

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/21 06:32:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618667.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_SRR618667 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618667_1.fastq.gz SRR618667_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Jan 21 06:32:53 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618667.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	104,860,252
Mapped reads	102,827,690 / 98.06%
Unmapped reads	2,032,562 / 1.94%
Mapped paired reads	102,827,690 / 98.06%
Mapped reads, first in pair	51,637,571 / 49.24%
Mapped reads, second in pair	51,190,119 / 48.82%
Mapped reads, both in pair	101,709,374 / 97%
Mapped reads, singletons	1,118,316 / 1.07%
Secondary alignments	0
Supplementary alignments	359,246 / 0.34%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	14,534,163 / 13.86%
Duplication rate	9.65%
Clipped reads	5,344,602 / 5.1%

2.2. ACGT Content

Number/percentage of A's	3,028,111,578 / 29.79%
Number/percentage of C's	2,055,156,558 / 20.22%
Number/percentage of T's	3,017,476,168 / 29.68%
Number/percentage of G's	2,059,901,145 / 20.26%
Number/percentage of N's	5,286,351 / 0.05%

GC Percentage	40.48%
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2.3. Coverage

Mean	3.285
Standard Deviation	35.938

2.4. Mapping Quality

Mean Mapping Quality	53.75
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2.5. Insert size

Mean	41,167.92
Standard Deviation	1,944,802.06
P25/Median/P75	163 / 170 / 177

2.6. Mismatches and indels

General error rate	0.52%
Mismatches	50,023,514
Insertions	1,066,796
Mapped reads with at least one insertion	1%
Deletions	1,314,282
Mapped reads with at least one deletion	1.24%
Homopolymer indels	41.5%

