

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/13 04:31:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438265.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_SRR8438265 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438265_1.fastq.gz SRR8438265_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 13 04:31:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8438265.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	660,138,950
Mapped reads	658,207,244 / 99.71%
Unmapped reads	1,931,706 / 0.29%
Mapped paired reads	658,207,244 / 99.71%
Mapped reads, first in pair	329,252,461 / 49.88%
Mapped reads, second in pair	328,954,783 / 49.83%
Mapped reads, both in pair	656,898,098 / 99.51%
Mapped reads, singletons	1,309,146 / 0.2%
Secondary alignments	0
Supplementary alignments	10,941,168 / 1.66%
Read min/max/mean length	28 / 151 / 146.01
Duplicated reads (estimated)	283,482,250 / 42.94%
Duplication rate	40.59%
Clipped reads	119,707,552 / 18.13%

2.2. ACGT Content

Number/percentage of A's	28,800,409,160 / 30.25%
Number/percentage of C's	19,021,219,051 / 19.98%
Number/percentage of T's	27,486,143,815 / 28.86%
Number/percentage of G's	19,915,315,288 / 20.91%
Number/percentage of N's	582,956 / 0%

GC Percentage	40.89%
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2.3. Coverage

Mean	30.7687
Standard Deviation	85.9921

2.4. Mapping Quality

Mean Mapping Quality	55.07
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2.5. Insert size

Mean	40,672.47
