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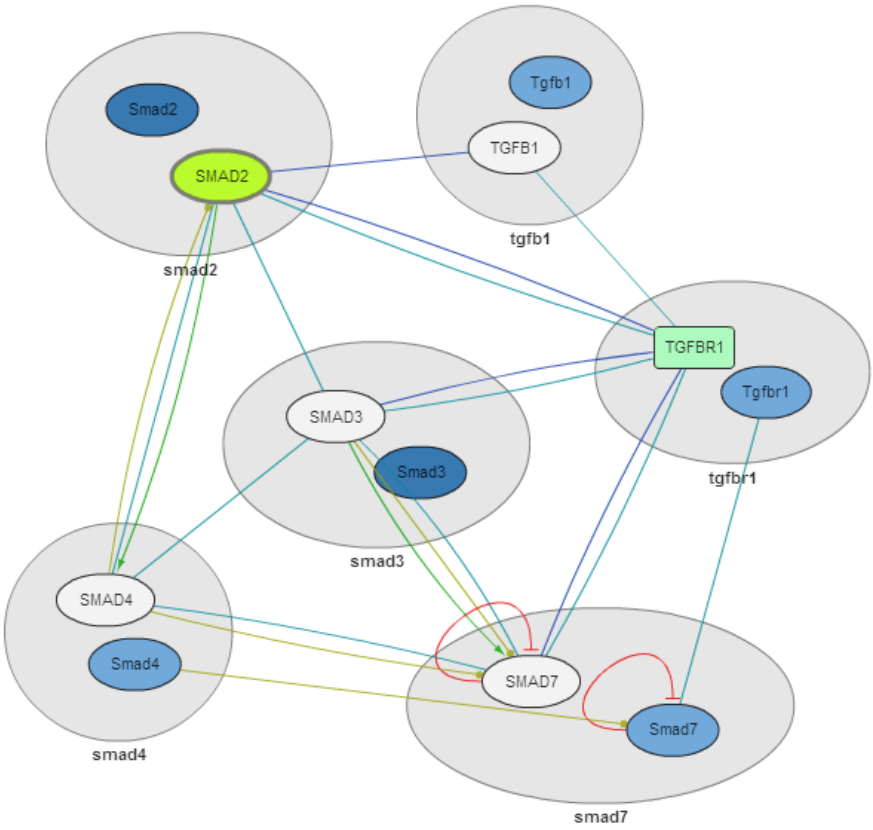
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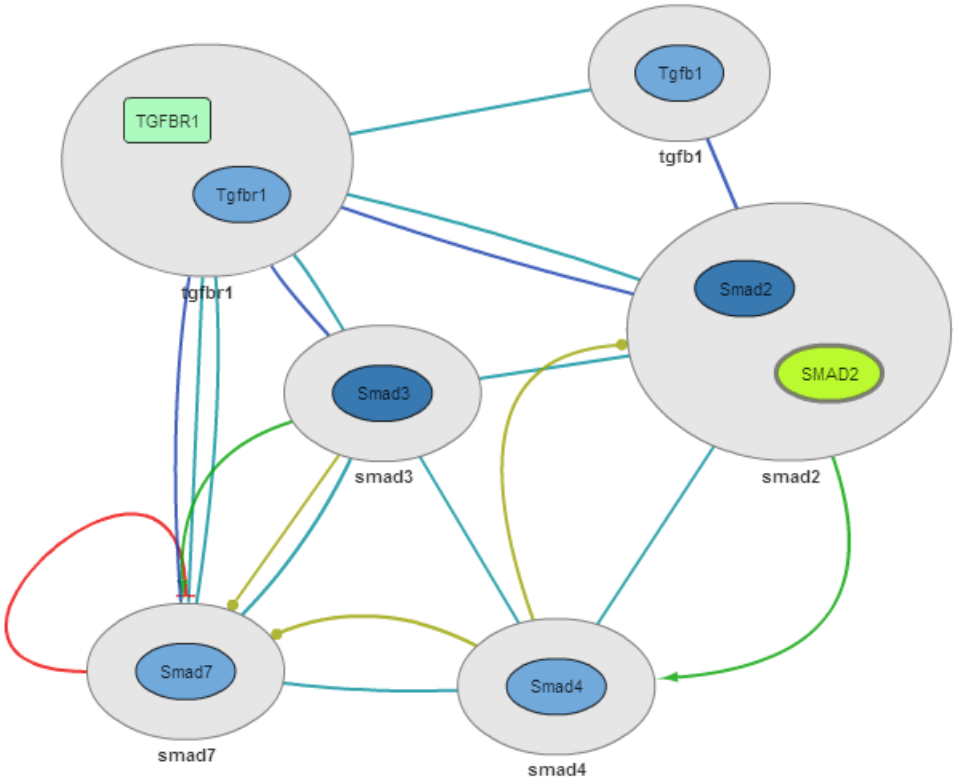
B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Smad7
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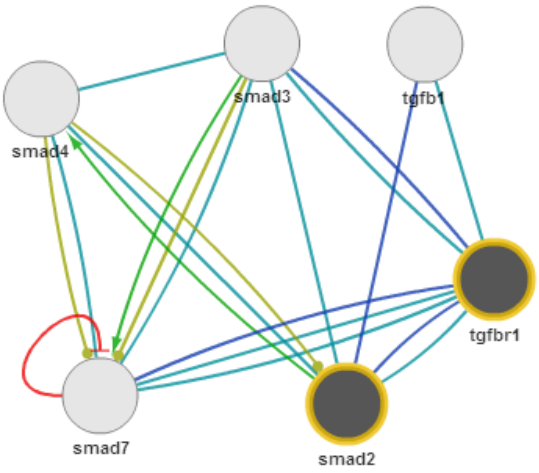
Smad4
smad4

C



Supplemental figure 1: Example of multi-species view in the KUPNetViz.
Orthologous genes are represented as compound nodes (‘supergenes’) in two possible ways: either as compound nodes encompassing single organism orthologs (A) or as simple compound nodes with hidden orthologs to reduce the complexity of the snapshot (B, C). In the first case (A), gene-to-gene relationships are organism specific while in the second case they are depicted as supergene-to-supergene relationships (‘superedges’, B, C). In the case of colored or multiple-colored nodes based on KUPKB expression data mapping to the network, the complexity can be further reduced by collapsing the colored nodes to a single colored node (C), when working in multi-species mode.