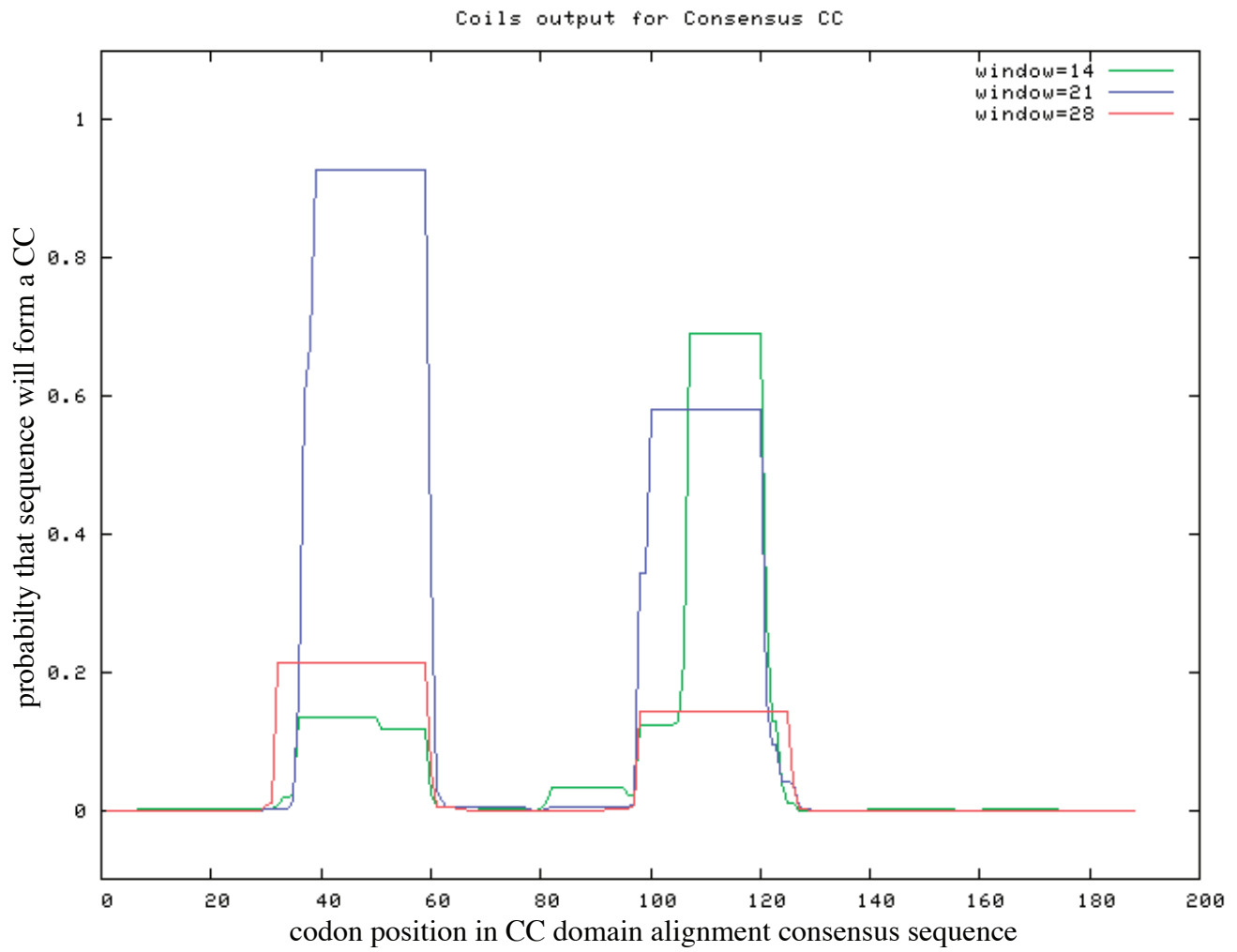


Supplementary Figure S2. A consensus sequence was generated from the alignment of 53 non-recombinant sequences corresponding to the CC domain such that only specific amino acids present in greater than 50% of the sequences represented at a given position in the alignment were retained. This consensus was then used as input for the COILS server.

A Using MTIDK matrix, without weighting



B Using MTIDK matrix, with weighting (weights: a,d=2.5 and b,c,e,f,g=1.0)

