Table 1A and 1B. Genes whose expressions are induced (A) and reduced (B) by exposure to LSS. Fold changes divisible by zero are listed by “-“. Genes with a chi2 score of at least 7.65 are obtained when FDR is controlled at 5%. A number of genes that would not be considered differentially expressed when FDR is controlled at 5%, but would be considered differentially expressed without FDR control, have been included in cases where they match genes of known biological significance (these tags have chi2 scores between 3.85 and 7.64). TGFB1 (marked “**”) did not reach statistical significance but has been included on the basis of its functional significance and likely downmodulation (confirmed by QRT-PCR, see Figure 1A).

Table 1A

Gene Function/ Name	*Symbol*	*Accession*	*Ratio*	*0h LSS*	*24h LSS*	*Tag*	*Chi2*
Adhesion							
carbohydrate sulfotransferase 5	CHST5	NM_012126	-	0.00	11.83	CCACTGCACC	13.36
Apoptosis							
Caspase 2	CASP2	NM_001224.2	-	0.00	4.30	ATCCACCCAC	4.86
DNA fragmentation factor, 45 kD, alpha polypeptide	DFFA	NM_004401	4.70	7.08	33.33	AACCTGGGAG	18.56
Cell Division							
cyclin-dependent kinase inhibitor 1A	CDKN1A	NM_000389.3	1.61	10.63	17.20	TGTCCTGGTT	
Polycystin 1	PKD1	NM_000296	3.85	5.31	20.43	AACCCAGGAG	9.6
Coagulation							
Coagulation factor II receptor-like 2	F2RL2	NM_004101	-	0.00	9.68	TTGACCAGGC	10.93
Cytoskeletal							
actin cross-linking factor	MACF1	NM_012090	-	0.00	7.53	CACTCCAGCC	8.5
calponin 2	CNN2	NM_004368	2.23	10.63	23.65	CCCCGCCAAG	5.24
gelsolin	GSN	NM_000177	3.03	3.54	10.75	TCACCGGTCA	3.9
Filamin A	FLNA	NM_001456	1.76	25.68	45.15	GTTCGTGCCA	5.61
transglutaminase 2	TGM2	NM_004613	10.93	0.89	9.68	ATTGCACCAC	8.12
Extracellular Matrix							
Collagen, type IV, alpha 1	COL4A1	NM_001845	1.54	32.77	50.53	GACCGCAGGA	3.95
Ion Channels							
cyclic nucleotide-gated potassium channel 2	HCN2	NM_001194	-	0.00	5.38	CCATTGCGCT	6.07
solute carrier family 11 member 1	SLC11A1	NM_000578	-	0.00	6.45	CTGGCCAGGC	7.28
solute carrier family 14 (urea transporter), member 1	SLC14A1	NM_015865	5.26	2.66	13.98	GTGGTGGGTG	8.41
solute carrier family 14 (urea transporter), member 2	SLC14A2	NM_007163	6.37	3.54	22.58	GTGGCGGGCA	15.23
Inflammation							
intercellular adhesion molecule 1	ICAM1	NM_000201	9.10	1.77	16.13	GTTCACTGCA	12.73
interleukin 2 receptor, alpha	IL2RA	NM_000417	-	0.00	8.60	ATGGCACCAC	9.71
TNF receptor-associated factor 5	TRAF5	NM_004619	15.78	0.89	13.98	ATCTCAGCTC	12.86
tumor necrosis factor receptor 1B	TNFRSF1B	NM_001066	4.86	1.77	8.60	GTAAAACCCC	4.9
