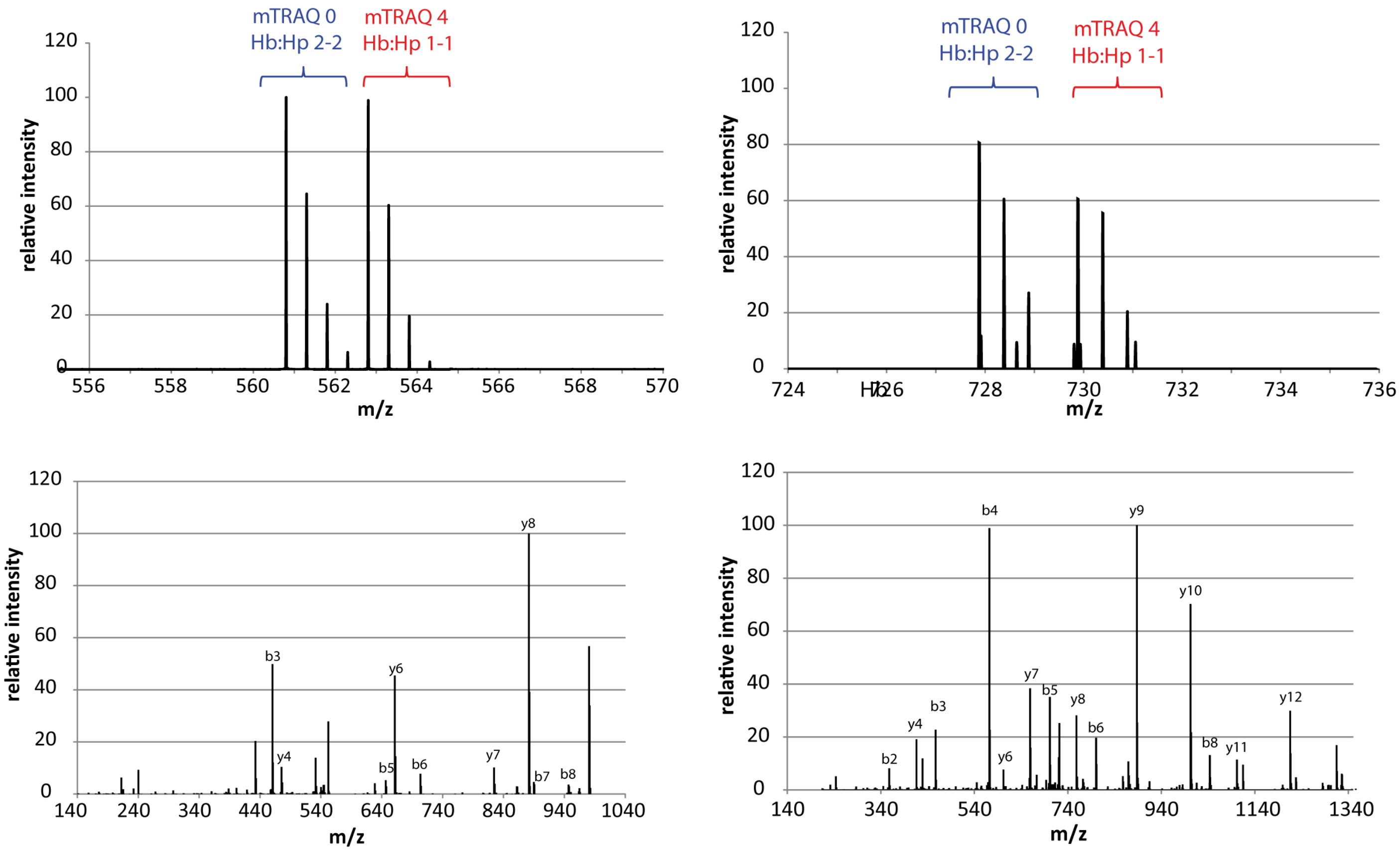
SUPPLEMENTARY FIGURE 2



(A) VGYVSGWGR (Hp 560)

(B) VNVDEVGGEALGR (Hb 727)

MS spectra of Hb:Hp peptides after mTRQA labeling.
The upper panels show MS1 spectra of peptide Hp560 and peptide Hb727. After adjustment for equal heme quantities in the two complexes by spectrophotometry and trypsin digestion, the peptides from the Hb:Hp 2-2 complex were labeled with mTRAQ label 0, the Hb:Hp 1-1 peptides were labeled with mTRAQ label 4. The resulting mass shift allowed assignment of mass intensities to the respective complex phenotype within the same MS1 spectrum. Complex specific ion chromatograms of each peptide were extracted from consecutive spectra across the LC-MSMS run as shown in Figure 1. The lower panels show representative MS2 fragmentation spectra of each peptide.