

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/20 23:21:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618665.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_SRR618665 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618665_1.fastq.gz SRR618665_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Jan 20 23:21:34 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618665.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	42,789,014
Mapped reads	40,969,892 / 95.75%
Unmapped reads	1,819,122 / 4.25%
Mapped paired reads	40,969,892 / 95.75%
Mapped reads, first in pair	20,532,077 / 47.98%
Mapped reads, second in pair	20,437,815 / 47.76%
Mapped reads, both in pair	40,334,830 / 94.26%
Mapped reads, singletons	635,062 / 1.48%
Secondary alignments	0
Supplementary alignments	159,798 / 0.37%
Read min/max/mean length	30 / 100 / 100.15
Duplicated reads (estimated)	3,647,095 / 8.52%
Duplication rate	4.99%
Clipped reads	2,556,948 / 5.98%

2.2. ACGT Content

Number/percentage of A's	1,206,607,818 / 29.89%
Number/percentage of C's	812,576,089 / 20.13%
Number/percentage of T's	1,202,541,667 / 29.79%
Number/percentage of G's	814,143,047 / 20.17%
Number/percentage of N's	330,044 / 0.01%

GC Percentage	40.3%
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2.3. Coverage

Mean	1.3042
Standard Deviation	14.4162

2.4. Mapping Quality

Mean Mapping Quality	53.66
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2.5. Insert size

Mean	49,367.35
Standard Deviation	2,115,710.12
P25/Median/P75	164 / 170 / 178

2.6. Mismatches and indels

General error rate	0.67%
Mismatches	25,781,356
Insertions	442,942
Mapped reads with at least one insertion	1.04%
Deletions	531,153
Mapped reads with at least one deletion	1.25%
Homopolymer indels	41.53%