Standard Deviation	1,969,837.18
P25/Median/P75	188 / 245 / 334

2.6. Mismatches and indels

General error rate	0.53%
Mismatches	483,620,717
Insertions	12,168,036
Mapped reads with at least one insertion	1.82%
Deletions	10,800,408
Mapped reads with at least one deletion	1.61%
Homopolymer indels	48.42%

2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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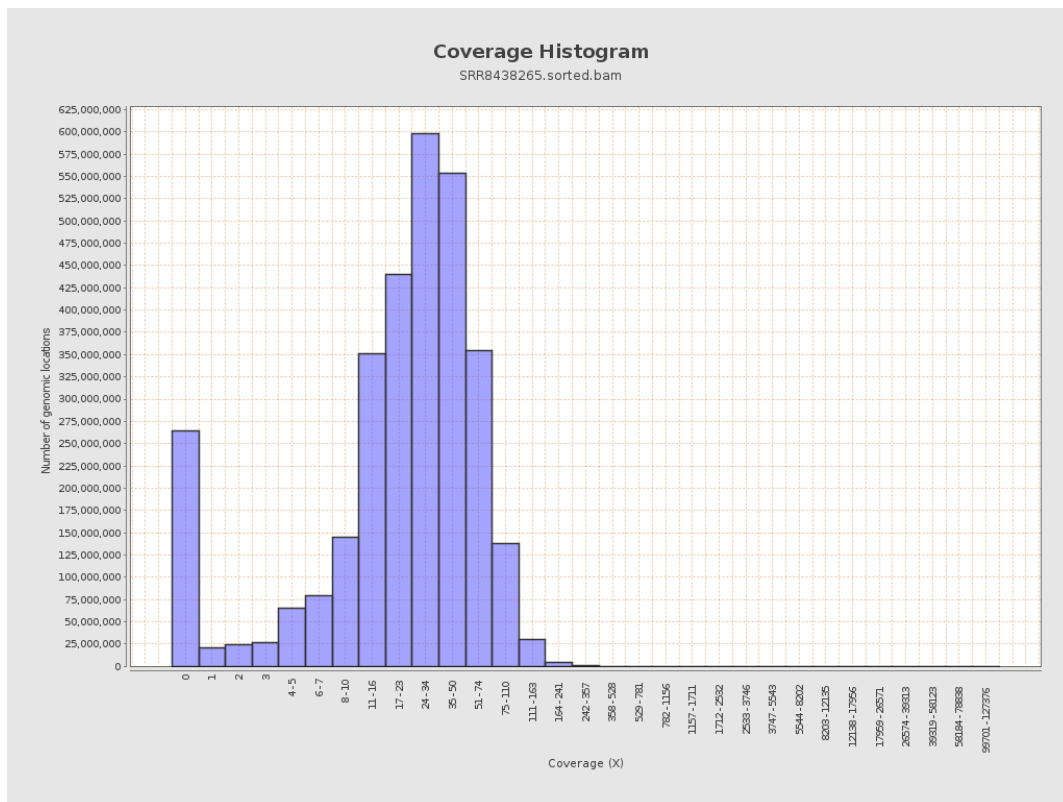
		bases	coverage	deviation
chr1	249250621	7744316370	31.0704	30.9956
chr2	243199373	8462095958	34.7949	116.3872
chr3	198022430	6859441648	34.6397	32.4349
chr4	191154276	6421458628	33.5931	24.3544
chr5	180915260	6187713528	34.2023	25.3914
chr6	171115067	5768508591	33.7113	26.5175
chr7	159138663	5188365411	32.6028	25.027
chr8	146364022	4906674286	33.5238	25.0094
chr9	141213431	4088047636	28.9494	31.9391
chr10	135534747	4541185513	33.5057	38.1194
chr11	135006516	4498110084	33.3177	26.0319
chr12	133851895	4484138438	33.5007	24.7994
chr13	115169878	3263887335	28.3398	25.1685
chr14	107349540	2931710075	27.3099	26.7578
chr15	102531392	2751537892	26.8361	26.8095
chr16	90354753	2627589270	29.0808	50.5798
chr17	81195210	2319432622	28.5661	34.4418
chr18	78077248	2627416571	33.6515	26.7777
chr19	59128983	1446940740	24.4709	39.3653
chr20	63025520	2072824035	32.8886	27.8628
chr21	48129895	1218513814	25.3172	30.9668
chr22	51304566	1017345545	19.8295	26.0586
chrMT	16571	495442305	29,898.1537	11,817.9494
chrX	155270560	2829312290	18.2218	15.9207

