Supplemental Figure 1

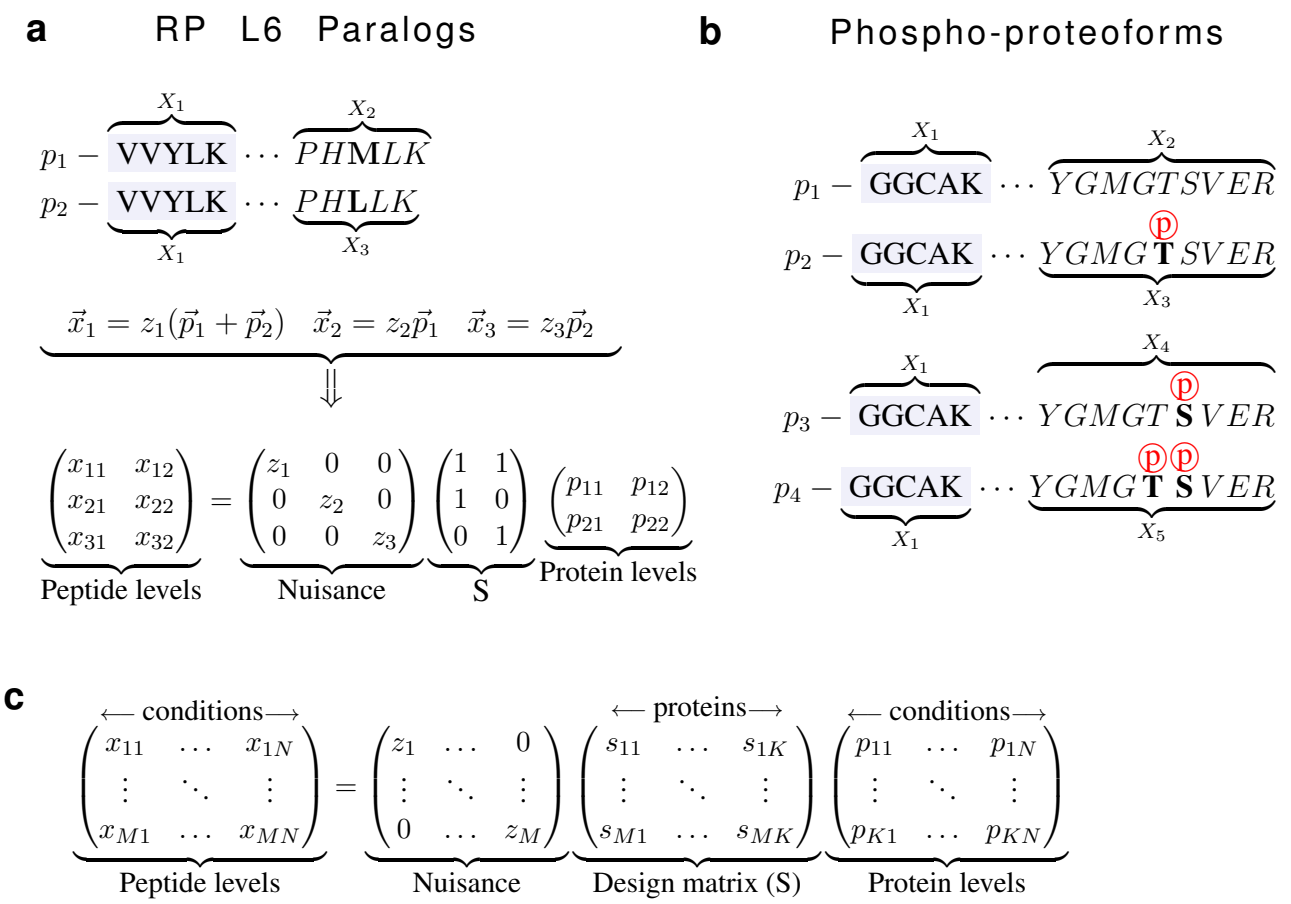

Figure S1 | Model for inferring stoichiometries among proteoforms and paralogous proteins independently from peptide-specific biases. (**a**) One shared (X_1) and two unique (X_2 and X_3) peptides from the two paralogs of ribosomal proteins L6 illustrate the simplest case of HI*quant*. HI*quant* models the peptide levels measured across two conditions ($\vec{x}$) as a supposition of the protein levels ($\vec{p}$), scaled by unknown peptide–specific nuisances (z). These coupled equations can be written in a matrix form whose solution infers the P_1/P_2 stoichiometry independently from the nuisances (z). (**b**) The shared and unique peptides of proteoforms (as illustrated by PDHA1 phospho-proteoforms) can be modeled as in panel (a); (**c**) The matrix system from (a) generalizes to K proteoforms (and homologous proteins) with M peptides quantified across N conditions. In many, albeit not all, cases an optimal and unique solution can be found, even in the absence of unique peptides. See Supplemental Information for details.