

Supplementary tables

Alignment quality							
	Replicate 1, left read	Replicate 1, right read	Replicate 2, left read	Replicate 2, right read	Replicate 3, left read	Replicate 3, right read	
Mapped reads %	76.10%	76.20%	79.20%	78.30%	75.90%	73.60%	
Multimapped reads %	5.10%	5.10%	4.90%	4.90%	5.30%	5.30%	
Concordant pairs among mapped pairs %	97.50%		97.40%		97.10%		
Sequencing quality							
	Replicate 1, left read	Replicate 1, right read	Replicate 2, left read	Replicate 2, right read	Replicate 3, left read	Replicate 3, right read	
No of sequenced reads	79,379,381	79,379,381	73,114,375	73,114,375	76,170,070	76,170,070	
Base position	Mean Phred score						
1	Mean Phred score	30.01	29.68	29.99	29.73	30.05	29.77
2	Mean Phred score	30.62	29.90	30.62	29.76	30.67	29.87
3	Mean Phred score	30.63	29.70	30.62	29.65	30.68	29.75
4	Mean Phred score	30.63	29.54	30.62	29.46	30.68	29.59
5	Mean Phred score	30.62	29.52	30.63	29.40	30.72	29.53
6	Mean Phred score	34.08	33.68	34.07	33.54	34.24	33.69
7	Mean Phred score	34.04	33.77	34.05	33.57	34.19	33.77
8	Mean Phred score	33.74	33.50	33.73	33.31	33.88	33.49
9	Mean Phred score	33.73	33.50	33.72	33.31	33.86	33.44
10	Mean Phred score	33.32	33.19	33.33	33.03	33.51	33.13
11	Mean Phred score	33.80	33.52	33.80	33.35	33.98	33.45
12	Mean Phred score	33.79	33.55	33.79	33.35	33.98	33.47
13	Mean Phred score	33.67	33.46	33.66	33.26	33.81	33.35
14	Mean Phred score	33.63	33.37	33.62	33.17	33.75	33.28
15	Mean Phred score	33.59	33.38	33.59	33.20	33.76	33.28
16	Mean Phred score	33.60	33.41	33.59	33.24	33.73	33.22
17	Mean Phred score	33.52	33.37	33.52	33.20	33.71	33.24
18	Mean Phred score	33.51	33.35	33.51	33.19	33.63	33.22
19	Mean Phred score	33.53	33.37	33.52	33.22	33.70	33.23
20	Mean Phred score	33.51	33.31	33.51	33.18	33.62	33.16
21	Mean Phred score	33.49	33.29	33.48	33.16	33.63	33.14
22	Mean Phred score	33.48	33.27	33.48	33.14	33.60	33.12
23	Mean Phred score	33.46	33.25	33.44	33.10	33.57	33.09
24	Mean Phred score	33.44	33.23	33.43	33.09	33.55	33.06
25	Mean Phred score	33.45	33.23	33.44	33.10	33.54	33.06
26	Mean Phred score	33.40	33.20	33.40	33.07	33.55	32.97
27	Mean Phred score	33.53	33.17	33.54	33.06	33.66	32.95
28	Mean Phred score	33.56	33.19	33.57	33.07	33.63	32.95
29	Mean Phred score	33.49	33.15	33.51	33.03	33.51	32.92
30	Mean Phred score	33.47	33.14	33.48	33.01	33.49	32.90
31	Mean Phred score	33.40	33.14	33.41	33.01	33.45	32.87
32	Mean Phred score	33.37	33.11	33.37	32.98	33.45	32.81
33	Mean Phred score	33.28	33.06	33.30	32.94	33.37	32.81
34	Mean Phred score	33.26	33.05	33.27	32.93	33.34	32.74
35	Mean Phred score	33.23	33.00	33.24	32.87	33.32	32.69
36	Mean Phred score	33.20	32.96	33.21	32.85	33.27	32.67
37	Mean Phred score	33.19	32.95	33.19	32.83	33.26	32.67
38	Mean Phred score	33.14	32.94	33.14	32.82	33.20	32.62
39	Mean Phred score	33.11	32.92	33.12	32.81	33.14	32.56
40	Mean Phred score	33.06	32.90	33.08	32.79	33.13	32.53
41	Mean Phred score	33.03	32.87	33.05	32.76	33.09	32.46
42	Mean Phred score	32.99	32.84	33.00	32.72	33.04	32.45
43	Mean Phred score	32.96	32.81	32.98	32.69	33.04	32.43
44	Mean Phred score	32.92	32.76	32.95	32.64	32.94	32.35
45	Mean Phred score	32.87	32.72	32.88	32.61	32.91	32.31
46	Mean Phred score	32.87	32.74	32.89	32.63	32.91	32.28
47	Mean Phred score	32.79	32.68	32.79	32.55	32.83	32.25
48	Mean Phred score	32.79	32.64	32.78	32.53	32.83	32.23
49	Mean Phred score	32.77	32.61	32.76	32.50	32.80	32.17
50	Mean Phred score	32.74	32.58	32.74	32.47	32.74	32.13
51	Mean Phred score	32.76	32.56	32.75	32.44	32.70	32.05
52	Mean Phred score	32.71	32.54	32.71	32.43	32.66	31.99
53	Mean Phred score	32.63	32.48	32.63	32.37	32.58	31.93
54	Mean Phred score	32.62	32.48	32.62	32.36	32.51	31.90
55	Mean Phred score	32.63	32.48	32.63	32.37	32.54	31.94
56	Mean Phred score	32.60	32.46	32.59	32.34	32.49	31.88
57	Mean Phred score	32.59	32.42	32.58	32.31	32.44	31.78
58	Mean Phred score	32.59	32.42	32.58	32.31	32.43	31.78
59	Mean Phred score	32.51	32.39	32.51	32.26	32.30	31.75
60	Mean Phred score	32.53	32.34	32.52	32.21	32.33	31.71
61	Mean Phred score	32.48	32.31	32.48	32.19	32.27	31.69
62	Mean Phred score	32.44	32.28	32.44	32.15	32.18	31.59
63	Mean Phred score	32.40	32.27	32.39	32.13	32.14	31.54
64	Mean Phred score	32.39	32.29	32.38	32.14	32.16	31.57
65	Mean Phred score	32.32	32.22	32.32	32.07	32.08	31.53
66	Mean Phred score	32.34	32.21	32.33	32.07	32.01	31.43
67	Mean Phred score	32.37	32.21	32.34	32.06	32.05	31.41
68	Mean Phred score	32.33	32.13	32.30	31.98	31.97	31.35
69	Mean Phred score	32.25	32.10	32.22	31.96	31.92	31.32
70	Mean Phred score	32.28	32.08	32.25	31.95	31.92	31.26
71	Mean Phred score	32.22	32.01	32.19	31.88	31.83	31.20
72	Mean Phred score	32.19	31.97	32.17	31.84	31.78	31.13
73	Mean Phred score	32.20	31.98	32.18	31.86	31.77	31.13
74	Mean Phred score	32.14	31.92	32.13	31.79	31.71	31.04
75	Mean Phred score	31.79	31.50	31.76	31.35	31.19	30.51

