SUPPLEMENTAL MATERIAL

Acknowledgments

The members of the CARDIoGRAM consortium are: Heribert Schunkert, Inke R. König, Sekar Kathiresan, Muredach P. Reilly, Themistocles L. Assimes, Hilma Holm, Michael Preuss, Alexandre F. R. Stewart, Maja Barbalic, Christian Gieger, Devin Absher, Zouhair Aherrahrou, Hooman Allayee, David Altshuler, Sonia S. Anand, Karl Andersen, Jeffrey L. Anderson, Diego Ardissino, Stephen G. Ball, Anthony J. Balmforth, Timothy A. Barnes, Diane M. Becker, Lewis C. Becker, Klaus Berger, Joshua C. Bis, S. Matthijs Boekholdt, Eric Boerwinkle, Peter S. Braund, Morris J. Brown, Mary Susan Burnett, Ian Buysschaert, Cardiogenics, John F. Carlquist, Li Chen, Sven Cichon, Veryan Codd, Robert W. Davies, George Dedoussis, Abbas Dehghan, Serkalem Demissie, Joseph M. Devaney, Ron Do, Angela Doering, Sandra Eifert, Nour Eddine El Mokhtari, Stephen G. Ellis, Roberto Elosua, James C. Engert, Stephen E. Epstein, Ulf de Faire, Marcus Fischer, Aaron R. Folsom, Jennifer Freyer, Bruna Gigante, Domenico Girelli, Solveig Gretarsdottir, Vilmundur Gudnason, Jeffrey R. Gulcher, Eran Halperin, Naomi Hammond, Stanley L. Hazen, Albert Hofman, Benjamin D. Horne, Thomas Illig, Carlos Iribarren, Gregory T. Jones, J.Wouter Jukema, Michael A. Kaiser, Lee M. Kaplan, John J.P. Kastelein, Kay-Tee Khaw, Joshua W. Knowles, Genovefa Kolovou, Augustine Kong, Reijo Laaksonen, Diether Lambrechts, Karin Leander, Guillaume Lettre, Mingyao Li, Wolfgang Lieb, Patrick Linsel-Nitschke, Christina Loley, Andrew J. Lotery, Pier M. Mannucci, Seraya Maouche, Nicola Martinelli, Pascal P. McKeown, Christa Meisinger, Thomas Meitinger, Olle Melander, Pier Angelica Merlini, Vincent Mooser, Thomas Morgan, Thomas W. Mühleisen, Joseph B. Muhlestein, Thomas Münzel, Kiran Musunuru, Janja Nahrstaedt, Christopher P. Nelson, Markus M. Nöthen, Oliviero Olivieri, Riyaz S. Patel, Chris C. Patterson, Annette Peters, Flora Peyvandi, Liming Qu, Arshed A. Quyyumi, Daniel J. Rader, Loukianos S. Rallidis, Catherine Rice, Frits R. Rosendaal, Diana Rubin, Veikko Salomaa, M. Lourdes Sampietro, Manj S. Sandhu, Eric Schadt, Arne Schäfer, Arne Schillert, Stefan Schreiber, Jürgen Schrezenmeir, Stephen M. Schwartz, David S. Siscovick, Mohan Sivananthan, Suthesh Sivapalaratnam, Albert Smith, Tamara B. Smith, Jaapjan D. Snoep, Nicole Soranzo, John A. Spertus, Klaus Stark, Kathy Stirrups, Monika Stoll, W. H. Wilson Tang, Stephanie Tennstedt, Gudmundur Thorgeirsson, Gudmar Thorleifsson, Maciej Tomaszewski, Andre G. Uitterlinden, Andre M. van Rij, Benjamin F. Voight, Nick J. Wareham, George A. Wells, H.-Erich Wichmann, Philipp S. Wild, Christina Willenborg, Jaqueline C. M. Witteman, Benjamin J. Wright, Shu Ye, Tanja Zeller, Andreas Ziegler, Francois Cambien, Alison H. Goodall, L. Adrienne Cupples, Thomas Quertermous, Winfried März, Christian Hengstenberg, Stefan Blankenberg, Willem H. Ouwehand, Alistair S. Hall, Panos Deloukas, John R. Thompson, Kari Stefansson,

Robert Roberts, Unnur Thorsteinsdottir, Christopher J. O'Donnell, Ruth McPherson, Jeanette Erdmann, and Nilesh J. Samani

Supplementary Methods

Gene-set enrichment analysis methods

Calculation of enrichment score in i-GSEA4GWAS: For enrichment score calculations, i-GSEA4GWAS first represents a gene by the max(–log(p-value) of all the SNPs mapped to that gene within the 100 kb window. Next, genes are ranked based on this association p-value. The ranked gene list is used to calculate the enrichment score (ES) of the pathways. The 'enrichment score' reflects the degree to which a pathway is over-represented at the extreme of the entire ranked list. The ES is then corrected by a 'k/K factor', where k and K are the proportions of significant genes in the pathway and among the total genes in GWAS, respectively (genes mapped with at least one of the top 5% of all SNPs are considered significant). A gene significance threshold is also calculated based on the number of genes that are mapped to one of the top 5% most associated SNPs out of all GWAS genes (in the current study, the threshold was 1.37). These corrected enrichment scores, also known as 'significance-proportion based enrichment scores', were used to calculate pathway association p-values and false discovery rates via SNP label permutation to correct for gene and gene set variation[1].

Pruning of SNPs in linkage disequilibrium (LD) : To test the effect of adjusting for differences in linkage disequilibrium (LD) patterns across the genome on our GSEA results, we generated two lists of pruned SNPs (SNPs that are in approximate linkage equilibrium to each other) using two different LD thresholds. Pruning was done using genotype data (2,239,392 SNPs) of 60 unrelated CEU individuals from Hapmap2 release 22, build 36 (hg18), and was executed using the --indep-pairwise function in PLINK[2]. SNPs with a pairwise r^2>0.2 or r^2>0.5 were removed within a sliding window of 200 SNPs, using window jumps of 5 SNPs. Pruning at r^2>0.2 or r^2>0.5 thresholds yielded 132,195 and 354,522 SNPs, respectively (5.4% or 14.6% of the full list of ~2.4 million unpruned SNPs).

Determination of LD among genes in a pathway: To test whether physical clustering of subsets of genes within each tested pathway could lead to biased estimates of pathway enrichment (due to linkage disequilibrium among the best scoring SNPs for those genes), we determined the degree of LD among the most significant SNPs mapped to genes within a pathway using the online SNP Annotation and Proxy Search tool (SNAP)[3]. We used the HapMap release 22 panel for CEU to calculate r^2 between the SNPs in gene sets that replicated.

ReactomeFI tool for network analysis: The gene sets employed in GSEA essentially represent 'lists' of genes that by themselves do not convey an understanding of the functional and topological relationships that may exist among such genes. However, such relationships are often crucial for biological function and can yield important information about the essentiality or vulnerability of different components of a pathway. The 'Reactome-FIs' (functional interactions) data set unites interactions from Reactome and other pathway databases, including KEGG, BioCyc, Panther, The Cancer Cell Map and Pathway Interaction Database (PID)[4-7] with pair-wise interactions gleaned from physical protein–protein interactions in human and model organisms, gene co-expression data, protein domain–domain interactions, text mining and GO annotation[8, 9]. As of December 2012, the 'Reactome-FIs' network contains 209,988 functional interactions encompassing 10,956 proteins (excluding splice isoforms), reflecting 46% of SwissProt proteins[10] and provides a pathway-informed data analysis system for high-throughput data analysis, leading to greater biological interpretability.

Network clustering: A larger network may be composed of smaller modules where the connections (edges) among members (nodes) within modules are dense but connections between modules are sparse. In technical terms, the modularity for a given division of a network can be defined as the fraction of edges within groups minus the expected fraction of such edges in an equivalent network with edges placed at random. Network clustering attempts to identify the modular substructure of networks by

using various algorithmic approaches (such as graph partitioning). The modules so identified may then be interrogated for specific functions which, if they exist, provides novel information about the functional architecture of the network and illuminate how modules may relate to one another. The clusters generated in our study were generated by spectral partitioning based methods detailed in Newman [9].

'Betweenness' as a network property: Betweenness of a node is defined as the fraction of the shortest paths between all pairs of nodes in a network that pass through that node and estimates the functional load through one node or link (assuming that information flows over a network predominantly via the shortest paths)[11]. For three nodes, *i, j, k*, the betweenness centrality measure C_i^{Btw} for node *i* is given by

$$C_i^{Btw} = \sum_{j=1}^{N} \sum_{k=1}^{j-1} \frac{g_{jk}(i)}{g_{jk}}$$

Where $g_{jk}(i)$ is the number of shortest paths from *j* to *k* through *i* and g_{jk} is the total number of shortest paths between j and k[12].

Supplementary Results:

Choice of window size for SNP-to-gene mapping: The choice of the window was determined after comparing the results of SNP-to-gene mapping at 100 kb and 500 kb intervals. Specifically, the larger interval resulted in more instances of the same SNP being mapped to multiple genes, leading to a reduction in the number of unique SNP-gene mappings and contracting the range of best scoring SNP p-values. Some of these results are most likely spurious, essentially being consequences of a larger window allowance around the gene. Conversely, a larger proportion of unique SNP-gene mappings were

obtained with the smaller interval (**Figure S1**). Additionally, the 100 kb region has also been reported to encompass the majority of regulatory regions, such as *cis*-eQTLs[13].

Frequency of gene occurrence among replicated pathways: Pathway multiplicity score was plotted against the pathway's association p-value (from iGSEA) to identify pathways that were enriched for genes with high gene multiplicity scores (**Figure S3**). Replicated but non overlapping pathways with the highest proportion of genes occurring in other replicated pathways are shown in the top right hand corner of the figure. In this analysis, pathways related to extracellular matrix organization and degradation, protein post-translational modification, amino acid metabolism, and lipid mobilization and transport were identified in the top quartile of pathway multiplicity scores.

Prioritization of network nodes based on "betweenness" measure of centrality: Referring to Figure 4, several of the larger red nodes with high "betweenness" measures are composed of complexes of various proteins e.g. 'GBR2:pFAK bound to NCAM:Pfyn' and 'SEMA3A:NRP1:PlexinA:Fyn', suggesting that these complexes play a key role in the function of this network. These red nodes contain at least one gene (in a complex) that was statistically significantly associated to CAD in the replication study (iGSEA score >1.37). Two nodes ('CREB1' and 'FGFR1c homodimer') are shown in yellow indicating that the iGSEA association statistic was less than 1.37 for these genes. In addition, the network contains some nodes colored in white, indicating that no SNP could be mapped to the genes in these nodes. However, these genes are included in the network to maintain network continuity.

Generic issues with pathway analysis: First, consensus is lacking regarding the optimal strategy for pathway-based approaches despite their enormous potential to extend the single SNP association tests of conventional GWAS analyses and to lead to the formulation of new biological hypotheses[14]. In the absence of such consensus, we chose to present the pathway results of a single GSEA algorithm, iGSEA4GWAS, using a single pathway database, REACTOME. This decision was made following

preliminary studies, comparing several tools including GSA-SNP and MAGENTA and additional pathway repositories including KEGG and Biocarta. The results of this comparative analysis will be the topic of a separate manuscript. Second, despite its improved algorithmic approach to identify significantly associated pathways, iGSEA4GWAS is unable to compute exact p-value when these values are <0.001 because the program is limited to the generation of 1000 permutation datasets to derive the null distribution. Thus, pathways with p <0.001 are hard to prioritize based solely on their level of significance. Third, the 100 kb window commonly used to map a SNP to a gene may not adequately account for the potential effects of more distal regulatory SNPs. However, a recent investigation of the distribution of association signals in 7 GWAS datasets detected significant enrichment up to 40 kb upstream and downstream of protein coding genes, suggesting that a 100 kb window is most likely adequate to capture the majority of cis-regulatory signals[15]. Fourth, the extent to which linkage disequilibrium between SNPs influences pathway analysis results remains an open question in the field. While it is easy to see how correlations among SNPs in LD can influence pathway analysis methods that utilize multiple SNPs to arrive at a gene significance score[16-18], the impact of LD on methods, such as i-GSEA4GWAS, that choose a single best SNP to tag a gene and correct for number of SNPs tested per gene is less clear. Pruning of SNPs (removal of SNPs above an LD-correlation threshold) has been proposed as a way to reduce the impact of LD on gene scores[1]. However, pruning also leads to significant loss of information and reduces power for pathway analysis methods that depend on the accumulated evidence from all genes within a pathway to estimate pathway significance. Nevertheless, we also examined the effect SNP pruning on replication of the 85 pathways identified as nominally significant in the Discovery cohort. Generally, pruning reduced the number of testable SNPs to 5-15% of the original number, and only a small subset of the original 32 replicated pathways could be identified with the pruned datasets. We believe this result to be most likely a consequence of reduced information content of the pruned datasets, so that only the most significantly associated pathways could be

identified. Hence, we chose to identify candidate associated pathways (accepting any inherent biases that might be present) and then to use additional methods to reduce the number of false positives. Lastly, LD among genes is another very relevant factor for pathway analysis, since inflation of pathway association score can occur if the index SNPs used to derive gene-based association p-values for proximally located genes are also in LD with each other. However, our LD analysis among the SNPs that were mapped to replicated gene sets suggests that over-inflation is unlikely to be a major concern in the current analysis given only 2 pairs of SNPs in 3 pathways were found to be in high LD (r2 > 0.8). Additionally, pathways with known instances of positionally clustered gene components (e.g. the HLA gene cluster or the chemokine gene cluster) were not significant in our analysis.

Supplementary References:

References

1. **Zhang K, Cui S, Chang S, Zhang L, and Wang J (2010) i-GSEA4GWAS: a web server for identification of pathways/gene sets associated with traits by applying an improved gene set enrichment analysis to genome-wide association study. Nucleic Acids Res 38 (Web Server issue):W90-W95**

2. **Purcell S, Neale B, Todd-Brown K, Thomas L, Ferreira MA, Bender D, Maller J, Sklar P, de Bakker PI, Daly MJ, and Sham PC (2007) PLINK: a tool set for whole-genome association and population-based linkage analyses. Am J Hum Genet 81 (3):559-575**

3. **Johnson AD, Handsaker RE, Pulit SL, Nizzari MM, O'Donnell CJ, and de Bakker PI (2008) SNAP: a web-based tool for identification and annotation of proxy SNPs using HapMap. Bioinformatics 24 (24):2938-2939**

4. **Caspi R, Altman T, Dreher K, Fulcher CA, Subhraveti P, Keseler IM, Kothari A, Krummenacker M, Latendresse M, Mueller LA, Ong Q, Paley S, Pujar A, Shearer AG, Travers M, Weerasinghe D, Zhang P, and Karp PD (2012) The MetaCyc database of metabolic pathways and enzymes and the BioCyc collection of pathway/genome databases. Nucleic Acids Res 40 (Database issue):D742-D753**

5. **Schaefer CF, Anthony K, Krupa S, Buchoff J, Day M, Hannay T, and Buetow KH (2009) PID: the Pathway Interaction Database. Nucleic Acids Res 37 (Database issue):D674-D679**

6. Mi H, Guo N, Kejariwal A, and Thomas PD (2007) PANTHER version 6: protein sequence and function evolution data with expanded representation of biological pathways. Nucleic Acids Res 35 (Database issue):D247-D252

7. Kanehisa M, Goto S, Kawashima S, Okuno Y, and Hattori M (2004) The KEGG resource for deciphering the genome. Nucleic Acids Res 32 (Database issue):D277-D280

8. Wu G, Feng X, and Stein L (2010) A human functional protein interaction network and its application to cancer data analysis. Genome Biol 11 (5):R53

9. Newman ME (2006) Modularity and community structure in networks. Proc Natl Acad Sci U S A 103 (23):8577-8582

10. Croft D, O'Kelly G, Wu G, Haw R, Gillespie M, Matthews L, Caudy M, Garapati P, Gopinath G, Jassal B, Jupe S, Kalatskaya I, Mahajan S, May B, Ndegwa N, Schmidt E, Shamovsky V, Yung C, Birney E, Hermjakob H, D'Eustachio P, and Stein L (2011) Reactome: a database of reactions, pathways and biological processes. Nucleic Acids Res 39 (Database issue):D691-D697

11. Girvan M and Newman ME (2002) Community structure in social and biological networks. Proc Natl Acad Sci U S A 99 (12):7821-7826

12. Freeman, L. C. A set of measures of centrality based on betweenness. Sociometry 40, 35-41. 1977.
Ref Type: Generic

13. Veyrieras JB, Kudaravalli S, Kim SY, Dermitzakis ET, Gilad Y, Stephens M, and Pritchard JK (2008) High-resolution mapping of expression-QTLs yields insight into human gene regulation. PLoS Genet 4 (10):e1000214

14. Wang K, Li M, and Bucan M (2007) Pathway-based approaches for analysis of genomewide association studies. Am J Hum Genet 81 (6):1278-1283

15. Lehne B, Lewis CM, and Schlitt T (2011) Exome localization of complex disease association signals. BMC Genomics 12:92

16. Yu K, Li Q, Bergen AW, Pfeiffer RM, Rosenberg PS, Caporaso N, Kraft P, and Chatterjee N (2009) Pathway analysis by adaptive combination of P-values. Genet Epidemiol 33 (8):700-709

17. O'Dushlaine C, Kenny E, Heron EA, Segurado R, Gill M, Morris DW, and Corvin A (2009) The SNP ratio test: pathway analysis of genome-wide association datasets. Bioinformatics 25 (20):2762-2763

18. Ballard D, Abraham C, Cho J, and Zhao H (2010) Pathway analysis comparison using Crohn's disease genome wide association studies. BMC Med Genomics 3:25

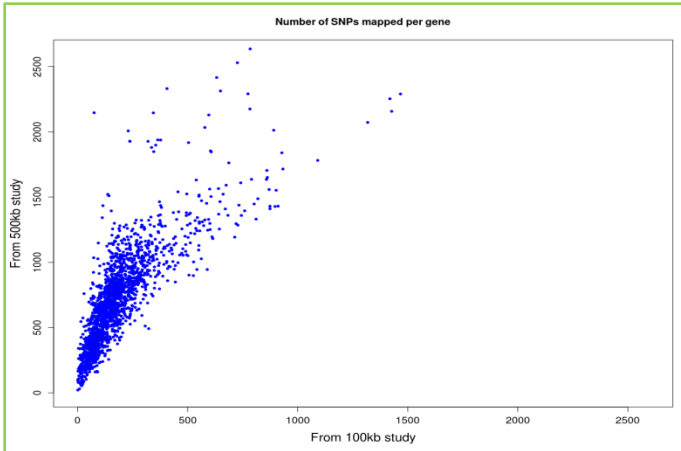
Supplementary Figure SI a-d: Comparison of SNP-to-gene mapping using 100 or 500 kb windows around genes.

a.

