Supplementary Material

Nawaz, M. and Rashid, S. 2012. *MotViz*: a tool for sequence motif prediction in parallel to structural visualization and analyses. *Genomics Proteomics Bioinformatics* 10(1): 35-43.

DOI: 10.1016/S1672-0229(11)60031-4.

Figure S1

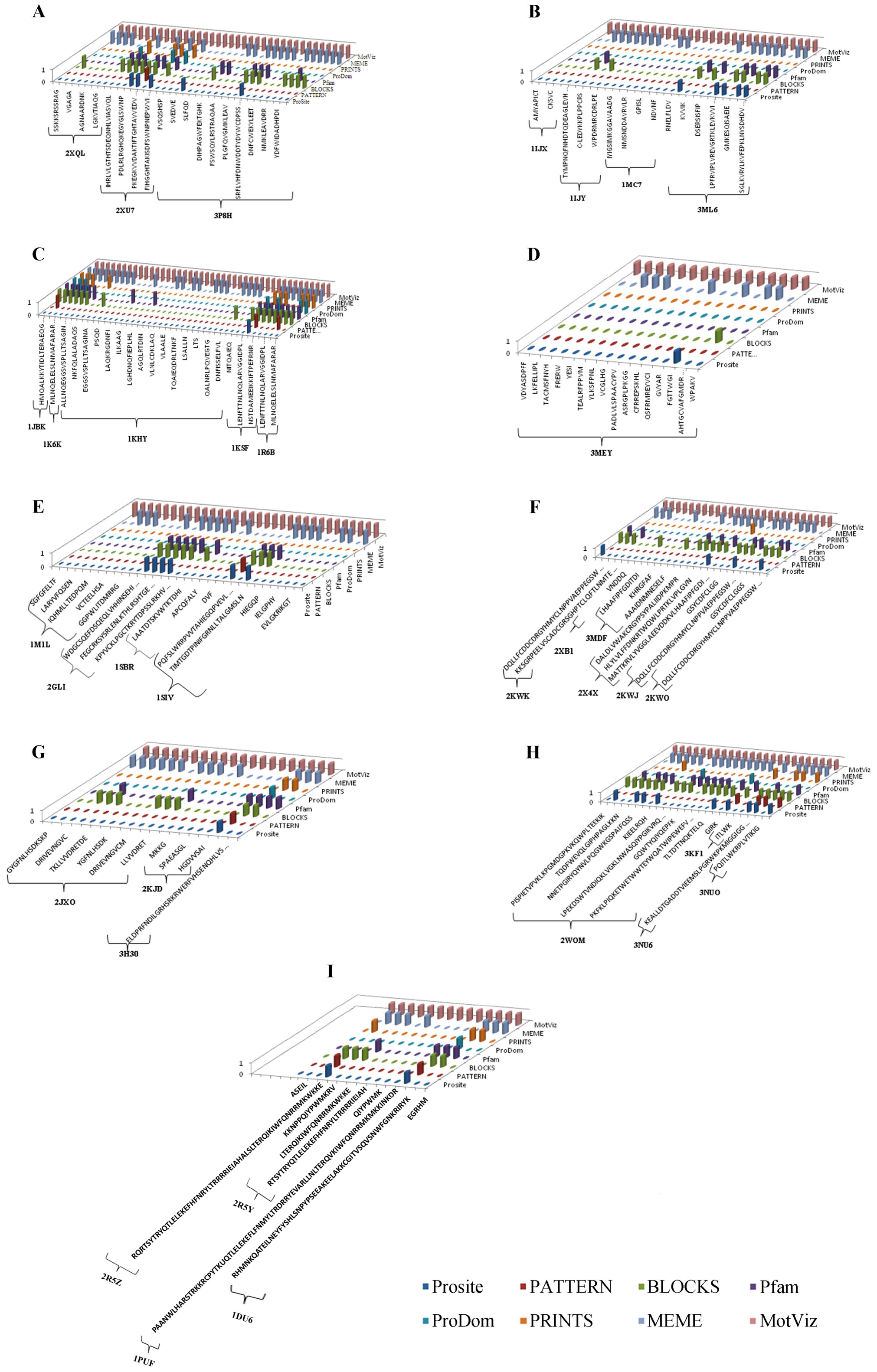

Figure S1 Graphical overview of predicted motifs by *MotViz* and other online tools. Graphical overview of predicted motifs by *MotViz*. The comparison was performed by dataset comprising histone family proteins (**A**), HSP100 family protein (**B**), Frizzled family proteins (**C**), ribosomal family proteins (**D**), Gli family proteins (**E**), PHD-finger family proteins (**F**), Wnt family proteins (**G**), HIV family proteins (**H**) and Hox family proteins (**I**). The predicted motifs by different tools were represented in different colors. The tools include Prosite, PATTERN, BLOCKS, Pfam, ProDom, PRINTS and MEME, respectively. X-axis represents predicted motifs. On Y-axis, the presence and absence of specific motif detected with various tools was indicated as 1 and 0, respectively.