Supplemental Material

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Supplemental Materials and Methods

Animal Studies

All procedures were performed and approved by the Institutional Animal Care and Use Committee at Columbia University. Genomic DNA was isolated from tail biopsies, and PCR analysis was used to identify the deficiency of both genes *ApoE* and *RAGE*. At age 6 weeks, certain mice were rendered diabetic by administration of 5 daily intraperitoneal injections of streptozotocin, 65 mg/kg in citrate buffer (0.05 mol/L; pH 4.5) (Sigma Aldrich). Control mice were treated with citrate buffer alone. Serum glucose was measured from tail vein blood using a glucometer; serum glucose on at least two separate occasions of >250 mg/dl was considered diabetic state. Beginning at age 9 or 14 weeks, certain diabetic and nondiabetic mice were euthanized. Serum glucose was measured again before euthanasia to ensure that mice remained diabetic and the mice were weighed.

Four mice in each of the four categories were sampled at age 9 weeks for glucose, body weight, serum cholesterol, and RNA experiments, with the exception that 3 non-diabetic ApoE null / RAGE null mice were sampled. Western blotting was performed on all 4 mice in each group. An additional set of 4 mice per group was prepared for ROCK1 activation experiments. Ten mice each in the ApoE null and ApoE /RAGE null categories were initially made diabetic for experiments at 14 weeks, but, of these, only 8 ApoE null mice, and only 7 ApoE /RAGE null mice, remained diabetic at 14 weeks and were the subjects of glucose, weight, cholesterol, and atherosclerotic lesion experiments. Total aortic segments from root to bifurcation were snap-frozen for further analysis. Aortic roots were embedded into OCT (Tissue-Tek) and further sectioned for histological and immunohistochemical analysis. To determine the cellular constituents of the lesions, 10 μm thick sections at the aortic sinus were cut and immunostaining was performed with a mouse monoclonal antibody raised to smooth muscle-actin (SMA, Dako Cytomation)

(Glostrup, Denmark), mouse monoclonal antibody raised to CD68 for detection of macrophages (Dako Cytomation), and a mouse monoclonal antibody to detect total T cells (BD Pharmingen). To detect collagen, Picrosirius Red staining with polarized microscopy was performed as described in Ref. 3 in the text. Immunostaining was performed using a two-step procedure (primary antibody followed by MOM fluorescein kit) (Vector Laboratories) (Burlingame CA). The % cellular component was determined by dividing the total % of cells/total lesion area using a Zeiss microscope and attached image analysis program. The image analysis program was set to determine the % area occupied by each of the cell types or collagen and in each case divided by the total lesion area (latter determined by Oil Red O on immediately adjacent section). In each case, staining with nonimmune control IgG was first performed to set background followed by analysis of sections stained with primary antigen-specific antibodies.

Assessment of statistical significance of changes in serum glucose levels between different genotype and disease states was determined using the 2 sample t-test. The statistical significance of the glucose concentration being above the diabetic threshold of 250 mg/ml, for nominally diabetic mice, and below the threshold for nominally non-diabetic mice, was determined using the 1 sample t-test. 95% confidence limits of the weight were calculated using the 1 sample t-test. All t-tests were performed in R (1).

Biochemical analyses

Levels of total cholesterol were determined in plasma of mice fasted for at least 8 hrs prior to euthanasia using chromogenic assays (Thermo Electron Corporation). The statistical significance of changes in cholesterol between different genotype and disease at 9 and 14 weeks was determined using the 2 sample t-test.

RNA Isolation and GeneChip Analysis.

All arrays in this study were normalized together using Robust Multiarray Average (RMA) (2). Log fold changes between conditions and the statistical significance of these fold changes were determined using contrasts in Linear Models for MicroArrays (LIMMA) (3). Both RMA and LIMMA are implemented in Bioconductor (4) which runs under R (2). The data have been deposited in the gene expression omnibus GEO (5), series accession number GSE15729 . Accession numbers (GeneIds) and gene symbols in NCBI Entrez Gene Database (where official symbols differ from that used in this paper, we give the official symbols first): Acta2/SMA(11475), Ager/RAGE (11596), ApoE(11816), Ltbp1(268977), PECAM1/CD31(18613), Ppp2r1b/PP2A(73699), Tgfbr1(21812), Tgfbr2(21813), RhoA (1848), Tgfb2/Tgf-b2 (21808), Thbs1(21825), Rock1(19877), and Smurf2(66313). Probesets were taken to be statistically significantly differentially expressed for a contrast between 2 conditions if their Bayesian log odds parameter, $B>0$. The Benjamini-Hochberg false discovery rate (P(BH)) (6) is also given for comparison for select genes.

Pathway Express Analysis

The KEGG Pathways (7) associated with differential expression between conditions were identified with Pathway Express which identifies the pathways associated with differential expression in a way that takes pathway structure into account. Pathways with a gamma p-value calculated using the hypergeometric distribution and corrected for false discoveries of ≤ 0.05 are taken to be statistically significantly associated with the differential expression of a given contrast.

Perturbation factors, as referred to in the manuscript text, are defined and discussed in detail by Draghici and colleagues (8) are effective $\log_2$ fold changes which take into account both any actual change in the expression of the gene and the effect of those genes in the pathway upstream from it upon the pathway at the protein level.

The perturbation factor, $PF(g)$, of a gene product, g, in a pathway is defined by Draghici et al. (8) as follows:

$$PF(g) = \log_2 FC + \sum_{u \in USg} \beta_{ug} \frac{PF(u)}{N_{ds}(u)}$$

Where $\log_2 FC$ is the base 2 logarithm of the fold-change of the gene. The second term is a sum over all of the genes, u, whose products are upstream in the pathway from gene g. $PF(u)$ is the perturbation factor of gene product u. β_{ug} is positive if gene product u is an activator in the pathway, and negative if it is an inhibitor. $N_{ds}(u)$ is the number of gene products downstream from gene u. For a thorough discussion of the implications of this equation, see the original paper by Draghici et. al. (8).

Real-Time RT-PCR validation

Data were analyzed by the $2^{-\Delta\Delta CT}$ method. The statistical significance (p-values and 95% confidence limits) of these measurements were determined by the t-test as implemented in R (1).

The t-test was applied to the count and log-fold change data so that reported 95% confidence limits for antilogs of counts and fold changes may be slightly asymmetric.

Western blot analysis

Total lysate from mouse aorta was immunoblotted and probed with Thbs1-specific antibody (Lifespan biosciences, catalog # LS-C33686), Tgf-β2-specific antibody (from Santa Cruz Biotechnology, catalog # sc-90) and ROCK1-specific antibody (Santa Cruz Biotechnology, catalog # sc-17794). HRP-conjugated donkey anti-rabbit IgG (Amersham Pharmacia Biotechnology, catalog # NA934) or HRP-conjugated sheep anti-mouse IgG (Amersham Pharmacia Biotechnology, catalog # NA931) was used to identify sites of binding of the primary antibody. After probing with the primary antibodies, membranes were stripped of bound immunoglobulins and reprobed with GAPDH (Abcam, catalog # ab8245). Blots were scanned with an AlfaImager TM 2200 scanner with AlfaEase (AlfaImager) FC 2200 software. Results are reported as a relative absorbance of test antigen to GAPDH.

Immunohistochemistry

Acetone-fixed cryostat aortic sections were preincubated with CAS-BLOCK (Zymed; Invitrogen) for 30 minutes followed by avidin-biotin block for 15 minutes; sections were then subjected to incubation with primary rabbit polyclonal RAGE IgG, (8-9) and Thbs1, TGF-β2, and ROCK1 antibodies as described above, followed by donkey anti-rabbit IgG as described above. Subsequently, Alexa Fluor 555 conjugate (Invitrogen) was incubated for 30 minutes. After washing, rat monoclonal CD31/PECAM1 antibody (Abcam, Catalog #ab7388) or mouse monoclonal smooth muscle actin (DakoCytomatin, CodeM0851) antibody were incubated for 1 hour followed by anti-rabbit or anti-mouse IgG, described above for 30 minutes, and then incubated with Alexa Fluor 488 conjugate (Invitrogen) for 30 minutes. Rabbit IgG (Zymed;

Invitrogen) or omission of the primary antibody was used as a negative control. Slides were mounted with Vectorshield mounting media (Vector) and observed with an oil immersion objective using a Nikon E800 microscope. Images were collected using a Bio-Rad Radiance 2000 Confocal System and the Lasersharp 2000 software (Bio-Rad).

ROCK1 activity assays.

Activation of ROCK1 was evaluated on lysates of aorta or primary murine aortic smooth muscle cells retrieved from wild-type or RAGE null mice. In the latter case, SMCs were stimulated with S100B (10 µg/ml for the indicated times and subjected to ROCK1 activity assays (9-10). Aortas or SMCs were lysed using a Triton X-100 lysis buffer containing 50 mM Tris (pH 7.5), 10 mM MgCl2, 0.5 M NaCl and 1% Triton X-100. The samples were incubated with Anti-ROCK1 antibody described above for 1hr further with Protein G coated agarose beads for overnight at 4°C, and the beads were washed three times with lysis buffer. The amount of ROCK1 associated with the beads was incubated with 50µl kinase buffer, 1 µl 10mM ATP (Cell Signalling) and 0.5 µg phosphorylated myosin phosphatase-1 (MYPT1)/protein phosphatase-1 regulatory (inhibitor) subunit 12A (Ppp1r12a) substrate (Upstate Biotech) at 30^0C for 30 min. Reaction was stopped by adding sample buffer, boiled for 5 min and the amount of phosphorylated MYPT1 was examined by immunoblotting using Thr850-phosphorylation specific antibody 36-003 (Upstate Biotechnology). After probing with the primary antibodies, membranes were stripped of bound immunoglobulins and reprobed with ROCK1 antibody as described above for normalization. Equal quantities of ROCK1 were treated with equal quantities of MYPT1/Ppp1r12a. Relative absorbances were measured as described above, and these were used to determine the relative activation of ROCK1. Statistical analysis was performed by the t-test and the results anti-log-transformed as above.

Smooth Muscle Cell Migration and Proliferation Assays. Wild-type and RAGE null mice vascular smooth muscle cells were isolated and cultured from the aorta and employed through passage 5 to 7. Migration assays were performed using the QCM Colorimetric Cell Migration Assay (Chemicon). Cells ($3x10^5$/well) were seeded into the upper chambers fitted with a lower 8 µm porous polycarbonate membrane, and the insert was placed in the lower chamber of a 24-well dish containing Dulbeccos' modified Eagle medium and no stimulant, S100B (10 µg/ml; generously provided by Dr. Guenter Fritz), Tgf-β2 (10 ng/ml; R&D Systems), or PDGF (10 ng/ml; R&D Systems) and incubated at 37°C for 5 hrs and relative migration was measured according to the manufacturer's instructions. In experiments using anti-Tgf-β2 IgG and nonimmune IgG (10 µg/ml, both from Santa Cruz Biotechnology, Santa Cruz, CA), Y27632 (10 µM, Sigma Aldrich) and fasudil hydrochloride (10 µM, Tocris Bioscience, Ellisville MO) cells were preincubated with these agents or vehicle alone for 2 hrs in the case of antibodies and 30 mins in the case of Y27632 or fasudil at 37°C prior to the addition to the chemotaxis chambers. Proliferation of cultured SMCs was quantified by measurement of incorporation of tritiated thymidine. SMCs were seeded at a density of $2x10^4$ cells/wells in 24-well tissue culture-treated plates and incubated in serum-free DMEM for 16 hrs. Following a 2 hr preincubation with the indicated concentration of anti-Tgf-β2, nonimmune IgG, Y27632 or fasudil, cells were exposed to serum-free DMEM containing the indicated concentration of S100B or PDGF (10 ng/ml) along with ^{3}H-thymidine (1 µCi/well). After the incubation period, cells were harvested 48 hrs later, and cellular proliferation was deermined based on the incorporation of tritiated thymidine.

Cell counting was performed and confirmed that increased trititated thymidine incorporation reflected an increase in cell number.

Inference of pathway model from gene expression data

It is useful and instructive to infer a working model of the effect of changes of gene expression on the flow of biochemical information through signaling pathways of interest. Such a model is of course approximate and must be tested by experiment at the protein level, and, if necessary, subsequently modified in the light of experiment. However, such a model helps us to predict tentatively the biological signaling consequences of observed changes in expression, which can be used to formulate falsifiable hypotheses, which can be tested experimentally. The model in Figure 7 was formulated according to the following qualitative, common sense rules:

1. The amount of activated protein changes in 2 ways: Changes in total quantity of protein (arrows with circles on bottom in left hand column of Figure 7) and changes in the fraction of protein that is activated at constant protein concentration (arrows with diamonds on bottom in center column of Figure 7). The direction of these two component changes determines the direction of the change of amount of activated protein (arrows in right hand column).

2. Arrows pointing up indicate an increase. Arrows pointing down indicate a decrease. Horizontal arrows indicate no change.

3. The pathway model is inferred entirely on the basis of gene expression data and prior

knowledge of pathway interactions. PCR and Western validation results are not included because we do not have this information for all proteins in the pathway and we wish to keep our inference for all genes on an equal footing.

4. If information is lacking on the direction of a change in the total quantity of protein (left hand column of arrows with circles on bottom) and/or fraction of protein that is activated at constant protein concentration (center column of arrows) then it is assumed that there will be no change in these quantities (horizontal arrows).

5. The direction of change of the total amount of activated protein within a step is determined by the following rules:

    A. If both of the arrows in the left hand and central columns point up (total amount of protein increases and fraction of protein which is activated at constant protein concentration increases) then the arrow in the right hand column points up (total amount of activated protein increases).
    B. If both of the arrows in the left hand and central columns point down (total amount of protein decreases and fraction of protein which is activated at constant protein concentration decreases) then the arrow in the right hand column points down (total amount of activated protein decreases).
    C. If both of the arrows in the left hand and central columns are horizontal (total amount of protein remains the same and fraction of protein which is activated at constant protein concentration remains the same) then the arrow in the right

hand column is horizontal (total amount of activated protein remains the same).

