

Table S1 Overrepresentation tests from RAGE knockdown in PANC-1 cells

PANTHER GO	Homo sapiens - REFLIST (21042)	Input (87)	Expected	Over/under	Fold Enrichment	P value	FDR
Biological Process							
Oxidative phosphorylation (GO:0006119)	47	4	0.19	+	20.58	5.78E-05	7.05E-03
Respiratory electron transport chain (GO:0022904)	107	4	0.44	+	9.04	1.15E-03	3.11E-02
RNA splicing, via transesterification reactions (GO:0000375)	156	5	0.64	+	7.75	5.39E-04	2.63E-02
mRNA splicing, via spliceosome (GO:0000398)	178	5	0.74	+	6.79	9.61E-04	2.93E-02
mRNA processing (GO:0006397)	244	6	1.01	+	5.95	5.86E-04	2.38E-02
Nucleobase-containing compound metabolic process (GO:0006139)	2797	23	11.56	+	1.99	1.22E-03	2.98E-02
Primary metabolic process (GO:0044238)	4753	39	19.65	+	1.98	4.45E-06	1.08E-03
Metabolic process (GO:0008152)	5878	42	24.3	+	1.73	6.17E-05	5.02E-03
Cellular process (GO:0009987)	8247	50	34.1	+	1.47	6.08E-04	2.12E-02
Unclassified (UNCLASSIFIED)	10206	26	42.2	-	0.62	5.24E-04	3.20E-02
Molecular Function							
Hydrogen ion transmembrane transporter activity (GO:0015078)	72	4	0.3	+	13.44	2.74E-04	1.32E-02
Oxidoreductase activity (GO:0016491)	503	12	2.08	+	5.77	1.31E-06	2.51E-04
RNA binding (GO:0003723)	385	7	1.59	+	4.4	1.17E-03	4.50E-02
Binding (GO:0005488)	4911	37	20.3	+	1.82	1.04E-04	9.95E-03
Unclassified (UNCLASSIFIED)	11852	31	49	-	0.63	1.27E-04	8.13E-03
Protein Class							
Oxidase (PC00175)	97	5	0.4	+	12.47	6.41E-05	3.45E-03
mRNA splicing factor (PC00148)	110	4	0.45	+	8.79	1.27E-03	4.54E-02
Reductase (PC00198)	114	4	0.47	+	8.49	1.44E-03	4.42E-02
Oxidoreductase (PC00176)	433	10	1.79	+	5.59	1.41E-05	1.01E-03
RNA binding protein (PC00031)	636	12	2.63	+	4.56	1.36E-05	1.46E-03
Nucleic acid binding (PC00171)	1585	20	6.55	+	3.05	6.21E-06	1.33E-03
Unclassified (UNCLASSIFIED)	12674	35	52.4	-	0.67	2.45E-04	1.06E-02

Table S2 PANTHER Reactome Pathways following RAGE knockdown in PANC-1 cells

Reactome pathways	Homo sapiens - REFLIST (21042)	Input (87)	Expected	Over/under	Fold Enrichment	P value	FDR
Eukaryotic Translation Termination (R-HSA-72764)	93	5	0.38	+	13	5.30E-05	1.05E-01
Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC) (R-HSA-975956)	95	5	0.39	+	12.73	5.83E-05	3.87E-02
Respiratory electron transport (R-HSA-611105)	97	5	0.4	+	12.47	6.41E-05	3.19E-02
SRP-dependent cotranslational protein targeting to membrane (R-HSA-1799339)	112	5	0.46	+	10.8	1.23E-04	4.89E-02
Nonsense-Mediated Decay (NMD) (R-HSA-927802)	113	5	0.47	+	10.7	1.28E-04	4.24E-02
Nonsense Mediated Decay (NMD) enhanced by the Exon Junction Complex (EJC) (R-HSA-975957)	113	5	0.47	+	10.7	1.28E-04	3.64E-02
Respiratory electron transport, ATP synthesis by chemiosmotic coupling, and heat production by uncoupling proteins (R-HSA-163200)	120	5	0.5	+	10.08	1.68E-04	4.17E-02
Translation (R-HSA-72766)	157	6	0.65	+	9.24	5.80E-05	5.77E-02

Table S3 Number of pathways observed with RAGE knockdown compared to scramble

Pathway	Down	Up
JAK/STAT signaling pathway	1	0
Apoptosis signaling pathway	1	1
Angiogenesis	1	0
Interleukin signaling pathway	1	0
Alzheimer disease-presenilin pathway	1	1
Interferon-gamma signaling pathway	1	0
Inflammation mediated by chemokine and cytokine signaling pathway	2	3
Ubiquitin proteasome pathway	2	0
Proline biosynthesis	1	0
p53 pathway feedback loops 2	2	0
EGF receptor signaling pathway	1	0
Parkinson disease	1	1
PDGF signaling pathway	1	0
Oxidative stress response	1	0
Ras Pathway	2	0
Cadherin signaling pathway	1	1
Heme biosynthesis	1	0
p53 pathway	2	0
Integrin signaling pathway	0	4
Pyridoxal-5-phosphate biosynthesis	0	1
Vitamin B6 metabolism	0	1
Huntington disease	0	3
Wnt signaling pathway	0	1
TCA cycle	0	1
Serine glycine biosynthesis	0	1
Cytoskeletal regulation by Rho GTPase	0	3
Nicotinic acetylcholine receptor signaling pathway	0	2
Fructose galactose metabolism	0	1

JAK/STAT, Janus kinase (JAK)-signal transducer and activator of transcription (STAT); EGF, Epithelial growth factor; PDGF, Platelet-derived growth factor; Ras, Rat sarcoma virus; Wnt, Wingless-related integration site; TCA, Tricarboxylic acid.