

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/19 15:35:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618625.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_SRR618625 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618625_1.fastq.gz SRR618625_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Jan 19 15:34:59 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618625.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	29,787,784
Mapped reads	27,975,502 / 93.92%
Unmapped reads	1,812,282 / 6.08%
Mapped paired reads	27,975,502 / 93.92%
Mapped reads, first in pair	14,290,215 / 47.97%
Mapped reads, second in pair	13,685,287 / 45.94%
Mapped reads, both in pair	26,973,422 / 90.55%
Mapped reads, singletons	1,002,080 / 3.36%
Secondary alignments	0
Supplementary alignments	151,628 / 0.51%
Read min/max/mean length	30 / 100 / 100.21
Duplicated reads (estimated)	5,604,590 / 18.82%
Duplication rate	17.44%
Clipped reads	6,488,705 / 21.78%

2.2. ACGT Content

Number/percentage of A's	722,436,980 / 27.46%
Number/percentage of C's	570,109,743 / 21.67%
Number/percentage of T's	732,728,936 / 27.86%
Number/percentage of G's	605,088,474 / 23%
Number/percentage of N's	90,117 / 0%

GC Percentage	44.68%
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2.3. Coverage

Mean	0.8503
Standard Deviation	3.6891

2.4. Mapping Quality

Mean Mapping Quality	53.26
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2.5. Insert size

Mean	136,824.09
Standard Deviation	3,717,822.42
P25/Median/P75	179 / 205 / 237

2.6. Mismatches and indels

General error rate	1.31%
Mismatches	33,622,676
Insertions	490,039
Mapped reads with at least one insertion	1.72%
Deletions	1,353,525
Mapped reads with at least one deletion	4.71%
Homopolymer indels	52.86%

