

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 05:18:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1298935.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_SRR1298935 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1298935_1.fastq.gz SRR1298935_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 05:18:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1298935.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	167,952,506
Mapped reads	139,472,246 / 83.04%
Unmapped reads	28,480,260 / 16.96%
Mapped paired reads	139,472,246 / 83.04%
Mapped reads, first in pair	74,275,816 / 44.22%
Mapped reads, second in pair	65,196,430 / 38.82%
Mapped reads, both in pair	127,571,580 / 75.96%
Mapped reads, singletons	11,900,666 / 7.09%
Secondary alignments	0
Supplementary alignments	907,198 / 0.54%
Read min/max/mean length	30 / 100 / 100.19
Duplicated reads (estimated)	134,996,358 / 80.38%
Duplication rate	53.23%
Clipped reads	138,233,959 / 82.31%

2.2. ACGT Content

Number/percentage of A's	3,457,702,498 / 30.41%
Number/percentage of C's	2,315,465,480 / 20.36%
Number/percentage of T's	3,291,177,845 / 28.94%
Number/percentage of G's	2,305,196,824 / 20.27%
Number/percentage of N's	2,416,853 / 0.02%

GC Percentage	40.63%
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2.3. Coverage

Mean	3.6769
Standard Deviation	514.1652

2.4. Mapping Quality

Mean Mapping Quality	51.63
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2.5. Insert size

Mean	548,997.43
Standard Deviation	7,246,271.18
P25/Median/P75	175 / 234 / 312

2.6. Mismatches and indels

General error rate	1.37%
Mismatches	122,525,697
Insertions	9,359,539
Mapped reads with at least one insertion	6.48%
Deletions	3,809,079
Mapped reads with at least one deletion	2.67%
Homopolymer indels	49.53%

