Supplementary Table 1: PCR primers used to assess transcription factor localization in ChIP assays or gene expression.

Supplementary Figure 1: Peaks of Egr1 binding are observed at start sites of many cholesterol biosynthetic promoters

The binding of Egr1 to many cholesterol biosynthetic genes was determined using ChIP-chip assays of H4IIE cells treated with insulin. The ChIP samples were labeled with Cy5 (Egr1+insulin) or Cy3 (Egr1-insulin control) for hybridization to the genomic tiling array. The enrichment ratio of Cy5 to Cy3 was plotted on a $\log_2$ scale and further processed to display a five-point moving average. Genomic location of peaks is displayed on the x-axis. Peaks of Egr1 binding coincide with transcription start sites of cholesterol biosynthetic genes such as *Hmgcs*, *Fdps*, *Nsdhl and Fdft1*. Arrows indicate gene location and transcriptional direction. These data are representative of 3 independent ChIP-chip experiments, and FDR values for these identified peaks are <0.05 using Nimblescan analysis.

Supplementary Figure 2: Verification of ChIP-chip results at *Hmgcs*, *Fdps*, and *Nsdhl*.

Gene elements identified as putative Egr1 binding sites were interrogated for Egr1 binding following insulin treatment for 1h using ChIP assays. Percentage recovery relative to input DNA was measured using qPCR with primers designed to detect putative EGR binding sites. The treatment of the cells is indicated on the x-axis (SF= serum free, Ins = 1h insulin) as is the promoter being tested, and darker bars indicate percent recovery of Egr1 at the locus while lighter bars indicate the level observed with nonspecific IgG immunoprecipitation.

Supplementary Figure 3: Two Nimblescan analyses ChIP-chip of the *Hmgcr* Locus

The binding of Egr1 to many cholesterol biosynthetic genes was determined using ChIP-chip assays of H4IIE cells treated with insulin. The ChIP samples were labeled with Cy5 (Egr1+insulin) or Cy3 (Egr1-insulin control) for hybridization to the genomic tiling array. Using Nimblescan software to analyze ChIP-chip data, peaks of binding can be identified that have a calculated false discovery rate of less than 0.05. These peaks are indicated in red as a separate track, indicating regions of strong binding of Egr1, and are coincident with the *Hmgcr* promoter. The *Hmgcr* locus is shown, as are the identified peaks from two separate experiments with H4IIEs treated with insulin for 1h.

Supplementary Figure 4: Egr1 siRNA Specifically Reduced both Egr1 mRNA and protein

