Accurate, flexible and low-cost method for normalizing Seahorse XF data to cell number

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There are many sources of stochastic noise in XF measurements and the unequal number of cellsin wells is a major one. A number of normalisation methods have been introduced including total cellular DNA or protein assays and cell counting using high-throughput plate readers. We present a low-cost microscopy-based cell counting method, which allows flexibly to choose areas of interest in relation to sensor response to limit data variability.