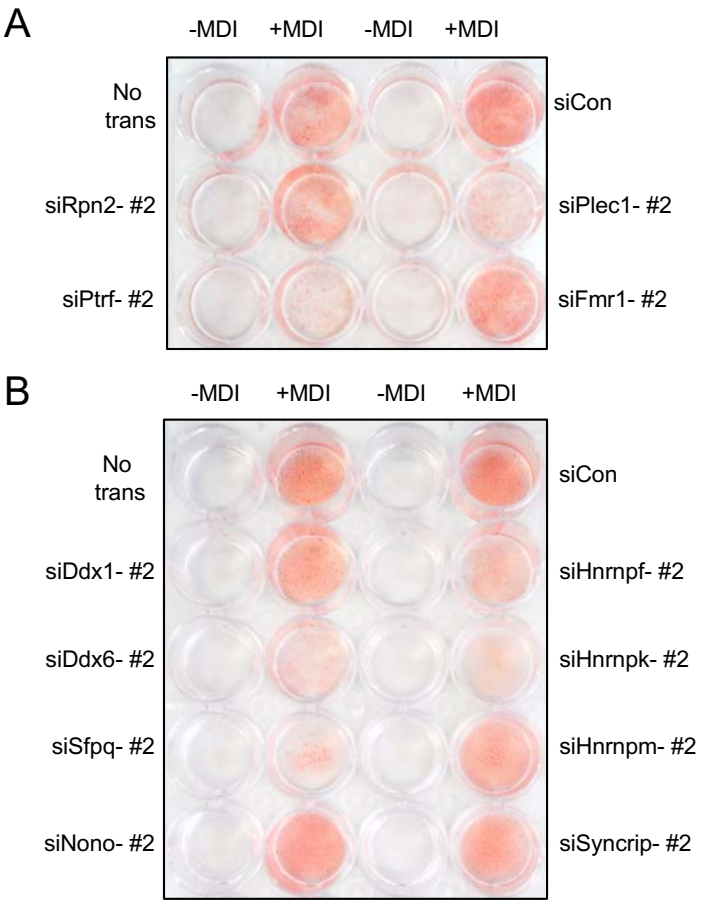
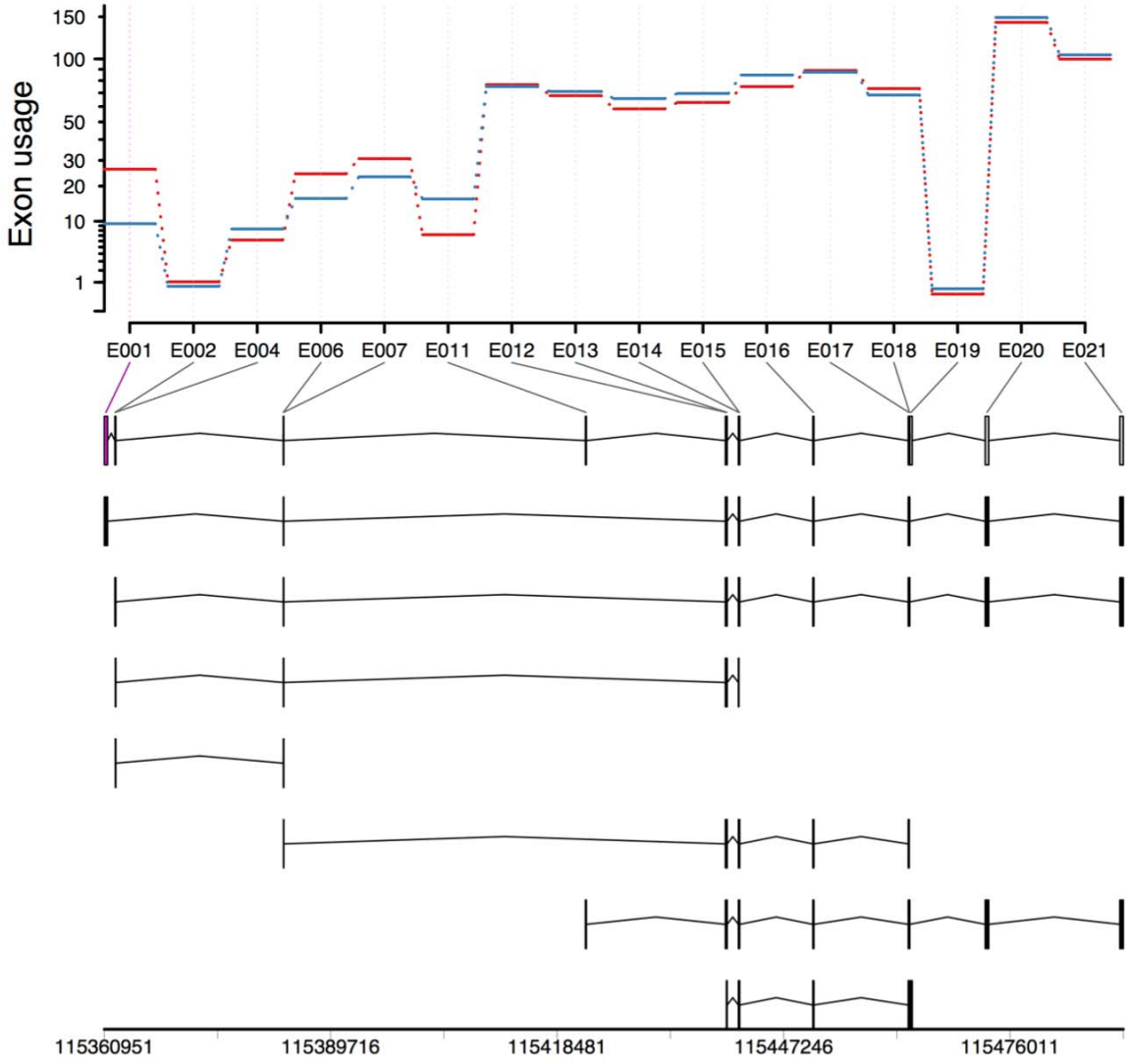
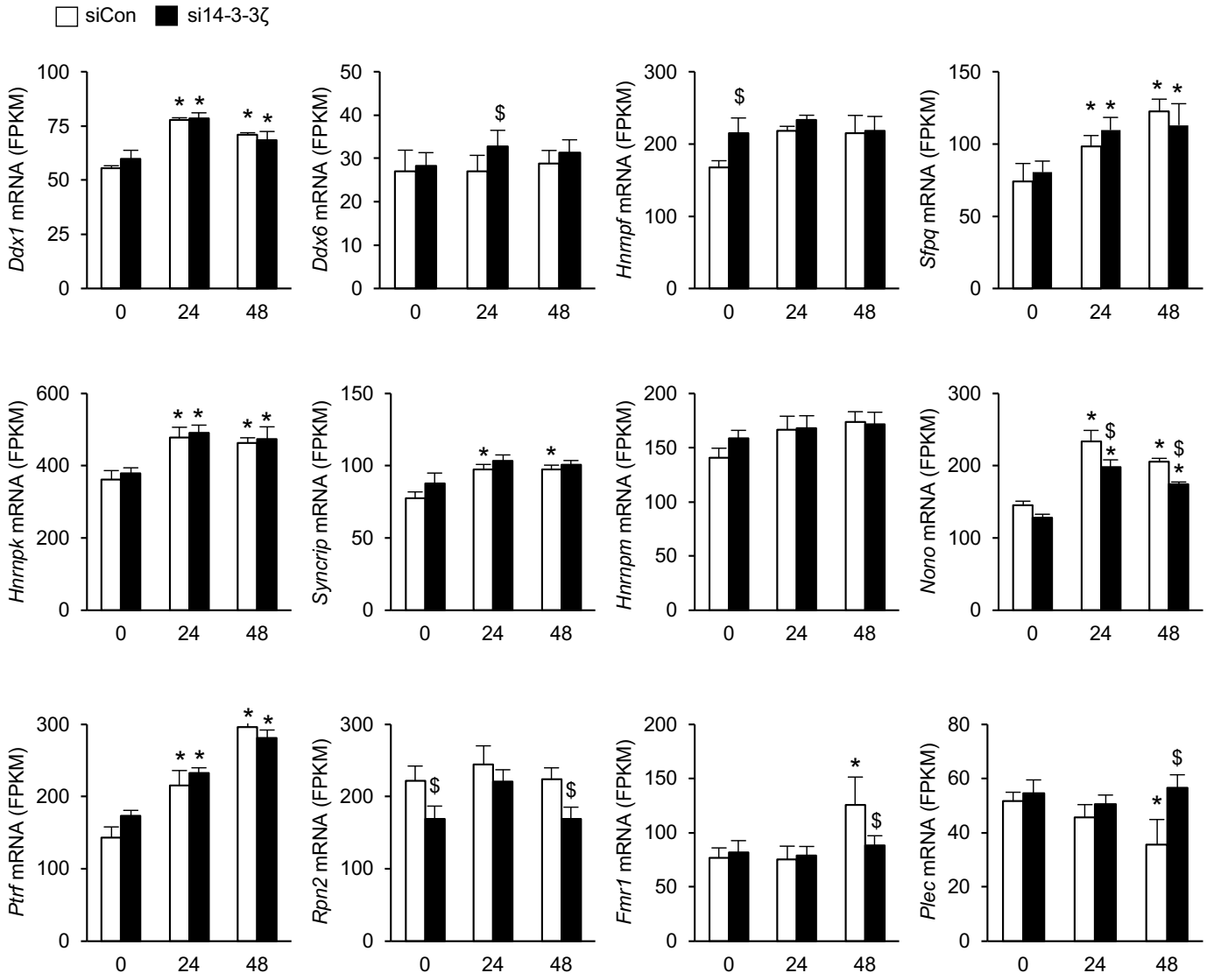


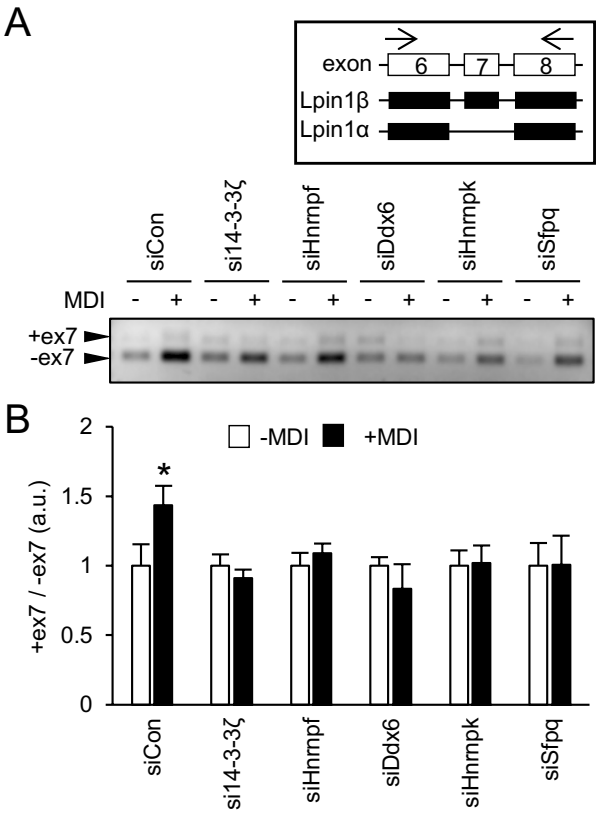
Supplemental figure 1: Knockdown of targets by independent siRNAs confirms the roles of 14-3-3ζ interacting partners in adipogenesis. (A,B) 3T3-L1 cells were transfected with a control siRNA (siCon) or siRNA#2 against established or putative adipogenic factors (A) or RNA splicing factors (B) (Knockdown efficiency of each siRNA is shown in Figure 2A and 4A) , followed by differentiation for up to 7 days. Adipocyte differentiation was assessed by Oil Red-O incorporation (representative of n=4 independent experiments).



Supplemental figure 2: *Pparg* exhibits differential exon usage during 3T3-L1 adipocyte differentiation. To confirm the ability of DEXSeq to detect genes exhibiting significant differential exon usage, transcriptomic data from