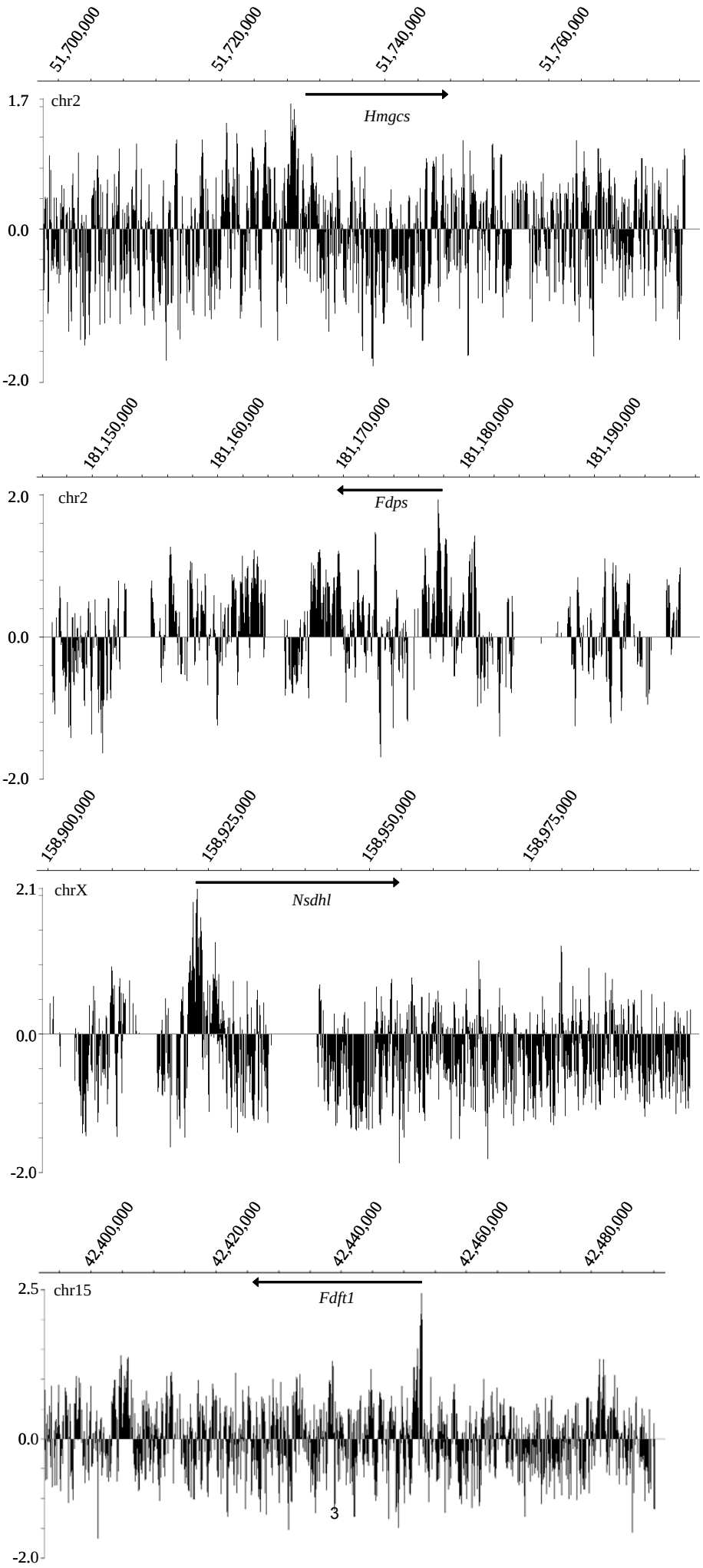
H4IIE cells were transfected with either control siRNA or Egr1 specific siRNAs. RT-qPCR indicated a 50% reduction in the response of *Egr1* mRNA to insulin in cells transfected with siRNA for Egr1 after treatment with insulin for 30 minutes. A similar reduction in Egr1 protein was observed after 1.5h of insulin treatment. Average values from four independent experiments are shown and error bars represent standard deviation (asterisk indicates $p<0.05$, error bars indicate standard deviation, Welch t-test, n=4).