chrY	59373566	498579929	8.3973	27.4368
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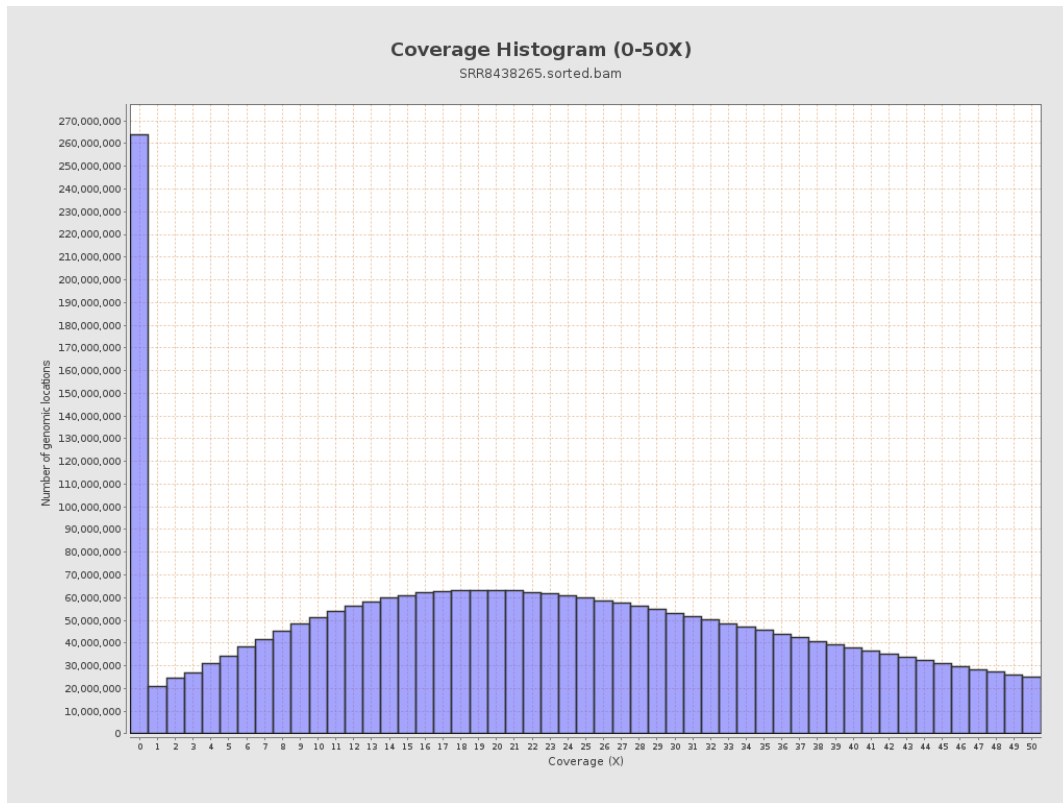
3. Results : Coverage across reference



