

Supplementary Table S5. Reactome pathway enrichment analysis results of CUPsig and CDPsig

Signatures	Reactome Pathways	P-values
CUPsig		
CTSB [50, 51]	Degradation of the extracellular matrix	0.002
	Caspase activation via Dependence Receptors in the absence of ligand	0.005
	Trafficking and processing of endosomal TLR	0.006
TIMP2 [52]	Extracellular matrix organization	0.007
	Caspase activation via extrinsic apoptotic signalling pathway	0.012
	Activation of Matrix Metalloproteinases	0.015
AHNAK2	NR1H3 & NR1H2 regulate gene expression linked to cholesterol transport and efflux	0.017
	Neutrophil degranulation	0.018
	RHOF GTPase cycle	0.019
ARHGAP5 [53]	RND3 GTPase cycle	0.019
	RND1 GTPase cycle	0.019
	RND2 GTPase cycle	0.02
ARL4C [54, 55]	NR1H2 and NR1H3-mediated signaling	0.021
	Netrin-1 signaling	0.023
	RHOD GTPase cycle	0.025
UNC5B [56]	RHOJ GTPase cycle	0.025
	RHOQ GTPase cycle	0.027
	Assembly of collagen fibrils and other multimeric structures	0.028
TGFB1I1 [57]	Collagen degradation	0.029
	RHOB GTPase cycle	0.032
	RHOC GTPase cycle	0.034
HOPX [58]	RHOG GTPase cycle	0.034
	Collagen formation	0.041
	RAC3 GTPase cycle	0.043
CDPsig		
DUS3L	RNA Polymerase I Transcription Termination	0.009
	RNA Polymerase I Transcription Initiation	0.013
AGMAT [59]	tRNA processing in the nucleus	0.016
	Metabolism of polyamines	0.016
POP1	B-WICH complex positively regulates rRNA expression	0.025
	RNA Polymerase I Promoter Escape	0.025
POLR1A	Positive epigenetic regulation of rRNA expression	0.029
	NoRC negatively regulates rRNA expression	0.029
DDX31	tRNA processing	0.029
	Negative epigenetic regulation of rRNA expression	0.03
ACTR3B	RNA Polymerase I Promoter Clearance	0.03

	RNA Polymerase I Transcription	0.031
NCOA5 [60]	Epigenetic regulation of gene expression	0.041