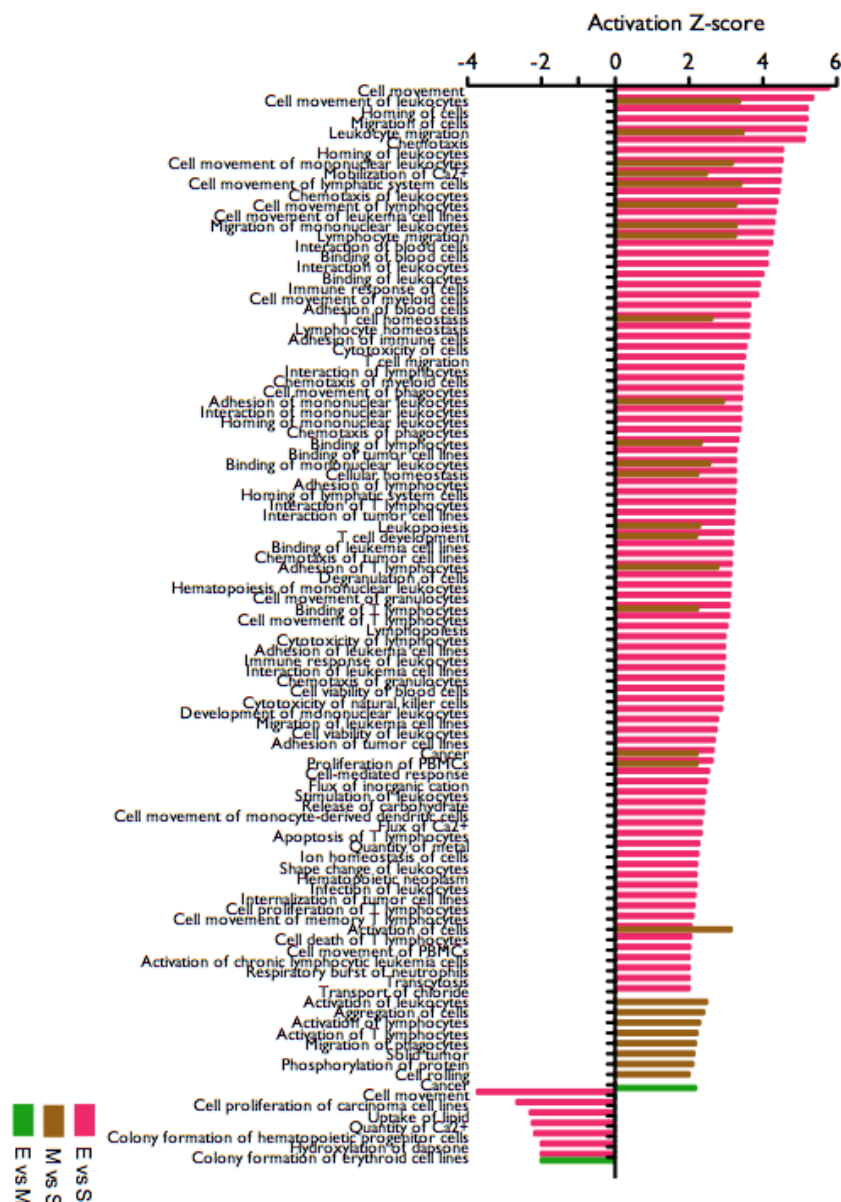


Online Supplement:

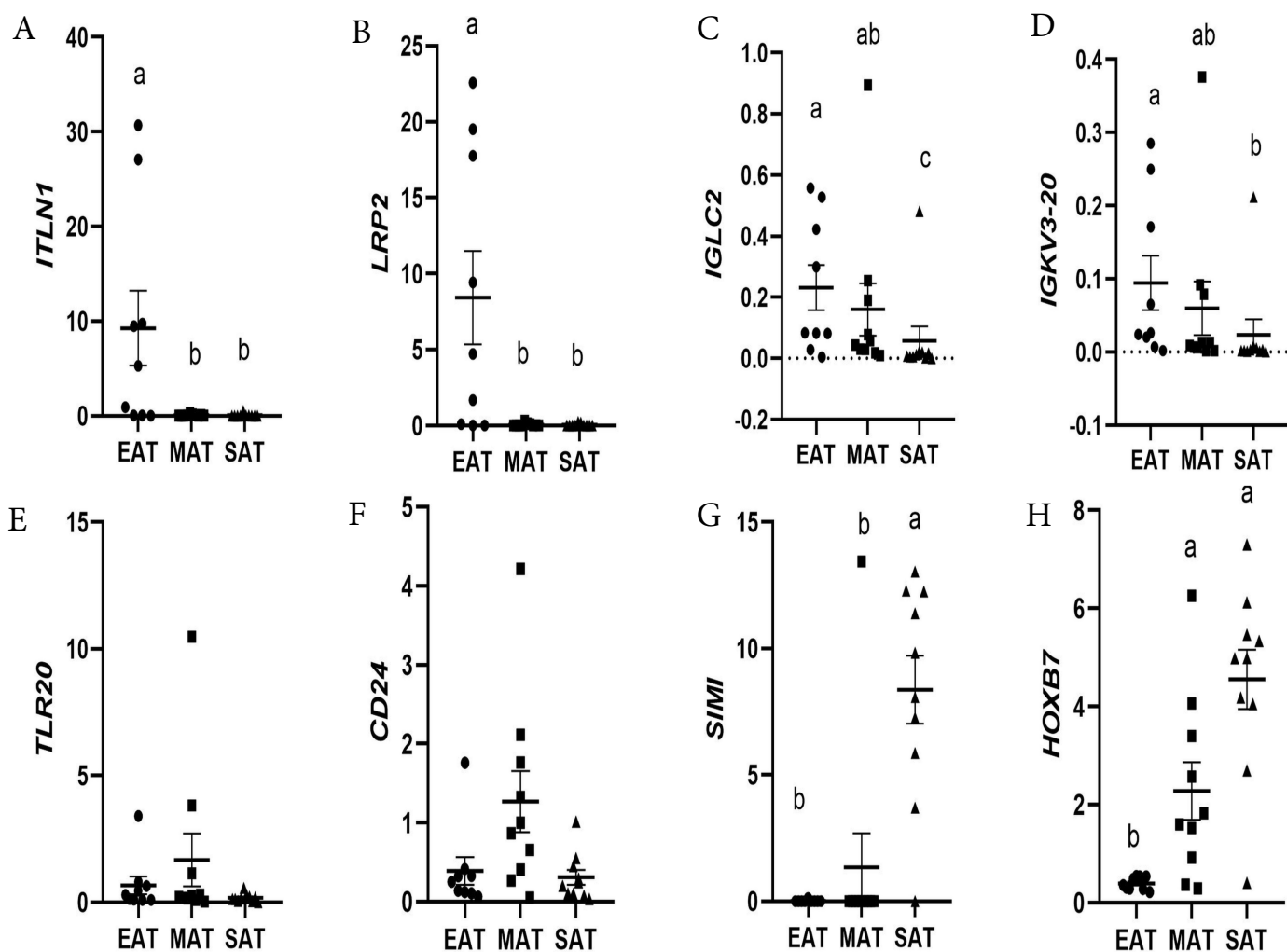
***UCP1*- expression associated gene signatures of human epicardial adipose tissue**

Kanta Chechi^{1,8}, Jinchu Vijay², Pierre Voisine^{3,8}, Patrick Mathieu^{4,8}, Yohan Bossé^{5,8}, Andre Tchernof^{6,8}, Elin Grundberg⁷, Denis Richard^{1,8}

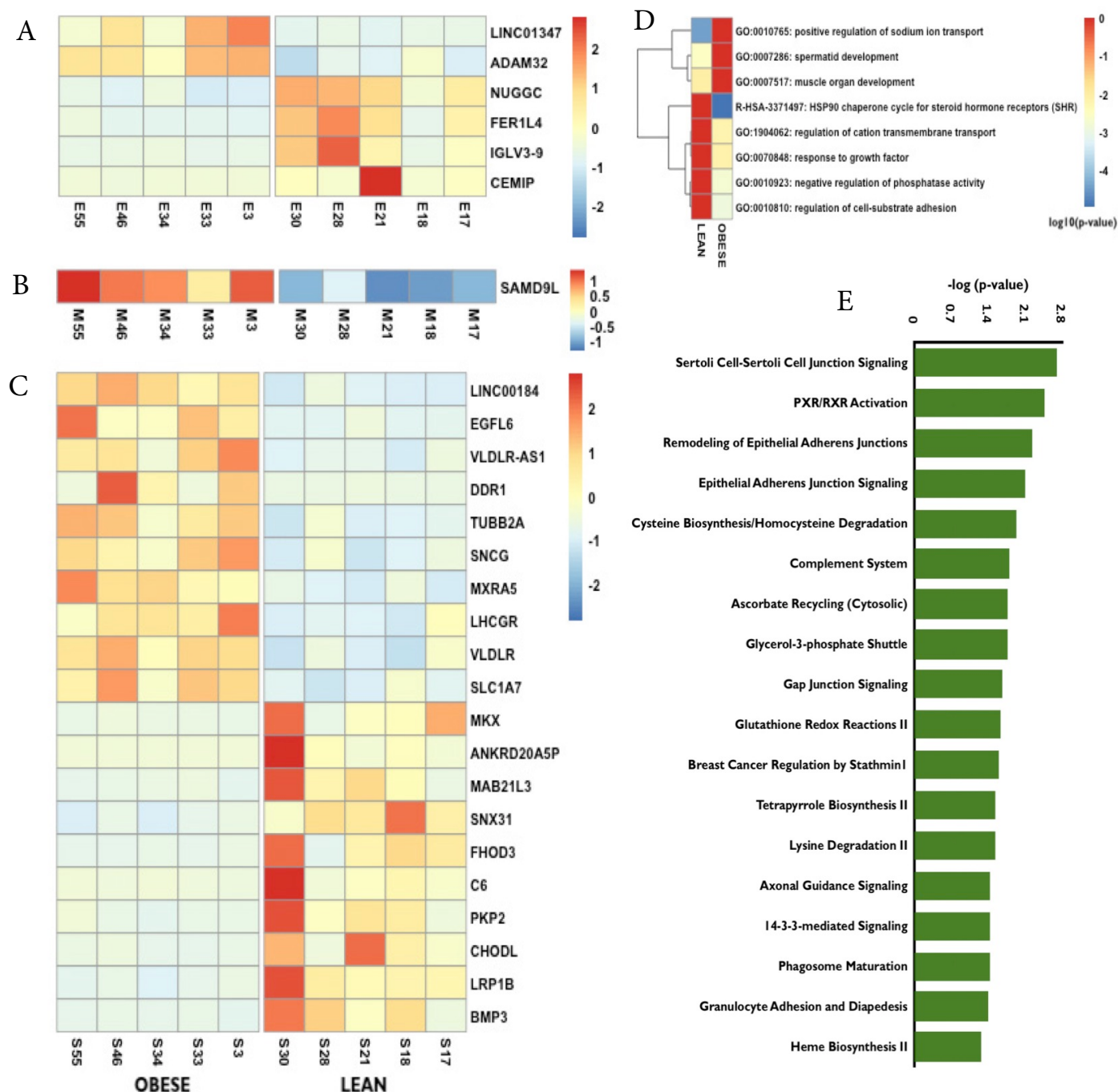
¹Department of Medicine, Faculty of Medicine, Université Laval, Québec, Québec, Canada. ²Institut universitaire de cardiologie et de pneumologie de Québec (IUCPQ), Chemin Sainte-Foy, Québec, Canada. ³Department of Human Genetics, McGill University, and Genome Québec Innovation Centre, Montreal, Québec, Canada. ⁴Department of Cardiovascular Surgery, ⁵Laboratory of Cardiovascular Pathobiology, Department of Surgery, Faculty of Medicine, and ⁶Department of Molecular Medicine, Université Laval, Québec, Québec, Canada. ⁷School of Nutrition, Université Laval, Québec, Québec, Canada. ⁸Children's Mercy Kansas City, Kansas City, Missouri, USA.



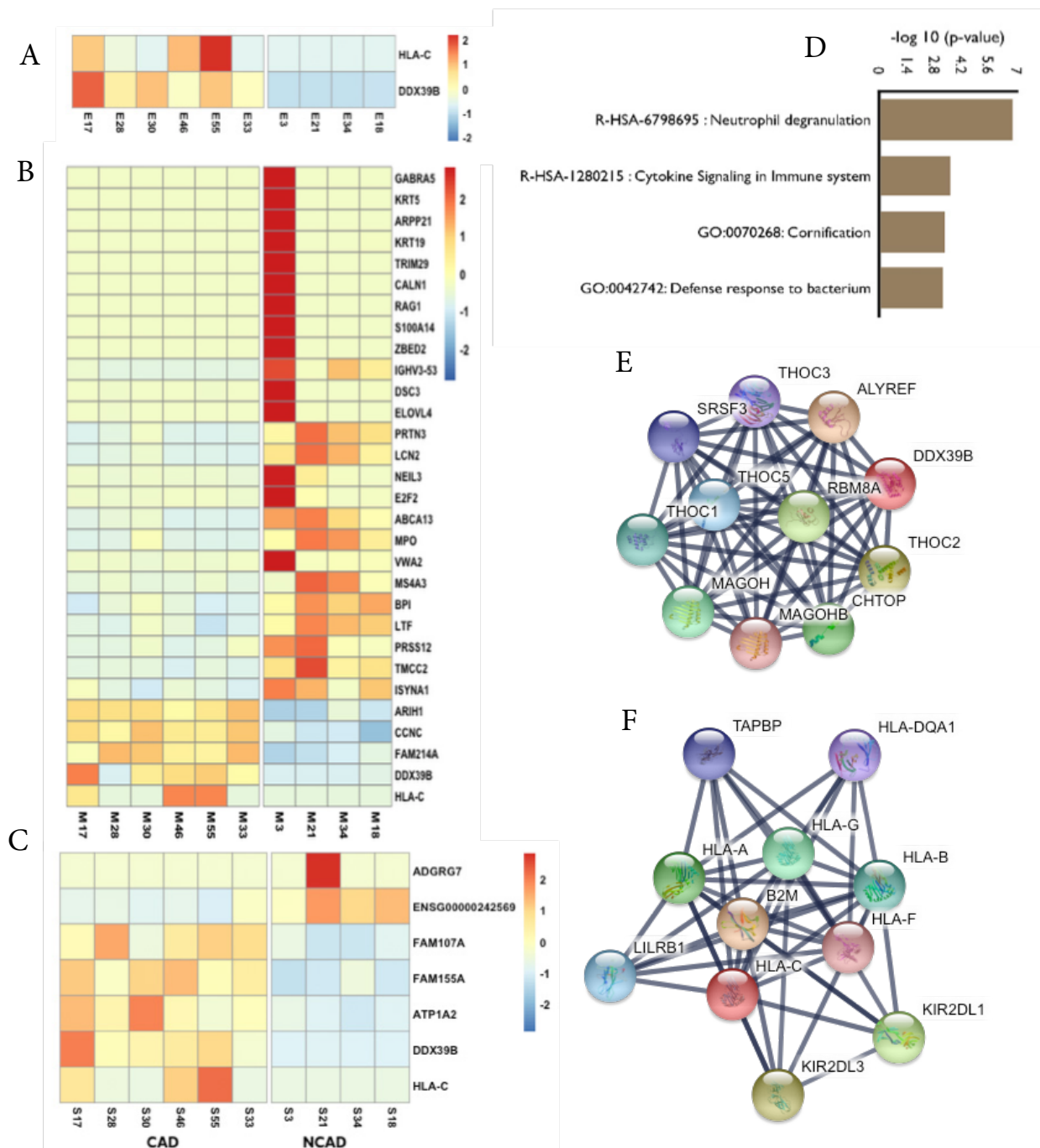
Supplementary Figure 1: Functions associated with significantly up- and down-regulated genes in eAT vs. sAT, mAT vs. sAT, and eAT vs. mAT groups identified using IPA's *Diseases and Functions* tool. eAT: epicardial adipose tissue; mAT: mediastinal adipose tissue; sAT: subcutaneous adipose tissue; IPA: Ingenuity Pathway Analysis.



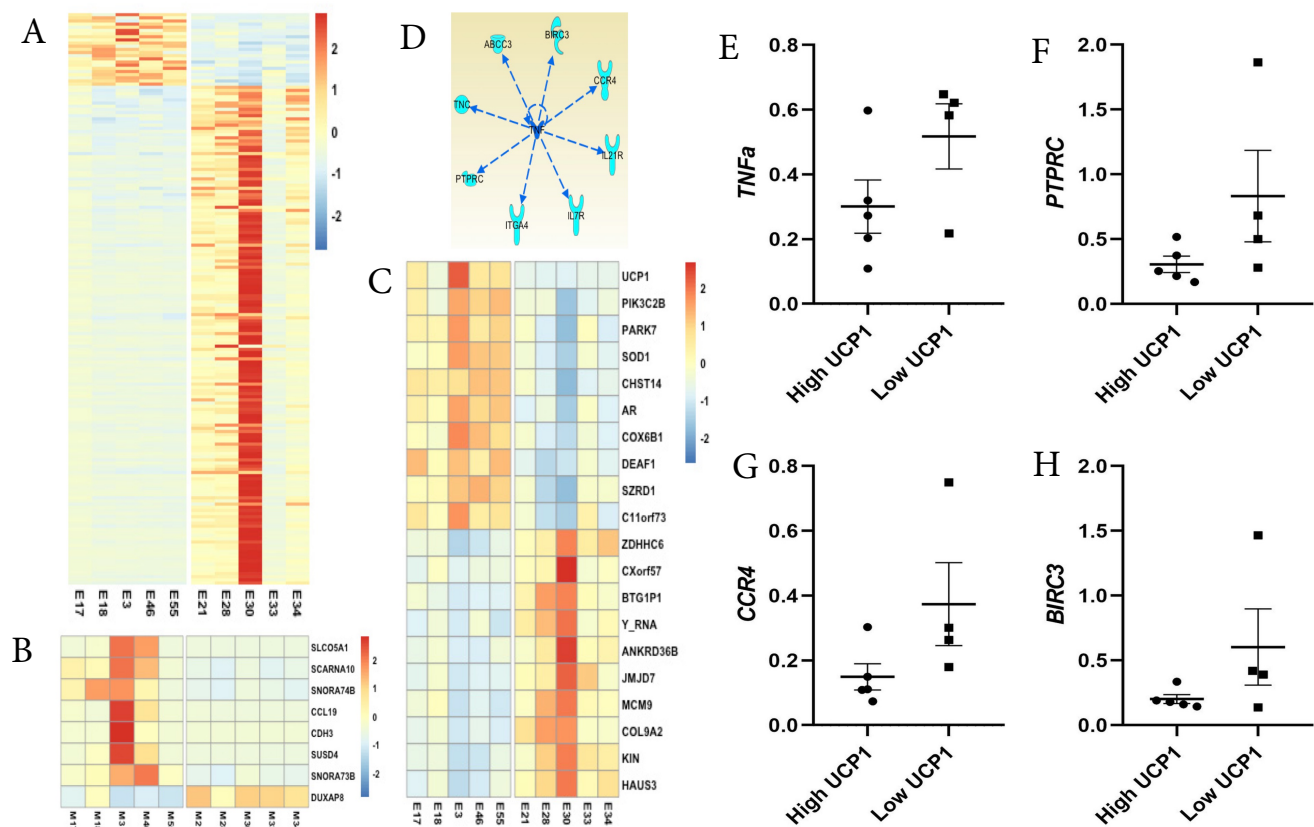
Supplementary Figure 3: Validation of top uniquely expressed genes in (A-C) eAT, (D-F) mAT and (G, H) sAT using qPCR. Data represent mean (n = 9) ± SEM. Superscripts represent $P \leq 0.05$ when log-transformed data were analyzed using repeated measures ANOVA with *Tukey's* post hoc test.



