xMWAS: R package for data integration and network analysis

xMWAS: an R package for data-driven integration and differential network analysis

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Abstract

Summary: Integrative omics is a central component of most systems biology studies. Computational methods are required for extracting meaningful relationships across different omics layers. Various tools have been developed to facilitate integration of paired heterogeneous omics data; however most existing tools allow integration of only two omics datasets. Furthermore, existing data integration tools do not incorporate additional steps of identifying sub-networks or communities of highly connected entities and evaluating the topology of the integrative network under different conditions. Here we present xMWAS, an R package for data integration, network visualization, clustering, differential network analysis of data from biochemical and phenotypic assays, and two or more omics platforms.

Availability: <https://sourceforge.net/projects/xmwas/>

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1 Introduction

Technological advances have led to a major paradigm shift where multi-assay molecular profiling of biological samples is increasingly being used to understand molecular mechanisms for diseases and host responses to environmental exposures (Hawkins 2010, Cancer Genome Atlas Network 2008). Most cellular processes in a biological system are dependent on complex molecular interactions (Barabasi 2011). Integrative omics allows researchers to address such complexity and answer challenging biological questions, such as function of genetic variants and unknown metabolites, mechanisms of gene regulation, signaling and metabolic pathway responses to infection and toxicity (Hawkins 2010, Chandler 2016, Uppal 2016).

Numerous data-driven/unsupervised and knowledge-based tools allow integration of data from different omics technologies and other molecular assays (Wanichthanarak 2015, Meng 2016). Most existing data integration tools allow integration of only two datasets and do not allow identification of community structure and evaluation of network changes between different conditions. Community detection reveals topological modules comprised of functionally related biomolecules (Barabasi 2011, Yang 2016). Differential network analysis (DiNA) allows characterization of

nodes that undergo changes in topological characteristics between different conditions, e.g. healthy vs disease (Lichtblau 2016).

To advance these capabilities, we present, xMWAS, an R package that provides an automated workflow for integrative analysis of more than two datasets, differential network analysis, and community detection to improve our understanding of complex molecular interactions and disease mechanisms.

Fig. 1. xMWAS workflow. A. Pairwise data integration and association analysis is performed using (sparse) partial least squares regression. The edge list matrices of significant associations from each pairwise comparison are merged to generate a global association network. Community detection is performed using the multilevel algorithm. B. Illustration of association network for the NCI60 dataset (Meng 2016): microRNAs (triangle), protein (circle) and transcripts (rectangle). C. Identification of communities in the NCI60 integrated network using the multilevel community detection algorithm.

2 Implementation

xMWAS provides an automated framework for integrative and differential network analysis. Figure 1A provides an overview of different stages of xMWAS. In stage one, xMWAS uses dimension reduction techniques such as Partial Least Squares (PLS), sparse Partial Least Squares (sPLS), and multilevel sparse Partial Least Squares (msPLS; for repeated measures) regression for

pairwise integrative and association analysis between data matrices (Le Cao 2009, Liqueur 2012, Gonzalez 2012). sPLS and msPLS methods perform simultaneous data integration and variable selection using a LASSO penalty for the loading vectors, which reduces the complexity of the networks (Liqueur 2012). R package *pls* is used to determine the optimal number of latent components. The *network()* function in the *mixOmics* package is used to generate the association matrix, A_{XY} , between matrices X and Y (Le Cao 2009, Gonzalez 2012). Student's t-test is used to evaluate the statistical significance of association scores. Only the associations that satisfy the user-defined thresholds, e.g. $|\text{association score}| > 0.7$ and $p\text{-value} < 0.01$, are used for downstream analysis. The resulting graph, $G_i = (V, E)$, where V is a set of nodes and E is a set of edges, is used to generate an edge list matrix, L_i , such that each row in L_i corresponds to an edge between nodes X_p and Y_q . The same process is repeated for generating edge list matrices from all pairwise association analyses between datasets, e.g. $L_i = \text{cor}(X, Y)$; $L_j = \text{cor}(Y, Z)$, and $L_k = \text{cor}(X, Z)$.

In stage two, the union of the individual edge list matrices from pairwise integrative analysis of the n datasets is used to generate a combined edge list matrix, $L_e = \bigcup_{i=1}^n L_i$. Matrix L_e is used to generate the integrative network graph, $G = (V, E)$, where V corresponds to nodes and E corresponds to edges or connections between the nodes, representing positive or negative associations between multiple datasets (Figure 1B). Network graphics are generated using the *igraph* package in R.

In stage three, the multilevel community detection algorithm (Blondel 2008) is used to identify communities of nodes that are tightly connected with each other, but sparsely connected with the rest of the network (Figure 1C). Comparative studies for community detection algorithms show that the multilevel algorithm is suitable for both small and large networks with varying connectivity patterns (Yang 2016). The quality of the community structure is evaluated using the network modularity measure (Newman 2006).

Differential network analysis is performed using the differential betweenness centrality and differential eigenvector centrality methods to identify nodes that undergo changes in their topological characteristics (Odibat 2012, Lichtblau 2016). Additional description about the software input and output is provided in Supplementary Section S1.

3 Example

We tested xMWAS in a three-way integrative analysis using cytokine, transcriptome, and metabolome datasets from a recently published study to examine H1N1 influenza virus infection-altered metabolic response in mouse lung (Chandler 2016). For comparisons, we used data from all samples (Supplementary Figure S1A), only control samples (Supplementary Figure S1B), and only H1N1 influenza samples (Supplementary Figure S1C). Supplementary Section S2 shows that the various stages of xMWAS capture biologically meaningful information and provide deeper insights into the underlying biology, which cannot be obtained by analyzing and exploring the different layers individually.

4 Conclusion

xMWAS provides a platform-independent framework for integrative network analysis of two or more datasets, identification of modules of functionally related biomolecules, and differential network analysis. The results show that xMWAS can improve our understanding of disease pathophysiology and complex molecular interactions across various functional levels.

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Conflict of Interest: none declared.

References

- Barabasi, A.L. et al. (2011) Network medicine: a network-based approach to human disease. *Nat Rev Genet*, 12, 56-68.
- Blondel VD. et al. (2008) Fast unfolding of communities in large networks. *Journal of Statistical Mechanics: Theory and Experiment*, 2008, P10008.
- Cancer Genome Atlas Research Network. (2008) Comprehensive genomic characterization defines human glioblastoma genes and core pathways. *Nature*, 455,1061-1068.
- Chandler JD. et al. (2016) Metabolic pathways of lung inflammation revealed by high-resolution metabolomics (HRM) of H1N1 influenza virus infection in mice. *Am J Physiol Regul Integr Comp Physiol*,311, R906-R916.
- Gonzalez, I. et al. (2012) Visualising associations between paired 'omics' data sets. *BioData Min*, 5, 19.
- Hawkins, R.D. et al. (2010) Next-generation genomics: an integrative approach. *Nat Rev Genet*, 11,476-486.
- Le Cao, K.A. et al. (2009) integrOmics: an R package to unravel relationships between two omics datasets. *Bioinformatics*, 25, 2855-2856.
- Lichtblau, Y. et al. (2016) Comparative assessment of differential network analysis methods. *Brief Bioinform* 2016.
- Liquet, B. et al. (2012) A novel approach for biomarker selection and the integration of repeated measures experiments from two assays. *BMC Bioinformatics*, 13, 325.
- Meng C. et al.. (2016) Dimension reduction techniques for the integrative analysis of multi-omics data. *Brief Bioinform*, 17, 628-41.
- Newman, M.E. (2006) Modularity and community structure in networks. *Proc Natl Acad Sci U S A*, 103, 8577-8582.
- Odibat, O. and Reddy, C.K. (2012) Ranking differential hubs in gene co-expression networks. *J Bioinform Comput Biol*, 10, 1240002.
- Uppal, K. et al. (2016) Computational Metabolomics: A Framework for the Million Metabolome. *Chem Res Toxicol*, 29, 1956-1975.
- Yang, Z.. et al. (2016) A Comparative Analysis of Community Detection Algorithms on Artificial Networks. *Sci Rep*, 6,30750.
- Wanichthanarak K. et al. (2015) Genomic, Proteomic, and Metabolomic Data Integration Strategies. *Biomark Insights*,10, 1-6.

Supplementary Material

xMWAS: an R package for data-driven integration and differential network analysis

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Supplementary Section S1. Description of input and output for xMWAS

The main input parameters include file paths or data matrices of input datasets, file with phenotypic labels (e.g. case, control), integration method (“pls”, “spl”), threshold for association score, and statistical significance. The software is designed to work with data from different sources and does not utilize any knowledgebase information for integration. For metabolomics studies, the software is designed to work with both targeted and untargeted datasets and does not require metabolite identification prior to integration. The output includes PDF of integrative network with cluster assignments, text files for association matrices and cluster assignments for each node and their centrality scores, and a GML format file that can be used for visualization with tools such as Cytoscape (Shannon 2003).

Figure S1. Integrative network analysis of cytokine, metabolome and transcriptome datasets from a study of H1N1 virus infection of mice. A. All samples; B. Only control samples; C. Only H1N1 infected samples. The results show that xMWAS analysis of the complex omics arrays allows identification and visualization of metabolite and transcript correlations with cytokines. The analysis further discriminates between correlations observed in controls from those observed in H1N1 virus infected mice and allows identification of nodes that undergo network changes. Details are provided in Supplementary Section S2.

Supplementary Section S2. Evaluation results using data from the H1N1 virus infection of mice

Pathway analysis of metabolic features (m/z and retention time) and genes that were significantly associated with cytokines at $p < 0.05$ across all samples was performed using Mummichog and MetaCore, respectively. Pathways related to immune response, lipid metabolism, amino acids metabolism, nitrogen metabolism, drug metabolism, vitamin metabolism, cytoskeleton remodeling, cell signaling, and energy metabolism were significantly enriched (Supplementary Tables S1 and S2). Previous studies have shown the role of these pathways in regulation of immune response and inflammation (Miyake 2000, Fortin 2009, Sadik 2012, Yin 2014, Chandler 2016)

Differential centrality analysis between control vs H1N1 samples showed dramatic change in the centrality of cytokines as well as genes and metabolites involved in immune response and defense mechanism (Supplementary Tables S3-6). Cytokines are known to be involved in the recruitment of the inflammatory cells and influence the adaptive immune response during influenza (Vareille 2011, Liu 2016, Chandler 2016).

Multilevel community detection identified four clusters in the integrative network generated using only H1N1 samples (Supplementary Figure S1C). Cluster 2 (blue), which comprised of four cytokines, 830 genes, and 437 metabolic features, was evaluated for significantly enriched pathways and biological processes. Pathway analysis of the metabolic features in this cluster showed enrichment of similar pathways as in the cytokine x metabolome association analysis across all samples described above (Supplementary Table S7). Pathway and process enrichment analysis using MetaCore showed enrichment of genes involved in immune responses, protein folding, signaling mechanisms, and various biological processes related to cilium movement, organization, assembly and organization (Supplementary Tables S8-S10). Previous studies have shown that the airway epithelium acts as a first layer of defense mechanism against respiratory viruses and that the respiratory viruses can lead to ciliary impairment (Vareille 2011).

xMWAS: R package for data integration and network analysis

Supplementary Table S1. Pathway analysis of metabolic features (*m/z* and retention time) that were found to be significantly associated with the six cytokines at $p < 0.05$ using Mummichog

Pathway Name	IL-1beta	IL-6	IL-10	TNFalpha	IP-1	IFNgamma
Carnitine shuttle	x	x	x	x	x	
Glycosphingolipid metabolism	x	x	x	x	x	
Vitamin D ₃ (cholecalciferol) metabolism	x	x	x	x	x	
Vitamin B ₆ (pyridoxine) metabolism		x		x	x	x
Bioppterin metabolism	x	x		x	x	
Saturated fatty acids beta-oxidation		x		x	x	
Vitamin E metabolism	x		x	x		
Nitrogen metabolism		x			x	
Urea cycle/amino group metabolism					x	x
Drug metabolism - cytochrome P450					x	x
Tryptophan metabolism					x	x
Arginine and proline metabolism						x
Bile acid biosynthesis				x		
Fatty acid metabolism			x			
Limonene and pinene degradation			x			
Linoleate metabolism			x			
Tyrosine metabolism		x				

Supplementary Table S2. Pathway analysis of genes that were found to be significantly associated with the six cytokines at $p < 0.05$ using MetaCore

Pathway Name	IL-1beta	IL-6	IL-10	TNFalpha	IP-1	IFNgamma
Immune response_Alternative complement pathway	x	x	x	x	x	x
GTP metabolism	x	x	x	x	x	
Cytoskeleton remodeling_TGF, WNT and cytoskeletal remodeling	x	x		x	x	x
Cytoskeleton remodeling_Cytoskeleton remodeling	x	x		x	x	x
Alternative complement cascade disruption in age-related macular degeneration	x	x		x	x	x
ATP metabolism	x	x		x	x	
Immune response_Lectin induced complement pathway		x	x		x	x
Regulation of lipid metabolism_Regulation of lipid metabolism by niacin and isoprenaline	x	x		x		
Development_Oligodendrocyte differentiation from adult stem cells		x			x	x
Cell adhesion_Chemokines and adhesion	x			x		
Expression targets of Tissue factor signaling in cancer	x			x		
Cell adhesion_ECM remodeling		x				x
Immune response_Classical complement pathway			x			x
Development_Regulation of epithelial-to-mesenchymal transition (EMT)					x	x
Protein folding and maturation_Insulin processing			x			
Glucocorticoid-induced elevation of intraocular pressure as glaucoma risk factor						x
Inhibition of neutrophil migration by proresolving lipid mediators in COPD						x

xMWAS: R package for data integration and network analysis

Supplementary Table S3. Eigenvector centrality measures for cytokines with delta centrality (control vs H1N1) greater than 0.3

Name	All samples	Control	H1N1	Delta (Control vs H1N1)
IL-10	0.61	0.00	1.00	1.00
IL-1beta	0.66	0.00	0.98	0.98
TNF-alpha	0.66	0.00	0.88	0.88
IL-6	0.34	0.50	0.00	0.50

Supplementary Table S4. Pathway analysis of metabolic features with delta centrality (control vs H1N1) greater than 0.3 using Mummichog

Pathways	Overlap_size	Pathway_size	p
Carnitine shuttle	16	18	0.00065
Vitamin D3 (cholecalciferol) metabolism	10	10	0.00065
Phytanic acid peroxisomal oxidation	4	4	0.00115
De novo fatty acid biosynthesis	8	14	0.00134
Leukotriene metabolism	11	23	0.00174
Valine, leucine and isoleucine degradation	10	22	0.00278
Fatty acid activation	6	11	0.00288
Fatty Acid Metabolism	6	11	0.00288
Vitamin E metabolism	7	15	0.00474
Squalene and cholesterol biosynthesis	7	15	0.00474
Pyruvate Metabolism	7	15	0.00474
Omega-6 fatty acid metabolism	2	2	0.01496
Benzoate degradation via CoA ligation	2	2	0.01496
Fatty acid oxidation, peroxisome	2	2	0.01496
Di-unsaturated fatty acid beta-oxidation	2	2	0.01496
Prostaglandin formation from arachidonate	14	40	0.01604
Biopterin metabolism	5	12	0.01882
Bile acid biosynthesis	16	47	0.01928
Glycosphingolipid metabolism	8	22	0.02174
Vitamin B5 - CoA biosynthesis from pantothenate	3	6	0.02583
Tryptophan metabolism	16	49	0.03124
Saturated fatty acids beta-oxidation	2	3	0.03833
Glyoxylate and Dicarboxylate Metabolism	3	7	0.04628

Supplementary Table S5. Pathway analysis of genes with delta centrality (control vs H1N1) greater than 0.3 using MetaCore. Only the top 20 significant pathways at FDR<0.1 are shown here.

