Pathfinder: Visual Analysis of Paths in Graphs

Supplementary Material

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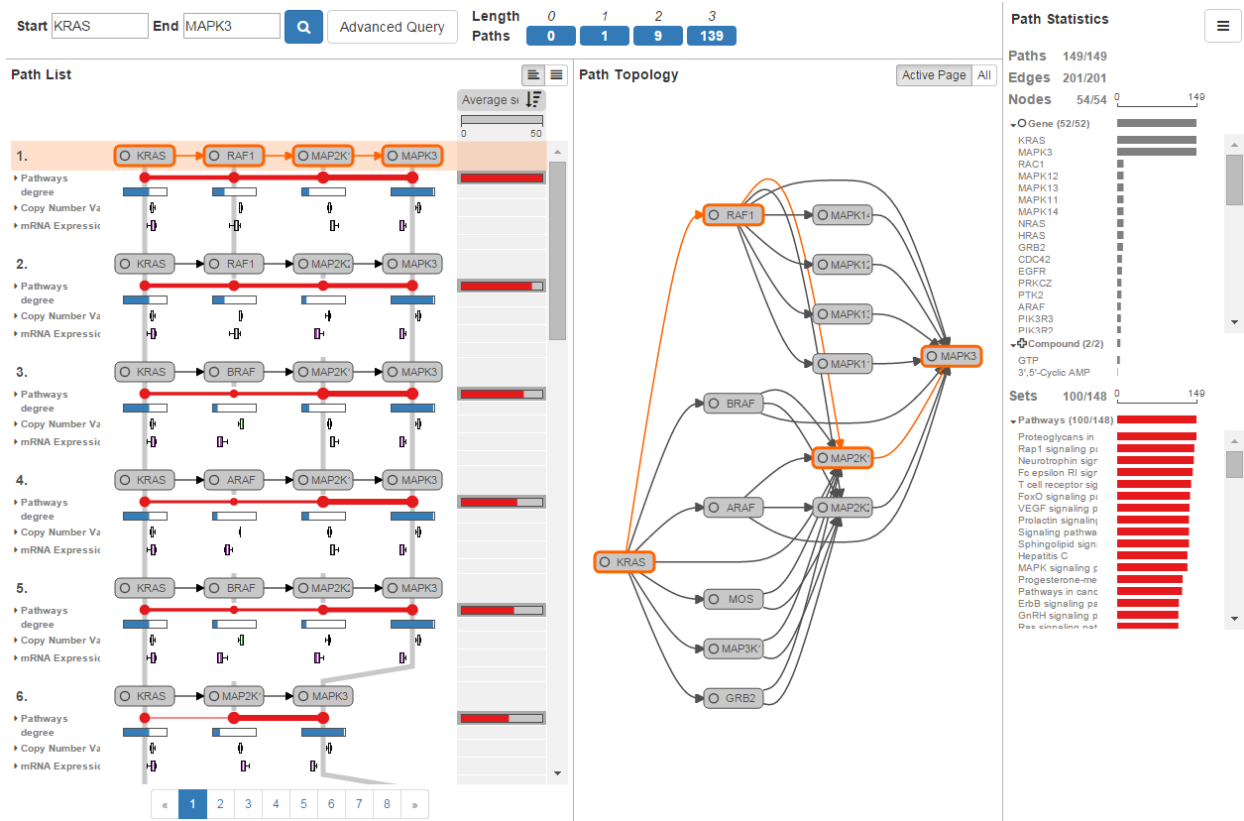
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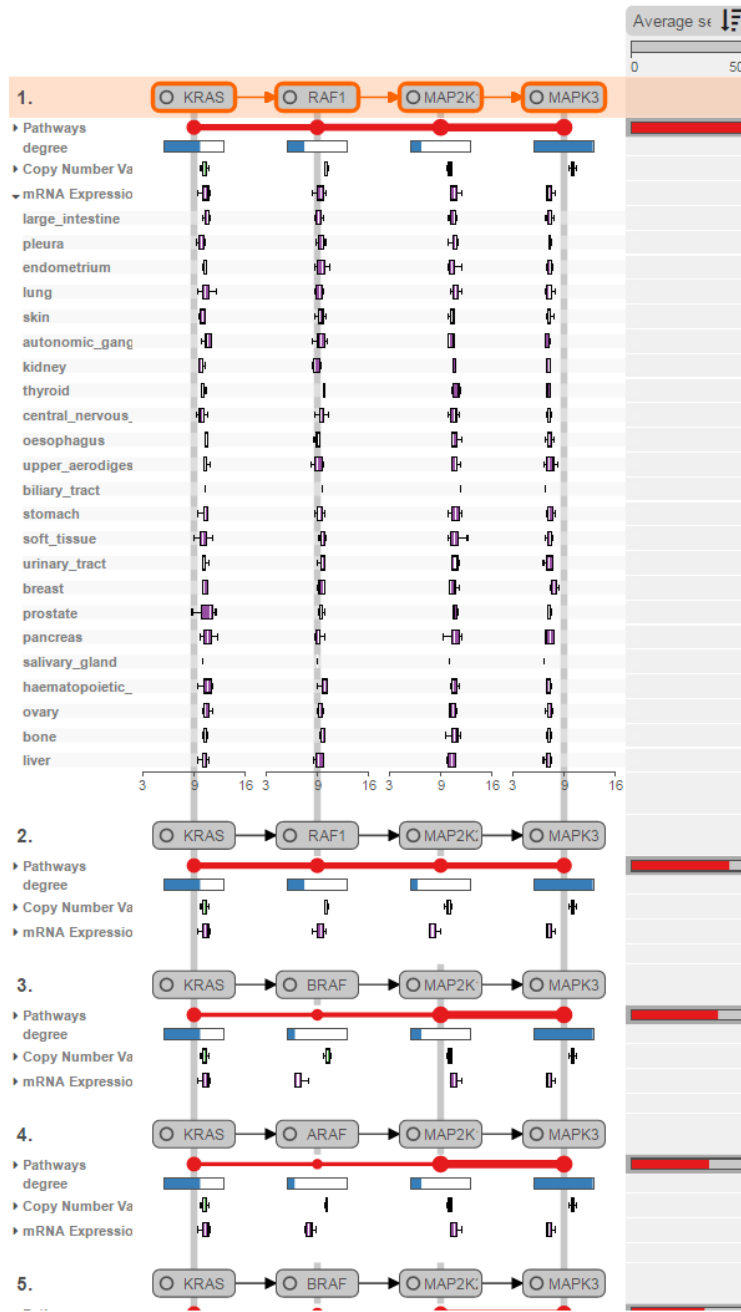
Supplementary Figure 1