Supplementary Table 1. Sequencing and alignment quality metrics for 3 hDRG RNA-seq replicates.

Gene list

SHOX2: DRG enriched in human and mouse, developmentally relevant in CNS.

Scott A, Hasegawa H, Sakurai K, Yaron A, Cobb J, Wang F. Transcription Factor Shox2 Is Required for Proper Development of TrkB-Expressing Mechanosensory Neurons. *The Journal of neuroscience: the official journal of the Society for Neuroscience* 2011;31(18):6741

SKOR2: DRG enriched in human and mouse, developmentally relevant in development of inner ear and related ganglion
Hori K, Hoshino M. GABAergic neuron specification in the spinal cord, the cerebellum, and the cochlear nucleus. *Neural plasticity* 2012;2012

SCRT2: DRG enriched in human and mouse. The Scratch family of genes are involved in neural development.

Vieceli FM, Simões-Costa M, Turri JA, Kanno T, Bronner M, Yan CY. The transcription factor chicken Scratch2 is expressed in a subset of early postmitotic neural progenitors. *Gene Expression Patterns* 2013;13(5):189-196.

INSM2: DRG enriched in human and mouse. INSM1 is involved in neural development.

Wildner H, Gierl MS, Strehle M, Pla P, Birchmeier C. *Insm1* (IA-1) is a crucial component of the transcriptional network that controls differentiation of the sympatho-adrenal lineage. *Development* 2008;135(3):473-481.

HMX1: TF known to be functional in DRG development, expressed but with divergent expression patterns in hDRG and mDRG.

Wang W, Lo P, Frasch M, Lufkin T. *Hmx*: an evolutionary conserved homeobox gene family expressed in the developing nervous system in mice and *Drosophila*. *Mechanisms of development* 2000;99(1):123-137.

SHH: Expressed but not enriched in hDRG, primary TF in Hedgehog signaling in DRG development.

Guan W, Wang G, Scott SA, Condic ML. *Shh* influences cell number and the distribution of neuronal subtypes in dorsal root ganglia. *Developmental biology* 2008;314(2):317-328.

