Table 4

| | EM | PL | ES | TS | Any tissue | All tissues |
|------------------------|---------|---------|---------|---------|------------|-------------|
| mRNAs/cell | 851,087 | 519,688 | 400,045 | 568,196 | | |
| Features ≥ I CpC | 13,718 | 10,559 | 9,667 | 9,840 | 14,908 | 8,073 |
| U-clusters ≥ I CpC | 11,360 | 8,828 | 8,101 | 8,271 | 12,264 | 6,838 |
| Transcripts ≥ I CpC | 11,762 | 9,108 | 8,357 | 8,534 | 12,739 | 7,037 |
| Mean copies per cell | 1.09 | 0.63 | 0.51 | 0.56 | | |
| Median copies per cell | 0.79 | 0.45 | 0.36 | 0.40 | | |

U-clusters and transcripts from the NIA mouse gene index were considered expressed if microarray features measured absolute expression estimated at one copy per cell or more. Copy-number estimates from expressed transcripts were summed to estimate the number of mRNA molecules per cell for each tissue, as well as the mean and median copy numbers. Microarray features corresponding to expressed genes and transcripts were mapped to the NIA Gene Index to calculate the number of U-clusters (loci) and transcripts expressed in each tissue.