Pathway Maps	Total	<i>p</i>	FDR	In D at a	Network Objects from Active Data
Expression targets of Tissue factor signaling in cancer	22	2.429E-04	5.928E-02	5	Tissue factor, PAR2, NFKBIE, PLA2 (UPA), CSF1
Signal transduction_Soluble CXCL16 signaling	49	3.036E-04	5.928E-02	7	STAT3, HIF1A, I-kB, JAK2, P-selectin, CD163, NF-kB
Immune response_IL-12 signaling pathway	23	3.036E-04	5.928E-02	5	STAT3, IRF1, JAK2, P-selectin, Perforin
Immune response_IFN alpha/beta signaling pathway	24	3.752E-04	5.928E-02	5	IRF1, STAT2, PTP-1B, PML, USP18
Development_Leptin signaling via JAK/STAT and MAPK cascades	25	4.588E-04	5.928E-02	5	STAT3, HIF1A, JAK2, cPLA2, PTP-1B
Platelet activation during ADAM-TS13-deficient thrombotic microangiopathy development	28	7.946E-04	7.381E-02	5	Calpain 1(mu), P-selectin, Histone H4, CD36, Fc gamma RII alpha
Retinal ganglion cell damage in glaucoma	44	1.059E-03	7.381E-02	6	Calpain 1(mu), TNF-R1, P2X7, Sortilin, NF-kB, MAP1LC3B
Myeloid-derived suppressor cells and M2 macrophages in cancer	64	1.560E-03	7.381E-02	7	STAT3, IRF8, ARG1, HIF1A, NF-kB, IL4RA, CSF1
Chemotaxis_CCR1 signaling	48	1.684E-03	7.381E-02	6	STAT3, I-kB, cPLA2, CCR1, NF-kB, CCL7
Bacterial infections in CF airways	48	1.684E-03	7.381E-02	6	IRF1, IKK-epsilon, MyD88, JAK2, Cathepsin S, NF-kB
Immune response_CD40 signaling	65	1.709E-03	7.381E-02	7	STAT3, IRF1, CCL2, I-kB, JAK2, Lyn, NF-

xMWAS: R package for data integration and network analysis

					kB
SLE genetic marker-specific pathways in antigen-presenting cells (APC)	84	1.813E-03	7.381E-02	8	IRF1, IKK-epsilon, IRF8, MyD88, I-kB, MICB, NF-kB, Fc gamma RII alpha
G-protein signaling_G-Protein alpha-q signaling cascades	34	1.973E-03	7.381E-02	5	I-kB, PKC-epsilon, RGS3, NF-kB, LARG
Development_GM-CSF signaling	50	2.085E-03	7.381E-02	6	STAT3, CCL2, I-kB, JAK2, Lyn, NF-kB
Transcription_Role of Akt in hypoxia induced HIF1 activation	21	2.118E-03	7.381E-02	4	Heme oxygenase 1, HIF1A, GLUT1, PGK1
Immune response_Inflammasome in inflammatory response	35	2.253E-03	7.381E-02	5	TNF-R1, P2X7, I-kB, Nod1, NF-kB
Development_Angiopoietin - Tie2 signaling	35	2.253E-03	7.381E-02	5	STAT3, I-kB, GRB7, NF-kB, NCK1
Signal transduction_NF-kB activation pathways	51	2.311E-03	7.381E-02	6	MyD88, TNF-R1, NF-kB2 (p52), I-kB, NF-kB2 (p100), NF-kB
Immune response_IL-15 signaling via JAK-STAT cascade	22	2.535E-03	7.381E-02	4	STAT3, IL-15, JAK2, STAT2
LRRK2 and immune function in Parkinson's disease	22	2.535E-03	7.381E-02	4	I-kB, JAK2, FCGR3A, NF-kB

Supplementary Table S6. Process networks enrichment analysis of genes with delta centrality (control vs H1N1) greater than 0.3 using MetaCore.

Process networks	Total	<i>p</i>	FDR	In Data	Network Objects from Active Data
Development_Regulation of angiogenesis	222	5.828E-05	4.303E-03	23	Ephrin-A, STAT3, IL-15, CCL2, S2P, HIF1A, I-kB, JAK2, HNF4-alpha, Osteonectin, Prolyl endopeptidase, Ephrin-B2, Ephrin-B, CCR1, Galpha(q)-specific peptide GPCRs, NF-kB, Ephrin-A1, BTG1, Ihh, PKC, NCK1, Hedgehog, Syndecan-3
Immune response_Antigen presentation	197	8.134E-05	4.303E-03	21	STAT3, PSMB1, RFX5, TNF-R1, NF-kB2 (p52), I-kB, JAK2, PSMD3, IP-30, STAT2, Cathepsin S, MICB, AP-3 beta subunits, PSMD14, NF-kB2 (p100), NFKBIE, NFKBIA, PSMB2, Legumain, NF-kB, TAP2 (PSF2)
Immune response_Phagosome in antigen presentation	243	8.663E-05	4.303E-03	24	PSMB1, Vinculin, NF-kB2 (p52), I-kB, PSMD3, CD63, Cathepsin S, FCGR3A, Lyn, Alpha-actinin, PSMD14, NF-kB2 (p100), NFKBIE, NFKBIA, VCP, PSMB2, Legumain, NF-kB, RalGDS, Alpha-actinin 3, TAP2 (PSF2), NCK1, FGR, Fc gamma RII alpha
Immune response_Phagocytosis	222	4.338E-04	1.616E-02	21	IL-15, Myosin I, Vinculin, NF-kB2 (p52), I-kB, MyHC, CD63, PKC-epsilon,

					FCGR3A, Lyn, Alpha-actinin, NF-kB2 (p100), NFKBIE, NFKBIA, MRLC, NF-kB, Alpha-actinin 3, HDL proteins, NCK1, FGR, Fc gamma RII alpha
Inflammation_Interferon signaling	110	7.078E-04	2.109E-02	13	STAT3, IRF1, IRF8, CCL2, JAK2, STAT2, MICB, Pyrin (MEFV), PTP-1B, TAP2 (PSF2), PML, GBP2, CCL7
Development_Blood vessel morphogenesis	228	1.520E-03	3.632E-02	20	STAT3, FOXC2, Furin, PLGF, PDE, HIF1A, Neuregulin 1, Galpha(q)-specific nucleotide-like GPCRs, VEGF-D, Galpha(q)-specific amine GPCRs, MMP-19, CCR1, FOXC1/2, ErbB4, PGK1, Galpha(q)-specific peptide GPCRs, GRB7, NF-kB, NCK1, FGF1
Inflammation_Protein C signaling	108	1.932E-03	3.632E-02	12	Tissue factor, MyD88, NF-kB2 (p52), I-kB, PAR2, Alpha-actinin, NF-kB2 (p100), NFKBIE, NFKBIA, PLA2 (UPA), NF-kB, Alpha-actinin 3
Cell adhesion_Synaptic contact	184	1.950E-03	3.632E-02	17	Ephrin-A, K(+) channel, subfamily J, Syntaxin 1A, GluR3, Synaptotagmin, GABA-A receptor beta-2 subunit, Ephrin-B2, Ephrin-B, Ephrin-B2 (CTF2), Alpha-actinin, SHANK, GABA-A receptor alpha-5 subunit, SHANK2, Neuroligin, Alpha-actinin 3, NCK1, Neuroligin 3

Supplementary Table S7. Pathway analysis of the 437 metabolic features in cluster 2 in the H1N1 integrative network using Mummichog

Pathways	Overlap_size	Pathway_size	<i>p</i>
Carnitine shuttle	9	18	0.00036
Vitamin D ₃ (cholecalciferol) metabolism	6	10	0.00037
Linoleate metabolism	7	21	0.00050
Vitamin E metabolism	5	15	0.00081
Glycosphingolipid metabolism	6	22	0.00100
Bile acid biosynthesis	10	47	0.00108
Saturated fatty acids beta-oxidation	2	3	0.00305
Pyruvate Metabolism	3	15	0.01784
C21-steroid hormone biosynthesis and metabolism	9	64	0.02414

Supplementary Table S8. Pathway analysis of the 830 genes in cluster 2 in the H1N1 integrative network using MetaCore

Pathway	Total	<i>p</i>	FDR	In Data	Network Objects from Active Data
Protein folding and maturation_Insulin processing	20	2.16E-10	1.45E-07	9	Des (64,65) proinsulin, Split (32,33) proinsulin, Insulin processed, Di-arginyl insulin, Proinsulin C-peptide, Split (64,65) proinsulin, Insulin, Proinsulin, Des(31,32) proinsulin
Immune response_IL-15 signaling via JAK-STAT cascade	22	1.20E-04	3.02E-02	5	STAT3, IL-15, JAK2, sIL-15RA, IL-15RA
Immune response_Lectin induced complement pathway	50	1.38E-04	3.02E-02	7	C2, C2b, C4a, C4, C2a, C3 convertase (C2aC4b), C4b
Immune response_Classical complement pathway	53	2.00E-04	3.02E-02	7	C2, C2b, C4a, C4, C2a, C3 convertase (C2aC4b), C4b
Role of IL-23/ T17 pathogenic axis in psoriasis	54	2.25E-04	3.02E-02	7	STAT3, IL-15, sIL-15RA, IL-15RA, CD86, CD40(TNFRSF5), HLA-C
Main growth factor signaling cascades in multiple myeloma cells	41	3.26E-04	3.64E-02	6	STAT3, MEK1(MAP2K1), HIF1A, I-kB, FGFR3, PI3K reg class IA
Cell adhesion_Integrin inside-out signaling in neutrophils	77	3.84E-04	3.67E-02	8	MEK1(MAP2K1), ARF6, LTBR1, MEK1/2, Cytohesin1, Lyn, Hck, GRO-1
Development_c-Kit ligand signaling pathway during hemopoiesis	61	4.84E-04	4.06E-02	7	STAT3, MGF, MEK1/2, DOK1, JAK2, Lyn, SLUG
Immune response_Fc gamma R-mediated phagocytosis in macrophages	46	6.16E-04	4.59E-02	6	ARF6, Vinculin, Lyn, Hck, Profilin, PI3K reg class IA
Immune response_CD40 signaling	65	7.15E-04	4.79E-02	7	STAT3, I-kB, JAK2, Lyn, A20, CD86, CD40(TNFRSF5)
Development_NOTCH-induced EMT	19	8.19E-04	4.85E-02	4	HEY1, VE-cadherin, NOTCH4, SLUG
Signal transduction_Soluble CXCL16 signaling	49	8.69E-04	4.85E-02	6	STAT3, HIF1A, I-kB, MEK1/2, JAK2, CD163
Development GM-CSF sig-	50	9.68E-04	4.99E-02	6	STAT3, MEK1(MAP2K1),

xMWAS: R package for data integration and network analysis

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I-kB, JAK2, Lyn, Hck

Supplementary Table S9. Process networks enrichment analysis of the 830 genes in cluster 2 in the H1N1 integrative network using MetaCore. Only the top 50 significantly enriched process networks are shown here.

Process networks	Total	<i>p</i>	FDR	In Data	Network Objects from Active Data
Immune re-sponse_Phagosome in antigen presentation	243	7.255E-05	1.110E-02	22	PSMA4, NFKBIB, ARF6, Vinculin, I-kB, PSMD3, Profilin II, Lyn, PSMA1, Alpha-actinin, PSMD14, Hck, TLR4, PSMA2, Profilin, PSMD12, HLA-C, HLA-B, Alpha-actinin 3, PI3K reg class IA (p55-gamma), NCK1, PI3K reg class IA
Immune re-sponse_Antigen presentation	197	2.965E-04	2.269E-02	18	PSMA4, STAT3, NFKBIB, RFX5, PSMD8, I-kB, JAK2, PSMD3, PSMA1, HLA-E, PSMD14, PSMA2, CD86, CD40(TNFRSF5), PSMD12, HLA-C, HLA-B, CD209
Inflammation_Interferon signaling	110	6.422E-04	3.275E-02	12	STAT3, MEK1(MAP2K1), MEK1/2, JAK2, MxA, Pyrin (MEFV), ISG20, CD86, SSAT, CD40(TNFRSF5), IFNAR2, SERPINB9
Signal transduction_Insulin signaling	171	1.428E-03	5.461E-02	15	Des (64,65) proinsulin, MEK1(MAP2K1), Split (32,33) proinsulin, Insulin processed, JAK2, Diarginyl insulin, Proinsulin C-peptide, PYGM, PKA-reg (cAMP-dependent), Split (64,65) proinsulin, Insulin, Proinsulin, Des(31,32) proinsulin, FADS2, PI3K reg class IA

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Cell adhesion_Synaptic contact	184	2.936E- 03	7.812E- 02	15	Syntaxin 4, Synaptotag- min II, Synaptotagmin, Profilin II, Ephrin-B2, Ephrin-B, Ephrin-B2 (CTF2), Alpha-actinin, SHANK, SynGAP, Profilin, SHANK2, Al- pha-actinin 3, Syntenin 1, NCK1
Immune re- sponse_Phagocytosis	222	3.063E- 03	7.812E- 02	17	IL-15, NFKBIB, Vincu- lin, I-kB, MyHC, Pro- filin II, Lyn, Alpha- actinin, IL-15RA, Hck, TLR4, Profilin, Alpha- actinin 3, HDL pro- teins, PI3K reg class IA (p55-gamma), NCK1, PI3K reg class IA

Supplementary Table S10. GO processes analysis of the 830 genes in cluster 2 in the H1N1 integrative network using MetaCore. Only the top 50 significantly enriched GO processes are shown here.

