

Supplementary Materials

Supplemental Tables

Table S1: List of primers sequences forward and reverse from 5'-3' used for RT-qPCR

RT-qPCR primers				
Genes				
<i>Rxrg</i>	Forward	TGAACTACCCATCCACCAGC	Reverse	GGCACTTCTGATAGCGACA
<i>Fosl2</i>	Forward	AGATGAGCAGCTGTCTCCTG	Reverse	GCTTGATGACAGAGCGCT
<i>Pml</i>	Forward	TTTCCGTGCAGAAGGTACCT	Reverse	GAACCAGTTTCCGTGCAGAA
<i>Ddit3</i>	Forward	CACCTGAAAGCAGAACCTGG	Reverse	GGACGCAGGGTCAAGAGTAG
<i>Tfap2b</i>	Forward	ACTTAGCTCGGGATTTCTGGG	Reverse	AGACTGAAGTGCCTGAGACA
<i>Fosl1</i>	Forward	CTCATTTCTGGGGCCCA	Reverse	ATTTTGAGATGGGTCGGTG
<i>Cx32</i>	Forward	GTACCCCACTTTGGGAGTCA	Reverse	TCCGATTTATCTGCCTGCTT
<i>Prx</i>	Forward	TGAGTGCCCGTGTGTTCTTT	Reverse	GCGCTTCAAGCAGAAGGAGA
<i>Chka</i>	Forward	GGCCAAGATCTCATCCATTGAA	Reverse	TGGTCAAAGTAGGCCTCGAATC
<i>Scd1</i>	Forward	CCTCTGGAGCCACAGAACTT	Reverse	GCCATGGTGTGGCAATGAT
<i>Cyp51</i>	Forward	ACGCTGCCTGGCTATTGC	Reverse	TTGATCTCTCGATGGGCTCTATC
<i>Hmgcr</i>	Forward	AACTGGTGCAGAAATCTCTAGC	Reverse	GGTTGAATAGCTCAGAACTAGCC
<i>Dhcr7</i>	Forward	CAAGACACCACCTGTGACAGCT	Reverse	CTGCTGGAGTAATGGCACCTTC
<i>Mag</i>	Forward	GTTTGCCCCCATAATCCTTCTG	Reverse	TCCCTCTCCGTCTATTACAGTC
<i>S100b</i>	Forward	GCTGAGCAAGAAAGAACTGAA	Reverse	AGCCACCAGCACAAACATAC
<i>Pou3f1</i>	Forward	TTCAAGCAACGACGCATCAA	Reverse	TGCGAGAACACGTTACCGTAGA

Table S2: List of 180 transcriptional regulators found in common in RNA-seq 1 and in RNA-seq 2 data sets (with FC >2)

Gene symbol	Full name	1st RNA-seq		2nd RNA-seq	
		Fold change	P-value	Fold change	P-value
Chp2	calcineurin-like EF hand protein 2	0,13	2,03E-34	0,07	6,84718E-37
Abca2	ATP-binding cassette, sub-family A (ABC1), member 2	0,14	2,20E-39	0,22	1,37891E-09
Wnt6	wingless-type MMTV integration site family, member 6	0,16	3,81E-35	0,40	0,000136894
Lmo1	LIM domain only 1	0,17	9,28E-05	0,19	2,63034E-09
Ldlr	low density lipoprotein receptor	0,2	4,14E-54	0,33	1,317E-09
Cdh1	cadherin 1	0,2	1,31E-02	0,18	8,95745E-06
Mitf	microphthalmia-associated transcription factor	0,2	6,09E-14	0,28	0,000494504
Ednrb	endothelin receptor type B	0,22	3,76E-53	0,32	7,48202E-07
Plp1	proteolipid protein (myelin) 1	0,22	1,10E-31	0,28	1,39242E-07
Rxrg	retinoid X receptor gamma	0,23	8,93E-23	0,18	1,1578E-15
Pou3f1	POU domain, class 3, transcription factor 1	0,23	1,62E-24	0,30	1,62105E-08
Rps6ka2	ribosomal protein S6 kinase, polypeptide 2	0,24	4,47E-21	0,29	5,147E-07
Mapre3	microtubule-associated protein, RP/EB family, member 3	0,24	2,05E-24	0,32	3,90711E-07
Bmp7	bone morphogenetic protein 7	0,26	3,59E-13	0,30	3,48314E-10
Cux1	cut-like homeobox 1	0,28	6,05E-25	0,41	0,00190925
Pf4	platelet factor 4	0,29	1,45E-21	0,18	9,41636E-05
Satb1	special AT-rich sequence binding protein 1	0,3	4,22E-12	0,28	2,17096E-11
Cntn1	contactin 1	0,3	1,01E-12	0,20	2,04809E-10
S100a1	S100 calcium binding protein A1	0,31	4,99E-22	0,18	2,06644E-10
Cdkn1c	cyclin-dependent kinase inhibitor 1C (P57)	0,32	1,02E-19	0,25	6,32991E-08
Mxd4	Max dimerization protein 4	0,33	1,20E-40	0,37	8,26742E-13
Arnt2	aryl hydrocarbon receptor nuclear translocator 2	0,33	1,34E-10	0,36	0,000810952
Crebl2	cAMP responsive element binding protein-like 2	0,33	5,22E-11	0,42	1,06238E-06
Pcx	pyruvate carboxylase	0,34	3,26E-02	0,32	7,35847E-10
Sirt2	sirtuin 2	0,34	1,98E-19	0,38	1,45367E-10
Itga6	integrin alpha 6	0,35	4,78E-22	0,49	0,000101818
Foxo4	forkhead box O4	0,35	1,04E-15	0,47	1,40326E-06
Tead4	TEA domain family member 4	0,35	1,21E-04	0,42	0,00046445
Hdac11	histone deacetylase 11	0,35	2,70E-11	0,37	1,14622E-07
Mt3	metallothionein 3	0,36	2,57E-05	0,14	8,68786E-09
Nacc2	nucleus accumbens associated 2, BEN and BTB (POZ) domain containing	0,37	7,23E-15	0,43	0,000108766
Cryab	crystallin, alpha B	0,38	4,71E-14	0,32	9,70727E-05
Pink1	PTEN induced putative kinase 1	0,38	2,03E-25	0,38	9,42704E-07
Mlip	muscular LMNA-interacting protein	0,38	2,09E-17	0,24	7,54258E-07
Kras	Kirsten rat sarcoma viral oncogene homolog	0,38	2,96E-24	0,37	8,611E-10
Ndfip2	Nedd4 family interacting protein 2	0,43	4,52E-13	0,39	1,2006E-08
Ndp	Norrie disease (pseudoglioma) (human)	0,43	6,41E-04	0,19	2,72185E-09
Med12l	mediator complex subunit 12-like	0,43	5,17E-12	0,44	0,0111337
Myo6	myosin VI	0,44	9,97E-11	0,33	2,37983E-09
Slc40a1	solute carrier family 40 (iron-regulated transporter), member 1	0,44	9,82E-05	0,33	3,52664E-05
Taf13	TATA-box binding protein associated factor 13	0,44	6,13E-17	0,42	0,000153922

