



Supplementary Figure 1 Selection of common targets both related to eligible ingredients of *Hovenia dulcis* seeds and alcoholic liver disease.
ALD: Alcoholic liver disease.

Supplementary Table 1 Eligible bioactive compounds of *Hovenia dulcis* seeds and their corresponding putative targets¹

Molecule ID	Molecule Name	Target	Symbol
MOL002140	Perlolyrine	Prostaglandin G/H synthase 2	PTGS2
MOL002140	Perlolyrine	Retinoic acid receptor RXR-alpha	RXRA
MOL000358	β -Sitosterol	Progesterone receptor	PGR
MOL000358	β -Sitosterol	Nuclear receptor coactivator 2	NCOA2
MOL000358	β -Sitosterol	Prostaglandin G/H synthase 1	PTGS1
MOL000358	β -Sitosterol	Prostaglandin G/H synthase 2	PTGS2
MOL000358	β -Sitosterol	Potassium voltage-gated channel subfamily H member 2	KCNH2
MOL000358	β -Sitosterol	Muscarinic acetylcholine receptor M3	CHRM3
MOL000358	β -Sitosterol	Muscarinic acetylcholine receptor M1	CHRM1
MOL000358	β -Sitosterol	Sodium channel protein type 5 subunit alpha	SCN5A
MOL000358	β -Sitosterol	Muscarinic acetylcholine receptor M4	CHRM4

MOL000358	β -Sitosterol	Alpha-1A adrenergic receptor	ADRA1A
MOL000358	β -Sitosterol	Muscarinic acetylcholine receptor M2	CHRM2
MOL000358	β -Sitosterol	Alpha-1B adrenergic receptor	ADRA1B
MOL000358	β -Sitosterol	Beta-2 adrenergic receptor	ADRB2
MOL000358	β -Sitosterol	Neuronal acetylcholine receptor subunit alpha-2	CHRNA2
MOL000358	β -Sitosterol	Sodium-dependent serotonin transporter	SLC6A4
MOL000358	β -Sitosterol	Mu-type opioid receptor	OPRM1
MOL000358	β -Sitosterol	Gamma-aminobutyric acid receptor subunit alpha-1	GABRA1
MOL000358	β -Sitosterol	Apoptosis regulator Bcl-2	BCL2
MOL000358	β -Sitosterol	Apoptosis regulator BAX	BAX
MOL000358	β -Sitosterol	Caspase-9	CASP9
MOL000358	β -Sitosterol	Transcription factor AP-1	JUN
MOL000358	β -Sitosterol	Caspase-3	CASP3

MOL000358	β -Sitosterol	Caspase-8	CASP8
MOL000358	β -Sitosterol	Protein kinase C alpha type	PRKCA
MOL000358	β -Sitosterol	Serum paraoxonase/arylesterase 1	PON1
MOL000358	β -Sitosterol	Microtubule-associated protein 2	MAP2
MOL000422	Kaempferol	Nitric oxide synthase, inducible	NOS2
MOL000422	Kaempferol	Prostaglandin G/H synthase 1	PTGS1
MOL000422	Kaempferol	Androgen receptor	AR
MOL000422	Kaempferol	Peroxisome proliferator activated receptor gamma	PPARG
MOL000422	Kaempferol	Prostaglandin G/H synthase 2	PTGS2
MOL000422	Kaempferol	Nuclear receptor coactivator 2	NCOA2
MOL000422	Kaempferol	Trypsin-1	PRSS1
MOL000422	Kaempferol	Progesterone receptor	PGR
MOL000422	Kaempferol	Muscarinic acetylcholine receptor M1	CHRM1

MOL000422	Kaempferol	Acetylcholinesterase	ACHE
MOL000422	Kaempferol	Sodium-dependent noradrenaline transporter	SLC6A2
MOL000422	Kaempferol	Muscarinic acetylcholine receptor M2	CHRM2
MOL000422	Kaempferol	Alpha-1B adrenergic receptor	ADRA1B
MOL000422	Kaempferol	Gamma-aminobutyric acid receptor subunit alpha-1	GABRA1
MOL000422	Kaempferol	Coagulation factor VII	F7
MOL000422	Kaempferol	Transcription factor p65	RELA
MOL000422	Kaempferol	Inhibitor of nuclear factor kappa-B kinase subunit beta	IKBKB
MOL000422	Kaempferol	RAC-alpha serine/threonine-protein kinase	AKT1
MOL000422	Kaempferol	Apoptosis regulator Bcl-2	BCL2
MOL000422	Kaempferol	Apoptosis regulator BAX	BAX
MOL000422	Kaempferol	Tumor necrosis factor	TNFSF15
MOL000422	Kaempferol	Transcription factor AP-1	JUN

MOL000422	Kaempferol	Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1
MOL000422	Kaempferol	Caspase-3	CASP3
MOL000422	Kaempferol	Mitogen-activated protein kinase 8	MAPK8
MOL000422	Kaempferol	Interstitial collagenase	MMP1
MOL000422	Kaempferol	Signal transducer and activator of transcription 1-alpha/beta	STAT1
MOL000422	Kaempferol	Peroxisome proliferator-activated receptor gamma	PPARG
MOL000422	Kaempferol	Heme oxygenase 1	HMOX1
MOL000422	Kaempferol	Cytochrome P450 3A4	CYP3A4
MOL000422	Kaempferol	Cytochrome P450 1A2	CYP1A2
MOL000422	Kaempferol	Cytochrome P450 1A1	CYP1A1
MOL000422	Kaempferol	Intercellular adhesion molecule 1	ICAM1
MOL000422	Kaempferol	E-selectin	SELE

MOL000422	Kaempferol	Vascular cell adhesion protein 1	VCAM1
MOL000422	Kaempferol	Nuclear receptor subfamily 1 group I member 2	NR1I2
MOL000422	Kaempferol	Cytochrome P450 1B1	CYP1B1
MOL000422	Kaempferol	Arachidonate 5-lipoxygenase	ALOX5
MOL000422	Kaempferol	Hyaluronan synthase 2	HAS2
MOL000422	Kaempferol	Glutathione S-transferase P	GSTP1
MOL000422	Kaempferol	Aryl hydrocarbon receptor	AHR
MOL000422	Kaempferol	26S proteasome non-ATPase regulatory subunit 3	PSMD3
MOL000422	Kaempferol	Solute carrier family 2, facilitated glucose transporter member 4	SLC2A4
MOL000422	Kaempferol	Nuclear receptor subfamily 1 group I member 3	NR1I3
MOL000422	Kaempferol	Insulin receptor	INSR
MOL000422	Kaempferol	Type I iodothyronine deiodinase	DIO1
MOL000422	Kaempferol	Serine/threonine-protein phosphatase 2B catalytic	PPP3CA

subunit alpha isoform

MOL000422	Kaempferol	Glutathione S-transferase Mu 1	GSTM1
MOL000422	Kaempferol	Glutathione S-transferase Mu 2	GSTM2
MOL000422	Kaempferol	Aldo-keto reductase family 1 member C3	AKR1C3
MOL000422	Kaempferol	Antileukoproteinase	SLPI
MOL004328	Naringenin	Prostaglandin G/H synthase 1	PTGS1
MOL004328	Naringenin	Estrogen receptor	ESR1
MOL004328	Naringenin	Prostaglandin G/H synthase 2	PTGS2
MOL004328	Naringenin	Transcription factor p65	RELA
MOL004328	Naringenin	RAC-alpha serine/threonine-protein kinase	AKT1
MOL004328	Naringenin	Apoptosis regulator Bcl-2	BCL2
MOL004328	Naringenin	Mitogen-activated protein kinase 3	MAPK3
MOL004328	Naringenin	Mitogen-activated protein kinase 1	MAPK1

MOL004328	Naringenin	Caspase-3	CASP3
MOL004328	Naringenin	Fatty acid synthase	FASN
MOL004328	Naringenin	Low-density lipoprotein receptor	LDLR
MOL004328	Naringenin	Superoxide dismutase [Cu-Zn]	SOD1
MOL004328	Naringenin	Catalase	CAT
MOL004328	Naringenin	Peroxisome proliferator-activated receptor gamma	PPARG
MOL004328	Naringenin	Microsomal triglyceride transfer protein large subunit	MTTP
MOL004328	Naringenin	Apolipoprotein B-100	APOB
MOL004328	Naringenin	Phospholipase B1, membrane-associated	PLB1
MOL004328	Naringenin	3-hydroxy-3-methylglutaryl-coenzyme A reductase	HMGCR
MOL004328	Naringenin	Glutathione S-transferase P	GSTP1
MOL004328	Naringenin	UDP-glucuronosyltransferase 1-1	UGT1A1
MOL004328	Naringenin	Peroxisome proliferator-activated receptor alpha	PPARA

MOL004328	Naringenin	Sterol regulatory element-binding protein 1	SREBF1
MOL004328	Naringenin	Glutathione reductase, mitochondrial	GSR
MOL004328	Naringenin	Multidrug resistance-associated protein 1	ABCC1
MOL004328	Naringenin	Adiponectin	ADIPOQ
MOL004328	Naringenin	Sterol O-acyltransferase 2	SOAT2
MOL004328	Naringenin	Aldo-keto reductase family 1 member C1	AKR1C1
MOL004328	Naringenin	Aspartate aminotransferase, cytoplasmic	GOT1
MOL004328	Naringenin	4-aminobutyrate aminotransferase, mitochondrial	ABAT
MOL004328	Naringenin	Liver carboxylesterase 1	CES1
MOL004328	Naringenin	Sterol O-acyltransferase 1	SOAT1
MOL000449	Stigmasterol	Progesterone receptor	PGR
MOL000449	Stigmasterol	Mineralocorticoid receptor	NR3C2
MOL000449	Stigmasterol	Nuclear receptor coactivator 2	NCOA2

MOL000449	Stigmasterol	Alcohol dehydrogenase 1C	ADH1C
MOL000449	Stigmasterol	Retinoic acid receptor RXR-alpha	RXRA
MOL000449	Stigmasterol	Nuclear receptor coactivator 1	NCOA1
MOL000449	Stigmasterol	Prostaglandin G/H synthase 1	PTGS1
MOL000449	Stigmasterol	Prostaglandin G/H synthase 2	PTGS2
MOL000449	Stigmasterol	Alpha-2A adrenergic receptor	ADRA2A
MOL000449	Stigmasterol	Sodium-dependent noradrenaline transporter	SLC6A2
MOL000449	Stigmasterol	Sodium-dependent dopamine transporter	SLC6A3
MOL000449	Stigmasterol	Beta-2 adrenergic receptor	ADRB2
MOL000449	Stigmasterol	Aldose reductase	AKR1B1
MOL000449	Stigmasterol	Urokinase-type plasminogen activator	PLAU
MOL000449	Stigmasterol	Leukotriene A-4 hydrolase	LTA4H
MOL000449	Stigmasterol	Amine oxidase [flavin-containing] B	MAOB

MOL000449	Stigmasterol	Amine oxidase [flavin-containing] A	MAOA
MOL000449	Stigmasterol	Chymotrypsinogen B	CTRB1
MOL000449	Stigmasterol	Muscarinic acetylcholine receptor M3	CHRM3
MOL000449	Stigmasterol	Muscarinic acetylcholine receptor M1	CHRM1
MOL000449	Stigmasterol	Beta-1 adrenergic receptor	ADRB1
MOL000449	Stigmasterol	Sodium channel protein type 5 subunit alpha	SCN5A
MOL000449	Stigmasterol	Alpha-1A adrenergic receptor	ADRA1A
MOL000449	Stigmasterol	Muscarinic acetylcholine receptor M2	CHRM2
MOL000449	Stigmasterol	Alpha-1B adrenergic receptor	ADRA1B
MOL000449	Stigmasterol	Gamma-aminobutyric acid receptor subunit alpha-1	GABRA1
MOL000098	Quercetin	Prostaglandin G/H synthase 1	PTGS1
MOL000098	Quercetin	Androgen receptor	AR
MOL000098	Quercetin	Peroxisome proliferator activated receptor gamma	PPARG

MOL000098	Quercetin	Prostaglandin G/H synthase 2	PTGS2
MOL000098	Quercetin	Nuclear receptor coactivator 2	NCOA2
MOL000098	Quercetin	Aldose reductase	AKR1B1
MOL000098	Quercetin	Trypsin-1	PRSS1
MOL000098	Quercetin	Potassium voltage-gated channel subfamily H member 2	KCNH2
MOL000098	Quercetin	Sodium channel protein type 5 subunit alpha	SCN5A
MOL000098	Quercetin	Beta-2 adrenergic receptor	ADRB2
MOL000098	Quercetin	Stromelysin-1	MMP3
MOL000098	Quercetin	Coagulation factor VII	F7
MOL000098	Quercetin	Retinoic acid receptor RXR-alpha	RXRA
MOL000098	Quercetin	Acetylcholinesterase	ACHE
MOL000098	Quercetin	Gamma-aminobutyric acid receptor subunit alpha-1	GABRA1
MOL000098	Quercetin	Amine oxidase [flavin-containing] B	MAOB

MOL000098	Quercetin	Transcription factor p65	RELA
MOL000098	Quercetin	Epidermal growth factor receptor	EGFR
MOL000098	Quercetin	RAC-alpha serine/threonine-protein kinase	AKT1
MOL000098	Quercetin	Vascular endothelial growth factor A	VEGFA
MOL000098	Quercetin	G1/S-specific cyclin-D1	CCND1
MOL000098	Quercetin	Apoptosis regulator Bcl-2	BCL2
MOL000098	Quercetin	Bcl-2-like protein 1	BCL2L1
MOL000098	Quercetin	Proto-oncogene c-Fos	FOS
MOL000098	Quercetin	Cyclin-dependent kinase inhibitor 1	CDKN1A
MOL000098	Quercetin	Eukaryotic translation initiation factor 6	EIF6
MOL000098	Quercetin	Apoptosis regulator BAX	BAX
MOL000098	Quercetin	Caspase-9	CASP9
MOL000098	Quercetin	Urokinase-type plasminogen activator	PLAU

MOL000098	Quercetin	72 kDa type IV collagenase	MMP2
MOL000098	Quercetin	Matrix metalloproteinase-9	MMP9
MOL000098	Quercetin	Mitogen-activated protein kinase 1	MAPK1
MOL000098	Quercetin	Interleukin-10	IL10
MOL000098	Quercetin	Pro-epidermal growth factor	EGF
MOL000098	Quercetin	Retinoblastoma-associated protein	RB1
MOL000098	Quercetin	Tumor necrosis factor	TNFSF15
MOL000098	Quercetin	Transcription factor AP-1	JUN
MOL000098	Quercetin	Interleukin-6	IL6
MOL000098	Quercetin	Activator of 90 kDa heat shock protein ATPase homolog 1	AHSA1
MOL000098	Quercetin	Caspase-3	CASP3
MOL000098	Quercetin	Cellular tumor antigen p53	TP63
MOL000098	Quercetin	ETS domain-containing protein Elk-1	ELK1

MOL000098	Quercetin	NF-kappa-B inhibitor alpha	NFKBIA
MOL000098	Quercetin	NADPH--cytochrome P450 reductase	POR
MOL000098	Quercetin	Ornithine decarboxylase	ODC1
MOL000098	Quercetin	Caspase-8	CASP8
MOL000098	Quercetin	DNA topoisomerase 1	TOP1
MOL000098	Quercetin	RAF proto-oncogene serine/threonine-protein kinase	RAF1
MOL000098	Quercetin	Superoxide dismutase [Cu-Zn]	SOD1
MOL000098	Quercetin	Protein kinase C alpha type	PRKCA
MOL000098	Quercetin	Interstitial collagenase	MMP1
MOL000098	Quercetin	Hypoxia-inducible factor 1-alpha	HIF1A
MOL000098	Quercetin	Signal transducer and activator of transcription 1-alpha/beta	STAT1
MOL000098	Quercetin	Protein CBFA2T1	RUNX1T1
MOL000098	Quercetin	Receptor tyrosine-protein kinase erbB-2	ERBB2

MOL000098	Quercetin	Peroxisome proliferator-activated receptor gamma	PPARG
MOL000098	Quercetin	Acetyl-CoA carboxylase 1	ACACA
MOL000098	Quercetin	Heme oxygenase 1	HMOX1
MOL000098	Quercetin	Cytochrome P450 3A4	CYP3A4
MOL000098	Quercetin	Cytochrome P450 1A2	CYP1A2
MOL000098	Quercetin	Caveolin-1	CAV1
MOL000098	Quercetin	Myc proto-oncogene protein	MYC
MOL000098	Quercetin	Tissue factor	F3
MOL000098	Quercetin	Gap junction alpha-1 protein	GJA1
MOL000098	Quercetin	Cytochrome P450 1A1	CYP1A1
MOL000098	Quercetin	Intercellular adhesion molecule 1	ICAM1
MOL000098	Quercetin	Interleukin-1 beta	IL1B
MOL000098	Quercetin	C-C motif chemokine 2	CCL2

MOL000098	Quercetin	E-selectin	SELE
MOL000098	Quercetin	Vascular cell adhesion protein 1	VCAM1
MOL000098	Quercetin	Prostaglandin E2 receptor EP3 subtype	PTGER3
MOL000098	Quercetin	Interleukin-8	CXCL8
MOL000098	Quercetin	Protein kinase C beta type	PRKCB
MOL000098	Quercetin	Baculoviral IAP repeat-containing protein 5	BIRC5
MOL000098	Quercetin	Dual oxidase 2	DUOX2
MOL000098	Quercetin	Nitric oxide synthase, endothelial	NOS3
MOL000098	Quercetin	Heat shock protein beta-1	HSPB1
MOL000098	Quercetin	Estrogen sulfotransferase	SULT1E1
MOL000098	Quercetin	Maltase-glucoamylase, intestinal	MGAM
MOL000098	Quercetin	Interleukin-2	IL2
MOL000098	Quercetin	Nuclear receptor subfamily 1 group I member 2	NR1I2

MOL000098	Quercetin	Cytochrome P450 1B1	CYP1B1
MOL000098	Quercetin	G2/mitotic-specific cyclin-B1	CCNB1
MOL000098	Quercetin	Tissue-type plasminogen activator	PLAT
MOL000098	Quercetin	Thrombomodulin	THBD
MOL000098	Quercetin	Plasminogen activator inhibitor 1	SERPINE1
MOL000098	Quercetin	Collagen alpha-1(I) chain	COL1A1
MOL000098	Quercetin	Interferon gamma	IFNG
MOL000098	Quercetin	Arachidonate 5-lipoxygenase	ALOX5
MOL000098	Quercetin	Interleukin-1 alpha	IL1A
MOL000098	Quercetin	Myeloperoxidase	MPO
MOL000098	Quercetin	DNA topoisomerase 2-alpha	TOP2A
MOL000098	Quercetin	Neutrophil cytosol factor 1	NCF1
MOL000098	Quercetin	ATP-binding cassette sub-family G member 2	ABCG2

MOL000098	Quercetin	Hyaluronan synthase 2	HAS2
MOL000098	Quercetin	Glutathione S-transferase P	GSTP1
MOL000098	Quercetin	Nuclear factor erythroid 2-related factor 2	NFE2L2
MOL000098	Quercetin	NAD(P)H dehydrogenase [quinone] 1	NQO1
MOL000098	Quercetin	Poly [ADP-ribose] polymerase 1	PARP1
MOL000098	Quercetin	Aryl hydrocarbon receptor	AHR
MOL000098	Quercetin	26S proteasome non-ATPase regulatory subunit 3	PSMD3
MOL000098	Quercetin	Solute carrier family 2, facilitated glucose transporter member 4	SLC2A4
MOL000098	Quercetin	Collagen alpha-1(III) chain	COL3A1
MOL000098	Quercetin	C-X-C motif chemokine 11	CXCL11
MOL000098	Quercetin	C-X-C motif chemokine 2	CXCL2
MOL000098	Quercetin	DDB1- and CUL4-associated factor 5	DCAF5
MOL000098	Quercetin	Nuclear receptor subfamily 1 group I member 3	NR1I3

MOL000098	Quercetin	Serine/threonine-protein kinase Chk2	CHEK2
MOL000098	Quercetin	Insulin receptor	INSR
MOL000098	Quercetin	Claudin-4	CLDN4
MOL000098	Quercetin	Peroxisome proliferator-activated receptor alpha	PPARA
MOL000098	Quercetin	Peroxisome proliferator-activated receptor delta	PPARD
MOL000098	Quercetin	Heat shock factor protein 1	HSF1
MOL000098	Quercetin	C-reactive protein	CRP
MOL000098	Quercetin	C-X-C motif chemokine 10	CXCL10
MOL000098	Quercetin	Inhibitor of nuclear factor kappa-B kinase subunit alpha	CHUK
MOL000098	Quercetin	Osteopontin	SPP1
MOL000098	Quercetin	Runt-related transcription factor 2	RUNX2
MOL000098	Quercetin	Ras association domain-containing protein 1	RASSF1
MOL000098	Quercetin	Transcription factor E2F1	E2F1

MOL000098	Quercetin	Transcription factor E2F2	E2F2
MOL000098	Quercetin	Prostatic acid phosphatase	ACPP
MOL000098	Quercetin	Cathepsin D	CTSD
MOL000098	Quercetin	Insulin-like growth factor-binding protein 3	IGFBP3
MOL000098	Quercetin	Insulin-like growth factor II	IGF2
MOL000098	Quercetin	CD40 ligand	CD40LG
MOL000098	Quercetin	Interferon regulatory factor 1	IRF1
MOL000098	Quercetin	Receptor tyrosine-protein kinase erbB-3	ERBB3
MOL000098	Quercetin	Serum paraoxonase/arylesterase 1	PON1
MOL000098	Quercetin	Type I iodothyronine deiodinase	DIO1
MOL000098	Quercetin	Procollagen C-endopeptidase enhancer 1	PCOLCE
MOL000098	Quercetin	Puromycin-sensitive aminopeptidase	NPEPPS
MOL000098	Quercetin	Hexokinase-2	HK2

MOL000098	Quercetin	Ras GTPase-activating protein 1	RASA1
MOL000098	Quercetin	Glutathione S-transferase Mu 1	GSTM1
MOL000098	Quercetin	Glutathione S-transferase Mu 2	GSTM2
MOL013129	(+)-3,3',5',5,7-Pentahydroflavanone	Prostaglandin G/H synthase 1	PTGS1
MOL013129	(+)-3,3',5',5,7-Pentahydroflavanone	Prostaglandin G/H synthase 2	PTGS2

¹The putative targets were 173 excluding the duplicates.

Supplementary Table 2 Node degrees of targets in protein-protein interaction network by STRING

No.	Target protein	Node degree	No.	Target protein	Node degree	No.	Target protein	Node degree
1	AKT1	107	57	RUNX2	32	113	PPARD	12
2	IL-6	95	58	CCNB1	30	114	TRP63	12
3	CASP3	84	59	NQO1	30	115	AKR1B3	11
4	MAPK3	83	60	PARP1	30	116	COL3A1	11
5	JUN	81	61	PGR	30	117	NR1I3	11
6	MMP9	78	62	HSPB1	28	118	PON1	11
7	PTGS2	77	63	IGF2	28	119	ADRB2	10
8	MAPK8	76	64	PLAU	28	120	BAX	10
9	EGF	75	65	PPARA	27	121	GSTM2	10
10	VEGFA	75	66	CD40LG	26	122	HK2	10
11	EGFR	73	67	F3	26	123	PTGS1	10
12	CAT	68	68	GJA1	26	124	RXRA	10
13	CCL2	67	69	IGFBP3	26	125	TOP2A	10
14	CCND1	65	70	SLC2A4	26	126	MTTP	9
15	IL-1B	64	71	FASN	25	127	RASA1	9
16	ESR1	63	72	GSR	25	128	RASSF1	9
17	HMOX1	63	73	IRF1	25	129	AKR1C6	8
18	IL-10	60	74	NCF1	25	130	CHRM4	8
19	MYC	60	75	CYP1A1	24	131	MAOA	8
20	ICAM1	58	76	CYP1A2	23	132	MAOB	8
21	PPARG	58	77	CXCR3	21	133	NR3C2	8
22	FOS	56	78	RAF1	21	134	PRSS1	8
23	MAPK1	55	79	COL1A1	20	135	CHRM1	7

24	SERPINE1	53	80	GSTP1	20	136	HAS2	7
25	RELA	50	81	ABCG2	19	137	PSMD3	7
26	AR	49	82	CHEK2	19	138	SLC6A4	7
27	VCAM1	49	83	CTSD	19	139	SLPI	7
28	BCL2L1	48	84	ERBB3	19	140	ELK1	6
29	STAT1	47	85	IL-1A	19	141	F7	6
30	CASP8	46	86	E2F1	18	142	LTA4H	6
31	ERBB2	45	87	IKBKB	18	143	POR	6
32	CRP	44	88	NCOA1	18	144	SLC6A2	6
33	IFNG	44	89	RB1	18	145	SULT1E1	6
34	NOS3	44	90	ACHE	17	146	CES1D	5
35	ADIPOQ	43	91	ALOX5	17	147	MAP2	5
36	MMP2	43	92	HSF1	17	148	SLC6A3	5
37	MPO	43	93	NR1I2	17	149	SOAT1	5
38	SPP1	42	94	PLAT	17	150	SOAT2	5
39	CXCL2	41	95	THBD	17	151	TOP1	5
40	HIF1A	41	96	CYP1B1	16	152	ABCC1	4
41	IL-2	41	97	HMGCR	16	153	ADRA1A	4
42	CDKN1A	39	98	INSR	16	154	ADRB1	4
43	CXCL10	39	99	PRKCB	16	155	AHSA1	4
44	NOS2	39	100	UGT1A1	16	156	CHRM3	4
45	SOD1	39	101	NCOA2	15	157	GOT1	4
46	CASP9	38	102	PRKCA	15	158	ADRA1B	3
47	MMP3	38	103	CHRM2	14	159	CHRNA2	3
48	AHR	37	104	ODC1	14	160	CLDN4	3
49	CAV1	37	105	OPRM1	14	161	MGAM	3

50	NFE2L2	37	106	PTGER3	14	162	PCOLCE	3
51	APOB	36	107	ACACA	13	163	SCN5A	3
52	SELE	36	108	BIRC5	13	164	ABAT	2
53	SREBF1	35	109	ADRA2A	12	165	CTRB1	2
54	MMP13	34	110	BCL2	12	166	GABRA1	2
55	LDLR	32	111	CHUK	12	167	KCNH2	2
56	NFKBIA	32	112	GSTM1	12	168	EIF6	1

Supplementary Table 3 Gene ontology enrichment analysis results (False discovery rate < 0.05)

Ontology	GO term	Description	FDR	Gene ID	Count
BP	GO:0032496	response to lipopolysaccharide	7.74E-30	PTGS2/OPRM1/CASP9/JUN/CASP3/CASP8/PRKCA/NOS2/RELA/AKT1/MAPK8/CYP1A2/CYP1A1/ICAM1/SELE/VCAM1/GSTP1/SLPI/MAPK3/MAPK1/APOB/UGT1A1/MAOB/FOS/IL10/IL6/NFKBIA/IL1B/CCL2/CXCL8/NOS3/THBD/SERPINE1/MPO/CXCL11/CXCL2/PPARD/HSF1/CXCL10/CHUK	40
BP	GO:0002237	response to molecule of bacterial origin	1.88E-29	PTGS2/OPRM1/CASP9/JUN/CASP3/CASP8/PRKCA/NOS2/RELA/AKT1/MAPK8/CYP1A2/CYP1A1/ICAM1/SELE/VCAM1/GSTP1/SLPI/MAPK3/MAPK1/APOB/UGT1A1/MAOB/FOS/IL10/IL6/NFKBIA/IL1B/CCL2/CXCL8/NOS3/THBD/SERPINE1/MPO/CXCL11/CXCL2/PPARD/HSF1/CXCL10/CHUK	40
BP	GO:0031667	response to nutrient levels	4.70E-28	PTGS2/ADRB2/SLC6A4/OPRM1/BCL2/JUN/PON1/PPARG/F7/RELA/AKT1/MAPK8/STAT1/HMOX1/CYP1A1/ICAM1/VCAM1/GSTP1/AKR1C3/MAPK3/MAPK1/LDLR/SOD1/CAT/HMGCR/UGT1A1/PPARA/SREBF1/ADIPOQ/NCOA1/ADRB1/EGFR/CC	44

				ND1/CDKN1A/POR/IL1B/COL1A1/MPO/NFE2L2/NQO1/PPARD/HSF1/CXCL10/SP P1	
BP	GO:0048545	response to steroid hormone	7.05E-25	PTGS2/RXRA/PGR/NCOA2/BCL2/CASP9/CASP3/AR/PPARG/RELA/ICAM1/NR1I2/GSTP1/NR1I3/AKR1C3/ESR1/UGT1A1/PPARA/SREBF1/ADIPOQ/GOT1/NR3C2/NCOA1/MAOB/EGFR/CCND1/FOS/CDKN1A/IL10/RB1/IL6/TP63/CAV1/COL1A1/PARP1/CLDN4/PPARD/SPP1	38
BP	GO:0010038	response to metal ion	5.50E-24	PTGS2/SCN5A/BCL2/CASP9/JUN/CASP3/CASP8/AKT1/MAPK8/HMOX1/CYP1A2/CYP1A1/ICAM1/VCAM1/AKR1C3/MAPK3/MAPK1/SOD1/CAT/GOT1/ABAT/SLC6A3/MAOB/EGFR/CCND1/FOS/MMP9/HIF1A/CAV1/CCNB1/IL1A/NCF1/NQO1/PARP1/HSF1/CHUK	36
BP	GO:0046677	response to antibiotic	3.07E-23	OPRM1/BCL2/CASP9/JUN/CASP3/CASP8/RELA/STAT1/HMOX1/CYP1A1/ICAM1/VCAM1/CYP1B1/GSTP1/AHR/SLC2A4/SOD1/CAT/HMGCR/UGT1A1/ADIPOQ/ABAT/SLC6A3/MAOB/CCND1/BCL2L1/IL10/IL6/IL2/COL1A1/NFE2L2/NQO1/HSF1/CHUK	34

