Supporting Information

Comprehensive prostate fluid-based spectral libraries for enhanced protein detection in urine.

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Table of Contents

Content	Page
Figure S1. Comparisons between DIA-MS data analysis approaches	S-3
Figure S2. Comparisons between DIA- and DDA-MS on matched EPS-urine samples.	S-5
Figure S3. Evaluation of the sample-relevant spectral libraries.	S-6
Figure S4. Detection results of the lib-EPS, DPHLv2, and library-free.	S-8
Table S1. Clinical information of the prostate cancer patients for EPS-urine cohort. (XLSX)	

Table S2. Detailed optimization parameters for DIA-MS methods tested. (XLSX)



Figure S1. Comparisons between DIA-MS data analysis approaches. (**A**) Intersection of peptides in the sample-specific generated spectral libraries. (**B**) Detection rates (**C**) Intersection of peptides

Figure S1

of the EPS-urine DIA-MS data searched against each sample-specific spectral libraries, DPHLv2, and library-free approach. (**D**) Percent observations of peptides detected in the EPS-urine DIA-MS data when searched against each subsampled library. (**E**) Boxplot of the log₂ peptide intensities of peptides detected. (**F**) Proportion of total peptides detected in DIA-MS data of each subset cohort using subsampled spectral libraries from DDA-MS of the corresponding subset cohort.



Figure S2. Comparisons between DIA- and DDA-MS on matched EPS-urine samples. (A) Number of peptides detected per sample with P-value calculated by Wilcoxon's signed-rank test. (B) Percent samples observed for detected proteins in both DIA- and DDA-MS, stratified by abundance quartile quantified by DDA-MS. (C) Spearman's correlation of run-to-run protein intensity correlation.





Figure S3. Evaluation of the sample-relevant spectral libraries. (**A**) Library size of the generated spectral libraries. (**B**) Percent observation of proteins detected by all libraries, or uniquely by each of the spectral libraries. (**C-E**) Percent observations of uniquely detected proteins by each spectral library in the corresponding DDA-MS samples of EPS-urine fractions.



Figure S4. Detection results of the lib-EPS library against DPHLv2 and library free. (**A**) Total number of peptide and proteins detected with each approach. (**B**) Number of peptides and proteins detected in more than 10% of samples with each approach.