

**Supplemental Table 1. Transcription factors enriched in the promoters of differentially expressed genes regulated by Neurog1/2 and Ascl1**

Term	Adjusted P-value	Genes
NEUROD4	3.55E-19	ROBO2;CHRNA3;ONECUT2;ELAVL4;EBF2;GFRA1;MYT1;POU3F2;ISL1;ELAVL3;DCX;INSM1;CHGB
NHLH2	3.97E-17	ROBO2;CHRNA3;ONECUT2;ELAVL4;DCX;EBF2;GFRA1;INSM1;MYT1;POU3F2;ISL1;ELAVL3
<b>ASCL1</b>	3.26E-15	PCDH9;ONECUT2;ELAVL4;DCX;GFRA1;INSM1;MYT1;POU3F2;ISL1;CHGB;ELAVL3
NHLH1	3.26E-15	ONECUT2;ELAVL4;DCX;EBF2;INSM1;MDGA1;MYT1;POU3F2;ISL1;CHGB;ELAVL3
SCRT2	2.72E-13	ROBO2;ONECUT2;ELAVL4;DCX;INSM1;MDGA1;MYT1;POU3F2;CHGB;ELAVL3
NEUROD1	2.72E-13	ROBO2;ONECUT2;ELAVL4;DCX;INSM1;MYT1;POU3F2;ISL1;CHGB;ELAVL3
INSM1	1.59E-11	ROBO2;ONECUT2;ELAVL4;DCX;MYT1;POU3F2;ISL1;CHGB;ELAVL3
ARX	1.59E-11	ROBO2;PCDH9;ONECUT2;DCX;EBF2;INSM1;POU3F2;ISL1;CHGB
POU3F4	1.59E-11	ROBO2;ONECUT2;ELAVL4;DCX;GFRA1;INSM1;MYT1;POU3F2;ISL1
FEZF2	1.59E-11	ROBO2;ONECUT2;ELAVL4;DCX;EBF2;GFRA1;INSM1;POU3F2;ISL1
ISL1	5.27E-10	ROBO2;ONECUT2;ELAVL4;EBF2;GFRA1;INSM1;POU3F2;CHGB
FOXG1	5.27E-10	ROBO2;PCDH9;ONECUT2;DCX;GFRA1;INSM1;POU3F2;ISL1
LHX9	5.27E-10	ROBO2;PCDH9;ONECUT2;EBF2;GFRA1;INSM1;POU3F2;ISL1
SOX1	5.27E-10	ONECUT2;ELAVL4;EBF2;GFRA1;INSM1;POU3F2;ISL1;ELAVL3
POU3F2	5.27E-10	ROBO2;PCDH9;ONECUT2;DCX;EBF2;GFRA1;INSM1;ISL1
SIM1	5.27E-10	ROBO2;PCDH9;ONECUT2;EBF2;GFRA1;INSM1;POU3F2;ISL1
PHOX2B	5.27E-10	ONECUT2;ELAVL4;EBF2;GFRA1;INSM1;POU3F2;ISL1;ELAVL3
MYT1	5.27E-10	ROBO2;ONECUT2;ELAVL4;DCX;INSM1;POU3F2;CHGB;ELAVL3
ATOH1	5.27E-10	ROBO2;ONECUT2;EBF2;GFRA1;INSM1;POU3F2;ISL1;CHGB
NEUROD2	5.27E-10	ONECUT2;ELAVL4;DCX;INSM1;MYT1;POU3F2;CHGB;ELAVL3
ST18	5.27E-10	ROBO2;PCDH9;ELAVL4;DCX;INSM1;MYT1;ISL1;CHGB