Ccdc85b	coiled-coil domain containing 85B	0,45	4,15E-17	0,40	4,56285E-05
Wwp1	WW domain containing E3 ubiquitin protein ligase 1	0,45	5,81E-13	0,32	1,66815E-07
Hes6	hairy and enhancer of split 6	0,46	1,30E-02	0,40	0,00017627
Acvr2b	activin receptor IIB	0,47	3,63E-09	0,49	2,58661E-05
Nfkbiz	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, zeta	2,02	1,65E-05	2,34	0,000108672
Aif1	allograft inflammatory factor 1	2,04	1,16E-05	2,81	0,007901834
Zfp217	zinc finger protein 217	2,06	1,71E-07	2,13	1,29565E-09
Lbh	limb-bud and heart	2,10	2,56E-14	2,40	2,13819E-08
Pprc1	peroxisome proliferative activated receptor, gamma, coactivator-related 1	2,12	1,48E-14	2,38	2,20134E-09
Sbno2	strawberry notch homolog 2 (Drosophila)	2,21	2,02E-16	2,30	4,01286E-06
Nr1d1	nuclear receptor subfamily 1, group D, member 1	2,27	2,38E-08	2,29	7,8723E-08
Havcr2	hepatitis A virus cellular receptor 2	2,28	9,60E-04	3,12	0,001866767
Rara	retinoic acid receptor, alpha	2,28	1,42E-16	2,37	2,02428E-16
Sap30	sin3 associated polypeptide	2,28	5,51E-11	2,02	0,01902268
Mafk	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein K (avian)	2,28	1,55E-17	2,26	6,7839E-10
Elf4	E74-like factor 4 (ets domain transcription factor)	2,30	4,26E-07	2,48	7,22031E-07
Akna	AT-hook transcription factor	2,33	5,66E-15	2,64	3,07559E-10
Nr4a3	nuclear receptor subfamily 4, group A, member 3	2,33	1,98E-02	3,81	3,7224E-12
Klf6	Kruppel-like factor 6	2,5	4,85E-15	2,05	4,27739E-07
Slc11a1	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	2,53	1,75E-10	2,82	0,001164602
Stat3	signal transducer and activator of transcription 3	2,56	9,34E-25	2,60	1,66724E-12
Hmga2	high mobility group AT-hook 2	2,60	1,31E-18	3,40	0,002863609
Itga3	integrin alpha 3	2,64	1,27E-03	2,06	0,001591151
Il18	interleukin 18	2,65	8,67E-06	2,43	0,009146839
Mdfic	MyoD family inhibitor domain containing	2,70	2,45E-12	2,25	6,39424E-14
Brip1	BRCA1 interacting protein C-terminal helicase 1	2,73	6,38E-13	2,21	2,17992E-06
Tox2	TOX high mobility group box family member 2	2,76	2,32E-12	2,38	0,001456075
Tnfrsf1a	tumor necrosis factor receptor superfamily, member 1a	2,82	2,18E-26	2,89	3,85969E-09
Fstl3	folliculin-like 3	2,84	4,75E-14	3,25	2,41436E-08
Anxa7	annexin A7	2,85	4,34E-28	2,09	6,10574E-08
Nfkbid	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, delta	2,95	6,30E-07	5,47	1,11452E-06
Ahr	aryl-hydrocarbon receptor	3,04	1,58E-30	2,93	4,66968E-16
Nampt	nicotinamide phosphoribosyltransferase	3,06	2,82E-30	2,64	5,28671E-12
Atp8b1	ATPase, class I, type 8B, member 1	3,17	1,53E-13	3,12	1,63129E-12
Twist2	twist basic helix-loop-helix transcription factor 2	3,18	2,07E-22	2,12	0,01154229
Ptgfr	prostaglandin F receptor	3,18	6,36E-03	2,53	0,000101028
Runx1	runt related transcription factor 1	3,18	2,72E-10	2,85	1,30824E-07
Slit2	slit homolog 2 (Drosophila)	3,29	1,84E-20	4,40	5,43469E-06
Tlr9	toll-like receptor 9	3,37	7,79E-09	6,10	1,30055E-05
Atad2	ATPase family, AAA domain containing 2	3,44	3,36E-12	3,00	7,69494E-16
Smad3	SMAD family member 3	3,54	9,02E-20	2,62	7,33453E-06
Cdk6	cyclin-dependent kinase 6	3,56	9,57E-08	2,38	3,9933E-05
Nfkb2	nuclear factor of kappa light polypeptide gene enhancer in B cells 2, p49/p100	3,59	3,37E-35	4,17	1,58577E-25

