

Table S1. Validation of gene chip data for selected differentially expressed transcripts by qPCR.

Gene symbol	mRNA description	Mean fold change ¹		<i>P</i> -value	
		Gene chip	qPCR	Gene chip	qPCR
<i>FGF21</i>	fibroblast growth factor 21	4.23	16.0	0.00001	0.0027
<i>MT1E</i>	metallothionein 1E	3.58	2.44	0.02151	0.0347
<i>GPX3</i>	glutathione peroxidase 3 (plasma)	2.90	1.75	0.04557	0.2142
<i>MT1A</i>	metallothionein-1A	2.64	2.84	0.01646	0.0447
<i>STEAP4</i>	STEAP family member 4	1.94	1.20	0.04495	0.3022
<i>MT2A</i>	metallothionein 2A	1.89	1.44	0.04520	0.1343
<i>STK39</i>	serine threonine kinase 39	1.81	1.54	0.00307	0.0626
<i>PPP1R3C</i>	protein phosphatase 1, regulatory subunit 3C	1.74	1.98	0.00644	0.0195
<i>INHBE</i>	inhibin, beta E	1.72	1.64	0.00014	0.0708
<i>PKD1L3</i>	polycystic kidney disease 1-like 3	1.67	1.32	0.01529	0.1226
<i>BCL6</i>	B-cell CLL/lymphoma 6	1.67	1.11	0.00271	0.3154
<i>LBP</i>	lipopolysaccharide binding protein	1.67	1.50	0.02337	0.2136
<i>HAL</i>	histidine ammonia-lyase	-1.91	-3.96	0.00167	0.0125
<i>MFSD2A</i>	major facilitator superfamily domain containing 2A	-1.89	-2.02	0.00185	0.0072

<i>LPIN1</i>	lipin 1	-1.77	-3.86	0.01014	0.0140
<i>GSTM2</i>	glutathione S-transferase M2	-1.75	-2.63	0.00998	0.0031
<i>GSTM1</i>	glutathione S-transferase M1	-1.68	-1.79	0.00878	0.0474
<i>ASCL1</i>	achaete-scute family bHLH transcription factor 1	-1.64	-2.58	0.02755	0.0199
<i>ERRFI1</i>	ERBB receptor feedback inhibitor 1	-1.60	-2.85	0.00724	0.0034
<i>VWA3B</i>	von Willebrand factor A domain containing 3B	-1.59	-2.50	0.01272	0.0221
<i>ATP10B</i>	ATPase, class V, type 10B	-1.57	-4.72	0.00278	0.0050
<i>LGR5</i>	leucine-rich repeat containing G protein-coupled receptor 5	-1.56	-1.69	0.01635	0.0369
<i>ZPR1</i>	ZPR1 zinc finger	-1.55	-2.93	0.00124	0.0001
<i>ZNF37A</i>	zinc finger protein 37A	-1.54	-1.64	0.00651	0.0737
<i>AMDHD1</i>	amidohydrolase domain containing 1	-1.53	-2.07	0.00206	0.0553

¹ Fold change was calculated from the signal log ratios as follows: $2^{\text{Signal log ratio}}$ if signal log ratio ≥ 0 and $(-1) \times 2^{-\text{(Signal log ratio)}}$ if signal log ratio < 0 . Signal log ratios were calculated from n = 8 microarrays per group.

Table S2 **Characteristics of gene-specific primers.**

Gene	Forward primer (from 5' to 3') Reverse primer (from 5' to 3')	PCR product size (bp)	NCBI GenBank Accession no.	Annealing temperature
<i>Reference genes</i>				
<i>EEF1A1</i>	GTCAAAGATGTCCGTVC GTGGC TGGCAGCGTCACCAGATTTC A	253	NM_174535.2	60
<i>H3F3A</i>	CTGTGGCACTCCGTGAAATTA ACTTGCCTCCTGCAAA.GCAC	154	NM_001014389.2	60
<i>RPL12</i>	GGCAACTGGTGATTGGAAGG TCTGCTTCTTTCTGTCCCTTGG	143	NM_205797.1	60
<i>Target genes</i>				
<i>FGF21</i>	TGTGGGTCCCTGTGCTGGCT CCACTGTGCCATCGGCCCTG	171	XM_001789587.1	65
<i>MT1E</i>	TTGCTTTGGACGACCACACTTC ATTGATACCTGGGGCAGGCTC	246	NM_001114857.2	63
<i>GPX3</i>	ACC ACC GCA CCA CGG TCA AC GCC CGT GTG GTG GAC TTG GG	127	NM_174077.3	63
<i>MT1A</i>	ATCCGACCAGTGGATCTGCTTTGCC AGACACAGCCCTGGGCACACT	209	NM_001040492.2	63
<i>STEAP4</i>	AGCACCTCTCCCGCAGTTATG GGACATCCCAGGGGTTCGAC	183	XM_002686859.5	60
<i>MT2A</i>	ACCCTCGCCATCCTTTGCTC AGGGATGTAACAAACGGGTCAGG	339	NM_001075140.1	60
<i>STK39</i>	AGGAGGTTATCGGCAGTGGC TGGGATGGCTGCACTGACTC	162	NM_001075826.1	60
<i>PPP1R3C</i>	TGCCATTGACCTACCCTCCG	142	NM_001076164.2	60