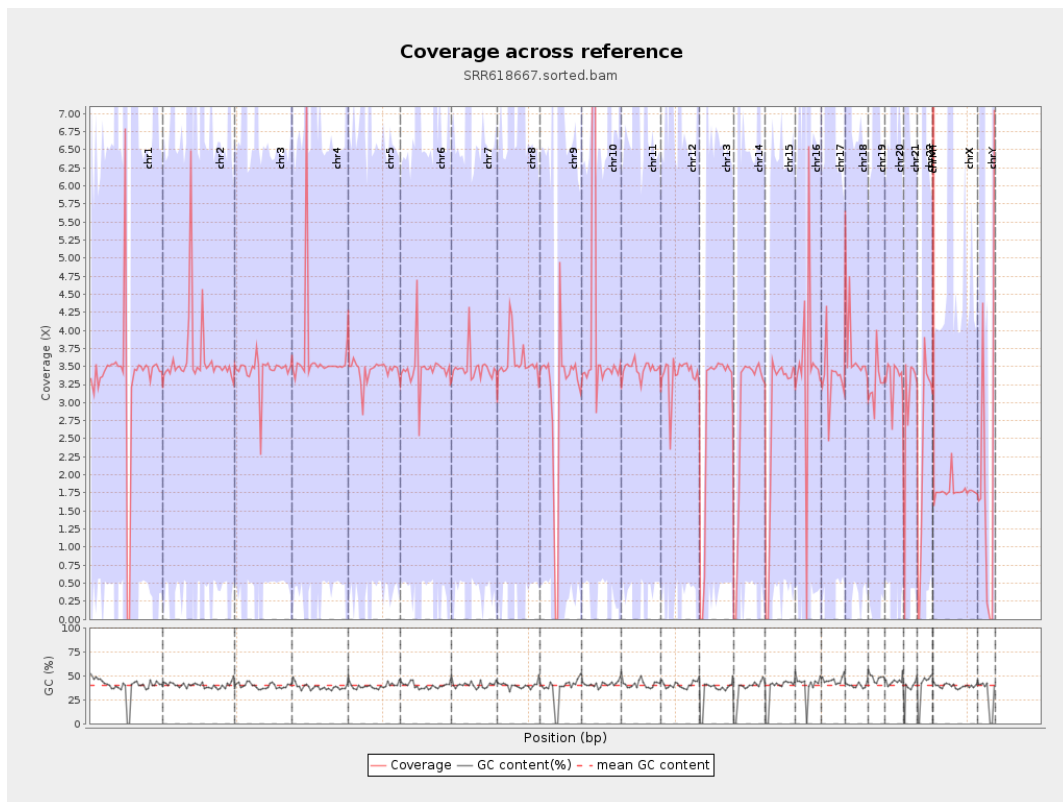
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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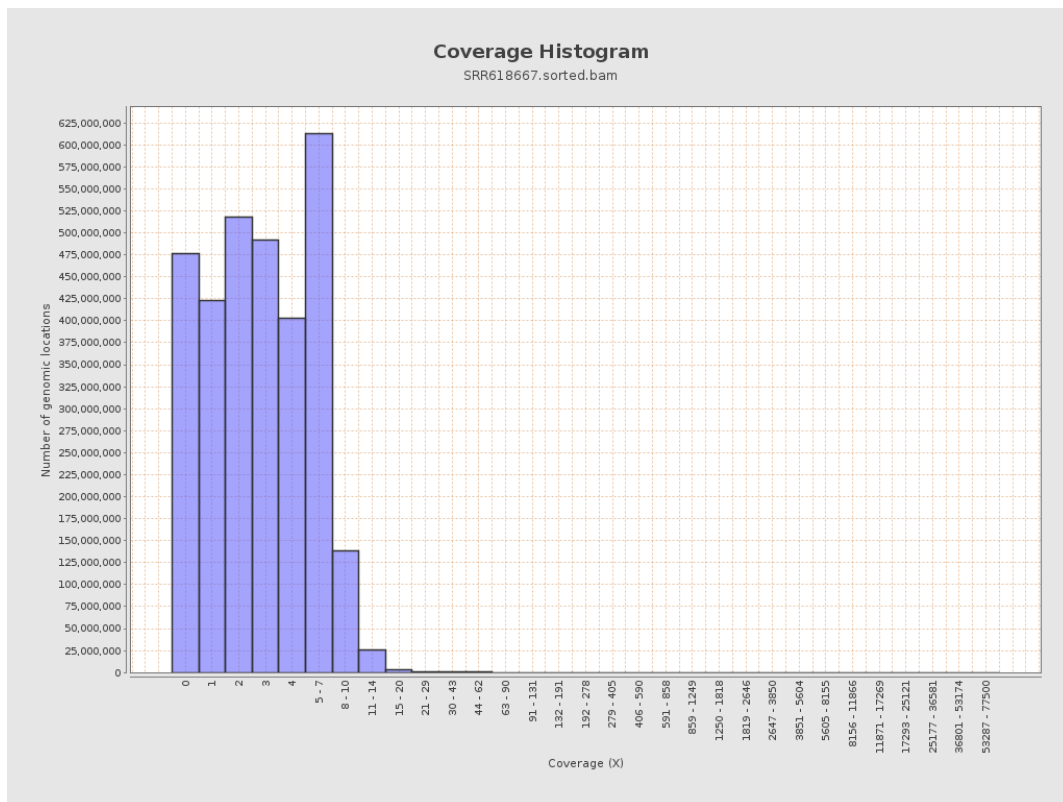
		bases	coverage	deviation
chr1	249250621	829168806	3.3266	79.364
chr2	243199373	880781854	3.6216	23.9035
chr3	198022430	682620251	3.4472	4.5974
chr4	191154276	699418309	3.6589	21.8985
chr5	180915260	622619024	3.4415	3.7213
chr6	171115067	594171730	3.4724	14.7862
chr7	159138663	553379513	3.4773	24.483
chr8	146364022	523542683	3.577	47.6237
chr9	141213431	436941265	3.0942	37.9758
chr10	135534747	536547880	3.9587	85.7341
chr11	135006516	468133236	3.4675	18.565
chr12	133851895	453501297	3.3881	3.6615
chr13	115169878	333511798	2.8958	2.7564
chr14	107349540	310294600	2.8905	3.86
chr15	102531392	288663235	2.8154	2.8261
chr16	90354753	314865983	3.4848	26.3622
chr17	81195210	273332363	3.3664	15.5812
chr18	78077248	289468030	3.7075	46.237
chr19	59128983	193786524	3.2774	34.2022
chr20	63025520	210021758	3.3323	12.3589
chr21	48129895	144396330	3.0001	18.1952
chr22	51304566	123175469	2.4009	16.2485
chrMT	16571	4844511	292.3487	46.7793
chrX	155270560	276833848	1.7829	8.2869

