Figure S1. Examples of structural variation detected by Stargazer.[15] Grey dots denote copy number calculated from read depth. Blue solid and green dashed lines represent two sequence structures that are being tested against the observed copy number of the sample. Purple and orange lines represent theoretical copy number profiles for *CYP2D6* and *CYP2D7*, respectively, formed by combining the two sequence structures. Each panel contains scaled *CYP2D6* and *CYP2D7* gene models, in which exons and introns are depicted with boxes and lines, respectively: (A) *CYP2D6*2/*4*: no structural variation; (B) *CYP2D6*2/*5*: gene deletion; (C) *CYP2D6*35/*2x2*: gene duplication; (D) *CYP2D6*9/*68+*4*: complex structural variation involving a gene duplication and a gene hybrid; (E) *CYP2D6 *41/*13+*2*: complex structural variation involving a gene hybrid; (F) *CYP2D6*68+*4/*36+*10*: complex structural variation involving multiple gene duplications and gene hybrids.