

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/21 07:10:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618668.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_SRR618668 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618668_1.fastq.gz SRR618668_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Jan 21 07:10:48 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618668.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	23,167,464
Mapped reads	21,049,955 / 90.86%
Unmapped reads	2,117,509 / 9.14%
Mapped paired reads	21,049,955 / 90.86%
Mapped reads, first in pair	10,457,961 / 45.14%
Mapped reads, second in pair	10,591,994 / 45.72%
Mapped reads, both in pair	20,491,290 / 88.45%
Mapped reads, singletons	558,665 / 2.41%
Secondary alignments	0
Supplementary alignments	89,524 / 0.39%
Read min/max/mean length	30 / 100 / 100.15
Duplicated reads (estimated)	1,270,540 / 5.48%
Duplication rate	2.99%
Clipped reads	2,293,076 / 9.9%

2.2. ACGT Content

Number/percentage of A's	601,180,079 / 29.55%
Number/percentage of C's	416,779,241 / 20.49%
Number/percentage of T's	596,683,680 / 29.33%
Number/percentage of G's	418,134,002 / 20.55%
Number/percentage of N's	1,739,029 / 0.09%

GC Percentage	41.04%
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2.3. Coverage

Mean	0.6574
Standard Deviation	6.5406

2.4. Mapping Quality

Mean Mapping Quality	53.43
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2.5. Insert size

Mean	58,865.54
Standard Deviation	2,416,875.24
P25/Median/P75	163 / 170 / 177

2.6. Mismatches and indels

General error rate	0.86%
Mismatches	16,916,735
Insertions	216,027
Mapped reads with at least one insertion	0.99%
Deletions	255,479
Mapped reads with at least one deletion	1.17%
Homopolymer indels	40.87%

