

Supplementary Material

Methods

Animals and ethics statement

Human IL-32 α -expressing transgenic (hIL-32 α -Tg) mice on a C57BL/6 background[1] (Disease Animal Model Research Center, Korea Research Institute of Bioscience and Biotechnology, Daejeon, Korea) were crossed with ApoE $^{-/-}$ mice (B6.129P2-*Apoe*^{tm1Unc}/J, Jackson Laboratory, Bar Harbor, ME, USA) to generate ApoE $^{-/-}$ /hIL-32 α -Tg mice. All genotyping was performed by polymerase chain reaction (PCR) amplification of tail-tip DNA to identify hIL-32 α -Tg and ApoE $^{-/-}$ /hIL-32 α -Tg mice with primers generating a 450-bp amplicon in Tg mice (primer 1: 5'-GAAGGT CCTCTCTGATGACA-3', primer 2: 5'-GGGGTTCAGAGCACTTCT-3'). The ApoE null and wild-type alleles were detected by PCR amplification using a set of 3 primers (primer 1: 5'-GCCTAGCCGAGGGAGAGCCG-3', primer 2: 5'-TGTGACTTGGGAGCTCTGCAGC-3', primer 3: 5'-GCCGCCCGACTGCATCT-3') that amplify a 155 bp wild-type band and a 245 bp targeted (null) band. All experiments were performed with littermate controls. This study was carried out in strict accordance with the Guide for the Care and Use of Laboratory Animals of Chungbuk National University (Cheongju, Chungbuk, Korea). All animal protocols were reviewed and approved by the Chungbuk National University Institutional Animal Care and Use Committee and compiled with the Korean National Institute of Health Guide for the Care and Use of Laboratory Animals (CBNUA-792-15-01).

Mouse partial carotid ligation surgery

Male mice were fed *ad libitum* with standard chow diet until surgery at 8–9 weeks of age. Animals were anaesthetized with 3.5% isoflurane initially; this dose was then reduced to 1.5–2% during the entire procedure while the mice were subjected to partial ligation of the left carotid artery (LCA). The LCA bifurcation was exposed by blunt dissection and 3 of 4 caudal LCA branches (the left external carotid, internal carotid, and occipital arteries) were ligated with 6-0 silk sutures, leaving the superior thyroid artery intact. The contralateral right carotid artery (RCA) was left intact as an internal control. Following surgery, analgesic buprenorphine (0.1 mg kg $^{-1}$) was administrated. The RCA and LCA were isolated at the indicated experimental end-points.

Microarray procedures

Endothelial-enriched total carotid intimal RNAs were separately obtained from the LCA and RCA of hIL-32 α -Tg and non-Tg mice after partial ligation as described previously[2]. At 48 h after partial ligation, intimal RNA samples from the carotid arteries of 4 mice were pooled to obtain ~50 ng of total RNA as 1 array sample, yielding 3 array samples from 12 mice per group. All RNA samples used for the DNA microarray study passed an initial quality control test by a BioAnalyzer 2100 instrument (Agilent Technologies, Santa Clara, CA, USA) and each sample was linearly amplified, as we described previously[3]. Each sample was then used for microarray studies using GeneChip® Mouse Gene 2.0 ST arrays (Affymetrix, Santa Clara, CA, USA) at BioCore Co. (Seoul, Korea). After hybridization in a GeneChip® Hybridization Oven 645 (Affymetrix), washing and staining steps proceeded in a GeneChip® Fluidics Station 450 (Affymetrix), and then the GeneChip® arrays were scanned on a GeneChip® 3000 7G

scanner (Affymetrix) to determine the probe fluorescence intensity. The raw probe intensities were then normalized by the quantile normalization algorithm[4].

Microarray data analysis and bioinformatics

The normalized microarray data were statistically analyzed by GeneSpring GX 13.0 software (Agilent Technologies). The differentially expressed genes between LCA and RCA that showed more than 2.0-fold changes at *p*-values of less than 0.05 by 1-way analysis of variance were identified. The lists of differentially expressed genes were interrogated for statistically significant overrepresented cellular functions and disorders using the Cluster 3.0, TreeView, DAVID, KEGG pathway, and GeneSpring GX 13.0 software programs.

Comparative network analysis and functional annotation

We constructed co-expression networks using microarray data obtained by analysis of the LCAs of hIL-32 α -Tg and non-Tg mice as well as publicly available microarray data from TNF- α treated HUVEC samples with and without exposure to apple OPC (dp3.9 apple procyanidin extract)[5]. The microarray data (GSE9647) from this study were downloaded from the GEO database (<http://www.ncbi.nlm.nih.gov/geo/>). The normalized microarray data were used to generate gene co-expression networks using WGCNA[6]. DAVID (<http://david.abcc.ncifcrf.gov/home.jsp>) was used to identify the biological processes that were significantly enriched in the genes included in the co-expression modules[7]. *p*-values < 0.05 were considered significant.

Quantitative real-time PCR

Total RNA was collected from mouse carotid endothelium or EC cultures in 700 μ L of QIAzol® and purified using the miRNeasy Mini Kit (Qiagen GmbH, Hilden, Germany) according to the manufacturer's protocol. Total RNA was reverse transcribed into complementary DNA (cDNA) using a High Capacity RNA-to-cDNA kit (Applied Biosystems, Foster City, CA), and then subjected to quantitative real-time PCR (qPCR) using QuantiFast® SYBR® Green PCR master mix (Qiagen) with custom-designed specific primers using 18S as house-keeping control on a StepOnePlus™ Real-Time PCR System (Applied Biosystems). Primer sequences can be found in Supplementary Table 9. For the detection of miRNA, cDNA was prepared in a reverse transcription reaction using a miScript II RT Kit (Qiagen). Mature miRNA expression was determined using a miRNA-specific miScript Primer Assay and a miScript SYBR® Green PCR Kit (Qiagen) on a StepOnePlus™ Real-Time PCR System (Applied Biosystems). Specific mature and pre-mature-miRNA primers were purchased from Qiagen. Relative fold-changes in target gene expression were calculated using *Rnub6B* as an internal control. The qPCR experiments were performed as described previously[8, 9]. The fold change between groups was determined for all targets using the $2^{\Delta\Delta Ct}$ method.

Dual-luciferase activity assay

Measurement of firefly luciferase activity was obtained at RT using the Luc-Pair miR Luciferase Assay Kit (GeneCopoeia, Rockville, MD, USA) and a luminometer (1420 Luminescence Counter, PerkinElmer, Waltham, MA, USA) as recently described[8]. Standard 3'-untranslated region (UTR) luciferase assays were performed to validate *in silico* target predictions. Dual-luciferase reporter constructs containing the Timp3 3'UTR containing a miR-205-binding site (5'- UGG AAG G-3') and Reck 3'UTR with miR-205 binding site (5'- AUG AAG G-3') (kindly provided by Dr. Hanjoong Jo of Georgia Institute of Technology and Emory University, Atlanta, GA, USA) or Timp3 3'UTR with mutated miR-205-binding site (5'- GAU

UCA AGG AAA GUC GGU U-3') and Reck 3'UTR with mutated miR-205-binding site (5'- GUC GGU U-3') (custom cloned at Cosmogenetech Co., Seoul, Korea) were transfected into iMAECs using a Nucleofection Kit (Lonza, Walkersville, MD, USA) and were allowed to recover for 24 h. The second transfection was performed using increasing concentrations of miR-205 mimic (*mirVana*TM, Ambion, Foster City, CA, USA) and control-miR (Ambion) with the Lipofectamine[®] RNAiMAX transfection reagent (ThermoFisher Scientific, Waltham, MA, USA). Firefly and *Renilla* luciferase activities were measured using a Luciferase assay system (Promega, Madison, WI, USA) as per manufacturer recommendation.

Arterial wall thickening and atherosclerotic plaque formation assessment

For studies on arterial wall thickening, animals were sacrificed by CO₂ gas inhalation, then aorta and carotid arteries from partial carotid-ligated hIL-32α-Tg and littermate non-Tg mice fed a high-fat diet for 4 weeks were carefully excised and the surrounding fat tissue was removed by dissection. Aortas and carotid arteries were photographed using a digital microscope device (ToupCam TPH02000A, ToupTek, Hangzhou, China) with a scale bar for reference. LCA and RCA tissues were embedded in Tissue-Tek[®] optimal cutting temperature compound (Sakura Finetek, Torrance, CA, USA), and cryosections (7-μm) were prepared as previously described[8]. Sections were stained with hematoxylin and eosin, then micrographs were taken using a light microscope (Axio Imager A2, Carl Zeiss, Oberkochen, Germany) at 10× magnification and images were analyzed using NIH ImageJ software. Lesion size (cross-sectional areas; intima-media area) and wall thickness (intima media thickness) were calculated using three sections from each LCA segment as described previously[10].

For studies of atherosclerotic plaque formation, aorta and carotid arteries from partial carotid-ligated ApoE^{-/-}/hIL-32α-Tg, littermate ApoE^{-/-}, and recombinant human IL-32α protein (rhIL-32α; R&D systems, 1 μg/mouse, administered intraperitoneally every 2 days)-injected ApoE^{-/-} mice fed a high-fat diet [11] for 2 weeks were carefully excised, and the surrounding fat tissue was removed by dissection. The RCA and LCA were photographed using a digital microscope device (ToupCam TPH02000A) as described above, and the opaque area covered by plaque and total artery area of LCA were quantified using NIH ImageJ software as described previously[8]. To visualize atherosclerotic plaques, oil red O staining of tissue sections (7-μm thick) was carried out, then micrographs were taken with a light microscope at 10× magnification and images were analyzed using NIH ImageJ software. The atherosclerotic lesion area and plaque size were calculated as described previously[8].

Immunohistochemical and Immunofluorescence staining

Cryosections were fixed in a 1:1 mixture of methanol/acetone for 5 min at -20 °C and then blocked (1 h, at room temperature) using 10% (v/v) donkey serum in phosphate-buffered saline (PBS). Immunohistochemical staining was carried out using the following antibodies: IL-32 (KU-32-52, 1:100), α-SMA (Abcam, Cambridge, UK, 1:200), CD31 (Abcam, 1:100), VCAM-1 (BD Biosciences, Franklin Lakes, NJ, USA, 1:50), ICAM-1 (Santa Cruz Biotechnology, Dallas, TX, USA, 1:100), MOMA2 (Abcam, 1: 100), TIMP3 (Abcam, 1:50), and (Cell Signaling Technology, Danvers, MA, USA, 1:100) overnight at 4 °C. The sections were incubated with biotinylated secondary antibodies for 2 h at room temperature. After washing in PBS, the immunocomplex was visualized using 3,3'-diaminobenzidine solution (2 mg/10 mL) containing 0.08% (v/v) hydrogen peroxide in PBS. Sections were dehydrated in a series of graded alcohols, cleared in xylene, and mounted with coverslips using PermountTM (Fisher Scientific, Suwanee, GA, USA).

Immunohistological images were acquired using a light microscope (Axio Imager A2, Carl Zeiss).

For immunofluorescence analysis, all sections were incubated with primary antibodies (VCAM-1 and ICAM-1 from Santa Cruz Biotechnology used at 1:200 dilution; CD31 from Abcam at 1:500) overnight at 4 °C, followed by staining with Alexa Flour 568-conjugated donkey anti-goat secondary antibody (Invitrogen, Carlsbad, CA, USA, 1:300) for VCAM-1 and ICAM-1. Alexa Flour 680-conjugated donkey anti-rat secondary antibody (Invitrogen, 1:300) was used for CD31. Nuclei were counterstained with DAPI and mounted with coverslips using an anti-fade fluorescent mounting media (DAKO, Santa Clara, CA, USA). Samples were imaged using Zeiss LSM 710 confocal microscope (Carl Zeiss).

ECs and VSMCs culture and treatment with siRNAs and miRNA mimic

Human umbilical vein endothelial cells (HUVECs; Lonza) were cultured and maintained as described previously[12]. Immortalized mouse aortic ECs (iMAECs) were generated from C57BL/6 mice as previously described[13]. Primary mouse arterial VSMCs were isolated from the thoracic aorta of hIL-32α-Tg mice and their littermate control (non-Tg) mice, and maintained as described previously[14]. Timp3, Reck, Dgcr8, Drosha, Dicer1, and Rprd2 siRNAs (Stealth RNAi™, ThermoFisher Scientific) or miR-205 mimic (Ambion) were transfected into cells using Lipofectamine® RNAiMAX transfection reagent (ThermoFisher Scientific) in normal culture medium, following the manufacturer's protocol.

Transient expression of hIL-32α in ECs

For the examination of gene expression and tests of cell functions *in vitro*, iMAECs or HUVECs were transiently transfected with the pcDNA3.1⁺-6×Myc-hIL-32α vector or a control vector using Lipofectamine® 3000 (Life Technologies, Carlsbad, CA, USA), following the manufacturer's protocol as described previously[15].

Smooth muscle cell proliferation and migration assay

VSMCs isolated from hIL-32α-Tg or non-Tg mice were used. Cells were seeded in a 96-well plate at a density of 5×10^3 cells/mL in Dulbecco's modified Eagle's medium for 24 h, and then transfected with siRNAs, miR-205 mimic, or rhIL-32α for 24 h before starving in serum-free medium for 24 h. The transfected cells were stimulated with 25 ng/mL of platelet-derived growth factor (PDGF)-BB (PeproTech, Rocky Hill, NJ, USA) for 24 h, and cell proliferation was determined using a BrdU cell proliferation assay kit (BioVision, Milpitas, CA, USA) according to the manufacturer's instructions. Briefly, cells were pulsed with BrdU for 2 h after 20 h PDGF-BB stimulation. ELISAs were performed using antibody for BrdU and the absorbance was measured by a plate reader at 450 nm. BrdU incorporation was calculated as the percentage of BrdU incorporated with respect to the untreated serum-free control. To determine migration, VSMCs were seeded in a μ-Dish with culture inserts (ibidi, Martinsried, Germany) and then maintained in serum-free media for 24 h before performing the migration assays. VSMCs were stimulated with PDGF-BB (25 ng/mL), and then cell migration was monitored for 24 h by taking a picture every 3 h. The area of the migrated cells was quantified using NIH ImageJ software.

Preparation of whole-cell lysates and immunoblotting

Following treatment, cells were washed 3 times with ice-cold PBS and lysed with radioimmunoprecipitation (RIPA) assay buffer. The protein content of each sample was determined using a DC assay kit (Bio-Rad, Hercules, CA, USA). Aliquots of cell lysates were resolved by 10% SDS-PAGE

and subsequently transferred to a polyvinylidene difluoride membrane (EMD Millipore, Billerica, MA, USA). The membrane was incubated with the following antibodies: Myc (Abcam; 1:1,000), IL-32 (KU-32-52; BioLegend, San Diego, CA, USA, 1:1,000), VCAM-1 (Santa Cruz Biotechnology; 1:500), ICAM-1 (Santa Cruz Biotechnology, 1:500), PCNA (Cell Signaling Technology; 1:500), p21 (Santa Cruz Biotechnology; 1:500), phospho-ERK1/2 (Cell Signaling Technology; 1:500), total-ERK1/2 (Cell Signaling Technology; 1:500), Timp3 (Abcam; 1:1,000), and Reck (Cell Signaling Technology; 1:1,000) overnight at 4 °C, followed by secondary antibody (1:2,000) for 1 h at room temperature. Immunoreactive bands were then detected by chemiluminescence. Full-sized scans of all western blots are provided in Supplementary Figs. 14–16.

Monocyte-EC adhesion assay

Following the transfection of iMAECs or HUVECs with hIL-32 α -expressing vector, siRNAs, or miR-205 mimic, or treatment with rhIL-32 α for 24 h, the cells were treated with TNF α (10 ng/mL) for 24 h, and a monocyte-EC binding assay was performed using fluorescently labeled THP-1 cells as described previously[16]. Adherent cells were quantified by fluorescence microscopy[12].

Enzyme-linked immunosorbent assay (ELISA)

Human IL-32 α (hIL-32 α) was transiently expressed in iMAECs as described above. Cells were then transfected with siRNAs for Timp3 or Reck or combination (final concentration, 100 nM) for 24 h, then starved in serum-free medium for 24 h and stimulated with 25 ng/mL of platelet-derived growth factor (PDGF)-BB for 24 h, then stimulated with IL-1 β (10 ng/mL) for 24 h. Soluble-TNF α or IL-10 in conditioned culture medium was measured using mouse soluble-TNF α or IL-10 ELISA kits (R&D Systems, Minneapolis, MN, USA) following the manufacturer's protocol.

In situ zymography

To measure the activity of MMPs in mouse carotid frozen sections, *in situ* zymography was performed in unfixed sections (30- μ m thick) using DQTM-gelatin substrate (Molecular Probes, Eugene, OR, USA) as described previously[8, 9]. DQTM-gelatin was dissolved in a concentration of 1 mg/mL in water and then diluted 1:10 in reaction buffer according to the manufacturer's protocol. The mixture (50 μ L) was put on top of the sections and incubated for 6 h at room temperature. Proteolytic activity was detected as green fluorescence (530 nm) by fluorescence microscopy.

MMP activity analysis

A cell-based ELISA using the DQTM-gelatin assay was employed to assess MMP activity as described previously[9]. VSMCs from non-Tg and hIL-32 α -Tg mice aorta were seeded in a 96-well plate and treated with PDGF-BB (25 ng/mL) in serum-free medium for 24 h, then DQTM-gelatin (100 μ g/mL) was added and incubated for 12 h. Product formation was determined by excitation 495 nm and emission at 515 nm (SpectraMax[®] Gemini EM Fluorescence Microplate Reader; Molecular Devices, Sunnyvale, CA, USA).

Gelatin zymography

For *in vitro* gelatinolytic activity of MMP-2 or MMP-9 assay, a gelatin zymography assay using the SDS-acrylamide gels containing 0.1% gelatin was employed. VSMCs from non-Tg and hIL-32 α -Tg mice aorta were cultured in 6-well plate to 90% confluence. Cells were then washed with phosphate-buffered saline

(PBS), and incubated with serum-free culture medium with or without PDGF-BB (25 ng/mL) for 24 h. Conditioned culture medium was then collected and their gelatinolytic activity was measured by gelatin zymography as described previously[17]. Gels were washed in renaturing buffer for 30 min, and at least 24 h in developing buffer at 37°C. Gels were staining with 0.5% (w/v) Coomassie brilliant blue R-250 solution for 30 min at room temperature, and destained with a destaining solution (methanol/acetic acid/water, 50/10/40, v/v) MMP activity in the gel was detected as white bands against a dark blue background. Band intensity was quantified using NIH ImageJ software. A full-sized scan of the gel is provided in Supplementary Fig. 17.

In situ ADAMs activity assay

ADAM activity was assessed by detection of a fragment peptide (DPEAAE) produced from the digestion of versican s by immunofluorescence staining. Sections were fixed in cold acetone for 5 min at -20 °C, and incubated with a primary antibody against the versican fragment (Abcam, 1:300) overnight at 4°C, followed by DyLight® 549-conjugated donkey anti-rabbit secondary antibody (Jackson ImmunoResearch, West Grove, PA, USA, 1:250). Nuclei were counterstained with DAPI. Samples were imaged using fluorescence microscopy

Statistical analysis

Statistical analysis was carried out using GraphPad Prism 5.0 (GraphPad Software Inc., La Jolla CA, USA). Pairwise comparisons were performed using 1-way Student's *t*-tests. Data are presented as means ± standard error of the mean (SEM) of the indicated number of experiments. Differences between groups were considered significant at *p* < 0.05.

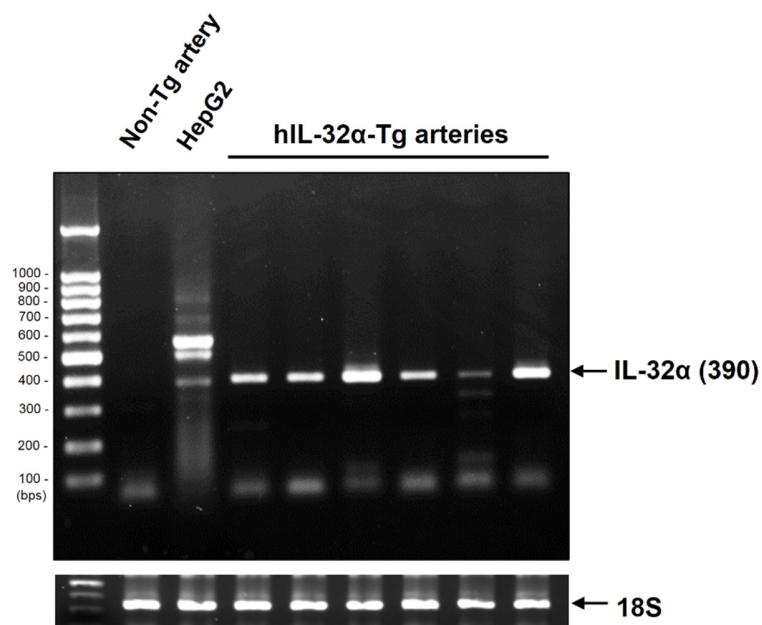
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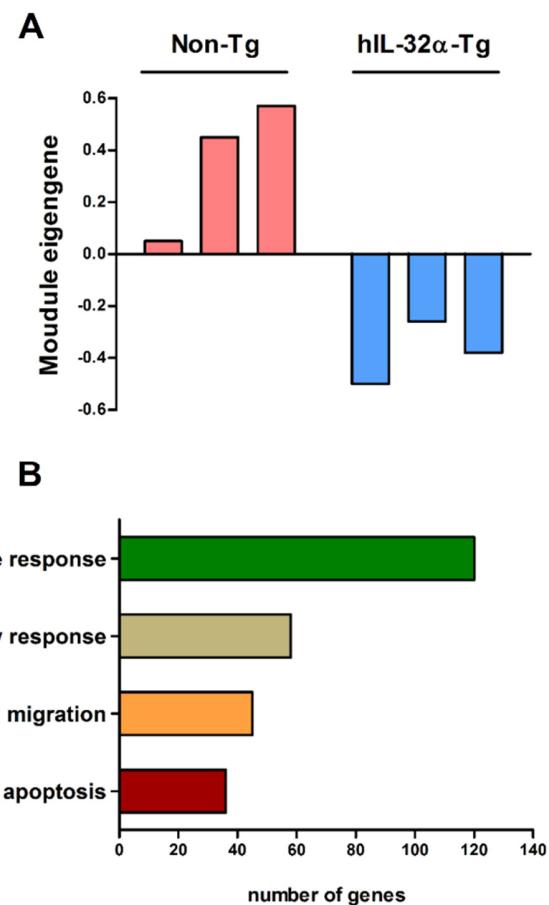
Supplementary Figures and Legends

Supplementary Figure 1.



