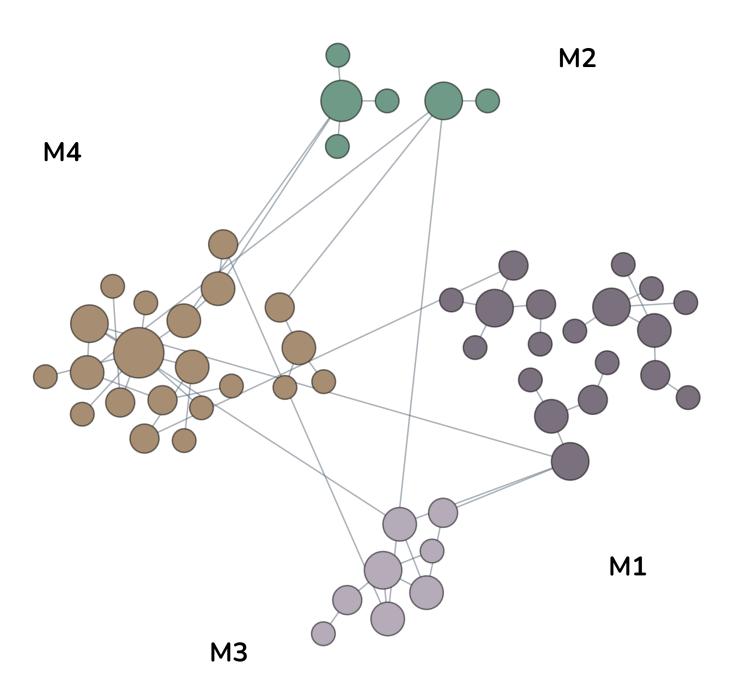


## HumanBase functional module discovery Tissue-specific network-based functional interpretation of genes and gene sets.

blood network version: dd4974d1f0dc5bb5b8b11b6c657f4cd6c1a65d28



**⊨** humanbase

MODULE	TOP TERMS (Max 10)	Q VAL	GENES	TERMS
M1	histone H3 acetylation	0.01080515	19	11
	histone acetylation	0.01452371		
	internal protein amino acid acetylation	0.01452371		
	internal peptidyl-lysine acetylation	0.01452371		
	peptidyl-lysine acetylation	0.01452371		
	protein acetylation	0.01766864		
	protein acylation	0.02123665		
	peptidyl-lysine modification	0.03287650		
	histone modification	0.03967589		
	covalent chromatin modification	0.03967589		
M2	response to endoplasmic reticulum stress	0.01080515	6	1
M3	membrane organization	0.01452371	8	1
M4	peptidyl-serine modification	0.01766864	21	3
	positive regulation of protein kinase activity	0.03287650		
	positive regulation of kinase activity	0.03287650		