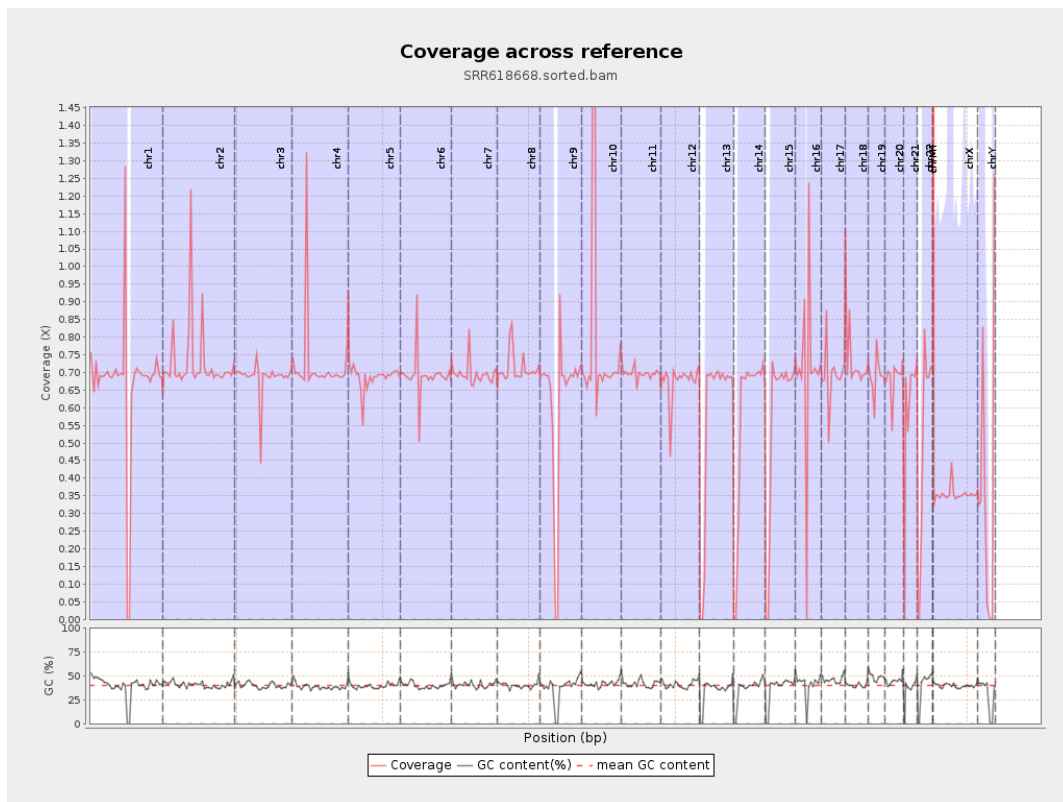
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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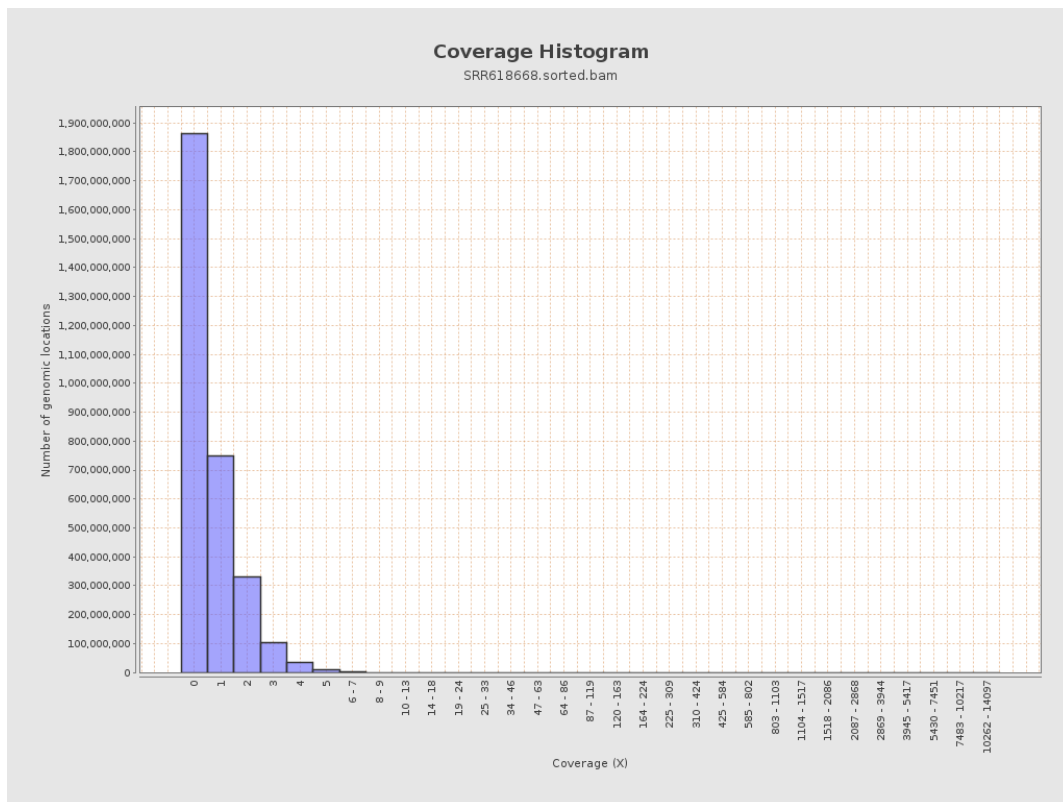
		bases	coverage	deviation
chr1	249250621	166641785	0.6686	14.4757
chr2	243199373	176911342	0.7274	5.9275
chr3	198022430	135952371	0.6866	1.2175
chr4	191154276	137864222	0.7212	3.808
chr5	180915260	124223028	0.6866	1.1266
chr6	171115067	118444234	0.6922	2.9124
chr7	159138663	110779681	0.6961	4.5366
chr8	146364022	104239261	0.7122	8.1417
chr9	141213431	87493825	0.6196	6.4782
chr10	135534747	105820575	0.7808	14.9359
chr11	135006516	94026734	0.6965	3.4318
chr12	133851895	90501661	0.6761	1.1025
chr13	115169878	66381401	0.5764	0.9635
chr14	107349540	62473927	0.582	1.2449
chr15	102531392	58153259	0.5672	1.0076
chr16	90354753	63873897	0.7069	4.929
chr17	81195210	56165438	0.6917	2.9432
chr18	78077248	57116313	0.7315	8.207
chr19	59128983	40759620	0.6893	6.3834
chr20	63025520	42844124	0.6798	2.364
chr21	48129895	29110683	0.6048	3.5059
chr22	51304566	25800785	0.5029	3.1606
chrMT	16571	920831	55.5688	12.2776
chrX	155270560	55112370	0.3549	1.619

