

Table S7. Description of 239 genes selected by machine learning

Gene	Sepsis Average (log2)	Control Average (log2)	Fold Change	FDR P value	Cellular source	Function	Number of classifiers it appears in
Solute Carrier Family 2 Member 3 (SLC2A3)	8.93	5.72	9.23	3.43E-07	Immune cell, genitourinary tract	Glucose transporter-3 protein; upregulation mediates tissue damage and dysfunction during inflammation (1)	2
S100 Calcium Binding Protein A12 (S100A12)	7.87	4.7	8.96	4.11E-11	Immune cell	Infection upregulates S100A12 proteins marked as Disease Associated Molecular Pattern Proteins (DAMPs); proposed biomarker for severe sepsis (2).	3
Secreted Phosphoprotein 1 (SPP1)	8.8	5.85	7.72	2.98E-07	Kidney	Cytokine upregulating interferon-gamma and interleukin-12; downregulated during sepsis (3)	2
Selectin L (SELL)	6.76	3.9	7.3	9.00E-08	Immune cell	L-selectin is a cell adhesion molecule found on lymphocytes. Ligands present on endothelial cells will bind to L-selectin, facilitating the entry of lymphocytes into a secondary lymphoid organ. Serum soluble L-selectin has been proposed as a marker of infection and are related to clinical severity in neonatal sepsis (4). In one study, soluble L-selectin has been seen to predict sepsis survival (5)	4
Lysosomal Protein Transmembrane 5 (LAPTM5)	8.88	6.23	6.28	2.11E-05	Immune cell	Encodes a transmembrane receptor associated with lysosomes, and may have a role in hematopoiesis. LAPTM5 interacts with the B-Cell receptor complex and promotes it's degradation in the lysosomal compartment in mouse B cells (6).	2
Chemokine (C-X-C motif) Ligand 8 (CXCL8)	5.99	3.43	5.89	5.00E-04	Immune cell	Chemotactic factor for neutrophils, promotes angiogenesis and cytosolic calcium. Biomarker of mortality in burn patients with sepsis (7). Urinary IL-8 has been identified as a marker of Acute Kidney Injury (8).	2
Hemoglobin, Beta (HBB)	6.97	4.51	5.52	4.00E-04	None	Controls production of cytophilic IgG subclasses (9) and HBB polymorphisms alter the anti-malarial IgG production (10)	2
RNA component of Mitochondrial RNA Processing Endoribonuclease (RMRP)	9.78	7.48	4.89	8.56E-13	N/A	Mutations cause Cartilage Hair Hypoplasia, associated with lymphomas (11); Severe sepsis is common complication in cancer patients (12).	4
Interleukin 1 Beta (IL1B)	7.62	5.34	4.84	2.00E-04	Immune cell	Associated with culture proven sepsis (13). Activates innate immune response; IL1B -/- mice show reduced inflammation and better renal function during sepsis (14). Associated with Cognitive impairment after sepsis (15).	2

S100 Calcium Binding Protein A9 (S100A9)	9.69	7.44	4.78	3.33E-08	Immune cell	DAMPS expressed in myeloid lineage cells, and proinflammatory mediators. Early septic mice have elevated levels in plasma and deficient mice are protected from late sepsis death (16). Potential biomarker for Renal Cell Carcinoma (17).	2
G0/G1 Switch 2 (G0S2)	9.53	7.37	4.46	4.77E-05	Immune cell	Inhibition of G0S2 ameliorates renal inflammation (18).	2
Prostaglandin-Endoperoxide Synthase 2 (prostaglandin G/H synthase and cyclooxygenase) (PTGS2)	6.46	4.34	4.36	2.00E-04	Immune cell, genitourinary tract	PTGS2 also known as cyclooxygenase-2 (COX2) is an isozyme of PTGS or cyclooxygenase which is the main enzyme in prostaglandin biosynthesis. COX2 is upregulated by many proinflammatory stimuli including TNF-alpha and IL1-beta (19). COX2 has been denoted as a stress molecule in Sepsis and SIRS (20).	2
Metastasis Associated Lung Adenocarcinoma Transcript 1 (MALAT1)	10.44	8.38	4.17	1.06E-05	Immune cell, genitourinary tract, Kidney	Aggravates cardiac inflammation and dysfunction in sepsis; may serve as a biomarker and therapeutic target (21).	2
6-Phosphofructo-2-Kinase/Fructose-2,6-Biphosphatase 3 (PFKFB3)	8.81	6.83	3.96	6.47E-09	Immune cell, Kidney	PFKFB3 inhibitors can diminish acute lung injuries induced by sepsis (22).	2
Nuclear Paraspeckle Assembly Transcript 1 (NEAT1)	9.23	7.35	3.68	2.98E-07	N/A	NEAT1 is a nuclear long non-coding RNA. Circulating lncRNA NEAT1 has been shown to be correlated with increased risk, elevated severity and unfavourable prognosis in sepsis patients (23). NEAT1 has also been shown to play an important role in sepsis-induced acute kidney injury by targeting miR-204 and modulating the NF-kB pathway (24). NEAT1 values of peripheral blood mononuclear cells has good diagnostic value for demarcating sepsis from SIRS (25).	2
Ferritin, Light Chain (FTL)	12.31	10.45	3.63	6.88E-07	Kidney, genitourinary tract, Immune cell	FTL encodes the light subunit of the protein ferritin. Ferritin is the major intracellular iron storage protein in prokaryotes and eukaryotes. Ferritin levels are raised in children with septic shock and high ferritin level is	2

						associated with poorer outcome (26). Increased mortality is associated with very high serum ferritin levels (27).	
Actin, Beta (ACTB)	11.25	9.41	3.57	3.29E-09	Immune cell, genitourinary tract, Kidney	Potentially used as internal standard for normalization of gene expression in organs of immune system (28).	2
Formyl Peptide Receptor 1 (FPR1)	6.49	4.7	3.45	3.23E-06	Immune cell	FPR1 recruits neutrophils to inflammation sites (29) and FPR1 antagonists have significant anti-inflammatory effects (30).	4
Oxidized Low-density Lipoprotein Receptor 1 (OLR1)	6.6	4.84	3.4	0.001	None	OLR1 also known as LOX1 is a receptor protein which binds, internalizes and degrades oxidized low-density lipoprotein. Oxidized low density lipoproteins (oxLDL) and lectin-like oxLDL receptor-1 (LOX-1) are upregulated in inflammation. The following review highlights evidence connecting oxLDL and LOX-1 to proinflammatory disease mechanisms. Modulation of LOX-1 response can also be utilized for treatment of local and systemic inflammation (31).	2
Heat Shock 70kDa Protein 1B; Heat Shock 70kDa Protein 1A (HSPA1B;HSPA1A)	8.95	7.19	3.39	1.64E-06	N/A	These genes encode heat shock proteins which stabilize existing proteins against aggregation and mediates proper folding of newly translated proteins. HSPA1B is one of the 12 candidate biomarkers in a pediatric sepsis biomarker risk model (32). HSPA1B was found among a small set of genes associated with sepsis gene expression quantitative trait loci (33)	2
NLR family, Apoptosis Inhibitory Protein (NAIP)	6.35	4.66	3.23	5.54E-08	Immune cell	NAIP is involved in suppression of apoptosis by inhibiting initiation of apoptosome formation. It has been shown that in vivo stimulation of NAIP inflammasome through flagellated pathogens in monocytes, macrophages, and neutrophils caused sepsis-like severe systemic inflammation (34)	2
Ras-related Protein (RAB1A)	7.17	5.51	3.17	1.55E-07	Kidney, Immune cell	RAB1A is a member of the small GTPases called Rab. They are key regulators of intracellular membrane trafficking, from the formation of transport vesicles to their fusion with membranes. Rab1a activity has been shown to be elevated in alveolar macrophages from septic patients and positively associated with severity of sepsis and respiratory dysfunction (35).	2
P21 Protein Activated Kinase 2 (PAK2)	6.15	4.53	3.06	2.08E-07	Immune cell	PAK2 is a protein kinase that plays a role in many different signaling pathways including cytoskeleton regulation, cell motility, cell cycle progression, apoptosis and proliferation. Sepsis associated eryptosis i.e suicidal erythrocyte death can be caused by deranged activity of many kinases including PAK2 (36). PAK2 is shown to be one of 12 cytoskeleton-related transcripts upregulated in the blood of sepsis patients (37).	2

