



Figure 2 – figure supplement 2. Comparison with previously published BLA scRNA-seq data.

A. t-SNE visualization of scRNA-seq from (Zeisel et al., 2018) excitatory basolateral amygdala neurons ("TEGLU22"). Example enriched genes listed, which tend to correlate with cell health (e.g., *Malat1*, *mt-Atp6*) or with neuronal populations outside of the BLA (e.g., *Zbtb20*, *Strip2*; see panels C-Q). B. As in (A), but for projection onto first two principal components. C. Expression of *Kcng1*, a marker restriction to the BLA, in the Allen Mouse Brain Atlas (AMBA) (Lein et al., 2007). D. Expression of *Kcng1* in the TEGLU22 scRNA-seq dataset. Most cells (76%) do not express this BLA marker. E. Expression of *Kcng1* in the dataset of our manuscript. Most cells (86%) express this BLA marker. F-H. As in (C-E), but for the LA marker *Negr1*. I-K. As in (C-E), but for the BA marker *Cplx1*. L-N. As in (C-E), but for the TEGLU22 marker *Strip2*, which is expressed outside the BLA. O-Q. As in (L-N), but for *Zbtb20*.