Supplemental Material
Alternative splicing analysis benchmark with DICAST

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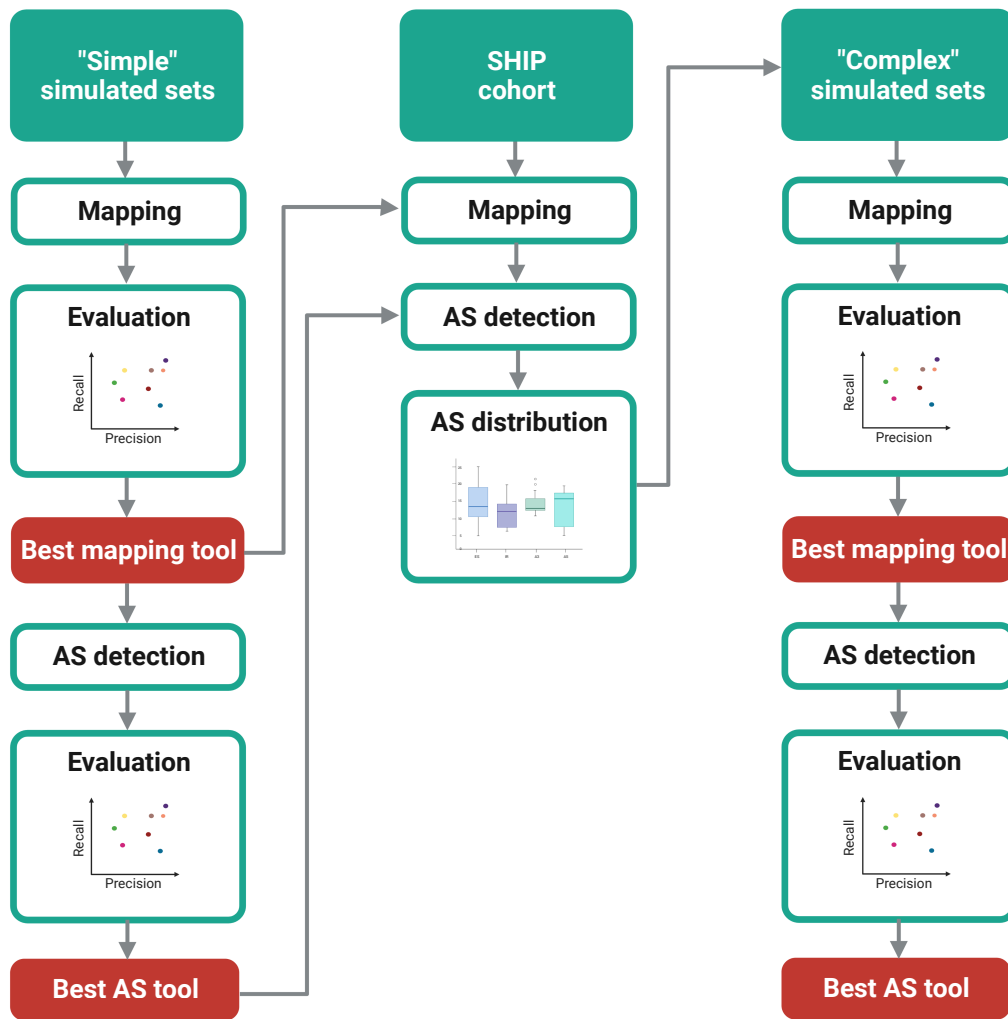[7]Braunschweig Integrated Centre of Systems Biology (BRICS), TU Braunschweig, Braunschweig, Germany
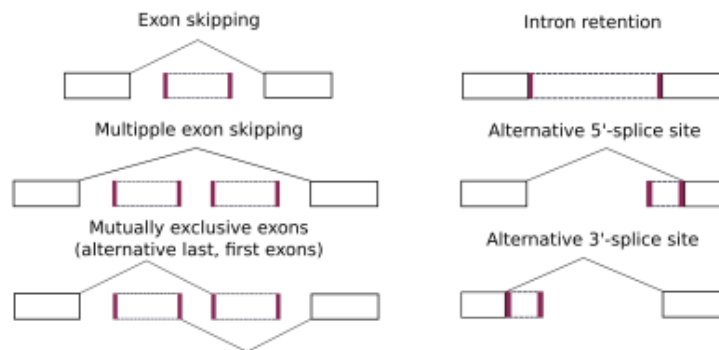[+]corresponding author: markus.list@tum.de
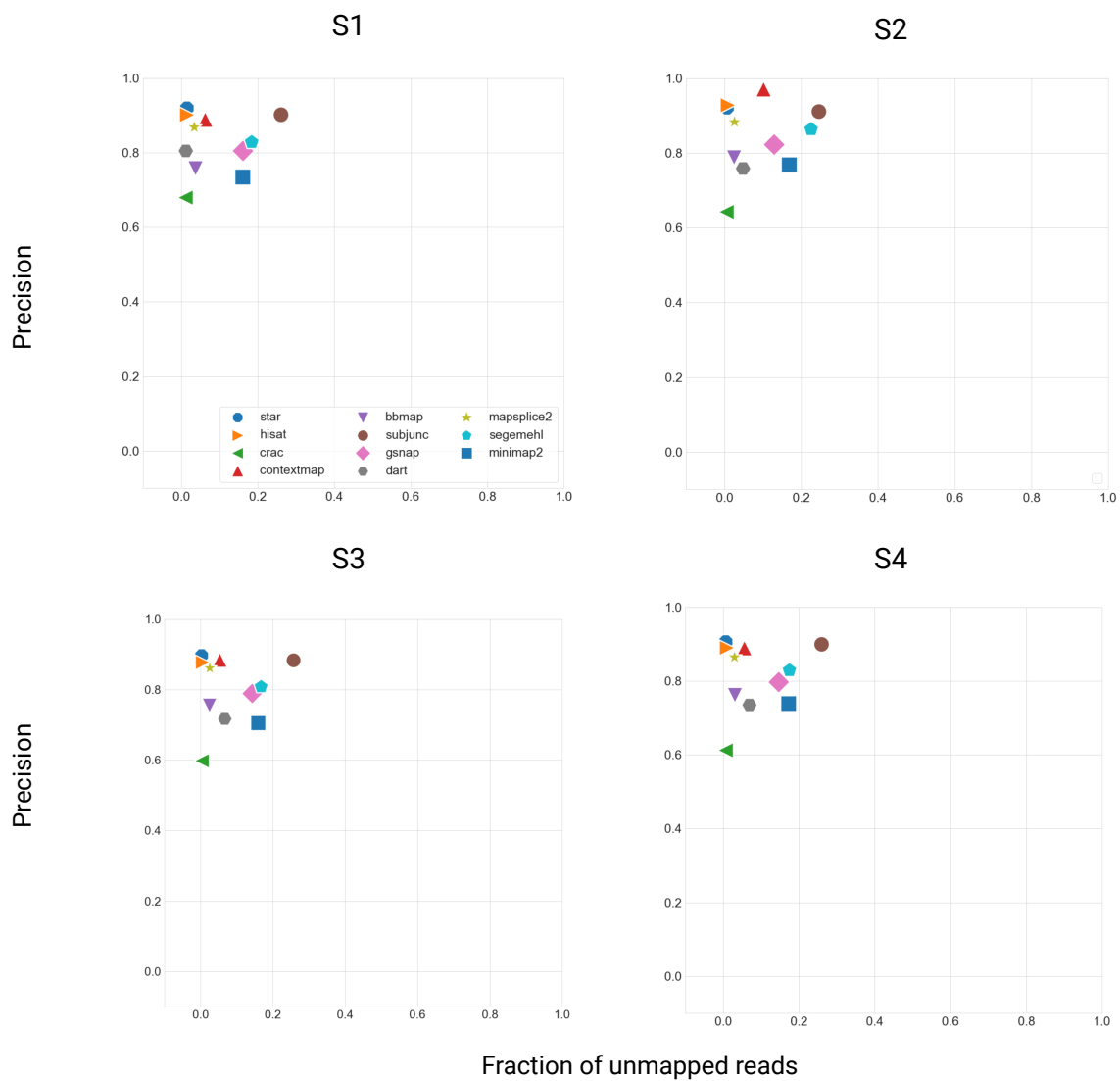[*]joint first authors
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ABSTRACT

