

Figure S2

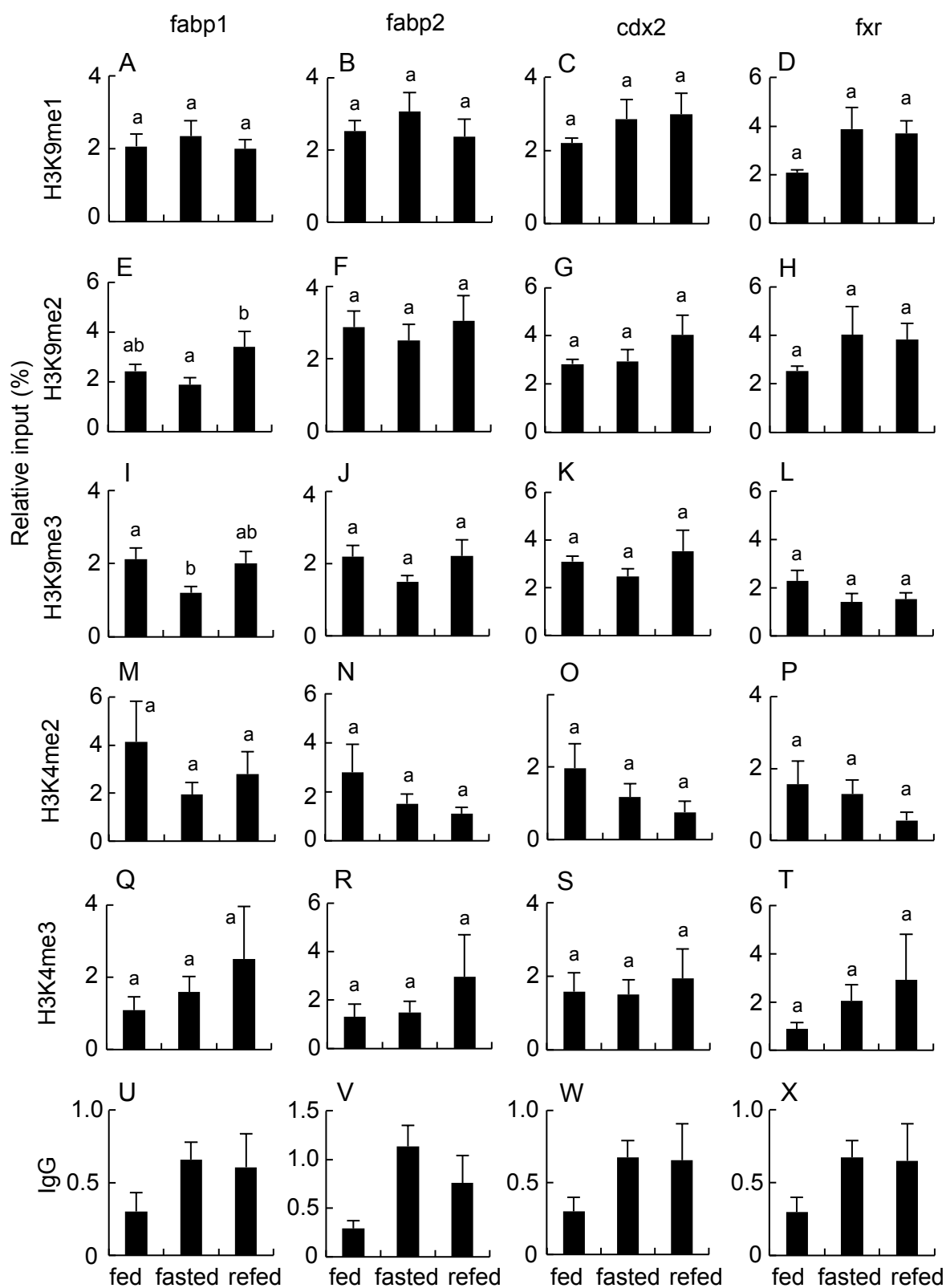


Fig. S2. Epigenetic modifications on *fabp1*, *fabp2*, *cdx2* and *fxr* genes in the intestines of fed, fasted and refed *X. laevis*. Chromatin samples were prepared from the intestines from animals that were fed for 22 days (*fed*), fasted for 22 days (*fasted*), and fasted for 21 days and then refed for 1 day (*refed*). Signals of ChIP on *fabp1* (A, E, I, M, Q and U), *fabp2* (B, F, J, N, R and V), *cdx2* (C, G, K, O, S and W), *fxr* (D, H, L, P, T and X) genes were detected by qPCR following immunoprecipitation with antibodies against H3K9me1 (A-D), H3K9me2 (E-H), H3K9me3 (I-L), H3K4me2 (M-P), H3K4me3 (Q-T), and normal IgG (U-X). Primers used in qPCR are shown in Table S2. Each value is the mean \pm SEM ($n = 8$). Distinct letters denote significantly different means, and were determined by one-way analysis of variance and Fisher's least significant difference test for multiple comparisons ($p < 0.05$).