

**Supplementary Table 2: List of probe sets differentially expressed between the high stress and low stress groups with annotation**

<b>Probe_Set_ID</b>	<b>Annotation</b>	<b>Gene_description</b>	<b>FC (H/L)</b>	<b>p-value</b>
Ssc.914.1.S1_at	<b>LOC100039095</b>	hypothetical protein LOC100039095	2.6	0.001
Ssc.3509.1.S1_at	<b>HK2</b>	hexokinase 2	1.9	0.046
Ssc.13604.1.A1_at	<b>HMGCS1</b>	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	1.8	0.007
Ssc.9200.1.A1_at	<b>ZCCHC18</b>	zinc finger, CCHC domain containing 18	1.7	0.026
Ssc.4875.1.S1_at	<b>GALP</b>	galanin-like peptide	1.7	0.043
Ssc.12454.1.A1_at	<b>HSD17B7</b>	hydroxysteroid (17-beta) dehydrogenase 7	1.6	0.011
Ssc.18654.2.A1_at	<b>ABCB1</b>	ATP-binding cassette, sub-family B (MDR/TAP), member 1	1.6	0.007
Ssc.13164.1.A1_at	<b>SLC6A17</b>	solute carrier family 6, member 17	1.6	0.023
Ssc.18298.1.A1_a_at	<b>RGS2</b>	regulator of G-protein signaling 2, 24kDa	1.6	0.007
Ssc.15598.1.S1_at	<b>INSIG1</b>	insulin induced gene 1	1.6	0.019
Ssc.24921.3.S1_a_at	<b>ALAS1</b>	aminolevulinate, delta-, synthase 1	1.6	0.054
Ssc.713.1.S1_at	<b>GAL</b>	galanin prepropeptide	1.6	0.038
Ssc.4715.1.S1_at	<b>TM7SF2</b>	transmembrane 7 superfamily member 2	1.5	0.035
Ssc.4922.1.A1_at	<b>ALPL</b>	alkaline phosphatase, liver/bone/kidney	1.5	0.036
Ssc.6196.1.S1_at	<b>NPM3</b>	nucleophosmin/nucleoplasmin, 3	1.5	0.000
Ssc.14477.1.S1_at	<b>CILP</b>	cartilage intermediate layer protein, nucleotide pyrophosphohydrolase	1.5	0.012
Ssc.6714.1.A1_at	<b>IDI1</b>	isopenentenyl-diphosphate delta isomerase 1	1.5	0.028
Ssc.19509.2.S1_at	<b>SOAT1</b>	sterol O-acyltransferase 1	1.5	0.005
Ssc.9013.1.S1_at	<b>CNN1</b>	calponin 1, basic, smooth muscle	1.5	0.001
Ssc.9340.1.A1_at	unknown		1.4	0.039
Ssc.16088.1.S1_at	<b>HMGCR</b>	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	1.4	0.035
Ssc.11913.1.S1_at	<b>TAGLN</b>	transgelin	1.4	0.002
Ssc.6352.1.S1_at	<b>LOC441481</b>	misc_RNA LOC441481	1.4	0.004
Ssc.13476.1.A1_at	<b>PEG10</b>	paternally expressed 10	1.4	0.024
Ssc.4934.1.S1_a_at	unknown		1.4	0.024
Ssc.20571.1.S1_a_at	<b>TPM2</b>	tropomyosin 2 (beta)	1.4	0.003
Ssc.16209.1.S1_at	<b>TNC</b>	tenascin C	1.4	0.047
Ssc.8225.1.A1_at	unknown		1.4	0.052
Ssc.20571.2.S1_a_at	<b>TPM2</b>	tropomyosin 2 (beta)	1.4	0.002
Ssc.7099.1.S1_at	<b>RFK</b>	riboflavin kinase	1.4	0.005
Ssc.5772.1.A1_at	<b>IL27RA</b>	interleukin 27 receptor, alpha	1.4	0.005
Ssc.6514.1.S1_at	<b>GALE</b>	UDP-galactose-4-epimerase	1.4	0.004
Ssc.2873.1.S1_at	<b>PDZK1IP1</b>	PDZK1 interacting protein 1	1.4	0.005

Supplementary Table 2 continued

<b>Probe_Set_ID</b>	<b>Annotation</b>	<b>Gene_description</b>	<b>FC (H/L)</b>	<b>p-value</b>
Ssc.8710.1.A1_at	<b>SLC4A7</b>	solute carrier family 4, sodium bicarbonate cotransporter, member 7	1.4	0.012
Ssc.4426.2.S1_at	<b>ACAT2</b>	acetyl-Coenzyme A acetyltransferase 2	1.4	0.012
Ssc.12475.1.A1_at	<b>LOC100133481</b>	similar to phosphoserine phosphatase	1.4	0.012
Ssc.5127.1.S1_at	<b>FBP1</b>	fructose-1,6-bisphosphatase 1	1.4	0.003
SscAffx.31.1.S1_at	<b>LOC100131385</b>	similar to hCG1788572	1.4	0.016
Ssc.24027.1.A1_at	<b>PPTC7</b>	Protein phosphatase PTC7 homolog	1.4	0.002
Ssc.5045.1.S1_at	<b>EBP</b>	emopamil binding protein (sterol isomerase)	1.4	0.053
Ssc.27507.1.S1_at	<b>ACOT7</b>	acyl-CoA thioesterase 7	1.4	0.008
Ssc.5382.1.A1_a_at	unknown		1.4	0.038
Ssc.29031.1.A1_at	<b>HIST1H2BE</b>	histone cluster 1, H2be	1.4	0.029
Ssc.27087.1.S1_at	<b>GOLT1B</b>	golgi transport 1 homolog B ( <i>S. cerevisiae</i> )	1.4	0.001
Ssc.8385.1.A1_at	<b>SQLE</b>	squalene epoxidase	1.4	0.021
Ssc.12202.2.S1_at	<b>FDPS</b>	farnesyl diphosphate synthase	1.4	0.023
Ssc.3994.1.S1_at	<b>PDCD2L</b>	Programmed cell death protein 2-like	1.4	0.008
Ssc.12523.1.A1_at	<b>CLIC4</b>	chloride intracellular channel 4	1.4	0.041
Ssc.4426.1.S1_at	<b>ACAT2</b>	acetyl-Coenzyme A acetyltransferase 2	1.4	0.014
Ssc.2576.1.A1_at	<b>PIR</b>	pirin (iron-binding nuclear protein)	1.4	0.029
Ssc.4565.1.A1_at	unknown		1.3	0.018
Ssc.28128.1.A1_at	unknown		1.3	0.008
Ssc.7519.1.A1_at	<b>C17ORF91</b>	chromosome 17 open reading frame 91 ( <i>Homo sapiens</i> )	1.3	0.000
Ssc.13189.1.A1_at	<b>HUBC-16</b>	ubiquitin-conjugating enzyme E2W (putative)	1.3	0.001
Ssc.772.1.S1_at	<b>CARHSP1</b>	calcium regulated heat stable protein 1, 24kDa	1.3	0.041
Ssc.15388.2.S1_at	<b>TH</b>	tyrosine hydroxylase	1.3	0.028
Ssc.331.2.S1_at	<b>LDLR</b>	low density lipoprotein receptor	1.3	0.033
Ssc.1527.2.A1_at	<b>SLC20A1</b>	solute carrier family 20, member 1	1.3	0.009
Ssc.3345.2.S1_at	<b>MVK</b>	mevalonate kinase	1.3	0.033
Ssc.24184.1.S1_at	<b>GPD1L</b>	glycerol-3-phosphate dehydrogenase 1-like	1.3	0.036
Ssc.17902.1.A1_at	<b>TDRD7</b>	tudor domain containing 7	1.3	0.043
Ssc.30585.1.A1_at	<b>FAM167B</b>	family with sequence similarity 167, member B	1.3	0.033
Ssc.13744.1.A1_at	unknown		1.3	0.029
Ssc.31064.1.A1_at	<b>TUSC3</b>	tumor suppressor candidate 3	1.3	0.011
Ssc.26594.1.S1_at	<b>C6ORF108</b>	chromosome 6 open reading frame 108 ( <i>Homo sapiens</i> )	1.3	0.021
Ssc.25948.1.S1_at	<b>SLC1A4</b>	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	1.3	0.013
Ssc.19883.1.S1_at	<b>COL15A1</b>	collagen, type XV, alpha 1	1.3	0.011

Supplementary Table 2 continued

Probe_Set_ID	Annotation	Gene_description	FC (H/L)	p-value
Ssc.19268.2.A1_at	<b>C14ORF143</b>	chromosome 14 open reading frame 143 ( <i>Homo sapiens</i> )	1.3	0.019
Ssc.18654.1.S1_at	<b>ABCB1</b>	ATP-binding cassette, sub-family B (MDR/TAP), member 1	1.3	0.021
Ssc.13131.1.A1_at	unknown		1.3	0.000
Ssc.22104.1.A1_at	<b>SLC23A2</b>	solute carrier family 23 (nucleobase transporters), member 2	1.3	0.023
Ssc.114.1.S1_at	<b>HSPA6</b>	heat shock 70kDa protein 6 (HSP70B')	1.3	0.022
Ssc.3476.1.A1_at	<b>PIR</b>	pirin (iron-binding nuclear protein)	1.3	0.040
Ssc.16097.1.S1_at	<b>SLC23A2</b>	solute carrier family 23 (nucleobase transporters), member 2	1.3	0.024
Ssc.6418.1.S1_at	<b>FDFT1</b>	farnesyl-diphosphate farnesyltransferase 1	1.3	0.038
Ssc.2516.2.S1_a_at	<b>SLC5A6</b>	solute carrier family 5 (sodium-dependent vitamin transporter), member 6	1.3	0.032
Ssc.13271.1.S1_at	<b>TRAM1</b>	translocation associated membrane protein 1	1.3	0.001
Ssc.11995.1.A1_at	<b>MTHFD2</b>	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase	1.3	0.007
Ssc.17886.1.A1_at	<b>SLC35E3</b>	solute carrier family 35, member E3	1.3	0.020
Ssc.18440.1.S1_at	<b>MTP18</b>	mitochondrial protein 18 kDa	1.3	0.003
Ssc.12207.1.A1_at	<b>DYNLL2</b>	dynein, light chain, LC8-type 2	1.3	0.031
Ssc.22221.1.S1_a_at	<b>GK</b>	glycerol kinase (GK)	1.3	0.021
Ssc.4698.1.A1_at	unknown		1.3	0.007
Ssc.12229.1.S1_at	<b>CKS1B</b>	CDC28 protein kinase regulatory subunit 1B	1.3	0.036
Ssc.997.3.A1_at	<b>KDELR2</b>	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	1.3	0.004
Ssc.2924.1.A1_at	<b>RAB8A</b>	RAB8A, member RAS oncogene family	1.3	0.028
Ssc.19659.2.S1_at	<b>LPCAT3</b>	lysophosphatidylcholine acyltransferase 3	1.3	0.001
Ssc.8359.2.A1_at	<b>SEMA6A</b>	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	1.3	0.035
Ssc.4899.1.S1_at	<b>SRPX2</b>	Sushi repeat-containing protein SRPX2 Precursor	1.3	0.016
Ssc.4999.2.S1_at	<b>LOC100155615</b>	similar to vasopressin-induced protein, 32kDa	1.3	0.001
Ssc.17815.1.S1_at	<b>LGALS3</b>	lectin, galactoside-binding, soluble, 3	1.3	0.024
Ssc.16774.1.A1_at	<b>SNORD31</b>	small nucleolar RNA, C/D box 31	1.3	0.035
Ssc.5712.1.S1_at	<b>CYP51A1</b>	cytochrome P450, family 51, subfamily A, polypeptide 1	1.3	0.046
Ssc.7306.1.A1_at	unknown		1.2	0.002
Ssc.16159.1.S1_at	<b>SCD</b>	stearoyl-CoA desaturase (delta-9-desaturase)	1.2	0.030
Ssc.10931.1.S1_at	<b>CRYAA</b>	crystallin, alpha A	1.2	0.017
Ssc.16770.1.S1_at	<b>EMG1</b>	EMG1 nucleolar protein homolog ( <i>S. cerevisiae</i> )	1.2	0.034
Ssc.10401.1.A1_at	unknown		1.2	0.012
Ssc.6901.3.A1_a_at	<b>LMBR1</b>	limb region 1 homolog (mouse)	1.2	0.014

