Proteomic analysis of descending thoracic aorta identifies unique and universal signatures of aneurysm and dissection

Louis Saddic, MD, PhD,[a] Amanda Orosco, BS,[b] Dongchuan Guo, PhD,[c] Dianna M. Milewicz, MD, PhD,[c] Dana Troxlair, MD,[d] Richard Vander Heide, MD,[d] David Herrington, MD,[e] Yue Wang, PhD,[f] Ali Azizzadeh, MD,[b] *and* Sarah J. Parker, PhD,[b] *Los Angeles, Calif; Houston, Tex; New Orleans, La; Winston-Salem, NC; and Arlington, Va*

ABSTRACT

Objective: Very few clinical predictors of descending thoracic aorta dissection have been determined. Although aneurysms can dissect in a size-dependent process, most descending dissections will occur without prior enlargement. We compared the proteomic profiles of normal, dissected, aneurysm, and both aneurysm and dissected descending thoracic aortas to identify novel biomarkers and further understand the molecular pathways that lead to tissue at risk of dissection.

Methods: We performed proteomic profiling of descending thoracic aortas with four phenotypes: normal ($n = 46$), aneurysm ($n = 22$), dissected ($n = 12$), and combined aneurysm and dissection ($n = 8$). Pairwise differential protein expression analyses using a Bayesian approach were then performed to identify common proteins that were dysregulated between each diseased tissue type and control aorta and to uncover unique proteins between aneurysmal and dissected aortas. Network and Markov cluster algorithms of differentially expressed proteins were used to find enriched ontology processes. A convex analysis of mixtures was also performed to identify the molecular subtypes within the different tissue types.

Results: The diseased aortas had 71 common differentially expressed proteins compared with the control, including higher amounts of the protein thrombospondin 1. We found 42 differentially expressed proteins between the aneurysm and dissected tissue, with an abundance of apolipoproteins in the former and higher quantities of extracellular matrix proteins in the latter. The convex analysis of mixtures showed enhancement of a molecular subtype enriched in contractile proteins within the control tissue compared with the diseased tissue, in addition to increased proportions of molecular subtypes enriched in inflammation and red blood cell expression in the aneurysmal compared with the dissected tissue.

Conclusions: We found some overlapping differentially expressed proteins in aneurysmal and nonaneurysmal descending thoracic aortas at risk of dissection compared with normal aortas. However, we also found uniquely altered molecular pathways that might uncover mechanisms for dissection. (JVS—Vascular Science 2022;3:85-181.)

Clinical Relevance: Diseases of the descending thoracic aorta such as aneurysms and dissections carry a high degree of morbidity and mortality. At present, a complete understanding is still lacking of the genetics that drive these diseases and why some aortic segments dissect in the presence or absence of an aneurysm. We compared and contrasted the whole proteome expression of descending aortas from patients with normal, dissected, aneurysmal, and aneurysmal with dissected pathology aortic tissue. We uncovered potential tissue markers that might serve as future targets for therapy or predictors of disease progression.

Keywords: Aneurysm; Descending thoracic aorta; Dissection; Proteomics

From the Department of Anesthesiology and Perioperative Medicine, David Geffen School of Medicine, University of California, Los Angeles, Los Angeles[a]; the Department of Cardiology, Smidt Heart Institute, Cedars-Sinai Medical Center, Los Angeles[b]; the Department of Internal Medicine, McGovern Medical School, University of Texas Health Science Center, Houston[c]; the Department of Pathology, Louisiana State University, New Orleans[d]; the Department of Cardiovascular Medicine, Wake Forest University, Winston-Salem[e]; and the Department of Electrical and Computer Engineering, Virginia Polytechnic Institute and State University, Arlington.[f]

The present study was funded by a Cedars-Sinai Institutional "Leon Fine" award (2018/2019; primary investigators S.J.P. and A.A.), the National Institutes of Health (grants R00HL128787 to S.J.P., 5R01HL111362-06 to D.H., and R01 HL146583-01 and 1P01HL110869-01A1 to D.M.M.), and a Foundation for Anesthesia Education and Research Mentored Training Grant (to L.S.).

Author conflict of interest: none.

Correspondence: Sarah J. Parker, PhD, Department of Cardiology, Smidt Heart Institute, Cedars Sinai Medical Center, AHSP A9228, 8700 Beverly Blvd, Los Angeles, CA 90048 (e-mail: sarah.parker@cshs.org).

The editors and reviewers of this article have no relevant financial relationships to disclose per the JVS-Vascular Science policy that requires reviewers to decline review of any manuscript for which they may have a conflict of interest.

2666-3503

https://doi.org/10.1016/j.jvssci.2022.01.001

Acute aortic syndromes are among the deadliest forms of cardiovascular disease. In particular, type A aortic dissections carry a high risk of mortality. In contrast, most patients with type B dissections will survive hospitalization, although the rates of morbidity and mortality have continued to be high.[1] Predicting which patients will be at risk of acute dissection is extremely difficult. The aortic size has continued to be one of the few risk factors routinely used in clinical practice. Pathologically, aneurysms of the thoracic aorta result from medial degeneration. This destruction causes the wall to thin, grow, and weaken, which is thought to increase the likelihood of dissection under pressure.[2] However, many recent studies have shown that a significant number of both type A and B dissections will occur at sizes well below the current guidelines for surgical management. More than 80% of type B dissections can occur at diameters <5.5 cm, with little to no enlargement at all.[3,4] The pathology underlying these nonaneurysmal dissections is much less understood. In addition, aneurysms will often be mostly silent, resulting in few clinical symptoms. At times, they will be identified incidentally on diagnostic imaging or through a family history. Nonaneurysmal aortas at risk of dissection go almost completely undetected.[5] As such, novel screening methods are desperately needed to help predict which patients are at risk of acute dissection.

In the present study, we surveyed the proteome of descending thoracic aortas from four different populations: normal descending thoracic aorta, type B aortic dissection (TBAD), descending thoracic aortic aneurysm (TAA), and combined type B dissection with aneurysm (TADA). Our goal was to identify a molecular signature that could be used to better understand the underlying pathology and, ultimately, predict the patients at risk of dissection, regardless of the presence of an aneurysm. The proteins unique to each pathology compared with the control tissue and the overlapping differentially expressed proteins from all disease states were identified using a pairwise Bayesian approach. We also identified a unique set of proteins and molecular subtypes that distinguished TBAD from TAA, which might provide insight into the mechanism of how aortic tissue dissects in the presence or absence of an aneurysm.

ARTICLE HIGHLIGHTS

- **Type of Research:** A single-center, prospective case-control study
- **Key Findings:** Proteomic profiling of 88 descending thoracic aortas uncovered increased levels of thrombospondin 1 as a universal marker of aneurysms and dissection. In contrast, the levels of key extracellular matrix proteins were greater in dissected tissue and the apolipoprotein levels were higher in aneurysms.
- **Take Home Message:** Descending thoracic aortas at risk of dissection from aneurysmal or nonaneurysmal precursors have common proteomic signatures, with the exception of certain key pathways.

METHODS

Patients and tissue samples. We prospectively enrolled 42 patients undergoing aortic surgery for aneurysm repair or chronic aortic dissection. Normally discarded descending thoracic aortic tissue was extracted from the operating room and flash frozen for later use. An additional 46 normal descending thoracic aortas were taken at autopsy <24 hours after death from individuals in accordance with approved procedures and institutional review board approval described in detail previously.[6] The University of Texas Medical Center review board approved the procedures for aneurysm and dissection sample acquisition (principal investigators, D.M.M. and A.A.). The patient demographics, including sex, were obtained from the electronic medical records (Table I). The cause of death for the control patients is listed in Supplementary Table I.

Sample preparation and mass spectrometry. The flash frozen tissue samples were pulverized over a bath of liquid nitrogen into a fine powder. The tissue powder was solubilized in a 6 M urea 0.1% RapiGest (Waters, Milford, Mass) lysis buffer, and the proteins were extracted using high pressure cycling on a barocyler instrument (Pressure Biosciences, Easton, Mass) with 45 × 60-second cycles consisting of 50 seconds at high pressure (40 PSI) followed by 10 seconds at normal atmospheric pressure. The protein concentration of the lysates was determined, and 50 μg of protein was allocated, reduced with 10 mM dithiothreitol, alkylated with 100 mM iodoacetamide, and digested with 1:20 trypsin/protein ratio using sequencing grade trypsin/LysC mix (Promega, Madison, Wis) in the presence of 10% acetonitrile. The digested peptides were partially dried, and the pH of the residual solution was adjusted to <2 with the addition of 10% formic acid (FA). Digested peptides were partially dried, and pH was lowered to <2 with the addition of 10% FA. The acidified samples were desalted on Waters C18 desalting plates (Waters) according to the manufacturer's protocol. Desalted peptides were dried and resuspended at 1 μg/μL in 0.1% FA in high-performance liquid chromatography–grade water and mixed 1:1 with a 1:20 dilution of indexed retention time standard peptides (Biogynosys, Schlieren, Switzerland) for a final loading concentration of 0.5 μg/μL.

A total of 4 μg of peptide was loaded onto a 15-cm C18 reverse-phase column attached to an Eksigent 415 HPLC system operating in microflow mode equipped with an Ekspert nanoLC 400 autosampler. The peptides were first loaded onto a trap column (10 × 0.3 mm, C18CL, 5 μm, 120Å; Sciex, Framingham, Mass) for 3 minutes at

Table I. Patient demographics

Aortic pathology	Age, years	Male sex	White race	CAD	COPD	HTN	PVD	CVA	Family history[a]
Control (n = 46)	41.93 ± 8.08	76	72	NA	NA	NA	NA	NA	NA
TAA (n = 22)	45.45 ± 7.96	86	45	20	10	100	0	0	0
TBAD (n = 12)	43.5 ± 11.49	75	33	0	0	50	0	0	25
TADA (n = 8)	48.13 ± 8.08	75	38	0	0	100	16.7	0	16.7

CAD, Coronary artery disease; *COPD,* chronic obstructive pulmonary disease; *CVA,* cerebrovascular accident; *HTN,* hypertension; *NA,* not available; *PVD,* peripheral vascular disease; *TAA,* thoracic aorta aneurysm; *TADA,* thoracic aorta dissection and aneurysm; *TBAD,* type B dissecting aorta.
Data presented as mean ± standard deviation or %.
[a]Family history of aortic dissection or aneurysm.

10 μL/min of solvent A (0.1% FA in water) followed by separation on an analytical column (ChromXP C18CL, 150 × 0.3 mm, 3 μm, 120Å; Sciex) at a flow rate of 5 μL/min using a linear AB gradient of 3% to 35% solvent B (0.1% FA in acetonitrile) for 60 minutes, 35% to 85% solvent B for 2 minutes, holding at 85% solvent B for 5 minutes, followed by reequilibration at 3% solvent B for 7 minutes. Mass spectra were collected in data independent acquisition mode, with the instrument looping through an initial MS1 scan of 250 ms (range, 400-1250 m/z), followed by acquisition of 100 MS2 scans of 30 ms (range, 100-1800 m/z) from peptide ions filtered through mass windows of variable width. The total cycle time was 3.3 seconds, allowing for a minimum of 10 sampled points across a given chromatographic peak for subsequent quantification of peptide MS2 fragments. Source gas 1 was set to 15 PSI, gas 2 was set to 20 PSI, and curtain gas was set to 25 PSI. The source temperature was set to 100°C, and source voltage was set to 5500 V.

Peptide library, normalization, and imputation. The peptide peak groups were extracted from a customized library consisting of an existing library of pooled human vascular lysates described previously[6] (available at: http://www.peptideatlas.org/PASS/PASS01066) merged with the Q1 pseudospectra files extracted from the sample-specific DIA files (generated as described) using the DIA-Umpire signal extraction module.[7] The groups were searched and formatted as a peptide library as described in detail previously.[8] Peptide groups containing up to six fragment ions were extracted from the library using the openSWATH workflow[9] and implemented in-house, as described previously.[6,10] In brief, the peptide peak groups were extracted from the raw data and the identifications scored according to multiple metrics. Decoy peak groups in the peptide assay facilitate modeling of the peptide score distributions and assignment of false discovery. The TRIC algorithm then aligns the peptide identifications across the experiment.[11] The fragment level intensities from each file were normalized to the total extracted MS2 signal intensity of that file (eg, akin to normalization to total protein in a Western blot), and normalized MSSTATS software was used to aggregate the fragment level data into protein intensities.[12]

Differential protein expression. Differential protein analysis was performed on log-transformed abundances using the LIMMA package in R studio.[13] A $\log_2$ fold change of 1.0 and an adjusted *P* value of < .05 (false discovery rate) was used for the cutoff parameters. A complete list of all pairwise analyses is presented in Supplementary Tables II and III.

Protein networks, heatmaps, and principal component analysis. Protein networks were constructed using the STRING interaction network, and their visualization was customized in cytoscape.[14,15] Clustering was performed using the MCL method with an inflation parameter set to 3. Gene ontology was conducted on clusters, and enrichments were considered significant at $P < .05$ (false discovery rate). Heatmaps and principal component analysis were conducted in R studio using the package ggplots2.[16]

Application of convex analysis of mixtures across the DIA-MS protein data from unselected specimens. To explore the underlying heterogeneity in molecular subtypes present within the tissue homogenates (eg, lysates reflecting multiple contributing cell types), we implemented the convex analysis of mixtures (CAM) pipeline,[17,18] the methods and function of which have been described in detail previously.[10] Pertinent modifiable settings were the elimination of signals outside of a 5%- to 95%-interval of total intensity and k for the minimum descriptive length parameterization set to test 2 to 10 putative subtypes. The most likely subtype number was determined from the minima of the minimum descriptive length plot, and the CAM workflow was then used to determine the protein markers of each subtype by first predicting the expression proportions for each protein across the six subtypes and identifying the proteins with dominant or exclusive predicted expression in one subtype relative to the others. Finally, the algorithm was used to estimate the relative proportions of each subtype present in each sample from the dataset. Marker protein gene ontology analysis was performed using the ShinyGO online

Table II. Common differentially expressed proteins between thoracic aneurysms, dissections, and aneurysms with dissection compared with control

Protein symbol	Protein name	Direction of expression	CAM subtype marker
IGDCC3	Immunoglobulin superfamily DCC subclass member 3	Down	
GLD2	Poly(A) RNA polymerase GLD2	Down	
FABP1	Fatty acid-binding protein 1	Down	S4
CELSR3	Cadherin EGF seven-pass G-type receptor 3	Down	S4
FURIN	Furin	Down	
MB	Myoglobin	Down	
XDH	Xanthine dehydrogenase	Down	S4
DCN	Decorin	Down	
GSS	Glutathion synthetase	Down	
MYO18A	Unconventional myosin-XVIIIa	Down	S4
ACAN	Aggrecan core protein	Down	S4
OR4C3	Olfactory receptor family 4 subfamily C member 3	Down	
PPM1F	Protein phosphatase Mg2+/Mn2+ dependent 1F	Down	
CA3	Carbonic anhydrase 3	Down	
DES	Desmin	Down	
CKM	Creatine kinase M-type	Down	
KRT73	Keratin 73	Down	S4
LSM7	U6 SnRNA-associated Sm-like protein LSm7	Down	
TPM2	Tropomyosin beta chain	Down	S4
APP	Amyloid-beta A4 protein	Down	S4
ERC2	ERC protein 2	Down	
RNASE1	Ribonuclease pancreatic	Down	
MFGE8	Lactadherin	Down	S4
CATSPERG	Cation channel sperm associated auxiliary subunit gamma	Down	S4
SBSPON	Somatomedin-B and thrombospondin type-1 domain-containing protein;	Down	
FAM198B	Golgi associated kinase 1B	Down	S4
SPON1	Spondin-1	Down	
SON	Protein SON	Down	S4
FILIP1L	Filamin A interacting protein 1 like	Down	S4
LGALS3BP	Galectin 3 binding protein	Down	
ADGRE5	Adhesion G protein-coupled receptor E5	Down	
DKK3	Dickkopf-related protein 3	Down	
TPM1	Tropomyosin alpha-1 chain	Down	S4
CFP	Properdin	Down	S4
SPARCL1	SPARC-like protein 1	Down	S4
CCN3	Cellular communication network factor 3	Down	
CKB	Creatine kinase B-type	Down	S4
SOD3	Extracellular superoxide dismutase Cu-Zn	Down	S4
FABP4	Fatty acid-binding protein 4	Down	
COL18A1	Collagen type 18 alpha 1 chain	Down	S4
THSD1	Thrombospondin type 1 domain-containing protein 1	Down	S4
VWA1	Von Willebrand factor A domain-containing protein 1	Down	
TINAGL1	Tubulointerstitial nephritis antigen-like precursor	Down	S4
ACAT1	Acetyl-coenzyme A acetyltransferase 1	Down	
RHOB	Ras homolog family member B	Down	
ITGA7	Integrin alpha-7	Down	S4

Table II. Continued.

Protein symbol	Protein name	Direction of expression	CAM subtype marker
SYNM	Synemin	Down	
GALM	Galactose mutarotase	Down	
CRYAB	Alpha-crystallin B chain	Down	
FLNC	Filamin-C	Down	
RILPL1	Rab interacting lysosomal protein like 1	Down	
ANXA5	Annexin A5	Down	
C11orf54	Chromosome 11 open reading frame 54	Down	
LHPP	Phospholysine phosphohistidine inorganic pyrophosphate phosphatase	Down	S4
VIM	Vimentin	Down	S4
ALDH1B1	Aldehyde dehydrogenase 1 family member B1	Down	S4
PSIP1	PC4 and SFRS1-interacting protein	Down	
ANXA4	Annexin A4	Down	
ACTN2	Alpha-actinin-2	Down	S4
PFKL	ATP-dependent 6-phosphofructokinase	Up	S2
SLC2A1	Solute carrier family 2	Up	
FERMT3	Fermitin family homolog 3	Up	
LMAN2	Lectin mannose binding 2	Up	
THBS1	Thrombospondin 1	Up	
PRTN3	Myeloblastin	Up	S6
ELANE	Neutrophil elastase	Up	
S100A8	S100 calcium binding protein A8	Up	S6
SH3RF2	SH3 domain containing ring finger 2	Up	
FANCA	FA complementation group A	Up	S6
c8orf74	Chromosome 8 open reading frame 74	Up	S6
COL3A1	Collagen type 3 alpha 1 chain	Up	S2

CAM, Convex analysis of mixtures.

portal.[19] The top five nonredundant gene otology biological process enrichments for each subtype were used to summarize the overall functional enrichment profile and infer the hypothesized subtype identity.

Histologic findings. Representative tissue samples from the diseased groups were fixed in formaldehyde and embedded in paraffin for sectioning. The samples were sliced in 5-μm sections and stained with hematoxylin and eosin, trichrome, and elastin (ELN)-Van Giessen. The images were captured using the ECHO Revolve microscope (ECHO, San Diego, Calif).

Western blot. Protein lysates were reduced in loading buffer, run on acrylamide gels, and transferred to polyvinylidene fluoride membrane. The membranes were subsequently probed with antibodies against thrombospondin 1 (THBS1; 1:500; sc-59887; Santa Cruz Biotechnology, Dallas, Tex), beta-tubulin (1:1000; Thermo Fisher, Waltham, Mass), and ELN (1:500; sc-166543; Santa Cruz Biotechnology).

RESULTS

Aneurysms and dissections share differentially expressed proteins. After quality measure and removing peptides not present in ≥50% of the samples, 1872 peptides were left. We performed differential protein analysis between the normal descending aorta tissue and each aortic pathology. At a $\log_2$ fold change cutoff of 1.0 and an adjusted *P* value of $< .05$, the number of differentially expressed proteins was 107 for TADA, 416 for TAA, and 272 for TBAD. A total of 71 proteins were shared among the three comparisons: 12 upregulated and 59 downregulated (Table II and Fig 1). Network analysis with MCL clustering generated 14 clusters of at least two proteins (Fig 2, *A*). One main cluster consisted of nine proteins. The top five biological process gene ontology enrichments for proteins in this cluster were positive regulation of endothelial cell apoptotic process, negative regulation of chemotaxis, regulation of mononuclear cell migration, peptide cross-linking, and integrin-mediated signaling pathway. The top molecular function enrichments

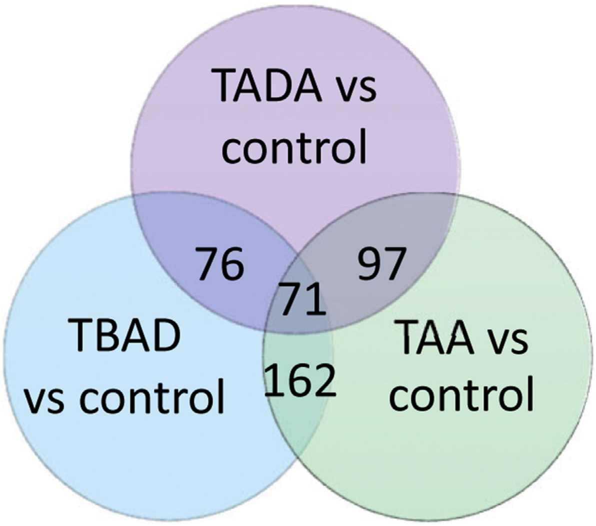

Fig 1. Degenerative aortic syndromes share dysregulated proteins. Venn diagram of overlapping differentially expressed proteins from comparisons between normal aorta and each aortic pathology.

included integrin binding, growth factor binding, and heparin binding. Finally, the top five cellular component enrichments included platelet alpha granule lumen, collagen trimer, endoplasmic reticulum lumen, extracellular matrix, and collagen-containing extracellular matrix (Fig 2, *B*). With 15 edges, THBS1 had the highest degree within this cluster and within the network. THBS1 was significantly upregulated in each disease group compared with the control. We validated this finding with Western blotting on representative samples from each pathology (Fig 2, *C*).

Unique proteins for aneurysms and dissections uncover classic genes associated with degenerative aortas. We next examined the differentially expressed proteins between the aortic pathologies. No proteins had met our predetermined cutoffs when comparing TADA to either TAA or TBAD. There were, however, 42 differentially expressed proteins between TAA and TBAD (Table III and Fig 3, *A* and *B*). Of these 42 proteins, 8 had higher expression in TBAD and 36 in TAA. Network analysis with MCL clustering generated six clusters with at least two proteins (Fig 4, *A*). The three largest clusters contained 12, 7, and 4 nodes. In the largest cluster, the nodes with the highest degree included apolipoprotein A1 (n = 14), apolipoprotein A-II (n = 13), apolipoprotein B (n = 13), and alpha-2-HS-glycoprotein (n= 12), all of which were upregulated in the TAA group compared with the TBAD group. Gene ontology for biological process, molecular function, and cellular component had enrichments for lipoprotein and cholesterol processes. The cluster with second highest number of nodes included fibrillin 1, ELN, collagen type 1 alpha 1 chain, and collagen type 4 alpha 2 chain, all of which were upregulated in the TBAD group compared with the TAA group. The top five biological process gene ontology enrichments were collagen-activated tyrosine kinase receptor signaling pathway, aortic valve morphogenesis, protein trimerization, negative regulation of angiogenesis, and negative regulation of transforming growth factor-beta (TGFβ) receptor signaling pathway. Enrichments in molecular function and cellular component also emphasized extracellular matrix, collagen, and integrin processes (Fig 4, *B*). ELN expression was validated using Western blotting (Fig 2, *C*). The cluster with four nodes included the hemoglobin subunit beta and hemoglobin subunit zeta proteins. Representative histologic images from all photographs of diseased aortic tissue are shown in Fig 4, *C*.

CAM identifies smooth muscle and inflammatory subtypes. The CAM approach uses unsupervised deconvolution of heterogeneous expression data (eg, homogenized arterial tissues with multiple cell types contributing to proteomic expression) to estimate detectable subtypes and their component marker proteins.[10] The CAM workflow identified the presence of at least six putative expression subtypes (Fig 5, *A*). Of these, subtypes S2, S4, and S6 had marker proteins that overlapped with the differentially expressed proteins shared among all disease comparisons, and subtypes S1 and S3 had marker proteins overlapping with the differentially expressed proteins between the aneurysm and dissection groups (Tables II and III). The proportion of each subtype present in each sample was also estimated using CAM, and these estimated proportions showed clear trends across the experimental groups that were consistent with the overlap between the subtype marker proteins and differentially expressed proteins. Specifically, subtypes S2 and S6 demonstrated elevated proportions in all three disease groups and subtype S4 demonstrated a clear reduction in the disease groups relative to the control (Fig 5, *B*). Subtypes S1 and S3 were more elevated in the aneurysm conditions relative to dissection. Gene ontology analysis of the marker proteins for each subtype indicated enrichment of the immune and inflammation pathways in subtype S1, endoplasmic reticulum-related proteins in subtype S2, pathways associated with red blood cells in subtype S3, contractile and cell adhesion pathways in subtype S4, and neutrophil-related pathways in subtype S6 (Fig 5, *C*). Subtype S5 did not exhibit sufficient pathway enrichment for clear interpretation.

DISCUSSION

Thoracic aortic dissection has continued to be one of the highest causes of morbidity and mortality among the cardiovascular diseases. However, few reliable risk factors are available, with the exception of aortic size.[2]

Table III. Differentially expressed proteins between thoracic aneurysms and dissections

Protein symbol	Protein name	Log_2FC	Adjusted *P* value[a]	CAM subtype marker
COL1A1	Collagen type 1 alpha 1 chain	−2.1	.0211	
ELN	Elastin	−1.9	.0211	
FBN1	Fibrillin 1	−1.6	.0353	S2
COL4A2	Collagen type 4 alpha 2 chain	−1.5	.0497	
NPNT	Nephronectin	−1.4	.0436	
LOXL1	Lysyl oxidase like 1	−1.3	.0369	
LAMB2	Laminin subunit beta 2	−1	.0421	
EMILIN1	Elastin micrifibril interfacer 1	−1	.343	
FUCA1	Alpha-L-fucosidase 1	1	.0394	
ECH1	Enoyl-coenzyme hydratase 1	1	.0369	
GSH1	Glutamine cysteine ligase	1	.228	
APOA2	Apolipoprotein A-II	1.1	.0344	S1
LAP3	Leucine aminopeptidase 3	1.1	.0228	
A1AT	Alpha-1 antitrypsin	1.1	.0244	
RBP4	Retinol binding protein 4	1.1	.0498	
FETUA	Alpha-2-HS-glycoprotein	1.1	.0228	
CA2	Carbonic anhydrase 2	1.1	.0394	S3
IGJ	Immunoglobulin J polypeptide	1.1	.0435	S1
SERPINA7	Serpin family A member 7	1.2	.03	S1
APOD	Apolipoprotein D	1.3	.0244	
HBB	Hemoglobin subunit beta	1.3	.0344	S3
APOL1	Apolipoprotein L1	1.4	.0369	
HBA	Hemoglobin subunit alpha	1.4	.0316	S3
CA1	Carbonic anhydrase 1	1.4	.0211	S3
PRTG	Protogenin	1.5	.0369	S3
TNR6C	Trinucleotide repeat containing adaptor 6C	1.5	.0435	
APOC2	Apolipoprotein C-II	1.6	.042	
ADGRF1	Adhesion G protein-coupled receptor F1	1.6	.0228	S3
APOC3	Apolipoprotein C-III	1.6	.0228	
IGKV3D-15	Immunoglobulin kappa variable 3D-15	1.6	.0344	S1
APOB	Apolipoprotein B	1.6	.0211	
HKDC1	Hexokinase domain containing 1	1.7	.0435	
HBAZ	Hemoglobin subunit zeta	1.7	.0376	S3
KANL3	KAT8 regulatory NSL complex subunit 3	1.7	.0228	S3
PGS2	Decorin	1.8	.0211	
EIF4G3	Eukaryotic translation initiation factor 4	1.8	.0344	S1
CYP27B1	Cytochrome p450 family 27 subfamily B member 1	1.8	.0368	
ERC2	ELKs/RAB6-interacting/CAST family member 2	1.9	.0344	
APOA1	Apolipoprotein A1	2	.0183	S1
IGLL5	Immunoglobulin lambda like polypeptide 5	2	.0228	S1
IDNK	Gluconokinase	2.6	.0183	S3
HSF1	Heat shock transcription factor 1	2.6	.0353	S3

CAM, Convex analysis of mixtures; *Log_2FC,* $\log_2$ fold change.
[a]False discovery rate.

Recent studies, however, have indicated that many descending thoracic aortas will dissect without any evidence of prior aneurysm growth and, of even greater concern, do so at less than the recommended thresholds currently set for surgical intervention.[3,4] These clinical findings beg the question of whether dissections with and without an aneurysm represent two different types of diseases. We found at least some

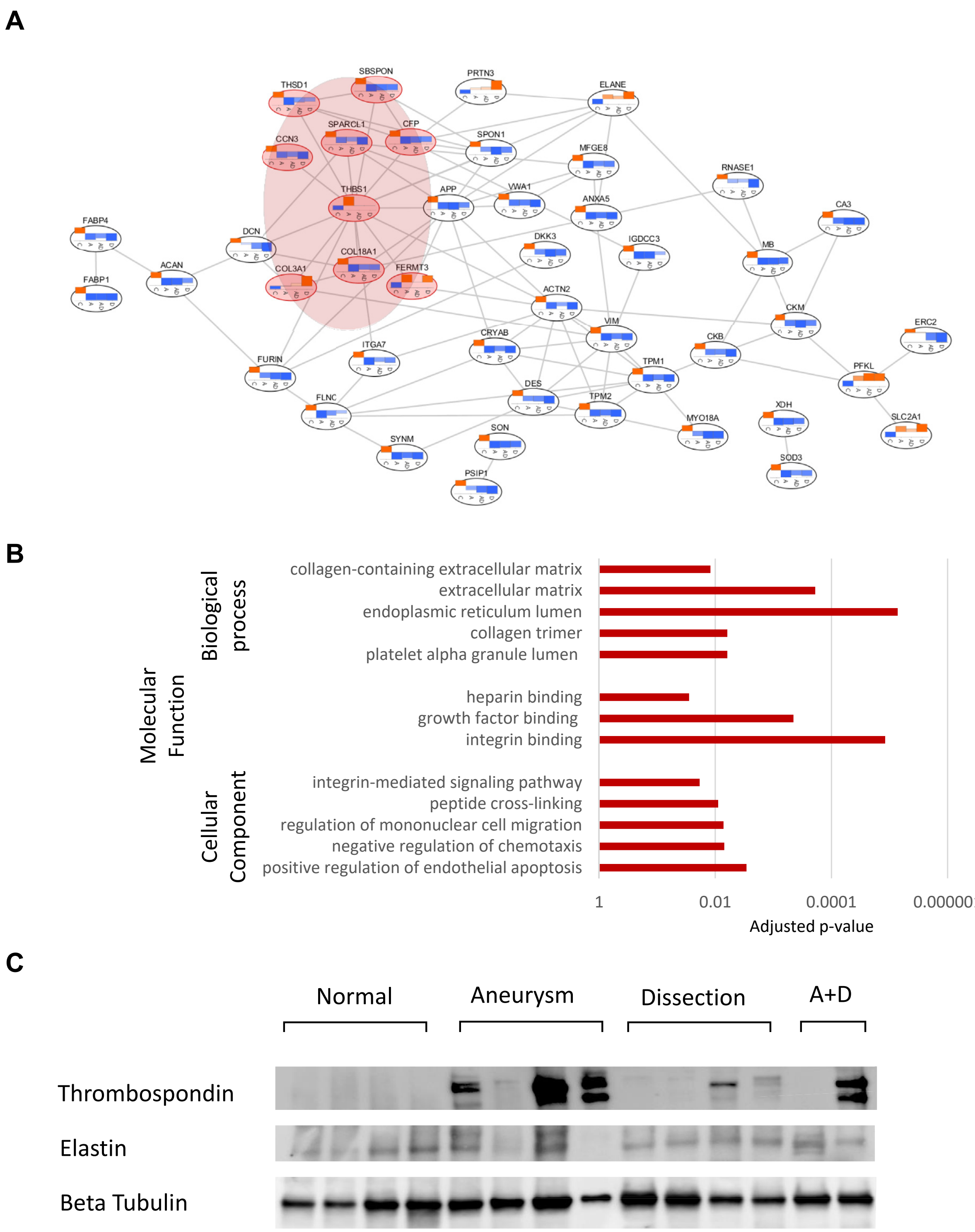

Fig 2. Degenerative aortic syndromes are enriched in extracellular matrix proteins. **A,** String network of overlapping proteins from Fig 1. Relative expression (average Z-scores for a given protein within each experimental group) of each protein in control (*C*), aneurysm (*A*), aneurysm with dissection (*AD*), and dissection (*D*) is displayed in that order as node bar charts, where *orange* indicates a relative increased expression and *blue*, a relative decreased expression. The largest cluster is highlighted in *red*. **B,** Biological process (*Top*), molecular function (*Middle*), and cellular component (*Bottom*) ontology analysis for the largest cluster in the network highlighted in *red*. **C,** Biomarker protein expression levels by Western blotting for representative samples from control and diseased tissue samples.

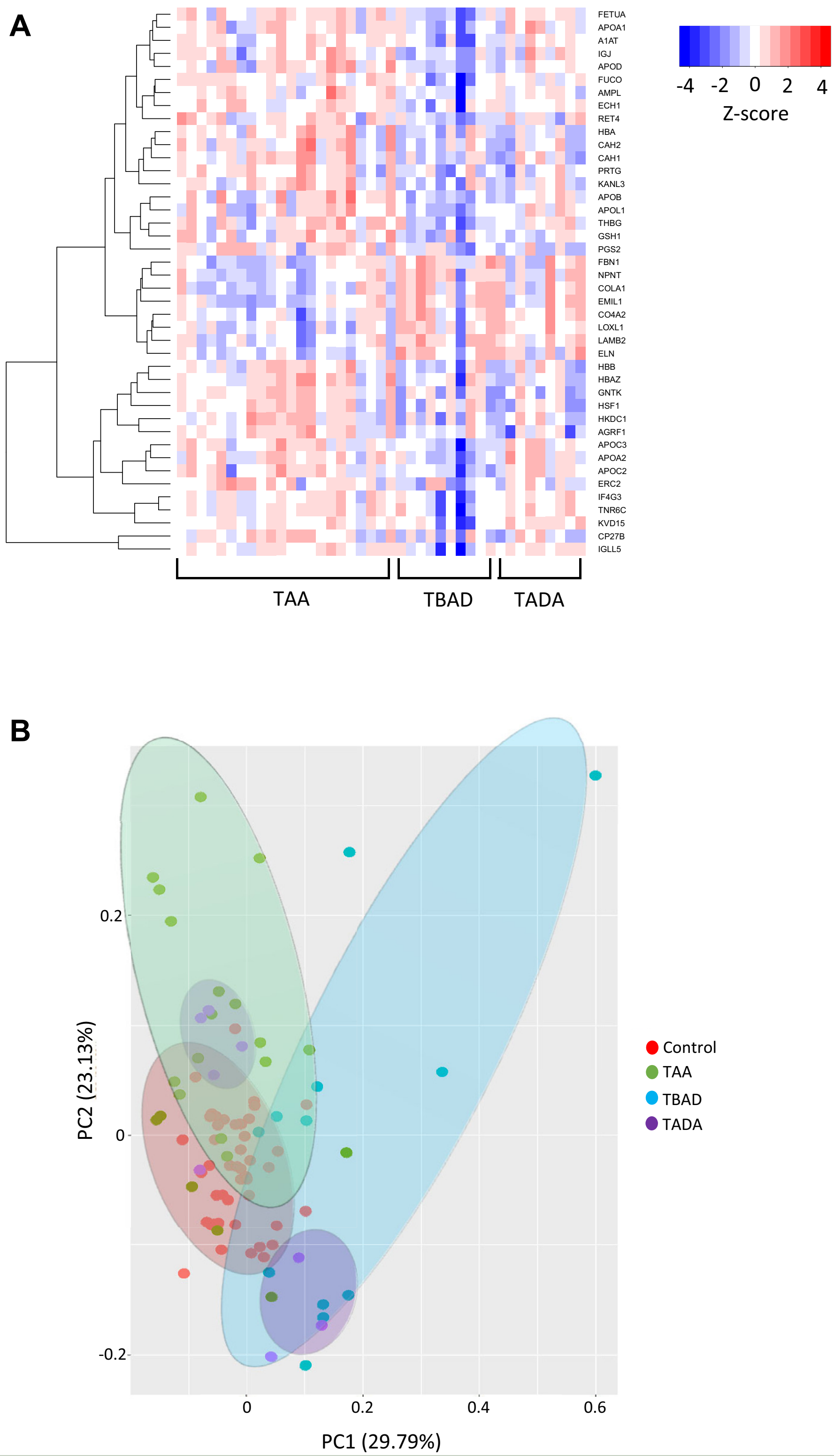

Fig 3. Thoracic aneurysms and dissections have a unique set of differentially expressed proteins. **A,** Heat map of the 43 differentially expressed proteins between aneurysmal and dissection tissue. Relative expression for each protein shown for aneurysmal, dissection, and aneurysm with dissection tissue, where *red* indicates a relative increase and *blue,* a relative decrease. **B,** Principal component analysis using the 43 differentially expressed proteins segregating the control and aortic disease tissue. *PC,* Principal component; *TAA,* thoracic aorta aneurysm; *TADA,* thoracic aorta dissection and aneurysm; *TBAD,* type B aortic dissection.

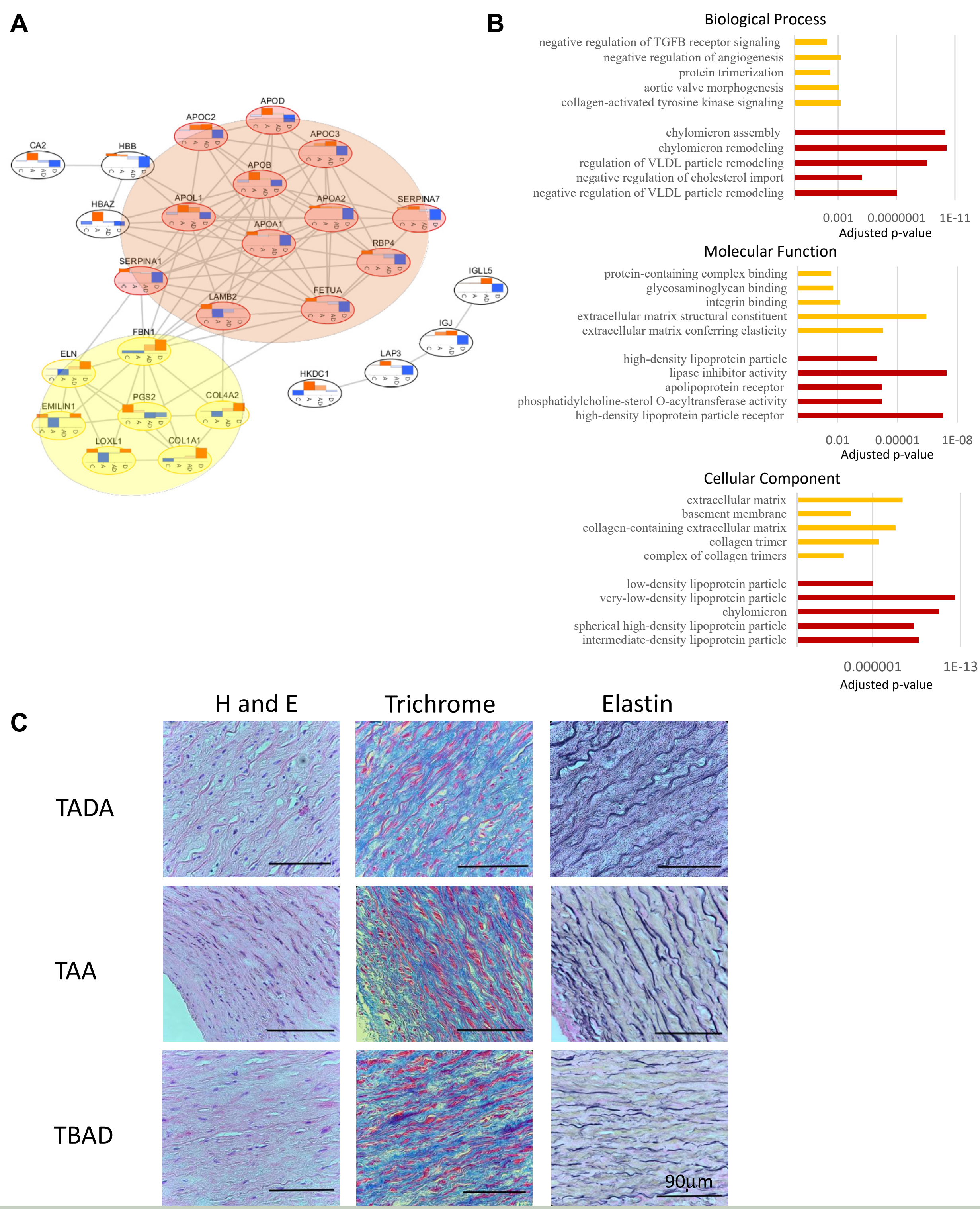

Fig 4. Aneurysm and dissection tissue have unique biological pathways. **A,** STRING protein network of differentially expressed proteins between aneurysms and dissection tissue. The two largest clusters are highlighted in *red* and *yellow*. Relative expression (average Z-scores for a given protein within each experimental group) of each protein in control (*C*), aneurysm (*A*), aneurysm with dissection (*AD*), and dissection (*D*) displayed in that order as node bar charts, where *orange* indicates a relative increased expression and *blue*, a relative decreased expression. The two largest clusters are highlighted in *red* and *yellow*. **B,** Biological process (*Top*), molecular function (*Middle*), and cellular component (*Bottom*) ontology analysis for the two largest clusters highlighted in **A**. *Red bars* indicate the largest cluster and *yellow bars*, the second largest cluster. **C,** Histologic staining from representative samples of diseased tissue.