Metabolic							
cytochrome c oxidase subunit VIIa polypeptide 2 like	COX7A2L	NM_004718	-	0.00	4.30	GCTTCGCAGC	4.86
glucose phosphate isomerase	GPI	NM_000175	-	0.00	4.30	ATCCGCCTGC	4.86
glucose-6-phosphatase	G6PC	NM_000151	4.25	1.77	7.53	AGCCACCGCA	3.86
NADH-coenzyme Q reductase Fe-S protein 6	NDUFS6		4.25	1.77	7.53	CGGTTACTGT	3.86
tyrosine aminotransferase	TAT	NM_000353	18.21	0.89	16.13	GGCGACAGAG	15.25
Ribsosomal							

ribosomal protein S27	RPS27	NM_001030	1.76	37.19	65.58	CACAAACGGT	8.23
ribosomal protein S3	RPS3	NM_001005	1.53	74.39	113.95	CCCCAGCCAG	8.68
ribosomal protein L10a	RPL10A	NM_007104	1.38	130.18	179.53	GGCAAGCCCC	8.19
ribosomal protein L13a	RPL13A	NM_012423	1.47	98.30	144.06	AGGCTACGGA	9.01
ribosomal protein L28	RPL28	NM_000991	2.12	80.59	170.93	GCAGCCATCC	34.43
ribosomal protein L29	RPL29	NM_000992	1.45	183.32	266.61	GGGCTGGGGT	16.14
Stress response							
DnaJ (Hsp40) homolog, subfamily B, member 1	HSPF1	NM_006145	15.98	5.31	84.93	AGACCAAAGT	78.44
DnaJ (Hsp40) homolog, subfamily B, member 1	HSPF1	NM_006145	-	0.00	27.95	AGAGGGTGGG	31.58
ferritin, light polypeptide	FLT	NM_000146	1.47	46.94	68.80	CCCTGGGTTC	4.3
folate transporter/carrier	SLC19A1	NM_003056	27.92	0.89	24.73	TTAGCCAGGA	24.88
heat shock 105kD	HSP105B	NM_006644	7.69	2.66	20.43	TGAAAGTGTG	15.08
heat shock 27kD protein 1	HSPB1	NM_001540	2.43	13.28	32.25	CCCAAGCTAG	8.4
heat shock 60kD protein 1	HSPD1	NM_002156	-	0.00	4.30	CCATTGCACC	4.86
heat shock 70kD protein 1A	HSPA1A	NM_005345	114.11	0.89	101.05	CAGAGATGAA	111.11
heat shock 70kD protein 1B	HSPA1B	NM_005346	-	0.00	44.08	AAGAGCGCCG	49.8
heat shock 70kD protein 5	HSPA5	NM_005347	5.58	48.71	271.98	TGCATCTGGT	170.87
heat shock 90kD protein 1, beta	HSPCB	NM_007355	2.65	9.74	25.80	GGCTCCCACT	7.74
heme oxygenase 1	HMOX1	NM_002133	22.21	8.86	196.73	CGTGGGTGGG	192.7
homocysteine-inducible ubiquitin-like domain member 1	HERPUD1	NM_014685	6.07	1.77	10.75	TTTTAGCAGG	7.06
immediate early response 5	IER5	NM_016545	-	0.00	4.30	AACCCCTGGA	4.86
metallothionein 1A	MT1A	K01383	-	0.00	5.38	AGCTGTGCCA	6.07
metallothionein 2A	MT2A	NM_005953	3.82	6.20	23.65	GCGAGCTGAA	11.04
novel SH2-containing protein 1	SH2D3A	NM_005490	-	0.00	4.30	GTGAGACCTC	4.86
superoxide dismutase 2, mitochondrial	SOD2	NM_000636	-	0.00	4.30	GCTTGCAAAA	4.86
Signal Transduction							
dual specificity phosphatase 6	DUSP6	NM_001946	-	0.00	4.30	GGCTCACTTT	4.86
hippocalcin-like 1	HPCAL1	NM_002149	4.05	2.66	10.75	TGTGCCCTGA	5.29

Table 1B.