<i>INHBE</i>	CCCGTCAGGCTTCCACTGTA TTGCTGTCCTCACAGACTCCT	101	NM_001205842.1	60
<i>PKD1L3</i>	CCAGAGGCGAGCATGATACA AGTGGCTAGACCATTCGACC	254	XM_010814701	60
<i>BCL6</i>	CTGCTGTTTCAACTGGCGAC TCATTTTAGAGTGCTCATTTGGTTT	248	NM_001206450.1	60
<i>LBP</i>	TGCTGTAGAACAGGCCACTG TGCGCAAGAGGATACTGAGAC	218	NM_001038674.2	60
<i>HAL</i>	TCGGAACCTGGACTCGATCT CTAAGCCCTGAGAGATGCCG	268	NM_001105440.1	60
<i>MFSD2A</i>	CATGAGCTGCGAGGACGTAT CGGTCCAGGTGAAGAAGGAA	231	NM_001101959.1	60
<i>LPIN1</i>	TAATGCAGAAGCCCACCAGG CTTCAGTTTCCCGACCGTCA	142	NM_001206156.2	60
<i>GSTM2</i>	TTGTGTGGCGAGGACTTTGT CTCCCCACCCCACATTATC	242	XM_005204221.4	60
<i>GSTM1</i>	CCAGGAGGGAATAAGCAGGTG GAGAAGACAAGTTTCAAGCCCA	193	NM_175825.3	60
<i>ASCL1</i>	CTGTCATAGTCGGGAGCATCT CCCCCAACTACTCCAACGAC	181	XM_002687640.5	60
<i>ERRFI1</i>	CCCTGCTTCCGAAGTCCATT GCGAGTTTGAGAACGGCTTT	292	NM_001077930.1	60
<i>VWA3B</i>	CTCTTGACAGGGGTAGCGG GAAGCTGGCAGCATATTGGC	112	XM_015473358.2	60
<i>ATP10B</i>	CCCAGGCGTCTTCTGGATTT GGGGTGGAGGAATTGTGTTCA	190	XM_010798068	60
<i>LGR5</i>	CTTGGGCCCTTCTTGGTTTC TGCAGTCAGGACACTCTCCA	192	NM_001192520.3	60

<i>ZPR1</i>	GCGCCATTCAAAGTCAGTGT GCCACCACAAGGATTCCAGA AGCTTCTTCGTTTCGCCCTTC	144	NM_001038504.1	60
<i>ZNF37A</i>	AGGAGAGGATTCCGGAGCTT AAACGGAGTCAGAGCCACAC	153	XM_010801271	60
<i>AMDHD1</i>	CGGCGAGCGCTTCCTAAC GTGGCTCCTGCCAACTTCAT	261	NM_001098872.2	60

Table S3 Fold change (FC) and *P*-value of all differentially expressed transcripts*

Gene Symbol	Gene Description	FGF21 high vs. FGF21 low	
		FC	<i>P</i> -value
<i>FGF21</i>	fibroblast growth factor 21	4.23	0.00001
<i>MT1E</i>	metallothionein 1E	3.58	0.02151
<i>GPX3</i>	glutathione peroxidase 3 (plasma)	2.90	0.04557
<i>MT1A</i>	metallothionein-1A	2.64	0.01646
<i>MT1E</i>	metallothionein 1E	2.11	0.04023
<i>MIR708</i>	microRNA mir-708	2.00	0.01304
<i>STEAP4</i>	STEAP family member 4	1.94	0.04495
<i>MT2A</i>	metallothionein 2A	1.89	0.04520
<i>SLC22A7</i>	solute carrier family 22 (organic anion transporter), member 7	1.85	0.00004
<i>STK39</i>	serine threonine kinase 39	1.81	0.00307
<i>PPP1R3C</i>	protein phosphatase 1, regulatory subunit 3C	1.74	0.00644
<i>INHBE</i>	inhibin, beta E	1.72	0.00014
<i>SPIDR</i>	scaffolding protein involved in DNA repair	1.70	0.02979
<i>PKD1L3</i>	polycystic kidney disease 1-like 3	1.67	0.01529
<i>BCL6</i>	B-cell CLL/lymphoma 6	1.67	0.00271
<i>LBP</i>	lipopolysaccharide binding protein	1.67	0.02337
<i>LOC788334</i>	apolipoprotein L3	1.66	0.02124
<i>SAA4</i>	serum amyloid A4, constitutive	1.64	0.04790
<i>WWC1</i>	WW and C2 domain containing 1	1.64	0.00131
<i>MANF</i>	mesencephalic astrocyte-derived neurotrophic factor	1.62	0.04617
<i>PFKFB3</i>	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	1.62	0.00081
<i>SLC25A33</i>	solute carrier family 25 (pyrimidine nucleotide carrier), member 33	1.60	0.00269
<i>PPP1R3B</i>	protein phosphatase 1, regulatory subunit 3B	1.59	0.01829
<i>INHBA</i>	inhibin, beta A	1.57	0.00081
<i>PFKFB2</i>	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	1.54	0.00229
<i>DCDC2</i>	doublecortin domain containing 2	1.54	0.01498
<i>HSPA5</i>	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	1.53	0.04974
<i>ARRDC3</i>	arrestin domain containing 3	1.49	0.00782
<i>MID1IP1</i>	MID1 interacting protein 1	1.49	0.00076
<i>LOC101908417</i>	complement C4-like	1.47	0.02331
<i>SERPINA3-8</i>	SERPINA3-8	1.47	0.03278
<i>SGPL1</i>	sphingosine-1-phosphate lyase 1	1.47	0.00895
<i>LOC104974345</i>	glycine N-acyltransferase-like	1.47	0.02243
<i>CPQ</i>	carboxypeptidase Q	1.46	0.02643
<i>DNAJB11</i>	DnaJ (Hsp40) homolog, subfamily B, member 11	1.44	0.01839
<i>MIR2284R</i>	microRNA mir-2284r	1.42	0.01088