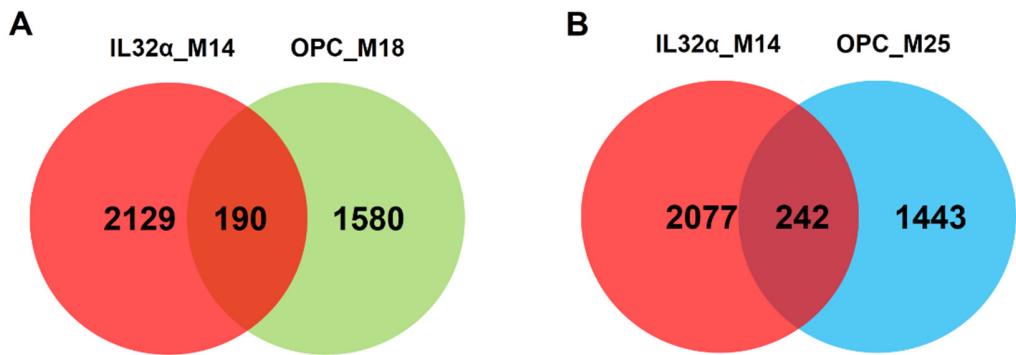
Supplementary Figure 1. Confirmation of hIL-32 α mRNA expression in aorta tissue from hIL-32 α -Tg mice. Total RNA samples were extracted from thoracic and abdominal aorta of hIL-32 α -Tg and non-Tg littermate control mice and analyzed by RT-PCR. Non-Tg littermate control mice aorta tissue and HepG2 cells served as negative and positive controls, respectively.

Supplementary Figure 2.



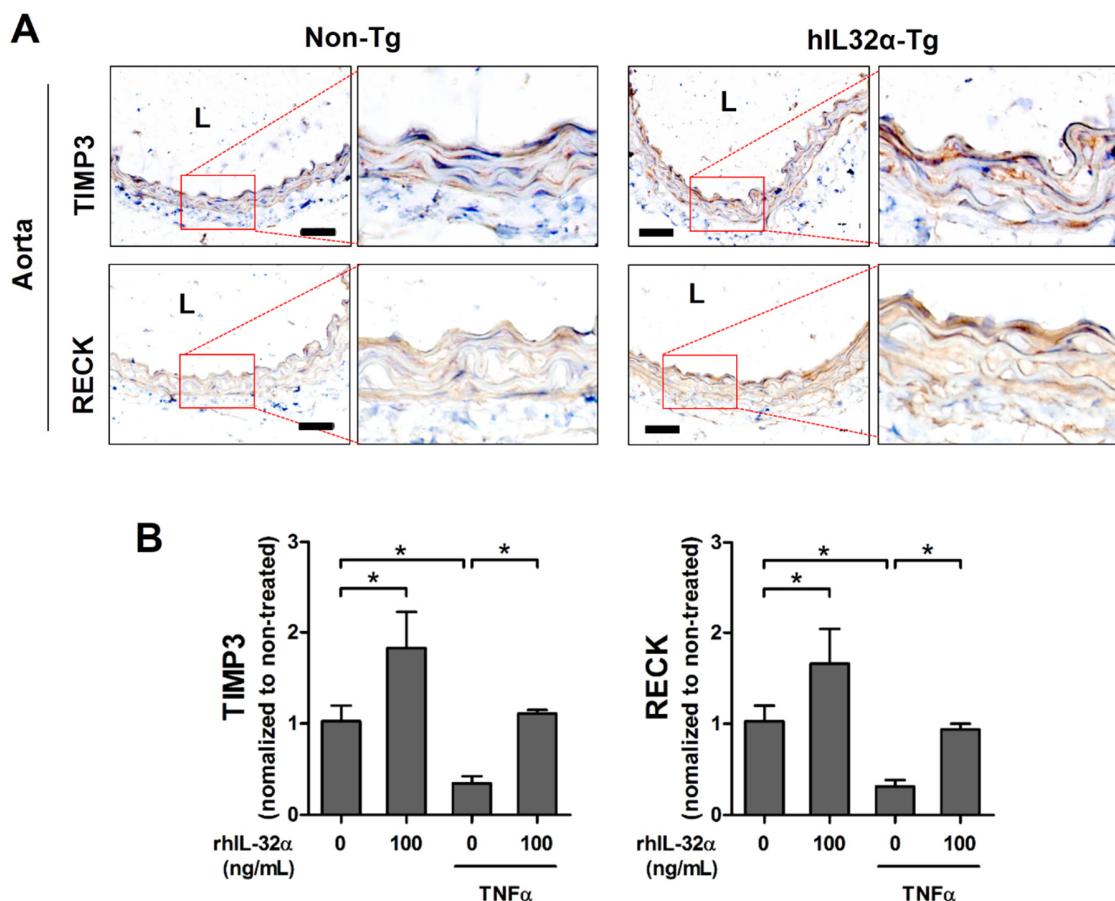
Supplementary Figure 2. Co-expression module associated with hIL-32 α . (A) The eigengene values across samples in the IL-32 α _M14. (B) Major biological processes (gene ontology) significantly enriched in the genes in the co-expression module.

Supplementary Figure 3.



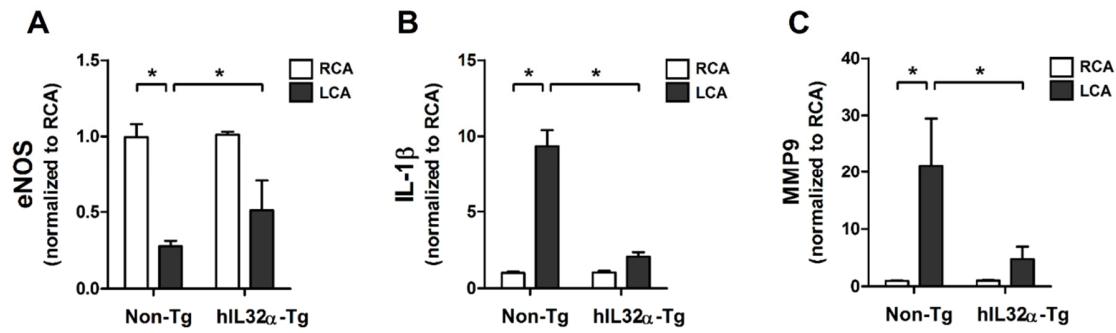
Supplementary Figure 3. Comparative network analysis of the hIL-32 α associated module. (a) Venn diagram showing the number of common and unique genes between the hIL-32 α -associated module IL-32 α _M14 and the two modules, OPC_M18 (A) and OPC_M25 (B), which associated with apple oligomeric procyanidin (OPC) treatment.

Supplementary Figure 4.



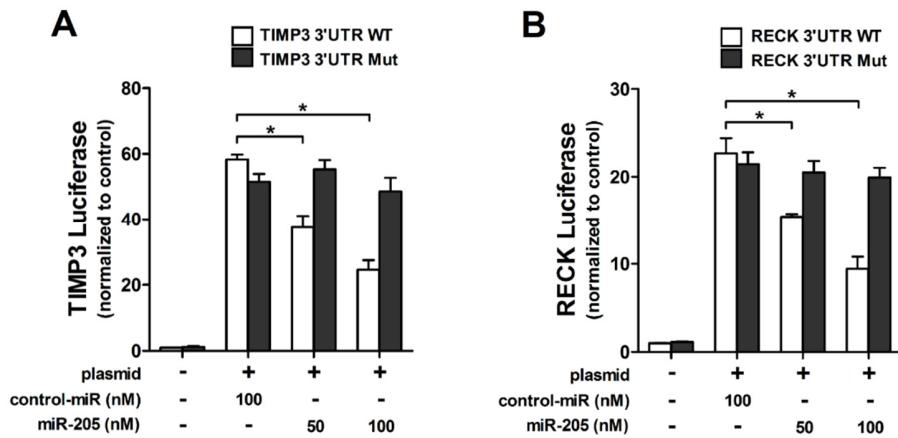
Supplementary Figure 4. Timp3 and Reck expression in the hIL-32 α -Tg mice aorta and hIL-32 α -overexpressing iMAECs. (A) Frozen sections of thoracic aorta tissues from hIL-32 α -Tg and littermate non-Tg control mice were stained with Timp3 and Reck antibodies. Representative microscopy images are shown. The red rectangle indicates the magnified area shown in the lower panel. Nuclei (blue); protein expression (brown). L, lumen. Scale bar, 100 μ m. (B) iMAECs were cultured in a 6-well culture plate for 24 h, then treated with recombinant human IL-32 α protein (rhIL-32 α). After 24 h, cells were treated with tumor necrosis factor α (TNF α) (10 ng/mL; 24 h), and *Timp3* and *Reck* mRNA expression was determined by qPCR (data shown as mean \pm SEM; $n=3$, * $P<0.05$ as determined by Student's *t*-test).

Supplementary Figure 5.



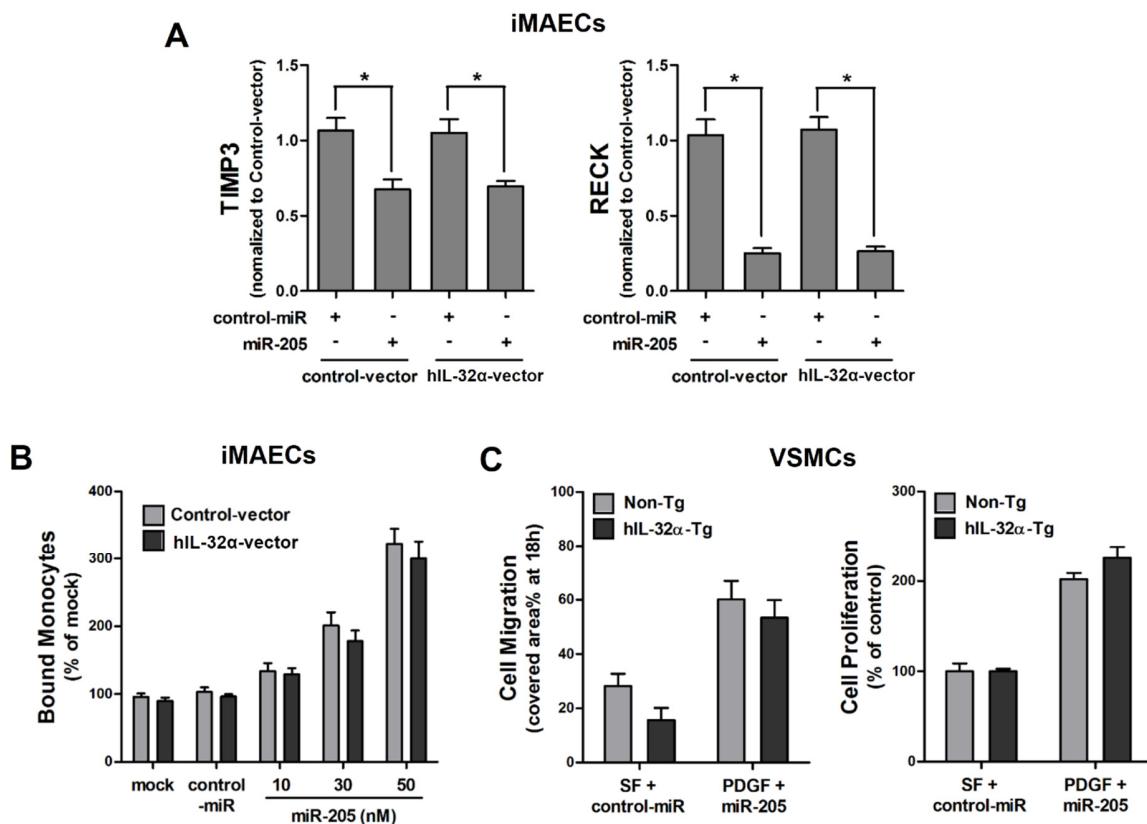
Supplementary Figure 5. eNOS, IL-1 β , and MMP9 expression in the hIL-32 α -Tg mice carotid endothelium. eNOS (*Nos3*) (A), IL-1 β (*Il1b*) (B), and MMP9 (*Mmp9*) (C) mRNA expression was determined by qPCR using endothelial-enriched RNA obtained from left carotid artery (LCA) and right carotid artery (RCA) following partial carotid ligation in hIL-32 α -Tg or non-Tg mice at 2 days post-ligation (data shown as mean \pm SEM; $n = 5$ each, * $P < 0.05$ as determined by Student's *t*-test).

Supplementary Figure 6.



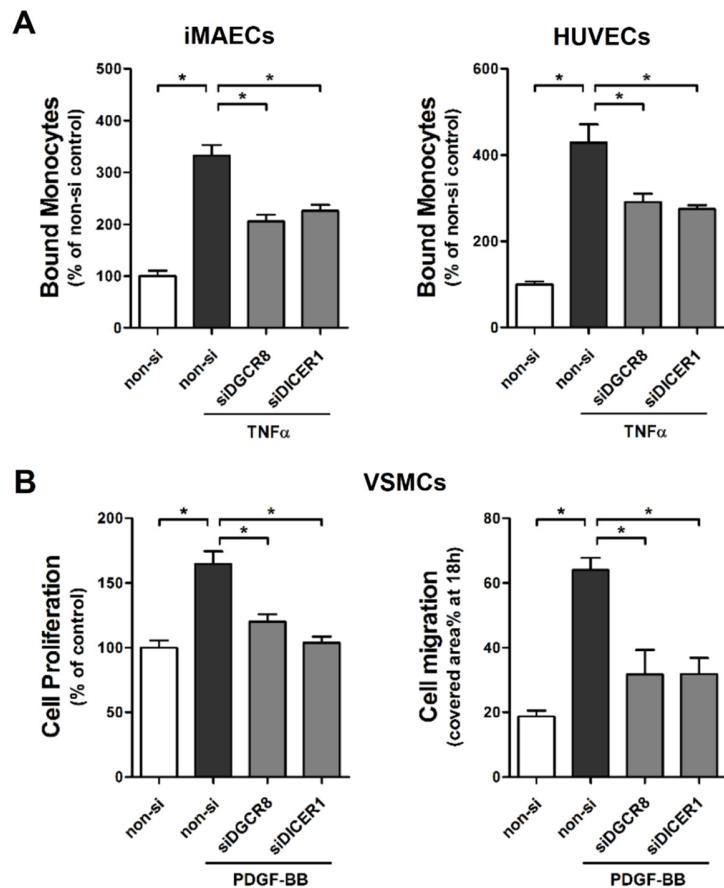
Supplementary Figure 6. miR-205 directly targets Timp3 and Reck. (A) iMAECs were cultured, then transfected with dual-luciferase reporter plasmids containing wild-type (WT) or mutant (Mut) of (A) Timp3-3'UTR and (B) Reck-3'UTR by electroporation. Cells were allowed to recover for 24 h, and treated with mature-miR-205 mimic or control-miR mimic. Firefly luciferase activity (normalized to control *Renilla* luciferase) indicating Timp3 and Reck expression was determined using a Luciferase assay system. ($n = 6$). All data shown as mean \pm SEM, * $P < 0.05$ as determined by Student's *t*-test.

Supplementary Figure 7.



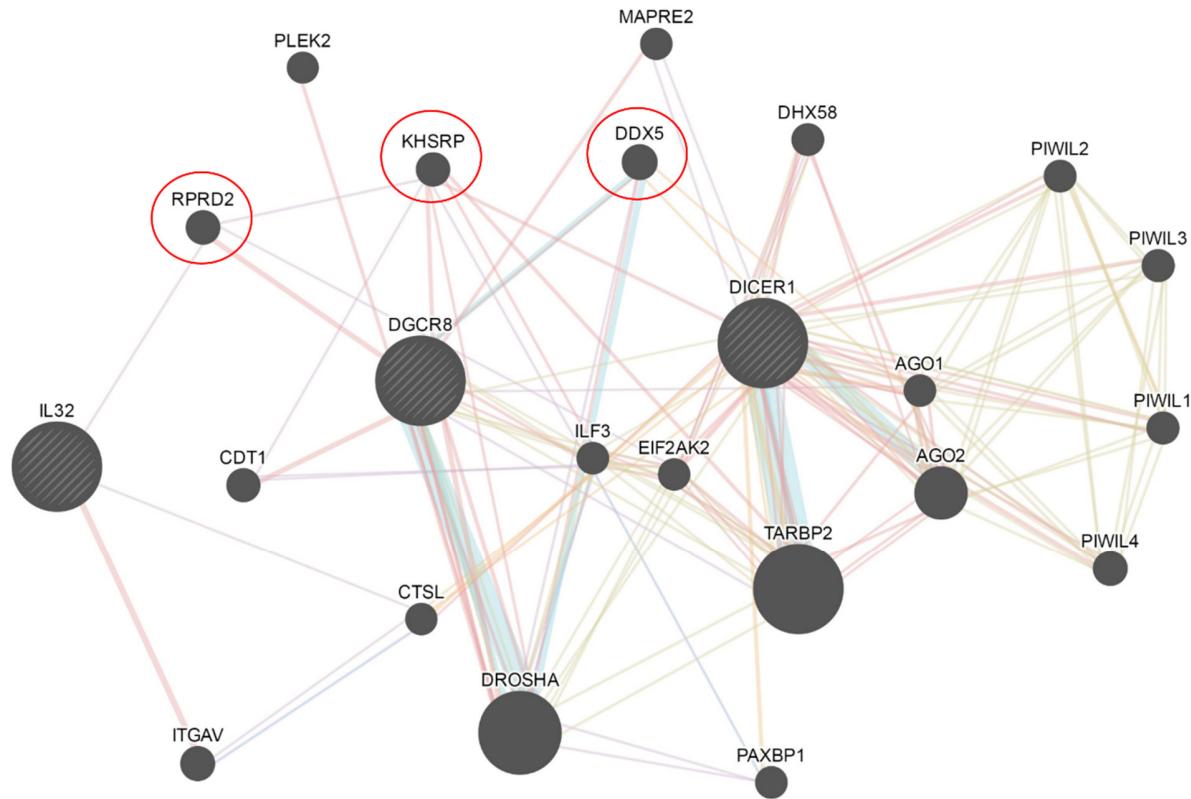
Supplementary Figure 7. hIL-32 α expression does not alter miR-205 biological function. (A) iMAECs were transfected with hIL-32 α -expressing pcDNA3.1⁺-6×Myc or control vector. After 24 h, cells were then transfected with mature-miR-205 mimic (50 nM; 24 h) or control-miR mimic, and *Timp3* and *Reck* mRNA expression was determined by qPCR ($n = 4$). (B) iMAECs were transfected with hIL-32 α or control vector, then treated with mature-miR-205 mimic (10–50 nM; 24 h), and THP-1 monocyte adhesion to iMAECs was determined ($n = 3$). (C) Primary cultured VSMCs from hIL-32 α -Tg or non-Tg mice aorta were transfected with mature-miR-205 mimic (50 nM) or control-miR mimic. Cells were then treated with PDGF-BB (25 ng/mL) in serum-free media, and cell migration ($n = 3$) and cell proliferation ($n = 5$) were determined. All data shown as mean \pm SEM, * $P < 0.05$ as determined by Student's *t*-test.

Supplementary Figure 8.



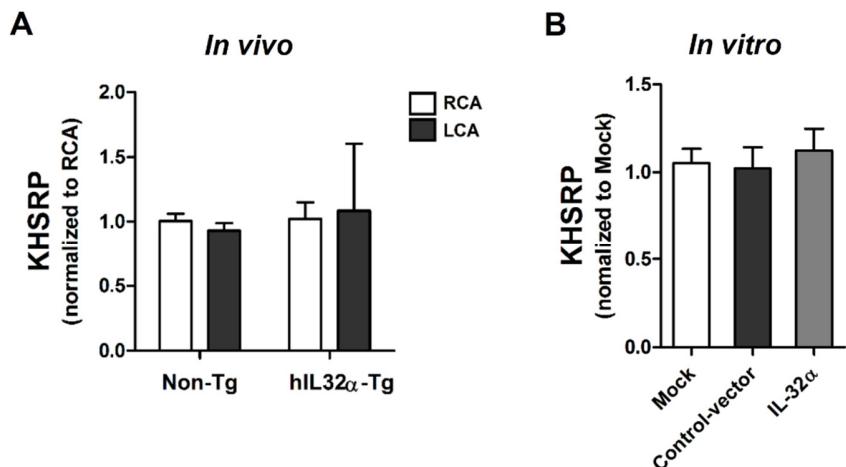
Supplementary Figure 8. Knockdown of Dgcr8 and Dicer1 inhibits EC inflammation and VSMC proliferation and migration. (A) iMAECs and HUVECs were transfected with Dgcr8 and Dicer1 siRNA (siDgcr8 or siDicer1, 150 nM) for 24 h. Cells were then treated with TNF α (10 ng/mL; 24 h), and monocyte-EC adherence was determined ($n = 6$ each). (B) VSMCs isolated from the thoracic aortas of non-Tg mice were transfected with siDgcr8 or siDicer1 (150 nM), then VSMC proliferation and migration were determined by wound healing ($n = 3$) and BrdU incorporation assays ($n = 6$), respectively, as described in the Methods. All data shown as mean \pm SEM, * $p < 0.05$ as determined by Student's t -test.

Supplementary Figure 9.



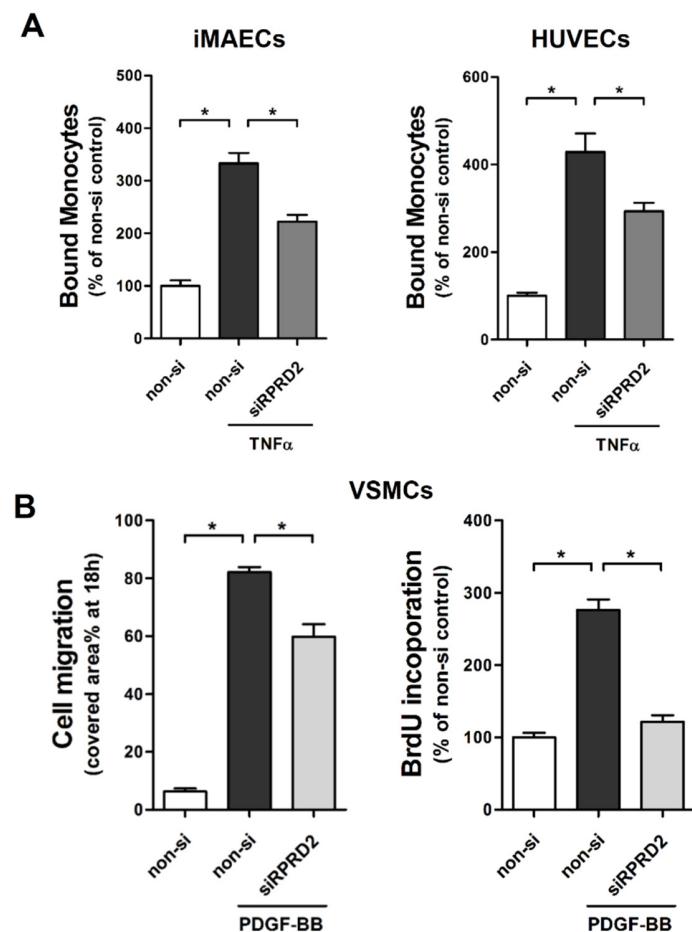
Supplementary Figure 9. Gene network analysis using GeneMANIA. The relationships between IL-32 and Dgcr8/Drosha/Dicer1 are shown based on known functional association networks.

Supplementary Figure 10.



