

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/03 10:37:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438297.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_SRR8438297 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438297_1.fastq.gz SRR8438297_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Jan 03 10:37:13 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438297.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	646,428,536
Mapped reads	644,293,356 / 99.67%
Unmapped reads	2,135,180 / 0.33%
Mapped paired reads	644,293,356 / 99.67%
Mapped reads, first in pair	322,388,275 / 49.87%
Mapped reads, second in pair	321,905,081 / 49.8%
Mapped reads, both in pair	642,709,808 / 99.42%
Mapped reads, singletons	1,583,548 / 0.24%
Secondary alignments	0
Supplementary alignments	10,932,484 / 1.69%
Read min/max/mean length	28 / 151 / 145.59
Duplicated reads (estimated)	332,330,251 / 51.41%
Duplication rate	47.34%
Clipped reads	115,470,640 / 17.86%

2.2. ACGT Content

Number/percentage of A's	27,553,826,665 / 29.64%
Number/percentage of C's	19,091,954,250 / 20.54%
Number/percentage of T's	26,182,854,997 / 28.16%
Number/percentage of G's	20,140,972,194 / 21.66%
Number/percentage of N's	694,728 / 0%

GC Percentage	42.2%
---------------	-------

2.3. Coverage

Mean	30.0415
Standard Deviation	144.2087

2.4. Mapping Quality

Mean Mapping Quality	54.7
----------------------	------

2.5. Insert size

Mean	47,289.03
Standard Deviation	2,129,015.51
P25/Median/P75	201 / 264 / 364

2.6. Mismatches and indels

General error rate	0.54%
Mismatches	475,759,457
Insertions	12,723,053
Mapped reads with at least one insertion	1.94%
Deletions	11,439,156
Mapped reads with at least one deletion	1.74%
Homopolymer indels	49.15%

