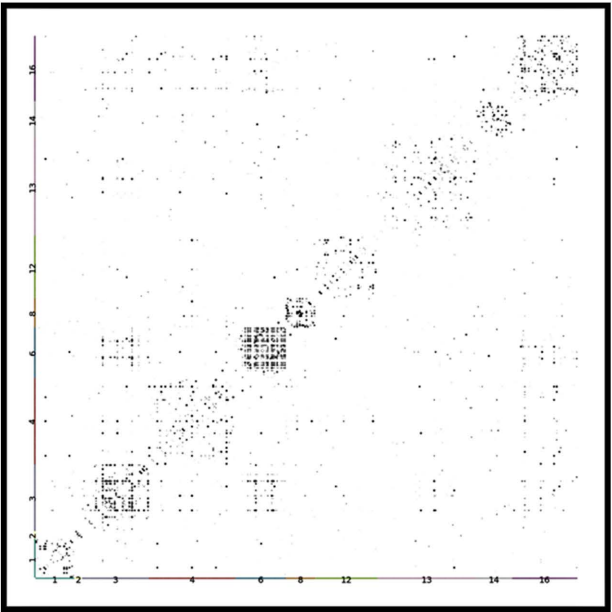


A

Network Properties		
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521	1821	n.a.

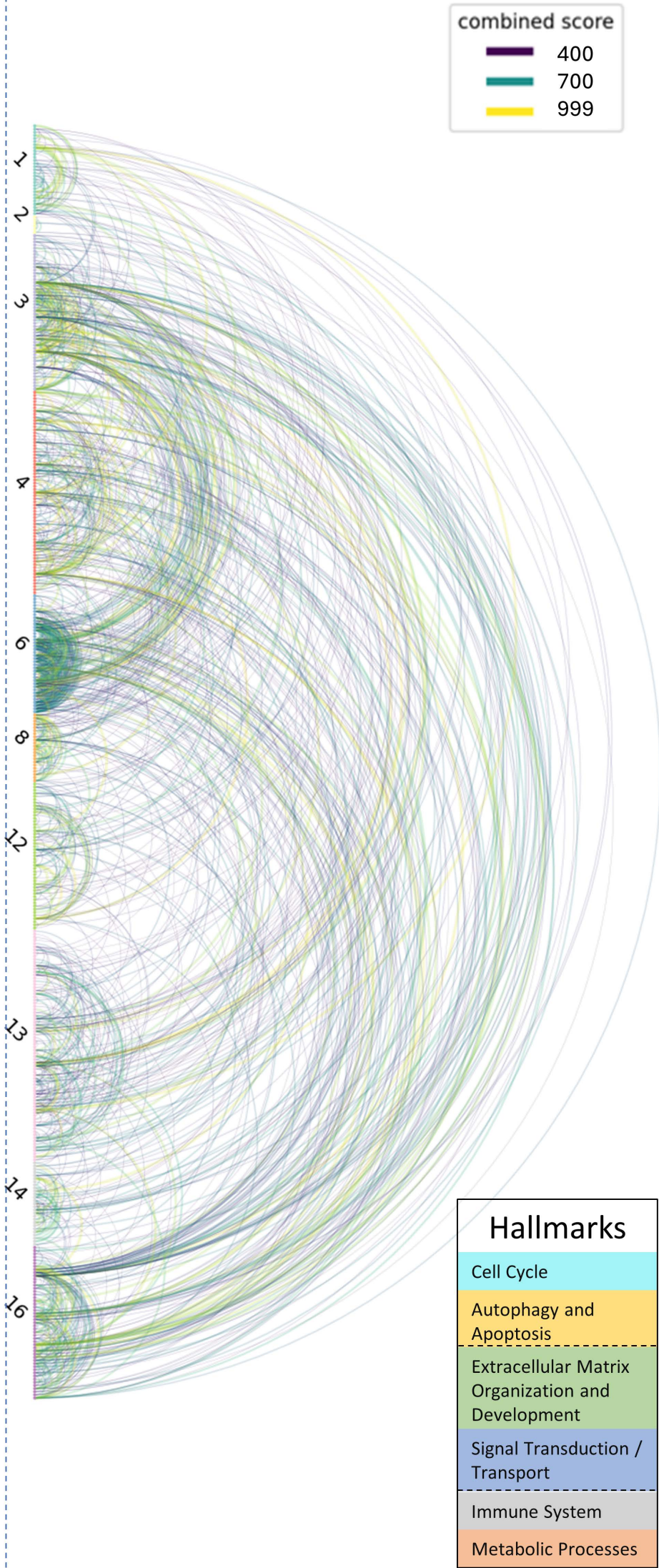
AD SNP

B



C

n	e	Hub Genes	Comm. Number: Associated Terms	
29	45	PSMA1	1:	Synapsis Receptor Activity
6	7	CACNA1G CATSPERB KCNN2	2:	Voltage-Gated Channel (Cardiac) Muscle Action Potential
49	126	APOB APOE APP	3:	Cholesterol, Lipoprotein
65	122	CDH1 ITGA6 CASP3	4:	ECM- and cytoskeleton organization Cell Adhesion Organ Development
38	284	BIN1 ABCA7 PICALM	6:	Proteolysis ECM- and cytoskeleton organization
22	52	ATM ERCC2 ERCC1	8:	DNA Repair Stress Response
47	61	BIRC3 MADD	12:	Autophagic Process
74	141	GRIN2B	13:	Cell Differentiation and Growth Synapsis Receptor Activity
25	31	EGR1 ADAR	14:	RNA Modification, Chromatin Interferon
48	113	IL6 SYK	16:	Cell Communication Defense Response to other Organisms Cytokine Leukocyte Activation

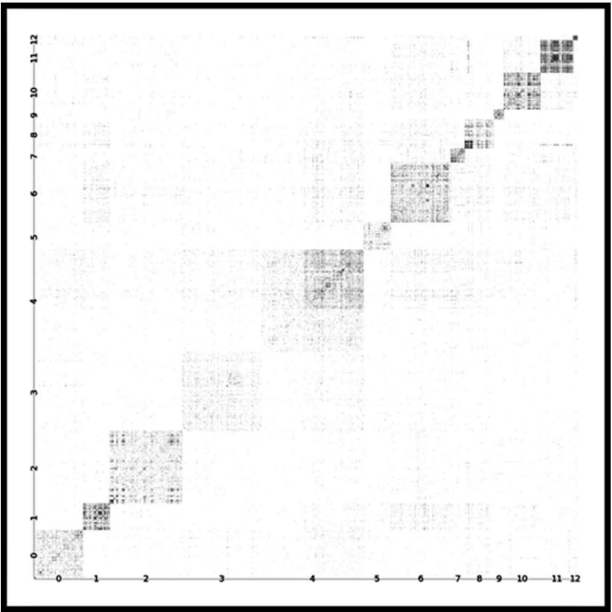


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Network Properties		
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14654	649843	0.13