GO Processes	Total	<i>p</i>	FDR	In Data	Network Objects from Active Data
cell projection assembly	367	1.09E-20	7.54E-17	51	FLJ13305, DNAH5, Dystrophin, CCDC39, SPEF2, ARMC4, DNAH1, SPAG17, Vinculin, IQCG, Rab8B, RABL2A, P2X7, DZIP1L, ATP6M, MIP-T3, LRRC50, MyHC, BBS9, WHDC1, Dynein, axonemal, heavy chains, RPGRIP1L, Oxygen-regulated protein 1, CFA54, MYH10, Dynein 2, cytoplasmic, heavy chain, CFA74, SPAG16, Alpha-actinin, RFX3, RAP2C, ABBA, KIAA1377(HIP5), CLR3, CYFIP1, HYDIN, TSGA2, CCDC176, DNAI1, DZIP, FGD3, Dynein, axonemal, intermediate chains, NME5, SNAP-29, Syntenin 1, LRGUK, NCK1, KAD7, C2orf39, RSPH4A, SNX10
cilium assembly	226	1.98E-19	5.75E-16	39	FLJ13305, DNAH5, Dystrophin, CCDC39, SPEF2, ARMC4, DNAH1, SPAG17, IQCG, Rab8B, RABL2A, DZIP1L, ATP6M, MIP-T3, LRRC50, BBS9, Dynein, axonemal, heavy chains, RPGRIP1L, Oxygen-regulated protein 1, CFA54, Dynein 2, cytoplasmic, heavy chain, CFA74, SPAG16, RFX3, KIAA1377(HIP5), CLR3, HYDIN, TSGA2, CCDC176, DNAI1, DZIP, Dynein, axonemal, inter-

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cilium organiza- tion	266	2.49E-19	5.75E-16	42	mediate chains, NME5, SNAP-29, LRGUK, KAD7, C2orf39, RSPH4A, SNX10 FLJ13305, DNAH5, Dystro- phin, CCDC39, SPEF2, ARMC4, DNAH1, SPAG17, IQCG, Rab8B, RABL2A, DZIP1L, ATP6M, MIP-T3, MNS1, LRRC50, BBS9, Dynein, axonemal, heavy chains, RPGRIP1L, Oxygen- regulated protein 1, CFA54, ENO4, Dynein 2, cyto- plasmic, heavy chain, CFA74, SPAG16, RFX3, KIAA1377(HIP5), CLR3, HYDIN, TSGA2, CCDC176, DNAI1, DZIP, Dynein, axonemal, inter- mediate chains, NME5, SNAP-29, LRGUK, KAD7, Nephrocystin-4, C2orf39, RSPH4A, SNX10
cilium morpho- genesis	274	4.97E-18	8.60E-15	41	FLJ13305, DNAH5, Dystro- phin, CCDC39, SPEF2, ARMC4, DNAH1, SPAG17, IQCG, Rab8B, RABL2A, DZIP1L, ATP6M, MIP-T3, LRRC50, BBS9, Dynein, axonemal, heavy chains, RPGRIP1L, Oxygen- regulated protein 1, CFA54, Alpha-parvin, Dynein 2, cytoplasmic, heavy chain, CFA74, SPAG16, RFX3, KIAA1377(HIP5), CLR3, Notch, HYDIN, TSGA2, CCDC176, DNAI1, DZIP, Dynein, axonemal, inter- mediate chains, NME5, SNAP-29, LRGUK, KAD7, C2orf39, RSPH4A, SNX10
cilium movement	61	1.46E-17	2.02E-14	21	DNAH5, CCDC39, ARMC4, DNAH1, SPAG17, Dynein, axonemal, light chains,

					LRRC50, DNAH6, Dynein, axonemal, heavy chains, CFA54, SPAG16, DNAH11, RFX3, Sp17, HYDIN, DNAI1, Dynein, axonemal, intermediate chains, NME5, KAD7, CABYR, RSPH4A
cell projection or- ganization	1348	2.17E-17	2.51E-14	98	FLJ13305, DNAH5, Dystrophin, C1orf88, CCDC39, SPEF2, OSF-2, MEK1(MAP2K1), ARMC4, SLIT3, DNAH1, SNX2, Hap-1, SNX1, Olfactory receptor, ARF6, SPAG17, Vinculin, APOD, HEY1, Dynein, axonemal, light chains, IQCG, Pleckstrin, Rab8B, RABL2A, P2X7, HES1, MEK1/2, B3GN1, ROBO1, DNAH9, JAK2, Islet-1, Galpha(q)-specific nucleotide-like GPCRs, DZIP1L, ATP6M, Rab-3, MIP-T3, MNS1, LRRC50, Ephrin-A receptor 5, FGFR3, MyHC, PMCA2b, Carbohydrate sulfotransferases, BBS9, WHDC1, Dynein, axonemal, heavy chains, RPGRIP1L, Oxygen-regulated protein 1, CFA54, Alpha-parvin, ENO4, MYH10, Lyn, Ephrin-B2, Ephrin-B, Dynein 2, cytoplasmic, heavy chain, NPX1, CFA74, SPAG16, Alpha-actinin, RFX3, MENA, RAP2C, ABBA, Ephrin-A receptors, SHANK, SynGAP, KIAA1377(HIP5), CLR3, Notch, Galpha(q)-specific peptide GPCRs, GFRalpha1, CYFIP1, HYDIN, Rab-3A, TSGA2,

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					ATF/CREB, MAP-1B, CCDC176, DNAI1, DZIP, FGD3, HDL proteins, Dynein, axonemal, intermediate chains, NME5, SNAP-29, Phosphatase regulator (inhibitor), Syntenin 1, LRGUK, NCK1, KAD7, Nephrocystin-4, ABI2, C2orf39, RSPH4A, SNX10
cellular component assembly involved in morphogenesis	360	6.90E-16	6.83E-13	44	FLJ13305, DNAH5, Dystrophin, CARP, CCDC39, SPEF2, ARMC4, DNAH1, SPAG17, IQCG, Rab8B, RABL2A, DZIP1L, ATP6M, MIP-T3, LRRC50, MyHC, BBS9, Dynein, axonemal, heavy chains, RPGRIP1L, Oxygen-regulated protein 1, CFA54, MYH10, Dynein 2, cytoplasmic, heavy chain, PKA-reg (cAMP-dependent), CFA74, SPAG16, Alpha-actinin, RFX3, KIAA1377(HIP5), CLR3, HYDIN, TSGA2, CCDC176, DNAI1, DZIP, Dynein, axonemal, intermediate chains, NME5, SNAP-29, LRGUK, KAD7, C2orf39, RSPH4A, SNX10
axoneme assembly	66	1.47E-15	1.28E-12	20	DNAH5, CCDC39, SPEF2, ARMC4, DNAH1, SPAG17, IQCG, LRRC50, Dynein, axonemal, heavy chains, Oxygen-regulated protein 1, CFA74, SPAG16, HYDIN, TSGA2, DNAI1, Dynein, axonemal, intermediate chains, LRGUK, KAD7, C2orf39, RSPH4A
cell part morphogenesis	923	1.88E-14	1.45E-11	72	FLJ13305, DNAH5, Dystrophin, CCDC39, PDIP38, SPEF2, OSF-2,

					<p>PNPase(old-35), MEK1(MAP2K1), ARMC4, SLIT3, DNAH1, SNX2, SNX1, Olfactory receptor, SPAG17, Vincu- lin, Dynein, axonemal, light chains, IQCG, Rab8B, RABL2A, MEK1/2, B3GN1, ROBO1, Islet-1, Galpha(q)-specific nucleo- tide-like GPCRs, DZIP1L, ATP6M, Rab-3, MIP-T3, LRRC50, Ephrin-A recep- tor 5, FGFR3, MyHC, BBS9, Dynein, axonemal, heavy chains, RPGRIP1L, Oxygen-regulated protein 1, CFA54, Alpha-parvin, MYH10, Ephrin-B2, Ephrin-B, Dynein 2, cyto- plasmic, heavy chain, NPX1, CFA74, SPAG16, RFX3, MENA, Ephrin-A receptors, SHANK, KIAA1377(HIP5), CLR3, Notch, Galpha(q)-specific peptide GPCRs, CYFIP1, HYDIN, Rab-3A, TSGA2, ATF/CREB, MAP-1B, CCDC176, DNAI1, DZIP, Dynein, axonemal, inter- mediate chains, NME5, SNAP-29, LRGUK, KAD7, C2orf39, RSPH4A, SNX10 FLJ13305, DNAH5, Dystro- phin, CCDC39, SPEF2, OSF-2, MEK1(MAP2K1), ARMC4, SLIT3, DNAH1, SNX2, SNX1, Olfactory receptor, SPAG17, Vincu- lin, Dynein, axonemal, light chains, IQCG, Rab8B, RABL2A, MEK1/2, B3GN1, ROBO1, Islet-1, Galpha(q)-specific nucleo- tide-like GPCRs, DZIP1L, ATP6M, Rab-3, MIP-T3,</p>
cell projection morphogenesis	889	2.84E-14	1.97E-11	70	

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					LRRC50, Ephrin-A receptor 5, FGFR3, MyHC, BBS9, Dynein, axonemal, heavy chains, RPGRIP1L, Oxygen-regulated protein 1, CFA54, Alpha-parvin, MYH10, Ephrin-B2, Ephrin-B, Dynein 2, cytoplasmic, heavy chain, NPX1, CFA74, SPAG16, RFX3, MENA, Ephrin-A receptors, SHANK, KIAA1377(HIP5), CLR3, Notch, Galpha(q)-specific peptide GPCRs, CYFIP1, HYDIN, Rab-3A, TSGA2, ATF/CREB, MAP-1B, CCDC176, DNAI1, DZIP, Dynein, axonemal, intermediate chains, NME5, SNAP-29, LRGUK, KAD7, C2orf39, RSPH4A, SNX10
cell morphogenesis	1193	9.55E-14	6.02E-11	83	FLJ13305, DNAH5, Dystrophin, CCDC39, SPEF2, OSF-2, MEK1(MAP2K1), ARMC4, SLIT3, DNAH1, SNX2, SNX1, Olfactory receptor, SPAG17, Vinculin, HEY1, Dynein, axonemal, light chains, IQCG, Rab8B, Ephrin-A receptor 1, HIF1A, RABL2A, FAT3, P2X7, NOTCH4, HES1, MEK1/2, B3GN1, ROBO1, Islet-1, Galpha(q)-specific nucleotide-like GPCRs, DZIP1L, ATP6M, Rab-3, MIP-T3, LRRC50, Ephrin-A receptor 5, FGFR3, MyHC, PMCA2b, BBS9, Dynein, axonemal, heavy chains, RPGRIP1L, Oxygen-regulated protein 1, CFA54, Alpha-parvin, CAP2, MYH10, Ephrin-B2, Ephrin-B, Dynein 2, cytoplasmic, heavy chain,

					NPX1, CFA74, SPAG16, Alpha-actinin, RFX3, SLUG, MENA, Ephrin-A receptors, SHANK, TMEM100, KIAA1377(HIP5), CLR3, Notch, Galpha(q)-specific peptide GPCRs, CYFIP1, HYDIN, Rab-3A, TSGA2, ATF/CREB, MAP-1B, CCDC176, DNAI1, DZIP, Dynein, axonemal, intermediate chains, NME5, SNAP-29, LRGUK, ILPIP, KAD7, C2orf39, RSPH4A, SNX10
microtubule bundle formation	95	2.91E-13	1.68E-10	21	DNAH5, CCDC39, SPEF2, ARMC4, DNAH1, SPAG17, IQCG, LRRC50, Dynein, axonemal, heavy chains, Oxygen-regulated protein 1, CFA74, SPAG16, HYDIN, TSGA2, MAP-1B, DNAI1, Dynein, axonemal, intermediate chains, LRGUK, KAD7, C2orf39, RSPH4A
cilium or flagellum-dependent cell motility	29	3.90E-13	1.77E-10	13	DNAH5, CCDC39, DNAH1, DNAH6, Dynein, axonemal, heavy chains, CFA54, SPAG16, DNAH11, RFX3, Sp17, DNAH3, DNAH2, C2orf39
cellular component morphogenesis	1316	3.93E-13	1.77E-10	87	FLJ13305, DNAH5, Dystrophin, CARP, CCDC39, PDIP38, SPEF2, OSF-2, PNPase(old-35), MEK1(MAP2K1), ARMC4, SLIT3, DNAH1, SNX2, SNX1, Olfactory receptor, SPAG17, Vinculin, HEY1, Dynein, axonemal, light chains, IQCG, Rab8B, Ephrin-A receptor 1, HIF1A, RABL2A, FAT3, P2X7, NOTCH4, HES1, MEK1/2, B3GN1,

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					ROBO1, Islet-1, Galpha(q)-specific nucleotide-like GPCRs, DZIP1L, ATP6M, Rab-3, MIP-T3, LRRC50, Ephrin-A receptor 5, FGFR3, MyHC, PMCA2b, BBS9, Dynein, axonemal, heavy chains, RPGRIP1L, Oxygen-regulated protein 1, CFA54, Alpha-parvin, CAP2, MYH10, Ephrin-B2, Ephrin-B, Dynein 2, cytoplasmic, heavy chain, NPX1, PKA-reg (cAMP-dependent), CFA74, SPAG16, Alpha-actinin, RFX3, SLUG, MENA, Ephrin-A receptors, SHANK, TMEM100, KIAA1377(HIP5), CLR3, Notch, Galpha(q)-specific peptide GPCRs, CYFIP1, HYDIN, Rab-3A, TSGA2, ATF/CREB, MAP-1B, CCDC176, DNAI1, DZIP, Dynein, axonemal, intermediate chains, NME5, SNAP-29, LRGUK, ILPIP, KAD7, C2orf39, RSPH4A, SNX10
microtubule-based movement	297	4.07E-13	1.77E-10	36	KIF21A, DNAH5, CCDC39, MEK1(MAP2K1), ARMC4, DNAH1, Hap-1, SPAG17, Dynein, axonemal, light chains, HIF1A, MEK1/2, DNAH9, MIP-T3, LRRC50, DNAH6, Dynein, axonemal, heavy chains, CFA54, Dynein 2, cytoplasmic, heavy chain, SPAG16, DNAH11, RFX3, Sp17, KIF3B, Huntingtin, HYDIN, DNAH3, MAP-1B, DNAH2, DNAI1, Dynein, axonemal, intermediate chains, NME5,

organelle assembly	692	4.08E-13	1.77E-10	58	DNAH12, KAD7, CABYR, RSPH4A, TCTE3
					FLJ13305, DNAH5, Dystrophin, CARP, CCDC39, WIP11, Rab20, SPEF2, ARMC4, DNAH1, SPAG17, CHMP6, Synaptotagmin, IQCG, Rab8B, RABL2A, P2X7, FLJ32658, DZIP1L, ATP6M, MIP-T3, LRRC50, MyHC, CD34, BBS9, Dynein, axonemal, heavy chains, RPGRIP1L, Oxygen-regulated protein 1, CFA54, MYH10, Dynein 2, cytoplasmic, heavy chain, PKA-reg (cAMP-dependent), CFA74, VTA1, SPAG16, Alpha-actinin, RFX3, KIF3B, SHANK, RPS27, KIAA1377(HIP5), CLR3, Trp53inp2, HYDIN, TSGA2, CCDC176, CCDC52, DNAI1, DZIP, Dynein, axonemal, intermediate chains, NME5, SNAP-29, LRGUK, KAD7, MAP1LC3B, C2orf39, RSPH4A, SNX10
single-organism organelle organization	1928	6.04E-13	2.46E-10	112	Bomapin, STAT3, FLJ13305, DNAH5, Dystrophin, CARP, C2CD4D, MPV17L, CCDC39, WIP11, Rab20, PDIP38, SPEF2, PNPase(old-35), MEK1(MAP2K1), ARMC4, DNAH1, ASCT1 (SLC1A4), Syntaxin 4, ARF6, SPAG17, CHMP6, Synaptotagmin II, Synaptotagmin, Dynein, axonemal, light chains, IQCG, Pleckstrin, Rab8B, VIPAR, ALPK1, RABL2A, FLJ32658, MEK1/2, ALKBH7, JAK2, DZIP1L,

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					ATP6M, Rab-3, MIP-T3, MNS1, LRRC50, MyHC, Carbohydrate sulfotransferases, YSK4, BBS9, WHDC1, WRCH-1, Dynein, axonemal, heavy chains, RPGRIP1L, Oxygen-regulated protein 1, CFA54, Alpha-parvin, ENO4, CAP2, MYH10, Profilin II, MRE11, Dynein 2, cytoplasmic, heavy chain, PKA-reg (cAMP-dependent), CFA74, SPAG16, Alpha-actinin, RFX3, MENA, KIF3B, Bim, SHANK, RPS27, GMIP, NMT1, KIAA1377(HIP5), GRO-1, SPATA18, CLR3, Galpha(q)-specific peptide GPCRs, Huntingtin, Profilin, HYDIN, Rab-3A, TSGA2, FGF10, ATF/CREB, EPS8, MAP1B, CCDC176, CCDC52, DNAI1, DZIP, FGD3, N-myristoyltransferase, PI4KII, Dynein, axonemal, intermediate chains, NUA2, FAT1, ANKFY1, NME5, SNAP-29, Phosphatase regulator (inhibitor), Syntenin 1, LRGUK, VAMP4, NCK1, Beta ad- ducin, KAD7, BET1, Nephrocystin-4, ABI2, MAP1LC3B, C2orf39, RSPH4A, Alpha- internexin, SNX10
movement of cell or subcellular component	1795	1.04E-12	3.99E-10	106	beta-MHC, KIF21A, CD84, STAT3, DNAH5, Dystrophin, CCDC39, MEK1(MAP2K1), ARMC4, SLIT3, DNAH1, PVR, PLET1, LYST, Hap- 1, MGF, Olfactory receptor,

