

GCOS_FC	Probe set ID	Symbol	Gene title	Main biological function	Bit Score	E-value	p-value
<i>p53-related process</i>							
2.4	Ssc.30871.1.A1_at	TP53INP1	Tumor protein p53 inducible nuclear protein 1	Cell cycle arrest & Apoptosis	93.7	2E-18	0.0100
1.7	Ssc.29750.1.A1_at			E3 ubiquitin ligase	268.1	5.8E-71	0.0143
1.9	Ssc.9522.1.A1_at	RNF144B	RNF144B ring finger 144B	_switching from p53-induced growth arrest to apoptosis.	137.3	3E-31	0.0252
1.6	Ssc.4271.1.S1_at	HTATIP2	HIV-1 Tat interactive protein 2, 30kDa	Nuclear translocation inhibitor	987.7	0	0.0143
1.6	Ssc.6154.1.S1_a_at	SLC6A6	Solute carrier family 6 (neurotransmitter transporter, taurine), member 6	_Apoptosis, tumor suppressor	44.1	0.042	0.0067
1.6	Ssc.6154.1.S1_at			Taurine uptake (down-regulated by p53)	44.1	0.042	0.0088
1.6	Ssc.14009.1.A1_at	MED17	Mediator complex subunit 17	Transcription machinery	1895.6	0	0.0286
1.5	Ssc.5695.1.A1_at	CKS1B	CDC28 protein kinase regulatory subunit 1B	_p53 signaling transducer	42.1	0.139	0.0268
-2.1	Ssc.16937.1.A1_at	TP53INP2	Tumor protein p53 inducible nuclear protein 2	Cell cycle promotion	274.1	1.9E-72	0.0209
-2.0	Ssc.11281.1.A1_at	PENK	Proenkephalin	Cell cycle promotion	506.0	4E-142	0.0145
				Apoptosis inducer			
<i>Cell proliferation & Differentiation signaling</i>							
1.9	Ssc.9883.1.A1_at	ADRBK2	Adrenergic, beta, receptor kinase 2	Desensitizing β -adrenergic receptors, thrombin receptors, and LPA receptors	46.1	0.013	0.0028
1.7	Ssc.6849.1.A1_at	NARG2	NMDA receptor regulated 2	Cell proliferation	63.9	6.1E-09	0.2674
1.7	Ssc.20175.1.S1_at	IGF1R	Insulin-like growth factor 1 receptor	_Differentiation (+)			
1.6	Ssc.11539.1.A1_at	MKRN1	Makorin, ring finger protein, 1	IGF signaling	450.5	3E-125	0.0188
1.5	Ssc.26274.1.S1_at	ETS1	V-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	_Cell growth	151.2	1.1E-35	0.0099
-4.5	Ssc.2841.1.S1_at	CREM	cAMP responsive element modulator	Transcription inhibitor	40.1	0.473	0.1508
-3.7	Ssc.2841.2.S1_a_at			E3 ubiquitin ligase	521.9	9E-147	0.0015
-4.2	Ssc.18764.1.A1_at	ITGB1BP3	Integrin beta 1 binding protein 3	transcription	521.9	6E-147	0.0026
-2.0	Ssc.92.1.S1_at	TGFB2	transforming growth factor, beta 2	_Transcription factor	654.7	0	0.0204
-2.0	Ssc.16434.1.A1_at	NOV	Nephroblastoma overexpressed gene	Inhibit myogenic differentiation	1790.6	0	0.1645
-1.9	Ssc.20906.1.A1_at	TAOK1	TAO kinase 1	Cell proliferation (+)	210.6	4.8E-53	0.0109
-1.9	Ssc.17238.1.A1_at	MUSTN1	Musculoskeletal, embryonic nuclear protein 1	Differentiation inhibitor	63.9	9.1E-09	0.0016
-1.8	Ssc.16910.2.S1_at	ROD1	ROD1 regulator of differentiation 1 (S. pombe)	Cell cycle check point	280.0	2E-74	0.0065
-1.8	Ssc.10952.1.S1_at	DLG1	Discs, large homolog 1 (Drosophila)	Differentiation marker	2698.5	0	0.2529
-1.5	Ssc.9766.2.S1_at	AK2	Adenylate kinase 2	Differentiation inhibitor	44.1	0.016	0.1275
				scaffolding protein			
				_target of CDK1 and CDK2 during mitosis			
				Apoptosis inducer	1094.8	0	0.1038
<i>Muscular system</i>							
1.7	Ssc.1290.1.S1_at	MYLK	Myosin, light chain kinase	Muscle contraction	44.1	0.026	0.0147
1.7	Ssc.13859.1.A1_at	UNC45B	Unc-45 homolog B (C. elegans)	Muscular system	176.9	2.1E-43	0.0597
-2.8	Ssc.1876.1.S1_at	MYH10	Myosin, heavy chain 10, non-muscle	_Myosin motor domain folding	807.3	0	0.0080
-2.1	Ssc.10392.1.A1_at	MYH11	Myosin, heavy chain 11, smooth muscle	Muscle fiber (z disc)	708.2	0	0.0424
				Muscle structure			