AD DEG

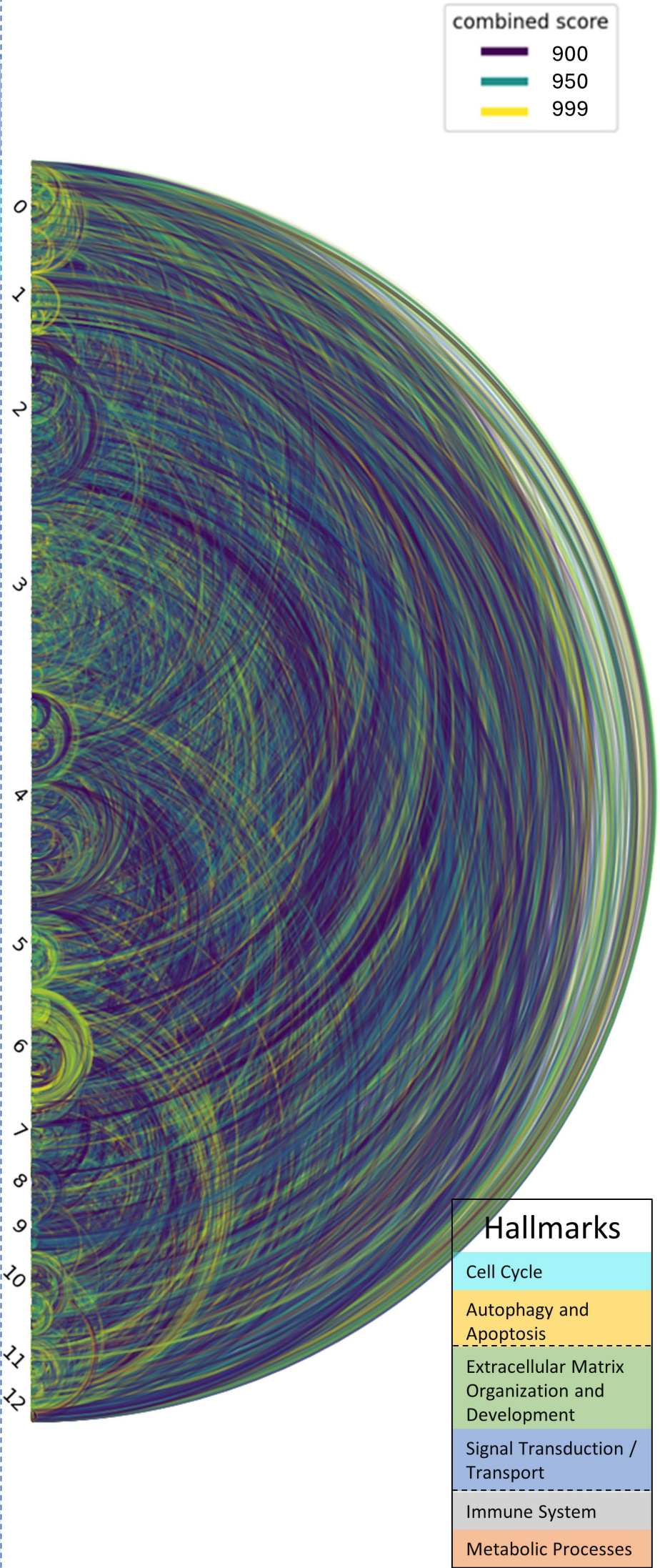
B



C

n	e	Hub Genes	Mean Reg Dir	Comm. Number: Associated Terms		
1278	24662	RAB5A RAB7A	0.04	0:	Auto-phagic Process	Local-ization SNARE Binding, Vesicle, ER to Golgi transport
683	22915		0.16	1:	Regulation of Cell Cycle, Spindle Apparatus, DNA Repair, Chromatin,	
1852	40486	CAT	0.05	2:	Trans-membranal Transport	Lipid, Branched AA Degradation, Carbohydrate, Nucleotide, Antioxidant (Mt.), Respiratory Chain Complex (Mt.)
2060	34465		0.06	3:	Neuronal Signaling, Synapsis, Voltage-Gated Channel, Neurotransmitter Secreton,	
2705	77466	SRC	0.33	4:	Apoptotic Process, Nfkb signaling pathway	Actin Cytosk. Collagen Cytosk. Cell Adhesion Cell Diff. & Growth Defense Resp. to other Organisms, Inflammation, Compl. & Coag. Cascade
694	7377	IFT88	0.14	5:	Spindle Apparatus	ECM- and cytoskeleton organization, Cilium
1575	38572	EP300 TP53 HDAC1	0.23	6:	Transcription, Chromatin	
357	4728	PPP2CA PPP2R1A	0.14	7:	Focal Adhesion, Cell Differentiation and Growth, Organ Development, Early Development	
759	13937	UBC UBB		8:	Proteolysis, Ubiquitinylation, Proteasome	
267	2615		0.16	9:	Sphingolipid, Proteoglycan, Glycosylation	
957	28314	SNRPD3	0.09	10:	Transcription, RNA Modification , Spliceosome	Chaperone Mediated Process
831	47025	RPS5	-0.08	11:	Translation, Mitochondrial Translation	
119	2064			12:	Stress Response, mTOR Sig. pathway	

D

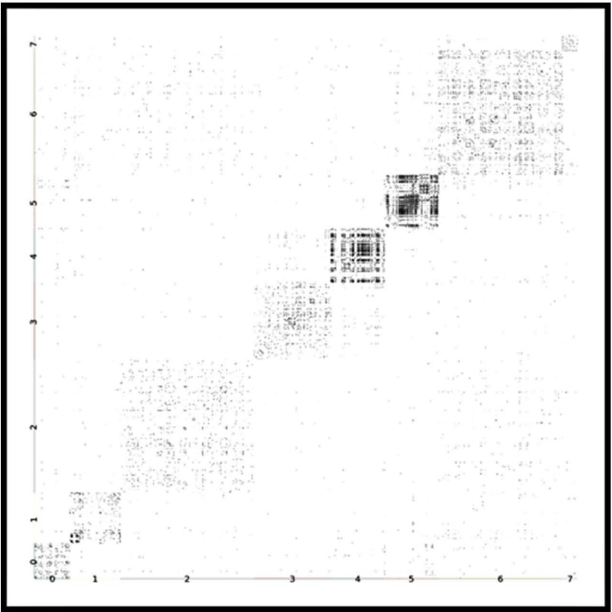


A

Network Properties		
n	e	Mean Reg. Dir.
1956	40482	-0.10

AD Prot

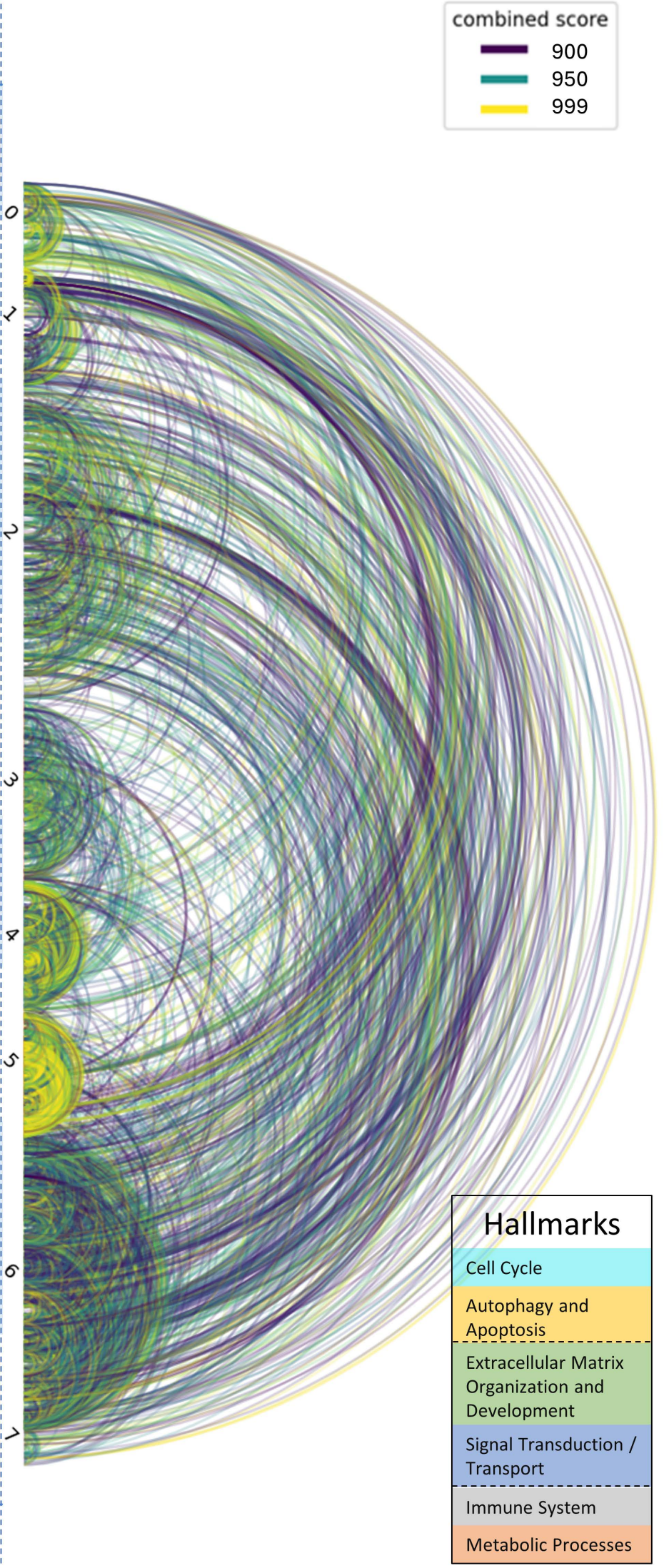
B



C

n	e	Hub Genes	Mean Reg Dir	Comm. Number: Associated Terms	
127	985			0:	RNA Modification, Spliceosome Chaperone Mediated Process
181	1224	CLTC	-0.13	1:	mTOR Signaling Pathway Vesicle Receptor Recycling
481	5317	SNAP25 DLG4	-0.2	2:	Synapsis Neurotransmitter Secretion SNARE Binding
277	3119	TPI1	0.13	3:	Fatty Acid Oxidation (Mt.) Carboxylic Acid (Mt.), Branched AA Degradation, Carbohydrate, Nucleotide, Antioxidant (Mt.)
193	3965	UQCRF51	-0.55	4:	NADH (Mt.), Respiratory Chain Complex (Mt.)
195	4714	RPL9	-0.31	5:	Translation Mitochondrial Translation Proteasome
444	5790	MAPK3 CDC42	0.13	6:	ECM- and cytoskeleton organization, Actin Cytoskeleton Cell Adhesion Organ Development Cell Communication
54	406	ALB C3	-0.27	7:	Inflammation Complement and Coagulation Cascade Leukocyte Activation Homeostasis