BP	GO:0070482	response to oxygen levels	3.46E-22	PTGS2/SLC6A4/BCL2/CASP3/NOS2/PPARG/F7/AKT1/HMOX1/CYP1A1/ICAM1/VCAM1/SLC2A4/CAT/PPARA/ADIPOQ/ABAT/PLAU/MMP3/VEGFA/CDKN1A/MMP2/RAF1/HIF1A/CAV1/MYC/CCNB1/PLAT/COL1A1/NFE2L2/PPARD/HSF1/E2F1/HK2	34
BP	GO:0000302	response to reactive oxygen species	3.49E-22	BCL2/JUN/CASP3/RELA/AKT1/MAPK8/STAT1/HMOX1/CYP1B1/GSTP1/AKR1C3/MAPK3/MAPK1/SOD1/CAT/MMP3/EGFR/FOS/MMP9/IL10/IL6/NOS3/COL1A1/MPO/NCF1/NFE2L2/NQO1/HSF1/CHUK	29
BP	GO:0072593	reactive oxygen species metabolic process	5.27E-22	PTGS2/BCL2/NOS2/AKT1/CYP1A2/CYP1A1/ICAM1/CYP1B1/GSTP1/INSR/AKR1C3/SOD1/CAT/MAOB/MMP3/EGFR/CDKN1A/EIF6/IL10/POR/HIF1A/CAV1/IL1B/NOS3/IFNG/MPO/NCF1/NFE2L2/NQO1/CRP/HK2	31
BP	GO:0006979	response to oxidative stress	3.86E-21	PTGS2/PTGS1/BCL2/JUN/CASP3/RELA/AKT1/MAPK8/STAT1/HMOX1/CYP1B1/GSTP1/AKR1C3/MAPK3/MAPK1/SOD1/CAT/GSR/ADIPOQ/MMP3/EGFR/FOS/MMP9/IL10/IL6/HIF1A/NOS3/HSPB1/COL1A1/MPO/NCF1/NFE2L2/NQO1/PARP1/HSF1/CHUK	36

BP	GO:0001666	response to hypoxia	2.20E-20	PTGS2/SLC6A4/BCL2/CASP3/NOS2/F7/AKT1/HMOX1/CYP1A1/ICAM1/VCAM1/SLC2A4/CAT/PPARA/ADIPOQ/ABAT/PLAU/MMP3/VEGFA/MMP2/RAF1/HIF1A/CAV1/MYC/CCNB1/PLAT/NFE2L2/PPARD/HSF1/E2F1/HK2	31
BP	GO:0007584	response to nutrient	2.86E-20	PTGS2/SLC6A4/PPARG/F7/RELA/STAT1/HMOX1/CYP1A1/VCAM1/GSTP1/AKR1C3/SOD1/CAT/HMGCR/UGT1A1/ADIPOQ/NCOA1/EGFR/CCND1/POR/IL1B/COL1A1/NQO1/PPARD/HSF1/CXCL10/SPP1	27
BP	GO:0036293	response to decreased oxygen levels	5.24E-20	PTGS2/SLC6A4/BCL2/CASP3/NOS2/F7/AKT1/HMOX1/CYP1A1/ICAM1/VCAM1/SLC2A4/CAT/PPARA/ADIPOQ/ABAT/PLAU/MMP3/VEGFA/MMP2/RAF1/HIF1A/CAV1/MYC/CCNB1/PLAT/NFE2L2/PPARD/HSF1/E2F1/HK2	31
BP	GO:0001101	response to acid chemical	9.23E-20	PTGS2/RXRA/SLC6A4/CASP3/PON1/PPARG/F7/RELA/AKT1/ICAM1/GSTP1/AKR1C3/LDLR/CAT/APOB/SREBF1/ADIPOQ/AKR1C1/AKR1B1/EGFR/VEGFA/BCL2L1/MMP2/ACACA/CCNB1/COL1A1/NQO1/COL3A1/HSF1/CHUK/E2F1	31

BP	GO:0097305	response to alcohol	1.33E-19	OPRM1/CASP8/PPARG/F7/AKT1/ICAM1/VCAM1/GSTP1/AHR/SLC2A4/AKR1C3/SOD1/CAT/HMGCR/UGT1A1/ADIPOQ/ABAT/SLC6A3/MAOB/CCND1/BCL2L1/FOS/CDKN1A/ACACA/IL2/NQO1/PARP1	27
BP	GO:0009410	response to xenobiotic stimulus	1.33E-19	PTGS1/OPRM1/CASP9/PPARG/F7/RELA/CYP3A4/CYP1A2/CYP1A1/ICAM1/NR1I2/CYP1B1/GSTP1/AHR/GSTM1/GSTM2/SOD1/UGT1A1/AKR1C1/ABAT/CES1/SLC6A3/EGFR/RB1/POR/NQO1/CHEK2/HSF1/E2F1	29
BP	GO:1901654	response to ketone	2.38E-19	NCOA2/CASP9/AR/PPARG/F7/RELA/AKT1/ICAM1/AHR/AKR1C3/SREBF1/AKR1B1/MAOB/EGFR/CCND1/BCL2L1/FOS/CDKN1A/ELK1/ACACA/CAV1/PARP1/CLDN4/HSF1/SPP1	25
BP	GO:0034599	cellular response to oxidative stress	2.38E-19	BCL2/JUN/RELA/AKT1/MAPK8/HMOX1/CYP1B1/AKR1C3/MAPK3/MAPK1/SOD1/CAT/GSR/MMP3/EGFR/FOS/MMP9/IL10/IL6/HIF1A/NOS3/HSPB1/MPO/NCF1/NFE2L2/NQO1/PARP1/HSF1/CHUK	29

BP	GO:0071276	cellular response to cadmium ion	3.35E-19	JUN/AKT1/MAPK8/HMOX1/CYP1A2/AKR1C3/MAPK3/MAPK1/SOD1/EGFR/FOS/MMP9/NCF1/HSF1/CHUK	15
BP	GO:0035690	cellular response to drug	4.54E-19	PTGS2/KCNH2/CHRM3/CHRM1/CHRM4/CHRM2/OPRM1/CASP9/NOS2/RELA/HMOX1/ICAM1/CYP1B1/AHR/GSTM2/MAPK3/MAPK1/SOD1/UGT1A1/ADIPOQ/NCOA1/MMP3/EGFR/IL10/IL6/MYC/IL1B/NFE2L2/NQO1/CHEK2/HSF1	31
BP	GO:0062012	regulation of small molecule metabolic process	4.54E-19	PTGS2/NCOA2/NOS2/PPARG/AKT1/HAS2/INSR/AKR1C3/FASN/LDLR/SOD1/APOB/HMGCR/PPARA/SREBF1/ADIPOQ/EIF6/EGF/POR/ODC1/HIF1A/ACACA/CAV1/IL1B/NOS3/CCNB1/IFNG/NQO1/PARP1/IGFBP3/IGF2	31
BP	GO:0046686	response to cadmium ion	1.88E-18	JUN/AKT1/MAPK8/HMOX1/CYP1A2/AKR1C3/MAPK3/MAPK1/SOD1/CAT/GOT1/EGFR/FOS/MMP9/NCF1/HSF1/CHUK	17

BP	GO:0008202	steroid metabolic process	2.73E-18	RXRA/PON1/CYP3A4/CYP1A2/CYP1A1/NR1I2/CYP1B1/AKR1C3/ESR1/FASN/LDLR/SOD1/CAT/APOB/HMGCR/UGT1A1/SREBF1/SOAT2/AKR1C1/CES1/SOAT1/AKR1B1/POR/ACACA/IL1B/SULT1E1/IFNG/PPARD/SPP1	29
BP	GO:0071466	cellular response to xenobiotic stimulus	4.76E-18	PTGS1/OPRM1/CASP9/CYP3A4/CYP1A2/CYP1A1/ICAM1/NR1I2/CYP1B1/GSTP1/AHR/GSTM1/GSTM2/UGT1A1/AKR1C1/CES1/EGFR/RB1/POR/NQO1/CHEK2/HSF1/E2F1	23
BP	GO:0008015	blood circulation	6.43E-18	PTGS2/PTGS1/KCNH2/CHRM3/SCN5A/ADRA1A/CHRM2/ADRA1B/ADRB2/SLC6A4/NOS2/AR/PPARG/AKT1/STAT1/HMOX1/ICAM1/GSTM2/SOD1/HMGCR/PPARA/SREBF1/ADIPOQ/ABAT/ADRA2A/ADRB1/EGFR/CAV1/GJA1/NOS3/IL2/PPARD/CRP/CXCL10	34
BP	GO:0003013	circulatory system process	1.03E-17	PTGS2/PTGS1/KCNH2/CHRM3/SCN5A/ADRA1A/CHRM2/ADRA1B/ADRB2/SLC6A4/NOS2/AR/PPARG/AKT1/STAT1/HMOX1/ICAM1/GSTM2/SOD1/HMGCR/PPARA/SREBF1/ADIPOQ/ABAT/ADRA2A/ADRB1/EGFR/CAV1/GJA1/NOS3/IL2/PPARD/CRP/CXCL10	34

BP	GO:0034614	cellular response to reactive oxygen species	2.37E-17	JUN/RELA/AKT1/MAPK8/CYP1B1/AKR1C3/MAPK3/MAPK1/SOD1/MMP3/EGFR/FOS/MMP9/IL10/IL6/NOS3/MPO/NCF1/NFE2L2/NQO1/HSF1/CHUK	22
BP	GO:0050878	regulation of body fluid levels	5.79E-17	CHRM3/CHRM1/PRKCA/F7/HAS2/MAPK3/MAPK1/ABAT/ADRA2A/SLC6A3/AKR1B1/PLAU/VEGFA/CCND1/IL6/TP63/RAF1/HIF1A/CAV1/F3/PRKCB/NOS3/HSPB1/PAT/THBD/SERPINE1/COL1A1/NFE2L2/COL3A1/CLDN4/CD40LG/IRF1/HK2	33
BP	GO:0071222	cellular response to lipopolysaccharide	2.03E-15	PRKCA/NOS2/RELA/AKT1/MAPK8/ICAM1/GSTP1/MAPK3/MAPK1/IL10/IL6/NFKBIA/IL1B/CCL2/CXCL8/NOS3/SERPINE1/CXCL11/CXCL2/PPARD/HSF1/CXCL10	22
BP	GO:0034612	response to tumor necrosis factor	3.12E-15	PTGS2/CASP3/CASP8/RELA/IKBKB/AKT1/STAT1/ICAM1/SELE/VCAM1/HAS2/GSTP1/SLC2A4/MAPK3/MAPK1/APOB/ADIPOQ/NFKBIA/CCL2/CXCL8/COL1A1/NFE2L2/CHUK/CD40LG	24

BP	GO:0071219	cellular response to molecule of bacterial origin	4.02E-15	PRKCA/NOS2/RELA/AKT1/MAPK8/ICAM1/GSTP1/MAPK3/MAPK1/IL10/IL6/NFKBIA/IL1B/CCL2/CXCL8/NOS3/SERPINE1/CXCL11/CXCL2/PPARD/HSF1/CXCL10	22
BP	GO:0071241	cellular response to inorganic substance	4.32E-15	PTGS2/SCN5A/JUN/AKT1/MAPK8/HMOX1/CYP1A2/CYP1A1/AKR1C3/MAPK3/MAPK1/SOD1/MMP3/EGFR/FOS/MMP9/CCNB1/NCF1/NQO1/PARP1/HSF1/CHUK	22
BP	GO:0071248	cellular response to metal ion	5.24E-15	PTGS2/SCN5A/JUN/AKT1/MAPK8/HMOX1/CYP1A2/CYP1A1/AKR1C3/MAPK3/MAPK1/SOD1/EGFR/FOS/MMP9/CCNB1/NCF1/NQO1/PARP1/HSF1/CHUK	21
BP	GO:2000377	regulation of reactive oxygen species metabolic process	5.69E-15	PTGS2/BCL2/AKT1/ICAM1/CYP1B1/GSTP1/INSR/AKR1C3/SOD1/MMP3/EGFR/CDKN1A/EIF6/IL10/HIF1A/CAV1/IL1B/IFNG/NFE2L2/CRP/HK2	21

BP	GO:0048608	reproductive structure development	6.01E-15	PTGS2/RXRA/PGR/BCL2/BAX/CASP3/CASP8/AR/PPARG/AKT1/ICAM1/INSR/AKR1C3/ESR1/MAPK1/SOD1/NCOA1/EGFR/VEGFA/CCND1/BCL2L1/IL10/TP63/HIF1A/NOS3/PPARD/HSF1/SPP1/IGF2	29
BP	GO:0061458	reproductive system development	7.05E-15	PTGS2/RXRA/PGR/BCL2/BAX/CASP3/CASP8/AR/PPARG/AKT1/ICAM1/INSR/AKR1C3/ESR1/MAPK1/SOD1/NCOA1/EGFR/VEGFA/CCND1/BCL2L1/IL10/TP63/HIF1A/NOS3/PPARD/HSF1/SPP1/IGF2	29
BP	GO:0048732	gland development	8.25E-15	RXRA/PGR/BCL2/BAX/JUN/AR/RELA/AKT1/HMOX1/CYP1A1/INSR/ESR1/MAPK3/MAPK1/FASN/SOD1/UGT1A1/SLC6A3/EGFR/VEGFA/CCND1/IL10/EGF/TP63/RAF1/HIF1A/CAV1/IGF2/HK2	29
BP	GO:0042133	neurotransmitter metabolic process	1.66E-14	PTGS2/SLC6A4/NOS2/ACHE/AKT1/ICAM1/CYP1B1/INSR/ABAT/SLC6A3/MAOB/MAOA/IL10/POR/CAV1/IL1B/NOS3/IFNG/NQO1	19

BP	GO:0032355	response to estradiol	1.71E-14	PTGS2/SLC6A4/CASP9/CASP3/CASP8/F7/CYP1A2/GSTP1/ESR1/CAT/APOB/UGT1A1/EGFR/CCND1/IL10/COL1A1/NQO1/HSF1	18
BP	GO:0007568	aging	1.71E-14	PTGS2/ADRA1A/BCL2/CASP9/JUN/RELA/AKT1/CYP1A1/ICAM1/VCAM1/SOD1/CAT/HMGCR/SREBF1/ABAT/SLC6A3/FOS/CDKN1A/IL10/TP63/SERPINE1/MPO/NFE2L2/NQO1/CHEK2	25
BP	GO:0035296	regulation of tube diameter	2.15E-14	PTGS2/CHRM3/ADRA1A/ADRA1B/ADRB2/SLC6A4/AKT1/HMOX1/ICAM1/SOD1/HMGCR/ADRA2A/ADRB1/EGFR/CAV1/NOS3/PPARD/CRP	18
BP	GO:0097746	regulation of blood vessel diameter	2.15E-14	PTGS2/CHRM3/ADRA1A/ADRA1B/ADRB2/SLC6A4/AKT1/HMOX1/ICAM1/SOD1/HMGCR/ADRA2A/ADRB1/EGFR/CAV1/NOS3/PPARD/CRP	18

BP	GO:0015850	organic hydroxy compound transport	2.28E-14	RXRA/NCOA2/SLC6A4/PON1/PPARG/SLC6A2/LDLR/APOB/ADIPOQ/SOAT2/AKR1C1/ABAT/CES1/SOAT1/NCOA1/ADRA2A/SLC6A3/MAOB/EGF/NFKBIA/CAV1/ABCG2/SPP1	23
BP	GO:0071216	cellular response to biotic stimulus	2.73E-14	PRKCA/NOS2/RELA/AKT1/MAPK8/ICAM1/GSTP1/MAPK3/MAPK1/IL10/IL6/NFKBIA/IL1B/CCL2/CXCL8/NOS3/SERPINE1/CXCL11/CXCL2/PPARD/HSF1/CXCL10	22
BP	GO:0009612	response to mechanical stimulus	3.23E-14	PTGS2/JUN/CASP8/PPARG/RELA/AKT1/MAPK8/STAT1/MAPK3/GOT1/EGFR/FOS/NFKBIA/RAF1/IL1B/CCNB1/COL1A1/MPO/COL3A1/CXCL10/IRF1	21
BP	GO:0010876	lipid localization	4.32E-14	RXRA/NCOA2/PON1/NOS2/PPARG/AKT1/LDLR/MTTP/APOB/PPARA/ABCC1/ADIPOQ/SOAT2/AKR1C1/CES1/SOAT1/NCOA1/EGF/IL6/NFKBIA/ACACA/CAV1/IL1B/ABCG2/PPARD/CRP/SPP1	27

BP	GO:1903409	reactive oxygen species biosynthetic process	4.88E-14	PTGS2/NOS2/AKT1/CYP1A2/CYP1A1/ICAM1/CYP1B1/INSR/SOD1/MAOB/IL10/CAV1/IL1B/NOS3/IFNG/MPO/NQO1	17
BP	GO:0050880	regulation of blood vessel size	4.88E-14	PTGS2/CHRM3/ADRA1A/ADRA1B/ADRB2/SLC6A4/AKT1/HMOX1/ICAM1/SOD1/HMGCR/ADRA2A/ADRB1/EGFR/CAV1/NOS3/PPARD/CRP	18
BP	GO:0071496	cellular response to external stimulus	4.88E-14	PTGS2/BCL2/JUN/CASP8/PPARG/AKT1/MAPK8/HMOX1/ICAM1/GSTP1/AKR1C3/MAPK3/MAPK1/SOD1/SREBF1/GOT1/NCOA1/EGFR/FOS/CDKN1A/IL1B/COL1A1/NFE2L2/HSF1/IRF1	25
BP	GO:0035150	regulation of tube size	5.41E-14	PTGS2/CHRM3/ADRA1A/ADRA1B/ADRB2/SLC6A4/AKT1/HMOX1/ICAM1/SOD1/HMGCR/ADRA2A/ADRB1/EGFR/CAV1/NOS3/PPARD/CRP	18

BP	GO:0009314	response to radiation	8.86E-14	PTGS2/OPRM1/BCL2/BAX/CASP9/JUN/CASP3/RELA/AKT1/MAPK8/ICAM1/VCAM1/CAT/HMGCR/EGFR/CCND1/BCL2L1/FOS/CDKN1A/ELK1/HIF1A/MYC/THBD/PARP1/COL3A1/CHEK2/HSF1/CXCL10	28
BP	GO:1901652	response to peptide	8.86E-14	PTGS2/ADRB2/PPARG/F7/RELA/AKT1/SAT1/ICAM1/GSTP1/SLC2A4/INSR/CAT/PPARA/SREBF1/ADIPOQ/GOT1/AKR1B1/EIF6/IL10/NFKBIA/POR/CAV1/IL1B/PRKCB/COL1A1/NFE2L2/PARP1/HSF1/IGF2	29
BP	GO:0031960	response to corticosteroid	1.05E-13	PTGS2/BCL2/CASP9/CASP3/ICAM1/GSTP1/AKR1C3/UGT1A1/ADIPOQ/GOT1/MAOB/EGFR/CCND1/FOS/CDKN1A/IL10/IL6/COL1A1/PARP1	19
BP	GO:0042136	neurotransmitter biosynthetic process	1.22E-13	PTGS2/SLC6A4/NOS2/ACHE/AKT1/ICAM1/CYP1B1/INSR/ABAT/SLC6A3/IL10/CAV1/IL1B/NOS3/IFNG/NQO1	16

BP	GO:0048660	regulation of smooth muscle cell proliferation	1.26E-13	PTGS2/JUN/PPARG/ AKT1/STAT1/HMOX1/GSTP1/HMGCR/ ADIPOQ/ AKR1B1/EGFR/CDKN1A/MMP2/MMP9/IL10/IL6/IFNG/PPARD/IGFBP3	19
BP	GO:0048659	smooth muscle cell proliferation	1.55E-13	PTGS2/JUN/PPARG/ AKT1/STAT1/HMOX1/GSTP1/HMGCR/ ADIPOQ/ AKR1B1/EGFR/CDKN1A/MMP2/MMP9/IL10/IL6/IFNG/PPARD/IGFBP3	19
BP	GO:0006066	alcohol metabolic process	1.67E-13	RXRA/PON1/CYP3A4/CYP1B1/ AKR1C3/FASN/LDLR/SOD1/CAT/APOB/HMGCR/SREBF1/SOAT2/ AKR1C1/GOT1/CES1/SOAT1/ADH1C/ AKR1B1/POR/ACACA/IL1B/SULT1E1/IFNG/PPARD	25
BP	GO:0097191	extrinsic apoptotic signaling pathway	1.68E-13	BCL2/BAX/CASP9/CASP3/CASP8/AR/RELA/ AKT1/HMOX1/ICAM1/GSTP1/BCL2L1/RAF1/CAV1/IL1B/NOS3/IL2/SERPINE1/IFNG/IL1A/ERBB3	21

BP	GO:0050673	epithelial cell proliferation	1.74E-13	PGR/SCN5A/BAX/JUN/PRKCA/AR/PPARG/ AKT1/STAT1/HMOX1/HAS2/ESR1/MAPK1/EGFR/VEGFA/CCND1/IL10/RB1/TP63/HIF1A/ERBB2/CAV1/MYC/F3/CCL2/PPARD/IGFBP3	27
BP	GO:0045471	response to ethanol	2.17E-13	OPRM1/CASP8/ICAM1/VCAM1/GSTP1/SLC2A4/SOD1/CAT/HMGCR/UGT1A1/ADIPOQ/ABAT/SLC6A3/MAOB/CCND1/IL2/NQO1	17
BP	GO:0019216	regulation of lipid metabolic process	2.17E-13	PTGS2/RXRA/NCOA2/PPARG/ AKT1/CYP1A1/AKR1C3/FASN/LDLR/SOD1/APOB/HMGCR/UGT1A1/PPARA/SREBF1/ADIPOQ/NCOA1/ADRA2A/EIF6/RB1/POR/ACACA/CAV1/IL1B/IFNG/PPARD	26
BP	GO:2001233	regulation of apoptotic signaling pathway	2.56E-13	PTGS2/BCL2/BAX/CASP8/AR/RELA/AKT1/MAPK8/HMOX1/ICAM1/GSTP1/SOD1/BCL2L1/MMP9/TP63/RAF1/HIF1A/CAV1/IL1B/NOS3/HSPB1/SERPINE1/IL1A/NFE2L2/PARP1/E2F1	26

BP	GO:0006869	lipid transport	3.10E-13	RXRA/NCOA2/PON1/NOS2/PPARG/AKT1/LDLR/MTTP/APOB/PPARA/ABCC1/ADIPOQ/SOAT2/AKR1C1/CES1/SOAT1/NCOA1/EGF/NFKBIA/ACACA/CAV1/IL1B/ABCG2/PPARD/SPP1	25
BP	GO:0048871	multicellular organismal homeostasis	3.37E-13	PTGS2/ADRB2/BCL2/BAX/PRKCA/ACHE/HAS2/SOD1/ADIPOQ/ABAT/AKR1B1/ADRB1/EGFR/VEGFA/RB1/IL6/TP63/ACACA/CAV1/GJA1/IL1B/PTGER3/NOS3/HSPB1/IL1A/CLDN4/HSF1/SPP1	28
BP	GO:0071356	cellular response to tumor necrosis factor	3.94E-13	CASP8/RELA/IKBKB/AKT1/STAT1/ICAM1/VCAM1/HAS2/GSTP1/SLC2A4/MAPK3/MAPK1/APOB/ADIPOQ/NFKBIA/CCL2/CXCL8/COL1A1/NFE2L2/CHUK/CD40LG	21
BP	GO:0033002	muscle cell proliferation	4.23E-13	PTGS2/RXRA/JUN/PPARG/AKT1/STAT1/HMOX1/GSTP1/HMGCR/ADIPOQ/AKR1B1/EGFR/CDKN1A/MMP2/MMP9/IL10/IL6/CCNB1/IFNG/PPARD/IGFBP3	21

BP	GO:0006631	fatty acid metabolic process	5.48E-13	PTGS2/PTGS1/PON1/PPARG/AKT1/CYP3A4/CYP1A2/CYP1A1/CYP1B1/ALOX5/GSTP1/GSTM2/AKR1C3/MAPK3/FASN/PPARA/SREBF1/ADIPOQ/CES1/LTA4H/EIF6/POR/ACACA/CAV1/PPARD	25
BP	GO:0003018	vascular process in circulatory system	7.18E-13	PTGS2/CHRM3/ADRA1A/ADRA1B/ADRB2/SLC6A4/AKT1/HMOX1/ICAM1/SOD1/HMGCR/ADRA2A/ADRB1/EGFR/CAV1/NOS3/PPARD/CRP	18
BP	GO:0048511	rhythmic process	8.76E-13	PGR/NCOA2/SLC6A4/OPRM1/JUN/CASP3/NOS2/PPARG/F7/MAPK8/HAS2/AHR/ESR1/PPARA/SREBF1/ADIPOQ/EGFR/TOPI1/NOS3/SERPINE1/TOP2A/CLDN4	22
BP	GO:0043434	response to peptide hormone	1.04E-12	PTGS2/PPARG/F7/RELA/AKT1/STAT1/ICAM1/GSTP1/SLC2A4/INSR/CAT/PPARA/SREBF1/ADIPOQ/GOT1/EIF6/IL10/POR/CAV1/IL1B/PRKCB/COL1A1/NFE2L2/PARP1/HSF1/IGF2	26

BP	GO:0062013	positive regulation of small molecule metabolic process	1.23E-12	PTGS2/NOS2/PPARG/AKT1/HAS2/INSR/PPARA/SREBF1/ADIPOQ/EGF/POR/HIF1A/IL1B/NOS3/CCNB1/IFNG/IGF2	17
BP	GO:0044706	multi-multicellular organism process	1.28E-12	PTGS2/RXRA/PGR/SLC6A4/BCL2/AR/AKT1/CYP1A1/ESR1/SOD1/AKR1B1/FOS/MMP2/MMP9/IL1B/THBD/CLDN4/PPARD/HSF1/SPP1	20
BP	GO:2001234	negative regulation of apoptotic signaling pathway	1.38E-12	PTGS2/BCL2/BAX/CASP8/AR/RELA/AKT1/HMOX1/ICAM1/GSTP1/BCL2L1/MMP9/RAF1/HIF1A/IL1B/NOS3/HSPB1/SERPINE1/IL1A/NFE2L2	20
BP	GO:0050678	regulation of epithelial cell proliferation	4.11E-12	PGR/SCN5A/BAX/JUN/PRKCA/AR/PPARG/AKT1/STAT1/HMOX1/HAS2/EGFR/VEGFA/CCND1/IL10/RB1/TP63/HIF1A/ERBB2/CAV1/MYC/F3/CCL2/PPARD	24

BP	GO:0051098	regulation of binding	4.30E-12	ADRB2/BCL2/BAX/JUN/PON1/MAP2/PPARG/AKT1/MAPK8/HMOX1/SLPI/MAPK3/PPARA/ADIPOQ/MMP9/IL10/EGF/RB1/NFKBIA/CAV1/IFNG/PARP1/HSF1/E2F1	24
BP	GO:0070997	neuron death	4.68E-12	BCL2/BAX/CASP9/JUN/CASP3/CASP8/AKT1/HMOX1/SOD1/PPARA/BCL2L1/FOS/IL10/RB1/TP63/ELK1/HIF1A/CCL2/NQO1/PARP1/HSF1/ERBB3/RASA1	23
BP	GO:0001505	regulation of neurotransmitter levels	9.13E-12	PTGS2/ADRA1A/CHRM2/SLC6A4/NOS2/ACHE/SLC6A2/AKT1/ICAM1/CYP1B1/INSR/ABAT/SLC6A3/MAOB/MAOA/IL10/POR/CAV1/IL1B/PRKCB/NOS3/IFNG/NQO1	23
BP	GO:0007565	female pregnancy	1.25E-11	PTGS2/RXRA/PGR/BCL2/AR/AKT1/ESR1/SOD1/AKR1B1/FOS/MMP2/MMP9/IL1B/THBD/CLDN4/PPARD/HSF1/SPP1	18

BP	GO:0006805	xenobiotic metabolic process	1.43E-11	PTGS1/CYP3A4/CYP1A2/CYP1A1/NR1I2/ CYP1B1/GSTP1/AHR/GSTM1/GSTM2/UG T1A1/AKR1C1/CES1/POR/NQO1	15
BP	GO:0071214	cellular response to abiotic stimulus	1.45E-11	PTGS2/BAX/CASP9/CASP3/CASP8/AKT1/ MAPK8/SLC2A4/MAPK3/GOT1/AKR1B1/ EGFR/BCL2L1/CDKN1A/ELK1/MYC/IL1B /COL1A1/PARP1/CHEK2/HSF1/IRF1	22
BP	GO:0104004	cellular response to environmental stimulus	1.45E-11	PTGS2/BAX/CASP9/CASP3/CASP8/AKT1/ MAPK8/SLC2A4/MAPK3/GOT1/AKR1B1/ EGFR/BCL2L1/CDKN1A/ELK1/MYC/IL1B /COL1A1/PARP1/CHEK2/HSF1/IRF1	22
BP	GO:0046209	nitric oxide metabolic process	1.46E-11	PTGS2/NOS2/AKT1/ICAM1/CYP1B1/INSR /IL10/POR/CAV1/IL1B/NOS3/IFNG/NQO 1	13

