1.0432	3.5991
chr13	115169878	101398867	0.8804	3.17
chr14	107349540	91309412	0.8506	3.2413
chr15	102531392	97970451	0.9555	3.396
chr16	90354753	94245214	1.0431	4.8434
chr17	81195210	76501106	0.9422	3.7871
chr18	78077248	88454873	1.1329	5.2921
chr19	59128983	47218661	0.7986	3.4875
chr20	63025520	63399411	1.0059	3.7317
chr21	48129895	39098861	0.8124	3.9389
chr22	51304566	31669335	0.6173	2.6873
chrMT	16571	890	0.0537	0.3062
chrX	155270560	165847999	1.0681	3.9182

chrY	59373566	4135129	0.0696	2.3491
------	----------	---------	--------	--------

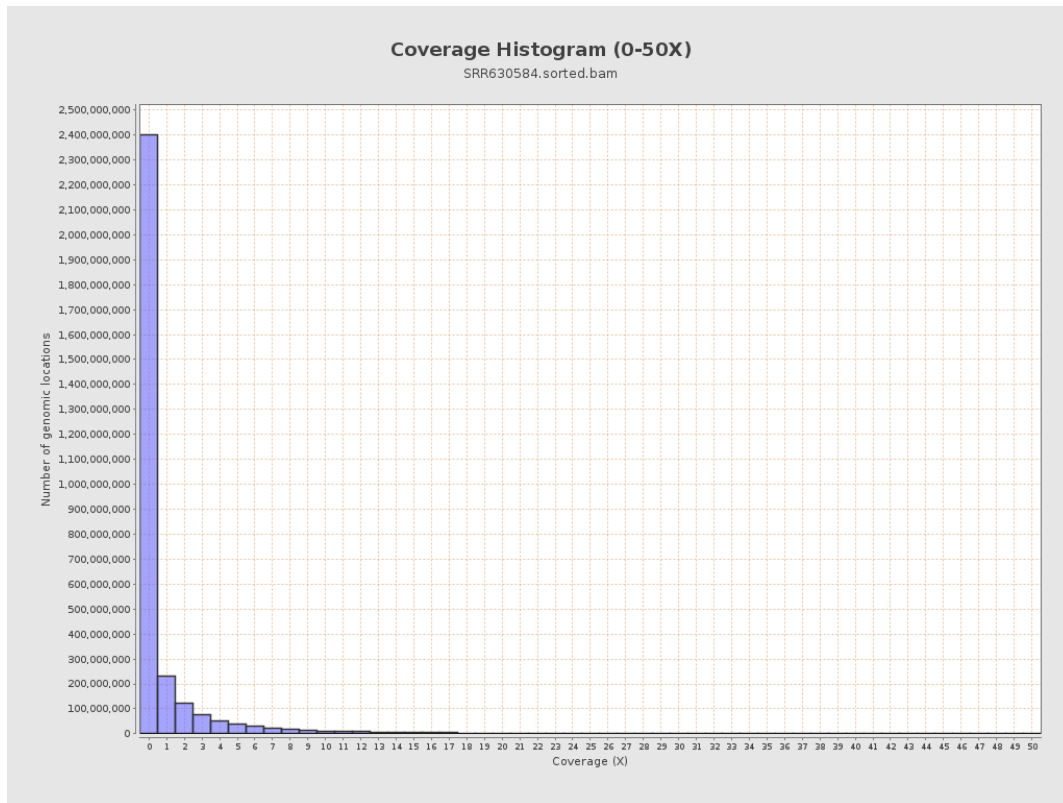
3. Results : Coverage across reference



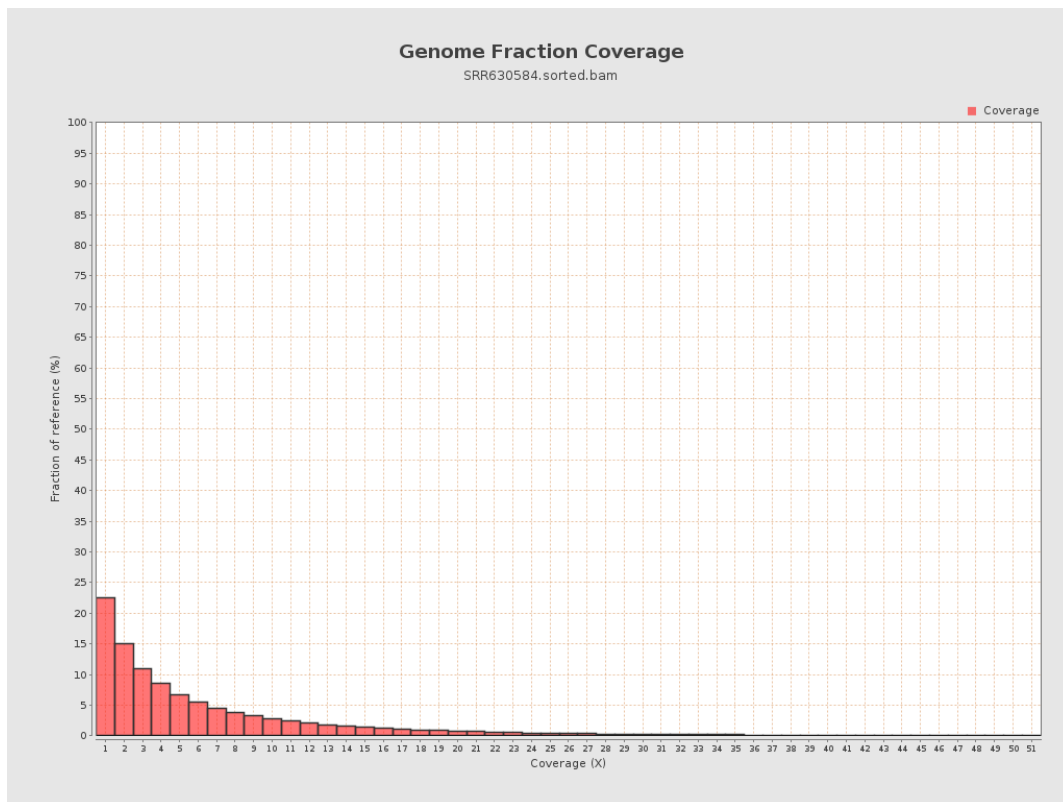
