

# Supplementary Material

This supplement has been provided by the authors to give readers additional information about their work.

Supplement to "***Deficits in prenatal serine biosynthesis underlie the mitochondrial dysfunction associated with the autism-linked FMR1 gene***" by Nolin S., Napoli E., Flores A., Hagerman R.J., and Giulivi C.

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## Supplementary Methods

### ***Metabolomics and proteomics***

For metabolomic analysis of AF, plasma biosamples (AF or plasma) or UCF, aliquots were extracted by 1 ml of degassed acetonitrile:isopropanol:water (3:3:2, V/V/V) at -20°C, centrifuged and decanted with subsequent evaporation of the solvent to complete dryness. After treatment with acetonitrile/water (1:1), to remove membrane lipids and triglycerides, the supernatant was dried down a second time. Internal standards C08-C30 FAMES were added and the samples derivatized with methoxyamine hydrochloride in pyridine and subsequently with *N*-methyl-*N*-trimethylsilyltrifluoroacetamide for trimethylsilylation of acidic protons. Data were acquired using the chromatographic parameters previously reported in detail [1, 2]. Metabolites were identified by matching ion chromatographic retention index, accurate mass, and mass spectral fragmentation signatures against library entries created from authentic standard metabolites obtained with the identical analytical procedure as the experimental samples. For proteomics analysis, total proteins from either AF samples or dermal fibroblasts were precipitated by the addition of 4 volumes of -20°C acetone as described before in detail [3]. All samples were submitted to the UC Davis Mass Spectrometry Core Facility, where this analysis was performed essentially as described before [4, 5].

### ***Validation cohorts characteristics and analyses***

Two external validation cohorts were identified constituted by dermal fibroblasts and plasma obtained from subjects recruited at the MIND Institute, Sacramento, CA. Demographic details of donors are reported in **Supplementary Table S2**. Twenty-five primary dermal fibroblasts were obtained from either carriers of the premutation ( $n = 14$ ) or controls ( $n = 11$ ; **Supplementary Table S2**). Their age (average  $\pm$  SEM) was  $46 \pm 17$  y (24-67 y old) for controls, and  $50 \pm 16$  y (24-71 y old) for premutation carriers, a M-to-F ratio of 1.3 with no differences between the two diagnostic groups. From the carriers ( $n = 14$ ), 6 had FXTAS. The other external validation cohort was constituted by plasma samples from (non-carriers) controls ( $n = 16$ ) and carriers ( $n = 23$ ). [6] Their age (average  $\pm$  SEM) was  $37 \pm 13$  for controls (ranging from 24 to 57 y old), and  $37 \pm 19$  y (ranging from 8 to 63 y old) for premutation carriers, with a M-to-F ratio of 1 and no differences between the two diagnostic groups. From the carriers ( $n = 23$ ), only 4 subjects were diagnosed with FXTAS. These external validation cohorts (to prevent bias-corrected estimates of model performance [7]) were chosen based on their availability on proteomics and metabolomics. One was constituted by proteomics data from 25 dermal fibroblasts obtained through the MIND Institute, Sacramento, CA (**Supplementary Table S2**). The other one was constituted by plasma metabolomics obtained from non-carriers and carriers (**Supplementary Table S2**) obtained at the same Institution [6]. The ROC analyses were performed by utilizing MetaboAnalyst [8]. The ROC curves with AF data were generated by Monte-Carlo cross validation (MCCV) using balanced sub-sampling. In each MCCV, two thirds (2/3) of the samples were used to evaluate the feature importance. The top 2, 3, 5, 10 ...100 (max) important features were then used to build the classification model which is validated on the 1/3 the (randomly selected) samples that were left out. The procedure was repeated multiple times to calculate the performance and confidence interval of the model. We utilized the SVM linear method for both the classification and the feature ranking method. As indicate din the text, two external cohorts were used to validate the model by utilizing the hold-out feature within the analysis. The predictive performance of each model was then quantified by measures of discrimination. We determined discrimination by the area under the receiver operating characteristic curve (AUROC) with 95% confidence interval (CI). Discrimination is the ability of the model to correctly separate samples from subjects who develop FXTAS (or associated phenotype) from those who will not. For comparability of the models, we used the validation cohort with our inclusion and exclusion criteria. A sensitivity analysis was performed to assess the predictive performance of each model according to its additionally defined eligibility criteria. The potential clinical utility was evaluated for the best discriminative models by means of decision curve analysis. Decision curve analysis provides insight into the net benefit (net proportion of true positives) of the models over a range of threshold risks as opposed to designating all or no women at high risk of having a child who may develop FXTAS [9, 10]. Finally, we composed tables for the models with the highest net benefit comparing sensitivity, specificity, and positive and negative predictive values for different risk thresholds.

## Supplementary Tables

**Table S1.** Proteins identified in this and another study utilizing AF

Protein name	Gene official name	This study	Cho et al.
		Rank	
Albumin	ALB	1	1
Immunoglobulins*		2	2
Alpha-1-antitrypsin	SERPRINA1	3	6
Serotransferrin	TF	4	4
Fibronectin 1 isoform 1	FN1	5	3
Vitamin D-binding protein	GC	6	9
Insulin growth factor binding protein 1	IGFBP1	7	
Alpha-fetoprotein	AFP	8	8
Complement C3	C3	9	5
Ceruloplasmin	CP	10	7
AMBP	AMBP	11	14
Apolipoprotein A1	APOA1	12	11
Alpha-2 <sub>HS</sub> -glycoprotein	AHSG	13	
Plasminogen	PLG	14	15
ORM1-like protein	ORM1	15	
Transforming growth factor-beta-induced protein ig-h3	TGFBI	20	13
Antithrombin III	SERPINC1	26	12
Periostin	POSTN	37	10

\*Collectively, immunoglobulin chains. Of the proteins identified by mass spectrometry in our study, 12 (in gray) matched the top 15 most abundant ones in AF samples as reported by Cho et al [11]. Rank is abundance with 1 as the most abundant protein group in each set.

**Table S2.** Demographics of the fibroblasts' donors included in the present study

Clinical Group	Age (y)	Sex	Diagnosis	Outcome
C1	23	F	Control	Metabolomics
C2	24	F	Control	Metabolomics
C3	24	M	Control	Metabolomics, Proteomics
C4	25	F	Control	Metabolomics
C5	26	F	Control	Metabolomics, Proteomics
C6	26	M	Control	Metabolomics
C7	29	F	Control	Metabolomics
C8	29	F	Control	Metabolomics, Proteomics
*C9	34	F	Control	Proteomics
*C10	39	F	Control	Proteomics
*C11	40	F	Control	Proteomics
C12	41	M	Control	Metabolomics
C13	42	M	Control	Metabolomics
C14	45	F	Control	Metabolomics
C15	51	M	Control	Metabolomics
C16	54	M	Control	Metabolomics
C17	54	M	Control	Metabolomics
C18	57	F	Control	Metabolomics
C19	59	M	Control	Proteomics
C20	60	F	Control	Metabolomics
C21	61	M	Control	Proteomics
C22	62	M	Control	Proteomics
C23	63	M	Control	Proteomics
C24	67	M	Control	Proteomics
P1	8	M	Premutation	Metabolomics
P2	8	M	Premutation	Metabolomics
P3	9	M	Premutation	Metabolomics
P4	10	F	Premutation	Metabolomics
P5	17	F	Premutation	Metabolomics
P6	20	M	Premutation	Metabolomics
P7	24	F	Premutation	Metabolomics, Proteomics
P8	24	F	Premutation	Metabolomics, Proteomics
P9	25	M	Premutation	Metabolomics
P10	33	F	Premutation	Proteomics
P11	38	F	Premutation	Metabolomics, Proteomics
P12	43	F	Premutation	Metabolomics, Proteomics
P13	45	M	Premutation	Metabolomics
P14	46	M	Premutation	Metabolomics
P15	49	F	Premutation	Metabolomics
P16	50	F	Premutation	Metabolomics, Proteomics
P17	50	M	Premutation	Proteomics
P18	52	M	Premutation	Metabolomics, Proteomics
P19	53	F	Premutation	Metabolomics
P20	55	F	Premutation	Metabolomics
P21	56	M	Premutation	Metabolomics
P22	58	M	FXTAS	Metabolomics, Proteomics
P23	59	F	FXTAS	Metabolomics
P24	60	M	FXTAS	Proteomics
P25	61	M	FXTAS	Metabolomics
P26	62	M	FXTAS	Proteomics
P27	63	M	FXTAS	Metabolomics
P28	67	M	FXTAS	Proteomics
P29	69	M	FXTAS	Proteomics
P30	71	M	FXTAS	Proteomics

\*Cell lines obtained from Coriell repository. All other samples (fibroblasts and plasmas) were obtained from participants previously enrolled in Genotype/Phenotype study [6].

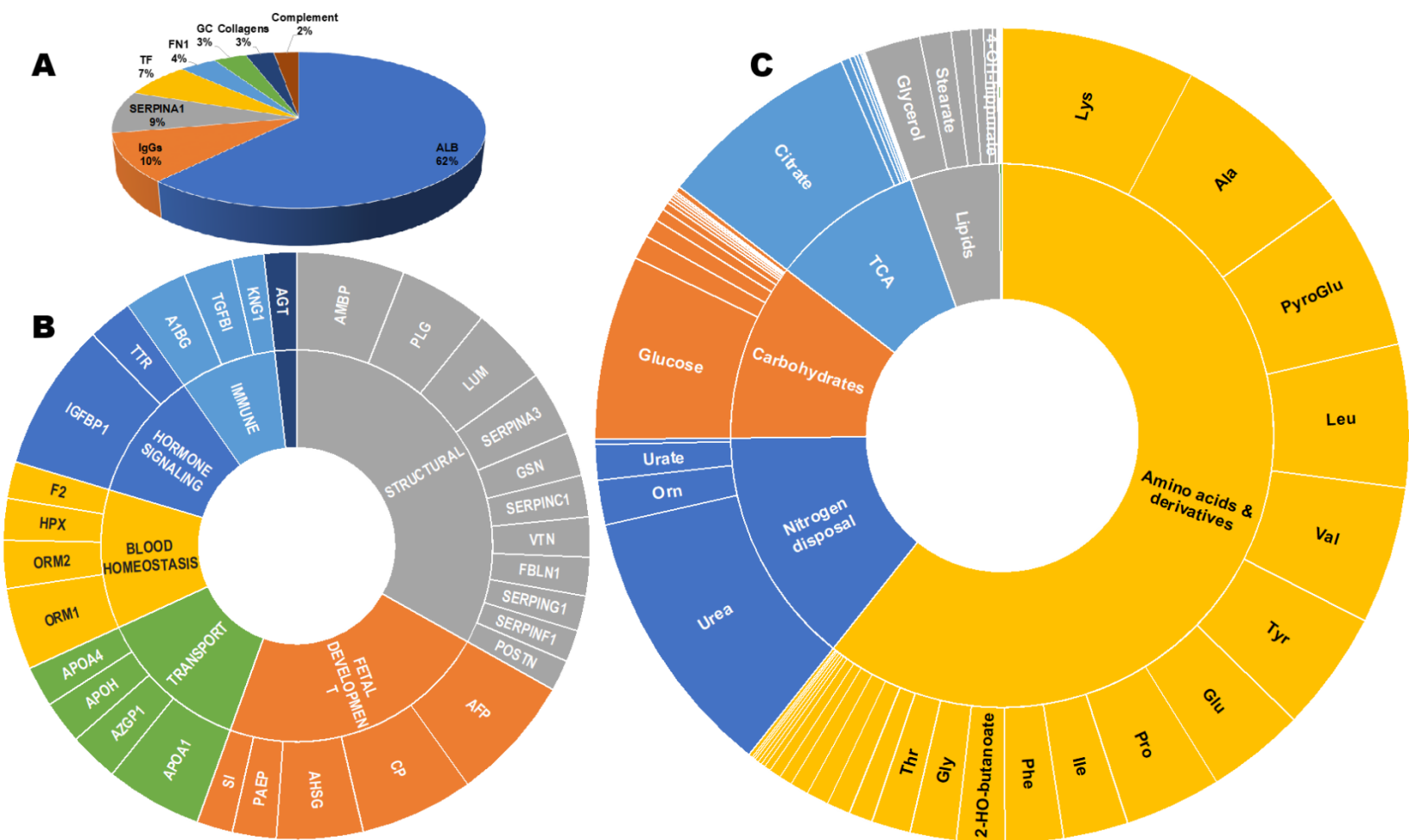
**Table S3.** Human disorders associated with premutation-linked proteins and metabolic patterns

ID	LABEL	Degree	Betweenness
181500	Schizophrenia	31	14381.05
104300	Alzheimer Disease	18	2604.56
616299	<b><i>Lipoyltransferase 1 Deficiency</i></b>	<b>12</b>	<b>1389.02</b>
211980	Lung Cancer	11	2549.07
246900	<b><i>Dihydrolipoamide Dehydrogenase Deficiency</i></b>	7	414.13
271900	Canavan Disease	6	723.64
607196	Microcephaly, Amish Type	6	264.28
203740	<b><i>Alpha-Ketoglutarate Dehydrogenase Deficiency</i></b>	<b>5</b>	<b>238.93</b>
606054	Propionic Acidemia	4	374.73
266150	Pyruvate Carboxylase Deficiency	4	322.24
220500	Deafness, Onychodystrophy, Osteodystrophy, Mental Retardation, And Seizures Syndrome	4	135.69
248600	Maple Syrup Urine Disease	4	31.68
605911	3-Hydroxy-3-Methylglutaryl-CoA Synthase-2 Deficiency	3	977.07
245450	<b><i>Lactic Aciduria Due To D-Lactic Acid</i></b>	<b>3</b>	<b>841.85</b>
600721	<b><i>D-2-Hydroxyglutaric Aciduria 1</i></b>	<b>3</b>	<b>710.56</b>
126200	Multiple Sclerosis, Susceptibility To	3	552.23
125853	Diabetes Mellitus, Noninsulin-Dependent	3	523.49
145500	Hypertension, Essential	3	521.6
608611	Ribose 5-Phosphate Isomerase Deficiency	3	473
246450	3-Hydroxy-3-Methylglutaryl-CoA Lyase Deficiency	3	433.46
237300	Carbamoyl Phosphate Synthetase I Deficiency, Due to Hyperammonemia	3	207.25
614741	Mitochondrial Pyruvate Carrier Deficiency	3	148.09
242600	Iminoglycinuria	3	138.39
252150	Molybdenum Cofactor Deficiency, Complementation Group A	3	123.31
557000	Pearson Marrow-Pancreas Syndrome	3	110.55
605814	Citrullinemia, Type II, Neonatal-Onset	3	109.97
261680	Phosphoenolpyruvate Carboxykinase Deficiency, Cytosolic	3	108.9
276700	Tyrosinemia, Type I	3	64.83
617290	Epilepsy, Early-Onset, Vitamin B6-Dependent	3	32.1
222730	Dicarboxylic Aminoaciduria	3	26.95
137215	Gastric Cancer, Hereditary Diffuse	2	705
105200	Amyloidosis, Familial Visceral	2	472
167320	Inclusion Body Myopathy Early Onset Paget Disease with or without Frontotemporal Dementia 1	2	401.11
220110	Mitochondrial Complex IV Deficiency	2	286.15
614105	Methylmalonate Semialdehyde Dehydrogenase Deficiency	2	237
614462	Hyperglycinemia, Lactic Acidosis, And Seizures	2	147.94
229600	Fructose Intolerance, Hereditary	2	136.85
229700	Fructose-1,6-Bisphosphatase Deficiency	2	136.85
612736	Cerebral Creatine Deficiency Syndrome 2	2	136.85
616034	2,4-Dienoyl-CoA Reductase Deficiency	2	115.5
600462	Myopathy, Lactic Acidosis, And Sideroblastic Anemia 1	2	55.38
614300	Hypermethioninemia Due to Adenosine Kinase Deficiency	2	47.88
608782	Pyruvate Dehydrogenase Phosphatase Deficiency	2	38.69
614654	Coenzyme Q10 Deficiency, Primary, 5	2	38.69
278300	Xanthinuria, Type I	2	27.18

ID	LABEL	Degree	Betweenness
300322	Lesch-Nyhan Syndrome	2	27.18
300661	Phosphoribosylpyrophosphate Synthetase Superactivity	2	27.18
613752	Hypermethioninemia with S-Adenosylhomocysteine Hydrolase Deficiency	2	27.17
312170	Pyruvate Dehydrogenase E1-Alpha Deficiency	2	17.6
266130	Glutathione Synthetase Deficiency	2	17.57
219150	Cutis Laxa, Autosomal Recessive, Type Iiia	2	16.08
606812	Fumarase Deficiency	2	4.58
256520	Neu-Laxova Syndrome 1	2	2.32
601815	<b>Phosphoglycerate Dehydrogenase Deficiency</b>	<b>2</b>	<b>2.32</b>
606904	Epilepsy, Myoclonic Juvenile	2	2.32
610992	<b>Phosphoserine Aminotransferase Deficiency</b>	<b>2</b>	<b>2.32</b>
614023	<b>Phosphoserine Phosphatase Deficiency</b>	<b>2</b>	<b>2.32</b>
614923	Branched-Chain Keto Acid Dehydrogenase Kinase Deficiency	2	0.92

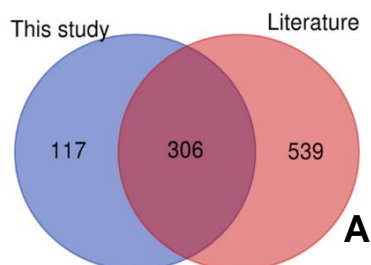
The combined omics dataset was analyzed against databases of human diseases. Schizophrenia and Alzheimer's disease were identified, along with lipolytransferase deficiency, AKG deficiency, amyloidosis as well as diseases associated with altered Ser biosynthesis. In bold, diseases discussed in the text.

Supplementary Figures



**Figure S1. Identification of the most abundant proteins and metabolites in AF.** **A.** A total of 423 unique proteins were identified by mass spectrometry in the AF supernatant samples. Albumin, immunoglobulins, SERPINA1, transferrin, fibronectin, vitamin D3 binding protein, collagens (all isoforms) and complement subunits were the most abundant proteins identified (with a relative abundance of  $\geq 2\%$ ). **B.** Analysis performed with the gene ontology molecular function feature. A significant fraction of the proteome was represented by proteins necessary for fetal development including structural ones. The rest were involved in blood homeostasis, hormone signaling, immune response and other functions. **C.** Of the total 129 metabolites identified, the largest category was represented by amino acids and derivatives, followed by carbohydrates and nitrogen disposal, tricarboxylic acid cycle (TCA) and lipids.

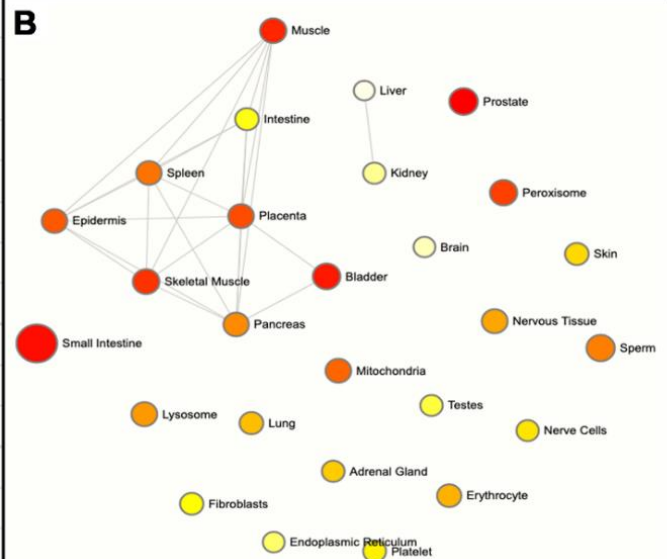




**Figure S2. Comparison of proteomic data from this study and those from other studies utilizing AF.** Proteomic data were collected from >150 studies [11-164], compared to those obtained in our study, and visualized by using a Venn diagram (A). List of proteins from AF supernatants and literature is reported in B.

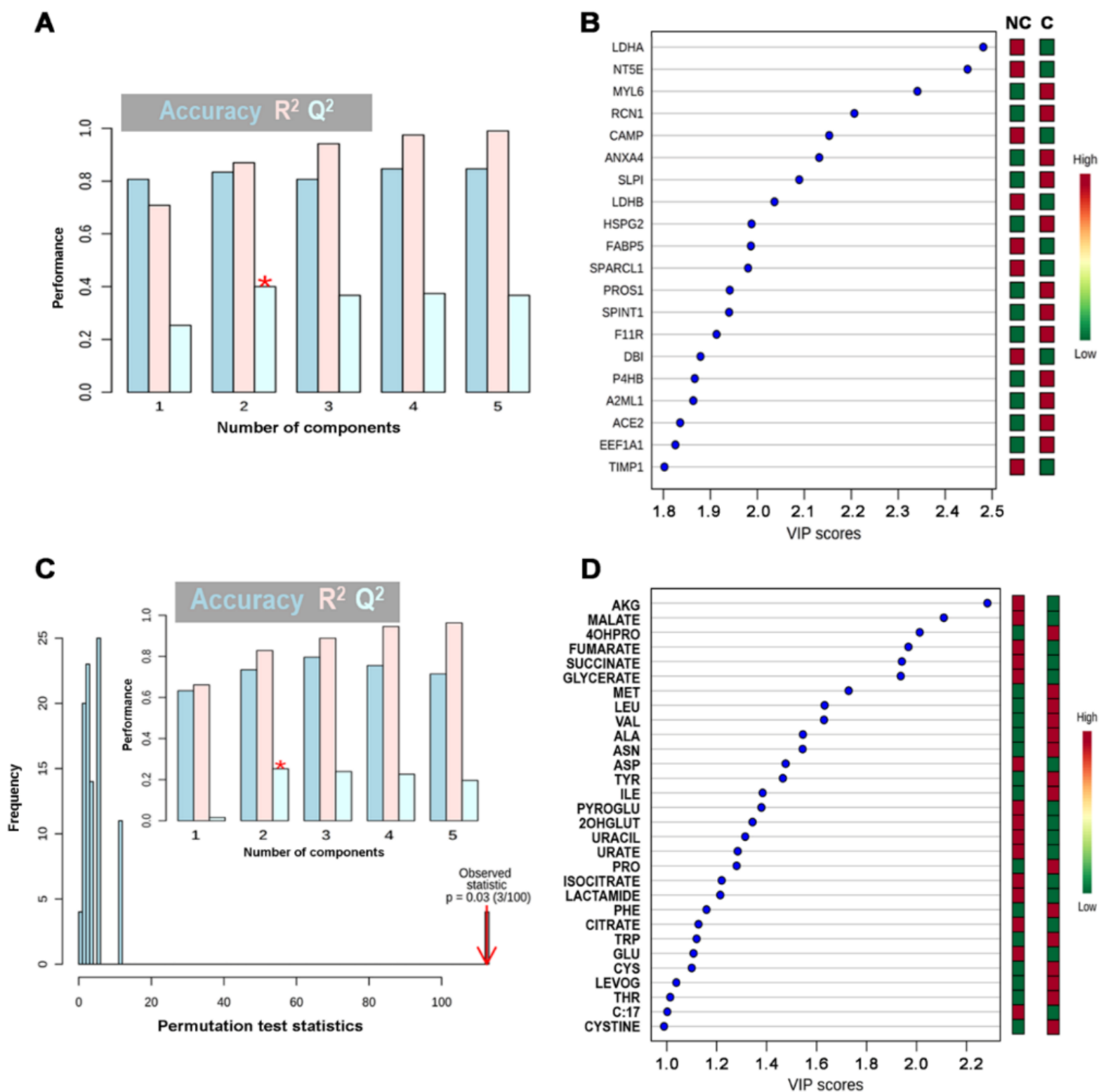
Literature AND This study (306)						This study (117)		Literature (539)															
elements						elements		elements															
A1BG	CDH11	F11R	KNG1	PRDX2	TNKB	A2M1	IGKV3D-11	ABAT	C1QB	CTHRC1	FCGR3A	HIST1H4	LRRC19	P4HA1	PSMC5	SOD1	VDAC3						
A2M	CDH13	F12	KRT1	PRDX6	TPI1	ACE	IGKV4-1	ABP1	CA2	CTNNA1	FCGR3B	HIST1H4E	LTBP4	P4HA2	PSMC6	SOD2	VIL2						
AB13BP	CDH5	F13B	KRT19	PRG2	TTR	ADAMTS2	IGLC7	ABRA	CALD1	CTS8	FDXR	HIST2H3C	LTF	PA2G4	PSMD11	SPAG9	VPS4B						
ACE2	CEL	F2	KRT2	PRL	TXN	AGRN	IGLL5	ACAA2	CALM2	CTSD	FES	HNRNPA1	MAT2A	PAK2	PSMD13	SRSF1	WARS						
ACTB	CFB	FABP1	KRT8	PROCR	VASN	AHSP	IGLV1-47	ACADM	CAP1	CTSG	FH	HNRNPA2B1	MATN3	PAPSS1	PSME1	SSB	WDR1						
ACTG2	CFD	FAM3C	KRT9	PROS1	VIM	ANXA13	IGLV1-51	ACAT1	CAPG	CTSL	FHL2	HNRNPC	MATN4	PBEF1	PTK7	ST13	XLKD1						
ACTN4	CFH	FBLN1	LAMC1	PRSS8	VTN	AOC1	IGLV10-54	ACLY	CAPZA1	CTSL1	FK506	HNRNPCL1	MCCC2	PCBP1	PTPN23	STCH	XRCC5						
ADAMTS1	CFHR1	FBLN2	LBP	PSAP	WFDC2	APOB	IGLV2-11	ACO1	CAPZA2	CTSZ	FKBP10	HNRNPH1	MDH1	PCCA	PVRL2	STIP1	YWHAB						
AFM	CFHR2	FBN1	LCN2	PSG9	YWHAE	C1RL	IGLV2-8	ACO2	CAPZB	CXCL10	FKBP1A	HNRNPH2	MDH2	PCK2	PXDN	STRAP	YWHAQ						
AFP	CFI	FCGBP	LCP1	PTGD5	YWHAG	C4B	IGLV3-10	ACOT2	CASP14	CXCL11	FKBP4	HNRNPK	MDN1	PCNA	PYCR1	SUCLG1	ZBTB33						
AGT	CFL1	FETUB	LDHA	PVR	YWHAZ	CD9	IGLV3-19	ACOT9	CAT	CXCL8	FLNA	HNRNPL	ME1	PDHA1	RAB7A	SULF2	ZYX						
AHSG	CHGA	FGA	LDHB	QSOX1		CDC5L	IGLV3-21	ACTA1	CAVIN1	CXCL9	FNDIC1	HNRPA1	METAP1	PDHB	RAC2	SUSD5							
ALB	CHRD1	FGB	LGALS1	RBP4		CDH15	IGSF1	ACTA2	CCT2	CYC5	FOLR1	HNRPA2B1	MICAL2	PDIA4	RACK1	SYCP3							
AMBP	CLCA1	FGG	LGALS3BP	RCN1		CDHR5	IL1R2	ACTG1	CCT3	DAAM2	FOLR2	HRP	MMP8	PDIA6	RAN	TAF1C							
ANGPTL2	CLEC3B	FLT1	LMAN2	RNASE1		CELA3A	IL1RAP	ACTN1	CCT4	DBN1	FRZB	HSD17B10	MMP9	PDLIM1	RANBP1	TAF3							
ANXA1	CLIC1	FMOD	LOX	S100A11		CGA	INA	ACTR1A	CCT5	DCTN2	FSCN1	HSD17B4	MMRN2	PDXK	RAP1B	TAGLN2							
ANXA2	CLIC4	FN1	LRG1	S100A8		CHRD12	ISLR	ACTR3	CCT6A	DDAH1	FTL	HSP90AE	MPO	PEBP1	RBBP4	TBCA							
ANXA4	CLPS	FSTL1	LTBP1	S100A9		COL16A1	ISM2	ADH5	CCT7	DDAH2	FUBP1	HSPA1A	MPST	PGD	RBMX	TCP1							
ANXA5	CLSTN1	FSTL3	LTBP2	SCGB1A1		EEF1A1	KLKB1	ADK	CD33L3	DDX1	G6PD	HSPA1B	MRC1	PGLS	RCN2	TFF2							
APOA1	CLU	GAPDH	LUM	SCGB3A1		F10A	KRT10	AEBP1	CD44	DDX17	GALK1	HSPA2	MRLC2	PGLYRP1	RCN3	THSA							
APOA2	COL12A1	GC	LYPD3	SCGB3A2		F10A	KRT13	AGPAT1	CDH2	DECR1	GALNT2	HSPA4	MROH8	PGM1	RETN	TINAGL1							
APOA4	COL15A1	GM2A	LYZ	SDF4		FABP5	KRT14	AGRIN	CEP192	DEFA1	GANAB	HSPA4L	MRPS22	PHB	RNASET2	TMOD3							
APOC1	COL1A1	GP2	MAN1A1	SERPINA1		FAM151A	KRT5	AK2	CGB	DES	GARS1	HSPA5	MTHFD1	PKM	RNH1	TMSL3							
APOC3	COL1A2	GPX3	MARCKS	SERPINA3		FLG	KRT79	AK4	CHI3L1	DKK2	GCN1L1	HSPA6	MUC5AC	PKM1	RPLP0	TNC							
APOD	COL2A1	GRN	MASP2	SERPINA4		FOLH1	KRT84	AKR1A1	CHP1	DKK3	GDF15	HSPA9	MUTED	PKM2	RPS27A	TNFRSF19							
APOE	COL3A1	GSN	MEP1A	SERPINA6		FUCA2	LAMB1	AKR1B1	CKAP4	DLD	GFAP	HSPD1	MVP	PLAUR	RPSA	TNFRSF1A							
APOH	COL4A2	GSTP1	MFAP4	SERPINA7		GGT1	LYVE1	ALDH1B1	CKB	DLST	GH2	HYOU1	MX1	PLIN3	RBBP1	TNFRSF8							
ATRN	COL5A1	HABP2	MIF	SERPINC1		GOLM1	MATN2	ALDH4A1	CLPB	DNAJB11	GIPC1	ICAM1	MXRA5	PLOD2	RTCB	TOMM40							
AXL	COL5A2	HAPLN1	MMP2	SERPIND1		HAPLN3	MUC1	ALDH7A1	CLPP	DNASE1	GLO1	IDH1	MYH9	PLOD3	RYR2	TPM1							
AZGP1	COL6A1	HBA1	MSLN	SERPINE2		HPR	MUC16	ALDOA	CMPK1	DPYSL2	GLS	IDH2	MYL12A	PLUNC	S100A12	TPM2							
B2M	COL6A3	HBB	MSN	SERPINF1		HRNR	MUC2	ALDOC	CNDP2	DPYSL3	GLUD1	IDH3A	MYL9	PMPCA	SAA4	TPM3							
B4GALT1	COLEC12	HBD	MUC13	SERPINF2		IGHA2	MUC5B	ANKAR	CNN2	DUS3L	GNB1	IGFALS	MYRF	PNP	SAMM50	TPM4							
BASP1	COMP	HP	MUC5AC	SERPING1		IGHG2	NOTUM	ANPEP	CNN3	DYNC112	GNB2	IGSF4C	NAMPT	PPA1	SCOTIN	TPT1							
BMP1	CP	HPX	MYDGF	SFTPB		IGHG3	NT5E	ANXA3	COIL	ECH1	GOLPH2	IL1RL1	NCL	PPBP	SDHA	TRAP1							
BP1FB1	CPA1	HRG	MYL6	SHBG		IGHV1-18	PAPLN	ANXA6	COL11A1	ECHS1	GOT1	IL6	NDST3	PPP1CA	SECTM1	TUBA1A							
BTD	CPM	HSP90AA1	NID1	SI		IGHV1-3	PLS3	APEX1	COL11A2	EEF1B2	GOT2	IMMT	NDUFA8	PPP1CB	SEPP1	TUBA1B							
C1R	CRISP3	HSP90B1	NID2	SLPI		IGHV10R15-1	PON1	APOC2	COL14A1	EEF1D	GP340	IRF7	NDUFS1	PRDX3	SEPTIN11	TUBA4A							
C1S	CST3	HSPA8	NPC2	SOD3		IGHV3-15	POTEI	APOM	COL6A2	EEF1G	GPI	ITGA3	NDUF53	PRDX4	SEPTIN2	TUBA8							
C2	CST6	HSPB1	NUCB1	SPARC		IGHV3-38	PPIAL4A	APP	CORO1C	EEF2	GPR115	ITGAM	NDUFV1	PRKCSH	SERPINA5	TUBB							
C3	CSTB	HSPG2	OGN	SPARCL1		IGHV3-43	PSG1	APRT	COTL1	EFNB2	GPR135	ITGAV	NDUFV2	PRND	SERPINB1	TUBB4A							
C4A	CTGF	HTRA1	OLFM13	SPINK1		IGHV3-49	PTMA	ARF1	CPA2	EHD1	GRB2	ITIH3	NEXN	PRPF19	SERPINB4	TUBB4B							
C5	DAG1	IGF2	ORM1	SPINK5		IGHV3-53	PZP	ARHGDI1A	CPB2	EIF3I	GRHPR	IVD	NFKB1Z	PRPS1	SERPINE1	TUFM							
C6	DBI	IGFBP1	ORM2	SPINT1		IGHV3-66	S100A6	ARHGEF19	CRISPLD1	EIF6	GSS	KLK3	NGFR	PSAT1	SERPINH1	TWF2							
C7	DCN	IGFBP2	P4HB	SPON1		IGHV3-7	SCUBE2	ARPC2	CRK	ELA2	GSTA1	KLK6	NIPSNAP3A	PSG10	SET	TWSG1							
C8A	DLK1	IGFBP3	PAEP	SPON2		IGHV3-72	SERPINA2	ARPC4	CRNN	ELA3A	GSTK1	KRT18	NME1	PSG11	SFTPA1	TXNRD1							
C8B	DMBT1	IGFBP4	PCOLCE	SPP1		IGHV3-73	SERPINB2	ASGR2	CRP	EMILIN2	GSTO1	KRT7	NME2	PSG2	SGCE	UBA1							
C8G	DMKN	IGFBP5	PDIA3	SPRR1B		IGHV3-9	SFN	ATIC	CRYAB	ENDOD1	GVIN1	LACTB	NNMT	PSMA1	SH2D3C	UBE2O							
C9	DPP4	IGFBP6	PFN1	SPRR3		IGHV3OR16-12	SHISA5	ATP5F1A	CRYZ	ENO2	HADHA	LAMA2	NOV	PSMA2	SH3BGR1	UBE2V2							
CA1	DSC2	IGFBP7	PGAM1	STC2		IGHV4-28	SLC15A1	ATP5F1B	CS	ERLIN2	HAUS3	LAP3	NRP1	PSMA3	SH3BGR3	UCHL1							
CALM1	DSC3	IGHA1	PGK1	TF		IGHV5-51	SLC38A10	ATP5PD	CSF1R	ERP29	HBE1	LF	NT5C3L	PSMA4	SHMT2	UGDH							
CALR	DSG2	IGHG1	PGLYRP2	TFF3		IGHV6-1	SLC9A3R1	ATP6V1A	CSH1	ESD	HBE2	LGALS3	OAT	PSMA5	SIGLEC5	UNC13A							
CALU	ECM1	IGHG4	PI16	TGFB1		IGKV1-16	TAGLN	AZU1	CSPG2	ETFA	HGB1	LMNA	OBP2A	PSMA6	SLC12A7	UQCRC							
CAMP	EFEMP1	IGHV1-69	PIGR	TGFB3		IGKV2-24	THBS4	BAMBI	CSPG4	ETFB	HDLBP	LMNB1	OGDH	PSMB1	SLC25A24	UQCRC1							
CD14	EFEMP2	IGKC	PLG	THBS1		IGKV2-28	TMSB10	BCAT2	CST1	ETHE1	HGFL	LOC139249	OLA1	PSMB2	SLC27A6	UQCRC2							
CD163	EFNB1	IGHV1-5	PLOD1	THY1		IGKV2-30	TTBK2	BP1	CST2	FAM71F1	HIBCH	LOC143244	OLFM4	PSMB5	SLC39A12	VCLM1							
CD248	ENO1	ITIH1	PLTP	TIMP1		IGKV3-15	TNNT1	BPNT1	CST4	FAM83B	HINT1	LOC730855	OTUB1	PSMC1	SLURP	VCLM							
CD55	ENPP2	ITIH2	POSTN	TIMP2		IGKV3-20	TXNDC5	BSG	CSTA	FBLN5	HIST1H1D	LONP1	OXCT1	PSMC2	SND1	VCP							
CD59	ENPP7	ITIH4	PPIA	TKT		IGKV3-7	VCAN	BST1	CSTF1	FBN2	HIST1H2BL	LOXL2	OXRP	PSMC3	SNRPA1	VDAC1							
CDH1	EZR	IVL	PRDX1	TMSB4X			VSIG4	BUB3				LPHN1	OXT	PSMC4	SNX6	VDAC2							

A	FROM PROTEOME			FROM METABOLOME		
		Fold Enrichment	p-value		Fold Enrichment	p-value
Plasma		17.81	1.64E-87	Prostate	2.62	1.47E-05
Liver		3.70	5.72E-46	Small Intestine	6.67	6.07E-02
Saliva		20.12	5.18E-19	Bladder	2.30	7.49E-02
Fetal brain cortex		6.58	3.51E-14	Muscle	1.88	1.37E-01
Cajal-Retzius cell		7.19	2.81E-14	Skeletal Muscle	1.95	1.42E-01
Bile		27.68	2.51E-13	Placenta	1.64	2.93E-01
Platelet		3.87	4.98E-11	Epidemis	1.57	3.38E-01
Serum		31.94	1.26E-10	Spleen	1.53	4.16E-01
Placenta		1.84	2.10E-10	Sperm	2.50	4.43E-01
Urine		21.29	8.69E-09	Pancreas	1.53	4.52E-01
Osteosarcoma		11.50	1.63E-05	Nervous Tissue	1.67	5.85E-01
Keratinocyte		5.67	1.92E-05	Erythrocyte	1.18	7.05E-01
Cerebrospinal fluid		41.06	4.50E-05	Lung	1.00	7.71E-01
Amniotic fluid		38.32	1.40E-03	Adrenal Gland	0.67	8.91E-01
Colon		1.79	6.14E-03	Skin	0.96	8.96E-01
Pancreas		1.84	8.74E-03	Nerve Cells	0.57	9.25E-01
Intestine		8.21	8.93E-03	Platelet	0.74	9.59E-01
Blood		2.04	9.23E-03	Fibroblasts	0.87	9.63E-01
Pituitary		3.27	3.64E-02	Intestine	0.96	9.65E-01
Fetal liver		3.01	3.54E-02	Testes	0.56	9.70E-01
Ascites		28.74	3.87E-02	Kidney	0.61	9.95E-01
Fibroblasts		3.47	3.91E-02	Brain	0.33	9.99E-01
Cartilage		8.84	7.56E-02	Liver	0.09	1.00E+00
Lung		1.32	9.75E-02			
Skin		1.40	9.63E-02			
Endothelial cell		4.79	1.30E-01			
Heart		1.72	1.99E-01			
Decidua		57.48	1.95E-01			
Tracheobronchial mucosa		57.48	1.95E-01			
Adipose tissue		2.46	2.42E-01			
Leukocyte		2.58	2.81E-01			
Adult brain		28.74	3.29E-01			
Erythrocyte		6.90	3.29E-01			
Foreskin		4.18	3.25E-01			
Epididymis		6.39	3.53E-01			
Aorta		2.61	3.49E-01			
Seminal plasma		22.99	3.56E-01			
Synovial fluid		22.99	3.56E-01			
Subthalamic nucleus		3.71	3.80E-01			

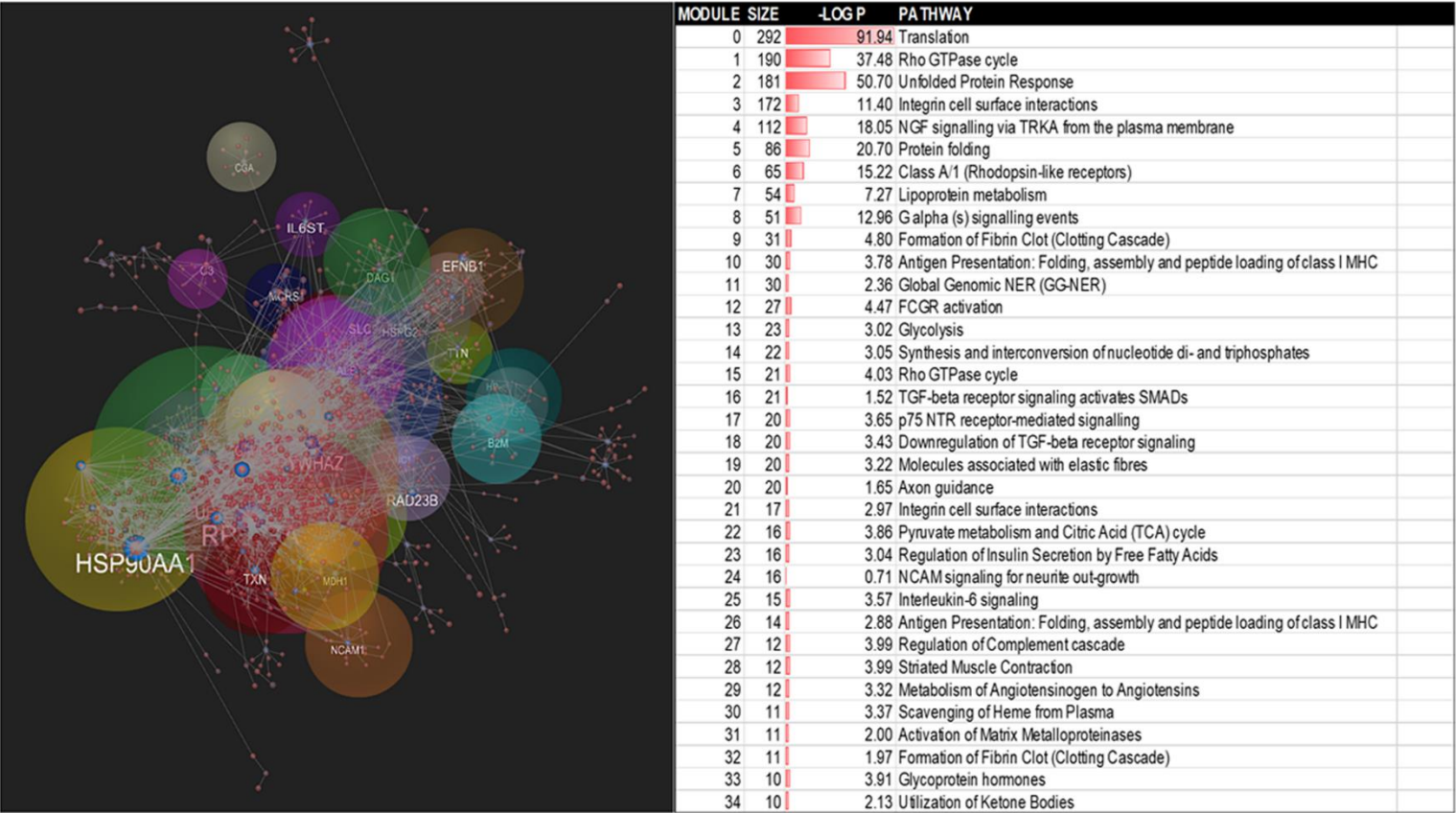


**Figure S3. Differential expression of metabolites and proteins and their tissue and subcellular distribution.**

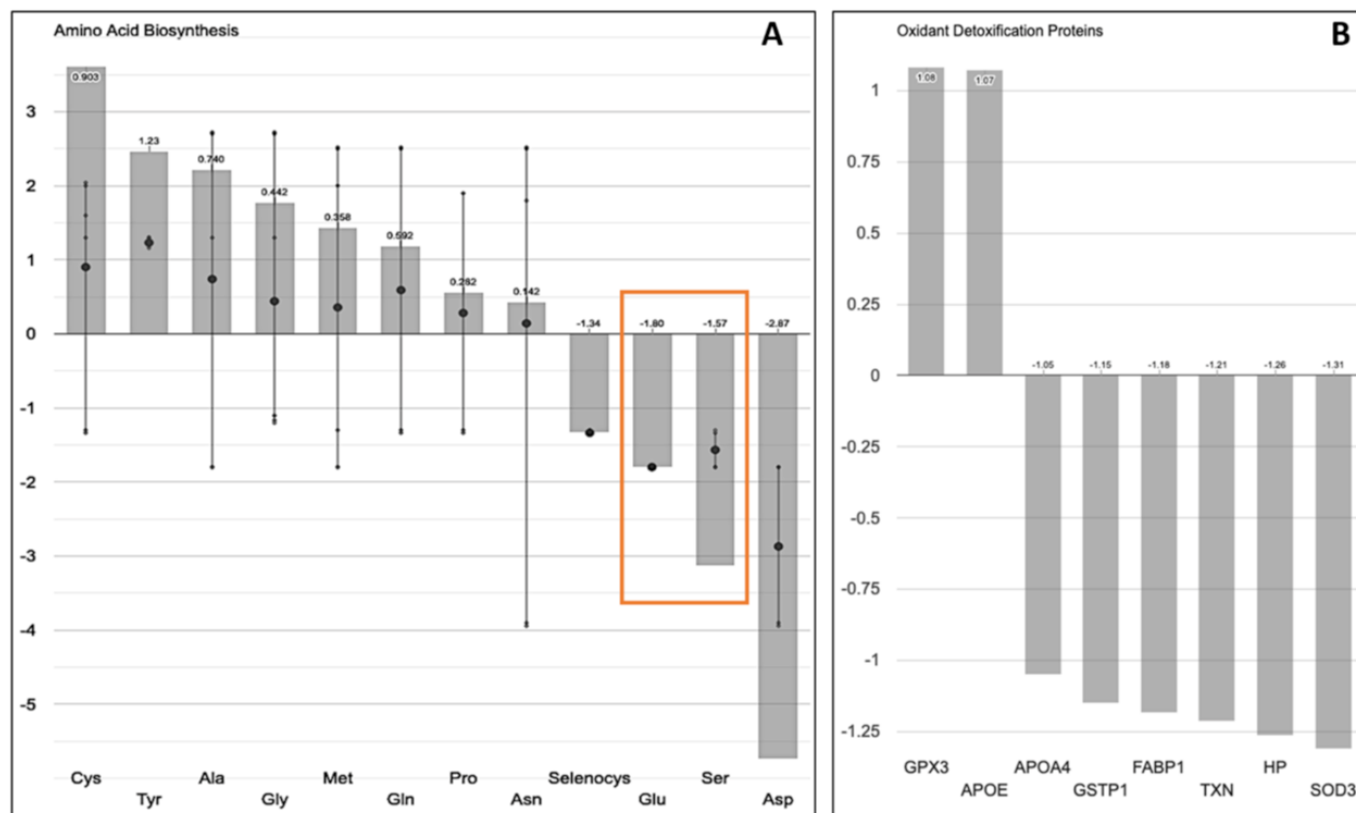
**A.** The enrichment of proteins and metabolites in AF was utilized to identify the associated tissues and subcellular compartments. In pink, tissues identified by the differential omics. **B.** Visualization of the combined data from A. Each node represents a protein-metabolite set with its color based on its *p* value and its size based on the fold enrichment. Two sets are connected by an edge if the number of their shared items is over 25% of the total number of their combined item sets. Analyses performed with DAVID and MetaboAnalyst.



**Figure S4. Differential expression of proteins and metabolites identified in AF of carriers and non-carrier fetuses.** To identify the proteins and metabolites that separated the most carriers and non-carriers (see **Figure 2**), a PLS-DA was performed. The two groups were separated by utilizing 2 components (**A** and **C**) which gave the most accurate separation. Asterisk identifies the component with the highest predictive value. The top 20 proteins (**B**) and the top 30 metabolites (**D**) identified based on the VIP scores are shown. Abbreviations: amino acids are referred by their 3-letter code; AKG, alpha-ketoglutarate; 4OHPRO, 4-hydroxyproline; PYROGLU, pyroglutamate; 2HOGLUT, 2-hydroxyglutarate; LEVOG, levoglucosan; C:17, heptanoic acid. Analysis was performed by utilizing MetaboAnalyst [8].

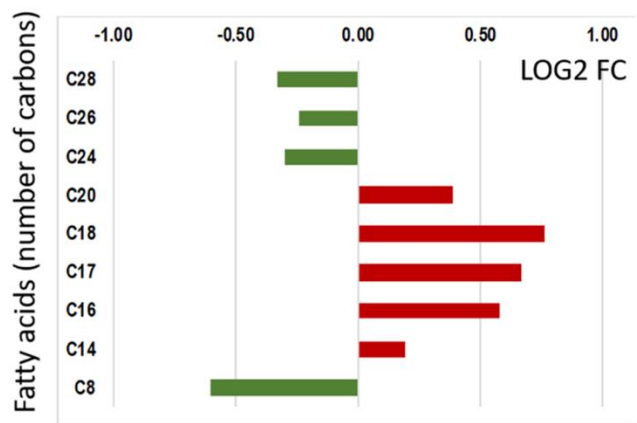


**Figure S5. Overrepresented pathways and energy metabolism in prenatal PM.** Differentially affected pathways between the genotypes were identified through a joint metabolome-proteome analysis performed with those with a  $VIP \geq 0.8$  by mining the WikiPathways and REACTOME pathway databases. Each module (**Supplementary Dataset 2**) was analyzed for pathway over-representation mining the REACTOME database. This last analysis revealed the presence of 34 modules (shown with size of nodes and significance) highlighting multiple interconnected pathways. The main pathway (292 between proteins and metabolites), regardless of the direction, was associated with translation, followed by unfolded protein response (UPR) and protein folding.

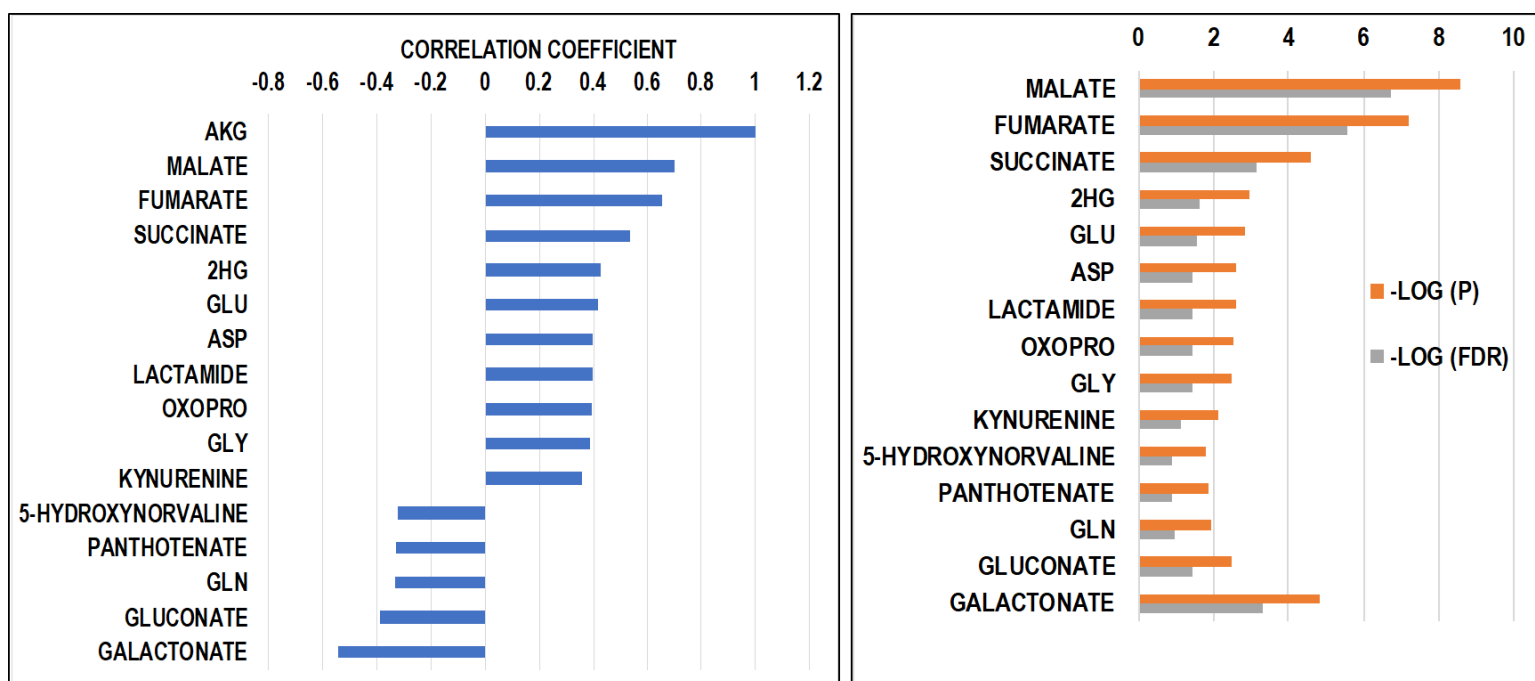


**Figure S6. Differentially expressed cellular processes linked to serine metabolism and antioxidant defenses.** The metabolism of Serine (A) as well as the detoxification pathway (B), the latter centered on antioxidant defenses against reactive oxygen species and derivatives, were down-regulated in AF from PM carriers. Analysis was obtained with BioCyc [165]. Abbreviations: APOA4, Apolipoprotein A4; APOE, Apolipoprotein E; GPX3, Glutathione Peroxidase 3; GSTP1, Glutathione S-Transferase Pi 1; FABP1, Fatty Acid-Binding Protein 1; HP, Haptoglobin; SOD3, Superoxide Dismutase 3; TXN, Thioredoxin.