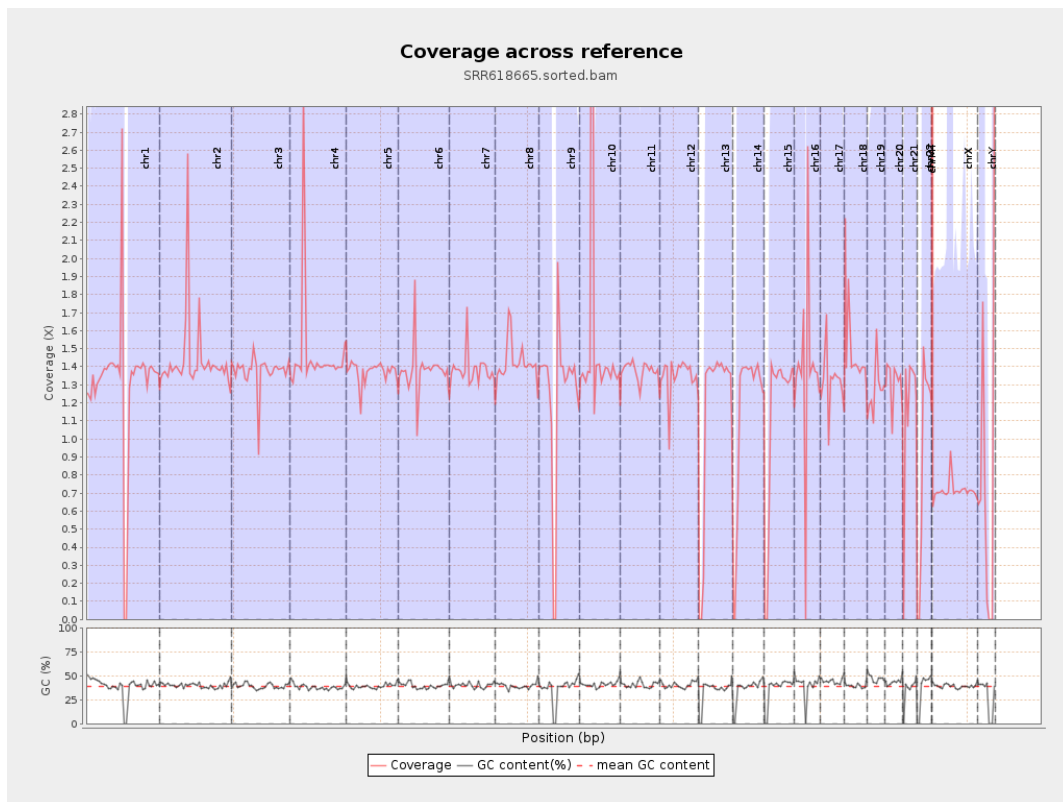
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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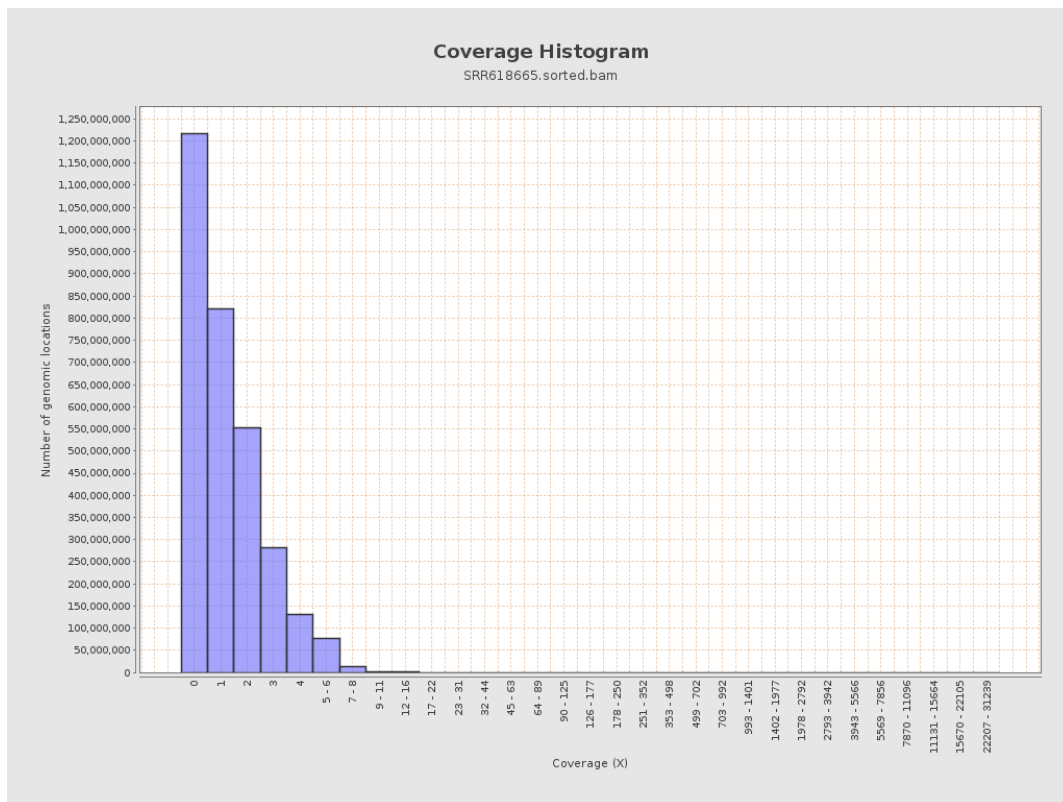
		bases	coverage	deviation
chr1	249250621	328411106	1.3176	32.0406
chr2	243199373	350135233	1.4397	9.4482
chr3	198022430	271848661	1.3728	2.0693
chr4	191154276	279495277	1.4621	8.876
chr5	180915260	247680430	1.369	1.8054
chr6	171115067	236907150	1.3845	6.0297
chr7	159138663	219973093	1.3823	10.0216
chr8	146364022	208419081	1.424	18.4585
chr9	141213431	173210615	1.2266	15.3011
chr10	135534747	213192661	1.573	34.2203
chr11	135006516	185717172	1.3756	7.37
chr12	133851895	180291104	1.3469	1.7199
chr13	115169878	132962342	1.1545	1.5014
chr14	107349540	123052655	1.1463	1.7969
chr15	102531392	114157065	1.1134	1.4935
chr16	90354753	124132952	1.3738	10.6159
chr17	81195210	106574185	1.3126	6.3879
chr18	78077248	115416224	1.4782	18.3832
chr19	59128983	75213410	1.272	14.0718
chr20	63025520	82621381	1.3109	4.8869
chr21	48129895	57159953	1.1876	7.2412
chr22	51304566	47692269	0.9296	6.5182
chrMT	16571	1988268	119.9848	21.0834
chrX	155270560	110851604	0.7139	3.3607

