Can one extend the above ideas beyond binary trees?

Earlier work in our group showed that the Haar-like wavelets associated with a large binary tree can significantly sparsify its phylogenetic covariance matrix with high probability. This paper shows that the same effect can be achieved on k-regular trees, i.e., trees where each interior node has k children. We accomplish this using generating functions to estimate the asymptotic expected value and variance of the internal path length of a uniformly random k-regular tree, which imply a lower bound on the number of non-zero entries in the phylogenetic covariance matrix after changing the basis to its Haar-like wavelets.