Table 1. Metadata from the 5 different sc/snRNA datasets analyzed in this study.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Study** | **Number of Cells** | **Number of Donors** | **Number of Samples** | **Donor Age Range** | **Donor Sex** | | | **Sampling Locations** | | | | **Method** | |
|  |  |  |  |  | **M** | **F** | **Not Reported** | **Cortex** | **Medulla** | **Both** | **Unknown/Other** |  |
| Menon et al. | 22,264 | 22 | 24 | <50 = 2  ≥50 = 13  Unknown = 7 | 7 | 6 | 9 | NA | NA | NA | 24 | (sc) 10X |
| Young et al. | 6,179 | 5 | 17 | 49-72 | 3 | 2 | 0 | 14 | 0 | 1 | 2 | (sc) 10X |
| Liao et al. | 16,145 | 2 | 2 | 59-65 | 1 | 1 | 0 | NA | NA | NA | 2 | (sc) 10X |
| Wu et al. | 4,432 | 1 | 4 | 21 | 1 | 0 | 0 | NA | NA | NA | 4 | (sc) InDrops |
| Lake et al. | 13,255 | 14 | 35 | <50 = 4  ≥50 = 7  Unknown = 3 | 10 | 4 | 0 | 15 | 14 | 6 | 0 | (sn) Drop\_Seq |
| **Total** | 62,275 | 40 | 82 |  | 22 | 13 | 9 | 29 | 14 | 7 | 32 |  |