chrY	59373566	23535807	0.3964	7.2637
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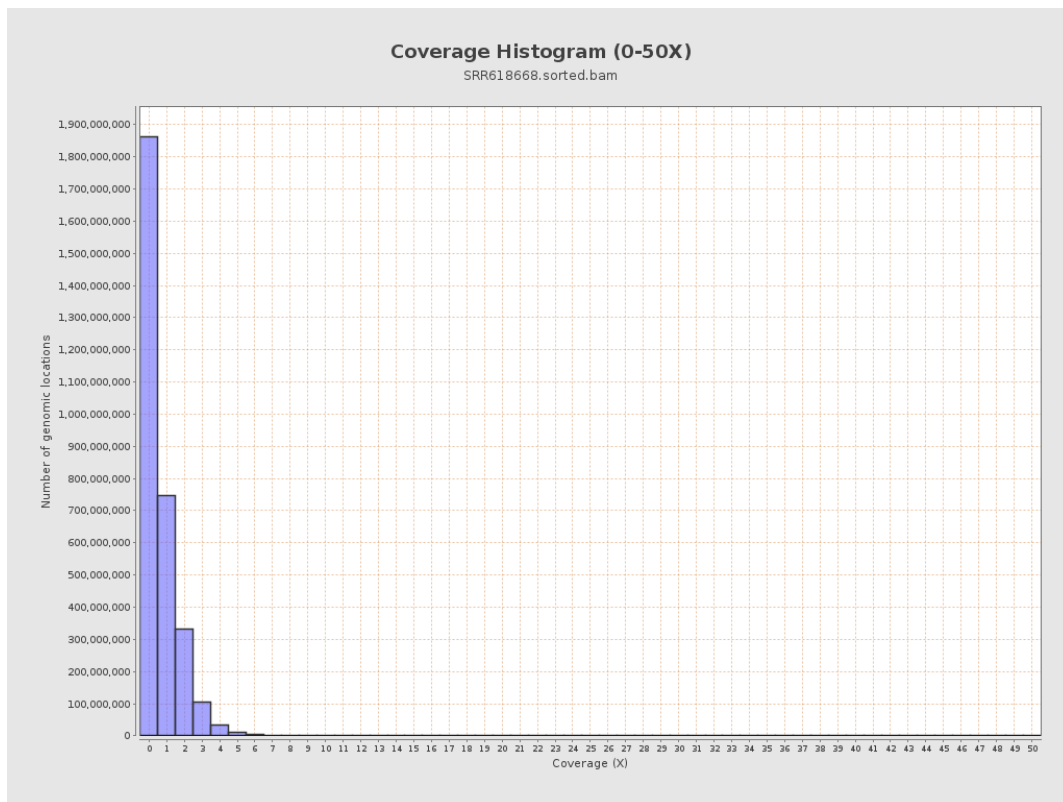
3. Results : Coverage across reference



