



**Figure 6 - figure supplement 3. Interneuron subtypes resolved by scRNA-seq and chromogenic ISH.**

A. t-SNE visualization of 51 interneurons, colored according to cluster identity. Inset numeric values denote number of enriched genes in each cluster, relative to the other interneuron cluster. Inset t-SNE visualization shows expression of interneuron marker *Gad1*. B. Examples of novel interneuron cluster-enriched genes obtained from scRNA-seq. C. Summary of all genes differentially expressed between the two interneuron clusters. Functional categories include calcium handling (*Hpcal*, *Wfs1*), synapses (*Gabra1*, *Cplx1*, *Syt5*), and regulation of transcription (*Tshz1*). D. Chromogenic ISH images for differentially expressed genes. Genes enriched in Int1 show diffuse spatial patterning across the BLA and absence of labeling of intercalated region. Genes enriched in Int2, conversely, show dense expression in the capsular region. Scale bar: 300  $\mu$ m.