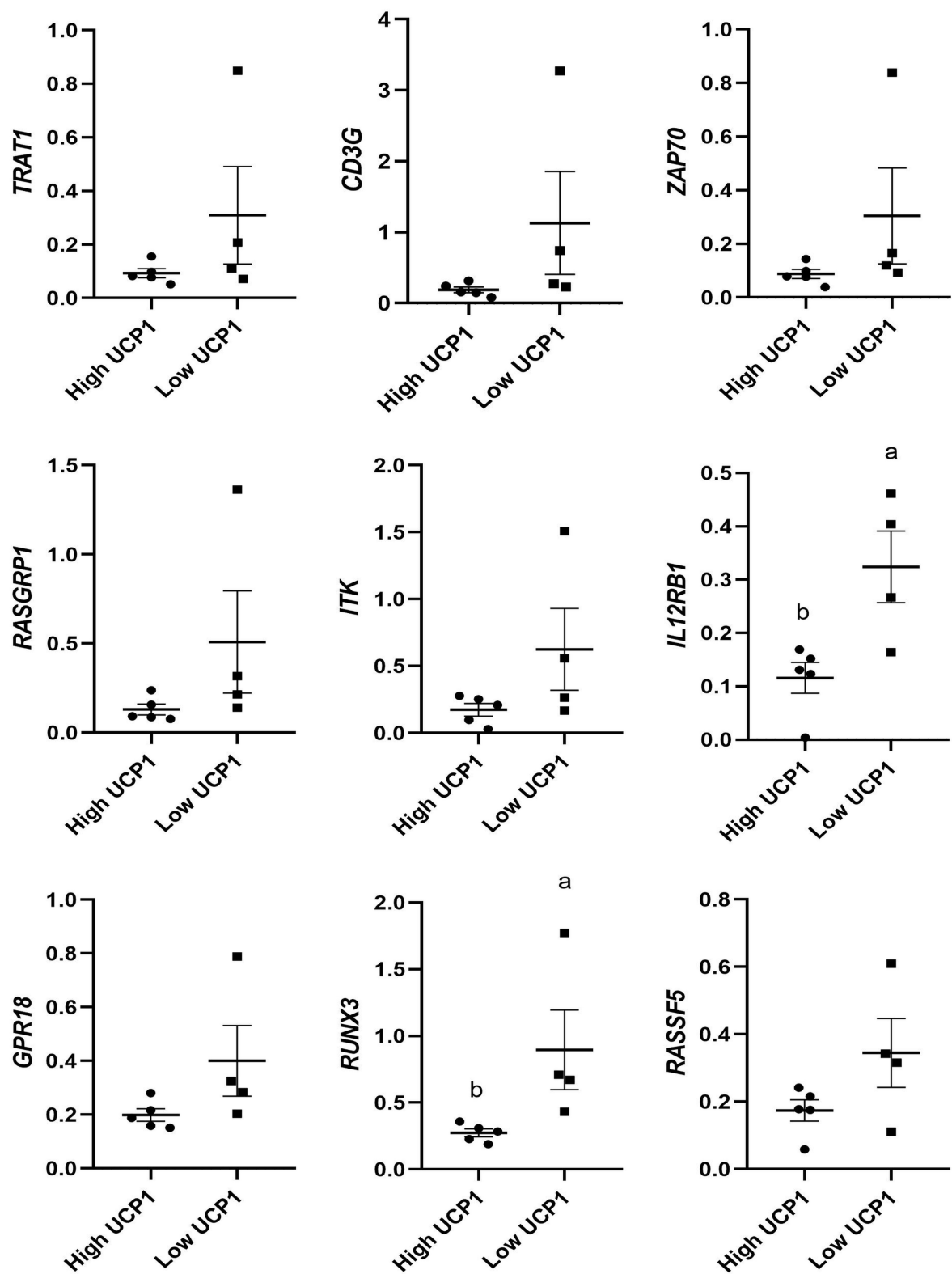
Supplementary Figure 4: Heatmaps representing the individual expression (data scaled to row) of DEGs in obese (n=5) vs. lean (n=5) (A) eAT, (B) mAT and (C). Heatmaps representing GO and Reactome pathways ($P \leq 0.05$) associated with up- and down-regulated genes analyzed separately in obese vs. lean sAT (D). IPA's canonical pathways exhibiting Benjamini and Hochberg corrected $P \leq 0.05$, identified by all of the DEGs in obese vs. lean sAT (E). GO: Gene ontology; DEGs: differentially expressed genes; eAT: epicardial adipose tissue; mAT: mediastinal adipose tissue; sAT: subcutaneous adipose tissue; IPA: Ingenuity Pathway Analysis.



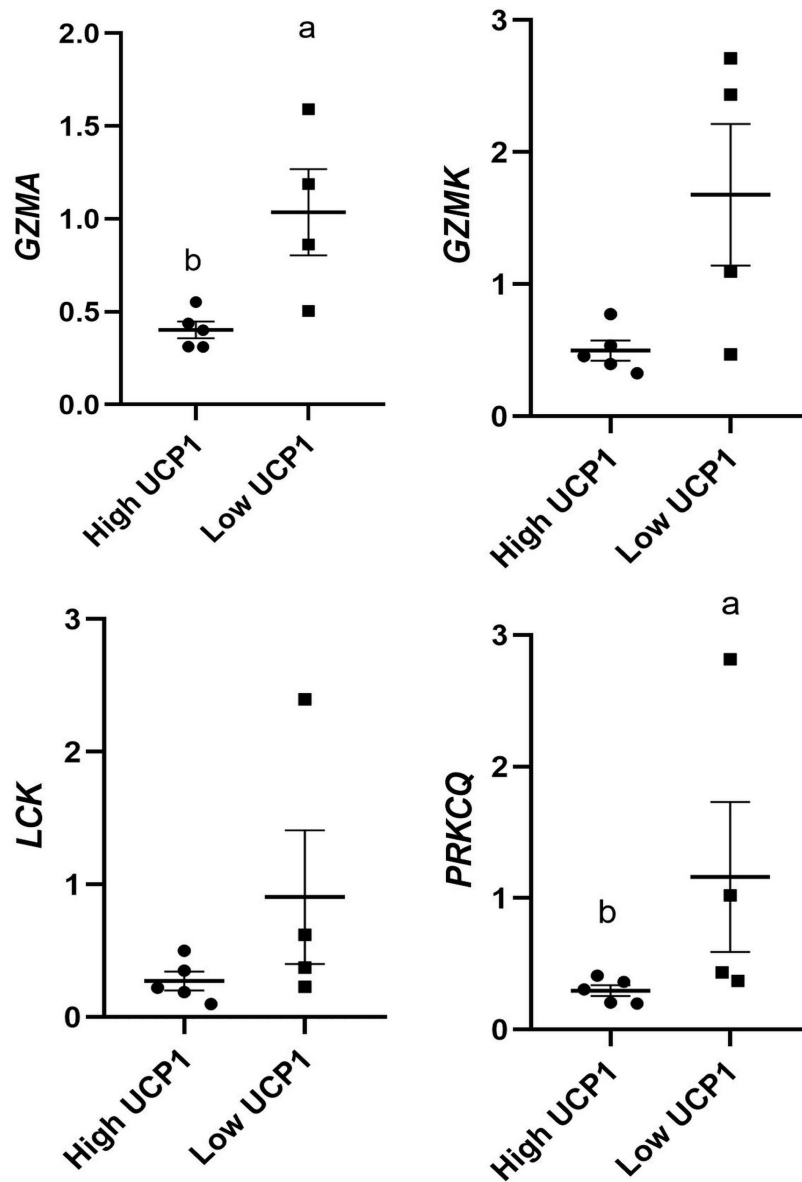
Supplementary Figure 5: Heatmaps representing the individual expression (data scaled to row) of DEGs in CAD (n=6) vs. NCAD (n=4) (A) eAT, (B) mAT and (C) sAT. GO and Reactome pathways ($P \leq 0.05$) associated with down-regulated genes in CAD vs. NCAD mAT (D). Protein-protein interaction network analysis of (E) *DDX39B* and (F) *HLA-C* using STRING platform, which can identify protein-protein interactions based on user-specified criteria. Our criteria for selection was based on published reports, experimental studies, curated databases and co-expression evidence. A maximum stringent interaction score of 0.90 was applied to generate the network where strength of nodes represents the evidence of interaction. GO: Gene ontology; DEGs: differentially expressed genes; eAT: epicardial adipose tissue; mAT: mediastinal adipose tissue; sAT: subcutaneous adipose tissue; CAD: coronary artery disease; NCAD: no-coronary artery disease.



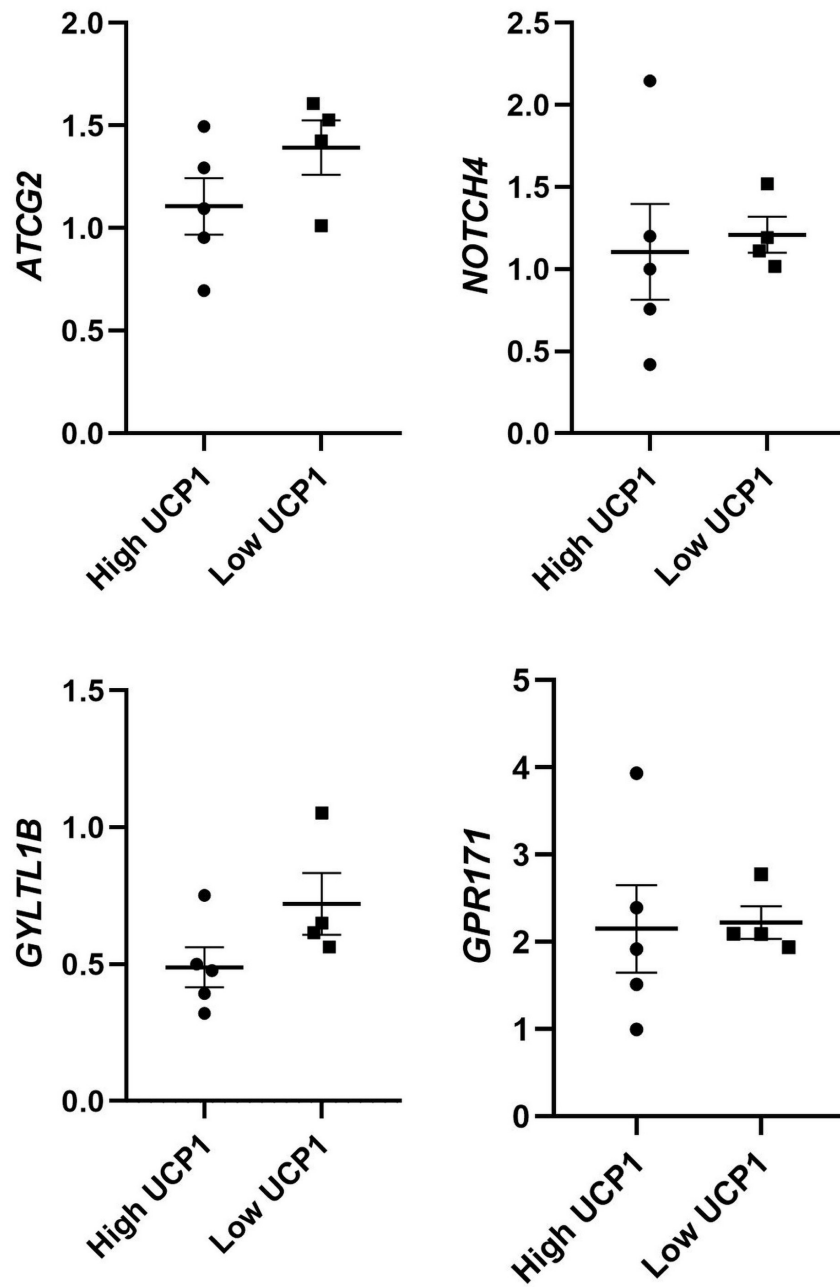
Supplementary Figure 6: Heatmaps representing the individual expression (data scaled to row) of DEGs in high vs. low *UCP1* groups in (A) eAT, (B) mAT and the top 10 genes exhibiting significant positive or negative ($r \geq 0.50$ or ≤ -0.50 ; $P \leq 0.05$) correlation with *UCP1* in eAT (C). *TNFA* and its network of genes identified by down-regulated genes in high vs. low *UCP1* comparison in eAT using IPA (D). Validation of expression pattern of (E) *TNFA*, (F) *PTPRC*, (G) *CCR4* and (H) *BIRC3* using qPCR approach in high (n=5) and low (n=4) *UCP1* expressing eAT.



Supplementary Figure 7: Validation of T-cell processes related genes in high (n=5) vs. low (n=4) *UCP1* expressing eAT samples. Superscripts represent $P \leq 0.05$ when data were analyzed using Mann-Whitney t-tests.



Supplementary Figure 8: Validation of redox-related related genes in high (n = 5) vs. low (n = 4) *UCP1* expressing eAT samples. Superscripts represent $P \leq 0.05$ when data were analyzed using Mann-Whitney t-tests.



Supplementary Figure 9: Validation of top differentially expressed genes in high (n=5) vs. low (n=4) *UCP1* expressing eAT samples.

Supplementary Table S1A: Clinical characteristics of all of the patients included in the study (n=10)

Parameters	Value
Age (years)	70.00 ± 1.44
Body mass index (kg/m ²)	30.46 ± 3.30
Body weight (kg)	73.75 ± 7.63
Body surface area (m ²)	1.72 ± 0.08
Triglycerides (mM)	1.33 ± 0.16
Total-cholesterol (mM)	4.39 ± 0.32
LDL-cholesterol (mM)	2.15 ± 0.28
HDL-cholesterol (mM)	1.64 ± 0.14
Sex (females/males)	(9/1)
Dyslipidemia (Yes/No)	(8/2)
Diabetes (Yes/No)	(2/8)
Heart surgeries (CABG/VR)	(6/4)
Hypertension (Yes/No)	(10/0)
Infarction (Yes/No)	(2/8)
Statins	(8/2)
ACE inhibitors	(6/4)
Calcium channel inhibitors	(5/5)
Beta-blocker (Yes/No)	(4/6)

ACE: Angiotensin converting enzyme; CABG: Coronary artery bypass grafting; VR: Valve replacement

Supplementary Table S1B: Individual anthropometric features and *UCPI* expression level for each patient included in the study (n=10).

Patient Number	CAD status	Obesity status	Age	Sex	BMI	UCPI expression (RPKM)
P3	NCAD	Obese	71	F	35.2	148.49
P17	CAD	Lean	65	F	23.4	66.32
P18	NCAD	Lean	77	F	20.7	18.88
P21	NCAD	Lean	75	F	18.8	9.72
P28	CAD	Lean	68	F	24.4	4.29
P30	CAD	Lean	69	F	17.5	1.57
P33	CAD	Obese	76	M	42.6	9.82
P34	NCAD	Obese	68	F	39.5	9.06
P46	CAD	Obese	66	F	39	71.88
P55	CAD	Obese	65	F	43.5	76.51

UCPI: Uncoupling protein 1; CAD: Coronary artery disease; NCAD; Non-CAD; RPKM: Reads per kilo base per million mapped reads. Expression values above and below 10 RPKM were considered as high and low-UCPI groups respectively.

Supplementary Table SIC: Clinical characteristics of patients when segregated as obese and lean groups.

Parameters	Lean (n=5) (BMI ≤ 25)	Obese (n=5) (BMI ≥ 30)
Sex (female/male)	5F	4F/1M
Age (years)	70.80 ± 2.24	69.20 ± 1.98
BMI (kg/m ²)	20.96 ± 1.33 ^b	39.96 ± 1.47 ^a
Body weight (kg)	52.10 ± 4.6 ^b	95.4 ± 2.50 ^a
BSA	1.50 ± 0.07 ^b	1.93 ± 0.04 ^a
Total-cholesterol (mM)	4.17 ± 0.33	4.60 ± 0.57
LDL-cholesterol (mM)	1.91 ± 0.26	2.39 ± 0.51
HDL-cholesterol (mM)	1.68 ± 0.21	1.59 ± 0.20
Triglycerides (mM)	1.27 ± 0.23	1.38 ± 0.24
Dyslipidemia (Yes/No)	(1/4)	(1/4)
Diabetes (Yes/No)	(0/5)	(2/3)
Heart surgeries (CABG/VR)	(3/2)	(3/2)
Hypertension (Yes/No)	(5/0)	(5/0)
Infarction (Yes/No)	(1/4)	(1/4)
Statins (Yes/No)	(4/1)	(4/1)
ACE inhibitors (Yes/No)	(2/3)	(4/1)
Calcium channel inhibitors (Yes/No)	(2/3)	(3/2)
Beta-blocker (Yes/No)	(3/2)	(1/4)

Groups were compared using unpaired t-tests. Superscripts represent $P \leq 0.05$.

