

<b>Functional Class</b>	<b>Gene Name</b>	<b>Gene ID (Entrez Gene)</b>	<b>Avg. Fold Expression</b>
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### **Inflammatory/Immune Response (n=53)**

	bone marrow stromal cell antigen 1	12182	<b>3.0</b> (2.3-3.8)
	chemokine (C-C motif) ligand 2	20296	<b>5.4</b> (3.2-9.1)
	chemokine (C-C motif) ligand 3	20302	<b>22.4</b> (13.9-36.0)
	chemokine (C-C motif) ligand 4	20303	<b>6.5</b> (3.7-11.4)
	chemokine (C-C motif) ligand 9	20308	<b>4.5</b> (4.0-5.1)
	chemokine (C-C motif) ligand 17	20295	<b>3.4</b> (3.2-3.7)
	chemokine (C-C motif) ligand 20	20297	<b>5.4</b> (4.1-7.0)
	chemokine (C-C motif) receptor 1	12768	<b>6.6</b> (5.4-8.0)
	chemokine (C-C motif) receptor 2	12772	<b>3.2</b> (2.2-4.6)
	chemokine (C-C motif) receptor-like 2	54199	<b>3.8</b> (2.8-5.1)
	chemokine (C-X-C motif) ligand 1	14825	<b>11.1</b> (8.1-15.0)
	chemokine (C-X-C motif) ligand 2	20310	<b>21.4</b> (15.2-30.2)
	chemokine (C-X-C motif) ligand 5	20311	<b>12.4</b> (9.3-16.5)
	chemokine (C-X-C motif) ligand 10	15945	<b>32.2</b> (21.6-48.0)
	colony stimulating factor 2 (granulocyte-macrophage)	12981	<b>2.6</b> (2.0-3.5)
	colony stimulating factor 2 receptor, beta 1, low-affinity	12983	<b>3.9</b> (2.9-5.2)
	colony stimulating factor 3 receptor (granulocyte)	12986	<b>3.3</b> (2.7-4.2)
	Complement component 5, receptor 1	12273	<b>3.1</b> (1.9-5.1)
	CD14 antigen	12475	<b>6.4</b> (6.1-6.7)
	c-type lectin domain family 4, member d	17474	<b>10.6</b> (8.3-13.5)
	c-type lectin domain family 4, member e	56619	<b>7.3</b> (5.4-9.9)
	c-type lectin domain family 4, member n	56620	<b>3.1</b> (2.2-4.4)
	Epstein-Barr virus induced gene 3	50498	<b>3.5</b> (2.2-5.5)
	Fc receptor, IgE, high affinity I, gamma polypeptide	14127	<b>3.4</b> (2.8-4.2)
	Fc receptor, IgG, high affinity I	14129	<b>6.8</b> (4.8-9.7)
	Fc receptor, IgG, low affinity III	14131	<b>4.3</b> (3.6-5.3)
	guanylate nucleotide binding protein 2	14469	<b>7.3</b> (5.78-9.3)
	guanylate nucleotide binding protein 4	55932	<b>4.5</b> (3.5-5.8)
	interleukin 1 alpha	16175	<b>3.6</b> (2.5-5.3)
	interleukin 1 beta	16176	<b>10.3</b> (7.7-13.8)
	interleukin 1 family, member 9	215257	<b>5.2</b> (3.6-7.6)
	interleukin 1 receptor, type II	16178	<b>13.7</b> (11.3-16.6)
	interleukin 1 receptor antagonist	16181	<b>7.0</b> (4.4-11.1)
	interleukin 6	16193	<b>9.1</b> (5.2-15.8)
	interleukin 15	16168	<b>3.0</b> (2.2-4.3)
	interferon, alpha-inducible protein	53606	<b>12.1</b> (9.3-15.8)
	interferon inducible protein 1	15944	<b>3.8</b> (3.1-4.8)
	interferon activated gene 203	15950	<b>5.3</b> (4.3-6.4)
	interferon gamma inducible protein 47	15953	<b>4.3</b> (3.5-5.2)
	interferon-induced protein with tetratricopeptide repeats 1	15957	<b>12.1</b> (9.3-15.8)
	interferon-induced protein with tetratricopeptide repeats 2	15958	<b>8.9</b> (6.2-12.8)