KCNIP3 (DREAM): Neuronally enriched, known to mediate inflammation and modulate pain.

Cheng H-YM, Pitcher GM, Laviolette SR, Whishaw IQ, Tong KI, Kockeritz LK, Wada T, Joza NA, Crackower M, Goncalves J. DREAM is a critical transcriptional repressor for pain modulation. *Cell* 2002;108(1):31-43.

TWIST1: Neuronally enriched, involved in Wnt signaling in human neural crest cells derived from pluripotent cells

Noisa P, Lund C, Kanduri K, Lund R, Lähdesmäki H, Laheesmaa R, Lundin K, Chokeywattanalert H, Otonkoski T, Tuuri T. Notch signaling regulates the differentiation of neural crest from human pluripotent stem cells. *J Cell Sci* 2014;127(9):2083-2094.

TFAP2A: Weakly enriched in hDRG and mDRG, key TF in neural crest lineage.

Barrallo-Gimeno A, Holzschuh J, Driever W, Knapik EW. Neural crest survival and differentiation in zebrafish depends on *mont blanc/ tfap2a* gene function. *Development* 2004;131(7):1463-1477.

SOX10, SOX12, MYT1L: Pan-neuronal TFs

NOVA1: Pan neuronally expressed splicing factor, but relatively less abundant in hDRG and mDRG. Along with NOVA2, known to regulate splicing in brain.

Ule J, Jensen KB, Ruggiu M, Mele A, Ule A, Darnell RB. CLIP identifies Nova-regulated RNA networks in the brain. *Science* 2003;302(5648):1212-1215.

RBFOX3: Pan neuronally expressed. Gene product NeuN is marker of neurons. Involved in neuronal splicing.

Duan W, Zhang Y-P, Hou Z, Huang C, Zhu H, Zhang CQ, Yin Q. Novel insights into NeuN: from neuronal marker to splicing regulator. *Molecular neurobiology* 2016;53(3):1637-1647.

CELF4: Pan neuronally expressed, implicated in splicing in retinal ganglion.

Guerrette TA. Alternative Splicing Factor CELF4 is Implicated in Regulation of Ganglion Cell Differentiation During Murine Retinal Development. 2012.

RBM11: Pan neuronally expressed gene whose product is an RNA binding protein.

KIF5C: Pan neuronally expressed. Shown to be involved in dendritic mRNA transport, role in pseudounipolar neurons unknown.

Kanai Y, Dohmae N, Hirokawa N. Kinesin transports RNA: isolation and characterization of an RNA transporting granule. *Neuron* 2004;43(4):513-525

CPEB1: Pan neuronally expressed. Involved in dendritic transport, trafficking role in pseudounipolar neurons unclear.

Implicated in translation regulation in hyperalgesic priming models in rats.

Bogen O, Alessandri-Haber N, Chu C, Gear RW, Levine JD. Generation of a pain memory in the primary afferent nociceptor triggered by PKC ϵ activation of CPEB. *Journal of Neuroscience* 2012;32(6):2018-2026

DDX25: Pan neuronally expressed, and shown to be involved in RNA transport during spermatogenesis.

Sheng Y, Tsai-Morris C-H, Gutti R, Maeda Y, Dufau ML. Gonadotropin-regulated testicular RNA helicase (GRTH/Ddx25) is a transport protein involved in gene specific mRNA export and protein translation during spermatogenesis. *Journal of Biological Chemistry* 2006;281(46):35048-35056.

ELAVL2 (HuB) and ELAVL4 (HuD): Pan neuronally expressed. Involved in PNS development and associated with axonal growth cones.

Smith CL, Afroz R, Bassell GJ, Furneaux HM, Perrone-Bizzozero NI, Burry RW. GAP-43 mRNA in growth cones is associated with HuD and ribosomes. *Journal of neurobiology* 2004;61(2):222-235.

Supplementary Table 2. Genes corresponding to TFs, co-factors, splicing factors and RNA binding and trafficking proteins expressed in the hDRG, but not strongly hDRG-enriched and mDRG-enriched. Some of these genes are likely functional in the mammalian DRG.

