

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/19 10:45:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618617.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_SRR618617 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618617_1.fastq.gz SRR618617_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Jan 19 10:45:47 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618617.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	36,190,550
Mapped reads	32,520,089 / 89.86%
Unmapped reads	3,670,461 / 10.14%
Mapped paired reads	32,520,089 / 89.86%
Mapped reads, first in pair	16,679,778 / 46.09%
Mapped reads, second in pair	15,840,311 / 43.77%
Mapped reads, both in pair	30,968,604 / 85.57%
Mapped reads, singletons	1,551,485 / 4.29%
Secondary alignments	0
Supplementary alignments	41,634 / 0.12%
Read min/max/mean length	30 / 100 / 100.04
Duplicated reads (estimated)	11,951,420 / 33.02%
Duplication rate	29.45%
Clipped reads	6,567,286 / 18.15%

2.2. ACGT Content

Number/percentage of A's	809,285,263 / 26.28%
Number/percentage of C's	720,945,240 / 23.41%
Number/percentage of T's	814,877,588 / 26.46%
Number/percentage of G's	732,382,086 / 23.78%
Number/percentage of N's	2,366,744 / 0.08%

GC Percentage	47.19%
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2.3. Coverage

Mean	0.9955
Standard Deviation	4.9494

2.4. Mapping Quality

Mean Mapping Quality	53.09
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2.5. Insert size

Mean	60,446.44
Standard Deviation	2,521,639.6
P25/Median/P75	183 / 212 / 252

2.6. Mismatches and indels

General error rate	1.49%
Mismatches	45,175,939
Insertions	538,599
Mapped reads with at least one insertion	1.63%
Deletions	1,286,180
Mapped reads with at least one deletion	3.87%
Homopolymer indels	51.37%