Tmem173	transmembrane protein 173	3,61	6,46E-24	2,61	0,000558315
Skil	SKI-like	3,65	8,27E-31	2,38	5,71751E-06
Tlr2	toll-like receptor 2	3,73	2,33E-22	4,12	2,07157E-07
Serpinb9	serine (or cysteine) peptidase inhibitor, clade B, member 9	3,87	2,82E-09	3,22	1,91432E-05
Tnfrsf10b	tumor necrosis factor receptor superfamily, member 10b	3,88	8,44E-08	5,48	1,2247E-22
Glis3	GLIS family zinc finger 3	3,93	5,75E-07	2,48	0,00118371
Trib1	tribbles pseudokinase 1	3,93	1,33E-32	2,51	0,000180333
Fhl2	four and a half LIM domains 2	3,94	1,27E-32	2,27	4,75296E-07
Relb	avian reticuloendotheliosis viral (v-rel) oncogene related B	3,94	4,76E-38	3,71	6,03492E-33
Cd44	CD44 antigen	4,01	1,43E-36	2,87	8,40137E-15
Plk3	polo-like kinase 3	4,11	3,11E-36	4,27	9,23557E-17
Nupr1	nuclear protein transcription regulator 1	4,13	1,23E-31	3,04	0,001415459
Plscr1	phospholipid scramblase 1	4,14	1,37E-31	4,02	2,75273E-13
Fosb	FBJ osteosarcoma oncogene B	4,17	1,03E-14	2,50	2,75806E-09
Pawr	PRKC, apoptosis, WT1, regulator	4,25	3,08E-17	2,57	0,000203418
Wnt10a	wingless-type MMTV integration site family, member 10A	4,25	3,61E-13	9,17	2,21255E-17
Lrrc32	leucine rich repeat containing 32	4,33	3,44E-70	3,73	4,95112E-11
Vegfa	vascular endothelial growth factor A	4,41	6,07E-45	2,28	8,77636E-05
Pcgf5	polycomb group ring finger 5	4,42	9,63E-33	3,83	4,51901E-26
Smad7	SMAD family member 7	4,43	1,82E-22	2,42	0,000106198
Fos	FBJ osteosarcoma oncogene	4,45	3,60E-38	2,68	1,45294E-07
Tgfb1	TGFB-induced factor homeobox 1	4,51	3,87E-79	3,71	1,82438E-22
Klf10	Kruppel-like factor 10	4,58	1,23E-37	4,30	1,0843E-19
Daxx	Fas death domain-associated protein	4,63	5,28E-43	5,35	3,05745E-17
Stc1	stanniocalcin 1	4,64	6,33E-11	2,31	0,002520536
Ccr5	chemokine (C-C motif) receptor 5	4,70	1,48E-24	7,80	4,331E-07
Atf5	activating transcription factor 5	4,78	9,09E-54	4,86	3,74928E-13
Nfkb1a	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, alpha	4,86	5,91E-39	3,01	1,47194E-05
Nr1h3	nuclear receptor subfamily 1, group H, member 3	4,98	2,33E-20	2,17	0,004106621
Hes1	hairly and enhancer of split 1 (Drosophila)	5,13	1,76E-23	3,34	2,04765E-09
Arid5a	AT rich interactive domain 5A (MRF1-like)	5,21	9,68E-36	3,12	4,42175E-24
Cebpg	CCAAT/enhancer binding protein (C/EBP), gamma	5,21	4,02E-32	3,08	3,12405E-11
F2rl1	coagulation factor II (thrombin) receptor-like 1	5,25	4,56E-27	4,17	1,98446E-05
Irf1	interferon regulatory factor 1	5,27	1,97E-03	9,85	6,13646E-35
Bhlhe40	basic helix-loop-helix family, member e40	5,30	1,80E-77	2,88	1,93539E-05
Hoxb9	homeobox B9	5,42	9,23E-50	11,66	3,37922E-58
Il33	interleukin 33	5,66	1,02E-27	3,32	3,92711E-06
Fosl2	fos-like antigen 2	5,69	2,13E-82	5,75	4,47782E-25
Pml	promyelocytic leukemia	5,72	2,99E-25	5,31	1,04565E-45
Arntl2	aryl hydrocarbon receptor nuclear translocator-like 2	5,92	2,21E-15	3,84	5,03252E-07
Csf1	colony stimulating factor 1 (macrophage)	6,09	2,42E-40	5,54	2,81091E-24
Bcl6	B cell leukemia/lymphoma 6	6,10	5,98E-30	2,31	4,93096E-05
Cebpb	CCAAT/enhancer binding protein (C/EBP), beta	6,17	4,48E-48	2,85	0,006042819

