

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/18 03:47:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618579.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_SRR618579 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618579_1.fastq.gz SRR618579_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jan 18 03:47:23 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618579.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	59,448,052
Mapped reads	56,974,832 / 95.84%
Unmapped reads	2,473,220 / 4.16%
Mapped paired reads	56,974,832 / 95.84%
Mapped reads, first in pair	28,715,841 / 48.3%
Mapped reads, second in pair	28,258,991 / 47.54%
Mapped reads, both in pair	55,987,386 / 94.18%
Mapped reads, singletons	987,446 / 1.66%
Secondary alignments	0
Supplementary alignments	133,798 / 0.23%
Read min/max/mean length	30 / 100 / 100.09
Duplicated reads (estimated)	12,891,316 / 21.69%
Duplication rate	19.61%
Clipped reads	11,365,606 / 19.12%

2.2. ACGT Content

Number/percentage of A's	1,464,516,547 / 27.14%
Number/percentage of C's	1,193,064,583 / 22.11%
Number/percentage of T's	1,481,090,802 / 27.44%
Number/percentage of G's	1,258,286,084 / 23.31%
Number/percentage of N's	163,059 / 0%

GC Percentage	45.42%
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2.3. Coverage

Mean	1.7446
Standard Deviation	7.0759

2.4. Mapping Quality

Mean Mapping Quality	52.06
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2.5. Insert size

Mean	41,293.37
Standard Deviation	2,013,654.58
P25/Median/P75	166 / 194 / 229

2.6. Mismatches and indels

General error rate	1.26%
Mismatches	66,430,973
Insertions	954,707
Mapped reads with at least one insertion	1.65%
Deletions	2,709,871
Mapped reads with at least one deletion	4.64%
Homopolymer indels	52.96%