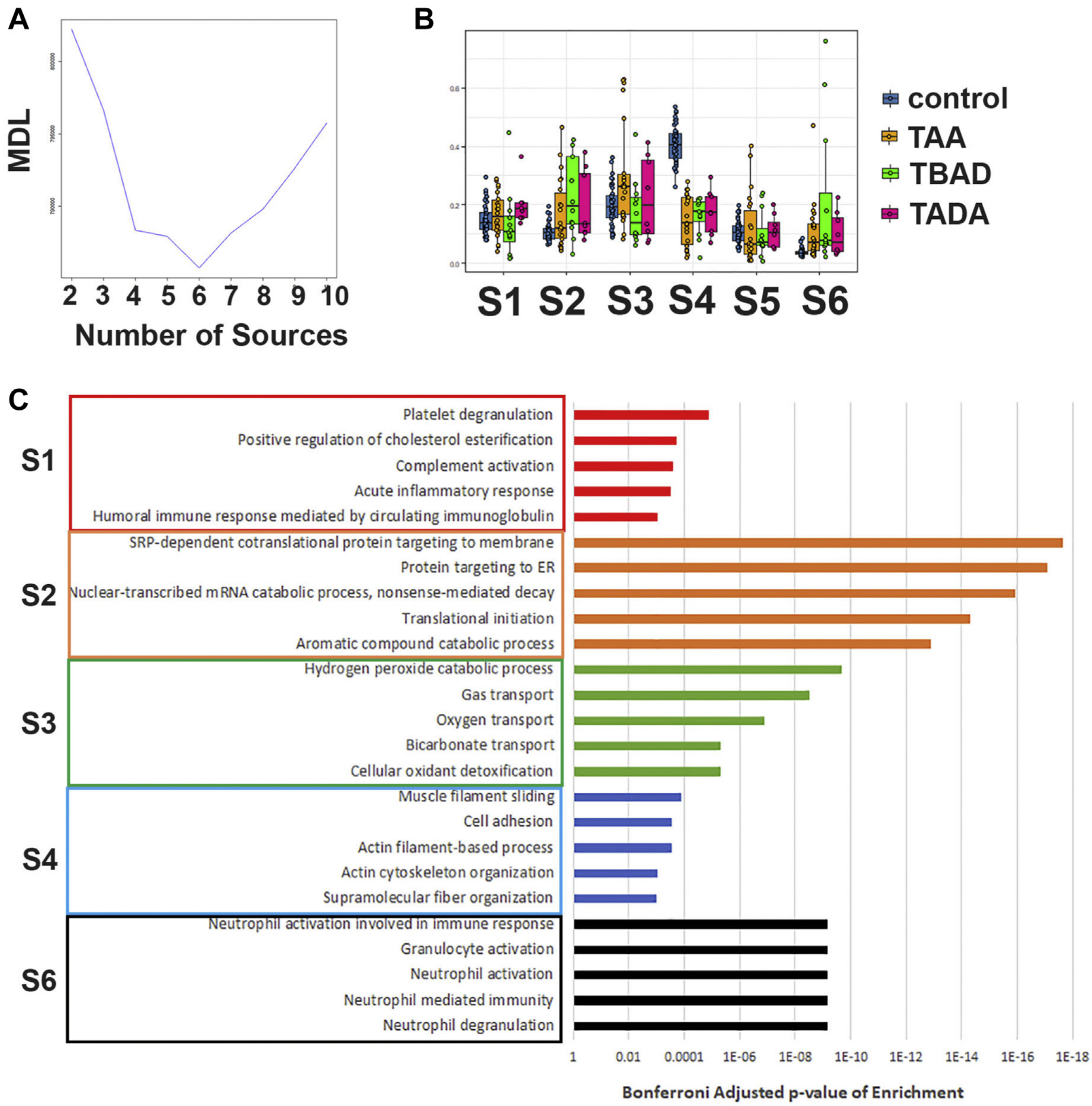

Fig 5. Convex analysis of mixtures (CAM) identified molecular subtypes for aortic disease. **A,** Minimum distance length plot generated in CAM for K = 2 to 10 potential sources, with minima indicated for 6 sources. **B,** Box plot of CAM-estimated subtype proportions present in each of the experimental samples, separated by disease category. **C,** Gene ontology enrichment analysis of the top representative biological process annotations for each subtype. Subtype 5 was omitted owing to the lack of enriched pathways. *ER,* Endoplasmic reticulum; *TAA,* thoracic aorta aneurysm; *TADA,* thoracic aorta dissection and aneurysm; *TBAD,* type B aortic dissection.

differences in the pathways that govern these two diseases, as indicated by the differential protein expression analysis between the TAAs and TBADs. No proteins, however, were significantly altered comparing TADA to TBAD or TAA. This finding was consistent with the CAM results, which showed that within most subtypes TADA was clustered between TBAD and TAA, with the exception of perhaps subtype S1, for which TADA clustered more closely with TAA than with TBAD. The inability to distinguish TADA from TBAD and TAA might have been because TADAs share a signature with both TAA and TBAD or because TADAs represent a mixture of signatures, such that each aorta behaves more like TAA or TBAD. Thus, given the low sample size, the differential expression and CAM were unable to identify significant distinguishing features. We favored the latter theory because the TADAs tended to cluster with either TAA or TBAD using principle component analysis. In addition, we lacked information regarding whether the TADA samples represented atherosclerotic aneurysms that had dissected or dissected tissue that had degenerated into an aneurysm or pseudoaneurysm.

The results of our analyses have shown that the normal tissue was molecularly different from the pathologic tissue. However, we also sought to determine whether any similarities were present between the different types of pathologic aortas. We found 71 proteins that were similarly differentially expressed between each pathology and normal tissue, representing 66%, 17%, and 21% of the differentially expressed proteins from TADA, TAA, and TBAD, respectively. Clearly, some common features exist among aneurysms at risk of dissection, aneurysms that dissect, and aortas without aneurysms that dissect. A network analysis of these 71 proteins generated one main cluster. THBS1 was at the center of this cluster, with a degree of 15. THBS1 was one of the few upregulated proteins in disease tissue compared with the normal tissue, and prior studies have demonstrated a pathologic role for increased THBS1 expression in both aneurysms and dissections. In the *Fbln4*^{SMKO} aneurysm mouse model, THBS1 is upregulated and causes disruption of the actin cytoskeleton and ELN-contractile apparatus. Deletion of this gene prevents aneurysm formation.[20] In humans, THBS1 is upregulated in the aortas and plasma of patients with acute dissection and might play a role in smooth muscle cell apoptosis and macrophage activation.[21] Thus, THBS1 might be a useful diagnostic marker for all types of aortic degeneration. In addition, THBS1 enzyme-linked immunosorbent assay kits are commercially available and have been used by others to easily detect plasma levels in patients, indicating the practicality of using this protein as a biomarker.[22] Further work in animal models is needed to determine whether THBS1 can be used to predict aneurysms at risk of dissection.

The proteome we analyzed represents a homogenate of multiple underlying cell types. Unsupervised deconvolution by CAM provided provisional insight into how the proteome is organized in terms of the molecular or cellular subtypes. When the proteins in our CAM were screened for those with the gene ontology annotation “contractile,” and their expression was compared across the six subtypes, subtypes S2 and S4 demonstrated a clear enrichment for contractile protein expression (Supplementary Fig). Nevertheless, subtype S4 was more abundant in normal tissue, and subtype S2 was more abundant in diseased tissue. Recent studies using single cell–based omics have shown different populations of smooth muscle cells with unique genetic signatures.[23] Subtypes S4 and S2 could represent two such unique populations of smooth muscle cells, and the shift in abundance of these two populations could be a phenotype of aortic disease. Infiltration of different cells, such as immune cells, from the blood also likely occurs. Subtypes S1 and S6 were enhanced in disease tissue compared with the control tissue, and this group was enriched in inflammatory proteins. Although subtype S6 was enriched for markers of neutrophils and was predicted to be upregulated in all three disease states, subtype S1 was marked by monocyte and IgG (eg, B cell) proteins, and its upregulation appeared limited to the cases with aneurysms. This suggests differences could exist in the nature of the inflammatory involvement between TAA and TBAD, favoring unique involvement of monocyte and B cell infiltration in the etiology of aneurysms but not dissections. Alternatively, this could reflect shifting proportions due to the loss of smooth muscle cells without a large amount of additional infiltration or, even, phenotype switching of smooth muscle cells to phagocytic or monocyte-like cells.[24] This will require significant additional study but presents one intriguing novel hypothesis to explain the differences between these two disease presentations in the descending aorta.

We also uncovered 42 differentially expressed proteins that could distinguish TAA from TBAD. These proteins were enriched in many canonical genes associated with aneurysms and dissections.[5,25] Only eight proteins were upregulated in the TBAD cohort compared with the TAA group, and seven of these eight genes formed the second largest cluster in the network of all dysregulated proteins. The central node of this cluster was fibrillin 1, and the network was enriched in many processes linked to dissection, including collagen, integrin, and TGFβ signaling.[26,27] These findings highlight the delicate balance governed by TGFβ signaling in maintaining the exact amount of extracellular matrix (ECM) content. Upregulation of TFGβ signaling can lead to both ECM destruction and deposition. Our findings suggest that aortas that dissect without aneurysm formation might have fragile media owing to excessive ECM composition and that aneurysms will be marked by a paucity of at least certain ECM components.[28] These findings are consistent with those from previous studies, which have shown that patients with thoracic aortic dissection tend to have increased collagen content and patients with aneurysms tend to have a loss of ELN and collagen.[29] Atherosclerosis can also be an important initiator of aneurysm formation. The largest cluster in the network of differentially expressed proteins contained 12 proteins, all upregulated in TAA compared with TBAD. Of these 12 proteins, 7 were apolipoproteins. Previous studies have demonstrated upregulation of apolipoproteins in thoracic aortic aneurysm samples compared with normal aortas.[30] This finding was also consistent with the CAM results, because subtype S1, which is enriched in cholesterol and inflammatory proteins, was enhanced in TAAs compared with TBADs. This could signify a shift toward more inflammatory cells in aneurysm tissue compared with dissected tissue, which is known to occur after TGFβ-mediated metalloproteinase destruction of ECM.[31] Finally, the third largest cluster included hemoglobin proteins, which have also been shown to be upregulated in proteomic studies of abdominal and thoracic aortas. Similarly, subtype 3 in the CAM profile, which was enriched in red blood cell markers, was enhanced in aneurysmal tissue. The significance of this trend is unclear but might represent mural thrombus, a stress response and upregulation of fetal proteins, a response to hypoxia locally, or contamination from the destruction of red blood cells in the turbulent flow that occurs in aneurysms.[32] The utility of using these targets to predict acute dissection can be elucidated from experimental serum proteomics in animal models of dissection with and without aneurysms and prospective proteomic analysis of patients with and without aneurysms.

The present study had some limitations. First, we were unable to obtain significant background information such as the comorbidities of the donor control patients. Furthermore, the proportion of white patients was greater in the control group than in the disease groups ($P = .03$, χ^2 analysis), although we did not observe significant differences in the differential protein analysis when race was added as a covariate (data not shown). Also, the donor control patients were slightly younger than the patients with aortic disease, although the difference was not statistically significant ($P = .18$, analysis of variance). In addition, although no significant sex differences were present between all groups in our study ($P = .78$, χ^2 analysis), men were overrepresented. As such, additional studies with female patients will be important to uncover potential sex differences. Finally, for the most part, TBAD and TADA represent aortic dissections that do not degenerate to aneurysms and those that do degenerate to aneurysms, respectively. However, we did not have sufficient clinical information to fully rule out a sample in the TADA group representing an aneurysm that had subsequently dissected. We also failed to detect significant differences between TADA and TBAD and TADA and TAA. This was likely in part due to the heterogeneous nature of TADA patients and the low sample size. Nevertheless, we have uncovered significant candidate proteins that could be used as biomarkers for degenerative diseases of the descending aorta and the risk of acute dissection pending serum validation.

CONCLUSIONS

We have presented a novel comparison of proteomic profiles from normal human descending thoracic aorta and tissue with aneurysmal growth, dissection, and aneurysm with dissection. Although most of the currently available proteomic profiles of the human aorta are from the ascending thoracic and abdominal segments, we have added profiles from the descending thoracic aorta. Because patients with diseases of the descending aorta have different treatment and diagnostic algorithms compared with diseases of other segments, we sought to share some of the protein signatures that could help explain these clinical differences. We were able to identify THBS1 as potential biomarker of degenerative diseases of the aorta such as aneurysms and dissections. A comparison between patients with TAA and TBAD highlighted the crucial balance of TGFβ signaling in ECM deposition and destruction and provided a potential mechanism for how this pathway could be responsible for two different types of pathology that can lead to the same clinical outcome, namely dissection.

We are grateful for the support of the Cedars-Sinai Proteomics and Metabolomics Core Facility, including Rakhi Pandey and Ron Holewinski, for technical support in MS data acquisition. We are also deeply grateful to the Genomic and Proteomic Architecture of Atherosclerosis project leadership for access to the control thoracic aortic tissue and the UTHealth SCCOR biorepository for collection, storage, and release of the aortic aneurysm and dissection specimens.

AUTHOR CONTRIBUTIONS

Conception and design: LS, DG, DM, DH, AA, SP
Analysis and interpretation: LS, AO, DG, DM, DT, RH, DH, YW, AA, SP
Data collection: DG, DM, AA, SP
Writing the article: LS, SP
Critical revision of the article: LS, AO, DG, DM, DT, RH, DH, YW, AA, SP
Final approval of the article: LS, AO, DG, DM, DT, RH, DH, YW, AA, SP
Statistical analysis: LS, SP
Obtained funding: DM, DH, AA, SP
Overall responsibility: SP

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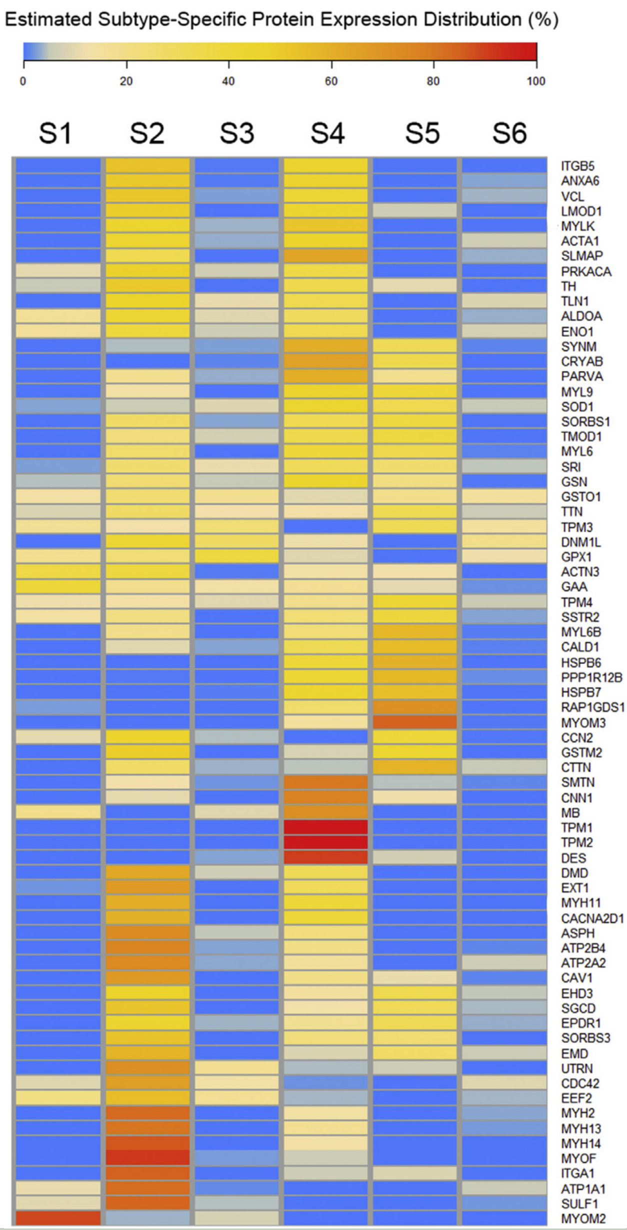
Submitted Jul 21, 2021; accepted Jan 5, 2022.

Appendix



Supplementary Fig. Convex analysis of mixtures (CAM) showing that subtypes 2 and 4 comprised the highest percentage of expressed contractile proteins. Heatmap displaying the proportion of the expression of all CAM genes with the gene ontology annotation "contractile" attributed to each subtype.

Supplementary Table I. Cause of death in control tissue

Cause of death	%
Drug overdose	43.50
Cardiovascular	34.80
Asphyxia	8.70
Trauma	6.50
Pneumonia	4.30
Other	2.20

Supplementary Table II. Complete differential expression analysis between aortic pathologies and normal aorta

Gene	Log_2FC TAA/ normal	Adjusted *P* value[a]	Log_2FC TBAD/ normal	Adjusted *P* value[a]	Log_2FC TADA/ normal	Adjusted *P* value[a]
A1BG	−0.2	.548	−0.9	.001	−0.2	.827
A2M	0.6	.087	−0.3	.487	0.8	.203
AAMDC	−1.2	<.001	−1	.004	−0.5	.458
AARS1	0.2	.651	−0.2	.672	0.1	.951
ABCA13	−1.4	<.001	−0.9	.045	−0.5	.59
ABCCB	−0.5	.332	−0.4	.583	0.3	.829
ABCD1	−0.5	.381	−0.9	.141	0.2	.914
ABCF1	0.5	.323	−1.1	.04	0.7	.469
ABHD14B	−0.7	.029	−1.2	.003	−0.3	.678
ABI3BP	−1.3	<.001	−0.9	.008	−0.8	.147
ACAA1	0.1	.872	−0.5	.295	−0.6	.538
ACAA2	−0.6	.109	−1.1	.017	−1	.157
ACADM	−0.3	.418	−0.6	.118	−0.7	.209
ACADVL	0.2	.563	−0.6	.045	−0.2	.759
ACAN	−2.7	<.001	−1.7	.001	−2.2	.002
ACAT1	−1.5	<.001	−1.8	<.001	−1.3	.01
ACAT2	−0.2	.737	−0.7	.074	−0.1	.949
ACLY	0.2	.593	0.1	.955	−0.2	.851
ACO1	−0.8	.003	−0.9	.01	−0.5	.369
ACO2	−0.3	.444	−0.7	.034	−0.5	.444
ACOT9	0.1	.864	−0.1	.885	0.4	.582
ACP1	−0.7	.004	−1.4	<.001	−0.5	.39
ACSF2	−1.2	.009	−0.8	.204	0.2	.933
ACSL1	−0.3	.585	−0.4	.556	−0.8	.369
ACTA1	−1	.001	−1	.007	−0.5	.458
ACTBL2	−1.1	<.001	−0.5	.127	−0.4	.504
ACTN1	−0.7	.002	−0.2	.53	−0.1	.879
ACTN2	−1.4	<.001	−1.5	<.001	−1	.02
ACTN3	0.2	.829	−0.6	.425	−0.3	.84
ACTN4	−0.9	.001	−0.7	.049	−0.3	.754
ACTR10	0.2	.554	0.2	.641	0.6	.276
ACTR1A	−0.3	.467	−0.8	.022	−0.2	.829
ACTR2	−0.1	.85	0.2	.452	0.1	.967
ACTR3	−0.1	.735	−0.1	.959	−0.1	.991
ACYP2	−1.1	.002	−1.3	.006	−1	.188
ADAM17	−1	.004	−0.8	.073	−0.2	.866
ADAMTS2	−0.8	.153	−2.6	<.001	−1.2	.242
ADAMTSL1	−1.1	.001	−0.2	.742	−0.5	.498
ADAMTSL2	0.3	.765	1.4	.069	1.1	.382
ADAMTSL4	−0.8	.024	−0.3	.602	−0.2	.827
ADARB1	0.1	.959	−0.3	.518	0.8	.167
ADD1	−0.3	.604	−1	.038	−0.7	.364
ADD3	0.1	.938	−0.2	.723	−0.1	.924
ADGRF1	0.8	.025	−0.9	.068	−0.3	.787
ADH1B	−0.9	.061	−0.8	.21	−0.2	.893
ADH5	−0.9	.001	−1.1	.002	−0.5	.369

Supplementary Table II. Continued.

Gene	Log_2FC TAA/ normal	Adjusted *P* value[a]	Log_2FC TBAD/ normal	Adjusted *P* value[a]	Log_2FC TADA/ normal	Adjusted *P* value[a]
ADIPOQ	−0.5	.225	−0.2	.683	0.8	.315
ADIRF	−0.9	.028	−0.7	.213	−0.3	.829
ADSL	0.3	.214	0.1	.893	−0.1	.999
ADSS1	−0.3	.594	0.9	.051	0.9	.245
AEBP1	0.3	.349	0.3	.542	0.4	.613
AFM	0.3	.459	−0.8	.024	0.5	.495
AGL	−0.3	.389	−0.4	.41	0.1	.917
AGRN	−0.7	.02	−0.9	.025	−0.5	.501
AGT	0.1	.965	−0.8	.02	0.2	.767
AHCY	0.1	.912	−0.4	.181	−0.1	.988
AHCYL1	0.1	.942	−0.4	.259	0.1	.988
AHNAK	−0.6	.013	−0.5	.089	−0.7	.179
AHSG	−0.4	.144	−1.5	<.001	−0.4	.449
AIFM1	−0.2	.606	−0.6	.059	−0.5	.283
AIMP2	0.2	.483	0.2	.723	0.3	.681
AIP	−0.5	.149	−0.3	.525	−0.1	.939
AK1	−0.8	<.001	−0.8	.001	−0.7	.028
AK2	−0.7	.052	−1.6	.001	−1	.173
AK3	0.1	.932	−0.4	.375	−0.5	.46
AK4	−1.1	.001	−0.6	.15	−0.7	.363
AK7	0.7	.109	−0.5	.402	−0.2	.87
AKAP12	0.1	.806	−0.4	.395	0.2	.847
AKR1A1	−0.4	.129	−1	.003	−0.1	.879
AKR1B1	−0.2	.516	−0.8	.002	−0.2	.713
AKR7A2	0.1	.806	−0.7	.1	−0.4	.666
AKR7A3	1.2	.043	0.8	.364	1	.48
ALAD	−0.1	.916	−0.7	.076	−0.2	.88
ALB	−0.2	.749	−1.2	.003	0.1	.986
ALCAM	−0.1	.794	0.4	.291	0.5	.521
ALDH1A1	−0.9	<.001	−1.1	<.001	−0.6	.171
ALDH1B1	−1.7	<.001	−1.4	.001	−1.2	.031
ALDH1L1	−1.1	<.001	−1.2	.001	−0.9	.097
ALDH2	−1	.001	−1.2	.001	−0.7	.241
ALDH6A1	−1.1	.001	−1.2	.004	−0.7	.352
ALDH7A1	−1	.001	−1.2	.001	−0.6	.283
ALDH9A1	−0.6	.032	−1	.006	−0.3	.676
ALDOA	−0.4	.046	−0.4	.11	−0.2	.746
ALDOC	−0.5	.02	−0.3	.36	0.1	.957
ALMS1	0.7	.021	0.2	.78	0.6	.423
ALOX15B	−0.7	.057	−0.9	.053	−0.6	.45
AMBP	−0.3	.338	−0.7	.051	−0.2	.851
AMIGO2	1.2	.006	0.7	.241	1.1	.18
AMN	−1.9	<.001	−2	.002	−1.7	.071
AMPD2	0.5	.099	0.7	.103	0.4	.602
ANG	−0.4	.339	−0.3	.46	0.1	.986
ANGPTL2	−0.7	.046	−0.6	.204	−0.5	.626

(Continued on next page)

Supplementary Table II. Continued.

Gene	Log$_2$FC TAA/ normal	Adjusted *P* value[a]	Log$_2$FC TBAD/ normal	Adjusted *P* value[a]	Log$_2$FC TADA/ normal	Adjusted *P* value[a]
ANK1	1.3	<.001	0.4	.306	0.4	.614
ANKRD31	−2.2	<.001	−1.9	.006	−1	.406
ANKS3	−2.3	.001	−1.7	.034	−1.2	.384
ANP32B	−0.6	.221	−0.8	.179	−0.1	.999
ANTXR1	−0.2	.742	0.5	.208	−0.3	.772
ANXA1	−0.4	.054	−0.2	.584	−0.2	.721
ANXA11	−0.9	<.001	−0.6	.032	−0.8	.05
ANXA2	−0.4	.176	−0.4	.202	−0.2	.762
ANXA3	−0.3	.531	0.1	.9	0.2	.784
ANXA4	−1.3	<.001	−1	.001	−1	.012
ANXA5	−1.5	<.001	−1.5	<.001	−1.2	.012
ANXA6	−1	<.001	−0.7	.019	−0.7	.137
ANXA7	−0.5	.027	−0.4	.189	−0.5	.217
AOC3	−1.4	.001	−0.3	.65	−0.3	.819
AP1B1	0.1	.937	−0.4	.15	−0.5	.264
AP2A1	−0.2	.536	−0.3	.547	0.1	.998
AP2A2	−0.2	.69	−0.6	.334	−0.4	.713
AP2B1	−0.4	.18	−0.8	.024	−0.5	.364
AP2M1	0.3	.499	0.1	.946	0.4	.637
AP3B1	0.4	.188	−0.2	.747	0.2	.807
AP3B2	−0.7	.126	−0.3	.63	0.2	.894
AP3S1	−0.3	.552	−0.2	.801	0.1	.959
APCS	−1.9	<.001	−2.1	<.001	−1.3	.059
APEH	−0.3	.493	−0.9	.045	−0.7	.293
APEX1	0.2	.576	0.7	.106	0.7	.266
APMAP	0.6	.002	0.5	.038	0.5	.262
APOA1	−0.3	.287	−1.3	.001	−0.3	.729
APOA2	−0.1	.828	−1.2	.001	−0.2	.83
APOA4	−0.9	<.001	−1.3	<.001	−1	.023
APOB	0.8	.021	−0.9	.05	0.7	.356
APOC1	−0.1	.964	−0.8	.07	−0.2	.844
APOC2	0.4	.372	−1.2	.017	0.6	.584
APOC3	0.1	.877	−1.6	.001	0.3	.792
APOD	0.7	.012	−0.6	.127	0.5	.432
APOE	0.5	.144	−0.6	.204	0.5	.468
APOF	0.1	.905	−0.4	.27	−0.1	.889
APOH	−0.9	.001	−1.1	.001	−0.7	.165
APOL1	0.7	.061	−0.8	.084	0.7	.362
APOM	0.8	.004	−0.2	.627	0.5	.378
APP	−1.9	<.001	−1.8	<.001	−1.9	.001
APPL1	−0.1	.941	−0.1	.862	−0.2	.773
APRT	0.3	.277	−0.6	.053	0.2	.762
AQP1	−0.5	.114	−0.6	.122	0.1	.979
ARCN1	0.3	.217	−0.1	.944	−0.1	.941
ARF4	0.7	.01	0.3	.455	0.7	.244
ARF5	−0.2	.554	0.5	.223	−0.1	.998

Supplementary Table II. Continued.

Gene	Log2FC TAA/ normal	Adjusted *P* value[a]	Log2FC TBAD/ normal	Adjusted *P* value[a]	Log2FC TADA/ normal	Adjusted *P* value[a]
ARFIP1	−1	<.001	−1.1	.001	−0.7	.154
ARG1	−1.9	<.001	−1.1	.012	−1.7	.01
ARHGAP1	−0.5	.003	−0.6	.009	−0.2	.714
ARHGAP11A	1.4	.009	1	.174	1.5	.147
ARHGAP31	−0.8	.155	−1	.174	0.5	.725
ARHGAP40	−0.6	.08	−0.8	.055	−0.3	.729
ARHGAP9	−1.1	.081	−1.1	.187	0.2	.907
ARHGDIA	−0.7	.001	−0.8	.002	−0.3	.48
ARHGDIB	0.6	.004	0.5	.09	0.3	.692
ARHGEF37	−2.1	<.001	−1.5	.024	−0.9	.432
ARL6IP5	0.2	.438	0.4	.095	0.3	.521
ARL8B	−0.8	.206	−0.2	.872	−0.1	.995
ARMC5	−0.1	.909	−0.5	.642	−0.7	.729
ARNTL2	−1	.042	−1.6	.012	−1	.369
ARPC1A	−0.7	.009	−0.6	.056	−0.3	.656
ARPC1B	0.4	.064	0.4	.151	0.3	.521
ARPC2	0.2	.548	0.2	.605	0.2	.768
ARPC3	0.1	.847	−0.1	.813	−0.1	.959
ARPC4	0.2	.408	−0.2	.651	0.2	.679
ARPC5	−0.4	.279	−1.1	.003	−0.4	.656
ARPC5L	−1.2	.001	−1.6	.001	−0.8	.294
ASAH1	0.2	.604	−0.6	.058	.1	.988
ASNA	−0.3	.336	−0.7	.021	−0.2	.777
ASPH	−0.5	.241	−0.7	.191	−0.8	.412
ASPN	1.3	.001	−0.1	.946	1.2	.118
ASS1	−1.1	.001	−1	.013	−0.6	.46
ATAD2B	0.5	.318	0.2	.847	1	.304
ATIC	0.1	.747	−0.2	.701	0.3	.676
ATL3	−0.2	.524	0.3	.523	0.2	.829
ATOX1	−1	.001	−1.5	.001	−0.9	.142
ATP1A1	0.4	.238	0.6	.189	0.6	.46
ATP2A2	−0.3	.542	0.3	.593	−0.1	.994
ATP2B4	−0.3	.479	0.1	.955	−0.3	.789
ATP5F1A	−0.3	.138	−0.5	.032	−0.3	.365
ATP5F1B	−0.4	.091	−1	.002	−0.6	.283
ATP5F1C	0.1	.8	−0.5	.067	−0.1	.912
ATP5F1D	−0.3	.323	−0.7	.026	−0.3	.555
ATP5ME	−1	.002	−0.8	.045	−0.3	.75
ATP5MF	1.1	.026	1	.107	0.9	.385
ATP5MG	−0.7	.046	−0.9	.048	−0.4	.676
ATP5PB	−0.2	.586	−0.7	.11	0.1	.944
ATP5PD	−0.7	.002	−0.9	.003	−0.6	.177
ATP5PF	−0.5	.105	−1.1	.005	−0.4	.546
ATP5PO	−0.2	.427	−0.8	.01	−0.4	.492
ATP6V1A	0.1	.937	−0.7	.043	−0.2	.864
ATP6V1B2	−0.1	.924	−0.7	.055	−0.2	.778

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Supplementary Table II. Continued.

Gene	Log_2FC TAA/ normal	Adjusted *P* value[a]	Log_2FC TBAD/ normal	Adjusted *P* value[a]	Log_2FC TADA/ normal	Adjusted *P* value[a]
ATP6V1E1	0.5	.071	−0.3	.355	0.2	.771
ATP6V1H	0.3	.25	−0.2	.619	−0.1	.994
ATP8A1	−0.2	.875	−0.7	.395	−0.2	.907
ATR	−0.3	.414	0.4	.432	0.8	.255
AXIN1	−0.1	.916	−0.3	.854	1.1	.562
AZGP1	−0.5	.135	−1.3	.001	−0.3	.734
B2M	0.4	.153	−0.5	.097	0.2	.731
BAG2	−1.1	.001	−0.4	.374	−0.6	.446
BANF1	−1.6	<.001	−2.1	<.001	−1.1	.132
BASP1	0.1	.881	0.3	.434	0.2	.792
BBS9	0.2	.55	0.4	.285	0.4	.498
BCAM	−1.2	<.001	−0.5	.202	−0.4	.589
BCAP31	0.8	.096	0.4	.555	1.1	.212
BCL10	0.4	.333	1	.023	0.5	.488
BDH2	−1.2	.003	−1.2	.02	−0.9	.309
BGN	−1.3	.001	−1.3	.011	−0.8	.345
BLM	−0.1	.979	−0.6	.449	0.3	.85
BLMH	0.5	.266	−0.2	.817	−0.2	.869
BLVRA	0.2	.604	−0.1	.745	0.1	.967
BLVRB	0.5	.06	−0.4	.204	0.3	.589
BNC2	−0.3	.46	−0.3	.476	0.1	.939
BPGM	0.6	.123	−0.5	.361	0.1	.939
BPNT1	−1.4	.001	−1.7	.001	−1.4	.052
BRK1	−0.1	.971	−0.2	.731	0.1	.959
BSG	−1	.052	0.1	.939	0.2	.917
C11orf54	−1.4	<.001	−1.6	<.001	−1.2	.03
C11orf96	−1.3	.002	−0.6	.334	−0.2	.889
C1orf198	−0.2	.657	−0.4	.347	−0.1	.919
C1QA	−1.2	.003	−0.6	.335	−0.4	.73
C1QB	−0.7	.07	−0.4	.549	−0.4	.677
C1QC	−0.9	.032	−0.8	.165	−0.5	.677
C1R	0.2	.604	0.1	.924	0.2	.841
C1S	0.3	.207	−0.1	.96	0.4	.431
C2	−0.5	.16	−0.7	.156	0.4	.715
C22orf23	−0.4	.41	0.1	.966	0.4	.761
C2orf78	−1.6	.001	−0.5	.398	−1.7	.034
C3	0.1	.957	−0.6	.043	0.2	.762
C4A	0.2	.537	−0.1	.901	0.6	.315
C4B	0.4	.196	−0.1	.962	0.4	.542
C4BPA	0.3	.342	−0.5	.179	0.3	.668
C4BPB	0.8	.038	−0.6	.196	0.6	.475
C5	0.1	.965	−0.4	.24	0.2	.781
C6	−0.4	.109	−0.4	.27	−0.1	.883
C7	−0.6	.031	−0.5	.213	−0.4	.582
C8A	−0.3	.276	−0.1	.854	0.3	.655
C8B	0.1	.899	−0.1	.825	0.5	.487

Supplementary Table II. Continued.

Gene	Log_2FC TAA/ normal	Adjusted *P* value[a]	Log_2FC TBAD/ normal	Adjusted *P* value[a]	Log_2FC TADA/ normal	Adjusted *P* value[a]
C8G	−0.5	.129	−0.9	.019	−0.2	.871
C8orf74	2	<.001	2.9	<.001	2	.013
C9	−0.6	.032	−0.5	.219	−0.3	.676
CA1	0.6	.06	−0.9	.019	−0.1	.997
CA123	−1.9	.001	−0.9	.211	−2.1	.032
CA2	0.3	.413	−0.9	.014	−0.4	.649
CA3	−1.8	<.001	−2.4	<.001	−2.1	0.004
CAB39	−0.3	.561	−0.4	.443	−0.4	.677
CACNA2D1	−1.1	.001	−0.8	.054	−0.7	.345
CACYBP	−0.3	.336	−0.3	.434	−0.4	.593
CALD1	−1.1	.002	−0.9	.045	−0.6	.446
CALR	−0.1	.873	−0.1	.82	0.1	.949
CALU	−0.3	.272	−0.5	.06	−0.6	.194
CAMK2G	−0.9	.004	0.2	.785	−0.5	.46
CAND1	0.4	.175	0.4	.218	0.8	.15
CANX	0.6	.003	0.6	.007	0.5	.153
CAP1	−0.6	<.001	−0.8	.001	−0.7	.025
CAP2	−1.4	<.001	−1.1	.005	−0.9	.129
CAPG	0.3	.413	−0.5	.17	−0.3	.759
CAPN1	0.1	.872	−0.1	.708	0.1	.903
CAPN2	−0.6	.011	−0.4	.196	−0.1	.967
CAPNS1	−0.6	.002	−0.7	.003	−0.5	.206
CAPZA1	0.6	.01	0.1	.872	0.2	.851
CAPZA2	−0.7	.002	−1.1	.001	−0.6	.177
CAPZB	0.1	.912	0.2	.431	0.2	.783
CARD10	1.6	.001	0.7	.289	0.6	.653
CASKIN2	−0.8	.024	−0.9	.053	−0.5	.553
CASP8	−0.4	.277	0.2	.759	0.3	.762
CAST	−0.1	.762	−0.6	.036	−0.4	.481
CAT	0.5	.038	−0.1	.924	0.2	.807
CATSPERG	−2.8	<.001	−2.5	<.001	−1.7	.048
CAV1	−0.5	.279	0.3	.606	0.3	.762
CAV2	0.6	.063	1	.008	1.2	.031
CAVIN1	−1.1	.002	−0.9	.053	−0.3	.771
CAVIN2	0.9	.002	0.5	.141	0.2	.783
CAVIN3	−1	.002	−0.5	.328	−0.2	.881
CBLN2	−0.7	.012	−0.9	.009	−0.3	.754
CBR1	−0.6	.022	−0.9	.008	−0.3	.691
CBR3	−1.3	.002	−1.1	.045	−1	.233
CCAR1	−0.4	.467	−1.8	.001	0.1	.967
CCDC158	−1.1	.007	−0.9	.107	−0.4	.739
CCDC194	−1.5	.001	−0.6	.252	−0.7	.444
CCDC25	3.7	.001	2.2	.116	0.8	.771
CCDC6	−1.5	<.001	−1.2	.001	−0.6	.272
CCDC69	0.1	.912	0.7	.336	0.6	.677
CCDC80	0.8	.004	0.6	.104	0.7	.281

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Supplementary Table II. Continued.

Gene	Log_2FC TAA/ normal	Adjusted *P* value[a]	Log_2FC TBAD/ normal	Adjusted *P* value[a]	Log_2FC TADA/ normal	Adjusted *P* value[a]
CCN3	−1.9	<.001	−1.9	<.001	−1.5	.021
CCS	−0.5	.199	−1.1	.022	−1.1	.153
CCT2	−0.1	.746	−0.4	.119	−0.2	.725
CCT3	−0.1	.856	−0.4	.294	0.1	.954
CCT4	0.5	.017	0.5	.054	0.4	.309
CCT5	0.1	.951	−0.3	.452	−0.2	.839
CCT6A	−0.2	.531	−0.1	.916	−0.2	.77
CCT7	0.5	.027	0.3	.374	0.4	.422
CCT8	0.2	.586	−0.2	.724	0.1	.939
CD109	−0.2	.774	−0.2	.754	0.4	.621
CD14	0.7	.107	0.3	.568	0.5	.634
CD151	−0.4	.301	0.1	.892	0.1	.96
CD163	1	<.001	0.9	.01	0.8	.137
CD34	−0.9	.003	−0.8	.055	−0.2	.81
CD44	−0.2	.322	0.1	.939	0.1	.946
CD47	0.1	.966	0.1	.889	0.2	.81
CD59	−0.2	.746	0.2	.675	0.4	.668
CD5L	0.1	.873	−1	.011	0.2	.885
CD81	−0.4	.431	−0.4	.521	0.1	.946
CD9	−0.1	.861	0.1	.854	0.4	.677
CD97	−1.5	<.001	−1.8	<.001	−1.6	0.019
CD99	−0.4	.374	−1.2	.005	−0.3	.77
CDC25C	−1	.034	−1.8	.002	−1.3	.138
CDC37	−0.1	.789	0.3	.391	0.2	.825
CDC42	0.5	.017	0.6	.039	0.6	.172
CDC5L	−0.2	.759	−1.2	.002	0.3	.719
CDH1	−0.6	.18	−0.4	.533	−0.4	.762
CDH13	−0.9	.007	−0.3	.606	0.3	.734
CDHR3	0.5	.368	−0.5	.401	0.6	.536
CDK5RAP3	−0.1	.87	−0.3	.607	−0.4	.729
CDKN2AIP	1.1	.069	0.4	.645	1.5	.206
CELSR3	−3.3	<.001	−2.3	.002	−3.2	.002
CENPE	−1.2	.007	−0.6	.327	−0.1	.972
CES1	−1.3	<.001	−0.4	.349	−0.4	.587
CFB	−0.3	.483	−0.6	.127	0.4	.648
CFD	−1.3	<.001	−1.9	<.001	−1	.066
CFH	0.1	.899	−0.5	.072	0.3	.545
CFHR1	−0.7	.103	−0.8	.122	0.2	.899
CFHR2	−0.3	.312	−0.5	.156	0.2	.792
CFHR5	−0.1	.837	−0.3	.654	0.7	.36
CFI	−0.1	.811	−1	.006	0.3	.659
CFL1	−0.6	.001	−0.7	.002	−0.5	.151
CFL2	−1.8	<.001	−1.5	.001	−0.9	.18
CFP	−1.8	<.001	−1.4	<.001	−1.5	.004
CHCHD3	−0.8	.028	−0.3	.632	−0.3	.734
CHD8	0.8	<.001	0.6	.024	0.6	.124

Supplementary Table II. Continued.