Supplementary Table S1D: Clinical characteristics of patients when segregated as CAD and non-CAD groups.

Parameters	CAD (n=6)	NCAD (n=4)
Sex (female/male)	5F/1M	4F
Age (years)	68.17 ± 1.70	72.75 ± 2.02
BMI (kg/m ²)	31.73 ± 4.60	28.55 ± 5.17
Body weight (Kg)	76.08 ± 9.98	70.25 ± 13.45
BSA	1.74 ± 0.10	1.68 ± 0.15
Total-cholesterol (mM)	4.23 ± 0.19	4.62 ± 0.80
LDL-cholesterol (mM)	1.88 ± 0.24	2.55 ± 0.59
HDL-cholesterol (mM)	1.76 ± 0.15	1.46 ± 0.26
Triglycerides (mM)	1.32 ± 0.24	1.35 ± 0.20
Dyslipidemia (Yes/No)	(5/1)	(3/1)
Diabetes (Yes/No)	(1/5)	(1/3)
Heart surgeries (CABG/VR)	(6/0)	(0/4)
Hypertension (Yes/No)	(6/0)	(4/0)
Infarction (Yes/No)	(2/4)	(0/4)
Statins (Yes/No)	(5/1)	(3/1)
ACE inhibitors (Yes/No)	(2/3)	(4/1)
Calcium channel inhibitors (Yes/No)	(4/2)	(1/3)
Beta-blocker (Yes/No)	(3/3)	(1/3)

Groups were compared using unpaired t-tests. Superscripts represent $P \leq 0.05$.

Supplementary Table S1E: Clinical characteristics of patients when segregated as high and low-UCPI expression in eAT groups.

Parameters	High UCPI (n=5)	Low UCPI (n=5)
UCPI-eAT	76.42 ± 20.77 ^a	6.89 ± 1.68 ^b
Sex (female/male)	5F	4F/1M
Age (years)	68.80 ± 2.33	71.20 ± 1.77
BMI (kg/m ²)	32.36 ± 4.43	28.56 ± 5.25
Body weight (kg)	79.90 ± 10.15	67.60 ± 11.84
BSA	1.80 ± 0.10	1.64 ± 0.13
Total-cholesterol (mM)	4.80 ± 0.53	3.98 ± 0.31
LDL-cholesterol (mM)	2.50 ± 0.51	1.80 ± 0.18
HDL-cholesterol (mM)	1.65 ± 0.12	1.63 ± 0.26
Triglycerides (mM)	1.44 ± 0.23	1.22 ± 0.23
Dyslipidemia (Yes/No)	(3/2)	(5/0)
Diabetes (Yes/No)	(1/4)	(1/4)
Heart surgeries (CABG/VR)	(3/2)	(3/2)
Hypertension (Yes/No)	(5/0)	(5/0)
Infarction (Yes/No)	(0/5)	(2/3)
Statins (Yes/No)	(4/1)	(4/1)
ACE inhibitors (Yes/No)	(4/1)	(2/3)
Calcium channel inhibitors (Yes/No)	(2/3)	(3/2)
Beta-blocker (Yes/No)	(1/4)	(3/2)

Groups were compared using unpaired t-tests. Superscripts represent $P \leq 0.05$.

Supplementary Table S2: Description of top 10 significantly up- and down-regulated genes ($FC \geq 2$ or ≤ -2 ; $FDR \leq 0.05$) in eAT vs. sAT, mAT vs. sAT and eAT vs. mAT groups (n=10).

Gene Name	log2 FC	FDR	Description	Biological Process (GO)
eAT vs. sAT				
GATA4	6.929823947	4.06E-67	GATA binding protein 4	GO:0003290 atrial septum secundum morphogenesis;GO:0003289 atrial septum primum morphogenesis;GO:0003285 septum secundum development
WT1	6.327429313	8.40E-45	Wilms tumor 1	GO:0072302 negative regulation of metanephric glomerular mesangial cell proliferation;GO:0072301 regulation of metanephric glomerular mesangial cell proliferation;GO:2001076 positive regulation of metanephric ureteric bud development
TBX20	6.017247473	4.91E-40	T-box 20	GO:0003193 pulmonary valve formation;GO:0060577 pulmonary vein morphogenesis;GO:0035922 foramen ovale closure
TCF21	5.869981817	2.21E-77	transcription factor 21	GO:0072277 metanephric glomerular capillary formation;GO:0072276 metanephric glomerulus vasculature morphogenesis;GO:0072104 glomerular capillary formation
STAB2	5.624809208	1.57E-43	stabilin 2	GO:0030214 hyaluronan catabolic process;GO:0030212 hyaluronan metabolic process;GO:0006027 glycosaminoglycan catabolic process
PKHD1L1	5.467870636	1.13E-36	PKHD1 like 1	GO:0006955 immune response;GO:0002376 immune system process;GO:0050896 response to stimulus
CGN	5.394894094	1.81E-27	cingulin	GO:0007179 transforming growth factor beta receptor signaling pathway;GO:0071560 cellular response to transforming growth factor beta stimulus;GO:0071559 response to transforming growth factor beta
CCL21	5.390192146	2.10E-64	C-C motif chemokine ligand 21	GO:2000529 positive regulation of myeloid dendritic cell chemotaxis;GO:2000527 regulation of myeloid dendritic cell chemotaxis;GO:2000548 negative regulation of dendritic cell dendrite assembly
BNC1	5.156288879	4.50E-30	basonuclin 1	GO:0007283 spermatogenesis;GO:0048232 male gamete generation;GO:0008544 epidermis development
WT1-AS	5.136912097	2.32E-28	WT1 antisense RNA	GO:0008150 biological_process

HOXA5	-4.688410991	1.05E-59	homeobox A5	GO:0060480 lung goblet cell differentiation;GO:0060574 intestinal epithelial cell maturation;GO:0060481 lobar bronchus epithelium development
IRX1	-5.216998439	3.25E-39	iroquois homeobox 1	GO:0072086 specification of loop of Henle identity;GO:0072081 specification of nephron tubule identity;GO:0072272 proximal/distal pattern formation involved in metanephric nephron development
HOXB8	-5.297118774	1.05E-25	homeobox B8	GO:0021516 dorsal spinal cord development;GO:0045638 negative regulation of myeloid cell differentiation;GO:0007625 grooming behavior
HOXA10	-5.555872969	6.76E-49	homeobox A10	GO:0060065 uterus development;GO:0008584 male gonad development;GO:0009954 proximal/distal pattern formation
EN1	-5.565830296	3.43E-32	engrailed homeobox 1	GO:0061743 motor learning;GO:0030917 midbrain-hindbrain boundary development;GO:0021903 rostrocaudal neural tube patterning
HOXC6	-5.728834003	4.49E-41	homeobox C6	GO:0048706 embryonic skeletal system development;GO:0009952 anterior/posterior pattern specification;GO:0043009 chordate embryonic development
HOXC9	-5.760576493	8.26E-36	homeobox C9	GO:0048704 embryonic skeletal system morphogenesis;GO:0048706 embryonic skeletal system development;GO:0048705 skeletal system morphogenesis
HOXC8	-6.110371459	1.49E-36	homeobox C8	GO:0000122 negative regulation of transcription by RNA polymerase II;GO:0048705 skeletal system morphogenesis;GO:0009952 anterior/posterior pattern specification
PAX3	-6.149806361	4.91E-40	paired box 3	GO:0007605 sensory perception of sound;GO:0050954 sensory perception of mechanical stimulus;GO:0045944 positive regulation of transcription by RNA polymerase II
SIM1	-6.866419972	2.67E-52	single-minded family bHLH transcription factor 1	GO:0001657 ureteric bud development;GO:0072164 mesonephric tubule development;GO:0072163 mesonephric epithelium development
mAT vs. sAT				
PKHD1L1	2.906044995	4.95E-08	PKHD1 like 1	GO:0006955 immune response;GO:0002376 immune system process;GO:0050896 response to stimulus
DCHS2	2.672645544	9.92E-06	dachsous cadherin-related 2	GO:0072137 condensed mesenchymal cell proliferation;GO:0072006 nephron development;GO:0010463 mesenchymal cell proliferation
STAB2	2.634047936	1.69E-05	stabilin 2	GO:0030214 hyaluronan catabolic process;GO:0030212 hyaluronan

				metabolic process;GO:0006027 glycosaminoglycan catabolic process
GATA4	2.554614516	1.19E-05	GATA binding protein 4	GO:0003290 atrial septum secundum morphogenesis;GO:0003289 atrial septum primum morphogenesis;GO:0003285 septum secundum development
CCL21	2.463869598	0.000104837	C-C motif chemokine ligand 21	GO:2000529 positive regulation of myeloid dendritic cell chemotaxis;GO:2000527 regulation of myeloid dendritic cell chemotaxis;GO:2000548 negative regulation of dendritic cell dendrite assembly
USH1C	2.385000299	0.000213007	USH1 protein network component harmonin	GO:0032532 regulation of microvillus length;GO:0030046 parallel actin filament bundle assembly;GO:0060122 inner ear receptor cell stereocilium organization
PROX1	2.369120944	7.80E-06	prospero homeobox 1	GO:0021707 cerebellar granule cell differentiation;GO:2000979 positive regulation of forebrain neuron differentiation;GO:0021684 cerebellar granular layer formation
COL19A1	2.352856208	0.000247594	collagen type XIX alpha 1 chain	GO:0030574 collagen catabolic process;GO:0007519 skeletal muscle tissue development;GO:0032963 collagen metabolic process
LRRC7	2.333973678	0.000188875	leucine rich repeat containing 7	GO:0043312 neutrophil degranulation;GO:0002283 neutrophil activation involved in immune response;GO:0010976 positive regulation of neuron projection development
POFIB	2.326638044	1.30E-05	POFIB, actin binding protein	GO:0070830 bicellular tight junction assembly;GO:0003382 epithelial cell morphogenesis;GO:0043297 apical junction assembly
IRX5	-1.642638102	0.011998156	iroquois homeobox 5	GO:0060040 retinal bipolar neuron differentiation;GO:0060042 retina morphogenesis in camera-type eye;GO:0048701 embryonic cranial skeleton morphogenesis
WTAPPI	-1.643729991	0.013843153	Wilms tumor 1 associated protein pseudogene 1	
NPM1P10	-1.656539703	0.01350982	nucleophosmin 1 pseudogene 10	
HOXA10	-1.697146701	0.002138474	homeobox A10	GO:0060065 uterus development;GO:0008584 male gonad development;GO:0009954 proximal/distal pattern formation
MIR4705	-1.717933286	0.007539502	microRNA 4705	
ALDOC	-1.740979992	0.00137941	aldolase, fructose-bisphosphate C	GO:0061621 canonical glycolysis;GO:0061620 glycolytic process through glucose-6-phosphate;GO:0061615 glycolytic process through fructose-6-phosphate
HOXB8	-1.769202592	0.00137941	homeobox B8	GO:0021516 dorsal spinal cord development;GO:0045638 negative regulation of myeloid cell

				differentiation;GO:0007625 grooming behavior
CI lorf53	-1.845984208	0.002073457	chromosome 11	open reading frame 53
GRM7	-2.214795442	4.61E-06	glutamate metabotropic receptor 7	GO:0014050 negative regulation of glutamate secretion;GO:0014048 regulation of glutamate secretion;GO:0051956 negative regulation of amino acid transport
APOB	-2.853889344	3.28E-10	apolipoprotein B	GO:0034371 chylomicron remodeling;GO:0034378 chylomicron assembly;GO:0010886 positive regulation of cholesterol storage
eAT vs. mAT				
TCF21	4.200306912	7.22E-37	transcription factor 21	GO:0072277 metanephric glomerular capillary formation;GO:0072276 metanephric glomerulus vasculature morphogenesis;GO:0072104 glomerular capillary formation
TBX20	4.076404722	3.73E-23	T-box 20	GO:0003193 pulmonary valve formation;GO:0060577 pulmonary vein morphogenesis;GO:0035922 foramen ovale closure
LHX9	3.906547238	2.84E-21	LIM homeobox 9	GO:0097380 dorsal spinal cord interneuron anterior axon guidance;GO:0097378 dorsal spinal cord interneuron axon guidance;GO:0097377 spinal cord interneuron axon guidance
CCL11	3.675257131	1.00E-16	C-C motif chemokine ligand 11	GO:0060763 mammary duct terminal end bud growth;GO:0048245 eosinophil chemotaxis;GO:0002551 mast cell chemotaxis
MSLN	3.617873218	1.27E-16	mesothelin	GO:0006501 C-terminal protein lipidation;GO:0018410 C-terminal protein amino acid modification;GO:0006497 protein lipidation
GATA4	3.416131903	9.10E-25	GATA binding protein 4	GO:0003290 atrial septum secundum morphogenesis;GO:0003289 atrial septum primum morphogenesis;GO:0003285 septum secundum development
LRRN4	3.339523387	2.18E-14	leucine rich repeat neuronal 4	GO:0008542 visual learning;GO:0007616 long-term memory;GO:0008306 associative learning
SYT4	3.324557155	4.18E-13	synaptotagmin 4	GO:1905433 negative regulation of retrograde trans-synaptic signaling by neuropeptide;GO:0048174 negative regulation of short-term neuronal synaptic plasticity;GO:1905432 regulation of retrograde trans-synaptic signaling by neuropeptide
GRID2	3.245799121	5.50E-16	glutamate ionotropic receptor delta type subunit 2	GO:0021707 cerebellar granule cell differentiation;GO:0021684 cerebellar granular layer formation;GO:1900454 positive regulation of long term synaptic depression

UPK3B	3.166636668	3.14E-15	uroplakin 3B	GO:0010629 negative regulation of gene expression;GO:0010605 negative regulation of macromolecule metabolic process;GO:0009892 negative regulation of metabolic process
HOXA5	-4.301948472	1.05E-37	homeobox A5	GO:0060480 lung goblet cell differentiation;GO:0060574 intestinal epithelial cell maturation;GO:0060481 lobar bronchus epithelium development
HOXC9	-3.979966757	8.23E-22	homeobox C9	GO:0048704 embryonic skeletal system morphogenesis;GO:0048706 embryonic skeletal system development;GO:0048705 skeletal system morphogenesis
HOXC6	-3.963388579	5.49E-22	homeobox C6	GO:0048706 embryonic skeletal system development;GO:0009952 anterior/posterior pattern specification;GO:0043009 chordate embryonic development
EN1	-3.70985832	8.53E-18	engrailed homeobox 1	GO:0061743 motor learning;GO:0030917 midbrain-hindbrain boundary development;GO:0021903 rostral-caudal neural tube patterning
HOXC8	-3.556387271	1.64E-15	homeobox C8	GO:0000122 negative regulation of transcription by RNA polymerase II;GO:0048705 skeletal system morphogenesis;GO:0009952 anterior/posterior pattern specification
HOXA6	-3.329002001	1.24E-17	homeobox A6	GO:0048704 embryonic skeletal system morphogenesis;GO:0048706 embryonic skeletal system development;GO:0048705 skeletal system morphogenesis
NPY1R	-3.325979802	1.60E-22	neuropeptide Y receptor Y1	GO:0003151 outflow tract morphogenesis;GO:0007193 adenylate cyclase-inhibiting G-protein coupled receptor signaling pathway;GO:0040014 regulation of multicellular organism growth
HOXA3	-3.217653057	1.23E-35	homeobox A3	GO:0021615 glossopharyngeal nerve morphogenesis;GO:0021563 glossopharyngeal nerve development;GO:0010159 specification of animal organ position
HOXA7	-3.177688107	3.48E-16	homeobox A7	GO:0045656 negative regulation of monocyte differentiation;GO:0045617 negative regulation of keratinocyte differentiation;GO:0045655 regulation of monocyte differentiation
IRX1	-3.145484948	5.71E-16	iroquois homeobox 1	GO:0072086 specification of loop of Henle identity;GO:0072081 specification of nephron tubule identity;GO:0072272 proximal/distal pattern formation involved in metanephric nephron development

Supplementary Table S3: Detailed description of top 25 genes uniquely expressed in eAT, mAT and sAT (n=10).

