

# **Bioinformatics Network Analyses of Growth differentiation factor 11 anti-aging study**

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Supplementary Information

Supplementary Table S1 GDF11 Genetic Co-expression Module Number of Each Human Tissue

	Tissue	Module Amount
<b>Adipose</b>	Visceral omentum	1
<b>Nervous System</b>	Cerebellum	1
	Cerebellar hemisphere	1
	Frontal cortex	1
	Hippocampus	1
	Nerve tibialis	1
<b>Cardiovascular System</b>	Left ventricle	1
<b>Digestive System</b>	Esophagus mucosa	1
	Esophagus muscle	1
	Stomach	1
	Small intestine terminal ileum	1
	Colon transverse	1
	Colon sigmoid	1
	<b>Liver</b>	
<b>Skeletal Muscle</b>		1
<b>Lung</b>		1
<b>Kidney</b>		1
<b>Endocrine System</b>	Pituitary	1
	Thyroid	1
	Adrenal gland	1
<b>Female Reproduction System</b>	Ovary	1
<b>Male Reproduction System</b>	Testis	1
	Prostate	1
	<b>Total</b>	<b>23</b>

**Supplementary Table S2 Pathways and Functions of GDF11 Gene Co-expression Networks of Human**

Tissue	Top pathways/functions	Overlaps	Genes belong to the pathway	Fold Enrichment	p-value	FDR q-value	
Adipose	Visceral omentum		121	352	6.35	1.79 e-63	1.92 e-60
		Genes involved in Generic Transcription Pathway ( <b>Transcription</b> )					
		DNA replication ( <b>Proliferation</b> )	13	36	6.67	2.36 e-8	6.36 e-6
		Genes involved in Lagging Strand Synthesis ( <b>Proliferation</b> )	9	19	8.75	2.21 e-7	2.86 e-5
		Genes involved in DNA strand elongation ( <b>Proliferation</b> )	11	30	6.77	2.39 e-7	2.86 e-5
		Genes involved in Extension of Telomeres ( <b>Telomere maintenance</b> )	10	27	6.84	7.63 e-7	8.21 e-5
		Genes involved in Global Genomic Nucleotide Excision Repair ( <b>DNA Repair</b> )	11	35	5.80	1.42 e-6	1.39 e-4
		Genes involved in Processive synthesis on the lagging strand ( <b>Proliferation</b> )	7	15	8.62	5.9 e-6	4.24 e-4
		Base excision repair ( <b>DNA Repair</b> )	10	35	5.27	1.11 e-5	6.67 e-4
		Genes involved in Activation of the pre-replicative complex ( <b>Proliferation</b> )	9	31	5.36	2.67 e-5	1.2 e-3
		Caspase Cascade in Apoptosis ( <b>Apoptosis</b> )	7	23	5.62	1.53 e-4	4.46 e-3
		Mismatch repair ( <b>DNA Repair</b> )	7	23	5.62	1.53 e-4	4.46 e-3
		Genes involved in Formation of incision complex in Global Genomic Nucleotide Excision Repair ( <b>DNA Repair</b> )	7	23	5.62	1.53 e-4	4.46 e-3
		Genes involved in Homologous recombination repair of replication-independent double-strand breaks ( <b>DNA Repair</b> )	6	17	6.52	1.84 e-4	4.79 e-3
		Genes involved in Inflammasomes ( <b>Immune</b> )	6	17	6.52	1.84 e-4	4.79 e-3
		Genes involved in Cholesterol biosynthesis ( <b>Metabolism of Cholesterol</b> )	7	24	5.38	2.06 e-4	4.93 e-3
Genes involved in Double-Strand Break Repair ( <b>DNA Repair</b> )	7	24	5.38	2.06 e-4	4.93 e-3		

		Genes involved in The NLRP3 inflammasome ( <b>Immune</b> )	5	12	7.69	2.66 e-4	6.09 e-3	
		Genes involved in Base Excision Repair ( <b>DNA Repair</b> )	6	19	5.83	3.67 e-4	7.61 e-3	
		Genes involved in Base Excision Repair ( <b>DNA Repair</b> )	6	19	5.83	3.67 e-4	7.61 e-3	
		Genes involved in Polymerase switching ( <b>Proliferation</b> )	5	13	7.10	4.12 e-4	8.08 e-3	
Nervous System	Cerebellum	Genes involved in NCAM signaling for neurite outgrowth ( <b>NCAM signaling</b> )	5	64	39.89	1.79 e-7	1.93 e-4	
		Genes involved in NCAM1 interactions ( <b>NCAM signaling</b> )	4	39	52.37	1.07 e-6	5.3 e-4	
		Extracellular matrix (ECM)-receptor interaction ( <b>Extracellular matrix</b> )	4	84	24.31	2.35 e-5	4.23 e-3	
		Multiple pathways from IGF-1R signaling lead to BAD phosphorylation ( <b>IGF-1 signaling pathway</b> )	5	23	21.12	3.27 e-6	1.09 e-3	
		IL-2 Receptor Beta Chain in T cell Activation ( <b>Immune</b> )	5	38	12.78	4.29 e-5	3.35 e-3	
			Genes involved in PI3K/AKT activation ( <b>PI3K/AKT pathway</b> )	5	38	12.78	4.29 e-5	3.35 e-3
			IGF-1 Signaling Pathway ( <b>IGF-1 signaling pathway</b> )	4	21	18.50	5.77 e-5	3.89 e-3
			Insulin Signaling Pathway ( <b>Insulin pathway</b> )	4	22	17.66	7 e-5	4.43 e-3
			CTCF: First Multivalent Nuclear Factor ( <b>Apoptosis</b> )	4	23	16.89	8.4 e-5	4.59 e-3
			Ras Signaling Pathway ( <b>Ras pathway</b> )	4	23	16.89	8.4 e-5	4.59 e-3
			Double Stranded RNA Induced Gene Expression ( <b>Immune</b> )	3	10	29.14	1.23 e-4	5.44 e-3
			Influence of Ras and Rho proteins on G1 to S Transition ( <b>Cell cycle</b> )	4	26	14.94	1.38 e-4	5.44 e-3
			Phospholipids as signalling intermediaries ( <b>Cell survival</b> )	4	27	14.39	1.61 e-4	5.79 e-3
			Inactivation of Gsk3 by AKT causes accumulation of b-catenin in Alveolar Macrophages ( <b>AKT pathway</b> )	4	27	14.39	1.61 e-4	5.79 e-3
			Growth Hormone Signaling Pathway ( <b>Growth</b> )	4	28	13.87	1.87 e-4	6.28 e-3