Zfp36	zinc finger protein 36	6,20	2,38E-95	4,29	2,39901E-18
Cited2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	6,31	5,26E-80	3,73	9,41158E-09
Irf5	interferon regulatory factor 5	6,55	3,13E-44	5,41	1,84498E-11
Trim6	tripartite motif-containing 6	6,73	5,80E-09	7,78	1,77033E-17
Ncoa7	nuclear receptor coactivator 7	6,75	4,93E-93	2,04	5,93745E-07
Nr1h4	nuclear receptor subfamily 1, group H, member 4	6,83	1,85E-05	3,38	0,000441343
Noct	nocturnin	6,98	3,31E-67	2,99	9,91041E-17
Lef1	lymphoid enhancer binding factor 1	6,98	2,93E-17	3,93	1,46723E-06
Dusp5	dual specificity phosphatase 5	7,02	3,92E-35	4,78	1,18189E-23
Myc	myelocytomatosis oncogene	7,13	5,82E-72	3,38	2,10193E-23
Irf9	interferon regulatory factor 9	7,24	1,10E-33	11,24	4,46792E-62
Plaur	plasminogen activator, urokinase receptor	7,32	2,26E-34	3,09	0,000188141
Arhgef2	rho/rac guanine nucleotide exchange factor (GEF) 2	7,40	1,33E-63	5,46	2,05032E-21
Cebpd	CCAAT/enhancer binding protein (C/EBP), delta	7,69	4,64E-116	4,69	4,9312E-08
Atf3	activating transcription factor 3	8,13	6,45E-65	4,99	5,47452E-19
Batf3	basic leucine zipper transcription factor, ATF-like 3	8,65	1,29E-34	6,90	1,79678E-17
Stat1	signal transducer and activator of transcription 1	9,20	5,82E-07	13,45	9,0428E-126
Nfkbie	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, epsilon	9,43	6,30E-61	7,44	7,75899E-41
Bcl3	B cell leukemia/lymphoma 3	9,43	3,40E-65	5,53	1,36978E-27
Lgals9	lectin, galactose binding, soluble 9	10,39	3,67E-46	9,44	1,803E-24
Runx2	runt related transcription factor 2	10,90	8,17E-20	6,67	8,92795E-13
Tnc	tenascin C	11,00	8,27E-111	13,44	5,77657E-58
Maff	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein F (avian)	11,80	2,18E-115	7,17	2,94135E-20
Egr1	early growth response 1	12,57	4,46E-193	9,98	1,26304E-61
Ddit3	DNA-damage inducible transcript 3	12,65	9,42E-76	5,56	1,49929E-10
Nfil3	nuclear factor, interleukin 3, regulated	13,56	7,69E-101	5,49	2,48454E-15
Helz2	helicase with zinc finger 2, transcriptional coactivator	14,24	4,39E-52	21,07	3,13212E-84
Lck	lymphocyte protein tyrosine kinase	14,91	1,08E-36	6,91	0,000104289
Mndal	myeloid nuclear differentiation antigen like	16,18	1,33E-17	18,10	1,74483E-24
Tlr3	toll-like receptor 3	16,58	1,07E-115	12,23	2,81941E-40
Serpine1	serine (or cysteine) peptidase inhibitor, clade E, member 1	17,11	2,33E-13	6,21	3,38861E-11
Tfap2a	transcription factor AP-2, alpha	18,35	4,02E-23	13,73	1,47763E-23
Batf2	basic leucine zipper transcription factor, ATF-like 2	19,72	1,51E-06	28,28	1,05768E-39
Ddx58	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	19,82	5,82E-27	19,85	5,9873E-147
Ucn2	urocortin 2	19,98	3,23E-51	45,07	1,84265E-07
Slfn1	schlafen 1	20,53	8,17E-05	152,54	2,40797E-14
Ifi203	interferon activated gene 203	20,62	6,97E-20	24,76	1,72926E-32
Calca	calcitonin/calcitonin-related polypeptide, alpha	22,78	4,81E-05	12,75	2,1416E-06
Lif	leukemia inhibitory factor	24,23	5,81E-158	23,94	7,2581E-101
Tnfsf8	tumor necrosis factor (ligand) superfamily, member 8	33,90	3,03E-03	5,41	2,54052E-25
Rorb	RAR-related orphan receptor beta	36,16	2,91E-10	15,49	4,45562E-16
Tfap2b	transcription factor AP-2 beta	36,84	1,80E-15	22,75	1,74538E-13
Ifi204	interferon activated gene 204	37,86	3,67E-32	43,50	7,63861E-42

Stc2	stanniocalcin 2	41,36	1,14E-89	5,07	3,7877E-05
Irf7	interferon regulatory factor 7	93,03	3,04E-13	251,37	1,1427E-142
Shh	sonic hedgehog	102,82	6,77E-05	267,80	3,80132E-14
Gdnf	glial cell line derived neurotrophic factor	104,43	3,28E-261	47,26	1,83713E-27
Fosl1	fos-like antigen 1	114,02	2,12E-123	5,53	7,99526E-06
Ptpm	protein tyrosine phosphatase, receptor type, N	114,74	1,36E-173	24,08	1,99716E-44
Nrg1	neuregulin 1	128,63	4,57E-12	20,73	5,29674E-36
Trib3	tribbles pseudokinase 3	131,41	4,15E-52	62,52	4,16474E-51
Trim66	tripartite motif-containing 66	155,01	4,44E-18	39,18	5,73698E-56
Ccl5	chemokine (C-C motif) ligand 5	1253,15	6,74E-87	188,95	2,67834E-29

Table S2: List of 180 transcriptional regulators found in common in RNA-seq 1 and in RNA-seq 2 data sets (with FC >2); gene symbol, gene name along with fold-change and P-value are indicated for each data set. Of note, only three transcripts were found to be upregulated in one set and downregulated in the other. The remaining discordant transcripts were found to have a $FC \leq 2$ in one data set and to be only modestly deregulated (with a $FC \leq 3$) in the other.

1 **Table S3:** List of 52 transcriptional regulators with Fold-change FC >5.

Gene symbol	Full name	1st RNA-seq		2nd RNA-seq		Pubmed search with key word		Encoded protein/ expected non-cell or cell autonomous function	Interferome	Repair	Mda5/Mavs pathway
		Fold change	P-value	Fold change	P-value	Neural crest	Schwann cells (SCs)		yess/no	yes/no	
Chp2	calcineurin-like EF hand protein 2	0,13	2,03E-34	0,07	6,84718E-37	nr	nr	small calcium-binding protein	no	yes	
Abca2	ATP-binding cassette, sub-family A (ABC1), member 2	0,14	2,2E-39	0,22	1,37891E-09	nr	yes, PMID 17240058 + PMID 36385764 showing expression in CNS neurons and association with neurodegeneration	membrane-associated protein, cell autonomous	yes	yes	
Lmo1	LIM domain only 1	0,17	0,0000928	0,19	2,63034E-09	neuroblastoma, PMID 33779609 + PMID 37183825 showing adrenergic cell identity of neuroblastoma requires LMO1	nr	transcriptional cofactor, non-cell autonomous	yes	yes	
Cdh1	cadherin 1	0,20	0,0132	0,18	8,95745E-06	yes, including PMID 37225711, PMID 27126000 + PMID 37183825 (craniofacial)	affect myelin in CNS, PMID 14716021	cell adhesion protein	yes	yes	
Rxrg	retinoid X receptor gamma	0,23	8,93E-23	0,18	1,1578E-15	migrating cranial neural crest cells + differentiating neurogenic derivatives (drg)	expressed in MPNST PMID: 29131833; downregulated upon nerve repair PMID: 29867349 ; RXRg-SREBP-Lipid Biosynthesis Axis control myelination in Schwann Cells PMID: 25310982	Nuclear Receptor, DNA binding receptor, negatively regulate Tfap2a expression PMID: 33774011	yes	yes	
Irf1	interferon regulatory factor 1	5,27	0,00198	9,85	6,13646E-35	nr	oligodendrocyte injury and inflammatory demyelination in MS and EAE, PMID 22499673	transcriptional regulator, no direct link with Egr1 or Tfap2a	yes	no	yes
Hoxb9	homeobox B9	5,42	9,23E-50	11,66	3,37922E-58	nr	nr	transcription factor	no	no	
Fosl2	fos-like antigen 2	5,69	2,13E-82	5,75	4,47782E-25	nr	activated after 7 days in repair PMID: 34744629	part of transcription factor complex AP-1	yes	yes	
Pml	promyelocytic leukemia	5,72	2,99E-25	5,31	1,04565E-45	sympathetic nervous system, PMID 28148693	Facial nerve schwannomas, PMID 32913501	phosphoprotein localizes to nuclear bodies where it functions as a transcription factor	yes	no	
Csf1	colony stimulating factor 1 (macrophage)	6,09	2,42E-40	5,54	2,81091E-24	expressed in iridophores and enteric neuron, PMID 27521479	SCs bearing phagocytic phenotypes, PMID 31859421 + PMID 23737760 showing demyelination-induced reactive astrocytes express numerous ligands including Csf1 that act on homeostatic as well as activated microglia	cytokine, cell autonomous	yes	yes	
Irf5	interferon regulatory factor 5	6,55	3,13E-44	5,41	1,84498E-11	nr	nr	transcription factor	yes	yes	yes
Trim6	tripartite motif-containing 6	6,73	5,8E-09	7,78	1,77033E-17	nr	nr	E3 ubiquitin ligase	yes	no	
Irf9	interferon regulatory factor 9	7,24	1,1E-33	11,24	4,46792E-62	nr	nr	transcription factor	yes	no	yes
Arhgef2	Rho guanine nucleotide exchange factor (GEF) 28	7,4	1,33E-63	5,46	2,05032E-21	Ifc increases ectodermal competence for neural induction and reduced NC formation PMID: 10525189	nr	Rho GTPase; cytoplasmic	yes	no	
Batf3	basic leucine zipper transcription factor, ATF-like 3	8,65	1,29E-34	6,90	1,79678E-17	nr	nr	transcription factor, JUN interactor	yes	no	