chrY	59373566	50419941	0.8492	16.9005
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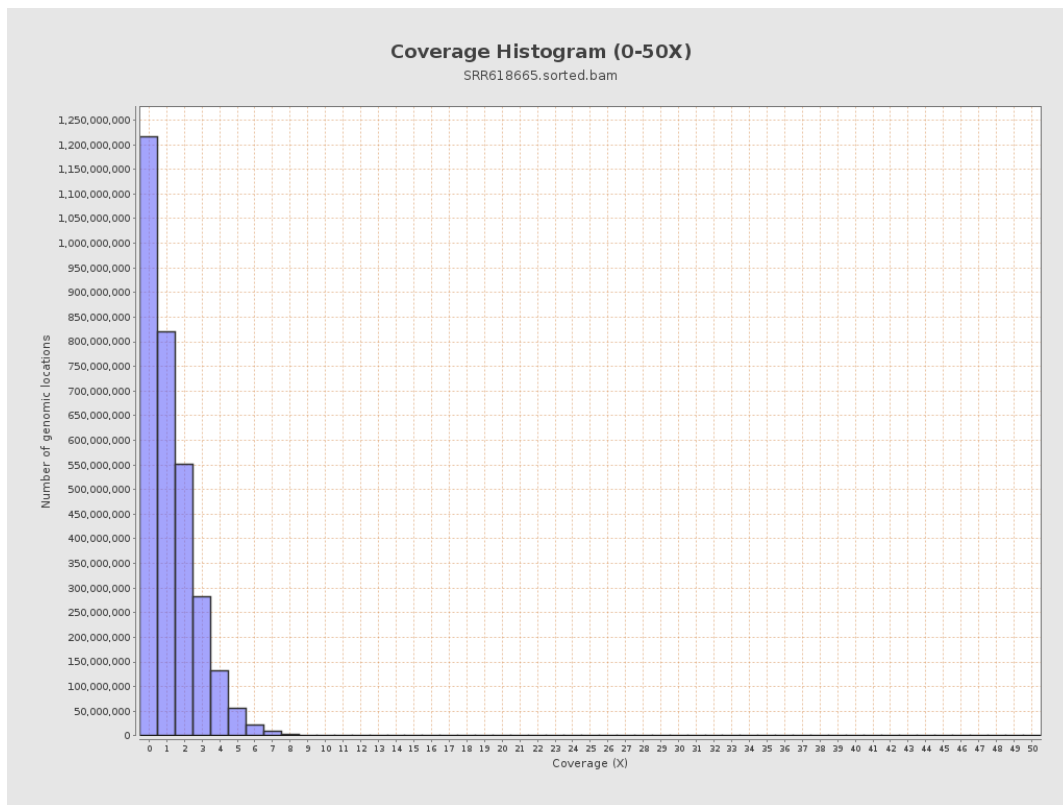
3. Results : Coverage across reference