Gene	Log_2FC TAA/ normal	Adjusted *P* value[a]	Log_2FC TBAD/ normal	Adjusted *P* value[a]	Log_2FC TADA/ normal	Adjusted *P* value[a]
CHMP2A	−0.2	.586	0.4	.418	−0.3	.704
CHMP4B	−0.9	.001	−0.9	.017	−0.7	.237
CHST14	−1.1	.008	−0.1	.903	−0.4	.714
CHTF18	−2.3	.001	−3.3	<.001	−1.5	.234
CILP2	−0.3	.653	0.1	.98	1.5	.084
CIRBP	−0.2	.742	−0.8	.072	−0.5	.611
CISD1	0.4	.212	0.3	.561	0.4	.659
CKAP2	0.5	.055	−0.2	.654	0.6	.219
CKAP4	0.5	.117	0.3	.583	0.3	.762
CKB	−1.8	<.001	−2	<.001	−1.4	.01
CKM	−1.6	<.001	−1.6	<.001	−2	<.001
CLEC11A	0.5	.218	−0.2	.848	−0.2	.907
CLEC3B	−0.7	0.012	−1.1	.002	−0.7	.248
CLIC1	0.5	.008	0.2	.609	0.2	.612
CLIC4	−0.8	.008	−0.9	.018	−0.3	.687
CLTA	0.7	.038	0.6	.184	0.1	.979
CLTB	−0.6	.041	−0.7	.055	−0.4	.582
CLTC	0.4	.133	0.3	.358	0.4	.422
CLU	−0.8	.004	−1.1	.004	−0.6	.308
CMA1	0.2	.64	−0.3	.41	0.1	.944
CMBL	−1.1	.001	−1.1	.004	−0.7	.291
CMPK1	−0.6	.007	−0.9	.002	−0.3	.639
CMYA5	0.2	.812	−1.1	.027	0.1	.976
CN166	−0.5	.416	−0.8	.215	−0.4	.773
CNBP	−0.3	.55	−0.4	.467	−0.4	.681
CNDP2	−0.5	.105	−0.9	.006	−0.2	.787
CNN1	−2.3	<.001	−1.6	.004	−1.2	.182
CNN2	0.1	.766	0.1	.837	0.2	.762
CNN3	−0.2	.774	−0.3	.645	0.3	.79
CNPY2	0.3	.482	−0.4	.331	−0.1	.956
CNRIP1	−0.7	.001	−1	.001	−0.7	.085
CNTN1	−0.9	.001	−0.7	.033	−0.5	.377
COASY	0.4	.37	−0.4	.518	0.3	.771
COG5	−0.4	.055	0.2	.492	−0.1	.881
COL12A1	0.8	.029	0.2	.81	0.5	.656
COL14A1	−0.8	.025	−0.4	.395	−0.3	.782
COL15A1	−0.4	.162	−0.6	.092	−0.4	.558
COL18A1	−2	<.001	−1.5	.001	−1.4	.031
COL1A1	0.7	.177	1.6	.009	1.7	.067
COL1A2	0.4	.493	1.3	.024	1.3	.149
COL21A1	−0.4	.52	1.9	.002	1.4	.115
COL3A1	1.2	.025	2.6	.001	2.4	.012
COL4A1	−1.6	<.001	−0.4	.396	−0.6	.503
COL4A2	−1.5	<.001	0.1	.987	−0.2	.851
COL4A3	−1.7	<.001	−0.5	.354	−0.8	.329
COL6A1	−0.2	.702	0.3	.473	0.2	.881

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Supplementary Table II. Continued.

Gene	Log_2FC TAA/ normal	Adjusted *P* value[a]	Log_2FC TBAD/ normal	Adjusted *P* value[a]	Log_2FC TADA/ normal	Adjusted *P* value[a]
COL6A2	−0.1	.952	0.6	.171	0.4	.687
COL6A3	0.2	.709	−0.2	.726	0.4	.538
COL7A1	0.2	.678	−1.1	.038	−0.3	.83
COL8A1	−0.6	.269	1.1	.074	0.8	.412
COLGALT1	0.2	.737	0.1	.84	0.4	.582
COMT	−0.3	.441	−0.3	.542	−0.2	.879
COPA	0.9	.005	0.9	.02	0.8	.237
COPB1	0.9	.004	0.7	.079	0.5	.533
COPB2	1	.003	0.6	.174	0.9	.177
COPG1	0.5	.088	0.4	.322	0.2	.845
COPS5	0.5	.052	0.3	.53	0.3	.743
COPS6	−0.7	.031	−0.5	.321	−0.3	.762
CORO1A	1.1	.001	1	.013	0.8	.25
CORO1B	−0.5	.08	−0.7	.028	−0.3	.713
CORO1C	−0.4	.121	−0.4	.234	−0.1	.957
COTL1	0.4	.147	−0.1	.928	0.2	.773
COX4I1	−0.3	.61	−0.6	.337	−0.5	.665
COX5A	−0.9	.001	−1.5	<.001	−1.1	.05
COX5B	−0.1	.792	−0.9	.013	−0.7	.276
COX6B1	−0.7	.042	−1	.021	−0.3	.797
COX6C	0.3	.704	0.4	.536	−0.4	.771
COX7A2	0.2	.679	−0.6	.202	−0.4	.666
CP	0.1	.871	−0.4	.24	0.4	.475
CPA3	0.3	.571	−0.6	.319	−0.5	.647
CPB2	0.8	.003	0.4	.237	0.6	.314
CPNE1	−0.7	.006	−0.3	.442	−0.5	.407
CPNE3	−0.5	.179	0.3	.614	−0.3	.734
CPPED1	−0.5	.181	−0.8	.064	−0.1	.954
CPQ	−1	.001	−1	.003	−0.7	.231
CPXM2	−1.3	.001	−1.1	.02	−0.8	.362
CREG1	−1	.019	−1	.051	−0.5	.626
CRIP1	1.9	.071	1.1	.428	1.5	.536
CRIP2	−0.9	.027	−0.5	.407	−0.2	.852
CRK	−1.1	.004	−1	.042	−0.7	.379
CRKL	−0.4	.244	−0.6	.086	0.1	.939
CRLF1	−0.7	.058	−1	.026	−1	.126
CRP	0.9	.053	0.4	.575	1.7	.055
CRYAB	−2	<.001	−1.6	<.001	−1.2	.04
CRYL1	−1.5	<.001	−1.3	.006	−0.8	.315
CRYZ	−1.1	<.001	−1.3	<.001	−0.7	.147
CS	0.3	.226	0.1	.811	−0.1	.899
CSDE1	−1.1	.051	−0.8	.259	1	.431
CSK	0.9	.004	0.4	.317	0.5	.485
CSPG4	−1.4	<.001	−1	.003	−0.9	.084
CSPG5	−1.3	.014	−1.1	.118	−0.3	.823
CSRP1	−1.4	.001	−1.1	.019	−0.6	.498

Supplementary Table II. Continued.

Gene	Log$_2$FC TAA/ normal	Adjusted *P* value[a]	Log$_2$FC TBAD/ normal	Adjusted *P* value[a]	Log$_2$FC TADA/ normal	Adjusted *P* value[a]
CSRP2	−0.8	.051	−0.4	.521	0.4	.712
CSTB	−0.5	.022	−0.8	.002	−0.2	.735
CTGF	1.2	.002	0.4	.445	0.4	.725
CTHRC1	−0.1	.839	−0.9	.013	−1	.056
CTNNA1	0.8	.233	0.6	.451	0.6	.731
CTNND1	0.7	.021	0.3	.523	0.4	.542
CTPS1	−0.7	.027	−0.6	.127	−0.5	.58
CTSB	0.5	.144	−0.1	.923	0.3	.78
CTSC	0.7	.019	−0.2	.787	0.8	.23
CTSD	0.2	.455	−0.5	.118	0.2	.815
CTSF	−1.2	.001	−0.9	.034	−0.5	.503
CTSG	1	.002	1.2	.008	0.5	.562
CTSZ	0.1	.946	−0.1	.765	−0.2	.815
CTTN	0.3	.451	0.5	.143	0.2	.771
CUL9	0.3	.773	−1.5	.073	−0.1	.956
CUTA	−1.4	<.001	−1.7	<.001	−0.9	.161
CXCL12	0.1	.965	0.3	.677	0.2	.88
CXCL16	−1.3	.003	−1.3	.02	−0.8	.422
CYB5R1	0.7	.057	0.6	.21	0.7	.349
CYB5R3	0.1	.949	−0.2	.765	0.4	.668
CYBRD1	0.8	.079	0.4	.597	1.6	.058
CYCS	0.3	.383	−0.4	.335	−0.3	.772
CYFIP1	0.4	.149	0.5	.221	0.5	.369
CYP20A1	0.2	.873	−0.5	.683	0.4	.852
CYP27B1	1	.028	−0.9	.129	0.4	.762
CYP2C8	0.2	.889	0.1	.949	0.5	.771
DAAM2	−0.3	.676	−0.8	.354	−0.9	.477
DAD1	1.2	.017	1.6	.009	1.5	.125
DAG1	−1.6	<.001	−1.1	.006	−0.8	.198
DARS1	0.3	.213	0.5	.119	0.3	.656
DBI	−1.2	<.001	−1	.001	−0.8	.067
DBN1	−0.5	.11	−0.8	.018	−0.7	.225
DBNL	−0.2	.418	−0.8	.006	−0.2	.725
DCN	−1.1	.003	−2.9	<.001	−2.4	.001
DCPS	0.1	.965	−0.7	.028	−0.2	.817
DCTN1	−0.4	.218	−0.3	.433	−0.4	.619
DCTN2	−0.6	.013	−0.8	.005	−0.5	.318
DCTN3	−0.7	.025	−0.7	.067	−0.3	.679
DDAH1	−2	<.001	−2	.001	−1.5	.056
DDAH2	−1	<.001	−1	.001	−0.5	.281
DDB1	0.3	.359	0.1	.928	0.5	.561
DDOST	0.4	.201	−0.2	.589	0.2	.773
DDR1	−2.1	<.001	−1.4	.036	−0.9	.407
DDT	−0.9	.002	−1.6	<.001	−0.6	.359
DDX1	−0.3	.479	−0.5	.201	−0.1	.959
DDX25	1.2	.001	1.5	.002	1.1	.125

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Supplementary Table II. Continued.

Gene	Log_2FC TAA/ normal	Adjusted *P* value[a]	Log_2FC TBAD/ normal	Adjusted *P* value[a]	Log_2FC TADA/ normal	Adjusted *P* value[a]
DDX39B	0.8	.063	0.9	.104	1.3	.129
DDX3X	−0.2	.705	0.3	.624	−0.3	.713
DDX6	−0.1	.942	−0.1	.888	−0.5	.665
DECR1	−0.3	.48	−0.8	.045	−0.8	.191
DES	−2	<.001	−2.7	<.001	−2	<.001
DHAK	−0.8	.009	−1.1	.003	−0.9	.102
DHRS7	0.2	.812	0.8	.337	0.6	.737
DHX37	−1.4	.008	−0.5	.531	0.6	.677
DHX9	0.4	.249	0.3	.537	0.5	.503
DIABLO	−0.9	.008	−0.7	.126	−0.6	.418
DKK3	−1.7	<.001	−2	<.001	−1.5	.021
DLAT	−0.7	.011	−0.7	.028	−0.6	.308
DLGAP1	−0.6	.372	−0.7	.372	−0.1	.953
DLST	−0.4	.084	−0.5	.109	−0.5	.359
DMD	−0.5	.103	−0.2	.649	−0.1	.998
DNAH5	−0.5	.336	−1.1	.069	0.4	.75
DNAH9	−2.6	<.001	−2	.005	−0.3	.881
DNAJA2	−0.5	.009	−0.7	.012	−0.5	.257
DNAJB11	0.4	.326	0.1	.987	−0.2	.874
DNAJB4	−0.5	.062	−0.5	.147	−0.2	.829
DNM1L	0.2	.637	0.1	.958	−0.1	.889
DNPEP	−0.4	.301	−0.4	.437	−0.2	.893
DNTTIP1	−2.1	<.001	−1.4	.012	−0.7	.474
DNTTIP2	0.4	.266	0.3	.555	0.8	.231
DPP3	0.3	.244	−0.3	.408	0.1	.989
DPT	−0.1	.988	−0.8	.114	0.1	.994
DPYSL2	−0.5	.027	−0.8	.008	−0.5	.345
DPYSL3	−0.9	<.001	−0.9	.002	−0.5	.264
DRAP1	0.1	.926	−0.4	.294	−0.1	.899
DSCAM	−1	.179	0.9	.347	0.7	.679
DSP	−0.4	.352	−1	.07	−0.6	.58
DST	−0.8	.151	−1	.147	−0.1	.989
DSTN	−1.3	<.001	−1.2	.001	−0.7	.172
DTWD2	−1.7	.003	−0.9	.237	−1.6	.195
DUSP3	−1	.001	−1	.003	−0.4	.458
DUT	−0.8	.084	−1.1	.045	−0.9	.345
DYNC1H1	0.4	.246	0.7	.072	0.6	.348
DYNC1I2	0.1	.95	−0.1	.855	0.4	.721
DYNC1LI1	−0.7	.035	−0.6	.18	−0.7	.349
DYNC1LI2	−0.3	.432	−0.3	.585	−0.1	.954
DYNLRB1	−1.6	<.001	−2	.001	−1.5	.069
ECH1	−0.2	.47	−1.3	.001	−0.4	.582
ECHS1	−0.9	.001	−1.2	.001	−0.8	.115
ECM1	−0.1	.842	−0.2	.724	0.1	.986
EEA1	−0.4	.096	−0.6	.045	−0.5	.283
EEF1A2	0.4	.296	−0.5	.288	0.3	.793

Supplementary Table II. Continued.

Gene	Log_2FC TAA/ normal	Adjusted *P* value[a]	Log_2FC TBAD/ normal	Adjusted *P* value[a]	Log_2FC TADA/ normal	Adjusted *P* value[a]
EEF1B2	−0.4	.195	−0.8	.04	−0.3	.771
EEF1D	−0.3	.266	−0.8	.008	−0.4	.553
EEF1DP3	0.1	.95	−0.2	.815	1.4	.231
EEF1G	0.7	.002	0.6	.025	0.6	.162
EEF2	0.3	.257	0.2	.716	0.2	.767
EFEMP1	−1.5	<.001	−0.9	.079	−0.7	.438
EFEMP2	−0.7	.012	−0.7	.062	−0.3	.721
EFHD1	−1.2	.001	−1.1	.021	−0.7	.369
EFHD2	1.4	<.001	0.5	.241	0.8	.217
EFL1	0.3	.576	−0.1	.914	0.6	.496
EGR4	−2.2	<.001	−2.3	.002	−1.2	.315
EHD1	0.3	.156	0.3	.346	0.3	.453
EHD2	−0.9	.005	−0.5	.251	0.1	.94
EHD3	−0.5	.214	0.2	.779	0.3	.8
EHD4	−0.8	.001	−0.7	.014	−0.4	.395
EIF1	−0.2	.69	−0.6	.054	0.2	.857
EIF2A	−1.5	<.001	−1	.005	−1.1	.025
EIF2B1	−0.4	.321	0.4	.431	0.1	.965
EIF2S1	−0.2	.604	−0.4	.208	−0.1	.971
EIF2S3	0.1	.845	0.2	.636	−0.1	.939
EIF3A	−0.2	.786	0.4	.421	0.1	.916
EIF3F	−0.3	.454	−0.9	.016	−0.6	.37
EIF3I	−0.1	.812	−0.6	.18	−0.2	.893
EIF4A1	0.1	.901	0.1	.959	0.2	.852
EIF4A2	−0.4	.128	−0.6	.062	−0.2	.756
EIF4A3	0.2	.583	−0.1	.923	0.3	.792
EIF4B	0.1	.929	−0.2	.802	−0.1	.939
EIF4G2	−0.2	.775	−0.1	.979	0.2	.891
EIF4G3	−0.1	.918	−1.9	.001	0.2	.894
EIF4H	−0.3	.566	0.1	.973	0.1	.987
EIF5	0.2	.683	0.2	.738	0.6	.317
EIF5A	0.2	.678	−0.3	.678	0.5	.661
EIF6	−0.7	.027	−1.1	.012	−0.3	.725
ELANE	1.3	.001	1.4	.004	1.7	.019
ELAVL1	−0.7	.058	−0.7	.147	−0.6	.553
ELN	−1.7	<.001	0.2	.73	−0.8	.362
ELOB	−0.4	.156	−0.5	.21	−0.1	.907
EMD	−0.2	.784	0.5	.318	0.6	.431
EMILIN1	−1.3	<.001	−0.3	.371	−0.5	.315
EMILIN2	−0.1	.851	−0.3	.539	−0.2	.851
EML2	−1.1	<.001	−1.2	<.001	−0.6	.283
EML3	0.3	.767	−0.1	.948	0.3	.899
ENAH	−0.7	.012	−0.6	.135	−0.5	.52
ENAM	−1.3	.001	−1.2	.014	−0.5	.551
ENDOD1	−0.1	.86	−0.2	.656	−0.1	.976
ENG	0.4	.215	0.7	.083	0.5	.475

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Supplementary Table II. Continued.

Gene	Log_2FC TAA/ normal	Adjusted *P* value[a]	Log_2FC TBAD/ normal	Adjusted *P* value[a]	Log_2FC TADA/ normal	Adjusted *P* value[a]
ENO1	−0.5	.005	−0.4	.135	−0.2	.762
ENO2	−0.7	.001	−0.5	.064	−0.3	.582
ENOPH1	−0.4	.478	−0.8	.153	−0.1	.969
ENPP1	−0.2	.608	0.1	.881	−0.2	.866
ENPP2	0.4	.193	0.1	.86	0.3	.77
EPB41L2	0.2	.645	0.3	.63	0.2	.899
EPDR1	−0.3	.392	−0.3	.503	−0.1	.995
EPHX1	−0.1	.864	−0.8	.008	0.1	.908
EPPK1	−0.8	.061	−0.9	.102	−0.8	.395
EPRS1	0.4	.227	0.3	.463	0.2	.86
EPS15L1	−0.3	.538	−0.3	.597	−0.3	.772
EPS8L1	−1.5	.003	−1.4	.035	−0.5	.699
ERBIN	−0.8	.018	−0.3	.643	0.2	.821
ERC2	−1	.027	−2.9	<.001	−1.9	.03
ERH	0.4	.271	0.2	.702	0.4	.578
ERI1	0.8	.454	0.5	.722	1.6	.412
ERLIN2	−1	.001	−0.5	.17	−0.7	.256
ERO1A	0.4	.448	0.2	.74	0.9	.311
ERP29	−0.4	.121	−0.9	.004	−0.5	.364
ERP44	0.1	.901	−0.6	.088	−0.1	.997
ES1	−0.7	.016	−0.9	.016	−0.4	.606
ESD	−0.8	.002	−1	.002	−0.5	.432
ESYT1	0.7	.027	0.6	.167	0.7	.291
ESYT2	−0.1	.936	0.2	.822	0.5	.572
ETF1	−0.2	.627	−0.5	.283	−0.2	.864
ETFA	−0.7	.008	−1.5	<.001	−0.9	.068
ETFB	−0.3	.281	−0.9	.007	−0.7	.231
EXOC3	−1.7	.001	−1.7	.003	−0.9	.356
EXT1	−1.3	.001	−0.6	.297	−0.8	.362
EYS	−1.6	.003	0.4	.647	−0.5	.729
EZR	−0.1	.844	−0.3	.395	−0.2	.696
F10	0.5	.241	−0.9	.121	0.4	.725
F11	−0.6	.144	−0.2	.854	0.2	.881
F12	−0.5	.121	−0.8	.045	−0.4	.602
F13A1	1	.001	0.4	.294	0.9	.137
F13B	0.6	.068	−0.3	.591	0.5	.44
F2	0.7	.003	0.3	.271	0.8	.05
F9	−0.5	.08	−0.1	.916	0.5	.458
FABP1	−3.4	<.001	−3.5	<.001	−3.2	<.001
FABP3	−2.2	<.001	−2.4	<.001	−1.4	.058
FABP4	−1.7	<.001	−2.1	<.001	−1.4	.028
FABP5	0.2	.691	−0.9	.06	−0.1	.959
FAH	−1.1	<.001	−1.5	<.001	−0.9	.023
FAM135A	1.3	.007	1.1	.086	1.3	.208
FAM180A	−1.4	.017	0.4	.63	−0.2	.908
FAM50B	0.8	.145	1.5	.024	1.9	.058

Supplementary Table II. Continued.

Gene	Log$_2$FC TAA/ normal	Adjusted *P* value[a]	Log$_2$FC TBAD/ normal	Adjusted *P* value[a]	Log$_2$FC TADA/ normal	Adjusted *P* value[a]
FANCA	1.7	.001	2.7	<.001	1.8	.043
FANK1	0.9	.091	−0.9	.179	0.4	.777
FARSB	0.2	.731	0.2	.801	0.3	.772
FASN	0.1	.8	−0.5	.311	−0.3	.749
FAU	1.7	<.001	1	.06	1.8	.012
FBLIM1	−1.5	<.001	−1.1	.013	−0.7	.328
FBLN1	−0.4	.086	−0.5	.147	0.2	.762
FBLN2	0.1	.92	−0.4	.348	0.1	.981
FBLN5	−2.1	<.001	−0.9	.095	−0.9	.297
FBN1	−0.4	.405	1.3	.011	0.8	.315
FCGBP	0.2	.616	0.1	.995	0.1	.928
FCGR3A	0.4	.422	−0.2	.854	0.9	.299
FDPS	−0.3	.369	−0.3	.415	−0.1	.907
FERMT2	−1.2	<.001	−0.7	.114	−0.4	.618
FERMT3	1.9	<.001	1.8	<.001	1.3	.031
FGA	0.9	.007	1.4	.002	1.1	.12
FGB	1.1	.006	1.6	.002	1.2	.168
FGG	1.2	.002	1.6	.002	1.1	.153
FGL2	−1.2	.001	−1.4	.002	−0.9	.18
FH	−1	.005	−1.8	<.001	−1.2	.091
FHL1	−1.5	<.001	−1	.044	−0.5	.65
FHL2	−0.2	.719	−0.2	.67	0.4	.582
FHL3	−0.7	.019	−0.6	.122	−0.3	.784
FHL5	−0.6	.037	−0.4	.292	−0.6	.356
FIGNL1	−1.6	.002	−1	.14	−1.6	.118
FILIP1L	−1.5	<.001	−1.3	<.001	−1.6	.001
FIS1	−0.4	.281	−1.1	.004	−0.4	.521
FKBP1A	−0.7	.007	−0.9	.005	−0.3	.685
FKBP2	−0.6	.028	−0.9	.003	−0.6	.237
FKBP3	−0.9	.007	−1.5	.002	−1.4	.027
FKBP4	−0.4	.222	−0.5	.18	−0.8	.153
FKBP5	0.5	.293	−0.9	.093	−0.3	.773
FKBP9	−0.1	.921	0.4	.536	0.6	.667
FLAD1	−1.8	.005	−1.1	.187	−1.2	.378
FLII	0.3	.336	0.5	.245	0.7	.212
FLNA	−1.3	<.001	−0.7	.084	−0.8	.165
FLNB	0.2	.666	−0.4	.456	−0.3	.799
FLNC	−1.7	<.001	−1.1	.002	−1.2	.009
FLOT1	0.1	.774	0.4	.156	0.2	.792
FLOT2	0.7	.022	1.2	.002	0.9	.118
FMOD	−1.2	.001	−1.1	.013	−0.7	.35
FN1	−0.4	.142	0.2	.731	0.1	.959
FN3K	−1.4	.013	−2.4	.001	−0.3	.837
FOXL1	0.1	.96	−1	.062	0.2	.881
FRMD6	0.1	.912	−0.7	.203	0.4	.72
FRZB	−1.3	.001	−1.1	.038	−0.9	.325

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Supplementary Table II. Continued.

Gene	Log_2FC TAA/ normal	Adjusted *P* value[a]	Log_2FC TBAD/ normal	Adjusted *P* value[a]	Log_2FC TADA/ normal	Adjusted *P* value[a]
FSCN1	0.4	.335	−0.1	.84	0.4	.668
FSIP2	−1.3	.002	−1.4	.006	−0.7	.403
FSTL1	−1	<.001	−0.8	.005	−0.8	.084
FTH1	0.4	.482	−0.3	.688	−0.3	.798
FUBP1	−0.4	.279	−0.6	.181	−0.5	.602
FUCA1	0.6	.033	−0.5	.135	0.4	.506
FURIN	−2.7	<.001	−3.1	<.001	−2.8	.012
G6PD	0.2	.462	0.3	.238	0.2	.773
GAA	−0.3	.413	−0.7	.03	−0.1	.923
GALM	−1.2	<.001	−1.8	<.001	−1.3	.013
GANAB	0.1	.662	0.1	.957	0.2	.806
GAPDH	−0.9	<.001	−1	.001	−0.7	.157
GAPDHS	−0.7	.249	−1	.165	−0.3	.821
GARS1	0.4	.46	−0.2	.783	−0.2	.879
GART	−0.5	.305	−0.5	.375	−0.1	.986
GAS6	−0.3	.492	−0.9	.038	−0.2	.889
GASK1B	−2.3	<.001	−1.7	.001	−1.7	.011
GBA	−0.4	.515	−0.3	.647	−0.7	.493
GBE1	−0.4	.208	0.3	.511	0.4	.536
GBLP	0.2	.621	−0.3	.506	−0.2	.827
GBP1	−1	.008	−1.2	.011	−0.5	.593
GC	0.3	.186	−0.3	.473	0.5	.357
GCA	1.1	.001	1.7	<.001	1.1	.091
GCLC	0.7	.003	−0.4	.234	0.4	.567
GDI1	−0.7	.015	−0.8	.019	−0.2	.829
GDI2	0.1	.719	−0.2	.6	0.2	.773
GFPT1	−0.4	.431	0.3	.631	−0.1	.968
GFUS	0.3	.478	0.3	.416	0.2	.773
GGT5	0.6	.108	0.1	.905	1.1	.095
GJA1	−0.7	.047	−0.2	.672	−0.2	.807
GLDC	−0.1	.971	−1.3	.017	0.5	.679
GLIPR2	−0.4	.219	−0.4	.349	0.2	.891
GLO1	−0.9	<.001	−1.1	<.001	−0.6	.091
GLOD4	−0.4	.136	−0.9	.004	−0.2	.852
GLRX	−0.2	.675	−0.9	.008	−0.3	.725
GLS	−0.6	.146	−0.5	.355	−0.2	.86
GLUD1	−0.6	.048	−0.7	.053	−0.8	.181
GM2A	0.2	.704	−1.2	.013	−0.1	.958
GMFG	0.4	.416	−0.2	.778	0.1	.953
GNA11	−0.6	.199	−0.3	.687	0.3	.847
GNA13	0.1	.946	−0.7	.2	0.1	.941
GNAI2	0.3	.413	0.3	.455	0.5	.422
GNAI3	0.5	.217	0.4	.372	0.5	.522
GNAQ	0.1	.832	0.4	.424	0.2	.889
GNB1	−0.6	.014	−0.6	.056	−0.4	.541
GNB2	−0.5	.088	−0.7	.048	−0.3	.718

Supplementary Table II. Continued.

Gene	Log_2FC TAA/ normal	Adjusted *P* value[a]	Log_2FC TBAD/ normal	Adjusted *P* value[a]	Log_2FC TADA/ normal	Adjusted *P* value[a]
GNB4	−0.4	.166	−0.5	.18	−0.1	.959
GNG12	−0.7	.089	−0.7	.189	−0.3	.824
GNPDA1	0.2	.748	0.1	.888	0.3	.75
GNPTAB	−0.2	.833	−0.1	.955	0.7	.458
GOLM1	−0.9	.239	−1.3	.143	−0.3	.888
GOT1	−1	.001	−1.3	.001	−1	.1
GOT2	−0.1	.946	−0.6	.11	0.1	.998
GPBP1L1	−4	<.001	−2.2	.011	−2	.137
GPC4	0.2	.79	−0.5	.35	0.2	.907
GPC6	−0.2	.704	−0.1	.872	0.3	.771
GPD1L	−1	.002	−1.1	.006	−0.6	.354
GPI	−0.2	.536	−0.1	.728	0.2	.676
GPM6A	−0.3	.584	0.6	.35	0.4	.725
GPNMB	1.1	.031	−0.1	.923	0.3	.871
GPX1	0.2	.611	−0.5	.156	0.3	.721
GPX3	−0.4	.125	−0.4	.269	−0.1	.944
GPX4	0.1	.893	−0.5	.358	−0.2	.91
GRB2	−0.4	.124	−1	.001	−0.4	.375
GRB7	0.1	.832	−0.3	.428	0.2	.826
GRHPR	−0.4	.145	−0.6	.084	−0.2	.77
GRP78	−0.5	.05	−0.3	.311	−0.6	.188
GSN	−0.8	<.001	−0.8	.002	−0.6	.128
GSR	−0.5	.003	−0.7	.001	−0.6	.056
GSS	−1.9	<.001	−3.2	<.001	−2.3	.003
GSTM2	−0.1	.966	−0.3	.584	0.4	.668
GSTM3	0.1	.924	−0.1	.862	0.5	.352
GSTO1	0.3	.031	0.1	.7	0.3	.464
GSTP1	−0.8	<.001	−0.6	.016	−0.5	.244
GSTT1	−0.4	.237	−0.5	.334	0.1	.917
GUK1	−0.8	.032	−0.8	.131	−0.3	.822
GULP1	−0.9	.003	−0.7	.098	−0.9	.152
GYG1	−0.5	.153	−0.7	.092	0.1	.986
H1-0	−0.2	.52	−0.2	.659	0.1	.899
H1-5	2	<.001	1.4	.026	1.7	.067
H2AC21	−0.7	.04	−1.1	.012	−0.9	.191
H3−3A	0.4	.275	0.4	.42	1.1	.129
H4−16	0.7	.151	0.2	.854	0.9	.348
HAAO	−1.6	<.001	−1.7	<.001	−0.8	.127
HABP2	−0.3	.491	−0.5	.207	−0.1	.919
HADH	−0.7	.002	−1.2	<.001	−0.9	.017
HADHA	−0.3	.337	−0.5	.092	−0.2	.729
HADHB	−0.3	.241	−0.4	.073	−0.3	.626
HAGH	−0.7	<.001	−1	<.001	−0.7	.015
HAPLN1	−1.6	<.001	−1.2	.007	−1.1	.118
HAPLN3	−1.4	.001	−0.9	.084	−0.4	.695
HARS2	−1	.009	−1	.035	−0.6	.533

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Supplementary Table II. Continued.

Gene	Log_2FC TAA/ normal	Adjusted *P* value[a]	Log_2FC TBAD/ normal	Adjusted *P* value[a]	Log_2FC TADA/ normal	Adjusted *P* value[a]
HBA1	0.5	.215	−1	.017	−0.5	.567
HBB	−0.1	.901	−1.4	.001	−0.6	.418
HBD	0.1	.969	−1.1	.005	−0.5	.563
HBZ	1	.019	−0.8	.179	−0.2	.917
HDGF	−0.3	.308	0.1	.992	0.1	.903
HDGFL3	−1.2	.003	−1.8	.001	−0.8	.362
HDHD2	−0.3	.309	−0.7	.041	−0.4	.596
HDLBP	0.4	.29	0.2	.678	0.5	.544
HEBP1	−0.5	.022	−1	.001	−0.4	.513
HEBP2	−1.2	<.001	−1.1	.002	−0.7	.256
HEXA	−1	.002	−0.9	.025	−1.5	.012
HEXB	0.1	.965	−0.5	.151	0.2	.872
HIBADH	−0.2	.558	−0.7	.072	0.3	.771
HIBCH	−0.3	.268	−0.8	.013	−0.4	.503
HINT1	−0.5	.041	−1.2	.001	−0.3	.675
HK1	0.3	.353	0.3	.379	0.3	.719
HKDC1	1.3	.002	−0.4	.53	0.7	.526
HLA-DRA	0.7	.013	−0.3	.568	0.1	.896
HLCS	0.3	.576	−0.3	.678	−0.4	.756
HMCN1	−1.1	.003	−0.4	.505	−0.4	.667
HMGB2	−0.1	.832	0.5	.078	0.1	.908
HMGCS2	0.7	.18	−0.1	.906	0.5	.692
HNRNPA1	1.5	.001	1.6	.002	0.8	.362
HNRNPA2B1	−0.2	.589	−0.2	.642	−0.2	.761
HNRNPA3	0.1	.953	0.1	.923	0.1	.939
HNRNPAB	−0.2	.644	−0.8	.006	−0.4	.446
HNRNPC	−0.4	.345	−1	.026	−0.3	.773
HNRNPD	−0.3	.377	−0.6	.122	−0.3	.73
HNRNPF	0.2	.753	−0.4	.562	−0.2	.916
HNRNPH3	−0.4	.079	−0.3	.432	−0.3	.714
HNRNPK	−0.3	.162	−0.5	.047	−0.2	.767
HNRNPL	−0.7	.006	−0.8	.026	−0.8	.138
HNRNPM	−0.2	.401	−0.2	.393	−0.4	.315
HNRNPR	−0.5	.036	−0.8	.008	−0.7	.167
HNRNPU	0.5	.216	0.1	.886	0.7	.384
HNRNPUL2	0.3	.604	0.3	.678	0.5	.677
HP	−0.5	.368	−1	.12	0.7	.529
HP1BP3	0.9	.012	0.8	.068	1	.147
HPR	0.3	.544	−1.1	.021	0.4	.702
HPRT1	1	.001	0.3	.462	0.6	.294
HPX	−1	.001	−1.8	<.001	−0.9	.068
HRG	−0.5	.024	−0.2	.557	−0.1	.994
HSD17B10	−0.6	.019	−1.1	.001	−0.8	.067
HSD17B12	0.2	.479	0.4	.22	0.4	.516
HSD17B3	−1	.012	−1	.044	−0.4	.741
HSD17B4	0.8	.011	0.3	.543	0.5	.544

Supplementary Table II. Continued.

Gene	Log_2FC TAA/ normal	Adjusted *P* value[a]	Log_2FC TBAD/ normal	Adjusted *P* value[a]	Log_2FC TADA/ normal	Adjusted *P* value[a]
HSF1	1.3	.042	−1.4	.094	−0.2	.939
HSP90AA1	−0.2	.418	−0.2	.701	0.1	.899
HSP90AB1	−0.4	.21	0.2	.7	0.2	.784
HSP90B1	−0.1	.898	−0.2	.435	−0.2	.821
HSPA2	−1.3	<.001	−0.9	.041	−0.3	.719
HSPA4	0.2	.788	−0.5	.266	−0.1	.954
HSPA4L	−0.1	.858	−0.6	.328	−0.5	.681
HSPA5	−0.2	.241	−0.4	.059	−0.4	.247
HSPA8	−0.6	.001	−0.8	.001	−0.6	.056
HSPA9	−0.1	.899	−0.3	.285	−0.1	.968
HSPB1	−1.6	<.001	−1.5	.001	−1.1	.068
HSPB6	−1.6	<.001	−1.9	<.001	−1	.167
HSPB7	−1.6	<.001	−1.5	.002	−0.8	.329
HSPB8	−1.9	<.001	−1.3	.011	−1.3	.085
HSPD1	−0.3	.178	−0.5	.017	−0.4	.248
HSPE1	−0.5	.127	−1.2	.001	−0.6	.33
HSPG2	−1.4	<.001	−0.6	.173	−0.7	.275
HTR3C	−0.5	.308	−1.6	.004	−0.8	.382
HTRA1	−1.4	.001	−1.4	.005	−0.9	.256
HV206	0.8	.214	0.1	.971	1.9	.112
HV209	0.6	.225	−0.6	.354	1.1	.282
HV306	0.3	.681	−0.9	.188	1.1	.324
HYOU1	−0.2	.526	−0.4	.346	−0.6	.345
IAH1	−0.7	.012	−0.7	.028	−0.3	.725
IARS1	0.4	.112	0.3	.539	0.3	.676
IARS2	−0.6	.131	−0.2	.817	−0.1	.979
IDH1	−0.3	.117	−0.6	.009	−0.2	.706
IDH2	0.8	.002	0.7	.046	0.6	.345
IDH3A	0.2	.621	−0.6	.139	−0.1	.998
IDNK	0.7	.184	−2	.003	−1.4	.199
IER5	0.2	.783	−0.7	.159	0.4	.693
IFT46	0.4	.325	−0.7	.127	0.7	.345
IGDCC3	−4.2	<.001	−2.4	.002	−3.6	.001
IGF2	−1	.001	−1.1	.003	−0.3	.735
IGFALS	0.8	.016	0.1	.987	0.9	.196
IGFBP2	−1.4	<.001	−1.3	.005	−1	.157
IGFBP3	−0.5	.304	0.5	.42	0.3	.79
IGFBP5	−1	.003	−0.3	.553	−0.4	.693
IGFBP6	−1.1	.002	−1.3	.003	−1	.116
IGFBP7	−1.9	<.001	−0.9	.049	−0.8	.315
IGHA1	−0.2	.774	−1.1	.009	0.3	.734
IGHA2	−0.3	.59	−1.3	.01	0.3	.777
IGHD	−0.1	.909	−1	.089	−0.1	.932
IGHG1	−0.2	.548	−0.7	.051	0.5	.484
IGHG2	−0.8	.018	−1.4	.002	−0.1	.974
IGHG3	−0.2	.666	−0.4	.383	−0.2	.888

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Supplementary Table II. Continued.

Gene	Log_2FC TAA/ normal	Adjusted *P* value[a]	Log_2FC TBAD/ normal	Adjusted *P* value[a]	Log_2FC TADA/ normal	Adjusted *P* value[a]
IGHG4	−0.2	.799	−0.5	.367	0.7	.455
IGHM	0.3	.526	−1	.046	0.6	.542
IGHV2-70D	−1.2	.046	−1.6	.035	−0.9	.499
IGHV3-20	−0.1	.988	−0.4	.457	0.4	.697
IGHV3-49	0.3	.527	−1.1	.038	0.7	.452
IGHV3-64D	0.2	.793	−0.7	.118	0.7	.372
IGHV3-7	0.2	.721	−0.8	.088	0.8	.283
IGHV3-72	−0.1	.873	−0.7	.143	0.7	.417
IGHV3-74	0.3	.609	−1	.041	0.8	.286
IGHV6-1	0.8	.126	−0.3	.675	1	.356
IGKC	−0.2	.6	−1	.007	0.3	.734
IGKV1-12	−0.2	.758	−0.5	.499	1	.284
IGKV1-16	−0.3	.649	−1.4	.009	0.2	.86
IGKV1-6	−0.1	.981	−0.8	.079	0.3	.782
IGKV2-24	0.2	.795	−1.2	.007	0.5	.582
IGKV3-20	−0.4	.266	−0.9	.013	0.3	.71
IGKV3D-15	0.2	.763	−1.5	.003	0.5	.607
IGKV3D-20	−0.4	.47	−1.6	.003	0.4	.746
IGKV4-1	−0.1	.998	−1	.02	0.6	.477
IGLC7	−0.3	.586	−1.3	.006	0.4	.737
IGLL1	−0.3	.435	−0.8	.041	0.3	.754
IGLL5	−0.1	.874	−2.2	.001	0.5	.725
IGLV1-47	−0.1	.986	−1.4	.005	0.4	.729
IGLV1-51	0.1	.943	−0.6	.456	1.2	.279
IGLV3-1	−0.5	.224	−1.6	.002	0.3	.809
IGLV3-12	−0.1	.819	−0.8	.032	0.6	.421
IGLV3-19	−0.5	.218	−1.3	.007	0.3	.762
IGLV4-3	1.1	.062	0.4	.642	1.6	.153
IGLV8-61	−0.3	.636	−0.3	.62	0.4	.772
IL12RB1	−3.7	<.001	−1.6	.044	−2.6	.026
IL1RAPL1	0.2	.863	−1.5	.028	0.8	.527
IL1RL1	0.3	.702	−1.2	.056	0.2	.91
IL34	−1.9	<.001	−1	.021	−1.7	.009
IL4I1	0.7	.005	−0.2	.568	0.5	.335
ILF2	−0.7	.121	−1.1	.039	−0.9	.294
ILK	−0.8	.001	−0.2	.557	−0.3	.656
IMMT	−0.5	.01	−0.4	.143	−0.5	.189
IMPA1	−0.9	.007	−1.4	.001	−0.5	.571
IMPDH2	−0.6	.097	−0.3	.553	0.1	.967
IMPG1	−0.8	.242	−0.4	.642	0.2	.907
INF2	−0.2	.819	−0.9	.282	−0.4	.792
INKA1	0.8	.033	−0.4	.397	0.3	.801
IPO5	0.7	.019	0.7	.106	0.6	.42
IPO7	−0.1	.785	0.1	.826	0.1	.906
IPO9	−0.2	.531	−0.3	.539	−0.2	.88
IQGAP1	0.1	.795	0.1	.926	0.3	.659

Supplementary Table II. Continued.

Gene	Log$_2$FC TAA/ normal	Adjusted *P* value[a]	Log$_2$FC TBAD/ normal	Adjusted *P* value[a]	Log$_2$FC TADA/ normal	Adjusted *P* value[a]
IRGC	−0.9	.067	0.2	.779	−0.4	.761
ISLR	−0.3	.574	−0.6	.311	−0.3	.793
ISYNA1	−0.7	.098	−0.6	.348	−0.1	.927
ITGA1	−0.4	.309	0.2	.688	0.6	.44
ITGA11	−0.6	.167	−0.3	.683	−0.2	.878
ITGA3	−1.5	<.001	−0.8	.035	−0.8	.177
ITGA5	−1	.002	−0.6	.203	−0.4	.611
ITGA7	−2	<.001	−1.6	<.001	−1.3	.012
ITGA8	−1.7	<.001	−1.1	.009	−1	.145
ITGAV	−1.1	<.001	−0.9	.003	−0.9	.047
ITGB1	−0.7	.014	−0.5	.2	−0.2	.844
ITGB2	1.1	.001	1.1	.004	0.9	.168
ITGB3	0.9	.009	1.6	.001	0.7	.315
ITGB5	−1	.001	−1	.008	−0.8	.192
ITIH1	0.3	.486	−0.4	.398	0.4	.675
ITIH2	0.4	.225	−0.4	.245	0.1	.923
ITIH3	0.7	.022	−0.1	.915	0.7	.275
ITIH4	0.2	.69	−0.7	.024	0.4	.511
ITIH5	−1.4	<.001	−1.2	.002	−0.6	.345
ITM2B	−1.1	.001	−1	.021	−0.5	.488
ITPR1	−0.5	.178	0.1	.889	0.2	.86
IVD	−0.7	.088	−0.5	.4	−0.7	.387
IVNS1ABP	−0.5	.12	−0.3	.605	−0.3	.688
JCHAIN	0.3	.38	−0.9	.018	0.3	.713
JMY	0.7	.258	1.4	.069	2	.068
K132L	−1.4	.002	−1.3	.036	−0.3	.807
KANK2	−1	.002	−0.6	.15	−0.4	.649
KANSL3	−0.2	.802	−1.9	.001	−0.6	.52
KAT6B	−0.6	.126	−0.1	.967	0.2	.878
KAT8	−1.7	.002	−1.4	.047	−0.4	.825
KCNF1	−1.1	.125	−2	.023	−1.1	.503
KCTD12	−0.2	.538	−0.9	.017	−0.3	.725
KDEL2	−0.6	.046	−0.5	.17	−0.6	.39
KHSRP	−0.3	.52	−0.3	.621	−0.4	.704
KIF26B	0.3	.799	−1.6	.12	0.4	.878
KIF2A	0.7	.233	0.7	.353	1.4	.244
KIF5B	−0.3	.467	−0.2	.73	−0.3	.765
KLB	−0.3	.29	−0.3	.491	−0.1	.899
KLC1	−0.5	.118	−0.6	.118	−0.3	.657
KLF10	−0.9	.049	−0.6	.33	−0.5	.677
KLKB1	−0.1	.781	−0.7	.049	0.1	.959
KMT5C	−0.3	.445	0.3	.478	0.5	.355
KNG1	−0.1	.903	−0.7	.01	0.1	.919
KNTC1	0.3	.733	−0.4	.642	1.1	.315
KPNB1	0.4	.154	0.2	.737	0.5	.364
KREMEN2	0.6	.301	−0.6	.428	0.5	.756

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Supplementary Table II. Continued.

