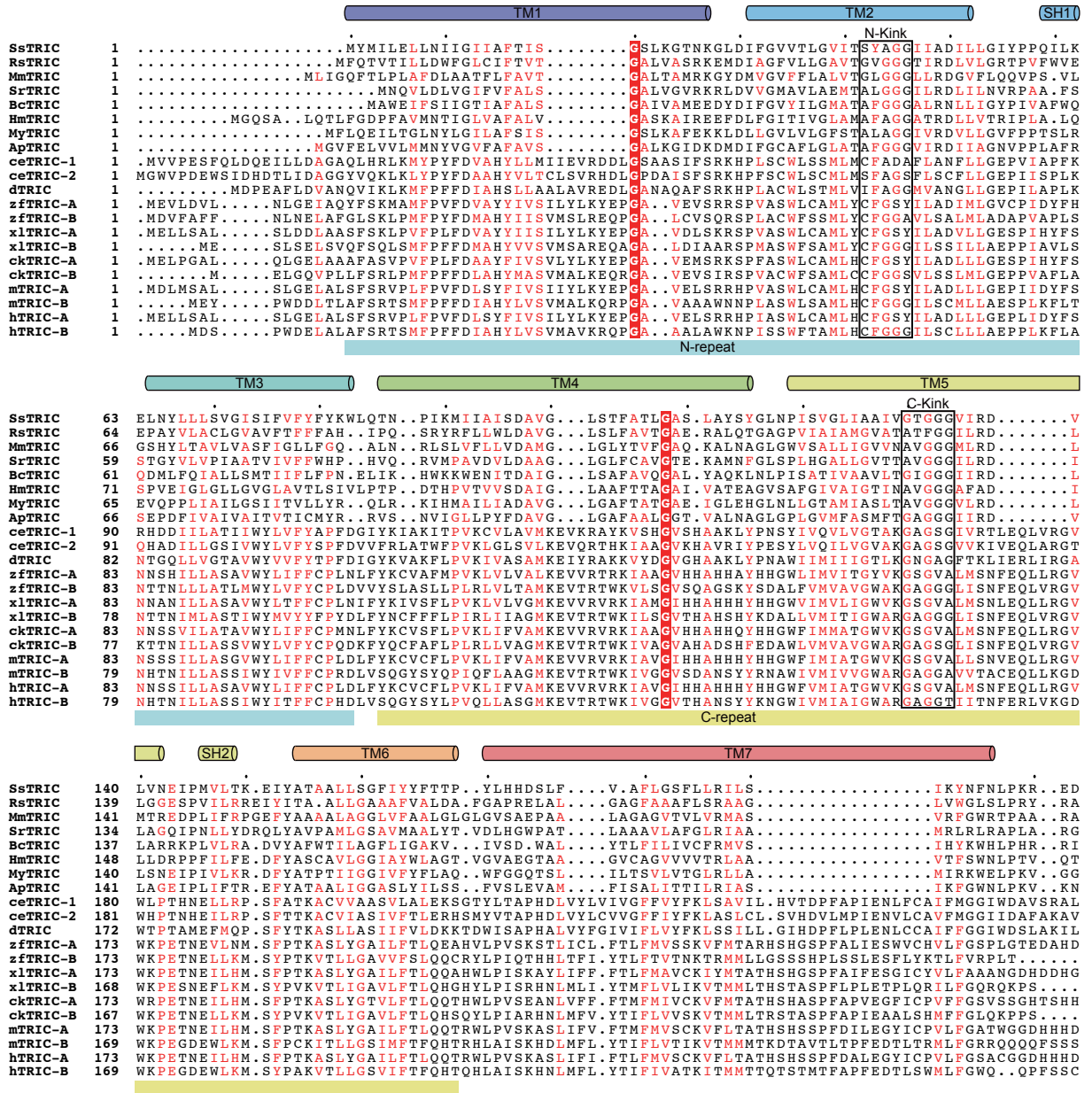
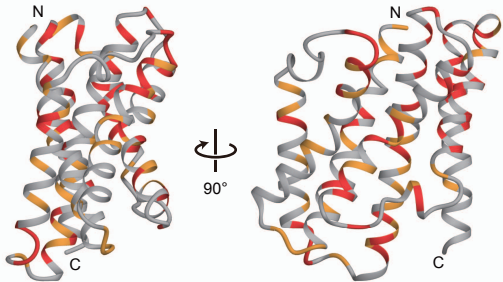


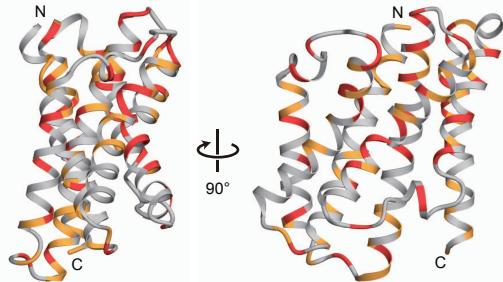
A



B



C



Supplementary information, Figure S3 Multiple amino acid sequence alignment of TRIC channels.

(A) Sequence alignment of SsTRIC (GI: 497675455), RsTRIC (488812244), *Magnetospirillum magnetotacticum* TRIC (MmTRIC, 497554682), *Streptosporangium roseum* TRIC (SrTRIC, 502656235), *Bacillus cereus* TRIC (BcTRIC, 487997996), *Halomicrobium mukohataei* TRIC (HmTRIC, 506243491), *Metallosphaera yellowstonensis* TRIC (MyTRIC, 496364148), *Archaeoglobus profundus* TRIC (ApTRIC, 502705752), *Caenorhabditis elegans* TRIC-1 (ceTRIC-1, 392892025), *C. elegans* TRIC-2 (ceTRIC-2, 34556095), *Drosophila melanogaster* TRIC-1 (dTRIC, 18859841), *Danio rerio* TRIC-A (zfTRIC-A, 41053814), *D. rerio* TRIC-B (zfTRIC-B, 41055766), *Xenopus laevis* TRIC-A (xlTRIC-A, 148237167), *X. laevis* TRIC-B (xlTRIC-B, 189083794), *Gallus gallus* TRIC-A (ckTRIC-A, 119331148), *G. gallus* TRIC-B (ckTRIC-B, 50761922), *Mus musculus* TRIC-A (mTRIC-A, 21362331), *M. musculus* TRIC-B (mTRIC-B, 21312532), *Homo sapiens* TRIC-A (hTRIC-A, 13129060) and *H. sapiens* TRIC-B (hTRIC-B, 8922461). SsTRIC shares sequence identities of 23% and 21% with hTRIC-A and hTRIC-B, respectively. RsTRIC shares sequence identities of 24% and 23% with hTRIC-A and hTRIC-B, respectively. The secondary structure of SsTRIC is indicated above the sequences. The conserved kinks in TM2 and TM5 are enclosed in black boxes. The red residues indicate similarly conserved residues. **(B, C)** Conserved residues between SsTRIC and hTRIC-A **(B)**, and between SsTRIC and hTRIC-B **(C)** mapped on the SsTRIC structure. The red and orange residues indicate strictly and similarly conserved residues, respectively. The sequence alignment and the identity percentages were calculated with ClustalW.