Supplemental Data

Fig.1. Molecular mass of DHMBP-1 determined by UV cross-linking and partial affinity purification. (A) UV cross-linking. The nuclear extracts of embryo (Em) and SG were UV cross-linked with S1, and the complexes were separated by SDS-PAGE. The molecular marker is shown on the left. Two bands were observed, as indicated by the arrows on the right. After correction for bound oligonucleotide, the molecular mass for protein 1 is about 40 kDa, and for protein 2 is about 20 kDa. (B) DHMBP-1 binding activity of eluted fractions from DNA affinity column. Presence of DHMBP-1 in different fractions obtained by affinity column was checked using EMSA with labeled S1. N represents EMSA reaction with the loaded fraction, F represents the flow-through fraction, and the numbers on top represent the fractions eluted by different concentrations of KCl (0.1 to 2.0 M). (C) SDS/PAGE and silver staining of DHMBP-1 positive fraction. M represents the molecular mass markers. Lane 1 represents the nuclear extract purified by sephacryl S-300 column, and lane 2 represents the concentrated fraction from affinity column with high DHMBP-1 binding activity.

Fig.2. Sequence comparison between POU-M1, POU-M2 and Har-POU

Comparison of the deduced amino acid sequence of POU-M2, POU-M1, and Har-POU cloned from *H. armigera*. Asterisks show the identical amino acids. The POU specific-and homeo-domains are underlined. The 28 amino acids (amino acid 109-136 of POU-M2) which are various between POU-M1 and POU-M2 are specified by shaded black if more than two amino acids are the same in one position.

Fig.3. **DHMBP-2 enhanced the binding of DHMBP-1**. (A) Probe S1 was incubated with increasing amounts (μ g) of nuclear protein extracts from SG of day 1 pupae. C, cytoplasm protein extract. (B) Probes S1, S7 and SC were incubated with 10 μ g nuclear protein extracts from SG of day 1 pupae. pro, probe.



Figure 1

Har-POU POU-M2 POU-M1	MAATTYMPADMDLGDIGGYHAASPRSAEPADMKYQHGLHAGGSPSPGAPVL-NPWTSLPP MAATTYMPAEMELGNIGGYHAASPRSAEPADMKYQHPLHSGGSPSPGAPVIGNPWTSLPP MAATTYMPAEMELGNIGGYHAASPRSAEPADMKYQHPLHSGGSPSPGAPVIGNPWTSLPP ********* * ** *********************	59 60 60
Har-POU POU-M2 POU-M1	ADPWAMHQHHAHAHQPDVKPPPAPHEHRHLQHGGWHAPVVSPHYGA <mark>GTPVALHGGYPM</mark> Adpwamhqhhahahqpdvkpppaphdhrhlqhaahgwhapvvsphyga <mark>gspvtlhggypm</mark> Adpwamhqhhahahqpdvkpppaphdhrhlqhaahgwhapvvsphygaar <mark>p</mark> shcmedtqc *************	117 120 120
Har-POU POU-M2 POU-M1	PMHQHHMLRDIQPSPHPLHHHAMEREPPEEDTPTSDDLEAFAKQFKQRRIKLGFTQADVG PV <mark>HQHHMLRDIQPSPH</mark> PLHHHAMERDQPEEDTPTSDDLEAFAKQFKQRRIKLGFTQADVG PCTNTICSETSS <mark>P</mark> R-DPLHHHAMERDQPEEDTPTSDDLEAFAKQFKQRRIKLGFTQADVG * * ******** ************************	177 180 179

Figure 2



Figure 3