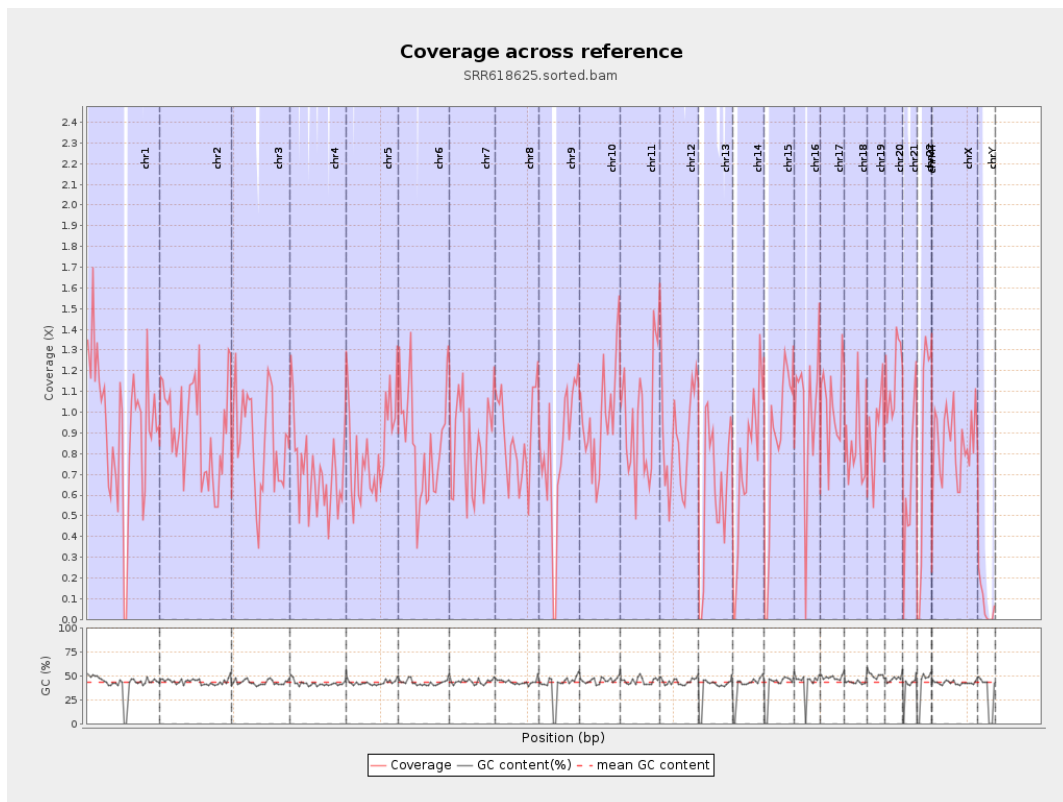
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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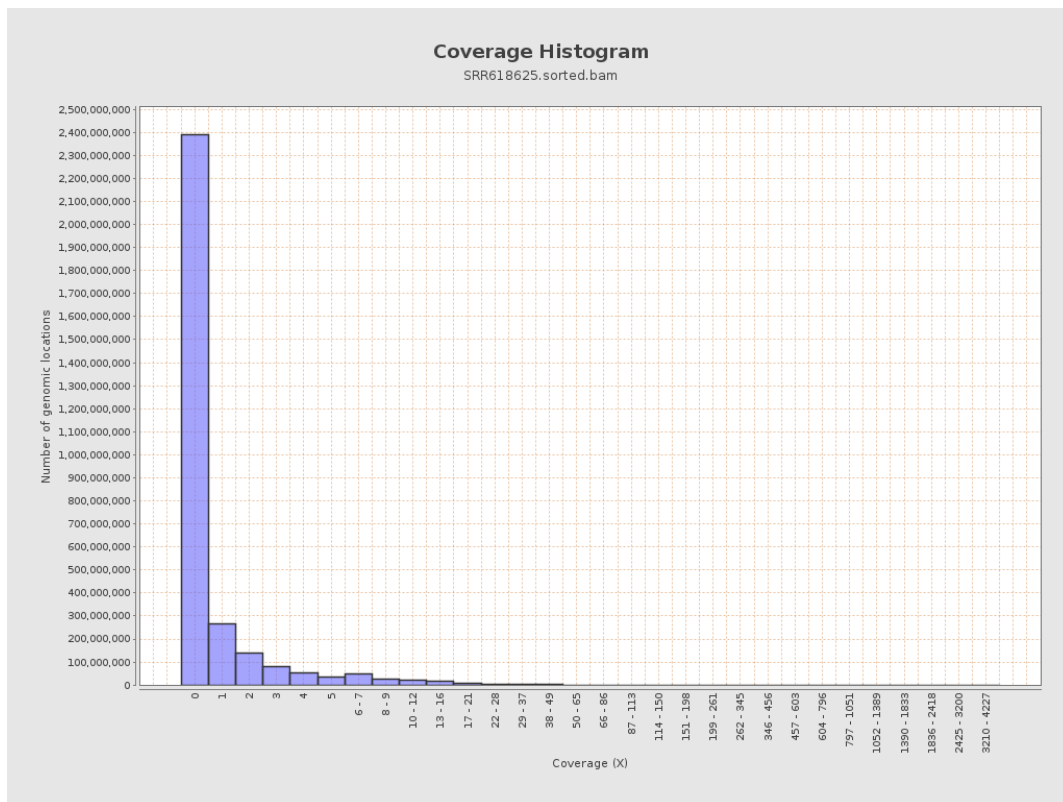
		bases	coverage	deviation
chr1	249250621	230817729	0.926	4.803
chr2	243199373	222946261	0.9167	4.659
chr3	198022430	170928537	0.8632	2.9771
chr4	191154276	135504115	0.7089	2.8115
chr5	180915260	148810888	0.8225	2.8823
chr6	171115067	145386929	0.8496	2.955
chr7	159138663	135342090	0.8505	3.2042
chr8	146364022	127666661	0.8723	2.9462
chr9	141213431	113531345	0.804	3.7926
chr10	135534747	131751061	0.9721	3.3712
chr11	135006516	130688712	0.968	3.4698
chr12	133851895	117440325	0.8774	3.3401
chr13	115169878	71752196	0.623	2.4675
chr14	107349540	79649783	0.742	2.7599
chr15	102531392	86513867	0.8438	3.3355
chr16	90354753	90124204	0.9974	7.6914
chr17	81195210	84317914	1.0385	3.8047
chr18	78077248	66300681	0.8492	3.7787
chr19	59128983	54431425	0.9206	4.2828
chr20	63025520	74057889	1.175	3.6187
chr21	48129895	33289455	0.6917	4.1609
chr22	51304566	44317873	0.8638	3.4781
chrMT	16571	3690	0.2227	1.1767
chrX	155270560	132450566	0.853	2.6798