	100kb	500kb
Total number of genes mapped	1834	1850
Number of different SNPs	1580	1177
Number of common SNPs	434	

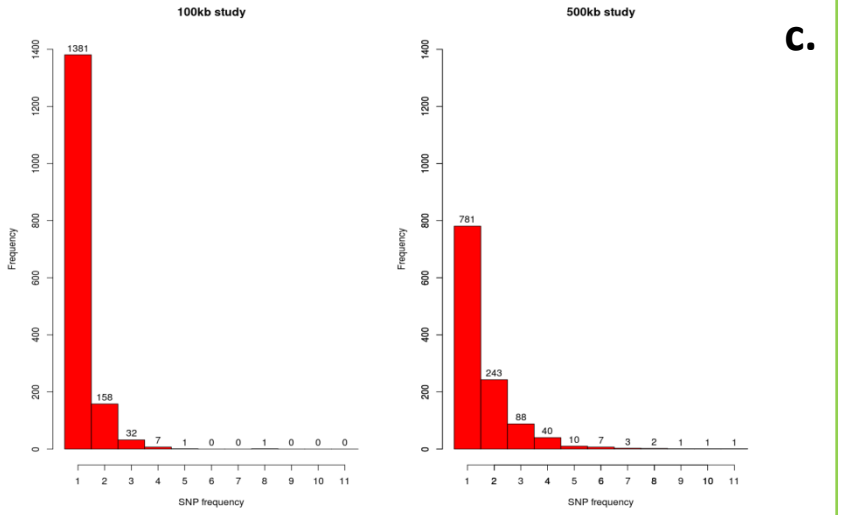
Summary of data used for the comparative analysis. Analysis was conducted on the set of genes present in pathways identified as nominally significant in the Discovery cohort (p<0.05)

b.



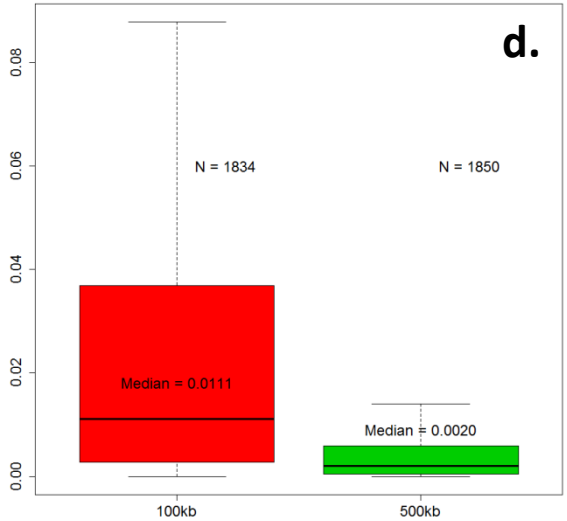
Bivariate plot, showing for each gene (blue dot) the total number of mapped SNPs. Expectedly, the number of mapped SNPs per gene is greater for the 500 kb window than for 100 kb.

c.



Histograms showing the distribution of SNPs mapping to 1, 2 or more genes when using a 500 vs. 100 kb window. The number of SNPs mapping to >1 gene is greater in the 500 kb window; conversely more unique SNP-to-gene mapping is observed with the 100 kb window.

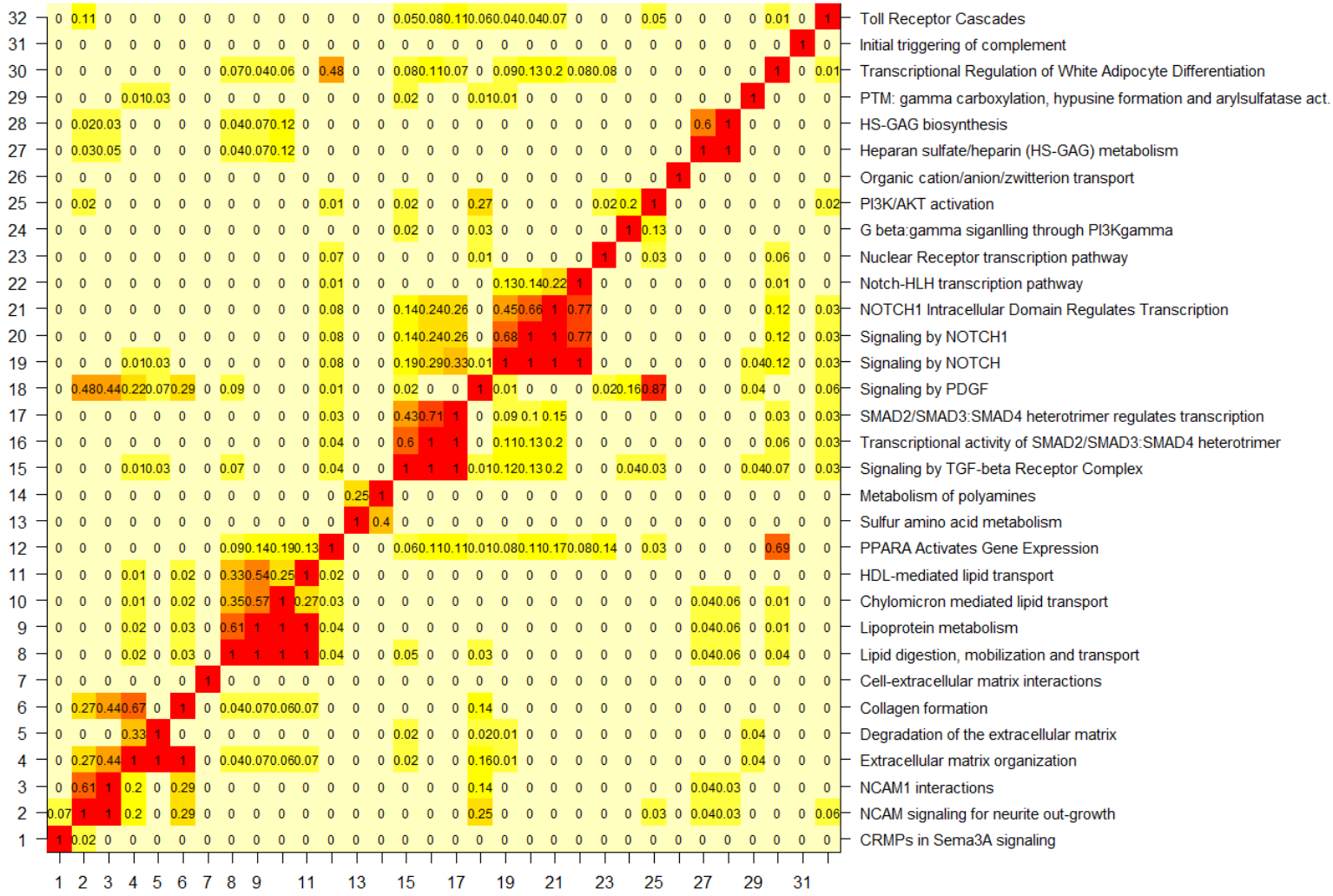
d.



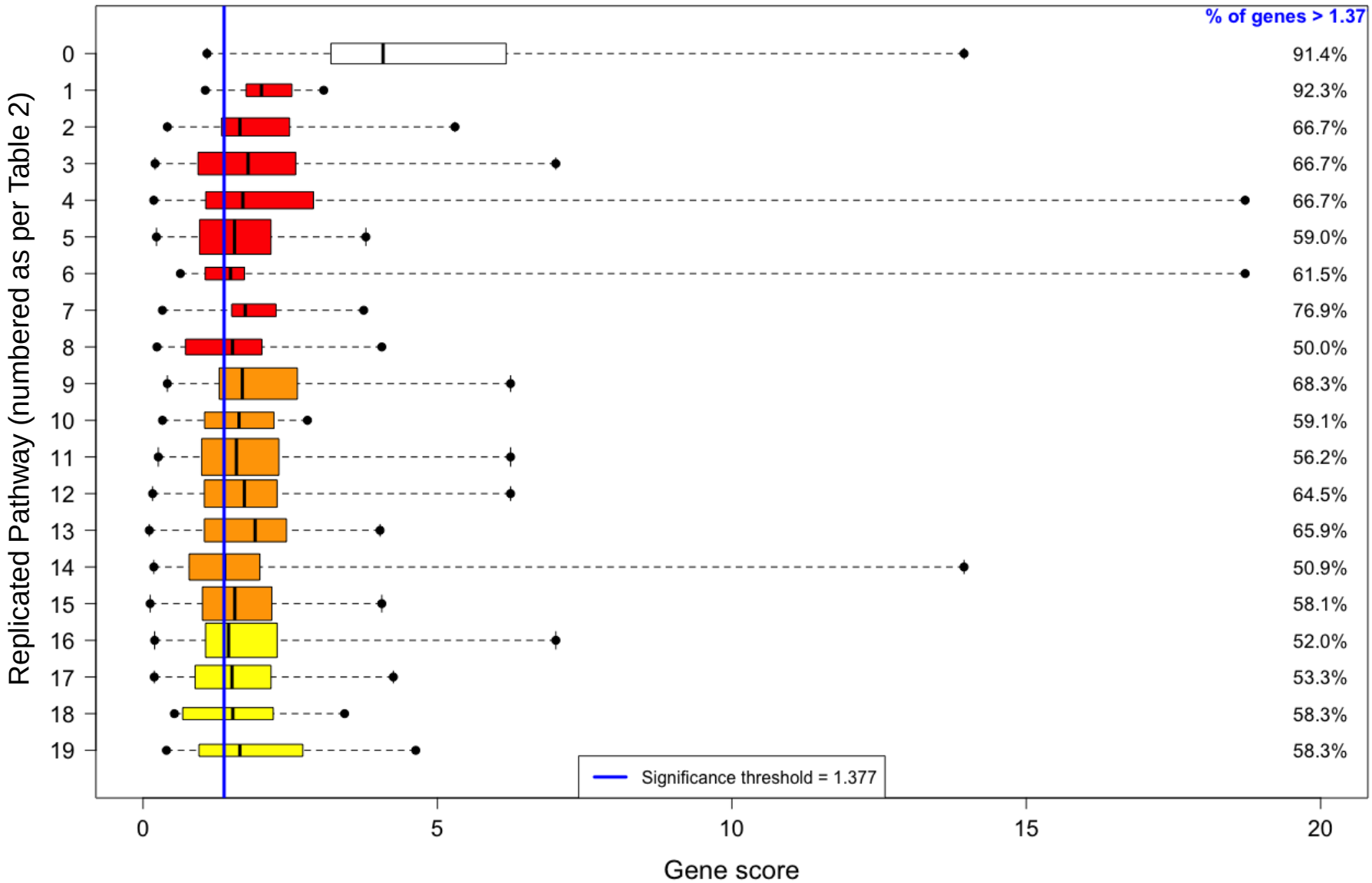
Boxplot showing the range of p-values observed for the best-scoring SNPs when using a 500 kb vs. a 100 kb window. The range is the expected 0-1 for the 100kb but much contracted for 500kb

Supplementary Figure SII: Degree of overlap among the 32 replicated pathways

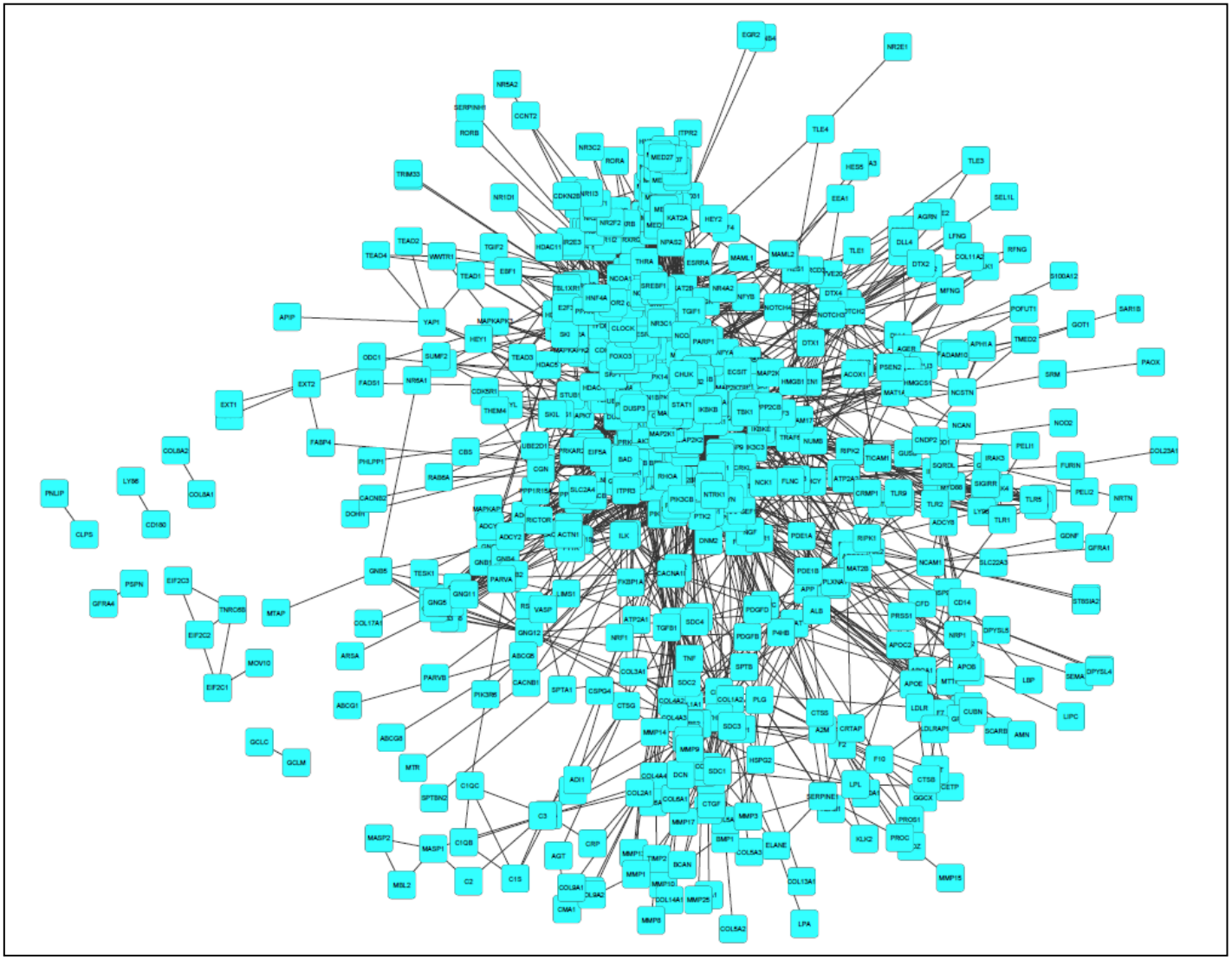
Overlap comparison among the replicated pathways. Pathways are listed in rows and again in columns (in same order) and overlap among the pathways is computed as a fraction of 1.0. The extent of overlap is always expressed as the overlap of a pathway in column to the pathways in rows.The degree of overlap is represented in a yellow-red color scale, with higher overlaps indicated in shades of red.