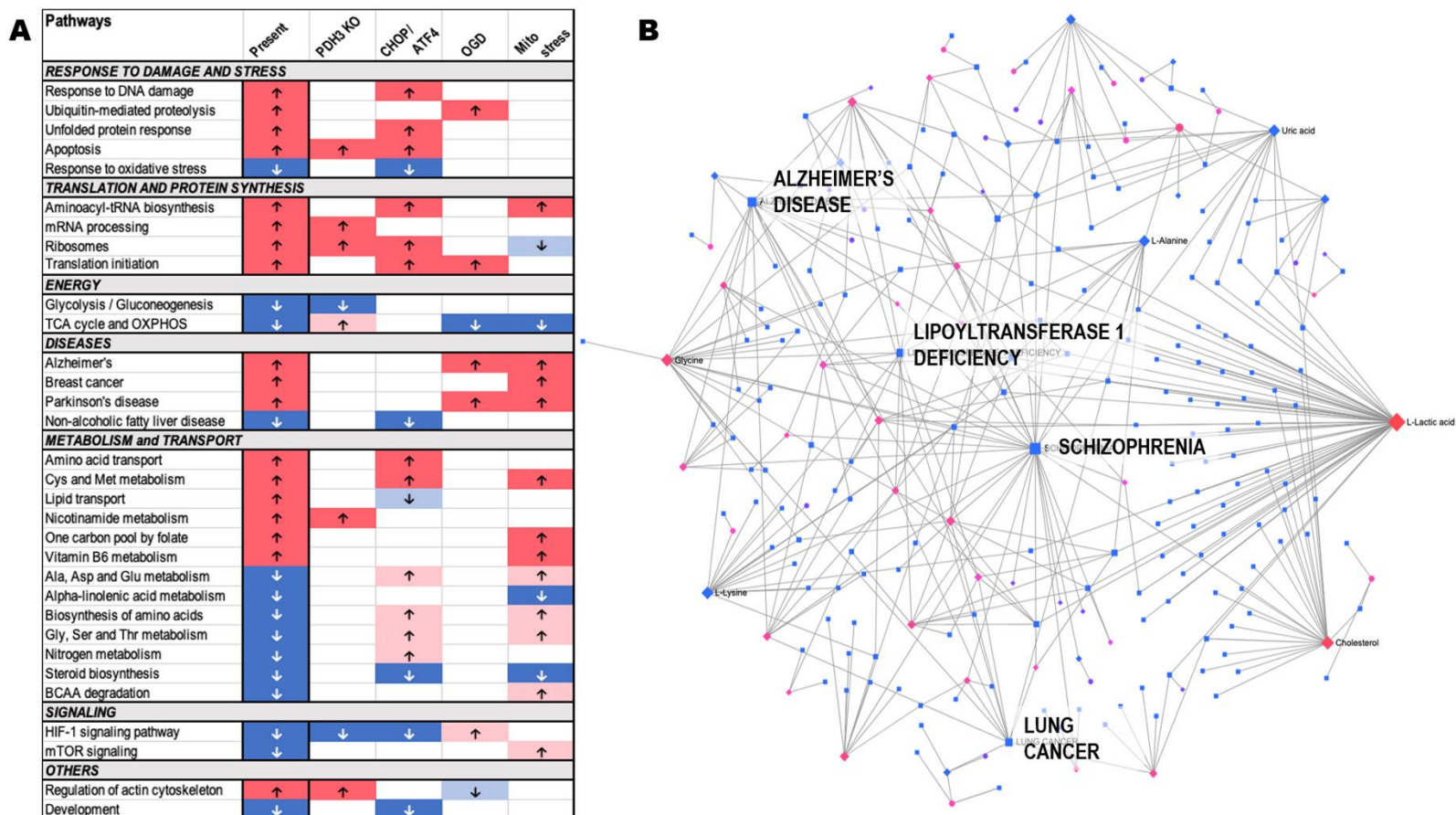




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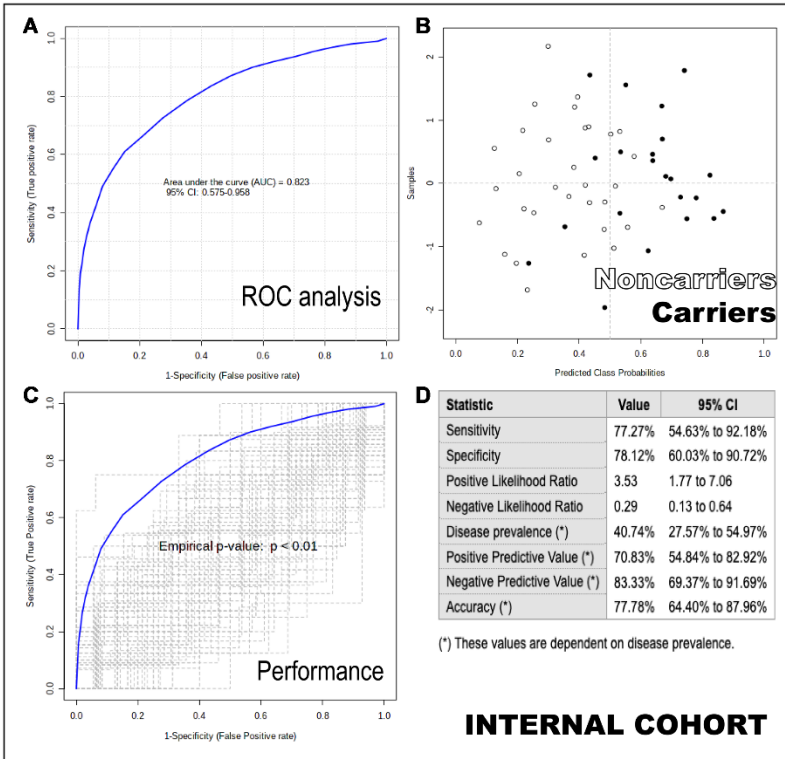


**Figure S8. TCA cycle metabolites correlation analysis.** A linear correlation analysis (Pearson's) was performed to explore whether a correlation existed among levels of metabolites belonging to the TCA cycle. The compound AKG directly correlated with malate, fumarate, succinate, 2-hydroxyglutarate, Glu, Asp and Gly, and inversely correlated with Gln and panthotenate. Log P values and false discovery rate (FDR) are shown, along with the correlation coefficients.

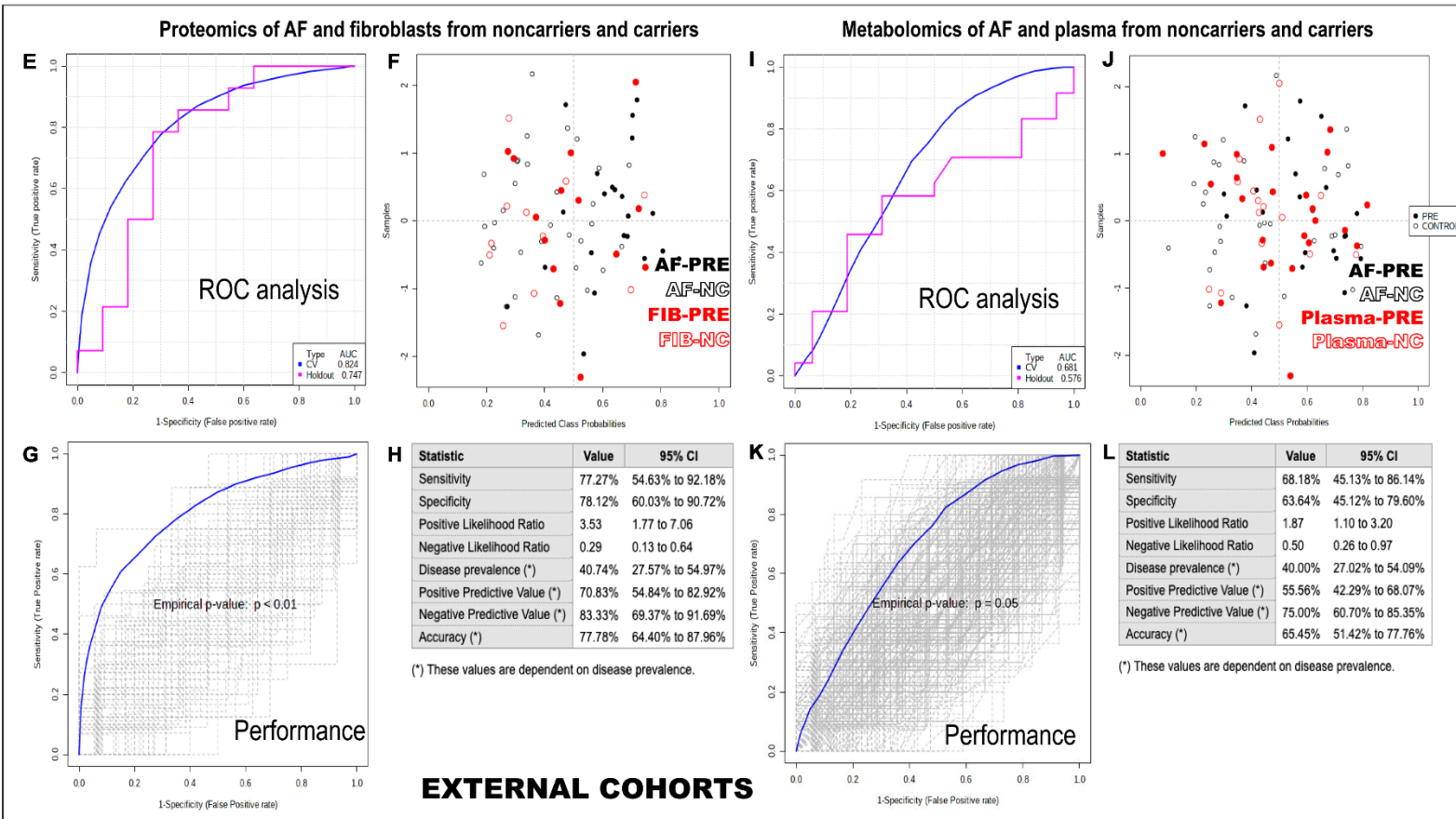


**Figure S9. Overlap of stress-related biological pathways and human disorders with the PM prenatal metabolic footprint.** **A.** Differentially regulated pathways from our study and those observed as a result of four stressors, namely (from left to right): PHD3 silencing [166]; tunicamycin-dependent ER stress [167]; OGD [168]; and mitochondrial stressors [169]. Up- and down-regulated in red and blue, respectively. Darker colors indicate a match with the direction of change observed in our study. Top, 95% confidence intervals (95%CI) of pathways that matched our study over all pathways for each of the stressors. **B.** Our combined omics dataset was analyzed via a network analysis utilizing databases of human diseases. The most significant ones associated with the PM were those with underlying MD (see also **Supplementary Table S3**).





**Figure S10. Receiver operating characteristic (ROC) curves built with proteomics and metabolomics data from AF, plasma and fibroblasts.** A ROC curve (**A**) for the predictive performance of the prenatal PM metabolic footprint was built utilizing 2/3 of the AF samples (internal cohort) and the top VIP predictors from both proteomic and metabolomic data, and then further tested by incorporating the remaining AF samples as holdout ones (internal cohort; **B-D**). In a second approach, we utilized the proteomics data from all AF samples and used as holdout samples those constituted by proteomics of skin fibroblasts from 25 subjects (**E-H**). We also utilized metabolomics from all AF samples and used as holdout ones those constituted by metabolomics data from 39 subjects (**I-L**). The performance of each model is shown after 100-cross validations (**C** with internal validation cohorts and **G** and **K** with external validation cohorts). The ROC curves (pink, **E**, **I**) and the predicted class probabilities for the AF (black) and their hold-out samples (red) are shown in panels **F**, **J**. From the confusion matrices, the diagnostic test evaluations, based on accuracy, were calculated (**D**, **H**, **L**).



## Supplementary References

1. Fiehn, O.; Wohlgemuth, G.; Scholz, M.; Kind, T.; Lee, D. Y.; Lu, Y.; Moon, S.; Nikolau, B. Quality control for plant metabolomics: reporting MSI-compliant studies. *Plant J.* **2008**, *53*, 691-704,doi:10.1111/j.1365-313X.2007.03387.x
2. Napoli, E.; Tassone, F.; Wong, S.; Angkustsiri, K.; Simon, T. J.; Song, G.; Giulivi, C. Mitochondrial Citrate Transporter-dependent Metabolic Signature in the 22q11.2 Deletion Syndrome. *J. Biol. Chem.* **2015**, *290*, 23240-53,doi:10.1074/jbc.M115.672360
3. Fujisawa, Y.; Napoli, E.; Wong, S.; Song, G.; Yamaguchi, R.; Matsui, T.; Nagasaki, K.; Ogata, T.; Giulivi, C. Impact of a novel homozygous mutation in nicotinamide nucleotide transhydrogenase on mitochondrial DNA integrity in a case of familial glucocorticoid deficiency. *BBA Clin.* **2015**, *3*, 70-78,doi:10.1016/j.bbacli.2014.12.003
4. Napoli, E.; Song, G.; Schneider, A.; Hagerman, R.; Eldeeb, M. A.; Azarang, A.; Tassone, F.; Giulivi, C. Warburg effect linked to cognitive-executive deficits in FMR1 premutation. *FASEB J.* **2016**, *30*, 3334-3351,doi:10.1096/fj.201600315R
5. Napoli, E.; Song, G.; Panoutsopoulos, A.; Riyadh, M. A.; Kaushik, G.; Halmai, J.; Levenson, R.; Zarbalis, K. S.; Giulivi, C. Beyond autophagy: a novel role for autism-linked Wdfy3 in brain mitophagy. *Sci. Rep.* **2018**, *8*, 11348,doi:10.1038/s41598-018-29421-7
6. Giulivi, C.; Napoli, E.; Tassone, F.; Halmai, J.; Hagerman, R. Plasma metabolic profile delineates roles for neurodegeneration, pro-inflammatory damage and mitochondrial dysfunction in the FMR1 premutation. *Biochem. J.* **2016**, *473*, 3871-3888,doi:10.1042/BCJ20160585
7. Bleeker, S. E.; Moll, H. A.; Steyerberg, E. W.; Donders, A. R. T.; Derksen-Lubsen, G.; Grobbee, D. E.; Moons, K. G. M. External validation is necessary in, prediction research: A clinical example. *J. Clin. Epidemiol.* **2003**, *56*, 826-832,doi:10.1016/S0895-4356(03)00207-5
8. Chong, J.; Wishart, D. S.; Xia, J. Using MetaboAnalyst 4.0 for Comprehensive and Integrative Metabolomics Data Analysis. *Curr. Protoc. Bioinformatics* **2019**, *68*, e86,doi:10.1002/cpbi.86
9. Vickers, A. J.; Cronin, A. M.; Elkin, E. B.; Gonen, M. Extensions to decision curve analysis, a novel method for evaluating diagnostic tests, prediction models and molecular markers. *BMC Med. Inform. Decis. Mak.* **2008**, *8*, 53,doi:10.1186/1472-6947-8-53
10. Vickers, A. J.; Elkin, E. B. Decision curve analysis: a novel method for evaluating prediction models. *Med. Decis. Making* **2006**, *26*, 565-74,doi:10.1177/0272989X06295361
11. Cho, C. K.; Shan, S. J.; Winsor, E. J.; Diamandis, E. P. Proteomics analysis of human amniotic fluid. *Mol. Cell. Proteomics: MCP* **2007**, *6*, 1406-15,doi:10.1074/mcp.M700090-MCP200
12. Abdel-Razeq, S. S.; Buhimschi, I. A.; Bahtiyar, M. O.; Rosenberg, V. A.; Dulay, A. T.; Han, C. S.; Werner, E. F.; Thung, S.; Buhimschi, C. S. Interpretation of amniotic fluid white blood cell count in "bloody tap" amniocenteses in women with symptoms of preterm labor. *Obstet. Gynecol.* **2010**, *116*, 344-54,doi:10.1097/AOG.0b013e3181e8fec6
13. Abu Shehab, M.; Inoue, S.; Han, V. K. M.; Gupta, M. B. Site Specific Phosphorylation of Insulin-Like Growth Factor Binding Protein-1 (IGFBP-1) for Evaluating Clinical Relevancy in Fetal Growth Restriction. *J. Proteome Res.* **2009**, *8*, 5325-5335,doi:10.1021/pr900633x
14. Abu Shehab, M.; Khosravi, J.; Han, V. K. M.; Shilton, B. H.; Gupta, M. B. Site-Specific IGFBP-1 Hyper-Phosphorylation in Fetal Growth Restriction: Clinical and Functional Relevance. *J. Proteome Res.* **2010**, *9*, 1873-1881,doi:10.1021/pr900987n
15. Aiello, D.; Giambona, A.; Leto, F.; Passarello, C.; Damiani, G.; Maggio, A.; Siciliano, C.; Napoli, A. Human coelomic fluid investigation: A MS-based analytical approach to prenatal screening. *Sci. Rep.* **2018**, *8*,doi:10.1038/s41598-018-29384-9
16. Alam, M.; Mahajan, M.; Raziuddin, M.; Singh, T. P.; Yadav, S. Proteomics-based approach for identification and purification of human phosphate binding apolipoprotein from amniotic fluid. *Genet. Mol. Res.* **2009**, *8*, 929-937,doi:10.4238/vol8-3gmr620
17. Anagnostopoulos, A. K.; Kolialexi, A.; Mavrou, A.; Vougas, K.; Papantoniou, N.; Antsaklis, A.; Kanavakis, E.; Fountoulakis, M.; Tsangaris, G. T. Proteomic analysis of amniotic fluid in pregnancies with Klinefelter syndrome fetuses. *J. Proteomics* **2010**, *73*, 943-950,doi:10.1016/j.jprot.2009.12.009
18. Arnon, S.; Litmanovitz, I. Diagnostic tests in neonatal sepsis. *Curr. Opin. Infect. Dis.* **2008**, *21*, 223-227,doi:DOI 10.1097/QCO.0b013e3282fa15dd

19. Bahtiyar, M. O.; Copel, J. A.; Mahoney, M. J.; Buhimschi, I. A.; Buhimschi, C. S. Proteomics: A novel methodology to complement prenatal diagnosis of chromosomal abnormalities and inherited human diseases. *Am. J. Perinat.* **2007**, *24*, 167-181,doi:10.1055/s-2007-972927
20. Bazrafshan, A.; Owji, M.; Yazdani, M.; Varedi, M. Activation of mitosis and angiogenesis in diabetes-impaired wound healing by processed human amniotic fluid. *J. Surg. Res.* **2014**, *188*, 545-552,doi:10.1016/j.jss.2014.01.041
21. Bitsika, V.; Roubelakis, M. G.; Zagoura, D.; Trohatou, O.; Makridakis, M.; Pappa, K. I.; Marini, F. C.; Vlahou, A.; Anagnou, N. P. Human Amniotic Fluid-Derived Mesenchymal Stem Cells As Therapeutic Vehicles: A Novel Approach For the Treatment of Bladder Cancer. *Stem Cells Dev.* **2012**, *21*, 1097-1111,doi:10.1089/scd.2011.0151
22. Bredeson, S.; Papaconstantinou, J.; Deford, J. H.; Kechichian, T.; Syed, T. A.; Saade, G. R.; Menon, R. HMGB1 Promotes a p38MAPK Associated Non-Infectious Inflammatory Response Pathway in Human Fetal Membranes. *Plos One* **2014**, *9*,doi:10.1371/journal.pone.0113799
23. Brown, K. J.; Formolo, C. A.; Seol, H.; Marathi, R. L.; Duguez, S.; An, E.; Pillai, D.; Nazarian, J.; Rood, B. R.; Hathout, Y. Advances in the proteomic investigation of the cell secretome. *Expert Rev. Proteomic* **2012**, *9*, 337-345,doi:10.1586/Epr.12.21
24. Buhimschi, C. S.; Abdel-Razeq, S.; Cackovic, M.; Pettker, C. M.; Dulay, A. T.; Bahtiyar, M. O.; Zambrano, E.; Martin, R.; Norwitz, E. R.; Bhandari, V., et al. Fetal heart rate monitoring patterns in women with amniotic fluid proteomic profiles indicative of inflammation. *Am. J. Perinat.* **2008**, *25*, 359-372,doi:10.1055/s-2008-1078761
25. Buhimschi, C. S.; Bhandari, V.; Hamar, B. D.; Bahtiyar, M. O.; Zhao, G. M.; Sfakianaki, A. K.; Pettker, C. M.; Magloire, L.; Funai, E.; Norwitz, E. R., et al. Proteomic profiling of the amniotic fluid to detect inflammation, infection, and neonatal sepsis. *Plos Med.* **2007**, *4*, 84-94,doi:10.1371/journal.pmed.0040018
26. Buhimschi, C. S.; Bhandari, V.; Han, Y. W.; Dulay, A. T.; Balumbusch, M. A.; Madri, J. A.; Buhimschi, I. A. Using proteomics in perinatal and neonatal sepsis: hopes and challenges for the future. *Curr. Opin. Infect. Dis.* **2009**, *22*, 235-243,doi:10.1097/QCO.0b013e32832a5963
27. Buhimschi, C. S.; Buhimschi, I. A.; Abdel-Razeq, S.; Rosenberg, V. A.; Thung, S. F.; Zhao, G. M.; Wang, E.; Bhandari, V. Proteomic biomarkers of intra-amniotic inflammation: Relationship with funisitis and early-onset sepsis in the premature neonate. *Ped. Res.* **2007**, *61*, 318-324,doi:10.1203/01.pdr.0000252439.48564.37
28. Buhimschi, C. S.; Dulay, A. T.; Abdel-Razeq, S.; Zhao, G.; Lee, S.; Hodgson, E. J.; Bhandari, V.; Buhimschi, I. A. Fetal inflammatory response in women with proteomic biomarkers characteristic of intra-amniotic inflammation and preterm birth. *Bjog-Int. J. Obstet. Gy.* **2009**, *116*, 257-267,doi:10.1111/j.1471-0528.2008.01925.x
29. Buhimschi, C. S.; Weiner, C. P.; Buhimschi, I. A. Proteomics, part II: The emerging role of proteomics over genomics in spontaneous preterm labor/birth. *Obstet. Gynecol. Surv.* **2006**, *61*, 543-553,doi:DOI 10.1097/01.ogx.0000228779.39568.59
30. Buhimschi, I. A. Using SELDI-TOF Mass Spectrometry on Amniotic Fluid and for Clinical Proteomics and Theranostics in Disorders of Pregnancy. *Methods Mol. Biol.* **2012**, *818*, 171-197,doi:10.1007/978-1-61779-418-6\_13
31. Buhimschi, I. A.; Buhimschi, C. S. Proteomics of the amniotic fluid in assessment of the placenta. Relevance for preterm birth. *Placenta* **2008**, *29*, S95-S101,doi:10.1016/j.placenta.2007.12.001
32. Buhimschi, I. A.; Buhimschi, C. S. Proteomics/diagnosis of chorioamnionitis and of relationships with the fetal exposome. *Semin. Fetal Neonat. M.* **2012**, *17*, 36-45,doi:10.1016/j.siny.2011.10.002
33. Buhimschi, I. A.; Buhimschi, C. S.; Christner, R.; Norwitz, E.; Weiner, C. P. Proteomic profiling and intra-amniotic infection. *Jama-J. Am. Med. Assoc.* **2004**, *292*, 2338-2338,doi:DOI 10.1001/jama.292.19.2338-a
34. Buhimschi, I. A.; Buhimschi, C. S.; Christner, R.; Weiner, C. P. Proteomics technology for the accurate diagnosis of inflammation in twin pregnancies. *Bjog-Int. J. Obstet. Gy.* **2005**, *112*, 250-255,doi:10.1111/j.1471-0528.2004.00341.x
35. Buhimschi, I. A.; Buhimschi, C. S.; Weiner, C. P.; Kimura, T.; Hamar, B. D.; Sfakianaki, A. K.; Norwitz, E. R.; Funai, E. F.; Ratner, E. Proteomic but not enzyme-linked immunosorbent assay technology detects amniotic fluid monomeric calgranulins from their complexed calprotectin form. *Clin. Diagn. Lab. Immun.* **2005**, *12*, 837-844,doi:10.1128/Cdli.12.7.837-844.2005
36. Buhimschi, I. A.; Christner, R.; Buhimschi, C. S. Proteomic biomarker analysis of amniotic fluid for identification of intra-amniotic inflammation. *Bjog-Int. J. Obstet. Gy.* **2005**, *112*, 173-181,doi:10.1111/j.1471-0528.2004.00340.x
37. Buhimschi, I. A.; Zambrano, E.; Pettker, C. M.; Bahtiyar, M. O.; Paidas, M.; Rosenberg, V. A.; Thung, S.; Salafia, C. M.; Buhimschi, C. S. Using proteomic analysis of the human amniotic fluid to identify histologic chorioamnionitis. *Obstet. Gynecol.* **2008**, *111*, 403-412,doi:DOI 10.1097/AOG.0b013e31816102aa

38. Buhimschi, I. A.; Zhao, G.; Rosenberg, V. A.; Abdel-Razeq, S.; Thung, S.; Buhimschi, C. S. Multidimensional Proteomics Analysis of Amniotic Fluid to Provide Insight into the Mechanisms of Idiopathic Preterm Birth. *Plos One* **2008**, 3,doi:10.1371/journal.pone.0002049
39. Bujold, E.; Romero, R.; Kusanovic, J. P.; Erez, O.; Gotsch, F.; Chaiworapongsa, T.; Gomez, R.; Espinoza, J.; Vaisbuch, E.; Kim, Y. M., et al. Proteomic profiling of amniotic fluid in preterm labor using two-dimensional liquid separation and mass spectrometry. *J. Matern.-Fetal Neo. M.* **2008**, 21, 697-713,doi:10.1080/14767050802053289
40. Cecconi, D.; Lonardoni, F.; Favretto, D.; Cosmi, E.; Tucci, M.; Visentin, S.; Cecchetto, G.; Fais, P.; Viel, G.; Ferrara, S. D. Changes in amniotic fluid and umbilical cord serum proteomic profiles of fetuses with intrauterine growth retardation. *Electrophoresis* **2011**, 32, 3630-3637,doi:10.1002/elps.201100256
41. Cen, J.; Lv, L.; Wei, Y.; Deng, L.; Huang, L.; Deng, X.; Qin, Q.; Sun, Y.; Pang, L. Comparative proteome analysis of amniotic fluids and placentas from patients with idiopathic polyhydramnios. *Placenta* **2020**, 89, 67-77,doi:10.1016/j.placenta.2019.10.010
42. Chen, C. P.; Lai, T. C.; Chern, S. R.; Li, S. H.; Chou, H. C.; Chen, Y. W.; Lin, S. T.; Lu, Y. C.; Wu, C. L.; Li, J. M., et al. Proteome differences between male and female fetal cells in amniotic fluid. *OMICS* **2013**, 17, 16-26,doi:10.1089/omi.2010.0145
43. Chen, W. Q.; Siegel, N.; Li, L.; Pollak, A.; Hengstschlager, M.; Lubec, G. Variations of protein levels in human amniotic fluid stem cells CD117/2 over passages 5-25. *J. Proteome Res.* **2009**, 8, 5285-95,doi:10.1021/pr900630s
44. Cheng, P. J.; Wang, T. H.; Huang, S. Y.; Kao, C. C.; Lu, J. H.; Hsiao, C. H.; Shaw, S. W. Differential proteomics analysis of amniotic fluid in pregnancies of increased nuchal translucency with normal karyotype. *Prenat. Diagn.* **2011**, 31, 274-81,doi:10.1002/pd.2719
45. Chevalier, R. L. Biomarkers of congenital obstructive nephropathy: past, present and future. *J. Urol.* **2004**, 172, 852-7,doi:10.1097/01.ju.0000129542.22043.ef
46. Chevalier, R. L. Prognostic factors and biomarkers of congenital obstructive nephropathy. *Pediatr. Nephrol.* **2016**, 31, 1411-20,doi:10.1007/s00467-015-3291-3
47. Cho, C. K.; Diamandis, E. P. Application of proteomics to prenatal screening and diagnosis for aneuploidies. *Clin. Chem. Lab. Med.* **2011**, 49, 33-41,doi:10.1515/CCLM.2011.002
48. Cho, C. K.; Drabovich, A. P.; Batruch, I.; Diamandis, E. P. Verification of a biomarker discovery approach for detection of Down syndrome in amniotic fluid via multiplex selected reaction monitoring (SRM) assay. *J. Proteomics* **2011**, 74, 2052-9,doi:10.1016/j.jprot.2011.05.025
49. Cho, C. K.; Smith, C. R.; Diamandis, E. P. Amniotic fluid proteome analysis from Down syndrome pregnancies for biomarker discovery. *J. Proteome Res.* **2010**, 9, 3574-82,doi:10.1021/pr100088k
50. Choolani, M.; Narasimhan, K.; Kolla, V.; Hahn, S. Proteomic technologies for prenatal diagnostics: advances and challenges ahead. *Expert Rev. Proteomics* **2009**, 6, 87-101,doi:10.1586/14789450.6.1.87
51. Cobo, T.; Palacio, M.; Grande, M.; Sanchez-Garcia, A. B.; Estanyol, J. M.; Lopez, M.; Bosch, J.; Marti, C.; Gratacos, E. Cervical Alpha-Actinin-4 Is Upregulated in Women with Threatened Preterm Labor and Microbial Invasion of the Amniotic Cavity. *Fetal Diagn. Ther.* **2018**, 44, 36-43,doi:10.1159/000478259
52. Cobo, T.; Palacio, M.; Navarro-Sastre, A.; Ribes, A.; Bosch, J.; Filella, X.; Gratacos, E. Predictive value of combined amniotic fluid proteomic biomarkers and interleukin-6 in preterm labor with intact membranes. *Am. J. Obstet. Gynecol.* **2009**, 200, 499 e1-6,doi:10.1016/j.ajog.2008.12.036
53. Conde-Agudelo, A.; Papageorgiou, A. T.; Kennedy, S. H.; Villar, J. Novel biomarkers for the prediction of the spontaneous preterm birth phenotype: a systematic review and meta-analysis. *BJOG* **2011**, 118, 1042-54,doi:10.1111/j.1471-0528.2011.02923.x
54. Consonni, S.; Mainini, V.; Pizzardi, A.; Gianazza, E.; Chinello, C.; Locatelli, A.; Magni, F. Non-invasively collected amniotic fluid as a source of possible biomarkers for premature rupture of membranes investigated by proteomic approach. *Arch. Gynecol. Obstet.* **2014**, 289, 299-306,doi:10.1007/s00404-013-2967-9
55. Crawford, J. T.; Pereira, L.; Buckmaster, J.; Gravett, M. G.; Tolosa, J. E. Amniocentesis results and novel proteomic analysis in a case of occult candidal chorioamnionitis. *J. Matern. Fetal Neonatal Med.* **2006**, 19, 667-70,doi:10.1080/14767050600738289
56. Croitor-Sava, A.; Beck, V.; Sandaite, I.; Van Huffel, S.; Dresselaers, T.; Claus, F.; Himmelreich, U.; Deprest, J. High-Resolution (1)H NMR Spectroscopy Discriminates Amniotic Fluid of Fetuses with Congenital Diaphragmatic Hernia from Healthy Controls. *J. Proteome Res.* **2015**, 14, 4502-10,doi:10.1021/acs.jproteome.5b00131
57. Cruickshank, J. K.; Mbanya, J. C.; Wilks, R.; Balkau, B.; McFarlane-Anderson, N.; Forrester, T. Sick genes, sick individuals or sick populations with chronic disease? The emergence of diabetes and high blood pressure in African-origin populations. *Int. J. Epidemiol.* **2001**, 30, 111-7,doi:10.1093/ije/30.1.111

58. Da Silva, M.; Dombre, C.; Brionne, A.; Monget, P.; Chesse, M.; De Pauw, M.; Mills, M.; Combes-Soia, L.; Labas, V.; Guyot, N., et al. The Unique Features of Proteins Depicting the Chicken Amniotic Fluid. *Mol. Cell Proteomics* **2019**, *18*, S174-S190,doi:10.1074/mcp.RA117.000459
59. Dasari, S.; Pereira, L.; Reddy, A. P.; Michaels, J. E.; Lu, X.; Jacob, T.; Thomas, A.; Rodland, M.; Roberts, C. T., Jr.; Gravett, M. G., et al. Comprehensive proteomic analysis of human cervical-vaginal fluid. *J. Proteome Res.* **2007**, *6*, 1258-68,doi:10.1021/pr0605419
60. De Seta, F.; Banco, R.; Guaschino, S.; De Santo, D.; Turrisi, A.; Piva, C. [Proteomic applications in gynecology-obstetrics]. *Minerva Ginecol.* **2011**, *63*, 39-46
61. Delanghe, J. R.; Speeckaert, M. M. Translational research and biomarkers in neonatal sepsis. *Clin. Chim. Acta* **2015**, *451*, 46-64,doi:10.1016/j.cca.2015.01.031
62. Deng, B.; Dong, Z.; Liu, Y.; Wang, C.; Liu, J.; Wang, C.; Qu, X. Effects of pretreatment protocols on human amniotic fluid protein profiling with SELDI-TOF MS using protein chips and magnetic beads. *Clin. Chim. Acta* **2010**, *411*, 1051-7,doi:10.1016/j.cca.2010.03.036
63. Di Venere, M.; Viglio, S.; Cagnone, M.; Bardoni, A.; Salvini, R.; Iadarola, P. Advances in the analysis of "less-conventional" human body fluids: An overview of the CE- and HPLC-MS applications in the years 2015-2017. *Electrophoresis* **2018**, *39*, 160-178,doi:10.1002/elps.201700276
64. Dixon, C. L.; Sheller-Miller, S.; Saade, G. R.; Fortunato, S. J.; Lai, A.; Palma, C.; Guanzon, D.; Salomon, C.; Menon, R. Amniotic Fluid Exosome Proteomic Profile Exhibits Unique Pathways of Term and Preterm Labor. *Endocrinology* **2018**, *159*, 2229-2240,doi:10.1210/en.2018-00073
65. Dudzik, D.; Revello, R.; Barbas, C.; Bartha, J. L. LC-MS-based metabolomics identification of novel biomarkers of chorioamnionitis and its associated perinatal neurological damage. *J. Proteome Res.* **2015**, *14*, 1432-44,doi:10.1021/pr501087x
66. Fotopoulou, C.; Kyeyamwa, S.; Linder, M.; Thieme, D.; Hartenstein, S.; Klein, O.; Dudenhausen, J. W.; Henrich, W.; Kalache, K. D.; Bamberg, C. Proteomic analysis of midtrimester amniotic fluid to identify novel biomarkers for preterm delivery. *J. Matern. Fetal Neonatal Med.* **2012**, *25*, 2488-93,doi:10.3109/14767058.2012.712565
67. Fu, W. Y.; Xu, L. H.; Yu, Y. N. Proteomic analysis of cellular response to microcystin in human amnion FL cells. *J. Proteome Res.* **2005**, *4*, 2207-15,doi:10.1021/pr050325k
68. Gianazza, E.; Miller, I.; Guerrini, U.; Palazzolo, L.; Parravicini, C.; Eberini, I. Gender proteomics II. Which proteins in sexual organs. *J. Proteomics* **2018**, *178*, 18-30,doi:10.1016/j.jprot.2017.10.001
69. Gianazza, E.; Wait, R.; Begum, S.; Eberini, I.; Campagnoli, M.; Labo, S.; Galliano, M. Mapping the 5-50-kDa fraction of human amniotic fluid proteins by 2-DE and ESI-MS. *Proteomics Clin. Appl.* **2007**, *1*, 167-75,doi:10.1002/prca.200600543
70. Gonzalez-Buitrago, J. M.; Ferreira, L.; Muniz, M. C. [Clinical proteomics and new biomarkers in biological fluids]. *Med. Clin. (Barc)* **2008**, *131*, 426-34,doi:10.1157/13126219
71. Govia, R. N. M.; Birse, K. D.; Sepehri, S.; Khafipour, E.; Menticoglou, S. M.; Burgener, A. D.; Poliquin, V. Amniotic fluid proteomic signatures of cervical insufficiency and their association with length of latency. *Am. J. Reprod. Immunol.* **2018**, *80*, e13030,doi:10.1111/aji.13030
72. Graca, G.; Duarte, I. F.; Barros, A. S.; Goodfellow, B. J.; Diaz, S.; Carreira, I. M.; Couceiro, A. B.; Galhano, E.; Gil, A. M. (1)H NMR based metabonomics of human amniotic fluid for the metabolic characterization of fetus malformations. *J. Proteome Res.* **2009**, *8*, 4144-50,doi:10.1021/pr900386f
73. Graca, G.; Duarte, I. F.; Barros, A. S.; Goodfellow, B. J.; Diaz, S. O.; Pinto, J.; Carreira, I. M.; Galhano, E.; Pita, C.; Gil, A. M. Impact of prenatal disorders on the metabolic profile of second trimester amniotic fluid: a nuclear magnetic resonance metabonomic study. *J. Proteome Res.* **2010**, *9*, 6016-24,doi:10.1021/pr100815q
74. Gravett, M. G.; Novy, M. J.; Rosenfeld, R. G.; Reddy, A. P.; Jacob, T.; Turner, M.; McCormack, A.; Lapidus, J. A.; Hitti, J.; Eschenbach, D. A., et al. Diagnosis of intra-amniotic infection by proteomic profiling and identification of novel biomarkers. *JAMA* **2004**, *292*, 462-9,doi:10.1001/jama.292.4.462
75. Hallingstrom, M.; Lenco, J.; Vajrychova, M.; Link, M.; Tambor, V.; Liman, V.; Bullarbo, M.; Nilsson, S.; Tsiartas, P.; Cobo, T., et al. Proteomic Analysis of Early Mid-Trimester Amniotic Fluid Does Not Predict Spontaneous Preterm Delivery. *Plos One* **2016**, *11*, e0155164,doi:10.1371/journal.pone.0155164
76. Hampton, T. Comprehensive "proteomic profile" of amniotic fluid may aid prenatal diagnosis. *JAMA* **2007**, *298*, 1751,doi:10.1001/jama.298.15.1751
77. Han, Y. W.; Shen, T.; Chung, P.; Buhimschi, I. A.; Buhimschi, C. S. Uncultivated bacteria as etiologic agents of intra-amniotic inflammation leading to preterm birth. *J. Clin. Microbiol.* **2009**, *47*, 38-47,doi:10.1128/JCM.01206-08
78. Hassan, M. I.; Kumar, V.; Singh, T. P.; Yadav, S. Proteomic analysis of human amniotic fluid from Rh(-) pregnancy. *Prenat. Diagn.* **2008**, *28*, 102-8,doi:10.1002/pd.1941

79. Hitti, J.; Lapidus, J. A.; Lu, X.; Reddy, A. P.; Jacob, T.; Dasari, S.; Eschenbach, D. A.; Gravett, M. G.; Nagalla, S. R. Noninvasive diagnosis of intraamniotic infection: proteomic biomarkers in vaginal fluid. *Am. J. Obstet. Gynecol.* **2010**, *203*, 32 e1-8,doi:10.1016/j.ajog.2010.03.037
80. Hsu, T. Y.; Lin, H.; Hung, H. N.; Yang, K. D.; Ou, C. Y.; Tsai, C. C.; Cheng, H. H.; Chung, S. H.; Cheng, B. H.; Wong, Y. H., et al. Two-Dimensional Differential Gel Electrophoresis to Identify Protein Biomarkers in Amniotic Fluid of Edwards Syndrome (Trisomy 18) Pregnancies. *Plos One* **2016**, *11*, e0145908,doi:10.1371/journal.pone.0145908
81. Hu, S.; Loo, J. A.; Wong, D. T. Human body fluid proteome analysis. *Proteomics* **2006**, *6*, 6326-53,doi:10.1002/pmic.200600284
82. Hui, L.; Bianchi, D. W. Cell-free fetal nucleic acids in amniotic fluid. *Hum. Reprod. Update* **2011**, *17*, 362-71,doi:10.1093/humupd/dmq049
83. Iadarola, P.; Fumagalli, M.; Bardoni, A. M.; Salvini, R.; Viglio, S. Recent applications of CE- and HPLC-MS in the analysis of human fluids. *Electrophoresis* **2016**, *37*, 212-30,doi:10.1002/elps.201500272
84. Isani, G.; Ferlizza, E.; Cuoghi, A.; Bellei, E.; Monari, E.; Bianchin Butina, B.; Castagnetti, C. Identification of the most abundant proteins in equine amniotic fluid by a proteomic approach. *Anim. Reprod. Sci.* **2016**, *174*, 150-160,doi:10.1016/j.anireprosci.2016.10.003
85. Joo, W. A.; Lee, D. Y.; Kim, C. W. Development of an effective sample preparation method for the proteome analysis of body fluids using 2-D gel electrophoresis. *Biosci. Biotechnol. Biochem.* **2003**, *67*, 1574-7,doi:10.1271/bbb.67.1574
86. Kamath-Rayne, B. D.; Smith, H. C.; Muglia, L. J.; Morrow, A. L. Amniotic fluid: the use of high-dimensional biology to understand fetal well-being. *Reprod. Sci.* **2014**, *21*, 6-19,doi:10.1177/1933719113485292
87. Klein, J.; Buffin-Meyer, B.; Mullen, W.; Carty, D. M.; Delles, C.; Vlahou, A.; Mischak, H.; Decramer, S.; Bascands, J. L.; Schanstra, J. P. Clinical proteomics in obstetrics and neonatology. *Expert Rev. Proteomics* **2014**, *11*, 75-89,doi:10.1586/14789450.2014.872564
88. Kolialexi, A.; Anagnostopoulos, A. K.; Mavrou, A.; Tsangaris, G. T. Application of proteomics for diagnosis of fetal aneuploidies and pregnancy complications. *J. Proteomics* **2009**, *72*, 731-9,doi:10.1016/j.jprot.2009.03.005
89. Kolialexi, A.; Mavrou, A.; Spyrou, G.; Tsangaris, G. T. Mass spectrometry-based proteomics in reproductive medicine. *Mass Spectrom Rev.* **2008**, *27*, 624-34,doi:10.1002/mas.20181
90. Kolialexi, A.; Mavrou, A.; Tsangaris, G. T. Proteomic analysis of human reproductive fluids. *Proteomics Clin. Appl.* **2007**, *1*, 853-60,doi:10.1002/prca.200700040
91. Kolialexi, A.; Tounta, G.; Mavrou, A.; Tsangaris, G. T. Proteomic analysis of amniotic fluid for the diagnosis of fetal aneuploidies. *Expert Rev. Proteomics* **2011**, *8*, 175-85,doi:10.1586/epr.10.112
92. Kolialexi, A.; Tsangaris, G. T.; Mavrou, A. Proteomics in prenatal diagnosis. *Expert Rev. Proteomics* **2009**, *6*, 111-3,doi:10.1586/epr.09.6
93. Kossowska, B.; Dudka, I.; Gancarz, R.; Antonowicz-Juchniewicz, J., [Proteomic analysis of protein profiles in some pathological stages of the human organism]. In *Postepy Hig. Med. Dosw. (Online)*, 2009/11/27 ed.; 2009; Vol. 63, pp 549-63.
94. Law, K. P.; Han, T. L.; Tong, C.; Baker, P. N. Mass spectrometry-based proteomics for pre-eclampsia and preterm birth. *Int. J. Mol. Sci.* **2015**, *16*, 10952-85,doi:10.3390/ijms160510952
95. Lee, J.; Park, J. S.; Norwitz, E. R.; Kim, B. J.; Park, C. W.; Jun, J. K.; Syn, H. C. Identification and characterization of proteins in amniotic fluid that are differentially expressed before and after antenatal corticosteroid administration. *Am. J. Obstet. Gynecol.* **2010**, *202*, 388 e1-388 e10,doi:10.1016/j.ajog.2010.01.056
96. Nath, A. K.; Krauthammer, M.; Li, P.; Davidov, E.; Butler, L. C.; Copel, J.; Katajamaa, M.; Oresic, M.; Buhimschi, I.; Buhimschi, C., et al. Proteomic-based detection of a protein cluster dysregulated during cardiovascular development identifies biomarkers of congenital heart defects. *Plos One* **2009**, *4*, e4221,doi:10.1371/journal.pone.0004221
97. Liu, H.; Shen, J.; Feng, L.; Yu, Y. Low concentration of anti-7,8-dihydroxy-9,10-epoxy-7,8,9,10-tetrahydrobenzo[a]pyrene induces alterations of extracellular protein profile of exposed epithelial cells. *Proteomics* **2009**, *9*, 4259-64,doi:10.1002/pmic.200700886
98. Liu, H.; Wang, H.; Zhu, H.; Zhang, H.; Liu, S. Preliminary study of protein changes in trisomy 21 fetus by proteomics analysis in amniocyte. *Prenat. Diagn.* **2018**, *38*, 435-444,doi:10.1002/pd.5259
99. Liu, X.; Song, Y.; Guo, Z.; Sun, W.; Liu, J. A comprehensive profile and inter-individual variations analysis of the human normal amniotic fluid proteome. *J. Proteomics* **2019**, *192*, 1-9,doi:10.1016/j.jprot.2018.04.023
100. Liu, Z.; Yuan, Z.; Zhao, Q. SELDI-TOF-MS proteomic profiling of serum, urine, and amniotic fluid in neural tube defects. *Plos One* **2014**, *9*, e103276,doi:10.1371/journal.pone.0103276



101. Lygirou, V.; Makridakis, M.; Vlahou, A. Biological sample collection for clinical proteomics: existing SOPs. *Methods Mol. Biol.* **2015**, *1243*, 3-27,doi:10.1007/978-1-4939-1872-0\_1
102. Makridakis, M.; Roubelakis, M. G.; Vlahou, A. Stem cells: insights into the secretome. *Biochim. Biophys. Acta* **2013**, *1834*, 2380-4,doi:10.1016/j.bbapap.2013.01.032
103. Martinez-Morillo, E.; Cho, C. K.; Drabovich, A. P.; Shaw, J. L.; Soosaipillai, A.; Diamandis, E. P. Development of a multiplex selected reaction monitoring assay for quantification of biochemical markers of down syndrome in amniotic fluid samples. *J. Proteome Res.* **2012**, *11*, 3880-7,doi:10.1021/pr300355a
104. Mavrou, A.; Anagnostopoulos, A. K.; Kolialexi, A.; Vougas, K.; Papantoniou, N.; Antsaklis, A.; Fountoulakis, M.; Tsangaris, G. T. Proteomic analysis of amniotic fluid in pregnancies with Turner syndrome fetuses. *J. Proteome Res.* **2008**, *7*, 1862-6,doi:10.1021/pr700588u
105. Mellows, B.; Mitchell, R.; Antonioli, M.; Kretz, O.; Chambers, D.; Zeuner, M. T.; Denecke, B.; Musante, L.; Ramachandra, D. L.; Debacq-Chainiaux, F., et al. Protein and Molecular Characterization of a Clinically Compliant Amniotic Fluid Stem Cell-Derived Extracellular Vesicle Fraction Capable of Accelerating Muscle Regeneration Through Enhancement of Angiogenesis. *Stem Cells Dev.* **2017**, *26*, 1316-1333,doi:10.1089/scd.2017.0089
106. Miceli, M.; Dell'Aversana, C.; Russo, R.; Rega, C.; Cupelli, L.; Ruvo, M.; Altucci, L.; Chambery, A. Secretome profiling of cytokines and growth factors reveals that neuro-glial differentiation is associated with the down-regulation of Chemokine Ligand 2 (MCP-1/CCL2) in amniotic fluid derived-mesenchymal progenitor cells. *Proteomics* **2016**, *16*, 674-88,doi:10.1002/pmic.201500223
107. Michaels, J. E.; Dasari, S.; Pereira, L.; Reddy, A. P.; Lapidus, J. A.; Lu, X.; Jacob, T.; Thomas, A.; Rodland, M.; Roberts, C. T., Jr., et al. Comprehensive proteomic analysis of the human amniotic fluid proteome: gestational age-dependent changes. *J. Proteome Res.* **2007**, *6*, 1277-85,doi:10.1021/pr060543t
108. Michel, P. E.; Crettaz, D.; Morier, P.; Heller, M.; Gallot, D.; Tissot, J. D.; Reymond, F.; Rossier, J. S. Proteome analysis of human plasma and amniotic fluid by Off-Gel isoelectric focusing followed by nano-LC-MS/MS. *Electrophoresis* **2006**, *27*, 1169-81,doi:10.1002/elps.200500680
109. Montemurro, T.; Andriolo, G.; Montelatici, E.; Weissmann, G.; Crisan, M.; Colnaghi, M. R.; Rebull, P.; Mosca, F.; Peault, B.; Lazzari, L. Differentiation and migration properties of human foetal umbilical cord perivascular cells: potential for lung repair. *J. Cell. Mol. Med.* **2011**, *15*, 796-808,doi:10.1111/j.1582-4934.2010.01047.x
110. Mukhopadhyay, R. Biomarkers for preterm birth. *J. Proteome Res.* **2005**, *4*, 1900,doi:10.1021/pr050532k
111. Musilova, I.; Kacerovsky, M.; Tambor, V.; Tosner, J. [Proteomics and biomarkers for detection of preterm labor: a systematic review]. *Ceska Gynekol.* **2011**, *76*, 37-45
112. Nakayama, A. [Proteomic analysis of urinary exosomes]. *Rinsho Byori* **2014**, *62*, 684-91
113. Nardelli, C.; Granata, I.; Iaffaldano, L.; D'Argenio, V.; Del Monaco, V.; Maruotti, G. M.; Del Vecchio, L.; Martinelli, P.; Salvatore, F.; Guarracino, M. R., et al. Sex-Comparative Analysis of the miRNome of Human Amniotic Mesenchymal Stem Cells During Obesity. *Stem Cells Dev.* **2017**, *26*, 1-3,doi:10.1089/scd.2016.0134
114. Nilsson, S.; Ramstrom, M.; Palmblad, M.; Axelsson, O.; Bergquist, J. Explorative study of the protein composition of amniotic fluid by liquid chromatography electrospray ionization Fourier transform ion cyclotron resonance mass spectrometry. *J. Proteome Res.* **2004**, *3*, 884-9,doi:10.1021/pr0499545
115. Nissum, M.; Abu Shehab, M.; Sukop, U.; Khosravi, J. M.; Wildgruber, R.; Eckerskorn, C.; Han, V. K.; Gupta, M. B. Functional and complementary phosphorylation state attributes of human insulin-like growth factor-binding protein-1 (IGFBP-1) isoforms resolved by free flow electrophoresis. *Mol. Cell. Proteomics* **2009**, *8*, 1424-35,doi:10.1074/mcp.M800571-MCP200
116. Ogge, G.; Romero, R.; Lee, D. C.; Gotsch, F.; Than, N. G.; Lee, J.; Chaiworapongsa, T.; Dong, Z.; Mittal, P.; Hassan, S. S., et al. Chronic chorioamnionitis displays distinct alterations of the amniotic fluid proteome. *J. Pathol.* **2011**, *223*, 553-65,doi:10.1002/path.2825
117. Park, J.; Cha, D. H.; Jung, J. W.; Kim, Y. H.; Lee, S. H.; Kim, Y.; Kim, K. P. Comparative proteomic analysis of human amniotic fluid supernatants with Down syndrome using mass spectrometry. *J. Microbiol. Biotechnol.* **2010**, *20*, 959-67,doi:10.4014/jmb.0912.12035
118. Park, J. S.; Oh, K. J.; Norwitz, E. R.; Han, J. S.; Choi, H. J.; Seong, H. S.; Kang, Y. D.; Park, C. W.; Kim, B. J.; Jun, J. K., et al. Identification of proteomic biomarkers of preeclampsia in amniotic fluid using SELDI-TOF mass spectrometry. *Reprod. Sci.* **2008**, *15*, 457-68,doi:10.1177/1933719108316909
119. Park, S. J.; Yoon, W. G.; Song, J. S.; Jung, H. S.; Kim, C. J.; Oh, S. Y.; Yoon, B. H.; Jung, G.; Kim, H. J.; Nirasawa, T. Proteome analysis of human amnion and amniotic fluid by two-dimensional electrophoresis and matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. *Proteomics* **2006**, *6*, 349-63,doi:10.1002/pmic.200500084

