

Table S2: Comparison matrix of available tools for functional prediction based on co-expression correlations

| Tool                 | Functional Prediction Method                                                                   | Tissue-specific | Disease-specific | Analysis Types                                                                            | Results presentation                                                 | Implementation                 | Publication                                          |
|----------------------|------------------------------------------------------------------------------------------------|-----------------|------------------|-------------------------------------------------------------------------------------------|----------------------------------------------------------------------|--------------------------------|------------------------------------------------------|
| COXPRESdb            | Over-representation analysis (ORA) from top 50 co-expressed genes                              | No              | No               | Single gene prediction; Gene comparison                                                   | Static results tables with minimal support for static visualizations | Web application; API           | Obayashi et al. 2008 [10]; Obayashi et al. 2019 [24] |
| GeneFriends          | ORA from top 5% of co-expressed genes                                                          | No              | No               | Single gene prediction                                                                    | Static tables with an option to export a network to Biolayout        | Web application                | van Dam et al. 2015 [11]                             |
| GeneMANIA            | ORA from co-expression and protein interaction network                                         | No              | No               | Single gene prediction                                                                    | Interactive network with summary tables                              | Web application; Cytoscape app | Franz et al. 2018 [12]                               |
| GIANT                | ORA from co-expression, protein interaction, gene-set co-membership, and TF binding prediction | Yes             | No               | Single gene prediction; Gene comparison; Network comparison                               | Interactive network and heatmaps with summary tables                 | Web application; API           | Wong et al. 2018 [13]                                |
| ARCHS4               | Gene sets ranked by mean correlation of member genes                                           | No              | No               | Single gene prediction                                                                    | Summary tables of top enrichment results                             | Web application; API           | Lachmann et al. 2018 [14]                            |
| Correlation AnalyzeR | GSEA of genome-wide correlation values (corGSEA)                                               | Yes             | Yes              | Single gene prediction; Gene comparison; Gene vs Gene list comparison; Gene list topology | Summary tables with interactive gene-level and pathway-level plots   | Web application; R package     | This article.                                        |