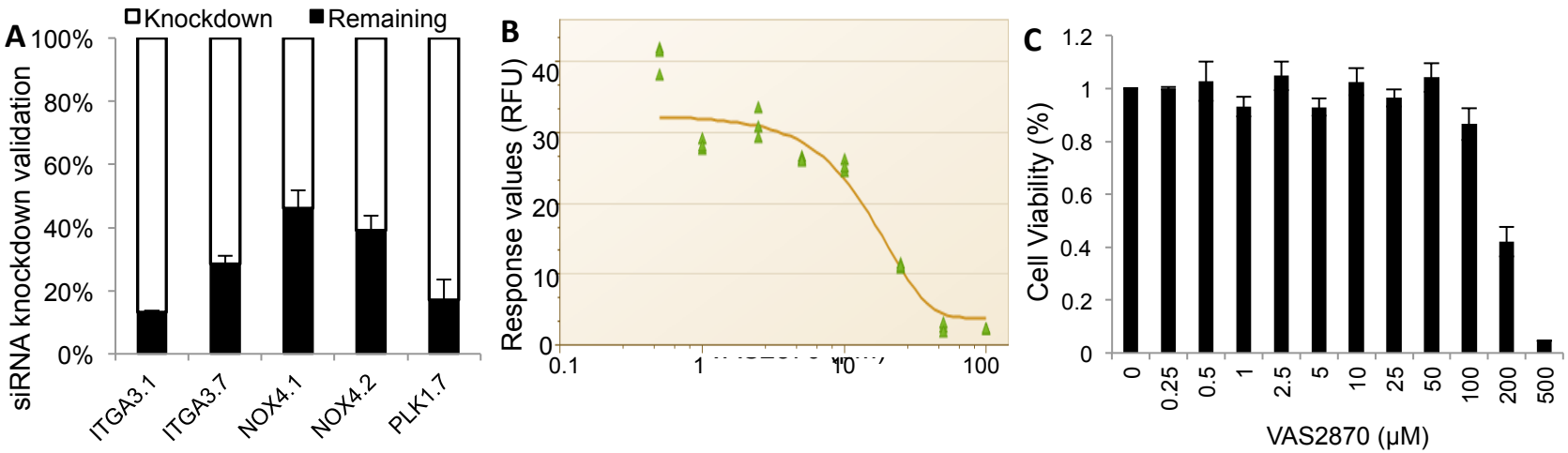
Supplemental Table S1. qRT-PCR primer sequences

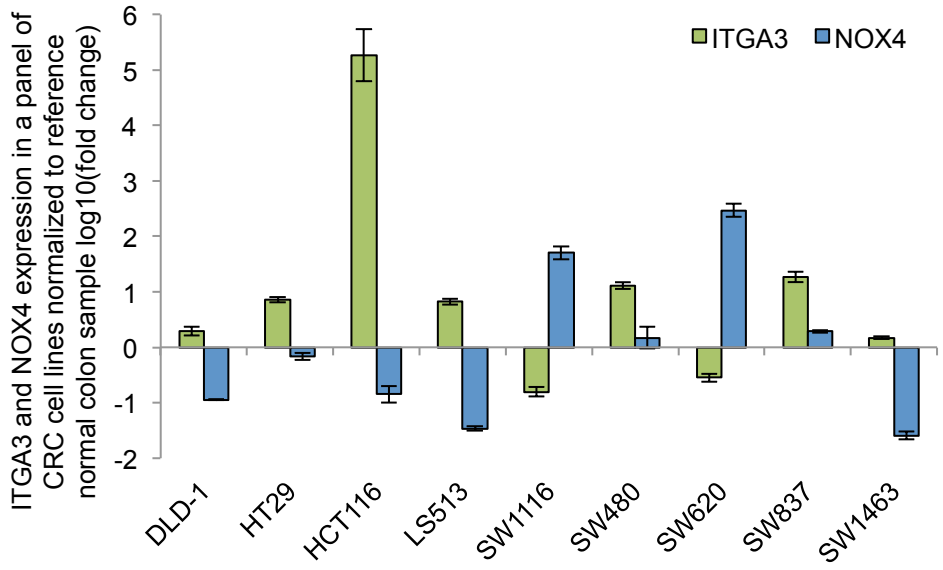
Gene	Forward primer sequence (5'-3')	Reverse primer sequence (5'-3')
Human ITGA3	TATTGAGGACATGTGGCTTG	ACAGCACCTGGGTGTAGC
Human NOX1	CATCATTGCACACCTGTTTA	CATCATGAGATAGGCTGGAG
Human NOX2	ATGGATGATTGCACTTCACT	TTCACACACCATTCCACATT
Human NOX3	AGCAGATTGCCTACAATCAC	TGTCCTCGAGAGAGCTTTAG
Human NOX4	GCCATGAAGCAGGACTCTAAAGA	TTGGCATAACACAGCTGATTGAT
Human NOX5	CTCCTCATGTTCATCTGCTC	AGGAGGTAGGACAGGTGAGT
Human ITGA3	TATTGAGGACATGTGGCTTG	ACAGCACCTGGGTGTAGC
Human PLK1	CCTGCACCTCAGCAACGGCA	CCATAGTGCGGGCGTAGCGG
Human YWAHZ	ACTTTTGGTACATTGTGGCTTCAA	CCGCCAGGACAAACCAGTAT