chrY	59373566	4286888	0.0722	2.609
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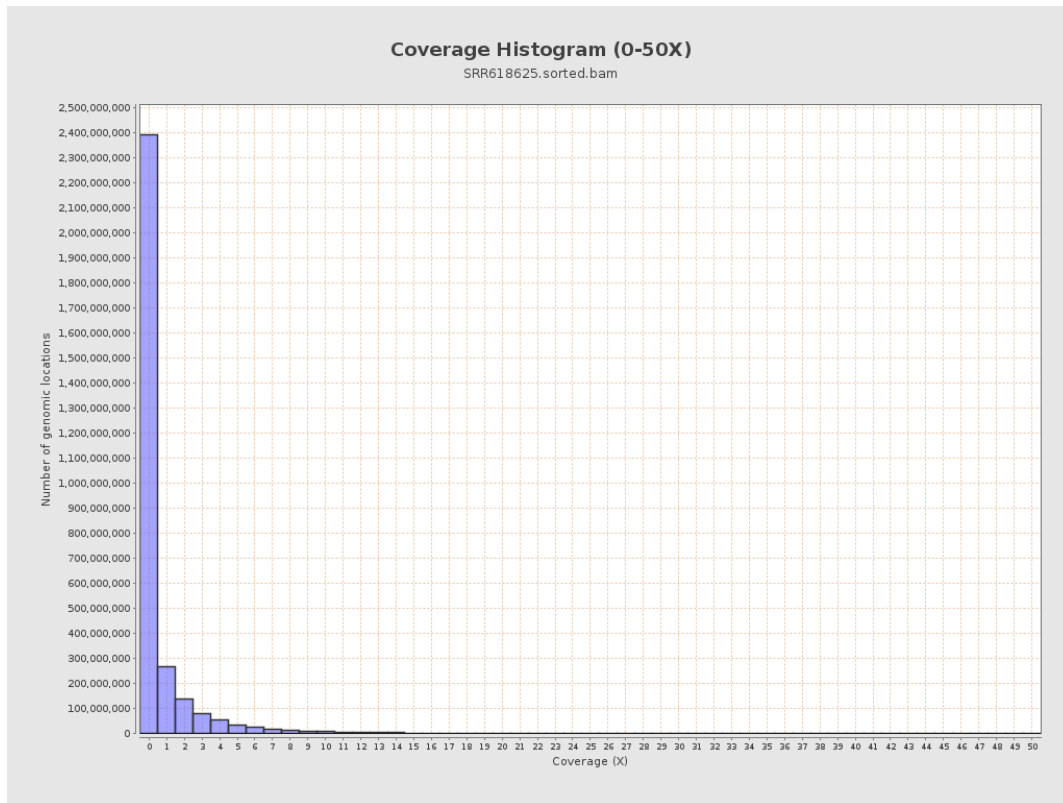
3. Results : Coverage across reference



