Clinical proteomics tumor analysis consortium breast cancer marker studies

Synopsis

A persistent central deficiency in our knowledge of cancer concerns how genomic changes drive the proteome and phosphoproteome to execute phenotypic characteristics. Furthermore, increasing evidence implicating epigenetic and post-translational changes in cancer biology reinforce the notion that molecular profiles based on nucleic acids are incomplete and are critically complemented by analyses of proteins and their post-translational modifications. We present the first integrated proteogenomic study on a prospectively collected breast cancer cohort, and provide new insights including on taxonomy, metabolic dependencies, and immune milieu.