Protein Kinase C Delta (PRKCD)	7.26	5.75	2.85	7.10E-07	Immune cell	PRKCD encodes the enzyme Protein Kinase C Delta. This enzyme functions as a pro-apoptotic protein during DNA damage-induced apoptosis, but acts as an anti-apoptotic protein during cytokine receptor-initiated cell death, is involved in tumor suppression, is required for oxygen radical production and regulates platelet functional responses. PRKCD has been found to be a critical regulator of the inflammatory response and its inhibition protected endothelial cells, decreased sepsis-mediated neutrophil influx and prevented tissue damage (38). PRKCD is one of the 20 genes central to a neonatal immune-metabolic response network in infection (39).	2
Ribosomal Protein L9 (RPL9)	7.42	5.95	2.77	3.28E-08	genitourinary tract, Immune cell	RPL9 encodes ribosomal protein 9 which is a component of the 60S subunit. RPL9 was shown to be one of the 3 key genes differentiating pediatric sepsis from healthy controls (40).	2
Toll-like Receptor 2 (TLR2)	6.43	4.97	2.76	4.28E-07	Immune cell	TLR2 encodes Toll-like receptor 2 which is a cell-surface protein that is fundamental in pathogen recognition and activation of innate immunity. Soluble TLR2 is a biomarker for sepsis in critically-ill patients with multi-organ failure within 12 hrs of ICU admission (41). TLR2 mediated neutrophil depletion exacerbates bacterial sepsis (42). TLR2 contributes to sepsis-induced depletion of spleen dendritic cells (43). Polymorphisms of TLR2 is associated with faster progression and more severe course of sepsis in critically ill patients (44). TLR2 and TLR4 have increased expression on leukocytes from patients with sepsis (45).	2
Heat Shock Protein 1 (HSPH1)	6.93	5.49	2.72	6.10E-06	genitourinary tract	HSPH1 encodes a member of the heat shock protein 70 family of proteins. It acts as a nucleotide exchange factor for the molecular chaperone Hsc70. HSPH1 occurs among the 18 genes described for mortality risk assessment in pediatric septic shock (46).	2
Interferon Induced Transmembrane Protein 3 (IFITM3)	8.38	6.97	2.66	2.48E-07	None	IFITM3 encodes an interferon-induced membrane protein that helps confer immunity to influenza A H1N1 virus, West Nile virus and dengue virus.	2
Interferon Gamma Receptor 2 (IFNGR2)	6.87	5.5	2.59	3.34E-08	Immune cell	IFNGR2 encodes the non-ligand-binding beta chain of the interferon gamma receptor.	2
V-Rel Avian Reticuloendotheliosis Viral Oncogene Homolog A (RELA)	7.24	5.93	2.47	4.22E-07	Immune cell	The most abundant form of NF-kappa-B is NFkB1 which is complexed with the product of this gene. Absence of RELA enhances mortality due to polymicrobial sepsis and leads to loss of spleen lymphoid dendritic cells in murine models (47).	2

Charged Multivesicular Body Protein 4B (CHMP4B)	7.71	6.42	2.45	1.23E-09	Immune cell	CHMP4B encodes Charged Multivesicular Body Protein 4B which is a part of the endosomal sorting complex required for transport (ESCRT) complex III, which functions in the sorting of endocytosed cell-surface receptors into multivesicular endosomes. Recombinant human Activated protein C (APC) which is a therapeutic agent for treatment of severe sepsis targets CHMP4B (48).	2
Prosaposin (PSAP)	8.39	7.11	2.43	5.46E-05	Immune cell	PSAP encodes prosaposin which is a preprotein that is proteolytically processed to generate saposins.	2
Glycogen Synthase Kinase 3 Beta (GSK3B)	6.66	5.39	2.42	7.52E-06	None	Glycogen synthase kinase 3 beta is an enzyme that negatively regulates glucose homeostasis and is involved in energy metabolism, inflammation, endoplasmic reticulum stress, mitochondrial dysfunction and apoptotic pathways. Inhibition of GS3KB improves the outcome in severe systemic inflammation, like sepsis, SIRS and shock (49). GSK3B is an important regulator of NF-kB and has the ability to modulate the inflammatory response (50). GSK3B has been described as a miRNA sponge in sepsis. This is specific to sepsis only and does not happen in other conditions characterized by an increased inflammatory response like post-surgery patients (51).	2
Ras-related Protein (RAB10)	6.76	5.5	2.4	2.61E-07	GI tract	RAB10 is a GTPase. RAB proteins localize to exocytic and endocytic compartments and regulate intracellular vesicle trafficking. Rab10 facilitates TLR4 signaling (52).	2
Cluster of Differentiation 14 (CD14)	6.56	5.31	2.38	5.60E-06	None	CD14 encodes a surface antigen that is preferentially expressed on monocytes/macrophages. It cooperates with other proteins to mediate innate immune response to bacterial lipopolysaccharide. Soluble CD14 can predict the outcome of critically ill patients (53). Soluble CD14 is a newly discovered marker for sepsis (54). Plasma levels of Presepsin (CD14) are useful for diagnoses of severe sepsis, septic shock and severe community-acquired pneumonia (55).	2
S100 Calcium Binding Protein A8 (S100A8)	7.39	6.16	2.35	5.67E-07	Immune cell	S100A8 is a member of the S100 family of proteins that contain 2 EF-hand calcium binding motifs. S100 proteins are localized in the cytoplasm and/or nucleus and involve in cell cycle progression and differentiation. The protein might function in the inhibition of casein kinase and as a cytokine. S100A8/A9 are important immunoregulators in newborns preventing excessive inflammation (56). S100A8 has been described as a hub gene in sepsis from analysing public datasets in sepsis from GEO (57).	4