chrY	59373566	125215185	2.1089	41.8917
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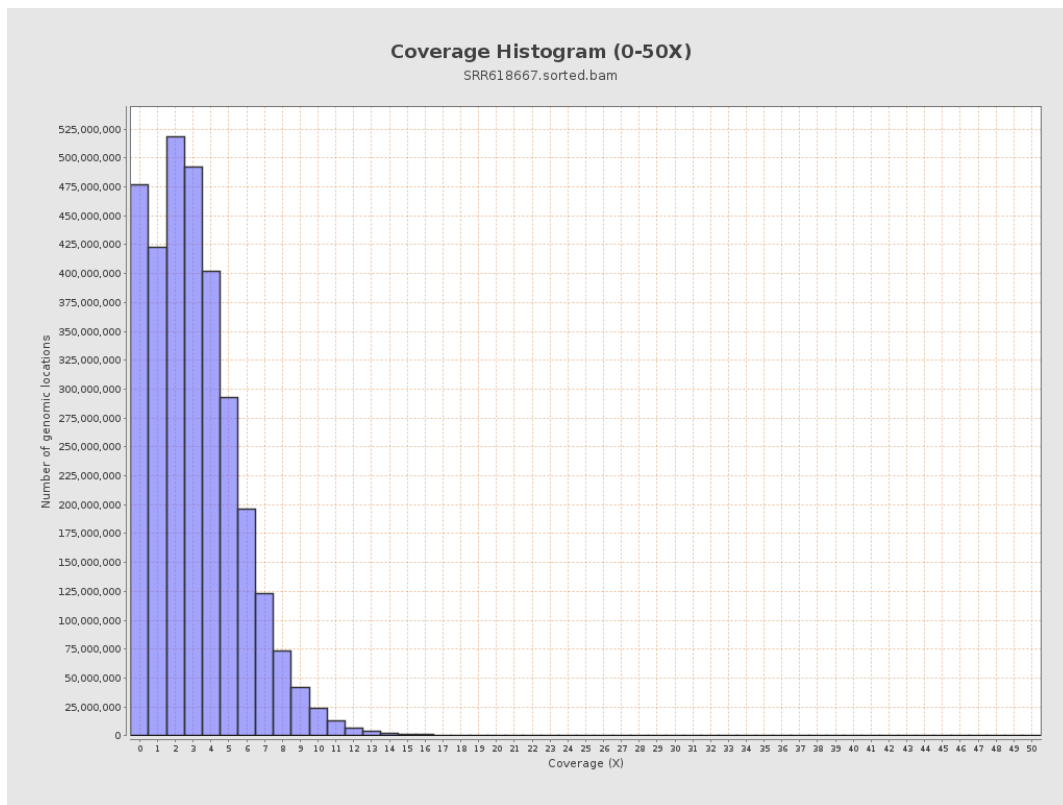
3. Results : Coverage across reference



