

## Supplemental Table 10. Top Canonical Pathways Identified by IPA

Carbon Nanotube/Pathway	P value*	Ratio**
<b>SWCNT-COOH 500 pg/ml</b>		
none	-	-
<b>MWCNT-COOH 500 pg/ml</b>		
Cardiac $\beta$ -adrenergic Signaling	0.00006	6/139
CDK5 Signaling	0.00008	5/89
EIF2 Signaling	0.00008	7/215
Glycolysis/Gluconeogenesis	0.00009	5/90
Inositol Metabolism	0.0004	2/6
<b>MWCNT-PVP 500 pg/ml</b>		
EIF2 Signaling	0.000000000003	19/215
Regulation of eIF4 and p70S6K Signaling	0.0000002	12/169
Protein Ubiquitination Pathway	0.000002	14/270
mTOR Signaling	0.000002	12/199
14-3-3-mediated Signaling	0.000008	9/118
<b>SWCNT-COOH 10 ug/ml</b>		
EIF2 Signaling	0.00001	5/215
Regulation of eIF4 and p70S6K Signaling	0.00006	4/169
mTOR Signaling	0.0002	4/199
Glutamate Metabolism	0.001	2/36
<b>MWCNT-COOH 10 ug/ml</b>		
EIF2 Signaling	0.00000002	11/215
RhoA Signaling	0.0004	5/111
Glutamate Metabolism	0.001	3/36
Actin Cytoskeleton Signaling	0.001	6/233
Virus Entry via Endocytic Pathways	0.002	4/93
<b>MWNT-PVP 10 ug/ml</b>		
EIF2 Signaling	0.001	5/215
Butanoate Metabolism	0.002	3/61
C21-Steroid Hormone Metabolism	0.003	2/21
Citrate Cycle	0.005	2/29
Glutamate Metabolism	0.008	2/36

Colored pathways denote commonality across f-CNTs (see Venn diagram in Figure 10 of text). Blue P values are down-regulated pathways, red P values are up-regulated pathways. Combination of Blue/Red signifies up- and down-regulation of various elements of a pathway.

\*P value is the probability that the proteins are associated with the pathway by chance.

\*\*Ratio is the number of differentially expressed proteins from dataset that are in the pathway relative to the total number of proteins in the pathway.