D

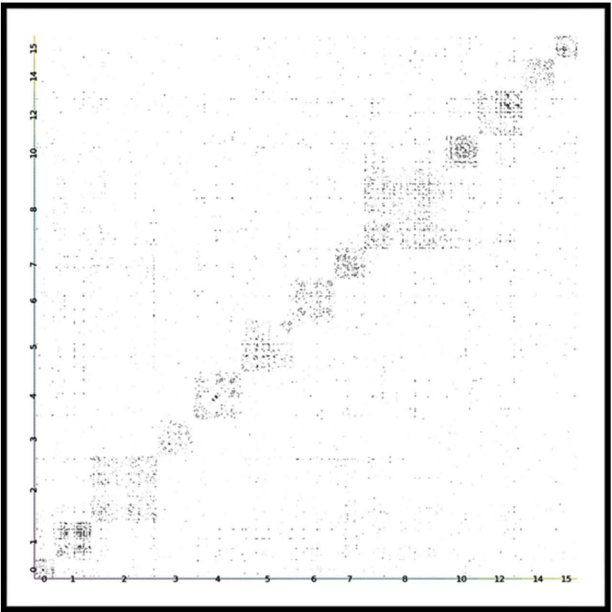


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Network Properties		
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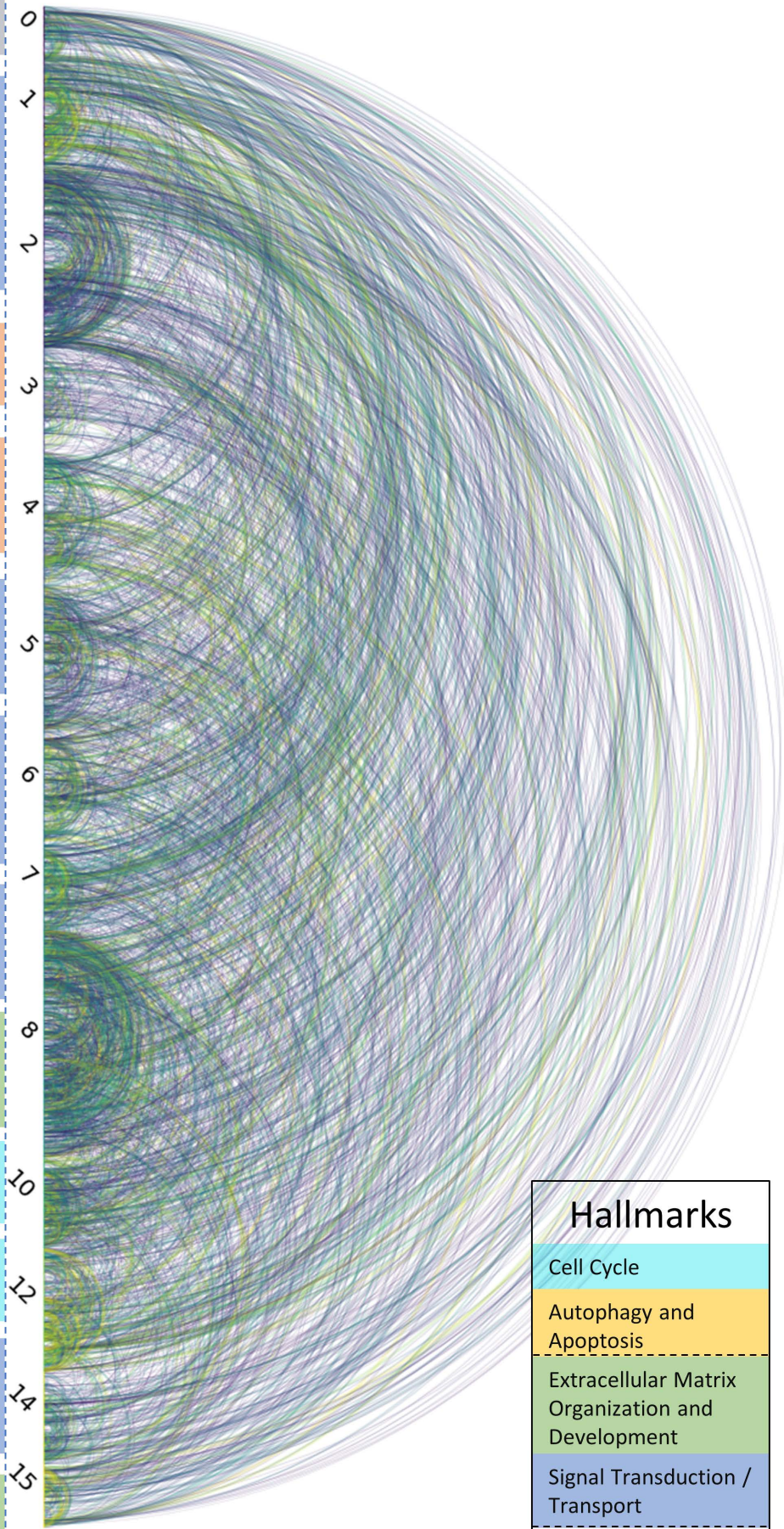
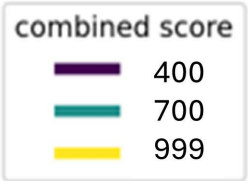
AD Meth

B



C

n	e	Hub Genes	Mean Reg Dir	Comm. Number: Associated Terms	
39	81	SORT1 DNM2		0:	Vesicle Trans-Golgi-Network
75	235	PLCG1 GRB2		1:	Cell Adhesion Immune Response Cytokine Interferon
131	555			2:	Cell Differentiation and Growth Cell Communication Synapsis Voltage-Gated Channel Receptor Activity
75	111	PFKL	-0.24	3:	Carbohydrate, Nucleotide
97	221	SREBF1 LEP SCD		4:	Lipid , Cholesterol, Fatty Acid Oxidation (Mt.)
104	315	NTN1 DOCK1		5:	Focal Adhesion Cell Differentiation and Growth Cell Communication
84	191	FN1 VWF		6:	ECM- and cytoskeleton organization Collagen Cytoskeleton Cell Migration Vesicle
61	168	CACNA1C CACNA1D		7:	Synapsis Voltage-Gated Channel Transmembranal Transport
162	719	NOTCH1 SOX2 HDAC2		8:	Transcription Cell Differentiation and Growth Early Development
66	221	ATM RPA2		10:	Regulation of Cell Cycle DNA Repair
89	259	RPS14 RPL4		12:	RNA Modification, Translation
67	128	PCNT		14:	ECM- and cytoskeleton organization Cilium Vesicle
46	84	SMAD7		15:	mTOR Signaling Pathway Organ Development Early Development



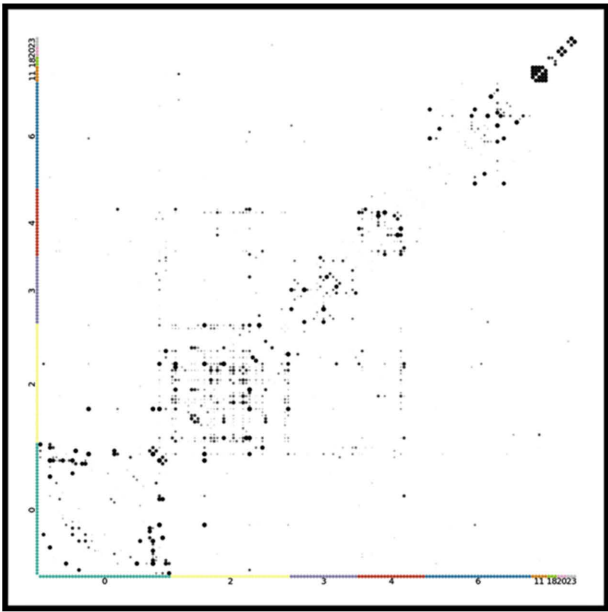
Hallmarks
Cell Cycle
Autophagy and Apoptosis
Extracellular Matrix Organization and Development
Signal Transduction / Transport
Immune System
Metabolic Processes

A

Network Properties		
n	e	Mean Reg. Dir.
246	629	n.a.

PD SNP

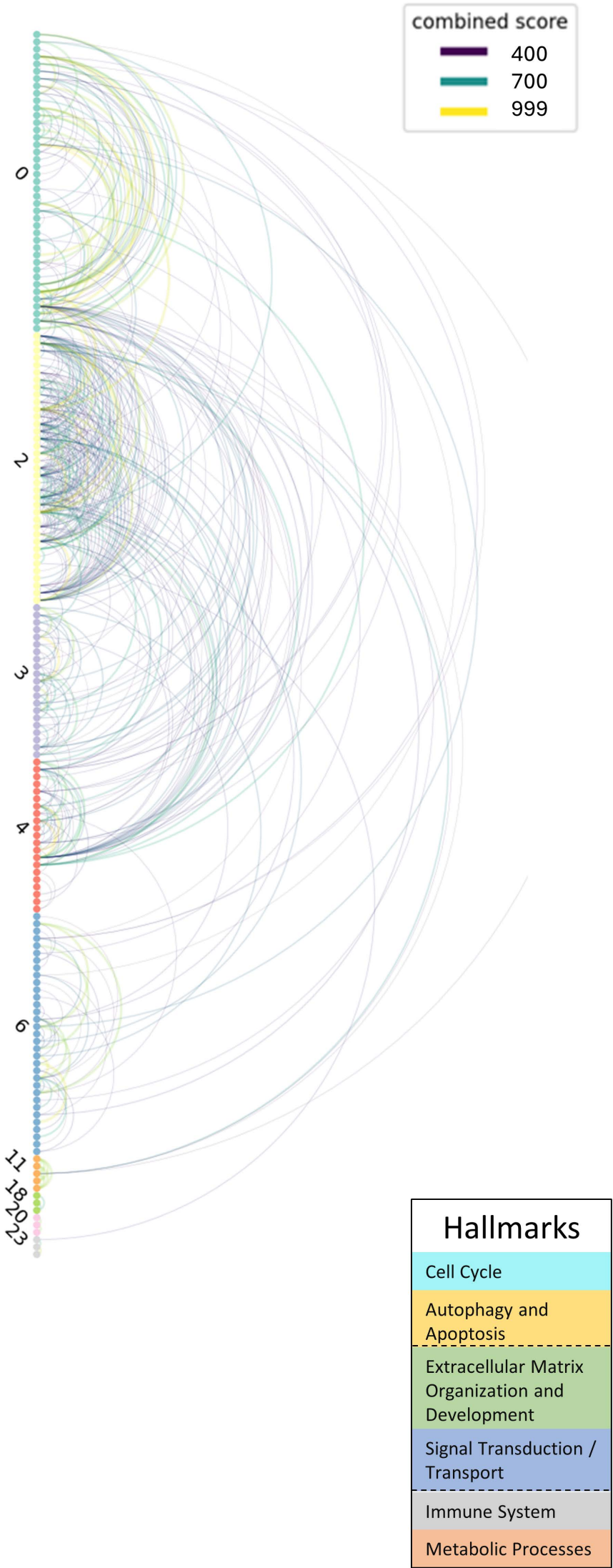
B



C

n	e	Hub Genes	Comm. Number: Associated Terms	
40	69	FYN MAPT	0:	Cell Communication Transmembranal Transport
37	210	LRRK2 CCDC62	2:	Synapsis Vesicle
21	34	KANSL1	3:	Early Development Cell Communication
21	38	STX1B VAMP4 UNC13B	4:	Neurotransmitter Secretion SNARE Binding Vesicle
33	38	POLR2A	6:	Transcription Nucleotide
5	10	ADAMTS16 THSD4	11:	Organ Development
3	2	*	18:	ECM- and cytoskeleton organization, Cilium
3	2	*	20:	Proteoglycan
3	2	*	23:	Cholesterol

