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**Figure S2.** WGCNA for CS group. **(a)** The dataset was fit to a scale-free model of proposed values for β ranging from 1 to 35 (numbers inside the plots). Left panel shows that approximate scale-free topology is attained around soft-thresholding power of 16. The right plot shows the mean connectivity along with the soft-thresholding power. **(b)** Gene co-expression dendrogram and module identification. **(c)** Module-trait correlation with time-intervals. In the rows, MEs are named by their module colors. In the column it is shown the trait of interest (time-interval: CS\_0h, T0; CS\_1h, T1; CS\_2h, T2). Numbers inside each colored box are the correlation coefficients (MS) between the ME and the specific trait, with p-value between brackets. The more intense the color of the box, the more negatively (green) or positively (red) correlated is the module with the trait. \* indicates the module highly correlated with the time-interval (MS < 0.85, p < 5e04).