Gene	Log_2FC TAA/ normal	Adjusted *P* value[a]	Log_2FC TBAD/ normal	Adjusted *P* value[a]	Log_2FC TADA/ normal	Adjusted *P* value[a]
KRT1	0.1	.791	−0.4	.41	−0.4	.661
KRT10	0.1	.953	−0.1	.876	−0.3	.768
KRT18	1.7	<.001	1.1	.019	2.3	.001
KRT19	−0.7	.02	−1.1	.006	0.3	.771
KRT2	0.4	.37	−0.4	.504	0.2	.868
KRT7	1.1	.004	0.7	.155	1.3	.079
KRT73	−1.7	<.001	−1.7	<.001	−2	.001
KRT77	−0.1	.986	−0.6	.452	−0.7	.652
KRT8	0.1	.882	−0.5	.289	0.8	.242
KRT9	−0.1	.792	−0.3	.449	−0.2	.767
KSR2	0.9	.041	−0.5	.433	1.2	.167
KTN1	−0.6	.008	−0.9	.004	−0.6	.245
KV204	−0.7	.04	−1.5	.001	−0.2	.793
KV303	0.5	.301	−1.1	.038	0.9	.299
KV304	0.2	.829	−1.2	.11	0.4	.813
KV308	0.5	.359	−0.7	.289	0.6	.656
KV402	−0.7	.096	−1.1	.033	0.3	.78
KY	−1	.081	−0.4	.649	0.1	.986
LACTB2	−0.3	.416	−0.8	.023	−0.8	.129
LAMA2	−1	.003	−0.9	.038	−0.7	.36
LAMA4	0.3	.368	−0.2	.703	0.8	.233
LAMA5	−1.8	<.001	−0.8	.032	−0.9	.118
LAMB1	−0.2	.756	0.1	.839	0.3	.729
LAMB2	−1.8	<.001	−0.8	.03	−0.9	.084
LAMC1	−1.3	<.001	−0.7	.065	−0.6	.329
LAMP1	0.5	.006	0.1	.903	0.4	.41
LAMP2	0.7	.002	0.4	.168	0.4	.369
LAMTOR1	0.2	.593	−0.1	.984	0.1	.918
LAMTOR3	0.7	.009	0.7	.033	0.4	.496
LANCL1	−0.8	.004	−0.5	.14	−0.2	.771
LAP3	0.2	.709	−1	.002	−0.2	.754
LASP1	−0.2	.766	−0.3	.584	0.3	.773
LBP	−0.1	.821	0.1	.899	0.6	.402
LBX1	−1.2	.008	−1.7	.004	−1.1	.262
LCA5L	1.1	.212	2.1	.055	1.5	.422
LCP1	1.3	<.001	0.9	.021	1.1	.056
LDB3	−1.8	<.001	−1.3	.002	−1.1	.103
LDHA	0.2	.621	0.2	.657	0.5	.29
LDHAL6A	0.4	.41	0.1	.984	1.1	.16
LDHB	−0.3	.128	−0.5	.024	−0.2	.729
LDLR	0.1	.856	−0.6	.187	0.3	.773
LECT2	−0.8	.146	−0.4	.605	−0.4	.756
LEFTY2	−1.5	.001	−0.9	.107	−0.9	.326
LEMD2	0.3	.483	−0.1	.881	0.8	.329
LETM1	−0.7	.007	−0.6	.045	−0.8	.106
LGALS1	−1	<.001	−0.9	.004	−0.5	.315

Supplementary Table II. Continued.

Gene	Log$_2$FC TAA/ normal	Adjusted *P* value[a]	Log$_2$FC TBAD/ normal	Adjusted *P* value[a]	Log$_2$FC TADA/ normal	Adjusted *P* value[a]
LGALS3	−0.5	.02	−1.2	<.001	−0.7	.147
LGALS3BP	−1.4	<.001	−1.5	.001	−1.6	.009
LHPP	−1.2	.001	−1.8	<.001	−1.2	.04
LIMS1	−1.1	.001	−0.9	.009	−0.7	.24
LIMS2	−1	<.001	−0.9	.004	−0.6	.283
LMAN2	1.4	<.001	1.3	.001	1.4	.009
LMCD1	−1.6	<.001	−1.1	.013	−0.8	.237
LMNA	−0.9	.005	−0.9	.018	−0.5	.498
LMNB1	0.8	.023	1.2	.009	1	.133
LMNB2	−0.5	.033	−0.4	.178	−0.1	.878
LMOD1	−1.4	<.001	−0.8	.067	−0.7	.316
LOXL1	−1.7	<.001	−0.4	.405	−0.6	.412
LPA	1.6	<.001	−0.5	.376	1.4	.05
LPCAT2	−0.2	.401	−0.4	.174	−0.1	.947
LPP	−1.5	<.001	−0.9	.034	−0.8	.259
LRG1	−0.3	.305	−1.1	.002	0.1	.999
LRP1	−0.2	.555	−0.2	.715	0.2	.815
LRP12	−2.3	<.001	−1.1	.127	−0.4	.772
LRP6	−2	.001	−1.6	.036	−1.4	.252
LRPAP1	−0.8	.015	−0.9	.043	−0.4	.666
LRRC47	−0.6	.063	−0.8	.049	−0.5	.496
LRRC59	1.7	<.001	1.1	.013	0.7	.378
LRRC72	−2.7	<.001	−1.1	.141	−1.8	.127
LRRC9	0.5	.219	−0.3	.499	−0.3	.767
LSM3	−0.3	.271	−1.1	.002	−0.3	.748
LSM6	−0.4	.121	−0.5	.167	−0.5	.337
LSM7	−1.8	.001	−2.4	.001	−2	.048
LSM8	−1	.037	−1.9	.002	−1.4	.153
LTA4H	0.1	.808	0.3	.476	0.2	.773
LTBP1	−1.1	<.001	−0.2	.713	−0.3	.737
LTBP2	−1.1	<.001	−0.9	.01	−0.5	.493
LTBP4	−2.2	<.001	−1.1	.011	−1.1	.083
LTF	1	.03	1.4	.012	1.4	.112
LUM	0.3	.548	−1.1	.019	−0.1	.993
LV106	−0.2	.808	−0.6	.356	0.3	.79
LXN	1.3	.004	−0.4	.571	0.9	.332
LYPLA1	−0.3	.488	−1.2	.015	−1.2	.12
LYST	−0.2	.785	−1.4	.003	0.5	.618
LYZ	−0.3	.363	−0.2	.795	0.3	.725
LZIC	−0.3	.237	−0.9	.005	−0.3	.677
LZTR1	0.1	.984	−0.6	.424	0.2	.9
MACF1	−0.7	.031	−0.4	.378	−0.6	.362
MACROH2A1	0.8	.011	0.5	.295	0.9	.137
MAGEE1	−2.8	<.001	−1.1	.054	−1.7	.056
MAGEH1	0.4	.211	−0.2	.651	0.2	.773
MAMDC2	−0.4	.374	−0.5	.332	−0.4	.718

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Supplementary Table II. Continued.

Gene	Log_2FC TAA/ normal	Adjusted *P* value[a]	Log_2FC TBAD/ normal	Adjusted *P* value[a]	Log_2FC TADA/ normal	Adjusted *P* value[a]
MAOA	0.1	.989	−0.3	.568	0.3	.762
MAOB	−0.1	.87	−0.2	.758	0.3	.773
MAP1B	−1.2	<.001	−0.9	.009	−1	.032
MAP4	−0.6	.044	−0.6	.112	−0.5	.407
MAPK1	−0.3	.246	−0.9	.003	−0.2	.767
MAPK10	−0.6	.448	0.5	.648	0.5	.771
MAPRE1	−0.4	.203	−0.6	.071	−0.3	.681
MARCKS	1.2	<.001	0.7	.067	0.9	.09
MAST3	−0.6	.113	−0.7	.159	0.1	.923
MAT2B	−0.5	.154	−0.7	.074	−0.4	.636
MB	−3.2	<.001	−2.5	<.001	−2.8	.001
MCAM	−0.7	.023	−0.6	.135	0.1	.953
MCEMP1	0.4	.627	−0.7	.474	−0.7	.714
MDFIC	0.6	.173	−0.7	.19	0.5	.675
MDH1	−0.6	.011	−1.2	.001	−0.6	.315
MDH2	−0.4	.184	−1.1	.001	−0.6	.237
MDM1	−1.9	<.001	−0.7	.177	−0.7	.476
ME1	−0.5	.401	−1.4	.052	−0.6	.676
ME2	0.5	.266	0.1	.981	0.6	.509
MECP2	−0.4	.083	−0.4	.215	−0.3	.602
MEGF6	−1	.003	−0.3	.591	−0.8	.244
MESD	−0.7	.033	−1.3	.003	−1	.147
METRNL	−0.5	.264	−0.1	.898	−0.4	.719
METTL25	−0.3	.717	−1	.145	0.8	.462
METTL7A	0.2	.746	−0.2	.738	1	.276
MFAP2	−0.9	.023	0.3	.558	0.2	.883
MFAP4	−2	<.001	−1.4	.016	−1	.325
MFAP5	−0.6	.072	−1.2	.002	−0.6	.39
MFGE8	−2.7	<.001	−1.9	.001	−1.8	.015
MGP	−1.9	<.001	−1.3	.039	−0.8	.503
MGST3	1.2	.004	1	.072	1.3	.118
MIF	−0.6	.019	−0.5	.133	−0.2	.814
MINPP1	0.5	.264	−0.9	.082	−0.7	.503
MLH1	0.3	.519	−0.8	.104	−0.5	.589
MLKL	0.3	.531	0.1	.971	0.8	.334
MLTK	0.4	.275	0.7	.066	0.7	.317
MMP2	−0.9	.011	−0.9	.032	−0.9	.212
MMP9	1	.029	1.6	.008	1.2	.209
MMRN1	0.8	.023	1.3	.004	0.2	.829
MOCS2	−1.3	<.001	−1.2	.001	−0.7	.188
MOS	−0.4	.529	−0.8	.314	−0.5	.765
MPDZ	0.6	.069	−0.6	.159	0.2	.82
MPO	1.1	.004	2.4	<.001	1.4	.054
MPST	−0.6	.032	−1.5	<.001	−0.4	.561
MRC2	0.4	.302	0.2	.783	0.3	.759
MRVI1	−0.8	.02	−0.5	.232	−0.6	.387

Supplementary Table II. Continued.

Gene	Log_2FC TAA/ normal	Adjusted *P* value[a]	Log_2FC TBAD/ normal	Adjusted *P* value[a]	Log_2FC TADA/ normal	Adjusted *P* value[a]
MSN	−0.7	<.001	−0.5	.022	−0.5	.195
MSRB3	−1.3	.001	−2.2	<.001	−0.9	.283
MST1	0.2	.784	0.3	.646	−0.1	.998
MT−CO2	0.5	.301	0.7	.186	1.2	.159
MTHFD1	0.1	.812	−0.2	.731	0.2	.889
MTPN	−0.2	.507	−0.7	.017	−0.1	.997
MVP	0.1	.726	0.2	.648	0.3	.589
MYADM	0.3	.574	1.5	.004	1	.244
MYCBP2	0.1	.986	−0.8	.38	0.7	.675
MYDGF	−0.2	.636	−0.8	.121	−0.5	.59
MYH10	−1.1	.001	−0.4	.41	−0.3	.767
MYH11	−1.5	<.001	−0.5	.299	−0.4	.699
MYH13	−0.5	.294	−0.3	.688	0.1	.923
MYH14	−0.6	.162	−0.1	.946	0.2	.903
MYH2	−0.4	.455	−0.1	.98	0.3	.771
MYH9	0.3	.359	0.6	.06	0.4	.503
MYL6	−1.3	<.001	−0.8	.027	−0.5	.477
MYL6B	−1.2	.001	−0.5	.381	−0.2	.891
MYL9	−1.4	<.001	−1.2	.002	−0.8	.195
MYLK	−1.1	<.001	−0.9	.006	−0.6	.276
MYO18A	−2.1	<.001	−2.7	.001	−2.3	.026
MYO1C	−0.4	.226	0.1	.855	0.3	.725
MYO1D	0.3	.556	0.4	.365	0.6	.472
MYO5B	−0.6	.352	0.2	.889	−0.4	.792
MYOF	0.2	.781	0.4	.397	0.3	.725
MYOM2	0.2	.737	−0.9	.066	0.3	.773
MYOM3	−1.2	.001	−1.3	.007	−0.5	.614
NAA15	−1.3	.202	−3.3	.006	0.2	.94
NAGK	0.3	.29	−0.2	.473	0.3	.578
NAMPT	0.6	.069	1.3	.002	1	.129
NAP1L1	0.2	.792	−0.3	.639	0.1	.976
NAP1L4	−0.8	.001	−0.9	.001	−0.6	.149
NAPA	−0.2	.691	−0.6	.14	−0.4	.545
NAPG	−0.2	.608	−0.2	.813	0.1	.944
NAPRT	−0.4	.412	−0.6	.248	0.1	.923
NARS1	−0.2	.722	−0.2	.799	−0.3	.771
NASP	0.2	.717	1.1	.019	0.7	.421
NAV1	−1.7	.001	−0.5	.41	−1.3	.127
NAV2	0.5	.413	−0.7	.263	0.4	.771
NAXE	−0.6	.148	−0.7	.197	0.3	.788
NCKAP1	−0.3	.55	0.3	.525	0.2	.871
NCL	−0.3	.389	−0.5	.191	0.1	.994
NCOA1	0.4	.476	−0.1	.914	−0.8	.466
NDRG1	−0.6	.04	−0.6	.079	−0.4	.536
NDRG3	−0.9	.001	−1.1	.001	−0.8	.12
NDUFA10	−0.5	.176	−1.2	.006	−0.2	.887

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Supplementary Table II. Continued.

Gene	Log_2FC TAA/ normal	Adjusted *P* value[a]	Log_2FC TBAD/ normal	Adjusted *P* value[a]	Log_2FC TADA/ normal	Adjusted *P* value[a]
NDUFA13	−0.5	.165	−0.5	.212	−0.3	.721
NDUFA4	0.5	.162	0.4	.395	0.7	.402
NDUFA5	−0.3	.411	−0.5	.165	−0.8	.165
NDUFA6	0.2	.417	−0.1	.732	0.1	.994
NDUFB11	−0.3	.46	−0.4	.479	−0.2	.817
NDUFB4	0.3	.548	0.2	.799	0.5	.582
NDUFS1	0.3	.437	−0.4	.383	0.1	.968
NDUFS3	−0.1	.926	−0.6	.395	0.1	.94
NDUFS8	−0.1	.964	−0.5	.067	−0.2	.72
NDUFV2	−0.4	.145	−0.8	.012	−0.4	.602
NECAP2	0.8	.162	1	.147	1.1	.33
NEDD8	−1.2	.002	−1.9	.001	−0.3	.773
NEGR1	−1	.002	−0.8	.053	−0.4	.598
NENF	−1.3	.002	−1.2	.028	−0.7	.469
NEXN	−1	.001	−1	.005	−0.8	.165
NHSL1	0.2	.853	−0.8	.367	−0.1	.998
NIBAN	−0.5	.046	−0.1	.788	0.1	.978
NIBL1	1	.008	0.4	.519	1	.239
NID1	−0.9	.001	−1	.002	−0.5	.329
NID2	−0.2	.604	−0.5	.171	0.4	.666
NIT2	−0.7	.002	−1	.001	−0.5	.335
NKX1−2	−0.3	.615	−1.1	.07	−0.5	.685
NLRC4	−1.4	.001	−1.2	.022	−0.7	.461
NLTP	0.5	.024	−0.1	.903	0.1	.999
NME1	0.4	.414	−0.5	.397	0.1	.964
NNMT	0.3	.523	0.1	.881	0.4	.677
NOLC1	2	.001	2.5	.001	1.6	.129
NOTCH3	−1	.003	−0.4	.431	−0.4	.668
NPC2	0.2	.727	−0.3	.587	0.1	.94
NPEPPS	−0.3	.428	−0.6	.084	0.2	.805
NPM1	0.3	.147	0.1	.836	0.3	.664
NPNT	−1.9	<.001	−0.6	.245	−0.8	.323
NPTN	−0.7	.009	−0.5	.174	−0.3	.729
NQO2	−1	.001	−1.1	.004	−0.6	.364
NRAP	−0.5	.162	−0.4	.376	0.4	.699
NSF	0.6	.046	0.4	.295	0.2	.821
NSFL1C	0.1	.899	−0.5	.233	0.1	1.00
NSMCE3	0.5	.103	−0.4	.383	0.8	.242
NT5E	−0.2	.786	0.1	.855	0.2	.889
NUCB1	−0.1	.971	−0.4	.186	−0.2	.753
NUCB2	−0.4	.193	−0.7	.041	−0.4	.606
NUCKS1	−0.2	.806	−0.9	.191	0.7	.549
NUDC	−0.5	.063	−0.4	.326	0.1	.998
NUDT2	−0.3	.351	−0.3	.452	0.1	.992
NUDT5	0.1	.817	−0.7	.052	0.4	.582
NUTF2	−0.7	.001	−0.8	.002	−0.6	.146

Supplementary Table II. Continued.

Gene	Log_2FC TAA/ normal	Adjusted *P* value[a]	Log_2FC TBAD/ normal	Adjusted *P* value[a]	Log_2FC TADA/ normal	Adjusted *P* value[a]
OAF	−2.2	.001	−2	.021	−1.9	.153
OAT	0.2	.615	0.2	.672	0.2	.829
OBSCN	−1.7	.01	−0.6	.529	0.4	.829
OGDH	0.3	.46	0.1	.862	0.2	.84
OGN	−0.9	.022	−1.2	.016	−0.4	.731
OLA1	−0.5	.013	−0.6	.007	−0.4	.379
OLFM1	0.7	.146	−0.2	.765	1.1	.217
OLFML1	0.3	.377	−0.2	.674	0.2	.889
OLFML3	0.3	.623	−0.2	.811	0.6	.535
OMD	0.7	.115	0.2	.826	0.6	.587
OPTN	0.2	.75	−0.3	.597	0.1	.91
OR10T2	−0.7	.135	0.3	.682	0.4	.762
OR4C3	−2.2	<.001	−1.8	.002	−2.1	.012
OR51Q1	−2.6	<.001	−2.5	.003	−0.9	.582
OR56B4	−0.5	.382	−0.3	.781	0.1	.961
ORM1	−0.4	.291	−0.9	.012	−0.1	.995
ORM2	0.1	.877	−0.9	.005	0.4	.59
OSTF1	0.6	.014	−0.1	.96	0.2	.781
OTUB1	−0.1	.891	−0.3	.543	0.3	.725
OVOS2	−0.4	.382	−1.4	.002	−0.9	.252
OXCT1	−1	<.001	−1.2	.001	−1.1	.012
OXSR1	0.3	.269	0.5	.133	0.2	.881
P4HB	0.1	.954	−0.1	.801	−0.1	.837
PA2G4	0.4	.296	0.2	.753	0.4	.66
PACSIN2	−1	<.001	−1	.004	−0.5	.36
PAFAH1B1	0.1	.949	−0.1	.886	0.1	.842
PAFAH1B2	−0.2	.553	−0.9	.002	−0.3	.696
PAFAH1B3	1.2	.001	0.1	.875	0.6	.464
PAICS	−0.3	.329	0.1	.959	−0.1	.907
PALLD	−1.2	<.001	−1.1	.001	−0.8	.092
PARK7	−0.9	<.001	−1.2	<.001	−0.8	.02
PARVA	−1.6	<.001	−1.2	.002	−0.7	.24
PAWR	−0.5	.131	−0.4	.375	−0.2	.827
PBXIP1	−2.2	<.001	−1	.083	−1.4	.091
PCBD1	−0.6	.21	−0.7	.234	−0.2	.881
PCBP1	−0.3	.067	−0.3	.137	−0.3	.378
PCBP2	−0.4	.22	−0.6	.06	−0.7	.212
PCDHB14	0.5	.238	0.3	.648	0.8	.253
PCMT1	−0.5	.017	−1	.001	−0.5	.237
PCOLCE	−0.1	.709	−0.4	.175	−0.3	.59
PCOLCE2	−1	.005	−0.9	.053	−1.1	.129
PCYOX1	−0.5	.035	−0.8	.013	−0.3	.703
PCYT2	−0.6	.104	−0.6	.171	−1	.146
PDAP1	−0.8	.106	−0.3	.654	−0.4	.772
PDCD10	−0.1	.892	−0.3	.512	−0.6	.387
PDCD5	−0.8	.003	−1.1	.002	−0.9	.071

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Supplementary Table II. Continued.

Gene	Log_2FC TAA/ normal	Adjusted *P* value[a]	Log_2FC TBAD/ normal	Adjusted *P* value[a]	Log_2FC TADA/ normal	Adjusted *P* value[a]
PDCD6	−1	.002	−0.7	.066	−0.5	.521
PDCD6IP	−0.6	.005	−0.4	.203	−0.6	.153
PDCD7	−1.1	.03	−1.1	.073	−0.1	.99
PDGFC	−2.3	<.001	−1.8	.004	−1.7	.067
PDHA1	−0.3	.57	−0.9	.039	−0.9	.217
PDHB	−1.3	.002	−1.3	.009	−1.6	.032
PDIA2	−1.9	<.001	−1.2	.036	−2.2	.009
PDIA3	−0.4	.031	−0.5	.019	−0.4	.214
PDIA4	−0.4	.171	−0.8	.009	−0.5	.329
PDIA5	0.8	.003	0.6	.06	0.3	.656
PDIA6	0.2	.615	−0.4	.15	−0.1	.918
PDLIM1	−1.3	<.001	−1.3	<.001	−0.9	.043
PDLIM2	−0.6	.091	−0.5	.369	0.1	.976
PDLIM3	−1.6	<.001	−1.3	.002	−0.8	.249
PDLIM4	−1.2	.001	−0.9	.043	−0.5	.537
PDLIM5	−0.8	.027	−0.8	.055	−0.5	.549
PDLIM7	−1.6	<.001	−1.3	.011	−0.7	.376
PDS5A	0.6	.018	0.3	.392	1	.05
PDXK	0.5	.064	−0.2	.723	0.6	.191
PEA15	−1.1	<.001	−1.2	.001	−0.8	.138
PEBP1	−1.2	<.001	−1.5	<.001	−0.8	.129
PEF1	−1.1	.001	−0.6	.174	−1.3	.032
PEPD	−0.5	.009	−1.2	<.001	−0.4	.356
PF4	0.6	.286	0.8	.232	0.4	.767
PFDN1	−0.9	.007	−1	.012	−0.6	.362
PFDN2	−1.3	<.001	−1.7	<.001	−1.2	.065
PFDN5	−0.5	.012	−0.9	.002	−0.5	.283
PFKL	1	.001	1.2	.002	1.1	.03
PFKM	−1	.002	−0.5	.29	−0.3	.756
PFKP	−0.5	.196	0.4	.424	0.1	.908
PFN1	−0.4	.012	−0.5	.045	−0.4	.332
PFN2	−1.3	<.001	−0.9	.003	−1	.031
PGAM1	−0.6	.029	−0.6	.085	−0.2	.851
PGD	1	.001	0.8	.041	0.9	.144
PGK1	−0.4	.075	−0.4	.203	−0.2	.773
PGK2	−0.8	.021	−1.1	.022	−0.4	.713
PGLS	−0.4	.043	−1	.001	−0.4	.455
PGLYRP2	−0.1	.757	−0.7	.045	−0.1	.939
PGM1	−0.6	.001	−0.5	.014	−0.4	.275
PGM2	0.1	.858	−0.5	.171	0.2	.89
PGM3	0.5	.115	0.1	.889	0.4	.619
PGM5	−1.7	<.001	−1.2	.006	−0.7	.315
PGP	−1.1	.004	−0.8	.095	0.1	.953
PGRMC1	−1.3	<.001	−1	.006	−0.7	.219
PHB	−0.1	.706	−0.5	.093	−0.2	.815
PHB2	0.3	.387	−0.2	.575	0.3	.647

Supplementary Table II. Continued.

Gene	Log_2FC TAA/ normal	Adjusted *P* value[a]	Log_2FC TBAD/ normal	Adjusted *P* value[a]	Log_2FC TADA/ normal	Adjusted *P* value[a]
PHGDH	−1.2	<.001	−1.2	.002	−0.6	.379
PHPT1	−0.8	.001	−0.9	.005	−0.6	.237
PI4KA	−1	.012	−1.1	.021	−0.2	.907
PIK3C3	−0.5	.201	−0.6	.288	−0.1	.94
PIMREG	0.3	.562	−0.4	.487	0.9	.253
PITHD1	−0.4	.156	−0.7	.018	−0.3	.635
PITPNB	−0.2	.738	−0.1	.9	0.4	.719
PITRM1	−1.4	.001	−1	.059	−0.6	.531
PKD2	−1.2	.001	−0.5	.32	−0.4	.675
PKM	0.1	.858	−0.1	.928	0.3	.647
PKP4	−2.1	.028	−0.5	.765	−1.3	.582
PLA2G2A	−1	.006	−0.5	.389	−0.2	.907
PLAUR	0.5	.479	0.3	.8	0.1	.988
PLCD1	−1.6	<.001	−1.3	.004	−1	.14
PLCH1	0.2	.699	0.1	.892	0.3	.734
PLD3	0.4	.302	−0.3	.615	0.4	.71
PLEC	0.7	.007	0.4	.35	0.5	.422
PLG	0.8	.009	0.6	.145	0.6	.356
PLIN1	−0.5	.141	−0.7	.11	−0.1	.959
PLIN3	−0.4	.233	−0.9	.011	−0.3	.729
PLOD1	0.4	.382	0.5	.374	0.2	.83
PLP2	−0.1	.874	0.3	.711	0.7	.563
PLS3	−0.6	.063	−0.6	.153	−0.1	.909
PLTP	0.8	.026	−0.2	.847	0.4	.722
PLXDC2	−0.3	.469	−0.9	.013	0.1	.998
PLXNB2	0.2	.788	0.2	.754	0.2	.849
PNP	0.7	.021	0.2	.716	0.3	.677
PODN	−0.3	.301	−1.2	.001	−0.6	.245
POLD1	−1.6	.026	−0.8	.447	−2.1	.147
PON1	0.9	.008	−0.3	.605	0.7	.413
POSTN	0.6	.221	−0.2	.811	0.1	.995
POTEF	−0.7	.081	−1.6	.002	−0.4	.725
POTEI	−1.4	.001	−1.7	.001	−0.7	.421
POTEJ	−0.8	.021	−1.3	.003	−0.4	.63
PPA1	−0.7	.008	−1.2	.001	−0.6	.369
PPA2	0.1	.874	−0.3	.389	−0.3	.725
PPBP	−0.8	.035	−0.9	.048	−1	.147
PPCS	−0.2	.732	−0.5	.171	−0.2	.817
PPFIBP1	−0.3	.335	−0.8	.03	−0.7	.275
PPIA	−0.5	.028	−0.6	.032	−0.3	.637
PPIB	0.2	.438	0.1	.906	0.2	.773
PPIC	−0.3	.531	−0.3	.479	−0.5	.474
PPM1F	−2	<.001	−1.6	.002	−2.1	.005
PPME1	0.8	.08	0.3	.627	0.5	.686
PPP1CB	−1.4	<.001	−0.9	.034	−0.7	.315
PPP1CC	−0.7	.296	−0.4	.699	−0.6	.719

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Supplementary Table II. Continued.

Gene	Log_2FC TAA/ normal	Adjusted *P* value[a]	Log_2FC TBAD/ normal	Adjusted *P* value[a]	Log_2FC TADA/ normal	Adjusted *P* value[a]
PPP1R12A	−0.7	.001	−0.7	.006	−0.7	.118
PPP1R12B	−1.7	<.001	−1.4	.003	−0.7	.327
PPP1R14A	−1.8	<.001	−1.4	.004	−0.7	.364
PPP1R7	−0.8	.016	−0.9	.045	−1.1	.102
PPP2R1A	−0.1	.702	0.1	.884	0.2	.772
PPP6R3	−1	.181	−1.4	.138	−0.5	.808
PPT1	−0.2	.576	−0.8	.034	−0.4	.541
PRAF2	0.2	.707	−0.1	.924	0.3	.772
PRDBP	−0.3	.6	0.5	.462	0.8	.436
PRDX1	−0.7	.001	−1	.001	−0.6	.138
PRDX2	0.3	.222	−0.5	.097	−0.1	.929
PRDX3	0.1	.988	−0.4	.06	−0.2	.63
PRDX4	0.4	.405	0.4	.473	−0.1	.998
PRDX5	−0.2	.537	−0.5	.043	−0.2	.668
PRDX6	−0.5	.006	−0.6	.004	−0.3	.46
PRELP	0.1	.836	−0.7	.061	0.2	.821
PRKACA	−0.6	.019	−0.6	.067	−0.3	.751
PRKACB	−1	.012	−0.5	.397	0.1	.955
PRKAR1A	−1	<.001	−1.2	<.001	−0.9	.034
PRKAR2A	−1.2	<.001	−1.1	.01	−0.7	.327
PRKCB	−2.5	.003	−2.4	.023	−1	.669
PRKCSH	0.1	.966	−0.4	.179	−0.1	.969
PRKG1	−1	.002	−0.4	.418	−0.2	.891
PROC	0.4	.154	−0.6	.067	0.2	.851
PROS1	0.6	.033	−0.3	.403	0.8	.158
PROSC	−1	.026	−1.2	.025	−1	.252
PROX2	−1.1	.003	−0.7	.138	−0.5	.618
PRPF4B	−0.8	.034	−0.8	.085	−1	.171
PRPS1	0.1	.877	−0.1	.862	−0.2	.827
PRR36	−0.6	.224	−0.6	.352	−0.3	.792
PRSS23	−0.6	.188	−0.6	.286	−0.7	.378
PRTG	0.8	.033	−0.8	.122	0.2	.878
PRTN3	1.3	.002	2	.001	1.5	.05
PRXL2A	0.1	.96	−0.6	.167	0.7	.281
PSAP	−0.6	.018	−0.6	.055	−0.2	.734
PSIP1	−1	<.001	−1.4	<.001	−1.1	.021
PSMA1	−0.1	.965	−0.7	.045	0.1	.98
PSMA2	−0.2	.575	−0.6	.039	−0.3	.691
PSMA3	0.2	.454	−0.2	.568	0.1	.998
PSMA4	0.2	.526	−0.5	.086	0.1	.889
PSMA5	−0.3	.35	−0.9	.002	−0.3	.594
PSMA6	0.1	.909	−0.6	.011	0.1	.889
PSMA7	−0.2	.534	−0.3	.424	0.3	.771
PSMB1	0.4	.263	0.1	.884	0.5	.393
PSMB2	0.3	.45	−0.3	.576	0.3	.696
PSMB3	0.4	.241	−0.6	.122	0.3	.677

Supplementary Table II. Continued.

Gene	Log_2FC TAA/ normal	Adjusted *P* value[a]	Log_2FC TBAD/ normal	Adjusted *P* value[a]	Log_2FC TADA/ normal	Adjusted *P* value[a]
PSMB4	−0.4	.223	−0.8	.014	−0.2	.815
PSMB5	−0.3	.314	−0.9	.013	−0.3	.721
PSMB6	−0.6	.004	−1	.001	−0.6	.149
PSMB7	0.8	.202	0.5	.543	0.9	.514
PSMB8	1.1	.005	0.9	.066	1.9	.008
PSMB9	0.9	.002	0.2	.652	0.8	.149
PSMC1	0.2	.544	−0.2	.716	0.1	.963
PSMC2	0.3	.448	0.3	.487	0.3	.676
PSMC3	0.5	.113	−0.2	.615	0.4	.676
PSMC4	0.1	.766	−0.2	.729	0.2	.776
PSMC5	−0.3	.221	−0.4	.237	−0.2	.849
PSMC6	0.4	.214	0.3	.546	−0.1	.998
PSMD1	0.3	.319	0.1	.817	0.4	.582
PSMD11	0.2	.439	−0.2	.647	0.3	.679
PSMD12	0.1	.999	−0.2	.781	0.2	.868
PSMD13	0.5	.101	0.1	.915	0.5	.424
PSMD14	−0.2	.548	−0.8	.004	−0.3	.608
PSMD2	0.6	.032	0.5	.219	0.5	.46
PSMD3	0.4	.217	0.3	.438	0.5	.475
PSMD5	−0.4	.182	−0.3	.594	0.1	.9
PSMD6	0.9	<.001	0.7	.033	0.9	.048
PSMD7	0.1	.889	−0.3	.537	0.3	.8
PSMD9	−0.3	.326	−0.8	.018	0.2	.767
PSME1	0.2	.322	−0.3	.345	0.2	.777
PSME2	0.3	.313	−0.4	.202	−0.1	.923
PSMF1	−1	.001	−1	.008	−0.6	.342
PTBP1	−0.3	.341	−0.8	.013	−0.4	.541
PTGES3	−0.7	.024	−0.8	.021	−0.3	.678
PTGIS	0.3	.365	1.1	.004	1.2	.04
PTGR1	−1.4	.001	−0.9	.067	−1.3	.091
PTK2	−0.5	.068	−0.7	.052	−0.1	.939
PTMA	−0.1	.923	−0.2	.754	0.2	.829
PTMS	−0.8	.007	−1	.007	−0.4	.631
PTPA	0.1	.879	−0.5	.105	0.1	.908
PTPN11	−0.8	.004	−0.6	.09	−0.6	.315
PTPN13	−1.8	<.001	−1	.044	−1.6	.026
PTPN4	−1.8	<.001	−0.7	.201	−0.9	.315
PTRF	−1.3	<.001	−1	.017	−0.9	.144
PURA	−0.8	.007	−0.6	.11	−0.3	.675
PUS10	−0.1	.967	−0.5	.606	0.7	.696
PXDN	−0.1	.874	−0.2	.697	0.3	.736
PYGB	−0.6	.066	−0.6	.132	−0.1	.903
PYGL	0.4	.245	0.8	.019	0.6	.345
PZP	−0.6	.204	0.2	.847	−0.3	.788
QARS1	0.5	.106	0.1	.915	−0.1	.956
QDPR	−0.9	.001	−1.3	<.001	−0.7	.191

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Supplementary Table II. Continued.

Gene	Log_2FC TAA/ normal	Adjusted *P* value[a]	Log_2FC TBAD/ normal	Adjusted *P* value[a]	Log_2FC TADA/ normal	Adjusted *P* value[a]
QSOX1	−0.6	.051	−0.6	.158	−0.3	.725
QTRT1	−0.6	.1	−1.2	.009	−0.3	.754
RAB10	0.6	.012	0.7	.026	0.7	.129
RAB11B	−2	.001	−1	.206	−1.2	.329
RAB14	−0.1	.875	−0.3	.41	−0.2	.775
RAB18	1.1	.02	0.8	.183	0.8	.469
RAB21	−0.1	.845	−0.4	.244	−0.1	.953
RAB23	−1.4	<.001	−1	.012	−0.5	.472
RAB2A	−0.1	.8	−0.5	.242	0.2	.807
RAB35	0.3	.392	0.3	.495	0.4	.582
RAB41	0.3	.512	−0.7	.104	0.8	.275
RAB5B	−0.9	.005	−1.2	.004	−0.2	.802
RAB5C	−0.4	.524	−1.7	.018	0.1	.976
RAB7A	0.3	.301	−0.3	.402	0.2	.772
RAC1	−0.3	.473	−0.7	.179	0.2	.905
RAC3	0.5	.354	0.6	.374	0.7	.6
RACK1	0.3	.114	0.2	.628	0.3	.554
RAD18	−2.4	<.001	−1.5	.025	−2.1	.032
RAD23A	−0.1	.844	−0.4	.575	0.4	.687
RAD23B	−0.3	.296	−0.8	.008	−0.4	.369
RALY	−0.2	.61	−0.2	.618	0.3	.714
RAN	0.1	.996	−0.1	.892	−0.1	.949
RANBP1	−0.2	.509	−0.6	.048	0.1	.968
RAP1A	−0.4	.488	0.1	.888	−0.2	.907
RAP1GDS1	−1	.008	−0.8	.077	−0.8	.318
RARRES2	−0.7	.066	−0.4	.402	−0.3	.771
RBBP8NL	−0.9	.081	−0.5	.519	−0.1	.982
RBCK1	0.4	.27	−0.5	.312	0.7	.326
RBMX	−0.7	.019	−0.9	.01	−0.6	.308
RBP1	−1.2	<.001	−0.8	.032	−0.4	.609
RBP4	−0.6	.034	−1.7	<.001	−0.9	.115
RBPMS	−1.3	<.001	−1.3	.001	−0.8	.203
RBX1	0.5	.327	−1.2	.043	−0.4	.719
RCN1	−0.5	.171	−0.8	.038	−0.2	.81
RCN3	0.6	.026	0.5	.151	0.5	.408
RDX	−0.9	.045	−0.4	.549	−1	.286
RECQL	0.8	.009	0.7	.087	0.8	.191
REEP5	0.1	.875	−0.7	.177	−0.2	.912
REEP6	−0.3	.483	−0.5	.33	0.1	.957
RFTN1	0.1	.953	−0.3	.514	0.3	.773
RGS22	−0.1	.893	−1	.036	0.4	.685
RHBDF1	−0.9	.049	−0.6	.293	−0.1	.967
RHOA	0.7	.022	0.9	.032	0.8	.244
RHOB	−1.6	<.001	−1.3	.001	−1.3	.01
RHOC	−1	.009	−1	.041	−0.6	.513
RHOG	0.6	.097	0.9	.024	0.7	.278

Supplementary Table II. Continued.

Gene	Log_2FC TAA/ normal	Adjusted *P* value[a]	Log_2FC TBAD/ normal	Adjusted *P* value[a]	Log_2FC TADA/ normal	Adjusted *P* value[a]
RIC8A	0.2	.692	0.5	.121	0.2	.792
RIF1	−0.5	.155	−0.6	.184	−0.2	.829
RILPL1	−1.5	<.001	−1.6	<.001	−1.2	.009
RINT1	0.2	.827	−0.4	.724	0.9	.578
RNASE1	−1.3	.003	−1.9	.001	−1.8	.021
RNASE4	−0.6	.141	−0.2	.781	−0.2	.828
RNF31	−0.4	.544	−1	.171	−0.3	.876
RNH1	−0.3	.131	−0.2	.518	−0.1	.983
RNPEP	−0.2	.611	−0.4	.421	−0.4	.656
RPL10	0.1	.966	0.2	.873	0.1	.988
RPL10A	0.6	.067	0.6	.141	0.7	.252
RPL11	0.2	.783	−0.2	.669	0.3	.792
RPL12	0.2	.522	0.3	.393	0.3	.675
RPL13	0.7	.024	0.5	.237	0.9	.167
RPL14	0.4	.225	−0.1	.96	0.3	.7
RPL15	1.1	.002	1.2	.005	1.2	.077
RPL17	1.2	.001	0.7	.17	1	.148
RPL18	1	.003	0.7	.089	1.2	.066
RPL18A	0.8	.022	1.1	.011	0.9	.234
RPL22	−0.1	.858	−0.2	.747	0.3	.725
RPL23	−0.1	.937	−0.4	.372	−0.2	.832
RPL23A	−0.4	.152	−0.8	.012	−0.5	.418
RPL24	1.1	.006	0.9	.11	0.6	.511
RPL27	1.6	<.001	1.3	.008	1.9	.008
RPL27A	0.6	.041	0.4	.335	0.6	.321
RPL28	1	.001	0.8	.033	1	.058
RPL29	1	.001	0.6	.132	0.8	.157
RPL3	1.1	.001	1	.013	1.2	.045
RPL30	−0.1	.816	−0.5	.374	0.5	.646
RPL31	0.3	.578	−0.4	.537	0.3	.762
RPL34	0.8	.062	0.7	.179	0.4	.719
RPL35	1.1	.035	0.6	.411	1.7	.083
RPL38	1.4	.007	1	.168	0.7	.575
RPL4	1	.004	0.7	.083	1	.151
RPL5	0.7	.048	0.4	.352	0.9	.199
RPL6	1.1	<.001	0.9	.006	1.2	.009
RPL7	0.8	.002	1	.005	1	.048
RPL7A	0.8	.01	0.6	.107	0.8	.212
RPL8	0.5	.306	−0.3	.688	0.2	.869
RPL9	0.6	.151	0.3	.672	0.6	.501
RPLP0	−0.4	.444	−0.6	.324	−0.1	.953
RPLP1	−0.6	.089	−0.9	.038	−0.5	.582
RPLP2	−0.5	.114	−0.7	.067	−0.3	.771
RPN1	0.4	.118	0.2	.65	0.3	.725
RPN2	0.8	.003	0.8	.024	0.7	.19
RPS10	1.1	.003	0.7	.159	1.2	.06

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Supplementary Table II. Continued.