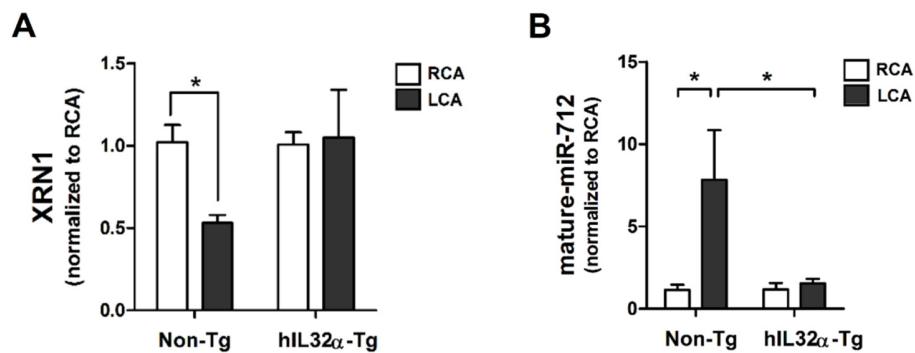
Supplementary Figure 10. Khsrp expression in hIL-32 α -Tg mice carotid endothelium and hIL-32 α -expressed iMAECs. (A) *Khsrp* mRNA expression was determined by qPCR using endothelial-enriched RNA obtained from left carotid artery (LCA) and right carotid artery (RCA) following partial carotid ligation in hIL-32 α -Tg or non-Tg mice at 2 days post-ligation ($n = 5$). (B) iMAECs were cultured in a 12-well culture plate for 24 h, then transfected with human IL-32 α expressing pcDNA3.1⁺-6 \times Myc vector (IL-32 α) or control-vector. After 24 h, cells were then treated with TNF α (10 ng/mL; 24 h), and *Khsrp* mRNA expression was determined by qPCR. All data shown as mean \pm SEM, * $P < 0.05$ as determined by Student's *t*-test.

Supplementary Figure 11.



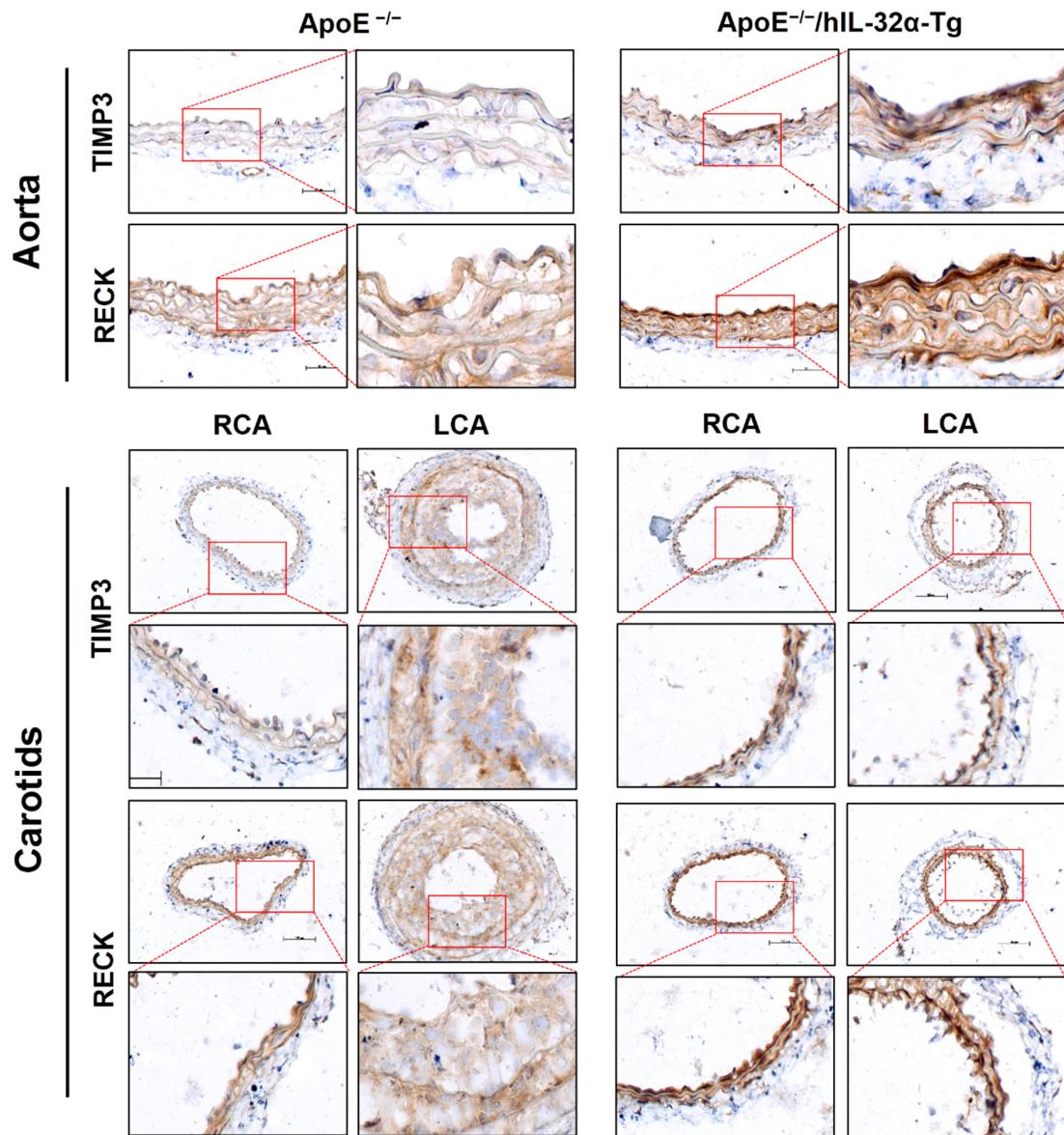
Supplementary Figure 11. Knockdown of Rprd2 inhibits EC inflammation and VSMC proliferation and migration. (A) iMAECs and HUVECs were transfected with Rprd2 siRNA (siRprd2, 200 nM) for 24 h. Cells were then treated with TNF α (10 ng/mL; 24 h), and monocyte-EC adherence was determined ($n = 6$ each). (B) VSMCs isolated from the thoracic aortas of non-Tg mice were transfected with siRprd2 (200 nM), then VSMC proliferation and migration were determined by wound healing ($n = 3$) and BrdU incorporation assays ($n = 6$), respectively, as described in the Methods. All data shown as mean \pm SEM, * $p < 0.05$ as determined by paired t -test.

Supplementary Figure 12.



Supplementary Figure 12. Effect of IL-32 α on expression of the noncanonical microRNA processor XRN1 and mature-microRNA-712 in the mouse endothelium. Expression of (A) *Xrn1* mRNA and (B) mature-microRNA-712 (miR-712) were determined by qPCR using endothelial-enriched RNA obtained from left carotid artery (LCA) and right carotid artery (RCA) following partial carotid ligation in hIL-32 α -Tg or non-Tg mice at 2 days post-ligation ($n = 5$ each, data shown as mean \pm SEM, * $P < 0.05$ as determined by Student's *t*-test).

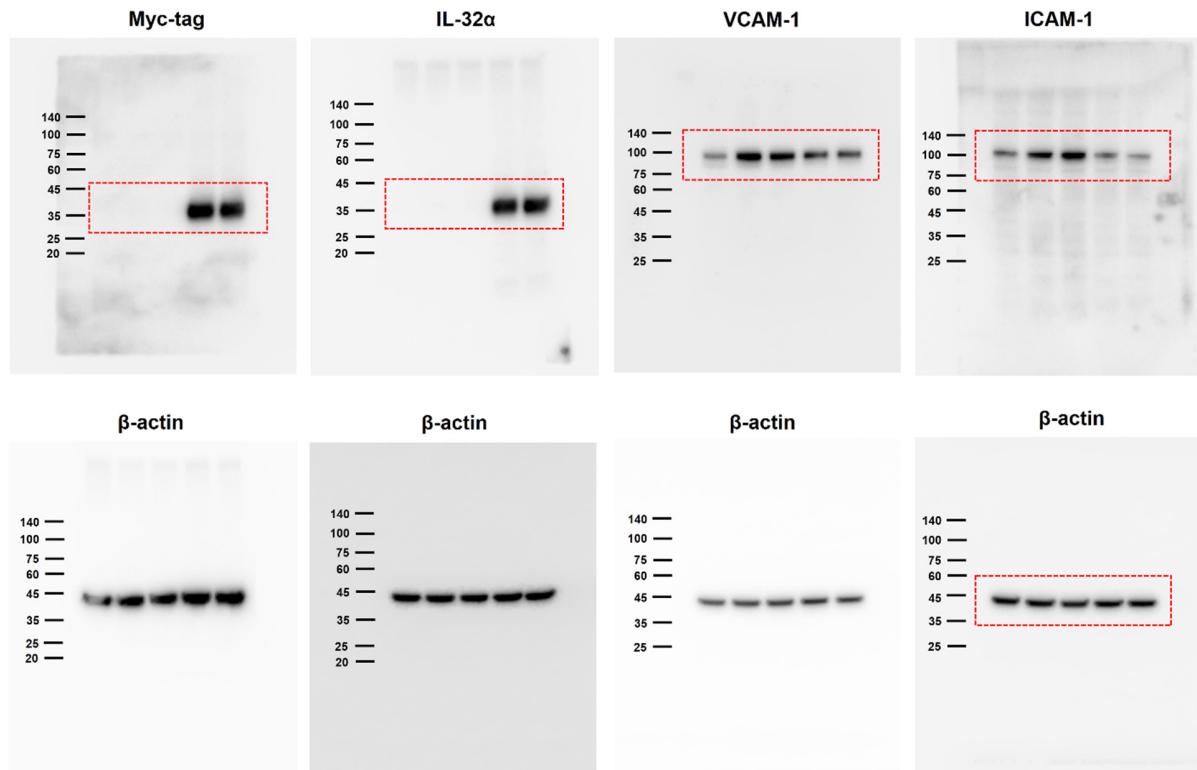
Supplementary Figure 13.



Supplementary Figure 13. Timp3 and Reck expression in *ApoE^{-/-}/hIL-32α-Tg* mice aorta and carotid arteries. *ApoE^{-/-}/hIL-32α-Tg* and littermate *ApoE^{-/-}/non-Tg* control mice were partially ligated and fed a high-fat diet for 2 weeks. Frozen sections of thoracic aorta and carotid tissues from *hIL-32α-Tg* and littermate non-Tg control mice were stained with Timp3 and Reck antibodies. Images shown are representative microscopy images. The red rectangle indicates the magnified area shown in the lower panel. Nuclei (blue); protein expression (brown).

Supplementary Figure 14.

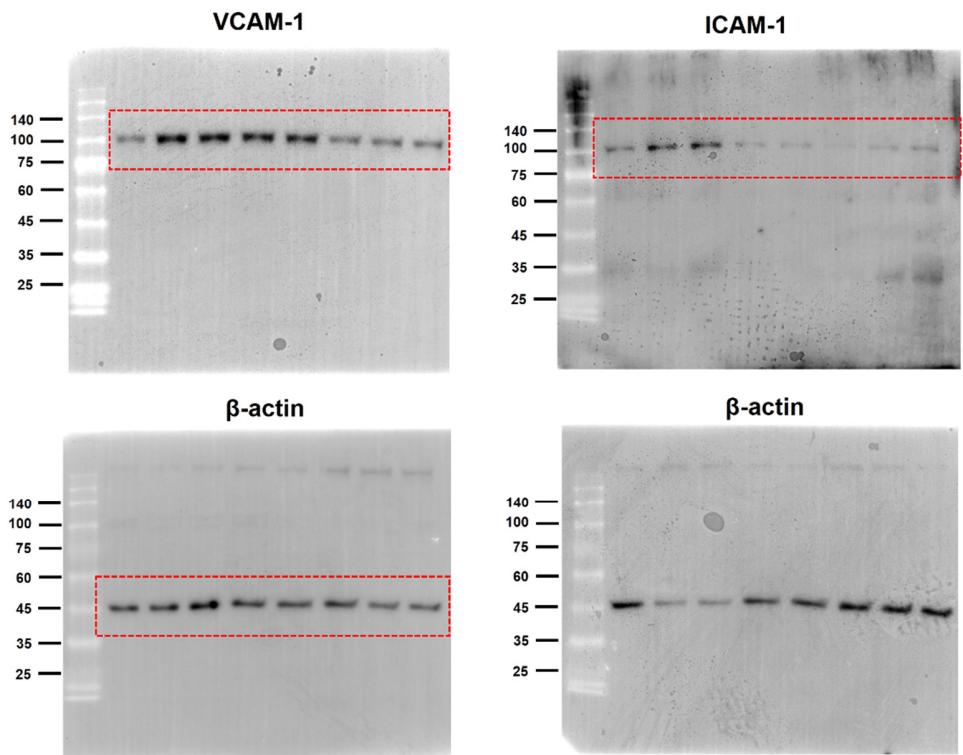
Fig. 1B



Supplementary Figure 14. Full western blot images for Myc-tag, IL-32, VCAM-1, ICAM-1, and respective β -actin control bands shown in Figure 1B. The red dotted rectangle indicates the area shown in Fig. 1B.

Supplementary Figure 15.

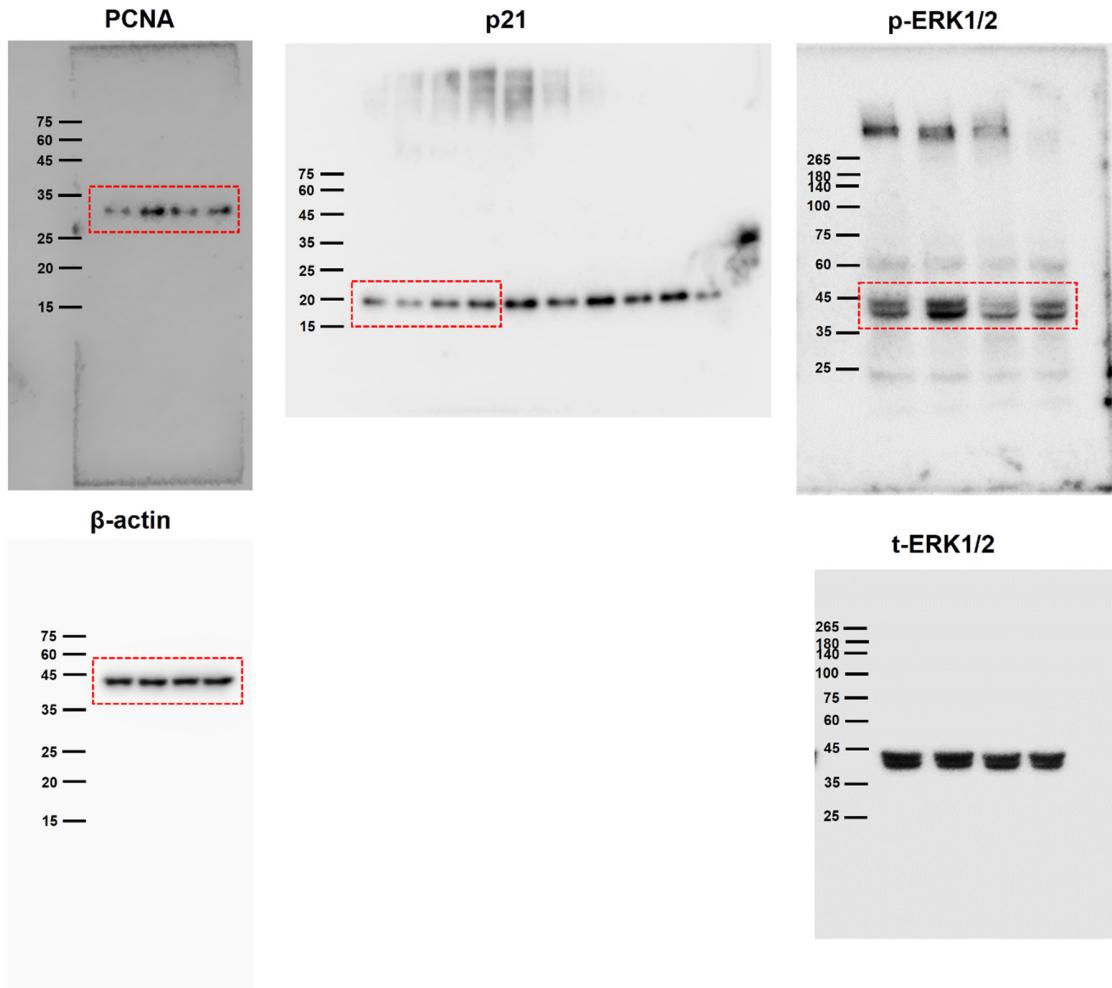
Fig. 1C



Supplementary Figure 15. Full western blot images for VCAM-1, ICAM-1, and the respective β -actin control bands shown in Figure 1C. The red dotted rectangle indicates the area shown in Fig. 1C.

Supplementary Figure 16.

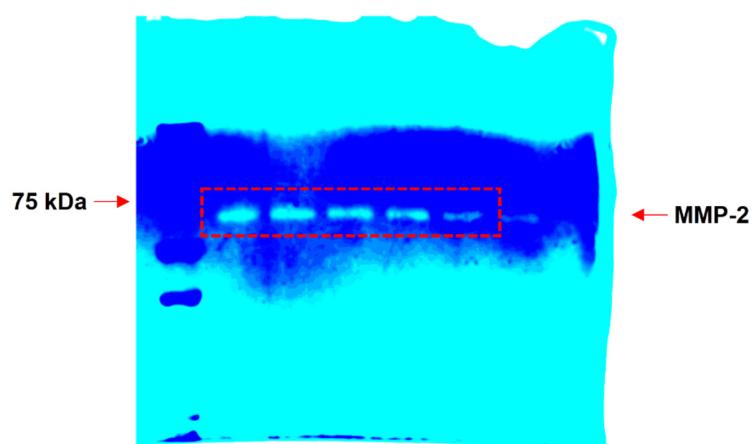
Fig. 2E



Supplementary Figure 16. Full western blot images for PCNA, p32, phospho-ERK1/2, total-ERK1/2, and the respective β-actin control bands in Figure 2E. The red dotted rectangle indicates the area shown in Fig. 2E.

Supplementary Figure 17.

Fig. 2G



Supplementary Figure 17. Full gelatin zymography gel image for MMP activity in Figure 2G. The red dotted rectangle indicates the area shown in Fig. 2G.

Supplementary Tables

Supplementary Table 1. Fold-change expression of endothelial genes in hIL-32 α -Tg mice LCA compared to non-Tg LCA *in vivo*.

Probe ID	Gene Symbol	IL-32 α LCA-1	IL-32 α LCA-2	IL-32 α LCA-3	Non-Tg LCA-1	Non-Tg LCA-2	Non-Tg LCA-3	IL-32 α LCA/Non-Tg LCA (Fold-Changes)	p-value
17459423	---	59.41696461	80.90236656	78.762773	6.642581391	5.161223121	8.978534601	10.542	1.19E-04
17248276	Hba-a2	342.9277874	461.0578596	445.9332609	37.32493907	38.67544537	49.39444851	9.968	9.14E-05
17491193	Saa3	36.63223957	37.15622425	31.47176096	6.270571777	7.073464484	6.001890507	5.441	4.21E-05
17290010	Esm1	180.5427904	220.3180675	228.9462302	43.32503471	42.43812466	46.88085577	4.748	3.42E-05
17302054	Snora31	150.796486	206.1879198	170.0398404	40.59508049	34.22356156	38.39738084	4.655	1.15E-04
17227892	Prg4	61.00155018	80.53148322	77.45690765	17.85330172	22.94630575	17.5222605	3.755	2.39E-04
17236182	Timp3	264.5308186	351.5239071	314.3382444	83.6673595	101.1526987	90.26301101	3.382	2.30E-04
17467458	---	16.45858041	8.925704224	12.6568106	3.413718271	3.934390073	4.091321755	3.325	1.03E-02
17284460	---	6.305164454	14.09138	16.1931528	3.806977386	4.70020278	2.921005349	3.202	4.35E-02
17232731	Rnu3a	69.21280168	85.61822373	71.39608197	18.8826717	27.71524777	29.11629739	2.988	1.31E-03
17508591	Snord13	638.6558895	707.5013056	593.4879797	175.3477368	259.1455841	243.2358382	2.862	1.05E-03
17547616	---	20.75508593	42.40492714	37.18469413	11.97940211	13.44114373	12.1087413	2.674	2.30E-02
17428477	Cyp4b1	93.78589118	76.49327437	75.83957635	23.30161429	36.900079	34.89007999	2.588	3.02E-03
17425523	Snora17	67.49089592	70.46075361	88.31049526	31.75326416	33.66606036	22.78963637	2.565	1.82E-03
17300929	---	83.81514206	66.92410337	90.45021331	29.9198907	31.47754235	32.78863641	2.561	9.29E-04
17225169	Snora75	70.01504209	84.42503692	84.09003847	28.69988399	29.44004558	36.37652939	2.524	4.83E-04
17469339	---	18.07946398	9.028854731	15.45940619	5.872044901	5.217797663	6.170498303	2.466	2.86E-02
17218927	Dpt	14.58304412	16.19661023	17.34164678	6.129481331	7.595258148	6.315259426	2.401	3.74E-04
17387517	Serpingle1	31.41659671	38.9540115	30.10126057	12.78716908	15.02438466	15.09442609	2.342	1.18E-03
17280493	---	125.9595763	136.0514007	121.6465842	50.65848405	65.13576426	48.58876977	2.334	8.73E-04
17385838	---	24.22392939	35.48912255	25.1584825	9.490742765	11.54305344	15.78261108	2.305	1.13E-02
17419405	Snora16a	115.8920666	111.9112297	107.8259039	46.915346	49.71550649	54.96094862	2.214	7.14E-05
17399176	5830417110Rik	27.75177223	16.42275202	15.66666286	11.73149525	6.600123408	8.801216828	2.205	4.36E-02
17547719	Ahnak2	54.43882413	84.89949104	76.34686435	31.8842712	33.94400756	32.38747294	2.196	5.90E-03
17383129	Snora17	112.4861057	112.4081633	106.2909533	43.35321259	57.72718618	50.88543973	2.179	5.08E-04
17284334	Ighg	10.82002554	9.971503154	8.084580972	5.184443004	4.399211613	3.802177806	2.157	4.37E-03
17281142	Cfl2	396.033044	414.3318743	458.539752	196.2629445	198.9153775	198.9088973	2.136	5.50E-05
17401066	Ngf	58.28274815	75.07340429	83.60903808	28.66864871	40.91383876	32.11599302	2.133	6.79E-03
17301340	---	69.67103064	75.59489993	105.5068604	29.60487793	38.23743913	50.41848979	2.121	1.70E-02
17513854	---	77.94469879	92.4222944	111.1197925	50.35094674	35.67792978	48.36474878	2.094	7.25E-03
17276906	Smoc1	172.8334917	200.5078625	171.3980636	81.70151922	88.6642738	91.6469523	2.079	2.10E-04
17257591	Snord104	234.4060507	235.3682645	225.9434619	94.53980606	119.0483653	121.533122	2.076	5.96E-04
17512852	---	56.63547115	54.97093068	48.06687145	32.36088146	22.26911006	22.69439306	2.065	4.03E-03

