

**Table S3. Genes downregulated in *or<sup>l</sup>* mutants by microarray analysis**

UNIQID	Unigene	Name	E12.5	E12.5 swap	E13.5-1	E13.5-1 swap	E13.5-2	E13.5-2 swap
AI852799	Mm.22231	synuclein, gamma	0.33	0.25	0.31	0.21	0.21	0.17
	Mm.4636	Neurogenic differentiation 1 (NeuroD)	0.24	0.21	0.31	0.27	0.23	0.23
AI841966	Mm.6670	protein kinase, AMP-activated, gamma 1 non-catalytic subunit	0.34	0.31	0.28	0.21	0.24	0.18
AI840972	Mm.29580	stathmin-like 2	0.28	0.3	0.32	0.24	0.26	0.26
AI836519	Mm.25165	ALL1-fused gene from chromosome 1q	0.34	0.28	0.32	0.22	0.36	0.27
AI841303	Mm.1222	growth associated protein 43	0.35	0.31	0.46	0.43	0.35	0.3
AI835930		Ribosomal RNA	0.25	0.31	0.44	0.32	0.53	0.54
AI848068	Mm.4323	microtubule-associated protein 1 B	0.48	0.4	0.43	0.44	0.36	0.3
AI851775	Mm.903	B-cell translocation gene 2, anti-proliferative	0.19	0.15	0.43	0.57	0.56	0.57
AI841267	Mm.2319	stathmin-like 3	0.49	0.65	0.35	0.43	0.33	0.25
	Mm.10695	Neurogenic differentiation 4 (Math3)	0.33	0.52	0.44	0.46	0.37	0.47
AI848445	Mm.27578	melanoma antigen, family D, 1	0.48	0.4	0.56	0.43	0.43	0.31
AI843116	Mm.61526	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	0.5	0.37	0.47	0.53	0.5	0.41
AI849592	Mm.3970	ELAV (Drosophila)-like 4 (Hu antigen D)	0.42	0.43	0.54	0.56	0.44	0.46
AI848983	Mm.32884	tubulin, alpha 8	0.52	0.42	0.54	0.37	0.6	0.47
AI848368	Mm.4435	synaptosomal-associated protein 25	0.42	0.45	0.7	0.54	0.38	0.44
AI850105	Mm.28479	stathmin 1	0.67	0.45	0.63	0.37	0.52	0.32
AI841233	Mm.101976	potassium voltage gated channel, Shaw-related subfamily, member 4	0.5	0.52	0.58	0.46	0.51	0.41
AI846286	Mm.218788	beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P)	0.66	0.47	0.64	0.4	0.51	0.35
	Mm.22288	Cyclin D1	0.33	0.36	0.74	0.68	0.47	0.47
AI845079		EST	0.54	0.52	0.54	0.41	0.58	0.47
AI851861	Mm.156164	RIKEN cDNA 6430547I21 gene	0.63	0.55	0.89	0.36	0.37	0.31
AI840604	Mm.1155	tubulin, alpha 4	0.6	0.43	0.58	0.41	0.68	0.42
AI854858	Mm.256966	microtubule-associated protein 2	0.52	0.56	0.61	0.58	0.43	0.44
AI850627		EST	0.63	0.42	0.61	0.39	0.68	0.42
AI838066	Mm.182912	growth hormone inducible transmembrane protein	0.57	0.52	0.61	0.42	0.53	0.51
AI835385	Mm.29324	lactate dehydrogenase 1, A chain	0.55	0.4	0.58	0.39	0.72	0.54
AI846851	Mm.39472	farnesyl diphosphate synthetase	0.62	0.5	0.58	0.43	0.6	0.46
AI837019	Mm.40068	tubulin, beta 3	0.8	0.61	0.57	0.39	0.51	0.35
AI837745	Mm.22421	telomerase binding protein, p23	0.66	0.4	0.66	0.4	0.73	0.41
AI848759	Mm.3204	farnesyl diphosphate farnesyl transferase 1	0.59	0.48	0.57	0.43	0.71	0.53
AI849399	Mm.45759	Musculus, clone IMAGE:5325914, mRNA	0.65	0.42	0.7	0.41	0.72	0.42
AI839893	Mm.231463	tubulin, alpha 2	0.64	0.44	0.54	0.44	0.76	0.51
AI839009	Mm.29902	phosphoserine aminotransferase 1	0.58	0.5	0.5	0.44	0.71	0.62
AI837103	Mm.40673	expressed sequence AI316785	0.68	0.52	0.62	0.4	0.67	0.46
AI850603	Mm.133615	RIKEN cDNA 2810457I06 gene	0.62	0.43	0.61	0.47	0.74	0.54
AI849291	Mm.3111	ribosomal protein L28	0.81	0.58	0.62	0.4	0.58	0.41
AI850549	Mm.37819	DNA segment, Chr 5, Brigham & Women's Genetics 0860 expressed	0.58	0.57	0.51	0.55	0.62	0.58
AI845046	Mm.4142	trans-golgi network protein 1	0.63	0.55	0.62	0.55	0.61	0.5
AI844837		EST	0.75	0.43	0.61	0.47	0.67	0.53
	Mm.8008	Cone-rod homeobox containing gene (Crx)	0.63	0.78	0.45	0.53	0.51	0.56
AI845893	Mm.42242	ISL1 transcription factor, LIM/homeodomain (islet 1)	0.76	0.6	0.65	0.55	0.48	0.44