DRGX	5.27E-10	ONECUT2;ELAVL4;EBF2;GFRA1;INSM1;POU3F2;ISL1;ELAVL3
SCRT1	5.27E-10	ONECUT2;ELAVL4;INSM1;MDGA1;MYT1;POU3F2;CHGB;ELAVL3
ONECUT2	1.78E-08	ROBO2;DCX;EBF2;GFRA1;INSM1;POU3F2;ISL1
HOXD3	1.78E-08	ROBO2;ONECUT2;EBF2;GFRA1;INSM1;POU3F2;ISL1
PAX2	1.78E-08	ONECUT2;EBF2;GFRA1;INSM1;MDGA1;POU3F2;ISL1
POU4F1	1.78E-08	ONECUT2;DCX;EBF2;INSM1;POU3F2;ISL1;ELAVL3
TBR1	1.78E-08	ROBO2;ONECUT2;ELAVL4;DCX;INSM1;POU3F2;ISL1
TFAP2B	1.78E-08	ROBO2;ONECUT2;EBF2;GFRA1;INSM1;POU3F2;ISL1
PAX3	1.78E-08	ROBO2;ONECUT2;EBF2;GFRA1;INSM1;POU3F2;ISL1
SP8	1.78E-08	ROBO2;ONECUT2;EBF2;GFRA1;INSM1;POU3F2;ISL1
<b>NEUROG1</b>	1.78E-08	ONECUT2;EBF2;INSM1;MDGA1;MYT1;POU3F2;ISL1
POU4F2	1.78E-08	ONECUT2;EBF2;GFRA1;INSM1;POU3F2;ISL1;ELAVL3
DLX6	1.78E-08	ROBO2;ONECUT2;EBF2;GFRA1;INSM1;POU3F2;ISL1
SALL3	1.78E-08	ROBO2;ONECUT2;EBF2;GFRA1;INSM1;POU3F2;ISL1
INSM2	1.78E-08	ONECUT2;ELAVL4;EBF2;INSM1;POU3F2;ISL1;CHGB
PAX4	1.78E-08	ONECUT2;DCX;INSM1;MYT1;POU3F2;ISL1;CHGB
ZIC4	1.78E-08	ROBO2;ONECUT2;EBF2;GFRA1;INSM1;POU3F2;ISL1
TFAP2D	1.78E-08	ROBO2;PCDH9;ONECUT2;ELAVL4;EBF2;POU3F2;ISL1
RFX6	1.78E-08	ROBO2;ONECUT2;ELAVL4;DCX;INSM1;ISL1;CHGB
BARHL1	1.78E-08	ONECUT2;EBF2;INSM1;MYT1;POU3F2;ISL1;CHGB
ISL2	4.26E-07	ONECUT2;EBF2;GFRA1;INSM1;POU3F2;ISL1
ONECUT1	4.26E-07	ONECUT2;EBF2;GFRA1;INSM1;POU3F2;ISL1
ALX1	4.26E-07	PCDH9;ONECUT2;EBF2;GFRA1;POU3F2;ISL1
FOXB1	4.26E-07	ONECUT2;EBF2;GFRA1;INSM1;POU3F2;ISL1
IRX6	4.26E-07	PCDH9;ONECUT2;EBF2;GFRA1;INSM1;POU3F2
<b>NEUROG2</b>	4.26E-07	ONECUT2;EBF2;INSM1;MYT1;POU3F2;ISL1
HMX1	4.26E-07	ONECUT2;EBF2;INSM1;POU3F2;ISL1;ELAVL3
HOXD13	4.26E-07	ONECUT2;EBF2;GFRA1;INSM1;POU3F2;ISL1
