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Supplementary Material

A $\text{Ca}_v1.1$ Ca^{2+} Channel Splice Variant with High Conductance and Voltage-Sensitivity Alters EC-Coupling in Developing Skeletal Muscle

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Supplementary results:

Table 1: Putatively non-functional splicing variants in the *CACNA1S* gene

<i>variant</i>	<i>protein length</i>	<i>nonsense residues</i>	<i>location in channel</i>	<i>% transcripts in adult muscle</i>
<i>deletion of exons 3-5</i>	187	101	IS1-S2	3,0
<i>deletion of exons 3-7</i>	111	25	IS1-S2	1,7
<i>deletion of exons 4-5</i>	140	8	IS3	1,0
<i>insertion of intron 4</i>	208	28	IS4-S5	2,4
<i>insertion of intron 8</i>	461	78	I-II	3,0
<i>insertion of intron 25</i>	1115	30	III-IV	3,6
<i>insertion of intron 26</i>	1147	9	IVS1	2,1
<i>insertion of intron 28</i>	1244	41	IVS3-S4	1,3
<i>deletion of exon 19</i>	1853	missing 20 in frame	IIIS1-S2, IIIS2	1,4

Table 2: Putatively functional splicing variants in the *CACNA1S* gene

<i>variant</i>	<i>protein length</i>	<i>nonsense residues</i>	<i>location in channel</i>	<i>% transcripts in adult muscle</i>
<i>deletion of exons 39-40</i>	1559	3	C-terminus	1,6
<i>alternate 5' site of exon 40</i>	1847	missing 26 in frame	C-terminus	1,5
<i>insertion of intron 43</i>	1851	61	C-terminus	3,0