BP	GO:0071383	cellular response to steroid hormone stimulus	2.24E-11	RXRA/PGR/CASP9/AR/PPARG/ICAM1/NR1I2/GSTP1/NR1I3/AKR1C3/ESR1/UGT1A1/PPARA/NR3C2/NCOA1/EGFR/RB1/TP63/PARP1/PPARD	20
BP	GO:2001057	reactive nitrogen species metabolic process	2.38E-11	PTGS2/NOS2/AKT1/ICAM1/CYP1B1/INSR/IL10/POR/CAV1/IL1B/NOS3/IFNG/NQO1	13
BP	GO:1901214	regulation of neuron death	2.87E-11	BCL2/BAX/CASP9/JUN/CASP3/CASP8/AKT1/HMOX1/SOD1/PPARA/BCL2L1/FOS/IL10/ELK1/HIF1A/CCL2/NQO1/PARP1/HSF1/ERBB3/RASA1	21
BP	GO:0051384	response to glucocorticoid	3.35E-11	PTGS2/BCL2/CASP9/CASP3/ICAM1/GSTP1/UGT1A1/ADIPOQ/GOT1/MAOB/EGFR/CCND1/FOS/CDKN1A/IL10/IL6	16

BP	GO:1902652	secondary alcohol metabolic process	3.35E-11	RXRA/PON1/CYP3A4/FASN/LDLR/SOD1/CAT/APOB/HMGCR/SREBF1/SOAT2/CE S1/SOAT1/POR/ACACA/PPARD	16
BP	GO:0007596	blood coagulation	3.36E-11	PRKCA/F7/MAPK3/MAPK1/ABAT/ADRA2A/PLAU/IL6/RAF1/CAV1/F3/PRKCB/NOS3/HSPB1/PLAT/THBD/SERPINE1/COL1A1/NFE2L2/COL3A1/CD40LG/IRF1	22
BP	GO:0097237	cellular response to toxic substance	3.66E-11	PTGS2/PTGS1/RELA/HMOX1/CYP1B1/GS TP1/GSTM1/GSTM2/SOD1/CAT/UGT1A1/GSR/IL10/IL6/NOS3/MPO/NFE2L2/NQO1/HSF1	19
BP	GO:0018209	peptidyl-serine modification	3.75E-11	PTGS2/BCL2/BAX/PRKCA/IKBKB/AKT1/MAPK8/MAPK3/MAPK1/EGFR/VEGFA/IL6/TOP1/RAF1/CAV1/PRKCB/CCNB1/IFN G/PARP1/CHEK2/CHUK	21

BP	GO:0071229	cellular response to acid chemical	3.90E-11	SLC6A4/PPARG/AKT1/AKR1C3/LDLR/APOB/SREBF1/AKR1C1/EGFR/VEGFA/BCL2L1/MMP2/ACACA/CCNB1/COL1A1/COL3A1/HSF1/E2F1	18
BP	GO:0014074	response to purine-containing compound	3.90E-11	PTGS2/SLC6A4/JUN/PPARG/RELA/STAT1/AHR/GSTM2/SOD1/SREBF1/ADIPOQ/SLC6A3/FOS/IL1B/THBD/COL1A1	16
BP	GO:2001237	negative regulation of extrinsic apoptotic signaling pathway	3.90E-11	BCL2/CASP8/AR/RELA/AKT1/HMOX1/ICAM1/GSTP1/BCL2L1/RAF1/IL1B/NOS3/SERPINE1/IL1A	14
BP	GO:0070542	response to fatty acid	4.09E-11	PTGS2/PON1/PPARG/AKT1/AKR1C3/LDLR/CAT/APOB/SREBF1/ADIPOQ/ACACA/CCNB1/E2F1	13

BP	GO:0007599	hemostasis	4.19E-11	PRKCA/F7/MAPK3/MAPK1/ABAT/ADRA2A/PLAU/IL6/RAF1/CAV1/F3/PRKCB/NOS3/HSPB1/PLAT/THBD/SERPINE1/COL1A1/NFE2L2/COL3A1/CD40LG/IRF1	22
BP	GO:0050817	coagulation	4.40E-11	PRKCA/F7/MAPK3/MAPK1/ABAT/ADRA2A/PLAU/IL6/RAF1/CAV1/F3/PRKCB/NOS3/HSPB1/PLAT/THBD/SERPINE1/COL1A1/NFE2L2/COL3A1/CD40LG/IRF1	22
BP	GO:0033273	response to vitamin	8.55E-11	PTGS2/PPARG/F7/RELA/CYP1A1/GSTP1/CAT/EGFR/CCND1/COL1A1/PPARD/CXCL10/SPP1	13
BP	GO:1903034	regulation of response to wounding	9.03E-11	PRKCA/F7/HMGCR/ABAT/ADRA2A/PLAU/IL10/CAV1/F3/NOS3/PLAT/THBD/SERPINE1/NFE2L2/PPARD/SPP1	16

BP	GO:0018105	peptidyl-serine phosphorylation	9.14E-11	PTGS2/BCL2/BAX/PRKCA/IKBKB/AKT1/MAPK8/MAPK3/MAPK1/EGFR/VEGFA/IL6/TOP1/RAF1/CAV1/PRKCB/CCNB1/IFNG/CHEK2/CHUK	20
BP	GO:0016125	sterol metabolic process	1.07E-10	RXRA/PON1/CYP1B1/FASN/LDLR/SOD1/CAT/APOB/HMGCR/SREBF1/SOAT2/CES1/SOAT1/POR/ACACA/PPARD	16
BP	GO:0046683	response to organophosphorus	1.17E-10	PTGS2/SLC6A4/JUN/RELA/STAT1/AHR/SOD1/SREBF1/ADIPOQ/AKR1C1/SLC6A3/FOS/IL1B/THBD/COL1A1	15
BP	GO:0097193	intrinsic apoptotic signaling pathway	1.23E-10	PTGS2/BCL2/BAX/CASP9/CASP3/AKT1/HMOX1/CYP1B1/SOD1/BCL2L1/CDKN1A/MMP9/TP63/HIF1A/CAV1/HSPB1/NFE2L2/PARP1/CHEK2/E2F1	20

BP	GO:0006809	nitric oxide biosynthetic process	1.36E-10	PTGS2/NOS2/ AKT1/ICAM1/CYP1B1/INSR /IL10/CAV1/IL1B/NOS3/IFNG/NQO1	12
BP	GO:0031668	cellular response to extracellular stimulus	1.65E-10	PTGS2/BCL2/JUN/PPARG/MAPK8/HMOX 1/ICAM1/GSTP1/ AKR1C3/MAPK3/MAPK 1/SOD1/SREBF1/NCOA1/FOS/CDKN1A/C OL1A1/NFE2L2/HSF1	19
BP	GO:0042542	response to hydrogen peroxide	1.71E-10	BCL2/JUN/CASP3/RELA/STAT1/HMOX1/ CYP1B1/SOD1/CAT/IL10/IL6/COL1A1/NF E2L2/NQO1/HSF1	15
BP	GO:0032868	response to insulin	1.73E-10	PPARG/RELA/ AKT1/STAT1/ICAM1/GSTP 1/SLC2A4/INSR/CAT/PPARA/SREBF1/AD IPOQ/GOT1/EIF6/IL10/IL1B/PRKCB/PAR P1/IGF2	19

BP	GO:0008203	cholesterol metabolic process	2.29E-10	RXRA/PON1/FASN/LDLR/SOD1/CAT/AP OB/HMGCR/SREBF1/SOAT2/CES1/SOAT1 /POR/ACACA/PPARD	15
BP	GO:0045766	positive regulation of angiogenesis	2.30E-10	PTGS2/PRKCA/HMOX1/CYP1B1/VEGFA/I L10/HIF1A/F3/IL1B/CXCL8/PRKCB/NOS3 /HSPB1/SERPINE1/IL1A/NFE2L2/HK2	17
BP	GO:0051090	regulation of DNA-binding transcription factor activity	2.40E-10	JUN/AR/PPARG/RELA/IKBKB/AKT1/HM OX1/ICAM1/CYP1B1/ESR1/MAPK3/MAP K1/CAT/VEGFA/FOS/IL10/RB1/IL6/NFK BIA/IL1B/PRKCB/CHUK/CD40LG	23
BP	GO:0071900	regulation of protein serine/threonine kinase activity	2.48E-10	ADRB2/CASP3/AKT1/GSTP1/INSR/MAPK 3/MAPK1/SOD1/HMGCR/ADIPOQ/ADRA 2A/EGFR/VEGFA/CCND1/CDKN1A/EGF /RAF1/ERBB2/CAV1/IL1B/HSPB1/CCNB1 /IFNG/IGF2/CD40LG	25

BP	GO:0030301	cholesterol transport	2.63E-10	PON1/PPARG/LDLR/APOB/ADIPOQ/SOAT2/AKR1C1/CES1/SOAT1/EGF/NFKBIA/CAV1/ABCG2	13
BP	GO:2000379	positive regulation of reactive oxygen species metabolic process	2.63E-10	PTGS2/AKT1/ICAM1/GSTP1/INSR/AKR1C3/SOD1/EGFR/CDKN1A/IL1B/IFNG/NFE2L2/CRP	13
BP	GO:0010212	response to ionizing radiation	2.65E-10	BCL2/BAX/CASP3/ICAM1/VCAM1/CCND1/BCL2L1/CDKN1A/ELK1/MYC/THBD/PARP1/CHEK2/HSF1/CXCL10	15
BP	GO:0045765	regulation of angiogenesis	3.51E-10	PTGS2/PRKCA/PPARG/STAT1/HMOX1/CYP1B1/VEGFA/IL10/IL6/HIF1A/ERBB2/F3/IL1B/CXCL8/PRKCB/NOS3/HSPB1/SERPINE1/IL1A/NFE2L2/CXCL10/HK2	22

BP	GO:0001890	placenta development	3.51E-10	PTGS2/RXRA/CASP8/PPARG/AKT1/MAPK1/SOD1/NCOA1/EGFR/IL10/HIF1A/PPARD/HSF1/SPP1/IGF2	15
BP	GO:0009266	response to temperature stimulus	4.03E-10	PTGS2/ADRB2/CASP8/PPARG/AKT1/HMOX1/MAPK3/MAPK1/SOD1/ADRB1/FOS/CDKN1A/NFKBIA/NOS3/IL1A/HSF1/CXCL10	17
BP	GO:0097756	negative regulation of blood vessel diameter	4.33E-10	PTGS2/CHRM3/ADRA1A/ADRA1B/SLC6A4/AKT1/ICAM1/HMGCR/ADRA2A/EGFR/CAV1/CRP	12
BP	GO:0070555	response to interleukin-1	4.56E-10	PRKCA/RELA/IKBKB/ICAM1/SELE/HAS2/MAPK3/IL6/NFKBIA/HIF1A/IL1B/CCL2/CXCL8/IL1A/CHUK	15

BP	GO:2001236	regulation of extrinsic apoptotic signaling pathway	6.59E-10	BCL2/CASP8/AR/RELA/AKT1/HMOX1/ICAM1/GSTP1/BCL2L1/RAF1/CAV1/IL1B/NOS3/SERPINE1/IL1A	15
BP	GO:0015918	sterol transport	8.69E-10	PON1/PPARG/LDLR/APOB/ADIPOQ/SOAT2/AKR1C1/CES1/SOAT1/EGF/NFKBIA/CAV1/ABCG2	13
BP	GO:0030522	intracellular receptor signaling pathway	9.67E-10	RXRA/PGR/CASP8/AR/PPARG/RELA/NR1I2/AHR/NR1I3/AKR1C3/ESR1/PPARA/SREBF1/NCOA1/RB1/TP63/NFKBIA/PARP1/PPARD	19
BP	GO:0061041	regulation of wound healing	1.00E-09	PRKCA/F7/HMGCR/ABAT/ADRA2A/PLAU/CAV1/F3/NOS3/PLAT/THBD/SERPINE1/NFE2L2/PPARD	14

BP	GO:0010742	macrophage derived foam cell differentiation	1.12E-09	PPARG/STAT1/APOB/PPARA/ADIPOQ/S OAT2/SOAT1/NFKBIA/CRP	9
BP	GO:0090077	foam cell differentiation	1.12E-09	PPARG/STAT1/APOB/PPARA/ADIPOQ/S OAT2/SOAT1/NFKBIA/CRP	9
BP	GO:0009411	response to UV	1.20E-09	PTGS2/BCL2/BAX/CASP9/CASP3/RELA/ AKT1/MAPK8/CAT/EGFR/CCND1/CDKN 1A/MYC/PARP1	14
BP	GO:0007623	circadian rhythm	1.24E-09	NCOA2/SLC6A4/JUN/NOS2/PPARG/F7/ MAPK8/AHR/PPARA/SREBF1/ADIPOQ/E GFR/TOP1/SERPINE1/TOP2A/CLDN4	16

BP	GO:0051100	negative regulation of binding	1.39E-09	ADRB2/BAX/JUN/MAP2/AKT1/MAPK8/HMOX1/SLPI/MAPK3/PPARA/ADIPOQ/IL10/NFKBIA/CAV1/E2F1	15
BP	GO:0032103	positive regulation of response to external stimulus	1.55E-09	PTGS2/OPRM1/PRKCA/F7/MAPK3/LDLR/EGFR/VEGFA/IL6/NFKBIA/F3/IL1B/PTGER3/CXCL8/HSPB1/IL2/THBD/SERPINE1/CXCL10	19
BP	GO:0031669	cellular response to nutrient levels	1.55E-09	PTGS2/BCL2/JUN/PPARG/MAPK8/HMOX1/ICAM1/AKR1C3/MAPK3/MAPK1/SOD1/SREBF1/NCOA1/CDKN1A/COL1A1/NFE2L2/HSF1	17
BP	GO:1904018	positive regulation of vasculature development	1.55E-09	PTGS2/PRKCA/HMOX1/CYP1B1/VEGFA/IL10/HIF1A/F3/IL1B/CXCL8/PRKCB/NOS3/HSPB1/SERPINE1/IL1A/NFE2L2/HK2	17

BP	GO:1903522	regulation of blood circulation	1.57E-09	PTGS2/KCNH2/CHRM3/SCN5A/ADRA1A/CHRM2/ADRA1B/AKT1/ICAM1/GSTM2/SREBF1/ADRA2A/ADRB1/EGFR/CAV1/GJA1/NOS3/IL2	18
BP	GO:0030879	mammary gland development	1.85E-09	PGR/BAX/AR/AKT1/ESR1/MAPK1/FASN/SLC6A3/VEGFA/CCND1/EGF/HIF1A/CAV1/HK2	14
BP	GO:1901655	cellular response to ketone	2.04E-09	CASP9/AR/PPARG/AKT1/ICAM1/AHR/AKR1C3/AKR1B1/EGFR/ELK1/ACACA/SPP1	12
BP	GO:1901342	regulation of vasculature development	2.09E-09	PTGS2/PRKCA/PPARG/STAT1/HMOX1/CYP1B1/VEGFA/IL10/IL6/HIF1A/ERBB2/F3/IL1B/CXCL8/PRKCB/NOS3/HSPB1/SERPINE1/IL1A/NFE2L2/CXCL10/HK2	22

BP	GO:0050679	positive regulation of epithelial cell proliferation	2.46E-09	SCN5A/JUN/PRKCA/AR/AKT1/HMOX1/HAS2/EGFR/VEGFA/CCND1/IL10/TP63/HIF1A/ERBB2/MYC/F3	16
BP	GO:0050727	regulation of inflammatory response	2.46E-09	PTGS2/NOS2/PPARG/RELA/SELE/GSTP1/ESR1/LDLR/PPARA/ADIPOQ/MMP3/EGFR/MMP9/IL10/RB1/IL6/NFKBIA/IL1B/PTGER3/IL2/SERPINE1/PPARD	22
BP	GO:0031649	heat generation	2.99E-09	PTGS2/ADRB2/ABAT/ADRB1/IL1B/PTGER3/IL1A	7
BP	GO:0008217	regulation of blood pressure	3.47E-09	PTGS2/PTGS1/ADRA1A/ADRA1B/ADRB2/NOS2/AR/PPARG/HMOX1/SOD1/PPARA/ADIPOQ/ABAT/ADRB1/NOS3	15

BP	GO:0048661	positive regulation of smooth muscle cell proliferation	3.65E-09	PTGS2/JUN/ AKT1/STAT1/HMOX1/HMGC R/ AKR1B1/EGFR/MMP2/MMP9/IL10/IL6	12
BP	GO:0030193	regulation of blood coagulation	3.97E-09	PRKCA/F7/ ABAT/PLAU/CAV1/F3/NOS3 /PLAT/THBD/SERPINE1/NFE2L2	11
BP	GO:1900046	regulation of hemostasis	3.97E-09	PRKCA/F7/ ABAT/PLAU/CAV1/F3/NOS3 /PLAT/THBD/SERPINE1/NFE2L2	11
BP	GO:1904951	positive regulation of establishment of protein localization	4.02E-09	PTGS2/CHRM1/BCL2/CASP8/ ACHE/MAP K8/MAPK3/MAPK1/ ABAT/EGFR/IL10/IL 6/TP63/HIF1A/ERBB2/IL1B/IL2/IFNG/IL1 A/PPARD/CHUK/E2F1	22

BP	GO:1901653	cellular response to peptide	4.28E-09	ADRB2/PPARG/RELA/AKT1/STAT1/GSTP1/SLC2A4/INSR/SREBF1/ADIPOQ/GOT1/AKR1B1/POR/CAV1/IL1B/PRKCB/NFE2L2/PARP1/HSF1/IGF2	20
BP	GO:0016999	antibiotic metabolic process	4.65E-09	CYP1A2/CYP1A1/AKR1C3/SOD1/CAT/UGT1A1/AKR1C1/ADH1C/AKR1B1/MAOB/MMP3/EGFR/SULT1E1/MPO	14
BP	GO:0030168	platelet activation	4.65E-09	PRKCA/MAPK3/MAPK1/ABAT/ADRA2A/IL6/RAF1/PRKCB/NOS3/HSPB1/THBD/COL1A1/COL3A1/CD40LG	14
BP	GO:0046890	regulation of lipid biosynthetic process	5.26E-09	PTGS2/AKT1/AKR1C3/FASN/LDLR/SOD1/APOB/HMGCR/SREBF1/ADIPOQ/EIF6/POR/ACACA/IL1B/IFNG	15

BP	GO:0051051	negative regulation of transport	6.97E-09	PTGS2/KCNH2/OPRM1/BCL2/AKT1/HMOX1/ICAM1/GSTM2/HMGCR/SREBF1/ADIPOQ/ABAT/ADRA2A/MAOB/MMP9/IL10/EGF/CAV1/IL1B/PTGER3/PRKCB/NOS3/ERBB3	23
BP	GO:0071453	cellular response to oxygen levels	7.05E-09	PTGS2/BCL2/PPARG/AKT1/HMOX1/ICAM1/SLC2A4/VEGFA/HIF1A/CAV1/MYC/CCNB1/NFE2L2/PPARD/E2F1	15
BP	GO:0071347	cellular response to interleukin-1	7.44E-09	RELA/IKBKB/ICAM1/HAS2/MAPK3/IL6/NFKBIA/HIF1A/IL1B/CCL2/CXCL8/IL1A/CHUK	13
BP	GO:0050818	regulation of coagulation	7.52E-09	PRKCA/F7/ABAT/PLAU/CAV1/F3/NOS3/PLAT/THBD/SERPINE1/NFE2L2	11

BP	GO:0032102	negative regulation of response to external stimulus	7.53E-09	PPARG/GSTP1/LDLR/HMGCR/PPARA/ADIPOQ/ABAT/SLC6A3/PLAU/IL10/RB1/CL2/NOS3/IL2/PLAT/THBD/SERPINE1/PARD/SPP1	19
BP	GO:0006940	regulation of smooth muscle contraction	7.53E-09	PTGS2/CHRM3/ADRA1A/CHRM2/ADRA1B/ADRB2/SOD1/ABAT/ADRA2A/CAV1	10
BP	GO:1990748	cellular detoxification	7.53E-09	PTGS2/PTGS1/GSTP1/GSTM1/GSTM2/SOD1/CAT/GSR/NOS3/MPO/NFE2L2/NQO1	12
BP	GO:0046394	carboxylic acid biosynthetic process	8.02E-09	PTGS2/PTGS1/CYP3A4/CYP1A2/CYP1A1/ALOX5/HAS2/INSR/AKR1C3/FASN/PPARA/ADIPOQ/GOT1/ABAT/LTA4H/EIF6/EGF/HIF1A/ACACA/IL1B/HK2	21

BP	GO:0003012	muscle system process	8.26E-09	PTGS2/KCNH2/CHRM3/SCN5A/ADRA1A/CHRM2/ADRA1B/ADRB2/PRKCA/HMOX1/GSTM2/SOD1/PPARA/ABAT/ADRA2A/CAV1/GJA1/IL1B/PTGER3/NOS3/PARP1/CHUK	22
BP	GO:0016053	organic acid biosynthetic process	8.27E-09	PTGS2/PTGS1/CYP3A4/CYP1A2/CYP1A1/ALOX5/HAS2/INSR/AKR1C3/FASN/PPARA/ADIPOQ/GOT1/ABAT/LTA4H/EIF6/EGF/HIF1A/ACACA/IL1B/HK2	21
BP	GO:0001676	long-chain fatty acid metabolic process	1.02E-08	PTGS2/PTGS1/CYP3A4/CYP1A2/CYP1A1/CYP1B1/ALOX5/GSTP1/GSTM2/AKR1C3/MAPK3/LTA4H	12
BP	GO:1904019	epithelial cell apoptotic process	1.02E-08	HMOX1/ICAM1/AKR1C3/BCL2L1/IL10/RB1/IL6/CCL2/SERPINE1/NFE2L2/E2F1/CD40LG	12

BP	GO:0010039	response to iron ion	1.12E-08	BCL2/HMOX1/CYP1A1/ABAT/SLC6A3/CND1/HIF1A/CCNB1	8
BP	GO:0035094	response to nicotine	1.15E-08	BCL2/CASP3/RELA/HMOX1/VCAM1/MAPK1/PPARA/ABAT/SLC6A3	9
BP	GO:0001819	positive regulation of cytokine production	1.19E-08	PTGS2/RELA/STAT1/HMOX1/CYP1B1/MAPK3/SOD1/ADIPOQ/ADRA2A/IL10/IL6/HIF1A/IL1B/HSPB1/IL2/SERPINE1/IFNG/IL1A/CHUK/CD40LG/IRF1	21
BP	GO:0001503	ossification	1.19E-08	PTGS2/ADRB2/BCL2/ACHE/AKT1/MAPK3/MAPK1/FASN/CAT/EGFR/MMP2/MMP9/IL6/TP63/HIF1A/COL1A1/SPP1/RUNX2/IGFBP3/IGF2	20

BP	GO:0051402	neuron apoptotic process	1.31E-08	BCL2/BAX/CASP9/JUN/CASP3/HMOX1/SOD1/BCL2L1/RB1/TP63/HIF1A/CCL2/NQO1/PARP1/ERBB3/RASA1	16
BP	GO:0019915	lipid storage	1.33E-08	PPARG/APOB/PPARA/SOAT1/IL6/NFKBIA/CAV1/IL1B/PPARD/CRP	10
BP	GO:0043200	response to amino acid	1.34E-08	CASP3/F7/RELA/ICAM1/GSTP1/EGFR/BCL2L1/MMP2/COL1A1/COL3A1/HSF1/CHUK	12
BP	GO:0071375	cellular response to peptide hormone stimulus	1.63E-08	PPARG/RELA/AKT1/STAT1/GSTP1/SLC2A4/INSR/SREBF1/ADIPOQ/GOT1/POR/CAV1/IL1B/PRKCB/NFE2L2/PARP1/HSF1/IGF2	18

BP	GO:0022407	regulation of cell-cell adhesion	1.66E-08	CASP3/PRKCA/ AKT1/ICAM1/VCAM1/HAS2/PPARA/ADIPOQ/ ABAT/IL10/IL6/ERBB2/CAV1/IL1B/CCL2/IL2/IFNG/IGF2/CD40LG/IRF1	20
BP	GO:0009416	response to light stimulus	1.70E-08	PTGS2/BCL2/BAX/CASP9/CASP3/RELA/ AKT1/MAPK8/ CAT/HMGCR/EGFR/CCND1/FOS/CDKN1A/ELK1/HIF1A/MYC/PARP1	18
BP	GO:0050900	leukocyte migration	1.84E-08	F7/ AKT1/MMP1/HMOX1/ICAM1/SELE/VCAM1/MAPK3/ APOB/VEGFA/MMP9/IL10/IL6/CAV1/IL1B/CCL2/CXCL8/SERPINE1/COL1A1/CXCL11/CXCL2/CXCL10	22
BP	GO:0001659	temperature homeostasis	1.90E-08	PTGS2/ ADRB2/ ACHE/ADIPOQ/ ABAT/ADRB1/VEGFA/RB1/CAV1/GJA1/IL1B/PTGER3/IL1A/HSF1	14

BP	GO:0006801	superoxide metabolic process	2.00E-08	NOS2/GSTP1/SOD1/EGFR/NOS3/MPO/N CF1/NFE2L2/NQO1/CRP	10
BP	GO:0050708	regulation of protein secretion	2.18E-08	OPRM1/PRKCA/NOS2/ACHE/MAPK3/H MGCR/SREBF1/ABAT/ADRA2A/EGFR/IL1 0/IL6/HIF1A/IL1B/IL2/IFNG/IL1A/PPAR D/CRP/CHUK/CD40LG	21
BP	GO:0052547	regulation of peptidase activity	2.55E-08	PTGS2/BAX/CASP9/CASP3/CASP8/PPAR G/AKT1/SLPI/MAPK3/VEGFA/MMP9/TP 63/POR/RAF1/CAV1/MYC/F3/BIRC5/SER PINE1/HSF1/PCOLCE	21
BP	GO:0046660	female sex differentiation	2.60E-08	PGR/BCL2/BAX/CASP3/ICAM1/INSR/ES R1/SOD1/VEGFA/BCL2L1/TP63/NOS3	12

BP	GO:0038034	signal transduction in absence of ligand	2.60E-08	BCL2/BAX/CASP9/CASP3/ AKT1/BCL2L1/ IL1B/IL2/IL1A/ERBB3	10
BP	GO:0097192	extrinsic apoptotic signaling pathway in absence of ligand	2.60E-08	BCL2/BAX/CASP9/CASP3/ AKT1/BCL2L1/ IL1B/IL2/IL1A/ERBB3	10
BP	GO:0043281	regulation of cysteine-type endopeptidase activity involved in apoptotic process	2.78E-08	PTGS2/BAX/CASP9/CASP3/CASP8/PPAR G/ AKT1/VEGFA/MMP9/TP63/POR/RAF1 /MYC/F3/HSF1	15
BP	GO:0019218	regulation of steroid metabolic process	2.81E-08	AKR1C3/FASN/LDLR/SOD1/ APOB/HMG CR/UGT1A1/SREBF1/POR/ ACACA/IL1B/I FNG	12

BP	GO:0043062	extracellular structure organization	2.86E-08	PRSS1/MMP1/ICAM1/VCAM1/CYP1B1/H AS2/MTTP/APOB/SOAT2/SOAT1/CTRB1/ MMP3/MMP2/MMP9/RB1/SERPINE1/COL 1A1/MPO/COL3A1/SPP1	20
BP	GO:0010332	response to gamma radiation	3.16E-08	BCL2/BAX/BCL2L1/ELK1/MYC/PARP1/C HEK2/HSF1/CXCL10	9
BP	GO:0030099	myeloid cell differentiation	3.22E-08	CASP9/JUN/CASP3/CASP8/PRKCA/PPAR G/STAT1/FASN/ADIPOQ/VEGFA/FOS/EI F6/MMP9/RB1/NFKBIA/HIF1A/MYC/PRK CB/IFNG/PARP1	20
BP	GO:0042310	vasoconstriction	3.33E-08	PTGS2/CHRM3/ADRA1A/ADRA1B/SLC6A 4/AKT1/ICAM1/ADRA2A/EGFR/CAV1	10

BP	GO:0071902	positive regulation of protein serine/threonine kinase activity	3.34E-08	ADRB2/INSR/MAPK3/MAPK1/SOD1/ADIPOQ/ADRA2A/EGFR/VEGFA/CCND1/EGF/RAF1/ERBB2/IL1B/CCNB1/IFNG/IGF2/CD40LG	18
BP	GO:0006352	DNA-templated transcription, initiation	3.46E-08	RXRA/PGR/BAX/JUN/AR/PPARG/NR1I2/NR1I3/ESR1/MAPK3/PPARA/NR3C2/CCND1/CDKN1A/PPARD/RUNX2	16
BP	GO:0090066	regulation of anatomical structure size	3.46E-08	PTGS2/CHRM3/ADRA1A/ADRA1B/ADRB2/SLC6A4/MAP2/AKT1/HMOX1/ICAM1/SOD1/HMGCR/ADRA2A/ADRB1/EGFR/VEGFA/CAV1/NOS3/PPARD/CRP/SPP1/ASA1	22
BP	GO:0098754	detoxification	3.95E-08	PTGS2/PTGS1/GSTP1/GSTM1/GSTM2/SOD1/CAT/GSR/NOS3/MPO/NFE2L2/NQO1	12