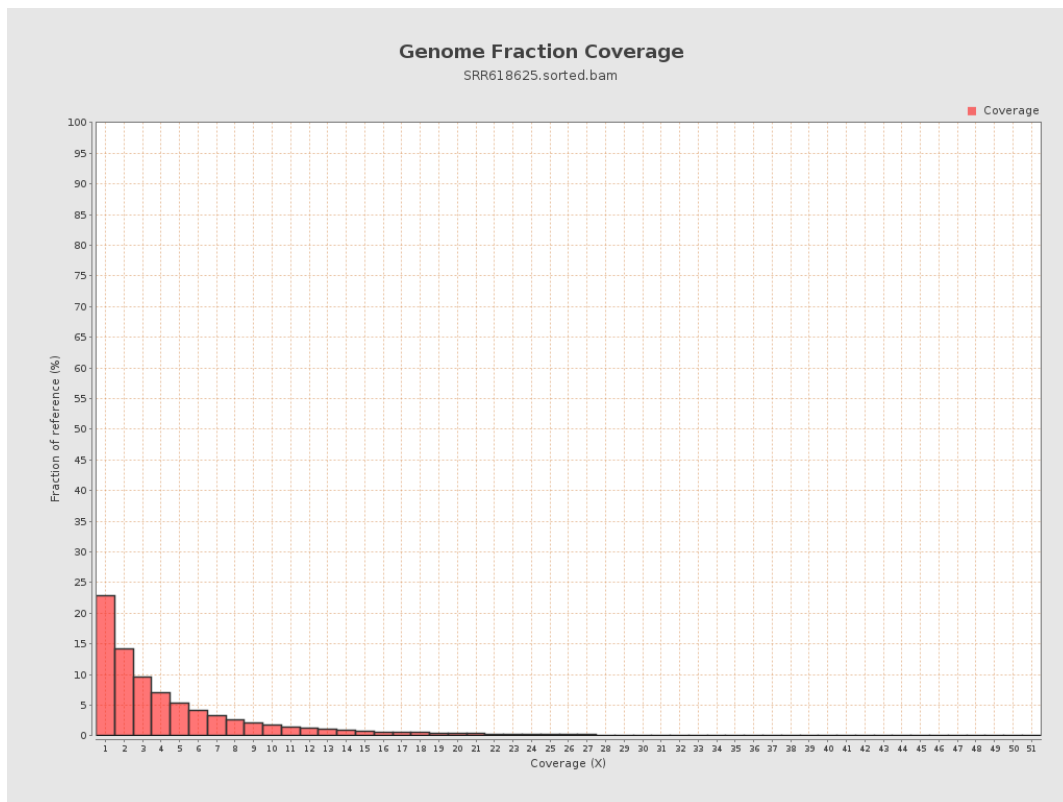
4. Results : Coverage Histogram



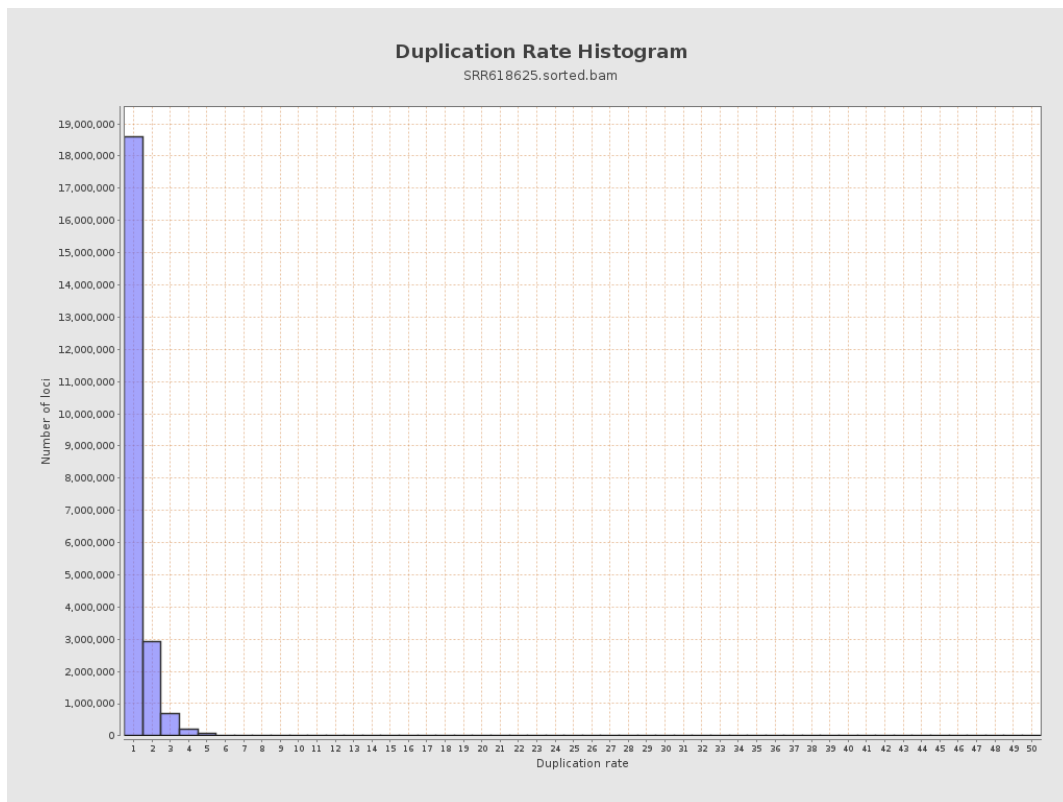
5. Results : Coverage Histogram (0-50X)