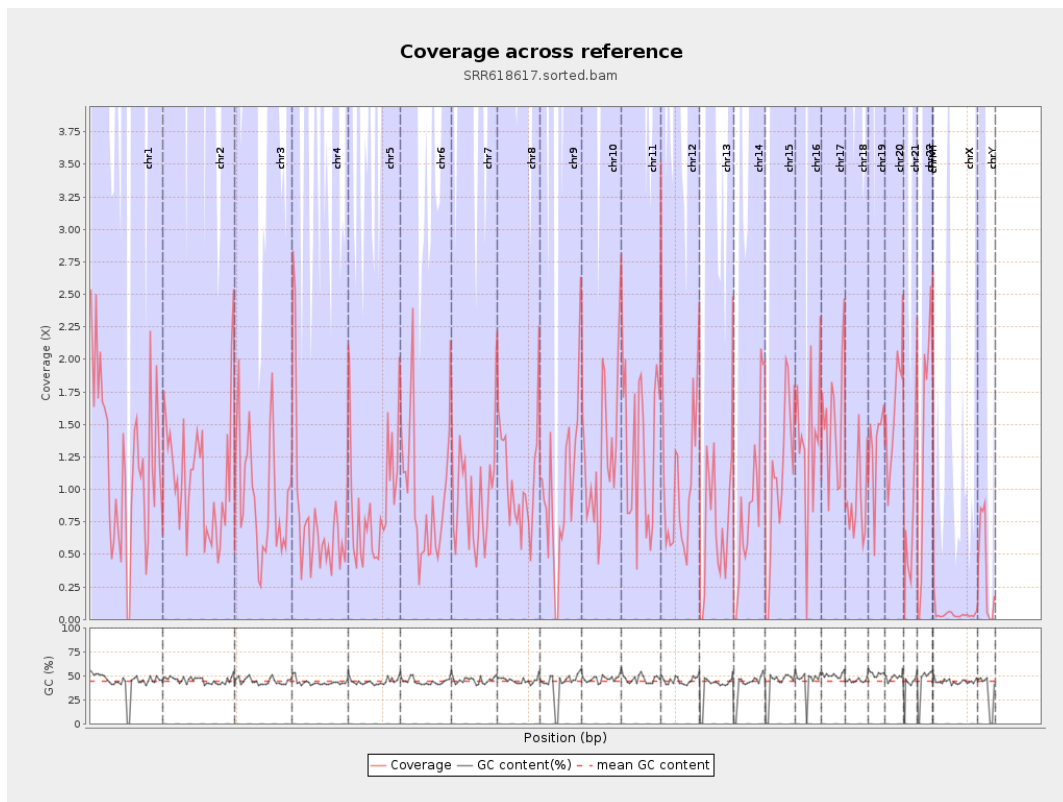
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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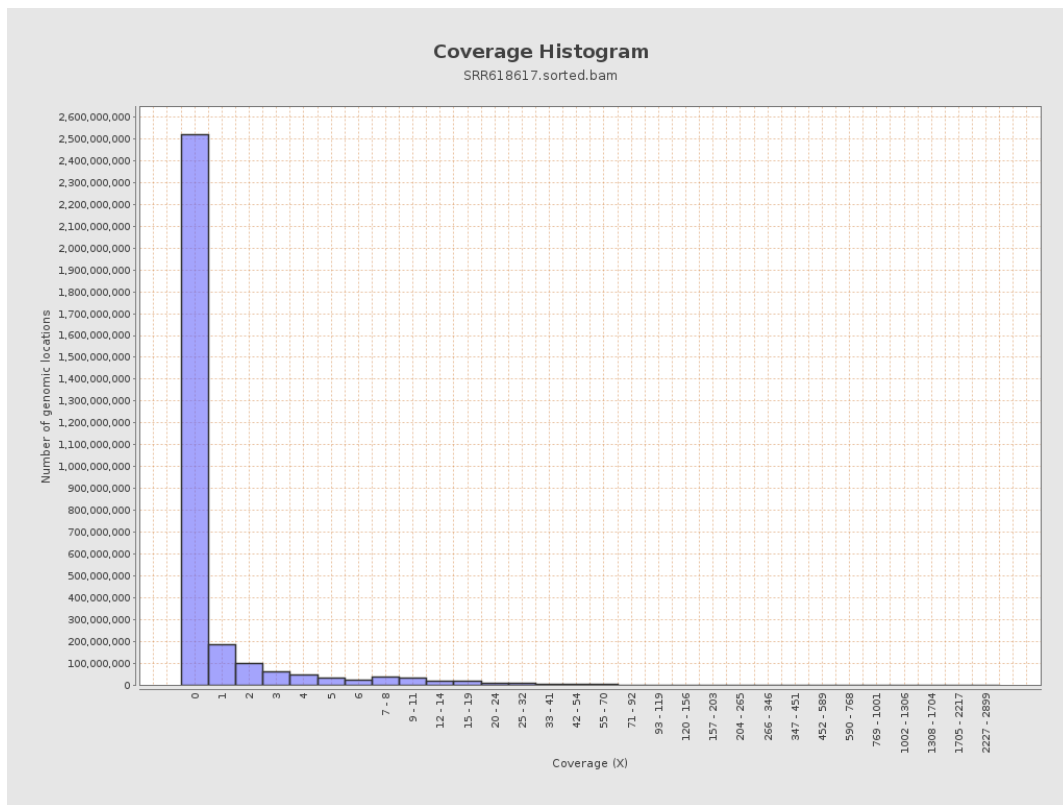
		bases	coverage	deviation
chr1	249250621	297318295	1.1928	6.1313
chr2	243199373	263436702	1.0832	5.1168
chr3	198022430	185007094	0.9343	4.3821
chr4	191154276	148166848	0.7751	4.4165
chr5	180915260	163631365	0.9045	4.0795
chr6	171115067	159819874	0.934	4.3098
chr7	159138663	151552565	0.9523	4.6792
chr8	146364022	156250432	1.0675	4.7384
chr9	141213431	140825018	0.9972	5.5864
chr10	135534747	169373598	1.2497	5.4555
chr11	135006516	177716311	1.3164	5.657
chr12	133851895	143530690	1.0723	5.1047
chr13	115169878	83834658	0.7279	3.7333
chr14	107349540	93951745	0.8752	3.9837
chr15	102531392	108601815	1.0592	5.2959
chr16	90354753	125067092	1.3842	6.2971
chr17	81195210	123336420	1.519	5.8669
chr18	78077248	68952918	0.8831	4.1351
chr19	59128983	78362768	1.3253	5.8639
chr20	63025520	100041440	1.5873	6.2941
chr21	48129895	39868021	0.8283	6.2219
chr22	51304566	72039609	1.4042	5.7281
chrMT	16571	44355	2.6767	11.4063
chrX	155270560	6604153	0.0425	1.9756

