

Additional File 1

Quantifying Engineered Nanomaterial Toxicity: Comparison of Common Cytotoxicity and Gene Expression Measurements

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Table S1. Quantitative RT-PCR of NHBE cells treated with CdSe or InP QDs. Cells were incubated with 5 µg/mL CdSe or InP QDs for 24 h or with 80 µg/mL CdSe or InP QDs for 6 h. Gene expression changes for different classes of cellular functions and processes were measured by quantitative qRT-PCR. Values are expressed as fold change relative to media controls (=1.0). Blue text indicates a 2-fold or greater decrease in gene expression relative to untreated cells (≤ 0.5) while red text highlights two-fold or greater increase in gene expression relative to untreated cells (≥ 2.0). All experiments were independently repeated three times (n=3). Errors represent one standard deviation.

CELL RESPONSE PATHWAY	GENE NAME	FOLD CHANGE (5 µg/mL, 24 hrs)	
		5 nm CdSe-MUA	5 nm InP-MUA
Adhesion and Invasion	ITGA2	1.45 ± 0.13	3.01 ± 0.26
	MMP1	1.03 ± 0.05	3.26 ± 0.33
Apoptosis	BAK1	1.22 ± 0.51	1.11 ± 0.68
	BCL2	0.77 ± 0.04	0.47 ± 0.03
Autophagy	ULK1	1.28 ± 0.02	1.68 ± 0.06
	WIPI1	1.47 ± 0.03	1.82 ± 0.15
DNA Damage	CDK1	0.50 ± 0.15	0.21 ± 0.09
	GADD45A	1.18 ± 0.02	1.00 ± 0.09
	SFN	1.50 ± 0.04	1.75 ± 0.04
DNA Repair	BRCA1	0.55 ± 0.07	0.18 ± 0.03
	BRCA2	0.57 ± 0.07	0.20 ± 0.02
	XPC	0.89 ± 0.02	0.79 ± 0.05
Mitochondrial Function and Metabolism	AHR	0.99 ± 0.04	1.11 ± 0.05
	CYP1A1	1.02 ± 0.11	1.17 ± 0.17
	CYP1B1	1.29 ± 0.02	1.16 ± 0.07
	DHFR	0.57 ± 0.02	0.40 ± 0.02
	UCP1	2.29 ± 0.50	2.20 ± 1.64
Proinflammatory Cytokines and Chemokines	CSF2	1.50 ± 0.04	5.01 ± 0.35
	FAS	1.18 ± 0.06	1.06 ± 0.11
	IFNA1	2.02 ± 0.38	4.05 ± 0.44
	IL1A	1.43 ± 0.11	2.88 ± 0.03
	IL1B	1.11 ± 0.07	1.24 ± 0.06
	IL6	1.40 ± 0.07	1.02 ± 0.05
	IL8	1.27 ± 0.07	6.56 ± 0.34
	TNF	0.64 ± 0.10	1.18 ± 0.38
CXCL1	1.27 ± 0.06	1.92 ± 0.15	
Proliferation	VEGFA	1.43 ± 0.05	1.44 ± 0.17
Signal Transduction and Transcription Factors	FOS	0.91 ± 0.02	1.07 ± 0.06
	JUN	1.12 ± 0.17	1.26 ± 0.30
	MYC	0.96 ± 0.03	1.01 ± 0.04
	PIK3R1	0.93 ± 0.04	0.99 ± 0.09

CELL RESPONSE PATHWAY	GENE NAME	FOLD CHANGE (80 µg/mL, 6 hrs)	
		5 nm CdSe-MUA	5 nm InP-MUA
Adhesion and Invasion	ITGA2	1.18 ± 0.20	1.19 ± 0.22
	MMP1	1.33 ± 0.07	1.05 ± 0.11
Apoptosis	BAK1	0.59 ± 0.25	2.56 ± 0.40
	BCL2	0.63 ± 0.12	5.77 ± 1.43
Autophagy	ULK1	1.90 ± 0.35	2.93 ± 0.26
	WIPI1	1.21 ± 0.16	2.97 ± 0.47
DNA Damage	CDK1	1.92 ± 0.10	1.15 ± 0.01
	GADD45A	4.17 ± 0.95	4.95 ± 0.66
	SFN	2.84 ± 0.50	0.86 ± 0.44
DNA Repair	BRCA1	1.20 ± 0.05	0.96 ± 0.22
	BRCA2	3.06 ± 0.48	0.43 ± 0.17
	XPC	0.84 ± 0.15	2.29 ± 0.15
Mitochondrial Function and Metabolism	AHR	2.18 ± 0.29	2.35 ± 0.43
	CYP1A1	1.38 ± 0.35	0.17 ± 0.04
	CYP1B1	3.19 ± 0.46	0.70 ± 0.09
	DHFR	1.10 ± 0.10	1.15 ± 0.07
	UCP1	4.32 ± 0.87	7.20 ± 0.51
Proinflammatory Cytokines and Chemokines	CSF2	3.24 ± 0.59	0.19 ± 0.09
	FAS	0.67 ± 0.12	0.50 ± 0.04
	IFNA1	2.25 ± 0.22	1.79 ± 0.37
	IL1A	2.62 ± 1.16	1.76 ± 1.42
	IL1B	0.41 ± 0.09	0.37 ± 0.06
	IL6	0.82 ± 0.17	0.40 ± 0.12
	IL8	18.36 ± 3.79	2.53 ± 0.23
	TNF	6.50 ± 1.61	5.24 ± 0.74
CXCL1	0.31 ± 0.07	0.27 ± 0.09	
Proliferation	VEGFA	2.18 ± 0.48	1.21 ± 0.16
Signal Transduction and Transcription Factors	FOS	0.17 ± 0.03	0.52 ± 0.07
	JUN	2.24 ± 0.58	0.82 ± 0.21
	MYC	0.08 ± 0.01	0.28 ± 0.06
	PIK3R1	0.36 ± 0.05	0.52 ± 0.05