Gene	NF1	NF2	NF3	NF4	NF5	NP1	NP2	NP3	PEP1	PEP2	TH	Detected in # cells / 706
Insm2	0.03	0.00	0.00	0.00	0.00	0.25	0.19	0.08	0.02	0.12	0.01	81
Ntrk1	0.00	0.00	0.00	0.05	0.00	0.07	0.59	0.17	0.50	0.88	0.03	212
Kcnh6	0.00	0.00	0.08	0.00	0.04	0.13	0.06	0.25	0.02	0.00	0.21	112
Ret	0.13	0.58	0.83	0.00	0.04	0.82	0.63	0.33	0.27	0.18	0.94	549
Stmn2	1.00	1.00	1.00	1.00	1.00	0.99	1.00	1.00	0.98	1.00	1.00	683
Trpv1	0.00	0.00	0.00	0.05	0.00	0.03	0.28	0.58	0.31	0.06	0.00	62
Amigo3	0.32	0.25	0.17	0.36	0.42	0.27	0.25	0.33	0.05	0.12	0.17	325
Tmem72	0.42	0.35	0.08	0.46	0.50	0.26	0.31	0.00	0.16	0.24	0.72	411
Nefh	0.81	0.96	0.92	0.73	1.00	0.01	0.00	0.00	0.13	0.65	0.01	518
Avil	0.94	0.96	1.00	0.68	0.73	0.96	0.88	1.00	0.47	0.94	0.86	601
Polr3g	0.16	0.54	1.00	0.27	0.31	0.45	0.53	0.58	0.16	0.71	0.31	355
Uchl1	1.00	1.00	1.00	1.00	1.00	1.00	0.97	1.00	0.97	1.00	1.00	687
Akap12	1.00	0.81	0.92	0.82	0.89	0.82	0.91	1.00	0.59	0.53	0.88	588
Nmb	0.00	0.02	0.58	0.00	0.00	0.94	0.75	0.67	0.39	1.00	0.16	389
Ppm1j	0.97	0.77	0.83	0.46	0.08	0.54	0.09	0.00	0.02	0.06	0.37	417
Sncg	0.97	1.00	1.00	1.00	0.69	1.00	1.00	1.00	0.95	1.00	0.99	690
Ahnak2	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Gng3	1.00	1.00	1.00	1.00	0.96	0.98	1.00	1.00	0.83	1.00	0.99	662
Kcnd1	0.48	0.42	0.67	0.27	0.19	0.38	0.22	0.08	0.05	0.29	0.35	274
Fkbp1b	0.61	0.42	0.42	0.55	0.15	0.38	0.28	0.00	0.34	0.59	0.61	499
Egr2	0.03	0.06	0.00	0.05	0.00	0.05	0.00	0.00	0.02	0.06	0.03	32
Susd2	0.77	0.88	0.92	0.36	0.35	0.34	0.13	0.25	0.31	0.88	0.67	482
Ngfr	0.90	0.71	1.00	0.18	0.42	0.02	0.31	0.00	0.42	1.00	0.47	379
Plekha4	0.00	0.04	0.00	0.05	0.00	0.02	0.03	0.00	0.02	0.00	0.00	27
Prx	0.00	0.02	0.00	0.00	0.08	0.01	0.00	0.00	0.02	0.12	0.03	27
Tubb3	1.00	1.00	1.00	1.00	1.00	0.97	0.97	1.00	0.95	1.00	0.92	671
Trim36	0.55	0.77	0.83	0.64	0.62	0.68	0.66	0.67	0.30	0.53	0.46	467
Ppp1r1c	1.00	0.85	1.00	0.77	0.62	0.95	0.78	1.00	0.56	0.94	0.91	600
Prune2	1.00	0.98	1.00	0.77	1.00	0.81	0.72	0.67	0.69	0.88	0.93	629
Accn3	0.00	0.31	0.00	0.27	0.00	0.00	0.00	0.00	0.14	0.59	0.00	140
Dusp15	0.19	0.08	0.17	0.00	0.08	0.06	0.03	0.00	0.03	0.12	0.03	83
Mpz	0.00	0.00	0.00	0.00	0.08	0.04	0.03	0.00	0.00	0.00	0.05	77
Tppp3	1.00	1.00	1.00	0.86	0.42	0.99	0.94	0.92	0.88	1.00	1.00	688
Col28a1	0.00	0.02	0.00	0.00	0.04	0.02	0.00	0.00	0.02	0.00	0.00	11
Prph	0.87	0.88	0.67	0.46	0.35	0.98	0.94	1.00	0.81	0.82	0.94	672
P2rx3	0.03	0.00	0.17	0.00	0.00	0.86	0.47	0.58	0.16	0.35	0.10	312
Isl1	0.10	0.40	0.08	0.77	0.46	0.29	0.38	0.00	0.09	0.29	0.37	428
Scn9a	0.39	0.52	0.67	0.23	0.00	0.54	0.66	0.75	0.39	0.77	0.78	569
Htr3a	0.52	0.27	0.00	0.05	0.00	0.00	0.13	0.00	0.05	0.82	0.00	128
Sfrp5	0.03	0.06	0.00	0.00	0.00	0.03	0.06	0.00	0.06	0.00	0.05	51
Pirt	0.13	0.38	0.92	0.18	0.04	0.82	0.81	0.67	0.63	0.88	0.38	530