	Role of fl-arrestins in the activation and targeting of MAP kinases ( <b>MAPK pathway</b> )	3	12	24.28	2.22 e-4	7.05 e-3
	EGF Signaling Pathway ( <b>EGF signaling</b> )	4	31	12.53	2.8 e-4	8.13 e-3
	Circadian rhythm – mammal ( <b>Circadian rhythm</b> )	3	13	22.42	2.87 e-4	8.13 e-3
Frontal cortex	Arginine and proline metabolism ( <b>Metabolism of amino acid</b> )	11	54	11.47	2.47 e-9	1.33 e-6
	Alanine, aspartate and glutamate metabolism ( <b>Metabolism of amino acid</b> )	8	32	14.07	6.89 e-8	1.48 e-5
	Genes involved in tRNA Aminoacylation ( <b>Expression</b> )	8	42	10.72	6.61 e-7	8.9 e-5
	Genes involved in Cytosolic tRNA aminoacylation ( <b>Expression</b> )	6	24	14.07	3.15 e-6	3.77 e-4
	Aminoacyl-tRNA biosynthesis ( <b>Expression</b> )	7	41	9.61	7.21 e-6	6.36 e-4
	Genes involved in Chondroitin sulfate biosynthesis ( <b>Metabolism of GAG</b> )	5	21	13.40	2.8 e-5	1.89 e-3
	Proximal tubule bicarbonate reclamation ( <b>Metabolism of ion</b> )	5	23	12.24	4.5 e-5	2.85 e-3
	Genes involved in Inhibition of voltage gated Ca <sup>2+</sup> channels via G beta/gamma subunits ( <b>Ca<sup>2+</sup> pathway</b> )	5	25	11.26	6.9 e-5	4.13 e-3
	Genes involved in Amino acid synthesis and interconversion ( <b>Metabolism of amino acid</b> )	4	17	13.25	1.95 e-4	8.06 e-3
	Genes involved in Rap1 signaling ( <b>Rap1 signaling</b> )	4	17	13.25	1.95 e-4	8.06 e-3
Hippocampus	Genes involved in Metabolism of nucleotides ( <b>Metabolism of nucleotides</b> )	8	72	6.78	2.38 e-5	3.6 e-3
	Sphingolipid metabolism ( <b>Metabolism of sphingolipid</b> )	6	40	9.15	4.53 e-5	4.88 e-3
	Genes involved in Apoptotic cleavage of cellular proteins ( <b>Apoptosis</b> )	6	40	9.15	4.53 e-5	4.88 e-3
	Axon guidance ( <b>Axon guidance</b> )	10	129	4.73	5.62 e-5	5.5 e-3
Nerve tibia	Genes involved in ER-Phagosome pathway ( <b>Phagocytosis</b> )	7	61	202.83	3.28 e-15	3.53 e-12

Genes involved in Antigen processing-Cross presentation ( <b>Immune</b> )	7	76	162.79	1.63 e-14	5.86 e-12
Antigen processing and presentation ( <b>Immune</b> )	6	89	119.15	9.92 e-12	1.23 e-9
Genes involved in Endosomal/Vacuolar pathway ( <b>Phagocytosis</b> )	4	9	785.57	1.01 e-11	1.23 e-9
Genes involved in Interferon alpha/beta signaling ( <b>Immune</b> )	5	64	138.08	2.87 e-10	3.09 e-8
Genes involved in Antigen Presentation: Folding, assembly and peptide loading of class I MHC ( <b>Immune</b> )	4	21	336.67	4.78 e-10	4.68 e-8
Genes involved in Interferon gamma signaling ( <b>Immune</b> )	4	63	112.22	4.69 e-8	3.88 e-6
Genes involved in Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell ( <b>Immune</b> )	4	70	101.00	7.19 e-8	5.53 e-6
Allograft rejection ( <b>Immune</b> )	3	38	139.54	1.34 e-6	8.48 e-5
Graft-versus-host disease ( <b>Immune</b> )	3	42	126.25	1.82 e-6	1.09 e-4
Type I diabetes mellitus ( <b>Immune</b> )	3	44	120.51	2.1 e-6	1.19 e-4
Proteasome ( <b>Proteasome pathway</b> )	3	48	110.47	2.73 e-6	1.34 e-4
Genes involved in CDK-mediated phosphorylation and removal of Cdc6 ( <b>DNA damage checkpoint</b> )	3	48	110.47	2.73 e-6	1.34 e-4
Genes involved in Cross-presentation of soluble exogenous antigens ( <b>Immune</b> )	3	48	110.47	2.73 e-6	1.34 e-4
Genes involved in Regulation of ornithine decarboxylase (ODC) ( <b>Metabolism of amino acid</b> )	3	49	108.21	2.91 e-6	1.36 e-4
Genes involved in Autodegradation of the E3 ubiquitin ligase COP1 ( <b>DNA damage checkpoint</b> )	3	51	103.97	3.29 e-6	1.36 e-4
Genes involved in p53-Independent G1/S DNA damage checkpoint ( <b>DNA damage checkpoint</b> )	3	51	103.97	3.29 e-6	1.36 e-4
Genes involved in SCF-beta-TrCP mediated degradation of Emil ( <b>DNA damage checkpoint</b> )	3	51	103.97	3.29 e-6	1.36 e-4

		Genes involved in Vif-mediated degradation of APOBEC3G ( <b>Proteasome pathway</b> )	3	52	101.97	3.49 e-6	1.37 e-4
		Autoimmune thyroid disease ( <b>Immune</b> )	3	53	100.04	3.7 e-6	1.37 e-4
		Genes involved in Destabilization of mRNA by AUF1 (hnRNP D0) ( <b>Metabolism of GDP</b> )	3	53	100.04	3.7 e-6	1.37 e-4
Cardiovascular System	Left ventricle	Genes involved in G alpha (12/13) signalling events ( <b>GPCR pathway</b> )	9	74	9.77	3.63 e-7	9.77 e-5
		Aminoacyl-tRNA biosynthesis ( <b>Expression</b> )	7	41	13.71	6.95 e-7	1.1 e-4
		Genes involved in NRAGE signals death through JNK ( <b>Apoptosis</b> )	7	43	13.07	9.75 e-7	1.17 e-4
		Genes involved in Cell death signalling via NRAGE, NRIF and NADE ( <b>Apoptosis</b> )	7	60	9.37	9.74 e-6	6.14 e-4
		Genes involved in trans-Golgi Network Vesicle Budding ( <b>Vesicle-mediated transport</b> )	7	60	9.37	9.74 e-6	6.14 e-4
		Genes involved in Double-Strand Break Repair ( <b>DNA repair</b> )	5	24	16.73	1.03 e-5	6.14 e-4
		Genes involved in tRNA Aminoacylation ( <b>Expression</b> )	6	42	11.47	1.3 e-5	6.99 e-4
		Glycerolipid metabolism ( <b>Metabolism of glycerolipid</b> )	6	49	9.83	3.22 e-5	1.24 e-3
		Genes involved in Metabolism of non-coding RNA ( <b>Metabolism of non-coding RNA</b> )	6	49	9.83	3.22 e-5	1.24 e-3
		Other glycan degradation ( <b>Metabolism of glycan</b> )	4	16	20.08	3.84 e-5	1.38 e-3
		Genes involved in Homologous recombination repair of replication-independent double-strand breaks ( <b>DNA repair</b> )	4	17	18.90	4.97 e-5	1.65 e-3
		Genes involved in RNA Polymerase III Transcription ( <b>Expression</b> )	5	33	12.17	5.22 e-5	1.65 e-3
		Telomeres, Telomerase, Cellular Aging, and Immortality ( <b>Telomere maintenance</b> )	4	18	17.85	6.33 e-5	1.84 e-3