Supplementary Figure SIII: Distribution of gene scores for replicated pathways

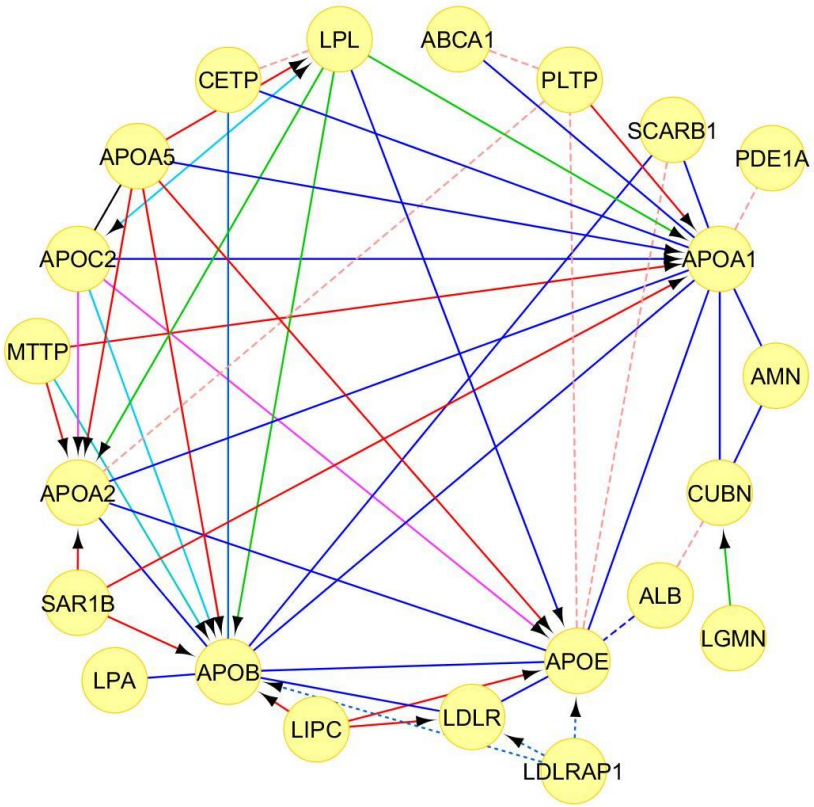


Supplementary Figure SIV: Protein-protein interaction network from replicated pathway genes

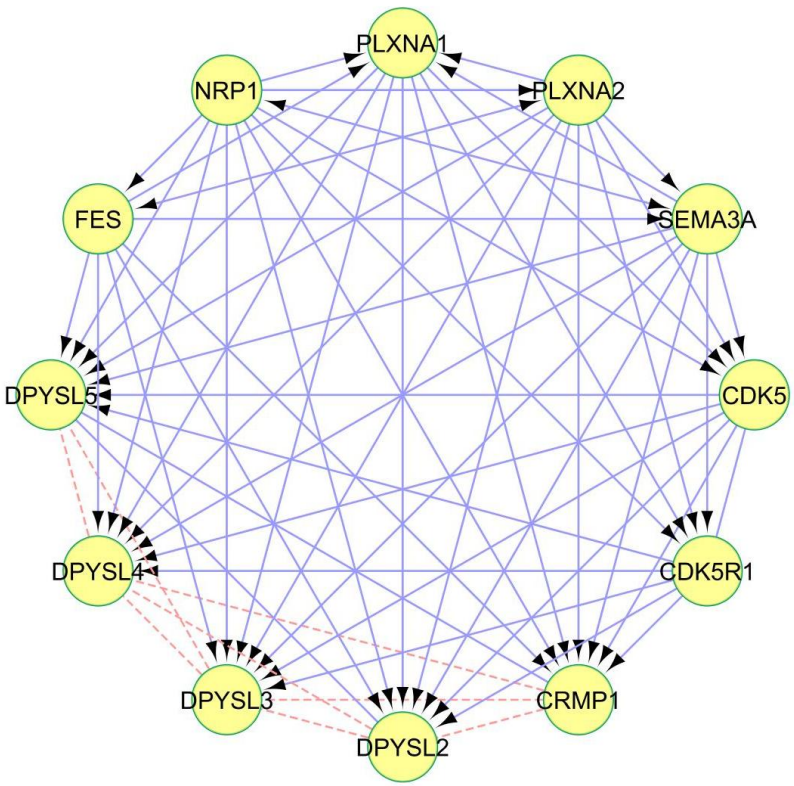


PARAMETER	OBSERVED	EXPECTED	P_VALUE
Direct Edge Count	3726	1548.137	0.001653
Seed Direct Degrees Mean	12	5.792583	0.001653
Seed Indirect Degrees Mean	587.8232	418.2798	0.001653
Seed CI Degrees Mean	6.464137	5.934328	0.001653

Supplementary Figure SV: Types of functional interactions observed within network clusters

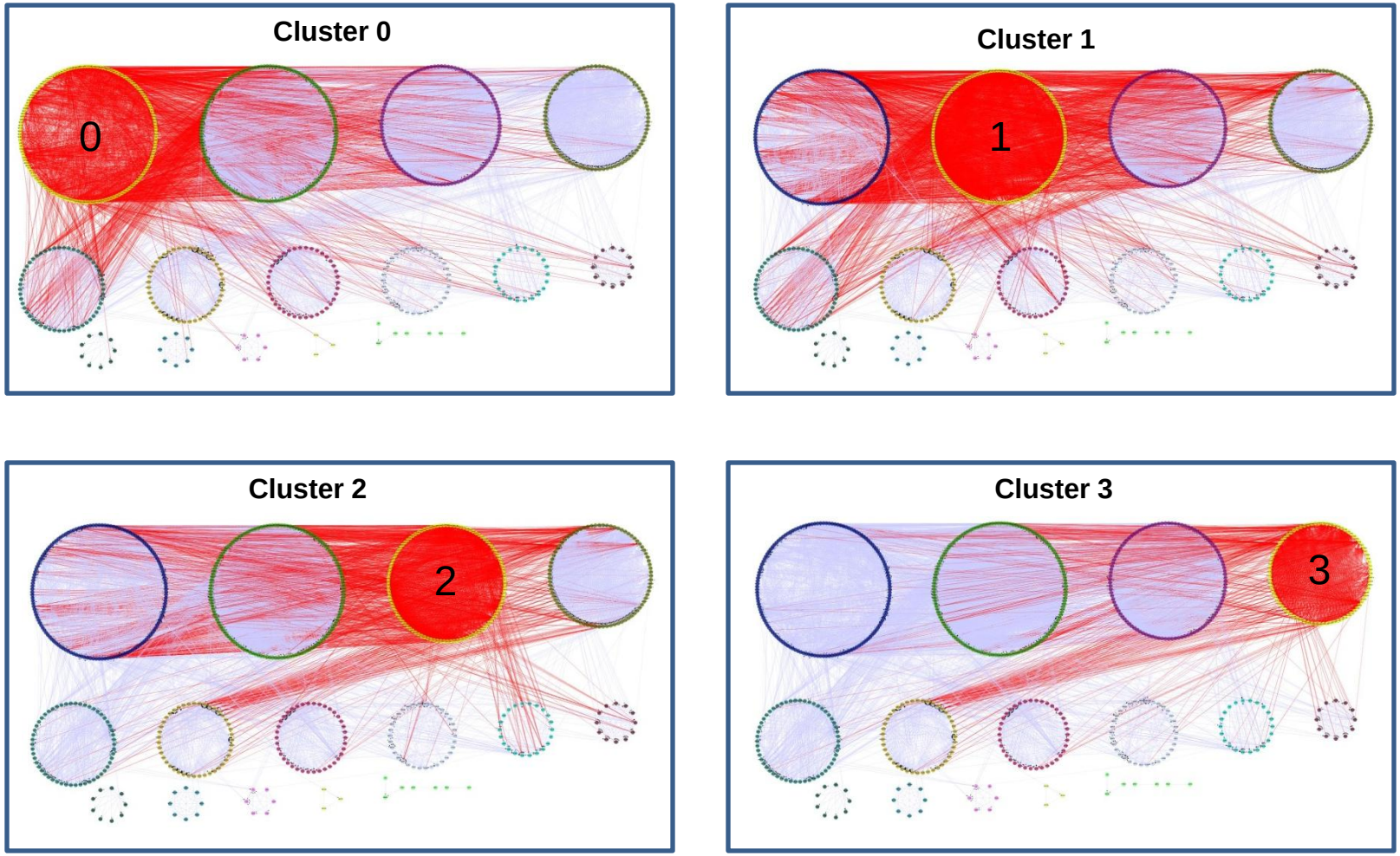


Cluster 8

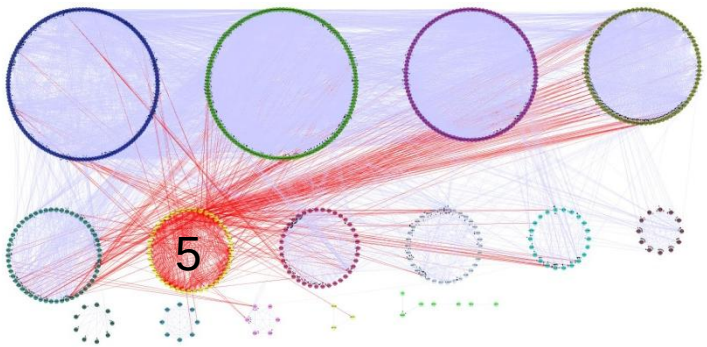


Cluster 9

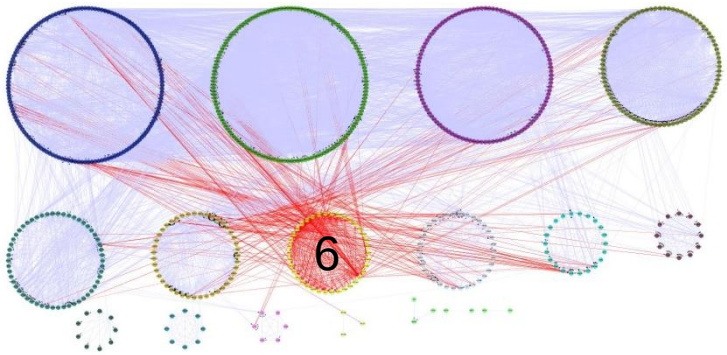
Supplementary Figure SVI: Inter-cluster connectivities among networked genes from the replicated pathways.



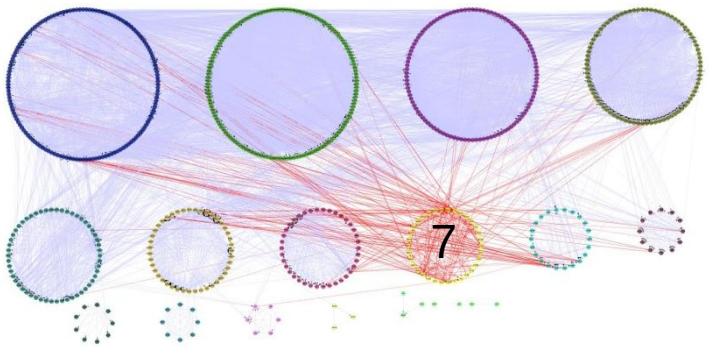
Cluster 5



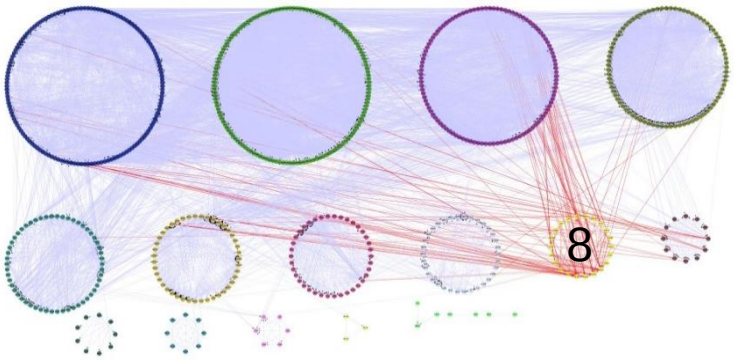
Cluster 6



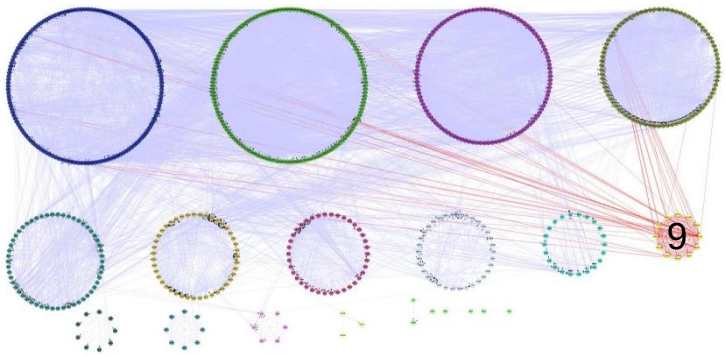
Cluster 7



Cluster 8



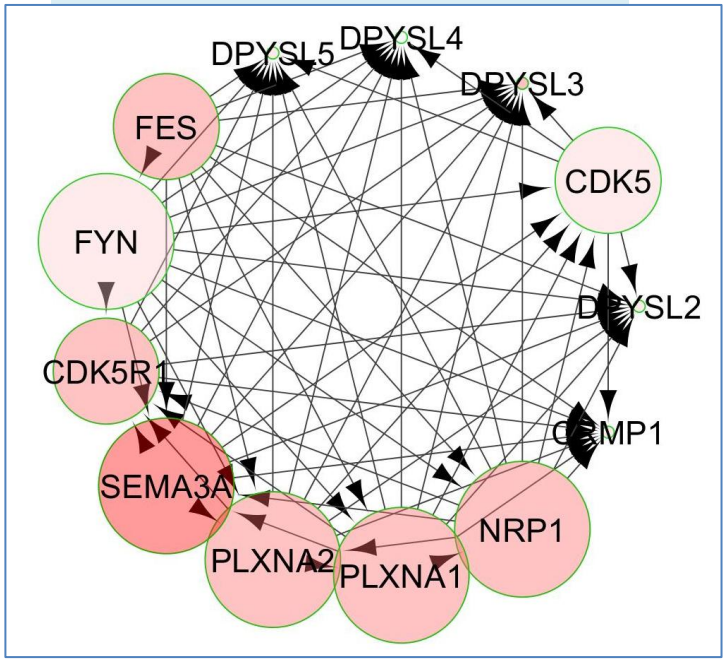
Cluster 9



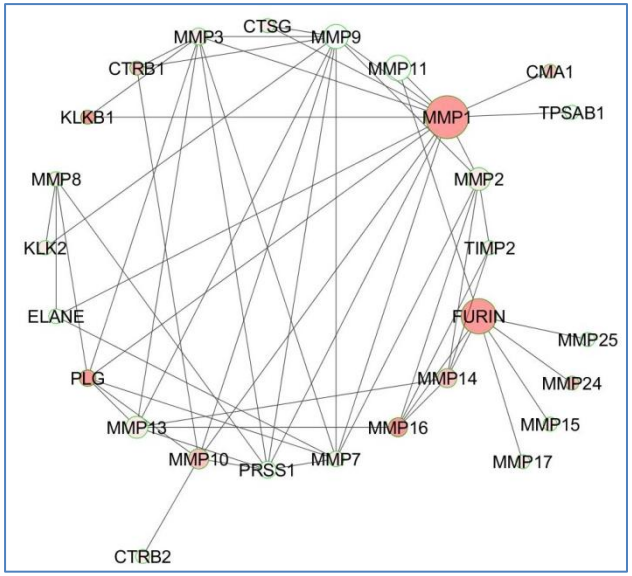
Supplementary Figure SVII

Topology based network analysis of replicated pathways. "Betweenness" measure of node centrality was determined for genes in the replicated pathways. Pathways were first represented as Reactome functional interaction networks in Cytoscape. Betweenness centrality in the network nodes (genes) was calculated via the Centiscape 2.0 Cytoscape plugin. In the following diagrams, genes are color coded by their Stage 2 analysis p-values (deep red, $p<0.001$; lighter red, $0.001<p<0.01$; lightest red, $0.01<p<0.05$; white, $p>0.05$) and sized by their betweenness score. The gene names and betweenness scores are listed beside each network. Betweenness scores are not calculated for genes that do not connect to at least one other gene in the network (these genes are indicated with #N/A for betweenness). No ReactomeFI networks exist for the '*organic anion, cation/zwitterion transport*', '*metabolism of polyamines*', and '*collagen formation*' pathways.