Ctnf	0.07	0.02	0.00	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.01	8
A330049M08rik / Ncmap	0.00	0.00	0.00	0.00	0.04	0.01	0.03	0.00	0.00	0.06	0.02	17
Hoxd1	0.58	0.25	0.75	0.05	0.04	0.03	0.03	0.08	0.06	0.53	0.04	104
Trim67	0.65	0.42	0.58	0.32	0.27	0.40	0.41	0.25	0.17	0.35	0.42	310
Cldn19	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	5
Ppef1	0.26	0.19	0.00	0.09	0.00	0.48	0.28	0.25	0.13	0.06	0.37	258
Stc17a6	0.90	0.71	0.92	0.05	0.35	0.48	0.44	0.08	0.36	0.77	0.64	478
Dhrs2	0.00	0.02	0.00	0.00	0.04	0.00	0.00	0.00	0.00	0.06	0.01	8
Shox2	0.07	0.13	0.00	0.14	0.42	0.01	0.03	0.00	0.00	0.00	0.00	42
Chrna6	0.36	0.02	0.00	0.00	0.00	0.32	0.31	0.42	0.13	0.00	0.02	147
Scn11a	0.00	0.00	0.00	0.00	0.00	0.90	0.78	0.83	0.31	0.18	0.33	443
Tusc5	0.81	0.54	1.00	0.05	0.00	0.90	0.88	0.58	0.42	0.47	0.91	559
Bet3l / Trappc3l	0.00	0.13	0.75	0.18	0.00	0.01	0.06	0.08	0.09	0.82	0.02	84
Kcnk18	0.45	0.04	0.00	0.00	0.00	0.19	0.34	0.00	0.00	0.06	0.00	85
Scn10a	0.00	0.00	0.00	0.00	0.00	0.76	0.63	0.42	0.28	0.59	0.23	482
Pou4f1	0.58	0.56	0.83	0.23	0.35	0.46	0.34	0.08	0.31	0.47	0.82	540
Pou4f2	0.16	0.06	0.00	0.00	0.12	0.07	0.00	0.00	0.05	0.00	0.47	285
Pou4f3	0.13	0.13	0.33	0.09	0.12	0.01	0.00	0.00	0.13	0.59	0.01	97
Mrgprx1	0.00	0.00	0.00	0.00	0.00	0.07	0.53	0.33	0.00	0.00	0.00	43
Tmem72	0.29	0.13	0.00	0.00	0.00	0.01	0.00	0.25	0.02	0.00	0.27	175
Prdm12	0.00	0.02	0.00	0.00	0.00	0.41	0.41	0.33	0.31	0.47	0.39	320
Calcb	0.03	0.25	0.17	0.00	0.00	0.88	0.78	0.00	0.44	0.71	0.60	526
Pla2g3	0.32	0.23	0.50	0.00	0.04	0.09	0.00	0.00	0.00	0.18	0.09	82
Mrgprd	0.03	0.02	0.00	0.00	0.04	0.84	0.22	0.00	0.02	0.00	0.01	161
Chrb3	0.00	0.00	0.00	0.00	0.00	0.05	0.00	0.00	0.08	0.00	0.00	20
Skor2	0.48	0.27	0.17	0.00	0.00	0.03	0.00	0.00	0.00	0.06	0.06	76
Isl2	0.36	0.25	0.25	0.00	0.04	0.52	0.63	0.42	0.14	0.47	0.72	442
Fam19a3	0.42	0.23	0.33	0.00	0.04	0.06	0.00	0.00	0.00	0.06	0.06	75
Foxd3	0.00	0.06	0.00	0.05	0.08	0.02	0.03	0.00	0.00	0.06	0.02	20
Gfra3	0.00	0.00	0.00	0.05	0.00	0.00	0.09	0.33	0.42	0.00	0.00	61
Il17b	0.00	0.00	0.00	0.00	0.04	0.00	0.00	0.00	0.00	0.00	0.00	1
Ptgdr	0.07	0.00	0.00	0.00	0.00	0.40	0.22	0.00	0.03	0.00	0.12	229
Tlx3	0.10	0.10	0.00	0.09	0.00	0.06	0.03	0.00	0.08	0.00	0.09	127
Dhh	0.03	0.00	0.00	0.00	0.00	0.04	0.00	0.00	0.00	0.00	0.05	40
Prrxl1 / Drgx	0.07	0.02	0.00	0.00	0.00	0.06	0.06	0.00	0.03	0.06	0.09	99
Calca	0.00	0.00	0.08	0.00	0.00	0.20	0.88	0.08	0.78	1.00	0.01	511
Scrt2	0.26	0.27	0.17	0.18	0.19	0.09	0.09	0.08	0.06	0.06	0.08	156
3830431G21rik / Plekhd1	0.42	0.29	0.33	0.46	0.62	0.01	0.00	0.00	0.08	0.35	0.22	212
Tlx2	0.10	0.04	0.25	0.05	0.23	0.22	0.13	0.17	0.09	0.24	0.19	229
Kcns1	0.42	0.52	0.75	0.59	0.92	0.09	0.03	0.00	0.02	0.18	0.06	142