Supplementary Table 2 continued

<b>Probe Set ID</b>	<b>Annotation</b>	<b>Gene description</b>	<b>FC (H/L)</b>	<b>p-value</b>
Ssc.12488.1.A1_at	<b>NOL3</b>	Nucleolar protein 3 (Apoptosis repressor with CARD domain)	1.2	0.048
Ssc.2699.1.S1_at	<b>ALG3</b>	asparagine-linked glycosylation 3, alpha-1,3- mannosyltransferase homolog (S. cerevisiae)	1.2	0.007
Ssc.2969.1.S1_at	<b>PYCR1</b>	pyrroline-5-carboxylate reductase 1	1.2	0.003
Ssc.11126.1.A1_at	<b>MGC90332</b>	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	1.2	0.045
Ssc.18621.1.S1_at	<b>PAGE4</b>	P antigen family, member 4 (prostate associated)	1.2	0.034
Ssc.25213.1.S1_at	<b>BCS1L</b>	BCS1-like (yeast)	1.2	0.007
Ssc.11969.1.A1_at	<b>FARP1</b>	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)	1.2	0.046
Ssc.6273.1.A1_at	<b>SLC25A38</b>	solute carrier family 25, member 38	1.2	0.011
Ssc.16336.1.S2_at	<b>ME1</b>	malic enzyme 1, NADP(+)-dependent, cytosolic	1.2	0.031
Ssc.7297.1.S1_at	<b>MAOB</b>	monoamine oxidase B	1.2	0.032
Ssc.20874.3.A1_at	<b>ACTR1A</b>	ARP1 actin-related protein 1 homolog A, contractin alpha (yeast)	1.2	0.047
Ssc.23808.2.S1_a_at	<b>CLIC4</b>	chloride intracellular channel 4	1.2	0.031
Ssc.23522.1.S1_at	<b>TRAM1</b>	translocation associated membrane protein 1	1.2	0.008
Ssc.1408.2.S1_at	<b>CDC19</b>	minichromosome maintenance complex component 2	1.2	0.011
Ssc.19073.1.S1_at	<b>PDE8A</b>	phosphodiesterase 8A	1.2	0.011
Ssc.5966.1.A1_at	<b>CRELD2</b>	cysteine-rich with EGF-like domains 2	1.2	0.014
Ssc.21897.1.S1_at	<b>RABL4</b>	RAB, member of RAS oncogene family-like 4	1.2	0.013
Ssc.7511.1.S1_at	<b>CUGBP1</b>	CUG triplet repeat, RNA binding protein 1	1.2	0.006
Ssc.12120.1.A1_at	<b>CHADL</b>	chondroadherin-like	1.2	0.025
Ssc.8774.1.S1_at	<b>SC4MOL</b>	sterol-C4-methyl oxidase-like	1.2	0.053
Ssc.18808.1.S1_at	<b>PAQR5</b>	progesterin and adipoQ receptor family member V	1.2	0.023
Ssc.18586.2.S1_at	<b>MAD2L2</b>	MAD2 mitotic arrest deficient-like 2 (yeast)	1.2	0.008
Ssc.5258.2.S1_at	<b>AATF</b>	apoptosis antagonizing transcription factor	1.2	0.034
Ssc.5477.1.A1_at	<b>DPAGT1</b>	dolichyl-phosphate (UDP-N-acetylglucosamine) N-acetylglucosaminophosphotransferase 1	1.2	0.007
Ssc.26985.1.S1_at	<b>LOC100130084</b>	hypothetical LOC100130084	1.2	0.019
Ssc.21691.1.A1_at	<b>FADS6</b>	fatty acid desaturase domain family, member 6	1.2	0.031
Ssc.30973.1.A1_at	<b>TBRG1</b>	transforming growth factor beta regulator 1	1.2	0.029
Ssc.29839.1.A1_at	<b>TROVE2</b>	TROVE domain family, member 2	1.2	0.017
Ssc.30044.1.A1_at	unknown		1.2	0.023
Ssc.5018.1.S1_at	<b>FKBP1A</b>	FK506 binding protein 1A, 12kDa	1.2	0.043
Ssc.23301.1.S1_at	<b>SLC39A1</b>	SLC39A1 solute carrier family 39 (zinc transporter), member 1	1.2	0.003
Ssc.4612.1.S1_at	<b>MCM4</b>	minichromosome maintenance complex component 4	1.2	0.001
Ssc.28155.1.A1_at	<b>C3ORF26</b>	Uncharacterized protein C3orf26	1.2	0.007
Ssc.2516.3.S1_a_at	<b>SLC5A6</b>	solute carrier family 5 (sodium-dependent vitamin transporter), member 6	1.2	0.024

Supplementary Table 2 continued

<b>Probe Set ID</b>	<b>Annotation</b>	<b>Gene description</b>	<b>FC (H/L)</b>	<b>p-value</b>
Ssc.28021.1.A1_at	<b>AGPAT5</b>	1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransferase, epsilon)	1.2	0.031
Ssc.12179.1.A1_at	<b>C17ORF68</b>	chromosome 17 open reading frame 68 ( <i>Homo sapiens</i> )	1.2	0.054
Ssc.828.1.S1_at	<b>SLC26A6</b>	solute carrier family 26, member 6	1.2	0.019
Ssc.21491.1.S1_at	<b>RNASEH2B</b>	ribonuclease H2, subunit B	1.2	0.041
Ssc.4999.1.S1_at	<b>AVP11</b>	arginine vasopressin-induced 1	1.2	0.010
Ssc.4436.1.S1_at	<b>EDNRB</b>	endothelin receptor type B	1.2	0.036
Ssc.9071.1.A1_at	<b>LOC729085</b>	hypothetical protein LOC729085	1.2	0.054
Ssc.22933.1.S1_at	<b>AMZ2</b>	archaelysin family metallopeptidase 2	1.2	0.025
Ssc.13276.1.A1_at	<b>CHRD1</b>	chordin-like 1	1.2	0.025
Ssc.30749.1.S1_at	<b>SSR1</b>	signal sequence receptor, alpha	1.2	0.011
Ssc.19914.1.S1_at	<b>MEST</b>	mesoderm specific transcript homolog (mouse)	1.2	0.033
Ssc.6034.1.S1_at	<b>SLC45A3</b>	solute carrier family 45, member 3	1.2	0.017
Ssc.24253.1.S1_at	<b>CYFIP2</b>	cytoplasmic FMR1 interacting protein 2	1.2	0.043
Ssc.7646.1.A1_at	<b>LOC668924</b>	similar to RIKEN cDNA 1110005A03 gene	1.2	0.006
Ssc.20071.1.S1_at	<b>ARMET</b>	arginine-rich, mutated in early stage tumors	1.2	0.010
Ssc.28555.2.S1_a_at	unknown		1.2	0.014
Ssc.12764.1.A1_at	<b>LOC100156657</b>	hypothetical protein LOC100156657	1.2	0.015
Ssc.15751.1.S1_a_at	<b>RAMP3</b>	receptor (G protein-coupled) activity modifying protein 3	1.2	0.021
Ssc.10948.1.S1_at	<b>RNF14</b>	ring finger protein 14	1.2	0.004
Ssc.9053.1.S1_at	<b>C1ORF144</b>	chromosome 1 open reading frame 144 ( <i>Homo sapiens</i> )	1.2	0.047
Ssc.5249.1.S1_at	<b>HMBS</b>	hydroxymethylbilane synthase	1.2	0.003
Ssc.18185.1.S1_at	<b>LOC643438</b>	misc_RNA LOC643438	1.2	0.011
Ssc.28253.1.A1_at	<b>IDS</b>	iduronate 2-sulfatase	1.2	0.008
Ssc.21641.1.A1_at	<b>VMA21</b>	VMA21 vacuolar H <sup>+</sup> -ATPase homolog ( <i>S. cerevisiae</i> )	1.2	0.010
Ssc.3893.1.S1_at	unknown		1.2	0.002
Ssc.24217.1.S1_at	<b>GINS3</b>	GINS complex subunit 3 (Psf3 homolog)	1.2	0.051
Ssc.24216.1.S1_at	<b>POP4</b>	Ribonuclease P protein subunit p29	1.2	0.021
Ssc.6545.1.S1_a_at	<b>RAB4B</b>	RAB4B, member RAS oncogene family	1.2	0.016
Ssc.16563.1.S1_at	<b>OSTC</b>	oligosaccharyltransferase complex subunit	1.2	0.001
Ssc.25217.1.S1_a_at	<b>SELM</b>	selenoprotein M	1.2	0.030
Ssc.3965.1.A1_at	<b>PIGN</b>	phosphatidylinositol glycan anchor biosynthesis, class N	1.2	0.007
Ssc.20323.1.S1_at	<b>EXOSC5</b>	exosome component 5	1.2	0.039
Ssc.22051.1.A1_at	<b>NSF</b>	N-ethylmaleimide-sensitive factor	1.2	0.020

Supplementary Table 2 continued

<b>Probe_Set_ID</b>	<b>Annotation</b>	<b>Gene_description</b>	<b>FC (HL)</b>	<b>p-value</b>
Ssc.18181.2.S1_at	<b>TMEM91</b>	transmembrane protein 91	1.2	0.012
Ssc.21216.2.A1_a_at	<b>PSMB3</b>	proteasome (prosome, macropain) subunit, beta type, 3	1.2	0.001
Ssc.25365.1.S1_at	unknown		1.2	0.009
Ssc.15283.1.A1_at	unknown		1.2	0.044
Ssc.18078.1.A1_at	<b>SFXN2</b>	sideroflexin 2	1.2	0.022
Ssc.3458.3.A1_a_at	<b>ACSL5</b>	acyl-CoA synthetase long-chain family member 5	1.2	0.034
Ssc.27233.1.S1_at	<b>SIGLEC10</b>	sialic acid binding Ig-like lectin 10	1.2	0.019
Ssc.11296.1.A1_at	<b>EIF3-ZETA</b>	eukaryotic translation initiation factor 3, subunit D	1.2	0.036
Ssc.1351.1.S1_at	<b>KIF1C</b>	kinesin family member 1C	1.2	0.003
Ssc.2178.1.A1_at	<b>ZNF134</b>	zinc finger protein 134	1.2	0.028
Ssc.4184.1.A1_at	<b>2610110G12RIK</b>	Mus musculus RIKEN cDNA 2610110G12 gene	1.2	0.006
Ssc.25131.1.S1_at	<b>NHP2</b>	NHP2 ribonucleoprotein homolog (yeast)	1.2	0.009
Ssc.26287.1.S1_at	<b>FUT4</b>	fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)	1.2	0.011
Ssc.29408.1.A1_at	unknown		1.2	0.040
Ssc.5062.1.S1_at	<b>SEPW1</b>	selenoprotein W, 1	1.2	0.005
Ssc.29960.1.A1_at	unknown		1.2	0.015
Ssc.1755.1.S1_at	<b>NANS</b>	N-acetylneuraminic acid synthase	1.2	0.042
Ssc.4188.1.S1_at	<b>HM13</b>	histocompatibility (minor) 13	1.2	0.006
Ssc.2821.1.A1_at	<b>LOC100154635</b>	similar to Uncharacterized protein C12orf43	1.2	0.036
Ssc.17900.1.S1_at	<b>C6ORF162</b>	chromosome 6 open reading frame 162 ( <i>Homo sapiens</i> )	1.2	0.009
Ssc.8305.1.A1_at	<b>ENTPD4</b>	ectonucleoside triphosphate diphosphohydrolase 4	1.2	0.009
Ssc.10107.1.S1_at	<b>SLC31A1</b>	solute carrier family 31 (copper transporters), member 1	1.2	0.025
Ssc.27963.1.A1_s_at	<b>SLC39A1</b>	solute carrier family 39 (zinc transporter), member 1	1.2	0.043
Ssc.12758.1.A1_at	<b>PSMB9</b>	proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional peptidase 2)	1.2	0.021
Ssc.11966.1.S1_at	<b>SHMT2</b>	Serine hydroxymethyltransferase, mitochondrial precursor	1.2	0.013
Ssc.3059.1.S1_at	<b>EFCAB2</b>	EF-hand calcium binding domain 2 (EFCAB2), transcript variant 2, mRNA	1.2	0.027
Ssc.11669.1.S1_at	<b>EIF5AL1</b>	eukaryotic translation initiation factor 5A-like 1	1.2	0.024
Ssc.5630.1.S1_at	<b>SLC25A11</b>	solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11	1.2	0.048
Ssc.18184.1.S1_at	<b>SERTAD4</b>	SERTA domain containing 4	1.2	0.009
Ssc.12206.1.S1_at	<b>GTPBP3</b>	GTP binding protein 3 (mitochondrial)	1.2	0.003
Ssc.17821.1.A1_at	<b>PLEK</b>	pleckstrin	1.2	0.054
Ssc.26215.1.S1_at	<b>POLE4</b>	polymerase (DNA-directed), epsilon 4 (p12 subunit)	1.2	0.002
Ssc.9133.1.A1_at	<b>REXO2</b>	REX2, RNA exonuclease 2 homolog ( <i>S. cerevisiae</i> )	1.2	0.015
Ssc.11072.1.S1_at	<b>ATF4</b>	activating transcription factor 4 (tax-responsive enhancer element B67)	1.2	0.011

