Supplemental Figure 1

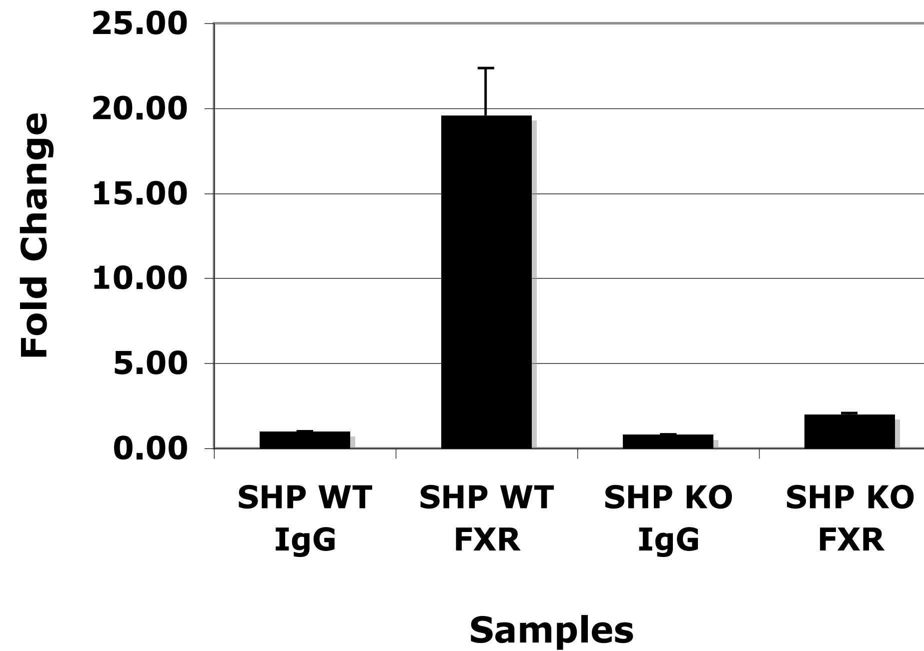

Figure S1. Confirmation of Chromatin and Antibody. Chromatin from WT or FXR KO mouse liver was used in gene specific ChIP analysis with control IgG or an FXR antibody and primers flanking the FXR binding site from the mouse SHP promoter. qPCR analysis was performed as described in the Methods.

Supplemental Figure 2

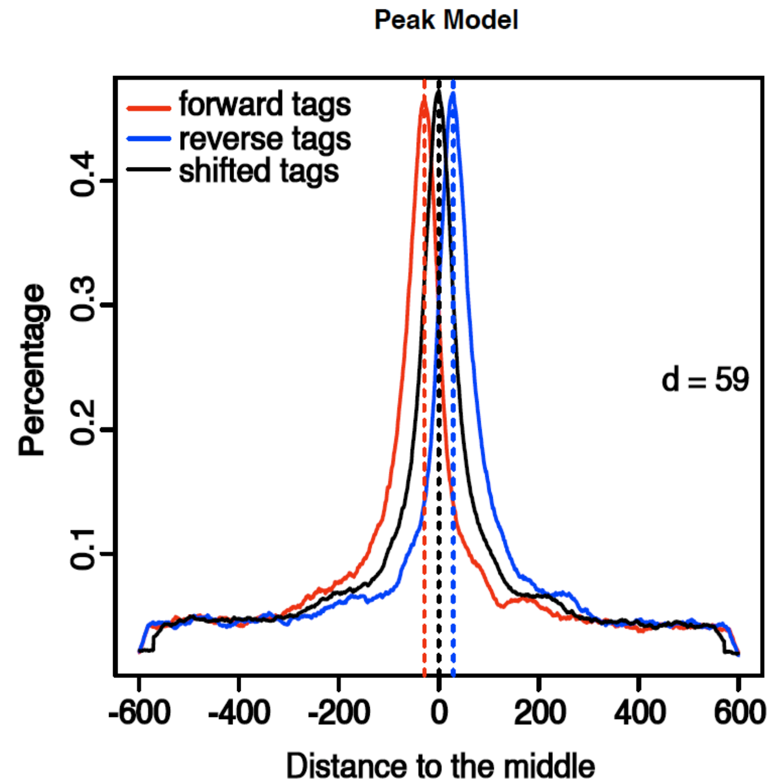

Figure S2. Peak model built by MACS. MACS estimated the *d* for FXR ChIP-seq data. MACS analysis of our data yielded 1656 peaks of FXR binding that are distributed throughout the genome.

