



Figure S1. Alignment of the sequences of CYP261C and CYP261D enzymes. Approximate positions of the main α -helices are shown with black frames. The residues conserved in all four sequences are shown in red letters. Amino acid substitutions in each of the CYP261C1/C2 and CYP261D1/D2 pairs are highlighted in blue boxes with white letters. Residues participating in a putative system of salt bridges between α -helices A and K are shown with connected green ovals. Red ovals indicate the position of spatially adjacent substitutions involved in the interactions of C-terminus with C/D and I/J loops.