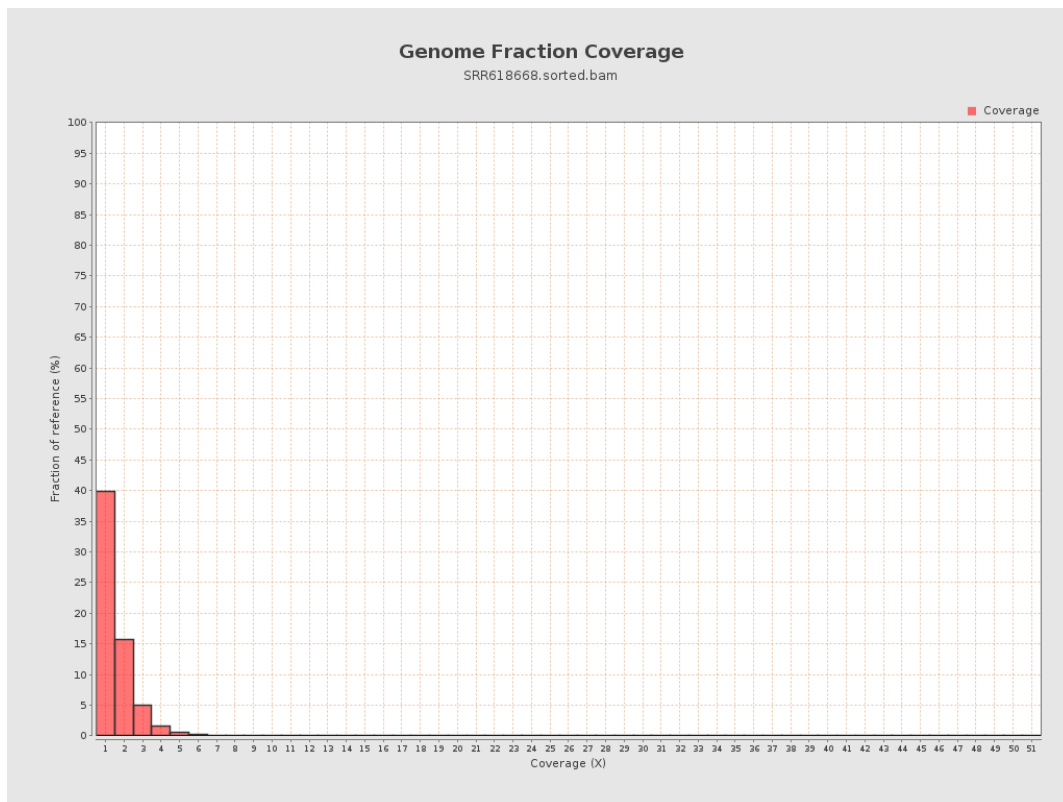
4. Results : Coverage Histogram



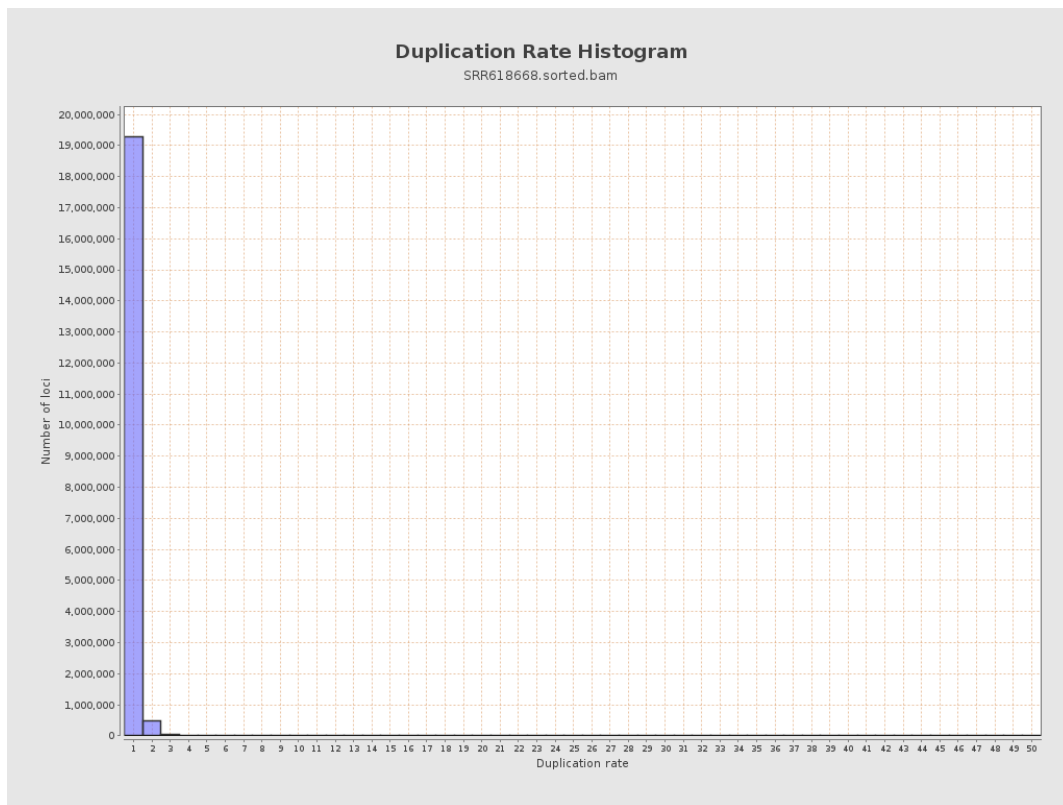
5. Results : Coverage Histogram (0-50X)