120. Perluigi, M.; Di Domenico, F.; Butterfield, D. A. Unraveling the complexity of neurodegeneration in brains of subjects with Down syndrome: insights from proteomics. *Proteomics Clin. Appl.* **2014**, *8*, 73-85,doi:10.1002/prca.201300066
121. Perluigi, M.; di Domenico, F.; Fiorini, A.; Cocciolo, A.; Giorgi, A.; Foppoli, C.; Butterfield, D. A.; Giorlandino, M.; Giorlandino, C.; Schinina, M. E., et al. Oxidative stress occurs early in Down syndrome pregnancy: A redox proteomics analysis of amniotic fluid. *Proteomics Clin. Appl.* **2011**, *5*, 167-78,doi:10.1002/prca.201000121
122. Pettker, C. M.; Buhimschi, I. A.; Magloire, L. K.; Sfakianaki, A. K.; Hamar, B. D.; Buhimschi, C. S. Value of placental microbial evaluation in diagnosing intra-amniotic infection. *Obstet. Gynecol.* **2007**, *109*, 739-49,doi:10.1097/01.AOG.0000255663.47512.23
123. Pipino, C.; Pierdomenico, L.; Di Tomo, P.; Di Giuseppe, F.; Cianci, E.; D'Alimonte, I.; Morabito, C.; Centurione, L.; Antonucci, I.; Mariggio, M. A., et al. Molecular and phenotypic characterization of human amniotic fluid-derived cells: a morphological and proteomic approach. *Stem Cells Dev.* **2015**, *24*, 1415-28,doi:10.1089/scd.2014.0453
124. Pogorelova, T. N.; Orlov, V. I.; Gunko, V. O. New approaches to molecular diagnostics of prenatal pathology. *Bull. Exp. Biol. Med.* **2011**, *151*, 567-70,doi:10.1007/s10517-011-1384-y
125. Queloz, P. A.; Crettaz, D.; Thadikkaran, L.; Sapin, V.; Gallot, D.; Jani, J.; Deprest, J.; Lemery, D.; Barelli, S.; Tissot, J. D. Proteomic analyses of amniotic fluid: potential applications in health and diseases. *J. Chromatogr. B Analyt. Technol. Biomed. Life Sci.* **2007**, *850*, 336-42,doi:10.1016/j.jchromb.2006.12.006
126. Raimondo, F.; Morosi, L.; Chinello, C.; Magni, F.; Pitto, M. Advances in membranous vesicle and exosome proteomics improving biological understanding and biomarker discovery. *Proteomics* **2011**, *11*, 709-20,doi:10.1002/pmic.201000422
127. Ramstrom, M.; Bergquist, J. Miniaturized proteomics and peptidomics using capillary liquid separation and high resolution mass spectrometry. *FEBS Lett* **2004**, *567*, 92-5,doi:10.1016/j.febslet.2004.04.074
128. Ridsdale, R.; Lewis, D. F.; Weaver, T. E.; Akinbi, H. T. Proteomic analysis of lamellar bodies isolated from amniotic fluid: implications for function. *Am. J. Perinatol.* **2012**, *29*, 419-28,doi:10.1055/s-0032-1304822
129. Romani, R.; Fallarino, F.; Pirisinu, I.; Calvitti, M.; Caselli, A.; Fiaschi, T.; Gamberi, T.; Matino, D.; Talesa, V. N.; Donti, E., et al. Comparative proteomic analysis of two distinct stem-cell populations from human amniotic fluid. *Mol. Biosyst.* **2015**, *11*, 1622-32,doi:10.1039/c5mb00018a
130. Romero, R.; Espinoza, J.; Gotsch, F.; Kusanovic, J. P.; Friel, L. A.; Erez, O.; Mazaki-Tovi, S.; Than, N. G.; Hassan, S.; Tromp, G. The use of high-dimensional biology (genomics, transcriptomics, proteomics, and metabolomics) to understand the preterm parturition syndrome. *BJOG* **2006**, *113 Suppl 3*, 118-35,doi:10.1111/j.1471-0528.2006.01150.x
131. Romero, R.; Espinoza, J.; Rogers, W. T.; Moser, A.; Nien, J. K.; Kusanovic, J. P.; Gotsch, F.; Erez, O.; Gomez, R.; Edwin, S., et al. Proteomic analysis of amniotic fluid to identify women with preterm labor and intra-amniotic inflammation/infection: the use of a novel computational method to analyze mass spectrometric profiling. *J. Matern. Fetal Neonatal Med.* **2008**, *21*, 367-88,doi:10.1080/14767050802045848
132. Romero, R.; Kusanovic, J. P.; Gotsch, F.; Erez, O.; Vaisbuch, E.; Mazaki-Tovi, S.; Moser, A.; Tam, S.; Leszyk, J.; Master, S. R., et al. Isobaric labeling and tandem mass spectrometry: a novel approach for profiling and quantifying proteins differentially expressed in amniotic fluid in preterm labor with and without intra-amniotic infection/inflammation. *J. Matern. Fetal Neonatal Med.* **2010**, *23*, 261-80,doi:10.3109/14767050903067386
133. Romero, R.; Mazaki-Tovi, S.; Vaisbuch, E.; Kusanovic, J. P.; Chaiworapongsa, T.; Gomez, R.; Nien, J. K.; Yoon, B. H.; Mazar, M.; Luo, J., et al. Metabolomics in premature labor: a novel approach to identify patients at risk for preterm delivery. *J. Matern. Fetal Neonatal Med.* **2010**, *23*, 1344-59,doi:10.3109/14767058.2010.482618
134. Roubelakis, M. G.; Pappa, K. I.; Bitsika, V.; Zagoura, D.; Vlahou, A.; Papadaki, H. A.; Antsaklis, A.; Anagnou, N. P. Molecular and proteomic characterization of human mesenchymal stem cells derived from amniotic fluid: comparison to bone marrow mesenchymal stem cells. *Stem Cells Dev.* **2007**, *16*, 931-52,doi:10.1089/scd.2007.0036
135. Roubelakis, M. G.; Trohatou, O.; Roubelakis, A.; Mili, E.; Kalaitzopoulos, I.; Papazoglou, G.; Pappa, K. I.; Anagnou, N. P. Platelet-rich plasma (PRP) promotes fetal mesenchymal stem/stromal cell migration and wound healing process. *Stem Cell Rev. Rep.* **2014**, *10*, 417-28,doi:10.1007/s12015-013-9494-8
136. Roubelakis, M. G.; Tsaknakis, G.; Pappa, K. I.; Anagnou, N. P.; Watt, S. M. Spindle shaped human mesenchymal stem/stromal cells from amniotic fluid promote neovascularization. *Plos One* **2013**, *8*, e54747,doi:10.1371/journal.pone.0054747
137. Ruetschi, U.; Rosen, A.; Karlsson, G.; Zetterberg, H.; Rymo, L.; Hagberg, H.; Jacobsson, B. Proteomic analysis using protein chips to detect biomarkers in cervical and amniotic fluid in women with intra-amniotic inflammation. *J. Proteome Res.* **2005**, *4*, 2236-42,doi:10.1021/pr050139e



138. Savickiene, J.; Treigyte, G.; Baronaite, S.; Valiuliene, G.; Kaupinis, A.; Valius, M.; Arlauskienė, A.; Navakauskienė, R. Human Amniotic Fluid Mesenchymal Stem Cells from Second- and Third-Trimester Amniocentesis: Differentiation Potential, Molecular Signature, and Proteome Analysis. *Stem Cells Int.* **2015**, *2015*, 319238,doi:10.1155/2015/319238
139. Shtam, T. A.; Burdakov, V. S.; Landa, S. B.; Naryzhny, S. N.; Bairamukov, V. Y.; Malek, A. V.; Orlov, Y. N.; Filatov, M. V. Aggregation by Lectin-Methodical Approach for Effective Isolation of Exosomes from Cell Culture Supernatant for Proteome Profiling. *Tsitologiya* **2017**, *59*, 5-12
140. Simpson, R. J.; Jensen, S. S.; Lim, J. W. Proteomic profiling of exosomes: current perspectives. *Proteomics* **2008**, *8*, 4083-99,doi:10.1002/pmic.200800109
141. Simpson, R. J.; Lim, J. W.; Moritz, R. L.; Mathivanan, S. Exosomes: proteomic insights and diagnostic potential. *Expert Rev. Proteomics* **2009**, *6*, 267-83,doi:10.1586/epr.09.17
142. Spivak, M.; Weston, J.; Tomazela, D.; MacCoss, M. J.; Noble, W. S. Direct maximization of protein identifications from tandem mass spectra. *Mol. Cell. Proteomics* **2012**, *11*, M111 012161,doi:10.1074/mcp.M111.012161
143. Stawicki, S. P.; Papadimos, T. J. Challenges in managing amniotic fluid embolism: an up-to-date perspective on diagnostic testing with focus on novel biomarkers and avenues for future research. *Curr. Pharm. Biotechnol.* **2014**, *14*, 1168-78,doi:10.2174/1389201015666140430163921
144. Tambor, V.; Hunter, C. L.; Seymour, S. L.; Kacerovsky, M.; Stulik, J.; Lenco, J. CysTRAQ - A combination of iTRAQ and enrichment of cysteinyl peptides for uncovering and quantifying hidden proteomes. *J. Proteomics* **2012**, *75*, 857-67,doi:10.1016/j.jprot.2011.09.027
145. Tambor, V.; Kacerovsky, M.; Andrys, C.; Musilova, I.; Hornychova, H.; Pliskova, L.; Link, M.; Stulik, J.; Lenco, J. Amniotic fluid cathelicidin in PPROM pregnancies: from proteomic discovery to assessing its potential in inflammatory complications diagnosis. *Plos One* **2012**, *7*, e41164,doi:10.1371/journal.pone.0041164
146. Tambor, V.; Kacerovsky, M.; Lenco, J.; Bhat, G.; Menon, R. Proteomics and bioinformatics analysis reveal underlying pathways of infection associated histologic chorioamnionitis in pPROM. *Placenta* **2013**, *34*, 155-61,doi:10.1016/j.placenta.2012.11.028
147. Tambor, V.; Vajrychova, M.; Kacerovsky, M.; Link, M.; Domasinska, P.; Menon, R.; Lenco, J. Potential Peripartum Markers of Infectious-Inflammatory Complications in Spontaneous Preterm Birth. *Biomed Res. Int.* **2015**, *2015*, 343501,doi:10.1155/2015/343501
148. Thadikkaran, L.; Crettaz, D.; Siegenthaler, M. A.; Gallot, D.; Sapin, V.; Iozzo, R. V.; Queloz, P. A.; Schneider, P.; Tissot, J. D. The role of proteomics in the assessment of premature rupture of fetal membranes. *Clin. Chim. Acta* **2005**, *360*, 27-36,doi:10.1016/j.cccn.2005.04.018
149. Tsangaris, G.; Weitzdorfer, R.; Pollak, D.; Lubec, G.; Fountoulakis, M. The amniotic fluid cell proteome. *Electrophoresis* **2005**, *26*, 1168-73,doi:10.1002/elps.200406183
150. Tsangaris, G. T.; Karamessinis, P.; Kolialexi, A.; Garbis, S. D.; Antsaklis, A.; Mavrou, A.; Fountoulakis, M. Proteomic analysis of amniotic fluid in pregnancies with Down syndrome. *Proteomics* **2006**, *6*, 4410-9,doi:10.1002/pmic.200600085
151. Tsangaris, G. T.; Kolialexi, A.; Karamessinis, P. M.; Anagnostopoulos, A. K.; Antsaklis, A.; Fountoulakis, M.; Mavrou, A. The normal human amniotic fluid supernatant proteome. *In Vivo* **2006**, *20*, 479-90
152. Vajrychova, M.; Kacerovsky, M.; Tambor, V.; Hornychova, H.; Lenco, J. Microbial invasion and histological chorioamnionitis upregulate neutrophil-gelatinase associated lipocalin in preterm prelabor rupture of membranes. *J. Matern. Fetal Neonatal Med.* **2016**, *29*, 12-21,doi:10.3109/14767058.2014.991305
153. Vascotto, C.; Salzano, A. M.; D'Ambrosio, C.; Fruscalzo, A.; Marchesoni, D.; di Loreto, C.; Scaloni, A.; Tell, G.; Quadrifoglio, F. Oxidized transthyretin in amniotic fluid as an early marker of preeclampsia. *J. Proteome Res.* **2007**, *6*, 160-70,doi:10.1021/pr060315z
154. Vento, G.; Tirone, C.; Aurilia, C.; Tana, M.; Piras, A.; Lio, A.; Tesfagabir, G.; Castagnola, M.; Fanali, C.; Romagnoli, C. Proteomics and neonatal infection. *Minerva Pediatr.* **2010**, *62*, 47-9
155. Virgiliou, C.; Gika, H. G.; Witting, M.; Bletsou, A. A.; Athanasiadis, A.; Zafrakas, M.; Thomaidis, N. S.; Raikos, N.; Makrydimas, G.; Theodoridis, G. A. Amniotic Fluid and Maternal Serum Metabolic Signatures in the Second Trimester Associated with Preterm Delivery. *J. Proteome Res.* **2017**, *16*, 898-910,doi:10.1021/acs.jproteome.6b00845
156. Vuadens, F.; Benay, C.; Crettaz, D.; Gallot, D.; Sapin, V.; Schneider, P.; Bienvenut, W. V.; Lemery, D.; Quadroni, M.; Dastugue, B., et al. Identification of biologic markers of the premature rupture of fetal membranes: proteomic approach. *Proteomics* **2003**, *3*, 1521-5,doi:10.1002/pmic.200300455
157. Wang, T.; Zhou, R.; Zhang, L.; Wang, Y.; Song, C.; Lin, W.; Niu, X.; Lin, Y.; Hu, H. Proteins in leaked amniotic fluid as biomarkers diagnostic for prelabor rupture of membranes. *Proteomics Clin. Appl.* **2011**, *5*, 415-21,doi:10.1002/prca.201000123

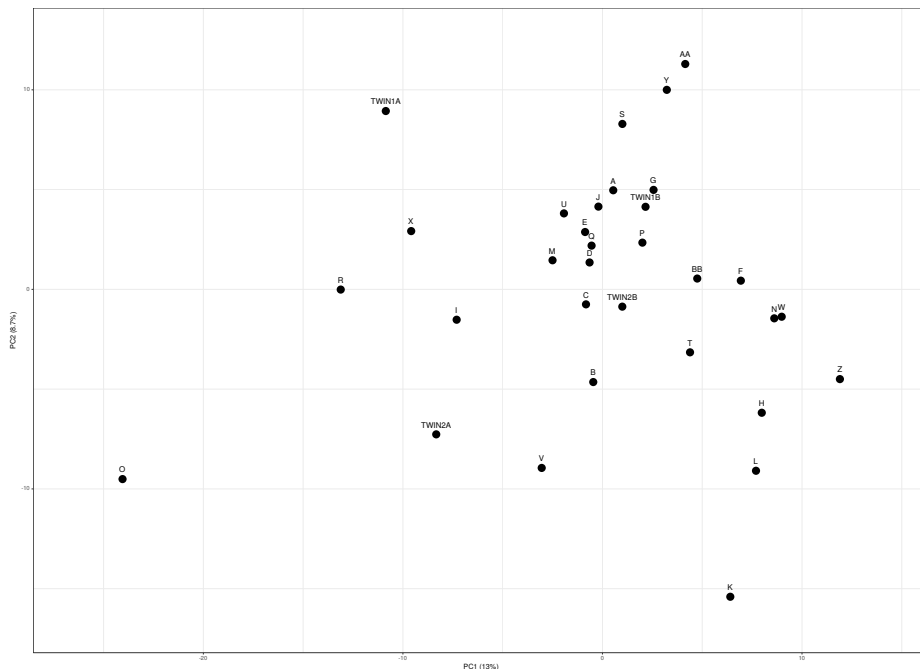
158. Wang, T. H.; Chang, Y. L.; Peng, H. H.; Wang, S. T.; Lu, H. W.; Teng, S. H.; Chang, S. D.; Wang, H. S. Rapid detection of fetal aneuploidy using proteomics approaches on amniotic fluid supernatant. *Prenat. Diagn.* **2005**, *25*, 559-66,doi:10.1002/pd.1186
159. Wang, T. H.; Chao, A. S.; Chen, J. K.; Chao, A.; Chang, Y. L.; Cheng, P. J.; Chang, S. D.; Wang, H. S. Network analyses of differentially expressed proteins in amniotic fluid supernatant associated with abnormal human karyotypes. *Fertil. Steril.* **2009**, *92*, 96-107,doi:10.1016/j.fertnstert.2008.05.038
160. Wang, Y.; Luo, H.; Che, G.; Li, Y.; Gao, J.; Yang, Q.; Zhou, B.; Gao, L.; Wang, T.; Liang, Y., et al. Placental protein 14 as a potential biomarker for diagnosis of preterm premature rupture of membranes. *Mol. Med. Rep.* **2018**, *18*, 113-122,doi:10.3892/mmr.2018.8967
161. Xanthopoulou, A. G.; Anagnostopoulos, A. K.; Thanasopoulou, A.; Anastasiadou, E.; Sifakis, S.; Siafaka-Kapadai, A.; Tsangaris, G. T. The proteome of normal human chorionic villus sampling cells. *In Vivo* **2011**, *25*, 945-61
162. Yu, B.; Zhang, B.; Wang, J.; Wang, Q. W.; Huang, R. P.; Yang, Y. Q.; Shao, S. H. Preliminary proteomic-based identification of a novel protein for Down's syndrome in maternal serum. *Exp. Biol. Med. (Maywood)* **2012**, *237*, 530-9,doi:10.1258/ebm.2012.011312
163. Zagoura, D. S.; Roubelakis, M. G.; Bitsika, V.; Trohatou, O.; Pappa, K. I.; Kapelouzou, A.; Antsaklis, A.; Anagnou, N. P. Therapeutic potential of a distinct population of human amniotic fluid mesenchymal stem cells and their secreted molecules in mice with acute hepatic failure. *Gut* **2012**, *61*, 894-906,doi:10.1136/gutjnl-2011-300908
164. Zhao, M.; Yang, Y.; Guo, Z.; Shao, C.; Sun, H.; Zhang, Y.; Sun, Y.; Liu, Y.; Song, Y.; Zhang, L., et al. A Comparative Proteomics Analysis of Five Body Fluids: Plasma, Urine, Cerebrospinal Fluid, Amniotic Fluid, and Saliva. *Proteomics Clin. Appl.* **2018**, *12*, e1800008,doi:10.1002/prca.201800008
165. Caspi, R.; Billington, R.; Ferrer, L.; Foerster, H.; Fulcher, C. A.; Keseler, I. M.; Kothari, A.; Krummenacker, M.; Latendresse, M.; Mueller, L. A., et al. The MetaCyc database of metabolic pathways and enzymes and the BioCyc collection of pathway/genome databases. *Nucl. Acids Res.* **2016**, *44*, D471-80,doi:10.1093/nar/gkv1164
166. Miikkulainen, P.; Hogel, H.; Rantanen, K.; Suomi, T.; Kouvonen, P.; Elo, L. L.; Jaakkola, P. M. HIF prolyl hydroxylase PHD3 regulates translational machinery and glucose metabolism in clear cell renal cell carcinoma. *Cancer Metab.* **2017**, *5*, 5,doi:10.1186/s40170-017-0167-y
167. Han, J.; Back, S. H.; Hur, J.; Lin, Y. H.; Gildersleeve, R.; Shan, J.; Yuan, C. L.; Krokowski, D.; Wang, S.; Hatzoglou, M., et al. ER-stress-induced transcriptional regulation increases protein synthesis leading to cell death. *Nat. Cell Biol.* **2013**, *15*, 481-90,doi:10.1038/ncb2738
168. Andreev, D. E.; O'Connor, P. B.; Zhdanov, A. V.; Dmitriev, R. I.; Shatsky, I. N.; Papkovsky, D. B.; Baranov, P. V. Oxygen and glucose deprivation induces widespread alterations in mRNA translation within 20 minutes. *Genome Biol.* **2015**, *16*, 90,doi:10.1186/s13059-015-0651-z
169. Quiros, P. M.; Prado, M. A.; Zamboni, N.; D'Amico, D.; Williams, R. W.; Finley, D.; Gygi, S. P.; Auwerx, J. Multi-omics analysis identifies ATF4 as a key regulator of the mitochondrial stress response in mammals. *J. Cell. Biol.* **2017**, *216*, 2027-2045,doi:10.1083/jcb.201702058

## Supplementary Dataset 1

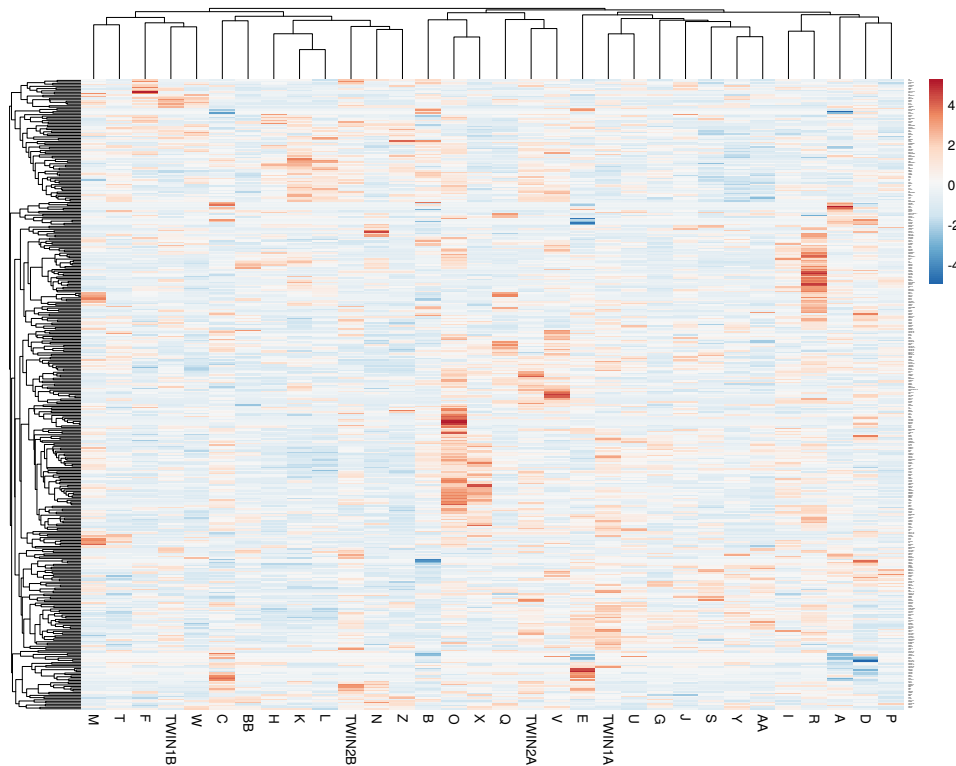
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Analysis performed with ClustVis v.2.0. Metsalu, Tauno and Vilo, Jaak. Clustvis: a web tool for visualizing clustering of multivariate data using Principal Component Analysis and heatmap. *Nucleic Acids Res.* 2015; 43, W566–W570,doi: 10.1093/nar/gkv468.

**Principal component analysis of all noncarrier samples based on the proteomics' data.**



**Agglomerative hierarchical clustering of the samples based on the proteomics' data visualized as a heat map.**



PCA SCORES																											
	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12	PC13	PC14	PC15	PC16	PC17	PC18	PC19	PC20	PC21	PC22	PC23	PC24	PC25	PC26	PC27
A	-0.54	4.97	-4.28	0.15	-1.00	2.74	-10.17	2.93	-5.18	8.23	3.42	-7.52	-6.42	2.27	5.28	-2.82	-0.75	-2.51	-0.60	1.26	1.69	1.70	-0.75	-0.18	-0.48	-0.58	-0.23
B	0.46	-4.64	8.75	-6.79	-1.80	-1.36	9.91	-5.93	7.50	-3.93	5.19	-3.62	-7.03	0.37	3.57	-1.84	-0.69	-4.13	0.53	1.08	-0.59	1.67	-1.47	0.59	-0.44	-0.97	1.15
C	0.83	-0.75	6.58	10.25	-4.97	-9.01	1.68	-8.70	-2.11	8.49	-7.10	2.31	-4.85	-1.30	0.05	-0.69	1.34	3.56	0.68	0.05	-1.44	-1.04	-1.36	1.14	0.23	-0.12	-0.39
D	0.65	1.35	-2.56	-9.22	-5.99	9.50	-8.17	-0.97	7.80	3.05	-0.76	9.55	-3.30	-4.21	-1.02	-1.29	-1.17	0.83	-1.78	-2.03	-1.68	-1.52	-1.18	0.69	-0.69	-0.01	-0.56
E	0.87	2.87	-6.09	15.42	3.56	-1.21	2.44	8.22	4.53	-3.93	-0.58	8.17	-3.25	3.56	3.13	-4.11	-2.43	-1.64	1.53	0.92	0.46	1.00	-0.09	1.05	-0.22	-0.74	0.80
F	-6.93	0.44	2.25	-0.76	2.90	6.04	3.46	3.36	-8.14	-7.64	-3.07	-0.34	-6.98	-5.76	0.79	0.58	0.62	5.61	-0.93	0.94	-2.15	0.65	1.71	-0.45	-2.52	0.75	0.02
G	-2.56	4.98	4.61	1.17	-2.01	-1.49	1.00	0.35	4.22	0.03	1.58	0.29	0.94	2.32	0.63	1.69	1.89	1.25	-5.61	-0.74	0.72	-3.23	0.48	-4.00	0.98	-4.63	1.74
H	-7.98	-6.18	0.24	-0.54	-3.40	-2.93	-2.04	4.54	-0.14	-2.80	-3.15	-1.69	-0.76	-2.25	1.34	1.68	0.94	-3.93	-1.36	-2.91	-0.13	1.70	-1.01	1.38	5.48	2.79	-0.51
I	7.31	-1.52	-3.30	-3.44	0.41	-1.37	1.36	0.23	-3.54	-1.96	0.02	-2.94	1.64	1.32	-0.64	-8.63	0.33	-1.09	3.03	-4.23	-5.19	-5.84	1.74	-0.05	-1.48	-2.96	-3.42
J	0.20	4.15	-0.21	-0.52	3.53	1.90	0.53	1.53	0.15	-2.71	-3.29	-3.28	-3.06	2.07	-2.17	4.27	0.65	1.66	-0.10	-6.14	6.86	-1.85	-3.06	2.30	0.88	-4.29	-2.08
K	-6.41	-15.41	-5.04	-0.55	1.46	-2.43	-2.14	2.60	1.62	0.79	-0.86	-3.52	1.76	-1.78	2.61	-1.55	-1.73	3.45	-4.77	2.42	-1.74	-0.24	0.91	-0.66	0.95	-0.78	2.15
L	-7.69	-9.09	-3.53	-2.33	2.18	-3.51	-0.17	1.26	3.47	2.27	-1.67	-0.95	3.50	1.65	1.02	0.81	1.81	3.78	0.30	-3.16	0.55	1.84	1.30	0.10	-3.81	-2.32	2.18
M	2.50	1.46	5.45	-9.33	4.47	-1.30	4.13	6.55	-3.23	5.14	2.22	3.01	-0.84	7.91	-3.06	2.84	-4.15	3.82	0.89	1.47	-4.36	0.77	-2.55	0.61	2.31	0.51	1.00
N	-8.61	-1.45	-2.43	2.63	-9.56	-1.22	-3.80	-0.18	-3.08	-3.45	3.76	0.91	2.51	-2.12	-3.39	0.45	-0.61	-0.38	6.17	2.77	-0.37	1.36	-3.55	-4.18	1.45	-5.14	1.62
O	24.05	-9.51	9.68	0.29	-6.47	5.52	-2.02	2.62	-2.17	-2.12	-5.63	0.20	4.40	1.24	5.70	2.23	-1.01	-0.52	1.63	1.19	1.63	-0.01	-0.41	-0.05	-0.28	-0.07	0.54
P	-2.00	2.34	-2.89	-5.03	2.65	-2.41	-4.12	-2.41	6.38	-1.19	-2.71	-0.73	1.11	3.18	2.04	-0.98	3.78	3.30	6.04	0.10	0.33	4.55	4.22	0.87	1.99	1.56	-2.35
Q	0.55	2.19	2.29	-0.80	7.33	-4.70	-4.40	-4.22	-4.96	-1.03	8.89	5.89	2.74	-3.34	6.79	4.73	1.49	-0.30	1.32	-0.77	-0.24	-0.89	0.29	3.93	-1.86	-1.31	0.56
R	13.12	-0.01	-21.01	-6.10	-6.61	-5.24	6.43	-2.39	-3.17	-1.21	1.15	1.92	-2.46	0.58	-0.57	2.72	1.65	0.89	-1.20	2.43	2.85	-0.90	0.40	-0.58	0.49	1.86	0.14
TWIN1A	10.86	8.94	-0.35	1.29	4.66	-2.54	4.46	3.26	3.26	3.94	0.55	-2.44	3.02	-9.20	-0.04	0.99	-3.31	-0.11	-1.71	0.98	-1.28	2.72	2.10	-1.16	3.70	-2.73	-3.53
TWIN1B	-2.16	4.14	-3.17	-1.33	0.70	6.41	7.27	-2.48	-3.48	3.30	-2.64	0.60	6.13	-0.94	-1.37	-5.68	1.43	-2.29	-2.76	-0.15	1.69	4.15	-2.22	4.73	-1.40	-1.27	3.89
S	-1.00	8.29	0.33	-2.02	2.62	-1.27	-4.46	-0.47	2.19	-4.17	-5.36	-3.21	1.46	-0.01	-2.68	1.20	3.52	-1.32	0.76	6.04	-3.51	0.33	-4.95	2.68	-1.09	-0.17	-0.96
T	-4.39	-3.16	4.01	-3.11	3.40	-3.00	0.51	5.39	-2.16	2.69	-1.60	3.74	-0.40	-0.51	-1.92	0.26	7.66	-6.95	-1.06	1.66	0.42	-4.31	2.26	-0.66	1.60	1.16	0.67
U	1.93	3.81	0.22	-1.23	4.31	-1.46	0.80	2.84	3.88	3.57	-2.62	-3.29	-0.63	-4.01	-2.34	2.21	-3.08	-2.05	5.74	0.07	2.42	-2.72	1.01	-3.07	-5.34	2.89	4.52
TWIN2A	8.33	-7.27	-1.78	7.93	6.83	3.90	-0.31	-1.06	2.87	0.58	6.69	-2.21	1.20	-1.32	-2.14	-1.29	4.37	2.92	-0.40	-2.10	-0.57	-0.67	-6.59	-2.34	0.51	4.90	-1.00
TWIN2B	-0.99	-0.87	-0.66	8.96	-6.11	10.88	3.93	0.19	1.27	3.21	4.26	-2.75	-0.33	2.27	-3.16	5.80	3.92	-0.68	1.24	0.36	-3.34	0.83	5.47	1.96	-0.72	-0.62	-0.69
V	3.04	-8.95	-2.81	2.07	11.48	3.52	-4.90	-10.12	-2.31	-1.80	-2.88	1.73	-1.82	2.63	-4.97	1.55	-4.66	-4.33	-1.68	1.37	0.09	1.34	2.41	-2.05	1.14	-1.63	-0.28
W	-8.98	-1.37	6.06	-3.27	-0.04	2.62	4.81	-0.45	-4.16	2.67	0.72	4.55	1.78	0.09	0.55	-2.96	0.65	-0.03	1.77	-0.35	4.60	3.26	0.00	-5.40	-0.38	1.62	-4.53
X	9.59	2.92	9.45	0.63	-4.10	-6.53	-6.75	1.72	-0.71	-4.16	5.09	-0.34	-0.66	0.14	-7.75	-4.58	0.32	2.28	-3.42	0.18	3.24	2.51	3.67	1.78	-1.18	1.58	1.55
Y	-3.22	10.00	0.10	1.04	-0.76	3.19	-0.10	-4.96	-2.05	-2.32	-0.28	-1.39	1.83	0.41	1.92	-1.20	-2.13	1.20	1.87	-4.12	-1.15	-2.26	1.62	-0.84	6.19	3.41	5.56
Z	-11.90	-4.50	1.15	1.54	-2.62	1.37	1.56	-0.63	1.50	0.58	2.50	-1.50	3.01	-0.41	-1.14	-0.65	-5.91	1.40	1.19	4.42	4.13	-5.92	0.52	5.41	0.81	2.05	-3.30
AA	-4.15	11.29	0.54	1.29	-1.01	1.06	-0.52	-3.26	1.24	-2.88	-1.64	-0.89	3.76	4.35	4.19	0.48	-0.14	0.57	-5.05	3.00	-0.29	-1.78	0.26	-3.83	-2.75	2.34	-1.98
BB	-4.75	0.54	-1.61	1.72	-6.06	-5.67	-0.21	0.67	-1.30	-1.22	-0.20	-0.25	1.99	0.80	-1.22	3.80	-4.62	-4.29	-2.24	-6.00	-3.66	2.80	-1.17	0.26	-4.07	2.93	-2.28

PC28	PC29	PC30	PC31	PC32
1.80	0.24	0.14	-0.80	0.00
-0.16	1.56	-0.63	-0.05	0.00
-0.81	-0.22	-0.69	0.19	0.00
-0.73	0.61	-0.31	-0.10	0.00
-0.27	0.56	0.88	-0.16	0.00
2.79	-0.96	-1.34	-0.28	0.00
4.49	-5.85	2.94	0.03	0.00
-4.06	-5.28	-0.91	-3.45	0.00
-1.67	-1.53	0.38	-0.46	0.00
-2.34	2.34	-0.74	2.47	0.00
-3.35	1.65	2.36	5.21	0.00
1.35	3.56	-0.56	-6.33	0.00
-0.96	-0.75	-1.29	-0.08	0.00
-0.03	0.62	-3.31	0.70	0.00
1.54	0.37	0.06	-0.01	0.00
2.77	-2.50	-1.98	3.21	0.00
-1.93	-1.25	0.83	0.45	0.00
0.24	-0.22	1.15	-0.73	0.00
0.65	1.96	-1.16	-1.05	0.00
0.40	-2.47	-1.82	1.33	0.00
-0.13	1.35	5.64	-1.27	0.00
2.52	3.73	-2.54	1.42	0.00
-2.19	-3.01	0.32	0.79	0.00
1.66	-0.51	-1.35	-0.02	0.00
-2.75	0.09	1.42	0.11	0.00
0.61	-0.85	-0.36	-1.07	0.00
-1.91	0.70	5.42	-0.17	0.00
-1.47	0.62	0.18	-0.41	0.00
0.91	3.86	2.38	-0.51	0.00
3.07	-0.57	-0.45	-1.04	0.00
-4.12	0.98	-5.29	-0.58	0.00
4.03	1.15	0.64	2.66	0.00

PCA LOADINGS													
	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12	
A1BG	0.04	-0.08	0.02	0.00	0.06	0.06	0.03	0.02	0.04	0.00	0.08	0.05	
AFP	0.01	0.05	-0.08	0.05	0.02	0.10	-0.06	-0.07	0.08	-0.03	0.01	0.00	
ALB	0.00	0.01	0.01	-0.02	-0.07	0.02	-0.08	-0.08	0.00	0.15	-0.05	0.04	
APOA1	0.01	-0.04	0.04	0.04	0.03	-0.02	0.02	0.07	0.00	0.05	-0.02	0.04	
APOC1	-0.03	-0.11	-0.03	0.07	-0.03	-0.03	0.00	0.03	0.03	0.02	-0.02	-0.03	
APOH	0.00	-0.02	0.03	0.00	0.09	0.02	-0.07	0.11	-0.03	0.02	-0.10	0.02	
B2M	0.05	0.09	0.05	-0.06	0.05	0.00	-0.03	0.04	-0.02	-0.04	-0.01	-0.04	
CD59	0.00	0.09	-0.02	-0.06	-0.02	0.06	0.08	0.01	0.08	0.00	-0.05	0.01	
CDH1	0.09	-0.01	-0.05	-0.03	0.01	0.06	0.03	-0.05	-0.05	-0.01	0.06	0.06	
CLU	0.02	-0.11	-0.01	-0.04	0.05	-0.03	-0.01	-0.01	0.05	0.03	-0.04	-0.05	
COL5A1	0.02	0.06	-0.07	0.07	-0.02	0.06	0.02	0.03	0.03	-0.01	-0.02	-0.03	
COL6A3	0.04	0.09	-0.08	0.05	0.05	0.05	0.03	-0.01	0.02	0.03	-0.01	-0.04	
CPM	0.04	0.02	-0.07	-0.09	0.04	0.06	0.00	-0.05	-0.01	0.07	-0.07	0.02	
FAM3C	-0.04	0.07	-0.02	-0.02	0.02	0.04	-0.03	-0.06	0.03	0.04	0.05	-0.03	
FBLN1	0.11	0.04	0.04	-0.02	-0.02	-0.03	0.05	0.01	0.02	0.03	-0.02	-0.04	
GC	-0.04	-0.05	0.03	-0.02	0.03	0.06	0.08	0.02	0.02	0.09	-0.03	0.01	
GP2	0.05	0.00	0.03	0.01	0.03	0.05	-0.06	-0.03	-0.10	-0.07	-0.12	-0.06	
GSN	0.03	-0.05	0.01	-0.03	0.04	0.00	0.12	0.07	0.04	-0.03	-0.08	0.02	
HBD	0.01	-0.01	-0.02	0.15	-0.04	-0.01	-0.02	0.02	0.00	0.08	0.01	0.04	
HP	-0.01	-0.05	-0.03	-0.05	0.01	-0.02	0.07	-0.01	-0.01	0.05	-0.08	-0.02	
HSPB1	0.02	-0.01	0.06	0.04	-0.01	0.02	0.00	-0.09	-0.10	0.01	0.07	0.04	
IGFBP1	0.08	0.06	0.08	-0.04	-0.03	-0.05	-0.01	0.04	-0.04	-0.02	-0.01	-0.03	
IGHG1	0.03	-0.03	0.00	-0.05	-0.02	-0.02	-0.12	0.04	-0.06	0.01	0.05	0.07	
ITIH4	-0.04	-0.08	-0.01	0.03	-0.03	0.04	-0.01	0.06	0.03	0.10	0.08	-0.05	
LMAN2	0.05	0.09	-0.02	-0.01	0.00	0.09	-0.05	0.04	-0.01	0.01	0.02	0.05	
LTBP1	0.02	0.05	-0.04	0.03	-0.02	-0.07	0.06	-0.01	-0.05	0.11	-0.02	-0.04	
MSLN	0.01	0.05	-0.01	0.00	-0.01	0.06	0.07	0.02	-0.05	0.07	0.06	-0.11	
PAEP	0.06	0.03	0.02	-0.07	-0.07	0.04	-0.08	-0.01	0.11	-0.03	-0.03	0.07	
RNASE1	0.08	0.05	-0.03	0.01	0.05	-0.04	-0.07	0.01	0.04	0.08	0.06	-0.04	

SERPINA1	0.00	-0.09	0.04	0.03	0.03	0.08	-0.01	0.04	0.06	0.06	0.03	0.04
SPARC	0.07	-0.01	-0.04	0.12	0.02	0.06	0.01	0.00	0.01	0.01	0.00	-0.04
SPINT1	0.03	0.04	-0.06	-0.03	0.04	0.01	-0.06	-0.05	0.08	0.01	-0.02	0.01
TF	0.00	0.01	0.07	-0.07	0.06	-0.02	0.06	-0.03	-0.02	0.04	0.01	0.01
TNXB	0.04	-0.02	-0.04	-0.04	0.10	0.00	0.02	0.05	0.00	-0.03	-0.05	0.01
VIM	0.06	-0.03	0.07	0.06	-0.10	-0.02	-0.06	0.00	-0.05	0.03	-0.01	-0.03
A2M	-0.01	-0.04	-0.05	0.05	-0.03	-0.04	-0.05	0.04	0.04	0.00	0.05	-0.01
A2ML1	0.04	-0.07	-0.03	-0.01	0.05	0.11	-0.06	-0.01	-0.01	0.01	0.00	-0.03
ABI3BP	0.11	-0.01	0.07	-0.01	-0.02	-0.01	-0.03	0.06	-0.02	-0.03	-0.01	-0.02
ACE	0.03	-0.01	-0.02	-0.04	0.01	-0.04	-0.03	0.01	-0.04	-0.01	-0.03	0.03
ACE2	0.01	0.04	-0.11	-0.04	-0.09	0.04	-0.03	0.00	0.01	0.05	0.01	0.03
ACTB	0.10	-0.04	-0.03	-0.03	-0.02	-0.05	-0.02	0.08	-0.04	-0.02	-0.01	-0.07
ACTG2	0.00	0.00	0.00	-0.12	-0.04	0.07	-0.09	-0.04	-0.03	0.08	0.03	-0.08
ACTN4	0.08	-0.06	-0.05	-0.06	-0.01	0.03	-0.01	-0.03	-0.04	-0.02	-0.06	0.02
ADAMTS1	0.05	0.00	0.06	-0.03	-0.08	-0.04	0.05	-0.02	0.00	-0.03	0.02	-0.04
ADAMTS2	0.06	0.01	-0.02	0.03	0.03	-0.07	0.03	0.02	0.05	0.01	-0.06	-0.01
AFM	-0.05	-0.01	0.01	-0.03	-0.01	0.03	0.04	0.05	-0.01	0.08	0.08	0.14
AGRN	-0.02	0.10	-0.04	0.02	0.01	0.11	0.01	0.04	-0.04	-0.05	-0.04	0.01
AGT	0.02	-0.08	0.03	-0.03	0.04	0.03	0.01	-0.05	0.09	0.03	0.08	0.02
AHSG	0.04	-0.08	-0.02	0.00	0.06	-0.01	0.02	0.01	0.04	0.03	-0.01	-0.01
AHSP	0.02	0.02	-0.03	0.03	0.05	0.05	-0.07	0.03	0.05	-0.02	0.02	-0.02
AMBP	0.03	0.07	-0.03	-0.02	0.04	0.06	0.03	0.02	0.04	-0.10	-0.03	-0.09
ANGPTL2	0.04	-0.03	-0.09	-0.02	0.03	-0.02	-0.01	0.01	0.00	0.09	-0.01	-0.07
ANXA1	0.07	-0.03	-0.03	-0.06	0.00	0.05	0.05	-0.08	-0.08	0.00	-0.04	0.05
ANXA13	0.00	0.03	-0.06	-0.01	-0.02	-0.01	-0.05	0.06	-0.02	-0.07	-0.07	-0.10
ANXA2	0.08	-0.06	-0.06	-0.05	-0.04	0.00	0.07	0.01	-0.03	-0.04	-0.09	0.02
ANXA4	0.04	-0.01	-0.11	-0.05	-0.05	-0.06	0.06	-0.03	0.01	-0.03	0.04	-0.01
ANXA5	0.02	-0.01	-0.12	-0.05	-0.03	-0.02	0.01	-0.02	-0.03	0.05	0.00	-0.04
AOC1	0.02	0.00	0.05	-0.03	0.06	0.08	0.08	-0.01	-0.10	0.09	0.03	0.06
APOA2	-0.07	-0.03	0.02	-0.01	-0.01	0.05	0.06	0.01	0.03	0.10	-0.02	0.03
APOA4	-0.05	-0.09	-0.02	0.08	-0.01	0.00	-0.05	0.01	-0.02	0.04	-0.07	-0.02

APOB	-0.02	0.01	-0.09	-0.02	-0.03	-0.04	-0.03	0.00	0.01	-0.09	-0.08	-0.04
APOC3	-0.05	-0.08	-0.01	0.02	-0.01	-0.07	0.01	0.03	0.08	0.04	-0.03	-0.03
APOD	0.08	0.01	0.07	-0.02	-0.03	-0.07	-0.02	0.01	-0.02	-0.06	0.04	0.00
APOE	0.00	-0.01	-0.03	0.02	-0.07	0.00	-0.11	0.01	0.01	-0.01	0.06	0.00
ATRN	0.00	-0.03	-0.05	0.01	0.05	-0.01	0.06	0.03	0.04	0.00	-0.01	-0.03
AXL	0.07	0.02	0.07	0.02	0.08	-0.03	0.06	-0.06	-0.03	0.05	0.03	-0.02
AZGP1	0.00	-0.13	-0.01	-0.02	0.04	0.00	0.02	0.00	0.01	-0.01	0.01	-0.02
B4GALT1	0.00	0.03	-0.01	0.00	0.05	0.01	-0.11	-0.06	-0.06	-0.07	-0.06	-0.06
BASP1	0.07	0.01	0.02	0.00	-0.10	0.04	0.00	-0.01	0.09	0.01	0.06	-0.03
BMP1	0.03	-0.05	0.05	0.02	-0.06	0.04	-0.01	0.01	0.01	0.00	-0.03	0.00
BPIFB1	0.08	-0.04	0.05	-0.02	-0.06	0.07	-0.04	0.03	0.00	-0.02	-0.08	0.04
BTD	0.03	-0.03	0.01	0.06	0.04	0.10	-0.02	-0.06	-0.04	-0.04	0.07	0.09
C1R	0.09	-0.01	-0.03	0.08	-0.02	0.00	0.02	0.06	0.03	-0.03	0.05	0.01
C1RL	-0.02	-0.01	0.04	0.01	-0.08	-0.01	0.08	-0.07	0.02	0.04	-0.01	-0.05
C1S	0.04	0.08	-0.04	0.04	0.00	0.04	0.04	0.01	0.05	-0.03	0.01	-0.06
C2	0.02	-0.10	0.01	0.05	0.07	0.06	-0.03	-0.02	0.04	0.02	0.02	-0.03
C3	0.02	-0.13	0.03	-0.02	0.00	0.00	-0.01	-0.02	0.03	-0.01	0.04	0.05
C4A	-0.02	-0.02	0.04	0.06	-0.04	-0.08	0.10	-0.09	0.06	0.00	-0.09	0.06
C4B	-0.01	-0.11	0.03	0.01	0.02	-0.01	0.03	0.00	0.05	0.02	-0.11	0.02
C5	-0.06	-0.10	-0.03	0.04	-0.01	0.03	0.01	0.05	-0.02	0.00	-0.04	-0.03
C6	0.05	-0.12	-0.02	-0.02	0.03	-0.04	0.02	0.02	0.05	0.01	-0.03	-0.07
C7	0.00	-0.06	0.00	0.02	-0.02	0.05	0.04	0.04	-0.04	-0.06	-0.01	-0.03
C8A	0.04	-0.07	0.01	0.00	0.03	-0.01	-0.04	0.12	0.01	0.06	0.03	0.00
C8B	0.04	-0.07	-0.02	0.04	0.08	0.05	-0.01	-0.04	-0.01	0.00	-0.02	0.01
C8G	-0.04	-0.04	-0.03	0.06	0.00	0.05	-0.04	0.01	-0.03	0.07	0.01	0.00
C9	0.00	-0.06	0.02	0.01	-0.03	0.10	0.04	-0.01	-0.06	-0.04	0.07	-0.09
CA1	0.01	-0.01	-0.05	0.14	-0.06	0.02	0.00	0.01	-0.01	0.02	0.03	0.03
CALM1	0.00	0.02	-0.05	-0.02	-0.02	0.08	-0.12	0.05	0.01	0.06	-0.04	0.12
CALR	0.04	-0.08	-0.06	0.02	-0.11	-0.05	-0.04	0.04	0.00	-0.02	0.00	-0.04
CALU	0.06	0.04	-0.08	0.06	0.04	0.01	0.05	-0.02	0.05	0.00	0.05	0.06
CAMP	0.08	-0.01	0.08	0.06	-0.09	0.01	-0.04	0.02	0.00	-0.02	0.01	-0.02



CD14	0.08	0.04	0.05	-0.03	-0.03	-0.06	-0.05	-0.04	0.03	-0.05	0.10	0.01
CD163	0.06	0.00	0.02	0.01	-0.09	0.00	-0.03	0.02	0.06	0.11	0.00	-0.04
CD248	0.10	0.00	0.07	-0.05	-0.01	-0.04	0.04	-0.02	-0.03	0.04	0.04	-0.02
CD55	0.10	0.02	0.00	-0.06	-0.04	0.04	0.02	0.03	0.01	0.00	-0.06	0.02
CD9	0.00	0.02	-0.03	0.00	0.01	0.02	-0.09	0.05	-0.08	0.08	0.06	-0.13
CDC5L	-0.03	-0.09	0.00	0.00	0.00	-0.08	0.03	-0.04	0.05	0.05	-0.05	-0.05
CDH11	0.04	0.06	-0.04	0.04	-0.02	0.09	0.01	-0.04	-0.03	-0.04	0.06	-0.04
CDH13	0.05	-0.01	-0.04	-0.06	0.09	0.03	0.07	-0.03	-0.07	-0.03	0.02	-0.01
CDH15	0.03	-0.08	-0.10	0.01	0.05	-0.03	0.00	-0.05	-0.01	0.00	-0.02	0.07
CDH5	0.01	-0.02	-0.03	-0.05	-0.06	0.04	0.06	-0.02	0.04	0.04	0.06	0.02
CDHR5	0.02	-0.01	-0.10	-0.02	-0.08	0.00	0.06	-0.02	-0.07	-0.04	0.04	0.01
CEL	0.01	-0.03	-0.02	-0.02	0.06	0.06	-0.09	-0.12	0.03	-0.02	-0.07	0.06
CELA3A	0.05	-0.05	0.01	-0.01	0.04	0.07	-0.09	-0.08	0.01	-0.04	-0.01	0.06
CFB	0.01	-0.01	-0.02	0.00	0.05	0.02	-0.01	-0.03	0.15	-0.04	-0.02	0.09
CFD	0.04	0.05	-0.02	0.02	-0.07	-0.01	0.10	-0.08	0.02	0.01	0.06	0.04
CFH	0.01	-0.10	0.06	0.05	0.03	0.04	0.02	0.04	0.01	0.03	0.04	0.02
CFHR1	-0.04	-0.04	-0.03	0.02	0.02	0.03	0.07	0.13	-0.01	0.00	0.02	0.07
CFHR2	-0.03	-0.06	-0.01	0.08	-0.04	0.08	0.01	0.07	0.00	-0.08	0.02	-0.03
CFI	-0.01	-0.10	0.02	0.05	-0.04	0.06	-0.02	0.02	0.04	-0.02	0.01	-0.01
CFL1	0.07	-0.02	-0.10	-0.02	-0.07	-0.02	0.03	0.04	0.00	-0.03	-0.04	0.05
CGA	0.00	-0.06	-0.01	-0.02	-0.02	0.07	-0.07	0.11	-0.05	-0.06	-0.06	-0.02
CHGA	0.03	-0.05	-0.13	-0.04	-0.02	-0.06	0.04	-0.04	0.00	-0.04	0.02	-0.03
CHRD1	0.09	0.03	0.05	-0.02	0.01	-0.03	0.03	-0.07	0.00	0.00	-0.03	0.01
CHRD2	0.03	-0.05	0.01	0.09	-0.08	0.07	-0.01	0.03	-0.03	0.01	0.04	-0.05
CLCA1	0.02	0.02	-0.04	-0.05	0.04	0.06	0.03	-0.02	-0.08	-0.08	-0.07	-0.04
CLEC3B	0.02	-0.03	0.04	0.01	0.01	0.08	0.12	-0.02	-0.01	0.00	0.08	-0.02
CLIC1	0.05	-0.05	-0.07	-0.02	-0.06	-0.02	-0.01	0.03	-0.03	-0.07	-0.05	0.00
CLIC4	0.05	-0.10	-0.05	-0.03	0.03	-0.01	0.01	-0.07	0.04	-0.04	-0.01	-0.05
CLPS	0.05	0.03	0.02	0.06	0.07	0.05	-0.04	-0.07	-0.02	-0.01	-0.03	0.00
CLSTN1	-0.01	-0.02	-0.02	0.02	0.05	0.02	-0.05	0.02	-0.02	-0.02	-0.02	-0.09
COL12A1	0.01	0.06	-0.07	0.06	0.01	0.02	0.12	0.03	-0.01	0.06	0.05	-0.01

COL15A1	0.06	0.00	-0.10	0.09	0.04	-0.01	0.01	-0.02	0.03	-0.01	0.06	-0.02
COL16A1	0.00	0.04	-0.06	0.04	-0.07	0.01	0.08	-0.05	-0.04	0.03	0.00	-0.03
COL1A1	-0.01	0.08	-0.02	0.10	0.04	0.06	0.03	-0.02	-0.02	-0.01	0.01	-0.08
COL1A2	0.01	0.09	-0.04	0.11	0.02	0.03	0.03	0.01	0.02	0.00	-0.03	-0.06
COL2A1	0.01	-0.02	-0.10	0.03	-0.02	0.04	0.04	0.02	0.00	0.04	0.06	-0.02
COL3A1	0.03	0.05	-0.04	0.11	0.02	0.04	0.01	-0.02	-0.03	-0.07	-0.02	-0.05
COL4A2	0.04	-0.03	-0.05	-0.02	0.07	-0.08	0.07	-0.01	0.02	0.07	0.05	0.05
COL5A2	0.05	0.09	0.00	0.06	0.07	0.02	0.00	-0.05	0.07	0.03	-0.07	-0.02
COL6A1	0.06	0.09	0.00	0.06	0.05	0.01	0.00	0.01	0.00	-0.03	0.02	0.01
COLEC12	0.07	-0.01	-0.06	-0.05	0.09	-0.03	-0.04	-0.01	0.04	-0.04	0.09	-0.04
COMP	0.08	0.05	0.00	0.02	0.00	0.02	0.02	0.04	0.10	0.02	-0.02	0.03
CP	-0.01	-0.02	0.04	-0.08	0.05	0.02	0.04	0.01	0.11	0.09	0.06	0.05
CPA1	0.05	-0.06	0.00	0.00	0.05	0.06	-0.11	-0.09	0.01	-0.01	-0.05	0.04
CRISP3	0.06	-0.07	-0.01	-0.01	0.02	0.00	0.02	-0.05	0.04	0.05	0.02	-0.03
CST3	0.10	0.03	-0.02	-0.06	0.04	0.03	-0.02	0.01	0.05	0.04	0.01	-0.03
CST6	0.05	0.01	-0.02	-0.11	0.05	0.00	0.08	-0.05	0.04	-0.02	0.05	0.02
CSTB	0.05	0.06	0.00	-0.07	0.01	0.05	0.07	0.06	-0.06	0.02	-0.01	0.01
CTGF	0.02	-0.04	-0.01	-0.01	0.07	0.04	0.03	-0.10	0.05	0.01	0.08	-0.02
DAG1	0.03	0.12	-0.04	-0.04	0.05	0.05	-0.02	0.00	0.07	0.04	0.02	0.01
DBI	0.06	0.07	-0.02	0.00	0.05	-0.06	0.00	0.05	0.01	0.04	-0.02	-0.02
DCN	0.07	0.06	-0.02	0.09	0.01	0.01	0.07	-0.01	0.00	-0.03	0.01	-0.01
DLK1	0.04	-0.04	-0.12	-0.03	-0.01	0.03	0.03	-0.10	0.02	0.01	-0.02	-0.01
DMBT1	0.03	0.01	-0.01	-0.04	0.07	0.00	-0.06	-0.08	-0.06	-0.06	0.03	-0.04
DMKN	0.07	-0.04	0.04	-0.03	-0.07	0.09	-0.05	0.02	0.02	-0.01	-0.07	0.07
DPP4	0.03	-0.03	-0.11	-0.03	0.00	-0.03	-0.04	0.02	0.01	0.01	-0.06	-0.09
DSC2	0.02	0.04	-0.08	0.01	-0.06	-0.03	0.02	-0.05	0.02	0.01	-0.04	0.10
DSC3	0.00	0.06	-0.03	0.01	0.05	0.03	0.02	-0.04	-0.02	0.02	-0.03	-0.07
DSG2	0.02	0.06	-0.04	0.03	0.08	0.03	-0.03	-0.02	0.03	-0.08	0.07	-0.01
ECM1	0.10	0.02	0.05	-0.03	0.01	-0.04	-0.01	0.01	-0.02	-0.01	0.05	-0.05
EEF1A1	0.00	-0.01	-0.07	-0.05	-0.08	-0.05	0.00	0.01	-0.04	-0.04	0.01	0.04
EFEMP1	0.11	0.01	-0.02	-0.04	0.06	-0.04	-0.03	0.00	0.00	0.03	0.00	-0.06