D

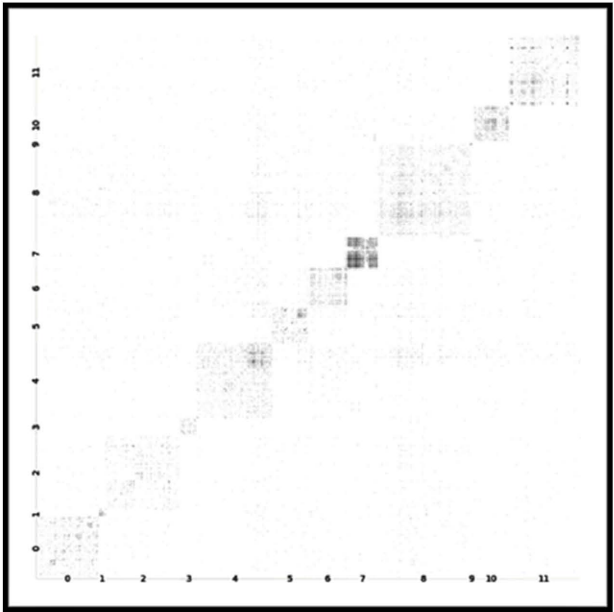


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Network Properties		
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PD DEG

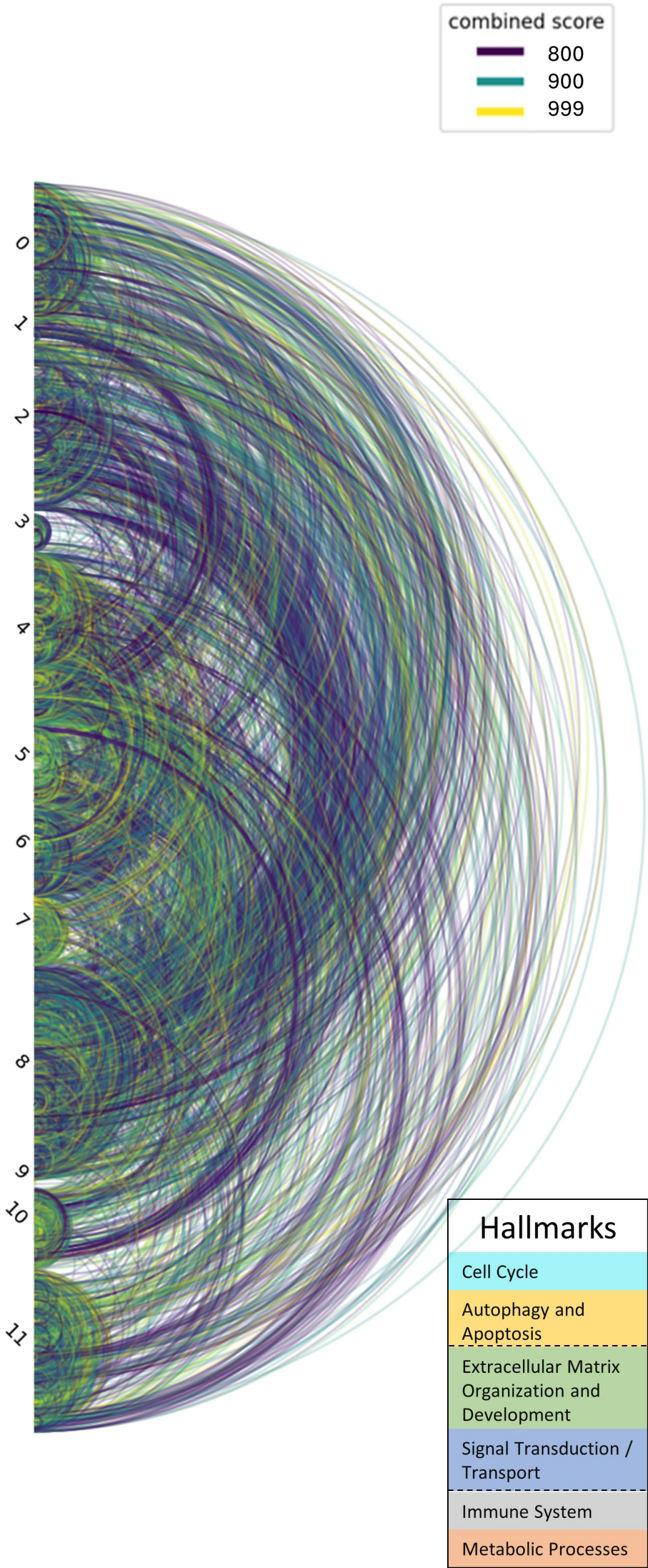
B



C

C n	e	Hub Genes	Mean Reg Dir	Comm. Number: Associated Terms				
550	4916	VAMP2 ARF1	-0.64	0:	Autophagic Process	SNARE Binding, Vesicle, Trans-Golgi-Network		
60	266	HLA-C	-0.57	1:	Immune Response Defense Response to Other Organism, Interferon			
655	5759		-0.67	2:	Cell Communication Synapsis, Voltage-Gated Channel			
148	535		-0.6	3:	Sphingolipid, Proteoglycan			
660	8015	HDAC1 MYC	-0.52	4:	Transcription, Chromatin		Early Development	
308	2287	HSP90AA1	-0.63	5:	Chaperone Mediated Process	ECM- & cytoskeleton organization, Cilium		Vesicle
354	3087	UBC UBB UBA52	-0.58	6:	Proteolysis, Ubiquitinylation			
259	5977	RPS5	-0.55	7:	Translation, Ribosome			
813	10173	FN1	-0.57	8:	Actin Cytoskeleton, Collagen Cytoskeleton, Cell Adhesion, Cell Migration			
32	145	SLC7A5 SLC1A7	-0.39	9:	Transmembranal Transport			
311	3601	HNRNPC SNRPE	-0.5	10:	RNA Modification, Spliceosome, Translation			
617	6270	ACO2	-0.65	11:	Branched AA Degradation, Carbohydrate, Antioxidant (Mt.), Respiratory Chain Complex (Mt.)			

D

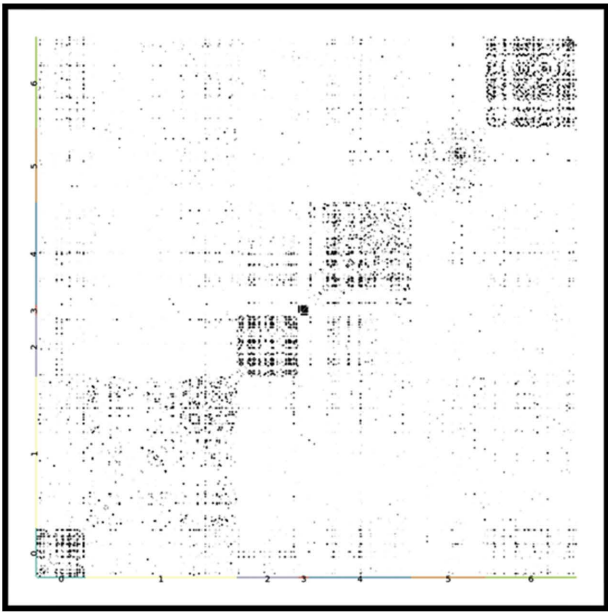


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Network Properties		
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421	4638	0.42

