

Article

Tristetraprolin/ZFP36 Regulates the Turnover of Autoimmune-Associated HLA-DQ mRNAs

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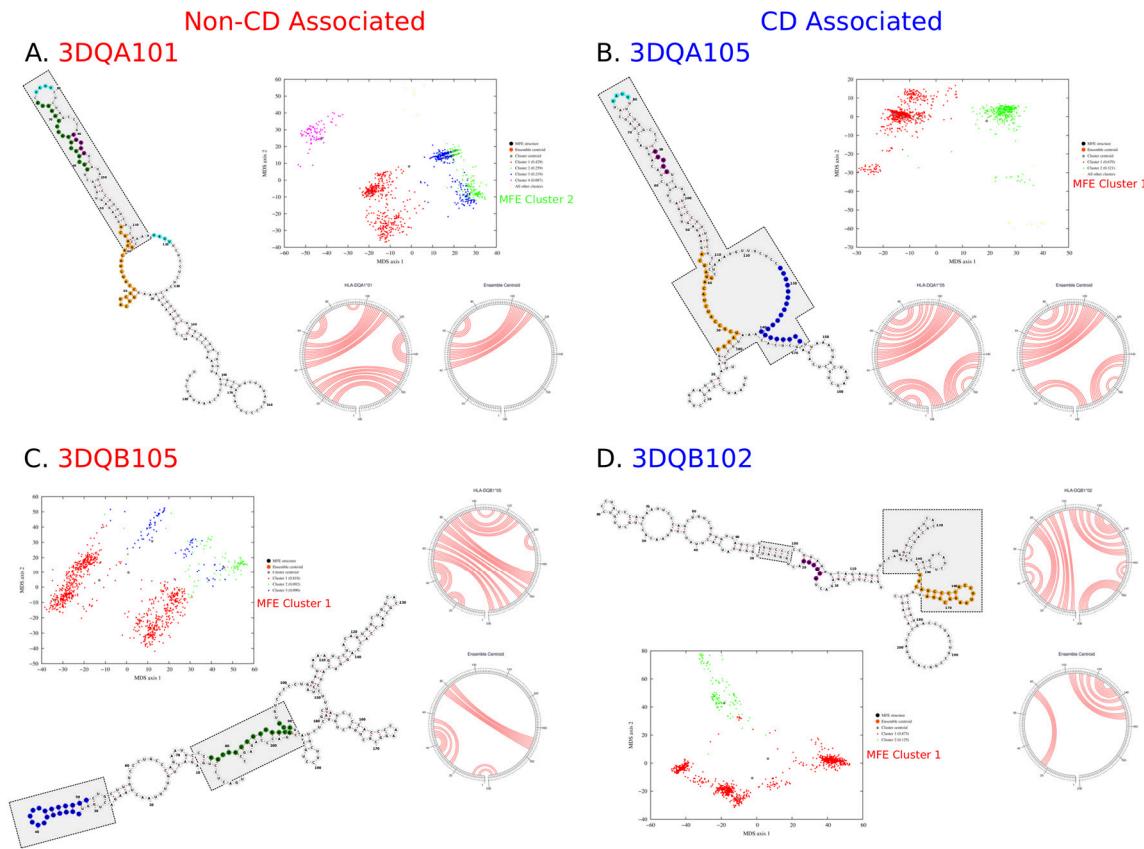


Figure S1. Sfold Structure Comparison of 3'UTR of DQA1* and DQB1*. Each of the riboprobe sequences was analysed with Sfold to predict statistical ensembles of structures. The ensembles permit many different conformations of the structures and clustering indicating the most likely conformations adopted by each sequence. The minimum-free energy (MFE) structure is also predicted and its parent cluster identified. **A.** 3DQA101, **B.** 3DQA105, **C.** 3DQB105 and **D.** 3DQB102 show the ensemble structures to contain fewer conserved base pairings (grey boxes) than the MFE structure indicating the structure is more dynamic/flexible outside of these regions. This is particularly evident in **D.** 3DQB102 where there is little conservation of base pairings in the large stem as seen in the other structures.

