Figure S1. (A) Mass error distribution of all phosphopeptides. (B) Distribution of phosphopeptides based on length (number of amino acids).
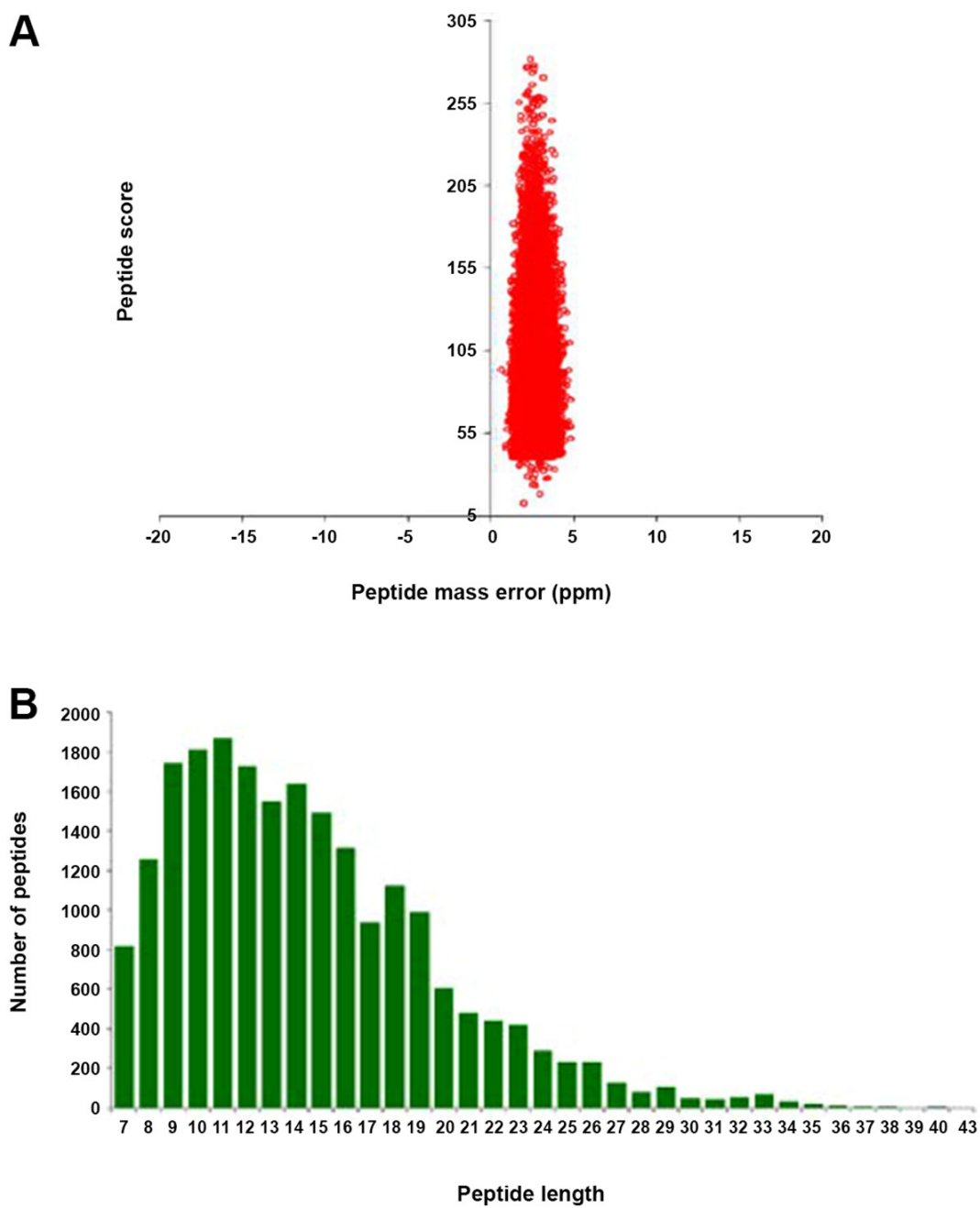
Figure S2. Heat maps of the amino acid composition around (A) serine phosphorylation sites and (B) threonine phosphorylation sites. Heat maps present the frequency of different types of amino acids around the residue.