

# Shared Nearest Neighbors Approach and Interactive Browser for Network Analysis of a Comprehensive Non-Small-Cell Lung Cancer Data Set

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\* Equal contribution

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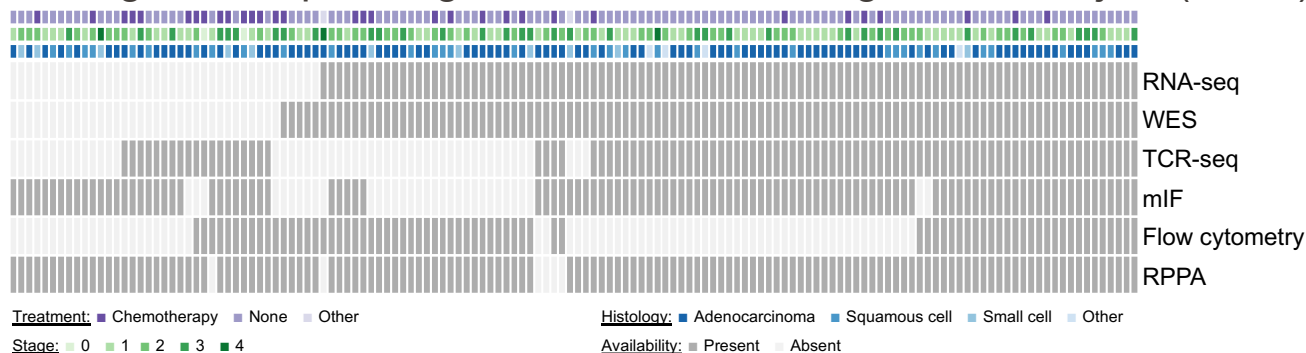
Presenter (STS) has no disclosures.

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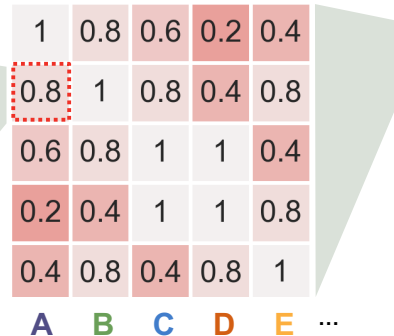
Making Cancer History®

## ImmunogenomiC prOfiling of Non-small cell lung cancer Project (ICON)

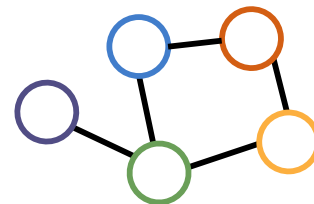


## Shared Nearest Neighbors (SNN) approach for multi-platform networks

Rank	Gene A	Gene B	...
1	Protein 1	Protein 2	
2	Protein 2	Protein 4	
3	Protein 3	Protein 1	...
4	Protein 4	Protein 6	
5	Protein 5	Protein 5	
...			

