Web Figure 2. Results of AlignACE analysis of the search results. The 34 elements found in the search were searched using AlignACE for over-represented subsequences. Of the 755 motifs found, 25 are perfectly conserved between *D. melanogaster* and *D. virilis* in either the Eve MHE or the Hbr DME. The 25 motifs cluster into 14 groups at a 0.8 correlation coefficient level. Seqence logos for each of the 25 motifs are shown below.