Gene	Log_2FC TAA/ normal	Adjusted *P* value[a]	Log_2FC TBAD/ normal	Adjusted *P* value[a]	Log_2FC TADA/ normal	Adjusted *P* value[a]
RPS11	0.5	.108	0.3	.476	0.6	.355
RPS12	0.1	.615	−0.1	.737	−0.1	.889
RPS13	1	.002	0.5	.294	1	.129
RPS14	0.4	.349	0.3	.551	0.8	.242
RPS15A	0.6	.048	0.7	.088	0.8	.242
RPS16	0.8	.022	0.7	.16	1.1	.103
RPS18	0.9	<.001	0.9	.002	1	.015
RPS19	0.2	.515	−0.2	.667	0.4	.554
RPS2	0.7	.032	0.6	.129	0.7	.262
RPS20	−0.1	.961	−0.3	.558	0.1	.939
RPS21	−0.3	.532	−0.9	.028	−0.2	.907
RPS23	0.6	.144	1	.044	0.7	.369
RPS24	0.4	.455	0.6	.243	0.9	.26
RPS25	0.6	.112	0.2	.672	0.6	.461
RPS27L	−2.4	<.001	−1.7	.01	−0.6	.687
RPS28	−1.2	.074	0.2	.885	−0.9	.575
RPS3	0.5	.045	0.2	.765	0.5	.422
RPS3A	0.7	.02	0.5	.145	0.7	.214
RPS4X	1.2	.001	1.2	.005	1.2	.071
RPS5	0.5	.088	0.3	.431	0.5	.469
RPS6	0.9	<.001	1.1	.001	0.8	.071
RPS6KA2	1	.057	0.2	.825	1.3	.246
RPS6KA3	−2	.001	−2.2	.004	−0.4	.83
RPS7	0.6	.077	0.5	.32	0.9	.195
RPS8	0.2	.43	0.3	.339	0.3	.677
RPS9	1	.001	1.2	.002	1.2	.019
RPSA	0.2	.546	−0.6	.099	−0.1	.961
RRAD	−0.3	.662	−0.1	.916	0.6	.648
RRAS	−1	.002	−0.6	.143	−0.4	.701
RRBP1	0.2	.614	−0.4	.418	−0.6	.355
RSAD2	−0.6	.363	0.7	.415	0.4	.797
RSU1	−1.1	<.001	−1.2	.002	−0.8	.182
RTCB	−0.8	.002	−0.7	.045	−0.5	.41
RTN4	0.1	.887	0.2	.747	−0.1	.986
RTRAF	−0.4	.072	−0.8	.007	−0.3	.591
RUNDC3A	0.8	.08	−0.2	.74	0.7	.514
RUVBL1	−0.3	.368	−0.3	.398	−0.2	.771
RUVBL2	−0.2	.705	−0.5	.168	−0.2	.826
S100A11	−0.2	.457	−0.4	.186	−0.3	.675
S100A13	0.4	.227	−0.1	.948	0.3	.748
S100A16	0.3	.279	0.1	.916	0.4	.533
S100A4	−0.9	.001	−0.7	.027	−0.6	.309
S100A6	−0.4	.111	−0.7	.019	−0.2	.741
S100A8	1.3	.004	1.7	.003	1.7	.047
SAA1	0.6	.38	0.7	.352	2.4	.021
SAMHD1	1	.002	0.4	.361	1	.09

Supplementary Table II. Continued.

Gene	Log_2FC TAA/ normal	Adjusted *P* value[a]	Log_2FC TBAD/ normal	Adjusted *P* value[a]	Log_2FC TADA/ normal	Adjusted *P* value[a]
SAMM50	0.7	.183	0.9	.151	1.8	.05
SARS1	−0.2	.558	−0.4	.325	0.1	.879
SBDS	−0.8	.009	−1	.01	−0.2	.792
SBSPON	−2.2	<.001	−1.9	<.001	−1.7	.003
SCARB2	1.2	.007	1.4	.012	1.7	.05
SCN8A	−0.8	.125	−0.7	.259	−0.3	.864
SCRN1	−0.9	.002	−1	.007	−0.3	.725
SCUBE3	−1.7	<.001	−0.8	.052	−1	.109
SCYL2	0.3	.785	−1	.312	1.1	.533
SDHA	−0.5	.133	−0.8	.05	−0.4	.656
SDHB	−0.2	.766	0.1	.915	0.2	.899
SEC11B	−0.1	.806	−0.7	.107	−0.1	.939
SEC13	−0.1	.949	−0.5	.362	−0.2	.86
SEC14L5	−0.2	.746	−0.4	.552	0.5	.649
SEC22B	0.9	.007	1	.02	0.7	.339
SEC23A	0.2	.79	−0.2	.71	−0.2	.876
SEC31A	0.7	.021	0.6	.121	0.4	.691
SELENBP1	−0.7	<.001	−1	<.001	−0.5	.182
SELENOM	−1.5	<.001	−1.2	.006	−1.3	.034
SELENOP	0.1	.901	−0.3	.564	0.2	.79
SEMA3B	−1.3	<.001	−0.7	.109	−0.6	.422
SEMA5B	−0.2	.8	−1.2	.066	0.8	.533
SERBP1	−0.5	.118	−0.4	.256	−0.5	.376
SERPINA1	−0.3	.29	−1.4	<.001	−0.3	.687
SERPINA10	0.2	.83	−0.8	.149	−0.1	.994
SERPINA3	−0.3	.526	−0.9	.038	0.3	.773
SERPINA4	−0.1	.908	−0.3	.376	0.1	.94
SERPINA5	−1	.001	−0.9	.027	−0.5	.445
SERPINA6	−0.2	.758	−1	.009	−0.2	.849
SERPINA7	−0.2	.64	−1.4	.001	−0.4	.554
SERPINB1	0.4	.167	0.5	.148	0.5	.369
SERPINB6	0.3	.437	0.3	.562	0.7	.345
SERPINC1	−0.2	.651	−0.4	.161	0.1	.916
SERPIND1	0.3	.263	−0.4	.193	0.5	.369
SERPINE2	0.9	.058	0.3	.716	0.7	.488
SERPINF1	−0.1	.783	−0.8	.008	−0.3	.602
SERPINF2	0.5	.117	0.8	.039	0.7	.294
SERPING1	0.1	.947	−0.8	.045	0.3	.687
SERPINH1	0.2	.776	−0.1	.977	0.2	.829
SETD1B	0.7	.031	0.1	.923	1.2	.074
SF3B6	0.3	.656	−1.4	.028	0.1	.958
SFPQ	0.1	.767	−0.3	.583	−0.5	.513
SFRP1	−1.5	<.001	−1.3	.002	−1.2	.051
SFXN3	0.1	.845	−0.1	.847	0.4	.542
SGCD	−0.6	.04	0.3	.438	0.4	.633
SH3BGRL	−1.1	<.001	−1.6	<.001	−0.8	.095

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Supplementary Table II. Continued.

Gene	Log_2FC TAA/ normal	Adjusted *P* value[a]	Log_2FC TBAD/ normal	Adjusted *P* value[a]	Log_2FC TADA/ normal	Adjusted *P* value[a]
SH3BGRL3	−0.1	.786	−0.6	.043	−0.2	.782
SH3BP5	−0.7	.007	−0.5	.125	−0.4	.582
SH3GLB1	−0.8	.004	−0.9	.005	−0.6	.249
SH3GLB2	−0.9	.004	−1.4	.001	−0.8	.203
SH3RF2	1.4	<.001	2.2	<.001	1.7	.008
SHMT1	−0.5	.067	−0.6	.092	−0.4	.568
SIN3B	−0.3	.494	−1.1	.036	−0.2	.9
SKP1	−0.3	.359	−0.5	.138	−0.2	.829
SLC22A17	0.4	.575	−1.1	.14	0.9	.498
SLC25A1	0.4	.291	0.4	.351	0.6	.33
SLC25A11	1.2	<.001	0.9	.01	1.1	.046
SLC25A12	0.4	.254	0.6	.122	0.2	.829
SLC25A24	0.2	.634	0.3	.515	0.3	.769
SLC25A3	1.2	.001	1.2	.01	1.2	.084
SLC25A4	−0.7	.084	0.2	.749	0.4	.677
SLC25A5	1	.052	0.6	.434	1	.364
SLC27A2	0.2	.684	−0.5	.153	0.1	.923
SLC27A3	−0.2	.769	−0.2	.69	−0.1	.94
SLC2A1	1.3	<.001	1.2	.002	1.2	.044
SLC2A12	−0.4	.233	−0.7	.138	0.6	.393
SLC30A10	1.3	.04	0.4	.731	1.7	.206
SLC3A2	1	.001	0.6	.138	0.5	.458
SLC4A1	1.8	<.001	0.8	.126	0.9	.219
SLC7A6	−0.7	.112	−0.1	.885	−0.2	.862
SLC9A3R1	−0.1	.893	−1	.074	0.2	.896
SLC9A5	0.1	.909	−0.7	.297	0.8	.476
SLC9A8	−0.9	.046	0.6	.294	0.6	.634
SLMAP	−1.7	<.001	−1.1	.004	−1	.081
SLPI	−1.8	<.001	−0.3	.606	−0.8	.364
SLX4	−1.8	.002	−1.7	.016	−0.8	.511
SMARCA5	−0.3	.445	−0.4	.34	0.3	.729
SMOC2	−0.9	.004	−0.8	.074	−0.8	.243
SMTN	−1.9	<.001	−1.4	.001	−1.1	.068
SNCA	0.5	.114	−0.7	.09	0.2	.899
SNCG	−0.1	.873	0.4	.512	1	.259
SND1	0.5	.084	0.6	.108	0.2	.791
SNRNP200	0.3	.704	−0.2	.812	0.9	.458
SNRPD1	0.1	.912	−0.4	.484	0.3	.756
SNRPD2	−0.6	.055	−0.9	.018	−0.8	.147
SNRPD3	0.2	.787	−0.6	.153	0.1	.993
SNTB2	−0.7	.007	−0.6	.073	−0.3	.697
SNX1	−0.2	.487	−0.5	.14	−0.6	.359
SNX12	−1.4	<.001	−1.1	.007	−0.9	.167
SNX18	−0.6	.099	−0.1	.829	−0.2	.879
SNX2	−0.4	.177	−0.9	.016	−0.7	.275
SNX29	0.2	.812	−0.1	.867	0.6	.493

Supplementary Table II. Continued.

Gene	Log$_2$FC TAA/ normal	Adjusted *P* value[a]	Log$_2$FC TBAD/ normal	Adjusted *P* value[a]	Log$_2$FC TADA/ normal	Adjusted *P* value[a]
SNX3	−0.6	<.001	−0.5	.009	−0.5	.085
SNX6	−0.1	.846	−0.5	.12	0.2	.777
SNX9	0.2	.733	0.2	.768	1	.218
SOD1	−0.9	<.001	−0.9	<.001	−0.7	.032
SOD2	0.3	.218	−0.3	.263	0.3	.582
SOD3	−2.4	<.001	−1.7	.001	−1.4	.04
SOGA1	0.5	.431	−0.1	.924	0.5	.703
SON	−1.8	<.001	−1.7	<.001	−1.6	.009
SORBS1	−1.2	.001	−0.6	.182	−0.4	.675
SORBS2	−1.1	.002	−0.7	.165	−0.1	.929
SORBS3	−0.6	.057	−0.2	.644	0.1	.986
SORD	−1.8	<.001	−1.6	.003	−1	.248
SOST	−2.1	<.001	−1	.085	−1.3	.145
SOX6	−0.1	.864	−0.8	.011	0.1	.889
SPARC	−0.3	.341	−0.8	.039	−0.7	.283
SPARCL1	−2	<.001	−2.4	<.001	−1.5	.001
SPCS2	0.5	.326	−0.5	.418	−1.5	.115
SPCS3	1.3	.001	1	.033	1	.177
SPON1	−1.4	<.001	−1.5	.001	−1.7	.004
SPR	−1.1	.002	−1.1	.014	−0.4	.647
SPTA1	1.4	<.001	0.9	.044	0.8	.237
SPTAN1	0.2	.705	−0.3	.432	0.3	.704
SPTB	1.4	<.001	0.7	.138	0.7	.378
SPTBN1	0.2	.593	−0.1	.848	0.3	.667
SQOR	0.3	.484	−0.5	.252	0.1	.916
SQRD	0.7	.177	0.7	.266	0.5	.692
SREBF2	−1.4	.026	−1	.2	−1	.473
SRFBP1	0.3	.549	−0.3	.702	1	.24
SRGAP3	−1.6	.001	−1.7	.007	−1.8	.048
SRI	−0.5	.005	−0.5	.012	−0.4	.315
SRM	0.1	.949	−0.6	.104	−0.2	.797
SRP9	−0.6	.036	−0.8	.024	−0.4	.634
SRPX	−1	.04	0.2	.832	−0.4	.781
SRRT	−1.2	.001	−0.3	.512	−0.9	.233
SRSF1	−0.3	.538	−0.4	.424	0.2	.894
SRSF3	−0.2	.499	0.1	.915	0.1	.949
SRSF7	−0.4	.305	0.2	.8	0.2	.86
SSB	−0.2	.482	−0.5	.087	0.3	.721
SSBP1	−1.4	.001	−0.7	.212	−1.7	.031
SSR1	0.5	.074	0.1	.96	−0.1	.993
SSR4	0.9	.071	0.6	.375	0.8	.452
SSTR2	−1.3	.09	−1.6	.078	−0.1	.974
ST3GAL6	−1.7	<.001	−0.6	.356	−0.3	.781
STAB1	0.5	.286	0.3	.583	0.9	.289
STAMBP	1.5	.151	1.2	.361	0.8	.77
STAT1	0.6	.278	0.1	.928	0.7	.58

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Supplementary Table II. Continued.

Gene	Log_2FC TAA/ normal	Adjusted *P* value[a]	Log_2FC TBAD/ normal	Adjusted *P* value[a]	Log_2FC TADA/ normal	Adjusted *P* value[a]
STAT6	0.3	.402	0.5	.119	0.5	.379
STIP1	−0.2	.42	−0.6	.041	0.1	.997
STK25	−1.7	.005	−1.6	.043	−1.1	.419
STK31	1.1	.022	0.1	.885	0.4	.773
STN1	−0.2	.783	−1.5	.002	0.4	.692
STOM	0.1	.846	0.2	.787	−0.1	.94
STT3A	1.2	.001	1.3	.006	1.3	.058
STX7	−0.4	.115	−0.6	.09	−0.3	.725
STXBP3	0.4	.132	0.1	.822	0.4	.416
SUCLA2	−0.2	.477	−0.7	.014	−0.3	.719
SUCLG1	−0.9	.128	−1.3	.073	−0.7	.606
SUCLG2	−0.2	.687	−0.5	.196	−0.1	.916
SULF1	0.4	.179	0.7	.073	0.4	.589
SUMF2	−0.9	.02	−0.7	.156	−0.3	.773
SUN2	−0.1	.892	0.6	.143	0.7	.329
SUSD2	−0.2	.786	0.3	.621	0.4	.702
SUSD5	−1.8	<.001	−1.1	.02	−1.1	.118
SVIL	−0.5	.118	−0.3	.436	−0.5	.444
SYG	0.8	.03	0.6	.271	0.5	.582
SYHC	−0.2	.746	−0.4	.393	−0.1	.936
SYNCRIP	−0.7	.04	−1	.02	−0.9	.182
SYNE1	−0.4	.229	−0.3	.6	0.2	.883
SYNM	−1.4	<.001	−1.3	<.001	−1.3	.008
SYNPO	−0.5	.101	−0.2	.626	−0.4	.649
SYNPO2	−1.3	<.001	−0.9	.013	−0.8	.147
SYPL1	0.4	.45	0.5	.456	0.9	.318
TAGLN	−2.1	<.001	−1.6	.002	−0.9	.29
TAGLN2	−0.6	.029	−0.7	.056	−0.3	.729
TALDO1	0.3	.103	−0.1	.946	0.1	.771
TARDBP	−0.4	.221	−0.8	.014	−0.3	.703
TARS1	0.6	.097	0.3	.556	0.2	.825
TARS2	−1.2	.029	−1.4	.057	−0.6	.719
TASOR2	−0.6	.099	−0.1	.969	−0.2	.889
TAX1BP3	−1.3	.008	−1.4	.028	−0.6	.631
TBC1D5	−1.3	.003	−0.3	.662	−0.2	.914
TBCA	−1.3	<.001	−1.4	<.001	−0.8	.116
TBCB	−1	<.001	−1.2	.001	−0.5	.369
TCP1	0.2	.594	−0.2	.731	0.3	.677
TENT2	−3.2	<.001	−3.5	<.001	−3.3	<.001
TES	−1.4	<.001	−0.9	.01	−0.8	.104
TF	−0.6	.048	−1.3	.001	−0.4	.589
TFEB	−1.2	.152	−1.3	.189	−0.3	.889
TFG	−0.3	.452	−0.6	.194	−0.3	.729
TGFB1	0.3	.575	0.9	.056	0.2	.907
TGFB1I1	−1.7	<.001	−1.1	.007	−0.8	.2
TGFBI	0.5	.133	0.4	.335	0.7	.252

Supplementary Table II. Continued.

Gene	Log$_2$FC TAA/ normal	Adjusted *P* value[a]	Log$_2$FC TBAD/ normal	Adjusted *P* value[a]	Log$_2$FC TADA/ normal	Adjusted *P* value[a]
TGM2	−0.1	.825	0.3	.606	0.7	.264
TH	−1.5	.001	−0.6	.312	−0.4	.767
THBS1	2.7	<.001	1.6	.002	1.5	.047
THBS2	1.4	.002	1.1	.052	1	.262
THOP1	−0.1	.879	−0.7	.166	0.4	.663
THSD1	−1.9	<.001	−1.1	.001	−1.3	.007
THSD4	−1.3	<.001	−0.6	.029	−1.1	.008
THTPA	0.4	.666	−0.3	.803	−1.3	.364
THY1	1.3	.001	0.4	.513	0.8	.333
TIMP1	0.8	.065	−0.1	.995	0.1	.994
TIMP2	−0.5	.241	−0.7	.171	−0.2	.914
TIMP3	0.7	.139	−0.2	.87	−0.3	.789
TINAGL1	−2.4	<.001	−1.5	.002	−1.3	.048
TJP2	−0.2	.718	−0.1	.887	−0.4	.679
TKT	−0.1	.673	−0.3	.078	0.2	.667
TLE7	−0.6	.006	−0.8	.003	−0.4	.526
TLN1	−0.6	.005	−0.3	.311	−0.5	.317
TLN2	−0.8	.01	−0.3	.499	−0.5	.513
TMC3	0.8	.312	0.2	.848	0.6	.732
TMCC2	0.3	.659	−1.1	.052	−0.4	.721
TMED7	0.4	.289	0.3	.443	0.7	.275
TMEM109	−0.3	.413	−0.4	.246	0.2	.767
TMEM198	0.6	.141	−0.2	.799	0.9	.283
TMEM214	−0.6	.157	−0.1	.9	0.2	.893
TMEM33	1	.154	1.9	.019	1.5	.267
TMEM43	−0.2	.58	−0.3	.605	0.1	.994
TMEM67	−0.3	.621	0.1	.966	1	.366
TMOD1	−1	.001	−1	.008	−0.3	.677
TMSB4X	−1.2	.001	−1.5	.001	−1.2	.075
TNC	1	.022	0.5	.395	1.2	.202
TNFRSF11B	−0.5	.155	−0.9	.033	−0.5	.474
TNFSF13	−1	.008	−0.6	.208	−0.6	.521
TNN	0.1	.817	−1	.029	0.3	.792
TNPO1	0.2	.556	0.1	.847	0.3	.677
TNPO2	0.5	.464	−0.6	.408	0.1	.989
TNRC6C	0.5	.286	−1.1	.027	0.8	.362
TNS1	−1.4	<.001	−0.6	.179	−0.6	.379
TNS2	−0.1	.812	0.2	.65	−0.1	.986
TNXB	−1.1	<.001	−1.2	.001	−0.4	.541
TOLLIP	−1.8	<.001	−1.3	.006	−1.7	.013
TOM1	0.1	.837	−0.2	.769	0.3	.675
TOM1L2	−0.7	.028	−0.7	.089	−1.1	.046
TOR1AIP1	0.5	.076	1	.003	0.7	.163
TPD52L2	−0.5	.129	−1	.013	−0.5	.472
TPI1	−0.3	.34	−0.4	.249	0.2	.756
TPM1	−2.4	<.001	−2.2	<.001	−1.5	.028

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Supplementary Table II. Continued.

Gene	Log_2FC TAA/ normal	Adjusted *P* value[a]	Log_2FC TBAD/ normal	Adjusted *P* value[a]	Log_2FC TADA/ normal	Adjusted *P* value[a]
TPM2	−3.1	<.001	−2.6	<.001	−1.9	.028
TPM3	0.9	<.001	0.3	.303	0.5	.242
TPM4	−0.3	.22	−0.4	.1	−0.2	.713
TPP1	0.2	.684	−0.6	.151	−0.5	.488
TPP2	−0.1	.875	−0.3	.68	0.6	.521
TPT1	−1.4	.001	−1.6	.005	−1.2	.198
TRIM38	−2.1	.001	−1.3	.078	−0.5	.762
TRIOBP	−0.3	.484	0.3	.426	−0.2	.813
TRIP6	−1	.002	−0.8	.07	−1.1	.085
TSG101	−0.4	.266	−0.8	.059	−0.4	.668
TSN	0.1	.89	−0.2	.677	0.1	.967
TTN	0.1	.999	−0.5	.127	0.1	.976
TTR	−0.6	.013	−1.3	<.001	−0.6	.203
TTYH2	−0.7	.007	−0.2	.632	−0.1	.916
TUBA4A	−0.3	.139	−0.4	.127	−0.4	.321
TUBB	−0.3	.511	−0.8	.049	−0.3	.748
TUBB1	−0.2	.83	0.5	.65	−0.2	.947
TUBB2A	−0.5	.144	−0.9	.017	−0.5	.452
TUBB4A	−0.1	.989	−0.2	.888	−0.5	.756
TUBB4B	−0.5	.177	−1.1	.007	−0.3	.773
TUBB6	−0.7	.021	−1	.009	−0.6	.344
TUFM	0.3	.278	0.1	.833	0.2	.714
TUT7	−0.9	.029	−0.7	.234	−0.3	.775
TWF1	−0.4	.176	−0.7	.056	−0.1	.951
TWF2	−0.4	.431	−0.4	.524	−0.6	.532
TXN	−0.5	.065	−0.7	.055	−0.3	.725
TXNDC12	−0.7	.155	−0.8	.16	−1.7	.048
TXNDC17	−0.8	.001	−1.2	<.001	−0.5	.29
TXNDC5	−0.2	.66	−0.8	.016	−0.4	.538
TXNL1	−0.5	.008	−0.8	.001	−0.3	.45
TXNRD1	−0.1	.873	−0.3	.396	0.4	.637
TYMP	1	.002	0.3	.505	0.5	.511
TYRP1	−0.3	.509	−0.5	.363	0.2	.88
U2AF2	−0.3	.411	−0.6	.155	−0.8	.275
UAP1	−0.7	.059	−0.3	.695	−0.2	.907
UBA1	−0.2	.307	−0.3	.255	−0.1	.998
UBAP2L	−0.4	.192	−0.5	.101	−0.6	.305
UBE2I	0.2	.717	0.6	.208	0.6	.39
UBE2K	−0.6	.046	−1.3	.001	−0.9	.114
UBE2L3	−0.4	.192	−0.4	.251	−0.4	.546
UBE2M	−0.8	.063	−0.9	.079	−0.7	.482
UBE2N	−1.2	.001	−1	.03	−0.8	.29
UBE2O	−1.3	.001	−0.4	.456	0.2	.894
UBE2V1	0.7	.023	0.5	.202	0.6	.329
UBL5	−0.4	.2	−0.5	.184	0.3	.725
UBR4	−1.2	.051	−0.1	.973	−0.4	.826

Supplementary Table II. Continued.

Gene	Log2FC TAA/ normal	Adjusted *P* value[a]	Log2FC TBAD/ normal	Adjusted *P* value[a]	Log2FC TADA/ normal	Adjusted *P* value[a]
UCHL1	−1	.001	−1.3	.002	−0.7	.329
UFC1	−0.6	.007	−0.8	.004	−0.3	.614
UFL1	0.2	.757	−0.3	.63	0.2	.88
UFM1	−0.3	.338	−1.1	.002	−0.3	.751
UGDH	−0.3	.451	−0.3	.625	−0.1	.964
UGGT1	0.5	.171	0.5	.241	0.1	.923
UGP2	−0.7	<.001	−0.6	.006	−0.4	.276
UNC45A	0.3	.569	−0.1	.884	0.4	.677
UQCR10	1.6	<.001	1.3	.002	1.1	.058
UQCRC1	−0.6	.113	−0.8	.072	−0.9	.229
UQCRC2	−0.9	.006	−0.8	.039	−1.1	.068
UQCRH	−0.4	.34	−0.6	.209	−0.3	.767
USO1	−0.2	.697	−0.7	.092	0.4	.667
USP14	0.2	.624	−0.3	.524	0.3	.765
USP15	−0.8	.064	−0.2	.728	0.3	.835
USP17L13	−0.2	.585	−0.6	.045	−0.2	.777
USP17L18	−0.1	.795	−0.2	.716	0.1	.894
USP17L19	−1.2	.003	−1.1	.033	−0.3	.781
USP17L20	−0.2	.569	−0.7	.049	−0.4	.52
USP17L22	−0.4	.175	−0.7	.069	−0.5	.475
USP5	−0.1	.898	−0.2	.7	−0.1	.959
UTP14A	−1.9	<.001	−2.1	.001	−1.3	.188
UTRO	0.5	.079	0.5	.154	0.8	.149
VAPA	−0.7	.138	−0.8	.165	−0.8	.44
VASP	−0.7	.001	−0.4	.142	−0.7	.075
VAT1	−0.3	.32	−0.6	.054	−0.3	.711
VCAN	−1.9	<.001	−1	.034	−1.3	.085
VCL	−1	<.001	−0.6	.053	−0.5	.364
VCP	−0.1	.881	−0.3	.296	−0.2	.719
VDAC1	−0.1	.873	−0.4	.104	−0.4	.36
VDAC2	−0.3	.283	−0.9	.012	−0.6	.345
VDAC3	0.5	.372	0.6	.335	0.3	.799
VILL	0.1	.819	−1.1	.011	0.4	.676
VIM	−1.6	<.001	−1.5	<.001	−1.2	.012
VIRMA	−0.4	.309	0.3	.564	0.6	.407
VPS11	−0.1	.774	−0.1	.973	0.1	.978
VPS29	−0.7	.028	−0.7	.071	−0.7	.333
VPS35	0.2	.684	−0.1	.851	0.5	.468
VPS4B	−0.6	.22	−0.6	.279	−0.6	.536
VTN	−0.6	.063	−0.9	.024	−0.6	.321
VWA1	−1.5	<.001	−1.7	<.001	−1.3	.034
VWA3A	0.2	.734	0.5	.233	0.2	.829
VWA3B	−0.1	.953	−0.9	.131	0.2	.899
WASHC1	−0.5	.624	−0.3	.847	−0.7	.773
WASHC4	−2.5	<.001	−0.6	.465	−0.4	.829
WBP11	−0.8	.113	0.6	.424	0.4	.792

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Supplementary Table II. Continued.

Gene	Log_2FC TAA/ normal	Adjusted *P* value[a]	Log_2FC TBAD/ normal	Adjusted *P* value[a]	Log_2FC TADA/ normal	Adjusted *P* value[a]
WDR1	−0.5	.005	−0.3	.166	−0.1	.865
WDR76	−0.3	.29	−0.9	.006	−0.2	.86
WDR82	−0.4	.504	−0.1	.928	0.1	.968
WDR83OS	−2.1	<.001	−1	.074	−1.1	.222
WISP2	−1	.003	−0.5	.254	0.2	.879
WRAP73	−0.8	.132	−0.8	.191	0.5	.714
WTIP	−0.8	.14	−0.7	.295	−0.1	.941
XDH	−3.2	<.001	−2.6	<.001	−2.7	<.001
XPO1	0.5	.127	0.6	.12	0.7	.329
XRCC5	0.8	.011	0.7	.103	0.9	.137
XRCC6	0.2	.612	0.2	.677	0.6	.32
XRN1	−1.4	.004	−1.3	.044	−0.4	.773
YAP1	−0.8	.002	−1	.004	−0.6	.283
YKT6	−0.4	.301	−0.4	.396	0.2	.889
YPEL1	0.2	.806	0.2	.839	1.2	.271
YWHAB	−0.3	.164	−0.3	.167	−0.1	.913
YWHAE	−0.3	.279	−0.6	.038	−0.2	.703
YWHAG	−0.6	.002	−0.7	.003	−0.3	.59
YWHAH	−0.4	.097	−0.6	.02	−0.3	.582
YWHAQ	−0.3	.301	−0.3	.424	0.1	.903
YWHAZ	−0.3	.225	−0.4	.135	−0.2	.681
ZBTB21	−0.9	.015	−0.1	.942	−0.1	.956
ZC2HC1C	−0.7	.103	0.5	.441	0.1	.955
ZMYND8	−1.5	<.001	−0.9	.067	−1	.152
ZNF350	1.1	.062	−0.6	.456	−0.5	.746
ZNF385A	0.5	.44	1.7	.014	1.7	.115
ZNF479	0.1	.871	0.2	.63	0.4	.438
ZNF507	−0.6	.091	−1.1	.014	−0.3	.773
ZNF597	−0.5	.232	−0.5	.398	0.3	.773
ZSCAN9	−0.8	.432	−0.4	.753	−0.2	.944
ZSWIM9	0.1	.864	−0.7	.048	0.4	.656
ZYX	−1	.001	−0.8	.013	−0.8	.132

Log_2FC, Log_2 fold change; *TAA,* thoracic aorta aneurysm; *TADA,* thoracic aorta dissection and aneurysm; *TBAD,* type B dissecting aorta.
[a]False discovery rate.

Supplementary Table III. Complete differential expression analysis between aortic pathologies

Gene	Log_2FC TAA/ TADA	Adjusted *P* value	Log_2FC TBAD/ TADA	Adjusted *P* value	Log_2FC TAA/ TBAD	Adjusted *P* value
A1BG	−0.1	.984	−0.8	.324	0.7	.068
A2M	−0.3	.966	−1.1	.363	0.8	.191
AAMDC	−0.8	.857	−0.6	.708	−0.2	.825
AARS1	0.1	.982	−0.2	.899	0.3	.684
ABCA13	−1	.862	−0.5	.822	−0.5	.591
ABCCB	−0.8	.9	−0.7	.821	−0.2	.943
ABCD1	−0.6	.929	−1	.685	0.5	.729
ABCF1	−0.3	.982	−1.7	.235	1.5	.066
ABHD14B	−0.4	.941	−0.9	.515	0.5	.441
ABI3BP	−0.5	.9	−0.2	.936	−0.4	.659
ACAA1	0.6	.9	0.1	.994	0.6	.506
ACAA2	0.5	.941	−0.1	.973	0.5	.561
ACADM	0.5	.9	0.2	.933	0.4	.676
ACADVL	0.4	.903	−0.5	.782	0.8	.108
ACAN	−0.6	.903	0.5	.822	−1	.195
ACAT1	−0.2	.972	−0.6	.713	0.4	.59
ACAT2	−0.1	.982	−0.6	.713	0.6	.407
ACLY	0.4	.941	0.2	.933	0.2	.865
ACO1	−0.3	.941	−0.4	.815	0.1	.924
ACO2	0.3	.966	−0.3	.853	0.5	.409
ACOT9	−0.4	.941	−0.5	.797	0.2	.899
ACP1	−0.3	.946	−1	.323	0.7	.179
ACSF2	−1.3	.857	−0.9	.759	−0.5	.732
ACSL1	0.6	.927	0.5	.844	0.1	.961
ACTA1	−0.6	.9	−0.5	.762	−0.1	.975
ACTBL2	−0.8	.857	−0.2	.942	−0.7	.176
ACTN1	−0.6	.862	−0.1	.942	−0.5	.307
ACTN2	−0.5	.9	−0.5	.677	0.1	.962
ACTN3	0.4	.969	−0.3	.933	0.7	.593
ACTN4	−0.7	.857	−0.5	.792	−0.3	.693
ACTR10	−0.4	.9	−0.4	.792	0.1	1.00
ACTR1A	−0.1	.982	−0.6	.652	0.6	.337
ACTR2	−0.1	.982	0.2	.891	−0.2	.634
ACTR3	−0.1	.982	−0.1	.997	−0.1	.922
ACYP2	−0.2	.982	−0.4	.891	0.2	.894
ADAM17	−0.8	.862	−0.6	.762	−0.2	.844
ADAMTS2	0.5	.957	−1.4	.553	1.9	.066
ADAMTSL1	−0.6	.9	0.4	.847	−1	.133
ADAMTSL2	−0.9	.903	0.3	.942	−1.2	.383
ADAMTSL4	−0.6	.9	−0.1	.985	−0.5	.526
ADARB1	−0.8	.862	−1.1	.328	0.3	.733
ADD1	0.5	.927	−0.3	.908	0.8	.35
ADD3	0.1	.982	−0.1	.973	0.2	.846
ADGRF1	1.1	.857	−0.6	.792	1.6	.023
ADH1B	−0.7	.903	−0.6	.822	−0.2	.945
ADH5	−0.4	.9	−0.6	.693	0.2	.84

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Supplementary Table III. Continued.

Gene	Log_2FC TAA/ TADA	Adjusted *P* value	Log_2FC TBAD/ TADA	Adjusted *P* value	Log_2FC TAA/ TBAD	Adjusted *P* value
ADIPOQ	−1.2	.857	−1	.574	−0.3	.819
ADIRF	−0.7	.9	−0.5	.847	−0.3	.855
ADSL	0.3	.927	0.1	.98	0.3	.688
ADSS1	−1.1	.857	0.1	.989	−1.1	.124
AEBP1	−0.1	.982	−0.2	.951	0.1	.966
AFM	−0.2	.972	−1.2	.225	1	.065
AGL	−0.4	.934	−0.5	.815	0.1	.962
AGRN	−0.3	.969	−0.4	.82	0.2	.862
AGT	−0.2	.972	−1	.324	0.8	.133
AHCY	0.1	.982	−0.4	.792	0.5	.413
AHCYL1	0.1	.993	−0.4	.796	0.4	.512
AHNAK	0.1	.982	0.2	.934	−0.1	.943
AHSG	0.1	.982	−1.1	.225	1.1	.023
AIFM1	0.4	.9	−0.1	.985	0.4	.429
AIMP2	−0.1	.982	−0.2	.933	0.1	.943
AIP	−0.4	.927	−0.2	.917	−0.2	.84
AK1	−0.1	.982	−0.2	.917	0.1	.943
AK2	0.3	.969	−0.7	.762	0.9	.203
AK3	0.5	.9	0.2	.942	0.4	.613
AK4	−0.5	.903	0.1	.993	−0.5	.529
AK7	0.9	.9	−0.3	.917	1.2	.179
AKAP12	−0.1	.982	−0.5	.792	0.5	.557
AKR1A1	−0.3	.941	−0.9	.391	0.6	.29
AKR1B1	0.1	.982	−0.6	.468	0.7	.094
AKR7A2	0.5	.903	−0.3	.861	0.7	.264
AKR7A3	0.3	.982	−0.3	.953	0.5	.785
ALAD	0.1	.982	−0.6	.762	0.7	.334
ALB	−0.2	.982	−1.2	.286	1.1	.071
ALCAM	−0.6	.9	−0.1	.993	−0.5	.459
ALDH1A1	−0.3	.903	−0.5	.642	0.2	.75
ALDH1B1	−0.6	.9	−0.3	.899	−0.3	.688
ALDH1L1	−0.3	.966	−0.4	.822	0.2	.902
ALDH2	−0.3	.947	−0.6	.762	0.3	.757
ALDH6A1	−0.5	.903	−0.6	.789	0.2	.927
ALDH7A1	−0.4	.9	−0.6	.674	0.2	.811
ALDH9A1	−0.3	.941	−0.7	.615	0.4	.561
ALDOA	−0.2	.941	−0.2	.826	0.1	.988
ALDOC	−0.5	.862	−0.3	.815	−0.2	.688
ALMS1	0.2	.982	−0.4	.819	0.6	.403
ALOX15B	−0.1	.982	−0.3	.899	0.2	.862
AMBP	−0.2	.982	−0.6	.742	0.5	.544
AMIGO2	0.1	.993	−0.5	.826	0.5	.652
AMN	−0.3	.982	−0.3	.933	0.1	.982
AMPD2	0.2	.982	0.3	.897	−0.2	.902
ANG	−0.4	.941	−0.4	.847	−0.1	.998
ANGPTL2	−0.3	.969	−0.2	.946	−0.2	.916

Supplementary Table III. Continued.

Gene	Log$_2$FC TAA/ TADA	Adjusted *P* value	Log$_2$FC TBAD/ TADA	Adjusted *P* value	Log$_2$FC TAA/ TBAD	Adjusted *P* value
ANK1	0.9	.857	0.1	.988	0.9	.178
ANKRD31	−1.3	.862	−1	.782	−0.4	.84
ANKS3	−1.2	.9	−0.6	.891	−0.7	.714
ANP32B	−0.6	.927	−0.8	.785	0.3	.889
ANTXR1	0.1	.982	0.8	.657	−0.7	.363
ANXA1	−0.2	.947	0.1	.985	−0.3	.663
ANXA11	−0.2	.957	0.2	.861	−0.4	.399
ANXA2	−0.2	.982	−0.2	.891	0.1	.945
ANXA3	−0.5	.912	−0.2	.938	−0.3	.757
ANXA4	−0.3	.941	−0.1	1.00	−0.3	.691
ANXA5	−0.3	.957	−0.3	.834	0.1	.962
ANXA6	−0.3	.941	−0.1	.997	−0.3	.705
ANXA7	0.1	.982	0.2	.897	−0.1	.873
AOC3	−1.2	.857	−0.1	.993	−1.1	.122
AP1B1	0.6	.862	0.1	.942	0.5	.383
AP2A1	−0.2	.972	−0.3	.895	0.1	.97
AP2A2	0.2	.982	−0.2	.956	0.4	.774
AP2B1	0.2	.982	−0.3	.865	0.4	.529
AP2M1	−0.2	.982	−0.4	.843	0.2	.829
AP3B1	0.2	.972	−0.3	.847	0.5	.429
AP3B2	−0.9	.9	−0.5	.853	−0.4	.753
AP3S1	−0.3	.969	−0.2	.935	−0.2	.932
APCS	−0.7	.9	−0.9	.614	0.3	.85
APEH	0.5	.903	−0.2	.953	0.6	.435
APEX1	−0.5	.9	−0.1	.973	−0.5	.552
APMAP	0.2	.972	0.1	.956	0.1	.913
APOA1	−0.1	.982	−1.1	.286	1	.061
APOA2	0.1	.982	−1	.288	1.1	.035
APOA4	0.1	.982	−0.4	.802	0.5	.394
APOB	0.2	.982	−1.6	.225	1.7	.022
APOC1	0.2	.982	−0.7	.769	0.8	.301
APOC2	−0.2	.982	−1.7	.225	1.6	.043
APOC3	−0.2	.982	−1.8	.225	1.6	.023
APOD	0.3	.969	−1.1	.327	1.3	.025
APOE	−0.1	.984	−1	.432	1	.116
APOF	0.2	.982	−0.3	.847	0.5	.503
APOH	−0.2	.969	−0.4	.792	0.2	.769
APOL1	−0.1	.992	−1.5	.258	1.5	.037
APOM	0.3	.947	−0.7	.592	1	.071
APP	−0.1	.997	0.2	.936	−0.2	.87
APPL1	0.2	.981	0.1	.942	0.1	.966
APRT	0.1	.982	−0.8	.433	0.9	.068
AQP1	−0.5	.9	−0.6	.718	0.2	.912
ARCN1	0.4	.903	0.1	.989	0.4	.572
ARF4	0.1	.982	−0.4	.815	0.5	.521
ARF5	−0.2	.975	0.5	.792	−0.7	.306

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Supplementary Table III. Continued.

Gene	Log_2FC TAA/ TADA	Adjusted *P* value	Log_2FC TBAD/ TADA	Adjusted *P* value	Log_2FC TAA/ TBAD	Adjusted *P* value
ARFIP1	−0.3	.941	−0.4	.792	0.2	.894
ARG1	−0.3	.974	0.6	.792	−0.8	.308
ARHGAP1	−0.4	.9	−0.5	.648	0.1	.899
ARHGAP11A	−0.2	.982	−0.6	.826	0.5	.768
ARHGAP31	−1.3	.862	−1.4	.583	0.2	.933
ARHGAP40	−0.3	.965	−0.5	.792	0.3	.825
ARHGAP9	−1.3	.9	−1.3	.732	−0.1	.989
ARHGDIA	−0.4	.9	−0.5	.583	0.2	.862
ARHGDIB	0.4	.9	0.3	.826	0.2	.811
ARHGEF37	−1.3	.862	−0.6	.826	−0.7	.613
ARL6IP5	−0.2	.981	0.2	.917	−0.3	.613
ARL8B	−0.8	.927	−0.2	.976	−0.6	.691
ARMC5	0.6	.972	0.2	.973	0.4	.868
ARNTL2	−0.1	.984	−0.7	.821	0.6	.657
ARPC1A	−0.4	.903	−0.4	.821	−0.1	.964
ARPC1B	0.1	.982	0.1	.951	0.1	1.00
ARPC2	−0.1	.988	−0.1	.995	−0.1	.991
ARPC3	0.1	.982	−0.1	.98	0.2	.855
ARPC4	−0.1	.982	−0.3	.792	0.3	.526
ARPC5	0.1	1.00	−0.8	.555	0.8	.182
ARPC5L	−0.5	.927	−0.9	.668	0.4	.704
ASAH1	0.2	.982	−0.6	.616	0.7	.134
ASNA	−0.1	.982	−0.6	.674	0.5	.391
ASPH	0.3	.982	0.1	.99	0.2	.889
ASPN	0.2	.982	−1.3	.451	1.4	.072
ASS1	−0.6	.9	−0.5	.792	−0.1	.951
ATAD2B	−0.6	.941	−0.9	.759	0.4	.795
ATIC	−0.2	.974	−0.4	.792	0.3	.741
ATL3	−0.4	.927	0.1	.956	−0.5	.506
ATOX1	−0.2	.982	−0.6	.718	0.5	.483
ATP1A1	−0.2	.982	0.1	.993	−0.2	.889
ATP2A2	−0.3	.976	0.3	.899	−0.6	.561
ATP2B4	−0.1	.984	0.3	.906	−0.4	.761
ATP5F1A	0.1	.982	−0.2	.897	0.2	.647
ATP5F1B	0.2	.982	−0.5	.77	0.6	.286
ATP5F1C	0.2	.982	−0.5	.721	0.6	.198
ATP5F1D	0.1	.982	−0.4	.808	0.4	.438
ATP5ME	−0.7	.862	−0.6	.789	−0.2	.858
ATP5MF	0.2	.982	0.2	.973	0.1	.968
ATP5MG	−0.4	.957	−0.6	.808	0.2	.863
ATP5PB	−0.3	.969	−0.7	.674	0.5	.556
ATP5PD	−0.1	.982	−0.3	.826	0.2	.797
ATP5PF	−0.1	.982	−0.7	.679	0.6	.383
ATP5PO	0.2	.974	−0.4	.785	0.6	.261
ATP6V1A	0.2	.982	−0.6	.707	0.7	.191
ATP6V1B2	0.2	.982	−0.5	.782	0.7	.286

Supplementary Table III. Continued.

