Supplementary Information S1 (Figure) | Sequence alignment of stromal interaction molecule1 (STIM1) and STIM2. Identity (red), similarity (blue) or differences (black and grey) between STIM1 and STIM2 are shown. Major structural features are also described and as shown in Fig. 1a. Note: the existence of an extended signal peptide in STIM2 is based on recent findings1 that disproved earlier suggestions of an alternative translational start site (TTG; L86) for STIM2 (REF. 2). Based on this new evidence, STIM2 has been renumbered to start at its originally predicted Kozak sequence (Accession #AAI71766.1). The three α-helices of the first coiled-coil domain (CC1) are predicted based on sequence analysis using JPred3 (REF. 3). The third of these helices (inhibitory helix) is supported by homology with the recently solved C. elegans structure4. cEF, canonical EF-hand; hEF, hidden EF-hand; ID, inhibitory domain; SOAR, STIM—Orai activating region.