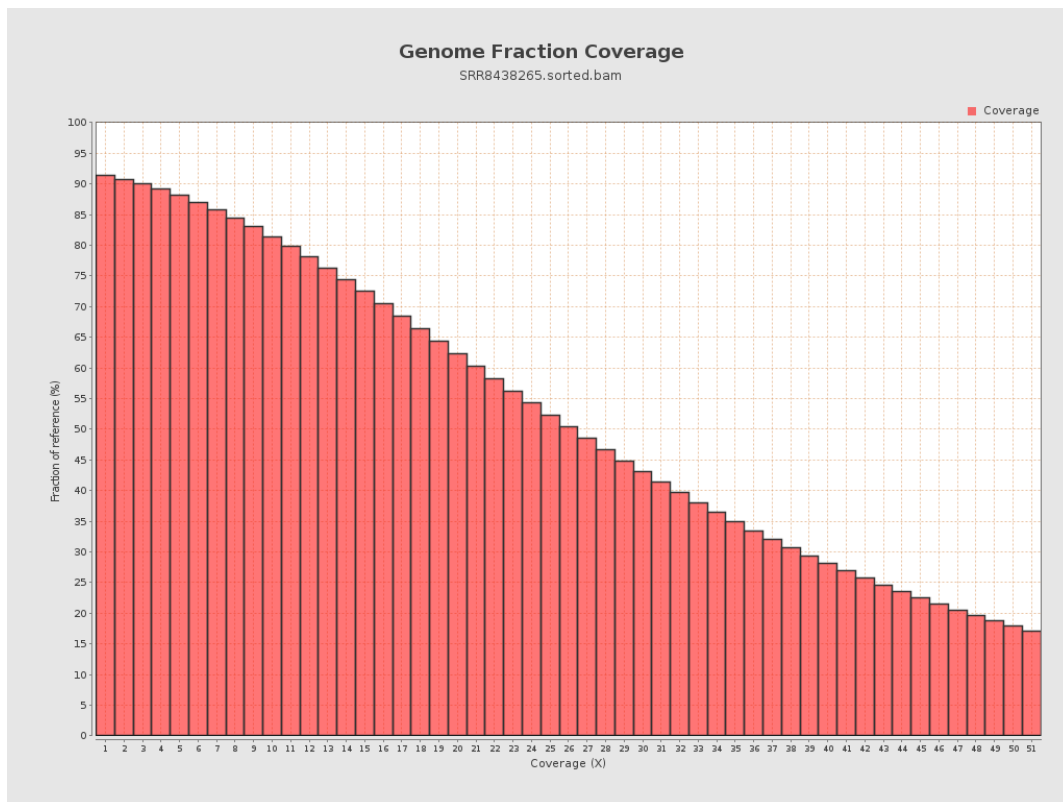
4. Results : Coverage Histogram



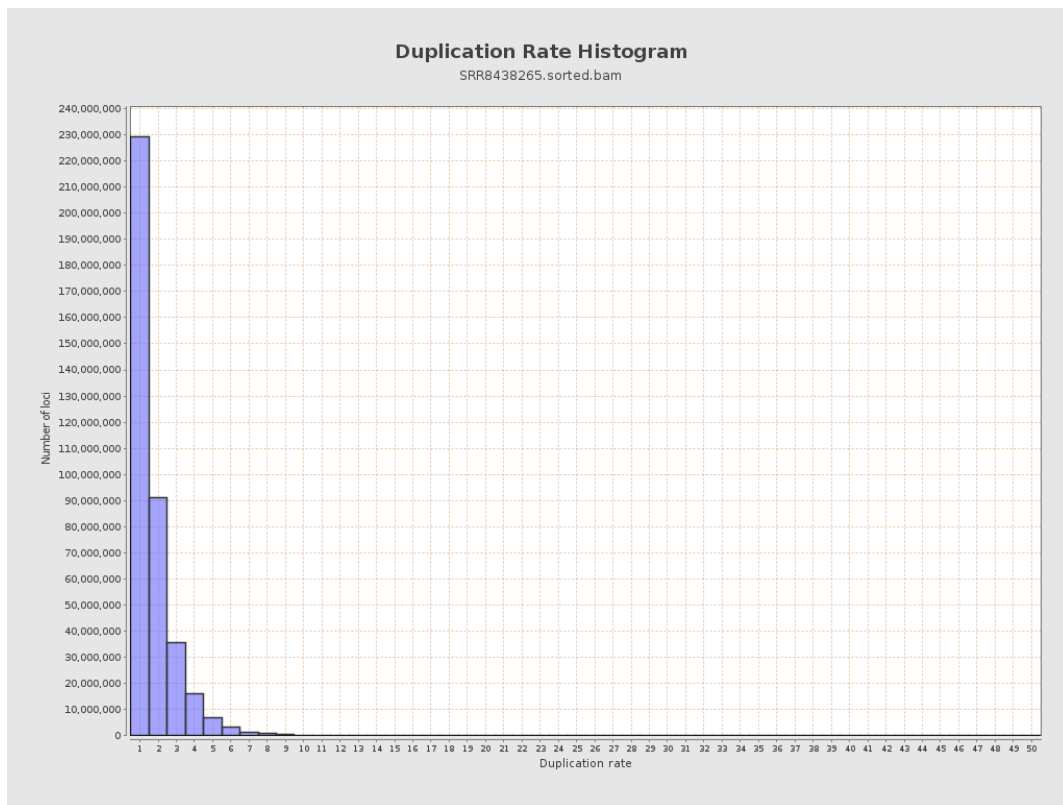
5. Results : Coverage Histogram (0-50X)