Gene	Log$_2$FC TAA/ TADA	Adjusted *P* value	Log$_2$FC TBAD/ TADA	Adjusted *P* value	Log$_2$FC TAA/ TBAD	Adjusted *P* value
ATP6V1E1	0.3	.941	−0.5	.746	0.8	.128
ATP6V1H	0.3	.927	−0.2	.917	0.5	.401
ATP8A1	0.1	.984	−0.6	.897	0.6	.729
ATR	−1	.857	−0.4	.821	−0.6	.388
AXIN1	−1.2	.903	−1.3	.792	0.2	.968
AZGP1	−0.2	.974	−1.1	.324	0.9	.129
B2M	0.2	.982	−0.7	.491	0.8	.069
BAG2	−0.6	.9	0.2	.939	−0.8	.301
BANF1	−0.6	.903	−1	.533	0.5	.581
BASP1	−0.1	.982	0.1	.951	−0.2	.757
BBS9	−0.3	.966	−0.1	.989	−0.2	.8
BCAM	−0.8	.862	−0.2	.953	−0.7	.306
BCAP31	−0.4	.966	−0.8	.785	0.4	.757
BCL10	−0.2	.982	0.5	.819	−0.6	.409
BDH2	−0.4	.969	−0.4	.899	0.1	.998
BGN	−0.5	.927	−0.5	.826	−0.1	.995
BLM	−0.3	.982	−0.9	.802	0.6	.72
BLMH	0.7	.9	0.1	.989	0.7	.529
BLVRA	0.1	.982	−0.2	.933	0.3	.703
BLVRB	0.2	.982	−0.7	.508	0.9	.071
BNC2	−0.4	.946	−0.4	.826	0.1	.968
BPGM	0.5	.92	−0.6	.808	1.1	.172
BPNT1	0.1	.982	−0.3	.928	0.3	.795
BRK1	−0.1	.982	−0.3	.922	0.2	.894
BSG	−1.2	.864	−0.1	.985	−1.1	.353
C11orf54	−0.2	.982	−0.4	.826	0.2	.825
C11orf96	−1.1	.862	−0.4	.88	−0.8	.444
C1orf198	−0.1	.982	−0.3	.861	0.3	.8
C1QA	−0.9	.9	−0.2	.951	−0.7	.491
C1QB	−0.3	.972	0.1	.973	−0.4	.715
C1QC	−0.5	.941	−0.3	.907	−0.2	.918
C1R	0.1	.99	−0.1	.952	0.2	.893
C1S	−0.1	.982	−0.4	.77	0.3	.576
C2	−0.9	.862	−1	.538	0.2	.911
C22orf23	−0.7	.9	−0.4	.906	−0.4	.729
C2orf78	0.2	.982	1.2	.524	−1.1	.247
C3	−0.2	.972	−0.8	.401	0.7	.198
C4A	−0.4	.903	−0.7	.674	0.3	.757
C4B	−0.1	.99	−0.5	.808	0.4	.567
C4BPA	−0.1	.988	−0.8	.524	0.8	.179
C4BPB	0.2	.982	−1.2	.431	1.3	.061
C5	−0.2	.979	−0.6	.679	0.4	.506
C6	−0.3	.927	−0.3	.848	−0.1	.962
C7	−0.3	.969	−0.1	.966	−0.2	.863
C8A	−0.5	.862	−0.3	.814	−0.2	.757
C8B	−0.4	.903	−0.5	.759	0.2	.883

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Supplementary Table III. Continued.

Gene	Log_2FC TAA/ TADA	Adjusted *P* value	Log_2FC TBAD/ TADA	Adjusted *P* value	Log_2FC TAA/ TBAD	Adjusted *P* value
C8G	−0.4	.941	−0.8	.592	0.5	.558
C8orf74	−0.1	.993	0.9	.753	−0.9	.372
C9	−0.3	.942	−0.2	.934	−0.2	.863
CA1	0.6	.9	−0.9	.497	1.5	.022
CA123	0.2	.982	1.3	.639	−1.1	.36
CA2	0.6	.9	−0.6	.742	1.2	.04
CA3	0.3	.982	−0.4	.891	0.6	.537
CAB39	0.2	.982	0.1	.997	0.2	.912
CACNA2D1	−0.5	.903	−0.2	.942	−0.4	.703
CACYBP	0.1	.982	0.1	.973	0.1	.998
CALD1	−0.5	.903	−0.3	.891	−0.2	.84
CALR	−0.1	.982	−0.1	.934	0.1	.97
CALU	0.3	.903	0.1	.973	0.3	.638
CAMK2G	−0.4	.929	0.6	.726	−1	.103
CAND1	−0.4	.903	−0.4	.822	−0.1	.962
CANX	0.1	.992	0.2	.928	−0.1	.863
CAP1	0.1	.982	−0.2	.906	0.2	.753
CAP2	−0.5	.9	−0.2	.917	−0.3	.719
CAPG	0.5	.9	−0.3	.865	0.7	.195
CAPN1	−0.1	.984	−0.2	.894	0.2	.811
CAPN2	−0.5	.862	−0.4	.792	−0.2	.762
CAPNS1	−0.2	.974	−0.3	.816	0.2	.812
CAPZA1	0.5	.9	−0.1	.973	0.6	.286
CAPZA2	−0.1	.982	−0.5	.682	0.4	.441
CAPZB	−0.1	.982	0.1	.951	−0.2	.742
CARD10	1	.878	0.2	.973	0.9	.399
CASKIN2	−0.3	.966	−0.4	.847	0.1	.957
CASP8	−0.6	.9	−0.1	.954	−0.5	.506
CAST	0.3	.934	−0.3	.839	0.6	.287
CAT	0.4	.903	−0.2	.906	0.6	.315
CATSPERG	−1.1	.862	−0.9	.773	−0.3	.863
CAV1	−0.8	.9	−0.1	.993	−0.7	.413
CAV2	−0.7	.878	−0.2	.917	−0.5	.523
CAVIN1	−0.8	.862	−0.6	.785	−0.3	.827
CAVIN2	0.7	.862	0.4	.826	0.4	.633
CAVIN3	−0.9	.862	−0.3	.886	−0.6	.457
CBLN2	−0.5	.9	−0.7	.604	0.3	.758
CBR1	−0.4	.927	−0.6	.65	0.3	.684
CBR3	−0.3	.982	−0.1	.989	−0.3	.873
CCAR1	−0.4	.957	−1.8	.225	1.5	.07
CCDC158	−0.8	.9	−0.5	.826	−0.3	.843
CCDC194	−0.9	.9	0.1	.981	−0.9	.296
CCDC25	2.9	.862	1.4	.821	1.6	.544
CCDC6	−0.9	.857	−0.6	.721	−0.4	.633
CCDC69	−0.5	.957	0.2	.973	−0.6	.669
CCDC80	0.2	.982	−0.1	.985	0.3	.797

Supplementary Table III. Continued.

Gene	Log_2FC TAA/ TADA	Adjusted *P* value	Log_2FC TBAD/ TADA	Adjusted *P* value	Log_2FC TAA/ TBAD	Adjusted *P* value
CCN3	−0.5	.903	−0.5	.826	−0.1	.962
CCS	0.6	.903	−0.1	.99	0.6	.504
CCT2	0.1	.982	−0.2	.836	0.3	.493
CCT3	−0.1	.982	−0.4	.792	0.3	.664
CCT4	0.1	.982	0.1	.962	−0.1	.979
CCT5	0.2	.982	−0.2	.937	0.3	.688
CCT6A	0.1	.992	0.1	.928	−0.1	.862
CCT7	0.1	.982	−0.2	.933	0.2	.715
CCT8	0.1	.982	−0.2	.911	0.3	.685
CD109	−0.5	.9	−0.6	.792	0.1	.979
CD14	0.2	.982	−0.2	.951	0.4	.761
CD151	−0.5	.929	0.1	.993	−0.5	.613
CD163	0.3	.958	0.1	.953	0.2	.862
CD34	−0.7	.862	−0.6	.762	−0.2	.87
CD44	−0.3	.927	−0.1	.992	−0.2	.666
CD47	−0.2	.982	−0.1	.951	−0.1	.968
CD59	−0.5	.903	−0.2	.934	−0.3	.722
CD5L	−0.1	.982	−1.1	.327	1	.078
CD81	−0.4	.942	−0.4	.847	0.1	.998
CD9	−0.5	.927	−0.3	.899	−0.2	.879
CD97	0.1	.992	−0.3	.907	0.3	.793
CD99	−0.1	.982	−1	.519	0.9	.191
CDC25C	0.4	.966	−0.6	.826	0.9	.363
CDC37	−0.2	.965	0.2	.932	−0.4	.539
CDC42	−0.1	.982	−0.1	.99	−0.1	.945
CDC5L	−0.4	.927	−1.5	.225	1.1	.065
CDH1	−0.3	.982	−0.1	.993	−0.3	.863
CDH13	−1.2	.857	−0.6	.792	−0.7	.383
CDHR3	−0.2	.982	−1.1	.592	0.9	.343
CDK5RAP3	0.3	.974	0.1	.985	0.2	.87
CDKN2AIP	−0.5	.972	−1.1	.757	0.7	.657
CELSR3	−0.2	.982	1	.792	−1.1	.391
CENPE	−1.2	.862	−0.6	.826	−0.7	.585
CES1	−0.9	.857	0.1	.994	−0.9	.164
CFB	−0.6	.9	−0.9	.457	0.4	.654
CFD	−0.3	.947	−0.9	.457	0.7	.328
CFH	−0.3	.927	−0.8	.327	0.6	.254
CFHR1	−0.8	.9	−0.9	.668	0.2	.925
CFHR2	−0.5	.9	−0.7	.616	0.2	.798
CFHR5	−0.8	.878	−0.9	.59	0.2	.913
CFI	−0.4	.903	−1.3	.225	0.9	.106
CFL1	−0.1	.982	−0.2	.826	0.2	.815
CFL2	−1	.857	−0.7	.753	−0.4	.705
CFP	−0.4	.941	0.1	.976	−0.4	.581
CHCHD3	−0.5	.927	0.1	.98	−0.6	.526
CHD8	0.2	.966	−0.1	.982	0.2	.699

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Supplementary Table III. Continued.

Gene	Log_2FC TAA/ TADA	Adjusted *P* value	Log_2FC TBAD/ TADA	Adjusted *P* value	Log_2FC TAA/ TBAD	Adjusted *P* value
CHMP2A	0.2	.982	0.6	.718	−0.5	.463
CHMP4B	−0.3	.966	−0.2	.928	−0.1	.945
CHST14	−0.7	.9	0.3	.899	−1	.247
CHTF18	−0.8	.941	−1.8	.497	1.1	.441
CILP2	−1.7	.857	−1.5	.418	−0.3	.862
CIRBP	0.3	.966	−0.4	.848	0.7	.401
CISD1	0.1	.982	−0.2	.957	0.2	.873
CKAP2	−0.2	.982	−0.8	.457	0.6	.22
CKAP4	0.3	.969	−0.1	.998	0.3	.767
CKB	−0.4	.927	−0.7	.706	0.3	.757
CKM	0.5	.9	0.5	.792	0.1	.996
CLEC11A	0.6	.9	0.1	.997	0.6	.513
CLEC3B	−0.1	.984	−0.5	.792	0.4	.526
CLIC1	0.3	.912	−0.1	.934	0.3	.401
CLIC4	−0.5	.9	−0.6	.742	0.2	.901
CLTA	0.6	.9	0.5	.792	0.2	.916
CLTB	−0.3	.972	−0.4	.831	0.2	.903
CLTC	−0.1	.982	−0.2	.935	0.1	.93
CLU	−0.3	.972	−0.5	.792	0.3	.764
CMA1	0.1	.982	−0.4	.821	0.5	.487
CMBL	−0.5	.903	−0.5	.792	0.1	.979
CMPK1	−0.4	.903	−0.6	.524	0.3	.585
CMYA5	0.1	.982	−1.1	.508	1.2	.123
CN166	−0.1	.982	−0.5	.89	0.4	.811
CNBP	0.2	.982	0.1	.993	0.2	.93
CNDP2	−0.3	.947	−0.8	.524	0.5	.413
CNN1	−1.2	.857	−0.5	.848	−0.8	.457
CNN2	−0.1	.982	−0.1	.937	0.1	.989
CNN3	−0.4	.947	−0.5	.821	0.2	.933
CNPY2	0.3	.957	−0.4	.826	0.6	.346
CNRIP1	−0.1	.982	−0.3	.792	0.3	.592
CNTN1	−0.4	.903	−0.3	.892	−0.2	.84
COASY	0.1	.982	−0.6	.792	0.7	.416
COG5	−0.4	.903	0.3	.819	−0.6	.161
COL12A1	0.4	.946	−0.3	.899	0.7	.429
COL14A1	−0.6	.903	−0.2	.942	−0.4	.691
COL15A1	−0.1	.992	−0.3	.899	0.2	.812
COL18A1	−0.7	.9	−0.2	.956	−0.5	.528
COL1A1	−1	.9	−0.1	.988	−1	.375
COL1A2	−1	.9	−0.1	1.00	−1	.338
COL21A1	−1.8	.857	0.5	.877	−2.2	.022
COL3A1	−1.3	.862	0.2	.966	−1.4	.179
COL4A1	−1.1	.857	0.2	.951	−1.2	.083
COL4A2	−1.3	.857	0.2	.935	−1.5	.05
COL4A3	−1	.862	0.3	.899	−1.3	.071
COL6A1	−0.3	.966	0.2	.933	−0.5	.561

Supplementary Table III. Continued.

Gene	Log_2FC TAA/ TADA	Adjusted *P* value	Log_2FC TBAD/ TADA	Adjusted *P* value	Log_2FC TAA/ TBAD	Adjusted *P* value
COL6A2	−0.4	.941	0.3	.906	−0.6	.419
COL6A3	−0.3	.947	−0.6	.757	0.3	.739
COL7A1	0.4	.947	−0.9	.706	1.2	.115
COL8A1	−1.3	.857	0.3	.936	−1.6	.08
COLGALT1	−0.3	.957	−0.3	.853	0.1	.975
COMT	−0.2	.982	−0.2	.947	−0.1	1.00
COPA	0.2	.982	0.2	.934	−0.1	.968
COPB1	0.5	.903	0.3	.899	0.2	.84
COPB2	0.1	.982	−0.4	.866	0.4	.63
COPG1	0.4	.929	0.3	.899	0.2	.902
COPS5	0.3	.941	0.1	.998	0.3	.691
COPS6	−0.5	.918	−0.2	.933	−0.3	.779
CORO1A	0.3	.963	0.3	.899	0.1	.979
CORO1B	−0.2	.969	−0.5	.762	0.3	.705
CORO1C	−0.4	.903	−0.4	.815	−0.1	.995
COTL1	0.2	.969	−0.2	.896	0.4	.496
COX4I1	0.3	.982	−0.1	.985	0.3	.814
COX5A	0.2	.982	−0.5	.78	0.6	.312
COX5B	0.6	.9	−0.3	.89	0.8	.164
COX6B1	−0.5	.903	−0.8	.668	0.4	.743
COX6C	0.6	.941	0.8	.792	−0.2	.905
COX7A2	0.5	.9	−0.2	.933	0.7	.334
CP	−0.4	.903	−0.8	.457	0.5	.452
CPA3	0.8	.9	−0.1	.985	0.9	.38
CPB2	0.2	.969	−0.2	.932	0.4	.572
CPNE1	−0.3	.957	0.2	.904	−0.4	.463
CPNE3	−0.2	.982	0.5	.792	−0.7	.343
CPPED1	−0.4	.93	−0.7	.682	0.4	.72
CPQ	−0.3	.941	−0.4	.818	0.1	.951
CPXM2	−0.6	.9	−0.4	.853	−0.3	.862
CREG1	−0.5	.941	−0.6	.822	0.1	.968
CRIP1	0.4	.982	−0.4	.953	0.8	.8
CRIP2	−0.7	.9	−0.3	.919	−0.4	.688
CRK	−0.4	.947	−0.3	.906	−0.1	.943
CRKL	−0.4	.903	−0.7	.632	0.3	.72
CRLF1	0.4	.941	0.1	.976	0.3	.739
CRP	−0.8	.9	−1.4	.519	0.6	.665
CRYAB	−0.8	.862	−0.4	.824	−0.4	.697
CRYL1	−0.8	.9	−0.6	.815	−0.3	.844
CRYZ	−0.4	.9	−0.7	.583	0.3	.701
CS	0.4	.9	0.2	.917	0.2	.746
CSDE1	−2	.857	−1.8	.451	−0.3	.881
CSK	0.4	.927	−0.1	.973	0.5	.533
CSPG4	−0.5	.9	−0.2	.942	−0.4	.628
CSPG5	−1	.9	−0.8	.808	−0.3	.898
CSRP1	−0.8	.878	−0.6	.808	−0.3	.811

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Supplementary Table III. Continued.

Gene	Log_2FC TAA/ TADA	Adjusted *P* value	Log_2FC TBAD/ TADA	Adjusted *P* value	Log_2FC TAA/ TBAD	Adjusted *P* value
CSRP2	−1.2	.857	−0.8	.762	−0.5	.694
CSTB	−0.3	.903	−0.7	.443	0.4	.43
CTGF	0.9	.862	0.1	.988	0.8	.33
CTHRC1	1	.857	0.2	.942	0.9	.147
CTNNA1	0.3	.982	0.1	.988	0.2	.953
CTNND1	0.3	.963	−0.2	.933	0.4	.561
CTPS1	−0.3	.966	−0.2	.919	−0.1	.951
CTSB	0.3	.969	−0.3	.898	0.6	.487
CTSC	−0.1	.984	−0.9	.519	0.9	.182
CTSD	0.1	.982	−0.6	.583	0.6	.164
CTSF	−0.7	.9	−0.4	.826	−0.3	.757
CTSG	0.6	.9	0.7	.721	−0.2	.916
CTSZ	0.2	.974	0.1	.985	0.2	.87
CTTN	0.1	.99	0.3	.826	−0.3	.697
CUL9	0.4	.982	−1.4	.707	1.7	.198
CUTA	−0.5	.903	−0.9	.583	0.4	.676
CXCL12	−0.2	.982	0.1	.985	−0.2	.863
CXCL16	−0.6	.927	−0.6	.826	−0.1	1.00
CYB5R1	−0.1	.99	−0.2	.953	0.1	.933
CYB5R3	−0.4	.947	−0.5	.799	0.2	.873
CYBRD1	−0.9	.9	−1.3	.519	0.5	.703
CYCS	0.6	.9	−0.2	.933	0.7	.307
CYFIP1	−0.2	.982	−0.1	.962	−0.1	.978
CYP20A1	−0.3	.982	−0.8	.848	0.6	.797
CYP27B1	0.7	.903	−1.3	.552	1.9	.037
CYP2C8	−0.4	.982	−0.5	.917	0.1	.983
DAAM2	0.7	.941	0.2	.956	0.5	.8
DAD1	−0.4	.974	0.2	.966	−0.5	.726
DAG1	−0.8	.862	−0.3	.868	−0.5	.511
DARS1	0.1	.982	0.2	.892	−0.2	.814
DBI	−0.4	.9	−0.3	.866	−0.2	.806
DBN1	0.3	.966	−0.2	.934	0.4	.578
DBNL	0.1	.997	−0.6	.583	0.6	.199
DCN	1.3	.857	−0.5	.821	1.8	.022
DCPS	0.2	.979	−0.6	.679	0.7	.161
DCTN1	−0.1	.992	0.1	.985	−0.1	.952
DCTN2	−0.1	.982	−0.4	.792	0.3	.658
DCTN3	−0.4	.941	−0.4	.821	0.1	.974
DDAH1	−0.5	.941	−0.5	.826	0.1	.998
DDAH2	−0.5	.862	−0.6	.609	0.1	.958
DDB1	−0.2	.982	−0.4	.826	0.3	.762
DDOST	0.2	.981	−0.4	.808	0.5	.346
DDR1	−1.2	.862	−0.5	.89	−0.8	.571
DDT	−0.3	.941	−1	.324	0.8	.198
DDX1	−0.2	.979	−0.5	.802	0.3	.757
DDX25	0.2	.982	0.4	.84	−0.3	.788

Supplementary Table III. Continued.

Gene	Log_2FC TAA/ TADA	Adjusted *P* value	Log_2FC TBAD/ TADA	Adjusted *P* value	Log_2FC TAA/ TBAD	Adjusted *P* value
DDX39B	−0.5	.941	−0.4	.878	−0.1	.957
DDX3X	0.2	.982	0.5	.792	−0.4	.676
DDX6	0.5	.946	0.4	.882	0.1	.974
DECR1	0.6	.9	0.1	.99	0.6	.442
DES	0.1	.984	−0.7	.713	0.7	.306
DHAK	0.2	.974	−0.2	.922	0.4	.623
DHRS7	−0.4	.982	0.3	.946	−0.6	.719
DHX37	−1.9	.857	−1	.758	−0.9	.441
DHX9	−0.2	.982	−0.3	.917	0.2	.915
DIABLO	−0.3	.966	−0.1	.975	−0.3	.827
DKK3	−0.2	.982	−0.5	.826	0.4	.757
DLAT	−0.1	.982	−0.2	.917	0.1	.939
DLGAP1	−0.5	.969	−0.6	.853	0.2	.95
DLST	0.1	.982	−0.1	.989	0.1	.93
DMD	−0.5	.9	−0.2	.922	−0.3	.705
DNAH5	−0.9	.9	−1.4	.457	0.6	.613
DNAH9	−2.4	.857	−1.8	.451	−0.7	.678
DNAJA2	−0.1	.982	−0.2	.892	0.2	.84
DNAJB11	0.6	.903	0.2	.942	0.4	.706
DNAJB4	−0.4	.927	−0.4	.82	−0.1	1.00
DNM1L	0.3	.957	0.2	.942	0.2	.889
DNPEP	−0.3	.972	−0.3	.917	−0.1	.991
DNTTIP1	−1.5	.857	−0.7	.792	−0.8	.447
DNTTIP2	−0.5	.927	−0.6	.792	0.2	.915
DPP3	0.3	.941	−0.3	.826	0.6	.286
DPT	−0.1	.992	−0.8	.718	0.8	.363
DPYSL2	−0.1	.982	−0.4	.812	0.3	.642
DPYSL3	−0.4	.9	−0.4	.759	0.1	.934
DRAP1	0.2	.982	−0.3	.848	0.4	.529
DSCAM	−1.6	.862	0.2	.976	−1.8	.198
DSP	0.2	.982	−0.4	.862	0.6	.598
DST	−0.8	.903	−1	.766	0.3	.906
DSTN	−0.6	.9	−0.5	.759	−0.1	.962
DTWD2	−0.2	.982	0.7	.846	−0.8	.581
DUSP3	−0.6	.878	−0.6	.674	0.1	.975
DUT	0.2	.982	−0.3	.933	0.4	.785
DYNC1H1	−0.3	.969	0.1	.964	−0.4	.691
DYNC1I2	−0.3	.966	−0.4	.826	0.2	.917
DYNC1LI1	−0.1	.986	0.1	.973	−0.2	.913
DYNC1LI2	−0.2	.974	−0.2	.933	−0.1	.977
DYNLRB1	−0.2	.982	−0.5	.826	0.4	.779
ECH1	0.2	.982	−0.9	.346	1.1	.037
ECHS1	−0.1	.982	−0.4	.808	0.4	.65
ECM1	−0.1	.982	−0.2	.933	0.1	.945
EEA1	0.2	.982	−0.1	.961	0.2	.759
EEF1A2	0.2	.982	−0.8	.721	0.9	.234

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Supplementary Table III. Continued.

Gene	Log_2FC TAA/ TADA	Adjusted *P* value	Log_2FC TBAD/ TADA	Adjusted *P* value	Log_2FC TAA/ TBAD	Adjusted *P* value
EEF1B2	−0.2	.982	−0.6	.759	0.4	.623
EEF1D	0.1	.982	−0.5	.721	0.5	.301
EEF1DP3	−1.3	.862	−1.5	.531	0.3	.901
EEF1G	0.1	.982	0.1	.993	0.1	.962
EEF2	0.1	.982	−0.1	.973	0.2	.824
EFEMP1	−0.9	.862	−0.2	.933	−0.7	.447
EFEMP2	−0.5	.9	−0.4	.808	−0.1	.978
EFHD1	−0.5	.903	−0.4	.848	−0.2	.913
EFHD2	0.6	.9	−0.4	.861	0.9	.172
EFL1	−0.3	.957	−0.6	.791	0.3	.791
EGR4	−1.1	.9	−1.1	.75	0.1	.97
EHD1	−0.1	.982	−0.1	.951	0.1	.962
EHD2	−1	.857	−0.6	.789	−0.4	.623
EHD3	−0.7	.9	−0.1	.974	−0.7	.463
EHD4	−0.4	.9	−0.3	.821	−0.1	.899
EIF1	−0.3	.957	−0.7	.508	0.5	.372
EIF2A	−0.5	.9	0.2	.92	−0.6	.313
EIF2B1	−0.4	.941	0.3	.876	−0.7	.341
EIF2S1	−0.1	.982	−0.3	.8	0.2	.703
EIF2S3	0.2	.982	0.3	.891	−0.2	.899
EIF3A	−0.3	.982	0.3	.899	−0.5	.567
EIF3F	0.3	.941	−0.4	.826	0.7	.301
EIF3I	0.1	.99	−0.5	.817	0.5	.557
EIF4A1	−0.2	.982	−0.2	.951	0.1	.983
EIF4A2	−0.2	.972	−0.4	.792	0.3	.776
EIF4A3	−0.1	.994	−0.3	.899	0.3	.8
EIF4B	0.2	.982	−0.1	.988	0.2	.887
EIF4G2	−0.3	.972	−0.2	.951	−0.2	.93
EIF4G3	−0.3	.982	−2	.225	1.8	.035
EIF4H	−0.3	.972	−0.1	.998	−0.3	.821
EIF5	−0.5	.9	−0.5	.792	0.1	1.00
EIF5A	−0.3	.976	−0.7	.791	0.5	.697
EIF6	−0.5	.927	−0.8	.668	0.4	.704
ELANE	−0.4	.941	−0.3	.917	−0.2	.902
ELAVL1	−0.2	.982	−0.2	.939	−0.1	.998
ELN	−1	.862	1	.634	−1.9	.022
ELOB	−0.4	.941	−0.4	.821	0.1	.966
EMD	−0.7	.9	−0.2	.951	−0.6	.48
EMILIN1	−0.8	.857	0.3	.88	−1	.035
EMILIN2	0.1	.982	−0.2	.953	0.3	.84
EML2	−0.6	.878	−0.7	.497	0.2	.792
EML3	0.1	.997	−0.3	.944	0.3	.891
ENAH	−0.3	.947	−0.2	.942	−0.2	.863
ENAM	−0.8	.9	−0.7	.782	−0.2	.913
ENDOD1	−0.1	.984	−0.2	.934	0.2	.905
ENG	−0.1	.982	0.2	.922	−0.3	.741

Supplementary Table III. Continued.

Gene	Log_2FC TAA/ TADA	Adjusted *P* value	Log_2FC TBAD/ TADA	Adjusted *P* value	Log_2FC TAA/ TBAD	Adjusted *P* value
ENO1	−0.4	.9	−0.2	.826	−0.2	.757
ENO2	−0.4	.862	−0.2	.848	−0.3	.65
ENOPH1	−0.3	.974	−0.8	.785	0.5	.697
ENPP1	−0.1	.984	0.2	.917	−0.3	.785
ENPP2	0.2	.982	−0.2	.937	0.4	.688
EPB41L2	0.1	.982	0.2	.957	−0.1	.968
EPDR1	−0.3	.96	−0.3	.891	−0.1	1.00
EPHX1	−0.2	.982	−0.9	.327	0.8	.112
EPPK1	−0.1	.99	−0.2	.966	0.1	.958
EPRS1	0.3	.969	0.2	.934	0.1	.944
EPS15L1	0.1	.993	−0.1	1.00	0.1	.991
EPS8L1	−1	.9	−0.9	.792	−0.2	.955
ERBIN	−1	.857	−0.5	.826	−0.6	.463
ERC2	0.9	.9	−1.1	.67	2	.035
ERH	−0.1	.982	−0.3	.899	0.2	.84
ERI1	−0.9	.957	−1.2	.822	0.3	.928
ERLIN2	−0.3	.947	0.2	.933	−0.5	.509
ERO1A	−0.6	.927	−0.7	.792	0.2	.913
ERP29	0.1	.982	−0.4	.774	0.5	.337
ERP44	0.1	.982	−0.6	.699	0.7	.286
ES1	−0.4	.941	−0.6	.764	0.2	.824
ESD	−0.4	.903	−0.6	.654	0.3	.757
ESYT1	−0.1	.997	−0.2	.951	0.2	.903
ESYT2	−0.5	.903	−0.4	.853	−0.2	.899
ETF1	−0.1	.988	−0.3	.865	0.3	.757
ETFA	0.3	.963	−0.6	.674	0.8	.112
ETFB	0.4	.927	−0.3	.861	0.6	.286
EXOC3	−0.8	.9	−0.8	.759	0.1	1.00
EXT1	−0.6	.912	0.3	.933	−0.8	.394
EYS	−1.1	.9	0.8	.8	−1.9	.071
EZR	0.2	.972	−0.1	.988	0.2	.75
F10	0.2	.982	−1.2	.512	1.4	.106
F11	−0.8	.9	−0.3	.917	−0.5	.641
F12	−0.1	.982	−0.4	.821	0.3	.726
F13A1	0.2	.982	−0.5	.792	0.6	.378
F13B	0.1	.984	−0.8	.632	0.8	.21
F2	−0.2	.972	−0.5	.674	0.4	.526
F9	−1	.857	−0.5	.769	−0.5	.495
FABP1	−0.2	.982	−0.3	.912	0.2	.93
FABP3	−0.9	.862	−1	.583	0.2	.913
FABP4	−0.4	.957	−0.7	.737	0.4	.701
FABP5	0.3	.982	−0.8	.674	1.1	.16
FAH	−0.3	.941	−0.6	.538	0.4	.494
FAM135A	0.1	.984	−0.2	.953	0.3	.875
FAM180A	−1.2	.9	0.6	.862	−1.8	.132
FAM50B	−1.1	.9	−0.4	.911	−0.8	.578

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Supplementary Table III. Continued.

Gene	Log_2FC TAA/ TADA	Adjusted *P* value	Log_2FC TBAD/ TADA	Adjusted *P* value	Log_2FC TAA/ TBAD	Adjusted *P* value
FANCA	−0.2	.982	0.9	.769	−1	.341
FANK1	0.5	.947	−1.2	.632	1.7	.08
FARSB	−0.1	.982	−0.2	.953	0.1	.991
FASN	0.4	.941	−0.2	.934	0.6	.483
FAU	−0.1	.982	−0.9	.674	0.8	.355
FBLIM1	−0.8	.862	−0.4	.831	−0.4	.658
FBLN1	−0.6	.862	−0.6	.583	0.1	.97
FBLN2	0.1	.993	−0.5	.819	0.5	.578
FBLN5	−1.3	.857	0.1	.994	−1.3	.102
FBN1	−1.2	.857	0.5	.826	−1.6	.036
FCGBP	0.2	.982	−0.1	.973	0.2	.862
FCGR3A	−0.6	.927	−1	.632	0.5	.674
FDPS	−0.2	.974	−0.3	.899	0.1	.97
FERMT2	−0.8	.862	−0.3	.899	−0.6	.427
FERMT3	0.6	.9	0.5	.815	0.2	.881
FGA	−0.2	.982	0.4	.847	−0.5	.537
FGB	−0.1	.992	0.5	.826	−0.6	.624
FGG	0.2	.982	0.5	.826	−0.4	.739
FGL2	−0.3	.972	−0.5	.808	0.3	.811
FH	0.2	.982	−0.7	.769	0.9	.286
FHL1	−1.1	.857	−0.6	.815	−0.6	.526
FHL2	−0.6	.9	−0.6	.759	0.1	.964
FHL3	−0.5	.9	−0.4	.821	−0.2	.917
FHL5	−0.1	.984	0.2	.933	−0.2	.824
FIGNL1	−0.1	.993	0.6	.826	−0.7	.638
FILIP1L	0.1	.982	0.3	.826	−0.2	.787
FIS1	0.1	.982	−0.7	.674	0.7	.199
FKBP1A	−0.5	.9	−0.7	.59	0.3	.744
FKBP2	0.1	.982	−0.4	.815	0.4	.486
FKBP3	0.5	.903	−0.1	.993	0.6	.514
FKBP4	0.4	.9	0.3	.836	0.2	.891
FKBP5	0.8	.9	−0.6	.808	1.3	.103
FKBP9	−0.6	.929	−0.2	.973	−0.5	.726
FLAD1	−0.6	.957	0.2	.985	−0.8	.688
FLII	−0.5	.903	−0.3	.853	−0.2	.878
FLNA	−0.5	.9	0.2	.933	−0.6	.324
FLNB	0.5	.941	−0.2	.952	0.6	.529
FLNC	−0.5	.9	0.2	.917	−0.7	.248
FLOT1	−0.1	.982	0.2	.826	−0.3	.539
FLOT2	−0.3	.969	0.3	.862	−0.5	.441
FMOD	−0.6	.903	−0.5	.826	−0.2	.931
FN1	−0.4	.9	0.1	.956	−0.5	.372
FN3K	−1.1	.9	−2.2	.323	1.1	.401
FOXL1	−0.2	.982	−1.1	.538	1	.259
FRMD6	−0.4	.969	−1	.588	0.7	.441
FRZB	−0.5	.941	−0.3	.933	−0.3	.855

Supplementary Table III. Continued.

Gene	Log_2FC TAA/TADA	Adjusted *P* value	Log_2FC TBAD/TADA	Adjusted *P* value	Log_2FC TAA/TBAD	Adjusted *P* value
FSCN1	−0.1	.99	−0.5	.815	0.5	.596
FSIP2	−0.6	.916	−0.7	.789	0.2	.916
FSTL1	−0.3	.947	−0.1	.965	−0.2	.818
FTH1	0.6	.903	0.1	.993	0.6	.592
FUBP1	0.1	.984	−0.2	.942	0.3	.852
FUCA1	0.2	.982	−0.9	.391	1	.04
FURIN	0.1	.993	−0.4	.933	0.4	.844
G6PD	0.1	.988	0.2	.897	−0.2	.811
GAA	−0.2	.979	−0.7	.605	0.5	.405
GALM	0.1	.993	−0.6	.679	0.6	.301
GANAB	−0.1	.986	−0.1	.933	0.1	.899
GAPDH	−0.3	.941	−0.4	.808	0.1	.916
GAPDHS	−0.4	.979	−0.7	.826	0.3	.851
GARS1	0.5	.929	0.1	.998	0.5	.652
GART	−0.4	.947	−0.5	.831	0.1	.975
GAS6	−0.2	.982	−0.8	.674	0.7	.403
GASK1B	−0.6	.9	−0.1	.988	−0.6	.543
GBA	0.4	.969	0.4	.882	−0.1	.98
GBE1	−0.8	.862	−0.2	.934	−0.7	.311
GBLP	0.3	.941	−0.1	.953	0.4	.543
GBP1	−0.5	.927	−0.7	.742	0.3	.825
GC	−0.2	.982	−0.7	.508	0.5	.286
GCA	0.1	.982	0.7	.759	−0.6	.447
GCLC	0.4	.9	−0.7	.511	1.1	.023
GDI1	−0.5	.9	−0.7	.631	0.2	.855
GDI2	−0.1	.982	−0.3	.808	0.2	.669
GFPT1	−0.3	.972	0.3	.899	−0.6	.526
GFUS	0.1	.99	0.2	.951	−0.1	.93
GGT5	−0.6	.9	−1	.468	0.5	.543
GJA1	−0.5	.912	0.1	.998	−0.5	.572
GLDC	−0.5	.941	−1.8	.264	1.3	.133
GLIPR2	−0.5	.9	−0.5	.792	−0.1	.998
GLO1	−0.3	.9	−0.6	.451	0.3	.561
GLOD4	−0.3	.944	−0.8	.421	0.5	.301
GLRX	0.2	.982	−0.7	.611	0.8	.151
GLS	−0.4	.946	−0.3	.899	−0.1	.945
GLUD1	0.2	.972	0.1	.975	0.2	.877
GM2A	0.3	.982	−1.2	.486	1.4	.068
GMFG	0.3	.972	−0.3	.933	0.6	.613
GNA11	−0.9	.9	−0.5	.847	−0.4	.795
GNA13	−0.1	.984	−0.8	.762	0.7	.451
GNAI2	−0.3	.966	−0.2	.906	−0.1	.974
GNAI3	−0.1	.982	−0.1	.972	0.1	.979
GNAQ	−0.1	.984	0.3	.915	−0.3	.779
GNB1	−0.3	.947	−0.3	.853	0.1	1.00
GNB2	−0.2	.969	−0.4	.792	0.2	.788

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Supplementary Table III. Continued.

Gene	Log_2FC TAA/ TADA	Adjusted *P* value	Log_2FC TBAD/ TADA	Adjusted *P* value	Log_2FC TAA/ TBAD	Adjusted *P* value
GNB4	−0.4	.927	−0.4	.792	0.1	.931
GNG12	−0.5	.941	−0.5	.83	−0.1	.998
GNPDA1	−0.2	.982	−0.3	.922	0.1	.962
GNPTAB	−0.8	.9	−0.8	.785	−0.1	.963
GOLM1	−0.6	.966	−1.1	.802	0.5	.825
GOT1	−0.1	.992	−0.4	.826	0.4	.658
GOT2	−0.1	.988	−0.6	.718	0.6	.378
GPBP1L1	−2	.857	−0.2	.966	−1.8	.195
GPC4	0.1	.997	−0.6	.792	0.6	.509
GPC6	−0.5	.941	−0.4	.862	−0.1	.958
GPD1L	−0.4	.941	−0.5	.792	0.2	.878
GPI	−0.3	.9	−0.3	.792	−0.1	.961
GPM6A	−0.7	.903	0.2	.953	−0.9	.409
GPNMB	0.9	.9	−0.3	.933	1.2	.296
GPX1	−0.1	.982	−0.7	.551	0.7	.266
GPX3	−0.4	.912	−0.4	.822	−0.1	.974
GPX4	0.2	.982	−0.4	.874	0.6	.572
GRB2	0.1	.982	−0.7	.508	0.7	.106
GRB7	−0.1	.982	−0.4	.792	0.3	.598
GRHPR	−0.2	.972	−0.4	.808	0.2	.812
GRP78	0.2	.973	0.3	.821	−0.2	.84
GSN	−0.2	.946	−0.3	.826	0.1	.974
GSR	0.2	.972	−0.1	.917	0.2	.581
GSS	0.4	.947	−1	.632	1.4	.083
GSTM2	−0.4	.941	−0.7	.762	0.3	.814
GSTM3	−0.5	.9	−0.6	.677	0.1	.913
GSTO1	0.1	.982	−0.2	.843	0.3	.498
GSTP1	−0.4	.9	−0.2	.917	−0.2	.682
GSTT1	−0.5	.903	−0.5	.792	0.1	.99
GUK1	−0.6	.9	−0.6	.815	−0.1	.962
GULP1	−0.1	.982	0.3	.907	−0.3	.753
GYG1	−0.5	.903	−0.7	.679	0.2	.822
H1-0	−0.3	.941	−0.3	.866	−0.1	.976
H1-5	0.4	.974	−0.4	.917	0.7	.593
H2AC21	0.2	.982	−0.2	.933	0.4	.669
H3-3A	−0.7	.9	−0.7	.755	0.1	.987
H4-16	−0.3	.982	−0.8	.789	0.6	.652
HAAO	−0.9	.857	−1	.346	0.1	.938
HABP2	−0.2	.982	−0.4	.818	0.3	.757
HADH	0.3	.922	−0.3	.814	0.6	.178
HADHA	−0.1	.984	−0.3	.822	0.3	.676
HADHB	−0.1	.997	−0.2	.847	0.2	.697
HAGH	0.1	.982	−0.3	.755	0.4	.316
HAPLN1	−0.6	.9	−0.2	.953	−0.5	.646
HAPLN3	−1.1	.862	−0.5	.826	−0.6	.567
HARS2	−0.5	.941	−0.5	.825	0.1	.971

Supplementary Table III. Continued.