Symbol	Gene Name	Expression Intensity (RPKM)	Biological processes (GO pathways)
Highly expressed eAT-specific genes			
<i>ITLN1</i>	omentin	17477.8	GO:0046326 positive regulation of glucose import;GO:0010828 positive regulation of glucose transport;GO:0046324 regulation of glucose import
<i>LRP2</i>	LDL receptor related protein 2	2218.8	GO:1904447 folic acid import across plasma membrane;GO:0003223 ventricular compact myocardium morphogenesis;GO:0140058 neuron projection arborization
<i>IGLC2</i>	immunoglobulin lambda constant 2	1928.3	GO:0002250 adaptive immune response;GO:0006955 immune response;GO:0002376 immune system process
<i>CDH19</i>	cadherin 19	1308.9	GO:0007156 homophilic cell adhesion via plasma membrane adhesion molecules;GO:0098742 cell-cell adhesion via plasma-membrane adhesion molecules;GO:0098609 cell-cell adhesion
<i>MUC16</i>	mucin 16, cell surface associated	915.7	GO:0002223 stimulatory C-type lectin receptor signaling pathway;GO:0002220 innate immune response activating cell surface receptor signaling pathway;GO:0016266 O-glycan processing
<i>KRT19</i>	keratin 19	896	GO:0070268 cornification;GO:0060706 cell differentiation involved in embryonic placenta development;GO:0045214 sarcomere organization
<i>COL4A3</i>	collagen type IV alpha 3 chain	869.4	GO:0032836 glomerular basement membrane development;GO:0006919 activation of cysteine-type endopeptidase activity involved in apoptotic process;GO:0038063 collagen-activated tyrosine kinase receptor signaling pathway
<i>IGHM</i>	immunoglobulin heavy constant mu	865.4	GO:0050853 B cell receptor signaling pathway;GO:0006958 complement activation, classical pathway;GO:0002455 humoral immune response mediated by circulating immunoglobulin
<i>MS4A1</i>	membrane spanning 4-domains A1	833.5	GO:0042100 B cell proliferation;GO:0046651 lymphocyte proliferation;GO:0042113 B cell activation
<i>CCL21</i>	C-C motif chemokine ligand 21	705.5	GO:2000529 positive regulation of myeloid dendritic cell chemotaxis;GO:2000527 regulation of myeloid dendritic cell chemotaxis;GO:2000548 negative regulation of dendritic cell dendrite assembly
<i>ALOX15</i>	arachidonate 15-lipoxygenase	685.3	GO:2001303 lipoxin A4 biosynthetic process;GO:2001301 lipoxin biosynthetic process;GO:2001302 lipoxin A4 metabolic process
<i>BNC1</i>	basonuclin 1	674.8	GO:0007283 spermatogenesis;GO:0048232 male gamete generation;GO:0008544 epidermis development
<i>MSLN</i>	mesothelin	663.8	GO:0006501 C-terminal protein lipidation;GO:0018410 C-terminal protein amino acid modification;GO:0006497 protein lipidation

<i>HLA-C</i>	major histocompatibility complex, class I, C	568.5	GO:0002480 antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-independent;GO:0002479 antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;GO:0042590 antigen processing and presentation of exogenous peptide antigen via MHC class I
<i>MYRF</i>	myelin regulatory factor	526	GO:0032286 central nervous system myelin maintenance;GO:0031643 positive regulation of myelination;GO:0022010 central nervous system myelination
<i>IGKV3-11</i>	immunoglobulin kappa variable 3-11	513.5	
<i>UPK3B</i>	uroplakin 3B	494.8	GO:0010629 negative regulation of gene expression;GO:0010605 negative regulation of macromolecule metabolic process;GO:0009892 negative regulation of metabolic process
<i>STAB2</i>	stabilin 2	482.5	GO:0030214 hyaluronan catabolic process;GO:0030212 hyaluronan metabolic process;GO:0006027 glycosaminoglycan catabolic process
<i>SBSPON</i>	somatomedin B and thrombospondin type I domain containing	403.6	GO:0006898 receptor-mediated endocytosis;GO:0006897 endocytosis;GO:0098657 import into cell
<i>TCF21</i>	transcription factor 21	381.3	GO:0072277 metanephric glomerular capillary formation;GO:0072276 metanephric glomerulus vasculature morphogenesis;GO:0072104 glomerular capillary formation
<i>TRIM55</i>	tripartite motif containing 55	365	GO:0007165 signal transduction;GO:0023052 signaling;GO:0007154 cell communication
<i>BICDL1</i>	BICD family like cargo adaptor 1	363	GO:0055107 Golgi to secretory granule transport;GO:0031175 neuron projection development;GO:0048666 neuron development
<i>CLDN1</i>	claudin 1	347.5	GO:1903348 positive regulation of bicellular tight junction assembly;GO:1903545 cellular response to butyrate;GO:0061772 drug transport across blood-nerve barrier
<i>CCR7</i>	C-C motif chemokine receptor 7	346.7	GO:2000525 positive regulation of T cell costimulation;GO:0097022 lymphocyte migration into lymph node;GO:2000523 regulation of T cell costimulation
<i>SYT4</i>	synaptotagmin 4	343.2	GO:1905433 negative regulation of retrograde trans-synaptic signaling by neuropeptide;GO:0048174 negative regulation of short-term neuronal synaptic plasticity;GO:1905432 regulation of retrograde trans-synaptic signaling by neuropeptide
Highly expressed <i>mAT</i>-specific genes			
<i>IGKV3-20</i>	immunoglobulin kappa variable 3-20	514.2	GO:0038096 Fc-gamma receptor signaling pathway involved in phagocytosis;GO:0002431 Fc receptor mediated stimulatory signaling pathway;GO:0006958 complement activation, classical pathway

<i>TLR10</i>	toll like receptor 10	365	GO:0034166 toll-like receptor 10 signaling pathway;GO:0002755 MyD88-dependent toll-like receptor signaling pathway;GO:0002224 toll-like receptor signaling pathway
<i>CD24</i>	CD24 molecule	295	GO:2000768 positive regulation of nephron tubule epithelial cell differentiation;GO:0072139 glomerular parietal epithelial cell differentiation;GO:0032597 B cell receptor transport into membrane raft
<i>SLC27A2</i>	solute carrier family 27 member 2	219	GO:0044539 long-chain fatty acid import;GO:0097089 methyl-branched fatty acid metabolic process;GO:0042760 very long-chain fatty acid catabolic process
<i>ASPM</i>	abnormal spindle microtubule assembly	138	GO:0045769 negative regulation of asymmetric cell division;GO:0021873 forebrain neuroblast division;GO:0051661 maintenance of centrosome location
<i>CD1C</i>	CD1c molecule	132.6	GO:0048007 antigen processing and presentation, exogenous lipid antigen via MHC class Ib;GO:0048003 antigen processing and presentation of lipid antigen via MHC class Ib;GO:0002475 antigen processing and presentation via MHC class Ib
<i>KCNMB1</i>	potassium calcium-activated channel subfamily M regulatory beta subunit 1	129.9	GO:1903413 cellular response to bile acid;GO:1901381 positive regulation of potassium ion transmembrane transport;GO:1903412 response to bile acid
<i>SIGLEC10</i>	sialic acid binding Ig like lectin 10	121.7	GO:0106015 negative regulation of inflammatory response to wounding;GO:0106014 regulation of inflammatory response to wounding;GO:0090594 inflammatory response to wounding
<i>KIAA1644</i>	KIAA1644	121.3	
<i>KCNN4</i>	potassium calcium-activated channel subfamily N member 4	116.7	GO:0050862 positive regulation of T cell receptor signaling pathway;GO:0050857 positive regulation of antigen receptor-mediated signaling pathway;GO:0050856 regulation of T cell receptor signaling pathway
<i>TOX</i>	thymocyte selection associated high mobility group box	109.6	
<i>FBN2</i>	fibrillin 2	108.5	GO:0035583 sequestering of TGFbeta in extracellular matrix;GO:0035581 sequestering of extracellular ligand from receptor;GO:0071694 maintenance of protein location in extracellular region
<i>BLM</i>	Bloom syndrome RecQ like helicase	105.6	GO:0072757 cellular response to camptothecin;GO:0048478 replication fork protection;GO:0061820 telomeric D-loop disassembly
<i>DACT2</i>	dishevelled binding antagonist of beta catenin 2	103.9	GO:1900108 negative regulation of nodal signaling pathway;GO:0072061 inner medullary collecting duct development;GO:1900107 regulation of nodal signaling pathway

<i>CYP4F3</i>	cytochrome P450 family 4 subfamily F member 3	94.3	GO:0036101 leukotriene B4 catabolic process;GO:0036100 leukotriene catabolic process;GO:0036102 leukotriene B4 metabolic process
<i>PAPPA2</i>	pappalysin 2	89	GO:0060349 bone morphogenesis;GO:0060348 bone development;GO:0009651 response to salt stress
<i>CD80</i>	CD80 molecule	86.2	GO:0045627 positive regulation of T-helper 1 cell differentiation;GO:0045625 regulation of T-helper 1 cell differentiation;GO:0045624 positive regulation of T-helper cell differentiation
<i>C2CD4B</i>	C2 calcium dependent domain containing 4B	82.9	GO:0048791 calcium ion-regulated exocytosis of neurotransmitter;GO:0016079 synaptic vesicle exocytosis;GO:0017158 regulation of calcium ion-dependent exocytosis
<i>SORCS2</i>	sortilin related VPS10 domain containing receptor 2	78.5	GO:0007218 neuropeptide signaling pathway;GO:0007186 G-protein coupled receptor signaling pathway;GO:0007165 signal transduction
<i>KCNK3</i>	potassium two pore domain channel subfamily K member 3	73.7	GO:0051481 negative regulation of cytosolic calcium ion concentration;GO:0071294 cellular response to zinc ion;GO:0090102 cochlea development
<i>PMAIP1</i>	phorbol-12-myristate-13-acetate-induced protein 1	71.3	GO:1900740 positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway;GO:1900739 regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway;GO:1901030 positive regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway
<i>SLAMF8</i>	SLAM family member 8	70	
<i>IL1R2</i>	interleukin 1 receptor type 2	69.1	GO:0050712 negative regulation of interleukin-1 alpha secretion;GO:0050705 regulation of interleukin-1 alpha secretion;GO:2000660 negative regulation of interleukin-1-mediated signaling pathway
<i>BMP8B</i>	bone morphogenetic protein 8b	67.6	GO:0010862 positive regulation of pathway-restricted SMAD protein phosphorylation;GO:0060393 regulation of pathway-restricted SMAD protein phosphorylation;GO:0060389 pathway-restricted SMAD protein phosphorylation
<i>CIQTNF2</i>	CIq and TNF related 2	67.4	GO:0045725 positive regulation of glycogen biosynthetic process;GO:0046326 positive regulation of glucose import;GO:0070875 positive regulation of glycogen metabolic process
Highly expressed sAT-specific genes			
<i>SIM1</i>	single-minded family bHLH transcription factor 1	547.8	GO:0001657 ureteric bud development;GO:0072164 mesonephric tubule development;GO:0072163 mesonephric epithelium development
<i>SPAG17</i>	sperm associated antigen 17	286.5	GO:1904158 axonemal central apparatus assembly;GO:0003351 epithelial cilium movement;GO:0035082 axoneme assembly

<i>HOXB7</i>	homeobox B7	182.1	GO:0090190 positive regulation of branching involved in ureteric bud morphogenesis;GO:0090189 regulation of branching involved in ureteric bud morphogenesis;GO:0001658 branching involved in ureteric bud morphogenesis
<i>SERPINE1</i>	serpin family E member 1	170.1	GO:0061044 negative regulation of vascular wound healing;GO:1901331 positive regulation of odontoblast differentiation;GO:0035491 positive regulation of leukotriene production involved in inflammatory response
<i>PDZRN4</i>	PDZ domain containing ring finger 4	159.6	
<i>MAP1LC3C</i>	microtubule associated protein 1 light chain 3 gamma	154	GO:0035973 aggrephagy;GO:0006995 cellular response to nitrogen starvation;GO:0043562 cellular response to nitrogen levels
<i>LINC00968</i>	long intergenic non-protein coding RNA 968	152.4	
<i>ABCB5</i>	ATP binding cassette subfamily B member 5	147.6	GO:0048058 compound eye corneal lens development;GO:0042908 xenobiotic transport;GO:0048749 compound eye development
<i>CDH20</i>	cadherin 20	129.5	GO:0007156 homophilic cell adhesion via plasma membrane adhesion molecules;GO:0098742 cell-cell adhesion via plasma-membrane adhesion molecules;GO:0098609 cell-cell adhesion
<i>IRX2</i>	iroquois homeobox 2	118	GO:0072086 specification of loop of Henle identity;GO:0072081 specification of nephron tubule identity;GO:0072272 proximal/distal pattern formation involved in metanephric nephron development
<i>DKK2</i>	dickkopf WNT signaling pathway inhibitor 2	114.6	GO:0090263 positive regulation of canonical Wnt signaling pathway;GO:0090090 negative regulation of canonical Wnt signaling pathway;GO:0030177 positive regulation of Wnt signaling pathway
<i>CXCR1</i>	C-X-C motif chemokine receptor 1	114.1	GO:0038112 interleukin-8-mediated signaling pathway;GO:0098759 cellular response to interleukin-8;GO:0098758 response to interleukin-8
<i>HOXA6</i>	homeobox A6	114.1	GO:0048704 embryonic skeletal system morphogenesis;GO:0048706 embryonic skeletal system development;GO:0048705 skeletal system morphogenesis
<i>IRX1</i>	iroquois homeobox 1	113.1	GO:0072086 specification of loop of Henle identity;GO:0072081 specification of nephron tubule identity;GO:0072272 proximal/distal pattern formation involved in metanephric nephron development
<i>ANGPTL8</i>	angiopoietin like 8	111.7	GO:0010954 positive regulation of protein processing;GO:0051004 regulation of lipoprotein lipase activity;GO:0070328 triglyceride homeostasis
<i>HOXC6</i>	homeobox C6	110.8	GO:0048706 embryonic skeletal system development;GO:0009952 anterior/posterior pattern specification;GO:1903507 negative regulation of nucleic acid-templated transcription

<i>HNRNPA1P6</i> 6	heterogeneous nuclear ribonucleoprotein A1 pseudogene 66	110.2	
<i>AQP7P2</i>	aquaporin 7 pseudogene 2	109.2	
<i>HOXA7</i>	homeobox A7	104.2	GO:0045656 negative regulation of monocyte differentiation;GO:0045617 negative regulation of keratinocyte differentiation;GO:0045655 regulation of monocyte differentiation
<i>LUCAT1</i>	lung cancer associated transcript 1 (non-protein coding)	93.5	
<i>SLC4A1</i>	solute carrier family 4 member 1 (Diego blood group)	92.2	GO:0051453 regulation of intracellular pH;GO:0015701 bicarbonate transport;GO:0030641 regulation of cellular pH
<i>HOXA9</i>	homeobox A9	89.6	GO:0035115 embryonic forelimb morphogenesis;GO:0042118 endothelial cell activation;GO:0035136 forelimb morphogenesis
<i>ARG2</i>	arginase 2	87.7	GO:1905403 negative regulation of activated CD8-positive, alpha-beta T cell apoptotic process;GO:2000562 negative regulation of CD4-positive, alpha-beta T cell proliferation;GO:2000666 negative regulation of interleukin-13 secretion
<i>PPBP</i>	pro-platelet basic protein	87.5	GO:0090023 positive regulation of neutrophil chemotaxis;GO:0071624 positive regulation of granulocyte chemotaxis;GO:1902624 positive regulation of neutrophil migration

Supplementary Table S4: Detailed description of DEGs (FDR $\leq$ 0.05) in eAT, mAT and sAT when patients were segregated as obese vs. lean individuals (n=5).

GeneName	Log2 FC	FDR	Description	Biological Process (GO)
eAT				
CEMIP	-2.128	0.006	cell migration inducing hyaluronan binding protein	GO:0051281 positive regulation of release of sequestered calcium ion into cytosol;GO:0051279 regulation of release of sequestered calcium ion into cytosol;GO:0010524 positive regulation of calcium ion transport into cytosol
IGLV3-9	-1.847	0.037	immunoglobulin lambda variable 3-9	GO:0002377 immunoglobulin production;GO:0002440 production of molecular mediator of immune response;GO:0002250 adaptive immune response
FER1L4	-1.577	0.006	fer-1 like family member 4, pseudogene	
NUGGC	-1.334	0.006	nuclear GTPase, germinal center associated	GO:0097752 regulation of DNA stability;GO:0071222 cellular response to lipopolysaccharide;GO:0071219 cellular response to molecule of bacterial origin
LINC01347	1.939	0.006	long intergenic non-protein coding RNA 1347	
mAT				
SAMD9L	0.754	0.000	sterile alpha motif domain containing 9 like	GO:0034058 endosomal vesicle fusion;GO:0006906 vesicle fusion;GO:0090174 organelle membrane fusion
sAT				
LINC00184	2.009	0.000	long intergenic non-protein coding RNA 184	
EGFL6	1.854	0.000	EGF like domain multiple 6	GO:0010811 positive regulation of cell-substrate adhesion;GO:0010810 regulation of cell-substrate adhesion;GO:0045785 positive regulation of cell adhesion
VLDLR-ASI	1.686	0.000	VLDLR antisense RNA 1	
DDR1	1.405	0.009	discoidin domain receptor tyrosine kinase 1	GO:0061302 smooth muscle cell-matrix adhesion;GO:0044319 wound healing, spreading of cells;GO:0060444 branching involved in mammary gland duct morphogenesis
TUBB2A	1.398	0.000	tubulin beta 2A class IIa	GO:0007017 microtubule-based process;GO:0007010 cytoskeleton organization;GO:0006996 organelle organization
SNCG	1.328	0.005	synuclein gamma	GO:0014059 regulation of dopamine secretion;GO:0014046 dopamine secretion;GO:0046928 regulation of neurotransmitter secretion
MXRA5	1.318	0.000	matrix remodeling associated 5	GO:0071559 response to transforming growth factor beta;GO:0070848 response to growth factor;GO:0009719 response to endogenous stimulus
LHCGR	1.308	0.019	luteinizing hormone/choriogonadotropin receptor	GO:0032962 positive regulation of inositol trisphosphate biosynthetic process;GO:0045762 positive regulation of adenylate cyclase activity;GO:0001545 primary ovarian follicle growth