AI836851	Mm.27307	guanine nucleotide binding protein (G protein), gamma 3 subunit	0.64	0.68	0.62	0.55	0.5	0.5
AI839739		EST	0.7	0.45	0.66	0.43	0.78	0.47
AI842035		EST	0.83	0.79	0.63	0.47	0.46	0.35
AI849910		EST	0.81	0.51	0.59	0.39	0.85	0.45
AI840446	Mm.24059	schwannomin interacting protein 1	0.62	0.56	0.68	0.65	0.59	0.49
AI840227	Mm.18923	minichromosome maintenance deficient 7 (S. cerevisiae)	0.74	0.61	0.52	0.5	0.67	0.57
AI849333	Mm.218657	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	0.7	0.67	0.51	0.44	0.67	0.63
AI843193	Mm.138083	RIKEN cDNA E130114P18 gene	0.57	0.64	0.63	0.7	0.56	0.55
AI838225	Mm.41484	RIKEN cDNA 1500015O20 gene	0.54	0.61	0.67	0.69	0.69	0.5
AI845505	Mm.246377	tubulin, beta 2	0.81	0.68	0.62	0.48	0.64	0.48
AI843805	Mm.4435	synaptosomal-associated protein 25	0.45	0.66	0.66	0.85	0.51	0.61
AI853846	Mm.741	fatty acid binding protein 5, epidermal	0.79	0.75	0.71	0.5	0.56	0.44
	Mm.20355	Wingless-related MMTV integration site 4 (Wnt4)	0.69	0.5	0.76	0.46	0.79	0.54
	Mm.1956	Neurofilament, light polypeptide (NF68)	0.8	0.85	0.64	0.51	0.49	0.47
AI845354	Mm.232930	neuritin 1	0.74	0.8	0.68	0.71	0.42	0.43
AI853301	Mm.16533	polymerase (RNA) II (DNA directed) polypeptide A	0.77	0.71	0.75	0.54	0.54	0.49
AI838520	Mm.41803	developmentally regulated GTP binding protein 2	0.82	0.59	0.72	0.49	0.72	0.47
AI844406	Mm.137278	RIKEN cDNA C030046I01 gene	0.67	0.57	0.8	0.59	0.64	0.55
AI843545	Mm.155896	heterogeneous nuclear ribonucleoprotein A2/B1	0.72	0.56	0.67	0.46	0.85	0.6
AI836520	Mm.268166	histone 3, H2bb	0.6	0.51	0.97	0.67	0.68	0.47
AI854838	Mm.42972	Ywhae	0.75	0.6	0.74	0.54		0.65
AI848998	Mm.29075	reticulon 1	0.67	0.7	0.8	0.78	0.52	0.49
AI849379	Mm.1147	Calmodulin 2	0.59	0.57	0.76	0.59	0.77	0.69
AI845040	Mm.254	tumor protein, translationally-controlled 1	0.86	0.66	0.64	0.48	0.75	0.57
AI852915	Mm.5101	synaptotagmin 1	0.67	0.52	0.86	0.75	0.74	0.43
AI845300	Mm.2223	t-complex protein 1	0.64	0.51	0.79	0.59	0.81	0.65
AI851946	Mm.140700	RIKEN cDNA 2610316D01 gene	0.69	0.85	0.44	0.67	0.62	0.74
AI845631	Mm.235585	dihydropyrimidinase-like 2	0.64	0.44	0.83	0.66	0.73	0.72
AI852614	Mm.28323	RIKEN cDNA G630055P03 gene	0.63	0.39	0.72	0.61	1.06	0.63
AI843214	Mm.36683	eukaryotic translation elongation factor 1 epsilon 1	0.55	0.59	0.65	0.79	0.7	0.77
AI841020	Mm.188	phosphoglycerate kinase 1	0.7	0.53	0.73	0.51	0.94	0.68
AI840089	Mm.6787	splicing factor, arginine/serine-rich 3 (SRp20)	0.75	0.57	0.74	0.54	0.83	0.68

AI841335		EST	0.91	0.67	0.73	0.51	0.75	0.56
AI835506		EST	0.66	0.65	0.67	0.61	0.79	0.75
AI852638	Mm.26381	spastic paraplegia 3A homolog (human)	0.86	0.76	0.74	0.71	0.59	0.47
AI841389	Mm.90587	enolase 1, alpha non-neuron	0.74	0.52	0.76	0.47	1	0.68
AI836137	Mm.216135	pyruvate kinase, muscle	0.57	0.61	0.62	0.51	1.04	0.84
AI849319	Mm.140672	Smarcd3	0.69	0.6	0.68	0.58	0.88	0.75
AI847555	Mm.4762	kinesin family member 1A	0.76	0.67	0.65	0.53	0.79	0.8
AI846050	Mm.196219	RIKEN cDNA 1110005A05 gene	0.82	0.6	0.82	0.64	0.75	0.6

Genes listed are those downregulated at least 0.7-fold, as represented by the ratio of signal in *or<sup>l</sup>* mutants relative to wild-type controls. Genes listed without unique IDs are full-length clones from within our laboratory. Unigene numbers and full names are indicated. Data points include one E12.5 sample and two E13.5 samples with associated color swaps.

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