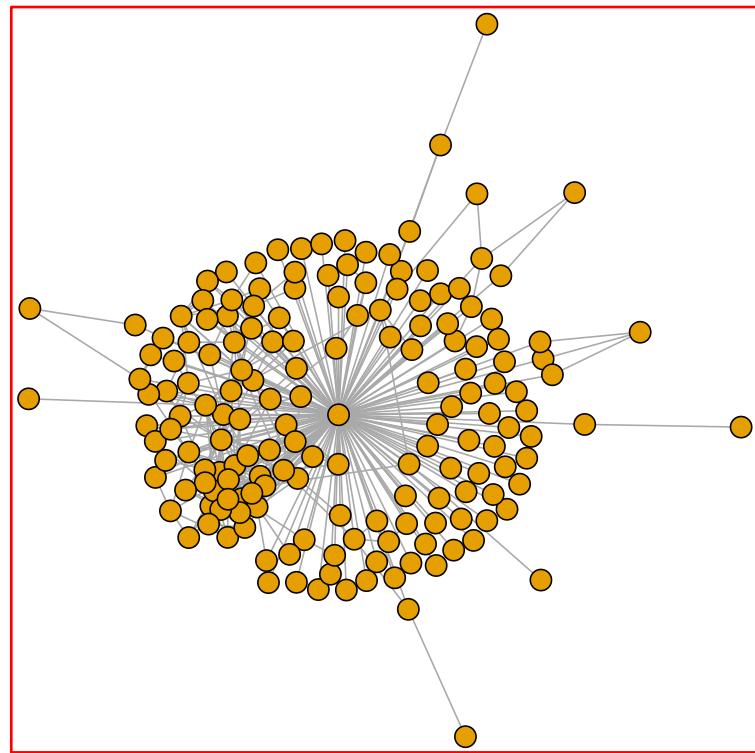
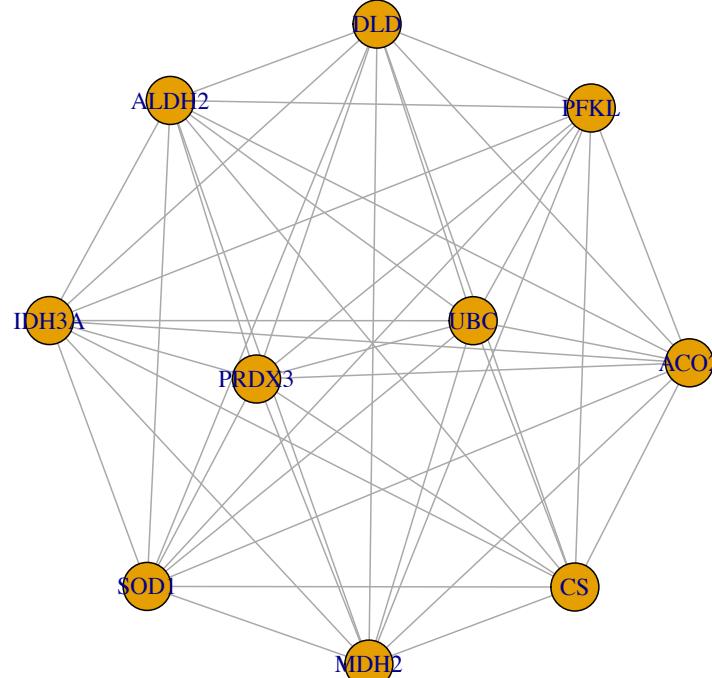


HALLMARKADIPOGENESIS



Subnetwork: 190 vertices, 445 edges
(unconnected vertices omitted)



5 largest cliques w/ degree = 10

NetBAS	DAVID
23.029	3.8E-7
22.952	1.7E-7
18.985	8.5E-8
16.609	8.5E-3
16.448	NA
15.334	1.9E-8
15.266	2.9E-12
15.249	5.4E-7
12.499	NA
12.331	6.6E-3

KEGG Pathways

Parkinson's disease
Oxidative phosphorylation
Alzheimer's disease
Glycolysis / Gluconeogenesis
Thermogenesis
Non-alcoholic fatty liver disease (NAFLD)
Citrate cycle (TCA cycle)
Huntington's disease
Fructose and mannose metabolism
Pyruvate metabolism

HALLMARK_AdIPOGENESIS

18.434	2.5E-5	GO:0006120
17.769	5.2E-3	GO:0032981
16.574	1.4E-36	GO:0055114
15.205	3.6E-13	GO:0006099
14.48	3.7E-5	GO:1902600
14.236	1.8E-5	GO:0006122
13.295	4.6E-15	GO:0009060
13.176	3.5E-2	GO:0006096
12.899	3.3E-2	GO:0061621
12.64	5.0E-15	GO:0022900

NetBAS DAVID Biological Process Terms

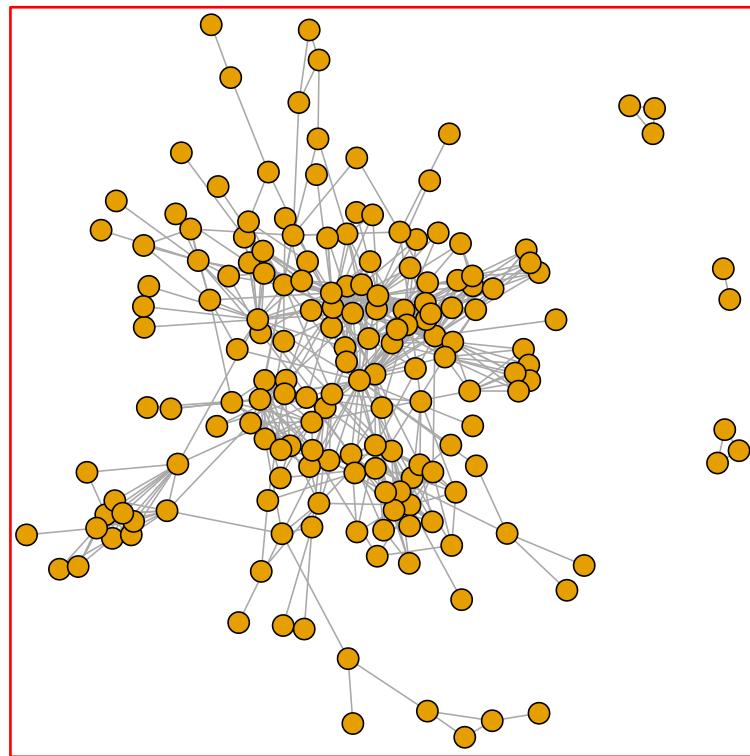
26.675	6.5E-32	GO:0005739
25.948	4.5E-14	GO:0005759
21.602	2.1E-26	GO:0005743
18.954	1.4E-2	GO:0005747
16.522	NA	GO:0005751
15.986	8.3E-13	GO:0070062
15.674	2.1E-6	GO:0043209
15.17	2.9E-4	GO:0005750
12.837	NA	GO:1904813
11.7	1.2E-3	GO:0005758

NetBAS DAVID Cellular Component Terms

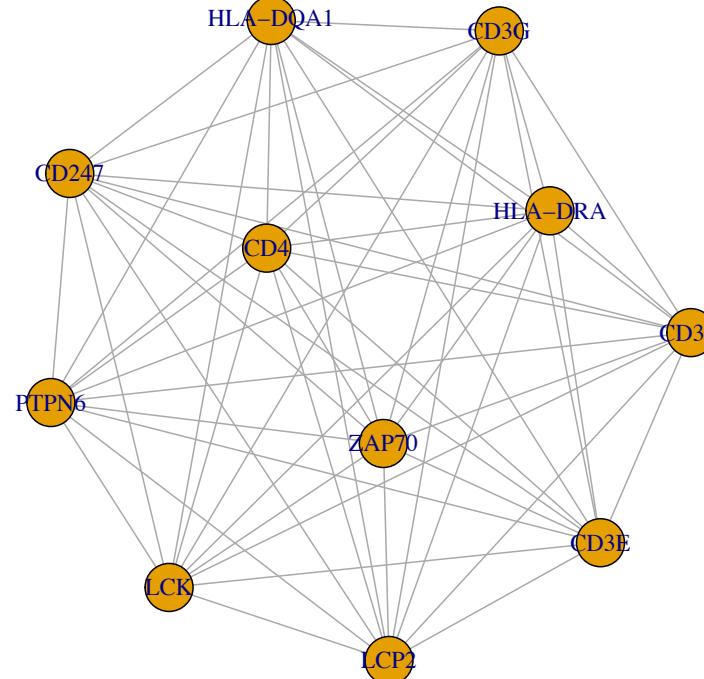
18.01	1.5E-2	GO:0008131
15.36	4.0E-2	GO:0004129
14.398	NA	GO:0004332
13.923	1.4E-4	GO:0008121
13.446	1.5E-13	GO:0009055
11.813	NA	GO:0051082
11.777	NA	GO:0005525
11.386	NA	GO:0030170
11.144	1.5E-2	GO:0003954
10.701	NA	GO:0061609

NetBAS DAVID Molecular Function Terms

HALLMARK_ALLOGRAFT_REJECTION



Subnetwork: 199 vertices, 616 edges
(unconnected vertices omitted)



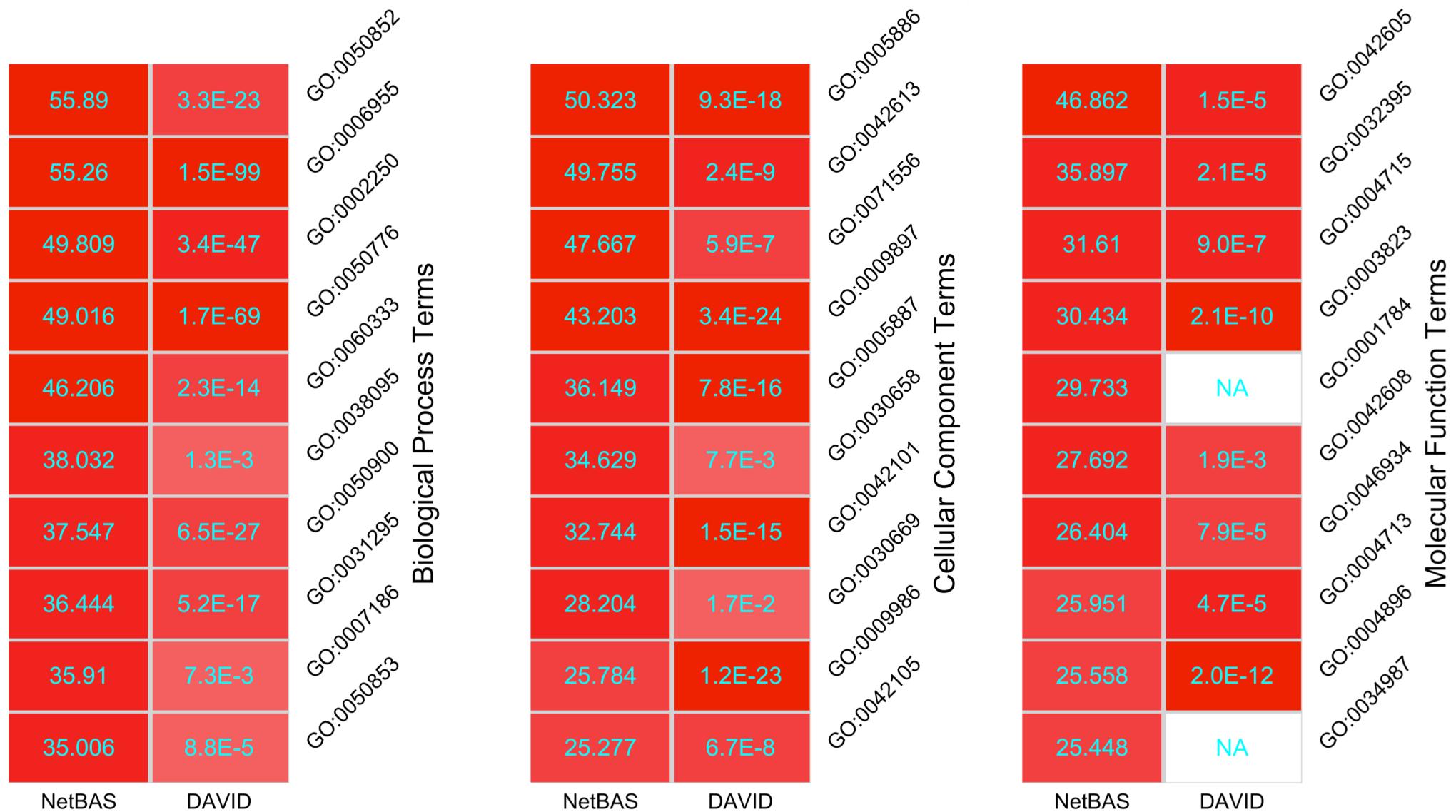
2 largest cliques w/ degree = 11

NetBAS	DAVID
52.186	1.6E-19
50.043	1.1E-24
49.944	1.6E-30
49.216	2.3E-12
45.403	3.6E-12
44.361	7.3E-14
42.576	1.3E-11
42.545	NA
42.055	5.8E-19
41.367	NA

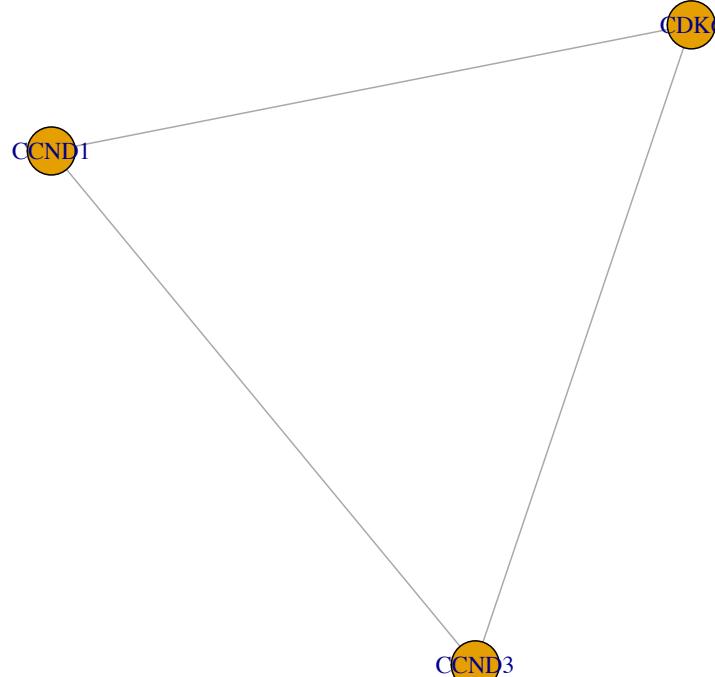
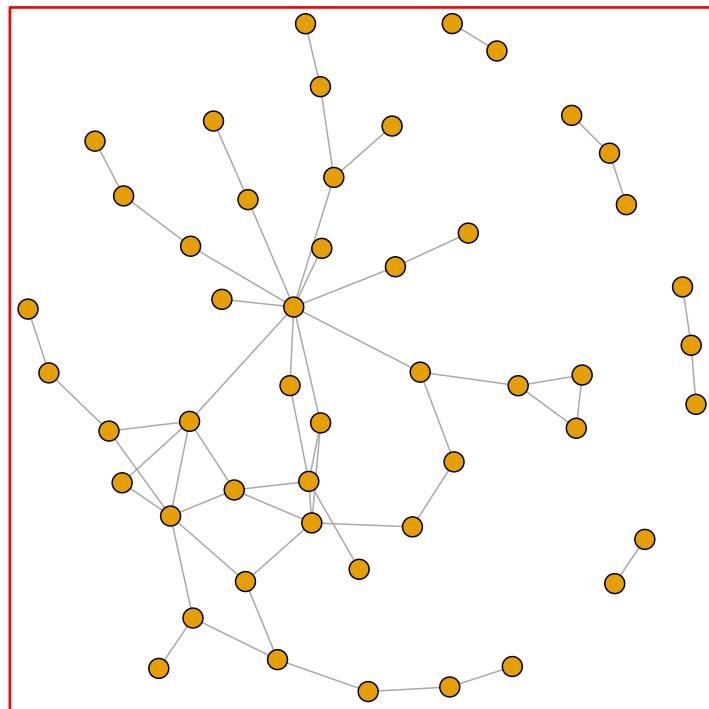
Autoimmune thyroid disease
Graft-versus-host disease
Allograft rejection
Hematopoietic cell lineage
Hemadhesion molecules (CAMs)
Cell adhesion mediated cytotoxicity
Asthma
Natural killer cell mediated differentiation
Th1 and Th2 cell differentiation
Jak-STAT signaling pathway
Th17 cell differentiation

KEGG Pathways

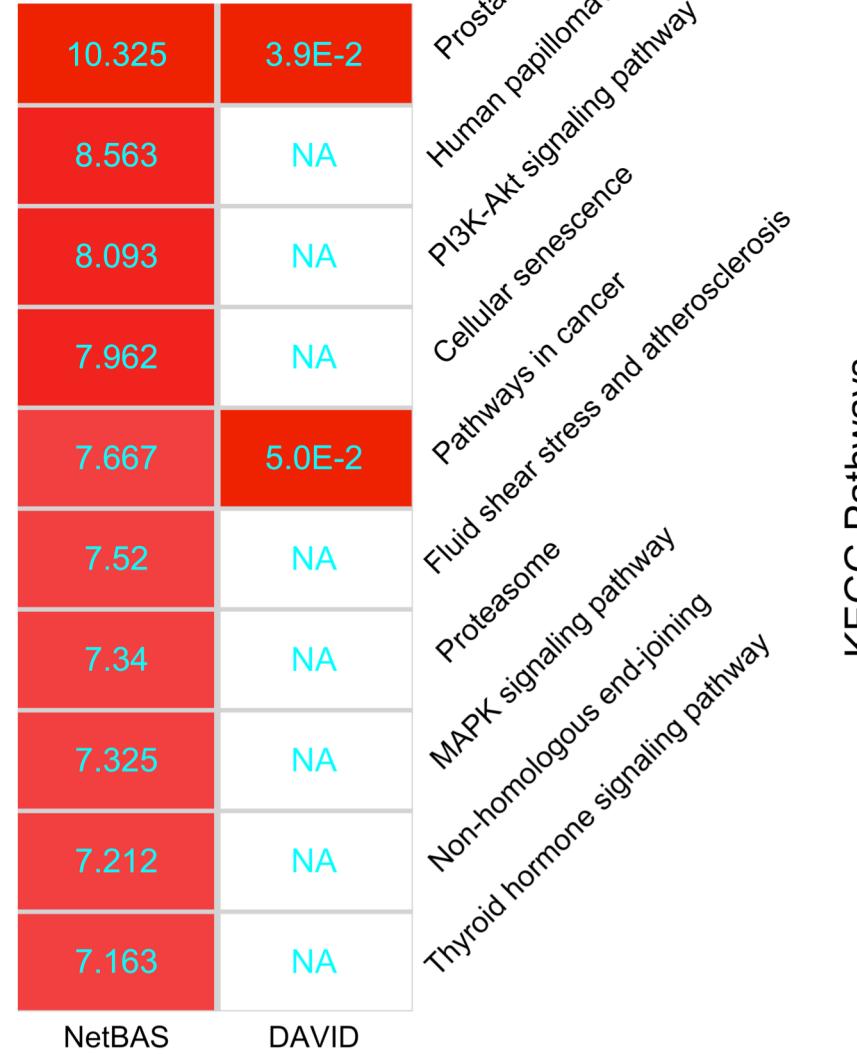
HALLMARK_ALLOGRAFT_REJECTION



HALLMARK_ANDROGEN_RESPONSE

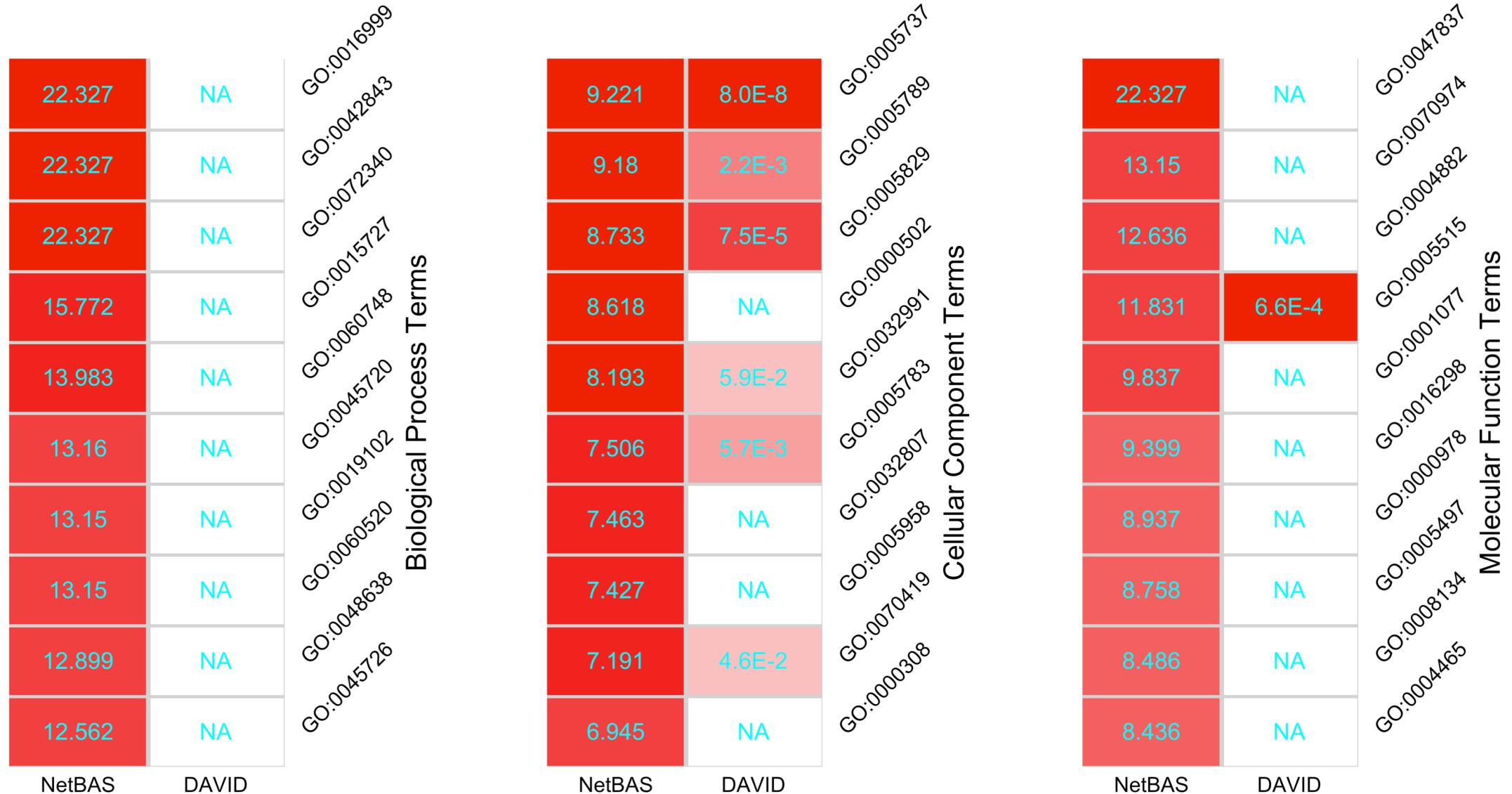


6 largest cliques w/ degree = 3

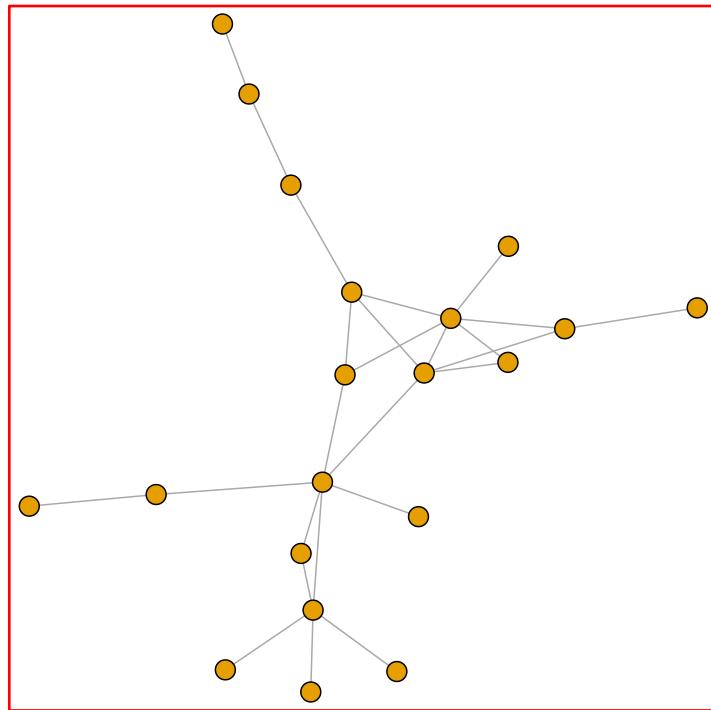


KEGG Pathways

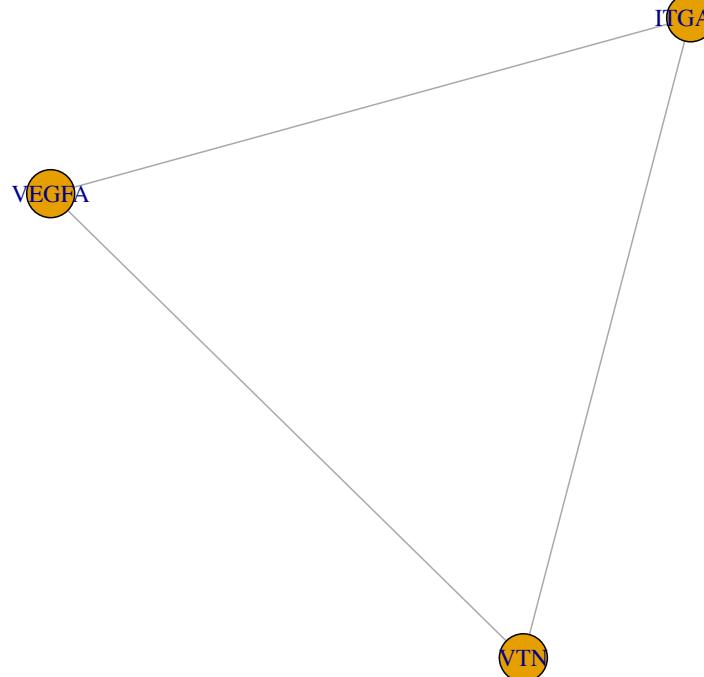
HALLMARK_ANDROGEN_RESPONSE



HALLMARK_ANGIOGENESIS



Subnetwork: 35 vertices, 25 edges
(unconnected vertices omitted)



5 largest cliques w/ degree = 3

KEGG Pathways	NetBAS	DAVID
Cytokine-cytokine receptor interaction	21.951	NA
Focal adhesion	21.212	5.5E-7
ECM-receptor interaction	20.528	4.1E-3
Chemokine signaling pathway	20.482	3.2E-2
Neuroactive ligand-receptor interaction	18.766	NA
Axon guidance	18.195	NA
Rap1 signaling pathway	17.501	NA
Taste transduction	16.315	NA
Regulation of actin cytoskeleton	15.366	7.4E-3
Phospholipase D signaling pathway	14.215	NA

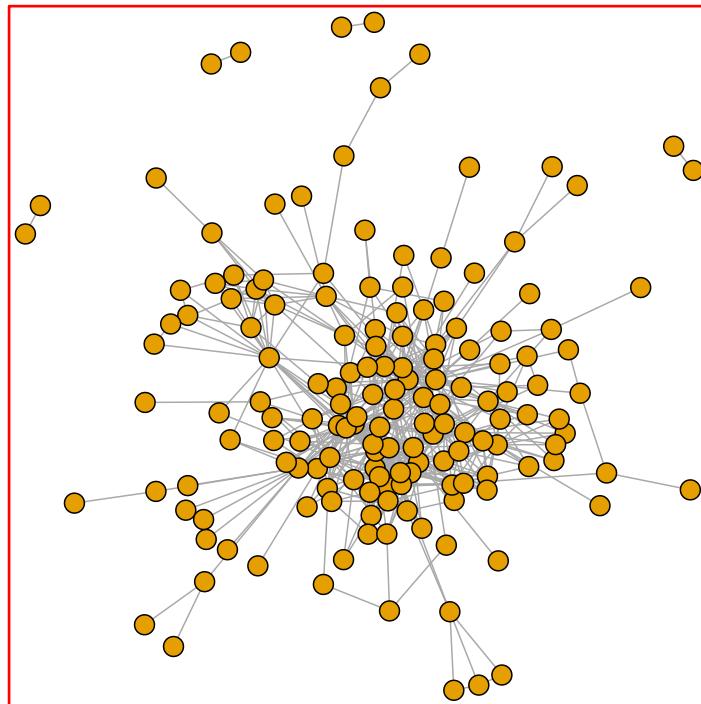
HALLMARK_ANGIOGENESIS

		GO:0007186
32.793	NA	GO:0002818
31.591	NA	GO:0000768
21.072	NA	GO:0010469
20.86	NA	GO:0006935
20.182	1.1E-5	GO:0048010
20.174	9.7E-7	GO:0070098
20.001	NA	GO:0030198
19.196	7.3E-10	GO:0060326
18.83	1.6E-3	GO:0006954
17.249	2.4E-4	

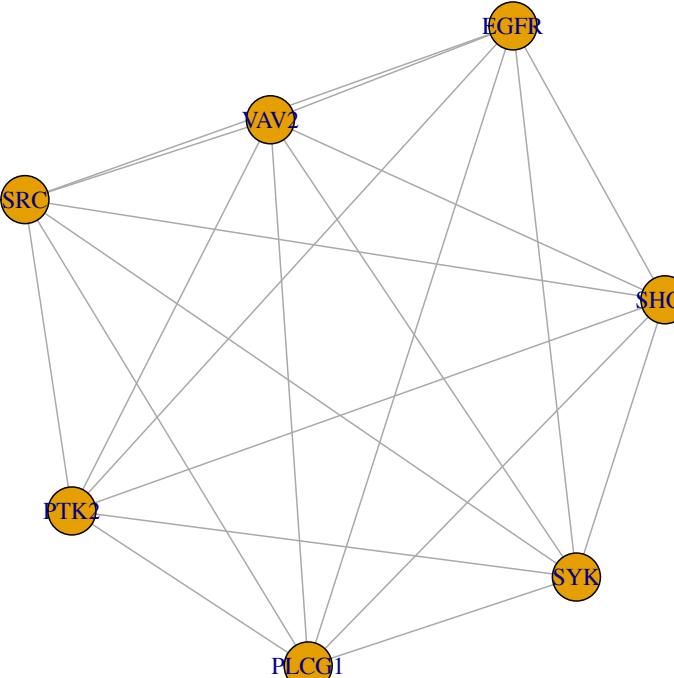
		GO:0005886
23.62	5.8E-3	GO:0005887
22.874	2.4E-3	GO:0005576
18.604	6.0E-10	GO:0031012
18.279	4.5E-6	GO:1990512
18.221	NA	GO:0005615
17.15	8.8E-12	GO:0009891
15.929	NA	GO:0009986
13.659	7.9E-6	GO:0034358
12.865	7.0E-2	GO:0043235
12.454	3.1E-3	

		GO:0004930
24.619	NA	GO:0008201
18.049	2.3E-18	GO:0008009
16.74	9.4E-2	GO:0050840
15.955	1.6E-4	GO:0005178
15.953	NA	GO:0033038
15.762	NA	GO:0043185
15.562	NA	GO:0008083
14.446	3.0E-4	GO:0046934
14.313	NA	GO:0008747
14.1	NA	

HALLMARK_APICAL_JUNCTION



Subnetwork: 194 vertices, 570 edges
(unconnected vertices omitted)

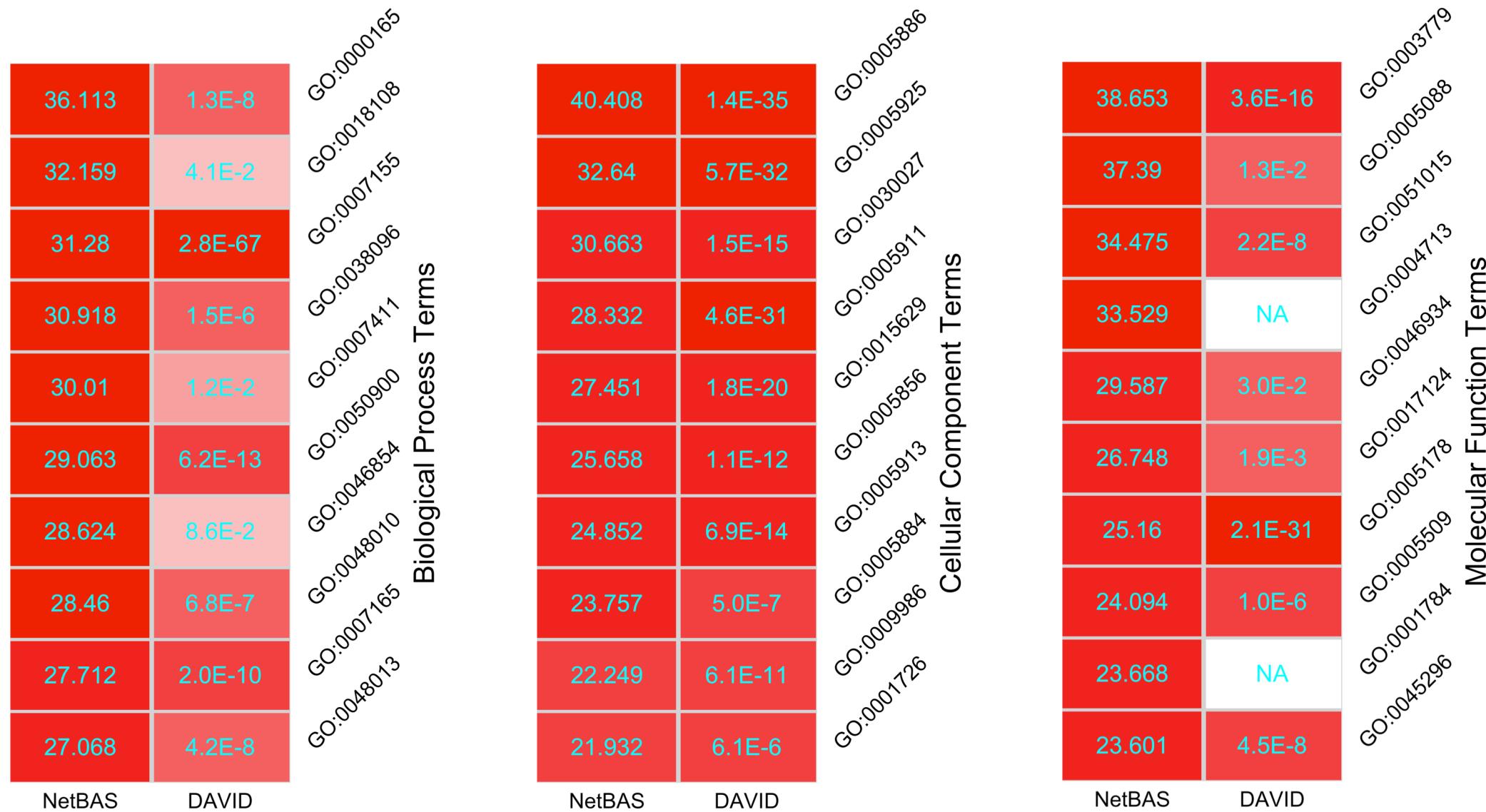


7 largest cliques w/ degree = 7

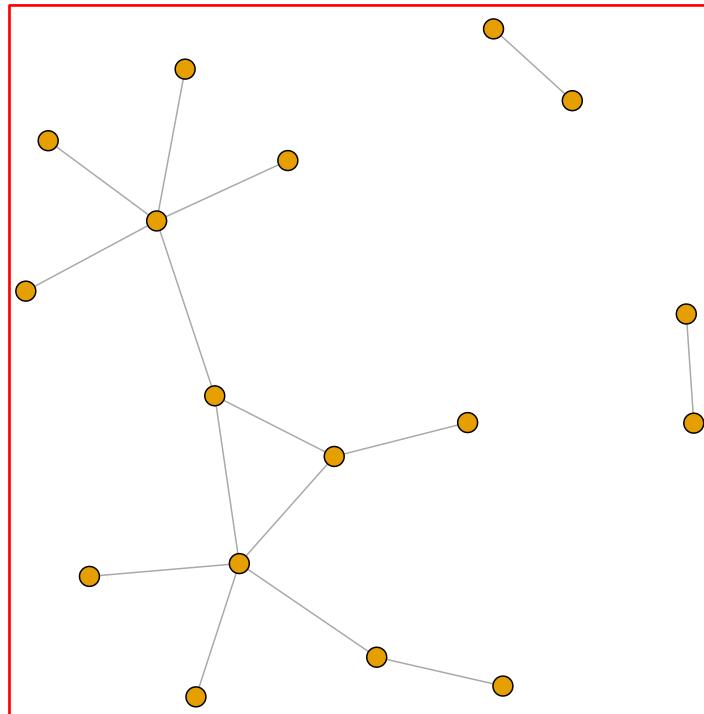
NetBAS	DAVID
43.193	1.0E-17
38.862	2.4E-23
34.213	5.8E-12
32.96	1.2E-3
32.702	1.0E-2
30.809	6.9E-45
29.119	4.8E-8
28.697	8.4E-10
28.364	2.0E-8
26.056	1.1E-7

Regulation of actin cytoskeleton
Focal adhesion
Rap1 signaling pathway
Ras signaling pathway
Axon guidance
Leukocyte transendothelial migration
Fc gamma R-mediated phagocytosis
Proteoglycans in cancer
Bacterial invasion of epithelial cells
PI3K-Akt signaling pathway

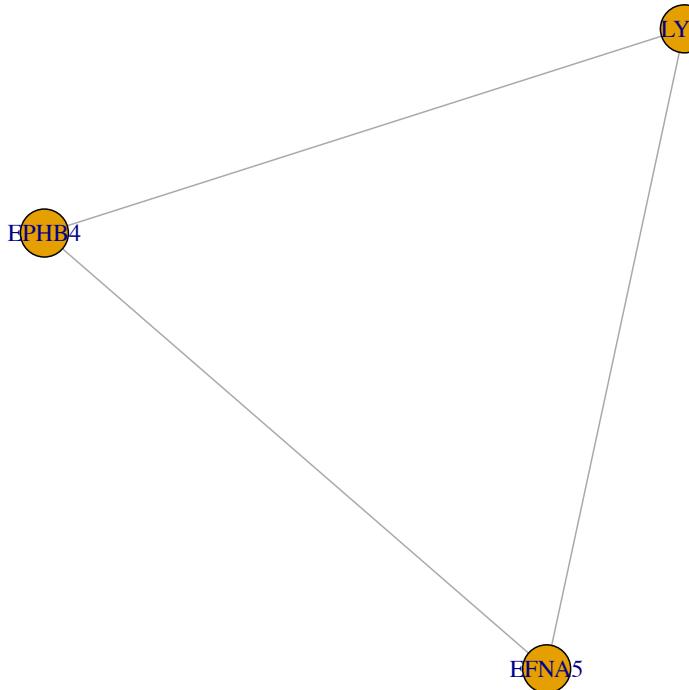
HALLMARK_APICAL_JUNCTION



HALLMARK_APICAL_SURFACE



Subnetwork: 42 vertices, 15 edges
(unconnected vertices omitted)



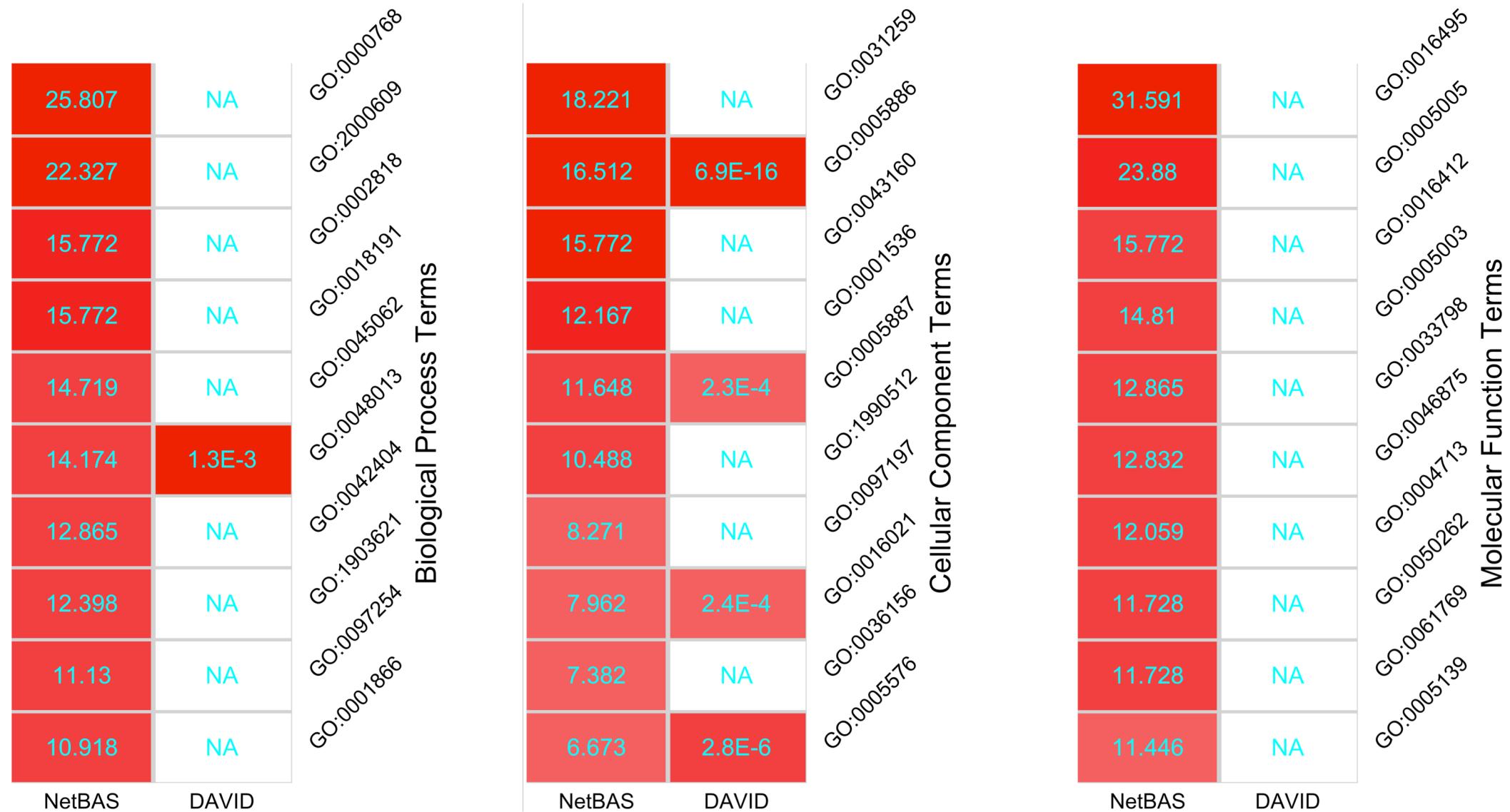
1 largest cliques w/ degree = 3

	NetBAS	DAVID
12.106	5.2E-2	
10.459	NA	
8.682	NA	
6.949	NA	
6.919	NA	
6.868	NA	
6.591	NA	
6.472	NA	
6.379	NA	
6.311	NA	

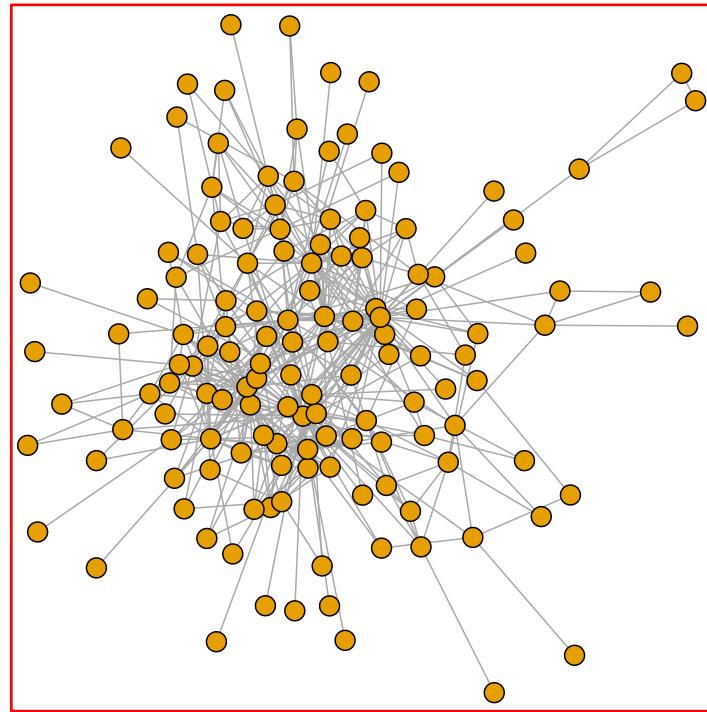
KEGG Pathways

- Axon guidance
- Jak-STAT signaling pathway
- Fc epsilon RI signaling pathway
- Phospholipase D signaling pathway
- Natural killer cell mediated cytotoxicity
- Prolactin signaling pathway
- Fc gamma R-mediated phagocytosis
- Osteoclast differentiation
- Chemokine signaling pathway
- Glycosaminoglycan degradation

