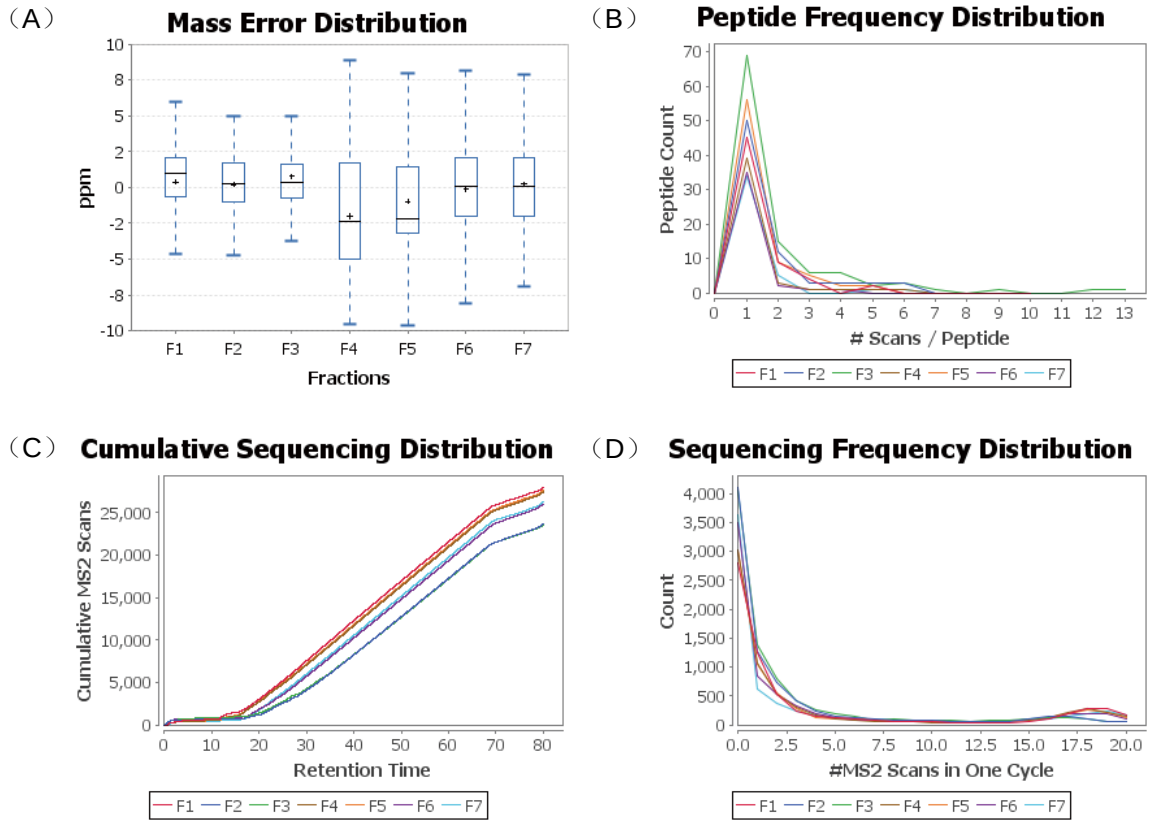

Figure S1. Statistics results of mass spectrometry data analysis. (F1: Eurasian elk, F2: Sika deer, F3: Red deer, F4: White-tailed deer, F5: Reindeer, F6: Fallow deer, F7: White-lipped deer)

（A）Precursor mass error for samples: This boxplot shows the precursor mass error for all the samples. (B) Peptide frequency distribution: This graph shows the peptide count in relation to the number of scans per peptide found for each fraction. (C) Cumulative sequencing distribution: This graph shows the acquired cumulative MS2 scans over retention time for each fraction. (D) Sequencing frequency distribution: This graph shows the sequencing count in relation to the number of MS2 scans in one cycle for each fraction.