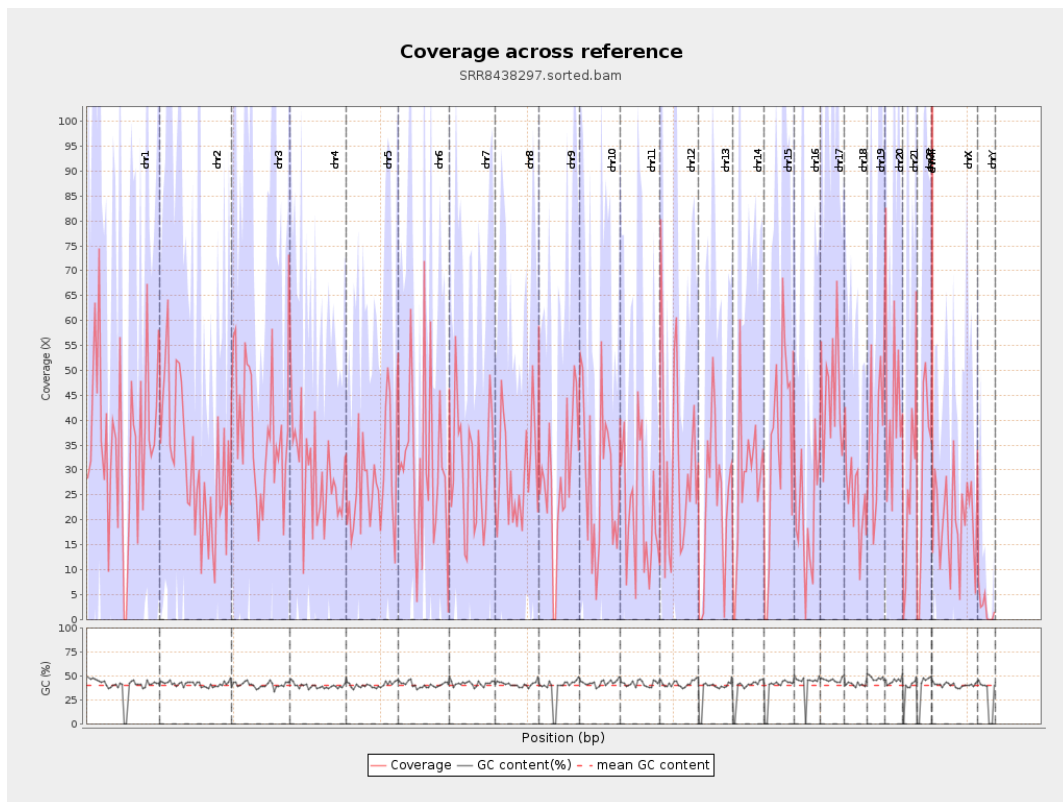
2.7. Chromosome stats

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

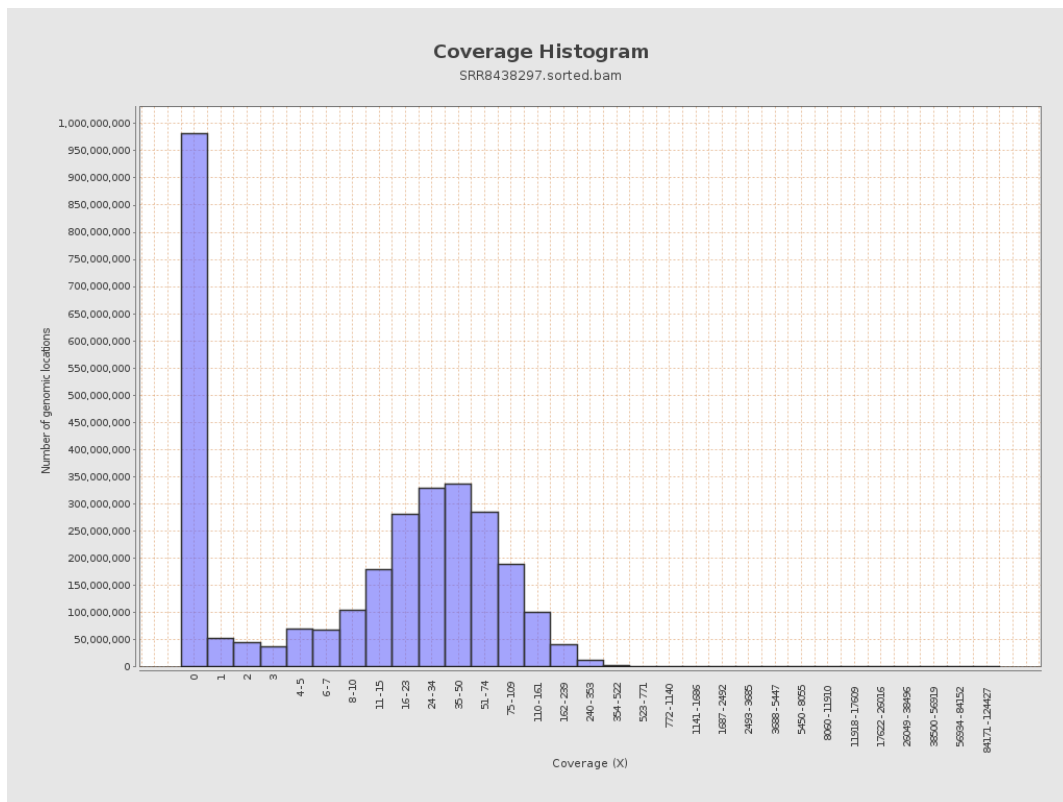
		bases	coverage	deviation
chr1	249250621	9033498481	36.2426	50.8301
chr2	243199373	7483838586	30.7724	103.9017
chr3	198022430	7438847280	37.5657	102.6221
chr4	191154276	5549390846	29.031	35.7189
chr5	180915260	5215354412	28.8276	37.1474
chr6	171115067	5314184819	31.0562	41.0586
chr7	159138663	4871201834	30.6098	41.3307
chr8	146364022	4288843406	29.3026	37.6265
chr9	141213431	4020480130	28.4709	40.8183
chr10	135534747	3816129734	28.1561	42.8735
chr11	135006516	3057200139	22.6448	38.5656
chr12	133851895	4246800775	31.7276	44.9683
chr13	115169878	2693696875	23.3889	37.3567
chr14	107349540	3012187898	28.0596	44.2479
chr15	102531392	3538499372	34.5114	47.456
chr16	90354753	1909262381	21.1307	55.2134
chr17	81195210	3663000153	45.1135	60.4555
chr18	78077248	1886622725	24.1635	34.1168
chr19	59128983	2228545643	37.6896	122.134
chr20	63025520	2740648411	43.4847	52.1796
chr21	48129895	1314489190	27.3113	59.6862
chr22	51304566	1580131791	30.799	48.9165
chrMT	16571	877029361	52,925.5543	21,314.6222
chrX	155270560	3087379396	19.8839	30.516

chrY	59373566	131896028	2.2215	18.9387
------	----------	-----------	--------	---------