undifferentiated and differentiating 3T3-L1 cells (48 hours post induction) were analyzed, and isoforms with differential use of exon 1 could be detected (n=4 per group).



Supplemental figure 3: Expression of candidate proteins from the 14-3-3ζ proteomic screen are largely unaffected by depletion of 14-3-3ζ. Transcriptomic data [GSE60745] (31) from 3T3-L1 cells transfected with control (siCon) or siRNA against 14-3-3ζ (si14-3-3ζ), followed by differentiation with an adipogenic cocktail (MDI) for up to 48 hours. The dataset was queried for expression profiles of 14-3-3ζ interacting partners that will be tested for their adipogenic contributions (Figure 3). (n=4 per group, *: $p<0.05$ when compared to t=0, $: $p<0.05$ when compared to siCon at respective time point; bar graphs represent mean ± std. dev.)



Supplemental figure 4: siRNA-mediated knockdown of RNA splicing factors affects the generationof *Lpin1* mRNA splice variants. (A) 3T3-L1 cells were transfected with siRNAs against various targets, induced to differentiate for 48 hours, and subjected to isolation of total RNA. RT-PCR was performed with primers specific for the detection of *Lpin1β* (+ex7) and *Lpin1α* (-ex7). PCR products were resolved on a 1% acrylamide gel. (Inset: Schematic diagram of the RT-PCR-based approach to detect alternative spliced isoforms of *Lpin1*. Arrows denote primers used to detect the inclusion or exclusion of exon 7) (representative of n=4 independent experiments). **(B)** Densitometric analysis of *Lpin1* PCR products from panel A to measure the ratio of *Lpin1β* (+ex7) to *Lpin1α* (-ex7) following knockdown of respective splicing factors or 14-3-3ζ or in repsone to differentiation (+MDI) (n=4 per group, *: $p<0.05$ when compared to undifferentiated (-MDI) 3T3-L1 cells; bar graphs represent mean ± std. dev.).