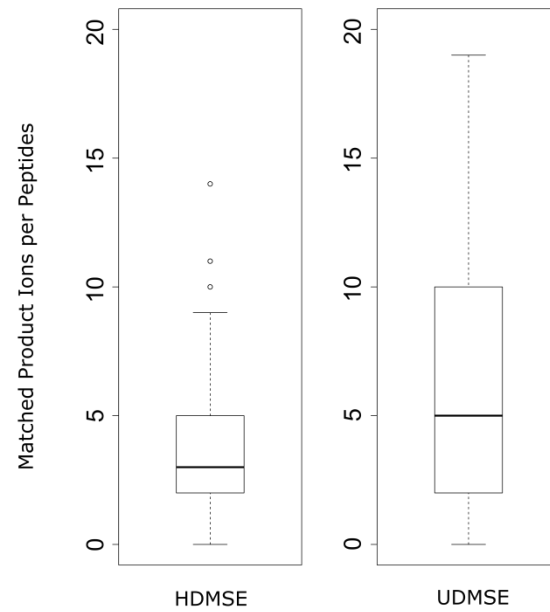
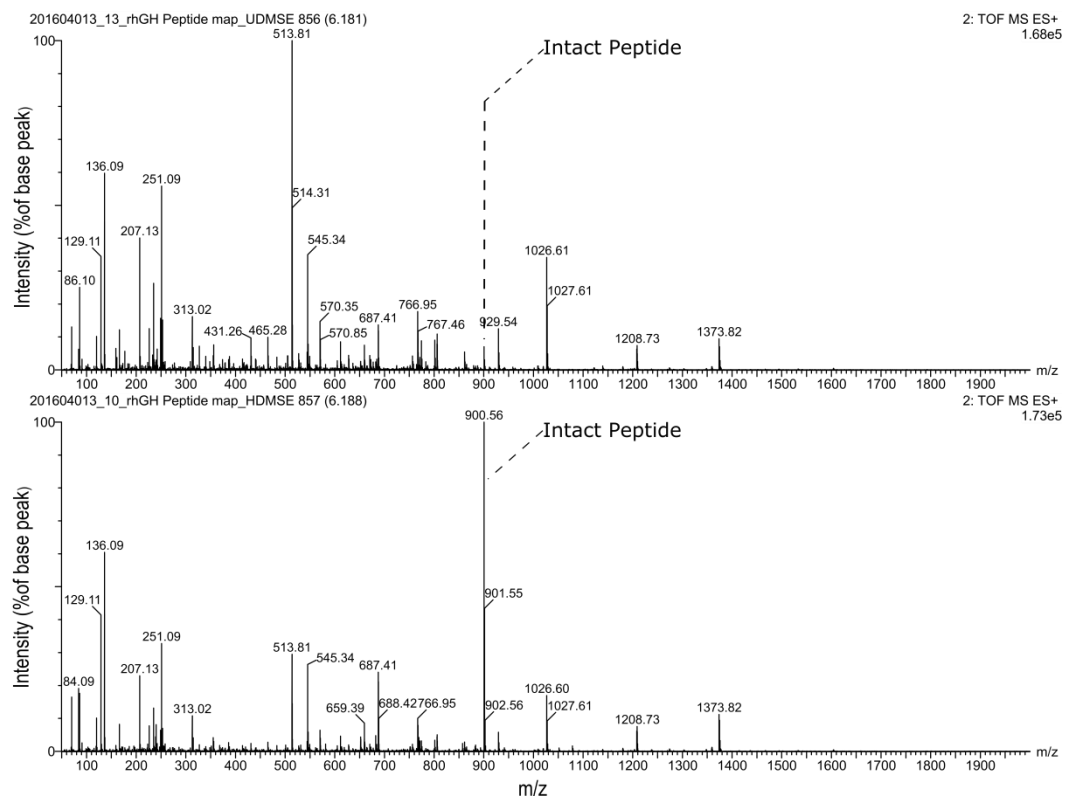


a)



b)



Supplementary Figure 1. UDMS^E peptide fragmentation efficiency is higher than HDMS^E. a) Boxplots of the number of matched product ions for rhGH proteolytic peptides, as identified by HDMS^E or UDMS^E analysis. b) Comparison of peptide high energy spectra acquired by HDMS^E and UDMS^E modes. Data has been combined over the same retention time window.