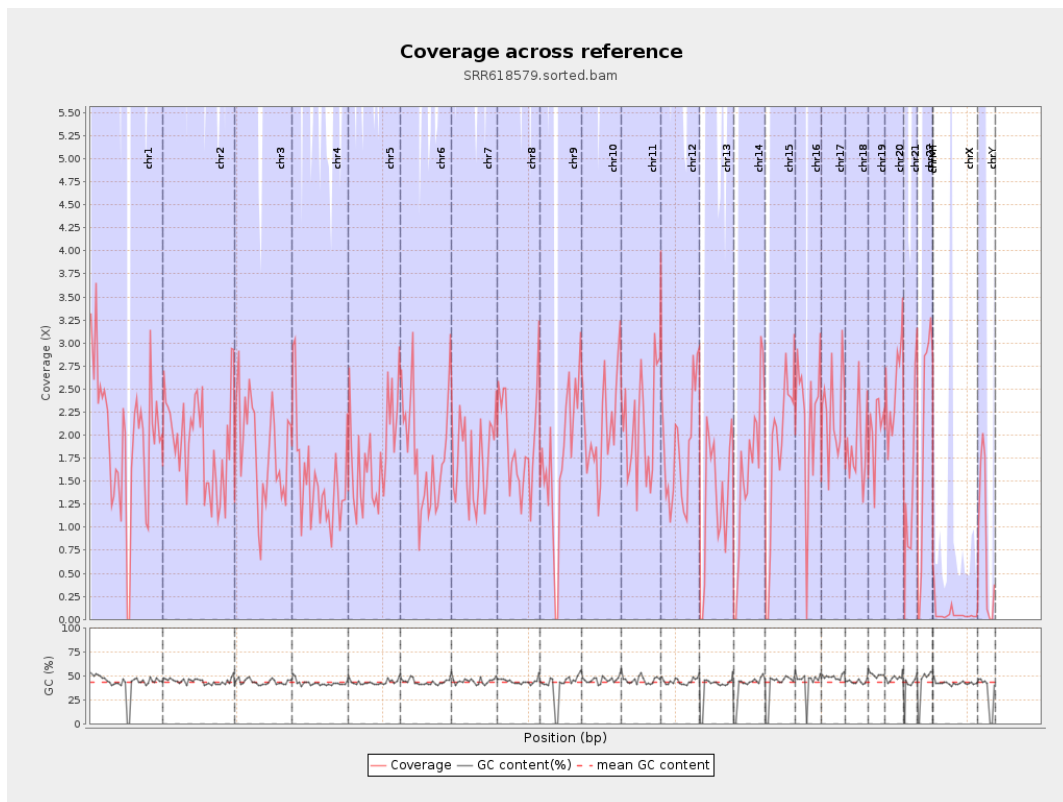
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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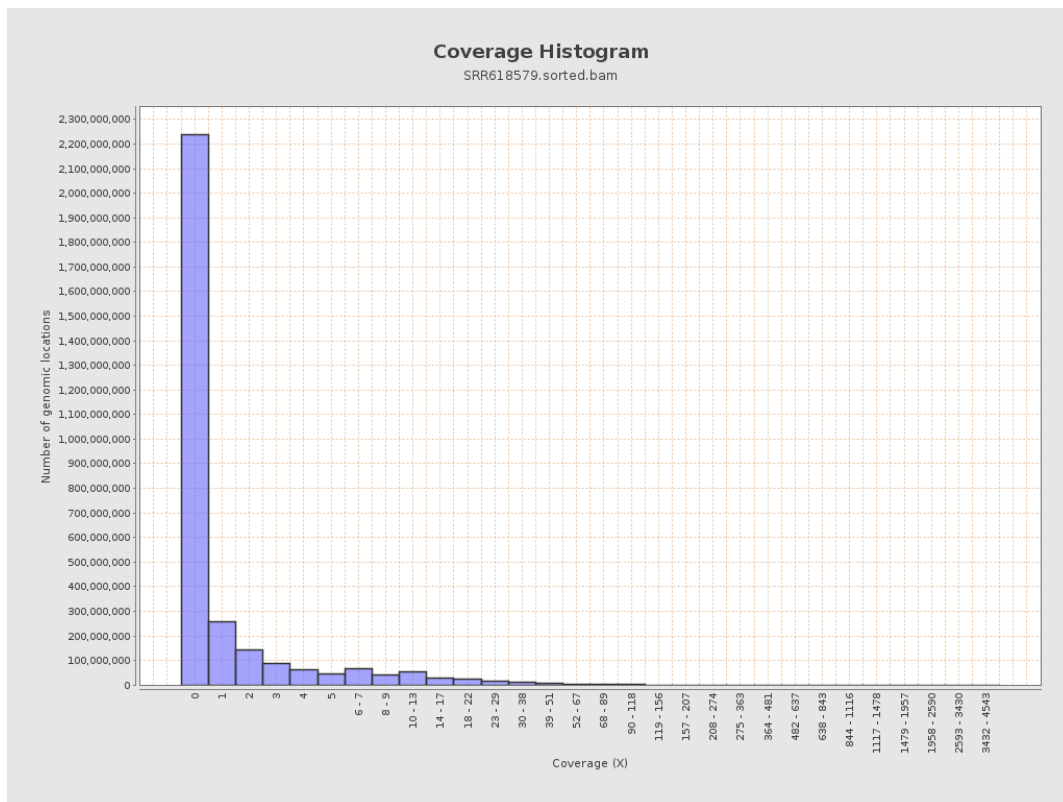
		bases	coverage	deviation
chr1	249250621	488059595	1.9581	8.6675
chr2	243199373	465507856	1.9141	7.4929
chr3	198022430	361575832	1.8259	5.9359
chr4	191154276	287956628	1.5064	5.8972
chr5	180915260	325590335	1.7997	5.7719
chr6	171115067	304347747	1.7786	6.6824
chr7	159138663	277244142	1.7422	6.0011
chr8	146364022	279148429	1.9072	6.2708
chr9	141213431	247282195	1.7511	8.6836
chr10	135534747	280978689	2.0731	6.8655
chr11	135006516	283449469	2.0995	9.0139
chr12	133851895	248509623	1.8566	6.1868
chr13	115169878	151451352	1.315	4.8695
chr14	107349540	175135453	1.6315	5.9788
chr15	102531392	186762692	1.8215	7.2202
chr16	90354753	197235447	2.1829	9.946
chr17	81195210	181824924	2.2394	7.8742
chr18	78077248	144048412	1.8449	8.7168
chr19	59128983	121536702	2.0555	8.2839
chr20	63025520	158395041	2.5132	7.9858
chr21	48129895	70957903	1.4743	9.8191
chr22	51304566	102814111	2.004	8.0387
chrMT	16571	9854	0.5947	2.9977
chrX	155270560	9140145	0.0589	1.9009