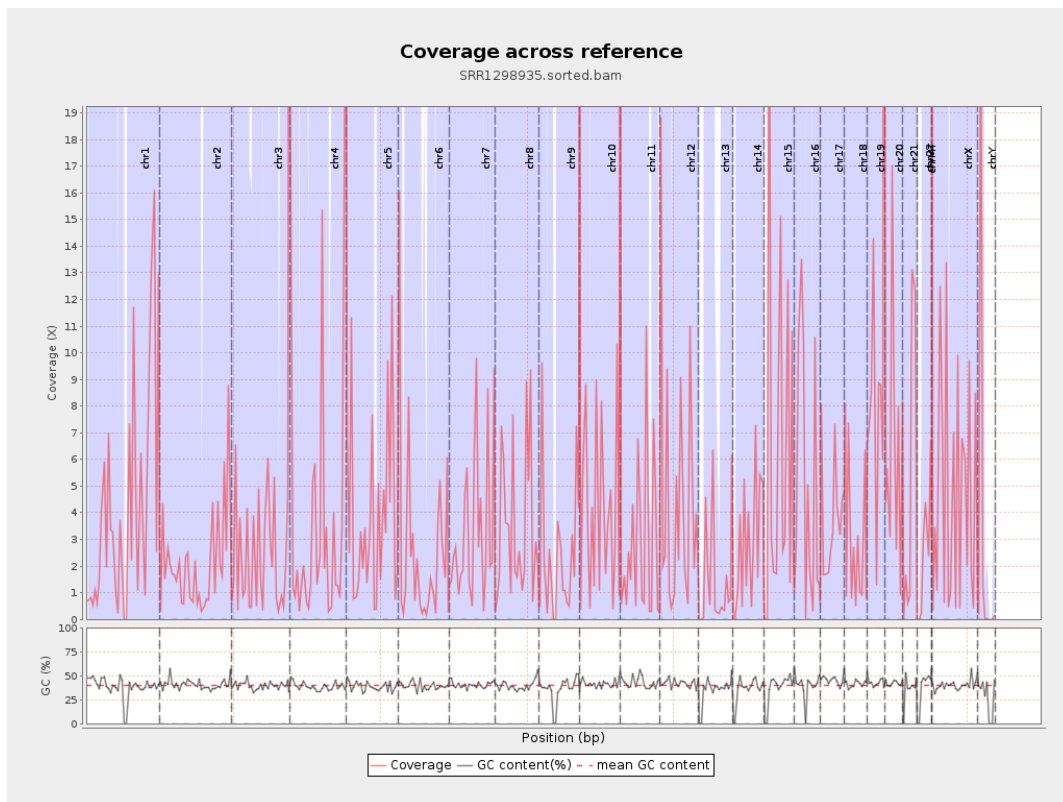
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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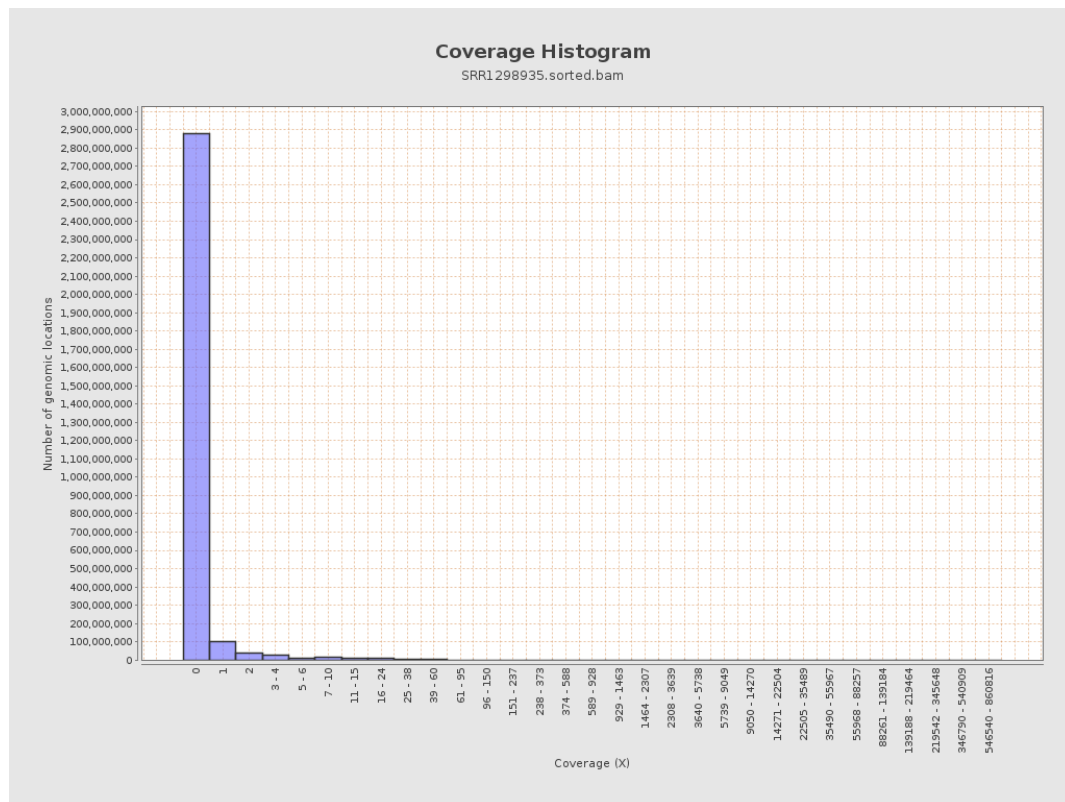
		bases	coverage	deviation
chr1	249250621	1052463677	4.2225	576.1106
chr2	243199373	519943228	2.1379	266.0847
chr3	198022430	516712499	2.6094	318.3215
chr4	191154276	681739731	3.5664	525.937
chr5	180915260	728109331	4.0246	587.6306
chr6	171115067	421016537	2.4604	383.333
chr7	159138663	555076850	3.488	437.9079
chr8	146364022	537219330	3.6704	460.7835
chr9	141213431	359929669	2.5488	308.5973
chr10	135534747	546386436	4.0313	487.6404
chr11	135006516	482739320	3.5757	407.7947
chr12	133851895	628116529	4.6926	632.6784
chr13	115169878	152382190	1.3231	241.2609
chr14	107349540	304092994	2.8327	337.8893
chr15	102531392	683585055	6.6671	810.7349
chr16	90354753	452931510	5.0128	628.3991
chr17	81195210	313304154	3.8587	319.5885
chr18	78077248	216622686	2.7745	300.3554
chr19	59128983	516884552	8.7416	790.6878
chr20	63025520	399737392	6.3425	677.0666
chr21	48129895	251958983	5.235	693.4979
chr22	51304566	136468811	2.66	327.8683
chrMT	16571	684082	41.2819	30.7667
chrX	155270560	724619408	4.6668	589.2251