chrY	59373566	24325277	0.4097	2.8383
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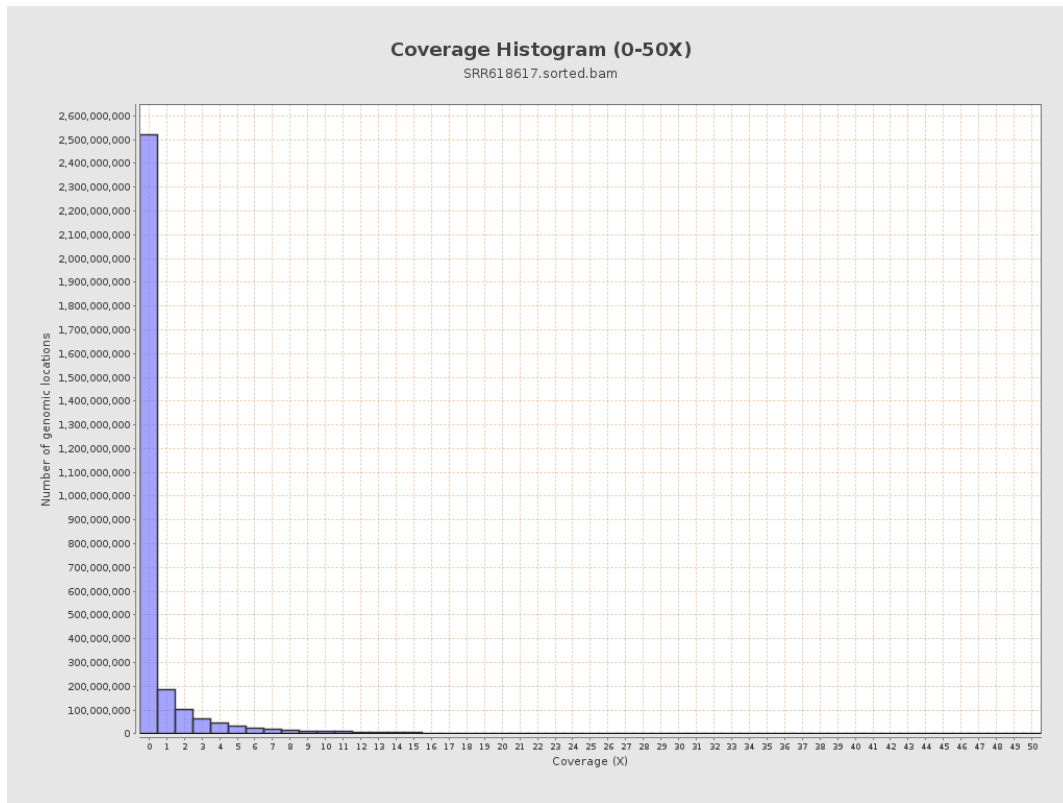
3. Results : Coverage across reference