Supplementary Table 2 continued

<b>Probe_Set_ID</b>	<b>Annotation</b>	<b>Gene_description</b>	<b>FC (H/L)</b>	<b>p-value</b>
Ssc.24317.1.A1_at	<b>EXOSC3</b>	exosome component 3	1.2	0.018
Ssc.9406.2.S1_at	<b>LYPLA1</b>	lysophospholipase I	1.2	0.009
Ssc.24381.1.S1_at	<b>PIGX</b>	phosphatidylinositol glycan anchor biosynthesis, class X	1.2	0.016
Ssc.6373.1.A1_at	<b>NOC4L</b>	Nucleolar complex protein 4 homolog	1.2	0.021
Ssc.21733.1.S1_at	<b>MBNL1</b>	muscleblind-like (Drosophila)	1.2	0.021
Ssc.21729.1.S1_at	<b>C16ORF61</b>	chromosome 16 open reading frame 61	1.2	0.052
Ssc.3266.1.S1_at	<b>TMEM5</b>	Transmembrane protein 5	1.2	0.010
Ssc.4364.1.S1_at	<b>LARGE</b>	like-glycosyltransferase	1.2	0.050
Ssc.24393.1.S1_at	<b>RCN1</b>	reticulocalbin 1, EF-hand calcium binding domain	1.2	0.014
Ssc.18465.1.A1_at	<b>C2ORF34</b>	chromosome 2 open reading frame 34	1.2	0.010
Ssc.29838.1.A1_at	<b>TTL5</b>	tubulin tyrosine ligase-like family, member 5	1.2	0.036
Ssc.24009.1.S1_at	<b>NT5M</b>	5',3'-nucleotidase, mitochondrial	1.2	0.048
Ssc.23363.1.S1_at	<b>LOC100153476</b>	similar to Ras association domain-containing protein 2	1.2	0.024
Ssc.29047.2.S1_at	<b>MGC138388</b>	hypoxia-inducible protein 2	1.2	0.035
Ssc.1649.1.A1_at	<b>ATP5G1</b>	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C1 (subunit 9)	1.2	0.011
Ssc.15592.1.S1_at	<b>OLFML3</b>	olfactomedin-like 3	1.2	0.010
Ssc.26408.1.S1_at	<b>ATP13A1</b>	ATPase type 13A1	1.2	0.046
Ssc.16083.1.S1_at	<b>MGC8394</b>	endosulfine alpha	1.2	0.051
Ssc.19231.2.S1_at	<b>FARSA</b>	phenylalanyl-tRNA synthetase, alpha subunit	1.2	0.028
Ssc.21425.1.S1_at	<b>RQCD1</b>	Cell differentiation protein RCD1 homolog	1.2	0.014
Ssc.17562.1.S1_at	<b>MBOAT7</b>	embrane bound O-acyltransferase domain containing 7	1.2	0.026
Ssc.1999.1.S1_at	<b>TBC1D9B</b>	TBC1 domain family, member 9B (with GRAM domain)	1.2	0.002
Ssc.18516.1.S1_at	<b>CLIP2</b>	CAP-GLY domain containing linker protein 2	1.2	0.043
Ssc.4345.1.S2_at	<b>COL4A1</b>	collagen, type IV, alpha 1	1.2	0.050
Ssc.22694.1.S1_at	<b>NDUFB6</b>	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6, 17kDa	1.2	0.022
Ssc.25550.1.S1_at	<b>LY96</b>	lymphocyte antigen 96	1.2	0.010
Ssc.11149.1.S1_at	<b>CA9</b>	carbonic anhydrase IX	1.2	0.014
Ssc.3987.1.S1_at	<b>SLC39A11</b>	solute carrier family 39 (metal ion transporter), member 11	1.2	0.013
Ssc.1198.1.S1_at	<b>DJ196E23.2</b>	protein-L-isoaspartate (D-aspartate) O-methyltransferase	1.2	0.011
Ssc.27616.1.S1_at	<b>CDK2</b>	cyclin-dependent kinase 2	1.2	0.011
Ssc.5650.1.S1_at	<b>ELOVL1</b>	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1	1.2	0.023
Ssc.12457.1.S1_at	<b>HN1A</b>	hematological and neurological expressed 1	1.2	0.004
Ssc.1537.1.S1_at	<b>YKT6</b>	YKT6 v-SNARE homolog ( <i>S. cerevisiae</i> )	1.2	0.039
Ssc.28420.1.A1_at	<b>ANAPC5</b>	anaphase promoting complex subunit 5	1.2	0.019

Supplementary Table 2 continued

<b>Probe Set ID</b>	<b>Annotation</b>	<b>Gene description</b>	<b>FC (H/L)</b>	<b>p-value</b>
Ssc.1095.2.S1_at	<b>TSPAN31</b>	tetraspanin 31	1.2	0.030
Ssc.9764.1.S1_a_at	<b>NGDN</b>	neuroguidin, EIF4E binding protein	1.2	0.007
Ssc.3768.1.S1_at	<b>LOC100048454</b>	Mus musculus hypothetical protein LOC100048454	1.2	0.009
Ssc.2804.2.A1_at	<b>CYB561D2</b>	cytochrome b-561 domain containing 2	1.2	0.008
Ssc.1755.2.A1_at	<b>NANS</b>	N-acetylneuraminic acid synthase	1.2	0.002
Ssc.30862.1.S1_a_at	<b>DNAJB9</b>	DnaJ homolog subfamily B member 9 (Microvascular endothelial differentiation gene 1 protein)	1.2	0.011
Ssc.22631.1.S1_at	<b>GFPT1</b>	glutamine-fructose-6-phosphate transaminase 1	1.2	0.017
Ssc.15824.1.S1_at	<b>LOC728860</b>	karyopherin alpha-2 subunit like, transcript variant 2	1.2	0.005
Ssc.17628.1.S1_at	<b>C6ORF226</b>	Uncharacterized protein C6orf226 ( <i>Homo sapiens</i> )	1.2	0.037
Ssc.9406.1.A1_at	<b>LYPLA1</b>	lysophospholipase I	1.2	0.003
Ssc.15727.1.A1_at	<b>SC5DL</b>	sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, <i>S. cerevisiae</i> )-like	1.2	0.046
Ssc.10866.1.A1_at	unknown		1.2	0.019
Ssc.9608.1.S1_at	<b>GINS4</b>	GINS complex subunit 4 (Sld5 homolog)	1.2	0.020
Ssc.17230.1.A1_at	<b>TMSB10</b>	thymosin beta 10	1.2	0.015
Ssc.27419.1.S1_at	<b>SLC25A13</b>	solute carrier family 25, member 13 (citrin)	1.2	0.002
Ssc.18095.1.A1_at	<b>EYA3</b>	eyes absent homolog 3 ( <i>Drosophila</i> )	1.2	0.015
Ssc.3629.1.S1_at	<b>OTUB1</b>	OTU domain, ubiquitin aldehyde binding 1	1.2	0.021
Ssc.16161.1.S1_at	<b>THOP1</b>	Thimet oligopeptidase	1.2	0.007
Ssc.14392.1.A1_at	<b>MSMB</b>	microseminoprotein, beta-	1.2	0.054
Ssc.10250.1.A1_at	<b>LTA4H</b>	Leukotriene A-4 hydrolase	1.2	0.022
Ssc.948.2.S1_at	<b>NUTF2</b>	nuclear transport factor 2	1.2	0.046
Ssc.13173.1.A1_at	<b>RAP1GDS1</b>	RAP1, GTP-GDP dissociation stimulator 1	1.2	0.009
Ssc.2487.2.S1_at	<b>AIFM2</b>	apoptosis-inducing factor, mitochondrion-associated, 2	1.2	0.037
Ssc.835.1.S1_at	<b>PFN1</b>	profilin 1	1.2	0.028
Ssc.28873.1.A1_at	unknown		1.2	0.011
Ssc.4925.1.S1_at	<b>HSPBP1</b>	HSPA (heat shock 70kDa) binding protein, cytoplasmic cochaperone 1	1.2	0.032
Ssc.18181.1.A1_at	<b>B9D2</b>	B9 protein domain 2	1.2	0.018
Ssc.1850.1.A1_at	<b>GLIPR2</b>	GLI pathogenesis-related 2	1.2	0.026
Ssc.11084.1.S1_at	<b>SRP72</b>	signal recognition particle 72kDa	1.2	0.024
Ssc.2981.1.S1_at	<b>PHKG1</b>	phosphorylase kinase, gamma 1 (muscle)	1.2	0.042
Ssc.30165.1.A1_at	<b>TMEM41B</b>	transmembrane protein 41B	1.1	0.029
Ssc.25889.1.S1_at	<b>CHCHD7</b>	coiled-coil-helix-coiled-coil-helix domain containing 7	1.1	0.037
Ssc.9901.1.A1_at	<b>ALS2CR4</b>	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 4	1.1	0.015



Supplementary Table 2 continued

<b>Probe_Set_ID</b>	<b>Annotation</b>	<b>Gene_description</b>	<b>FC (H/L)</b>	<b>p-value</b>
Ssc.9951.2.A1_at	<b>GNPNAT1</b>	glucosamine-phosphate N-acetyltransferase 1	1.1	0.024
Ssc.24620.3.A1_a_at	<b>LOC100043490</b>	similar to Ran-interacting protein MOG1	1.1	0.012
Ssc.9332.1.A1_at	<b>MID2</b>	midline 2	1.1	0.054
Ssc.17315.1.S1_at	<b>EIF3I</b>	eukaryotic translation initiation factor 3, subunit I	1.1	0.005
Ssc.21889.1.S1_at	<b>AGK</b>	acylglycerol kinase	1.1	0.012
Ssc.27900.1.S1_at	<b>WDR68</b>	WD repeat domain 68	1.1	0.049
Ssc.20162.1.S1_at	<b>ERH</b>	enhancer of rudimentary homolog (Drosophila)	1.1	0.015
Ssc.2271.1.S1_at	<b>SURF4</b>	surfeit 4	1.1	0.019
Ssc.6768.1.A1_at	<b>UBE2J1</b>	ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)	1.1	0.015
Ssc.5682.1.A1_at	<b>RAP1GDS1</b>	RAP1, GTP-GDP dissociation stimulator 1	1.1	0.041
Ssc.2087.1.S1_at	<b>HYOU1</b>	hypoxia up-regulated 1	1.1	0.021
Ssc.26072.1.S1_at	<b>TTC7A</b>	tetratricopeptide repeat domain 7A	1.1	0.013
Ssc.21959.1.S1_at	<b>CARS</b>	cysteinyl-tRNA synthetase	1.1	0.032
Ssc.9174.2.A1_a_at	<b>PTPMT1</b>	protein tyrosine phosphatase, mitochondrial 1	1.1	0.047
Ssc.23511.1.S1_at	<b>C5ORF32</b>	chromosome 5 open reading frame 32	1.1	0.032
Ssc.21182.1.S1_at	<b>PFDN6</b>	prefoldin subunit 6	1.1	0.018
Ssc.20426.1.S1_at	<b>GLRX3</b>	glutaredoxin 3	1.1	0.012
Ssc.10351.1.A1_at	<b>PLAUR</b>	plasminogen activator, urokinase receptor	1.1	0.026
Ssc.19737.2.S1_at	<b>STX4</b>	Syntaxin-4	1.1	0.022
Ssc.7022.1.A1_at	<b>LRRC42</b>	leucine rich repeat containing 42	1.1	0.001
Ssc.8895.1.S1_at	<b>SERPINB6</b>	serpin peptidase inhibitor, clade B (ovalbumin), member 6	1.1	0.048
Ssc.4903.1.A1_at	<b>CCDC115</b>	coiled-coil domain containing 115	1.1	0.040
Ssc.12661.1.A1_at	<b>HINT1</b>	histidine triad nucleotide binding protein 1	1.1	0.020
Ssc.2237.1.A1_at	<b>VGLL3</b>	vestigial like 3 (Drosophila)	1.1	0.023
Ssc.16459.1.S1_at	<b>SAR1A</b>	SAR1 homolog A (S. cerevisiae)	1.1	0.045
Ssc.1311.1.A1_at	<b>NDUFB2</b>	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 2, mitochondrial precursor	1.1	0.011
Ssc.5287.1.S1_at	<b>ARSB</b>	arylsulfatase B	1.1	0.012
Ssc.19737.1.S1_at	<b>STX4</b>	Syntaxin-4	1.1	0.022
Ssc.4060.1.S1_at	<b>SLCO2A1</b>	solute carrier organic anion transporter family, member 2A1	1.1	0.030
Ssc.8163.1.A1_at	<b>HDDC2</b>	HD domain containing 2	1.1	0.036
Ssc.6687.2.S1_a_at	<b>CDC42</b>	cell division cycle 42 (GTP binding protein, 25kDa)	1.1	0.006
Ssc.1797.1.S1_a_at	<b>IMP4</b>	U3 small nucleolar ribonucleoprotein protein IMP4	1.1	0.025
Ssc.1662.1.S1_at	<b>PRDX1</b>	peroxiredoxin 1	1.1	0.006
Ssc.19258.2.A1_at	<b>KCNJ8</b>	potassium inwardly-rectifying channel, subfamily J, member 8	1.1	0.030