Supplemental Figure 3

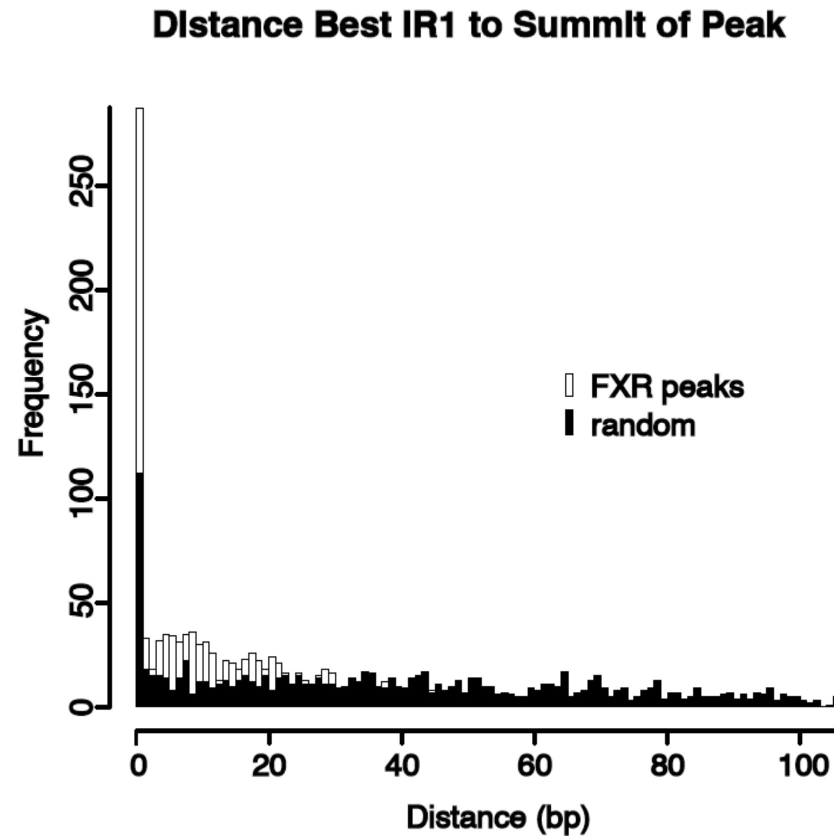

Figure S3. Distribution of the distance from the best IR-1 site to the summit of each peak with an IR-1 site. An arbitrarily located site of the same length in each peak was placed for 'random' peaks.

Supplemental Figure 4

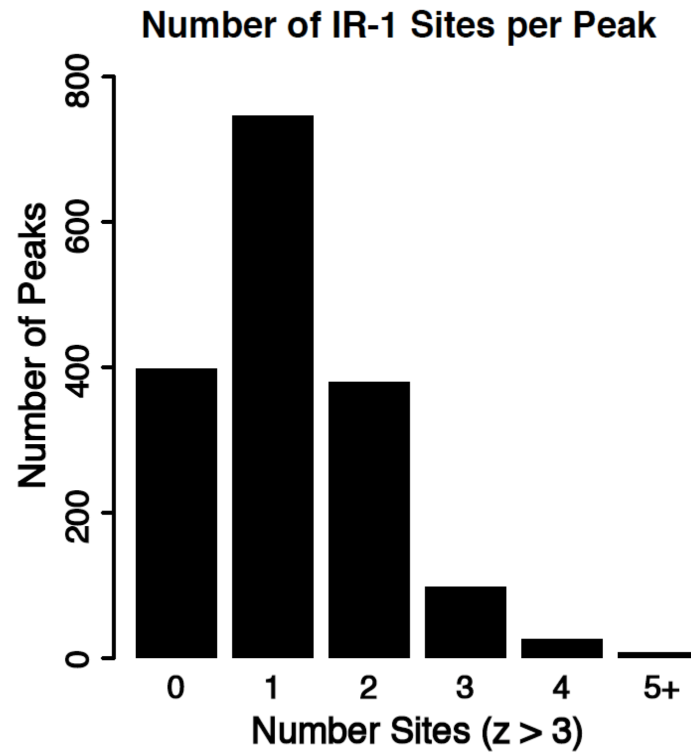

Figure S4. Number of IR-1 motif in a peak identified by ChIP-seq ($p<0.001$).