PD Prot

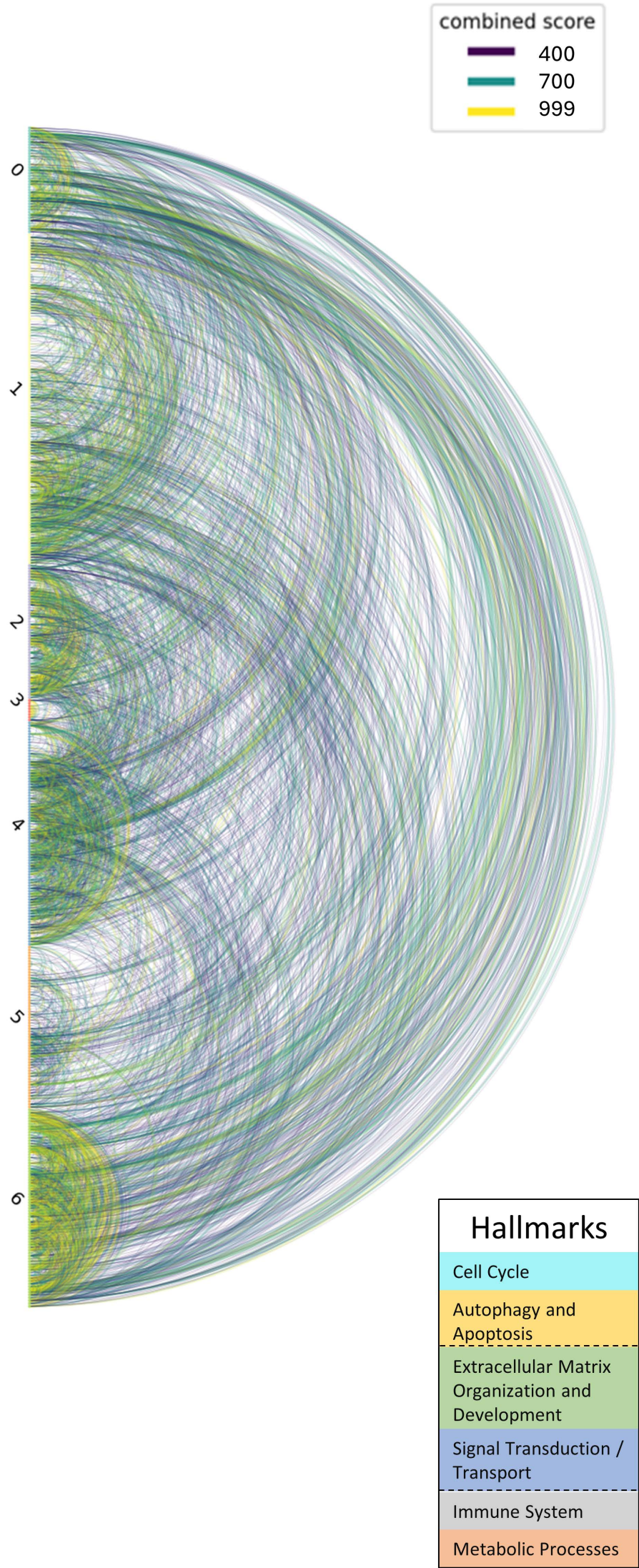
B



C

n	e	Hub Genes	Mean Reg Dir	Comm. Number: Associated Terms		
38	187	HSPA5 HSP90AA1		0:	Chaperone Mediated Process Stress Response	
118	572	ACTB ACTG1	0.49	1:	ECM- and Cytoskeleton Organization Actin Cytoskeleton	Vesicle
48	328		0.52	2:	Fatty Acid Oxidation (Mt.) Branched AA Degradation, Antioxidant (Mt.) Respiratory Chain Complex (Mt.)	
8	22	ATP6V1A	0.62	3:	mTOR Signaling Pathway	Receptor Recycling Respiratory Chain Complex (Mt.)
79	658	TPI1 ENO1	0.66	4:	Carbohydrate, Antioxidant (Mt.)	
58	223	SYN1		5:	Neuronal Signaling Synapsis Voltage-Gated Channel	
71	725	EEF1A1	0.36	6:	Translation	Proteasome

D

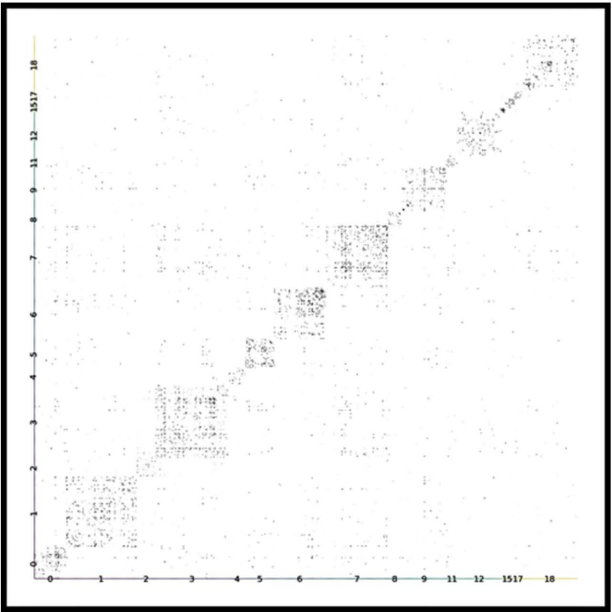


A

Network Properties		
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PD Meth

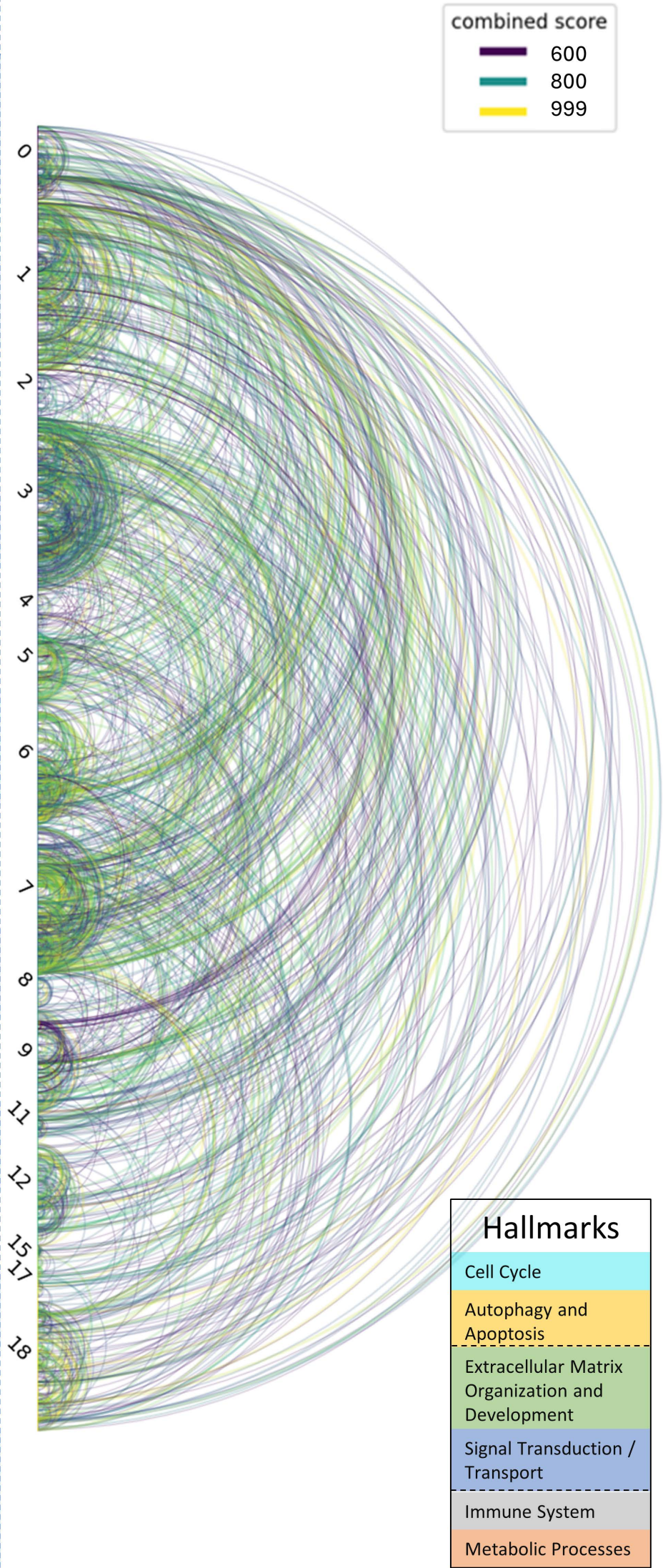
B



C

n	e	Hub Genes	Mean Reg Dir	Comm. Number: Associated Terms	
71	207	DCTN1 DYNC1H1	0.43	0:	ECM- and cytoskeleton organization, Cilium Axonal Transport
161	532	CREBBP STAT3	0.38	1:	Transcription Chromatin
43	81	POU3F2	0.38	2:	Transcription Organ Development Early Development
165	997	DLG4	0.3	3:	Synapsis Voltage-Gated Channel Axonal Transport Receptor Activity
40	55	ARFGAP1		4:	ER to Golgi transport
65	138	RPTOR YWHAZ	0.2	5:	Autophagic Process Apoptotic Process mTOR Signaling Pathway
117	385	SNRPE PABPC1	0.35	6:	RNA Modification, Spliceosome, Translation
142	550	CDC42 GRB2 PLCG1	0.23	7:	Cell Migration Cell Differentiation and Growth Cell Communication
32	38	PLA2G6	0.57	8:	Lipid Sphingolipid
102	244	UBC	0.39	9:	Regulation of Cell Cycle Proteolysis Ubiquitinylation
26	69	CTNNA1 CDH5		11:	Cell Junction Cell Adhesion
95	200		0.3	12:	Lipid Respiratory Chain Complex (Mt.)
32	68	GDI2		15:	Localization SNARE Binding Vesicle
17	26	PTPRF PTPRD	0.53	17:	Synapsis Transmembranal Transport
127	339	CD44 ACAN BMP4	0.38	18:	ECM- and cytoskeleton organization, Cell Adhesion Organ Development Early Development

D

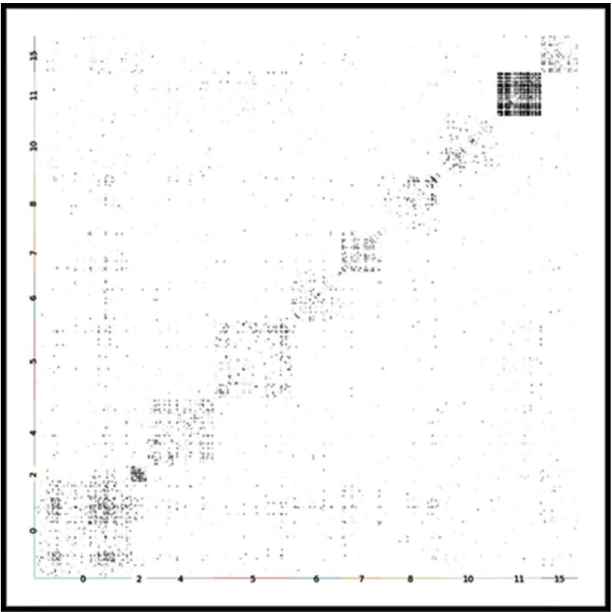


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Network Properties		
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ALS DEG