Supplementary Table 2 continued

<b>Probe_Set_ID</b>	<b>Annotation</b>	<b>Gene_description</b>	<b>FC (H/L)</b>	<b>p-value</b>
Ssc.8970.1.S1_at	<b>PDIA4</b>	protein disulfide isomerase family A, member 4	1.1	0.005
Ssc.6627.1.A1_at	<b>C17ORF59</b>	chromosome 17 open reading frame 59 ( <i>Homo sapiens</i> )	1.1	0.010
Ssc.12259.1.A1_at	<b>MARS</b>	methionyl-tRNA synthetase	1.1	0.025
Ssc.18416.1.A1_at	<b>LEPROTL1</b>	leptin receptor overlapping transcript-like 1	1.1	0.051
Ssc.24642.1.S1_at	<b>PSTK</b>	L-seryl-tRNA(Sec) kinase	1.1	0.054
Ssc.18581.1.S1_at	<b>USP5</b>	ubiquitin specific peptidase 5 (isopeptidase T)	1.1	0.047
Ssc.26294.1.S1_at	<b>KIF2A</b>	kinesin heavy chain member 2A	1.1	0.035
Ssc.5401.1.S1_at	<b>GIN51</b>	GIN5 complex subunit 1 (Psf1 homolog)	1.1	0.029
Ssc.29223.1.A1_at	<b>NDUFB1</b>	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1, 7kDa	1.1	0.024
Ssc.1436.1.S1_at	<b>SEC13</b>	SEC13 homolog ( <i>S. cerevisiae</i> )	1.1	0.007
Ssc.3286.1.S1_at	<b>MTPN</b>	myotrophin	1.1	0.030
Ssc.8818.1.A1_at	<b>RFC3</b>	replication factor C (activator 1) 3, 38kDa	1.1	0.007
Ssc.19420.1.S1_at	<b>RUVBL1</b>	RuvB-like 1 ( <i>E. coli</i> )	1.1	0.009
Ssc.21403.1.S1_at	<b>ALG5</b>	asparagine-linked glycosylation 5, dolichyl-phosphate beta-glucosyltransferase homolog ( <i>S. cerevisiae</i> )	1.1	0.012
Ssc.24245.1.S1_at	<b>POLR2H</b>	polymerase (RNA) II (DNA directed) polypeptide H	1.1	0.034
Ssc.5412.2.A1_at	<b>LOC100154621</b>	similar to potassium channel tetramerisation domain containing 20	1.1	0.005
Ssc.19354.1.S1_at	<b>CHCHD4</b>	coiled-coil-helix-coiled-coil-helix domain containing 4	1.1	0.017
Ssc.16936.2.S1_a_at	<b>NOP16</b>	Nucleolar protein 16 (HBV pre-S2 trans-regulated protein 3)	1.1	0.006
Ssc.30690.1.A1_at	<b>PPRC1</b>	peroxisome proliferator-activated receptor gamma, coactivator-related 1	1.1	0.045
Ssc.21926.1.S1_at	<b>LDLR</b>	low density lipoprotein receptor	1.1	0.025
Ssc.9387.1.A1_at	<b>PCNA</b>	proliferating cell nuclear antigen	1.1	0.032
Ssc.28091.1.A1_at	<b>FANK1</b>	fibronectin type III and ankyrin repeat domains 1	1.1	0.035
Ssc.10800.2.A1_at	<b>SLC25A14</b>	solute carrier family 25 (mitochondrial carrier, brain), member 14	1.1	0.023
Ssc.854.1.S1_at	<b>ROBLD3</b>	roadblock domain containing 3	1.1	0.042
Ssc.20659.1.S1_at	<b>MRPS23</b>	mitochondrial ribosomal protein S23	1.1	0.053
Ssc.26880.1.A1_s_at	<b>CD40</b>	CD40 molecule, TNF receptor superfamily member 5	1.1	0.043
Ssc.20874.1.S1_at	<b>ACTR1A</b>	ARP1 actin-related protein 1 homolog A, cetractin alpha (yeast)	1.1	0.013
Ssc.6903.1.S1_at	<b>LOC92755</b>	misc_RNA LOC92755	1.1	0.010
Ssc.1918.1.S1_at	<b>MRPS7</b>	mitochondrial ribosomal protein S7	1.1	0.029
Ssc.1006.1.S1_at	<b>PGM1</b>	phosphoglucomutase 1	1.1	0.049
Ssc.16410.1.A1_at	<b>SIGMAR1</b>	sigma non-opioid intracellular receptor 1	1.1	0.039
Ssc.5746.1.S1_at	<b>IMPAD1</b>	inositol monophosphatase domain containing 1	1.1	0.008
Ssc.22027.1.S1_at	<b>SRPRB</b>	signal recognition particle receptor, B subunit	1.1	0.005

Supplementary Table 2 continued

<b>Probe_Set_ID</b>	<b>Annotation</b>	<b>Gene_description</b>	<b>FC (H/L)</b>	<b>p-value</b>
Ssc.7670.1.S1_at	<b>SNRPB2</b>	small nuclear ribonucleoprotein polypeptide B''	1.1	0.048
Ssc.1420.1.S1_at	<b>PSMB6</b>	proteasome (prosome, macropain) subunit, beta type, 6	1.1	0.043
Ssc.4453.1.S1_at	<b>COPE</b>	coatomer protein complex, subunit epsilon	1.1	0.010
Ssc.25892.1.S1_at	<b>DET1</b>	de-etiolated homolog 1 (Arabidopsis)	1.1	0.007
Ssc.6681.1.A1_at	<b>DDX39</b>	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	1.1	0.003
Ssc.6696.1.S1_at	<b>TXN</b>	thioredoxin	1.1	0.016
Ssc.20612.1.S1_at	<b>UFM1</b>	ubiquitin-fold modifier 1	1.1	0.040
Ssc.6463.1.A1_at	<b>MYD88</b>	myeloid differentiation primary response gene (88)	1.1	0.009
Ssc.21422.1.S1_at	<b>SF4</b>	splicing factor 4	1.1	0.003
Ssc.22038.1.S1_at	<b>DNAJB11</b>	DnaJ (Hsp40) homolog, subfamily B, member 11	1.1	0.019
Ssc.3237.1.S1_at	<b>LOC100132279</b>	hypothetical protein LOC100132279	1.1	0.005
Ssc.9215.1.A1_at	<b>FLRT2</b>	fibronectin leucine rich transmembrane protein 2	1.1	0.031
Ssc.8786.1.A1_at	<b>SPATA2</b>	spermatogenesis associated 2	1.1	0.019
Ssc.15656.1.S1_at	<b>FBL</b>	fibrillarin	1.1	0.039
Ssc.14281.3.A1_at	<b>C10ORF26</b>	chromosome 10 open reading frame 26 ( <i>Homo sapiens</i> )	1.1	0.021
Ssc.27390.1.A1_at	<b>FGL2</b>	fibrinogen-like 2	1.1	0.025
Ssc.29067.1.A1_s_at	<b>BZW2</b>	basic leucine zipper and W2 domains 2	1.1	0.043
Ssc.20362.1.S1_at	<b>C7ORF59</b>	chromosome 7 open reading frame 59 ( <i>Homo sapiens</i> )	1.1	0.034
Ssc.14323.1.A1_at	<b>C1ORF192</b>	chromosome 1 open reading frame 192 ( <i>Homo sapiens</i> )	1.1	0.040
Ssc.6685.2.A1_at	<b>CALU</b>	calumenin	1.1	0.009
Ssc.27254.1.S1_at	<b>SEC13</b>	SEC13 homolog ( <i>S. cerevisiae</i> )	1.1	0.039
Ssc.4513.2.A1_a_at	<b>EMD</b>	emerin	1.1	0.038
Ssc.23470.1.S1_at	<b>BAX</b>	BCL2-associated X protein	1.1	0.050
Ssc.11114.1.A1_at	<b>RPA1</b>	replication protein A1, 70kDa	1.1	0.020
Ssc.997.1.S1_at	<b>KDELR2</b>	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	1.1	0.049
Ssc.11668.1.A1_at	<b>MGC40489</b>	misc_RNA MGC40489	1.1	0.025
Ssc.15456.1.S1_at	<b>LOC653888</b>	similar to p41-Arc	1.1	0.051
Ssc.26414.1.S1_at	<b>WDR8</b>	WD repeat domain 8	1.1	0.003
Ssc.10426.1.S1_at	<b>EIF3B</b>	eukaryotic translation initiation factor 3, subunit B	1.1	0.036
Ssc.4097.1.S1_at	<b>SLC12A7</b>	solute carrier family 12 (potassium/chloride transporters), member 7	1.1	0.049
Ssc.11791.1.S1_at	<b>SCARB1</b>	scavenger receptor class B, member 1	1.1	0.040
Ssc.16699.1.S1_at	<b>WDR5</b>	WD repeat domain 5	1.1	0.045
Ssc.830.1.S1_at	<b>PSME2</b>	proteasome (prosome, macropain) activator subunit 2 (PA28 beta)	1.1	0.002
Ssc.21435.1.S1_a_at	<b>ANAPC5</b>	anaphase promoting complex subunit 5	1.1	0.022

Supplementary Table 2 continued

<b>Probe_Set_ID</b>	<b>Annotation</b>	<b>Gene_description</b>	<b>FC (HL)</b>	<b>p-value</b>
Ssc.3107.1.S1_at	<b>CLEC14A</b>	C-type lectin domain family 14, member A	1.1	0.054
Ssc.7750.1.S1_at	<b>AKAP8</b>	A kinase (PRKA) anchor protein 8	1.1	0.040
Ssc.27516.1.S1_at	<b>LOC100131294</b>	similar to RAB13 protein	1.1	0.046
Ssc.16336.1.S1_at	<b>ME1</b>	malic enzyme 1, NADP(+)-dependent, cytosolic	1.1	0.028
Ssc.9555.1.A1_at	<b>PTPN3</b>	protein tyrosine phosphatase, non-receptor type 3	1.1	0.019
Ssc.23760.1.S1_at	<b>ECSIT</b>	ECSIT homolog (Drosophila)	1.1	0.044
Ssc.5332.1.S1_at	<b>APOBEC3H</b>	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3H	1.1	0.054
Ssc.17618.1.S1_at	<b>C19ORF60</b>	chromosome 19 open reading frame 60 ( <i>Homo sapiens</i> )	1.1	0.050
Ssc.19390.1.S1_at	<b>RAB5C</b>	RAB5C, member RAS oncogene family	1.1	0.053
Ssc.29105.1.A1_at	<b>ERCC1</b>	excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence)	1.1	0.047
Ssc.7608.2.S1_at	<b>ARL8B</b>	ADP-ribosylation factor-like 8B	1.1	0.043
Ssc.3494.1.A1_at	<b>NKTR</b>	natural killer-tumor recognition sequence (NKTR), mRNA	1.1	0.044
Ssc.27512.1.A1_at	<b>RNF123</b>	ring finger protein 123	1.1	0.054
Ssc.3205.1.S1_at	<b>MIC2Y</b>	CD99 molecule	1.1	0.050
Ssc.5957.1.S1_at	<b>THOC6</b>	THO complex 6 homolog (Drosophila)	1.1	0.036
Ssc.7506.1.S1_at	<b>CHCHD3</b>	coiled-coil-helix-coiled-coil-helix domain containing 3	1.1	0.008
Ssc.26271.1.S1_at	<b>EBNA1BP2</b>	EBNA1 binding protein 2	1.1	0.018
Ssc.22306.1.A1_at	<b>CD164</b>	CD164 molecule, sialomucin	1.1	0.034
Ssc.21644.1.S1_a_at	<b>STT3A</b>	STT3, subunit of the oligosaccharyltransferase complex, homolog A ( <i>S. cerevisiae</i> )	1.1	0.019
Ssc.9128.1.A1_at	<b>FBXO9</b>	F-box protein 9	1.1	0.001
Ssc.2719.1.A1_at	<b>MTA1</b>	metastasis associated 1	1.1	0.050
Ssc.30612.1.S1_at	<b>AP1G2</b>	adaptor-related protein complex 1, gamma 2 subunit	1.1	0.006
Ssc.1537.1.S2_at	<b>YKT6</b>	YKT6 v-SNARE homolog ( <i>S. cerevisiae</i> )	1.1	0.006
Ssc.27454.1.S1_at	<b>ATIC</b>	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase	1.1	0.030
Ssc.4094.1.S1_at	<b>MRPL55</b>	mitochondrial ribosomal protein L55	1.1	0.039
Ssc.1080.1.A1_at	<b>RTN3</b>	reticulon 3	1.1	0.048
Ssc.25198.1.A1_at	<b>OAT</b>	ornithine aminotransferase (gyrate atrophy)	1.1	0.053
Ssc.25077.1.S1_at	<b>SLC20A2</b>	solute carrier family 20 (phosphate transporter), member 2	1.1	0.044
Ssc.11103.1.S1_at	<b>MDH1</b>	malate dehydrogenase 1, NAD (soluble)	1.1	0.039
Ssc.21861.1.S1_at	<b>PYCR1</b>	pyrroline-5-carboxylate reductase-like	1.1	0.043
Ssc.22511.1.S1_at	<b>C3ORF1</b>	chromosome 3 open reading frame 1	1.1	0.049
Ssc.8512.1.S1_a_at	<b>METTL3</b>	methyltransferase like 3	1.1	0.003
Ssc.27457.1.A1_at	<b>SFRS7</b>	splicing factor, arginine/serine-rich 7, 35kDa	1.1	0.042