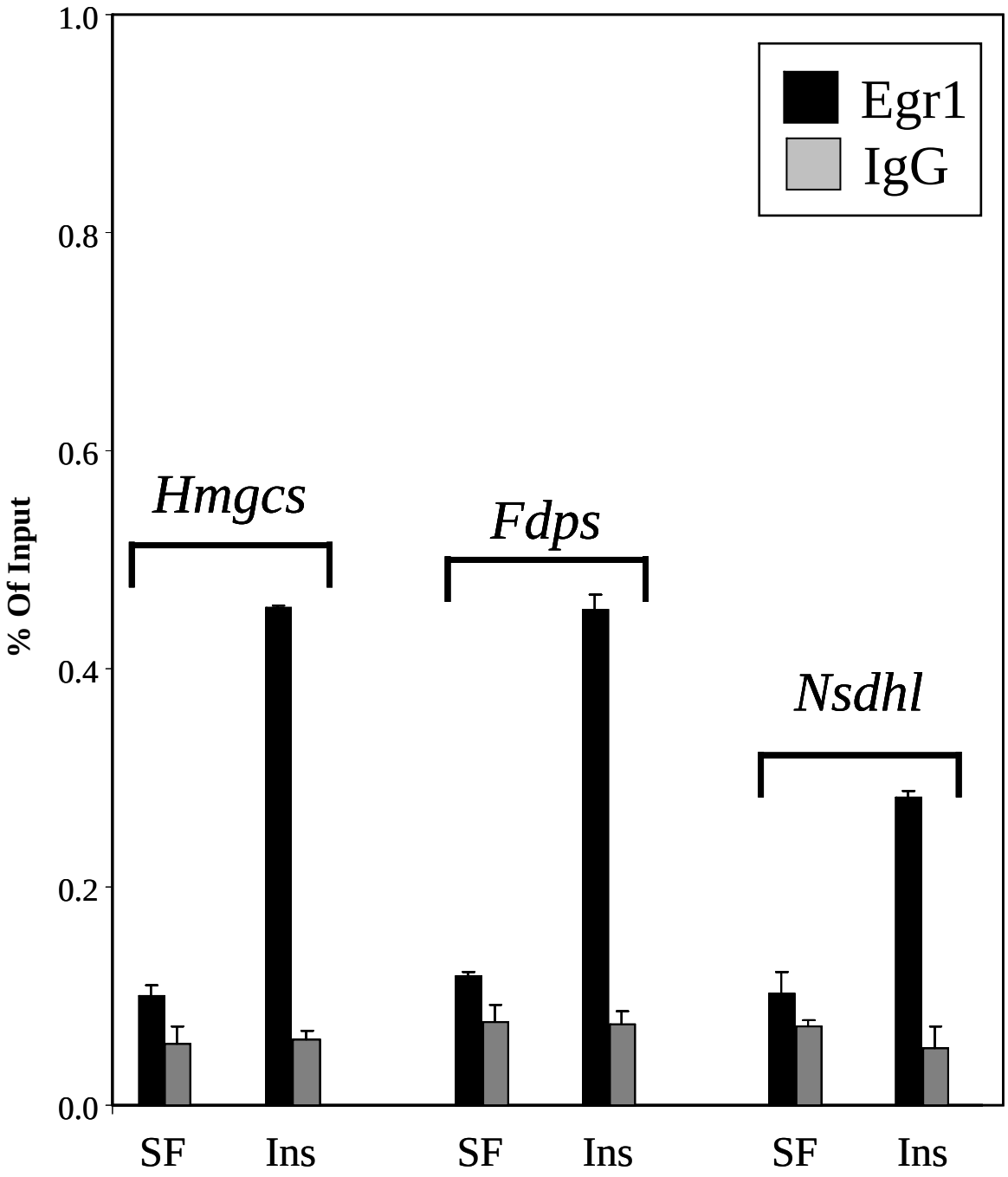
Supplementary Figure 5: $Egr1^{-/-}$ mice have reduced serum cholesterol profiles

