Figure S4. The position of 10 individual mutations found within an active site region of MT-CO1 (Left) and a binding pocket of MT-CYB (Right) of Complex IV and III, respectively. The mutations are shown as side-chains rendered as spheres and coloured according to their associated disease (see Figure 2 legend). Heme groups are shown as green stick models with bound substrate ubiquinone molecule in red (PDB 1NTZ). Multiple mutation sites clustering around, and directly interacting with, the heme group a and those corresponding to the side-chains that make direct contributions to the ubiquinone binding pocket are shown. T6721C (M273T), T6742C (I280T), G6955A (G352D), T14849C (S35P), G14846A (G34S), A15579G (Y278C) and G15762A (G339E) are confirmed mutations, while G7041A (V380I), G7023A (V374M) and A14841G (N32S) are unconfirmed (see main text for definitions).