EFEMP2	0.06	0.02	0.01	0.07	0.00	0.06	0.01	0.07	0.04	0.04	0.01	-0.08
EFNA1	0.03	0.08	-0.02	0.00	-0.02	0.04	-0.07	0.05	0.08	-0.05	-0.04	-0.01
EFNB1	0.04	0.00	-0.07	0.04	0.07	-0.01	-0.03	-0.04	-0.03	-0.01	0.07	0.03
ENO1	0.07	-0.02	-0.02	0.04	-0.03	-0.07	-0.02	-0.01	0.00	0.00	-0.02	-0.02
ENPP2	0.11	-0.03	0.04	-0.04	-0.02	-0.04	-0.03	0.02	0.01	-0.02	0.01	0.01
ENPP7	0.00	0.05	-0.05	-0.04	0.01	0.01	-0.07	-0.10	0.03	0.02	-0.12	-0.01
EZR	0.07	-0.06	-0.05	-0.03	0.07	-0.01	-0.06	0.04	0.03	0.05	-0.05	-0.04
F10	0.04	-0.09	-0.09	-0.01	-0.09	-0.06	0.00	0.01	-0.02	-0.03	-0.03	-0.03
F11R	-0.04	0.03	-0.03	0.00	-0.06	0.05	-0.03	-0.01	-0.06	0.03	0.02	0.03
F12	0.00	-0.14	-0.01	0.02	0.02	0.03	0.05	0.00	-0.02	0.04	0.02	0.01
F13B	-0.02	0.00	0.02	0.03	-0.02	0.09	0.05	0.01	-0.07	-0.02	0.03	-0.09
F2	0.02	-0.11	-0.08	-0.01	-0.08	-0.05	-0.01	0.04	-0.02	-0.03	-0.02	-0.01
FABP1	-0.01	0.04	-0.07	0.00	0.00	0.12	0.00	-0.01	-0.04	-0.03	-0.08	-0.05
FABP5	0.10	-0.04	0.00	0.01	0.00	0.04	0.02	-0.01	-0.06	-0.01	-0.02	-0.03
FAM151A	0.01	0.02	-0.06	0.00	-0.08	0.03	-0.02	0.03	0.04	0.02	-0.01	0.05
FBLN2	0.06	-0.04	-0.10	0.03	-0.06	-0.06	0.02	0.01	-0.04	-0.01	0.03	0.02
FBN1	0.05	-0.01	-0.02	0.04	0.01	-0.03	0.07	0.06	-0.06	0.07	-0.02	0.04
FCGBP	0.03	-0.03	0.02	-0.08	0.04	0.04	0.02	-0.06	-0.07	-0.08	0.05	-0.03
FETUB	0.00	-0.09	0.03	0.06	-0.01	0.05	0.00	-0.02	0.01	0.05	-0.01	0.02
FGA	0.00	-0.03	-0.04	0.10	-0.08	-0.03	-0.01	-0.06	0.04	0.02	0.09	-0.01
FGB	0.08	-0.01	0.04	0.03	-0.06	0.05	0.03	0.01	0.05	0.04	0.07	0.02
FGG	0.04	0.00	0.06	0.04	-0.08	0.09	0.03	0.01	-0.02	-0.03	0.04	0.02
FLG	0.02	-0.04	0.05	-0.09	0.04	-0.02	0.04	0.04	-0.09	0.05	0.05	0.06
FLT1	0.02	0.04	0.04	-0.03	0.04	0.11	0.09	0.01	-0.11	0.03	-0.01	0.04
FMOD	0.03	0.07	-0.07	0.07	0.01	0.05	0.00	-0.02	0.06	-0.02	-0.01	0.02
FN1	0.08	0.08	0.00	0.04	0.02	0.01	0.11	0.00	-0.05	0.02	0.03	0.00
FOLH1	0.05	0.00	-0.12	-0.05	-0.02	-0.07	-0.03	0.00	0.03	-0.03	-0.03	0.00
FSTL1	0.08	0.02	0.06	0.10	0.05	0.03	0.00	0.03	-0.03	0.05	-0.01	-0.03
FSTL3	0.04	0.02	-0.07	-0.02	-0.04	0.07	0.09	-0.06	0.00	0.05	0.07	0.05
FUCA2	0.04	0.00	-0.12	-0.07	-0.06	0.00	0.02	-0.02	0.00	-0.02	0.02	0.07
GAPDH	0.09	-0.06	-0.01	0.06	0.03	0.00	0.00	-0.05	-0.01	0.00	-0.01	-0.04

GGT1	0.00	0.03	-0.07	0.00	0.00	0.09	-0.12	0.10	0.02	0.04	0.01	0.09
GM2A	0.06	0.04	-0.02	-0.02	-0.01	0.08	0.05	0.08	-0.04	-0.02	-0.01	0.01
GOLM1	0.03	0.06	-0.03	0.04	0.00	-0.02	0.01	-0.09	0.10	0.09	0.01	-0.03
GPX3	0.05	0.04	-0.07	-0.02	-0.08	0.04	0.04	-0.01	0.06	0.08	0.01	0.03
GRN	0.07	-0.04	0.04	-0.05	-0.03	0.06	-0.06	-0.05	0.02	-0.04	-0.06	0.07
GSTP1	0.09	-0.03	-0.02	-0.04	0.00	0.00	0.00	0.02	-0.04	-0.05	0.02	-0.01
HABP2	-0.03	-0.12	-0.05	0.01	0.02	0.04	0.01	-0.01	0.00	-0.02	0.02	-0.02
HAPLN1	0.06	0.01	-0.05	0.05	0.06	-0.03	0.07	0.05	0.01	-0.03	0.05	-0.03
HAPLN3	0.00	0.01	-0.04	0.10	0.05	-0.01	0.03	0.11	0.02	-0.10	-0.02	0.11
HBA1	0.00	0.02	-0.01	0.14	0.00	-0.07	0.00	0.02	-0.03	0.07	-0.07	0.05
HBB	0.00	-0.03	-0.02	0.13	-0.08	0.00	-0.03	0.02	-0.02	0.03	0.04	-0.01
HPR	0.00	-0.02	0.05	0.01	0.00	-0.08	0.07	-0.09	-0.07	0.01	-0.07	-0.05
HPX	-0.03	-0.11	0.03	-0.01	0.05	0.02	0.04	0.00	0.04	0.05	0.00	-0.03
HRG	-0.01	-0.05	-0.04	0.03	0.00	0.11	0.08	-0.03	0.02	-0.06	-0.06	-0.02
HRNR	0.04	0.01	-0.07	-0.08	-0.02	-0.01	0.04	0.05	-0.02	0.02	0.02	0.11
HSP90AA1	0.06	-0.07	-0.09	-0.05	-0.07	-0.02	0.02	0.01	-0.04	-0.02	-0.04	0.00
HSP90B1	-0.01	-0.03	-0.07	0.01	-0.12	-0.02	0.04	-0.04	-0.05	-0.07	0.07	0.03
HSPA8	0.00	0.01	0.01	0.05	-0.01	-0.06	-0.05	-0.04	-0.13	0.14	-0.04	-0.11
HSPG2	0.04	0.03	-0.12	-0.05	0.00	0.06	0.05	-0.02	-0.01	-0.01	0.04	-0.01
HTRA1	0.07	0.02	-0.02	0.02	0.04	0.00	0.05	0.02	0.07	0.11	-0.02	0.01
IGF2	0.04	0.01	0.01	0.05	0.08	0.09	0.02	0.00	-0.01	-0.04	-0.01	-0.01
IGFBP2	0.09	0.04	0.06	-0.02	0.01	-0.05	0.02	0.00	0.05	-0.01	0.02	-0.02
IGFBP3	0.08	0.03	-0.04	0.03	-0.06	-0.08	0.03	0.07	0.02	0.00	0.04	0.02
IGFBP4	0.09	0.06	0.04	-0.04	-0.03	-0.02	0.04	0.05	0.01	0.02	0.00	-0.01
IGFBP5	0.04	0.02	0.06	0.00	-0.01	-0.03	0.02	-0.03	0.14	0.03	-0.11	-0.04
IGFBP6	0.07	-0.04	0.05	0.01	0.04	-0.03	0.03	-0.02	-0.01	0.02	0.01	0.01
IGFBP7	0.08	0.05	0.03	-0.03	-0.06	0.00	0.02	-0.01	0.08	-0.01	-0.06	0.00
IGHA1	-0.04	-0.04	0.02	0.02	-0.05	-0.01	-0.04	-0.02	-0.13	-0.02	0.06	0.00
IGHA2	-0.03	-0.01	-0.02	-0.08	-0.07	0.07	-0.11	-0.01	-0.04	0.01	0.01	-0.02
IGHG2	0.01	0.00	0.03	0.11	0.04	-0.09	0.05	-0.02	-0.04	-0.04	-0.02	0.08
IGHG3	0.00	0.00	0.02	0.11	0.05	-0.08	0.03	0.01	-0.04	-0.01	0.07	0.05

IGHG4	-0.03	0.00	-0.02	-0.01	0.00	-0.05	-0.02	0.09	-0.06	0.05	-0.07	-0.06
IGHV1-18	0.02	0.09	-0.01	-0.02	0.05	0.00	-0.06	0.04	0.05	-0.02	0.05	0.00
IGHV1-3	0.00	0.00	0.04	0.01	-0.04	-0.06	0.00	-0.10	-0.06	0.13	-0.02	-0.11
IGHV1-69	0.02	-0.01	0.03	-0.02	0.04	-0.01	-0.09	0.09	0.00	0.04	0.05	0.08
IGHV10R15-	-0.03	0.01	0.01	-0.05	-0.01	0.03	-0.08	-0.03	-0.05	-0.02	0.11	0.02
IGHV3-15	0.04	0.01	0.01	0.07	0.00	-0.02	0.09	-0.04	0.06	0.03	0.02	0.05
IGHV3-38	0.01	0.00	0.03	0.07	0.03	0.01	-0.01	-0.11	-0.01	0.04	-0.09	0.00
IGHV3-43	0.00	-0.01	0.02	0.07	-0.02	-0.03	0.02	0.06	-0.07	-0.08	-0.12	0.08
IGHV3-49	0.04	0.01	0.03	0.09	0.04	-0.08	0.03	0.01	0.02	-0.01	-0.01	0.02
IGHV3-53	0.01	-0.02	0.01	0.03	0.08	-0.03	0.01	-0.07	-0.03	0.01	-0.08	-0.03
IGHV3-66	-0.01	0.05	0.00	0.00	-0.03	-0.03	-0.06	-0.09	0.03	-0.02	0.07	0.07
IGHV3-7	-0.04	0.05	0.06	0.05	-0.05	0.00	0.07	0.00	0.00	-0.01	-0.10	0.06
IGHV3-72	0.04	0.04	0.04	0.03	0.02	0.00	-0.01	0.02	0.00	-0.04	-0.09	0.08
IGHV3-73	0.03	0.02	-0.04	0.00	0.01	0.01	-0.01	-0.07	-0.03	0.09	0.00	0.04
IGHV3-9	0.00	-0.01	0.02	0.12	0.01	-0.09	0.09	-0.02	0.02	-0.02	-0.07	0.08
IGHV3OR16-	0.04	-0.06	-0.02	0.04	0.09	0.02	-0.06	-0.06	0.01	-0.01	0.07	0.05
IGHV4-28	0.02	-0.03	0.03	0.02	0.07	-0.02	-0.04	0.02	-0.03	-0.01	0.02	0.03
IGHV5-51	0.04	-0.03	0.06	-0.08	-0.05	0.03	-0.04	-0.06	-0.07	0.05	-0.02	-0.13
IGHV6-1	0.00	-0.02	-0.02	0.07	0.02	-0.03	-0.03	-0.08	-0.01	0.00	-0.08	0.09
IGKC	0.00	0.00	0.01	0.08	0.03	-0.08	-0.09	-0.06	-0.09	-0.06	0.05	0.08
IGKV1-16	0.04	-0.01	0.02	-0.06	0.07	0.04	-0.08	0.02	0.03	-0.06	0.02	0.04
IGKV1-5	0.04	-0.07	-0.07	0.04	0.06	0.03	-0.05	-0.10	-0.02	-0.05	-0.01	0.03
IGKV2-24	0.02	0.01	0.03	0.00	0.07	-0.01	0.01	-0.09	-0.06	-0.08	-0.04	-0.02
IGKV2-28	0.03	-0.02	0.04	0.03	0.09	-0.07	-0.05	-0.10	-0.04	-0.02	-0.05	0.04
IGKV2-30	0.03	0.00	0.08	0.03	0.04	-0.04	-0.03	-0.06	0.00	-0.05	-0.07	0.06
IGKV3-15	0.00	-0.02	-0.01	0.08	0.08	-0.03	-0.04	0.01	-0.07	0.04	-0.06	0.05
IGKV3-20	0.00	0.01	0.01	0.03	0.02	-0.07	-0.09	-0.05	-0.05	-0.04	0.01	0.12
IGKV3-7	0.00	0.02	-0.06	0.01	0.02	0.06	-0.07	0.10	0.00	-0.04	-0.03	0.11
IGKV3D-11	0.05	0.00	0.04	-0.01	0.07	-0.12	-0.03	-0.04	-0.03	0.05	0.04	0.06
IGKV4-1	0.04	-0.02	0.01	0.05	0.09	0.01	-0.06	-0.03	-0.09	0.07	0.02	0.07
IGLC7	0.00	0.02	-0.01	0.03	-0.04	0.01	-0.09	-0.01	-0.01	0.15	-0.01	0.01

IGLL5	-0.04	0.04	0.00	0.05	-0.02	0.00	-0.06	-0.09	-0.04	0.11	0.10	0.03
IGLV1-47	-0.07	-0.03	0.02	0.01	-0.03	-0.05	0.05	-0.07	-0.02	0.04	-0.01	0.05
IGLV1-51	-0.01	-0.01	0.08	0.03	0.04	0.06	-0.04	-0.05	-0.09	-0.05	0.05	0.01
IGLV10-54	-0.02	0.00	0.02	0.00	0.01	0.05	0.04	0.01	-0.06	-0.09	-0.06	0.05
IGLV2-11	0.02	0.06	0.09	-0.02	0.07	-0.02	-0.05	0.05	-0.08	-0.02	0.00	0.01
IGLV2-8	0.04	0.07	0.09	-0.03	-0.02	-0.02	0.00	-0.07	-0.01	0.04	0.01	-0.02
IGLV3-10	0.01	0.01	0.02	-0.01	0.01	-0.05	-0.07	0.00	0.02	-0.02	-0.03	0.02
IGLV3-19	0.04	-0.03	0.05	0.03	0.01	0.02	-0.04	-0.01	0.07	-0.05	0.00	-0.10
IGLV3-21	0.02	-0.02	-0.03	0.05	0.04	-0.02	-0.01	0.03	-0.02	0.09	0.01	0.04
IGSF1	0.02	0.01	-0.10	0.00	-0.03	0.06	-0.04	-0.07	0.07	0.02	-0.01	0.00
IL1R2	0.06	0.01	0.03	0.03	-0.09	-0.07	0.02	-0.06	0.00	-0.02	-0.05	0.04
IL1RAP	0.00	0.09	-0.02	0.01	-0.02	0.06	0.01	0.03	0.04	0.01	-0.06	0.05
INA	-0.03	-0.03	0.04	-0.03	-0.02	0.00	0.07	-0.05	0.07	-0.04	0.07	-0.06
ISLR	0.08	-0.01	0.03	0.03	-0.01	-0.03	0.05	0.04	0.02	-0.02	-0.08	0.01
ISM2	0.09	-0.01	-0.01	-0.04	0.00	-0.03	0.06	-0.01	-0.03	0.05	-0.06	0.02
ITIH1	0.05	-0.08	0.07	0.02	0.00	0.07	0.03	0.06	0.04	-0.03	-0.03	-0.01
ITIH2	0.00	-0.08	0.00	0.01	0.01	0.06	0.07	0.03	0.05	0.01	-0.06	0.02
IVL	0.07	-0.04	0.01	-0.07	0.07	0.00	0.03	-0.02	-0.03	0.04	0.01	0.01
KLKB1	0.01	-0.08	0.02	-0.02	0.03	0.01	0.04	0.05	-0.05	0.01	-0.07	0.03
KNG1	-0.05	-0.05	0.04	0.03	-0.01	0.08	0.10	-0.04	-0.03	0.04	0.03	0.08
KRT1	0.02	0.00	-0.07	-0.05	0.05	-0.03	-0.03	0.06	-0.09	0.04	0.09	0.07
KRT10	0.02	0.01	-0.05	-0.02	0.06	-0.04	-0.01	0.05	-0.10	0.03	0.10	0.09
KRT13	-0.01	0.02	0.01	-0.05	0.03	0.06	0.00	0.10	-0.08	0.00	-0.01	0.07
KRT14	0.02	0.01	-0.04	-0.04	0.05	-0.04	-0.01	0.03	-0.09	0.05	0.09	0.09
KRT19	0.10	0.00	-0.03	0.00	0.01	0.01	-0.04	0.01	0.01	0.00	0.04	0.01
KRT2	0.02	0.03	-0.06	-0.03	0.02	-0.03	-0.01	0.10	-0.09	0.05	0.04	0.06
KRT5	0.00	-0.02	0.02	-0.02	0.03	-0.04	0.07	-0.02	-0.07	-0.08	0.00	-0.09
KRT79	0.00	0.01	-0.03	0.12	0.05	-0.05	0.05	0.09	-0.01	-0.08	-0.02	0.05
KRT8	0.06	0.04	-0.02	-0.02	-0.11	-0.01	0.00	0.03	0.00	0.01	0.06	0.04
KRT84	0.00	0.02	-0.01	-0.02	-0.05	0.02	-0.12	-0.04	-0.06	0.16	-0.05	-0.01
KRT9	0.02	0.03	-0.09	-0.02	-0.01	-0.05	0.03	0.08	-0.04	0.03	0.01	0.06

LAMB1	0.07	-0.03	0.02	0.07	0.03	0.02	0.00	0.00	0.03	-0.01	0.07	-0.02
LAMC1	0.09	0.04	-0.03	0.02	0.01	-0.07	0.05	-0.01	0.05	0.01	0.06	-0.06
LBP	-0.01	-0.10	-0.01	0.02	-0.03	-0.02	0.05	-0.01	0.05	0.04	0.00	-0.06
LCN2	0.09	0.04	0.04	0.04	-0.05	-0.01	0.00	-0.04	-0.02	0.07	0.09	-0.03
LCP1	0.08	-0.03	0.05	0.08	-0.07	0.06	-0.04	0.01	-0.03	0.00	0.03	-0.03
LDHA	0.10	-0.05	0.03	0.04	-0.04	-0.01	0.00	-0.03	0.02	-0.04	0.00	0.00
LDHB	0.09	-0.04	-0.01	0.02	-0.04	0.08	-0.02	-0.04	-0.04	0.06	-0.05	-0.02
LGALS1	0.10	-0.01	0.04	0.04	-0.02	0.04	0.03	0.05	-0.01	0.01	-0.06	0.03
LGALS3BP	0.07	0.06	-0.02	-0.01	0.05	0.02	0.06	0.01	-0.06	0.00	0.01	0.00
LOX	0.09	-0.02	-0.05	0.04	0.03	-0.03	-0.05	-0.04	0.05	0.02	-0.02	0.05
LRG1	0.00	-0.10	0.04	-0.04	0.01	0.02	0.03	0.02	0.10	0.05	0.06	-0.02
LTBP2	0.05	0.04	0.06	0.03	0.06	0.02	-0.01	-0.02	0.03	0.01	0.02	-0.06
LUM	0.07	0.07	0.09	-0.03	0.00	-0.06	0.03	0.00	-0.02	0.01	0.01	-0.01
LYPD3	0.05	-0.02	-0.06	-0.07	0.06	-0.03	-0.05	0.09	0.07	0.02	-0.02	0.02
LYVE1	-0.05	0.00	0.01	0.00	-0.03	0.15	-0.01	-0.03	0.01	0.05	-0.03	-0.01
LYZ	0.07	-0.05	0.03	0.03	0.05	-0.01	-0.07	-0.01	0.01	-0.03	0.06	0.04
MAN1A1	0.00	0.02	-0.12	-0.04	-0.01	-0.01	-0.01	0.01	-0.05	-0.05	-0.05	-0.08
MARCKS	0.07	-0.05	0.00	0.02	0.02	0.04	-0.02	-0.10	-0.04	-0.06	0.01	0.05
MASP2	0.01	-0.06	-0.03	-0.03	0.01	0.04	0.08	0.09	-0.01	0.08	-0.04	0.01
MATN2	0.06	-0.01	0.02	0.09	-0.03	0.04	0.03	0.04	-0.05	-0.03	0.06	0.03
MEP1A	0.02	0.02	-0.08	0.00	0.08	0.06	-0.10	-0.02	-0.02	-0.04	-0.06	-0.07
MFAP4	0.00	-0.01	0.00	0.07	0.04	0.04	0.05	-0.05	0.03	0.02	-0.01	-0.04
MIF	0.07	0.01	0.02	-0.03	-0.05	0.01	0.02	0.01	0.06	0.00	0.05	-0.05
MMP2	0.11	-0.03	0.04	-0.02	0.00	-0.03	-0.01	0.07	-0.03	0.00	0.02	-0.05
MSN	0.07	0.00	0.05	-0.01	-0.04	0.00	-0.09	0.08	-0.03	-0.04	0.04	0.02
MUC1	0.06	-0.07	-0.05	0.00	0.06	0.00	-0.02	-0.01	-0.01	-0.02	0.03	0.11
MUC13	0.00	-0.03	-0.13	-0.03	0.00	-0.01	0.00	-0.02	-0.07	-0.06	-0.02	-0.04
MUC16	0.04	-0.07	0.00	-0.03	0.09	0.04	0.00	-0.01	-0.03	-0.03	-0.10	0.00
MUC2	0.03	-0.03	-0.04	-0.05	0.00	0.01	0.08	-0.15	0.00	0.01	-0.02	0.04
MUC5AC	0.02	0.01	-0.11	-0.08	0.00	-0.03	0.06	-0.06	-0.04	-0.03	-0.01	-0.01
MUC5B	0.05	-0.03	0.01	-0.07	-0.04	0.03	0.05	0.00	-0.09	-0.07	-0.06	0.02

MYDGF	0.03	0.02	-0.03	0.08	0.02	0.02	-0.02	0.01	-0.02	0.00	0.13	-0.03
MYL6	0.00	0.04	0.01	0.02	0.02	-0.07	-0.02	0.06	0.02	0.07	-0.08	-0.09
NID1	0.07	0.00	0.00	-0.01	-0.05	-0.01	0.04	-0.03	-0.13	0.05	-0.02	0.01
NID2	0.08	0.04	0.06	-0.02	0.03	0.02	0.01	0.01	-0.01	-0.06	0.01	-0.09
NOTUM	-0.02	0.03	0.01	-0.04	0.01	0.06	0.04	-0.09	-0.06	0.03	0.03	0.09
NPC2	0.09	0.03	0.05	-0.05	-0.06	0.03	-0.02	-0.01	0.01	-0.01	-0.05	0.01
NT5E	0.00	0.05	-0.07	0.00	-0.05	0.09	-0.06	-0.03	0.04	0.00	-0.09	0.06
NUCB1	0.11	0.01	-0.03	0.02	-0.06	-0.07	0.01	0.01	0.02	0.01	-0.01	0.02
OGN	0.02	0.02	-0.02	-0.05	0.12	-0.05	-0.04	0.06	0.01	-0.01	0.01	-0.02
OLFML3	0.06	0.05	-0.02	0.08	0.02	-0.01	0.03	0.05	0.05	0.05	-0.10	-0.03
ORM1	0.03	-0.09	0.06	-0.05	-0.05	-0.01	-0.03	0.00	0.09	-0.01	0.02	-0.07
ORM2	0.00	-0.08	0.06	-0.06	-0.03	0.01	-0.04	0.01	0.07	-0.01	0.05	0.00
P4HB	0.09	0.02	0.01	0.03	-0.03	-0.03	-0.03	0.03	0.02	-0.05	0.04	-0.02
PAPLN	0.06	-0.01	0.10	-0.01	-0.05	-0.05	-0.03	0.02	0.00	-0.05	0.04	-0.01
PCOLCE	0.04	0.07	-0.03	0.10	0.02	0.05	0.05	-0.01	-0.06	-0.04	-0.02	-0.03
PDIA3	0.03	0.03	0.04	-0.06	0.02	-0.03	-0.01	0.10	0.01	0.05	0.05	0.07
PFN1	0.06	-0.01	0.05	0.01	-0.06	0.11	0.01	0.00	0.01	0.01	-0.03	-0.01
PGAM1	0.10	-0.02	0.08	0.02	-0.04	0.01	-0.03	0.02	0.02	-0.05	0.02	-0.03
PGK1	0.09	-0.02	0.07	0.00	-0.04	-0.05	0.02	0.05	-0.03	0.00	-0.04	-0.03
PGLYRP2	0.03	-0.04	-0.02	0.04	0.03	0.07	-0.01	0.04	-0.05	-0.07	-0.09	-0.07
PI16	0.00	0.00	0.03	-0.03	0.01	0.08	0.10	0.08	-0.04	0.00	0.02	0.01
PIGR	0.03	0.08	0.03	-0.05	0.00	0.03	0.03	0.02	0.10	0.04	-0.04	0.01
PLG	-0.02	-0.13	-0.02	0.02	0.06	0.04	0.04	0.02	-0.01	0.07	0.00	0.00
PLOD1	0.00	0.01	0.00	0.12	-0.01	-0.05	0.02	0.00	0.03	0.04	-0.09	0.14
PLS3	0.05	-0.04	0.02	0.06	0.00	0.01	-0.07	-0.07	-0.06	0.07	-0.10	0.01
PLTP	0.03	-0.08	-0.03	0.09	-0.04	-0.03	-0.05	-0.04	-0.04	-0.01	0.07	-0.03
PON1	-0.05	-0.06	0.00	0.03	-0.08	0.00	-0.03	0.09	-0.03	0.00	-0.01	-0.06
POSTN	0.02	0.06	-0.09	0.06	-0.02	0.00	0.03	-0.02	-0.02	0.02	0.04	-0.04
POTEI	0.00	-0.02	0.02	0.01	0.03	-0.03	0.12	0.00	0.07	-0.16	0.00	0.07
PPIA	0.06	-0.03	-0.02	0.04	0.01	0.03	-0.03	-0.06	0.01	0.10	-0.08	0.00
PPIAL4A	0.00	0.00	0.01	0.06	-0.01	-0.06	0.01	-0.05	-0.04	0.05	-0.12	0.09



PRDX1	-0.02	0.00	-0.02	-0.03	-0.09	0.04	-0.07	-0.01	0.01	-0.03	0.03	0.08
PRDX2	0.03	-0.03	-0.06	0.10	-0.04	0.04	0.03	-0.07	-0.02	0.03	0.04	0.02
PRDX6	0.00	0.00	0.02	0.01	-0.05	0.01	0.01	-0.05	0.12	0.03	-0.04	0.15
PRG2	0.04	-0.01	0.02	-0.03	0.04	0.08	0.08	-0.01	-0.12	0.04	0.03	0.09
PRL	0.07	0.05	0.06	0.00	-0.06	-0.06	0.04	-0.06	-0.08	-0.05	0.03	0.02
PROCR	0.00	0.03	0.03	0.00	0.05	-0.04	0.06	-0.02	-0.03	0.13	0.01	0.03
PROS1	0.03	-0.06	-0.06	-0.02	-0.09	-0.07	-0.01	0.02	-0.04	-0.06	-0.02	-0.01
PRSS8	0.05	0.03	-0.06	-0.07	-0.05	-0.01	-0.02	0.03	-0.02	0.01	-0.06	0.09
PSAP	0.09	0.00	0.04	0.04	-0.01	0.04	-0.06	0.04	-0.01	-0.06	-0.04	0.06
PSG1	0.06	-0.06	-0.06	0.00	0.06	0.01	-0.07	-0.03	-0.04	0.04	0.10	-0.03
PSG9	0.00	0.03	-0.04	0.10	0.00	0.00	-0.09	0.06	-0.05	0.11	-0.05	0.05
PTGDS	0.04	0.05	0.01	-0.06	-0.05	0.08	0.06	-0.08	-0.08	0.01	0.00	-0.02
PTMA	-0.05	0.00	0.00	0.07	-0.12	-0.03	-0.01	-0.04	-0.02	0.00	0.02	-0.01
PVR	0.03	0.02	0.05	-0.05	0.03	-0.01	-0.02	0.10	-0.02	0.08	-0.03	-0.01
PZP	0.00	-0.02	0.02	-0.10	0.00	0.05	0.06	-0.01	0.11	-0.13	0.07	0.02
QSOX1	0.04	-0.04	-0.10	-0.07	0.07	-0.03	0.03	0.04	-0.02	0.04	0.00	0.00
RBP4	-0.02	-0.08	-0.04	0.00	0.00	0.04	-0.05	-0.04	0.11	0.00	0.08	-0.07
RCN1	0.03	0.06	-0.02	0.04	0.05	0.00	0.02	0.05	0.12	-0.01	0.05	-0.02
S100A11	0.00	0.03	-0.07	0.03	-0.11	0.02	0.04	0.01	-0.09	-0.02	-0.06	0.01
S100A6	0.02	-0.03	0.08	-0.04	-0.04	0.00	0.01	0.08	-0.02	0.11	-0.04	0.05
S100A8	0.07	-0.05	0.06	0.01	-0.08	0.07	-0.01	0.01	-0.01	-0.01	-0.06	0.01
S100A9	0.08	-0.06	0.06	0.03	-0.05	0.09	0.00	-0.01	0.04	-0.04	0.00	0.02
SCGB1A1	-0.01	0.06	0.02	-0.06	0.07	-0.02	0.08	-0.03	-0.07	0.02	-0.06	-0.02
SCGB3A1	0.02	-0.07	-0.08	-0.06	-0.05	-0.04	0.06	-0.03	-0.05	-0.03	-0.04	-0.01
SCGB3A2	0.01	-0.10	0.03	-0.05	0.04	0.02	0.04	-0.07	0.01	0.06	-0.02	-0.03
SCUBE2	0.04	0.02	-0.06	-0.01	0.08	-0.07	-0.02	0.02	0.01	0.03	0.05	0.00
SDF4	-0.01	0.05	-0.03	0.04	-0.04	0.11	-0.06	0.02	0.00	0.06	0.05	-0.02
SERPINA2	0.00	-0.01	0.04	0.01	-0.04	-0.04	0.03	-0.08	0.03	0.07	0.02	-0.05
SERPINA3	0.01	-0.06	0.06	0.01	0.02	-0.02	0.06	0.04	-0.02	0.01	0.02	-0.06
SERPINA4	-0.06	-0.06	-0.04	0.03	-0.03	0.08	0.06	0.06	-0.08	0.04	-0.02	0.04
SERPINA6	0.03	-0.05	-0.03	0.02	0.11	0.05	0.02	0.02	0.06	0.09	0.00	0.02

SERPINA7	0.02	0.00	0.00	-0.05	0.00	0.04	0.01	0.11	-0.02	0.09	-0.05	-0.04
SERPINB2	0.03	-0.01	-0.04	-0.05	-0.01	-0.04	0.05	-0.07	0.04	-0.06	0.10	0.12
SERPINC1	-0.08	-0.05	-0.02	0.01	-0.02	0.05	0.07	0.02	0.02	-0.03	0.00	0.01
SERPIND1	-0.02	-0.09	-0.03	0.06	-0.03	0.00	0.04	0.04	0.03	0.01	0.01	0.01
SERPINE2	0.08	-0.01	0.00	0.08	0.06	0.03	0.03	-0.02	-0.02	-0.02	-0.08	0.03
SERPINF1	0.03	0.01	-0.06	0.02	0.08	0.02	0.06	0.06	-0.03	0.07	0.04	0.01
SERPINF2	0.03	-0.11	0.01	-0.01	0.04	0.05	-0.04	-0.01	0.06	0.02	-0.02	0.01
SERPING1	0.10	0.03	0.09	-0.04	-0.02	0.01	0.04	0.00	0.01	-0.02	-0.01	0.01
SFN	0.03	-0.03	0.04	-0.01	-0.10	0.10	-0.02	0.05	-0.01	-0.01	-0.04	0.06
SFTPB	0.05	-0.02	0.04	-0.07	0.02	-0.02	0.03	0.04	-0.10	0.04	0.00	0.07
SHBG	0.02	-0.07	0.01	0.07	0.08	0.07	0.02	-0.01	-0.01	-0.04	0.08	-0.01
SHISA5	0.01	0.03	-0.04	-0.05	-0.02	0.04	0.03	0.00	0.08	0.09	-0.08	0.01
SI	0.03	-0.04	-0.13	0.00	-0.01	-0.02	-0.03	-0.04	-0.04	-0.05	-0.06	-0.01
SLC15A1	0.00	-0.01	0.01	0.03	0.05	-0.06	0.06	0.01	-0.10	-0.06	0.00	-0.12
SLC38A10	0.00	-0.01	0.00	0.00	0.02	0.03	0.07	0.05	0.13	-0.12	0.06	0.07
SLC9A3R1	0.01	-0.04	-0.14	-0.03	0.01	-0.04	0.00	0.03	0.00	0.00	-0.02	-0.03
SLPI	0.06	-0.03	0.04	-0.03	-0.08	0.05	-0.02	-0.01	0.01	0.02	-0.08	0.09
SOD3	0.06	-0.03	0.00	-0.05	-0.09	-0.03	0.03	-0.08	0.09	0.00	0.01	0.03
SPARCL1	0.10	-0.01	-0.02	-0.01	-0.01	-0.02	-0.04	0.02	-0.07	-0.04	0.04	0.01
SPINK1	0.04	0.02	-0.06	-0.02	0.06	0.06	-0.09	-0.04	0.03	0.02	0.01	0.00
SPINK5	0.04	-0.02	0.07	-0.10	0.02	0.03	0.05	0.03	-0.02	0.02	-0.03	0.01
SPON1	0.04	-0.01	-0.03	0.11	-0.01	-0.01	0.02	-0.03	0.00	0.05	-0.05	-0.02
SPON2	0.06	-0.04	0.06	-0.01	0.05	0.05	0.01	-0.04	0.01	0.00	0.00	0.02
SPP1	0.09	0.03	-0.03	0.01	-0.10	-0.04	-0.01	0.02	0.04	0.00	0.00	-0.02
SPRR1B	0.01	0.02	0.02	0.00	0.00	0.04	0.02	0.01	-0.05	0.11	0.04	-0.01
SPRR3	0.03	0.05	-0.02	-0.06	0.02	0.10	0.06	0.01	0.02	0.05	0.01	0.01
STC2	0.08	-0.01	-0.01	0.04	0.03	-0.09	0.00	-0.01	0.05	0.04	-0.03	-0.02
TAGLN	-0.01	0.07	0.02	0.06	-0.03	0.04	0.08	0.00	0.01	0.06	-0.02	-0.07
TFF3	-0.02	0.01	0.05	0.00	-0.04	0.11	0.11	-0.07	-0.08	-0.02	-0.04	0.00
TGFBI	0.04	-0.01	-0.06	0.06	0.05	-0.04	0.01	0.06	0.03	0.06	-0.05	-0.09
TGFBR3	-0.03	0.06	0.00	-0.02	-0.01	0.11	0.04	0.04	-0.05	0.07	0.02	-0.04

THBS1	0.04	-0.05	-0.03	0.05	0.04	0.07	0.07	0.05	-0.04	0.00	0.02	-0.07
THBS4	0.00	0.01	-0.04	0.10	0.05	-0.01	0.03	0.11	0.03	-0.09	0.01	0.07
THY1	0.04	0.00	0.03	0.03	0.06	-0.01	-0.01	-0.14	-0.02	-0.05	-0.02	-0.04
TIMP1	0.05	-0.05	-0.02	0.11	-0.05	-0.02	-0.04	-0.03	-0.07	0.02	0.06	0.03
TIMP2	0.08	-0.02	0.09	-0.01	-0.03	0.01	0.00	0.08	-0.02	0.04	0.04	-0.03
TKT	0.08	-0.04	0.07	0.05	-0.07	0.05	-0.02	0.01	-0.01	-0.01	-0.02	-0.02
TMSB10	0.03	0.04	-0.07	0.04	-0.04	0.03	0.02	0.03	0.00	0.02	0.05	0.04
TMSB4X	0.03	0.03	0.01	0.03	-0.06	0.08	-0.05	-0.04	0.00	-0.06	0.08	-0.07
TPI1	0.06	0.01	0.01	0.03	-0.02	0.11	0.00	-0.03	0.04	0.00	-0.07	-0.04
TTBK2	0.00	-0.01	0.01	-0.02	-0.03	0.00	-0.03	-0.07	-0.02	0.05	-0.09	0.08
TTN	-0.01	0.04	0.03	0.04	0.06	0.03	0.05	0.08	-0.02	-0.03	-0.03	0.03
TTR	-0.06	-0.04	0.02	0.01	-0.02	0.03	0.02	0.02	0.01	-0.10	-0.04	-0.02
TXN	0.07	0.06	0.01	0.02	-0.02	0.04	-0.06	0.04	-0.04	-0.03	0.00	-0.03
TXNDC5	-0.02	0.01	0.01	0.03	0.01	0.07	0.00	-0.04	-0.01	-0.02	-0.02	0.00
VASN	0.10	-0.01	-0.01	-0.06	-0.03	-0.01	0.00	0.02	0.01	0.02	-0.01	-0.06
VCAN	0.05	0.00	-0.06	0.01	-0.11	-0.06	0.02	0.01	-0.06	0.00	0.01	-0.01
VSIG4	0.03	-0.01	-0.10	-0.07	0.01	0.01	0.00	-0.05	-0.08	0.03	-0.02	0.00
VTN	0.00	-0.12	-0.02	-0.02	0.09	-0.01	0.01	0.02	-0.02	0.05	0.01	-0.01
WFDC2	0.03	0.08	0.01	-0.03	0.00	0.05	0.02	-0.04	0.08	0.05	-0.08	0.05
YWHAE	0.09	-0.01	-0.03	0.00	0.07	-0.04	-0.03	0.04	0.04	0.07	-0.04	0.00
YWHAG	0.11	-0.01	0.01	0.03	-0.08	-0.02	-0.01	0.06	0.00	0.01	0.03	-0.01
YWHAZ	0.09	-0.05	0.00	0.06	-0.06	0.03	0.00	-0.04	-0.03	0.00	0.06	0.05

PC13	PC14	PC15	PC16	PC17	PC18	PC19	PC20	PC21	PC22	PC23	PC24	PC25
0.01	-0.10	0.05	0.03	0.05	-0.02	-0.02	0.05	-0.03	-0.01	0.00	0.02	-0.09
0.04	0.05	0.00	0.00	0.03	0.06	-0.03	-0.01	0.00	0.02	0.00	-0.01	-0.03
-0.10	-0.07	0.00	-0.02	0.01	0.06	-0.03	-0.03	-0.04	-0.04	-0.05	0.02	-0.01
-0.03	0.01	0.09	-0.04	0.11	-0.09	-0.11	-0.04	0.01	0.02	-0.09	-0.05	0.10
0.00	0.03	0.03	0.02	-0.02	0.00	-0.07	-0.01	-0.01	0.02	-0.02	0.03	0.06
-0.02	-0.11	-0.03	0.07	0.03	0.02	0.00	0.07	-0.01	-0.03	-0.03	-0.03	-0.01
0.00	0.03	0.01	0.03	0.05	-0.04	0.04	0.01	0.04	-0.08	-0.04	-0.04	0.03
-0.02	0.01	0.00	0.06	-0.02	-0.02	0.02	-0.06	0.01	0.05	-0.05	-0.04	0.01
0.00	0.02	0.03	-0.03	-0.01	0.03	0.02	0.01	0.01	-0.02	-0.01	0.00	-0.03
0.02	0.02	0.06	0.05	0.08	0.01	0.08	-0.01	-0.05	0.02	-0.04	-0.01	-0.07
0.07	-0.06	0.04	-0.01	0.11	-0.04	-0.01	0.06	0.00	0.10	0.05	-0.02	-0.01
0.03	0.02	0.01	0.04	0.01	-0.01	0.00	0.06	0.03	0.03	-0.05	-0.01	-0.04
0.03	0.03	-0.03	-0.02	-0.04	-0.09	0.01	0.01	-0.05	-0.08	0.04	0.02	0.07
-0.03	0.09	0.06	0.10	0.02	-0.06	0.02	-0.07	-0.03	-0.04	0.12	-0.05	-0.05
0.02	-0.08	0.01	0.02	-0.03	0.01	0.02	-0.01	0.00	0.01	0.02	0.01	0.03
-0.03	-0.08	-0.02	-0.03	-0.07	0.01	-0.02	-0.02	0.10	0.03	-0.03	-0.03	0.02
-0.05	0.01	-0.01	-0.01	-0.04	-0.07	0.00	-0.04	0.09	0.00	-0.02	0.04	0.04
-0.04	-0.02	-0.01	0.01	0.10	-0.05	-0.02	-0.03	-0.03	0.00	-0.01	0.09	0.08
-0.07	0.05	-0.01	-0.01	0.05	0.02	0.04	-0.01	-0.05	0.04	0.02	0.03	-0.02
0.12	-0.02	-0.02	-0.05	0.02	0.02	-0.06	-0.09	0.06	0.00	0.00	0.06	-0.08
0.06	0.09	-0.10	-0.05	-0.05	-0.02	0.00	-0.05	0.03	-0.01	0.02	0.00	0.06
-0.02	0.01	-0.02	-0.01	-0.02	-0.04	-0.03	0.02	-0.05	-0.04	0.00	0.02	-0.01
-0.04	-0.05	0.06	0.03	0.02	0.08	0.06	-0.02	0.05	0.03	-0.02	-0.04	-0.05
-0.02	0.03	0.02	-0.01	-0.01	0.02	-0.09	0.08	0.05	-0.01	-0.02	0.07	-0.01
-0.01	-0.05	0.01	0.01	0.01	0.01	0.05	0.00	0.01	-0.06	0.14	0.02	-0.07
0.03	-0.07	-0.02	0.06	-0.10	0.01	0.09	0.09	0.02	0.00	0.05	-0.03	0.01
-0.02	0.06	0.03	-0.09	0.03	-0.05	-0.06	0.01	-0.11	-0.04	0.05	0.01	0.00
-0.01	-0.01	-0.03	0.00	0.03	0.04	-0.04	0.01	-0.02	-0.02	-0.02	0.00	-0.03
0.02	0.03	-0.03	0.01	0.00	-0.08	-0.01	0.02	0.07	-0.01	0.03	0.02	-0.02

-0.09	-0.04	0.01	-0.06	-0.05	-0.02	-0.05	0.05	0.00	0.04	-0.06	0.00	-0.01
0.01	0.07	0.02	0.05	0.01	0.00	-0.11	0.00	0.00	-0.04	0.01	-0.01	-0.05
0.01	-0.02	0.01	0.01	0.00	0.03	0.10	-0.04	-0.05	0.02	0.13	0.02	0.14
0.00	-0.01	-0.05	-0.06	0.02	-0.04	-0.08	0.08	0.08	0.03	0.04	-0.14	-0.02
-0.06	0.01	-0.06	0.02	0.13	-0.04	0.09	-0.03	0.10	-0.01	-0.07	0.01	-0.03
0.00	0.02	-0.03	0.00	0.03	0.06	-0.03	0.05	0.04	0.03	0.08	0.02	-0.02
0.05	-0.05	0.03	0.11	-0.17	-0.02	0.04	0.00	0.05	-0.10	-0.04	-0.01	-0.03
0.07	0.00	0.01	-0.05	-0.03	-0.04	-0.09	0.02	0.03	0.06	-0.07	-0.01	0.00
0.02	0.00	-0.04	-0.03	-0.03	0.01	0.02	-0.03	0.04	-0.02	0.09	0.01	-0.05
0.07	0.02	0.09	0.10	0.14	-0.04	-0.01	0.10	0.02	-0.05	-0.02	0.04	-0.09
-0.03	-0.03	0.00	0.04	-0.02	-0.01	-0.04	0.00	0.07	0.03	-0.01	0.05	0.03
0.01	-0.02	-0.04	-0.02	-0.01	0.01	-0.02	-0.04	0.00	-0.02	-0.03	0.03	0.01
0.00	-0.06	-0.02	0.04	0.02	0.01	-0.05	-0.03	0.00	-0.02	-0.01	-0.02	-0.01
0.01	0.03	-0.01	0.01	-0.04	-0.08	-0.02	0.03	-0.03	-0.02	0.04	-0.02	0.04
0.00	0.11	0.01	0.02	-0.07	0.00	-0.10	0.04	0.10	0.00	-0.04	0.07	-0.05
0.01	0.10	-0.02	-0.03	-0.05	0.00	-0.04	-0.11	0.04	0.07	-0.02	-0.02	-0.04
0.01	-0.01	-0.04	0.05	-0.01	-0.07	0.03	0.01	0.10	0.08	0.00	0.01	0.00
0.01	0.04	-0.01	-0.01	-0.02	0.02	-0.06	-0.04	0.04	0.01	0.02	0.01	-0.02
0.01	0.03	0.04	0.01	0.12	0.01	0.03	-0.06	0.05	0.00	0.03	-0.06	0.01
0.02	-0.02	0.03	0.03	0.13	0.00	-0.08	0.00	-0.06	-0.02	0.06	-0.04	-0.01
0.01	-0.01	-0.04	-0.03	0.09	0.01	0.00	0.06	-0.06	0.00	-0.22	0.01	-0.02
-0.04	0.00	-0.05	0.02	0.08	0.00	-0.03	0.01	0.01	-0.04	-0.06	0.05	-0.03
-0.03	-0.01	0.08	0.02	-0.08	-0.01	0.03	-0.08	0.01	0.03	0.00	0.02	0.00
-0.01	0.04	0.02	-0.08	-0.04	-0.07	0.00	0.02	0.02	-0.01	0.04	0.01	0.02
0.04	-0.02	0.00	-0.08	0.02	-0.01	0.02	-0.01	-0.03	0.06	-0.11	0.06	0.02
-0.01	-0.02	0.05	-0.04	-0.01	-0.01	-0.01	0.01	0.00	0.00	-0.01	0.03	-0.03
-0.03	-0.03	0.01	0.03	0.02	0.03	0.01	0.09	0.05	0.04	0.02	-0.05	0.07
-0.02	0.03	0.05	-0.04	0.05	0.03	-0.04	0.08	0.07	0.09	0.03	0.04	0.02
0.09	0.01	-0.01	0.01	0.00	-0.04	0.01	0.02	-0.01	0.10	0.00	-0.04	0.02
-0.03	0.06	-0.05	0.06	-0.03	0.04	0.11	0.03	0.03	-0.04	0.04	-0.05	0.06
0.04	0.06	0.04	0.03	0.01	0.01	-0.05	0.00	0.02	-0.07	-0.09	-0.04	0.06

-0.03	0.01	-0.02	0.05	0.08	0.06	0.12	0.07	0.04	0.10	-0.06	0.00	0.05
-0.02	0.06	0.07	-0.01	-0.06	0.10	-0.05	0.01	-0.03	0.02	0.03	0.07	0.04
-0.02	0.02	-0.05	-0.06	0.00	-0.01	-0.03	0.00	-0.02	-0.07	0.05	0.03	-0.08
0.02	-0.06	-0.04	-0.06	-0.05	-0.06	-0.01	0.11	-0.07	0.03	0.06	0.03	0.05
0.02	0.00	-0.13	-0.07	-0.14	0.03	-0.02	0.04	-0.08	0.02	0.00	0.11	0.03
0.04	0.02	-0.04	0.03	-0.01	0.01	-0.02	0.01	0.04	0.02	0.01	0.02	-0.07
-0.01	-0.04	0.01	-0.01	-0.03	-0.02	-0.12	-0.01	-0.02	-0.09	0.03	0.02	0.03
-0.03	0.03	-0.08	0.01	-0.03	-0.02	-0.01	0.05	-0.06	0.10	0.04	0.02	0.00
-0.03	0.02	-0.06	-0.05	0.01	-0.01	-0.11	-0.04	0.05	0.04	0.01	0.02	-0.04
0.05	0.01	0.08	0.00	-0.11	0.01	0.05	0.10	0.10	-0.11	-0.01	0.12	0.01
0.07	0.00	0.09	0.04	-0.03	0.00	0.02	0.01	0.03	-0.01	-0.02	0.00	-0.01
0.08	0.07	-0.03	-0.04	0.05	-0.03	-0.02	0.07	0.02	-0.04	-0.01	0.01	-0.02
-0.05	-0.01	-0.03	-0.01	-0.03	-0.02	-0.01	-0.01	0.02	0.04	0.04	-0.04	-0.08
-0.01	0.00	-0.02	0.06	0.05	-0.09	-0.09	-0.09	-0.07	0.07	-0.01	0.07	0.00
0.01	0.02	0.07	0.06	-0.02	-0.02	-0.04	0.04	0.03	-0.02	0.01	-0.07	0.03
-0.03	0.02	-0.05	0.07	0.05	0.04	0.05	0.04	-0.02	-0.03	0.06	-0.03	-0.02
-0.02	-0.03	0.04	0.06	0.02	0.03	0.00	-0.05	-0.01	0.07	0.04	-0.02	-0.06
-0.04	-0.02	0.00	0.00	0.02	0.06	0.03	0.01	-0.05	0.00	-0.02	0.03	-0.01
-0.01	-0.01	0.01	-0.03	0.05	0.04	0.05	-0.04	0.03	0.11	0.07	-0.02	0.03
-0.02	-0.01	0.02	0.01	-0.06	0.04	-0.07	-0.06	-0.04	-0.03	0.01	0.04	0.01
-0.01	0.03	-0.02	-0.01	0.00	0.00	0.00	0.00	0.01	-0.09	0.00	-0.01	-0.02
-0.01	-0.04	0.08	0.07	-0.05	0.13	0.00	0.04	0.05	0.09	-0.02	0.06	0.06
0.01	0.00	-0.07	-0.08	0.01	-0.04	0.06	-0.01	-0.03	-0.07	-0.02	-0.03	0.04
0.01	0.00	-0.02	-0.01	-0.07	-0.06	0.04	0.00	-0.03	0.08	0.13	-0.08	0.03
0.03	-0.01	-0.07	0.01	-0.10	-0.01	0.08	0.11	0.07	-0.02	0.08	-0.09	-0.03
-0.10	-0.04	-0.05	0.04	-0.05	-0.03	0.09	0.02	-0.06	-0.01	0.00	0.00	-0.02
-0.07	0.05	-0.05	0.01	0.04	-0.02	0.08	0.03	-0.05	0.03	0.00	0.00	0.03
0.04	-0.05	-0.05	0.01	-0.01	0.06	-0.04	-0.05	-0.02	-0.05	0.01	0.00	-0.01
0.02	-0.02	-0.01	0.03	-0.02	-0.05	-0.01	-0.07	-0.05	0.04	-0.01	-0.03	0.00
0.05	0.00	0.04	0.00	0.10	0.01	-0.04	0.04	-0.02	0.00	-0.01	-0.02	0.05
0.00	0.01	0.00	0.00	-0.02	0.02	-0.01	-0.03	0.06	0.05	0.00	0.00	0.02