Supplementary Table 2 continued

<b>Probe_Set_ID</b>	<b>Annotation</b>	<b>Gene_description</b>	<b>FC (H/L)</b>	<b>p-value</b>
Ssc.27928.1.S1_at	<b>OGFR</b>	opioid growth factor receptor	1.1	0.028
Ssc.9655.1.A1_at	<b>LOC440359</b>	misc_RNA LOC440359	1.1	0.035
Ssc.18045.1.S1_a_at	<b>GPR89C</b>	G protein-coupled receptor 89C	1.1	0.023
Ssc.17546.1.A1_at	<b>TTC13</b>	tetratricopeptide repeat domain 13	1.1	0.023
Ssc.5389.1.S1_at	<b>IDH3A</b>	isocitrate dehydrogenase 3 (NAD+) alpha	1.1	0.001
Ssc.25651.1.S1_at	unknown		1.1	0.031
Ssc.30862.1.S1_at	<b>DNAJB9</b>	DnaJ homolog subfamily B member 9	1.1	0.014
Ssc.8483.1.A1_at	<b>IARS</b>	Isoleucyl-tRNA synthetase, cytoplasmic	1.1	0.012
Ssc.12439.1.A1_at	<b>PLA2G16</b>	phospholipase A2, group XVI	1.1	0.028
Ssc.5102.1.S1_at	<b>MRPS27</b>	mitochondrial ribosomal protein S27	1.1	0.032
Ssc.18110.1.A1_at	<b>TUBGCP4</b>	tubulin, gamma complex associated protein 4	1.1	0.053
Ssc.3178.1.S1_at	<b>CCT5</b>	chaperonin containing TCP1, subunit 5 (epsilon)	1.1	0.026
Ssc.15672.1.S1_at	<b>RRAS</b>	related RAS viral (r-ras) oncogene homolog	1.1	0.042
Ssc.5315.1.S1_at	<b>COX6B2</b>	cytochrome c oxidase subunit VIb polypeptide 2 (testis)	1.1	0.014
Ssc.5886.1.S1_at	<b>MRPS17</b>	mitochondrial ribosomal protein S17	1.1	0.054
Ssc.30927.1.A1_at	<b>RSU1</b>	Ras suppressor protein 1	1.1	0.030
Ssc.3286.2.S1_at	<b>MTPN</b>	myotrophin	1.1	0.042
Ssc.17842.2.S1_a_at	<b>STX8</b>	syntaxin 8	1.1	0.030
Ssc.22034.1.S1_at	<b>EIF4A1</b>	eukaryotic translation initiation factor 4A, isoform 1	1.1	0.025
Ssc.2373.1.A1_at	<b>LOC100156038</b>	similar to methylosome protein 50	1.1	0.030
Ssc.1413.1.S1_at	<b>FAM49B</b>	Protein FAM49B	1.1	0.034
Ssc.8970.1.S2_at	<b>Q29305</b>	Disulfide isomerase related protein (ERP72) Fragment	1.1	0.042
Ssc.4158.1.S1_at	<b>HPRT1</b>	hypoxanthine phosphoribosyltransferase 1	1.1	0.049
Ssc.24195.1.A1_at	<b>ARHGAP19</b>	Rho GTPase activating protein 19	1.1	0.045
Ssc.22027.2.A1_at	<b>SRPRB</b>	signal recognition particle receptor, B subunit	1.1	0.007
Ssc.7927.1.S1_at	<b>2500003M10RIK</b>	Mus musculus RIKEN cDNA 2500003M10 gene	1.1	0.011
Ssc.16835.1.S1_at	<b>COPS6</b>	COP9 constitutive photomorphogenic homolog subunit 6 (Arabidopsis)	1.1	0.013
Ssc.10592.1.A1_at	<b>DGUOK</b>	deoxyguanosine kinase	1.1	0.042
Ssc.11719.1.A1_at	<b>BAT1</b>	HLA-B associated transcript 1	1.1	0.054
Ssc.21027.2.A1_a_at	<b>BNIP3L</b>	BCL2/adenovirus E1B 19kDa interacting protein 3-like	1.1	0.003
Ssc.3447.1.S1_at	<b>ULK3</b>	unc-51-like kinase 3 ( <i>C. elegans</i> )	1.1	0.049
Ssc.1549.1.A1_at	<b>STIP1</b>	stress-induced-phosphoprotein 1	1.1	0.032
Ssc.122.1.S1_at	<b>DGKA</b>	diacylglycerol kinase, alpha 80kDa	1.1	0.011
Ssc.3664.1.S1_at	<b>EIF2B5</b>	eukaryotic translation initiation factor 2B, subunit 5 epsilon, 82kDa	1.1	0.035

Supplementary Table 2 continued

<b>Probe Set ID</b>	<b>Annotation</b>	<b>Gene description</b>	<b>FC (H/L)</b>	<b>p-value</b>
Ssc.1005.2.S1_at	<b>MRLC2</b>	myosin regulatory light chain	1.1	0.037
Ssc.30778.1.S1_at	<b>YIF1B</b>	Yip1 interacting factor homolog B ( <i>S. cerevisiae</i> )	1.1	0.018
Ssc.1226.1.S1_at	<b>SNUPN</b>	snurportin 1	1.1	0.039
Ssc.1067.1.S1_at	<b>PSMB2</b>	proteasome (prosome, macropain) subunit, beta type, 2	1.1	0.017
Ssc.11169.1.A1_at	<b>LOC100157270</b>	similar to WD repeat domain 23, transcript variant 1	1.1	0.045
Ssc.23545.2.A1_at	<b>PIP5K1A</b>	phosphatidylinositol-4-phosphate 5-kinase, type I, alpha	1.1	0.043
Ssc.29109.1.A1_at	<b>WIBG</b>	within bgcn homolog ( <i>Drosophila</i> )	1.1	0.013
Ssc.19541.1.A1_at	unknown		1.1	0.037
Ssc.21644.1.S1_at	<b>STT3A</b>	STT3, subunit of the oligosaccharyltransferase complex, homolog A ( <i>S. cerevisiae</i> )	1.1	0.006
Ssc.19613.2.S1_at	<b>ARMC6</b>	armadillo repeat containing 6	1.1	0.054
Ssc.19212.1.S1_at	<b>SLC25A20</b>	solute carrier family 25 (carnitine/acylcarnitine translocase), member 20	1.1	0.051
Ssc.3129.1.A1_at	<b>HMGN3</b>	high mobility group nucleosomal binding domain 3	1.1	0.040
Ssc.856.1.S1_at	<b>VCP</b>	valosin-containing protein	1.1	0.000
Ssc.1639.3.S1_a_at	<b>GALT</b>	galactose-1-phosphate uridylyltransferase	1.1	0.054
Ssc.30995.1.A1_at	unknown		1.1	0.002
Ssc.10766.1.A1_at	<b>RNF135</b>	ring finger protein 135	1.1	0.043
Ssc.7444.1.A1_at	<b>CREM</b>	cAMP responsive element modulator	1.1	0.024
Ssc.7483.1.A1_at	<b>LOC100155503</b>	similar to rCG62611	1.1	0.036
Ssc.14201.1.S1_at	<b>RAB14</b>	RAB14, member RAS oncogene family	1.1	0.033
Ssc.6193.1.A1_at	<b>RAB24</b>	RAB24, member RAS oncogene family	1.1	0.033
Ssc.5797.1.A1_at	<b>CECR5</b>	cat eye syndrome chromosome region, candidate 5	1.1	0.047
Ssc.9477.1.A1_at	<b>CTNND1</b>	catenin (cadherin-associated protein), delta 1	1.1	0.031
Ssc.3954.1.A1_at	<b>COPG</b>	coatomer protein complex, subunit gamma	1.1	0.024
Ssc.183.1.S1_at	<b>GSTO1</b>	Glutathione S-transferase omega-1	1.1	0.023
Ssc.5355.1.S1_at	<b>H2AFY</b>	H2A histone family, member Y	1.1	0.022
Ssc.2456.1.S1_at	<b>YWHAQ</b>	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	1.1	0.020
Ssc.2957.1.S1_at	<b>ATP5L</b>	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit G	1.1	0.035
Ssc.6696.1.A1_at	<b>TXN</b>	thioredoxin	1.1	0.014
Ssc.13371.1.S1_at	<b>P3</b>	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C3 (subunit 9)	1.1	0.043
Ssc.19975.1.S1_at	<b>PTGES3</b>	prostaglandin E synthase 3 (cytosolic)	1.1	0.045
Ssc.4235.1.S1_at	<b>PSMD4</b>	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4	1.1	0.040
Ssc.16756.1.S1_at	<b>HLA-A</b>	major histocompatibility complex, class I, A	1.1	0.038
Ssc.7608.1.A1_at	<b>ARL8B</b>	ADP-ribosylation factor-like 8B	1.0	0.049
Ssc.11132.1.S1_a_at	<b>RPS18</b>	ribosomal protein S18	1.0	0.038

Supplementary Table 2 continued

<b>Probe Set ID</b>	<b>Annotation</b>	<b>Gene description</b>	<b>FC (H/L)</b>	<b>p-value</b>
Ssc.6675.1.S1_a_at	<b>GNAS</b>	GNAS complex locus	-1.1	0.008
Ssc.6868.1.A1_at	<b>COX7A2L</b>	cytochrome c oxidase subunit VIIa polypeptide 2 like	-1.1	0.050
Ssc.11159.1.A2_at	<b>CSNK1A1</b>	casein kinase 1, alpha 1	-1.1	0.029
Ssc.19910.1.S1_at	<b>RPS24</b>	ribosomal protein S24	-1.1	0.035
Ssc.5142.1.S1_at	<b>ENPP2</b>	ectonucleotide pyrophosphatase/phosphodiesterase 2	-1.1	0.036
Ssc.8312.1.A1_at	<b>CDYL</b>	chromodomain protein, Y-like	-1.1	0.014
Ssc.3684.1.S1_at	<b>ZC3H7B</b>	zinc finger CCCH-type containing 7B	-1.1	0.044
Ssc.29480.1.A1_at	unknown		-1.1	0.049
Ssc.14051.1.S1_at	<b>DNAJA2</b>	DnaJ (Hsp40) homolog, subfamily A, member 2	-1.1	0.043
Ssc.4144.1.A1_at	<b>LOC666726</b>	Mus musculus similar to 4932441K18Rik protein	-1.1	0.029
Ssc.13158.1.A1_at	<b>UBR5</b>	ubiquitin protein ligase E3 component n-recogin 5	-1.1	0.037
Ssc.21474.1.S1_at	<b>BAZ1B</b>	bromodomain adjacent to zinc finger domain, 1B	-1.1	0.023
Ssc.2417.1.S1_at	<b>DENND1A</b>	DENN/MADD domain containing 1A	-1.1	0.050
Ssc.6364.1.S1_at	<b>DDX20</b>	DEAD (Asp-Glu-Ala-Asp) box polypeptide 20	-1.1	0.021
Ssc.11757.1.S1_at	<b>SMAD1</b>	SMAD family member 1	-1.1	0.017
Ssc.5506.1.A1_at	<b>FAM168B</b>	family with sequence similarity 168, member B	-1.1	0.028
Ssc.26261.1.A1_at	<b>SON</b>	SON DNA binding protein	-1.1	0.019
Ssc.10324.1.A1_at	<b>RAB14</b>	RAB14, member RAS oncogene family	-1.1	0.028
Ssc.13939.1.A1_at	<b>FAM164C</b>	family with sequence similarity 164, member C	-1.1	0.005
Ssc.2374.1.A1_at	<b>STAU1</b>	staufer, RNA binding protein, homolog 1 (Drosophila)	-1.1	0.003
Ssc.7358.1.A1_at	<b>CNOT2</b>	CCR4-NOT transcription complex, subunit 2	-1.1	0.052
Ssc.26090.1.A1_at	<b>CAPRIN1</b>	cell cycle associated protein 1	-1.1	0.047
Ssc.3236.1.A1_at	<b>RRP15</b>	ribosomal RNA processing 15 homolog ( <i>S. cerevisiae</i> )	-1.1	0.045
Ssc.11420.1.A1_at	<b>PARP16</b>	poly (ADP-ribose) polymerase family, member 16	-1.1	0.036
Ssc.6470.1.A1_at	<b>GLO1</b>	glyoxalase I	-1.1	0.051
Ssc.20400.1.S1_at	<b>CTBP2</b>	C-terminal binding protein 2	-1.1	0.032
Ssc.10483.1.S1_at	<b>SAFB2</b>	scaffold attachment factor B2	-1.1	0.048
Ssc.9245.1.S1_at	<b>GALM</b>	Aldose 1-epimerase	-1.1	0.023
Ssc.1414.1.A1_a_at	<b>NCOA1</b>	nuclear receptor coactivator 1	-1.1	0.035
Ssc.10865.1.A1_at	<b>NVL</b>	nuclear VCP-like	-1.1	0.045
Ssc.9084.1.S1_at	<b>SCOX</b>	acyl-Coenzyme A oxidase 1, palmitoyl	-1.1	0.032
Ssc.16539.1.S1_at	<b>ANKRD13A</b>	ankyrin repeat domain 13A	-1.1	0.043
Ssc.8415.1.A1_at	<b>BACE1</b>	beta-site APP-cleaving enzyme 1	-1.1	0.013
Ssc.21913.1.S1_at	<b>LOC100153912</b>	similar to single-strand selective monofunctional uracil DNA glycosylase	-1.1	0.031

