Supplementary information

Discrepancies between high-resolution native and glycopeptide-centric mass spectrometric approaches: A case study into the glycosylation of erythropoietin variants

Tomislav Čaval[1,2,*], Alexander Buettner[3], Markus Haberger[3], Dietmar Reusch[3], Albert J.R. Heck[1,2,#]

[1]Biomolecular Mass Spectrometry and Proteomics, Bijvoet Center for Biomolecular Research and Utrecht Institute for Pharmaceutical Sciences, University of Utrecht, Padualaan 8, Utrecht, 3584 CH, The Netherlands
[2]Netherlands Proteomics Center, Padualaan 8, Utrecht, 3584 CH, The Netherlands

[3]Pharma Technical Development, Roche Diagnostics GmbH, Penzberg 82377, Germany

[#]Corresponding author

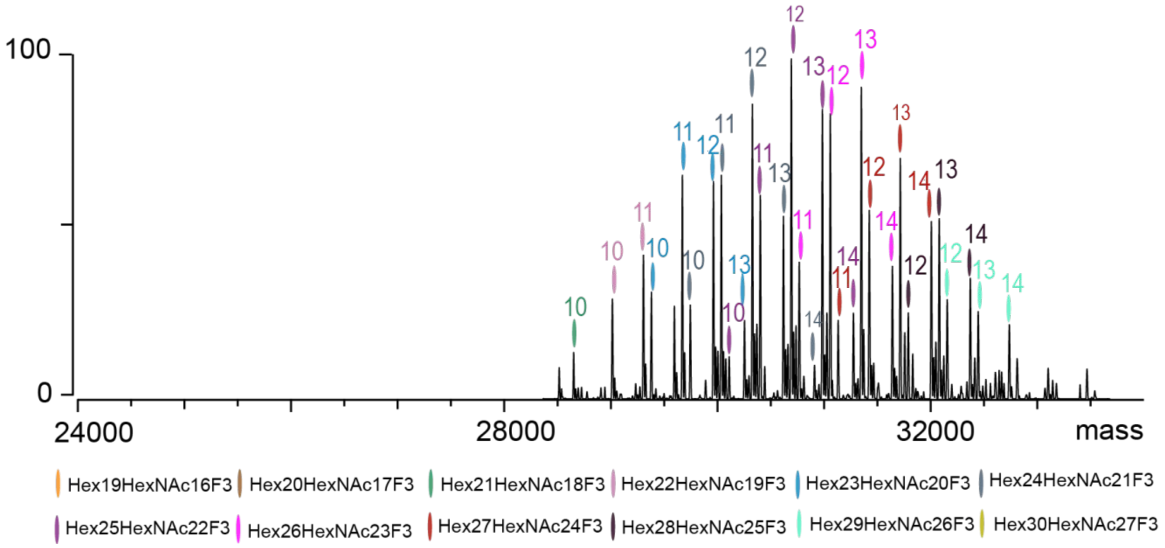

Figure S1. **Upsized spectrum of EPO-1**) Native MS spectrum of non-sialidase treated EPO-1. Each peak is color coded and represents a unique $Hex_{x+3}HexNAc_xF_3$ composition where the numbers above the color codes indicate the cumulative number of sialic acid residues attached to the EPO glycans.