D. If one of the arrows in the left hand or central columns points up and the other is horizontal (total amount of protein increases (remains the same) or fraction of protein which is activated at constant protein concentration increases (or remains the same) then the arrow in the right hand column points up (total amount of activated protein increases).

E. If one of the arrows in the left hand or central columns points down and the other is horizontal (total amount of protein decreases (remains the same) or fraction of protein which is activated at constant protein concentration decreases (or remains the same) then the arrow in the right hand column points down (total amount of activated protein decreases).

F. If one of the arrows in the left hand or central columns points up and the other points down (total amount of protein increases (decreases) or fraction of protein which is activated at constant protein concentration decreases (increases) then the arrow in the right hand column in horizontal (total amount of activated protein remains the same).

6. Between successive steps:

   A. The amount of protein activated at constant protein concentration in the succeeding step (central column) has the same direction as the total change in activated protein of the preceding step (right hand column) if the interaction connecting genes (line connecting boxes) is an activation.

B. The amount of protein activated at constant protein concentration in the succeeding step (central column) has the opposite direction as the total change in activated protein of the preceding step (right hand column) if the interaction connecting genes (line connecting boxes) is an inhibition.

C. If two proteins precede a protein then their interactions add according to the rules for addition of different components in the step outlined in rule 5 A-G.

Supplementary References

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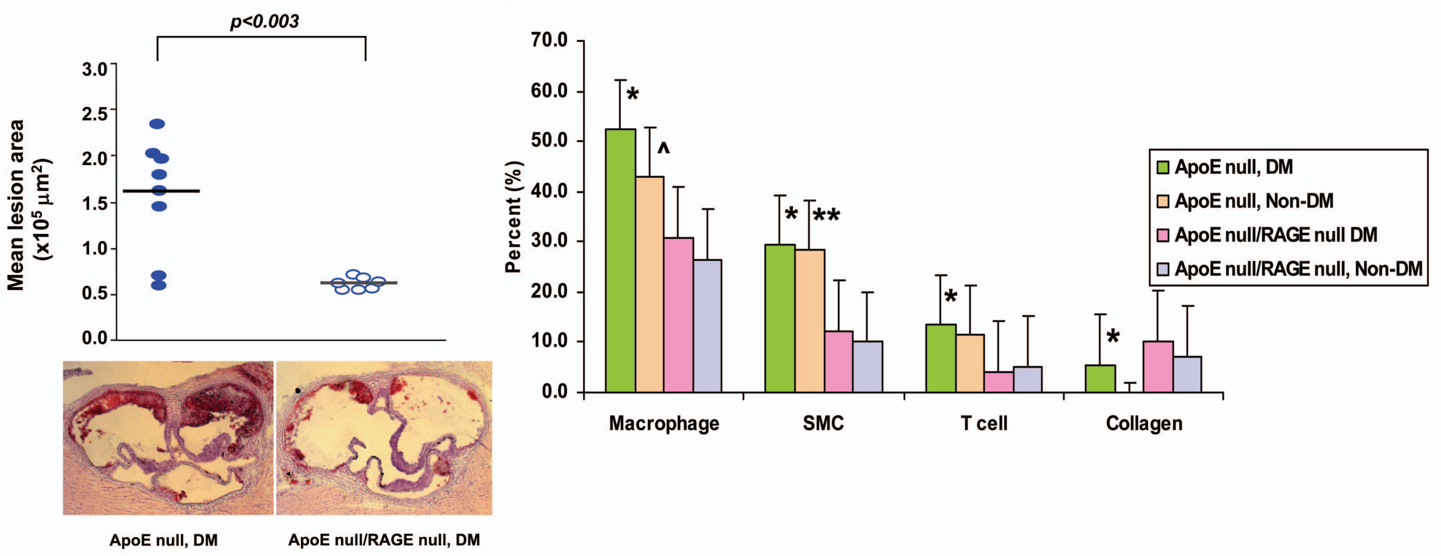
Legends to Online Figures

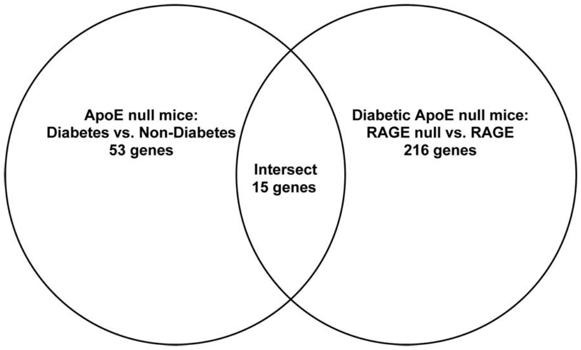
Online Figure I. Deletion of RAGE suppresses diabetes-accelerated atherosclerosis and effect of diabetes and RAGE deficiency on macrophage and smooth muscle content. (A). Male ApoE null (N=8) and Apo E null / RAGE null mice (N=7) were rendered diabetic with streptozotocin at age 6 weeks. Mice were sacrificed at age 14 weeks and aortas were retrieved. Mean atherosclerotic lesion area at the aortic sinus is reported; statistical considerations are indicated in the text. (B). Immunostaining and Picrosirius Red staining of atherosclerotic lesions from the indicated ApoE null mice was performed for detection of macrophages, smooth muscle cells, T cells, and collagen (the latter using picrosirius red and polarizing microscopy) at age 24 weeks. Note that the lesions in the non-diabetic or any RAGE-deficient ApoE null mice were quite small at age 14 weeks; hence, detailed lesion characterization was performed at age 24 weeks (after 18 weeks of established hyperglycemia). Lesion areas at the aortic sinus were 6.8×10^5 vs. 0.9×10^5 μm^2 in ApoE null diabetic vs. non-diabetic ApoE null mice, respectively; $p<0.02$. Lesions areas in non-diabetic ApoE null/RAGE null mice were 0.5×10^5 μm^2; $p<0.05$ vs. non-diabetic ApoE null mice. Lesion areas in diabetic ApoE null/RAGE null mice were 3.8×10^5 μm^2; $p<0.05$ vs. diabetic ApoE null mice. Once we established these relationships at 24 weeks of age, we then proceeded to analyze lesion composition. In all cases, the percent of cell type/lesion area, or %collagen/lesion area was then calculated using Zeiss Imaging analysis program. N=5 mice/group. Error bars are standard deviations. Statistical considerations are indicated in the figure. In B, each distinct set of bars represents the cell type or collagen content. The four bars in each set represent the genotype and the diabetic state (*indicates $p<0.03$ vs. ApoE null/RAGE null diabetic. ** indicates $p<0.01$ vs. ApoE null/RAGE null non-diabetic. ^indicates $p<0.02$ vs. ApoE null RAGE null non-diabetic.

Online Figure II. **Venn diagram depicting the effect of diabetes and RAGE deletion in ApoE null mouse aorta.** The Venn diagram shows the intersection of comparison 1, diabetic ApoE null relative to non-diabetic ApoE null, with comparison 4, diabetic ApoE null / RAGE null relative to diabetic ApoE null. Although there are 53 genes which are statistically significantly differentially expressed in diabetic ApoE null relative to the non-diabetic ApoE null state, and 216 genes which are statistically significantly differentially expressed in diabetic ApoE null / RAGE null relative to diabetic ApoE null, only 15 of these genes are statistically significantly differentially expressed in both comparisons. Note that there is very little overlap of the genes which are differentially expressed both in the onset of diabetes in apoE null mice and in the effect of RAGE deletion in diabetic ApoE null mice.

Online Figure I



Online Figure II



Online Table I

		glucose concentration (mg/ml)							
Comparison #	Comparison	Change in glucose concentration	P-value change	Reference condition	95% confidence limits reference condition	P-value glucose concentration in accordance with disease state reference condition	Experimental condition	95% confidence limits experimental condition	P-value glucose concentration in accordance with disease state experimental condition
1	Diabetic ApoE null relative to Non-diabetic ApoE null 9 weeks	249.75 (206.07,293.42)	2.E-05	Non-diabetic ApoE null 9 weeks	128.00 (97.17,158.82)	5.E-04	Diabetic ApoE null 9 weeks	377.75 (332.28,423.21)	1.E-03
2	Non-diabetic ApoE null / RAGE null relative to non-diabetic ApoE null 9 weeks	6.33 (-24.02,36.69)	1	Non-diabetic ApoE null 9 weeks	128.00 (97.17,158.82)	5.E-04	Non-diabetic ApoE null / RAGE null 9 weeks	134.33 (106.08,162.58)	2.E-03
3	Diabetic ApoE null / RAGE null relative to non-diabetic ApoE null / RAGE null 9 weeks	264.16 (219.03,309.3)	8.E-05	Non-diabetic ApoE null / RAGE null 9 weeks	134.33 (106.08,162.58)	2.E-03	Diabetic ApoE null / RAGE null 9 weeks	398.5 (350.93,446.06)	1.E-03
4	Diabetic ApoE null / RAGE null relative to diabetic ApoE null 9 weeks	20.7 (-29.86,71.36)	0.4	Diabetic ApoE null 9 weeks	377.75 (332.28,423.21)	1.E-03	Diabetic ApoE null / RAGE null 9 weeks	398.5 (350.93,446.06)	1.E-03
5	Diabetic ApoE null 14 weeks relative to Diabetic ApoE null 9 weeks	-32 (-75.60,11.60)	0.1	Diabetic ApoE null 9 weeks	377.75 (332.28,423.21)	1.E-03	Diabetic ApoE null 14 weeks	345.75 (318.18,373.32)	4.E-05
6	Diabetic ApoE null / RAGE null 14 weeks relative to Diabetic ApoE null / RAGE null 9 weeks	-60.21 (-104.57,-15.85)	2.E-02	Diabetic ApoE null / RAGE null 9 weeks	398.5 (350.93,446.06)	1.E-03	Diabetic ApoE null / RAGE null 14 weeks	338.28 (315.25, 361.3186)	8.E-05
7	Diabetic ApoE null / RAGE null 14 weeks relative to Diabetic ApoE null 14 weeks	-7.46 (-39.89,24.96)	0.6	Diabetic ApoE null 14 weeks	345.75 (318.18,373.32)	4.E-05	Diabetic ApoE null / RAGE null 14 weeks	338.28 (315.25, 361.3186)	8.E-05

Online Table II	Weight of mice (gm)
Condition	95% confidence limits
Non-diabetic ApoE null 9 weeks	22.96(20.88,25.03)
Diabetic ApoE null 9 weeks	20.36(17.79,22.93)
Non-diabetic ApoE null / RAGE null 9 weeks	17.97(17.47,18.47)
Diabetic ApoE null / RAGE null 9 weeks	18.56(16.95,20.17)
Diabetic ApoE null 14 weeks	22.67(22.26, 23.08)
Diabetic ApoE null / RAGE null 14 weeks	21.65(21.06,22.24)

Online Table III Cholesterol

Concentration (mmol/L)

comparison #	Comparison	Change in concentration	P-value change	Reference condition	95% confidence limits reference condition	Experimental condition	95% confidence limits experimental condition
1	Diabetic ApoE null relative to Non-diabetic ApoE null 9 weeks	0.03 (-1.43,1.51)	0.9	Non-diabetic ApoE null 9 weeks	10.11 (8.72, 11.50)	Diabetic ApoE null 9 weeks	10.15 (8.83,11.46)
2	Non-diabetic ApoE null / RAGE null relative to non-diabetic ApoE null 9 weeks	0.90 (-1.30,3.10)	0.3	Non-diabetic ApoE null 9 weeks	10.11 (8.72, 11.50)	Non-diabetic ApoE null / RAGE null 9 weeks	11.01 (8.26,13.76)
3	Diabetic ApoE null / RAGE null relative to non-diabetic ApoE null / RAGE null 9 weeks	-0.66 (0.4,1.55)	0.4	Non-diabetic ApoE null / RAGE null 9 weeks	11.01 (8.26,13.76)	Diabetic ApoE null / RAGE null 9 weeks	10.35 (8.76,11.93)
4	Diabetic ApoE null / RAGE null relative to diabetic ApoE null 9 weeks	0.20 (-1.39, 1.79)	0.7	Diabetic ApoE null 9 weeks	10.15 (8.83,11.46)	Diabetic ApoE null / RAGE null 9 weeks	10.35 (8.76,11.93)
5	Diabetic ApoE null 14 weeks relative to Diabetic ApoE null 9 weeks	0.35 (-0.87,1.58)	0.4	Diabetic ApoE null 9 weeks	10.15 (8.83,11.46)	Diabetic ApoE null 14 weeks	10.99 (10.16,11.82)
6	Diabetic ApoE null / RAGE null 14 weeks relative to Diabetic ApoE null / RAGE null 9 weeks	0.64 (-0.84,2.13)	0.3	Diabetic ApoE null / RAGE null 9 weeks	10.35 (8.76,11.93)	Diabetic ApoE null / RAGE null 14 weeks	10.50 (10.05,10.95)
7	Diabetic ApoE null / RAGE null 14 weeks relative to Diabetic ApoE null 14 weeks	0.49 (-0.38,1.36)	0.2	Diabetic ApoE null 14 weeks	10.99 (10.16,11.82)	Diabetic ApoE null / RAGE null 14 weeks	10.50 (10.05,10.95)

Online Table IV. Differentially Expressed Genes in Diabetic ApoE null Relative to Non-Diabetic ApoE null mice