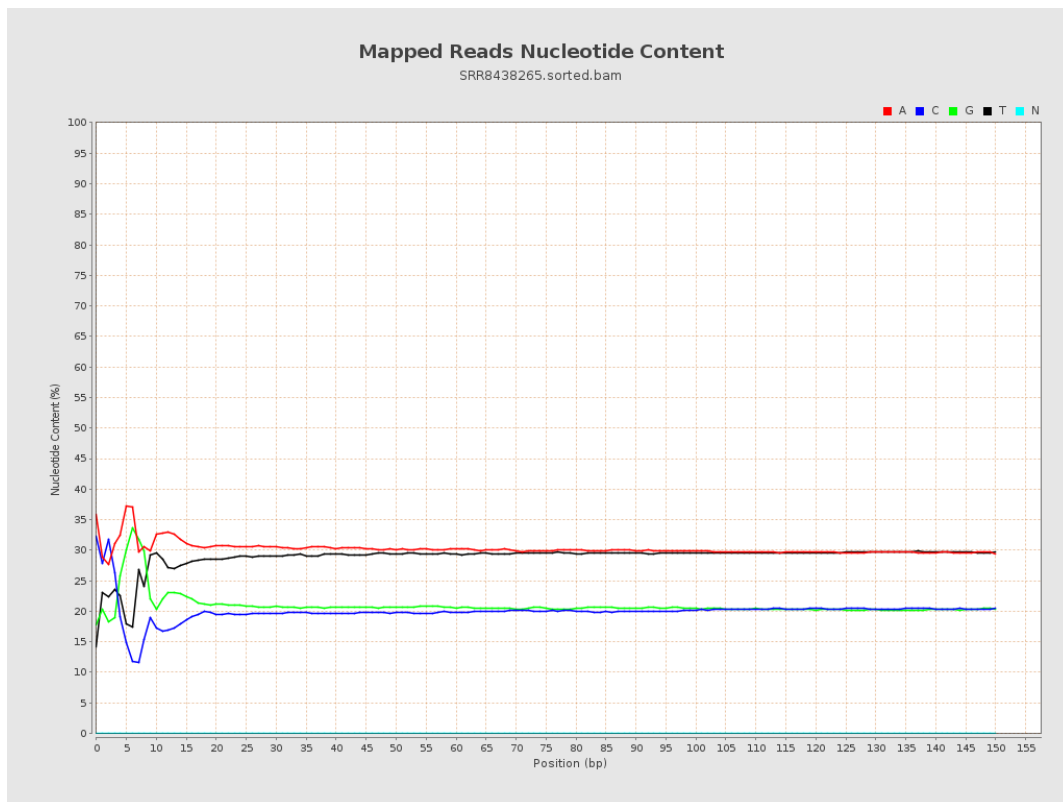
6. Results : Genome Fraction Coverage



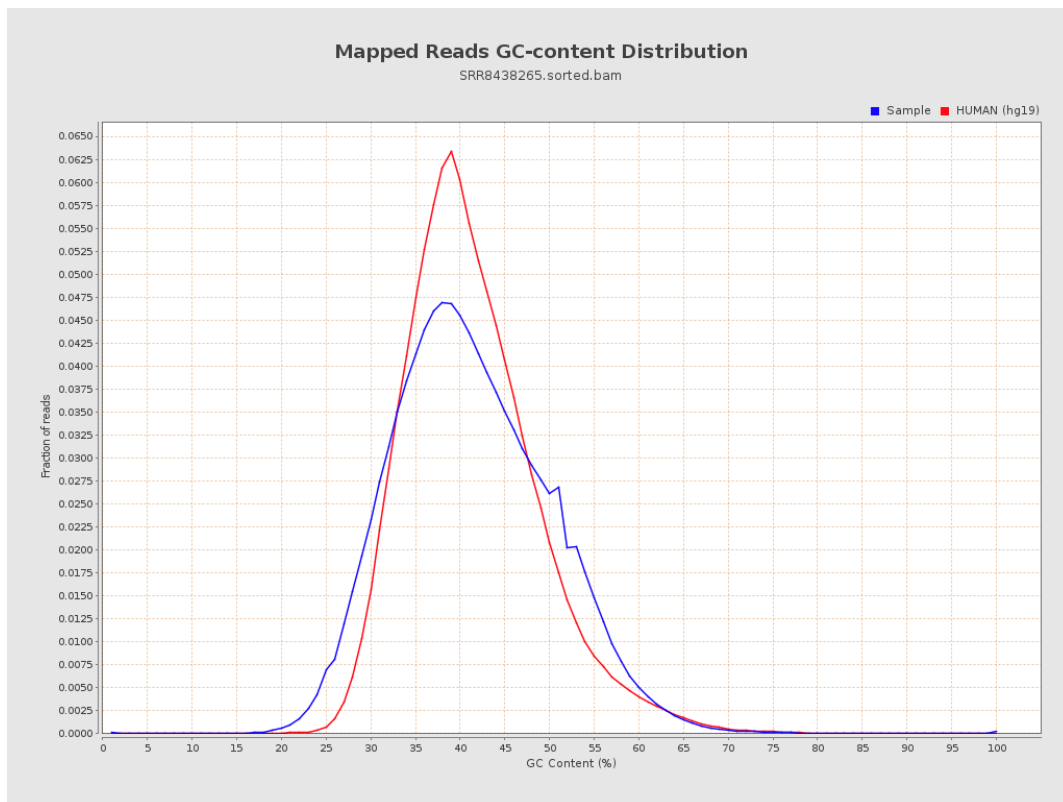
