

Description of Supplementary Files

File Name: Supplementary Dataset 1. Amplicon sequence variants (ASVs) identified from corisin/corisin-like peptide amplicon sequencing in BALF samples.

Description: The file summarizes the amplicon sequence variants (ASVs) detected by sequencing of the corisin/corisin-like peptide region in bronchoalveolar lavage fluid (BALF) samples. Each row represents a unique ASV, identified by its ASV ID, along with the closest species match from sequence similarity analysis. The numbers shown for each sample correspond to the total sequencing reads assigned to the respective ASV. The final column ("ASV Sum") indicates the cumulative number of reads for each ASV across all analyzed samples. Samples with insufficient amplicon yield were pooled prior to sequencing as follows: HC2 and HC4 (HC2_HC4), patients 1, 4, and 7 (Japan_1_4_7), and patients 15 and 16 (P15_P16). Species assignments are provided for reference only and should be interpreted with caution because the approximately 150-bp corisin-targeted amplicon does not constitute a phylogenetic marker and may not allow unambiguous taxonomic identification. The dataset includes only samples that generated sufficient amplicon signal for reliable sequencing and downstream sequence analysis. Organisms with extremely low counts were not shown.

File Name: Supplementary Dataset 2. Identification of human proteins interacting with corisin by high-throughput protein array screening.

Description: This dataset summarizes the results of a large-scale protein–protein interaction screen performed using the Ehime Kazusa Human Protein Array containing 9,263 recombinant human proteins. Interactions between biotinylated wild-type corisin and arrayed human proteins were assessed using the AlphaScreen luminescence assay. An inactive biotinylated corisin mutant (N14S), which lacks proapoptotic activity, was used as a negative control to identify interaction partners preferentially recognized

29 by biologically active corisin. For each recombinant protein, AlphaScreen
30 luminescence signals generated by binding of wild-type corisin and N14S corisin are
31 shown. The ratio of signal intensity obtained with wild-type corisin relative to N14S
32 corisin (Posi/Nega) was calculated and used to rank candidate interaction partners.
33 Higher Posi/Nega ratios indicate preferential binding to biologically active corisin and
34 therefore a greater likelihood of representing specific corisin-interacting proteins. The
35 table includes protein array positions, AlphaScreen signal intensities, rankings based
36 on the Posi/Nega ratio, clone information, UniProt and RefSeq identifiers, protein
37 annotations, and functional classifications from the Kazusa Human Protein Array
38 database. Candidate proteins are listed in descending order of the Posi/Nega ratio.
39 This screening was intended to identify potential host intracellular proteins capable of
40 interacting with corisin and to provide mechanistic insight into pathways involved in
41 corisin-induced cellular injury