Affymetrix ID	Gene Symbol	Gene Name	$\log_2$ FC	B
1423828_at	Fasn	fatty acid synthase	-2.33	4.36
1417877_at	2310005P05Rik	RIKEN cDNA 2310005P05 gene	-0.63	2.96
1424542_at	S100a4	S100 calcium binding protein A4	0.88	2.34
1416288_at	Dnaja1	DnaJ (Hsp40) homolog, subfamily A, member 1	0.76	2.29
1425993_a_at	Hsp110	heat shock protein 110	1.12	2.05
1419359_at	Hexim1	hexamethylene bis-acetamide inducible 1	0.51	2.05
1434185_at	Acaca	acetyl-Coenzyme A carboxylase alpha	-1.57	1.81
1460179_at	Dnaja1	DnaJ (Hsp40) homolog, subfamily A, member 1	0.69	1.71
1460645_at	Chordc1	cysteine and histidine-rich domain (CHORD)-containing, zinc-binding protein 1	0.48	1.62
1416872_at	Tspan6	tetraspanin 6	0.70	1.61
1427127_x_at	Hspa1b	heat shock protein 1B	1.49	1.56
1460302_at	Thbs1	thrombospondin 1	1.32	1.50
1423566_a_at	Hsp110	heat shock protein 110	1.41	1.50
1437218_at	Fn1	fibronectin 1	0.76	1.42
1460011_at	Cyp26b1	cytochrome P450, family 26, subfamily b, polypeptide 1	0.70	1.40
1428190_at	Slc25a1	solute carrier family 25 (mitochondrial carrier, citrate transporter), member 1	-1.37	1.30
1456081_a_at	Aacs	acetoacetyl-CoA synthetase	-1.13	1.24
1428219_at	Rybp	RING1 and YY1 binding protein	0.56	1.24
1452318_a_at	Hspa1b	heat shock protein 1B	1.27	1.10
1439200_x_at	NA	NA	-1.75	1.00
1431802_a_at	D5Wsu178e	DNA segment, Chr 5, Wayne State University 178, expressed	0.40	0.99
1428973_s_at	0610012D17Rik	RIKEN cDNA 0610012D17 gene	0.53	0.98
1422478_a_at	Acss2	acyl-CoA synthetase short-chain family member 2	-1.63	0.95
1423797_at	Aacs	acetoacetyl-CoA synthetase	-1.22	0.95
1427126_at	Hspa1b	heat shock protein 1B	1.77	0.94
1448501_at	Tspan6	tetraspanin 6	0.76	0.94
1451979_at	Kras	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	0.43	0.93
1435337_at	Tshz3	teashirt zinc finger family member 3	0.59	0.88
1424737_at	Thrsp	thyroid hormone responsive SPOT14 homolog (Rattus)	-1.16	0.88
1450541_at	Pvt1	plasmacytoma variant translocation 1	0.54	0.88
1415860_at	Kpna2	karyopherin (importin) alpha 2	0.53	0.79
1459874_s_at	Mtmr4	myotubularin related protein 4	0.63	0.79
1448531_at	Lmnb2	lamin B2	0.50	0.75

1416563_at	Ctps	cytidine 5'-triphosphate synthase	0.73	0.74
1416529_at	Emp1	epithelial membrane protein 1	0.64	0.68
1452805_at	D11Wsu47e	DNA segment, Chr 11, Wayne State University 47, expressed	0.42	0.62
1449609_at	NA	NA	-0.40	0.61
1449528_at	Figf	c-fos induced growth factor	0.61	0.59
1418659_at	Tparl	TPA regulated locus	0.59	0.54
1452619_a_at	Agbl3	ATP/GTP binding protein-like 3	-0.43	0.51
1449044_at	Eef1e1	eukaryotic translation elongation factor 1 epsilon 1	0.65	0.48
1418322_at	Crem	cAMP responsive element modulator	0.61	0.48
1452406_x_at	Erdr1	erythroid differentiation regulator 1	-1.43	0.46
1439443_x_at	Tkt	transketolase	-0.79	0.43
1451015_at	Tkt	transketolase	-1.16	0.39
1447476_at	NA	NA	-0.37	0.39
1417196_s_at	Wwc2	WW, C2 and coiled-coil domain containing 2	0.51	0.37
1435484_at	BF642829	expressed sequence BF642829	0.80	0.37
1428989_at	0710001D07Rik	RIKEN cDNA 0710001D07 gene	-0.84	0.36
1417741_at	Pygl	liver glycogen phosphorylase	-1.48	0.35
1435294_at	Mtmr11	myotubularin related protein 11	-0.37	0.30
1460330_at	Anxa3	annexin A3	0.62	0.29
1428944_at	Ube1l2	ubiquitin-activating enzyme E1-like 2	0.45	0.26
1416632_at	Mod1	malic enzyme, supernatant	-1.20	0.25
1451666_at	Acly	ATP citrate lyase	-1.55	0.23
1454991_at	Slc7a1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	0.61	0.22
1456626_a_at	1110005A23Rik	RIKEN cDNA 1110005A23 gene	0.41	0.21
1422479_at	Acss2	acyl-CoA synthetase short-chain family member 2	-1.57	0.19
1452433_at	NA	NA	-0.46	0.18
1454993_a_at	Sfrs3	splicing factor, arginine/serine-rich 3 (SRp20)	0.46	0.16
1425326_at	Acly	ATP citrate lyase	-1.86	0.15
1418119_at	Rbm8a	RNA binding motif protein 8a	0.41	0.14
1433897_at	AI597468	expressed sequence AI597468	0.58	0.12
1460583_at	Golt1b	golgi transport 1 homolog B (S. cerevisiae)	0.48	0.12
1416629_at	Slc1a5	solute carrier family 1 (neutral amino acid transporter), member 5	-0.59	0.11
1423796_at	Sfpq	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)	0.71	0.10
1435902_at	Nudt18	nudix (nucleoside diphosphate linked moiety X)-type motif 18	-0.41	0.09
1417460_at	Ifitm2	interferon induced transmembrane protein 2	0.39	0.09
1450958_at	Tm4sf1	transmembrane 4 superfamily member 1	0.64	0.09

1459835_s_at	Reln	reelin	0.67	0.07
1436338_at	Ppp2r1b	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform	-0.53	0.05
1440899_at	Fmo5	flavin containing monooxygenase 5	-0.48	0.05
1444560_at	NA	NA	0.49	0.05
1425137_a_at	H2-Q10	histocompatibility 2, Q region locus 10	-1.34	0.04
1445894_at	NA	NA	0.42	0.03
1427052_at	Acacb	acetyl-Coenzyme A carboxylase beta	-1.59	0.01

Online Table V. Differentially Expressed Genes in Diabetic ApoE null/RAGE null Relative to Diabetic ApoE null mice

Affymetrix ID	Gene Symbol	Gene Name	$\log_2$ FC	B
1452707_at	4631423F02Rik	RIKEN cDNA 4631423F02 gene	-1.23	4.90
1439200_x_at	NA	NA	2.45	4.43
1421834_at	Pip5k1a	phosphatidylinositol-4-phosphate 5-kinase, type 1 alpha	-0.82	4.28
1431413_at	Ramp1	receptor (calcitonin) activity modifying protein 1	-0.77	4.07
1435606_at	Gal3st4	galactose-3-O-sulfotransferase 4	-0.84	4.05
1460583_at	Golt1b	golgi transport 1 homolog B (S. cerevisiae)	-0.73	4.03
1447886_at	0610040B09Rik	RIKEN cDNA 0610040B09 gene	-0.80	3.81
1419431_at	Ereg	epiregulin	-1.52	3.77
1450742_at	Bysl	bystin-like	-0.72	3.76
1426319_at	Pdgfd	platelet-derived growth factor, D polypeptide	-1.24	3.67
1416121_at	Lox	lysyl oxidase	-0.96	3.62
1452406_x_at	Erdr1	erythroid differentiation regulator 1	1.96	3.56
1418322_at	Crem	cAMP responsive element modulator	-0.84	3.52
1456791_at	AA407452	EST AA407452	-0.50	3.35
1439849_at	NA	NA	-0.67	3.28
1425425_a_at	Wif1	Wnt inhibitory factor 1	-1.55	3.21
1447490_at	NA	NA	-1.49	3.20
1423250_a_at	Tgfb2	transforming growth factor, beta 2	-1.12	3.19
1418572_x_at	Tnfrsf12a	tumor necrosis factor receptor superfamily, member 12a	-1.41	3.13
1437498_at	NA	NA	-0.50	3.06
1436002_at	C230013L11Rik	RIKEN cDNA C230013L11 gene	-1.45	3.04
1429637_at	2210419I08Rik	RIKEN cDNA 2210419I08 gene	-1.14	2.88
1458573_at	9530026P05Rik	RIKEN cDNA 9530026P05 gene	0.88	2.84
1417430_at	Cdr2	cerebellar degeneration-related 2	-0.99	2.77
1456532_at	Pdgfd	platelet-derived growth factor, D polypeptide	-0.81	2.71
1460645_at	Chordc1	cysteine and histidine-rich domain (CHORD)-containing, zinc-binding protein 1	-0.51	2.70
1424373_at	Armcx3	armadillo repeat containing, X-linked 3	-0.46	2.68
1448501_at	Tspan6	tetraspanin 6	-0.89	2.66
1427127_x_at	Hspa1b	heat shock protein 1B	-1.59	2.57
1439779_at	NA	NA	0.56	2.55
1429564_at	Pcgf5	polycomb group ring finger 5	-0.69	2.52
1435337_at	Tshz3	teashirt zinc finger family member 3	-0.68	2.50
1440534_at	NA	NA	-1.20	2.50
1419149_at	Serpine1	serine (or cysteine) peptidase inhibitor, clade E, member 1	-1.88	2.47
1452318_a_at	Hspa1b	heat shock protein 1B	-1.41	2.42
1422307_at	NA	NA	-0.47	2.38
1452284_at	Ptprz1	protein tyrosine phosphatase, receptor type Z, polypeptide 1	-1.20	2.36
1422587_at	Tmem45a	transmembrane protein 45a	-0.77	2.36
1460011_at	Cyp26b1	cytochrome P450, family 26, subfamily b, polypeptide 1	-0.75	2.32
1424483_at	Mobk1b	MOB1, Mps One Binder kinase activator-like 1B (yeast)	-0.39	2.28

1433651_at	Wtip	WT1-interacting protein	-0.74	2.28
1446541_at	4930434E21Rik	RIKEN cDNA 4930434E21 gene	-0.76	2.27
1448201_at	Sfrp2	secreted frizzled-related protein 2	-1.20	2.26
1433481_at	Fkbp14	FK506 binding protein 14	-0.79	2.23
1434572_at	Hdac9	histone deacetylase 9	-1.05	2.23
1433897_at	AI597468	expressed sequence AI597468	-0.72	2.12
1448892_at	Dock7	dedicator of cytokinesis 7	-0.73	2.12
1418571_at	Tnfrsf12a	tumor necrosis factor receptor superfamily, member 12a	-1.22	2.11
1435106_at	3732412D22Rik	RIKEN cDNA 3732412D22 gene	-0.81	2.11
1430798_x_at	Mrpl15	mitochondrial ribosomal protein L15	0.81	2.08
1448487_at	Lrrfip1	leucine rich repeat (in FLII) interacting protein 1	-0.80	2.07
1427484_at	Eml5	echinoderm microtubule associated protein like 5	0.63	2.06
1420696_at	Sema3c	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C	-0.89	2.05
1452257_at	Bdh1	3-hydroxybutyrate dehydrogenase, type 1	-0.90	2.04
1425185_at	5830417C01Rik	RIKEN cDNA 5830417C01 gene	-0.50	2.04
1435248_a_at	Btaf1	BTAF1 RNA polymerase II, B-TFIID transcription factor-associated, (Mot1 homolog, S. cerevisiae)	-0.48	2.04
1416288_at	Dnaja1	DnaJ (Hsp40) homolog, subfamily A, member 1	-0.70	2.03
1449065_at	Acot1	acyl-CoA thioesterase 1	1.26	2.02
1428910_at	2310022B05Rik	RIKEN cDNA 2310022B05 gene	-0.82	2.02
1450389_s_at	Pip5k1a	phosphatidylinositol-4-phosphate 5-kinase, type 1 alpha	-0.68	1.94
1435473_at	Gm347	gene model 347, (NCBI)	-0.64	1.93
1440215_at	C130086A10	NA	-0.79	1.93
1420688_a_at	Sgce	sarcoglycan, epsilon	-0.50	1.92
1438328_at	Hcfc2	host cell factor C2	-0.63	1.92
1448228_at	Lox	lysyl oxidase	-0.92	1.91
1448648_at	9130005N14Rik	RIKEN cDNA 9130005N14 gene	-0.88	1.87
1448468_a_at	Kcnab1	potassium voltage-gated channel, shaker-related subfamily, beta member 1	-0.95	1.86
1427448_at	Rabep1	rabaptin, RAB GTPase binding effector protein 1	-0.39	1.86
1435574_at	NA	NA	-0.88	1.85
1418852_at	Chrna1	cholinergic receptor, nicotinic, alpha polypeptide 1 (muscle)	-0.84	1.82
1427126_at	Hspa1b	heat shock protein 1B	-1.88	1.81
1417877_at	2310005P05Rik	RIKEN cDNA 2310005P05 gene	0.52	1.80
1439089_at	Zbtb41	zinc finger and BTB domain containing 41 homolog	-0.49	1.79
1419595_a_at	Ggh	gamma-glutamyl hydrolase	-0.51	1.79
1421624_a_at	Enah	enabled homolog (Drosophila)	-1.00	1.77
1456483_at	Zfp9	zinc finger protein 9	-0.73	1.77
1451240_a_at	Glo1	glyoxalase 1	0.81	1.76
1426306_a_at	Maged2	melanoma antigen, family D, 2	-0.84	1.76
1436319_at	Sulf1	sulfatase 1	-0.73	1.74
1444418_at	NA	NA	0.60	1.72
1421833_at	Pip5k1a	phosphatidylinositol-4-phosphate 5-kinase, type 1 alpha	-0.50	1.72

