

Table 2

Representation of the differentially expressed genes comparing the groups l_GFR (calculated GFR < 45ml/min/1.73 m²) and h_GFR (calculated GFR ≥ 45ml/min/1.73 m²). Genes are categorized based on gene ontology terms and PANTHER classifications and are ranked by difference of mean expression between the two groups under study. Values represent ratios of sample to standard reference expression on a log2 scale.

Accession Number	Gene Name	Gene Symbol	Mean Expression group l_GFR	Mean Expression group h_GFR
Cell adhesion				
AA228380	Integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)	ITGAV	1.79	0.57
Cell cycle, cell proliferation, cell growth				
AA625655	Regenerating islet-derived 1 alpha (pancreatic stone protein, pancreatic thread protein)	REG1A	5.10	3.45
AA844864	Regenerating islet-derived 1 beta (pancreatic stone protein, pancreatic thread protein)	REG1B	2.44	1.11
AA456653	Polybromo 1	PB1	-1.65	-2.76
N89676	Osteoglycin (osteoinductive factor, mimecan)	OGN	-0.19	0.91
AA029185	Prokineticin 1	PROK1	0.17	1.21
Immune response				
T90492	Immunoglobulin J polypeptide, linker protein for immunoglobulin alpha and mu polypeptides	IGJ	-2.26	-3.79
AA486362	Immunoglobulin kappa variable 1-5	IGKC	2.75	1.26
A1820828	Immunoglobulin lambda joining 3	IGLC2	-3.17	-4.48
AA826328	Mucosa associated lymphoid tissue lymphoma translocation gene 1	MALT1	1.39	0.13
AA521362	Complement component (3d/Epstein Barr virus) receptor 2	CR2	1.17	-0.03
AA401441	B-factor, properdin	BF	2.28	1.22
AA926680	Doublecortin domain containing 2	DCDC2	-0.83	0.28
Ion binding				
H77597	Metallothionein 1H	MT1H	3.53	4.53
R43566	Testis expressed sequence 27	TEX27	-0.09	1.02
N73883	Phospholipase A2, group XIIB	PLA2G12B	1.02	2.49
Membrane				
R27335	Plexin A2	PLXNA2	-0.51	0.55
Metabolism				
AW005857	Retinol dehydrogenase 5 (11-cis and 9-cis)	RDH5	-0.80	0.26
AA508861	Regenerating islet-derived family, member 4	REG4	1.18	2.27
AA070357	Transketolase (Wernicke-Korsakoff syndrome)	TKT	-0.85	0.43
AA995921	Uridine phosphorylase 2	UPP2	3.94	5.55
Nucleus				
AA701964	Polymerase (DNA directed), alpha	POLA	-1.51	-2.55
AA670391	HCCA2 protein	HCCA2	-0.30	0.79
Protein modification				
AA421258	Proteasome (prosome, macropain) inhibitor subunit 1 (PI31)	PSMF1	1.74	0.28
AA883775	ADAM metallopeptidase domain 30	ADAM30	-0.95	0.10
Signal transduction				
AA476918	G protein-coupled receptor kinase 5	GRK5	2.86	0.61
AA680106	RAB12, member RAS oncogene family	RAB12	-2.17	-3.23
N77731	Signal transducer and activator of transcription 3 interacting protein 1	STATIP1	-0.77	-1.82
AA076085	Signal transducer and activator of transcription 1, 91kDa	STAT1	2.82	1.78
R95749	Membrane-spanning 4-domains, subfamily A, member 7	MS4A7	2.30	1.26
AA427595	Src homology 2 domain containing adaptor protein B	SHB	-1.04	0.22

Accession Number	Gene Name	Gene Symbol	Mean Expression group l_GFR	Mean Expression group h_GFR
Structural				
AI015991	Claudin 2	CLDN2	2.58	3.71
Transcription				
AA488871	MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C)	MEF2C	0.41	-0.77
H61303	E2F transcription factor 1	E2F1	-2.88	-3.91
R53527	Trinucleotide repeat containing 4	TNRC4	-1.52	-0.49
AA973580	Achaete-scute complex-like 1 (Drosophila)	ASCL1	0.96	2.02
AA913906	Myeloid/lymphoid or mixed-lineage leukemia 3	MLL3	-1.26	-0.15
Transport				
N90388	Transferrin	TF	1.47	0.25
AA666312	Vesicle-associated membrane protein 1 (synaptobrevin 1)	VAMP1	0.80	1.86
AI241088	Solute carrier family 6 (neurotransmitter transporter, GABA), member 13	SLC6A13	0.93	2.13
AA863145	D-amino-acid oxidase	DAO	2.33	3.37
AA708152	Transmembrane emp24 protein transport domain containing 6	TMED6	1.91	3.03
Others				
N51547	Transcribed locus		2.08	0.34
AA693501	Chromosome 7 open reading frame 34	C7orf34	0.42	1.42
AA582497	Transcribed locus		0.69	1.71
AI017053	SRSR846	UNQ846	1.23	2.28
AA020011	Metallophosphoesterase domain containing 2	C11orf8	-0.47	0.60
AI277451	Transcribed locus		-1.01	0.13
AA101631	Transcribed locus		0.51	1.74
AA913902	Transcribed locus		-0.09	1.16
AA666255	DnaJ (Hsp40) homolog, subfamily C, member 9	KIAA0974	0.57	1.86
AA620787	Transcribed locus		-0.67	0.76