BP	GO:0007159	leukocyte cell-cell adhesion	3.97E-08	CASP3/AKT1/ICAM1/SELE/VCAM1/HAS2/PPARA/IL10/IL6/ERBB2/CAV1/IL1B/CC L2/IL2/IFNG/IGF2/CD40LG/IRF1	18
BP	GO:1905952	regulation of lipid localization	4.13E-08	PON1/PPARG/AKT1/APOB/PPARA/ADIP OQ/EGF/IL6/NFKBIA/IL1B/PPARD/CRP/ SPP1	13
BP	GO:0008585	female gonad development	4.20E-08	PGR/BCL2/BAX/CASP3/ICAM1/INSR/ES R1/SOD1/VEGFA/BCL2L1/NOS3	11
BP	GO:0071398	cellular response to fatty acid	4.22E-08	PPARG/AKT1/AKR1C3/LDLR/APOB/SRE BF1/ACACA/CCNB1/E2F1	9

BP	GO:0090257	regulation of muscle system process	4.23E-08	PTGS2/CHRM3/SCN5A/ADRA1A/CHRM2/ADRA1B/ADRB2/PRKCA/GSTM2/SOD1/PPARA/ABAT/ADRA2A/CAV1/NOS3/PARP1	16
BP	GO:0042445	hormone metabolic process	4.59E-08	ACHE/CYP3A4/CYP1A1/CYP1B1/AKR1C3/ESR1/UGT1A1/AKR1C1/AKR1B1/POR/HIF1A/IL1B/SULT1E1/IFNG/SPP1	15
BP	GO:0019229	regulation of vasoconstriction	4.91E-08	PTGS2/CHRM3/ADRA1A/ADRA1B/AKT1/ICAM1/ADRA2A/EGFR/CAV1	9
BP	GO:0006367	transcription initiation from RNA polymerase II promoter	4.96E-08	RXRA/PGR/BAX/AR/PPARG/NR1I2/NR1I3/ESR1/PPARA/NR3C2/CCND1/CDKN1A/PPARD/RUNX2	14

BP	GO:0072330	monocarboxylic acid biosynthetic process	4.96E-08	PTGS2/PTGS1/CYP3A4/CYP1A2/CYP1A1/ALOX5/INSR/AKR1C3/FASN/PPARA/ADIPOQ/ABAT/LTA4H/EIF6/HIF1A/ACACA/HK2	17
BP	GO:1903037	regulation of leukocyte cell-cell adhesion	4.96E-08	CASP3/AKT1/ICAM1/VCAM1/HAS2/PPARA/IL10/IL6/ERBB2/CAV1/IL1B/CCL2/IL2/IFNG/IGF2/CD40LG/IRF1	17
BP	GO:0048638	regulation of developmental growth	5.27E-08	ADRB2/SLC6A4/BCL2/MAP2/AR/AKT1/INSR/SOD1/PPARA/SLC6A3/ADRB1/VEGFA/POR/CCNB1/PPARD/HSF1/SPP1/IGF2	18
BP	GO:0002791	regulation of peptide secretion	5.50E-08	OPRM1/PRKCA/NOS2/ACHE/MAPK3/HMGCR/SREBF1/ABAT/ADRA2A/EGFR/IL10/IL6/HIF1A/IL1B/IL2/IFNG/IL1A/PPARD/CRP/CHUK/CD40LG	21

BP	GO:0098869	cellular oxidant detoxification	5.52E-08	PTGS2/PTGS1/GSTP1/GSTM2/SOD1/CAT/ GSR/NOS3/MPO/NFE2L2/NQO1	11
BP	GO:0031099	regeneration	5.57E-08	BCL2/JUN/PPARG/F7/HMOX1/GSTP1/U GT1A1/EGFR/CCND1/CDKN1A/IL10/CC NB1/PPARD/SPP1	14
BP	GO:0060359	response to ammonium ion	5.79E-08	CHRM3/CHRM1/CHRM4/CHRM2/OPRM1 /GABRA1/CASP3/RELA/MAPK3/MAPK1/ ABAT/SLC6A3	12
BP	GO:0071260	cellular response to mechanical stimulus	5.83E-08	PTGS2/CASP8/AKT1/MAPK8/MAPK3/GO T1/EGFR/IL1B/COL1A1/IRF1	10

BP	GO:0009743	response to carbohydrate	5.93E-08	PTGS2/CASP3/ICAM1/GSTP1/CAT/APOB/HMGCR/SREBF1/ADIPOQ/GOT1/ADRA2A/RAF1/HIF1A/PRKCB/PPARD	15
BP	GO:0046165	alcohol biosynthetic process	6.13E-08	CYP3A4/FASN/SOD1/APOB/HMGCR/SREBF1/GOT1/CES1/AKR1B1/POR/ACACA/IL1B/IFNG	13
BP	GO:0042180	cellular ketone metabolic process	6.21E-08	PTGS2/PPARG/AKT1/AKR1C3/HMGCR/PARA/SREBF1/ADIPOQ/AKR1C1/AKR1B1/EIF6/ODC1/CAV1/NQO1	14
BP	GO:0042391	regulation of membrane potential	6.21E-08	KCNH2/CHRM1/SCN5A/ADRA1A/ADRB2/CHRNA2/OPRM1/GABRA1/BCL2/BAX/JUN/AKT1/SOD1/GOT1/ABAT/ADRB1/BCL2L1/CAV1/GJA1/PARP1	20

BP	GO:0060249	anatomical structure homeostasis	6.44E-08	ADRB2/BCL2/BAX/PRKCA/SLC6A2/MAP K3/MAPK1/SOD1/AKR1B1/EGFR/VEGFA /RB1/IL6/HIF1A/ACACA/MYC/NOS3/HS PB1/PARP1/SPP1	20
BP	GO:0032091	negative regulation of protein binding	6.49E-08	ADRB2/BAX/MAP2/AKT1/MAPK8/SLPI/ MAPK3/PPARA/ADIPOQ/IL10/CAV1	11
BP	GO:0046545	development of primary female sexual characteristics	6.49E-08	PGR/BCL2/BAX/CASP3/ICAM1/INSR/ES R1/SOD1/VEGFA/BCL2L1/NOS3	11
BP	GO:0006091	generation of precursor metabolites and energy	6.49E-08	NOS2/AKT1/CYP1A2/INSR/CAT/PPARA/ GSR/ADIPOQ/ADH1C/AKR1B1/MAOB/EI F6/POR/HIF1A/MYC/CCNB1/NCF1/NQO 1/PPARD/IGF2/HK2	21

BP	GO:0043401	steroid hormone mediated signaling pathway	6.49E-08	RXRA/PGR/AR/PPARG/NR1I2/NR1I3/ESR1/PPARA/NR3C2/NCOA1/RB1/TP63/PARP1/PPARD	14
BP	GO:0070371	ERK1 and ERK2 cascade	6.79E-08	ADRA1A/OPRM1/JUN/PRKCA/ICAM1/GSTP1/INSR/MAPK3/MAPK1/HMGCR/ADIPOQ/EGFR/EGF/ERBB2/MYC/IL1B/CCL2/ERBB3	18
BP	GO:0071456	cellular response to hypoxia	6.81E-08	PTGS2/BCL2/AKT1/HMOX1/ICAM1/SLC2A4/VEGFA/HIF1A/MYC/CCNB1/NFE2L2/PPARD/E2F1	13
BP	GO:1901568	fatty acid derivative metabolic process	6.81E-08	PTGS2/PTGS1/PON1/CYP1A2/CYP1A1/CYP1B1/ALOX5/AKR1C3/MAPK3/FASN/ABCC1/LTA4H/ACACA	13

BP	GO:0006939	smooth muscle contraction	7.75E-08	PTGS2/CHRM3/ADRA1A/CHRM2/ADRA1B/ADRB2/SOD1/ABAT/ADRA2A/CAV1/PTGER3	11
BP	GO:0060135	maternal process involved in female pregnancy	8.30E-08	PTGS2/RXRA/PGR/AR/AKT1/ESR1/AKR1B1/PPARD/SPP1	9
BP	GO:0032963	collagen metabolic process	8.50E-08	PPARG/MMP1/GOT1/MMP3/MMP2/MMP9/IL6/HIF1A/COL1A1/PPARD/CTSD	11
BP	GO:2000116	regulation of cysteine-type endopeptidase activity	9.47E-08	PTGS2/BAX/CASP9/CASP3/CASP8/PPARG/AKT1/VEGFA/MMP9/TP63/POR/RAF1/MYC/F3/HSF1	15

BP	GO:0010634	positive regulation of epithelial cell migration	9.69E-08	PTGS2/JUN/PRKCA/AKT1/HMOX1/HAS2/VEGFA/MMP9/HIF1A/NOS3/HSPB1/IFNG/NFE2L2	13
BP	GO:0006690	icosanoid metabolic process	1.02E-07	PTGS2/PTGS1/PON1/CYP1A2/CYP1A1/CYP1B1/ALOX5/AKR1C3/MAPK3/ABCC1/LTA4H	11
BP	GO:0019932	second-messenger-mediated signaling	1.05E-07	ADRA1A/ADRA1B/ADRB2/OPRM1/PRKCA/NOS2/SELE/VCAM1/AHR/GSTM2/ADRA2A/ADRB1/EGFR/VEGFA/PTGER3/CXCL8/NOS3/CXCL11/CXCL10/ERBB3	20
BP	GO:1901215	negative regulation of neuron death	1.19E-07	BCL2/BAX/JUN/AKT1/HMOX1/SOD1/PPARA/BCL2L1/IL10/HIF1A/CCL2/HSF1/ERBB3/RASA1	14

BP	GO:0061614	pri-miRNA transcription by RNA polymerase II	1.22E-07	JUN/PPARG/RELA/PPARA/FOS/IL10/HIF1A/PPARD	8
BP	GO:0043523	regulation of neuron apoptotic process	1.26E-07	BCL2/BAX/CASP9/JUN/CASP3/HMOX1/SOD1/BCL2L1/HIF1A/CCL2/NQO1/PARP1/ERBB3/RASA1	14
BP	GO:0036294	cellular response to decreased oxygen levels	1.35E-07	PTGS2/BCL2/AKT1/HMOX1/ICAM1/SLC2A4/VEGFA/HIF1A/MYC/CCNB1/NFE2L2/PPARD/E2F1	13
BP	GO:0032869	cellular response to insulin stimulus	1.42E-07	PPARG/RELA/AKT1/STAT1/GSTP1/SLC2A4/INSR/SREBF1/ADIPOQ/GOT1/IL1B/PKCB/PARP1/IGF2	14

BP	GO:0071242	cellular response to ammonium ion	1.42E-07	CHRM3/CHRM1/CHRM4/CHRM2/OPRM1/GABRA1/CASP3/MAPK3/MAPK1	9
BP	GO:0008631	intrinsic apoptotic signaling pathway in response to oxidative stress	1.43E-07	BCL2/AKT1/CYP1B1/SOD1/HIF1A/HSPB1/NFE2L2/PARP1	8
BP	GO:0045776	negative regulation of blood pressure	1.43E-07	ADRA1A/ADRB2/NOS2/PPARA/ADIPOQ/ABAT/ADRB1/NOS3	8
BP	GO:0051235	maintenance of location	1.44E-07	BAX/PPARG/AKT1/GSTM2/APOB/PPARA/SOAT1/IL10/IL6/NFKBIA/CAV1/IL1B/CXCL11/PPARD/CRP/CXCL10/HK2	17

BP	GO:0042110	T cell activation	1.58E-07	BCL2/BAX/CASP3/CASP8/ AKT1/ICAM1/ VCAM1/SOD1/IL10/IL6/ERBB2/CAV1/IL1 B/CCL2/IL2/IFNG/RUNX2/IGF2/CD40LG /IRF1	20
BP	GO:0045907	positive regulation of vasoconstriction	1.67E-07	PTGS2/ ADRA1A/ ADRA1B/ AKT1/ICAM1/ EGFR/CAV1	7
BP	GO:0055123	digestive system development	1.77E-07	BCL2/CYP1A1/INSR/EGFR/CDKN1A/RB1 /TP63/HIF1A/CXCL8/CCNB1/COL3A1/IG F2	12
BP	GO:0060749	mammary gland alveolus development	1.81E-07	AR/ESR1/VEGFA/CCND1/EGF/HIF1A	6

BP	GO:0061377	mammary gland lobule development	1.81E-07	AR/ESR1/VEGFA/CCND1/EGF/HIF1A	6
BP	GO:0050730	regulation of peptidyl-tyrosine phosphorylation	1.83E-07	ADRA1A/ICAM1/ADIPOQ/ADRA2A/EGFR/VEGFA/EGF/IL6/CAV1/IL2/IFNG/NCF1/HSF1/IGF2/ERBB3	15
BP	GO:0014909	smooth muscle cell migration	2.04E-07	BCL2/HAS2/GSTP1/ADIPOQ/PLAU/PLAT/SERPINE1/NFE2L2/PPARD/IGFBP3	10
BP	GO:0048145	regulation of fibroblast proliferation	2.04E-07	BAX/JUN/PPARG/GSTP1/ESR1/EGFR/CDKN1A/MYC/CCNB1/E2F1	10

BP	GO:0048144	fibroblast proliferation	2.26E-07	BAX/JUN/PPARG/GSTP1/ESR1/EGFR/CDKN1A/MYC/CCNB1/E2F1	10
BP	GO:0050810	regulation of steroid biosynthetic process	2.26E-07	AKR1C3/FASN/SOD1/APOB/HMGCR/SREBF1/POR/ACACA/IL1B/IFNG	10
BP	GO:1901617	organic hydroxy compound biosynthetic process	2.48E-07	CYP3A4/AKR1C3/FASN/SOD1/APOB/HMGCR/SREBF1/GOT1/CES1/SLC6A3/AKR1B1/POR/ACACA/IL1B/IFNG	15
BP	GO:0010888	negative regulation of lipid storage	2.55E-07	PPARG/PPARA/IL6/NFKBIA/PPARD/CRP	6

BP	GO:0008406	gonad development	2.73E-07	PGR/BCL2/BAX/CASP3/AR/ICAM1/INSR /AKR1C3/ESR1/SOD1/VEGFA/CCND1/BC L2L1/NOS3	14
BP	GO:0036473	cell death in response to oxidative stress	2.75E-07	BCL2/AKT1/CYP1B1/SOD1/MMP3/IL10/H IF1A/HSPB1/NFE2L2/PARP1	10
BP	GO:0043393	regulation of protein binding	2.87E-07	ADRB2/BCL2/BAX/MAP2/AKT1/MAPK8/ SLPI/MAPK3/PPARA/ADIPOQ/MMP9/IL1 0/CAV1/HSF1	14
BP	GO:0048662	negative regulation of smooth muscle cell proliferation	2.96E-07	PPARG/HMOX1/GSTP1/ADIPOQ/CDKN1 A/IL10/IFNG/PPARD/IGFBP3	9

BP	GO:0051091	positive regulation of DNA-binding transcription factor activity	2.99E-07	AR/PPARG/RELA/IKBKB/AKT1/ICAM1/ESR1/CAT/VEGFA/IL10/IL6/IL1B/PRKCB/CHUK/CD40LG	15
BP	GO:0008637	apoptotic mitochondrial changes	3.03E-07	BCL2/BAX/JUN/CASP8/AKT1/MAPK8/BCL2L1/MMP9/TP63/E2F1/HK2	11
BP	GO:0060326	cell chemotaxis	3.06E-07	F7/VCAM1/GSTP1/MAPK3/ABCC1/VEGFA/IL10/IL6/IL1B/CCL2/CXCL8/HSPB1/SELPINE1/CXCL11/CXCL2/CXCL10	16
BP	GO:0007187	G protein-coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger	3.11E-07	CHRM3/CHRM1/CHRM4/ADRA1A/CHRM2/ADRA1B/ADRB2/OPRM1/PRKCA/ADRA2A/ADRB1/CCL2/PTGER3/CXCL11/CXCL10	15

BP	GO:0051101	regulation of DNA binding	3.26E-07	JUN/PPARG/MAPK8/HMOX1/MMP9/EGF/RB1/NFKBIA/IFNG/PARP1/E2F1	11
BP	GO:0031349	positive regulation of defense response	3.30E-07	PTGS2/CASP8/RELA/IKBKB/ESR1/MAPK3/LDLR/APOB/EGFR/IL6/NFKBIA/RAF1/CAV1/IL1B/PTGER3/IL2/SERPINE1/CHUK/IRF1	19
BP	GO:0007249	I-kappaB kinase/NF-kappaB signaling	3.41E-07	CASP8/RELA/IKBKB/AKT1/STAT1/HMOX1/GSTP1/ESR1/ADIPOQ/NFKBIA/GJA1/IL1B/PRKCB/HSPB1/CHUK	15
BP	GO:0001894	tissue homeostasis	3.48E-07	ADRB2/BCL2/BAX/PRKCA/SOD1/AKR1B1/EGFR/VEGFA/RB1/IL6/ACACA/NOS3/HSPB1/SPP1	14

BP	GO:0007188	adenylate cyclase-modulating G protein-coupled receptor signaling pathway	3.48E-07	CHRM3/CHRM1/CHRM4/ADRA1A/CHRM2/ADRA1B/ADRB2/OPRM1/PRKCA/ADRA2A/ADRB1/PTGER3/CXCL11/CXCL10	14
BP	GO:0006720	isoprenoid metabolic process	3.48E-07	CYP3A4/CYP1A2/CYP1A1/CYP1B1/AKR1C3/APOB/HMGCR/UGT1A1/AKR1C1/EGFR/PPARD	11
BP	GO:0050731	positive regulation of peptidyl-tyrosine phosphorylation	3.50E-07	ADRA1A/ICAM1/ADIPOQ/ADRA2A/VEGFA/EGF/IL6/IL2/IFNG/NCF1/HSF1/IGF2/ERBB3	13
BP	GO:0045137	development of primary sexual characteristics	3.64E-07	PGR/BCL2/BAX/CASP3/AR/ICAM1/INSR/AKR1C3/ESR1/SOD1/VEGFA/CCND1/BCL2L1/NOS3	14

BP	GO:0043271	negative regulation of ion transport	3.67E-07	PTGS2/KCNH2/BCL2/AKT1/ICAM1/GSTM2/ABAT/ADRA2A/MAOB/MMP9/CAV1/NOS3	12
BP	GO:0043270	positive regulation of ion transport	3.68E-07	KCNH2/CHRM1/SCN5A/ADRB2/SLC6A4/BAX/AKT1/GSTM2/ABAT/ADRA2A/CAV1/IL1B/CCL2/CXCL11/CXCL10	15
BP	GO:0018108	peptidyl-tyrosine phosphorylation	3.92E-07	ADRA1A/ICAM1/INSR/MAPK3/ADIPOQ/ADRA2A/EGFR/VEGFA/EGF/IL6/ERBB2/CAV1/IL2/IFNG/NCF1/HSF1/IGF2/ERBB3	18
BP	GO:0010565	regulation of cellular ketone metabolic process	4.03E-07	PTGS2/PPARG/AKT1/AKR1C3/PPARA/SREBF1/ADIPOQ/EIF6/ODC1/CAV1/NQO1	11

BP	GO:0007566	embryo implantation	4.12E-07	PTGS2/RXRA/SOD1/MMP2/MMP9/IL1B/P PARD/SPP1	8
BP	GO:0006633	fatty acid biosynthetic process	4.16E-07	PTGS2/PTGS1/CYP3A4/CYP1A2/CYP1A1/ ALOX5/AKR1C3/FASN/ADIPOQ/LTA4H/ EIF6/ACACA	12
BP	GO:0051591	response to cAMP	4.22E-07	JUN/RELA/STAT1/AHR/SREBF1/ADIPOQ /SLC6A3/FOS/THBD/COL1A1	10
BP	GO:0018212	peptidyl-tyrosine modification	4.33E-07	ADRA1A/ICAM1/INSR/MAPK3/ADIPOQ/ ADRA2A/EGFR/VEGFA/EGF/IL6/ERBB2/ CAV1/IL2/IFNG/NCF1/HSF1/IGF2/ERBB3	18

BP	GO:0043122	regulation of I-kappaB kinase/NF-kappaB signaling	4.40E-07	CASP8/RELA/IKBKB/AKT1/STAT1/HMOX1/GSTP1/ESR1/ADIPOQ/GJA1/IL1B/PRKCB/HSPB1/CHUK	14
BP	GO:0031331	positive regulation of cellular catabolic process	4.49E-07	ADRB2/BAX/AKT1/HMOX1/INSR/MAPK3/LDLR/PPARA/ADRA2A/EGF/HIF1A/CAV1/IL1B/IFNG/NFE2L2/HSF1/HK2	17
BP	GO:0055093	response to hyperoxia	4.52E-07	PPARG/CYP1A1/CAT/CDKN1A/CAV1/COL1A1	6
BP	GO:0015718	monocarboxylic acid transport	4.69E-07	RXRA/NCOA2/NOS2/PPARG/AKT1/PPARA/AKR1C1/ABAT/NCOA1/ACACA/IL1B/PPARD	12

BP	GO:0042063	gliogenesis	4.78E-07	PPARG/RELA/AKT1/GSTP1/MAPK3/MAPK1/LDLR/SOD1/EGFR/IL6/ERBB2/IL1B/CL2/E2F1/ERBB3	15
BP	GO:0006694	steroid biosynthetic process	5.13E-07	CYP3A4/AKR1C3/FASN/SOD1/APOB/HMGCR/SREBF1/CES1/AKR1B1/POR/ACACA/IL1B/IFNG	13
BP	GO:0007548	sex differentiation	5.24E-07	PGR/BCL2/BAX/CASP3/AR/ICAM1/INSR/AKR1C3/ESR1/SOD1/VEGFA/CCND1/BCL2L1/TP63/NOS3	15
BP	GO:0045862	positive regulation of proteolysis	5.41E-07	BAX/CASP9/CASP3/CASP8/PPARG/AKT1/MAPK3/ADRA2A/EGF/CAV1/MYC/F3/IL1B/IFNG/NFE2L2/HSF1/PCOLCE	17

BP	GO:2001242	regulation of intrinsic apoptotic signaling pathway	5.68E-07	PTGS2/BCL2/BAX/AKT1/SOD1/BCL2L1/ MMP9/HIF1A/CAV1/HSPB1/NFE2L2/PAR P1	12
BP	GO:0006766	vitamin metabolic process	5.76E-07	RXRA/PRSS1/CYP3A4/CYP1A1/AKR1C3/ ABCC1/CTRB1/IL1B/IFNG/PPARD/ACPP	11
BP	GO:0001701	in utero embryonic development	5.76E-07	RXRA/CASP8/AR/AKT1/MAPK1/APOB/ NCOA1/EGFR/VEGFA/BCL2L1/IL10/HIF1 A/NOS3/CCNB1/HSF1/IGF2	16
BP	GO:0070498	interleukin-1-medi ated signaling pathway	6.16E-07	RELA/IKBKB/MAPK3/IL6/NFKBIA/IL1B/I L1A/CHUK	8

BP	GO:0002573	myeloid leukocyte differentiation	6.38E-07	JUN/CASP8/PRKCA/PPARG/FASN/ADIP OQ/VEGFA/FOS/MMP9/RB1/MYC/IFNG/ PARP1	13
BP	GO:0014812	muscle cell migration	6.46E-07	BCL2/HAS2/GSTP1/ADIPOQ/PLAU/PLAT /SERPINE1/NFE2L2/PPARD/IGFBP3	10
BP	GO:1902042	negative regulation of extrinsic apoptotic signaling pathway via death domain receptors	6.56E-07	CASP8/HMOX1/ICAM1/BCL2L1/RAF1/N OS3/SERPINE1	7
BP	GO:1902893	regulation of pri-miRNA transcription by RNA polymerase II	6.56E-07	JUN/RELA/PPARA/FOS/IL10/HIF1A/PPA RD	7

BP	GO:0060627	regulation of vesicle-mediated transport	6.68E-07	ADRA1A/CHRM2/MAP2/PPARG/HMOX1/SELE/SLC2A4/MAPK3/MAPK1/LDLR/A DIPOQ/ADRA2A/VEGFA/EGF/CAV1/IL1 B/CCL2/PRKCB/SERPINE1/IFNG	20
BP	GO:0031100	animal organ regeneration	6.73E-07	PPARG/F7/HMOX1/GSTP1/UGT1A1/EGF R/CCND1/CDKN1A/IL10	9
BP	GO:0006937	regulation of muscle contraction	6.73E-07	PTGS2/CHRM3/SCN5A/ADRA1A/CHRM2 /ADRA1B/ADRB2/GSTM2/SOD1/ABAT/A DRA2A/CAV1	12
BP	GO:0031663	lipopolysaccharide-mediated signaling pathway	6.91E-07	PRKCA/AKT1/MAPK3/MAPK1/NFKBIA/I L1B/CCL2/NOS3	8

BP	GO:0006721	terpenoid metabolic process	6.91E-07	CYP3A4/CYP1A2/CYP1A1/CYP1B1/AKR1C 3/APOB/UGT1A1/AKR1C1/EGFR/PPARD	10
BP	GO:0023061	signal release	7.38E-07	ADRA1A/CHRM2/OPRM1/PRKCA/NOS2/ HMGCR/SREBF1/ADIPOQ/ABAT/ADRA2 A/EGFR/IL6/RAF1/HIF1A/IL1B/PRKCB/I FNG/PPARD/SPP1	19
BP	GO:0043536	positive regulation of blood vessel endothelial cell migration	7.42E-07	PTGS2/PRKCA/AKT1/HMOX1/VEGFA/HI F1A/NOS3/HSPB1/NFE2L2	9
BP	GO:0033344	cholesterol efflux	7.86E-07	PON1/APOB/ADIPOQ/SOAT2/SOAT1/EG F/NFKBIA/ABCG2	8

BP	GO:0042743	hydrogen peroxide metabolic process	7.86E-07	CYP1A2/CYP1A1/SOD1/CAT/MAOB/MM P3/EGFR/MPO	8
BP	GO:1902930	regulation of alcohol biosynthetic process	8.21E-07	FASN/SOD1/APOB/HMGCR/SREBF1/POR /ACACA/IL1B/IFNG	9
BP	GO:0009755	hormone-mediated signaling pathway	8.52E-07	RXRA/PGR/AR/PPARG/NR1I2/NR1I3/ES R1/PPARA/NR3C2/NCOA1/RB1/TP63/PA RP1/PPARD	14
BP	GO:1905953	negative regulation of lipid localization	8.95E-07	PPARG/AKT1/PPARA/EGF/IL6/NFKBIA/ PPARD/CRP	8

BP	GO:1901216	positive regulation of neuron death	9.06E-07	BAX/CASP9/JUN/CASP3/CASP8/FOS/ELK1/NQO1/PARP1	9
BP	GO:0032800	receptor biosynthetic process	9.96E-07	PPARG/ACHE/PPARA/ADIPOQ/IL10/HIF1A	6
BP	GO:0052548	regulation of endopeptidase activity	1.07E-06	PTGS2/BAX/CASP9/CASP3/CASP8/PPARG/AKT1/SLPI/VEGFA/MMP9/TP63/POR/RAF1/MYC/F3/BIRC5/SERPINE1/HSF1	18
BP	GO:0030225	macrophage differentiation	1.10E-06	CASP8/PRKCA/ADIPOQ/VEGFA/MMP9/RB1/PARP1	7

BP	GO:1903706	regulation of hemopoiesis	1.10E-06	JUN/CASP8/PRKCA/STAT1/SOD1/ADIPOQ/FOS/EIF6/RB1/NFKBIA/HIF1A/ERBB2/MYC/PRKCB/IL2/IFNG/NFE2L2/IRF1	18
BP	GO:0014910	regulation of smooth muscle cell migration	1.11E-06	BCL2/HAS2/GSTP1/ADIPOQ/PLAU/SERPINE1/NFE2L2/PPARD/IGFBP3	9
BP	GO:0010745	negative regulation of macrophage derived foam cell differentiation	1.12E-06	PPARG/PPARA/ADIPOQ/NFKBIA/CRP	5
BP	GO:0042737	drug catabolic process	1.13E-06	ACHE/CYP3A4/CYP1A2/NR1I2/CAT/SLC6A3/MAOB/MAOA/POR/SULT1E1/MPO	11

BP	GO:0008625	extrinsic apoptotic signaling pathway via death domain receptors	1.22E-06	BCL2/BAX/CASP8/HMOX1/ICAM1/BCL2L1/RAF1/NOS3/SERPINE1	9
BP	GO:0001936	regulation of endothelial cell proliferation	1.29E-06	JUN/PRKCA/PPARG/AKT1/STAT1/HMOX1/VEGFA/IL10/HIF1A/CAV1/F3/CCL2	12
BP	GO:0002526	acute inflammatory response	1.31E-06	PTGS2/OPRM1/PPARG/ICAM1/VCAM1/GSTP1/UGT1A1/IL6/F3/IL1B/PTGER3/IL1A/CRP	13
BP	GO:0010821	regulation of mitochondrion organization	1.37E-06	BCL2/BAX/CASP8/AKT1/MAPK8/SREBF1/BCL2L1/MMP9/TP63/HIF1A/E2F1/HK2	12