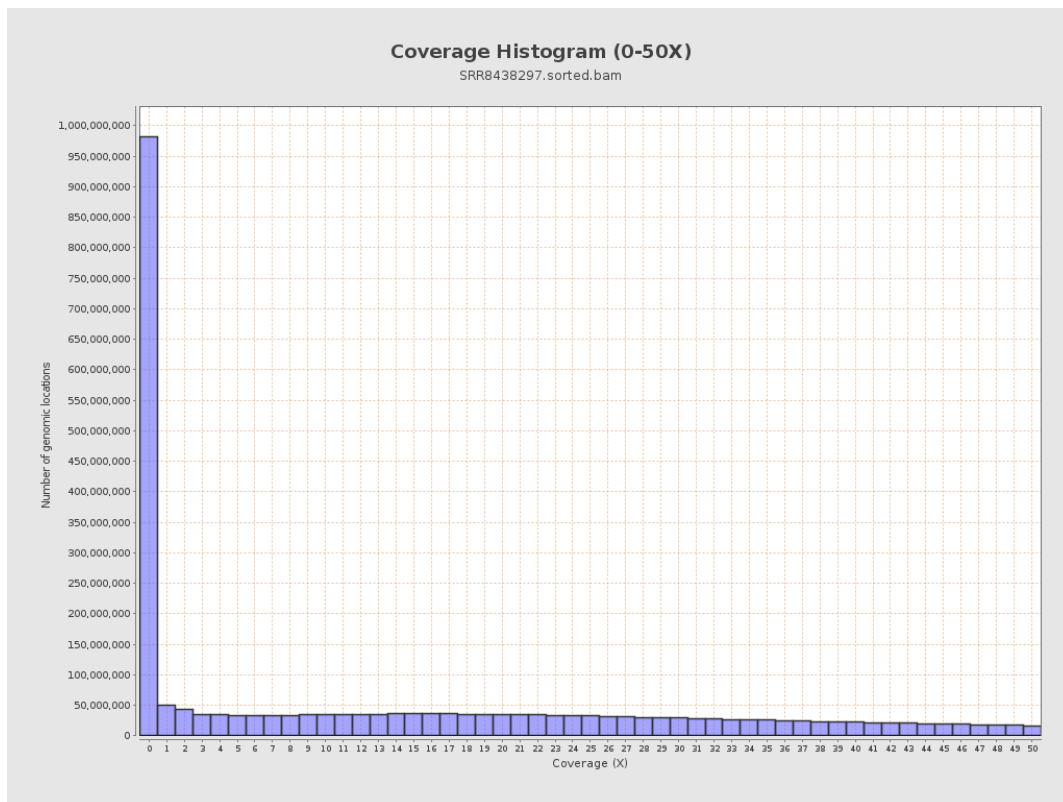
3. Results : Coverage across reference



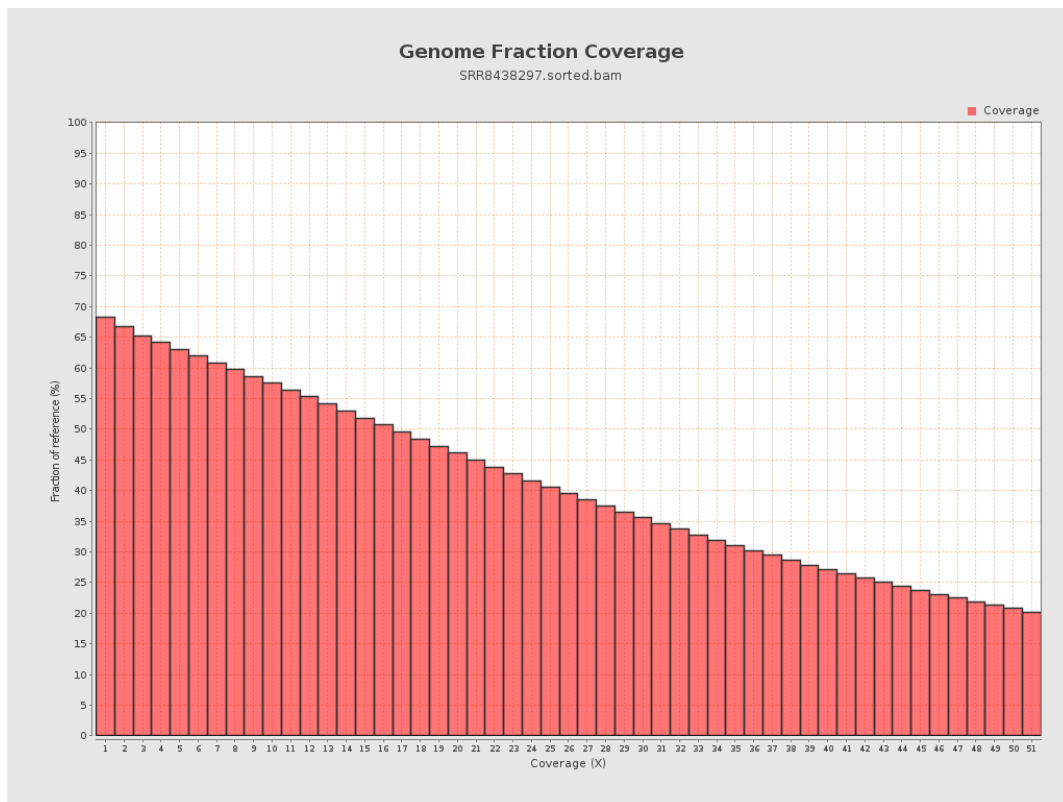
