Supplementary note

Methods for **figure 4**, in brief, pathway-level heatmaps **(a)** were derived with different color ranges with a maximum color threshold at two to show the ListHits or number of genes from each tissue type involved in the composite metabolic pathways from the KEGG database (described at www.genome.jp/kegg/pathway.html#metabolism). Gene-level heatmaps **(b)** were derived for each corresponding pathway to show actual driver mutation genes from the tissue types. The driver genes involved in each metabolic pathway are plotted for each tissue. **c.** With Clarivate Analytics' network-building tool (https://clarivate.com/cortellis), they were built into a relation network by using a shortest-path algorithm with a maximum number of two steps in the path, the goal being to maximize their connections as much as the algorithm setting allowed. The lines or edges between the gene nodes in the network indicate interaction either genetically or physically supported by published studies with assessed high confidence.