| Dataset | Quintile 1 (lowest 20\%) | Quintile 2 | Quintile 3 | Quintile 4 | Quintile 5 (highest 20\%) |
| :---: | :---: | :---: | :---: | :---: | :---: |
| SMARTseq dispersion | $\begin{gathered} \text { mean: } 2.05 \\ \text { median: } 1.606 \end{gathered}$ | mean: 0.984 <br> median: 0.66 | mean: 0.465 median: 0.304 | $\begin{gathered} \text { mean: } 0.277 \\ \text { median: } 0.181 \end{gathered}$ | $\begin{gathered} \text { mean: } 0.204 \\ \text { median: } 0.134 \end{gathered}$ |
| SoLo dispersion | $\begin{gathered} \text { mean: } 0.686 \\ \text { median: } 0.369 \end{gathered}$ | $\begin{gathered} \text { mean: } 0.367 \\ \text { median: } 0.160 \end{gathered}$ | $\begin{gathered} \text { mean: } 0.169 \\ \text { median: } 0.081 \end{gathered}$ | $\begin{gathered} \text { mean: } 0.104 \\ \text { median: } 0.058 \end{gathered}$ | $\begin{gathered} \text { mean: } 0.092 \\ \text { median: } 0.056 \end{gathered}$ |
| SMARTseq normalized confidence interval size | mean: 2.469 median: 2.417 | $\begin{gathered} \text { mean: } 1.876 \\ \text { median: } 1.900 \end{gathered}$ | $\begin{gathered} \text { mean: } 1.369 \\ \text { median: } 1.236 \end{gathered}$ | $\begin{gathered} \text { mean: } 1.053 \\ \text { median: } 0.901 \end{gathered}$ | $\begin{gathered} \text { mean: } 0.841 \\ \text { median: } 0.677 \end{gathered}$ |
| SoLo normalized confidence interval size | $\begin{gathered} \text { mean: } 2.043 \\ \text { median: } 1.995 \end{gathered}$ | $\begin{gathered} \text { mean: } 1.426 \\ \text { median: } 1.270 \end{gathered}$ | $\begin{gathered} \text { mean: } 0.966 \\ \text { median: } 0.776 \end{gathered}$ | $\begin{gathered} \text { mean: } 0.713 \\ \text { median: } 0.573 \end{gathered}$ | $\begin{gathered} \text { mean: } 0.630 \\ \text { median: } 0.503 \end{gathered}$ |

Table S2: Mean and Median variance in each quintile of gene expression