4. Results : Coverage Histogram



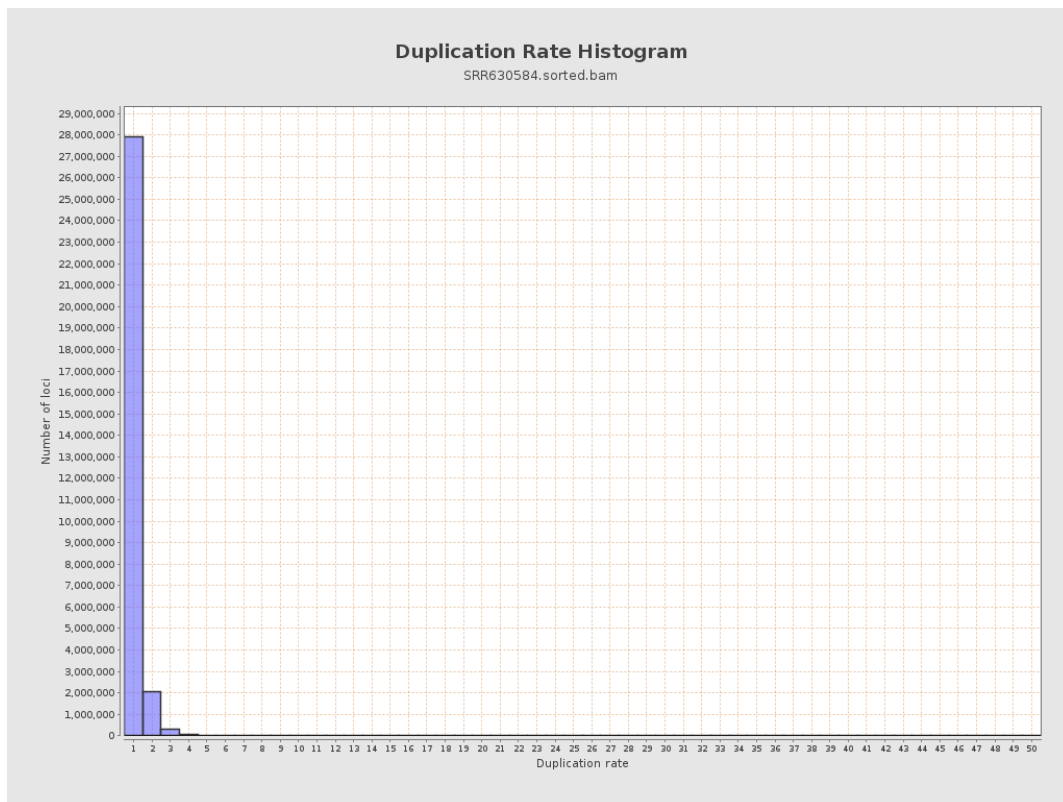
5. Results : Coverage Histogram (0-50X)



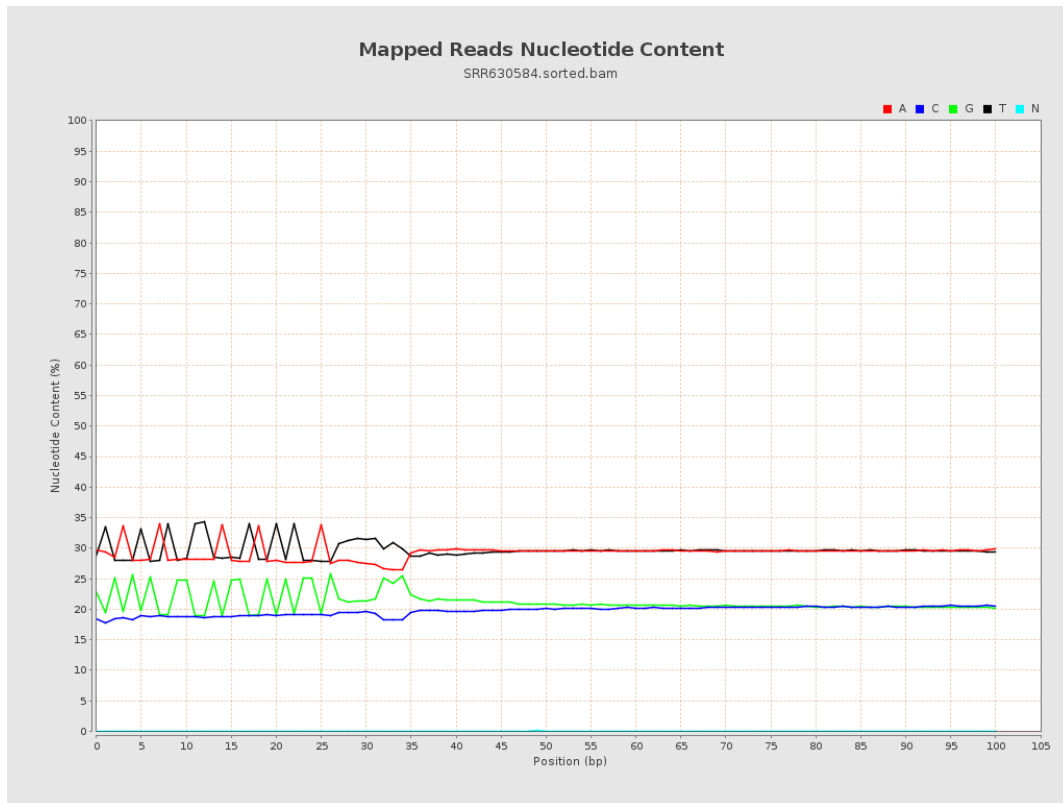
6. Results : Genome Fraction Coverage