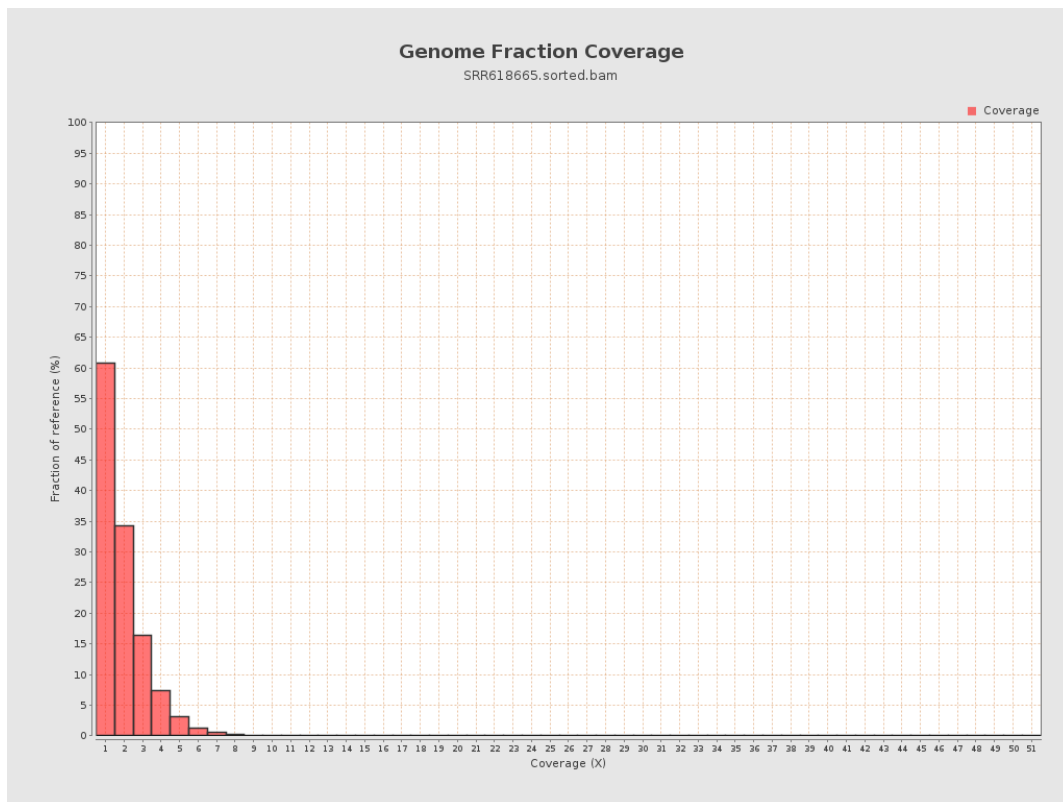
4. Results : Coverage Histogram



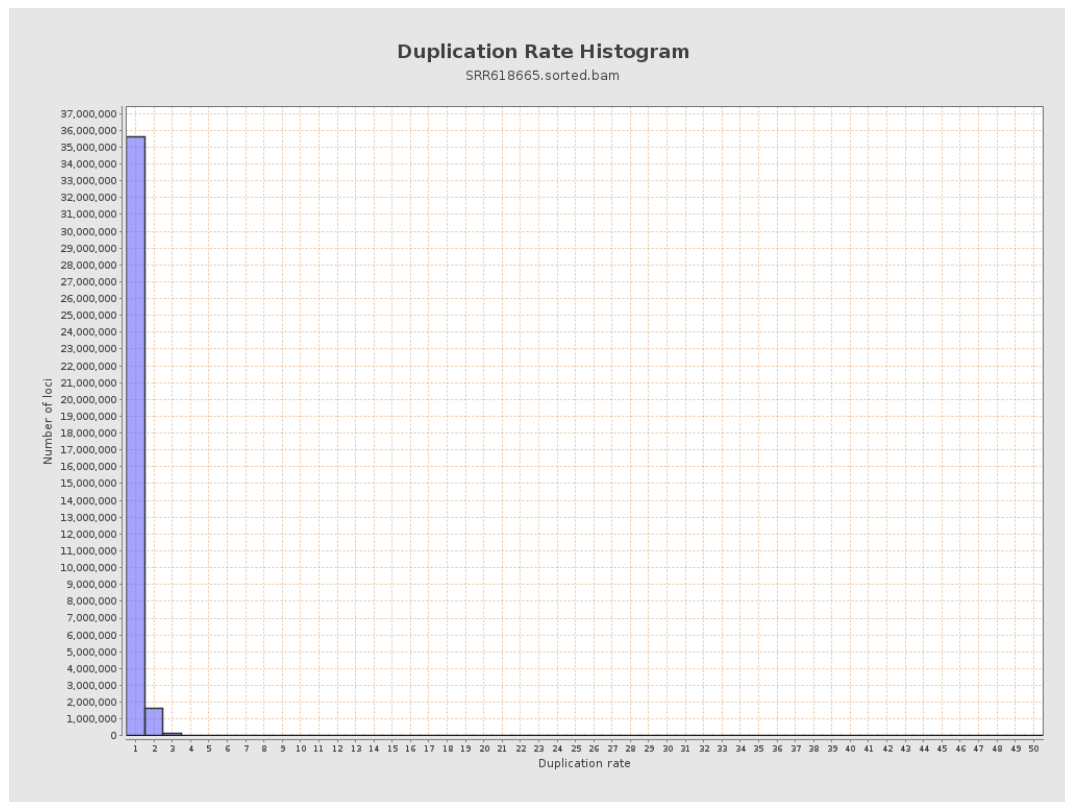
5. Results : Coverage Histogram (0-50X)