<i>S100A12</i>	S100 calcium binding protein A12	1.42	0.00605
<i>PSPH</i>	phosphoserine phosphatase	1.42	0.00009
<i>LOC785811</i>	olfactory receptor 12D2	1.41	0.01320
<i>LOC100336476</i>	granulocyte-macrophage colony-stimulating factor receptor subunit alpha	1.41	0.01720
<i>TIMD4</i>	T-cell immunoglobulin and mucin domain containing 4	1.40	0.03793
<i>CRELD2</i>	cysteine-rich with EGF-like domains 2	1.40	0.01898
<i>LOC104968675</i>	apolipoprotein L3-like	1.39	0.02347
<i>G0S2</i>	G0/G1 switch 2	1.39	0.00901
<i>SLC39A14</i>	solute carrier family 39 (zinc transporter), member 14	1.39	0.00064
<i>LOC786942</i>	uncharacterized LOC786942	1.39	0.03517
<i>LOC100300896</i>	sulfotransferase 1C4	1.39	0.01453
<i>LEAP2</i>	liver expressed antimicrobial peptide 2	1.38	0.00339
<i>SLC20A1</i>	solute carrier family 20 (phosphate transporter), member 1	1.37	0.00127
<i>SLC1A1</i>	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1	1.37	0.01857
<i>ATP6V0D2</i>	ATPase, H ⁺ transporting, lysosomal 38kDa, V0 subunit d2	1.37	0.01956
<i>ASNS</i>	asparagine synthetase (glutamine-hydrolyzing)	1.37	0.03515
<i>MIR874</i>	microRNA mir-874	1.36	0.01771
<i>MAMSTR</i>	MEF2 activating motif and SAP domain containing transcriptional regulator	1.36	0.00082
<i>CITED4</i>	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 4	1.36	0.00001
<i>ZCCHC10</i>	zinc finger, CCHC domain containing 10	1.36	0.03243
<i>ALDH1L2</i>	aldehyde dehydrogenase 1 family, member L2	1.35	0.02364
<i>LARP1B</i>	La ribonucleoprotein domain family, member 1B	1.35	0.00307
<i>GZMK</i>	granzyme K (granzyme 3; tryptase II)	1.35	0.02657
<i>GRAMD4</i>	GRAM domain containing 4	1.34	0.00752
<i>C15H11orf96</i>	chromosome 15 open reading frame, human C11orf96	1.34	0.00691
<i>SLC16A1</i>	solute carrier family 16 (monocarboxylate transporter), member 1	1.34	0.00055
<i>MEIOB</i>	meiosis specific with OB domains	1.34	0.00973
<i>CS</i>	citrate synthase	1.34	0.00356
<i>GLUL</i>	glutamate-ammonia ligase	1.33	0.03033
<i>HDHD3</i>	haloacid dehalogenase-like hydrolase domain containing 3	1.33	0.00211
<i>MICAL2</i>	microtubule associated monooxygenase, calponin and LIM domain containing 2	1.33	0.03967
<i>SELK</i>	selenoprotein K	1.32	0.00698
<i>UAP1</i>	UDP-N-acetylglucosamine pyrophosphorylase 1	1.32	0.00463
<i>PPL</i>	periplakin	1.32	0.00366

<i>HERPUD1</i>	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	1.32	0.04380
<i>EPHA2</i>	EPH receptor A2	1.32	0.00227
<i>MIR2372</i>	microRNA mir-2372	1.32	0.03830
<i>MDM4</i>	MDM4, p53 regulator	1.32	0.00673
<i>PLK2</i>	polo-like kinase 2	1.32	0.01037
<i>LOC785803</i>	lysozyme 14D	1.32	0.02452
<i>RAP1GAP</i>	RAP1 GTPase activating protein	1.31	0.00384
<i>HES1</i>	hes family bHLH transcription factor 1	1.31	0.01160
<i>NPR3</i>	natriuretic peptide receptor 3	1.31	0.02876
<i>XPO1</i>	exportin 1	1.31	0.01228
<i>ATF4</i>	activating transcription factor 4	1.31	0.00130
<i>RORC</i>	RAR-related orphan receptor C	1.31	0.02388
<i>IL4R</i>	interleukin 4 receptor	1.31	0.00097
<i>TMEM86A</i>	transmembrane protein 86A	1.31	0.02259
<i>WDR76</i>	WD repeat domain 76	1.30	0.02358
<i>LOC782221</i>	olfactory receptor 8B3	1.30	0.00747
<i>AGPAT9</i>	1-acylglycerol-3-phosphate O-acyltransferase 9	1.30	0.02074
<i>LYVE1</i>	lymphatic vessel endothelial hyaluronan receptor 1	1.30	0.01631
<i>KIF23</i>	kinesin family member 23	1.30	0.04910
<i>LOC101904076</i>	glutathione S-transferase theta-1-like	1.30	0.02855
<i>LOC784376</i>	olfactory receptor 52D1	1.29	0.04756
<i>LOC528329</i>	uncharacterized LOC528329	1.29	0.01205
<i>LOC787740</i>	olfactory receptor 2A12	1.29	0.01747
<i>ENTPD7</i>	ectonucleoside triphosphate diphosphohydrolase 7	1.29	0.01661
<i>NFIL3</i>	nuclear factor, interleukin 3 regulated	1.29	0.01156
<i>ALPI</i>	alkaline phosphatase, intestinal	1.29	0.03577
<i>C6H4orf19</i>	chromosome 6 open reading frame, human C4orf19	1.29	0.01004
<i>STK38</i>	serine/threonine kinase 38	1.28	0.00037
<i>HS3ST3A1</i>	heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1	1.28	0.02186
<i>LOC619125</i>	putative SEC14-like protein 6	1.28	0.02206
<i>ZFAND2A</i>	zinc finger, AN1-type domain 2A	1.28	0.01425
<i>RGL1</i>	ral guanine nucleotide dissociation stimulator-like 1	1.28	0.00155
<i>CISD2</i>	CDGSH iron sulfur domain 2	1.28	0.01803
<i>STARD6</i>	StAR-related lipid transfer (START) domain containing 6	1.28	0.02658
<i>ASPHD2</i>	aspartate beta-hydroxylase domain containing 2	1.28	0.02626
<i>DENND2A</i>	DENN/MADD domain containing 2A	1.28	0.04855
<i>LOC101907658</i>	60S ribosomal protein L22-like 1	1.27	0.02534
<i>SOWAHB</i>	sosondowah ankyrin repeat domain family member B	1.27	0.00575
<i>LOC784623</i>	olfactory receptor 5B12	1.27	0.01102
<i>BOSTAUV1R403</i>	vomer nasal 1 receptor bosTauV1R403	1.27	0.00838
<i>SH3BP2</i>	SH3-domain binding protein 2	1.27	0.02830
<i>UGDH</i>	UDP-glucose 6-dehydrogenase	1.27	0.00037