Supplementary Table 2 continued

<b>Probe Set ID</b>	<b>Annotation</b>	<b>Gene description</b>	<b>FC (H/L)</b>	<b>p-value</b>
Ssc.26919.1.S1_at	<b>DDX6</b>	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6	-1.1	0.006
Ssc.26076.1.S1_at	<b>TBL1X</b>	transducin (beta)-like 1X-linked	-1.1	0.034
Ssc.20300.1.S1_at	<b>KIAA0323</b>	KIAA0323	-1.1	0.053
Ssc.1082.1.S1_at	<b>TIMP2</b>	TIMP metalloproteinase inhibitor 2	-1.1	0.041
Ssc.2425.1.S1_at	<b>TJP1</b>	tight junction protein 1 (zona occludens 1)	-1.1	0.042
Ssc.231.1.S2_at	<b>FDX1</b>	ferredoxin 1	-1.1	0.041
Ssc.1106.1.S1_at	<b>UPF1</b>	UPF1 regulator of nonsense transcripts homolog (yeast)	-1.1	0.017
Ssc.26147.1.S1_at	<b>SORT1</b>	sortilin 1	-1.1	0.023
Ssc.19324.1.A1_at	<b>ZNF846</b>	zinc finger protein 846	-1.1	0.052
Ssc.20531.1.S1_at	<b>FOXO3</b>	forkhead box O3	-1.1	0.035
Ssc.153.1.S1_at	<b>DPYD</b>	dihydropyrimidine dehydrogenase	-1.1	0.048
Ssc.20199.1.S1_at	<b>HIVEP2</b>	human immunodeficiency virus type I enhancer binding protein 2	-1.1	0.017
Ssc.22091.1.A1_at	<b>ADNP2</b>	ADNP homeobox 2	-1.1	0.005
Ssc.6754.1.A1_at	<b>ST13</b>	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein)	-1.1	0.045
Ssc.5330.1.A1_at	<b>TGFBR2</b>	transforming growth factor, beta receptor II (70/80kDa)	-1.1	0.045
Ssc.2407.1.S1_at	<b>G3BP2</b>	GTPase activating protein (SH3 domain) binding protein 2	-1.1	0.014
Ssc.5032.1.S1_at	<b>MPHOSPH8</b>	M-phase phosphoprotein 8 (Two hybrid-associated protein 3 with RanBPM)	-1.1	0.045
Ssc.1647.1.S1_at	<b>1500035H01RIK</b>	Mus musculus RIKEN cDNA 1500035H01 gene	-1.1	0.030
Ssc.22553.2.A1_at	unknown		-1.1	0.044
Ssc.29040.2.S1_at	<b>HMBOX1</b>	homeobox containing 1	-1.1	0.032
Ssc.25638.1.S1_at	<b>UBE4A</b>	ubiquitination factor E4A (UFD2 homolog, yeast)	-1.1	0.029
Ssc.8329.2.A1_at	<b>UBE4A</b>	ubiquitination factor E4A (UFD2 homolog, yeast)	-1.1	0.054
Ssc.26083.1.S1_at	<b>BAZ1B</b>	bromodomain adjacent to zinc finger domain, 1B	-1.1	0.016
Ssc.22089.2.S1_at	<b>TAF1B</b>	TATA box binding protein (TBP)-associated factor, RNA polymerase I, B, 63kDa	-1.1	0.024
Ssc.10583.1.A1_at	<b>BA462D18.2</b>	destrin (actin depolymerizing factor)	-1.1	0.051
Ssc.11177.1.S1_at	<b>TET3</b>	tet oncogene family member 3	-1.1	0.030
Ssc.5709.1.S1_at	<b>IPO11</b>	importin 11	-1.1	0.040
Ssc.28928.1.A1_at	<b>ANP32B</b>	acidic (leucine-rich) nuclear phosphoprotein 32 family, member B	-1.1	0.052
Ssc.1339.1.A1_at	<b>SMARCA2</b>	SWI/SNF related, matrix associated, actin dependent regulator of chromatin subfamily a, member 2	-1.1	0.049
Ssc.9202.1.A1_at	<b>IQWD1</b>	IQ motif and WD repeats 1	-1.1	0.047
Ssc.7712.3.S1_at	<b>TACC1</b>	transforming, acidic coiled-coil containing protein 1	-1.1	0.031
Ssc.16046.1.S1_s_at	<b>SPTBN1</b>	spectrin, beta, non-erythrocytic 1	-1.1	0.016
Ssc.3568.1.S1_at	<b>ZBTB4</b>	zinc finger and BTB domain containing 4	-1.1	0.019



Supplementary Table 2 continued

<b>Probe_Set_ID</b>	<b>Annotation</b>	<b>Gene_description</b>	<b>FC (H/L)</b>	<b>p-value</b>
Ssc.24537.1.A1_at	unknown		-1.1	0.009
Ssc.8430.1.A1_at	<b>ANKRD46</b>	ankyrin repeat domain 46	-1.1	0.046
Ssc.5907.1.S1_at	<b>CUL1</b>	cullin 1	-1.1	0.043
Ssc.2820.1.A1_at	<b>RAB6B</b>	RAB6A, member RAS oncogene family	-1.1	0.021
Ssc.20175.1.S1_at	<b>IGF1R</b>	insulin-like growth factor 1 receptor	-1.1	0.018
Ssc.28049.1.A1_at	<b>LOC100156219</b>	similar to cutA divalent cation tolerance homolog	-1.1	0.021
Ssc.22344.1.A1_at	<b>TNKS2</b>	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2	-1.1	0.038
Ssc.27969.1.A1_at	<b>PHF20L1</b>	PHD finger protein 20-like 1	-1.1	0.040
Ssc.26309.1.A1_at	<b>FOXN3</b>	forkhead box N3	-1.1	0.050
Ssc.25709.1.A1_at	<b>FAM105B</b>	family with sequence similarity 105, member B	-1.1	0.036
Ssc.19103.1.A1_at	<b>BRWD1</b>	bromodomain and WD repeat domain containing 1	-1.1	0.038
Ssc.12899.1.S1_at	<b>SERP1</b>	stress-associated endoplasmic reticulum protein 1	-1.1	0.044
Ssc.1969.1.A1_at	<b>TSC22D1</b>	TSC22 domain family, member 1	-1.1	0.023
Ssc.8455.1.A1_at	unknown		-1.1	0.033
Ssc.10953.1.A1_at	<b>NDUFS1</b>	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)	-1.1	0.009
Ssc.29447.1.A1_at	<b>CCDC6</b>	coiled-coil domain containing 6	-1.1	0.043
Ssc.31074.2.S1_at	<b>LOC728732</b>	misc_RNA LOC728732	-1.1	0.030
Ssc.18323.2.S1_at	<b>EIF4B</b>	eukaryotic translation initiation factor 4B	-1.1	0.029
Ssc.7572.1.A1_at	<b>ACADSB</b>	acyl-Coenzyme A dehydrogenase, short/branched chain	-1.1	0.024
Ssc.5769.1.S1_at	<b>RASSF3</b>	Ras association (RalGDS/AF-6) domain family member 3	-1.1	0.021
Ssc.4842.1.S1_at	<b>HCN4</b>	hyperpolarization activated cyclic nucleotide-gated potassium channel 4	-1.1	0.023
Ssc.3364.1.A1_at	<b>PUM1</b>	pumilio homolog 1 (Drosophila)	-1.1	0.002
Ssc.7235.1.A1_at	<b>UBE2H</b>	ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)	-1.1	0.014
Ssc.30704.1.S1_at	<b>TSHZ1</b>	teashirt zinc finger homeobox 1	-1.1	0.006
Ssc.2878.1.A1_at	<b>PAK2</b>	p21 protein (Cdc42/Rac)-activated kinase 2	-1.1	0.045
Ssc.23048.1.S1_at	unknown		-1.1	0.040
Ssc.20251.1.S1_at	<b>TSPAN3</b>	tetraspanin 3	-1.1	0.040
Ssc.11516.1.S1_at	<b>CALM1</b>	calmodulin 1 (phosphorylase kinase, delta)	-1.1	0.039
Ssc.16686.1.A1_at	<b>FAM48A</b>	family with sequence similarity 48, member A	-1.1	0.051
Ssc.10326.1.A1_at	unknown		-1.1	0.034
Ssc.2111.1.S1_at	<b>AFTPH</b>	aftiphilin	-1.1	0.049
Ssc.7769.2.S1_at	<b>LPGAT1</b>	lysophosphatidylglycerol acyltransferase 1	-1.1	0.047
Ssc.16961.1.A1_at	<b>SENP5</b>	SUMO1/sentrin specific peptidase 5	-1.1	0.015
Ssc.2647.1.S1_at	<b>ADIPOR2</b>	adiponectin receptor 2	-1.1	0.041

Supplementary Table 2 continued

<b>Probe Set ID</b>	<b>Annotation</b>	<b>Gene description</b>	<b>FC (H/L)</b>	<b>p-value</b>
Ssc.12255.1.A1_at	<b>VEZF1</b>	vascular endothelial zinc finger 1	-1.1	0.023
Ssc.1827.1.S1_at	<b>INTS6</b>	integrator complex subunit 6	-1.1	0.047
Ssc.16429.1.A1_at	<b>CCNI</b>	Cyclin-I	-1.1	0.020
Ssc.29080.1.A1_at	<b>ST8SIA2</b>	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 2	-1.1	0.033
Ssc.16444.1.S1_at	<b>PTPRK</b>	tyrosine phosphatase, receptor type, K	-1.1	0.016
Ssc.18411.1.A1_at	<b>CHD2</b>	chromodomain helicase DNA binding protein 2	-1.1	0.044
Ssc.2886.1.S1_at	<b>UTP14C</b>	UTP14, U3 small nucleolar ribonucleoprotein, homolog C (yeast)	-1.1	0.026
Ssc.6363.1.A1_at	<b>DAAM1</b>	dishevelled associated activator of morphogenesis 1	-1.1	0.036
Ssc.7770.1.A1_at	<b>TARDBP</b>	TAR DNA binding protein	-1.1	0.045
Ssc.24383.1.S1_at	<b>FOXO1</b>	forkhead box O1	-1.1	0.032
Ssc.25093.1.S1_at	<b>HMGXB4</b>	HMG box domain containing 4	-1.1	0.005
Ssc.11832.1.S1_at	<b>RNMT</b>	RNA (guanine-7-) methyltransferase	-1.1	0.026
Ssc.7099.2.A1_a_at	<b>RFK</b>	riboflavin kinase	-1.1	0.035
Ssc.20714.1.S1_at	<b>CNOT6LP1</b>	CCR4-NOT transcription complex, subunit 6-like pseudogene 1	-1.1	0.048
Ssc.11316.1.A1_at	unknown		-1.1	0.004
Ssc.1294.1.S1_at	<b>DEDD</b>	death effector domain containing	-1.1	0.042
Ssc.9792.1.S1_at	<b>FAM160B1</b>	family with sequence similarity 160, member B1	-1.1	0.045
Ssc.14267.1.A1_at	<b>LOC727732</b>	hypothetical LOC727732	-1.1	0.003
Ssc.4900.2.S1_at	<b>CRIM1</b>	cysteine rich transmembrane BMP regulator 1 (chordin-like)	-1.1	0.032
Ssc.1876.1.S1_at	<b>MYH10</b>	myosin, heavy chain 10, non-muscle	-1.1	0.013
Ssc.27267.1.A1_at	<b>DDHD2</b>	DDHD domain containing 2	-1.1	0.017
Ssc.2807.1.A1_at	<b>DAB2</b>	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	-1.1	0.021
Ssc.23549.1.A1_at	<b>CYORF15B</b>	chromosome Y open reading frame 15B	-1.1	0.008
Ssc.25655.1.S1_at	<b>DEFB133</b>	defensin, beta 133	-1.1	0.048
Ssc.25257.1.S1_at	<b>ARGLU1</b>	arginine and glutamate rich 1	-1.1	0.041
Ssc.19273.3.S1_at	<b>JARID1A</b>	jumonji, AT rich interactive domain 1A	-1.1	0.019
Ssc.4641.1.A1_at	<b>LOC100044756</b>	similar to PX domain-containing protein kinase-like protein	-1.1	0.044
Ssc.27572.1.S1_at	<b>MCCC2</b>	methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	-1.1	0.042
Ssc.1796.1.A1_at	<b>DDHD2</b>	DDHD domain containing 2	-1.1	0.025
Ssc.25107.1.S1_at	<b>BAT2D1</b>	BAT2 domain containing 1	-1.1	0.035
Ssc.6461.1.A1_at	<b>ACER2</b>	alkaline ceramidase 2	-1.1	0.054
Ssc.8143.1.A1_at	<b>RAPGEF2</b>	Rap guanine nucleotide exchange factor (GEF) 2	-1.1	0.004
Ssc.20986.1.S1_at	<b>FKBP14</b>	FK506 binding protein 14, 22 kDa	-1.1	0.047
Ssc.28076.1.A1_at	<b>DNMT1</b>	DNA (cytosine-5-)-methyltransferase 1	-1.1	0.027