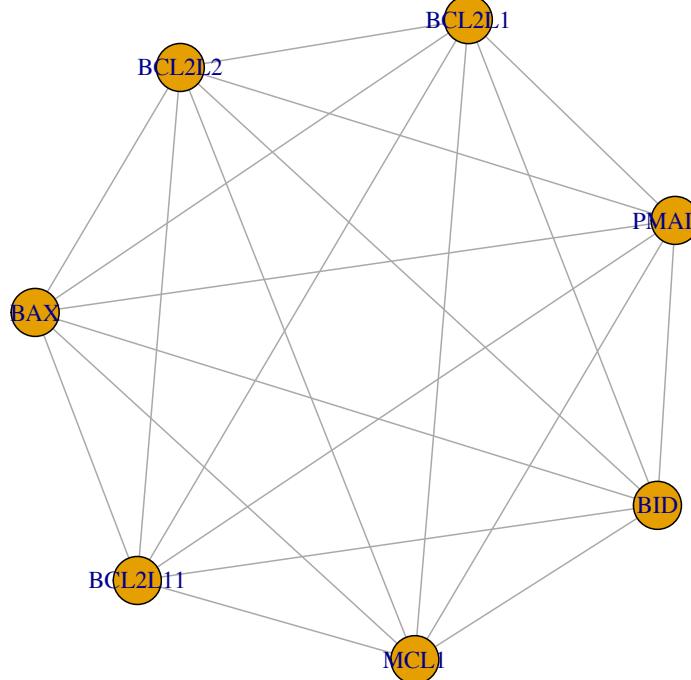
HALLMARK_APICAL_SURFACE



HALLMARK_APOPTOSIS



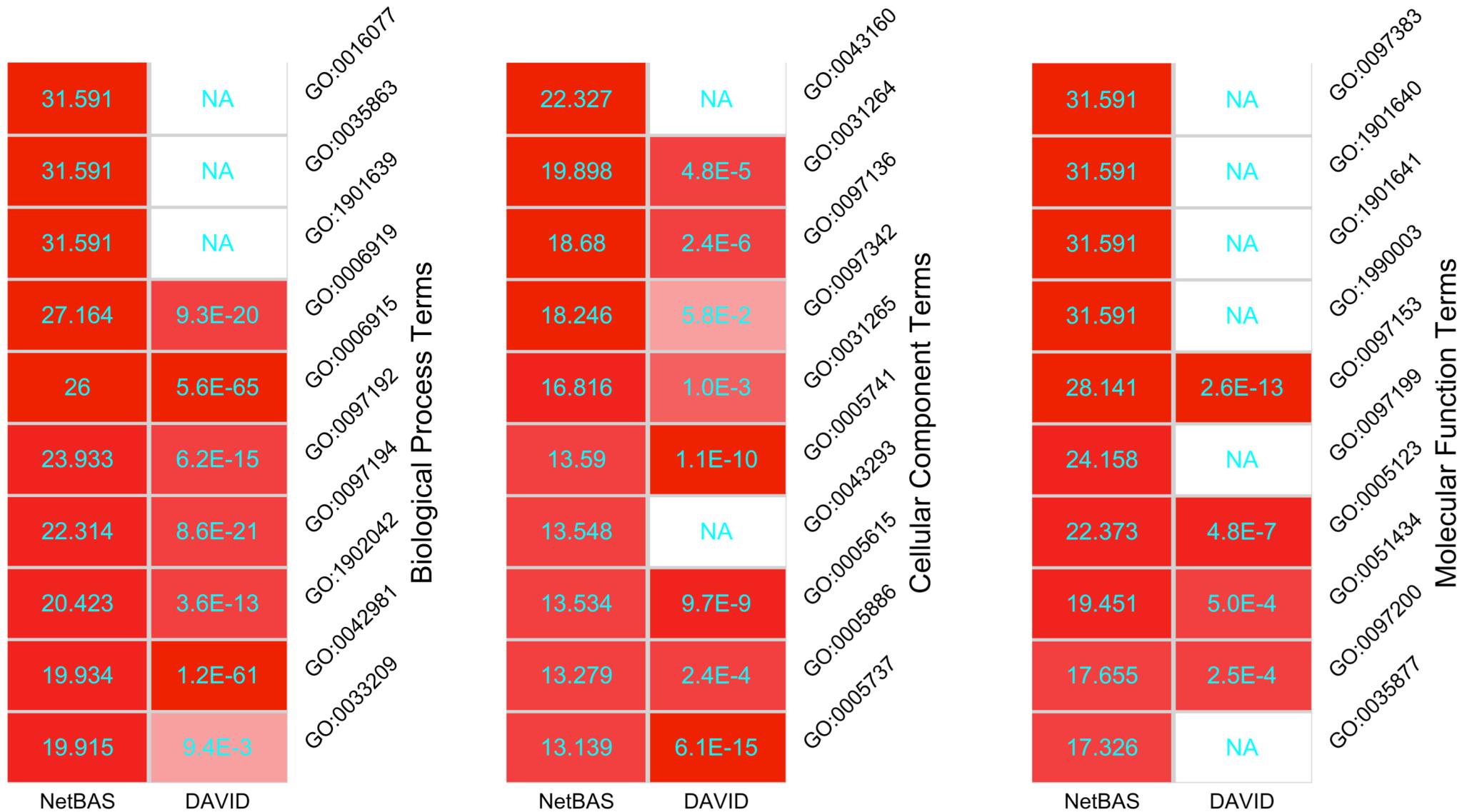
Subnetwork: 159 vertices, 467 edges
(unconnected vertices omitted)



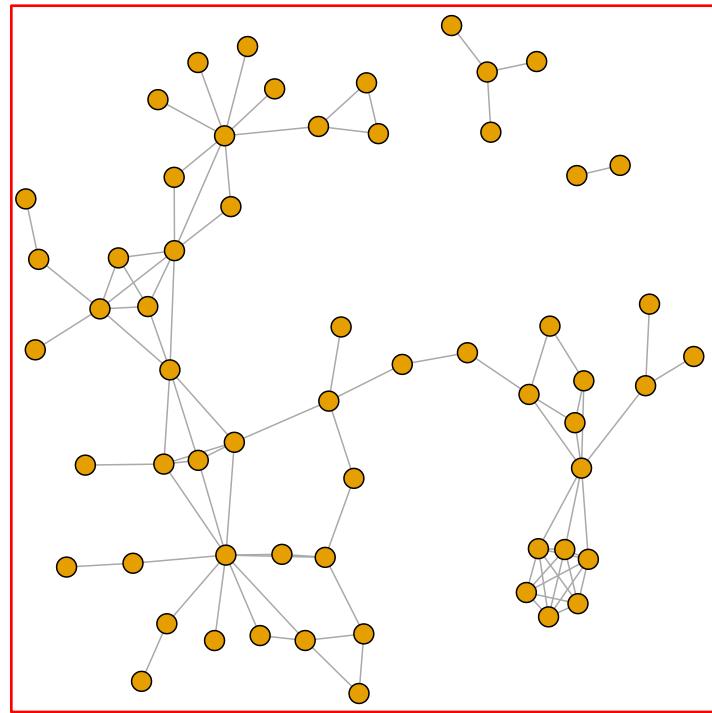
NetBAS	DAVID
34.192	NA
29.849	2.6E-11
29.473	1.2E-12
26.252	1.7E-6
26.148	2.5E-15
22.999	8.9E-5
22.567	NA
22.442	4.0E-5
21.473	2.1E-3
21.028	4.8E-3

KEGG Pathways	Apoptosis - multiple species
Hepatitis B	
Pathways in cancer	
TNF signalling pathway	
Apoptosis	
Small cell lung cancer	
AGE-RAGE signalling pathway in diabetic complications	
NOD-like receptor signalling pathway	
Toll-like receptor signalling pathway	
Pancreatic cancer	

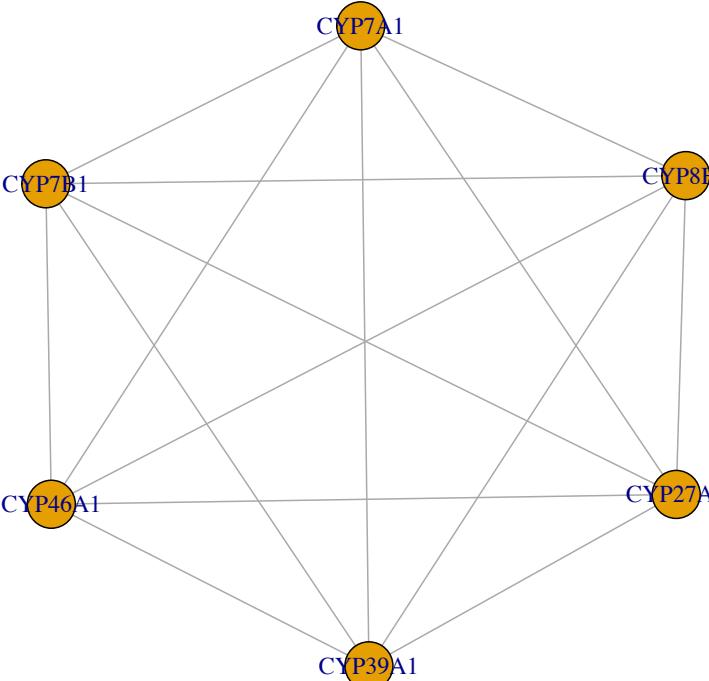
HALLMARK_APOPTOSIS



HALLMARK_BILE_ACID_METABOLISM



Subnetwork: 111 vertices, 89 edges
(unconnected vertices omitted)

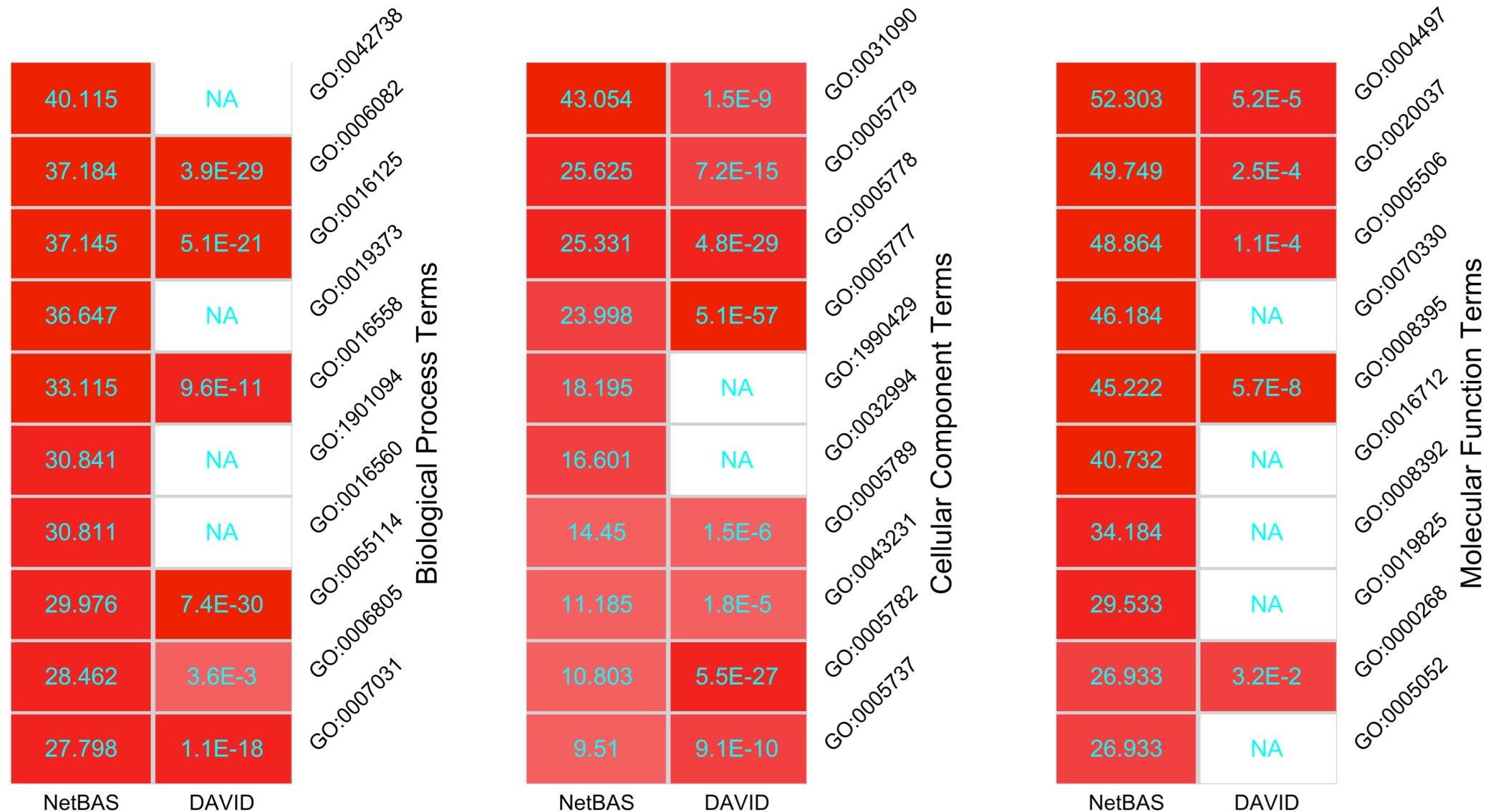


1 largest cliques w/ degree = 6

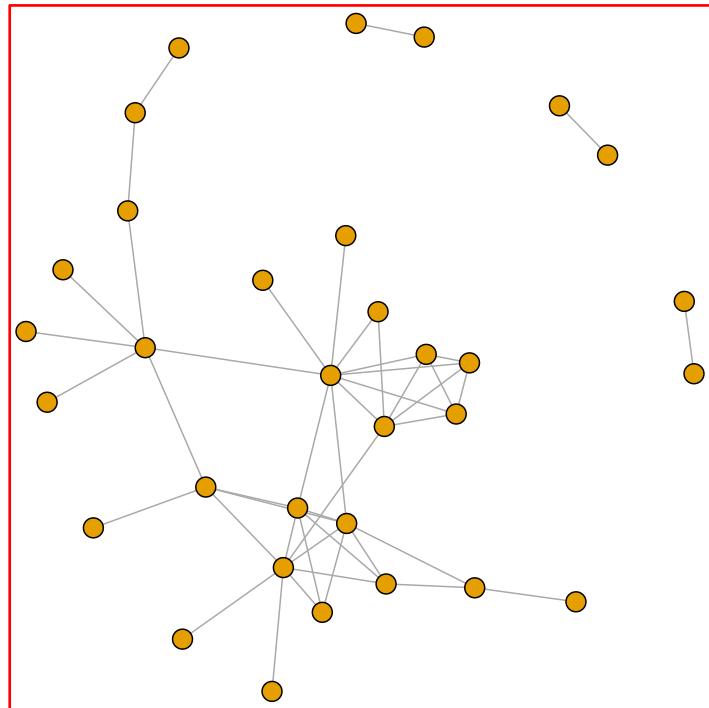
NetBAS	DAVID
27.057	7.8E-4
26.108	2.9E-51
22.025	NA
22.002	NA
21.492	NA
21.017	NA
19.969	NA
17.25	NA
16.91	4.5E-20
11.787	NA

Steroid hormone biosynthesis
Peroxisome
Chemical carcinogenesis
Linoleic acid metabolism
Retinol metabolism
Metabolism of xenobiotics by cytochrome P450
Arachidonic acid metabolism
Drug metabolism - cytochrome P450
Primary bile acid biosynthesis
Steroid biosynthesis

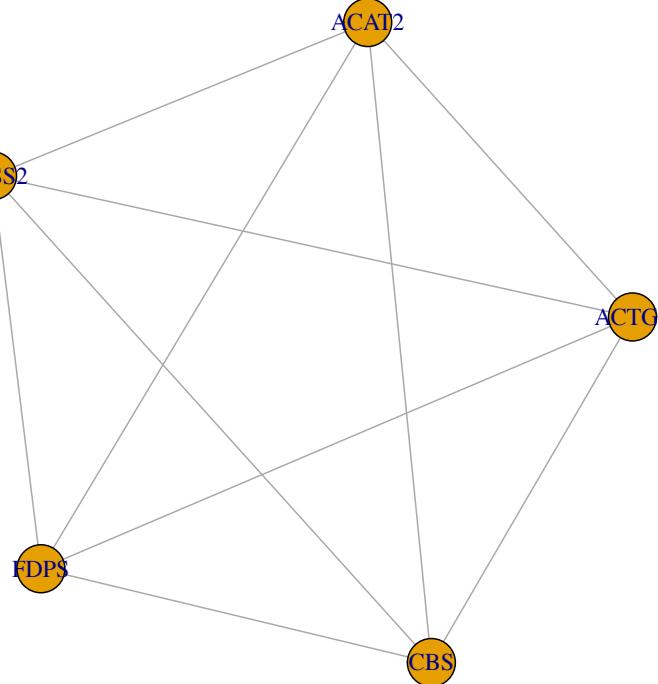
HALLMARK_BILE_ACID_METABOLISM



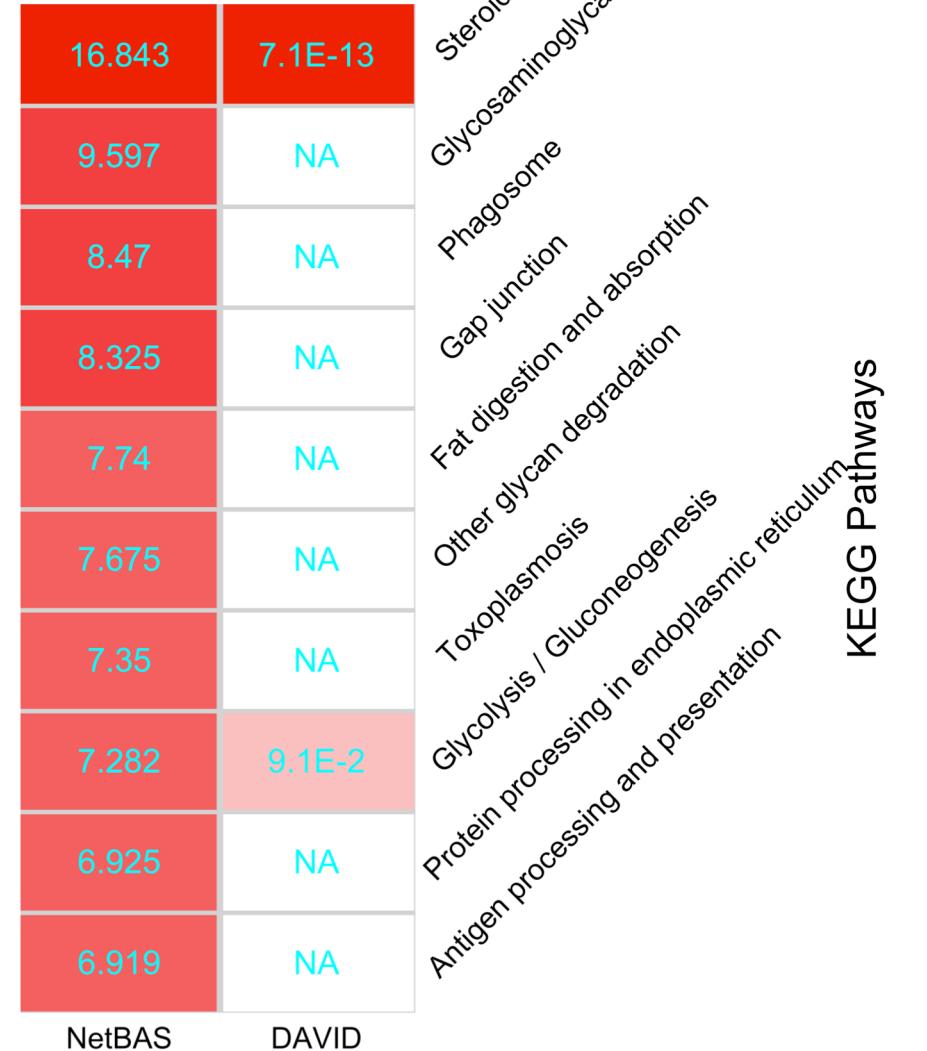
HALLMARK_CHOLESTEROL_HOMEOSTASIS



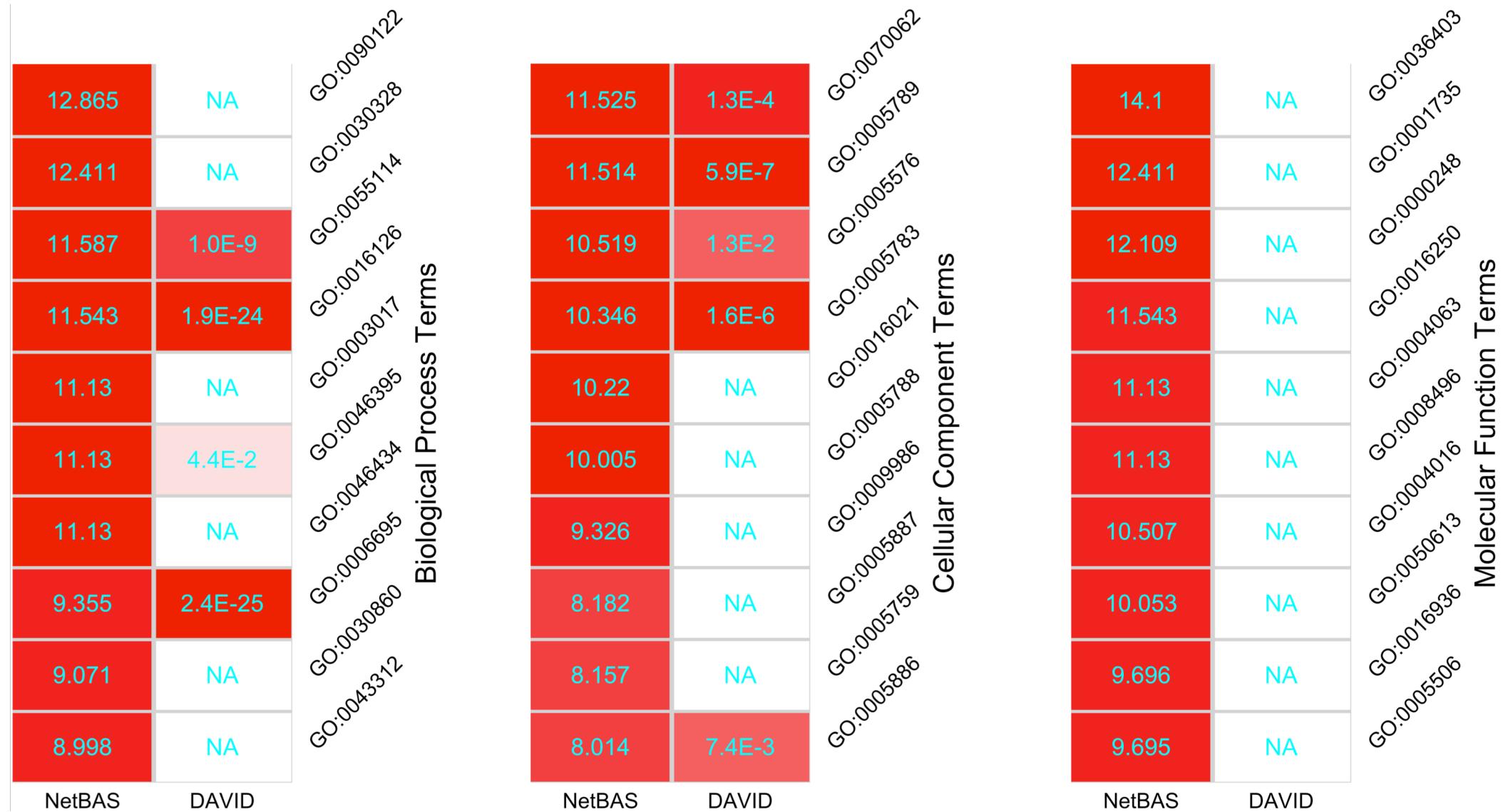
Subnetwork: 73 vertices, 46 edges
(unconnected vertices omitted)



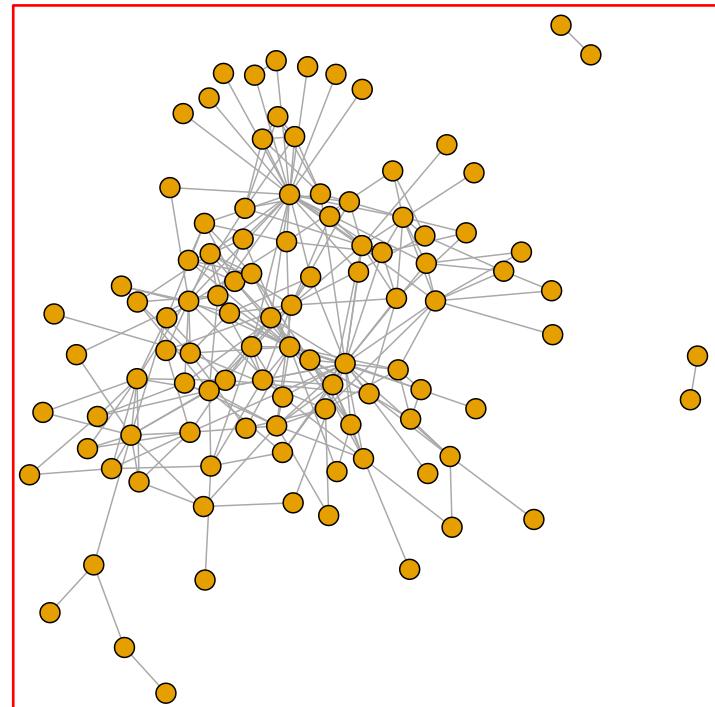
1 largest cliques w/ degree = 5



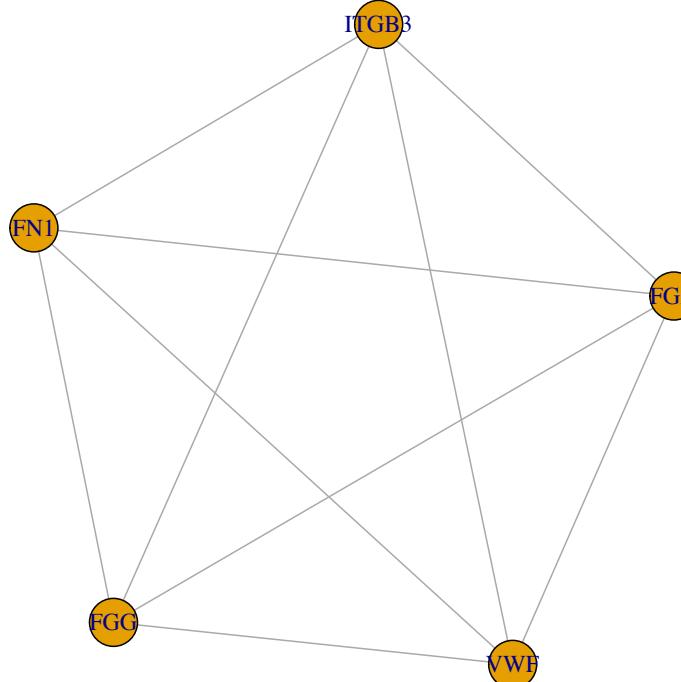
HALLMARK_CHOLESTEROL_HOMEOSTASIS



HALLMARK_COAGULATION



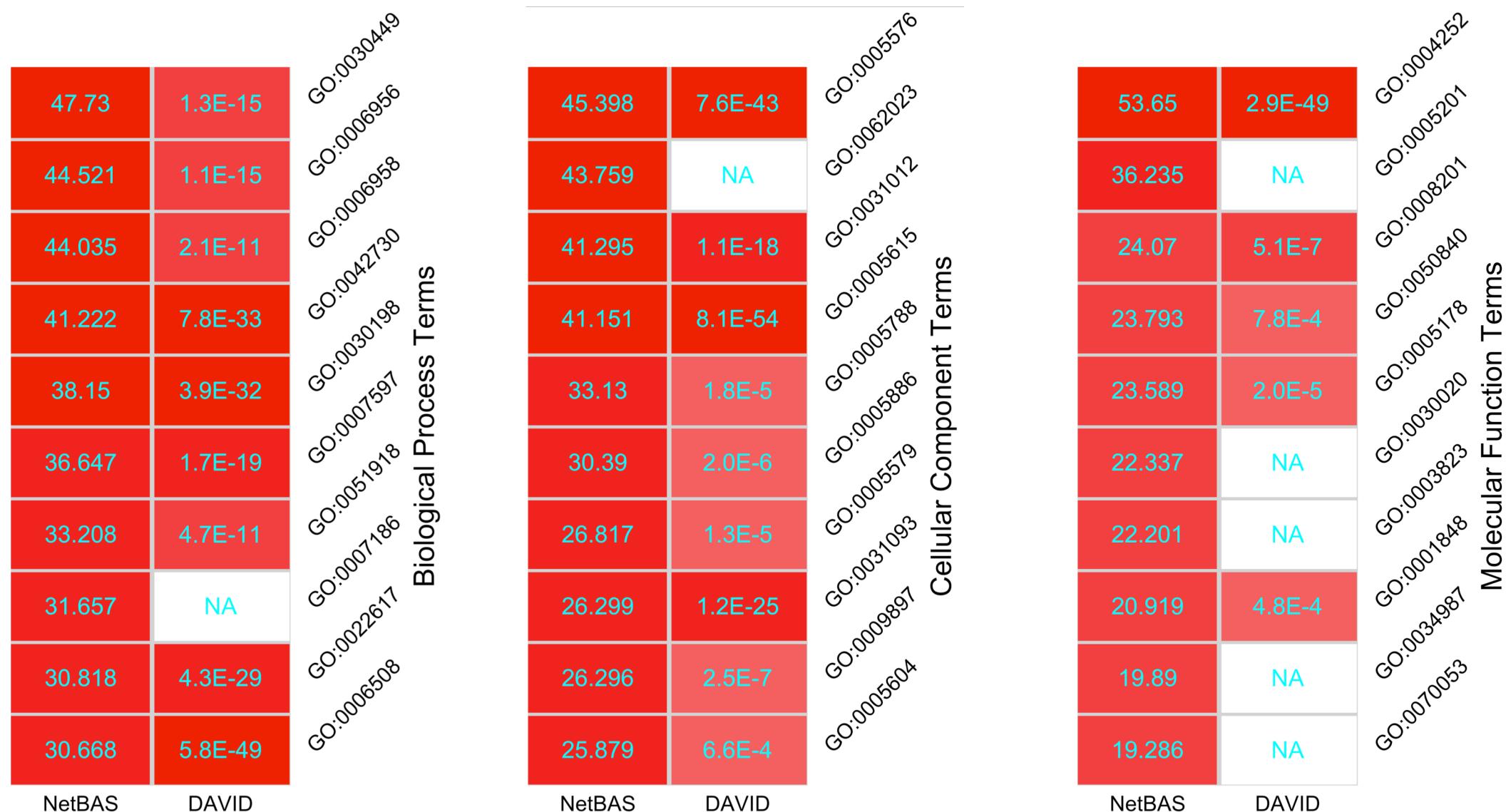
Subnetwork: 136 vertices, 260 edges
(unconnected vertices omitted)



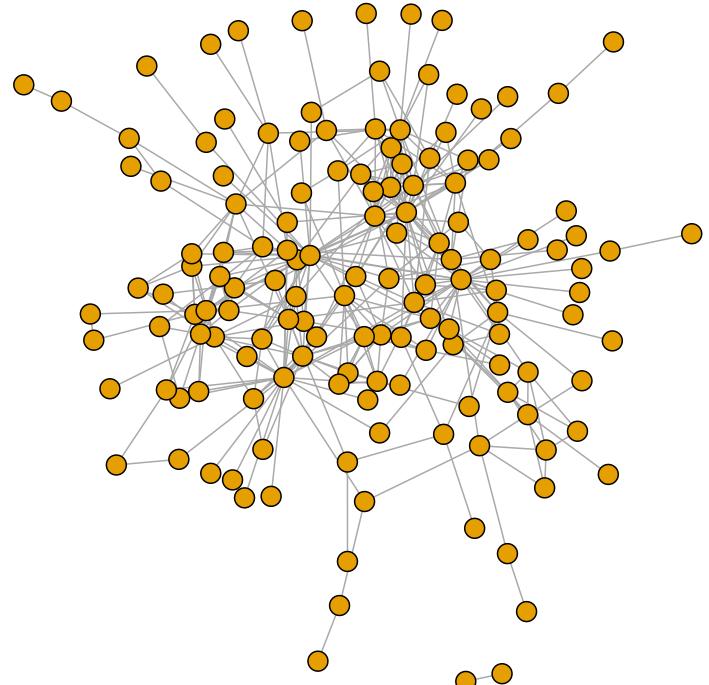
3 largest cliques w/ degree = 5

KEGG Pathways	NetBAS	DAVID
Complement and coagulation cascades	62.947	1.3E-55
ECM-receptor interaction	42.66	1.8E-4
Focal adhesion	25.56	2.1E-3
Staphylococcus aureus infection	24.414	NA
Neuroactive ligand-receptor interaction	21.182	NA
Protein digestion and absorption	19.1	NA
Amoebiasis	17.914	1.5E-2
Malaria	17.449	3.0E-2
Regulation of actin cytoskeleton	16.961	2.6E-2
Proteoglycans in cancer	15.85	6.2E-3

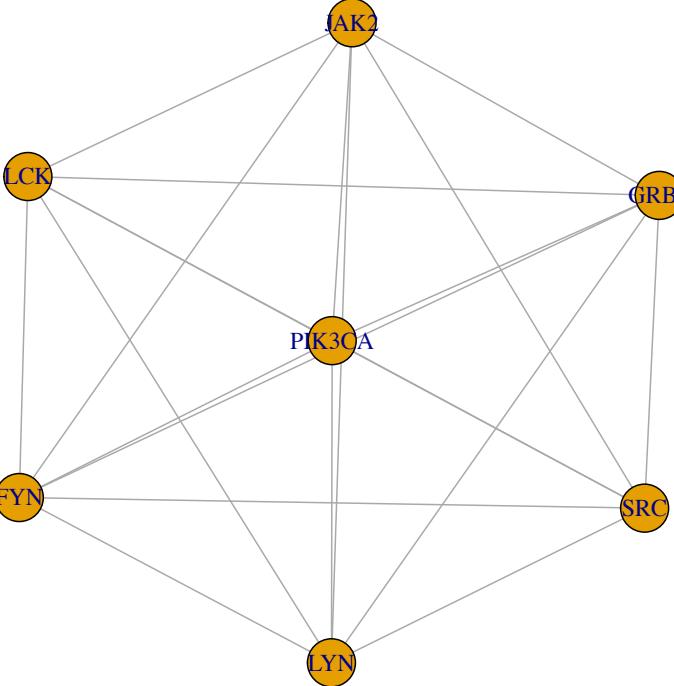
HALLMARK_COAGULATION



HALLMARK_COMPLEMENT



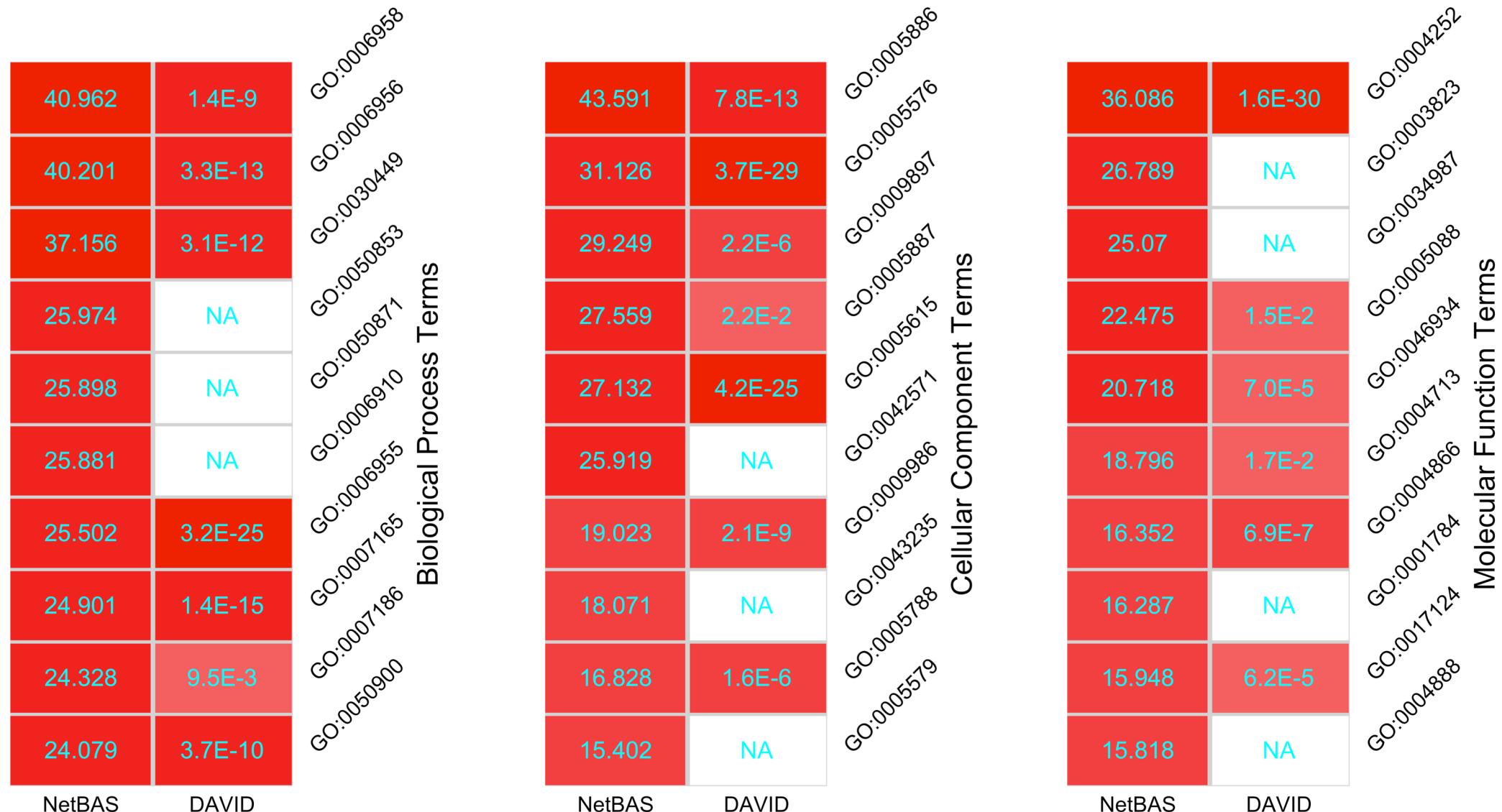
Subnetwork: 193 vertices, 356 edges
(unconnected vertices omitted)



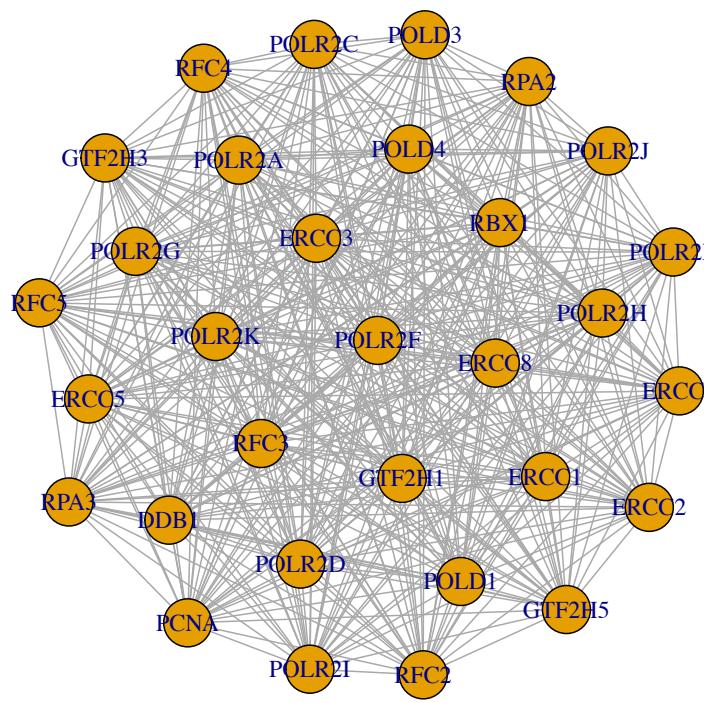
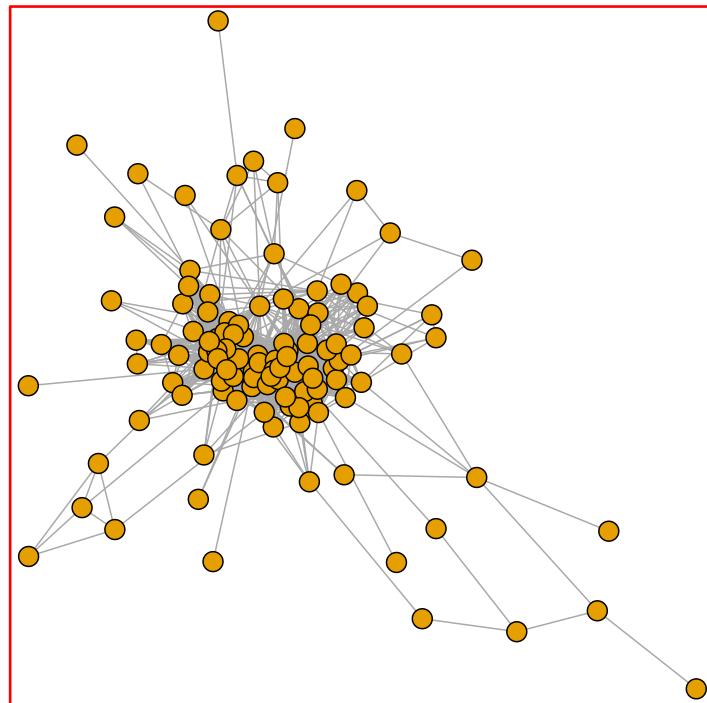
2 largest cliques w/ degree = 7

KEGG Pathways	NetBAS	DAVID
Complement and coagulation cascades	36.839	7.2E-31
Chemokine signaling pathway	26.257	1.1E-7
Focal adhesion	23.339	7.1E-3
Staphylococcus aureus infection	23.32	8.3E-7
Ras signaling pathway	22.968	4.6E-4
Rap1 signaling pathway	22.572	2.3E-4
Pathways in cancer	22.49	6.2E-4
Natural killer cell mediated cytotoxicity	21.509	1.3E-4
Cytokine-cytokine receptor interaction	21.239	NA
PI3K-Akt signaling pathway	21.199	3.0E-3

HALLMARK_COMPLEMENT

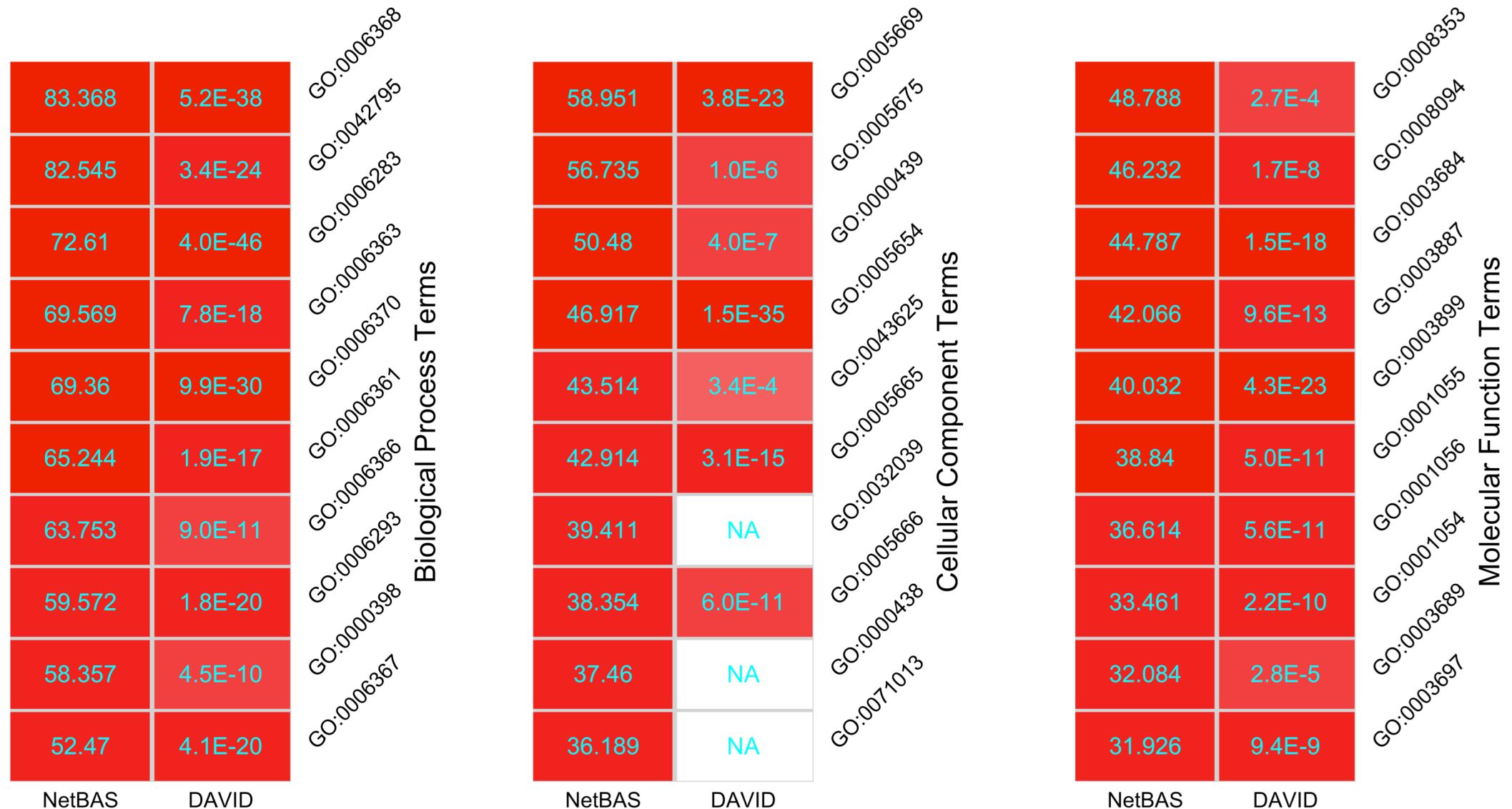


HALLMARK_DNA_REPAIR

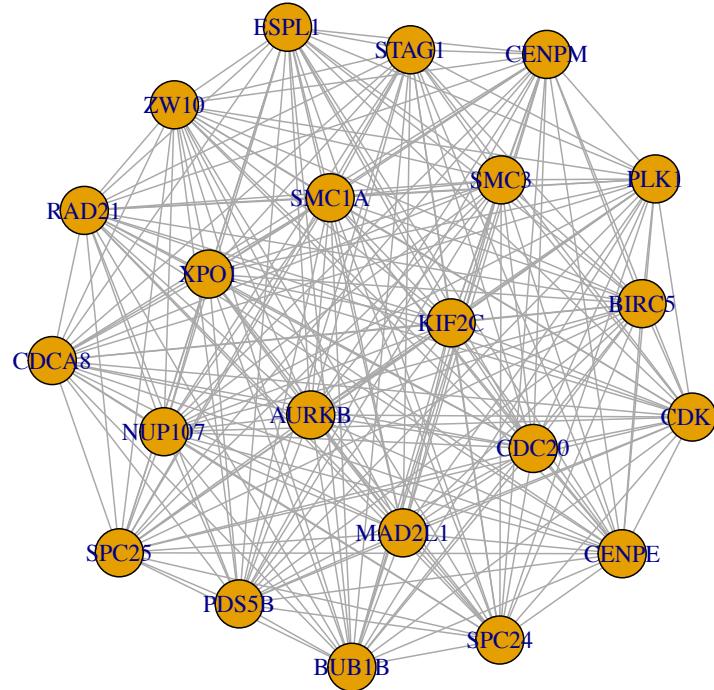
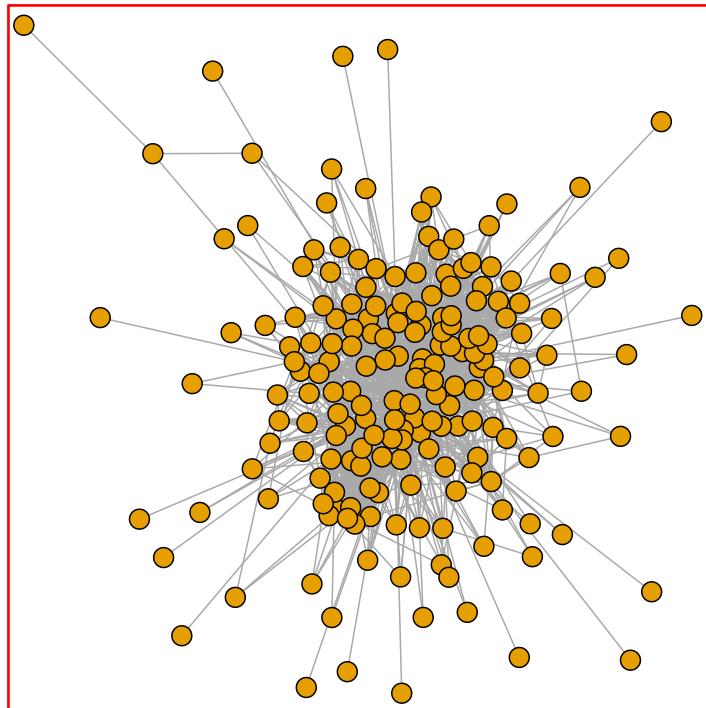