Myosin, Heavy Chain 9 (MYH9)	7.59	6.45	2.2	3.83E-08	Immune cell, genitourinary tract	MYH9 gene encodes a conventional non-muscle myosin which is involved in several important functions, including cytokinesis, cell motility and maintenance of cell shape.	2
Glutathione Peroxidase 3 (GPX3)	6.93	5.81	2.18	5.05E-05	Kidney	GPX3 encodes a glutathione peroxidase which protect cells against oxidative damage. Serum GPX3 protein concentration is significantly lowered in sepsis patients (58).	2
Aquaporin 2 (AQP2)	6.94	5.83	2.17	7.73E-07	Kidney	AQP2 encodes a water channel protein located in the kidney collecting tubule. In kidney, AQP2 expression is downregulated during sepsis and cause renal failure (59).	4
Translocated Promoter Region (TPR)	5.49	4.39	2.14	1.65E-05	genitourinary tract, immune cell	TPR encodes a large coiled-coil protein that forms intranuclear filaments attached to the inner surface of nuclear pore complexes. It is required for nuclear export of mRNAs and some proteins.	2
Thioredoxin (TXN)	6.98	5.9	2.12	9.24E-08	GI tract, Kidney	TXN is a homodimer that is involved in many redox reactions. It is part of the response to intracellular nitric oxide. It is one of the 17 recognized oxidative stress genes upregulated in septic patients (60).	2
Endoplasmic Reticulum Protein 44 (ERP44)	5.7	4.64	2.08	6.38E-05	None	ERP44 is an endoplasmic reticulum protein which functions as a pH-regulated chaperone of the secretory pathway and likely plays a role in protein quality control at the endoplasmic reticulum - Golgi interface. ERP44 is an endoplasmic reticulum stress marker and its expression is much more elevated in sepsis in a rat model and this lead to weakened diaphragm contractibility and damaged endoplasmic reticulum (61).	4
MicroRNA 297 (MIR297)	3.31	4.31	-2	4.95E-12	N/A	MiR-297 upregulated in extravasated neutrophils in response to infection. Also upregulated in patients who expired from Sepsis compared to controls (62, 63).	3
MicroRNA 1302-11 (MIR1302-11)	1.48	2.49	-2.01	1.88E-14	N/A	Mir-1302-11 is a novel microRNA in which limited validation studies exist. It is predicted to target S100 Calcium binding protein a10, endoplasmic reticular protein (Target Scan, release 7.1)	3
MicroRNA 548ac (MIR548AC)	8.92	10.04	-2.17	7.12E-10	N/A	The MiR-548 family has been validated to repress TLR6/8 and INF-gamma1 (64, 65). MiRNA 548ac is known to be downregulated via TGF-b and complement activation invitro (66).	4
MicroRNA 3689b (MIR3689B)	7.12	8.24	-2.18	1.35E-09	N/A	Mir-3689b is a novel microRNA in which limited validation studies exist. It is predicted to target phospholipase C, various chemokines, and hypoxia inducible factor 3 (Target Scan, release 7.1)	2
MicroRNA 548a-2 (MIR548A2)	3.58	4.71	-2.2	6.67E-09	N/A	The MiR-548 family has been validated to repress TLR6/8 and INF-gamma1 (64, 65). Specifically, mir-548a-2, or mir-548a-3p, regulates inflammatory responses in the TLR4/NFkB pathway (67)	4

MicroRNA 548i-4 (MIR548I4)	10.6	11.74	-2.2	4.11E-10	N/A	The MiR-548 family has been validated to repress TLR6/8 and INF-gamma1 (64, 65).	2
MicroRNA 548m (MIR548M)	6.45	7.61	-2.23	6.02E-09	N/A	The MiR-548 family has been validated to repress TLR6/8 and INF-gamma1 (64, 65).	2
MicroRNA 1261 (MIR1261)	2.38	3.54	-2.24	1.02E-10	N/A	MirR-1261 is a novel microRNA where the function has yet to be elucidated. However, invitro it has been shown to be downregulated in Macrophages activated by LPS stimulation (68). Top predicted targets include Cadherin, ZincFingers, NFKB, IFN-regulatory Factors	4
MicroRNA 3689a; MicroRNA 3689e (MIR3689A; MIR3689E)	6.98	8.16	-2.26	1.14E-09	N/A	Mir-3689e is a novel microRNA in which limited validation studies exist. It is predicted to target phospholipase C, various chemokines, and hypoxia inducible factor 3 (Target Scan, release 7.1)	2
MicroRNA 548i-1 (MIR548I1)	4.08	5.26	-2.27	4.00E-11	N/A	The MiR-548 family has been validated to repress TLR6/8 and INF-gamma1 (64, 65).	2
MicroRNA 3689c (MIR3689C)	6.63	7.83	-2.29	3.24E-09	N/A	Limited studies exist on miRNA3689c. It has been found to be upregulated in circulating microparticles in polycystic ovary syndrome (69)	4
MicroRNA 548h-3 (MIR548H3)	9.4	10.6	-2.3	2.93E-10	N/A	The MiR-548 family has been validated to repress TLR6/8 and INF-gamma1 (64, 65).	2
MicroRNA 548f-3 (MIR548F3)	9.38	10.65	-2.41	1.83E-10	N/A	The MiR-548 family has been validated to repress TLR6/8 and INF-gamma1 (64, 65).	2
MicroRNA 548t (MIR548T)	9.35	10.64	-2.45	6.64E-11	N/A	The MiR-548 family has been validated to repress TLR6/8 and INF-gamma1 (64, 65).	3
MicroRNA 548aa-2 (MIR548AA2)	9.09	10.44	-2.54	6.26E-10	N/A	The MiR-548 family has been validated to repress TLR6/8 and INF-gamma1 (64, 65). Specifically, mir-548aa-2 regulates inflammatory responses in the TLR4/NFkB pathway (67)	2
MicroRNA 1299 (MIR1299)	8.06	9.41	-2.55	8.03E-11	N/A	Mir-1299 has been validated to target IL6-receptor to increase the expression of CD4/CD25 expressing cells (TH-17 cells) (70). In addition, MiR1299 has been reported to be microvesicle fractions in the peripheral blood (71)	2
MicroRNA 548o-2 (MIR548O2)	7.73	9.16	-2.68	6.17E-10	N/A	The MiR-548 family has been validated to repress TLR6/8 and INF-gamma1 (64, 65).	4
Small Nucleolar RNA, C/D Box 116-15 (SNORD116-15)	8.74	5.94	6.96	1.03E-10	N/A	SNORD116-15 is an RNA Gene, and is affiliated with the snoRNA class.	4
Small Nucleolar RNA, C/D Box 116-14 (SNORD116-14)	6.4	3.64	6.77	1.85E-10	N/A	SNORD116-14 is an RNA Gene, and is affiliated with the snoRNA class.	4
Influenza Virus NS1A Binding Protein (IVNS1ABP)	7.35	4.61	6.68	1.11E-06	Immune cell, Kidney	IVNS1ABP involves in many cell functions, including pre-mRNA splicing, the aryl hydrocarbon receptor (AHR) pathway, F-actin organization and protein ubiquitination.	2