VLDLR	1.268	0.007	very low density lipoprotein receptor	GO:0034436 glycoprotein transport;GO:0034447 very-low-density lipoprotein particle clearance;GO:0032802 low-density lipoprotein particle receptor catabolic process
SLC1A7	1.245	0.003	solute carrier family 1 member 7	GO:0014047 glutamate secretion;GO:0015800 acidic amino acid transport;GO:0006835 dicarboxylic acid transport
FAM72A	1.224	0.021	family with sequence similarity 72 member A	
FGF1	1.215	0.009	fibroblast growth factor 1	GO:0060681 branch elongation involved in ureteric bud branching;GO:0060677 ureteric bud elongation;GO:0001658 branching involved in ureteric bud morphogenesis
MTND2P28	1.212	0.049	mitochondrially encoded NADH:ubiquinone oxidoreductase core subunit 2 pseudogene 28	
KRT8P36	1.194	0.028	keratin 8 pseudogene 36	
TENM4	1.171	0.005	teneurin transmembrane protein 4	GO:0032289 central nervous system myelin formation;GO:0048714 positive regulation of oligodendrocyte differentiation;GO:0060912 cardiac cell fate specification
THY1	1.125	0.012	Thy-1 cell surface antigen	GO:0051281 positive regulation of release of sequestered calcium ion into cytosol;GO:0051279 regulation of release of sequestered calcium ion into cytosol;GO:0050860 negative regulation of T cell receptor signaling pathway
LRRN3	1.113	0.021	leucine rich repeat neuronal 3	GO:0051965 positive regulation of synapse assembly;GO:0051963 regulation of synapse assembly;GO:0007409 axonogenesis
IGSF1	1.094	0.019	immunoglobulin superfamily member 1	GO:0006355 regulation of transcription, DNA-templated;GO:1903506 regulation of nucleic acid-templated transcription;GO:0006351 transcription, DNA-templated
DOK5	1.052	0.040	docking protein 5	GO:0051386 regulation of neurotrophin TRK receptor signaling pathway;GO:0048011 neurotrophin TRK receptor signaling pathway;GO:0038179 neurotrophin signaling pathway
NTM	1.042	0.033	neurotrimin	GO:0006501 C-terminal protein lipidation;GO:0008038 neuron recognition;GO:0018410 C-terminal protein amino acid modification
PHACTR1	0.981	0.025	phosphatase and actin regulator 1	GO:0032515 negative regulation of phosphoprotein phosphatase activity;GO:0043149 stress fiber assembly;GO:0035308 negative regulation of protein dephosphorylation
OSGIN1	0.976	0.044	oxidative stress induced growth inhibitor 1	GO:0030308 negative regulation of cell growth;GO:0045926 negative regulation of growth;GO:0043065 positive regulation of apoptotic process
MSTO1	0.969	0.012	misato 1, mitochondrial distribution and morphology regulator	GO:0048311 mitochondrion distribution;GO:0051646 mitochondrion localization;GO:0007005 mitochondrion organization
SH2D4A	0.945	0.025	SH2 domain containing 4A	GO:0010923 negative regulation of phosphatase activity;GO:0035305 negative regulation of

				dephosphorylation;GO:0010921 regulation of phosphatase activity
ADAM12	0.911	0.021	ADAM metallopeptidase domain 12	GO:0045766 positive regulation of angiogenesis;GO:0007520 myoblast fusion;GO:0045765 regulation of angiogenesis
PEMT	0.903	0.009	phosphatidylethanolamine N-methyltransferase	GO:0006686 sphingomyelin biosynthetic process;GO:0046498 S-adenosylhomocysteine metabolic process;GO:0050747 positive regulation of lipoprotein metabolic process
METTL1	0.900	0.012	methyltransferase like 1	GO:0106004 tRNA (guanine-N7)-methylation;GO:0036265 RNA (guanine-N7)-methylation;GO:0030488 tRNA methylation
BHLHE41	0.876	0.042	basic helix-loop-helix family member e41	GO:0010832 negative regulation of myotube differentiation;GO:0010944 negative regulation of transcription by competitive promoter binding;GO:0051154 negative regulation of striated muscle cell differentiation
TPST2	0.873	0.009	tyrosylprotein sulfotransferase 2	GO:0006478 peptidyl-tyrosine sulfation;GO:0050427 3'-phosphoadenosine 5'-phosphosulfate metabolic process;GO:0034035 purine ribonucleoside bisphosphate metabolic process
LINC00152	0.843	0.005	cytoskeleton regulator RNA	
DZIP1L	0.839	0.045	DAZ interacting zinc finger protein 1 like	GO:0060271 cilium assembly;GO:0044782 cilium organization;GO:0120031 plasma membrane bounded cell projection assembly
OPRL1	0.836	0.024	opioid related nociceptin receptor 1	GO:1901386 negative regulation of voltage-gated calcium channel activity;GO:0060454 positive regulation of gastric acid secretion;GO:0106072 negative regulation of adenylate cyclase-activating G-protein coupled receptor signaling pathway
ITIH5	0.787	0.028	inter-alpha-trypsin inhibitor heavy chain family member 5	GO:0030212 hyaluronan metabolic process;GO:1903510 mucopolysaccharide metabolic process;GO:0010951 negative regulation of endopeptidase activity
GLRX	0.787	0.044	glutaredoxin	GO:2000651 positive regulation of sodium ion transmembrane transporter activity;GO:1902307 positive regulation of sodium ion transmembrane transport;GO:0080058 protein deglutathionylation
ITGB1BP1	0.780	0.007	integrin subunit beta 1 binding protein 1	GO:0090051 negative regulation of cell migration involved in sprouting angiogenesis;GO:0051895 negative regulation of focal adhesion assembly;GO:0090315 negative regulation of protein targeting to membrane
NCKAP5	0.776	0.005	NCK associated protein 5	GO:0008150 biological_process
SCO2	0.773	0.040	SCO2, cytochrome c oxidase assembly protein	GO:0006878 cellular copper ion homeostasis;GO:0055070 copper ion homeostasis;GO:0006825 copper ion transport
PP1L1	0.771	0.043	peptidylprolyl isomerase like 1	GO:0000413 protein peptidyl-prolyl isomerization;GO:0018208 peptidyl-proline modification;GO:0000398 mRNA splicing, via spliceosome
NEK6	0.771	0.00	NIMA related kinase 6	GO:0007077 mitotic nuclear envelope

		1		disassembly;GO:0030071 regulation of mitotic metaphase/anaphase transition;GO:0007091 metaphase/anaphase transition of mitotic cell cycle
TNS3	0.765	0.045	tensin 3	GO:0048286 lung alveolus development;GO:0030324 lung development;GO:0030323 respiratory tube development
STK38L	0.749	0.043	serine/threonine kinase 38 like	GO:0018105 peptidyl-serine phosphorylation;GO:0018209 peptidyl-serine modification;GO:0018193 peptidyl-amino acid modification
TOMM40L	0.650	0.018	translocase of outer mitochondrial membrane 40 like	GO:0030150 protein import into mitochondrial matrix;GO:0044743 protein transmembrane import into intracellular organelle;GO:0065002 intracellular protein transmembrane transport
PALMD	0.634	0.009	palmdelphin	GO:0008360 regulation of cell shape;GO:0022604 regulation of cell morphogenesis;GO:0000902 cell morphogenesis
TUBB4B	0.626	0.013	tubulin beta 4B class IVb	GO:0097711 ciliary basal body-plasma membrane docking;GO:0042267 natural killer cell mediated cytotoxicity;GO:0043312 neutrophil degranulation
SDC3	0.615	0.015	syndecan 3	GO:0001523 retinoid metabolic process;GO:0006027 glycosaminoglycan catabolic process;GO:0016101 diterpenoid metabolic process
ALAS1	0.594	0.027	5'-aminolevulinate synthase 1	GO:0006782 protoporphyrinogen IX biosynthetic process;GO:0046501 protoporphyrinogen IX metabolic process;GO:0006783 heme biosynthetic process
RGL1	0.585	0.011	ral guanine nucleotide dissociation stimulator like 1	GO:0019216 regulation of lipid metabolic process;GO:0007264 small GTPase mediated signal transduction;GO:0006629 lipid metabolic process
TUBB6	0.575	0.049	tubulin beta 6 class V	GO:0007017 microtubule-based process;GO:0007010 cytoskeleton organization;GO:0006996 organelle organization
TSPAN17	0.555	0.044	tetraspanin 17	GO:0072594 establishment of protein localization to organelle;GO:0016567 protein ubiquitination;GO:0032446 protein modification by small protein conjugation
TAF1B	0.553	0.043	TATA-box binding protein associated factor, RNA polymerase I subunit B	GO:0006362 transcription elongation from RNA polymerase I promoter;GO:0006361 transcription initiation from RNA polymerase I promoter;GO:0006363 termination of RNA polymerase I transcription
FAM49B	0.543	0.040	family with sequence similarity 49 member B	GO:2000568 positive regulation of memory T cell activation;GO:2000567 regulation of memory T cell activation;GO:0035709 memory T cell activation
HSPA5	0.536	0.001	heat shock protein family A (Hsp70) member 5	GO:1903895 negative regulation of IRE1-mediated unfolded protein response;GO:0021589 cerebellum structural organization;GO:1903891 regulation of ATF6-mediated unfolded protein response
OPA3	0.536	0.040	OPA3, outer mitochondrial membrane lipid metabolism regulator	GO:0070584 mitochondrion morphogenesis;GO:0007601 visual perception;GO:0050905 neuromuscular process
SI00A16	0.489	0.005	SI00 calcium binding protein A16	GO:0051592 response to calcium ion;GO:0010038 response to metal ion;GO:0010035 response to

				inorganic substance
OSBPL11	0.470	0.044	oxysterol binding protein like 11	GO:0010890 positive regulation of sequestering of triglyceride;GO:0010889 regulation of sequestering of triglyceride;GO:0010884 positive regulation of lipid storage
FKBP1A	0.414	0.028	FK506 binding protein 1A	GO:0060315 negative regulation of ryanodine-sensitive calcium-release channel activity;GO:0051280 negative regulation of release of sequestered calcium ion into cytosol;GO:0060314 regulation of ryanodine-sensitive calcium-release channel activity
STIP1	0.400	0.044	stress induced phosphoprotein 1	
AHSA1	0.329	0.022	activator of HSP90 ATPase activity 1	GO:0032781 positive regulation of ATPase activity;GO:0043462 regulation of ATPase activity;GO:0051345 positive regulation of hydrolase activity
ZC3H6	-0.319	0.005	zinc finger CCCH-type containing 6	GO:0008150 biological_process
RAD54L2	-0.345	0.042	RAD54 like 2	
ATL2	-0.444	0.045	atlastin GTPase 2	GO:1990809 endoplasmic reticulum tubular network membrane organization;GO:0090158 endoplasmic reticulum membrane organization;GO:0071786 endoplasmic reticulum tubular network organization
RFTN2	-0.492	0.044	raftlin family member 2	GO:0032596 protein transport into membrane raft;GO:0033227 dsRNA transport;GO:1903044 protein localization to membrane raft
MX11	-0.548	0.010	MAX interactor 1, dimerization protein	GO:0042994 cytoplasmic sequestering of transcription factor;GO:0042992 negative regulation of transcription factor import into nucleus;GO:0042308 negative regulation of protein import into nucleus
ING5	-0.571	0.024	inhibitor of growth family member 5	GO:0043966 histone H3 acetylation;GO:0016573 histone acetylation;GO:0018393 internal peptidyl-lysine acetylation
ICA1L	-0.572	0.044	islet cell autoantigen 1 like	GO:0007286 spermatid development;GO:0048515 spermatid differentiation;GO:0007283 spermatogenesis
CCNB1IP1	-0.583	0.003	cyclin B1 interacting protein 1	GO:0051026 chiasma assembly;GO:0001825 blastocyst formation;GO:0007129 synapsis
LAMB1	-0.601	0.025	laminin subunit beta 1	GO:0021812 neuronal-glia interaction involved in cerebral cortex radial glia guided migration;GO:0021801 cerebral cortex radial glia guided migration;GO:0021799 cerebral cortex radially oriented cell migration
RNF125	-0.619	0.019	ring finger protein 125	GO:0039536 negative regulation of RIG-I signaling pathway;GO:0039532 negative regulation of viral-induced cytoplasmic pattern recognition receptor signaling pathway;GO:0039535 regulation of RIG-I signaling pathway
KLHL23	-0.634	0.022	kelch like family member 23	GO:0016567 protein ubiquitination;GO:0032446 protein modification by small protein conjugation;GO:0070647 protein modification by small protein conjugation or removal
PAIP2B	-	0.01	poly(A) binding protein	GO:0045947 negative regulation of translational

	0.719	0	interacting protein 2B	initiation;GO:0006446 regulation of translational initiation;GO:0006413 translational initiation
LINC01359	- 0.737	0.02 2	long intergenic non-protein coding RNA 1359	
CDKN1C	- 0.761	0.02 2	cyclin dependent kinase inhibitor 1C	GO:0030511 positive regulation of transforming growth factor beta receptor signaling pathway;GO:1904030 negative regulation of cyclin-dependent protein kinase activity;GO:1903846 positive regulation of cellular response to transforming growth factor beta stimulus
FOXP2	- 0.779	0.04 5	forkhead box P2	GO:0021757 caudate nucleus development;GO:0021758 putamen development;GO:0060501 positive regulation of epithelial cell proliferation involved in lung morphogenesis
CRHR1-IT1	- 0.789	0.01 3	long intergenic non-protein coding RNA 2210	
PRKAG2	- 0.854	0.00 6	protein kinase AMP-activated non-catalytic subunit gamma 2	GO:0006853 carnitine shuttle;GO:0006110 regulation of glycolytic process;GO:1902001 fatty acid transmembrane transport
RAMP2-AS1	- 0.867	0.02 2	RAMP2 antisense RNA 1	
SFXN2	- 0.888	0.00 3	sideroflexin 2	GO:0055072 iron ion homeostasis;GO:0055076 transition metal ion homeostasis;GO:0055065 metal ion homeostasis
HMGN2P15	- 0.911	0.04 4	high mobility group nucleosomal binding domain 2 pseudogene 15	
FAM161A	- 0.922	0.04 5	family with sequence similarity 161 member A	GO:1901985 positive regulation of protein acetylation;GO:1901983 regulation of protein acetylation;GO:0007601 visual perception
AASS	- 0.956	0.03 3	amino adipate-semialdehyde synthase	GO:0033512 L-lysine catabolic process to acetyl-CoA via saccharopine;GO:0019474 L-lysine catabolic process to acetyl-CoA;GO:0019477 L-lysine catabolic process
C5	- 0.973	0.00 2	complement C5	GO:0010760 negative regulation of macrophage chemotaxis;GO:0090197 positive regulation of chemokine secretion;GO:1905522 negative regulation of macrophage migration
CDNF	- 0.975	0.00 4	cerebral dopamine neurotrophic factor	GO:0071542 dopaminergic neuron differentiation;GO:0010469 regulation of signaling receptor activity;GO:0031175 neuron projection development
GPD1L	- 1.023	0.02 5	glycerol-3-phosphate dehydrogenase 1 like	GO:0086005 ventricular cardiac muscle cell action potential;GO:0060373 regulation of ventricular cardiac muscle cell membrane depolarization;GO:0090038 negative regulation of protein kinase C signaling
GOLGA2P5	- 1.041	0.00 9	golgin A2 pseudogene 5	
ADH1B	- 1.086	0.01 2	alcohol dehydrogenase 1B (class I), beta polypeptide	GO:0006069 ethanol oxidation;GO:0006067 ethanol metabolic process;GO:0034308 primary alcohol metabolic process
SLC25A21-AS1	- 1.100	0.01 4	SLC25A21 antisense RNA 1	
DLGAP2	-	0.03	DLG associated protein 2	GO:0007270 neuron-neuron synaptic

	1.214	9		transmission;GO:0007268 chemical synaptic transmission;GO:0098916 anterograde trans-synaptic signaling
ALDH1L1-AS2	- 1.273	0.00 4	ALDH1L1 antisense RNA 2	
NLRP14	- 1.277	0.04 5	NLR family pyrin domain containing 14	GO:0007283 spermatogenesis;GO:0048232 male gamete generation;GO:0007276 gamete generation
PRUNE2	- 1.278	0.02 8	prune homolog 2	GO:0006915 apoptotic process;GO:0012501 programmed cell death;GO:0008219 cell death
FXYP1	- 1.355	0.01 0	FXYP domain containing ion transport regulator 1	GO:1903278 positive regulation of sodium ion export across plasma membrane;GO:0010734 negative regulation of protein glutathionylation;GO:1903276 regulation of sodium ion export across plasma membrane
SCN7A	- 1.355	0.01 8	sodium voltage-gated channel alpha subunit 7	GO:0055078 sodium ion homeostasis;GO:0019228 neuronal action potential;GO:0086010 membrane depolarization during action potential
CBS	- 1.359	0.00 6	cystathionine-beta-synthase	GO:0019448 L-cysteine catabolic process;GO:0009093 cysteine catabolic process;GO:0019343 cysteine biosynthetic process via cystathionine
TSHR	- 1.394	0.01 9	thyroid stimulating hormone receptor	GO:0045762 positive regulation of adenylate cyclase activity;GO:1905229 cellular response to thyrotropin-releasing hormone;GO:0030819 positive regulation of cAMP biosynthetic process
SPTB	- 1.400	0.01 8	spectrin beta, erythrocytic	GO:0051693 actin filament capping;GO:0030835 negative regulation of actin filament depolymerization;GO:0030837 negative regulation of actin filament polymerization
ABCB11	- 1.404	0.00 1	ATP binding cassette subfamily B member 11	GO:0015722 canalicular bile acid transport;GO:0006699 bile acid biosynthetic process;GO:0015721 bile acid and bile salt transport
ARHGEF26-AS1	- 1.413	0.00 9	ARHGEF26 antisense RNA 1	
DMC1	- 1.424	0.00 7	DNA meiotic recombinase 1	GO:0001556 oocyte maturation;GO:0000730 DNA recombinase assembly;GO:0007141 male meiosis I
MKX	- 1.472	0.01 0	mohawk homeobox	GO:0007517 muscle organ development;GO:0061061 muscle structure development;GO:0006355 regulation of transcription, DNA-templated
ANKRD20A5P	- 1.512	0.00 7	ankyrin repeat domain 20 family member A5, pseudogene	
MAB21L3	- 1.532	0.00 5	mab-21 like 3	
SNX31	- 1.541	0.00 6	sorting nexin 31	GO:1990126 retrograde transport, endosome to plasma membrane;GO:0098876 vesicle-mediated transport to the plasma membrane;GO:0016197 endosomal transport
FHOD3	- 1.543	0.00 3	formin homology 2 domain containing 3	GO:0055003 cardiac myofibril assembly;GO:0030837 negative regulation of actin filament polymerization;GO:0051639 actin filament network formation
C6	- 1.619	0.00 3	complement C6	GO:0001970 positive regulation of activation of membrane attack complex;GO:0045917 positive regulation of complement activation;GO:0001969

				regulation of activation of membrane attack complex
PKP2	- 1.697	0.00 1	plakophilin 2	GO:0086073 bundle of His cell-Purkinje myocyte adhesion involved in cell communication;GO:0098911 regulation of ventricular cardiac muscle cell action potential;GO:0086064 cell communication by electrical coupling involved in cardiac conduction
CHODL	- 1.698	0.00 1	chondrolectin	GO:0010975 regulation of neuron projection development;GO:0045664 regulation of neuron differentiation;GO:0031175 neuron projection development
LRP1B	- 1.957	0.00 0	LDL receptor related protein 1B	GO:0006898 receptor-mediated endocytosis;GO:0006897 endocytosis;GO:0098657 import into cell
BMP3	- 2.354	0.00 0	bone morphogenetic protein 3	GO:0010862 positive regulation of pathway-restricted SMAD protein phosphorylation;GO:0060393 regulation of pathway-restricted SMAD protein phosphorylation;GO:0060389 pathway-restricted SMAD protein phosphorylation

Supplementary Table S5: Detailed description of DEGs (FDR $\leq$ 0.05) in eAT, mAT and sAT when patients were segregated as CAD (n=6) vs. NCAD (n=4).