-0.01	0.05	-0.01	0.01	0.03	0.06	-0.03	0.04	0.04	-0.04	0.02	0.02	0.00
0.04	-0.08	0.04	0.06	0.01	0.00	0.06	0.02	0.08	0.02	0.02	-0.04	0.05
-0.02	-0.01	-0.04	-0.03	-0.03	0.02	-0.01	0.00	-0.01	0.00	0.04	-0.05	0.06
-0.02	-0.07	-0.02	0.02	-0.01	-0.06	-0.06	0.03	-0.04	-0.04	-0.06	-0.03	0.01
-0.07	0.05	0.09	-0.04	-0.01	-0.06	-0.01	0.03	0.06	0.05	-0.01	-0.02	-0.01
0.01	-0.01	0.05	-0.01	0.02	0.11	-0.05	0.00	-0.04	0.02	0.02	0.01	-0.05
-0.03	-0.05	0.04	0.06	-0.01	0.05	0.06	-0.08	-0.02	-0.03	0.09	-0.09	0.04
-0.03	-0.04	0.02	-0.05	-0.04	0.01	0.04	-0.06	0.07	0.00	-0.02	0.04	0.07
-0.04	0.03	-0.05	-0.04	0.03	-0.03	-0.05	0.01	-0.01	-0.07	0.03	-0.06	0.01
-0.10	0.00	-0.02	0.06	0.13	-0.12	-0.02	0.05	-0.02	-0.05	0.09	0.02	0.01
-0.05	-0.02	-0.05	0.03	0.02	0.05	0.04	0.08	0.01	-0.09	0.05	0.01	-0.01
-0.02	0.03	-0.09	-0.01	-0.08	-0.05	0.00	-0.01	-0.02	0.02	0.08	-0.04	0.03
-0.02	0.02	-0.10	-0.04	-0.08	-0.06	-0.05	-0.01	0.00	0.01	0.05	-0.04	0.00
-0.11	0.02	0.01	-0.05	-0.08	-0.08	0.10	0.02	0.01	0.05	0.06	-0.02	-0.05
0.02	-0.06	0.01	0.02	0.01	-0.05	-0.06	0.05	-0.01	-0.03	0.06	0.06	0.07
-0.01	-0.03	-0.04	0.03	0.07	0.02	0.02	-0.01	0.05	0.01	0.01	0.06	-0.05
0.02	-0.05	-0.02	-0.08	0.01	-0.02	-0.03	0.08	0.01	0.00	0.04	-0.03	-0.03
-0.02	-0.01	0.02	0.06	-0.03	0.02	-0.05	-0.04	-0.11	0.00	0.07	0.02	0.00
-0.08	-0.04	0.00	0.00	0.10	0.05	-0.01	-0.05	0.09	-0.03	0.11	-0.02	-0.05
-0.04	-0.02	0.05	0.03	-0.04	-0.02	-0.04	-0.02	0.04	-0.02	-0.01	0.02	0.03
-0.03	-0.07	0.11	0.01	-0.03	0.03	-0.07	0.01	-0.02	0.03	0.02	0.00	0.04
-0.03	0.03	0.02	0.00	0.01	0.01	-0.04	-0.02	0.00	0.01	0.03	-0.03	0.06
0.01	0.02	0.00	0.02	-0.01	-0.08	-0.06	-0.03	-0.02	-0.08	-0.09	0.01	-0.03
0.04	0.03	0.01	0.07	0.04	-0.01	0.10	0.07	-0.04	0.04	0.02	-0.04	0.01
-0.11	-0.06	-0.04	-0.07	-0.03	0.05	0.02	0.03	-0.04	-0.01	0.02	-0.01	-0.09
-0.07	-0.07	0.02	0.12	-0.03	-0.03	0.03	-0.07	0.05	-0.04	0.01	-0.02	0.03
-0.02	-0.03	0.03	-0.08	-0.05	-0.04	0.09	-0.04	-0.06	-0.06	0.00	-0.05	0.02
0.02	0.05	0.04	-0.05	0.03	0.05	0.03	-0.01	-0.03	0.01	0.03	-0.05	-0.01
0.06	-0.01	-0.04	-0.01	0.00	-0.04	-0.08	0.00	0.01	0.10	0.06	0.12	-0.01
-0.07	0.02	-0.02	0.06	0.01	-0.06	-0.04	-0.13	0.12	0.02	-0.12	0.02	0.13
0.01	-0.01	0.04	-0.06	0.05	-0.03	-0.02	-0.01	0.00	-0.05	0.01	-0.06	0.02

0.02	-0.03	0.00	0.01	0.00	-0.01	0.05	-0.05	-0.04	0.05	-0.02	-0.02	0.05
0.03	0.08	0.01	0.04	0.02	-0.07	-0.10	0.01	-0.03	0.08	0.03	0.04	-0.12
0.03	0.02	-0.01	0.00	0.00	0.00	-0.10	-0.10	0.03	-0.03	-0.02	-0.03	-0.03
0.01	0.07	0.00	0.05	-0.01	0.01	-0.09	-0.01	0.01	-0.02	-0.04	0.02	-0.01
0.07	0.04	-0.04	0.04	0.06	-0.01	-0.05	-0.09	-0.01	0.10	-0.03	0.05	-0.12
-0.02	0.05	0.00	0.08	-0.05	0.00	-0.09	0.04	-0.01	-0.07	-0.03	-0.01	-0.07
-0.03	0.03	-0.01	0.09	-0.06	0.09	-0.04	0.05	-0.03	-0.01	-0.04	-0.06	0.01
-0.01	-0.06	-0.03	-0.04	0.02	0.03	-0.01	-0.01	0.03	-0.06	-0.04	0.03	0.02
0.00	-0.05	-0.03	0.02	-0.10	0.04	0.04	0.02	0.07	0.02	-0.07	0.03	-0.02
-0.05	0.00	-0.05	-0.02	0.01	0.01	0.02	-0.01	0.02	0.02	0.02	-0.02	-0.01
-0.04	-0.11	-0.09	0.02	-0.07	0.00	-0.03	0.01	-0.04	0.00	0.00	-0.03	-0.05
-0.07	-0.04	-0.04	0.04	-0.01	0.06	-0.04	-0.02	-0.03	-0.01	0.03	-0.10	-0.04
-0.01	0.00	-0.09	-0.01	-0.04	-0.03	-0.07	0.03	0.00	0.05	-0.02	-0.03	0.03
-0.02	-0.06	0.01	-0.01	-0.04	0.02	-0.08	0.05	0.09	0.07	-0.01	-0.17	0.01
-0.04	-0.01	0.02	0.05	0.08	-0.04	-0.01	-0.02	0.00	-0.06	-0.07	0.04	0.04
-0.04	0.06	0.02	0.01	-0.06	-0.02	0.02	-0.05	0.03	0.07	-0.03	0.02	0.03
-0.03	-0.03	-0.07	-0.03	0.07	-0.03	-0.03	-0.08	-0.03	0.04	0.07	0.04	0.04
0.05	0.01	0.07	-0.01	-0.06	-0.01	-0.02	0.15	-0.02	-0.04	-0.03	0.03	-0.05
-0.01	0.00	0.01	0.01	0.03	-0.02	-0.02	-0.05	-0.02	-0.11	-0.01	-0.04	0.00
0.04	-0.01	0.10	0.07	-0.04	0.01	0.06	0.14	-0.01	0.06	0.02	-0.01	0.01
0.00	0.00	0.04	0.01	-0.04	0.01	0.03	-0.08	0.04	-0.05	0.02	-0.07	0.03
0.06	-0.03	0.03	-0.02	0.04	0.03	-0.02	0.02	0.00	0.02	0.03	0.04	0.03
-0.09	-0.01	-0.01	0.04	-0.01	-0.01	0.02	0.14	0.03	-0.02	0.06	0.13	-0.02
0.05	-0.02	0.07	0.03	-0.03	0.00	0.01	0.00	0.02	-0.02	-0.02	0.00	-0.02
-0.06	-0.08	-0.05	0.01	-0.02	-0.05	-0.05	0.03	-0.02	0.03	0.04	-0.01	-0.05
-0.05	0.04	0.06	0.00	0.01	0.04	-0.09	0.08	0.02	-0.06	-0.01	-0.05	-0.05
0.09	0.06	0.05	0.03	0.11	-0.05	0.04	-0.08	-0.04	0.05	-0.07	0.01	-0.17
-0.03	0.00	0.00	0.04	0.03	-0.04	0.04	0.01	0.02	0.04	-0.06	0.06	-0.14
0.02	0.01	0.01	0.01	0.01	-0.08	-0.05	0.04	0.04	-0.01	0.03	0.00	-0.02
0.03	-0.04	-0.10	-0.02	0.12	-0.07	0.04	0.06	0.02	-0.02	-0.05	-0.03	0.03
0.04	-0.05	0.05	0.01	0.02	-0.03	0.01	0.00	-0.03	0.03	0.04	0.02	0.01



0.02	-0.03	0.07	-0.01	-0.07	-0.01	0.05	-0.04	0.05	-0.09	0.02	-0.01	0.06
-0.05	0.04	0.03	0.02	0.08	0.06	-0.05	0.08	0.02	0.05	0.05	0.01	0.00
-0.07	0.05	0.02	-0.01	0.03	-0.01	-0.04	-0.09	0.06	-0.12	-0.06	-0.02	0.00
0.03	-0.03	-0.13	-0.10	0.03	0.03	0.07	0.06	0.00	0.09	-0.04	-0.03	-0.04
0.03	-0.01	0.02	-0.02	-0.05	0.00	0.00	0.01	0.00	0.04	0.02	0.05	-0.05
-0.02	0.05	-0.02	0.00	0.08	0.03	0.00	0.08	0.02	0.07	-0.06	0.08	-0.01
0.06	-0.01	0.06	0.00	0.00	-0.02	0.03	0.00	0.02	-0.01	0.07	-0.01	0.01
0.03	0.00	0.04	-0.01	-0.02	0.03	0.01	-0.02	-0.02	0.01	0.00	-0.01	0.01
0.10	-0.02	-0.02	-0.07	0.00	0.01	0.05	-0.03	0.04	0.06	-0.07	-0.09	0.07
-0.01	0.03	-0.06	0.02	0.04	0.00	-0.01	0.03	0.01	-0.02	-0.02	-0.01	0.02
-0.13	-0.03	0.01	0.07	0.07	0.04	0.01	0.04	-0.09	0.05	0.12	0.03	-0.07
-0.01	0.00	0.03	0.04	-0.04	-0.03	-0.05	-0.04	-0.04	0.00	0.00	-0.01	0.02
-0.07	0.00	-0.02	-0.05	0.00	0.02	0.09	-0.03	0.02	-0.03	0.03	0.07	-0.07
-0.01	0.08	-0.01	-0.06	0.01	-0.06	0.05	-0.03	0.01	-0.08	-0.01	-0.01	0.00
0.03	0.01	-0.07	-0.07	0.04	-0.09	0.12	0.08	0.01	-0.07	0.07	0.08	-0.10
-0.01	-0.02	0.00	0.02	-0.08	-0.01	0.00	-0.04	-0.02	0.00	-0.01	-0.08	-0.01
0.05	0.06	0.03	-0.11	0.06	-0.05	0.01	0.07	-0.08	-0.10	-0.08	-0.02	-0.02
-0.07	-0.04	0.05	-0.10	-0.02	-0.04	0.10	-0.03	-0.01	-0.01	-0.04	-0.03	-0.04
0.06	0.00	0.03	0.11	-0.07	-0.04	0.06	0.01	0.11	-0.10	-0.02	-0.02	-0.04
0.01	-0.02	-0.06	0.00	-0.07	-0.03	-0.02	-0.01	0.06	-0.01	-0.06	0.10	0.01
-0.08	-0.08	-0.04	-0.01	0.05	-0.08	0.01	-0.03	0.03	0.02	-0.01	0.03	0.00
-0.07	-0.04	-0.07	-0.04	-0.01	0.06	0.05	-0.05	0.07	0.08	-0.03	0.03	-0.01
0.02	0.10	0.03	-0.01	-0.01	-0.01	0.06	-0.01	-0.09	-0.05	-0.01	-0.01	0.03
0.06	-0.03	0.03	-0.05	0.01	0.02	-0.01	-0.03	-0.04	0.06	-0.02	0.04	0.03
-0.04	0.02	0.02	-0.01	-0.02	0.04	-0.01	0.01	0.01	-0.13	0.00	-0.08	0.07
0.02	-0.07	0.01	0.02	-0.02	-0.01	0.00	0.01	0.00	-0.01	0.00	-0.03	-0.01
-0.05	-0.03	-0.06	0.01	0.03	0.00	0.05	-0.02	0.07	0.02	0.02	0.00	0.01
-0.03	-0.01	0.00	-0.01	0.05	-0.04	0.03	0.00	-0.02	0.00	-0.04	-0.04	0.00
0.02	-0.10	0.04	-0.01	0.02	0.02	0.00	0.02	0.03	0.00	0.04	0.10	0.00
-0.03	-0.02	-0.03	0.05	0.02	0.02	-0.04	0.03	0.05	-0.04	0.01	-0.02	0.01
0.04	-0.03	-0.03	-0.05	0.07	0.08	-0.02	-0.04	0.00	0.00	-0.06	-0.01	0.01

-0.02	0.00	0.02	-0.04	-0.04	-0.01	-0.03	-0.02	0.02	-0.01	0.00	0.00	-0.02
-0.06	0.02	0.05	0.02	0.02	0.10	0.01	-0.06	0.02	0.00	0.10	-0.07	0.08
0.01	-0.09	-0.03	-0.09	0.01	0.06	0.02	-0.05	-0.05	-0.04	0.01	-0.04	-0.02
-0.01	-0.02	-0.09	0.04	0.08	0.01	0.02	-0.03	-0.04	0.03	0.04	0.05	0.01
0.02	-0.02	0.07	0.01	-0.02	-0.05	0.03	0.01	-0.06	-0.05	-0.04	0.05	-0.04
-0.01	-0.05	0.10	0.00	0.03	0.00	0.04	-0.05	-0.01	0.06	-0.07	-0.04	-0.01
0.00	0.00	-0.03	0.07	-0.02	0.07	0.00	0.01	0.06	0.05	-0.02	0.01	-0.03
0.05	-0.06	-0.01	-0.10	-0.01	0.00	0.03	-0.04	-0.08	-0.05	0.00	-0.05	0.05
0.07	0.05	-0.01	-0.02	-0.03	0.00	0.03	0.01	0.02	0.00	0.04	0.01	0.01
-0.08	0.05	0.06	-0.06	-0.01	0.03	0.03	0.03	0.01	0.01	-0.02	0.03	0.00
-0.06	0.03	-0.07	0.06	0.04	-0.04	0.06	-0.02	-0.10	0.05	0.03	-0.01	-0.02
0.09	-0.03	-0.08	0.08	0.06	0.08	0.01	-0.01	-0.02	-0.04	0.02	-0.01	0.03
0.00	0.08	-0.04	0.05	-0.01	0.05	-0.09	0.02	0.02	-0.09	-0.01	0.01	0.03
0.01	-0.03	0.04	-0.01	-0.06	0.03	-0.14	0.03	0.03	-0.04	-0.02	0.00	-0.05
-0.03	0.08	-0.06	0.06	-0.05	0.08	-0.01	0.04	-0.04	-0.02	-0.04	0.01	0.05
0.03	0.01	0.05	0.01	0.00	-0.01	-0.03	-0.02	-0.02	-0.06	0.04	0.00	0.00
0.00	-0.03	-0.03	0.00	-0.03	-0.04	0.01	0.04	0.04	0.01	-0.07	-0.03	0.06
-0.04	0.02	0.03	0.00	0.04	0.04	0.00	0.02	0.02	0.01	-0.01	-0.01	0.01
-0.07	0.04	-0.01	0.03	0.01	-0.02	0.00	0.00	0.01	0.00	-0.02	-0.07	0.05
0.01	-0.09	-0.02	0.00	-0.02	0.05	0.08	0.02	0.01	0.04	-0.08	-0.04	0.00
0.01	0.02	0.08	0.04	-0.02	0.04	0.08	0.09	0.00	-0.03	0.08	-0.03	0.06
0.01	-0.03	0.01	0.06	-0.02	-0.08	-0.03	-0.04	-0.05	-0.01	-0.01	-0.05	0.00
-0.05	0.02	-0.05	0.07	-0.03	0.01	-0.03	0.00	-0.03	0.07	0.03	-0.03	-0.03
-0.04	0.08	0.00	0.05	-0.06	0.03	0.00	-0.03	-0.01	-0.02	0.01	-0.04	0.03
-0.01	-0.06	0.05	0.04	0.02	-0.01	0.05	-0.03	-0.01	-0.06	-0.07	-0.07	-0.07
0.05	-0.03	0.11	-0.06	0.06	-0.05	0.06	0.00	0.10	0.07	0.01	0.06	0.00
-0.04	0.04	0.04	0.04	0.04	0.04	-0.02	0.04	-0.03	-0.09	0.00	-0.05	-0.04
-0.04	-0.08	-0.04	-0.04	-0.01	-0.04	-0.01	-0.04	0.01	-0.02	0.05	-0.03	0.12
-0.01	-0.11	-0.02	0.02	-0.01	0.04	-0.01	-0.02	-0.05	-0.01	-0.04	-0.07	0.08
-0.08	0.03	0.05	-0.02	-0.01	-0.01	-0.04	0.03	0.02	0.05	0.04	0.07	-0.01
-0.11	0.00	0.04	-0.03	0.02	-0.02	0.03	0.08	0.00	0.01	-0.08	0.04	0.02

-0.06	-0.02	0.06	-0.02	0.02	-0.10	-0.06	-0.02	0.07	-0.02	0.08	-0.13	-0.08
0.07	-0.11	0.04	0.03	-0.03	-0.03	-0.05	0.09	-0.03	0.02	0.01	0.00	-0.05
-0.11	0.00	0.05	-0.01	0.03	0.01	0.00	0.02	-0.01	0.01	-0.04	0.01	0.00
0.04	-0.04	-0.05	0.03	0.00	-0.11	-0.04	0.07	-0.01	-0.01	-0.05	-0.12	-0.01
0.03	-0.01	0.13	0.05	-0.03	-0.03	-0.01	-0.03	-0.04	-0.11	0.01	-0.06	-0.04
-0.04	0.01	-0.02	0.10	0.05	-0.06	0.03	0.04	-0.07	0.09	-0.04	0.06	0.06
-0.01	0.03	-0.06	0.07	0.00	-0.07	-0.06	0.00	-0.02	-0.10	0.02	-0.03	0.11
0.02	-0.03	0.02	0.04	0.01	-0.03	0.00	-0.08	-0.06	-0.03	0.04	0.01	0.08
0.00	-0.12	-0.01	0.04	-0.06	-0.08	0.04	-0.05	0.02	0.05	-0.01	-0.02	0.11
0.04	-0.02	-0.12	0.08	-0.07	-0.03	0.06	0.02	0.03	-0.04	0.08	-0.10	-0.06
0.06	0.01	0.04	0.05	0.08	0.04	0.05	0.09	0.08	-0.06	0.05	0.04	0.16
-0.02	-0.03	0.02	0.07	0.00	-0.07	-0.01	-0.07	-0.04	-0.03	-0.06	0.02	0.03
-0.06	0.04	-0.01	0.11	0.09	0.10	-0.07	0.00	-0.05	-0.02	-0.04	-0.02	0.09
0.06	-0.10	-0.08	0.07	0.09	-0.05	0.02	0.11	0.05	0.01	-0.02	-0.09	-0.10
-0.05	0.03	0.01	-0.03	0.00	0.03	0.05	0.02	-0.02	0.00	-0.01	0.04	0.01
0.02	-0.04	-0.09	-0.03	0.01	0.06	-0.02	0.06	-0.05	-0.02	0.02	0.01	0.02
-0.03	-0.07	0.02	0.09	0.03	-0.01	0.07	-0.10	0.07	-0.06	0.06	0.19	-0.07
0.04	-0.02	0.04	0.07	0.02	0.00	-0.01	0.01	0.02	0.00	-0.01	-0.02	0.00
-0.02	0.03	-0.08	0.05	-0.13	-0.08	-0.05	-0.08	-0.08	0.05	0.01	-0.01	-0.06
0.01	-0.02	0.07	0.04	0.03	-0.05	-0.02	-0.02	0.01	0.02	-0.01	-0.02	0.00
0.06	-0.06	-0.04	0.06	0.00	0.12	-0.08	0.05	-0.07	0.04	0.01	-0.01	0.04
-0.04	0.03	-0.05	0.03	-0.05	0.01	0.06	0.00	0.02	0.04	-0.01	-0.04	0.02
0.01	-0.10	-0.02	0.11	0.01	-0.08	0.03	0.05	-0.07	-0.02	-0.04	0.08	-0.01
-0.03	-0.06	0.01	0.04	0.03	0.00	-0.02	-0.05	-0.04	0.09	0.09	-0.01	0.04
-0.05	-0.06	0.06	0.00	0.04	-0.07	0.05	-0.06	-0.07	0.06	0.04	0.01	0.08
-0.06	0.07	-0.03	-0.02	0.03	-0.15	-0.02	0.07	0.03	-0.03	0.08	-0.03	0.05
-0.02	0.02	0.04	0.07	0.00	-0.07	-0.11	-0.04	0.10	0.02	0.06	-0.04	-0.02
0.13	-0.01	-0.07	0.02	-0.01	0.05	-0.02	-0.04	0.01	-0.04	0.05	-0.02	0.00
0.03	-0.02	0.03	0.05	0.04	-0.02	0.02	-0.01	0.00	0.06	0.06	0.03	0.02
-0.06	-0.02	0.07	0.05	-0.02	0.03	-0.05	-0.08	0.10	0.01	0.05	0.00	0.01
-0.16	0.01	0.08	-0.08	-0.02	-0.01	-0.01	0.01	0.00	0.01	-0.05	0.03	-0.02

0.07	0.04	0.04	-0.07	-0.01	-0.01	-0.03	0.08	0.03	-0.04	0.03	0.02	0.01
-0.02	-0.10	-0.01	0.07	-0.05	-0.05	0.01	0.10	-0.02	0.04	-0.05	0.02	-0.08
0.02	-0.05	0.07	-0.01	-0.03	0.00	-0.05	-0.09	-0.12	-0.01	0.00	0.05	-0.06
-0.14	-0.12	0.01	0.00	0.01	0.13	-0.02	0.01	-0.07	0.00	0.03	0.00	-0.08
-0.04	-0.03	0.01	0.02	0.06	0.06	0.01	0.04	-0.06	0.05	-0.02	-0.05	-0.04
0.04	0.00	0.06	0.00	-0.01	0.03	-0.10	0.07	-0.05	0.03	-0.06	0.06	0.04
-0.04	-0.11	0.06	0.13	0.07	-0.08	-0.06	0.07	0.02	-0.04	0.11	0.11	0.02
-0.03	0.06	-0.07	0.06	-0.07	0.07	-0.03	0.05	0.01	0.13	-0.10	-0.09	0.02
-0.07	-0.09	-0.05	0.04	-0.06	-0.03	-0.06	-0.08	-0.03	-0.11	0.10	0.08	-0.10
0.06	0.00	-0.04	-0.12	0.05	0.04	-0.01	0.04	-0.06	0.02	-0.02	0.05	-0.03
0.01	0.05	0.01	0.02	0.04	0.08	-0.12	0.06	0.06	-0.06	0.03	-0.06	-0.03
0.04	0.05	0.05	-0.05	-0.01	0.04	-0.07	0.09	0.01	-0.02	0.07	0.02	-0.03
-0.02	0.00	0.02	-0.02	-0.10	-0.03	0.03	0.10	0.07	-0.10	-0.01	0.13	0.01
0.01	0.10	0.05	-0.04	0.00	-0.01	-0.02	0.05	-0.03	-0.07	0.07	0.00	0.04
-0.01	-0.07	0.02	-0.04	-0.02	0.03	0.03	-0.10	0.05	-0.04	0.04	-0.07	-0.02
0.02	0.06	0.03	0.03	0.00	0.07	0.01	-0.02	0.05	0.08	-0.07	0.06	0.04
0.08	0.03	-0.05	0.04	0.05	-0.04	-0.08	0.06	-0.07	0.08	-0.11	0.03	0.05
-0.03	0.11	-0.05	-0.01	-0.07	0.00	0.08	0.03	-0.06	0.00	0.01	-0.01	0.01
-0.02	0.01	-0.06	0.03	0.02	0.04	0.05	-0.04	0.04	0.03	-0.04	-0.15	-0.17
-0.03	-0.04	0.02	0.00	0.03	-0.01	-0.08	-0.02	0.04	0.03	0.00	-0.07	-0.01
0.00	0.05	0.08	0.11	-0.03	0.07	-0.03	-0.01	-0.02	0.03	-0.05	0.07	-0.02
0.02	0.06	0.09	0.09	-0.01	0.07	0.01	0.03	-0.03	-0.01	-0.02	0.07	-0.02
-0.09	0.02	-0.03	0.03	-0.06	0.15	-0.01	0.03	-0.12	0.02	-0.02	0.01	-0.01
0.00	0.05	0.08	0.10	0.00	0.09	0.01	0.02	-0.04	-0.01	-0.03	0.09	-0.02
0.00	0.02	-0.06	-0.04	0.07	-0.04	-0.01	-0.05	-0.02	-0.02	-0.07	0.04	-0.04
-0.01	0.13	-0.02	0.10	-0.09	0.04	-0.01	-0.03	-0.04	0.02	-0.06	0.04	0.00
0.16	0.00	-0.08	0.10	0.05	0.03	0.01	0.00	0.01	-0.01	0.05	-0.04	0.03
0.03	0.08	0.03	-0.03	-0.03	-0.02	0.05	0.03	0.03	0.03	0.03	0.01	0.01
0.02	0.04	-0.07	0.08	0.04	-0.04	-0.01	-0.08	-0.02	0.03	0.01	0.13	0.04
-0.03	-0.05	-0.02	0.01	0.02	0.07	-0.04	-0.03	-0.01	-0.04	-0.02	0.00	0.00
0.02	0.03	-0.05	0.15	-0.07	0.05	-0.02	-0.02	-0.06	0.05	-0.03	0.06	0.00

0.03	-0.04	0.04	-0.06	0.00	0.02	0.04	-0.08	-0.03	-0.04	-0.13	-0.03	0.01
-0.02	-0.04	-0.05	0.01	-0.04	0.00	-0.02	-0.04	-0.01	0.04	-0.01	-0.04	-0.02
0.02	0.02	0.06	0.04	0.08	0.09	-0.06	-0.01	-0.02	0.04	0.04	-0.04	-0.02
-0.04	-0.02	-0.01	-0.06	0.07	0.02	0.01	-0.01	-0.01	0.03	-0.03	0.03	0.00
0.01	0.01	-0.01	0.01	0.04	0.05	0.04	0.00	0.05	0.04	-0.04	-0.04	0.04
-0.01	-0.02	0.03	-0.02	-0.01	0.03	0.00	0.05	0.01	-0.01	0.00	0.02	-0.01
0.04	-0.03	0.06	-0.03	-0.02	0.00	-0.02	0.00	-0.04	-0.01	0.01	0.00	0.06
0.04	0.06	0.05	0.00	-0.04	0.00	0.04	0.04	-0.03	0.02	-0.02	0.02	0.05
0.05	-0.10	-0.04	-0.06	-0.05	0.00	0.02	0.06	0.05	-0.05	-0.04	-0.03	-0.03
0.06	-0.06	0.05	0.02	-0.02	0.03	-0.02	0.01	-0.04	0.09	0.02	0.03	-0.05
0.00	0.04	0.00	0.03	0.03	0.03	0.01	0.02	-0.02	-0.06	0.02	0.04	0.05
0.07	-0.08	0.05	-0.05	-0.10	0.08	-0.03	-0.11	-0.06	0.03	0.05	0.05	0.07
-0.01	0.05	-0.04	-0.02	0.00	-0.03	-0.04	0.04	0.02	-0.05	0.00	-0.04	-0.03
0.01	-0.06	0.03	0.03	0.05	-0.04	0.00	0.04	-0.01	0.05	-0.05	0.07	0.06
0.02	0.03	-0.08	0.03	0.01	-0.04	0.02	0.00	0.04	0.03	-0.06	0.04	0.05
0.03	-0.02	0.01	-0.03	0.12	0.03	0.04	-0.07	0.04	0.02	0.00	0.03	0.00
-0.04	0.01	0.01	0.01	0.01	0.02	-0.05	-0.02	0.08	-0.03	0.02	0.08	-0.09
0.08	-0.01	0.03	-0.03	-0.01	-0.03	0.08	0.01	-0.04	-0.09	-0.10	0.05	0.01
0.07	-0.04	-0.05	0.03	0.00	0.08	0.00	-0.09	0.01	-0.05	0.01	0.02	-0.13
-0.04	-0.01	0.05	0.01	0.07	0.10	-0.02	0.05	-0.12	-0.06	0.03	-0.06	0.03
-0.08	-0.03	0.00	0.03	-0.02	0.00	0.00	0.03	0.01	0.04	0.04	0.01	-0.06
-0.02	-0.02	-0.09	0.10	-0.09	-0.01	0.00	0.02	0.07	-0.04	0.09	0.10	0.09
0.08	0.06	-0.02	0.03	-0.01	0.04	0.01	-0.04	-0.12	0.00	0.01	0.04	0.01
0.00	0.02	-0.01	-0.02	-0.04	-0.01	-0.01	-0.02	0.01	0.00	0.04	0.02	-0.04
0.02	0.05	-0.08	-0.09	-0.03	0.05	-0.04	0.00	0.04	0.03	0.08	0.05	-0.03
0.02	0.02	0.04	-0.02	0.07	-0.06	0.02	-0.04	-0.01	-0.10	0.01	0.00	-0.05
0.01	0.02	0.02	-0.09	0.05	0.00	0.02	0.05	-0.03	-0.04	0.01	0.05	0.00
-0.07	-0.02	-0.02	0.04	-0.01	-0.01	-0.05	0.12	-0.01	0.04	-0.02	-0.04	0.02
-0.06	0.00	-0.05	-0.03	-0.02	-0.08	-0.07	0.04	0.03	0.06	-0.03	0.05	0.00
-0.06	0.02	-0.01	-0.05	-0.04	0.00	0.04	-0.06	0.01	-0.07	0.03	0.02	-0.02
-0.09	0.00	0.00	0.02	0.03	0.03	-0.01	0.06	0.05	0.06	-0.05	0.04	0.04

-0.03	0.04	-0.07	0.04	0.07	-0.05	0.00	-0.09	-0.08	-0.03	-0.08	-0.02	0.15
-0.04	-0.12	-0.01	0.05	-0.01	-0.15	0.02	0.04	-0.05	0.03	-0.05	0.00	0.02
0.01	-0.10	0.01	-0.05	0.00	0.01	-0.12	-0.03	-0.02	0.04	0.00	-0.06	0.03
0.00	0.02	-0.05	0.03	-0.03	0.06	-0.07	0.03	-0.02	-0.06	0.01	0.04	-0.01
0.10	-0.06	0.04	-0.06	0.02	-0.01	0.00	-0.07	0.05	0.06	-0.03	0.07	0.02
0.01	0.06	0.04	-0.02	-0.01	-0.01	0.09	0.02	0.10	-0.01	-0.01	-0.01	0.04
0.05	-0.01	0.02	0.00	-0.04	-0.02	-0.07	-0.03	-0.03	0.05	-0.02	0.03	0.08
-0.02	-0.05	-0.03	-0.03	-0.02	0.04	-0.02	-0.05	0.04	0.00	0.01	-0.02	-0.02
-0.08	0.04	-0.04	0.10	-0.04	0.01	-0.05	-0.04	0.04	-0.02	-0.03	-0.01	0.05
0.03	-0.05	0.03	-0.04	0.02	0.01	0.05	0.04	0.01	-0.01	0.03	-0.02	-0.03
-0.04	0.07	0.00	-0.04	-0.02	0.04	0.03	0.01	0.00	-0.04	0.07	-0.02	0.04
-0.06	-0.04	0.01	0.00	0.04	-0.03	0.07	0.06	-0.04	-0.03	0.06	0.03	0.12
0.00	-0.03	-0.11	-0.02	0.05	0.05	-0.06	0.05	0.07	0.06	0.00	0.06	0.00
-0.01	0.05	-0.07	-0.05	-0.01	0.05	-0.07	0.03	0.07	0.05	0.06	0.03	-0.01
0.00	-0.06	0.01	0.00	0.02	0.01	-0.05	0.05	0.03	0.00	0.05	-0.09	0.04
0.00	-0.04	-0.12	-0.01	0.00	-0.01	-0.07	0.04	-0.04	0.01	0.07	0.01	0.09
0.02	0.06	0.01	0.04	-0.03	-0.13	0.04	-0.03	-0.08	0.02	0.02	0.01	-0.01
0.01	0.03	-0.07	-0.06	0.00	0.02	0.00	-0.01	0.00	-0.03	0.02	0.01	-0.04
0.04	0.02	-0.06	-0.03	0.07	-0.02	0.01	0.01	0.03	-0.03	0.07	0.06	0.00
0.03	-0.06	0.01	-0.06	0.04	-0.05	-0.03	0.14	-0.09	-0.03	-0.04	-0.01	0.05
-0.11	0.03	-0.01	0.05	0.05	-0.01	0.07	0.00	0.06	-0.08	-0.03	-0.07	-0.07
0.05	0.01	0.04	-0.01	-0.01	0.01	-0.06	0.06	-0.08	0.02	-0.06	-0.08	0.01
0.00	-0.01	-0.02	0.01	0.05	0.00	-0.05	0.04	0.00	-0.01	0.06	0.02	-0.01
-0.08	0.01	0.02	-0.06	-0.02	0.05	0.03	0.00	-0.03	-0.02	-0.03	0.05	0.00
-0.07	0.05	0.05	0.00	-0.07	-0.04	0.01	0.05	0.03	0.03	0.00	-0.01	0.01
0.05	0.01	-0.03	0.03	0.01	0.04	-0.01	0.02	0.00	0.01	-0.08	0.01	0.04
-0.01	-0.04	0.01	0.08	0.00	-0.13	0.03	-0.01	-0.02	0.00	0.03	0.04	0.04
0.12	-0.04	0.10	0.02	-0.10	0.00	0.05	0.02	-0.02	-0.01	0.01	-0.01	0.05
0.10	0.00	-0.06	0.04	0.00	0.00	0.03	-0.01	-0.02	-0.01	0.03	0.00	0.01
0.04	0.05	0.04	0.08	0.03	-0.07	-0.03	0.00	-0.15	0.00	0.07	0.00	0.01
0.07	-0.04	-0.09	0.04	0.04	0.13	0.01	-0.03	-0.04	-0.07	0.01	0.01	0.02

0.04	-0.08	-0.09	0.01	-0.01	0.02	0.09	0.02	-0.03	0.00	-0.09	-0.10	0.03
-0.05	0.04	-0.09	0.01	0.06	-0.01	0.08	0.01	-0.10	-0.03	0.03	-0.03	0.01
-0.13	-0.04	0.02	-0.06	-0.03	0.01	0.00	-0.02	-0.06	-0.02	-0.06	0.05	-0.02
0.01	-0.06	0.03	-0.04	0.00	-0.01	-0.08	0.03	-0.02	0.09	-0.04	-0.01	-0.01
-0.04	-0.01	-0.04	0.05	0.00	-0.01	-0.02	-0.01	0.00	-0.04	-0.01	-0.05	-0.03
0.07	-0.09	-0.02	0.04	-0.10	0.04	0.05	0.06	0.01	-0.04	-0.02	0.14	-0.02
0.01	-0.03	0.03	0.01	-0.06	-0.09	-0.01	-0.08	-0.07	0.05	-0.04	-0.02	0.02
0.00	0.06	-0.04	0.03	0.05	-0.03	0.06	0.00	-0.06	-0.05	-0.02	0.03	-0.02
-0.01	-0.02	0.00	0.02	0.00	0.01	0.08	-0.02	0.09	0.03	0.00	0.03	0.01
-0.03	0.03	0.02	-0.04	0.02	0.05	-0.05	-0.05	0.00	-0.04	-0.10	-0.01	-0.02
-0.07	0.04	0.05	-0.06	-0.02	0.02	0.01	0.01	0.02	0.00	-0.01	0.02	-0.01
-0.09	0.02	0.02	0.03	-0.06	0.00	0.04	-0.02	-0.04	0.03	-0.08	-0.01	0.05
0.04	0.01	-0.04	0.07	-0.06	-0.03	0.05	0.03	-0.06	0.00	-0.05	-0.02	-0.03
-0.02	0.11	-0.01	0.07	0.00	-0.03	0.02	0.10	-0.05	-0.06	-0.08	-0.04	0.00
0.04	-0.03	-0.03	0.02	-0.01	-0.06	-0.01	-0.02	-0.02	0.00	0.01	-0.01	-0.01
0.01	-0.04	0.03	0.01	-0.01	0.07	0.03	-0.01	-0.11	0.06	-0.04	-0.03	-0.02
-0.04	0.10	-0.02	0.04	0.00	0.00	0.01	-0.01	-0.02	-0.09	-0.02	-0.03	0.05
0.03	-0.03	0.08	-0.03	-0.01	0.01	-0.06	0.03	-0.01	0.07	0.02	-0.11	0.08
0.00	0.04	-0.04	0.04	0.04	0.00	0.00	0.08	0.09	-0.04	-0.04	-0.07	0.02
-0.06	0.07	-0.01	0.05	0.02	-0.07	0.03	-0.05	0.05	0.04	0.00	-0.02	-0.03
0.06	0.01	0.07	0.07	0.00	-0.01	0.06	0.03	0.00	0.00	0.01	0.00	-0.01
0.01	0.03	0.02	0.05	0.00	-0.03	0.02	0.02	0.00	0.03	0.04	0.02	-0.02
-0.01	0.11	-0.06	-0.05	-0.04	0.02	-0.01	0.00	0.00	0.06	0.02	-0.04	0.06
0.02	0.01	0.02	0.00	0.00	-0.07	-0.06	-0.04	0.03	0.06	0.00	-0.01	0.02
0.06	0.08	0.01	-0.11	-0.03	0.07	0.04	0.02	0.00	0.04	-0.03	0.02	0.00
-0.04	-0.03	0.05	0.01	0.01	0.03	0.01	-0.07	0.05	0.05	0.07	0.06	0.16
-0.06	0.04	0.04	0.00	-0.01	-0.03	0.03	-0.05	-0.05	0.00	0.10	0.03	0.08
-0.19	0.01	0.09	-0.06	-0.01	-0.05	0.01	0.03	-0.01	0.04	-0.06	0.03	-0.01
-0.09	-0.13	0.04	0.01	-0.02	0.05	0.00	0.15	-0.03	0.01	-0.01	-0.01	0.05
-0.03	0.00	0.00	-0.04	0.00	-0.02	0.02	0.02	-0.04	0.05	0.05	0.00	-0.05
0.04	0.04	0.00	0.04	-0.07	-0.06	-0.05	-0.04	0.04	0.01	-0.01	-0.03	-0.01

0.04	-0.01	-0.04	0.01	0.02	-0.07	-0.06	-0.01	0.02	-0.08	-0.05	0.18	0.08
-0.06	-0.04	0.09	0.05	0.02	-0.03	0.00	0.02	0.01	-0.02	-0.02	0.08	-0.04
0.01	0.00	-0.04	0.06	-0.07	-0.04	-0.06	0.06	0.06	-0.07	-0.03	-0.01	-0.05
0.09	-0.09	0.08	-0.03	-0.04	-0.05	-0.07	-0.03	0.01	-0.01	0.03	-0.04	0.07
-0.03	0.04	-0.05	0.04	-0.02	-0.04	0.00	-0.02	0.02	0.02	-0.11	0.04	-0.02
0.00	-0.08	0.03	0.00	0.07	-0.01	-0.03	-0.01	0.11	0.00	0.04	-0.01	0.05
0.02	0.03	-0.04	0.02	-0.01	-0.07	-0.06	-0.02	0.02	-0.03	0.03	0.04	-0.07
0.00	-0.01	-0.01	0.00	0.00	-0.01	-0.03	0.01	0.06	0.00	0.02	0.01	-0.01
0.06	0.01	0.08	0.02	0.01	-0.14	0.00	0.00	0.02	0.06	-0.03	-0.03	-0.03
0.00	0.07	-0.07	-0.07	-0.02	-0.03	-0.02	0.04	-0.02	-0.06	0.02	-0.01	0.12
0.01	-0.07	0.02	0.00	-0.05	0.00	-0.05	0.06	0.01	0.00	-0.03	0.06	0.08
0.00	-0.03	-0.04	0.00	-0.02	-0.01	0.13	-0.09	0.09	-0.06	-0.03	0.10	0.01
-0.03	-0.04	0.05	0.02	-0.05	0.02	0.03	0.00	-0.04	-0.03	0.04	0.02	-0.03
0.13	0.05	-0.03	0.06	0.04	0.01	0.03	0.03	0.04	0.01	0.05	-0.04	0.03
-0.06	0.03	0.05	-0.06	-0.05	-0.09	0.02	0.01	0.00	0.04	-0.01	0.02	-0.02
0.00	0.04	0.04	-0.02	0.00	0.05	-0.02	0.03	0.07	0.03	0.07	-0.01	-0.02
0.03	0.01	0.09	0.01	0.01	0.03	0.03	0.01	0.08	0.02	0.00	-0.07	0.00
-0.09	0.02	0.03	0.00	-0.03	-0.01	-0.05	-0.02	-0.05	0.05	0.00	0.01	-0.05
0.02	0.00	0.09	0.07	0.00	0.07	0.00	0.00	0.00	0.07	-0.06	0.00	-0.03
-0.01	0.10	0.00	-0.01	-0.13	0.03	0.01	-0.04	-0.06	0.10	0.04	0.03	0.02
-0.02	0.11	0.00	0.04	-0.07	0.06	0.04	0.01	-0.06	0.06	-0.09	0.03	0.04
0.01	-0.01	0.01	-0.02	-0.07	0.07	0.00	0.05	0.10	-0.09	0.00	0.03	0.04
-0.06	0.02	0.05	0.06	-0.08	0.00	0.04	0.05	-0.03	-0.01	-0.09	-0.06	-0.08
0.00	0.01	0.02	0.02	-0.03	-0.04	-0.03	0.01	-0.02	0.00	0.03	-0.06	-0.01
0.01	0.07	0.02	0.01	0.01	-0.02	0.13	-0.04	-0.06	0.10	0.12	-0.02	-0.10
-0.03	0.08	-0.03	0.05	0.03	0.02	0.06	0.03	0.00	0.07	0.08	-0.04	0.10
-0.03	-0.07	-0.05	0.03	-0.10	-0.01	0.08	0.00	0.01	0.04	-0.03	-0.05	-0.10
0.01	-0.02	-0.06	0.13	-0.05	0.01	-0.04	-0.02	-0.10	0.01	0.06	0.07	-0.03
0.02	-0.03	0.04	-0.08	0.03	0.04	0.01	-0.01	-0.02	0.02	0.06	0.00	-0.04
0.03	-0.03	-0.08	-0.03	0.07	-0.04	0.09	0.00	0.05	-0.04	-0.04	0.06	-0.03
0.01	-0.05	-0.03	-0.05	-0.07	-0.02	0.07	0.10	0.00	0.08	-0.05	0.05	0.00



-0.03	0.03	0.01	-0.02	0.07	0.03	0.05	-0.03	-0.11	-0.10	-0.03	0.04	-0.06
0.00	0.08	0.05	-0.06	-0.05	-0.05	0.04	0.03	0.03	0.04	0.02	0.01	0.00
0.01	0.07	0.09	-0.01	0.03	0.03	0.07	-0.09	0.00	-0.06	-0.02	-0.01	0.05
0.01	0.02	-0.05	-0.04	0.03	0.03	-0.01	0.06	-0.04	-0.02	-0.04	-0.04	-0.01
0.00	0.01	-0.05	-0.07	-0.03	0.02	-0.04	0.01	-0.05	-0.03	0.03	0.03	0.01
0.02	0.03	-0.01	0.05	0.05	0.04	0.01	-0.01	0.06	0.02	0.03	0.05	-0.02
-0.02	-0.01	-0.09	0.01	0.06	0.05	-0.05	-0.05	0.17	0.04	-0.06	-0.03	0.04
-0.03	-0.04	-0.04	0.15	-0.02	0.00	0.02	0.02	0.00	0.00	-0.09	-0.08	0.02
-0.01	0.08	-0.01	0.09	0.05	0.04	0.07	0.00	0.05	0.10	0.06	0.05	0.01
0.09	-0.09	-0.11	0.07	0.04	0.12	-0.02	-0.05	-0.05	-0.08	0.01	0.00	0.01
-0.09	-0.08	-0.03	-0.02	0.04	0.00	-0.10	-0.05	0.05	0.03	0.04	0.04	-0.01
-0.10	-0.06	-0.01	0.01	0.11	-0.03	0.01	0.07	-0.02	-0.01	-0.01	-0.03	0.17
-0.09	-0.02	-0.03	-0.07	-0.03	-0.02	-0.09	-0.01	-0.09	-0.04	-0.04	-0.05	-0.02
-0.08	-0.07	-0.02	0.00	-0.02	0.16	0.01	-0.09	0.06	-0.14	-0.10	0.07	0.08
-0.01	0.00	0.03	-0.08	-0.07	0.03	0.02	0.06	-0.07	0.00	0.09	0.01	0.04
0.02	-0.02	0.00	0.02	-0.08	-0.08	0.05	-0.07	-0.05	0.05	-0.06	0.00	-0.03
-0.05	0.05	-0.07	0.07	-0.02	-0.03	-0.07	0.01	0.09	0.03	-0.02	0.01	0.08
0.00	-0.02	-0.07	0.01	0.09	-0.04	0.05	-0.03	-0.01	0.03	-0.01	0.04	0.03
0.02	0.10	0.06	0.01	0.03	0.03	0.00	-0.04	0.00	0.04	0.01	-0.08	0.03
-0.05	0.04	-0.05	-0.03	0.03	0.01	0.01	0.01	-0.04	0.01	0.00	0.07	0.07
0.02	-0.01	-0.05	-0.02	-0.02	0.05	0.01	0.02	0.01	0.00	0.00	0.04	0.02
0.00	0.06	-0.05	-0.07	0.03	0.03	0.01	-0.01	-0.03	0.02	-0.04	-0.04	-0.03

PC26	PC27	PC28	PC29	PC30	PC31	PC32
-0.09	0.03	0.04	0.03	0.04	0.05	0.26
0.02	-0.02	-0.03	-0.01	-0.10	-0.03	-0.04
0.00	-0.03	-0.01	0.00	-0.03	-0.01	-0.01
0.03	-0.07	-0.09	-0.06	0.03	0.00	0.27
0.08	-0.05	-0.10	-0.02	0.07	-0.06	0.08
0.03	0.06	-0.06	0.00	-0.02	-0.04	0.05
0.06	-0.05	-0.11	0.04	0.00	0.02	0.12
0.09	0.08	-0.06	0.02	0.01	0.04	0.11
-0.06	-0.11	-0.01	0.00	-0.01	-0.07	0.03
-0.06	0.04	0.01	0.00	0.01	-0.02	-0.02
0.00	0.05	0.05	-0.07	-0.03	-0.01	-0.34
-0.06	-0.03	-0.03	-0.02	0.04	-0.04	0.07
0.06	0.00	-0.04	0.07	0.01	0.00	0.10
-0.02	0.01	0.11	-0.03	0.03	0.01	0.39
-0.01	0.01	0.02	-0.03	-0.03	-0.03	-0.11
-0.11	0.05	0.00	-0.02	-0.08	-0.11	0.13
-0.09	0.03	-0.03	0.02	-0.04	-0.03	-0.15
-0.03	0.04	0.04	-0.06	-0.01	-0.03	-0.34
-0.01	-0.01	-0.02	0.01	0.00	0.00	0.19
-0.13	-0.04	0.01	0.13	0.03	-0.06	-0.02
0.03	0.02	0.05	-0.01	0.15	0.00	-0.11
0.01	-0.02	0.01	0.00	-0.01	-0.01	0.23
-0.11	0.05	-0.07	-0.09	0.02	-0.02	0.18
-0.04	-0.05	0.05	0.03	0.02	0.04	0.14
-0.05	-0.03	0.02	0.01	-0.01	0.00	0.14
0.06	0.04	0.06	0.04	-0.01	-0.01	0.12
-0.08	-0.04	0.03	-0.09	0.08	0.01	0.04
0.01	-0.01	0.00	-0.01	0.02	0.03	0.02
-0.05	0.03	0.04	-0.03	-0.04	-0.01	-0.18

-0.05	-0.01	-0.02	-0.01	-0.08	0.00	0.07
0.00	0.04	0.04	-0.02	-0.07	0.02	-0.11
0.09	-0.03	0.04	0.03	0.01	0.04	0.02
0.01	-0.09	-0.01	-0.10	-0.03	-0.03	0.00
-0.02	0.02	0.01	-0.01	-0.07	0.02	0.03
-0.03	0.06	-0.02	0.00	0.02	0.03	0.01
-0.05	0.05	0.01	-0.04	0.03	-0.05	0.00
0.01	0.07	0.03	-0.02	-0.01	0.10	0.02
-0.02	0.00	-0.01	-0.01	-0.02	0.02	0.00
0.00	0.03	0.03	0.13	0.03	-0.15	-0.02
0.02	-0.10	0.00	-0.02	-0.09	0.01	-0.03
-0.05	-0.02	-0.04	0.04	-0.02	0.01	0.03
0.01	-0.03	0.03	-0.01	-0.02	-0.01	-0.03
-0.04	-0.05	-0.02	-0.03	0.04	-0.14	0.03
0.01	0.02	0.07	-0.02	-0.06	0.03	0.03
0.00	-0.01	0.01	-0.14	-0.13	-0.07	0.03
-0.01	-0.05	0.02	-0.11	-0.10	-0.02	-0.03
-0.03	-0.03	-0.01	0.11	-0.03	0.07	0.00
-0.02	-0.06	0.02	-0.07	-0.08	-0.07	0.01
0.04	-0.05	0.01	0.00	-0.18	0.09	-0.01
0.10	-0.05	0.05	0.03	0.12	-0.05	0.02
-0.02	0.04	-0.06	0.08	0.07	0.02	0.00
0.04	0.12	-0.07	-0.03	0.02	0.09	0.00
-0.02	0.02	-0.04	0.02	0.04	0.01	-0.01
-0.17	-0.03	-0.07	0.08	0.03	-0.03	0.03
-0.01	0.01	0.01	-0.01	-0.02	0.01	0.01
0.00	0.00	0.01	0.02	0.00	0.06	0.00
0.03	0.05	0.03	-0.05	0.01	0.14	0.02
0.02	-0.03	-0.06	-0.02	0.03	0.01	-0.01
0.00	-0.05	-0.01	-0.03	0.01	-0.14	-0.01
0.00	0.00	-0.07	0.01	0.03	-0.05	-0.03

-0.05	0.00	-0.01	0.00	0.02	0.05	0.02
-0.03	0.02	-0.01	-0.01	0.04	0.13	-0.02
0.05	-0.03	-0.08	-0.02	-0.04	-0.01	0.00
0.09	0.04	-0.17	-0.01	-0.07	-0.02	-0.01
-0.11	-0.03	0.00	-0.10	-0.02	0.03	0.00
0.01	0.06	0.09	-0.09	-0.01	-0.03	0.02
0.03	0.04	0.08	0.04	0.06	-0.03	0.01
0.06	-0.01	0.13	0.03	0.12	-0.01	0.00
0.00	0.04	-0.03	-0.08	0.02	-0.02	0.00
0.04	-0.07	0.12	0.00	-0.01	-0.04	0.01
0.00	0.01	0.05	0.02	0.00	0.00	0.01
0.01	-0.03	-0.04	-0.02	-0.07	0.05	-0.01
0.08	0.01	0.06	-0.02	0.04	-0.01	0.00
-0.02	0.04	0.02	-0.17	0.01	0.02	0.00
0.03	-0.04	-0.12	0.14	-0.06	-0.04	-0.02
-0.01	0.06	-0.05	-0.03	0.00	-0.06	-0.01
0.01	-0.01	-0.07	0.02	0.03	0.05	0.00
0.00	0.04	-0.05	0.01	0.00	-0.01	0.01
0.03	-0.10	-0.05	0.00	-0.01	0.02	0.02
0.04	0.02	0.05	0.05	-0.04	-0.11	0.01
0.00	0.02	-0.04	0.05	-0.03	0.08	0.00
0.11	-0.15	-0.01	-0.08	-0.01	0.00	0.04
0.09	-0.02	0.03	-0.12	0.03	-0.02	0.02
0.08	0.00	-0.10	-0.09	-0.03	-0.06	0.00
-0.02	-0.01	-0.08	-0.03	0.09	0.08	-0.05
0.00	0.00	-0.01	-0.05	-0.04	0.09	0.00
-0.05	-0.02	-0.08	-0.02	-0.01	-0.04	-0.01
0.02	-0.04	-0.01	-0.02	0.01	0.00	-0.02
-0.02	0.01	0.00	-0.01	-0.04	0.05	0.01
0.04	-0.04	0.05	-0.05	-0.02	0.00	0.02
-0.02	0.05	0.06	0.07	0.01	0.02	0.01

0.00	-0.06	-0.03	-0.04	0.08	0.01	-0.03
-0.03	-0.01	-0.06	-0.02	0.08	-0.05	0.00
0.02	-0.03	0.01	-0.02	-0.04	0.03	-0.01
-0.08	0.00	0.01	-0.06	0.02	-0.03	-0.01
-0.01	-0.01	0.07	0.00	0.01	-0.04	-0.02
-0.07	0.10	-0.06	0.13	0.02	-0.03	-0.02
-0.03	0.04	0.00	-0.01	0.01	0.02	-0.02
0.06	0.08	-0.05	-0.08	-0.01	0.08	-0.01
0.00	0.01	0.01	0.06	0.00	-0.06	0.00
0.02	0.01	0.00	0.10	-0.02	0.01	-0.01
0.00	-0.05	0.02	-0.03	0.00	-0.05	0.03
-0.05	0.00	0.01	-0.02	-0.03	-0.01	0.01
-0.02	-0.01	0.01	-0.01	-0.02	-0.06	0.00
0.01	0.05	0.00	-0.05	-0.03	0.05	0.00
-0.06	-0.02	-0.08	0.00	0.04	-0.05	-0.01
0.07	-0.01	-0.11	-0.01	0.10	-0.06	-0.02
-0.07	0.02	0.11	0.09	-0.08	-0.08	0.02
0.03	-0.01	0.04	-0.07	0.05	0.01	-0.01
0.03	-0.06	0.01	-0.05	0.02	-0.05	-0.02
0.00	-0.05	-0.03	0.02	0.05	0.02	0.00
0.04	0.03	-0.03	-0.07	0.01	0.02	0.01
0.09	0.03	0.00	0.01	0.06	0.01	0.03
0.01	0.07	0.03	0.04	-0.02	0.05	0.00
-0.08	0.03	-0.04	0.03	-0.01	0.06	0.01
-0.05	0.02	0.00	-0.02	-0.12	-0.05	0.01
-0.02	-0.01	-0.07	-0.02	0.04	0.02	-0.02
-0.11	-0.06	-0.07	-0.06	-0.03	0.05	-0.01
0.00	-0.02	0.04	0.02	-0.01	0.00	0.00
-0.05	0.00	-0.05	-0.02	-0.09	-0.08	0.03
0.00	-0.07	-0.10	-0.08	-0.06	-0.06	-0.01
-0.03	0.10	-0.01	-0.02	0.05	-0.01	0.02