Probe Set ID	Gene Symbol	IL-32 α LCA-1	IL-32 α LCA-2	IL-32 α LCA-3	Non-Tg LCA-1	Non-Tg LCA-2	Non-Tg LCA-3	IL-32 α LCA/Non-Tg LCA Fold-Changes	p-value
17358266	Pgm5	13.55672695	13.25979899	10.23648143	93.62494104	119.7442856	170.8802675	0.096429554	4.98E-04
17528586	Ccnb2	12.4519346	21.09593316	19.74847027	136.7301886	165.4919234	160.3906242	0.115207243	5.67E-05
17277876	---	15.40183136	21.07313425	23.05094513	123.622197	130.8441851	147.3420081	0.148145017	4.94E-05
17504138	Ccl17	6.359811475	8.058693703	8.504208687	50.59005842	55.24216667	47.52421857	0.149473431	1.54E-05
17483615	Itgax	10.77753513	18.03351848	17.15566328	65.35741417	94.01975396	93.82652962	0.18153184	8.21E-04
17514495	Mmp12	7.375930183	11.764091146	9.109949142	41.62669173	55.14235585	57.58287833	0.183023118	3.53E-04
17321768	---	29.74390165	49.38664295	37.04453964	231.0156854	194.9964434	202.8984453	0.18472433	2.17E-04
17454166	Pilra	14.46006367	16.32446719	21.13808827	83.9196642	83.30908919	106.4897675	0.189693481	0.00020295
17271724	Cd300ld	21.32531283	31.37250884	27.8649952	135.7728304	122.4550957	135.9541142	0.204379725	8.96E-05
17277794	Gpr65	8.773235528	9.841976011	11.12949325	40.54482836	60.14025167	43.58331413	0.206176169	0.000671995
17325608	Cd80	46.94865752	63.323057	43.70934943	251.7972995	220.0262739	271.8580993	0.207052385	0.000193798
17404217	LOC10003894	11.63237678	23.34223825	11.95284382	52.81090649	77.57565135	92.48810976	0.210555373	0.003885379
17490149	Cd33 // Cd33	46.1102953	80.28814076	92.56391631	362.6273677	342.1601655	321.1910762	0.213418048	0.001290414
17405082	Slc7a11	6.381355909	8.533573454	6.332025213	24.71186518	36.46958809	37.90932859	0.214419083	0.001559442
17260474	Igfbp3	17.03435009	36.11962476	27.14229863	99.41578276	112.8528467	155.7943388	0.218159066	2.69E-03
17248809	Havcr2	11.55534957	17.66665499	13.94153008	51.35276312	67.55759195	77.38312039	0.219892865	7.22E-04
17418485	Csf3r	79.17653352	101.8766066	104.2935408	378.6176877	424.9752462	467.3880377	0.224509011	0.000159703
17485510	Tarm1	40.81526729	48.34282912	46.23245281	190.0072951	190.7963815	220.2511894	0.225254892	2.38E-05
17212174	Il1r2	35.2749712	35.89569685	37.49374425	141.7595383	166.1634194	173.4154948	0.225754688	2.66E-05
17333731	Fpr2	4.257300719	3.369968252	3.232505893	21.37608878	12.44877605	14.15128346	0.226357789	6.98E-03
17494370	Trim30b	6.948063793	6.47118835	5.177038331	24.86076869	31.79449303	24.85646102	0.228142546	0.000393958
17517097	1600029D21Ri	7.92160629	8.496513734	8.224961923	28.54564983	43.43915096	35.95655755	0.228300647	6.38E-04
17325324	Stfa21	9.086205911	12.41394712	11.28135926	40.25346305	46.83983212	52.22841438	0.235293641	0.000216839
17408856	I830077J02Rik	26.8826415	34.9792633	36.66376402	142.9644861	119.4591871	143.8987251	0.24248151	0.000194631
17536383	F630028010R	19.05571716	33.93927872	30.5374142	114.4589923	123.0994922	106.6847385	0.242655206	6.48E-04

17233210	Gp49a	28.82574521	50.30165631	32.13080007	131.554884	164.8125165	159.5678285	0.244021945	0.000964482
17222566	---	8.101112262	14.82558369	12.06491628	32.39054864	50.12943261	60.40051728	0.244832705	5.78E-03
17419437	Ptafr	30.64515295	49.07886567	40.84764501	153.4518257	161.1463834	177.4826267	0.245024099	0.00030259
17430906	BC013712	24.00797805	24.94334424	18.48952171	80.66293525	97.00599474	93.29151715	0.24889553	0.000147787
17405478	P2ry13	6.925071659	7.708627419	6.470270376	18.50530489	27.37346195	38.43529936	0.250301882	0.008538476
17371427	Dhrs9	8.795045248	8.682502975	7.091776157	23.63242874	42.81151545	29.89598832	0.255027419	5.30E-03
17462788	Clec4n	17.69597074	18.19774774	23.37283774	73.52775341	75.69809033	81.950209924	0.256367694	8.56E-05
17466228	Clec5a	12.00365621	11.80698742	11.10526566	38.65239755	39.76267745	52.16459312	0.267391622	0.000465142
17337152	---	37.519611191	68.72113695	58.45501916	234.6729913	175.1724397	199.2699007	0.270385195	0.001940909
17271776	Cd300lf	12.45310848	12.57285165	15.17738146	35.56383501	44.83740878	67.17939975	0.272416088	0.005905675
17379606	Mmp9	25.92893419	36.37191547	27.30217535	109.3838548	110.1200989	109.2979855	0.272513676	0.000134737
17367652	Il1f9	8.13470484	8.72452145	8.852788777	22.78684055	31.59304306	38.54476428	0.276697471	0.003188121
17525894	Sorl1	23.69860117	29.14343447	25.78623074	92.66939193	93.00342876	96.52247473	0.278630678	1.45E-05
17404200	Sirpb1a	28.00751346	78.8783244	66.30638974	195.8004133	220.8542829	203.7741164	0.279149234	0.008644897
17349433	Kif20a	9.597901452	8.793466458	8.5583341	25.19141054	32.59396593	37.75971577	0.282062651	0.001272753
17336494	H2-Ab1	258.3537474	301.7171723	327.568314	1093.236638	1051.424834	992.3587797	0.282956169	6.54E-05
17214142	Cxcr2	59.02212669	95.58246043	105.0428387	278.7785983	292.4590859	338.1571387	0.285516719	0.001783479
17462796	Clec4d	14.48656858	25.97016005	18.65941692	68.37116012	67.14616042	70.86444221	0.286440743	0.000648648
17495839	Igsv6	69.54944032	117.2030253	123.6825364	354.2013744	335.7400886	383.5596106	0.289179964	0.002100556
17322355	Gpr84	6.180596149	8.289620176	6.883827759	27.53086435	27.67760109	17.72456112	0.29278977	0.003989032
17419483	Fgr	23.82169228	21.80362337	18.46179596	61.2992705	72.6892946	82.952928	0.29541196	0.000456543
17548238	Fabp5	5.442830091	7.950981702	5.701735045	20.29891907	22.51257223	21.37527388	0.297499754	0.000172521
17359098	Cep55	5.789035486	6.603408973	6.678069001	18.38704836	20.61832171	25.09164237	0.297525777	0.001210968
17219382	Cd244	9.157012551	14.14203667	13.0183166	43.50230681	44.10777253	34.24809886	0.298029778	0.000877923
17357640	Ms4a4a	31.68611768	47.28592783	50.27331787	130.0789764	130.7072178	169.7336735	0.300207663	0.001507361
17214197	Slc11a1	27.27333085	36.82166605	40.04518835	119.3073406	117.3806669	107.841675	0.302267672	0.000580146
17335480	Rab44	18.00284488	18.96734706	17.43911593	58.38132302	67.1092161	53.52615067	0.303934275	6.32E-05
17479575	Prc1	10.06445398	14.56425499	10.41741916	29.11391603	41.00375135	44.52451527	0.305700113	0.003557469
17254166	Sifn2	49.61904282	92.96971964	71.13708732	212.2875568	228.3001504	257.548263	0.306137857	0.002235726
17248380	Lcp2	42.940557	54.83503332	55.23259476	159.6249104	175.5413382	162.760973	0.307290259	0.00124009
17440768	Selpg // Selpk	15.82833939	17.67717708	21.38413581	42.6091687	72.38219735	62.56825659	0.309133639	0.004398338
17507161	Cd209a	13.85845958	30.395735	22.66256103	57.43514906	76.34829319	81.92443994	0.310219334	0.005587827
17408960	Cd53	87.55453489	117.478912	105.9030992	314.3957707	361.4246263	325.8355034	0.310422517	0.00020467
17212252	Il18rap	5.544817589	8.526762068	6.895704728	19.43047144	21.02701275	26.75146509	0.311971614	0.001738361
17227536	Ptprc	50.64135142	71.31996056	76.26710326	201.5016721	214.0283356	212.5201756	0.315625121	0.000471381
17529575	Bcl2a1d	7.558164927	14.82682717	13.51764569	31.39006258	46.77776411	35.47739068	0.315918598	0.005076137
17229658	Fcer1g	192.9953129	216.3165144	235.5440371	725.1969262	655.167962	646.9525083	0.318083328	5.85E-05
17373177	Sfp11	45.83996381	38.19296451	36.33454663	89.94193393	119.2193829	167.3319353	0.319706859	0.006253722
17309981	Fyb	7.592089501	11.17600759	8.857858801	23.82463159	28.44227578	33.96690821	0.320361052	0.002083411
17391565	Il1b	275.4466296	356.2968701	300.5203755	914.8459375	1019.605256	970.8603628	0.320882583	0.000127808
17223069	Stk17b	36.79928933	37.84594957	35.3791627	110.6739595	122.1632891	107.7875695	0.32300759	2.26E-05
17391094	Hdc	20.03350573	20.42529486	26.08470116	47.92119568	66.96665492	91.0917145	0.323058351	0.008606852
17548717	Fabp5 // Fabp!	5.424946838	7.546909636	6.669464823	18.48763786	21.52754651	20.58689003	0.324103118	0.000181612
17338364	Trem1	28.87505922	26.56888906	25.9624747	72.52583021	95.30374491	82.28673641	0.325474266	0.000240547
17222149	Neurl3	86.27771122	81.45865001	81.96641532	229.9218875	263.1993288	269.4169857	0.327462645	2.50E-05
17236892	---	7.384079061	5.504116476	7.535963618	18.444733	20.20343925	23.65801294	0.327803076	0.000551608
17471541	Clec7a	38.63059518	47.27865209	46.36112289	136.7998654	126.1742762	141.7201414	0.328322825	9.16E-05
17482739	Plk1	13.8857866	16.50736566	15.15011668	34.66053456	51.03881753	52.84569338	0.328725353	0.00271872
17230034	Al607873	8.806727339	12.63131556	10.06570279	23.53984637	29.10630907	42.81561075	0.330014276	0.011845345
17451437	Selpg	97.23117158	116.1091614	103.4463549	312.5250454	318.125013	320.4185807	0.33308499	1.44E-05
17343813	H2-Aa	89.21806787	107.4984464	95.0674791	290.2264105	291.2695346	294.4461501	0.333108769	1.83E-05
17274099	Fam49a	17.1939606	22.5273858	21.31431817	56.1944599	60.16330847	64.69695915	0.337111687	0.000149377
17322437	Glycam1	6.354462067	6.233852415	4.772830162	13.82978669	17.46382895	20.04757736	0.338152342	0.00160305
17485609	Lilra6	13.53018818	17.40901895	14.39520072	29.93854077	58.60809339	45.39926387	0.338453126	0.01023964
17335467	Cdkn1a	79.85041497	82.3547524	85.15716405	224.8721209	258.7415612	245.1374341	0.339433211	9.49E-06
17520162	Bcl2a1a	10.50979774	7.354758652	10.2904916	28.48848506	14.76688885	39.46363654	0.340369739	0.04652139
17532569	Ccr1	14.8508438	32.79679654	26.83972529	56.74557536	81.75646993	79.79895783	0.341214033	0.008562314
17547744	Cks2	7.510265967	5.292355595	10.51582403	15.96549081	29.41277502	22.91329449	0.34145428	0.016786924
17548303	Cks2 // Cks2	7.510265967	5.292355595	10.51582403	15.96549081	29.41277502	22.91329449	0.34145428	0.016786924
17548955	Cks2 // Cks2	7.510265967	5.292355595	10.51582403	15.96549081	29.41277502	22.91329449	0.34145428	0.016786924
17342642	Dusp1	73.07201065	80.62123622	63.8109847	203.3508203	219.8002169	212.1820789	0.342346764	8.06E-05
17339772	Rasgrp3	5.358514096	5.535758477	5.099507778	17.90912566	12.83448053	15.96945309	0.342383492	0.001375177
17497334	Mki67	31.65871952	36.91875507	27.83366533	81.44244678	94.51589063	105.4990356	0.342542599	0.000561668
17537081	Tir13	17.87583837	17.57617215	19.02610052	40.83244353	62.77333705	54.81679216	0.343878464	0.002720885
17404209	Sirpb1b	69.75452969	80.87982665	78.62329928	213.9073137	226.2409072	226.0178648	0.344144892	1.80E-05
17520171	Bcl2a1b	6.486134767	7.207895025	9.489631067	17.38909565	22.47639883	27.44445909	0.344431319	0.004157796

17296128	Gapt	11.14171953	11.82987562	11.75072609	33.83292489	32.09680968	34.73025263	0.344946609	7.46E-06
17251303	Plk3r5	15.44768772	11.75800996	13.89495252	39.21595966	40.08690138	39.09385638	0.347143494	6.48E-05
17352036	PstPIP2 // Pstp	11.07570018	13.86670394	14.39233732	35.09403674	27.80331498	50.29011683	0.347518519	0.009718806
17472114	Plbd1	79.81920475	85.91743391	80.26838691	209.6763014	255.5209905	241.0522357	0.348325933	5.09E-05
17404195	Gm9733	13.63947302	39.59910724	40.59744418	73.42421341	97.37489754	98.41361408	0.348557166	0.020459749
17367686	Il1rn	29.07914609	22.25802994	17.18289239	67.62833827	70.24915662	57.65692536	0.350424587	0.001649428
17244949	Krr1	12.75622903	21.25196004	15.4572525	49.85022116	47.45926985	43.60643065	0.351028053	0.000846283
17498730	1810033B17Ri	17.78438278	17.27828355	17.82638173	45.27638912	60.21303783	44.60547821	0.352370708	0.000807827
17344140	D17H6S56E-5	41.30195022	42.59921677	40.77135502	122.2836746	112.2425593	118.4263247	0.353227421	7.17E-06
17491941	Aldh1a3	10.23897931	11.47567412	12.98751941	26.40199423	35.43263862	35.824707	0.355339007	0.001264777
17385405	Cytip	9.951368935	8.993713956	17.77125916	28.17729079	37.24188005	37.684282	0.356111663	0.005343999
17351053	Csf1r	50.99761948	40.34376999	58.68532991	126.1291562	138.6814485	156.2475762	0.356308762	0.000987159
17435089	Fgl2	53.90577746	54.00174044	57.38127024	121.4816838	162.9741115	179.2852512	0.356424753	0.000964824
17470796	Ptpn6	44.23722552	58.35991998	59.22900725	150.2639373	162.9788561	139.8907733	0.357126827	0.000407028
17257100	Fmn1	22.4617122	34.49864994	28.08490465	75.02663767	74.05175386	87.47767673	0.359514205	0.0007532
17317637	Sla	13.36899397	14.96800458	16.16952059	32.13215866	48.23899682	43.28580245	0.359919247	0.00262095
17406760	Sema4a	18.64321801	22.25719684	19.99649167	48.13935811	62.21118147	58.35534908	0.360964914	0.000472377
17411545	6330407A03Ri	11.01498786	13.75844959	13.87513593	37.79587804	31.17820573	37.70029742	0.362304172	0.000596641
17404821	Ccna2	16.47684368	19.20904646	12.83428482	45.72340693	42.34832492	45.84269644	0.362322235	0.000440699
17266590	Evi2a	24.4415352	29.09164558	36.38530502	66.1762667	88.79158191	92.18550386	0.363816573	0.002275833
17300279	Mmp14	114.537801	148.4741538	155.2314427	389.9558543	379.5297059	379.5281275	0.364002102	0.000337399
17229607	Fcgr2b	141.6891032	110.2390079	107.3902346	298.0246805	330.6577716	357.8472295	0.364224567	0.000605433
17351330	Malt1	23.01058888	28.0594145	25.48642298	52.69499371	81.91308359	75.49786803	0.364370586	0.003295062
17226593	Cxcr4	75.5436193	71.79716632	64.30339483	178.6175465	210.2956212	191.4670067	0.364664732	9.40E-05
17318950	Csf2rb2	8.641669163	12.87768178	17.76148839	42.69943278	40.91627773	24.52151143	0.365099441	0.019195989
17350982	Cd74	429.5112174	489.924626	501.201527	1306.417223	1211.106483	1362.263431	0.36616374	7.47E-05
17281721	Pygl	10.76998996	13.67186356	14.0384427	34.54696337	36.35628795	33.73656072	0.367740495	0.000131222
17304406	Prkcd	37.68258419	54.05458163	52.86467105	109.9314979	163.7246799	118.3427077	0.368883286	0.004104526
17536665	Gm19763	15.85372553	35.37232146	24.61372322	62.14123462	68.88266237	74.04195072	0.369831306	0.006373902
17233226	Lilrb4	466.4552918	473.0680771	470.0961321	1375.566337	1167.882972	1258.674912	0.370745252	2.97E-05
17452054	Oas2	21.26665166	18.01817515	16.87632651	38.96351696	59.86516737	52.5599865	0.370995346	0.004199449
17516718	Amica1	9.16319677	8.936810295	11.38439721	25.41550514	29.60721736	24.08449886	0.372714447	0.000332445
17347042	Ndc80	6.234785816	10.57528765	17.03390141	21.4334324	31.88729912	37.29377671	0.373493997	0.027078167
17527934	Kif23	7.352368112	7.820143059	7.409036803	20.65332276	16.88898825	22.77225098	0.374396286	0.001262314
17388435	Tspan18	13.64473055	18.37000355	13.63866944	25.92679554	47.1561163	48.52451876	0.375416233	0.018205523
17407363	S100a9	14.39380387	23.7989167	13.77272379	33.42211206	54.18016943	50.0078266	0.377628105	0.012436997
17223169	Ankrd44	8.341032618	17.85924269	9.994310223	24.44277196	36.29824774	34.92879579	0.378328163	0.015054221
17353747	Cd14	40.9673594	57.46852038	48.35747464	93.44314976	149.0067628	144.7345959	0.379130237	0.006292551
17377793	Tpx2	13.94749375	13.07699362	16.74769912	34.60817595	38.13104066	42.61150199	0.379470427	0.000536625
17360344	LOC73899	12.25235357	13.41918362	13.83809073	33.94337231	41.76675052	28.3927759	0.379524763	0.001917456
17334419	Sepx1	50.06422006	59.94094817	45.37378165	122.0772874	147.1003634	139.0861543	0.380584681	0.000550309
17504122	Ccl22	8.692053172	12.56264201	7.191989926	24.54708827	29.53277463	20.63367653	0.380743374	0.005265445
17264651	Kdm6b	39.03645124	45.9952827	45.66031793	111.3975737	116.2141557	115.62191	0.380767025	4.00E-05
17526492	Il10ra	11.54668648	21.29674441	12.62838286	28.38437362	42.18084232	48.69629143	0.381278207	0.014505218
17240226	Marcks	24.93490843	38.37444553	32.70367819	70.53287785	87.28422306	93.67024932	0.381780762	0.00266296
17449673	Naaa	46.23472812	51.40764435	55.88162233	133.2357103	129.9846091	137.0631558	0.383538178	4.59E-05
17332236	Runx1	25.2552952	22.35856977	28.91846359	62.28992801	85.45482219	51.28976301	0.384517877	0.006719173
17405482	P2ry12	9.078047267	9.556603746	7.238119869	17.30534742	21.9711427	27.91194975	0.385077715	0.004989254
17470627	Clec4e	24.57751246	33.83339392	24.86917942	61.39618041	72.68113278	81.36091506	0.38656132	0.001448694
17280609	Pik3cg	10.38510574	18.04550985	16.10540461	34.99408061	39.60251094	40.46618673	0.387058446	0.002372711
17358544	Cd274	14.1557276	14.54392742	13.06845785	27.52794482	33.61368952	46.72860294	0.387207018	0.010022169
17327580	Mefv	11.89351297	11.00533381	7.318662413	25.75441741	25.08786854	27.18166641	0.387285036	0.001050581
17524969	Anln	10.29994694	15.01635753	15.69503129	30.37143142	37.09181605	38.32046068	0.387690472	0.002138585
17490160	Siglece	10.38848234	7.96177444	14.39844393	25.29776453	31.61549713	27.40830109	0.388378721	0.003384671
17291057	Hist1h2ag	3.515446649	4.804349147	5.48240535	8.56006054	15.23953523	11.54073337	0.390551007	0.01948906
17374765	Sprint1	15.21451036	14.60422605	15.40200217	34.00712172	39.45070016	42.0888154	0.391363519	0.000127551
17444009	C130050018R	19.50265995	18.88566919	19.74187346	49.90584882	47.19483256	51.28531928	0.391749911	1.21E-05
17372307	Itga4	17.81668467	17.51877509	22.01750365	53.25665825	48.98350147	44.0369608	0.392084307	0.000433955
17229620	Fcgr3	35.30229326	48.87737835	45.65883044	112.1747377	100.2310714	118.3820882	0.392512855	0.00062212
17483577	Itgam	50.57014465	75.49682142	60.21040848	144.6910625	155.8627105	173.0988104	0.393278494	0.001251599
17393658	Samhd1	142.181702	163.3910331	145.6017616	376.695764	373.8417797	394.6976174	0.39395795	2.20E-05
17234647	Itgb2	43.38721265	59.0574844	58.46251546	126.0574872	138.5674891	142.2600731	0.395461108	0.000682838
17464950	Tfec	6.653677771	5.633127009	6.840809239	17.83603462	14.9780406	15.48382498	0.396034071	0.000590015
17264835	Cd68	112.1734159	146.9027914	157.4616837	320.3592862	360.644847	370.0452789	0.396306669	0.000950834
17290083	Emb	20.38470255	31.21775747	31.44629187	63.47977018	64.10166832	81.31998252	0.397549962	0.00369789
17265386	A430084P05Ri	6.489057725	8.462500418	6.086323424	15.87062457	18.41517242	18.59569805	0.397830688	0.000838861