Gene name	Log2 FC	FDR	Description	Biological process (GO)
eAT				
HLA-C*	-7.531	0.053	DExD-box helicase 39B	GO:0061051 positive regulation of cell growth involved in cardiac muscle cell development;GO:2000002 negative regulation of DNA damage checkpoint;GO:0046784 viral mRNA export from host cell nucleus
DDX39B	-6.745	0.000	major histocompatibility complex, class I, C	GO:0002480 antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-independent;GO:0002479 antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;GO:0042590 antigen processing and presentation of exogenous peptide antigen via MHC class I
mAT				
GABRA5	21.070	0.000	gamma-aminobutyric acid type A receptor alpha5 subunit	GO:0060119 inner ear receptor cell development;GO:0090102 cochlea development;GO:0060384 innervation
KRT5	7.512	0.042	keratin 5	GO:0031581 hemidesmosome assembly;GO:0070268 cornification;GO:0031424 keratinization
ARPP21	6.915	0.025	cAMP regulated phosphoprotein 21	GO:0034605 cellular response to heat;GO:0009408 response to heat;GO:0009266 response to temperature stimulus
KRT19	6.556	0.025	keratin 19	GO:0070268 cornification;GO:0060706 cell differentiation involved in embryonic placenta development;GO:0045214 sarcomere organization
TRIM29	5.977	0.024	tripartite motif containing 29	GO:1900181 negative regulation of protein localization to nucleus;GO:1903828 negative regulation of cellular protein localization;GO:1900180 regulation of protein localization to nucleus
CALN1	5.645	0.015	calneuron 1	
RAG1	5.587	0.006	recombination activating 1	GO:0002331 pre-B cell allelic exclusion;GO:0070244 negative regulation of thymocyte apoptotic process;GO:0002329 pre-B cell differentiation
SI00A14	5.526	0.038	SI00 calcium binding protein A14	GO:0034142 toll-like receptor 4 signaling pathway;GO:0090026 positive regulation of monocyte chemotaxis;GO:0071624 positive regulation of granulocyte chemotaxis
ZBED2	5.401	0.046	zinc finger BED-type containing 2	
IGHV3-53	5.385	0.013	immunoglobulin heavy variable 3-53	GO:0038096 Fc-gamma receptor signaling pathway involved in phagocytosis;GO:0002431 Fc receptor mediated stimulatory signaling pathway;GO:0006958 complement activation, classical pathway
DSC3	5.034	0.022	desmocollin 3	GO:0070268 cornification;GO:0031424 keratinization;GO:0030216 keratinocyte differentiation
ELOVL4	4.178	0.038	ELOVL fatty acid elongase 4	GO:0034625 fatty acid elongation, monounsaturated fatty acid;GO:0034626 fatty acid elongation, polyunsaturated fatty

				acid;GO:0019367 fatty acid elongation, saturated fatty acid
PRTN3	3.730	0.003	proteinase 3	GO:0097029 mature conventional dendritic cell differentiation;GO:0072672 neutrophil extravasation;GO:0050765 negative regulation of phagocytosis
LCN2	3.604	0.000	lipocalin 2	GO:0015891 siderophore transport;GO:0015688 iron chelate transport;GO:0006879 cellular iron ion homeostasis
NEIL3	3.235	0.015	nei like DNA glycosylase 3	GO:0006284 base-excision repair;GO:0006289 nucleotide-excision repair;GO:0006281 DNA repair
E2F2	3.226	0.046	E2F transcription factor 2	GO:1990086 lens fiber cell apoptotic process;GO:0072332 intrinsic apoptotic signaling pathway by p53 class mediator;GO:1904019 epithelial cell apoptotic process
ABCA13	3.116	0.000	ATP binding cassette subfamily A member 13	GO:0043312 neutrophil degranulation;GO:0002283 neutrophil activation involved in immune response;GO:0042119 neutrophil activation
MPO	2.916	0.005	myeloperoxidase	GO:0002149 hypochlorous acid biosynthetic process;GO:0044130 negative regulation of growth of symbiont in host;GO:1990268 response to gold nanoparticle
VWA2	2.898	0.035	von Willebrand factor A domain containing 2	GO:0007161 calcium-independent cell-matrix adhesion;GO:0046626 regulation of insulin receptor signaling pathway;GO:1900076 regulation of cellular response to insulin stimulus
MS4A3	2.661	0.037	membrane spanning 4-domains A3	GO:0043312 neutrophil degranulation;GO:0002283 neutrophil activation involved in immune response;GO:0042119 neutrophil activation
BPI	2.660	0.037	bactericidal/permeability-increasing protein	GO:0043031 negative regulation of macrophage activation;GO:0032717 negative regulation of interleukin-8 production;GO:0032720 negative regulation of tumor necrosis factor production
LTF	2.067	0.004	lactotransferrin	GO:1900159 positive regulation of bone mineralization involved in bone maturation;GO:0034145 positive regulation of toll-like receptor 4 signaling pathway;GO:1900229 negative regulation of single-species biofilm formation in or on host organism
PRSS12	2.051	0.037	protease, serine 12	GO:0031638 zymogen activation;GO:0006898 receptor-mediated endocytosis;GO:0016485 protein processing
TMCC2	1.651	0.000	transmembrane and coiled-coil domain family 2	GO:0042982 amyloid precursor protein metabolic process;GO:0019538 protein metabolic process;GO:1901564 organonitrogen compound metabolic process
ISYNA1	1.039	0.037	inositol-3-phosphate synthase 1	GO:0006021 inositol biosynthetic process;GO:0006020 inositol metabolic process;GO:0043647 inositol phosphate metabolic process
ARIH1	-0.290	0.021	ariadne RBR E3 ubiquitin protein ligase 1	GO:0032436 positive regulation of proteasomal ubiquitin-dependent protein catabolic process;GO:2000060 positive regulation of ubiquitin-dependent protein catabolic process;GO:1901800 positive regulation of proteasomal protein catabolic process
CCNC	-0.494	0.003	cyclin C	GO:1901409 positive regulation of phosphorylation of RNA polymerase II C-terminal domain;GO:0045737 positive regulation of cyclin-dependent protein serine/threonine kinase activity;GO:1901407 regulation of phosphorylation of RNA polymerase II C-terminal domain
FAM214A	-0.921	0.000	family with sequence similarity 214 member A	

DDX39B	-4.972	0.037	DExD-box helicase 39B	GO:0061051 positive regulation of cell growth involved in cardiac muscle cell development;GO:2000002 negative regulation of DNA damage checkpoint;GO:0046784 viral mRNA export from host cell nucleus
HLA-C	-8.621	0.002	major histocompatibility complex, class I, C	GO:0002480 antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-independent;GO:0002479 antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;GO:0042590 antigen processing and presentation of exogenous peptide antigen via MHC class I
			sAT	
ADGRG7	23.698	0.000	adhesion G protein-coupled receptor G7	GO:0007186 G-protein coupled receptor signaling pathway;GO:0007166 cell surface receptor signaling pathway;GO:0007165 signal transduction
DDX39B	-6.767	0.000	DExD-box helicase 39B	GO:0061051 positive regulation of cell growth involved in cardiac muscle cell development;GO:2000002 negative regulation of DNA damage checkpoint;GO:0046784 viral mRNA export from host cell nucleus
ATPIA2	-1.510	0.004	ATPase Na ⁺ /K ⁺ transporting subunit alpha 2	GO:0010881 regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion;GO:0051946 regulation of glutamate uptake involved in transmission of nerve impulse;GO:0010880 regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum
FAM107A	-1.484	0.005	family with sequence similarity 107 member A	GO:0001558 regulation of cell growth;GO:0016049 cell growth;GO:0040008 regulation of growth
FAM155A	-1.491	0.010	family with sequence similarity 155 member A	GO:0098703 calcium ion import across plasma membrane;GO:1902656 calcium ion import into cytosol;GO:0097553 calcium ion transmembrane import into cytosol
HLA-C*	-6.782	0.070	major histocompatibility complex, class I, C	GO:0002480 antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-independent;GO:0002479 antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;GO:0042590 antigen processing and presentation of exogenous peptide antigen via MHC class I

* Please note that FDR for HLA-C in eAT and sAT is above 0.05.

Supplementary Table S6: Detailed description of top up- and down-regulated genes ($FC \geq 2$ or ≤ -2 ; $FDR \leq 0.05$) in eAT, mAT and sAT when segregated as per the high and low UCPI-expression in eAT (n=5).

Gene Name	Log2 FC	FDR	Description	Biological Process (GO)
eAT				
UCPI	2.409	0.000	uncoupling protein 1	GO:0002024 diet induced thermogenesis;GO:1990845 adaptive thermogenesis;GO:0002021 response to dietary excess
ACTG2	1.726	0.023	actin, gamma 2, smooth muscle, enteric	GO:0090131 mesenchyme migration;GO:0072132 mesenchyme morphogenesis;GO:0060485 mesenchyme development
NOTCH4	1.629	0.038	notch 4	GO:0045602 negative regulation of endothelial cell differentiation;GO:0001886 endothelial cell morphogenesis;GO:0007221 positive regulation of transcription of Notch receptor target
LINC00993	1.621	0.033	long intergenic non-protein coding RNA 993	
AC018647.3	1.602	0.031	None	None
PCDH11X	1.593	0.033	protocadherin 11 X-linked	GO:0010923 negative regulation of phosphatase activity;GO:0035305 negative regulation of dephosphorylation;GO:0007156 homophilic cell adhesion via plasma membrane adhesion molecules
TMEM155	1.590	0.044	transmembrane protein 155	
RP11-402C9.1	1.566	0.038	None	None
HBA2	1.515	0.038	hemoglobin subunit alpha 2	GO:0015671 oxygen transport;GO:0015701 bicarbonate transport;GO:0042744 hydrogen peroxide catabolic process
ISLR2	1.515	0.004	immunoglobulin superfamily containing leucine rich repeat 2	GO:0045773 positive regulation of axon extension;GO:0050772 positive regulation of axonogenesis;GO:0030516 regulation of axon extension
HBA1	1.500	0.038	hemoglobin subunit alpha 1	GO:0015671 oxygen transport;GO:0015701 bicarbonate transport;GO:0042744 hydrogen peroxide catabolic process
ANO3	1.493	0.002	anoctamin 3	GO:0061590 calcium activated phosphatidylcholine scrambling;GO:0061591 calcium activated galactosylceramide scrambling;GO:0061588 calcium activated phospholipid scrambling
RNF208	1.473	0.028	ring finger protein 208	GO:0051865 protein autoubiquitination;GO:0016567 protein ubiquitination;GO:0032446 protein modification by small protein conjugation

LINC01186	1.435	0.023	long intergenic non-protein coding RNA 1186	
SLC27A6	1.375	0.026	solute carrier family 27 member 6	GO:0015909 long-chain fatty acid transport;GO:0000038 very long-chain fatty acid metabolic process;GO:0015908 fatty acid transport
ENSG00000184674	1.355	0.045	None	None
DEFB132	1.301	0.013	defensin beta 132	GO:0031640 killing of cells of other organism;GO:0050829 defense response to Gram-negative bacterium;GO:0044364 disruption of cells of other organism
ZNF536	1.260	0.045	zinc finger protein 536	GO:0048387 negative regulation of retinoic acid receptor signaling pathway;GO:0048385 regulation of retinoic acid receptor signaling pathway;GO:0048384 retinoic acid receptor signaling pathway
SIX1	1.157	0.045	SIX homeobox 1	GO:0072107 positive regulation of ureteric bud formation;GO:0072095 regulation of branch elongation involved in ureteric bud branching;GO:0090191 negative regulation of branching involved in ureteric bud morphogenesis
GPLD1	1.147	0.038	glycosylphosphatidylinositol specific phospholipase D1	GO:0010897 negative regulation of triglyceride catabolic process;GO:0010983 positive regulation of high-density lipoprotein particle clearance;GO:0006507 GPI anchor release
CIB2	1.121	0.031	calcium and integrin binding family member 2	GO:0071318 cellular response to ATP;GO:0045494 photoreceptor cell maintenance;GO:0033198 response to ATP
SLC25A10	1.117	0.047	solute carrier family 25 member 10	GO:1902356 oxaloacetate(2-) transmembrane transport;GO:0071423 malate transmembrane transport;GO:0071422 succinate transmembrane transport
ENSG00000203415	1.088	0.047	None	None
ARHGEF4	1.088	0.027	Rho guanine nucleotide exchange factor 4	GO:0030032 lamellipodium assembly;GO:0046847 filopodium assembly;GO:0035023 regulation of Rho protein signal transduction
STBD1	1.081	0.025	starch binding domain 1	GO:0061723 glycophagy;GO:0005980 glycogen catabolic process;GO:0043312 neutrophil degranulation
CHADL	1.071	0.031	chondroadherin like	GO:1904027 negative regulation of collagen fibril organization;GO:1904026 regulation of collagen fibril organization;GO:1903054 negative regulation of extracellular matrix organization
LINC00982	1.002	0.038	long intergenic non-protein coding RNA 982	
RPI1-410E4.1	-1.019	0.043	None	None

SLC15A2	-1.038	0.033	solute carrier family 15 member 2	GO:0035672 oligopeptide transmembrane transport;GO:0006857 oligopeptide transport;GO:0015893 drug transport
CKLF	-1.052	0.038	chemokine like factor	GO:0048246 macrophage chemotaxis;GO:0030593 neutrophil chemotaxis;GO:1905517 macrophage migration
ZNF92	-1.058	0.028	zinc finger protein 92	GO:0006355 regulation of transcription, DNA-templated;GO:1903506 regulation of nucleic acid-templated transcription;GO:0006351 transcription, DNA-templated
HACD4	-1.071	0.038	3-hydroxyacyl-CoA dehydratase 4	GO:0042761 very long-chain fatty acid biosynthetic process;GO:0030497 fatty acid elongation;GO:0000038 very long-chain fatty acid metabolic process
RP11-395I6.3	-1.078	0.038	None	None
EMB	-1.091	0.038	embigin	GO:0035879 plasma membrane lactate transport;GO:0035873 lactate transmembrane transport;GO:0015727 lactate transport
TLR6	-1.092	0.040	toll like receptor 6	GO:0034136 negative regulation of toll-like receptor 2 signaling pathway;GO:0042496 detection of diacyl bacterial lipopeptide;GO:0034150 toll-like receptor 6 signaling pathway
COL9A2	-1.107	0.028	collagen type IX alpha 2 chain	GO:0030198 extracellular matrix organization;GO:0043062 extracellular structure organization;GO:0001501 skeletal system development
HIST1H1B	-1.135	0.050	histone cluster 1 H1 family member b	GO:0051574 positive regulation of histone H3-K9 methylation;GO:0071169 establishment of protein localization to chromatin;GO:0051570 regulation of histone H3-K9 methylation
BTG1P1	-1.146	0.038	BTG anti-proliferation factor 1 pseudogene 1	
LINC00920	-1.183	0.050	long intergenic non-protein coding RNA 920	
ASF1B	-1.212	0.040	anti-silencing function 1B histone chaperone	GO:0006335 DNA replication-dependent nucleosome assembly;GO:0006336 DNA replication-independent nucleosome assembly;GO:0034723 DNA replication-dependent nucleosome organization
KLRG1	-1.225	0.000	killer cell lectin like receptor G1	GO:0006968 cellular defense response;GO:0006954 inflammatory response;GO:0045087 innate immune response
MIAT	-1.228	0.031	myocardial infarction associated transcript (non-protein coding)	
GZMA	-1.235	0.005	granzyme A	GO:0032078 negative regulation of endodeoxyribonuclease activity;GO:0032076 negative regulation of deoxyribonuclease activity;GO:0032071 regulation of endodeoxyribonuclease activity
RP11-248J18.3	-1.250	0.036	None	None
ABCC3	-1.260	0.044	ATP binding cassette subfamily C member 3	GO:0015722 canalicular bile acid transport;GO:0099133 ATP hydrolysis coupled anion transmembrane transport;GO:0015721 bile acid and bile salt transport
IL12RB1	-1.285	0.033	interleukin 12 receptor subunit beta 1	GO:2000330 positive regulation of T-helper 17 cell lineage commitment;GO:2000328 regulation of T-helper 17 cell lineage commitment;GO:2000321 positive regulation of T-helper 17 cell differentiation
SLA	-1.287	0.045	Src like adaptor	GO:0038083 peptidyl-tyrosine autophosphorylation;GO:0018108 peptidyl-tyrosine phosphorylation;GO:0046777 protein autophosphorylation
TNFSF8	-1.298	0.028	TNF	GO:0043374 CD8-positive, alpha-beta T cell

