Supplemental Table 7: Enriched KEGG pathway annotations among the 4040 transcripts regulated in HaCaT cells upon I-125-dU incorporation.

Term	Count	%	P-Value	Benjamini
AXON GUIDANCE	37	1.2	2.50E-03	3.80E-01
VALINE, LEUCINE AND ISOLEUCINE DEGRADATION	19	0.6	2.70E-03	2.30E-01
LYSINE DEGRADATION	20	0.7	3.80E-03	2.20E-01
INSULIN SIGNALING PATHWAY	36	1.2	4.60E-03	2.00E-01
GAMMA-HEXACHLOROCYCLOHEXANE DEGRADATION	11	0.4	9.30E-03	3.00E-01
PHOSPHATIDYLINOSITOL SIGNALING SYSTEM	26	0.9	1.10E-02	3.00E-01
TGF-BETA SIGNALING PATHWAY	23	0.8	1.60E-02	3.60E-01
INOSITOL PHOSPHATE METABOLISM	20	0.7	1.70E-02	3.50E-01
APOPTOSIS	24	0.8	2.10E-02	3.60E-01
TRYPTOPHAN METABOLISM	23	0.8	2.30E-02	3.70E-01
LIMONENE AND PINENE DEGRADATION	11	0.4	2.50E-02	3.60E-01
MAPK SIGNALING PATHWAY	58	1.9	2.60E-02	3.50E-01
REGULATION OF ACTIN CYTOSKELETON	45	1.5	4.10E-02	4.70E-01
FC EPSILON RI SIGNALING PATHWAY	20	0.7	4.90E-02	5.00E-01
BUTANOATE METABOLISM	15	0.5	5.00E-02	4.90E-01
BETA-ALANINE METABOLISM	9	0.3	5.80E-02	5.10E-01
ASCORBATE AND ALDARATE METABOLISM	6	0.2	6.10E-02	5.10E-01
HISTIDINE METABOLISM	14	0.5	6.60E-02	5.20E-01
FOCAL ADHESION	44	1.5	8.20E-02	5.80E-01
ARACHIDONIC ACID METABOLISM	15	0.5	8.30E-02	5.70E-01
TOLL-LIKE RECEPTOR SIGNALING PATHWAY	22	0.7	8.40E-02	5.60E-01
GLUTAMATE METABOLISM	9	0.3	9.80E-02	6.00E-01
SELENOAMINO ACID METABOLISM	10	0.3	9.90E-02	5.90E-01