1427019_at	Ptprz1	protein tyrosine phosphatase, receptor type Z, polypeptide 1	-0.99	1.70
1424607_a_at	Xdh	xanthine dehydrogenase	0.59	1.69
1429417_at	4833446K15Rik	RIKEN cDNA 4833446K15 gene	-1.18	1.67
1418349_at	Hbegf	heparin-binding EGF-like growth factor	-1.28	1.66
1434316_at	Chsy1	carbohydrate (chondroitin) synthase 1	-0.82	1.64
1460080_at	AI645535	expressed sequence AI645535	-0.55	1.63
1428638_at	Efhc2	EF-hand domain (C-terminal) containing 2	-1.07	1.62
1433529_at	E430002G05Rik	RIKEN cDNA E430002G05 gene	-0.92	1.61
1450416_at	Cbx5	chromobox homolog 5 (Drosophila HP1a)	-0.51	1.60
1426782_at	Gpr125	G protein-coupled receptor 125	-0.65	1.59
1423347_at	Sec23a	SEC23A (S. cerevisiae)	-0.55	1.55
1452388_at	Hspa1a	heat shock protein 1A	-1.68	1.53
1434158_at	Gmds	GDP-mannose 4, 6-dehydratase	-0.52	1.53
1425806_a_at	Surb7	SRB7 (suppressor of RNA polymerase B) homolog (S. cerevisiae)	-0.43	1.52
1452238_at	Hrb	HIV-1 Rev binding protein	-0.55	1.52
1449584_at	Dgkg	diacylglycerol kinase, gamma	-0.75	1.49
1429888_a_at	Hspb2	heat shock protein 2	-0.92	1.49
1418538_at	Kdelr3	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3	-0.77	1.47
1436826_at	Tmtc3	transmembrane and tetratricopeptide repeat containing 3	-0.51	1.46
1452093_at	2500001K11Rik	RIKEN cDNA 2500001K11 gene	-0.52	1.45
1418964_at	Pigm	phosphatidylinositol glycan, class M	-0.69	1.45
1427475_a_at	NA	NA	-0.70	1.44
1443939_at	LOC230628	NA	-0.61	1.41
1450029_s_at	Itga9	integrin alpha 9	-1.00	1.41
1441989_at	Bnip2	BCL2/adenovirus E1B interacting protein 1, NIP2	-0.69	1.40
1417730_at	Ext1	exostoses (multiple) 1	-0.61	1.37
1458719_at	Glp1r	glucagon-like peptide 1 receptor	1.91	1.36
1429232_at	2610528B01Rik	RIKEN cDNA 2610528B01 gene	-0.48	1.35
1432417_a_at	Tspan2	tetraspanin 2	-1.09	1.33
1438004_at	Pols	polymerase (DNA directed) sigma	-0.82	1.30
1418802_at	R74862	expressed sequence R74862	-0.41	1.30
1422118_at	Sync	syncoilin	-0.78	1.29
1447547_at	Ltbp1	latent transforming growth factor beta binding protein 1	-1.31	1.28
1455316_x_at	Ccrn4l	CCR4 carbon catabolite repression 4-like (S. cerevisiae)	0.57	1.28
1417272_at	9130005N14Rik	RIKEN cDNA 9130005N14 gene	-0.60	1.28
1444396_at	Trp53inp2	tumor protein p53 inducible nuclear protein 2	0.65	1.27
1456823_at	Gm70	gene model 70, (NCBI)	-0.73	1.26
1422862_at	Pdlim5	PDZ and LIM domain 5	-0.85	1.24
1437523_s_at	Sgcg	sarcoglycan, gamma (dystrophin-associated glycoprotein)	-0.83	1.24
1457092_at	C630007B19Rik	RIKEN cDNA C630007B19 gene	-1.15	1.24
1422772_at	C1galt1	core 1 UDP-galactose:N-acetylgalactosamine-alpha-R beta 1,3-galactosyltransferase	-0.88	1.20
1449063_at	Sec22l1	SEC22 vesicle trafficking protein-like 1 (S. cerevisiae)	-0.40	1.20

1436101_at	Pank2	pantothenate kinase 2 (Hallervorden-Spatz syndrome)	-0.74	1.20
1429065_at	1200009F10Rik	RIKEN cDNA 1200009F10 gene	-0.79	1.19
1438566_at	St8sia6	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 6	0.43	1.19
1419667_at	Sgcb	sarcoglycan, beta (dystrophin-associated glycoprotein)	-0.55	1.16
1427560_at	Six5	sine oculis-related homeobox 5 homolog (Drosophila)	-0.45	1.16
1424609_a_at	Xdh	xanthine dehydrogenase	0.57	1.15
1431693_a_at	Il17b	interleukin 17B	-0.73	1.14
1457817_at	Bcas3	breast carcinoma amplified sequence 3	0.56	1.12
1435878_at	Stk38l	serine/threonine kinase 38 like	-0.82	1.12
1453172_at	Stch	stress 70 protein chaperone, microsome-associated, human homolog	-0.51	1.12
1417866_at	Tnfaip1	tumor necrosis factor, alpha-induced protein 1 (endothelial)	-0.38	1.08
1455197_at	Rnd1	Rho family GTPase 1	-0.65	1.08
1423824_at	Gpr177	G protein-coupled receptor 177	-0.75	1.07
1454991_at	Slc7a1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	-0.65	1.06
1439817_at	2900064A13Rik	RIKEN cDNA 2900064A13 gene	-0.51	1.06
1417205_at	Kdelr2	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	-0.63	1.06
1440435_at	Ky	kyphoscoliosis peptidase	-1.17	1.06
1450243_a_at	Dscr1l1	Down syndrome critical region gene 1-like 1	-1.60	1.02
1453087_at	6330403L08Rik	RIKEN cDNA 6330403L08 gene	-0.72	1.01
1434883_at	Mtdh	Metadherin	-0.62	1.01
1426755_at	Ckap4	cytoskeleton-associated protein 4	-0.63	1.00
1450922_a_at	Tgfb2	transforming growth factor, beta 2	-1.25	0.99
1436203_a_at	1110059G02Rik	RIKEN cDNA 1110059G02 gene	-0.92	0.97
1445421_at	NA	NA	-0.67	0.96
1421012_at	Srprb	signal recognition particle receptor, B subunit	-0.36	0.95
1428896_at	Pdgfrl	platelet-derived growth factor receptor-like	-0.75	0.92
1445848_at	LOC384500	NA	0.81	0.92
1448682_at	Dynll1	dynein light chain LC8-type 1	-0.64	0.92
1419015_at	Wisp2	WNT1 inducible signaling pathway protein 2	-0.82	0.92
1448556_at	Prlr	prolactin receptor	0.67	0.91
1423405_at	Timp4	tissue inhibitor of metalloproteinase 4	0.91	0.91
1424542_at	S100a4	S100 calcium binding protein A4	-0.71	0.90
1422437_at	Col5a2	procollagen, type V, alpha 2	-0.71	0.89
1431714_at	2310015D24Rik	RIKEN cDNA 2310015D24 gene	-0.82	0.88
1452740_at	Myh10	myosin, heavy polypeptide 10, non-muscle	-0.85	0.88
1435985_at	Stk25	serine/threonine kinase 25 (yeast)	-0.54	0.85
1460302_at	Thbs1	thrombospondin 1	-1.17	0.84
1429508_at	2310057M21Rik	RIKEN cDNA 2310057M21 gene	-0.64	0.84
1458566_at	Gpatc2	G patch domain containing 2	0.54	0.83
1449096_at	0610011N22Rik	RIKEN cDNA 0610011N22 gene	-0.55	0.83
1437902_s_at	Lrrc61	leucine rich repeat containing 61	-0.51	0.82
1416174_at	Rbbp9	retinoblastoma binding protein 9	-0.43	0.82

1433934_at	Sec24a	SEC24 related gene family, member A (S. cerevisiae)	-0.42	0.82
1418820_s_at	Zcchc10	zinc finger, CCHC domain containing 10	-0.49	0.81
1416441_at	Pgcp	plasma glutamate carboxypeptidase	-0.60	0.80
1451975_at	2810453I06Rik	RIKEN cDNA 2810453I06 gene	-0.54	0.79
1415988_at	Hdlbp	high density lipoprotein (HDL) binding protein	-0.55	0.79
1448251_at	9030425E11Rik	RIKEN cDNA 9030425E11 gene	-0.88	0.79
1423316_at	Tmem39a	transmembrane protein 39a	-0.74	0.78
1437370_at	Sgol2	shugoshin-like 2 (S. pombe)	0.45	0.76
1459495_at	NA	NA	-0.50	0.75
1448207_at	Lasp1	LIM and SH3 protein 1	-0.45	0.75
1420636_a_at	Dusp12	dual specificity phosphatase 12	-0.42	0.73
1460260_s_at	Kpna1	karyopherin (importin) alpha 1	-0.39	0.72
1415741_at	Tparl	TPA regulated locus	-0.52	0.71
1442148_at	Psip1	PC4 and SFRS1 interacting protein 1	-0.58	0.71
1454842_a_at	B3galnt2	UDP-GalNAc:betaGlcNAc beta 1,3-galactosaminyltransferase, polypeptide 2	-0.69	0.69
1416554_at	Pdlim1	PDZ and LIM domain 1 (elfin)	-0.84	0.67
1442257_at	NA	NA	-1.03	0.67
1455583_at	Gne	glucosamine	-0.44	0.67
1426468_at	0610037L13Rik	RIKEN cDNA 0610037L13 gene	-0.36	0.66
1450784_at	Reck	reversion-inducing-cysteine-rich protein with kazal motifs	-0.49	0.66
1440397_at	Cacna2d1	calcium channel, voltage-dependent, alpha2/delta subunit 1	-0.70	0.66
1434950_a_at	Armc8	armadillo repeat containing 8	-0.41	0.65
1435641_at	9530018I07Rik	RIKEN cDNA 9530018I07 gene	-0.73	0.64
1418455_at	Copz2	coatomer protein complex, subunit zeta 2	-0.47	0.63
1451629_at	Lbh	limb-bud and heart	-0.70	0.63
1450994_at	Rock1	Rho-associated coiled-coil forming kinase 1	-0.66	0.60
1456798_at	9330118A15Rik	RIKEN cDNA 9330118A15 gene	-0.78	0.60
1430479_at	2010007H06Rik	RIKEN cDNA 2010007H06 gene	0.43	0.60
1428983_at	Scx	scleraxis	-0.77	0.60
1432494_a_at	1700019E19Rik	RIKEN cDNA 1700019E19 gene	-0.73	0.60
1425921_a_at	1810055G02Rik	RIKEN cDNA 1810055G02 gene	-0.66	0.58
1431079_at	C1qtnf2	C1q and tumor necrosis factor related protein 2	-0.81	0.58
1425913_a_at	2810022L02Rik	RIKEN cDNA 2810022L02 gene	-0.80	0.58
1437259_at	Slc9a2	solute carrier family 9 (sodium/hydrogen exchanger), member 2	-0.67	0.57
1433670_at	Emp2	epithelial membrane protein 2	-0.55	0.57
1424568_at	Tspan2	tetraspanin 2	-0.78	0.56
1450728_at	Fjx1	four jointed box 1 (Drosophila)	-0.73	0.56
1423352_at	Crispld1	cysteine-rich secretory protein LCCL domain containing 1	-0.52	0.56
1433543_at	Anln	anillin, actin binding protein (scraps homolog, Drosophila)	-0.95	0.55
1445969_at	NA	NA	-0.65	0.54
1418722_at	Ngp	neutrophilic granule protein	0.53	0.53
1441904_x_at	9130005N14Rik	RIKEN cDNA 9130005N14 gene	-0.63	0.53

1416686_at	Plod2	procollagen lysine, 2-oxoglutarate 5-dioxygenase 2	-0.78	0.53
1450943_at	2010012C16Rik	RIKEN cDNA 2010012C16 gene	-0.56	0.53
1428219_at	Rybp	RING1 and YY1 binding protein	-0.50	0.53
1453993_a_at	Bnip2	BCL2/adenovirus E1B interacting protein 1, NIP2	-0.55	0.53
1428538_s_at	Rarres2	retinoic acid receptor responder (tazarotene induced) 2	-0.57	0.51
1433929_at	Nhlrc2	NHL repeat containing 2	-0.40	0.51
1418413_at	Cav3	caveolin 3	-0.75	0.50
1460203_at	Itpr1	inositol 1,4,5-triphosphate receptor 1	-0.57	0.49
1424556_at	Pycr1	pyrroline-5-carboxylate reductase 1	-0.98	0.49
1426540_at	Endod1	endonuclease domain containing 1	-0.83	0.48
1419169_at	Mapk6	mitogen-activated protein kinase 6	-0.46	0.48
1455294_at	1110029L17Rik	RIKEN cDNA 1110029L17 gene	-0.36	0.48
1417104_at	Emp3	epithelial membrane protein 3	-0.52	0.47
1452521_a_at	Plaur	plasminogen activator, urokinase receptor	-0.59	0.46
1455320_at	Pbef1	pre-B-cell colony-enhancing factor 1	0.76	0.45
1416165_at	Rab31	RAB31, member RAS oncogene family	-0.51	0.45
1422818_at	Nedd9	neural precursor cell expressed, developmentally down-regulated gene 9	-0.90	0.44
1437637_at	Phtf2	putative homeodomain transcription factor 2	-0.98	0.44
1418454_at	Mfap5	microfibrillar associated protein 5	-0.60	0.44
1435981_at	NA	NA	-0.70	0.43
1424800_at	Enah	enabled homolog (Drosophila)	-0.77	0.43
1437101_at	Lats2	large tumor suppressor 2	-0.65	0.43
1429823_at	5430420E18Rik	RIKEN cDNA 5430420E18 gene	-0.95	0.42
1428668_at	Acbd3	acyl-Coenzyme A binding domain containing 3	-0.45	0.42
1427730_a_at	Zfp148	zinc finger protein 148	-0.34	0.41
1415758_at	Fryl	furry homolog-like (Drosophila)	-0.40	0.41
1443916_at	2900026A02Rik	RIKEN cDNA 2900026A02 gene	-0.55	0.40
1443501_at	NA	NA	0.44	0.40
1452094_at	P4ha1	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha 1 polypeptide	-0.77	0.40
1423440_at	1110001A07Rik	RIKEN cDNA 1110001A07 gene	-0.37	0.39
1423566_a_at	Hsp110	heat shock protein 110	-1.19	0.39
1417570_at	Anapc1	anaphase promoting complex subunit 1	-0.83	0.39
1431166_at	Chd1	chromodomain helicase DNA binding protein 1	0.57	0.38
1455375_at	NA	NA	-0.84	0.38
1425993_a_at	Hsp110	heat shock protein 110	-0.88	0.37
1454876_at	Rab23	RAB23, member RAS oncogene family	-0.67	0.37
1424801_at	Enah	enabled homolog (Drosophila)	-0.78	0.37
1448810_at	Gne	glucosamine	-0.37	0.37
1423649_at	Tmem68	transmembrane protein 68	-0.35	0.37
1458667_at	4930519N13Rik	RIKEN cDNA 4930519N13 gene	0.48	0.36
1450923_at	Tgfb2	transforming growth factor, beta 2	-1.09	0.36