Supplementary Table 3. Putative assignment of cell type expression for hDRG enriched genes based on single cell RNA seq data from mouse. DRG neuron cell type-specific values for hDRG-enriched genes based on mDRG scRNA-seq data from Usoskin et al. Color coding in expression value cells (in TPMs) shows low (blue) to high expression (red). Purple highlighted gene names do not show expression in any DRG neuron subclass. (NF = neurofilament; NP = non-peptidergic; PEP = peptidergic ; TH = tyrosine hydroxylase).

Gene list

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- EGR2:** hDRG and mDRG enriched, low or no detectable expression in mDRG neuronal scRNA-seq dataset. TF involved in Schwann cell development.
Warner LE, Mancias P, Butler IJ, McDonald CM, Keppen L, Koob KG, Lupski JR. Mutations in the early growth response 2 (EGR2) gene are associated with hereditary myelinopathies. *Nature genetics* 1998;18(4):382-384
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- FOXD3:** hDRG and mDRG enriched, low or no detectable expression in mDRG neuronal scRNA-seq dataset. TF involved in Schwann cell development.
Thomas AJ, Erickson CA. FOXD3 regulates the lineage switch between neural crest-derived glial cells and pigment cells by repressing MITF through a noncanonical mechanism. *Development* 2009;136(11):1849-1858.
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- DUSP15:** hDRG and mDRG enriched, low or no detectable expression in mDRG neuronal scRNA-seq dataset. Phosphatase involved in myelinating cell development in both CNS (oligodendrocyte) and PNS (Schwann cells)
Rodríguez-Molina JF, Lopez-Anido C, Ma KH, Zhang C, Olson T, Muth KN, Weider M, Svaren J. Dual specificity phosphatase 15 regulates Erk activation in Schwann cells. *Journal of Neurochemistry* 2017.
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- PLEKHA4:** hDRG and mDRG enriched, low or no detectable expression in mDRG neuronal scRNA-seq dataset. Known expression in Schwann cells.
Schmid D, Zeis T, Schaeren-Wiemers N. Transcriptional regulation induced by cAMP elevation in mouse Schwann cells. *ASN neuro* 2014; 6(3): AN20130031.
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- COL28A1:** hDRG and mDRG enriched, low or no detectable expression in mDRG neuronal scRNA-seq dataset. Known expression in Schwann cells.
Hubert T, Grimal S, Carroll P, Fichard-Carroll A. Collagens in the developing and diseased nervous system. *Cellular and molecular life sciences* 2009;66(7):1223-1238.
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- SFRP5:** hDRG and mDRG enriched, low or no detectable expression in mDRG neuronal scRNA-seq dataset. Known expression in Schwann cells.
Luscan A, Masliah-Planchon J, Laurendeau I, Ortonne N, Varin J, Lallemand F, Leroy K, Dumaine V, Hivelin M, Borderie D. The activation of the WNT signalling pathway is a hallmark in Neurofibromatosis type 1 tumorigenesis. *Clinical Cancer Research* 2013;clincanres. 0780.2013.
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- CLDN19:** hDRG and mDRG enriched, low or no detectable expression in mDRG neuronal scRNA-seq dataset. Known expression in Schwann cells involved in cell – cell junction maintenance.
Kikuchi S, Ninomiya T, Tatsumi H, Sawada N, Kojima T. Tricellulin is expressed in autotypic tight junctions of peripheral myelinating Schwann cells. *Journal of Histochemistry & Cytochemistry* 2010;58(12):1067-1073.
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- PRX:** hDRG and mDRG enriched, low or no detectable expression in mDRG neuronal scRNA-seq dataset. Known expression in myelinating Schwann cells.
Gillespie CS, Sherman DL, Blair GE, Brophy PJ. Periaxin, a novel protein of myelinating Schwann cells with a possible role in axonal ensheathment. *Neuron* 1994;12(3):497-508.