0.02	-0.01	0.02	0.04	-0.04	0.01	0.03
0.07	-0.01	-0.03	0.00	-0.07	0.06	0.02
-0.03	0.02	-0.01	0.01	0.02	-0.02	0.01
-0.01	0.03	0.03	0.02	-0.02	-0.05	0.02
0.07	0.03	0.09	0.03	0.00	-0.07	0.02
0.04	-0.05	0.06	0.02	-0.04	-0.02	0.02
-0.02	0.10	-0.01	-0.05	0.03	-0.05	-0.01
0.00	-0.03	-0.08	0.01	-0.03	0.04	0.03
-0.02	-0.05	-0.06	0.05	0.03	0.06	-0.01
0.05	-0.01	0.04	-0.02	0.02	0.05	-0.02
-0.04	-0.02	-0.01	-0.03	0.04	-0.01	-0.02
-0.09	0.01	-0.01	0.07	0.08	0.03	-0.04
0.02	0.00	0.01	-0.03	0.00	-0.02	0.00
0.01	-0.01	0.01	0.04	0.11	-0.02	0.00
-0.03	0.00	0.05	0.02	-0.04	0.05	-0.01
-0.01	-0.04	0.07	0.07	-0.02	-0.01	-0.04
-0.03	0.03	0.05	0.00	0.04	0.04	0.01
0.07	-0.09	-0.11	-0.03	-0.02	0.08	0.00
0.02	0.06	-0.02	-0.01	-0.04	0.07	0.00
0.01	-0.05	-0.02	-0.01	-0.03	-0.02	0.01
-0.04	0.05	0.00	-0.03	0.05	0.01	-0.01
0.04	0.06	0.07	-0.03	-0.01	0.01	0.04
-0.03	-0.05	0.06	-0.02	0.03	-0.04	0.00
0.00	0.01	0.04	0.02	0.00	0.00	-0.04
-0.05	0.02	-0.06	0.04	0.00	0.11	-0.02
0.07	-0.04	-0.11	0.03	-0.10	-0.04	-0.01
0.00	-0.02	-0.04	-0.05	-0.10	-0.01	0.01
0.13	0.08	-0.02	-0.02	0.06	0.06	0.00
0.07	-0.01	-0.04	0.06	-0.02	-0.04	-0.01
-0.07	0.06	-0.01	0.04	-0.07	-0.08	0.02
0.01	0.01	0.05	0.03	-0.05	-0.01	0.01

-0.06	-0.04	0.08	0.01	0.04	-0.03	-0.01
-0.07	-0.08	0.09	-0.06	0.08	0.02	-0.02
-0.12	-0.06	0.03	-0.11	0.05	0.00	-0.01
-0.06	0.01	-0.02	0.06	0.00	0.01	0.03
0.00	0.06	-0.01	-0.06	0.03	-0.03	-0.02
-0.01	-0.08	0.00	-0.02	-0.01	0.07	0.04
-0.09	0.03	0.06	0.04	0.00	0.05	0.00
0.00	0.01	0.01	0.02	-0.01	-0.02	0.04
-0.12	0.17	0.07	0.02	0.00	-0.04	0.00
0.00	0.01	-0.01	0.13	-0.04	-0.02	-0.01
-0.01	-0.01	0.02	-0.01	-0.01	-0.01	-0.01
-0.02	-0.01	0.00	-0.03	-0.02	0.05	0.01
-0.08	0.09	-0.03	0.00	-0.01	0.06	-0.01
0.01	0.03	0.01	0.00	-0.01	-0.01	0.01
0.02	-0.01	0.03	-0.03	-0.09	0.10	0.01
0.03	0.04	0.08	0.06	0.02	0.04	0.00
0.00	-0.06	-0.01	0.02	0.00	0.07	-0.01
-0.02	-0.07	-0.05	-0.06	0.06	-0.06	0.01
0.03	0.07	0.01	0.02	0.01	-0.02	0.01
0.05	-0.04	0.06	0.05	0.03	-0.09	-0.02
0.07	-0.04	0.00	0.04	-0.01	-0.02	-0.02
0.04	0.01	0.04	0.03	0.03	-0.03	0.01
-0.02	-0.05	-0.08	0.00	0.03	-0.02	-0.04
-0.01	0.01	-0.03	0.03	-0.01	0.02	0.02
-0.07	-0.02	-0.03	-0.06	0.00	0.02	-0.03
0.00	-0.03	0.01	-0.05	0.02	-0.02	-0.01
-0.05	-0.05	-0.04	0.01	0.00	-0.09	0.00
0.04	0.03	-0.04	0.00	0.00	-0.01	-0.01
0.05	-0.03	0.00	0.00	0.02	-0.05	0.00
0.06	0.00	0.00	0.00	0.04	-0.03	0.01
0.05	0.02	0.02	-0.04	0.00	-0.04	0.02

0.00	-0.02	0.02	0.00	0.03	-0.02	-0.02
-0.07	0.00	0.03	0.04	-0.10	0.01	0.00
0.00	0.01	-0.03	0.02	0.03	-0.05	0.00
-0.03	0.03	0.03	0.03	0.01	0.01	0.02
-0.06	-0.03	-0.01	0.01	0.05	-0.03	0.00
0.04	-0.03	0.15	-0.02	0.01	0.04	-0.02
-0.04	0.00	-0.02	0.03	-0.03	-0.15	0.00
-0.04	-0.14	0.00	0.00	-0.01	-0.05	0.00
0.00	0.02	-0.02	-0.01	0.04	0.01	0.01
-0.02	0.00	0.00	-0.01	0.01	-0.01	0.00
-0.06	-0.01	-0.01	0.02	-0.02	0.04	-0.01
0.02	-0.01	-0.03	-0.04	-0.02	0.03	0.02
0.02	-0.04	-0.04	0.05	0.01	0.09	-0.02
-0.01	-0.05	-0.08	0.03	0.06	-0.02	0.00
0.05	0.02	-0.03	-0.02	0.00	-0.03	-0.02
-0.01	0.00	-0.03	0.03	0.05	-0.01	-0.04
-0.04	0.05	0.04	-0.11	-0.01	-0.01	0.00
0.00	-0.02	0.03	-0.03	-0.01	-0.01	-0.02
0.07	-0.01	0.01	0.02	-0.03	0.01	0.01
0.10	0.03	0.03	-0.08	-0.09	0.04	0.00
0.10	-0.03	-0.07	0.05	-0.10	-0.12	-0.01
-0.07	-0.03	0.07	-0.06	0.03	0.02	0.00
0.04	0.06	0.03	-0.06	-0.06	-0.02	0.03
-0.10	-0.05	-0.01	-0.03	-0.03	-0.01	0.00
0.00	0.03	0.02	-0.02	-0.01	-0.03	-0.01
0.00	-0.07	0.04	0.03	-0.02	0.18	0.01
-0.02	0.03	-0.01	-0.09	0.03	0.05	-0.01
0.02	-0.06	-0.06	0.03	0.11	0.10	-0.05
-0.02	0.05	-0.02	0.00	-0.05	0.02	-0.02
-0.01	0.00	-0.01	0.06	0.09	0.02	-0.01
0.02	0.05	-0.06	-0.02	0.02	0.00	-0.01



0.09	-0.05	0.00	0.03	-0.05	0.12	-0.03
-0.02	-0.07	-0.10	0.05	0.00	-0.07	-0.01
-0.01	-0.01	0.02	0.00	-0.03	-0.01	-0.02
-0.01	0.02	0.08	0.06	0.08	0.11	-0.02
-0.10	0.04	-0.09	0.00	-0.04	0.03	-0.03
-0.13	-0.04	0.06	0.03	-0.03	0.09	-0.03
0.02	-0.02	0.10	0.11	-0.01	0.00	0.01
0.13	0.05	0.08	0.03	-0.01	0.01	0.03
-0.02	0.00	-0.01	0.08	-0.07	0.00	0.02
0.04	0.08	-0.05	-0.11	0.00	0.01	0.02
0.01	-0.01	0.10	-0.05	0.01	-0.02	-0.02
0.06	0.04	-0.04	-0.02	0.04	0.03	-0.01
-0.06	0.02	0.03	-0.08	0.04	0.00	-0.01
0.04	0.02	-0.09	0.02	-0.02	-0.06	0.01
-0.01	0.02	-0.04	0.01	0.00	0.02	0.02
0.01	0.10	0.04	-0.02	0.01	0.03	-0.01
-0.05	-0.07	0.01	-0.08	0.03	0.03	-0.03
0.01	-0.01	0.05	0.00	-0.03	0.00	0.02
0.03	-0.06	0.08	0.00	0.01	0.06	0.00
-0.01	0.07	-0.03	-0.01	0.00	0.11	0.02
-0.01	-0.02	0.06	-0.07	0.05	0.07	0.00
0.00	-0.03	0.03	-0.07	-0.03	0.01	0.02
-0.05	-0.02	0.06	0.09	0.07	0.00	0.04
-0.07	0.01	0.01	0.01	0.05	-0.05	0.00
0.04	0.04	0.03	-0.01	0.03	-0.11	0.00
-0.02	0.01	0.08	0.06	-0.05	0.00	0.02
-0.05	-0.02	0.01	0.10	-0.01	0.04	0.01
0.03	-0.02	-0.01	-0.03	0.03	0.00	0.01
0.01	0.05	0.03	0.07	-0.06	-0.02	0.00
0.00	-0.04	-0.03	-0.02	0.04	-0.02	-0.02
-0.02	-0.01	0.02	0.02	-0.01	-0.03	-0.05

-0.05	0.00	-0.02	-0.05	-0.02	-0.01	0.00
-0.06	-0.07	0.06	0.02	0.03	-0.03	-0.03
0.00	-0.01	-0.01	0.05	-0.08	-0.01	-0.03
0.02	0.00	0.08	-0.03	-0.06	-0.01	0.01
0.00	-0.06	0.00	0.10	-0.01	0.04	-0.02
-0.04	0.10	-0.01	0.00	0.01	-0.04	-0.01
-0.05	-0.02	-0.07	-0.08	0.07	0.11	0.00
0.03	0.00	0.01	0.04	-0.03	-0.08	0.03
0.02	0.09	0.11	-0.03	0.05	0.00	0.00
0.07	-0.05	0.00	0.01	0.01	0.05	0.03
0.01	0.03	-0.01	-0.07	-0.03	-0.03	-0.02
0.08	0.12	0.02	0.05	-0.10	-0.08	-0.01
0.03	-0.06	0.08	0.02	-0.03	-0.04	0.00
-0.04	-0.09	0.06	-0.14	0.04	0.00	0.02
-0.05	-0.06	0.01	0.03	0.05	0.04	0.00
0.02	-0.05	0.00	-0.04	-0.03	0.08	0.01
0.01	-0.05	0.01	-0.03	0.04	-0.02	0.01
-0.01	-0.01	-0.03	-0.04	-0.01	-0.01	-0.02
0.00	-0.02	0.03	0.05	0.05	0.06	-0.01
-0.06	-0.03	0.02	0.05	0.04	0.02	-0.03
0.01	0.02	-0.02	-0.01	0.00	-0.02	-0.04
-0.03	0.04	-0.06	-0.02	-0.01	-0.03	0.00
0.03	0.01	0.05	-0.04	-0.06	-0.02	-0.01
-0.03	0.03	-0.07	-0.01	-0.03	-0.03	-0.02
0.12	-0.08	-0.05	-0.05	-0.07	0.01	0.00
0.04	-0.02	0.02	-0.01	0.01	0.05	-0.02
0.03	0.00	0.00	-0.04	0.00	0.03	0.01
-0.01	0.03	0.00	-0.01	0.04	0.00	0.01
0.01	0.03	-0.05	-0.04	-0.02	0.02	0.02
0.01	-0.05	0.01	-0.03	-0.02	-0.01	-0.01
0.00	-0.07	0.03	0.05	0.03	-0.07	-0.02

0.13	-0.01	0.07	0.03	-0.02	-0.01	0.00
0.06	-0.01	0.02	0.05	0.07	-0.02	-0.01
-0.04	0.06	-0.08	0.05	0.11	-0.07	-0.03
0.01	0.02	-0.04	-0.03	0.03	-0.02	-0.01
0.01	0.04	0.02	0.05	-0.02	0.00	0.02
0.05	0.07	-0.05	0.06	0.07	0.04	0.01
-0.01	0.03	0.02	0.04	0.02	0.03	0.02
-0.06	-0.02	0.01	0.03	0.07	-0.04	0.00
0.02	-0.02	0.01	-0.01	0.09	0.05	0.00
0.02	-0.01	0.03	0.09	0.03	-0.06	0.01
-0.03	0.14	-0.05	-0.04	0.01	0.08	-0.01
0.03	-0.04	-0.02	0.02	0.07	-0.07	0.01
-0.02	0.00	-0.07	-0.02	-0.01	0.01	-0.01
0.03	0.01	-0.06	-0.01	0.03	-0.08	-0.01
-0.07	0.07	0.07	-0.02	0.11	0.04	0.03
-0.02	-0.04	0.07	0.02	-0.11	-0.03	0.01
0.02	0.03	-0.10	-0.02	0.03	-0.04	-0.03
-0.02	0.01	0.03	-0.03	0.02	-0.04	-0.01
0.01	-0.04	0.04	0.12	0.00	-0.04	-0.04
0.01	0.04	0.01	0.03	-0.05	0.04	0.01
0.06	-0.04	-0.04	-0.04	0.00	0.03	-0.01
-0.11	-0.15	-0.02	0.06	-0.03	-0.01	0.01
-0.15	-0.01	-0.09	0.10	-0.10	-0.02	0.04
-0.04	0.04	-0.04	0.02	0.05	-0.05	-0.01
0.02	0.03	-0.03	0.01	0.01	-0.03	0.01
-0.01	0.00	0.05	0.06	-0.03	-0.14	0.01
-0.05	0.00	0.04	-0.05	0.01	-0.03	0.03
-0.03	0.01	0.05	0.09	0.02	0.07	0.02
-0.03	0.08	0.00	-0.04	-0.04	-0.01	0.02
-0.04	0.06	-0.03	0.03	0.04	-0.06	0.00
0.09	0.05	0.02	0.00	0.04	0.00	0.01

0.05	0.02	0.03	0.04	0.05	-0.04	-0.01
0.06	-0.02	-0.03	-0.04	0.05	-0.08	0.01
-0.03	0.04	0.00	-0.02	-0.08	0.00	0.04
-0.04	0.00	-0.07	-0.01	-0.08	-0.01	0.02
0.03	0.11	-0.05	0.00	0.09	0.04	0.01
0.03	0.06	-0.02	0.07	-0.05	-0.03	0.01
0.01	0.04	-0.08	0.06	-0.05	0.07	0.00
0.03	-0.08	0.06	0.00	0.00	0.02	0.02
0.06	0.05	-0.03	0.09	-0.01	0.04	-0.01
-0.03	0.08	0.04	-0.05	0.06	0.01	0.00
0.01	0.00	0.01	-0.01	-0.07	-0.01	-0.02
0.04	0.13	0.00	-0.07	-0.01	-0.07	0.02
0.05	-0.02	-0.03	0.07	0.07	-0.05	0.02
0.01	0.08	0.00	-0.02	0.01	-0.02	0.00
-0.06	0.01	-0.06	-0.01	0.01	-0.06	-0.01
0.01	-0.01	0.01	0.11	-0.09	-0.01	-0.01
0.03	0.03	-0.10	0.02	-0.02	-0.01	-0.01
-0.04	0.00	-0.02	-0.02	0.03	-0.02	0.01
-0.01	-0.05	0.01	0.05	0.01	-0.02	0.03
0.02	0.03	-0.04	-0.03	0.06	-0.03	-0.01
0.04	-0.06	-0.08	-0.04	0.02	0.02	-0.05
-0.10	-0.09	0.04	-0.05	0.09	-0.04	0.00
0.00	-0.05	0.04	0.01	-0.02	0.04	-0.03
-0.01	0.00	-0.04	0.00	0.01	0.00	-0.02
-0.04	0.00	0.05	-0.01	-0.01	-0.04	-0.01
-0.04	0.01	-0.01	0.00	-0.04	0.17	0.03
0.06	0.00	0.00	-0.05	-0.08	-0.07	0.03
0.02	-0.04	0.05	0.00	-0.05	0.02	-0.01
0.01	0.03	-0.05	0.00	0.01	0.03	0.04
0.02	0.05	-0.01	-0.05	0.01	-0.03	0.01
0.02	-0.03	-0.05	-0.04	-0.01	0.03	0.01

-0.13	0.03	-0.02	0.02	-0.11	0.03	0.00
-0.05	-0.05	-0.07	-0.02	-0.01	-0.02	0.01
-0.02	0.01	-0.05	0.04	-0.02	0.00	-0.03
0.05	0.00	0.03	-0.01	-0.03	0.04	0.00
0.00	0.00	0.01	0.02	-0.03	0.04	-0.03
0.00	0.04	-0.03	-0.10	-0.07	0.01	0.00
-0.01	-0.05	0.00	-0.05	-0.04	-0.01	0.04
0.07	-0.10	0.12	0.00	0.01	-0.02	-0.02
-0.04	0.04	0.03	-0.03	-0.05	0.01	0.01
0.02	-0.02	-0.02	0.01	0.01	0.00	-0.03
-0.01	-0.02	0.02	-0.01	0.02	-0.02	-0.01
0.03	0.01	-0.01	0.05	0.02	0.00	-0.02
-0.01	-0.08	-0.01	0.01	-0.14	0.04	-0.02
-0.01	0.10	0.07	-0.06	0.05	0.00	-0.04
0.00	0.02	-0.02	0.03	-0.01	0.01	0.00
0.00	-0.02	0.00	-0.03	0.03	0.04	-0.02
-0.04	0.01	0.07	0.02	-0.03	-0.03	-0.03
-0.03	-0.11	0.09	-0.03	-0.09	0.00	-0.02
-0.01	-0.01	0.10	0.05	0.03	0.03	0.01
0.06	-0.02	-0.05	0.09	0.02	-0.03	-0.02
-0.03	0.02	0.02	0.02	-0.01	0.01	-0.02
0.01	0.02	0.00	0.03	0.01	-0.01	0.01
0.00	0.10	0.02	0.01	-0.04	-0.11	0.05
0.05	-0.01	-0.06	-0.07	0.07	-0.09	0.03
0.01	-0.06	0.04	-0.02	-0.01	0.01	-0.02
-0.06	-0.07	-0.03	0.07	-0.05	0.01	0.00
0.04	0.09	-0.01	0.10	0.09	-0.04	-0.05
-0.03	0.02	0.01	0.05	-0.03	-0.01	-0.01
-0.01	-0.08	-0.01	0.05	-0.10	0.00	0.00
0.02	-0.08	-0.07	0.02	0.03	0.08	-0.05
0.01	-0.02	-0.10	0.03	0.04	0.07	-0.04

-0.05	-0.01	-0.08	-0.07	-0.01	0.05	0.01
-0.01	0.03	-0.06	0.01	0.03	-0.01	0.00
0.01	0.01	0.08	-0.02	-0.08	0.03	0.00
0.01	0.05	-0.07	-0.02	-0.09	0.01	0.01
-0.05	-0.09	-0.02	0.06	0.01	0.03	-0.01
-0.03	0.09	0.08	0.00	-0.12	0.04	0.02
-0.12	0.06	-0.01	-0.05	0.05	0.02	0.01
0.00	-0.02	-0.03	-0.01	0.04	0.07	0.01
0.02	-0.02	-0.01	0.03	-0.06	0.02	-0.01
-0.01	0.05	-0.03	0.10	-0.02	0.06	0.00
-0.03	-0.02	0.09	-0.07	0.03	0.01	0.01
0.12	0.03	0.01	0.00	0.02	0.03	0.03
-0.03	0.03	-0.02	0.01	0.01	-0.04	0.01
0.02	0.01	0.02	-0.04	0.01	0.01	0.02
-0.03	0.04	-0.02	0.05	0.01	0.00	0.01
-0.02	0.06	-0.03	0.01	0.06	0.09	-0.01
0.01	-0.06	0.06	-0.04	0.09	0.02	-0.02
0.03	-0.03	0.05	0.04	-0.03	0.04	0.00
-0.02	0.09	0.01	-0.03	-0.03	-0.05	-0.01
0.02	0.05	-0.02	0.02	0.02	0.01	0.00
-0.06	-0.01	-0.01	0.02	-0.04	-0.01	0.02
0.12	0.09	-0.05	0.04	0.01	0.07	0.04
0.08	0.07	-0.01	-0.05	-0.10	-0.02	-0.02
0.09	0.03	-0.04	-0.03	0.03	-0.07	-0.02
0.06	-0.16	0.01	0.01	0.10	-0.05	-0.03
0.05	-0.01	-0.05	0.08	0.05	0.01	0.01
0.02	0.03	-0.01	0.01	-0.01	0.04	-0.02
-0.01	-0.04	0.02	0.02	0.03	0.05	0.02
0.05	0.00	-0.04	0.01	0.03	0.00	0.00
0.02	0.05	-0.02	-0.02	-0.01	-0.02	0.02
-0.01	0.08	0.03	0.00	0.05	-0.02	0.01

-0.02	0.07	0.06	0.01	0.02	-0.03	-0.01
-0.02	0.03	0.00	0.01	0.04	-0.01	0.01
0.01	-0.05	-0.04	0.02	-0.10	0.06	-0.01
-0.03	0.02	-0.03	-0.04	0.02	0.08	-0.01
0.05	0.05	0.07	0.04	-0.04	0.04	0.03
0.01	0.00	-0.03	0.04	0.00	0.02	0.02
-0.11	-0.05	-0.03	0.00	0.04	0.05	0.03
-0.03	0.03	-0.03	0.07	0.06	0.02	-0.03
-0.08	0.03	0.01	0.00	-0.06	0.06	0.03
0.03	-0.04	-0.04	-0.04	-0.02	0.03	-0.02
-0.03	0.14	0.01	-0.09	-0.12	-0.06	0.04
0.06	0.02	0.05	-0.05	0.02	-0.02	0.02
0.03	-0.06	-0.07	-0.03	0.02	-0.01	-0.02
0.10	-0.02	0.08	0.08	-0.04	0.01	0.02
0.04	-0.01	0.01	0.04	-0.01	0.09	-0.02
-0.05	-0.06	0.05	-0.01	-0.01	0.04	-0.01
0.00	0.00	-0.03	-0.08	-0.02	-0.06	0.01
-0.01	-0.03	-0.02	0.03	0.01	-0.06	0.03
-0.02	0.00	0.01	-0.09	0.10	-0.02	0.00
-0.03	0.02	-0.02	0.08	0.03	0.09	-0.01
-0.03	-0.01	-0.03	0.01	0.01	-0.09	0.01
0.02	0.01	-0.04	0.00	0.00	-0.03	0.00

EXPLAINED PCA VARIANCE													
	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12	
Individual	0.13	0.09	0.08	0.06	0.05	0.05	0.05	0.04	0.04	0.03	0.03	0.03	0.03
Cumulative	0.13	0.22	0.29	0.36	0.41	0.46	0.51	0.55	0.58	0.62	0.65	0.68	



PC13	PC14	PC15	PC16	PC17	PC18	PC19	PC20	PC21	PC22	PC23	PC24	PC25	
0.03	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.01	0.01
0.70	0.73	0.75	0.78	0.80	0.82	0.84	0.85	0.87	0.89	0.90	0.92	0.93	

PC26	PC27	PC28	PC29	PC30	PC31	PC32	
0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.00
0.94	0.96	0.97	0.98	0.99	1.00	1.00	

## SUPPLEMENTARY DATASET 2

MODULE 0					
Pathway	Total	Expected	Hits	P.Value	FDR
Translation	249	9.58	113	5.3E-101	7.41E-98
Metabolism of mRNA	317	12.2	116	1.06E-90	7.41E-88
Metabolism of RNA	339	13	116	9.47E-87	4.42E-84
GTP hydrolysis and joining of the 60S ribosomal subunit	201	7.74	95	1.56E-85	5.46E-83
Eukaryotic Translation Initiation	209	8.04	96	5.57E-85	1.30E-82
Cap-dependent Translation Initiation	209	8.04	96	5.57E-85	1.30E-82
3' -UTR-mediated translational regulation	201	7.74	94	5.36E-84	9.40E-82
L13a-mediated translational silencing of Ceruloplasmin expression	201	7.74	94	5.36E-84	9.40E-82
Formation of a pool of free 40S subunits	189	7.27	88	5.36E-78	8.35E-76
SRP-dependent cotranslational protein targeting to membrane	204	7.85	90	3.11E-77	4.36E-75
Eukaryotic Translation Elongation	186	7.16	84	8.86E-73	1.13E-70
Nonsense Mediated Decay Independent of the Exon Junction Complex	184	7.08	83	8.46E-72	9.89E-70
Nonsense Mediated Decay Enhanced by the Exon Junction Complex	203	7.81	86	1.18E-71	1.18E-69
Nonsense-Mediated Decay	203	7.81	86	1.18E-71	1.18E-69
Peptide chain elongation	178	6.85	81	2.41E-70	2.26E-68
Eukaryotic Translation Termination	178	6.85	80	7.13E-69	6.25E-67
Influenza Viral RNA Transcription and Replication	176	6.77	79	6.67E-68	5.19E-66
Viral mRNA Translation	176	6.77	79	6.67E-68	5.19E-66
Influenza Life Cycle	180	6.93	79	6.19E-67	4.57E-65
Influenza Infection	185	7.12	79	9.10E-66	6.38E-64
Gene Expression	1090	41.8	157	2.75E-62	1.84E-60
Metabolism of proteins	689	26.5	113	1.69E-46	1.08E-44
Ribosomal scanning and start codon recognition	91	3.5	48	6.35E-45	3.87E-43
Translation initiation complex formation	92	3.54	48	1.29E-44	7.52E-43
Activation of the mRNA upon binding of the cap-binding complex and eIFs, and subsequent binding to 43S	93	3.58	48	2.58E-44	1.45E-42
Switching of origins to a post-replicative state	69	2.66	42	5.91E-43	3.07E-41
Orc1 removal from chromatin	69	2.66	42	5.91E-43	3.07E-41
Disease	945	36.4	126	1.45E-42	7.28E-41
Removal of licensing factors from origins	71	2.73	42	3.39E-42	1.58E-40

Regulation of DNA replication	71	2.73	42	3.39E-42	1.58E-40
Assembly of the pre-replicative complex	63	2.42	40	5.28E-42	2.39E-40
Formation of the ternary complex, and subsequently, the 43S complex	83	3.19	44	2.75E-41	1.21E-39
Cell Cycle Checkpoints	131	5.04	52	1.33E-40	5.64E-39
Regulation of APC/C activators between G1/S and early anaphase	84	3.23	42	5.46E-38	2.25E-36
Activation of APC/C and APC/C:Cdc20 mediated degradation of mitotic proteins	77	2.96	40	4.60E-37	1.84E-35
APC/C-mediated degradation of cell cycle proteins	89	3.43	42	1.26E-36	4.76E-35
Regulation of mitotic cell cycle	89	3.43	42	1.26E-36	4.76E-35
Synthesis of DNA	95	3.66	43	1.63E-36	6.01E-35
DNA Replication Pre-Initiation	80	3.08	40	3.47E-36	1.22E-34
M/G1 Transition	80	3.08	40	3.47E-36	1.22E-34
APC/C:Cdc20 mediated degradation of mitotic proteins	76	2.93	39	7.25E-36	2.48E-34
Antigen processing: Ubiquitination & Proteasome degradation	224	8.62	60	1.42E-35	4.75E-34
G1/S Transition	113	4.35	45	3.63E-35	1.18E-33
DNA Replication	102	3.93	43	7.03E-35	2.24E-33
Cdc20:Phospho-APC/C mediated degradation of Cyclin A	76	2.93	38	2.17E-34	6.52E-33
APC/C:Cdh1 mediated degradation of Cdc20 and other APC/C:Cdh1 targeted proteins in late mitosis/early G1	76	2.93	38	2.17E-34	6.52E-33
CDT1 association with the CDC6:ORC:origin complex	57	2.19	34	2.19E-34	6.52E-33
APC/C:Cdc20 mediated degradation of Securin	71	2.73	36	6.92E-33	2.02E-31
Class I MHC mediated antigen processing & presentation	267	10.3	62	7.43E-33	2.13E-31
SCF-beta-TrCP mediated degradation of Emi1	53	2.04	32	1.22E-32	3.42E-31
S Phase	122	4.7	44	3.54E-32	9.74E-31
Vif-mediated degradation of APOBEC3G	55	2.12	32	6.70E-32	1.81E-30
CDK-mediated phosphorylation and removal of Cdc6	49	1.89	30	6.63E-31	1.75E-29
Autodegradation of Cdh1 by Cdh1:APC/C	68	2.62	34	8.13E-31	2.11E-29
Vpu mediated degradation of CD4	50	1.92	30	1.60E-30	4.09E-29
Mitotic G1-G1/S phases	140	5.39	45	2.21E-30	5.54E-29
Ubiquitin Mediated Degradation of Phosphorylated Cdc25A	52	2	30	8.60E-30	2.04E-28
p53-Independent DNA Damage Response	52	2	30	8.60E-30	2.04E-28
p53-Independent G1/S DNA damage checkpoint	52	2	30	8.60E-30	2.04E-28
Regulation of activated PAK-2p34 by proteasome mediated degradation	48	1.85	29	1.18E-29	2.76E-28

G1/S DNA Damage Checkpoints	62	2.39	32	1.28E-29	2.94E-28
Autodegradation of the E3 ubiquitin ligase COP1	53	2.04	30	1.92E-29	4.33E-28
Ubiquitin-dependent degradation of Cyclin D1	49	1.89	29	2.80E-29	6.13E-28
Ubiquitin-dependent degradation of Cyclin D	49	1.89	29	2.80E-29	6.13E-28
Stabilization of p53	54	2.08	30	4.17E-29	8.86E-28
Destabilization of mRNA by AUF1 (hnRNP D0)	54	2.08	30	4.17E-29	8.86E-28
p53-Dependent G1/S DNA damage checkpoint	59	2.27	31	4.92E-29	1.02E-27
p53-Dependent G1 DNA Damage Response	59	2.27	31	4.92E-29	1.02E-27
Degradation of beta-catenin by the destruction complex	65	2.5	32	9.27E-29	1.86E-27
Signaling by Wnt	65	2.5	32	9.27E-29	1.86E-27
Activation of NF-kappaB in B Cells	66	2.54	32	1.74E-28	3.44E-27
ER-Phagosome pathway	63	2.42	31	7.13E-28	1.39E-26
Cross-presentation of soluble exogenous antigens (endosomes)	48	1.85	27	1.78E-26	3.43E-25
Mitotic M-M/G1 phases	266	10.2	55	2.56E-26	4.86E-25
Regulation of ornithine decarboxylase (ODC)	49	1.89	27	3.84E-26	7.18E-25
Regulation of Apoptosis	59	2.27	29	4.17E-26	7.70E-25
Cyclin A:Cdk2-associated events at S phase entry	66	2.54	30	1.09E-25	1.99E-24
Antigen processing-Cross presentation	78	3	32	1.30E-25	2.33E-24
SCF(Skp2)-mediated degradation of p27/p21	58	2.23	28	5.94E-25	1.05E-23
Cyclin E associated events during G1/S transition	65	2.5	29	1.44E-24	2.53E-23
Separation of Sister Chromatids	186	7.16	42	1.16E-21	2.00E-20
Regulation of mRNA Stability by Proteins that Bind AU-rich Elements	88	3.39	30	2.81E-21	4.80E-20
Mitotic Anaphase	198	7.62	42	1.50E-20	2.53E-19
Mitotic Metaphase and Anaphase	199	7.66	42	1.84E-20	3.07E-19
Cell Cycle, Mitotic	411	15.8	60	1.90E-20	3.14E-19
M Phase	233	8.97	44	2.10E-19	3.43E-18
Host Interactions of HIV factors	141	5.43	33	1.16E-17	1.88E-16
Cell Cycle	508	19.6	61	1.77E-16	2.82E-15
Downstream Signaling Events Of B Cell Receptor (BCR)	173	6.66	33	7.57E-15	1.19E-13
Adaptive Immune System	654	25.2	67	1.47E-14	2.29E-13
Signaling by the B Cell Receptor (BCR)	199	7.66	34	8.69E-14	1.34E-12

HIV Infection	214	8.24	35	1.41E-13	2.15E-12
Apoptosis	158	6.08	30	1.59E-13	2.39E-12
Immune System	1140	43.8	85	1.28E-10	1.91E-09
Downregulation of SMAD2/3:SMAD4 transcriptional activity	23	0.885	11	2.00E-10	2.94E-09
Metabolism of amino acids and derivatives	190	7.31	27	2.75E-09	4.02E-08
APC/C:Cdc20 mediated degradation of Cyclin B	29	1.12	11	4.15E-09	6.00E-08
Activation of the pre-replicative complex	32	1.23	11	1.40E-08	2.00E-07
G2/M Checkpoints	48	1.85	13	1.74E-08	2.47E-07
Oxygen-dependent Proline Hydroxylation of Hypoxia-inducible Factor Alpha	20	0.77	9	1.87E-08	2.62E-07
Unwinding of DNA	11	0.423	7	3.34E-08	4.64E-07
E2F mediated regulation of DNA replication	35	1.35	11	4.08E-08	5.60E-07
NOD1/2 Signaling Pathway	38	1.46	11	1.06E-07	1.44E-06
APC-Cdc20 mediated degradation of Nek2A	31	1.19	10	1.30E-07	1.75E-06
TRIF-mediated TLR3/TLR4 signaling	87	3.35	16	1.48E-07	1.98E-06
MyD88-independent cascade	88	3.39	16	1.75E-07	2.30E-06
Toll Like Receptor 3 (TLR3) Cascade	88	3.39	16	1.75E-07	2.30E-06
Phosphorylation of the APC/C	25	0.962	9	1.92E-07	2.49E-06
Activation of ATR in response to replication stress	41	1.58	11	2.51E-07	3.23E-06
Negative regulators of RIG-I/MDA5 signaling	33	1.27	10	2.54E-07	3.23E-06
Cellular responses to stress	27	1.04	9	4.11E-07	5.10E-06
Cellular response to hypoxia	27	1.04	9	4.11E-07	5.10E-06
Regulation of Hypoxia-inducible Factor (HIF) by Oxygen	27	1.04	9	4.11E-07	5.10E-06
Transcriptional activity of SMAD2/SMAD3:SMAD4 heterotrimer	43	1.66	11	4.27E-07	5.25E-06
Phosphorylation of Emi1	6	0.231	5	4.73E-07	5.76E-06
E2F-enabled inhibition of pre-replication complex formation	10	0.385	6	5.66E-07	6.84E-06
Endosomal Sorting Complex Required For Transport (ESCRT)	28	1.08	9	5.86E-07	7.02E-06
TAK1 activates NFkB by phosphorylation and activation of IKKs complex	22	0.847	8	8.65E-07	1.03E-05
Activated TLR4 signalling	100	3.85	16	1.07E-06	1.27E-05
RIG-I/MDA5 mediated induction of IFN-alpha/beta pathways	67	2.58	13	1.19E-06	1.39E-05

## MODULE 1

Pathway	Total	Expected	Hits	P.Value	FDR
Rho GTPase cycle	123	2.62	61	1.10E-73	7.70E-71
Signaling by Rho GTPases	123	2.62	61	1.10E-73	7.70E-71
G alpha (12/13) signalling events	80	1.7	29	3.51E-29	1.64E-26
NRAGE signals death through JNK	45	0.957	23	1.53E-27	5.36E-25
Signal Transduction	1690	35.9	96	9.56E-27	2.68E-24
p75 NTR receptor-mediated signalling	85	1.81	26	5.61E-24	1.31E-21
Cell death signalling via NRAGE, NRIF and NADE	62	1.32	23	1.65E-23	3.31E-21
Signalling by NGF	290	6.17	38	1.47E-20	2.58E-18
Axon guidance	292	6.21	32	5.28E-15	8.23E-13
Sema4D in semaphorin signaling	34	0.723	13	6.63E-14	9.29E-12
Sema4D induced cell migration and growth-cone collapse	29	0.617	12	2.04E-13	2.60E-11
Semaphorin interactions	72	1.53	16	1.11E-12	1.30E-10
Signaling by Robo receptor	34	0.723	12	1.97E-12	2.13E-10
Developmental Biology	417	8.87	33	2.04E-11	2.04E-09
GPVI-mediated activation cascade	33	0.702	11	3.54E-11	3.31E-09
Activation of Rac	15	0.319	8	1.95E-10	1.71E-08
Fcgamma receptor (FCGR) dependent phagocytosis	86	1.83	13	2.42E-08	1.99E-06
Smooth Muscle Contraction	25	0.532	8	2.74E-08	2.13E-06
CD28 co-stimulation	30	0.638	8	1.35E-07	9.99E-06
Hemostasis	511	10.9	29	7.36E-07	5.16E-05
Platelet activation, signaling and aggregation	220	4.68	18	7.80E-07	5.21E-05
Interleukin-3, 5 and GM-CSF signaling	51	1.08	9	9.83E-07	6.26E-05
GPCR downstream signaling	812	17.3	38	1.36E-06	8.31E-05
CD28 dependent Vav1 pathway	12	0.255	5	2.85E-06	0.000166
Regulation of signaling by CBL	22	0.468	6	4.69E-06	0.000263
Regulation of actin dynamics for phagocytic cup formation	62	1.32	9	5.37E-06	0.00029
Signaling by GPCR	931	19.8	40	5.82E-06	0.000302
DCC mediated attractive signaling	14	0.298	5	6.96E-06	0.000348
Downstream signal transduction	163	3.47	14	8.17E-06	0.000395

DAP12 signaling	164	3.49	14	8.77E-06	0.00041
Muscle contraction	52	1.11	8	1.17E-05	0.00053
DAP12 interactions	182	3.87	14	2.88E-05	0.00126
NGF signalling via TRKA from the plasma membrane	207	4.4	15	2.99E-05	0.00127
Signaling by PDGF	189	4.02	14	4.38E-05	0.00181
Costimulation by the CD28 family	68	1.45	8	8.65E-05	0.00346
Signaling by FGFR in disease	178	3.79	13	9.61E-05	0.00374
Signaling by EGFR	179	3.81	13	0.000102	0.00385
Signaling by EGFR in Cancer	181	3.85	13	0.000114	0.0042
Signaling by FGFR	162	3.45	12	0.000157	0.00566
Signaling by ERBB2	164	3.49	12	0.000177	0.0062
Cell-Cell communication	143	3.04	11	0.000214	0.00732
Innate Immune System	521	11.1	24	0.000227	0.00758
Interleukin-2 signaling	42	0.893	6	0.000232	0.00758
Interleukin receptor SHC signaling	28	0.595	5	0.000269	0.00856
Downstream signaling of activated FGFR	150	3.19	11	0.000325	0.0101
TGF-beta receptor signaling in EMT (epithelial to mesenchymal transition)	17	0.362	4	0.000376	0.0115
Regulation of PAK-2p34 activity by PS-GAP/RHG10	2	0.0425	2	0.000449	0.0134
Nef and signal transduction	8	0.17	3	0.000488	0.014
Sema4D mediated inhibition of cell attachment and migration	8	0.17	3	0.000488	0.014
Antigen Activates B Cell Receptor Leading to Generation of Second Messengers	32	0.681	5	0.000514	0.0144
Netrin-1 signaling	49	1.04	6	0.000548	0.0151
Synthesis of PIPs at the plasma membrane	33	0.702	5	0.000595	0.0161
Axonal growth inhibition (RHOA activation)	9	0.191	3	0.00072	0.0191
Signaling by Interleukins	116	2.47	9	0.000764	0.0198
Signaling by SCF-KIT	142	3.02	10	0.000837	0.0213
p75NTR regulates axonogenesis	10	0.213	3	0.00101	0.0249
Inactivation of Cdc42 and Rac	10	0.213	3	0.00101	0.0249
PLCG1 events in ERBB2 signaling	38	0.808	5	0.00116	0.028
Factors involved in megakaryocyte development and platelet production	155	3.3	10	0.00164	0.0389
GAB1 signalosome	106	2.25	8	0.00179	0.0412



PI3K/AKT activation	106	2.25	8	0.00179	0.0412
Integrin alphaIIb beta3 signaling	27	0.574	4	0.00235	0.0532
Constitutive PI3K/AKT Signaling in Cancer	89	1.89	7	0.00273	0.0608
G-protein beta:gamma signalling	30	0.638	4	0.0035	0.0766
FCGR activation	15	0.319	3	0.00355	0.0766
Striated Muscle Contraction	31	0.659	4	0.00395	0.0833
PI Metabolism	50	1.06	5	0.00398	0.0833
Sema3A PAK dependent Axon repulsion	16	0.34	3	0.0043	0.0875
Disinhibition of SNARE formation	5	0.106	2	0.00431	0.0875
Signaling by ERBB4	152	3.23	9	0.00493	0.0988
Regulation of KIT signaling	17	0.362	3	0.00515	0.102
PI3K events in ERBB4 signaling	103	2.19	7	0.00615	0.113
PIP3 activates AKT signaling	103	2.19	7	0.00615	0.113
PI-3K cascade	103	2.19	7	0.00615	0.113
PI3K/AKT Signaling in Cancer	103	2.19	7	0.00615	0.113
PI3K events in ERBB2 signaling	103	2.19	7	0.00615	0.113
Regulation of PLK1 Activity at G2/M Transition	6	0.128	2	0.00637	0.116
Platelet Aggregation (Plug Formation)	36	0.766	4	0.00681	0.122
Signaling by constitutively active EGFR	19	0.404	3	0.00711	0.125
CD28 dependent PI3K/Akt signaling	19	0.404	3	0.00711	0.125
Signalling to ERKs	37	0.787	4	0.00751	0.128
EGFR interacts with phospholipase C-gamma	37	0.787	4	0.00751	0.128
G alpha (z) signalling events	38	0.808	4	0.00826	0.14
Cell-cell junction organization	60	1.28	5	0.00867	0.145
Signaling by the B Cell Receptor (BCR)	199	4.23	10	0.00965	0.159
Cell junction organization	89	1.89	6	0.0114	0.186
GRB2 events in ERBB2 signaling	23	0.489	3	0.0122	0.197
CTLA4 inhibitory signaling	24	0.51	3	0.0137	0.217
Nephrin interactions	24	0.51	3	0.0137	0.217
EGFR Transactivation by Gastrin	9	0.191	2	0.0147	0.226
eNOS activation	9	0.191	2	0.0147	0.226

SHC1 events in ERBB2 signaling	25	0.532	3	0.0154	0.234
Signaling by TGF-beta Receptor Complex	70	1.49	5	0.0162	0.245
COPI Mediated Transport	10	0.213	2	0.0181	0.264
Golgi to ER Retrograde Transport	10	0.213	2	0.0181	0.264
GP1b-IX-V activation signalling	10	0.213	2	0.0181	0.264
Signalling to RAS	27	0.574	3	0.019	0.269
G beta:gamma signalling through PI3Kgamma	27	0.574	3	0.019	0.269
Role of phospholipids in phagocytosis	27	0.574	3	0.019	0.269
mTOR signalling	29	0.617	3	0.023	0.319
Tight junction interactions	29	0.617	3	0.023	0.319
PKB-mediated events	30	0.638	3	0.0251	0.346
Netrin mediated repulsion signals	12	0.255	2	0.0258	0.351
The role of Nef in HIV-1 replication and disease pathogenesis	31	0.659	3	0.0274	0.363
Trafficking of AMPA receptors	31	0.659	3	0.0274	0.363
Glutamate Binding, Activation of AMPA Receptors and Synaptic Plasticity	31	0.659	3	0.0274	0.363
p38MAPK events	13	0.276	2	0.03	0.386
PECAM1 interactions	13	0.276	2	0.03	0.386
Downregulation of ERBB2:ERBB3 signaling	13	0.276	2	0.03	0.386
Downstream Signaling Events Of B Cell Receptor (BCR)	173	3.68	8	0.0307	0.392
Gastrin-CREB signalling pathway via PKC and MAPK	209	4.44	9	0.0336	0.425
Immune System	1140	24.2	33	0.0342	0.429
GRB2 events in EGFR signaling	14	0.298	2	0.0346	0.429
IRS-mediated signalling	87	1.85	5	0.0373	0.454
Signal transduction by L1	35	0.744	3	0.0375	0.454
DAG and IP3 signaling	35	0.744	3	0.0375	0.454
SHC1 events in EGFR signaling	15	0.319	2	0.0393	0.467
GRB2:SOS provides linkage to MAPK signaling for Intergrins	15	0.319	2	0.0393	0.467
Activation, translocation and oligomerization of BAX	2	0.0425	1	0.0421	0.485
Activation and oligomerization of BAK protein	2	0.0425	1	0.0421	0.485

## MODULE 2

Pathway	Total	Expected	Hits	P.Value	FDR
Unfolded Protein Response	66	0.751	9	4.34E-08	6.09E-05
Activation of Chaperones by IRE1alpha	49	0.558	6	1.69E-05	0.0118
Mitochondrial Protein Import	59	0.672	6	4.97E-05	0.0135
Inflammasomes	19	0.216	4	5.28E-05	0.0135
Innate Immune System	521	5.93	17	5.66E-05	0.0135
Immune System	1140	13	27	7.45E-05	0.0135
Activation of Chaperones by ATF6-alpha	8	0.0911	3	7.62E-05	0.0135
Signaling by ERBB2	164	1.87	9	9.08E-05	0.0135
Interferon alpha/beta signaling	68	0.774	6	0.000111	0.0135
G2/M Transition	102	1.16	7	0.000146	0.0135
PI3K events in ERBB4 signaling	103	1.17	7	0.000155	0.0135
PIP3 activates AKT signaling	103	1.17	7	0.000155	0.0135
PI-3K cascade	103	1.17	7	0.000155	0.0135
PI3K/AKT Signaling in Cancer	103	1.17	7	0.000155	0.0135
PI3K events in ERBB2 signaling	103	1.17	7	0.000155	0.0135
Mitotic G2-G2/M phases	105	1.2	7	0.000175	0.0135
GAB1 signalosome	106	1.21	7	0.000185	0.0135
PI3K/AKT activation	106	1.21	7	0.000185	0.0135
Signaling by SCF-KIT	142	1.62	8	0.000191	0.0135
Signaling by EGFR in Cancer	181	2.06	9	0.000193	0.0135
Signaling by ERBB4	152	1.73	8	0.000305	0.0204
Nucleotide-binding domain, leucine rich repeat containing receptor (NLR) signaling pathways	55	0.626	5	0.000373	0.0238
The NLRP3 inflammasome	14	0.159	3	0.000471	0.0287
Cell Cycle	508	5.78	15	0.000497	0.029
Sema3A PAK dependent Axon repulsion	16	0.182	3	0.000713	0.0391
Downstream Signaling Events Of B Cell Receptor (BCR)	173	1.97	8	0.000726	0.0391
Polo-like kinase mediated events	4	0.0455	2	0.000756	0.0393
Trafficking and processing of endosomal TLR	17	0.194	3	0.000859	0.043
Activation of Chaperone Genes by ATF6-alpha	5	0.0569	2	0.00125	0.0605

Cytokine Signaling in Immune system	286	3.26	10	0.00138	0.0646
Downstream signaling of activated FGFR	150	1.71	7	0.0015	0.0679
Metabolism of proteins	689	7.84	17	0.00155	0.0681
Activation of Chaperone Genes by XBP1(S)	46	0.524	4	0.00176	0.074
Signaling by the B Cell Receptor (BCR)	199	2.27	8	0.00179	0.074
Activation of PKB	6	0.0683	2	0.00186	0.0746
Cell Cycle, Mitotic	411	4.68	12	0.00214	0.0834
Signaling by FGFR	162	1.84	7	0.00233	0.0884
Downstream signal transduction	163	1.86	7	0.00241	0.0891
DAP12 signaling	164	1.87	7	0.0025	0.0899
Post-transcriptional Silencing By Small RNAs	7	0.0797	2	0.00259	0.0907
Centrosome maturation	86	0.979	5	0.00284	0.0949
Recruitment of mitotic centrosome proteins and complexes	86	0.979	5	0.00284	0.0949
Constitutive PI3K/AKT Signaling in Cancer	89	1.01	5	0.0033	0.107
Interferon Signaling	173	1.97	7	0.00337	0.107
IRS-related events	90	1.02	5	0.00346	0.108
Signaling by FGFR in disease	178	2.03	7	0.00395	0.12
Signaling by EGFR	179	2.04	7	0.00407	0.121
eNOS activation	9	0.102	2	0.00437	0.123
Small Interfering RNA (siRNA) Biogenesis	9	0.102	2	0.00437	0.123
Insulin receptor signalling cascade	95	1.08	5	0.00437	0.123
DAP12 interactions	182	2.07	7	0.00446	0.123
Signaling by PDGF	189	2.15	7	0.00548	0.148
Loss of proteins required for interphase microtubule organizationVÇ-†from the centrosome	65	0.74	4	0.00621	0.161
Loss of Nlp from mitotic centrosomes	65	0.74	4	0.00621	0.161
Pre-NOTCH Transcription and Translation	12	0.137	2	0.00784	0.2
Intrinsic Pathway for Apoptosis	37	0.421	3	0.00834	0.208
NGF signalling via TRKA from the plasma membrane	207	2.36	7	0.00889	0.208
DAI mediated induction of type I IFNs	13	0.148	2	0.0092	0.208
AKT phosphorylates targets in the cytosol	13	0.148	2	0.0092	0.208
PERK regulated gene expression	13	0.148	2	0.0092	0.208

Downregulation of ERBB2:ERBB3 signaling	13	0.148	2	0.0092	0.208
Tetrahydrobiopterin (BH4) synthesis, recycling, salvage and regulation	13	0.148	2	0.0092	0.208
Signaling by Insulin receptor	117	1.33	5	0.0104	0.231
Cyclin A/B1 associated events during G2/M transition	14	0.159	2	0.0106	0.231
PI3K Cascade	76	0.865	4	0.0107	0.231
t(4;14) translocations of FGFR3	1	0.0114	1	0.0114	0.242
Toll-Like Receptors Cascades	123	1.4	5	0.0128	0.267
Interleukin-1 signaling	45	0.512	3	0.0143	0.294
Activation of BAD and translocation to mitochondria	17	0.194	2	0.0156	0.312
TRAF6 mediated IRF7 activation in TLR7/8 or 9 signaling	17	0.194	2	0.0156	0.312
IRS-mediated signalling	87	0.99	4	0.0169	0.334
GABA synthesis, release, reuptake and degradation	18	0.205	2	0.0174	0.339
Cytosolic sensors of pathogen-associated DNA	19	0.216	2	0.0193	0.361
Signaling by constitutively active EGFR	19	0.216	2	0.0193	0.361
CD28 dependent PI3K/Akt signaling	19	0.216	2	0.0193	0.361
IRS-related events triggered by IGF1R	91	1.04	4	0.0197	0.363
Metabolism of nitric oxide	20	0.228	2	0.0213	0.378
eNOS activation and regulation	20	0.228	2	0.0213	0.378
Signaling by Type 1 Insulin-like Growth Factor 1 Receptor (IGF1R)	94	1.07	4	0.0219	0.378
IGF1R signaling cascade	94	1.07	4	0.0219	0.378
PDE3B signalling	2	0.0228	1	0.0226	0.378
Inhibition of HSL	2	0.0228	1	0.0226	0.378
Telomere Extension By Telomerase	2	0.0228	1	0.0226	0.378
NOSIP mediated eNOS trafficking	2	0.0228	1	0.0226	0.378
Pre-NOTCH Expression and Processing	22	0.25	2	0.0255	0.421
Activation of BH3-only proteins	24	0.273	2	0.03	0.478
Cytosolic tRNA aminoacylation	24	0.273	2	0.03	0.478
CTLA4 inhibitory signaling	24	0.273	2	0.03	0.478
MicroRNA (miRNA) Biogenesis	25	0.285	2	0.0324	0.504
IRF3 mediated activation of type 1 IFN	3	0.0341	1	0.0338	0.504
Formation of apoptosome	3	0.0341	1	0.0338	0.504

Inhibition of TSC complex formation by PKB	3	0.0341	1	0.0338	0.504
The NLRP1 inflammasome	3	0.0341	1	0.0338	0.504
Localization of the PINCH-ILK-PARVIN complex to focal adhesions	3	0.0341	1	0.0338	0.504
Integrin alphaIIb beta3 signaling	27	0.307	2	0.0374	0.535
G beta:gamma signalling through PI3Kgamma	27	0.307	2	0.0374	0.535
Nitric oxide stimulates guanylate cyclase	27	0.307	2	0.0374	0.535
Cyclin E associated events during G1/S transition	65	0.74	3	0.0374	0.535
Regulatory RNA pathways	28	0.319	2	0.0399	0.566
RIG-I/MDA5 mediated induction of IFN-alpha/beta pathways	67	0.763	3	0.0404	0.566
Antiviral mechanism by IFN-stimulated genes	69	0.785	3	0.0435	0.594
ISG15 antiviral mechanism	69	0.785	3	0.0435	0.594
G2/M DNA replication checkpoint	4	0.0455	1	0.0448	0.594
SHC activation	4	0.0455	1	0.0448	0.594
AKT-mediated inactivation of FOXO1A	4	0.0455	1	0.0448	0.594
CD28 co-stimulation	30	0.341	2	0.0453	0.594
G-protein beta:gamma signalling	30	0.341	2	0.0453	0.594
Signalling by NGF	290	3.3	7	0.0461	0.598
Semaphorin interactions	72	0.82	3	0.0483	0.622