Gene	Log_2FC TAA/ TADA	Adjusted *P* value	Log_2FC TBAD/ TADA	Adjusted *P* value	Log_2FC TAA/ TBAD	Adjusted *P* value
HBA1	0.9	.862	−0.6	.792	1.5	.032
HBB	0.6	.9	−0.9	.583	1.4	.035
HBD	0.5	.903	−0.7	.674	1.2	.066
HBZ	1.1	.862	−0.7	.808	1.8	.038
HDGF	−0.4	.903	−0.1	.961	−0.3	.688
HDGFL3	−0.5	.941	−1	.616	0.6	.567
HDHD2	0.1	.982	−0.4	.821	0.4	.526
HDLBP	−0.1	.982	−0.3	.897	0.2	.863
HEBP1	−0.2	.969	−0.7	.401	0.6	.21
HEBP2	−0.6	.9	−0.5	.792	−0.1	.945
HEXA	0.5	.903	0.6	.762	−0.1	.931
HEXB	−0.1	.982	−0.6	.674	0.5	.399
HIBADH	−0.4	.903	−0.9	.476	0.5	.486
HIBCH	0.1	.982	−0.4	.792	0.5	.372
HINT1	−0.3	.957	−0.9	.327	0.7	.185
HK1	0.1	.992	0.1	.973	−0.1	.962
HKDC1	0.7	.9	−1	.668	1.7	.044
HLA-DRA	0.6	.9	−0.4	.826	1	.104
HLCS	0.7	.903	0.2	.973	0.6	.652
HMCN1	−0.7	.9	0.1	.98	−0.8	.342
HMGB2	−0.2	.982	0.5	.753	−0.6	.234
HMGCS2	0.2	.982	−0.6	.826	0.8	.518
HNRNPA1	0.8	.9	0.8	.718	−0.1	.951
HNRNPA2B1	0.1	.982	0.1	.987	0.1	.994
HNRNPA3	−0.1	.982	−0.1	.992	−0.1	.987
HNRNPAB	0.3	.941	−0.4	.764	0.7	.137
HNRNPC	−0.1	.982	−0.8	.708	0.7	.426
HNRNPD	−0.1	.99	−0.3	.834	0.3	.703
HNRNPF	0.4	.974	−0.3	.934	0.6	.658
HNRNPH3	−0.2	.969	−0.1	.989	−0.2	.811
HNRNPK	−0.2	.974	−0.4	.78	0.2	.688
HNRNPL	0.1	.982	0.1	.989	0.1	.974
HNRNPM	0.3	.93	0.2	.862	0.1	.95
HNRNPR	0.2	.974	−0.2	.917	0.3	.593
HNRNPU	−0.3	.982	−0.6	.792	0.4	.691
HNRNPUL2	−0.3	.982	−0.3	.941	0.1	1.00
HP	−1.1	.862	−1.6	.391	0.5	.704
HP1BP3	−0.2	.982	−0.2	.933	0.1	.968
HPR	−0.2	.982	−1.5	.288	1.4	.068
HPRT1	0.4	.941	−0.4	.826	0.7	.287
HPX	−0.1	.982	−0.9	.401	0.8	.112
HRG	−0.5	.867	−0.2	.899	−0.4	.557
HSD17B10	0.3	.941	−0.4	.818	0.6	.228
HSD17B12	−0.2	.972	0.1	.989	−0.2	.783
HSD17B3	−0.7	.9	−0.7	.789	0.1	.979
HSD17B4	0.4	.941	−0.2	.933	0.6	.48

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Supplementary Table III. Continued.

Gene	Log_2FC TAA/ TADA	Adjusted *P* value	Log_2FC TBAD/ TADA	Adjusted *P* value	Log_2FC TAA/ TBAD	Adjusted *P* value
HSF1	1.5	.862	−1.3	.755	2.7	.036
HSP90AA1	−0.3	.93	−0.2	.891	−0.1	.917
HSP90AB1	−0.5	.9	−0.1	.988	−0.5	.416
HSP90B1	0.1	.982	−0.1	.942	0.2	.754
HSPA2	−1	.857	−0.6	.792	−0.5	.587
HSPA4	0.2	.982	−0.5	.821	0.6	.441
HSPA4L	0.4	.969	−0.2	.972	0.5	.688
HSPA5	0.2	.941	−0.1	.998	0.2	.658
HSPA8	0.1	.982	−0.2	.822	0.3	.529
HSPA9	−0.1	.993	−0.3	.821	0.3	.627
HSPB1	−0.6	.9	−0.5	.808	−0.2	.889
HSPB6	−0.6	.9	−0.9	.668	0.3	.797
HSPB7	−0.9	.862	−0.7	.75	−0.2	.878
HSPB8	−0.6	.9	0.1	.993	−0.7	.487
HSPD1	0.2	.947	−0.2	.917	0.3	.486
HSPE1	0.2	.982	−0.7	.592	0.8	.133
HSPG2	−0.7	.862	0.2	.934	−0.9	.144
HTR3C	0.4	.97	−0.8	.762	1.2	.199
HTRA1	−0.5	.941	−0.6	.82	0.1	.961
HV206	−1.2	.9	−1.9	.462	0.8	.633
HV209	−0.5	.947	−1.7	.377	1.2	.234
HV306	−0.8	.9	−1.9	.323	1.1	.324
HYOU1	0.4	.927	0.3	.907	0.2	.862
IAH1	−0.4	.9	−0.5	.759	0.1	.922
IARS1	0.2	.982	−0.1	.973	0.2	.792
IARS2	−0.5	.903	−0.1	.973	−0.5	.65
IDH1	−0.2	.981	−0.4	.653	0.3	.451
IDH2	0.3	.941	0.2	.933	0.2	.87
IDH3A	0.2	.982	−0.6	.759	0.7	.247
IDNK	2	.857	−0.7	.826	2.7	.019
IER5	−0.3	.974	−1	.526	0.8	.328
IFT46	−0.3	.957	−1.3	.287	1	.133
IGDCC3	−0.6	.959	1.3	.727	−1.8	.147
IGF2	−0.8	.862	−0.9	.49	0.2	.894
IGFALS	−0.1	.982	−0.9	.586	0.8	.28
IGFBP2	−0.5	.929	−0.3	.899	−0.2	.89
IGFBP3	−0.7	.9	0.2	.946	−0.9	.325
IGFBP5	−0.7	.9	0.1	.981	−0.7	.344
IGFBP6	−0.1	.99	−0.3	.9	0.3	.82
IGFBP7	−1.1	.857	−0.2	.951	−1	.203
IGHA1	−0.4	.93	−1.4	.237	1	.135
IGHA2	−0.5	.927	−1.6	.286	1.1	.19
IGHD	0.1	.988	−0.9	.755	0.9	.36
IGHG1	−0.7	.862	−1.2	.283	0.5	.429
IGHG2	−0.8	.862	−1.4	.302	0.6	.487
IGHG3	−0.1	.984	−0.3	.899	0.3	.825

Supplementary Table III. Continued.

Gene	Log_2FC TAA/ TADA	Adjusted *P* value	Log_2FC TBAD/ TADA	Adjusted *P* value	Log_2FC TAA/ TBAD	Adjusted *P* value
IGHG4	−0.8	.9	−1.2	.519	0.4	.751
IGHM	−0.3	.972	−1.5	.287	1.3	.104
IGHV2-70D	−0.3	.982	−0.7	.826	0.4	.818
IGHV3-20	−0.5	.947	−0.8	.742	0.4	.72
IGHV3-49	−0.4	.957	−1.8	.225	1.4	.089
IGHV3-64D	−0.6	.9	−1.4	.297	0.8	.286
IGHV3-7	−0.7	.9	−1.5	.225	0.9	.204
IGHV3-72	−0.8	.9	−1.4	.327	0.7	.466
IGHV3-74	−0.6	.9	−1.8	.225	1.2	.111
IGHV6-1	−0.2	.982	−1.3	.592	1.1	.328
IGKC	−0.4	.903	−1.2	.225	0.8	.156
IGKV1-12	−1.2	.862	−1.5	.457	0.3	.862
IGKV1-16	−0.4	.947	−1.6	.323	1.2	.164
IGKV1-6	−0.3	.972	−1.1	.508	0.8	.312
IGKV2-24	−0.4	.947	−1.6	.225	1.3	.055
IGKV3-20	−0.6	.899	−1.2	.262	0.6	.372
IGKV3D-15	−0.4	.965	−2	.225	1.7	.035
IGKV3D-20	−0.7	.9	−1.9	.225	1.3	.123
IGKV4-1	−0.6	.9	−1.6	.225	1	.137
IGLC7	−0.6	.903	−1.6	.225	1.1	.151
IGLL1	−0.5	.9	−1	.391	0.5	.447
IGLL5	−0.5	.941	−2.6	.225	2.1	.023
IGLV1-47	−0.4	.958	−1.7	.225	1.4	.07
IGLV1-51	−1.2	.878	−1.7	.432	0.6	.688
IGLV3-1	−0.8	.9	−1.8	.225	1.1	.176
IGLV3-12	−0.6	.9	−1.4	.225	0.8	.247
IGLV3-19	−0.8	.9	−1.5	.235	0.8	.328
IGLV4-3	−0.6	.954	−1.2	.682	0.7	.644
IGLV8-61	−0.6	.927	−0.6	.814	0.1	.968
IL12RB1	−1.1	.9	1	.792	−2.1	.083
IL1RAPL1	−0.7	.927	−2.2	.235	1.6	.133
IL1RL1	0.1	.982	−1.4	.553	1.5	.156
IL34	−0.2	.982	0.7	.742	−0.9	.213
IL4I1	0.2	.972	−0.7	.526	0.9	.071
ILF2	0.3	.982	−0.2	.942	0.5	.698
ILK	−0.6	.862	0.1	.957	−0.7	.179
IMMT	0.1	.986	0.2	.902	−0.2	.827
IMPA1	−0.5	.927	−1	.452	0.6	.413
IMPDH2	−0.6	.9	−0.4	.872	−0.3	.757
IMPG1	−1	.903	−0.6	.866	−0.4	.857
INF2	0.3	.982	−0.5	.899	0.7	.674
INKA1	0.6	.903	−0.7	.78	1.2	.103
IPO5	0.2	.982	0.1	.961	0.1	.945
IPO7	−0.2	.974	−0.1	1.00	−0.2	.828
IPO9	−0.1	.982	−0.2	.945	0.1	.968
IQGAP1	−0.2	.969	−0.2	.859	0.1	.962

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Supplementary Table III. Continued.

Gene	Log_2FC TAA/ TADA	Adjusted *P* value	Log_2FC TBAD/ TADA	Adjusted *P* value	Log_2FC TAA/ TBAD	Adjusted *P* value
IRGC	−0.6	.944	0.6	.826	−1.1	.306
ISLR	0.1	.997	−0.3	.913	0.3	.812
ISYNA1	−0.6	.903	−0.5	.857	−0.2	.899
ITGA1	−0.9	.857	−0.4	.826	−0.6	.488
ITGA11	−0.4	.947	−0.1	.987	−0.4	.762
ITGA3	−0.8	.862	0.1	.998	−0.8	.212
ITGA5	−0.6	.9	−0.2	.951	−0.5	.572
ITGA7	−0.8	.857	−0.4	.821	−0.4	.537
ITGA8	−0.8	.862	−0.2	.944	−0.7	.36
ITGAV	−0.3	.957	−0.1	.998	−0.3	.733
ITGB1	−0.6	.9	−0.4	.826	−0.3	.795
ITGB2	0.3	.969	0.3	.865	−0.1	.968
ITGB3	0.2	.982	0.9	.592	−0.7	.343
ITGB5	−0.2	.972	−0.3	.9	0.1	.99
ITIH1	−0.1	.982	−0.7	.679	0.6	.401
ITIH2	0.3	.947	−0.5	.776	0.7	.177
ITIH3	−0.1	.997	−0.7	.632	0.7	.261
ITIH4	−0.3	.946	−1.1	.225	0.8	.089
ITIH5	−0.9	.857	−0.6	.713	−0.3	.792
ITM2B	−0.6	.9	−0.5	.816	−0.2	.906
ITPR1	−0.6	.9	−0.1	.972	−0.5	.503
IVD	0.1	.986	0.3	.913	−0.3	.844
IVNS1ABP	−0.2	.982	0.1	.964	−0.3	.757
JCHAIN	−0.1	.997	−1.2	.286	1.2	.044
JMY	−1.3	.862	−0.7	.826	−0.7	.676
K132L	−1.2	.862	−1	.718	−0.2	.902
KANK2	−0.6	.9	−0.3	.916	−0.4	.593
KANSL3	0.5	.941	−1.3	.391	1.8	.023
KAT6B	−0.8	.9	−0.2	.941	−0.6	.528
KAT8	−1.4	.862	−1.1	.75	−0.4	.84
KCNF1	−0.1	.992	−1	.815	0.9	.596
KCTD12	0.1	.982	−0.6	.7	0.7	.276
KDEL2	−0.1	.982	0.1	.993	−0.1	.956
KHSRP	0.1	.982	0.1	.966	−0.1	.998
KIF26B	−0.1	.984	−1.9	.632	1.8	.286
KIF2A	−0.7	.941	−0.7	.826	−0.1	1.00
KIF5B	−0.1	.997	0.2	.966	−0.2	.93
KLB	−0.2	.969	−0.2	.931	−0.1	.962
KLC1	−0.2	.982	−0.3	.891	0.2	.901
KLF10	−0.4	.957	−0.2	.973	−0.3	.825
KLKB1	−0.2	.982	−0.8	.583	0.6	.324
KMT5C	−0.8	.857	−0.3	.858	−0.5	.438
KNG1	−0.1	.982	−0.8	.346	0.7	.113
KNTC1	−0.9	.9	−1.4	.538	0.6	.697
KPNB1	−0.2	.982	−0.4	.808	0.3	.719
KREMEN2	0.2	.982	−1	.761	1.2	.328

Supplementary Table III. Continued.

Gene	Log_2FC TAA/ TADA	Adjusted *P* value	Log_2FC TBAD/ TADA	Adjusted *P* value	Log_2FC TAA/ TBAD	Adjusted *P* value
KRT1	0.5	.903	0.1	.998	0.5	.561
KRT10	0.3	.969	0.2	.934	0.2	.931
KRT18	−0.6	.903	−1.2	.474	0.6	.519
KRT19	−0.9	.857	−1.3	.225	0.4	.638
KRT2	0.2	.982	−0.5	.818	0.7	.408
KRT7	−0.2	.982	−0.6	.792	0.4	.707
KRT73	0.4	.941	0.4	.847	0.1	.989
KRT77	0.7	.941	0.1	.988	0.6	.719
KRT8	−0.7	.862	−1.2	.323	0.5	.506
KRT9	0.2	.982	−0.1	.973	0.2	.818
KSR2	−0.4	.972	−1.7	.323	1.4	.123
KTN1	−0.1	.982	−0.4	.815	0.3	.666
KV204	−0.5	.903	−1.3	.253	0.9	.179
KV304	−0.2	.982	−1.9	.225	1.5	.061
KV308	−0.1	.982	−1.5	.583	1.3	.286
KY	−1	.9	−1.2	.592	1.1	.273
LACTB2	0.6	.9	−1.4	.391	0.5	.705
LAMA2	−0.4	.941	−0.4	.916	−0.6	.676
LAMA4	−0.5	.903	0.1	.989	0.5	.363
LAMA5	−0.9	.857	−0.3	.913	−0.2	.916
LAMB1	−0.5	.927	−1	.492	0.5	.529
LAMB2	−0.9	.857	0.1	.953	−1	.066
LAMC1	−0.7	.862	−0.2	.933	−0.3	.824
LAMP1	0.2	.957	0.2	.933	−1.1	.043
LAMP2	0.3	.927	−0.1	.965	−0.6	.328
LAMTOR1	0.1	.982	−0.3	.792	0.5	.216
LAMTOR3	0.3	.944	−0.1	.989	0.3	.581
LANCL1	−0.6	.9	−0.1	.965	0.2	.84
LAP3	0.3	.927	0.3	.826	−0.1	.968
LASP1	−0.4	.941	−0.4	.826	−0.3	.742
LBP	−0.7	.9	−0.8	.421	1.1	.023
LBX1	−0.2	.982	−0.5	.808	0.2	.906
LCA5L	−0.4	.982	−0.6	.792	−0.2	.889
LCP1	0.2	.974	−0.7	.815	0.5	.688
LDB3	−0.8	.862	0.6	.916	−1	.675
LDHA	−0.4	.9	−0.3	.917	0.4	.591
LDHAL6A	−0.8	.9	−0.3	.891	−0.5	.557
LDHB	−0.2	.974	−0.4	.792	−0.1	.99
LDLR	−0.2	.982	−1.1	.538	0.4	.757
LECT2	−0.4	.974	−0.4	.742	0.3	.598
LEFTY2	−0.7	.9	−0.9	.632	0.7	.393
LEMD2	−0.5	.927	0.1	.99	−0.4	.796
LETM1	0.2	.982	0.1	1.00	−0.7	.517
LGALS1	−0.5	.9	−0.8	.674	0.4	.719
LGALS3	0.2	.982	0.2	.919	−0.1	.968
LGALS3BP	0.2	.982	−0.4	.792	−0.1	.913

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Supplementary Table III. Continued.

Gene	Log_2FC TAA/ TADA	Adjusted *P* value	Log_2FC TBAD/ TADA	Adjusted *P* value	Log_2FC TAA/ TBAD	Adjusted *P* value
LHPP	0.1	.99	−0.6	.583	0.7	.11
LIMS1	−0.4	.912	0.1	.961	0.1	.968
LIMS2	−0.5	.9	−0.6	.753	0.6	.363
LMAN2	−0.1	.996	−0.3	.882	−0.2	.887
LMCD1	−0.8	.862	−0.4	.805	−0.1	.962
LMNA	−0.4	.927	−0.2	.951	0.2	.913
LMNB1	−0.3	.972	−0.3	.906	−0.6	.496
LMNB2	−0.4	.9	−0.5	.808	0.1	.957
LMOD1	−0.8	.862	0.2	.953	−0.4	.688
LOXL1	−1.2	.857	−0.3	.821	−0.1	.912
LPA	0.2	.982	−0.1	.973	−0.7	.363
LPCAT2	−0.2	.972	0.3	.917	−1.4	.037
LPP	−0.8	.862	−1.9	.225	2	.019
LRG1	−0.3	.941	−0.4	.792	0.2	.765
LRP1	−0.3	.927	−0.2	.951	−0.7	.343
LRP12	−1.9	.857	−1.1	.286	0.8	.152
LRP6	−0.6	.947	−0.3	.839	−0.1	.968
LRPAP1	−0.5	.927	−0.7	.826	−1.3	.308
LRRC47	−0.2	.982	−0.2	.961	−0.4	.824
LRRC59	1.1	.857	−0.5	.808	0.1	.962
LRRC72	−1	.9	−0.3	.866	0.2	.839
LRRC9	0.7	.9	0.5	.821	0.6	.452
LSM3	−0.1	.982	0.7	.826	−1.6	.179
LSM6	0.2	.982	−0.1	.985	0.8	.313
LSM7	0.2	.982	−0.9	.406	0.8	.133
LSM8	0.4	.972	0.1	.973	0.1	.961
LTA4H	−0.1	.982	−0.5	.895	0.6	.68
LTBP1	−0.9	.857	−0.6	.826	1	.383
LTBP2	−0.7	.862	0.1	.973	−0.2	.825
LTBP4	−1.1	.857	0.1	.956	−1	.075
LTF	−0.5	.947	−0.5	.785	−0.3	.792
LUM	0.3	.972	0.1	.99	−1.1	.106
LV106	−0.5	.957	0.1	.993	−0.5	.699
LXN	0.4	.969	−1.1	.497	1.4	.066
LYPLA1	0.9	.862	−0.9	.759	0.5	.734
LYST	−0.6	.9	−1.3	.526	1.6	.068
LYZ	−0.6	.9	−0.1	.998	0.9	.286
LZIC	−0.1	.982	−1.9	.225	1.3	.072
LZTR1	−0.2	.982	−0.4	.822	−0.2	.844
MACF1	−0.1	.982	−0.6	.586	0.6	.264
MACROH2A1	−0.2	.982	−0.7	.815	0.6	.688
MAGEE1	−1.2	.862	0.3	.905	−0.3	.729
MAGEH1	0.2	.982	−0.5	.792	0.4	.676
MAMDC2	−0.1	.997	0.6	.826	−1.7	.053
MAOA	−0.3	.972	−0.4	.819	0.6	.391
MAOB	−0.3	.957	−0.2	.953	0.2	.917

Supplementary Table III. Continued.

Gene	Log_2FC TAA/ TADA	Adjusted *P* value	Log_2FC TBAD/ TADA	Adjusted *P* value	Log_2FC TAA/ TBAD	Adjusted *P* value
MAP1B	−0.2	.972	−0.6	.792	0.3	.785
MAP4	−0.1	.982	−0.4	.826	0.1	.952
MAPK1	−0.2	.982	0.2	.917	−0.4	.572
MAPK10	−1.1	.9	−0.1	.973	0.1	.998
MAPRE1	−0.1	.982	−0.7	.474	0.6	.206
MARCKS	0.3	.957	−0.1	.989	−1	.543
MAST3	−0.7	.9	−0.3	.822	0.3	.72
MAT2B	−0.1	.982	−0.3	.866	0.6	.402
MB	−0.4	.947	−0.7	.718	0.1	.961
MCAM	−0.7	.862	−0.4	.844	0.3	.779
MCEMP1	1.1	.903	0.4	.904	−0.8	.452
MDFIC	0.2	.982	−0.6	.713	−0.1	.921
MDH1	−0.1	.982	−0.1	.998	1.1	.526
MDH2	0.3	.941	−1.2	.538	1.3	.123
MDM1	−1.2	.857	−0.7	.586	0.6	.311
ME1	0.1	.982	−0.6	.677	0.8	.096
ME2	−0.2	.982	−0.1	.986	−1.2	.172
MECP2	−0.2	.982	−0.8	.815	0.9	.512
MEGF6	−0.2	.982	−0.6	.808	0.5	.675
MESD	0.3	.969	−0.1	.956	−0.1	.968
METRNL	−0.2	.982	0.6	.792	−0.7	.307
METTL25	−1.1	.9	−0.4	.853	0.6	.438
METTL7A	−0.8	.9	0.4	.905	−0.5	.719
MFAP2	−1	.862	−1.8	.364	0.8	.553
MFAP4	−1.1	.862	−1.1	.553	0.4	.76
MFAP5	0.1	.997	0.2	.951	−1.2	.128
MFGE8	−1	.862	−0.5	.861	−0.6	.602
MGP	−1.2	.862	−0.7	.677	0.7	.306
MGST3	−0.1	.982	−0.2	.951	−0.8	.363
MIF	−0.5	.9	−0.6	.834	−0.7	.587
MINPP1	1.1	.862	−0.4	.899	0.3	.857
MLH1	0.8	.9	−0.4	.818	−0.1	.91
MLKL	−0.6	.927	−0.3	.914	1.4	.083
MLTK	−0.3	.957	−0.4	.899	1.1	.172
MMP2	0.1	.997	−0.8	.744	0.3	.829
MMP9	−0.2	.982	0.1	.973	−0.4	.653
MMRN1	0.6	.9	−0.1	.978	0.1	.953
MOCS2	−0.6	.864	0.4	.891	−0.6	.624
MOS	0.1	.99	1.1	.438	−0.6	.526
MPDZ	0.4	.927	−0.5	.759	−0.1	.917
MPO	−0.4	.966	−0.4	.933	0.4	.835
MPST	−0.2	.972	−0.8	.642	1.2	.066
MRC2	0.1	.982	1	.583	−1.4	.071
MRVI1	−0.2	.982	−1.2	.225	1	.071
MSN	−0.3	.927	−0.2	.951	0.3	.818
MSRB3	−0.5	.941	0.1	.966	−0.3	.8

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Supplementary Table III. Continued.

Gene	Log_2FC TAA/ TADA	Adjusted *P* value	Log_2FC TBAD/ TADA	Adjusted *P* value	Log_2FC TAA/ TBAD	Adjusted *P* value
MST1	0.2	.982	−0.1	.962	−0.2	.705
MT-CO2	−0.7	.9	−1.4	.346	1	.247
MTHFD1	−0.1	.988	0.3	.917	−0.2	.931
MTPN	−0.2	.972	−0.5	.84	−0.3	.84
MVP	−0.2	.965	−0.3	.892	0.3	.797
MYADM	−0.7	.9	−0.7	.48	0.6	.286
MYCBP2	−0.7	.941	−0.2	.917	−0.1	.957
MYDGF	0.3	.972	0.6	.815	−1.3	.115
MYH10	−0.9	.862	−1.5	.674	0.8	.654
MYH11	−1.2	.857	−0.3	.913	0.6	.549
MYH13	−0.6	.912	−0.2	.956	−0.8	.306
MYH14	−0.7	.9	−0.2	.951	−1	.157
MYH2	−0.6	.9	−0.4	.898	−0.3	.862
MYH9	−0.2	.982	−0.2	.947	−0.6	.59
MYL6	−0.9	.857	−0.3	.899	−0.3	.791
MYL6B	−1.1	.857	0.3	.891	−0.4	.563
MYL9	−0.7	.878	−0.4	.826	−0.5	.457
MYLK	−0.5	.9	−0.3	.899	−0.8	.35
MYO18A	0.2	.982	−0.4	.815	−0.3	.787
MYO1C	−0.6	.878	−0.4	.826	−0.2	.84
MYO1D	−0.3	.957	−0.5	.899	0.6	.707
MYO5B	−0.3	.982	−0.2	.919	−0.5	.526
MYOF	−0.2	.982	−0.2	.951	−0.2	.862
MYOM2	−0.2	.982	0.5	.895	−0.7	.654
MYOM3	−0.8	.9	0.1	.974	−0.3	.787
NAA15	−1.5	.903	−1.2	.474	1.1	.179
NAGK	−0.1	.982	−0.8	.674	0.1	.97
NAMPT	−0.4	.941	−3.5	.323	2.1	.307
NAP1L1	0.1	.982	−0.5	.67	0.4	.343
NAP1L4	−0.2	.965	0.4	.826	−0.8	.283
NAPA	0.3	.957	−0.4	.904	0.5	.722
NAPG	−0.3	.969	−0.3	.808	0.2	.855
NAPRT	−0.4	.941	−0.2	.937	0.4	.558
NARS1	0.2	.982	−0.2	.933	−0.1	.951
NASP	−0.5	.927	−0.7	.78	0.3	.84
NAV1	−0.4	.972	0.2	.951	−0.1	.99
NAV2	0.1	.982	0.5	.822	−0.9	.21
NAXE	−0.8	.889	0.9	.755	−1.2	.198
NCKAP1	−0.4	.941	−1.1	.679	1.1	.28
NCL	−0.3	.957	−0.9	.668	0.1	.962
NCOA1	1.2	.862	0.2	.945	−0.6	.523
NDRG1	−0.2	.982	−0.5	.789	0.3	.8
NDRG3	−0.2	.982	0.8	.808	0.5	.734
NDUFA10	−0.4	.947	−0.3	.899	0.1	.961
NDUFA13	−0.2	.982	−0.4	.802	0.3	.712
NDUFA4	−0.2	.982	−1.1	.459	0.8	.341

Supplementary Table III. Continued.

Gene	Log_2FC TAA/ TADA	Adjusted *P* value	Log_2FC TBAD/ TADA	Adjusted *P* value	Log_2FC TAA/ TBAD	Adjusted *P* value
NDUFA5	0.5	.9	−0.3	.917	0.1	.962
NDUFA6	0.2	.966	−0.3	.917	0.2	.933
NDUFB11	−0.1	.982	0.3	.862	0.3	.752
NDUFB4	−0.3	.974	−0.2	.934	0.3	.585
NDUFS1	0.3	.972	−0.2	.952	0.1	.968
NDUFS3	−0.2	.982	−0.4	.866	0.1	.931
NDUFS8	0.2	.966	−0.5	.821	0.7	.363
NDUFV2	−0.1	.982	−0.6	.818	0.5	.705
NECAP2	−0.4	.982	−0.3	.815	0.5	.296
NEDD8	−0.9	.862	−0.5	.755	0.5	.463
NEGR1	−0.6	.9	−0.1	.985	−0.3	.898
NENF	−0.6	.903	−1.6	.225	0.8	.375
NEXN	−0.2	.982	−0.4	.826	−0.3	.822
NHSL1	0.2	.982	−0.5	.826	−0.1	.955
NIBAN	−0.6	.9	−0.3	.893	0.1	.933
NIBL1	0.1	.982	−0.8	.826	1	.557
NID1	−0.4	.9	−0.2	.942	−0.4	.496
NID2	−0.5	.9	−0.6	.792	0.7	.452
NIT2	−0.3	.941	−0.5	.75	0.1	.943
NKX1-2	0.3	.982	−0.8	.519	0.4	.658
NLRC4	−0.8	.9	−0.6	.609	0.3	.59
NLTP	0.5	.862	−0.6	.822	0.8	.451
NME1	0.3	.972	−0.5	.822	−0.3	.84
NNMT	−0.2	.982	−0.1	.985	0.5	.262
NOLC1	0.4	.972	−0.5	.822	0.8	.363
NOTCH3	−0.6	.9	−0.3	.895	0.2	.878
NPC2	0.1	.982	0.9	.792	−0.6	.729
NPEPPS	−0.4	.903	0.1	.994	−0.7	.383
NPM1	0.1	.982	−0.4	.866	0.5	.663
NPNT	−1.2	.857	−0.7	.526	0.4	.59
NPTN	−0.5	.9	−0.2	.899	0.3	.657
NQO2	−0.5	.903	0.2	.933	−1.4	.044
NRAP	−0.9	.862	−0.3	.891	−0.3	.779
NSF	0.4	.903	−0.6	.77	0.2	.913
NSFL1C	0.1	.982	−0.8	.69	−0.1	.945
NSMCE3	−0.3	.972	0.3	.899	0.2	.841
NT5E	−0.3	.972	−0.5	.792	0.5	.463
NUCB1	0.2	.969	−1.1	.346	0.9	.164
NUCB2	−0.1	.988	−0.1	.989	−0.3	.846
NUCKS1	−0.9	.9	−0.2	.891	0.4	.48
NUDC	−0.5	.9	−0.4	.818	0.4	.63
NUDT2	−0.3	.946	−1.5	.468	0.7	.572
NUDT5	−0.3	.944	−0.4	.821	−0.2	.862
NUTF2	−0.2	.982	−0.3	.848	0.1	1.00
OAF	−0.4	.982	−1	.323	0.8	.179
OAT	0.1	.996	−0.3	.826	0.1	.863

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Supplementary Table III. Continued.

Gene	Log_2FC TAA/ TADA	Adjusted *P* value	Log_2FC TBAD/ TADA	Adjusted *P* value	Log_2FC TAA/ TBAD	Adjusted *P* value
OBSCN	−2	.857	−0.1	.989	−0.3	.901
OGDH	0.1	.982	0.1	.993	−0.1	.998
OGN	−0.6	.903	−1	.815	−1.1	.466
OLA1	−0.1	.982	−0.1	.973	0.2	.862
OLFM1	−0.5	.946	−0.9	.683	0.3	.785
OLFML1	0.2	.982	−0.3	.792	0.2	.707
OLFML3	−0.4	.965	−1.3	.502	0.9	.394
OMD	0.2	.982	−0.3	.866	0.5	.523
OPTN	0.1	.99	−0.7	.773	0.4	.75
OR10T2	−1.1	.862	−0.4	.862	0.6	.613
OR4C3	−0.2	.982	−0.4	.853	0.4	.681
OR51Q1	−1.8	.857	−0.1	.975	−1	.342
OR56B4	−0.6	.941	0.3	.917	−0.5	.742
ORM1	−0.4	.941	−1.7	.583	−0.2	.945
ORM2	−0.3	.941	−0.3	.933	−0.3	.863
OSTF1	0.5	.9	−0.9	.452	0.6	.343
OTUB1	−0.4	.941	−1.3	.225	1	.053
OVOS2	0.5	.903	−0.2	.904	0.6	.239
OXCT1	0.2	.982	−0.6	.784	0.2	.825
OXSR1	0.2	.972	−0.6	.792	1.1	.123
P4HB	0.2	.982	−0.1	.985	0.2	.813
PA2G4	−0.1	.997	0.4	.792	−0.2	.795
PACSIN2	−0.5	.9	0.1	.985	0.1	.898
PAFAH1B1	−0.1	.982	−0.3	.917	0.2	.825
PAFAH1B2	0.1	.982	−0.5	.762	−0.1	.979
PAFAH1B3	0.7	.9	−0.2	.911	0.1	.934
PAICS	−0.2	.972	−0.7	.492	0.8	.093
PALLD	−0.4	.903	−0.5	.815	1.1	.08
PARK7	−0.2	.947	0.2	.951	−0.4	.685
PARVA	−0.9	.857	−0.3	.826	−0.1	.945
PAWR	−0.4	.947	−0.5	.583	0.3	.493
PBXIP1	−0.8	.9	−0.6	.766	−0.4	.63
PCBD1	−0.4	.959	−0.2	.919	−0.2	.915
PCBP1	0.1	.997	0.5	.847	−1.3	.145
PCBP2	0.4	.927	−0.5	.826	0.1	.949
PCDHB14	−0.4	.941	−0.1	.993	0.1	.984
PCMT1	0.1	.992	0.1	.988	0.3	.682
PCOLCE	0.2	.966	−0.6	.789	0.2	.846
PCOLCE2	0.1	.982	−0.5	.586	0.6	.197
PCYOX1	−0.3	.941	−0.1	.942	0.3	.602
PCYT2	0.5	.927	0.2	.933	−0.2	.926
PDAP1	−0.5	.957	−0.6	.68	0.3	.688
PDCD10	0.5	.9	0.4	.826	0.1	.975
PDCD5	0.2	.982	0.1	.989	−0.5	.705
PDCD6	−0.5	.9	0.3	.872	0.3	.811
PDCD6IP	0.1	.99	−0.2	.899	0.4	.647

Supplementary Table III. Continued.

Gene	Log_2FC TAA/ TADA	Adjusted *P* value	Log_2FC TBAD/ TADA	Adjusted *P* value	Log_2FC TAA/ TBAD	Adjusted *P* value
PDCD7	−1	.9	−0.3	.891	−0.3	.785
PDGFC	−0.7	.927	0.3	.826	−0.3	.681
PDHA1	0.7	.9	−1.1	.677	0.1	.972
PDHB	0.4	.966	−0.1	.98	−0.6	.684
PDIA2	0.4	.972	−0.1	.989	0.7	.367
PDIA3	0.1	.982	0.3	.917	0.1	.962
PDIA4	0.2	.977	1	.694	−0.7	.561
PDIA5	0.5	.9	−0.1	.942	0.2	.763
PDIA6	0.2	.967	−0.3	.821	0.5	.388
PDLIM1	−0.4	.9	0.3	.825	0.2	.855
PDLIM2	−0.7	.9	−0.4	.792	0.6	.261
PDLIM3	−0.8	.862	−0.4	.792	−0.1	1.00
PDLIM4	−0.7	.9	−0.5	.821	−0.2	.87
PDLIM5	−0.3	.969	−0.6	.792	−0.3	.825
PDLIM7	−0.9	.862	−0.4	.826	−0.3	.77
PDS5A	−0.4	.912	−0.4	.848	0.1	.945
PDXK	−0.2	.969	−0.6	.815	−0.4	.757
PEA15	−0.4	.927	−0.7	.589	0.3	.654
PEBP1	−0.4	.9	−0.8	.457	0.6	.28
PEF1	0.3	.974	−0.5	.755	0.2	.82
PEPD	−0.2	.982	−0.7	.583	0.3	.691
PF4	0.2	.982	0.7	.674	−0.5	.515
PFDN1	−0.3	.972	−0.8	.225	0.7	.05
PFDN2	−0.2	.982	0.4	.899	−0.3	.898
PFDN5	−0.1	.982	−0.4	.822	0.2	.865
PFKL	−0.2	.982	−0.6	.789	0.5	.607
PFKM	−0.7	.862	−0.4	.762	0.4	.509
PFKP	−0.6	.9	0.1	.993	−0.2	.873
PFN1	−0.1	.982	−0.2	.932	−0.6	.483
PFN2	−0.4	.9	0.3	.899	−0.8	.262
PGAM1	−0.5	.9	−0.1	.934	0.1	.982
PGD	0.1	.982	0.1	.989	−0.4	.457
PGK1	−0.3	.941	−0.5	.789	0.1	.998
PGK2	−0.5	.927	−0.1	.962	0.2	.827
PGLS	−0.1	.982	−0.2	.872	−0.1	.968
PGLYRP2	−0.1	.982	−0.7	.75	0.3	.839
PGM1	−0.3	.903	−0.6	.474	0.6	.185
PGM2	−0.1	.982	−0.6	.668	0.6	.324
PGM3	0.2	.982	−0.2	.892	−0.1	.851
PGM5	−1	.857	−0.6	.704	0.6	.372
PGP	−1.1	.857	−0.3	.853	0.4	.567
PGRMC1	−0.6	.9	−0.5	.808	−0.6	.525
PHB	0.1	.984	−0.9	.67	−0.3	.797
PHB2	−0.1	.982	−0.3	.847	−0.3	.707
PHGDH	−0.7	.862	−0.4	.792	0.4	.463
PHPT1	−0.3	.947	−0.5	.753	0.4	.462

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Supplementary Table III. Continued.

Gene	Log_2FC TAA/ TADA	Adjusted *P* value	Log_2FC TBAD/ TADA	Adjusted *P* value	Log_2FC TAA/ TBAD	Adjusted *P* value
PI4KA	−0.9	.878	−0.7	.677	−0.1	.958
PIK3C3	−0.5	.941	−0.3	.826	0.1	.966
PIMREG	−0.7	.9	−1	.583	0.2	.887
PITHD1	−0.1	.982	−0.5	.826	0.1	.983
PITPNB	−0.5	.927	−1.3	.421	0.6	.505
PITRM1	−0.8	.9	−0.5	.765	0.4	.515
PKD2	−0.8	.862	−0.4	.832	−0.1	.957
PKM	−0.3	.957	−0.4	.866	−0.4	.729
PKP4	−0.9	.966	−0.1	.973	−0.8	.346
PLA2G2A	−0.9	.862	−0.3	.821	0.1	.916
PLAUR	0.5	.972	0.9	.891	−1.7	.447
PLCD1	−0.7	.9	−0.3	.895	−0.6	.518
PLCH1	−0.2	.982	0.2	.962	0.3	.902
PLD3	0.1	.984	−0.3	.906	−0.4	.674
PLEC	0.3	.957	−0.2	.917	0.1	.945
PLG	0.2	.982	−0.6	.792	0.7	.44
PLIN1	−0.5	.912	−0.2	.939	0.4	.571
PLIN3	−0.1	.982	−0.1	.992	0.2	.818
PLOD1	0.2	.982	−0.6	.759	0.2	.863
PLP2	−0.8	.9	−0.7	.657	0.6	.368
PLS3	−0.5	.9	0.3	.917	−0.1	.945
PLTP	0.5	.927	−0.5	.895	−0.4	.812
PLXDC2	−0.3	.969	−0.5	.792	−0.1	.998
PLXNB2	−0.1	.982	−0.5	.826	0.9	.234
PNP	0.4	.929	−0.9	.452	0.7	.28
PODN	0.4	.927	−0.1	.993	−0.1	.974
POLD1	0.5	.974	−0.2	.933	0.5	.441
PON1	0.3	.967	−0.6	.703	0.9	.08
POSTN	0.5	.927	1.4	.761	−0.9	.657
POTEF	−0.4	.966	−0.9	.614	1.2	.093
POTEI	−0.7	.9	−0.2	.952	0.7	.493
POTEJ	−0.4	.941	−1.2	.421	0.9	.258
PPA1	−0.2	.972	−1	.583	0.4	.774
PPA2	0.3	.941	−1	.552	0.6	.484
PPBP	0.3	.969	−0.7	.64	0.5	.483
PPCS	0.1	.982	−0.1	.973	0.4	.588
PPFIBP1	0.4	.927	0.2	.953	0.2	.899
PPIA	−0.3	.947	−0.4	.826	0.4	.587
PPIB	0.1	.984	−0.2	.937	0.5	.451
PPIC	0.3	.959	−0.4	.792	0.2	.862
PPM1F	0.2	.982	−0.2	.933	0.2	.824
PPME1	0.4	.972	0.2	.917	0.1	.945
PPP1CB	−0.7	.9	0.5	.824	−0.4	.728
PPP1CC	−0.1	.982	−0.2	.953	0.5	.688
PPP1R12A	−0.1	.982	−0.2	.932	−0.5	.526
PPP1R12B	−1	.857	0.3	.951	−0.4	.862

Supplementary Table III. Continued.