		NetBAS	DAVID
Nucleotide excision repair	77.438	2.1E-33	
Basal transcription factors	67.095	4.3E-12	
Pyrimidine metabolism	47.736	5.1E-37	
RNA polymerase	46.512	1.9E-17	
Mismatch repair	43.533	1.0E-12	
Purine metabolism	43.371	1.8E-40	
DNA replication	41.895	3.1E-18	
Base excision repair	41.196	1.9E-9	
Spliceosome	39.717	NA	
Fanconi anemia pathway	34.44	2.2E-4	

HALLMARK_DNA_REPAIR



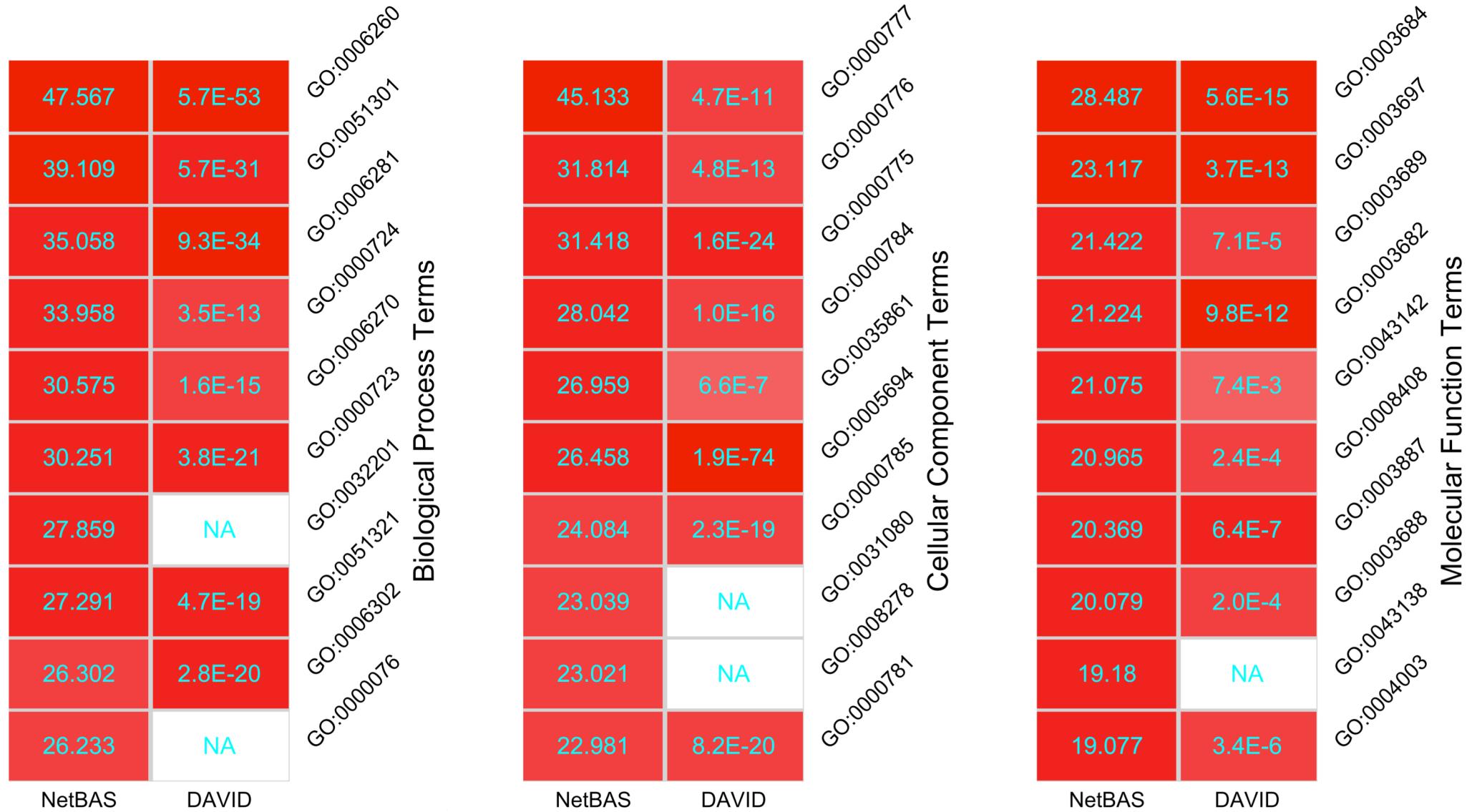
HALLMARK_E2F_TARGETS



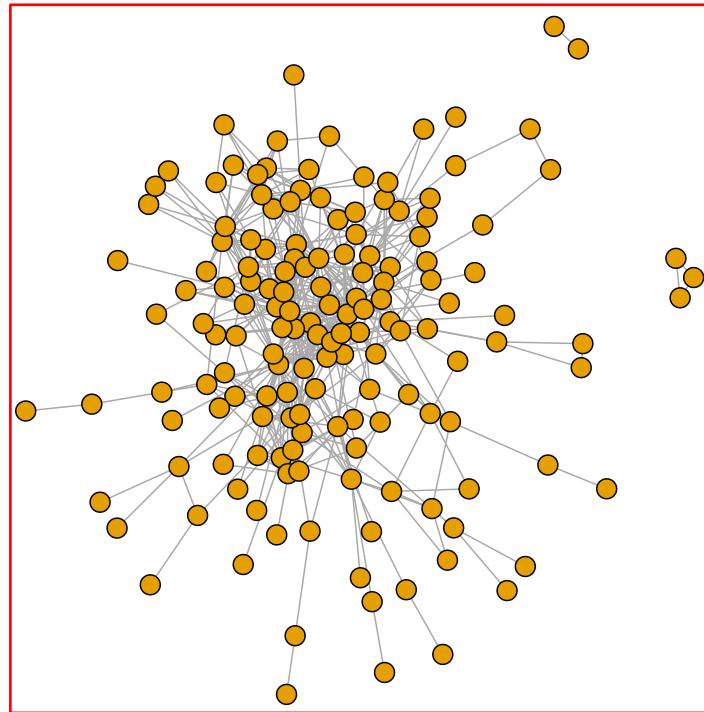
	NetBAS	DAVID
Fanconi anemia pathway	36.701	9.5E-8
Homologous recombination	34.19	8.5E-12
Cell cycle	32.522	4.4E-33
DNA replication	31.647	6.2E-30
Mismatch repair	26.752	1.5E-18
Nucleotide excision repair	24.223	3.6E-12
Base excision pathway	20.634	5.5E-7
p53 signaling pathway	19.036	6.4E-8
Systemic lupus erythematosus	16.418	NA
Cellular senescence	13.681	NA

KEGG Pathways

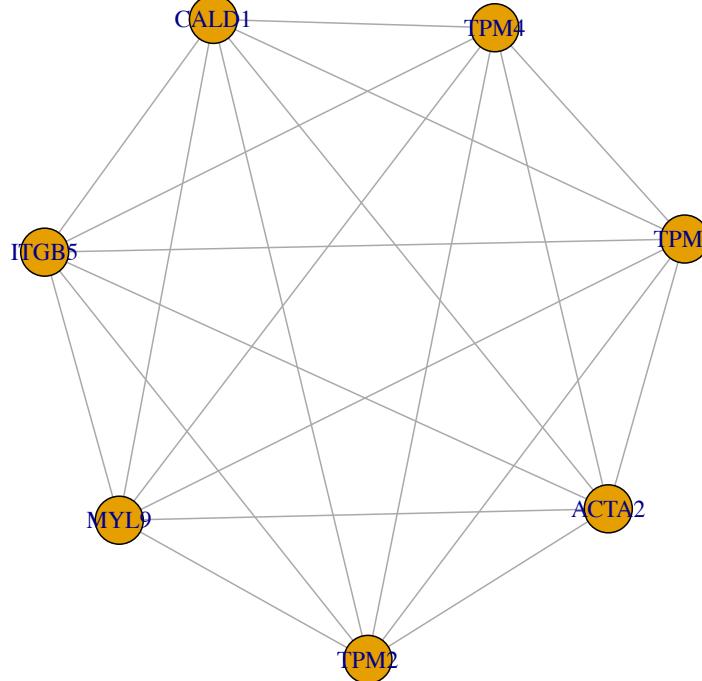
HALLMARK_E2F_TARGETS



HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION



Subnetwork: 196 vertices, 503 edges
(unconnected vertices omitted)

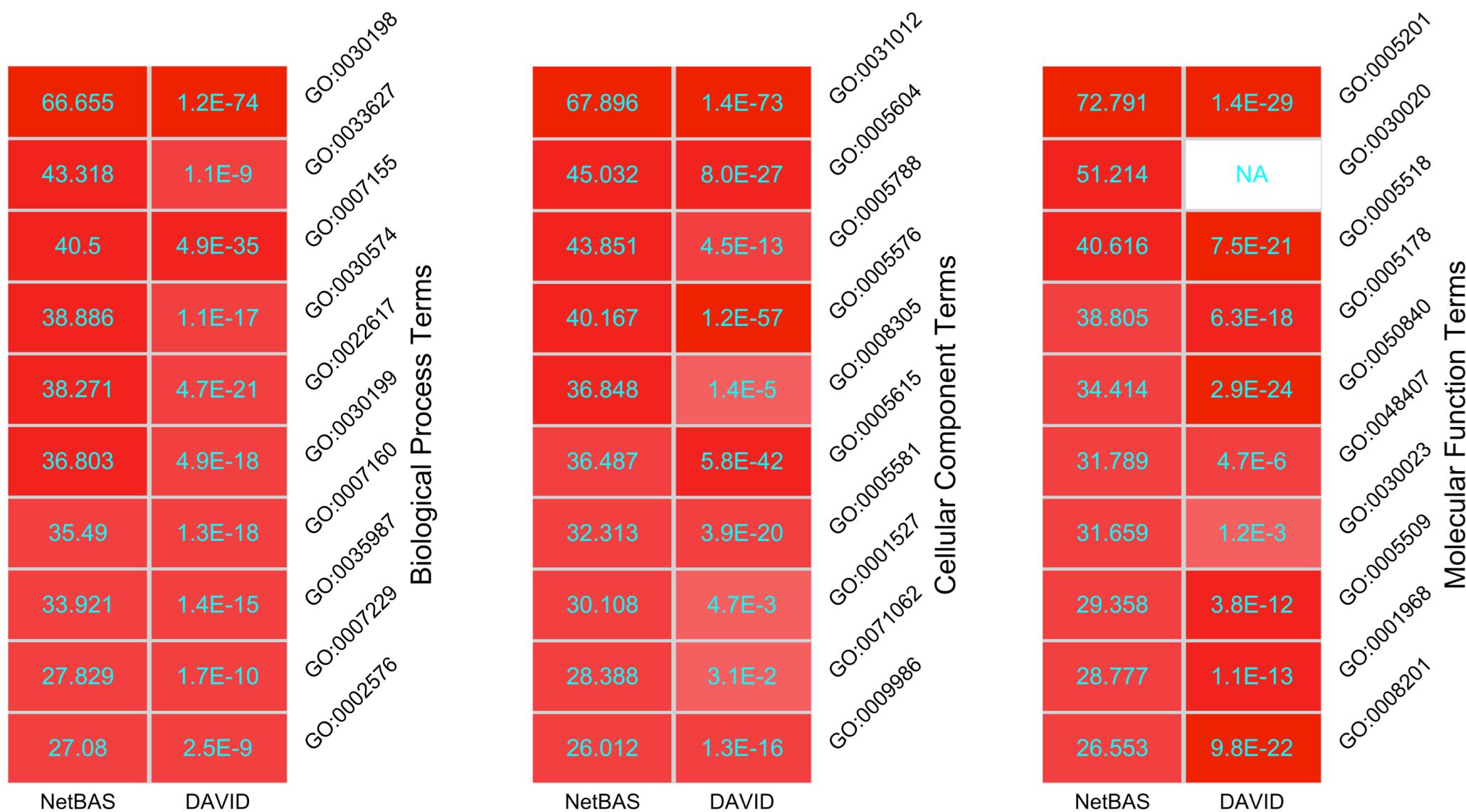


1 largest cliques w/ degree = 7

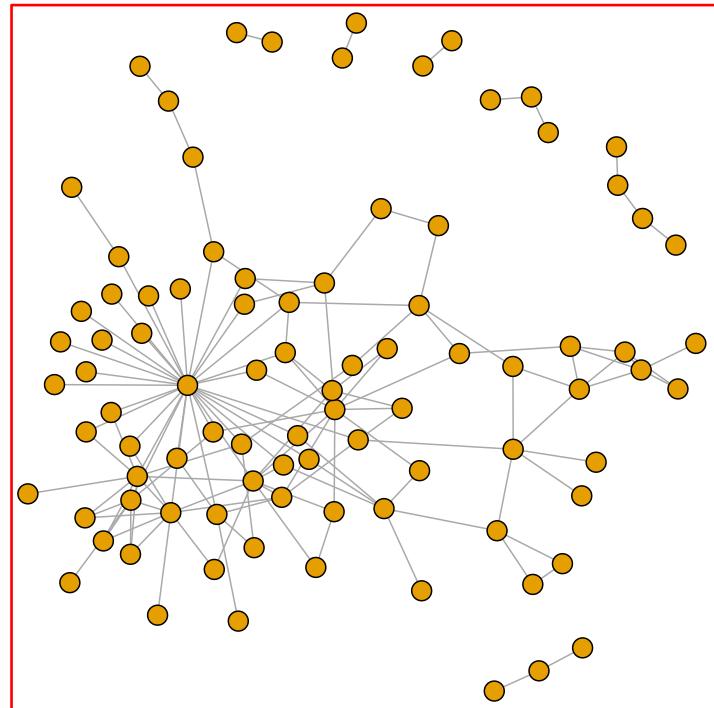
	NetBAS	DAVID
62.841	1.8E-31	ECM-receptor interaction
42.09	1.7E-24	Focal adhesion
38.867	1.5E-8	Protein digestion and absorption
32.021	6.3E-4	Regulation of actin cytoskeleton
27.599	2.8E-10	Hypertrophic cardiomyopathy (HCM)
26.874	7.2E-13	Proteoglycans in cancer
25.603	9.0E-9	Dilated cardiomyopathy (DCM)
25.259	1.1E-7	Arrhythmogenic right ventricular cardiomyopathy
23.396	NA	Glycosaminoglycan biosynthesis - chondroitin sulphate
22.06	1.8E-15	PI3K-Akt signalling pathway

KEGG Pathways

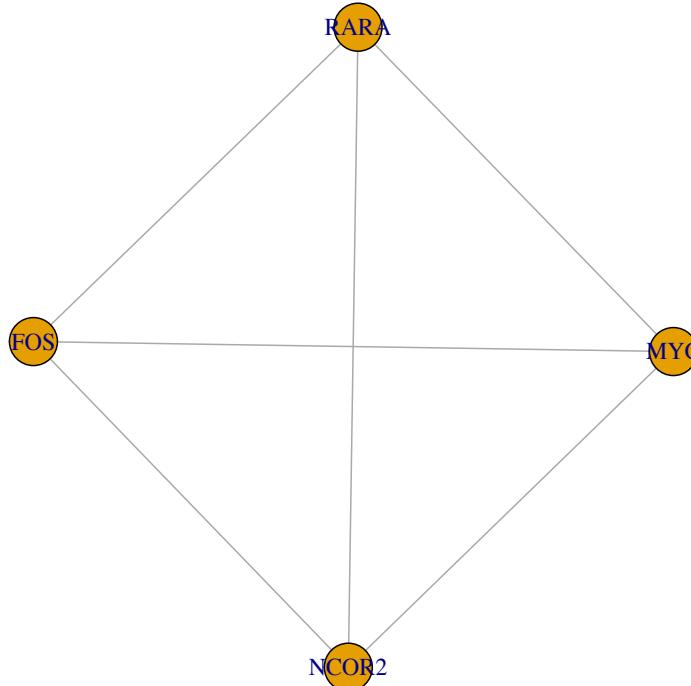
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION



HALLMARK_ESTROGEN_RESPONSE_EARLY



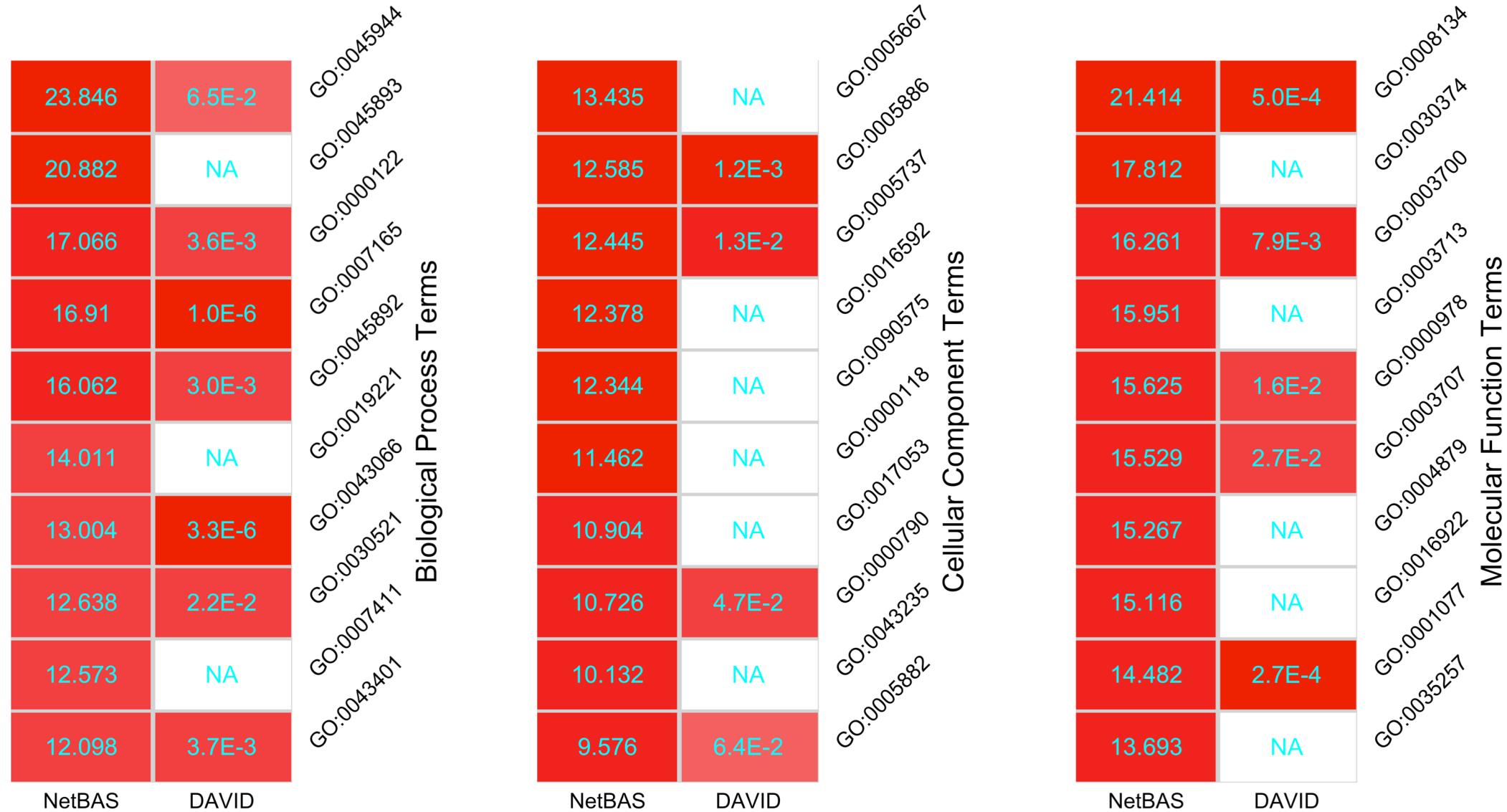
Subnetwork: 195 vertices, 134 edges
(unconnected vertices omitted)



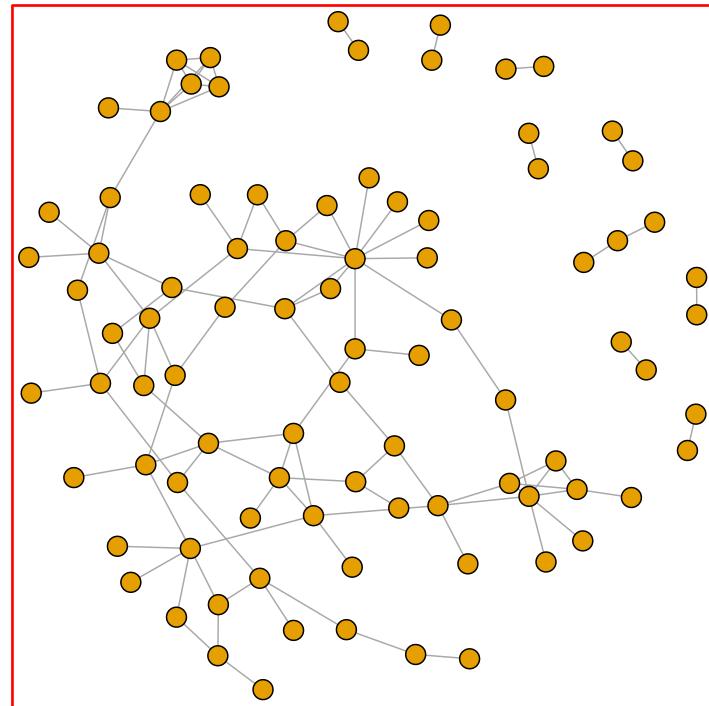
2 largest cliques w/ degree = 4

NetBAS	DAVID	KEGG Pathways
21.797	5.8E-3	Pathways in cancer
20.499	NA	Jak-STAT signaling pathway
19.671	NA	Thyroid hormone signaling pathway
18.95	NA	MicroRNAs in cancer
17.615	NA	Hepatitis B
16.8	NA	Chronic myeloid leukemia
15.801	NA	Breast cancer
15.134	NA	ErbB signaling pathway
15.052	NA	Prostate cancer
14.762	NA	Non-small cell lung cancer

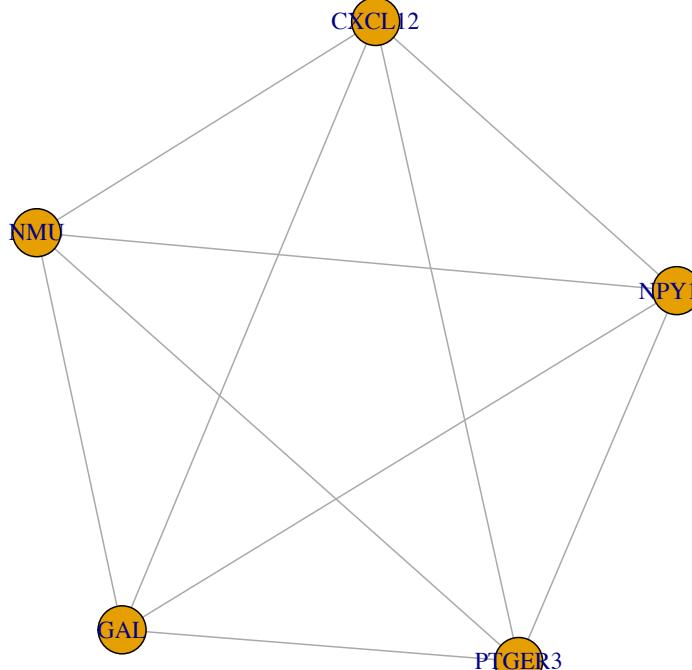
HALLMARK_ESTROGEN_RESPONSE_EARLY



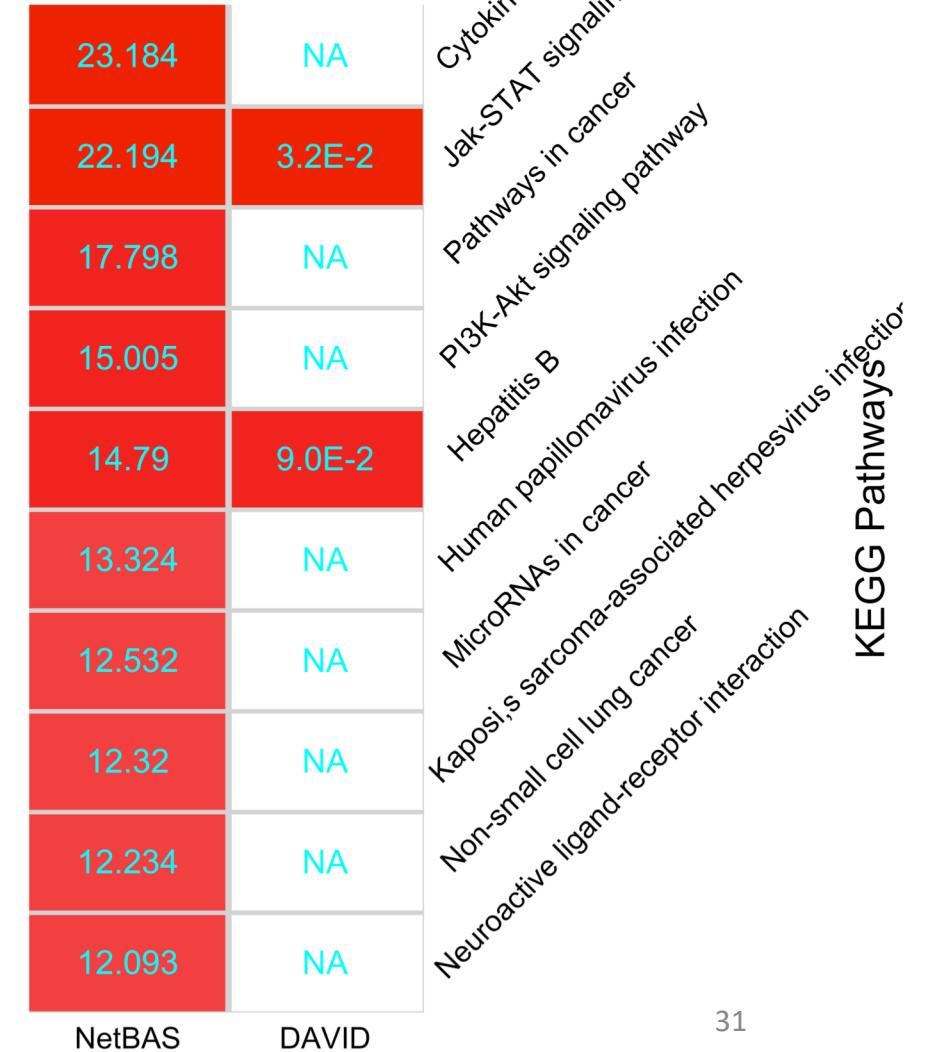
HALLMARK_ESTROGEN_RESPONSE_LATE



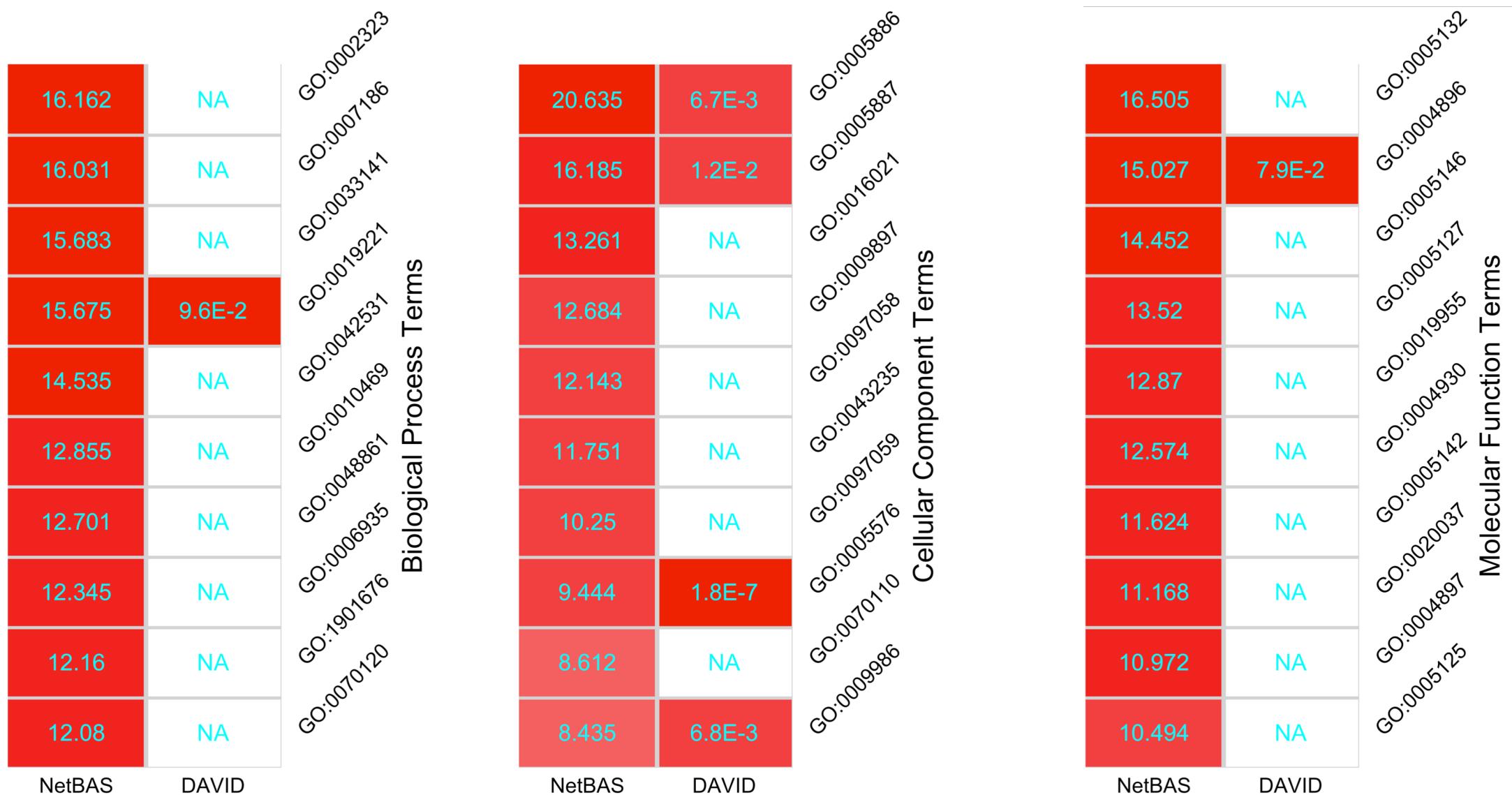
Subnetwork: 197 vertices, 106 edges
(unconnected vertices omitted)



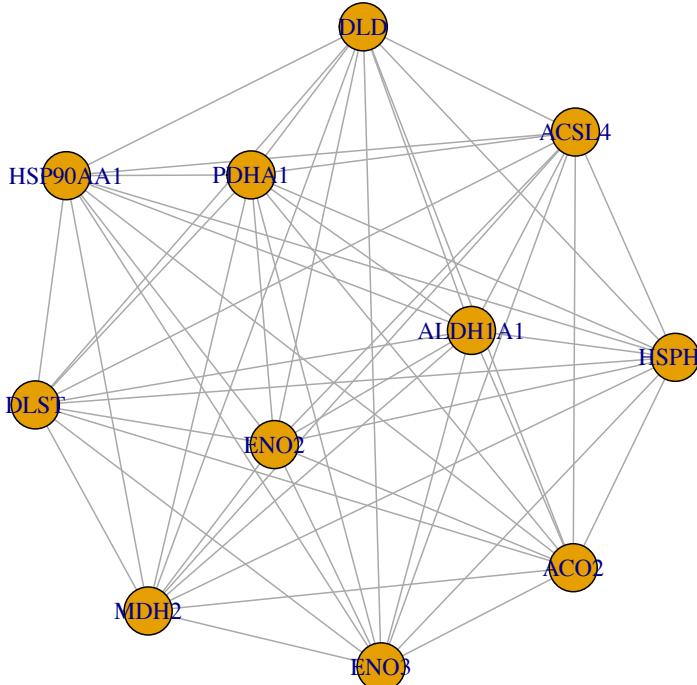
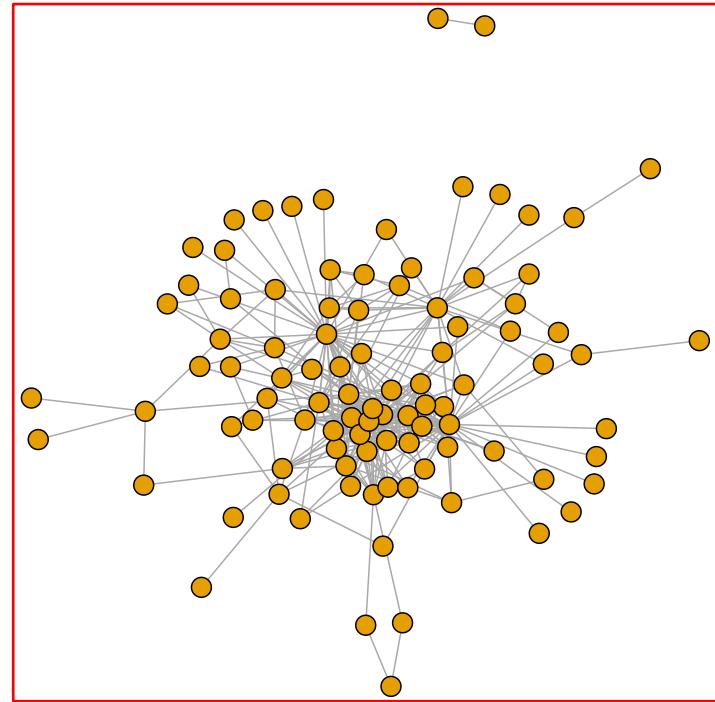
1 largest cliques w/ degree = 5



HALLMARK_ESTROGEN_RESPONSE_LATE



HALLMARK_FATTY_ACID_METABOLISM

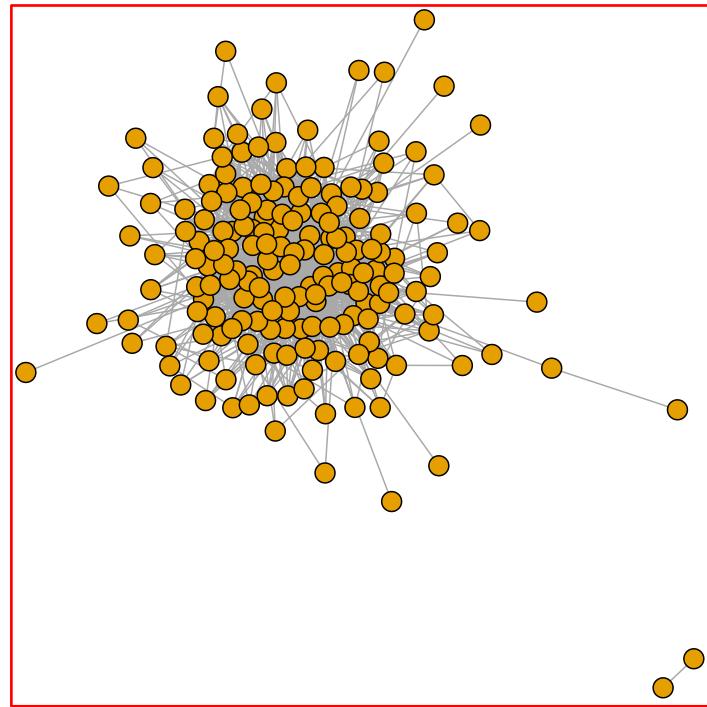


KEGG Pathways	NetBAS	DAVID
Glycolysis / Gluconeogenesis	29.986	2.8E-10
Citrate cycle (TCA cycle)	21.601	1.5E-20
Pyruvate metabolism	21.47	5.3E-12
Valine, leucine and isoleucine degradation	21.187	6.5E-23
Glycine, serine and threonine metabolism	18.449	3.8E-2
Propanoate metabolism	16.967	1.4E-12
Proteasome	16.523	NA
Cysteine and methionine metabolism	16.486	5.8E-3
Glyoxylate and dicarboxylate pathway	16.486	2.4E-8
Pentose phosphate pathway	16.214	NA

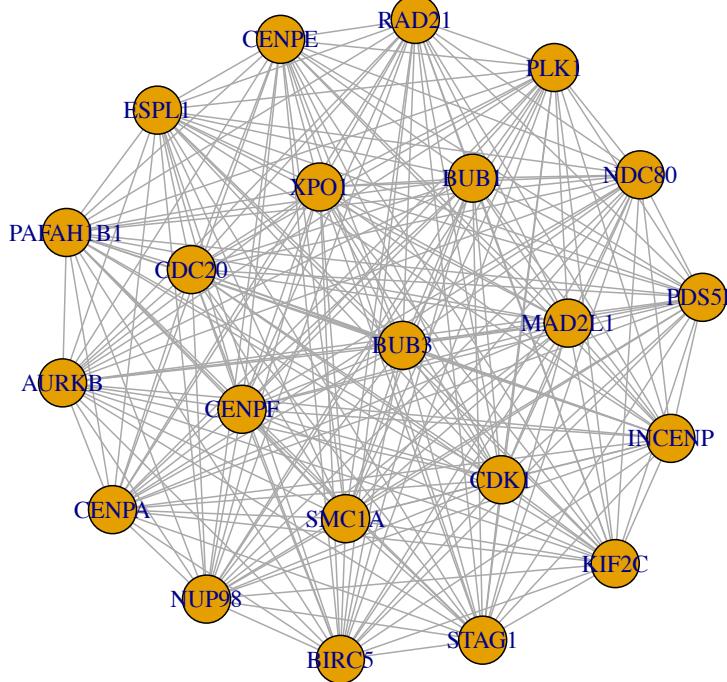
HALLMARK_FATTY_ACID_METABOLISM

		Biological Process Terms		Cellular Component Terms		Molecular Function Terms	
		NetBAS	DAVID	NetBAS	DAVID	NetBAS	DAVID
GO:0006096	22.927	2.9E-5		32.894	6.8E-26	26.219	NA
	22.405	1.7E-3		28.191	1.4E-12	25.839	NA
	22.39	3.4E-7		24.473	1.8E-40	25.839	8.8E-4
	22.301	2.3E-76		22.088	NA	22.327	NA
	21.594	6.9E-26		19.354	7.7E-8	19.828	NA
	19.704	2.4E-5		19.2	NA	19.392	NA
	18.566	NA		18.771	3.1E-8	17.771	NA
	18.325	NA		16.859	NA	17.264	NA
	18.018	NA		15.727	1.2E-23	17.264	NA
	16.988	NA		15.352	NA	17.264	NA

HALLMARK_G2M_CHECKPOINT



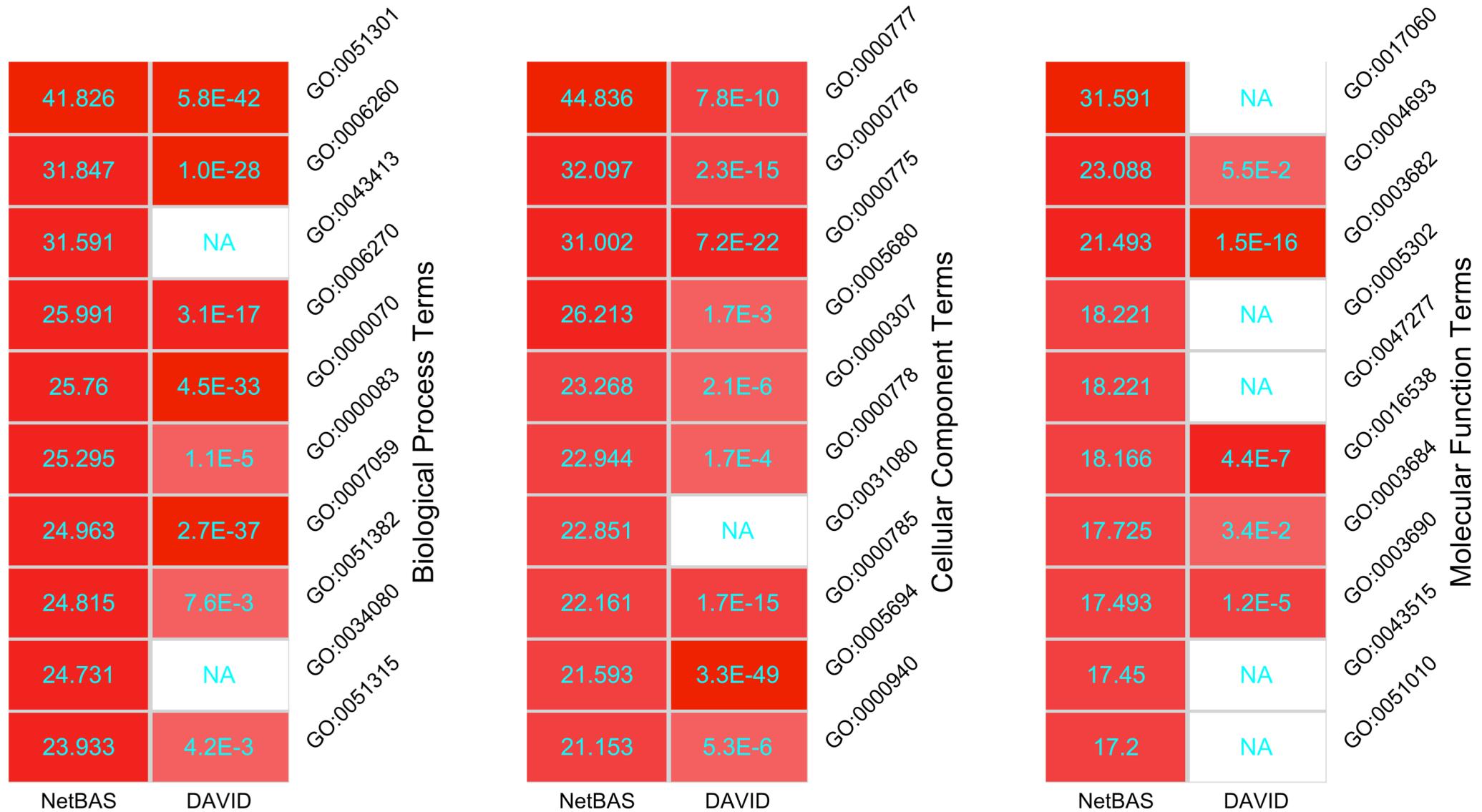
Subnetwork: 193 vertices, 1597 edges
(unconnected vertices omitted)



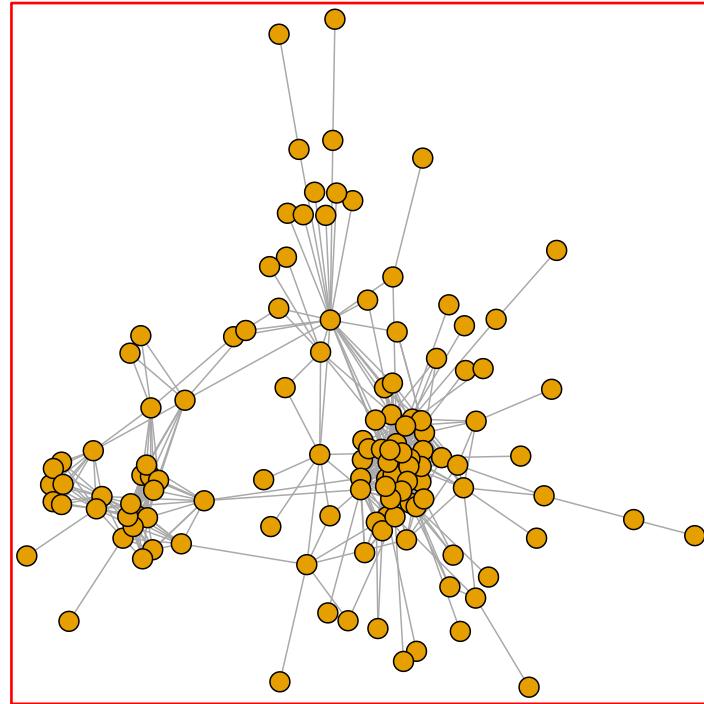
2 largest cliques w/ degree = 22

KEGG Pathways	NetBAS	DAVID
Cell cycle	35.262	2.1E-44
Homologous recombination	21.003	8.4E-2
DNA replication	19.291	1.7E-6
Fanconi anemia pathway	18.906	NA
p53 signaling pathway	17.88	2.5E-2
Oocyte meiosis	15.187	2.6E-7
Progesterone-mediated oocyte maturation	15.122	1.3E-5
Mismatch repair	15.029	NA
Cellular senescence	14.16	NA
Nucleotide excision repair	13.535	7.6E-3