## MODULE 3

Pathway	Total	Expected	Hits	P.Value	FDR
Integrin cell surface interactions	85	1.77	37	2.73E-41	3.83E-38
Hemostasis	511	10.6	54	1.34E-25	9.37E-23
Platelet degranulation	89	1.85	25	2.77E-22	1.29E-19
Platelet activation, signaling and aggregation	220	4.58	35	4.26E-22	1.49E-19
Response to elevated platelet cytosolic Ca <sup>2+</sup>	94	1.96	25	1.24E-21	3.49E-19
Regulation of Insulin-like Growth Factor (IGF) Transport and Uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs)	21	0.437	13	1.38E-17	3.23E-15
Extracellular matrix organization	157	3.27	25	7.12E-16	1.43E-13
Cell surface interactions at the vascular wall	99	2.06	20	6.28E-15	1.10E-12
Signal Transduction	1690	35.1	74	1.03E-12	1.60E-10
Integrin alphaIIb beta3 signaling	27	0.562	11	2.10E-12	2.94E-10
Platelet Aggregation (Plug Formation)	36	0.749	11	8.24E-11	1.05E-08
GRB2:SOS provides linkage to MAPK signaling for Intergrins	15	0.312	8	1.64E-10	1.77E-08
p130Cas linkage to MAPK signaling for integrins	15	0.312	8	1.64E-10	1.77E-08
Axon guidance	292	6.08	25	1.02E-09	1.02E-07
Developmental Biology	417	8.68	30	1.19E-09	1.11E-07
Degradation of collagen	61	1.27	12	3.00E-09	2.63E-07
Degradation of the extracellular matrix	77	1.6	13	4.62E-09	3.72E-07
Cell-Cell communication	143	2.98	17	4.78E-09	3.72E-07
Assembly of collagen fibrils and other multimeric structures	54	1.12	11	9.54E-09	7.04E-07
Collagen formation	85	1.77	13	1.61E-08	1.13E-06
Elastic fibre formation	45	0.937	10	1.89E-08	1.26E-06
Molecules associated with elastic fibres	38	0.791	9	5.53E-08	3.52E-06
L1CAM interactions	112	2.33	14	6.26E-08	3.82E-06
Signaling by PDGF	189	3.93	17	3.11E-07	1.82E-05
Signal transduction by L1	35	0.729	8	4.22E-07	2.37E-05
Signaling by VEGF	10	0.208	5	8.43E-07	4.38E-05
VEGF ligand-receptor interactions	10	0.208	5	8.43E-07	4.38E-05
FasL/ CD95L signaling	5	0.104	4	8.85E-07	4.43E-05
SHC-related events triggered by IGF1R	18	0.375	6	1.10E-06	5.34E-05

Common Pathway	11	0.229	5	1.52E-06	7.10E-05
Tie2 Signaling	20	0.416	6	2.23E-06	0.000101
Collagen biosynthesis and modifying enzymes	62	1.29	9	4.51E-06	0.000197
Nephrin interactions	24	0.5	6	7.22E-06	0.000307
Fibronectin matrix formation	3	0.0625	3	8.83E-06	0.000364
VEGF binds to VEGFR leading to receptor dimerization	8	0.167	4	1.18E-05	0.00046
CHL1 interactions	8	0.167	4	1.18E-05	0.00046
Signal attenuation	16	0.333	5	1.32E-05	0.000501
Dimerization of procaspase-8	9	0.187	4	2.09E-05	0.000751
Caspase-8 activation	9	0.187	4	2.09E-05	0.000751
Formation of Fibrin Clot (Clotting Cascade)	29	0.604	6	2.34E-05	0.00082
Death Receptor Signalling	12	0.25	4	7.82E-05	0.00255
Platelet Adhesion to exposed collagen	12	0.25	4	7.82E-05	0.00255
Extrinsic Pathway for Apoptosis	12	0.25	4	7.82E-05	0.00255
Apoptosis	158	3.29	12	0.000101	0.00322
Caspase-mediated cleavage of cytoskeletal proteins	13	0.271	4	0.000111	0.00346
Signaling by Type 1 Insulin-like Growth Factor 1 Receptor (IGF1R)	94	1.96	9	0.000134	0.00401
IGF1R signaling cascade	94	1.96	9	0.000134	0.00401
DCC mediated attractive signaling	14	0.291	4	0.000153	0.00447
Apoptotic execution phase	57	1.19	7	0.000162	0.00462
Anchoring fibril formation	15	0.312	4	0.000205	0.00576
Apoptotic cleavage of cellular proteins	43	0.895	6	0.000236	0.00637
Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell	80	1.67	8	0.000236	0.00637
NGF signalling via TRKA from the plasma membrane	207	4.31	13	0.000349	0.00923
SHC-related events	18	0.375	4	0.000439	0.0114
Netrin-1 signaling	49	1.02	6	0.000489	0.0125
GPVI-mediated activation cascade	33	0.687	5	0.00054	0.0135
Downstream signal transduction	163	3.39	11	0.000551	0.0136
Interleukin-3, 5 and GM-CSF signaling	51	1.06	6	0.000609	0.0147
Signal regulatory protein (SIRP) family interactions	20	0.416	4	0.000672	0.016
Semaphorin interactions	72	1.5	7	0.000694	0.0162



Insulin receptor signalling cascade	95	1.98	8	0.000763	0.0175
Signalling to ERKs	37	0.77	5	0.000928	0.021
Regulation of signaling by CBL	22	0.458	4	0.000983	0.0219
Signaling by EGFR	179	3.73	11	0.0012	0.0263
Signaling by EGFR in Cancer	181	3.77	11	0.00131	0.0284
GAB1 signalosome	106	2.21	8	0.00156	0.0332
Netrin mediated repulsion signals	12	0.25	3	0.00169	0.0354
DAP12 signaling	164	3.41	10	0.00212	0.0438
Constitutive PI3K/AKT Signaling in Cancer	89	1.85	7	0.00242	0.0492
SHC activation	4	0.0833	2	0.00251	0.0496
Neurophilin interactions with VEGF and VEGFR	4	0.0833	2	0.00251	0.0496
SEMA3A-Plexin repulsion signaling by inhibiting Integrin adhesion	14	0.291	3	0.00272	0.0514
Signaling by SCF-KIT	142	2.96	9	0.00272	0.0514
Signalling by NGF	290	6.04	14	0.00273	0.0514
IRS-related events triggered by IGF1R	91	1.89	7	0.00275	0.0514
Signaling by Insulin receptor	117	2.44	8	0.00292	0.0539
SHC-mediated signalling	15	0.312	3	0.00334	0.0609
Activation of Matrix Metalloproteinases	31	0.645	4	0.00366	0.0657
Downstream signaling of activated FGFR	150	3.12	9	0.00393	0.0697
Basigin interactions	32	0.666	4	0.00411	0.0715
TRAIL signaling	5	0.104	2	0.00413	0.0715
Signaling by ERBB4	152	3.16	9	0.00428	0.0728
Muscle contraction	52	1.08	5	0.00431	0.0728
DAP12 interactions	182	3.79	10	0.00451	0.0753
PI3K events in ERBB4 signaling	103	2.14	7	0.00548	0.0863
PIP3 activates AKT signaling	103	2.14	7	0.00548	0.0863
PI-3K cascade	103	2.14	7	0.00548	0.0863
PI3K/AKT Signaling in Cancer	103	2.14	7	0.00548	0.0863
PI3K events in ERBB2 signaling	103	2.14	7	0.00548	0.0863
PI3K/AKT activation	106	2.21	7	0.0064	0.0997
Signaling by FGFR	162	3.37	9	0.00648	0.0999

Signaling by ERBB2	164	3.41	9	0.00701	0.107
TNF signaling	7	0.146	2	0.00844	0.127
Fcgamma receptor (FCGR) dependent phagocytosis	86	1.79	6	0.00879	0.131
SHC1 events in ERBB4 signaling	21	0.437	3	0.00892	0.132
Regulation of actin dynamics for phagocytic cup formation	62	1.29	5	0.0091	0.133
Signaling by Interleukins	116	2.41	7	0.0103	0.148
Cell junction organization	89	1.85	6	0.0103	0.148
NCAM signaling for neurite out-growth	65	1.35	5	0.0111	0.154
Cross-presentation of particulate exogenous antigens (phagosomes)	8	0.167	2	0.0111	0.154
Sema4D mediated inhibition of cell attachment and migration	8	0.167	2	0.0111	0.154
Innate Immune System	521	10.8	19	0.0112	0.154
Signaling by FGFR in disease	178	3.71	9	0.0117	0.159
Costimulation by the CD28 family	68	1.42	5	0.0133	0.179
SHC1 events in ERBB2 signaling	25	0.52	3	0.0145	0.192
Smooth Muscle Contraction	25	0.52	3	0.0145	0.192
Adaptive Immune System	654	13.6	22	0.0157	0.205
Dissolution of Fibrin Clot	10	0.208	2	0.0174	0.223
Dermatan sulfate biosynthesis	10	0.208	2	0.0174	0.223
Signalling to RAS	27	0.562	3	0.0179	0.226
A tetrasaccharide linker sequence is required for GAG synthesis	27	0.562	3	0.0179	0.226
SHC-mediated cascade	28	0.583	3	0.0198	0.245
Interleukin receptor SHC signaling	28	0.583	3	0.0198	0.245
Crosslinking of collagen fibrils	11	0.229	2	0.0209	0.253
TRIF-mediated programmed cell death	11	0.229	2	0.0209	0.253
DSCAM interactions	11	0.229	2	0.0209	0.253
Signaling by the B Cell Receptor (BCR)	199	4.14	9	0.0227	0.271
CD28 co-stimulation	30	0.625	3	0.0238	0.283
CD28 dependent Vav1 pathway	12	0.25	2	0.0248	0.285
Type I hemidesmosome assembly	12	0.25	2	0.0248	0.285

## MODULE 4

Pathway	Total	Expected	Hits	P.Value	FDR
NGF signalling via TRKA from the plasma membrane	207	2.82	30	1.31E-23	1.84E-20
G2/M Transition	102	1.39	23	1.17E-22	8.18E-20
Mitotic G2-G2/M phases	105	1.43	23	2.40E-22	1.12E-19
Signaling by FGFR	162	2.21	26	1.43E-21	5.00E-19
Signaling by FGFR in disease	178	2.43	26	1.73E-20	4.85E-18
Signalling by NGF	290	3.95	31	2.35E-20	5.48E-18
Signalling to ERKs	37	0.504	15	2.30E-19	4.61E-17
SOS-mediated signalling	14	0.191	11	5.70E-19	9.99E-17
Cell Cycle, Mitotic	411	5.6	34	8.08E-19	1.26E-16
Cell Cycle	508	6.92	37	1.03E-18	1.45E-16
Downstream signaling of activated FGFR	150	2.04	23	1.28E-18	1.63E-16
Signalling to RAS	27	0.368	13	3.97E-18	4.51E-16
Loss of proteins required for interphase microtubule organization	65	0.886	17	4.50E-18	4.51E-16
Loss of Nlp from mitotic centrosomes	65	0.886	17	4.50E-18	4.51E-16
Signaling by EGFR	179	2.44	24	5.14E-18	4.81E-16
Signaling by SCF-KIT	142	1.94	22	6.35E-18	5.22E-16
ARMS-mediated activation	16	0.218	11	6.69E-18	5.22E-16
Signaling by EGFR in Cancer	181	2.47	24	6.71E-18	5.22E-16
Downstream signal transduction	163	2.22	23	8.80E-18	6.49E-16
Signaling by ERBB2	164	2.24	23	1.01E-17	6.76E-16
DAP12 signaling	164	2.24	23	1.01E-17	6.76E-16
Centrosome maturation	86	1.17	18	3.33E-17	2.03E-15
Recruitment of mitotic centrosome proteins and complexes	86	1.17	18	3.33E-17	2.03E-15
Frs2-mediated activation	18	0.245	11	4.77E-17	2.79E-15
RAF/MAP kinase cascade	10	0.136	9	1.07E-16	5.91E-15
DAP12 interactions	182	2.48	23	1.10E-16	5.91E-15
Prolonged ERK activation events	20	0.273	11	2.46E-16	1.28E-14
Signaling by PDGF	189	2.58	23	2.58E-16	1.29E-14
Signalling to p38 via RIT and RIN	15	0.204	10	3.79E-16	1.83E-14

Rap1 signalling	17	0.232	10	2.40E-15	1.12E-13
Signaling by ERBB4	152	2.07	20	6.53E-15	2.96E-13
IRS-mediated signalling	87	1.19	16	1.97E-14	8.64E-13
GRB2 events in EGFR signaling	14	0.191	9	2.05E-14	8.72E-13
IRS-related events	90	1.23	16	3.46E-14	1.43E-12
IRS-related events triggered by IGF1R	91	1.24	16	4.15E-14	1.66E-12
SHC-mediated signalling	15	0.204	9	5.08E-14	1.92E-12
SHC1 events in EGFR signaling	15	0.204	9	5.08E-14	1.92E-12
RAF phosphorylates MEK	7	0.0954	7	6.92E-14	2.42E-12
MEK activation	7	0.0954	7	6.92E-14	2.42E-12
Signaling by Type 1 Insulin-like Growth Factor 1 Receptor (IGF1R)	94	1.28	16	7.08E-14	2.42E-12
IGF1R signaling cascade	94	1.28	16	7.08E-14	2.42E-12
Insulin receptor signalling cascade	95	1.29	16	8.43E-14	2.81E-12
SHC-related events	18	0.245	9	4.77E-13	1.52E-11
SHC-related events triggered by IGF1R	18	0.245	9	4.77E-13	1.52E-11
Signaling by Insulin receptor	117	1.59	16	2.43E-12	7.56E-11
SHC1 events in ERBB4 signaling	21	0.286	9	2.79E-12	8.50E-11
Immune System	1140	15.5	44	3.85E-12	1.15E-10
Translocation of GLUT4 to the Plasma Membrane	71	0.968	13	7.09E-12	2.07E-10
GRB2 events in ERBB2 signaling	23	0.313	9	7.58E-12	2.17E-10
SHC1 events in ERBB2 signaling	25	0.341	9	1.85E-11	5.20E-10
Activation of BAD and translocation to mitochondria	17	0.232	8	1.92E-11	5.27E-10
Adaptive Immune System	654	8.91	32	3.44E-11	9.28E-10
Innate Immune System	521	7.1	28	1.00E-10	2.65E-09
p38MAPK events	13	0.177	7	1.11E-10	2.88E-09
Interleukin-2 signaling	42	0.572	10	1.37E-10	3.50E-09
RAF activation	5	0.0681	5	4.21E-10	1.05E-08
Activation of BH3-only proteins	24	0.327	8	5.36E-10	1.32E-08
Intrinsic Pathway for Apoptosis	37	0.504	9	9.87E-10	2.39E-08
FRS2-mediated cascade	39	0.532	9	1.65E-09	3.91E-08
Signaling by Interleukins	116	1.58	13	4.09E-09	9.57E-08

G2/M Checkpoints	48	0.654	9	1.18E-08	2.71E-07
Regulation of mRNA Stability by Proteins that Bind AU-rich Elements	88	1.2	11	2.21E-08	4.99E-07
Disease	945	12.9	34	2.62E-08	5.84E-07
MAP kinase activation in TLR cascade	55	0.75	9	4.13E-08	9.05E-07
Signaling by the B Cell Receptor (BCR)	199	2.71	15	5.73E-08	1.22E-06
Activation of ATR in response to replication stress	41	0.559	8	5.77E-08	1.22E-06
Downstream Signaling Events Of B Cell Receptor (BCR)	173	2.36	14	6.83E-08	1.43E-06
Mitotic M-M/G1 phases	266	3.63	17	7.79E-08	1.61E-06
TRAF6 Mediated Induction of proinflammatory cytokines	62	0.845	9	1.22E-07	2.48E-06
ERK activation	5	0.0681	4	1.60E-07	3.20E-06
Signal Transduction	1690	23	46	1.66E-07	3.28E-06
NCAM signaling for neurite out-growth	65	0.886	9	1.86E-07	3.62E-06
Cytokine Signaling in Immune system	286	3.9	17	2.23E-07	4.29E-06
Constitutive PI3K/AKT Signaling in Cancer	89	1.21	10	2.82E-07	5.33E-06
Resolution of Sister Chromatid Cohesion	118	1.61	11	4.73E-07	8.84E-06
Toll Like Receptor 10 (TLR10) Cascade	74	1.01	9	5.81E-07	1.04E-05
Toll Like Receptor 5 (TLR5) Cascade	74	1.01	9	5.81E-07	1.04E-05
MyD88 cascade initiated on plasma membrane	74	1.01	9	5.81E-07	1.04E-05
Nuclear Events (kinase and transcription factor activation)	24	0.327	6	6.00E-07	1.06E-05
TRAF6 mediated induction of NFkB and MAP kinases upon TLR7/8 or 9 activation	76	1.04	9	7.32E-07	1.28E-05
Toll Like Receptor 7/8 (TLR7/8) Cascade	77	1.05	9	8.20E-07	1.40E-05
MyD88 dependent cascade initiated on endosome	77	1.05	9	8.20E-07	1.40E-05
Mitotic Prometaphase	127	1.73	11	9.94E-07	1.68E-05
Toll Like Receptor 9 (TLR9) Cascade	79	1.08	9	1.02E-06	1.71E-05
PI3K events in ERBB4 signaling	103	1.4	10	1.12E-06	1.76E-05
PIP3 activates AKT signaling	103	1.4	10	1.12E-06	1.76E-05
PI-3K cascade	103	1.4	10	1.12E-06	1.76E-05
PI3K/AKT Signaling in Cancer	103	1.4	10	1.12E-06	1.76E-05
PI3K events in ERBB2 signaling	103	1.4	10	1.12E-06	1.76E-05
MyD88:Mal cascade initiated on plasma membrane	81	1.1	9	1.27E-06	1.91E-05
Toll Like Receptor TLR1:TLR2 Cascade	81	1.1	9	1.27E-06	1.91E-05

Toll Like Receptor TLR6:TLR2 Cascade	81	1.1	9	1.27E-06	1.91E-05
Toll Like Receptor 2 (TLR2) Cascade	81	1.1	9	1.27E-06	1.91E-05
Cell Cycle Checkpoints	131	1.79	11	1.36E-06	2.02E-05
GAB1 signalosome	106	1.44	10	1.46E-06	2.13E-05
PI3K/AKT activation	106	1.44	10	1.46E-06	2.13E-05
TRIF-mediated TLR3/TLR4 signaling	87	1.19	9	2.33E-06	3.37E-05
Developmental Biology	417	5.68	19	2.39E-06	3.42E-05
Processing of DNA double-strand break ends	3	0.0409	3	2.45E-06	3.47E-05
MAPK targets/ Nuclear events mediated by MAP kinases	30	0.409	6	2.48E-06	3.47E-05
MyD88-independent cascade	88	1.2	9	2.57E-06	3.53E-05
Toll Like Receptor 3 (TLR3) Cascade	88	1.2	9	2.57E-06	3.53E-05
M Phase	233	3.18	14	2.63E-06	3.57E-05
Membrane Trafficking	203	2.77	13	3.07E-06	4.14E-05
Hemostasis	511	6.96	21	3.36E-06	4.48E-05
EGFR Transactivation by Gastrin	9	0.123	4	3.86E-06	5.11E-05
Activation of the AP-1 family of transcription factors	10	0.136	4	6.37E-06	8.35E-05
ERK/MAPK targets	21	0.286	5	7.21E-06	9.36E-05
Activated TLR4 signalling	100	1.36	9	7.48E-06	9.63E-05
Apoptosis	158	2.15	11	8.51E-06	0.000108
Toll Like Receptor 4 (TLR4) Cascade	103	1.4	9	9.55E-06	0.000121
AKT phosphorylates targets in the cytosol	13	0.177	4	2.10E-05	0.000263
Recruitment of NuMA to mitotic centrosomes	26	0.354	5	2.21E-05	0.000274
Activation of RAS in B Cells	5	0.0681	3	2.40E-05	0.00029
Assembly of the RAD51-ssDNA nucleoprotein complex	5	0.0681	3	2.40E-05	0.00029
Cyclin B2 mediated events	5	0.0681	3	2.40E-05	0.00029
Axon guidance	292	3.98	14	3.50E-05	0.000419
Repair synthesis of patch ~27-30 bases long by DNA polymerase	15	0.204	4	3.93E-05	0.000462
Repair synthesis for gap-filling by DNA polymerase in TC-NER	15	0.204	4	3.93E-05	0.000462
Separation of Sister Chromatids	186	2.53	11	3.96E-05	0.000462

## MODULE 5

Pathway	Total	Expected	Hits	P.Value	FDR
Protein folding	56	0.453	22	1.20E-33	1.69E-30
Cooperation of Prefoldin and TriC/CCT in actin and tubulin folding	30	0.243	18	7.42E-32	5.20E-29
Prefoldin mediated transfer of substrate to CCT/TriC	29	0.235	17	8.00E-30	3.74E-27
Chaperonin-mediated protein folding	51	0.412	18	2.15E-26	7.53E-24
Fcgamma receptor (FCGR) dependent phagocytosis	86	0.696	20	3.43E-25	9.63E-23
Regulation of actin dynamics for phagocytic cup formation	62	0.501	17	9.58E-23	2.24E-20
Formation of tubulin folding intermediates by CCT/TriC	23	0.186	13	1.44E-22	2.88E-20
Post-chaperonin tubulin folding pathway	20	0.162	10	8.64E-17	1.49E-14
Folding of actin by CCT/TriC	9	0.0728	8	9.54E-17	1.49E-14
Innate Immune System	521	4.21	22	2.03E-11	2.85E-09
Translocation of GLUT4 to the Plasma Membrane	71	0.574	10	1.59E-10	2.02E-08
Immune System	1140	9.2	29	8.03E-10	9.38E-08
Microtubule-dependent trafficking of connexons from Golgi to the plasma membrane	16	0.129	6	1.58E-09	1.71E-07
Association of TriC/CCT with target proteins during biosynthesis	29	0.235	7	2.06E-09	2.06E-07
Transport of connexons to the plasma membrane	17	0.137	6	2.43E-09	2.27E-07
Metabolism of proteins	689	5.57	22	4.59E-09	4.02E-07
Recruitment of NuMA to mitotic centrosomes	26	0.21	6	4.28E-08	3.40E-06
Gap junction trafficking	44	0.356	7	4.61E-08	3.40E-06
Recycling pathway of L1	44	0.356	7	4.61E-08	3.40E-06
Gap junction trafficking and regulation	46	0.372	7	6.36E-08	4.46E-06
Gap junction assembly	33	0.267	6	1.97E-07	1.32E-05
Kinesins	41	0.332	6	7.62E-07	4.85E-05
Membrane Trafficking	203	1.64	10	4.02E-06	0.000245
L1CAM interactions	112	0.906	7	2.86E-05	0.00167
MHC class II antigen presentation	118	0.954	7	4.01E-05	0.00216
Resolution of Sister Chromatid Cohesion	118	0.954	7	4.01E-05	0.00216
Centrosome maturation	86	0.696	6	6.03E-05	0.00302
Recruitment of mitotic centrosome proteins and complexes	86	0.696	6	6.03E-05	0.00302
Mitotic Prometaphase	127	1.03	7	6.43E-05	0.00311

Axon guidance	292	2.36	10	9.48E-05	0.00443
G2/M Transition	102	0.825	6	0.000156	0.00707
Mitotic G2-G2/M phases	105	0.849	6	0.000183	0.00804
Factors involved in megakaryocyte development and platelet production	155	1.25	7	0.000225	0.00955
Separation of Sister Chromatids	186	1.5	7	0.00068	0.028
Mitotic Anaphase	198	1.6	7	0.000985	0.0394
Mitotic Metaphase and Anaphase	199	1.61	7	0.00101	0.0395
Role of phospholipids in phagocytosis	27	0.218	3	0.00128	0.0483
Synthesis of PG	7	0.0566	2	0.00131	0.0485
Developmental Biology	417	3.37	10	0.00162	0.0582
M Phase	233	1.88	7	0.00252	0.0882
Hormone-sensitive lipase (HSL)-mediated triacylglycerol hydrolysis	12	0.097	2	0.00402	0.138
Mitotic M-M/G1 phases	266	2.15	7	0.00524	0.175
Muscle contraction	52	0.421	3	0.00836	0.272
Signaling by TGF-beta Receptor Complex	70	0.566	3	0.0187	0.596
Downregulation of TGF-beta receptor signaling	27	0.218	2	0.0198	0.613
Hemostasis	511	4.13	9	0.0201	0.613
Synthesis of PA	28	0.226	2	0.0212	0.633
Sema4D induced cell migration and growth-cone collapse	29	0.235	2	0.0227	0.662
TGF-beta receptor signaling activates SMADs	30	0.243	2	0.0242	0.691
Striated Muscle Contraction	31	0.251	2	0.0257	0.721
Sema4D in semaphorin signaling	34	0.275	2	0.0305	0.839
Lipid digestion, mobilization, and transport	41	0.332	2	0.0431	1
Cell Cycle, Mitotic	411	3.32	7	0.0462	1



## MODULE 6

Pathway	Total	Expected	Hits	P.Value	FDR
Class A/1 (Rhodopsin-like receptors)	312	1.68	10	3.69E-06	0.00517
GPCR ligand binding	415	2.24	10	4.54E-05	0.021
G alpha (i) signalling events	184	0.992	7	4.57E-05	0.021
Peptide ligand-binding receptors	192	1.04	7	5.99E-05	0.021
Amyloids	84	0.453	5	7.76E-05	0.0217
Signal Transduction	1690	9.1	19	0.000363	0.0849
p75 NTR receptor-mediated signalling	85	0.458	4	0.00106	0.212
Apoptotic cleavage of cellular proteins	43	0.232	3	0.00153	0.268
Caspase-mediated cleavage of cytoskeletal proteins	13	0.0701	2	0.00212	0.298
Apoptotic cleavage of cell adhesion proteins	13	0.0701	2	0.00212	0.298
NRIF signals cell death from the nucleus	15	0.0809	2	0.00284	0.362
G alpha (q) signalling events	188	1.01	5	0.00311	0.364
Apoptotic execution phase	57	0.307	3	0.00345	0.372
Cell death signalling via NRAGE, NRIF and NADE	62	0.334	3	0.00438	0.438
Gastrin-CREB signalling pathway via PKC and MAPK	209	1.13	5	0.0049	0.438
Cell-Cell communication	143	0.771	4	0.00698	0.438
Signaling by NOTCH1 t(7;9)(NOTCH1:M1580_K2555) Translocation Mutant	74	0.399	3	0.00718	0.438
Signaling by NOTCH1 in Cancer	74	0.399	3	0.00718	0.438
Signaling by NOTCH1 PEST Domain Mutants in Cancer	74	0.399	3	0.00718	0.438
FBXW7 Mutants and NOTCH1 in Cancer	74	0.399	3	0.00718	0.438
Signaling by NOTCH1 HD Domain Mutants in Cancer	74	0.399	3	0.00718	0.438
Signaling by NOTCH1 HD+PEST Domain Mutants in Cancer	74	0.399	3	0.00718	0.438
Signaling by NOTCH1	74	0.399	3	0.00718	0.438
GPCR downstream signaling	812	4.38	10	0.00879	0.514
Apoptosis	158	0.852	4	0.00986	0.52
Activated NOTCH1 Transmits Signal to the Nucleus	29	0.156	2	0.0105	0.52
G-protein activation	29	0.156	2	0.0105	0.52
Translesion synthesis by Pol zeta	2	0.0108	1	0.0108	0.52
Stimulation of the cell death response by PAK-2p34	2	0.0108	1	0.0108	0.52

Adherens junctions interactions	31	0.167	2	0.0119	0.557
Signaling by NOTCH	95	0.512	3	0.0142	0.642
Activation of BIM and translocation to mitochondria	3	0.0162	1	0.0161	0.684
Activation of BMF and translocation to mitochondria	3	0.0162	1	0.0161	0.684
Intrinsic Pathway for Apoptosis	37	0.199	2	0.0167	0.69
Signalling by NGF	290	1.56	5	0.0186	0.747
Cyclin D associated events in G1	41	0.221	2	0.0203	0.769
G1 Phase	41	0.221	2	0.0203	0.769
DNA Damage Bypass	4	0.0216	1	0.0214	0.769
Translesion synthesis by DNA polymerases bypassing lesion on DNA template	4	0.0216	1	0.0214	0.769
Signaling by GPCR	931	5.02	10	0.0219	0.769
Disease	945	5.1	10	0.0241	0.813
SMAC-mediated dissociation of IAP:caspase complexes	5	0.027	1	0.0267	0.813
SMAC-mediated apoptotic response	5	0.027	1	0.0267	0.813
Activation of caspases through apoptosome-mediated cleavage	5	0.027	1	0.0267	0.813
SMAC binds to IAPs	5	0.027	1	0.0267	0.813
Cytochrome c-mediated apoptotic response	5	0.027	1	0.0267	0.813
Constitutive Signaling by NOTCH1 HD+PEST Domain Mutants	52	0.28	2	0.0317	0.914
p75NTR negatively regulates cell cycle via SC1	6	0.0323	1	0.0319	0.914
Formyl peptide receptors bind formyl peptides and many other ligands	6	0.0323	1	0.0319	0.914
Apoptotic factor-mediated response	7	0.0377	1	0.0372	1
Neurotransmitter Clearance In The Synaptic Cleft	7	0.0377	1	0.0372	1
NADE modulates death signalling	7	0.0377	1	0.0372	1
Constitutive Signaling by NOTCH1 PEST Domain Mutants	59	0.318	2	0.0399	1
Cell-cell junction organization	60	0.323	2	0.0411	1
Peptide hormone metabolism	60	0.323	2	0.0411	1
Lysosphingolipid and LPA receptors	8	0.0431	1	0.0423	1
TRAF6 Mediated Induction of proinflammatory cytokines	62	0.334	2	0.0437	1
A third proteolytic cleavage releases NICD	9	0.0485	1	0.0475	1
Peptide hormone biosynthesis	9	0.0485	1	0.0475	1
Relaxin receptors	9	0.0485	1	0.0475	1

Role of Abl in Robo-Slit signaling

9    0.0485    1    0.0475    1

## MODULE 7

Pathway	Total	Expected	Hits	P.Value	FDR
Lipoprotein metabolism	22	0.119	13	1.34E-25	1.88E-22
Lipid digestion, mobilization, and transport	41	0.221	13	4.47E-21	3.13E-18
HDL-mediated lipid transport	13	0.0701	9	9.18E-19	4.29E-16
Retinoid metabolism and transport	41	0.221	10	5.29E-15	1.86E-12
Chylomicron-mediated lipid transport	12	0.0647	7	5.54E-14	1.55E-11
Visual phototransduction	56	0.302	10	1.59E-13	3.72E-11
Diseases associated with visual transduction	57	0.307	10	1.93E-13	3.86E-11
Scavenging of Heme from Plasma	15	0.0809	5	9.86E-09	1.54E-06
Binding and Uptake of Ligands by Scavenger Receptors	15	0.0809	5	9.86E-09	1.54E-06
Metabolism of lipids and lipoproteins	507	2.73	15	1.64E-08	2.30E-06
Platelet degranulation	89	0.48	7	3.59E-07	4.58E-05
Response to elevated platelet cytosolic Ca2+	94	0.507	7	5.24E-07	6.12E-05
LDL-mediated lipid transport	4	0.0216	3	5.74E-07	6.19E-05
Vitamin D (calciferol) metabolism	7	0.0377	3	4.96E-06	0.000497
Platelet activation, signaling and aggregation	220	1.19	7	0.000142	0.0132
Metabolism of steroid hormones and vitamin D	26	0.14	3	0.000344	0.0283
Steroid hormones	26	0.14	3	0.000344	0.0283
Hemostasis	511	2.76	9	0.00122	0.0913
Retinoid cycle disease events	10	0.0539	2	0.00124	0.0913
The canonical retinoid cycle in rods (twilight vision)	15	0.0809	2	0.00284	0.199
PPARA Activates Gene Expression	59	0.318	3	0.0038	0.254
Platelet sensitization by LDL	19	0.102	2	0.00456	0.291
Metabolism	1490	8.02	15	0.00707	0.431
Regulation of Lipid Metabolism by Peroxisome proliferator-activated receptor alpha (PPARalpha)	76	0.41	3	0.00773	0.451
Transferrin endocytosis and recycling	26	0.14	2	0.00847	0.474
Disease	945	5.1	11	0.0088	0.474
Activation, translocation and oligomerization of BAX	2	0.0108	1	0.0108	0.558
Iron uptake and transport	38	0.205	2	0.0176	0.881
Processing of DNA ends prior to end rejoining	6	0.0323	1	0.0319	1

Fatty acid, triacylglycerol, and ketone body metabolism	139	0.749	3	0.0382	1
Nonhomologous End-joining (NHEJ)	8	0.0431	1	0.0423	1
2-LTR circle formation	9	0.0485	1	0.0475	1

## MODULE 8

Pathway	Total	Expected	Hits	P.Value	FDR
G alpha (s) signalling events	127	0.913	32	2.33E-45	3.26E-42
Opioid Signalling	86	0.618	29	7.65E-45	5.36E-42
Glucagon signaling in metabolic regulation	37	0.266	23	5.23E-43	2.44E-40
G alpha (z) signalling events	38	0.273	23	1.32E-42	4.62E-40
Regulation of Water Balance by Renal Aquaporins	47	0.338	24	5.03E-42	1.41E-39
GABA B receptor activation	40	0.288	23	7.51E-42	1.50E-39
Activation of GABAB receptors	40	0.288	23	7.51E-42	1.50E-39
Integration of energy metabolism	109	0.784	29	2.42E-41	4.24E-39
Aquaporin-mediated transport	55	0.395	24	7.56E-40	1.18E-37
G-protein activation	29	0.208	20	1.30E-38	1.83E-36
GABA receptor activation	55	0.395	23	1.50E-37	1.91E-35
Signal amplification	33	0.237	19	2.40E-34	2.80E-32
Inhibition of Insulin Secretion by Adrenaline/Noradrenaline	28	0.201	18	8.65E-34	9.33E-32
ADP signalling through P2Y purinoceptor 12	23	0.165	17	1.45E-33	1.46E-31
GPCR downstream signaling	812	5.84	42	8.55E-33	7.99E-31
G alpha (i) signalling events	184	1.32	28	2.72E-32	2.39E-30
Signaling by GPCR	931	6.69	43	5.86E-32	4.77E-30
Prostacyclin signalling through prostacyclin receptor	21	0.151	16	6.12E-32	4.77E-30
Neurotransmitter Receptor Binding And Downstream Transmission In The Postsynaptic Cell	143	1.03	26	6.97E-32	5.14E-30
Thrombin signalling through proteinase activated receptors (PARs)	34	0.244	18	1.42E-31	9.93E-30
Transmission across Chemical Synapses	196	1.41	28	1.77E-31	1.18E-29
Regulation of Insulin Secretion	82	0.589	22	9.35E-31	5.96E-29
Thromboxane signalling through TP receptor	25	0.18	16	6.04E-30	3.68E-28
Regulation of Insulin Secretion by Glucagon-like Peptide-1	47	0.338	18	2.78E-28	1.62E-26
Glucagon-type ligand receptors	32	0.23	16	1.72E-27	9.65E-26
ADP signalling through P2Y purinoceptor 1	27	0.194	15	1.02E-26	5.51E-25
Neuronal System	292	2.1	28	1.86E-26	9.67E-25
G beta:gamma signalling through PLC beta	22	0.158	14	3.75E-26	1.88E-24
Adenylate cyclase inhibitory pathway	13	0.0935	12	5.55E-26	2.59E-24

Inhibition of adenylate cyclase pathway	13	0.0935	12	5.55E-26	2.59E-24
Presynaptic function of Kainate receptors	23	0.165	14	9.53E-26	4.31E-24
Signal Transduction	1690	12.1	46	1.38E-25	6.03E-24
G beta:gamma signalling through PI3Kgamma	27	0.194	14	2.30E-24	9.75E-23
G-protein beta:gamma signalling	30	0.216	14	1.64E-23	6.76E-22
Activation of Kainate Receptors upon glutamate binding	34	0.244	14	1.54E-22	6.17E-21
PLC beta mediated events	46	0.331	15	2.75E-22	1.07E-20
G-protein mediated events	47	0.338	15	4.02E-22	1.52E-20
G alpha (12/13) signalling events	80	0.575	16	6.20E-20	2.29E-18
Adenylate cyclase activating pathway	10	0.0719	9	2.31E-19	8.30E-18
Class B/2 (Secretin family receptors)	87	0.625	16	2.64E-19	9.25E-18
Platelet activation, signaling and aggregation	220	1.58	21	2.94E-19	1.01E-17
Platelet homeostasis	88	0.633	16	3.21E-19	1.07E-17
Activation of G protein gated Potassium channels	27	0.194	11	9.29E-18	2.89E-16
G protein gated Potassium channels	27	0.194	11	9.29E-18	2.89E-16
Inhibition of voltage gated Ca2+ channels via Gbeta/gamma subunits	27	0.194	11	9.29E-18	2.89E-16
PKA activation in glucagon signalling	19	0.137	10	1.20E-17	3.65E-16
GPCR ligand binding	415	2.98	24	4.67E-17	1.39E-15
Inwardly rectifying K+ channels	33	0.237	11	1.34E-16	3.91E-15
G alpha (q) signalling events	188	1.35	18	1.91E-16	5.48E-15
PKA activation	18	0.129	9	1.08E-15	3.02E-14
Gastrin-CREB signalling pathway via PKC and MAPK	209	1.5	18	1.28E-15	3.52E-14
PKA-mediated phosphorylation of CREB	19	0.137	9	2.03E-15	5.48E-14
Transmembrane transport of small molecules	504	3.62	24	4.03E-15	1.07E-13
Hemostasis	511	3.67	23	6.70E-14	1.74E-12
Calmodulin induced events	30	0.216	9	2.97E-13	7.44E-12
CaM pathway	30	0.216	9	2.97E-13	7.44E-12
Ca-dependent events	32	0.23	9	5.76E-13	1.42E-11
DAG and IP3 signaling	35	0.252	9	1.43E-12	3.45E-11
PLC-gamma1 signalling	37	0.266	9	2.49E-12	5.82E-11
EGFR interacts with phospholipase C-gamma	37	0.266	9	2.49E-12	5.82E-11

PLCG1 events in ERBB2 signaling	38	0.273	9	3.24E-12	7.46E-11
Potassium Channels	103	0.74	11	9.63E-11	2.18E-09
Phospholipase C-mediated cascade	57	0.41	9	1.62E-10	3.60E-09
Metabolism	1490	10.7	29	1.25E-08	2.75E-07
NGF signalling via TRKA from the plasma membrane	207	1.49	11	1.61E-07	3.47E-06
Downstream signaling of activated FGFR	150	1.08	9	9.10E-07	1.93E-05
Signaling by FGFR	162	1.16	9	1.74E-06	3.64E-05
Downstream signal transduction	163	1.17	9	1.83E-06	3.77E-05
Signaling by ERBB2	164	1.18	9	1.93E-06	3.86E-05
DAP12 signaling	164	1.18	9	1.93E-06	3.86E-05
CREB phosphorylation through the activation of Adenylate Cyclase	5	0.0359	3	3.45E-06	6.82E-05
Signaling by FGFR in disease	178	1.28	9	3.80E-06	7.41E-05
Signaling by EGFR	179	1.29	9	3.98E-06	7.65E-05
Signaling by EGFR in Cancer	181	1.3	9	4.37E-06	8.27E-05
DAP12 interactions	182	1.31	9	4.57E-06	8.50E-05
Signalling by NGF	290	2.08	11	4.61E-06	8.50E-05
Signaling by PDGF	189	1.36	9	6.23E-06	0.000113
Prostanoid ligand receptors	11	0.0791	3	5.53E-05	0.000993
Eicosanoid ligand-binding receptors	17	0.122	3	0.000221	0.00392
Innate Immune System	521	3.75	11	0.000929	0.0163
Class A/1 (Rhodopsin-like receptors)	312	2.24	8	0.00153	0.0264
Post NMDA receptor activation events	35	0.252	3	0.00194	0.0332
Hormone ligand-binding receptors	10	0.0719	2	0.0022	0.0371
Activation of NMDA receptor upon glutamate binding and postsynaptic events	39	0.28	3	0.00266	0.0441
DSCAM interactions	11	0.0791	2	0.00267	0.0441
Depolarization of the Presynaptic Terminal Triggers the Opening of Calcium Channels	12	0.0863	2	0.00319	0.052
p38MAPK events	13	0.0935	2	0.00375	0.0605
Signalling to RAS	27	0.194	2	0.0158	0.252
Signalling to ERKs	37	0.266	2	0.0287	0.453
NOD1/2 Signaling Pathway	38	0.273	2	0.0302	0.465
Amine ligand-binding receptors	38	0.273	2	0.0302	0.465



Vasopressin-like receptors

6    0.0431    1    0.0424    0.646

## MODULE 9

Pathway	Total	Expected	Hits	P.Value	FDR
Formation of Fibrin Clot (Clotting Cascade)	29	0.104	11	2.86E-21	4.01E-18
Hemostasis	511	1.84	20	2.66E-19	1.87E-16
Intrinsic Pathway	17	0.0611	9	4.33E-19	2.02E-16
Platelet activation, signaling and aggregation	220	0.791	11	6.64E-11	2.33E-08
Dissolution of Fibrin Clot	10	0.0359	5	9.59E-11	2.69E-08
Peptide ligand-binding receptors	192	0.69	8	2.00E-07	4.68E-05
G alpha (q) signalling events	188	0.676	7	2.89E-06	0.00058
Transport of gamma-carboxylated protein precursors from the endoplasmic reticulum to the Golgi apparatus	9	0.0323	3	3.38E-06	0.000592
Gamma-carboxylation of protein precursors	10	0.0359	3	4.82E-06	0.000614
Removal of aminoterminal propeptides from gamma-carboxylated proteins	10	0.0359	3	4.82E-06	0.000614
GP1b-IX-V activation signalling	10	0.0359	3	4.82E-06	0.000614
Thrombin signalling through proteinase activated receptors (PARs)	34	0.122	4	5.54E-06	0.000632
Gastrin-CREB signalling pathway via PKC and MAPK	209	0.751	7	5.86E-06	0.000632
Common Pathway	11	0.0395	3	6.61E-06	0.000655
Platelet Aggregation (Plug Formation)	36	0.129	4	7.01E-06	0.000655
Class A/1 (Rhodopsin-like receptors)	312	1.12	8	7.93E-06	0.000685
Platelet Adhesion to exposed collagen	12	0.0431	3	8.79E-06	0.000685
Gamma-carboxylation, transport, and amino-terminal cleavage of proteins	12	0.0431	3	8.79E-06	0.000685
GPCR ligand binding	415	1.49	8	6.32E-05	0.00467
PTM: gamma carboxylation, hypusine formation and arylsulfatase activation	29	0.104	3	0.00014	0.00983
Platelet degranulation	89	0.32	4	0.000256	0.0171
Response to elevated platelet cytosolic Ca <sup>2+</sup>	94	0.338	4	0.000315	0.0201
Cell surface interactions at the vascular wall	99	0.356	4	0.000385	0.0235
Regulation of Complement cascade	15	0.0539	2	0.00126	0.0738
Regulation of Insulin-like Growth Factor (IGF) Transport and Uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs)	21	0.0755	2	0.00249	0.14
Activation of Matrix Metalloproteinases	31	0.111	2	0.0054	0.291
GPCR downstream signaling	812	2.92	8	0.00569	0.295
Complement cascade	33	0.119	2	0.00611	0.306
Signaling by GPCR	931	3.35	8	0.0129	0.625

Signal Transduction	1690	6.07	11	0.0229	1
G alpha (i) signalling events	184	0.661	3	0.0272	1
Degradation of the extracellular matrix	77	0.277	2	0.0308	1
Relaxin receptors	9	0.0323	1	0.0319	1
Post-translational protein modification	200	0.719	3	0.0337	1
BMAL1:CLOCK/NPAS2 Activates Circadian Expression	14	0.0503	1	0.0492	1

## MODULE 10

Pathway	Total	Expected	Hits	P.Value	FDR
Antigen Presentation: Folding, assembly and peptide loading of class I MHC	25	0.0637	5	2.89E-09	4.05E-06
Calnexin/calreticulin cycle	11	0.028	4	9.39E-09	6.58E-06
N-glycan trimming in the ER and Calnexin/Calreticulin cycle	13	0.0331	4	2.03E-08	9.48E-06
Collagen biosynthesis and modifying enzymes	62	0.158	5	3.33E-07	0.000117
Collagen formation	85	0.216	5	1.63E-06	0.000457
Extracellular matrix organization	157	0.4	5	3.32E-05	0.00776
Asparagine N-linked glycosylation	86	0.219	4	5.37E-05	0.0108
Chylomicron-mediated lipid transport	12	0.0306	2	0.000397	0.0639
Class I MHC mediated antigen processing & presentation	267	0.68	5	0.00041	0.0639
Unfolded Protein Response	66	0.168	3	0.000568	0.0797
Metabolism of proteins	689	1.75	7	0.00093	0.118
Lipoprotein metabolism	22	0.056	2	0.00137	0.148
Post-translational protein modification	200	0.509	4	0.00137	0.148
Lipid digestion, mobilization, and transport	41	0.104	2	0.00472	0.473
Signalling to STAT3	3	0.00764	1	0.00762	0.712
Assembly of the RAD50-MRE11-NBS1 complex at DNA double-strand breaks	4	0.0102	1	0.0101	0.837
MRN complex relocates to nuclear foci	4	0.0102	1	0.0101	0.837
ER-Phagosome pathway	63	0.16	2	0.0109	0.847
Activation of Chaperone Genes by ATF6-alpha	5	0.0127	1	0.0127	0.935
ATM mediated phosphorylation of repair proteins	6	0.0153	1	0.0152	1
ATM mediated response to DNA double-strand break	6	0.0153	1	0.0152	1
Antigen processing-Cross presentation	78	0.199	2	0.0164	1
Recycling of eIF2:GDP	8	0.0204	1	0.0202	1
Activation of Chaperones by ATF6-alpha	8	0.0204	1	0.0202	1
Adaptive Immune System	654	1.67	5	0.0202	1
Recruitment of repair and signaling proteins to double-strand breaks	9	0.0229	1	0.0227	1
PERK regulated gene expression	13	0.0331	1	0.0326	1
Interleukin-6 signaling	14	0.0356	1	0.0351	1
Homologous recombination repair of replication-independent double-strand breaks	16	0.0407	1	0.04	1

Homologous Recombination Repair	16	0.0407	1	0.04	1
Signaling by FGFR1 fusion mutants	20	0.0509	1	0.0498	1

## MODULE 11

Pathway	Total	Expected	Hits	P.Value	FDR
Global Genomic NER (GG-NER)	36	0.124	12	1.01E-22	1.41E-19
Nucleotide Excision Repair	53	0.183	12	2.09E-20	9.30E-18
Dual incision reaction in GG-NER	23	0.0792	10	2.65E-20	9.30E-18
Formation of incision complex in GG-NER	23	0.0792	10	2.65E-20	9.30E-18
DNA Repair	117	0.403	13	7.35E-18	2.06E-15
HIV Infection	214	0.737	14	5.01E-16	1.17E-13
S Phase	122	0.42	12	9.13E-16	1.83E-13
Synthesis of DNA	95	0.327	11	3.14E-15	5.51E-13
Cyclin E associated events during G1/S transition	65	0.224	10	3.85E-15	6.00E-13
Cyclin A:Cdk2-associated events at S phase entry	66	0.227	10	4.53E-15	6.35E-13
DNA Replication	102	0.351	11	7.09E-15	9.03E-13
Regulation of activated PAK-2p34 by proteasome mediated degradation	48	0.165	9	1.76E-14	1.77E-12
Cross-presentation of soluble exogenous antigens (endosomes)	48	0.165	9	1.76E-14	1.77E-12
Ubiquitin-dependent degradation of Cyclin D1	49	0.169	9	2.15E-14	1.77E-12
CDK-mediated phosphorylation and removal of Cdc6	49	0.169	9	2.15E-14	1.77E-12
Ubiquitin-dependent degradation of Cyclin D	49	0.169	9	2.15E-14	1.77E-12
Regulation of ornithine decarboxylase (ODC)	49	0.169	9	2.15E-14	1.77E-12
G1/S Transition	113	0.389	11	2.27E-14	1.77E-12
Vpu mediated degradation of CD4	50	0.172	9	2.62E-14	1.93E-12
DNA Replication Pre-Initiation	80	0.276	10	3.45E-14	2.24E-12
M/G1 Transition	80	0.276	10	3.45E-14	2.24E-12
Ubiquitin Mediated Degradation of Phosphorylated Cdc25A	52	0.179	9	3.83E-14	2.24E-12
p53-Independent DNA Damage Response	52	0.179	9	3.83E-14	2.24E-12
p53-Independent G1/S DNA damage checkpoint	52	0.179	9	3.83E-14	2.24E-12
SCF-beta-TrCP mediated degradation of Emi1	53	0.183	9	4.61E-14	2.48E-12
Autodegradation of the E3 ubiquitin ligase COP1	53	0.183	9	4.61E-14	2.48E-12
Stabilization of p53	54	0.186	9	5.52E-14	2.76E-12
Destabilization of mRNA by AUF1 (hnRNP D0)	54	0.186	9	5.52E-14	2.76E-12
Vif-mediated degradation of APOBEC3G	55	0.189	9	6.59E-14	3.18E-12

CDT1 association with the CDC6:ORC:origin complex	57	0.196	9	9.28E-14	4.34E-12
SCF(Skp2)-mediated degradation of p27/p21	58	0.2	9	1.10E-13	4.96E-12
p53-Dependent G1/S DNA damage checkpoint	59	0.203	9	1.29E-13	5.33E-12
p53-Dependent G1 DNA Damage Response	59	0.203	9	1.29E-13	5.33E-12
Regulation of Apoptosis	59	0.203	9	1.29E-13	5.33E-12
G1/S DNA Damage Checkpoints	62	0.214	9	2.07E-13	8.31E-12
Assembly of the pre-replicative complex	63	0.217	9	2.41E-13	9.15E-12
ER-Phagosome pathway	63	0.217	9	2.41E-13	9.15E-12
Mitotic G1-G1/S phases	140	0.482	11	2.53E-13	9.34E-12
Degradation of beta-catenin by the destruction complex	65	0.224	9	3.25E-13	1.14E-11
Signaling by Wnt	65	0.224	9	3.25E-13	1.14E-11
Activation of NF-kappaB in B Cells	66	0.227	9	3.75E-13	1.28E-11
Autodegradation of Cdh1 by Cdh1:APC/C	68	0.234	9	4.98E-13	1.66E-11
Switching of origins to a post-replicative state	69	0.238	9	5.72E-13	1.82E-11
Orc1 removal from chromatin	69	0.238	9	5.72E-13	1.82E-11
Removal of licensing factors from origins	71	0.245	9	7.48E-13	2.23E-11
Regulation of DNA replication	71	0.245	9	7.48E-13	2.23E-11
APC/C:Cdc20 mediated degradation of Securin	71	0.245	9	7.48E-13	2.23E-11
Cdc20:Phospho-APC/C mediated degradation of Cyclin A	76	0.262	9	1.42E-12	3.98E-11
APC/C:Cdh1 mediated degradation of Cdc20 and other APC/C:Cdh1 targeted proteins in late mitosis/early G1	76	0.262	9	1.42E-12	3.98E-11
APC/C:Cdc20 mediated degradation of mitotic proteins	76	0.262	9	1.42E-12	3.98E-11
Activation of APC/C and APC/C:Cdc20 mediated degradation of mitotic proteins	77	0.265	9	1.60E-12	4.41E-11
Antigen processing-Cross presentation	78	0.269	9	1.81E-12	4.88E-11
Regulation of APC/C activators between G1/S and early anaphase	84	0.289	9	3.61E-12	9.55E-11
Regulation of mRNA Stability by Proteins that Bind AU-rich Elements	88	0.303	9	5.56E-12	1.44E-10
APC/C-mediated degradation of cell cycle proteins	89	0.307	9	6.17E-12	1.55E-10
Regulation of mitotic cell cycle	89	0.307	9	6.17E-12	1.55E-10
Cell Cycle, Mitotic	411	1.42	13	9.84E-11	2.42E-09
Transcription-coupled NER (TC-NER)	47	0.162	7	1.21E-10	2.93E-09
Cell Cycle Checkpoints	131	0.451	9	2.12E-10	5.03E-09
Host Interactions of HIV factors	141	0.486	9	4.11E-10	9.61E-09

Apoptosis	158	0.544	9	1.14E-09	2.62E-08
Cell Cycle	508	1.75	13	1.39E-09	3.14E-08
Downstream Signaling Events Of B Cell Receptor (BCR)	173	0.596	9	2.56E-09	5.69E-08
Separation of Sister Chromatids	186	0.641	9	4.86E-09	1.06E-07
Metabolism of amino acids and derivatives	190	0.654	9	5.87E-09	1.27E-07
Mitotic M-M/G1 phases	266	0.916	10	6.16E-09	1.31E-07
Mitotic Anaphase	198	0.682	9	8.44E-09	1.77E-07
Mitotic Metaphase and Anaphase	199	0.685	9	8.82E-09	1.79E-07
Signaling by the B Cell Receptor (BCR)	199	0.685	9	8.82E-09	1.79E-07
Antigen processing: Ubiquitination & Proteasome degradation	224	0.772	9	2.49E-08	4.99E-07
M Phase	233	0.803	9	3.51E-08	6.93E-07
Dual incision reaction in TC-NER	31	0.107	5	4.88E-08	9.38E-07
Formation of transcription-coupled NER (TC-NER) repair complex	31	0.107	5	4.88E-08	9.38E-07
Class I MHC mediated antigen processing & presentation	267	0.92	9	1.14E-07	2.16E-06
Disease	945	3.26	14	2.77E-07	5.19E-06
Metabolism of mRNA	317	1.09	9	4.96E-07	9.15E-06
RNA Polymerase I Chain Elongation	21	0.0723	4	6.16E-07	1.12E-05
RNA Polymerase I Promoter Escape	22	0.0758	4	7.51E-07	1.35E-05
Metabolism of RNA	339	1.17	9	8.76E-07	1.55E-05
RNA Polymerase I Transcription Initiation	23	0.0792	4	9.07E-07	1.57E-05
RNA Polymerase I Transcription Termination	23	0.0792	4	9.07E-07	1.57E-05
RNA Polymerase I Promoter Clearance	24	0.0827	4	1.09E-06	1.86E-05
RNA Polymerase I Transcription	26	0.0896	4	1.52E-06	2.57E-05
RNA Pol II CTD phosphorylation and interaction with CE	28	0.0965	4	2.07E-06	3.42E-05
RNA Pol II CTD phosphorylation and interaction with CE	28	0.0965	4	2.07E-06	3.42E-05
mRNA Capping	30	0.103	4	2.76E-06	4.51E-05
Formation of the Early Elongation Complex	34	0.117	4	4.63E-06	7.38E-05
Formation of the HIV-1 Early Elongation Complex	34	0.117	4	4.63E-06	7.38E-05
RNA Polymerase II Promoter Escape	41	0.141	4	9.96E-06	0.000149
RNA Polymerase II Transcription Pre-Initiation And Promoter Opening	41	0.141	4	9.96E-06	0.000149
RNA Polymerase II Transcription Initiation	41	0.141	4	9.96E-06	0.000149



