Supplementary Table 1 Functional analysis of genes that are differentially expressed in the mouse brain following reovirus infection at early times post infection[a]

General function	Specific function	Biological process	Gene symbol	Description	3D	6D	8D
Immune response	Transcription	Interferon type 1 biosynthetic process	Irf9	Interferon regulatory factor 9	4.0	5.6	9.2
			Irf7	Interferon regulatory factor 7	11.7	24.7	65.0
		Cytokine and chemokine signaling	STAT1	Signal transducer and activator of transcription 1	8.4	11.8	33.9
			Stat2	Signal transducer and activator of transcription 2	1.8	0	6.3
			Nmi	N-myc (and Stat1) interactor	2.0	2.8	9.7
		PML body	Pml	Promylocytic leukemia	9.5	0	11.3
			Sp100	Nuclear antigen Sp100	0	35.5	81.1
	Endopeptidase	Antigen presentation	Psmb8	Proteosome (prosome. macropain) subunit, beta type 8 (large multifunctional protease 7)	7.2	14.3	92.3
			Psmb9	Proteosome (prosome, macropain) subunit, beta type 9 (large multifunctional protease 2)	1.3	5.2	27.3
	MHC class II presentation	Antigen presentation	Ctss	Cathepsin C	1.5	1.6	4.2
	MHC class I presentation	Antigen presentation	H2-K1	Histocompatibility 2, K1, K region	1.5	3.5	19.6
			H2-T10	Histocompatibility 2, T region locus 10	2.4	0	21.7
			H2-T23	Histocompatibility 2, T region locus 23	4.3	0	64.7
			B2M	Beta-2 microglobulin	2.6	3.7	9.6
			Fcg	Fc receptor, IgG, high affinity 1	1.9	0	17.1
			Fcer1g	Fc receptor, IgE, high affinity 1 gamma polypyptide	0	1.9	9.4
			Tapbp	TAP binding protein	1.9	0	12.7
	GTP binding	Interferon induced	Gbp2	Guanylate nucleotide binding protein 2	8.9	53.6	111.4
			Gbp3	Guanylate nucleotide binding protein 3	5.2	14.2	36.8
			Gbp6	Guanylate nucleotide binding protein 6	6.5	10.1	32.9
			Irgm1	Immunity related GTPase family M1	7.2	8.8	41.4
			Mpa2l	Macrophage activation like 2	9.2	13.4	83.6
	GTPase	Interferon induced	Igtp	Interferon gamma induced GTPase	15.6	18.5	163.1
			Mx1	Myxovirus (influenza virus) resistance 1	7.0	0	84.2
			Mx2	Myxovirus (influenza virus) resistance 2	31.9	38.1	129.7
			Iigp1	Interferon inducible GTPase 1	25.6	22.2	295.5
			Iigp2	Interferon inducible GTPase 2	9.7	10.7	96.2
			Tgtp	T cell specific GTPase	16.9	31.3	508.4
	RNA binding	Interferon induced	Oas1b	2′-5′oligoadenylate synthetase 1b	5.3	0	24.9
			Oas1g	2′-5′oligoadenylate synthetase 1g	5.8	12.4	33.7
			Oas2	2′-5′oligoadenylate synthetase 2	2.8	0	20.7
			Oasl1	2′-5′oligoadenylate synthetase-like 1	3.3	0	29.0
			Oasl2	2′-5′oligoadenylate synthetase-like 2	32.9	80.3	259.6
	DNA binding	Interferon induced	Ifit1	Interferon-induced protein with tetracopeptide repeats 1	46.6	104.9	233.9
			Ifit2	Interferon-induced protein with tetracopeptide repeats 2	2.7	0	25.8