Gene	Log_2FC TAA/ TADA	Adjusted *P* value	Log_2FC TBAD/ TADA	Adjusted *P* value	Log_2FC TAA/ TBAD	Adjusted *P* value
PPP1R14A	−1.1	.857	−0.1	.942	−0.1	1.00
PPP1R7	0.3	.969	−0.7	.759	−0.4	.688
PPP2R1A	−0.3	.941	−0.7	.762	−0.4	.681
PPP6R3	−0.6	.969	0.3	.917	0.1	.963
PPT1	0.3	.969	−0.1	.934	−0.2	.825
PRAF2	−0.1	.982	−1	.821	0.4	.863
PRDBP	−1	.862	−0.4	.821	0.6	.343
PRDX1	−0.2	.974	−0.3	.891	0.2	.855
PRDX2	0.3	.903	−0.4	.911	−0.7	.506
PRDX3	0.3	.93	−0.4	.746	0.3	.602
PRDX4	0.4	.957	−0.4	.759	0.7	.083
PRDX5	0.1	.982	−0.2	.826	0.4	.262
PRDX6	−0.2	.941	0.4	.862	−0.1	.988
PRELP	−0.1	.982	−0.3	.808	0.3	.402
PRKACA	−0.4	.903	−0.4	.703	0.2	.697
PRKACB	−1.1	.862	−0.9	.497	0.8	.198
PRKAR1A	−0.1	.982	−0.4	.802	0.1	1.00
PRKAR2A	−0.6	.9	−0.6	.821	−0.6	.591
PRKCB	−1.6	.9	−0.4	.762	0.3	.585
PRKCSH	0.1	.982	−0.4	.826	−0.2	.863
PRKG1	−0.9	.857	−1.5	.769	−0.1	.998
PROC	0.3	.954	−0.4	.792	0.5	.441
PROS1	−0.2	.974	−0.3	.911	−0.7	.344
PROSC	0.1	.982	−0.7	.526	0.9	.057
PROX2	−0.6	.9	−1	.288	0.9	.105
PRPF4B	0.3	.981	−0.3	.937	0.3	.834
PRPS1	0.2	.972	−0.3	.917	−0.4	.704
PRR36	−0.3	.981	0.2	.933	0.1	.979
PRSS23	0.2	.982	0.1	.965	0.2	.894
PRTG	0.7	.9	−0.3	.93	−0.1	.998
PRTN3	−0.3	.982	0.2	.942	0.1	.991
PRXL2A	−0.7	.878	−0.9	.638	1.6	.037
PSAP	−0.4	.903	0.5	.826	−0.7	.452
PSIP1	0.1	.982	−1.2	.286	0.6	.416
PSMA1	−0.1	.984	−0.4	.792	0.1	.979
PSMA2	0.1	.982	−0.3	.826	0.4	.544
PSMA3	0.2	.969	−0.7	.583	0.7	.234
PSMA4	0.1	.982	−0.4	.792	0.5	.366
PSMA5	0.1	.982	−0.2	.899	0.4	.497
PSMA6	−0.1	.982	−0.6	.587	0.6	.153
PSMA7	−0.4	.903	−0.6	.526	0.7	.123
PSMB1	−0.2	.976	−0.7	.327	0.7	.083
PSMB2	−0.1	.982	−0.6	.769	0.2	.912
PSMB3	0.1	.982	−0.5	.792	0.3	.728
PSMB4	−0.2	.974	−0.6	.776	0.5	.499
PSMB5	−0.1	.984	−0.8	.474	0.9	.107

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Supplementary Table III. Continued.

Gene	Log_2FC TAA/ TADA	Adjusted *P* value	Log_2FC TBAD/ TADA	Adjusted *P* value	Log_2FC TAA/ TBAD	Adjusted *P* value
PSMB6	−0.1	.997	−0.7	.592	0.5	.409
PSMB7	−0.1	.982	−0.7	.677	0.6	.342
PSMB8	−0.8	.878	−0.5	.718	0.5	.35
PSMB9	0.1	.982	−0.4	.917	0.3	.878
PSMC1	0.2	.982	−1	.583	0.2	.898
PSMC2	−0.1	.982	−0.6	.674	0.7	.21
PSMC3	0.2	.982	−0.2	.917	0.4	.657
PSMC4	−0.1	.982	−0.1	.988	−0.1	.974
PSMC5	−0.2	.969	−0.6	.776	0.7	.286
PSMC6	0.4	.927	−0.3	.826	0.3	.763
PSMD1	−0.1	.982	−0.3	.848	0.1	.945
PSMD11	−0.1	.982	0.3	.895	0.2	.888
PSMD12	−0.2	.982	−0.3	.862	0.3	.811
PSMD13	−0.1	.992	−0.4	.792	0.4	.537
PSMD14	0.2	.982	−0.4	.895	0.2	.906
PSMD2	0.2	.982	−0.5	.792	0.5	.526
PSMD3	−0.1	.982	−0.6	.632	0.7	.133
PSMD5	−0.5	.9	−0.1	.993	0.2	.863
PSMD6	0.1	.982	−0.2	.933	0.1	.945
PSMD7	−0.2	.982	−0.4	.847	−0.2	.836
PSMD9	−0.5	.9	−0.3	.848	0.3	.631
PSME1	0.1	.982	−0.5	.808	0.4	.707
PSME2	0.3	.927	−0.9	.323	0.5	.376
PSMF1	−0.4	.927	−0.4	.75	0.5	.286
PTBP1	0.2	.982	−0.4	.815	0.7	.185
PTGES3	−0.4	.941	−0.4	.816	0.1	.994
PTGIS	−0.9	.857	−0.5	.782	0.6	.328
PTGR1	−0.1	.982	−0.6	.759	0.2	.818
PTK2	−0.5	.9	−0.1	.978	−0.8	.185
PTMA	−0.2	.974	0.4	.866	−0.5	.675
PTMS	−0.4	.903	−0.7	.674	0.2	.835
PTPA	−0.1	.984	−0.3	.862	0.1	.925
PTPN11	−0.2	.972	−0.7	.674	0.3	.784
PTPN13	−0.3	.982	−0.6	.647	0.5	.301
PTPN4	−1	.862	−0.1	.996	−0.2	.814
PTRF	−0.4	.941	0.6	.792	−0.9	.307
PURA	−0.5	.9	0.2	.942	−1.2	.137
PUS10	−0.7	.944	−0.1	.989	−0.4	.707
PXDN	−0.4	.942	−0.3	.865	−0.2	.835
PYGB	−0.5	.903	−1.1	.789	0.5	.825
PYGL	−0.3	.969	−0.5	.815	0.2	.916
PZP	−0.3	.974	−0.5	.792	0.1	.979
QARS1	0.6	.9	0.3	.861	−0.5	.441
QDPR	−0.3	.957	0.4	.869	−0.7	.497
QSOX1	−0.3	.941	0.1	.961	0.5	.532
QTRT1	−0.4	.966	−0.7	.596	0.4	.497

Supplementary Table III. Continued.

Gene	Log_2FC TAA/ TADA	Adjusted *P* value	Log_2FC TBAD/ TADA	Adjusted *P* value	Log_2FC TAA/ TBAD	Adjusted *P* value
RAB10	−0.2	.982	−0.3	.877	−0.1	.97
RAB11B	−0.8	.903	−1	.604	0.6	.483
RAB14	0.2	.982	−0.1	.985	−0.1	.915
RAB18	0.4	.974	0.3	.948	−1.1	.421
RAB21	−0.1	.992	−0.2	.951	0.3	.743
RAB23	−0.9	.857	0.1	.989	0.3	.848
RAB2A	−0.3	.957	−0.4	.818	0.4	.618
RAB35	−0.1	.982	−0.5	.792	−0.5	.578
RAB41	−0.5	.903	−0.6	.706	0.4	.646
RAB5B	−0.7	.878	−0.1	.951	−0.1	1.00
RAB5C	−0.5	.969	−1.4	.225	0.9	.17
RAB7A	0.1	.982	−1	.452	0.3	.714
RAC1	−0.4	.941	−1.7	.459	1.3	.287
RAC3	−0.2	.982	−0.4	.762	0.5	.308
RACK1	0.1	.982	−0.8	.718	0.4	.733
RAD18	−0.3	.982	−0.1	.993	−0.2	.961
RAD23A	−0.5	.927	−0.2	.913	0.2	.739
RAD23B	0.2	.969	0.6	.826	−0.9	.452
RALY	−0.5	.903	−0.7	.769	0.3	.863
RAN	0.1	.982	−0.4	.802	0.5	.287
RANBP1	−0.2	.966	−0.5	.792	0.1	.974
RAP1A	−0.2	.982	−0.1	.998	0.1	.961
RAP1GDS1	−0.2	.982	−0.7	.583	0.5	.441
RARRES2	−0.4	.941	0.3	.934	−0.4	.726
RBBP8NL	−0.9	.9	−0.1	.985	−0.2	.913
RBCK1	−0.3	.957	−0.2	.951	−0.3	.811
RBMX	−0.1	.982	−0.5	.899	−0.5	.757
RBP1	−0.8	.862	−1.1	.391	0.8	.234
RBP4	0.3	.946	−0.3	.826	0.3	.726
RBPMS	−0.6	.9	−0.5	.808	−0.4	.65
RBX1	0.9	.9	−0.9	.524	1.1	.05
RCN1	−0.3	.969	−0.6	.759	0.1	1.00
RCN3	0.2	.982	−0.8	.792	1.6	.068
RDX	0.1	.982	−0.6	.718	0.4	.633
RECQL	−0.1	.992	0.1	.993	0.1	.913
REEP5	0.2	.982	0.6	.815	−0.6	.658
REEP6	−0.4	.957	−0.2	.942	0.2	.906
RFTN1	−0.2	.979	−0.6	.808	0.8	.391
RGS22	−0.5	.941	−0.6	.808	0.2	.863
RHBDF1	−0.8	.9	−0.5	.792	0.3	.726
RHOA	−0.1	.984	−1.4	.324	0.9	.229
RHOB	−0.4	.93	−0.6	.822	−0.3	.855
RHOC	−0.5	.941	0.2	.953	−0.2	.883
RHOC	−0.5	.941	0.1	.998	−0.4	.638
RHOG	−0.2	.982	−0.5	.833	0.1	.995
RIC8A	−0.1	.982	0.2	.923	−0.4	.657

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Supplementary Table III. Continued.

Gene	Log_2FC TAA/ TADA	Adjusted *P* value	Log_2FC TBAD/ TADA	Adjusted *P* value	Log_2FC TAA/ TBAD	Adjusted *P* value
RIF1	−0.3	.957	0.4	.818	−0.4	.525
RILPL1	−0.3	.963	−0.4	.826	0.1	.945
RINT1	−0.7	.941	−0.4	.792	0.2	.811
RNASE1	0.6	.912	−1.2	.762	0.5	.797
RNASE4	−0.4	.957	−0.2	.972	0.7	.487
RNF31	−0.2	.982	0.1	.986	−0.4	.684
RNH1	−0.3	.903	−0.7	.819	0.6	.688
RNPEP	0.2	.982	−0.2	.899	−0.2	.825
RPL10	−0.1	.997	0.1	.993	0.2	.871
RPL10A	−0.2	.982	0.1	.985	−0.1	.962
RPL11	−0.2	.982	−0.2	.942	−0.1	.99
RPL12	−0.1	.982	−0.5	.826	0.4	.739
RPL13	−0.2	.982	0.1	.993	−0.2	.897
RPL14	0.1	.982	−0.4	.826	0.3	.818
RPL15	−0.1	.982	−0.4	.848	0.4	.593
RPL17	0.2	.982	0.1	.973	−0.2	.893
RPL18	−0.2	.982	−0.4	.836	0.6	.487
RPL18A	−0.1	.982	−0.5	.818	0.3	.77
RPL22	−0.4	.941	0.3	.899	−0.4	.72
RPL23	0.2	.982	−0.5	.818	0.1	.952
RPL23A	0.1	.982	−0.2	.917	0.3	.688
RPL24	0.5	.927	−0.4	.808	0.5	.447
RPL27	−0.3	.972	0.3	.933	0.3	.82
RPL27A	−0.1	.992	−0.7	.792	0.4	.74
RPL28	−0.1	.982	−0.3	.899	0.3	.8
RPL29	0.2	.974	−0.3	.891	0.2	.827
RPL3	−0.1	.982	−0.3	.891	0.5	.523
RPL30	−0.6	.903	−0.2	.917	0.2	.913
RPL31	−0.1	.982	−0.9	.653	0.4	.744
RPL34	0.4	.957	−0.7	.792	0.6	.543
RPL35	−0.7	.927	0.4	.899	0.1	.968
RPL38	0.7	.927	−1.2	.674	0.5	.719
RPL4	0.1	.997	0.3	.944	0.5	.753
RPL5	−0.2	.981	−0.3	.917	0.3	.825
RPL6	−0.2	.982	−0.5	.818	0.3	.811
RPL7	−0.2	.974	−0.4	.818	0.3	.757
RPL7A	−0.1	.997	−0.1	.988	−0.2	.863
RPL8	0.3	.978	−0.2	.942	0.2	.888
RPL9	−0.1	.992	−0.5	.859	0.7	.487
RPLP0	−0.3	.974	−0.4	.872	0.4	.757
RPLP1	−0.2	.982	−0.5	.826	0.3	.881
RPLP2	−0.3	.966	−0.5	.819	0.3	.742
RPN1	0.2	.972	−0.5	.792	0.2	.811
RPN2	0.1	.982	−0.1	.972	0.3	.726
RPS10	−0.2	.982	0.1	.974	0.1	.974
RPS11	−0.1	.982	−0.6	.78	0.4	.655

Supplementary Table III. Continued.

Gene	Log$_2$FC TAA/ TADA	Adjusted *P* value	Log$_2$FC TBAD/ TADA	Adjusted *P* value	Log$_2$FC TAA/ TBAD	Adjusted *P* value
RPS12	0.2	.957	−0.3	.859	0.2	.824
RPS13	0.1	.993	−0.1	.989	0.2	.703
RPS14	−0.5	.903	−0.6	.792	0.6	.483
RPS15A	−0.2	.982	−0.6	.792	0.1	.962
RPS16	−0.4	.957	−0.1	.973	−0.1	.961
RPS18	−0.1	.982	−0.5	.815	0.2	.887
RPS19	−0.2	.974	−0.2	.935	0.1	.962
RPS2	−0.1	.982	−0.5	.742	0.4	.595
RPS20	−0.1	.982	−0.2	.953	0.1	.962
RPS21	−0.2	.982	−0.4	.853	0.3	.801
RPS23	−0.2	.982	−0.8	.615	0.7	.342
RPS24	−0.6	.903	0.3	.917	−0.4	.697
RPS25	−0.1	.997	−0.4	.899	−0.3	.815
RPS27L	−1.9	.857	−0.4	.848	0.4	.705
RPS28	−0.3	.982	−1.2	.674	−0.8	.532
RPS3	0.1	.982	1.1	.792	−1.4	.363
RPS3A	−0.1	.982	−0.4	.821	0.4	.506
RPS4X	0.1	.982	−0.2	.917	0.2	.894
RPS5	0.1	.984	0.1	.985	0.1	.989
RPS6	0.2	.982	−0.2	.933	0.2	.824
RPS6KA2	−0.3	.982	0.4	.792	−0.3	.704
RPS6KA3	−1.7	.857	−1.1	.718	0.8	.506
RPS7	−0.3	.969	−1.9	.442	0.3	.909
RPS8	−0.1	.982	−0.5	.821	0.2	.889
RPS9	−0.3	.946	0.1	.974	−0.1	.901
RPSA	0.3	.969	−0.1	.966	−0.3	.8
RRAD	−0.8	.9	−0.6	.745	0.8	.173
RRAS	−0.7	.878	−0.7	.821	−0.2	.916
RRBP1	0.8	.862	−0.3	.888	−0.5	.609
RSAD2	−0.9	.9	0.3	.891	0.6	.483
RSU1	−0.4	.927	0.3	.942	−1.2	.347
RTCB	−0.4	.927	−0.4	.812	0.1	.97
RTN4	0.1	.982	−0.2	.899	−0.2	.863
RTRAF	−0.2	.982	0.2	.934	−0.1	.939
RUNDC3A	0.2	.982	−0.5	.679	0.4	.471
RUVBL1	−0.1	.982	−0.9	.75	1	.306
RUVBL2	0.1	.984	−0.1	.951	0.1	.965
S100A11	0.1	.982	−0.3	.826	0.4	.592
S100A13	0.2	.982	−0.2	.922	0.2	.753
S100A16	−0.1	.982	−0.3	.877	0.4	.59
S100A4	−0.4	.903	−0.4	.821	0.3	.719
S100A6	−0.2	.969	−0.2	.917	−0.3	.763
S100A8	−0.4	.963	−0.5	.699	0.3	.578
SAA1	−1.9	.857	0.1	.993	−0.5	.726
SAMHD1	−0.1	.982	−1.7	.474	−0.2	.931
SAMM50	−1.2	.862	−0.7	.718	0.6	.437

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Supplementary Table III. Continued.

Gene	Log_2FC TAA/ TADA	Adjusted *P* value	Log_2FC TBAD/ TADA	Adjusted *P* value	Log_2FC TAA/ TBAD	Adjusted *P* value
SARS1	−0.3	.941	−0.9	.762	−0.3	.883
SBDS	−0.6	.9	−0.5	.785	0.2	.825
SBSPON	−0.5	.903	−0.8	.583	0.3	.811
SCARB2	−0.5	.946	−0.2	.939	−0.4	.699
SCN8A	−0.6	.941	−0.3	.934	−0.3	.865
SCRN1	−0.6	.862	−0.5	.853	−0.1	.979
SCUBE3	−0.7	.9	−0.7	.586	0.1	.921
SCYL2	−0.8	.941	0.3	.916	−0.9	.187
SDHA	−0.2	.982	−2	.537	1.2	.474
SDHB	−0.3	.972	−0.5	.818	0.3	.729
SEC11B	−0.1	.99	−0.1	.983	−0.2	.868
SEC13	0.2	.982	−0.6	.762	0.6	.441
SEC14L5	−0.7	.9	−0.3	.904	0.4	.674
SEC22B	0.3	.974	−0.9	.745	0.2	.898
SEC23A	0.3	.972	0.3	.872	−0.1	.941
SEC31A	0.4	.927	−0.1	.989	0.3	.765
SELENBP1	−0.2	.927	0.3	.862	0.1	.932
SELENOM	−0.2	.982	−0.6	.391	0.4	.335
SELENOP	−0.2	.982	0.2	.951	−0.3	.757
SEMA3B	−0.8	.862	−0.5	.808	0.3	.734
SEMA5B	−0.9	.9	−0.2	.961	−0.7	.399
SERBP1	0.1	.982	−2	.323	1.1	.36
SERPINA1	−0.1	.988	0.2	.951	−0.1	.974
SERPINA10	0.2	.982	−1.2	.225	1.1	.025
SERPINA3	−0.5	.903	−0.8	.762	0.9	.337
SERPINA4	−0.1	.982	−1.1	.401	0.6	.389
SERPINA5	−0.5	.9	−0.4	.815	0.3	.702
SERPINA6	0.1	.984	−0.4	.826	−0.2	.862
SERPINA7	0.3	.966	−0.8	.519	0.9	.135
SERPINB1	−0.2	.982	−1	.363	1.2	.03
SERPINB6	−0.5	.941	−0.1	.998	−0.1	.894
SERPINC1	−0.2	.969	−0.5	.826	0.1	.991
SERPIND1	−0.2	.972	−0.5	.717	0.3	.613
SERPINE2	0.2	.982	−0.9	.346	0.7	.161
SERPINF1	0.3	.957	−0.5	.848	0.7	.572
SERPINF2	−0.2	.982	−0.5	.706	0.7	.128
SERPING1	−0.3	.957	0.2	.944	−0.3	.705
SERPINH1	−0.1	.982	−1	.346	0.8	.198
SETD1B	−0.5	.927	−0.2	.933	0.2	.911
SF3B6	0.2	.982	−1.1	.421	0.7	.366
SFPQ	0.6	.9	−1.5	.497	1.6	.094
SFRP1	−0.4	.941	0.3	.907	0.4	.681
SFXN3	−0.3	.941	−0.2	.933	−0.2	.863
SGCD	−0.9	.857	−0.5	.791	0.2	.863
SH3BGRL	−0.3	.947	−0.1	.985	−0.9	.123
SH3BGRL3	0.1	.982	−0.8	.452	0.6	.329

Supplementary Table III. Continued.

Gene	Log_2FC TAA/ TADA	Adjusted *P* value	Log_2FC TBAD/ TADA	Adjusted *P* value	Log_2FC TAA/ TBAD	Adjusted *P* value
SH3BP5	−0.4	.927	−0.5	.759	0.6	.305
SH3GLB1	−0.2	.982	−0.2	.917	−0.2	.825
SH3GLB2	−0.1	.982	−0.4	.821	0.2	.791
SH3RF2	−0.4	.947	−0.7	.722	0.6	.441
SHMT1	−0.2	.982	0.5	.815	−0.8	.276
SIN3B	−0.2	.982	−0.3	.899	0.1	.93
SKP1	−0.2	.982	−1	.667	0.8	.394
SLC22A17	−0.5	.959	−0.4	.816	0.3	.739
SLC25A1	−0.3	.957	−1.9	.391	1.4	.226
SLC25A11	0.1	.982	−0.3	.899	−0.1	.97
SLC25A12	0.2	.974	−0.2	.937	0.3	.768
SLC25A24	−0.1	.982	0.5	.808	−0.3	.787
SLC25A3	0.1	.984	0.1	.988	−0.2	.916
SLC25A4	−1	.857	−0.1	.993	0.1	.961
SLC25A5	0.1	.997	−0.3	.928	−0.8	.313
SLC27A2	0.1	.982	−0.5	.891	0.5	.753
SLC27A3	−0.1	.983	−0.6	.713	0.6	.286
SLC2A1	0.2	.982	−0.2	.956	0.1	.961
SLC2A12	−1	.857	0.1	.988	0.2	.916
SLC30A10	−0.4	.982	−1.2	.324	0.3	.825
SLC3A2	0.6	.9	−1.4	.718	1	.514
SLC4A1	0.9	.862	0.1	.972	0.5	.447
SLC7A6	−0.5	.941	−0.2	.933	1.1	.164
SLC9A3R1	−0.3	.982	0.2	.973	−0.6	.567
SLC9A5	−0.7	.903	−1.1	.583	0.9	.339
SLC9A8	−1.4	.857	−1.5	.497	0.8	.526
SLMAP	−0.8	.862	0.1	.98	−1.5	.084
SLPI	−1	.862	−0.2	.951	−0.6	.328
SLX4	−1	.9	0.5	.826	−1.5	.08
SMARCA5	−0.5	.9	−0.9	.792	−0.1	.971
SMOC2	−0.2	.982	−0.6	.699	0.2	.894
SMTN	−0.9	.857	0.1	.988	−0.2	.84
SNCA	0.4	.927	−0.4	.826	−0.5	.467
SNCG	−1	.862	−0.8	.604	1.2	.058
SND1	0.3	.941	−0.6	.812	−0.5	.688
SNRNP200	−0.7	.94	0.4	.815	−0.1	.928
SNRPD1	−0.3	.974	−1.1	.742	0.5	.787
SNRPD2	0.3	.957	−0.6	.78	0.4	.691
SNRPD3	0.1	.982	−0.1	.988	0.4	.688
SNTB2	−0.5	.9	−0.6	.759	0.7	.324
SNX1	0.4	.941	−0.4	.821	−0.1	.911
SNX12	−0.6	.9	0.1	.994	0.3	.674
SNX18	−0.4	.927	−0.3	.917	−0.4	.664
SNX2	0.3	.965	0.1	.989	−0.5	.584
SNX29	−0.5	.927	−0.3	.899	0.5	.478
SNX3	−0.1	.972	−0.7	.77	0.3	.863

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Supplementary Table III. Continued.

Gene	Log_2FC TAA/ TADA	Adjusted *P* value	Log_2FC TBAD/ TADA	Adjusted *P* value	Log_2FC TAA/ TBAD	Adjusted *P* value
SNX6	−0.3	.957	−0.1	1.00	−0.1	.815
SNX9	−0.8	.9	−0.6	.574	0.4	.444
SOD1	−0.2	.941	−0.8	.713	−0.1	1.00
SOD2	−0.1	.993	−0.3	.785	0.1	.863
SOD3	−1	.862	−0.6	.537	0.6	.179
SOGA1	−0.1	.984	−0.3	.899	−0.7	.394
SON	−0.2	.982	−0.6	.833	0.5	.719
SORBS1	−0.8	.862	−0.2	.953	−0.1	.958
SORBS2	−1	.857	−0.3	.919	−0.6	.452
SORBS3	−0.6	.9	−0.6	.792	−0.5	.635
SORD	−0.8	.9	−0.3	.912	−0.4	.624
SOST	−0.8	.9	−0.6	.814	−0.3	.863
SOX6	−0.2	.982	0.4	.911	−1.1	.285
SPARC	0.4	.93	−0.9	.327	0.7	.128
SPARCL1	−0.6	.862	−0.2	.951	0.5	.495
SPCS2	2	.857	−1	.286	0.5	.451
SPCS3	0.3	.972	1	.721	1	.334
SPON1	0.3	.947	0.1	.998	0.3	.808
SPR	−0.7	.9	0.2	.944	0.2	.862
SPTA1	0.6	.9	−0.7	.75	0.1	.985
SPTAN1	−0.2	.982	0.1	.988	0.6	.523
SPTB	0.7	.9	−0.6	.725	0.5	.529
SPTBN1	−0.2	.982	0.1	.993	0.7	.377
SQOR	0.2	.982	−0.4	.815	0.3	.757
SQRD	0.2	.982	−0.6	.776	0.7	.301
SREBF2	−0.4	.982	0.2	.942	−0.1	.988
SRFBP1	−0.7	.9	−0.1	.993	−0.4	.862
SRGAP3	0.3	.982	−1.2	.497	0.5	.652
SRI	−0.1	.974	0.2	.966	0.2	.953
SRM	0.2	.972	−0.2	.844	0.1	.898
SRP9	−0.3	.963	−0.4	.808	0.6	.326
SRPX	−0.7	.916	−0.5	.792	0.3	.784
SRRT	−0.4	.946	0.5	.861	−1.1	.28
SRSF1	−0.4	.944	0.6	.792	−0.9	.209
SRSF3	−0.3	.957	−0.5	.812	0.2	.911
SRSF7	−0.6	.9	−0.1	.997	−0.3	.752
SSB	−0.4	.9	−0.1	.989	−0.5	.552
SSBP1	0.4	.972	−0.8	.459	0.4	.564
SSR1	0.6	.9	1	.632	−0.7	.467
SSR4	0.1	.982	0.1	.989	0.5	.452
SSTR2	−1.2	.9	−0.3	.942	0.3	.84
ST3GAL6	−1.4	.857	−1.6	.701	0.4	.863
STAB1	−0.4	.941	−0.3	.933	−1.2	.203
STAMBP	0.7	.972	−0.6	.808	0.2	.913
STAT1	−0.1	.982	0.5	.942	0.3	.945
STAT6	−0.3	.957	−0.6	.826	0.5	.707

Supplementary Table III. Continued.

Gene	Log$_2$FC TAA/ TADA	Adjusted *P* value	Log$_2$FC TBAD/ TADA	Adjusted *P* value	Log$_2$FC TAA/ TBAD	Adjusted *P* value
STIP1	−0.2	.96	0.1	.986	−0.3	.688
STK25	−0.7	.947	−0.6	.583	0.4	.453
STK31	0.7	.9	−0.6	.897	−0.1	.966
STN1	−0.5	.922	−0.3	.936	1	.35
STOM	0.2	.982	−1.9	.225	1.4	.064
STT3A	−0.1	.982	0.3	.93	−0.1	.968
STX7	−0.2	.972	−0.1	.997	−0.1	.962
STXBP3	−0.1	.982	−0.3	.822	0.2	.862
SUCLA2	0.1	.982	−0.3	.809	0.3	.647
SUCLG1	−0.2	.982	−0.5	.679	0.6	.28
SUCLG2	−0.1	.982	−0.6	.853	0.4	.811
SULF1	0.1	.988	−0.4	.815	0.4	.654
SUMF2	−0.6	.9	0.3	.861	−0.3	.753
SUN2	−0.7	.864	−0.5	.836	−0.2	.878
SUSD2	−0.5	.927	−0.1	.985	−0.7	.354
SUSD5	−0.7	.9	−0.2	.965	−0.4	.707
SVIL	0.1	.988	0.1	.989	−0.8	.346
SYG	0.3	.966	0.2	.917	−0.2	.862
SYHC	−0.1	.982	0.1	.988	0.3	.812
SYNCRIP	0.2	.979	−0.3	.88	0.3	.799
SYNE1	−0.6	.9	−0.1	.966	0.3	.743
SYNM	−0.2	.974	−0.4	.831	−0.2	.865
SYNPO	−0.2	.982	−0.1	.961	−0.1	.912
SYNPO2	−0.5	.9	0.2	.941	−0.3	.719
SYPL1	−0.6	.927	−0.1	.972	−0.4	.59
TAGLN	−1.2	.857	−0.5	.839	−0.1	.963
TAGLN2	−0.4	.927	−0.8	.769	−0.5	.668
TALDO1	0.2	.957	−0.5	.792	0.1	.945
TARDBP	−0.1	.982	−0.2	.897	0.3	.447
TARS1	0.4	.941	−0.6	.704	0.5	.416
TARS2	−0.7	.929	0.1	.973	0.3	.757
TASOR2	−0.5	.927	−0.9	.808	0.2	.945
TAX1BP3	−0.7	.903	0.2	.957	−0.6	.492
TBC1D5	−1.1	.862	−0.8	.792	0.1	.962
TBCA	−0.5	.9	−0.2	.961	−1	.278
TBCB	−0.5	.9	−0.7	.624	0.2	.82
TCP1	−0.2	.982	−0.7	.519	0.3	.769
TENT2	0.1	.982	−0.4	.792	0.3	.691
TES	−0.6	.9	−0.3	.934	0.4	.811
TF	−0.2	.974	−0.1	.989	−0.5	.363
TFEB	−0.9	.941	−1	.346	0.8	.157
TFG	0.1	.992	−1.1	.821	0.2	.956
TGFB1	0.2	.982	−0.3	.899	0.3	.762
TGFB1I1	−0.9	.857	0.8	.708	−0.7	.438
TGFBI	−0.3	.969	−0.3	.891	−0.7	.368
TGM2	−0.8	.862	−0.3	.847	0.1	.945

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Supplementary Table III. Continued.

Gene	Log_2FC TAA/ TADA	Adjusted *P* value	Log_2FC TBAD/ TADA	Adjusted *P* value	Log_2FC TAA/ TBAD	Adjusted *P* value
TH	−1.2	.862	−0.5	.792	−0.3	.72
THBS1	1.3	.857	−0.3	.933	−1	.343
THBS2	0.4	.97	0.2	.953	1.1	.16
THOP1	−0.5	.927	0.1	.985	0.3	.84
THSD1	−0.6	.862	−1.1	.508	0.6	.497
THSD4	−0.3	.941	0.2	.904	−0.8	.135
THTPA	1.6	.862	0.5	.691	−0.7	.094
THY1	0.6	.9	1.1	.792	0.6	.761
TIMP1	0.8	.9	−0.4	.826	1	.179
TIMP2	−0.4	.957	−0.1	.994	0.8	.409
TIMP3	1	.878	−0.6	.808	0.2	.863
TINAGL1	−1.1	.857	0.2	.95	0.8	.447
TJP2	0.3	.981	−0.2	.942	−1	.182
TKT	−0.3	.9	0.3	.895	−0.1	.957
TLE7	−0.3	.927	−0.5	.401	0.3	.447
TLN1	−0.2	.974	−0.5	.632	0.3	.671
TLN2	−0.4	.941	0.2	.904	−0.4	.557
TMC3	0.2	.982	0.2	.933	−0.5	.489
TMCC2	0.7	.903	−0.4	.932	0.6	.791
TMED7	−0.4	.941	−0.7	.792	1.3	.135
TMEM109	−0.5	.9	−0.4	.826	0.1	.979
TMEM198	−0.3	.972	−0.6	.674	0.2	.84
TMEM214	−0.7	.9	−1.1	.586	0.8	.406
TMEM33	−0.6	.969	−0.2	.933	−0.5	.623
TMEM43	−0.2	.974	0.5	.917	−1	.526
TMEM67	−1.2	.862	−0.3	.904	0.1	.978
TMOD1	−0.7	.862	−0.9	.762	−0.3	.84
TMSB4X	0.1	.988	−0.7	.656	−0.1	.97
TNC	−0.2	.982	−0.3	.896	0.4	.74
TNFRSF11B	0.1	.984	−0.7	.808	0.5	.676
TNFSF13	−0.4	.941	−0.4	.83	0.4	.623
TNN	−0.2	.982	−0.1	.986	−0.4	.72
TNPO1	−0.2	.982	−1.2	.391	1.1	.128
TNPO2	0.4	.972	−0.2	.899	0.1	.913
TNRC6C	−0.4	.969	−0.7	.826	1.1	.397
TNS1	−0.8	.862	−1.9	.225	1.6	.044
TNS2	−0.1	.982	0.1	.988	−0.8	.273
TNXB	−0.8	.857	0.2	.916	−0.3	.743
TOLLIP	−0.1	.982	−0.9	.392	0.1	.933
TOM1	−0.3	.967	0.4	.847	−0.5	.616
TOM1L2	0.5	.9	−0.5	.802	0.2	.825
TOR1AIP1	−0.3	.947	0.5	.792	−0.1	1.00
TPD52L2	0.1	.992	0.3	.826	−0.6	.334
TPI1	−0.4	.9	−0.5	.792	0.5	.489
TPM1	−0.9	.862	−0.5	.67	0.2	.878
TPM2	−1.3	.862	−0.7	.78	−0.3	.811

Supplementary Table III. Continued.

Gene	Log_2FC TAA/ TADA	Adjusted *P* value	Log_2FC TBAD/ TADA	Adjusted *P* value	Log_2FC TAA/ TBAD	Adjusted *P* value
TPM3	0.4	.9	−0.7	.815	−0.6	.626
TPM4	−0.1	.982	−0.3	.848	0.6	.198
TPP1	0.6	.9	−0.3	.826	0.2	.77
TPP2	−0.7	.9	−0.1	.966	0.7	.286
TPT1	−0.3	.974	−0.8	.721	0.2	.911
TRIM38	−1.6	.857	−0.5	.853	0.2	.916
TRIOBP	−0.1	.982	−0.8	.808	−0.8	.561
TRIP6	0.1	.982	0.5	.792	−0.6	.42
TSG101	−0.1	.99	0.4	.853	−0.3	.811
TSN	0.1	.993	−0.5	.821	0.4	.641
TTN	−0.1	.988	−0.2	.914	0.3	.8
TTR	0.1	.984	−0.6	.718	0.5	.378
TTYH2	−0.6	.862	−0.7	.583	0.7	.179
TUBA4A	0.1	.982	−0.1	.951	−0.5	.363
TUBB	0.1	.987	0.1	.988	0.1	.893
TUBB1	−0.1	.99	−0.5	.792	0.6	.441
TUBB2A	0.1	.982	0.6	.899	−0.6	.753
TUBB4A	0.5	.969	−0.4	.815	0.5	.521
TUBB4B	−0.3	.974	0.4	.93	0.2	.962
TUBB6	−0.1	.982	−0.9	.552	0.7	.352
TUFM	0.1	.982	−0.4	.818	0.4	.697
TUT7	−0.6	.903	−0.2	.917	0.2	.769
TVC2	−1	.862	−0.4	.895	−0.3	.84
TWF1	−0.4	.93	−0.6	.674	0.3	.705
TWF2	0.3	.982	0.3	.933	0.1	1.00
TXN	−0.3	.957	−0.4	.792	0.2	.849
TXNDC12	1.1	.862	0.9	.755	0.2	.916
TXNDC17	−0.4	.9	−0.7	.401	0.4	.441
TXNDC5	0.3	.957	−0.5	.792	0.7	.21
TXNL1	−0.2	.957	−0.6	.477	0.4	.344
TXNRD1	−0.4	.912	−0.6	.668	0.3	.734
TYMP	0.5	.9	−0.2	.932	0.7	.328
TYRP1	−0.5	.941	−0.7	.792	0.2	.878
U2AF2	0.5	.912	0.2	.944	0.3	.737
UAP1	−0.6	.9	−0.1	.973	−0.5	.59
UBA1	−0.2	.941	−0.3	.808	0.1	.902
UBAP2L	0.2	.969	0.1	.993	0.2	.8
UBE2I	−0.5	.903	−0.1	.978	−0.4	.654
UBE2K	0.4	.941	−0.4	.808	0.7	.199
UBE2L3	0.1	.992	−0.1	.989	0.1	.968
UBE2M	−0.2	.982	−0.3	.917	0.2	.913
UBE2N	−0.4	.941	−0.3	.933	−0.2	.863
UBE2O	−1.4	.857	−0.6	.818	−0.9	.306
UBE2V1	0.1	.982	−0.2	.951	0.2	.841
UBL5	−0.7	.862	−0.8	.583	0.2	.911
UBR4	−0.9	.903	0.4	.934	−1.2	.399

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Supplementary Table III. Continued.

Gene	Log_2FC TAA/ TADA	Adjusted *P* value	Log_2FC TBAD/ TADA	Adjusted *P* value	Log_2FC TAA/ TBAD	Adjusted *P* value
UCHL1	−0.4	.927	−0.7	.703	0.3	.76
UFC1	−0.3	.903	−0.5	.614	0.3	.693
UFL1	−0.1	.993	−0.4	.844	0.4	.701
UFM1	−0.1	.982	−0.9	.457	0.8	.145
UGDH	−0.3	.974	−0.2	.933	−0.1	.968
UGGT1	0.4	.941	0.4	.822	−0.1	.974
UGP2	−0.3	.9	−0.2	.822	−0.1	.913
UNC45A	−0.2	.982	−0.5	.821	0.3	.761
UQCR10	0.5	.903	0.2	.922	0.3	.779
UQCRC1	0.3	.966	0.1	.982	0.3	.825
UQCRC2	0.3	.972	0.3	.895	−0.1	.977
UQCRH	−0.1	.982	−0.3	.892	0.3	.843
USO1	−0.6	.9	−1.1	.431	0.6	.463
USP14	−0.1	.982	−0.5	.792	0.4	.561
USP15	−1	.862	−0.5	.855	−0.6	.581
USP17L13	0.1	.99	−0.4	.762	0.5	.391
USP17L18	−0.2	.974	−0.3	.891	0.1	.961
USP17L19	−0.9	.862	−0.8	.721	−0.1	.958
USP17L20	0.3	.967	−0.3	.853	0.5	.409
USP17L22	0.1	.982	−0.2	.911	0.3	.744
USP5	−0.1	.997	−0.1	.951	0.1	.911
UTP14A	−0.7	.903	−0.9	.759	0.2	.902
UTRO	−0.3	.941	−0.3	.853	−0.1	.989
VAPA	0.1	.982	−0.1	.989	0.2	.943
VASP	0.1	.992	0.3	.797	−0.3	.543
VAT1	−0.1	.988	−0.4	.808	0.3	.572
VCAN	−0.7	.9	0.3	.922	−0.9	.286
VCL	−0.6	.862	−0.2	.933	−0.4	.457
VCP	0.2	.972	−0.1	.944	0.3	.652
VDAC1	0.3	.9	−0.1	.988	0.4	.402
VDAC2	0.3	.966	−0.4	.826	0.6	.342
VDAC3	0.2	.982	0.3	.917	−0.2	.922
VILL	−0.3	.969	−1.5	.225	1.2	.071
VIM	−0.4	.9	−0.4	.816	−0.1	.962
VIRMA	−0.9	.857	−0.3	.861	−0.6	.409
VPS11	−0.2	.982	−0.1	.988	−0.1	.931
VPS29	−0.1	.982	−0.1	.972	0.1	.974
VPS35	−0.4	.941	−0.5	.759	0.2	.8
VPS4B	0.1	.982	0.1	1.00	0.1	.968
VTN	0.1	.982	−0.3	.899	0.3	.715
VWA1	−0.3	.976	−0.4	.826	0.2	.873
VWA3A	−0.1	.984	0.3	.858	−0.4	.674
VWA3B	−0.2	.982	−1	.674	0.8	.408
WASHC1	0.2	.982	0.4	.946	−0.3	.944
WASHC4	−2.2	.857	−0.3	.944	−1.9	.108
WBP11	−1.1	.862	0.2	.946	−1.3	.188

Supplementary Table III. Continued.

Gene	Log_2FC TAA/ TADA	Adjusted *P* value	Log_2FC TBAD/ TADA	Adjusted *P* value	Log_2FC TAA/ TBAD	Adjusted *P* value
WDR1	−0.4	.862	−0.3	.819	−0.2	.71
WDR76	−0.2	.974	−0.8	.474	0.7	.262
WDR82	−0.5	.966	−0.2	.973	−0.4	.84
WDR83OS	−1	.872	0.1	.974	−1.1	.26
WISP2	−1.2	.857	−0.7	.759	−0.5	.526
WRAP73	−1.2	.862	−1.3	.583	0.1	.968
WTIP	−0.7	.927	−0.6	.826	−0.1	.971
XDH	−0.5	.934	0.2	.962	−0.6	.526
XPO1	−0.2	.982	−0.1	.993	−0.2	.894
XRCC5	−0.2	.982	−0.3	.891	0.2	.9
XRCC6	−0.4	.903	−0.4	.802	−0.1	1.00
XRN1	−1.1	.9	−0.9	.762	−0.2	.945
YAP1	−0.3	.969	−0.4	.808	0.2	.84
YKT6	−0.5	.903	−0.5	.8	0.1	.993
YPEL1	−1.1	.9	−1.1	.742	−0.1	1.00
YWHAB	−0.2	.941	−0.3	.808	0.1	.916
YWHAE	−0.1	.982	−0.4	.792	0.4	.526
YWHAG	−0.4	.9	−0.5	.583	0.2	.795
YWHAH	−0.1	.982	−0.4	.792	0.3	.613
YWHAQ	−0.4	.903	−0.4	.815	−0.1	.998
YWHAZ	−0.1	.982	−0.2	.891	0.2	.825
ZBTB21	−0.8	.862	0.1	.993	−0.8	.287
ZC2HC1C	−0.8	.9	0.4	.891	−1.1	.187
ZMYND8	−0.5	.927	0.2	.934	−0.7	.431
ZNF350	1.5	.862	−0.1	.985	1.6	.157
ZNF385A	−1.3	.862	0.1	.998	−1.3	.287
ZNF479	−0.4	.903	−0.3	.853	−0.2	.886
ZNF507	−0.4	.947	−0.9	.634	0.5	.563
ZNF597	−0.8	.9	−0.8	.762	−0.1	.974
ZSCAN9	−0.6	.974	−0.3	.973	−0.4	.902
ZSWIM9	−0.3	.957	−1.1	.327	0.8	.179
ZYX	−0.2	.969	−0.1	.983	−0.2	.84

Log_2FC, Log_2 fold change; *TAA*, thoracic aorta aneurysm; *TADA*, thoracic aorta dissection and aneurysm; *TBAD*, type B aortic dissection.
[a]False discovery rate.