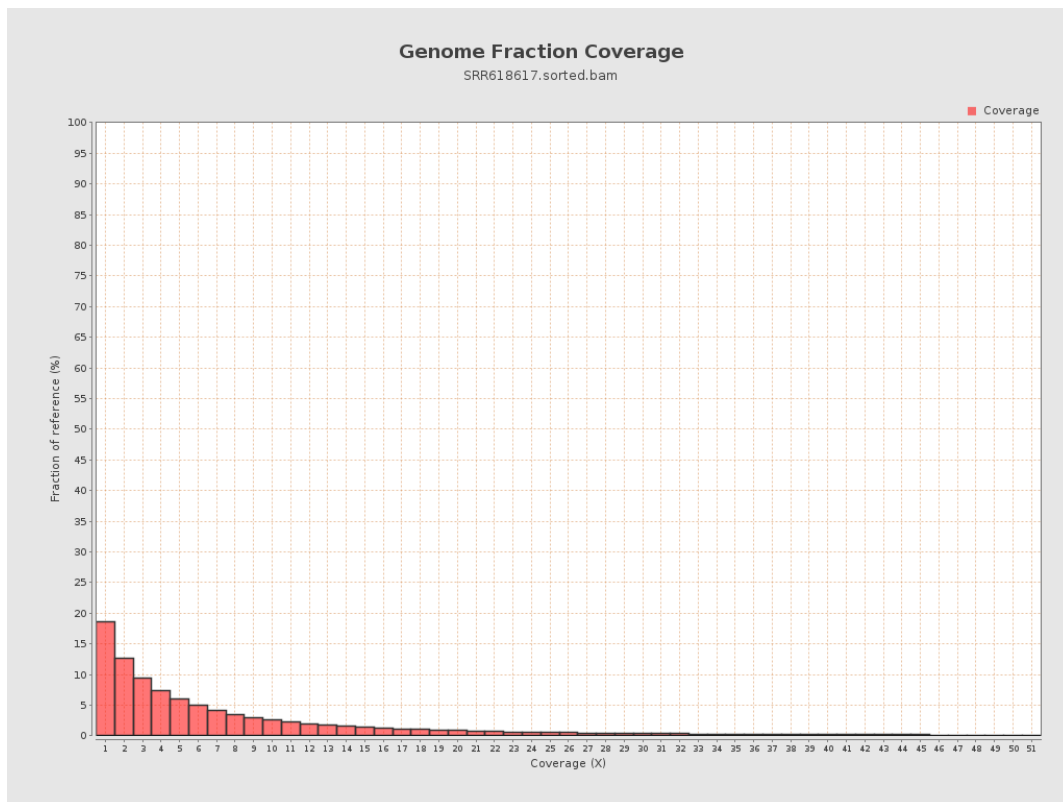
4. Results : Coverage Histogram



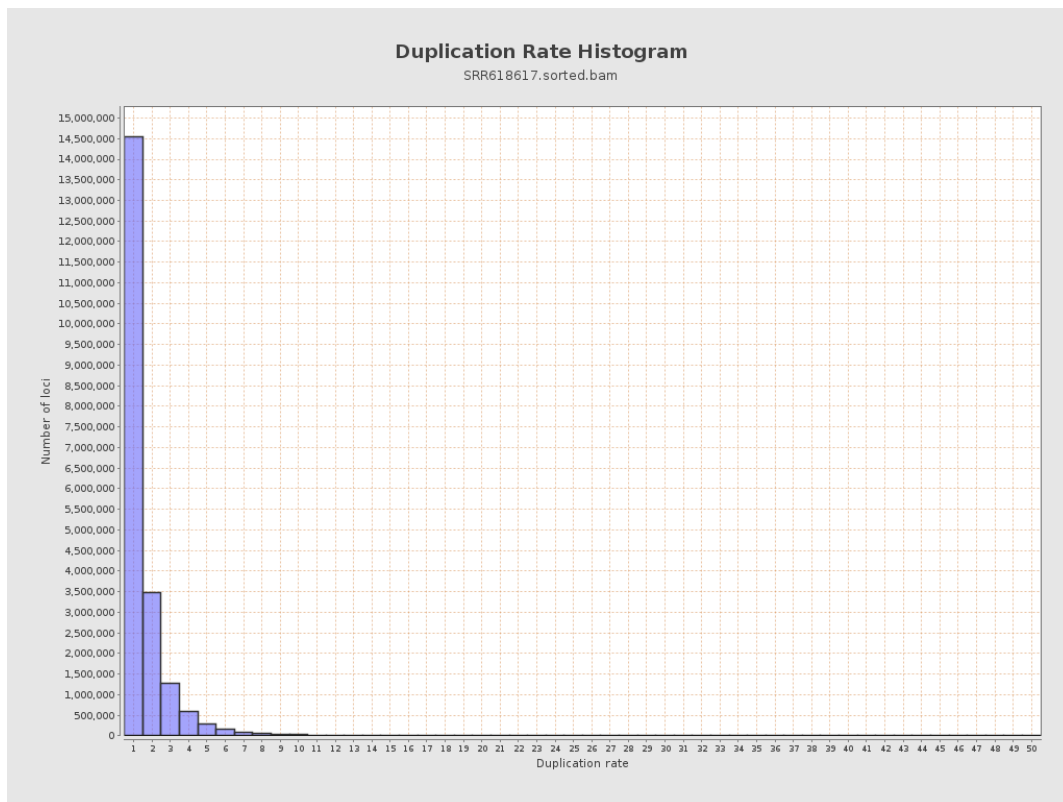
5. Results : Coverage Histogram (0-50X)



