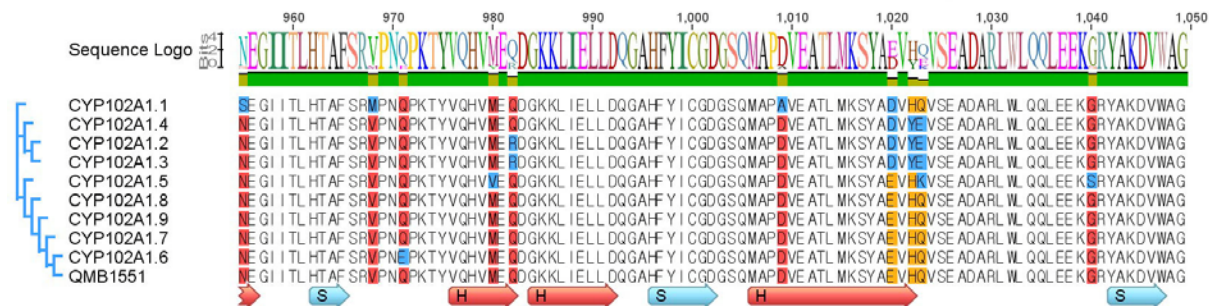




**Additional file 1. Amino acid sequence alignment of CYP102A1 and its variants.** CYP102A1 variants are arranged in order corresponding to the molecular phylogeny (Fig. 1a) as indicated by the simplified schematic to the left of the amino acid alignment. Secondary structures are shown below the CYP102A1 variant sequences:  $\alpha$ -helices, red;  $\beta$ -sheets, blue. Binding sites of cofactors are shown: heme (yellow), FMN (dark blue), and FAD (gray).