					<p>ARF6, LTBR1, SPAG17, Vinculin, DHSO, Dynein, axonemal, light chains, PDE, HIF1A, RABL2A, FAT3, HES1, MEK1/2, B3GN1, ROBO1, DNAH9, JAK2, Islet-1, Galpha(q)-specific nucleotide-like GPCRs, MIP-T3, LRRC50, Ephrin-A receptor 5, DNAH6, MyHC, CD34, Carbohydrate sulfotransferases, Dynein, axonemal, heavy chains, CFA54, Alpha-parvin, ENO4, MYH10, Lyn, Ephrin-B2, Ephrin-B, Dynein 2, cytoplasmic, heavy chain, STRBP, CAPZA1, SPAG16, Alpha-actinin, DNAH11, GRO-3, RFX3, SLUG, MENA, Ephrin-A receptors, Sp17, KIF3B, DAGK, CCR1, Hck, GRO-1, SPP lyase, CAPZA, CLR3, Notch, SLAM, Galpha(q)-specific peptide GPCRs, Huntingtin, GFRalpha1, HYDIN, CCL27, FGF10, ATF/CREB, EPS8, C4orf31, DNAH3, MAP1B, CAPZA2, DNAH2, DNAI1, Alpha-actinin 3, HDL proteins, Dynein, axonemal, intermediate chains, FAT1, PLTP, NME5, Syntenin 1, NCK1, RANK(TNFRSF11A), DNAH12, KAD7, Nephrocystin-4, ABI2, CABYR, PI3K reg class IA, C2orf39, RSPH4A, CCNYL1, PSTPIP2, TCTE3</p>
anatomical structure formation involved in	1410	6.56E-12	2.39E-09	88	<p>FLJ13305, DNAH5, Dystrophin, CARP, IL-15, CCDC39, SF3B14a,</p>

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morphogenesis					SPEF2, MEK1(MAP2K1), ARMC4, DNAH1, SPAG17, EPAS1, APOD, HEY1, PDE, IQCG, Rab8B, Ephrin-A receptor 1, HIF1A, Polycystin, RABL2A, FAT3, NOTCH4, MEK1/2, MIRK, ROBO1, Apaf-1, Is- let-1, DMP4, DZIP1L, ATP6M, MIP-T3, LRRC50, MyHC, CD34, PMCA2b, BBS9, Dynein, axonemal, heavy chains, RPGRIP1L, Oxygen- regulated protein 1, CFA54, Alpha-parvin, MYH10, Ephrin-B2, Ephrin-B, Dynein 2, cytoplasmic, heavy chain, TRIM15, PKA-reg (cAMP- dependent), CFA74, SPAG16, Alpha-actinin, RFX3, SLUG, MENA, Ephrin-A receptors, Bim, FAIM2, SHANK, TMEM100, Insulin, KIAA1377(HIP5), DUSP5, CLR3, Notch, Galpha(q)- specific peptide GPCRs, Huntingtin, Profilin, HYDIN, TSGA2, SSAT, FGF10, ATF/CREB, C4orf31, CCDC176, DNAI1, DZIP, HDL pro- teins, Dynein, axonemal, intermediate chains, NME5, SNAP-29, LRGUK, KAD7, AL1A1, Perlecan, C2orf39, RSPH4A, SNX10
epithelial cilium movement	29	1.03E-11	3.55E-09	12	CCDC39, DNAH1, SPAG17, LRRC50, Dynein, ax- onemal, heavy chains, RFX3, Sp17, DNAI1, Dynein, axonemal, inter- mediate chains, NME5, KAD7, CABYR
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intracellular signal transduction	2102	6.31E-11	2.08E-08	113	PSMA4, STAT3, G3BP2, Dystrophin, IL-15, Rab20, p200RhoGAP, MEK1(MAP2K1), AM-R, SP100, RIPK2, MDA-5, MGF, PRKAR2B, IL- 31RA, ARF6, Guanylate cyclase, Sec3, PDE, PSMD8, Pleckstrin, Guanylate cyclase alpha, Galpha(q)-specific Class A Orphan/other GPCRs, Rab8B, Polycystin, RABL2A, I-kB, HES1, MEK1/2, PPP4C, DOK1, Apaf-1, JAK2, PLEKHM1, SGK3, GUCY1A2, Gal- pha(q)-specific nucleotide- like GPCRs, PSMD3, Rab- 3, Ephrin-A receptor 5, FGFR3, Galectin-9, Neu- regulin 4, WRCH-1, ATP1A2, Oxygen- regulated protein 1, PKA- reg type II (cAMP- dependent), Lyn, PSMA1, Centaurin alpha 1, CENTA2, DMPK, RGS11, PKA-reg (cAMP- dependent), Alpha-actinin, IL-15RA, PDE2A, RAP2C, A20, AZI2, Ephrin-A re- ceptors, NPR3, GSTO1, Bim, FNIP2, SHANK, SynGAP, DAGK, PSMD14, GMIP, TLR4, TMEM100, Insulin, PSMA2, GRO-1, DUSP5, TANK, Galpha(q)-specific peptide GPCRs, GFRal- pha1, CYFIP1, CD86, NUDT4, Rab-3A, TOX3, FGF10, CD40(TNFRSF5), PNPH, ATF/CREB, Rhov, ERK3, EPS8, C4orf31, PSMD12, ASB14, DGKH, RGS6, DIRAS2, CD209,
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					HDL proteins, NUA2, Phosphatase regulator (inhibitor), Syntenin 1, ILPIP, IFNAR2, Protein p8, TRIM23, PLCL2, Nephrocystin-4, ABI2, CABYR, PI3K reg class IA, RGS9, Galpha(s)-specific peptide GPCRs
positive regulation of molecular function	2442	9.59E-10	3.02E-07	122	PSMA4, CD84, FAM13A1, STAT3, Dystrophin, C1orf88, p200RhoGAP, NFKBIB, MEK1(MAP2K1), DNAJB11, SP100, ELMOD1, RIPK2, DENND1A, Hap-1, MGF, PRKAR2B, Syntaxin 4, EFP, Vsm-RhoGEF, PDE, PSMD8, Pleckstrin, Galpha(q)-specific Class A Orphan/other GPCRs, Ephrin-A receptor 1, FLJ32810, Tbc1d9, HIF1A, Polycystin, P2X7, I-kB, ORP-family, HES1, MEK1/2, MAPRE3(EB3), DENND1B, TRIM14, ROBO1, Apaf-1, JAK2, SGK3, ORP8, SMIF, ARHGEF19, Islet-1, Galpha(q)-specific nucleotide-like GPCRs, PSMD3, Rab3, Cytohesin1, Ephrin-A receptor 5, FGFR3, TRIB2, Galectin-9, Neuregulin 4, PLEKHG1, MUL, PKA-reg type II (cAMP-dependent), CAP2, Profilin II, Lyn, PSMA1, Centaurin alpha 1, CENTA2, MRE11, hRap1, PKI, RGS11, TRIM15, PKA-reg (cAMP-dependent), PKIB, Alpha-actinin, Ephrin-A receptors, NPR3, GSTO1, Bim, SHANK, SynGAP,

					PSMD14, CREB3, GMIP, TLR4, RGSS22, Insulin, Fibulin-1, Pyrin (MEFV), PSMA2, GRO-1, DUSP5, TANK, Galpha(q)-specific peptide GPCRs, Huntingtin, GFRalpha1, Profilin, Rab-3A, NEK5, FGF10, CD40(TNFRSF5), ATF/CREB, FAM116B, PSMD12, SERINC5, GITRL, Glutaredoxin, FGD3, RGS6, DIRAS2, HDL proteins, Phosphatase regulator (inhibitor), ILPIP, NCK1, RANK(TNFRSF11A), Beta adducin, AL1A1, TRIM23, PLCL2, LULL1, PI3K reg class IA, RGS9, Galpha(s)-specific peptide GPCRs, MAP1LC3B, NPNT, Glutaredoxin 1
regulation of response to stimulus	4960	1.14E-09	3.42E-07	209	Bomapin, beta-MHC, PSMA4, CD84, FAM13A1, STAT3, G3BP2, PODN, Dystrophin, CARP, MPV17L, IL-15, WFDC1, H-2L(d), p200RhoGAP, FLJ20898, OSF-2, REVERBalpha, NFKBIB, TR-alpha, MHC Class I alpha chain, PNPase(old-35), MEK1(MAP2K1), C2, DOT1, SLIT3, SP100, PVR, RIPK2, MDA-5, DENND1A, Hap-1, MGF, SNX1, IL-31RA, Syntaxin 4, Trim30, ARF6, Guanylate cyclase, PRAM-1, APOD, EFP, HEY1, Vsm-RhoGEF, Synaptotagmin, Dynein, axonemal, light chains, PDE, TREML2, ACP33, PSMD8, Pleckstrin, Galpha(q)-specific Class A Orphan/other

GPCRs, CD300LG,
 ZNF364, FLJ32810,
 ALPK1, HIF1A, Fibulin-5,
 Peregrin, P2X7, I-kB, ORP-
 family, NOTCH4, HES1,
 MEK1/2, ATF-3, PPP4C,
 DENND1B, SAMHD1,
 DOK1, C3orf58, ROBO1,
 Apaf-1, JAK2, SGK3,
 ORP8, ARHGEF19, Islet-1,
 DMP4, Galpha(q)-specific
 nucleotide-like GPCRs,
 PSMD3, MIP-T3, Cytohe-
 sin1, Ephrin-A receptor 5,
 FGFR3, MyHC, TRIB2,
 CD34, Galectin-9, Carbo-
 hydrate sulfotransferases,
 Neuregulin 4, Ceb1,
 TRAFD1, PLEKHG1,
 WRCH-1, Krm1,
 RPGRIP1L, C4B protein,
 Lyn, PSMA1, HLA-E,
 Ephrin-B2, DMPK,
 MRE11, Ephrin-B, Dynein
 2, cytoplasmic, heavy
 chain, hRap1, CysLT2 re-
 ceptor, RGS11, TRIM15,
 HA12 (rodent), Alpha-
 actinin, GRO-3, TOP3A,
 SLUG, MENA, PDE2A,
 Coagulation factor X, Orex-
 in receptor 1, A20, Ephrin-
 A receptors, GSTO1, Bim,
 FAIM2, SCAI, SHANK,
 SynGAP, Fibrinogen gam-
 ma, DAGK, PSMD14, IL-1
 alpha, CREB3, CCR1, Hck,
 GMIP, TLR4, C4,
 RGSS22, NMT1,
 TMEM100, Insulin, Fibu-
 lin-1, Pyrin (MEFV),
 PSMA2, ADAR1, GRO-1,
 DUSP5, CD276, TANK,
 BTNL2, Asporin, Notch,
 Orexin receptor, SLAM,
 Galpha(q)-specific peptide
 GPCRs, Huntingtin,

					CYFIP1, HA11, CD86, CCL27, FGF10, CD40(TNFRSF5), PNPB, ATF/CREB, Rhov, RNF34, EPS8, PSMD12, CQ087, GITRL, Glutaredoxin, HLA-C, PEAR1, FGD3, PCPH, N- myristoyltransferase, PIP1, RGS6, DIRAS2, HLA-B, Alpha-actinin 3, CD209, HDL proteins, BCAP, NME5, Phosphatase regula- tor (inhibitor), Syntenin 1, MPP1, PI3K reg class IA (p55-gamma), ILPIP, NCK1, RANK(TNFRSF11A), USP18, IFNAR2, GREM2, Thyroid hormone receptor, PLCL2, Nephrocystin-4, PI3K reg class IA, RGS9, CD300LF, IPP-2, Gal- pha(s)-specific peptide GPCRs, DUSP18, TIG2, DDX60, NPNT, SERPINB9, Glutaredoxin 1
microtubule-based process	696	3.79E-09	1.09E-06	50	KIF21A, DNAH5, CCDC39, SPEF2, MEK1(MAP2K1), ARMC4, DNAH1, LYST, Hap-1, SPAG17, Dynein, axonemal, light chains, IQCG, HIF1A, FLJ32658, MEK1/2, DNAH9, MIP- T3, LRRC50, DNAH6, MyHC, Dynein, axonemal, heavy chains, Oxygen- regulated protein 1, CFA54, Dynein 2, cytoplasmic, heavy chain, CFA74, SPAG16, DNAH11, RFX3, Sp17, KIF3B, KIAA1377(HIP5), Hun- tingtin, HYDIN, TSGA2, FGF10, DNAH3, MAP-1B, DNAH2, CCDC52, DNAI1, Dynein, axonemal,

regulation of transport	2558	4.23E-09	1.17E-06	124	intermediate chains, NME5, LRGUK, VAMP4, DNAH12, KAD7, CABYR, C2orf39, RSPH4A, TCTE3 PAM, CD84, G3BP2, Dystrophin, CARP, C2CD4D, NHE3, MPV17L, OSF-2, REV-ERBalpha, CLCN7, NFKBIB, TR-alpha, MHC Class I alpha chain, MEK1(MAP2K1), C2, SP100, ELMOD1, Hap-1, ARG1, Olfactory receptor, Syntaxin 4, ARF6, CHMP6, Guanylate cyclase, Sec3, PRAM-1, APOD, Synaptotagmin II, Synaptotagmin, PDE, PSMD8, Galpha(q)-specific Class A Orphan/other GPCRs, Rab8B, KCNRG, Tbc1d9, HIF1A, Polycystin, P2X7, I-kB, ORP-family, HES1, MEK1/2, DGAT1, SLC24A6, JAK2, SGK3, ORP8, PDE1, Islet-1, Galpha(q)-specific nucleotide-like GPCRs, Rab-3, Ephrin-A receptor 5, MyHC, CD34, Galectin-9, PMCA2b, WRCH-1, ATP1A2, C4B protein, Profilin II, Lyn, HLA-E, DMPK, PKI, TRIM15, WWP2, Bestrophin-4, Alpha-actinin, RFX3, SLUG, PDE2A, ATP4A, Ephrin-A receptors, GSTO1, KCNE4, Bim, SHANK, Fibrinogen gamma, IL-1 alpha, CREB3, CCR1, Hck, TLR4, C4, NMT1, Insulin, Fibulin-1, CD276, IDH2, BTNL2, Notch, SLAM, Galpha(q)-specific peptide GPCRs, Huntingtin, Profilin, NUDT4, Rab-3A,
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					<p>FGF10, CD40(TNFRSF5), ATF/CREB, DNAJC13, SCN3A, MAP-1B, Glu- taredoxin, N- myristoyltransferase, HLA- B, CHD7, HDL proteins, PLTP, ANKFY1, Phospha- tase regulator (inhibitor), Syntenin 1, UGCG, PI3K reg class IA (p55-gamma), PARP-10, VAMP4, RANK(TNFRSF11A), Thyroid hormone receptor, PI3K reg class IA, Gal- pha(s)-specific peptide GPCRs, TIG2, MAP1LC3B, Glutaredoxin 1</p>
phosphorus meta- bolic process	2600	5.92E-09	1.54E-06	125	<p>beta-MHC, RPS6KL1, PSMA4, STAT3, GNPTA, CTP synthase, IL-15, DDHD1, MEK1(MAP2K1), PLB1, PHEX, Stk33, RIPK2, KIAA1274, LYST, MGF, PRKAR2B, IL-31RA, Mdh1b, Guanylate cyclase, Glycogen phosphorylase, CDP-diacylglycerol syn- thase, DHSO, PDE, PSMD8, Pleckstrin, Guanylate cyclase alpha, Ephrin-A receptor 1, ALPK1, Polycystin, P2X7, MEK1/2, PPP4C, MIRK, SAMHD1, DOK1, JAK2, SGK3, GUCY1A2, PDE1, DMP4, Galpha(q)-specific nucleotide-like GPCRs, PSMD3, Ephrin-A receptor 5, FGFR3, IDH1, MyHC, TRIB2, Galectin-9, PMCA2b, Neuregulin 4, YSK4, PGS1, ATP1A2, NNTM, PKA-reg type II (cAMP-dependent), ENO4, ATP6V1B2, MANA, Lyn,</p>