BP	GO:0030258	lipid modification	1.37E-06	PPARG/AKT1/CYP3A4/CYP1A1/ESR1/PPARA/ADIPOQ/SOAT2/SOAT1/EGFR/EGF/POR/ERBB2/PPARD/ERBB3	15
BP	GO:0043405	regulation of MAP kinase activity	1.44E-06	GSTP1/INSR/MAPK3/MAPK1/SOD1/HMGCR/ADIPOQ/ADRA2A/EGFR/VEGFA/EGF/RAF1/ERBB2/CAV1/IL1B/CD40LG	16
BP	GO:0019748	secondary metabolic process	1.45E-06	BCL2/CYP1A2/CYP1A1/CYP1B1/AKR1C3/AKR1C1/AKR1B1/NFE2L2	8
BP	GO:0032768	regulation of monooxygenase activity	1.45E-06	AKT1/EGFR/POR/HIF1A/CAV1/IL1B/NO S3/IFNG	8

BP	GO:0045428	regulation of nitric oxide biosynthetic process	1.45E-06	PTGS2/ AKT1/ICAM1/INSR/IL10/CAV1/IL1B/IFNG	8
BP	GO:0009408	response to heat	1.57E-06	PTGS2/ AKT1/HMOX1/MAPK3/MAPK1/SOD1/CDKN1A/NOS3/IL1A/HSF1/CXCL10	11
BP	GO:1904705	regulation of vascular smooth muscle cell proliferation	1.60E-06	JUN/PPARG/HMOX1/GSTP1/ADIPOQ/CDKN1A/MMP2/MMP9/IL10	9
BP	GO:1990874	vascular smooth muscle cell proliferation	1.60E-06	JUN/PPARG/HMOX1/GSTP1/ADIPOQ/CDKN1A/MMP2/MMP9/IL10	9

BP	GO:0090181	regulation of cholesterol metabolic process	1.62E-06	FASN/LDLR/SOD1/APOB/HMGCR/SREBF1/POR/ACACA	8
BP	GO:0034349	glial cell apoptotic process	1.64E-06	CASP9/CASP3/PRKCA/RB1/CCL2	5
BP	GO:0034754	cellular hormone metabolic process	1.64E-06	CYP3A4/CYP1A1/CYP1B1/AKR1C3/ESR1/UGT1A1/AKR1C1/AKR1B1/SULT1E1/SPP1	10
BP	GO:0070663	regulation of leukocyte proliferation	1.65E-06	BCL2/CASP3/VCAM1/GSTP1/AHR/IL10/IL6/ERBB2/IL1B/IL2/IGF2/CD40LG/IRF1	13

BP	GO:0045444	fat cell differentiation	1.73E-06	PTGS2/ ADRB2/PPARG/ AKT1/SLC2A4/SR EBF1/ ADIPOQ/ ADRB1/CCND1/IL6/SULT 1E1/PPARD/E2F1	13
BP	GO:0001892	embryonic placenta development	1.73E-06	CASP8/ AKT1/MAPK1/NCOA1/EGFR/IL10 /HIF1A/HSF1/IGF2	9
BP	GO:0045787	positive regulation of cell cycle	2.02E-06	SLC6A4/BAX/PRKCA/CYP1A1/INSR/CCN D1/CDKN1A/IL10/EGF/RB1/IL1B/CCNB1 /IL1A/CHEK2/HSF1/E2F1/IGF2	17
BP	GO:0045926	negative regulation of growth	2.08E-06	ADRB2/SLC6A4/BCL2/MAP2/PPARG/PPA RA/ ADRB1/CDKN1A/IL10/HIF1A/GJA1/ MPO/PPARD/SPP1	14

BP	GO:0010631	epithelial cell migration	2.14E-06	PTGS2/JUN/PRKCA/PPARG/AKT1/HMOX1/CYP1B1/HAS2/VEGFA/MMP9/HIF1A/NOS3/HSPB1/IFNG/NFE2L2/PPARD	16
BP	GO:0051048	negative regulation of secretion	2.22E-06	OPRM1/HMOX1/HMGCR/SREBF1/ADIPOQ/ABAT/ADRA2A/MAOB/IL10/EGF/IL1B/PTGER3/ERBB3	13
BP	GO:0010883	regulation of lipid storage	2.36E-06	PPARG/APOB/PPARA/IL6/NFKBIA/PPARD/CRP	7
BP	GO:0090132	epithelium migration	2.37E-06	PTGS2/JUN/PRKCA/PPARG/AKT1/HMOX1/CYP1B1/HAS2/VEGFA/MMP9/HIF1A/NOS3/HSPB1/IFNG/NFE2L2/PPARD	16

BP	GO:0050863	regulation of T cell activation	2.37E-06	CASP3/AKT1/VCAM1/SOD1/IL10/IL6/ERBB2/CAV1/IL1B/CCL2/IL2/IFNG/IGF2/C D40LG/IRF1	15
BP	GO:0001844	protein insertion into mitochondrial membrane involved in apoptotic signaling pathway	2.43E-06	BCL2/BAX/CASP8/MAPK8/TP63/E2F1	6
BP	GO:0036296	response to increased oxygen levels	2.43E-06	PPARG/CYP1A1/CAT/CDKN1A/CAV1/C OL1A1	6
BP	GO:0046879	hormone secretion	2.45E-06	PRKCA/NOS2/HMGCR/SREBF1/ADIPOQ/ ABAT/ADRA2A/EGFR/IL6/RAF1/HIF1A/I L1B/IFNG/PPARD/SPP1	15

BP	GO:0006936	muscle contraction	2.53E-06	PTGS2/KCNH2/CHRM3/SCN5A/ADRA1A/ CHRM2/ADRA1B/ADRB2/GSTM2/SOD1/ ABAT/ADRA2A/CAV1/GJA1/PTGER3/CH UK	16
BP	GO:0001935	endothelial cell proliferation	2.90E-06	JUN/PRKCA/PPARG/AKT1/STAT1/HMO X1/VEGFA/IL10/HIF1A/CAV1/F3/CCL2	12
BP	GO:0001959	regulation of cytokine-mediated signaling pathway	2.90E-06	CASP8/PPARG/IKBKB/STAT1/GSTP1/ADI POQ/IL6/HIF1A/CAV1/IFNG/CHUK	11
BP	GO:0090130	tissue migration	2.92E-06	PTGS2/JUN/PRKCA/PPARG/AKT1/HMO X1/CYP1B1/HAS2/VEGFA/MMP9/HIF1A/ NOS3/HSPB1/IFNG/NFE2L2/PPARD	16

BP	GO:0051222	positive regulation of protein transport	2.97E-06	PTGS2/CHRM1/ACHE/MAPK3/MAPK1/BAT/EGFR/IL10/IL6/HIF1A/ERBB2/IL1B/IL2/IFNG/IL1A/PPARD/CHUK	17
BP	GO:0042759	long-chain fatty acid biosynthetic process	2.97E-06	PTGS2/CYP3A4/CYP1A2/CYP1A1/ALOX5/LTA4H	6
BP	GO:1902175	regulation of oxidative stress-induced intrinsic apoptotic signaling pathway	2.97E-06	AKT1/SOD1/HIF1A/HSPB1/NFE2L2/PARP1	6
BP	GO:0006953	acute-phase response	3.07E-06	PTGS2/UGT1A1/IL6/IL1B/PTGER3/IL1A/CRP	7

BP	GO:0051205	protein insertion into membrane	3.07E-06	BCL2/BAX/CASP8/MAPK8/EGFR/TP63/E 2F1	7
BP	GO:0150076	neuroinflammator y response	3.07E-06	JUN/LDLR/MMP3/EGFR/MMP9/IL6/IL1B	7
BP	GO:1903524	positive regulation of blood circulation	3.09E-06	PTGS2/ADRA1A/ADRA1B/AKT1/ICAM1/ ADRB1/EGFR/CAV1	8
BP	GO:0031098	stress-activated protein kinase signaling cascade	3.16E-06	IKBKB/AKT1/MAPK8/GSTP1/MAPK3/MA PK1/HMGCR/AKR1B1/EGFR/VEGFA/MY C/IL1B/NCF1/CHUK/CD40LG	15

BP	GO:0045931	positive regulation of mitotic cell cycle	3.21E-06	PRKCA/CYP1A1/INSR/CCND1/EGF/RB1/IL1B/CCNB1/IL1A/HSF1/IGF2	11
BP	GO:0009615	response to virus	3.41E-06	CHRM2/BCL2/RELA/IKBKB/STAT1/CYP1A1/APOB/BCL2L1/IL6/ODC1/HSPB1/IFNG/CXCL10/CHUK/IRF1	15
BP	GO:0009896	positive regulation of catabolic process	3.43E-06	ADRB2/BAX/AKT1/HMOX1/INSR/MAPK3/LDLR/PPARA/ADRA2A/EGF/HIF1A/CAV1/IL1B/IFNG/NFE2L2/HSF1/HK2	17
BP	GO:0009409	response to cold	3.50E-06	ADRB2/CASP8/PPARG/ADRB1/FOS/NFKBIA/CXCL10	7

BP	GO:0070849	response to epidermal growth factor	3.50E-06	AKT1/GSTP1/MAPK3/MAPK1/EGFR/ERB B2/COL1A1	7
BP	GO:0009914	hormone transport	3.51E-06	PRKCA/NOS2/HMGCR/SREBF1/ADIPOQ/ABAT/ADRA2A/EGFR/IL6/RAF1/HIF1A/IL1B/IFNG/PPARD/SPP1	15
BP	GO:0010743	regulation of macrophage derived foam cell differentiation	3.56E-06	PPARG/APOB/PPARA/ADIPOQ/NFKBIA/CRP	6
BP	GO:0061180	mammary gland epithelium development	3.76E-06	PGR/BAX/AR/AKT1/ESR1/MAPK1/CCND1/HIF1A	8

BP	GO:0007162	negative regulation of cell adhesion	3.96E-06	CASP3/ AKT1/ CYP1B1/ PPARA/ ADIPOQ/ A BAT/ IL10/ ERBB2/ IL2/ SERPINE1/ COL1A1/ IRF1/ ERBB3/ RASA1	14
BP	GO:0016042	lipid catabolic process	4.24E-06	AKT1/ CYP3A4/ CYP1A2/ CYP1B1/ AKR1C3/ LDLR/ APOB/ PPARA/ ADIPOQ/ CES1/ ADR A2A/ IL1B/ SULT1E1/ PPARD/ SPP1	15
BP	GO:0006109	regulation of carbohydrate metabolic process	4.27E-06	NCOA2/ AKT1/ HAS2/ INSR/ PPARA/ ADIP OQ/ EIF6/ EGF/ HIF1A/ IGFBP3/ IGF2	11
BP	GO:0051204	protein insertion into mitochondrial membrane	4.32E-06	BCL2/ BAX/ CASP8/ MAPK8/ TP63/ E2F1	6

BP	GO:0001655	urogenital system development	4.38E-06	RXRA/BCL2/BAX/CASP9/AR/STAT1/HAS2/ESR1/CAT/ADIPOQ/AKR1B1/VEGFA/TP63/ODC1/MYC	15
BP	GO:0010878	cholesterol storage	4.40E-06	PPARG/APOB/PPARA/SOAT1/PPARD	5
BP	GO:0097164	ammonium ion metabolic process	4.45E-06	PON1/ACHE/AKR1C3/LDLR/AKR1C1/ABAT/SLC6A3/AKR1B1/MAOB/MAOA/POR/ODC1	12
BP	GO:0045540	regulation of cholesterol biosynthetic process	4.51E-06	FASN/SOD1/APOB/HMGCR/SREBF1/POR/ACACA	7

BP	GO:0106118	regulation of sterol biosynthetic process	4.51E-06	FASN/SOD1/APOB/HMGCR/SREBF1/POR/ACACA	7
BP	GO:0046902	regulation of mitochondrial membrane permeability	4.55E-06	BCL2/BAX/CASP8/MAPK8/BCL2L1/TP63/E2F1/HK2	8
BP	GO:0070372	regulation of ERK1 and ERK2 cascade	4.66E-06	ADRA1A/OPRM1/JUN/PRKCA/ICAM1/GSTP1/INSR/MAPK3/HMGCR/ADIPOQ/EGFR/ERBB2/IL1B/CCL2/ERBB3	15
BP	GO:0048565	digestive tract development	4.87E-06	BCL2/CYP1A1/EGFR/CDKN1A/RB1/TP63/HIF1A/CXCL8/CCNB1/COL3A1	10

BP	GO:0034284	response to monosaccharide	4.87E-06	PTGS2/CASP3/ICAM1/GSTP1/CAT/HMGCR/SREBF1/ADIPOQ/ADRA2A/RAF1/HIF1A/PPARD	12
BP	GO:0060759	regulation of response to cytokine stimulus	4.98E-06	CASP8/PPARG/IKBKB/STAT1/GSTP1/ADIPOQ/IL6/HIF1A/CAV1/IFNG/CHUK	11
BP	GO:1904659	glucose transmembrane transport	5.00E-06	AKT1/SLC2A4/INSR/ADIPOQ/IL1B/PRKCB/NFE2L2/PPARD/HK2	9
BP	GO:0019369	arachidonic acid metabolic process	5.06E-06	PTGS2/PTGS1/CYP1A2/CYP1A1/CYP1B1/AKR1C3/MAPK3	7

BP	GO:0002064	epithelial cell development	5.06E-06	PGR/ AR/IKBKB/ICAM1/ESR1/FASN/SOD1/ ADIPOQ/CDKN1A/TP63/HIF1A/IL1B	12
BP	GO:0010574	regulation of vascular endothelial growth factor production	5.06E-06	PTGS2/CYP1B1/IL6/HIF1A/IL1B/IL1A	6
BP	GO:1901030	positive regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway	5.06E-06	BCL2/BAX/CASP8/MAPK8/TP63/E2F1	6
BP	GO:0070661	leukocyte proliferation	5.08E-06	BCL2/BAX/CASP3/VCAM1/GSTP1/AHR/IL10/IL6/ERBB2/IL1B/IL2/IGF2/CD40LG/IRF1	14

BP	GO:0010632	regulation of epithelial cell migration	5.27E-06	PTGS2/JUN/PRKCA/PPARG/AKT1/HMOX1/HAS2/VEGFA/MMP9/HIF1A/NOS3/SPB1/IFNG/NFE2L2	14
BP	GO:0051403	stress-activated MAPK cascade	5.27E-06	IKBKB/AKT1/MAPK8/GSTP1/MAPK3/MAK1/HMGCR/EGFR/VEGFA/MYC/IL1B/NCF1/CHUK/CD40LG	14
BP	GO:0033559	unsaturated fatty acid metabolic process	5.32E-06	PTGS2/PTGS1/CYP1A2/CYP1A1/CYP1B1/GSTP1/GSTM2/AKR1C3/MAPK3	9
BP	GO:0006695	cholesterol biosynthetic process	5.40E-06	FASN/SOD1/APOB/HMGCR/SREBF1/CES1/POR/ACACA	8

BP	GO:1903201	regulation of oxidative stress-induced cell death	5.40E-06	AKT1/SOD1/MMP3/IL10/HIF1A/HSPB1/NFE2L2/PARP1	8
BP	GO:0010959	regulation of metal ion transport	5.60E-06	PTGS2/KCNH2/SCN5A/ADRB2/BCL2/BAX/AKT1/ICAM1/GSTM2/ADRA2A/EGF/CAV1/CCL2/NOS3/CXCL11/CXCL10	16
BP	GO:0030072	peptide hormone secretion	5.63E-06	PRKCA/NOS2/HMGCR/SREBF1/ABAT/ADRA2A/EGFR/IL6/RAF1/HIF1A/IL1B/IFNG/PPARD	13
BP	GO:0060047	heart contraction	5.63E-06	KCNH2/SCN5A/ADRA1A/CHRM2/ADRA1B/GSTM2/SOD1/SREBF1/ADRB1/CAV1/GJA1/NOS3/IL2	13

BP	GO:0033138	positive regulation of peptidyl-serine phosphorylation	5.69E-06	PTGS2/BCL2/AKT1/EGFR/VEGFA/IL6/RAF1/CAV1/IFNG	9
BP	GO:0050670	regulation of lymphocyte proliferation	5.74E-06	BCL2/CASP3/VCAM1/AHR/IL10/IL6/ERBB2/IL1B/IL2/IGF2/CD40LG/IRF1	12
BP	GO:1902653	secondary alcohol biosynthetic process	5.89E-06	FASN/SOD1/APOB/HMGCR/SREBF1/CES1/POR/ACACA	8
BP	GO:0032944	regulation of mononuclear cell proliferation	6.02E-06	BCL2/CASP3/VCAM1/AHR/IL10/IL6/ERBB2/IL1B/IL2/IGF2/CD40LG/IRF1	12

BP	GO:0007586	digestion	6.08E-06	CHRM3/CHRM1/PRSS1/LDLR/SOAT2/AKR1C1/ADRA2A/CTRB1/PTGER3/MGAM	10
BP	GO:0033135	regulation of peptidyl-serine phosphorylation	6.08E-06	PTGS2/BCL2/BAX/AKT1/EGFR/VEGFA/IL6/RAF1/CAV1/IFNG	10
BP	GO:0048771	tissue remodeling	6.35E-06	ADRB2/BAX/PRKCA/EGFR/IL6/HIF1A/CAV1/NOS3/IL2/IL1A/SPP1	11
BP	GO:0045637	regulation of myeloid cell differentiation	6.61E-06	JUN/CASP8/PRKCA/STAT1/ADIPOQ/FOS/EIF6/RB1/NFKBIA/HIF1A/MYC/PRKCB/IFNG	13

BP	GO:0048872	homeostasis of number of cells	6.61E-06	BCL2/BAX/CASP3/AKT1/STAT1/HMOX1/ SOD1/VEGFA/RB1/IL6/HIF1A/NOS3/IL2	13
BP	GO:0010573	vascular endothelial growth factor production	7.03E-06	PTGS2/CYP1B1/IL6/HIF1A/IL1B/IL1A	6
BP	GO:0043279	response to alkaloid	7.09E-06	OPRM1/CASP3/PPARG/RELA/ICAM1/GS TM2/ABAT/SLC6A3/BCL2L1	9
BP	GO:0045834	positive regulation of lipid metabolic process	7.33E-06	PTGS2/PPARG/AKT1/LDLR/PPARA/SREB F1/ADIPOQ/POR/IL1B/IFNG	10

BP	GO:0035994	response to muscle stretch	7.41E-06	JUN/RELA/FOS/NFKBIA/RAF1	5
BP	GO:0022409	positive regulation of cell-cell adhesion	7.47E-06	AKT1/ICAM1/VCAM1/HAS2/IL10/IL6/CAV1/IL1B/CCL2/IL2/IFNG/IGF2/CD40LG	13
BP	GO:0007189	adenylate cyclase-activating G protein-coupled receptor signaling pathway	7.78E-06	ADRA1A/ADRA1B/ADRB2/OPRM1/PRKCA/ADRA2A/ADRB1/PTGER3/CXCL11/CXCL10	10
BP	GO:0003015	heart process	7.78E-06	KCNH2/SCN5A/ADRA1A/CHRM2/ADRA1B/GSTM2/SOD1/SREBF1/ADRB1/CAV1/GJA1/NOS3/IL2	13

BP	GO:0048146	positive regulation of fibroblast proliferation	7.99E-06	JUN/ESR1/EGFR/CDKN1A/MYC/CCNB1/E2F1	7
BP	GO:0090303	positive regulation of wound healing	7.99E-06	F7/ADRA2A/F3/THBD/SERPINE1/NFE2L2/PPARD	7
BP	GO:0043491	protein kinase B signaling	8.07E-06	F7/AKT1/INSR/AKR1C3/ESR1/EGFR/EGF/ERBB2/F3/IL1B/CCL2/IGF2/ERBB3	13
BP	GO:0008645	hexose transmembrane transport	8.12E-06	AKT1/SLC2A4/INSR/ADIPOQ/IL1B/PRKC B/NFE2L2/PPARD/HK2	9

BP	GO:1903039	positive regulation of leukocyte cell-cell adhesion	8.64E-06	AKT1/ICAM1/VCAM1/HAS2/IL6/CAV1/IL1B/CCL2/IL2/IFNG/IGF2/CD40LG	12
BP	GO:0001541	ovarian follicle development	8.97E-06	BCL2/BAX/ICAM1/ESR1/SOD1/VEGFA/BCL2L1	7
BP	GO:1905475	regulation of protein localization to membrane	9.10E-06	BCL2/CASP8/AR/AKT1/MAPK8/EGFR/BCL2L1/TP63/ERBB2/IFNG/E2F1	11
BP	GO:0016126	sterol biosynthetic process	9.13E-06	FASN/SOD1/APOB/HMGCR/SREBF1/CES1/POR/ACACA	8

BP	GO:0090559	regulation of membrane permeability	9.13E-06	BCL2/BAX/CASP8/MAPK8/BCL2L1/TP63/E2F1/HK2	8
BP	GO:0015749	monosaccharide transmembrane transport	9.34E-06	AKT1/SLC2A4/INSR/ADIPOQ/IL1B/PRKCB/NFE2L2/PPARD/HK2	9
BP	GO:0042098	T cell proliferation	9.53E-06	BAX/CASP3/VCAM1/IL10/IL6/ERBB2/IL1B/IL2/IGF2/CD40LG/IRF1	11
BP	GO:0038127	ERBB signaling pathway	9.78E-06	PRKCA/AKT1/MAPK1/ADRA2A/EGFR/MMP9/EGF/ERBB2/NCF1/ERBB3	10

BP	GO:0008016	regulation of heart contraction	9.79E-06	KCNH2/SCN5A/ADRA1A/CHRM2/ADRA1B/GSTM2/SREBF1/ADRB1/CAV1/GJA1/NOS3/IL2	12
BP	GO:0030595	leukocyte chemotaxis	9.79E-06	F7/MAPK3/VEGFA/IL10/IL6/IL1B/CCL2/CXCL8/SERPINE1/CXCL11/CXCL2/CXCL10	12
BP	GO:0097755	positive regulation of blood vessel diameter	9.92E-06	ADRB2/HMOX1/SOD1/ADRB1/EGFR/NOS3/PPARD	7
BP	GO:0030198	extracellular matrix organization	1.01E-05	PRSS1/MMP1/ICAM1/VCAM1/CYP1B1/HAS2/CTRB1/MMP3/MMP2/MMP9/RB1/SERPINE1/COL1A1/COL3A1/SPP1	15

BP	GO:0055088	lipid homeostasis	1.03E-05	PPARG/LDLR/MTTP/APOB/SOAT2/AKR1C1/GOT1/SOAT1/ACACA/CAV1	10
BP	GO:0002685	regulation of leukocyte migration	1.04E-05	F7/AKT1/HMOX1/ICAM1/MAPK3/VEGFA/IL6/CCL2/CXCL8/SERPINE1/CXCL10	11
BP	GO:0045785	positive regulation of cell adhesion	1.04E-05	PRKCA/AKT1/ICAM1/VCAM1/HAS2/VEGFA/IL10/IL6/ERBB2/CAV1/IL1B/CCL2/IL2/IFNG/IGF2/CD40LG	16
BP	GO:0010822	positive regulation of mitochondrion organization	1.06E-05	BCL2/BAX/CASP8/MAPK8/MMP9/TP63/HIF1A/E2F1/HK2	9

BP	GO:0034219	carbohydrate transmembrane transport	1.06E-05	AKT1/SLC2A4/INSR/ADIPOQ/IL1B/PRKCB/NFE2L2/PPARD/HK2	9
BP	GO:0042326	negative regulation of phosphorylation	1.08E-05	BAX/JUN/CASP3/AKT1/GSTP1/HMGCR/PPARA/ADIPOQ/CDKN1A/RB1/CAV1/MYC/IL1B/HSPB1/IL2/CCNB1/IGFBP3	17
BP	GO:0046883	regulation of hormone secretion	1.09E-05	PRKCA/NOS2/HMGCR/SREBF1/ADIPOQ/ABAT/ADRA2A/EGFR/HIF1A/IL1B/IFNG/PPARD/SPP1	13
BP	GO:1902041	regulation of extrinsic apoptotic signaling pathway via death domain receptors	1.10E-05	CASP8/HMOX1/ICAM1/BCL2L1/RAF1/NOS3/SERPINE1	7

BP	GO:0014912	negative regulation of smooth muscle cell migration	1.10E-05	GSTP1/ADIPOQ/SERPINE1/NFE2L2/PPAR D/IGFBP3	6
BP	GO:0032094	response to food	1.10E-05	OPRM1/AKT1/CYP1A1/PPARA/SREBF1/MPO	6
BP	GO:1903035	negative regulation of response to wounding	1.16E-05	HMGCR/ABAT/PLAU/NOS3/PLAT/THBD /SERPINE1/SPP1	8
BP	GO:0042135	neurotransmitter catabolic process	1.18E-05	ACHE/ABAT/MAOB/MAOA/POR	5

BP	GO:1901522	positive regulation of transcription from RNA polymerase II promoter involved in cellular response to chemical stimulus	1.18E-05	RELA/VEGFA/HIF1A/NFE2L2/RUNX2	5
BP	GO:0042594	response to starvation	1.20E-05	BCL2/JUN/PPARG/MAPK8/AKR1C3/MAPK3/MAPK1/UGT1A1/SREBF1/CDKN1A/NFE2L2	11
BP	GO:2000134	negative regulation of G1/S transition of mitotic cell cycle	1.20E-05	BCL2/BAX/CCND1/CDKN1A/RB1/CCL2/CCNB1/CHEK2/E2F1	9
BP	GO:0007259	JAK-STAT cascade	1.20E-05	STAT1/CYP1B1/AKR1B1/EGF/IL6/CAV1/CCL2/IL2/IFNG/HSF1	10

BP	GO:0043524	negative regulation of neuron apoptotic process	1.20E-05	BCL2/BAX/JUN/HMOX1/SOD1/BCL2L1/HIF1A/CCL2/ERBB3/RASA1	10
BP	GO:0033013	tetrapyrrole metabolic process	1.20E-05	PRSS1/HMOX1/CYP1A2/CYP1A1/UGT1A1/ABCC1/CTRB1	7
BP	GO:0046651	lymphocyte proliferation	1.20E-05	BCL2/BAX/CASP3/VCAM1/AHR/IL10/IL6/ERBB2/IL1B/IL2/IGF2/CD40LG/IRF1	13
BP	GO:1904035	regulation of epithelial cell apoptotic process	1.24E-05	HMOX1/ICAM1/AKR1C3/IL6/CCL2/SERPINE1/NFE2L2/CD40LG	8

BP	GO:0043112	receptor metabolic process	1.24E-05	PPARG/ACHE/SELE/PPARA/ADIPOQ/VEGFA/IL10/EGF/HIF1A/CAV1/CXCL8	11
BP	GO:0032570	response to progesterone	1.26E-05	NCOA2/RELA/SREBF1/FOS/CAV1/CLDN4	6
BP	GO:0032943	mononuclear cell proliferation	1.30E-05	BCL2/BAX/CASP3/VCAM1/AHR/IL10/IL6/ERBB2/IL1B/IL2/IGF2/CD40LG/IRF1	13
BP	GO:0019933	cAMP-mediated signaling	1.37E-05	ADRA1A/ADRA1B/ADRB2/OPRM1/PRKCA/AHR/ADRA2A/ADRB1/PTGER3/CXCL11/CXCL10	11

BP	GO:0001660	fever generation	1.40E-05	PTGS2/IL1B/PTGER3/IL1A	4
BP	GO:0046886	positive regulation of hormone biosynthetic process	1.40E-05	POR/HIF1A/IL1B/IFNG	4
BP	GO:0001933	negative regulation of protein phosphorylation	1.41E-05	BAX/JUN/CASP3/AKT1/GSTP1/HMGCR/ADIPOQ/CDKN1A/RB1/CAV1/MYC/IL1B/HSPB1/IL2/CCNB1/IGFBP3	16
BP	GO:1900407	regulation of cellular response to oxidative stress	1.46E-05	AKT1/SOD1/MMP3/IL10/HIF1A/HSPB1/NFE2L2/PARP1	8

BP	GO:0071379	cellular response to prostaglandin stimulus	1.46E-05	PPARG/AKT1/AKR1C3/APOB/ACACA	5
BP	GO:0097696	STAT cascade	1.48E-05	STAT1/CYP1B1/AKR1B1/EGF/IL6/CAV1/CCL2/IL2/IFNG/HSF1	10
BP	GO:0019217	regulation of fatty acid metabolic process	1.57E-05	PTGS2/PPARG/AKT1/PPARA/SREBF1/ADIPOQ/EIF6/CAV1	8
BP	GO:0010952	positive regulation of peptidase activity	1.57E-05	BAX/CASP9/CASP3/CASP8/PPARG/MAPK3/CAV1/MYC/F3/HSF1/PCOLCE	11

BP	GO:0033209	tumor necrosis factor-mediated signaling pathway	1.65E-05	CASP8/RELA/IKBKB/STAT1/GSTP1/ADIP OQ/NFKBIA/CHUK/CD40LG	9
BP	GO:1905477	positive regulation of protein localization to membrane	1.65E-05	BCL2/CASP8/AKT1/MAPK8/EGFR/TP63/ ERBB2/IFNG/E2F1	9
BP	GO:0042129	regulation of T cell proliferation	1.65E-05	CASP3/VCAM1/IL10/IL6/ERBB2/IL1B/IL2 /IGF2/CD40LG/IRF1	10
BP	GO:1903829	positive regulation of cellular protein localization	1.69E-05	PTGS2/CHRM1/BCL2/CASP8/AKT1/MAP K8/MAPK1/EGFR/TP63/ERBB2/IL1B/IFN G/PARP1/E2F1	14