PAX6	4.26E-07	ONECUT2;ELAVL4;GFRA1;INSM1;POU3F2;ISL1
HELT	4.26E-07	ONECUT2;EBF2;GFRA1;INSM1;POU3F2;ISL1
FEZF1	4.26E-07	ONECUT2;EBF2;GFRA1;INSM1;POU3F2;ISL1
BARHL2	4.26E-07	ONECUT2;EBF2;GFRA1;INSM1;POU3F2;ISL1
FOXO4	4.26E-07	ONECUT2;EBF2;GFRA1;INSM1;POU3F2;ISL1
LBX1	4.26E-07	ONECUT2;EBF2;GFRA1;INSM1;POU3F2;ISL1
POU3F3	4.26E-07	ONECUT2;EBF2;INSM1;POU3F2;ISL1;ELAVL3
OLIG3	4.26E-07	ONECUT2;EBF2;GFRA1;INSM1;POU3F2;ISL1
DMRTA2	4.26E-07	ONECUT2;ELAVL4;EBF2;INSM1;POU3F2;ISL1
LHX8	4.26E-07	ONECUT2;EBF2;GFRA1;INSM1;POU3F2;ISL1
SOX11	4.26E-07	ROBO2;ONECUT2;DCX;GFRA1;INSM1;ISL1
DMRT3	4.26E-07	ONECUT2;EBF2;GFRA1;INSM1;POU3F2;ISL1
PAX7	4.26E-07	ONECUT2;EBF2;GFRA1;INSM1;POU3F2;ISL1
UNCX	4.26E-07	ONECUT2;EBF2;INSM1;MYT1;POU3F2;ISL1
LMX1A	4.26E-07	ONECUT2;EBF2;GFRA1;INSM1;POU3F2;ISL1
DBX1	4.26E-07	ONECUT2;EBF2;GFRA1;INSM1;POU3F2;ISL1
SIX3	4.26E-07	ONECUT2;EBF2;GFRA1;INSM1;POU3F2;ISL1
LHX4	4.26E-07	ONECUT2;EBF2;INSM1;MDGA1;POU3F2;ISL1
SIX6	4.26E-07	ONECUT2;EBF2;GFRA1;INSM1;POU3F2;ISL1
ZNF454	4.26E-07	ROBO2;ONECUT2;ELAVL4;EBF2;GFRA1;ISL1
NEUROD6	4.26E-07	ROBO2;ELAVL4;DCX;INSM1;POU3F2;CHGB
PAX1	4.26E-07	ONECUT2;EBF2;GFRA1;INSM1;POU3F2;ISL1
TLX3	4.26E-07	ONECUT2;EBF2;GFRA1;INSM1;POU3F2;ISL1
FOXO2	4.26E-07	ONECUT2;EBF2;GFRA1;INSM1;POU3F2;ISL1
VSX2	4.26E-07	ONECUT2;EBF2;INSM1;MDGA1;POU3F2;ISL1
VSX1	4.26E-07	ONECUT2;EBF2;GFRA1;INSM1;POU3F2;ISL1
EMX1	4.26E-07	ONECUT2;EBF2;GFRA1;INSM1;POU3F2;ISL1
VAX1	4.26E-07	ONECUT2;EBF2;GFRA1;INSM1;POU3F2;ISL1
FERD3L	4.26E-07	ROBO2;ONECUT2;GFRA1;INSM1;POU3F2;ISL1
LHX5	4.26E-07	ONECUT2;EBF2;GFRA1;INSM1;POU3F2;ISL1
POU4F3	4.26E-07	ONECUT2;EBF2;GFRA1;INSM1;POU3F2;ISL1
PRDM12	4.26E-07	ONECUT2;EBF2;INSM1;MDGA1;POU3F2;ISL1