RNA, 5S Ribosomal Pseudogene 348 (RNA5SP348)	6.06	3.37	6.44	1.41E-10	N/A	RNA5SP348 is a Pseudogene.	2
Small Nucleolar RNA, C/D Box 61 (SNORD61)	6.13	3.47	6.32	5.03E-09	N/A	SNORD61 is involved in site-specific 2-prime-O-ribose methylation of preribosomal RNA precursors.	2
RNA, U4 Small Nuclear 2 (RNU4-2)	9.88	7.37	5.71	7.09E-14	N/A	RNU4-2 is an RNA Gene, and is affiliated with the snRNA class.	3
Protein Tyrosine Phosphatase Type IVA, Member 1 (PTP4A1)	7.18	4.67	5.7	3.54E-08	Immune cell	PTP4A1 encodes a cell signaling molecule that plays regulatory roles in a variety of cellular processes, including cell proliferation and migration.	2
Small Nucleolar RNA, C/D box 116-24 (SNORD116-24)	7.57	5.08	5.62	4.11E-11	N/A	SNORD116-24 is an RNA Gene, and is affiliated with the snoRNA class.	4
Metallothionein 1X (MT1X)	8.64	6.16	5.59	3.70E-07	Kidney, GI tract	MT1X is a Protein Coding gene that has a high content of cysteine residues that bind various heavy metals; these proteins are transcriptionally regulated by both heavy metals and glucocorticoids.	2
Small Nucleolar RNA, C/D box 116-18 (SNORD116-18)	8.32	6	4.98	2.89E-10	N/A	SNORD116-18 is an RNA Gene, and is affiliated with the snoRNA class.	2
Small Nucleolar RNA, C/D box 97 (SNORD97)	8.44	6.28	4.48	1.39E-08	N/A	SNORD97 is an RNA Gene, and is affiliated with the snoRNA class.	2
Potassium Channel, Inwardly Rectifying Subfamily J, Member 15 (KCNJ15)	6.49	4.33	4.48	5.14E-07	Kidney	KCNJ15 encodes an integral membrane protein and inward-rectifier type potassium channel, it has a greater tendency to allow potassium to flow into a cell rather than out of it.	2
Small Nucleolar RNA, C/D Box 58A (SNORD58A)	6.58	4.45	4.37	5.07E-08	N/A	SNORD58A is an RNA Gene, and is affiliated with the snoRNA class.	2
Small Nucleolar RNA, H/ACA Box 12 (SNORA12)	5.72	3.62	4.27	3.62E-11	N/A	SNORA12 is small noncoding RNA that directs the conversion of uridine to pseudouridine at specific residues of ribosomal RNAs or small nuclear RNAs.	3
Kruppel-like Factor 6 (KLF6)	8.22	6.13	4.24	8.26E-10	Immune cell, GI tract	KLF6 encodes a transcriptional activator, and functions as a tumor suppressor.	2
RAB31, Member RAS Oncogene Family (RAB31)	7.45	5.38	4.2	5.26E-08	None	RAB31 is a GTP-binding protein that plays essential roles in vesicle and granule targeting.	2
RNA, U1 Small Nuclear 13, Pseudogene (RNU1-13P)	9.42	7.36	4.19	2.08E-14	N/A	RNU1-13P is a Pseudogene, and is affiliated with the snRNA class.	3
RNA, U1 Small Nuclear 12, Pseudogene (RNU1-12P)	9.42	7.36	4.19	2.08E-14	N/A	RNU1-12P is a Pseudogene, and is affiliated with the snRNA class.	3

Small Nucleolar RNA, H/ACA Box 72 (SNORA72)	4.75	2.7	4.12	6.13E-11	N/A	SNORA72 is an RNA Gene, and is affiliated with the snoRNA class.	3
MAX Dimerization Protein 1 (MXD1)	8.35	6.32	4.07	2.40E-06	None	MXD1 encodes protein that antagonizes MYC-mediated transcriptional activation of target genes by competing for the binding partner MAX and recruiting repressor complexes containing histone deacetylases.	2
RNA, Variant U1 Small Nuclear 14 (RNVU1-14)	7.97	5.96	4.03	5.52E-15	N/A	RNVU1-14 is an RNA Gene, and is affiliated with the snRNA class.	3
RAB18, Member RAS Oncogene Family (RAB18)	5.72	3.72	4.02	1.15E-07	Immune cell, genitourinary tract	RAB18 encodes a protein that regulates membrane trafficking in organelles and transport vesicles.	2
Metallothionein 1F (MT1F)	8.11	6.13	3.95	2.29E-05	Kidney	MT1F is a protein coding gene that has a high content of cysteine residues that bind various heavy metals; these proteins are transcriptionally regulated by both heavy metals and glucocorticoids.	2
RNA, U4 Small Nuclear 1 (RNU4-1)	8.85	6.88	3.91	1.14E-12	N/A	RNU4-1 is an RNA Gene, and is affiliated with the snRNA class.	3
RNA, Variant U1 Small Nuclear 17 (RNVU1-17)	9.93	7.96	3.91	7.41E-15	N/A	RNVU1-17 is an RNA Gene, and is affiliated with the snRNA class.	3
RNA, U5E Small Nuclear 1 (RNU5E-1)	6.15	4.21	3.84	2.30E-11	N/A	RNU5E-1 is an RNA Gene, and is affiliated with the snRNA class.	3
Small Nucleolar RNA, C/D Box 41 (SNORD41)	7.12	5.18	3.82	2.78E-07	N/A	SNORD41 is an RNA Gene, and is affiliated with the snoRNA class.	2
Lymphocyte Cytosolic Protein 2 (LCP2)	6.95	5.03	3.79	1.00E-04	Immune cell	LCP2 encodes an adapter protein that acts as a substrate of the T cell antigen receptor (TCR)-activated protein tyrosine kinase pathway.	2
Small Cajal BodySspecific RNA 9; Small Cajal Body Specific RNA 9 Like (SCARNA9; SCARNA9L)	6.68	4.77	3.76	4.52E-08	N/A	SCARNA9 is an RNA Gene, and is affiliated with the scaRNA class; SCARNA9L is a Pseudogene, and is affiliated with the lncRNA class.	2
Small Nucleolar RNA, C/D Box 63 (SNORD63)	5.73	3.83	3.72	1.04E-11	N/A	SNORD63 is an RNA Gene, and is affiliated with the snoRNA class.	3
Small Nucleolar RNA, H/ACA Box 14B (SNORA14B)	6.27	4.37	3.72	9.07E-12	N/A	SNORA14B is guide for the isomerization of uridine residues into pseudouridine.	2
Glycerophosphocholine Phosphodiesterase 1 (GPCPD1)	5.93	4.04	3.7	3.48E-06	Immune cell	GPCPD1 is a Protein Coding gene. Gene Ontology annotations related to this gene include carbohydrate binding and starch binding.	2

RNA, U1 Small Nuclear 3 (RNU1-3)	12.03	10.16	3.64	1.13E-13	N/A	RNU1-3 is an RNA Gene, and is affiliated with the snRNA class. Among its related pathways are Spliceosomal Splicing Cycle.	2
RNA, U1 Small Nuclear 1 (RNU1-1)	12.03	10.16	3.64	1.13E-13	N/A	RNU1-1 is an RNA Gene, and is affiliated with the snRNA class. Among its related pathways are Spliceosomal Splicing Cycle.	2
RNA, U1 Small Nuclear 4 (RNU1-4)	12.03	10.16	3.64	1.13E-13	N/A	RNU1-4 is an RNA Gene, and is affiliated with the snRNA class. Among its related pathways are Spliceosomal Splicing Cycle.	2
RNA, U1 Small Nuclear 28, Pseudogene (RNU1-28P)	12.03	10.16	3.64	1.13E-13	N/A	RNU1-28P is a Pseudogene, and is affiliated with the snRNA class.	2
RNA, Variant U1 Small Nuclear 18 (RNVU1-18)	12.03	10.16	3.64	1.13E-13	N/A	RNVU1-18 is an RNA Gene, and is affiliated with the snRNA class.	2
RNA, U1 Small Nuclear 27, Pseudogene (RNU1-27P)	12.03	10.16	3.64	1.13E-13	N/A	RNU1-27P is a Pseudogene, and is affiliated with the snRNA class.	2
RNA, U1 Small Nuclear 2 (RNU1-2)	12.03	10.16	3.64	1.13E-13	N/A	RNU1-2 is an RNA Gene, and is affiliated with the snRNA class. Among its related pathways are Spliceosomal Splicing Cycle.	2
RNA, Variant U1 Small Nuclear 7 (RNVU1-7)	12.01	10.16	3.62	1.13E-13	N/A	RNVU1-7 is an RNA Gene, and is affiliated with the snRNA class.	2
Small Nucleolar RNA, H/ACA Box 49 (SNORA49)	7.43	5.58	3.62	1.55E-09	N/A	SNORA49 is an RNA Gene, and is affiliated with the snoRNA class.	2
RNA, Variant U1 Small Nuclear 9; RNA, Variant U1 Small Nuclear 7 (RNVU1-9; RNVU1-7)	12.01	10.16	3.62	1.13E-13	N/A	RNVU1-7(RNVU1-9) is an RNA Gene, and is affiliated with the snRNA class.	2
Protein Kinase, cAMP-Dependent, Regulatory, Type I, Alpha (PRKAR1A)	5.5	3.65	3.6	2.55E-07	None	PRKAR1A encodes protein that was found to be a tissue-specific extinguisher that down-regulates the expression of seven liver genes in hepatoma x fibroblast hybrids.	2
Small Nucleolar RNA, C/D Box 12 (SNORD12)	5.63	3.8	3.56	2.96E-07	N/A	SNORD12 is an RNA Gene, and is affiliated with the snoRNA class.	2
RNA, Variant U1 Small Nuclear 1 (RNVU1-1)	11.29	9.45	3.56	3.34E-14	N/A	RNVU1-1 is an RNA Gene, and is affiliated with the snRNA class.	2
RNA, U1 Small Nuclear 10, Pseudogene (RNU1-10P)	11.29	9.45	3.56	3.34E-14	N/A	RNU1-10P is an RNA Gene, and is affiliated with the snRNA class.	2
Small Nucleolar RNA, C/D Box 59A (SNORD59A)	6.21	4.38	3.55	3.53E-09	N/A	SNORD59A is an RNA Gene, and is affiliated with the snoRNA class.	2