BP	GO:0022612	gland morphogenesis	1.76E-05	RXRA/PGR/BCL2/BAX/AR/ESR1/EGFR/T P63/CAV1	9
BP	GO:0009308	amine metabolic process	1.84E-05	CYP1A1/VCAM1/ABAT/SLC6A3/MAOB/ MAOA/ODC1/NQO1	8
BP	GO:1902807	negative regulation of cell cycle G1/S phase transition	1.87E-05	BCL2/BAX/CCND1/CDKN1A/RB1/CCL2/ CCNB1/CHEK2/E2F1	9
BP	GO:0042593	glucose homeostasis	1.87E-05	ADRA1B/PPARG/AKT1/ICAM1/SLC2A4/I NSR/HMGCR/ADIPOQ/ADRA2A/RAF1/H IF1A/HK2	12

BP	GO:1901028	regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway	1.91E-05	BCL2/BAX/CASP8/MAPK8/TP63/E2F1	6
BP	GO:1904706	negative regulation of vascular smooth muscle cell proliferation	1.91E-05	PPARG/HMOX1/GSTP1/ADIPOQ/CDKN1A/IL10	6
BP	GO:0033500	carbohydrate homeostasis	1.94E-05	ADRA1B/PPARG/AKT1/ICAM1/SLC2A4/INSR/HMGCR/ADIPOQ/ADRA2A/RAF1/HIF1A/HK2	12
BP	GO:0045639	positive regulation of myeloid cell differentiation	1.97E-05	JUN/CASP8/PRKCA/STAT1/FOS/RB1/HIF1A/IFNG	8

BP	GO:0010001	glial cell differentiation	1.97E-05	PPARG/RELA/ AKT1/GSTP1/MAPK3/MAP K1/LDLR/SOD1/EGFR/ERBB2/ERBB3	11
BP	GO:0010595	positive regulation of endothelial cell migration	1.97E-05	PTGS2/PRKCA/ AKT1/HMOX1/VEGFA/HIF1A/NOS3/HSPB1/NFE2L2	9
BP	GO:0032368	regulation of lipid transport	1.97E-05	PON1/PPARG/ AKT1/PPARA/ADIPOQ/EGF/NFKBIA/IL1B/SPP1	9
BP	GO:0072577	endothelial cell apoptotic process	1.97E-05	ICAM1/AKR1C3/IL10/CCL2/SERPINE1/NFE2L2/CD40LG	7

BP	GO:1903036	positive regulation of response to wounding	1.97E-05	F7/ADRA2A/F3/THBD/SERPINE1/NFE2L2/PPARD	7
BP	GO:0051249	regulation of lymphocyte activation	1.98E-05	BCL2/CASP3/AKT1/VCAM1/AHR/SOD1/IL10/IL6/ERBB2/CAV1/IL1B/CCL2/IL2/IFNG/IGF2/CD40LG/IRF1	17
BP	GO:0035265	organ growth	2.04E-05	RXRA/ADRA1A/SLC6A4/BCL2/AR/AKT1/ESR1/SOD1/PPARA/POR/CCNB1	11
BP	GO:0031652	positive regulation of heat generation	2.04E-05	PTGS2/ABAT/IL1B/PTGER3	4

BP	GO:0033197	response to vitamin E	2.04E-05	PPARG/CAT/CCND1/COL1A1	4
BP	GO:0034379	very-low-density lipoprotein particle assembly	2.04E-05	MTTP/APOB/SOAT2/SOAT1	4
BP	GO:0042178	xenobiotic catabolic process	2.04E-05	CYP1A1/GSTM1/GSTM2/UGT1A1	4
BP	GO:0051188	cofactor biosynthetic process	2.05E-05	PTGS2/CYP1A2/CYP1A1/INSR/FASN/SOD 1/PPARA/MAOB/EIF6/HIF1A/ACACA/N FE2L2/HK2	13

BP	GO:0016101	diterpenoid metabolic process	2.09E-05	CYP1A1/CYP1B1/AKR1C3/APOB/UGT1A1 /AKR1C1/EGFR/PPARD	8
BP	GO:0043535	regulation of blood vessel endothelial cell migration	2.10E-05	PTGS2/PRKCA/PPARG/AKT1/HMOX1/VE GFA/HIF1A/NOS3/HSPB1/NFE2L2	10
BP	GO:0045429	positive regulation of nitric oxide biosynthetic process	2.13E-05	PTGS2/AKT1/ICAM1/INSR/IL1B/IFNG	6
BP	GO:1904407	positive regulation of nitric oxide metabolic process	2.13E-05	PTGS2/AKT1/ICAM1/INSR/IL1B/IFNG	6

BP	GO:1900739	regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway	2.16E-05	BCL2/CASP8/MAPK8/TP63/E2F1	5
BP	GO:1900740	positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway	2.16E-05	BCL2/CASP8/MAPK8/TP63/E2F1	5
BP	GO:0045930	negative regulation of mitotic cell cycle	2.18E-05	BCL2/BAX/EGFR/CCND1/BCL2L1/CDKN1A/IL10/RB1/CCL2/CCNB1/TOP2A/CHEK2/E2F1	13
BP	GO:0042176	regulation of protein catabolic process	2.20E-05	NOS2/RELA/AKT1/PSMD3/LDLR/ADRA2A/EGFR/IL10/EGF/ODC1/CAV1/IL1B/IFNG/NFE2L2/CHEK2	15

BP	GO:0007589	body fluid secretion	2.23E-05	CHRM3/CHRM1/SLC6A3/VEGFA/CCND1/HIF1A/CAV1/HK2	8
BP	GO:0051924	regulation of calcium ion transport	2.30E-05	PTGS2/BCL2/BAX/ICAM1/GSTM2/ADRA2A/EGF/CAV1/CCL2/NOS3/CXCL11/CXCL10	12
BP	GO:0042035	regulation of cytokine biosynthetic process	2.40E-05	RELA/HMOX1/IL10/IL6/IL1B/HSPB1/IL1A/IRF1	8
BP	GO:1900542	regulation of purine nucleotide metabolic process	2.40E-05	NOS2/INSR/PPARA/EIF6/HIF1A/NOS3/CNB1/PARP1	8

BP	GO:1903426	regulation of reactive oxygen species biosynthetic process	2.40E-05	PTGS2/AKT1/ICAM1/INSR/IL10/CAV1/IL1B/IFNG	8
BP	GO:0046688	response to copper ion	2.40E-05	CYP1A2/CYP1A1/ICAM1/SOD1/IL1A/HSF1	6
BP	GO:0007050	cell cycle arrest	2.49E-05	BAX/CCND1/CDKN1A/RB1/MYC/CXCL8/CCNB1/IFNG/CHEK2/RASSF1/E2F1/IRF1	12
BP	GO:0090068	positive regulation of cell cycle process	2.60E-05	BAX/CYP1A1/INSR/CCND1/CDKN1A/EGF/RB1/IL1B/CCNB1/IL1A/CHEK2/E2F1/IGF2	13

BP	GO:0019430	removal of superoxide radicals	2.60E-05	SOD1/NOS3/MPO/NFE2L2/NQO1	5
BP	GO:0030194	positive regulation of blood coagulation	2.60E-05	F7/F3/THBD/SERPINE1/NFE2L2	5
BP	GO:0046885	regulation of hormone biosynthetic process	2.60E-05	AKR1C3/POR/HIF1A/IL1B/IFNG	5
BP	GO:0150077	regulation of neuroinflammatory response	2.60E-05	LDLR/MMP3/MMP9/IL6/IL1B	5

BP	GO:1900048	positive regulation of hemostasis	2.60E-05	F7/F3/THBD/SERPINE1/NFE2L2	5
BP	GO:0120162	positive regulation of cold-induced thermogenesis	2.75E-05	ADRB2/ACHE/ADIPOQ/ADRB1/VEGFA/CAV1/GJA1/HSF1	8
BP	GO:1902882	regulation of response to oxidative stress	2.75E-05	AKT1/SOD1/MMP3/IL10/HIF1A/HSPB1/NFE2L2/PARP1	8
BP	GO:2001243	negative regulation of intrinsic apoptotic signaling pathway	2.75E-05	PTGS2/BCL2/AKT1/BCL2L1/MMP9/HIF1A/HSPB1/NFE2L2	8

BP	GO:0031670	cellular response to nutrient	2.77E-05	PTGS2/PPARG/HMOX1/SOD1/NCOA1/COL1A1/HSF1	7
BP	GO:0042698	ovulation cycle	2.77E-05	PGR/OPRM1/CASP3/HAS2/ESR1/EGFR/NOS3	7
BP	GO:0051881	regulation of mitochondrial membrane potential	2.77E-05	BCL2/BAX/AKT1/SOD1/GOT1/BCL2L1/PARP1	7
BP	GO:0030073	insulin secretion	2.82E-05	PRKCA/NOS2/HMGCR/SREBF1/ABAT/ADRA2A/RAF1/HIF1A/IL1B/IFNG/PPARD	11

BP	GO:0090276	regulation of peptide hormone secretion	2.82E-05	PRKCA/NOS2/HMGCR/SREBF1/ABAT/ADRA2A/EGFR/HIF1A/IL1B/IFNG/PPARD	11
BP	GO:0070374	positive regulation of ERK1 and ERK2 cascade	2.86E-05	ADRA1A/OPRM1/JUN/PRKCA/ICAM1/INSR/MAPK3/HMGCR/EGFR/ERBB2/CCL2/ERBB3	12
BP	GO:0007200	phospholipase C-activating G protein-coupled receptor signaling pathway	2.93E-05	CHRM1/ADRA1A/CHRM2/ADRA1B/OPRM1/ESR1/ADRA2A/PTGER3	8
BP	GO:0040014	regulation of multicellular organism growth	3.03E-05	ADRB2/BCL2/SOD1/SLC6A3/ADRB1/HSF1/IGF2	7

BP	GO:0034383	low-density lipoprotein particle clearance	3.04E-05	HMOX1/LDLR/APOB/ADIPOQ/SOAT2/SOAT1	6
BP	GO:0050921	positive regulation of chemotaxis	3.05E-05	F7/MAPK3/VEGFA/IL6/F3/CXCL8/HSPB1/SERPINE1/CXCL10	9
BP	GO:2000045	regulation of G1/S transition of mitotic cell cycle	3.06E-05	BCL2/BAX/CYP1A1/CCND1/CDKN1A/RB1/CCL2/CCNB1/CHEK2/E2F1	10
BP	GO:0050820	positive regulation of coagulation	3.10E-05	F7/F3/THBD/SERPINE1/NFE2L2	5

BP	GO:0006140	regulation of nucleotide metabolic process	3.13E-05	NOS2/INSR/PPARA/EIF6/HIF1A/NOS3/CNB1/PARP1	8
BP	GO:0051341	regulation of oxidoreductase activity	3.37E-05	AKT1/EGFR/POR/HIF1A/CAV1/IL1B/NO S3/IFNG	8
BP	GO:0051897	positive regulation of protein kinase B signaling	3.38E-05	F7/INSR/AKR1C3/ESR1/EGFR/EGF/ERBB 2/F3/IGF2/ERBB3	10
BP	GO:0050729	positive regulation of inflammatory response	3.64E-05	PTGS2/LDLR/EGFR/IL6/NFKBIA/IL1B/PT GER3/IL2/SERPINE1	9

BP	GO:0010575	positive regulation of vascular endothelial growth factor production	3.70E-05	PTGS2/CYP1B1/HIF1A/IL1B/IL1A	5
BP	GO:0035902	response to immobilization stress	3.70E-05	PPARG/CYP1A2/CYP1A1/GOT1/FOS	5
BP	GO:0071450	cellular response to oxygen radical	3.70E-05	SOD1/NOS3/MPO/NFE2L2/NQO1	5
BP	GO:0071451	cellular response to superoxide	3.70E-05	SOD1/NOS3/MPO/NFE2L2/NQO1	5

BP	GO:1902895	positive regulation of pri-miRNA transcription by RNA polymerase II	3.70E-05	JUN/RELA/FOS/IL10/HIF1A	5
BP	GO:1990776	response to angiotensin	3.70E-05	PTGS2/RELA/CAV1/NFE2L2/HSF1	5
BP	GO:2001235	positive regulation of apoptotic signaling pathway	3.70E-05	BCL2/BAX/CASP8/MAPK8/SOD1/BCL2L1/MMP9/TP63/CAV1/E2F1	10
BP	GO:0050920	regulation of chemotaxis	3.76E-05	F7/GSTP1/MAPK3/VEGFA/IL6/F3/CCL2/CXCL8/HSPB1/SERPINE1/CXCL10	11

BP	GO:0071901	negative regulation of protein serine/threonine kinase activity	3.80E-05	CASP3/AKT1/GSTP1/HMGCR/ADIPOQ/C DKN1A/CAV1/IL1B/HSPB1	9
BP	GO:0007595	lactation	3.81E-05	SLC6A3/VEGFA/CCND1/HIF1A/CAV1/H K2	6
BP	GO:0061045	negative regulation of wound healing	3.89E-05	HMGCR/ABAT/PLAU/NOS3/PLAT/THBD /SERPINE1	7
BP	GO:0031650	regulation of heat generation	3.92E-05	PTGS2/ABAT/IL1B/PTGER3	4

BP	GO:0008584	male gonad development	4.00E-05	BCL2/BAX/ AR/ICAM1/INSR/ AKR1C3/ESR1/CCND1/BCL2L1	9
BP	GO:0072655	establishment of protein localization to mitochondrion	4.00E-05	BCL2/BAX/CASP8/AKT1/MAPK8/SREBF1/TP63/E2F1/HK2	9
BP	GO:0050796	regulation of insulin secretion	4.04E-05	PRKCA/NOS2/HMGCR/SREBF1/ABAT/ADRA2A/HIF1A/IL1B/IFNG/PPARD	10
BP	GO:0008630	intrinsic apoptotic signaling pathway in response to DNA damage	4.07E-05	BCL2/BAX/CASP9/HMOX1/BCL2L1/TP63/CHEK2/E2F1	8

BP	GO:0043627	response to estrogen	4.20E-05	PPARG/F7/HMOX1/ESR1/MAPK1/CCND1/CAV1	7
BP	GO:1900371	regulation of purine nucleotide biosynthetic process	4.20E-05	NOS2/INSR/PPARA/EIF6/HIF1A/NOS3/PARP1	7
BP	GO:0014065	phosphatidylinositol 3-kinase signaling	4.20E-05	AKT1/MAPK3/MAPK1/CAT/EGFR/ERBB2/NCF1/PPARD/ERBB3	9
BP	GO:0046546	development of primary male sexual characteristics	4.20E-05	BCL2/BAX/AR/ICAM1/INSR/AKR1C3/ESR1/CCND1/BCL2L1	9

BP	GO:0050999	regulation of nitric-oxide synthase activity	4.24E-05	AKT1/EGFR/HIF1A/CAV1/IL1B/NOS3	6
BP	GO:0001649	osteoblast differentiation	4.37E-05	ACHE/AKT1/FASN/CAT/IL6/TP63/COL1 A1/SPP1/RUNX2/IGFBP3/IGF2	11
BP	GO:0019935	cyclic-nucleotide- mediated signaling	4.37E-05	ADRA1A/ADRA1B/ADRB2/OPRM1/PRKC A/AHR/ADRA2A/ADRB1/PTGER3/CXCL1 1/CXCL10	11
BP	GO:0010506	regulation of autophagy	4.44E-05	ADRA1A/ADRB2/BCL2/CASP3/AKT1/MA PK8/HMOX1/MAPK3/SREBF1/HIF1A/HSP B1/IFNG/HK2	13

BP	GO:0043406	positive regulation of MAP kinase activity	4.53E-05	INSR/MAPK3/MAPK1/SOD1/ADRA2A/EGFR/VEGFA/EGF/RAF1/ERBB2/IL1B/CD40LG	12
BP	GO:0010827	regulation of glucose transmembrane transport	4.54E-05	AKT1/INSR/ADIPOQ/IL1B/PRKCB/NFE2L2/HK2	7
BP	GO:0030808	regulation of nucleotide biosynthetic process	4.54E-05	NOS2/INSR/PPARA/EIF6/HIF1A/NOS3/PARP1	7
BP	GO:0034605	cellular response to heat	4.60E-05	PTGS2/HMOX1/MAPK3/MAPK1/CDKN1A/IL1A/HSF1/CXCL10	8

BP	GO:0001667	ameboidal-type cell migration	4.78E-05	PTGS2/JUN/PRKCA/PPARG/AKT1/HMOX1/CYP1B1/HAS2/VEGFA/MMP9/HIF1A/NOS3/HSPB1/IFNG/NFE2L2/PPARD	16
BP	GO:0051047	positive regulation of secretion	4.81E-05	SLC6A4/ACHE/MAPK3/ABAT/EGFR/IL10/IL6/HIF1A/IL1B/IL2/IFNG/IL1A/PPARD/CHUK/SPP1	15
BP	GO:0042089	cytokine biosynthetic process	4.88E-05	RELA/HMOX1/IL10/IL6/IL1B/HSPB1/IL1A/IRF1	8
BP	GO:0043467	regulation of generation of precursor metabolites and energy	4.88E-05	NOS2/AKT1/INSR/PPARA/EIF6/HIF1A/CNB1/IGF2	8

BP	GO:0097006	regulation of plasma lipoprotein particle levels	4.88E-05	HMOX1/LDLR/MTTP/APOB/ADIPOQ/SOAT2/SOAT1/MPO	8
BP	GO:0050728	negative regulation of inflammatory response	4.88E-05	PPARG/GSTP1/LDLR/PPARA/ADIPOQ/IL10/RB1/IL2/PPARD	9
BP	GO:0070585	protein localization to mitochondrion	4.88E-05	BCL2/BAX/CASP8/AKT1/MAPK8/SREBF1/TP63/E2F1/HK2	9
BP	GO:0032642	regulation of chemokine production	4.88E-05	HMOX1/GSTP1/ADIPOQ/IL10/IL6/HIF1A/IL1B	7

BP	GO:0032770	positive regulation of monooxygenase activity	5.05E-05	AKT1/POR/HIF1A/IL1B/IFNG	5
BP	GO:0032352	positive regulation of hormone metabolic process	5.19E-05	POR/HIF1A/IL1B/IFNG	4
BP	GO:0042107	cytokine metabolic process	5.19E-05	RELA/HMOX1/IL10/IL6/IL1B/HSPB1/IL1A/IRF1	8
BP	GO:0008643	carbohydrate transport	5.43E-05	AKT1/SLC2A4/INSR/ADIPOQ/IL1B/PRKCB/NFE2L2/PPARD/HK2	9

BP	GO:0071236	cellular response to antibiotic	5.43E-05	RELA/CYP1B1/AHR/UGT1A1/IL10/IL6/NFE2L2/NQO1/HSF1	9
BP	GO:0071887	leukocyte apoptotic process	5.54E-05	BAX/CASP9/CASP3/AKT1/IL10/IL6/HIF1A/IL2	8
BP	GO:0106106	cold-induced thermogenesis	5.72E-05	ADRB2/ACHE/ADIPOQ/ADRB1/VEGFA/RB1/CAV1/GJA1/HSF1	9
BP	GO:0120161	regulation of cold-induced thermogenesis	5.72E-05	ADRB2/ACHE/ADIPOQ/ADRB1/VEGFA/RB1/CAV1/GJA1/HSF1	9

BP	GO:1902105	regulation of leukocyte differentiation	5.73E-05	JUN/CASP8/PRKCA/SOD1/ADIPOQ/FOS/RB1/ERBB2/MYC/IL2/IFNG/IRF1	12
BP	GO:0045840	positive regulation of mitotic nuclear division	5.79E-05	INSR/EGF/RB1/IL1B/IL1A/IGF2	6
BP	GO:0097345	mitochondrial outer membrane permeabilization	5.79E-05	BCL2/BAX/CASP8/MAPK8/TP63/E2F1	6
BP	GO:0000303	response to superoxide	5.90E-05	SOD1/NOS3/MPO/NFE2L2/NQO1	5

BP	GO:0043123	positive regulation of I-kappaB kinase/NF-kappaB signaling	5.96E-05	CASP8/RELA/IKBKB/AKT1/HMOX1/ADIP OQ/GJA1/IL1B/PRKCB/CHUK	10
BP	GO:0006816	calcium ion transport	6.03E-05	PTGS2/ADRA1A/OPRM1/BCL2/BAX/ICA M1/GSTM2/ADRA2A/EGF/CAV1/CCL2/P RKCB/NOS3/CXCL11/CXCL10	15
BP	GO:0045927	positive regulation of growth	6.12E-05	BCL2/AKT1/INSR/SLC6A3/EGFR/VEGFA/ ERBB2/IL2/CCNB1/PPARD/HSF1/IGF2	12
BP	GO:0046889	positive regulation of lipid biosynthetic process	6.16E-05	PTGS2/AKT1/LDLR/SREBF1/POR/IL1B/IF NG	7

BP	GO:0043534	blood vessel endothelial cell migration	6.20E-05	PTGS2/PRKCA/PPARG/ AKT1/HMOX1/VE GFA/HIF1A/NOS3/HSPB1/NFE2L2	10
BP	GO:0061138	morphogenesis of a branching epithelium	6.20E-05	RXRA/PGR/BCL2/ AR/ESR1/VEGFA/IL10/ EGF/TP63/MYC	10
BP	GO:0002688	regulation of leukocyte chemotaxis	6.20E-05	F7/MAPK3/VEGFA/IL6/CCL2/CXCL8/SER PINE1/CXCL10	8
BP	GO:0002763	positive regulation of myeloid leukocyte differentiation	6.37E-05	JUN/CASP8/PRKCA/FOS/RB1/IFNG	6

BP	GO:0030195	negative regulation of blood coagulation	6.37E-05	ABAT/PLAU/NOS3/PLAT/THBD/SERPINE1	6
BP	GO:1900047	negative regulation of hemostasis	6.37E-05	ABAT/PLAU/NOS3/PLAT/THBD/SERPINE1	6
BP	GO:0001558	regulation of cell growth	6.47E-05	BCL2/MAP2/PPARG/AKT1/PPARA/EGFR/VEGFA/CDKN1A/RB1/ERBB2/GJA1/IL2/PPARD/SPP1/IGFBP3	15
BP	GO:0010885	regulation of cholesterol storage	6.73E-05	PPARG/APOB/PPARA/PPARD	4

BP	GO:0050665	hydrogen peroxide biosynthetic process	6.73E-05	CYP1A2/CYP1A1/SOD1/MAOB	4
BP	GO:0050866	negative regulation of cell activation	6.73E-05	CASP3/HMOX1/LDLR/ABAT/IL10/ERBB2/NOS3/IL2/THBD/IRF1	10
BP	GO:0000305	response to oxygen radical	6.73E-05	SOD1/NOS3/MPO/NFE2L2/NQO1	5
BP	GO:0001893	maternal placenta development	6.73E-05	PTGS2/RXRA/AKT1/PPARD/SPP1	5

BP	GO:0034694	response to prostaglandin	6.73E-05	PPARG/AKT1/AKR1C3/APOB/ACACA	5
BP	GO:0038128	ERBB2 signaling pathway	6.73E-05	PRKCA/EGFR/EGF/ERBB2/ERBB3	5
BP	GO:0042554	superoxide anion generation	6.73E-05	GSTP1/SOD1/EGFR/NCF1/CRP	5
BP	GO:0045742	positive regulation of epidermal growth factor receptor signaling pathway	6.73E-05	AKT1/ADRA2A/MMP9/EGF/NCF1	5

BP	GO:0071880	adenylate cyclase-activating adrenergic receptor signaling pathway	6.73E-05	ADRA1A/ADRA1B/ADRB2/ADRA2A/ADRB1	5
BP	GO:0002262	myeloid cell homeostasis	6.82E-05	BAX/CASP3/STAT1/HMOX1/SOD1/VEGFA/RB1/IL6/HIF1A	9
BP	GO:0009267	cellular response to starvation	6.82E-05	BCL2/JUN/MAPK8/AKR1C3/MAPK3/MAPK1/SREBF1/CDKN1A/NFE2L2	9
BP	GO:0051092	positive regulation of NF-kappaB transcription factor activity	6.82E-05	AR/RELA/IKBKB/ICAM1/CAT/IL1B/PRKCB/CHUK/CD40LG	9

BP	GO:1902806	regulation of cell cycle G1/S phase transition	6.92E-05	BCL2/BAX/CYP1A1/CCND1/CDKN1A/RB1/CCL2/CCNB1/CHEK2/E2F1	10
BP	GO:0045913	positive regulation of carbohydrate metabolic process	7.02E-05	AKT1/HAS2/INSR/PPARA/EGF/HIF1A/IGF2	7
BP	GO:0071478	cellular response to radiation	7.23E-05	PTGS2/BAX/CASP9/BCL2L1/CDKN1A/ELK1/MYC/PARP1/CHEK2/HSF1	10
BP	GO:0051896	regulation of protein kinase B signaling	7.25E-05	F7/AKT1/INSR/AKR1C3/ESR1/EGFR/EGF/ERBB2/F3/IGF2/ERBB3	11

BP	GO:0001938	positive regulation of endothelial cell proliferation	7.30E-05	JUN/PRKCA/ AKT1/HMOX1/VEGFA/IL10/HIF1A/F3	8
BP	GO:0032386	regulation of intracellular transport	7.42E-05	PTGS2/CHRM1/ADRA1A/CHRM2/MAP2/HMOX1/SLC2A4/MAPK3/MAPK1/SREBF1/ADIPOQ/ERBB2/IL1B/PRKCB/IFNG	15
BP	GO:0043620	regulation of DNA-templated transcription in response to stress	7.56E-05	JUN/RELA/HMOX1/VEGFA/HIF1A/NFE2L2/HSF1	7
BP	GO:0006749	glutathione metabolic process	7.65E-05	GSTP1/GSTM1/GSTM2/SOD1/GSR/NFE2L2	6

BP	GO:0045987	positive regulation of smooth muscle contraction	7.75E-05	PTGS2/CHRM3/ADRA1A/ADRA1B/ABAT	5
BP	GO:0032147	activation of protein kinase activity	7.94E-05	ADRB2/AKT1/INSR/MAPK3/MAPK1/SOD1/ADRA2A/EGFR/VEGFA/EGF/RAF1/IL1B/CD40LG	13
BP	GO:1903532	positive regulation of secretion by cell	7.97E-05	SLC6A4/ACHE/MAPK3/ABAT/EGFR/IL10/IL6/HIF1A/IL2/IFNG/IL1A/PPARD/CHUK/SPP1	14
BP	GO:0032602	chemokine production	8.12E-05	HMOX1/GSTP1/ADIPOQ/IL10/IL6/HIF1A/IL1B	7

BP	GO:0097194	execution phase of apoptosis	8.12E-05	BAX/CASP3/CASP8/AKT1/BCL2L1/TOP2A/HSF1	7
BP	GO:0030336	negative regulation of cell migration	8.15E-05	BCL2/PPARG/AKT1/HMOX1/CYP1B1/GS TP1/ADIPOQ/CCL2/SERPINE1/NFE2L2/C OL3A1/PPARD/IGFBP3	13
BP	GO:0002761	regulation of myeloid leukocyte differentiation	8.17E-05	JUN/CASP8/PRKCA/ADIPOQ/FOS/RB1/ MYC/IFNG	8
BP	GO:1990845	adaptive thermogenesis	8.25E-05	ADRB2/ACHE/ADIPOQ/ADRB1/VEGFA/ RB1/CAV1/GJA1/HSF1	9

BP	GO:0051146	striated muscle cell differentiation	8.29E-05	RXRA/ADRA1A/BCL2/CASP3/AKT1/PPARA/VEGFA/RB1/CCNB1/CXCL10/CHUK/IGF2	12
BP	GO:1903428	positive regulation of reactive oxygen species biosynthetic process	8.38E-05	PTGS2/AKT1/ICAM1/INSR/IL1B/IFNG	6
BP	GO:0032930	positive regulation of superoxide anion generation	8.45E-05	GSTP1/SOD1/EGFR/CRP	4
BP	GO:0070293	renal absorption	8.45E-05	HAS2/AKR1C3/ADIPOQ/CLDN4	4

BP	GO:0044262	cellular carbohydrate metabolic process	8.54E-05	NCOA2/ AKT1/HAS2/INSR/PPARA/ ADIP OQ/GOT1/ AKR1B1/MGAM/IGFBP3/IGF2/ HK2	12
BP	GO:0030856	regulation of epithelial cell differentiation	8.62E-05	IKBKB/STAT1/ ADIPOQ/CCND1/TP63/CA V1/IL1B/SERPINE1/IFNG	9
BP	GO:0071312	cellular response to alkaloid	8.84E-05	OPRM1/CASP3/ICAM1/GSTM2/BCL2L1	5
BP	GO:1901186	positive regulation of ERBB signaling pathway	8.84E-05	AKT1/ ADRA2A/MMP9/EGF/NCF1	5