7. Results : Duplication Rate Histogram



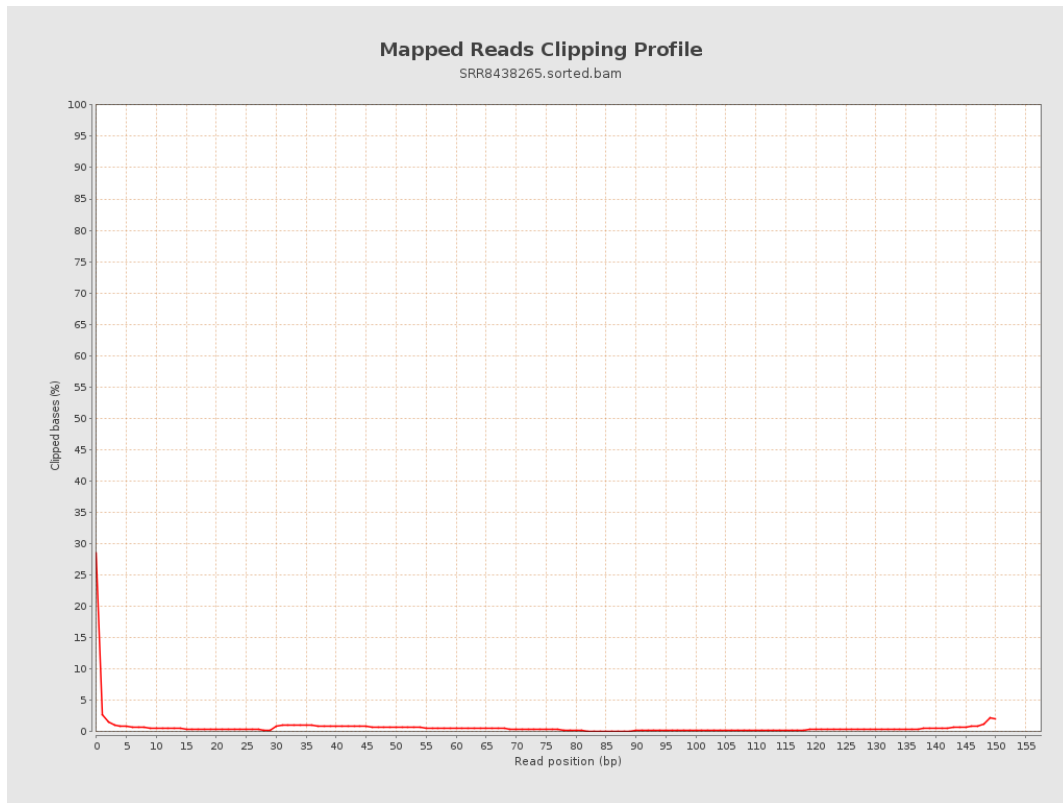
8. Results : Mapped Reads Nucleotide Content