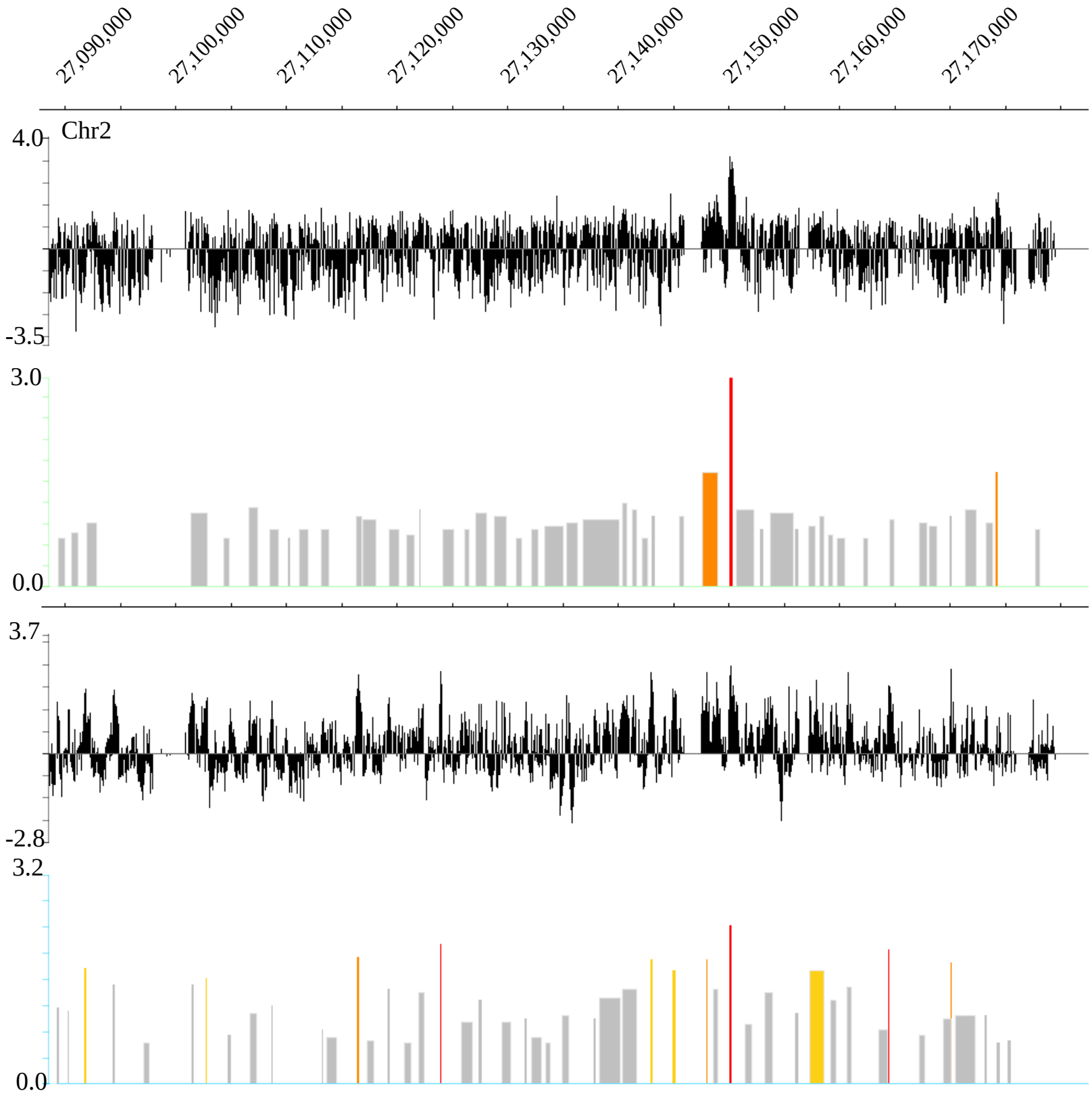
Serum from wild type and *Egr1 null* mice was extracted and fractionated using FPLC and total cholesterol was assayed for each fraction. Average cholesterol values from each fraction are displayed as area under the curve from 10 wild-type and 10 knockout mice. The HDL containing portion of the serum is located in fractions 33-41, which are statistically reduced in transgenic mice ($P<0.005$). Error bars represent standard deviation.

