

Supplemental Table 1. Summary of Mass Spectrometry Method Parameters for Different Sets of Acquired Proteome Profiling Data .

	TMT HeLa/3T3 Mixture	Label-Free HeLa and 3T3 Profiling	Label-Free WHIM-PDX Profiling	Label-Free BCM-PDX 1-hour QC Runs	
Figure #	3	1&4	2&5	4	
sRP Method	18F6R	15F5R	9F6R	no off-line fractionation	
HPLC	Instrument	Ultimate3000	Ultimate3000	Ultimate3000	EASY-nLC1200
	Pre-column	2cm 100umID C18	2cm 100umID C18	2cm 100umID C18	2cm 100umID C18
	Column	10cm 100umID C18	10cm 100umID C18	10cm 100umID C18	5cm 150umID C18
	Loading	10 min @ 2%B	10 min @ 2%B	10 min @ 2%B	Auto
	Gradient(s)	2%-28%B	2%-28%B	2-24%B (fractions 06+25, 09+30, and 12+35); 4-24%B (fraction 15); 8-26%B (fractions 18 and 21)	5-28%B
	Flow Rate	500nl/min	500nl/min	500nl/min	750nl/min
	Gradient Length	110 min	120 min	90 min	55 min
	Wash	10 min @ 90%B	10 min @ 90%B	10 min @ 90%B	5 min @ 95%B
	Instrument	Fusion	Fusion	Fusion	LumosETD
	Method	SPS-MS3	MS2	MS2	MS2
Spray Voltage	2200 V	2200 V	2400 V	2400 V	
Transfer Tube Temp	300 C	300 C	325 C	300 C	
S-Lens RF	60%	60%	65%	50%	
MS1 Analyzer	Orbitrap	Orbitrap	Orbitrap	Orbitrap	
MS1 Resolution	120,000	120,000	120,000	120,000	
MS1 Scan Range	380-1500 m/z	300-1400 m/z	300-1400 m/z	300-1400 m/z	
MS1 Max Inj Time	500 ms	500 ms	50 ms	50 ms	
MS1 AGC Target	200,000	400,000	500,000	500,000	
MS2 Analyzer	IonTrap	IonTrap	IonTrap	IonTrap	
MS2 Top Method	Speed, 3 sec	Top20	Top20	Top30	
MS2 Dynamic Excl	70 sec	15 sec	20 sec	15 sec	
MS2 Charge States	2 to 7	2 to 6	2 to 4	2 to 6	
MS2 Isolation Window	0.7 Da	2 Da	3 Da	2 Da	
MS2 Fragmentation	CID	HCD	HCD	HCD	
MS2 Collision Energy	35%	35%	35%	32%	
MS2 Ion Trap Mode	Turbo	Rapid	Rapid	Rapid	
MS2 Max Inj Time		30 ms	50 ms	35 ms	
MS2 AGC Target		50,000	10,000	5,000	
MS3 Analyzer	Orbitrap				
MS3 Fragmentation	HCD				
MS3 Collision Energy	65%				
MS3 Resolution	30,000				
MS3 Scan Range	120-500 m/z				
MS3 AGC Target	100,000				