Supplementary Table 1. Chromatography and MS instrument acquisition settings for DDA

Sample Volume	5 µL	***MS^2 Acquisition***	Data dependent, 3 s cycle time, Centroid
Stationary Phase	PicoChip; C_{18} 75 µm × 10.5 cm	***MS^2 Fragmentation***	HCD
LC Solvent A	100% H2O, 0.1% formic acid	***MS^2 Detection***	Orbitrap
LC Solvent B	80% ACN, 0.1% formic acid	***MS^2 fixed first mass***	110 *m/z*
Gradient Ramp ***Duration*** ***Flow Rate***	6-36% B 95 minutes 300 nL/min	***Isolation Window***	1.6 m/z
Mass Spectrometer	Thermo Orbitrap Fusion Lumos	***MS^2 AGC Target***	5e4
Spray Voltage	2.0 kV	***MS^2 Maximum IT***	100 ms
In-Source CID	0.0 eV	***Normalized Collision Energy***	30
MS^1 Scan Range	375-1500 m/z	***Minimum Intensity Req.***	5e4
MS^1 Resolution	120,000 @ 200 *m/z*	***Dynamic Exclusion***	60.0 s
MS^1 AGC Target	4e5	***MS^2 resolution***	30,000 @ 200 *m/z*
MS^1 Maximum IT	50 ms		

Supplementary Table 2. Chromatography and MS instrument acquisition settings for DIA

Sample Volume	5 µL, Microliter Pickup	***MS^2 Acquisition***	Data independent, Profile
Stationary Phase	PicoChip; C_{18} 75 µm × 10.5 cm	***MS^2 Fragmentation***	HCD
LC Solvent A	100% H2O, 0.1% formic acid	***MS^2 Detection***	Orbitrap
LC Solvent B	80% ACN, 0.1% formic acid	***MS^2 scan isolation windows***	400-600 *m/z* by 20 *m/z* windows 600-1000 *m/z* by 40 *m/z* windows
Gradient Ramp ***Duration*** ***Flow Rate***	6-36% B 95 minutes 300 nL/min	***MS^2 scan range***	120-1200 *m/z*
Mass Spectrometer	Thermo Orbitrap Fusion Lumos	***MS^2 resolution***	30,000 @ 200 *m/z*
Spray Voltage	2.0 kV	***MS^2 AGC Target***	1e5
In-Source CID	0.0 eV	***MS^2 Maximum IT***	100 ms
MS^1 Scan Range	375-1500 m/z	***Normalized Collision Energy***	30
MS^1 Resolution	120,000 @ 200 *m/z*	***Max Cycle Time***	3s
MS^1 AGC Target	4e5		
MS^1 Maximum IT	50 ms		

Supplementary Table 3. Chromatography and MS instrument acquisition settings for PRM

Sample Volume	20 µL, full-loop Injection	***MS^2 Detection***	Orbitrap
Stationary Phase	Thermo Acclaim PepMap C$_{18}$ 75 µm × 25 cm	***MS^2 m/z range***	120-1200 m/z
LC Solvent A	100% H2O, 0.1% formic acid	***Isolation Window***	1.6 m/z
LC Solvent B	80% ACN, 0.1% formic acid	***MS^2 AGC Target***	5e4
Gradient Ramp ***Duration*** ***Flow Rate***	2-28% B in 52 minutes 28-40% B in 7 minutes 300 nL/min	***MS^2 Maximum IT***	54 ms
Mass Spectrometer	Thermo Orbitrap Fusion Lumos	***Normalized Collision Energy***	Variable
Spray Voltage	2.0 kV	***MS^2 resolution***	30,000 @ 200 *m/z*
In-Source CID	0.0 eV	***MS^2 Detection***	Orbitrap
MS^1 Scan Range	325-1500 m/z	***MS^2 m/z range***	120-1200 m/z
MS^1 Resolution	120,000 @ 200 *m/z*	***Isolation Window***	1.6 m/z
MS^1 AGC Target	4e5		
MS^1 Maximum IT	50 ms		

Supplementary Table 4. DDA search parameters

Platform	ProteomeDiscoverer 2.2	***Quantitation***	Precursor Ions Quantifier, Peak Area
Search Algorithms	SequestHT	***Normalization***	Total Peptide Amount
Validation	Percolator Peptide Validator Protein FDR Validator	***Scaling***	On All Average (to value of 100)
Database	UniProt; Rabbit; created 10/03/2017 MaxQuant Contaminants Database; 10/03/2017	***Ratio Calculation***	Summed Abundance Based
Digest	Trypsin (full) 2 Missed Cleavages Allowed	***Hypothesis Test***	ANOVA (Individual Proteins)
Precursor mass tolerance	10 ppm	***Target FDR (Strict) for PSMs:***	0.01
Fragment mass tolerance	0.02 Da	***Target FDR (Relaxed) for PSMs:***	0.05
Static Modifications	Carbamidomethyl (C)	***Target FDR (Strict) for Peptides:***	0.01
Dynamic Modifications	Oxidation (M), Acetylation (protein N-terminus)	***Target FDR (Relaxed) for Peptides:***	0.05