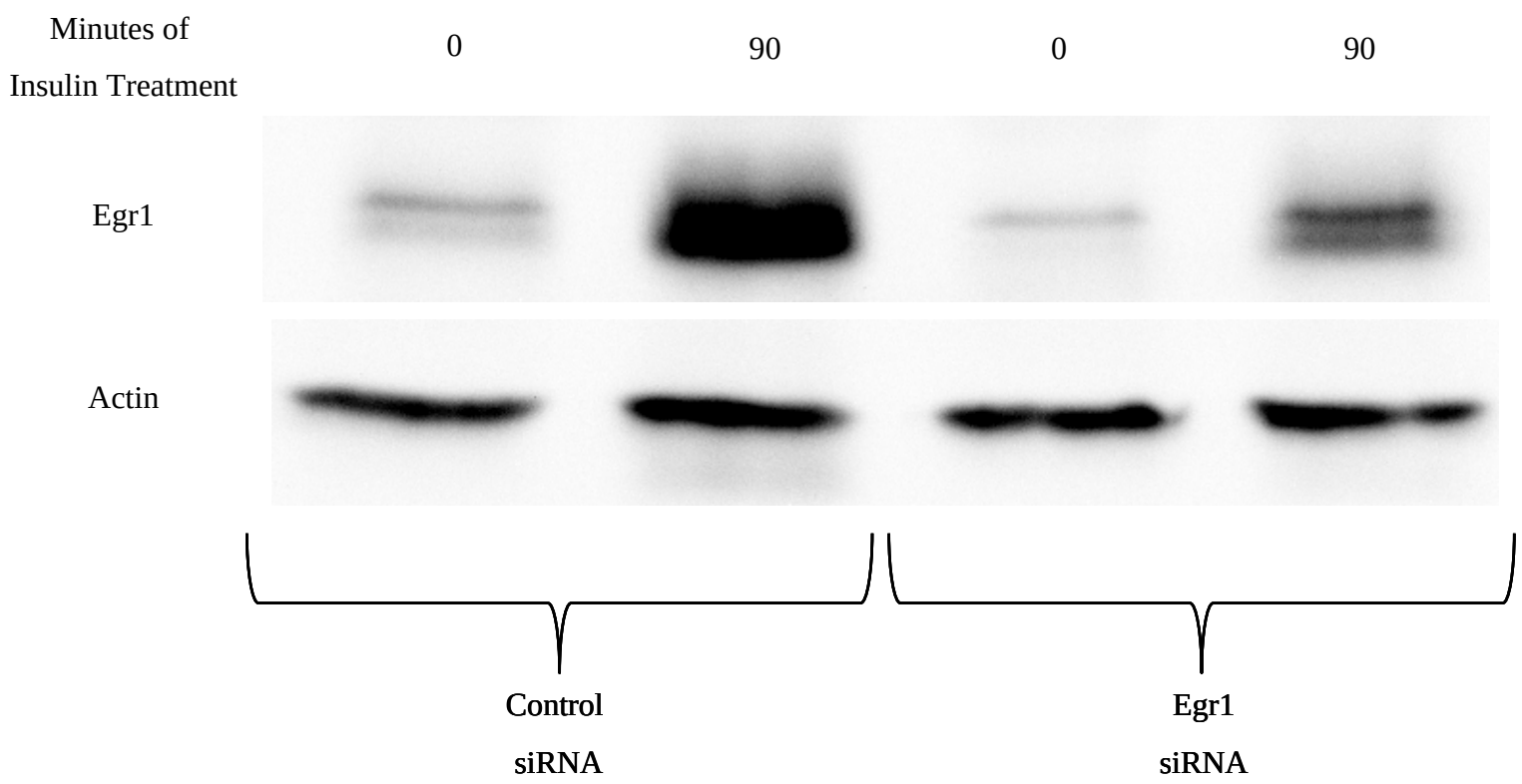
Supplementary Table 1: List of Primers

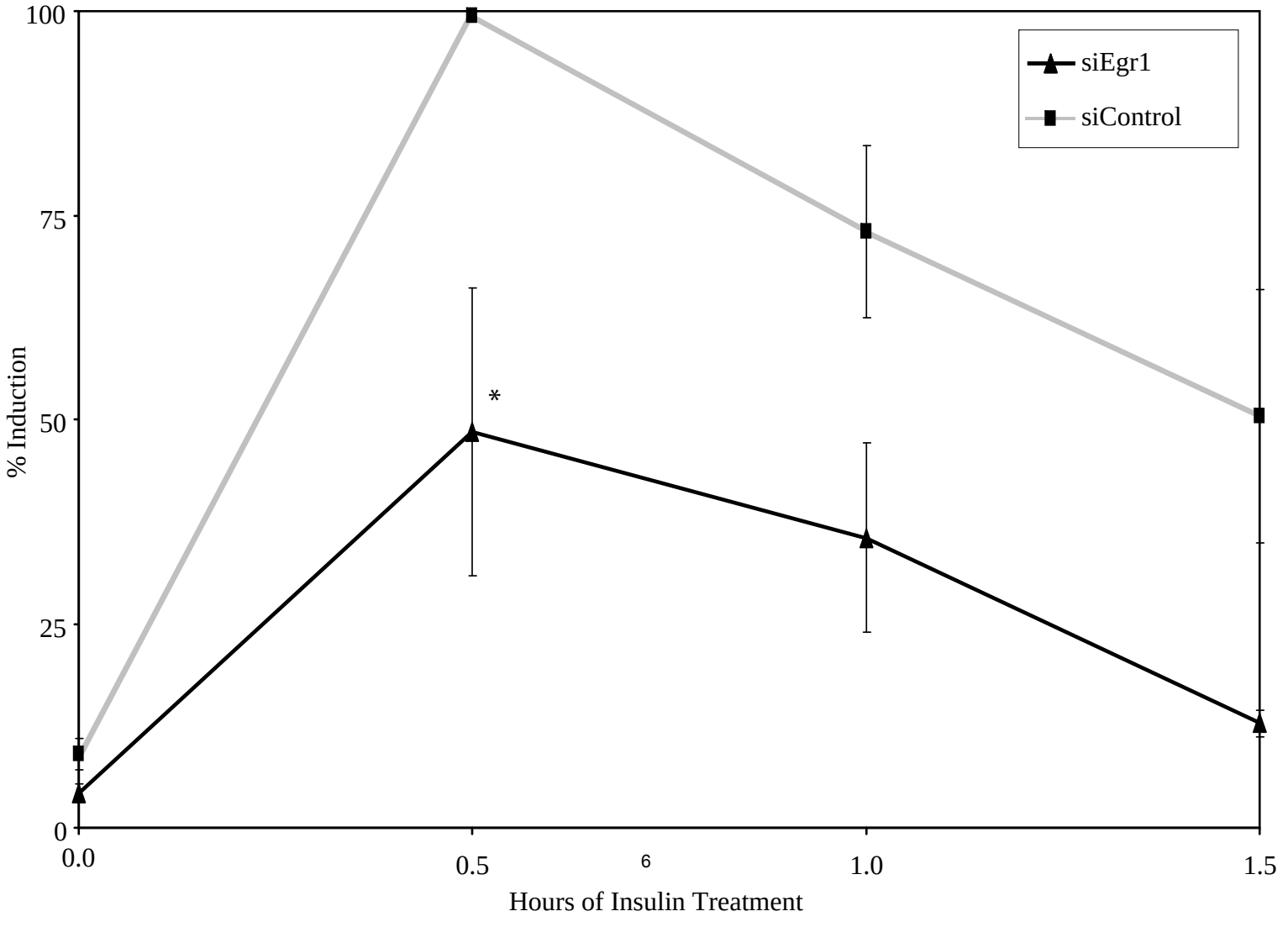
Mouse Hmgcr Promoter ChIP F	TCGTGACGTAGGCCGTCAG
Mouse Hmgcr Promoter ChIP R	CCAATAAGGAAGGATCGTCCG
Mouse Hmgcr +4kb ChIP F	GGATTGCTCCCATTTCACACA
Mouse Hmgcr +4kb ChIP R	TTTCCAATTGATTCAAGTTGTTTAGAC
Mouse Mod1 Promoter ChIP F	ACGAGCCGAGGAAGCGA
Mouse Mod1 Promoter ChIP R	GGTGAACGCCAAGCGAGA
Mouse Cyp51 Promoter ChIP F	AAGGCGCTCTGTGATTGCA
Mouse Cyp51 Promoter ChIP R	ACATAGGCCGAGATCACCTCA
Mouse Sqle Promoter ChIP F	CCTGTAGCTCTCTTGCGTTTGA
Mouse Sqle Promoter ChIP R	GCTCGCTCTGGAGGAACTCTT
Rat Cyp51 Promoter ChIP F	AAGGCGCTCTGTGATTGCA
Rat Cyp51 Promoter ChIP R	ACATAGGCCGAGATCACCTCA
Rat Hmgcr Promoter ChIP F	TCGTGACGTAGGCCGTCAG
