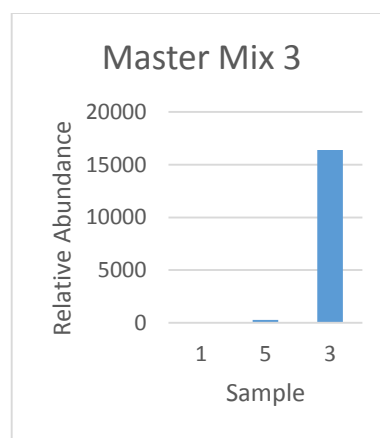
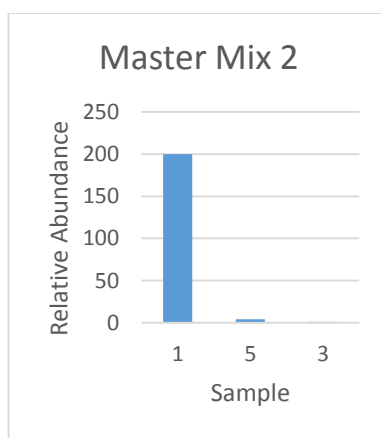
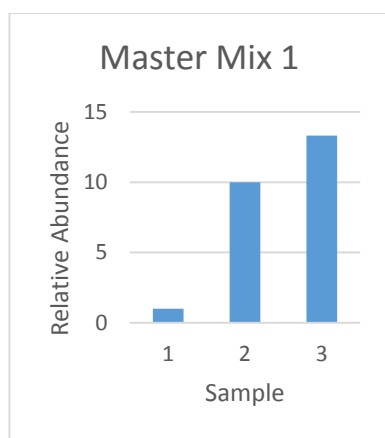


Spectronaut 7 – Demo Dataset

The demo experiment consists of 3 samples each having 3 technical replicates. The samples all contain a HEK-293 human cell line extract as stable background matrix. Additionally, 12 non-human proteins have been added to the in the following concentration ranges:

	Master Mix1		Master Mix 2		Master Mix 3	
	<i>P02754</i>		<i>P61823</i>		<i>P02666</i>	
	<i>P80025</i>		<i>P02789</i>		<i>P68082</i>	
	<i>P00921</i>		<i>P12799</i>			
	<i>P00366</i>		<i>P02676</i>			
	<i>P02662</i>		<i>P02672</i>			

Sample	Relative	fmol/ μ l	Relative	fmol/ μ l	Relative	fmol/ μ l
1	1	1.5	200	100	1	0.05
5	10	15	4	2	256	12.8
8	13.33	19.995	1	0.5	16384	819.2



The provided spectral library (HEK293_SN7_Demo.kit) can be imported using the Prepare perspective in Spectronaut. The library contains ~35,000 precursors including peptides representing the 12 non-human spike in proteins.

The spectral library was generated from 24 shotgun replicates on the same LC-MS setup. The LC-MS runs were analyzed with MaxQuant and the library generated with Spectronaut using the default settings in the Prepare perspective.

This demo data-set is part of a larger experiment that was published in MCP¹. Additional material can be obtained from there.

References

[1] Bruderer, Roland, et al. "Extending the limits of quantitative proteome profiling with data-independent acquisition and application to acetaminophen treated 3D liver microtissues." *Molecular & Cellular Proteomics* (2015): mcp-M114.