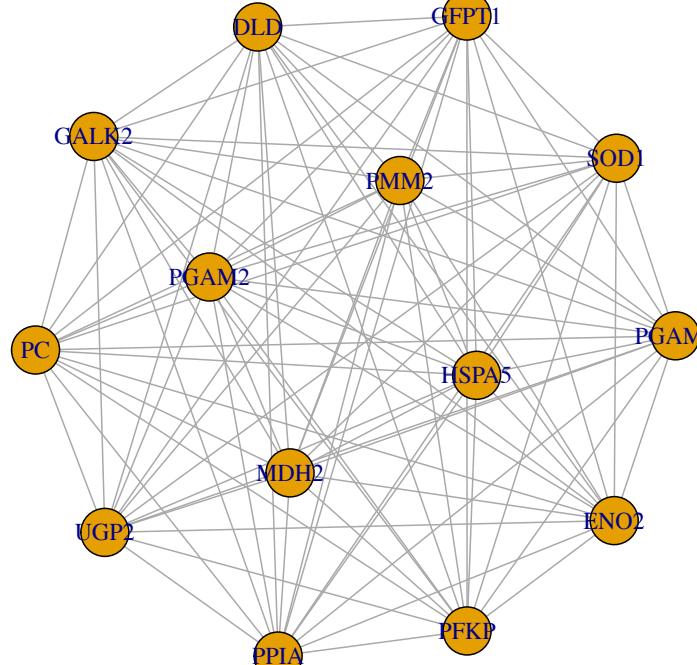
HALLMARK_G2M_CHECKPOINT



HALLMARK_GLYCOLYSIS



Subnetwork: 196 vertices, 605 edges
(unconnected vertices omitted)



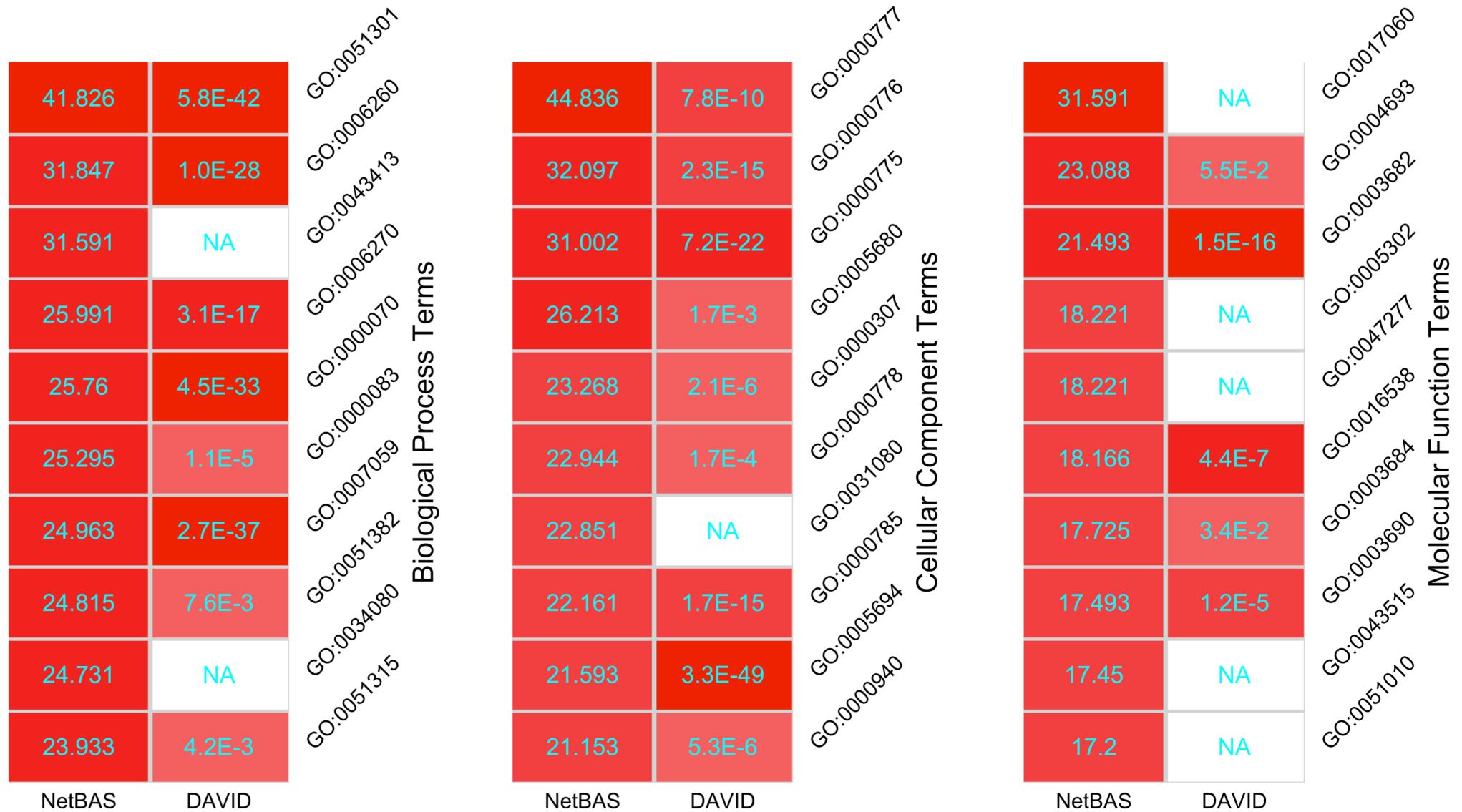
4 largest cliques w/ degree = 14

NetBAS	DAVID
50.951	5.0E-10
32.497	4.1E-5
28.483	5.2E-16
21.925	7.9E-8
20.26	3.2E-4
19.055	3.6E-6
18.822	1.1E-4
18.449	8.0E-3
18.112	NA
17.933	NA

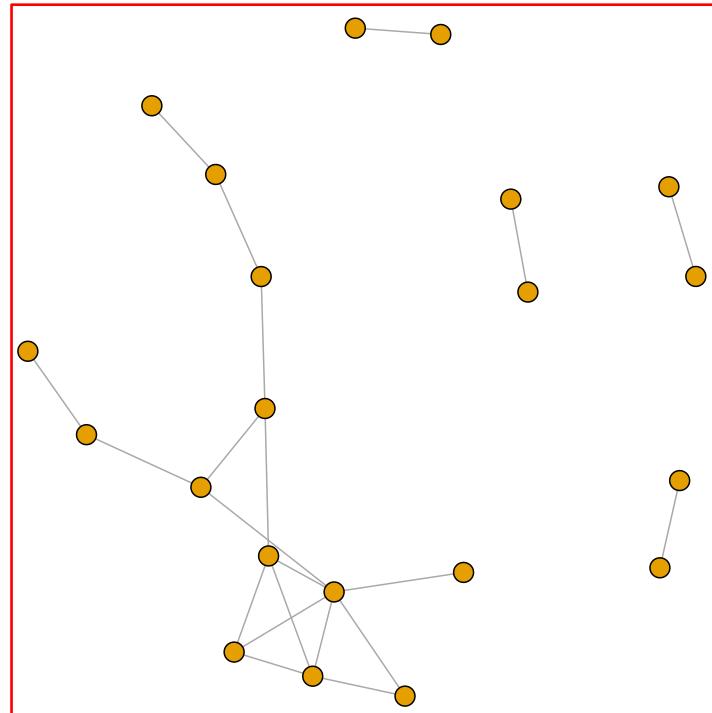
KEGG Pathways

Glycosaminoglycan biosynthesis - heparan sulfate
Glycosaminoglycan biosynthesis - chondroitin sulfate
Glycosaminoglycan / Glucuronogenesis
Glycolysis / Pyruvate metabolism
Pyruvate cycle (TCA cycle)
Citrate cycle and sucrose metabolism
Starch and methionine metabolism
Cysteine and serine and threonine metabolism
Glycine, serine and proline metabolism
Propanoate metabolism
Aminoacyl-tRNA biosynthesis

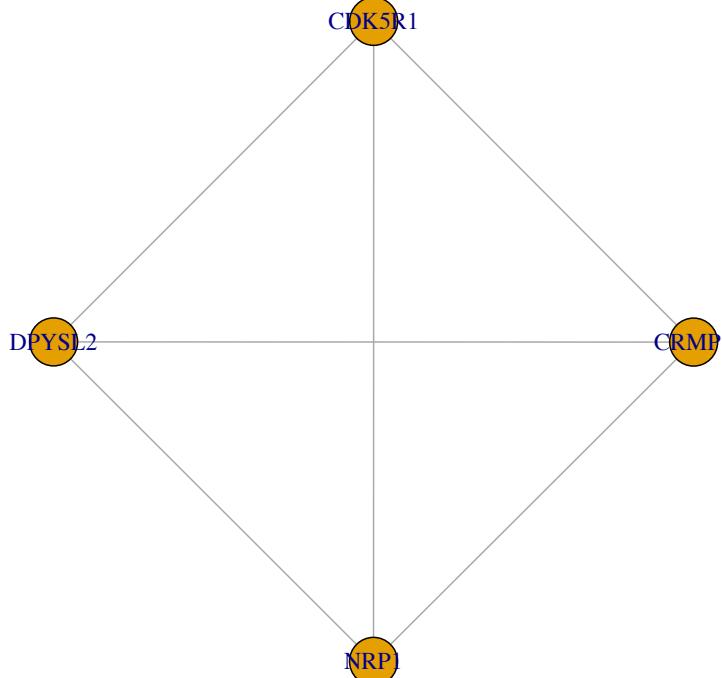
HALLMARK_GLYCOLYSIS



HALLMARK_HEDGEHOG_SIGNALING



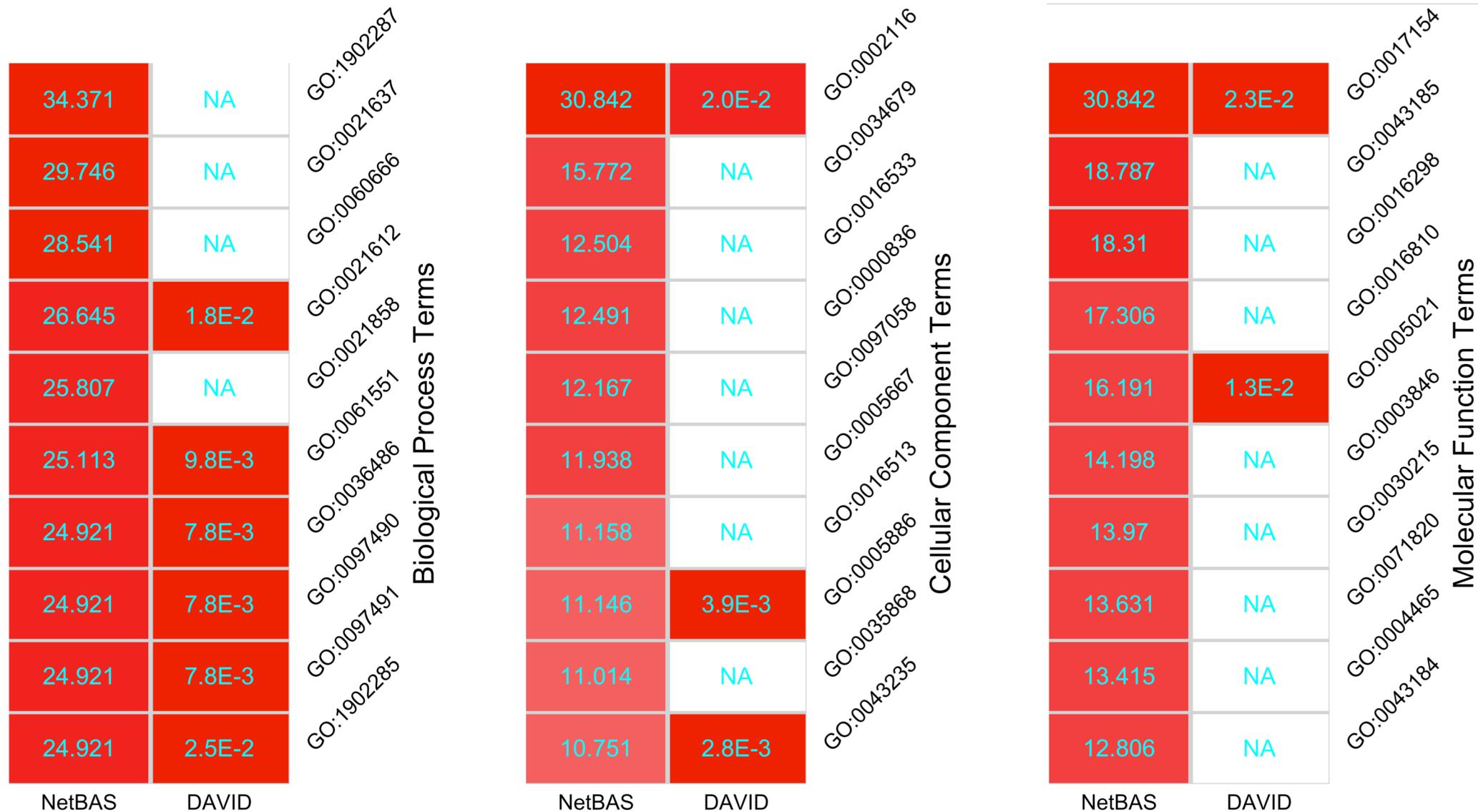
Subnetwork: 35 vertices, 21 edges
(unconnected vertices omitted)



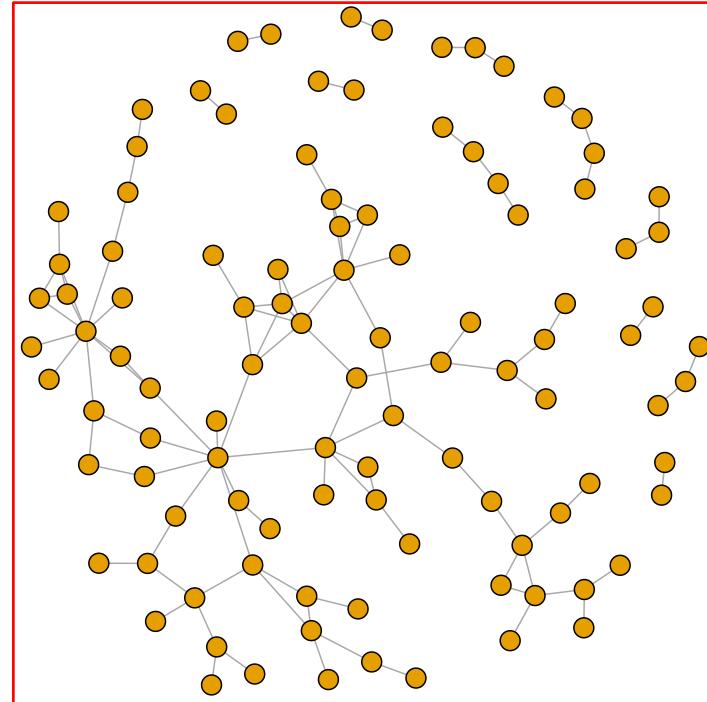
1 largest cliques w/ degree = 4

KEGG Pathways	NetBAS	DAVID
Axon guidance	20.03	4.1E-5
Focal adhesion	16.563	NA
Pathways in cancer	15.221	7.0E-3
Human papillomavirus infection	13.326	NA
Ras signaling pathway	13.038	3.4E-2
Proteoglycans in cancer	12.828	NA
Adherens junction	12.721	NA
Regulation of actin cytoskeleton	11.719	NA
Rap1 signaling pathway	11.698	NA
Chronic myeloid leukemia	10.654	NA

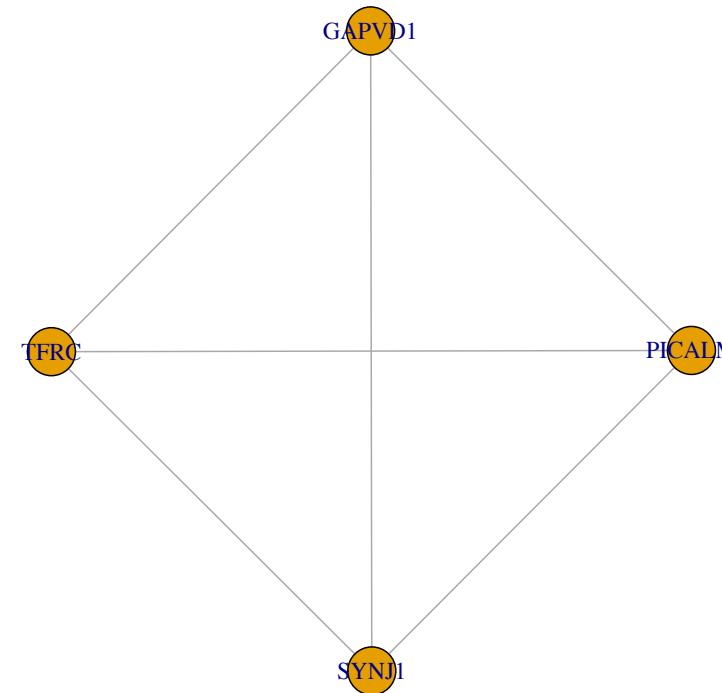
HALLMARK_HEDGEHOG_SIGNALING



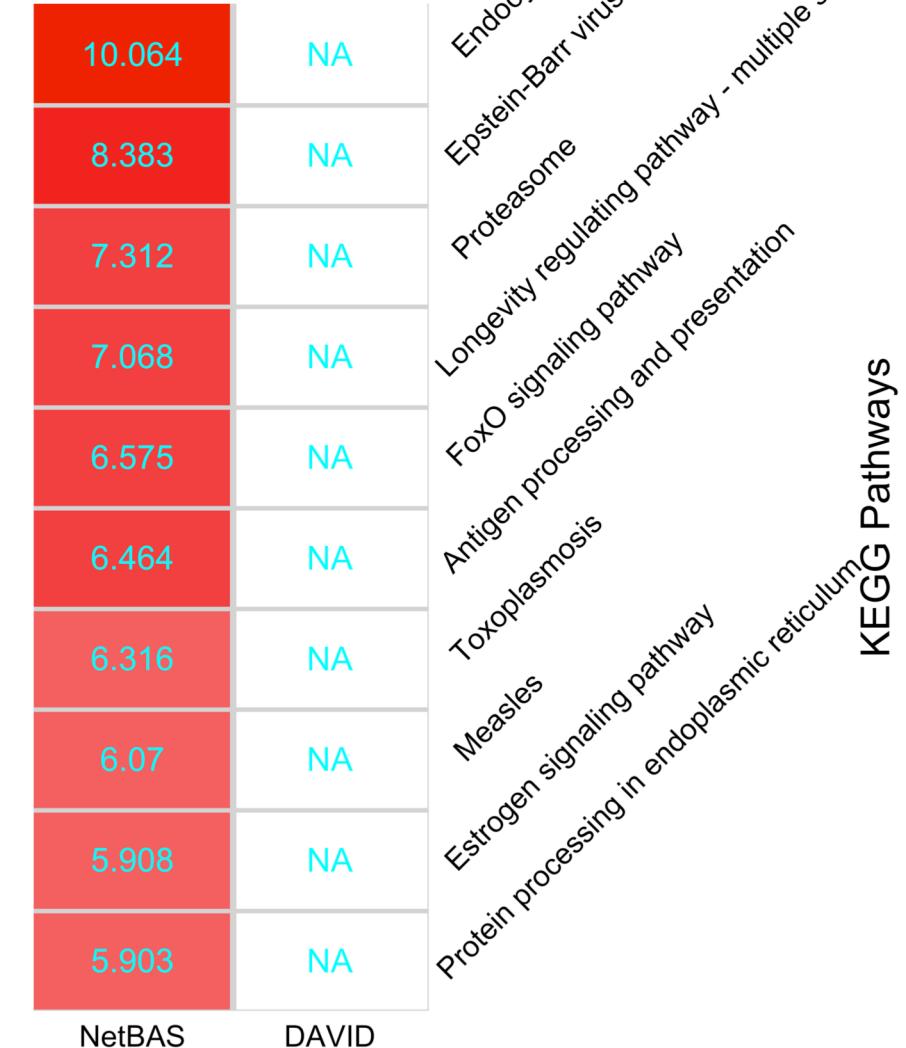
HALLMARK_HEME_METABOLISM



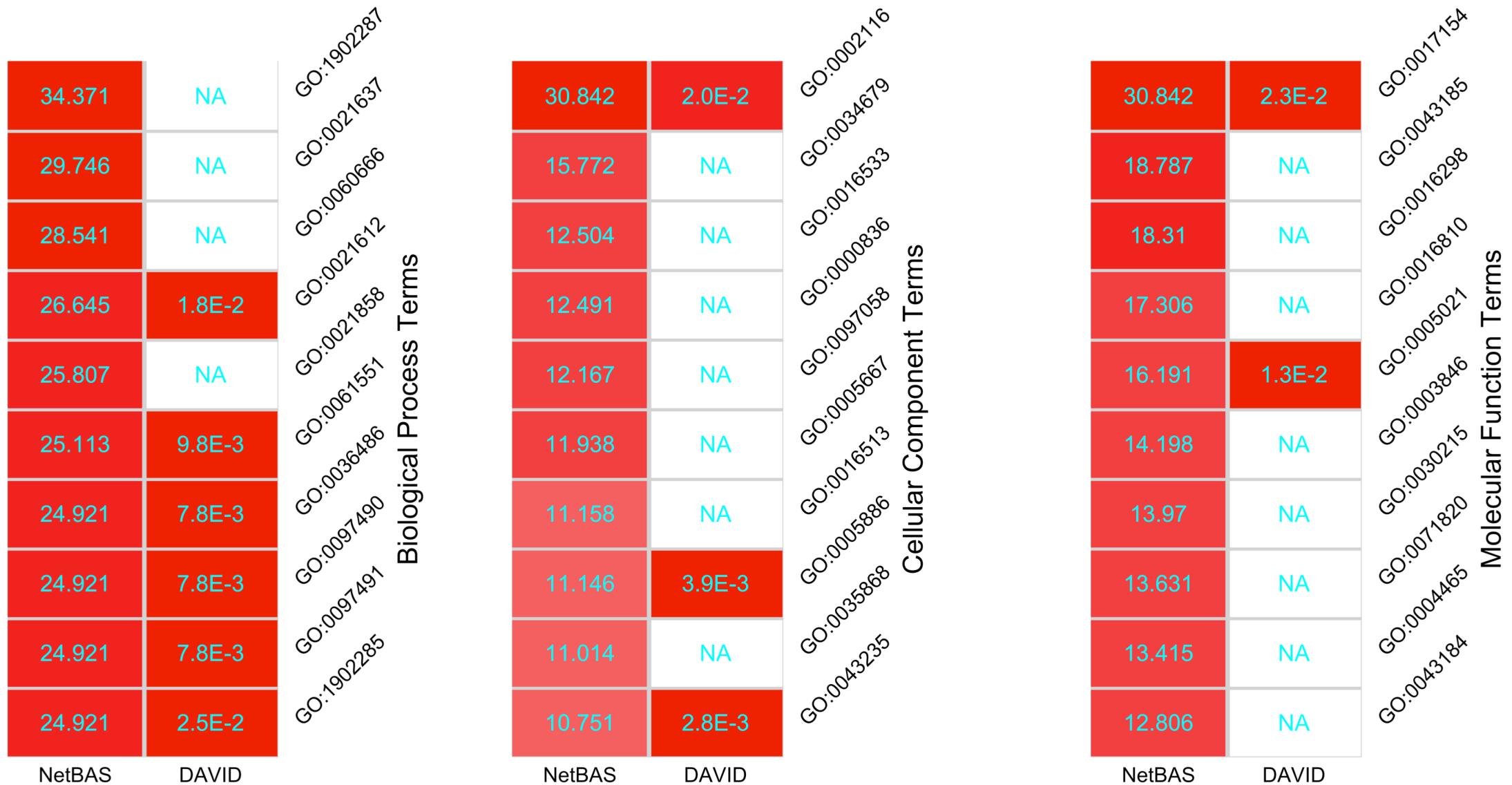
Subnetwork: 190 vertices, 111 edges
(unconnected vertices omitted)



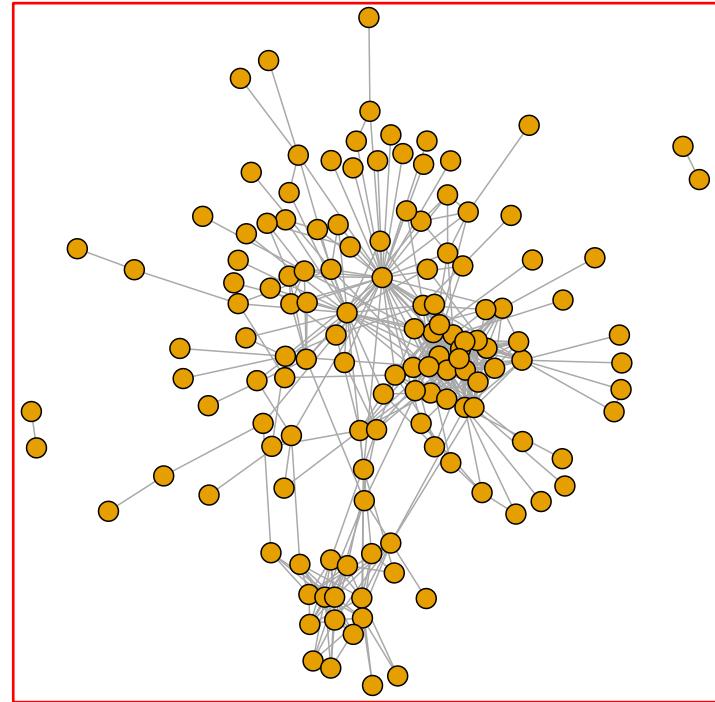
3 largest cliques w/ degree = 4



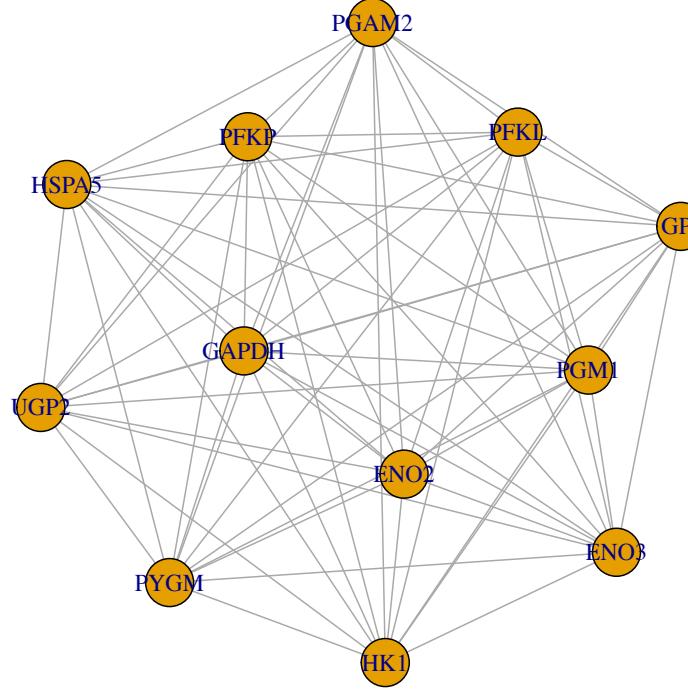
HALLMARK_HEME_METABOLISM



HALLMARK_HYPOXIA



Subnetwork: 192 vertices, 435 edges
(unconnected vertices omitted)



2 largest cliques w/ degree = 12

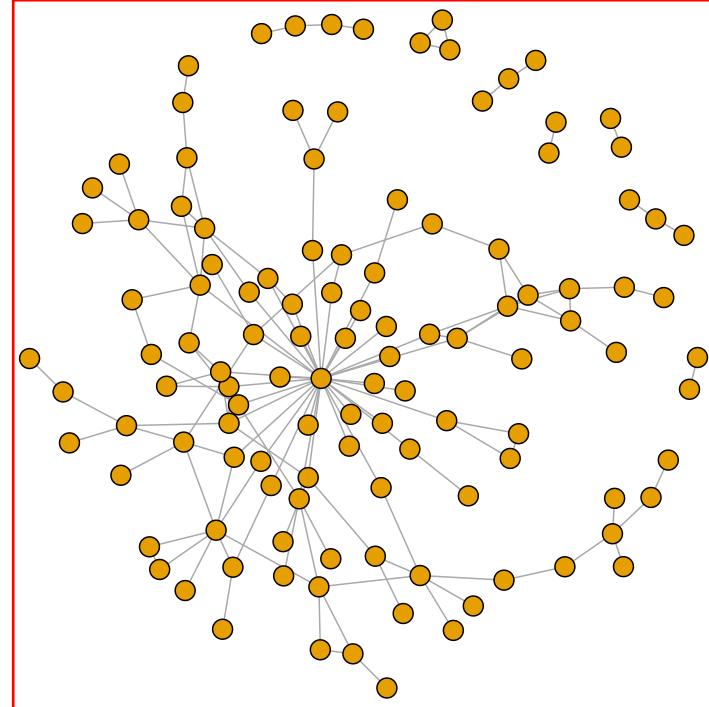
NetBAS	DAVID
38.435	8.3E-4
35.715	NA
15.587	7.1E-5
14.707	3.0E-24
14.06	5.7E-3
13.958	3.7E-5
13.078	NA
12.508	NA
12.072	3.4E-3
12.049	NA

Glycosaminoglycan biosynthesis - heparan sulfate
Glycosaminoglycan biosynthesis pathway
Glycosaminoglycan signaling pathway
Glucagon signaling pathway
Glucagon / Gluconeogenesis
Glycolysis / Pyruvate metabolism
Pyruvate metabolism
Pyruvate signaling pathway
Insulin signaling pathway
Insulin and methionine metabolism
Cysteine and methionine metabolism
Propanoate metabolism
Propanoate resistance
Insulin resistance
Aminoacyl-tRNA biosynthesis

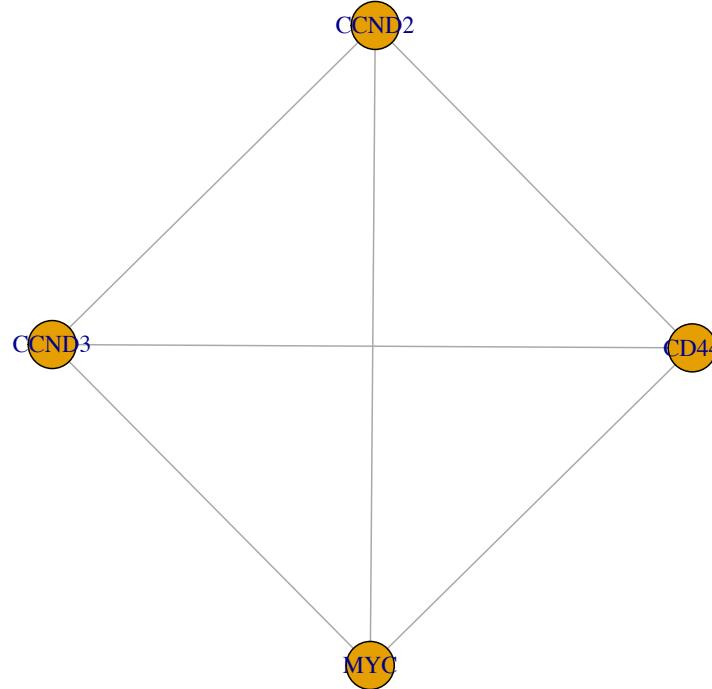
HALLMARK_HYPOXIA

		Biological Process Terms		Cellular Component Terms		Molecular Function Terms	
		NetBAS	DAVID	NetBAS	DAVID	NetBAS	DAVID
GO:0006024	35.609	1.5E-18		22.241	1.1E-11	26.9	2.7E-5
	30.139	1.2E-17		18.12	NA	22.953	NA
	29.937	3.2E-3		13.59	1.7E-13	21.959	NA
	29.335	2.1E-5		13.27	2.4E-9	18.904	NA
	28.037	8.4E-6		12.947	5.9E-12	16.38	NA
	20.088	NA		12.398	NA	16.16	NA
	19.364	8.8E-2		12.318	3.8E-2	16.13	NA
	18.398	NA		12.19	NA	15.893	NA
	18.388	7.8E-2		12.047	NA	15.772	NA
	17.915	3.6E-3		11.787	1.1E-2	15.772	NA

HALLMARK_IL2_STAT5_SIGNALING



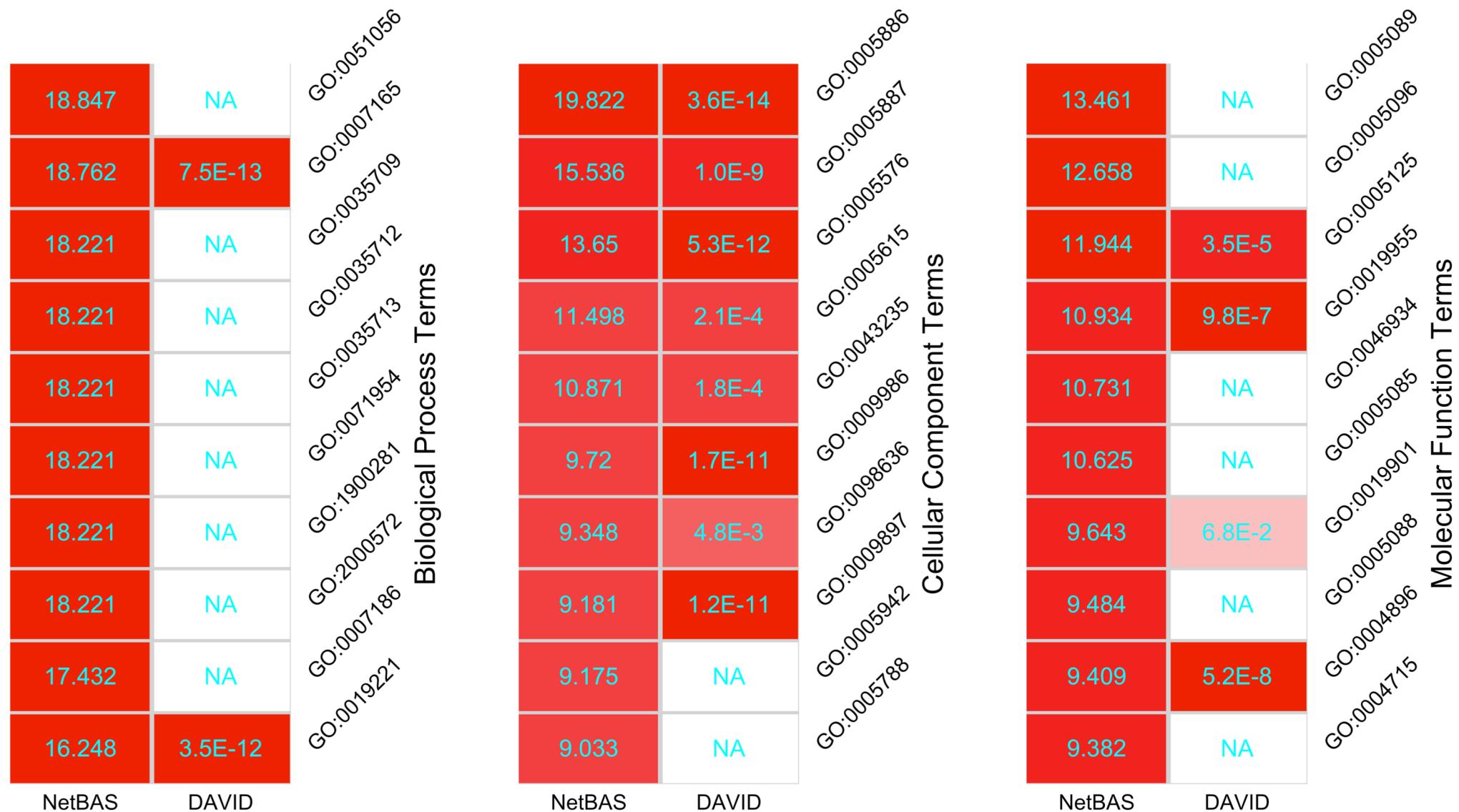
Subnetwork: 192 vertices, 145 edges
(unconnected vertices omitted)



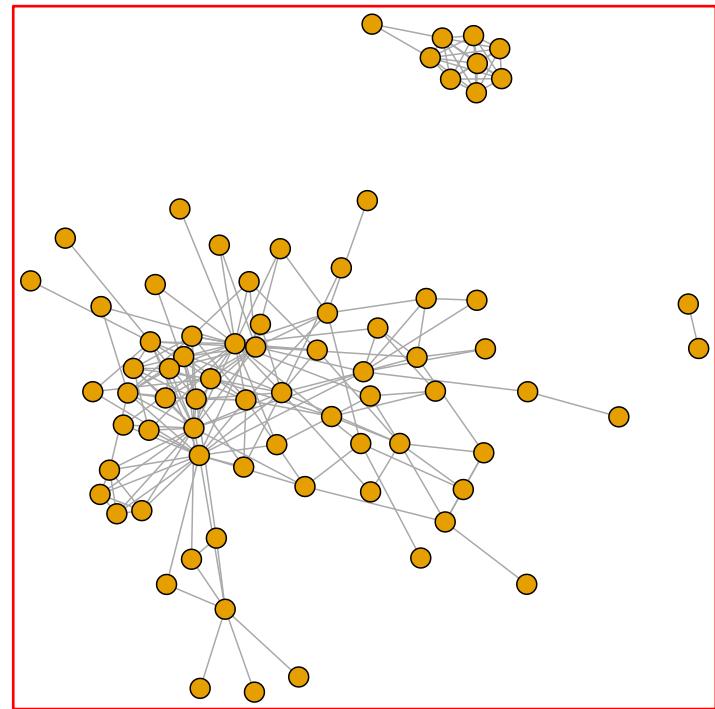
2 largest cliques w/ degree = 4

	NetBAS	DAVID	KEGG Pathways
22.052	9.0E-11		Jak-STAT signaling pathway
20.362	2.3E-2		Pathways in cancer
18.397	3.3E-13		Cytokine-cytokine receptor interaction
14.855	3.6E-4		PI3K-Akt signaling pathway
14.662	NA		Hepatitis B
14.117	NA		Proteoglycans in cancer
13.957	NA		Human papillomavirus infection
13.862	3.9E-2		MicroRNAs in cancer
13.82	2.3E-3		Small cell lung cancer
13.801	4.6E-2		Focal adhesion

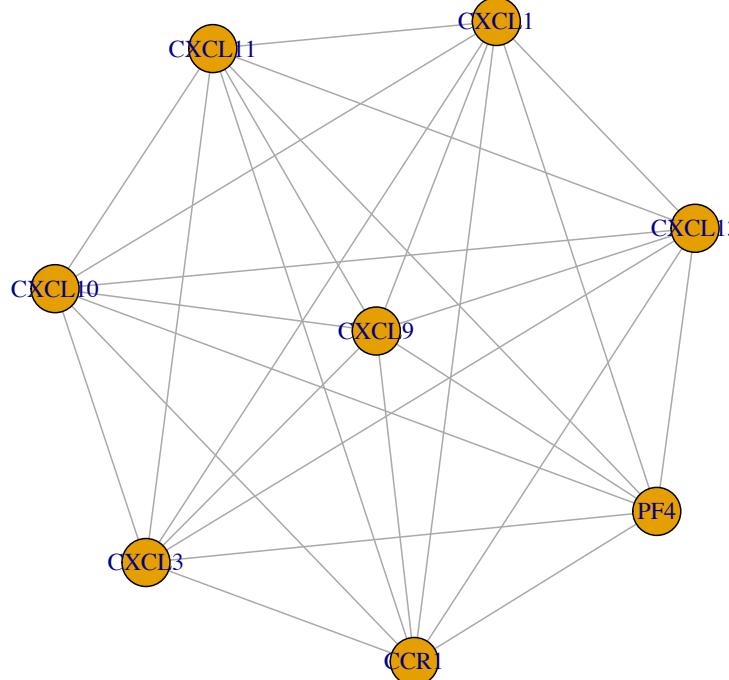
HALLMARK_IL2_STAT5_SIGNALING



HALLMARK_IL6_JAK_STAT3_SIGNALING



Subnetwork: 87 vertices, 206 edges
(unconnected vertices omitted)



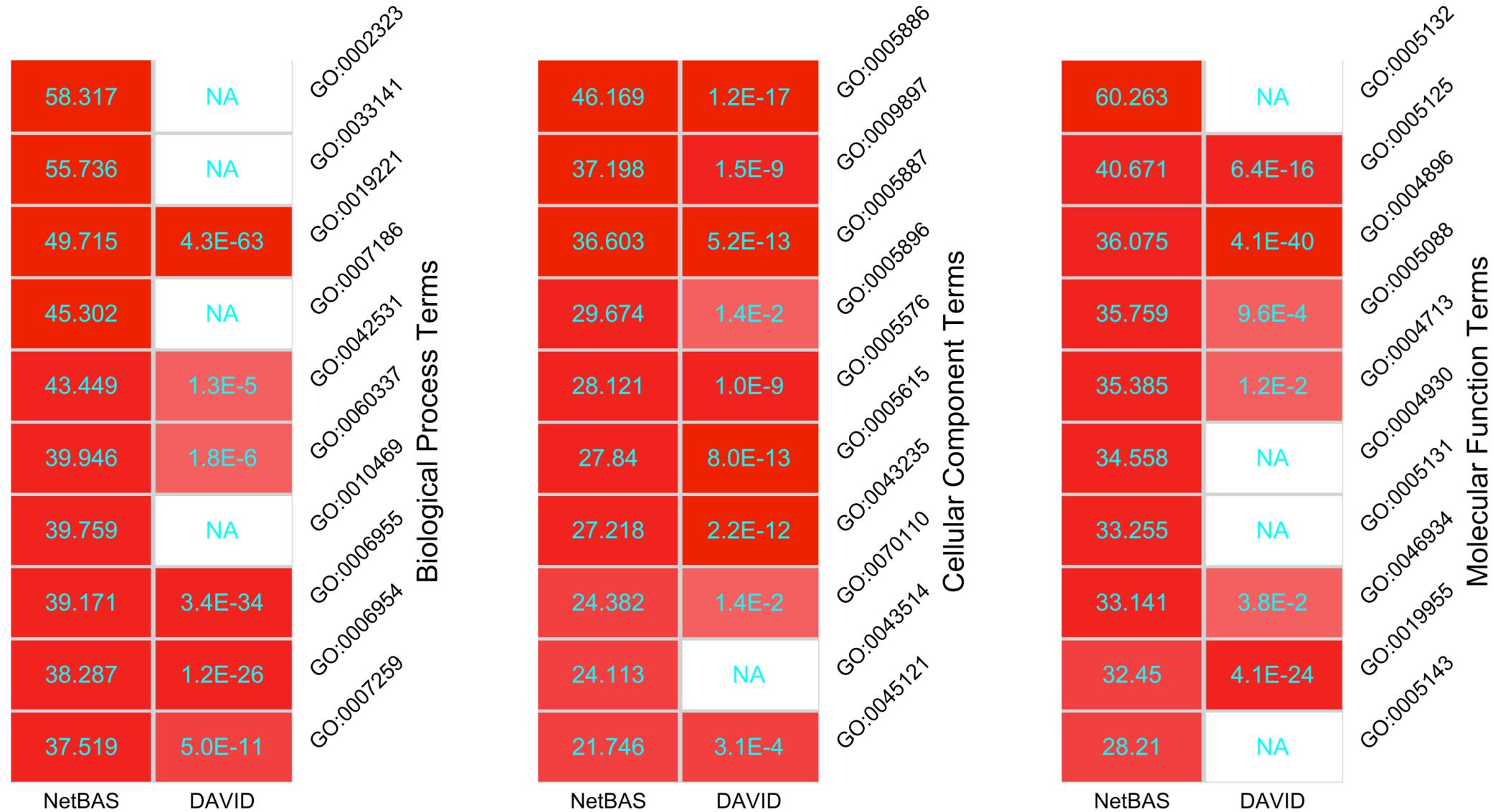
1 largest cliques w/ degree = 8

NetBAS	DAVID
68.965	1.4E-50
67.279	3.4E-37
37.545	1.8E-7
36.764	1.7E-10
36.444	1.5E-2
34.869	7.8E-5
33.201	NA
32.685	3.1E-7
30.825	2.0E-11
30.475	7.9E-6

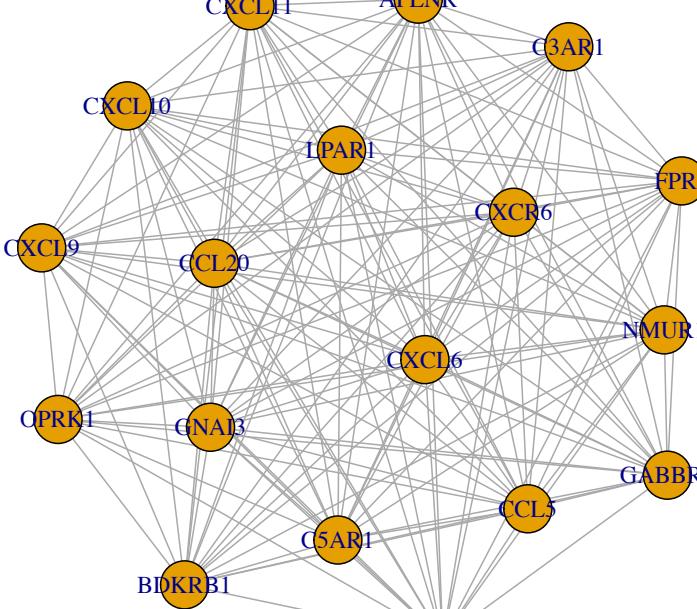
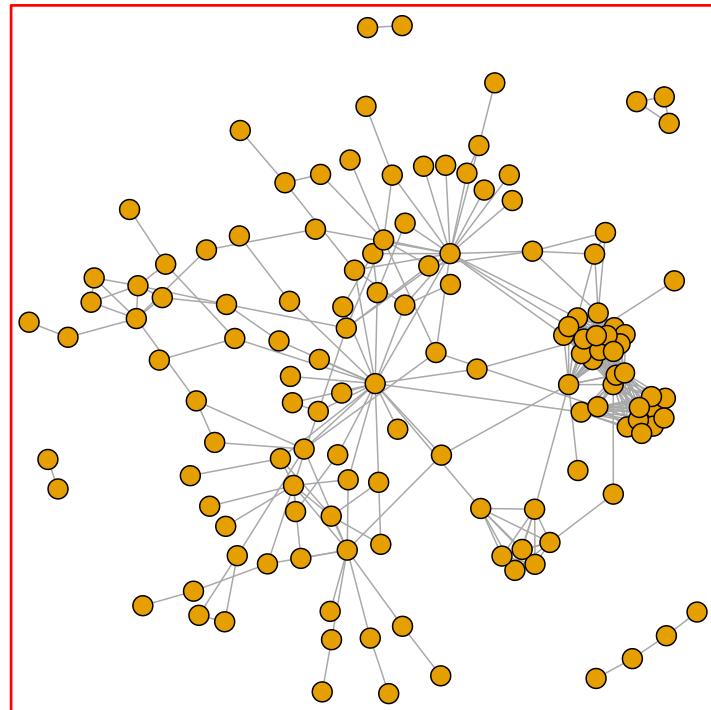
KEGG Pathways