Rat Hmgcr Promoter ChIP R	CCAATAAGGAAGGATCGTCCG
Rat Hmgcr -1.5kb ChIP F	CACCACACACTGGGCATAATG
Rat Hmgcr -1.5kb ChIP R	GGGACGGCTCCTGTTTCACAC
Rat Me1 Promoter ChIP F	ACAGTGGACGAGCGGAGG
Rat Me1 Promoter ChIP R	AGCTGGTGAGCGCCGA
Rat Hmgcs Promoter ChIP F	CGTCATTGGCAGGCTTGTT
Rat Hmgcs Promoter ChIP R	AAAGTCGGAGGACCTGGGA
Rat Mvd Promoter ChIP F	AGAGCAAGAGGCTACTCCTCAGAA
Rat Mvd Promoter ChIP R	GCCTCTATTGTCACTCCAAAGCTT
Rat Fdps Promoter ChIP F	GAGAGGAAGGTTCGGGCTCTT
Rat Fdps Promoter ChIP R	CGGTTCAAGGCCCCTCAT
Rat Sqle Promoter ChIP F	CAGCGGCCGGGTTAAGT
Rat Sqle Promoter ChIP R	GGCTAGCTCTGGAGGAGTTCC
Rat Lss Promoter ChIP F	TGAATAAAAACATCACACACCAAAATTA
Rat Lss Promoter ChIP R	TCAAACGCCAAGGACATTAAGTT
Rat Nsdhl Promoter ChIP F	CGGATACGGATGATCAATTGTACA