1436737_a_at	Sorbs1	sorbin and SH3 domain containing 1	0.46	0.35
1431340_a_at	2310002J21Rik	RIKEN cDNA 2310002J21 gene	-0.46	0.35
1422919_at	Hrasls	HRAS-like suppressor	-0.59	0.35
1436178_at	Leprel1	leprecan-like 1	-0.85	0.35
1431131_s_at	A630007B06Rik	RIKEN cDNA A630007B06 gene	-0.35	0.35
1415856_at	Emb	embigin	-0.88	0.33
1444289_at	Yipf5	Yip1 domain family, member 5	-0.73	0.32
1420855_at	Eln	elastin	-0.89	0.32
1424318_at	1110067D22Rik	RIKEN cDNA 1110067D22 gene	-0.47	0.31
1417629_at	Prodh	proline dehydrogenase	1.13	0.30
1423790_at	Dap	death-associated protein	-0.52	0.30
1454916_s_at	Arfip1	ADP-ribosylation factor interacting protein 1	-0.41	0.29
1423841_at	Bxdc2	brix domain containing 2	-0.67	0.29
1451453_at	Dapk2	death-associated kinase 2	-0.62	0.29
1434802_s_at	Ntf3	neurotrophin 3	-0.69	0.28
1457042_at	AI256396	EST AI256396	-0.85	0.28
1434787_at	Arf3	ADP-ribosylation factor 3	-0.43	0.27
1451469_at	D530005L17Rik	RIKEN cDNA D530005L17 gene	-0.49	0.27
1418792_at	Sh3gl2	SH3-domain GRB2-like 2	0.39	0.26
1453189_at	Ube2i	ubiquitin-conjugating enzyme E2I	0.47	0.26
1418350_at	Hbegf	heparin-binding EGF-like growth factor	-1.32	0.26
1452283_at	Rassf8	Ras association (RalGDS/AF-6) domain family 8	-0.71	0.25
1436181_at	Itgb1bp1	integrin beta 1 binding protein 1	-0.77	0.25
1438271_at	Lpp	LIM domain containing preferred translocation partner in lipoma	-0.64	0.25
1422568_at	Ndel1	nuclear distribution gene E-like homolog 1 (A. nidulans)	-0.35	0.24
1452968_at	Cthrc1	collagen triple helix repeat containing 1	-0.53	0.23
1452145_at	H6pd	hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)	0.46	0.23
1433761_at	NA	NA	-0.63	0.22
1450079_at	Nrk	Nik related kinase	-0.85	0.22
1456415_at	Zfp451	zinc finger protein 451	-0.79	0.21
1430259_at	Tnfrsf11a	tumor necrosis factor receptor superfamily, member 11a	-0.47	0.21
1428644_at	Mgat5	mannoside acetylglucosaminyltransferase 5	-0.65	0.20
1455570_x_at	Cnn3	calponin 3, acidic	-0.60	0.20
1423825_at	Gpr177	G protein-coupled receptor 177	-0.57	0.20
1456626_a_at	1110005A23Rik	RIKEN cDNA 1110005A23 gene	-0.40	0.20
1435160_at	1110064P04Rik	RIKEN cDNA 1110064P04 gene	-0.49	0.19
1434869_at	Tdrd3	tudor domain containing 3	-0.48	0.19
1455862_at	9630054F20Rik	RIKEN cDNA 9630054F20 gene	-0.63	0.18
1437268_at	Lancl3	LanC lantibiotic synthetase component C-like 3 (bacterial)	-0.88	0.18
1423033_at	Stt3a	STT3, subunit of the oligosaccharyltransferase complex, homolog A (S. cerevisiae)	-0.57	0.17
1426584_a_at	Sord	sorbitol dehydrogenase	0.40	0.16
1439837_at	Tnrc15	trinucleotide repeat containing 15	-0.58	0.15

1429045_at	Smurf2	SMAD specific E3 ubiquitin protein ligase 2	-0.43	0.15
1456763_at	AA536749	expressed sequence AA536749	-0.46	0.15
1436297_a_at	Grina	glutamate receptor, ionotropic, N-methyl D-asparate-associated protein 1 (glutamate binding)	0.60	0.13
1452770_at	Vkorc1	vitamin K epoxide reductase complex, subunit 1	-0.44	0.13
1423915_at	Olfml2b	olfactomedin-like 2B	-0.66	0.13
1421818_at	Bcl6	B-cell leukemia/lymphoma 6	-0.83	0.12
1429027_at	0610007N19Rik	RIKEN cDNA 0610007N19 gene	-0.60	0.12
1434958_at	Sacs	sacsin	-0.83	0.12
1428097_at	2510009E07Rik	RIKEN cDNA 2510009E07 gene	-0.55	0.11
1434078_at	D7Wsu128e	DNA segment, Chr 7, Wayne State University 128, expressed	-0.40	0.11
1423136_at	Fgf1	fibroblast growth factor 1	-0.49	0.10
1422644_at	Sh3bgr	SH3-binding domain glutamic acid-rich protein	-0.78	0.10
1443550_at	NA	NA	-0.33	0.08
1417965_at	Plekha1	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 1	-0.63	0.07
1449324_at	Ero1l	ERO1-like (S. cerevisiae)	-0.48	0.07
1431381_at	3110005L24Rik	RIKEN cDNA 3110005L24 gene	0.71	0.07
1437396_at	Creb3l2	cAMP responsive element binding protein 3-like 2	-0.61	0.06
1421260_a_at	Srm	spermidine synthase	-0.35	0.05
1436204_at	1110059G02Rik	RIKEN cDNA 1110059G02 gene	-0.73	0.04
1454043_a_at	Kcnab1	potassium voltage-gated channel, shaker-related subfamily, beta member 1	-1.44	0.04
1455779_at	Hisppd2a	histidine acid phosphatase domain containing 2A	-0.62	0.04
1444246_at	Chd2	chromodomain helicase DNA binding protein 2	0.44	0.03
1425066_a_at	1110061O04Rik	RIKEN cDNA 1110061O04 gene	0.64	0.03
1440484_at	Unc5d	unc-5 homolog D (C. elegans)	-0.50	0.03
1416749_at	Htra1	HtrA serine peptidase 1	-0.63	0.03
1416469_at	Luzp1	leucine zipper protein 1	-0.40	0.02
1433877_at	4732473B16Rik	RIKEN cDNA 4732473B16 gene	-0.78	0.01
1438993_a_at	Atp6v1d	ATPase, H+ transporting, lysosomal V1 subunit D	0.42	0.01

Online Table VI. Statistically Significant KEGG Pathways Associated with Differentially-Expressed Genes for Diabetic ApoE null Relative to Non-Diabetic ApoE null mice

Rank	Pathway Name	Number of differentially expressed genes in KEGG pathway	Total number of genes in KEGG pathway on chip	False discovery rate corrected gamma p-value
1	Insulin signaling pathway	5	137	1.5E-03
2	Bladder cancer	3	42	9.6E-03
3	Cell Communication	4	130	0.01
4	ECM-receptor interaction	3	84	0.01
5	Focal adhesion	4	192	0.01
6	TGF-beta signaling pathway	2	89	0.01
7	Antigen processing and presentation	1	99	0.01
8	Adipocytokine signaling pathway	1	71	0.02
9	Long-term depression	2	76	0.02

Online Table VII. Statistically Significant KEGG Pathways Associated with Differentially Expressed Genes for Diabetic ApoE null/RAGE null Relative to Diabetic ApoE null mice

Rank	Pathway Name	Number of differentially expressed genes in KEGG pathway	Number of genes in KEGG pathway on chip	False discovery rate corrected gamma p-value
1	Phosphatidylinositol signaling system	3	70	9.7E-12
2	Wnt signaling pathway	3	141	0.02
3	Focal adhesion	6	186	0.02
4	MAPK signaling pathway	5	249	0.02
5	Melanoma	2	70	0.02
6	Gap junction	2	84	0.02
7	ErbB signaling pathway	2	85	0.02
8	TGF-beta signaling pathway	5	86	0.02

Online Table VIII. Fold Changes of Differentially Expressed Tgf-β Pathway Genes in Diabetic ApoE null Relative to Non-Diabetic ApoE null mice

Gene Symbol	Gene Name	$\log_2$ FC
Ppp2r1b	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform	-0.53
Thbs1	thrombospondin 1	1.32

Online Table IX. Fold Changes of Differentially Expressed Tgf-β Pathway Genes in Diabetic ApoE null/RAGE null Relative to Diabetic ApoE null mice

Gene Symbol	Gene Name	$\log_2$ FC
Ltbp1	latent transforming growth factor beta binding protein 1	-1.3
Rock1	Rho-associated coiled-coil containing protein kinase 1	-0.66
Smurf2	SMAD specific E3 ubiquitin protein ligase 2	-0.43
Tgfb2	transforming growth factor, beta 2	-1.1
Thbs1	thrombospondin 1	-1.2

Online Table X. Perturbation Factors of Differentially Expressed Tgf-β Pathway Genes in Diabetic ApoE null Relative to Non-Diabetic ApoE null mice

Gene Symbol	Gene Name	Perturbation Factor	$\log_2$ FC	Is Input Gene
Ltbp1	latent transforming growth factor beta binding protein 1	-1.32	0	No
Ppp2ca	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha	0.12	0	No
Ppp2cb	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	0.12	0	No
Ppp2r1a	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform	0.12	0	No
Ppp2r1b	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform	-0.41	-0.53	Yes
Ppp2r2b	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), beta isoform	0.12	0	No
Ppp2r2c	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), gamma isoform	0.12	0	No
Ppp2r2d	protein phosphatase 2, regulatory subunit B, delta isoform	0.12	0	No
Rhoa	ras homolog gene family, member A	0.12	0	No
Rock1	Rho-associated coiled-coil containing protein kinase 1	0.12	0	No
Rock2	Rho-associated coiled-coil containing protein kinase 2	0.12	0	No
Rps6kb1	ribosomal protein S6 kinase, polypeptide 1	0.16	0	No
Rps6kb2	ribosomal protein S6 kinase, polypeptide 2	0.16	0	No
Smad2	MAD homolog 2 (Drosophila)	0.12	0	No
Smad3	MAD homolog 3 (Drosophila)	0.12	0	No
Smad4	MAD homolog 4 (Drosophila)	0.24	0	No
Tgfb1	transforming growth factor, beta 1	0.44	0	No
Tgfb2	transforming growth factor, beta 2	0.44	0	No
Tgfb3	transforming growth factor, beta 3	0.44	0	No
Tgfbr1	transforming growth factor, beta receptor I	0.66	0	No
Tgfbr2	transforming growth factor, beta receptor II	0.66	0	No
Thbs1	thrombospondin 1	1.32	1.32	Yes

Online Table XI. Perturbation Factors of Differentially Expressed Tgf-β Pathway Genes in Diabetic ApoE null/RAGE null Relative to Diabetic ApoE null mice

Gene Symbol	Gene Name	Perturbation Factor	Fold change	Is Input Gene
Ltbp1	latent transforming growth factor beta binding protein 1	-0.14	-1.31	Yes
Ppp2ca	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha	-0.05	0.00	No
Ppp2cb	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	-0.05	0.00	No
Ppp2r1a	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform	-0.05	0.00	No
Ppp2r1b	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform	-0.05	0.00	No
Ppp2r2b	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), beta isoform	-0.05	0.00	No
Ppp2r2c	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), gamma isoform	-0.05	0.00	No
Ppp2r2d	protein phosphatase 2, regulatory subunit B, delta isoform	-0.05	0.00	No
Rhoa	ras homolog gene family, member A	-0.05	0.00	No
Rock1	Rho-associated coiled-coil containing protein kinase 1	-0.71	-0.66	Yes
Rock2	Rho-associated coiled-coil containing protein kinase 2	-0.05	0.00	No
Rps6kb1	ribosomal protein S6 kinase, polypeptide 1	-0.17	0.00	No
Rps6kb2	ribosomal protein S6 kinase, polypeptide 2	-0.17	0.00	No
Smad2	MAD homolog 2 (Drosophila)	-0.05	0.00	No
Smad3	MAD homolog 3 (Drosophila)	-0.05	0.00	No
Smad4	MAD homolog 4 (Drosophila)	-0.10	0.00	No
Smurf2	SMAD specific E3 ubiquitin protein ligase 2	-0.43	-0.43	Yes
Tgfb1	transforming growth factor, beta 1	0.05	0.00	No
Tgfb2	transforming growth factor, beta 2	-1.07	-1.12	Yes
Tgfb3	transforming growth factor, beta 3	0.05	0.00	No
Tgfbr1	transforming growth factor, beta receptor I	-0.27	0.00	No
Tgfbr2	transforming growth factor, beta receptor II	-0.27	0.00	No
Thbs1	thrombospondin 1	-1.17	-1.17	Yes

Online Table XII.

