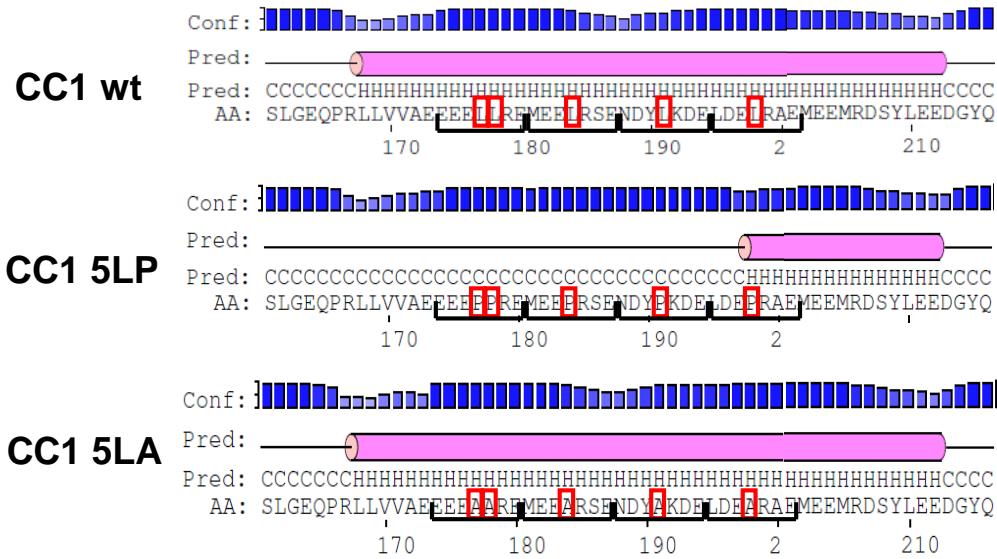


A

1 METLNGPAGG GAPDTKPQPA GQHHRHHHLH PLAERRRLHR APPSPARPFLK  
 50 DLHTRPATAT PSAGRAPHPTA APRSPSLAGK APPSPGPAA PGRLSRRSGV  
 100 VPGAKDKPPP GAGARSAGGA KAVPGTRRAA RAGPAEPLSR VGRPTGAEPP  
 150 PAVAKGRKTK RGPGTTPPARA VVPPARASRV PAVTLSVTSV AGCRINHTDS  
 200 SSDLSDCASE PLSDEQRLLP AASSDAESGT GSSDREPIRG APTPSSGSRG  
 250 PPPGSPEPPI LLAAPP VASA CLGGRSSPGG ASTGSPGPGS QEDVGGRAPP  
 300 ERTILGTSKE PSLGEQPRLLL VVA[EEEELLR EMEELRSEND YLKDELDEL R]  
 350 [AEMEEMRDSY LE[E]DGYQLQE LRRELDRAK NCRI[LQYRLR KAEQKSLKVA]  
 400 ETGQVDGELI RSLEQD[LKVA KDVSVRLHHE LETVEEKRAK AEDDNETLRQ]

The diagram shows the MTCL1 sequence from 1 to 450. Red boxes highlight N-MTBD regions, and a green box highlights a proline-rich region. Black boxes group sequences into CC1 and CC2. CC1 starts at position 170 and ends at 210. CC2 starts at 211 and ends at 450. Proline residues are shown in red. Asterisks above the sequence indicate specific residues: \* at 171, \*\* at 181, \* at 191, \* at 201, \* at 211, \* at 221, \* at 231, and \* at 241. An arrow points to the start of CC1 at position 170, and another arrow points to the start of CC2 at position 211.

B



**S2 Fig. The amino acid sequence of the MTCL1 N-terminal region and the predicted secondary structure of the first half of CC1.**

(A) The amino acid sequence of mouse MTCL1 from 1 to 450 is shown. Red and green boxes indicate N-MTBD and the proline-rich region, respectively. Proline residues are red. The sequences corresponding to CC1 and CC2 are boxed by black, in which

residues in the “*d*” position of the heptad repeat (***a-b-c-d-e-f-g***)<sub>n</sub> are blue. The amino acids in the first half of CC1 are bold, and the mutated residues are indicated by asterisks. Note that the heptad pattern of the first and latter half of CC1 is interrupted by a single residue, glutamate (red arrow). (B) Secondary structures of the first half of CC1 wt and its mutants were predicted by the PSIPRED program (<http://bioinf.cs.ucl.ac.uk/psipred/>). Positions of mutated leucine residues are indicated by red rectangles. Seven residue repeats, (***a-b-c-d-e-f-g***), are indicated by black brackets under the sequences.<sup>4</sup>