4. Results : Coverage Histogram



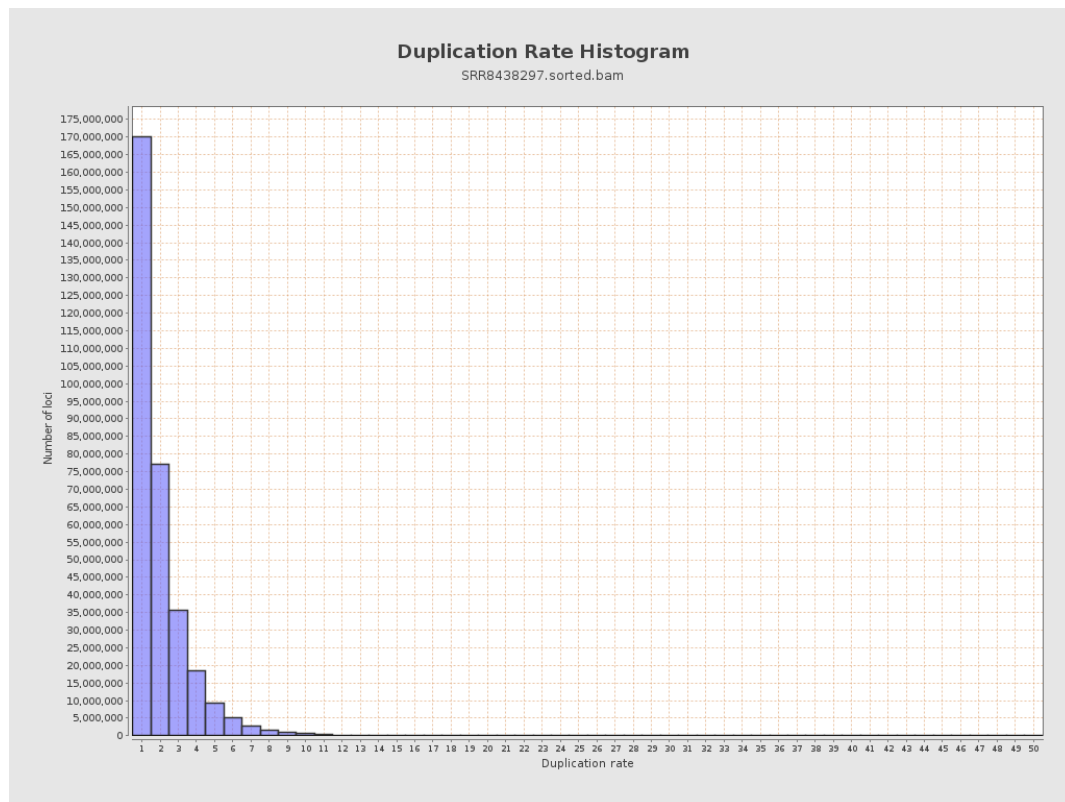
5. Results : Coverage Histogram (0-50X)



