

APPENDIX

Appendix A. Gene identification and primer sets used for realtime PCR reactions. Accession numbers provided for each gene of interest. Primer sets were obtained from PrimerBank (Spandidos et al., 2010) or generated *de novo* using PRIMER3 software. All primer sets were validated before use (See Garcia et al. 2014).

Gene name	Accession #	Gene Function	Forward primer (5'–3')	Reverse Primer (5'–3')
<i>HTR1A</i>	NM_008308	5HT _{1A}	ACTCACCTCTCACAGTATCCA	CTTTTGCTCCTTACCTCCTCTAC
<i>HTR2A</i>	NM_172812	5HT _{2A}	CGAAGCCTCGAACTGGACAAT	CCGCAATGGTGAGAATAATCACG
<i>HTR2C</i>	NM_008312	5HT _{2C}	TGCTGGTGGGACTACTTGTC	GACGCAGTTGAAAATAGCACATC
<i>HTR7</i>	NM_008315	5HT ₇	TGAGAGAAGCGAGTTTGTGC	AGTTCTGTTGTGCAGTCTCAG
<i>CHRNA2</i>	NM_144803	Nicotinic α 2	TTATCTCTGGTGTCTGCTTCTGA	CCCAGCGATTGTAGCCTCC
<i>CHRNA3</i>	NM_145129	Nicotinic α 3	TCCAGTTTGAGGTGTCTATGTCT	TGGTAGTCAGAGGGTTTCCATTT
<i>CHRNA4</i>	NM_015730	Nicotinic α 4	CTAGCAGCCACATAGAGACCC	GACAAGCCAAAGCGGACAAG
<i>CHRNA5</i>	NM_176844	Nicotinic α 5	ATCCTCTGTGCAAAACATGA	TCCACGTCCACTAAGTGTGAT
<i>CHRNA6</i>	NM_021369	Nicotinic α 6	TAAAGGCAGTACAGGCTGTGA	AAAATGCACCGTGACGGGAT
<i>CHRNA7</i>	NM_007390	Nicotinic α 7	CACATTCACACCAACGTCTT	AAAAGGGAACCAGCGTACATC
<i>CHRM2</i>	NM_203491	Muscarinic M2	TGTGATTGGCTACTGGCCTTT	GGGTAGGTTAGAGGTTTTGTGAC
<i>CHRM4</i>	NM_007699	Muscarinic M4	AGATGGTGTTCATTGCGACAG	GAGAACGCCCTATGATGAGA
<i>GLRA1</i>	NM_020492	Glycine α 1	CCGCCCTCAACTTTGTGTCT	GGGGAAACCGATGCGAGATA
<i>GLRA2</i>	NM_183427	Glycine α 2	CATCCCTCGACAGCCCTATCT	CCAGCCGTGAATCATTCCAC
<i>GLRA3</i>	NM_080438	Glycine α 3	AGTGCGGATCTCGAAGTG	ATGGAGCCAAAGCTGTTTTATGA
<i>GLRA4</i>	NM_010297	Glycine α 4	TCCCCAGCCTACTCATCGTC	CAAGCAAGGCAGCAAATACAAA
<i>GABBR1</i>	NM_019439	GABA-Br1	ACGTCACCTCGAAGGTTG	CACAGGCAGGAAATTGATGGC
<i>GABBR2</i>	NM_001081141	GABA-Br2	AAGACCCCATAGAGGACATCAA	GGGTGGTACGTGTCTGTGG
<i>GABRA1</i>	NM_010250	GABA-Ar1	AAAAGTCGGGGTCTCTCTGAC	CAGTCGGTCCAAAATCTTTGTGA
<i>GABRA3</i>	NM_008067	GABA-Ar3	ATGTGGCACTTTTATGTGACCA	CCCAGGTTCTTGTCTGCTTG
<i>GABRA5</i>	NM_176942	GABA-Ar5	TGACCCAAACCCCTCCTGTCT	GTGATGTTGTCATTGGTCTCGT
<i>SERT</i>	NM_010484	5HT transporter	CTCCGCAGTCCCAGTACAAG	CTCCGCAGTCCCAGTACAAG
<i>ACHE</i>	NM_009599	Acetylcholin-esterase	CTCCCTGGTATCCCCTGCATA	GGATGCCAGAAAAGCTGAGA
<i>CACNA1A</i>	NM_007578	P/Q-type Ca ²⁺ (Ca _v 2.1)	AAAGGCTCCTACCTGAGGAAT	CTCAGTGTCCGTAGGTCAAC
<i>CACNA1B</i>	NM_007579	N-type Ca ²⁺ (Ca _v 2.2)	ACAACGTCTCCGCAAATAC	CAGGGCCAGAACAAATGCAGT
