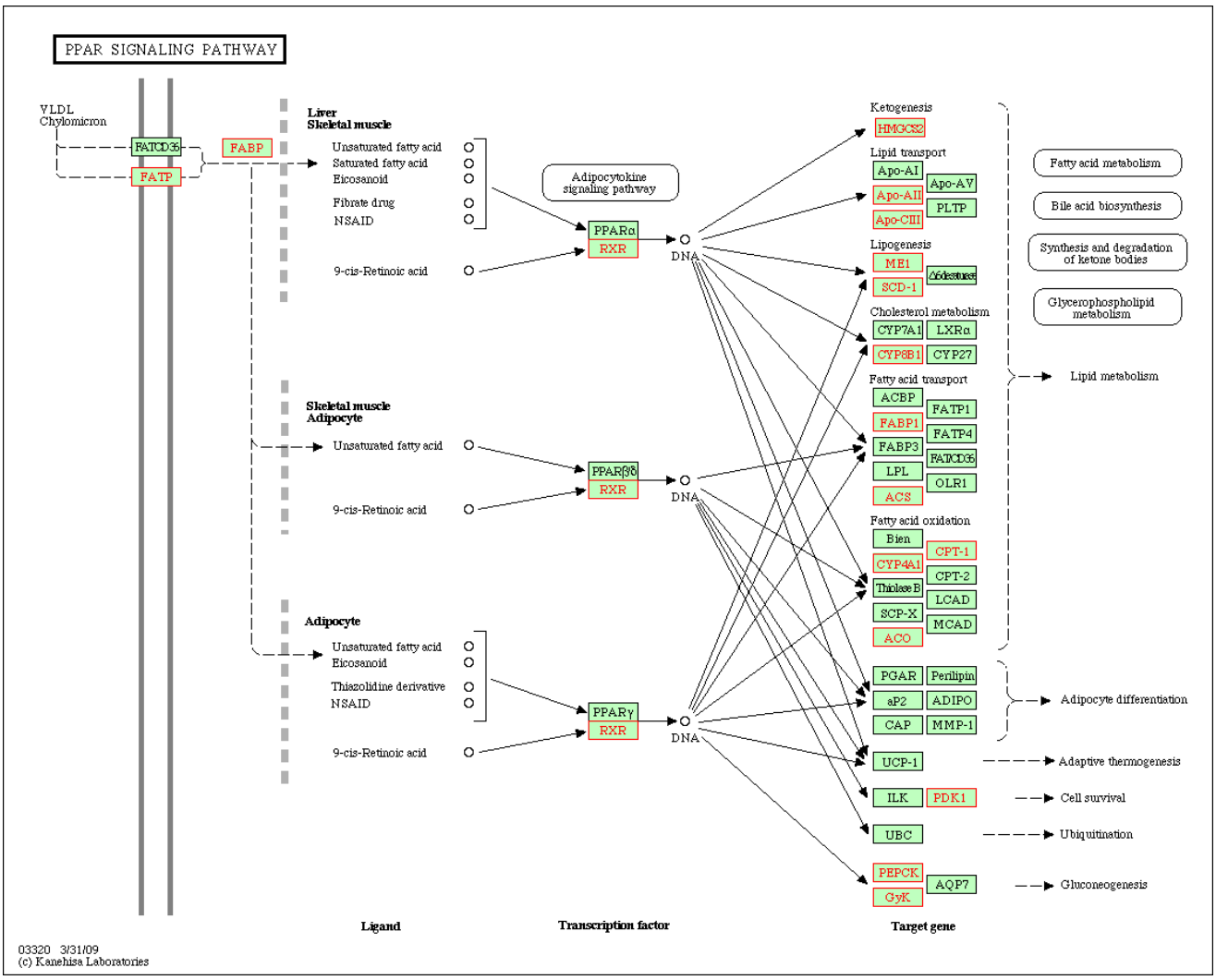
SUPPLEMENTARY FIGURES

Supplementary Fig. 2. Complete data set of the GO analysis using Ontologizer. Data sets were analyzed using the gene set provided by Illumina as the background. Analysis for over-represented terms was performed using the term-for-term algorithm with the Benjamini-Hochberg correction, and a corrected p value of 0.05 was used as the cutoff for significance. Colored circles are processes with significant changes. A) Biological process enriched in up-regulated genes. B) Molecular function enriched in up-regulated genes. C) Cellular components enriched in up-regulated genes. D) Biological processes enriched in down-regulated genes. E) Molecular functions enriched in down-regulated genes. F) Cellular components enriched in down-regulated genes.