xMWAS: R package for data integration and network analysis

					<p>PSMA1, DMPK, PKI, CDS2, PKA-reg (cAMP-dependent), PKIB, Alpha-actinin, PDE2A, Ephrin-A receptors, NPR3, AKD1, FNIP2, SHANK, SynGAP, DAGK, PSMD14, Hck, TLR4, Insulin, PBEF, PSMA2, DUSP5, NT5C3, IDH2, Galpha(q)-specific peptide GPCRs, GFRalpha1, CD86, NUDT4, FLAD1, NEK5, MOK, FGF10, PNPH, ATF/CREB, ERK3, PSMD12, SERINC5, ADSSL1, LDHB, MTHFD2L, ATP6V1B, PDE1B, DGKH, PCPH, PI4KII, AGPHD1, TXL-2, HDL proteins, PPP1R3B, BCAP, NUA2, C9orf98, NME5, Phosphatase regulator (inhibitor), MPP1, LRGUK, PI3K reg class IA (p55-gamma), ILPIP, NCK1, KAD7, AL1A1, ABI2, PI3K reg class IA, DUSP18, FRK</p>
regulation of cell communication	4033	5.99E-09	1.54E-06	175	<p>PSMA4, CD84, FAM13A1, STAT3, G3BP2, PODN, Dystrophin, CARP, MPV17L, IL-15, p200RhoGAP, FLJ20898, OSF-2, REV-ERBalpha, NFKBIB, TR-alpha, MEK1(MAP2K1), DOT1, SLIT3, SP100, RIPK2, DENND1A, Hap-1, MGF, SNX1, IL-31RA, Syntaxin 4, Trim30, ARF6, Guanylate cyclase, APOD, EFP, HEY1, Vsm-RhoGEF, Synaptotagmin, Dynein, axonemal, light chains, PDE, PSMD8, Pleckstrin, Galpha(q)-specific Class A</p>

Orphan/other GPCRs,
Rab8B, ZNF364,
FLJ32810, HIF1A, Pere-
grin, P2X7, I-kB, ORP-
family, NOTCH4, HES1,
MEK1/2, ATF-3, DOK1,
C3orf58, SLC24A6,
ROBO1, Apaf-1, JAK2,
SGK3, ORP8, ARHGEF19,
PDE1, Islet-1, DMP4, Gal-
pha(q)-specific nucleotide-
like GPCRs, PSMD3, Rab-
3, MIP-T3, Cytohesin1,
Ephrin-A receptor 5,
FGFR3, TRIB2, Galectin-9,
PMCA2b, Neuregulin 4,
PLEKHG1, WRCH-1,
Krm1, ATP1A2,
RPGRI1L, Profilin II,
Lyn, PSMA1, DMPK,
MRE11, Dynein 2, cyto-
plasmic, heavy chain,
hRap1, CysLT2 receptor,
RGS11, TRIM15, Alpha-
actinin, TOP3A, RFX3,
SLUG, Coagulation factor
X, Orexin receptor 1, A20,
Ephrin-A receptors,
GSTO1, Bim, FAIM2,
SCAI, SHANK, SynGAP,
Fibrinogen gamma, DAGK,
PSMD14, IL-1 alpha,
CREB3, CCR1, GMIP,
TLR4, RGSS22, NMT1,
TMEM100, Insulin, Fibu-
lin-1, PSMA2, ADAR1,
DUSP5, TANK, BTNL2,
Asporin, Notch, Orexin re-
ceptor, SLAM, Galpha(q)-
specific peptide GPCRs,
Huntingtin, CD86, Profilin,
Rab-3A, FGF10,
CD40(TNFRSF5),
ATF/CREB, Rhov, RNF34,
EPS8, MAP-1B, PSMD12,
CQ087, GITRL,
Calsyntenin-2, Glutaredox-

					in, PEAR1, SHANK2, FGD3, PCPH, N- myristoyltransferase, PIP1, RGS6, DIRAS2, CHD7, Alpha-actinin 3, HDL pro- teins, BCAP, NME5, Phos- phatase regulator (inhibi- tor), Syntenin 1, ILPIP, NCK1, RANK(TNFRSF11A), USP18, IFNAR2, GREM2, Thyroid hormone receptor, PLCL2, Nephrocystin-4, PI3K reg class IA, RGS9, IPP-2, Galpha(s)-specific peptide GPCRs, DUSP18, DDX60, NPNT, Glu- taredoxin 1
regulation of lo- calization	3402	7.46E-09	1.85E-06	153	PAM, CD84, STAT3, G3BP2, PODN, Dystro- phin, CARP, C2CD4D, NHE3, MPV17L, CCDC39, OSF-2, REV- ERBalpha, CLCN7, NFKBIB, TR-alpha, MHC Class I alpha chain, MEK1(MAP2K1), C2, ARMC4, SP100, PLET1, ELMOD1, Hap-1, MGF, ARG1, Olfactory receptor, Syntaxin 4, ARF6, CHMP6, Guanylate cyclase, Sec3, PRAM-1, Vinculin, APOD, Synapto- tagmin II, Synaptotagmin, PDE, PSMD8, Galpha(q)- specific Class A Or- phan/other GPCRs, Rab8B, Ephrin-A receptor 1, KCNRG, Tbc1d9, HIF1A, Polycystin, LDB2, P2X7, I- kB, ORP-family, NOTCH4, HES1, MEK1/2, DGAT1, ALKBH7, SLC24A6, ROBO1, JAK2, SGK3, ORP8, PDE1, Islet-1, Gal- pha(q)-specific nucleotide-

like GPCRs, Rab-3, LRRC50, Ephrin-A receptor 5, MyHC, CD34, Galectin-9, PMCA2b, Carbohydrate sulfotransferases, Neuregulin 4, WRCH-1, ATP1A2, Dynein, axonemal, heavy chains, C4B protein, Profilin II, Lyn, HLA-E, DMPK, PKI, TRIM15, WWP2, Bestrophin-4, Alpha-actinin, DNAH11, GRO-3, RFX3, SLUG, PDE2A, RAP2C, ATP4A, Coagulation factor X, Ephrin-A receptors, GSTO1, KCNE4, Bim, SCAI, SHANK, Fibrinogen gamma, IL-1 alpha, CREB3, CCR1, Hck, TLR4, PLEKHM2, C4, NMT1, Insulin, Fibulin-1, GRO-1, CD276, IDH2, BTNL2, CLR3, Notch, SLAM, Galpha(q)-specific peptide GPCRs, Huntingtin, Trp53inp2, Profilin, NUDT4, Rab-3A, CCL27, FGF10, CD40(TNFRSF5), ATF/CREB, DNAJC13, SCN3A, MAP-1B, GITRL, Glutaredoxin, N-myristoyltransferase, HLA-B, CHD7, HDL proteins, PLTP, ANKFY1, Phosphatase regulator (inhibitor), Syntenin 1, MPP1, UGCG, PI3K reg class IA (p55-gamma), PARP-10, VAMP4, NCK1, RANK(TNFRSF11A), Thyroid hormone receptor, PI3K reg class IA, Galpha(s)-specific peptide GPCRs, TIG2, MAP1LC3B, Glutaredoxin

xMWAS: R package for data integration and network analysis

locomotion	1497	8.10E-09	1.93E-06	83	CD84, DNAH5, CCDC39, MEK1(MAP2K1), SLIT3, DNAH1, PVR, PLET1, LYST, MGF, Olfactory receptor, DHSO, PDE, Galpha(q)-specific Class A Orphan/other GPCRs, HIF1A, RABL2A, FAT3, HES1, MEK1/2, B3GN1, ROBO1, JAK2, Islet-1, Galpha(q)-specific nucleotide-like GPCRs, Ephrin-A receptor 5, DNAH6, MyHC, CD34, Galectin-9, PMCA2b, Carbohydrate sulfotransferases, ATP1A2, Dynein, axonemal, heavy chains, CFA54, Alpha-parvin, ENO4, MYH10, Lyn, Ephrin-B2, Ephrin-B, SPAG16, DNAH11, GRO-3, RFX3, SLUG, MENA, Ephrin-A receptors, Sp17, SHANK, DAGK, CREB3, CCR1, CCR9, Hck, GRO-1, SPP lyase, CLR3, Notch, SLAM, Galpha(q)-specific peptide GPCRs, GFRalpha1, CCL27, FGF10, ATF/CREB, EPS8, C4orf31, DNAH3, DNAH2, DNAI1, HDL proteins, Dynein, axonemal, intermediate chains, FAT1, PLTP, Syntenin 1, NCK1, RANK(TNFRSF11A), Nephrocystin-4, ABI2, PI3K reg class IA, TIG2, C2orf39, CCNYL1, PSTPIP2
regulation of signaling	4089	9.74E-09	2.25E-06	176	PSMA4, CD84, FAM13A1, STAT3, G3BP2, PODN, Dystrophin, CARP, MPV17L, IL-15, p200RhoGAP, FLJ20898, OSF-2, REV-ERBalpha,

NFKBIB, TR-alpha,
 MEK1(MAP2K1), DOT1,
 SLIT3, SP100, RIPK2,
 DENND1A, Hap-1, MGF,
 SNX1, IL-31RA, Syntaxin
 4, Trim30, ARF6, Guanyl-
 ate cyclase, APOD, EFP,
 HEY1, Vsm-RhoGEF,
 Synaptotagmin, Dynein,
 axonemal, light chains,
 PDE, PSMD8, Pleckstrin,
 Galpha(q)-specific Class A
 Orphan/other GPCRs,
 Rab8B, ZNF364,
 FLJ32810, HIF1A, Pere-
 grin, P2X7, I-kB, ORP-
 family, NOTCH4, HES1,
 MEK1/2, ATF-3, DOK1,
 C3orf58, SLC24A6,
 ROBO1, Apaf-1, JAK2,
 SGK3, ORP8, ARHGEF19,
 PDE1, Islet-1, DMP4, Gal-
 pha(q)-specific nucleotide-
 like GPCRs, PSMD3, Rab-
 3, MIP-T3, Cytohesin1,
 Ephrin-A receptor 5,
 FGFR3, TRIB2, Galectin-9,
 Ca-ATPase3, PMCA2b,
 Neuregulin 4, PLEKHG1,
 WRCH-1, Krm1, ATP1A2,
 RPGRIP1L, Profilin II,
 Lyn, PSMA1, DMPK,
 MRE11, Dynein 2, cyto-
 plasmic, heavy chain,
 hRap1, CysLT2 receptor,
 RGS11, TRIM15, Alpha-
 actinin, TOP3A, RFX3,
 SLUG, Coagulation factor
 X, Orexin receptor 1, A20,
 Ephrin-A receptors,
 GSTO1, Bim, FAIM2,
 SCAI, SHANK, SynGAP,
 Fibrinogen gamma, DAGK,
 PSMD14, IL-1 alpha,
 CREB3, CCR1, GMIP,
 TLR4, RGSS22, NMT1,
 TMEM100, Insulin, Fibu-

					lin-1, PSMA2, ADAR1, DUSP5, TANK, BTNL2, Asporin, Notch, Orexin receptor, SLAM, Galpha(q)-specific peptide GPCRs, Huntingtin, CD86, Profilin, Rab-3A, FGF10, CD40(TNFRSF5), ATF/CREB, Rhov, RNF34, EPS8, MAP-1B, PSMD12, CQ087, GITRL, Calsyntenin-2, Glutaredoxin, PEAR1, SHANK2, FGD3, PCPH, N-myristoyltransferase, PIP1, RGS6, DIRAS2, CHD7, Alpha-actinin 3, HDL proteins, BCAP, NME5, Phosphatase regulator (inhibitor), Syntenin 1, ILPIP, NCK1, RANK(TNFRSF11A), USP18, IFNAR2, GREM2, Thyroid hormone receptor, PLCL2, Nephrocystin-4, PI3K reg class IA, RGS9, IPP-2, Galpha(s)-specific peptide GPCRs, DUSP18, DDX60, NPNT, Glutaredoxin 1
phosphate-containing compound metabolic process	2595	1.85E-08	3.97E-06	123	beta-MHC, RPS6KL1, PSMA4, STAT3, GNPTA, CTP synthase, IL-15, MEK1(MAP2K1), PLB1, Stk33, RIPK2, KIAA1274, LYST, MGF, PRKAR2B, IL-31RA, Mdh1b, Guanylate cyclase, Glycogen phosphorylase, CDP-diacylglycerol synthase, DHSO, PDE, PSMD8, Pleckstrin, Guanylate cyclase alpha, Ephrin-A receptor 1, ALPK1, Polycystin, P2X7, MEK1/2, PPP4C, MIRK, SAMHD1, DOK1, JAK2, SGK3,

					<p>GUCY1A2, PDE1, DMP4, Galpha(q)-specific nucleotide-like GPCRs, PSMD3, Ephrin-A receptor 5, FGFR3, IDH1, MyHC, TRIB2, Galectin-9, PMCA2b, Neuregulin 4, YSK4, PGS1, ATP1A2, NNTM, PKA-reg type II (cAMP-dependent), ENO4, ATP6V1B2, MANA, Lyn, PSMA1, DMPK, PKI, CDS2, PKA-reg (cAMP-dependent), PKIB, Alpha-actinin, PDE2A, Ephrin-A receptors, NPR3, AKD1, FNIP2, SHANK, SynGAP, DAGK, PSMD14, Hck, TLR4, Insulin, PBEF, PSMA2, DUSP5, NT5C3, IDH2, Galpha(q)-specific peptide GPCRs, GFRalpha1, CD86, NUDT4, FLAD1, NEK5, MOK, FGF10, PNPH, ATF/CREB, ERK3, PSMD12, SERINC5, ADSSL1, LDHB, MTHFD2L, ATP6V1B, PDE1B, DGKH, PCPH, PI4KII, AGPHD1, TXL-2, HDL proteins, PPP1R3B, BCAP, NUA2, C9orf98, NME5, Phosphatase regulator (inhibitor), MPP1, LRGUK, PI3K reg class IA (p55-gamma), ILPIP, NCK1, KAD7, AL1A1, ABI2, PI3K reg class IA, DUSP18, FRK</p>
regulation of molecular function	3799	1.86E-08	3.97E-06	165	<p>Bomapin, PSMA4, CD84, FAM13A1, STAT3, PODN, Dystrophin, C1orf88, WFDC1, p200RhoGAP, NFKBIB, TR-alpha, MEK1(MAP2K1), DOT1,</p>