		Thrombin signaling and protease-activated receptors ( <b>Thrombin signaling</b> )	5	37	10.85	9.21 e-5	2.36 e-3
		Genes involved in Mitochondrial tRNA aminoacylation ( <b>Expression</b> )	4	21	15.30	1.2 e-4	2.94 e-3
		Genes involved in Lysosome Vesicle Biogenesis ( <b>Vesicle-mediated transport</b> )	4	23	13.97	1.74 e-4	3.84 e-3
		Regulation of eIF4e and p70 S6 Kinase ( <b>Expression</b> )	4	24	13.39	2.07 e-4	4.21 e-3
		Genes involved in Synthesis of PIPs at the late endosome membrane ( <b>Metabolism of phospholipids</b> )	3	10	24.10	2.16 e-4	4.3 e-3
		Regulation of BAD phosphorylation ( <b>Apoptosis</b> )	4	26	12.36	2.86 e-4	5.46 e-3
		Phospholipids as signalling intermediaries ( <b>Metabolism of phospholipids</b> )	4	27	11.90	3.32 e-4	5.46 e-3
		Inactivation of Gsk3 by AKT causes accumulation of b-catenin in Alveolar Macrophages ( <b>Proteasome pathway</b> )	4	27	11.90	3.32 e-4	5.46 e-3
		Genes involved in Synthesis of PIPs at the early endosome membrane ( <b>Metabolism of phospholipids</b> )	3	12	20.08	3.88 e-4	6.24 e-3
		EGF Signaling Pathway ( <b>EGF pathway</b> )	4	31	10.36	5.72 e-4	8.81 e-3
		PKC-catalyzed phosphorylation of inhibitory phosphoprotein of myosin phosphatase ( <b>Smooth muscle contraction</b> )	4	31	10.36	5.72 e-4	8.81 e-3
		Non-homologous end-joining ( <b>DNA repair</b> )	3	14	17.21	6.3 e-4	9.56 e-3
		PDGF Signaling Pathway ( <b>PDGF pathway</b> )	4	32	10.04	6.48 e-4	9.56 e-3
Digestive System	Esophagus mucosa	Genes involved in Regulation of Complement cascade ( <b>Immune</b> )	3	14	83.45	5.88 e-6	2.11 e-3
		Glycosaminoglycan biosynthesis - chondroitin sulfate ( <b>Metabolism of GAG</b> )	3	22	53.10	2.45 e-5	6.6 e-3
	Esophagus muscle	Genes involved in Unfolded Protein Response ( <b>ER stress</b> )	9	80	94.00	5.49 e-16	4.12 e-13
		Genes involved in Activation of Chaperone Genes by XBP1(S) ( <b>ER stress</b> )	5	46	90.82	2.69 e-9	7.24 e-7



	Protein export ( <b>Metabolism of protein</b> )	4	24	139.26	1.92 e-8	4.13 e-6
	Genes involved in Activation of Chaperone Genes by ATF6-alpha ( <b>ER stress</b> )	3	11	227.88	2.66 e-7	4.09 e-5
	Genes involved in Activation of Chaperones by ATF6-alpha ( <b>ER stress</b> )	3	13	192.82	4.6 e-7	6.19 e-5
	Genes involved in Antigen Presentation: Folding, assembly and peptide loading of class I MHC ( <b>Metabolism of protein</b> )	3	21	119.36	2.12 e-6	2.16 e-4
Stomach	Genes involved in Extracellular matrix organization ( <b>Extracellular matrix</b> )	17	87	6.55	7.19 e-10	7.74 e-7
	Genes involved in Collagen formation ( <b>Collagen formation</b> )	13	58	7.52	1.25 e-8	3.36 e-6
	Neuropeptides VIP and PACAP inhibit the apoptosis of activated T cells ( <b>Immune</b> )	8	29	9.26	1.49 e-6	2.01 e-4
	Genes involved in Response to elevated platelet cytosolic Ca <sup>2+</sup> ( <b>DAG/IP3/Ca<sup>2+</sup> pathway</b> )	13	89	4.90	2.37 e-6	2.83 e-4
	Amino sugar and nucleotide sugar metabolism ( <b>Metabolism of amino sugar and nucleotide sugar</b> )	9	44	6.86	4.98 e-6	4.47 e-4
	Phosphatidylinositol signaling system ( <b>PI signaling</b> )	11	76	4.85	1.53 e-5	9.87 e-4
	VEGF signaling pathway ( <b>PI signaling</b> )	11	76	4.85	1.53 e-5	9.87 e-4
	Genes involved in Semaphorin interactions ( <b>Axon guidance</b> )	10	68	4.93	3.22 e-5	1.8 e-3
	Genes involved in CRMPs in Sema3A signaling ( <b>Axon guidance</b> )	5	14	11.98	3.72 e-5	1.91 e-3
	Genes involved in Glutamate Neurotransmitter Release Cycle ( <b>Neurotransmitter release cycle</b> )	5	15	11.18	5.45 e-5	2.55 e-3
	Signaling Pathway from G-Protein Families ( <b>DAG/IP3/Ca<sup>2+</sup> pathway</b> )	7	37	6.35	9.65 e-5	4 e-3
	Basal cell carcinoma ( <b>Hedgehog signaling</b> )	8	55	4.88	2.13 e-4	6.56 e-3
	Effects of calcineurin in Keratinocyte Differentiation ( <b>DAG/IP3/Ca<sup>2+</sup> pathway</b> )	5	21	7.99	3.18 e-4	8.61 e-3

	Phospholipase C-epsilon pathway ( <b>DAG/IP3/Ca2+ pathway</b> )	4	12	11.18	3.2 e-4	8.61 e-3
Small intestine terminal ileum	Genes involved in Biological oxidations ( <b>Biological oxidation</b> )	31	139	7.51	1.26 e-18	4.54 e-16
	Genes involved in Phase II conjugation ( <b>Biological oxidation</b> )	17	70	8.18	1.72 e-11	2.32 e-9
	Genes involved in Glycerophospholipid biosynthesis ( <b>Metabolism of glycerophospholipid</b> )	17	82	6.99	2.53 e-10	3.03 e-8
	Retinol metabolism ( <b>Metabolism of retinol</b> )	15	64	7.90	4.57 e-10	4.48 e-8
	Genes involved in Lipid digestion, mobilization, and transport ( <b>Metabolism of lipids</b> )	13	46	9.52	5.32 e-10	4.77 e-8
	PPAR signaling pathway ( <b>PPAR signaling pathway</b> )	15	69	7.32	1.41 e-9	1.17 e-7
	Drug metabolism - other enzymes ( <b>Metabolism of drug</b> )	12	51	7.93	2.41 e-8	1.23 e-6
	Genes involved in Cytochrome P450 - arranged by substrate type ( <b>Biological oxidation</b> )	12	51	7.93	2.41 e-8	1.23 e-6
	Genes involved in Lipoprotein metabolism ( <b>Metabolism of lipids</b> )	9	28	10.83	7.18 e-8	3.22 e-6
	Genes involved in Amino acid and oligopeptide SLC transporters ( <b>Metabolism of amino acid</b> )	11	49	7.56	1.55 e-7	5.58 e-6
	Genes involved in Nuclear Receptor transcription pathway ( <b>Transcription</b> )	11	49	7.56	1.55 e-7	5.58 e-6
	Sphingolipid metabolism ( <b>Metabolism of sphingolipid</b> )	10	40	8.42	1.92 e-7	6.67 e-6
	Genes involved in Gluconeogenesis ( <b>Metabolism of gluconeogenesis</b> )	9	34	8.92	4.65 e-7	1.52 e-5
	Genes involved in Glycosphingolipid metabolism ( <b>Metabolism of glycosphingolipid</b> )	9	38	7.98	1.3 e-6	3.68 e-5
Genes involved in Transport of vitamins, nucleosides, and related molecules ( <b>Membrane transport</b> )	8	31	8.70	2.52 e-6	6.63 e-5	