RNA Polymerase II Transcription Initiation And Promoter Clearance	41	0.141	4	9.96E-06	0.000149
HIV-1 Transcription Initiation	41	0.141	4	9.96E-06	0.000149
RNA Polymerase II HIV-1 Promoter Escape	41	0.141	4	9.96E-06	0.000149
DNA Damage Recognition in GG-NER	2	0.00689	2	1.14E-05	0.000168
Gene Expression	1090	3.74	13	1.20E-05	0.000175
Tat-mediated elongation of the HIV-1 transcript	45	0.155	4	1.45E-05	0.000206
Formation of HIV-1 elongation complex containing HIV-1 Tat	45	0.155	4	1.45E-05	0.000206
HIV-1 Transcription Elongation	45	0.155	4	1.45E-05	0.000206
RNA Polymerase II Transcription Elongation	46	0.158	4	1.59E-05	0.000218
Formation of RNA Pol II elongation complex	46	0.158	4	1.59E-05	0.000218
Formation of HIV-1 elongation complex in the absence of HIV-1 Tat	46	0.158	4	1.59E-05	0.000218
RNA Polymerase I, RNA Polymerase III, and Mitochondrial Transcription	59	0.203	4	4.30E-05	0.000585
RNA Polymerase II Pre-transcription Events	62	0.214	4	5.23E-05	0.000705
Transcription of the HIV genome	64	0.22	4	5.93E-05	0.000792
HIV Life Cycle	128	0.441	5	6.11E-05	0.000808
Adaptive Immune System	654	2.25	9	0.000182	0.00238
RNA Polymerase II Transcription	107	0.369	4	0.000437	0.00567
Late Phase of HIV Life Cycle	108	0.372	4	0.000452	0.00582
Repair synthesis of patch ~27-30 bases long by DNA polymerase	15	0.0517	2	0.00116	0.0146
Repair synthesis for gap-filling by DNA polymerase in TC-NER	15	0.0517	2	0.00116	0.0146
mRNA Processing	140	0.482	4	0.0012	0.0151
Gap-filling DNA repair synthesis and ligation in GG-NER	16	0.0551	2	0.00132	0.0161
Gap-filling DNA repair synthesis and ligation in TC-NER	16	0.0551	2	0.00132	0.0161
Cytosolic Iron-sulfur Cluster Assembly	16	0.0551	2	0.00132	0.0161
Transcription	149	0.513	4	0.00152	0.0183
Telomere C-strand (Lagging Strand) Synthesis	22	0.0758	2	0.00251	0.0301
Extension of Telomeres	24	0.0827	2	0.00299	0.0355
Metabolism	1490	5.13	11	0.00599	0.0705
Immune System	1140	3.92	9	0.00984	0.115

## MODULE 12

Pathway	Total	Expected	Hits	P.Value	FDR
FCGR activation	15	0.0225	4	3.44E-09	4.82E-06
Signaling by Interleukins	116	0.174	5	3.41E-07	0.000239
PECAM1 interactions	13	0.0195	3	6.87E-07	0.000321
Regulation of KIT signaling	17	0.0255	3	1.63E-06	0.00057
Regulation of signaling by CBL	22	0.0329	3	3.67E-06	0.00102
CTLA4 inhibitory signaling	24	0.0359	3	4.82E-06	0.00102
Fcgamma receptor (FCGR) dependent phagocytosis	86	0.129	4	5.08E-06	0.00102
CD28 co-stimulation	30	0.0449	3	9.62E-06	0.00169
Cytokine Signaling in Immune system	286	0.428	5	2.94E-05	0.00458
Innate Immune System	521	0.78	6	3.51E-05	0.00492
Interleukin-3, 5 and GM-CSF signaling	51	0.0764	3	4.85E-05	0.00618
Nef and signal transduction	8	0.012	2	5.63E-05	0.00657
Costimulation by the CD28 family	68	0.102	3	0.000115	0.0124
Signaling by the B Cell Receptor (BCR)	199	0.298	4	0.00014	0.014
Immune System	1140	1.7	7	0.000305	0.0285
Cell surface interactions at the vascular wall	99	0.148	3	0.000352	0.0308
The role of Nef in HIV-1 replication and disease pathogenesis	31	0.0464	2	0.000917	0.0729
Antigen Activates B Cell Receptor Leading to Generation of Second Messengers	32	0.0479	2	0.000978	0.0729
Signaling by SCF-KIT	142	0.213	3	0.00101	0.0729
GPVI-mediated activation cascade	33	0.0494	2	0.00104	0.0729
Adaptive Immune System	654	0.979	5	0.00147	0.0982
Downstream TCR signaling	48	0.0719	2	0.0022	0.14
TCR signaling	65	0.0973	2	0.00399	0.243
Hemostasis	511	0.765	4	0.0049	0.286
Nef Mediated CD4 Down-regulation	9	0.0135	1	0.0134	0.752
IRAK2 mediated activation of TAK1 complex upon TLR7/8 or 9 stimulation	10	0.015	1	0.0149	0.773
IRAK2 mediated activation of TAK1 complex	10	0.015	1	0.0149	0.773
Host Interactions of HIV factors	141	0.211	2	0.0178	0.834
Platelet Adhesion to exposed collagen	12	0.018	1	0.0178	0.834

CD28 dependent Vav1 pathway	12	0.018	1	0.0178	0.834
Activation of Rac	15	0.0225	1	0.0223	0.978
Downstream signal transduction	163	0.244	2	0.0234	0.978
Signaling by ERBB2	164	0.246	2	0.0237	0.978
TRAF6 mediated induction of TAK1 complex	16	0.024	1	0.0237	0.978
Downstream Signaling Events Of B Cell Receptor (BCR)	173	0.259	2	0.0262	1
Translocation of ZAP-70 to Immunological synapse	18	0.027	1	0.0267	1
CD28 dependent PI3K/Akt signaling	19	0.0285	1	0.0281	1
Platelet sensitization by LDL	19	0.0285	1	0.0281	1
Phosphorylation of CD3 and TCR zeta chains	20	0.03	1	0.0296	1
JNK (c-Jun kinases) phosphorylation and activation mediated by activated human TAK1	20	0.03	1	0.0296	1
Signaling by PDGF	189	0.283	2	0.0309	1
TAK1 activates NFkB by phosphorylation and activation of IKKs complex	22	0.0329	1	0.0325	1
Growth hormone receptor signaling	23	0.0344	1	0.0339	1
activated TAK1 mediates p38 MAPK activation	23	0.0344	1	0.0339	1
Nef-mediates down modulation of cell surface receptors by recruiting them to clathrin adapters	24	0.0359	1	0.0354	1
Nephrin interactions	24	0.0359	1	0.0354	1
PD-1 signaling	25	0.0374	1	0.0368	1
HIV Infection	214	0.321	2	0.0388	1
Platelet activation, signaling and aggregation	220	0.329	2	0.0409	1
Generation of second messenger molecules	31	0.0464	1	0.0455	1
Signaling by Robo receptor	34	0.0509	1	0.0498	1

**MODULE 13**

Pathway	Total	Expected	Hits	P.Value	FDR
Glycolysis	30	0.0809	12	9.75E-26	1.37E-22
Gluconeogenesis	35	0.0944	11	4.44E-22	3.11E-19
Glucose metabolism	70	0.189	12	1.16E-20	5.42E-18
Metabolism of carbohydrates	258	0.696	13	2.29E-15	8.04E-13
Metabolism	1490	4.01	13	8.73E-06	0.00245
Fructose catabolism	2	0.00539	1	0.00538	1
Nuclear Receptor transcription pathway	53	0.143	2	0.00872	1
Facilitative Na <sup>+</sup> -independent glucose transporters	12	0.0323	1	0.0319	1
Golgi Cisternae Pericentriolar Stack Reorganization	14	0.0377	1	0.0371	1
Mitotic Prophase	36	0.097	1	0.0928	1

## MODULE 14

Pathway	Total	Expected	Hits	P.Value	FDR
Synthesis and interconversion of nucleotide di- and triphosphates	20	0.0479	7	7.46E-15	1.05E-11
Metabolism of nucleotides	81	0.194	8	3.92E-12	2.75E-09
RIG-I/MDA5 mediated induction of IFN-alpha/beta pathways	67	0.161	4	1.54E-05	0.00719
IKK complex recruitment mediated by RIP1	25	0.0599	3	2.52E-05	0.00882
TRIF-mediated TLR3/TLR4 signaling	87	0.208	4	4.34E-05	0.0091
MyD88-independent cascade	88	0.211	4	4.54E-05	0.0091
Toll Like Receptor 3 (TLR3) Cascade	88	0.211	4	4.54E-05	0.0091
Activated TLR4 signalling	100	0.24	4	7.51E-05	0.0131
Toll Like Receptor 4 (TLR4) Cascade	103	0.247	4	8.43E-05	0.0131
Interleukin-1 signaling	45	0.108	3	0.000151	0.0211
Toll-Like Receptors Cascades	123	0.295	4	0.000168	0.0214
Downstream TCR signaling	48	0.115	3	0.000183	0.0214
Regulated proteolysis of p75NTR	10	0.024	2	0.00024	0.0258
Nucleotide-binding domain, leucine rich repeat containing receptor (NLR) signaling pathways	55	0.132	3	0.000275	0.0275
NF-kB is activated and signals survival	13	0.0312	2	0.000414	0.0377
TCR signaling	65	0.156	3	0.00045	0.0377
p75NTR signals via NF-kB	16	0.0383	2	0.000634	0.0377
IRAK1 recruits IKK complex upon TLR7/8 or 9 stimulation	16	0.0383	2	0.000634	0.0377
IRAK1 recruits IKK complex	16	0.0383	2	0.000634	0.0377
TRAF6 mediated NF-kB activation	16	0.0383	2	0.000634	0.0377
Toll Like Receptor 10 (TLR10) Cascade	74	0.177	3	0.00066	0.0377
Toll Like Receptor 5 (TLR5) Cascade	74	0.177	3	0.00066	0.0377
MyD88 cascade initiated on plasma membrane	74	0.177	3	0.00066	0.0377
TRAF6 mediated induction of NFkB and MAP kinases upon TLR7/8 or 9 activation	76	0.182	3	0.000713	0.0377
TRAF6 mediated IRF7 activation in TLR7/8 or 9 signaling	17	0.0407	2	0.000717	0.0377
Toll Like Receptor 7/8 (TLR7/8) Cascade	77	0.185	3	0.000741	0.0377
MyD88 dependent cascade initiated on endosome	77	0.185	3	0.000741	0.0377
Toll Like Receptor 9 (TLR9) Cascade	79	0.189	3	0.000799	0.0377
MyD88:Mal cascade initiated on plasma membrane	81	0.194	3	0.00086	0.0377

Toll Like Receptor TLR1:TLR2 Cascade	81	0.194	3	0.00086	0.0377
Toll Like Receptor TLR6:TLR2 Cascade	81	0.194	3	0.00086	0.0377
Toll Like Receptor 2 (TLR2) Cascade	81	0.194	3	0.00086	0.0377
Innate Immune System	521	1.25	6	0.000891	0.0379
TAK1 activates NFkB by phosphorylation and activation of IKKs complex	22	0.0527	2	0.00121	0.0499
Signaling by Interleukins	116	0.278	3	0.00243	0.0958
Immune System	1140	2.73	8	0.00246	0.0958
Negative regulators of RIG-I/MDA5 signaling	33	0.0791	2	0.00272	0.103
Adaptive Immune System	654	1.57	6	0.00293	0.108
Class I MHC mediated antigen processing & presentation	267	0.64	4	0.00311	0.112
NOD1/2 Signaling Pathway	38	0.0911	2	0.0036	0.126
Cytokine Signaling in Immune system	286	0.685	4	0.00399	0.136
TRAF6 Mediated Induction of proinflammatory cytokines	62	0.149	2	0.00936	0.313
Metabolism	1490	3.57	8	0.0136	0.436
Synthesis of 12-eicosatetraenoic acid derivatives	6	0.0144	1	0.0143	0.436
Synthesis of 5-eicosatetraenoic acids	6	0.0144	1	0.0143	0.436
Synthesis of 15-eicosatetraenoic acid derivatives	6	0.0144	1	0.0143	0.436
Antigen processing: Ubiquitination & Proteasome degradation	224	0.537	3	0.0151	0.45
p75 NTR receptor-mediated signalling	85	0.204	2	0.0171	0.5
Cross-presentation of particulate exogenous antigens (phagosomes)	8	0.0192	1	0.019	0.544
Displacement of DNA glycosylase by APE1	9	0.0216	1	0.0214	0.599
Base-free sugar-phosphate removal via the single-nucleotide replacement pathway	10	0.024	1	0.0237	0.628
IRAK2 mediated activation of TAK1 complex upon TLR7/8 or 9 stimulation	10	0.024	1	0.0237	0.628
IRAK2 mediated activation of TAK1 complex	10	0.024	1	0.0237	0.628
Purine catabolism	11	0.0264	1	0.0261	0.664
RIP-mediated NFkB activation via DAI	11	0.0264	1	0.0261	0.664
Resolution of AP sites via the single-nucleotide replacement pathway	12	0.0288	1	0.0284	0.711
DAI mediated induction of type I IFNs	13	0.0312	1	0.0307	0.743
p75NTR recruits signalling complexes	13	0.0312	1	0.0307	0.743
The NLRP3 inflammasome	14	0.0335	1	0.0331	0.786
NRIF signals cell death from the nucleus	15	0.0359	1	0.0354	0.827

G1/S-Specific Transcription	16	0.0383	1	0.0377	0.853
TRAF6 mediated induction of TAK1 complex	16	0.0383	1	0.0377	0.853
Resolution of AP sites via the multiple-nucleotide patch replacement pathway	17	0.0407	1	0.04	0.863
Removal of DNA patch containing abasic residue	17	0.0407	1	0.04	0.863
Regulation of IFNG signaling	17	0.0407	1	0.04	0.863
Resolution of Abasic Sites (AP sites)	19	0.0455	1	0.0446	0.907
Base Excision Repair	19	0.0455	1	0.0446	0.907
Inflammasomes	19	0.0455	1	0.0446	0.907
Cytosolic sensors of pathogen-associated DNA	19	0.0455	1	0.0446	0.907
Oxygen-dependent Proline Hydroxylation of Hypoxia-inducible Factor Alpha	20	0.0479	1	0.0469	0.926
JNK (c-Jun kinases) phosphorylation and activation mediated by activated human TAK1	20	0.0479	1	0.0469	0.926

## MODULE 15

Pathway	Total	Expected	Hits	P.Value	FDR
Rho GTPase cycle	123	0.332	14	7.01E-22	4.91E-19
Signaling by Rho GTPases	123	0.332	14	7.01E-22	4.91E-19
Sema4D induced cell migration and growth-cone collapse	29	0.0782	4	8.42E-07	0.000394
Sema4D in semaphorin signaling	34	0.0917	4	1.63E-06	0.000572
Signal Transduction	1690	4.55	14	4.41E-06	0.00124
Semaphorin interactions	72	0.194	4	3.39E-05	0.00793
G alpha (12/13) signalling events	80	0.216	4	5.15E-05	0.0103
GPVI-mediated activation cascade	33	0.089	3	8.53E-05	0.015
Axon guidance	292	0.787	4	0.00674	1
Axonal growth stimulation	4	0.0108	1	0.0107	1
Platelet activation, signaling and aggregation	220	0.593	3	0.02	1
Developmental Biology	417	1.12	4	0.0228	1
Axonal growth inhibition (RHOA activation)	9	0.0243	1	0.024	1
p75NTR regulates axonogenesis	10	0.027	1	0.0267	1
Golgi Cisternae Pericentriolar Stack Reorganization	14	0.0377	1	0.0371	1



## MODULE 16

Pathway	Total	Expected	Hits	P.Value	FDR
TGF-beta receptor signaling activates SMADs	30	0.0674	5	3.76E-09	5.27E-06
TGF-beta receptor signaling in EMT (epithelial to mesenchymal transition)	17	0.0382	4	3.86E-08	2.71E-05
Signaling by BMP	24	0.0539	4	1.71E-07	7.98E-05
Downregulation of TGF-beta receptor signaling	27	0.0607	4	2.81E-07	8.51E-05
Signaling by TGF-beta Receptor Complex	70	0.157	5	3.03E-07	8.51E-05
Molecules associated with elastic fibres	38	0.0854	2	0.00316	0.739
Elastic fibre formation	45	0.101	2	0.00441	0.789
Signal Transduction	1690	3.79	9	0.0045	0.789
Stimuli-sensing channels	63	0.142	2	0.0085	1
Platelet activation, signaling and aggregation	220	0.494	3	0.012	1
Release of eIF4E	6	0.0135	1	0.0134	1
Platelet degranulation	89	0.2	2	0.0165	1
Response to elevated platelet cytosolic Ca2+	94	0.211	2	0.0183	1
S6K1-mediated signalling	9	0.0202	1	0.02	1
Regulation of Signaling by NODAL	9	0.0202	1	0.02	1
mTORC1-mediated signalling	11	0.0247	1	0.0245	1
Elevation of cytosolic Ca2+ levels	12	0.027	1	0.0266	1
Keratan sulfate degradation	12	0.027	1	0.0266	1
Signaling by Activin	12	0.027	1	0.0266	1
Ion channel transport	128	0.288	2	0.0325	1
Regulation of AMPK activity via LKB1	16	0.0359	1	0.0354	1
Signaling by NODAL	17	0.0382	1	0.0376	1
Energy dependent regulation of mTOR by LKB1-AMPK	19	0.0427	1	0.0419	1
cGMP effects	21	0.0472	1	0.0462	1
Extracellular matrix organization	157	0.353	2	0.0472	1
Platelet calcium homeostasis	22	0.0494	1	0.0483	1

## MODULE 17

Pathway	Total	Expected	Hits	P.Value	FDR
p75 NTR receptor-mediated signalling	85	0.165	8	6.03E-13	8.45E-10
p75NTR regulates axonogenesis	10	0.0195	5	2.92E-12	2.05E-09
Signalling by NGF	290	0.565	10	5.23E-12	2.44E-09
Axonal growth inhibition (RHOA activation)	9	0.0175	4	1.08E-09	3.80E-07
p75NTR recruits signalling complexes	13	0.0253	4	6.12E-09	1.72E-06
NRIF signals cell death from the nucleus	15	0.0292	4	1.17E-08	2.72E-06
p75NTR signals via NF-kB	16	0.0312	4	1.55E-08	3.11E-06
Activation of TRKA receptors	6	0.0117	3	1.15E-07	2.01E-05
NF-kB is activated and signals survival	13	0.0253	3	1.63E-06	0.000254
TRKA activation by NGF	2	0.00389	2	3.50E-06	0.000491
Cell death signalling via NRAGE, NRIF and NADE	62	0.121	4	4.53E-06	0.000577
Ceramide signalling	3	0.00584	2	1.05E-05	0.00105
NFG and proNGF binds to p75NTR	3	0.00584	2	1.05E-05	0.00105
Signalling to STAT3	3	0.00584	2	1.05E-05	0.00105
Signal Transduction	1690	3.29	11	1.22E-05	0.00114
Axonal growth stimulation	4	0.00779	2	2.10E-05	0.00184
NGF-independant TRKA activation	5	0.00973	2	3.49E-05	0.00288
p75NTR negatively regulates cell cycle via SC1	6	0.0117	2	5.23E-05	0.00407
NADE modulates death signalling	7	0.0136	2	7.31E-05	0.00539
Regulated proteolysis of p75NTR	10	0.0195	2	0.000156	0.0109
Retrograde neurotrophin signalling	13	0.0253	2	0.00027	0.018
Signalling to p38 via RIT and RIN	15	0.0292	2	0.000362	0.0231
ARMS-mediated activation	16	0.0312	2	0.000414	0.0252
Frs2-mediated activation	18	0.035	2	0.000526	0.0307
Prolonged ERK activation events	20	0.0389	2	0.000652	0.0366
Signalling to RAS	27	0.0526	2	0.0012	0.0644
PLC-gamma1 signalling	37	0.072	2	0.00224	0.112
Signalling to ERKs	37	0.072	2	0.00224	0.112
NRAGE signals death through JNK	45	0.0876	2	0.0033	0.154

Interleukin-1 signaling	45	0.0876	2	0.0033	0.154
NGF signalling via TRKA from the plasma membrane	207	0.403	3	0.00667	0.302
NGF processing	4	0.00779	1	0.00777	0.34
PI3K/AKT activation	106	0.206	2	0.0174	0.717
A third proteolytic cleavage releases NICD	9	0.0175	1	0.0174	0.717
Signaling by Interleukins	116	0.226	2	0.0206	0.804
Signaling by NOTCH3	11	0.0214	1	0.0212	0.804
Signaling by NOTCH4	11	0.0214	1	0.0212	0.804
Signaling by NOTCH2	18	0.035	1	0.0345	1
NOTCH2 Activation and Transmission of Signal to the Nucleus	18	0.035	1	0.0345	1
JNK (c-Jun kinases) phosphorylation and activation mediated by activated human TAK1	20	0.0389	1	0.0383	1
TAK1 activates NFkB by phosphorylation and activation of IKKs complex	22	0.0428	1	0.042	1
activated TAK1 mediates p38 MAPK activation	23	0.0448	1	0.0439	1
Activation of Gene Expression by SREBP (SREBF)	26	0.0506	1	0.0495	1

MODULE 18					
Pathway	Total	Expected	Hits	P.Value	FDR
Downregulation of TGF-beta receptor signaling	27	0.00809	1	0.00807	1
TGF-beta receptor signaling activates SMADs	30	0.00899	1	0.00897	1
Deposition of New CENPA-containing Nucleosomes at the Centromere	65	0.0195	1	0.0194	1
Nucleosome assembly	65	0.0195	1	0.0194	1
Signaling by TGF-beta Receptor Complex	70	0.021	1	0.0209	1
Chromosome Maintenance	124	0.0371	1	0.0368	1
Cell Cycle	508	0.152	1	0.146	1
Signal Transduction	1690	0.506	1	0.442	1

## MODULE 19

Pathway	Total	Expected	Hits	P.Value	FDR
Molecules associated with elastic fibres	38	0.0797	6	6.53E-11	9.16E-08
Elastic fibre formation	45	0.0944	6	1.91E-10	1.34E-07
Extracellular matrix organization	157	0.329	7	1.04E-08	4.86E-06
Lipoprotein metabolism	22	0.0461	2	0.000921	0.132
A tetrasaccharide linker sequence is required for GAG synthesis	27	0.0566	2	0.00139	0.132
Glycosaminoglycan metabolism	118	0.247	3	0.0017	0.132
MPS VI - Maroteaux-Lamy syndrome	118	0.247	3	0.0017	0.132
Mucopolysaccharidoses	118	0.247	3	0.0017	0.132
MPS IX - Natowicz syndrome	118	0.247	3	0.0017	0.132
MPS IIIB - Sanfilippo syndrome B	118	0.247	3	0.0017	0.132
MPS I - Hurler syndrome	118	0.247	3	0.0017	0.132
MPS II - Hunter syndrome	118	0.247	3	0.0017	0.132
MPS VII - Sly syndrome	118	0.247	3	0.0017	0.132
MPS IV - Morquio syndrome A	118	0.247	3	0.0017	0.132
MPS IIIC - Sanfilippo syndrome C	118	0.247	3	0.0017	0.132
MPS IV - Morquio syndrome B	118	0.247	3	0.0017	0.132
MPS IIIA - Sanfilippo syndrome A	118	0.247	3	0.0017	0.132
MPS IIID - Sanfilippo syndrome D	118	0.247	3	0.0017	0.132
Lipid digestion, mobilization, and transport	41	0.086	2	0.0032	0.224
Nuclear signaling by ERBB4	41	0.086	2	0.0032	0.224
Signaling by ERBB4	152	0.319	3	0.0035	0.234
Chondroitin sulfate/dermatan sulfate metabolism	53	0.111	2	0.00529	0.337
Heparan sulfate/heparin (HS-GAG) metabolism	56	0.117	2	0.00589	0.359
Disease	945	1.98	6	0.00861	0.503
FGFR1b ligand binding and activation	5	0.0105	1	0.0104	0.586
FGFR2b ligand binding and activation	6	0.0126	1	0.0125	0.67
Amyloids	84	0.176	2	0.0129	0.67
Constitutive Signaling by NOTCH1 t(7;9)(NOTCH1:M1580_K2555) Translocation Mutant	7	0.0147	1	0.0146	0.705
FGFR3b ligand binding and activation	7	0.0147	1	0.0146	0.705

Metabolism of carbohydrates	258	0.541	3	0.0151	0.707
Dermatan sulfate biosynthesis	10	0.021	1	0.0208	0.793
Crosslinking of collagen fibrils	11	0.0231	1	0.0228	0.793
FGFR1c ligand binding and activation	11	0.0231	1	0.0228	0.793
FGFR3c ligand binding and activation	11	0.0231	1	0.0228	0.793
FGFR3 ligand binding and activation	11	0.0231	1	0.0228	0.793
Signaling by activated point mutants of FGFR3	11	0.0231	1	0.0228	0.793
Signaling by activated point mutants of FGFR1	11	0.0231	1	0.0228	0.793
Signaling by FGFR3 mutants	11	0.0231	1	0.0228	0.793
Signaling by NOTCH3	11	0.0231	1	0.0228	0.793
Signaling by NOTCH4	11	0.0231	1	0.0228	0.793
Chylomicron-mediated lipid transport	12	0.0252	1	0.0249	0.793
FGFR2c ligand binding and activation	12	0.0252	1	0.0249	0.793
FGFR4 ligand binding and activation	12	0.0252	1	0.0249	0.793
Keratan sulfate degradation	12	0.0252	1	0.0249	0.793
HDL-mediated lipid transport	13	0.0273	1	0.0269	0.829
Receptor-ligand binding initiates the second proteolytic cleavage of Notch receptor	14	0.0294	1	0.029	0.829
FGFR1 ligand binding and activation	14	0.0294	1	0.029	0.829
Constitutive Signaling by NOTCH1 HD Domain Mutants	14	0.0294	1	0.029	0.829
CS/DS degradation	14	0.0294	1	0.029	0.829
Anchoring fibril formation	15	0.0315	1	0.031	0.87
FGFR2 ligand binding and activation	16	0.0335	1	0.0331	0.875
Signaling by FGFR2 mutants	16	0.0335	1	0.0331	0.875
Activated point mutants of FGFR2	16	0.0335	1	0.0331	0.875
Prolactin receptor signaling	17	0.0356	1	0.0351	0.911
Signaling by NOTCH2	18	0.0377	1	0.0371	0.929
NOTCH2 Activation and Transmission of Signal to the Nucleus	18	0.0377	1	0.0371	0.929
FGFR ligand binding and activation	22	0.0461	1	0.0452	1
HS-GAG degradation	22	0.0461	1	0.0452	1
Growth hormone receptor signaling	23	0.0482	1	0.0472	1
Chondroitin sulfate biosynthesis	23	0.0482	1	0.0472	1

## MODULE 20

Pathway	Total	Expected	Hits	P.Value	FDR
Axon guidance	292	0.7	9	4.52E-09	6.34E-06
Developmental Biology	417	0.999	9	1.03E-07	7.19E-05
Signaling by Robo receptor	34	0.0815	4	9.77E-07	0.000457
Cell-extracellular matrix interactions	19	0.0455	3	1.07E-05	0.00375
Cell-Cell communication	143	0.343	5	1.52E-05	0.00425
Platelet degranulation	89	0.213	4	4.75E-05	0.00951
Cell junction organization	89	0.213	4	4.75E-05	0.00951
Response to elevated platelet cytosolic Ca2+	94	0.225	4	5.89E-05	0.0103
Platelet activation, signaling and aggregation	220	0.527	5	0.00012	0.0188
Role of Abl in Robo-Slit signaling	9	0.0216	2	0.000192	0.0269
Regulation of actin dynamics for phagocytic cup formation	62	0.149	3	0.000392	0.0499
Semaphorin interactions	72	0.173	3	0.000609	0.0711
Fcgamma receptor (FCGR) dependent phagocytosis	86	0.206	3	0.00102	0.11
Sema4D induced cell migration and growth-cone collapse	29	0.0695	2	0.0021	0.211
Adherens junctions interactions	31	0.0743	2	0.0024	0.225
Sema4D in semaphorin signaling	34	0.0815	2	0.00289	0.253
Hemostasis	511	1.22	5	0.00553	0.456
Muscle contraction	52	0.125	2	0.00666	0.519
Cell-cell junction organization	60	0.144	2	0.00879	0.648
NOSTRIN mediated eNOS trafficking	5	0.012	1	0.0119	0.836
Regulation of cytoskeletal remodeling and cell spreading by IPP complex components	9	0.0216	1	0.0214	1
Formation of annular gap junctions	11	0.0264	1	0.0261	1
Gap junction degradation	12	0.0288	1	0.0284	1
DCC mediated attractive signaling	14	0.0335	1	0.0331	1
GRB2:SOS provides linkage to MAPK signaling for Integrins	15	0.0359	1	0.0354	1
p130Cas linkage to MAPK signaling for integrins	15	0.0359	1	0.0354	1
Sema3A PAK dependent Axon repulsion	16	0.0383	1	0.0377	1
Metabolism of nitric oxide	20	0.0479	1	0.0469	1
eNOS activation and regulation	20	0.0479	1	0.0469	1

## MODULE 21

Pathway	Total	Expected	Hits	P.Value	FDR
Integrin cell surface interactions	85	0.0891	6	2.47E-11	3.46E-08
Type I hemidesmosome assembly	12	0.0126	2	6.19E-05	0.0434
Anchoring fibril formation	15	0.0157	2	9.83E-05	0.0459
L1CAM interactions	112	0.117	3	0.000153	0.0537
Assembly of collagen fibrils and other multimeric structures	54	0.0566	2	0.00131	0.333
Signal Transduction	1690	1.77	6	0.00142	0.333
Axon guidance	292	0.306	3	0.00254	0.509
Collagen formation	85	0.0891	2	0.00323	0.55
Cell junction organization	89	0.0933	2	0.00353	0.55
Developmental Biology	417	0.437	3	0.00701	0.982
Cell-Cell communication	143	0.15	2	0.00891	1
Extracellular matrix organization	157	0.165	2	0.0107	1
Striated Muscle Contraction	31	0.0325	1	0.0321	1



## MODULE 22

Pathway	Total	Expected	Hits	P.Value	FDR
Pyruvate metabolism and Citric Acid (TCA) cycle	49	0.0954	6	1.88E-10	2.64E-07
The citric acid (TCA) cycle and respiratory electron transport	145	0.282	6	1.43E-07	7.01E-05
Metabolism	1490	2.9	12	1.50E-07	7.01E-05
Pyruvate metabolism	21	0.0409	3	7.52E-06	0.00263
Citric acid cycle (TCA cycle)	26	0.0506	3	1.46E-05	0.0041
Glucose metabolism	70	0.136	3	0.000293	0.0684
Metabolism of carbohydrates	258	0.502	4	0.00118	0.237
Gluconeogenesis	35	0.0681	2	0.00201	0.352
Abnormal metabolism in phenylketonuria	4	0.00779	1	0.00777	1
Galactose catabolism	5	0.00973	1	0.0097	1
Glycogen synthesis	8	0.0156	1	0.0155	1
ChREBP activates metabolic gene expression	8	0.0156	1	0.0155	1
Pentose phosphate pathway (hexose monophosphate shunt)	9	0.0175	1	0.0174	1
Regulation of Gene Expression by Hypoxia-inducible Factor	9	0.0175	1	0.0174	1
Regulation of pyruvate dehydrogenase (PDH) complex	13	0.0253	1	0.025	1
Fatty acid, triacylglycerol, and ketone body metabolism	139	0.271	2	0.0289	1
Glycogen breakdown (glycogenolysis)	18	0.035	1	0.0345	1
Fatty Acyl-CoA Biosynthesis	18	0.035	1	0.0345	1

## MODULE 23

Pathway	Total	Expected	Hits	P.Value	FDR
Regulation of Insulin Secretion by Free Fatty Acids	8	0.0144	2	8.24E-05	0.0578
Regulation of Insulin Secretion by Fatty Acids Bound to GPR40 (FFAR1)	8	0.0144	2	8.24E-05	0.0578
Regulation of Insulin Secretion by Acetylcholine	11	0.0198	2	0.000161	0.0754
Transport of inorganic cations/anions and amino acids/oligopeptides	96	0.173	3	0.000577	0.202
Thromboxane signalling through TP receptor	25	0.0449	2	0.000868	0.237
ADP signalling through P2Y purinoceptor 1	27	0.0485	2	0.00101	0.237
Signal amplification	33	0.0593	2	0.00152	0.282
Thrombin signalling through proteinase activated receptors (PARs)	34	0.0611	2	0.00161	0.282
Type II Na <sup>+</sup> /Pi cotransporters	4	0.00719	1	0.00717	0.866
SLC-mediated transmembrane transport	251	0.451	3	0.00897	0.866
Regulation of Insulin Secretion	82	0.147	2	0.00908	0.866
Constitutive PI3K/AKT Signaling in Cancer	89	0.16	2	0.0106	0.866
Sodium-coupled phosphate cotransporters	6	0.0108	1	0.0107	0.866
The retinoid cycle in cones (daylight vision)	7	0.0126	1	0.0125	0.866
PI3K events in ERBB4 signaling	103	0.185	2	0.0141	0.866
PIP3 activates AKT signaling	103	0.185	2	0.0141	0.866
PI-3K cascade	103	0.185	2	0.0141	0.866
PI3K/AKT Signaling in Cancer	103	0.185	2	0.0141	0.866
PI3K events in ERBB2 signaling	103	0.185	2	0.0141	0.866
Adrenoceptors	8	0.0144	1	0.0143	0.866
GAB1 signalosome	106	0.191	2	0.0149	0.866
PI3K/AKT activation	106	0.191	2	0.0149	0.866
Signal Transduction	1690	3.03	7	0.0151	0.866
Integration of energy metabolism	109	0.196	2	0.0157	0.866
Bicarbonate transporters	9	0.0162	1	0.0161	0.866
Sodium/Proton exchangers	9	0.0162	1	0.0161	0.866
Retinoid cycle disease events	10	0.018	1	0.0178	0.926
Negative regulation of the PI3K/AKT network	11	0.0198	1	0.0196	0.982
G alpha (s) signalling events	127	0.228	2	0.0209	1

Role of second messengers in netrin-1 signaling	13	0.0234	1	0.0231	1
Signaling by SCF-KIT	142	0.255	2	0.0258	1
The canonical retinoid cycle in rods (twilight vision)	15	0.027	1	0.0266	1
Downstream signaling of activated FGFR	150	0.27	2	0.0285	1
Signaling by ERBB4	152	0.273	2	0.0293	1
Signaling by FGFR	162	0.291	2	0.0329	1
Downstream signal transduction	163	0.293	2	0.0333	1
Signaling by ERBB2	164	0.295	2	0.0337	1
DAP12 signaling	164	0.295	2	0.0337	1
Downstream Signaling Events Of B Cell Receptor (BCR)	173	0.311	2	0.0371	1
Signaling by FGFR in disease	178	0.32	2	0.0391	1
Signaling by EGFR	179	0.322	2	0.0395	1
Signaling by EGFR in Cancer	181	0.325	2	0.0403	1
DAP12 interactions	182	0.327	2	0.0408	1
G alpha (q) signalling events	188	0.338	2	0.0432	1
Signaling by PDGF	189	0.34	2	0.0437	1
Synthesis of IP3 and IP4 in the cytosol	27	0.0485	1	0.0475	1
Signaling by the B Cell Receptor (BCR)	199	0.358	2	0.0479	1
GPCR downstream signaling	812	1.46	4	0.0483	1

## MODULE 24

Pathway	Total	Expected	Hits	P.Value	FDR
NCAM signaling for neurite out-growth	65	0.146	8	3.16E-13	4.42E-10
Interaction between L1 and Ankyrins	29	0.0651	6	1.89E-11	1.32E-08
L1CAM interactions	112	0.252	8	2.84E-11	1.33E-08
Axon guidance	292	0.656	9	2.06E-09	7.21E-07
Developmental Biology	417	0.937	9	4.75E-08	1.33E-05
Interferon gamma signaling	74	0.166	5	4.02E-07	9.39E-05
Interferon Signaling	173	0.389	6	1.14E-06	0.000229
Interferon alpha/beta signaling	68	0.153	4	1.23E-05	0.00216
Cytokine Signaling in Immune system	286	0.643	6	2.12E-05	0.00329
Immune System	1140	2.56	10	2.61E-05	0.00367
Signaling by FGFR mutants	45	0.101	3	0.000123	0.0157
Phospholipase C-mediated cascade	57	0.128	3	0.00025	0.0292
Downstream signaling of activated FGFR	150	0.337	4	0.000275	0.0297
Signaling by FGFR	162	0.364	4	0.00037	0.032
Downstream signal transduction	163	0.366	4	0.000379	0.032
Signaling by ERBB2	164	0.368	4	0.000388	0.032
DAP12 signaling	164	0.368	4	0.000388	0.032
Signaling by FGFR in disease	178	0.4	4	0.000529	0.0385
Signaling by EGFR	179	0.402	4	0.000541	0.0385
Signaling by EGFR in Cancer	181	0.407	4	0.000564	0.0385
DAP12 interactions	182	0.409	4	0.000576	0.0385
Signaling by PDGF	189	0.425	4	0.000664	0.0423
Signaling by the B Cell Receptor (BCR)	199	0.447	4	0.000807	0.0492
Constitutive PI3K/AKT Signaling in Cancer	89	0.2	3	0.000928	0.0525
NGF signalling via TRKA from the plasma membrane	207	0.465	4	0.000936	0.0525
FGFR ligand binding and activation	22	0.0494	2	0.00106	0.0572
Nephrin interactions	24	0.0539	2	0.00126	0.0621
PI3K events in ERBB4 signaling	103	0.231	3	0.00142	0.0621
PIP3 activates AKT signaling	103	0.231	3	0.00142	0.0621

PI-3K cascade	103	0.231	3	0.00142	0.0621
PI3K/AKT Signaling in Cancer	103	0.231	3	0.00142	0.0621
PI3K events in ERBB2 signaling	103	0.231	3	0.00142	0.0621
GAB1 signalosome	106	0.238	3	0.00154	0.0635
PI3K/AKT activation	106	0.238	3	0.00154	0.0635
SHC-mediated cascade	28	0.0629	2	0.00172	0.069
Signaling by FGFR1 mutants	31	0.0696	2	0.00211	0.0822
Signaling by FGFR1 amplification mutants	1	0.00225	1	0.00225	0.0829
Signaling by FGFR2 amplification mutants	1	0.00225	1	0.00225	0.0829
Signal transduction by L1	35	0.0786	2	0.00269	0.0965
Signalling by NGF	290	0.651	4	0.00325	0.114
FRS2-mediated cascade	39	0.0876	2	0.00333	0.114
Signaling by SCF-KIT	142	0.319	3	0.00355	0.119
Negative regulation of FGFR signaling	41	0.0921	2	0.00367	0.12
Signaling by ERBB4	152	0.341	3	0.0043	0.137
Downstream Signaling Events Of B Cell Receptor (BCR)	173	0.389	3	0.00618	0.193
FGFR1c and Klotho ligand binding and activation	3	0.00674	1	0.00673	0.205
Adaptive Immune System	654	1.47	5	0.0116	0.345
PI3K Cascade	76	0.171	2	0.0122	0.356
FGFR2b ligand binding and activation	6	0.0135	1	0.0134	0.376
Klotho-mediated ligand binding	6	0.0135	1	0.0134	0.376
IRS-mediated signalling	87	0.195	2	0.0158	0.434
IRS-related events	90	0.202	2	0.0168	0.454
IRS-related events triggered by IGF1R	91	0.204	2	0.0172	0.455
Signaling by Type 1 Insulin-like Growth Factor 1 Receptor (IGF1R)	94	0.211	2	0.0183	0.466
IGF1R signaling cascade	94	0.211	2	0.0183	0.466
Insulin receptor signalling cascade	95	0.213	2	0.0186	0.467
FGFR1c ligand binding and activation	11	0.0247	1	0.0245	0.591
Signaling by activated point mutants of FGFR1	11	0.0247	1	0.0245	0.591
Innate Immune System	521	1.17	4	0.025	0.594
FGFR2c ligand binding and activation	12	0.027	1	0.0266	0.623

Signaling by Insulin receptor	117	0.263	2	0.0275	0.632
PECAM1 interactions	13	0.0292	1	0.0288	0.632
Caspase-mediated cleavage of cytoskeletal proteins	13	0.0292	1	0.0288	0.632
Role of second messengers in netrin-1 signaling	13	0.0292	1	0.0288	0.632
FGFR1 ligand binding and activation	14	0.0315	1	0.031	0.669
FGFR2 ligand binding and activation	16	0.0359	1	0.0354	0.73
Signaling by FGFR2 mutants	16	0.0359	1	0.0354	0.73
Activated point mutants of FGFR2	16	0.0359	1	0.0354	0.73
Regulation of KIT signaling	17	0.0382	1	0.0376	0.763
Frs2-mediated activation	18	0.0404	1	0.0397	0.787
Cell-Cell communication	143	0.321	2	0.0399	0.787
Signaling by constitutively active EGFR	19	0.0427	1	0.0419	0.816
Prolonged ERK activation events	20	0.0449	1	0.044	0.834
Signaling by FGFR1 fusion mutants	20	0.0449	1	0.044	0.834

## MODULE 25

Pathway	Total	Expected	Hits	P.Value	FDR
Interleukin-6 signaling	14	0.0126	6	2.45E-17	3.43E-14
Signaling by Interleukins	116	0.104	6	2.42E-11	1.69E-08
Cytokine Signaling in Immune system	286	0.257	6	5.87E-09	2.74E-06
Regulation of IFNG signaling	17	0.0153	3	2.73E-07	9.57E-05
Regulation of IFNA signaling	27	0.0243	3	1.17E-06	0.000328
Interferon alpha/beta signaling	68	0.0611	3	1.98E-05	0.00447
Immune System	1140	1.02	6	2.42E-05	0.00447
Interferon gamma signaling	74	0.0665	3	2.55E-05	0.00447
Growth hormone receptor signaling	23	0.0207	2	0.000169	0.0263
Interferon Signaling	173	0.155	3	0.000323	0.0453
Antiviral mechanism by IFN-stimulated genes	69	0.062	2	0.00154	0.18
ISG15 antiviral mechanism	69	0.062	2	0.00154	0.18
Interleukin-7 signaling	12	0.0108	1	0.0107	1
Signaling by FGFR1 fusion mutants	20	0.018	1	0.0178	1
Interleukin receptor SHC signaling	28	0.0252	1	0.0249	1
Signaling by FGFR1 mutants	31	0.0279	1	0.0275	1
Interleukin-2 signaling	42	0.0377	1	0.0372	1
Signaling by FGFR mutants	45	0.0404	1	0.0398	1
Interleukin-3, 5 and GM-CSF signaling	51	0.0458	1	0.045	1

## MODULE 26

Pathway	Total	Expected	Hits	P.Value	FDR
Antigen Presentation: Folding, assembly and peptide loading of class I MHC	25	0.0412	7	1.34E-15	1.88E-12
Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell	80	0.132	8	4.76E-14	3.34E-11
Endosomal/Vacuolar pathway	10	0.0165	5	1.05E-12	4.91E-10
Adaptive Immune System	654	1.08	10	7.66E-10	2.69E-07
ER-Phagosome pathway	63	0.104	5	2.82E-08	7.89E-06
Class I MHC mediated antigen processing & presentation	267	0.44	7	4.35E-08	1.02E-05
Interferon gamma signaling	74	0.122	5	6.40E-08	1.28E-05
Antigen processing-Cross presentation	78	0.129	5	8.36E-08	1.47E-05
Immune System	1140	1.87	10	1.86E-07	2.90E-05
Interferon alpha/beta signaling	68	0.112	4	3.08E-06	0.000431
Interferon Signaling	173	0.285	5	4.49E-06	0.000572
Nef-mediates down modulation of cell surface receptors by recruiting them to clathrin adapters	24	0.0395	3	6.61E-06	0.000772
The role of Nef in HIV-1 replication and disease pathogenesis	31	0.0511	3	1.46E-05	0.00157
Cytokine Signaling in Immune system	286	0.471	5	5.20E-05	0.00521
COPII (Coat Protein 2) Mediated Vesicle Transport	9	0.0148	2	8.83E-05	0.00774
ER to Golgi Transport	9	0.0148	2	8.83E-05	0.00774
Nef mediated downregulation of MHC class I complex cell surface expression	13	0.0214	2	0.000191	0.0157
Host Interactions of HIV factors	141	0.232	3	0.00134	0.105
Transport to the Golgi and subsequent modification	35	0.0577	2	0.00143	0.105
HIV Infection	214	0.353	3	0.00443	0.31
Asparagine N-linked glycosylation	86	0.142	2	0.00836	0.558
Nef Mediated CD8 Down-regulation	7	0.0115	1	0.0115	0.732
MHC class II antigen presentation	118	0.194	2	0.0153	0.936
Crosslinking of collagen fibrils	11	0.0181	1	0.018	1
DAP12 signaling	164	0.27	2	0.0285	1
DAP12 interactions	182	0.3	2	0.0346	1
Post-translational protein modification	200	0.329	2	0.0411	1
Membrane Trafficking	203	0.334	2	0.0422	1



MODULE 27					
Pathway	Total	Expected	Hits	P.Value	FDR
Regulation of Complement cascade	15	0.0157	5	5.70E-13	7.99E-10
Complement cascade	33	0.0346	5	4.48E-11	3.14E-08
Alternative complement activation	6	0.00629	3	1.41E-08	6.59E-06
Activation of C3 and C5	7	0.00734	3	2.47E-08	8.64E-06
Initial triggering of complement	17	0.0178	3	4.77E-07	0.000134
Innate Immune System	521	0.546	5	5.22E-05	0.0122
Immune System	1140	1.19	5	0.00221	0.443
G alpha (i) signalling events	184	0.193	2	0.0145	1
Peptide ligand-binding receptors	192	0.201	2	0.0157	1
Class A/1 (Rhodopsin-like receptors)	312	0.327	2	0.0391	1

## MODULE 28

Pathway	Total	Expected	Hits	P.Value	FDR
Striated Muscle Contraction	31	0.0371	6	1.67E-13	2.34E-10
Muscle contraction	52	0.0623	6	4.59E-12	3.22E-09
NRAGE signals death through JNK	45	0.0539	1	0.0527	1
Cell death signalling via NRAGE, NRIF and NADE	62	0.0743	1	0.072	1
G alpha (12/13) signalling events	80	0.0959	1	0.092	1
p75 NTR receptor-mediated signalling	85	0.102	1	0.0975	1
Rho GTPase cycle	123	0.147	1	0.138	1
Signaling by Rho GTPases	123	0.147	1	0.138	1
Antigen processing: Ubiquitination & Proteasome degradation	224	0.268	1	0.239	1
Class I MHC mediated antigen processing & presentation	267	0.32	1	0.279	1

## MODULE 29

Pathway	Total	Expected	Hits	P.Value	FDR
Metabolism of Angiotensinogen to Angiotensins	14	0.0252	9	6.08E-24	8.52E-21
Peptide hormone metabolism	60	0.108	9	4.41E-17	3.09E-14
Metabolism of proteins	689	1.24	9	2.09E-07	9.75E-05
Peptide ligand-binding receptors	192	0.345	3	0.00425	1
Class A/1 (Rhodopsin-like receptors)	312	0.561	3	0.0162	1
Activation of the AP-1 family of transcription factors	10	0.018	1	0.0178	1
GPCR ligand binding	415	0.746	3	0.0344	1
G alpha (i) signalling events	184	0.331	2	0.0416	1
G alpha (q) signalling events	188	0.338	2	0.0432	1
Lysosome Vesicle Biogenesis	27	0.0485	1	0.0475	1

MODULE 30					
Pathway	Total	Expected	Hits	P.Value	FDR
Scavenging of Heme from Plasma	15	0.0157	5	5.70E-13	3.99E-10
Binding and Uptake of Ligands by Scavenger Receptors	15	0.0157	5	5.70E-13	3.99E-10
Uptake of Oxygen and Release of Carbon Dioxide by Erythrocytes	10	0.0105	3	8.44E-08	2.37E-05
Uptake of Carbon Dioxide and Release of Oxygen by Erythrocytes	10	0.0105	3	8.44E-08	2.37E-05
O2/CO2 exchange in erythrocytes	10	0.0105	3	8.44E-08	2.37E-05
Factors involved in megakaryocyte development and platelet production	155	0.162	3	0.000401	0.0937
Hemostasis	511	0.536	3	0.0124	1
Metabolism	1490	1.56	3	0.189	1

## MODULE 31

Pathway	Total	Expected	Hits	P.Value	FDR
Activation of Matrix Metalloproteinases	31	0.0511	10	1.01E-23	1.41E-20
Degradation of the extracellular matrix	77	0.127	10	2.48E-19	1.74E-16
Extracellular matrix organization	157	0.259	10	4.18E-16	1.96E-13
Degradation of collagen	61	0.1	7	1.20E-12	4.19E-10
Assembly of collagen fibrils and other multimeric structures	54	0.089	2	0.00337	0.945
Collagen formation	85	0.14	2	0.00818	1
Platelet degranulation	89	0.147	2	0.00894	1
Response to elevated platelet cytosolic Ca <sup>2+</sup>	94	0.155	2	0.00993	1
EGFR Transactivation by Gastrin	9	0.0148	1	0.0147	1
Regulation of Insulin-like Growth Factor (IGF) Transport and Uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs)	21	0.0346	1	0.0341	1
Hemostasis	511	0.842	3	0.0463	1
Platelet activation, signaling and aggregation	220	0.362	2	0.0489	1

## MODULE 32

Pathway	Total	Expected	Hits	P.Value	FDR
Formation of Fibrin Clot (Clotting Cascade)	29	0.0347	7	1.06E-16	1.49E-13
Extrinsic Pathway	5	0.00599	5	5.07E-16	3.55E-13
Gamma-carboxylation of protein precursors	10	0.012	4	1.77E-10	8.28E-08
Gamma-carboxylation, transport, and amino-terminal cleavage of proteins	12	0.0144	4	4.17E-10	1.46E-07
PTM: gamma carboxylation, hypusine formation and arylsulfatase activation	29	0.0347	4	1.99E-08	5.57E-06
Transport of gamma-carboxylated protein precursors from the endoplasmic reticulum to the Golgi apparatus	9	0.0108	3	9.45E-08	2.21E-05
Hemostasis	511	0.612	7	1.11E-07	2.21E-05
Removal of aminoterminal propeptides from gamma-carboxylated proteins	10	0.012	3	1.35E-07	2.37E-05
Common Pathway	11	0.0132	3	1.85E-07	2.89E-05
Post-translational protein modification	200	0.24	4	4.98E-05	0.00698
Intrinsic Pathway	17	0.0204	2	0.000169	0.0216
Metabolism of proteins	689	0.826	4	0.0056	0.654
BMAL1:CLOCK/NPAS2 Activates Circadian Expression	14	0.0168	1	0.0167	1
Circadian Clock	35	0.0419	1	0.0412	1

## MODULE 33

Pathway	Total	Expected	Hits	P.Value	FDR
Glycoprotein hormones	7	0.0105	7	1.03E-21	1.44E-18
Peptide hormone biosynthesis	9	0.0135	7	3.69E-20	2.59E-17
Peptide hormone metabolism	60	0.0899	7	3.88E-13	1.81E-10
Hormone ligand-binding receptors	10	0.015	5	5.73E-13	2.01E-10
G alpha (s) signalling events	127	0.19	5	5.37E-07	0.000151
Metabolism of proteins	689	1.03	7	1.10E-05	0.00257
Class A/1 (Rhodopsin-like receptors)	312	0.467	5	4.48E-05	0.00897
GPCR ligand binding	415	0.622	5	0.000176	0.0308
Signal regulatory protein (SIRP) family interactions	20	0.03	2	0.000378	0.0589
GPCR downstream signaling	812	1.22	5	0.00391	0.548
Signaling by GPCR	931	1.39	5	0.00715	0.912
Cell surface interactions at the vascular wall	99	0.148	2	0.00906	1
Cell-Cell communication	143	0.214	2	0.0183	1

## MODULE 34

Pathway	Total	Expected	Hits	P.Value	FDR
Utilization of Ketone Bodies	3	0.0018	1	0.0018	1
Ketone body metabolism	5	0.003	1	0.00299	1
Attachment of GPI anchor to uPAR	7	0.00419	1	0.00419	1
Dissolution of Fibrin Clot	10	0.00599	1	0.00598	1
Interleukin-6 signaling	14	0.00839	1	0.00836	1
Post-translational modification: synthesis of GPI-anchored proteins	26	0.0156	1	0.0155	1
Regulation of IFNA signaling	27	0.0162	1	0.0161	1
Golgi Associated Vesicle Biogenesis	57	0.0341	1	0.0337	1
trans-Golgi Network Vesicle Budding	64	0.0383	1	0.0378	1
Clathrin derived vesicle budding	64	0.0383	1	0.0378	1
Interferon alpha/beta signaling	68	0.0407	1	0.0401	1