<i>CACNA1C</i>	NM_001159534	L-type Ca ²⁺ (Ca _v 1.2)	GGAGGCGGTGCAATAAGCATT	AGGAAGAGATACTCCAATCGTTC
<i>CACNA1D</i>	NM_001083616	L-type Ca ²⁺ (Ca _v 1.3)	GCTTACGTTAGGAATGGATGGAA	GAAGTGGTCTTAACACTCGGAAG
<i>CACNA1E</i>	NM_009782	R-type Ca ²⁺ (Ca _v 2.1)	CAGTCCGGCAGAACTGTTTCA	GAGACATTGGGGTCTTGTCTATC
<i>CACNA1G</i>	NM_001112813	T-type Ca ²⁺ (Ca _v 3.1)	AGAGTCCGCTGACCATGAAAT	CCGGAATGTGTGCGAGATCA
<i>KCNN1</i>	NM_032397	K _{Ca} 2.1	CAAGCGGGTCAAAAATGCTG	GAAGGAACCTACGCTGGTGT
<i>KCNN2</i>	NM_080465	K _{Ca} 2.2	AGCCGGAGCACACAATCTA	CCCAGTCTAGCCGATG
<i>KCNN3</i>	NM_080466	K _{Ca} 2.3	CTCGGAGAAACCTTATCGAGGC	GGTTGTGGGTACGGTTGGG
<i>KCNMA1</i>	NM_010610	K _{Ca} 1.1	CAGGCAGATGGTACTCTCAAGC	TTGGGTTTGACGAGTCTATGAAG
<i>KCNA1</i>	NM_010595	K _V 1.1	CCCCTCCTACCCCTCTTC	CTGCCGATTGAGACTCT
<i>KCNA2</i>	NM_008417	K _V 1.2	GTCTGAGCTTCTGCAGGAAA	CCTATTTGTGTATCTGTGCCATC
<i>KCNA3</i>	NM_008418	K _V 1.3	CTGCCATTACCTTGTCTGTT	CAGTAAAGCCACTTCTCCA
<i>KCNA4</i>	NM_021275	K _V 1.4	GAAAGCAGGAAATGAAGAGCATC	GTTGACAGGTGAAAAGG
<i>KCNA5</i>	NM_145983	K _V 1.5	GCAGAGCTTCCAAGCAGAAG	TCTTCAATACCCAGAAAAGCTC
<i>KCNA6</i>	NM_013568	K _V 1.6	CAGAGAAGTTCAAGATCGGGTA	ATTTCTGCTTGGGATGAGGAC
<i>KCNB1</i>	NM_008420	K _V 2.1	GGTGGAGAGGACAATGAACA	GAGTTCGACAACACGTGCT
<i>KCNB2</i>	NM_001098528	K _V 2.2	AAGTGTGTTGAGAGACAGAGC	TTGCTGGAGAAAACCTAACTCG
<i>KCNC1</i>	NM_001112739	K _V 3.1	TTCCGGTCTTGTTCACGATGG	CCCTACTCATCCCGCTACG
<i>KCNC2</i>	NM_001025581	K _V 3.2	TTGTGTCTCCTTTAGTCTGTGC	AACGTGTTTCTGTTGACGA
<i>KCNC3</i>	NM_008422	K _V 3.3	CACAATGCTGCTCAGGCT	GAAGACAAGAGCCCAATCACT
<i>KCNC4</i>	NM_145922	K _V 3.4	CTTGGCAGGTCTCTGTGTT	GGACTATGCCTGTGCTGATG
<i>KCND2</i>	NM_019697	K _V 4.2	CTGTGGTCACGTAAGGTTGT	GTGCAAGAAGTCAAGTCAATTCAG
<i>KCND3</i>	NM_001039347	K _V 4.3	ATCGAGCTCTCCATGCAG	CAAGACCACCTCACTCATCG
<i>KCNQ1</i>	NM_008434	K _V 7.1	GTAAGTCTCGATGACATCTCG	CCCATACCCATGTGTCA
<i>SCN8A</i>	NM_001077499	Na _v 1.6	GTGACGAAATCAAAGACAATCCC	GACATGAGGAACGAAGAAGTACTAC
<i>SLC12A5</i>	NM_020333	Cl ⁻ /K ⁺ symporter	ATGTCTTCTCGTAGGTGTATGC	GACCACGTTTCTGTACCACTT
<i>ACTB</i>	NM_007393	Beta-actin	GATGACCCAGATCATGTTTGAGACC	AGATGGGCACAGTGTGGGTGA
<i>GAPDH</i>	NM_008084	Glyceraldehyde 3-phosphate dehydrogenase	TGCACCACCACCTGCTTAGC	GGCATGGACTGTGGTTCATGAG

Appendix B. ANOVA results for mRNA levels across cord levels and injury. Values for *F* and *P* for two-way ANOVAs are reported for the interaction of 2 slice levels (motor- and interneuron) and injury (SCI and control). *P*-values lower than 0.05 are noted in bold.