chrY	59373566	51841192	0.8731	5.2392
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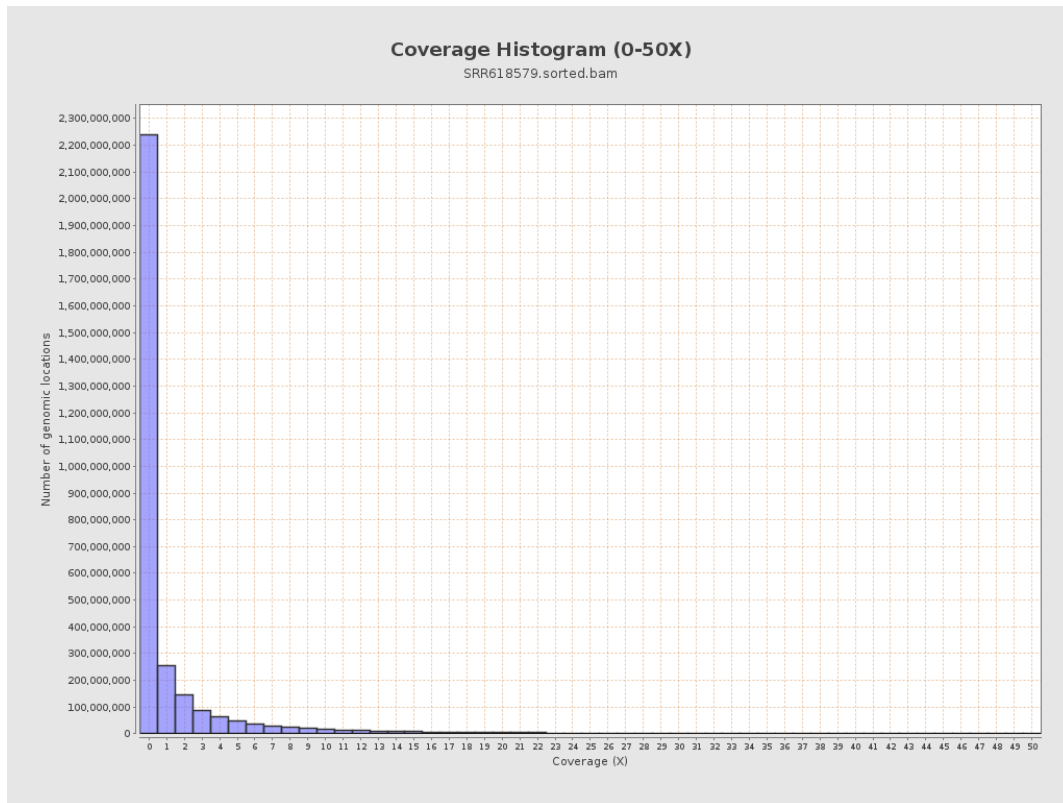
3. Results : Coverage across reference



