Primary Motif

Secondary Motif

Tertiary Motif

Construct	SELEX Consensus Site
POU	TATGCAAAT
POU$_{HD}$	RTAATNA
POU$_S$	GAATATKC

Verrijzer, et al., EMBO Journal (1992), 11:4993-5003

R = A or G; K = T or G; N = A, C, G, or T

Figure S10: Primary, secondary, and tertiary Seed-and-Wobble motifs for the human POU homeodomain Oct-1. We searched for secondary and tertiary motifs in previously generated universal PBM data [Berger, *et al*., *Nature Biotechnology* (2007), 24:1429-1435] using our modified Seed-and-Wobble algorithm [Berger, *et al*., *Nature Biotechnology* (2007), 24:1429-1435] described in **Materials and Methods**. For one protein, human Oct-1, which has a bipartite POU DNA-binding domain, another group had already determined the consensus binding sites by *in vitro* selection (SELEX) for three separate constructs: the entire POU domain, the POU-specific subdomain (POU$_S$), and the POU-type homeodomian (POU$_{HD}$) [Verrijzer, *et al*., *EMBO Journal* (1992), 11:4993-5003]. The three motifs we derived from our universal PBM data correspond exactly to the previously-identified binding sites for these three constructs, suggesting to us that we can capture multiple modes of DNA-protein interactions *in vitro* from a single experiment.