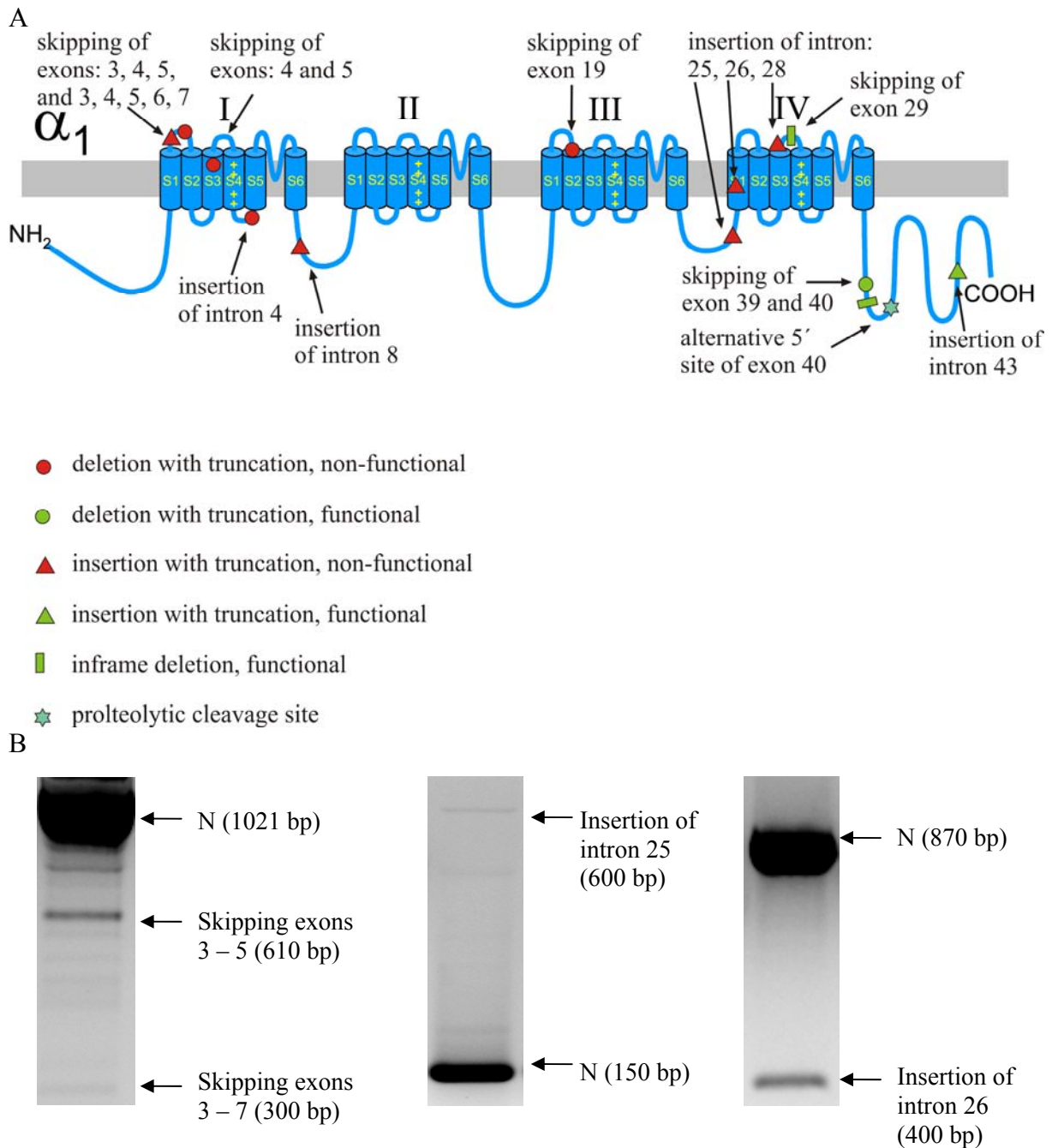


Figure 1. 13 splicing variants found in the *CACNAIS* gene. A. Schematic representation of pore forming α_1 subunit of $\text{Ca}_v1.1$. Arrows point to segments encoded by alternative splice variants. **B.** Examples of scanning of *CACNAIS* gene uncovered splice variations revealed by different reverse transcriptase PCR product size. Standard band marked with N.

Table 3: RT-PCR and cloning primers

<i>Exons/name</i>	<i>Forward Primer</i>	<i>Reverse Primer</i>	<i>T_m</i> °C	<i>Product</i> <i>length bp</i>
1-9	ttcctgagattctgccaagg	ctgtgtcagagccacctca	51	1129
2-8	atcatcttgctcaccatctttgc	ccccgaaggtcctcatcta	51	929
7-10	tattttgtcacctcattttgctg	tgcggctggttgtgggtct	54	437
8-10	accaaggagcgggagaag	aggcgatagacagggtgtg	52	340
9-15	atgaaggtggctctgacaca	ggtttctgtccagcttctg	51	961
10-14	ccgacattggaggcagtggga	atcttctgcggtttttctcctc	51	825
13-18	acttcatcatcctttctgctgt	catggaatcagcccggatg	52	563
14-18	cccagaaggccaaggctgag	cgatgcgggtgacacaggacacg	55	369
17-26	acgaggaagatgagcctgag	tgggttttgggaatgtagc	51	1084
18-25	atgccacctggtttaccaac	tcatgaagaaggcaatgagg	52	780
24-27	tctcagccatgatgtcctctt	gtggttcatctgctccgactg	54	443
25-26	catctttgtgggcttctgctcatt	tggtatgggttttgggaatgt	54	150
26-35	cacctctcctactttgaatacct	agaacttcccaaagcccaga	52	971
27-34	agtccggagcagatgaaccac	atggccttgaactcatccag	51	790
34-40	actacctcaccgggactg	cgttggcattgttgattg	51	843
37-42	aaccagcatgaagctcttgg	agcagtccttcagcatctc	52	678
39-44	cggaccattgaggaagagg	cattggtcatgccagctcta	51	990
34-44	actacctcaccgggactg	cattggtcatgccagctcta	51	1514
<i>P1/P4</i>	gcacaagggctccttctgccgcaac	atgcgggcgctctcgtctgggtcgtcgatctcg ctgaggatgacgtcaatgat	60	1059
<i>P3/P2</i>	atcattgacgtcatcctcagcgagatcg acgaccagacgagagcggccgcat	ggaagtgctcctgaatgaggaatgtggc	60	1021
<i>Taqman RT-PCR probes</i>				
28/29	ctaategtcatcggcagcat	cagtctcatgaccgggaaca (for template only)		168
	ctaategtcatcggcagcat	ctccaccaggcaatacagt		91
	Taqman MGB Probe:	attgacgtcatcctgagc		
28/30	ctaategtcatcggcagcat	tctcatctgggtcatcgatct		61
	Taqman MGB Probe:	attgacgtcatcctgagc		

