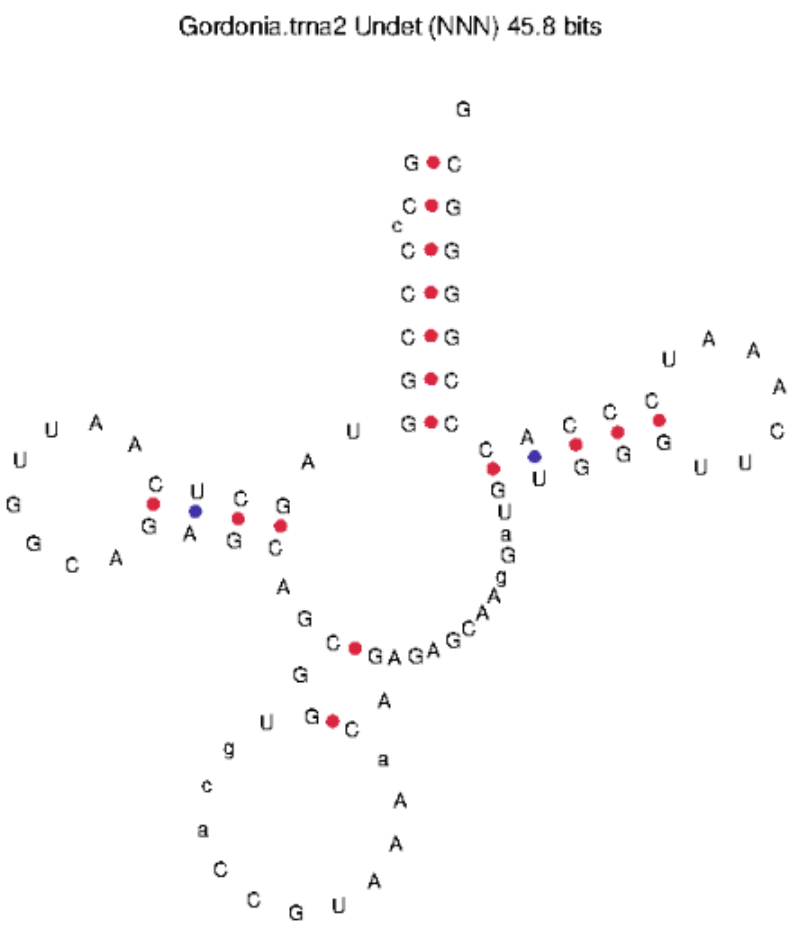
Phage: Culver CQ1

tRNA Scan SE
Start: 6057
End: 6138
Anti-codon: Undetermined
Infernal Score: 45.8
Isotype score: 50.8



If you look at the bp downstream of the “G” listed on the 3’ end, they are CATACG

bp 6139

So, I was thinking that we cut it at 6139, as after that “C”, it deviates from the CCA sequence.

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Gordonia.trna2 (6057-6138)      Length: 82 bp
Type: Undet     Anticodon: NNN at 0-0 (0-0)     Score: 45.8
          *    |    *    |    *    |    *    |    *    |    *    |    *    |    *    |
Seq: GCcCCCGGTAGCTCAATTGGCAGAGCAGCGGTgcaCCGTAAAaCAGAGAGCAAgGaTGTGGGTTCAAATCCCACCCGGGGCG
Str: >>.>>>>>..>>>>........<<<<..>.>............<.<............>>>>.......<<<<<<<<<<<<.
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