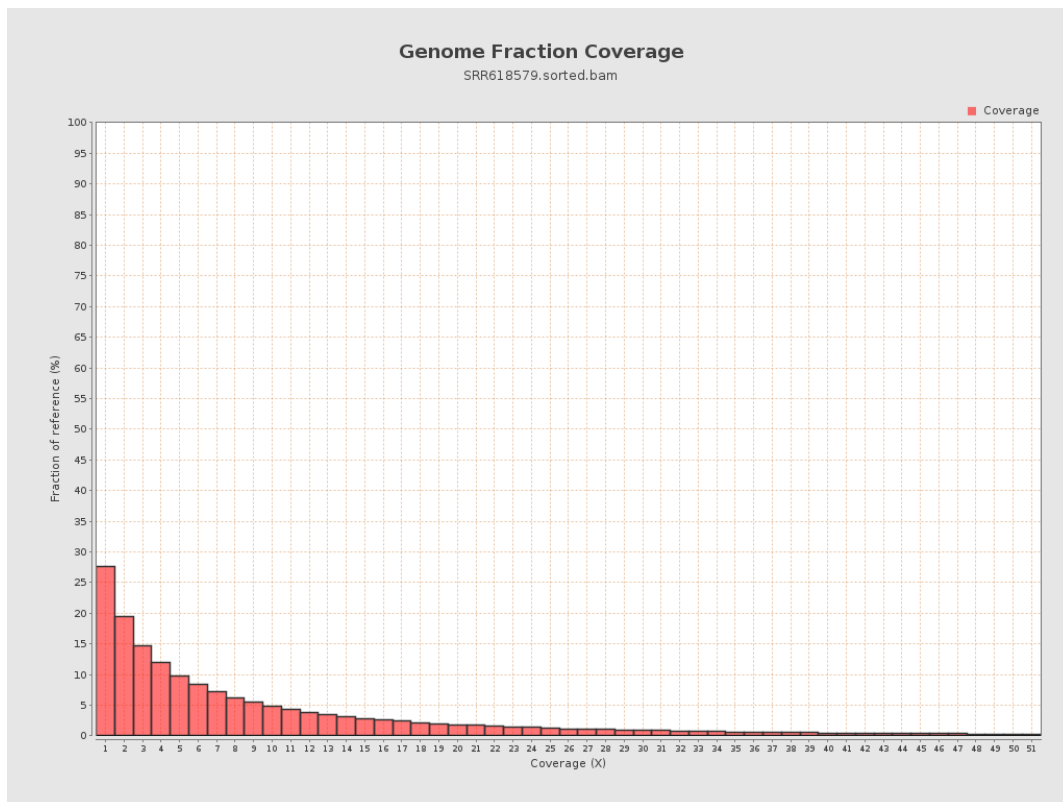
4. Results : Coverage Histogram



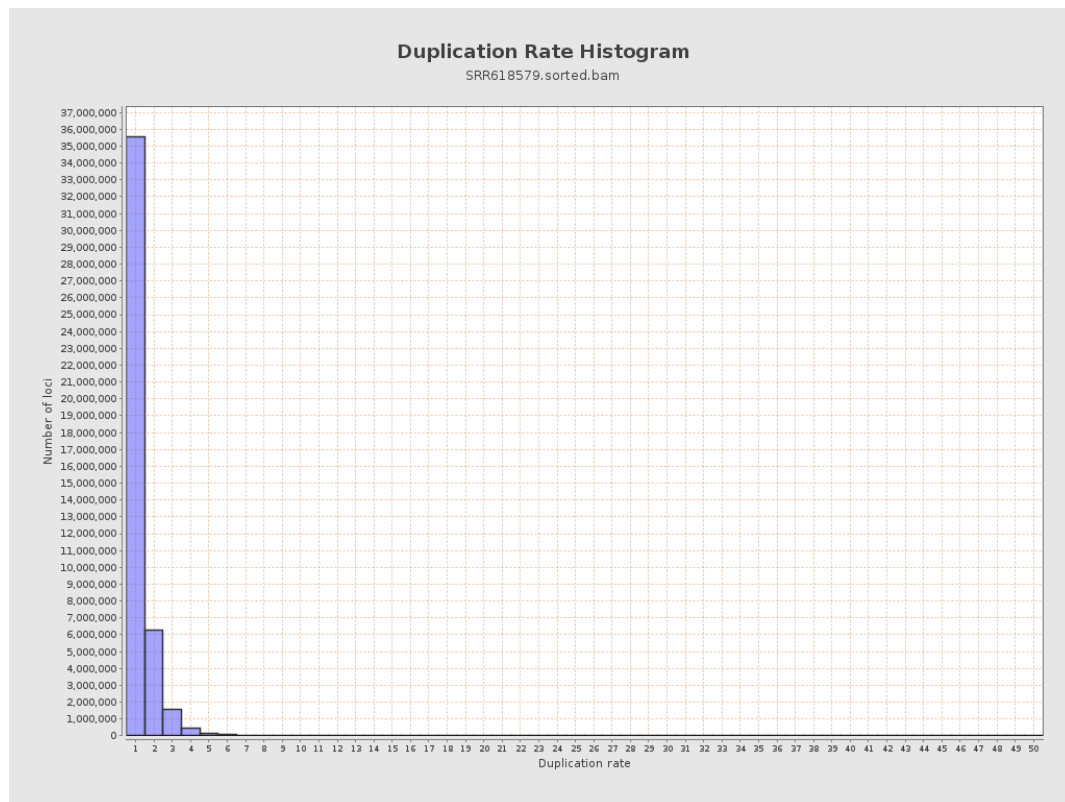
5. Results : Coverage Histogram (0-50X)