chrY	59373566	199955283	3.3677	1,222.8778
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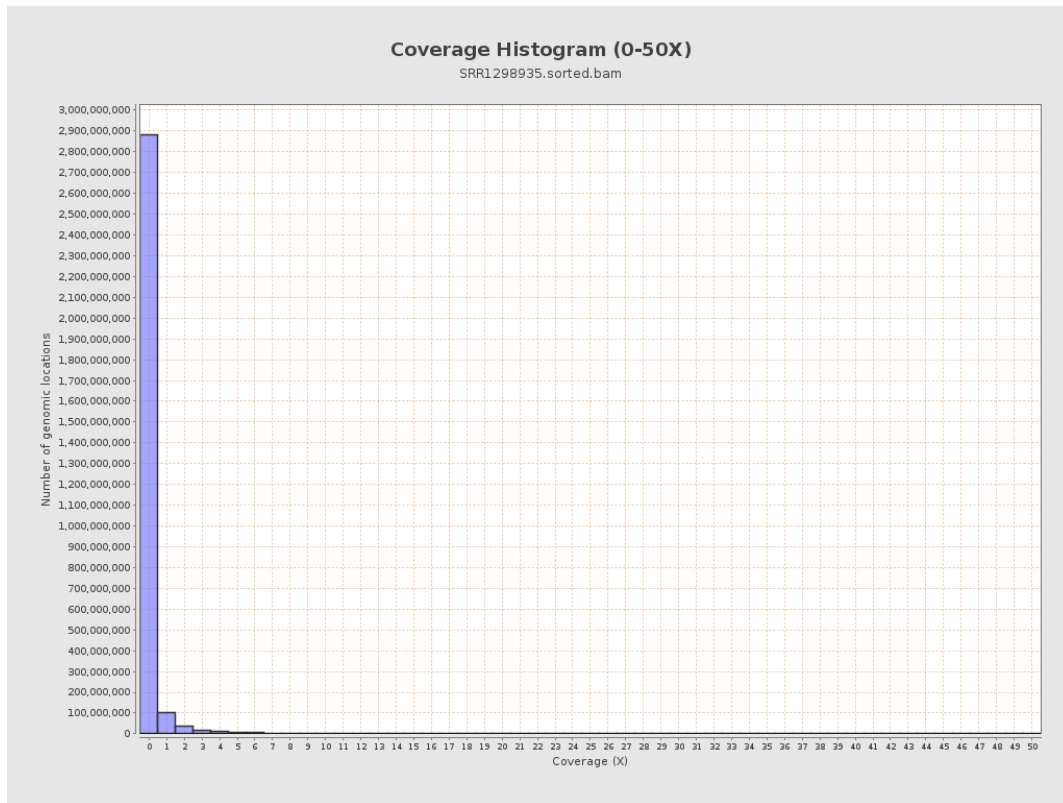
3. Results : Coverage across reference