			superfamily member 8	differentiation;GO:0036037 CD8-positive, alpha-beta T cell activation;GO:0046632 alpha-beta T cell differentiation
EVI2B	-1.309	0.038	ecotropic viral integration site 2B	GO:0045660 positive regulation of neutrophil differentiation;GO:0045658 regulation of neutrophil differentiation;GO:0030854 positive regulation of granulocyte differentiation
BIN2	-1.325	0.045	bridging integrator 2	GO:0097320 plasma membrane tubulation;GO:0043312 neutrophil degranulation;GO:0071800 podosome assembly
MYO1G	-1.331	0.047	myosin 1G	GO:0071976 cell gliding;GO:0038096 Fc-gamma receptor signaling pathway involved in phagocytosis;GO:0002431 Fc receptor mediated stimulatory signaling pathway
Clorf189	-1.332	0.038	chromosome 1 open reading frame 189	
RPII-91P24.7	-1.335	0.041	None	None
TTC9	-1.350	0.050	tetratricopeptide repeat domain 9	GO:0060348 bone development;GO:0001501 skeletal system development;GO:0048513 animal organ development
SEMA4D	-1.350	0.050	semaphorin 4D	GO:0048672 positive regulation of collateral sprouting;GO:0010693 negative regulation of alkaline phosphatase activity;GO:1900220 semaphorin-plexin signaling pathway involved in bone trabecula morphogenesis
KBTBD8	-1.352	0.042	kelch repeat and BTB domain containing 8	GO:0014029 neural crest formation;GO:0014032 neural crest cell development;GO:0006513 protein monoubiquitination
PBX4	-1.368	0.037	PBX homeobox 4	GO:0045893 positive regulation of transcription, DNA-templated;GO:1903508 positive regulation of nucleic acid-templated transcription;GO:1902680 positive regulation of RNA biosynthetic process
SAMD3	-1.379	0.015	sterile alpha motif domain containing 3	
ENSG00000197459	-1.379	0.038	None	None
FCHO1	-1.398	0.045	FCH domain only 1	GO:0072583 clathrin-dependent endocytosis;GO:0048268 clathrin coat assembly;GO:0006898 receptor-mediated endocytosis
LY75	-1.398	0.045	lymphocyte antigen 75	GO:0006954 inflammatory response;GO:0006897 endocytosis;GO:0098657 import into cell
Y_RNA	-1.398	0.047	None	None
RUNX3	-1.402	0.040	runt related transcription factor 3	GO:0048935 peripheral nervous system neuron development;GO:0048934 peripheral nervous system neuron differentiation;GO:0002062 chondrocyte differentiation
RPII-75L1.2	-1.405	0.038	None	None
FYB	-1.408	0.047	FYN binding protein 1	GO:0006607 NLS-bearing protein import into nucleus;GO:0050852 T cell receptor signaling pathway;GO:0050851 antigen receptor-mediated signaling pathway
CD8A	-1.408	0.025	CD8a molecule	GO:0045065 cytotoxic T cell differentiation;GO:0002456 T cell mediated immunity;GO:0030217 T cell differentiation
PTPN7	-1.419	0.038	protein tyrosine phosphatase, non-receptor type 7	GO:0035335 peptidyl-tyrosine dephosphorylation;GO:0006470 protein dephosphorylation;GO:0071345 cellular response to cytokine stimulus

ENSG00000270107	-1.424	0.037	None	None
CCR4	-1.431	0.038	C-C motif chemokine receptor 4	GO:0050927 positive regulation of positive chemotaxis;GO:0050926 regulation of positive chemotaxis;GO:0007204 positive regulation of cytosolic calcium ion concentration
EVI2A	-1.437	0.031	ecotropic viral integration site 2A	GO:0007165 signal transduction;GO:0023052 signaling;GO:0007154 cell communication
ITGA4	-1.452	0.038	integrin subunit alpha 4	GO:1903238 positive regulation of leukocyte tethering or rolling;GO:1990771 clathrin-dependent extracellular exosome endocytosis;GO:1903236 regulation of leukocyte tethering or rolling
RPI1-438L19.1	-1.454	0.041	None	None
CYFIP2	-1.458	0.048	cytoplasmic FMR1 interacting protein 2	GO:0051388 positive regulation of neurotrophin TRK receptor signaling pathway;GO:0097202 activation of cysteine-type endopeptidase activity;GO:0051386 regulation of neurotrophin TRK receptor signaling pathway
KLRK1	-1.465	0.038	killer cell lectin like receptor K1	GO:2000502 negative regulation of natural killer cell chemotaxis;GO:1901624 negative regulation of lymphocyte chemotaxis;GO:2000501 regulation of natural killer cell chemotaxis
KIF14	-1.469	0.028	kinesin family member 14	GO:0021685 cerebellar granular layer structural organization;GO:0021693 cerebellar Purkinje cell layer structural organization;GO:0021698 cerebellar cortex structural organization
IKZF1	-1.470	0.036	IKAROS family zinc finger 1	GO:0030218 erythrocyte differentiation;GO:0034101 erythrocyte homeostasis;GO:0051291 protein heterooligomerization
BIRC3	-1.473	0.038	baculoviral IAP repeat containing 3	GO:0039535 regulation of RIG-I signaling pathway;GO:0070424 regulation of nucleotide-binding oligomerization domain containing signaling pathway;GO:0035666 TRIF-dependent toll-like receptor signaling pathway
TNC	-1.476	0.038	tenascin C	GO:0060447 bud outgrowth involved in lung branching;GO:0060739 mesenchymal-epithelial cell signaling involved in prostate gland development;GO:0014012 peripheral nervous system axon regeneration
KMO	-1.483	0.036	kynurenine 3-monooxygenase	GO:0019441 tryptophan catabolic process to kynurenine;GO:0019805 quinolinate biosynthetic process;GO:0006569 tryptophan catabolic process
CD48	-1.484	0.047	CD48 molecule	GO:0002819 regulation of adaptive immune response;GO:0050900 leukocyte migration;GO:0002250 adaptive immune response
GOLGA5P1	-1.491	0.038	golgin A5 pseudogene 1	
SNX22	-1.492	0.047	sorting nexin 22	GO:0015031 protein transport;GO:0015833 peptide transport;GO:0042886 amide transport
RCAN3	-1.495	0.039	RCAN family member 3	GO:0070884 regulation of calcineurin-NFAT signaling cascade;GO:0106056 regulation of calcineurin-mediated signaling;GO:0033173 calcineurin-NFAT signaling cascade
ZNF831	-1.498	0.038	zinc finger protein 831	GO:0000122 negative regulation of transcription by RNA polymerase II;GO:0045892 negative regulation of transcription,

				DNA-templated;GO:1903507 negative regulation of nucleic acid-templated transcription
TTC16	-1.498	0.033	tetratricopeptide repeat domain 16	
ASPM	-1.500	0.029	abnormal spindle microtubule assembly	GO:0045769 negative regulation of asymmetric cell division;GO:0021873 forebrain neuroblast division;GO:0051661 maintenance of centrosome location
ACAP1	-1.505	0.047	ArfGAP with coiled-coil, ankyrin repeat and PH domains 1	GO:0043547 positive regulation of GTPase activity;GO:0043087 regulation of GTPase activity;GO:0051345 positive regulation of hydrolase activity
PTPRC	-1.506	0.031	protein tyrosine phosphatase, receptor type C	GO:0001915 negative regulation of T cell mediated cytotoxicity;GO:2000473 positive regulation of hematopoietic stem cell migration;GO:0050857 positive regulation of antigen receptor-mediated signaling pathway
SPI40	-1.507	0.045	SPI40 nuclear body protein	GO:0006952 defense response;GO:0006355 regulation of transcription, DNA-templated;GO:1903506 regulation of nucleic acid-templated transcription
TMC8	-1.507	0.050	transmembrane channel like 8	GO:0032460 negative regulation of protein oligomerization;GO:1902041 regulation of extrinsic apoptotic signaling pathway via death domain receptors;GO:0055069 zinc ion homeostasis
FAM65B	-1.507	0.044	RHO family interacting cell polarization regulator 2	GO:1903904 negative regulation of establishment of T cell polarity;GO:2000391 positive regulation of neutrophil extravasation;GO:2000405 negative regulation of T cell migration
MIR155HG	-1.525	0.038	MIR155 host gene	
STAG3	-1.527	0.038	stromal antigen 3	GO:0007130 synaptonemal complex assembly;GO:0007129 synapsis;GO:0045143 homologous chromosome segregation
NLRC3	-1.536	0.037	NLR family CARD domain containing 3	GO:1900226 negative regulation of NLRP3 inflammasome complex assembly;GO:0032687 negative regulation of interferon-alpha production;GO:1900016 negative regulation of cytokine production involved in inflammatory response
ARRDC5	-1.539	0.048	arrestin domain containing 5	GO:0007165 signal transduction;GO:0023052 signaling;GO:0007154 cell communication
FCRL3	-1.539	0.044	Fc receptor like 3	GO:0050859 negative regulation of B cell receptor signaling pathway;GO:0034163 regulation of toll-like receptor 9 signaling pathway;GO:0034162 toll-like receptor 9 signaling pathway
IL21R	-1.544	0.044	interleukin 21 receptor	GO:0038114 interleukin-21-mediated signaling pathway;GO:0098757 cellular response to interleukin-21;GO:0098756 response to interleukin-21
AC104820.2	-1.548	0.044	None	None
PRKCQ	-1.549	0.038	protein kinase C theta	GO:2000570 positive regulation of T-helper 2 cell activation;GO:2000569 regulation of T-helper 2 cell activation;GO:0035712 T-helper 2 cell activation
PRKCQ-AS1	-1.549	0.047	PRKCQ antisense RNA 1	
SIRPG	-1.550	0.048	signal regulatory protein	GO:0050870 positive regulation of T cell activation;GO:1903039 positive regulation of leukocyte cell-cell adhesion;GO:0022409 positive regulation of cell-cell

			gamma	adhesion
PYHIN1	-1.551	0.031	pyrin and HIN domain family member 1	GO:1902164 positive regulation of DNA damage response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator;GO:1902162 regulation of DNA damage response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator;GO:0043517 positive regulation of DNA damage response, signal transduction by p53 class mediator
CNR2	-1.554	0.048	cannabinoid receptor 2	GO:0032229 negative regulation of synaptic transmission, GABAergic;GO:0051001 negative regulation of nitric-oxide synthase activity;GO:0033004 negative regulation of mast cell activation
IPCEF1	-1.555	0.038	interaction protein for cytohesin exchange factors 1	GO:0015671 oxygen transport;GO:0015669 gas transport;GO:0098869 cellular oxidant detoxification
TRAJ51	-1.557	0.045	T cell receptor alpha joining 51 (pseudogene)	
CD19	-1.558	0.047	CD19 molecule	GO:0051281 positive regulation of release of sequestered calcium ion into cytosol;GO:0051279 regulation of release of sequestered calcium ion into cytosol;GO:0010524 positive regulation of calcium ion transport into cytosol
SPIB	-1.559	0.044	Spi-B transcription factor	GO:0045944 positive regulation of transcription by RNA polymerase II;GO:0045893 positive regulation of transcription, DNA-templated;GO:1903508 positive regulation of nucleic acid-templated transcription
CRTAM	-1.562	0.015	cytotoxic and regulatory T cell molecule	GO:0002860 positive regulation of natural killer cell mediated cytotoxicity directed against tumor cell target;GO:0002857 positive regulation of natural killer cell mediated immune response to tumor cell;GO:0002858 regulation of natural killer cell mediated cytotoxicity directed against tumor cell target
TPRKBP2	-1.563	0.023	TP53RK binding protein pseudogene 2	
ENSG00000264198	-1.564	0.038	None	None
FAM129C	-1.564	0.046	family with sequence similarity 129 member C	
TRAV38-2DV8	-1.565	0.049	T cell receptor alpha variable 38-2/delta variable 8	
ZC3H12D	-1.570	0.031	zinc finger CCCH-type containing 12D	GO:0061158 3'-UTR-mediated mRNA destabilization;GO:0061157 mRNA destabilization;GO:0061014 positive regulation of mRNA catabolic process
AC007381.3	-1.571	0.041	None	None
PLAC8	-1.574	0.038	placenta specific 8	GO:0040015 negative regulation of multicellular organism growth;GO:0043312 neutrophil degranulation;GO:0002283 neutrophil activation involved in immune response
TRAJ24	-1.576	0.047	T cell receptor alpha joining 24	
LY9	-1.579	0.044	lymphocyte antigen 9	GO:0072540 T-helper 17 cell lineage commitment;GO:0002295 T-helper cell lineage commitment;GO:0072539 T-helper 17 cell differentiation
PRAME	-1.580	0.045	preferentially expressed antigen in melanoma	GO:0048387 negative regulation of retinoic acid receptor signaling pathway;GO:0048385 regulation of retinoic acid receptor signaling pathway;GO:0048384 retinoic acid receptor signaling pathway
SLAMF1	-1.582	0.028	signaling	GO:2000349 negative regulation of CD40 signaling

			lymphocytic activation molecule family member 1	pathway;GO:0002277 myeloid dendritic cell activation involved in immune response;GO:2000348 regulation of CD40 signaling pathway
ZAP70	-1.583	0.038	zeta chain of T cell receptor associated protein kinase 70	GO:0043366 beta selection;GO:0070489 T cell aggregation;GO:0045060 negative thymic T cell selection
SKAP1	-1.585	0.038	src kinase associated phosphoprotein 1	GO:0050852 T cell receptor signaling pathway;GO:0050851 antigen receptor-mediated signaling pathway;GO:0002429 immune response-activating cell surface receptor signaling pathway
PRR13P5	-1.586	0.037	proline rich 13 pseudogene 5	
TRAJ20	-1.586	0.045	T cell receptor alpha joining 20	
TRAJ50	-1.587	0.045	T cell receptor alpha joining 50	
RASGRP1	-1.587	0.033	RAS guanyl releasing protein 1	GO:0033089 positive regulation of T cell differentiation in thymus;GO:0032825 positive regulation of natural killer cell differentiation;GO:1902715 positive regulation of interferon-gamma secretion
TRAF3IP3	-1.593	0.035	TRAF3 interacting protein 3	
ERMN	-1.594	0.038	ermin	GO:0008360 regulation of cell shape;GO:0001763 morphogenesis of a branching structure;GO:0007015 actin filament organization
SIT1	-1.597	0.037	signaling threshold regulating transmembrane adaptor 1	GO:0043029 T cell homeostasis;GO:0002260 lymphocyte homeostasis;GO:0001776 leukocyte homeostasis
RPI1-75L1.1	-1.608	0.042	None	None
TRAJ6	-1.609	0.040	T cell receptor alpha joining 6	
CD8B	-1.612	0.015	CD8b molecule	GO:0050690 regulation of defense response to virus by virus;GO:0042110 T cell activation;GO:0016032 viral process
KB-226F1.2	-1.614	0.039	None	None
LCK	-1.615	0.038	LCK proto-oncogene, Src family tyrosine kinase	GO:0050862 positive regulation of T cell receptor signaling pathway;GO:0050857 positive regulation of antigen receptor-mediated signaling pathway;GO:0051209 release of sequestered calcium ion into cytosol
GCSAM	-1.615	0.036	germinal center associated signaling and motility	GO:0050855 regulation of B cell receptor signaling pathway;GO:2000402 negative regulation of lymphocyte migration;GO:0050854 regulation of antigen receptor-mediated signaling pathway
BTLA	-1.617	0.038	B and T lymphocyte associated	GO:0031295 T cell costimulation;GO:0031294 lymphocyte costimulation;GO:0050870 positive regulation of T cell activation
CD3D	-1.623	0.038	CD3d molecule	GO:0045059 positive thymic T cell selection;GO:0045061 thymic T cell selection;GO:0043368 positive T cell selection
IGHV10R15-1	-1.624	0.038	immunoglobulin heavy variable	GO:0038096 Fc-gamma receptor signaling pathway involved in phagocytosis;GO:0002431 Fc receptor mediated stimulatory signaling pathway;GO:0006958 complement activation, classical

			I/ORI5-I (non-functional)	pathway
HKDCI	-1.626	0.038	hexokinase domain containing 1	GO:0006096 glycolytic process;GO:0006757 ATP generation from ADP;GO:0046031 ADP metabolic process
RASSF5	-1.626	0.038	Ras association domain family member 5	GO:0031398 positive regulation of protein ubiquitination;GO:1903322 positive regulation of protein modification by small protein conjugation or removal;GO:0031396 regulation of protein ubiquitination
IKZF3	-1.628	0.031	IKAROS family zinc finger 3	GO:0045577 regulation of B cell differentiation;GO:0030888 regulation of B cell proliferation;GO:0030183 B cell differentiation
BLK	-1.631	0.038	BLK proto-oncogene, Src family tyrosine kinase	GO:0050855 regulation of B cell receptor signaling pathway;GO:0050854 regulation of antigen receptor-mediated signaling pathway;GO:0032024 positive regulation of insulin secretion
EPHA1	-1.631	0.038	EPH receptor A1	GO:0051496 positive regulation of stress fiber assembly;GO:0051492 regulation of stress fiber assembly;GO:0032233 positive regulation of actin filament bundle assembly
RPI1-693J15.5	-1.633	0.038	None	None
TRAJ30	-1.638	0.038	T cell receptor alpha joining 30	
ENSG00000262134	-1.640	0.038	None	None
ACSL6	-1.641	0.028	acyl-CoA synthetase long chain family member 6	GO:0035338 long-chain fatty-acyl-CoA biosynthetic process;GO:0046949 fatty-acyl-CoA biosynthetic process;GO:0035336 long-chain fatty-acyl-CoA metabolic process
P2RX5-TAX1BP3	-1.645	0.038	P2RX5-TAX1BP3 readthrough (NMD candidate)	
IGKJ3	-1.646	0.038	immunoglobulin kappa joining 3	
LINC00426	-1.648	0.031	long intergenic non-protein coding RNA 426	
SCML4	-1.649	0.035	Scm polycomb group protein like 4	GO:0006355 regulation of transcription, DNA-templated;GO:1903506 regulation of nucleic acid-templated transcription;GO:0006351 transcription, DNA-templated
TRAJ21	-1.651	0.038	T cell receptor alpha joining 21	
RHOH	-1.651	0.038	ras homolog family member H	GO:0034260 negative regulation of GTPase activity;GO:0043124 negative regulation of I-kappaB kinase/NF-kappaB signaling;GO:0045576 mast cell activation
RP3-455J7.4	-1.658	0.031	None	None
P2RX5	-1.658	0.038	purinergic receptor P2X 5	GO:0010524 positive regulation of calcium ion transport into cytosol;GO:0010522 regulation of calcium ion transport into cytosol;GO:0060402 calcium ion transport into cytosol
LINC00494	-1.659	0.038	long intergenic non-protein coding RNA 494	
PARP15	-1.661	0.027	poly(ADP-ribose) polymerase family member 15	GO:0070212 protein poly-ADP-ribosylation;GO:0006471 protein ADP-ribosylation;GO:0000122 negative regulation of transcription by RNA polymerase II