MicroRNA 5047 (MIR5047)	7.93	6.12	3.49	8.14E-07	N/A	MIR5047 is an RNA Gene, and is affiliated with the miRNA class. Among its related pathways are mRNA Splicing - Major Pathway and Circadian rhythm related genes.	2
Ubiquitin Specific Peptidase 15 (USP15)	5.59	3.78	3.49	1.35E-05	Immune cell	USP15 encodes protein that associates with the COP9 signalosome, and also plays a role in transforming growth factor beta signalling through deubiquitination of receptor-activated SMAD transcription factors.	2
ATPase, H ⁺ Transporting, Lysosomal 9kDa, V0 Subunit E1 (ATP6V0E1)	8.21	6.44	3.41	7.96E-09	Kidney, genitourinary tract	ATP6V0E1 encodes a component of vacuolar ATPase (V-ATPase), a multisubunit enzyme that mediates acidification of eukaryotic intracellular organelles.	2
Proteolipid Protein 2 (colonic epithelium-enriched) (PLP2)	7.47	5.7	3.41	1.75E-07	GI tract, Immune cell, genitourinary tract	PLP2 encodes an integral membrane protein that localizes to the endoplasmic reticulum in colonic epithelial cells, it can multimerize and may function as an ion channel.	2
Metallothionein 1A (MT1A)	7.43	5.67	3.39	0.001	GI tract	MT1A encodes anti-oxidants that protect against hydroxyl free radicals, are important in homeostatic control of metal in the cell, and play a role in detoxification of heavy metals.	2
Ribonuclease P RNA Component H1 (RPPH1)	9.21	7.45	3.38	1.10E-12	N/A	RPPH1 is the RNA component of the RNase P ribonucleoprotein, an endoribonuclease that cleaves tRNA precursor molecules to form the mature 5-prime termini of their tRNA sequences.	3
Small Nucleolar RNA, C/D Box 3B-1 (SNORD3B-1)	9.03	7.32	3.27	2.94E-10	N/A	SNORD3B-1 is an RNA Gene, and is affiliated with the lncRNA class. Among its related pathways are Ribosome biogenesis in eukaryotes and RNA transport.	4
Small Nucleolar RNA, C/D Box 3B-2 (SNORD3B-2)	9.03	7.32	3.27	2.94E-10	N/A	SNORD3B-2 is an RNA Gene, and is affiliated with the lncRNA class. Among its related pathways are Ribosome biogenesis in eukaryotes and RNA transport.	2
Transforming Growth Factor Beta 1 (TGFB1)	6.99	5.31	3.2	9.43E-08	Immune cell	TGFB1 encodes protein that regulates cell proliferation, differentiation and growth, and can modulate expression and activation of other growth factors including interferon gamma and tumor necrosis factor alpha.	2
Microsomal Glutathione S-Transferase 1 (MGST1)	7.58	5.91	3.18	2.00E-04	None	MGST1 encodes a protein that catalyzes the conjugation of glutathione to electrophiles and the reduction of lipid hydroperoxides.	2
Small Nucleolar RNA, C/D Box 3D (SNORD3D)	8.88	7.22	3.17	3.16E-10	N/A	SNORD3D is an RNA Gene, and is affiliated with the snoRNA class.	2

Small Nucleolar RNA, C/D Box 99 (SNORD99)	7.71	6.06	3.14	2.11E-07	N/A	SNORD99 is an RNA Gene, and is affiliated with the snoRNA class.	2
Small Nucleolar RNA, H/ACA Box 31 (SNORA31)	7.49	5.84	3.14	1.33E-09	N/A	SNORA31 is an RNA Gene, and is affiliated with the snoRNA class.	2
Protein Phosphatase 1, Regulatory Subunit 15B (PPP1R15B)	6.56	4.91	3.13	2.43E-07	Immune cell	PPP1R15B encodes a phosphatase I-interacting protein that promotes the dephosphorylation of eukaryotic translation initiation factor 2A to regulate translation under conditions of cellular stress.	2
RNA, U5A Small Nuclear 1 (RNU5A-1)	4.66	3.03	3.09	7.21E-09	N/A	RNU5A-1 is an RNA Gene, and is affiliated with the snRNA class.	4
Jumonji Domain Containing 1C (JMJD1C)	6.55	4.93	3.07	1.65E-05	Immune cell	JMJD1C encodes protein that interacts with thyroid hormone receptors and contains a jumonji domain.	2
Small Nucleolar RNA, H/ACA Box 2C; MicroRNA 1291 (SNORA2C; MIR1291)	6.92	5.3	3.07	1.06E-08	N/A	SNORA2C is an RNA Gene, and is affiliated with the snoRNA class. MIR1291 is an RNA Gene, and is affiliated with the miRNA class.	2
DEAD (Asp-Glu-Ala-Asp) Box Helicase 5; MicroRNA 3064 (DDX5; MIR3064)	7.8	6.25	2.92	9.14E-06	Immune cell	DDX5 encodes protein that is involved in pathways that include the alteration of RNA structures, it plays a role as a coregulator of transcription, a regulator of splicing, and in the processing of small noncoding RNAs. MIR3064 is an RNA Gene, and is affiliated with the miRNA class. Among its related pathways are mRNA Splicing - Major Pathway and Circadian rhythm related genes.	2
Hexosaminidase B (Beta Polypeptide) (HEXB)	6.14	4.6	2.91	5.00E-04	None	HEXB is the beta subunit of the lysosomal enzyme beta-hexosaminidase that, together with the cofactor GM2 activator protein, catalyzes the degradation of the ganglioside GM2, and other molecules containing terminal N-acetyl hexosamines.	2
Ornithine Decarboxylase Antizyme 1 (OAZ1)	8.5	6.98	2.87	4.39E-09	Immune cell	OAZ1 encodes protein that belongs to the ornithine decarboxylase antizyme family, which plays a role in cell growth and proliferation by regulating intracellular polyamine levels.	2
Capping Protein (Actin Filament) Muscle Z-line, Alpha 1 (CAPZA1)	7.49	6	2.81	4.14E-05	Immune cell	CAPZA1 encodes the alpha subunit of the barbed-end actin binding protein that regulates growth of the actin filament by capping the barbed end of growing actin filaments.	2
Mast Cell-Expressed Membrane Protein 1 (MCEMP1)	6.92	5.44	2.79	6.54E-07	Immune cell	MCEMP1 encodes a single-pass transmembrane protein that is speculated to be involved in regulating mast cell differentiation or immune responses.	2