17486864	C5ar1	12.67305112	10.25599103	13.36011017	18.63802389	33.8463651	38.65783667	0.398159602	0.028280027
17461414	Bhlhe40	61.78758153	60.73035932	60.93237208	132.4037341	168.4067319	159.1859283	0.398808154	0.000277287
17344303	Lst1	12.56353024	12.75606103	16.83611075	24.14269793	44.11651732	37.38407677	0.399038133	0.015947783
17254171	Sifn1	34.03511313	27.72581569	31.17569895	79.08718284	76.42925169	77.30372343	0.399177754	5.34E-05
17486859	Gpr77	16.50923082	21.58418928	20.70900022	43.81120529	47.85527321	55.30902481	0.400083136	0.000911311
17480924	Gm19765 // G	5.14386935	7.11358593	5.775856904	13.14026076	14.7985098	17.12007361	0.400216928	0.001742511
17357810	Mpeg1	23.07180546	29.81108543	25.62911932	53.99796003	74.05041933	67.91201812	0.400652434	0.001447183
17312700	Ncf4	20.31640171	15.46387526	22.41132436	33.49235693	48.88100357	62.47802743	0.401733129	0.016333638
17281084	Egln3	17.33854582	17.2365484	17.13395144	41.62669173	46.8367154	40.12312306	0.402134233	4.10E-05
17287827	Tgfb1	322.2360291	360.7566053	354.5238806	856.3145329	858.7575098	864.3201589	0.402232942	6.23E-06
17510136	Ilf30	138.4723386	167.3944633	168.8036162	372.9359331	418.5017949	386.6646326	0.402911015	0.000228712
17268909	Top2a	12.02010006	10.59943897	13.6001815	21.52996397	31.6975186	36.29857482	0.404571826	0.010335378
17337796	Pla2g7	22.45981283	23.66157167	37.48093402	61.82935284	68.74548216	75.84867115	0.405003868	0.003692763
17462729	Clec4a1	14.09248376	15.33484841	16.00068762	28.81469812	35.89985222	47.30667966	0.40553045	0.007916278
17484701	Iifitm1 // Iifitm1	16.1310674	14.87057987	12.61114183	34.26802165	29.21576174	43.93805188	0.405995569	0.004027533
17218261	Ncf2	34.07406111	50.22145774	37.85940939	109.383779	89.54227077	101.5839734	0.406492026	0.001593133
17362973	Ms4a6d	13.23103485	19.09462921	18.35182965	42.28444096	41.48658499	40.7523966	0.406971578	0.000602136
17404402	Ect2	11.87524193	14.13231592	17.96689249	26.28360025	42.68377884	38.87648826	0.407760324	0.011890342
17374792	Dll4	29.42158369	26.08061528	25.47503106	52.5073325	78.28147311	67.47662918	0.408428378	0.002588244
17460465	Asprv1	6.417258059	6.984355533	6.935014986	16.2208442	13.71150474	19.79993789	0.408922048	0.003490054
17424090	---	10.62866135	11.17225111	10.45391189	22.93746418	30.04160527	25.85784248	0.409133534	0.00087719
17230111	Ilf205	20.80590301	21.61501601	23.62620488	52.92828489	52.56483215	55.92288947	0.409173324	2.36E-05
17401530	Al504432	4.524884603	4.257188585	4.240269613	9.625083123	11.0718009	11.11279645	0.409383012	0.000143966
17266967	Ccl3	14.22035918	24.19328888	20.91334604	40.55542477	50.22358124	54.13219561	0.409402403	0.003761064
17318967	Gm20024	23.10219456	20.77572618	15.60390268	56.12275789	47.25080489	41.6309334	0.410206752	0.003485135
17336414	H2-DMb2	6.680110651	5.56023169	6.742665369	12.72666934	13.69716107	19.83789439	0.410339385	0.011402445
17315570	Nckap1I	25.19313928	26.53940277	34.53920569	59.36122668	70.3625079	79.83159884	0.411689583	0.002171839
17267418	A130040M12R	44.97679641	86.97603279	87.37895821	174.4630855	186.4911037	171.3683651	0.412027981	0.011235187
17296355	Itga2	17.47043953	19.98025374	16.16916194	40.24389394	43.7300775	46.15787813	0.41204252	0.000157767
17485589	Lilrb3	16.611778279	15.75776478	11.08056852	31.77781444	33.16645701	39.81483021	0.41481948	0.002532074
17547608	Actg1 // Actg1	39.13083525	54.81709613	54.0904127	115.8185877	118.5108223	120.0399656	0.417751517	0.001216113
17377870	Hck	21.48571675	28.2361405	33.9352562	64.0437997	66.509568223	69.55074195	0.418067942	0.001735626
17244439	Plxnc1	6.924961258	7.306213944	7.805304957	14.96012163	15.40710607	22.30198162	0.418393981	0.008464054
17304177	D14Ertd449e	84.60881067	114.5064456	100.945095	241.7592031	237.0126087	238.0794024	0.418581074	0.000473409
17330203	Cd86	11.30616695	13.91937955	11.77654958	27.44862545	23.84693589	37.0878569	0.418654277	0.006398809
17468511	Mxd1	62.1070871	56.92971609	67.31919407	132.0364093	158.1214193	154.7074648	0.418904329	0.000323561
17476364	Tyrobp	70.39621713	80.41451336	85.2314517	156.8406809	203.0525029	202.5137422	0.419699992	0.001083802
17487805	Atp1a3	7.311224236	6.642581391	13.43218406	26.35169761	18.78145594	19.99373362	0.420502052	0.018890887
17287381	Syk	15.76847242	15.23048523	12.15181579	31.40780031	34.16153744	36.83031931	0.421395683	0.000572204
17405458	Gpr171	12.92355433	12.67977289	14.30547007	22.94148699	33.92982303	37.82974116	0.421418736	0.008723428
17338617	Emr4	10.891811139	13.58638748	16.97909901	22.75457917	35.08143848	40.42186551	0.421923377	0.018165782
17227764	Rgs2	54.39616356	73.94014666	65.60223219	145.0409028	161.9398235	151.7417215	0.422779708	0.000525271
17304162	D14Ertd449e	83.90750783	114.8035942	107.2117338	244.3611289	233.9577116	242.863353	0.424196322	0.000637676
17435055	Pion	9.309314903	13.9905328	9.4961584	23.00244001	27.37661178	26.63685779	0.425834172	0.001969044
17338371	Trem3	9.288830712	12.26581337	9.406760675	22.69612348	23.54092329	26.44637352	0.425976167	0.000517473
17272619	Socs3	35.711152901	39.42910341	44.39945307	66.95370562	103.2932378	109.5548087	0.427231369	0.006074954
17316197	Fam105a	5.005419551	9.404830873	9.52013479	15.84247683	22.37073884	17.77060631	0.427451795	0.013572673
17219789	Kmo	8.179042725	6.383483832	7.044239691	13.73443826	17.81342468	18.98968409	0.42753888	0.003214715
17249801	Gm2a	172.44202729	189.5333612	202.185118	418.963572	462.2046616	433.8507461	0.429013239	5.78E-05
17312759	Cyth4	64.85864595	66.5725719	63.89534834	148.0887258	153.0234559	153.3481551	0.429798929	6.50E-07
17546101	Tlr8	6.685113247	7.782766102	4.810007022	16.21603272	15.93365127	12.62966966	0.430508366	0.004223416
17286365	Serpinb9	19.63701856	20.29770908	20.9048386	47.58731002	42.63756074	51.08734302	0.430532964	0.000121663
17301968	Lcp1	102.9911099	109.7979265	112.8705266	260.7649217	220.3122645	273.6369036	0.431500574	0.000358037
17325438	Hcls1	25.94347807	23.72290859	28.29270086	52.44822342	54.03630045	74.02901871	0.431873899	0.003385256
17265164	Bcl6b	35.60448303	47.60779812	44.71168466	75.75357135	108.1967984	112.2378914	0.431900864	0.00481725
17367536	Apbb1ip	12.35873349	14.77110653	16.3986938	29.0638919	30.98151954	40.5620876	0.432656951	0.003505172
17483264	Itgal	20.99610773	19.74892199	19.70311735	36.43661418	56.65620249	46.50358391	0.433020814	0.005608296
17218835	Sell	34.53585415	28.90415517	32.64551736	77.84238456	68.05456341	75.85550612	0.433300849	0.000226702
17407138	Il6ra	35.47753823	39.37213387	51.76478223	98.48451512	101.4997948	91.96665738	0.433683969	0.001499989
17508850	Msr1	7.733411597	14.97653528	14.96769333	27.08512793	27.74300197	31.7480923	0.435196169	0.007282885
17485673	Lair1	7.613231776	13.19881954	9.973113714	20.78559296	28.65617207	21.29594728	0.435201592	0.008307863
17399823	S100a8	39.11789952	42.44386115	54.66839063	100.2124539	108.2701697	103.0485932	0.437292136	0.000973403
17304193	D14Ertd449e	94.3088333	122.3396293	116.3569036	268.1917411	244.5768425	247.61536	0.437943711	0.000655085
17327465	Ets2	41.55444781	35.88417879	41.81019886	84.3003666	90.42495062	95.72063085	0.440934044	0.000118946
17222549	Rnf149	26.33752731	43.31419501	28.30058559	63.35901492	84.35355701	74.12082324	0.441557989	0.007649247
17337927	Nfkbie	11.33411625	13.7340765	13.5141044	28.18834751	28.968137	30.14097122	0.441963592	0.000106797

17290894	Gpr141	2.943213094	3.366337909	3.950945649	6.367592446	6.33535736	10.49782101	0.442248093	0.039152287
17471828	Klra2	10.78682965	14.45170695	14.80767263	24.23437549	31.72721538	34.57887434	0.442301783	0.00517791
17410492	Tet2	25.7783854	29.78196417	30.01396471	64.55428692	60.63281925	68.24346524	0.442403254	0.000198954
17260761	Plek	58.53647639	86.87294255	75.67925597	170.9949609	155.8574168	172.6816532	0.442589816	0.001676411
17462351	Il17ra	21.32920074	25.33969053	31.32023213	44.32930995	65.68695573	65.96720158	0.443161648	0.010358757
17540521	Cfp	31.4834121	30.96713479	25.25093667	52.50926149	65.70644577	79.40780985	0.443780603	0.006414862
17499394	---	66.52570551	109.5533659	104.5509239	239.7169312	217.3498063	175.288556	0.443785318	0.008573031
17472030	Dusp16	22.04815454	26.11415289	19.23840114	43.91138093	52.98202206	54.61642582	0.444860304	0.001824911
17253235	Ssh2	25.23683351	30.69521777	31.30330327	59.46422224	62.17626285	74.39119666	0.445006408	0.000970331
17345775	A530064D06R	6.213736225	4.547564184	6.569952773	9.485836487	11.79897802	17.65719168	0.44505291	0.035229437
17506081	Osgin1	19.99984619	17.20075517	25.7963671	45.5714699	52.41566004	43.45399759	0.445393568	0.00253919
17322842	Ciita	14.35413013	21.28573497	17.53850657	44.19937303	39.58118774	35.13923796	0.447178453	0.002536013
17250249	Nlrp3	9.091390708	10.91837312	9.913709608	19.61374335	20.96600381	26.125396	0.448593197	0.002145569
17499224	F10	15.22828953	14.65770166	15.28399727	28.8750392	37.42519686	34.35516245	0.448758727	0.000614186
17540154	Cybb	37.2724565	53.97909934	43.4038466	84.54033945	97.89918877	117.1891343	0.449407614	0.004686845
17357671	Ms4a6c	17.52646335	26.01770854	24.53052151	45.04365524	55.58007977	50.21265136	0.451314799	0.003542502
17468612	Arhgap25	17.63600639	20.12134724	15.45909544	33.99324068	36.6212213	47.27711188	0.451401634	0.003734288
17374833	Nusap1	11.58322436	13.2017383	12.33304383	23.93619619	33.83219791	24.45582112	0.451424272	0.004805882
17476076	Rasgrp4	16.244119632	14.50109561	12.31664141	26.42779218	26.97716799	41.5677859	0.453381998	0.014069894
17484233	Ptpre	34.4303514	36.25414386	42.33150863	73.94773226	80.29977276	94.91011863	0.453592398	0.001110454
17292450	Fgd3	9.40361843	6.461056092	8.486131296	12.24147927	19.59140555	21.83710951	0.45371359	0.029133597
17224813	Dock10	19.39410104	23.75743208	22.6879759	44.94824868	51.41494965	48.73525878	0.453757472	0.000340693
17438963	Ppbp	6.433313527	7.086935899	8.068463706	13.38947975	20.57706053	13.57287087	0.454122435	0.015265055
17221756	Ogfr1	6.03283866	10.69320187	9.84635667	14.52385976	20.38775477	23.56203105	0.454433736	0.020101149
17310637	Fam134b	7.06954321	8.582411051	11.45710784	15.23424397	22.10446635	22.27692193	0.454730766	0.015126145
17336407	H2-DMa	18.88409839	18.57611624	22.84467479	37.2415961	48.45917706	46.76097155	0.455262684	0.002013788
17359020	Kif11	8.206346096	7.679961081	7.54683117	15.97153423	17.96872327	17.51221904	0.455432662	7.19E-05
17288876	Arrdc3	31.29382277	29.11875968	29.51765076	52.45425858	74.105668668	70.70189605	0.45589274	0.00255163
17218328	Rnasel	11.28846173	13.38283628	10.54427502	16.2871808	28.48475318	32.13973214	0.45787037	0.038060024
17222825	Obfc2a	7.797258692	10.00922939	9.226151611	14.87935414	22.71373415	21.36964446	0.458469926	0.013096948
17261650	Dock2	15.09711524	15.63194076	15.51424947	28.69417519	34.40296493	37.4860264	0.459751935	0.000777385
17212724	Stat4	6.279366418	6.574749827	6.15510727	13.96400622	18.6307778	8.598905261	0.461459603	0.049863975
17254176	Sifn4	18.95090709	20.30568794	23.66803453	37.83978536	55.34319389	42.95180931	0.462222994	0.006512963
17428803	Kif2c	5.139931027	4.799053845	4.991951785	10.02375394	11.71417949	10.54059206	0.462565636	0.000167104
17497525	Adam8	36.18831426	27.93916501	29.93235737	67.26266334	60.39997302	75.59867271	0.462753276	0.001395474
17297537	Plau	25.27023193	24.736989	25.58960548	43.76540452	58.86527806	60.7151649	0.462802254	0.002664441
17462738	Clec4a3	12.83932097	19.85418176	21.44199147	34.33768802	46.22630041	36.30232389	0.463225827	0.009111363
17389481	Arhgap11a	6.991422396	9.319238027	7.974201162	14.67321394	20.59124277	17.15459309	0.463283132	0.003881403
17411527	Lyn	59.52715336	61.89427215	63.56201695	119.3916392	160.6846159	116.7810194	0.466120831	0.002457049
17286707	Gcnt2	15.79422234	12.33869576	13.11288294	26.53717698	25.33951489	36.50623546	0.466671588	0.007219069
17309154	Kctd12	25.58772539	42.17204275	29.37964381	57.01533114	75.73039585	75.37546019	0.466738409	0.01104417
17319037	Rac2	69.45260971	70.63645325	89.59255832	170.9815681	156.4136923	163.6587582	0.467731884	0.000744844
17247225	Upp1	11.52842882	17.79668957	19.98826022	30.07644193	40.36172698	34.62446801	0.469371225	0.009825703
17336114	Myo1f	17.2297158	15.50334909	20.22315243	37.63515479	41.71001714	33.38499687	0.469760827	0.001222474
17543572	Il2rg	128.6940907	162.2190005	163.0132021	313.7174568	337.8689586	314.6877044	0.46976969	0.00056649
17362223	Fermt3	11.4677146	19.08332953	14.05484852	30.22002607	34.70638025	29.97132583	0.470041714	0.004345545
17456131	Tes	14.76655108	20.3344068	23.30259954	29.17753297	39.42795556	55.64287272	0.470054952	0.031302173
17480216	Prcp	64.73028721	63.03529719	75.75288875	141.565509	155.52762	135.7813948	0.470155812	0.000373985
17496310	Cln3	19.44654562	20.71230199	20.87621124	39.51539707	54.05600543	36.08236507	0.470754225	0.005871419
17290997	Hist1h2bl	268.7338042	354.585566	285.5597829	629.9563252	626.2582962	672.4396572	0.471250427	0.000937277
17282216	Zfp361	56.76449771	65.99926258	64.52404596	105.8749149	126.6534003	164.7093906	0.4714754	0.00688205
17219324	Arhgap30	16.45467926	19.04550979	25.11283501	41.27124344	45.89776507	41.34640529	0.471640111	0.002310951
17500478	Gsr	56.60776269	64.50942266	72.26138493	136.2538325	131.0132577	141.6906746	0.47285707	0.000378584
17236900	Kitl	18.115943	9.545739723	11.57194928	21.86355354	26.42676638	34.65253521	0.473020032	0.028194273
17229433	Nuf2	8.775297278	8.493245782	9.630969273	17.65731407	19.00794946	20.17395445	0.4732562	0.000150635
17431174	Cd52	42.48182971	47.94820285	50.93879759	81.73607154	104.3552954	112.3841679	0.473636258	0.003334178
17319738	Nfam1	17.10943246	27.79639727	31.56073722	50.67509559	50.76879103	59.65821884	0.474646602	0.009798232
17490702	Cd37	16.69320424	20.50558504	23.8115396	44.73384927	38.8719614	44.31987785	0.476920074	0.001970989
17402797	Cenpe	7.187992981	6.645892698	7.010269949	12.84317505	14.10481658	16.75744159	0.47692367	0.001774594
17515238	AB124611	32.61048517	29.31416383	32.0727688	60.17127408	69.27951859	67.48158712	0.477308089	0.000152541
17475342	Tgfb1	174.6093495	216.8195446	182.6481081	391.2809331	407.9094161	400.1516367	0.478659973	0.000306721
17493632	Dgat2	14.09249353	14.91875252	15.43196638	27.41029595	41.17780433	24.26037591	0.478663886	0.01619201
17386709	---	3.614928219	4.322820706	4.052611839	6.245283226	7.416111835	11.38659114	0.478695599	0.039234813
17444961	Alox5ap	74.59034528	85.2433272	81.3631145	148.962977	179.7416574	174.9633574	0.478880514	0.000414091
17510948	Cd97	208.5333042	244.5253115	257.1531472	487.0746199	494.1382756	498.0814943	0.480101708	0.000426012
17476372	Nfkbid	14.12777141	9.315078971	11.42605124	17.9788894	25.19507769	29.4188103	0.480335687	0.019286554

17262065	Cyfip2	11.33125695	7.029241394	10.70969879	20.15842474	21.60505502	18.65817533	0.481122159	0.004234064
17501311	---	50.69343431	52.02769906	52.37447601	126.0935789	88.75989157	106.5412277	0.482570529	0.00277724
17400599	Txnip	238.6912714	262.007264	268.2116327	528.2975833	525.7914967	537.0028743	0.483259416	4.56E-05
17338378	Treml4	16.80800976	19.62175256	24.02770581	30.72923614	43.91077219	50.38568483	0.483560352	0.017313072
17316956	Trps1	15.1312262	22.24035637	20.08467206	31.84303627	40.58748384	46.33710478	0.483770343	0.008660136
17532257	Csrnp1	15.72595799	16.12032584	19.92541683	37.89351329	36.42439236	32.52508676	0.484558692	0.000903211
17505148	Cdh1	12.05703278	11.60949248	11.72554439	23.21069794	22.93264728	26.75480298	0.485500256	0.000249658
17374632	D2Ertd750e	19.11905087	17.37145872	14.2268563	32.11770717	35.89223856	36.42095887	0.48565476	0.001241064
17276776	Arg2	14.79312557	16.64280843	16.50953979	31.25744605	37.10037849	30.23913571	0.486277403	0.000729789
17219248	Adamts4	11.54453373	10.40549722	8.18116331	24.64981647	14.06025642	23.14314459	0.487140289	0.033949554
17454179	Pilrb1	16.8029193	15.52297313	14.56338683	27.82380844	35.09739379	33.29422377	0.487336399	0.001436232
17229782	Slamf7	11.955994624	9.470719284	8.683718747	19.49542904	24.07867332	18.19826491	0.487505751	0.005647957
17406279	Tlr2	12.08051455	15.14716612	15.57067951	22.90498956	28.28930836	36.56706676	0.487667441	0.015318361
17232112	H60a // H60a	7.582433815	6.193010963	7.638985219	11.36779864	14.41531043	18.11316811	0.487841598	0.016340595
17471528	Clec1a	12.0034482	20.1823463	22.96793106	28.90772159	39.40183733	44.60343765	0.488462154	0.028491344
1739156	Atp8b4	5.65162601	9.948437817	9.277441507	15.9875393	18.43742148	16.47817998	0.488722404	0.00570665
17261107	Rel	25.91398532	36.69863091	43.35062836	72.873784	73.52846693	70.8517214	0.489078489	0.005559218
17373550	Trp53i11	19.69219465	26.64847371	20.81693842	43.98699071	45.66493897	47.53456326	0.489535124	0.001266611
17400555	Hist2h3c2 // H	48.39077031	50.14100472	51.7945358	102.3038054	112.9538786	91.66785436	0.489781045	0.000516886
17430861	Sesn2	12.76696766	9.696364952	7.748102288	18.42270497	22.66221545	20.57145596	0.489996926	0.006583059
17285867	Hist1h2ab	4.787840195	4.453380864	5.629871525	6.754626513	11.39138295	12.19144308	0.490189233	0.037324276
17321597	Racgap1	14.21409163	12.53201069	12.22519863	23.47053788	21.79709548	34.2006064	0.490400958	0.014593916
17302141	Epst1	13.2500693	13.27377666	9.47747667	18.18992892	28.49604906	26.70733281	0.490525938	0.017099334
17436607	Sh3bp2	15.37301252	15.6097443	14.61714856	27.3896704	26.95027333	38.61498752	0.490559293	0.007922712
17532137	Myd88	39.6674843	35.87719016	34.3238148	69.55175434	68.1920665	86.12970591	0.490761417	0.001823127
17451297	Adrbk2	10.36028654	9.804037483	7.536715844	15.26115238	22.75211883	18.40070325	0.491031524	0.009080079
17432674	Tnfrsf1b	28.04072994	41.684467479	30.42674289	65.05797444	75.62047467	63.20649894	0.491217921	0.005259261
17454187	Pilrb2	8.92146107	7.956213552	7.57668096	17.53419145	20.97649892	11.22558714	0.491680456	0.038764507
17312341	Grina	98.4731839	112.1604319	95.64383014	194.3282723	220.3173039	208.1468622	0.491780932	0.000265231
17317486	Fam49b	64.35302229	59.08811212	74.97158511	116.3753745	151.6420442	135.2683024	0.49199044	0.002224009
17338388	Treml2	4.565921322	6.849311623	6.170960243	9.174630145	13.62286273	12.90635761	0.492557328	0.016853053
17454283	BC037034	25.75034756	19.52252832	26.1724849	39.70384988	43.63618285	61.69561292	0.492605528	0.015538089
17309935	Dab2	59.91569237	66.61194488	72.05696588	144.7170405	131.2141048	126.8147722	0.493076638	0.000555823
17324745	Bex6 // Bex6	4.582913322	4.810983995	3.437028942	5.753991142	9.98301781	10.22849464	0.494146042	0.04093412
17321078	Vdr	11.28541057	13.05136684	15.41839833	26.81460321	27.12766559	26.47535273	0.49435901	0.000690923
17449939	Antxr2	32.31578204	35.10152974	40.12156566	64.25442917	73.4991673	79.5890472	0.494789589	0.001082409
17277387	Fos	24.62379123	36.30750781	28.35411064	50.30280691	60.69038216	69.26084098	0.495331004	0.007773755
17236787	Btg1	43.31581629	50.0679333	56.8324892	94.80366973	110.7808728	97.61344709	0.495439429	0.001234206
17548348	Actg1 // Actg1	106.138702	122.6335573	136.489256	245.0421296	251.8041063	239.8949537	0.495780011	0.000500888
17294738	Vcan	24.01471863	25.10834444	24.61839836	39.80202701	55.05554618	53.78988502	0.496082895	0.003350976
17283380	Fbln5	105.1648666	109.9353841	103.5836866	195.9568235	214.2857346	230.0242256	0.497736171	0.000101105
17489304	Ffar2	8.890151471	9.50103709	7.672990667	17.51395494	14.08279707	20.74891511	0.497924292	0.009809245
17284247	Gpr132	16.30066594	15.46635149	24.02092829	34.02386192	31.12554083	46.62190339	0.499125828	0.02234895
17246803	Osm	13.16298697	13.41728625	12.98597111	21.5469386	22.4819458	35.23814317	0.499151356	0.024790684
17391920	Rassf2	16.44210378	18.27266303	15.22186262	32.72993881	29.57132536	37.67929326	0.499463403	0.001603643
17494081	Rhog	53.24418254	63.24563464	58.72634723	106.6135501	117.4928374	126.6753496	0.499501958	0.000548526
17379938	Cebpb	28.99809054	28.83118041	26.32393026	60.67229589	48.89232137	58.84573701	0.499691373	0.001250896

Supplementary Table 2. Correlation coefficients and p-values between co-expression modules and human IL-32 α .

