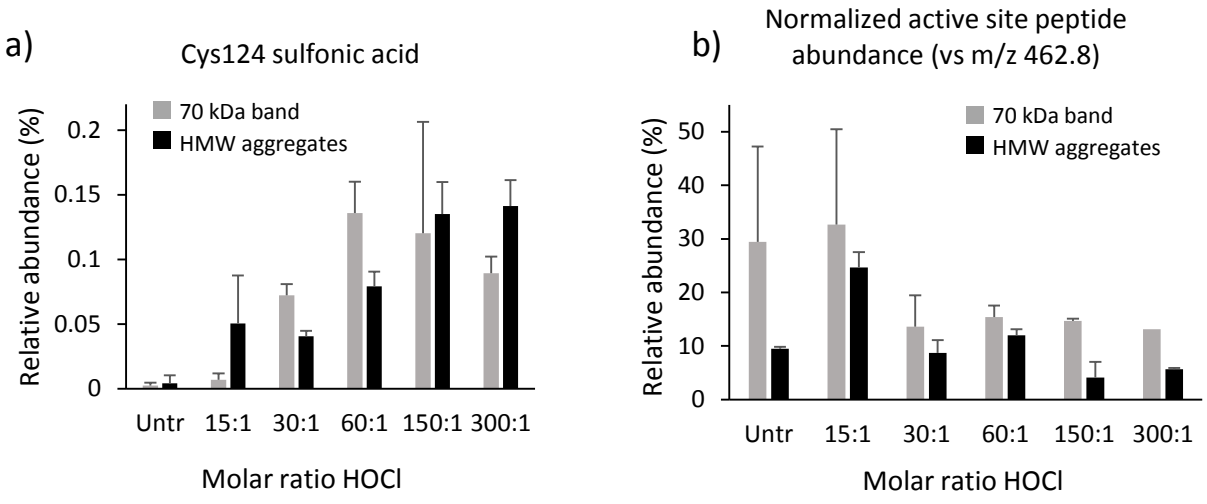
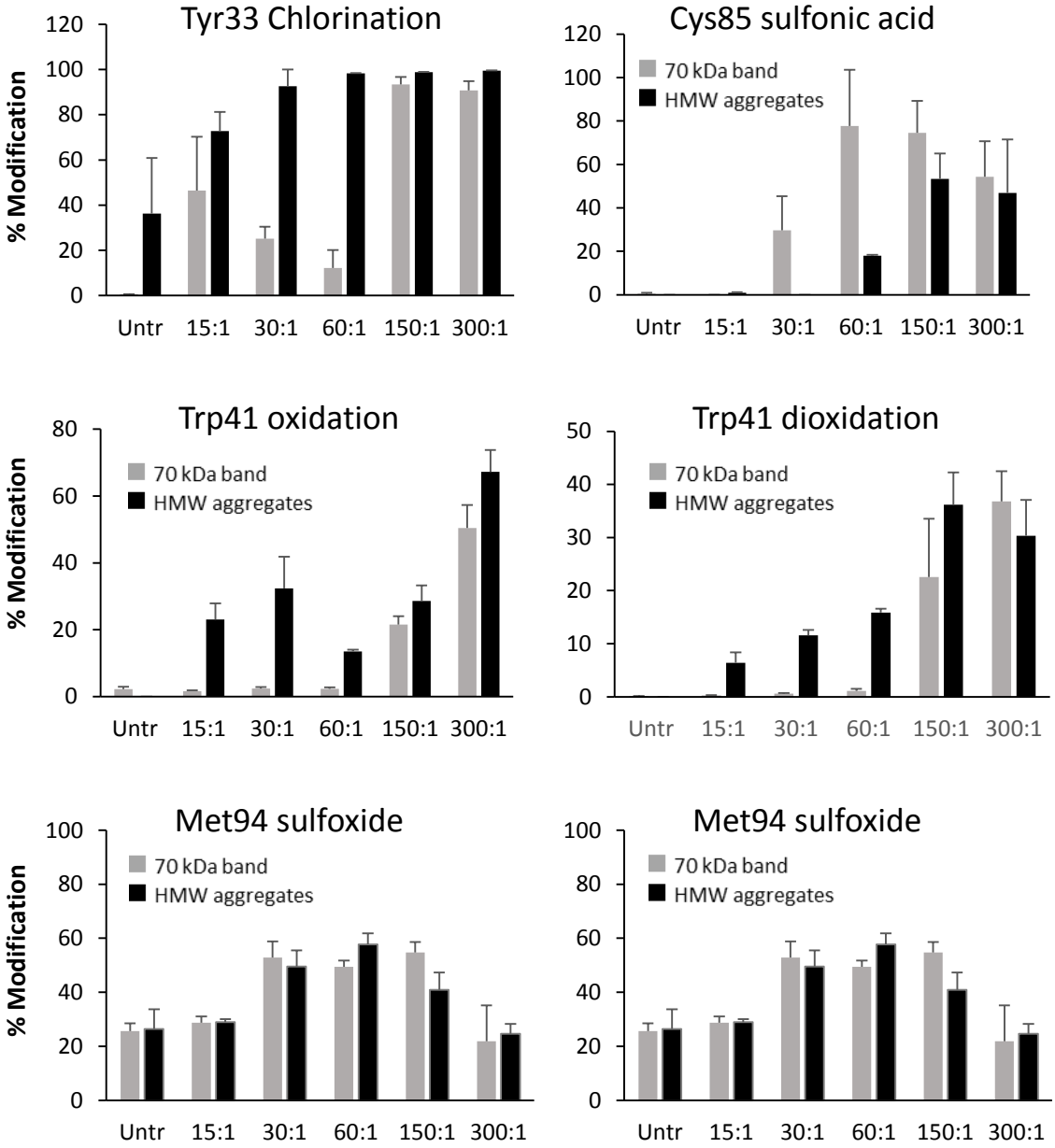



**Supplementary figure 1. Active site cysteine modification.** Quantification of a) the cysteine sulfonic acid forms of the observed active site (Cys124) containing peptide and b) the intensity of the unmodified active site containing peptide normalized to another PTEN peptide (m/z 462.8, residues 190-197, PVALLFHK). Light grey bars represent the monomeric protein band at 70 kDa and black bars the high molecular weight aggregates isolated from the top of the gel. The vertical axes are % modification, the horizontal axes are the molar ratio of HOCl to protein (Untr = no oxidant), and data are presented as mean ± SD (n = 3).




**Supplementary figure 2. Relative quantitation of selected GST oxPTMs upon HOCl treatment.** Quantification of 6 different modifications detected in either the monomeric protein band at 70 kDa (light grey bars) or the high molecular weight aggregates isolated from the top of the gel (black bars), or both. The vertical axes are the percentage (%) of peptide modified, the horizontal axes are the molar ratio of HOCl to protein (Untr = no oxidant), and data are presented as mean ± SD (n = 3).