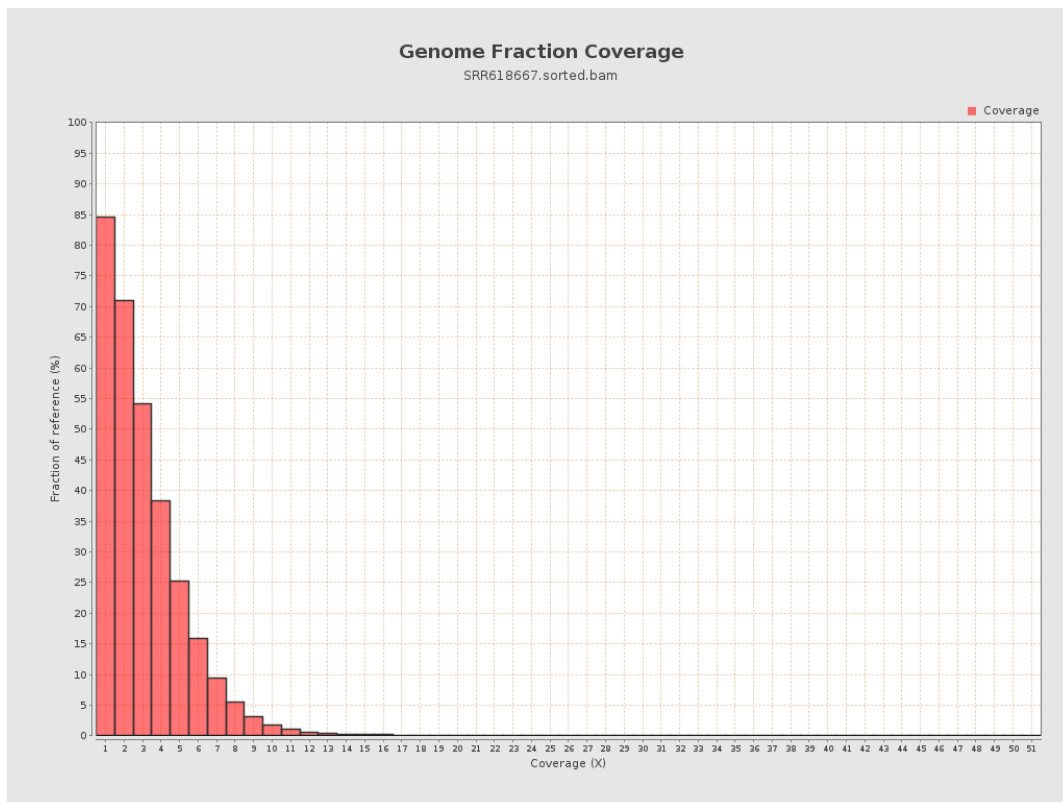
4. Results : Coverage Histogram



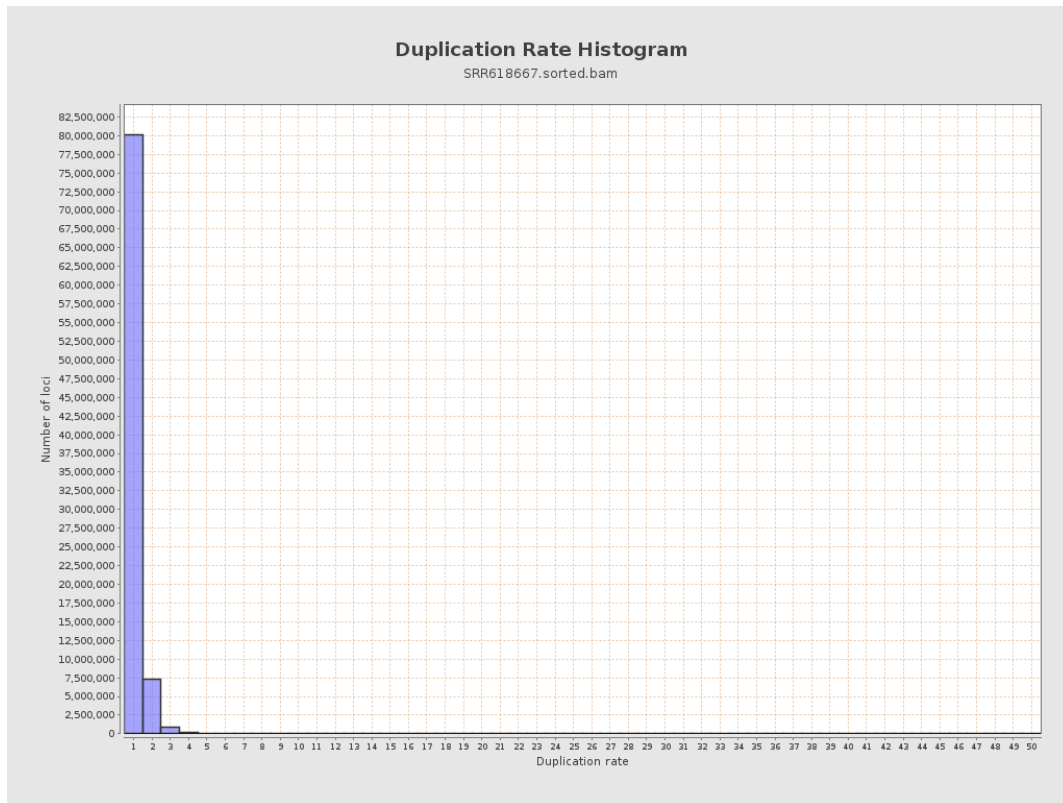
5. Results : Coverage Histogram (0-50X)