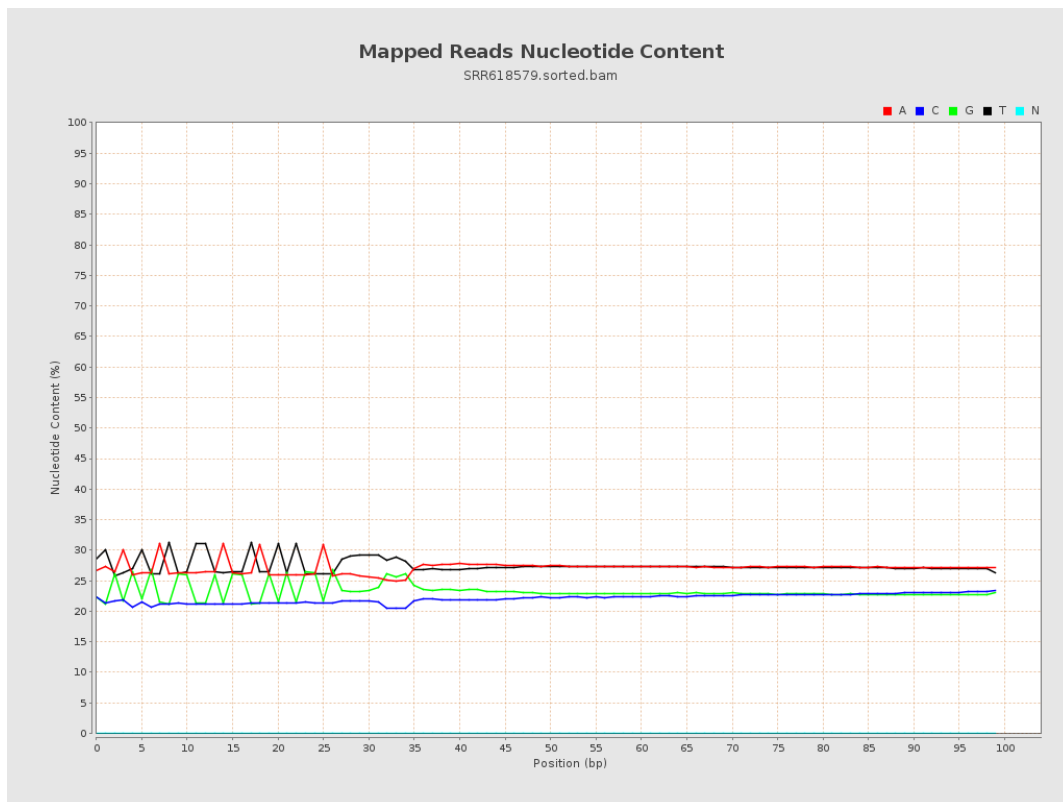
6. Results : Genome Fraction Coverage



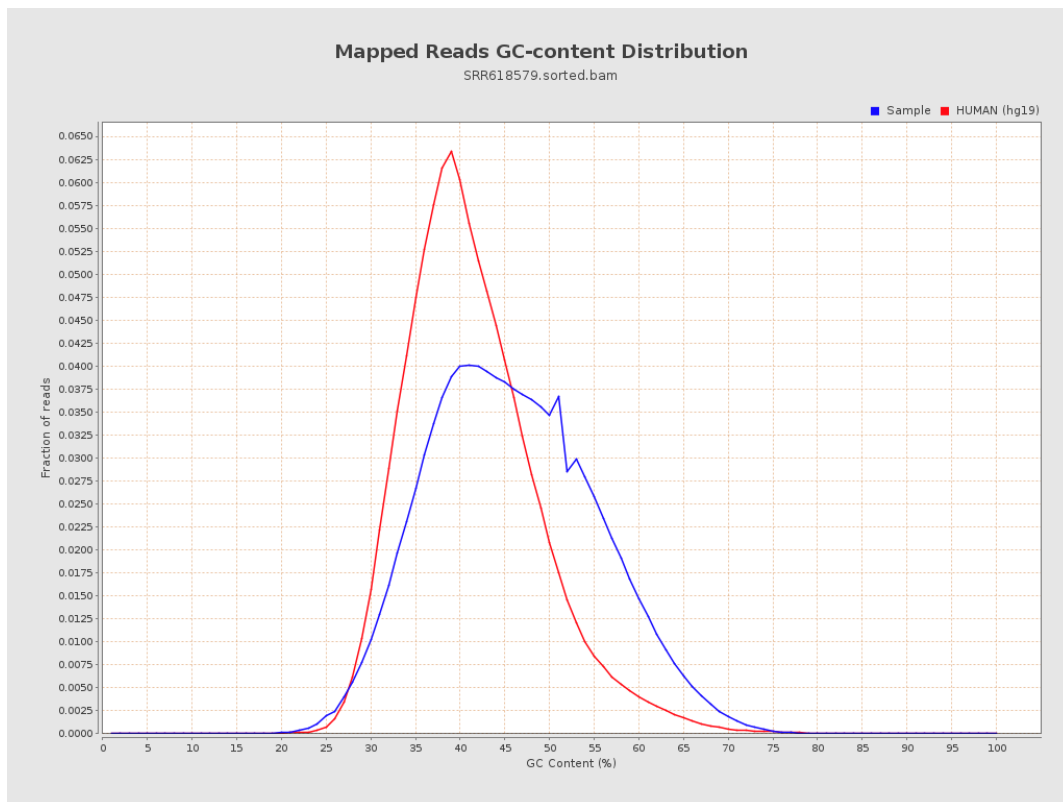
7. Results : Duplication Rate Histogram