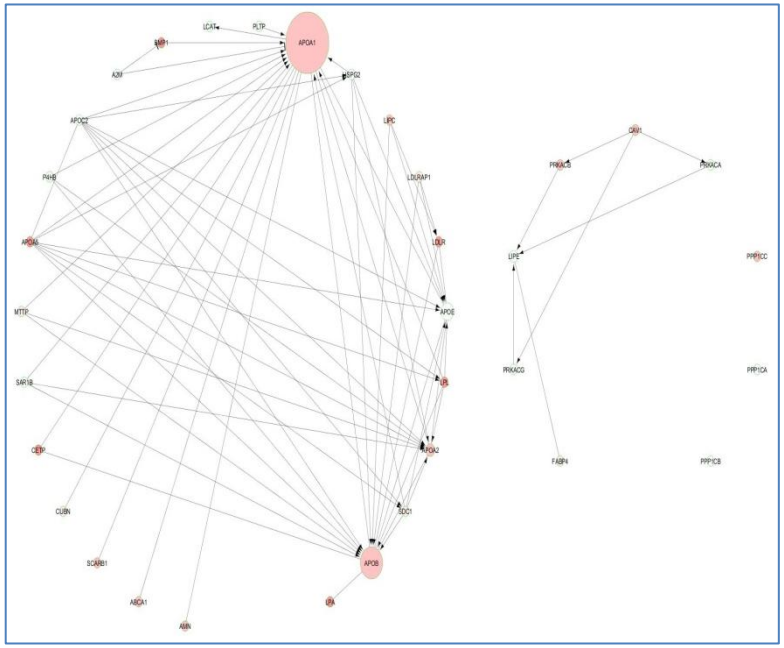
Crmps in Sema3A signaling



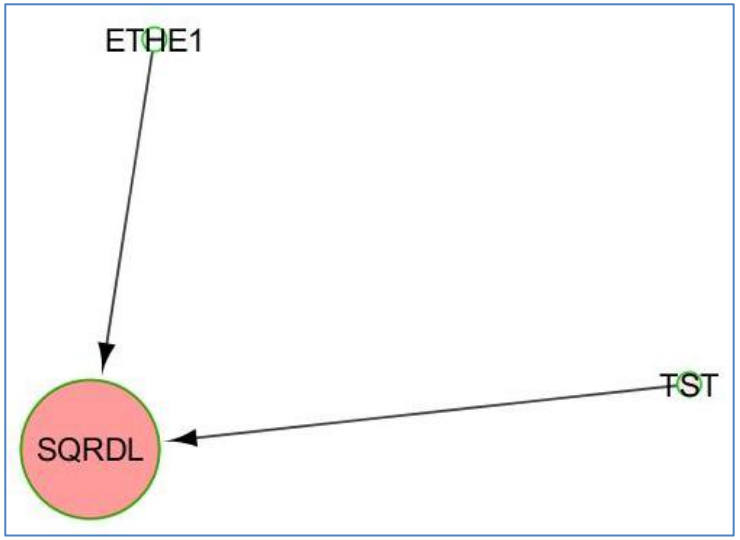
Degradation of the extracellular matrix



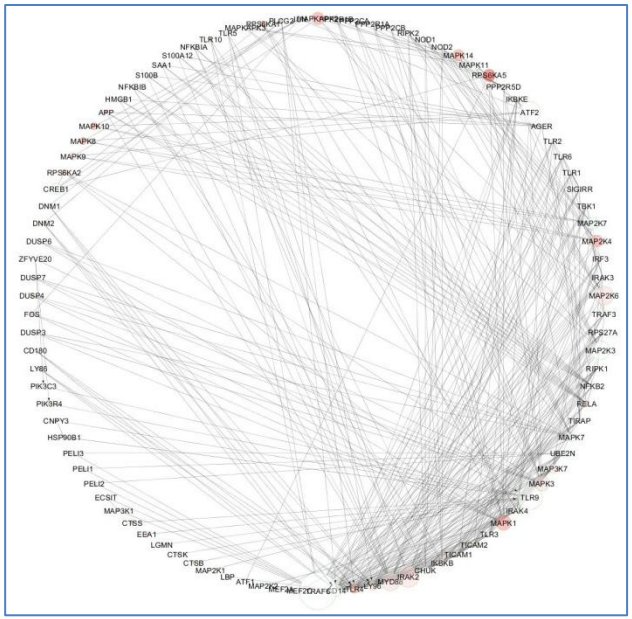
Lipid digestion, mobilization and transp