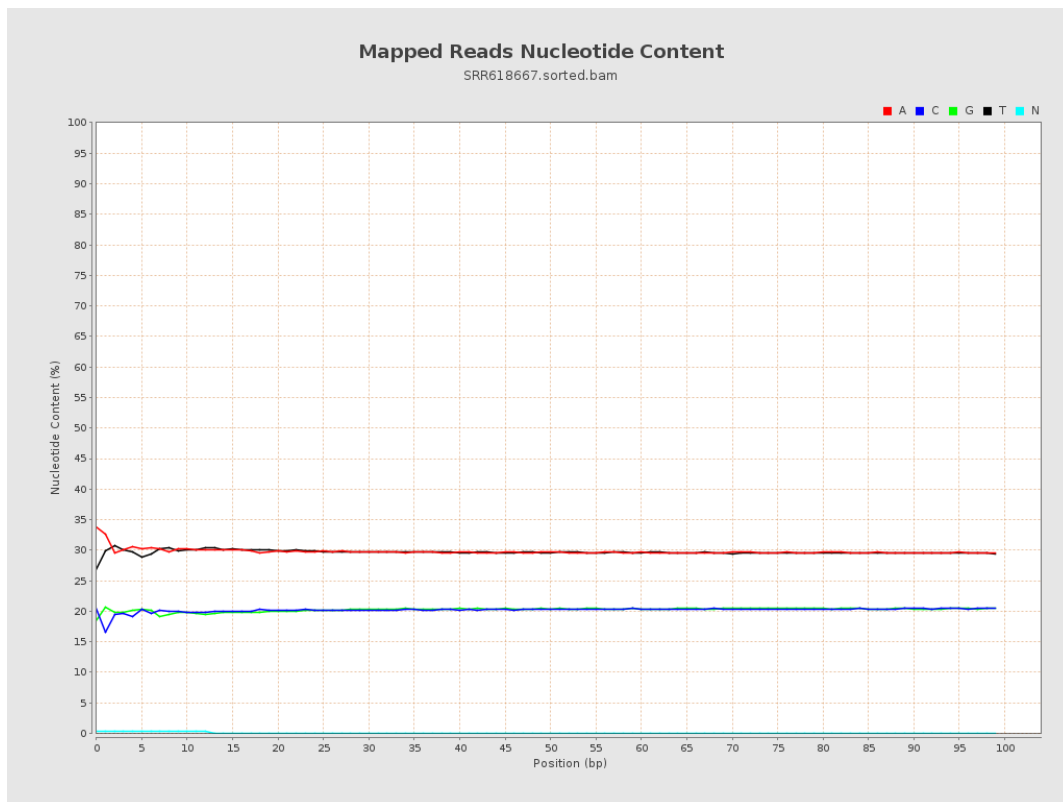
6. Results : Genome Fraction Coverage



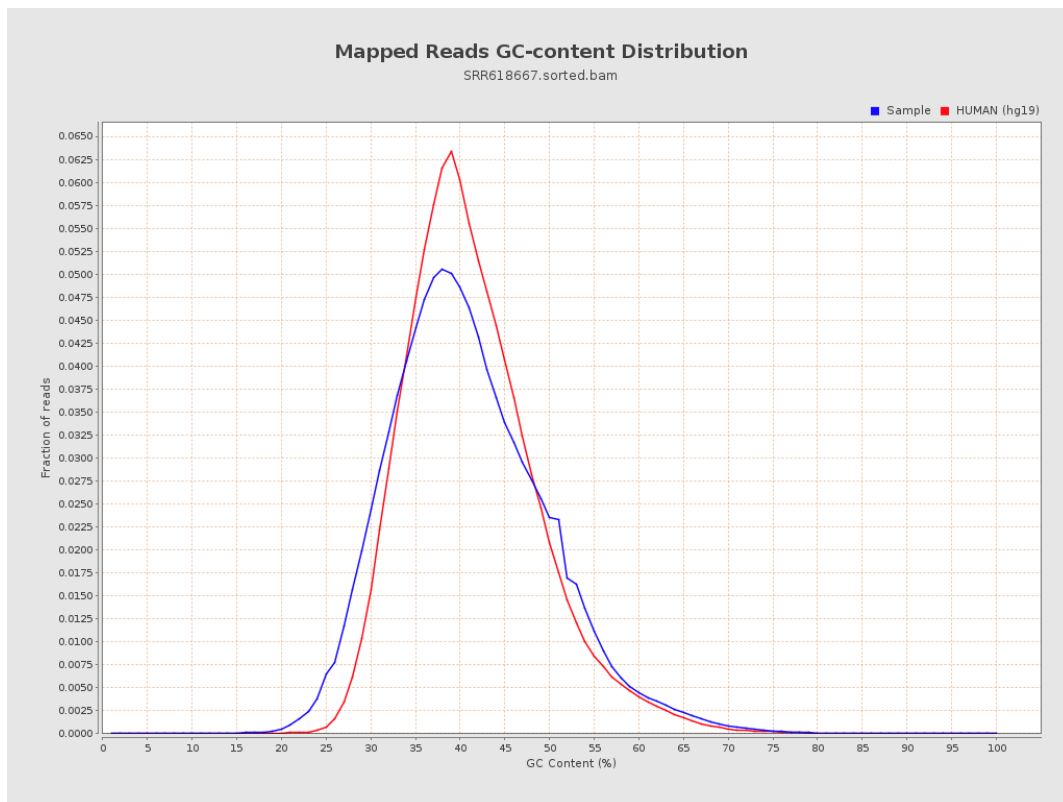