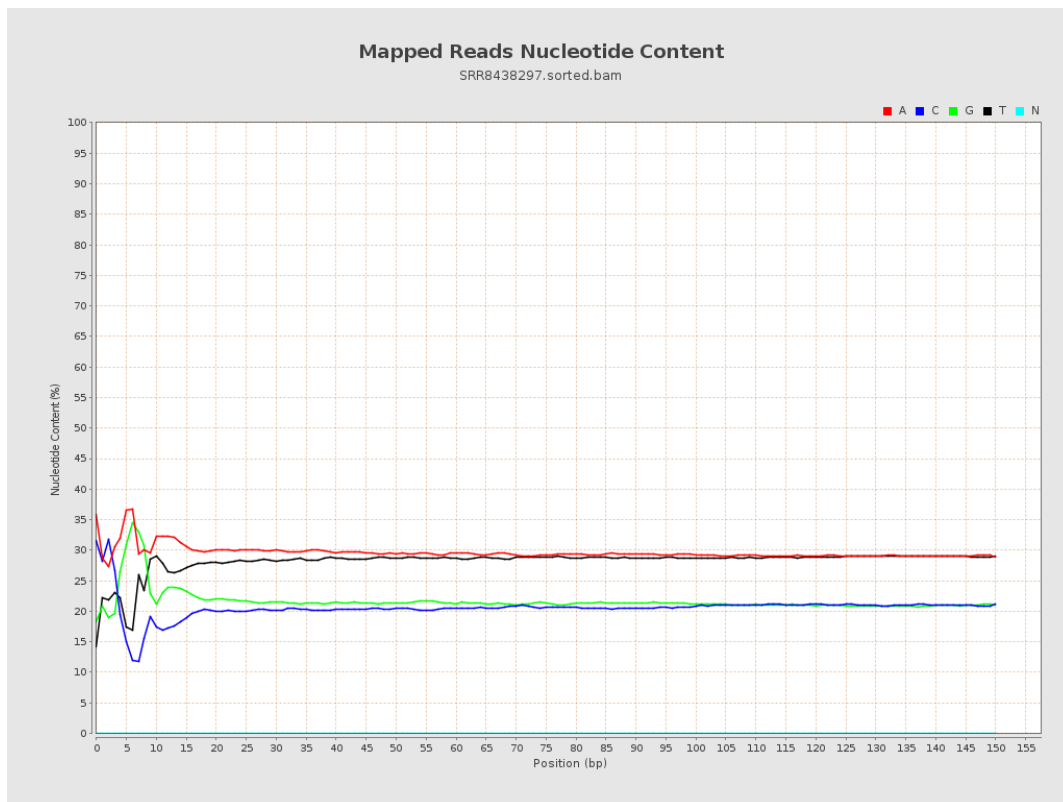
6. Results : Genome Fraction Coverage



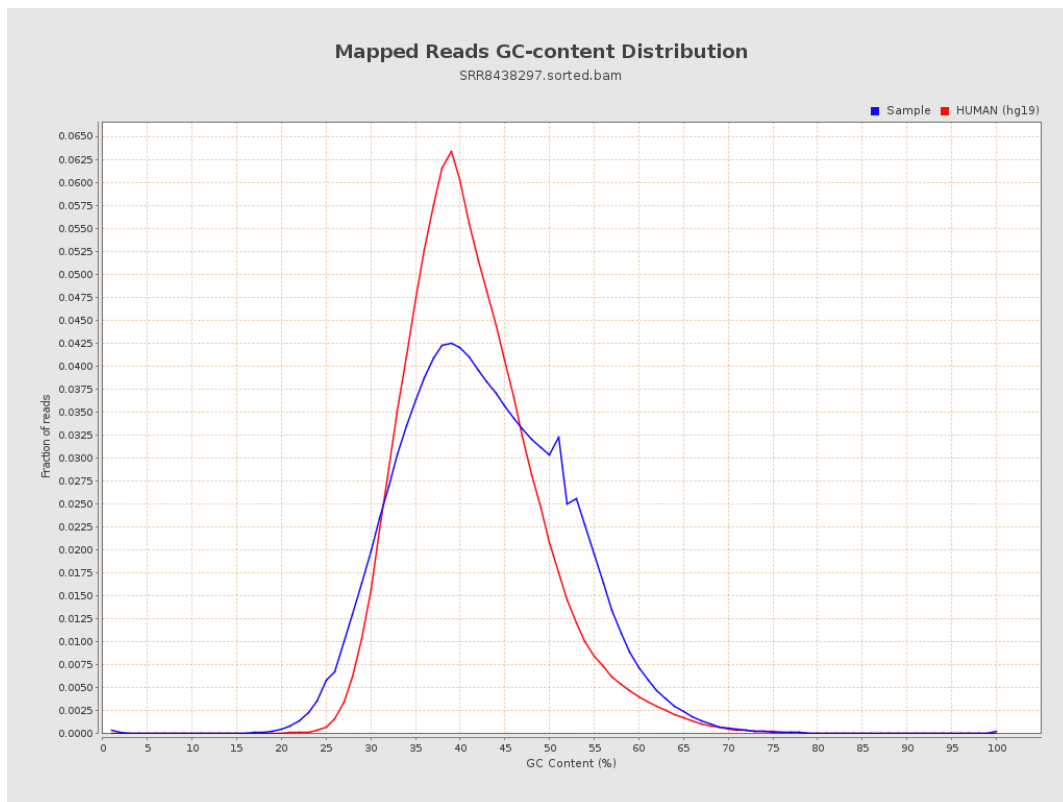