Supplementary Table 2 continued

<b>Probe_Set_ID</b>	<b>Annotation</b>	<b>Gene_description</b>	<b>FC (HL)</b>	<b>p-value</b>
Ssc.23006.1.S1_at	<b>NUCKS1</b>	nuclear casein kinase and cyclin-dependent kinase substrate 1	-1.1	0.020
Ssc.17507.1.S1_at	<b>TNRC6C</b>	trinucleotide repeat containing 6C	-1.1	0.011
Ssc.14094.1.A1_at	<b>SAR1B</b>	SAR1 homolog B ( <i>S. cerevisiae</i> )	-1.1	0.023
Ssc.9572.1.A1_at	<b>MYO10</b>	myosin X	-1.1	0.012
Ssc.23791.1.A1_at	<b>ARNT</b>	aryl hydrocarbon receptor nuclear translocator	-1.1	0.038
Ssc.18929.1.S1_s_at	<b>RNF128</b>	ring finger protein 128	-1.1	0.051
Ssc.18220.3.A1_at	<b>CDC37L1</b>	cell division cycle 37 homolog ( <i>S. cerevisiae</i> )-like 1	-1.1	0.050
Ssc.3813.1.S1_at	<b>OSBP</b>	oxysterol binding protein	-1.1	0.013
Ssc.6425.3.A1_at	<b>ABCC5</b>	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	-1.1	0.049
Ssc.11618.2.S1_at	<b>ITM2A</b>	integral membrane protein 2A	-1.1	0.033
Ssc.12761.1.A1_at	<b>KIAA1671</b>	Uncharacterized protein KIAA1671	-1.1	0.050
Ssc.17838.1.A1_at	unknown		-1.1	0.040
Ssc.6872.1.S1_at	<b>UBL3</b>	ubiquitin-like 3	-1.1	0.052
Ssc.25326.1.S1_at	unknown		-1.1	0.012
Ssc.1295.1.A1_at	<b>SETX</b>	senataxin	-1.1	0.054
Ssc.18178.2.S1_at	<b>ITPRIP</b>	inositol 1,4,5-triphosphate receptor interacting protein	-1.1	0.017
Ssc.7222.1.S1_at	<b>SERINC3</b>	serine incorporator 3	-1.1	0.049
Ssc.27613.1.S1_at	<b>OPTN</b>	optineurin	-1.1	0.050
Ssc.19076.1.S1_at	unknown		-1.1	0.046
Ssc.30904.1.S1_at	<b>ZKSCAN1</b>	zinc finger with KRAB and SCAN domains 1	-1.1	0.003
Ssc.20570.1.S1_at	<b>ACAD11</b>	acyl-Coenzyme A dehydrogenase family, member 11	-1.1	0.010
Ssc.9714.1.S1_at	<b>LMO4</b>	LIM domain only 4	-1.2	0.054
Ssc.13713.1.A1_at	<b>ASH1L</b>	ash1 (absent, small, or homeotic)-like ( <i>Drosophila</i> )	-1.2	0.051
Ssc.11404.1.A1_at	<b>ATXN1</b>	ataxin 1	-1.2	0.022
Ssc.29640.1.A1_at	<b>RBM39</b>	RNA binding motif protein 39	-1.2	0.047
Ssc.3070.3.S1_at	<b>GAPVD1</b>	GTPase activating protein and VPS9 domains 1	-1.2	0.046
Ssc.19579.2.S1_at	<b>B5A7P0</b>	Orphan nuclear receptor COUP-TFII	-1.2	0.019
Ssc.19342.1.A1_at	<b>RNF145</b>	ring finger protein 145	-1.2	0.010
Ssc.10185.1.S1_at	<b>RSF1</b>	remodeling and spacing factor 1	-1.2	0.023
Ssc.26701.2.A1_at	<b>ZCCHC8</b>	zinc finger, CCHC domain containing 8	-1.2	0.003
Ssc.8647.1.A1_at	<b>LONRF3</b>	LON peptidase N-terminal domain and ring finger 3	-1.2	0.043
Ssc.27050.1.A1_at	<b>NVL</b>	nuclear VCP-like	-1.2	0.001
Ssc.16504.1.S1_at	<b>CXORF42</b>	misc_RNA CXorf42	-1.2	0.021
Ssc.5729.2.S1_at	<b>PHKA2</b>	phosphorylase kinase, alpha 2 (liver)	-1.2	0.025

Supplementary Table 2 continued

<b>Probe Set ID</b>	<b>Annotation</b>	<b>Gene description</b>	<b>FC (HL)</b>	<b>p-value</b>
Ssc.2877.1.A1_at	<b>ANP32A</b>	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	-1.2	0.001
Ssc.19311.1.A1_at	<b>KLF13</b>	Kruppel-like factor 13	-1.2	0.029
Ssc.10110.1.A1_at	<b>MEIS2</b>	Meis homeobox 2	-1.2	0.027
Ssc.22369.1.A1_at	<b>NR3C1</b>	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)	-1.2	0.029
Ssc.3364.2.S1_at	<b>PUM1</b>	pumilio homolog 1 (Drosophila)	-1.2	0.028
Ssc.16940.1.A1_at	<b>KAT2B</b>	K(lysine) acetyltransferase 2B	-1.2	0.052
Ssc.3791.1.S1_at	<b>CTSF</b>	cathepsin F	-1.2	0.031
Ssc.16966.1.S1_at	<b>DTX4</b>	deltex 4 homolog (Drosophila)	-1.2	0.051
Ssc.22181.1.S1_at	<b>CTR9</b>	Ctr9, Paf1/RNA polymerase II complex component, homolog ( <i>S. cerevisiae</i> )	-1.2	0.031
Ssc.18120.2.S1_at	<b>RAD18</b>	RAD18 homolog ( <i>S. cerevisiae</i> )	-1.2	0.050
Ssc.21951.1.S1_at	<b>WASL</b>	Wiskott-Aldrich syndrome-like	-1.2	0.001
Ssc.9941.1.A1_at	unknown		-1.2	0.010
Ssc.18546.1.S1_at	<b>CRIM1</b>	cysteine rich transmembrane BMP regulator 1 (chordin-like)	-1.2	0.025
Ssc.10308.1.A1_at	<b>PCMTD1</b>	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	-1.2	0.033
Ssc.2898.1.S1_at	<b>MTRR</b>	5-methyltetrahydrofolate-homocysteine methyltransferase reductase	-1.2	0.038
Ssc.14249.1.A1_at	<b>LOC653753</b>	misc_RNA LOC653753	-1.2	0.028
Ssc.17091.1.A1_at	unknown		-1.2	0.040
Ssc.7572.2.S1_at	<b>ACADSB</b>	acyl-Coenzyme A dehydrogenase, short/branched chain	-1.2	0.048
Ssc.23768.1.S1_at	<b>RTF1</b>	Rtf1, Paf1/RNA polymerase II complex component, homolog ( <i>S. cerevisiae</i> )	-1.2	0.012
Ssc.22944.1.S1_at	<b>LOC729920</b>	notch1-induced protein	-1.2	0.014
Ssc.494.1.S1_at	<b>TMEM56</b>	transmembrane protein 56	-1.2	0.047
Ssc.7597.1.S1_at	<b>FAM179B</b>	family with sequence similarity 179, member B	-1.2	0.024
Ssc.7980.1.A1_at	<b>ZNF22</b>	zinc finger protein 22 (KOX 15)	-1.2	0.042
Ssc.2558.1.S1_at	<b>DCI</b>	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)	-1.2	0.043
Ssc.24140.1.S1_at	<b>ZC3H13</b>	zinc finger CCCH-type containing 13	-1.2	0.052
Ssc.29807.1.A1_at	<b>TLE2</b>	transducin-like enhancer of split 2 (E(sp1) homolog, Drosophila)	-1.2	0.050
Ssc.20236.1.A1_at	unknown		-1.2	0.045
Ssc.25863.1.S1_at	<b>ME3</b>	malic enzyme 3, NADP(+)-dependent, mitochondrial	-1.2	0.023
Ssc.4942.2.S1_at	<b>LOC100293849</b>	hypothetical protein LOC100293849	-1.2	0.018
Ssc.4348.2.S1_at	<b>MFAP1</b>	microfibrillar-associated protein 1	-1.2	0.033
Ssc.8270.1.S1_at	<b>CEP57</b>	centrosomal protein 57kDa	-1.2	0.044
Ssc.15800.1.S1_at	<b>IGFBP5</b>	insulin-like growth factor binding protein 5	-1.2	0.050
Ssc.17359.1.S1_at	<b>MED4</b>	Mediator of RNA polymerase II transcription subunit 4	-1.2	0.037
Ssc.5001.2.A1_at	<b>SNX29</b>	sorting nexin 29	-1.2	0.029

Supplementary Table 2 continued

<b>Probe Set ID</b>	<b>Annotation</b>	<b>Gene description</b>	<b>FC (H/L)</b>	<b>p-value</b>
Ssc.18497.1.S1_at	<b>NEIL1</b>	nei endonuclease VIII-like 1 ( <i>E. coli</i> )	-1.2	0.033
Ssc.30607.1.A1_at	<b>CALM1</b>	calmodulin 1 (phosphorylase kinase, delta)	-1.2	0.003
Ssc.486.1.A1_at	<b>LOC100154615</b>	similar to AP-4 complex subunit sigma-1	-1.2	0.044
Ssc.11082.1.A1_at	<b>WDR26</b>	WD repeat domain 26	-1.2	0.051
Ssc.30704.3.A1_at	<b>TSHZ1</b>	teashirt zinc finger homeobox 1	-1.2	0.008
Ssc.25097.1.S1_at	<b>CTCF</b>	CCCTC-binding factor (zinc finger protein)	-1.2	0.006
Ssc.27478.1.A1_at	<b>RECQL</b>	RecQ protein-like (DNA helicase Q1-like)	-1.2	0.013
Ssc.30970.1.S1_at	<b>KIAA1009</b>	KIAA1009	-1.2	0.003
Ssc.9246.1.S1_a_at	<b>SCYE1</b>	small inducible cytokine subfamily E, member 1 (endothelial monocyte-activating)	-1.2	0.015
Ssc.25894.1.S1_at	<b>ASH1L</b>	ash1 (absent, small, or homeotic)-like ( <i>Drosophila</i> )	-1.2	0.053
Ssc.3599.1.S1_at	<b>ZFP91</b>	zinc finger protein 91	-1.2	0.032
Ssc.2026.1.S1_at	<b>CSDE1</b>	cold shock domain containing E1, RNA-binding	-1.2	0.051
Ssc.75.2.S1_a_at	<b>CDH5</b>	cadherin 5, type 2 (vascular endothelium)	-1.2	0.037
Ssc.26236.1.S1_at	<b>LIN7C</b>	lin-7 homolog C ( <i>C. elegans</i> )	-1.2	0.002
Ssc.26415.1.A1_at	<b>ING3</b>	inhibitor of growth family, member 3	-1.2	0.048
Ssc.8346.1.A1_at	unknown		-1.2	0.016
Ssc.8000.1.A1_at	<b>OGT</b>	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)	-1.2	0.049
Ssc.27250.1.S1_at	<b>EXOSC7</b>	exosome component 7	-1.2	0.030
Ssc.26737.1.S1_at	unknown		-1.2	0.044
Ssc.17766.1.A1_at	<b>ENAH</b>	enabled homolog ( <i>Drosophila</i> )	-1.2	0.046
Ssc.12453.1.S1_a_at	<b>SFRS18</b>	splicing factor, arginine/serine-rich 18	-1.2	0.048
Ssc.10575.1.A1_at	unknown		-1.2	0.016
Ssc.7037.2.A1_at	<b>ZNF709</b>	zinc finger protein 709	-1.2	0.034
Ssc.14189.1.A1_at	<b>LOC100153420</b>	hypothetical protein LOC100153420	-1.2	0.038
Ssc.6737.1.S1_at	<b>ITGAV</b>	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)	-1.2	0.030
Ssc.18803.1.S1_at	<b>LOC100133975</b>	hypothetical LOC100133975	-1.2	0.037
Ssc.8920.1.A1_at	<b>TMEM106B</b>	transmembrane protein 106B	-1.2	0.045
Ssc.31072.1.S1_at	<b>SMARCE1</b>	SWI/SNF related, matrix associated, actin dependent regulator of chromatin subfamily e, member 1	-1.2	0.026
Ssc.30487.1.A1_at	unknown		-1.2	0.046
Ssc.17389.1.S1_at	<b>ZFP91</b>	zinc finger protein 91 homolog (mouse)	-1.2	0.024
Ssc.1852.1.S1_at	<b>TMEM87A</b>	transmembrane protein 87A	-1.2	0.027
Ssc.7176.1.A1_at	<b>CXCR4</b>	chemokine (C-X-C motif) receptor 4	-1.2	0.038

