



**Supplemental Figure S2 – Benchmarking of *vast-tools*: performance and sensitivity on AS identification**

A) User time and maximal memory usage for each tool required to process 50 [light] or 150 [dark] million paired-end reads. B) Number of differentially included ( $\Delta\text{PSI} > 15$  [light],  $\Delta\text{PSI} < -15$  [dark]) alternative exons by size category (3-9 nt, 10-15 nt, 16-27 nt and  $> 27$  nt) identified by each tool when comparing RNA-seq data from ESC (DIV -8) and differentiated neurons (DIV 28) from (Hubbard et al. 2013). C) Number of AS events by type identified by each tool in our simulated dataset, as well as the total number of events (TOTAL) and those identified by all tools (COM). AS events are separated into complex (light) or simple (dark), depending on whether multiple competing splice sites are present or not.