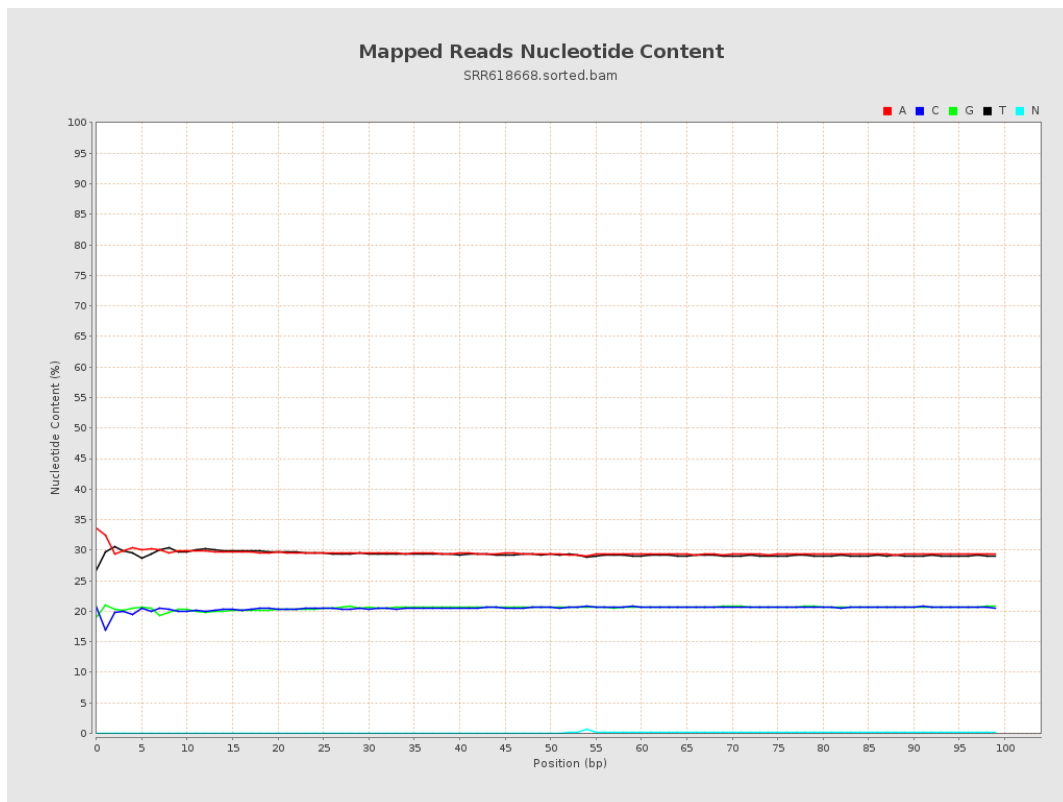
6. Results : Genome Fraction Coverage



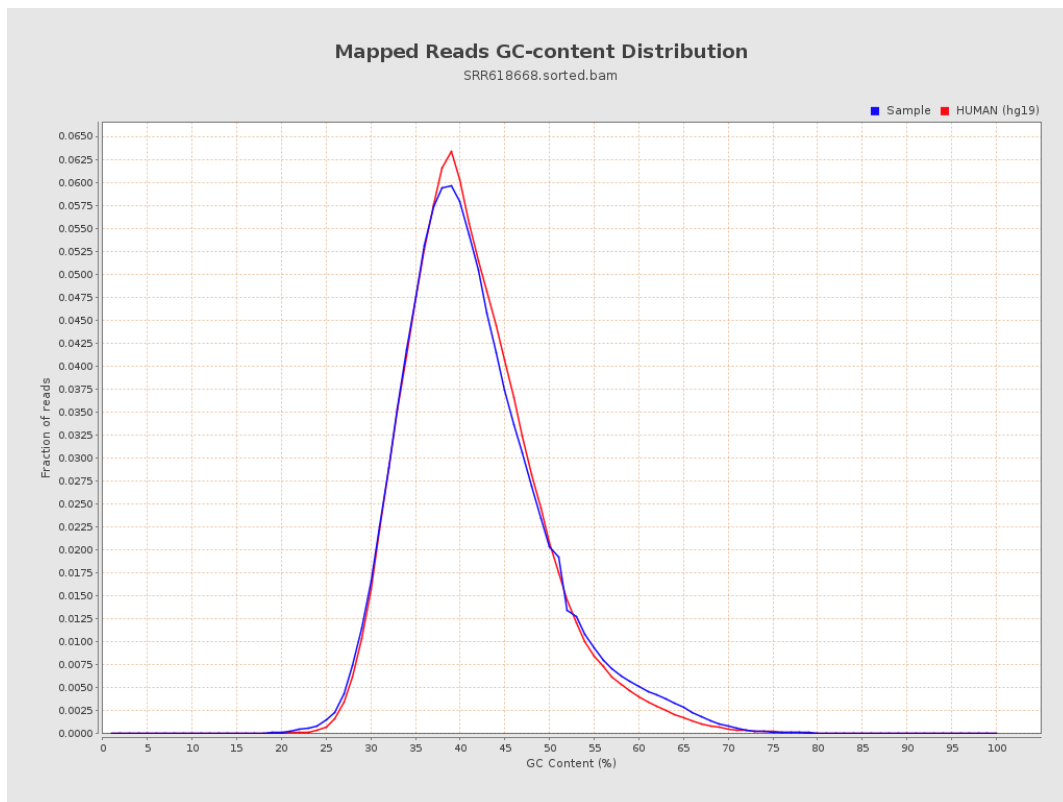
7. Results : Duplication Rate Histogram



