Supplementary Table S3. Gene ontology analysis of pathways significantly regulated in SUM149PT cells ectopically expressing the EN1 cDNA using the DAVID database.

Term	RT	Count	%	P-Value	Benjamini
KEGG_PATHWAY	Cytokine-cytokine receptor interaction	11	9	3.80E-05	2.40E-03
KEGG_PATHWAY	Chemokine signaling pathway	6	4.9	1.80E-02	4.50E-01
KEGG_PATHWAY	Bladder cancer	3	2.5	4.70E-02	6.40E-01
KEGG_PATHWAY	Cell adhesion molecules (CAMs)	4	3.3	9.40E-02	8.00E-01

RT	Genes	Count	%	P-Value	Benjamini
GOTERM_MF_FAT	cytokine activity	11	9	6.80E-07	1.80E-04
GOTERM_MF_FAT	chemokine activity	5	4.1	2.50E-04	3.20E-02
GOTERM_MF_FAT	chemokine receptor binding	5	4.1	3.20E-04	2.70E-02
GOTERM_MF_FAT	glycosaminoglycan binding	5	4.1	1.40E-02	6.10E-01
GOTERM_MF_FAT	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amidines	3	2.5	1.80E-02	6.20E-01
GOTERM_MF_FAT	polysaccharide binding	5	4.1	2.00E-02	5.80E-01
GOTERM_MF_FAT	pattern binding	5	4.1	2.00E-02	5.80E-01
GOTERM_MF_FAT	growth factor activity	5	4.1	2.30E-02	5.80E-01
GOTERM_MF_FAT	carbohydrate binding	7	5.7	3.10E-02	6.50E-01
GOTERM_MF_FAT	heparin binding	4	3.3	3.20E-02	6.10E-01
GOTERM_MF_FAT	interleukin-1 receptor activity	2	1.6	4.60E-02	7.10E-01
GOTERM_MF_FAT	5'-nucleotidase activity	2	1.6	5.20E-02	7.20E-01
GOTERM_MF_FAT	hedgehog receptor activity	2	1.6	5.90E-02	7.30E-01
GOTERM_MF_FAT	nucleotidase activity	2	1.6	5.90E-02	7.30E-01
GOTERM_MF_FAT	interleukin-1 binding	2	1.6	6.50E-02	7.40E-01
GOTERM_MF_FAT	enzyme activator activity	6	4.9	7.40E-02	7.60E-01
GOTERM_MF_FAT	chloride channel activity	3	2.5	8.40E-02	7.80E-01
GOTERM_MF_FAT	chloride ion binding	3	2.5	9.40E-02	8.00E-01
GOTERM_MF_FAT	anion channel activity	3	2.5	9.60E-02	7.90E-01