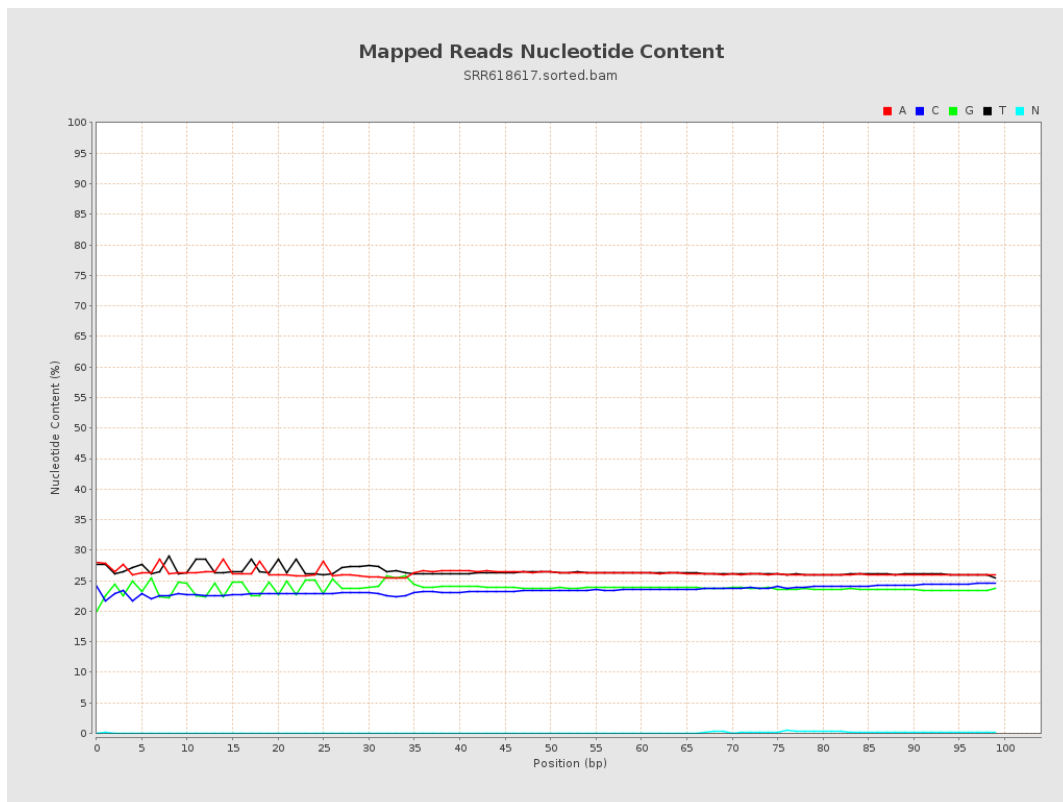
6. Results : Genome Fraction Coverage



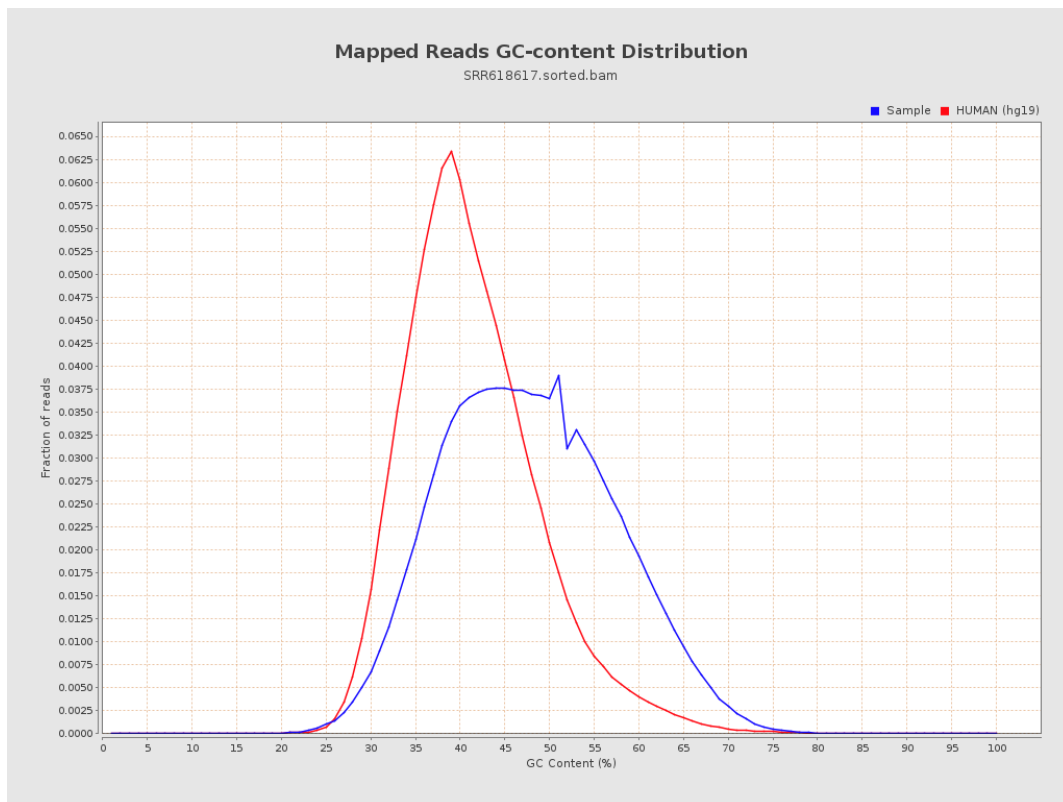
7. Results : Duplication Rate Histogram