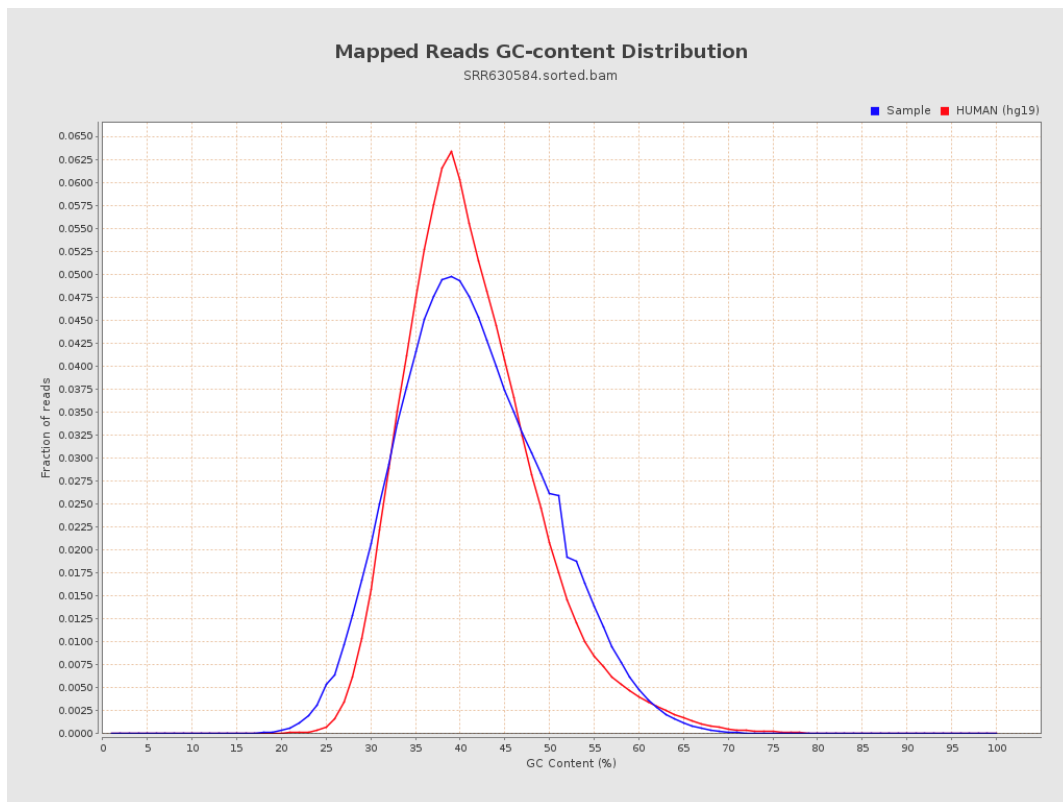
7. Results : Duplication Rate Histogram



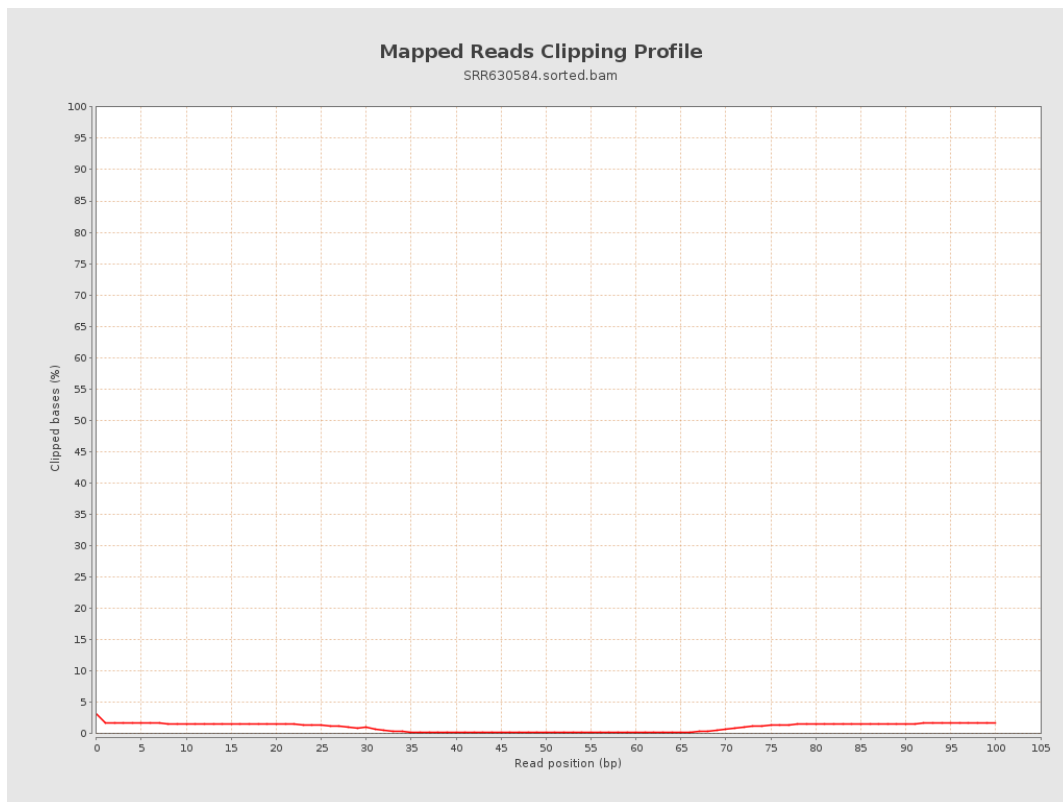
8. Results : Mapped Reads Nucleotide Content



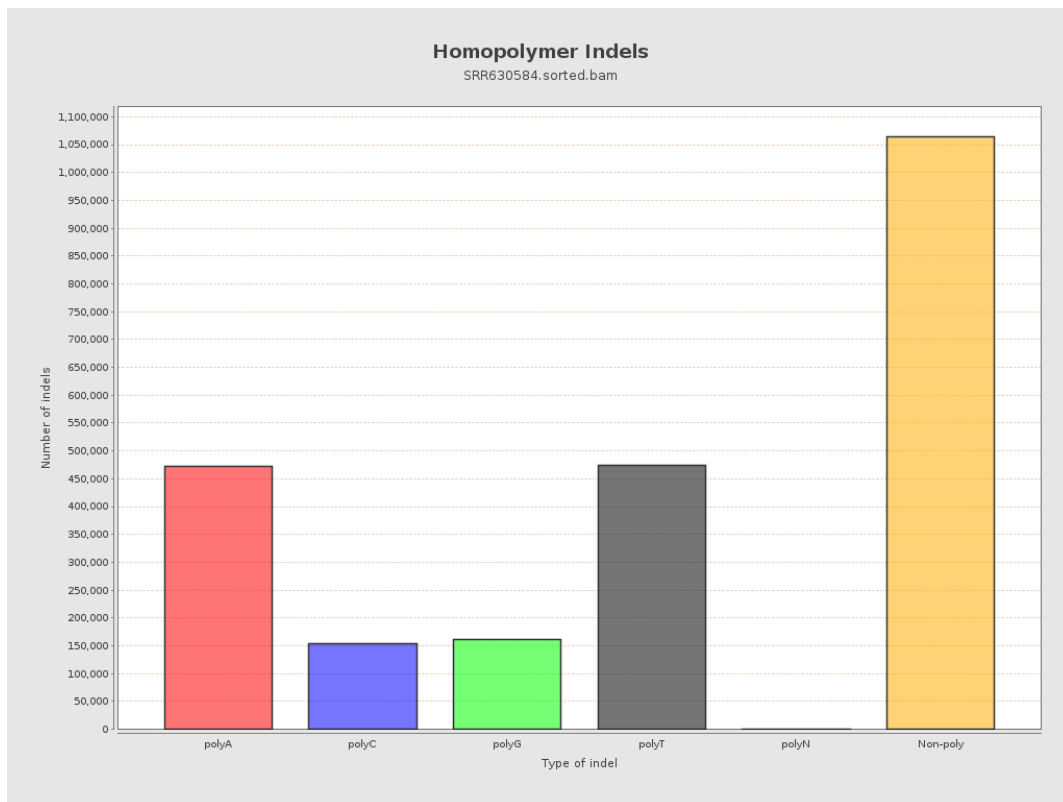
