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.