



**Figure 1 | Reproducibility of unbiased, global mRNA amplification of mouse cardiomyocytes.** **a**, Typical morphology of cardiomyocytes after enzymatic dissociation. Original magnification,  $\times 400$ . **b**, Schematic representation of the strategy to validate cell-to-cell variation in gene expression as compared with the experimental variation in repeated global mRNA amplification. The single-cell equivalents were made from a pool of lysed cardiomyocytes. Fifteen single cells and ten single-cell equivalents were separately subjected

to mRNA isolation, reverse transcription and global cDNA amplification. **c**, Relative expression of the *Myl2* gene (over *COX1*). Significantly increased variability was observed among the single cells as compared with the single-cell equivalents ( $P = 0.0026$ ). Boxes in the box plots indicate the interquartile range (IQR) with the median; the whiskers indicate  $1.5\times$  the IQR.