Table S1. Differential gene expression in Lasp1$^{-/-}$ MEFs (>2-fold change; P<0.05).

Gene Symbol	Description	Accession Number	Fold Change(s)	P Value(s)
Col2a1*	procollagen, type II, alpha 1	NM_031163	15.171; 6.674; 3.020	0.002; 0.000; 0.000
Kng1*	kininogen 1	NM_023125	6.137; 2.662	0.0001; 0.0003
Inmt*	indolethylamine N-methyltransferase	NM_009349	7.755; 2.762	0.0001; 0.0002
Sim2	single-minded homolog 2 (Drosophila)	NM_011377	5.114	0.0001
Serpina3g	serine (or cysteine) peptidase inhibitor, clade A, member 3G	XM_354694	4.906	0.0001
Il1rn	interleukin 1 receptor antagonist	NM_031167	4.745	0.0002
Lcn2	lipocalin 2	NM_008491	4.209	0.0004
Serpina3h*	serine (or cysteine) peptidase inhibitor, clade A, member 3H	NM_001034870	3.844; 2.654	0.0025; 0.0103
Hoxa5	homeo box A5	NM_010453	3.701	0.0004
Sncg*	synuclein, gamma	NM_011430	3.683; 2.222	0.0034; 0.0001
Saa3	Serum amyloid A3	NM_011315	3.661	0.0004
CRG-L1	N-acylsphingosine amidohydrolase 3-like	NM_139306	3.296	0.0002
Cxcl1	chemokine (C-X-C motif) ligand 1	NM_008176	3.199	0.0007
Ankrd1	ankyrin repeat domain 1 (cardiac muscle)	NM_013468	3.197	0.002
A730017D01Rik	RIKEN cDNA A730017D01 gene		3.069	0.0003
Diras2	DIRAS family, GTP-binding RAS-like 2	NM_001024474	2.976	0.008
Sox5*	SRY-box containing gene 5	AK081802	2.915; 2.279	0.006; 0.005
Acta1	actin, alpha 1, skeletal muscle	NM_009606	2.870	0.0146
Smoc1	SPARC related modular calcium binding 1	NM_022316	2.851	0.0064
Chst1	carbohydrate (keratan sulfate Gal-6) sulfotransferase 1	NM_023850	2.836	0.001
P2ry14*	purinergic receptor P2Y, G-protein coupled, 14	NM_133200	2.828; 2.070	0.000; 0.001
6330404C01Rik	RIKEN cDNA 9930013L23 gene	AK018112	2.762	0.0012
LOC217066*	hypothetical LOC217066	NM_001025564	2.725; 2.474	0.0263; 0.027
9430064K01Rik	RIKEN cDNA 9430064K01 gene		2.673	0.0062
Nfkbiz	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta	NM_030612	2.657	0.0022
Ccdc68	coiled-coil domain containing 68	NM_201362	2.612	0.0017
1300002F13Rik	ERBB receptor feedback inhibitor 1	NM_133753	2.601	0.01
LOC381284	RIKEN cDNA E030010N08 gene	XM_355224	2.515	0.0006
9830143E02Rik		AK036626	2.510	0.0377
Nes	nestin	NM_016701	2.503	0.0098
Kng2	kininogen 2	NM_201375	2.498	0.0009

Fst	follistatin	NM_008046	2.471	0.0035
Nrp	neuropilin 1	AK030358	2.454	0.0388
Car12	carbonic anyhydrase 12	NM_178396	2.452	0.0016
Cbr2	carbonyl reductase 2	NM_007621	2.442	0
Nid1	nidogen 1	AK049585	2.435	0.0259
Fgf7	fibroblast growth factor 7	NM_008008	2.430	0.0007
Klra18	killer cell lectin-like receptor, subfamily A, member 18	NM_053153	2.430	0.0163
Mmp13	matrix metallopeptidase 13	NM_008607	2.375	0.006
Nr2f1	nuclear receptor subfamily 2, group F, member 1	NM_010151	2.371	0.0048
Cgnl1	cingulin-like 1	NM_026599	2.353	0.0028
Tgm2	transglutaminase 2, C polypeptide	NM_009373	2.344	0.0007
scl0001276.1_18	epidermal growth factor-containing fibulin-like extracellular matrix protein 1	AK077302	2.320	0.0201
Serpine2	serine (or cysteine) peptidase inhibitor, clade E, member 2	NM_009255	2.299	0.0157
LPP*	LIM domain containing preferred translocation partner in lipoma	AK040185	2.298; 2.262; 2.24	0.002; 0.038; 0.0386
Uncx4.1	Unc4.1 homeobox (C. elegans)	NM_013702	2.260	0.0145
Cyp1b1	cytochrome P450, family 1, subfamily b, polypeptide 1	NM_009994	2.260	0.0034
Cp	ceruloplasmin	NM_007752	2.259	0.0008
Tinagl*	tubulointerstitial nephritis antigen-like 1	NM_023476	2.259; 2.235	0.0054; 0.0049
Foxc1	forkhead box C1	NM_008592	2.256	0.0025
Gata2	GATA binding protein 2	NM_008090	2.250	0.0005
Klra4	killer cell lectin-like receptor, subfamily A, member 4	NM_010649	2.228	0.0018
Pde1a	phosphodiesterase 1A, calmodulin-dependent	NM_016744	2.224	0.0015
Aldh1a7	aldehyde dehydrogenase family 1, subfamily A7	NM_011921	2.215	0.0006
Phlda1	pleckstrin homology-like domain, family A, member 1	NM_009344	2.206	0.0008
9130004J05Rik	RIKEN cDNA 9130004J05 gene		2.194	0.0434
Col10a1	procollagen, type X, alpha 1	NM_009925	2.181	0.0046
9930105H17Rik	RIKEN cDNA 9930105H17 gene		2.165	0.0007
Ccl9	chemokine (C-C motif) ligand 9	NM_011338	2.163	0.0003
Hoxa2*	homeo box A2	NM_010451	2.150; 2.083	0.001; 0.003
Enah	enabled homolog (Drosophila)	AK020248	2.141	0.0296
Angptl7	angiopoietin-like 7	NM_001039554	2.102	0.004
1700038P13Rik	RIKEN cDNA 1700038P13 gene		2.089	0.0013
C730013O11Rik		AK050083	2.086	0.0049
Adora2b	adenosine A2b receptor	NM_007413	2.075	0.0011
Sh3md2	SH3 domain containing ring finger 1	NM_198678	2.063	0.0007