Genes involved in Xenobiotics ( <b>Biological oxidation</b> )	6	16	12.64	4.18 e-6	1.02 e-4
Renin-angiotensin system ( <b>Renin-angiotensin system</b> )	6	17	11.90	6.29 e-6	1.51 e-4
Genes involved in Triglyceride Biosynthesis ( <b>Metabolism of lipids</b> )	8	38	7.09	1.3 e-5	2.91 e-4
Linoleic acid metabolism ( <b>Metabolism of linoleic acid</b> )	7	29	8.13	1.75 e-5	3.7 e-4
Genes involved in Glycolysis ( <b>Metabolism of glycolysis</b> )	7	29	8.13	1.75 e-5	3.7 e-4
Genes involved in ERK/MAPK targets ( <b>ERK/MAPK pathway</b> )	6	21	9.63	2.49 e-5	5.06 e-4
Genes involved in Amino acid transport across the plasma membrane ( <b>Membrane transport</b> )	7	31	7.61	2.8 e-5	5.43 e-4
Nuclear Receptors in Lipid Metabolism and Toxicity ( <b>Metabolism of lipids and toxin</b> )	5	15	11.23	5.34 e-5	8.98 e-4
Genes involved in HDL-mediated lipid transport ( <b>Metabolism of lipids</b> )	5	15	11.23	5.34 e-5	8.98 e-4
Genes involved in Nuclear Events ( <b>Transcription</b> )	6	24	8.42	5.73 e-5	9.49 e-4
Genes involved in Chylomicron-mediated lipid transport ( <b>Metabolism of lipids</b> )	5	16	10.53	7.57 e-5	1.2 e-3
Genes involved in Recycling pathway of L1 ( <b>Axon guidance</b> )	6	27	7.49	1.17 e-4	1.7 e-3
Genes involved in Synthesis of PA ( <b>Metabolism of phospholipids</b> )	6	27	7.49	1.17 e-4	1.7 e-3
Pentose and glucuronate interconversions ( <b>Metabolism of glucose</b> )	6	28	7.22	1.45 e-4	2.03 e-3
Genes involved in Peroxisomal lipid metabolism ( <b>Metabolism of lipids</b> )	5	21	8.02	3.12 e-4	3.65 e-3
Cystic Fibrosis Transmembrane Conductance Regulator And Beta 2 Adrenergic Receptor Pathway ( <b>cAMP related signaling</b> )	4	12	11.23	3.15 e-4	3.65 e-3
Genes involved in Apoptotic cleavage of cell adhesion proteins ( <b>Apoptosis</b> )	4	12	11.23	3.15 e-4	3.65 e-3

	Genes involved in ERKs are inactivated ( <b>ERK/MAPK pathway</b> )	4	12	11.23	3.15 e-4	3.65 e-3
	Genes involved in Metal ion SLC transporters ( <b>Membrane transport</b> )	5	22	7.66	3.94 e-4	4.24 e-3
Colon transverse	Extracellular matrix (ECM)-receptor interaction ( <b>Extracellular matrix</b> )	10	84	6.40	3.72 e-6	5.73 e-4
	Genes involved in Sphingolipid metabolism ( <b>Metabolism of phospholipids</b> )	9	69	7.01	5.3 e-6	7.14 e-4
	Fructose and mannose metabolism ( <b>Metabolism of glycose</b> )	6	34	9.49	3.49 e-5	2.92 e-3
	Genes involved in Synthesis of PE ( <b>Metabolism of phospholipids</b> )	4	11	19.56	3.52 e-5	2.92 e-3
	Genes involved in NCAM1 interactions ( <b>NCAM signaling</b> )	6	39	8.27	7.82 e-5	4.6 e-3
	Genes involved in Effects of PIP2 hydrolysis ( <b>Metabolism of phospholipids</b> )	5	25	10.76	8.54 e-5	4.6 e-3
	Mechanism of Gene Regulation by Peroxisome Proliferators via PPAR $\alpha$ ( <b>Transcription regulation</b> )	7	58	6.49	9.85 e-5	4.82 e-3
	Genes involved in Collagen formation ( <b>Collagen formation</b> )	7	58	6.49	9.85 e-5	4.82 e-3
	Genes involved in Regulation of Insulin Secretion by Glucagon-like Peptide-1 ( <b>GLP-1 and insulin secretion</b> )	6	43	7.50	1.37 e-4	5.91 e-3
Colon sigmoid	Genes involved in Cytosolic tRNA aminoacylation ( <b>Expression</b> )	8	24	62.27	4.11 e-13	2.21 e-10
	Genes involved in tRNA Aminoacylation ( <b>Expression</b> )	9	42	40.03	1.19 e-12	4.28 e-10
	Aminoacyl-tRNA biosynthesis ( <b>Expression</b> )	7	41	31.89	2.23 e-9	5.99 e-7
	Genes involved in Metabolism of non-coding RNA ( <b>Metabolism of non-coding RNA</b> )	7	49	26.68	8.2 e-9	1.77 e-6
	Genes involved in Protein folding ( <b>Expression</b> )	7	53	24.67	1.44 e-8	2.59 e-6
	Genes involved in Prefoldin mediated transfer of substrate to CCT/TriC ( <b>Expression</b> )	5	28	33.35	3.75 e-7	4.04 e-5

	Glutathione metabolism <b>(Metabolism of glutathione)</b>	5	50	18.68	7.34 e-6	4.65 e-4
	Genes involved in Association of TriC/CCT with target proteins during biosynthesis <b>(Expression)</b>	4	27	27.67	1.28 e-5	6.87 e-4
	Genes involved in NEP/NS2 Interacts with the Cellular Export Machinery <b>(Expression)</b>	4	27	27.67	1.28 e-5	6.87 e-4
	Genes involved in Purine ribonucleoside monophosphate biosynthesis <b>(Metabolism of purine ribonucleoside)</b>	3	11	50.94	2.42 e-5	1.19 e-3
	One carbon pool by folate <b>(Biological oxidation)</b>	3	17	32.96	9.75 e-5	3.89 e-3
	Genes involved in Formation of tubulin folding intermediates by CCT/TriC <b>(Expression)</b>	3	22	25.47	2.16 e-4	7.06 e-3
	Genes involved in RNA Polymerase I Transcription Termination <b>(Expression)</b>	3	22	25.47	2.16 e-4	7.06 e-3
	Genes involved in RNA Polymerase I Transcription Initiation <b>(Expression)</b>	3	25	22.41	3.19 e-4	9.05 e-3
Liver	Genes involved in Extracellular matrix organization <b>(Extracellular matrix)</b>	17	87	21.38	4.32 e-18	4.65 e-15
	Genes involved in Signaling by PDGF <b>(PDGF signaling)</b>	18	122	16.14	8.65 e-17	4.66 e-14
	Genes involved in Collagen formation <b>(Collagen formation)</b>	14	58	26.41	1.61 e-16	5.77 e-14
	Extracellular matrix (ECM)-receptor interaction <b>(Extracellular matrix)</b>	13	84	16.93	8.97 e-13	1.38 e-10
	Genes involved in NCAM1 interactions <b>(NCAM signaling)</b>	9	39	25.25	6.79 e-11	8.13 e-9
	Genes involved in NCAM signaling for neurite out-growth <b>(NCAM signaling)</b>	10	64	17.09	3.57 e-10	3.84 e-8
	Genes involved in Muscle contraction <b>(Muscle contraction)</b>	7	48	15.95	2.7 e-7	1.94 e-5
	Genes involved in Chondroitin sulfate/dermatan sulfate <b>(metabolism Metabolism of GAG )</b>	7	49	15.63	3.13 e-7	2.1 e-5

