

Titles and Legends to Supplementary Figures and Tables

Table S1: Gene Ontology pathways over-represented in the list of IR-regulated genes. The list of IR-regulated genes in the absence of IR was compared to lists of genes grouped by pathways in the Gene Ontology data base. The expected number of genes regulated by chance in each pathway was compared to the actual number of genes regulated by IR. Over-represented pathways are listed.

Table S2: Gene Ontology pathways over-represented in the list of p53 shRNA-regulated genes. The list of p53 shRNA-regulated genes in the absence of IR was compared to lists of genes grouped by pathways in the Gene Ontology data base. The expected number of genes regulated by chance in each pathway was compared to the actual number of genes regulated by p53 shRNA. Over-represented pathways are listed.

Figure S1: Effect of NFBD1 knockdown on *CAVI* and *CAV2* mRNA levels in HFFs. HFF cells were infected with control or NFBD1a shRNA-expressing retroviruses and RNA was isolated following puromycin selection. cDNA was synthesized and real-time PCR was performed using primers towards *CAVI*, *CAV2*, or *NFBD1*. Error bars represent the standard error of the mean among three technical replicates.