Supplementary Figures: Quality control for the target decoy approach for peptide identification

Elke Debrie,[†] Milan Malfait,[†,‡] Ralf Gabriels,[¶,§] Arthur Declerq,[¶,§] Adriaan Sticker,[†,¶,§] Lennart Martens,[¶,§] and Lieven Clement[*,†]

[†]Department of Applied Mathematics, Computer Science and Statistics, Ghent University, Ghent University, Ghent, Belgium

[‡]Statistics and Decision Sciences, Janssen Pharmaceutical Companies of Johnson and Johnson, Beerse, Belgium

[¶]VIB-UGent Center for Medical Biotechnology, VIB, Ghent, Belgium

[§]Department of Biomolecular Medicine, Ghent University, Ghent, Belgium

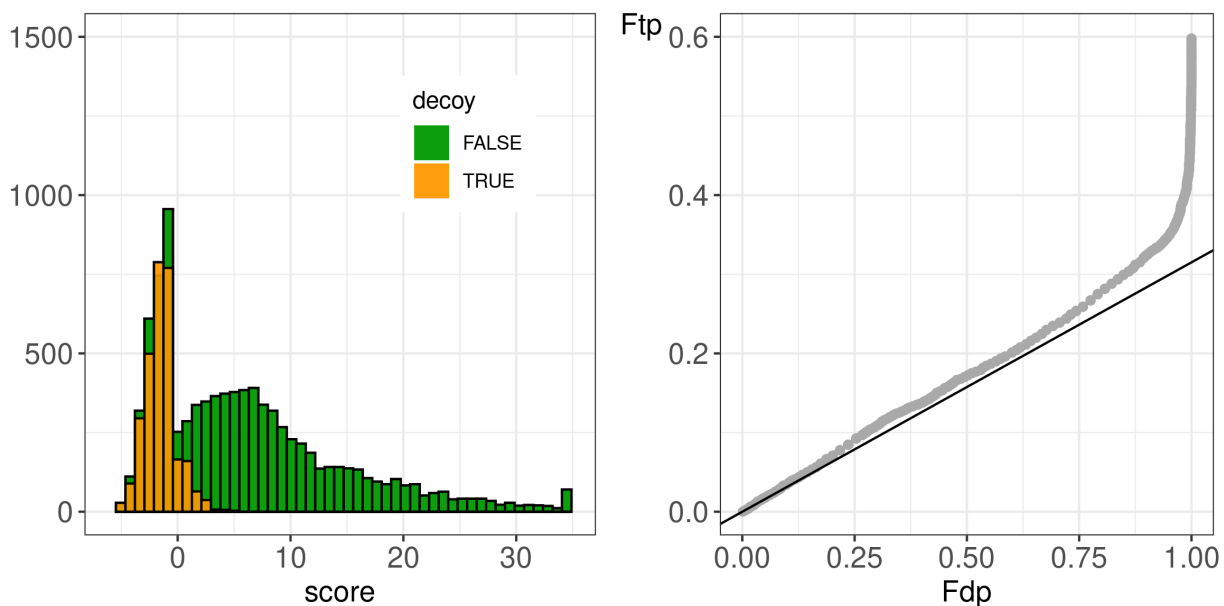E-mail: lieven.clement@ugent.be

References

Figure 1: Histogram and PP-plot for a concatenated search on a *Pyrococcus* run against a database of canonical *P. furiosus* sequences from Swiss-Prot using X!Tandem without refinement. Both the histogram and the P-P plot show no violation of the TDA assumptions.
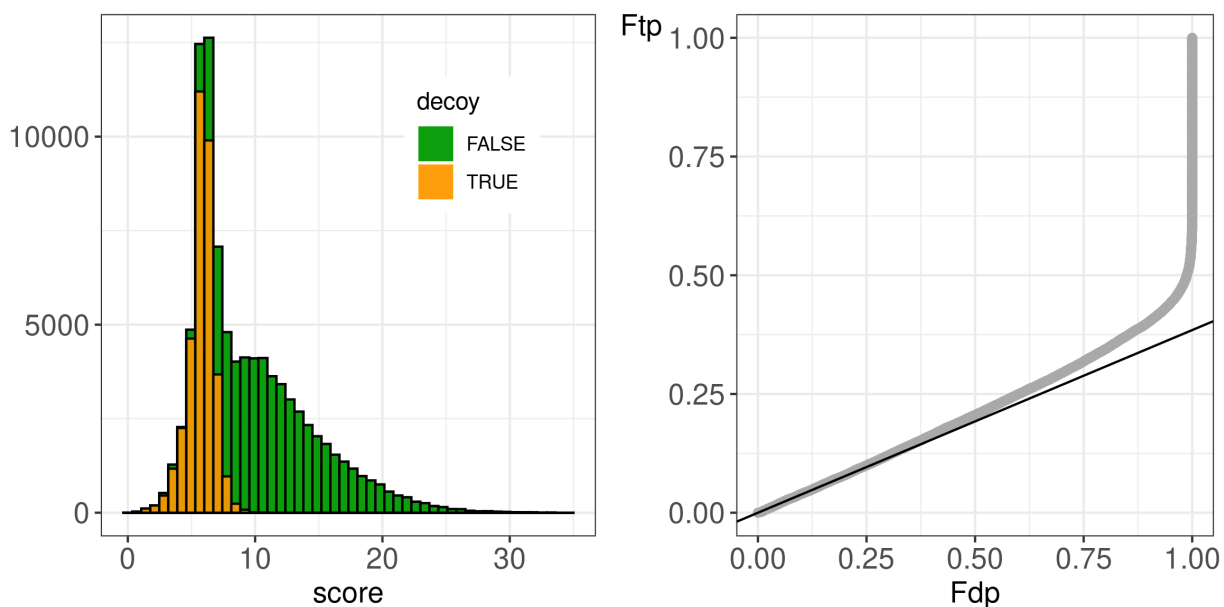