Ybx3	RIKEN cDNA 1200016E24 gene	AK029441	2.062	0.0045
Grem1	gremlin 1	NM_011824	2.044	0.0034
LOC214403	predicted gene, EG214403	XM_129490	2.043	0.0005
Hoxa7	homeo box A7	NM_010455	2.027	0.0213
Msn	moesin	AK031171	2.026	0.0224
Dgkh	diacylglycerol kinase, eta	XM_484397	2.025	0.0256
9830134K01Rik	mannoside acetylglucosaminyltransferase 5	AK036567	2.023	0.0259
Cfd	complement factor D (adipsin)	NM_013459	-7.092	0.000
Gpr49	leucine rich repeat containing G protein coupled receptor 5	NM_010195	-6.270	0.006
Msx1	homeo box, msh-like 1	NM_010835	-6.165	0.001
Adh7	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide	NM_009626	-6.031	0.000
Krt1-14	keratin 14	NM_016958	-6.013	0.003
Tcfap2b*	transcription factor AP-2 beta	NM_001025305	-5.434;-3.367;-3.289	0.000;0.012; 0.008
Apod	apolipoprotein D	NM_007470	-4.914	0.011
Acdc	adiponectin, C1Q and collagen domain containing	NM_009605	-4.047	0.001
BC054438	cDNA sequence BC054438	NM_001001183	-3.964	0.005
Slc14a2*	solute carrier family 14 (urea transporter), member 2	NM_030683	-3.940; -3.786	0.0016; 0.0061
G1p2	ISG15 ubiquitin-like modifier	NM_015783	-3.865	0.023
Bcl11b	B-cell leukemia/lymphoma 11B	NM_021399	-3.740	0.009
Usp18*	ubiquitin specific peptidase 18	NM_011909	-3.646; -2.850	0.004; 0.000
Chodl	chondrolectin	NM_139134	-3.587	0.001
Ndg2	Nur77 downstream gene 2	NM_175329	-3.583	0.002
Matn4	matrilin 4	NM_013592	-3.357	0.039
Oasl2*	2'-5' oligoadenylate synthetase-like 2	NM_011854	-3.505; -2.157	0.004; 0.0244
Cxcl15	chemokine (C-X-C motif) ligand 15	NM_011339	-3.257	0.014
9130430L19Rik	RIKEN cDNA 9130430L19 gene		-3.108	0.000
Adh1*	alcohol dehydrogenase 1 (class I)	NM_007409	-3.066; -2.428	0.0034; 0.0004
Tbxa2r*	thromboxane A2 receptor	NM_009325	-3.058; -2.890	0.004; 0.004
Slpi	secretory leukocyte peptidase inhibitor	NM_011414	-2.953	0.000
Slit3*	slit homolog 3 (Drosophila)	XM_203363	-2.892; -2.042	0.0019; 0.0011
Odz4	odd Oz/ten-m homolog 4 (Drosophila)	NM_011858	-2.874	0.011
Ifit3	interferon-induced protein with tetratricopeptide repeats 3	NM_010501	-2.854	0.005
Ldb2*	LIM domain binding 2	NM_010698	-2.820; -2.686	0.0163; 0.01
Lpl	lipoprotein lipase	NM_008509	-2.811	0.001
C2	complement component 2 (within H-2S)	NM_013484	-2.796	0.029
LOC226866	gene model 106, (NCBI)	XM_129714	-2.731	0