<i>ZNF608</i>	zinc finger protein 608	1.27	0.02961
<i>KRT6B</i>	keratin 6B	1.27	0.01084
<i>CCDC79</i>	coiled-coil domain containing 79	1.26	0.02048
<i>CDKN1A</i>	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	1.26	0.04303
<i>USP50</i>	ubiquitin specific peptidase 50	1.26	0.00089
<i>LOC786352</i>	apolipoprotein L3	1.26	0.01865
<i>MAP1LC3A</i>	microtubule-associated protein 1 light chain 3 alpha	1.26	0.00757
<i>CCDC134</i>	coiled-coil domain containing 134	1.26	0.03557
<i>WFS1</i>	Wolfram syndrome 1 (wolframin)	1.26	0.03334
<i>HPX</i>	hemopexin	1.26	0.02358
<i>RIOK1</i>	RIO kinase 1	1.26	0.00319
<i>RNF144B</i>	ring finger protein 144B	1.26	0.00606
<i>TBC1D9</i>	TBC1 domain family, member 9 (with GRAM domain)	1.25	0.03029
<i>C8H9orf89</i>	chromosome 8 open reading frame, human C9orf89	1.25	0.00062
<i>RRH</i>	retinal pigment epithelium-derived rhodopsin homolog	1.25	0.00829
<i>HAMP</i>	hepcidin antimicrobial peptide	1.25	0.04570
<i>FSTL1</i>	folliculin-like 1	1.25	0.02243
<i>ATP8B1</i>	ATPase, aminophospholipid transporter, class I, type 8B, member 1	1.25	0.01479
<i>TMEM41B</i>	transmembrane protein 41B	1.25	0.01878
<i>RNF43</i>	ring finger protein 43	1.25	0.00907
<i>CDC42EP3</i>	CDC42 effector protein (Rho GTPase binding) 3	1.25	0.02708
<i>FXVD6</i>	FXVD domain containing ion transport regulator 6	1.25	0.00515
<i>FBXO21</i>	F-box protein 21	1.25	0.01659
<i>ZHX3</i>	zinc fingers and homeoboxes 3	1.24	0.00127
<i>HSPB8</i>	heat shock 22kDa protein 8	1.24	0.00307
<i>TRIB3</i>	tribbles pseudokinase 3	1.24	0.03366
<i>IRF1</i>	interferon regulatory factor 1	1.24	0.04070
<i>MIR1197</i>	microRNA mir-1197	1.24	0.04820
<i>RNF144A</i>	ring finger protein 144A	1.24	0.00219
<i>CDC37L1</i>	cell division cycle 37-like 1	1.24	0.01153
<i>C3H1orf52</i>	chromosome 3 open reading frame, human C1orf52	1.24	0.02196
<i>FYN</i>	FYN proto-oncogene, Src family tyrosine kinase	1.24	0.00232
<i>CLDN15</i>	claudin 15	1.23	0.03785
<i>FNDC3B</i>	fibronectin type III domain containing 3B	1.23	0.03420
<i>CHAC1</i>	ChaC glutathione-specific gamma-glutamylcyclotransferase 1	1.23	0.02543
<i>IRF2BPL</i>	interferon regulatory factor 2 binding protein-like	1.23	0.00737
<i>ZMYND10</i>	zinc finger, MYND-type containing 10	1.23	0.00808
<i>FGL1</i>	fibrinogen-like 1	1.23	0.01453
<i>CTPS1</i>	CTP synthase 1	1.23	0.02064
<i>SLC4A7</i>	solute carrier family 4, sodium bicarbonate cotransporter, member 7	1.23	0.00159
<i>LITAF</i>	lipopolysaccharide-induced TNF factor	1.23	0.02406