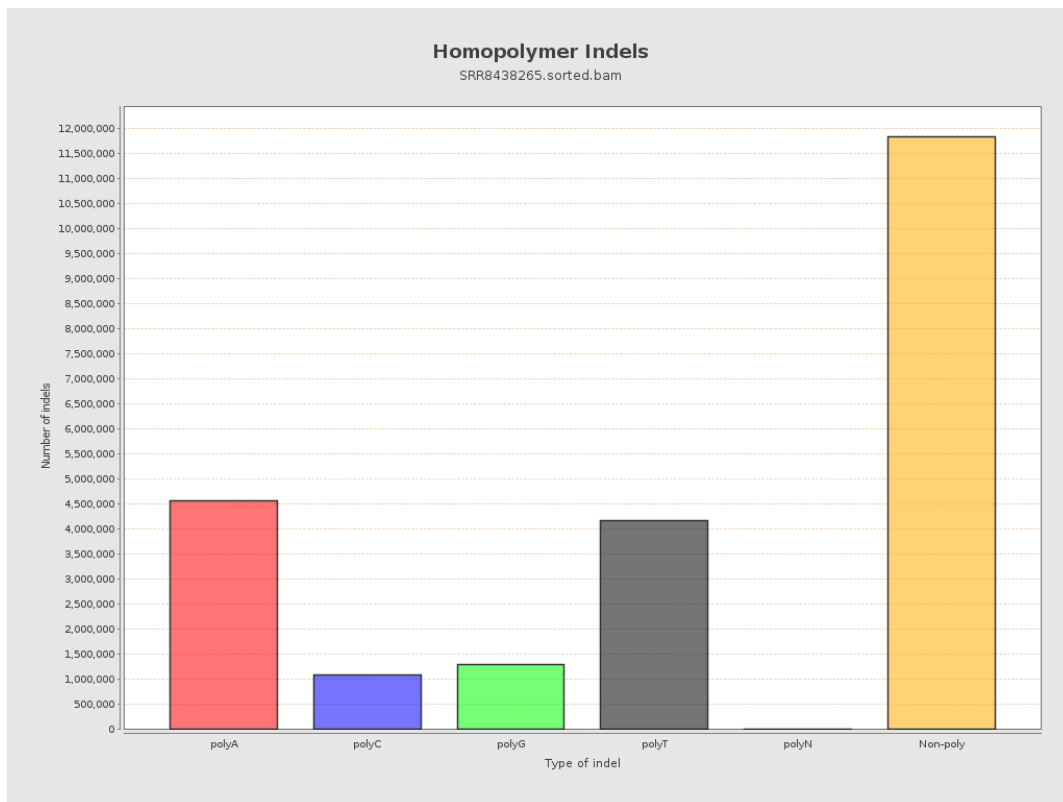
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