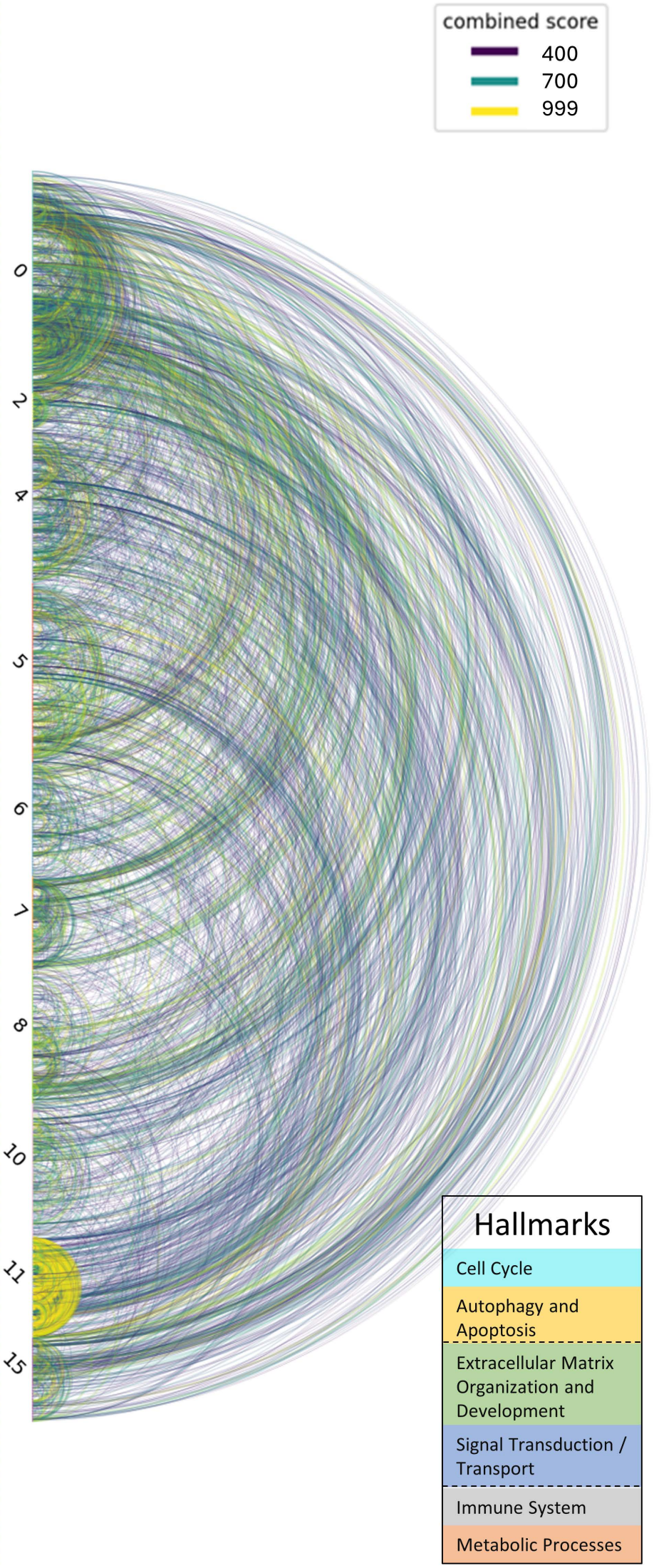
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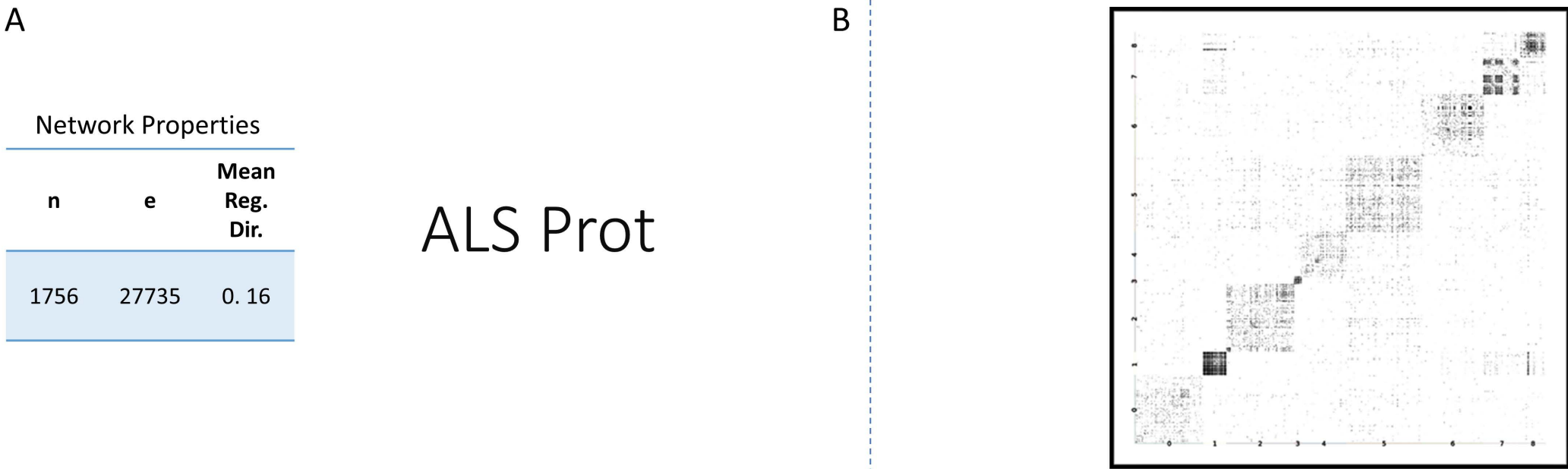


C

n	e	Hub Genes	Mean Reg Dir	Comm. Number: Associated Terms	
148	929	STAT3 CD4	0.35	0:	Apoptotic Process
24	89	HLA-B ISG15	0.5	2:	Defense Response to Other Organism, Interferon
103	288	HSPA4 HSP90AB1		4:	Autophagic Process, Chaperone Mediated Process Trans-Golgi- Network
119	274	HDAC1 CCND1		5:	Regulation of Cell Cycle, Transcription, Chromatin
76	143	ACTN1 FLNA		6:	Actin Cytoskeleton
63	219	COL1A1 COL4A1 COL4A2	0.36	7:	Collagen Cytoskeleton, Organ Development
89	166	RAF1 AKT2		8:	Cell Communication Protein
89	152	VAMP2	-0.14	10:	Carboxylic Acid (Mt.), Respiratory Chain Complex (Mt.)
67	881	RPS6		11:	Translation
56	140	APOE	0.21	15:	Complement and Coagulation Cascade, Immune Response

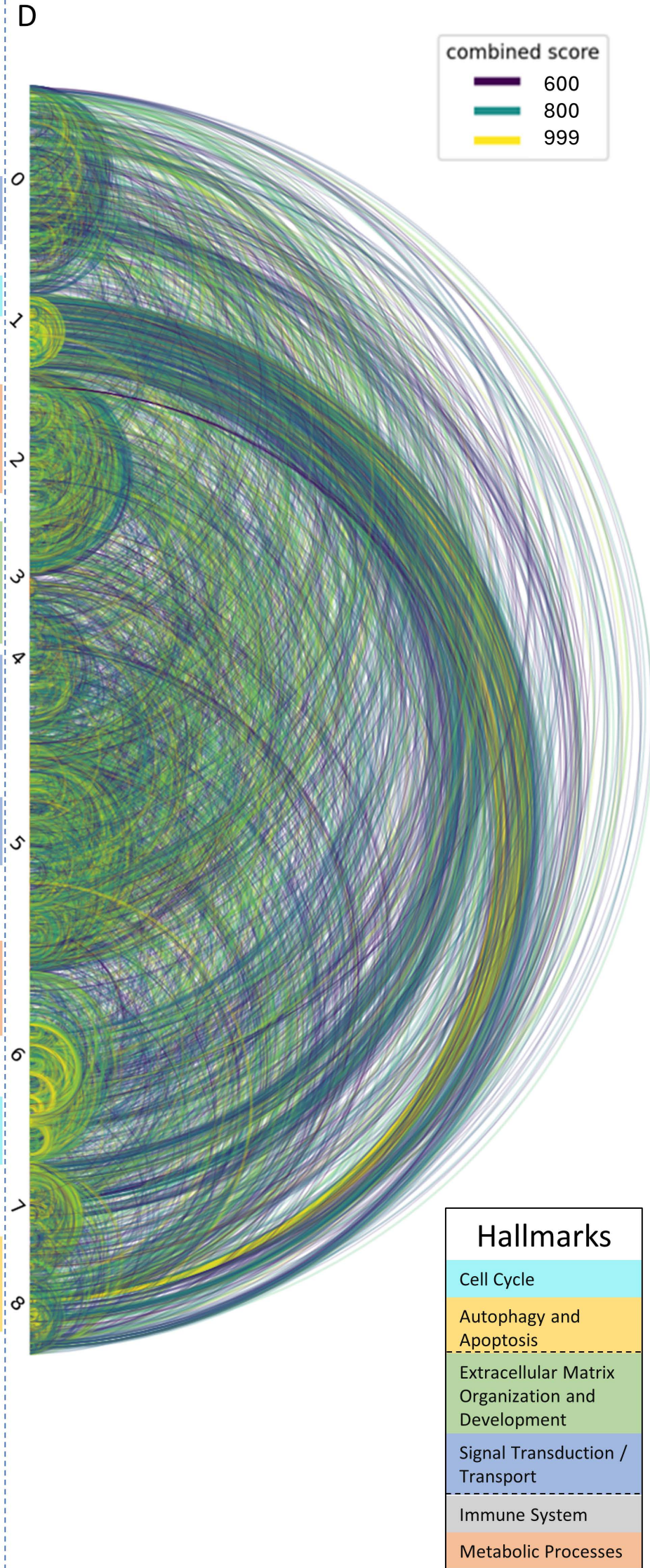
D





C

n	e	Hub Genes	Mean Reg Dir	Comm. Number: Associated Terms		
292	1601	CLTC CANX		0:	SNARE Binding Vesicle	
98	2283			1:	Translation	
286	3497	ALB	0.74	2:	ECM & Cyto- skeleton Organization	Complement & Coagulation Cascade Lipoprotein
32	197	RPTOR		3:	Autophagic Process mTOR Signaling Pathway	Cell Differentiation and Growth
190	974	DCTN1 DYNC1H1	-0.24	4:	ECM and Cytoskeleton Organization	Vesicle
323	3008	HRAS		5:	Actin Cytoskeleton	Cell Communication
260	2258	GOT2 GAPDH		6:	Carbohydrate, Antioxidant (Mt.), Respiratory Chain Complex (Mt.)	
157	2487		0.67	7:	RNA Modification, Spliceosome	
108	1194	RPS27A UBA52		8:	Proteolysis Ubiquitylation Proteasome	