Stat1	signal transducer and activator of transcription 1	9,20	0,000000582	13,45	9,0428E-126	nr	yes, regulate oct6 expression, PMID 20687925 + The transcription factor Stat-1 is essential for Schwann cell differentiation, myelination and myelin sheath regeneration PMID 37365519	Signal transducer and transcription activator, cell autonomous	yes	no	yes
Bcl3	B cell leukemia/lymphoma 3	9,43	3,4E-65	5,53	1,36978E-27	nr	nr	transcriptional co-activator	no	yes	
Nfkbie	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, epsilon	9,43	6,3E-61	7,44	7,75899E-41	nr	nr	Inhibits NF-kappa-B by complexing with and trapping it in the cytoplasm	yes	no	
Lgals9	lectin, galactose binding, soluble 9	10,39	3,67E-46	9,44	1,803E-24	nr	nr	cell-cell and cell-matrix interactions	yes	yes	
Runx2	runt related transcription factor 2	10,90	8,17E-20	6,67	8,92795E-13	Osteoblastic differentiation and skeletal morphogenesis, including PMID 32417535, PMID 38063851	Schwann cell differentiation and migration after sciatic nerve injury PMID 30374602, PMID 34744629, PMID, 38051902 + regulated by c-Jun- PMID 25614629, but not in SC PMID: 27581455 + PMID 34902518 showing that curcumin promoted Schwann cell proliferation and myelination through Runx2	transcription factor, cell autonomous + RUNX2 and EGR1 co-repressed Htra1 and increased the expression levels of other osteoblast marker genes, such as osterix, osteocalcin PMID 32324256	yes	yes	
Tnc	tenascin C	11,00	8,27E-111	13,44	5,77657E-58	yes, PMID 23958436 and references therein	PMID: 38951719 expression of Tnc in sciatic nerve; PMID 26497118 nerve fibroblasts accumulating at the lesion site + PMID 35681468 Tnc has an inhibitory effect on the differentiation of OPCs and the remyelination efficiency of oligodendrocytes.	extracellular matrix glycoprotein, non cell autonomous	yes	yes	
Maff	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein F (avian)	11,80	2,18E-115	7,17	2,94135E-20	nr	nr	transcription factor	yes	no	
Egr1	early growth response 1	12,57	4,46E-193	9,98	1,26304E-61	cranial cartilage PMID 23209659	yes, during development PMID 9418958 and upon injury PMID 27058953, myelin inhibitor	transcription factor, cell autonomous	yes	yes	
Ddit3	DNA-damage inducible transcript 3	12,65	9,42E-76	5,56	1,49929E-10	nr	Ablation of Chop, from POS63del mice rescues their motor deficit and reduces active demyelination PMID 23547100	transcription factor, cell autonomous, regulate Egr1 expression PMID 22496745	yes	no	PERK signalling
Nfil3	nuclear factor, interleukin 3, regulated	13,56	7,69E-101	5,49	2,48454E-15	nr	mutation lead to sensory autonomic neuropathy	transcriptional regulator, non cell autonomous	yes	yes	
Helz2	helicase with zinc finger 2, transcriptional coactivator	14,24	4,39E-52	21,07	3,13212E-84	nr	nr	transcriptional co-activator	yes	no	yes
Lck	lymphocyte protein tyrosine kinase	14,91	1,08E-36	6,91	0,000104289	nr	Lck mediates β 1-integrin signalling to regulate Schwann cell migration and myelination , PMID 23715271	Src family of protein tyrosine kinase, cell autonomous	yes	no	-