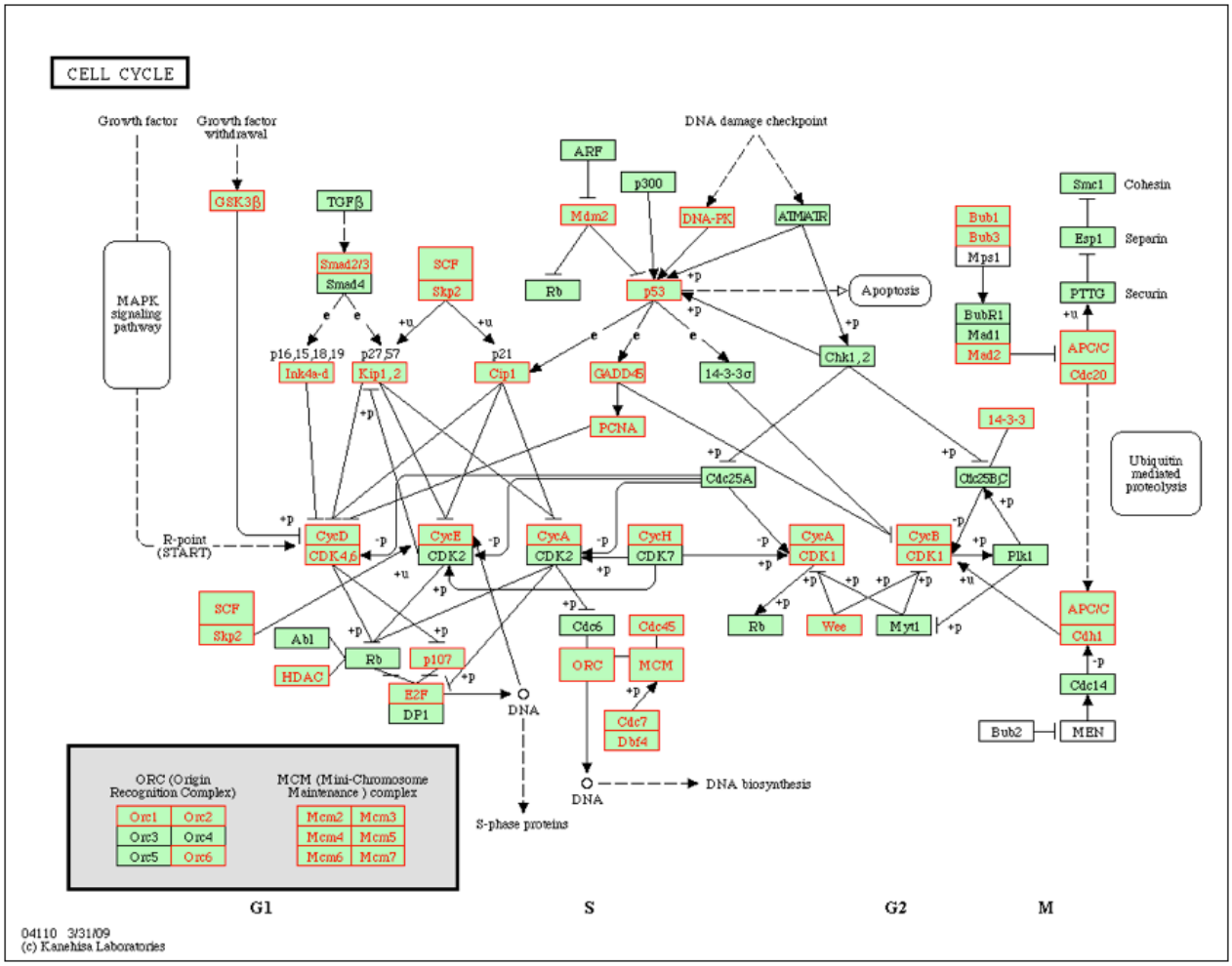
See attached PDF file labeled 'Supplementary Fig. 2

Supplementary Fig. 3. Graphical representation of the top pathways in the KEGG analysis. The p value is calculated using the hypergeometric test. Differentially expressed genes that changed more than 1.5-fold are indicated in red. A) PPAR signaling pathway, enriched in down-regulated genes. B) Cell cycle, enriched in up-regulated genes.