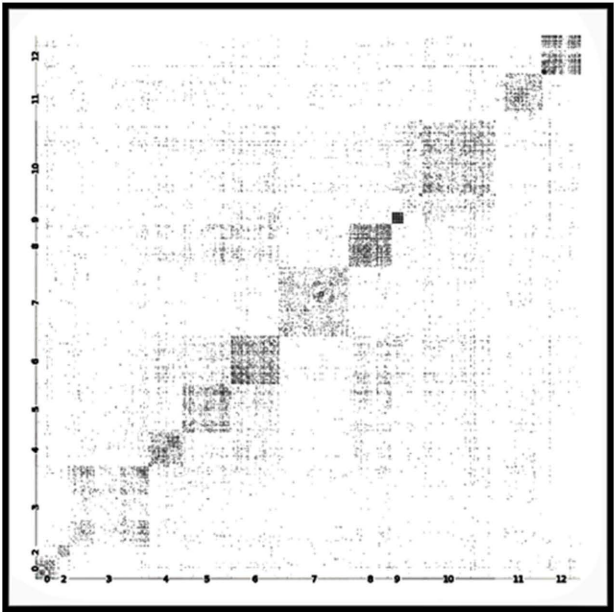


A

Network Properties		
n	e	Mean Reg. Dir.
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HD DEG

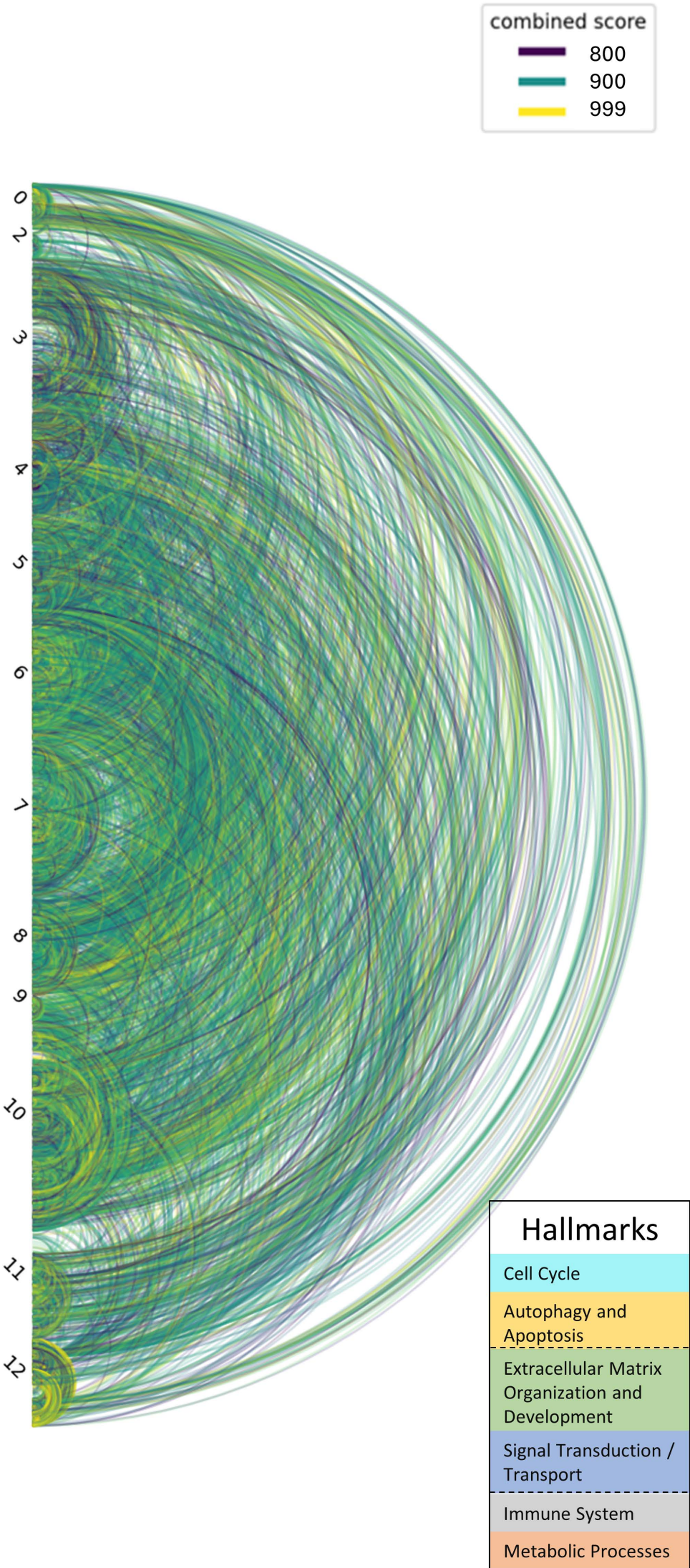
B



C

n	e	Hub Genes	Mean Reg Dir	Comm. Number: Associated Terms	
172	1046	HSPA9 HSP90AA1	-0.16	0:	Respiratory Chain Complex (Mt.) Chaperone Mediated Process
81	253	SLC30A1		2:	Sphingolipid, Homeostasis
617	6729	GRIA2	-0.42	3:	Ion Channels Synapsis Neurotransmitter Secretion
262	1628	GNB1		4:	Cell Communication Vesicle
375	2559	CDC42	0.18	5:	Actin Cytoskeleton Cell differentiation and growth
364	5507	CD4 TLR4	0.55	6:	Apoptotic Process Complement and coagulation cascade
541	2929	PPARA		7:	Lipid, Cholesterol, Fatty Acid Oxidation (Mt.), Branched AA Degradation
332	3794	FN1 ITGB1	0.29	8:	Collagen Cell Adhesion
81	687		0.39	9:	Ubiquitinylation Interferon
716	6272	TP53 MYC HDAC1	0.17	10:	Cell differentiation and growth Early Development
363	1675			11:	Autophagic Process Trans-membranal Transport
294	3010		-0.11	12:	Translation RNA Modification

D

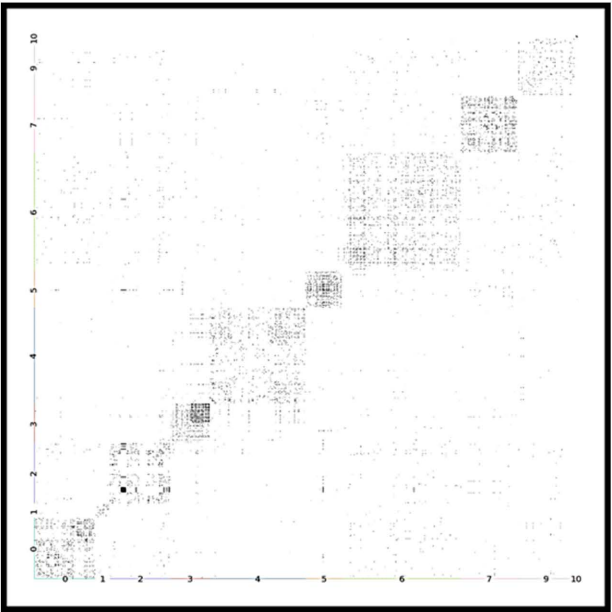


A

Network Properties		
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HD Prot