	Genes involved in Smooth Muscle Contraction ( <b>Smooth Muscle Contraction</b> )	5	25	21.88	2.85 e-6	1.7 e-4
	PKC-catalyzed phosphorylation of inhibitory phosphoprotein of myosin phosphatase ( <b>Smooth muscle contraction</b> )	5	31	17.64	8.7 e-6	4.46 e-4
	Role of EGF Receptor Transactivation by GPCRs in Cardiac Hypertrophy ( <b>GRCP signaling pathway</b> )	4	18	24.31	1.9 e-5	8.67 e-4
	Genes involved in Chondroitin sulfate biosynthesis ( <b>Metabolism of GAG</b> )	4	21	20.84	3.64 e-5	1.22 e-3
	Genes involved in A tetrasaccharide linker sequence is required for GAG synthesis ( <b>Metabolism of GAG</b> )	4	25	17.50	7.47 e-5	2.3 e-3
	Genes involved in Keratan sulfate degradation ( <b>Metabolism of GAG</b> )	3	11	29.84	1.18 e-4	3.54 e-3
	Genes involved in Receptor-ligand binding initiates the second proteolytic cleavage of Notch receptor ( <b>NOTCH pathway</b> )	3	12	27.35	1.57 e-4	4.22 e-3
	Genes involved in Signaling by NOTCH3 ( <b>NOTCH pathway</b> )	3	12	27.35	1.57 e-4	4.22 e-3
Skeletal Muscle	Genes involved in Fatty acid, triacylglycerol, and ketone body metabolism ( <b>Metabolism of lipids</b> )	29	168	6.10	6.2 e-15	6.68 e-12
	HIV-I Nef: negative effector of Fas and TNF ( <b>Immune</b> )	14	58	8.53	6.16 e-10	1.58 e-7
	Genes involved in Muscle contraction ( <b>Muscle contraction</b> )	12	48	8.84	6.73 e-9	1.04 e-6
	Genes involved in Striated Muscle Contraction ( <b>Muscle contraction</b> )	9	27	11.79	3.32 e-8	3.97 e-6
	Genes involved in TRIF mediated TLR3 signaling ( <b>Toll-like receptor pathway</b> )	13	74	6.21	1.46 e-7	9.18 e-6
	Genes involved in NFkB and MAP kinases activation mediated by TLR4 signaling repertoire ( <b>Toll-like receptor pathway, NF-κB pathway and MAPK pathway</b> )	12	72	5.89	7.95 e-7	3.43 e-5

Genes involved in Transcriptional Regulation of White Adipocyte Differentiation <b>(Transcription regulation)</b>	12	72	5.89	7.95 e-7	3.43 e-5
Induction of apoptosis through DR3 and DR4/5 Death Receptors ( <b>Apoptosis</b> )	8	33	8.57	2.95 e-6	9.63 e-5
Genes involved in Activation of Chaperone Genes by XBP1(S) ( <b>ER stress</b> )	9	46	6.92	4.81 e-6	1.4 e-4
Genes involved in MAP kinase activation in TLR cascade ( <b>Toll-like receptor pathway</b> )	9	50	6.36	9.89 e-6	2.6 e-4
FAS signaling pathway ( CD95 ) ( <b>Apoptosis</b> )	7	30	8.25	1.63 e-5	3.91 e-4
Inositol phosphate metabolism ( <b>Metabolism of phospholipids</b> )	9	54	5.89	1.9 e-5	4.35 e-4
Apoptotic Signaling in Response to DNA Damage ( <b>Apoptosis</b> )	6	22	9.64	2.55 e-5	5.32 e-4
Rho cell motility signaling pathway ( <b>Muscle contraction</b> )	7	32	7.73	2.57 e-5	5.32 e-4
Alanine, aspartate and glutamate metabolism ( <b>Metabolism of amino acid</b> )	7	32	7.73	2.57 e-5	5.32 e-4
Valine, leucine and isoleucine degradation ( <b>Metabolism of amino acid</b> )	8	44	6.43	2.86 e-5	5.72 e-4
N-Glycan biosynthesis ( <b>Metabolism of glycoprotein</b> )	8	46	6.15	4.01 e-5	7.31 e-4
Genes involved in RORA Activates Circadian Expression ( <b>Circadian rhythm</b> )	6	24	8.84	4.38 e-5	7.74 e-4
SNARE interactions in vesicular transport ( <b>Vesicular transport</b> )	7	38	6.51	8.31 e-5	1.36 e-3
Genes involved in Triglyceride Biosynthesis ( <b>Metabolism of lipids</b> )	7	38	6.51	8.31 e-5	1.36 e-3
Genes involved in Branched-chain amino acid catabolism ( <b>Metabolism of amino acid</b> )	5	17	10.40	8.34 e-5	1.36 e-3
Fatty acid metabolism ( <b>Metabolism of lipids</b> )	7	42	5.89	1.61 e-4	2.38 e-3
Genes involved in Intrinsic Pathway for Apoptosis ( <b>Apoptosis</b> )	6	30	7.07	1.67 e-4	2.43 e-3

	Genes involved in ERK/MAPK targets ( <b>ERK/MAPK pathway</b> )	5	21	8.42	2.5 e-4	3.4 e-3
	Genes involved in ERKs are inactivated ( <b>ERK/MAPK pathway</b> )	4	12	11.79	2.62 e-4	3.53 e-3
	Signal transduction through IL1R ( <b>NF-κB pathway and MAPK pathway</b> )	6	33	6.43	2.9 e-4	3.83 e-3
	Genes involved in Gluconeogenesis ( <b>Metabolism of glucose</b> )	6	34	6.24	3.44 e-4	4.41 e-3
	Circadian rhythm – mammal ( <b>Circadian rhythm</b> )	4	13	10.88	3.7 e-4	4.64 e-3
	Genes involved in Circadian Repression of Expression by REV-ERBA ( <b>Circadian rhythm</b> )	5	23	7.69	3.94 e-4	4.88 e-3
	Genes involved in BMAL1:CLOCK/NPAS2 Activates Circadian Expression ( <b>Circadian rhythm</b> )	6	36	5.89	4.75 e-4	5.69 e-3
	Nicotinate and nicotinamide metabolism ( <b>Metabolism of vitamin</b> )	5	24	7.37	4.86 e-4	5.69 e-3
	Genes involved in Nuclear Events (kinase and transcription factor activation) ( <b>Transcription</b> )	5	24	7.37	4.86 e-4	5.69 e-3
	Cell to Cell Adhesion Signaling ( <b>Cellular activities</b> )	4	14	10.10	5.07 e-4	5.87 e-3
	Genes involved in Smooth Muscle Contraction ( <b>Muscle contraction</b> )	5	25	7.07	5.94 e-4	6.66 e-3
Lung	Genes involved in Ion transport by P-type ATPases ( <b>Ion transport</b> )	5	34	17.32	9.75 e-6	1.68 e-3
	Genes involved in Acyl chain remodelling of phosphatidylcholine ( <b>Metabolism of phospholipids</b> )	4	22	21.42	3.31 e-5	3.56 e-3
	Genes involved in Metabolism of vitamins and cofactors ( <b>Metabolism of vitamin</b> )	5	51	11.55	7.31 e-5	6.56 e-3
	Genes involved in Ion channel transport ( <b>Ion transport</b> )	5	55	10.71	1.05 e-4	8.1 e-3
	Genes involved in HS-GAG biosynthesis ( <b>Metabolism of GAG</b> )	4	31	15.20	1.34 e-4	7.21 e-3



