Malte D Luecken & Fabian J Theis

Expanded View Figures

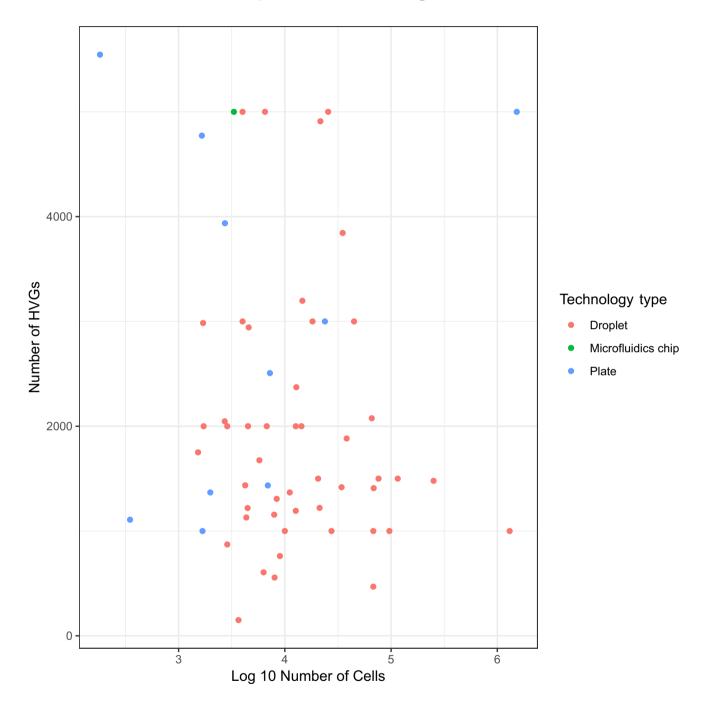
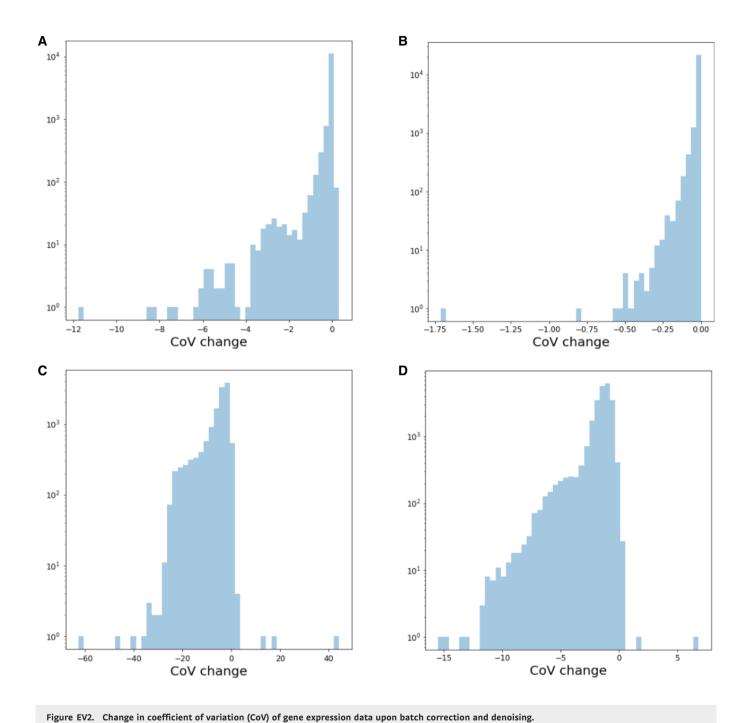


Figure EV1. The number of highly variable genes (HVGs) used for datasets of different sizes.

The data were obtained by a brief manual survey of recent scRNA-seq analysis papers. The plotted data, along with further information on scRNA-seq technology, publication year, reference and the number of reads per cell, are available in Dataset EV1.



Negative values represent a reduction in CoV upon data correction. The top row shows CoV changes upon ComBat batch correction for (A) mouse intestinal epithelium (mIE) and (B) mouse embryonic stem cell (mESC) data. The lower row depicts CoV changes upon DCA denoising for (C) mIE and (D) mESC data. mIE data were obtained from Haber et al (2017) and mESC from Klein et al (2015).