Module	R	P-value
IL32α_M1	0.28	0.59
IL32α_M2	0.70	0.12
IL32α_M3	0.05	0.93
IL32α_M4	0.03	0.96
IL32α_M5	0.28	0.60
IL32α_M6	0.72	0.11
IL32α_M7	0.19	0.72
IL32α_M8	-0.43	0.40
IL32α_M9	-0.22	0.68
IL32α_M10	-0.74	0.09
IL32α_M11	-0.67	0.15
IL32α_M12	-0.59	0.22
IL32α_M13	-0.38	0.46
IL32α_M14	-0.90	0.01
IL32α_M15	0.11	0.84
IL32α_M16	0.63	0.18
IL32α_M17	-0.04	0.95
IL32α_M18	-0.11	0.83
IL32α_M19	0.00	1.00
IL32α_M20	0.11	0.84
IL32α_M21	0.55	0.26
IL32α_M22	0.46	0.36
IL32α_M23	0.08	0.87

Supplementary Table 3. Biological processes enriched in the genes in the IL32 α _M14 module

Term	Count	p-Value
GO:0006955~immune response	121	1.21E-20
GO:0001775~cell activation	72	1.58E-15
GO:0045321~leukocyte activation	63	2.61E-13
GO:0007242~intracellular signaling cascade	168	7.63E-13
GO:0002684~positive regulation of immune system process	58	6.72E-12
GO:0006952~defense response	97	1.16E-11
GO:0046649~lymphocyte activation	53	1.09E-10
GO:0006954~inflammatory response	57	8.71E-10
GO:0006796~phosphate metabolic process	149	2.29E-09
GO:0006793~phosphorus metabolic process	149	2.29E-09
GO:0050865~regulation of cell activation	44	2.94E-09
GO:0016310~phosphorylation	128	4.17E-09
GO:0002694~regulation of leukocyte activation	43	6.33E-09
GO:0042110~T cell activation	36	6.73E-09
GO:0009611~response to wounding	74	8.27E-09
GO:0048534~hemopoietic or lymphoid organ development	63	1.74E-08
GO:0002252~immune effector process	37	2.03E-08
GO:0051249~regulation of lymphocyte activation	40	2.70E-08
GO:0002520~immune system development	64	4.88E-08
GO:0050778~positive regulation of immune response	38	5.36E-08
GO:0006935~chemotaxis	33	6.09E-08
GO:0042330~taxis	33	6.09E-08
GO:0006468~protein amino acid phosphorylation	113	6.49E-08
GO:0002250~adaptive immune response	28	8.24E-08
GO:0002460~adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	28	8.24E-08
GO:0001817~regulation of cytokine production	38	9.93E-08
GO:0043067~regulation of programmed cell death	101	1.26E-07
GO:0045087~innate immune response	32	1.36E-07
GO:0010941~regulation of cell death	101	1.64E-07
GO:0019884~antigen processing and presentation of exogenous antigen	15	2.23E-07
GO:0042981~regulation of apoptosis	99	2.44E-07
GO:0030097~hemopoiesis	55	3.43E-07
GO:0050867~positive regulation of cell activation	30	4.22E-07
GO:0002449~lymphocyte mediated immunity	25	6.18E-07
GO:0048584~positive regulation of response to stimulus	44	7.07E-07
GO:0002764~immune response-regulating signal transduction	20	7.43E-07
GO:0044092~negative regulation of molecular function	35	7.49E-07
GO:0019886~antigen processing and presentation of exogenous peptide antigen via MHC class II	11	8.18E-07
GO:0002495~antigen processing and presentation of peptide antigen via MHC class II	11	8.18E-07
GO:0002478~antigen processing and presentation of exogenous peptide antigen	13	9.23E-07
GO:0002757~immune response-activating signal transduction	19	9.30E-07
GO:0002696~positive regulation of leukocyte activation	29	9.33E-07
GO:0051251~positive regulation of lymphocyte activation	28	1.04E-06
GO:0002443~leukocyte mediated immunity	27	1.15E-06
GO:0002237~response to molecule of bacterial origin	19	1.32E-06
GO:0002253~activation of immune response	26	2.03E-06
GO:0009617~response to bacterium	38	2.55E-06
GO:0002697~regulation of immune effector process	26	3.23E-06
GO:0001816~cytokine production	17	4.21E-06
GO:0050900~leukocyte migration	17	4.21E-06
GO:0002521~leukocyte differentiation	35	4.43E-06

GO:0048002~antigen processing and presentation of peptide antigen	15	6.25E-06
GO:0002504~antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	11	6.97E-06
GO:0007243~protein kinase cascade	49	7.84E-06
GO:0030595~leukocyte chemotaxis	13	7.89E-06
GO:0060326~cell chemotaxis	13	7.89E-06
GO:0070663~regulation of leukocyte proliferation	24	9.98E-06
GO:0019221~cytokine-mediated signaling pathway	19	1.17E-05
GO:0042098~T cell proliferation	13	1.25E-05
GO:0016477~cell migration	49	1.26E-05
GO:0031349~positive regulation of defense response	19	1.54E-05
GO:0042127~regulation of cell proliferation	90	1.54E-05
GO:0030029~actin filament-based process	39	1.67E-05
GO:0030098~lymphocyte differentiation	29	1.82E-05
GO:0070661~leukocyte proliferation	16	2.08E-05
GO:0032943~mononuclear cell proliferation	16	2.08E-05
GO:0032944~regulation of mononuclear cell proliferation	23	2.18E-05
GO:0050670~regulation of lymphocyte proliferation	23	2.18E-05
GO:0008283~cell proliferation	49	2.76E-05
GO:0002218~activation of innate immune response	9	2.76E-05
GO:0002703~regulation of leukocyte mediated immunity	21	2.78E-05
GO:0019724~B cell mediated immunity	20	3.08E-05
GO:0002274~myeloid leukocyte activation	14	3.43E-05
GO:0043068~positive regulation of programmed cell death	49	3.80E-05
GO:0043086~negative regulation of catalytic activity	26	4.38E-05
GO:0010942~positive regulation of cell death	49	4.69E-05
GO:0045088~regulation of innate immune response	16	5.15E-05
GO:0050863~regulation of T cell activation	27	5.18E-05
GO:0030036~actin cytoskeleton organization	36	5.23E-05
GO:0007049~cell cycle	97	5.82E-05
GO:0042325~regulation of phosphorylation	54	6.19E-05
GO:0043065~positive regulation of apoptosis	48	6.38E-05
GO:0051101~regulation of DNA binding	21	6.65E-05
GO:0016064~immunoglobulin mediated immune response	19	6.90E-05
GO:0046651~lymphocyte proliferation	15	6.94E-05
GO:0042108~positive regulation of cytokine biosynthetic process	15	6.94E-05
GO:0002758~innate immune response-activating signal transduction	8	7.61E-05
GO:0019220~regulation of phosphate metabolic process	55	8.84E-05
GO:0051174~regulation of phosphorus metabolic process	55	8.84E-05
GO:0009891~positive regulation of biosynthetic process	89	9.79E-05
GO:0007626~locomotory behavior	46	1.06E-04
GO:0002706~regulation of lymphocyte mediated immunity	19	1.08E-04
GO:0002768~immune response-regulating cell surface receptor signaling pathway	15	1.23E-04
GO:0051726~regulation of cell cycle	42	1.43E-04
GO:0030593~neutrophil chemotaxis	9	1.66E-04
GO:0009620~response to fungus	9	1.66E-04
GO:0001819~positive regulation of cytokine production	18	1.90E-04
GO:0031328~positive regulation of cellular biosynthetic process	87	1.91E-04
GO:0002221~pattern recognition receptor signaling pathway	7	2.11E-04
GO:0010604~positive regulation of macromolecule metabolic process	97	2.16E-04
GO:0002429~immune response-activating cell surface receptor signaling pathway	14	2.22E-04
GO:0045089~positive regulation of innate immune response	13	2.28E-04
GO:0048514~blood vessel morphogenesis	39	2.37E-04
GO:0048870~cell motility	51	2.54E-04
GO:0051674~localization of cell	51	2.54E-04
GO:0043549~regulation of kinase activity	38	2.62E-04

GO:0051338~regulation of transferase activity	39	2.64E-04
GO:0042035~regulation of cytokine biosynthetic process	18	2.88E-04
GO:0043388~positive regulation of DNA binding	14	2.91E-04
GO:0002683~negative regulation of immune system process	20	3.05E-04
GO:0051090~regulation of transcription factor activity	17	3.34E-04
GO:0048585~negative regulation of response to stimulus	18	3.52E-04
GO:0010324~membrane invagination	37	3.57E-04
GO:0006897~endocytosis	37	3.57E-04
GO:0007010~cytoskeleton organization	56	3.89E-04
GO:0032496~response to lipopolysaccharide	13	4.02E-04
GO:0051130~positive regulation of cellular component organization	27	4.25E-04
GO:0006909~phagocytosis	15	4.33E-04
GO:0042113~B cell activation	20	4.35E-04
GO:0045576~mast cell activation	8	4.63E-04
GO:0051240~positive regulation of multicellular organismal process	33	4.72E-04
GO:0006928~cell motion	61	5.04E-04
GO:0010557~positive regulation of macromolecule biosynthetic process	82	5.41E-04
GO:0051091~positive regulation of transcription factor activity	12	5.53E-04
GO:0051094~positive regulation of developmental process	40	5.84E-04
GO:0001944~vasculature development	45	5.84E-04
GO:0002819~regulation of adaptive immune response	16	5.86E-04
GO:0002822~regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	16	5.86E-04
GO:0010648~negative regulation of cell communication	36	5.99E-04
GO:0045859~regulation of protein kinase activity	36	5.99E-04
GO:0051099~positive regulation of binding	14	6.13E-04
GO:0000278~mitotic cell cycle	44	6.52E-04
GO:0001568~blood vessel development	44	6.52E-04
GO:0000087~M phase of mitotic cell cycle	37	6.61E-04
GO:0050764~regulation of phagocytosis	10	7.33E-04
GO:0051092~positive regulation of NF-kappaB transcription factor activity	10	7.33E-04
GO:0045577~regulation of B cell differentiation	8	7.47E-04
GO:0002700~regulation of production of molecular mediator of immune response	11	7.54E-04
GO:0010647~positive regulation of cell communication	36	8.10E-04
GO:0044093~positive regulation of molecular function	52	8.30E-04
GO:0070665~positive regulation of leukocyte proliferation	15	8.36E-04
GO:0030217~T cell differentiation	19	8.71E-04
GO:0045619~regulation of lymphocyte differentiation	16	8.74E-04
GO:0010627~regulation of protein kinase cascade	31	8.90E-04
GO:0050866~negative regulation of cell activation	15	0.001027
GO:0002695~negative regulation of leukocyte activation	15	0.001027
GO:0030099~myeloid cell differentiation	22	0.001029
GO:0051173~positive regulation of nitrogen compound metabolic process	80	0.001045
GO:0051098~regulation of binding	21	0.001092
GO:0009967~positive regulation of signal transduction	33	0.001225
GO:0051254~positive regulation of RNA metabolic process	66	0.001242
GO:0050870~positive regulation of T cell activation	17	0.001269
GO:0032675~regulation of interleukin-6 production	11	0.001328
GO:0008284~positive regulation of cell proliferation	48	0.001511
GO:0050864~regulation of B cell activation	15	0.001517
GO:0045123~cellular extravasation	5	0.001627
GO:0045597~positive regulation of cell differentiation	33	0.001643
GO:0045893~positive regulation of transcription, DNA-dependent	65	0.001661
GO:0019882~antigen processing and presentation	20	0.001785
GO:0010628~positive regulation of gene expression	74	0.001789
GO:0032946~positive regulation of mononuclear cell proliferation	14	0.001797

GO:0050671~positive regulation of lymphocyte proliferation	14	0.001797
GO:0050766~positive regulation of phagocytosis	9	0.001867
GO:0050830~defense response to Gram-positive bacterium	9	0.001867
GO:0007264~small GTPase mediated signal transduction	44	0.002041
GO:0045941~positive regulation of transcription	72	0.002076
GO:0042742~defense response to bacterium	23	0.002105
GO:0006469~negative regulation of protein kinase activity	14	0.00218
GO:0033673~negative regulation of kinase activity	14	0.00218
GO:0007610~behavior	63	0.002189
GO:0009968~negative regulation of signal transduction	32	0.002215
GO:0043122~regulation of I-kappaB kinase/NF-kappaB cascade	12	0.002453
GO:0045428~regulation of nitric oxide biosynthetic process	8	0.002468
GO:0002285~lymphocyte activation during immune response	8	0.002468
GO:0030183~B cell differentiation	13	0.002583
GO:0051250~negative regulation of lymphocyte activation	14	0.002628
GO:0008285~negative regulation of cell proliferation	39	0.002629
GO:0043405~regulation of MAP kinase activity	19	0.002901
GO:0006917~induction of apoptosis	31	0.002978
GO:0012502~induction of programmed cell death	31	0.002978
GO:0007265~Ras protein signal transduction	15	0.00309
GO:0042129~regulation of T cell proliferation	15	0.00309
GO:0051607~defense response to virus	7	0.003134
GO:0032655~regulation of interleukin-12 production	7	0.003134
GO:0002712~regulation of B cell mediated immunity	10	0.003141
GO:0002889~regulation of immunoglobulin mediated immune response	10	0.003141
GO:0051348~negative regulation of transferase activity	14	0.003148
GO:0008219~cell death	75	0.003163
GO:0016044~membrane organization	45	0.003269
GO:0007067~mitosis	34	0.003323
GO:0000280~nuclear division	34	0.003323
GO:0002335~mature B cell differentiation	5	0.003475
GO:0051301~cell division	46	0.003595
GO:0032844~regulation of homeostatic process	15	0.003643
GO:0032494~response to peptidoglycan	6	0.003666
GO:0051640~organelle localization	14	0.003749
GO:0045935~positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	75	0.003757
GO:0016265~death	76	0.003857
GO:0043069~negative regulation of programmed cell death	41	0.00386
GO:0000279~M phase	46	0.004116
GO:0060548~negative regulation of cell death	41	0.004151
GO:0051347~positive regulation of transferase activity	26	0.004233
GO:0010876~lipid localization	25	0.004254
GO:0012501~programmed cell death	70	0.004331
GO:0050871~positive regulation of B cell activation	11	0.004373
GO:0050777~negative regulation of immune response	9	0.004448
GO:0043392~negative regulation of DNA binding	9	0.004448
GO:0030101~natural killer cell activation	7	0.004565
GO:0043487~regulation of RNA stability	7	0.004565
GO:0009142~nucleoside triphosphate biosynthetic process	20	0.005052
GO:0032649~regulation of interferon-gamma production	10	0.005065
GO:0033674~positive regulation of kinase activity	25	0.005209
GO:0006754~ATP biosynthetic process	18	0.005336
GO:0030003~cellular cation homeostasis	28	0.005468
GO:0044087~regulation of cellular component biogenesis	19	0.00554
GO:0032680~regulation of tumor necrosis factor production	9	0.00574

GO:0048285~organelle fission	34	0.005878
GO:0046034~ATP metabolic process	19	0.006252
GO:0043123~positive regulation of I-kappaB kinase/NF-kappaB cascade	10	0.006317
GO:0045059~positive thymic T cell selection	5	0.006364
GO:0050732~negative regulation of peptidyl-tyrosine phosphorylation	5	0.006364
GO:0007059~chromosome segregation	15	0.006713
GO:0007249~I-kappaB kinase/NF-kappaB cascade	9	0.007298
GO:0010638~positive regulation of organelle organization	13	0.007523
GO:0030005~cellular di-, tri-valent inorganic cation homeostasis	25	0.007654
GO:0043254~regulation of protein complex assembly	15	0.007736
GO:0051656~establishment of organelle localization	10	0.007794
GO:0045807~positive regulation of endocytosis	10	0.007794
GO:0045621~positive regulation of lymphocyte differentiation	10	0.007794
GO:0002699~positive regulation of immune effector process	12	0.007802
GO:0002708~positive regulation of lymphocyte mediated immunity	11	0.007922
GO:0002705~positive regulation of leukocyte mediated immunity	11	0.007922
GO:0043066~negative regulation of apoptosis	39	0.007924
GO:0051051~negative regulation of transport	16	0.008183
GO:0002823~negative regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	6	0.008512
GO:0043488~regulation of mRNA stability	6	0.008512
GO:0050854~regulation of antigen receptor-mediated signaling pathway	6	0.008512
GO:0042089~cytokine biosynthetic process	6	0.008512
GO:0002820~negative regulation of adaptive immune response	6	0.008512
GO:0019915~lipid storage	6	0.008512
GO:0032755~positive regulation of interleukin-6 production	7	0.008782
GO:0043408~regulation of MAPKK cascade	19	0.008844
GO:0009206~purine ribonucleoside triphosphate biosynthetic process	19	0.008844
GO:0009201~ribonucleoside triphosphate biosynthetic process	19	0.008844
GO:0009152~purine ribonucleotide biosynthetic process	21	0.008879
GO:0045449~regulation of transcription	271	0.009062
GO:0006334~nucleosome assembly	16	0.00931
GO:0022403~cell cycle phase	50	0.009477
GO:0050672~negative regulation of lymphocyte proliferation	10	0.00952
GO:0032945~negative regulation of mononuclear cell proliferation	10	0.00952
GO:0070664~negative regulation of leukocyte proliferation	10	0.00952
GO:0006915~apoptosis	67	0.009554
GO:0009145~purine nucleoside triphosphate biosynthetic process	19	0.009878
GO:0009205~purine ribonucleoside triphosphate metabolic process	20	0.009888
GO:0006323~DNA packaging	20	0.009888
GO:0022402~cell cycle process	58	0.010037
GO:0045351~type I interferon biosynthetic process	4	0.010294
GO:0032606~type I interferon production	4	0.010294
GO:0002312~B cell activation during immune response	4	0.010294
GO:0002313~mature B cell differentiation during immune response	4	0.010294
GO:0045736~negative regulation of cyclin-dependent protein kinase activity	5	0.010495
GO:0045075~regulation of interleukin-12 biosynthetic process	5	0.010495
GO:0045580~regulation of T cell differentiation	12	0.010845
GO:0010740~positive regulation of protein kinase cascade	18	0.010961
GO:0009199~ribonucleoside triphosphate metabolic process	20	0.010971
GO:0034220~ion transmembrane transport	11	0.011303
GO:0002260~lymphocyte homeostasis	9	0.01134
GO:0031341~regulation of cell killing	9	0.01134
GO:0001910~regulation of leukocyte mediated cytotoxicity	9	0.01134
GO:0051100~negative regulation of binding	9	0.01134
GO:0050851~antigen receptor-mediated signaling pathway	10	0.01152

GO:0006672~ceramide metabolic process	10	0.01152
GO:0045860~positive regulation of protein kinase activity	23	0.011545
GO:0055066~di-, tri-valent inorganic cation homeostasis	26	0.01159
GO:0048535~lymph node development	7	0.011697
GO:0031497~chromatin assembly	16	0.01193
GO:0007159~leukocyte adhesion	6	0.012094
GO:0006825~copper ion transport	6	0.012094
GO:0042107~cytokine metabolic process	6	0.012094
GO:0051050~positive regulation of transport	24	0.01231
GO:0006665~sphingolipid metabolic process	14	0.012611
GO:0045944~positive regulation of transcription from RNA polymerase II promoter	53	0.013106
GO:0009260~ribonucleotide biosynthetic process	21	0.013206
GO:0007585~respiratory gaseous exchange	8	0.013312
GO:0009615~response to virus	16	0.013439
GO:0065004~protein-DNA complex assembly	16	0.013439
GO:0034728~nucleosome organization	16	0.013439
GO:0007015~actin filament organization	13	0.013677
GO:0016049~cell growth	10	0.013817
GO:0015986~ATP synthesis coupled proton transport	10	0.013817
GO:0015985~energy coupled proton transport, down electrochemical gradient	10	0.013817
GO:0002366~leukocyte activation during immune response	9	0.013888
GO:0007595~lactation	9	0.013888
GO:0002263~cell activation during immune response	9	0.013888
GO:0009150~purine ribonucleotide metabolic process	22	0.014184
GO:0006357~regulation of transcription from RNA polymerase II promoter	84	0.014555
GO:0003018~vascular process in circulatory system	12	0.014721
GO:0002698~negative regulation of immune effector process	7	0.015231
GO:0050727~regulation of inflammatory response	13	0.01569
GO:0048872~homeostasis of number of cells	21	0.015921
GO:0043368~positive T cell selection	5	0.01603
GO:0009144~purine nucleoside triphosphate metabolic process	20	0.016279
GO:0006643~membrane lipid metabolic process	14	0.016336
GO:0046519~sphingoid metabolic process	10	0.016436
GO:0032760~positive regulation of tumor necrosis factor production	6	0.016574
GO:0045840~positive regulation of mitosis	6	0.016574
GO:0006911~phagocytosis, engulfment	6	0.016574
GO:0051785~positive regulation of nuclear division	6	0.016574
GO:0070201~regulation of establishment of protein localization	15	0.016721
GO:0045582~positive regulation of T cell differentiation	9	0.016829
GO:0052547~regulation of peptidase activity	12	0.017012
GO:0051056~regulation of small GTPase mediated signal transduction	36	0.017492
GO:0048732~gland development	32	0.017608
GO:0010033~response to organic substance	70	0.018116
GO:0046328~regulation of JNK cascade	11	0.018283
GO:0032886~regulation of microtubule-based process	11	0.018283
GO:0051223~regulation of protein transport	14	0.018486
GO:0002467~germinal center formation	4	0.018961
GO:0009141~nucleoside triphosphate metabolic process	21	0.019056
GO:0051252~regulation of RNA metabolic process	184	0.019116
GO:0001776~leukocyte homeostasis	10	0.019401
GO:0060322~head development	7	0.019441
GO:0030100~regulation of endocytosis	12	0.019557
GO:0051235~maintenance of location	9	0.020193
GO:0043406~positive regulation of MAP kinase activity	13	0.020378
GO:0070302~regulation of stress-activated protein kinase signaling pathway	11	0.021194