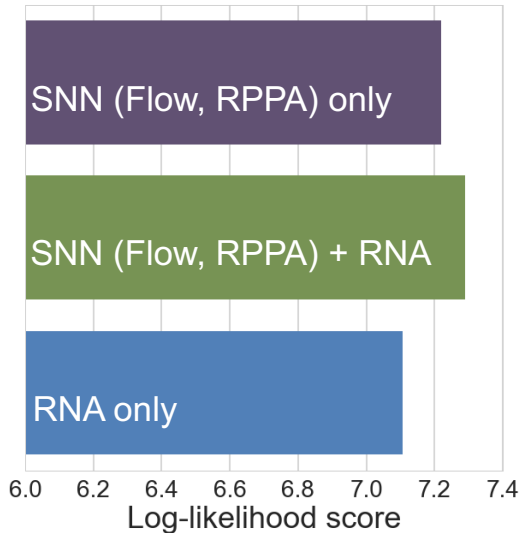


Qualifying pairs:  
A-B, B-C, B-E, C-D, D-E

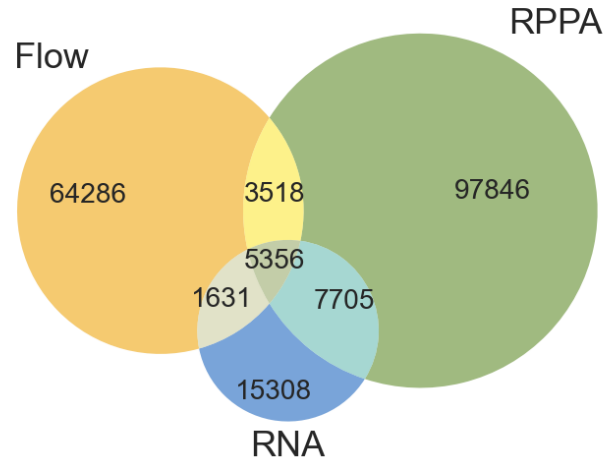


# ICON data network highlights new connections based on interplay between integrated platforms

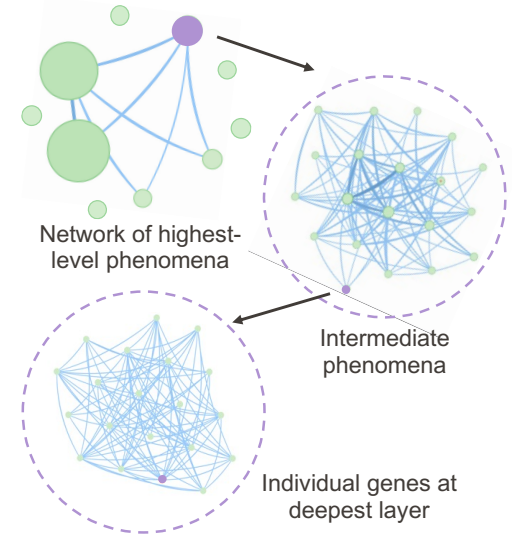
Selection of SNN with RNA-based edges  
Improved performance over SNN, RNA alone



SNN platforms provide more edges per node  
Overlaps in network edges from each platform shown



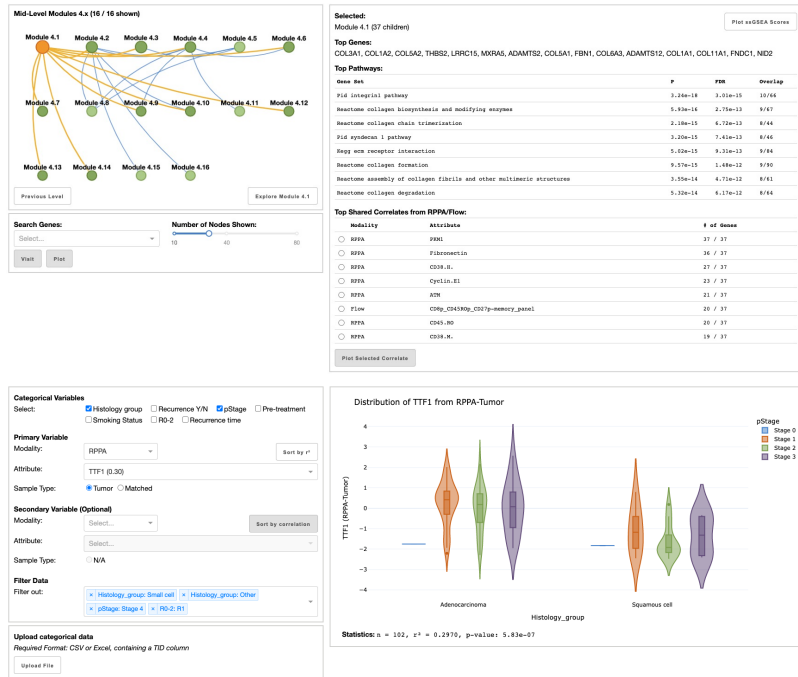
Community detection identifies modules  
10 top-level and 93 mid-level modules with 10+ genes



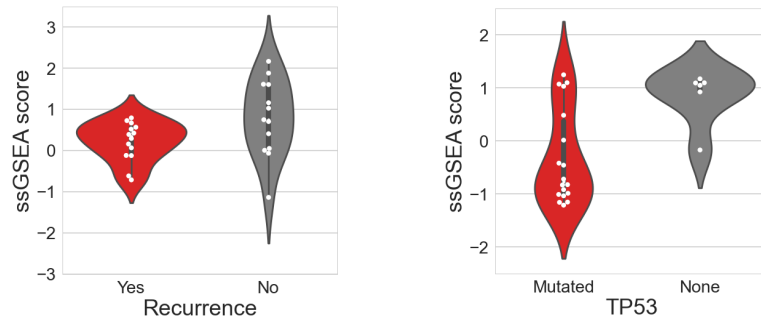
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# ICON data browser enables interactive network exploration for insights into tumor characteristics of interest

Network panel (top) and plotting/modeling panel (bottom) of the ICON data browser



Score distributions for highlighted modules relevant to selected features



Recurrence in Stage 2+, non-LUSC tumors

TP53 oncogenotype in LUSC tumors



To learn more, please see our recent publication in *JCO CCI*.

Ongoing: Expansion of approach to NEOSTAR to enable multi-cohort, multi-platform integration

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