-1.7	Ssc.8574.1.A1_at	TMOD1	tropomodulin 1	Muscular system _Regulation of thin filament (±)	561.5	2E-158	0.1031
-7.2	Ssc.761.1.S1_at	NR4A3	Nuclear receptor subfamily 4, group A, member 3	Actin repolymerization	1854.0	0	0.0032
-1.9	Ssc.1664.1.A1_at	NRN1	Neuritin 1	High level in muscle regeneration	1370.3	0	0.0342

Metabolism

Glucose metabolism

2.0	Ssc.8241.1.A1_at	PPM2C	Protein phosphatase 2C, magnesium-dependent, catalytic subunit	Glycogen metabolism _Acetyl-CoA synthesis transcription factor	178.9	1.2E-43	0.0295
1.7	Ssc.26463.1.S1_at	KLF15	Kruppel-like factor 15	_acetyl-CoA(+)/GLUT4(+)/ gluconeogenesis(-)	393.0	3E-108	0.1136
1.7	Ssc.8506.1.A1_at	PHKB	Phosphorylase kinase, beta	Glycogen metabolism _Glycogenolysis	40.1	0.386	0.0153
1.5	Ssc.4307.1.A1_at	PGM3	Phosphoglucomutase 3	Glycogen metabolism _Glycolysis // Glycosylation	1195.9	0	0.0122

Lipid metabolism

1.7	Ssc.2874.1.S1_at	LIPH	Lipase, member H	LPA generator (sn-2-acylated LPA)	44.1	0.049	0.0135
1.6	Ssc.21972.1.A1_at	DGKG	Diacylglycerol kinase, gamma 90kDa	Phosphatidic acid generator	44.1	0.044	0.0066

Protein metabolism

2.0	Ssc.29341.1.A1_at	FBXL4	F-box and leucine-rich repeat protein 4	Ubiquitin-ligase activity / Post- translational modification	73.8	1.8E-12	0.0336
1.6	Ssc.13572.1.A1_at	CPN1	Carboxypeptidase N, polypeptide 1	Protein catabolism	58.0	0.000005	0.0109
1.6	Ssc.13262.1.S1_at	EIF4EBP1	Eukaryotic translation initiation factor 4E binding protein 1	translation	490.1	2E-137	0.1351
1.6	Ssc.3669.1.A1_at	TRSPAP1	tRNA selenocysteine associated protein 1	_translation initiation repressor	470.3	2E-131	0.1022
1.6	Ssc.3669.1.A1_a_at			Translation _Selenoprotein biosynthesis	470.3	2E-131	0.0187
1.6	Ssc.4805.1.S1_at	RPS27	Ribosomal protein S27 (metalloprotein 1)	Translation	490.1	3E-137	0.0119
-1.8	Ssc.4538.1.S1_at	PRSS23	Protease, serine, 23	_Ribosomal protein Protein catabolism	1104.7	0	0.0014

Others

1.7	Ssc.22641.3.S1_at	RDH16	Retinol dehydrogenase 16 (all-trans)	Retinol metabolism	589.3	6E-167	0.0216
1.7	Ssc.4571.1.A1_at	GNPTG	N-acetylglucosamine-1-phosphate transferase, gamma subunit	mannose 6-phosphate synthesis _lysosomal signaling	617.0	4E-175	0.1262
-2.4	Ssc.16041.1.S1_at	DHDH	Dihydrodiol dehydrogenase (dimeric)	Detoxification process detoxification	773.6	0	0.0273
-1.7	Ssc.11186.1.S1_at	NUDT7	Nudix (nucleoside diphosphate linked moiety X)-type motif 7	_CoA diphosphatase _CoA turnover (maybe)	186.8	5.1E-46	0.1352

Transcription/RNA metabolism

Transcription factor & cofactor

2.0	Ssc.24043.1.S1_at	LCORL	Ligand dependent nuclear receptor corepressor-like	Transcription _Transcription factor (+)	60.0	2.E-06	0.1933
1.7	Ssc.2836.1.S1_at	POLR1D	Polymerase (RNA) I polypeptide D, 16kDa	Transcription _RNA polymerase subunit	638.8	0	0.0038
1.5	Ssc.6157.1.A1_at	ZNF521	Zinc finger protein 521	Transcription _Transcription factor (±)	313.7	9.1E-85	0.0464