**Supplemental Table 2. Biological process enriched in the differentially expressed genes regulated by Neurog1/2 and Asc1**

Term	Adjusted P-value	Genes
neuron fate specification (GO:0048665)	1.21E-03	<i>POU3F2;ISL1</i>
cell differentiation in spinal cord (GO:0021515)	1.21E-03	<i>MDGA1;ISL1</i>
nervous system development (GO:0007399)	1.21E-03	<i>ROBO2;CHRNA3;DCX;GFRA1;POU3F2</i>
neuron fate commitment (GO:0048663)	2.31E-03	<i>POU3F2;ISL1</i>
generation of neurons (GO:0048699)	4.91E-03	<i>DCX;MDGA1;POU3F2</i>
central nervous system neuron differentiation (GO:0021953)	8.85E-03	<i>MDGA1;ISL1</i>
neuron migration (GO:0001764)	1.17E-02	<i>DCX;MDGA1</i>
central nervous system development (GO:0007417)	1.32E-02	<i>ROBO2;DCX;MDGA1</i>
axonogenesis (GO:0007409)	1.32E-02	<i>ROBO2;GFRA1;ISL1</i>
retinal ganglion cell axon guidance (GO:0031290)	4.34E-02	<i>ROBO2</i>
spinal cord motor neuron differentiation (GO:0021522)	4.34E-02	<i>ISL1</i>
norepinephrine biosynthetic process (GO:0042421)	4.34E-02	<i>INSM1</i>
norepinephrine metabolic process (GO:0042415)	4.34E-02	<i>INSM1</i>
activation of transmembrane receptor protein tyrosine kinase activity (GO:0007171)	4.34E-02	<i>CHRNA3</i>
negative regulation of chemotaxis (GO:0050922)	4.34E-02	<i>ROBO2</i>
response to ammonium ion (GO:0060359)	4.34E-02	<i>CHRNA3</i>
trigeminal nerve development (GO:0021559)	4.34E-02	<i>ISL1</i>
negative regulation of synapse organization (GO:1905809)	4.34E-02	<i>ROBO2</i>
atrial septum morphogenesis (GO:0060413)	4.34E-02	<i>ISL1</i>
sympathetic ganglion development (GO:0061549)	4.34E-02	<i>INSM1</i>
type B pancreatic cell differentiation (GO:0003309)	4.34E-02	<i>INSM1</i>
positive regulation of interleukin-1 production (GO:0032732)	4.34E-02	<i>ISL1</i>
cardiac right ventricle morphogenesis (GO:0003215)	4.34E-02	<i>ISL1</i>
negative regulation of intracellular estrogen receptor signaling pathway (GO:0033147)	4.34E-02	<i>ISL1</i>
peripheral nervous system neuron development (GO:0048935)	4.34E-02	<i>ISL1</i>
adrenal gland development (GO:0030325)	4.34E-02	<i>INSM1</i>
regulation of granulocyte macrophage CSF production (GO:0032645)	4.34E-02	<i>ISL1</i>
cranial nerve development (GO:0021545)	4.34E-02	<i>ISL1</i>
positive regulation of granulocyte macrophage CSF production (GO:0032725)	4.34E-02	<i>ISL1</i>
regulation of cell differentiation (GO:0045595)	4.34E-02	<i>INSM1;ISL1</i>
atrial septum development (GO:0003283)	4.34E-02	<i>ISL1</i>
ganglion development (GO:0061548)	4.34E-02	<i>INSM1</i>
cardiac atrium morphogenesis (GO:0003209)	4.34E-02	<i>ISL1</i>
mesonephric tubule development (GO:0072164)	4.34E-02	<i>ROBO2</i>
regulation of interleukin-1 beta production (GO:0032651)	4.34E-02	<i>ISL1</i>
pancreas development (GO:0031016)	4.34E-02	<i>ISL1</i>
regulation of neural precursor cell proliferation (GO:2000177)	4.34E-02	<i>INSM1</i>
catecholamine biosynthetic process (GO:0042423)	4.34E-02	<i>INSM1</i>
mesenchyme morphogenesis (GO:0072132)	4.34E-02	<i>ISL1</i>
cellular response to corticosteroid stimulus (GO:0071384)	4.34E-02	<i>ISL1</i>
sympathetic nervous system development (GO:0048485)	4.34E-02	<i>INSM1</i>
cellular response to glucocorticoid stimulus (GO:0071385)	4.34E-02	<i>ISL1</i>
noradrenergic neuron differentiation (GO:0003357)	4.34E-02	<i>INSM1</i>
pharyngeal system development (GO:0060037)	4.34E-02	<i>ISL1</i>
positive regulation of neural precursor cell proliferation (GO:2000179)	4.34E-02	<i>INSM1</i>
regulation of protein homodimerization activity (GO:0043496)	4.34E-02	<i>ISL1</i>
endocardial cushion morphogenesis (GO:0003203)	4.34E-02	<i>ISL1</i>
ureteric bud development (GO:0001657)	4.34E-02	<i>ROBO2</i>
acetylcholine receptor signaling pathway (GO:0095500)	4.58E-02	<i>CHRNA3</i>
endocardial cushion development (GO:0003197)	4.58E-02	<i>ISL1</i>
response to nicotine (GO:0035094)	4.87E-02	<i>CHRNA3</i>
neuromuscular synaptic transmission (GO:0007274)	4.88E-02	<i>CHRNA3</i>
outflow tract septum morphogenesis (GO:0003148)	4.88E-02	<i>ISL1</i>
regulation of smooth muscle contraction (GO:0006940)	4.88E-02	<i>CHRNA3</i>