<i>GALNTL6</i>	polypeptide N-acetylgalactosaminyltransferase-like 6	1.23	0.00361
<i>OR1L6</i>	olfactory receptor, family 1, subfamily L, member 6	1.23	0.01562
<i>SH2D1A</i>	SH2 domain containing 1A	1.23	0.00434
<i>ID1</i>	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	1.23	0.00571
<i>GZMB</i>	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)	1.22	0.02274
<i>TTC7A</i>	tetratricopeptide repeat domain 7A	1.22	0.00660
<i>UBE2L6</i>	ubiquitin-conjugating enzyme E2L 6	1.22	0.02858
<i>FAM134B</i>	family with sequence similarity 134, member B	1.22	0.00625
<i>LOC785981</i>	olfactory receptor 7A17	1.22	0.01594
<i>MTHFD1L</i>	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like	1.22	0.01228
<i>CAGE1</i>	cancer antigen 1	1.22	0.03954
<i>LOC513333</i>	olfactory receptor 151	1.22	0.02806
<i>SLC38A7</i>	solute carrier family 38, member 7	1.22	0.03120
<i>CNOT1</i>	CCR4-NOT transcription complex, subunit 1	1.22	0.02638
<i>BCAR3</i>	breast cancer anti-estrogen resistance 3	1.22	0.00482
<i>SLC30A1</i>	solute carrier family 30 (zinc transporter), member 1	1.22	0.00688
<i>CEBPA</i>	CCAAT/enhancer binding protein (C/EBP), alpha	1.22	0.01341
<i>LRCH1</i>	leucine-rich repeats and calponin homology (CH) domain containing 1	1.21	0.00884
<i>SKIL</i>	SKI-like proto-oncogene	1.21	0.01870
<i>BIN2</i>	bridging integrator 2	1.21	0.01017
<i>MIR487A</i>	microRNA mir-487a	1.21	0.04780
<i>RCN2</i>	reticulocalbin 2, EF-hand calcium binding domain	1.21	0.02028
<i>SDC4</i>	syndecan 4	1.21	0.01125
<i>LRAT</i>	lecithin retinol acyltransferase (phosphatidylcholine-retinol O-acyltransferase)	1.21	0.01511
<i>MIR144</i>	microRNA mir-144	1.21	0.02171
<i>PSMG4</i>	proteasome (prosome, macropain) assembly chaperone 4	1.21	0.02158
<i>LOC515150</i>	apolipoprotein R	1.21	0.03285
<i>CORO1C</i>	coronin, actin binding protein, 1C	1.21	0.00772
<i>PARM1</i>	prostate androgen-regulated mucin-like protein 1	1.21	0.00159
<i>C6H4orf32</i>	chromosome 6 open reading frame, human C4orf32	1.21	0.00220
<i>IHH</i>	indian hedgehog	1.21	0.02710
<i>MIR208A</i>	microRNA mir-208a	1.21	0.04147
<i>GPRC5C</i>	G protein-coupled receptor, class C, group 5, member C	1.21	0.00374
<i>AGFG1</i>	ArfGAP with FG repeats 1	1.21	0.01705
<i>TMEM50B</i>	transmembrane protein 50B	1.21	0.03759
<i>PLAGL1</i>	pleiomorphic adenoma gene-like 1	1.21	0.01149
<i>FLOT2</i>	flotillin 2	1.21	0.01589
<i>LOC783070</i>	60S ribosomal protein L5 pseudogene	-1.21	0.01177

<i>PRR29</i>	proline rich 29	-1.21	0.00032
<i>BVD1.15</i>	T cell receptor delta chain variable region BVd1.15	-1.21	0.01706
<i>BCL11B</i>	B-cell CLL/lymphoma 11B (zinc finger protein)	-1.21	0.03007
<i>SMO</i>	smoothened, frizzled class receptor	-1.21	0.00139
<i>ATP8A1</i>	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1	-1.21	0.00893
<i>FRMPD3</i>	FERM and PDZ domain containing 3	-1.21	0.01367
<i>NPAS4</i>	neuronal PAS domain protein 4	-1.21	0.00828
<i>TMEM38B</i>	transmembrane protein 38B	-1.21	0.02574
<i>GAS2</i>	growth arrest-specific 2	-1.21	0.02180
<i>TTC21B</i>	tetratricopeptide repeat domain 21B	-1.21	0.04557
<i>PPFIA3</i>	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 3	-1.21	0.00022
<i>SLC51B</i>	solute carrier family 51, beta subunit	-1.21	0.04918
<i>HRH3</i>	histamine receptor H3	-1.21	0.01832
<i>KRT26</i>	keratin 26	-1.21	0.04773
<i>STARD13</i>	StAR-related lipid transfer (START) domain containing 13	-1.21	0.00033
<i>FAAH</i>	fatty acid amide hydrolase	-1.21	0.01007
<i>IFNAH</i>	interferon alpha H	-1.21	0.02866
<i>LOC100300010</i>	olfactory receptor 8S1	-1.21	0.01270
<i>LONRF1</i>	LON peptidase N-terminal domain and ring finger 1	-1.21	0.01748
<i>SEL1L3</i>	sel-1 suppressor of lin-12-like 3 (C. elegans)	-1.21	0.04107
<i>C5H12orf71</i>	chromosome 5 open reading frame, human C12orf71	-1.21	0.02732
<i>ANTXR2</i>	anthrax toxin receptor 2	-1.21	0.01263
<i>LOC101906359</i>	Y-box-binding protein 3-like	-1.21	0.03913
<i>MMP12</i>	matrix metalloproteinase 12 (macrophage elastase)	-1.21	0.02363
<i>G6PC</i>	glucose-6-phosphatase, catalytic subunit	-1.21	0.01044
<i>ASPRV1</i>	aspartic peptidase, retroviral-like 1	-1.22	0.00223
<i>GRIN2C</i>	glutamate receptor, ionotropic, N-methyl D-aspartate 2C	-1.22	0.00711
<i>PPM1K</i>	protein phosphatase, Mg ²⁺ /Mn ²⁺ dependent, 1K	-1.22	0.01647
<i>PROX2</i>	prospero homeobox 2	-1.22	0.00111
<i>MIR184</i>	microRNA mir-184	-1.22	0.04469
<i>ENO2</i>	enolase 2 (gamma, neuronal)	-1.22	0.02159
<i>CLDN1</i>	claudin 1	-1.22	0.02000
<i>LOC100848786</i>	lipid phosphate phosphatase-related protein type 5	-1.22	0.01549
<i>SCN9A</i>	sodium channel, voltage-gated, type IX, alpha subunit	-1.22	0.04638
<i>HCRTR2</i>	hypocretin (orexin) receptor 2	-1.22	0.04439
<i>ZNF319</i>	zinc finger protein 319	-1.22	0.00919
<i>CCDC7</i>	coiled-coil domain containing 7	-1.22	0.01962
<i>DMP1</i>	dentin matrix acidic phosphoprotein 1	-1.22	0.00336
<i>INSIG2</i>	insulin induced gene 2	-1.22	0.03109
<i>GJA3</i>	gap junction protein, alpha 3, 46kDa	-1.22	0.00165

