Abstract
The sensitivity and specificity of current breast cancer biomarkers are not sufficient for early diagnosis. Identification of more sensitive and specific biomarkers to provide accurate information about disease at the molecular level is of great significance to establish new breast cancer diagnosis model. To achieve this goal, one of prerequisites is to accurately profile the expression of biomarker candidates. However, most of the currently available assays frequently fail to provide adequate reproducibility and specificity for the quantification of biomolecules. Liquid chromatography-tandem mass spectrometry (LC-MS/MS)-based targeted proteomics emerges as alternative technique. Recent work in our lab has shown a clear advantage of targeted proteomics in quantitative analysis of proteins, modified proteins, protein complexes and other biomolecules.