Figure S1. The workflow used to benchmark AS analysis tools. Created with BioRender.com


Figure S2. The coordinates of AS events reported in the unified format output of DICAST are shown as bold purple lines in the corresponding splice graph

Figure S3. The plots for precision and fraction of unmapped reads for splicing-aware mapping tools for the S1-S4 simulated sets

Figure S4. Precision/recall plots for AS event detection tools for the S1-S4 simulated sets
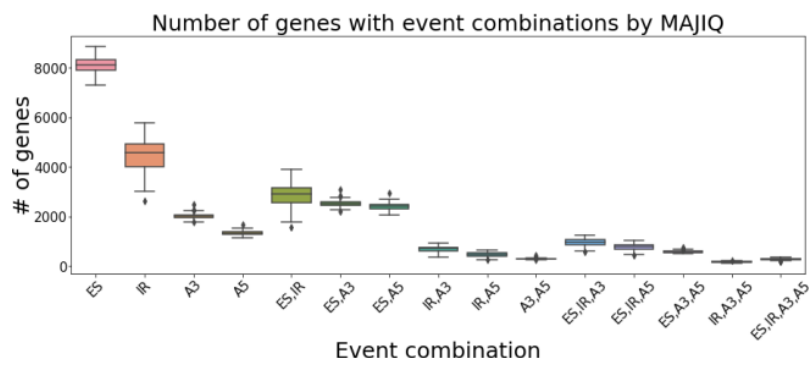
Figure S5. Number of genes with AS event types found by MAJIQ in the SHIP cohort data set