Rat Nsdhl Promoter ChIP R	TTTATAGAACGGAGATTCCCGAAA
Rat Sc5d Promoter ChIP F	GGCAGAGTCATTTGTCCCGTT
Rat Sc5d Promoter ChIP R	AGTGCGGGTTGATGAATGTTT
18S rRNA qPCR F	CGCCGCTAGAGGTGAAATTCT
18S rRNA qPCR R	CCAACCTCCGACTTTCGTTCT
Rat Egr2 qPCR F	GCACTCTGTGGCCCTAGAACA
Rat Egr2 qPCR R	GGCTGAGATGGCTCGAGAAA
Rat Egr1 qPCR F	AGAAGCCTTTTGCCTGTGACA
Rat Egr1 qPCR R	CGTTCATCACTCCTGGCAAAC
Rat Hmgcr qPCR F	CGCCCCTTAGGAGAATGACAT
Rat Hmgcr qPCR R	GAGGTCGGTACAGGCAAAGCTA
Rat Me1 qPCR F	GTGGCCTGTGGACTGAGACA
Rat Me1 qPCR R	TCAGCCGTGGTGAGGAAGA
Rat Sqle qPCR F	GTTGTGAACGTGCTGGCTCA
Rat Sqle qPCR R	CGGAGCTGACGCAAGGAAT
Mouse Egr1 qPCR F	AAGACACCCCCCCATGAAC
Mouse Egr1 qPCR R	CTCATCCGAGCGAGAAAAGC
Mouse Egr2 qPCR F	TGCTAGCCCTTTCCGTTGA
Mouse Egr2 qPCR R	TCTTTTCCGCTGTCCTCGAT

