*Proteomics analysis.* Trypsin digestion and analysis of peptides by LC MS/MS was performed by the Core Facility Proteomics, Center for Biological Systems Analysis, University of Freiburg, Germany. Samples were supplemented with Laemmli buffer 6 × containing 1 mm DTT and boiled for 5 min at 95 °C. Subsequently, they were alkylated using 5.5 mm iodoacetamide for 30 min at 25 °C. Protein mixtures were separated by SDS/PAGE (4-12% Bis-Tris mini gradient gel), and gel lanes were cut into 10 equal slices. Gel fractions were in-gel digested using trypsin (Promega, Mannheim, Germany) [23]. Digests were performed overnight at 37 °C in 0.05 m NH4HCO3 (pH 7.5). About 0.1 μg of protease was used for each gel band. Peptides were extracted from the gel slices with ethanol, and resulting peptide mixtures were processed on STAGE tips as described [24]. Samples analyzed by MS were measured on LTQ Orbitrap XL mass spectrometer (Thermo Fisher Scientific, Bremen, Germany) coupled either to an Agilent 1200 nanoflow-HPLC (Agilent Technologies GmbH, Waldbronn, Germany). HPLC-column tips (fused silica) with 75-μm inner diameter were self-packed with Reprosil-Pur 120 ODS-3 to a length of 20 cm. No precolumn was used. Peptides were injected at a flow of 500 nL·min−1 in 92% buffer A (0.5% acetic acid in HPLC gradient grade water) and 2% buffer B (0.5% acetic acid in 80% acetonitrile, 20% water). Separation was achieved by a linear gradient from 10% to 30% of buffer B at a flow rate of 250 nL·min−1. The mass spectrometer was operated in the data-dependent mode and switched automatically between MS (max. of 1 × 10 ions) and MS/MS. Each MS scan was followed by a maximum of five MS/MS scans in the linear ion trap using normalized collision energy of 35% and a target value of 5000. Parent ions with a charge states of z = 1 and unassigned charge states were excluded from fragmentation. The mass range for MS was m/z = 370 to 2000. The resolution was set to 60 000. MS parameters were as follows: spray voltage 2.3 kV; no sheath and auxiliary gas flow; ion transfer tube temperature 125 °C.

Software Xcalibur (Thermo Scientific, Schwerte, Germany) and MaxQuant 1.4.1.2 were used for data acquisition and processing.