<i>SGCZ</i>	sarcoglycan, zeta	-1.22	0.01501
<i>KRT1</i>	keratin 1	-1.22	0.00436
<i>IP6K2</i>	inositol hexakisphosphate kinase 2	-1.22	0.02957
<i>ATL1</i>	atlastin GTPase 1	-1.22	0.01418
<i>LOC538872</i>	dual specificity phosphatase 18-like	-1.22	0.02587
<i>CRABP2</i>	cellular retinoic acid binding protein 2	-1.22	0.00698
<i>PBLD</i>	phenazine biosynthesis-like protein domain containing	-1.23	0.02703
<i>LOC787011</i>	uncharacterized protein CXorf66 homolog	-1.23	0.00691
<i>RIMBP3B</i>	RIMS binding protein 3B	-1.23	0.02487
<i>LOC100300695</i>	intelectin-2	-1.23	0.01674
<i>ZNF750</i>	zinc finger protein 750	-1.23	0.01019
<i>NT5DC1</i>	5-nucleotidase domain containing 1	-1.23	0.01786
<i>LOC504344</i>	olfactory receptor 4F15	-1.23	0.02552
<i>LOC784187</i>	olfactory receptor 51L1	-1.23	0.04964
<i>RAB3C</i>	RAB3C, member RAS oncogene family	-1.23	0.00064
<i>LOC101906200</i>	ninjurin-1 pseudogene	-1.23	0.01542
<i>LOC537188</i>	UDP-glucuronosyltransferase 3A1-like	-1.24	0.00249
<i>AGL</i>	amylase-1, 6-glucosidase, 4-alpha-glucanotransferase	-1.24	0.01408
<i>RBMS2</i>	RNA binding motif, single stranded interacting protein 2	-1.24	0.01436
<i>MBNL3</i>	muscleblind-like splicing regulator 3	-1.24	0.02344
<i>LOC784679</i>	peptidyl-prolyl cis-trans isomerase A	-1.24	0.03099
<i>FAM71B</i>	family with sequence similarity 71, member B	-1.24	0.00498
<i>LOC100125266</i>	alkaline phosphatase-like	-1.24	0.04400
<i>OR2G6</i>	olfactory receptor, family 2, subfamily G, member 6	-1.24	0.00475
<i>PK2</i>	pyruvate dehydrogenase kinase, isozyme 2	-1.24	0.01237
<i>FST</i>	follistatin	-1.24	0.00289
<i>MYBL2</i>	v-myb avian myeloblastosis viral oncogene homolog-like 2	-1.24	0.00132
<i>LOC785899</i>	olfactory receptor 1440	-1.24	0.02496
<i>AQP9</i>	aquaporin 9	-1.24	0.00390
<i>GABRQ</i>	gamma-aminobutyric acid (GABA) A receptor, theta	-1.24	0.00578
<i>TMEM184C</i>	transmembrane protein 184C	-1.25	0.04891
<i>OPN1SW</i>	opsin 1 (cone pigments), short-wave-sensitive	-1.25	0.01030
<i>SLC16A10</i>	solute carrier family 16 (aromatic amino acid transporter), member 10	-1.25	0.00681
<i>MIR2475</i>	microRNA mir-2475	-1.25	0.01011
<i>MIR1603</i>	microRNA mir-1603	-1.25	0.00738
<i>LOC511642</i>	olfactory receptor 18	-1.25	0.03583
<i>LOC788998</i>	olfactory receptor, family 9, subfamily K, member 2-like	-1.25	0.01252
<i>PLCG2</i>	phospholipase C, gamma 2 (phosphatidylinositol-specific)	-1.25	0.00039

<i>ABCB11</i>	ATP-binding cassette, sub-family B (MDR/TAP), member 11	-1.25	0.01637
<i>ELL2</i>	elongation factor, RNA polymerase II, 2	-1.25	0.02513
<i>OTC</i>	ornithine carbamoyltransferase	-1.25	0.00401
<i>TMEM144</i>	transmembrane protein 144	-1.25	0.04843
<i>FIGF</i>	c-fos induced growth factor (vascular endothelial growth factor D)	-1.25	0.00748
<i>TAT</i>	tyrosine aminotransferase	-1.25	0.03960
<i>LOC100848572</i>	keratin-associated protein 4-7-like	-1.25	0.03490
<i>MIR23A</i>	microRNA mir-23a	-1.26	0.01646
<i>SERPINE3</i>	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 3	-1.26	0.00217
<i>MIR105B</i>	microRNA mir-105b	-1.26	0.02745
<i>HSD11B1</i>	hydroxysteroid (11-beta) dehydrogenase 1	-1.26	0.00165
<i>LOC101903205</i>	alpha-2-macroglobulin receptor-associated protein pseudogene	-1.26	0.01288
<i>SALL1</i>	spalt-like transcription factor 1	-1.26	0.03715
<i>OR51E1</i>	olfactory receptor, family 51, subfamily E, member 1	-1.26	0.00028
<i>LOC785144</i>	olfactory receptor, family 51, subfamily E, member 2-like	-1.26	0.04072
<i>JAKMIP2</i>	janus kinase and microtubule interacting protein 2	-1.26	0.00166
<i>IQCF1</i>	IQ motif containing F1	-1.26	0.01104
<i>LOC100297248</i>	Ig kappa chain V-III region PC 7210	-1.26	0.02055
<i>LOC504570</i>	olfactory receptor 1L4	-1.27	0.03432
<i>MYC</i>	v-myc avian myelocytomatosis viral oncogene homolog	-1.27	0.04674
<i>C18H16orf87</i>	chromosome 18 open reading frame, human C16orf87	-1.27	0.00823
<i>LOC104975671</i>	ubiquitin D-like	-1.27	0.00977
<i>GLP1R</i>	glucagon-like peptide 1 receptor	-1.27	0.01386
<i>MAT1A</i>	methionine adenosyltransferase I, alpha	-1.27	0.00005
<i>ZNF883</i>	zinc finger protein 883	-1.27	0.01005
<i>RASSF6</i>	Ras association (RalGDS/AF-6) domain family member 6	-1.27	0.03790
<i>KCNJ2</i>	potassium inwardly-rectifying channel, subfamily J, member 2	-1.27	0.04198
<i>LOC101905711</i>	heme-binding protein 1	-1.28	0.03768
<i>LOC787624</i>	ADAMTS-like protein 3	-1.28	0.01883
<i>LOC783144</i>	60S ribosomal protein L13 pseudogene	-1.28	0.00231
<i>LOC787129</i>	glycine cleavage system H protein, mitochondrial	-1.28	0.00175
<i>ARHGEF9</i>	Cdc42 guanine nucleotide exchange factor (GEF) 9	-1.28	0.03088
<i>GRIK3</i>	glutamate receptor, ionotropic, kainate 3	-1.28	0.00036
<i>LOC504233</i>	olfactory receptor 2A1/2A42	-1.28	0.04420
<i>LOC789943</i>	olfactory receptor 13C2	-1.28	0.02491
<i>LOC100299372</i>	olfactory receptor 2S2	-1.28	0.02331
<i>STXBP6</i>	syntaxin binding protein 6 (amisyn)	-1.28	0.02821