Supplementary Table 1 *(Continued)*

General function	Specific function	Biological process	Gene symbol	Description	3D	6D	8D
			Ifit3	Interferon-induced protein with tetracopeptide repeats 3	14.6	25.2	127.7
	Helicase	Interferon induced	Ifih1	Interferon-induced protein with helicase C domain 1	6.7	9.7	45.1
		Interferon type I biosynthetic process	Dhx58	DEXH (Asp-glu-X-His) box polypeptide 58	7.7	27.8	49.0
			Ddx58	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	4.9	0	11.9
	Protein binding	NC	Ifi203	Interferon-activated gene 203	0	3.3	15.7
		Interferon induced	Pyhin1	Pyrin and HIN domain family, member 1	5.1	0	81.5
	Receptor activity	Tlr signaling	TLR3	Toll-like receptor 3	2.5	0	8.8
		Interferon induced	Ifitm1	Interferon-induced transmembrane protein 1	0	1.9	6.0
			Ifitm3	Interferon-induced transmembrane protein 3	6.3	9.3	20.9
		Cell adhesion	Lgals9	Lectin, galactosidase-binding, soluble 9	4.4	6.1	22.6
			Lgals3bp	Lectin, galactosidase-binding, soluble, 3 binding protein	8.2	12.9	34.5
			Icam1	Intercellular adhesion molecule 1	0	2.2	10.0
		NC	Itgb2	Integrin beta 2	0	1.3	7.7
			Ly6e	Lymphocyte antigen 6complex, locus e	1.6	2.5	5.0
	Exonuclease	Interferon induced	Isg20	Interferon-stimulated protein	4.5	0	33.6
	Kinase	Interferon induced	Eif2ak2	Eukaryotic translation initiation factor 2-alpha kinase 2	3.3	0	10.8
	Cytokine/ chemokine	Chemotaxis	Ccl12	Chemokine (C-C motif) ligand 12	0	20.5	53.2
			Cxcl10	Chemokine (C-X-C motif) ligand 10	23.1	0	248.8
			Cxcl11	Chemokine (C-X-C motif) ligand 11	7.5	0	198.6
		Apoptosis	Tnfsf10	Tumor necrosis factor (ligand) superfamily, member 10	1.7	2.1	10.8
	Peptidase	Complement activation	C2	Complement component 2 (within H2-S)	0	3.5	10.7
	Phosphate transport	Complement activation	C1qb	Complement component 1, q subcomponent, beta polypeptide	1.8	0	7.5
			C1qa	Complement component 1, q subcomponent, alpha polypeptide	1.6	1.9	5.2
			C1qc	Complement component 1, q subcomponent, C chain	1.5	2.1	7.9
	Complement binding	Complement activation	Serping1	Serine (or cysteine) peptidase inhibitor, clade G member 1	0	1.8	18.3
	Poly-A-polymerase	NC	Parp 9	Poly (ADP-ribose) polymerase family, member 9	8.3	11.7	46.4
	Catalytic activity	Virus response IFN induced	Rsad2	Radical *S*-adenosyl methionine domain containing 2	6.7	0	70.8
	NC	Interferon induced	Ifi44	Interferon-induced protein 44	17.5	33.4	152.2
			Ifi47	Interferon gamma inducible protein 47	7.7	11.9	154.9
	NC	NC	Ifi202b	Interferon-activated 202B	21.9	35.5	353.8
			Plac8	Placenta specific 8	6.1	17.6	93.1
	NC	Natural killer cell mediated cytotoxicity	Cd48	CD48 antigen	0	1.9	8.4
			Tyrobp	TYRO protein tyrosine kinase binding protein	0	1.4	3.2
Defense response	GPI anchored	Cell proliferation	Ly6a	Lymphocyte antigen 6 complex, locus A	4.3	14.7	45.5
	Macrophage associated	NC	Mpeg1	Macrophage expressed gene 1	1.1	0	8.9
	Lysozyme activity	Defense response to bacteria	Lyz2	Lysozyme 2	2.0	2.3	14.5
			Lyz1	Lysozyme 1	2	2.9	15.2

Supplementary Table 1 *(Continued)*

General function	Specific function	Biological process	Gene symbol	Description	3D	6D	8D
Ubiquitin cycle	Ubiquitin ligase	Interferon induced	Dtx31	Deltrex 3-like (*Drosophila*)	3.9	5.9	21.6
		NC	Herc5	Hect domain and RLD5	2.9	0	25.9
		Protein modification	Trim25	Tripartate motif protein 25	2.1	2.6	7.5
			Trim21	Tripartate motif protein 21	3.2	2.5	12.7
			Ube2l6	Ubiquitin conjugating enzymeE2L6	0	2.6	15.7
	Ubiquitin activating	Protein modification	Ube1l		4.8	2.9	24.4
	Peptidase	Interferon induced	Usp18	Ubiquitin specific protease	34.0	84.4	206.1
Signal transduction	Receptor	NC	Ms4a4d	Membrane-spanning 4-domains, subfamily A, member 4d	1.6	3.2	24.3
			Ms4a4c	Membrane-spanning 4-domains, subfamily A, member4c	0	11.2	116.6
			Ms4a4b	Membrane-spanning 4-domains, subfamily A, member 4b	2.1	2.2	25.0
	Transmembrane receptor protein tyrosine kinase activity	NC	Pik3ap1	Phosphoinositide 3 kinase adaptor protein 1	1.5	2.1	12.6
Chaperone	ATP binding	Protein folding	Tor3a	Torsin family 3, member A	2.8	0	15.9
Metabolism	Phospholipase	Lipid catabolism	Pld4	Phospholipase D family member 4	0	1.6	4.2
	Acyltransferase activity	Lipid metabolism	Lpcat1	Lysophosphatidylcholine acetyltransferase 1	-2.2	0	0
	Inflammatory response	Protein binding	Apoptosis	Pycard	PYD and CARD		
domain containing	1.6	0	8.4				
NC	P53 signal transduction	Apoptosis	Nupr1	Nuclear protein 1	0	1.6	3.1
	Poly-A-polymerase	Transcription regulation	Parp14		5.6	6.8	47.7
		NC	Parp12		4.6	6.3	22.4
	Transcriptional regulation	IL6 biosynthetic process	Cebpb (C/EBP), beta	CCAAT enhancer binding protein	0	1.4	4.7
	Apoptosis	Interferon induced	XAF-1	XIAP associated factor 1	14.1	17.8	65.3
	Caspase activity	Apoptosis	Casp 4	Casapse 4	0	48.3	198.4
	P53 signaling	Apoptosis	Shisa5	Shisa homolog 5	1.4	0	2.8
	Ras protein signal transduction	Cytokine-cytokine receptor interaction	Csf1	Colony-stimulating factor 1	0	2.0	4.1
	Helicase	NC	Mov10	Moloney leukemia virus 10	1.3	0	3.3
	Protein transport	NC	Mitd1	RMIT, microtubule interacting and transport, domain containing 1	1.9	0	4.7
	GTP binding	G protein coupled receptor protein signaling	Tgm2	Transglutaminase 2, C polypeptide	0	1.2	8.6
	GTPase	Small GTPase mediated signal transduction	Rac2	Ras-related C3 botulinum substrate 2	0	1.5	4.4
	GTP cyclohydrolase I activity	Neuromuscular process	Gch1	GTP cyclohydrolase 1	0	1.5	5.0
	Ferroxidase activity	Oxidation/reduction	Cp	Ceruloplasmin	0	1.7	6.4
	Iron ion binding	Oxidation/reduction	Cyba	Cytochrome b-245, alpha polypeptide	0	1.4	4.5
	Transport	NC	Apod	Apolipoprotein D	1.8	2.9	7.5
	Receptor		Rtp4	Receptor transporter protein 4	15.3	32.3	58.7