Cytokine-cytokine receptor interaction
Jak-STAT signaling pathway
Chemokine signaling pathway
Toll-like receptor signaling pathway
Pathways in cancer
Natural killer cell mediated cytotoxicity
Kaposi's sarcoma-associated herpesvirus infection
Hepatitis C
Measles
PI3K-Akt signaling pathway

HALLMARK_IL6_JAK_STAT3_SIGNALING



HALLMARK_INFLAMMATORY_RESPONSE

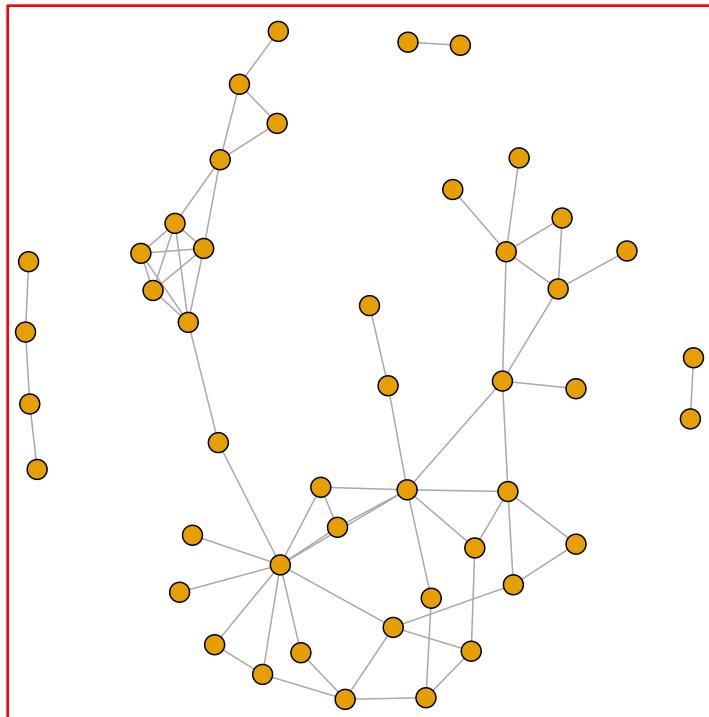


NetBAS	DAVID	KEGG Pathways
105.084	4.4E-7	Neuroactive ligand-receptor interaction
62.501	6.7E-32	Cytokine-cytokine receptor interaction
53.174	NA	Taste transduction
51.623	2.4E-9	Chemokine signaling pathway
35.664	1.7E-2	Calcium signaling pathway
31.281	NA	Phospholipase D signaling pathway
29.265	1.1E-2	cAMP signaling pathway
29.16	3.6E-3	Complement and coagulation cascades
26.391	1.6E-5	NF-kappa B signaling pathway
26.04	7.6E-11	Toll-like receptor signaling pathway

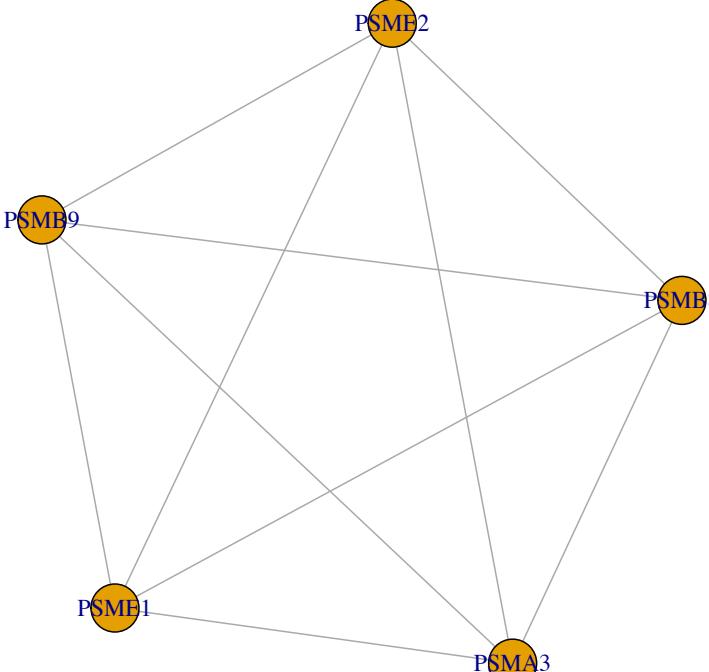
HALLMARK_INFLAMMATORY_RESPONSE

		Biological Process Terms		Cellular Component Terms		Molecular Function Terms	
		NetBAS	DAVID	NetBAS	DAVID	NetBAS	DAVID
GO:0007186	157.204	1.8E-16		96.487	3.1E-54	107.292	2.5E-7
	77.471	5.4E-12		79.193	2.1E-42	53.009	5.8E-12
	77.066	NA		41.515	6.9E-23	49.565	NA
	72.394	NA		40.289	6.4E-9	46.06	NA
	69.574	2.9E-52		40.154	1.8E-11	43.754	NA
	67.93	4.6E-17		32.13	8.2E-17	43.661	NA
	61.535	6.0E-22		31.804	NA	43.413	2.3E-2
	61.491	5.6E-49		28.207	NA	42.184	NA
	58.771	2.6E-6		27.968	NA	41.688	3.3E-8
	56.946	6.8E-7		24.883	3.4E-3	40.787	NA

HALLMARK_INTERFERON_ALPHA_RESPONSE



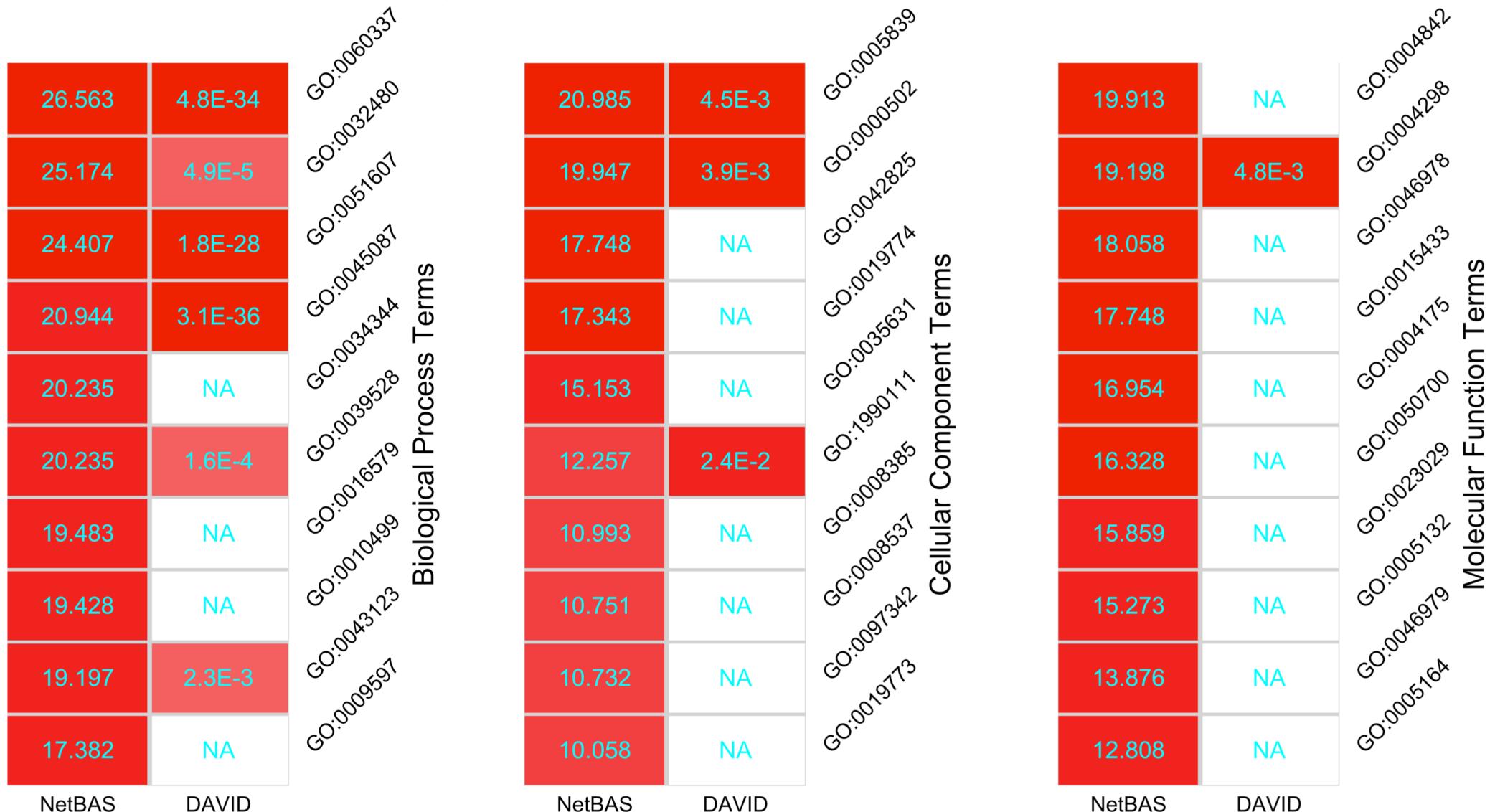
Subnetwork: 91 vertices, 65 edges
(unconnected vertices omitted)



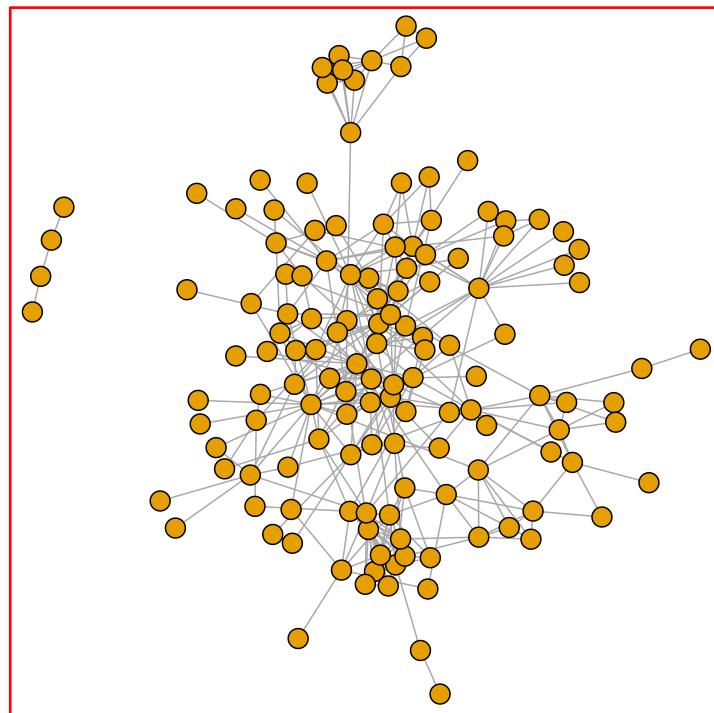
1 largest cliques w/ degree = 5

NetBAS	DAVID	KEGG Pathways
27.377	5.3E-5	RIG-I-like receptor signaling pathway
22.698	2.2E-3	Proteasome
21.761	4.4E-2	NOD-like receptor signaling pathway
17.816	NA	NF-kappa B signaling pathway
16.39	1.1E-3	Hepatitis C
15.955	7.6E-8	Herpes simplex infection
15.867	2.5E-2	Toll-like receptor signaling pathway
14.245	6.4E-3	Cytosolic DNA-sensing pathway
11.989	5.5E-2	Hepatitis B
11.938	NA	Autoimmune thyroid disease

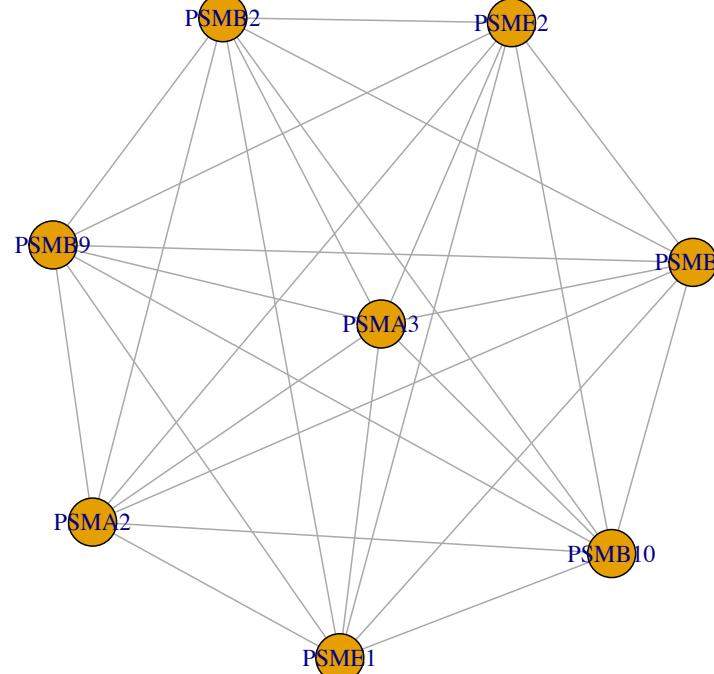
HALLMARK_INTERFERON_ALPHA_RESPONSE



HALLMARK_INTERFERON_GAMMA_RESPONSE



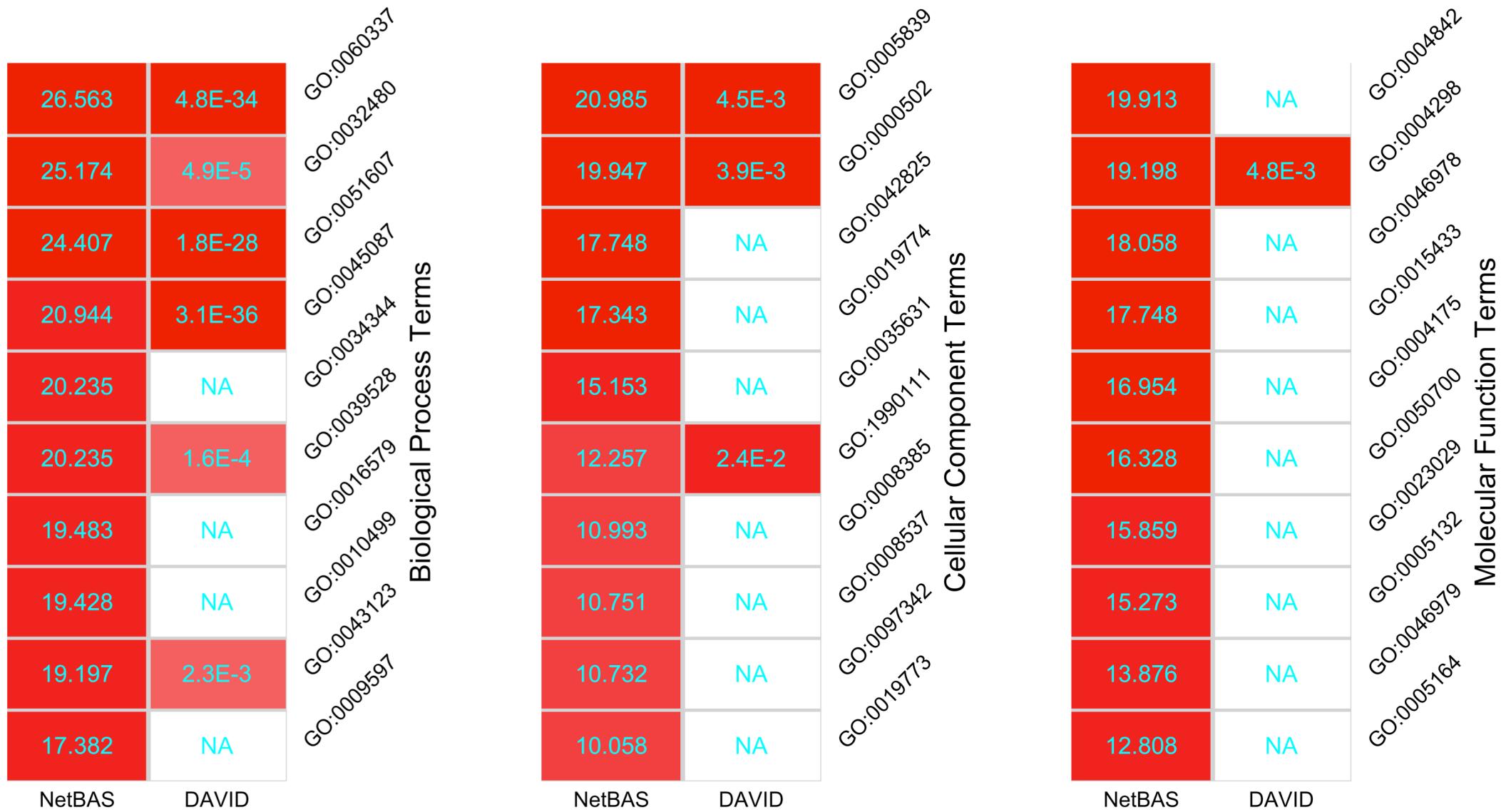
Subnetwork: 194 vertices, 371 edges
(unconnected vertices omitted)



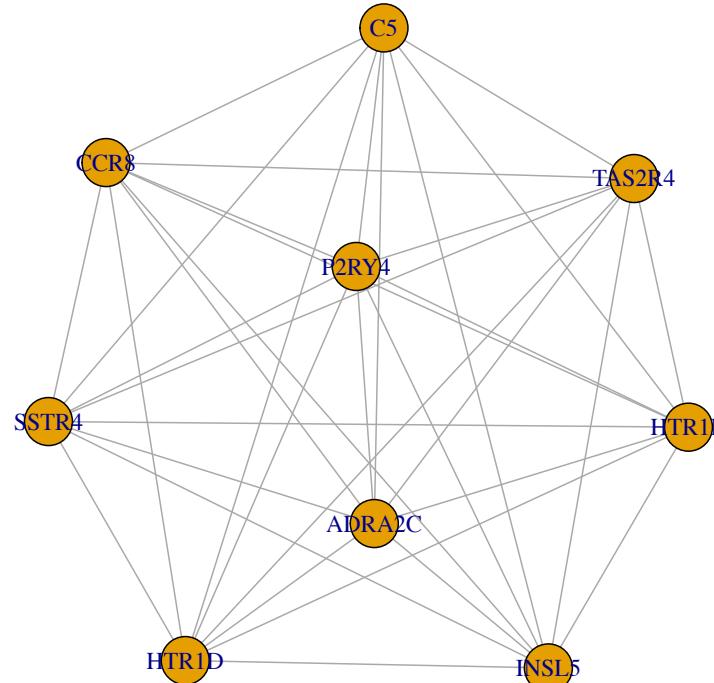
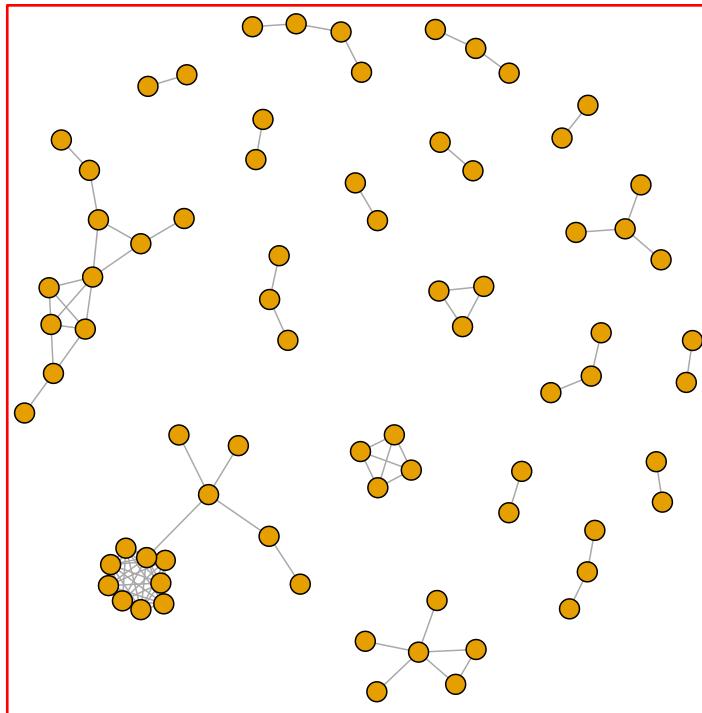
1 largest cliques w/ degree = 8

NetBAS	DAVID	KEGG Pathways
43.898	3.4E-6	RIG-I-like receptor signaling pathway
42.876	2.2E-7	Cytokine-cytokine receptor interaction
39.99	5.4E-11	Jak-STAT signaling pathway
36.386	3.8E-10	Toll-like receptor signaling pathway
35.901	3.0E-6	Autoimmune thyroid disease
35.626	4.9E-7	NOD-like receptor signaling pathway
34.682	1.2E-22	Herpes simplex infection
33.523	1.1E-9	Hepatitis C
32.063	2.1E-5	NF-kappa B signaling pathway
30.638	NA	Th1 and Th2 cell differentiation

HALLMARK_INTERFERON_GAMMA_RESPONSE



HALLMARK_KRAS_SIGNALING_DN



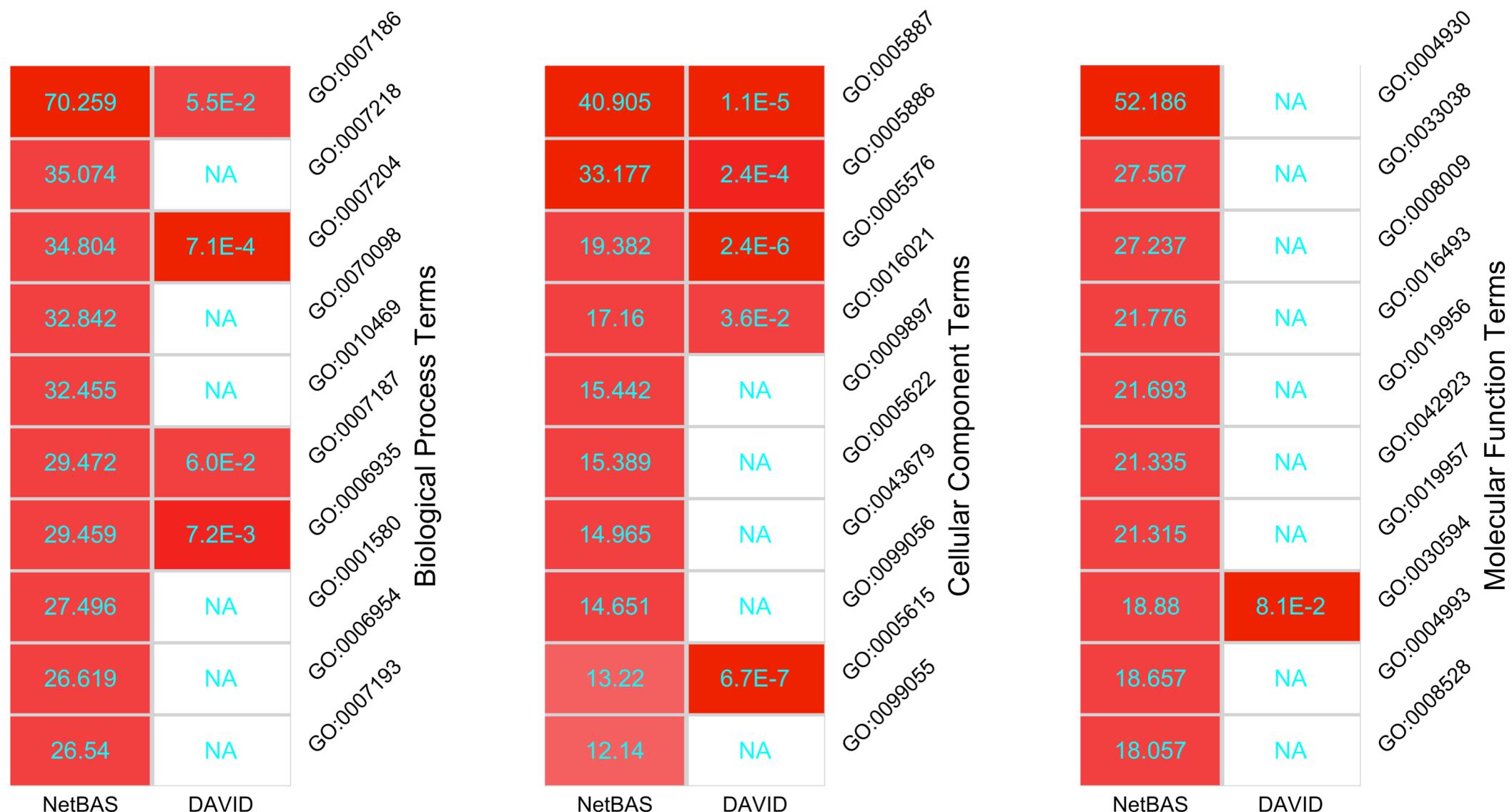
NOTE: the clique-only NetBAS result is consistent with the whole set

	NetBAS	DAVID
50.515	2.3E-3	
28.25	NA	
24.339	2.6E-2	
22.97	NA	
17.217	7.0E-2	
17.005	NA	
15.953	NA	
15.261	1.6E-2	
13.917	NA	
13.873	NA	

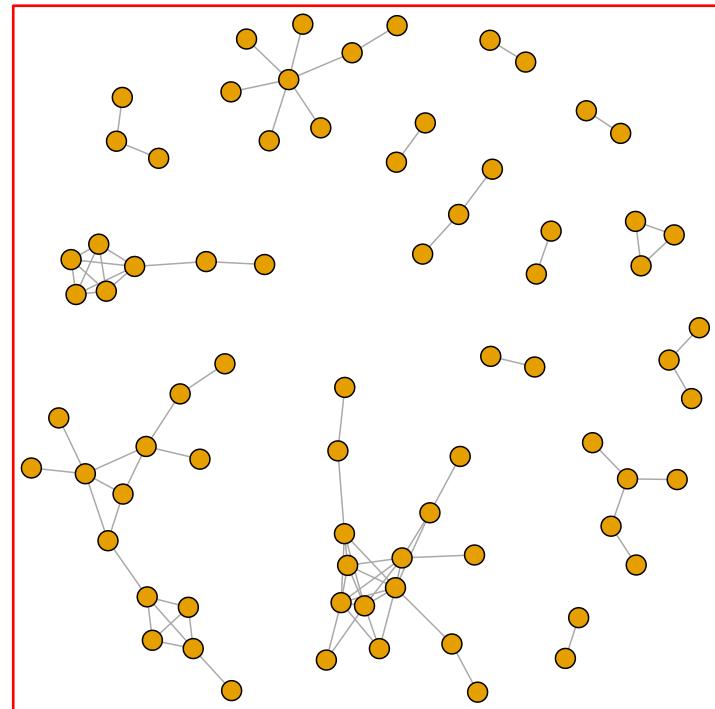
KEGG Pathways

- Neuroactive ligand-receptor interaction
- Taste transduction
- Cytokine-cytokine receptor interaction
- Chemokine signaling pathway
- cAMP signaling pathway
- Phospholipase D signaling cascades
- Complement and coagulation pathway
- Calcium signaling pathway
- Rap1 signaling pathway
- Serotonergic synapse

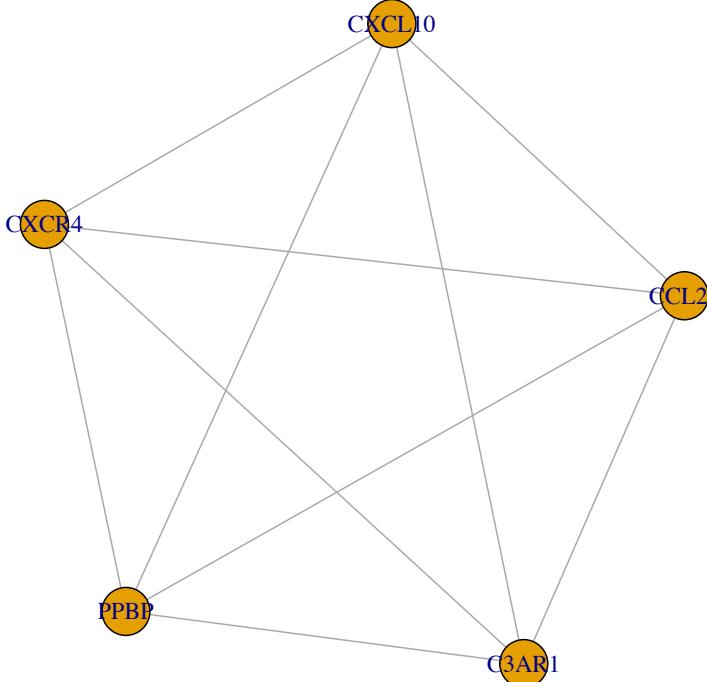
HALLMARK_KRAS_SIGNALING_DN



HALLMARK_KRAS_SIGNALING_UP



Subnetwork: 188 vertices, 83 edges
(unconnected vertices omitted)

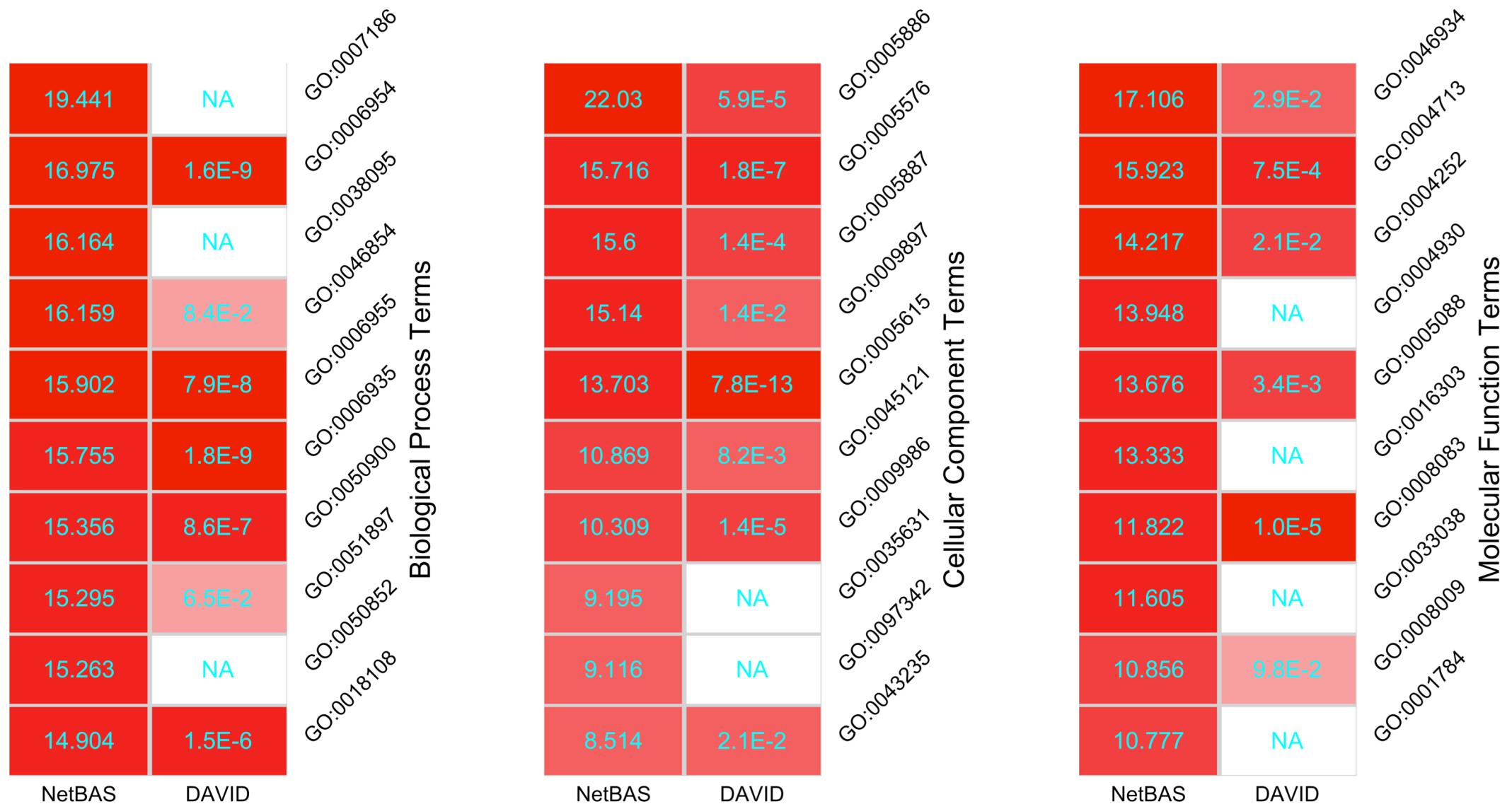


3 largest cliques w/ degree = 5

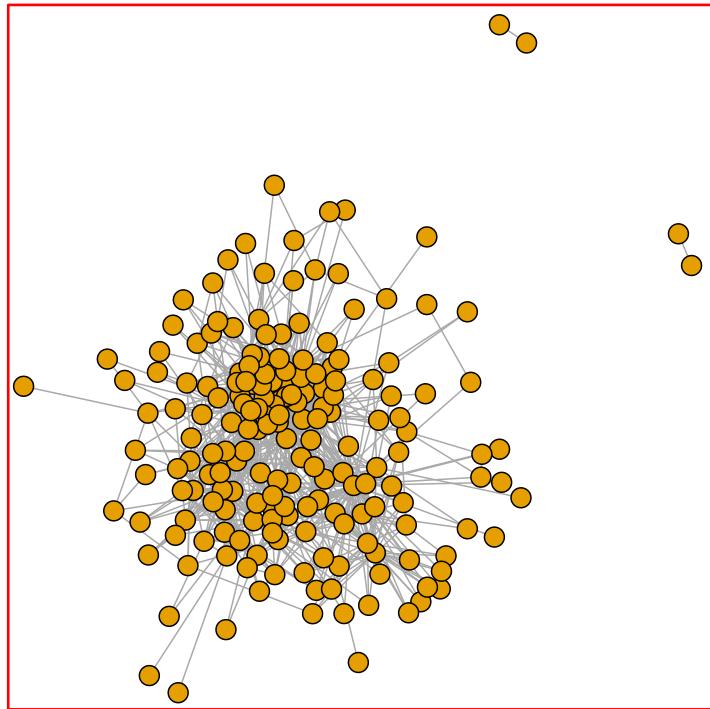
	NetBAS	DAVID
Cytokine-cytokine receptor interaction	20.983	4.7E-4
Chemokine signaling pathway	18.551	7.7E-2
Pathways in cancer	15.985	3.8E-3
Toll-like receptor signaling pathway	15.024	2.7E-2
Ras signaling pathway	14.916	NA
PI3K-Akt signaling pathway	14.859	4.9E-2
TNF signaling pathway	14.483	7.0E-6
Regulation of actin cytoskeleton	14.2	NA
Chagas disease (American trypanosomiasis)	14.197	NA
Fc epsilon RI signaling pathway	14.086	NA

KEGG Pathways

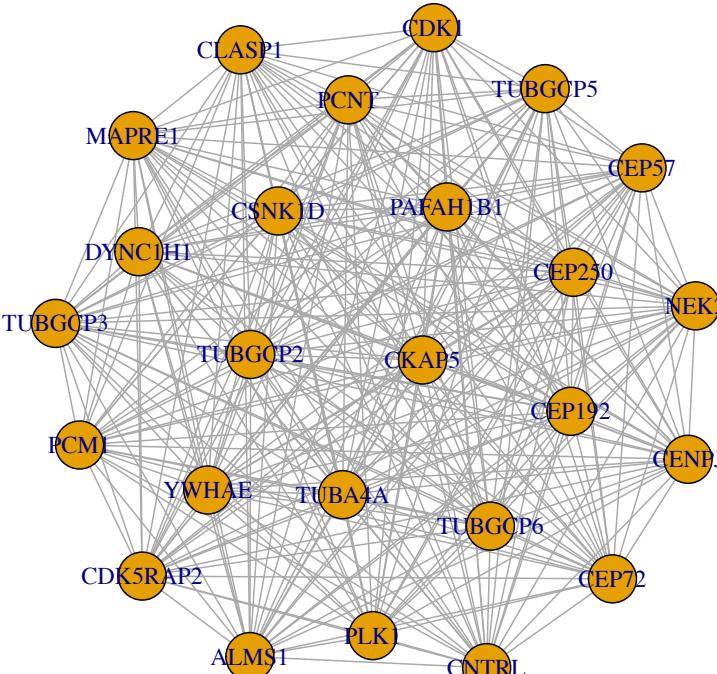
HALLMARK_KRAS_SIGNALING_UP



HALLMARK_MITOTIC_SPINDLE



Subnetwork: 198 vertices, 1228 edges
(unconnected vertices omitted)



1 largest cliques w/ degree = 25

NetBAS	DAVID
27.658	5.6E-9
22.635	1.1E-3
22.195	5.2E-3
21.406	3.9E-8
20.702	1.1E-6
19.515	9.4E-6
19.134	5.2E-4
17.417	5.9E-4
17.248	NA
15.969	3.1E-6

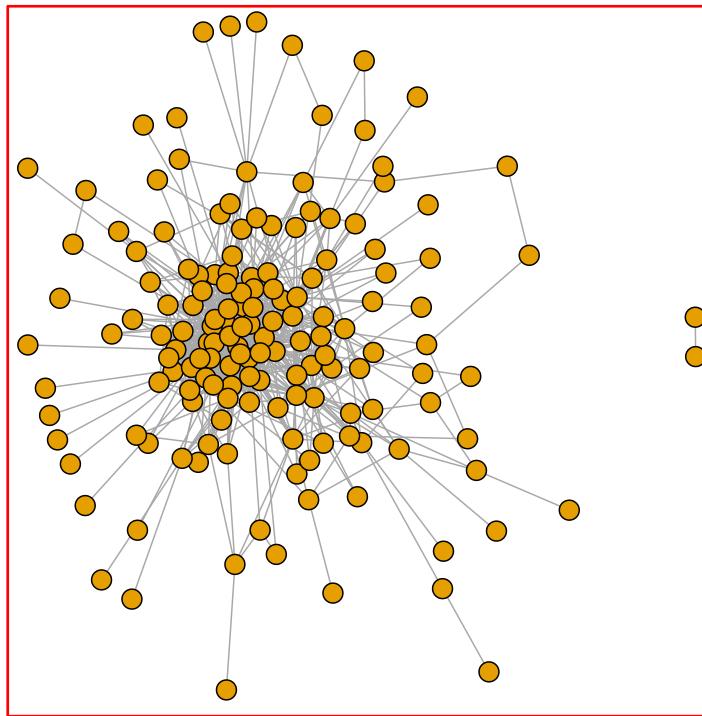
KEGG Pathways

- Regulation of actin cytoskeleton
- Focal adhesion
- Axon guidance
- Bacterial invasion of epithelial cells
- Oocyte meiosis
- Oc gamma R-mediated phagocytosis
- Fc gamma R-signaling pathway
- Ras signaling pathway
- Leukocyte transendothelial migration
- Vasopressin-regulated water reabsorption
- Cell cycle

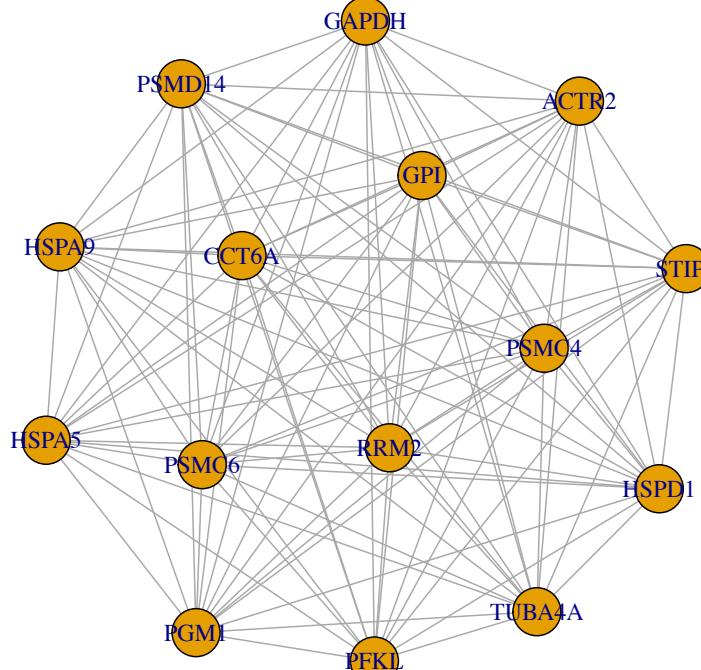
HALLMARK_MITOTIC_SPINDLE

		Biological Process Terms		Cellular Component Terms		Molecular Function Terms	
		NetBAS	DAVID	NetBAS	DAVID	NetBAS	DAVID
GO:0097711	66.593	NA		66.347	2.2E-41	40.223	4.6E-45
	58.884	NA		59.075	1.2E-9	35.222	8.4E-12
	56.84	1.2E-39		49.77	2.0E-11	31	7.8E-9
	54.93	4.5E-21		43.496	2.0E-21	28.527	4.5E-24
	54.488	6.8E-30		43.241	6.8E-14	27.888	7.2E-13
	44.656	1.3E-8		41.173	1.1E-4	26.195	8.4E-5
	41.225	8.4E-3		38.126	2.1E-25	24.98	4.6E-2
	40.7	1.7E-46		37.662	NA	22.074	3.9E-11
	40.299	3.8E-29		36.672	4.9E-60	21.777	4.2E-13
	35.544	2.4E-20		34.503	9.2E-51	20.988	1.2E-21

HALLMARK_MTORC1_SIGNALING



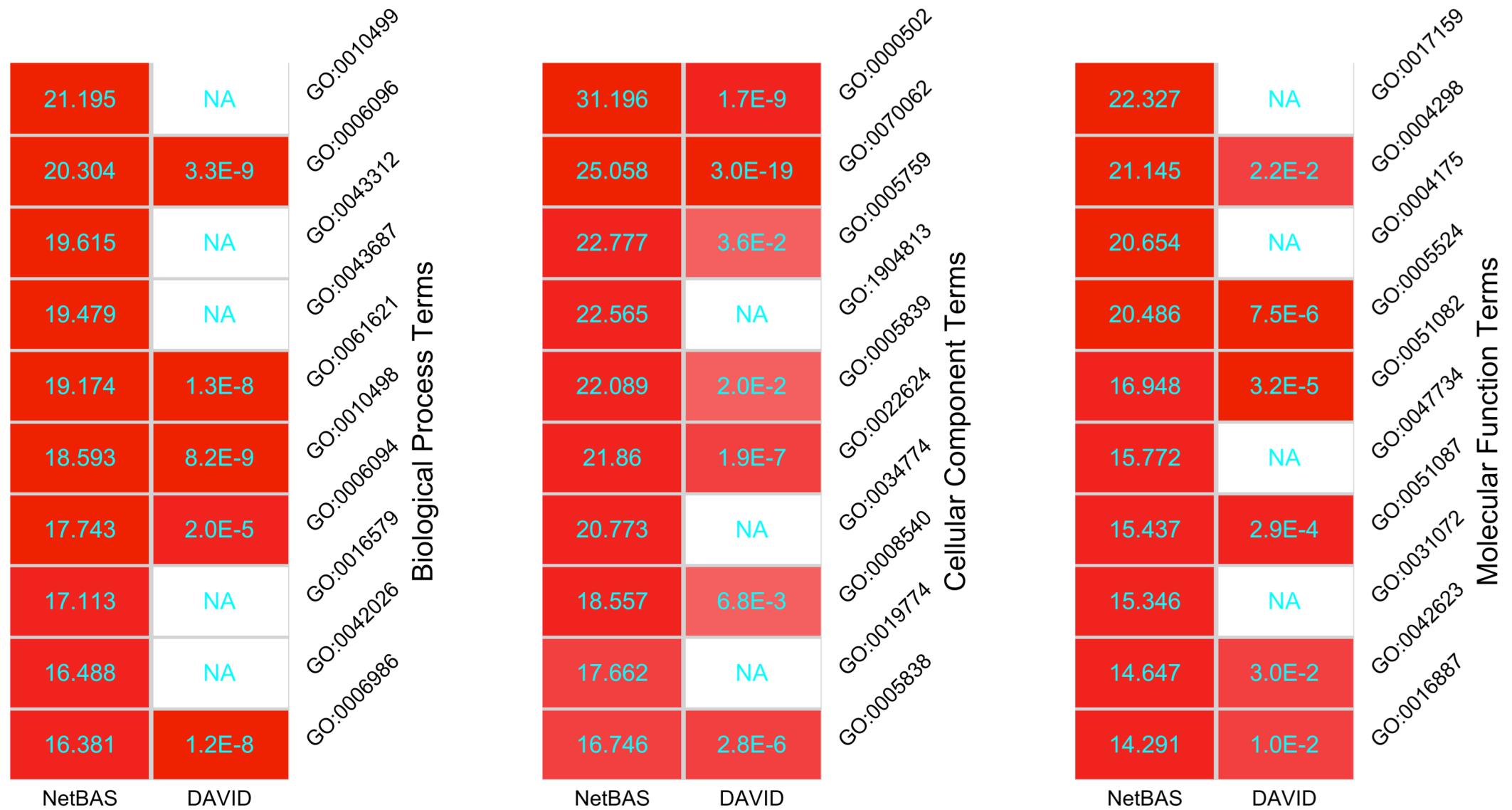
Subnetwork: 196 vertices, 903 edges
(unconnected vertices omitted)