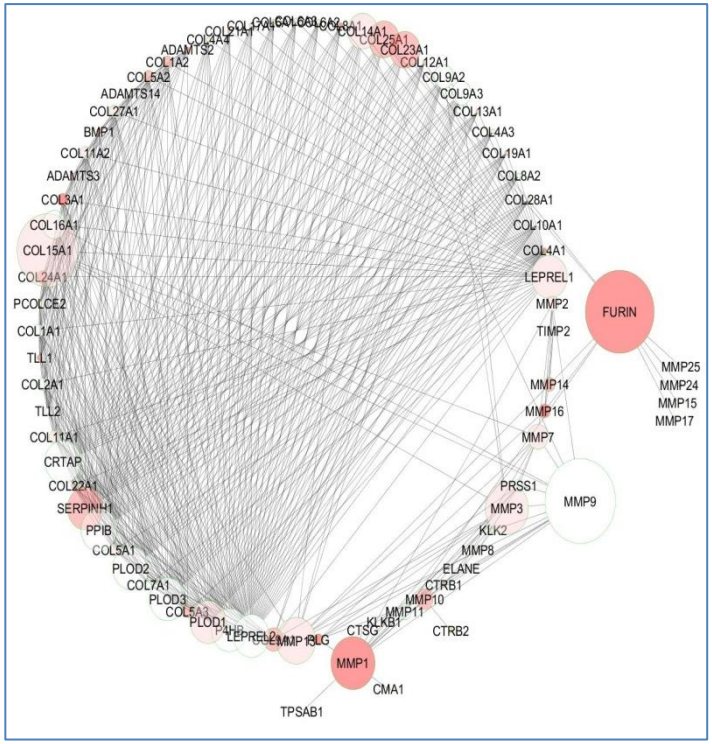
Sulfur amino acid metabolism



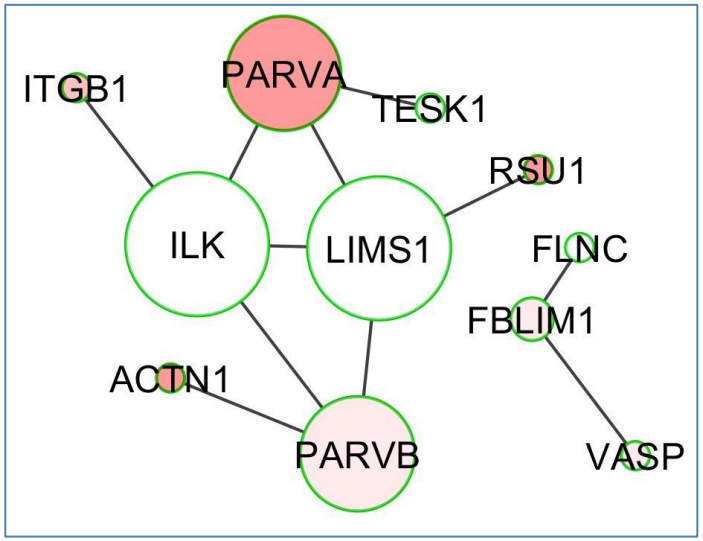
Toll receptor cascades



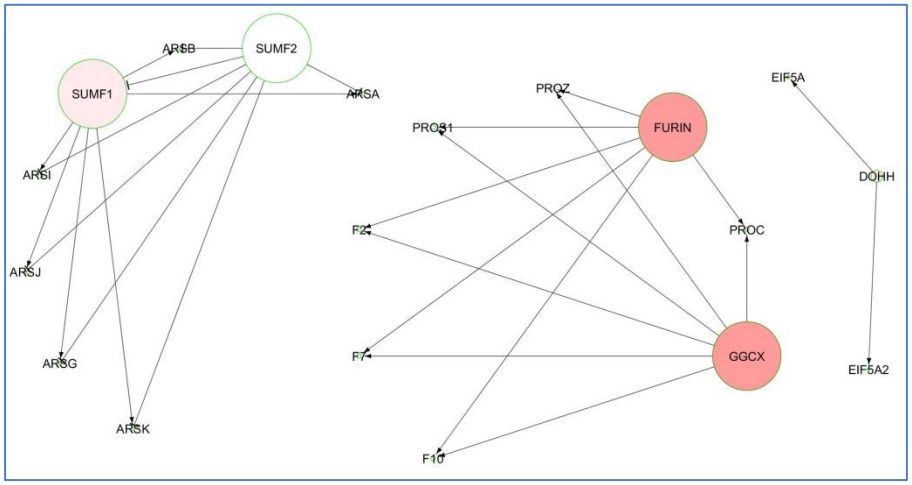
Extracellular matrix organization



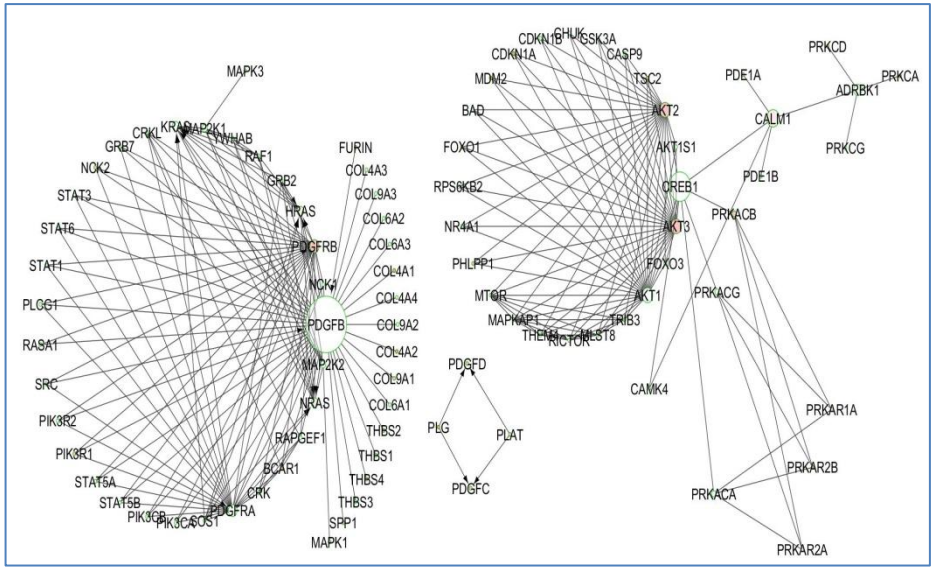
Cell extracellular matrix interactions



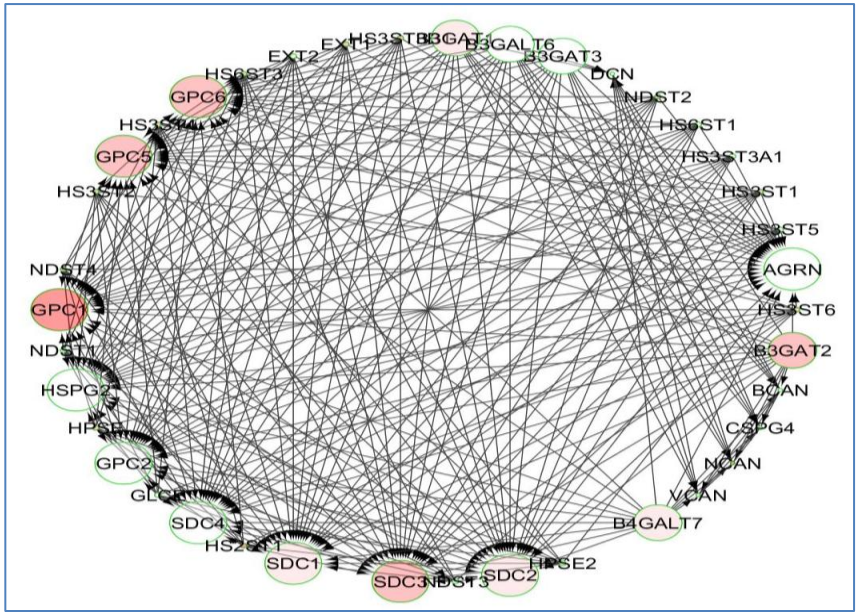
PTM γ carboxylation hypusine formation



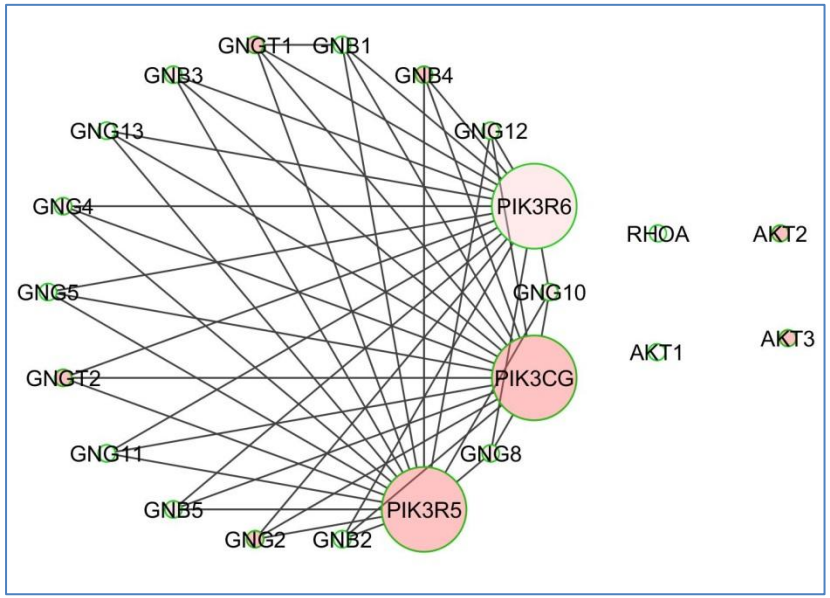
Signaling by PDGF



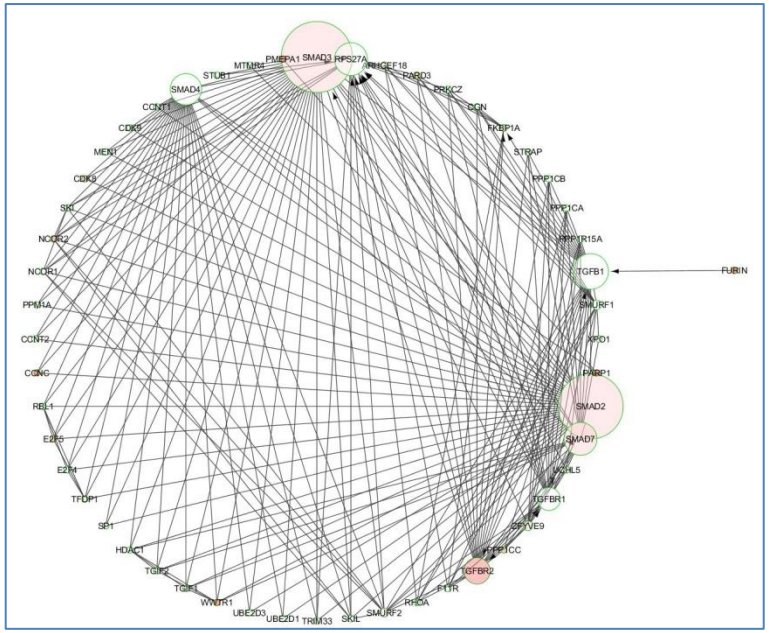
Heparan sulfate heparin HS GAG metabo



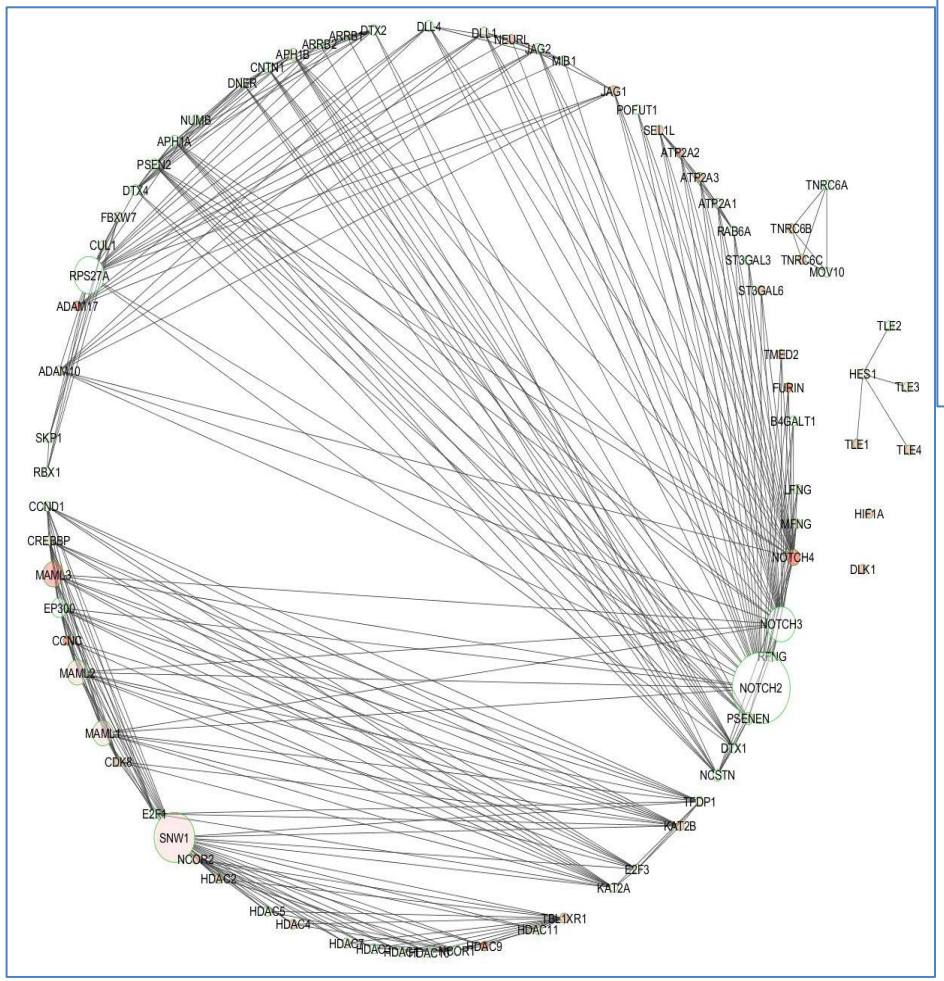
G βγ signaling through PI3Kγ



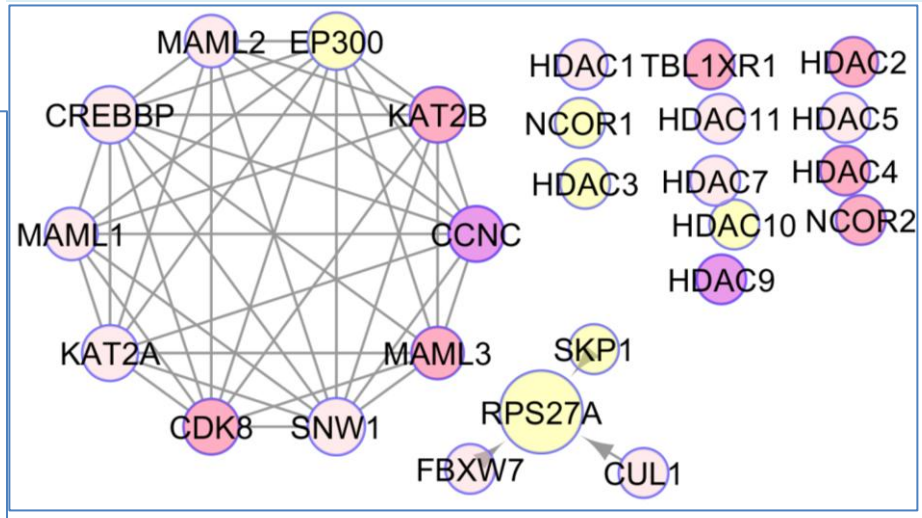
Signaling by TGF β receptor complex



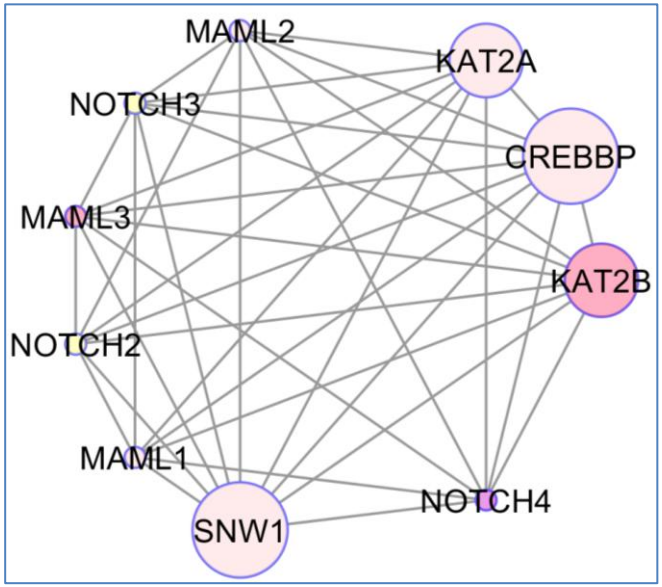
Signaling by Notch



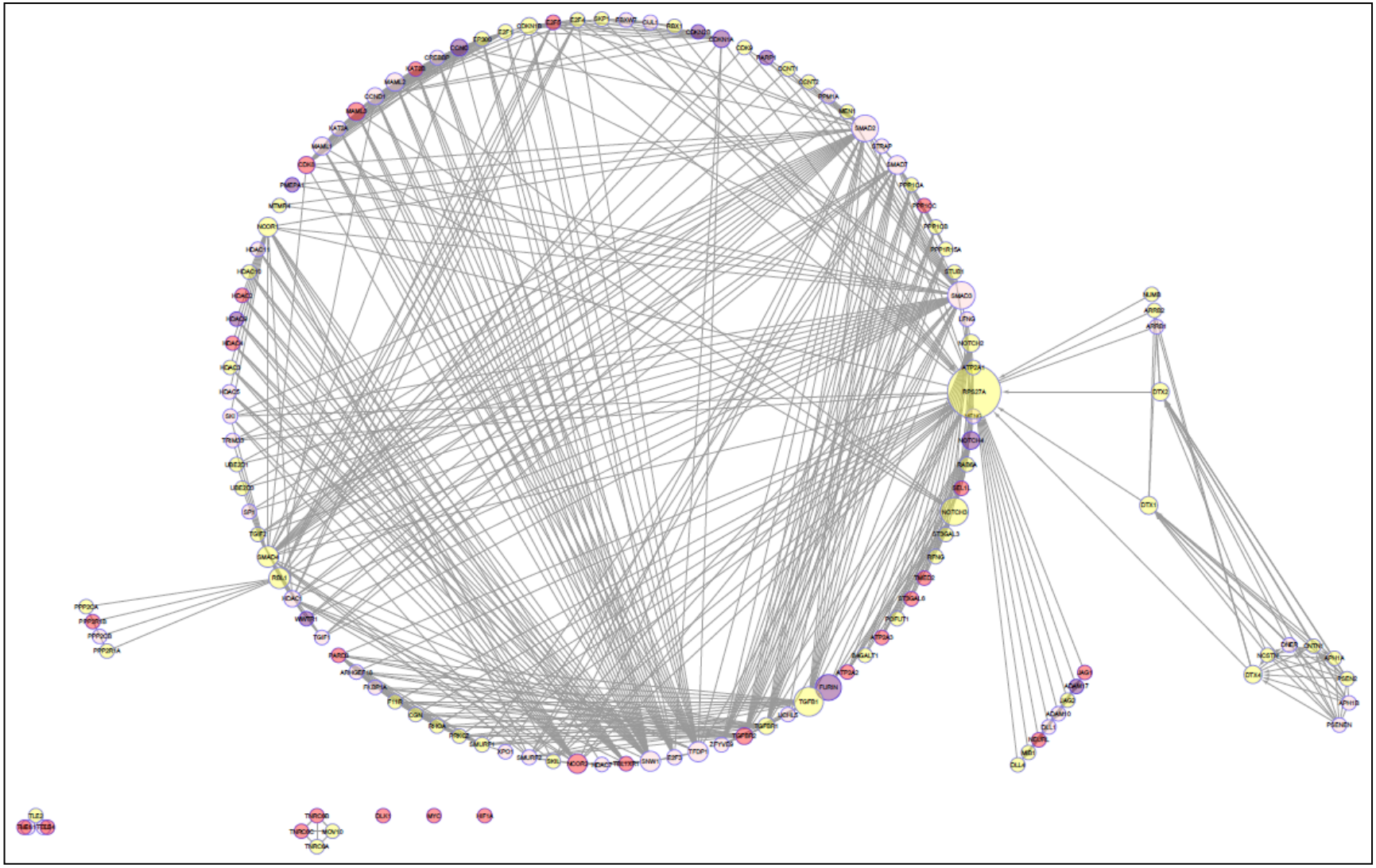
Notch1 intracellular domain regulates transcrip



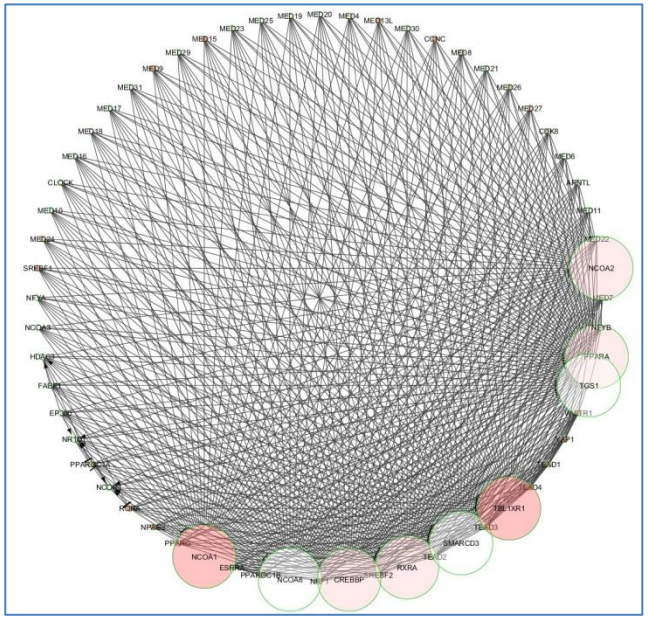
Notch HLH transcription pathway



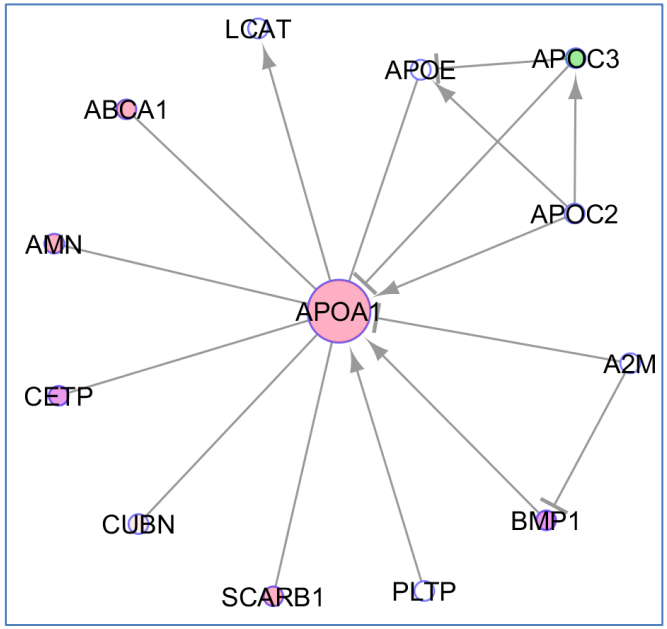
Signaling by Notch 1



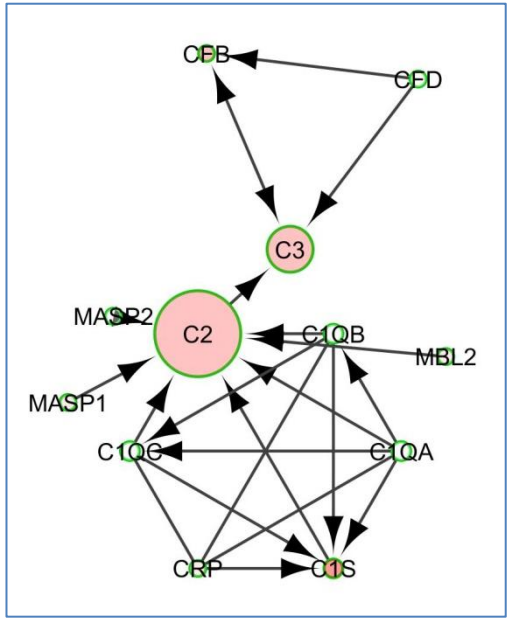
PPARA activates gene expression



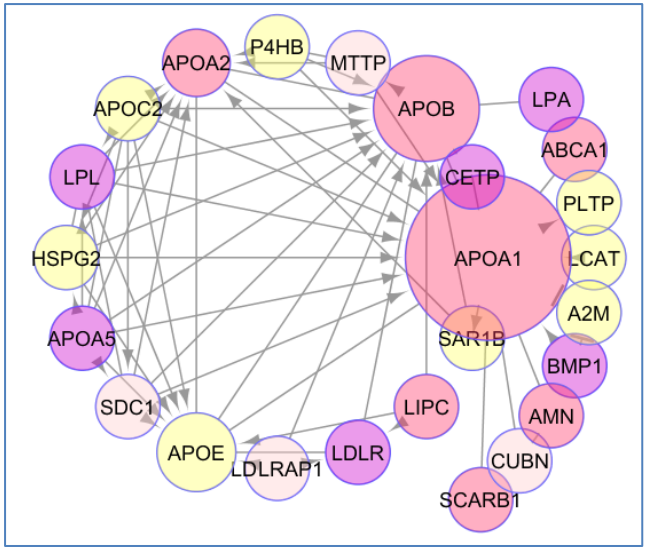
HDL mediated lipid transport



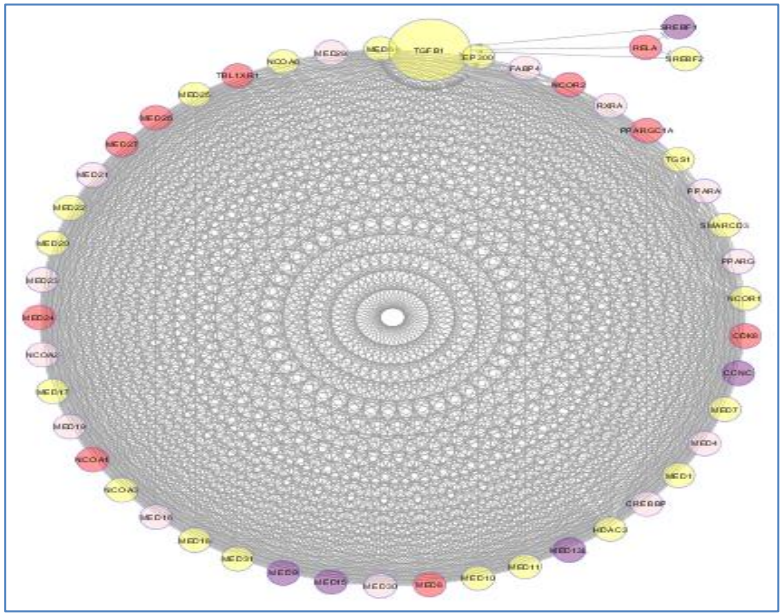
Triggering of complement



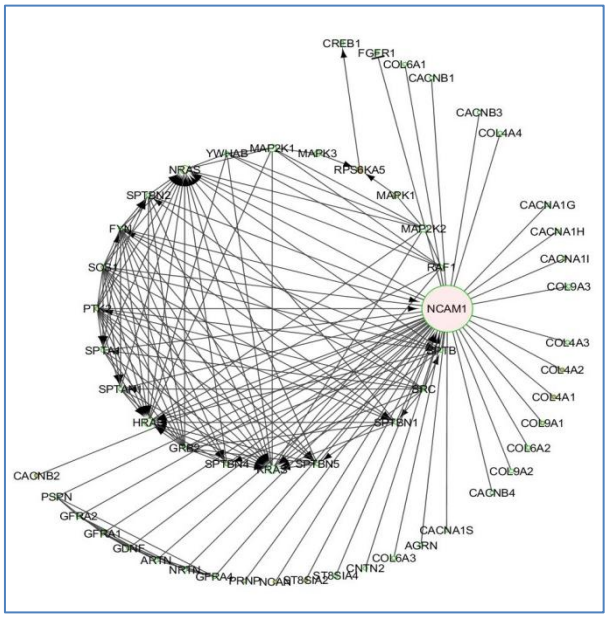
Lipoprotein metabolism



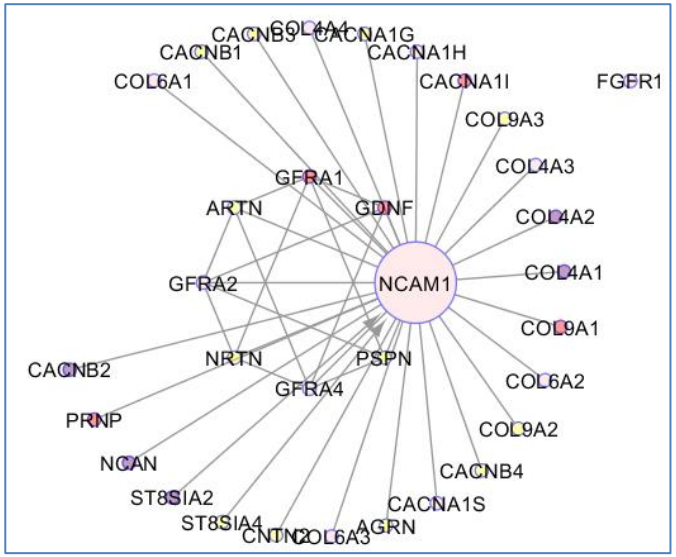
Transcriptional regulation of white adipocyte differentiation