7. Results : Duplication Rate Histogram



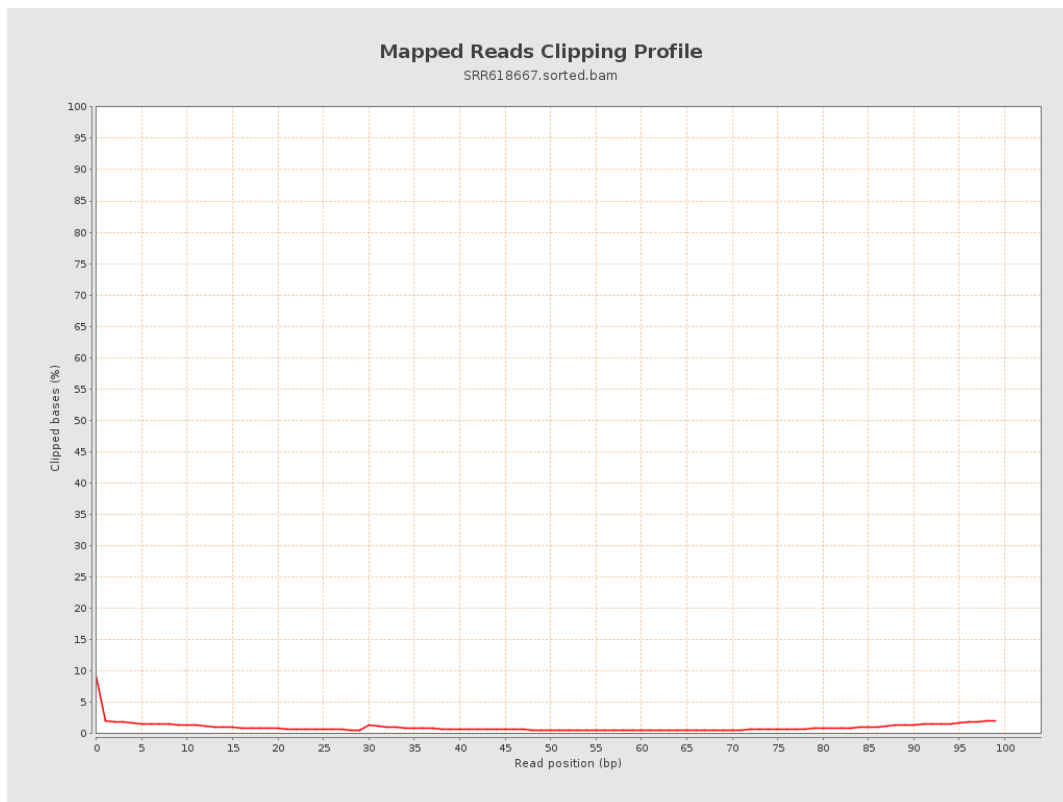
8. Results : Mapped Reads Nucleotide Content