DNAJB11, SP100,
ELMOD1, RIPK2,
DENND1A, Hap-1, MGF,
PRKAR2B, Syntaxin 4,
EFP, HEY1, Vsm-
RhoGEF, Dynein, ax-
onemal, light chains, PDE,
PSMD8, Pleckstrin, Gal-
pha(q)-specific Class A Or-
phan/other GPCRs, Ephrin-
A receptor 1, KCNRG,
FLJ32810, Tbc1d9, HIF1A,
Polycystin, LDB2, P2X7, I-
kB, ORP-family, HES1,
MEK1/2, MAPRE3(EB3),
DENND1B, TRIM14,
ROBO1, Apaf-1, JAK2,
SGK3, ORP8, SMIF,
ARHGEF19, Islet-1, Gal-
pha(q)-specific nucleotide-
like GPCRs, PSMD3, Rab-
3, MIP-T3, Cytohesin1,
Ephrin-A receptor 5,
FGFR3, SERPINB7, Sor-
tilin, MyHC, TRIB2,
Spp24, Galectin-9, Neureg-
ulin 4, ITIH2, Ceb1,
PLEKHG1, ATP1A2,
MUL, Antileukoproteinase
1, PKA-reg type II (cAMP-
dependent), CAP2, C4B
protein, Profilin II, Lyn,
PSMA1, Centaurin alpha 1,
CENTA2, DMPK, MRE11,
hRap1, PKI, RGS11,
TRIM15, PKA-reg (cAMP-
dependent), ELL, WWP2,
PKIB, Alpha-actinin,
RAP2C, A20, Ephrin-A re-
ceptors, NPR3, GSTO1,
Bim, SHANK, SynGAP,
DAGK, PSMD14, CREB3,
Hck, GMIP, TLR4, C4,
RGSS22, Insulin, Fibulin-1,
Pyrin (MEFV), PSMA2,
ADAR1, GRO-1, DUSP5,
TANK, Asporin, Notch,

					SLAM, Galpha(q)-specific peptide GPCRs, Huntingtin, GFRalpha1, Mitd1, Profilin, Rab-3A, NEK5, FGF10, CD40(TNFRSF5), ATF/CREB, FAM116B, RNF34, PSMD12, SERINC5, GITRL, Glutaredoxin, AGAL, FGD3, RGS6, DIRAS2, HDL proteins, PPP1R3B, Phosphatase regulator (inhibitor), PI3K reg class IA (p55-gamma), PARP-10, ILPIP, NCK1, RANK(TNFRSF11A), Beta adducin, GREM2, AL1A1, Thyroid hormone receptor, TRIM23, PLCL2, LULL1, PI3K reg class IA, RGS9, IPP-2, Galpha(s)-specific peptide GPCRs, DUSP18, MAP1LC3B, CCNYL1, NPNT, SERPINB9, Glutaredoxin 1
regulation of signal transduction	3625	1.93E-08	3.97E-06	159	PSMA4, CD84, FAM13A1, STAT3, G3BP2, PODN, Dystrophin, CARP, MPV17L, IL-15, p200RhoGAP, FLJ20898, OSF-2, REV-ERBalpha, NFKBIB, TR-alpha, MEK1(MAP2K1), DOT1, SLIT3, SP100, RIPK2, DENND1A, Hap-1, MGF, SNX1, IL-31RA, Syntaxin 4, Trim30, ARF6, Guanylate cyclase, APOD, EFP, HEY1, Vsm-RhoGEF, Dynein, axonemal, light chains, PDE, PSMD8, Pleckstrin, Galpha(q)-specific Class A Orphan/other GPCRs, ZNF364, FLJ32810, HIF1A, Peregrin, P2X7, I-kB, ORP-family, NOTCH4,

HES1, MEK1/2, ATF-3,
DOK1, C3orf58, ROBO1,
Apaf-1, JAK2, SGK3,
ORP8, ARHGEF19, Islet-1,
DMP4, Galpha(q)-specific
nucleotide-like GPCRs,
PSMD3, MIP-T3, Cytohe-
sin1, FGFR3, TRIB2, Ga-
lectin-9, Neuregulin 4,
PLEKHG1, WRCH-1,
Krm1, RPGRIP1L, Lyn,
PSMA1, DMPK, MRE11,
Dynein 2, cytoplasmic,
heavy chain, hRap1,
CysLT2 receptor, RGS11,
TRIM15, Alpha-actinin,
TOP3A, SLUG, Coagula-
tion factor X, Orexin recep-
tor 1, A20, Ephrin-A recep-
tors, GSTO1, Bim, FAIM2,
SCAI, SHANK, SynGAP,
Fibrinogen gamma, DAGK,
PSMD14, IL-1 alpha,
CREB3, CCR1, GMIP,
TLR4, RGSS22, NMT1,
TMEM100, Insulin, Fibu-
lin-1, PSMA2, ADAR1,
DUSP5, TANK, BTNL2,
Asporin, Notch, Orexin re-
ceptor, SLAM, Galpha(q)-
specific peptide GPCRs,
Huntingtin, CD86, FGF10,
CD40(TNFRSF5),
ATF/CREB, Rhov, RNF34,
EPS8, PSMD12, CQ087,
GITRL, Glutaredoxin,
PEAR1, FGD3, PCPH, N-
myristoyltransferase, PIP1,
RGS6, DIRAS2, Alpha-
actinin 3, HDL proteins,
BCAP, NME5, Phosphatase
regulator (inhibitor),
Syntenin 1, ILPIP, NCK1,
RANK(TNFRSF11A),
USP18, IFNAR2, GREM2,
Thyroid hormone receptor,
PLCL2, Nephrocystin-4,

					PI3K reg class IA, RGS9, IPP-2, Galpha(s)-specific peptide GPCRs, DUSP18, DDX60, NPNT, Glutaredoxin 1
immune system process	3048	1.95E-08	3.97E-06	139	PSMA4, CD84, CTP synthase, IL-15, H-2L(d), Mca32, SPEF2, TR-alpha, MHC Class I alpha chain, MEK1(MAP2K1), C2, SP100, RIPK2, MDA-5, LYST, MGF, IL-31RA, LTBR1, EPAS1, EFP, PDE, TREML2, ACP33, PSMD8, Pleckstrin, Galpha(q)-specific Class A Orphan/other GPCRs, Rab8B, CD300LG, HIF1A, SUSD2, ADAMDEC1, P2X7, I-kB, ORP-family, NOTCH4, HES1, MEK1/2, DENND1B, SAMHD1, TRIM14, JAK2, MR1, PDE1, DMP4, Galpha(q)-specific nucleotide-like GPCRs, PSMD3, FLVCR, Rab-3, MxA, Ku70, MyHC, CD34, Galectin-9, Carbohydrate sulfotransferases, Ceb1, Antileukoproteinase 1, TFE3, C4B protein, Lyn, PSMA1, HLA-E, Ephrin-B2, Ephrin-B, Dynein 2, cytoplasmic, heavy chain, CysLT2 receptor, TRIM15, CAPZA1, HA12 (rodent), Alpha-actinin, GRO-3, MENA, PDE2A, A20, OASL, AZI2, Ephrin-A receptors, KIF3B, Bim, Fibrinogen gamma, PSMD14, IL-1 alpha, CCR1, CCR9, Hck, TLR4, C4, Insulin, Pyrin (MEFV), PSMA2, ADAR1, GRO-1, CD276, SPP lyase, TANK, Galectin-8,

xMWAS: R package for data integration and network analysis

					CAPZA, Notch, SLAM, Galpha(q)-specific peptide GPCRs, ISG20, CYFIP1, HA11, CD86, CCL27, TAPBPL, FGF10, CD40(TNFRSF5), PNPB, ATF/CREB, EPS8, PSMD12, SERINC5, ADSSL1, CAPZA2, GITRL, HLA-C, PDE1B, HLA-B, Artemis, CHD7, PI4KII, CD209, HDL pro- teins, BCAP, OSTM1 (grey-lethal), NCK1, RANK(TNFRSF11A), Beta adducin, IFNAR2, KAD7, Thyroid hormone receptor, PLCL2, RPESP, PI3K reg class IA, CD300LF, DDX60, FRK, SERPINB9, SNX10
single-organism cellular process	14419	2.55E-08	5.05E-06	482	Bomapin, beta-MHC, RPS6KL1, PAM, KIF21A, PSMA4, CD84, FAM13A1, B4GT4, STAT3, G3BP2, FLJ13305, PODN, DNAH5, Dystrophin, GNPTA, CARP, CTP syn- thase, C2CD4D, NHE3, MPV17L, IL-15, OLFML2A, C1orf88, CCDC39, H-2L(d), Mca32, WIPI1, Trehalase, DPYD, Rab20, PDIP38, p200RhoGAP, SPEF2, FLJ20898, OSF-2, REV- ERBalpha, HDAC11, NFKBIB, STOML3, ZNF281, TR-alpha, MHC Class I alpha chain, PNPase(old-35), GPR141, MEK1(MAP2K1), C2, ARMC4, DOT1, SLIT3, PLB1, AM-R, DNAH1, PHEX, DNAJB11, SNX2, SP100, PVR, PLET1, RIPK2, MDA-5, ASCT1

(SLC1A4), ZNF313,
 LYST, Hap-1, MGF,
 SNX1, PRKAR2B, ARG1,
 IL-31RA, Olfactory recep-
 tor, Syntaxin 4, ARF6,
 LTBR1, SPAG17,
 SCPEP1, CHMP6, Mdh1b,
 Guanylate cyclase, EPAS1,
 DMKN, Sec3, PRAM-1,
 Vinculin, APOD, EFP,
 Glycogen phosphorylase,
 HEY1, CEP78, Synapto-
 tagmin II, VE-cadherin,
 NCKX3, Synaptotagmin,
 CD-MPR, CDP-
 diacylglycerol synthase,
 DHSO, HIST3H2A,
 Dynein, axonemal, light
 chains, PDE, IQCG,
 TREML2, MGAT4A,
 ACP33, KCNQ1OT1,
 PSMD8, Pleckstrin,
 LRP12, Guanylate cyclase
 alpha, Galpha(q)-specific
 Class A Orphan/other
 GPCRs, Rab8B, HPLC2,
 Ephrin-A receptor 1,
 VIPAR, FLJ32810,
 ALPK1, HIF1A, Polycys-
 tin, Fibulin-5, Tmem195,
 RABL2A, FAT3, P2X7, I-
 kB, ORP-family, NOTCH4,
 HES1, FLJ32658, Vitrin,
 MEK1/2, DGAT1, ATF-3,
 Olr1598, PPP4C, MIRK,
 OLAH, MAPRE3(EB3),
 DENND1B, SAMHD1,
 VN1R4, B3GN1, DOK1,
 C3orf58, Egflam,
 ALKBH7, SLC24A6,
 ROBO1, DNAH9, Apaf-1,
 HAT1, JAK2, PLEKHM1,
 MR1, SGK3, ORP8, SMIF,
 GUCY1A2, ARHGEF19,
 ZCCHC14, PDE1, Islet-1,
 DMP4, Galpha(q)-specific
 nucleotide-like GPCRs,

WDR93, PSMD3, FLVCR,
 DZIP1L, ATP6M, Rab-3,
 MIP-T3, Cytohesin1,
 MNS1, LRRC50, Ephrin-A
 receptor 5, MxA, FGFR3,
 FANCM, DNAH6,
 DYDC1, IDH1, RETSAT,
 Ku70, Sortilin, MyHC, V-
 ATPase E subunit, OGFR,
 CD34, Spp24, Galectin-9,
 Ca-ATPase3, PCDHB8,
 NHLRC2, PMCA2b, Car-
 bohydrate sulfotransferases,
 Neuregulin 4, Ceb1, Scd2,
 YSK4, BBS9, PGS1,
 TRAP25, WHDC1,
 WRCH-1, Krm1, ATP1A2,
 Dynein, axonemal, heavy
 chains, RPGRIP1L, Oxy-
 gen-regulated protein 1,
 NNTM, CFA54, Alpha-
 parvin, PKA-reg type II
 (cAMP-dependent), ENO4,
 CAP2, MYH10,
 ATP6V1B2, VANG1,
 MANA, Profilin II, Lyn,
 PSMA1, Centaurin alpha 1,
 CENTA2, HLA-E, Ephrin-
 B2, DMPK, PRIC285,
 MRE11, Ephrin-B, Dynein
 2, cytoplasmic, heavy
 chain, PYGM, LMLN,
 NPX1, STRBP, CNBP2,
 PKI, CysLT2 receptor,
 RGS11, CDS2, TRIM15,
 G-protein alpha-14,
 CAPZA1, PKA-reg
 (cAMP-dependent), HA12
 (rodent), CFA74,
 KIAA1340, VTA1,
 SPAG16, Alpha-actinin, c-
 Maf, DNAH11, IL-15RA,
 GRO-3, TOP3A, RFX3,
 SLUG, MENA, PDE2A,
 RAP2C, ATP4A, Orexin
 receptor 1, A20, OASL,
 AZI2, ABBA, Ephrin-A re-

ceptors, GALRL, NPR3,
 GSTO1, Sp17, AKD1,
 KCNE4, KIF3B, Bim,
 SLC4A11, FAIM2, FNIP2,
 SHANK, SynGAP, Fibrin-
 ogen gamma, DAGK,
 PSMD14, IL-1 alpha,
 CREB3, CCR1, CCR9,
 RPS27, TFIIF, beta subunit,
 Hck, GMIP, TLR4, NAR4,
 SCO2, NMT1, TMEM100,
 Insulin, Fibulin-1, PBEF,
 PSMA2, GNT-IV, Ces1
 (mouse), ADAR1,
 KIAA1377(HIP5), GRO-1,
 DUSP5, CD276, SPP lyase,
 TANK, Galectin-8, NT5C3,
 PADI6, IDH2, SPATA18,
 CAPZA, CLR3, Asporin,
 FLJ46266, Notch, Orexin
 receptor, SLAM,
 APBA2BP, MCFD2, Gal-
 pha(q)-specific peptide
 GPCRs, ISG20, Huntingtin,
 GFRalpha1, CYFIP1,
 HA11, CD86, Mitd1,
 POLR2G, Trp53inp2, Pro-
 filin, NUDT4, HYDIN,
 Rab-3A, CCL27, TOX3,
 TSGA2, ACADM, CBR1,
 FLAD1, ES130 (p180),
 MOK, FGF10,
 CD40(TNFRSF5),
 OR52N5, PNPH, T6441,
 ATF/CREB, Rhov, RNF34,
 ERK3, DNAJC13, EPS8,
 C4orf31, SCN3A, DNAH3,
 MAP-1B, PSMD12,
 SERINC5, ADSSL1,
 CQ087, LDHB, CAPZA2,
 FADS2, MTHFD2L,
 GITRL, CCDC176,
 Calsyntenin-2, SETDB2,
 ASB14, Glutaredoxin,
 DNAH2, MMSA, HLA-C,
 PEAR1, ATP6V1B,
 CCDC52, DNAIL1,

SHANK2, AGAL, DZIP,
 CGI-128, ZNF541, AL3A1,
 Heme oxygenase 2,
 PDE1B, WDT2, FGD3,
 DGKH, PCPH, N-
 myristoyltransferase,
 PCDHB16, RGS6, GPR35,
 DIRAS2, HLA-B,
 ATP6V1E, Artemis,
 CHD7, Alpha-actinin 3,
 PI4KII, FBX6, AGPHD1,
 TXL-2, ANKRD28,
 CD209, HDL proteins,
 PPP1R3B, SIX5, BCAP,
 Dynein, axonemal, inter-
 mediate chains, NUA2,
 C9orf98, FAT1, NRIF2,
 PLTP, ANKFY1, NME5,
 SNAP-29, Phosphatase
 regulator (inhibitor),
 OSTM1 (grey-lethal),
 Syntenin 1, ATP8B3,
 MPP1, UGCG, LRGUK,
 PI3K reg class IA (p55-
 gamma), PARP-10,
 VAMP4, ILPIP, NCK1,
 RANK(TNFRSF11A),
 P2Y4, NABP1, DNAH12,
 Beta adducin, IFNAR2,
 GREM2, KAD7, Protein
 p8, AL1A1, Thyroid hor-
 mone receptor, BET1,
 TRIM23, UOX, PLCL2,
 Nephrocystin-4, DIP13 be-
 ta, GSTT2, ACSS1, PTER,
 ABI2, TSNAXIP1,
 CABYR, LULL1,
 KIAA0317, PI3K reg class
 IA, RGS9, CD300LF,
 HPSE2, IPP-2, Galpha(s)-
 specific peptide GPCRs,
 C8orf34, DUSP18, TIG2,
 MAP1LC3B, Perlecan,
 C2orf39, FAM188A,
 RSPH4A, Olfr554,
 CCNYL1, NPNT, Alpha-
 internexin, MCEE, FRK,