**Supplemental Table 3. crRNA, tracrRNA, and PCR primer nucleotide sequences used for this study**

name	sequence (5'-3')
c3orf70a_crRNA1	cagauggauaguccaucgaguuuagagcuaugcuguuuug
c3orf70a_crRNA2	gcagcuugaaacaauuuccgguuuagagcuaugcuguuuug
c3orf70b_crRNA1	agauggacaguccaucacagguuuuagagcuaugcuguuuug
c3orf70b_crRNA2	gcucuggccaaaagcugugcguuuuagagcuaugcuguuuug
tracrRNA	aaacagcauagcaaguuaaaauaaggcuaguccguuaacaacuugaaaaaguggcaccgagucggugcu
c3orf70a F for mutation	ggcggacagaagagtggagaa
c3orf70a R for mutation	aaccagatgacagcaccag
c3orf70b F for mutation	ctacagtggagcgcagaagg
c3orf70b R for mutation	caccagtgcagttgaaacact
c3orf70a F for cloning and WISH	aagtggaactgggtagccg
c3orf70a R for cloning and WISH	aggagtgtgtgcttgactg
c3orf70b F for cloning and WISH	ggatcttaatacagatgtgtggga
c3orf70b R for cloning and WISH	agtgaagcattgtcctctacata
neurod1 F for WISH	tcgaactggaccgacaagtg
neurod1 R for WISH	ggagcgtctcgtcttgag
elavl3 F for WISH	cgacaaacggaacgaagcag
elavl3 R for WISH	catggtgacgaagccaaagc
neurod1 F for qPCR	accacgaagggcatgaaact
neurod1 R for qPCR	gtccacgtctcgtctctt
elavl3 F for qPCR	atcaacacgctcaacggtct
elavl3 R for qPCR	ttaccagatgctgtaggtg
irx3b F for qPCR	caccggctctgttctctg
irx3b R for qPCR	tgcgagctcagctggtg
actb F for qPCR	cgagcaggagatgggaacc
actb R for qPCR	caacggaaacgctcattgc

**A****Neurog2 binding motif**

				Score
Human C3orf70	-2243	ACCATG <u>T</u> GGT	-2252	7.0
	-1374	ACCAT <u>T</u> TGCT	-1383	6.3
Mouse C3orf70	-1926	AACATCTGTT	-1935	10.4
	-1223	TGCATATGTC	-1232	8.6
Zebrafish C3orf70a	- 713	AACATATGCT	- 722	14.1
	-1812	GACAGATGCC	-1803	10.9
Zebrafish C3orf70b	- 139	AACATATTTTC	- 148	10.4
	-1956	ACCACATGTC	-1965	9.8

**B****Ascl1 binding motif**

				Score
Human C3orf70	-1218	CCAGCAGG <u>T</u> GTGA	-1230	10.9
	-1907	GGAGCAG <u>T</u> TGGG	-1895	9.7
Mouse C3orf70	-1398	TGGGCACCTGGGA	-1386	8.8
	-1666	CAACCAGCTGTAT	-1654	7.8
Zebrafish C3orf70a	- 682	GTTGCAGCTGGAA	- 694	12.4
Zebrafish C3orf70b	- 59	ACTGCAGCTGTGT	- 47	11.4
	- 838	GCAGCAGCAGCAA	- 850	9.4

**Supplemental Figure 1.** Comparison of the putative binding sites for Neurog2 and Ascl1 in the promoter sequence of C3orf70. Potential binding sites for Neurog2 (A) and Ascl1 (B) in the promoters of human, mouse, and zebrafish C3orf70 are shown below the motifs.