Supplementary Table 2 continued

<b>Probe Set ID</b>	<b>Annotation</b>	<b>Gene description</b>	<b>FC (H/L)</b>	<b>p-value</b>
Ssc.27344.1.A1_at	<b>PHF14</b>	PHD finger protein 14	-1.2	0.051
Ssc.8209.1.A1_at	<b>PHLDA1</b>	pleckstrin homology-like domain, family A, member 1	-1.2	0.031
Ssc.20580.2.S1_at	<b>SLU7</b>	SLU7 splicing factor homolog ( <i>S. cerevisiae</i> )	-1.2	0.029
Ssc.1698.1.S1_at	<b>C20ORF3</b>	Adipocyte plasma membrane-associated protein	-1.2	0.051
Ssc.29999.1.A1_at	unknown		-1.2	0.002
Ssc.9118.1.S1_at	<b>DAB2</b>	disabled homolog 2, mitogen-responsive phosphoprotein ( <i>Drosophila</i> )	-1.2	0.013
Ssc.6910.1.A1_at	<b>EIF2A</b>	eukaryotic translation initiation factor 2A, 65kDa	-1.2	0.019
Ssc.21876.1.S1_at	<b>ATM</b>	ataxia telangiectasia mutated	-1.2	0.036
Ssc.20172.1.A1_at	<b>ANTXR1</b>	anthrax toxin receptor 1	-1.2	0.021
Ssc.7079.1.A1_at	<b>MALAT1</b>	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	-1.2	0.047
Ssc.8030.1.A1_at	<b>LOC100130195</b>	hypothetical protein LOC100130195	-1.2	0.053
Ssc.6106.1.S1_at	<b>R-PTP-DELTA</b>	protein tyrosine phosphatase, receptor type, D	-1.2	0.029
Ssc.3403.1.S1_a_at	<b>PCF11</b>	PCF11, cleavage and polyadenylation factor subunit, homolog ( <i>S. cerevisiae</i> )	-1.2	0.037
Ssc.8552.3.S1_a_at	<b>GLT6D1</b>	glycosyltransferase 6 domain containing 1	-1.2	0.020
Ssc.19090.1.A1_at	<b>SETD7</b>	SET domain containing (lysine methyltransferase) 7	-1.2	0.001
Ssc.27189.1.A1_at	<b>KIAA2026</b>	KIAA2026	-1.2	0.038
Ssc.19579.3.S1_at	<b>LOC100129010</b>	hypothetical protein LOC100129010	-1.2	0.001
Ssc.4959.1.A1_at	<b>ARSK</b>	arylsulfatase family, member K	-1.2	0.004
Ssc.11079.1.A1_at	<b>RNASE4</b>	ribonuclease, RNase A family, 4	-1.2	0.020
Ssc.3477.3.S1_at	<b>SENP6</b>	SUMO1/sentrin specific peptidase 6	-1.2	0.045
Ssc.272.1.S1_a_at	<b>CD55</b>	CD55 molecule, decay accelerating factor for complement (Cromer blood group)	-1.2	0.039
Ssc.6788.1.A1_at	<b>SORBS2</b>	sorbin and SH3 domain containing 2	-1.2	0.002
Ssc.5937.1.S1_at	unknown		-1.2	0.045
Ssc.29025.1.A1_at	<b>NOL8</b>	nucleolar protein 8	-1.2	0.030
Ssc.27442.1.A1_at	<b>ZNF326</b>	zinc finger protein 326	-1.2	0.029
Ssc.26317.1.S1_at	<b>A2M</b>	alpha-2-macroglobulin	-1.2	0.007
Ssc.14238.1.S1_a_at	<b>NAP1L1</b>	nucleosome assembly protein 1-like 1	-1.2	0.032
Ssc.26113.1.S1_at	<b>FAM134B</b>	family with sequence similarity 134, member B	-1.2	0.033
Ssc.17222.1.S1_at	<b>MUC1</b>	mucin 1, cell surface associated	-1.2	0.039
Ssc.8581.1.A1_at	<b>SFRS12</b>	splicing factor, arginine/serine-rich 12	-1.2	0.053
Ssc.5070.1.A1_at	<b>CCNG1</b>	cyclin G1	-1.2	0.044
Ssc.24452.1.S1_at	<b>C5ORF41</b>	chromosome 5 open reading frame 41	-1.2	0.036
Ssc.20017.1.A1_at	<b>MYH10</b>	myosin, heavy chain 10, non-muscle	-1.2	0.028
Ssc.17745.1.S1_at	<b>NFAT5</b>	nuclear factor of activated T-cells 5, tonicity-responsive	-1.2	0.048

Supplementary Table 2 continued

<b>Probe_Set_ID</b>	<b>Annotation</b>	<b>Gene_description</b>	<b>FC (H/L)</b>	<b>p-value</b>
Ssc.8461.1.S1_a_at	<b>OA48-18</b>	cisplatin resistance-associated overexpressed protein	-1.2	0.046
Ssc.11574.1.A1_at	<b>GLT8D1</b>	glycosyltransferase 8 domain containing 1	-1.2	0.019
Ssc.20883.1.S1_at	<b>SELENBP1</b>	Selenium-binding protein 1 (56 kDa selenium-binding protein)	-1.2	0.032
Ssc.1429.1.A1_at	<b>NAP1L1</b>	nucleosome assembly protein 1-like 1	-1.2	0.016
Ssc.25107.2.A1_at	<b>BAT2D1</b>	BAT2 domain containing 1	-1.2	0.020
Ssc.24254.1.S1_at	<b>CASC4</b>	cancer susceptibility candidate 4	-1.2	0.035
Ssc.18246.1.S1_at	<b>MLLT3</b>	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3	-1.2	0.040
Ssc.24155.1.S1_at	<b>ARID4A</b>	AT rich interactive domain 4A (RBP1-like)	-1.2	0.028
Ssc.1012.1.S1_at	<b>ZNF277</b>	zinc finger protein 277	-1.2	0.054
Ssc.17091.2.A1_s_at	unknown		-1.2	0.004
Ssc.13037.1.A1_at	<b>TLK1</b>	tousled-like kinase 1	-1.2	0.037
Ssc.26393.1.S1_at	<b>ANKHD1-EIF4EBP3</b>	ANKHD1-EIF4EBP3 readthrough transcript	-1.2	0.003
Ssc.25208.2.S1_at	<b>COL4A3BP</b>	collagen, type IV, alpha 3 (Goodpasture antigen) binding protein	-1.2	0.029
Ssc.30838.1.A1_at	<b>PHIP</b>	pleckstrin homology domain interacting protein	-1.2	0.051
Ssc.27044.1.A1_at	<b>ZBU1</b>	helicase-like transcription factor	-1.2	0.045
Ssc.12837.1.A1_at	<b>GPBP1</b>	GC-rich promoter binding protein 1	-1.2	0.005
Ssc.18528.2.A1_at	<b>MFSD1</b>	major facilitator superfamily domain containing 1	-1.2	0.004
Ssc.10036.1.A1_at	<b>ARSK</b>	arylsulfatase family, member K	-1.2	0.050
Ssc.3802.1.S1_at	<b>NRP</b>	nucleosome assembly protein 1-like 1	-1.2	0.013
Ssc.10329.1.S1_at	<b>LONRF3</b>	LON peptidase N-terminal domain and ring finger 3	-1.2	0.022
Ssc.23780.1.S1_at	<b>SFRS11</b>	splicing factor, arginine/serine-rich 11	-1.3	0.039
Ssc.26113.2.S1_at	<b>FAM134B</b>	family with sequence similarity 134, member B	-1.3	0.037
Ssc.9311.1.A1_at	<b>PHLDA1</b>	pleckstrin homology-like domain, family A, member 1	-1.3	0.051
Ssc.13479.1.A1_at	<b>LRRC34</b>	leucine rich repeat containing 34	-1.3	0.028
SscAffx.28.1.S1_at	<b>NU5M</b>	NADH-ubiquinone oxidoreductase chain 5	-1.3	0.007
Ssc.5407.1.A1_at	<b>FAM134B</b>	family with sequence similarity 134, member B	-1.3	0.047
Ssc.14238.2.S1_at	<b>NAP1L1</b>	nucleosome assembly protein 1-like 1	-1.3	0.005
Ssc.15827.1.S1_at	<b>KPNA5</b>	karyopherin alpha 5 (importin alpha 6)	-1.3	0.038
Ssc.18878.1.A1_at	<b>C5ORF41</b>	chromosome 5 open reading frame 41	-1.3	0.016
Ssc.22797.1.S1_at	<b>TOP2B</b>	topoisomerase (DNA) II beta 180kDa	-1.3	0.042
Ssc.12416.1.S1_at	<b>FNBP4</b>	formin binding protein 4	-1.3	0.030
Ssc.1026.2.S1_at	<b>BBX</b>	bobby sox homolog (Drosophila)	-1.3	0.043
Ssc.24696.2.S1_at	<b>IRS2</b>	insulin receptor substrate 2	-1.3	0.011
Ssc.235.3.S1_a_at	<b>CAST</b>	calpastatin	-1.3	0.007

Supplementary Table 2 continued

<b>Probe_Set_ID</b>	<b>Annotation</b>	<b>Gene_description</b>	<b>FC (H/L)</b>	<b>p-value</b>
Ssc.24696.1.S1_at	<b>IRS2</b>	insulin receptor substrate 2	-1.3	0.007
Ssc.3920.1.S1_at	<b>PMEPA1</b>	prostate transmembrane protein, androgen induced 1	-1.3	0.010
Ssc.9439.3.S1_at	<b>FUBP1</b>	far upstream element (FUSE) binding protein 1	-1.3	0.005
Ssc.26224.1.S1_at	<b>PMEPA1</b>	prostate transmembrane protein, androgen induced 1	-1.3	0.006
Ssc.5239.1.S1_at	<b>TGM2</b>	transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)	-1.3	0.026
Ssc.21290.1.S1_at	<b>TSC22D2</b>	TSC22 domain family, member 2	-1.3	0.039
Ssc.27228.1.S1_at	<b>SEC63</b>	SEC63 homolog ( <i>S. cerevisiae</i> )	-1.3	0.010
Ssc.11292.1.A1_at	unknown		-1.3	0.051
Ssc.3654.1.A1_at	<b>B3VKM1</b>	Membrane-associated ring finger 6	-1.3	0.005
Ssc.21643.1.A1_at	<b>PATL1</b>	protein associated with topoisomerase II homolog 1 (yeast)	-1.3	0.016
Ssc.26185.1.S1_at	<b>ACSL6</b>	acyl-CoA synthetase long-chain family member 6	-1.3	0.004
Ssc.11255.1.A1_at	<b>ACSL6</b>	acyl-CoA synthetase long-chain family member 6	-1.3	0.032
Ssc.27228.2.S1_at	<b>SEC63</b>	SEC63 homolog ( <i>S. cerevisiae</i> )	-1.3	0.010
Ssc.6338.1.S1_at	<b>USP1</b>	ubiquitin specific peptidase 1	-1.3	0.030
Ssc.14386.1.A1_at	<b>CCNG2</b>	cyclin G2	-1.3	0.010
Ssc.19643.1.A1_at	<b>COL4A4</b>	collagen, type IV, alpha 4	-1.3	0.003
Ssc.25523.1.S1_at	<b>WHSC1L2P</b>	Wolf-Hirschhorn syndrome candidate 1-like 2 (pseudogene)	-1.3	0.024
Ssc.28309.1.A1_at	<b>TAX1BP1</b>	Tax1 (human T-cell leukemia virus type I) binding protein 1	-1.3	0.049
Ssc.15952.1.S1_at	<b>NR3C1</b>	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)	-1.3	0.004
Ssc.1285.1.S1_at	<b>C3ORF64</b>	chromosome 3 open reading frame 64 ( <i>Homo sapiens</i> )	-1.3	0.047
Ssc.26267.1.S1_at	<b>CRY2</b>	cryptochrome 2 (photolyase-like)	-1.3	0.000
Ssc.3966.1.S1_at	<b>KIAA1147</b>	KIAA1147	-1.3	0.001
Ssc.22165.1.A1_at	<b>ELMO3</b>	engulfment and cell motility 3	-1.3	0.037
Ssc.20017.2.S1_at	<b>MYH10</b>	myosin, heavy chain 10, non-muscle	-1.3	0.004
Ssc.211.1.S1_at	<b>RNS10</b>	Ribonuclease-like protein 10 Precursor (Protein Train A)	-1.3	0.005
Ssc.3207.1.S1_at	<b>CSDC2</b>	cold shock domain containing C2, RNA binding	-1.4	0.025
Ssc.3271.1.A1_at	<b>ABCA1</b>	ATP-binding cassette, sub-family A (ABC1), member 1	-1.4	0.021
Ssc.15128.1.S1_at	<b>ARID4B</b>	AT rich interactive domain 4B (RBP1-like)	-1.4	0.021
Ssc.9301.1.A1_at	<b>BAT2D1</b>	BAT2 domain containing 1	-1.4	0.013
Ssc.15741.1.S1_s_at	<b>CYP2E1</b>	cytochrome P450, family 2, subfamily E, polypeptide 1	-1.4	0.034
Ssc.3417.1.A1_at	<b>SNORD50B</b>	small nucleolar RNA, C/D box 50B	-1.4	0.031
Ssc.15463.1.S1_at	<b>LOC731605</b>	similar to BCL2-associated transcription factor 1	-1.4	0.052
Ssc.23853.1.A1_at	unknown		-1.4	0.030
Ssc.15480.1.S1_at	<b>F2RL2</b>	coagulation factor II (thrombin) receptor-like 2	-1.4	0.035



Supplementary Table 2 continued

<b>Probe_Set_ID</b>	<b>Annotation</b>	<b>Gene_description</b>	<b>FC (H/L)</b>	<b>p-value</b>
Ssc.25716.1.S1_at	<b>KN</b>	complement component (3b/4b) receptor 1 (Knops blood group)	-1.4	0.026
Ssc.27786.2.S1_at	<b>LOC100128774</b>	hypothetical protein LOC100128774	-1.5	0.013
Ssc.4804.1.S1_at	<b>AGT</b>	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	-1.5	0.024
Ssc.25292.1.S1_at	<b>LOC254028</b>	misc_RNA LOC254028	-1.5	0.008
Ssc.7146.1.A1_at	<b>ABCA1</b>	ATP-binding cassette, sub-family A (ABC1), member 1	-1.5	0.004
Ssc.18996.2.A1_a_at	<b>TM4SF5</b>	transmembrane 4 L six family member 5	-1.5	0.031
Ssc.14367.1.S1_at	unknown		-1.5	0.054
Ssc.28613.1.S1_at	unknown		-1.6	0.029
Ssc.11273.2.A1_at	unknown		-1.9	0.029
Ssc.21856.1.S1_at	<b>LOC100157073</b>	similar to angiotensinogen	-1.9	0.008