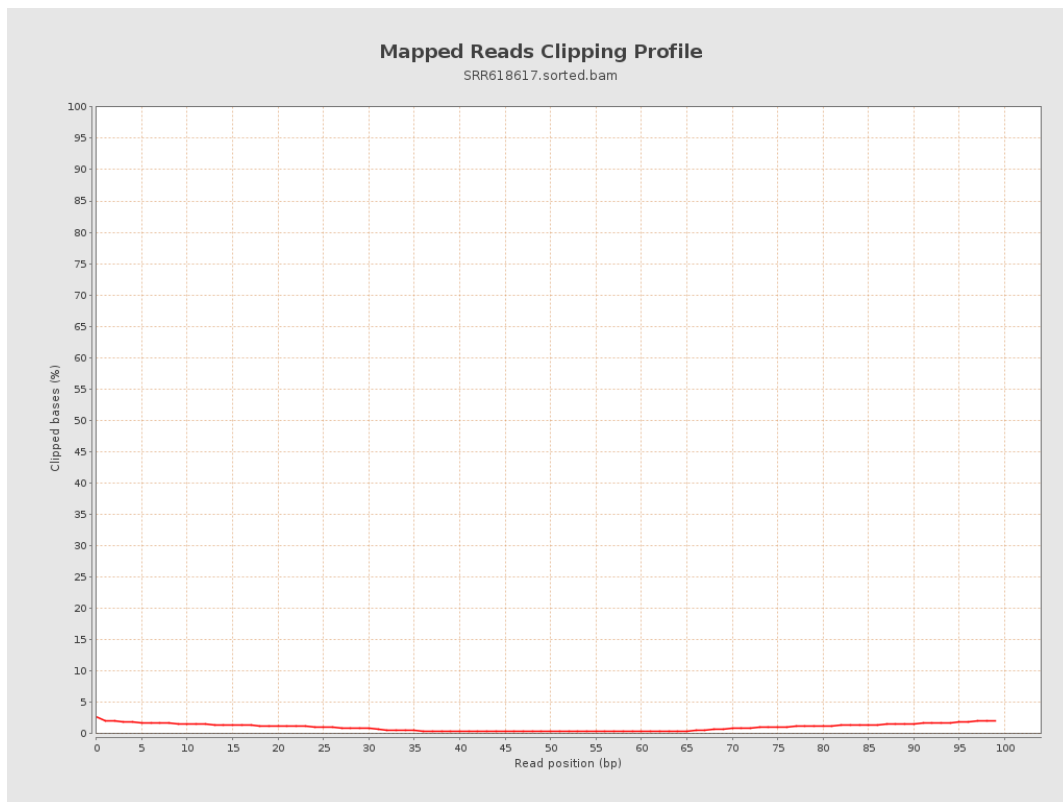
8. Results : Mapped Reads Nucleotide Content



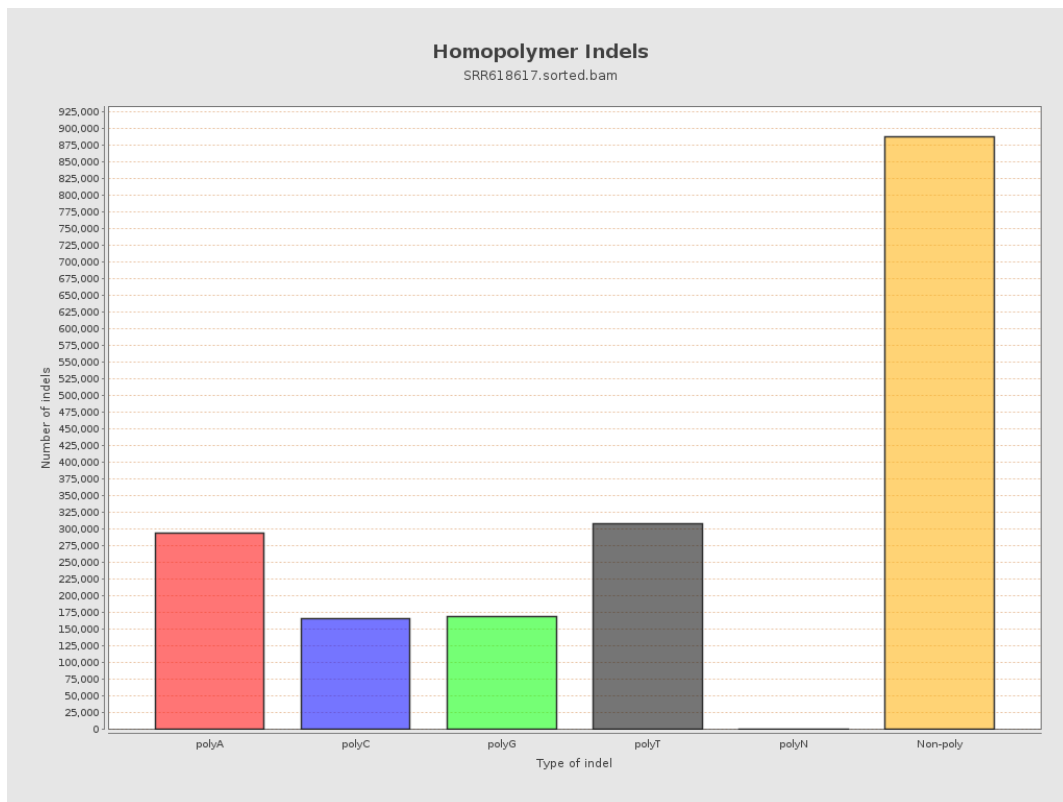
9. Results : Mapped Reads GC-content Distribution