Numbers of Differentially Expressed Genes with Unique Entrez Gene Symbols
for Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice
and for Diabetic ApoE null / RAGE null vs. Diabetic ApoE null mice,
and their Directional and Boolean Subsets

Online Table	Gene set or subset	
XIII	Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice All	53
	Diabetic ApoE null/RAGE null vs. Diabetic ApoE null mice All	216
	Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice All UNION Diabetic ApoE null/RAGE null vs. Diabetic ApoE null mice All	254
	Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice All INTERSECTION Diabetic ApoE null / RAGE null vs. Diabetic ApoE null mice All	15
	Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice All NOT Diabetic ApoE null / RAGE null vs. Diabetic ApoE null mice All	38
	Diabetic ApoE null/RAGE null vs. diabetic ApoE null mice All NOT Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice All	201
XIV	Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice Positive	34
	Diabetic ApoE null/RAGE null vs. Diabetic ApoE null mice Positive	27
	Diabetic ApoE null mice vs. non-diabetic ApoE null mice Positive UNION Diabetic ApoE null / RAGE null vs. Diabetic ApoE null mice Positive	61
	Diabetic ApoE null mice vs. non-diabetic ApoE null mice Positive INTERSECTION Diabetic ApoE null / RAGE null vs. Diabetic ApoE null mice Positive	0
	Diabetic ApoE null mice vs. non-diabetic ApoE null mice Positive NOT Diabetic ApoE null / RAGE null vs. Diabetic ApoE null mice Positive	34
	Diabetic ApoE null/RAGE null vs. diabetic ApoE null mice Positive NOT Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice Positive	27
XV	Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice Negative	19
	Diabetic ApoE null/RAGE null vs. Diabetic ApoE null mice Negative	189
	Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice Negative UNION Diabetic ApoE null / RAGE null vs. Diabetic ApoE null mice Positive	208
	Diabetic ApoE null mice vs. Non-Diabetic ApoE null miceNegative INTERSECTION Diabetic ApoE null / RAGE null vs. Diabetic ApoE null mice Positive	0
	Diabetic ApoE null mice vs. Non-Diabetic ApoE null miceNegative NOT Diabetic ApoE null / RAGE null vs. Diabetic ApoE null mice Positive	19
	Diabetic ApoE null/RAGE null vs. diabetic ApoE null mice Positive NOT Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice Negative	189
XVI	Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice Positive	34
	Diabetic ApoE null/RAGE null vs. Diabetic ApoE null mice Negative	189
	Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice Positive UNION Diabetic ApoE null / RAGE null vs. Diabetic ApoE null mice Positive	210
	Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice Positive INTERSECTION Diabetic ApoE null / RAGE null vs. Diabetic ApoE null mice Positive	14
	Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice Positive NOT Diabetic ApoE null / RAGE null vs. Diabetic ApoE null mice Positive	21
	Diabetic ApoE null/RAGE null vs. Diabetic ApoE null mice Positive NOT Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice Positive	175

XVII	Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice Negative	19
	Diabetic ApoE null/RAGE null vs. Diabetic ApoE null mice Positive	27
	Diabetic ApoE null mice vs. non-diabetic ApoE null mice Negative UNION Diabetic ApoE null / RAGE null vs. Diabetic ApoE null mice Positive	45
	Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice Negative INTERSECTION Diabetic ApoE null / RAGE null vs. Diabetic ApoE null mice Positive	1
	Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice Negative NOT Diabetic ApoE null / RAGE null vs. Diabetic ApoE null mice Positive	18
	Diabetic ApoE null/RAGE null vs. Diabetic ApoE null mice Positive NOT Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice Negative	26

Online Table XIII.

Differentially Expressed Genes with Unique Entrez Gene Symbols
for Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice
and for Diabetic ApoE null / RAGE null vs. Diabetic ApoE null mice,
and their Boolean Subsets

Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice All	Diabetic ApoE null / RAGE null vs. Diabetic ApoE null mice All	Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice All UNION Diabetic ApoE null / RAGE null vs. Diabetic ApoE null mice All	Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice All INTERSECTION Diabetic ApoE null / RAGE null vs. Diabetic ApoE null mice All	Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice All NOT Diabetic ApoE null / RAGE null vs. Diabetic ApoE null mice All	Diabetic ApoE null / RAGE null vs. Diabetic ApoE null mice All NOT Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice All
Aacs	Acbd3	Aacs	Chordc1	Aacs	Acbd3
Acaca	Acot1	Acaca	Crem	Acaca	Acot1
Acacb	Anapc1	Acacb	Cyp26b1	Acacb	Anapc1
Acly	Anln	Acbd3	Dnaja1	Acly	Anln
Acss2	Arf3	Acly	Erdr1	Acss2	Arf3
Agbl3	Arfip1	Acot1	Golt1b	Agbl3	Arfip1
Anxa3	Armc8	Acss2	Hsp110	Anxa3	Armc8
Chordc1	Armcx3	Agbl3	Hspa1b	Ctps	Armcx3
Crem	Atp6v1d	Anapc1	Rybp	Eef1e1	Atp6v1d
Ctps	B3galnt2	Anln	S100a4	Emp1	B3galnt2
Cyp26b1	Bcas3	Anxa3	Slc7a1	Fasn	Bcas3
Dnaja1	Bcl6	Arf3	Thbs1	Figf	Bcl6
Eef1e1	Bdh1	Arfip1	Tparl	Fmo5	Bdh1
Emp1	Bnip2	Armc8	Tshz3	Fn1	Bnip2
Erdr1	Btaf1	Armcx3	Tspan6	H2-Q10	Btaf1
Fasn	Bxdc2	Atp6v1d		Hexim1	Bxdc2
Figf	Bysl	B3galnt2		Ifitm2	Bysl
Fmo5	C1galt1	Bcas3		Kpna2	C1galt1
Fn1	C1qtnf2	Bcl6		Kras	C1qtnf2
Golt1b	Cacna2d1	Bdh1		Lmnb2	Cacna2d1
H2-Q10	Cav3	Bnip2		Mod1	Cav3
Hexim1	Cbx5	Btaf1		Mtmr11	Cbx5
Hsp110	Ccrn4l	Bxdc2		Mtmr4	Ccrn4l
Hspa1b	Cdr2	Bysl		Nudt18	Cdr2
Ifitm2	Chd1	C1galt1		Ppp2r1b	Chd1
Kpna2	Chd2	C1qtnf2		Pvt1	Chd2
Kras	Chordc1	Cacna2d1		Pygl	Chrna1
Lmnb2	Chrna1	Cav3		Rbm8a	Chsy1
Mod1	Chsy1	Cbx5		Reln	Ckap4
Mtmr11	Ckap4	Ccrn4l		Sfpq	Cnn3
Mtmr4	Cnn3	Cdr2		Sfrs3	Col5a2
Nudt18	Col5a2	Chd1		Slc1a5	Copz2
Ppp2r1b	Copz2	Chd2		Slc25a1	Creb3l2
Pvt1	Creb3l2	Chordc1		Thrsp	Crispld1

Pygl
Rbm8a
Reln
Rybp
S100a4
Sfpq
Sfrs3
Slc1a5
Slc25a1
Slc7a1
Thbs1
Thrsp
Tkt
Tm4sf1
Tparl
Tshz3
Tspan6
Ube1l2
Wwc2

Crem
Crispld1
Cthrc1
Cyp26b1
Dap
Dapk2
Dgkg
Dnaja1
Dock7
Dscr1l1
Dusp12
Dynll1
Efhc2
Eln
Emb
Eml5
Emp2
Emp3
Enah
Endod1
Erdr1
Ereg
Ero1l
Ext1
Fgf1
Fjx1
Fkbp14
Fryl
Gal3st4
Ggh
Glo1
Glp1r
Gm347
Gm70
Gmds
Gne
Golt1b
Gpatc2
Gpr125
Gpr177
Grina
H6pd
Hbegf
Hcfc2
Hdac9

Chrna1
Chsy1
Ckap4
Cnn3
Col5a2
Copz2
Creb3l2
Crem
Crispld1
Cthrc1
Ctps
Cyp26b1
Dap
Dapk2
Dgkg
Dnaja1
Dock7
Dscr1l1
Dusp12
Dynll1
Eef1e1
Efhc2
Eln
Emb
Eml5
Emp1
Emp2
Emp3
Enah
Endod1
Erdr1
Ereg
Ero1l
Ext1
Fasn
Fgf1
Figf
Fjx1
Fkbp14
Fmo5
Fn1
Fryl
Gal3st4
Ggh
Glo1

Tkt
Tm4sf1
Ube1l2
Wwc2

Cthrc1
Dap
Dapk2
Dgkg
Dock7
Dscr1l1
Dusp12
Dynll1
Efhc2
Eln
Emb
Eml5
Emp2
Emp3
Enah
Endod1
Ereg
Ero1l
Ext1
Fgf1
Fjx1
Fkbp14
Fryl
Gal3st4
Ggh
Glo1
Glp1r
Gm347
Gm70
Gmds
Gne
Gpatc2
Gpr125
Gpr177
Grina
H6pd
Hbegf
Hcfc2
Hdac9
Hdlbp
Hisppd2a
Hrasls
Hrb
Hspa1a
Hspb2

Hdlbp
Hisppd2a
Hrasls
Hrb
Hsp110
Hspa1a
Hspa1b
Hspb2
Htra1
Il17b
Itga9
Itgb1bp1
Itpr1
Kcnab1
Kdelr2
Kdelr3
Kpna1
Ky
Lancl3
Lasp1
Lats2
Lbh
Leprel1
Lox
Lpp
Lrrc61
Lrrfip1
Ltbp1
Luzp1
Maged2
Mapk6
Mfap5
Mgat5
Mobk1b
Mrpl15
Mtdh
Myh10
Ndel1
Nedd9
Ngp
Nhlrc2
Nrk
Ntf3
Olfml2b
P4ha1

Glp1r
Gm347
Gm70
Gmds
Gne
Golt1b
Gpatc2
Gpr125
Gpr177
Grina
H2-Q10
H6pd
Hbegf
Hcfc2
Hdac9
Hdlbp
Hexim1
Hisppd2a
Hrasls
Hrb
Hsp110
Hspa1a
Hspa1b
Hspb2
Htra1
Ifitm2
Il17b
Itga9
Itgb1bp1
Itpr1
Kcnab1
Kdelr2
Kdelr3
Kpna1
Kpna2
Kras
Ky
Lancl3
Lasp1
Lats2
Lbh
Leprel1
Lmnb2
Lox
Lpp

Htra1
Il17b
Itga9
Itgb1bp1
Itpr1
Kcnab1
Kdelr2
Kdelr3
Kpna1
Ky
Lancl3
Lasp1
Lats2
Lbh
Leprel1
Lox
Lpp
Lrrc61
Lrrfip1
Ltbp1
Luzp1
Maged2
Mapk6
Mfap5
Mgat5
Mobk1b
Mrpl15
Mtdh
Myh10
Ndel1
Nedd9
Ngp
Nhlrc2
Nrk
Ntf3
Olfml2b
P4ha1
Pank2
Pbef1
Pcgf5
Pdgfd
Pdgfrl
Pdlim1
Pdlim5
Pgcp

Pank2
Pbef1
Pcgf5
Pdgfd
Pdgfrl
Pdlim1
Pdlim5
Pgcp
Phtf2
Pigm
Pip5k1a
Plaur
Plekha1
Plod2
Pols
Prlr
Prodh
Psip1
Ptprz1
Pycr1
Rab23
Rab31
Rabep1
Ramp1
Rarres2
Rassf8
Rbbp9
Reck
Rnd1
Rock1
Rybp
S100a4
Sacs
Scx
Sec22l1
Sec23a
Sec24a
Sema3c
Serpine1
Sfrp2
Sgcb
Sgce
Sgcg
Sgol2
Sh3bgr

Lrrc61
Lrrfip1
Ltbp1
Luzp1
Maged2
Mapk6
Mfap5
Mgat5
Mobk1b
Mod1
Mrpl15
Mtdh
Mtmr11
Mtmr4
Myh10
Ndel1
Nedd9
Ngp
Nhlrc2
Nrk
Ntf3
Nudt18
Olfml2b
P4ha1
Pank2
Pbef1
Pcgf5
Pdgfd
Pdgfrl
Pdlim1
Pdlim5
Pgcp
Phtf2
Pigm
Pip5k1a
Plaur
Plekha1
Plod2
Pols
Ppp2r1b
Prlr
Prodh
Psip1
Ptprz1
Pvt1

Phtf2
Pigm
Pip5k1a
Plaur
Plekha1
Plod2
Pols
Prlr
Prodh
Psip1
Ptprz1
Pycr1
Rab23
Rab31
Rabep1
Ramp1
Rarres2
Rassf8
Rbbp9
Reck
Rnd1
Rock1
Sacs
Scx
Sec22l1
Sec23a
Sec24a
Sema3c
Serpine1
Sfrp2
Sgcb
Sgce
Sgcg
Sgol2
Sh3bgr
Sh3gl2
Six5
Slc9a2
Smurf2
Sorbs1
Sord
Srm
Srprb
St8sia6
Stch

Sh3gl2
Six5
Slc7a1
Slc9a2
Smurf2
Sorbs1
Sord
Srm
Srprb
St8sia6
Stch
Stk25
Stk38l
Stt3a
Sulf1
Surb7
Sync
Tdrd3
Tgfb2
Thbs1
Timp4
Tmem39a
Tmem45a
Tmem68
Tmtc3
Tnfaip1
Tnfrsf11a
Tnfrsf12a
Tnrc15
Tparl
Trp53inp2
Tshz3
Tspan2
Tspan6
Ube2i
Unc5d
Vkorc1
Wif1
Wisp2
Wtip
Xdh
Yipf5
Zbtb41
Zcchc10
Zfp148

Pycr1
Pygl
Rab23
Rab31
Rabep1
Ramp1
Rarres2
Rassf8
Rbbp9
Rbm8a
Reck
Reln
Rnd1
Rock1
Rybp
S100a4
Sacs
Scx
Sec22l1
Sec23a
Sec24a
Sema3c
Serpine1
Sfpq
Sfrp2
Sfrs3
Sgcb
Sgce
Sgcg
Sgol2
Sh3bgr
Sh3gl2
Six5
Slc1a5
Slc25a1
Slc7a1
Slc9a2
Smurf2
Sorbs1
Sord
Srm
Srprb
St8sia6
Stch
Stk25