Supplemental Table S2. Patient Characteristics from GSE14333

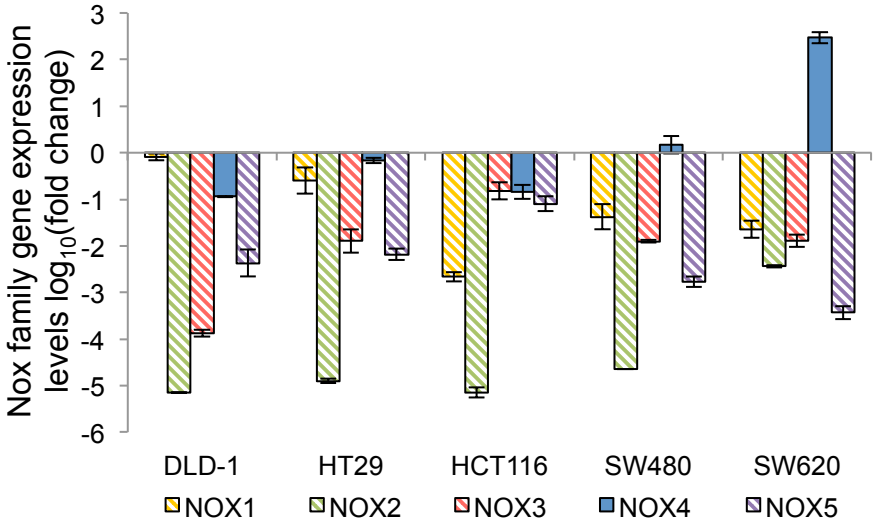
No.	Gender (M/F)	Location		Duke's Stage	
250	137/113	Left	122	A	36
		Right	125	B	82
		Colon	3	C	81
				D	51



Supplemental Figure S1. (A) Confirmation of siRNA gene silencing. Black portion of bars represent percent of RNA remaining relative to siNeg transfected cells as assessed by qRT-PCR 48 h post-transfection. Percent RNA remaining is presented as the average of multiple independent transfections ± SD. Gene silencing is relative to gene expression in siNeg transfected cells using YWAHZ as a normalization gene. (B) VAS2870 IC50 determination . Response values to a range of VAS2870 concentrations were fitted with the five parameter logistic model to determine the IC50 (18 μM). (C) Confirmation that VAS2870 treatment at the IC50 does not affect SW620 cell viability. Bars represent cell viability (%) following 24 h treatment with VAS2870 concentration (μM) indicated. Cell viability is not significantly impacted until treatment with 200 μM VAS2870. Data is the average of three measurements ± SD.



Supplemental Figure S2. ITGA3 and NOX4 expression levels in colorectal cancer cell line panel. Gene expression is based on qRT-PCR comparative C_T normalized to reference normal colon mucosa tissue. ITGA3 is most highly expressed in HCT116 cells. NOX4 is most highly expressed in SW620 cells. Data is shown as mean ± SD.