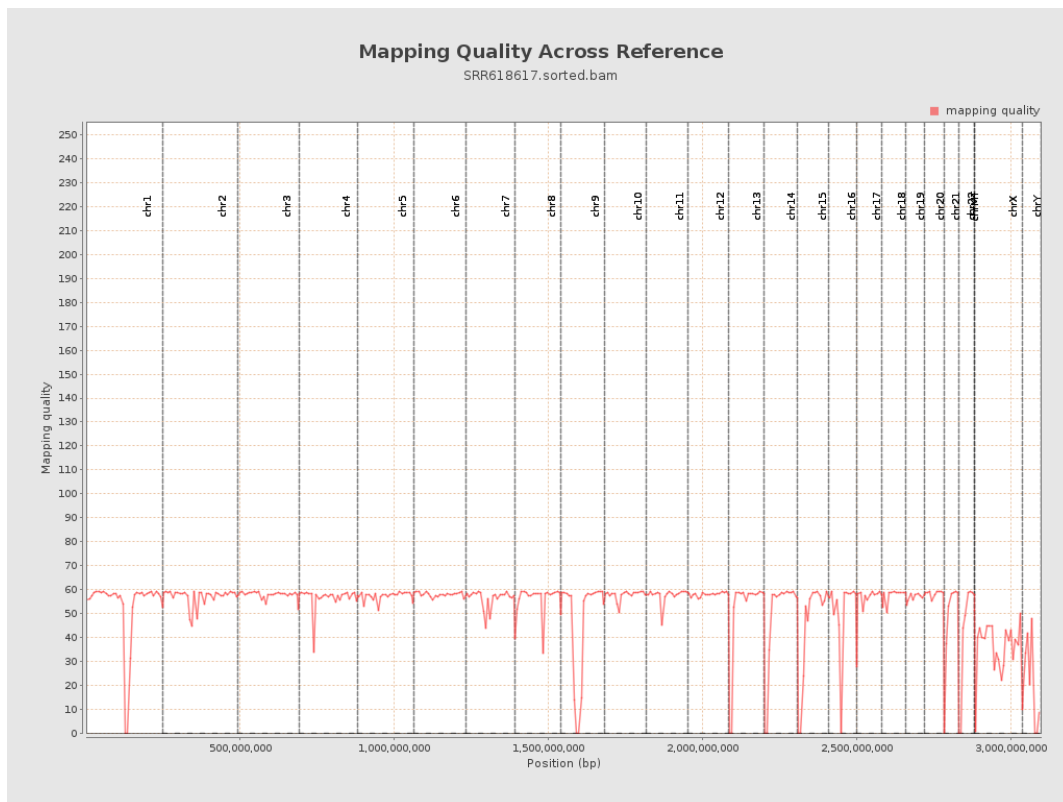
10. Results : Mapped Reads Clipping Profile



