Correlation analysis between the differential expression fold-change (FC), and the number of CAG repeats, indicates a strong inverse relationship between glial gene expression and the CAG repeat number. A, Expression heat map based on transcripts per million (TPM) values calculated from raw counts of 429 differentially expressed genes (DEGs) (1% FDR, FC>2.0) found in the intersection of DEGs by comparisons of hGPCs derived from each of the three different HD patients against pooled control hGPCs from two different donors. Row side colors show the Pearson’s R correlation coefficient between fold change of that gene in each HD-derived hGPC line against pooled controls and the corresponding CAG repeat number in that HD line (HD17 = 40x CAG, HD18 = 46x CAG, and HD20 = 48x CAG). Selected genes encoding transcription factors and stage-regulated proteins involved in glial differentiation and myelination are listed. B, Combined scatterplot with linear fit lines, obtained by regression of fold-changes of each of the 429 DEGs shown in heat map in A, against the CAG repeat number in the corresponding hGPC line. C, Histogram showing the distribution of Pearson’s R coefficients for correlation between fold changes of DEGs in 3 HD lines, to corresponding CAG length. For 255 of the 429 genes (|Pearson’s R| > 0.75), the correlation analysis indicated that the absolute magnitude of the fold-change increased with CAG repeat number; 228 of these genes displayed an inverse correlation of gene expression level to the CAG repeat number, with longer repeats associated with diminished glial gene expression.