					PSTPIP2, SERPINB9, Glutaredoxin 1, SNX10, TCTE3
negative regulation of intracellular transport	156	2.67E-08	5.07E-06	20	CD84, G3BP2, NFKBIB, TR-alpha, SP100, APOD, PDE, Polycystin, I-kB, Galectin-9, PKI, TRIM15, SLUG, PDE2A, CREB3, ATF/CREB, MAP-1B, HDL proteins, PARP-10, Thyroid hormone receptor
localization of cell	1212	2.78E-08	5.07E-06	70	CD84, DNAH5, CCDC39, MEK1(MAP2K1), SLIT3, DNAH1, PVR, PLET1, LYST, MGF, DHOS, PDE, HIF1A, RABL2A, FAT3, HES1, MEK1/2, ROBO1, JAK2, Islet-1, Galpha(q)-specific nucleotide-like GPCRs, DNAH6, MyHC, CD34, Carbohydrate sulfotransferases, Dynein, axonemal, heavy chains, CFA54, Alpha-parvin, ENO4, MYH10, Lyn, Ephrin-B2, Ephrin-B, SPAG16, DNAH11, GRO-3, RFX3, SLUG, Ephrin-A receptors, Sp17, DAGK, CCR1, Hck, GRO-1, SPP lyase, CLR3, Notch, SLAM, Galpha(q)-specific peptide GPCRs, GFRalpha1, CCL27, FGF10, EPS8, C4orf31, DNAH3, DNAH2, DNAI1, HDL proteins, Dynein, axonemal, intermediate chains, FAT1, PLTP, Syntenin 1, NCK1, RANK(TNFRSF11A), Nephrocystin-4, ABI2, PI3K reg class IA, C2orf39, CCNYL1, PSTPIP2
cell motility	1212	2.78E-08	5.07E-06	70	CD84, DNAH5, CCDC39, MEK1(MAP2K1), SLIT3, DNAH1, PVR, PLET1,

					<p>LYST, MGF, DHOS, PDE, HIF1A, RABL2A, FAT3, HES1, MEK1/2, ROBO1, JAK2, Islet-1, Galpha(q)- specific nucleotide-like GPCRs, DNAH6, MyHC, CD34, Carbohydrate sul- fotransferases, Dynein, ax- onemal, heavy chains, CFA54, Alpha-parvin, ENO4, MYH10, Lyn, Ephrin-B2, Ephrin-B, SPAG16, DNAH11, GRO- 3, RFX3, SLUG, Ephrin-A receptors, Sp17, DAGK, CCR1, Hck, GRO-1, SPP lyase, CLR3, Notch, SLAM, Galpha(q)-specific peptide GPCRs, GFRal- pha1, CCL27, FGF10, EPS8, C4orf31, DNAH3, DNAH2, DNAI1, HDL proteins, Dynein, ax- onemal, intermediate chains, FAT1, PLTP, Syntenin 1, NCK1, RANK(TNFRSF11A), Nephrocystin-4, ABI2, PI3K reg class IA, C2orf39, CCNYL1, PSTPIP2 Bomapiin, beta-MHC, RPS6KL1, PAM, KIF21A, PSMA4, CD84, FAM13A1, B4GT4, STAT3, G3BP2, EG1, FLJ13305, PODN, DNAH5, Dystrophin, GNPTA, MCT8, CARP, CTP synthase, C2CD4D, NHE3, MPV17L, IL-15, OLFML2A, C1orf88, CCDC39, DDHD1, H- 2L(d), Mca32, WIPI1, Tre- halase, DPYD, Rab20, PDIP38, p200RhoGAP, SF3B14a, SPEF2, FLJ20898, OSF-2, REV- ERBalpha, HDAC11,</p>
single-organism process	16117	3.41E-08	6.05E-06	526	

NFKBIB, STOML3,
ZNF281, TR-alpha, MHC
Class I alpha chain,
PNPase(old-35), GPR141,
MEK1(MAP2K1), CTRL,
C2, ARMC4, DOT1,
SLIT3, C10orf58, PLB1,
AM-R, DNAH1, PHEX,
DNAJB11, SNX2, SP100,
PVR, PLET1, ELMOD1,
RIPK2, MDA-5, ASCT1
(SLC1A4), ZNF313,
LYST, DENND1A, Hap-1,
MGF, SNX1, MAD,
PRKAR2B, ARG1, IL-
31RA, Olfactory receptor,
Syntaxin 4, ARF6, LTBR1,
TMEM2, SPAG17,
SCPEP1, CHMP6, Mdh1b,
Guanylate cyclase, EPAS1,
DMKN, Sec3, PRAM-1,
Vinculin, APOD, EFP,
Glycogen phosphorylase,
HEY1, Vsm-RhoGEF,
CEP78, Synaptotagmin II,
ASCC3, VE-cadherin,
NCKX3, Synaptotagmin,
CD-MPR, CDP-
diacylglycerol synthase,
DHSO, HIST3H2A,
Dynein, axonemal, light
chains, PDE, IQCG,
TREML2, MGAT4A,
ACP33, KCNQ1OT1,
PSMD8, Pleckstrin,
LRP12, Spermine oxidase,
Guanylate cyclase alpha,
Galpha(q)-specific Class A
Orphan/other GPCRs,
Rab8B, HPLC2,
CD300LG, Ephrin-A recep-
tor 1, VIPAR, FLJ32810,
ALPK1, NAT-1, HIF1A,
Polycystin, LDB2, Fibulin-
5, Tmem195, RABL2A,
FAT3, P2X7, I-kB, ORP-
family, NOTCH4, HES1,

FLJ32658, Vitrin, MEK1/2, DGAT1, ATF-3, Olf1598, PPP4C, C20orf26, PAFAH gamma, MIRK, OLAH, MAPRE3(EB3), DENND1B, SAMHD1, VN1R4, B3GN1, DOK1, C3orf58, Egflam, ALKBH7, SLC24A6, ROBO1, DNAH9, Apaf-1, HAT1, JAK2, PLEKHM1, MR1, SGK3, ORP8, SMIF, GUCY1A2, DUS4L, ARHGEF19, ZCCHC14, PDE1, Islet-1, DMP4, Galpha(q)-specific nucleotide-like GPCRs, WDR93, PSMD3, FLVCR, DZIP1L, ATP6M, Rab-3, MIP-T3, Cytohesin1, MNS1, LRRC50, Ephrin-A receptor 5, MxA, FGFR3, FANCM, DNAH6, DYDC1, IDH1, RETSAT, SERPINB7, Ku70, Sortilin, MyHC, V-ATPase E subunit, OGFR, CD34, Spp24, Galectin-9, Ca-ATPase3, PCDHB8, Adipophilin, NHLRC2, PMCA2b, Carbohydrate sulfotransferases, Neuregulin 4, Ceb1, Scd2, YSK4, BBS9, PGS1, TRAP25, WHDC1, WRCH-1, Krm1, ATP1A2, Dynein, axonemal, heavy chains, RPGRIP1L, Oxygen-regulated protein 1, NNTM, CFA54, Alpha-parvin, PKA-reg type II (cAMP-dependent), ENO4, CAP2, MYH10, ATP6V1B2, VANGL1, C4B protein, MANA, Profilin II, Lyn, PSMA1, Centaurin alpha 1, CENTA2, HLA-E, Ephrin-B2,

DMPK, RNPEP, PRIC285, MRE11, Ephrin-B, Dynein 2, cytoplasmic, heavy chain, PYGM, LMLN, NPX1, STRBP, CNBP2, PKI, CysLT2 receptor, RGS11, CDS2, TRIM15, G-protein alpha-14, CAPZA1, PKA-reg (cAMP-dependent), HA12 (rodent), ELL, CFA74, KIAA1340, VTA1, SPAG16, Alpha-actinin, CREG2, c-Maf, DNAH11, IL-15RA, GRO-3, TOP3A, RFX3, SLUG, MENA, PDE2A, RAP2C, ATP4A, Coagulation factor X, Orexin receptor 1, A20, OASL, AZI2, ABBA, Ephrin-A receptors, GALRL, NPR3, GSTO1, Sp17, AKD1, KCNE4, KIF3B, Bim, SLC4A11, FAIM2, FNIP2, SHANK, Tryptase delta, SynGAP, Fibrinogen gamma, DAGK, PSMD14, IL-1 alpha, CREB3, CHST2, CCR1, CCR9, SULT1D1, RPS27, TFIIF, beta subunit, Hck, Hapln4, GMIP, TLR4, NAR4, C4, SCO2, NMT1, TMEM100, CYP2S1, Insulin, Fibulin-1, PBEF, PSMA2, GNT-IV, Ces1 (mouse), ADAR1, KIAA1377(HIP5), GRO-1, DUSP5, CD276, SPP lyase, TANK, Galectin-8, NT5C3, PHTF1, HYEP, PADI6, IDH2, SPATA18, CAPZA, CLR3, Asporin, FLJ46266, DSCR2, Notch, Orexin receptor, SLAM, APBA2BP, MCFD2, CAC, Galpha(q)-specific peptide GPCRs, ISG20, PLEKHA5, Hun-

tingtin, GFRalpha1,
 CYFIP1, HA11, CD86,
 Mitd1, POLR2G,
 Trp53inp2, Profilin,
 NUDT4, HYDIN, Rab-3A,
 CCL27, TOX3, TSGA2,
 SSAT, ACADM, CBR1,
 FLAD1, ES130 (p180),
 MOK, FGF10,
 CD40(TNFRSF5),
 OR52N5, PNPH, T6441,
 ATF/CREB, Rhov, RNF34,
 ERK3, DNAJC13, EPS8,
 C4orf31, SCN3A, DNAH3,
 MAP-1B, PSMD12,
 SERINC5, ADSSL1,
 CQ087, LDHB, CAPZA2,
 FADS2, MTHFD2L,
 GITRL, CCDC176,
 Calsyntenin-2, SETDB2,
 ASB14, Glutaredoxin,
 DNAH2, MMSA, HLA-C,
 PEAR1, ATP6V1B,
 CCDC52, DNAI1,
 SHANK2, AGAL, DZIP,
 CGI-128, ZNF541, AL3A1,
 Heme oxygenase 2,
 PDE1B, WDT2, FGD3,
 DGKH, PCPH, N-
 myristoyltransferase,
 PCDHB16, PIP1, RGS6,
 GPR35, DIRAS2, HLA-B,
 ATP6V1E, Artemis,
 CHD7, Alpha-actinin 3,
 PI4KII, FBX6, AGPHD1,
 TXL-2, ANKRD28,
 CD209, HDL proteins,
 PPP1R3B, SIX5, BCAP,
 Dynein, axonemal, inter-
 mediate chains, NUA2,
 C9orf98, FAT1, NRIF2,
 PLTP, ANKFY1, NME5,
 SNAP-29, Phosphatase
 regulator (inhibitor),
 OSTM1 (grey-lethal),
 Syntenin 1, TRIML1,
 ATP8B3, MPP1, UGCG,

					LRGUK, PI3K reg class IA (p55-gamma), PARP-10, VAMP4, ILPIP, NCK1, RANK(TNFRSF11A), P2Y4, NABP1, DNAH12, Beta adducin, IFNAR2, GREM2, KAD7, Protein p8, AL1A1, Thyroid hormone receptor, BET1, TRIM23, UOX, PLCL2, Nephrocystin-4, DIP13 beta, GSTT2, ACSS1, Lrig3, PTER, STOX2, ABI2, TSNAXIP1, CABYR, LULL1, KIAA0317, ANKFN1, PI3K reg class IA, RGS9, CD300LF, HPSE2, IPP-2, Galpha(s)-specific peptide GPCRs, C8orf34, DUSP18, TIG2, MAP1LC3B, Perlecan, C2orf39, FAM188A, RSPH4A, Olfr554, CCNYL1, NPNT, Alpha-internexin, MCEE, FRK, RNF22, PSTPIP2, SERPINB9, Glutaredoxin 1, SNX10, TCTE3
negative regulation of protein import	92	5.89E-08	9.96E-06	15	G3BP2, NFKB1B, TR-alpha, APOD, PDE, Polycystin, I-kB, PKI, SLUG, PDE2A, CREB3, ATF/CREB, HDL proteins, PARP-10, Thyroid hormone receptor
negative regulation of protein import into nucleus	92	5.89E-08	9.96E-06	15	G3BP2, NFKB1B, TR-alpha, APOD, PDE, Polycystin, I-kB, PKI, SLUG, PDE2A, CREB3, ATF/CREB, HDL proteins, PARP-10, Thyroid hormone receptor
negative regulation of nucleocytoplasmic transport	106	6.58E-08	1.09E-05	16	G3BP2, NFKB1B, TR-alpha, SP100, APOD, PDE, Polycystin, I-kB, PKI, SLUG, PDE2A, CREB3, ATF/CREB, HDL proteins, PARP-10, Thyroid hormone receptor
regulation of immune system process	2131	7.05E-08	1.14E-05	104	Bomapin, PSMA4, CD84, IL-15, H-2L(d), Mca32, REV-ERBalpha, MHC Class I alpha chain, C2, C10orf58, PVR, RIPK2, MDA-5, LYST, MGF, IL-31RA, Syntaxin 4, Trim30, ARF6, PRAM-1, APOD, PDE, TREML2, ACP33, PSMD8, CD300LG, ALPK1, HIF1A, P2X7, I-