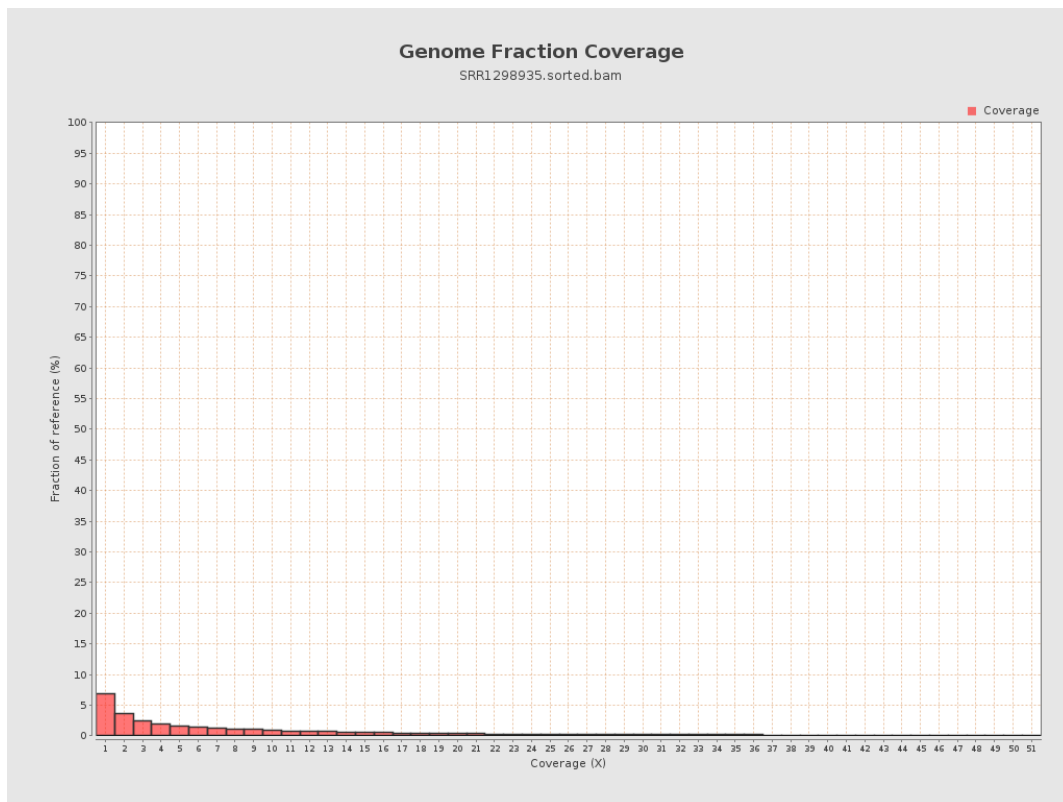
4. Results : Coverage Histogram



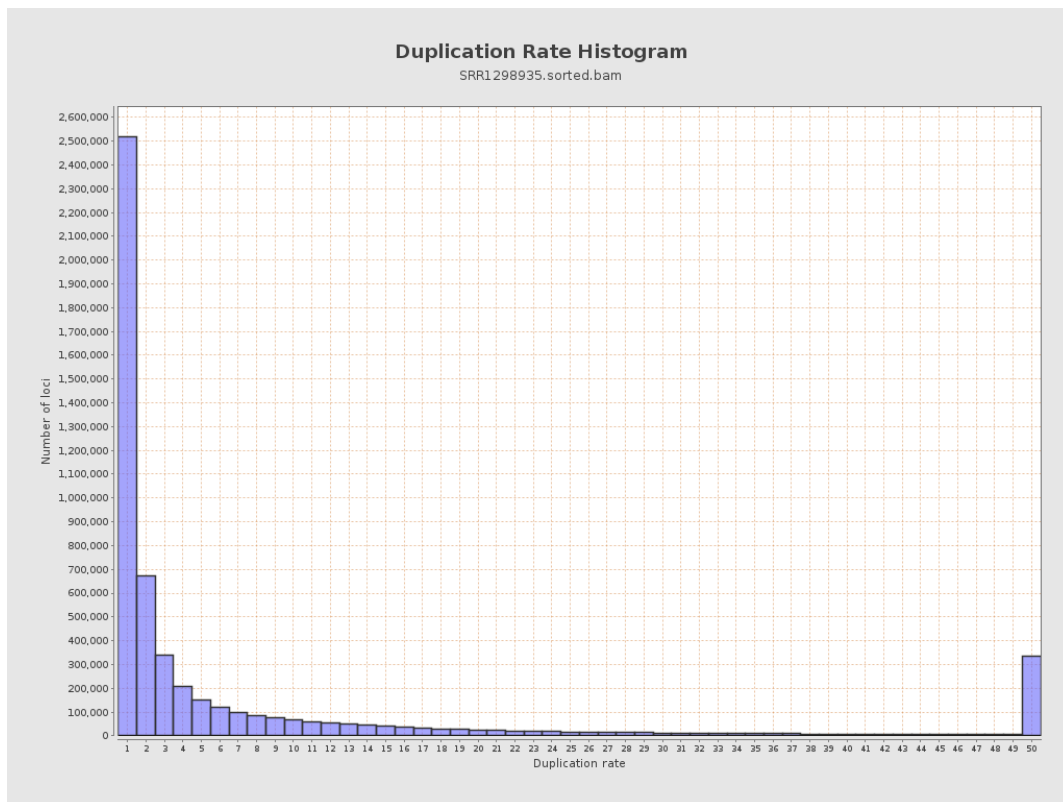
5. Results : Coverage Histogram (0-50X)