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- CNTF:** hDRG and mDRG enriched, low or no detectable expression in mDRG neuronal scRNA-seq dataset. Known expression in myelinating Schwann cells, involved in regulating tyrosine phosphorylation of STAT3, which is an important TF in Schwann cell repair mechanism.
Friedman B, Scherer SS, Rudge JS, Helgren M, Morrisey D, McClain J, Wang D-y, Wiegand SJ, Furth ME, Lindsay RM. Regulation of ciliary neurotrophic factor expression in myelin-related Schwann cells in vivo. *Neuron* 1992;9(2):295-305
Benito C, Davis CM, Gomez-Sanchez JA, Turmaine M, Meijer D, Poli V, Mirsky R, Jessen KR. STAT3 controls the long-term survival and phenotype of repair Schwann cells during nerve regeneration. *Journal of Neuroscience* 2017:3481-3416.
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- NCMAP:** hDRG and mDRG enriched, low or no detectable expression in mDRG neuronal scRNA-seq dataset. Known expression in myelinating Schwann cells, involved in Myelin assembly.
Ryu EJ, Yang M, Gustin JA, Chang L-W, Freimuth RR, Nagarajan R, Milbrandt J. Analysis of peripheral nerve expression profiles identifies a novel myelin glycoprotein, MP11. *Journal of Neuroscience* 2008;28(30):7563-7573.
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- MPZ:** hDRG and mDRG enriched, low or no detectable expression in mDRG neuronal scRNA-seq dataset. Known expression in myelinating Schwann cells.
Nagarajan R, Le N, Mahoney H, Araki T, Milbrandt J. Deciphering peripheral nerve myelination by using Schwann cell expression profiling. *Proceedings of the National Academy of Sciences* 2002;99(13):8998-9003.
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- DHH:** hDRG and mDRG enriched, low or no detectable expression in mDRG neuronal scRNA-seq dataset. Known expression in myelinating Schwann cells.
Parmantier E, Lynn B, Lawson D, Turmaine M, Namini SS, Chakrabarti L, McMahon AP, Jessen KR, Mirsky R. Schwann cell-derived Desert hedgehog controls the development of peripheral nerve sheaths. *Neuron* 1999;23(4):713-724.
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- GFRA3:** hDRG and mDRG enriched, low or no detectable expression in mDRG neuronal scRNA-seq dataset. Known to be expressed in both neurons and Schwann cells, potentially low or condition-specific expression in neurons avoids detection in scRNA-seq dataset.
Widenfalk J, Tomac A, Lindqvist E, Hoffer B, Olson L. GFR α -3, a protein related to GFR α -1, is expressed in developing peripheral neurons and ensheathing cells. *European journal of neuroscience* 1998;10(4):1508-1517.
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- CHRN3:** hDRG and mDRG enriched, low or no detectable expression in mDRG neuronal scRNA-seq dataset in spite of known neuronal expression.
Albers KM, Zhang XL, Diges CM, Schwartz ES, Yang CI, Davis BM, Gold MS. Artemin growth factor increases nicotinic cholinergic receptor subunit expression and activity in nociceptive sensory neurons. *Molecular pain* 2014;10(1):31.
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- IL17B:** hDRG and mDRG enriched, low or no detectable expression in mDRG neuronal scRNA-seq dataset in spite of known neuronal expression.
Moore EE, Presnell S, Garrigues U, Guillot A, LeGuern E, Smith D, Yao L, Whitmore TE, Gilbert T, Palmer TD. Expression of IL-17B in neurons and evaluation of its possible role in the chromosome 5q-linked form of Charcot-Marie-Tooth disease. *Neuromuscular Disorders* 2002;12(2):141-150.
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Supplementary Table 4. DRG enriched genes that are undetected in Usoskin *et al* dataset. hDRG and mDRG enriched genes detected in less than 10% of sequenced mDRG neurons, and stably expressed in less than half of any of the sensory neuronal subpopulations based on analysis in Usoskin *et al*. Literature driven search suggests a distinctive transcriptional program for peripheral glia conserved between human and mouse.