7. Results : Duplication Rate Histogram



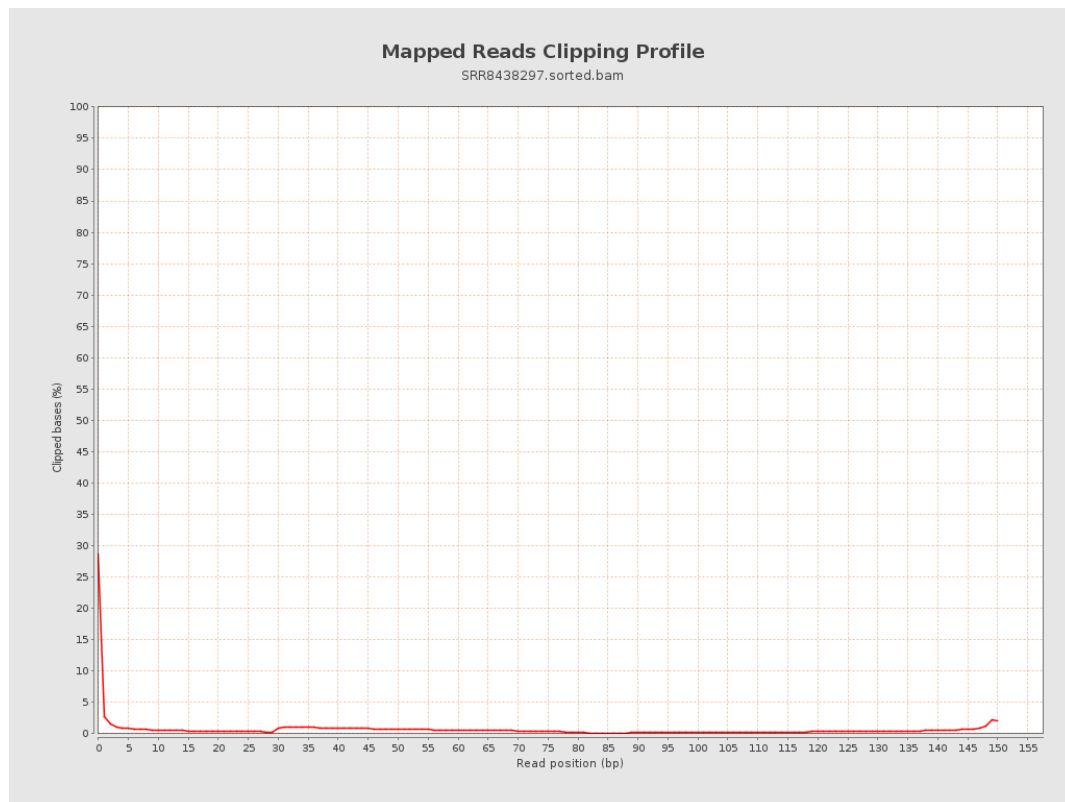
8. Results : Mapped Reads Nucleotide Content