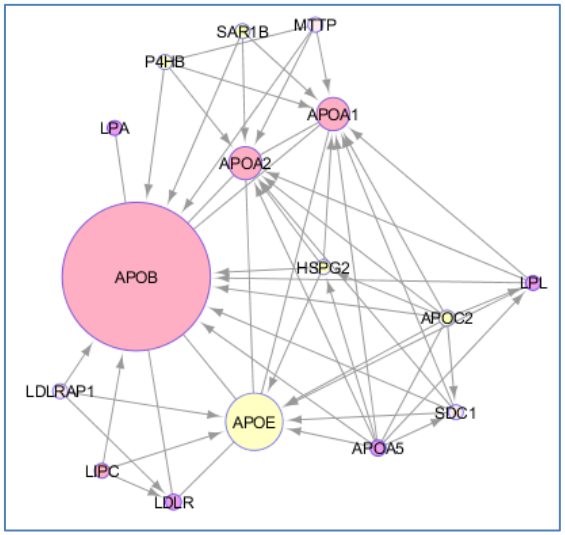
NCAM signaling for neurite outgrowth



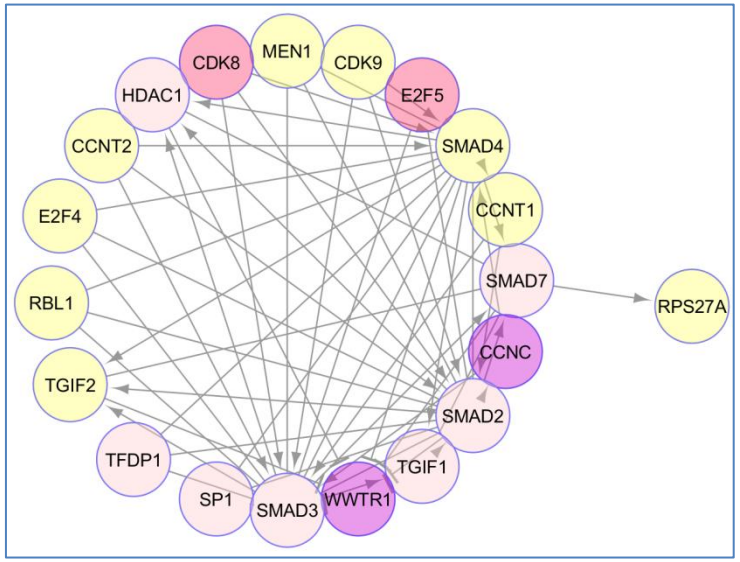
NCAM1 interactions



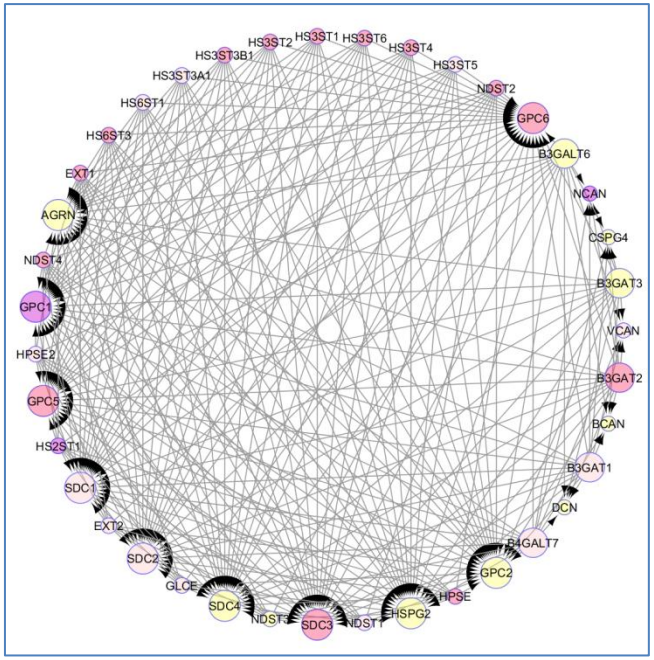
Chylomicron mediated lipid transport



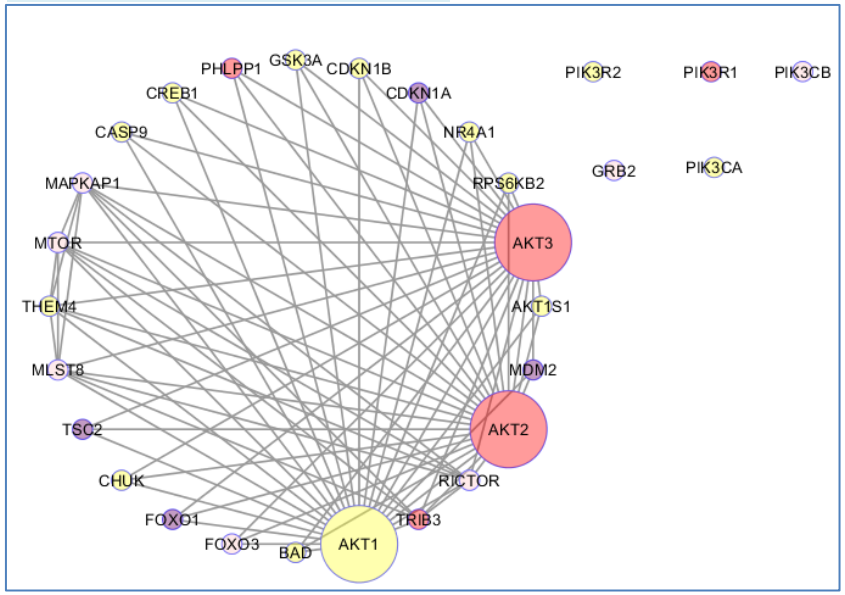
SMAD2_SMAD3_SMAD4 heterotrimer Regulates transcription



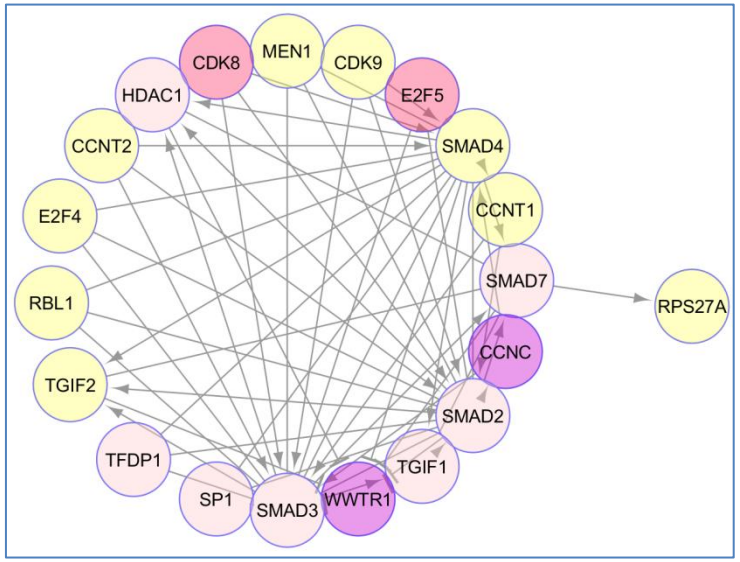
HS GAG biosynthesis



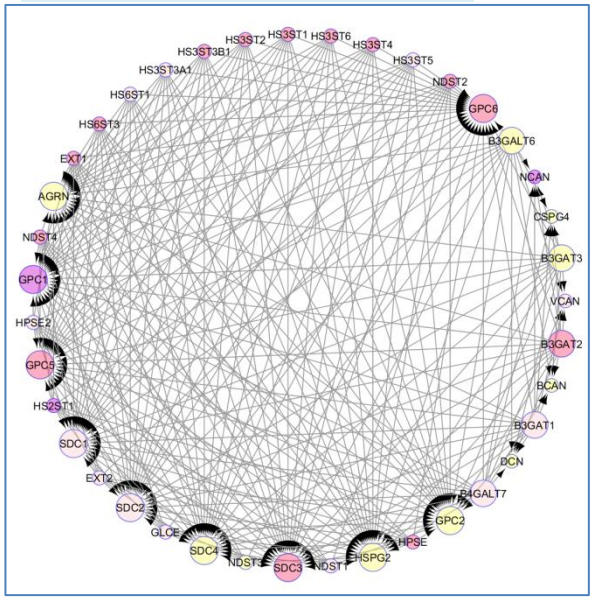
PI3K_AKT activation



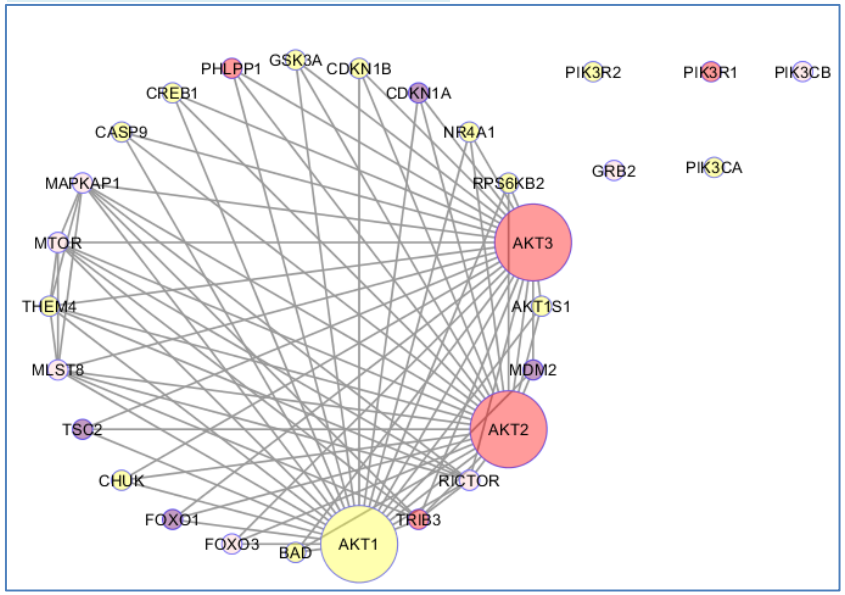
SMAD2_SMAD3_SMAD4 heterotrimer Regulates transcription



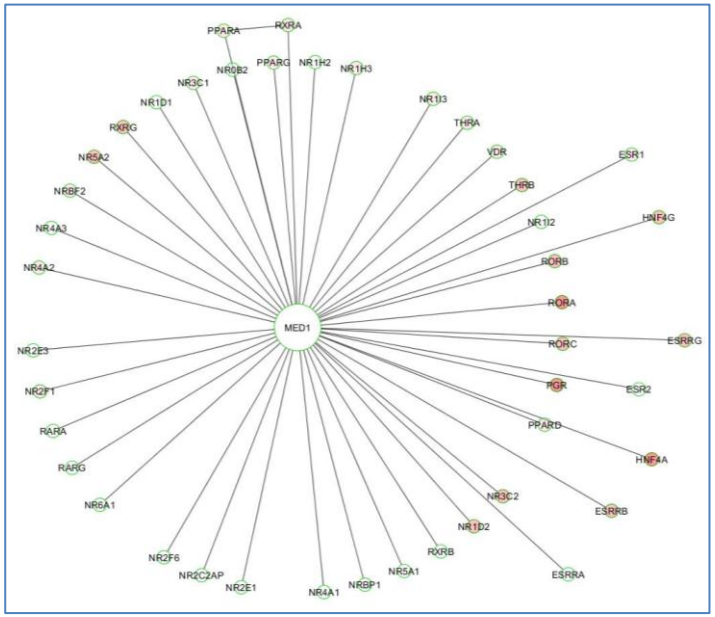
HS GAG biosynthesis



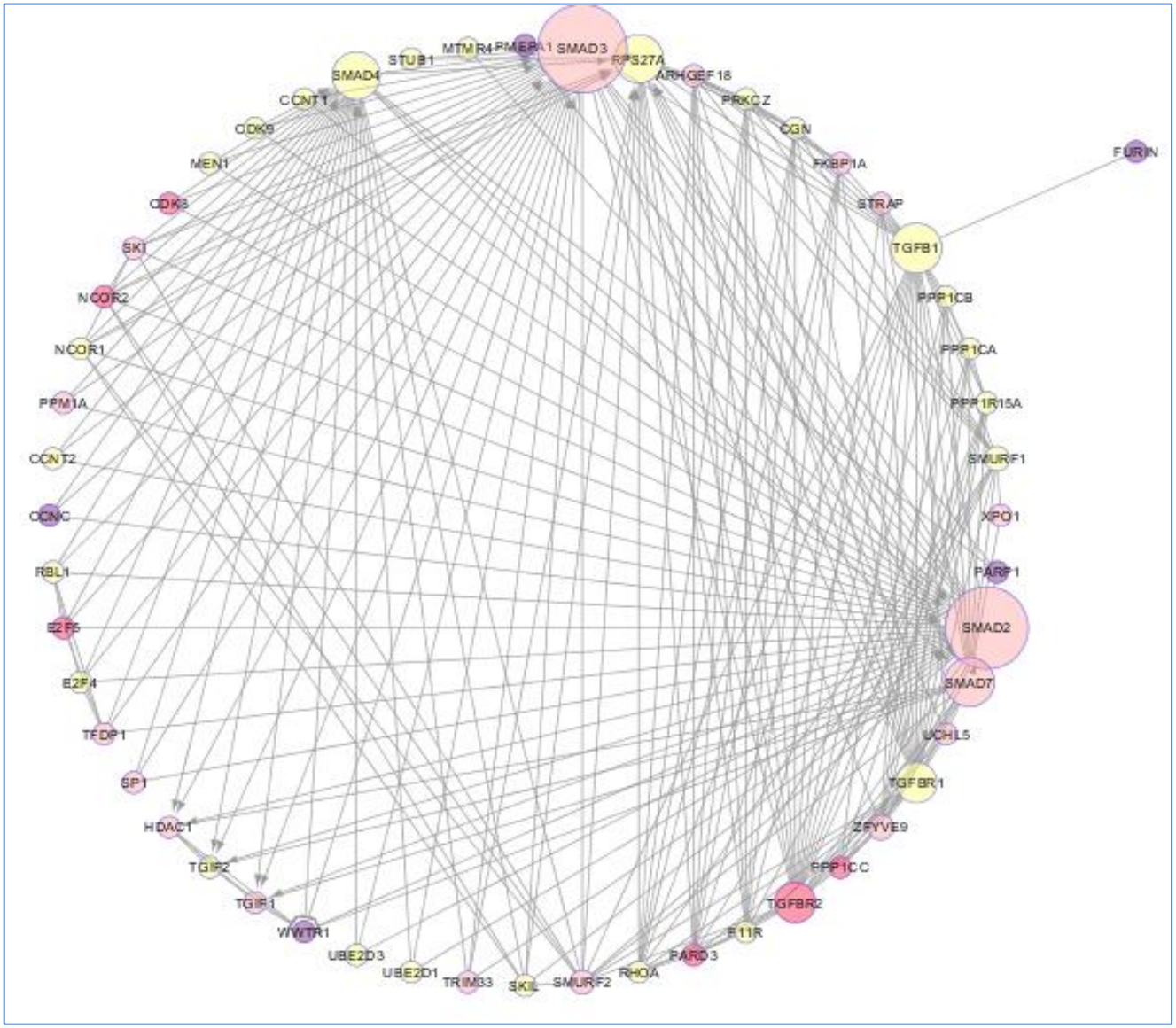
PI3K_AKT activation



Nuclear receptor transcription pathway



Transcriptional activity of SMAD2_SMAD3_ SMAD4 heterotrimer



Supplementary Table I

Supplementary Table S1: Hierarchical organization of replicated and non-replicated Reactome pathways. Pathway hierarchy is represented by levels, with the root level being indicated as Level 1. The 9 root level pathways that contain at least one replicated pathway (at any level) are shown. Pathways are highlighted according to their gene-set enrichment p-values obtained from the replication stage data analysis (see legend at right).Non-replicated pathways (p>0.05) are indicated with a red box around the pathway name. Pathways with greater than 50% overlap with an upper level pathway are indicated with a blue box. Pathways with >200 or <10 genes were not tested.