8. Results : Mapped Reads Nucleotide Content



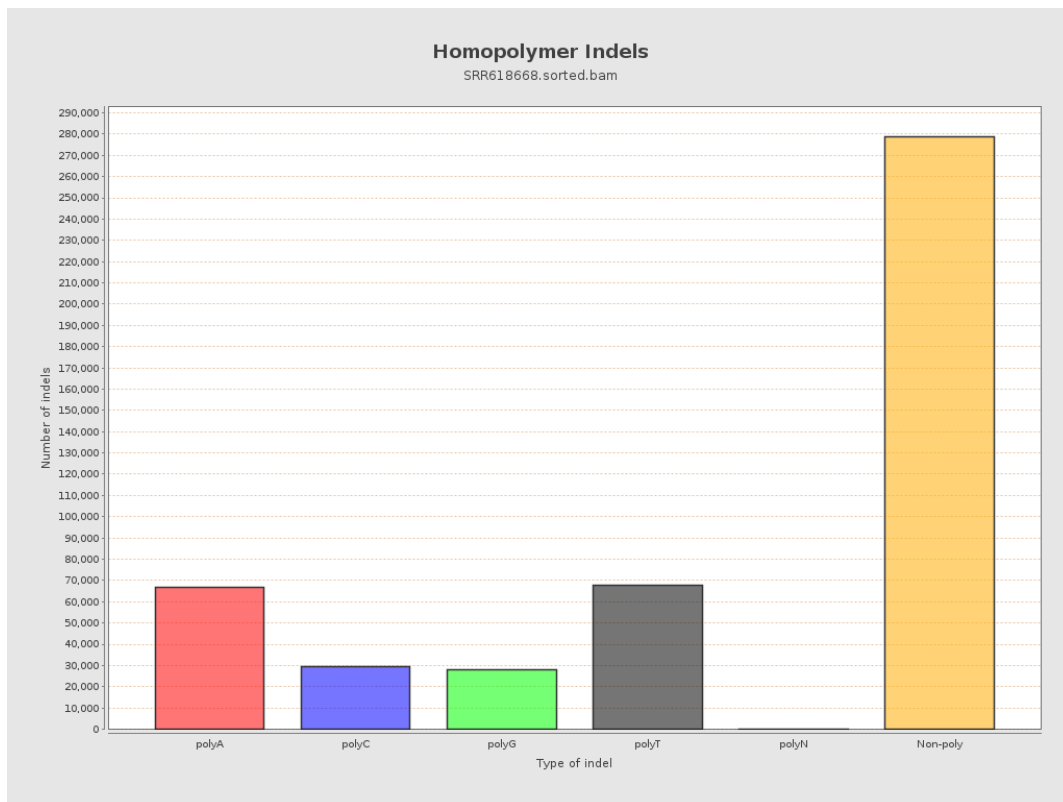
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