Supplemental Figure 5

Gene Name	*Fold Change*	*p-value*
Accb	**0.8**	**0.0700**
Atg4b	**0.5**	**0.0503**
Atg4d	**0.6**	**0.0649**
DGAT1	**0.9**	**0.5746**
Elovl6	**0.8**	**0.2326**
Mtf2	***0.8***	***0.4860***
MTTP	**0.7**	**0.2965**
Scd1	**0.3**	**0.0732**
Snx2	**0.4**	**0.0885**
SREBP2	**1.0**	**0.9332**
SHP	*9.8*	*0.0010*

Supplemental figure 5_. Random binding for non-FXR target genes by qPCR. Ten random primer pairs were chosen for gene-specific ChIP qPCR. Fold Change is the fold increase for the signal from DNA enriched by FXR antibody relative to a control IgG. SHP was used as a positive control. Data were normalized to the housekeeping gene L32.

Supplemental Figure 6

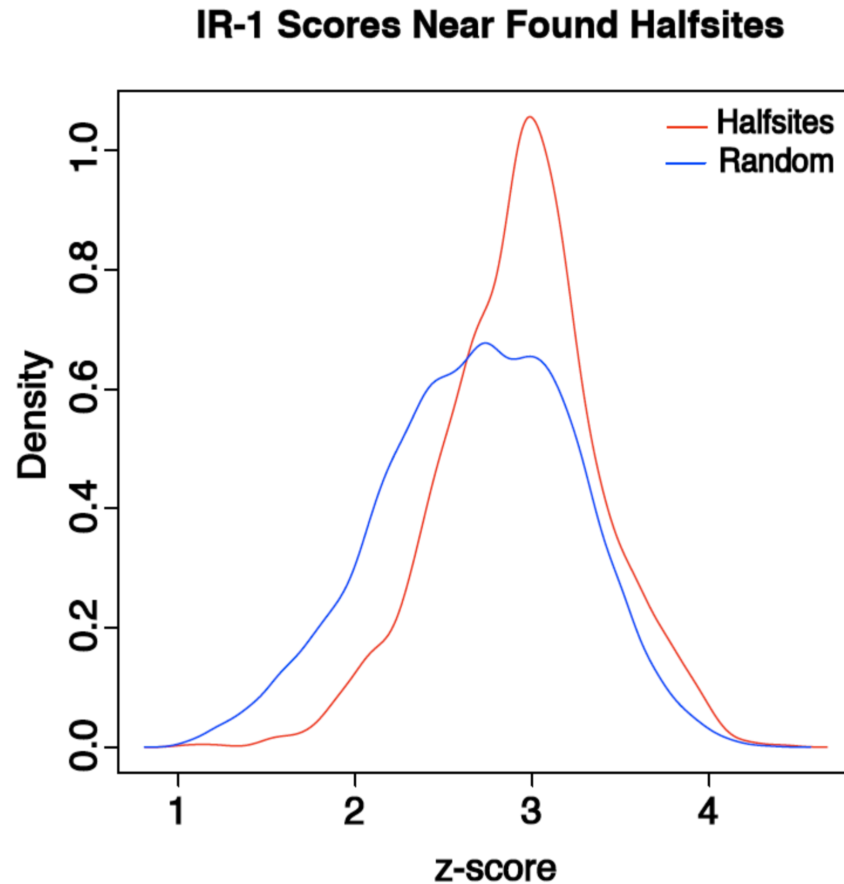

Figure S6. Hall-Site analysis: To confirm that the half-sites we identified were not merely weak IR-1 sites, we took all the half-sites we found and replaced them with AGGTCA and calculated the IR-1 score for them. We plotted a histogram of these scores. Next, we took random promoter sequence, selected a location at random, and inserted AGGTCA, then found the IR-1 score. We plotted the histogram of these scores on the same graph, normalizing the total area under each graph to be one. The scores from the found half-sites were slightly higher than from random sequence; the area of the higher curve to the right of the background was 0.20, which implies that 80% of the found half-sites are likely true half-sites, and not part of a “weak” IR-1.