Legend:

- p<0.001
- 0.001<p<0.01
- 0.01<p<0.05
- p>0.05
- >50% overlap with another pathway
- not tested, number of genes > 200

Level 1	Level 2	Level 3	Level 4	Level 5
Metabolism	Metabolism of lipids and lipoproteins	Lipid Digestion, Mobilization and Transport	Lipoprotein metabolism	Chylomicron mediated lipid transport
				HDL mediated lipid transport
				LDL mediated lipid transport
			Digestion of dietary lipids	
			Trafficking of dietary sterols	
			TG lipolysis by hormone sensitive lipase	
		Fatty acid, triglyceride and ketone body metabolism	Regulation of lipid metabolism by PPARA	PPARA activates gene expression
			Triglyceride biosynthesis	
			Import of palmitoyl-CoA into mitochondria	
			Ketone body metabolism	
			Mitochondrial fatty acid beta oxidation	
	Metabolism of amino acids and derivatives	Sulfur amino acid metabolism		
		Metabolism of polyamines		
	Metabolism of carbohydrates	Glycosaminoglycan metabolism	Heparan sulfate heparin (HS-GAG) metabolism	HS-GAG biosynthesis
			Hyaluronan metabolism	
			Keratin metabolism	
			Transport and synthesis of PAPS	
			Heparan sulfate metabolism	
			Chondroitin sulfate metabolism	
Signal Transduction	Signaling by PDGF			
	Signaling by NOTCH	Signaling by NOTCH1	NOTCH1 intracellular domain regulates transcription	
	Signaling by TGF-beta receptor complex	Transcriptional activity of SMAD2/3:SMAD4 heterotrimer	SMAD 2/3:SMAD4 heterotrimer regulates transcription	
			Downregulation of SMAD2/3:SMAD4 transcriptional activity	
	Signaling by NGF	NGF signaling via TRKA from plasma membrane	PI3K AKT activation	
			Signaling to ERKs	
			PLC gamma 1 signaling	
			Retrograde neurotropin signaling	
	Signaling by GPCR	GPCR downstream signaling	G protein beta:gamma signaling	G beta:gamma signaling through PI3K gamma
			G alpha signaling	
			Opioid signaling	
Developmental Biology	Axon guidance	NCAM signaling for neurite outgrowth	NCAM1 interactions	
		Semaphorin interactions	CRMPS in SEMA3A signaling	
			Sema4D in semaphorin signaling	
			Sema3A PAK dependent axon repulsion	
	Transcriptional regulation of white adipocyte differentiation			
Extracellular matrix organization	Collagen formation			
	Degradation of the extracellular matrix			
Immune system	Innate immunity	Toll receptor cascades		
		Complement cascade	Initial triggering of complement	
			Activation of C3 and C5	
			Terminal pathway of complement	
			Regulation of complement cascade	
Metabolism of proteins	Post-translational protein modification (PTM)	PTM: gamma carboxylation, hypusine formation and arylsulfatase action		
Cell-cell communication	Cell-cell junction organization	Cell extracellular matrix interaction		
Transmembrane transport of small molecules	SLC-mediated transmembrane transport	Transport of glucose and other sugars, bile salts and organic acids, metal ions and amine compounds	Organic cation anion zwitterion transport	
			Na+ dependent/independent glucose transporters	
			Inositol transporters	
			Na+ coupled sulfate, di-, tricarboxylate transporters	
			Metal ion SLC transporters	
			H+ coupled monocarboxylate transporters	
			Na+/Cl- dependent neurotransporters	
Gene Expression	Generic transcription pathway	NOTCH HLH transcription pathway		
		Nuclear receptor transcription pathway		

Supplementary Table II

Supplementary Table S2. Replication studies on 85 Discovery pathways using pruned lists of SNPs

SNPs were pruned if they were in LD, defined as r2>0.2 or r2>0.5. Pathways that also replicated with the pruned list are highlighted in yellow.

Replicated pathways (SNPs with **r2>0.2** pruned)	Number of genes	P	FDR	Replicated in unpruned list
REACTOME_LIPID_DIGESTION_MOBILIZATION_AND_TRANSPORT	46	< 0.001	0.007	Yes
REACTOME_MUSCLE_CONTRACTION	48	< 0.001	0.013	No
REACTOME_EXTRACELLULAR_MATRIX_ORGANIZATION	87	< 0.001	0.033	Yes
REACTOME_LIPOPROTEIN_METABOLISM	28	0.001	0.033	Yes
REACTOME_ORGANIC_CATION_ANION_ZWITTERION_TRANSPORT	13	0.002	0.012	No
REACTOME_SIGNALING_BY_PDGF	122	0.003	0.071	Yes
REACTOME_COLLAGEN_FORMATION	58	0.004	0.052	Yes
REACTOME_SMOOTH_MUSCLE_CONTRACTION	25	0.005	0.052	No
REACTOME_HDL_MEDIATED_LIPID_TRANSPORT	15	0.011	0.097	Yes
REACTOME_TOLL_RECEPTOR_CASCADES	118	0.012	0.105	Yes
REACTOME_SIGNALING_BY_RHO_GTPASES	113	0.017	0.134	No
REACTOME_PI_METABOLISM	48	0.022	0.107	No
REACTOME_NCAM_SIGNALING_FOR_NEURITE_OUT_GROWTH	64	0.022	0.157	Yes
REACTOME_DEGRADATION_OF_THE_EXTRACELLULAR_MATRIX	29	0.047	0.210	Yes

Replicated pathways (SNPs with **r2>0.5** pruned)	Number of genes	P	FDR	Replicated in unpruned list
REACTOME_LIPID_DIGESTION_MOBILIZATION_AND_TRANSPORT	46	< 0.001	0.001	Yes
REACTOME_LIPOPROTEIN_METABOLISM	28	< 0.001	0.006	Yes
REACTOME_SULFUR_AMINO_ACID_METABOLISM	24	< 0.001	0.010	Yes
REACTOME_CHYLOMICRON_MEDIATED_LIPID_TRANSPORT	16	< 0.001	0.011	Yes
REACTOME_ORGANIC_CATION_ANION_ZWITTERION_TRANSPORT	13	0.002	0.009	No
REACTOME_DEGRADATION_OF_THE_EXTRACELLULAR_MATRIX	29	0.005	0.028	Yes
REACTOME_TRANSCRIPTIONAL_ACTIVITY_OF_SMAD2_SMAD3_SMAD4_HETEROTRIMER	38	0.005	0.068	Yes
REACTOME_NOTCH_HLH_TRANSCRIPTION_PATHWAY	13	0.011	0.099	Yes
REACTOME_SIGNALING_BY_TGF_BETA_RECEPTOR_COMPLEX	63	0.013	0.120	Yes
REACTOME_PI3K_AKT_ACTIVATION	38	0.02	0.126	Yes
REACTOME_TOLL_RECEPTOR_CASCADES	118	0.02	0.134	Yes
REACTOME_NOTCH1_INTRACELLULAR_DOMAIN_REGULATES_TRANSCRIPTION	46	0.02	0.140	Yes
REACTOME_SMAD2_SMAD3_SMAD4_HETEROTRIMER_REGULATES_TRANSCRIPTION	27	0.021	0.124	Yes
REACTOME_SYNTHESIS_OF_PIPS_AT_THE_PLASMA_MEMBRANE	31	0.023	0.145	No

Supplementary Table III

Supplementary Table S3. Summary of linkage disequilibirum between mapped SNPs in the 32 replicated pathways

	REPLICATED PATHWAY NAME	# of SNPs	SNPs with pairwise r^2 ≥ 0.2	≥ 0.5	≥ 0.8	rs# of SNPs in LD
31	CELL EXTRACELLULAR MATRIX INTERACTIONS	14	0	0	0	
1	CHYLOMICRON MEDIATED LIPID TRANSPORT	16	0	0	0	
32	COLLAGEN FORMATION	58	0	0	0	
2	CRMPS IN SEMA3A SIGNALING	14	0	0	0	
3	DEGRADATION OF THE EXTRACELLULAR MATRIX	29	0	0	0	
15	EXTRACELLULAR MATRIX ORGANIZATION	87	0	0	0	
17	G BETA GAMMA SIGNALLING THROUGH PI3KGAMMA	25	0	0	0	
26	HDL MEDIATED LIPID TRANSPORT	15	0	0	0	
21	HEPARAN SULFATE HEPARIN HS GAG METABOLISM	52	2	2	2	rs1509558, rs2663905
13	HS GAG BIOSYNTHESIS	31	2	2	2	rs1509558, rs2663905
30	INITIAL TRIGGERING OF COMPLEMENT	16	0	0	0	
4	LIPID DIGESTION MOBILIZATION AND TRANSPORT	46	0	0	0	
5	LIPOPROTEIN METABOLISM	28	0	0	0	
9	METABOLISM OF POLYAMINES	15	0	0	0	
20	NCAM SIGNALING FOR NEURITE OUT GROWTH	64	0	0	0	
29	NCAM1 INTERACTIONS	39	0	0	0	
12	NOTCH HLH TRANSCRIPTION PATHWAY	13	0	0	0	
6	NOTCH1 INTRACELLULAR DOMAIN REGULATES TRANSCRIPTION	46	0	0	0	
28	NUCLEAR RECEPTOR TRANSCRIPTION PATHWAY	49	0	0	0	
11	ORGANIC CATION ANION ZWITTERION TRANSPORT	13	2	0	0	
25	PI3K AKT ACTIVATION	38	0	0	0	
24	PPARA ACTIVATES GENE EXPRESSION	104	0	0	0	
14	PTM GAMMA CARBOXYLATION HYPUSINE FORMATION AND ARYLSULFATASE ACTIVAT	27	0	0	0	
22	SIGNALING BY NOTCH	103	2	2	2	rs709308, rs12143347
18	SIGNALING BY NOTCH1	70	0	0	0	
19	SIGNALING BY PDGF	122	0	0	0	
23	SIGNALING BY TGF BETA RECEPTOR COMPLEX	63	0	0	0	
10	SMAD2 SMAD3 SMAD4 HETEROTRIMER REGULATES TRANSCRIPTION	27	0	0	0	
7	SULFUR AMINO ACID METABOLISM	24	0	0	0	
8	TOLL RECEPTOR CASCADES	118	2	0	0	
16	TRANSCRIPTIONAL ACTIVITY OF SMAD2 SMAD3 SMAD4 HETEROTRIMER	38	0	0	0	
27	TRANSCRIPTIONAL REGULATION OF WHITE ADIPOCYTE DIFFERENTIATION	72	0	0	0	

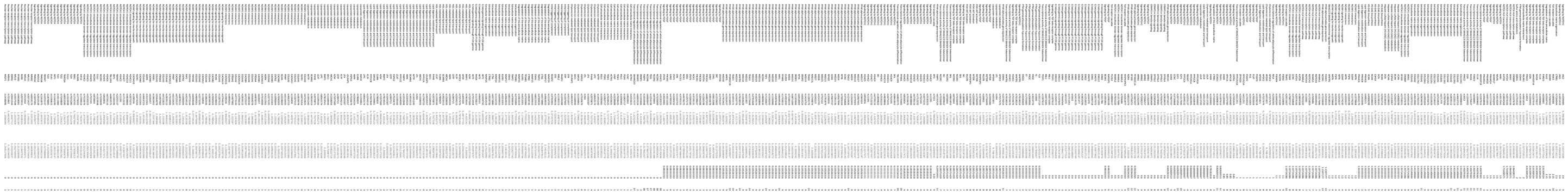
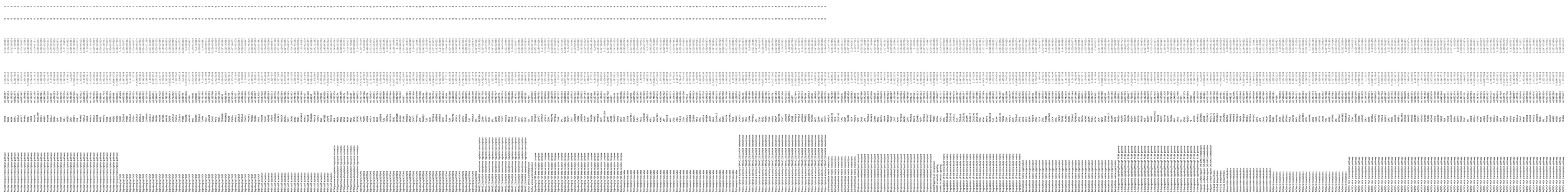
Supplementary Table 12

Supplementary Table 12. Coding of protein-coding genes in the genome of Ficedula albicollis

Scaffold	Gene	Start	End	Strand	Exons	Transcripts	Mean exon length	Mean CDS length
chr1A	ENSFALG00000000001	1,000,000	1,000,000	+	1	1	1,000	1,000
chr1A	ENSFALG00000000002	1,000,000	1,000,000	+	1	1	1,000	1,000
chr1A	ENSFALG00000000003	1,000,000	1,000,000	+	1	1	1,000	1,000
chr1A

Supplementary Table 55. Enrichment analysis (by Gene Ontology Biological Process, GO-BP) of the functionality interacting network clusters derived from the genes in the 29 replicated pathways.