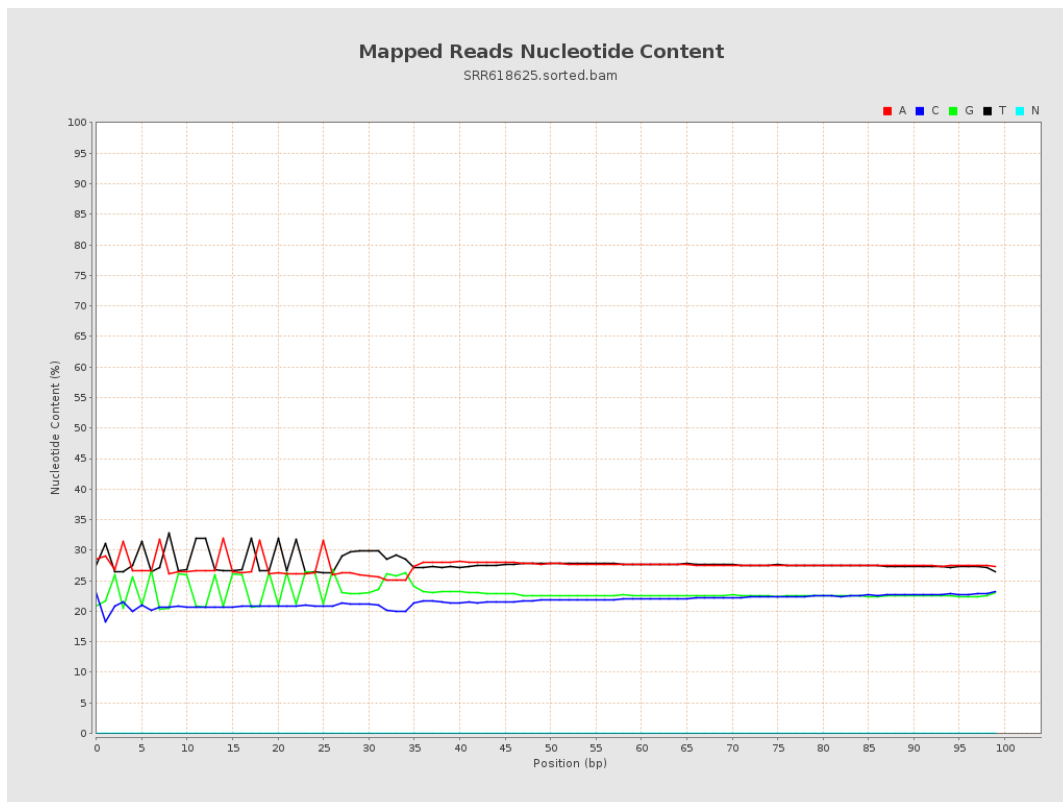
6. Results : Genome Fraction Coverage



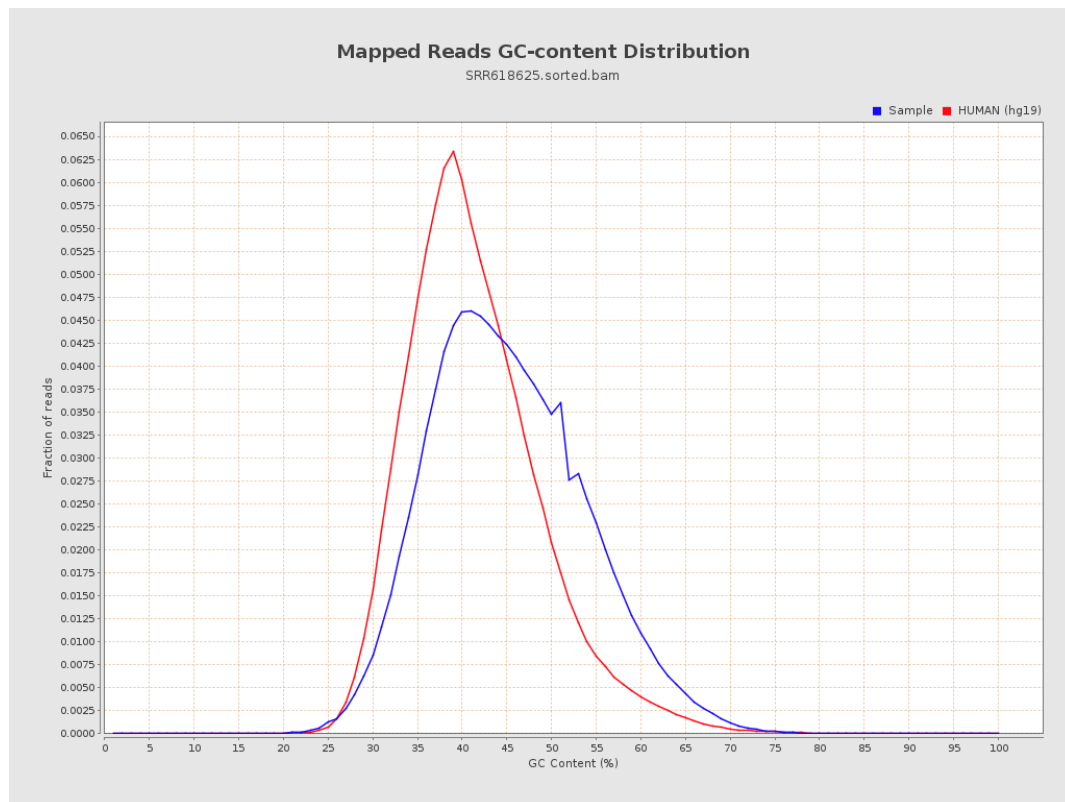
