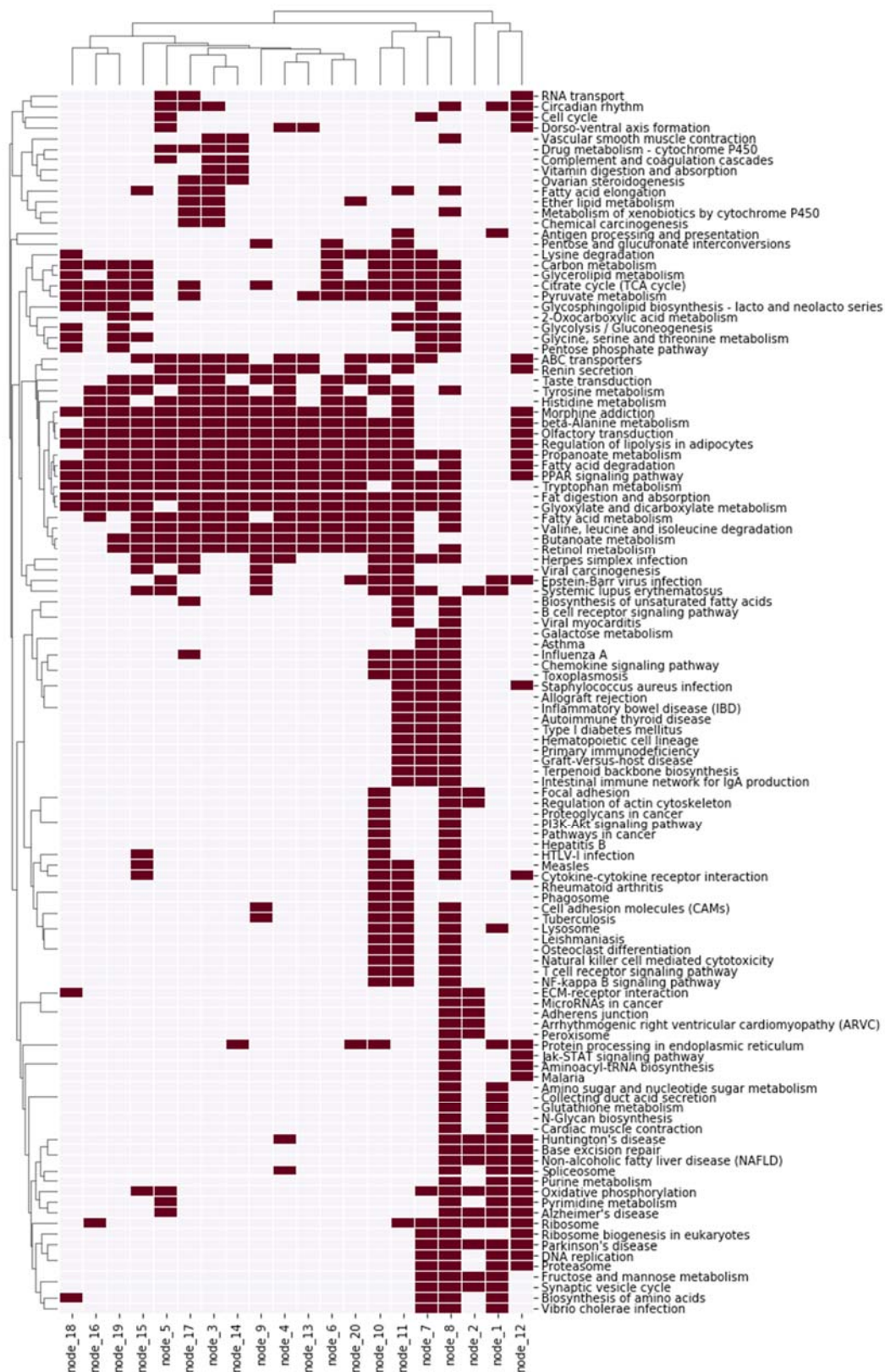


Supplementary file for Kim et al. (2020), Improved survival analysis by learning shared genomic information from pan-cancer data



Suppl. Fig S1. Enriched KEGG pathways for each hidden node of the Cox layer in the BRCA dataset. The pathway enrichment test is conducted using the correlation values between a vector of hidden node and a vector of gene expression value across all BRCA samples.

Group	Hyperparameter	Size
VAE	number of nodes in first layer of encoder	4096
	number of nodes in second layer of encoder	128
Cox-model	number of nodes in first layer	12
	number of nodes in second layer	1
Training	batch size	1000
	learning rate	1e-3
	weight decay	1e-5
	dropout rate	0.3
	model optimizer	Adam
	activation function	Tanh

Suppl. Table S1. Hyperparameters used to train VAECoX.