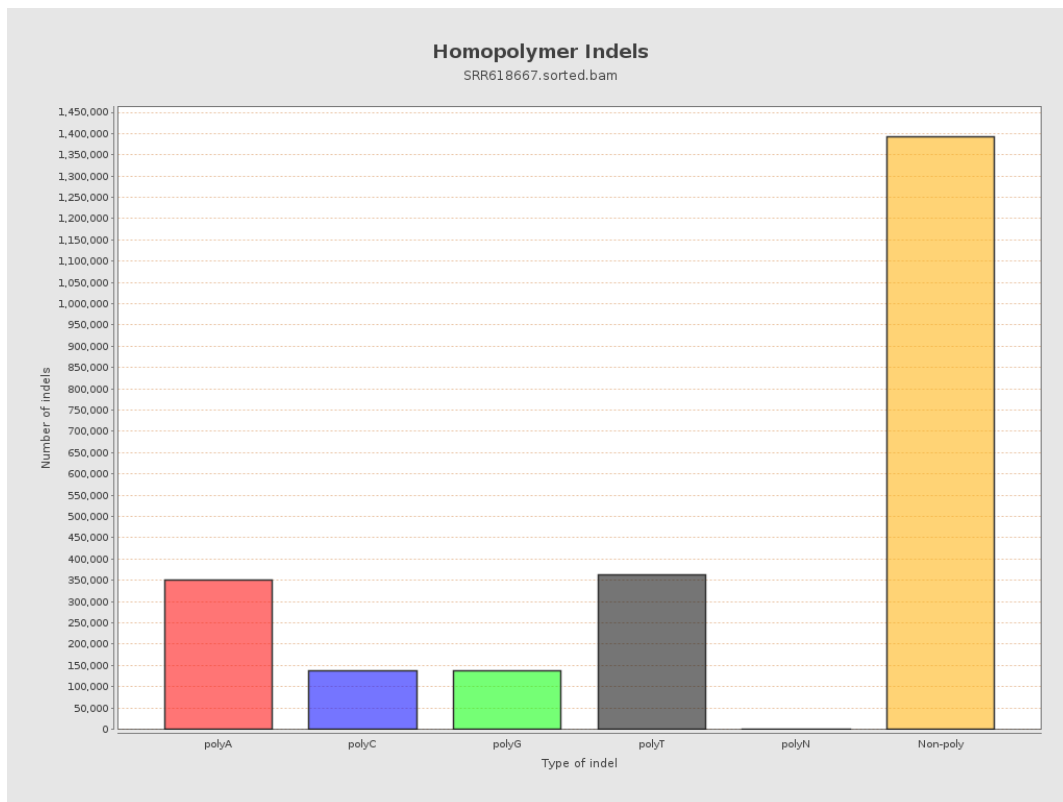
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