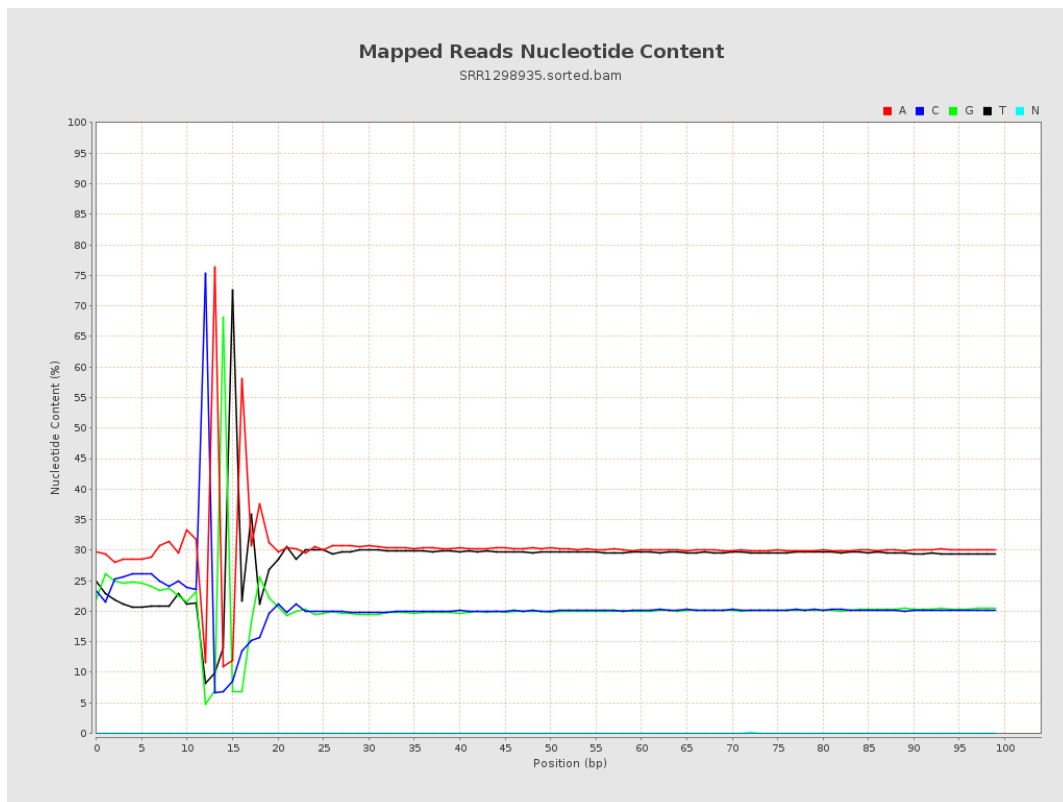
6. Results : Genome Fraction Coverage



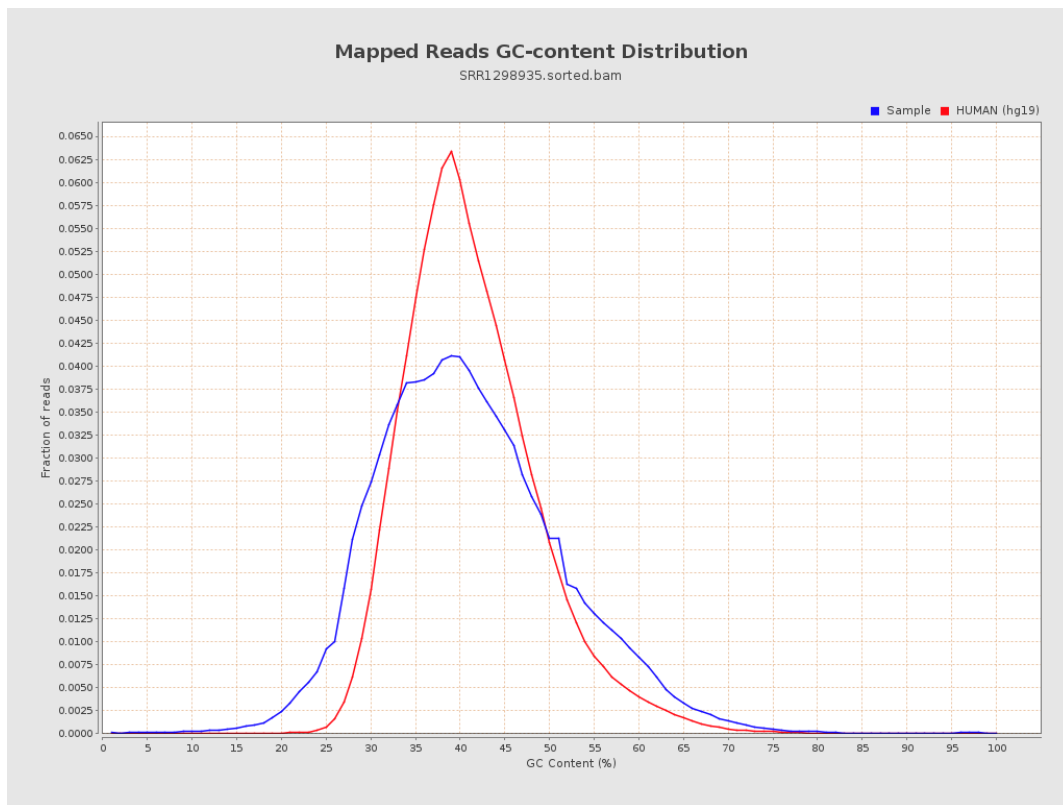
