

Supplemental Figure for online distribution.

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T V * CfE19 V S P Q A P T Q T T R P P R L

Jiao et al., 2008. Developmentally-regulated alternative splicing of densin modulates protein-protein interaction and subcellular localization. (JNC-W-2008-0001)

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I P S S Q A T R G P Q P G R C L I Q T K	1440

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T V *	1542
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ctagcacaaggtatatgttggcatg	5250

Notes:

- 1) The nucleotide sequence of the predicted longest mRNA variant of densin is shown along with the resulting amino acid sequence below. Nucleotides and amino acids are numbered at the right in normal and bold font, respectively, based on the longest theoretical sequence.
- 2) The beginning of each exon is indicated with a solid arrow and cryptic starts are indicated as dashed arrows. Each star site is labeled with the corresponding exon number (E#). The splice donor exon for the alternative splicing events is indicated by "Cf" (continues from).
- 3) Nucleotide sequences of exons that are known to be alternatively spliced are indicated in blue. The corresponding amino acid sequences are in red if skipping of the exon would shift the reading frame and in green if the reading frame remains the same.
- 4) The conventional start and stop codons for the longest variant are highlighted in solid green and red boxes, respectively. An alternative start codons due to frame shift splicing is indicated by an open green box. Novel stop codons created by frame shift splicing are indicated by open colored boxes to match a second line of colored amino acid sequence showing the novel downstream residues underneath the "normal" residues. [For the skipping of Exon21-24 (CfE20), the first novel amino acid is Ser which is encoded by the last two bases in E20 and the first base in E25: for simplicity, this Ser is shown under E25, along with the rest of the novel C-terminal domain.)