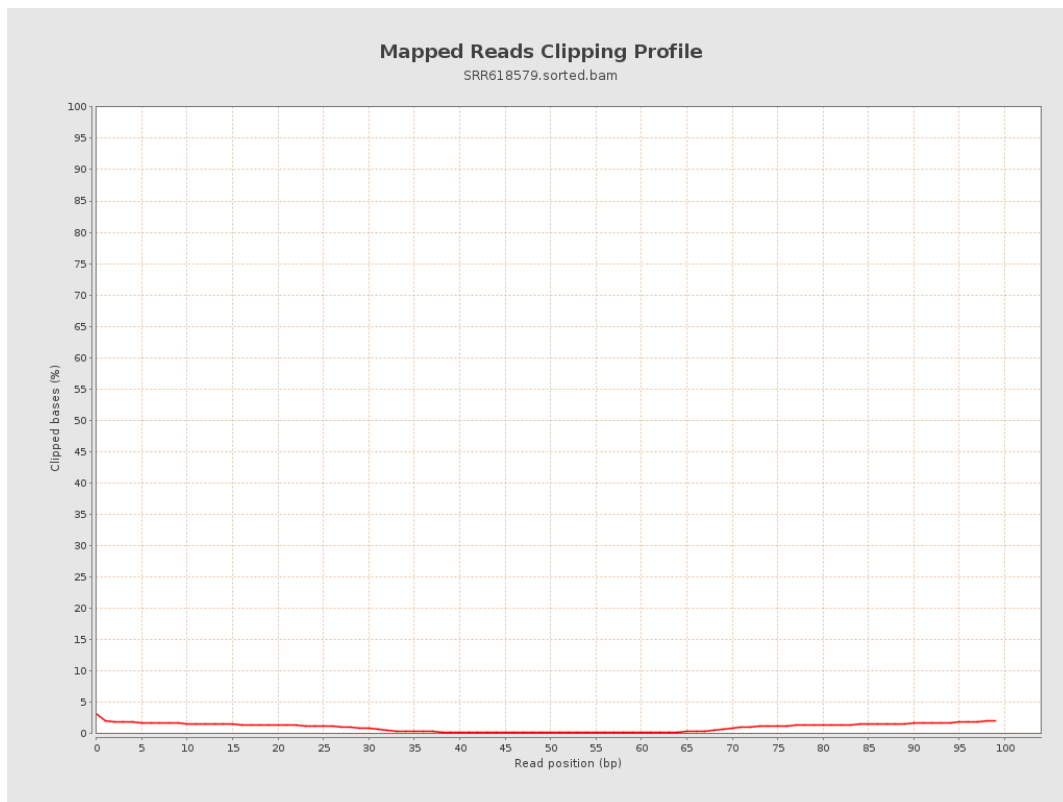
8. Results : Mapped Reads Nucleotide Content



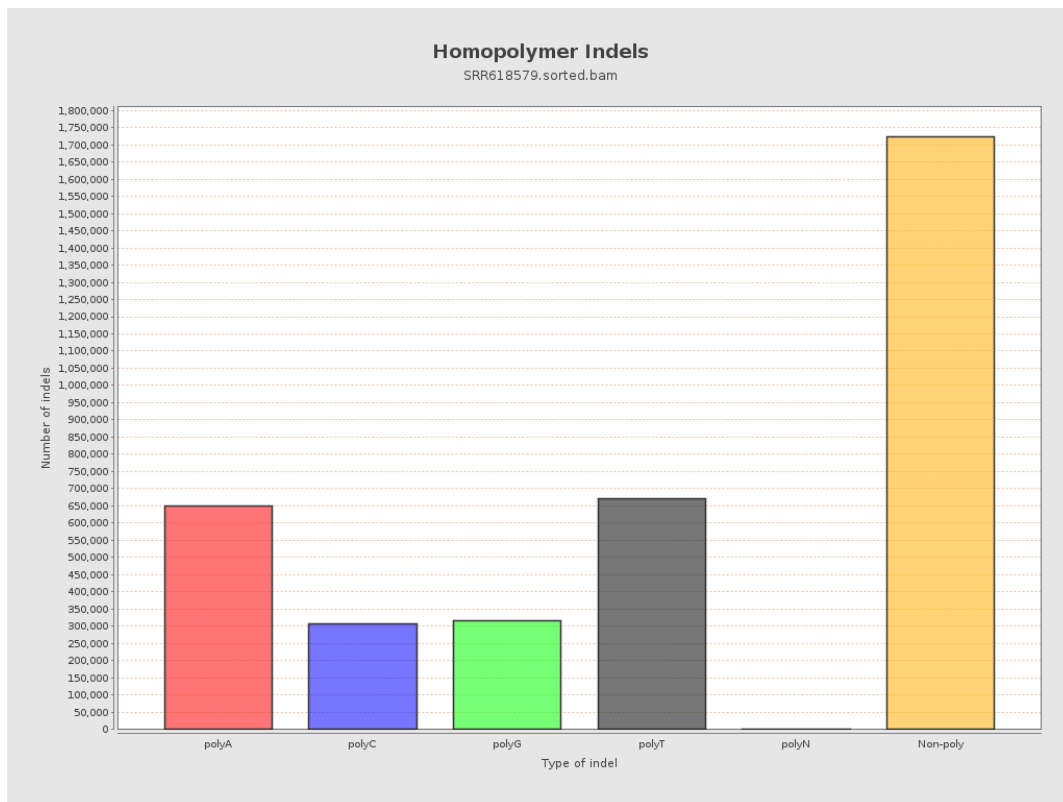
9. Results : Mapped Reads GC-content Distribution