Figure S1: Pathfinder is used to search for paths between KRAS and MAPK3. Ranking the paths by set connection strength places the path KRAS-RAF1-MAP2K1-MAPK3 on top, which corresponds to the ERK-MAPK signaling cascade.
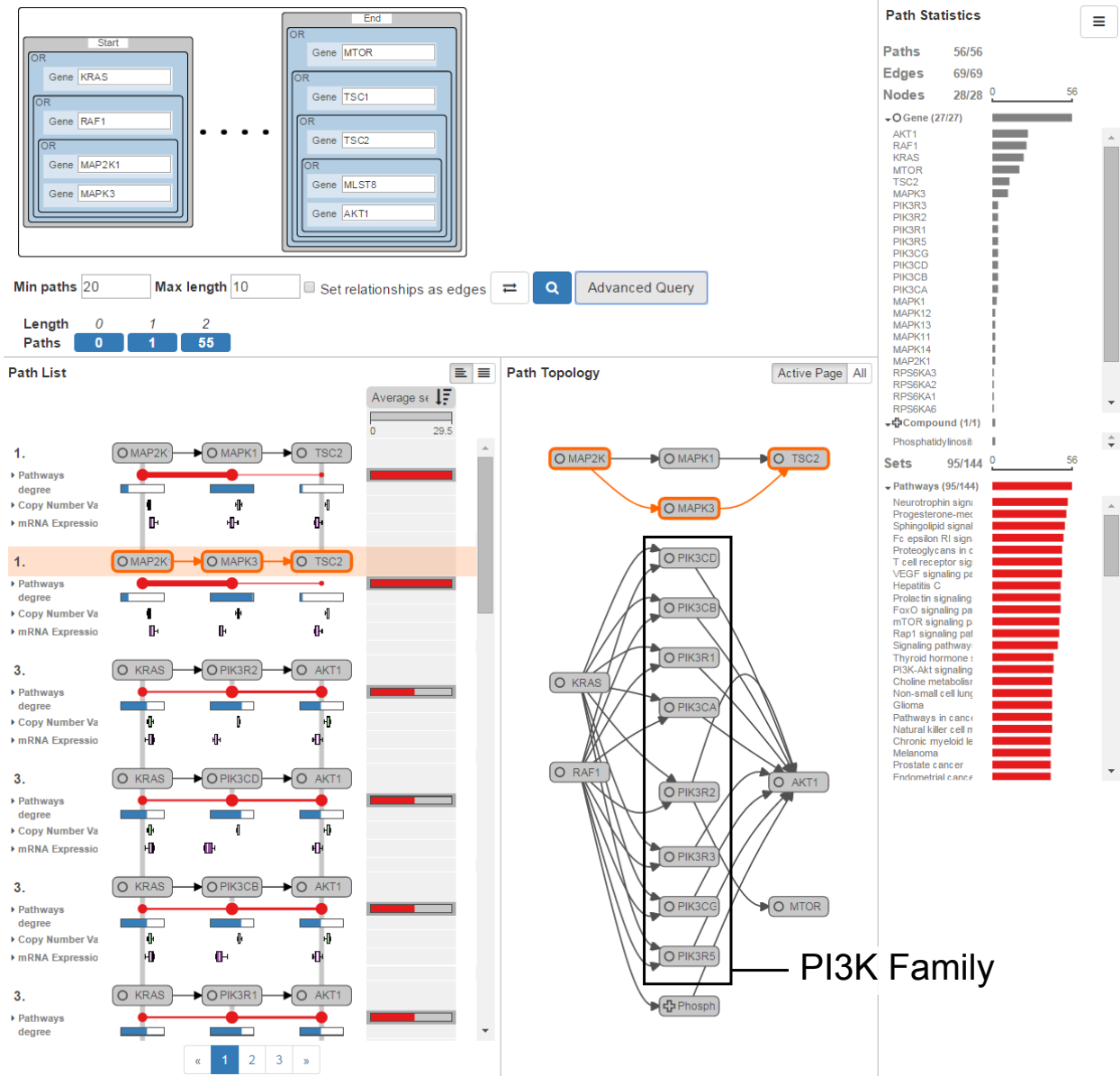
Supplementary Figure 2

