

**Table S8. Inventory of datasets deposited at external repositories.**

| <b>Data</b>                                    | <b>Repository</b>                | <b>Link</b>                                                                                                                                                                   | <b>Description</b>                                                                                                                                                                     |
|------------------------------------------------|----------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| snRNA-seq count tables                         | GEO,<br>GSE239854                | <a href="https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE239854">https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE239854</a>                                       | Data for samples MB266, MB295, MB299 from ref. [1].                                                                                                                                    |
| MC transcript count tables                     | GEO,<br>GSE247736                | <a href="https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE247736">https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE247736</a>                                       | Data for samples MB263, MB266, MB295, MB299 from ref. [1]                                                                                                                              |
| RNAscope                                       | BiolImage Archive,<br>S-BIAD826  | <a href="https://www.ebi.ac.uk/bio-studies/bioimages/studies/S-BIAD826">https://www.ebi.ac.uk/bio-studies/bioimages/studies/S-BIAD826</a>                                     | Raw and processed data from ref. [1]                                                                                                                                                   |
| MC (Molecular Cartography)                     | BiolImage Archive,<br>S-BIAD825  | <a href="https://www.ebi.ac.uk/bio-studies/bioimages/studies/S-BIAD825?query=S-BIAD825">https://www.ebi.ac.uk/bio-studies/bioimages/studies/S-BIAD825?query=S-BIAD825</a>     | Raw and processed data for samples MB263, MB266, MB295, MB299 from ref. [1]                                                                                                            |
| Visium                                         | Zenodo                           | <a href="https://doi.org/10.5281/zenodo.10863259">https://doi.org/10.5281/zenodo.10863259</a>                                                                                 | Raw and filtered feature bc matrix and spatial data for samples MB263, MB266, MB295, MB299, this study.                                                                                |
| MC (additional data), Merscope, Xenium         | BiolImage Archive,<br>S-BIAD1093 | <a href="https://www.ebi.ac.uk/bio-studies/bioimages/studies/S-BIAD1093?query=S-BIAD1093">https://www.ebi.ac.uk/bio-studies/bioimages/studies/S-BIAD1093?query=S-BIAD1093</a> | Raw and processed data for samples MB263, MB266, MB295, MB299, this study.                                                                                                             |
| Seurat objects for cell-based analysis         | Zenodo                           | <a href="https://doi.org/10.5281/zenodo.10863259">https://doi.org/10.5281/zenodo.10863259</a>                                                                                 | Seurat objects for cell-based analysis of shared set of 96 genes for snRNA-seq, Merscope, MC and Xenium for and for shared set of 10 genes when including RNAscope, this study.        |
| Seurat objects for segmentation-free analysis  | Zenodo                           | <a href="https://doi.org/10.5281/zenodo.10863259">https://doi.org/10.5281/zenodo.10863259</a>                                                                                 | Seurat objects for segmentation-free analysis of shared set of 96 genes for snRNA-seq, Merscope, MC and Xenium for and for shared set of 10 genes when including RNAscope, this study. |
| Data for image analysis with fluorescent beads | Zenodo                           | <a href="https://doi.org/10.5281/zenodo.10863259">https://doi.org/10.5281/zenodo.10863259</a>                                                                                 | Data associated with the FWHM, signal-tonoise and signal-to-background analysis                                                                                                        |