TESPA1	-1.664	0.035	thymocyte expressed, positive selection associated 1	GO:0050862 positive regulation of T cell receptor signaling pathway;GO:0033089 positive regulation of T cell differentiation in thymus;GO:0050857 positive regulation of antigen receptor-mediated signaling pathway
TRAJ16	-1.665	0.038	T cell receptor alpha joining 16	
RPII-291B21.2	-1.667	0.038	None	None
ENSG00000260424	-1.671	0.038	None	None
SLAMF6	-1.672	0.028	SLAM family member 6	GO:0072540 T-helper 17 cell lineage commitment;GO:0002295 T-helper cell lineage commitment;GO:0072539 T-helper 17 cell differentiation
CD5	-1.675	0.037	CD5 molecule	GO:0031295 T cell costimulation;GO:0031294 lymphocyte costimulation;GO:0050870 positive regulation of T cell activation
GPR174	-1.676	0.031	G protein-coupled receptor 174	GO:0043029 T cell homeostasis;GO:0002260 lymphocyte homeostasis;GO:0001776 leukocyte homeostasis
HNRNPA1P70	-1.677	0.031	heterogeneous nuclear ribonucleoprotein A1 pseudogene 70	
GZMK	-1.679	0.005	granzyme K	GO:0006508 proteolysis;GO:0019538 protein metabolic process;GO:1901564 organonitrogen compound metabolic process
CTB-133G6.1	-1.679	0.037	None	None
KCNA3	-1.682	0.028	potassium voltage-gated channel subfamily A member 3	GO:0071805 potassium ion transmembrane transport;GO:0071804 cellular potassium ion transport;GO:0006813 potassium ion transport
UBASH3A	-1.683	0.035	ubiquitin associated and SH3 domain containing A	GO:0050860 negative regulation of T cell receptor signaling pathway;GO:0050858 negative regulation of antigen receptor-mediated signaling pathway;GO:0050856 regulation of T cell receptor signaling pathway
LINC01215	-1.691	0.037	long intergenic non-protein coding RNA 1215	
TRAJ5	-1.694	0.033	T cell receptor alpha joining 5	
CD3G	-1.694	0.033	CD3g molecule	GO:0038096 Fc-gamma receptor signaling pathway involved in phagocytosis;GO:0031295 T cell costimulation;GO:0002431 Fc receptor mediated stimulatory signaling pathway
RPII-115N12.1	-1.702	0.020	None	None
VSIG1	-1.707	0.035	V-set and immunoglobulin domain containing 1	GO:0030277 maintenance of gastrointestinal epithelium;GO:0010669 epithelial structure maintenance;GO:0003382 epithelial cell morphogenesis
IFNG-AS1	-1.712	0.027	IFNG antisense RNA 1	
TRAJ39	-1.723	0.033	T cell receptor alpha joining 39	
ORM1	-1.727	0.032	orosomucoid 1	GO:0050718 positive regulation of interleukin-1 beta secretion;GO:1904469 positive regulation of tumor necrosis factor secretion;GO:0050716 positive regulation of interleukin-1 secretion

TRAJ28	-1.729	0.031	T cell receptor alpha joining 28	
CD2	-1.730	0.015	CD2 molecule	GO:0030887 positive regulation of myeloid dendritic cell activation;GO:1902715 positive regulation of interferon-gamma secretion;GO:2000484 positive regulation of interleukin-8 secretion
CD3E	-1.733	0.028	CD3e molecule	GO:0002669 positive regulation of T cell anergy;GO:0045060 negative thymic T cell selection;GO:0002913 positive regulation of lymphocyte anergy
TIGIT	-1.741	0.015	T cell immunoreceptor with Ig and ITIM domains	GO:0032695 negative regulation of interleukin-12 production;GO:0032733 positive regulation of interleukin-10 production;GO:0050868 negative regulation of T cell activation
ENSG00000229164	-1.745	0.028	None	None
IL7R	-1.756	0.028	interleukin 7 receptor	GO:0001915 negative regulation of T cell mediated cytotoxicity;GO:0033089 positive regulation of T cell differentiation in thymus;GO:0033081 regulation of T cell differentiation in thymus
THEMIS	-1.762	0.019	thymocyte selection associated	GO:0043383 negative T cell selection;GO:0043368 positive T cell selection;GO:0045058 T cell selection
SH2D1A	-1.765	0.013	SH2 domain containing 1A	GO:0045954 positive regulation of natural killer cell mediated cytotoxicity;GO:0002717 positive regulation of natural killer cell mediated immunity;GO:0042269 regulation of natural killer cell mediated cytotoxicity
TRATI	-1.766	0.028	T cell receptor associated transmembrane adaptor 1	GO:0050862 positive regulation of T cell receptor signaling pathway;GO:0050857 positive regulation of antigen receptor-mediated signaling pathway;GO:0050856 regulation of T cell receptor signaling pathway
C12orf42	-1.771	0.028	chromosome 12 open reading frame 42	
LINC00861	-1.772	0.028	long intergenic non-protein coding RNA 861	
GPR18	-1.777	0.028	G protein-coupled receptor 18	GO:0002300 CD8-positive, alpha-beta intraepithelial T cell differentiation;GO:0002305 CD8-positive, gamma-delta intraepithelial T cell differentiation;GO:0002299 alpha-beta intraepithelial T cell differentiation
ADAMDEC1	-1.777	0.028	ADAM like decysin 1	GO:0007162 negative regulation of cell adhesion;GO:0030155 regulation of cell adhesion;GO:0007155 cell adhesion
ITK	-1.786	0.027	IL2 inducible T cell kinase	GO:0001865 NK T cell differentiation;GO:0007202 activation of phospholipase C activity;GO:0010863 positive regulation of phospholipase C activity
TRAJ19	-1.787	0.028	T cell receptor alpha joining 19 (non-functional)	
TRAV8-3	-1.797	0.028	T cell receptor alpha variable 8-3	
CD6	-1.800	0.028	CD6 molecule	GO:1900017 positive regulation of cytokine production involved in inflammatory response;GO:0031663 lipopolysaccharide-mediated signaling pathway;GO:0042102 positive regulation of T cell proliferation
TRAJ12	-1.810	0.028	T cell receptor alpha joining 12	
TRAJ29	-1.815	0.028	T cell receptor alpha joining 29	
RTKN2	-1.817	0.025	rhoteikin 2	GO:0030097 hemopoiesis;GO:0048534 hematopoietic or lymphoid organ development;GO:0002520 immune system development

TRAJ23	-1.841	0.025	T cell receptor alpha joining 23	
TRAJ38	-1.845	0.025	T cell receptor alpha joining 38	
GPR171	-1.871	0.015	G protein-coupled receptor 171	GO:0035589 G-protein coupled purinergic nucleotide receptor signaling pathway;GO:0035590 purinergic nucleotide receptor signaling pathway;GO:0045638 negative regulation of myeloid cell differentiation
RPII-284N8.3	-1.945	0.013	None	None
GYLTLIB	-1.967	0.007	LARGE xylosyl- and glucuronyltransferase 2	GO:0035269 protein O-linked mannosylation;GO:0035268 protein mannosylation;GO:0046716 muscle cell cellular homeostasis
TRAJ17	-1.969	0.015	T cell receptor alpha joining 17	
GTSFI	-2.007	0.005	gametocyte specific factor 1	GO:0007283 spermatogenesis;GO:0048232 male gamete generation;GO:0007276 gamete generation
			mAT	
SLCO5A1	2.706	0.010	solute carrier organic anion transporter family member 5A1	GO:0043252 sodium-independent organic anion transport;GO:0015711 organic anion transport;GO:0006820 anion transport
SCARNA10	1.597	0.010	small Cajal body-specific RNA 10	
SNORA74B	1.877	0.013	small nucleolar RNA, H/ACA box 74B	
CCL19	2.534	0.017	C-C motif chemokine ligand 19	GO:0045627 positive regulation of T-helper 1 cell differentiation;GO:0045625 regulation of T-helper 1 cell differentiation;GO:0045624 positive regulation of T-helper cell differentiation
CDH3	2.459	0.047	cadherin 3	GO:1902910 positive regulation of melanosome transport;GO:0051796 negative regulation of timing of catagen;GO:1902908 regulation of melanosome transport
SUSD4	2.332	0.047	sushi domain containing 4	GO:0006958 complement activation, classical pathway;GO:0030449 regulation of complement activation;GO:0002455 humoral immune response mediated by circulating immunoglobulin
SNORA73B	1.604	0.047	small nucleolar RNA, H/ACA box 73B	
DUXAP8	-1.058	0.047	double homeobox A pseudogene 8	

Supplementary Table S7: Top 10 genes exhibiting significant ($P \leq 0.05$) positive and negative correlation ($r \geq 0.50$ or ≤ -0.50) with UCPI in eAT.

Gene Name	Description	Cor Coef	Cor P value	log2FoldChange	FDR	Biological Process (GO)
UCPI	uncoupling protein 1	1	1.06E-62	2.409228702	2.83E-05	GO:0002024 diet induced thermogenesis;GO:1990845 adaptive thermogenesis;GO:0002021 response to dietary excess
AR	androgen receptor	0.935482718	7.01E-05	0.878084334	0.032923116	GO:0060520 activation of prostate induction by androgen receptor signaling pathway;GO:0060514 prostate induction;GO:0060515 prostate field specification
JMJD8	jumonji domain containing 8	0.929579575	9.88E-05	0.537510062	0.027579945	jumonji domain containing 8
POLR2J	RNA polymerase II subunit J	0.920400055	0.000159415	0.448182808	0.041304778	GO:0050434 positive regulation of viral transcription;GO:0046782 regulation of viral transcription;GO:0006370 7-methylguanosine mRNA capping
UNG	uracil DNA glycosylase	0.905315077	0.000313243	0.578792412	0.032836958	GO:0045830 positive regulation of isotype switching;GO:0045008 depyrimidination;GO:0045191 regulation of isotype switching
C6orf106	chromosome 6 open reading frame 106	0.902527059	0.000350581	0.509892143	0.036553009	GO:0016236 macroautophagy;GO:0006914 autophagy;GO:0061919 process utilizing autophagic mechanism
NDUFA2	NADH:ubiquinone oxidoreductase subunit A2	0.900716855	0.00037651	0.468960909	0.039287195	GO:0006120 mitochondrial electron transport, NADH to ubiquinone;GO:0042775 mitochondrial ATP synthesis coupled electron transport;GO:0042773 ATP synthesis coupled electron transport
GPRI	G protein-coupled estrogen receptor 1	0.886387191	0.000634181	0.857041717	0.039678842	GO:0051281 positive regulation of release of sequestered calcium ion into cytosol;GO:2000724 positive regulation of cardiac vascular smooth muscle cell differentiation;GO:0032962 positive regulation of inositol trisphosphate biosynthetic process
RILP	Rab interacting lysosomal protein	0.882918507	0.000712148	0.809872762	0.032836958	GO:0010796 regulation of multivesicular body size;GO:0070676 intraluminal vesicle formation;GO:0051036 regulation of endosome size
VEGFB	vascular endothelial growth factor	0.881796051	0.000738812	0.829346404	0.046679163	GO:0060754 positive regulation of mast cell chemotaxis;GO:0060753 regulation of mast cell

	B					chemotaxis;GO:0050930 induction of positive chemotaxis
COL9A2	collagen type IX alpha 2 chain	-0.946165706	3.44E-05	-1.106651742	0.027579945	GO:0030198 extracellular matrix organization;GO:0043062 extracellular structure organization;GO:0001501 skeletal system development
BTGIP1	BTG anti-proliferation factor 1 pseudogene 1	-0.928471797	0.000104982	-1.145864733	0.037558113	BTG anti-proliferation factor 1 pseudogene 1
GTSF1	gametocyte specific factor 1	-0.921113483	0.000153912	-2.006974371	0.005265372	GO:0007283 spermatogenesis;GO:0048232 male gamete generation;GO:0007276 gamete generation
TRAV8-3	T cell receptor alpha variable 8-3	-0.917250387	0.00018546	-1.797435682	0.027579945	T cell receptor alpha variable 8-3
PIK3C3	phosphatidylinositol 3-kinase catalytic subunit type 3	-0.901156945	0.000370081	-0.236178747	0.040209357	GO:0034162 toll-like receptor 9 signaling pathway;GO:0036092 phosphatidylinositol-3-phosphate biosynthetic process;GO:0034497 protein localization to phagophore assembly site
PAXBPI	PAX3 and PAX7 binding protein 1	-0.89076617	0.000544894	-0.416638112	0.045151002	GO:0014842 regulation of skeletal muscle satellite cell proliferation;GO:0014841 skeletal muscle satellite cell proliferation;GO:0014857 regulation of skeletal muscle cell proliferation
PBX4	PBX homeobox 4	-0.890214101	0.000555609	-1.368036837	0.036553009	GO:0045893 positive regulation of transcription, DNA-templated;GO:1903508 positive regulation of nucleic acid-templated transcription;GO:1902680 positive regulation of RNA biosynthetic process
CD8B	CD8b molecule	-0.881161132	0.000754213	-1.61201989	0.015269061	GO:0050690 regulation of defense response to virus by virus;GO:0042110 T cell activation;GO:0016032 viral process
THAP5	THAP domain containing 5	-0.875735544	0.000895548	-0.576928031	0.038403802	GO:0045786 negative regulation of cell cycle;GO:0051726 regulation of cell cycle;GO:0007049 cell cycle
TRAJ23	T cell receptor alpha joining 23	-0.874095151	0.000941836	-1.840631594	0.024899961	T cell receptor alpha joining 23

Supplementary Table S8: KEGG pathways identified by top 10 matching proteins in the DDX39B network that were pulled when active interaction sources included Textmining, Databases, Experiments and Co-expression parameters with highest confidence level (0.900) in the STRING 11.0 platform.

ID	Pathway description	Observed gene count	FDR	Matching proteins in the network (labels)
hsa03040	Spliceosome	9	9.58E-18	ALYREF,DDX39B,MAGOH,MAGOHB,RBM8A,SRSF3,THOC1,THOC2,THOC3
hsa03013	RNA transport	9	2.75E-17	ALYREF,DDX39B,MAGOH,MAGOHB,RBM8A,THOC1,THOC2,THOC3,THOC5
hsa03015	mRNA surveillance pathway	5	1.72E-09	ALYREF,DDX39B,MAGOH,MAGOHB,RBM8A
hsa05168	Herpes simplex infection	2	0.0057	ALYREF,SRSF3

Supplementary Table S9: KEGG pathways identified by top 10 matching proteins in the HLA-C network that were pulled when active interaction sources included Textmining, Databases, Experiments and Co-expression parameters with highest confidence level (0.900) in the STRING 11.0 platform.

#pathway ID	pathway description	observed gene count	FDR	Matching proteins in the network (labels)
hsa04612	Antigen processing and presentation	10	1.43E-22	B2M,HLA-A,HLA-B,HLA-C,HLA-DQA1,HLA-F,HLA-G,KIR2DL1,KIR2DL3,TAPBP
hsa05332	Graft-versus-host disease	8	8.44E-19	HLA-A,HLA-B,HLA-C,HLA-DQA1,HLA-F,HLA-G,KIR2DL1,KIR2DL3
hsa05330	Allograft rejection	6	2.73E-13	HLA-A,HLA-B,HLA-C,HLA-DQA1,HLA-F,HLA-G
hsa04940	Type I diabetes mellitus	6	4.26E-13	HLA-A,HLA-B,HLA-C,HLA-DQA1,HLA-F,HLA-G
hsa05320	Autoimmune thyroid disease	6	1.05E-12	HLA-A,HLA-B,HLA-C,HLA-DQA1,HLA-F,HLA-G
hsa05416	Viral myocarditis	6	1.86E-12	HLA-A,HLA-B,HLA-C,HLA-DQA1,HLA-F,HLA-G
hsa04218	Cellular senescence	7	3.46E-12	HLA-A,HLA-B,HLA-C,HLA-F,HLA-G,KIR2DL1,KIR2DL3
hsa04650	Natural killer cell mediated cytotoxicity	6	1.33E-10	HLA-A,HLA-B,HLA-C,HLA-G,KIR2DL1,KIR2DL3
hsa04514	Cell adhesion molecules (CAMs)	6	2.30E-10	HLA-A,HLA-B,HLA-C,HLA-DQA1,HLA-F,HLA-G
hsa04145	Phagosome	6	2.64E-10	HLA-A,HLA-B,HLA-C,HLA-DQA1,HLA-F,HLA-G
hsa05168	Herpes simplex infection	6	8.77E-10	HLA-A,HLA-B,HLA-C,HLA-DQA1,HLA-F,HLA-G
hsa05169	Epstein-Barr virus infection	6	1.21E-09	HLA-A,HLA-B,HLA-C,HLA-DQA1,HLA-F,HLA-G
hsa05166	HTLV-I infection	6	4.92E-09	HLA-A,HLA-B,HLA-C,HLA-DQA1,HLA-F,HLA-G
hsa05167	Kaposi's sarcoma-associated herpesvirus infection	5	7.56E-08	HLA-A,HLA-B,HLA-C,HLA-F,HLA-G
hsa05203	Viral carcinogenesis	5	7.56E-08	HLA-A,HLA-B,HLA-C,HLA-F,HLA-G
hsa04144	Endocytosis	5	2.58E-07	HLA-A,HLA-B,HLA-C,HLA-F,HLA-G
hsa05165	Human papillomavirus infection	5	9.07E-07	HLA-A,HLA-B,HLA-C,HLA-F,HLA-G