Stk25
Stk38l
Stt3a
Sulf1
Surb7
Sync
Tdrd3
Tgfb2
Timp4
Tmem39a
Tmem45a
Tmem68
Tmtc3
Tnfaip1
Tnfrsf11a
Tnfrsf12a
Tnrc15
Trp53inp2
Tspan2
Ube2i
Unc5d
Vkorc1
Wif1
Wisp2
Wtip
Xdh
Yipf5
Zbtb41
Zcchc10
Zfp148
Zfp451
Zfp9

Zfp451
Zfp9

Stk38l
Stt3a
Sulf1
Surb7
Sync
Tdrd3
Tgfb2
Thbs1
Thrsp
Timp4
Tkt
Tm4sf1
Tmem39a
Tmem45a
Tmem68
Tmtc3
Tnfaip1
Tnfrsf11a
Tnfrsf12a
Tnrc15
Tparl
Trp53inp2
Tshz3
Tspan2
Tspan6
Ube1l2
Ube2i
Unc5d
Vkorc1
Wif1
Wisp2
Wtip
Wwc2
Xdh
Yipf5
Zbtb41
Zcchc10
Zfp148
Zfp451
Zfp9

Online Table XIV.
Differentially Expressed Genes with Unique Entrez Gene Symbols for Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice and for Diabetic ApoE null / RAGE null vs. Diabetic ApoE null mice both with Positive log2 Fold Change and their Boolean Subsets

Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice Positive	Diabetic ApoE null / RAGE null vs. Diabetic ApoE null mice Positive	Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice Positive UNION Diabetic ApoE null / RAGE null vs. Diabetic ApoE null mice Positive	Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice Positive INTERSECTION Diabetic ApoE null / RAGE null vs. Diabetic ApoE null mice Positive	Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice Positive NOT Diabetic ApoE null / RAGE null vs. Diabetic ApoE null mice Positive	Diabetic ApoE null / RAGE null vs. Diabetic ApoE null mice Positive NOT Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice Positive
Anxa3	Acot1	Acot1		Anxa3	Acot1
Chordc1	Atp6v1d	Anxa3		Chordc1	Atp6v1d
Crem	Bcas3	Atp6v1d		Crem	Bcas3
Ctps	Ccrn4l	Bcas3		Ctps	Ccrn4l
Cyp26b1	Chd1	Ccrn4l		Cyp26b1	Chd1
Dnaja1	Chd2	Chd1		Dnaja1	Chd2
Eef1e1	Eml5	Chd2		Eef1e1	Eml5
Emp1	Erdr1	Chordc1		Emp1	Erdr1
Figf	Glo1	Crem		Figf	Glo1
Fn1	Glp1r	Ctps		Fn1	Glp1r
Golt1b	Gpatc2	Cyp26b1		Golt1b	Gpatc2
Hexim1	Grina	Dnaja1		Hexim1	Grina
Hsp110	H6pd	Eef1e1		Hsp110	H6pd
Hspa1b	Mrpl15	Eml5		Hspa1b	Mrpl15
Ifitm2	Ngp	Emp1		Ifitm2	Ngp
Kpna2	Pbef1	Erdr1		Kpna2	Pbef1
Kras	Prlr	Figf		Kras	Prlr
Lmnb2	Prodh	Fn1		Lmnb2	Prodh
Mtmr4	Sgol2	Glo1		Mtmr4	Sgol2
Pvt1	Sh3gl2	Glp1r		Pvt1	Sh3gl2
Rbm8a	Sorbs1	Golt1b		Rbm8a	Sorbs1
Reln	Sord	Gpatc2		Reln	Sord
Rybp	St8sia6	Grina		Rybp	St8sia6
S100a4	Timp4	H6pd		S100a4	Timp4
Sfpq	Trp53inp2	Hexim1		Sfpq	Trp53inp2
Sfrs3	Ube2i	Hsp110		Sfrs3	Ube2i
Slc7a1	Xdh	Hspa1b		Slc7a1	Xdh
Thbs1		Ifitm2		Thbs1	

Tm4sf1
Tparl
Tshz3
Tspan6
Ube1l2
Wwc2

Kpna2
Kras
Lmnb2
Mrpl15
Mtmr4
Ngp
Pbef1
Prlr
Prodh
Pvt1
Rbm8a
Reln
Rybp
S100a4
Sfpq
Sfrs3
Sgol2
Sh3gl2
Slc7a1
Sorbs1
Sord
St8sia6
Thbs1
Timp4
Tm4sf1
Tparl
Trp53inp2
Tshz3
Tspan6
Ube1l2
Ube2i
Wwc2
Xdh

Tm4sf1
Tparl
Tshz3
Tspan6
Ube1l2
Wwc2

Online Table XV.
Differentially Expressed Genes with Unique Entrez Gene Symbols for
Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice
and for Diabetic ApoE null / RAGE null vs. Diabetic ApoE null mice
both with Negative log2 Fold Change and their Boolean Subsets

Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice Negative	Diabetic ApoE null / RAGE null vs. Diabetic ApoE null mice Negative	Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice Negative UNION Diabetic ApoE null / RAGE null vs. Diabetic ApoE null mice Negative	Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice Negative INTERSECTION Diabetic ApoE null / RAGE null vs. Diabetic ApoE null mice Negative	Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice Negative NOT Diabetic ApoE null / RAGE null vs. Diabetic ApoE null mice Negative	Diabetic ApoE null / RAGE null vs. Diabetic ApoE null mice Negative NOT Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice Negative
Aacs	Acbd3	Aacs	No Entries	Aacs	Acbd3
Acaca	Anapc1	Acaca		Acaca	Anapc1
Acacb	Anln	Acacb		Acacb	Anln
Acly	Arf3	Acly		Acly	Arf3
Acss2	Arfip1	Acss2		Acss2	Arfip1
Agbl3	Armc8	Agbl3		Agbl3	Armc8
Erdr1	Armcx3	Erdr1		Erdr1	Armcx3
Fasn	B3galnt2	Fasn		Fasn	B3galnt2
Fmo5	Bcl6	Fmo5		Fmo5	Bcl6
H2-Q10	Bdh1	H2-Q10		H2-Q10	Bdh1
Mod1	Bnip2	Mod1		Mod1	Bnip2
Mtmr11	Btaf1	Mtmr11		Mtmr11	Btaf1
Nudt18	Bxdc2	Nudt18		Nudt18	Bxdc2
Ppp2r1b	Bysl	Ppp2r1b		Ppp2r1b	Bysl
Pygl	C1galt1	Pygl		Pygl	C1galt1
Slc1a5	C1qtnf2	Slc1a5		Slc1a5	C1qtnf2
Slc25a1	Cacna2d1	Slc25a1		Slc25a1	Cacna2d1
Thrsp	Cav3	Thrsp		Thrsp	Cav3
Tkt	Cbx5	Tkt		Tkt	Cbx5
	Cdr2	Acbd3			Cdr2
	Chordc1	Anapc1			Chordc1
	Chrna1	Anln			Chrna1
	Chsy1	Arf3			Chsy1
	Ckap4	Arfip1			Ckap4
	Cnn3	Armc8			Cnn3
	Col5a2	Armcx3			Col5a2
	Copz2	B3galnt2			Copz2

Creb3l2
Crem
Crispld1
Cthrc1
Cyp26b1
Dap
Dapk2
Dgkg
Dnaja1
Dock7
Dscr1l1
Dusp12
Dynll1
Efhc2
Eln
Emb
Emp2
Emp3
Enah
Endod1
Ereg
Ero1l
Ext1
Fgf1
Fjx1
Fkbp14
Fryl
Gal3st4
Ggh
Gm347
Gm70
Gmds
Gne
Golt1b
Gpr125
Gpr177
Hbegf
Hcfc2
Hdac9
Hdlbp
Hisppd2a
Hrasls

Bcl6
Bdh1
Bnip2
Btaf1
Bxdc2
Bysl
C1galt1
C1qtnf2
Cacna2d1
Cav3
Cbx5
Cdr2
Chordc1
Chrna1
Chsy1
Ckap4
Cnn3
Col5a2
Copz2
Creb3l2
Crem
Crispld1
Cthrc1
Cyp26b1
Dap
Dapk2
Dgkg
Dnaja1
Dock7
Dscr1l1
Dusp12
Dynll1
Efhc2
Eln
Emb
Emp2
Emp3
Enah
Endod1
Ereg
Ero1l
Ext1

Creb3l2
Crem
Crispld1
Cthrc1
Cyp26b1
Dap
Dapk2
Dgkg
Dnaja1
Dock7
Dscr1l1
Dusp12
Dynll1
Efhc2
Eln
Emb
Emp2
Emp3
Enah
Endod1
Ereg
Ero1l
Ext1
Fgf1
Fjx1
Fkbp14
Fryl
Gal3st4
Ggh
Gm347
Gm70
Gmds
Gne
Golt1b
Gpr125
Gpr177
Hbegf
Hcfc2
Hdac9
Hdlbp
Hisppd2a
Hrasls

Hrb
Hsp110
Hspa1a
Hspa1b
Hspb2
Htra1
Il17b
Itga9
Itgb1bp1
Itpr1
Kcnab1
Kdelr2
Kdelr3
Kpna1
Ky
Lancl3
Lasp1
Lats2
Lbh
Leprel1
Lox
Lpp
Lrrc61
Lrrfip1
Ltbp1
Luzp1
Maged2
Mapk6
Mfap5
Mgat5
Mobk1b
Mtdh
Myh10
Ndel1
Nedd9
Nhlrc2
Nrk
Ntf3
Olfml2b
P4ha1
Pank2
Pcgf5

Fgf1
Fjx1
Fkbp14
Fryl
Gal3st4
Ggh
Gm347
Gm70
Gmds
Gne
Golt1b
Gpr125
Gpr177
Hbegf
Hcfc2
Hdac9
Hdlbp
Hisppd2a
Hrasls
Hrb
Hsp110
Hspa1a
Hspa1b
Hspb2
Htra1
Il17b
Itga9
Itgb1bp1
Itpr1
Kcnab1
Kdelr2
Kdelr3
Kpna1
Ky
Lancl3
Lasp1
Lats2
Lbh
Leprel1
Lox
Lpp
Lrrc61

Hrb
Hsp110
Hspa1a
Hspa1b
Hspb2
Htra1
Il17b
Itga9
Itgb1bp1
Itpr1
Kcnab1
Kdelr2
Kdelr3
Kpna1
Ky
Lancl3
Lasp1
Lats2
Lbh
Leprel1
Lox
Lpp
Lrrc61
Lrrfip1
Ltbp1
Luzp1
Maged2
Mapk6
Mfap5
Mgat5
Mobk1b
Mtdh
Myh10
Ndel1
Nedd9
Nhlrc2
Nrk
Ntf3
Olfml2b
P4ha1
Pank2
Pcgf5

Pdgfd	Lrrfip1	Pdgfd
Pdgfrl	Ltbp1	Pdgfrl
Pdlim1	Luzp1	Pdlim1
Pdlim5	Maged2	Pdlim5
Pgcp	Mapk6	Pgcp
Phtf2	Mfap5	Phtf2
Pigm	Mgat5	Pigm
Pip5k1a	Mobk1b	Pip5k1a
Plaur	Mtdh	Plaur
Plekha1	Myh10	Plekha1
Plod2	Ndel1	Plod2
Pols	Nedd9	Pols
Psip1	Nhlrc2	Psip1
Ptprz1	Nrk	Ptprz1
Pycr1	Ntf3	Pycr1
Rab23	Olfml2b	Rab23
Rab31	P4ha1	Rab31
Rabep1	Pank2	Rabep1
Ramp1	Pcgf5	Ramp1
Rarres2	Pdgfd	Rarres2
Rassf8	Pdgfrl	Rassf8
Rbbp9	Pdlim1	Rbbp9
Reck	Pdlim5	Reck
Rnd1	Pgcp	Rnd1
Rock1	Phtf2	Rock1
Rybp	Pigm	Rybp
S100a4	Pip5k1a	S100a4
Sacs	Plaur	Sacs
Scx	Plekha1	Scx
Sec22l1	Plod2	Sec22l1
Sec23a	Pols	Sec23a
Sec24a	Psip1	Sec24a
Sema3c	Ptprz1	Sema3c
Serpine1	Pycr1	Serpine1
Sfrp2	Rab23	Sfrp2
Sgcb	Rab31	Sgcb
Sgce	Rabep1	Sgce
Sgcg	Ramp1	Sgcg
Sh3bgr	Rarres2	Sh3bgr
Six5	Rassf8	Six5
Slc7a1	Rbbp9	Slc7a1
Slc9a2	Reck	Slc9a2

Smurf2
Srm
Srprb
Stch
Stk25
Stk38l
Stt3a
Sulf1
Surb7
Sync
Tdrd3
Tgfb2
Thbs1
Tmem39a
Tmem45a
Tmem68
Tmtc3
Tnfaip1
Tnfrsf11a
Tnfrsf12a
Tnrc15
Tparl
Tshz3
Tspan2
Tspan6
Unc5d
Vkorc1
Wif1
Wisp2
Wtip
Yipf5
Zbtb41
Zcchc10
Zfp148
Zfp451
Zfp9

Rnd1
Rock1
Rybp
S100a4
Sacs
Scx
Sec22l1
Sec23a
Sec24a
Sema3c
Serpine1
Sfrp2
Sgcb
Sgce
Sgcg
Sh3bgr
Six5
Slc7a1
Slc9a2
Smurf2
Srm
Srprb
Stch
Stk25
Stk38l
Stt3a
Sulf1
Surb7
Sync
Tdrd3
Tgfb2
Thbs1
Tmem39a
Tmem45a
Tmem68
Tmtc3
Tnfaip1
Tnfrsf11a
Tnfrsf12a
Tnrc15
Tparl
Tshz3

Smurf2
Srm
Srprb
Stch
Stk25
Stk38l
Stt3a
Sulf1
Surb7
Sync
Tdrd3
Tgfb2
Thbs1
Tmem39a
Tmem45a
Tmem68
Tmtc3
Tnfaip1
Tnfrsf11a
Tnfrsf12a
Tnrc15
Tparl
Tshz3
Tspan2
Tspan6
Unc5d
Vkorc1
Wif1
Wisp2
Wtip
Yipf5
Zbtb41
Zcchc10
Zfp148
Zfp451
Zfp9

Tspan2
Tspan6
Unc5d
Vkorc1
Wif1
Wisp2
Wtip
Yipf5
Zbtb41
Zcchc10
Zfp148
Zfp451
Zfp9

Online Table XVI.

