Supplemental Table 1. mRNA levels in tongue and distal intestine of mice.

Gene	Fold Regulation	
	Tongue	**Distal Intestine**
SREBP-2	1.5 ± 0.4	1.4 ± 0.2
HMGR	2.2 ± 0.6	1.5 ± 0.1
T2R102	0.6 ± 0.0	N.D.
T2R104	0.7 ± 0.0	0.7 ± 0.1
T2R105	0.4 ± 0.1	N.D.
T2R106	0.6 ± 0.0	N.D.
T2R107	0.7 ± 0.0	1.1 ± 0.3
T2R108	0.4 ± 0.1	N.D.
T2R109	0.3 ± 0.1	N.D.
T2R110	1.0 ± 0.1	N.D.
T2R113	0.3 ± 0.1	N.D.
T2R114	0.8 ± 0.1	N.D.
T2R115	N.D.	N.D.
T2R116	0.7 ± 0.0	N.D.
T2R117	0.6 ± 0.1	N.D.
T2R118	0.5 ± 0.1	N.D.
T2R119	0.8 ± 0.1	0.6 ± 0.1
T2R120	0.8 ± 0.1	N.D.
T2R121	0.4 ± 0.0	N.D.
T2R122	0.5 ± 0.1	N.D.
T2R123	0.6 ± 0.1	N.D.
T2R124	0.8 ± 0.0	N.D.
T2R125	0.6 ± 0.0	N.D.
T2R126	0.6 ± 0.1	1.4 ± 0.3
T2R129	0.6 ± 0.0	1.0 ± 0.3
T2R130	0.7 ± 0.2	N.D.
T2R131	0.6 ± 0.1	N.D.
T2R134	0.8 ± 0.2	N.D.
T2R135	0.5 ± 0.1	N.D.
T2R136	0.6 ± 0.0	N.D.
T2R137	0.7 ± 0.0	N.D.
T2R138	0.9 ± 0.0	N.D.
T2R139	0.5 ± 0.0	0.8 ± 0.2
T2R140	0.6 ± 0.0	N.D.
T2R143	0.5 ± 0.0	N.D.
T2R144	0.4 ± 0.1	N.D.

Supplemental Figure 1. mT2R138 promoter sequence.

-900 ACCACCACCA CCACCACCAT CTGTATTGAT CAGGCTCTAG AGAGCCTCT
-850 CAGGGGACAG CTATACCAGA CTCCTGTCAG CAAGTGCTTC TGGCATCAG
                                              SRE2
-800 CAATAGTGTC TGAGTTTGGT GGCTG**CATGT GGGATGAATC CCAGGTGGG**
-750 GCAGTATCTG GATGGCCTGT CCTTCAGTCT CTGCTCTACT CATTGTCCCT
-700 GGATCTCCTT TAGACAGGAG CAATTCTGGA TTAAAAATTT TTGAATGAGT
                                          NF-Y
-650 GGGTAGCCCC CTTCCTCAAC TGGGGTCTAG GCTATGTAGA TGG**ATTGG**C
-600 TGTACATTAT GGAGGGTAAG GATTAAGACT TCTTGGATAG AACAGTCAC
-550 CTAATCATAT TAAAGTATAT TTATAGTAGG TGAGGCCTCA GTTGTGAAAT
-500 GAGAAATGCA AATGTGAAGA GACCCCATTT CAAAGCCTAA TCACTTACA
-450 GCATCTGTTT TGCCTACAGG CAGTGTCCCT GGGCCCATAA CAAATCCTC
-400 CTCTTCTCTG TGCATACAAG TCCATGTGGG CATGTAAAAC AGACCCTGC
-350 CTGGTTAGGG AACTGAAACT CAATCTTGTT TACATTCCTG TTGCTGCAAT
                 Sp1
-300 ATGACTG**GGG GTGGGG**CTGT TGGGTAGGTA ACACCTGGAT TATTAAAGC
-250 TTTTGCATCA TCCAAGAGGT AGGCCGATCA TTACTCCTCC CTTACCATAA
-200 GCTTTCGTGC CAAATCACAA GATACTGTAA AGTGACAACA CCCCTCCAG
               NF-Y
-150 GTTTCCT**ATT GG**GGATTTGG GTTCATAAGG GGAAATTCTG GCAAGATTT
-100 GGAATCCTTG CGAAGGAAAG CTCTCCATTC AAAAGATACC CTTTCCTGCT
 -50 CTGGTGGGTG AAATCGGAGT TTTAGATTAG TTAATCAGAG AAGGGCATC
  +1 ATGCTGAGTC