Figure S1. An interaction network of some of the identified ITAM partners highlights relevant connections. (A) Venn diagram representing the overlap between the 3 ITAM interactomes (ζa, ζaP and ζcP) identified in resting and stimulated Jurkat cells (15 min with anti-CD3 antibody). The proteins highlighted in bold were identified in both conditions (see Table S1). The number of proteins binding to each ITAM and condition is indicated inside the circles. (B) Network diagram of the physical interactions (binding, purple lines) and direct/indirect relationships (regulation, gray dashed lines) among a set of identified ITAM partners (blue) and other interacting proteins (red). A significant number of over-represented pathways and cellular process are interconnected in this illustration, including signal transduction pathways (e.g., Ras, Rho, G-protein), actin cytoskeleton assembly, endocytosis, T cell development, activation and differentiation, and the regulation of apoptosis. Moreover, all these processes are implicated in important diseases (violet). This network was generated using Pathway Studio software (http://www.ariadnegenomics.com).