Mfap4	microfibrillar-associated protein 4	NM_029568	-2.725	0.040
LOC380706	gene model 881, (NCBI)	XM_354621	-2.679	0.018
Plvap	plasmalemma vesicle associated protein	NM_032398	-2.667	0.010
Osr2	odd-skipped related 2 (Drosophila)	NM_054049	-2.519; -2.331	0.013; 0.005
Fgf21	fibroblast growth factor 21	NM_020013	-2.516	0.008
Adamts2*	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 2	NM_175643	-2.489; -2.435	0.0204; 0.0259
Pcdha1	protocadherin alpha 1	NM_054072	-2.484	0.001
Sorcs2	sortilin-related VPS10 domain containing receptor 2	NM_030889	-2.477	0.007
C130057K09	ADAMTS-like 3	XM_194370	-2.466	0.000
1110062M06Rik	RIKEN cDNA 1110062M06 gene		-2.399	0.015
Tnfrsf5	CD40 antigen	NM_170704	-2.385	0.000
Tmem119	transmembrane protein 119	NM_146162	-2.350	0.004
Socs2	suppressor of cytokine signaling 2	NM_007706	-2.346	0.007
Ctsk	cathepsin K	NM_007802	-2.340	0.002
Egfl3 (Megf6)	multiple EGF-like-domains 6	NM_172273	-2.317	0.018
Tnn	tenascin N	NM_177839	-2.316	0.000
Pdgfrl	platelet-derived growth factor receptor-like	NM_026840	-2.300	0.016
D330027H18Rik	RIKEN cDNA D330027H18 gene	XM_149840	-2.264	0.002
Tbx4	T-box 4	NM_011536	-2.264	0.006
Angptl1	angiopoietin-like 1	NM_028333	-2.261	0.048
Vegfc	vascular endothelial growth factor C	NM_009506	-2.254	0.000
Igtp	interferon gamma induced GTPase	NM_018738	-2.253	0.018
Megf10*	multiple EGF-like-domains 10	NM_001001979	-2.235; -2.199	0.008; 0.0051
Trib3*	tribbles homolog 3 (Drosophila)	NM_144554	-2.231;-2.228;-2.278	0.003;0.0017;0.0021
Cdh3	cadherin 3	NM_007665	-2.231	0.007
Lgi2	leucine-rich repeat LGI family, member 2	NM_144945	-2.228	0.024
Irf7	interferon regulatory factor 7	NM_016850	-2.220	0.041
Mfap5	microfibrillar associated protein 5	NM_015776	-2.220	0.003
Sema5a*	sema domain, (semaphorin) 5A	NM_009154	-2.212; -2.06	0.0006; 0.0064
Epb4.1l4b*	erythrocyte protein band 4.1-like 4b	NM_019427	-2.208; -2.205	0.0015; 0.0018
Parp14	poly (ADP-ribose) polymerase family, member 14	NM_001039530	-2.206	0.038
Hoxd8	homeo box D8	XM_355338	-2.192	0.001
Dpt	dermatopontin	NM_019759	-2.179	0.002
Slc7a3	solute carrier family 7 (cationic amino acid transporter, y+ system), member 3	NM_007515	-2.177	0.000
Hsd17b1	hydroxysteroid (17-beta) dehydrogenase 1	NM_010475	-2.163	0.011

Cd40	CD40 antigen	NM_170702	-2.160	0.001
Tcfap2a	transcription factor AP-2, alpha	NM_011547	-2.160; -2.387	0.001; 0.000
Lgals3bp	lectin, galactoside-binding, soluble, 3 binding protein	NM_011150	-2.139	0.019
3830422K02Rik	inscuteable homolog (Drosophila)	NM_173767	-2.133	0.014
Flt1	FMS-like tyrosine kinase 1	NM_010228	-2.128	0.035
Igfbp3	insulin-like growth factor binding protein 3	NM_008343	-2.124	0.015
Mmp11	matrix metallopeptidase 11	NM_008606	-2.117	0.007
Hey1	hairy/enhancer-of-split related with YRPW motif 1	NM_010423	-2.107	0.000
BC046404*	cDNA sequence BC046404	NM_198861	-2.105; -2.012	0.0; 0.0098
2810032G03Rik	RIKEN cDNA 2810032G03 gene	NM_028318	-2.093	0.001
Comp	cartilage oligomeric matrix protein	NM_016685	-2.074	0.044
D230005D02Rik	RIKEN cDNA D230005D02 gene	NM_172813	-2.067	0.001
Htra1*	HtrA serine peptidase 1	NM_019564	-2.062; -2.016	0.001; 0.002
C1qtnf3	C1q and tumor necrosis factor related protein 3	NM_030888	-2.054	0.011
Cox6a2	cytochrome c oxidase, subunit VI a, polypeptide 2	NM_009943	-2.029	0.005
Qpct	glutaminyl-peptide cyclotransferase (glutaminyl cyclase)	NM_027455	-2.026	0.000
H2-T23	histocompatibility 2, T region locus 23	NM_010398	-2.005	0.011

* Genes identified by multiple probes. The corresponding fold changes and P values are listed for each probe.