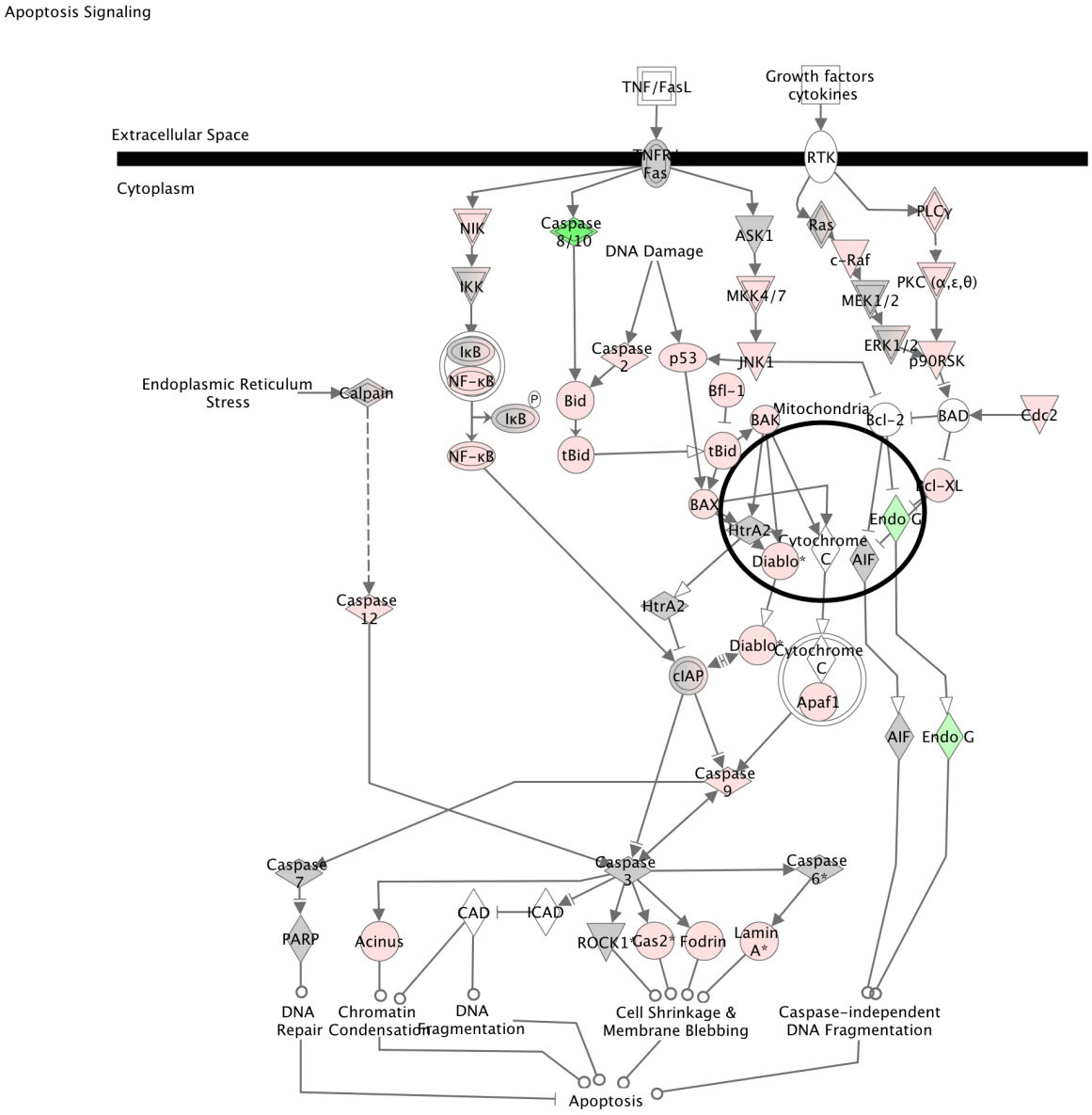
A.