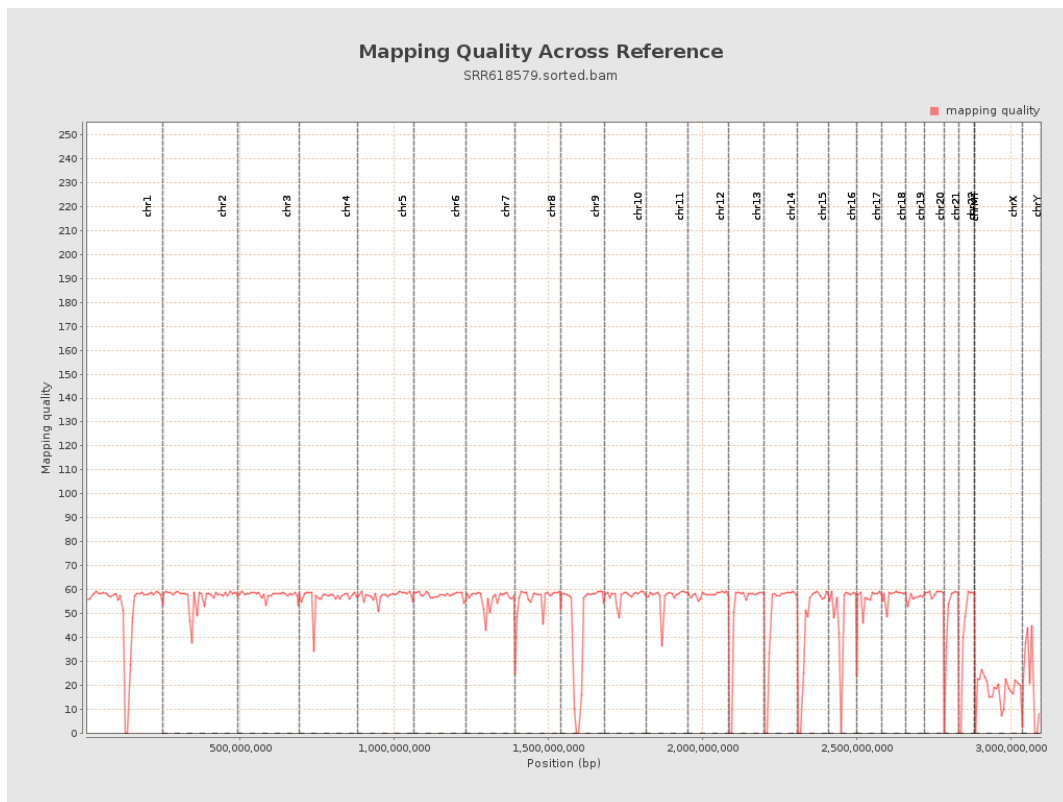
10. Results : Mapped Reads Clipping Profile