Figure 2: Histogram and PP-plot for a concatenated search on a *H. sapiens* run against a database of *H. Sapiens* sequences from UniProt using MS-GF+. Both the histogram and the P-P plot show no violation of the TDA assumptions.
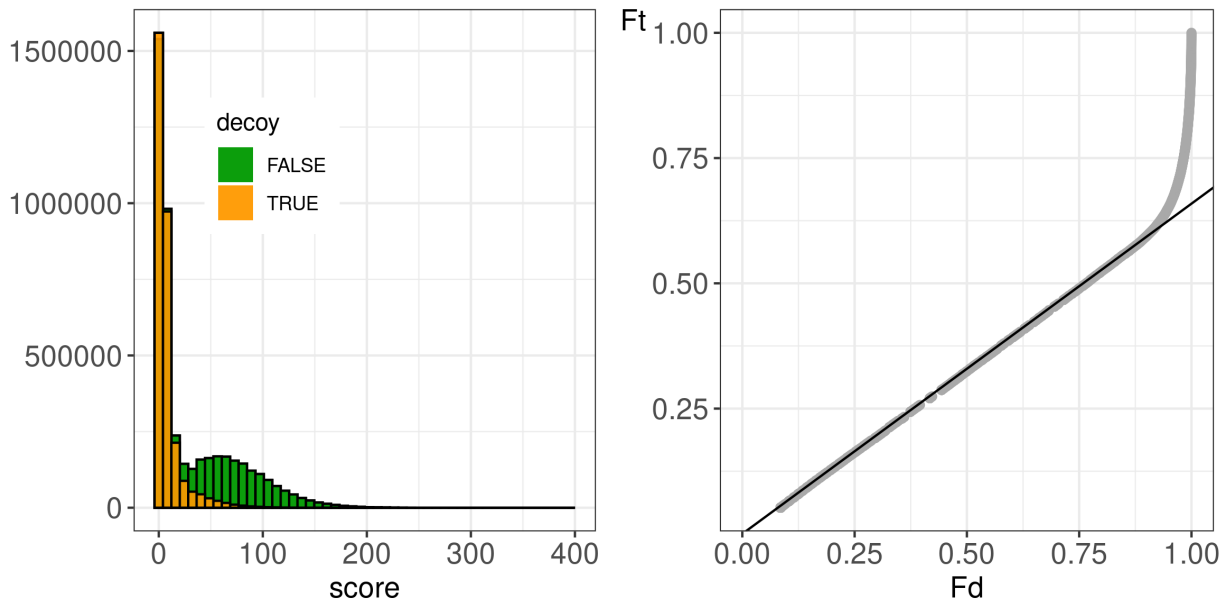
Figure 3: Histogram and PP-plot for a concatenated search on an immunopeptidomics run using Andromeda. Both the histogram and the P-P plot show no violation of the TDA assumptions.
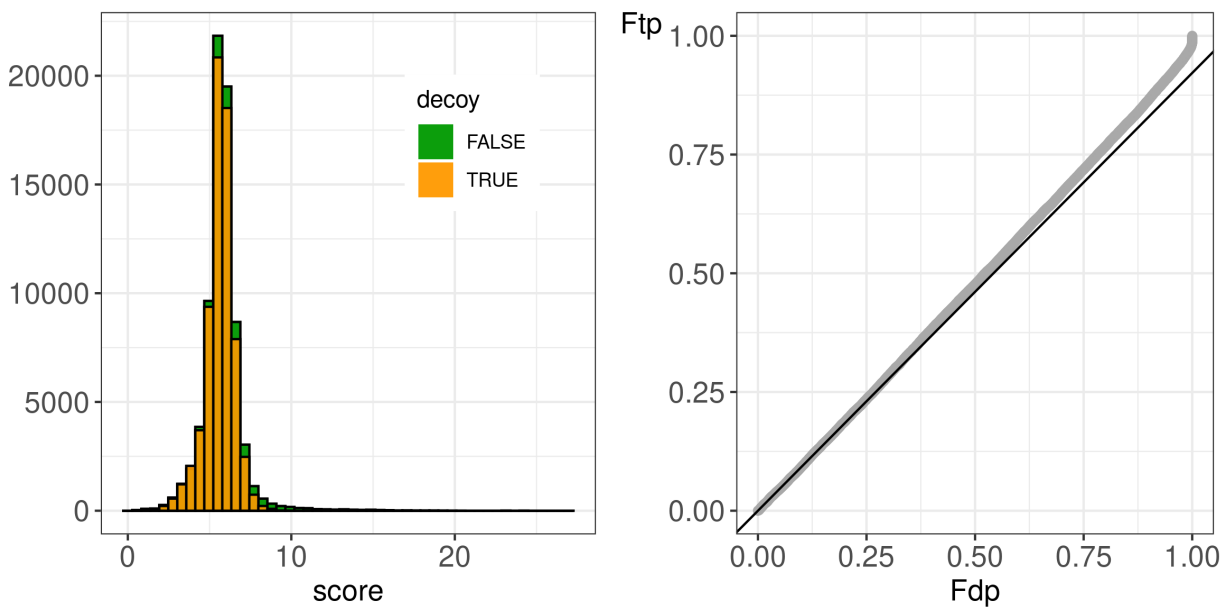

Figure 4: Histogram and PP-plot for rank 2 target and decoy PSM scores of a concatenated search on a H. sapiens run against a database of H. Sapiens sequences from UniProt using MS-GF+.