c3orf70a_cDNA	ATGGCCGCTTCGGGCGGACAGAAGAGTGAGAAGTTAGATGAAGCTCAGGCTTTAGCCAGG	60
c3orf70a_NM_001126467	ATGGCCGCTTCGGGCGGACAGAAGAGTGAGAAGTTAGATGAAGCTCAGGCTTTAGCCAGG	60
	*****	
c3orf70a_cDNA	AGTTGCGCAGGACGACCGGACTTTCTGCCCTGCGATGGACTATCCATCTGCGCCACACAC	120
c3orf70a_NM_001126467	AGTTGCGCAGGACGACCGGACTTTCTGCCCTGCGATGGACTATCCATCTGCGCCACACAC	120
	*****	
c3orf70a_cDNA	AGCCACGGGAAATGTTTCAAGCTGCACTGGTGCTGTCATCTGGGTTGGTGCCACTGTAAA	180
c3orf70a_NM_001126467	AGCCACGGGAAATGTTTCAAGCTGCACTGGTGCTGTCATCTGGGTTGGTGCCACTGTAAA	180
	*****	
c3orf70a_cDNA	TACGTCTACCAACCTATGACCAGCGTATGCCAACTTCCCAGCACAGCGGTTCCAGTCGCT	240
c3orf70a_NM_001126467	TACGTCTACCAACCTATGACCAGCGTATGCCAACTTCCCAGCACAGCGGTTCCAGTCGCT	240
	*****	
c3orf70a_cDNA	CCCTCAGGTCATACGCACACTATGAACTTGTCCATCTCGCTGGCTGAACGTTTTCTCAGG	300
c3orf70a_NM_001126467	CCCTCAGGTCATACGCACACTATGAACTTGTCCATCTCGCTGGCTGAACGTTTTCTCAGG	300
	*****	
c3orf70a_cDNA	ACAGCTCCCAAGTTCAGGCTCCACCCTGCCCTGAGTCTCCCAAGTTCGTGTGCATCTCT	360
c3orf70a_NM_001126467	ACAGCTCCCAAGTTCAGGCTCCACCCTGCCCTGAGTCTCCCAAGTTCGTGTGCATCTCT	360
	*****	
c3orf70a_cDNA	GACCTCTTTGTGGATGATTACATGGTCAAGCGTATCAATGGTAAAATGTGTTACGTGCAA	420
c3orf70a_NM_001126467	GACCTCTTTGTGGATGATTACATGGTCAAGCGTATTAATGGTAAAATGTGTTACGTGCAA	420
	*****	
c3orf70a_cDNA	AGGCCTCCCCGCCTACACCAAATCCCACACACCAACCTCAAACGGCGGCACCTCAGCCT	480
c3orf70a_NM_001126467	AGGCCTCCCCGCCTACACCAAATCCCACACACCAACCTCAAACGGCGGCACCTCAGCCT	480
	*****	
c3orf70a_cDNA	GTGCCCCAACGTTCCAAAAACAGTCATCAAGTGGGCCCAACTGTTAAACAAGGCCAAGCA	540
c3orf70a_NM_001126467	GTGCCCCAACGTTCCAAAAACAGTCATCAAGTGGGCCCAACTGTTAAACAAGGCCAAGCA	540
	*****	
c3orf70a_cDNA	AAGGAGAAGATCTCAGCCCCATAAATGGACCACCTGCTCCTCTCCCTCCAGCTCAGAGGAC	600
c3orf70a_NM_001126467	AAGGAGAAGATCTCAGCCCCATAAATGGACCACCTGCTCCTCTCCCTCCAGCTCAGAGGAC	600
	*****	
c3orf70a_cDNA	TCTGGAATCAATGCATTGGGTTTGCACACTACATGGAATCATGCGACGAGGACTCTTGTGTA	660
c3orf70a_NM_001126467	TCTGGAATCAATGCATTGGGTTTGCACACTACATGGAATCATGCGACGAGGACTCTTGTGTA	660
	*****	
c3orf70a_cDNA	GATGACGATGACGAGGAAGAAGAGGACGATGAGCTGAGTACTGATGGAACTCCAGCCCA	720
c3orf70a_NM_001126467	GATGACGATGACGAGGAAGAAGAGGACGATGAGCTGAGTACTGATGGAACTCCAGCCCA	720
	*****	
c3orf70a_cDNA	GGTAGCTTCTGGGACCAGGACGAGTGCACCTTACTATCACCATCTAAATCAATCGTTGAG	780
c3orf70a_NM_001126467	GGTAGCTTCTGGGACCAGGACGAGTGCACCTTACTATCACCATCTAAATCAATCGTTGAG	780
	*****	
c3orf70a_cDNA	ATCATTGAGAAGATTGAGACTACAGTTTGA	810
c3orf70a_NM_001126467	ATCATTGAGAAGATTGAGACTACAGTTTGA	810
	*****	



**Supplemental Figure 2.** Comparison of the nucleotide sequences of c3orf70a open reading frame determined in this study and human sequence NM\_001126467 in the NCBI Reference Sequence Database. Red arrowhead indicates the single nucleotide difference between the cDNA and reference sequences.

