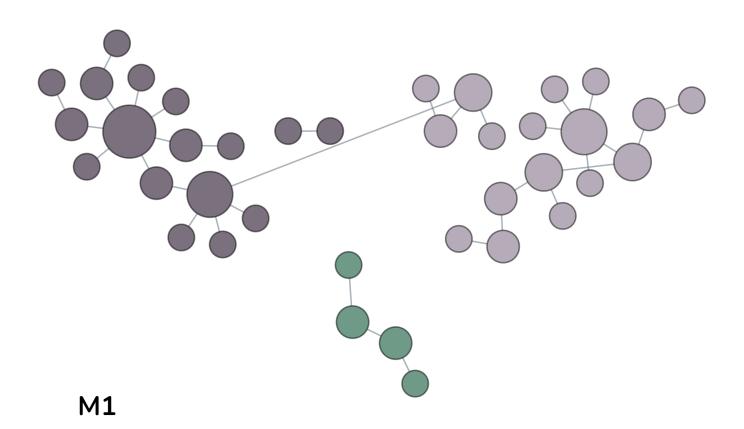
HumanBase functional module discovery Tissue-specific network-based functional interpretation of genes and gene sets.

blood network version: dd4974d1f0dc5bb5b8b11b6c657f4cd6c1a65d28





M2

⊨ humanbase

MODULE	TOP TERMS (Max 10)	Q VAL	GENES	TERMS
M1	peptide hormone processing	0.00136176	17	66
	positive regulation of stress-activated MAPK cascade	0.00162943		
	positive regulation of stress-activated protein kinase signaling cascade	0.00162943		
	positive regulation of p38MAPK cascade	0.00162943		
	regulation of stress-activated MAPK cascade	0.00171633		
	regulation of stress-activated protein kinase signaling cascade	0.00171633		
	p38MAPK cascade	0.00171633		
	regulation of p38MAPK cascade	0.00171633		
	negative regulation of intracellular signal transduction	0.00171633		
	stress-activated MAPK cascade	0.00177419		
M2	histone H3-K4 methylation	0.00136176	4	11
	histone lysine methylation	0.00162943		
	peptidyl-lysine methylation	0.00171633		
	histone methylation	0.00171633		
	protein methylation	0.00175485		
	protein alkylation	0.00175485		
	macromolecule methylation	0.00293012		
	methylation	0.00339052		
	peptidyl-lysine modification	0.00578586		
	histone modification	0.00649252		
M3	protein modification by small protein removal	0.00937742	17	3
	DNA repair	0.02663025		
	negative regulation of cell cycle	0.02914055		