(a)

(b)

Figure S2: (a)Expanding the pathways reveals that this cascade plays a role in many biological processes and diseases. Many of the pathways are cancer related, e.g., colorectal cancer, pancreatic cancer, glioma, prostate cancer, and non-small cell lung cancer. (b) The analyst can use a direct link to the original pathway map to show the whole pathway.
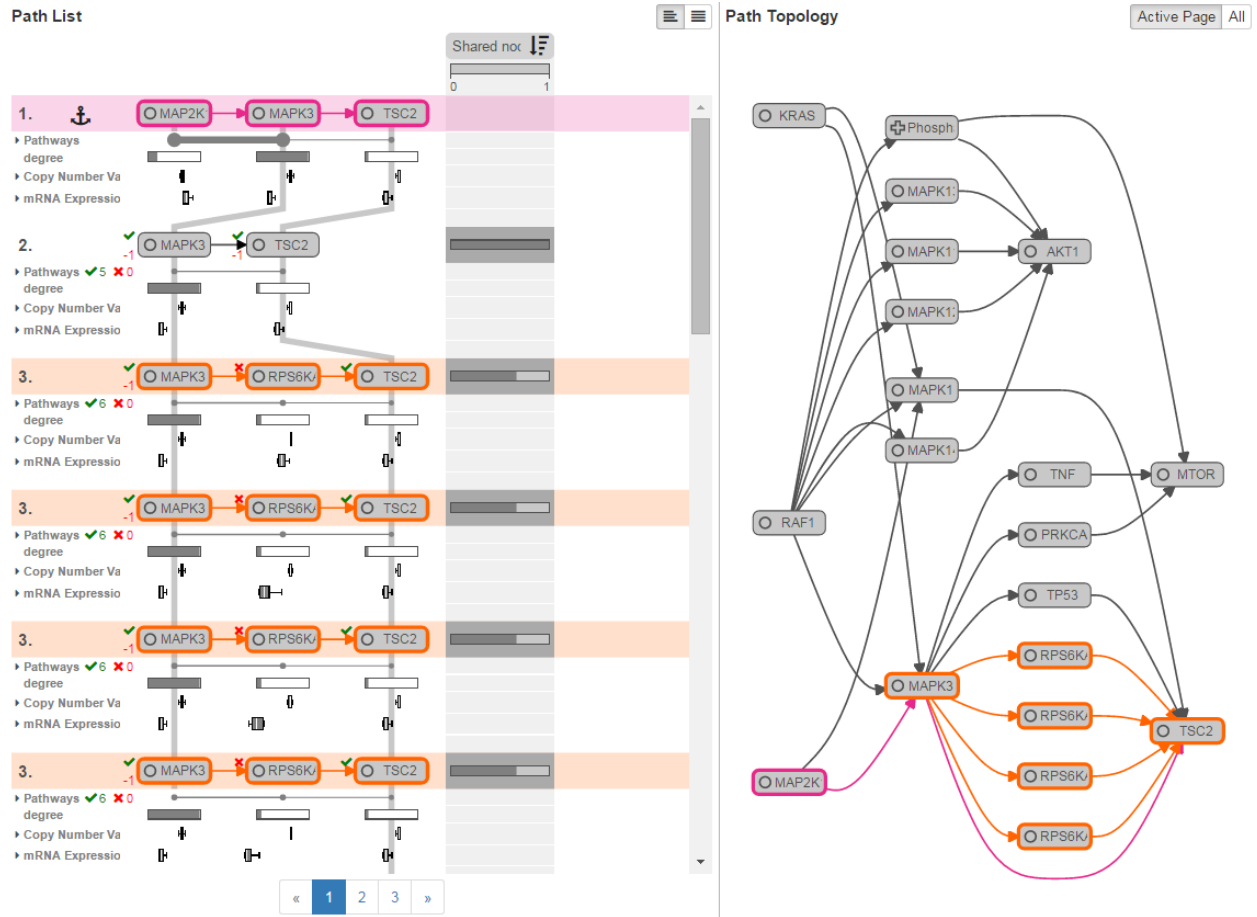
Supplementary Figure 3

Figure S3: The associated mRNA expression dataset is expanded to investigate the expression across different tissue types in more detail. The data shown in the box plots emphasize the importance of this path, as all four genes are ubiquitously expressed in all tissue types.

Supplementary Figure 4

Figure S4: To investigate whether there is any cross-talk between the path discussed previously and the mTOR signaling cascade, which is another well-known cancer-related pathway, the analyst defines a complex query between multiple nodes of each path. The query is composed of several *OR* queries for the start and end, i.e., from (KRAS or RAF1 or MAP2K1 or MAPK3) to (MTOR or TSC1 or TSC2 or MLST8 or AKT1). The paths in the result set are again ranked by set connection strength. The topology view reveals that the mTOR pathway can be influenced via the gene PI3K. In this case, the gene is represented by various subtypes (PIK3*). The original path, specifically its node TSC2, can also be modulated via MAPK3, as shown by the path highlighted in orange.

Supplementary Figure 5

Figure S5: To learn more about paths similar to the MAPK3 path, the analyst selected it as a reference. The list was then ranked by the number of shared nodes, which revealed another way to modulate TSC2: via RPS6K. This gene is represented by various subtypes (RPS6K*). The corresponding paths are highlighted in orange.