c3orf70b_cDNA	ATGGCCTACAGTGGAGCGCAGAAGGCTTTGAAGAGTGATAAGTTAGATGAAGCTCAAGCT	60
c3orf70b_NM_001089454	ATGGCCTACAGTGGAGCGCAGAAGGCTTTGAAGAGTGATAAGTTAGATGAAGCTCAAGCT	60
	*****	
c3orf70b_cDNA	CTGGCCAAAAGCTGTGCGGGCAGACCGGACTTCCTCCCCTGTGATGGACTGTCCATCTGC	120
c3orf70b_NM_001089454	CTGGCCAAAAGCTGTGCGGGCAGACCGGACTTCCTCCCCTGTGATGGACTGTCCATCTGC	120
	*****	
c3orf70b_cDNA	GCAACACACAGCCATGGAAAGTGTTCAAACTGCACTGGTGCTGCCATTTGGGCTGGTGT	180
c3orf70b_NM_001089454	GCAACACACAGCCATGGAAAGTGTTCAAACTGCACTGGTGCTGCCATTTGGGCTGGTGT	180
	*****	
c3orf70b_cDNA	CACTGTAAATATGTGTACCAGCCCATGACCAACGTGGCTCAGCTGCCAGCACACCTGTG	240
c3orf70b_NM_001089454	CACTGTAAATATGTGTACCAGCCCATGACCAACGTGGCTCAGCTGCCAGCACACCTGTG	240
	*****	
c3orf70b_cDNA	CTGCGGCTCCGTCTGACTGCCCGACACCATTGATCTGTCCATTTCTCTGACCGAACGC	300
c3orf70b_NM_001089454	CTGCGGCTCCGTCTGACTGCCCGACACCATTGATCTGTCCATTTCTCTGACCGAACGC	300
	*****	
c3orf70b_cDNA	TTCTCCGCATCTCCCCCTGCTTCCAGCTCCACCCTGTCCAGAATCGCCCAAATACTGC	360
c3orf70b_NM_001089454	TTCTCCGCATCTCCCCCTGCTTCCAGCTCCACCCTGTCCAGAATCGCCCAAATACTGC	360
	*****	
c3orf70b_cDNA	AACATCGCCGAACTCTTTATTGACGACTATATCGTTAAACGAATCAACGGCAAGATGTGC	420
c3orf70b_NM_001089454	AACATCGCCGAACTCTTTATTGACGACTATATCGTTAAACGAATCAACGGCAAGATGTGC	420
	*****	
c3orf70b_cDNA	TACGTGCAGCGGCCCCAGGCTCATGTGGAGCCTGTCAAATGAACCCAATTCAGAAACAG	480
c3orf70b_NM_001089454	TACGTGCAGCGGCCCCAGGCTCATGTGGAGCCTGTCAAATGAACCCAATTCAGAAACAG	480
	*****	
c3orf70b_cDNA	CACACCGAAGACAAACAGATTGTTGAGGAGACTGTCAAAGGACCAAAAATGGGCCACTGC	540
c3orf70b_NM_001089454	CACACCGAAGACAAACAGATTGTTGAGGAGACTGTCAAAGGACCAAAAATGGGCCACTGC	540
	*****	
c3orf70b_cDNA	TC'TTCGCCCTCTACCTCCGAGGACTCAGGGATCAACGCTTTGGGAGGACACTTCCTGGAG	600
c3orf70b_NM_001089454	TC'TTCGCCCTCTACCTCCGAGGACTCAGGGATCAACGCTTTGGGAGGACACTTCCTGGAG	600
	*****	
c3orf70b_cDNA	TCCTGCGAGGAAGAGTCTGAGGAAGAGGATGAGCTCAGCACGGATGGACACTCCAGTCCG	660
c3orf70b_NM_001089454	TCCTGCGAGGAAGAGTCTGAGGAAGAGGATGAGCTCAGCACGGATGGACACTCCAGTCCA	660
	*****	
c3orf70b_cDNA	GGGAGTCTATGGGACCAGGACGAATGCACCCTGCTTTCCCCTTCCAAATCCATGGTGGAG	720
c3orf70b_NM_001089454	GGGAGTCTATGGGACCAGGACGAATGCACCCTGCTTTCCCCTTCCAAATCCATGGTGGAG	720
	*****	
c3orf70b_cDNA	ATTATTGAAAACATCGAAACGACCGTGTGA	750
c3orf70b_NM_001089454	ATTATTGAAAACATCGAAACGACCGTGTGA	750
	*****	