ATP Synthase, H+ Transporting, Mitochondrial F1 Complex, O Subunit (ATP5O)	7.16	5.69	2.77	1.53E-06	Kidney, GI tract	ATP5O encodes a component of the F-type ATPase found in the mitochondrial matrix, it may be involved in transmission of conformational changes or proton conductance.	2
LUC7-Like 3 Pre-mRNA Splicing Factor (LUC7L3)	6.57	5.13	2.71	3.00E-04	genitourinary tract, Immune cell	LUC7L3 encodes a protein with an N-terminal half that contains cysteine/histidine motifs and leucine zipper-like repeats, this protein localizes with a speckled pattern in the nucleus, and could be involved in the formation of spliceosome via the RE and RS domains.	2
Ubiquitin Protein Ligase E3 Component N-Recognin 1 (UBR1)	4.87	3.44	2.7	1.59E-05	genitourinary tract	UBR1 encodes the recognition component of N-end rule pathway that binds to a destabilizing N-terminal residue of a substrate protein and participates in the formation of a substrate-linked multiubiquitin chain.	2
RNA, Variant U1 Small Nuclear 6 (RNVU1-6)	6.37	4.94	2.69	5.12E-14	N/A	RNVU1-6 is an RNA Gene, and is affiliated with the snRNA class.	3
DEAD (Asp-Glu-Ala-Asp) Box Helicase 17 (DDX17)	7.43	6.02	2.66	7.07E-06	Immune cell, genitourinary tract	DDX17 encodes a DEAD box protein, which is an ATPase activated by a variety of RNA species. This gene can encode multiple isoforms due to both alternative splicing and the use of alternative translation initiation codons, including a non-AUG (CUG) start codon.	2
RNA, 5S Ribosomal 15 (RNA5S15)	11.15	9.75	2.64	5.11E-08	N/A	RNA5S15 is an RNA Gene, and is affiliated with the non-coding RNA class. Among its related pathways are Ribosome biogenesis in eukaryotes and Viral mRNA Translation.	2
RNA, 5S Ribosomal 12 (RNA5S12)	11.15	9.75	2.64	5.11E-08	N/A	RNA5S12 is an RNA Gene, and is affiliated with the non-coding RNA class. Among its related pathways are Ribosome biogenesis in eukaryotes and Viral mRNA Translation.	2
RNA, 5S Ribosomal 14 (RNA5S14)	11.15	9.75	2.64	5.11E-08	N/A	RNA5S14 is an RNA Gene, and is affiliated with the non-coding RNA class. Among its related pathways are Ribosome biogenesis in eukaryotes and Viral mRNA Translation.	2
RNA, 5S Ribosomal 10 (RNA5S10)	11.15	9.75	2.64	5.11E-08	N/A	RNA5S10 is an RNA Gene, and is affiliated with the non-coding RNA class. Among its related pathways are Ribosome biogenesis in eukaryotes and Viral mRNA Translation.	2
RNA, 5S Ribosomal 17 (RNA5S17)	11.15	9.75	2.64	5.11E-08	N/A	RNA5S17 is an RNA Gene, and is affiliated with the non-coding RNA class. Among its related pathways are Ribosome biogenesis in eukaryotes and Viral mRNA Translation.	2
RNA, 5S Ribosomal 16 (RNA5S16)	11.15	9.75	2.64	5.11E-08	N/A	RNA5S16 is an RNA Gene, and is affiliated with the non-coding RNA class. Among its related pathways	2

						are Ribosome biogenesis in eukaryotes and Viral mRNA Translation.	
RNA, 5S Ribosomal 8 (RNA5S8)	11.15	9.75	2.64	5.11E-08	N/A	RNA5S8 is an RNA Gene, and is affiliated with the non-coding RNA class. Among its related pathways are Ribosome biogenesis in eukaryotes and Viral mRNA Translation.	2
RNA, 5S Ribosomal 11 (RNA5S11)	11.15	9.75	2.64	5.11E-08	N/A	RNA5S11 is an RNA Gene, and is affiliated with the non-coding RNA class. Among its related pathways are Ribosome biogenesis in eukaryotes and Viral mRNA Translation.	2
RNA, 5S Ribosomal 6 (RNA5S6)	11.15	9.75	2.64	5.11E-08	N/A	RNA5S6 is an RNA Gene, and is affiliated with the non-coding RNA class. Among its related pathways are Ribosome biogenesis in eukaryotes and Viral mRNA Translation.	2
RNA, 5S Ribosomal 5 (RNA5S5)	11.15	9.75	2.64	5.11E-08	N/A	RNA5S5 is an RNA Gene, and is affiliated with the non-coding RNA class. Among its related pathways are Ribosome biogenesis in eukaryotes and Viral mRNA Translation.	2
RNA, 5S Ribosomal 13 (RNA5S13)	11.15	9.75	2.64	5.11E-08	N/A	RNA5S13 is an RNA Gene, and is affiliated with the non-coding RNA class. Among its related pathways are Ribosome biogenesis in eukaryotes and Viral mRNA Translation.	2
RNA, 5S ribosomal 7 (RNA5S7)	11.15	9.75	2.64	5.11E-08	N/A	RNA5S7 is an RNA Gene, and is affiliated with the non-coding RNA class. Among its related pathways are Ribosome biogenesis in eukaryotes and Viral mRNA Translation.	2
RNA, 5S ribosomal 3 (RNA5S3)	11.15	9.75	2.64	5.11E-08	N/A	RNA5S3 is an RNA Gene, and is affiliated with the non-coding RNA class. Among its related pathways are Ribosome biogenesis in eukaryotes and Viral mRNA Translation.	2
Lung Cancer Associated Transcript 1 (Non-Protein Coding) (LUCAT1)	5.76	4.36	2.64	0.0026	Immune cell	LUCAT1 is an RNA Gene, and is affiliated with the non-coding RNA class. Diseases associated with LUCAT1 include Clear Cell Renal Cell Carcinoma and Squamous Cell Carcinoma, Head And Neck.	2
RNA, 5S Ribosomal 2 (RNA5S2)	11.15	9.75	2.64	5.11E-08	N/A	RNA5S2 is an RNA Gene, and is affiliated with the non-coding RNA class. Among its related pathways are Ribosome biogenesis in eukaryotes and Viral mRNA Translation.	2
Ankyrin Repeat Domain 12 (ANKRD12)	5.57	4.19	2.61	1.69E-06	Immune cell	ANKRD12 encodes a member of the ankyrin repeats-containing cofactor family, it interacts with p160 coactivators and also represses transcription mediated by the coactivator alteration/deficiency in activation 3 (ADA3).	2