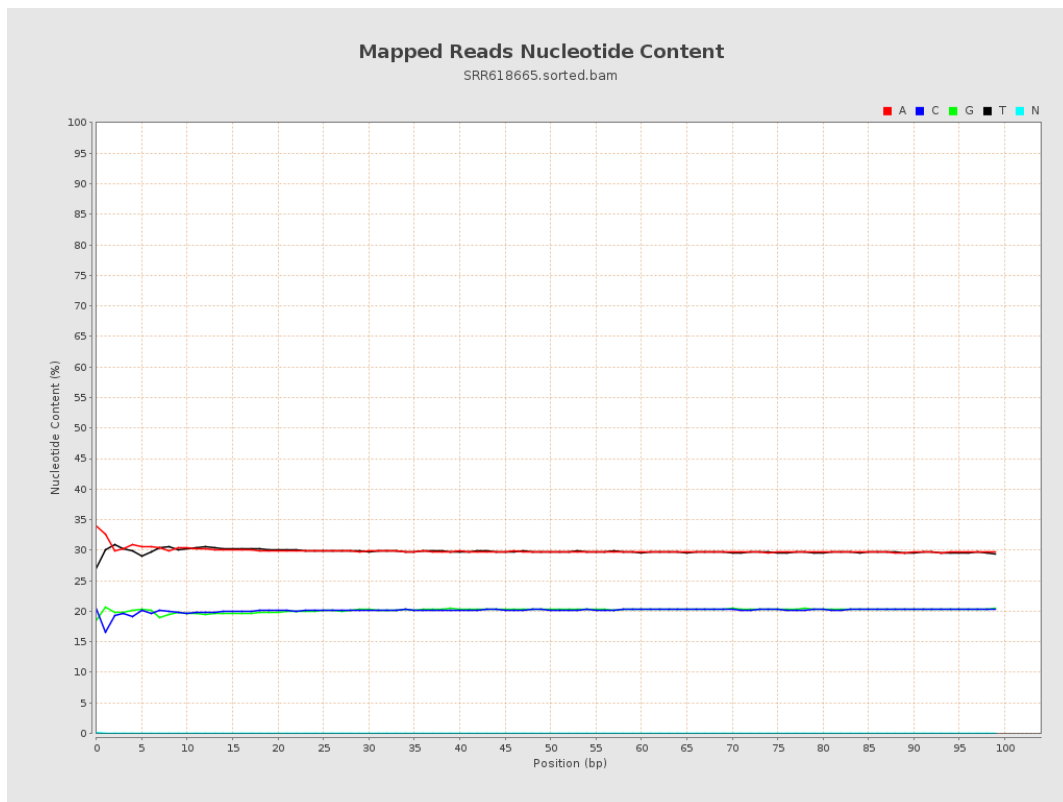
6. Results : Genome Fraction Coverage



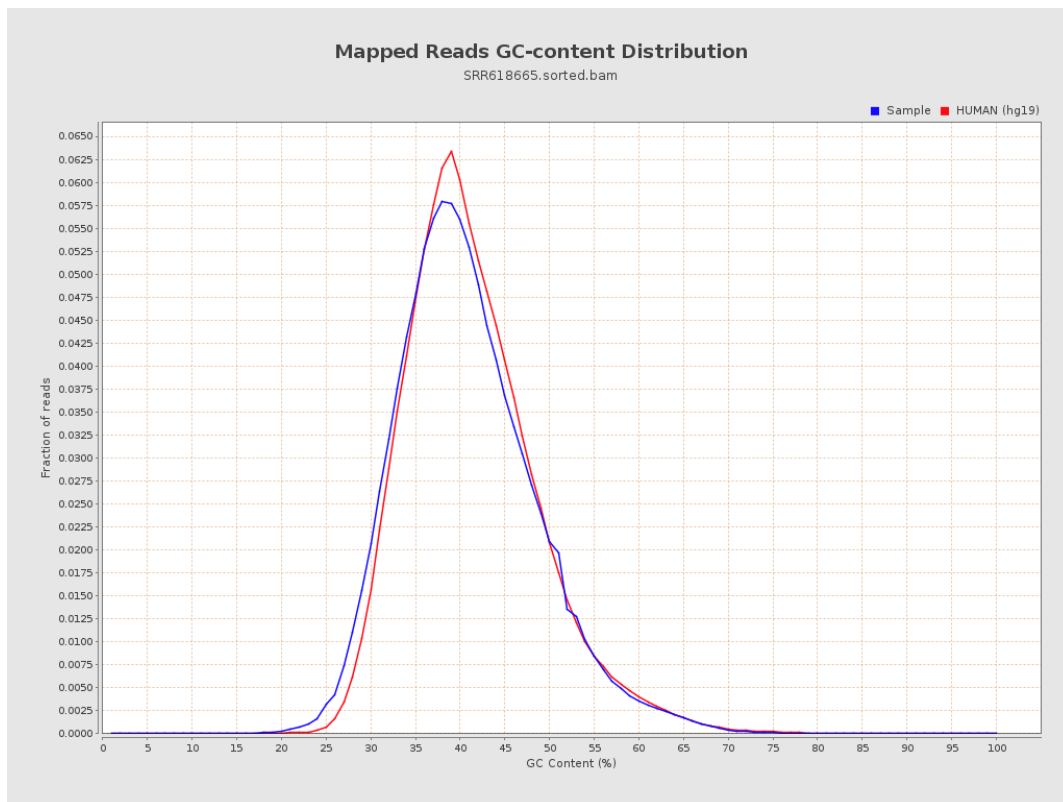
