Supplementary figure 1  

(a) **Cross-species precision-recall**: Precision-recall within tissue training dataset for the pathway fingerprint (red, mean average precision 0.90), unthresholded POE (dashed, 0.88), random gene sets (black, 0.83), gene-expression barcode (blue, 0.73), Spearman gene-expression correlation (green, 0.71).  

(b) Comparison of distance metrics: Precision-recall curves for aggregated mouse to human tissues data based on a thresholded fingerprint build using Euclidean (blue), Manhattan (green) and Mahalanobis distances (red).  

Tissue- vs platform/species-dominated clustering: Plots of the two most significant principal components (PC) for (c) the pathway fingerprint and (d) the gene expression barcode, brain = red, kidney = yellow, liver = green, lung = light blue, muscle = dark blue, spleen = pink, Mouse 430A2 = circles, Human 133plus2 = diamonds, Human 133A = crosses  

(e) **Functional classification of tissues and blood cell types**: Hierarchical clustering of consensus fingerprints for human and mouse tissues on three platforms. Colors indicate 1 (red), 0 (white) and -1 (blue).  

a) Wikipathway and Reactome pathways significantly contributing the clustering