Gene Name/function	***Symbol***	***Accession***	***Ratio***	***0h LSS***	***24h LSS***	***Tag***	***Chi2***
Angiogenesis							
connective tissue growth factor	CTGF	NM_001901	0.25	142.58	35.48	TTTGCACCTT	62.30
cysteine-rich, angiogenic inducer, 61	CYR61	NM_001554	0.36	15.05	5.38	AGTGTCTGTG	4.48
phosphoglycerate dehydrogenase	PHGDH	NM_006623	0.16	27.45	4.30	TTACCTCCTT	16.10
phosphoglycerate kinase 1	PGK1	NM_000291	0.34	15.94	5.38	GAAACAAGAT	5.10
secreted protein, acidic,	SPARC	NM_003118	0.00	4.43	0.00	AATGCTTGG	4.12

cysteine-rich (osteonectin)								
Thrombospondin 1	THBS1	NM_003246	0.20	10.63	2.15	AGGTCTTCAA	5.39
angiopoietin-like 4	ANGPTL4	NM_139314	0.30	10.63	3.23	GTGCTGGTGC	3.85
endoglin	ENG	NM_000118	0.04	30.11	1.08	AAACCAAAAA	25.31
Apoptosis							
death-associated protein kinase 3	DAPK3	NM_001348	0.00	6.20	0.00	TGGAGCATCG	5.77
Intercellular adhesion molecule 2	ICAM2	NM_000873	0.33	23.03	7.53	GCCACCACCA	7.65
poly(rC)-binding protein 4	PCBP4	NM_020418.2	0.00	4.43	0.00	GGGCAGGGGC	4.12
Cell-Cell Communication							
cadherin 5, type 2, VE-cadherin	CDH5	NM_001795	0.51	31.88	16.13	ACAAGTACTG	5.12
talin 1	TLN1	NM_006289	0.00	5.31	0.00	CTCCAATAAA	4.94
Cell Division							
CDC10 (cell division cycle 10, S. cerevisiae, homolog)	CDC10	NM_001788	0.00	4.43	0.00	GCCTCTTGAA	4.12
CDC20 (cell division cycle 20, S. cerevisiae, homolog)	CDC20	NM_001255	0.00	6.20	0.00	TCTCCCTTCA	5.77
Cdc42 effector protein 2	CDC42EP2	NM_006779	0.24	8.86	2.15	CTGCTGCTGG	3.94
calpain, small subunit 1	CAPNS1	NM_001749	0.69	73.50	50.53	CCCCAGTTGC	4.27
cyclin B1	CCNB1	NM_031966	0.32	13.28	4.30	TGCCATCTGT	4.46
cyclin D1	CCND1	NM_053056	0.00	6.20	0.00	AAAGTCTAGA	5.77
enhancer of rudimentary (Drosophila) homolog	ERH	NM_004450	0.15	7.08	1.08	TCCTCAAGAT	4.22
nucleophosmin (nucleolar phosphoprotein B23, numatrin)	NPM1	NM_002520	0.15	14.17	2.15	TGAAATAAAA	8.43
PDGFA associated protein 1	PDAP1	NM_014891	0.00	7.08	0.00	CTCCACAAAT	6.59
Cell Motility							
tetraspan 3	TSPAN-3	NM_005724	0.32	13.28	4.30	TAGACTAGCA	4.46
Cell Surface Structure							
galectin 1	LGALS1	NM_002305	0.59	325.89	192.43	GCCCCCAATA	34.51
galectin 3	LGALS3	NM_002306	0.00	6.20	0.00	TTCACTGTGA	5.77
moesin	MSN	NM_002444	0.27	15.94	4.30	TTCTATTTCA	6.47
Cytoskeletal							
actin, beta	ACTB	NM_001101	0.21	41.62	8.60	GCTTTATTTG	20.84
capping protein muscle Z-line, beta	CAPZB	NM_004930	0.00	4.43	0.00	CTAACCAGAC	4.12
Cofilin 1	CFL1	NM_005507	0.64	219.62	140.83	GAAGCAGGAC	17.31
filamin A, alpha	FLNA	NM_001456	0.42	20.37	8.60	GCCCAAGGAC	4.69
