Figure S5. Composite of mapped reads across all samples for exon 3b. The depth of mapped reads is indicated by the gray histogram in the upper panel, while HTR2A gene structure is depicted in the lower panel (5'-to-3' direction from left-to-right). The histogram depicts exon 3b starting adjacent to the 3' splice acceptor site and continuing approximately 1.2kB to the poly-A signal cluster, proximal to where read depth noticeably decreases. Canonical and non-canonical poly-A sites are marked in the lower panel as red dots. Note: read depth is presented in linear scale.