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	interferon-induced protein with tetratricopeptide repeats 3	15959	<b>10.0</b> (8.0-12.6)
	leukocyte specific transcript 1	16988	<b>3.1</b> (2.4-4.0)
	mediterranean fever	54483	<b>3.6</b> (2.5-5.2)
	myxovirus (influenza virus) resistance 1	17857	<b>5.8</b> (4.0-8.4)
	2'-5' oligoadenylate synthetase 2	246728	<b>3.5</b> (2.8-4.4)
	2'-5' oligoadenylate synthetase 3	246727	<b>5.6</b> (3.9-7.9)
	2'-5' oligoadenylate synthetase-like 2	23962	<b>8.4</b> (6.9-10.1)
	paired-Ig-like receptor B	18733	<b>3.4</b> (2.6-4.3)
	phospholipase A2, group VII	27226	<b>3.9</b> (3.0-4.9)
	toll-like receptor 2	24088	<b>6.3</b> (5.0-8.1)
	triggering receptor expressed on myeloid cells 3	58218	<b>3.0</b> (2.2-4.0)
	tumor necrosis factor (ligand) superfamily, member 9	21950	<b>3.1</b> (2.8-3.4)

### **Apoptosis (n=4)**

B-cell leukemia/lymphoma 2 related protein A1 (a,b,d)	12044/12045/12047	<b>5.1</b> (3.7-7.0)
caspase 11, apoptosis- related cysteine protease	12363	<b>6.2</b> (5.2-7.5)
interferon-induced with helicase C domain 1	71586	<b>4.7</b> (3.8-5.8)
tumor necrosis factor, alpha- induced protein 3	21929	<b>3.4</b> (2.5-4.5)

### **Signal Transduction - Intracellular (n=18)**

A kinase (PRKA) anchor protein (gravin) 12	83397	<b>3.6</b> (2.7-5.0)
down syndrome critical region homolog 1 (human)	54720	<b>3.1</b> (2.6-3.5)
growth arrest and DNA-damage-inducible 45 gamma	23882	<b>3.9</b> (3.6-4.3)
GTP binding protein (overexpressed in skeletal muscle)	14579	<b>3.3</b> (2.4-4.6)
G protein-coupled receptor 109B	80885	<b>5.9</b> (4.6-7.5)
G protein-coupled receptor 65	14744	<b>3.4</b> (2.7-4.3)
G protein-coupled receptor 84	80910	<b>3.0</b> (1.9-4.6)
interferon gamma induced GTPase	16145	<b>4.0</b> (3.2-5.0)
lymphocyte cytosolic protein 2	16822	<b>4.3</b> (3.0-6.1)
MARCKS-like protein	17357	<b>9.5</b> (6.1-14.8)
Metallothionein 1	17748	<b>3.3</b> (3.1-3.5)
Metallothionein 2	17750	<b>3.9</b> (3.7-4.2)
mitogen activated protein kinase kinase kinase 8	26410	<b>3.7</b> (2.5-5.4)
Pleckstrin	56193	<b>4.2</b> (3.3-5.2)
RAB20, member RAS oncogene family	19332	<b>4.8</b> (3.8-6.0)
src-like adaptor	20491	<b>3.5</b> (2.7-4.6)
suppressor of cytokine signaling 3	12702	<b>4.6</b> (3.7-5.6)
Traf2 binding protein	211550	<b>4.3</b> (3.1-6.0)

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<b>Signal Transduction – Cell Surface Receptor (non-immune) (n=6)</b>			
	formyl peptide receptor, related sequence 2	14289	<b>5.0</b> (3.8-6.6)
	MAS-related GPR, member A2	235712	<b>6.9</b> (4.4-10.8)
	membrane-spanning 4-domains, subfamily A, member 6B	69774	<b>4.8</b> (3.7-6.2)
	membrane-spanning 4-domains, subfamily A, member 6C	73656	<b>5.1</b> (3.7-7.0)
	oncostatin M receptor	18414	<b>3.0</b> (2.7-3.3)
	urokinase plasminogen activator receptor	18793	<b>3.5</b> (2.8-4.3)
<b>Transcriptional Regulation (n=17)</b>			
	activating transcription factor 3	11910	<b>4.9</b> (3.6-6.6)
	avian reticuloendotheliosis viral (v-rel) oncogene related B	19698	<b>3.3</b> (2.6-4.2)
	B-cell leukemia/lymphoma 3	12051	<b>4.4</b> (3.3-5.7)
	CCAAT/enhancer binding protein (C/EBP), delta	12609	<b>3.5</b> (3.1-3.9)
	interferon regulatory factor 7	54123	<b>6.9</b> (5.2-9.1)
	Jun-B oncogene	16477	<b>3.2</b> (2.2-4.5)
	LPS-induced TN factor	56722	<b>3.4</b> (3.0-3.9)
	Max dimerization protein	17119	<b>3.1</b> (2.0-4.9)
	nuclear factor, interleukin 3, regulated	18030	<b>4.5</b> (3.6-5.6)
	nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, alpha	18035	<b>3.2</b> (2.8-3.8)
	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta	80859	<b>4.4</b> (3.0-6.4)
	sin3 associated polypeptide	60406	<b>3.0</b> (2.5-3.5)
	signal transducer and activator of transcription 1	20846	<b>3.3</b> (2.6-4.1)
	signal transducer and activator of transcription 2	20847	<b>3.0</b> (2.5-3.6)
	transcription factor EC	21426	<b>3.7</b> (2.9-4.6)
	tripartite motif protein 30	20128	<b>5.0</b> (4.2-6.0)
	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein F (avian)	17133	<b>3.3</b> (2.9-3.7)
<b>Cell Proliferation (n=4)</b>			
	fibrinogen-like protein 2	14190	<b>4.0</b> (3.3-4.7)
	schlafen 1	20555	<b>10.7</b> (7.8-14.6)
	schlafen 2	20556	<b>4.2</b> (3.5-5.1)
	schlafen 4	20558	<b>20.8</b> (16.1-26.8)
<b>Matrix (n=1)</b>			
	chondroitin sulfate proteoglycan 2	13003	<b>6.3</b> (4.1-9.8)
<b>Angiogenesis (n=3)</b>			
	serine (or cysteine) proteinase inhibitor, clade E, member 1	18787	<b>7.7</b> (5.0-11.9)
	thrombospondin 1	21825	<b>3.3</b> (2.4-4.6)
	tumor necrosis factor, alpha- induced protein 2	21928	<b>3.5</b> (2.6-4.8)