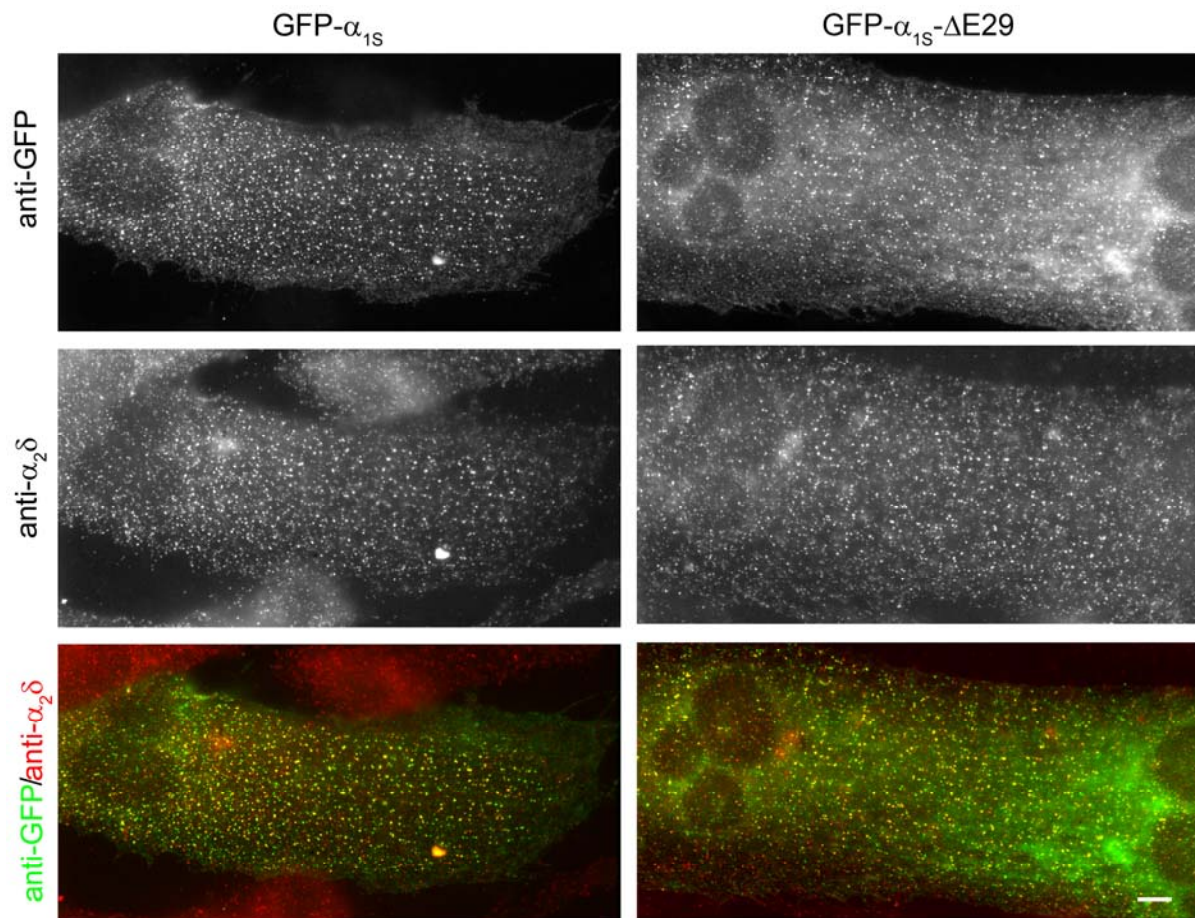


Figure 2. Deletion of exon 29 does not disturb the colocalization of α_{1S} and $\alpha_2\delta$ -1 subunit. Dysgenic myotubes transfected with GFP- α_{1S} (**left**) or GFP- $\alpha_{1S}\Delta 29$ splice variant (**right**) were double immunolabeled with anti-GFP (**top**) and anti- $\alpha_2\delta$ -1 (**middle**). Clusters of GFP- α_{1S} or GFP- $\alpha_{1S}\Delta 29$ colocalize with clusters of $\alpha_2\delta$ -1 subunit (**color overlay**). Bar, 10 μm .