	Kidney	Extracellular matrix (ECM)-receptor interaction <b>(Extracellular matrix)</b>	8	31	18.38	2.46 e-5	8.84 e-3
Endocrine System	Thyroid	Genes involved in Generic Transcription Pathway <b>(Transcription)</b>	20	352	9.46	6.37 e-14	6.86 e-11
	Pituitary	Axon guidance ( <b>Axon guidance</b> )	31	129	5.72	1.94 e-15	4.18 e-13
		Arginine and proline metabolism ( <b>Metabolism of amino acid</b> )	18	54	7.93	3.49 e-12	4.18 e-10
		Fc gamma R-mediated phagocytosis ( <b>Phagocytosis</b> )	23	97	5.64	1.07 e-11	1.15 e-9
		Extracellular matrix (ECM)-receptor interaction <b>(Extracellular matrix)</b>	21	84	5.95	2.83 e-11	2.54 e-9
		Genes involved in HDL-mediated lipid transport <b>(Metabolism of lipids)</b>	10	15	15.87	4.13 e-11	3.42 e-9
		Genes involved in Integrin cell surface interactions <b>(Extracellular matrix)</b>	18	79	5.42	3.65 e-9	1.87 e-7
		Genes involved in Glycerophospholipid biosynthesis ( <b>Metabolism of phospholipids</b> )	18	82	5.22	6.88 e-9	3.37 e-7
		Genes involved in Lipoprotein metabolism <b>(Metabolism of lipids)</b>	11	28	9.35	7.72 e-9	3.62 e-7
		Arrhythmogenic right ventricular cardiomyopathy (ARVC) ( <b>Ca<sup>2+</sup> pathway</b> )	17	76	5.32	1.33 e-8	5.72 e-7
		Phosphoinositides and their downstream targets <b>(Metabolism of phospholipids)</b>	9	23	9.31	1.91 e-7	6.63 e-6
		Genes involved in Lipid digestion, mobilization, and transport ( <b>Metabolism of lipids</b> )	12	46	6.21	2.99 e-7	1.01 e-5
		Genes involved in CRMPs in Sema3A signaling ( <b>Axon guidance</b> )	7	14	11.90	6.03 e-7	1.8 e-5
		Genes involved in Collagen formation ( <b>Collagen formation</b> )	13	58	5.33	6.54 e-7	1.9 e-5
		Genes involved in Netrin-1 signaling ( <b>Axon guidance</b> )	11	41	6.38	6.86 e-7	1.9 e-5
	Glutathione metabolism <b>(Metabolism of glutathione)</b>	12	50	5.71	8 e-7	2.15 e-5	
	Genes involved in Cell death signalling via NUAGE, NRIF and NADE <b>(Apoptosis)</b>	13	60	5.15	9.89 e-7	2.54 e-5	

Genes involved in NRAGE signals death through JNK ( <b>Apoptosis</b> )	11	43	6.09	1.16 e-6	2.86 e-5
Base excision repair ( <b>DNA repair</b> )	10	35	6.80	1.17 e-6	2.86 e-5
Endometrial cancer ( <b>Cancer</b> )	12	52	5.49	1.26 e-6	2.95 e-5
Cyclins and Cell Cycle Regulation ( <b>Cell cycle</b> )	8	23	8.28	2.66 e-6	5.61 e-5
Genes involved in Glutathione conjugation ( <b>Metabolism of glutathione</b> )	8	23	8.28	2.66 e-6	5.61 e-5
PKC-catalyzed phosphorylation of inhibitory phosphoprotein of myosin phosphatase ( <b>Smooth muscle contraction</b> )	9	31	6.91	3.47 e-6	6.8 e-5
Genes involved in Regulation of signaling by CBL ( <b>Phagocytosis</b> )	7	18	9.25	4.82 e-6	8.95 e-5
DNA replication ( <b>Proliferation</b> )	9	36	5.95	1.34 e-5	1.99 e-4
Genes involved in Myogenesis ( <b>Myogenesis</b> )	8	28	6.80	1.4 e-5	2.03 e-4
Keratinocyte Differentiation ( <b>Differentiation</b> )	10	46	5.17	1.7 e-5	2.38 e-4
Glycosaminoglycan biosynthesis - chondroitin sulfate ( <b>Metabolism of GAG</b> )	7	22	7.57	2.23 e-5	2.93 e-4
O-Glycan biosynthesis ( <b>Metabolism of glycan</b> )	8	30	6.34	2.44 e-5	3.09 e-4
Proximal tubule bicarbonate reclamation ( <b>Metabolism of ion</b> )	7	23	7.24	3.09 e-5	3.69 e-4
Genes involved in Transport of vitamins, nucleosides, and related molecules ( <b>Molecules transport</b> )	8	31	6.14	3.16 e-5	3.74 e-4
Genes involved in Sulfur amino acid metabolism ( <b>Metabolism of amino acid</b> )	7	24	6.94	4.2 e-5	4.92 e-4
Genes involved in Dopamine Neurotransmitter Release Cycle ( <b>Neurotransmitter Release</b> )	5	11	10.82	4.86 e-5	5.56 e-4
Genes involved in Neurotransmitter Release Cycle ( <b>Neurotransmitter Release</b> )	8	34	5.60	6.51 e-5	7.11 e-4
Genes involved in Synthesis of phosphatidylcholine ( <b>metabolism of phospholipids</b> )	6	18	7.93	6.53 e-5	7.11 e-4

	Adrenal gland	Genes involved in GAB1 signalosome ( <b>PI3K/AKT pathway</b> )	7	38	13.69	6.76 e-7	2.74 e-4
		Genes involved in PI3K events in ERBB2 signaling ( <b>PI3K/AKT pathway</b> )	6	44	10.14	2.64 e-5	2.84 e-3
		Genes involved in PIP3 activates AKT signaling ( <b>PI3K/AKT pathway</b> )	5	29	12.82	3.93 e-5	3.85 e-3
		Genes involved in Nuclear Receptor transcription pathway ( <b>Nuclear receptor transcription pathway</b> )	6	49	9.10	4.94 e-5	4.09 e-3
		Fructose and mannose metabolism ( <b>Metabolism of glucide</b> )	5	34	10.93	8.72 e-5	5.64 e-3
		Genes involved in PI3K/AKT activation ( <b>PI3K/AKT pathway</b> )	5	38	9.78	1.5 e-4	7.72 e-3
		Genes involved in PI3K events in ERBB4 signaling ( <b>PI3K/AKT pathway</b> )	5	38	9.78	1.5 e-4	7.72 e-3
Female Reproductive System	Ovary	Ribosome ( <b>Expression</b> )	61	88	107.62	8.72 e-115	9.39 e-112
		Genes involved in 3' -UTR-mediated translational regulation ( <b>Translational regulation</b> )	65	176	57.33	1.56 e-97	8.42 e-95
		Genes involved in Peptide chain elongation ( <b>Expression</b> )	60	153	60.88	7.53 e-92	2.03 e-89
		Genes involved in Activation of the mRNA upon binding of the cap-binding complex and eIFs, and subsequent binding to 43S ( <b>Expression</b> )	32	84	59.14	1.6 e-48	1.43 e-46
		Genes involved in Formation of the ternary complex, and subsequently, the 43S complex ( <b>Expression</b> )	30	74	62.94	1.5 e-46	1.24 e-44
Male Reproductive System	Testis	Genes involved in Generic Transcription Pathway ( <b>Transcription regulation</b> )	39	352	4.67	2.04 e-15	2.2 e-12
	Prostate	Regulation of BAD phosphorylation ( <b>Apoptosis</b> )	4	26	28.05	1.2 e-5	1.18 e-3
		Genes involved in Keratan sulfate biosynthesis ( <b>Metabolism of GAG</b> )	4	26	28.05	1.2 e-5	1.18 e-3
		Genes involved in Keratan sulfate/keratin metabolism ( <b>Metabolism of GAG</b> )	4	30	24.31	2.16 e-5	1.79 e-3
		Genes involved in HS-GAG biosynthesis ( <b>Metabolism of GAG</b> )	4	31	23.53	2.47 e-5	1.87 e-3