7. Results : Duplication Rate Histogram



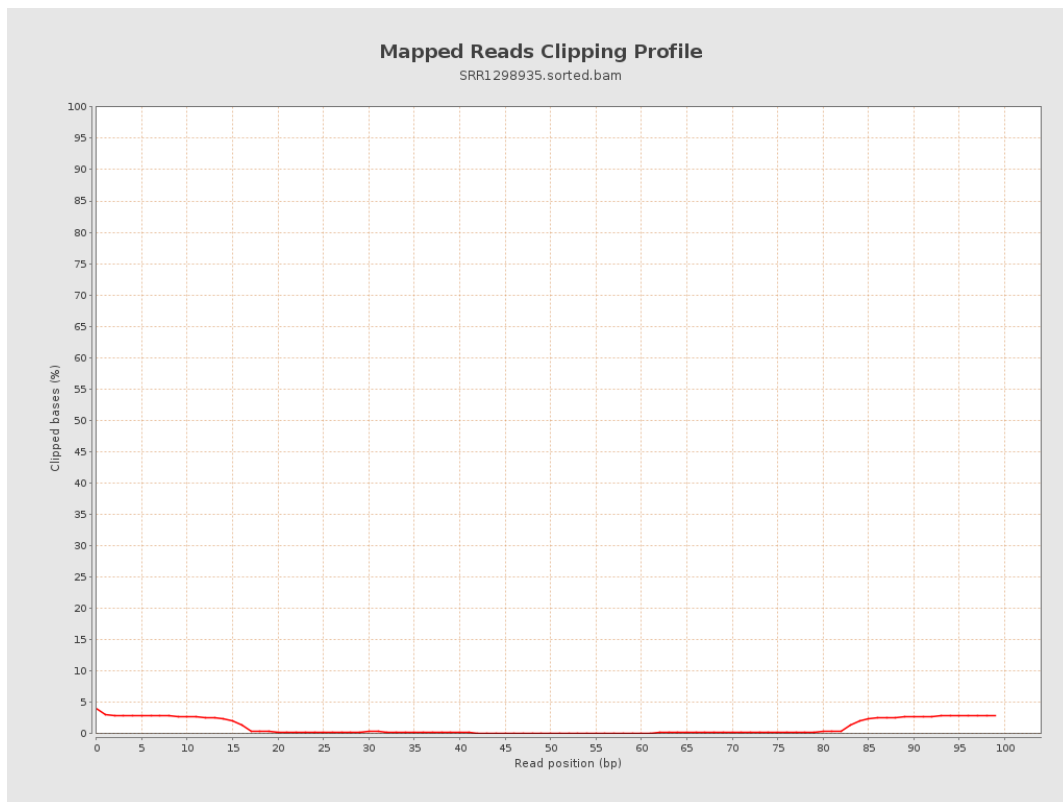
8. Results : Mapped Reads Nucleotide Content