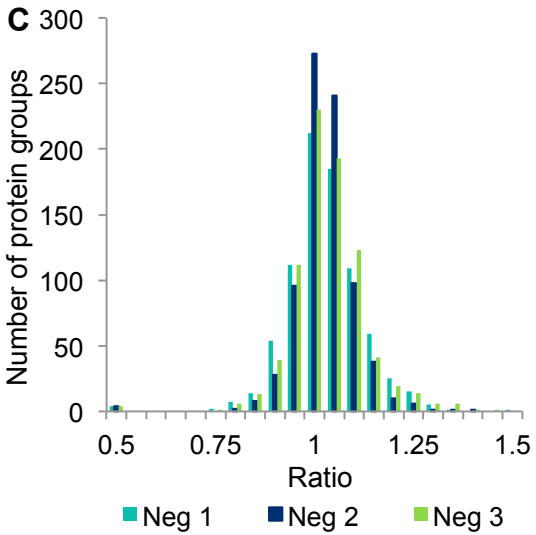
Supplemental Figure S3. NOX family expression levels in colon cancer cell lines. Gene expression is based on qRT-PCR comparative Ct normalized to reference colon tissue. NOX4 is the only NOX family member with high expression in the colon cancer cell lines, with the highest expression seen in the metastatic cell line, SW620. Data is shown as mean ± SD.

A Descriptive statistics of global proteomic profiling of control samples

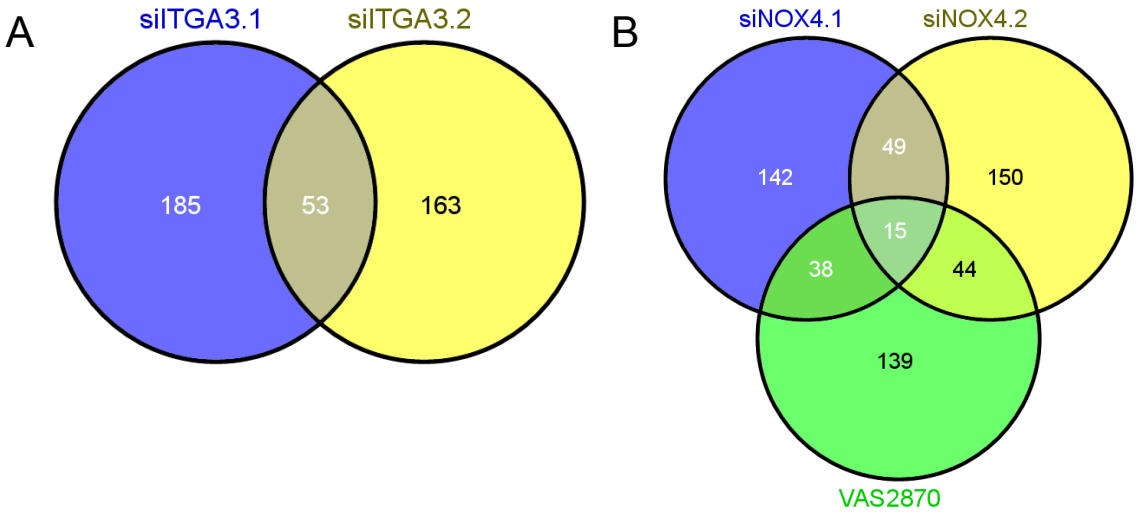
Statistic	*Neg 1 (Tech)*	*Neg 2*	*Neg 3*	*Biol*
Mean	1.01	1.00	1.01	1.00
Median	1.00	1.00	1.00	1.00
Mode	0.98	1.01	0.97	1.01
Standard Deviation	0.11	0.09	0.10	0.10
Range	1.93	1.55	1.41	1.93
Confidence Level (95.0%)	0.0078	0.0059	0.0069	0.0040

B Fold change threshold based on global standard deviation

	Median	Stdev	± 3x Stdev
Experimental variation	1.0	0.11	0.33
Biological variation	1.0	0.10	0.30



Supplemental Figure S4. (A) Descriptive statistics of global proteomics profiling of control samples. (B) A threshold for biological significance based on the variation of the biological system itself compared to an arbitrary threshold combats the dynamic range compression inherent in the chemical isobaric iTRAQ tagging used for quantitative analysis. Combined criterion based on expression fold changes and a p-value threshold will address the reduction in quantitative accuracy from precursor interference associated with iTRAQ labeling. (C) Normal distribution of global proteomic data is seen with this method.



Supplemental Figure S5. Venn diagram comparison of differentially expressed proteins following treatment of (A) HCT116 cells with siITGA3.1 or siITGA3.2 and (B) SW620 cells with siNOX4.1, siNOX4.2, or VAS2870. The differentially expressed proteins that were common among the treatment groups had to correspond in direction of change and meet the fold-change cutoff and p-value criteria.