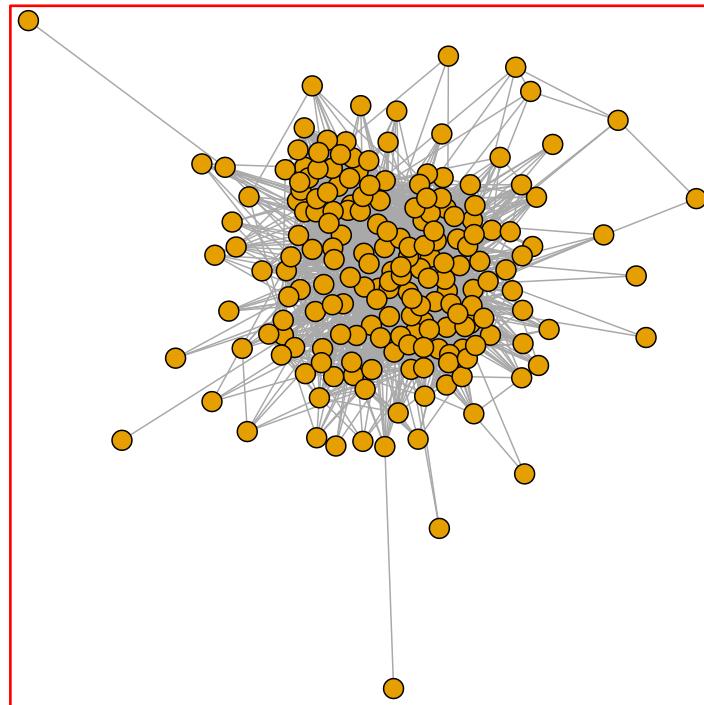
5 largest cliques w/ degree = 15

	NetBAS	DAVID	KEGG Pathways
	31.533	2.0E-7	Proteasome
	25.354	8.2E-6	Glycolysis / Gluconeogenesis
	17.457	NA	Pyruvate metabolism
	17.063	NA	Amino sugar and nucleotide sugar metabolism
	16.799	8.1E-3	Protein processing in endoplasmic reticulum
	16.179	3.5E-2	Phagosome
	15.809	NA	Citrate cycle (TCA cycle)
	14.995	8.2E-3	Glycine, serine and threonine metabolism
	14.477	NA	Cysteine and methionine metabolism
	14.173	4.0E-3	Fructose and mannose metabolism

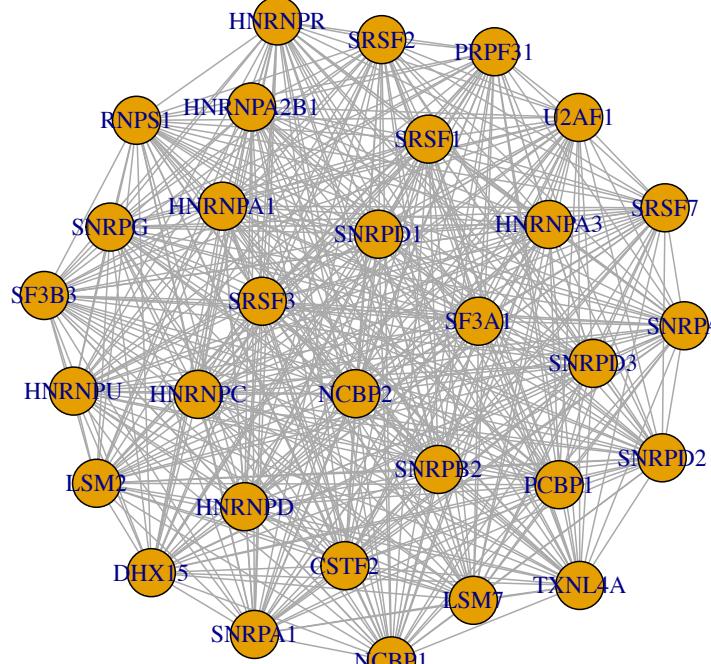
HALLMARK_MTORC1_SIGNALING



HALLMARK_MYC_TARGETS_V1



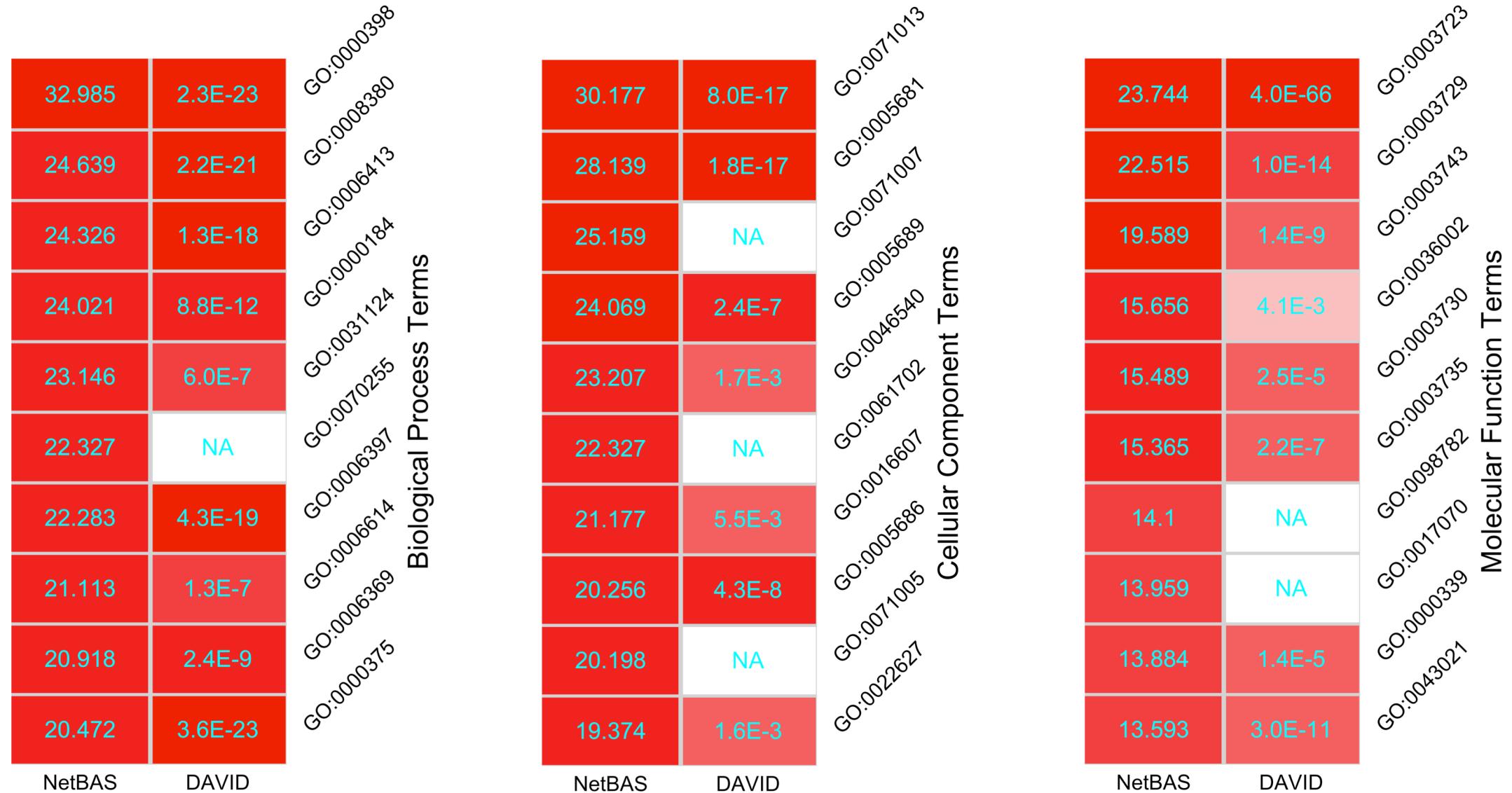
Subnetwork: 197 vertices, 3018 edges
(unconnected vertices omitted)



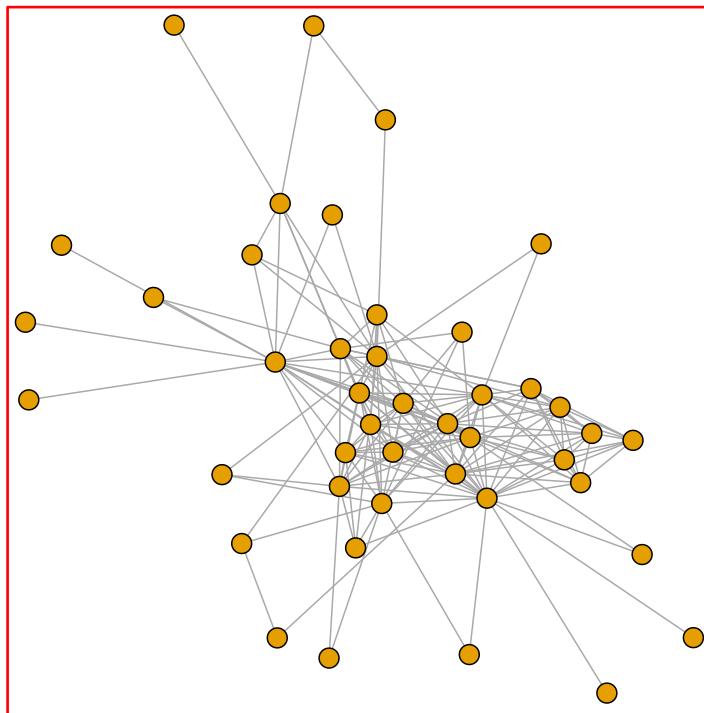
1 largest cliques w/ degree = 31

KEGG Pathways	NetBAS	DAVID
Spliceosome	28.748	6.4E-18
mRNA surveillance pathway	21.311	1.0E-2
Proteasome	17.772	1.8E-12
RNA transport	17.363	5.7E-8
Ribosome	17.158	1.8E-5
RNA degradation	16.573	7.1E-2
Systemic lupus erythematosus	15.562	NA
Glycolysis / Gluconeogenesis	13.416	NA
Amino sugar and nucleotide sugar metabolism	12.931	NA
Ribosome biogenesis in eukaryotes	12.641	NA

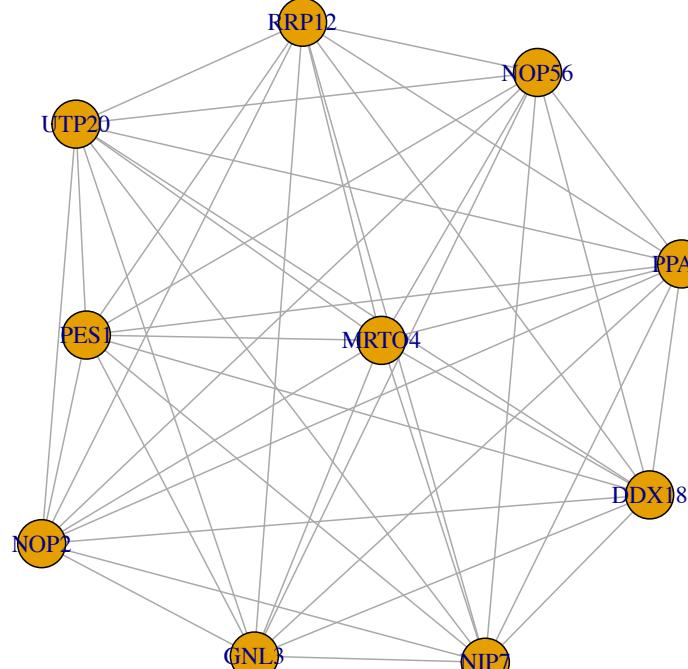
HALLMARK_MYC_TARGETS_V1



HALLMARK_MYC_TARGETS_V2



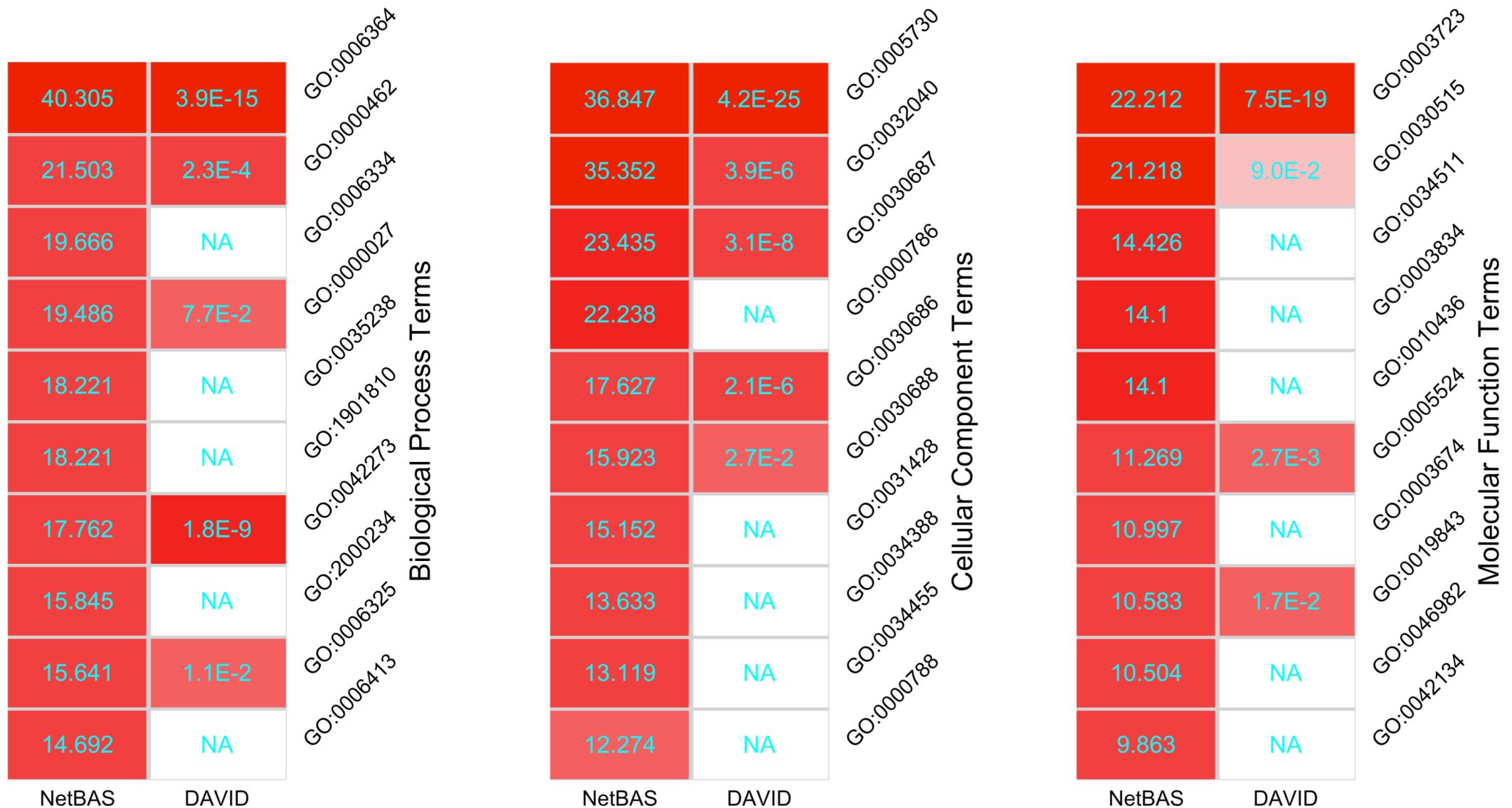
Subnetwork: 58 vertices, 181 edges
(unconnected vertices omitted)



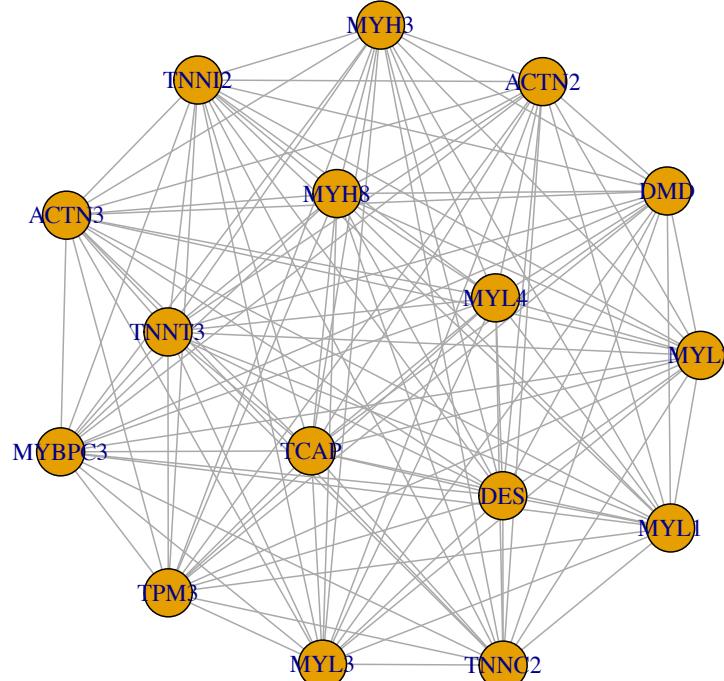
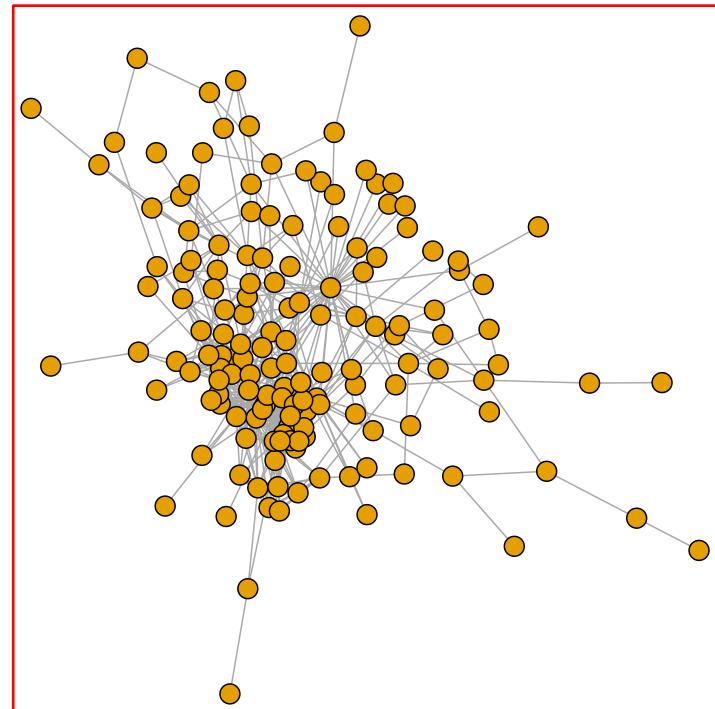
2 largest cliques w/ degree = 10

	NetBAS	DAVID	KEGG Pathways
	35.618	6.4E-6	Ribosome biogenesis in eukaryotes
	20.239	NA	Systemic lupus erythematosus
	14.564	NA	Alcoholism
	9.904	NA	Necroptosis
	9.829	NA	Ribosome
	9.282	NA	RNA degradation
	8.643	NA	RNA transport
	7.563	NA	Glycolysis / Gluconeogenesis
	7.504	NA	Pathogenic Escherichia coli infection
	7.246	NA	Amino sugar and nucleotide sugar metabolism

HALLMARK_MYC_TARGETS_V2



HALLMARK_MYOGENESIS



NetBAS	DAVID	KEGG Pathways
41.149	1.1E-17	Dilated cardiomyopathy (DCM)
40.821	4.7E-17	Hypertrophic cardiomyopathy (HCM)
33.742	7.7E-8	Cardiac muscle contraction
23.79	9.9E-7	Adrenergic signaling in cardiomyocytes
21.425	2.7E-6	Arrhythmogenic right ventricular cardiomyopathy (ARVC)
21.026	1.3E-7	Focal adhesion
20.011	9.5E-5	Regulation of actin cytoskeleton
18.168	NA	Vascular smooth muscle contraction
17.623	3.1E-6	Vascular smooth muscle interaction
17.465	5.5E-3	ECM-receptor interaction
		Oxytocin signaling pathway

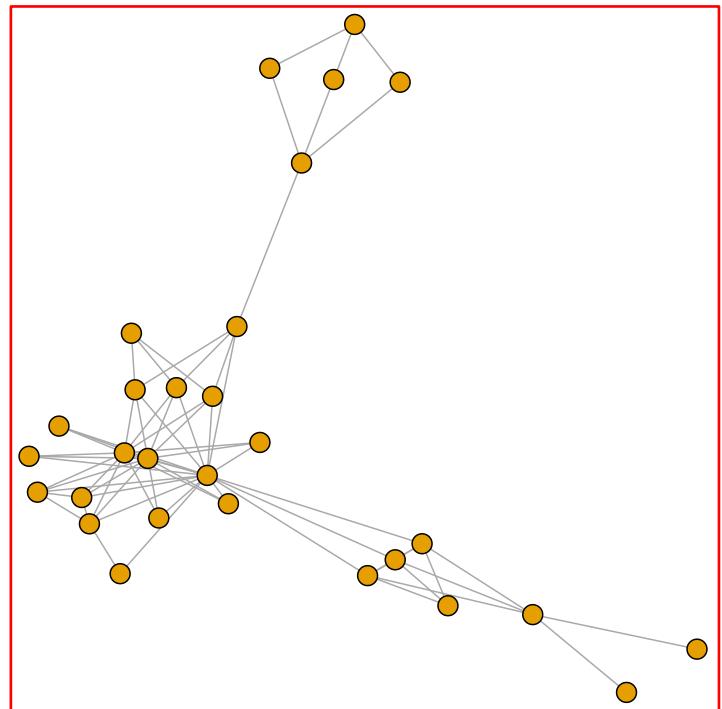
HALLMARK_MYOGENESIS

73.619	8.8E-43	GO:0030049
50.681	2.2E-71	GO:0006936
43.844	4.1E-18	GO:0060048
40.777	8.6E-17	GO:0045214
38.57	5.4E-8	GO:0055010
35.622	4.8E-8	GO:003009
34.157	1.4E-26	GO:0048739
30.8	9.7E-2	GO:0032972
29.732	2.2E-2	GO:0035995
29.5	7.4E-4	
NetBAS	DAVID	

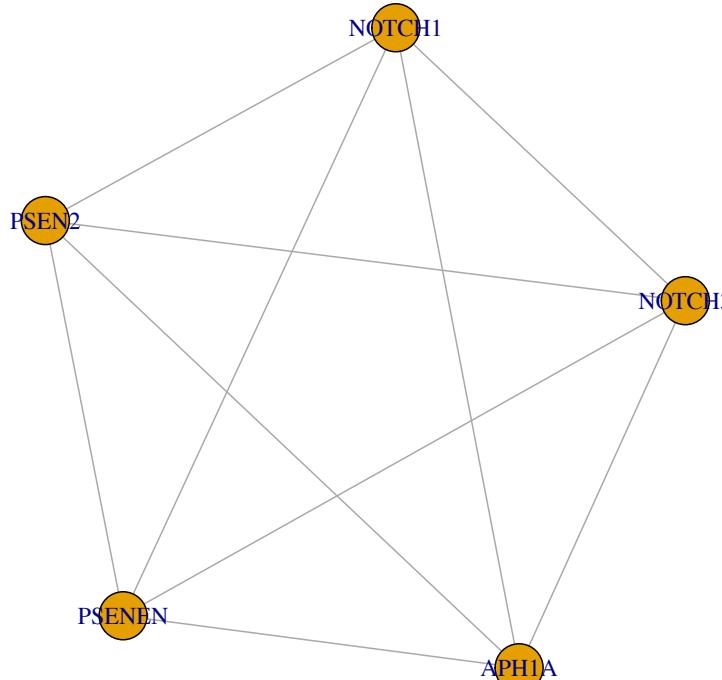
56.463	3.4E-11	GO:0005861
35.973	4.1E-2	GO:0005862
35.704	NA	GO:1990584
35.556	6.0E-15	GO:0030018
34.119	NA	GO:0097512
31.287	5.8E-20	GO:0005859
31.009	2.2E-47	GO:0030017
28.257	5.6E-13	GO:0005865
27.897	6.3E-48	GO:0030016
25.711	7.9E-17	GO:0032982
NetBAS	DAVID	

59.723	1.1E-26	GO:0008307
44.385	2.8E-8	GO:0051015
37.306	3.3E-2	GO:0030172
36.919	7.3E-4	GO:0031014
35.545	1.8E-3	GO:0031013
35.034	6.4E-26	GO:0032038
32.031	2.2E-2	GO:0003779
30.233	NA	GO:0030899
28.884	5.1E-6	GO:0005509
28.028	1.0E-2	GO:0005523
NetBAS	DAVID	

HALLMARK_NOTCH_SIGNALING



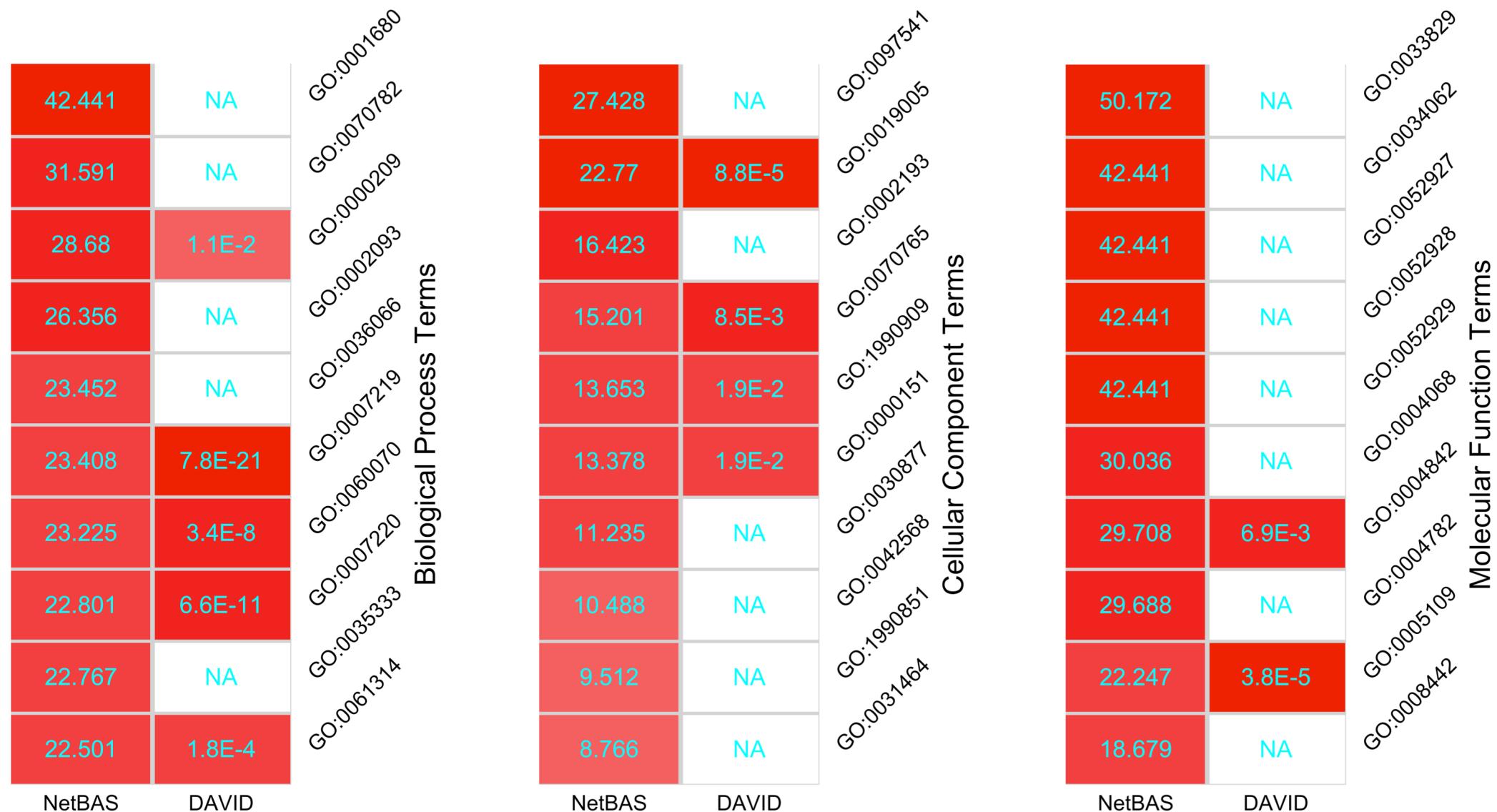
Subnetwork: 32 vertices, 68 edges
(unconnected vertices omitted)



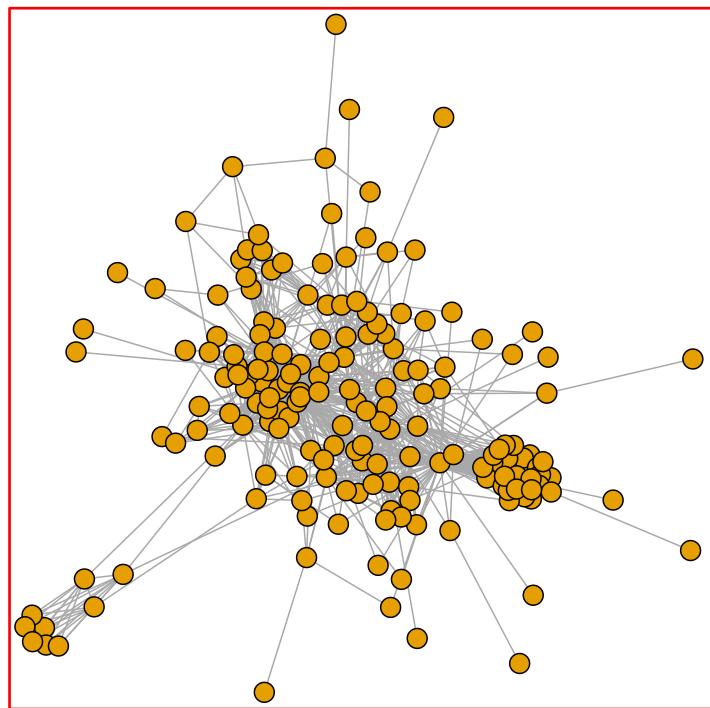
2 largest cliques w/ degree = 5

	NetBAS	DAVID
Notch signaling pathway	35.248	5.8E-24
Basal cell carcinoma	25.417	2.5E-6
Human papillomavirus infection	18.11	NA
Breast cancer	16.807	NA
Wnt signaling pathway	14.923	1.0E-13
Hippo signaling pathway	13.644	2.2E-6
Ubiquitin mediated proteolysis	13.088	1.9E-2
Pathways in cancer	12.23	2.1E-5
Other types of O-glycan biosynthesis	11.853	NA
Th1 and Th2 cell differentiation	11.615	NA

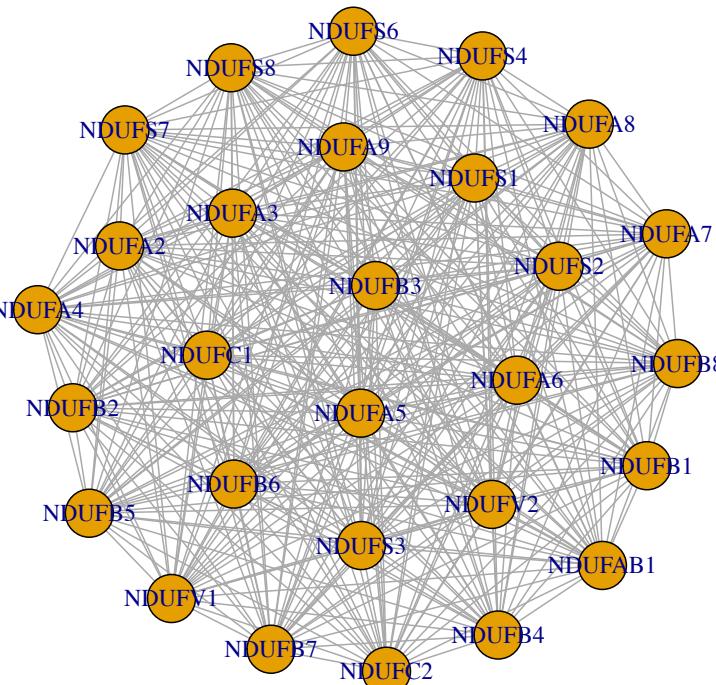
HALLMARK_NOTCH_SIGNALING



HALLMARK_OXIDATIVE_PHOSPHORYLATION



Subnetwork: 189 vertices, 1380 edges
(unconnected vertices omitted)



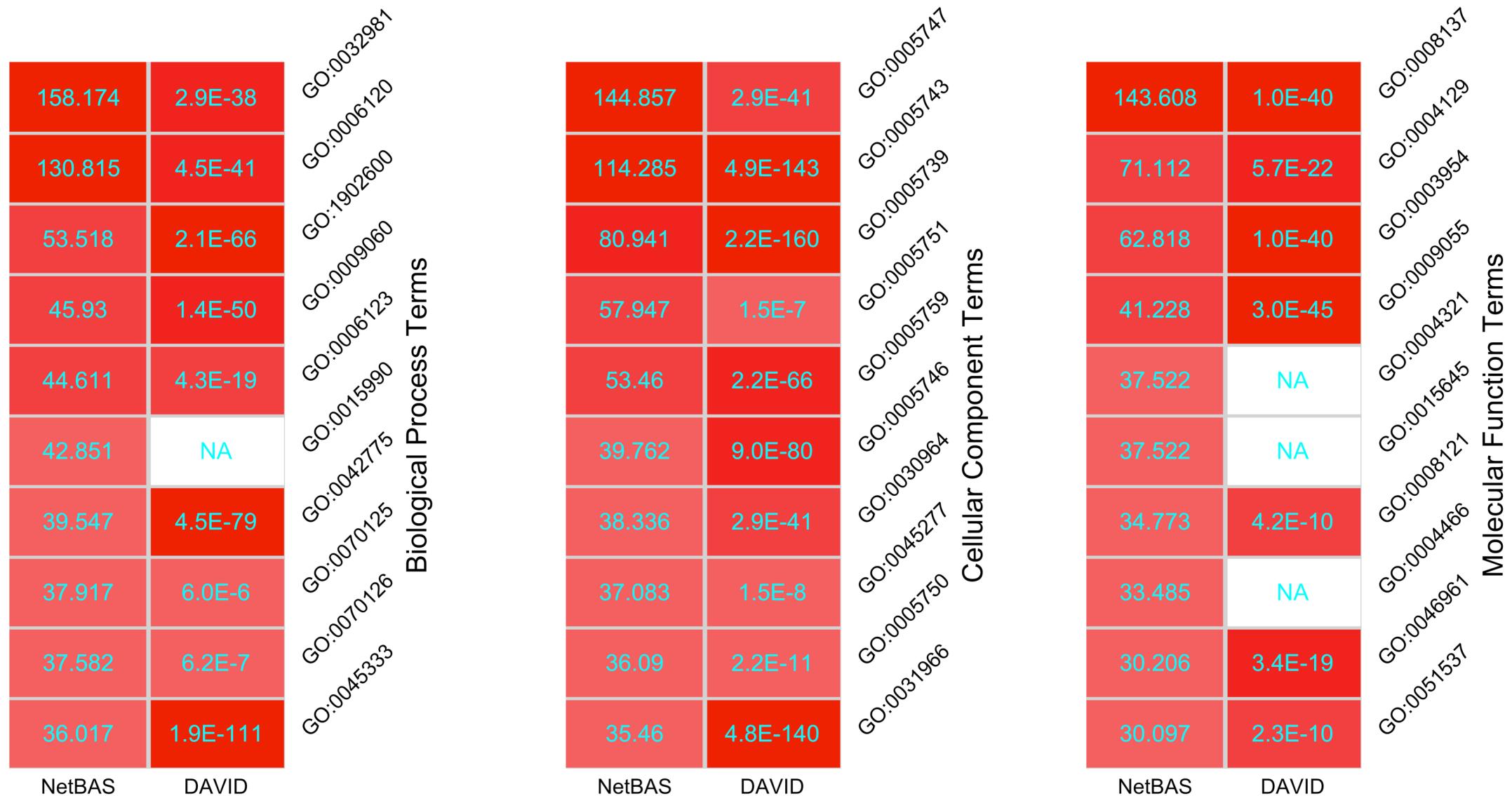
2 largest cliques w/ degree = 28

	NetBAS	DAVID
Oxidative phosphorylation	131.407	4.0E-106
Parkinson's disease	106.522	4.7E-83
Alzheimer's disease	89.046	7.3E-68
Thermogenesis	88.015	NA
Non-alcoholic fatty liver disease (NAFLD)	75.753	8.0E-52
Retrograde endocannabinoid signaling	75.041	NA
Huntington's disease	66.045	4.5E-73
Cardiac muscle contraction	39.95	1.5E-15
Collecting duct acid secretion	29.452	1.5E-6
Glycolysis / Gluconeogenesis	28.487	3.7E-3

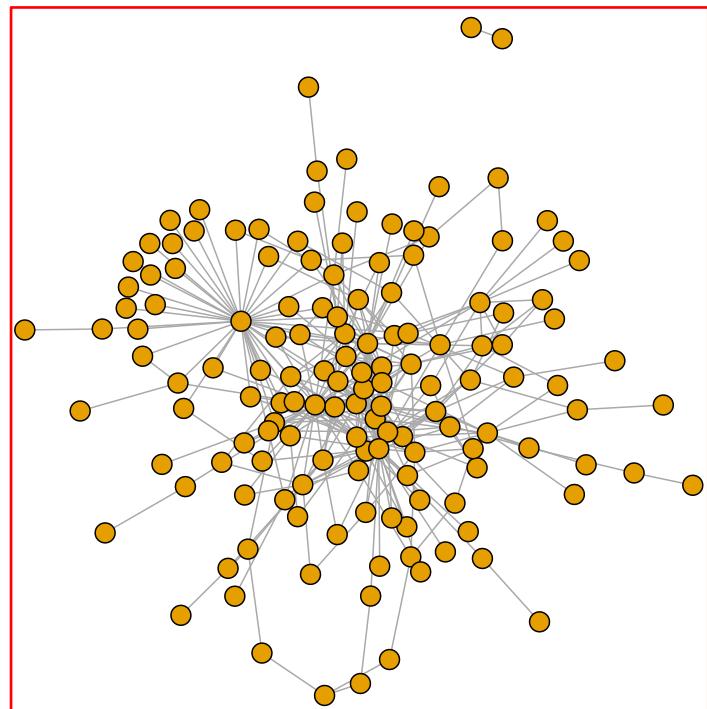
KEGG Pathways

- Oxidative phosphorylation
- Parkinson's disease
- Alzheimer's disease
- Thermogenesis
- Non-alcoholic fatty liver disease (NAFLD)
- Retrograde endocannabinoid signaling
- Huntington's disease
- Cardiac muscle contraction
- Collecting duct acid secretion
- Glycolysis / Gluconeogenesis

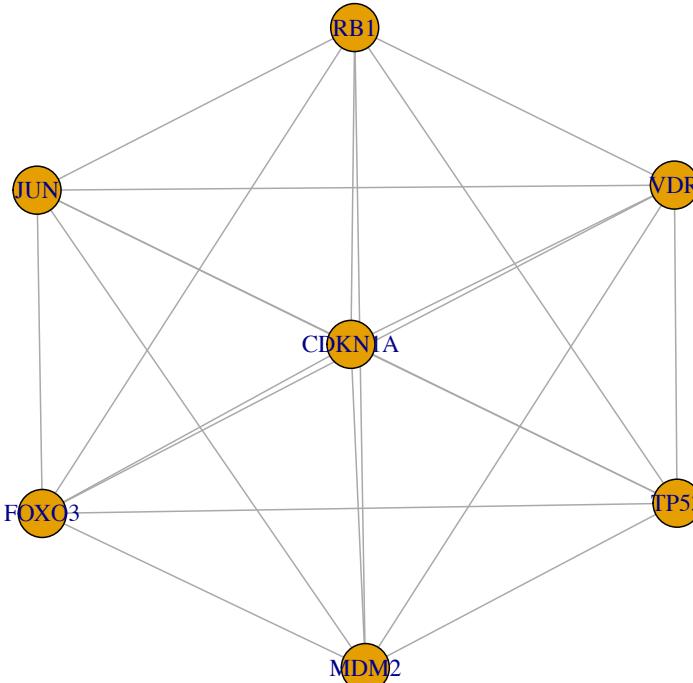
HALLMARK_OXIDATIVE_PHOSPHORYLATION



HALLMARK_P53_PATHWAY



Subnetwork: 195 vertices, 342 edges
(unconnected vertices omitted)



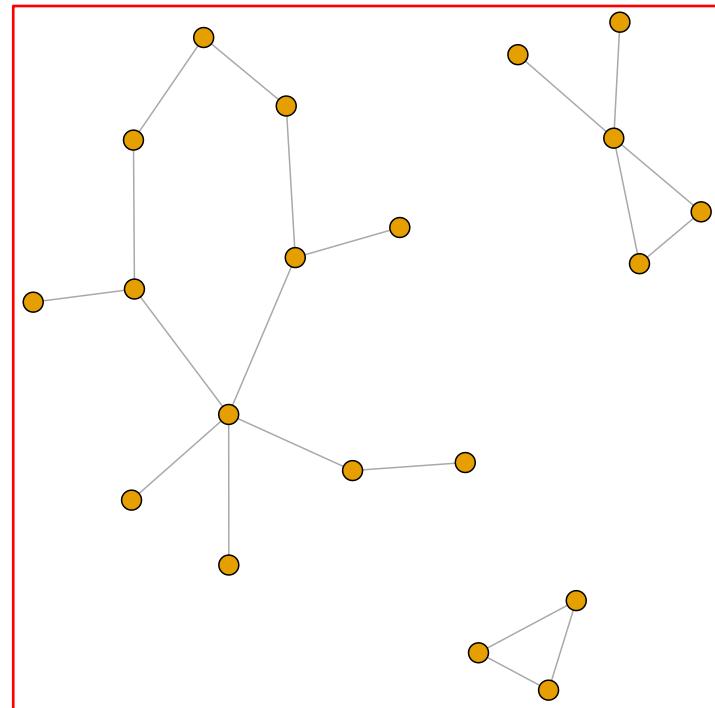
1 largest cliques w/ degree = 7

KEGG Pathways	NetBAS	DAVID
p53 signaling pathway	19.611	2.2E-21
Pathways in cancer	18.31	5.1E-6
Cell cycle	18.283	1.2E-5
Hepatitis B	17.954	5.1E-5
Pancreatic cancer	17.647	5.9E-3
Chronic myeloid leukemia	17.41	1.7E-3
Cellular senescence	16.128	NA
MicroRNAs in cancer	15.975	4.4E-5
FoxO signaling pathway	15.846	1.3E-4
Colorectal cancer	15.807	4.8E-3

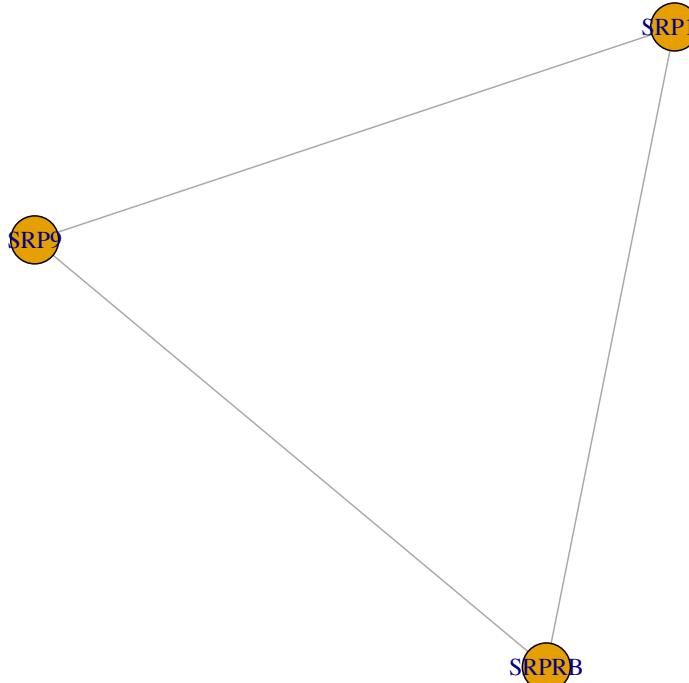
HALLMARK_P53_PATHWAY

		Biological Process Terms		Cellular Component Terms		Molecular Function Terms	
		NetBAS	DAVID	NetBAS	DAVID	NetBAS	DAVID
GO:0045893	20.454	2.2E-6		16.217	4.6E-5	19.387	1.7E-3
	20.411	1.7E-6		15.655	1.1E-4	18.455	NA
	18.294	3.4E-6		11.959	5.8E-4	18.221	NA
	18.221	NA		11.836	6.0E-3	16.202	NA
	18.221	NA		11.658	1.2E-7	15.397	5.4E-2
	16.048	NA		10.422	1.3E-4	14.334	NA
	15.915	3.0E-6		10.226	4.2E-7	13.985	5.4E-2
	15.848	8.5E-13		10.005	1.7E-6	13.489	7.3E-7
	14.169	1.6E-9		9.482	4.6E-4	13.182	9.7E-12
	14.124	1.5E-5		8.655	NA	13.066	1.4E-2