myosin, heavy polypeptide 9, non-muscle	MYH9	NM_002473	0.28	23.03	6.45	TGCTAAAAAA	9.02
profilin 1	PFN1	NM_005022	0.12	8.86	1.08	TGGTTTTGGC	5.78
singed (Drosophila)-like	FSCN1	NM_003088	0.38	14.17	5.38	ATAGTAGCTT	3.87
thymosin, beta 4, X chromosome	TMSB4X	NM_021109	0.20	15.94	3.23	AGTTTCCCAA	8.09
thymosin, beta 4, X chromosome	TMSB4X	NM_021109	0.71	139.92	99.98	TTGGTGAAGG	6.70
Tropomyosin 2 (beta)	TPM2	NM_003289	0.36	15.05	5.38	GACCAGGCCC	4.48
tubulin alpha 6	TUBA6	NM_032704	0.38	16.83	6.45	GCTGCCCTTG	4.53
tubulin, alpha 3	TUBA3	NM_006009	0.19	11.51	2.15	AATGCTTTGT	6.14
tubulin, alpha, ubiquitous	K-	NM_006082	0.13	83.24	10.75	TGTACCTGTA	53.17

	ALPHA-1						
tubulin, beta, 2	TUBB2	NM_006088	0.24	40.74	9.68	CTGTACAGAC	18.44
ENOS							
dimethylarginine dimethylaminohydrolase 1	DDAH1	NM_012137	0.00	4.43	0.00	TATACCAATC	4.12
Extracellular Matrix							
EGF-containing fibulin-like extracellular matrix protein 1	EFEMP1	NM_004105	0.47	118.67	55.90	CAAGGGTAAG	22.31
fibrillin 1	FBN1	NM_000138	0.13	7.97	1.08	TGCAATATGC	4.99
fibronectin 1	FN1	NM_002026	0.29	15.05	4.30	ATCTTGTTAC	5.79
hyaluronoglucosaminidase 2	HYAL2	NM_003773	0.22	9.74	2.15	TAGGACCCTG	4.66
integrin, alpha 5	ITGA5	NM_002205	0.37	31.88	11.83	ATGGCAACAG	9.00
integrin, alpha E	ITGAE	NM_002208	0.00	5.31	0.00	GAGCTGTTGG	4.94
integrin, alpha V	ITGAV	NM_002210	0.45	23.91	10.75	TAACTTGTGA	4.92
integrin-linked kinase	ILK	NM_004517	0.28	23.03	6.45	GGAGGGATCA	9.02
laminin receptor 1	LAMR1	NM_002295	0.51	80.59	40.85	GAAAAATGGT	12.88
lysyl oxidase-like 2	LOXL2	NM_002318	0.50	45.16	22.58	TGTCATCACA	7.45
procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide	P4HB	NM_000918	0.36	15.05	5.38	CCTGGAAGAG	4.48
Vimentin	VIM	NM_003380	0.60	52.25	31.18	TCCAAATCGA	5.31
Immune Response							
HLA class II region expressed gene KE2	HKE2	NM_014260	0.12	8.86	1.08	GTGGGGGGAG	5.78
major histocompatibility complex, class I, A	HLA-A	NM_002116	0.24	17.71	4.30	AGAAAAAAAA	7.88
Inflammation							
pentaxin-related gene, rapidly induced by IL-1 beta	PTX3	NM_002852	0.00	15.94	0.00	GTGCTTTCAG	14.83
Intracellular Motility							
sorting nexin 3	SNX3	NM_003795	0.00	7.08	0.00	GAAGATTAAT	6.59
Ion Channels							
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3	ATP5G3	NM_001689	0.47	23.03	10.75	GGAATGTACG	4.40
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, isoform 2	ATP5J2	NM_004889	0.00	7.08	0.00	ACTGGTAAAA	6.59
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit g	ATP5L	NM_006476	0.51	38.08	19.35	TGTGATCAGA	6.05
ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit	ATP5D	NM_001687	0.00	4.43	0.00	GGGCTCTCCT	4.12
ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit	ATP5D	NM_001687	0.24	8.86	2.15	TTGGACCTGG	3.94
chloride intracellular channel 1	CLIC1	NM_001288	0.30	10.63	3.23	GTACTGTGGC	3.85
solute carrier family 1, member 5	SLC1A5	NM_005628	0.00	8.86	0.00	TGCCTGCTCC	8.24
solute carrier family 2 member 1	SLC2A1	NM_006516	0.00	6.20	0.00	GAGAGCTCCC	5.77

solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulatory factor 2	SLC9A3R2	NM_004785	0.26	12.40	3.23	CGCGCTCTCA	5.20
WD repeat domain 1	WDR1	NM_005112	0.00	7.08	0.00	AAAAATAAAG	6.59
voltage-dependent anion channel 3	VDAC3	NM_005662	0.00	7.08	0.00	ACTGGTAAAA	6.59
Metabolic							
branched chain alpha-ketoacid dehydrogenase kinase	BCKDK	NM_005881	0.00	7.08	0.00	GAGCTGGGCA	6.59
glyceraldehyde-3-phosphate dehydrogenase	GAPD	NM_002046	0.27	137.27	36.55	TACCATCAAT	56.55
lactate dehydrogenase A	LDHA	NM_005566	0.00	4.43	0.00	TCTTGTGCAT	4.12
lactate dehydrogenase B	LDHB	NM_002300	0.19	11.51	2.15	GATCACAGTT	6.14
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7	NDUFA7	NM_005001	0.00	6.20	0.00	TCGTCGCAGA	5.77
NADH dehydrogenase (ubiquinone) flavoprotein 1	NDUFV1	NM_007103	0.17	18.60	3.23	TGGAATGCTG	10.35
pyruvate carboxylase	PC	NM_000920	0.00	4.43	0.00	CAGCAAAAAA	4.12
pyruvate dehydrogenase (lipoamide) alpha 1	PDHA1	NM_000284	0.15	7.08	1.08	CAGTTTGTAC	4.22
Nuclear Matrix							
matrin 3	MATR3	NM_018834	0.00	5.31	0.00	TTTGGAATGT	4.94
Nucleolin	NCL	NM_005381	0.12	8.86	1.08	TACAAAACCA	5.78
Ribosomal							
mitochondrial ribosomal protein 64	MRPL51	NM_016497	0.00	5.31	0.00	GGAAGTTTCG	4.94
mitochondrial ribosomal protein L3	MRPL3	NM_007208	0.00	5.31	0.00	TCATCTTTGT	4.94
Signal Transduction							
guanine nucleotide binding protein alpha inhibiting activity polypeptide 2	GNAI2	NM_002070	0.00	5.31	0.00	TTTTATGGAA	4.94
myotubularin related protein 4	MTMR4	NM_004687	0.00	4.43	0.00	CAATGTGCTG	4.12
non-metastatic cells 2, protein (NM23B) expressed in	NME2	NM_002512	0.17	12.40	2.15	ACTGGGTCTA	6.90
Phosphatidylethanolamine-binding protein (PBP)	PBP	NM_002567	0.20	10.63	2.15	GGGGTAAGAA	5.39
RAB32, member RAS oncogene family	RAB32	NM_006834	0.00	4.43	0.00	TGGCACTTCA	4.12
Ral guanine nucleotide exchange factor	RALGPS1A	NM_014636	0.00	4.43	0.00	ATCACTTGGG	4.12
RAN, member RAS oncogene family	RAN	NM_006325	0.17	12.40	2.15	TGCTTCATCT	6.90
ras homolog gene family, member B	ARHB	NM_004040	0.15	7.08	1.08	CACACAGTTT	4.22