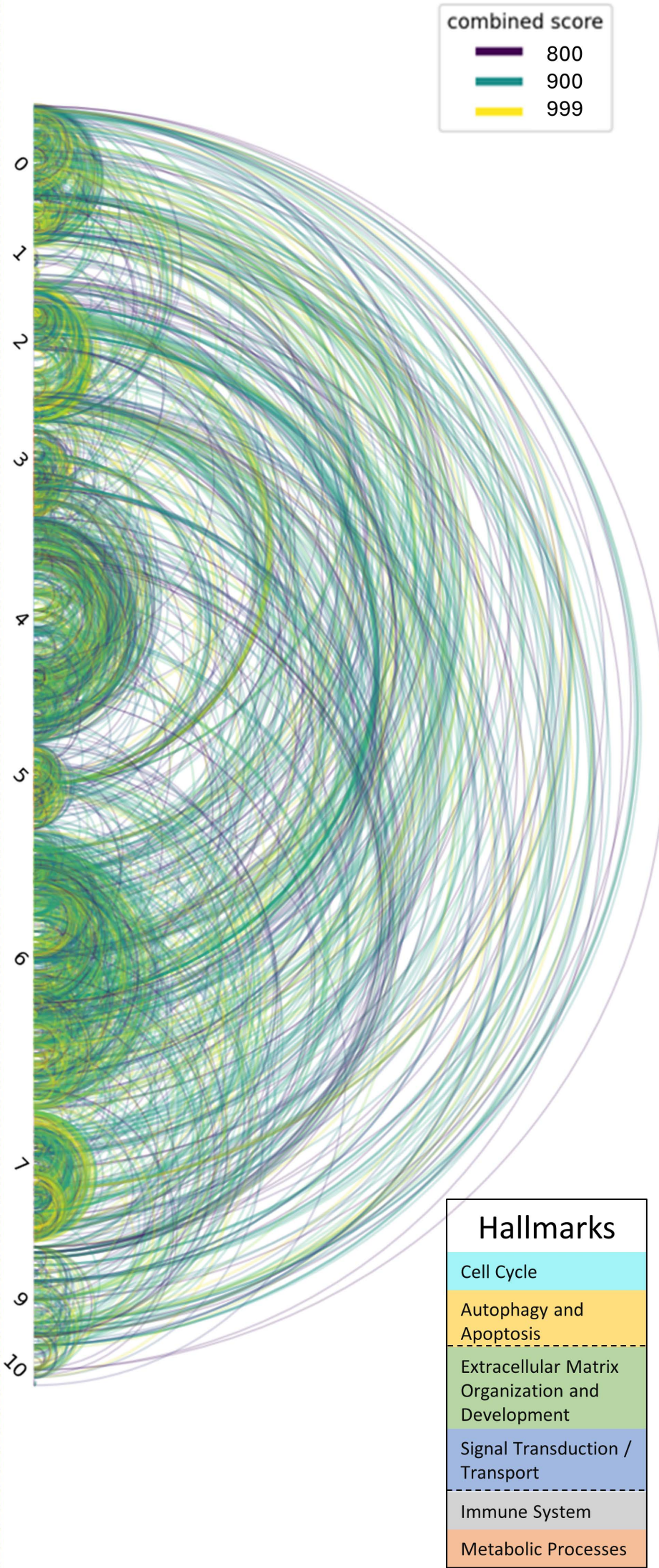
B



C

n	e	Hub Genes	Mean Reg Dir	Comm. Number: Associated Terms	
157	1269	RAB5A CLTC	-0.26	0:	SNARE Binding Vesicle
36	85	APOC3 CLU		1:	Complement and coagulation cascadeLipoprotein
158	987	HSP90AB1 PSMD4		2:	Chaperone Mediated Process, Proteasome
97	1039	NDUFS3	-0.78	3:	Respiratory Chain Complex (Mt.)
247	2415	ACO2 FH		4:	Fatty Acid Oxidation (Mt.), Carbohydrate
94	808		-0.36	5:	Translation
303	2683	CDC42 ACTB CTNNB1		6:	Actin Cytoskeleton, Cell Adhesion
145	1571	SRSF1 HNRNPK		7:	RNA Modification, Spliceosome
148	978	DLG4	-0.27	9:	Synapsis, Neurotransmitter Secretion
7	13	KRT1 KRT2 KRT5	1.0	10:	Keratin Cytoskeleton

D

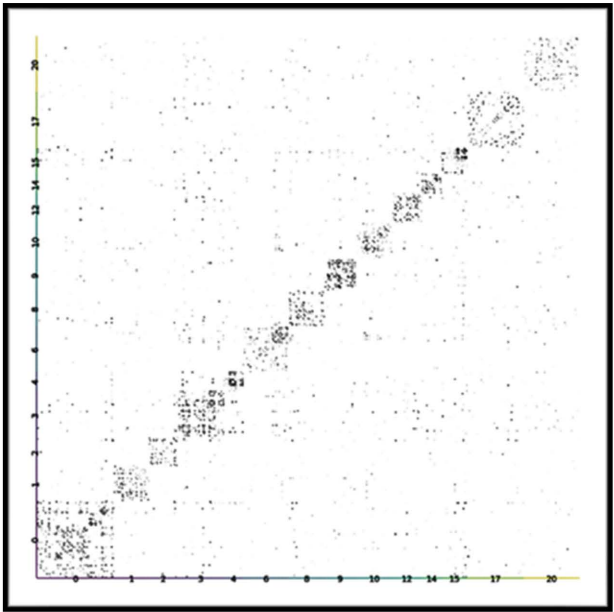


A

Network Properties		
n	e	Mean Reg. Dir.
806	2862	-0.80

HD Meth

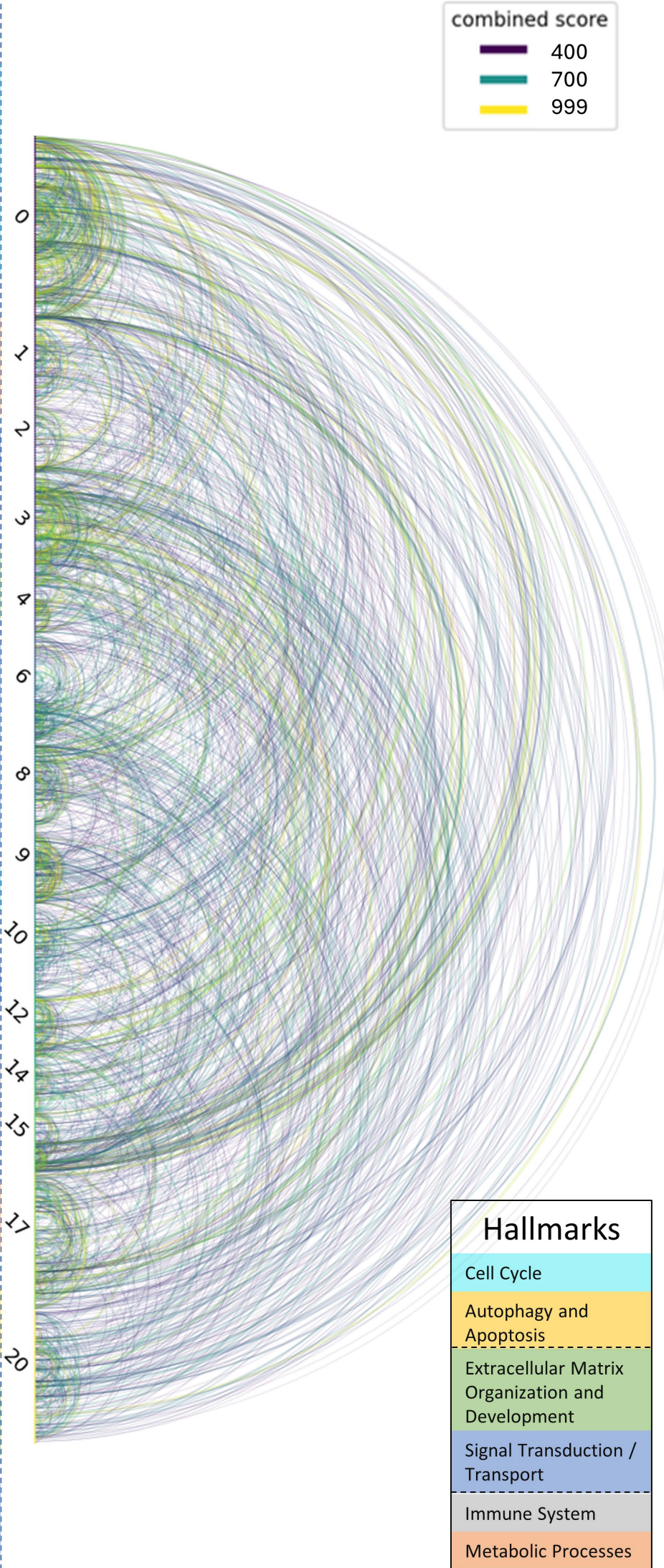
B



C

n	e	Hub Genes	Mean Reg Dir	Comm. Number: Associated Terms	
112	336	CDK2 DNMT1	-0.74	0:	Regulation of Cell Cycle, DNA Repair, Transcription, Chromatin
50	83	SNRPN LSM7	-0.83	1:	RNA Modification, Spliceosome
39	56	PPARGC1A	-0.67	2:	Fatty Acid Oxidation (Mt.), Carboxylic Acid (Mt.), Carbohydrate
67	168	RAF1	-0.8	3:	Cell Communication
28	49	DVL2 LRP5 LRP6	-0.95	4:	Apoptotic Process Cell differentiation & growth
66	136	CACNA1C KCNQ1 KCNJ2	-0.86	6:	Ion Channels, Voltage-gated Channel (Cardiac) Muscle Action Potential
52	93	PAFAH1B1	-0.78	8:	ECM- & cytoskeleton organization Axonal Transport
45	122	RPS6 RPL19 RPS15	-0.67	9:	Translation
53	83	ADCY6 ADCY9 GNAS	-0.82	10:	Cell Communication
42	88	IRF1 IRF4	-0.9	12:	Immune Response, Defense Response to Other Organism, Cytokine, Interferon
29	53	NDUFAB1	-0.76	14:	Mitochondrial Translation Respiratory Chain Complex (Mt.)
37	87	PSMA6 USP14 PSMA3	-0.68	15:	Ubiquitylation, Proteasome
82	144	CAV1 THBS1	-0.89	17:	ECM- and cytoskeleton organization, Cell Migration
81	127	GAK	-0.79	20:	Localization Trans-Golgi-Network

D



A

Network Properties		
n	e	Mean Reg. Dir.
16	13	n.a.

HD SNP

n	e	Hub Genes	Comm. Number: Associated Terms
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None

B

Network Properties		
n	e	Mean Reg. Dir.
18	12	-0.75

ALS Meth

n	e	Hub Genes	Mean Reg Dir	Comm. Number: Associated Terms
2	1	*	*	1: Protein

C

n	e	Mean Reg. Dir.
147	214	n.a.

ALS SNP

n	e	Hub Genes	Comm. Number: Associated Terms
20	35	NRXN3 ANK3	1: Cell Adhesion
9	9	MAT2B SQLE STOX1	2: Cholesterol
2	1	*	6: Spindle Apparatus
6	6	LAMA3 LAMA2 ITGA9	19:
5	6	*	20: Fatty Acid Oxidation (Mt.) Lipid

Hallmarks
Cell Cycle
Autophagy and Apoptosis
Extracellular Matrix Organization and Development
Signal Transduction / Transport
Immune System
Metabolic Processes