BP	GO:0016049	cell growth	9.15E-05	ADRA1A/BCL2/MAP2/PPARG/AKT1/PPARA/EGFR/VEGFA/CDKN1A/RB1/ERBB2/GJA1/IL2/PPARD/SPP1/IGFBP3	16
BP	GO:0034764	positive regulation of transmembrane transport	9.18E-05	KCNH2/ADRB2/BAX/AKT1/INSR/GSTM2/ADIPOQ/NFE2L2/CXCL11/CXCL10	10
BP	GO:0050819	negative regulation of coagulation	9.18E-05	ABAT/PLAU/NOS3/PLAT/THBD/SERPINE1	6
BP	GO:0032872	regulation of stress-activated MAPK cascade	9.24E-05	AKT1/GSTP1/MAPK3/MAPK1/HMGCR/EGFR/VEGFA/MYC/IL1B/NCF1/CD40LG	11

BP	GO:0002690	positive regulation of leukocyte chemotaxis	9.25E-05	F7/MAPK3/VEGFA/IL6/CXCL8/SERPINE1/CXCL10	7
BP	GO:0042446	hormone biosynthetic process	9.25E-05	CYP3A4/AKR1C3/AKR1B1/POR/HIF1A/IL1B/IFNG	7
BP	GO:0038095	Fc-epsilon receptor signaling pathway	9.63E-05	JUN/RELA/IKBKB/MAPK8/MAPK3/MAPK1/FOS/CHUK	8
BP	GO:0070302	regulation of stress-activated protein kinase signaling cascade	9.94E-05	AKT1/GSTP1/MAPK3/MAPK1/HMGCR/EGFR/VEGFA/MYC/IL1B/NCF1/CD40LG	11

BP	GO:0042108	positive regulation of cytokine biosynthetic process	0.0001	RELA/HMOX1/IL1B/HSPB1/IL1A/IRF1	6
BP	GO:1902110	positive regulation of mitochondrial membrane permeability involved in apoptotic process	0.0001	BCL2/BAX/CASP8/MAPK8/TP63/E2F1	6
BP	GO:0030224	monocyte differentiation	0.0001	JUN/PPARG/FASN/VEGFA/MYC	5
BP	GO:0043276	anoikis	0.0001	BCL2/AKT1/CAV1/CHEK2/E2F1	5

BP	GO:0071392	cellular response to estradiol stimulus	0.0001	ESR1/UGT1A1/EGFR/IL10/HSF1	5
BP	GO:0071875	adrenergic receptor signaling pathway	0.0001	ADRA1A/ADRA1B/ADRB2/ADRA2A/ADRB1	5
BP	GO:0090322	regulation of superoxide metabolic process	0.0001	GSTP1/SOD1/EGFR/NFE2L2/CRP	5
BP	GO:1903131	mononuclear cell differentiation	0.0001	JUN/PPARG/FASN/VEGFA/MYC	5

BP	GO:0002683	negative regulation of immune system process	0.000106	CASP3/PPARG/ AKT1/HMOX1/LDLR/ ADIPOQ/IL10/NFKBIA/ERBB2/MYC/CCL2/IL2/NFE2L2/COL3A1/IRF1	15
BP	GO:0050890	cognition	0.000106	PTGS2/CHRM1/SLC6A4/JUN/CASP3/INSR/MAPK1/LDLR/HMGCR/EGFR/FOS/HIF1A	12
BP	GO:0032966	negative regulation of collagen biosynthetic process	0.000106	PPARG/GOT1/IL6/PPARD	4
BP	GO:0001523	retinoid metabolic process	0.000106	CYP1A1/CYP1B1/AKR1C3/APOB/UGT1A1/AKR1C1/PPARD	7

BP	GO:0001763	morphogenesis of a branching structure	0.000106	RXRA/PGR/BCL2/ AR/ESR1/VEGFA/IL10/EGF/TP63/MYC	10
BP	GO:0009746	response to hexose	0.000106	PTGS2/CASP3/ICAM1/HMGCR/SREBF1/ADIPOQ/ADRA2A/RAF1/HIF1A/PPARD	10
BP	GO:1903531	negative regulation of secretion by cell	0.000106	OPRM1/HMOX1/HMGCR/SREBF1/ADIPOQ/ABAT/ADRA2A/MAOB/IL10/IL1B	10
BP	GO:0001836	release of cytochrome c from mitochondria	0.000108	BCL2/BAX/JUN/ AKT1/BCL2L1/MMP9	6

BP	GO:0043388	positive regulation of DNA binding	0.000108	PPARG/MMP9/EGF/RB1/IFNG/PARP1	6
BP	GO:2000351	regulation of endothelial cell apoptotic process	0.000108	ICAM1/AKR1C3/CCL2/SERPINE1/NFE2L2/CD40LG	6
BP	GO:2000378	negative regulation of reactive oxygen species metabolic process	0.000108	BCL2/MMP3/IL10/HIF1A/CAV1/HK2	6
BP	GO:0005996	monosaccharide metabolic process	0.000111	NCOA2/AKT1/INSR/UGT1A1/PPARA/AD IPOQ/GOT1/AKR1B1/PPARD/IGFBP3/IGF 2/HK2	12

BP	GO:0009895	negative regulation of catabolic process	0.000111	ADRA1A/BCL2/NOS2/RELA/AKT1/HMO X1/PPARA/ADRA2A/EGFR/IL10/IL1B/E2 F1	12
BP	GO:0046661	male sex differentiation	0.000112	BCL2/BAX/AR/ICAM1/INSR/AKR1C3/ES R1/CCND1/BCL2L1	9
BP	GO:0032885	regulation of polysaccharide biosynthetic process	0.000113	AKT1/HAS2/INSR/EGF/IGF2	5
BP	GO:0051385	response to mineralocorticoid	0.000113	MAOB/CCND1/FOS/CDKN1A/PARP1	5

BP	GO:1901099	negative regulation of signal transduction in absence of ligand	0.000113	BCL2/ AKT1/ BCL2L1/ IL1B/ IL1A	5
BP	GO:2001240	negative regulation of extrinsic apoptotic signaling pathway in absence of ligand	0.000113	BCL2/ AKT1/ BCL2L1/ IL1B/ IL1A	5
BP	GO:0002687	positive regulation of leukocyte migration	0.000118	F7/ ICAM1/ MAPK3/ VEGFA/ IL6/ CXCL8/ S ERPINE1/ CXCL10	8
BP	GO:1902686	mitochondrial outer membrane permeabilization involved in programmed cell death	0.000118	BCL2/ BAX/ CASP8/ MAPK8/ TP63/ E2F1	6

BP	GO:0097529	myeloid leukocyte migration	0.000118	MAPK3/VEGFA/IL6/IL1B/CCL2/CXCL8/SERPINE1/CXCL11/CXCL2/CXCL10	10
BP	GO:0001776	leukocyte homeostasis	0.000119	BCL2/BAX/CASP3/AKT1/IL6/HIF1A/IL2	7
BP	GO:2000146	negative regulation of cell motility	0.000121	BCL2/PPARG/AKT1/HMOX1/CYP1B1/GS TP1/ADIPOQ/CCL2/SERPINE1/NFE2L2/COL3A1/PPARD/IGFBP3	13
BP	GO:0019318	hexose metabolic process	0.000124	NCOA2/AKT1/INSR/PPARA/ADIPOQ/GOT1/AKR1B1/PPARD/IGFBP3/IGF2/HK2	11

BP	GO:0032350	regulation of hormone metabolic process	0.000128	AKR1C3/POR/HIF1A/IL1B/IFNG	5
BP	GO:0034405	response to fluid shear stress	0.000128	PTGS2/AKT1/HAS2/NOS3/NFE2L2	5
BP	GO:0007213	G protein-coupled acetylcholine receptor signaling pathway	0.000129	CHRM3/CHRM1/CHRM4/CHRM2	4
BP	GO:0010713	negative regulation of collagen metabolic process	0.000129	PPARG/GOT1/IL6/PPARD	4

BP	GO:0033189	response to vitamin A	0.000129	PPARG/CYP1A1/CAT/PPARD	4
BP	GO:0050714	positive regulation of protein secretion	0.000132	ACHE/MAPK3/ABAT/EGFR/IL10/IL6/HIF1A/IL2/IL1A/PPARD/CHUK	11
BP	GO:0050870	positive regulation of T cell activation	0.000133	AKT1/VCAM1/IL6/CAV1/IL1B/CCL2/IL2/IFNG/IGF2/CD40LG	10
BP	GO:0051899	membrane depolarization	0.000136	KCNH2/SCN5A/BCL2/JUN/GOT1/CAV1/PARP1	7

BP	GO:1901184	regulation of ERBB signaling pathway	0.000136	AKT1/ ADRA2A/EGFR/MMP9/EGF/ERBB2 /NCF1	7
BP	GO:0007611	learning or memory	0.000136	PTGS2/SLC6A4/JUN/CASP3/INSR/MAPK1 /LDLR/HMGCR/EGFR/FOS/HIF1A	11
BP	GO:0034763	negative regulation of transmembrane transport	0.000137	KCNH2/ AKT1/GSTM2/ ADRA2A/MMP9/C AV1/IL1B/PRKCB	8
BP	GO:0035794	positive regulation of mitochondrial membrane permeability	0.00014	BCL2/BAX/CASP8/MAPK8/TP63/E2F1	6

BP	GO:0006006	glucose metabolic process	0.000143	NCOA2/ AKT1/INSR/PPARA/ADIPOQ/GO T1/PPARD/IGFBP3/IGF2/HK2	10
BP	GO:0016572	histone phosphorylation	0.000144	PRKCA/MAPK3/IL1B/PRKCB/CCNB1	5
BP	GO:0038083	peptidyl-tyrosine autophosphorylation	0.000144	INSR/MAPK3/EGFR/VEGFA/CAV1	5
BP	GO:0042100	B cell proliferation	0.000144	BCL2/BAX/CASP3/AHR/IL10/IL2/CD40LG	7

BP	GO:1901570	fatty acid derivative biosynthetic process	0.000144	PTGS2/PTGS1/ ALOX5/ AKR1C3/FASN/LT A4H/ ACACA	7
BP	GO:0035051	cardiocyte differentiation	0.000144	RXRA/ ADRA1A/ VCAM1/ MAPK3/ MAPK1 /PPARA/ EGFR/ VEGFA/ CCNB1	9
BP	GO:0048015	phosphatidylinosit ol-mediated signaling	0.000151	AKT1/ MAPK3/ MAPK1/ CAT/ EGFR/ ERBB2 /NCF1/ PPARD/ ERBB3	9
BP	GO:0043280	positive regulation of cysteine-type endopeptidase activity involved in apoptotic process	0.000152	BAX/ CASP9/ CASP3/ CASP8/ PPARG/ MYC /F3/ HSF1	8

BP	GO:0042632	cholesterol homeostasis	0.000154	LDLR/MTTP/APOB/SOAT2/AKR1C1/SOA T1/CAV1	7
BP	GO:0043255	regulation of carbohydrate biosynthetic process	0.000154	AKT1/HAS2/INSR/PPARA/ADIPOQ/EGF/ IGF2	7
BP	GO:0017000	antibiotic biosynthetic process	0.000158	CYP1A2/CYP1A1/SOD1/MAOB	4
BP	GO:0030949	positive regulation of vascular endothelial growth factor receptor signaling pathway	0.000158	VEGFA/HIF1A/IL1B/PRKCB	4

BP	GO:1902176	negative regulation of oxidative stress-induced intrinsic apoptotic signaling pathway	0.000158	AKT1/HIF1A/HSPB1/NFE2L2	4
BP	GO:0000060	protein import into nucleus, translocation	0.000162	AKT1/ AKR1C3/MAPK1/NFKBIA/IFNG	5
BP	GO:0033238	regulation of cellular amine metabolic process	0.000162	ABAT/SLC6A3/MAOB/ODC1/NQO1	5
BP	GO:0015908	fatty acid transport	0.000163	NOS2/PPARG/ AKT1/PPARA/ACACA/IL1B/PPARD	7

BP	GO:0055092	sterol homeostasis	0.000163	LDLR/MTTP/APOB/SOAT2/AKR1C1/SOAT1/CAV1	7
BP	GO:0007093	mitotic cell cycle checkpoint	0.000163	BAX/CCND1/BCL2L1/CDKN1A/RB1/CCNB1/TOP2A/CHEK2/E2F1	9
BP	GO:0031571	mitotic G1 DNA damage checkpoint	0.000163	BAX/CCND1/CDKN1A/CCNB1/CHEK2/E2F1	6
BP	GO:0044819	mitotic G1/S transition checkpoint	0.000163	BAX/CCND1/CDKN1A/CCNB1/CHEK2/E2F1	6

BP	GO:0046323	glucose import	0.000163	AKT1/SLC2A4/INSR/ADIPOQ/NFE2L2/HK2	6
BP	GO:1902108	regulation of mitochondrial membrane permeability involved in apoptotic process	0.000163	BCL2/BAX/CASP8/MAPK8/TP63/E2F1	6
BP	GO:1905710	positive regulation of membrane permeability	0.000163	BCL2/BAX/CASP8/MAPK8/TP63/E2F1	6
BP	GO:2000027	regulation of animal organ morphogenesis	0.000163	RXRA/BCL2/BAX/AR/STAT1/ESR1/VEGFA/POR/MYC/RUNX2	10

BP	GO:0045598	regulation of fat cell differentiation	0.000166	PTGS2/PPARG/ AKT1/ADIPOQ/IL6/SULT1 E1/PPARD/E2F1	8
BP	GO:0048017	inositol lipid-mediated signaling	0.00017	AKT1/MAPK3/MAPK1/CAT/EGFR/ERBB2 /NCF1/PPARD/ERBB3	9
BP	GO:0070838	divalent metal ion transport	0.00017	PTGS2/ ADRA1A/OPRM1/BCL2/BAX/ICA M1/GSTM2/ ADRA2A/EGF/CAV1/CCL2/P RKCB/NOS3/CXCL11/CXCL10	15
BP	GO:0070301	cellular response to hydrogen peroxide	0.000172	RELA/CYP1B1/IL10/IL6/NFE2L2/NQO1/H SF1	7

BP	GO:0015711	organic anion transport	0.000174	RXRA/NCOA2/NOS2/PPARG/AKT1/LDL R/MTTP/PPARA/ABCC1/AKR1C1/ABAT/NCOA1/ACACA/IL1B/PPARD	15
BP	GO:0046425	regulation of JAK-STAT cascade	0.000174	CYP1B1/AKR1B1/EGF/IL6/CAV1/IL2/IFN G/HSF1	8
BP	GO:0002260	lymphocyte homeostasis	0.000175	BCL2/BAX/CASP3/AKT1/HIF1A/IL2	6
BP	GO:0044783	G1 DNA damage checkpoint	0.000175	BAX/CCND1/CDKN1A/CCNB1/CHEK2/E 2F1	6

BP	GO:0051785	positive regulation of nuclear division	0.000175	INSR/EGF/RB1/IL1B/IL1A/IGF2	6
BP	GO:0071384	cellular response to corticosteroid stimulus	0.000175	CASP9/ICAM1/GSTP1/AKR1C3/UGT1A1/EGFR	6
BP	GO:0043029	T cell homeostasis	0.000179	BCL2/BAX/CASP3/AKT1/IL2	5
BP	GO:0072511	divalent inorganic cation transport	0.000181	PTGS2/ADRA1A/OPRM1/BCL2/BAX/ICAM1/GSTM2/ADRA2A/EGF/CAV1/CCL2/PKCB/NOS3/CXCL11/CXCL10	15

BP	GO:0048469	cell maturation	0.000183	PGR/BCL2/PPARG/VEGFA/CDKN1A/RB1/HIF1A/CCNB1/RUNX2	9
BP	GO:0010869	regulation of receptor biosynthetic process	0.000188	PPARG/PPARA/ADIPOQ/HIF1A	4
BP	GO:0010893	positive regulation of steroid biosynthetic process	0.000188	SREBF1/POR/IL1B/IFNG	4
BP	GO:0032928	regulation of superoxide anion generation	0.000188	GSTP1/SOD1/EGFR/CRP	4

BP	GO:0014823	response to activity	0.000189	CAT/ADIPOQ/IL10/HIF1A/PPARD/HSF1	6
BP	GO:0051926	negative regulation of calcium ion transport	0.000189	PTGS2/BCL2/ICAM1/GSTM2/ADRA2A/NOS3	6
BP	GO:0022408	negative regulation of cell-cell adhesion	0.00019	CASP3/AKT1/PPARA/ADIPOQ/ABAT/IL10/ERBB2/IL2/IRF1	9
BP	GO:0002224	toll-like receptor signaling pathway	0.000191	CASP8/IKBKB/ESR1/APOB/NFKBIA/CAV1/CHUK/IRF1	8

BP	GO:0007006	mitochondrial membrane organization	0.000191	BCL2/BAX/CASP8/MAPK8/BCL2L1/TP63/ E2F1/HK2	8
BP	GO:0032881	regulation of polysaccharide metabolic process	0.0002	AKT1/HAS2/INSR/EGF/IGF2	5
BP	GO:0050873	brown fat cell differentiation	0.0002	PTGS2/ADRB2/SLC2A4/ADIPOQ/ADRB1	5
BP	GO:0051052	regulation of DNA metabolic process	0.000201	BAX/JUN/PPARG/AKT1/MAPK3/MAPK1 /ADIPOQ/EGFR/IL10/MYC/IL2/PARP1/C HEK2/HSF1	14

BP	GO:0030100	regulation of endocytosis	0.000203	PPARG/SELE/SLC2A4/LDLR/ADIPOQ/VEGFA/EGF/CAV1/IL1B/CCL2/SERPINE1	11
BP	GO:0022600	digestive system process	0.000205	CHRM3/CHRM1/LDLR/SOAT2/AKR1C1/ADRA2A/PTGER3	7
BP	GO:1904892	regulation of STAT cascade	0.000211	CYP1B1/AKR1B1/EGF/IL6/CAV1/IL2/IFNG/HSF1	8
BP	GO:0071230	cellular response to amino acid stimulus	0.000222	EGFR/BCL2L1/MMP2/COL1A1/COL3A1/HSF1	6

BP	GO:0030574	collagen catabolic process	0.000224	MMP1/MMP3/MMP2/MMP9/CTSD	5
BP	GO:0000082	G1/S transition of mitotic cell cycle	0.000224	BCL2/BAX/CYP1A1/CCND1/CDKN1A/RB1/MYC/CCL2/CCNB1/CHEK2/E2F1	11
BP	GO:0031281	positive regulation of cyclase activity	0.000225	NOS2/MAPK8/MAPK3/NOS3	4
BP	GO:0042359	vitamin D metabolic process	0.000225	CYP3A4/CYP1A1/IL1B/IFNG	4

BP	GO:0045649	regulation of macrophage differentiation	0.000225	CASP8/PRKCA/ADIPOQ/RB1	4
BP	GO:0045088	regulation of innate immune response	0.000235	CASP8/PPARG/RELA/IKBKB/STAT1/ESR1/APOB/NFKBIA/RAF1/CAV1/IFNG/CHUK/IRF1	13
BP	GO:0002793	positive regulation of peptide secretion	0.000238	ACHE/MAPK3/ABAT/EGFR/IL10/IL6/HIF1A/IL2/IL1A/PPARD/CHUK	11
BP	GO:0043542	endothelial cell migration	0.000246	PTGS2/PRKCA/PPARG/AKT1/HMOX1/CYP1B1/VEGFA/HIF1A/NOS3/HSPB1/NFE2L2	11

BP	GO:0006775	fat-soluble vitamin metabolic process	0.000249	CYP3A4/CYP1A1/IL1B/IFNG/PPARD	5
BP	GO:0043124	negative regulation of I-kappaB kinase/NF-kappaB signaling	0.000249	CASP8/STAT1/GSTP1/ESR1/ADIPOQ	5
BP	GO:0051054	positive regulation of DNA metabolic process	0.000249	BAX/JUN/ AKT1/MAPK3/MAPK1/EGFR/ MYC/IL2/PARP1/HSF1	10
BP	GO:0015849	organic acid transport	0.000251	RXRA/NCOA2/NOS2/PPARG/ AKT1/PPA RA/ AKR1C1/ ABAT/NCOA1/ ACACA/IL1B /PPARD	12

BP	GO:0046942	carboxylic acid transport	0.000251	RXRA/NCOA2/NOS2/PPARG/ AKT1/PPA RA/ AKR1C1/ ABAT/NCOA1/ ACACA/IL1B /PPARD	12
BP	GO:0048568	embryonic organ development	0.000254	CASP8/ AKT1/MAPK3/MAPK1/SOD1/NC OA1/EGFR/VEGFA/IL10/HIF1A/CXCL8/ HSF1/RUNX2/IGF2	14
BP	GO:0001889	liver development	0.000254	JUN/RELA/HMOX1/CYP1A1/UGT1A1/EG FR/CCND1/IL10	8
BP	GO:0006469	negative regulation of protein kinase activity	0.000266	CASP3/ AKT1/GSTP1/HMGCR/ADIPOQ/C DKN1A/RB1/CAV1/IL1B/HSPB1	10

BP	GO:0010594	regulation of endothelial cell migration	0.000266	PTGS2/PRKCA/PPARG/ AKT1/HMOX1/VE GFA/HIF1A/NOS3/HSPB1/NFE2L2	10
BP	GO:0060485	mesenchyme development	0.000268	BCL2/STAT1/HAS2/MAPK3/MAPK1/HIF1 A/MYC/IL1B/NOS3/COL1A1/ERBB3	11
BP	GO:0043900	regulation of multi-organism process	0.000273	BCL2/JUN/PRKCA/NOS2/STAT1/SLPI/M APK3/IL10/CAV1/CXCL8/IFNG/MPO/TO P2A	13
BP	GO:0002221	pattern recognition receptor signaling pathway	0.000274	CASP8/RELA/IKBKB/ESR1/APOB/NFKBI A/CAV1/CHUK/IRF1	9

BP	GO:1903747	regulation of establishment of protein localization to mitochondrion	0.000277	BCL2/CASP8/MAPK8/SREBF1/TP63/E2F1	6
BP	GO:0060078	regulation of postsynaptic membrane potential	0.000279	CHRM1/ADRB2/CHRNA2/OPRM1/GABRA1/AKT1/ABAT/ADRB1	8
BP	GO:0048639	positive regulation of developmental growth	0.000285	BCL2/AKT1/INSR/SLC6A3/VEGFA/CCNB1/PPARD/HSF1/IGF2	9
BP	GO:0001822	kidney development	0.000285	BCL2/BAX/CASP9/STAT1/HAS2/CAT/ADIPOQ/AKR1B1/VEGFA/ODC1/MYC	11

BP	GO:0061008	hepaticobiliary system development	0.000293	JUN/RELA/HMOX1/CYP1A1/UGT1A1/EGFR/CCND1/IL10	8
BP	GO:0051271	negative regulation of cellular component movement	0.000294	BCL2/PPARG/AKT1/HMOX1/CYP1B1/GS TP1/ADIPOQ/CCL2/SERPINE1/NFE2L2/C OL3A1/PPARD/IGFBP3	13
BP	GO:0051099	positive regulation of binding	0.000296	PON1/PPARG/MMP9/EGF/RB1/CAV1/IF NG/PARP1/HSF1	9
BP	GO:0034381	plasma lipoprotein particle clearance	0.000297	HMOX1/LDLR/APOB/ADIPOQ/SOAT2/S OAT1	6

BP	GO:0034105	positive regulation of tissue remodeling	0.000304	BAX/PRKCA/EGFR/IL2/SPP1	5
BP	GO:0071364	cellular response to epidermal growth factor stimulus	0.000304	AKT1/GSTP1/EGFR/ERBB2/COL1A1	5
BP	GO:0045807	positive regulation of endocytosis	0.000306	PPARG/SELE/LDLR/VEGFA/EGF/IL1B/CL2/SERPINE1	8
BP	GO:0051348	negative regulation of transferase activity	0.000311	CASP3/PPARG/ AKT1/GSTP1/HMGCR/AD IPOQ/CDKN1A/RB1/CAV1/IL1B/HSPB1	11

BP	GO:0046777	protein autophosphorylation	0.000314	JUN/AKT1/INSR/MAPK3/ADIPOQ/EGFR /VEGFA/ERBB2/CAV1/CHEK2	10
BP	GO:0051043	regulation of membrane protein ectodomain proteolysis	0.000315	ADRA2A/IL10/IL1B/IFNG	4
BP	GO:0051412	response to corticosterone	0.000315	MAOB/CCND1/FOS/CDKN1A	4
BP	GO:1903708	positive regulation of hemopoiesis	0.000318	JUN/CASP8/PRKCA/STAT1/FOS/RB1/HIF 1A/IL2/IFNG	9

BP	GO:0030518	intracellular steroid hormone receptor signaling pathway	0.000319	PGR/ AR/NR1I3/ ESR1/NCOA1/RB1/TP63/ PARP1	8
BP	GO:2001056	positive regulation of cysteine-type endopeptidase activity	0.000334	BAX/CASP9/CASP3/CASP8/PPARG/MYC /F3/HSF1	8
BP	GO:0048538	thymus development	0.000335	BCL2/MAPK3/MAPK1/SOD1/RAF1	5
BP	GO:0071827	plasma lipoprotein particle organization	0.000335	MTPP/APOB/SOAT2/SOAT1/MPO	5

BP	GO:0014066	regulation of phosphatidylinosit ol 3-kinase signaling	0.000341	MAPK3/MAPK1/CAT/EGFR/NCF1/PPAR D/ERBB3	7
BP	GO:0032637	interleukin-8 production	0.000341	NOS2/ADIPOQ/IL10/IL1B/SERPINE1/CRP	6
BP	GO:0051260	protein homooligomerizati on	0.000345	RXRA/SLC6A4/BAX/HMOX1/CAT/ADIPO Q/AKR1C1/TP63/ACACA/CAV1/HSF1/A CPP	12
BP	GO:0044774	mitotic DNA integrity checkpoint	0.000361	BAX/CCND1/CDKN1A/CCNB1/TOP2A/C HEK2/E2F1	7

BP	GO:0033044	regulation of chromosome organization	0.000364	MAPK8/MAPK3/MAPK1/SREBF1/VEGFA/RB1/MYC/IL1B/CCNB1/TOP2A/PARP1/IGF2	12
BP	GO:0022617	extracellular matrix disassembly	0.000366	PRSS1/MMP1/CTRB1/MMP3/MMP2/MMP9	6
BP	GO:1903578	regulation of ATP metabolic process	0.000366	INSR/PPARA/EIF6/HIF1A/CCNB1/PARP1	6
BP	GO:1904385	cellular response to angiotensin	0.000367	RELA/CAV1/NFE2L2/HSF1	4

BP	GO:0030857	negative regulation of epithelial cell differentiation	0.000367	STAT1/CCND1/TP63/CAV1/IFNG	5
BP	GO:0031279	regulation of cyclase activity	0.000367	OPRM1/NOS2/MAPK8/MAPK3/NOS3	5
BP	GO:0045981	positive regulation of nucleotide metabolic process	0.000367	NOS2/INSR/HIF1A/NOS3/CCNB1	5
BP	GO:0060443	mammary gland morphogenesis	0.000367	PGR/BAX/AR/ESR1/CAV1	5

BP	GO:1900544	positive regulation of purine nucleotide metabolic process	0.000367	NOS2/INSR/HIF1A/NOS3/CCNB1	5
BP	GO:2001239	regulation of extrinsic apoptotic signaling pathway in absence of ligand	0.000367	BCL2/AKT1/BCL2L1/IL1B/IL1A	5
BP	GO:0002758	innate immune response-activating signal transduction	0.000379	CASP8/RELA/IKBKB/ESR1/APOB/NFKBIA/RAF1/CAV1/CHUK/IRF1	10
BP	GO:0040013	negative regulation of locomotion	0.000389	BCL2/PPARG/AKT1/HMOX1/CYP1B1/GS TP1/ADIPOQ/CCL2/SERPINE1/NFE2L2/C OL3A1/PPARD/IGFBP3	13

BP	GO:0044843	cell cycle G1/S phase transition	0.000389	BCL2/BAX/CYP1A1/CCND1/CDKN1A/RB 1/MYC/CCL2/CCNB1/CHEK2/E2F1	11
BP	GO:0043618	regulation of transcription from RNA polymerase II promoter in response to stress	0.000389	JUN/HMOX1/VEGFA/HIF1A/NFE2L2/HSF 1	6
BP	GO:0051193	regulation of cofactor metabolic process	0.000389	INSR/PPARA/MMP3/EIF6/HIF1A/NFE2L2	6
BP	GO:0035264	multicellular organism growth	0.000395	ADRB2/BCL2/AR/SOD1/SLC6A3/ADRB1/ HSF1/IGF2	8

BP	GO:0018107	peptidyl-threonine phosphorylation	0.000397	BCL2/PRKCA/ AKT1/MAPK8/MAPK1/EGF /PRKCB	7
BP	GO:0006970	response to osmotic stress	0.000417	PTGS2/BAX/CASP3/SLC2A4/ AKR1B1/EGF R	6
BP	GO:0034308	primary alcohol metabolic process	0.000417	CYP1B1/ AKR1C3/ AKR1C1/ ADH1C/ AKR1B 1/SULT1E1	6
BP	GO:0009749	response to glucose	0.000424	CASP3/ICAM1/HMGCR/SREBF1/ ADIPOQ /ADRA2A/RAF1/HIF1A/PPARD	9

