Abstract

Cardiac transcription factor (cardiac TF) are essential for proper heart development and function. Not surprisingly, numerous non-synonymous mutations identified in patients with congenital heart defects map to the DNA-binding domain of cardiac TFs. However, the consequences these mutations have on cardiac TF-DNA interactions remain unknown. Our working hypothesis is that non-synonymous CHD mutations in the DNA-binding domains (DBD) of cardiac TFs perturb their DNA-recognition properties, potentially re-wiring the transcriptional networks indispensable for normal heart development and function. To test this hypothesis, we propose to systematically and comprehensively characterize the DNA binding landscapes of cardiac TF mutants found CHD.