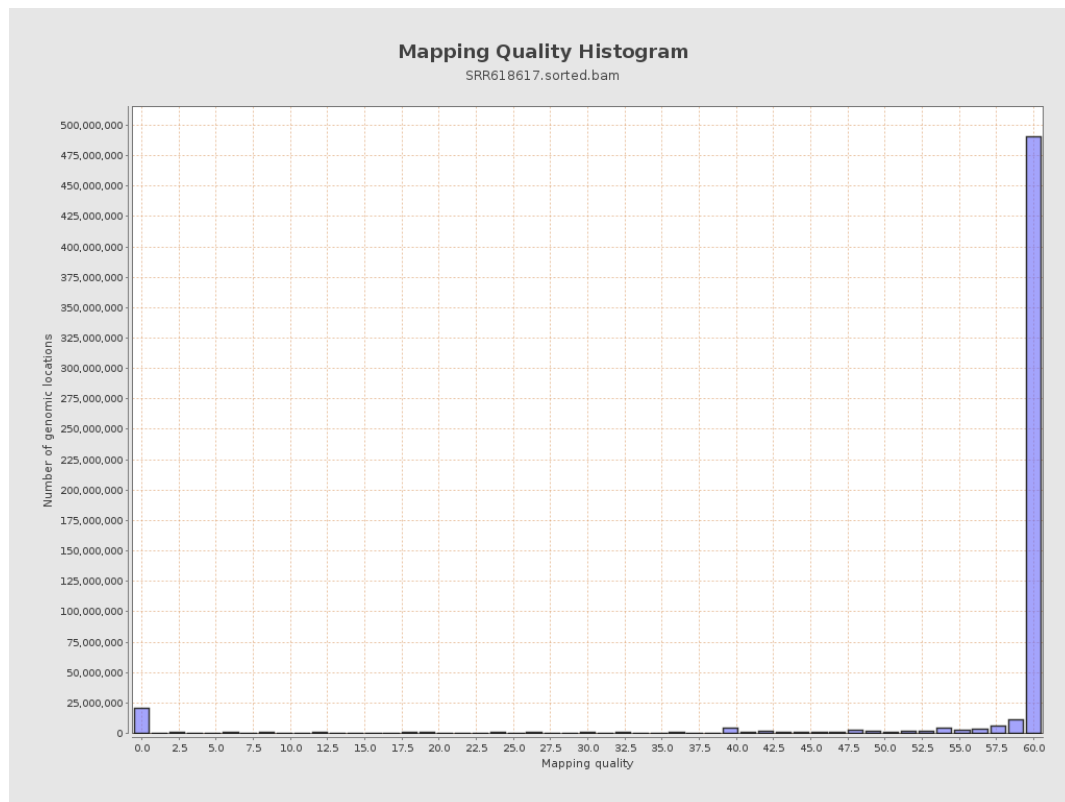
11. Results : Homopolymer Indels



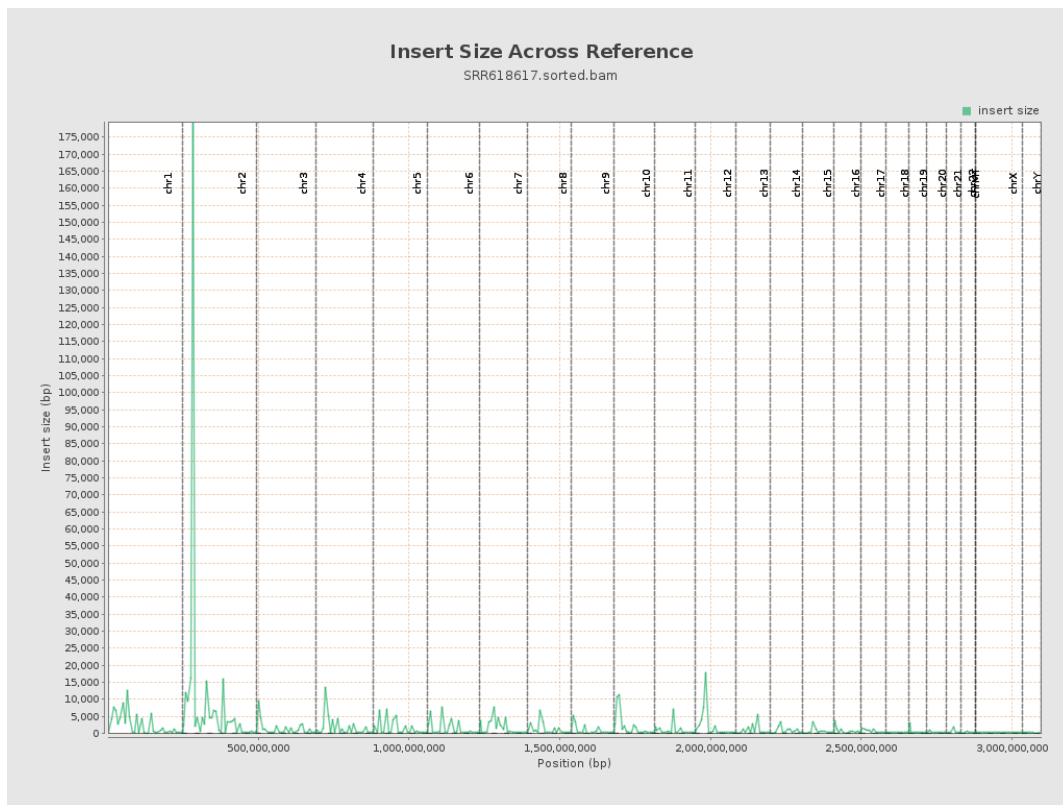
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