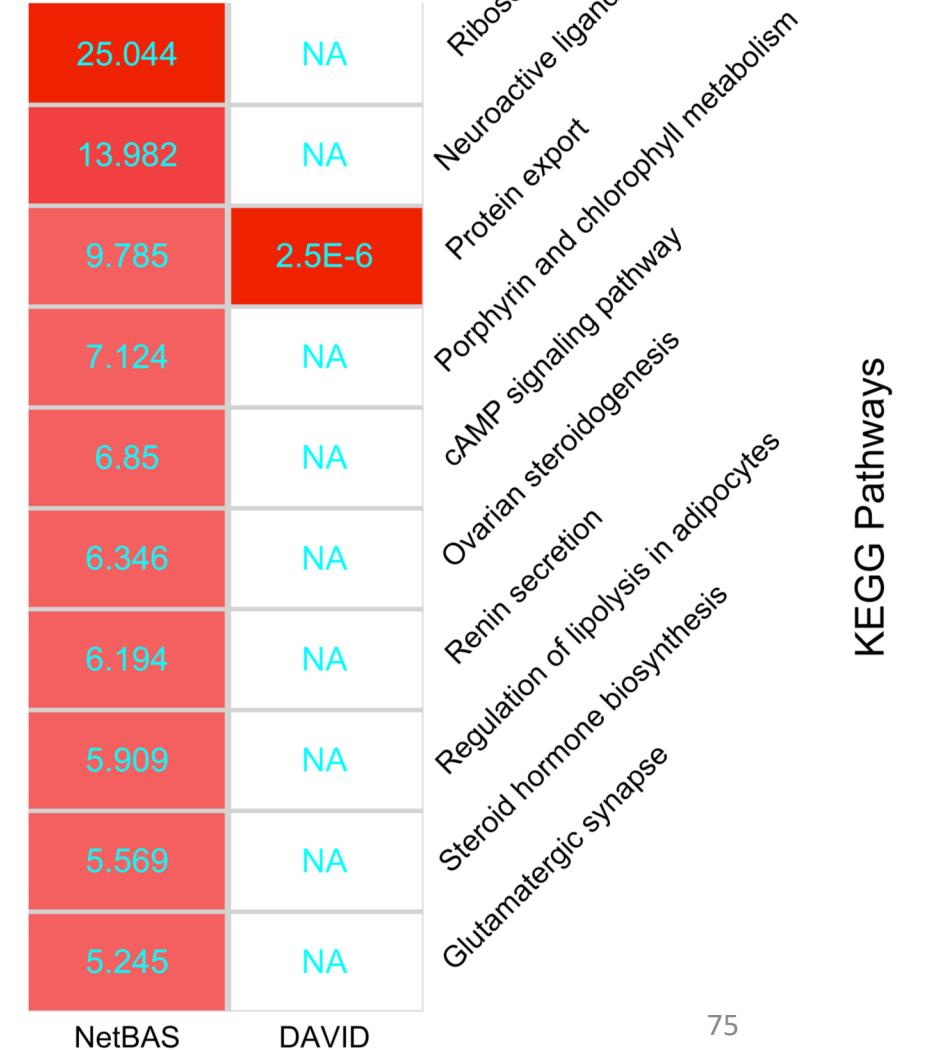
HALLMARK_PANCREAS_BETA_CELLS



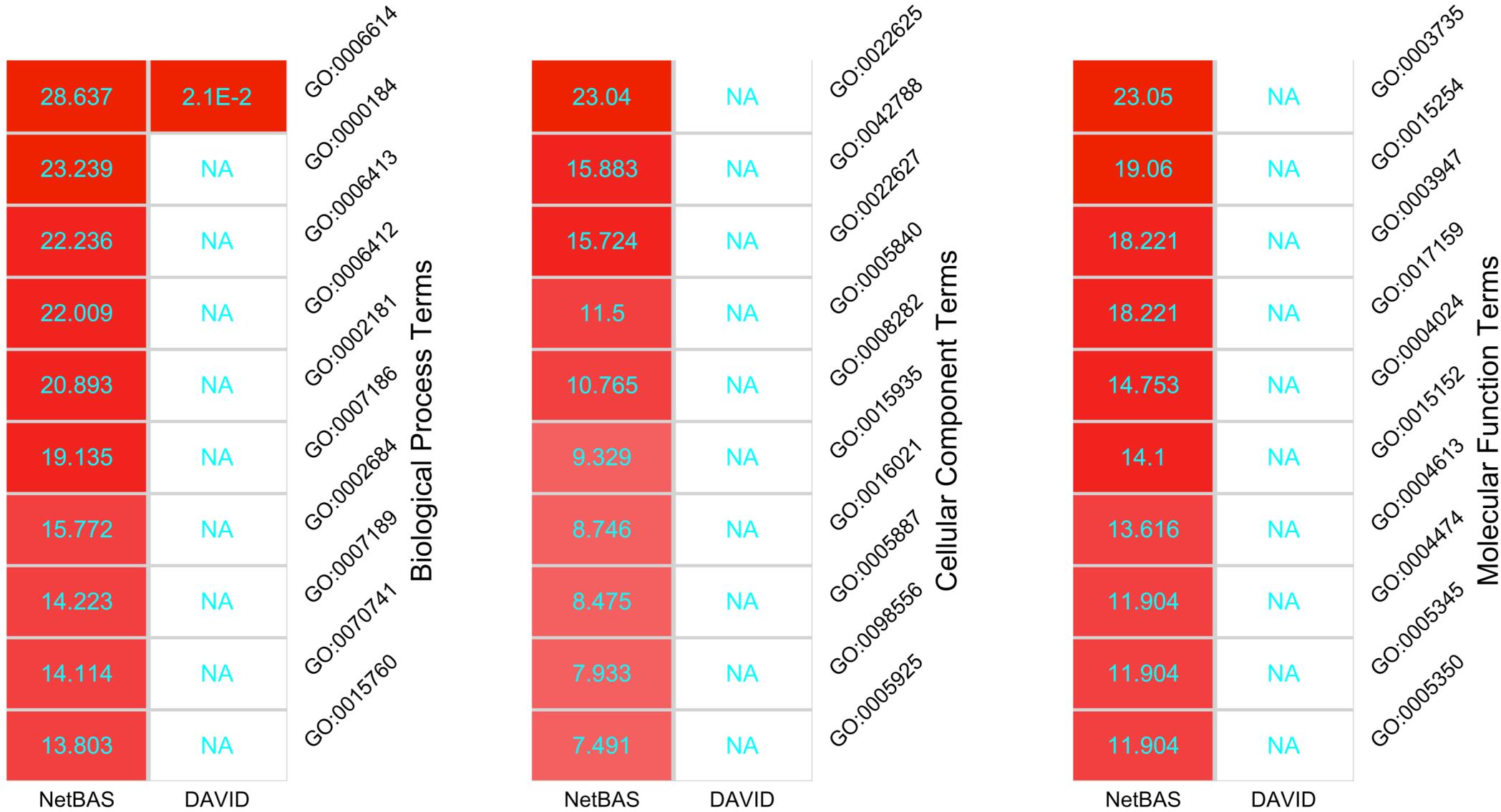
Subnetwork: 39 vertices, 20 edges
(unconnected vertices omitted)



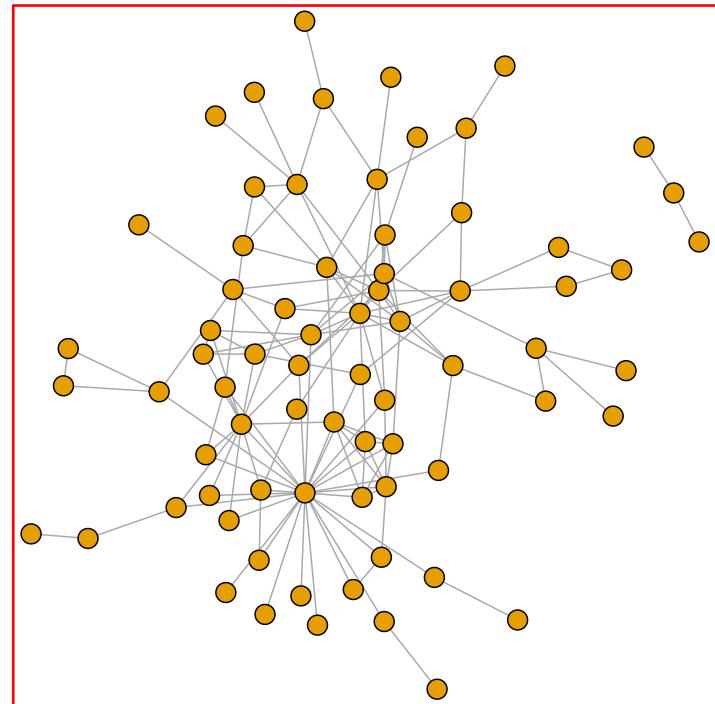
2 largest cliques w/ degree = 3



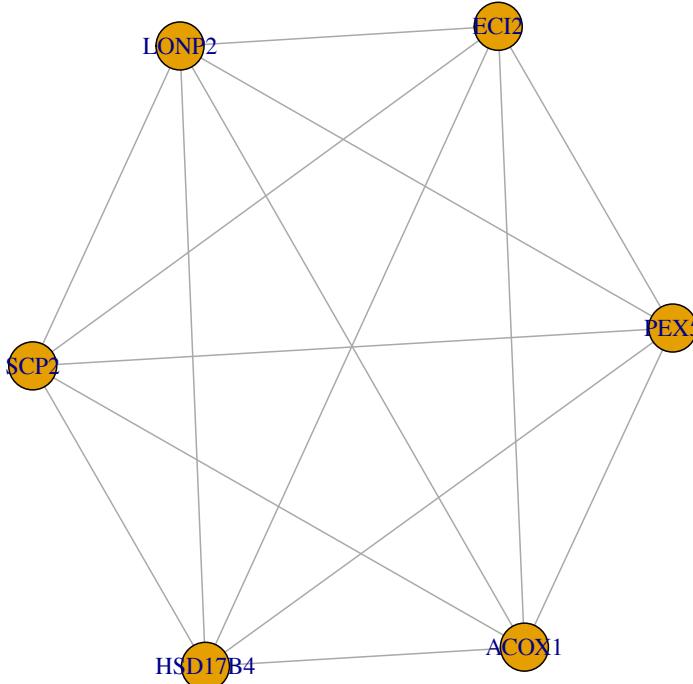
HALLMARK_PANCREAS_BETA_CELLS



HALLMARK_PEROXISOME



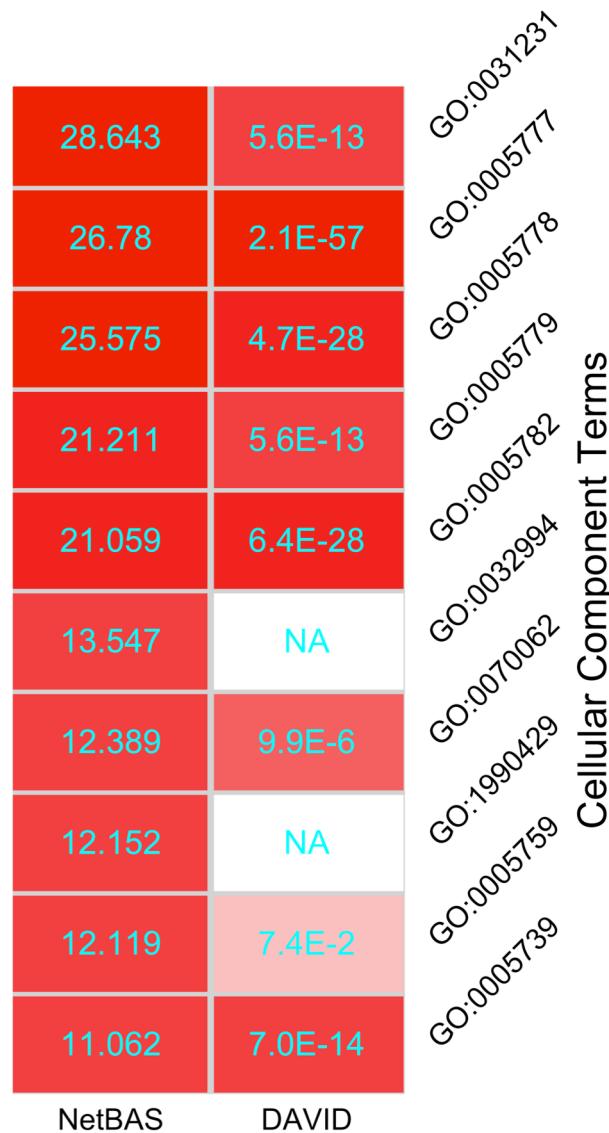
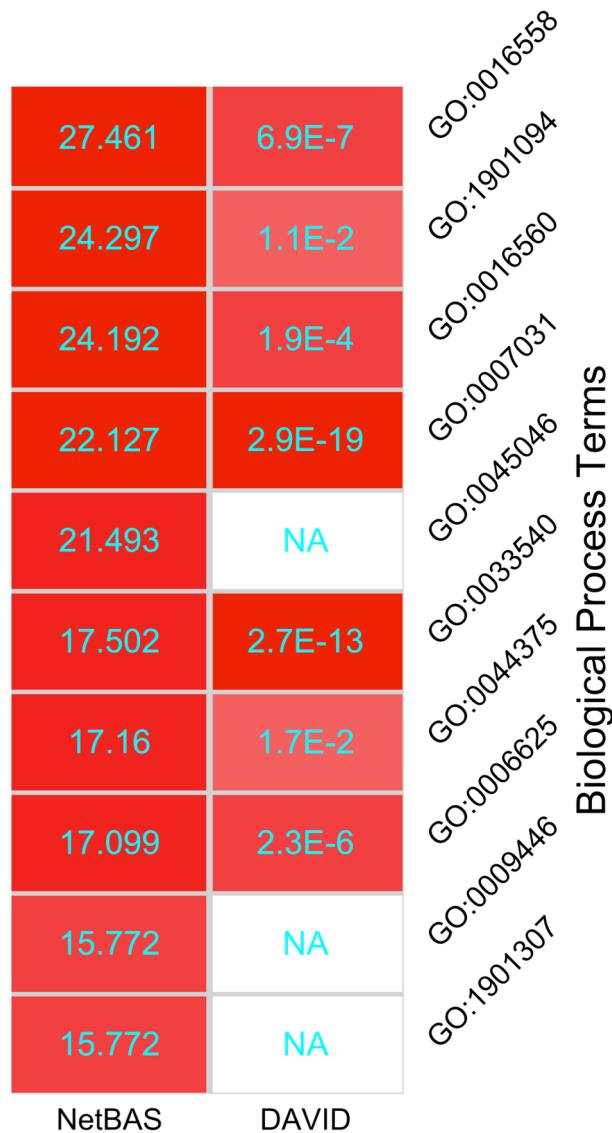
Subnetwork: 103 vertices, 142 edges
(unconnected vertices omitted)



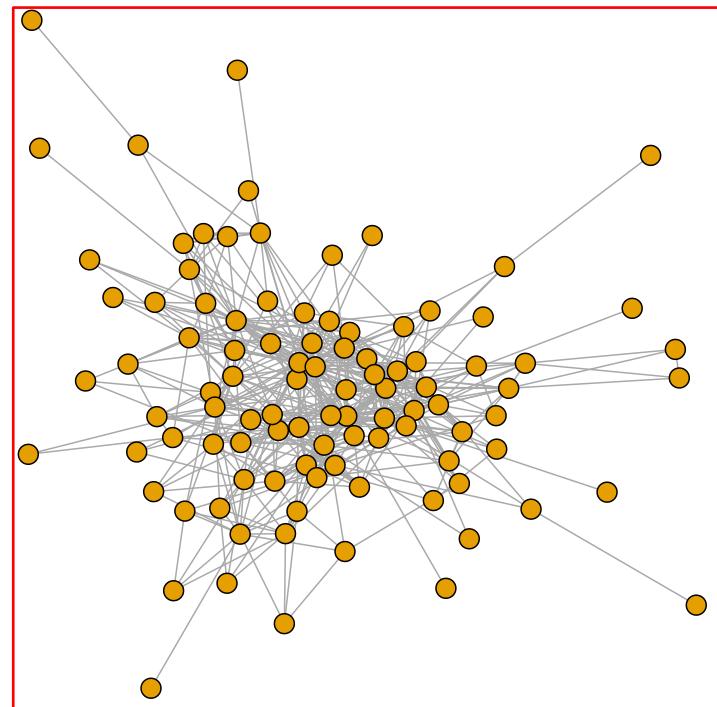
1 largest cliques w/ degree = 6

KEGG Pathways	NetBAS	DAVID
Peroxisome	27.134	1.0E-51
Glycolysis / Gluconeogenesis	10.061	NA
Necroptosis	9.114	NA
Nucleotide excision repair	8.838	9.7E-2
Drug metabolism	8.709	NA
Pyruvate metabolism	8.436	NA
D-Arginine and D-ornithine metabolism	8.388	NA
Citrate cycle (TCA cycle)	8.012	NA
Fatty acid degradation	7.687	3.3E-7
Legionellosis	7.396	NA

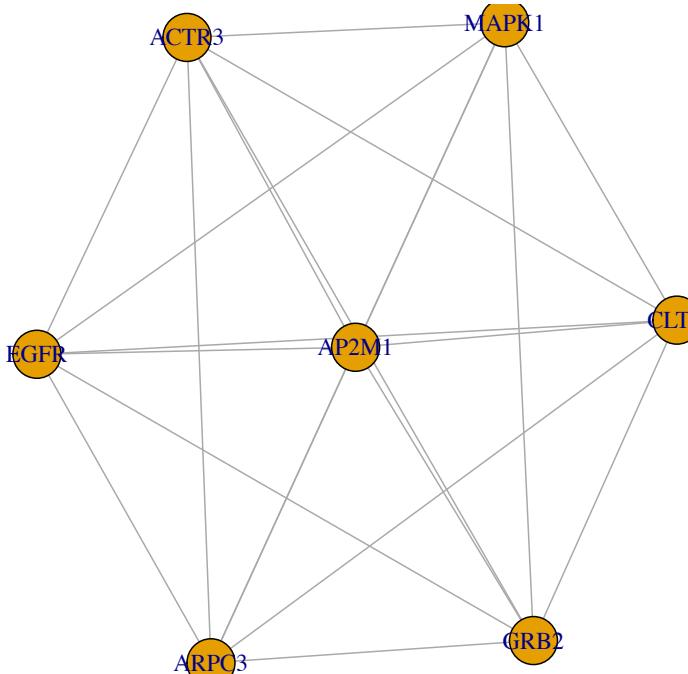
HALLMARK_PEROXISOME



HALLMARK_PI3K_AKT_MTOR_SIGNALING



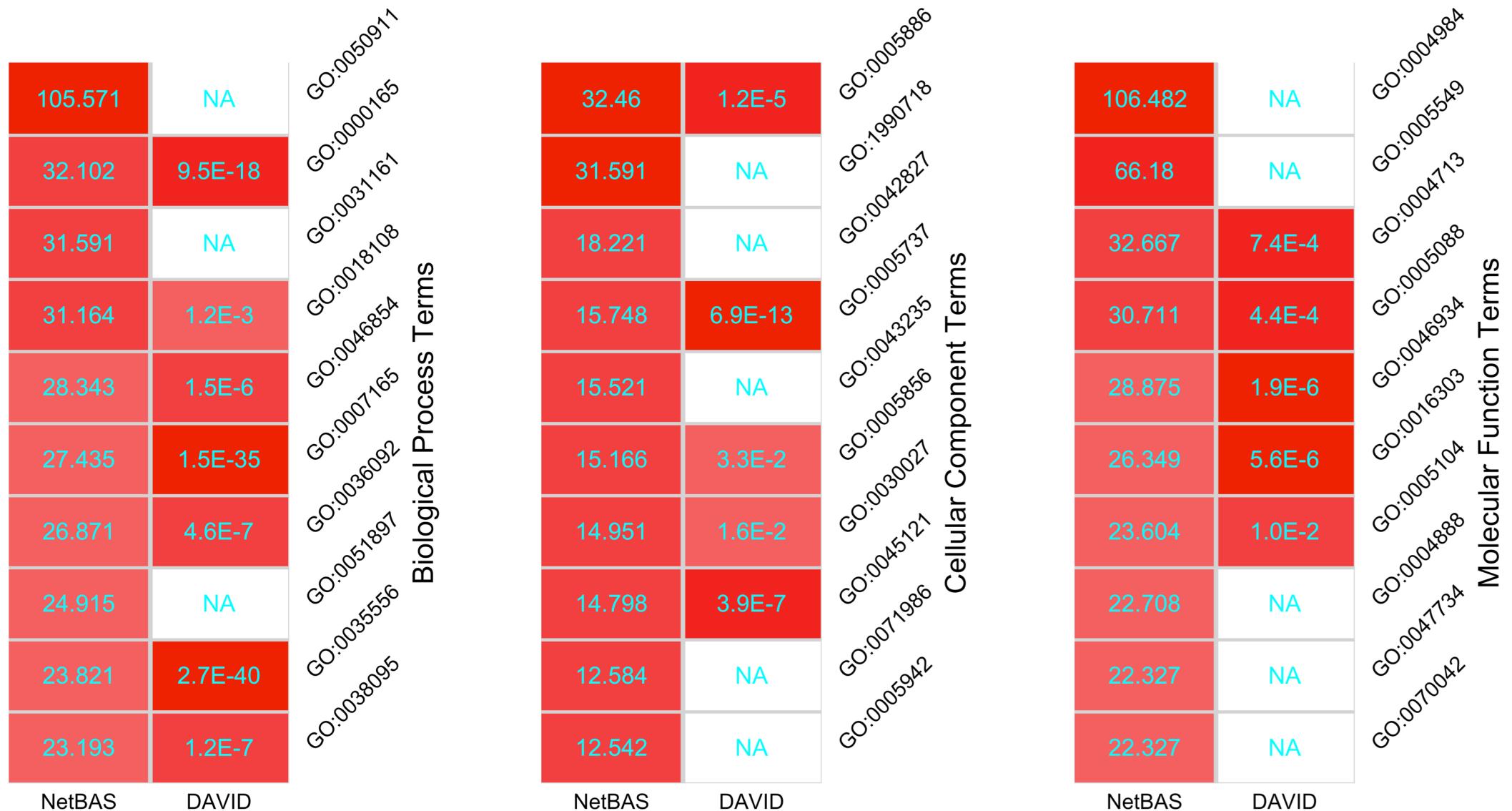
Subnetwork: 104 vertices, 463 edges
(unconnected vertices omitted)



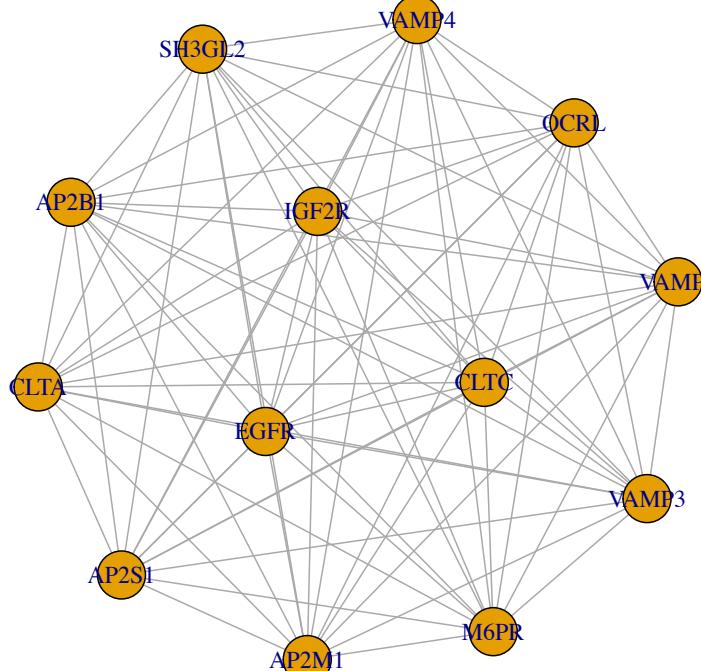
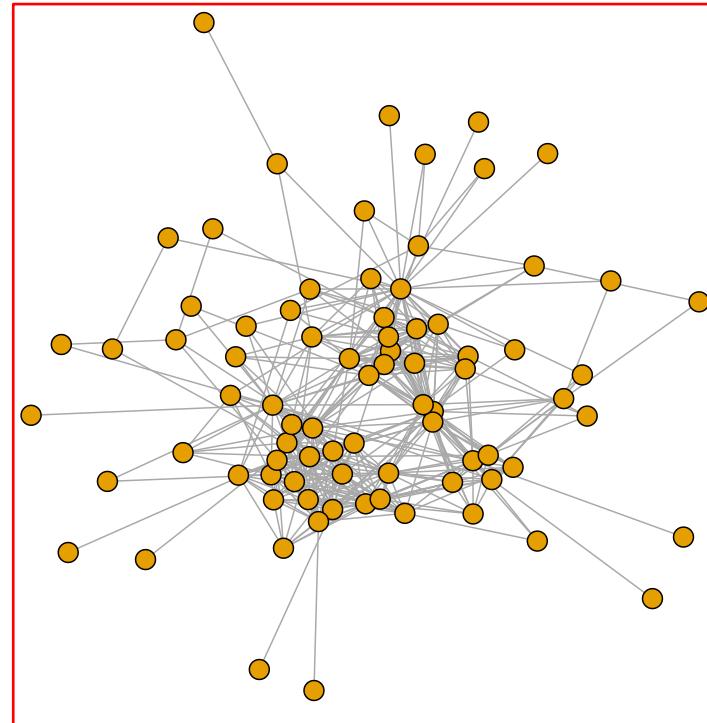
3 largest cliques w/ degree = 7

KEGG Pathways	NetBAS	DAVID
Olfactory transduction	33.228	NA
Ras signalling pathway	30.423	2.4E-15
MAPK signalling pathway	29.43	2.4E-17
PI3K-Akt signalling pathway	26.933	8.0E-15
Rap1 signalling pathway	24.68	5.1E-11
Regulation of actin cytoskeleton	23.904	2.5E-8
Pathways in cancer	22.853	3.9E-16
Jak-STAT signalling pathway	22.824	1.6E-2
Neurotrophin signalling pathway	22.661	9.2E-17
Toll-like receptor signalling pathway	22.606	1.8E-9

HALLMARK_PI3K_AKT_MTOR_SIGNALING



HALLMARK_PROTEIN_SECRETION



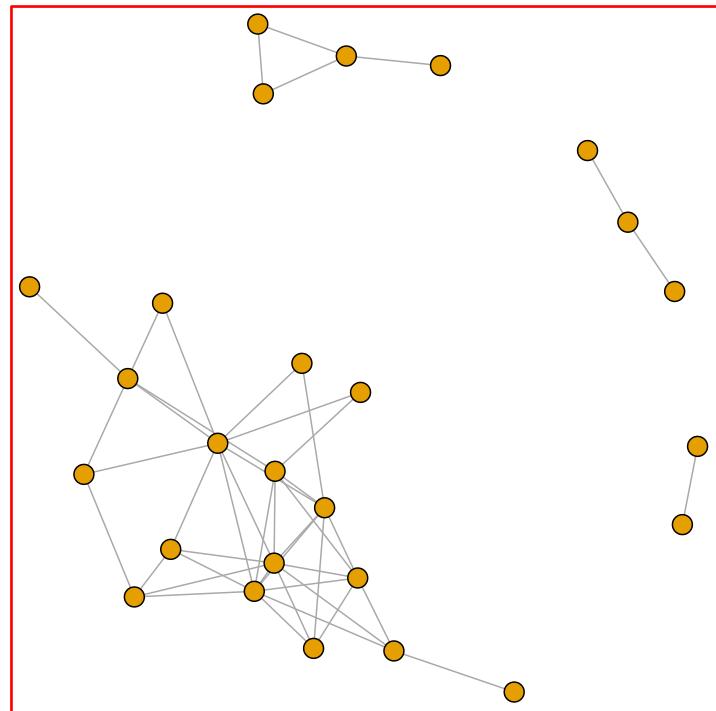
	NetBAS	DAVID
SNARE interactions in vesicular transport	59.573	8.1E-12
Endocytosis	30.663	8.8E-14
Synaptic vesicle cycle	27.941	1.1E-6
Lysosome	24.444	1.4E-12
Phagosome	23.842	4.7E-5
Vasopressin-regulated water reabsorption	21.608	NA
Hematopoietic cell lineage	20.868	NA
Asthma	18.415	NA
Graft-versus-host disease	17.022	NA
Allograft rejection	16.436	NA

KEGG Pathways

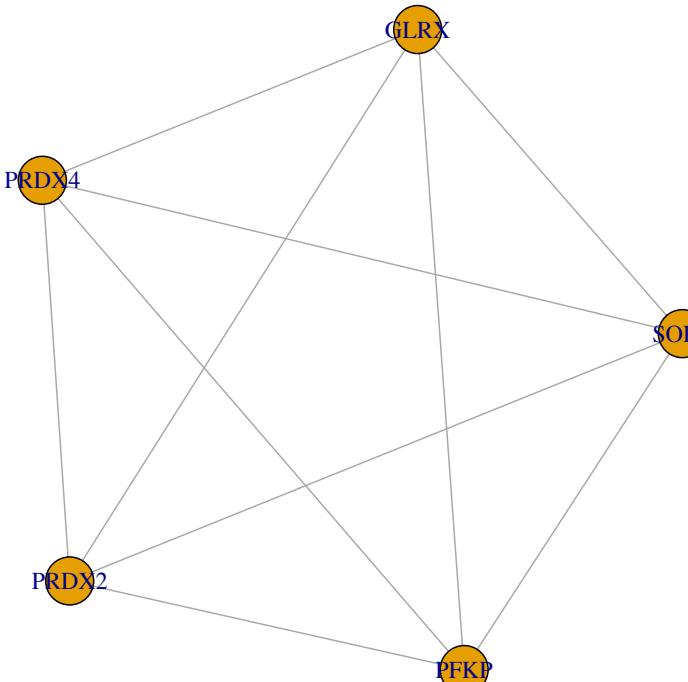
HALLMARK_PROTEIN_SECRETION

		Biological Process Terms		Cellular Component Terms		Molecular Function Terms	
		NetBAS	DAVID	NetBAS	DAVID	NetBAS	DAVID
GO:0006888	75.723	6.7E-24		67.963	4.6E-40	53.439	4.8E-13
	56.713	1.3E-12		60.171	6.2E-17	44.318	5.9E-15
	54.865	9.4E-13		53.635	1.5E-8	42.595	5.6E-11
	53.917	2.0E-15		52.335	3.8E-11	25.693	3.0E-5
	45.45	4.1E-43		47.749	3.4E-10	23.631	1.3E-3
	45.337	4.0E-19		47.293	4.5E-13	20.973	NA
	43.51	4.5E-8		46.826	2.7E-36	20.748	NA
	37.284	9.7E-9		40.85	1.4E-47	20.07	NA
	36.529	1.2E-12		40.296	5.2E-9	19.463	NA
	35.685	1.9E-7		36.112	2.6E-15	18.821	NA

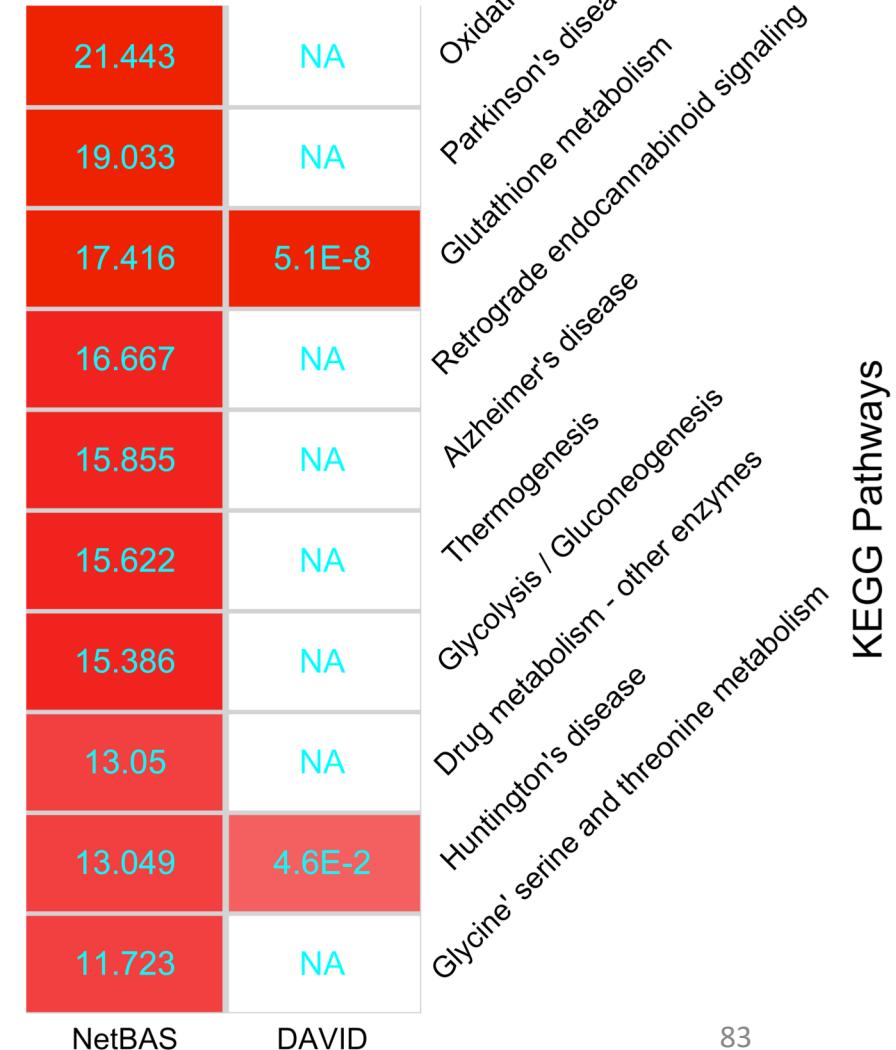
HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY



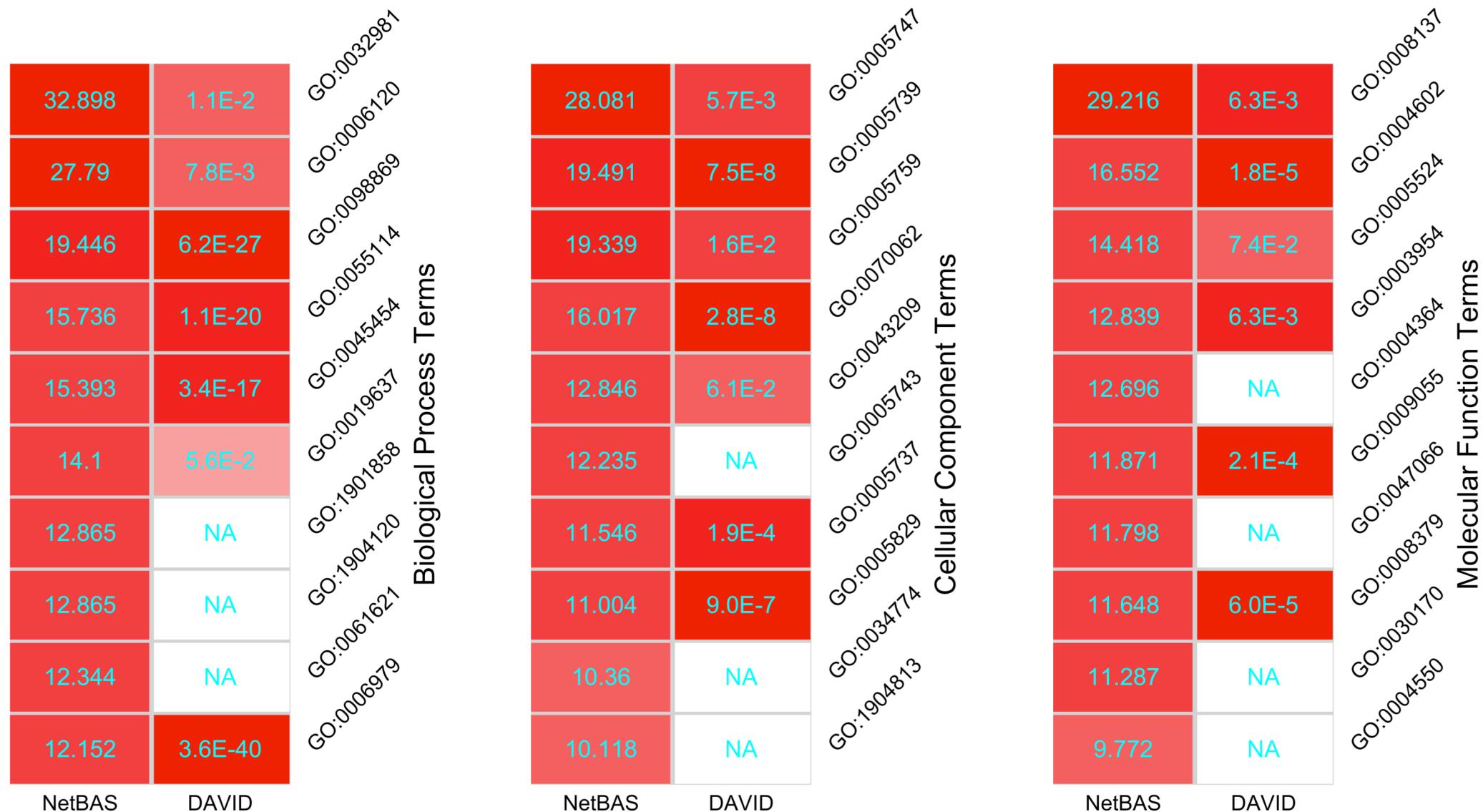
Subnetwork: 46 vertices, 46 edges
(unconnected vertices omitted)



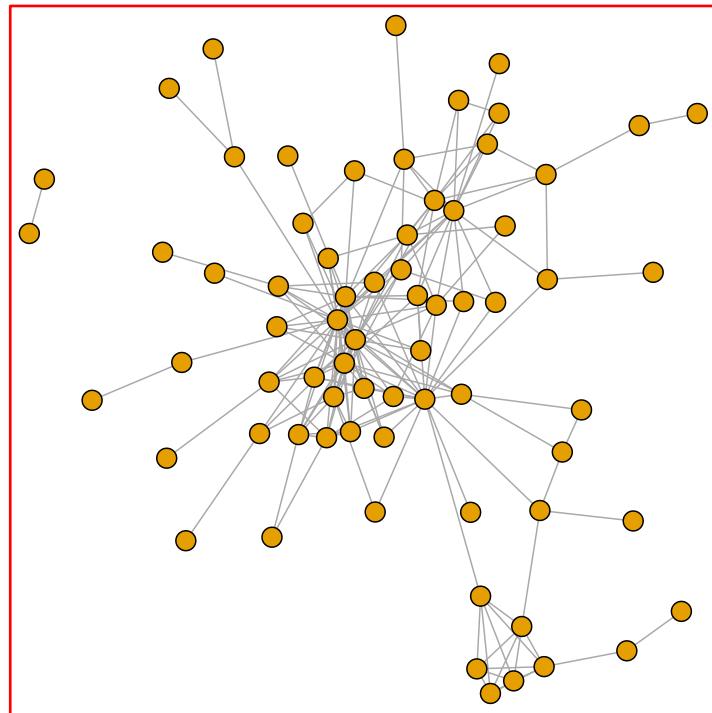
2 largest cliques w/ degree = 5



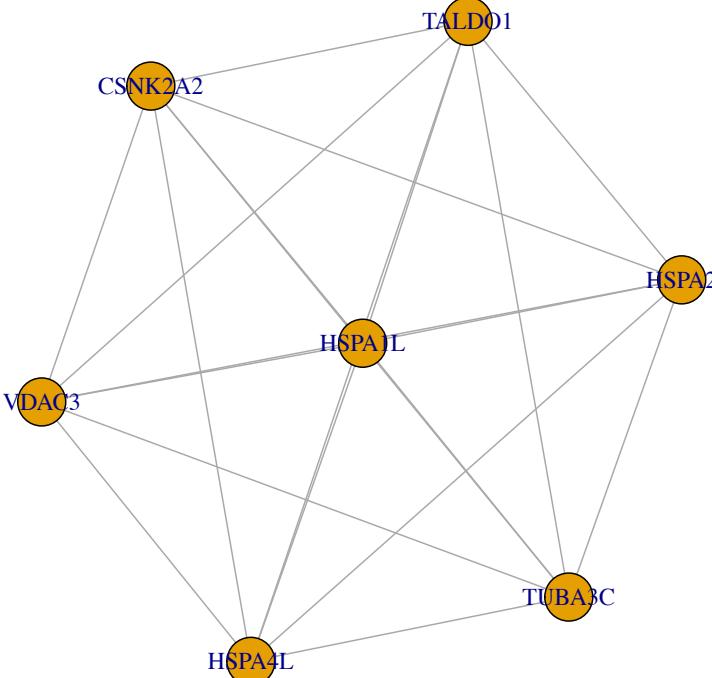
HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY



HALLMARK_SPERMATOGENESIS



Subnetwork: 130 vertices, 185 edges
(unconnected vertices omitted)

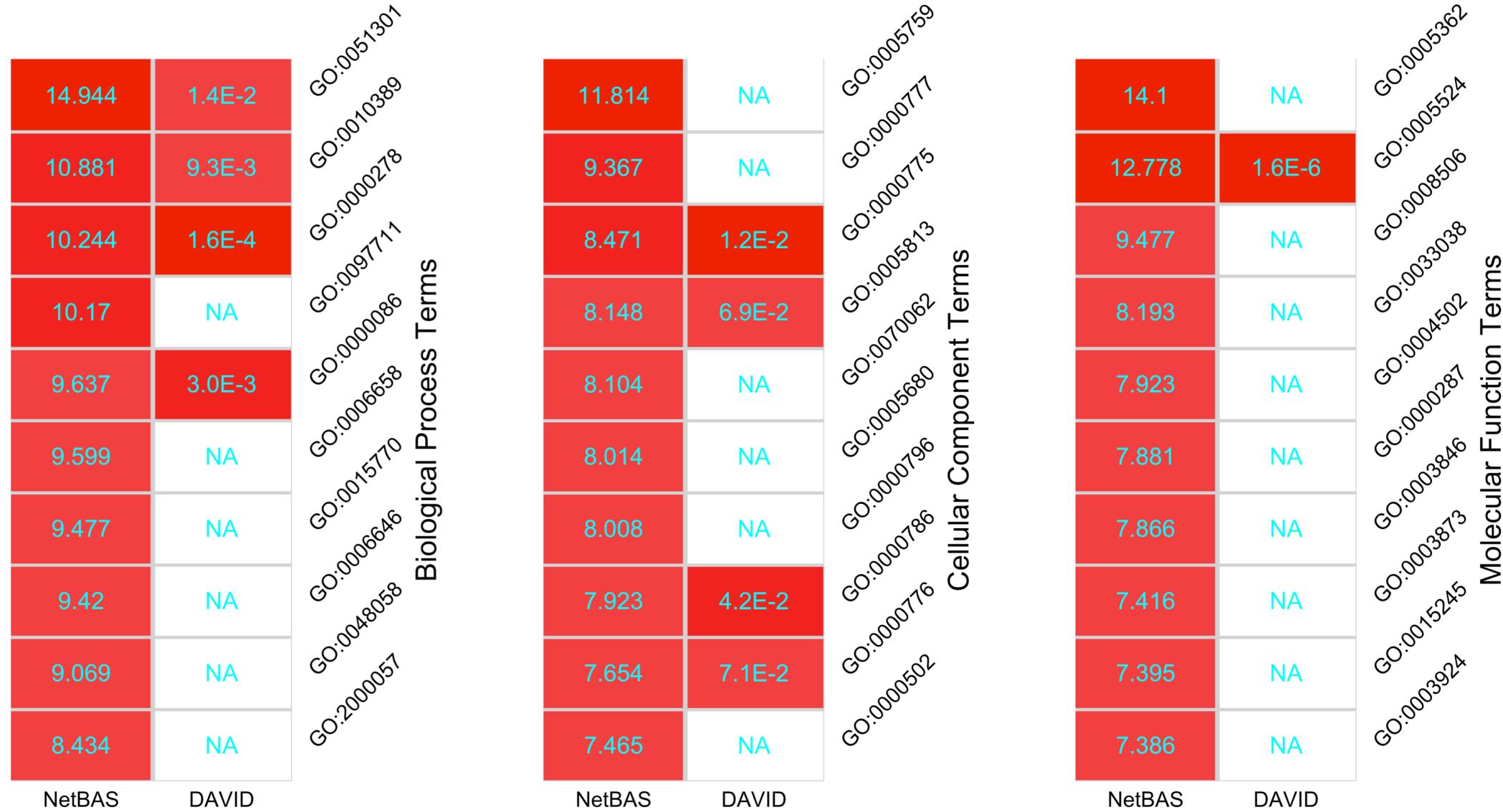


1 largest cliques w/ degree = 7

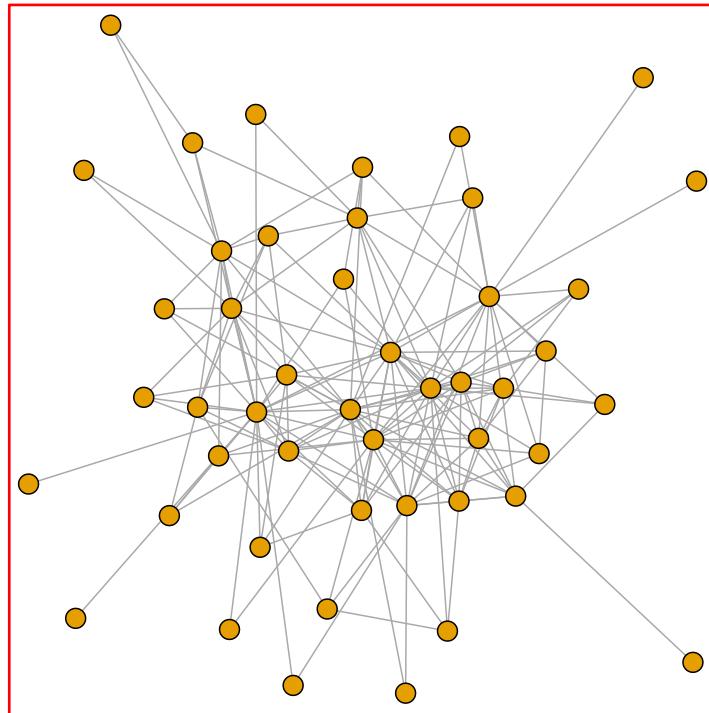
	NetBAS	DAVID
Glycolysis / Gluconeogenesis	9.722	2.0E-2
Glycerophospholipid metabolism	8.561	NA
Taste transduction	8.387	NA
Oocyte meiosis	8.042	7.2E-2
Progesterone-mediated oocyte maturation	7.539	6.8E-3
Proteasome	7.279	NA
Alcoholism	6.956	NA
Pentose phosphate pathway	6.913	NA
Cell cycle	6.83	4.3E-3
Thiamine metabolism	6.789	NA