Cluster	Genesets	BaitsOfOrtologsIn	NumberOfOrtologsIn	BaitsFromHuman	p-value	FDR	NodeSeqIntersection
1	cell cycle arrest	11	116	11	0.0306-05	0.1	CNKN2B,SKI,TGFBR1,SMAD3,CDKN1A,CDKN2B,NEU1,NFC,TP53,PPP1R15A,KAT2B
1	cellular lipid metabolic process	9	112	9	0.0114	0.1	HMGCR,NAMPT,GFPT1,PMCD,HMGCS1,ABCB4,ALAS1,GOS2,PHL2,TAOS1
1	cytoarmin remodeling	8	53	8	0.0052	0.1	HDAC5,HDAC8,HDAC2,HDAC1,NEU1,NFC,KAT2A,KAT2B
1	cellular response to polyglutamic acid	13	138	15	0.0126	0.1	CDY2,CDY1,MAT1A,TADA1,CCC,MYC,SIN3A,CCC,CSE1L,MTR,CDK1,MAT2A,KAP1,CBS
1	6 G1 phase of mitotic cell cycle	34	11	11	0.0033	0.1	CDKN2B,SKP2,RB1,SPC1,CDKN1A,CDKN1B,E2F1,E2F2,E2F3,CCND1
1	histone H3 deacetylation	5	3	3	0.0005	0.1	HDAC6,HDAC1,HDAC2
1	histone deacetylation	18	6	6	0.0018	0.1	HDAC10,HDAC2,HDAC1,HDAC3
1	6 G1 phase of mitotic cell cycle	34	11	11	0.0033	0.1	CDKN2B,SKP2,RB1,SPC1,CDKN1A,CDKN1B,E2F1,E2F2,E2F3,CCND1
1	neutrophil degranulation	62	21	21	0.0061	0.1	MYH9,CFL1,CFL2,GSN,PFN1,PFN2,PLCG1,GRB2,RAC1,MAPK1,MAPK3,RAC2,MAPK14,RHOA,GSK3A
1	negative regulation of cell cycle	72	15	15	0.0071	0.1	MYH9,CFL1,CFL2,GSN,PFN1,PFN2,PLCG1,GRB2,RAC1,MAPK1,MAPK3,RAC2,MAPK14,RHOA,GSK3A
1	negative regulation of growth of whole or part of a cell	8	5	5	0.0018	0.1	HDAC6,HDAC1,HDAC2,HDAC3,CCND1
1	negative regulation of cell cycle	64	17	17	0.0025	0.1	MYH9,MYH10,MYH11,MYH14,CFL1,CFL2,GRB2,RAC1,MAPK1,MAPK3,RAC2,MAPK14,RHOA,GSK3A
1	7 cellular response to amino acid stimulus	33	7	7	0.0033	0.1	CDKN2A,CDKN1A,CDKN1B,CDKN1C,CDKN2B,CDKN2C,CCND1,CCND2,CCND3,CDK4,CDK6,RB1,SKP2,CDC20,CDC27
1	collagen biosynthetic process	4	3	3	0.0004	0.1	COL1A1,COL1A2,COL6A3
1	collagen fibril organization	6	3	3	0.0006	0.1	COL1A1,COL1A2,COL6A3
1	extracellular matrix disassembly	22	6	6	0.0022	0.1	COL1A1,COL1A2,COL6A3,COL9A1,COL9A2,COL9A3
1	extracellular matrix organization	75	14	14	0.0016	0.1	COL1A1,COL1A2,COL11A1,COL11A2,COL12A1,COL14A1,COL15A1,COL16A1,COL4A3,COL5A1,COL5A2,COL5A3,COL6A3,COL9A1,COL9A2,COL9A3
1	collagen metabolic process	33	8	8	0.0033	0.1	COL1A1,COL1A2,COL11A1,COL11A2,COL12A1,COL14A1,COL15A1,COL16A1,COL4A3,COL5A1,COL5A2,COL5A3,COL6A3,COL9A1,COL9A2,COL9A3
1	3 cellular response to fibroblast growth factor stimulus	6	3	3	0.0006	0.1	FGF2,FGF9,FGF18
1	3 cellular response to insulin stimulus	21	7	7	0.0021	0.1	INS,IGF1,IGF2,IGFBP1,IGFBP2,IGFBP3,IGFBP4
1	3 cellular response to platelet-derived growth factor stimulus	8	3	3	0.0008	0.1	PDGFA,PDGFB,PDGFC
1	3 cellular response to vitamin D	8	3	3	0.0008	0.1	VDR,RXRA,RXRB
1	3 cellular response to zinc ion	8	3	3	0.0008	0.1	MTF1,MT1A,MT2A
1	3 collagen fibril organization	14	4	4	0.0014	0.1	COL1A1,COL1A2,COL6A3,COL9A3
1	3 collagen metabolic process	18	5	5	0.0018	0.1	COL1A1,COL1A2,COL6A3,COL9A1,COL9A2
1	3 connective tissue development	75	14	14	0.0016	0.1	COL1A1,COL1A2,COL11A1,COL11A2,COL12A1,COL14A1,ADAMTS2,ADAMTS5,COL15A1,COL16A1,COL4A3,COL5A1,COL5A2,COL5A3,COL6A3,COL9A1,COL9A2,COL9A3
1	3 cellular response to platelet-derived growth factor stimulus	8	3	3	0.0008	0.1	PDGFA,PDGFB,PDGFC
1	3 cellular response to vitamin D	8	3	3	0.0008	0.1	VDR,RXRA,RXRB
1	3 cellular response to zinc ion	8	3	3	0.0008	0.1	MTF1,MT1A,MT2A
1	3 connective tissue development	75	14	14	0.0016	0.1	COL1A1,COL1A2,COL11A1,COL11A2,COL12A1,COL14A1,ADAMTS2,ADAMTS5,COL15A1,COL16A1,COL4A3,COL5A1,COL5A2,COL5A3,COL6A3,COL9A1,COL9A2,COL9A3
1	3 extracellular matrix disassembly	22	6	6	0.0022	0.1	COL1A1,COL1A2,COL6A3,COL9A1,COL9A2,COL9A3
1	3 extracellular matrix organization	75	14	14	0.0016	0.1	COL1A1,COL1A2,COL11A1,COL11A2,COL12A1,COL14A1,ADAMTS2,ADAMTS5,COL15A1,COL16A1,COL4A3,COL5A1,COL5A2,COL5A3,COL6A3,COL9A1,COL9A2,COL9A3
1	3 fibroblast growth factor receptor signaling pathway	8	3	3	0.0008	0.1	FGF2,FGF9,FGF18
1	3 gene expression	40	9	9	0.0040	0.1	CDKN2B,SKP2,RB1,SPC1,CDKN1A,CDKN1B,E2F1,E2F2,E2F3
1	3 insulin receptor signaling pathway	24	7	7	0.0024	0.1	INS,IGF1,IGF2,IGFBP1,IGFBP2,IGFBP3,IGFBP4
1	3 intracellular signal transduction	26	7	7	0.0026	0.1	INS,IGF1,IGF2,IGFBP1,IGFBP2,IGFBP3,IGFBP4
1	3 JUN phosphorylation	4	3	3	0.0004	0.1	MAPK9,MAPK8,MAPK10
1	3 keratinocyte differentiation	20	6	6	0.0020	0.1	CDKN2B,SKP2,RB1,SPC1,CDKN1A,CDKN1B,E2F1,E2F2,E2F3,CCND1
1	3 keratinocyte signal activity	12	4	4	0.0012	0.1	INS,IGF1,IGF2,IGFBP1
1	3 negative regulation of cell cycle	117	17	17	0.0117	0.1	CDKN2B,SKP2,RB1,SPC1,CDKN1A,CDKN1B,E2F1,E2F2,E2F3,CCND1
1	3 negative regulation of cell cycle, G1/S phase	42	6	6	0.0042	0.1	CDKN2B,SKP2,RB1,SPC1,CDKN1A,CDKN1B
1	3 negative regulation of cell proliferation	123	17	17	0.0123	0.1	CDKN2B,SKP2,RB1,SPC1,CDKN1A,CDKN1B,E2F1,E2F2,E2F3,CCND1
1	3 negative regulation of cell-cell signaling	54	9	9	0.0054	0.1	CDKN2B,SKP2,RB1,SPC1,CDKN1A,CDKN1B,E2F1,E2F2,E2F3
1	3 negative regulation of cell-matrix adhesion	20	6	6	0.0020	0.1	CDKN2B,SKP2,RB1,SPC1,CDKN1A,CDKN1B
1	3 negative regulation of cell-substrate adhesion	20	6	6	0.0020	0.1	CDKN2B,SKP2,RB1,SPC1,CDKN1A,CDKN1B
1	3 negative regulation of epithelial cell proliferation	75	14	14	0.0016	0.1	CDKN2B,SKP2,RB1,SPC1,CDKN1A,CDKN1B,E2F1,E2F2,E2F3,CCND1
1	3 negative regulation of epithelial cell proliferation involved in wound healing	4	3	3	0.0004	0.1	CDKN2B,CDKN1A,CDKN1B
1	3 negative regulation of fibroblast proliferation	8	3	3	0.0008	0.1	CDKN2B,CDKN1A,CDKN1B
1	3 negative regulation of G1/S transition of mitotic cell cycle	8	3	3	0.0008	0.1	CDKN2B,CDKN1A,CDKN1B
1	3 negative regulation of growth	8	3	3	0.0008	0.1	CDKN2B,CDKN1A,CDKN1B
1	3 negative regulation of mitotic cell cycle	8	3	3	0.0008	0.1	CDKN2B,CDKN1A,CDKN1B
1	3 negative regulation of mitotic cell cycle, G1/S phase	8	3	3	0.0008	0.1	CDKN2B,CDKN1A,CDKN1B
1	3 negative regulation of neuroblast proliferation	4	3	3	0.0004	0.1	CDKN2B,CDKN1A,CDKN1B
1	3 negative regulation of osteoblast proliferation	4	3	3	0.0004	0.1	CDKN2B,CDKN1A,CDKN1B
1	3 negative regulation of smooth muscle cell proliferation	8	3	3	0.0008	0.1	CDKN2B,CDKN1A,CDKN1B
1	3 neuroblast proliferation	4	3	3	0.0004	0.1	CDKN2B,CDKN1A,CDKN1B
1	3 osteoblast proliferation	4	3	3	0.0004	0.1	CDKN2B,CDKN1A,CDKN1B
1	3 positive regulation of cell cycle arrest	8	3	3	0.0008	0.1	CDKN2B,CDKN1A,CDKN1B
1	3 positive regulation of cell proliferation involved in wound healing	4	3	3	0.0004	0.1	CDKN2B,CDKN1A,CDKN1B
1	3 positive regulation of fibroblast proliferation	8	3	3	0.0008	0.1	CDKN2B,CDKN1A,CDKN1B
1	3 positive regulation of smooth muscle cell proliferation	8	3	3	0.0008	0.1	CDKN2B,CDKN1A,CDKN1B
1	3 regulation of cell-substrate adhesion	20	6	6	0.0020	0.1	CDKN2B,SKP2,RB1,SPC1,CDKN1A,CDKN1B
1	3 regulation of epithelial cell proliferation	75	14	14	0.0016	0.1	CDKN2B,SKP2,RB1,SPC1,CDKN1A,CDKN1B,E2F1,E2F2,E2F3,CCND1
1	3 regulation of fibroblast proliferation	8	3	3	0.0008	0.1	CDKN2B,CDKN1A,CDKN1B
1	3 regulation of neuroblast proliferation	4	3	3	0.0004	0.1	CDKN2B,CDKN1A,CDKN1B
1	3 regulation of osteoblast proliferation	4	3	3	0.0004	0.1	CDKN2B,CDKN1A,CDKN1B
1	3 regulation of smooth muscle cell proliferation	8	3	3	0.0008	0.1	CDKN2B,CDKN1A,CDKN1B
1	3 response to cytokine	54	9	9	0.0054	0.1	CDKN2B,SKP2,RB1,SPC1,CDKN1A,CDKN1B,E2F1,E2F2,E2F3
1	3 response to growth factor	75	14	14	0.0016	0.1	CDKN2B,SKP2,RB1,SPC1,CDKN1A,CDKN1B,E2F1,E2F2,E2F3,CCND1
1	3 response to insulin	20	6	6	0.0020	0.1	CDKN2B,SKP2,RB1,SPC1,CDKN1A,CDKN1B
1	3 response to platelet-derived growth factor	8	3	3	0.0008	0.1	CDKN2B,CDKN1A,CDKN1B
1	3 response to vitamin D	8	3	3	0.0008	0.1	CDKN2B,CDKN1A,CDKN1B
1	3 response to zinc ion	8	3	3	0.0008	0.1	CDKN2B,CDKN1A,CDKN1B
1	3 T-helper 1 cell differentiation	4	3	3	0.0004	0.1	CDKN2B,CDKN1A,CDKN1B
1	3 T-helper 1 cell lineage commitment	4	3	3	0.0004	0.1	CDKN2B,CDKN1A,CDKN1B
1	3 T-helper 2 cell differentiation	4	3	3	0.0004	0.1	CDKN2B,CDKN1A,CDKN1B
1	3 T-helper 2 cell lineage commitment	4	3	3	0.0004	0.1	CDKN2B,CDKN1A,CDKN1B
1	3 transforming growth factor beta receptor signaling pathway	62	11	11	0.0062	0.1	CDKN2B,SKP2,RB1,SPC1,CDKN1A,CDKN1B,E2F1,E2F2,E2F3
1	3 vitamin D receptor signaling pathway	8	3	3	0.0008	0.1	CDKN2B,CDKN1A,CDKN1B
1	3 wound healing, spreading of epithelial cells	4	3	3	0.0004	0.1	CDKN2B,CDKN1A,CDKN1B
1	4 activation of JNK activity	8	4	4	0.0008	0.1	TAB1,MAPK9,MAPK8,MAPK10
1	4 activation of protein kinase activity	15	5	5	0.0015	0.1	TAB1,MAPK9,MAPK8,MAPK10,MAPK12
1	4 activation of phospholipase A2 activity	50	8	8	0.0050	0.1	PRKCB,MAPK9,MAPK8,MAPK10,MAPK12,MAPK14,PRKCD,PRKCE,PRKCG,PRKCH,PRKCQ,PLCB1,AGT,TP53,RPS6KA5,CALM1
1	4 activation of MAPKK activity	50	8	8	0.0050	0.1	MAPK9,MAPK8,MAPK10,MAPK12,MAPK14,PRKCB,PRKCD,PRKCE,PRKCG,PRKCH,PRKCQ
1	4 activation of phospholipase A2 activity	15	5	5	0.0015	0.1	PRKCB,PRKCD,PRKCE,PRKCG,PRKCH
1	4 activation of protein kinase C activity	26	6	6	0.0026	0.1	PRKCB,PRKCD,PRKCE,PRKCG,PRKCH,PRKCQ
1	4 activation of transcription factor activity	8	4	4	0.0008	0.1	PRKCB,PRKCD,PRKCE,PRKCG
1	4 activation of transcription factor binding	15	5	5	0.0015	0.1	PRKCB,PRKCD,PRKCE,PRKCG,PRKCH

Supplementary Table 6. Models to predict the presence of Degree and Assessment. The given percentage is the coefficient (Exp(coef.)) – 100% of variation

Variable	Coef.	Exp(coef.)	Pr(>|z|)	Coef.	Exp(coef.)	Pr(>|z|)	Coef.	Exp(coef.)	Pr(>|z|)	Coef.	Exp(coef.)	Pr(>|z|)
(Intercept)	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Degree.Bachelor's degree	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Degree.Doctorate	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Degree.Master's	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Degree.Other	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Degree.Other degree	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Degree.Other degree or certificate	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Degree.Pre-school	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Degree.Primary	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Degree.Secondary	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Degree.Technical	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Degree.Vocational	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Female	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Male	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Other	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Female	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Male	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Male/Female	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Male/Female/Other	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Male/Female/Other/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Male/Female/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Male/Other	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Male/Other/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Male/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Other	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Other/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Prefer not to answer/Other	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Prefer not to answer/Other/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Prefer not to answer/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Female	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Female/Male	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Female/Male/Other	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Female/Male/Other/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Female/Male/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Female/Other	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Female/Other/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Female/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Male	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Male/Female	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Male/Female/Other	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Male/Female/Other/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Male/Female/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Male/Other	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Male/Other/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Male/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Other	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Other/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Prefer not to answer/Other	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Prefer not to answer/Other/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Prefer not to answer/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Female	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Female/Male	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Female/Male/Other	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Female/Male/Other/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Female/Male/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Female/Other	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Female/Other/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Female/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Male	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Male/Female	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Male/Female/Other	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Male/Female/Other/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Male/Female/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Male/Other	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Male/Other/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Male/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Other	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Other/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Prefer not to answer/Other	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Prefer not to answer/Other/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Prefer not to answer/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Female	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Female/Male	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Female/Male/Other	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Female/Male/Other/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Female/Male/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Female/Other	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Female/Other/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Female/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Male	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Male/Female	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Male/Female/Other	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Male/Female/Other/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Male/Female/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Male/Other	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Male/Other/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Male/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Other	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Other/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Prefer not to answer/Other	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Prefer not to answer/Other/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Prefer not to answer/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Female	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Female/Male	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Female/Male/Other	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Female/Male/Other/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Female/Male/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Female/Other	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Female/Other/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Female/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Male	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Male/Female	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Male/Female/Other	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Male/Female/Other/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Male/Female/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Male/Other	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Male/Other/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Male/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Other	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Other/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Prefer not to answer/Other	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Prefer not to answer/Other/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Prefer not to answer/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Transgender Female	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Transgender Female/Male	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Transgender Female/Male/Other	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Transgender Female/Male/Other/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Transgender Female/Male/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Transgender Female/Other	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Transgender Female/Other/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Transgender Female/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Transgender Male	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Transgender Male/Female	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Transgender Male/Female/Other	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Transgender Male/Female/Other/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Transgender Male/Female/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Transgender Male/Other	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Transgender Male/Other/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Transgender Male/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Transgender Other	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Transgender Other/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Transgender Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Transgender Prefer not to answer/Other	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Transgender Prefer not to answer/Other/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Transgender Prefer not to answer/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Transgender Transgender Female	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Transgender Transgender Female/Male	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Transgender Transgender Female/Male/Other	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Transgender Transgender Female/Male/Other/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Transgender Transgender Female/Male/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Transgender Transgender Female/Other	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Transgender Transgender Female/Other/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Transgender Transgender Female/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Transgender Transgender Male	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Transgender Transgender Male/Female	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Transgender Transgender Male/Female/Other	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender Transgender Transgender Transgender Transgender Transgender Male/Female/Other/Prefer not to answer	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000	0.000	1.000	0.000
Sex.Transgender Transgender