Gene name	<i>F</i> (Level)	<i>P</i> (Level)	<i>F</i> (Injury)	<i>P</i> (Injury)	<i>F</i> (Interaction)	<i>P</i> (Interaction)
<i>HTR1A</i>	34.575	<0.001	16.682	<0.001	0.324	0.573
<i>HTR2A</i>	0.113	0.739	3.650	0.065	19.754	<0.001
<i>HTR2C</i>	58.618	<0.001	0.00418	0.949	4.953	0.033
<i>HTR7</i>	33.097	<0.001	0.0961	0.759	5.569	0.024
<i>CHRNA2</i>	4.227	0.048	28.659	<0.001	21.367	<0.001
<i>CHRNA3</i>	122.144	<0.001	19.722	<0.001	7.50	0.010
<i>CHRNA4</i>	119.458	<0.001	18.417	<0.001	0.493	0.488
<i>CHRNA5</i>	1.698	0.202	1.993	0.168	0.159	0.693
<i>CHRNA6</i>	0.899	0.350	11.220	0.002	1.414	0.243
<i>CHRNA7</i>	21.250	<0.001	12.821	0.001	2.107	0.156
<i>CHRM2</i>	9.239	0.005	46.010	<0.001	4.675	0.038
<i>CHRM4</i>	1.721	0.199	0.113	0.739	1.940	0.173
<i>GLRA1</i>	13.443	<0.001	19.594	<0.001	0.734	0.398
<i>GLRA2</i>	98.336	<0.001	0.273	0.605	4.827	0.035
<i>GLRA3</i>	89.110	<0.001	8.088	0.007	1.718	0.199
<i>GABBR1</i>	18.695	<0.001	0.0079	0.930	19.507	<0.001
<i>GABBR2</i>	6.406	0.016	1.847	0.184	26.804	<0.001
<i>GABRA1</i>	29.977	<0.001	0.0326	0.858	0.655	0.424
<i>GABRA3</i>	66.594	<0.001	1.531	0.224	0.017	0.897
<i>GABRA5</i>	71.280	<0.001	3.180	0.083	1.091	0.304
<i>ACHE</i>	49.189	<0.001	13.185	<0.001	0.887	0.353
<i>CACNA1A</i>	9.328	0.004	0.00285	0.958	3.865	0.058
<i>CACNA1B</i>	44.325	<0.001	3.548	0.068	5.582	0.024
<i>CACNA1C</i>	47.365	<0.001	25.546	<0.001	31.136	<0.001
<i>CACNA1D</i>	8.935	0.005	11.529	0.002	22.019	<0.001
<i>CACNA1E</i>	39.226	<0.001	0.713	0.404	1.090	0.304
<i>CACNA1G</i>	3.338	0.076	20.730	<0.001	4.844	0.035
<i>KCNN1</i>	30.252	<0.001	5.777	0.022	54.369	<0.001
<i>KCNN2</i>	18.519	<0.01	1.619	0.212	30.776	<0.001
<i>KCNN3</i>	22.848	<0.001	39.580	<0.001	16.225	<0.001
<i>KCNMA1</i>	12.602	0.001	1.050	0.313	21.024	<0.001
<i>KCNA1</i>	0.635	0.431	1.188	0.283	8.852	0.005
<i>KCNA2</i>	23.147	<0.001	7.505	0.010	3.777	0.060
<i>KCNA3</i>	64.577	<0.001	34.750	<0.001	0.632	0.433
<i>KCNA6</i>	2.473	0.125	0.113	0.738	0.039	0.844
<i>KCNB1</i>	0.021	0.886	0.410	0.526	10.349	0.003
<i>KCNB2</i>	10.112	0.003	0.002	0.963	0.584	0.450
<i>KCNC3</i>	1.996	0.167	0.268	0.608	18.398	<0.001
<i>KCNC4</i>	2.663	0.112	0.001	0.972	18.827	<0.001
<i>KCND2</i>	70.159	<0.001	1.179	0.286	25.838	<0.001
<i>SCN8A</i>	43.839	<0.001	40.502	<0.001	100.155	<0.001
<i>SLC12A5</i>	1.972	0.170	0.014	0.908	0.243	0.625

(Received 14 May 2018, Accepted 24 September 2018)
(Available online 30 September 2018)