<i>LOC783917</i>	olfactory receptor 187	-1.28	0.02245
<i>LOC785712</i>	olfactory receptor 12D2	-1.29	0.02805
<i>GSAP</i>	gamma-secretase activating protein	-1.29	0.04778
<i>LOC751804</i>	WC1 isolate DV100	-1.29	0.01612
<i>SOX5</i>	SRY (sex determining region Y)-box 5	-1.29	0.00356
<i>BPIFA2B</i>	BPI fold containing family A, member 2B	-1.29	0.00986
<i>PIGP</i>	phosphatidylinositol glycan anchor biosynthesis, class P	-1.29	0.04820
<i>SNCAIP</i>	synuclein, alpha interacting protein	-1.29	0.01033
<i>MIR27B</i>	microRNA mir-27b	-1.29	0.00498
<i>LOC522775</i>	olfactory receptor 8J2	-1.29	0.00738
<i>LOC618034</i>	olfactory receptor 12D3	-1.29	0.02320
<i>UHRF1</i>	ubiquitin-like with PHD and ring finger domains 1	-1.29	0.01016
<i>FGF12</i>	fibroblast growth factor 12	-1.29	0.00191
<i>SLC25A30</i>	solute carrier family 25, member 30	-1.29	0.01297
<i>LOC100337180</i>	eukaryotic translation elongation factor 1 alpha 1 pseudogene	-1.30	0.03742
<i>IVD</i>	isovaleryl-CoA dehydrogenase	-1.30	0.00096
<i>LOC788079</i>	olfactory receptor 2L8	-1.30	0.04603
<i>FOXP1</i>	forkhead box P1	-1.30	0.02469
<i>NECAB2</i>	N-terminal EF-hand calcium binding protein 2	-1.30	0.02836
<i>LOC100337053</i>	multidrug resistance-associated protein 4-like	-1.30	0.04205
<i>LOC617135</i>	interferon omega-1	-1.31	0.00591
<i>TDH</i>	L-threonine dehydrogenase	-1.31	0.00025
<i>MIR940</i>	microRNA mir-940	-1.31	0.00153
<i>PNP</i>	purine nucleoside phosphorylase	-1.31	0.00171
<i>EDNRA</i>	endothelin receptor type A	-1.31	0.01341
<i>ADH4</i>	alcohol dehydrogenase 4 (class II), pi polypeptide	-1.31	0.00334
<i>OR5D18</i>	olfactory receptor, family 5, subfamily D, member 18	-1.31	0.02317
<i>ZNF679</i>	zinc finger protein 679	-1.32	0.00631
<i>FBP1</i>	fructose-1,6-bisphosphatase 1	-1.32	0.00134
<i>SMARCA1</i>	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1	-1.32	0.00123
<i>LOC515551</i>	protein DDI1 homolog 2	-1.32	0.00613
<i>BOSTAUUV1R414</i>	vomeroneasal 1 receptor bosTauV1R414	-1.32	0.02124
<i>LOC515540</i>	olfactory receptor 1E2	-1.32	0.04412
<i>CITED1</i>	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 1	-1.32	0.00302
<i>LOC508595</i>	olfactory receptor 51G2	-1.33	0.03560
<i>PCTP</i>	phosphatidylcholine transfer protein	-1.33	0.00697
<i>LOC531650</i>	H2B histone family, member W, testis-specific-like pseudogene	-1.33	0.01198
<i>LOC782554</i>	putative olfactory receptor 2W6	-1.33	0.04590
<i>LOC100298264</i>	uncharacterized LOC100298264	-1.33	0.01968
<i>BTG2</i>	BTG family, member 2	-1.33	0.02334
<i>LOC513329</i>	major allergen Equ c 1	-1.34	0.01500