Differentially Expressed Genes with Unique Entrez Gene Symbols for Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice with Positive log Fold Change, and for Diabetic ApoE null/RAGE null vs. Diabetic ApoE null with Negative log Fold Change and their Boolean Subsets

Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice Positive	Diabetic ApoE null / RAGE null vs. Diabetic ApoE null mice Negative	Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice Positive UNION Diabetic ApoE null / RAGE null vs. Diabetic ApoE null mice Negative	Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice Positive INTERSECTION Diabetic ApoE null / RAGE null vs. Diabetic ApoE null mice Negative	Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice Positive NOT Diabetic ApoE null / RAGE null vs. Diabetic ApoE null mice Negative	Diabetic ApoE null / RAGE null vs. Diabetic ApoE null mice Negative NOT Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice Positive
Anxa3	Acbd3	Anxa3	Chordc1	Anxa3	Acbd3
Chordc1	Anapc1	Chordc1	Crem	Ctps	Anapc1
Crem	Anln	Crem	Cyp26b1	Eef1e1	Anln
Ctps	Arf3	Ctps	Dnaja1	Emp1	Arf3
Cyp26b1	Arfip1	Cyp26b1	Golt1b	Figf	Arfip1
Dnaja1	Armc8	Dnaja1	Hsp110	Fn1	Armc8
Eef1e1	Armcx3	Eef1e1	Hspa1b	Hexim1	Armcx3
Emp1	B3galnt2	Emp1	Rybp	Ifitm2	B3galnt2
Figf	Bcl6	Figf	S100a4	Kpna2	Bcl6
Fn1	Bdh1	Fn1	Slc7a1	Kras	Bdh1
Golt1b	Bnip2	Golt1b	Thbs1	Lmnb2	Bnip2
Hexim1	Btaf1	Hexim1	Tparl	Mtmr4	Btaf1
Hsp110	Bxdc2	Hsp110	Tshz3	Pvt1	Bxdc2
Hspa1b	Bysl	Hspa1b	Tspan6	Rbm8a	Bysl
Ifitm2	C1galt1	Ifitm2		Reln	C1galt1
Kpna2	C1qtnf2	Kpna2		Sfpq	C1qtnf2
Kras	Cacna2d1	Kras		Sfrs3	Cacna2d1
Lmnb2	Cav3	Lmnb2		Tm4sf1	Cav3
Mtmr4	Cbx5	Mtmr4		Ube1l2	Cbx5
Pvt1	Cdr2	Pvt1		Wwc2	Cdr2
Rbm8a	Chordc1	Rbm8a			Chrna1
Reln	Chrna1	Reln			Chsy1
Rybp	Chsy1	Rybp			Ckap4
S100a4	Ckap4	S100a4			Cnn3
Sfpq	Cnn3	Sfpq			Col5a2
Sfrs3	Col5a2	Sfrs3			Copz2
Slc7a1	Copz2	Slc7a1			Creb3l2

Thbs1
Tm4sf1
Tparl
Tshz3
Tspan6
Ube1l2
Wwc2

Creb3l2
Crem
Crispld1
Cthrc1
Cyp26b1
Dap
Dapk2
Dgkg
Dnaja1
Dock7
Dscr1l1
Dusp12
Dynll1
Efhc2
Eln
Emb
Emp2
Emp3
Enah
Endod1
Ereg
Ero1l
Ext1
Fgf1
Fjx1
Fkbp14
Fryl
Gal3st4
Ggh
Gm347
Gm70
Gmds
Gne
Golt1b
Gpr125
Gpr177
Hbegf
Hcfc2
Hdac9
Hdlbp
Hisppd2a

Thbs1
Tm4sf1
Tparl
Tshz3
Tspan6
Ube1l2
Wwc2

Acbd3
Anapc1
Anln
Arf3
Arfip1
Armc8
Armcx3
B3galnt2
Bcl6
Bdh1
Bnip2
Btaf1
Bxdc2
Bysl
C1galt1
C1qtnf2
Cacna2d1
Cav3
Cbx5
Cdr2
Chrna1
Chsy1
Ckap4
Cnn3
Col5a2
Copz2
Creb3l2
Crispld1
Cthrc1
Dap
Dapk2
Dgkg
Dock7

Crispld1
Cthrc1
Dap
Dapk2
Dgkg
Dock7
Dscr1l1
Dusp12
Dynll1
Efhc2
Eln
Emb
Emp2
Emp3
Enah
Endod1
Ereg
Ero1l
Ext1
Fgf1
Fjx1
Fkbp14
Fryl
Gal3st4
Ggh
Gm347
Gm70
Gmds
Gne
Gpr125
Gpr177
Hbegf
Hcfc2
Hdac9
Hdlbp
Hisppd2a
Hrasls
Hrb
Hspa1a
Hspb2
Htra1

Hrasls
Hrb
Hsp110
Hspa1a
Hspa1b
Hspb2
Htra1
Il17b
Itga9
Itgb1bp1
Itpr1
Kcnab1
Kdelr2
Kdelr3
Kpna1
Ky
Lancl3
Lasp1
Lats2
Lbh
Leprel1
Lox
Lpp
Lrrc61
Lrrfip1
Ltbp1
Luzp1
Maged2
Mapk6
Mfap5
Mgat5
Mobk1b
Mtdh
Myh10
Ndel1
Nedd9
Nhlrc2
Nrk
Ntf3
Olfml2b
P4ha1

Dscr1l1
Dusp12
Dynll1
Efhc2
Eln
Emb
Emp2
Emp3
Enah
Endod1
Ereg
Ero1l
Ext1
Fgf1
Fjx1
Fkbp14
Fryl
Gal3st4
Ggh
Gm347
Gm70
Gmds
Gne
Gpr125
Gpr177
Hbegf
Hcfc2
Hdac9
Hdlbp
Hisppd2a
Hrasls
Hrb
Hspa1a
Hspb2
Htra1
Il17b
Itga9
Itgb1bp1
Itpr1
Kcnab1
Kdelr2

Il17b
Itga9
Itgb1bp1
Itpr1
Kcnab1
Kdelr2
Kdelr3
Kpna1
Ky
Lancl3
Lasp1
Lats2
Lbh
Leprel1
Lox
Lpp
Lrrc61
Lrrfip1
Ltbp1
Luzp1
Maged2
Mapk6
Mfap5
Mgat5
Mobk1b
Mtdh
Myh10
Ndel1
Nedd9
Nhlrc2
Nrk
Ntf3
Olfml2b
P4ha1
Pank2
Pcgf5
Pdgfd
Pdgfrl
Pdlim1
Pdlim5
Pgcp

Pank2
Pcgf5
Pdgfd
Pdgfrl
Pdlim1
Pdlim5
Pgcp
Phtf2
Pigm
Pip5k1a
Plaur
Plekha1
Plod2
Pols
Psip1
Ptprz1
Pycr1
Rab23
Rab31
Rabep1
Ramp1
Rarres2
Rassf8
Rbbp9
Reck
Rnd1
Rock1
Rybp
S100a4
Sacs
Scx
Sec22l1
Sec23a
Sec24a
Sema3c
Serpine1
Sfrp2
Sgcb
Sgce
Sgcg
Sh3bgr

Kdelr3
Kpna1
Ky
Lancl3
Lasp1
Lats2
Lbh
Leprel1
Lox
Lpp
Lrrc61
Lrrfip1
Ltbp1
Luzp1
Maged2
Mapk6
Mfap5
Mgat5
Mobk1b
Mtdh
Myh10
Ndel1
Nedd9
Nhlrc2
Nrk
Ntf3
Olfml2b
P4ha1
Pank2
Pcgf5
Pdgfd
Pdgfrl
Pdlim1
Pdlim5
Pgcp
Phtf2
Pigm
Pip5k1a
Plaur
Plekha1
Plod2

Phtf2
Pigm
Pip5k1a
Plaur
Plekha1
Plod2
Pols
Psip1
Ptprz1
Pycr1
Rab23
Rab31
Rabep1
Ramp1
Rarres2
Rassf8
Rbbp9
Reck
Rnd1
Rock1
Sacs
Scx
Sec22l1
Sec23a
Sec24a
Sema3c
Serpine1
Sfrp2
Sgcb
Sgce
Sgcg
Sh3bgr
Six5
Slc9a2
Smurf2
Srm
Srprb
Stch
Stk25
Stk38l
Stt3a

Six5
Slc7a1
Slc9a2
Smurf2
Srm
Srprb
Stch
Stk25
Stk38l
Stt3a
Sulf1
Surb7
Sync
Tdrd3
Tgfb2
Thbs1
Tmem39a
Tmem45a
Tmem68
Tmtc3
Tnfaip1
Tnfrsf11a
Tnfrsf12a
Tnrc15
Tparl
Tshz3
Tspan2
Tspan6
Unc5d
Vkorc1
Wif1
Wisp2
Wtip
Yipf5
Zbtb41
Zcchc10
Zfp148
Zfp451
Zfp9

Pols
Psip1
Ptprz1
Pycr1
Rab23
Rab31
Rabep1
Ramp1
Rarres2
Rassf8
Rbbp9
Reck
Rnd1
Rock1
Sacs
Scx
Sec22l1
Sec23a
Sec24a
Sema3c
Serpine1
Sfrp2
Sgcb
Sgce
Sgcg
Sh3bgr
Six5
Slc9a2
Smurf2
Srm
Srprb
Stch
Stk25
Stk38l
Stt3a
Sulf1
Surb7
Sync
Tdrd3
Tgfb2
Tmem39a

Sulf1
Surb7
Sync
Tdrd3
Tgfb2
Tmem39a
Tmem45a
Tmem68
Tmtc3
Tnfaip1
Tnfrsf11a
Tnfrsf12a
Tnrc15
Tspan2
Unc5d
Vkorc1
Wif1
Wisp2
Wtip
Yipf5
Zbtb41
Zcchc10
Zfp148
Zfp451
Zfp9

Tmem45a
Tmem68
Tmtc3
Tnfaip1
Tnfrsf11a
Tnfrsf12a
Tnrc15
Tspan2
Unc5d
Vkorc1
Wif1
Wisp2
Wtip
Yipf5
Zbtb41
Zcchc10
Zfp148
Zfp451
Zfp9

Online Table XVII.

Differentially Expressed Genes with Unique Entrez Gene Symbols for Diabetic ApoE null vs. Non-Diabetic ApoE null mice with Negative log Fold Change, and for Diabetic ApoE null/RAGE null vs. Diabetic ApoE null mice with Positive log Fold Change and their Boolean Subsets

Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice Negative	Diabetic ApoE null / RAGE null vs. Diabetic ApoE null mice Positive	Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice Negative UNION Diabetic ApoE null / RAGE null vs. Diabetic ApoE null mice Positive	Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice Negative INTERSECTION Diabetic ApoE null / RAGE null vs. Diabetic ApoE null mice Positive	Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice Negative NOT Diabetic ApoE null / RAGE null vs. Diabetic ApoE null mice Positive	Diabetic ApoE null / RAGE null vs. Diabetic ApoE null mice Positive NOT Diabetic ApoE null mice vs. Non-Diabetic ApoE null mice Negative
Aacs	Acot1	Aacs	Erdr1	Aacs	Acot1
Acaca	Atp6v1d	Acaca		Acaca	Atp6v1d
Acacb	Bcas3	Acacb		Acacb	Bcas3
Acly	Ccrn4l	Acly		Acly	Ccrn4l
Acss2	Chd1	Acss2		Acss2	Chd1
Agbl3	Chd2	Agbl3		Agbl3	Chd2
Erdr1	Eml5	Erdr1		Fasn	Eml5
Fasn	Erdr1	Fasn		Fmo5	Glo1
Fmo5	Glo1	Fmo5		H2-Q10	Glp1r
H2-Q10	Glp1r	H2-Q10		Mod1	Gpatc2
Mod1	Gpatc2	Mod1		Mtmr11	Grina
Mtmr11	Grina	Mtmr11		Nudt18	H6pd
Nudt18	H6pd	Nudt18		Ppp2r1b	Mrpl15
Ppp2r1b	Mrpl15	Ppp2r1b		Pygl	Ngp
Pygl	Ngp	Pygl		Slc1a5	Pbef1
Slc1a5	Pbef1	Slc1a5		Slc25a1	Prlr
Slc25a1	Prlr	Slc25a1		Thrsp	Prodh
Thrsp	Prodh	Thrsp		Tkt	Sgol2
Tkt	Sgol2	Tkt			Sh3gl2
	Sh3gl2	Acot1			Sorbs1
	Sorbs1	Atp6v1d			Sord
	Sord	Bcas3			St8sia6
	St8sia6	Ccrn4l			Timp4
	Timp4	Chd1			Trp53inp2
	Trp53inp2	Chd2			Ube2i
	Ube2i	Eml5			Xdh
	Xdh	Glo1			
		Glp1r			
		Gpatc2			

Grina
H6pd
Mrpl15
Ngp
Pbef1
Prlr
Prodh
Sgol2
Sh3gl2
Sorbs1
Sord
St8sia6
Timp4
Trp53inp2
Ube2i
Xdh