Term (GO ID)	P-value	Adjusted P-value	Genes
nerve development (GO:0021675)	1.5E-07	0.000109	NTRK1; NGFR; POU4F1; POU4F3; DRGX
detection of temperature stimulus (GO:0016048)	4E-07	0.000146	NTRK1; NGFR; CALCA; DRGX
cranial nerve development (GO:0021545)	1.2E-06	0.000297	NTRK1; POU4F1; POU4F3; DRGX
regulation of neuron differentiation (GO:0045664)	4.6E-06	0.000841	NTRK1; RET; NGFR; ISL2; SKOR2; TLX3; TLX2; STMN2; KLK8
retinal ganglion cell axon guidance (GO:0031290)	4.3E-05	0.002424	ISL2; POU4F2; POU4F3
neuron differentiation (GO:0030182)	6.6E-06	0.000957	NTRK1; ISL2; SKOR2; HOXD1; POU4F1; POU4F2; POU4F3
negative regulation of neuron differentiation (GO:0045665)	7.8E-06	0.000957	NGFR; ISL2; TLX3; TLX2; STMN2; KLK8
neuron projection guidance (GO:0097485)	1.9E-05	0.001642	NTRK1; NGFR; ISL2; TUBB3; GFRA3; POU4F2; POU4F3; DRGX
axon guidance (GO:0007411)	1.9E-05	0.001642	NTRK1; NGFR; ISL2; TUBB3; GFRA3; POU4F2; POU4F3; DRGX
regulation of neuron projection development (GO:0010975)	2.6E-05	0.001709	NTRK1; RET; NGFR; SKOR2; TLX2; STMN2; KLK8
detection of abiotic stimulus (GO:0009582)	2.2E-05	0.001642	NTRK1; NGFR; CALCA; CHRNA9; PPEF1; DRGX
detection of external stimulus (GO:0009581)	2E-05	0.001642	NTRK1; NGFR; CALCA; CHRNA9; PPEF1; DRGX
neuron fate specification (GO:0048665)	7.2E-05	0.003296	ISL2; TLX3; POU4F1
negative regulation of neurogenesis (GO:0050768)	3.4E-05	0.002069	NGFR; ISL2; TLX3; TLX2; STMN2; KLK8
negative regulation of nervous system development (GO:0051961)	5.6E-05	0.002761	NGFR; ISL2; TLX3; TLX2; STMN2; KLK8
response to temperature stimulus (GO:0009266)	4.7E-05	0.002453	NTRK1; NGFR; CALCA; P2RX3; DRGX
neuronal action potential (GO:0019228)	0.00011	0.004296	SCN10A; P2RX3; SCN11A
sensory perception (GO:0007600)	8.8E-05	0.003783	SCN10A; P2RX3; HOXD1; SFRP5; POU4F1; POU4F2; POU4F3; DRGX
negative regulation of cell development (GO:0010721)	0.00011	0.004296	NGFR; ISL2; TLX3; TLX2; STMN2; KLK8
response to pain (GO:0048265)	0.00018	0.006507	RET; CALCA; P2RX3
regulation of cell projection organization (GO:0031344)	0.00022	0.007425	NTRK1; RET; NGFR; SKOR2; TLX2; STMN2; KLK8
negative regulation of neuron projection development (GO:0010977)	0.00022	0.007425	NGFR; TLX2; STMN2; KLK8
synaptic transmission (GO:0007268)	0.00041	0.012682	CHRN3; P2RX3; CHRNA6; CHRNA9; SNCG; HTR3A; KCNK18

Supplementary Table 5. Overlap of hDRG-enriched genes with biological processes in the Gene Ontology database. Three broad categories are highlighted: differentiation and development (blue), growth and regeneration (orange), sensory perception and signal transduction (green)

Term (GO ID)	P-value	Adjusted P-value	Genes
Activation of Nicotinic Acetylcholine Receptors H. sapiens (R-HSA-629602)	1.3E-05	0.00043	CHRNA6;CHRNA9;CHRNA3
Acetylcholine Binding And Downstream Events H. sapiens (R-HSA-181431)	1.3E-05	0.00043	CHRNA6;CHRNA9;CHRNA3
Postsynaptic nicotinic acetylcholine receptors H. sapiens (R-HSA-622327)	1.3E-05	0.00043	CHRNA6;CHRNA9;CHRNA3
Highly calcium permeable postsynaptic nicotinic acetylcholine receptors H. sapiens (R-HSA-629594)	1.3E-05	0.00043	CHRNA6;CHRNA9;CHRNA3
Highly calcium permeable postsynaptic nicotinic acetylcholine receptors H. sapiens (R-HSA-629594)	6.8E-06	0.00043	CHRNA6;CHRNA9;CHRNA3
Presynaptic nicotinic acetylcholine receptors H. sapiens (R-HSA-622323)	0.00066	0.012933	CHRNA6;CHRNA3
Highly calcium permeable nicotinic acetylcholine receptors H. sapiens (R-HSA-629597)	0.0004	0.01098	CHRNA6;CHRNA3
Regulation of TP53 Activity through Association with Co-factors H. sapiens (R-HSA-6804759)	0.00087	0.014872	POU4F1;POU4F2
Calcitonin-like ligand receptors H. sapiens (R-HSA-419812)	0.00048	0.01098	CALCA;CALCB

Supplementary Table 6. Overlap of hDRG-enriched genes with molecular pathways in the Reactome database.