Ribosomal Protein S15 (RPS15)	7.91	6.54	2.6	1.09E-07	Immune cell, genitourinary tract	RPS15 encodes a ribosomal protein that is a component of the 40S subunit. This gene has been found to be activated in various tumors, such as insulinomas, esophageal cancers, and colon cancers.	2
Chromosome 6 Open Reading Frame 62 (C6orf62)	6.57	5.22	2.55	2.70E-06	genitourinary tract, immune cell	C6orf62 is a Protein Coding gene.	2
Hydroxysteroid Dehydrogenase Like 2 (HSDL2)	6.07	4.73	2.53	4.35E-07	Kidney	HSDL2 is a Protein Coding gene. Gene Ontology annotations related to this gene include oxidoreductase activity.	2
Chromosome 20 Open Reading Frame 24 (C20orf24)	6.98	5.65	2.52	2.53E-09	Immune cell, GI tract	C20orf24 is a Protein Coding gene.	4
Fibronectin Type III Domain Containing 3A (FNDC3A)	5.47	4.15	2.51	2.86E-07	None	FNDC3A is a Protein Coding gene.	2
Cathepsin S (CTSS)	6.58	5.26	2.51	0.0017	Immune cell	CTSS encodes a lysosomal cysteine proteinase that may participate in the degradation of antigenic proteins to peptides for presentation on MHC class II molecules. It can function as an elastase over a broad pH range in alveolar macrophages.	2
Small Cajal Body-Specific RNA 10 (SCARNA10)	5.94	4.64	2.45	3.70E-12	N/A	SCARNA10 is an RNA Gene, and is affiliated with the scaRNA class.	4
Cathepsin H (CTSH)	7.06	5.78	2.44	5.68E-07	Kidney	CTSH encodes a lysosomal cysteine proteinase important in the overall degradation of lysosomal proteins. It can act both as an aminopeptidase and as an endopeptidase.	2
Histone Cluster 2, H2be (HIST2H2BE)	7.05	5.77	2.43	3.21E-05	N/A	HIST2H2BE encodes a replication-dependent histone that is a member of the histone H2B family. It has antibacterial and antifungal antimicrobial activity.	2
WD Repeat and FYVE Domain Containing 3 (WDFY3)	5.6	4.33	2.41	4.10E-07	Kidney	WDFY3 encodes a phosphatidylinositol 3-phosphate-binding protein that functions as a master conductor for aggregate clearance by autophagy.	2
Vanin 1 (VNN1)	5.24	3.98	2.39	3.01E-07	GI tract	VNN1 encodes a member of the vanin family of proteins, it possesses pantetheinase activity, which may play a role in oxidative-stress response.	4
Cystatin F (Leukocystatin) (CST7)	7.63	6.38	2.38	1.34E-06	Immune cell	CST7 encodes a glycosylated cysteine protease inhibitor with a putative role in immune regulation through inhibition of a unique target in the hematopoietic system.	4
AT Rich Interactive Domain 4A (RBP1-like) (ARID4A)	4.75	3.54	2.32	2.67E-05	Immune cell	ARID4A encodes a ubiquitously expressed nuclear protein, it serves as a bridging molecule to recruit HDACs and, in addition, provides a second HDAC-independent repression function.	2

Vault RNA 1-1 (VTRNA1-1)	4.17	2.96	2.32	7.40E-08	N/A	VTRNA1-1 is a nontranslated RNA component of Vaults, large cytoplasmic ribonucleoproteins of about 13 MD.	2
Heterogeneous Nuclear Ribonucleoprotein D Like (HNRNPDL)	7.17	5.96	2.31	3.38E-05	genitourinary tract, immune cell	HNRNPDL is RNA binding protein that is associated with pre-mRNAs in the nucleus and appear to influence pre-mRNA processing and other aspects of mRNA metabolism and transport.	2
Eukaryotic Translation Elongation Factor 1 Alpha 1 (EEF1A1)	11.96	10.76	2.3	1.41E-05	genitourinary tract, immune cell, kidney	EEF1A1 encodes an isoform of the alpha subunit of the elongation factor-1 complex, which is responsible for the enzymatic delivery of aminoacyl tRNAs to the ribosome.	2
Epithelial Membrane Protein 3 (EMP3)	7.35	6.15	2.3	0.0027	Immune cell	EMP3 encodes protein that contains four transmembrane domains and two N-linked glycosylation sites. It is thought to be involved in cell proliferation, cell-cell interactions and function as a tumor suppressor.	2
Metallothionein 1L (Gene/Pseudogene) (MT1L)	7.21	6.01	2.3	0.0015	None	MT1L is a pseudogene that has a high content of cysteine residues that bind various heavy metals; these proteins are transcriptionally regulated by both heavy metals and glucocorticoids.	2
Guanine Nucleotide Binding Protein (G Protein), Alpha 13 (GNA13)	6.48	5.29	2.29	2.27E-06	Immune cell	GNA13 is a Protein Coding gene that is involved as modulators or transducers in various transmembrane signaling systems.	2
Transaldolase 1 (TALDO1)	7.44	6.26	2.27	9.35E-08	Immune cell	TALDO1 is a key enzyme of the nonoxidative pentose phosphate pathway providing ribose-5-phosphate for nucleic acid synthesis and NADPH for lipid biosynthesis.	2
Echinoderm Microtubule Associated Protein Like 4 (EML4)	5.59	4.43	2.23	3.88E-05	GI tract, Immune cell	EML4 is a member of the echinoderm microtubule associated protein-like family. The encoded WD-repeat protein may be involved in microtubule formation.	2
Bromodomain Containing 2 (BRD2)	7.35	6.19	2.23	1.66E-05	Immune cell, genitourinary tract	BRD2 encodes a transcriptional regulator that belongs to the BET family of proteins. This protein associates with transcription complexes and with acetylated chromatin during mitosis, and it selectively binds to the acetylated lysine-12 residue of histone H4 via its two bromodomains.	2
Ribosomal Protein L6 (RPL6)	8.81	7.66	2.22	2.00E-04	genitourinary tract, immune cell	RPL6 encodes the protein that can bind specifically to domain C of the tax-responsive enhancer element of human T-cell leukemia virus type 1, and may participate in tax-mediated transactivation of transcription.	2

Small Nucleolar RNA, C/D Box 17 (SNORD17)	6.09	4.95	2.21	2.19E-08	N/A	SNORD17 is an RNA Gene, and is affiliated with the snoRNA class.	2
Protein Disulfide Isomerase Family A Member 3 (PDIA3)	6.69	5.56	2.19	8.73E-05	genitourinary tract	PDIA3 encodes a protein of the endoplasmic reticulum that interacts with lectin chaperones calreticulin and calnexin to modulate folding of newly synthesized glycoproteins. It functions as a molecular chaperone that prevents the formation of protein aggregates.	2
Small Nucleolar RNA, H/ACA Box 22 (SNORA22)	5.88	4.76	2.18	5.10E-05		SNORA22 is an RNA Gene, and is affiliated with the snoRNA class.	2
Histone Acetyltransferase 1 (HAT1)	5.56	4.45	2.15	5.60E-05	Immune cell	HAT1 encodes a type B histone acetyltransferase (HAT) that is involved in the rapid acetylation of newly synthesized cytoplasmic histones, which are in turn imported into the nucleus for de novo deposition onto nascent DNA chains.	2
GABA(A) Receptor-Associated Protein Like 2 (GABARAPL2)	6.66	5.57	2.13	1.43E-08	Kidney	GABARAPL2 is a Protein Coding gene. Among its related pathways are Autophagy Pathway and Toll-like Receptor Signaling Pathway. Gene Ontology (GO) annotations related to this gene include microtubule binding and SNARE binding.	2
RNA, Variant U1 Small Nuclear 3 (RNVU1-3)	5.52	4.44	2.12	4.95E-12	N/A	RNVU1-3 is an RNA Gene, and is affiliated with the snRNA class.	3
DEAD (Asp-Glu-Ala-Asp) Box Helicase 21 (DDX21)	5.71	4.64	2.09	5.07E-08	Immune cell	DDX21 an antigen recognized by autoimmune antibodies from a patient with watermelon stomach disease. It unwinds double-stranded RNA, folds single-stranded RNA, and may play important roles in ribosomal RNA biogenesis, RNA editing, RNA transport, and general transcription.	2
Cytochrome C Oxidase Subunit VIc (COX6C)	4.27	3.21	2.08	7.20E-07	None	COX6C encodes subunits that function in electron transfer, and the nuclear-encoded subunits may be involved in the regulation and assembly of the complex.	4
BRE Antisense RNA 1 (BRE-AS1)	4.72	3.67	2.06	4.00E-04	N/A	BRE-AS1 is an RNA Gene, and is affiliated with the antisense RNA class.	2
Myosin IXB (MYO9B)	6.88	5.85	2.04	9.83E-07	Immune cell	MYO9B encodes an unconventional myosin, it has four IQ motifs located in the neck domain that bind calmodulin, which serves as a light chain.	2