Mndal	myeloid nuclear differentiation antigen like	16,18	1,33E-17	18,10	1,74483E-24	nr	nr	ISG	yes	no	
Tlr3	toll-like receptor 3	16,58	1,07E-115	12,23	2,81941E-40	nr	yes, all tlr PMID 29113341	single transmembrane cell-surface receptor, cell autonomous	yes	no	
Serpine1	serine (or cysteine) peptidase inhibitor, clade E, member 1	17,11	2,33E-13	6,21	3,38861E-11	nr	nr	serine proteinase inhibitor	yes	no	
Tfap2a	transcription factor AP-2, alpha	18,35	4,02E-23	13,73	1,47763E-23	yes, PMID 29852131 Tfap2a in early NCC + PMID 37398373 PMID 38063857 Tfap paralogs control craniofacial development through Alx + PMID 36563566 Zebrafish anterior segment mesenchyme progenitors are defined by function of tfap2a	yes, PMID 11553286, PMID 31650361, PMID 39009095 myelin inhibitor	transcription factor, cell autonomous	yes	yes	
Batf2	basic leucine zipper transcription factor, ATF-like 2	19,72	0,00000151	28,28	1,05768E-39	nr	nr	AP1 transcription factor family	yes	no	
Ddx58	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	19,82	5,82E-27	19,85	5,9873E-147	nr	nr	viral double-stranded (ds) RNA recognition RNA Helicase RIG-I	yes	yes	
Ucn2	urocortin 2	19,98	3,23E-51	45,07	1,84265E-07	nr	nr	endogenous ligand for CRF type 2 receptor	no	yes	
Slfn1	schlafen 1	20,53	0,0000817	152,54	2,40797E-14	nr	nr	ISG	yes	yes	
Ifi203	interferon activated gene 203	20,62	6,97E-20	24,76	1,72926E-32	nr	nr	ISG	yes	no	
Calca	calcitonin/calcitonin-related polypeptide, alpha	22,78	0,0000481	12,75	2,1416E-06	affected in frontal bone of dlx3 mutant, PMID 22886599 + PMID 37044067 sensory neuron marker	nr	peptide hormones calcitonin	yes	no	
Lif	leukemia inhibitory factor	24,23	5,81E-158	23,94	7,2581E-101	NSC reprogramming	PMID: 10386959, expressed in Schwann cells after rat sciatic nerve injury. Affect proliferation and migration ability of Schwann cells	cytokine, cell autonomous	yes	yes	
Tnfsf8	tumor necrosis factor (ligand) superfamily, member 8	33,90	0,00304	5,41	2,54052E-25	nr	nr	cytokine	yes	no	
Rorb	RAR-related orphan receptor beta	36,16	2,91E-10	15,49	4,45562E-16	nr	nr	nuclear hormone receptors	no	yes	
Tfap2b	transcription factor AP-2 beta	36,84	1,8E-15	22,75	1,74538E-13	PMID 31848212, pair with tfap2a during NC differentiation	nr	transcription factor	no	no	
Ifi204	interferon activated gene 204	37,86	3,67E-32	43,50	7,63861E-42	nr	nr	ISG	yes	no	
Stc2	stannocalcin 2	41,36	1,14E-89	5,07	3,7877E-05	nr	nr	secreted, homodimeric glycoprotein	no	yes	
Irf7	interferon regulatory factor 7	93,03	3,04E-13	251,37	1,1427E-142	nr	myelin alterations are associated to IRF7 deregulation during acute demyelination, PMID 19121307	TF, cell autonomous	yes	yes	yes
Shh	sonic hedgehog	102,82	0,0000677	267,80	3,80132E-14	various NCC derivatives	PMID 27581455 activated during SC repair, but not necessary for myelin formation PMID: 38771121	secreted protein, cell autonomous	no	yes	

Gdnf	glial cell line derived neurotrophic factor	104,43	3,28E-261	47,26	1,83713E-27	various NCC derivatives	PMID 32562261 Gdnf induces migration of Schwann cell precursors. Role in repair PMID: 38995011 and pain sensitivity PMID: 38258905	secreted ligand of the TGF-beta family, cell autonomous	no	yes	
Fosl1	fos-like antigen 1	114,02	2,12E-123	5,53	7,99526E-06	FOSL1 causes melanocyte reprogramming and transformation and induces neuronal genes PMID: 28481878	activated early in repair PMID: 34744629, but not in SC PMID: 27581455. PMID 37949219 modulates Schwann cell responses in the wound microenvironment and regulates peripheral nerve regeneration	AP1 trascription factor subnit, leucine zipper proteins that can dimerize with proteins of the JUN family	yes	yes	
Ptpn	protein tyrosine phosphatase, receptor type, N	114,74	1,36E-173	24,08	1,99716E-44	nr	nr	protein tyrosine phosphatase	no	no	
Nrg1	neuregulin 1	128,63	4,57E-12	20,73	5,29674E-36	PMID 17432114, several neurocristopathies	PMID: 31229498, role in SC development and repair	ligand for ERBB3 and ERBB4, non cell autonomous	yes	no	
Trib3	tribbles pseudokinase 3	131,41	4,15E-52	62,52	4,16474E-51	nr	PMID 27977799 in CNS repair	protein kinase	yes	no	
Trim66	tripartite motif-containing 66	155,01	4,44E-18	39,18	5,73698E-56	nr	nr	transcriptional repressor	no	no	
Ccl5	chemokine (C-C motif) ligand 5	1253,15	6,74E-87	188,95	2,67834E-29	nr	PMID 9521605 and PMID 36611893 showing gene is expressed in E12.5 DRG, Schwann cells, spinal cord and skin following infection	chemoattractant	yes	yes	

Table S3: List of 52 transcriptional regulators with FC >5; gene symbol, full name, Fold change (FC) and P-value in each RNA-seq are indicated. Pubmed search colums indicate references (PMID) found upon use of "Neural crest" or "Schwann cells" key words. nr: not reported; Encoded protein/ expected non-cell or cell autonomous function column indicates main functions/localisation and PMID references (Columns indicated in green show genes encoding membrane-associated proteins, cytokine, or neurotrophic factors, and /or genes with a main function in sensory neurons). Interferome column indicates if genes are within the interferome database; Repair column shows RNAs in common with (Kim et al.,2012-Arthur-Farraj et al.,2017). Network analysis and interferome confirm central role of IFN signaling,. Last column (and blue color) indicates the genes previously described within Mda5/Mavs pathway.