Supplementary Table 1 *(Continued)*

General function	Specific function	Biological process	Gene symbol	Description	3D	6D	8D
		Interferon-induced					
	Protein/nucleic acid binding	Interferon induced	Trim 34	Tripartite motif protein 34	2.3	0	7.7
		NC	Trim 30	Tripartite motif protein 30	3.4	2.8	23.4
			Phf20l1	PHD finger protein 20-like 1	3.0	4.3	13.2
			Brd4	Bromodomain containing 4	12.0	21.9	114.3
	Actin binding	NC	Plec1	Plectin 1	2.5	0	23.5
			Lcp-1	Lymphocyte cytosolic	0	1.8	6.8
		Regulation of actin cytoskeleton	Arpc1b	protein 1 Actin-related protein 2/3 complex, subunit 1b	0	1.3	2.9
	NC	Interferon induced	Ifi35	Interferon-induced protein 35	6.2	9.7	56.1
		Cell-cell adhesion	Itgal	Integrin alpha L	0	1.7	4.3
		NC	CD52	CD52 antigen	0	4.1	27.1
			Epsti1	Epithelial stromal interaction 1 (breast)	7.2	1.9	31.1
			D12Ertd647e	DNA segment, Chr 12, ERATO Doi 668 expressed	3.2	4.3	3.4
			Samd9l	Sterile alpha motif domain containing 9 like	2.6	3.5	21.7
			Phf11	PHD finger protein 11	4.8	0	39.3
			Slfn2	Schlafen 2	4.0	0	27.6
			Slfn8	Schlafen 8	6.9	0	56.7
			Rnf213	Ring finger protein 213 9830115L13Rik	4	1.4	24.9
			RIKEN		4.2	18.0	
			cDNA	3.6			
			9830115L13 gene				
				0610037M15Rik			
			RIKEN		3.2	20.3	
			cDNA	0			
					2.6	2.8	9.7
				0610037M15 gene cDNA sequence			
			BC006779	BC006779			
			Ddx60	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60	17.4	9.6	54.6
				Expressed sequence	1.5	0	5.0
			Al413194	Al413194 Predicted gene	8.5	11.4	33.7
			100042856	100042856			
				Predicted gene 677168	15.5	49.8	167.3
				Transmembrane protein	0	2.4	8.5
			677168				
			Tmem140	140			
				Apolipoprotein L9a	0	4.6	35.9
			Apol 9a	NLR family CARD containing 5	0	4.6	55.3
			Nlrc5	Probe set ID:1438027	4.8	3.8	33.0
Probe set ID:	2.4						
1442201		5.6		20.2			
Probe set ID:							
1447213	0	3.2		6.7			

[a] Identified genes were differentially regulated in the brains of reovirus infected mice at day 3 and/or day 6 post infection. Probe sets from Table 1 representing the same gene were combined and the fold increases for these probe sets were averaged. All genes that were not differentially regulated by at least 2-fold at any day post infection were excluded from the table. All identified differentially regulated genes (except one) were up-regulated in reovirus-infected, compared to mock-infected, animals, with a false detection rate (FDR) of.1 and $P < .002$. These genes were also up-regulated at day 8 post infection.