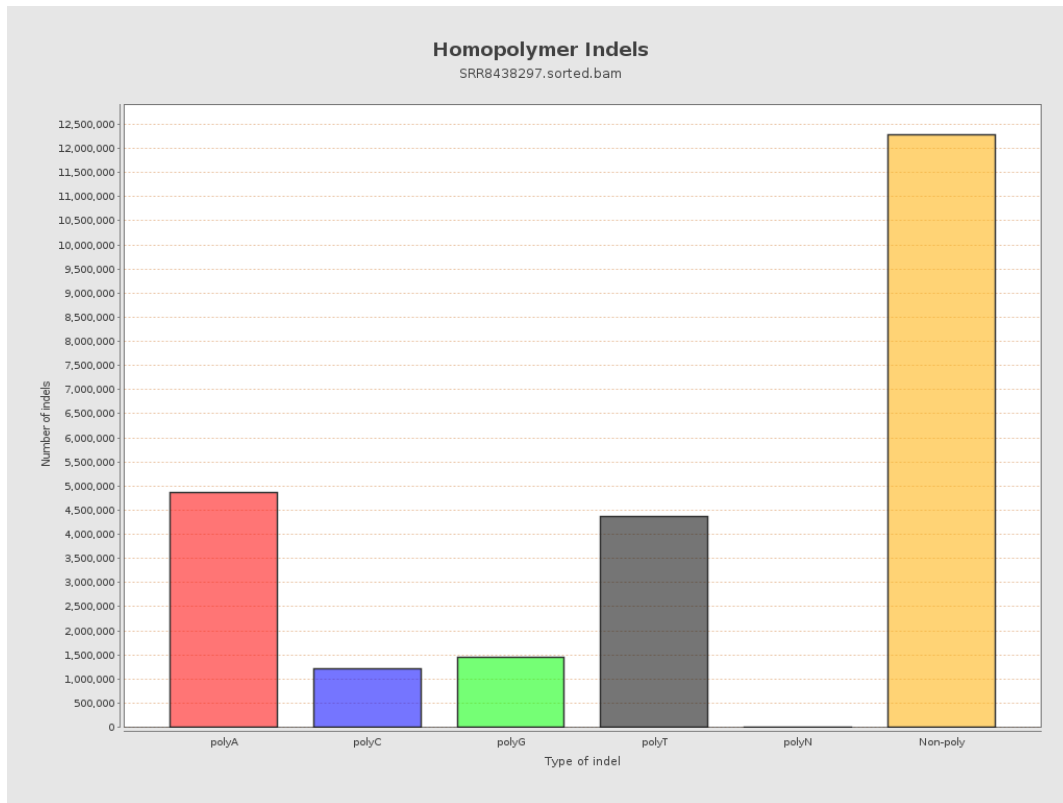
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