Genes involved in Keratan sulfate degradation <b>(Metabolism of GAG)</b>	3	11	49.73	2.6 e-5	1.87 e-3
Genes involved in Regulation of Insulin-like Growth Factor (IGF) Activity by Insulin-like Growth Factor Binding Proteins (IGFBPs) <b>(IGF signaling)</b>	3	16	34.19	8.65 e-5	5.48 e-3
Genes involved in Regulation of KIT signaling <b>(Proliferation)</b>	3	17	32.18	1.05 e-4	5.93 e-3

**Supplementary Table S3 Transcription Factor Network of GDF11 in Different Human Cells**

System	Tissue	Amount	Network Member
Nervous System	Neural Stem Cell	22	SP3, RARG, KLF14, KLF12, KLF7, NFIC, CPEB1, SP8, CREB1, NFYA, IKZF2, MYF6, SP1, NFY, SP4, RFX3, RFX4, RFX1, KLF4, ATF1, RFX5, KLF16
	Neuron	8	CREB1, NFYA, NFY, ATF1, SP1, SP4, KLF16, IKZF2
	Brain	20	SP3, RARG, KLF14, KLF12, KLF7, NFIC, SP8, CREB1, NFYA, MYF6, SP1, NFY, SP4, RFX3, RFX4, RFX1, KLF4, ATF1, RFX5, KLF16
	Occipital Cortex	21	SP3, RARG, KLF14, KLF12, KLF7, NFIC, SP8, CREB1, NFYA, AP1, MYF6, SP1, NFY, SP4, RFX3, RFX4, RFX1, KLF4, ATF1, RFX5, KLF16
	Occipital Lobe	8	CREB1, NFYA, NFY, ATF1, SP1, SP4, KLF16, IKZF2
	Occipital Pole	20	SP3, RARG, KLF14, KLF12, KLF7, NFIC, SP8, CREB1, NFYA, MYF6, SP1, NFY, SP4, RFX3, RFX4, RFX1, KLF4, ATF1, RFX5, KLF16
	Paracentral Gyrus	10	CREB1, NFYA, NFY, ATF1, SP1, SP4, KLF16, RFX1, RFX4, RFX5
	Postcentral Gyrus	7	CREB1, NFYA, NFY, ATF1, SP1, SP4, KLF16
	Parietal Lobe	20	SP3, RARG, KLF14, KLF12, KLF7, NFIC, SP8, CREB1, NFYA, MYF6, SP1, NFY, SP4, RFX3, RFX4, RFX1, KLF4, ATF1, RFX5, KLF16
	Frontal Lobe	20	SP3, RARG, KLF14, KLF12, KLF7, NFIC, SP8, CREB1, NFYA, MYF6, SP1, NFY, SP4, RFX3, RFX4, RFX1, KLF4, ATF1, RFX5, KLF16
	Medial Frontal Gyrus	21	SP3, RARG, KLF14, KLF12, KLF7, NFIC, SP8, CREB1, NFYA, IKZF2, MYF6, SP1, NFY, SP4, RFX3, RFX4, RFX1, KLF4, ATF1, RFX5, KLF16
	Medial Temporal Gyrus	20	SP3, RARG, KLF14, KLF12, KLF7, NFIC, SP8, CREB1, NFYA, MYF6, SP1, NFY, SP4, RFX3, RFX4, RFX1, KLF4, ATF1, RFX5, KLF16
	Temporal Lobe	7	CREB1, NFYA, NFY, ATF1, SP1, SP4, KLF16
	Hippocampus	21	SP3, RARG, KLF14, KLF12, KLF7, NFIC, SP8, CREB1, NFYA, IKZF2, MYF6, SP1, NFY, SP4, RFX3, RFX4, RFX1, KLF4, ATF1, RFX5, KLF16
	Amygdala	20	SP3, RARG, KLF14, KLF12, KLF7, NFIC, SP8, CREB1, NFYA, MYF6, SP1, NFY, SP4, RFX3, RFX4, RFX1, KLF4, ATF1, RFX5, KLF16
	Putamen	20	SP3, RARG, KLF14, KLF12, KLF7, NFIC, SP8, CREB1, NFYA, MYF6, SP1, NFY, SP4, RFX3, RFX4, RFX1, KLF4, ATF1, RFX5, KLF16
	Caudate Nucleus	20	SP3, RARG, KLF14, KLF12, KLF7, NFIC, SP8, CREB1, NFYA, MYF6, SP1, NFY, SP4, RFX3, RFX4, RFX1, KLF4, ATF1, RFX5, KLF16
	Corpus Callosum	7	CREB1, NFYA, NFY, ATF1, SP1, SP4, KLF16
	Globus Pallidus	20	SP3, RARG, KLF14, KLF12, KLF7, NFIC, SP8, CREB1, NFYA, MYF6, SP1, NFY, SP4, RFX3, RFX4, RFX1, KLF4, ATF1, RFX5, KLF16
	Nucleus Accumbens	20	SP3, RARG, KLF14, KLF12, KLF7, NFIC, SP8, CREB1, NFYA, MYF6, SP1, NFY, SP4, RFX3, RFX4, RFX1, KLF4, ATF1, RFX5, KLF16
Thalamus	4	CREB1, NFYA, NFY, ATF1	
Pineal Gland	7	CREB1, NFYA, NFY, ATF1, SP1, SP4, KLF16	
Substantia Nigra	5	CREB1, NFYA, NFY, ATF1, IKZF2	