<i>GNAT3</i>	guanine nucleotide binding protein, alpha transducing 3	-1.34	0.00017
<i>TDRD10</i>	tudor domain containing 10	-1.34	0.04056
<i>GYS2</i>	glycogen synthase 2 (liver)	-1.34	0.01646
<i>LOC524160</i>	olfactory receptor 2T3	-1.34	0.01028
<i>LOC523582</i>	olfactory receptor 12	-1.34	0.03900
<i>LOC100298605</i>	olfactory receptor 5T2	-1.34	0.03626
<i>GLYATL3</i>	glycine-N-acyltransferase-like 3	-1.34	0.00768
<i>ARG2</i>	arginase 2	-1.35	0.00066
<i>MIR103-2</i>	microRNA mir-103-2	-1.35	0.04396
<i>GSTA2</i>	glutathione S-transferase alpha 2	-1.36	0.03955
<i>LOC100336901</i>	olfactory receptor 8J3	-1.36	0.04626
<i>SLC25A15</i>	solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 15	-1.36	0.00889
<i>MIR339B</i>	microRNA mir-339b	-1.37	0.02691
<i>LOC510712</i>	olfactory receptor 7A17	-1.37	0.00005
<i>BICC1</i>	BicC family RNA binding protein 1	-1.38	0.00169
<i>LOC523530</i>	nuclear RNA export factor 3	-1.38	0.01477
<i>ADRA1A</i>	adrenoceptor alpha 1A	-1.38	0.00143
<i>MOGAT1</i>	monoacylglycerol O-acyltransferase 1	-1.38	0.00184
<i>LOC788220</i>	olfactory receptor 6C76	-1.38	0.00570
<i>ADRB2</i>	adrenoceptor beta 2, surface	-1.39	0.00079
<i>PCDH19</i>	protocadherin 19	-1.39	0.00243
<i>SLC4A4</i>	solute carrier family 4 (sodium bicarbonate cotransporter), member 4	-1.39	0.03198
<i>DBP</i>	D site of albumin promoter (albumin D-box) binding protein	-1.40	0.01658
<i>CCRN4L</i>	CCR4 carbon catabolite repression 4-like (S. cerevisiae)	-1.40	0.01715
<i>ATP10B</i>	ATPase, class V, type 10B	-1.40	0.01451
<i>ACMSD</i>	aminocarboxymuconate semialdehyde decarboxylase	-1.40	0.04530
<i>LOC786363</i>	tumor susceptibility gene 101 protein pseudogene	-1.41	0.00950
<i>LOC100138638</i>	retinol dehydrogenase 16-like	-1.41	0.01970
<i>IRS2</i>	insulin receptor substrate 2	-1.41	0.00418
<i>LOC104976490</i>	complement factor H-like	-1.41	0.00587
<i>LRP2</i>	low density lipoprotein receptor-related protein 2	-1.42	0.00660
<i>VNN1</i>	vanin 1	-1.42	0.04659
<i>LOC100337097</i>	cationic amino acid transporter 3-like	-1.42	0.01886
<i>ARG1</i>	arginase 1	-1.42	0.01348
<i>PPARGC1A</i>	peroxisome proliferator-activated receptor gamma, coactivator 1 alpha	-1.42	0.01809
<i>LOC618124</i>	olfactory receptor, family 1, subfamily E, member 2-like	-1.44	0.04559
<i>LOC527057</i>	multidrug resistance-associated protein 4-like	-1.45	0.03897
<i>LOC531237</i>	olfactory receptor 4C13	-1.45	0.00140

<i>SLC7A2</i>	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	-1.46	0.00679
<i>SOCS2</i>	suppressor of cytokine signaling 2	-1.47	0.02636
<i>DIRAS3</i>	DIRAS family, GTP-binding RAS-like 3	-1.47	0.00187
<i>TDO2</i>	tryptophan 2,3-dioxygenase	-1.47	0.00534
<i>TLE1</i>	transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila)	-1.48	0.00092
<i>XPNPEP2</i>	X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound	-1.49	0.03487
<i>PPAP2B</i>	phosphatidic acid phosphatase type 2B	-1.49	0.00067
<i>LURAP1L</i>	leucine rich adaptor protein 1-like	-1.49	0.01546
<i>TEX12</i>	testis expressed 12	-1.51	0.02480
<i>RALGPS2</i>	Ral GEF with PH domain and SH3 binding motif 2	-1.53	0.02406
<i>AMDHD1</i>	amidohydrolase domain containing 1	-1.53	0.00206
<i>ZNF37A</i>	zinc finger protein 37A	-1.54	0.00651
<i>ZPR1</i>	ZPR1 zinc finger	-1.55	0.00124
<i>LGR5</i>	leucine-rich repeat containing G protein-coupled receptor 5	-1.56	0.01635
<i>ATP10B</i>	ATPase, class V, type 10B	-1.57	0.00278
<i>VWA3B</i>	von Willebrand factor A domain containing 3B	-1.58	0.01272
<i>GLS2</i>	glutaminase 2 (liver, mitochondrial)	-1.59	0.00007
<i>ERRFI1</i>	ERBB receptor feedback inhibitor 1	-1.60	0.00724
<i>ASCL1</i>	achaete-scute family bHLH transcription factor 1	-1.64	0.02755
<i>GSTM1</i>	glutathione S-transferase M1	-1.68	0.00878
<i>GSTM2</i>	glutathione S-transferase M2	-1.75	0.00998
<i>LPIN1</i>	lipin 1	-1.77	0.01014
<i>MFSD2A</i>	major facilitator superfamily domain containing 2A	-1.89	0.00185
<i>HAL</i>	histidine ammonia-lyase	-1.91	0.00167
<i>PDK4</i>	pyruvate dehydrogenase kinase, isozyme 4	-1.93	0.00002

*Filter criteria: FC > 1.2 and < -1.2 and P < 0.05 between FGF21 high vs. FGF21 low group. FCs were calculated from the signal log ratios, which were calculated from n = 8 microarrays per group.