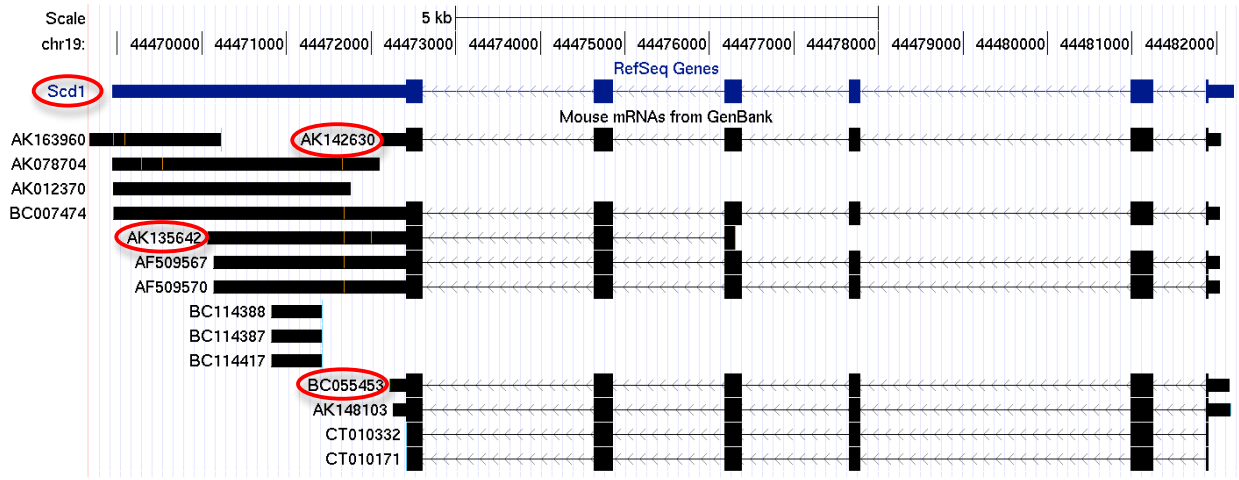
B.


CELL CYCLE
Growth factor
Growth factor withdrawal
GSK3β
TGFβ
MAPK signaling pathway
Smad2/3
Smad4
SCF
Skp2
p16,15,18,19
Ink4a-d
p27,57
Kip1,2
p21
Cip1
R-point (START)
CycD
CDK4,6
CycE
CDK2
CycA
CDK2
CycH
CDK7
CycA
CDK1
CycB
CDK1
Plk1
SCF
Skp2
Abl
HDAC
Rb
p107
E2F
DP1
DNA
Cdc6
ORC
Cdc45
MCM
Cdc7
Dbf4
S-phase proteins
DNA
DNA biosynthesis
ORC (Origin Recognition Complex)
Orc1
Orc2
Orc3
Orc4
Orc5
Orc6
MCM (Mini-Chromosome Maintenance) complex
Mcm2
Mcm3
Mcm4
Mcm5
Mcm6
Mcm7
G1
S
G2
M
04110 3/31/09
(c) Kanehisa Laboratories
DNA damage checkpoint
ARF
p300
Mdm2
DNA-PK
ATM/ATR
Rb
p53
Apoptosis
Chk1,2
GADD45
14-3-3σ
PCNA
Cdc25A
Rb
Wee
Myt1
Bub1
Bub3
Mps1
BubR1
Mad1
Mad2
APC/C
Cdc20
14-3-3
Cdc25B/C
APC/C
Cdh1
Cdc14
Bub2
MEN
Smc1
Cohesin
Esp1
Separin
PTTG
Securin
Ubiquitin mediated proteolysis

Supplementary Fig. 4. Graphical representation of the apoptosis pathway. The apoptosis pathway is presented from Ingenuity Pathway Analysis, with up-regulated genes in red, and down-regulated genes in green.



Supplementary Fig. 5. Graphical view of the genomic locus of Scd1. Scd1 is located on mouse chr19:44,465,670-44,485,318 (UCSC Genome Browser mm9). There are variable polyA sites, resulting in different lengths of 3' -UTR. There are four different tags that match the transcripts whose accession numbers are circled in red. All but AK135642 show differential expression in the DGE, with BC055453 going up, and AK142630 and the reference sequence going down.



Note that the expression patterns seen in DGE are complex. A classic example is Scd1, one of the mouse models chosen for comparison. There are four different tags, each representing an alternative 3' UTR (Supplementary Table 4). The order of UTRs from shortest to longest is: BC055453, AK142630, AK135642, NM_009127. This also roughly matches the fold changes, which are, respectively 1.6, 2.3, 1.1, and 1.5. The third mRNA, AK135642, does not change, and its annotation is problematic, as it is missing the first few exons of the gene (see above), and is predicted to encode a different protein. There are also very different expression levels, with all except for NM_009127 in the range of tens of reads, while NM_009127 is in the thousands of reads (this is also reflected in the corrected p values, Supplementary Table 4.) There are several possible biological explanations for these differences, the two most plausible being i) a mix of tissue types, with different transcripts expressed in different cell types, and ii) different types are expressed by the same cell, but there is one major isoform which decreases, while the minor isoform increases.