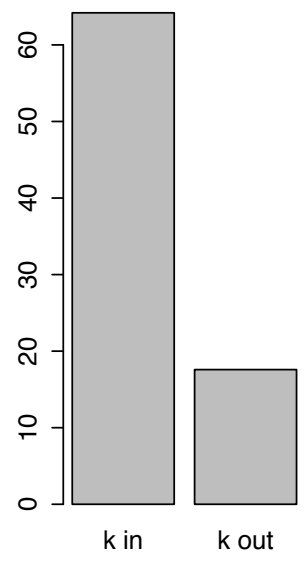
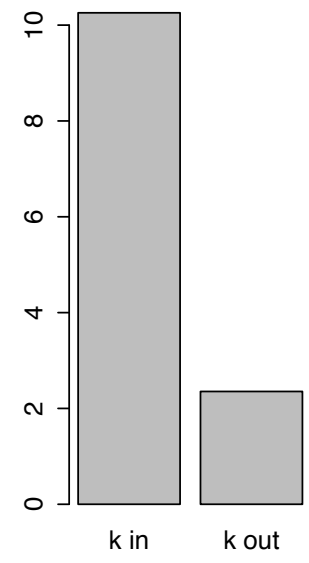


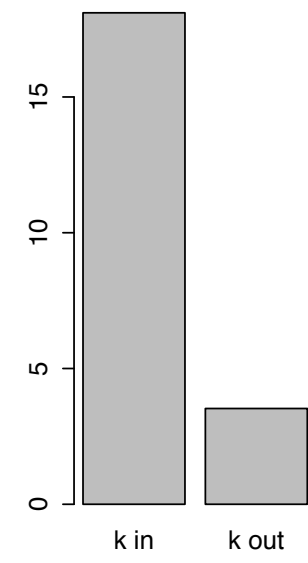
black



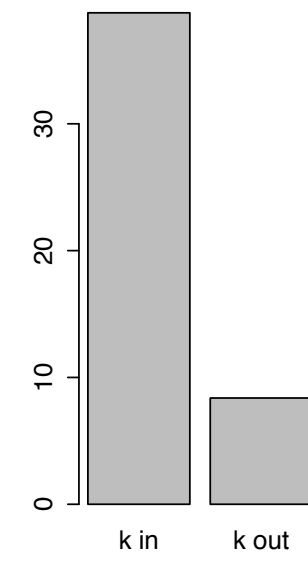
darkred



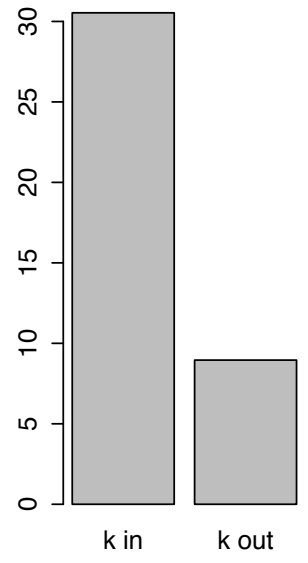
lightcyan



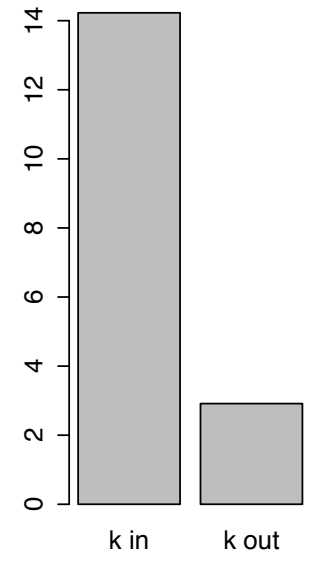
magenta



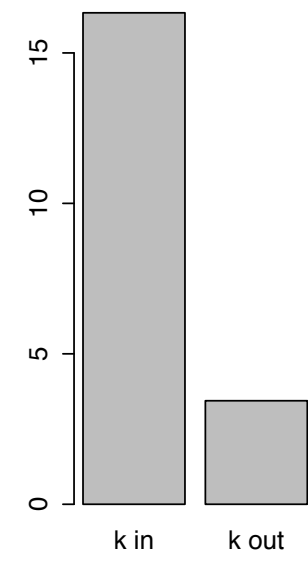
purple



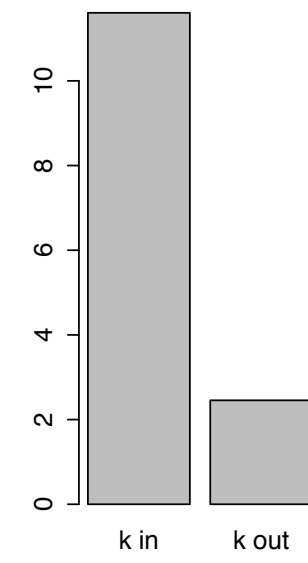
lightgreen



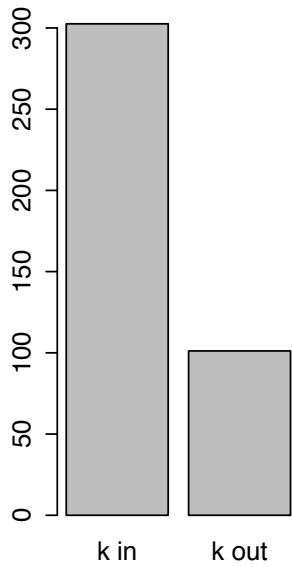
grey60



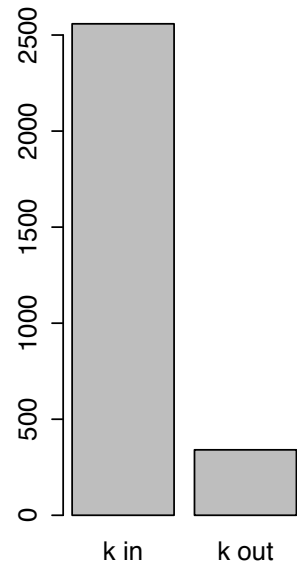
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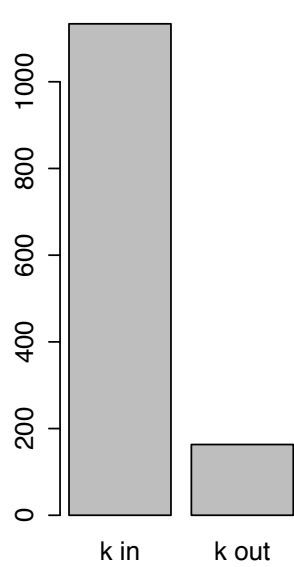
brown



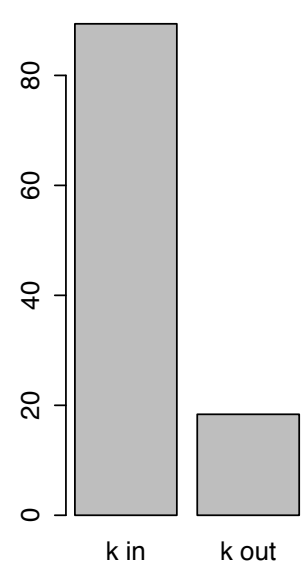
turquoise



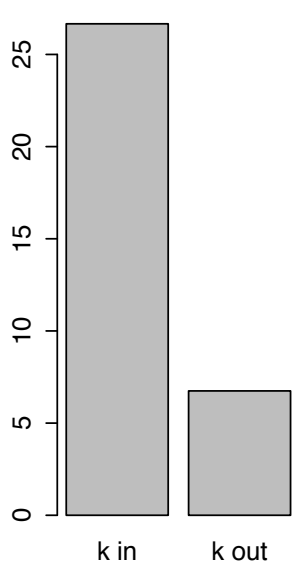
blue



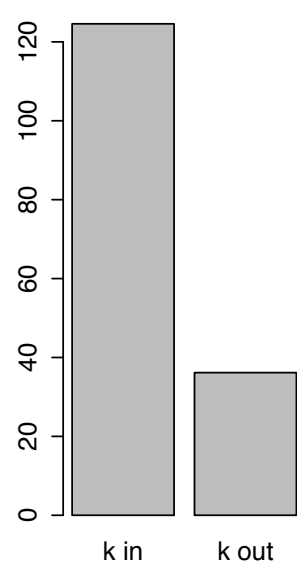
greenyellow



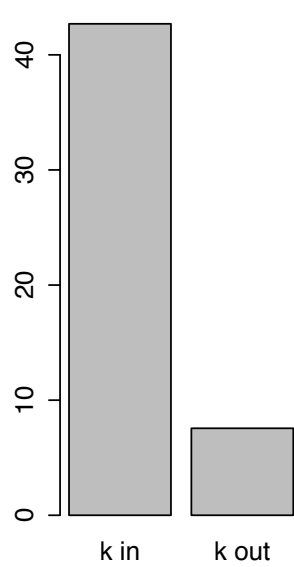
tan



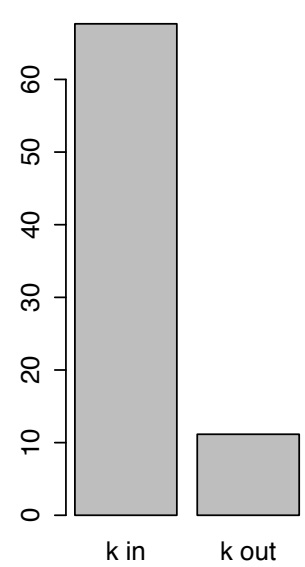
yellow



cyan



green



The figures depict the scaled intramodular connectivity (k_{in}) compared to the scaled intermodular connectivity (k_{out}) for each of the sixteen modules. Both “ k_{in} ” and “ k_{out} ” are summations of each gene’s scaled connectivity in each module. Connectivity scores were generated using the `intramodularConnectivity` function in the WGCNA package. Intramodular connectivity scores were scaled by the number of genes in the module, and intermodular connectivity scores were scaled by the number of genes not in the module. In each module, scaled intramodular connectivity is higher compared to scaled intermodular connectivity. Note that the y-axes are different scales.