7. Results : Duplication Rate Histogram



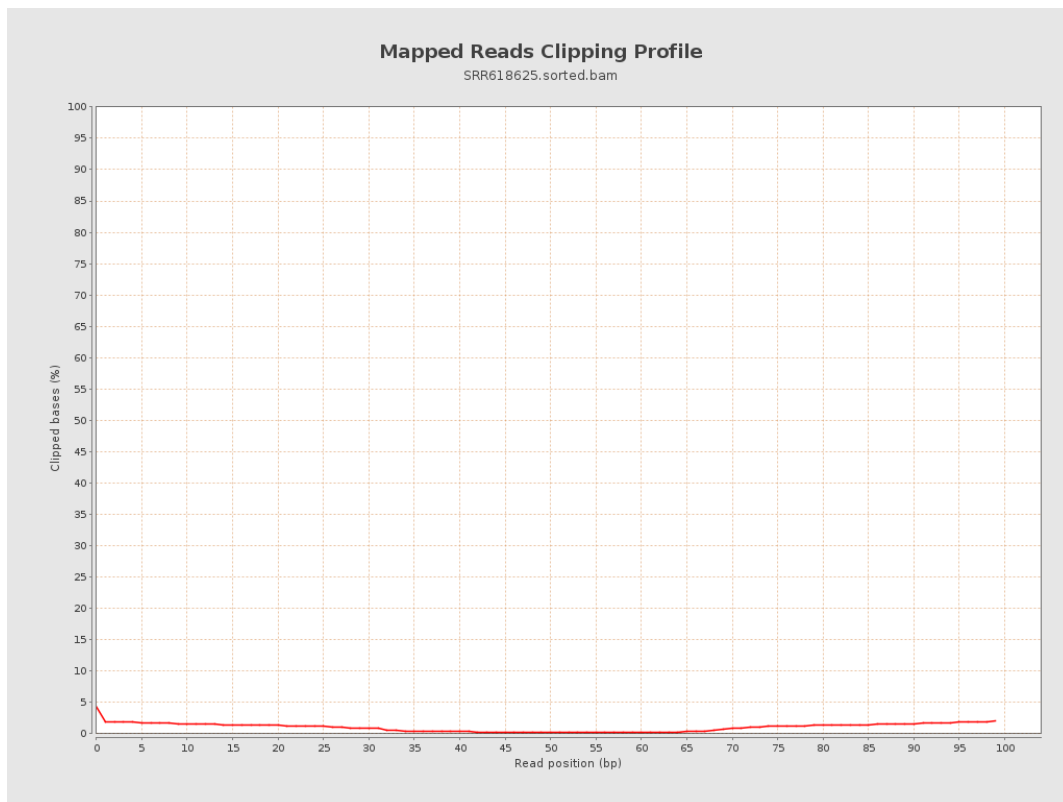
8. Results : Mapped Reads Nucleotide Content