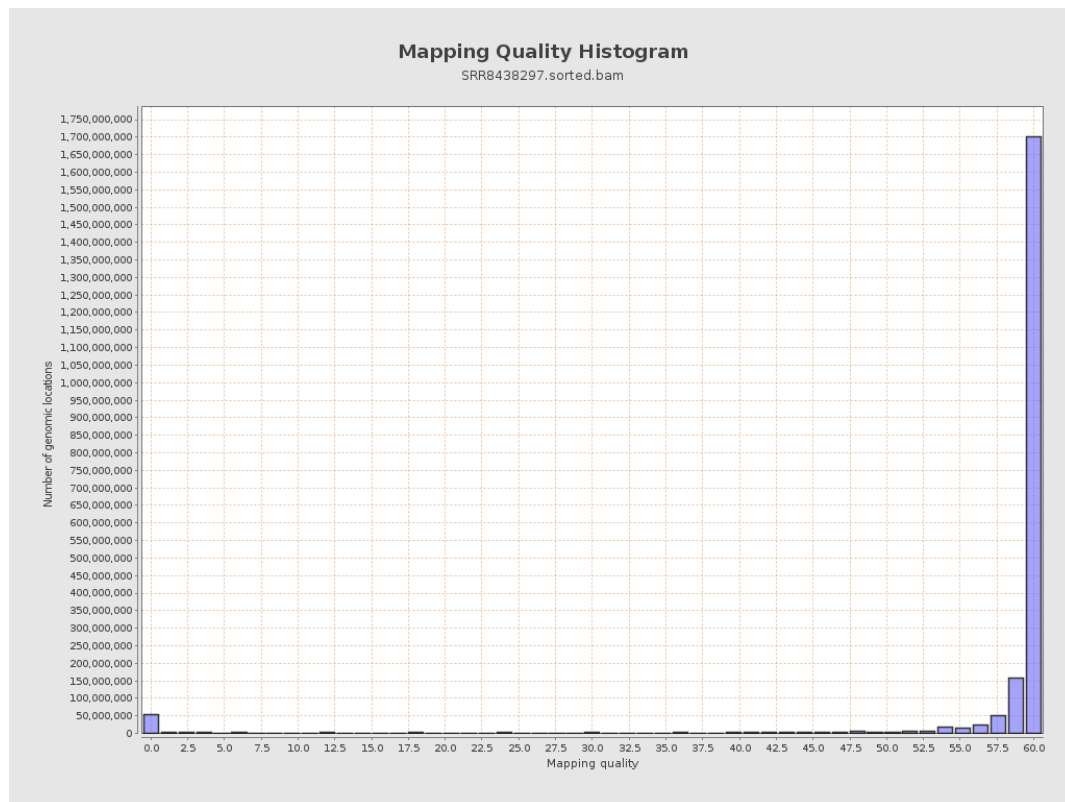
11. Results : Homopolymer Indels



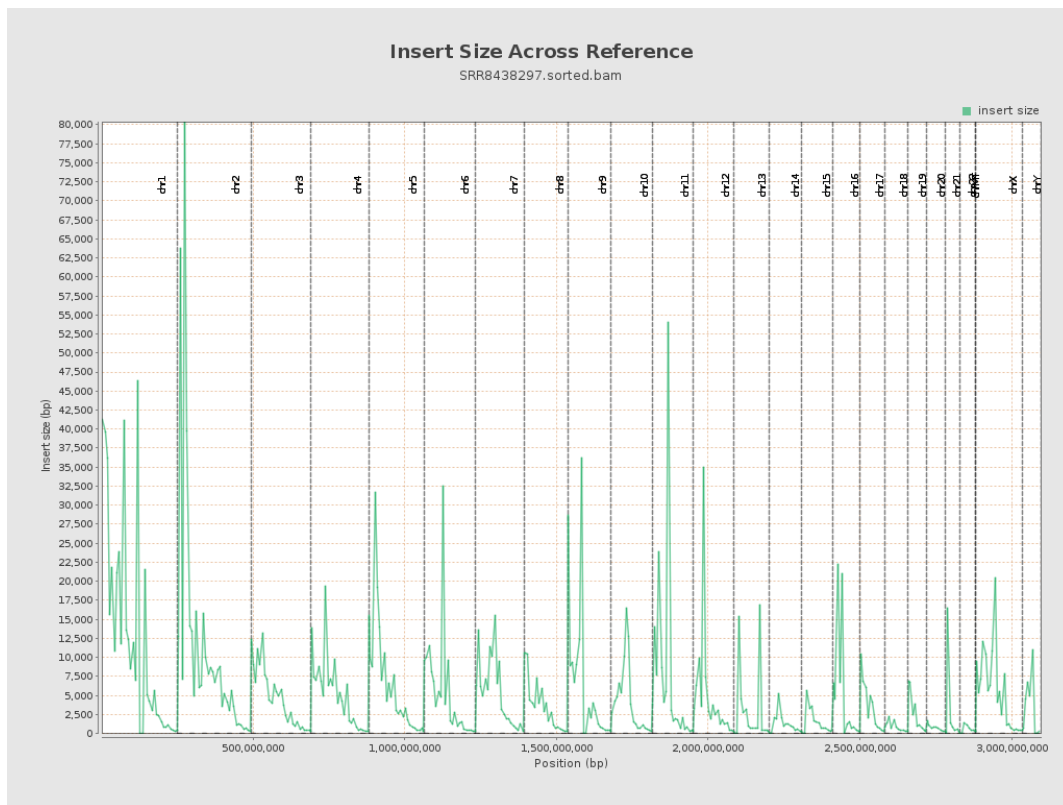
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