Table S4: List of 174 genes identified in common among EGR1and EGR2 ChIPseq datasets and current *Adar1*cKO RNA-seq

	EGR2 mutant	<i>Adar1</i>cKO mutant
CHDH		
MBP		
PLLP		
KCNK1		
MME		
ELOVL7		
FA2H		
SLC6A1		
DUSP15		
GJB1		
ELOVL6		
HMGCS1		
FRZB		
IDI1		
GPM6A		
FDPS		
LSS		
SECISBP2L		
EFHD1		
CHST2		
MT3		
ALDOC		
MAL		
DHCR24		
ACSS2		
TM7SF2		
PCYT2		
APOBEC2		
SLC7A2		
NSDHL		
PRX		
ACAT2		
SCN3B		
HMGCR		
GPR155		
SEMA5A		
IL16		
TNNI2		
CASQ1		
ENO3		
PGAM2		
CNTN1		
SC5D		
FDFT1		
CKM		
MBOAT1		
SNCG		
NEK1		
TMEM38A		
ABCA2		
TESK2		
DHCR7		
NDRG1		
CD9		
SH3BGR		
TPM2		
RAB40B		
TMEM40		
HSD17B7		
TTN		
RYR1		
AACS		
MAPK8IP1		
ACSL1		
S100B		

ELOVL1		
PMVK		
BMP7		
SQLC		
ST6GAL1		
TBXA2R		
SEMA3B		
SLC6A15		
MRAS		
LDLR		
EXTL1		
PANK3		
CASKIN2		
AK3		
GLOD4		
ADAM10		
VWF		
SIRT2		
PACS2		
UTRN		
CD55		
TM6SF1		
MGST3		
RNF13		
STARD4		
LIMK2		
PIP4K2A		
SLC20A2		
LIMCH1		
EPDR1		
EPHB6		
DNAJA4		
RAP1GDS1		
TRIM59		
CCNA2		
NTM		
GPC1		
NR4A1		
MKI67		
PLK4		
DCK		
PLEKHO1		
RAB32		
INCENP		
MCM6		
NCAPD2		
AURKB		
DNMT1		
MCM2		
DCLK1		
RACGAP1		
CEP55		
MIDN		
TOP2A		
ECT2		
RBL1		
BUB1		
ZWILCH		
RAD51AP1		
MCM3		
SORCS2		
BRCA1		
RRM2		
FOS		
MCM5		
LRRFIP1		
CD44		
KIF2C		
SPATA13		
PLK2		
CDC45		
ALCAM		

HMGA2		
UHRF1		
COL18A1		
KLF10		
ATF3		
THBS2		
PHLDA1		
RUNX2		
TNFRSF12A		
LGALS3		
TRIM25		
PARP14		
HMGA1		
GPR37		
ABHD3		
GRIA2		
SLAIN1		
SPOCK1		
CUEDC2		
CSRP2		
WASF1		
SH3GL3		
CDKN1C		
RNF103		
TMPRSS5		
POU3F1		
BZW2		
GSTA4		
LPCAT1		
ICK		
PPP1R14C		
PDGFC		
CADM1		
TMEM189		
ME1		
SLIT2		
SPP1		

Table S4: List of 174 transcriptional regulators evidenced in Chip-seq of EGR1, EGR2 and deregulated in current *Adar1* cKO RNA-seq; Red : up-regulated and green : down-regulated in hypomorphic *Egr2* mutant or upon *Adar1* invalidation in NC compared to controls.

Supplemental Figures

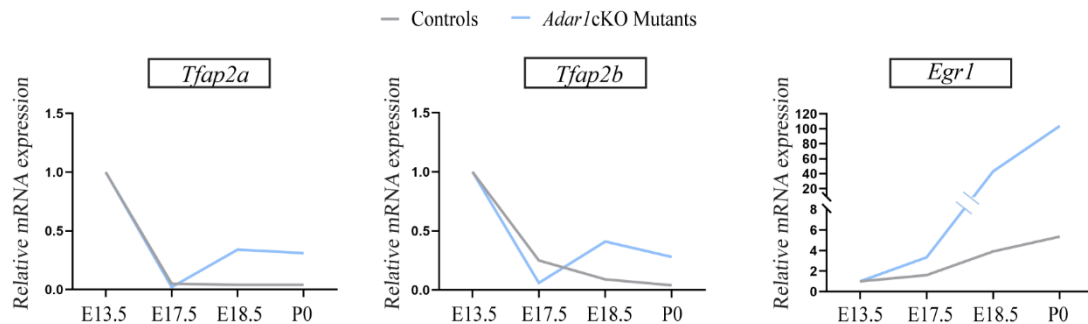


Figure S1. Expression level of *Tfap2a*, *Tfap2b* and *Egr1* in DRG or sciatic nerves isolated from controls and *Adar1*cKO mutants at E13.5, E17.5, E18.5 and birth (new born, P0). The relative abundance values of each transcripts was normalized to the internal control β -actin, and expression level in controls and *Adar1*cKO mutants represented relative to level quantified at E13.5. Note that although expressed at similar levels in E13.5 DRG of wild-type and *Adar1*cKO mutants, *Tfap2a* and *Tfap2b* are drastically downregulated from E17.5 onwards in controls (grey), but aberrantly re-expressed from E18.5 onwards in *Adar1*cKO mutants (blue). In contrast, *Egr1* expression is maintained at all stages analyzed in controls, but strikingly upregulated from E18.5 onwards in *Adar1*cKO mutants.