KEGG Pathways

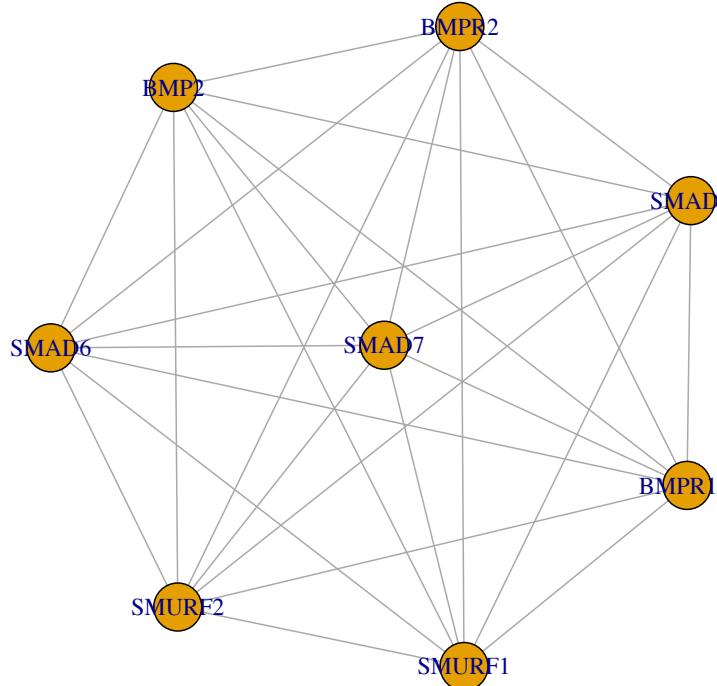
HALLMARK_SPERMATOGENESIS



HALLMARK_TGF_BETA_SIGNALING



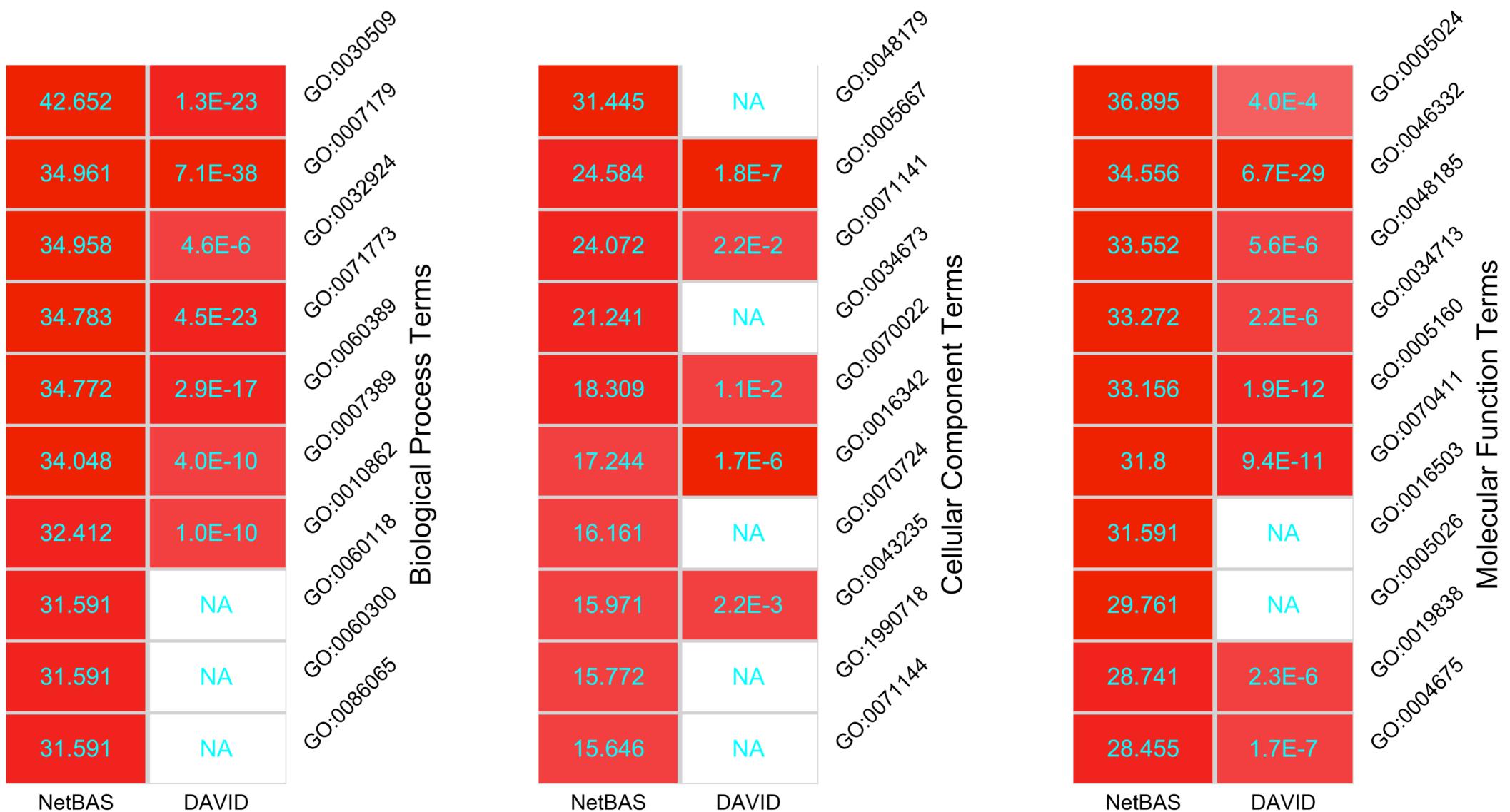
Subnetwork: 54 vertices, 174 edges
(unconnected vertices omitted)



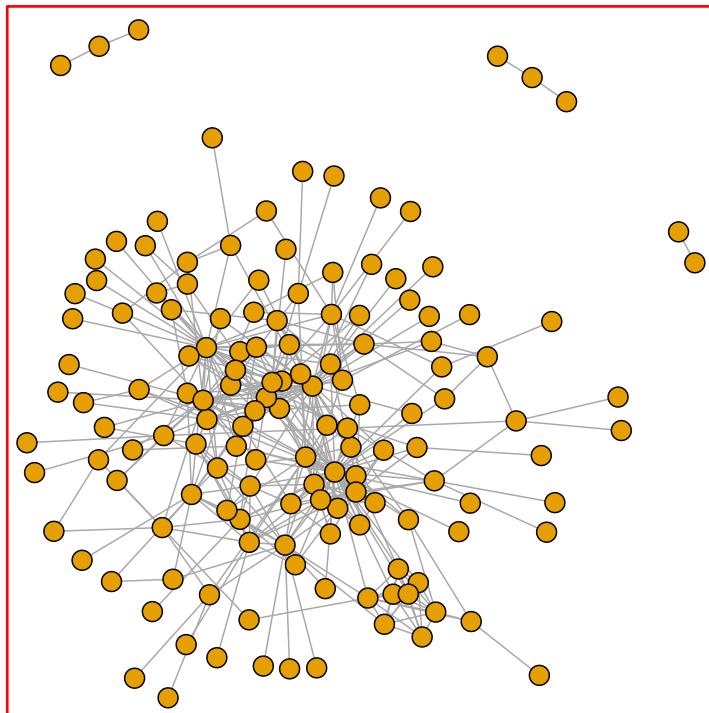
NetBAS	DAVID
36.326	5.4E-27
25.44	4.7E-14
25.026	2.3E-10
19.049	3.3E-4
17.911	NA
17.35	4.6E-2
17.295	2.8E-6
17.092	NA
16.525	2.6E-5
16.484	NA

TGF-beta signaling pathway
Hippo signaling pathway
Signaling pathways regulating pluripotency of stem
Pathways in cancer
Gastric cancer
Wnt signaling pathway
Adherens junction
Hepatocellular carcinoma
Colorectal cancer
AGE-RAGE signaling pathway in diabetic complications

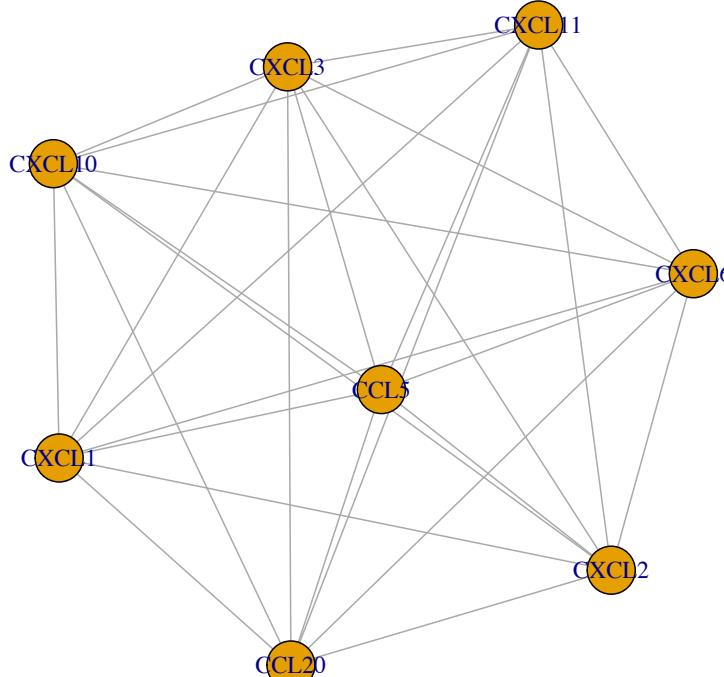
HALLMARK_TGF_BETA_SIGNALING



HALLMARK_TNFA_SIGNALING_VIA_NFKB



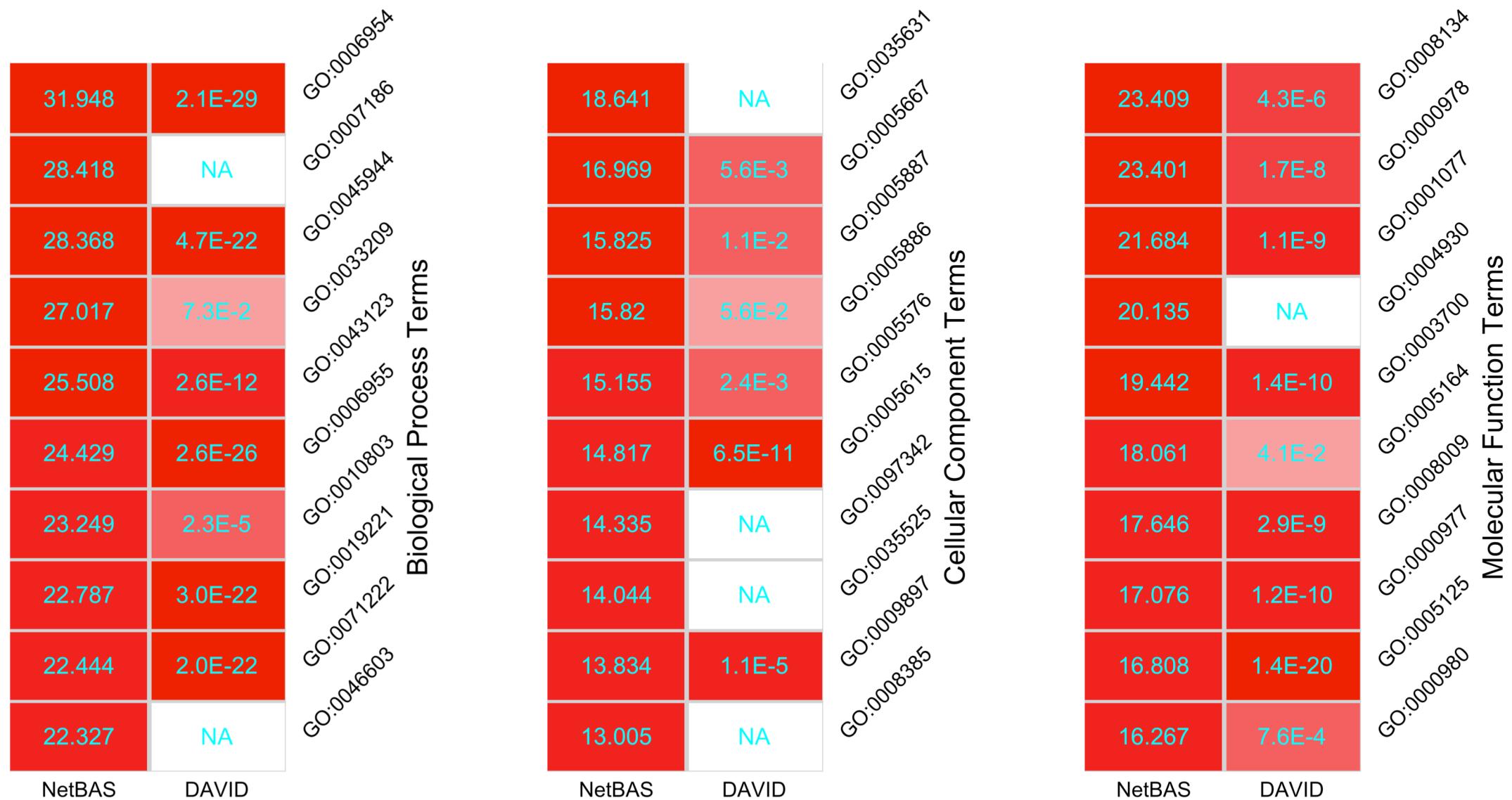
Subnetwork: 198 vertices, 390 edges
(unconnected vertices omitted)



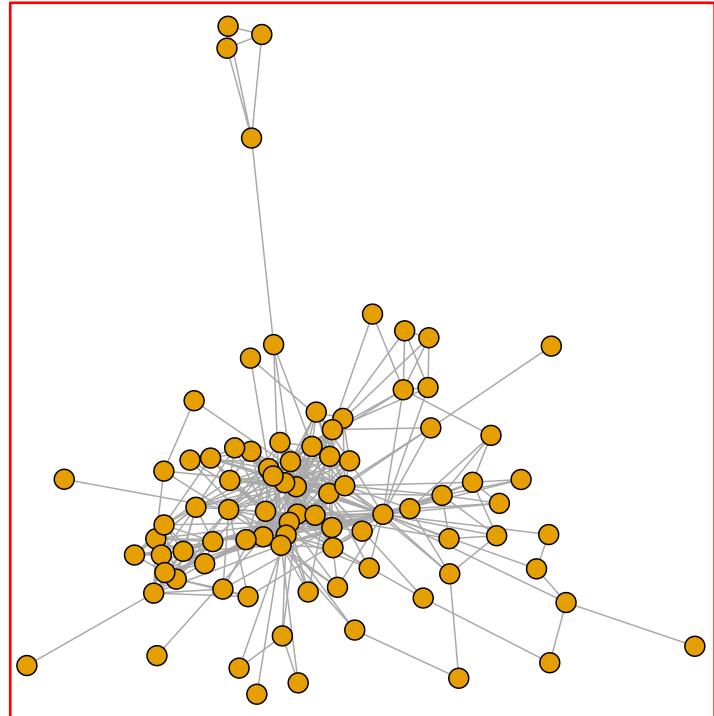
1 largest cliques w/ degree = 8

NetBAS	DAVID	KEGG Pathways
32.845	1.2E-28	TNF signaling pathway
32.353	1.8E-14	Cytokine-cytokine receptor interaction
31.79	6.7E-5	RIG-I-like receptor signaling pathway
31.684	2.0E-10	Toll-like receptor signaling pathway
30.441	6.8E-13	NF-kappa B signaling pathway
29.058	1.5E-7	Hepatitis B
27.775	7.4E-4	Pathways in cancer
26.759	2.2E-12	NOD-like receptor signaling pathway
26.703	NA	IL-17 signaling pathway
25.632	6.1E-10	Osteoclast differentiation

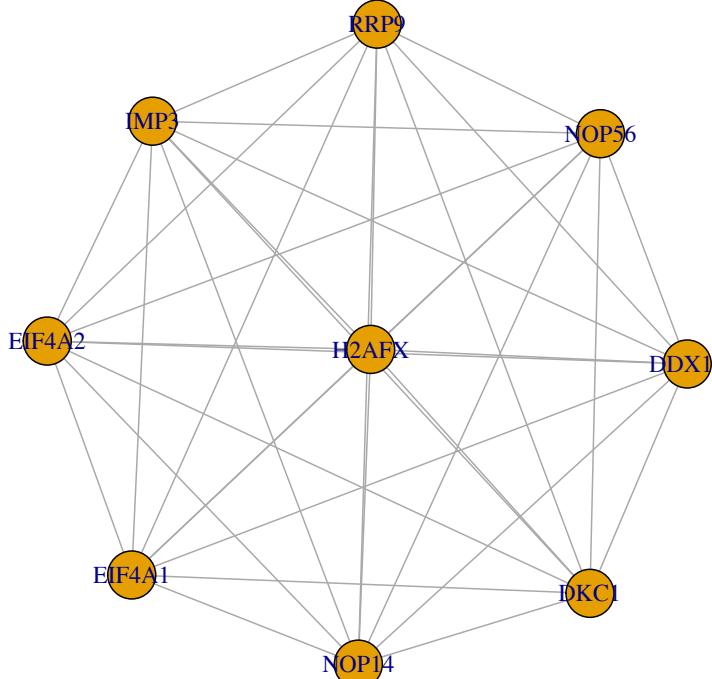
HALLMARK_TNFA_SIGNALING_VIA_NFKB



HALLMARK_UNFOLDED_PROTEIN_RESPONSE



Subnetwork: 109 vertices, 401 edges
(unconnected vertices omitted)



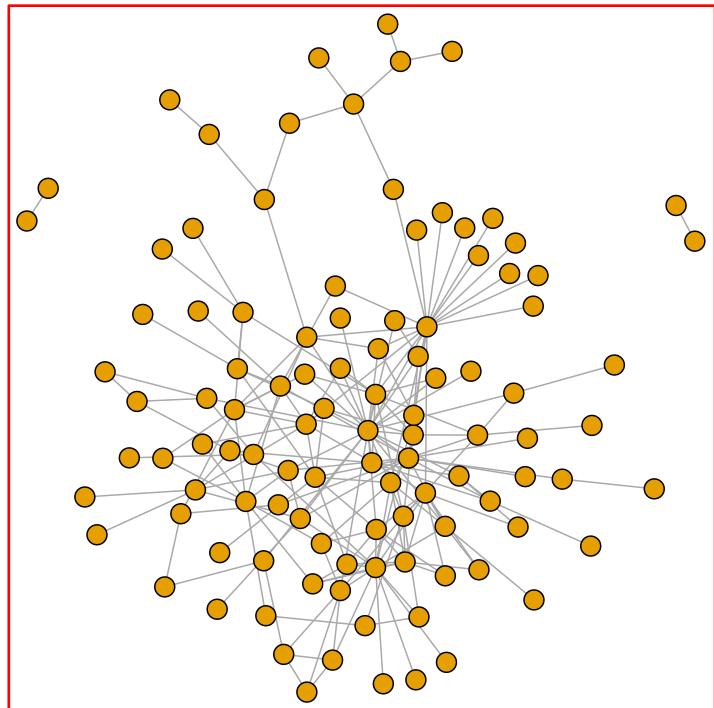
10 largest cliques w/ degree = 9

NetBAS	DAVID	KEGG Pathways
23.655	1.8E-16	RNA degradation
22.618	NA	Ribosome
18.027	NA	Ribosome biogenesis in eukaryotes
13.152	1.6E-4	RNA transport
11.138	6.0E-11	Protein processing in endoplasmic reticulum
8.255	NA	Cysteine and methionine pathway
8.027	NA	mRNA surveillance pathway
7.98	NA	Antigen processing and presentation
7.741	NA	Amino sugar and nucleotide sugar metabolism
7.114	NA	Phagosome

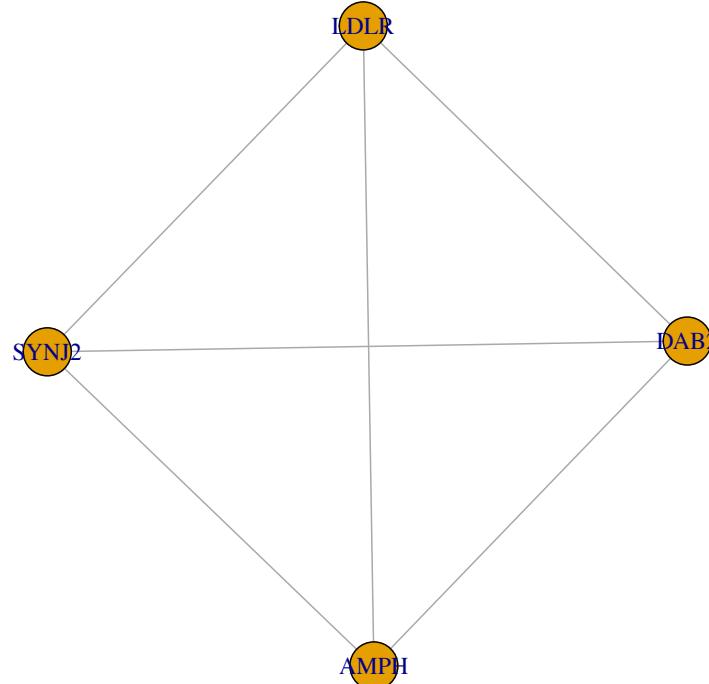
HALLMARK_UNFOLDED_PROTEIN_RESPONSE

		Biological Process Terms		Cellular Component Terms		Molecular Function Terms	
		NetBAS	DAVID	NetBAS	DAVID	NetBAS	DAVID
GO:0006364	31.834	7.7E-10		24.479	1.5E-7	22.384	6.1E-14
	31.534	2.0E-7		23.523	1.2E-6	22.327	NA
	28.206	NA		22.536	NA	22.327	NA
	27.594	9.8E-5		22.095	3.0E-3	20.561	2.6E-11
	24.131	9.2E-14		20.514	1.6E-2	19.685	NA
	23.811	1.2E-9		20.23	1.2E-8	18.73	1.7E-8
	21.355	1.7E-9		20.059	NA	18.337	4.8E-4
	20.235	1.6E-4		18.046	3.5E-3	13.871	2.6E-3
	19.127	9.8E-4		16.435	NA	12.658	5.3E-2
	19.015	1.6E-3		16.319	NA	12.181	3.2E-2

HALLMARK_UV_RESPONSE_DN



Subnetwork: 140 vertices, 198 edges
(unconnected vertices omitted)

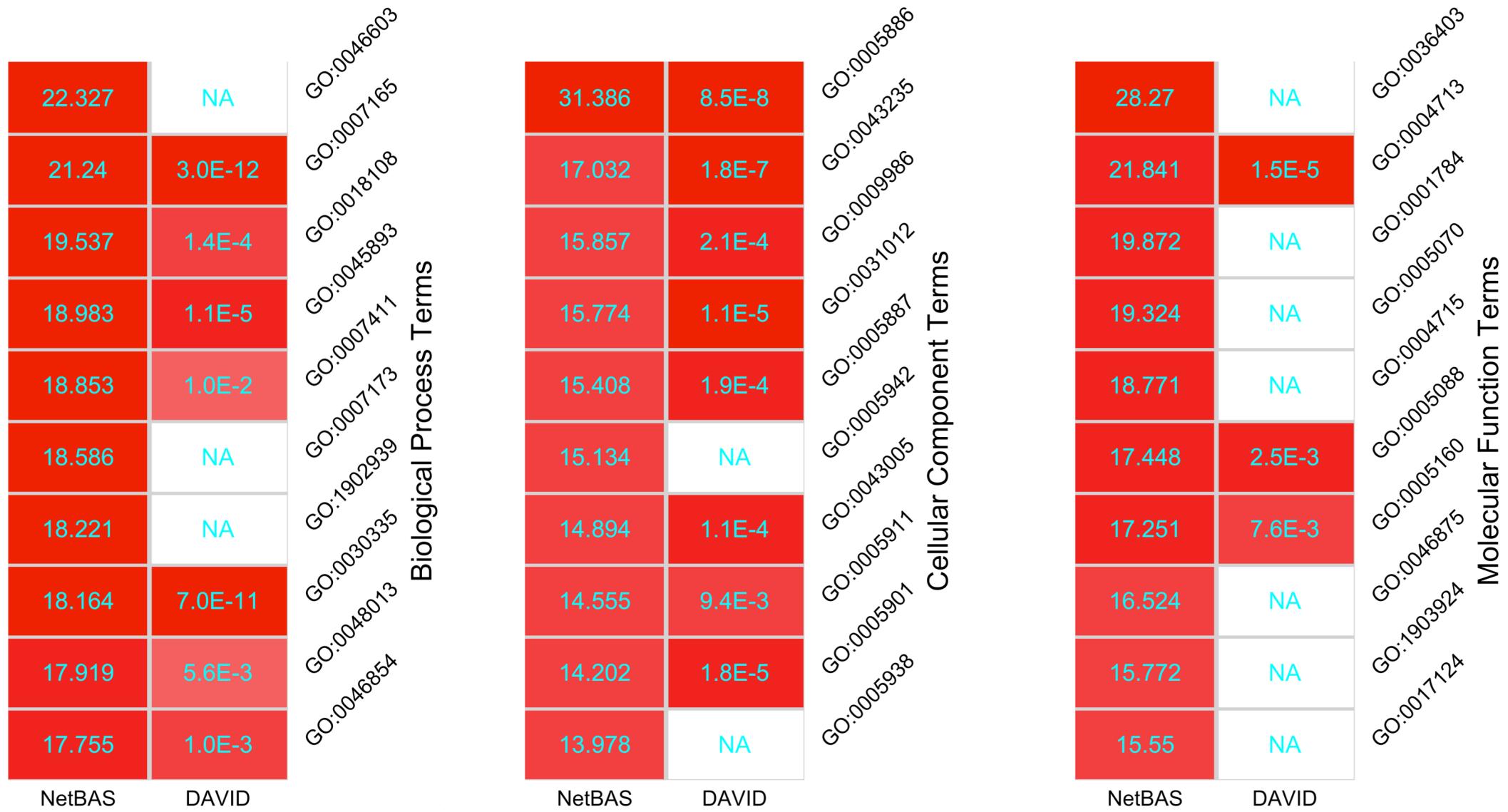


9 largest cliques w/ degree = 4

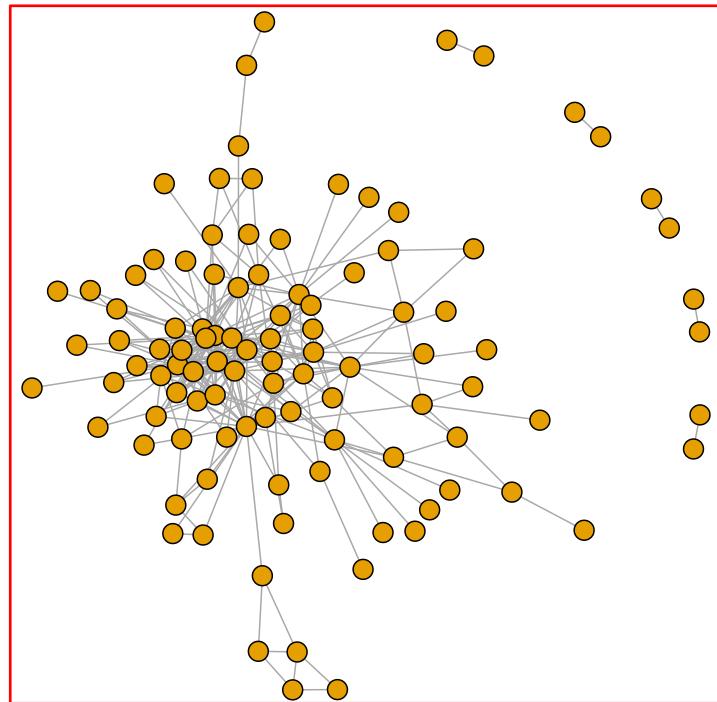
NetBAS	DAVID
24.283	8.1E-11
23.233	7.8E-9
23.113	NA
21.499	2.1E-6
20.502	9.0E-9
20.416	9.6E-4
20.239	4.3E-4
19.806	8.2E-2
18.603	NA
18.582	3.1E-6

Focal adhesion
Pathways in cancer
Axon guidance
Proteoglycans in cancer
Rap1 signaling pathway
Ras signaling pathway
ErbB signaling pathway
Jak-STAT signaling pathway
Hepatocellular carcinoma
MicroRNAs in cancer

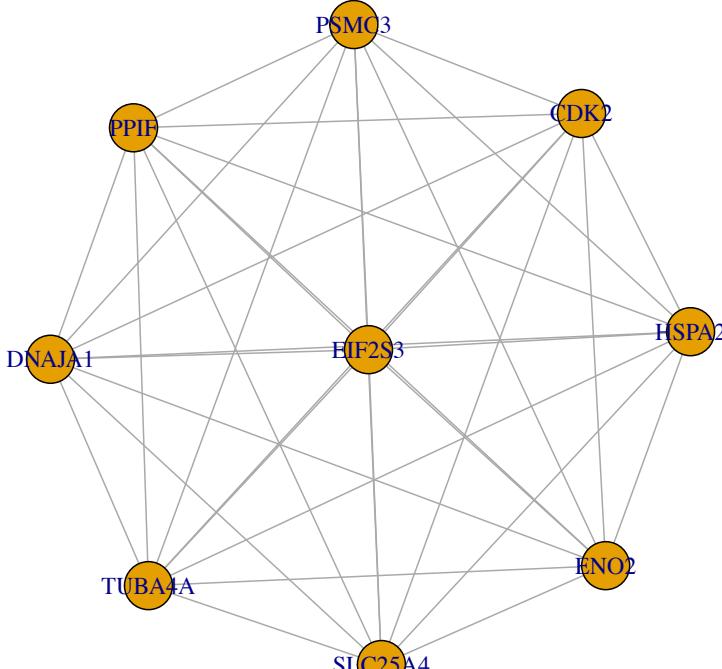
HALLMARK_UV_RESPONSE_DN



HALLMARK_UV_RESPONSE_UP



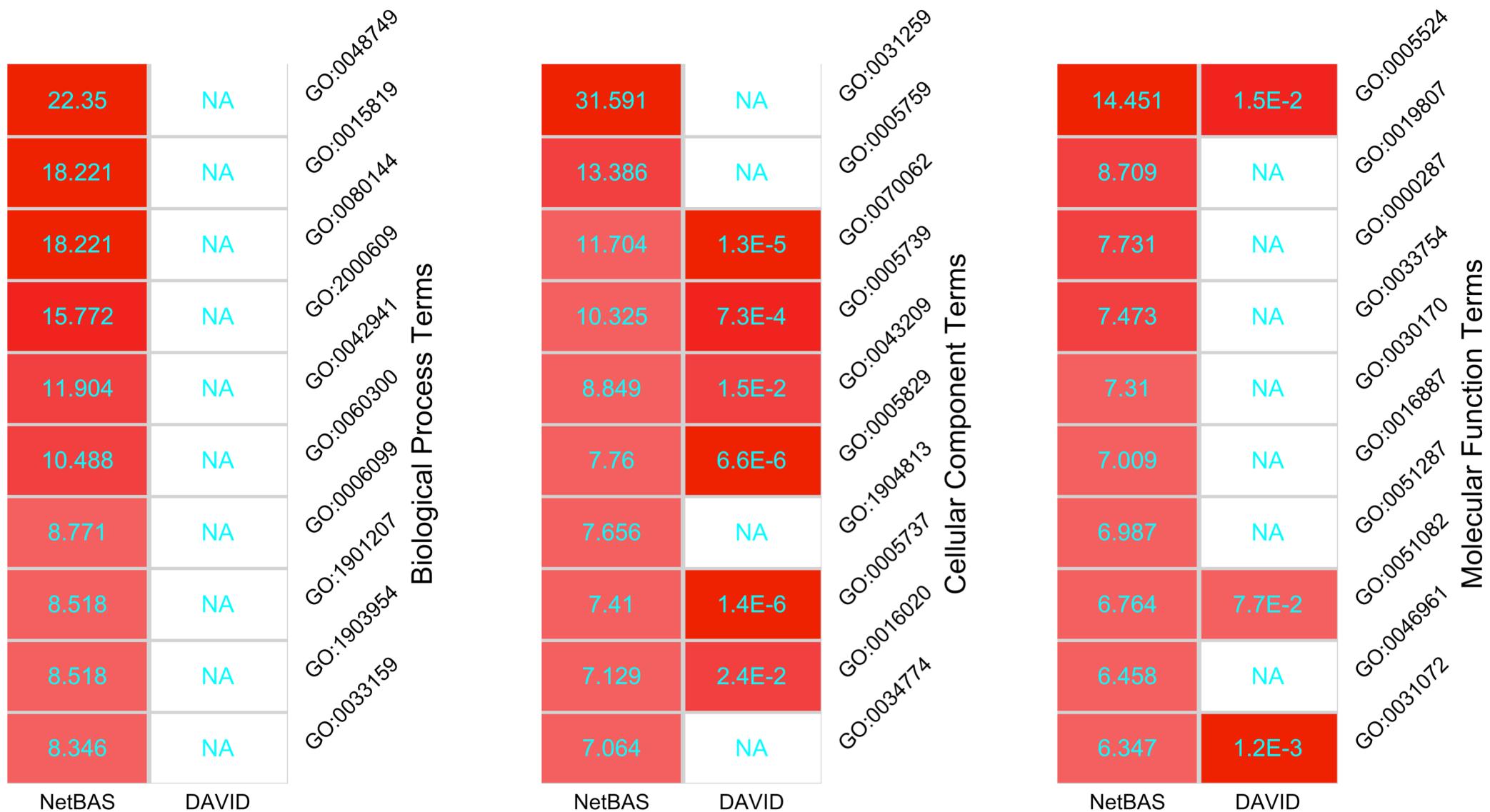
Subnetwork: 153 vertices, 287 edges
(unconnected vertices omitted)



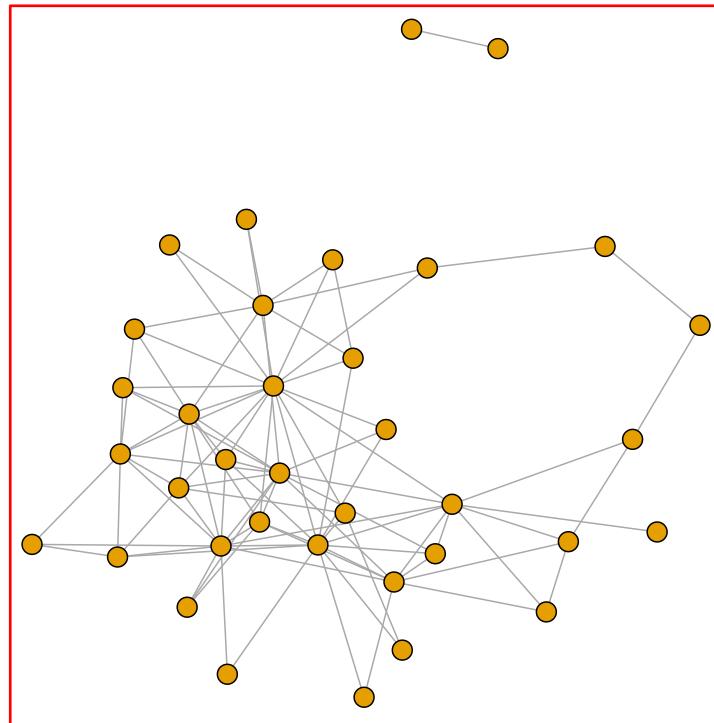
1 largest cliques w/ degree = 9

		KEGG Pathways
NetBAS	10.499	NA
NetBAS	9.238	NA
NetBAS	8.819	NA
NetBAS	7.503	NA
NetBAS	7.177	NA
NetBAS	7.068	9.5E-2
NetBAS	7.015	NA
NetBAS	6.946	7.0E-2
NetBAS	6.823	NA
NetBAS	6.658	NA
DAVID		

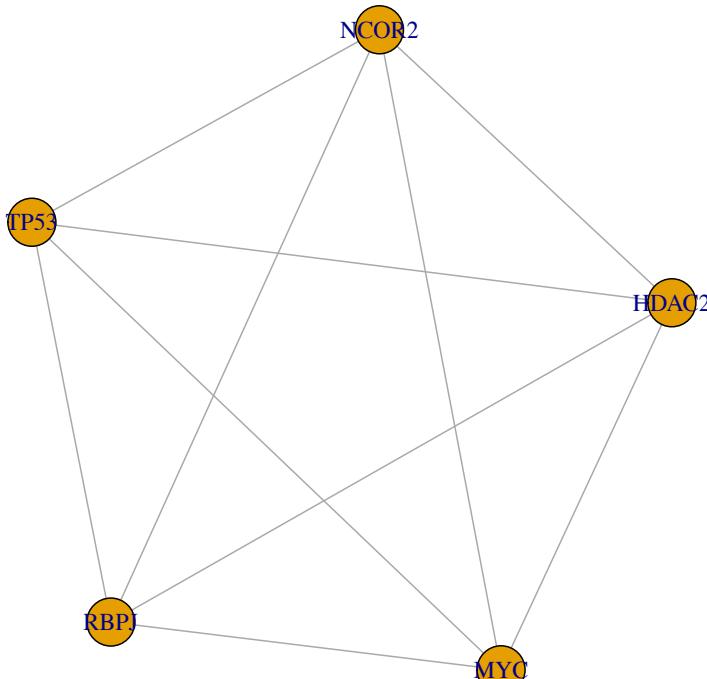
HALLMARK_UV_RESPONSE_UP



HALLMARK_WNT_BETA_CATENIN_SIGNALING



Subnetwork: 41 vertices, 94 edges
(unconnected vertices omitted)



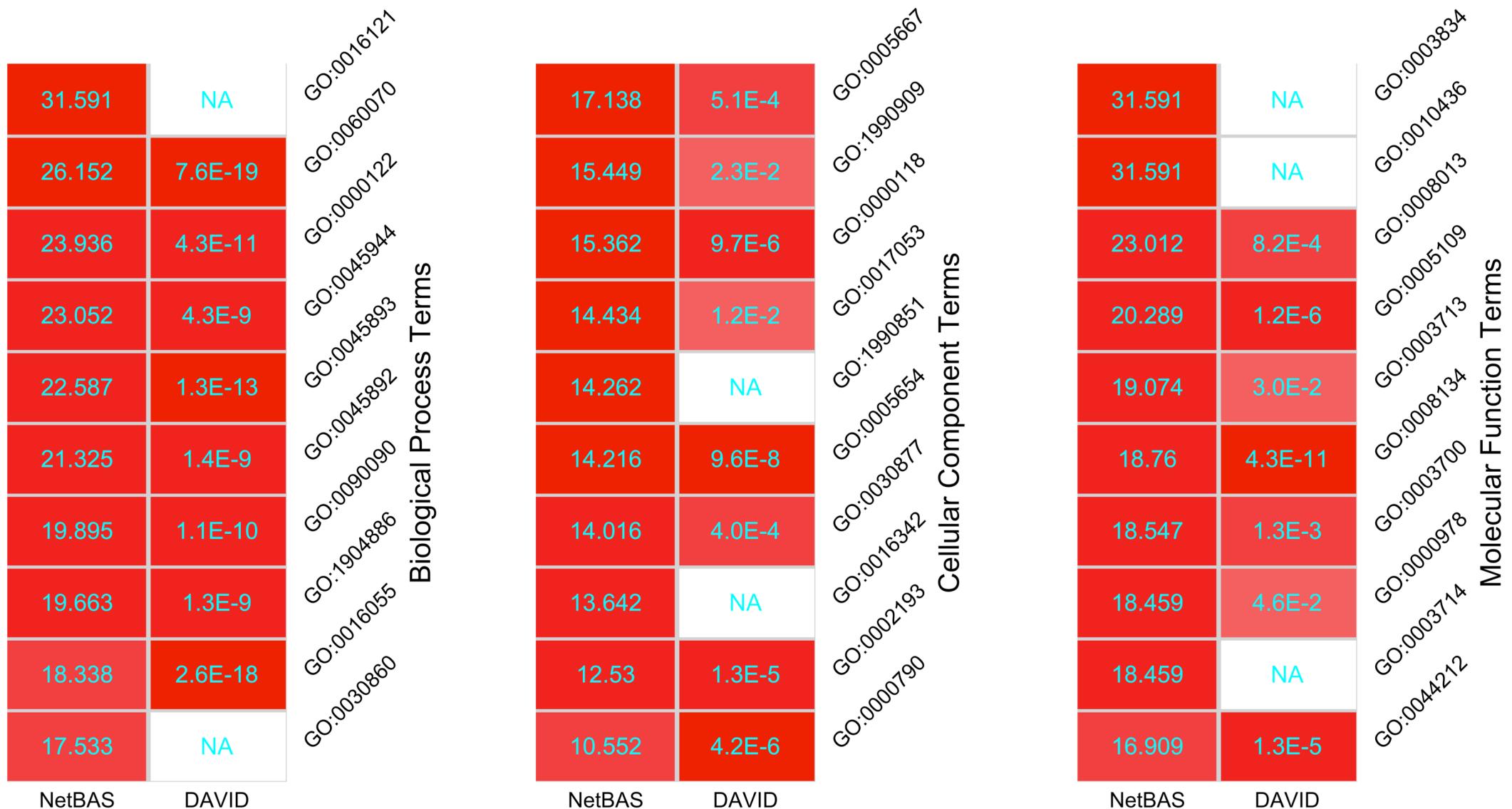
1 largest cliques w/ degree = 5

NetBAS	DAVID
26.747	5.0E-20
23.374	1.7E-15
19.697	2.0E-23
17.204	NA
15.686	NA
14.96	NA
14.307	4.1E-11
14.134	NA
13.852	9.3E-12
13.205	NA

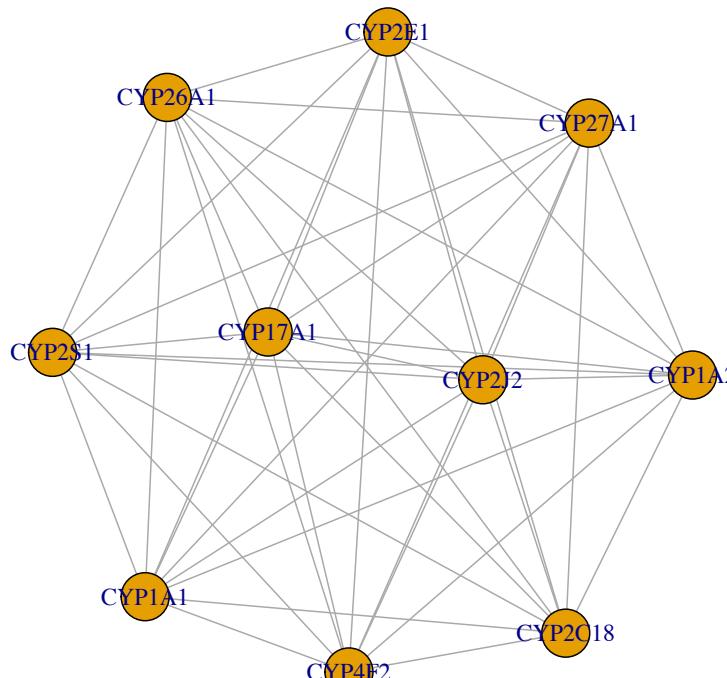
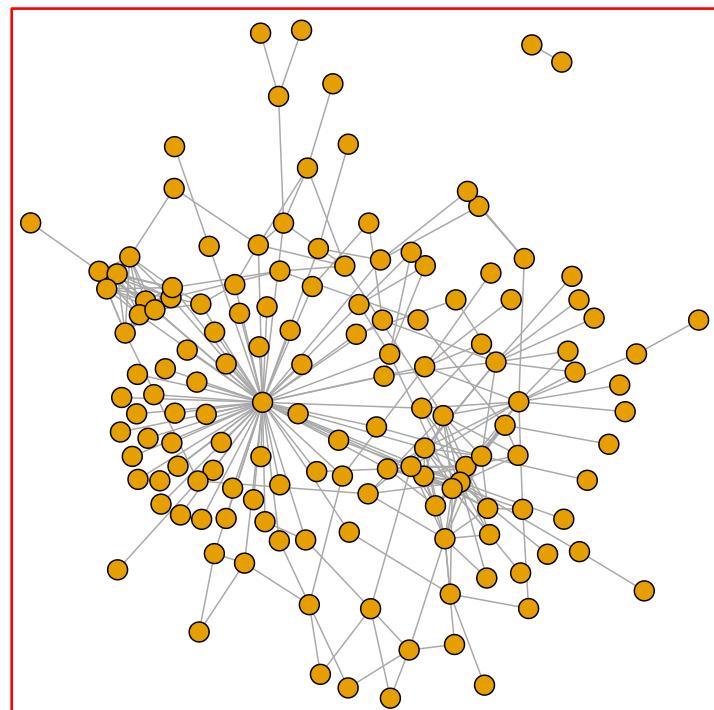
KEGG Pathways

Notch signaling pathway
Basal cell carcinoma
Wnt signaling pathway
Breast cancer
Human papillomavirus infection
Hepatocellular carcinoma
Pathways in cancer
Gastric cancer
Hippo signaling pathway
Cushing's syndrome

HALLMARK_WNT_BETA_CATENIN_SIGNALING



HALLMARK_XENOBIOTIC_METABOLISM



NetBAS	DAVID
39.389	2.4E-11
39.221	9.1E-10
38.885	1.2E-9
33.971	2.0E-4
32.789	7.0E-6
29.176	NA
27.19	2.8E-4
22.135	NA
19.516	2.7E-3
17.482	5.0E-4

KEGG Pathways

Metabolism of xenobiotics by cytochrome P450
Chemical carcinogenesis
Drug metabolism - cytochrome P450
Steroid hormone biosynthesis
Retinol metabolism
Linoleic acid metabolism
Arachidonic acid metabolism
Primary bile acid biosynthesis
Drug metabolism - other enzymes
Glycolysis / Gluconeogenesis

HALLMARK_XENOBIOTIC_METABOLISM

		Biological Process Terms		Cellular Component Terms		Molecular Function Terms	
		NetBAS	DAVID	NetBAS	DAVID	NetBAS	DAVID
GO:0042738	47.245	NA		53.678	9.7E-5	59.328	9.3E-12
	44.93	1.8E-50		23.992	6.7E-8	57.571	6.1E-8
	44.464	1.4E-6		21.431	1.2E-5	56.727	4.0E-11
	43.907	9.0E-30		21.417	7.6E-14	53.61	1.6E-6
	42.493	1.2E-4		17.48	1.8E-8	49.728	1.6E-5
	40.364	2.1E-14		14.849	1.8E-14	49.101	2.2E-4
	33.235	3.2E-9		14.4	NA	42.02	5.8E-4
	32.213	NA		13.812	NA	31.573	2.0E-5
	31.884	4.7E-5		13.36	2.4E-4	26.689	NA
	31.833	NA		12.03	3.0E-4	25.759	NA