7. Results : Duplication Rate Histogram



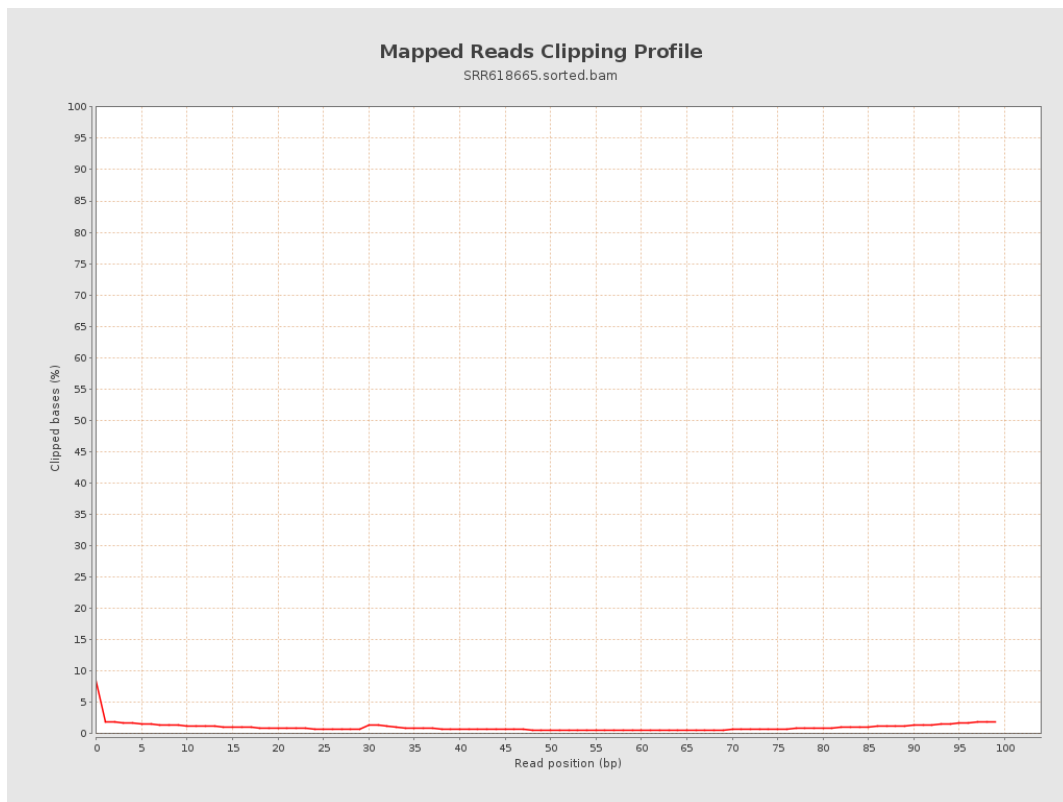
8. Results : Mapped Reads Nucleotide Content