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



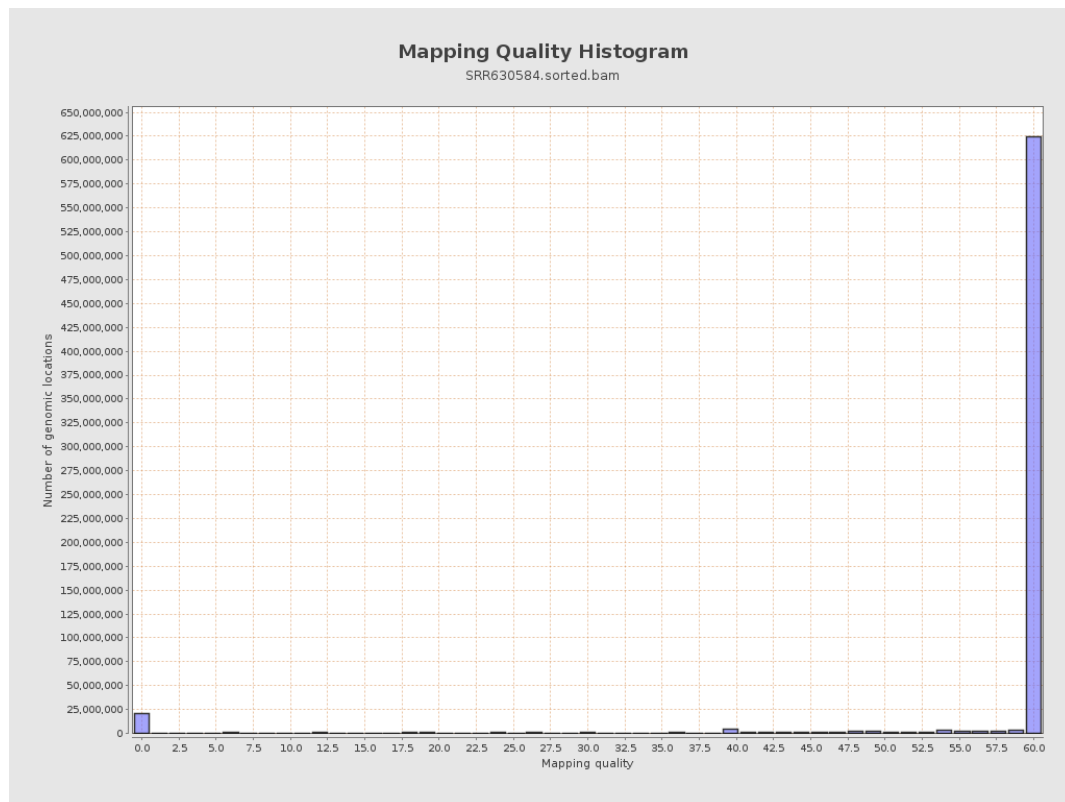
11. Results : Homopolymer Indels



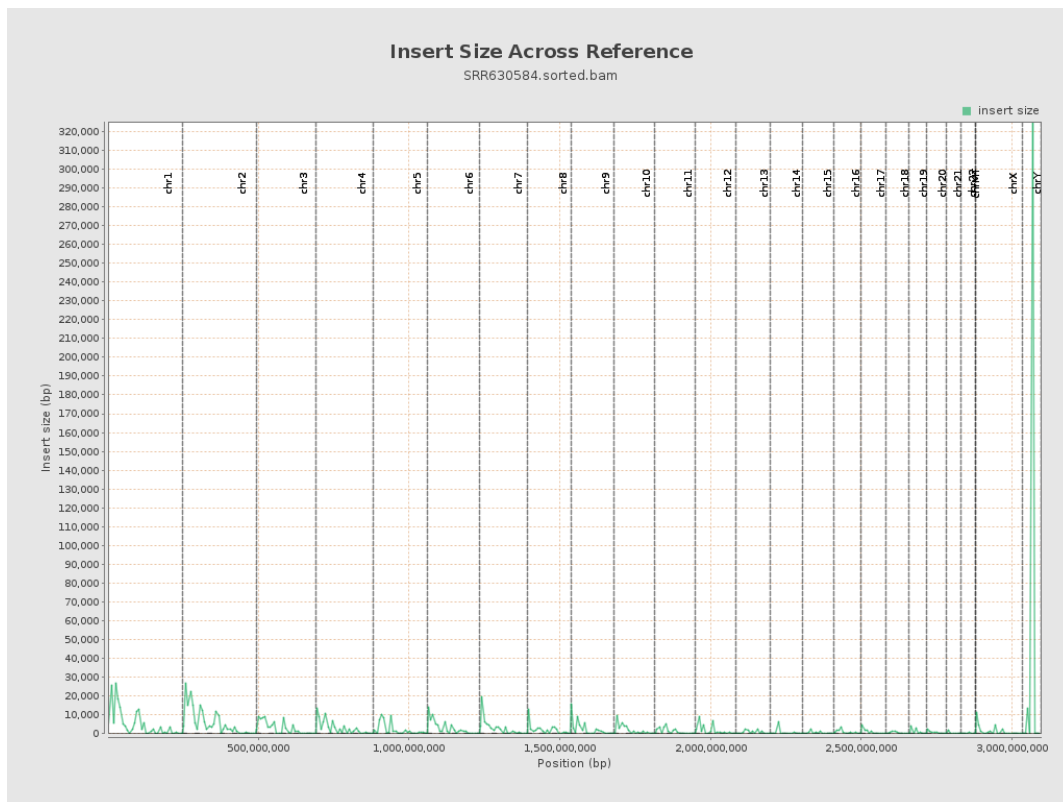
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