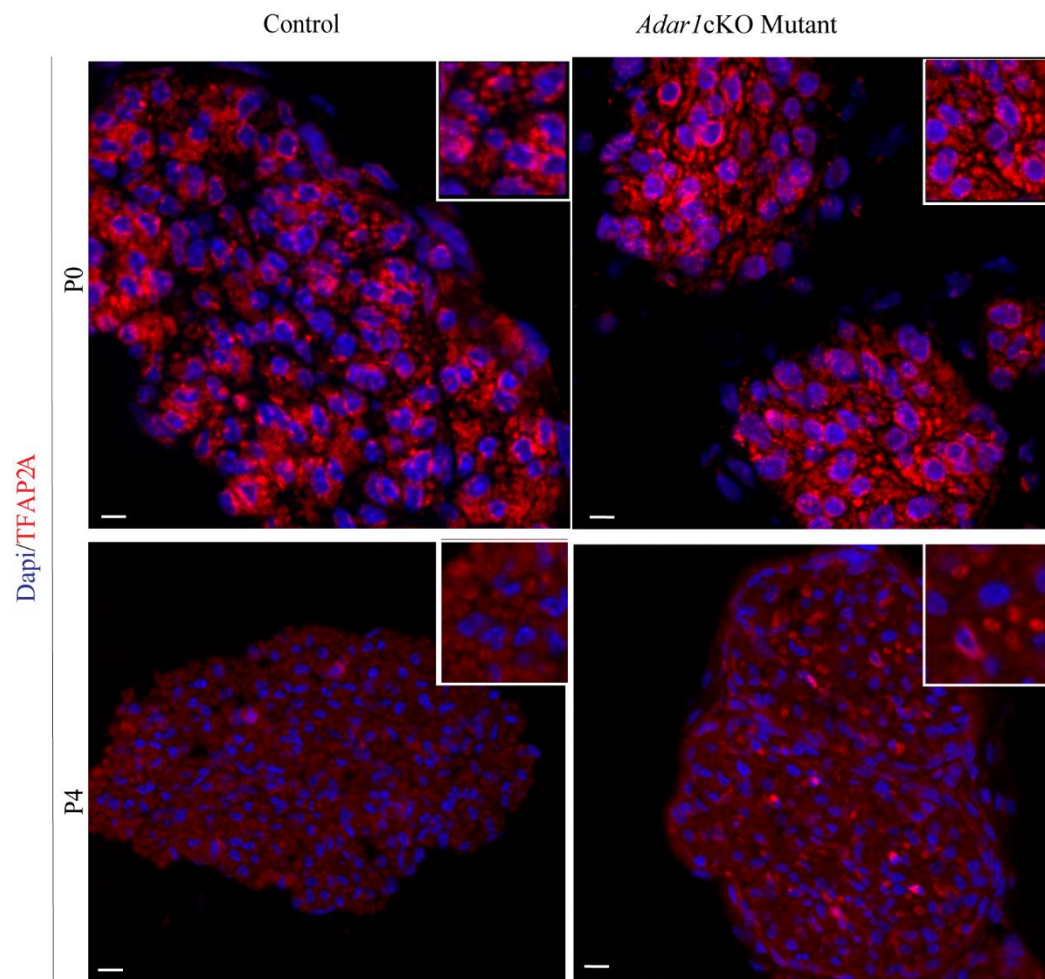


Figure S2. Expression of TFAP2A protein in the sciatic nerves of *Adar1*cKO compared to controls at P0 and P4. TFAP2A (red) immunostainings were performed on sections of sciatic nerves of *Adar1*cKO and controls mice at P0 and P4. Counter staining with DAPI is shown to identify nuclei. Scale bar: 60 μ m at P0 and 30 μ m at P4 .

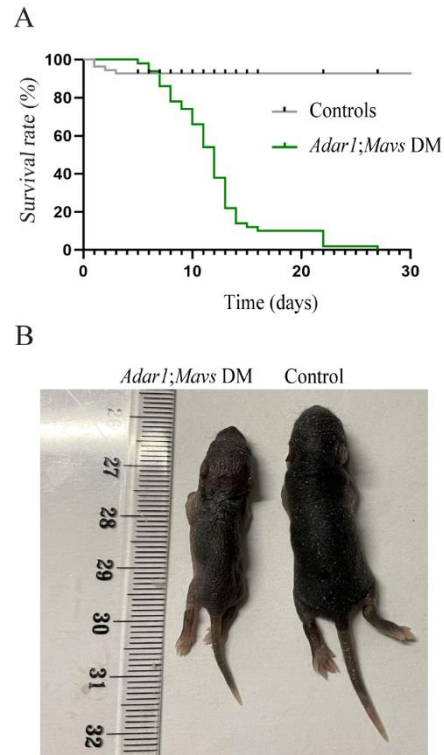


Figure S3. Survival curve and pigmentation of *Adar1;Mavs* DM versus controls. (A) Survival rate (%) of controls (grey), and *Adar1;Mavs* DM (green) over time (days) and **(B)** picture of *Adar1;Mavs* DM (left) and controls (right) showing normal pigmentation of animals of both genotypes.

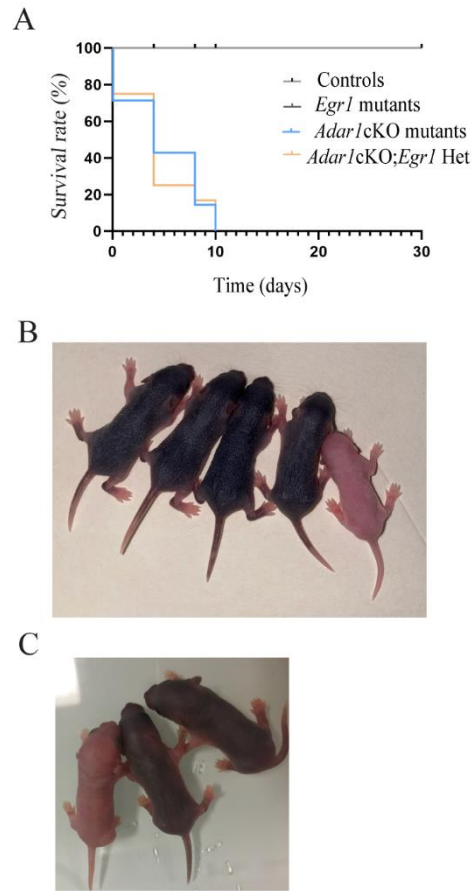


Figure S4. Survival curve and pigmentation of *Adar1cKO;Egr1*Het and *Adar1cKO* mutants versus controls **(A)** Survival rate (%) of controls (light grey), *Egr1* homozygous (grey), *Adar1cKO* (blue) and *Adar1cKO;Egr1*Het (orange) over time (days). Note that deletion of one copy of *Egr1* does not rescue survival rate of *Adar1cKO* animals. **(B)** Picture of *Adar1cKO;Egr1*Het (right) compared to controls and **(C)** Picture of *Adar1cKO* (left) compared to controls. Note total depigmentation of *Adar1cKO;Egr1*Het and *Adar1cKO* mutants, demonstrating absence of pigmentation rescue upon deletion of one allele of *Egr1*.