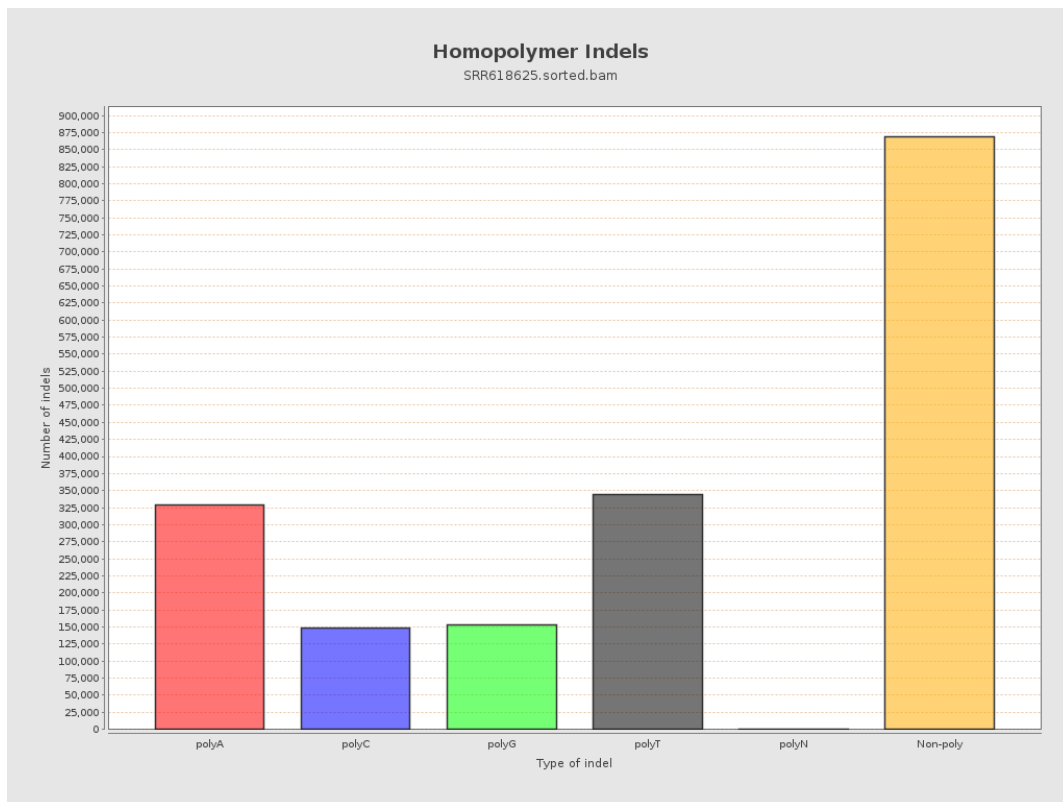
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