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<b>Coagulation (n=3)</b>			
	coagulation factor III	14066	<b>3.0</b> (2.2-4.1)
	coagulation factor VIII, A1 subunit	74145	<b>8.2</b> (5.5-12.1)
	tissue factor pathway inhibitor 2	21789	<b>3.8</b> (2.5-5.8)
<b>Proteolysis (n=2)</b>			
	a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 4	240913	<b>3.8</b> (2.6-5.6)
	tissue inhibitor of metalloproteinase 1	21857	<b>5.9</b> (4.3-8.0)
<b>Metabolism (n=12)</b>			
	arginase type II	11847	<b>4.6</b> (4.1-5.2)
	cholesterol 25-hydroxylase	12642	<b>8.0</b> (6.6-9.7)
	cytidine 5'- triphosphate synthase	51797	<b>3.4</b> (3.2-3.6)
	GTP cyclohydrolase 1	14528	<b>3.7</b> (3.1-4.4)
	glycerol kinase	14933	<b>4.3</b> (3.7-5.0)
	guanine deaminase	14544	<b>3.0</b> (2.1-4.2)
	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	170768	<b>3.4</b> (2.7-4.3)
	superoxide dismutase 2, mitochondrial	20656	<b>3.3</b> (3.0-3.6)
	ST3 beta-galactoside alpha-2,3-sialyltransferase 1	20442	<b>4.4</b> (3.4-5.5)
	transglutaminase 1, K polypeptide	21816	<b>3.2</b> (2.5-4.2)
	uridine phosphorylase 1	22271	<b>6.9</b> (5.0-9.6)
	ubiquitin specific protease 18	24110	<b>7.5</b> (5.8-9.6)
<b>Miscellaneous (n=12)</b>			
	adrenomedullin	11535	<b>6.7</b> (4.8-9.3)
	cytochrome b-245, beta polypeptide	13058	<b>3.7</b> (3.2-4.2)
	hemopexin	15458	<b>2.8</b> (2.5-3.1)
	interleukin 4 induced 1	14204	<b>3.4</b> (3.1-3.8)
	integrin alpha M	16409	<b>4.2</b> (2.6-6.9)
	L-selectin	20343	<b>6.1</b> (4.8-7.7)
	P-selectin	20344	<b>3.7</b> (2.7-5.1)
	serum amyloid A 3	20210	<b>22.8</b> (20.3-25.6)
	solute carrier family 15, member 3	65221	<b>5.8</b> (4.0-8.3)
	solute carrier family 26, member 4	23985	<b>4.5</b> (4.0-5.0)
	three prime repair exonuclease 1	22040	<b>4.0</b> (3.0-5.4)
	thymidylate kinase family LPS-inducible member	22169	<b>6.3</b> (4.6-8.6)

**Supplemental Table 1:** Selected gene expression in the MV+LPS group with 95% confidence intervals relative to mean expression in the Control group. Included genes are those that were upregulated  $\geq 3$ -fold in one or more of the MV-only, LPS-only, and MV+LPS groups as compared with the Control group. Genes are grouped by broad functional classification using the gene ontology classification Mouse Genome Informatics website (<http://www.informatics.jax.org/>) and or published papers.