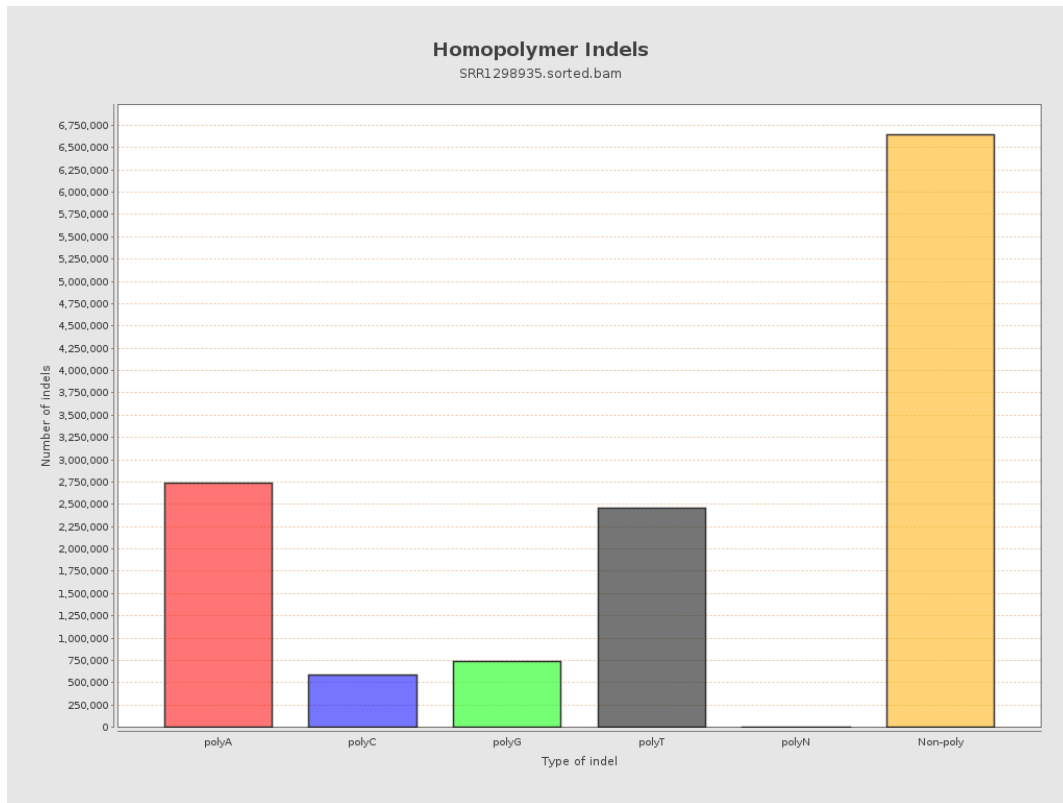
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