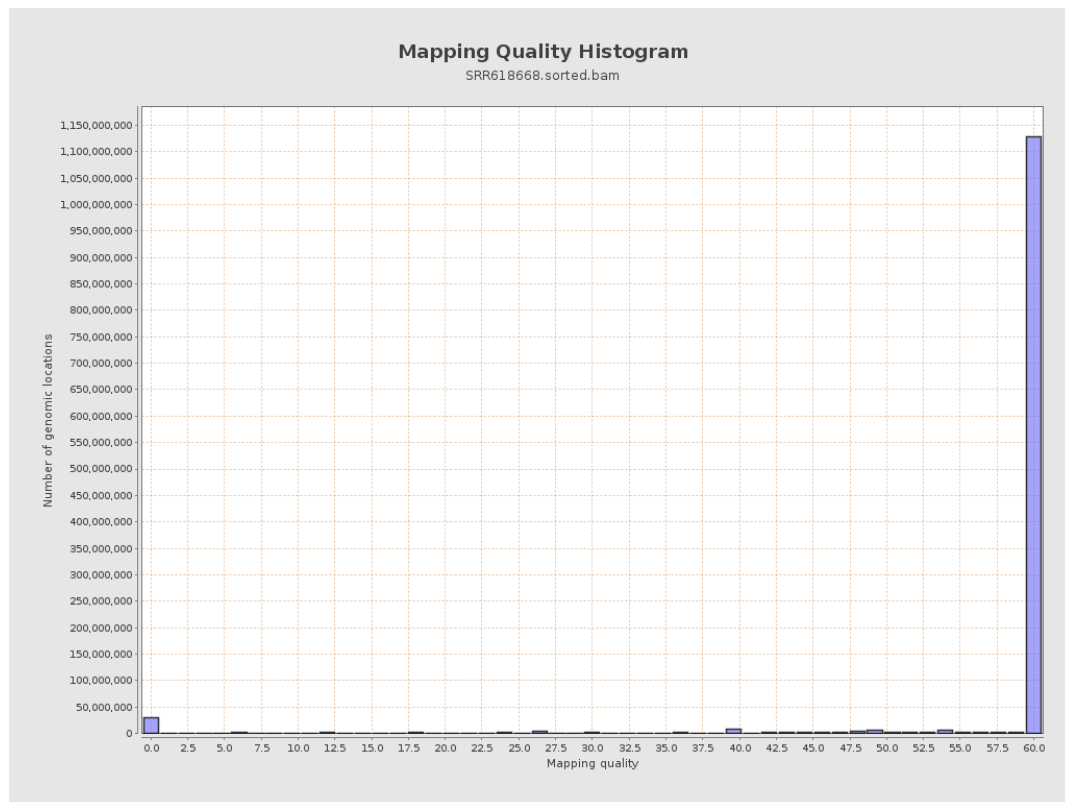
11. Results : Homopolymer Indels



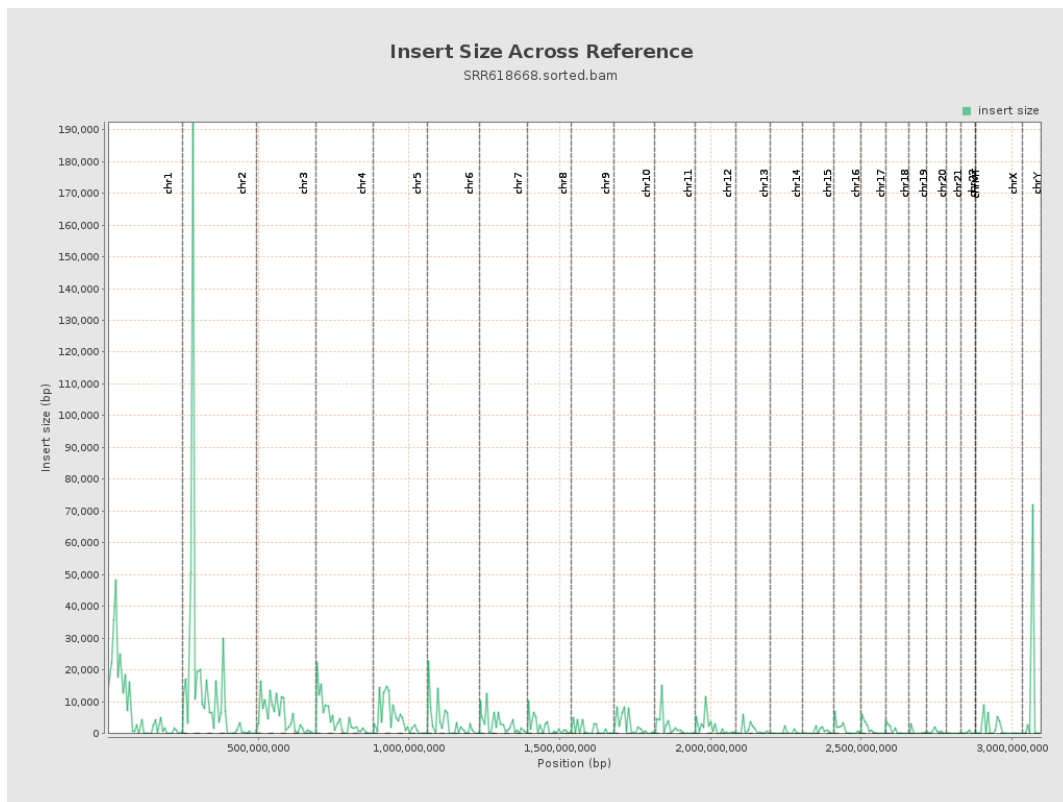
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

