

S1 Text. Normalisation methods. We applied different combinations of normalization methods to get phenotypes that are comparable between the studies. In summary, we used the following methods for normalization:

- **Logarithm.** Compute the natural logarithm over every well-readout separately, such that a well's new readout y_{ij} is computed as $y_{ij}^{\text{norm}} = \log(y_{ij})$.
- **Background correction.** Subtract the mean/median of a row/column from every well of every plate separately.
- **Robust Z-scores.** Subtract by median and divide by median absolute deviation over every plate separately. The new readout is computed as $y_{ij}^{\text{norm}} = \frac{y_{ij} - \text{med}(\mathbf{Y})}{\text{mad}(\mathbf{Y})}$, where $\text{med}(\mathbf{Y})$ is the median of plate readouts and $\text{mad}(\mathbf{Y})$ is the median absolute deviation of plate readouts.
- **Loess.** Fits a locally-weighted polynomial regression model between well cell counts x_i and averaged well readout y_i separately on every plate using R's `lowess` function. The procedure estimates a new readout \hat{y}_i for every cell counts covariable x . The new normalized value is computed as $y_i^{\text{norm}} = y_i - \hat{y}_i$, i.e. the residual.
- **B-scores.** B-scores are computed using R's `medpolish` function on every plate separately. Input to `medpolish` is a matrix \mathbf{Y} where every element y_{ij} is the readout from the i -th row and j -th column from a plate. The new normalized value per row and column is computed as $y_{ij}^{\text{norm}} = \frac{r_{ij}}{\text{mad}(\mathbf{R})}$, where \mathbf{R} are the computed residuals for every well ij and $\text{mad}(\mathbf{R})$ is the median absolute deviation of the residuals.

The implementation of the described methods can be found in Supplement S1 Code.