Small Nucleolar RNA, C/D Box 16 (SNORD16)	4.23	3.2	2.04	1.21E-10	N/A	SNORD16 is an RNA Gene, and is affiliated with the snoRNA class.	4
Histone Cluster 1, H4e (HIST1H4E)	7.62	6.59	2.04	4.41E-08	N/A	HIST1H4E is intronless and encodes a replication-dependent histone that is a member of the histone H4 family.	2
Torsin A Interacting Protein 2 (TOR1AIP2)	4.91	3.89	2.02	9.30E-06	None	TOR1AIP2 encodes a cofactor for the ATPase TorsinA, regulating the amount of TorsinA present in the ER compared to that found in the nuclear envelope.	2
Small Nucleolar RNA, H/ACA Box 75 (SNORA75)	3.39	2.39	2	3.83E-07	N/A	SNORA75 is an RNA Gene, and is affiliated with the snoRNA class.	2
Olfactory Receptor, Family 51, Subfamily B, Member 6 (OR51B6)	3.14	4.14	-2	1.55E-11	N/A	OR51B6 interacts with odorant molecules in the nose, to initiate a neuronal response that triggers the perception of a smell.	4
Olfactory Receptor, Family 4, Subfamily F, Member 2 Pseudogene (OR4F2P)	3.93	4.94	-2.01	2.41E-10	N/A	OR4F2P interacts with odorant molecules in the nose, to initiate a neuronal response that triggers the perception of a smell.	3
Mucin 3A, Cell Surface Associated (MUC3A)	5.17	6.18	-2.03	1.16E-07	GI tract	MUC3A encodes epithelial glycoproteins that contain at least one large domain of tandemly repeated sequence that encodes the peptide sequence rich in serine and/or threonine residues, which carries most of the O-linked glycosylation.	4
LOC101928495	8.81	9.84	-2.04	3.74E-10	N/A	LOC101928495 (Uncharacterized) is an RNA Gene, and is affiliated with the ncRNA class.	2
Family With Sequence Similarity 138, Member D; Family With Sequence Similarity 138, Member C (FAM138D; FAM138C)	4.06	5.11	-2.07	1.68E-09	genitourinary tract	FAM138D is an RNA Gene, and is affiliated with the non-coding RNA class. FAM138C is an RNA Gene, and is affiliated with the non-coding RNA class.	4
Olfactory Receptor, Family 5, Subfamily I, Member 1 (OR5I1)	3.31	4.36	-2.07	8.00E-11	N/A	OR5I1 interacts with odorant molecules in the nose, to initiate a neuronal response that triggers the perception of a smell.	2
Olfactory Receptor, Family 8, Subfamily G, Member 2 (OR8G2)	3.77	4.84	-2.09	7.27E-10	N/A	OR8G2 interacts with odorant molecules in the nose, to initiate a neuronal response that triggers the perception of a smell.	2

LOC100508046; LOC101929572	4.37	5.45	-2.11	2.48E-10	genitourinary tract	LOC100508046 (Uncharacterized) is an RNA Gene, and is affiliated with the ncRNA class. LOC101929572 (Uncharacterized) is an RNA Gene, and is affiliated with the ncRNA class.	2
LOC339539	5.79	6.88	-2.12	7.34E-11	Immune cell	LOC339539 (Uncharacterized) is an RNA Gene, and is affiliated with the ncRNA class.	4
Ubiquitin Specific Peptidase 17-Like Family Member 4 (USP17L4)	4.48	5.58	-2.14	3.85E-10	N/A	USP17L4 is a Protein Coding gene. Among its related pathways are Metabolism of proteins and Deubiquitination. Gene Ontology annotations related to this gene include thiol-dependent ubiquitinyl hydrolase activity.	2
Dynamin 1 Pseudogene 46 (DNM1P46)	7.37	8.47	-2.15	1.71E-07	genitourinary tract	DNM1P46 is a Pseudogene. Gene Ontology annotations related to this gene include GTPase activity.	2
LOC105376796	4.12	5.22	-2.15	1.14E-07	N/A	Uncharacterized.	4
Mucin 17, Cell Surface Associated (MUC17)	3.85	4.96	-2.16	3.68E-06	GI tract	MUC17 encodes a membrane-bound mucin that provides protection to gut epithelial cells.	4
Mucin 12, Cell Surface Associated (MUC12)	7.19	8.41	-2.33	1.97E-08	GI tract	MUC12 encodes an integral membrane glycoprotein that plays an essential role in forming protective mucous barriers on epithelial surfaces and have been implicated in epithelial renewal and differentiation.	4
BX571672.3	3.8	5.05	-2.37	1.38E-09	N/A	Uncharacterized.	2
AL583842.1	3.64	4.95	-2.48	1.47E-08	N/A	Uncharacterized.	2
RP11-327I22.4	5.33	6.64	-2.48	1.36E-10	N/A	Uncharacterized.	3
RNA, 5S ribosomal pseudogene 316 (RNA5SP316)	4.88	6.22	-2.52	1.07E-10	N/A	RNA5SP316 is a Pseudogene.	4
REX1, RNA Exonuclease 1 Homolog-like 1, Pseudogene; REX1, RNA Exonuclease 1 Homolog-like 2, Pseudogene (REXO1L1P; REXO1L2P)	7.01	8.38	-2.59	3.29E-09	N/A	REXO1L1P is a Pseudogene. Gene Ontology annotations related to this gene include nucleic acid binding and exonuclease activity. REXO1L2P is a Pseudogene.	4
BX004987.7	3.75	5.13	-2.59	9.01E-09	N/A	Uncharacterized.	4

RNA, 5S Ribosomal Pseudogene 314 (RNA5SP314)	4.98	6.4	-2.67	8.45E-11	N/A	RNA5SP314 is a Pseudogene.	4
RNA, 5S Ribosomal Pseudogene 313 (RNA5SP313)	4.91	6.36	-2.72	5.34E-11	N/A	RNA5SP313 is a Pseudogene.	3
Ubiquitin specific peptidase 17-like family members (USP17L5; USP17L6P; USP17L9P; USP17L10; USP17L11; USP17L12; USP17L13; USP17L15; USP17L18; USP17L19; USP17L20; USP17L21; USP17L24; USP17L25; USP17L26; USP17L27; USP17L28; USP17L29; USP17L30)	5.6	7.07	-2.78	4.21E-10	N/A	Deubiquitinating enzyme that removes conjugated ubiquitin from specific proteins to regulate different cellular processes that may include cell proliferation, progression through the cell cycle, apoptosis, cell migration, and the cellular response to viral infection.	4
	6.2	7.73	-2.9	2.43E-10	None		2
	7.14	8.72	-3	9.53E-10	N/A		4
	7.14	8.72	-3	9.53E-10	N/A		4
	6.74	8.32	-3	6.08E-10	N/A		4
	7.14	8.72	-3	9.53E-10	N/A		4
	7.14	8.72	-3	9.53E-10	N/A		4
	6.95	8.53	-3	6.77E-10	N/A		4
	7.14	8.72	-3	9.53E-10	N/A		2
	7.14	8.72	-3	9.53E-10	N/A		4
	7.08	8.68	-3.03	1.46E-09	N/A		2
	6.35	7.98	-3.08	4.86E-10	N/A		2
	6.35	7.99	-3.11	4.28E-10	N/A		2
	7.1	8.74	-3.12	1.30E-09	N/A		3
	6.4	8.05	-3.15	4.65E-10	N/A		2

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