**Supplemental Figure 3.** Comparison of the nucleotide sequences of c3orf70b open reading frame determined in this study and NM\_001089454 in the NCBI Reference Sequence Database. Red arrowhead indicates the single nucleotide difference between the cDNA and reference sequences.

c3orf70a_cDNA	MAASGGQKSEKLDEAQUALARSCAGRPDFLPCDGLSICATHSHGKCFKLHWCCHLGWCHCK	60
c3orf70a_NM001126467	MAASGGQKSEKLDEAQUALARSCAGRPDFLPCDGLSICATHSHGKCFKLHWCCHLGWCHCK	60
	*****	
c3orf70a_cDNA	YVYQPMTSVCQLPSTAVPVAPSGHTHTMNLISLAERFLRTAPKFQAPPCPESPKFCVIS	120
c3orf70a_NM001126467	YVYQPMTSVCQLPSTAVPVAPSGHTHTMNLISLAERFLRTAPKFQAPPCPESPKFCVIS	120
	*****	
c3orf70a_cDNA	DLFVDDYMKRINGKMCYVQRPPPTPNPTHQPQTAAQPVPQRSKNSHQVGPTVKQGQA	180
c3orf70a_NM001126467	DLFVDDYMKRINGKMCYVQRPPPTPNPTHQPQTAAQPVPQRSKNSHQVGPTVKQGQA	180
	*****	
c3orf70a_cDNA	KEKISAPKMDHCSSPSSSEDSGINALGLHYMESCEDEDSCVDDDDDEEEEDDELSTDGNSSP	240
c3orf70a_NM001126467	KEKISAPKMDHCSSPSSSEDSGINALGLHYMESCEDEDSCVDDDDDEEEEDDELSTDGNSSP	240
	*****	
c3orf70a_cDNA	GSFWDQDECTLLSPSKSIVEIIEKIETTV	269
c3orf70a_NM001126467	GSFWDQDECTLLSPSKSIVEIIEKIETTV	269
	*****	
c3orf70b_cDNA	MAYSGAQKALKSDKLDEAQUALAKSCAGRPDFLPCDGLSICATHSHGKCFKLHWCCHLGWC	60
c3orf70b_NM_001089454	MAYSGAQKALKSDKLDEAQUALAKSCAGRPDFLPCDGLSICATHSHGKCFKLHWCCHLGWC	60
	*****	
c3orf70b_cDNA	HCKYVYQPMTNVAQLPSTPVPAAPSDCPD'TIDLSISLTERFLRISPCFQPPPCPESPKYC	120
c3orf70b_NM_001089454	HCKYVYQPMTNVAQLPSTPVPAAPSDCPD'TIDLSISLTERFLRISPCFQPPPCPESPKYC	120
	*****	
c3orf70b_cDNA	NIAELFIDDIYVCRINGKMCYVQRQAHVEPAQMNP'IQKHTEDEKQIVEETVKGPKMGHC	180
c3orf70b_NM_001089454	NIAELFIDDIYVCRINGKMCYVQRQAHVEPAQMNP'IQKHTEDEKQIVEETVKGPKMGHC	180
	*****	
c3orf70b_cDNA	SSPSTSEDSGINALGGHFLESCEEESEEEDELSTDGHSSPSGLWDQDECTLLSPSKSMVE	240
c3orf70b_NM_001089454	SSPSTSEDSGINALGGHFLESCEEESEEEDELSTDGHSSPSGLWDQDECTLLSPSKSMVE	240
	*****	
c3orf70b_cDNA	IIENIETTV	249
c3orf70b_NM_001089454	IIENIETTV	249
	*****	

**Supplemental Figure 4.** Comparison of the inferred amino acid sequences of c3orf70a and c3orf70b open reading frames obtained in this study and NCBI reference sequences NM\_001126467 and NM\_001089454.