

Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: List of differentially expressed genes from comparative analysis of RNA-seq samples, the comparisons are indicated in the worksheet titles.

File Name: Supplementary Data 2

Description: List of differentially expressed genes associated with clusters generated from 10X Genomics C-Loupe analysis of control tongue scRNA-seq datasets.

File Name: Supplementary Data 3

Description: List of 100 genes/probes that were added (custom add-on 100 probes worksheet) to the Xenium Mouse Brain panel (248 probes) – used in all subsequent spatial transcriptomic analyses.

File Name: Supplementary Data 4

Description: List of genes associated with each cell type annotation – generated from analysis of Xenium datasets from control tongue samples.

File Name: Supplementary Data 5

Description: ScRNA-seq data expressed as CPM generated from tongue tumours (tSRC1-3) and controls (Tongue1 and 2).

File Name: Supplementary Data 6

Description: List of genes associated with each cell type annotation – generated from analysis of Xenium datasets from tongue SyS tumours.

File Name: Supplementary Data 7

Description: List of differentially expressed genes from analysis of scRNA-seq datasets derived from stifle and tongue tumours along with controls (i.e., tongue and skeletal muscle).

File Name: Supplementary Data 8

Description: List of differentially expressed genes from analysis of stifle tumours and skeletal muscle scRNA-seq datasets.

File Name: Supplementary Data 9

Description: List of genes associated with each cell type annotation – generated from analysis of Xenium datasets from stifle SyS tumours.

File Name: Supplementary Data 10

Description: List of genes associated with each cell type annotation – generated from integrated analysis of Xenium datasets from tongue and stifle SyS tumours.

File Name: Supplementary Data 11

Description: Differential expression analysis of tumours from WNT/ β -catenin activated background, generated through 10X Genomics C-Loupe.

File Name: Supplementary Data 12

Description: ScRNA-seq data expressed as CPM, additional worksheets contain lists of SAT, MAT, SST and Hox genes.