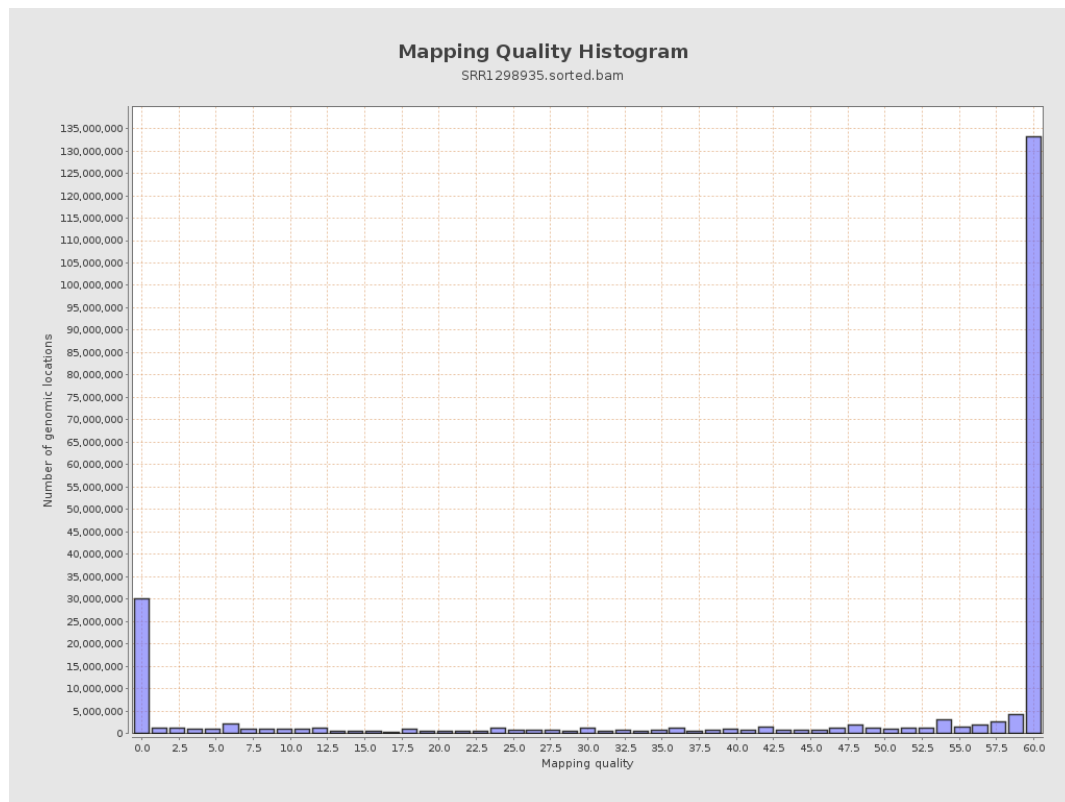
11. Results : Homopolymer Indels



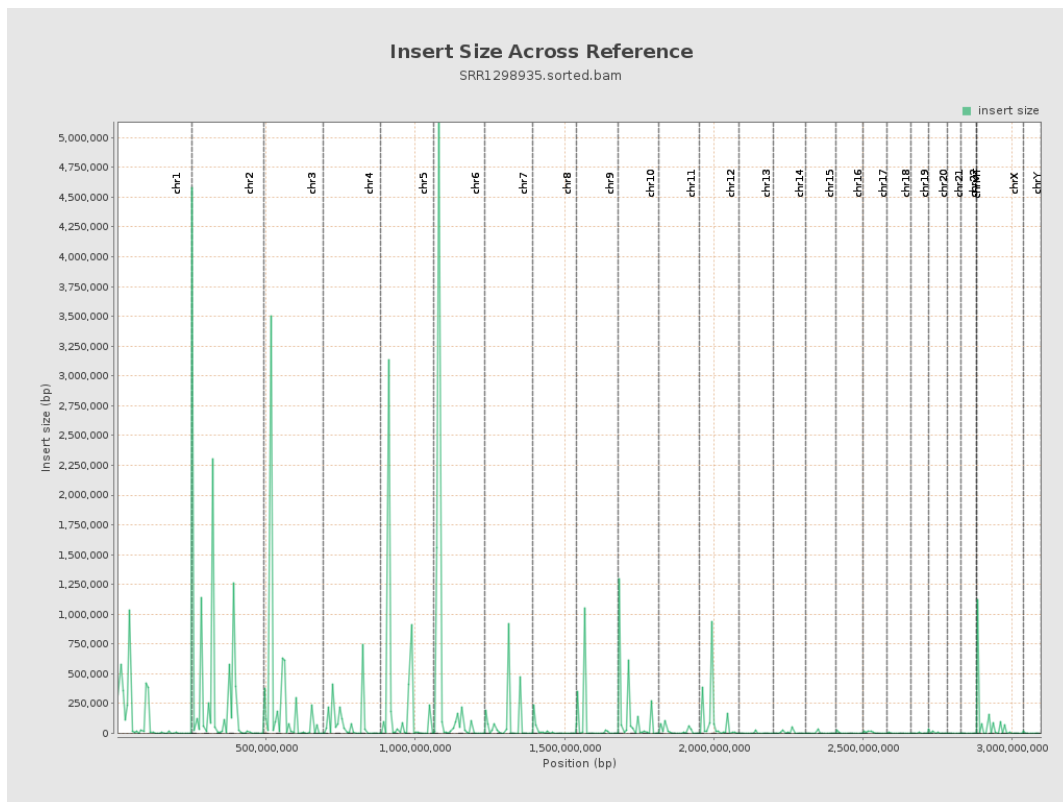
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