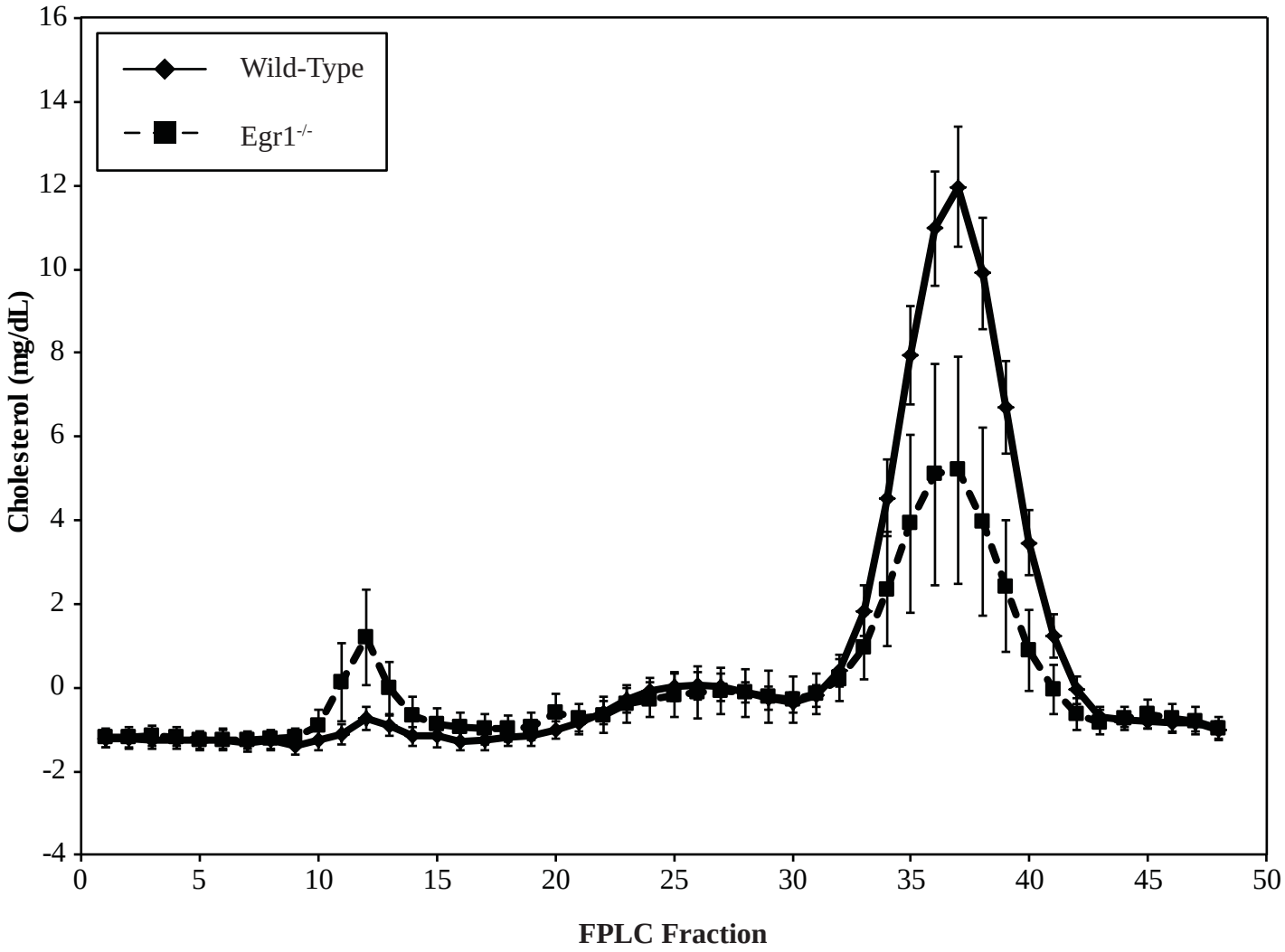

51,700,000
51,720,000
51,740,000
51,760,000
1.7
chr2
Hmgcs
0.0
-2.0
181,150,000
181,160,000
181,170,000
181,180,000
181,190,000
2.0
chr2
Fdps
0.0
-2.0
158,900,000
158,925,000
158,950,000
158,975,000
2.1
chrX
Nsdhl
0.0
-2.0
42,400,000
42,420,000
42,440,000
42,460,000
42,480,000
2.5
chr15
Fdft1
0.0
-2.0


1.0
0.8
0.6
0.4
0.2
0.0
% Of Input
Egr1
IgG
Hmgcs
Fdps
Nsdhl
SF
Ins
SF
Ins
SF
Ins


27,090,000
27,100,000
27,110,000
27,120,000
27,130,000
27,140,000
27,150,000
27,160,000
27,170,000
Chr2
4.0
-3.5
3.0
0.0
3.7
-2.8
3.2
0.0


Minutes of
Insulin Treatment
0
90
0
90
Egr1
Actin
Control
siRNA
Egr1
siRNA


100
75
50
25
0
% Induction
*
siEgr1
siControl
0.0
0.5
1.0
1.5
Hours of Insulin Treatment


Wild-Type
Egr1-/-
Cholesterol (mg/dL)
FPLC Fraction
16
14
12
10
8
6
4
2
0
-2
-4
0
5
10
15
20
25
30
35
40
45
50