GO:0033043~regulation of organelle organization	26	0.021708
GO:0008354~germ cell migration	5	0.023096
GO:0046823~negative regulation of nucleocytoplasmic transport	5	0.023096
GO:0009259~ribonucleotide metabolic process	22	0.02373
GO:0007033~vacuole organization	9	0.024008
GO:0050885~neuromuscular process controlling balance	9	0.024008
GO:0002824~positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	9	0.024008
GO:0045787~positive regulation of cell cycle	9	0.024008
GO:0002821~positive regulation of adaptive immune response	9	0.024008
GO:0002573~myeloid leukocyte differentiation	9	0.024008
GO:0032101~regulation of response to external stimulus	19	0.024124
GO:0043433~negative regulation of transcription factor activity	7	0.024379
GO:0001974~blood vessel remodeling	7	0.024379
GO:0048771~tissue remodeling	11	0.024429
GO:0019362~pyridine nucleotide metabolic process	8	0.024728
GO:0045185~maintenance of protein location	8	0.024728
GO:0080135~regulation of cellular response to stress	15	0.026124
GO:0006869~lipid transport	21	0.02674
GO:0051336~regulation of hydrolase activity	31	0.027234
GO:0009725~response to hormone stimulus	27	0.027474
GO:0032880~regulation of protein localization	17	0.027894
GO:0035150~regulation of tube size	11	0.028003
GO:0050880~regulation of blood vessel size	11	0.028003
GO:0042102~positive regulation of T cell proliferation	9	0.028301
GO:0046578~regulation of Ras protein signal transduction	29	0.028353
GO:0060627~regulation of vesicle-mediated transport	16	0.028515
GO:0016051~carbohydrate biosynthetic process	16	0.028515
GO:0060324~face development	6	0.028535
GO:0045766~positive regulation of angiogenesis	6	0.028535
GO:0032729~positive regulation of interferon-gamma production	6	0.028535
GO:0043933~macromolecular complex subunit organization	52	0.02951
GO:0043085~positive regulation of catalytic activity	39	0.029513
GO:0048536~spleen development	7	0.030088
GO:0031343~positive regulation of cell killing	7	0.030088
GO:0001912~positive regulation of leukocyte mediated cytotoxicity	7	0.030088
GO:0001933~negative regulation of protein amino acid phosphorylation	7	0.030088
GO:0002224~toll-like receptor signaling pathway	4	0.030576
GO:0045084~positive regulation of interleukin-12 biosynthetic process	4	0.030576
GO:0010812~negative regulation of cell-substrate adhesion	4	0.030576
GO:0002718~regulation of cytokine production during immune response	4	0.030576
GO:0002456~T cell mediated immunity	4	0.030576
GO:0050798~activated T cell proliferation	4	0.030576
GO:0051452~intracellular pH reduction	4	0.030576
GO:0050868~negative regulation of T cell activation	10	0.030588
GO:0032763~regulation of mast cell cytokine production	3	0.031757
GO:0046633~alpha-beta T cell proliferation	3	0.031757
GO:0002238~response to molecule of fungal origin	3	0.031757
GO:0006021~inositol biosynthetic process	3	0.031757
GO:0031113~regulation of microtubule polymerization	5	0.031775
GO:0002920~regulation of humoral immune response	5	0.031775
GO:0032387~negative regulation of intracellular transport	5	0.031775
GO:0010829~negative regulation of glucose transport	5	0.031775
GO:0046486~glycerolipid metabolic process	22	0.032419
GO:0034637~cellular carbohydrate biosynthetic process	12	0.032595
GO:0006119~oxidative phosphorylation	12	0.032595

GO:0070507~regulation of microtubule cytoskeleton organization	9	0.033095
GO:0051969~regulation of transmission of nerve impulse	19	0.034028
GO:0055080~cation homeostasis	29	0.03423
GO:0001570~vasculogenesis	10	0.03515
GO:0065003~macromolecular complex assembly	48	0.035248
GO:0033157~regulation of intracellular protein transport	8	0.035265
GO:0060341~regulation of cellular localization	26	0.035293
GO:0007167~enzyme linked receptor protein signaling pathway	40	0.036024
GO:0043281~regulation of caspase activity	11	0.036238
GO:0052548~regulation of endopeptidase activity	11	0.036238
GO:0001818~negative regulation of cytokine production	7	0.036605
GO:0050729~positive regulation of inflammatory response	7	0.036605
GO:0009820~alkaloid metabolic process	7	0.036605
GO:0031646~positive regulation of neurological system process	7	0.036605
GO:0046496~nicotinamide nucleotide metabolic process	7	0.036605
GO:0006769~nicotinamide metabolic process	7	0.036605
GO:0032271~regulation of protein polymerization	12	0.036637
GO:0018212~peptidyl-tyrosine modification	9	0.038413
GO:0046165~alcohol biosynthetic process	9	0.038413
GO:0018108~peptidyl-tyrosine phosphorylation	9	0.038413
GO:0006333~chromatin assembly or disassembly	19	0.039977
GO:0045637~regulation of myeloid cell differentiation	11	0.040928
GO:0007163~establishment or maintenance of cell polarity	8	0.041501
GO:0006910~phagocytosis, recognition	5	0.042114
GO:0045408~regulation of interleukin-6 biosynthetic process	5	0.042114
GO:0055074~calcium ion homeostasis	17	0.043456
GO:0010741~negative regulation of protein kinase cascade	7	0.043961
GO:0002637~regulation of immunoglobulin production	7	0.043961
GO:0051651~maintenance of location in cell	7	0.043961
GO:0051224~negative regulation of protein transport	6	0.04486
GO:0033032~regulation of myeloid cell apoptosis	4	0.045103
GO:0045579~positive regulation of B cell differentiation	4	0.045103
GO:0001810~regulation of type I hypersensitivity	4	0.045103
GO:0042308~negative regulation of protein import into nucleus	4	0.045103
GO:0015992~proton transport	11	0.046016
GO:0051276~chromosome organization	55	0.048184
GO:0009165~nucleotide biosynthetic process	27	0.048542

Supplementary Table 4. Correlation coefficients and p-values between co-expression modules and oligomeric procyanidins treatment.

Module	R	P-value
OPC_M1	0.15	0.77
OPC_M2	0.41	0.42
OPC_M3	0.36	0.48
OPC_M4	0.23	0.66
OPC_M5	-0.37	0.47
OPC_M6	-0.35	0.49
OPC_M7	0.79	0.06
OPC_M8	0.15	0.78
OPC_M9	0.15	0.78
OPC_M10	-0.45	0.38
OPC_M11	-0.02	0.98
OPC_M12	0.12	0.82
OPC_M13	0.06	0.91
OPC_M14	0.63	0.18
OPC_M15	-0.25	0.64
OPC_M16	-0.65	0.16
OPC_M17	-0.66	0.15
OPC_M18	-0.94	0.006
OPC_M19	-0.46	0.36
OPC_M20	0.49	0.32
OPC_M21	-0.43	0.39
OPC_M22	-0.08	0.87
OPC_M23	-0.21	0.70
OPC_M24	0.54	0.27
OPC_M25	0.97	0.001

Supplementary Table 5. Biological processes enriched in the genes in the OPC_M18 module

Term	Count	PValue
GO:0008219~cell death	107	5.05E-06
GO:0016265~death	107	6.92E-06
GO:0006468~protein amino acid phosphorylation	100	7.79E-06
GO:0009725~response to hormone stimulus	63	8.21E-06
GO:0045859~regulation of protein kinase activity	60	9.23E-06
GO:0051338~regulation of transferase activity	63	1.27E-05
GO:0043549~regulation of kinase activity	61	1.35E-05
GO:0019220~regulation of phosphate metabolic process	77	1.37E-05
GO:0051174~regulation of phosphorus metabolic process	77	1.37E-05
GO:0010033~response to organic substance	105	1.64E-05
GO:0006793~phosphorus metabolic process	134	1.67E-05
GO:0006796~phosphate metabolic process	134	1.67E-05
GO:0012501~programmed cell death	91	2.73E-05
GO:0007242~intracellular signaling cascade	164	3.35E-05
GO:0042325~regulation of phosphorylation	73	3.71E-05
GO:0043627~response to estrogen stimulus	25	4.83E-05
GO:0009719~response to endogenous stimulus	65	5.03E-05
GO:0006915~apoptosis	88	7.46E-05
GO:0006396~RNA processing	80	1.61E-04
GO:0048545~response to steroid hormone stimulus	36	1.67E-04
GO:0051270~regulation of cell motion	36	1.85E-04
GO:0044093~positive regulation of molecular function	84	2.17E-04
GO:0042254~ribosome biogenesis	26	2.20E-04
GO:0031327~negative regulation of cellular biosynthetic process	81	2.24E-04
GO:0022613~ribonucleoprotein complex biogenesis	34	2.27E-04
GO:0030334~regulation of cell migration	32	3.43E-04
GO:0045860~positive regulation of protein kinase activity	39	3.72E-04
GO:0010629~negative regulation of gene expression	73	4.30E-04
GO:0010558~negative regulation of macromolecule biosynthetic process	78	4.31E-04
GO:0009890~negative regulation of biosynthetic process	81	4.37E-04
GO:0010604~positive regulation of macromolecule metabolic process	113	4.74E-04
GO:0010605~negative regulation of macromolecule metabolic process	99	5.10E-04
GO:0016310~phosphorylation	106	6.04E-04
GO:0031399~regulation of protein modification process	47	7.40E-04
GO:0033674~positive regulation of kinase activity	39	7.50E-04
GO:0008630~DNA damage response, signal transduction resulting in induction of apoptosis	11	7.90E-04
GO:0051272~positive regulation of cell motion	21	9.54E-04
GO:0006261~DNA-dependent DNA replication	15	9.92E-04
GO:0016481~negative regulation of transcription	66	0.001014
GO:0043067~regulation of programmed cell death	106	0.00103
GO:0043085~positive regulation of catalytic activity	73	0.001046
GO:0010941~regulation of cell death	106	0.001155
GO:0007049~cell cycle	101	0.001501
GO:0040012~regulation of locomotion	33	0.001517
GO:0042981~regulation of apoptosis	104	0.001526
GO:0051347~positive regulation of transferase activity	39	0.001549
GO:0051172~negative regulation of nitrogen compound metabolic process	72	0.001584
GO:0045934~negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	71	0.001701
GO:0042771~DNA damage response, signal transduction by p53 class mediator resulting in induction of apoptosis	7	0.001861
GO:0030335~positive regulation of cell migration	19	0.001868
GO:0030330~DNA damage response, signal transduction by p53 class mediator	9	0.002361
GO:0040017~positive regulation of locomotion	20	0.002367
GO:0051491~positive regulation of filopodium assembly	5	0.002383
GO:0051489~regulation of filopodium assembly	5	0.002383

GO:0006350~transcription	240	0.002388
GO:0009891~positive regulation of biosynthetic process	90	0.003203
GO:0022604~regulation of cell morphogenesis	24	0.003389
GO:0008285~negative regulation of cell proliferation	52	0.003537
GO:0007243~protein kinase cascade	53	0.003614
GO:0042770~DNA damage response, signal transduction	17	0.003666
GO:0034470~ncRNA processing	31	0.003767
GO:0007178~transmembrane receptor protein serine/threonine kinase signaling pathway	20	0.004228
GO:0045892~negative regulation of transcription, DNA-dependent	51	0.004338
GO:0031328~positive regulation of cellular biosynthetic process	88	0.004562
GO:0000079~regulation of cyclin-dependent protein kinase activity	13	0.004641
GO:0042060~wound healing	31	0.005153
GO:0060491~regulation of cell projection assembly	7	0.00536
GO:0048701~embryonic cranial skeleton morphogenesis	7	0.00536
GO:0033993~response to lipid	7	0.00536
GO:0032268~regulation of cellular protein metabolic process	64	0.005412
GO:0043065~positive regulation of apoptosis	59	0.005449
GO:0032270~positive regulation of cellular protein metabolic process	36	0.005528
GO:0051253~negative regulation of RNA metabolic process	51	0.006008
GO:0045449~regulation of transcription	287	0.006014
GO:0035023~regulation of Rho protein signal transduction	19	0.006165
GO:0051247~positive regulation of protein metabolic process	37	0.00618
GO:0043068~positive regulation of programmed cell death	59	0.006408
GO:0006364~rRNA processing	18	0.006482
GO:0010942~positive regulation of cell death	59	0.006932
GO:0008286~insulin receptor signaling pathway	10	0.007312
GO:0010557~positive regulation of macromolecule biosynthetic process	83	0.007732
GO:0006357~regulation of transcription from RNA polymerase II promoter	91	0.007822
GO:0043069~negative regulation of programmed cell death	50	0.008095
GO:0001817~regulation of cytokine production	29	0.008262
GO:0055088~lipid homeostasis	12	0.00832
GO:0007167~enzyme linked receptor protein signaling pathway	48	0.008347
GO:0001932~regulation of protein amino acid phosphorylation	28	0.008357
GO:0070482~response to oxygen levels	24	0.008473
GO:0043405~regulation of MAP kinase activity	24	0.008473
GO:0060548~negative regulation of cell death	50	0.008507
GO:0042127~regulation of cell proliferation	97	0.009018
GO:0001666~response to hypoxia	23	0.009174
GO:0044087~regulation of cellular component biogenesis	24	0.009215
GO:0015031~protein transport	94	0.00973
GO:0016072~rRNA metabolic process	18	0.009941
GO:0006917~induction of apoptosis	45	0.01028
GO:0048534~hemopoietic or lymphoid organ development	38	0.010512
GO:0006974~response to DNA damage stimulus	51	0.010514
GO:0006730~one-carbon metabolic process	20	0.010547
GO:0012502~induction of programmed cell death	45	0.010842
GO:0007264~small GTPase mediated signal transduction	43	0.011676
GO:0070201~regulation of establishment of protein localization	21	0.011715
GO:0043255~regulation of carbohydrate biosynthetic process	7	0.01219
GO:0045184~establishment of protein localization	94	0.012321
GO:0016311~dephosphorylation	25	0.012609
GO:0033554~cellular response to stress	72	0.012681
GO:0031346~positive regulation of cell projection organization	11	0.012777
GO:0007005~mitochondrion organization	23	0.012802
GO:0032880~regulation of protein localization	23	0.012802
GO:0008629~induction of apoptosis by intracellular signals	12	0.012815
GO:0034660~ncRNA metabolic process	34	0.013434
GO:0051789~response to protein stimulus	19	0.01367

GO:0048703~embryonic viscerocranium morphogenesis	4	0.014357
GO:0010887~negative regulation of cholesterol storage	4	0.014357
GO:0043066~negative regulation of apoptosis	48	0.015118
GO:0007507~heart development	32	0.015177
GO:0002520~immune system development	39	0.015919
GO:0007010~cytoskeleton organization	57	0.016123
GO:0051271~negative regulation of cell motion	13	0.016151
GO:0006984~ER-nuclear signaling pathway	9	0.016328
GO:0019637~organophosphate metabolic process	30	0.017137
GO:0051301~cell division	41	0.017256
GO:0043406~positive regulation of MAP kinase activity	18	0.017716
GO:0043009~chordate embryonic development	45	0.017751
GO:0000165~MAPKKK cascade	28	0.018124
GO:0002474~antigen processing and presentation of peptide antigen via MHC class I	6	0.019187
GO:0045935~positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	77	0.019429
GO:0014706~striated muscle tissue development	20	0.019435
GO:0051173~positive regulation of nitrogen compound metabolic process	79	0.020331
GO:0009792~embryonic development ending in birth or egg hatching	45	0.020606
GO:0006259~DNA metabolic process	64	0.020812
GO:0060627~regulation of vesicle-mediated transport	17	0.020987
GO:0031401~positive regulation of protein modification process	28	0.021955
GO:0030509~BMP signaling pathway	10	0.022663
GO:0031344~regulation of cell projection organization	16	0.022699
GO:0010888~negative regulation of lipid storage	5	0.022739
GO:0006264~mitochondrial DNA replication	4	0.023338
GO:0032365~intracellular lipid transport	4	0.023338
GO:0090003~regulation of establishment of protein localization to plasma membrane	4	0.023338
GO:0008380~RNA splicing	39	0.024033
GO:0051291~protein heterooligomerization	11	0.025195
GO:0006605~protein targeting	31	0.025197
GO:0051130~positive regulation of cellular component organization	27	0.025649
GO:0033630~positive regulation of cell adhesion mediated by integrin	3	0.026145
GO:0060317~cardiac epithelial to mesenchymal transition	3	0.026145
GO:0006644~phospholipid metabolic process	28	0.026391
GO:0006260~DNA replication	28	0.026391
GO:0007179~transforming growth factor beta receptor signaling pathway	12	0.027023
GO:0032869~cellular response to insulin stimulus	13	0.028287
GO:0045669~positive regulation of osteoblast differentiation	7	0.028551
GO:0030036~actin cytoskeleton organization	32	0.028654
GO:0032259~methylation	14	0.029105
GO:0008104~protein localization	103	0.029173
GO:0065003~macromolecular complex assembly	80	0.029583
GO:0045937~positive regulation of phosphate metabolic process	17	0.029718
GO:0010562~positive regulation of phosphorus metabolic process	17	0.029718
GO:0030100~regulation of endocytosis	12	0.030196
GO:0032870~cellular response to hormone stimulus	21	0.030268
GO:0006470~protein amino acid dephosphorylation	21	0.030268
GO:0017015~regulation of transforming growth factor beta receptor signaling pathway	9	0.030313
GO:0030097~hemopoiesis	33	0.030632
GO:0060537~muscle tissue development	20	0.03091
GO:0043414~biopolymer methylation	13	0.031345
GO:0051254~positive regulation of RNA metabolic process	60	0.031955
GO:0008360~regulation of cell shape	11	0.032018
GO:0042476~odontogenesis	11	0.032018
GO:0030099~myeloid cell differentiation	16	0.03243
GO:0035295~tube development	31	0.033169
GO:0030857~negative regulation of epithelial cell differentiation	4	0.034699
GO:0046321~positive regulation of fatty acid oxidation	4	0.034699

GO:0032042~mitochondrial DNA metabolic process	4	0.034699
GO:0046785~microtubule polymerization	4	0.034699
GO:0030278~regulation of ossification	14	0.035179
GO:0006195~purine nucleotide catabolic process	8	0.035189
GO:0051592~response to calcium ion	11	0.035875
GO:0032570~response to progesterone stimulus	6	0.037757
GO:0010627~regulation of protein kinase cascade	34	0.037804
GO:0006986~response to unfolded protein	13	0.038161
GO:0045893~positive regulation of transcription, DNA-dependent	59	0.03848
GO:0006869~lipid transport	22	0.03862
GO:0006461~protein complex assembly	62	0.03864
GO:0070271~protein complex biogenesis	62	0.03864
GO:0005979~regulation of glycogen biosynthetic process	5	0.039376
GO:0010962~regulation of glucan biosynthetic process	5	0.039376
GO:0032885~regulation of polysaccharide biosynthetic process	5	0.039376
GO:0008624~induction of apoptosis by extracellular signals	18	0.040106
GO:0010628~positive regulation of gene expression	70	0.040749
GO:0034976~response to endoplasmic reticulum stress	8	0.040753
GO:0051252~regulation of RNA metabolic process	197	0.041535
GO:0051094~positive regulation of developmental process	37	0.041934
GO:0042157~lipoprotein metabolic process	14	0.04211
GO:0045596~negative regulation of cell differentiation	30	0.042567
GO:0051056~regulation of small GTPase mediated signal transduction	34	0.043629
GO:0030336~negative regulation of cell migration	11	0.044531
GO:0042327~positive regulation of phosphorylation	16	0.044902
GO:0034620~cellular response to unfolded protein	6	0.045746
GO:0030968~endoplasmic reticulum unfolded protein response	6	0.045746
GO:0008283~cell proliferation	54	0.046341
GO:0017038~protein import	20	0.046812
GO:0051259~protein oligomerization	25	0.046869
GO:0032319~regulation of Rho GTPase activity	7	0.047465
GO:0010876~lipid localization	23	0.047768
GO:0044272~sulfur compound biosynthetic process	10	0.04778
GO:0010746~regulation of plasma membrane long-chain fatty acid transport	3	0.048958
GO:0010891~negative regulation of sequestering of triglyceride	3	0.048958
GO:0032367~intracellular cholesterol transport	3	0.048958
GO:0032366~intracellular sterol transport	3	0.048958
GO:0010748~negative regulation of plasma membrane long-chain fatty acid transport	3	0.048958
GO:0007032~endosome organization	5	0.049712
GO:0032881~regulation of polysaccharide metabolic process	5	0.049712

Supplementary Table 6. Biological processes enriched in the genes in the OPC_M25 module

Term	Count	PValue
GO:0009615~response to virus	36	1.91E-11
GO:0042127~regulation of cell proliferation	124	2.30E-09
GO:0042981~regulation of apoptosis	124	8.77E-09
GO:0010941~regulation of cell death	125	1.02E-08
GO:0043067~regulation of programmed cell death	124	1.50E-08
GO:0010033~response to organic substance	113	1.78E-08
GO:0008285~negative regulation of cell proliferation	64	5.08E-07
GO:0030335~positive regulation of cell migration	25	1.06E-06
GO:0016477~cell migration	52	1.10E-06
GO:0009891~positive regulation of biosynthetic process	103	1.29E-06
GO:0010942~positive regulation of cell death	72	1.31E-06
GO:0030334~regulation of cell migration	37	1.44E-06
GO:0043065~positive regulation of apoptosis	71	1.71E-06
GO:0040017~positive regulation of locomotion	26	1.95E-06
GO:0031328~positive regulation of cellular biosynthetic process	101	2.04E-06
GO:0043068~positive regulation of programmed cell death	71	2.22E-06
GO:0040012~regulation of locomotion	39	4.83E-06
GO:0051270~regulation of cell motion	39	5.49E-06
GO:0007242~intracellular signaling cascade	162	6.19E-06
GO:0034097~response to cytokine stimulus	22	6.33E-06
GO:0051272~positive regulation of cell motion	25	6.71E-06
GO:0010557~positive regulation of macromolecule biosynthetic process	95	8.19E-06
GO:0048660~regulation of smooth muscle cell proliferation	16	9.06E-06
GO:0048661~positive regulation of smooth muscle cell proliferation	13	9.72E-06
GO:0010604~positive regulation of macromolecule metabolic process	117	1.27E-05
GO:0051173~positive regulation of nitrogen compound metabolic process	92	2.25E-05
GO:0051674~localization of cell	52	2.49E-05
GO:0048870~cell motility	52	2.49E-05
GO:0001525~angiogenesis	31	2.91E-05
GO:0001666~response to hypoxia	29	2.99E-05
GO:0009725~response to hormone stimulus	59	3.22E-05
GO:0010324~membrane invagination	40	5.17E-05
GO:0006897~endocytosis	40	5.17E-05
GO:0046697~decidualization	8	5.86E-05
GO:0010628~positive regulation of gene expression	83	5.94E-05
GO:0007167~enzyme linked receptor protein signaling pathway	55	6.05E-05
GO:0009611~response to wounding	77	6.55E-05
GO:0033273~response to vitamin	18	7.32E-05
GO:0070482~response to oxygen levels	29	7.77E-05
GO:0002237~response to molecule of bacterial origin	21	8.46E-05
GO:0009719~response to endogenous stimulus	62	8.56E-05
GO:0045935~positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	87	9.19E-05
GO:0006928~cell motion	70	9.48E-05
GO:0051789~response to protein stimulus	24	9.49E-05
GO:0045941~positive regulation of transcription	80	1.05E-04
GO:0045893~positive regulation of transcription, DNA-dependent	70	1.09E-04
GO:0006955~immune response	94	1.12E-04
GO:0042330~taxis	31	1.31E-04
GO:0006935~chemotaxis	31	1.31E-04
GO:0051254~positive regulation of RNA metabolic process	70	1.40E-04
GO:0048545~response to steroid hormone stimulus	35	1.56E-04
GO:0016265~death	97	1.59E-04
GO:0008284~positive regulation of cell proliferation	62	1.60E-04
GO:0001893~maternal placenta development	8	1.86E-04
GO:0008219~cell death	96	1.92E-04

