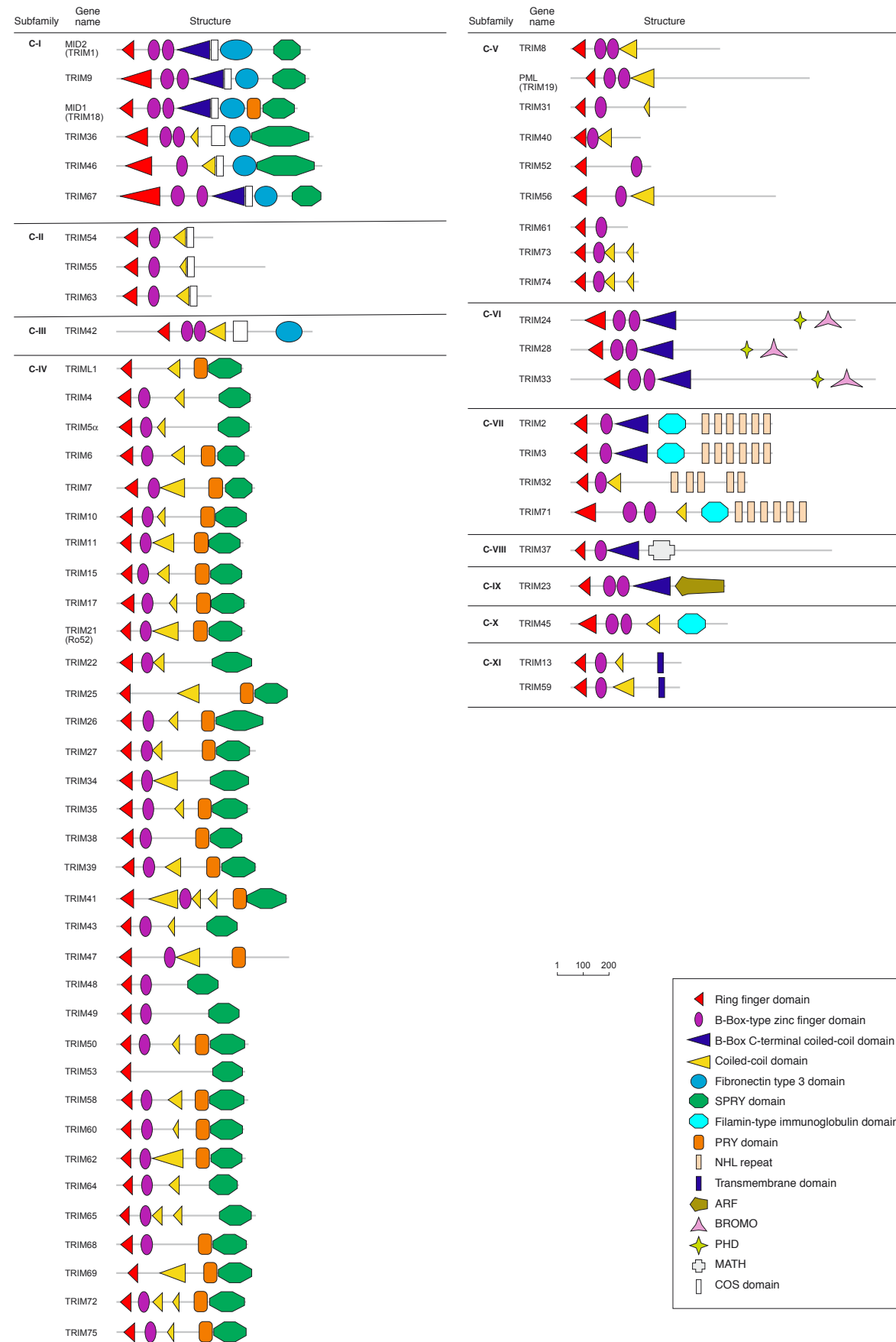


S1 Figure



Structural features and domain-based classification of TRIM superfamily members.

Allocation of tripartite motif-containing (TRIM) superfamily members to subfamilies is based on differences in the composition of domains in the C-terminal region relative to the RBCC elements. Subfamilies C-I through C-IX follow the classification scheme of Short and Cox¹. New C-terminal subfamilies, C-X and C-XI, are proposed to accommodate new sequence information. Domains depicted in the key and shown for each TRIM member are primarily those that have been identified and ordered using the Normal [SMART](#) mode and/or [UniProt](#). Exceptions are the location and topology of the transmembrane helices, which were predicted by the [TMHMM2](#) programme, the coiled-coil regions that were not defined as B-Box C-terminal coiled-coil domains by SMART were determined by the [Coils2](#) programme (independent keys are given for coiled-coil domains that have been predicted by SMART and Coils2), and COS domains, which were defined by Short and Cox¹. Alternatively spliced isoforms are not shown. For some family members, commonly used names or prior TRIM designations are given in parentheses under the formal gene name.

1. Short, K. M. & Cox, T. C. Subclassification of the RBCC/TRIM superfamily reveals a novel motif necessary for microtubule binding. *J. Biol. Chem.* **281**, 8970–8980 (2006).