**Supplementary table 1 RNA expression level of genes in multiple transcriptome datasets**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Mouse DRG neuron (Usoskin D, et al. 2015) | Human DRG tissue  (Flegel C, et al. 2015) | Mouse TG neuron  (Lopes DM, et al. 2017) | Human TG tissue  (Flegel C, et al. 2015) |
|  | Normalized mean RPM | Normalized mean FPKM | Normalized mean FPKM | Normalized mean FPKM |
| *CACNA1D* | 64.72007161 | 0.700975257 | 0.150168784 | 0.708819467 |
| *KCNC3* | 124.6112206 | 0.542891422 | 0.922562008 | 0.527374613 |
| *KCND2* | 18.80736621 | 0.106868365 | 0.088061475 | 0.032271345 |
| *KCNH2* | 248.4659451 | 12.21456404 | 1.407409256 | 6.663263383 |
| *TRPM8* | 33.24266245 | 1.087603349 | 5.415630672 | 1.223017589 |
| *GAPDH* | 1000 | 1000 | 1000 | 1000 |

Note: all values are normalized by the housekeeping gene (GAPDH). RPM: Reads Per Million; FPKM: Fragments Per Kilobase Million.

**Supplementary Fig. 1**

A B

 

**Effect of co-expression of wild-type TRPM8 and R30Q mutant channels in HEK293 cells. A**) Average increase in Fura-2 ratio in response to Menthol (100 M) in wild-type TRPM8 and wild-type TRPM8+R30Q (1:1) transfected cells (n=8 cells, 2 transfections). \*P<0.05, unpaired Student’s t test. **B**) Basal Fura-2 ratio, in wild-type TRPM8 and wild-type TRPM8+R30Q (1:1) transfected cells (n=8 cells, 2 transfections). \*P<0.05, unpaired Student’s t test.