GO:0012501~programmed cell death	84	1.95E-04
GO:0048514~blood vessel morphogenesis	37	2.18E-04
GO:0031349~positive regulation of defense response	18	2.77E-04
GO:0006917~induction of apoptosis	50	2.79E-04
GO:0042254~ribosome biogenesis	25	2.85E-04
GO:0006357~regulation of transcription from RNA polymerase II promoter	96	2.91E-04
GO:0012502~induction of programmed cell death	50	3.01E-04
GO:0016044~membrane organization	57	3.13E-04
GO:0010629~negative regulation of gene expression	71	3.28E-04
GO:0006915~apoptosis	82	3.29E-04
GO:0007626~locomotory behavior	44	3.79E-04
GO:0007584~response to nutrient	27	4.19E-04
GO:0048584~positive regulation of response to stimulus	39	4.87E-04
GO:0032496~response to lipopolysaccharide	18	5.40E-04
GO:0003006~reproductive developmental process	42	5.44E-04
GO:0032103~positive regulation of response to external stimulus	16	5.79E-04
GO:0032101~regulation of response to external stimulus	29	6.27E-04
GO:0051384~response to glucocorticoid stimulus	18	6.32E-04
GO:0031960~response to corticosteroid stimulus	19	6.38E-04
GO:0006796~phosphate metabolic process	120	7.37E-04
GO:0006793~phosphorus metabolic process	120	7.37E-04
GO:0006351~transcription, DNA-dependent	45	7.85E-04
GO:0045785~positive regulation of cell adhesion	15	9.15E-04
GO:0045071~negative regulation of viral genome replication	5	9.31E-04
GO:0001568~blood vessel development	39	0.00101
GO:0032774~RNA biosynthetic process	45	0.001046
GO:0007178~transmembrane receptor protein serine/threonine kinase signaling pathway	21	0.001051
GO:0034341~response to interferon-gamma	6	0.001129
GO:0033189~response to vitamin A	12	0.001159
GO:0042493~response to drug	35	0.001405
GO:0045944~positive regulation of transcription from RNA polymerase II promoter	53	0.001505
GO:0045765~regulation of angiogenesis	15	0.001519
GO:0006366~transcription from RNA polymerase II promoter	37	0.001565
GO:0043066~negative regulation of apoptosis	51	0.001569
GO:0001944~vasculature development	39	0.001588
GO:0030155~regulation of cell adhesion	25	0.001597
GO:0043434~response to peptide hormone stimulus	27	0.001809
GO:0007264~small GTPase mediated signal transduction	45	0.001909
GO:0006468~protein amino acid phosphorylation	85	0.001932
GO:0048525~negative regulation of viral reproduction	5	0.002014
GO:0050792~regulation of viral reproduction	8	0.002049
GO:0010605~negative regulation of macromolecule metabolic process	92	0.002057
GO:0043069~negative regulation of programmed cell death	51	0.002103
GO:0060548~negative regulation of cell death	51	0.002215
GO:0031667~response to nutrient levels	32	0.002239
GO:0006916~anti-apoptosis	33	0.002369
GO:0031327~negative regulation of cellular biosynthetic process	73	0.002438
GO:0009890~negative regulation of biosynthetic process	74	0.002777
GO:0016310~phosphorylation	98	0.002925
GO:0070555~response to interleukin-1	7	0.003101
GO:0051094~positive regulation of developmental process	41	0.003135
GO:0030031~cell projection assembly	17	0.003456
GO:0009628~response to abiotic stimulus	51	0.003506
GO:0030030~cell projection organization	51	0.003506
GO:0050727~regulation of inflammatory response	16	0.003612
GO:0006984~ER-nuclear signaling pathway	10	0.00367
GO:0002831~regulation of response to biotic stimulus	9	0.003798
GO:0045087~innate immune response	24	0.003806
GO:0009612~response to mechanical stimulus	13	0.004421

GO:0010558~negative regulation of macromolecule biosynthetic process	70	0.004527
GO:0030278~regulation of ossification	16	0.004667
GO:0050729~positive regulation of inflammatory response	9	0.004767
GO:0007169~transmembrane receptor protein tyrosine kinase signaling pathway	34	0.004788
GO:0045892~negative regulation of transcription, DNA-dependent	49	0.004875
GO:0009967~positive regulation of signal transduction	42	0.005214
GO:0043281~regulation of caspase activity	16	0.005282
GO:0051726~regulation of cell cycle	46	0.005364
GO:0016481~negative regulation of transcription	60	0.005545
GO:0048732~gland development	23	0.006024
GO:0007243~protein kinase cascade	50	0.006287
GO:0009991~response to extracellular stimulus	33	0.006546
GO:0045069~regulation of viral genome replication	6	0.006551
GO:0051253~negative regulation of RNA metabolic process	49	0.006649
GO:0002230~positive regulation of defense response to virus by host	4	0.006808
GO:0043280~positive regulation of caspase activity	13	0.006856
GO:0010952~positive regulation of peptidase activity	13	0.006856
GO:0016192~vesicle-mediated transport	72	0.006932
GO:0045859~regulation of protein kinase activity	47	0.007029
GO:0001936~regulation of endothelial cell proliferation	9	0.007262
GO:0051101~regulation of DNA binding	21	0.007325
GO:0006952~defense response	76	0.007337
GO:0052548~regulation of endopeptidase activity	16	0.007528
GO:0045934~negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	65	0.007533
GO:0000122~negative regulation of transcription from RNA polymerase II promoter	38	0.007588
GO:0045766~positive regulation of angiogenesis	8	0.007705
GO:0030330~DNA damage response, signal transduction by p53 class mediator	8	0.007705
GO:0007179~transforming growth factor beta receptor signaling pathway	13	0.007869
GO:0010647~positive regulation of cell communication	45	0.007875
GO:0022613~ribonucleoprotein complex biogenesis	28	0.007951
GO:0030522~intracellular receptor-mediated signaling pathway	15	0.008057
GO:0001816~cytokine production	11	0.008116
GO:0043549~regulation of kinase activity	48	0.008177
GO:0070271~protein complex biogenesis	64	0.008266
GO:0006461~protein complex assembly	64	0.008266
GO:0002683~negative regulation of immune system process	16	0.008426
GO:0060348~bone development	21	0.008775
GO:0032526~response to retinoic acid	9	0.008827
GO:0001503~ossification	20	0.008849
GO:0042771~DNA damage response, signal transduction by p53 class mediator resulting in induction of apoptosis	6	0.00909
GO:0001938~positive regulation of endothelial cell proliferation	6	0.00909
GO:0032355~response to estradiol stimulus	12	0.009325
GO:0051240~positive regulation of multicellular organismal process	35	0.009918
GO:0051172~negative regulation of nitrogen compound metabolic process	65	0.009978
GO:0006350~transcription	224	0.010431
GO:0030099~myeloid cell differentiation	17	0.010656
GO:0002697~regulation of immune effector process	18	0.010723
GO:0009617~response to bacterium	29	0.010849
GO:0043242~negative regulation of protein complex disassembly	10	0.011032
GO:0052547~regulation of peptidase activity	16	0.01164
GO:0045449~regulation of transcription	272	0.011682
GO:0007565~female pregnancy	19	0.011724
GO:0022407~regulation of cell-cell adhesion	7	0.012532
GO:0051797~regulation of hair follicle development	4	0.012684
GO:0002755~MyD88-dependent toll-like receptor signaling pathway	4	0.012684
GO:0042634~regulation of hair cycle	4	0.012684
GO:0016126~sterol biosynthetic process	9	0.012693
GO:0007610~behavior	59	0.01296

GO:0051098~regulation of binding	24	0.013228
GO:0050921~positive regulation of chemotaxis	8	0.014333
GO:0008610~lipid biosynthetic process	43	0.014546
GO:0010038~response to metal ion	21	0.014557
GO:0043407~negative regulation of MAP kinase activity	9	0.015035
GO:0009057~macromolecule catabolic process	91	0.015501
GO:0006576~biogenic amine metabolic process	17	0.015692
GO:0002221~pattern recognition receptor signaling pathway	6	0.016039
GO:0051338~regulation of transferase activity	48	0.016637
GO:0019220~regulation of phosphate metabolic process	60	0.016772
GO:0051174~regulation of phosphorus metabolic process	60	0.016772
GO:0042325~regulation of phosphorylation	58	0.016791
GO:0030595~leukocyte chemotaxis	9	0.017673
GO:0051336~regulation of hydrolase activity	44	0.018236
GO:0051222~positive regulation of protein transport	13	0.018594
GO:0001501~skeletal system development	42	0.018648
GO:0043405~regulation of MAP kinase activity	22	0.019115
GO:0045778~positive regulation of ossification	7	0.019291
GO:0010740~positive regulation of protein kinase cascade	25	0.019339
GO:0008354~germ cell migration	5	0.019565
GO:0006809~nitric oxide biosynthetic process	5	0.019565
GO:0014910~regulation of smooth muscle cell migration	5	0.019565
GO:0032870~cellular response to hormone stimulus	21	0.019844
GO:0009743~response to carbohydrate stimulus	12	0.02012
GO:0050920~regulation of chemotaxis	8	0.020549
GO:0030501~positive regulation of bone mineralization	6	0.020558
GO:0002645~positive regulation of tolerance induction	4	0.020686
GO:0002643~regulation of tolerance induction	4	0.020686
GO:0044265~cellular macromolecule catabolic process	84	0.022458
GO:0050866~negative regulation of cell activation	12	0.022567
GO:0002274~myeloid leukocyte activation	10	0.022926
GO:0045669~positive regulation of osteoblast differentiation	7	0.023454
GO:0043331~response to dsRNA	7	0.023454
GO:0051345~positive regulation of hydrolase activity	26	0.023805
GO:0060326~cell chemotaxis	9	0.023918
GO:0007182~common-partner SMAD protein phosphorylation	3	0.023984
GO:0006970~response to osmotic stress	8	0.024269
GO:0006919~activation of caspase activity	11	0.02439
GO:0045088~regulation of innate immune response	11	0.02439
GO:0006954~inflammatory response	42	0.02461
GO:0043388~positive regulation of DNA binding	13	0.025592
GO:0045637~regulation of myeloid cell differentiation	13	0.025592
GO:0051099~positive regulation of binding	14	0.02561
GO:0045184~establishment of protein localization	88	0.025752
GO:0050688~regulation of defense response to virus	6	0.025832
GO:0048008~platelet-derived growth factor receptor signaling pathway	6	0.025832
GO:0002758~innate immune response-activating signal transduction	6	0.025832
GO:0070169~positive regulation of biomineral formation	6	0.025832
GO:0002218~activation of innate immune response	6	0.025832
GO:0006525~arginine metabolic process	5	0.026237
GO:0046209~nitric oxide metabolic process	5	0.026237
GO:0006730~one-carbon metabolic process	18	0.027758
GO:0006469~negative regulation of protein kinase activity	15	0.027761
GO:0015031~protein transport	87	0.027885
GO:0008630~DNA damage response, signal transduction resulting in induction of apoptosis	8	0.028427
GO:0030097~hemopoiesis	32	0.02845
GO:0042060~wound healing	27	0.028671
GO:0009259~ribonucleotide metabolic process	22	0.029012
GO:0018212~peptidyl-tyrosine modification	10	0.029597

GO:0040007~growth	26	0.030268
GO:0031958~corticosteroid receptor signaling pathway	4	0.030857
GO:0007184~SMAD protein nuclear translocation	4	0.030857
GO:0043627~response to estrogen stimulus	17	0.031072
GO:0051092~positive regulation of NF-kappaB transcription factor activity	9	0.031564
GO:0050714~positive regulation of protein secretion	9	0.031564
GO:0051607~defense response to virus	6	0.031898
GO:0032570~response to progesterone stimulus	6	0.031898
GO:0043123~positive regulation of I-kappaB kinase/NF-kappaB cascade	16	0.032106
GO:0000060~protein import into nucleus, translocation	8	0.03304
GO:0048520~positive regulation of behavior	8	0.03304
GO:0001952~regulation of cell-matrix adhesion	7	0.033491
GO:0045428~regulation of nitric oxide biosynthetic process	7	0.033491
GO:0030728~ovulation	5	0.034112
GO:0002224~toll-like receptor signaling pathway	5	0.034112
GO:0050900~leukocyte migration	11	0.0343
GO:0048754~branching morphogenesis of a tube	12	0.034553
GO:0031589~cell-substrate adhesion	16	0.0348
GO:0042592~homeostatic process	85	0.035657
GO:0033673~negative regulation of kinase activity	15	0.035927
GO:0051591~response to cAMP	9	0.035951
GO:0043122~regulation of I-kappaB kinase/NF-kappaB cascade	17	0.036237
GO:0051129~negative regulation of cellular component organization	21	0.037073
GO:0048534~hemopoietic or lymphoid organ development	34	0.03746
GO:0035023~regulation of Rho protein signal transduction	16	0.037654
GO:0001763~morphogenesis of a branching structure	13	0.037681
GO:0010035~response to inorganic substance	28	0.037719
GO:0045884~regulation of survival gene product expression	6	0.038781
GO:0001569~patterning of blood vessels	6	0.038781
GO:0045429~positive regulation of nitric oxide biosynthetic process	6	0.038781
GO:0002252~immune effector process	20	0.038997
GO:0007507~heart development	29	0.039464
GO:0048872~homeostasis of number of cells	16	0.040673
GO:0043244~regulation of protein complex disassembly	10	0.04197
GO:0043392~negative regulation of DNA binding	10	0.04197
GO:0051100~negative regulation of binding	11	0.042289
GO:0009199~ribonucleoside triphosphate metabolic process	18	0.043028
GO:0022408~negative regulation of cell-cell adhesion	4	0.043168
GO:0052173~response to defenses of other organism during symbiotic interaction	4	0.043168
GO:0060416~response to growth hormone stimulus	4	0.043168
GO:0050691~regulation of defense response to virus by host	4	0.043168
GO:0009125~nucleoside monophosphate catabolic process	4	0.043168
GO:0045684~positive regulation of epidermis development	4	0.043168
GO:0052200~response to host defenses	4	0.043168
GO:0075136~response to host	4	0.043168
GO:0021700~developmental maturation	16	0.04386
GO:0016311~dephosphorylation	22	0.044962
GO:0051798~positive regulation of hair follicle development	3	0.045043
GO:0010544~negative regulation of platelet activation	3	0.045043
GO:0045091~regulation of retroviral genome replication	3	0.045043
GO:0045896~regulation of transcription, mitotic	3	0.045043
GO:0006926~virus-infected cell apoptosis	3	0.045043
GO:0070498~interleukin-1-mediated signaling pathway	3	0.045043
GO:0001757~somite specification	3	0.045043
GO:0007568~aging	17	0.045114
GO:0030509~BMP signaling pathway	9	0.045914
GO:0016568~chromatin modification	35	0.046203
GO:0010212~response to ionizing radiation	11	0.046723
GO:0051091~positive regulation of transcription factor activity	11	0.046723

GO:0051241~negative regulation of multicellular organismal process	23	0.047682
GO:0046700~heterocycle catabolic process	13	0.049058

Supplementary Table 7. Overrepresented Gene Ontology categories regulated by IL-32 α in mouse carotid endothelium *in vivo*.

Molecular and Cellular Functions	Number of Changed Genes			
	Non-Tg_LCA vs. Non-Tg RCA	IL-32 α -Tg LCA vs. IL-32 α -Tg RCA	IL-32 α -Tg RCA vs. Non-Tg RCA	IL-32 α -Tg LCA vs. Non-Tg LCA
Transport	639	344	49	47
Translation	136	108	10	0
Response to stress	463	280	57	82
Cell cycle	254	135	20	35
Cell adhesion	131	89	28	32
Signal transduction	614	270	81	103
Cell proliferation	121	70	12	21
Homeostasis	208	103	22	28
Cell differentiation	473	237	59	48
Immune response	136	84	18	47
Inflammatory response	86	50	6	33
Behavior	73	36	12	9
Apoptotic process	235	109	24	25
Total	4251	2195	547	379

Supplementary Table 8. Changed genes that are involved in inflammation and cell growth and proliferation that regulated by IL-32 α in mouse carotid endothelium *in vivo*.

Gene Symbol	hIL-32 α -Tg LCA vs. Non-Tg LCA					
Inflammation						
Down-regulated	Fold-Changes	P value	Up-regulated	Fold-Changes	P value	
Ptafr	0.24	<0.001	Saa3	5.44	<0.001	
BC013712	0.25	<0.001				
Slc11a1	0.30	<0.001				
Fcer1g	0.32	<0.001				
Il1b	0.32	<0.001				
Clec7a	0.33	<0.001				
Ccr1	0.34	0.008				
Tlr13	0.34	0.002				
Il1rn	0.35	0.001				
Csf1r	0.36	<0.001				
Cd14	0.38	0.006				
Ccl22	0.38	0.005				
Kdm6b	0.38	<0.001				
Pik3cg	0.39	0.002				
Mefv	0.39	0.001				
Fcgr3	0.39	<0.001				
Itgb2	0.39	<0.001				
Pla2g7	0.40	0.003				
Ccl3	0.40	0.003				
Hck	0.42	0.001				
Syk	0.42	<0.001				
Tlr8	0.43	0.004				
Serpinp9b	0.43	<0.001				
Nlrp3	0.45	0.002				
Adam8	0.46	0.001				
Lyn	0.47	0.002				
Tgfb1	0.48	<0.001				
Alox5ap	0.48	<0.001				
Tlr2	0.48	0.015				
Myd88	0.49	0.001				
Tnfrsf1b	0.49	0.005				
Osm	0.50	0.024				

Cell Cycle and Cell Proliferation					
Down-regulated	Fold-Changes	P value	Up-regulated	Fold-Changes	P value
Ccnb2	0.12	<0.001	None		
Itgax	0.18	<0.001			
Igfbp3	0.21	0.002			
Kif20a	0.28	0.001			
Cep55	0.29	0.001			
Slc11a1	0.30	<0.001			
Ptprc	0.31	<0.001			
Il1b	0.32	<0.001			
Plk1	0.32	0.002			
Cdkn1a	0.33	<0.001			
Cks2	0.34	0.016			

Dusp1	0.34	<0.001
Mki67	0.34	<0.001
Ptpn6	0.35	<0.001
Ccna2	0.36	<0.001
Malt1	0.36	0.003
Cxcr4	0.36	<0.001
Cd74	0.36	<0.001
Prked	0.36	0.004
Ndc80	0.37	0.027
Kif23	0.37	0.001
Tpx2	0.37	<0.001
Anln	0.38	0.002
Itgam	0.39	0.001
C5ar1	0.39	0.028
Slfn1	0.39	<0.001
Top2a	0.40	0.010
Ect2	0.40	0.011
Rgs2	0.42	<0.001
Itgal	0.43	0.005
Tet2	0.44	<0.001
Nusap1	0.45	0.004
Rasgrp4	0.45	0.014
Kif11	0.45	<0.001
Dock2	0.45	<0.001
Stat4	0.46	0.049
Kif2c	0.46	<0.001
Nuf2	0.47	<0.001
Txnip	0.48	<0.001
D2Ertd750e	0.48	0.001
Sesn2	0.48	0.006
Racgap1	0.49	0.014
Gpr132	0.49	0.022
Rassf2	0.49	0.001

Supplementary Table 9. List and sequences of qPCR primers for mRNA expression.

Primer Name		Sequences
18s	For	5'-AGGAATTGACGGAAGGGCACCA-3'
	Rev	5'-GTGCAGCCCCGGACATCTAAG-3'
VCAM-1	For	5'-TCTTGGGAGCCTCAACGGTA-3'
	Rev	5'-CAAGTGAGGGCCATGGAGTC-3'
ICAM-1	For	5'-GGACTCACCTGCTGGTCTCT-3'
	Rev	5'-CCCCTGCGATCTAGGAATT-3'
TIMP3	For	5'-CACGGAAGCCTCTGAAAGTC-3'
	Rev	5'-TCCCACCTCTCCACAAAGTT-3'
RECK	For	5'-ATAGGCTGCAAACCCATCAT-3'
	Rev	5'-CCGTAACATCCCAGCACATA-3'
IL-1 β	For	5'-AGAGCCTGTGTTTCCTCCT-3'
	Rev	5'-GAGAGTGCTGCCTAATGTCC-3'
eNOS	For	5'-ATCCAGTGCCTGCTTC-3'
	Rev	5'-GCAGGGCAAGTTAGGATCAG-3'
MMP9	For	5'-ACGACATAGACGGCATCCA-3'
	Rev	5'-GCTGTGGTCAGTTGTGGTG-3'
DGCR8	For	5'-GGGGTTCCCTTACTACGCATGT-3'
	Rev	5'-CACACTCTGTCAGAGGTCTCCT-3'
DROSHA	For	5'- ATGCAAGGCAATACGTGTCAT -3'
	Rev	5'- TTTTGGGGTCTGAAAGCTGGT-3'
DICER1	For	5'-AGATGGAGGCGGGAGTCAG-3'
	Rev	5'-CAATGAGCAGGTTGGTCTCA-3'
RPRD2	For	5'-GCAGCTTCCCATAATGCCAG-3'
	Rev	5'-TTGGATTCTGGATGTTGTGA-3'
DDX5	For	5'-GCACCGCACAAAGAGGTAGAT-3'
	Rev	5'-ATCCACTGAGAGCACTGGC-3'
KHSRP	For	5'-GCTGGAAGATGGAGACCAGC-3'
	Rev	5'-GGGTCCCAGTTGAGAACCAA-3'
XRN1	For	5'-GGTCTTATGCTGGAACCTCCT-3'
	Rev	5'-AATCAAGTCTCCTGAATCCTGAA-3'