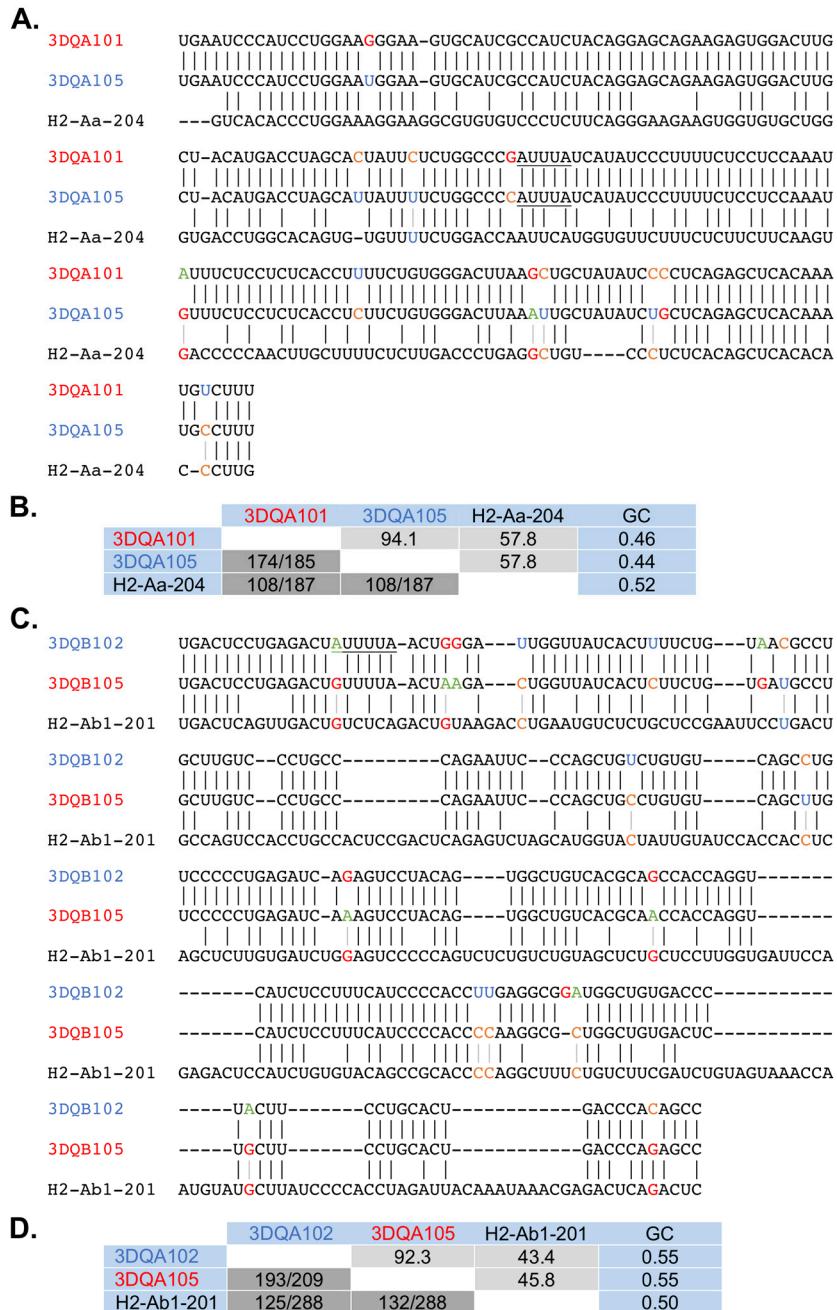


Figure S2. Sequence Alignment for human and mouse homologs for DQA1* and DQB1* alleles. The sequence alignments for the human DQA1* and DQB1* 3'UTR sequences in Figure 1A and B have been extended to include the mouse homologs H2-Aa and H2-Ab1. **A.** The DQA1* alignment for the human alleles and mouse homolog show high sequence identity between the human alleles at 94.1% but a much lower identity between the human and mouse sequences (<60%) as summarised in **B.** **C.** The DQB1* alignment for the human alleles and mouse homolog show a low sequence identity of <45% between species but >90% for the human sequences as summarised in **D.** The low level of conservation between human and mouse (<60% for DQA and <45%DQB) will result in different locations of AU rich motifs and affect their presentation in single stranded RNA structure regions.