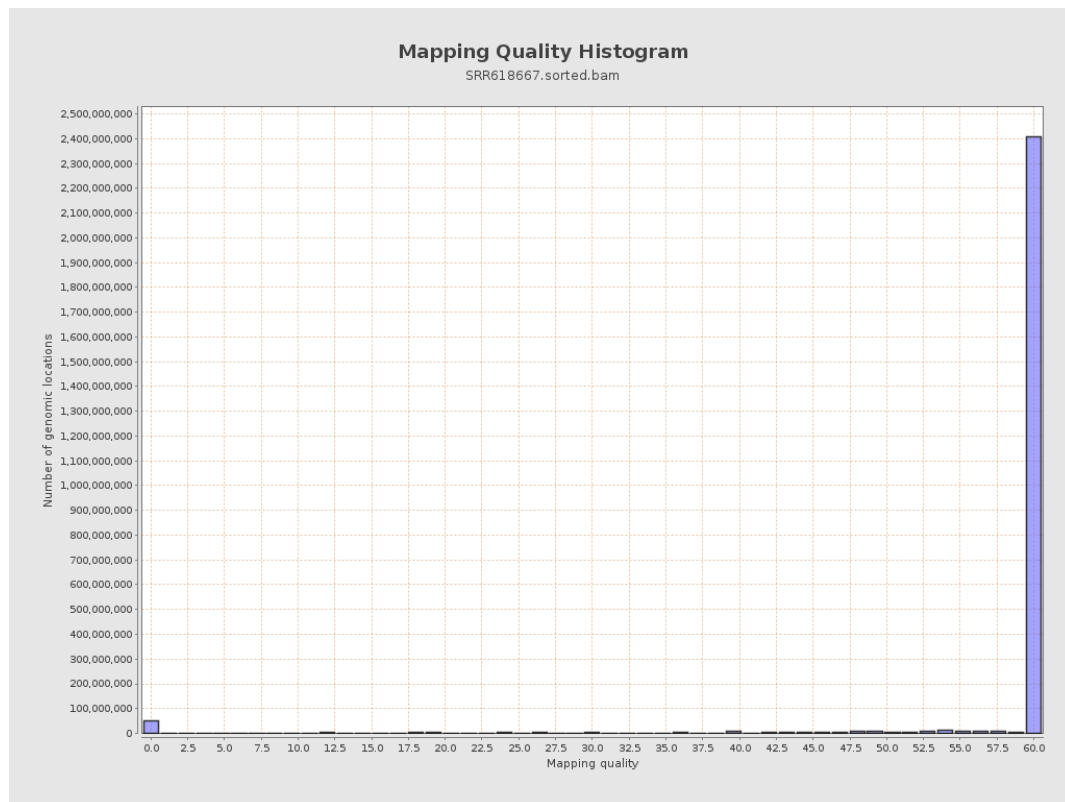
11. Results : Homopolymer Indels



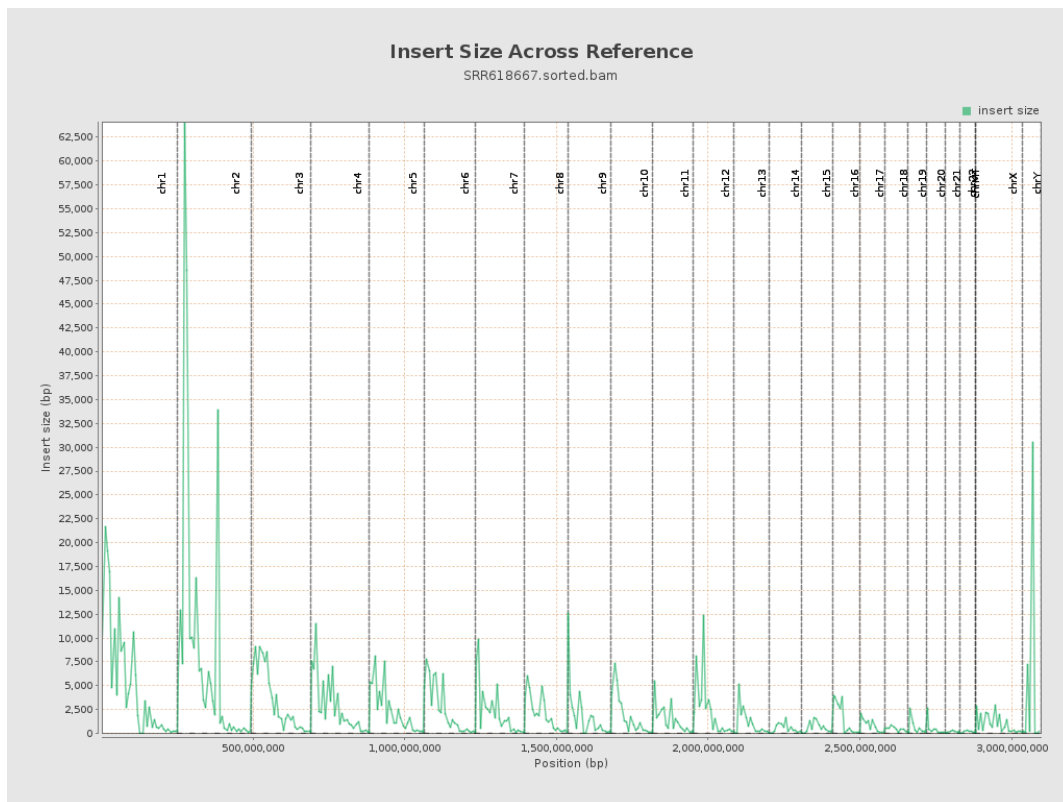
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