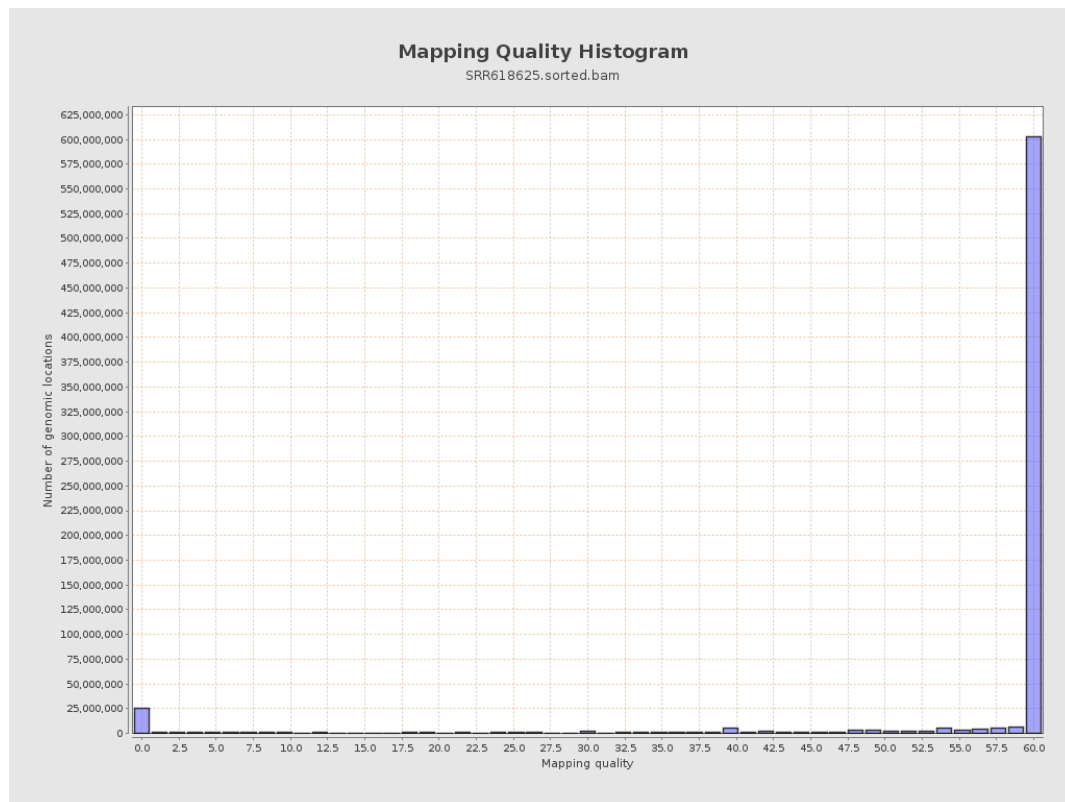
11. Results : Homopolymer Indels



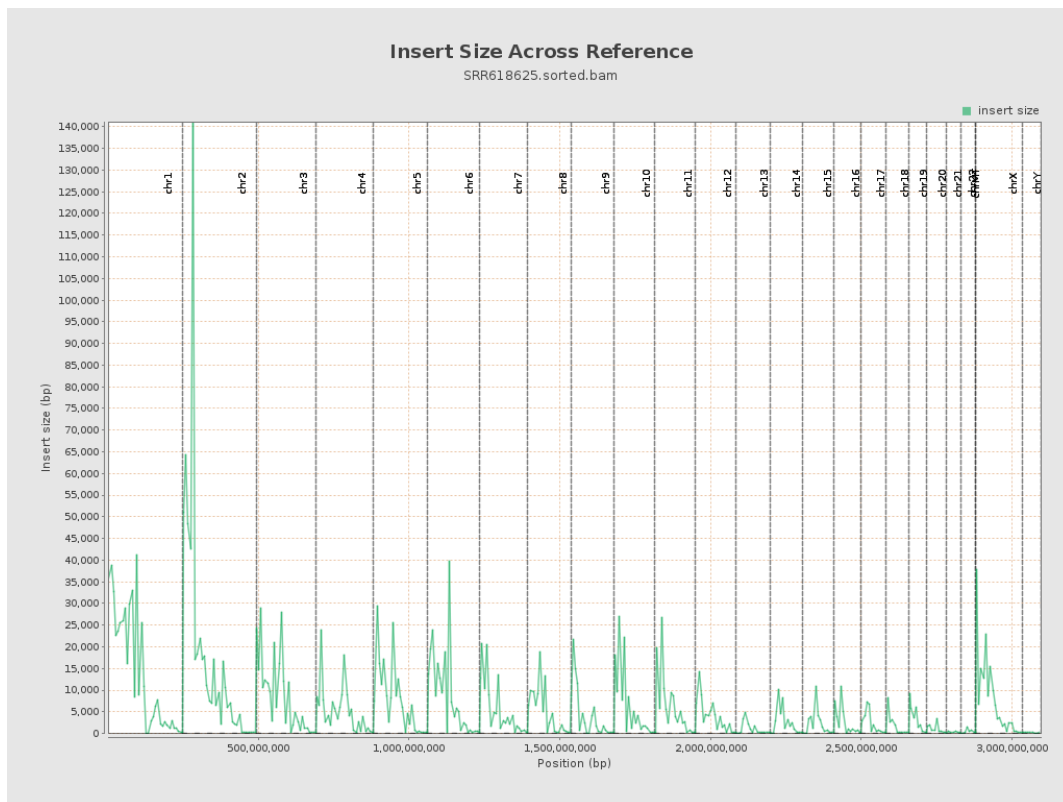
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

