

The GM_{combined} dataset was used to generate this figure, which is the dataset containing both the positively selected reads from the AS pores and all the reads from the conventionally sequencing pores. The positions of the gRNAs are indicated with vertical lines and the sequencing direction is indicated with arrows on top of the vertical lines. Reads are split by allele. gRNA2* indicates the position where gRNA2 cuts before the *CYP2D6-CYP2D7* *13 hybrid. The reads of the hybrid map on the *CYP2D7* gene, but the first part of the hybrid originates from the *CYP2D6* gene, resulting in a visual gap in the alignment.