Supplementary figures 1-3

Supplementary figure 1: Scatter plot of codon position of mutation by age of onset of disease for the youngest affected patient in each pedigree.

Supplementary figure 2: The conservation of the homeodomain in CRX across multiple species generated by Clustal Omega. # (hashtag) indicates position of reported mutations, * (asterisk) indicates positions which have a single, fully conserved residue, a : (colon) indicates conservation between groups of strongly similar properties, a . (period) indicates conservation between groups of weakly similar properties. All mutations arise within highly conserved residues.
Supplementary figure 3: The conservation of the homeodomain in CRX across multiple human paralogues as generated by Clustal Omega. # (hashtag) indicates position of previously reported mutations, * (asterisk) indicates positions which have a single, fully conserved residue, a : (colon) indicates conservation between groups of strongly similar properties, a . (period) indicates conservation between groups of weakly similar properties. Three mutation locations are not conserved between paralogues.