	Pituitary	16	SP3, RARG, KLF14, KLF12, KLF7, NFIC, SP8, MYF6, SP1, SP4, RFX3, RFX4, RFX1, KLF4, RFX5, KLF16
	Diencephalon	7	CREB1, NFYA, NFY, ATF1, SP1, SP4, KLF16
	Pons	7	CREB1, NFYA, NFY, ATF1, SP1, SP4, KLF16
	Medulla Oblongata	20	SP3, RARG, KLF14, KLF12, KLF7, NFIC, SP8, CREB1, NFYA, MYF6, SP1, NFY, SP4, RFX3, RFX4, RFX1, KLF4, ATF1, RFX5, KLF16
	Cerebellum	21	SP3, RARG, KLF14, KLF12, KLF7, NFIC, SP8, CREB1, NFYA, IKZF2, MYF6, SP1, NFY, SP4, RFX3, RFX4, RFX1, KLF4, ATF1, RFX5, KLF16
	Cerebral Meninges	7	CREB1, NFYA, NFY, ATF1, SP1, SP4, KLF16
	Spinal Cord	4	CREB1, NFYA, NFY, ATF1
	Olfactory Region	20	SP3, RARG, KLF14, KLF12, KLF7, NFIC, SP8, CREB1, NFYA, MYF6, SP1, NFY, SP4, RFX3, RFX4, RFX1, KLF4, ATF1, RFX5, KLF16
	Optic Nerve	7	CREB1, NFYA, NFY, ATF1, SP1, SP4, KLF16
	Retina	20	SP3, RARG, KLF14, KLF12, KLF7, NFIC, SP8, CREB1, NFYA, MYF6, SP1, NFY, SP4, RFX3, RFX4, RFX1, KLF4, ATF1, RFX5, KLF16
Cardiovascular System	Heart	4	CREB1, NFYA, NFY, ATF1
	Left Atrium	20	SP3, RARG, KLF14, KLF12, KLF7, NFIC, SP8, CREB1, NFYA, MYF6, SP1, NFY, SP4, RFX3, RFX4, RFX1, KLF4, ATF1, RFX5, KLF16
	Left Ventricle	4	CREB1, NFYA, NFY, ATF1
	Heart Mitral Valve	10	CREB1, NFYA, NFY, ATF1, SP1, SP4, KLF16, IKZF2, FEV, AP1
	Heart Pulmonic Valve	22	SP3, RARG, KLF14, KLF12, KLF7, NFIC, AP1, SP8, CREB1, NFYA, IKZF2, MYF6, SP1, NFY, SP4, RFX3, RFX4, RFX1, KLF4, ATF1, RFX5, KLF16
	Heart Tricuspid Valve	4	CREB1, NFYA, NFY, AP1
	Blood	4	CREB1, NFYA, NFY, ATF1
	Aorta	2	CREB1, NFYA
	Endothelial Cell Aorta	20	SP3, RARG, KLF14, KLF12, KLF7, NFIC, SP8, CREB1, NFYA, MYF6, SP1, NFY, SP4, RFX3, RFX4, RFX1, KLF4, ATF1, RFX5, KLF16
	Endothelial Cell Artery	7	CREB1, NFYA, NFY, ATF1, SP1, SP4, KLF16
	Endothelial Cell Microvascular Vein	4	CREB1, NFYA, NFY, ATF1
	Pericyte	19	SP3, RARG, KLF14, KLF12, KLF7, NFIC, SP8, CREB1, NFYA, MYF6, SP1, NFY, SP4, RFX3, RFX4, RFX1, KLF4, RFX5, KLF16
		20	SP3, RARG, KLF14, KLF12, KLF7, NFIC, SP8, CREB1, NFYA, MYF6, SP1, NFY, SP4, RFX3, RFX4, RFX1, KLF4, ATF1, RFX5, KLF16
Digestive System	Hepatocyte	20	SP3, RARG, KLF14, KLF12, KLF7, NFIC, SP8, CREB1, NFYA, MYF6, SP1, NFY, SP4, RFX3, RFX4, RFX1, KLF4, ATF1, RFX5, KLF16
	Hepatic Sinusoid Endothelial Cell	7	CREB1, NFYA, NFY, ATF1, SP1, SP4, KLF16
	Hepatic Stellate Cell	7	CREB1, NFYA, NFY, ATF1, SP1, SP4, KLF16
	Lipocyte	7	CREB1, NFYA, NFY, ATF1, SP1, SP4, KLF16
	Gall Bladder	6	CREB1, NFYA, NFY, ATF1, SP1, SP4

	Insula	20	SP3, RARG, KLF14, KLF12, KLF7, NFIC, SP8, CREB1, NFYA, MYF6, SP1, NFY, SP4, RFX3, RFX4, RFX1, KLF4, ATF1, RFX5, KLF16
	Spleen	6	CREB1, NFYA, NFY, ATF1, SP1, SP4
	Appendix	7	CREB1, NFYA, NFY, ATF1, SP1, SP4, KLF16
Respiratory System	Small Intestine	2	CREB1, NFYA
	Throat	6	CREB1, NFYA, NFY, ATF1, SP1, SP4
	Trachea	3	CREB1, NFYA, NFY
Urinary system	Bladder	5	CREB1, NFYA, NFY, SP1, SP4
Skeletal Muscle	Osteoblast	20	SP3, RARG, KLF14, KLF12, KLF7, NFIC, SP8, CREB1, NFYA, MYF6, SP1, NFY, SP4, RFX3, RFX4, RFX1, KLF4, ATF1, RFX5, KLF16
	Osteoblast Differentiated	20	SP3, RARG, KLF14, KLF12, KLF7, NFIC, SP8, CREB1, NFYA, MYF6, SP1, NFY, SP4, RFX3, RFX4, RFX1, KLF4, ATF1, RFX5, KLF16
	Skeletal Muscle Cell Differentiated Into Myotube	19	SP3, RARG, KLF14, KLF12, KLF7, SP8, CREB1, NFYA, MYF6, SP1, NFY, SP4, RFX3, RFX4, RFX1, KLF4, ATF1, RFX5, KLF16
	Smooth Muscle	6	CREB1, NFYA, NFY, ATF1, SP1, SP4
Female Reproductive System	Ovary	7	CREB1, NFYA, NFY, ATF1, SP1, SP4, KLF16
	Uterus	20	SP3, RARG, KLF14, KLF12, KLF7, NFIC, SP8, CREB1, NFYA, MYF6, SP1, NFY, SP4, RFX3, RFX4, RFX1, KLF4, ATF1, RFX5, KLF16
Male Reproductive System	Cervix	7	CREB1, NFYA, NFY, ATF1, SP1, SP4, KLF16
	Prostate	6	CREB1, NFYA, NFY, ATF1, SP1, SP4
	Testis	16	SP3, RARG, KLF14, KLF12, KLF7, NFIC, SP8, MYF6, SP1, SP4, RFX3, RFX4, RFX1, KLF4, RFX5, KLF16
	Seminal Vesicle	21	SP3, RARG, KLF14, KLF12, KLF7, NFIC, SP8, CREB1, NFYA, AP1, MYF6, SP1, NFY, SP4, RFX3, RFX4, RFX1, KLF4, ATF1, RFX5, KLF16
	Ductus Deferens	7	CREB1, NFYA, NFY, ATF1, SP1, SP4, KLF16
	Epididymis	2	CREB1, NFYA
	Penis	1	IKZF2
Endocrine System	Salivary Gland	7	CREB1, NFYA, NFY, ATF1, SP1, SP4, KLF16
	Parotid Gland	4	CREB1, NFYA, NFY, ATF1
	Thyroid	16	SP3, RARG, KLF14, KLF12, KLF7, NFIC, SP8, MYF6, SP1, SP4, RFX3, RFX4, RFX1, KLF4, RFX5, KLF16
Immune System	Tonsil	2	SP1, SP4
	Thymus	22	SP3, RARG, KLF14, KLF12, KLF7, NFIC, SP8, CREB1, NFYA, IKZF2, MYF6, SP1, NFY, SP4, RFX3, ZNF219, RFX4, RFX1, KLF4, ATF1, RFX5, KLF16
	Lymph Node	7	CREB1, NFYA, NFY, ATF1, SP1, SP4, KLF16