Supplemental information

Emergence of rich-club topology and coordinated dynamics in development of hippocampal functional networks in vitro

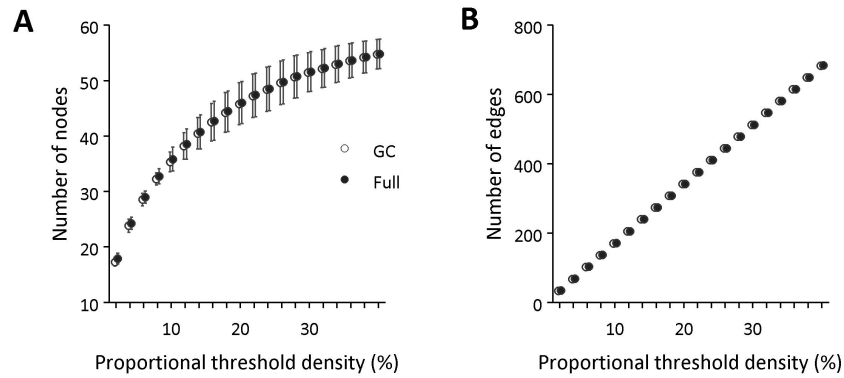by Schröter et al., 2015 (under review)

Supplemental information for Schröter et al. (under review), "Emergence of rich-club topology and coordinated dynamics in development of hippocampal functional networks in vitro"

Figure S1 Consistency analysis across range of thresholds. (A-B) The number of edges and nodes (with degree >=1) between the largest connected component (GC) and the overall network (Full) were very similar across the range of proportional thresholds used (2-40% density); values represent mean ± standard deviation (n = 10 cultures, D28).
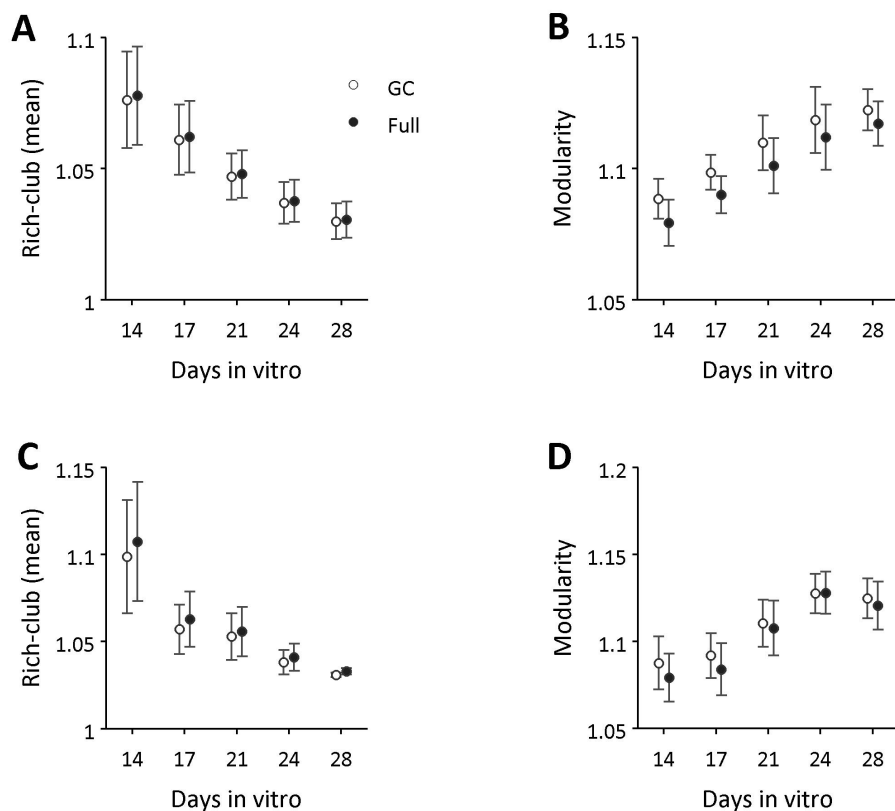
Figure S2 Consistency analysis for topological metrics. (A-B) Rich-club and modularity metrics calculated on the largest connected component (GC) and the overall network (Full) were highly consistent. Results are depicted for the proportional thresholding scheme (Fig.S2*A-B*) and a single absolute threshold (median + 1.5SD; Fig.S2*C-D*). Values represent mean ± standard error of the mean (*n* = 6 cultures).
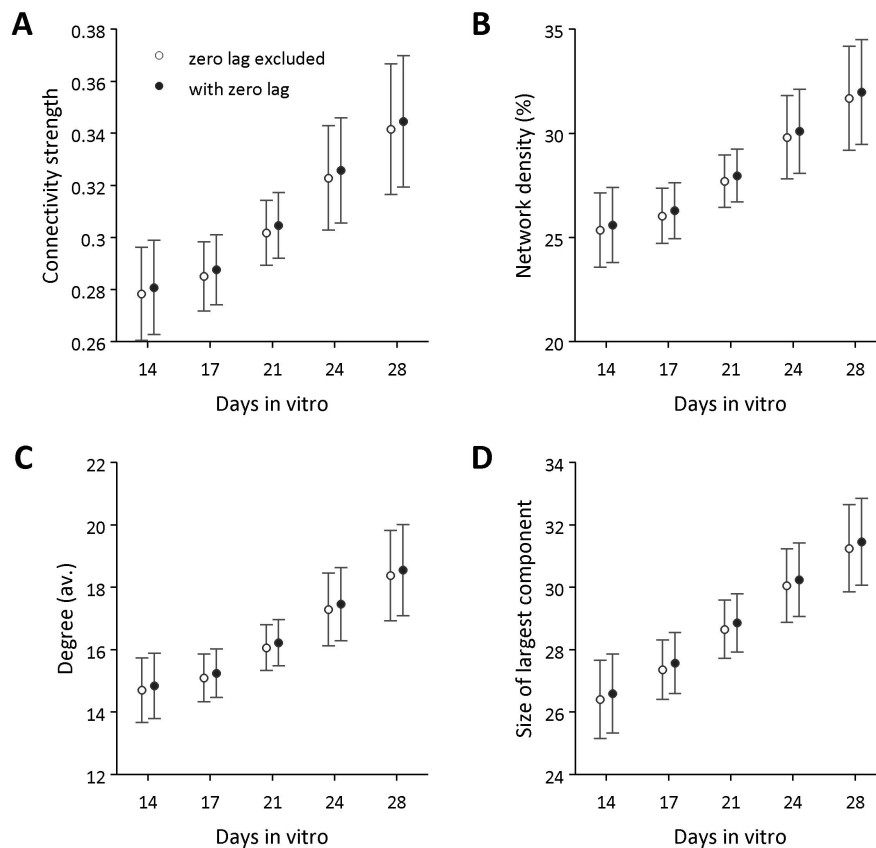
Figure S3 Comparison of cross-covariance estimates with (without) zero-lag. Basic connectivity metrics (connectivity strength, density, degree and size of largest component) calculated on MUA functional connectivity matrices with not zero-lag were very similar to results with with zero-lag included. Results are depicted over developmental time and for the absolute thresholding scheme (averaged over 0.05-1 threshold weights). Values represent mean ± standard error of the mean (n = 6 cultures).