2 Supplemental Table S1. S-nitrosylated proteins/peptides from non-GSNO-treated heart 3 homogenates as identified via SNO-RAC proteomic analysis with a false discovery rate of 4 1%. LC-MS/MS derived peptide sequences and MASCOT MS/MS search identifications. 5 Peptide identifications with ion scores below 25 were not accepted; non-cysteine containing 6 peptides were filtered from the data set. To view peptide sequences, click on the '+' symbol 7 found on the left side of the spreadsheet. Each of 4 biological replicates was run in triplicate in 8 order to increase protein/peptide identifications; replicates are identified in column headings as 9 A2 (Heart 1), B2 (Heart 2), C2 (Heart 3), and D2 (Heart 4). 11 Supplemental Table S2. S-nitrosylated proteins/peptides from GSNO-treated heart

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homogenates as identified via SNO-RAC proteomic analysis with a false discovery rate of 1%. LC-MS/MS derived peptide sequences and MASCOT MS/MS search identifications. Peptide identifications with ion scores below 25 were not accepted; non-cysteine containing peptides were filtered from the data set. To view peptide sequences, click on the '+' symbol found on the left side of the spreadsheet. Each of 4 biological replicates was run in triplicate in order to increase protein/peptide identifications; replicates are identified in column headings as A2 (Heart 1), B2 (Heart 2), C2 (Heart 3), and D2 (Heart 4).