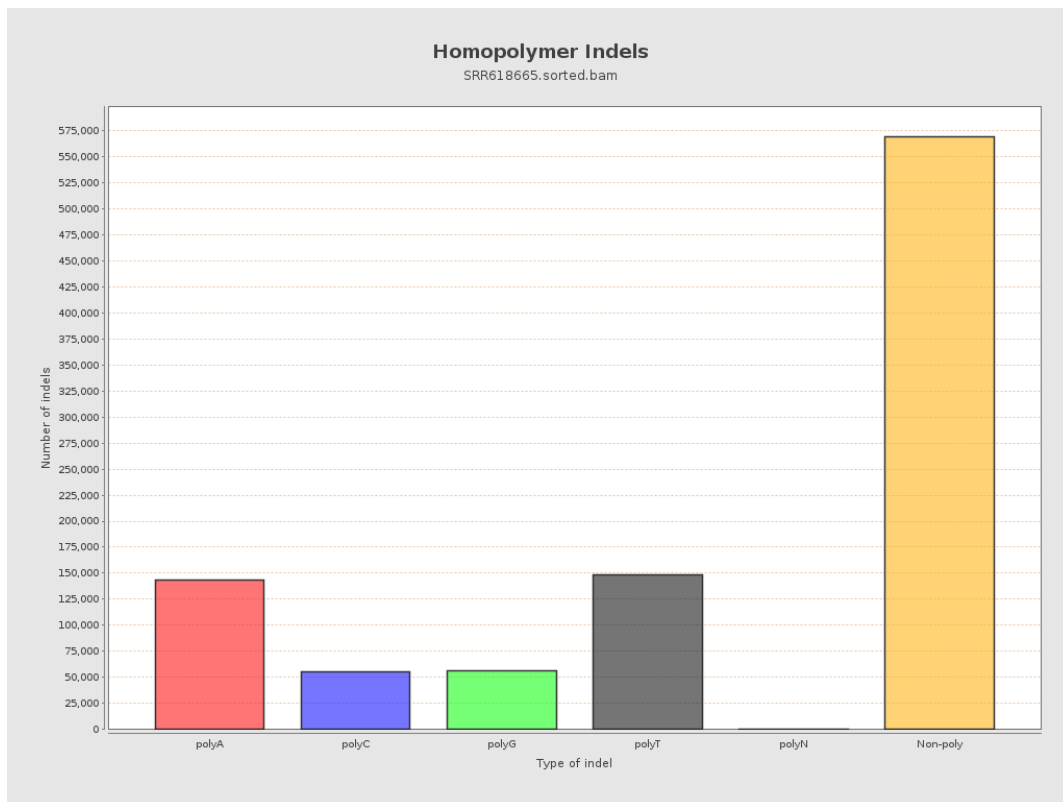
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