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					<p> kB, HES1, DENND1B, SAMHD1, JAK2, Gal- pha(q)-specific nucleotide- like GPCRs, PSMD3, MIP- T3, FGFR3, MyHC, CD34, Galectin-9, Carbohydrate sulfotransferases, Ceb1, TRAFD1, CCDC88, TFE3, C4B protein, Lyn, PSMA1, HLA-E, Ephrin-B2, Ephrin- B, TRIM15, PKA-reg (cAMP-dependent), HA12 (rodent), IL-15RA, GRO-3, MENA, A20, PSMD14, IL- 1 alpha, CREB3, CCR1, Hck, GMIP, TLR4, C4, In- sulin, PSMA2, ADAR1, GRO-1, CD276, TANK, Galectin-8, BTNL2, Notch, SLAM, Galpha(q)-specific peptide GPCRs, CYFIP1, HA11, CD86, CCL27, TAPBPL, FGF10, CD40(TNFRSF5), PNPH, ATF/CREB, PSMD12, GITRL, HLA-C, HLA-B, CD209, HDL proteins, BCAP, MPP1, NCK1, USP18, IFNAR2, PLCL2, PI3K reg class IA, CD300LF, TIG2, DDX60, SERPINB9, STA13, FLJ13305, DNAH5, Dystrophin, GNPTA, CARP, IL-15, CCDC39, H- 2L(d), PDIP38, SPEF2, FLJ20898, OSF-2, REV- ERBalpha, HDAC11, ZNF281, TR-alpha, MHC Class I alpha chain, PNPase(old-35), MEK1(MAP2K1), ARMC4, SLIT3, DNAH1, SNX2, PLET1, ZNF313, Hap-1, MGF, SNX1, IL- 31RA, Olfactory receptor, ARF6, SPAG17, EPAS1, DMKN, Vinculin, APOD, HEY1, Synaptotagmin II, Synaptotagmin, Dynein, axonemal, light chains, PDE, IQCG, Pleckstrin, Rab8B, Ephrin-A receptor 1, VIPAR, HIF1A, RABL2A, FAT3, P2X7, ORP-family, NOTCH4, HES1, FLJ32658, MEK1/2, ATF-3, MIRK, B3GN1, ROBO1, Apaf-1, JAK2, ORP8, PDE1, Islet-1, DMP4, Galpha(q)-specific nucleotide-like GPCRs, FLVCR, DZIP1L, ATP6M, Rab-3, MIP-T3, LRRC50, Ephrin-A receptor 5, FGFR3, Ku70, Sortilin, MyHC, CD34, Galectin-9, PMCA2b, Carbohydrate sulfotransferases, Ceb1, BBS9, Dynein, axonemal, heavy chains, RPGRIP1L, Oxygen-regulated protein 1, CFA54, Alpha-parvin, </p>
cellular develop- mental process	4943	8.59E-08	1.34E-05	200	

localization

6321

8.71E-08

1.34E-05

244

CAP2, MYH10, Lyn, Ephrin-B2, Ephrin-B, Dynein 2, cytoplasmic, heavy chain, NPX1, STRBP, TRIM15, PKA-reg (cAMP-dependent), HA12 (rodent), CFA74, SPAG16, Alpha-actinin, c-Maf, IL-15RA, RFX3, SLUG, MENA, PDE2A, RAP2C, A20, AZI2, Ephrin-A receptors, FAIM2, SHANK, SynGAP, Fibrinogen gamma, DAGK, IL-1 alpha, CCR1, CCR9, Hck, TLR4, TMEM100, Insulin, ADAR1, KIAA1377(HIP5), SPP lyase, Galectin-8, IDH2, SPATA18, CAPZA, CLR3, FLJ46266, Notch, SLAM, Galpha(q)-specific peptide GPCRs, Huntingtin, GFRalpha1, CYFIP1, HA11, CD86, Trp53imp2, HYDIN, Rab-3A, TSGA2, ACADM, CBR1, ES130 (p180), FGF10, T6441, ATF/CREB, ERK3, DNAJC13, C4orf31, MAP1B, CCDC176, Glutaredoxin, MMSA, HLA-C, DNAA1, DZIP, ZNF541, PDE1B, WDT2, RGS6, HLA-B, Artemis, CHD7, Alpha-actinin 3, HDL proteins, SIX5, Dynein, axonemal, intermediate chains, NME5, SNAP-29, Phosphatase regulator (inhibitor), OSTM1 (grey-lethal), LRGUK, ILPIP, NCK1, RANK(TNFRSF11A), KAD7, Protein p8, Thyroid hormone receptor, PLCL2, Nephrocystin-4, PTER, ABI2, TSNA XIPI, CABYR, PI3K reg class IA, CD300LF, TIG2, Perlecan, C2orf39, RSPH4A, NPNT, Alpha-internexin, FRK, SNX10, SLC06A1, PAM, C1cal (rodent), CD84, STAT3, G3BP2, DNAH5, Dystrophin, GNPTA, MCT8, SNX5, C2CD4D, NHE3, MPV17L, CCDC39, Mca32, WIP1, Rab20, CLCN7, NFKB1B, TR-alpha, PNPase(old-35), MEK1(MAP2K1), SLIT3, DNAH1, SNX2, PVR, PLET1, ELMOD1, ASCT1 (SLC1A4), LYST, DENND1A, Hap-1, MGF, SNX1, Olfactory receptor, Syntaxin 4, ARF6, CHMP6, Guanylate cyclase, Sec3, Vinculin, APOD, Synaptotagmin II, NCKX3, Synaptotagmin,

CD-MPR, DH50, Dynein, axonemal, light chains, PDE, Pleckstrin, LRP12, Galpha(q)-specific Class A Orphan/other GPCRs, Rab8B, CD300LG, VIPAR, Tbc1d9, HIF1A, SUS2, Polycystin, Fibulin-5, RABL2A, FAT3, P2X7, I-kB, ORP-family, HES1, FLJ32658, MEK1/2, DGAT1, DENND1B, C3orf58, ALKBH7, SLC24A6, ROBO1, JAK2, PLEKHM1, SGK3, ORP8, SMIF, Islet-1, Galpha(q)-specific nucleotide-like GPCRs, FLVCR, ATP6M, Rab-3, GOLT1A, MIP-T3, Cytohesin1, FAM38B, DNAH6, SERPINB7, Sortilin, MyHC, V-ATPase E subunit, CD34, Spp24, Galectin-9, Ca-ATPase3, Adipophilin, PMCA2b, Carbohydrate sulfotransferases, BBS9, C9orf72, UGRP1, WHDC1, ATP1A2, Dynein, axonemal, heavy chains, NNTM, CFA54, Alpha-parvin, ENO4, MYH10, ATP6V1B2, C4B protein, Lyn, Ephrin-B2, CCDC46, Ephrin-B, Dynein 2, cytoplasmic heavy chain, hRap1, NPX1, NIPA2, VTA1, SPAG16, Bestrophin-4, Alpha-actinin, DNAH11, GRO-3, MEX3D, RFX3, SLUG, MENA, PDE2A, ATP4A, Coagulation factor X, A20, Ephrin-A receptors, NPR3, Sp17, KCNE4, KIF3B, Bim, SLC4A11, SHANK, SynGAP, Fibrinogen gamma, DAGK, CREB3, CCR1, RPS27, Hck, TLR4, PLEKHM2, C4, SCO2, NMT1, Insulin, ADAR1, GRO-1, SPP lyase, PADI6, IMP2, CLR3, Asporin, Notch, SLAM, APBA2BP, MCFD2, CAC, Galpha(q)-specific peptide GPCRs, Huntingtin, GFRalpha1, CYFIP1, Mitd1, Profilin, NUDT4, Rab-3A, CCL27, DHX38, ES130 (p180), FGF10, PNPH, ATF/CREB, DNAJC13, EPS8, C4orf31, SCN3A, DNAH3, MAP-1B, SERINC5, CD163, FADS2, Glutaredoxin, DNAH2, PEAR1, ATP6V1B, CCDC52, DNAI1, DZIP, WDT2, N-myristoyltransferase, ATP6V1E, MARCH5, PI4KII, ANKRD28, CD209, HDL proteins, Dynein, axonemal, inter-

					mediate chains, FAT1, PLTP, ANKFY1, SNAP-29, Phosphatase regulator (inhibitor), OSTM1 (grey-lethal), Syntenin 1, ATP8B3, VAMP4, ILPIP, NCK1, RANK(TNFRSF11A), P2Y4, Beta adducin, Thyroid hormone receptor, BET1, NXT2, Nephrocystin-4, GPP130, ABI2, RPESP, LULL1, PI3K reg class 1A, Galpha(s)-specific peptide GPCRs, DUSP18, TIG2, Perlecan, C2orf39, UBAP1, CCNYL1, NPNT, RNF22, PSTPIP2, Glutaredoxin 1, SNX10, TCTE3
axonemal dynein complex assembly	30	1.11E-07	1.68E-05	9	DNAH5, CCDC39, ARMC4, DNAH1, LRRC50, Dynein, axonemal, heavy chains, DNAI1, Dynein, axonemal, intermediate chains, C2orf39
regulation of innate immune response	514	1.43E-07	2.05E-05	38	PSMA4, REV-ERBalpha, MHC Class I alpha chain, PVR, RIPK2, MDA-5, Trim30, ARF6, PSMD8, I-kB, SAMHD1, JAK2, PSMD3, Galectin-9, TRAFD1, Lyn, PSMA1, HLA-E, TRIM15, A20, PSMD14, CCR1, Hck, TLR4, Insulin, PSMA2, ADAR1, TANK, Galpha(q)-specific peptide GPCRs, CD86, PSMD12, HLA-B, CD209, BCAP, USP18, IFNAR2, DDX60, SERPINB9
regulation of defense response	1116	1.48E-07	2.05E-05	64	Bomapin, PSMA4, IL-15, WFDC1, REV-ERBalpha, MHC Class I alpha chain, C2, PVR, RIPK2, MDA-5, Trim30, ARF6, APOD, Synaptotagmin, PDE, PSMD8, Galpha(q)-specific Class A Orphan/other GPCRs, ALPK1, I-kB, SAMHD1, JAK2, Islet-1, Galpha(q)-specific nucleotide-like GPCRs, PSMD3, MIP-T3, Galectin-9, Carbohydrate sulfotransferases, Ceb1, TRAFD1, C4B protein, Lyn, PSMA1, HLA-E, TRIM15, PDE2A, A20, SHANK, PSMD14, CREB3, CCR1, Hck, GMIP, TLR4, C4, Insulin, Pyrin (MEFV), PSMA2, ADAR1, CD276, TANK, Galpha(q)-specific peptide GPCRs, CD86, ATF/CREB, PSMD12, GITRL, HLA-B, CD209, HDL proteins, BCAP, RANK(TNFRSF11A), USP18, IFNAR2, DDX60, SERPINB9
developmental	7554	1.49E-07	2.05E-05	281	beta-MHC, PAM, STAT3,

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process

EG1, FLJ13305, DNAH5,
Dystrophin, GNPTA,
CARP, MPV17L, IL-15,
CCDC39, H-2L(d), Trehalase,
DPYD, PDIP38, SF3B14a, SPEF2,
FLJ20898, OSF-2, REV-ERBalpha, HDAC11,
ZNF281, TR-alpha, MHC Class I alpha chain,
PNPase(old-35), MEK1(MAP2K1),
ARMC4, SLIT3, DNAH1, PHEX, SNX2, PLET1, ZNF313, Hap-1, MGF, SNX1, MAD, ARG1, IL-31RA, Olfactory receptor, ARF6, TMEM2, SPAG17, Guanylate cyclase, EPAS1, DMKN, Vinculin, APOD, HEY1, Vsm-RhoGEF, Synaptotagmin II, VECadherin, Synaptotagmin, Dynein, axonemal, light chains, PDE, IQCG, Plectstrin, Galpha(q)-specific Class A Orphan/other GPCRs, Rab8B, Ephrin-A receptor 1, VIPAR, NAT-1, HIF1A, Polycystin, LDB2, RABL2A, FAT3, P2X7, 1-kB, ORP-family, NOTCH4, HES1, FLJ32658, MEK1/2, ATF-3, PAFAH gamma, MIRK, B3GN1, C3orf58, ROBO1, Apaf-1, JAK2, ORP8, PDE1, Islet-1, DMP4, Galpha(q)-specific nucleotide-like GPCRs, FLVCR, DZIP1L, ATP6M, Rab-3, MIP-T3, MNS1, LRRC50, Ephrin-A receptor 5, FGFR3, IDH1, Ku70, Sortilin, MyHC, CD34, Spp24, Galectin-9, PCDHB8, PMCA2b, Carbohydrate sulfotransferases, Neuregulin 4, Ceb1, Scd2, BBS9, TRAP25, Krm1, Dynein, axonemal, heavy chains, RPGRIP1L, Oxygen-regulated protein 1, CFA54, Alpha-parvin, CAP2, MYH10, VANG1, Lyn, CENTA2, HLA-E, Ephrin-B2, RNPEP, MRE11, Ephrin-B, Dynein 2, cytoplasmic, heavy chain, NPX1, STRBP, TRIM15, PKA-reg (cAMP-dependent), HA12 (rodent), ELL, CFA74, SPAG16, Alpha-actinin, c-Maf, DNAH11, IL-15RA, RFX3, SLUG, MENA, PDE2A, RAP2C, A20, AZI2, Ephrin-A receptors, NPR3, KIF3B, Bim, FAIM2, SHANK, Tryptase delta, SynGAP, Fibrinogen gamma, DAGK, IL-1 alpha, CHST2, CCR1, CCR9, Hck, Hapln4, TLR4, SC02,

					<p>NMT1, TMEM100, Insulin, Fibulin-1, PBEF, ADAR1, KIAA1377(HIP5), GRO-1, DUSP5, SPP lyase, Galectin-8, HYEP, IDH2, IMP2, SPATA18, CAPZA, CLR3, Asporin, FLJ46266, DSCR2, Notch, SLAM, MCFD2, Galpha(q)-specific peptide GPCRs, PLEKHA5, Huntingtin, GFRalpha1, CYFIP1, HA11, CD86, POLR2G, Trp53inp2, Profilin, HYDIN, Rab-3A, TSGA2, SSAT, ACADM, CBR1, ES130 (p180), FGF10, CD40(TNFRSF5), T6441, ATF/CREB, ERK3, DNAJC13, C4orf31, SCN3A, MAP-1B, SERINC5, CCDC176, SETDB2, Glutaredoxin, MMSA, HLA-C, ATP6V1B, DNAI1, SHANK2, AGAL, DZIP, ZNF541, AL3A1, PDE1B, WDT2, N-myristoyltransferase, PCDHB16, PIP1, RGS6, HLA-B, Artemis, CHD7, Alpha-actinin 3, HDL proteins, SIX5, Dynein, axonemal, intermediate chains, C9orf98, FAT1, NME5, SNAP-29, Phosphatase regulator (inhibitor), OSTM1 (grey-lethal), TRIML1, UGCG, LRGUK, ILPIP, NCK1, RANK(TNFRSF11A), Beta adducin, GREM2, KAD7, Protein p8, AL1A1, Thyroid hormone receptor, PLCL2, Nephrocystin-4, Lrig3, PTER, STOX2, ABI2, TSNAXIP1, CABYR, PI3K reg class IA, RGS9, CD300LF, Galpha(s)-specific peptide GPCRs, TIG2, Perlecan, C2orf39, RSPH4A, NPNT, Alpha-internexin, FRK, RNF22, Glutaredoxin 1, SNX10</p>
cilium-dependent cell motility	16	1.49E-07	2.05E-05	7	<p>CCDC39, DNAH1, Dynein, axonemal, heavy chains, CFA54, SPAG16, RFX3, C2orf39</p>

References for Supplementary Material

Chandler, J.D., *et al.* (2016) Metabolic pathways of lung inflammation revealed by high-resolution metabolomics (HRM) of H1N1 influenza virus infection in mice. *Am J Physiol Regul Integr Comp Physiol*, 311, R906-R916.

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- Fortin, G., *et al.* (2009) L-carnitine, a diet component and organic cation transporter OCTN ligand, displays immunosuppressive properties and abrogates intestinal inflammation. *Clin Exp Immunol*, 156, 161-171.
- Kohlmeier, J.E. and Woodland, D.L. (2009) Immunity to respiratory viruses. *Annu Rev Immunol*, 27, 61-82.
- Liu, Q. *et al.* (2016) The cytokine storm of severe influenza and development of immunomodulatory therapy. *Cell Mol Immunol*, 13, 3-10.
- Miyake, J.H. *et al.* (2000) Bile acid induction of cytokine expression by macrophages correlates with repression of hepatic cholesterol 7alpha-hydroxylase. *J Biol Chem*, 275, 21805-21808.
- Sadik, C.D. and Luster, A.D. (2012) Lipid-cytokine-chemokine cascades orchestrate leukocyte recruitment in inflammation. *J Leukoc Biol*, 91, 207-215.
- Shannon P. *et al.* (2003) Cytoscape: a software environment for integrated models of biomolecular interaction networks. *Genome Res*, 13, 2498-2504.
- Yin, K. and Agrawal, D.K. Vitamin D and inflammatory diseases. (2014) *J Inflamm Res* 7, 69-87.