Stress Response							
heat shock 60kD protein 1	HSPD1	NM_002156	0.00	7.97	0.00	TACCAGTGTA	7.42
HS1 binding protein	HAX1	NM_006118	0.00	4.43	0.00	TCAGTTTGTC	4.12
TGFβ Signaling							
endoglin	ENG	NM_000118	0.04	30.11	1.08	AAACCAAAAA	25.31
latent transforming growth factor beta binding protein 2	LTBP2	NM_000428	0.40	18.60	7.53	GTGGAATAAA	4.60
ret finger protein	RFP	NM_006510	0.00	4.43	0.00	CAGATTGTGA	4.12

transforming growth factor, beta-induced, 68kD	TGFBI	NM_000358	0.22	29.22	6.45	GTGTGTTTGT	13.98
Transforming growth factor beta 1	TGFB1	NM_000660	0.57	13.28	7.53	GGGGCTGTAT	**
Coagulation							
plasminogen activator inhibitor type 1	SERPINE1	NM_000602	0.21	60.22	12.90	TAAAAATGTT	29.44
Transcription							
high-mobility group protein 14	HMGN1	NM_004965	0.15	7.08	1.08	GCTTTTTAGA	4.22
high-mobility group protein 17	HMGN2	NM_005517.1	0.17	12.40	2.15	ATTGTTTATG	6.90
histone acetyltransferase	HBOA	NM_007067	0.10	10.63	1.08	CACGCAATGC	7.37
endothelial PAS domain protein 1	EPAS1	NM_001430	0.00	6.20	0.00	AACGTTATTA	5.77
MORF-related gene 15	MORF4L1	NM_006791	0.30	14.17	4.30	ATAGACGCAA	5.12
MYC-associated zinc finger protein	MAZ	NM_002383	0.29	18.60	5.38	TACCCCACCC	7.07
poly(A)-binding protein, nuclear 1	PABPN1	NM_004643.1	0.00	6.20	0.00	GTATTCCCCT	5.77
small nuclear ribonucleoprotein polypeptide E	SNRPD1	NM_006938	0.00	4.43	0.00	CTAAAAGGAG	4.12
Translation							
cyclophilin A	PPIA	NM_021130.1	0.64	137.27	88.15	CCTAGCTGGA	10.73
eukaryotic translation elongation factor 1 beta 2	EEF1B2	NM_001959	0.20	15.94	3.23	GCATTTAAAT	8.09
eukaryotic translation initiation factor 5A	EIF5A	NM_001970	0.33	35.42	11.83	GGCTTTACCC	11.48
glutamyl-prolyl-tRNA synthetase	EPRS	NM_004446	0.30	21.25	6.45	AACTAAAAAA	7.68
poly(A)-binding protein, cytoplasmic 1	PABPC1	NM_002568	0.00	4.43	0.00	AAAAGAAACT	4.12
putative translation initiation factor	SUI1	NM_005801	0.07	29.22	2.15	CAATAAACTG	22.01
ribosomal protein L14	RPL14	NM_003973	0.30	24.80	7.53	CAGCTCACTG	8.96
ribosomal protein L23	RPL23	NM_000978	0.49	56.68	27.95	ATTCTCCAGT	9.64
ribosomal protein L37	RPL37	NM_000997	0.32	40.74	12.90	CAATAAATGT	14.05
ribosomal protein L39	RPL39	NM_001000	0.32	20.37	6.45	TTACCATATC	7.02
ribosomal protein S19	RPS19	NM_001022	0.71	174.46	123.63	CTGGGTTAAT	8.74
ribosomal protein S8	RPS8	NM_001012	0.51	48.71	24.73	TAATAAAGGT	7.75
Vascular Reactivity							
endothelin 1	EDN1	NM_001955	0.43	17.71	7.53	CTTTGTTTTG	4.04
insulin-like growth factor binding protein 7	IGFBP7	NM_001553	0.19	50.48	9.68	CATATCATTA	26.52