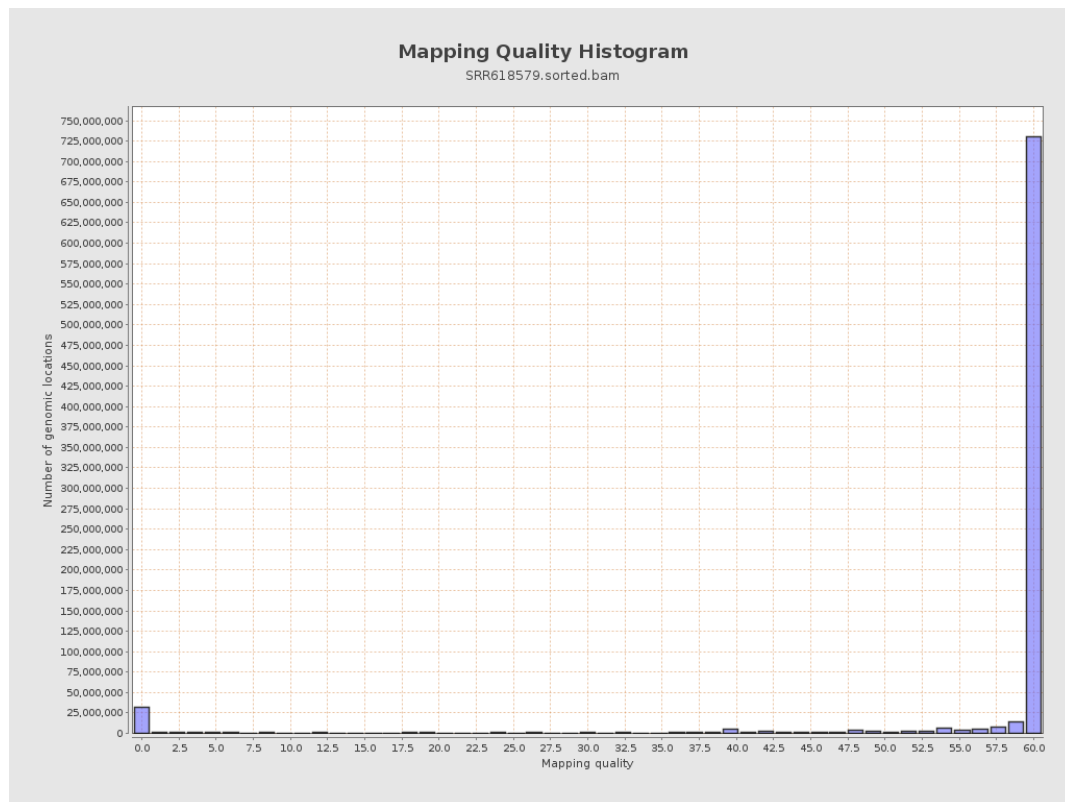
11. Results : Homopolymer Indels



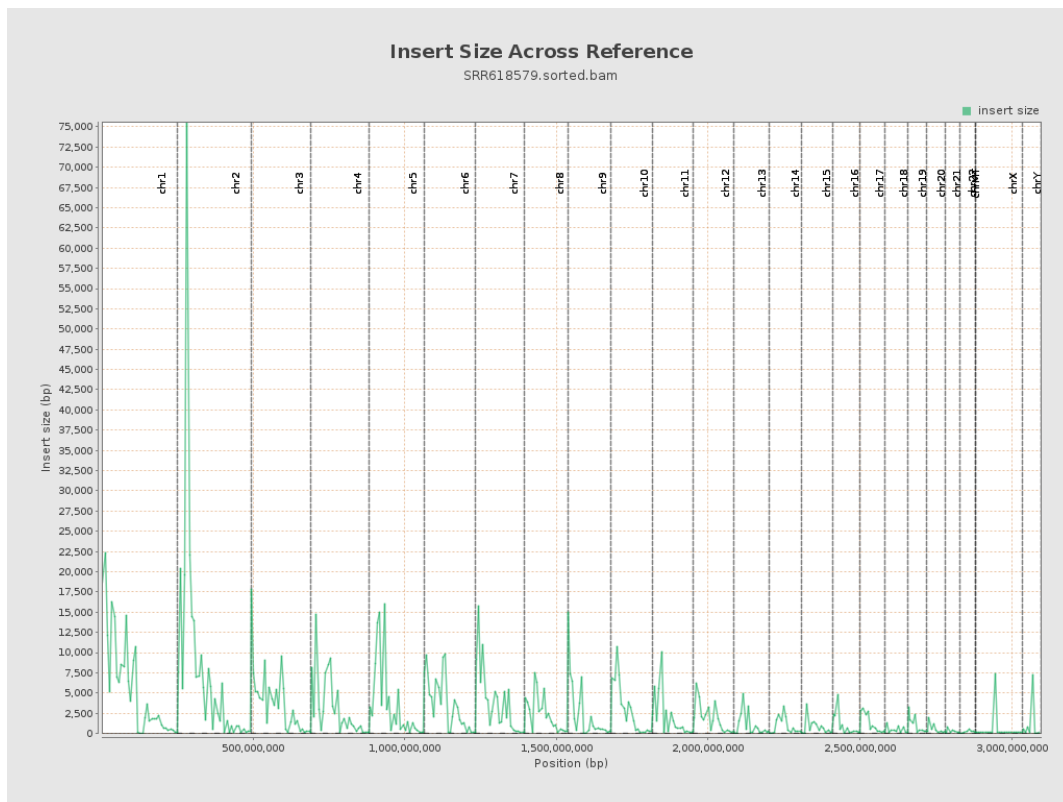
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