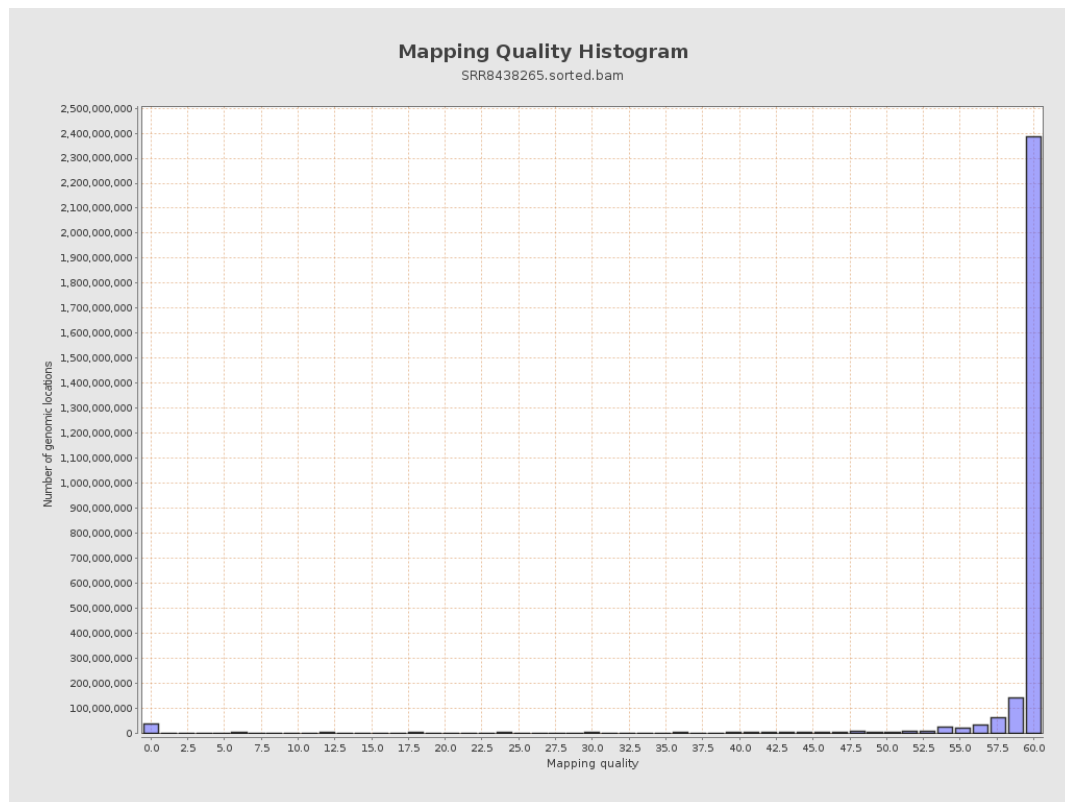
11. Results : Homopolymer Indels



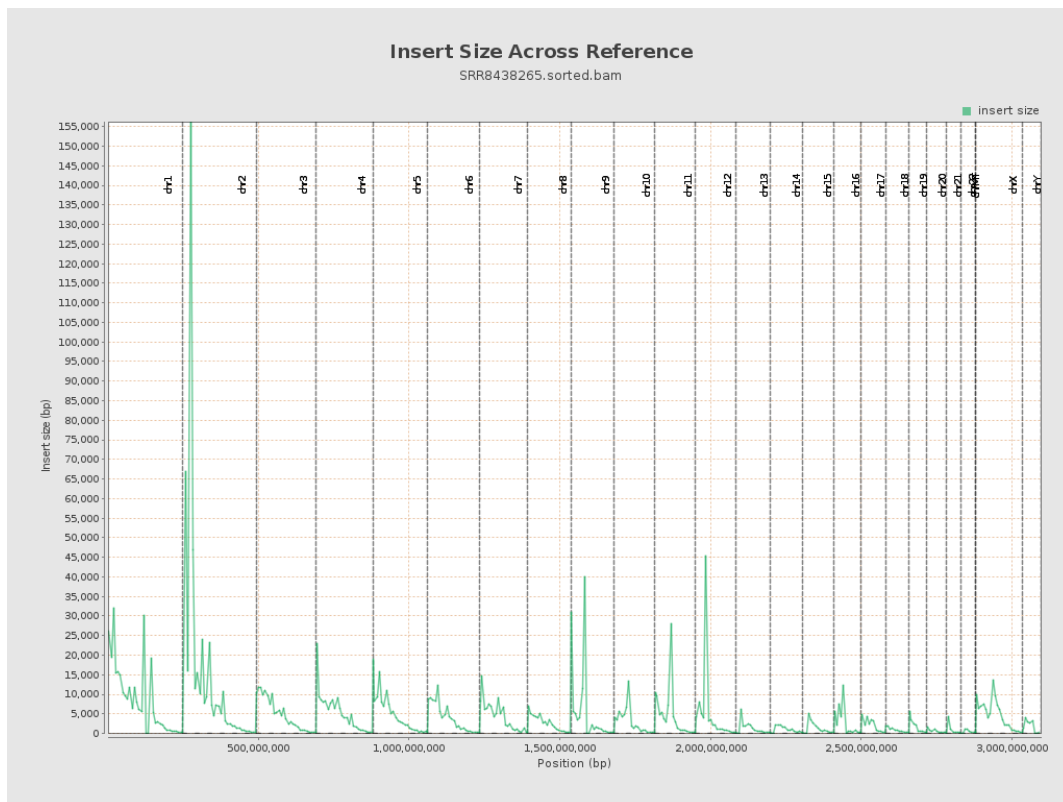
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