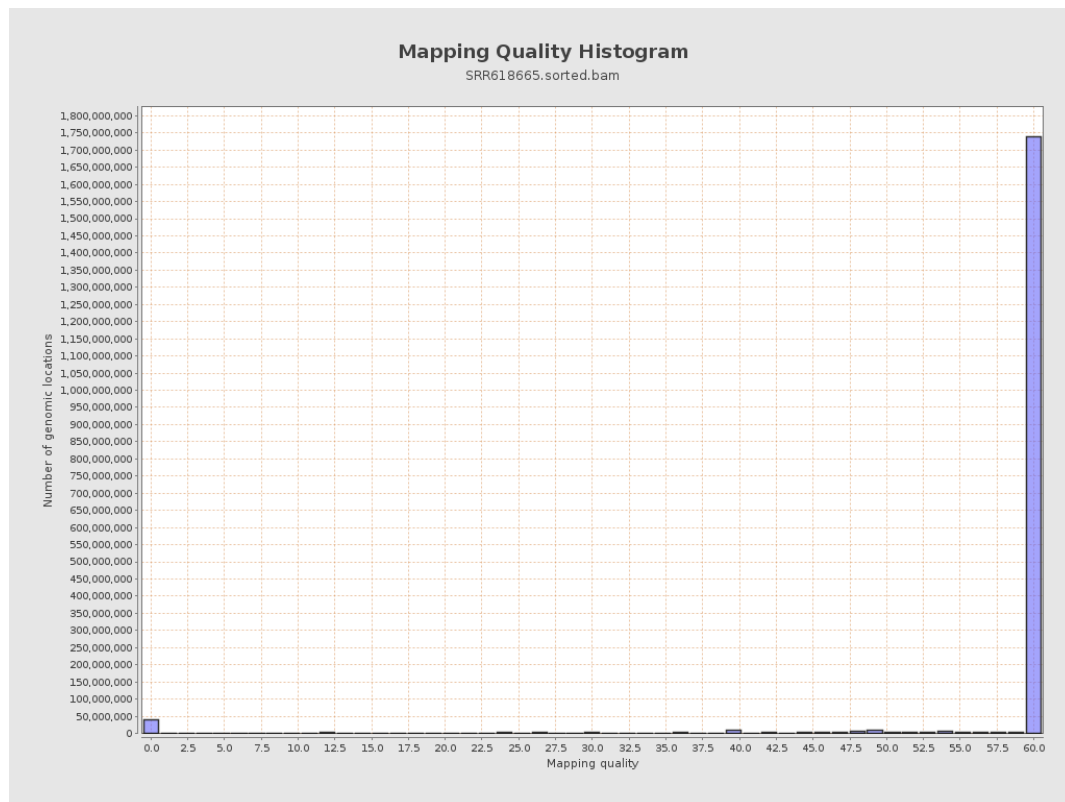
11. Results : Homopolymer Indels



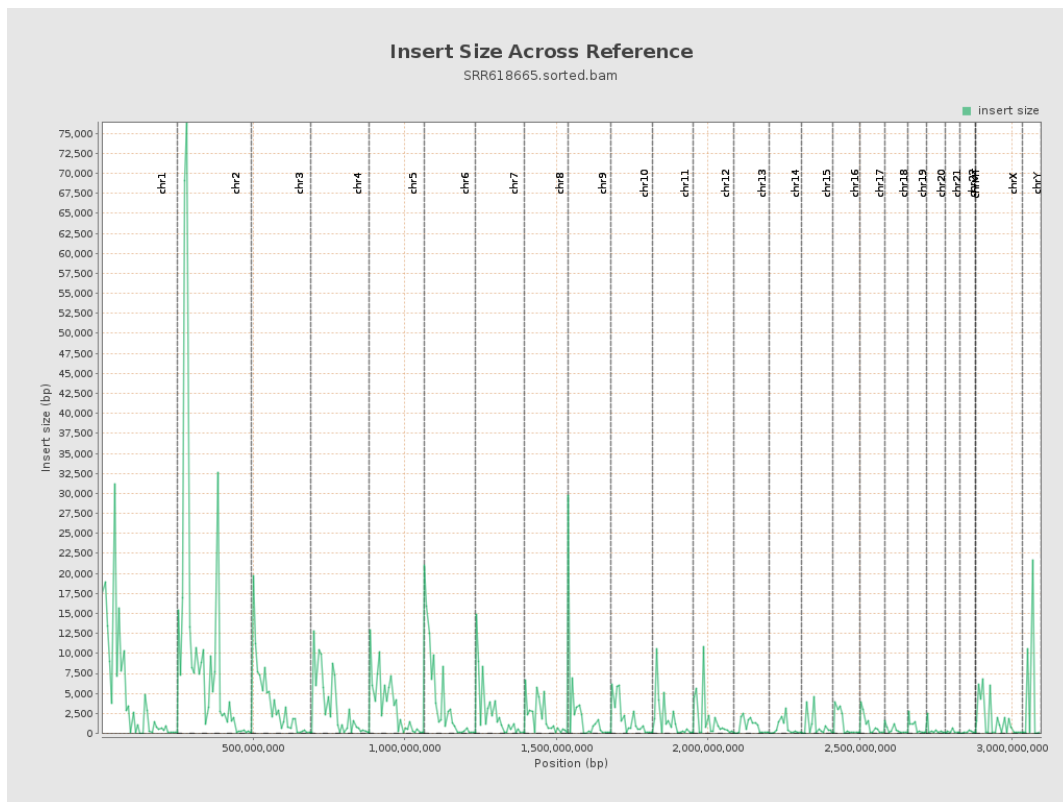
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