RNA processing

2.2	Ssc.4676.1.A1_at	RAVER2	Ribonucleoprotein, PTB-binding 2	mRNA processing	123.4	4.2E-27	0.0379
1.9	Ssc.7191.1.A1_at	LSM14A	LSM14A, SCD6 homolog A (S. cerevisiae)	_mRNA splicing inhibitor modulator mRNA degradation	60.0	4.2E-08	0.0025
1.7	Ssc.14456.1.S1_at	PCBP2	Poly(rC) binding protein 2	Poly(rC) binding protein	963.9	0	0.0092
1.6	Ssc.14431.1.S1_at	FTSJ2	FtsJ homolog 2 (E. coli)	RNA modification	440.6	3E-122	0.0070
<i>Other</i>							
-1.6	Ssc.25399.1.S1_at	FBXL11	F-box and leucine-rich repeat protein 11	Transcription _Histone demethylation	44.1	0.044	0.0192
Miscellaneous							
2.2	Ssc.27198.1.A1_at	ASB3	Ankyrin repeat and SOCS box-containing 3	Scaffold protein (SOCS box domain)	121.4	3.3E-26	0.0107
2.0	Ssc.13952.1.A1_at	MBP	Myelin basic protein	Neurogenesis	56.0	0.000017	0.0058
1.6	Ssc.27826.1.S1_at	EPB41L5	Erythrocyte membrane protein band 4.1 like 5	Modulator _Cell polarity Endocytosis	44.1	0.015	0.0008
1.6	Ssc.23484.1.A1_a_at	SCARB2	Scavenger receptor class B, member 2	_Reorganizing the endosomal/lysosomal comprtments Pigmentation (-)/ Metabolism (homeostasis)/ Immune status (+)/ Neurodegeneration (+)	1542.8	0	0.0330
1.5	Ssc.7686.1.S1_at	ATRN	Attractin	hydrolysis of some nucleoside diphosphate derivatives	264.1	3.6E-69	0.0209
1.5	Ssc.20597.1.S1_at	NUDT18	Nudix (nucleoside diphosphate linked moiety X)-type motif 18	Wide range of cellular processes	956.0	0	0.0433
-2.4	Ssc.12492.1.A1_at	SORT1	Sortilin 1	Bone formation inhibitor/ Vascular calcification inhibitor	676.5	0	0.0017
-2.1	Ssc.373.1.S1_at	MGP	Matrix Gla protein	Lactate transport	210.6	1.9E-53	0.0409
-2.0	Ssc.3909.1.A1_at	SLC16A9	Solute carrier family 16, member 9 (monocarboxylic acid transporter 9)	Secretary protein	220.5	2E-56	0.0220
-1.9	Ssc.14368.1.A1_at	MMRN1	Multimerin 1	_Coagulation Purine nucleotide biosynthesis _De novo biosynthesis of AMP	763.7	0	0.0728
-1.8	Ssc.24153.1.S1_at	ADSSL1	Adenylosuccinate synthase like 1	Protein phosphorylation	484.2	1E-135	0.0194
-1.7	Ssc.5624.1.A1_at	NEK4	NIMA (never in mitosis gene a)-related kinase 4	Ca2+ influx inhibitor	333.5	1.7E-90	0.1204
-1.6	Ssc.4109.1.S1_at	STIM2	stromal interaction molecule 2	Structure _Membrane trafficking	605.1	7E-172	0.2342
-1.6	Ssc.12989.1.A1_at	YIPF6	Yip1 domain family, member 6	Signaling molecules kinase	270.1	1.6E-71	0.0493
-1.6	Ssc.2429.1.S1_at	ROCK2	Rho-associated, coiled-coil containing protein kinase 2		174.9	3.8E-41	0.0021
Unknown							
2.2	Ssc.4368.1.S1_at	---	CDNA FLJ39585 fis, clone SKMUS2006633	?	1709.3	0	0.0882
1.7	Ssc.13394.1.A1_at	PCNX	pecanex homolog (Drosophila)	?	42.1	0.125	0.0587
1.5	Ssc.12870.1.A1_at	CAMSAP1L1	Calmodulin regulated spectrin-associated protein 1-like 1	?	52.0	1.E-04	0.0002
1.5	Ssc.4818.1.A1_at	C7orf60	C7orf60 chromosome 7 open reading frame 60	?	682.4	0	0.1123
1.5	Ssc.15352.1.S1_at	FAM117A	family with sequence similarity 117, member A	?	535.7	3E-151	0.0992
-2.7	Ssc.10752.1.A1_at	TMEM65	Transmembrane protein 65	?	174.9	3.1E-41	0.0083
-2.1	Ssc.21490.1.S1_a_at	C12orf45	Chromosome 12 open reading frame 45	?	416.8	2E-115	0.0064
-1.7	Ssc.4081.1.A1_at	FAM13A1	family with sequence similarity 13, member A1	?	212.6	8.7E-54	0.0541
-1.6	Ssc.7768.1.A1_at	KIAA0701	KIAA0701 protein	?	46.1	0.021	0.0074
-1.5	Ssc.13584.1.A1_at	NHLRC2	NHL repeat containing 2	?	83.8	3.8E-14	0.1198