



Similarity ratios and membership grades for the dysregulated genes obtained from Table 1 and 2. TCGA/HPA-f1 and TCGA/HPA-f2 denoted as similarity ratio and membership grade are computed using the GSMNs reconstructed by TCGA or HPA database, respectively. The iMAT algorithm was applied to reconstruct GSMN of LUAD and LUSC by integrated TCGA or HPA database, respectively.

Zur, H.; Ruppın, E.; Shlomi, T.; iMAT: an integrative metabolic analysis tool. *Bioinformatics*, 2010, 26, 24:3140-3142.