Supplemental Figure 4

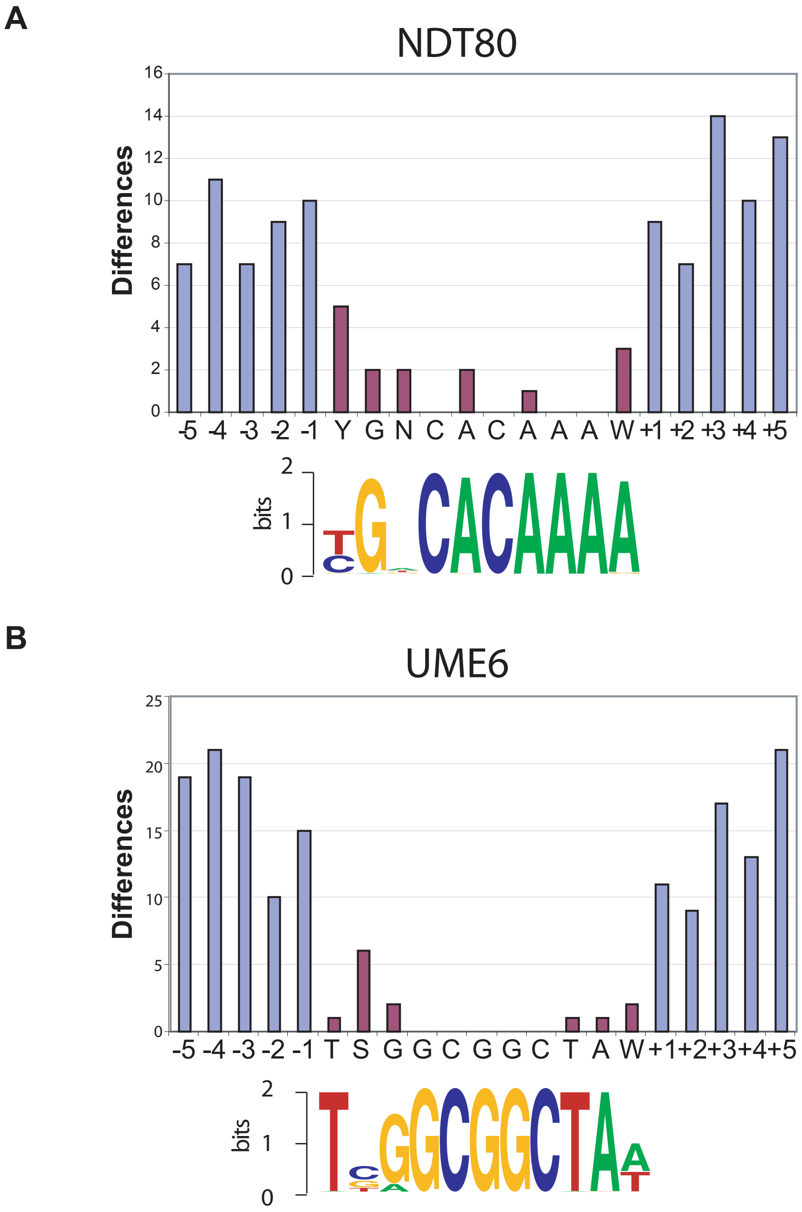

Figure S4. Using evolutionary data to build PWMs. For all sites with 1 difference between species, the number of differences found at each position within Ndt80 (A) and Ume6 (B) sites is shown in red. The differences were tabulated from 13 Ndt80 and 15 Ume6 motifs with a single difference among the three species. The number of differences found in the 5 nucleotides adjacent to the two motifs is shown in blue for reference. Using this substitution data, and the perfectly conserved sequences matching the NDT80 (YGNCACAAAW) or UME6 (TSGGCGGCTAW) consensus motifs, PWMs were constructed. Below each graph is the PWM constructed from the 39 NDT80 and 35 UME6 sites with zero or one difference. Each position weight matrix is displayed graphically as a motif logo. The frequency of each base at each position is represented by the height of A, G, C or T.