Family history evaluation is considered to be one of the most effective tools for predicting disease (Alspach, 2011; Leach & Eng, 2010) and is used for risk stratification, individualized screening for cancer detection and prevention, and targeted genetic services (Berg et al., 2009). Leach and Eng (2010) compared family history assessment to commercial personal genomic testing, often referred to as direct-to-consumer genetic testing, and family history assessment was found to be superior in stratifying population risk, moderate risk, and high risk for breast, prostate, or colon cancers. Although family history is one of the least expensive and most important genomic tools, it frequently is underused and underdocumented (Freezo, Rubenstein, Dunham, & Ormond, 2003; Murff, Greevy, & Syngal, 2007). Family history information is key for studying single-gene disorders and identifying the shared risk factors, gene alternations (single-nucleotide polymorphisms), lifestyle patterns, and environment of common complex diseases (Berg et al., 2009). Although the presence or absence of family history may be documented in