BP	GO:1901991	negative regulation of mitotic cell cycle phase transition	0.000424	BCL2/BAX/CCND1/CDKN1A/RB1/CCL2/CCNB1/CHEK2/E2F1	9
BP	GO:0009299	mRNA transcription	0.000424	SREBF1/HIF1A/PPARD/HSF1	4
BP	GO:0009404	toxin metabolic process	0.000424	CYP1A2/CYP1A1/CYP1B1/NFE2L2	4
BP	GO:0015721	bile acid and bile salt transport	0.000424	RXRA/NCOA2/AKR1C1/NCOA1	4

BP	GO:0050927	positive regulation of positive chemotaxis	0.000424	F7/VEGFA/F3/CXCL8	4
BP	GO:0060571	morphogenesis of an epithelial fold	0.000424	AR/EGFR/TP63/HIF1A	4
BP	GO:0072001	renal system development	0.000433	BCL2/BAX/CASP9/STAT1/HAS2/CAT/AD IPOQ/ AKR1B1/VEGFA/ODC1/MYC	11
BP	GO:0010906	regulation of glucose metabolic process	0.000439	NCOA2/ AKT1/INSR/PPARA/ADIPOQ/IG FBP3/IGF2	7

BP	GO:0043525	positive regulation of neuron apoptotic process	0.000439	BAX/CASP9/JUN/CASP3/NQO1	5
BP	GO:0045933	positive regulation of muscle contraction	0.000439	PTGS2/CHRM3/ADRA1A/ADRA1B/ABAT	5
BP	GO:0060711	labyrinthine layer development	0.000439	CASP8/AKT1/MAPK1/NCOA1/IL10	5
BP	GO:0034644	cellular response to UV	0.000474	PTGS2/BAX/CASP9/CDKN1A/MYC/PARP 1	6

BP	GO:0032025	response to cobalt ion	0.000479	CASP9/CASP3/CASP8	3
BP	GO:0033483	gas homeostasis	0.000479	GSTP1/HIF1A/CAV1	3
BP	GO:0045741	positive regulation of epidermal growth factor-activated receptor activity	0.000479	ADRA2A/EGF/NCF1	3
BP	GO:0072584	caveolin-mediated endocytosis	0.000479	MAPK3/MAPK1/CAV1	3

BP	GO:0090594	inflammatory response to wounding	0.000479	HMOX1/HIF1A/IL1A	3
BP	GO:0003044	regulation of systemic arterial blood pressure mediated by a chemical signal	0.000479	ADRA1A/ADRA1B/ADRB2/ADRB1/NOS3	5
BP	GO:0046456	icosanoid biosynthetic process	0.000479	PTGS2/PTGS1/ALOX5/AKR1C3/LTA4H	5
BP	GO:0060324	face development	0.000479	MAPK3/MAPK1/MMP2/RAF1/COL1A1	5

BP	GO:0071825	protein-lipid complex subunit organization	0.000479	MTTP/APOB/SOAT2/SOAT1/MPO	5
BP	GO:0006839	mitochondrial transport	0.000482	BCL2/BAX/CASP8/MAPK8/SREBF1/BCL2 L1/TP63/ACACA/E2F1/HK2	10
BP	GO:0007569	cell aging	0.000482	BCL2/ICAM1/SOD1/CDKN1A/TP63/SERPI NE1/CHEK2	7
BP	GO:0043950	positive regulation of cAMP-mediated signaling	0.000483	PRKCA/ADRB1/CXCL11/CXCL10	4

BP	GO:0050926	regulation of positive chemotaxis	0.000483	F7/VEGFA/F3/CXCL8	4
BP	GO:0060740	prostate gland epithelium morphogenesis	0.000483	RXRA/AR/ESR1/TP63	4
BP	GO:0095500	acetylcholine receptor signaling pathway	0.000483	CHRM3/CHRM1/CHRM4/CHRM2	4
BP	GO:1903831	signal transduction involved in cellular response to ammonium ion	0.000483	CHRM3/CHRM1/CHRM4/CHRM2	4

BP	GO:1905144	response to acetylcholine	0.000483	CHRM3/CHRM1/CHRM4/CHRM2	4
BP	GO:1905145	cellular response to acetylcholine	0.000483	CHRM3/CHRM1/CHRM4/CHRM2	4
BP	GO:1905954	positive regulation of lipid localization	0.000497	PON1/APOB/ADIPOQ/NFKBIA/IL1B/SPP 1	6
BP	GO:0051262	protein tetramerization	0.000499	RXRA/ACHE/INSR/CAT/HMGCR/TP63/ ACACA/ACPP	8

BP	GO:0009165	nucleotide biosynthetic process	0.000505	PTGS2/NOS2/INSR/MAPK1/FASN/PPAR A/EIF6/HIF1A/ACACA/NOS3/PARP1/HK2	12
BP	GO:0030098	lymphocyte differentiation	0.000505	BCL2/BAX/VCAM1/SOD1/IL10/IL6/ERBB2/IL2/IFNG/RUNX2/CD40LG/IRF1	12
BP	GO:0032655	regulation of interleukin-12 production	0.000519	RELA/IL10/IFNG/CD40LG/IRF1	5
BP	GO:0033673	negative regulation of kinase activity	0.000525	CASP3/AKT1/GSTP1/HMGCR/ADIPOQ/C DKN1A/RB1/CAV1/IL1B/HSPB1	10

BP	GO:0003014	renal system process	0.000529	ADRA1A/BCL2/HAS2/ AKR1C3/ ADIPOQ/ AKR1B1/CLDN4	7
BP	GO:1901293	nucleoside phosphate biosynthetic process	0.000545	PTGS2/NOS2/INSR/MAPK1/FASN/PPAR A/EIF6/HIF1A/ ACACA/NOS3/PARP1/HK 2	12
BP	GO:0031348	negative regulation of defense response	0.000555	PPARG/GSTP1/LDLR/PPARA/ADIPOQ/IL 10/RB1/IL2/PPARD	9
BP	GO:0006706	steroid catabolic process	0.000555	CYP3A4/CYP1A2/SULT1E1/SPP1	4

BP	GO:0018210	peptidyl-threonine modification	0.000556	BCL2/PRKCA/ AKT1/MAPK8/MAPK1/EGF /PRKCB	7
BP	GO:0044106	cellular amine metabolic process	0.000564	ABAT/SLC6A3/MAOB/MAOA/ODC1/NQO1	6
BP	GO:0051480	regulation of cytosolic calcium ion concentration	0.000587	ADRA1A/ADRA1B/BCL2/BAX/GSTM2/ESR1/GOT1/CAV1/PTGER3/IL2/CXCL11/CXCL10	12
BP	GO:0032615	interleukin-12 production	0.000617	RELA/IL10/IFNG/CD40LG/IRF1	5

BP	GO:0032964	collagen biosynthetic process	0.000617	PPARG/GOT1/IL6/COL1A1/PPARD	5
BP	GO:0050994	regulation of lipid catabolic process	0.000617	AKT1/LDLR/PPARA/ADRA2A/IL1B	5
BP	GO:0051353	positive regulation of oxidoreductase activity	0.000617	AKT1/POR/HIF1A/IL1B/IFNG	5
BP	GO:2001169	regulation of ATP biosynthetic process	0.000617	INSR/PPARA/EIF6/HIF1A/PARP1	5

BP	GO:0010623	programmed cell death involved in cell development	0.000625	BCL2/BAX/IL1A	3
BP	GO:0019336	phenol-containing compound catabolic process	0.000625	SLC6A3/MAOB/MAOA	3
BP	GO:0019371	cyclooxygenase pathway	0.000625	PTGS2/PTGS1/ AKR1C3	3
BP	GO:0042368	vitamin D biosynthetic process	0.000625	CYP3A4/IL1B/IFNG	3

BP	GO:0043619	regulation of transcription from RNA polymerase II promoter in response to oxidative stress	0.000625	HMOX1/HIF1A/NFE2L2	3
BP	GO:0060525	prostate glandular acinus development	0.000625	RXRA/ESR1/TP63	3
BP	GO:0002026	regulation of the force of heart contraction	0.000626	ADRA1A/ADRB1/CAV1/NOS3	4
BP	GO:0002675	positive regulation of acute inflammatory response	0.000626	PTGS2/IL6/IL1B/PTGER3	4

BP	GO:0007263	nitric oxide mediated signal transduction	0.000626	NOS2/EGFR/VEGFA/NOS3	4
BP	GO:0033598	mammary gland epithelial cell proliferation	0.000626	BAX/ESR1/MAPK1/CCND1	4
BP	GO:0034377	plasma lipoprotein particle assembly	0.000626	MTTP/APOB/SOAT2/SOAT1	4
BP	GO:0042730	fibrinolysis	0.000626	PLAU/PLAT/THBD/SERPINE1	4

BP	GO:0060512	prostate gland morphogenesis	0.000626	RXRA/AR/ESR1/TP63	4
BP	GO:0071480	cellular response to gamma radiation	0.000626	BCL2L1/ELK1/CHEK2/HSF1	4
BP	GO:1902932	positive regulation of alcohol biosynthetic process	0.000626	SREBF1/POR/IL1B/IFNG	4
BP	GO:0043903	regulation of symbiosis, encompassing mutualism through parasitism	0.000626	BCL2/JUN/STAT1/SLPI/IL10/CAV1/CXCL8/MPO/TOP2A	9

BP	GO:0034637	cellular carbohydrate biosynthetic process	0.000627	AKT1/HAS2/INSR/GOT1/AKR1B1/IGF2	6
BP	GO:0042058	regulation of epidermal growth factor receptor signaling pathway	0.000627	AKT1/ADRA2A/EGFR/MMP9/EGF/NCF1	6
BP	GO:0043433	negative regulation of DNA-binding transcription factor activity	0.000652	HMOX1/CYP1B1/ESR1/CAT/IL10/RB1/NF KBIA/CHUK	8
BP	GO:0002218	activation of innate immune response	0.000658	CASP8/RELA/IKBKB/ESR1/APOB/NFKBI A/RAF1/CAV1/CHUK/IRF1	10

BP	GO:0032722	positive regulation of chemokine production	0.000659	HMOX1/ADIPOQ/IL6/HIF1A/IL1B	5
BP	GO:0043500	muscle adaptation	0.000663	ADRA1A/PRKCA/HMOX1/PPARA/IL1B/ NOS3/PARP1	7
BP	GO:0071621	granulocyte chemotaxis	0.000663	MAPK3/IL1B/CCL2/CXCL8/CXCL11/CXC L2/CXCL10	7
BP	GO:0034103	regulation of tissue remodeling	0.000663	BAX/PRKCA/EGFR/IL6/IL2/SPP1	6

BP	GO:0043154	negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	0.000663	PTGS2/ AKT1/ VEGFA/ MMP9/ POR/ RAF1	6
BP	GO:0097306	cellular response to alcohol	0.000663	PPARG/ AKT1/ AHR/ AKR1C3/ UGT1A1/ ACA	6
BP	GO:0042113	B cell activation	0.000663	BCL2/ BAX/ CASP3/ CASP8/ VCAM1/ AHR/ IL10/ IL6/ PRKCB/ IL2/ CD40LG	11
BP	GO:0035821	modification of morphology or physiology of other organism	0.000674	RXRA/ JUN/ CASP8/ NOS2/ INSR/ SLPI/ BCL2L1/ IFNG	8

BP	GO:0051302	regulation of cell division	0.000702	CAT/VEGFA/BCL2L1/TP63/MYC/IL1B/IL1A/IGF2	8
BP	GO:0045833	negative regulation of lipid metabolic process	0.000704	AKT1/AKR1C3/SOD1/UGT1A1/ADRA2A/IL1B	6
BP	GO:0046427	positive regulation of JAK-STAT cascade	0.000704	CYP1B1/AKR1B1/IL6/IL2/IFNG/HSF1	6
BP	GO:0045940	positive regulation of steroid metabolic process	0.000706	SREBF1/POR/IL1B/IFNG	4

BP	GO:0006584	catecholamine metabolic process	0.000708	ABAT/SLC6A3/AKR1B1/MAOB/MAOA	5
BP	GO:0009712	catechol-containin g compound metabolic process	0.000708	ABAT/SLC6A3/AKR1B1/MAOB/MAOA	5
BP	GO:0010524	positive regulation of calcium ion transport into cytosol	0.000708	BAX/GSTM2/CAV1/CXCL11/CXCL10	5
BP	GO:0043949	regulation of cAMP-mediated signaling	0.000708	OPRM1/PRKCA/ADRB1/CXCL11/CXCL10	5

BP	GO:0061098	positive regulation of protein tyrosine kinase activity	0.000708	ADRA1A/ADRA2A/EGF/NCF1/ERBB3	5
BP	GO:1903038	negative regulation of leukocyte cell-cell adhesion	0.000722	CASP3/AKT1/PPARA/IL10/ERBB2/IL2/IRF1	7
BP	GO:0016051	carbohydrate biosynthetic process	0.000758	AKT1/HAS2/INSR/PPARA/ADIPOQ/GOT1/AKR1B1/EGF/IGF2	9
BP	GO:0051701	interaction with host	0.000758	RXRA/CASP8/ICAM1/INSR/LDLR/EGFR/BCL2L1/CAV1/CXCL8	9

BP	GO:0050804	modulation of chemical synaptic transmission	0.000763	PTGS2/ ADRA1A/CHRM2/ ADRB2/SLC6A4 /ACHE/MAPK1/ ADIPOQ/ ABAT/EGFR/IL1B/PRKCB/PLAT	13
BP	GO:0046324	regulation of glucose import	0.000766	AKT1/INSR/ ADIPOQ/NFE2L2/HK2	5
BP	GO:1900408	negative regulation of cellular response to oxidative stress	0.000766	AKT1/IL10/HIF1A/HSPB1/NFE2L2	5
BP	GO:1903202	negative regulation of oxidative stress-induced cell death	0.000766	AKT1/IL10/HIF1A/HSPB1/NFE2L2	5

BP	GO:0007204	positive regulation of cytosolic calcium ion concentration	0.000771	ADRA1A/ADRA1B/BCL2/BAX/GSTM2/ESR1/CAV1/PTGER3/IL2/CXCL11/CXCL10	11
BP	GO:0006164	purine nucleotide biosynthetic process	0.000773	NOS2/INSR/FASN/PPARA/EIF6/HIF1A/CACA/NOS3/PARP1/HK2	10
BP	GO:0099177	regulation of trans-synaptic signaling	0.000775	PTGS2/ADRA1A/CHRM2/ADRB2/SLC6A4/ACHE/MAPK1/ADIPOQ/ABAT/EGFR/IL1B/PRKCB/PLAT	13
BP	GO:0042475	odontogenesis of dentin-containing tooth	0.000781	SCN5A/BAX/PPARA/TP63/SERPINE1/RUNX2	6

BP	GO:0061097	regulation of protein tyrosine kinase activity	0.000781	ADRA1A/ADRA2A/EGF/CAV1/NCF1/ERBB3	6
BP	GO:0070098	chemokine-mediated signaling pathway	0.000781	HIF1A/CCL2/CXCL8/CXCL11/CXCL2/CXCL10	6
BP	GO:0007077	mitotic nuclear envelope disassembly	0.000781	PRKCA/PRKCB/CCNB1	3
BP	GO:0030656	regulation of vitamin metabolic process	0.000781	AKR1C3/IL1B/IFNG	3

BP	GO:0031953	negative regulation of protein autophosphorylation	0.000781	JUN/ADIPOQ/CAV1	3
BP	GO:0042908	xenobiotic transport	0.000781	NR1I2/ABCC1/ABCG2	3
BP	GO:0060742	epithelial cell differentiation involved in prostate gland development	0.000781	RXRA/AR/TP63	3
BP	GO:0001782	B cell homeostasis	0.000783	BCL2/BAX/CASP3/HIF1A	4

BP	GO:0010165	response to X-ray	0.000783	CASP3/CCND1/CDKN1A/THBD	4
BP	GO:0010543	regulation of platelet activation	0.000783	PRKCA/ABAT/NOS3/THBD	4
BP	GO:0046685	response to arsenic-containing substance	0.000783	HMOX1/CYP1A1/CDKN1A/HSF1	4
BP	GO:1901661	quinone metabolic process	0.000783	AKR1C3/HMGCR/AKR1C1/AKR1B1	4

BP	GO:1901988	negative regulation of cell cycle phase transition	0.000795	BCL2/BAX/CCND1/CDKN1A/RB1/CCL2/CCNB1/CHEK2/E2F1	9
BP	GO:0002009	morphogenesis of an epithelium	0.000795	RXRA/PGR/BCL2/AR/STAT1/ESR1/EGFR/VEGFA/IL10/EGF/TP63/HIF1A/MYC/CXCL10	14
BP	GO:0001960	negative regulation of cytokine-mediated signaling pathway	0.000814	PPARG/GSTP1/ADIPOQ/IL6/CAV1	5
BP	GO:0006977	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	0.000814	BAX/CDKN1A/CCNB1/CHEK2/E2F1	5

BP	GO:0048008	platelet-derived growth factor receptor signaling pathway	0.000814	F7/ADIPOQ/VEGFA/F3/PLAT	5
BP	GO:1903749	positive regulation of establishment of protein localization to mitochondrion	0.000814	BCL2/CASP8/MAPK8/TP63/E2F1	5
BP	GO:0006919	activation of cysteine-type endopeptidase activity involved in apoptotic process	0.000816	BAX/CASP9/CASP3/CASP8/PPARG/F3	6
BP	GO:0015844	monoamine transport	0.000816	SLC6A4/SLC6A2/ABAT/ADRA2A/SLC6A3/MAOB	6

BP	GO:1904894	positive regulation of STAT cascade	0.000816	CYP1B1/ AKR1B1/ IL6/ IL2/ IFNG/ HSF1	6
BP	GO:0042476	odontogenesis	0.00085	SCN5A/ BAX/ PPARA/ TP63/ SERPINE1/ CO L1A1/ RUNX2	7
BP	GO:0006941	striated muscle contraction	0.000859	KCNH2/ SCN5A/ ADRA1A/ ADRA1B/ GSTM 2/ CAV1/ GJA1/ CHUK	8
BP	GO:1904062	regulation of cation transmembrane transport	0.000859	KCNH2/ SCN5A/ ADRB2/ OPRM1/ BAX/ GS TM2/ ADRA2A/ MMP9/ CAV1/ CXCL11/ CX CL10	11

BP	GO:0007193	adenylate cyclase-inhibiting G protein-coupled receptor signaling pathway	0.000865	CHRM3/CHRM1/CHRM4/CHRM2/OPRM1/ADRA2A	6
BP	GO:0017001	antibiotic catabolic process	0.000874	AKR1C3/CAT/UGT1A1/SULT1E1/MPO	5
BP	GO:0072431	signal transduction involved in mitotic G1 DNA damage checkpoint	0.000874	BAX/CDKN1A/CCNB1/CHEK2/E2F1	5
BP	GO:1902400	intracellular signal transduction involved in G1 DNA damage checkpoint	0.000874	BAX/CDKN1A/CCNB1/CHEK2/E2F1	5

BP	GO:1902883	negative regulation of response to oxidative stress	0.000874	AKT1/IL10/HIF1A/HSPB1/NFE2L2	5
BP	GO:2001244	positive regulation of intrinsic apoptotic signaling pathway	0.000874	BCL2/BAX/SOD1/BCL2L1/CAV1	5
BP	GO:0030324	lung development	0.000887	PGR/CYP1A2/MAPK3/MAPK1/SREBF1/E GFR/VEGFA/NOS3	8
BP	GO:0003073	regulation of systemic arterial blood pressure	0.000911	ADRA1A/ADRA1B/ADRB2/AR/ADRB1/N OS3	6

BP	GO:0060333	interferon-gamma-mediated signaling pathway	0.000911	PPARG/STAT1/ICAM1/VCAM1/IFNG/IRF1	6
BP	GO:0035270	endocrine system development	0.000924	AKT1/INSR/MAPK3/MAPK1/SLC6A3/IL6/RAF1	7
BP	GO:0000075	cell cycle checkpoint	0.000924	BAX/CCND1/BCL2L1/CDKN1A/RB1/CCNB1/TOP2A/CHEK2/E2F1	9
BP	GO:0002696	positive regulation of leukocyte activation	0.000932	BCL2/AKT1/VCAM1/IL10/IL6/CAV1/IL1B/CCL2/IL2/IFNG/IGF2/CD40LG	12

BP	GO:0045453	bone resorption	0.000942	ADRB2/PRKCA/EGFR/IL6/SPP1	5
BP	GO:0042692	muscle cell differentiation	0.000953	RXRA/ADRA1A/BCL2/CASP3/AKT1/PPARA/VEGFA/RB1/CCNB1/CXCL10/CHUK/IGF2	12
BP	GO:0010950	positive regulation of endopeptidase activity	0.000953	BAX/CASP9/CASP3/CASP8/PPARG/MYC/F3/HSF1	8
BP	GO:0048010	vascular endothelial growth factor receptor signaling pathway	0.00096	VEGFA/HIF1A/IL1B/PRKCB/HSPB1/NCF1	6

BP	GO:2000117	negative regulation of cysteine-type endopeptidase activity	0.00096	PTGS2/ AKT1/ VEGFA/ MMP9/ POR/ RAF1	6
BP	GO:0030213	hyaluronan biosynthetic process	0.000967	HAS2/ EGF/ IL1B	3
BP	GO:0033127	regulation of histone phosphorylation	0.000967	MAPK3/ IL1B/ CCNB1	3
BP	GO:0042574	retinal metabolic process	0.000967	CYP1B1/ AKR1C3/ AKR1C1	3

BP	GO:1902894	negative regulation of pri-miRNA transcription by RNA polymerase II	0.000967	RELA/PPARA/PPARD	3
BP	GO:0044282	small molecule catabolic process	0.000969	PON1/NOS2/AKT1/CYP1A1/AKR1C3/PPARA/ADIPOQ/GOT1/ABAT/NOS3/SULT1E1/PPARD/HK2	13
BP	GO:0032735	positive regulation of interleukin-12 production	0.000971	RELA/IFNG/CD40LG/IRF1	4
BP	GO:0042311	vasodilation	0.000971	ADRB2/SOD1/ADRB1/NOS3	4

BP	GO:0065005	protein-lipid complex assembly	0.000971	MTTP/APOB/SOAT2/SOAT1	4
BP	GO:0010803	regulation of tumor necrosis factor-mediated signaling pathway	0.001001	CASP8/IKBKB/GSTP1/ADIPOQ/CHUK	5
BP	GO:0030888	regulation of B cell proliferation	0.001001	BCL2/CASP3/AHR/IL10/IL2	5
BP	GO:0032370	positive regulation of lipid transport	0.001001	PON1/ADIPOQ/NFKBIA/IL1B/SPP1	5

BP	GO:0033619	membrane protein proteolysis	0.001001	RELA/ADRA2A/IL10/IL1B/IFNG	5
BP	GO:0072413	signal transduction involved in mitotic cell cycle checkpoint	0.001001	BAX/CDKN1A/CCNB1/CHEK2/E2F1	5
BP	GO:1902402	signal transduction involved in mitotic DNA damage checkpoint	0.001001	BAX/CDKN1A/CCNB1/CHEK2/E2F1	5
BP	GO:1902403	signal transduction involved in mitotic DNA integrity checkpoint	0.001001	BAX/CDKN1A/CCNB1/CHEK2/E2F1	5

BP	GO:0010660	regulation of muscle cell apoptotic process	0.001001	PPARG/HMOX1/HMGCR/IFNG/NFE2L2/ HSF1	6
BP	GO:0030323	respiratory tube development	0.00101	PGR/CYP1A2/MAPK3/MAPK1/SREBF1/E GFR/VEGFA/NOS3	8
BP	GO:0021700	developmental maturation	0.001072	PGR/BCL2/PPARG/VEGFA/CDKN1A/MM P2/RB1/HIF1A/CCNB1/RUNX2	10
BP	GO:0072522	purine-containing compound biosynthetic process	0.001072	NOS2/INSR/FASN/PPARA/EIF6/HIF1A/A CACA/NOS3/PARP1/HK2	10

BP	GO:0060761	negative regulation of response to cytokine stimulus	0.001075	PPARG/GSTP1/ADIPOQ/IL6/CAV1	5
BP	GO:0071385	cellular response to glucocorticoid stimulus	0.001075	CASP9/ICAM1/GSTP1/UGT1A1/EGFR	5
BP	GO:0030947	regulation of vascular endothelial growth factor receptor signaling pathway	0.001075	VEGFA/HIF1A/IL1B/PRKCB	4
BP	GO:0036003	positive regulation of transcription from RNA polymerase II promoter in response to stress	0.001075	VEGFA/HIF1A/NFE2L2/HSF1	4

BP	GO:0040018	positive regulation of multicellular organism growth	0.001075	BCL2/SLC6A3/HSF1/IGF2	4
BP	GO:0046326	positive regulation of glucose import	0.001075	AKT1/INSR/ADIPOQ/NFE2L2	4
BP	GO:0048147	negative regulation of fibroblast proliferation	0.001075	BAX/PPARG/GSTP1/MYC	4
BP	GO:0071354	cellular response to interleukin-6	0.001075	RELA/STAT1/ICAM1/IL6	4

BP	GO:0008286	insulin receptor signaling pathway	0.001075	RELA/ AKT1/INSR/SREBF1/IL1B/PRKCB/IGF2	7
BP	GO:0050671	positive regulation of lymphocyte proliferation	0.001075	BCL2/VCAM1/IL6/IL1B/IL2/IGF2/CD40LG	7
BP	GO:0042119	neutrophil activation	0.001112	ALOX5/GSTP1/PSMD3/SLPI/MAPK1/CAT/PLAU/LTA4H/MMP9/CXCL8/MGAM/MPO/ACPP/CTSD	14
BP	GO:0002700	regulation of production of molecular mediator of immune response	0.001121	HMOX1/MAPK3/IL10/IL6/IL1B/IL2/CD40LG	7

BP	GO:0032946	positive regulation of mononuclear cell proliferation	0.001121	BCL2/VCAM1/IL6/IL1B/IL2/IGF2/CD40LG	7
BP	GO:0060048	cardiac muscle contraction	0.001121	KCNH2/SCN5A/ADRA1A/ADRA1B/GSTM2/CAV1/GJA1	7
BP	GO:0002446	neutrophil mediated immunity	0.00113	ALOX5/GSTP1/PSMD3/SLPI/MAPK1/CAT/PLAU/LTA4H/MMP9/IL6/MGAM/MPO/ACPP/CTSD	14
BP	GO:0032371	regulation of sterol transport	0.001145	PON1/PPARG/ADIPOQ/EGF/NFKBIA	5

BP	GO:0032374	regulation of cholesterol transport	0.001145	PON1/PPARG/ADIPOQ/EGF/NFKBIA	5
BP	GO:0007088	regulation of mitotic nuclear division	0.001154	INSR/CCND1/EGF/RB1/IL1B/CCNB1/IL1A/IGF2	8
BP	GO:0097327	response to antineoplastic agent	0.001161	CASP9/F7/HMOX1/ICAM1/EGFR/HSF1	6
BP	GO:1990868	response to chemokine	0.001161	HIF1A/CCL2/CXCL8/CXCL11/CXCL2/CXCL10	6

BP	GO:1990869	cellular response to chemokine	0.001161	HIF1A/CCL2/CXCL8/CXCL11/CXCL2/CXCL10	6
BP	GO:0007292	female gamete generation	0.001161	PTGS2/PGR/BCL2/NOS3/CCNB1/TOP2A/HSF1	7
BP	GO:0010675	regulation of cellular carbohydrate metabolic process	0.001161	NCOA2/AKT1/INSR/PPARA/ADIPOQ/IGFBP3/IGF2	7
BP	GO:0097530	granulocyte migration	0.001161	MAPK3/IL1B/CCL2/CXCL8/CXCL11/CXCL2/CXCL10	7

BP	GO:0014854	response to inactivity	0.001166	SCN5A/CAT/IL10	3
BP	GO:0019372	lipxygenase pathway	0.001166	PTGS2/PON1/ALOX5	3
BP	GO:0042362	fat-soluble vitamin biosynthetic process	0.001166	CYP3A4/IL1B/IFNG	3
BP	GO:0045651	positive regulation of macrophage differentiation	0.001166	CASP8/PRKCA/RB1	3

BP	GO:0090399	replicative senescence	0.001166	CDKN1A/SERPINE1/CHEK2	3
BP	GO:0050867	positive regulation of cell activation	0.001175	BCL2/AKT1/VCAM1/IL10/IL6/CAV1/IL1B/CCL2/IL2/IFNG/IGF2/CD40LG	12
BP	GO:0030262	apoptotic nuclear changes	0.001178	BAX/CASP3/TOP2A/HSF1	4
BP	GO:0097421	liver regeneration	0.001178	HMOX1/EGFR/CCND1/IL10	4

BP	GO:0098664	G protein-coupled serotonin receptor signaling pathway	0.001178	CHRM3/CHRM1/CHRM4/CHRM2	4
BP	GO:0071346	cellular response to interferon-gamma	0.001179	NOS2/PPARG/STAT1/ICAM1/VCAM1/CC L2/IFNG/IRF1	8
BP	GO:0010657	muscle cell apoptotic process	0.001212	PPARG/HMOX1/HMGCR/IFNG/NFE2L2/HSF1	6
BP	GO:0006879	cellular iron ion homeostasis	0.001212	HMOX1/SOD1/HIF1A/MYC/ABCG2	5

BP	GO:0042102	positive regulation of T cell proliferation	0.001278	VCAM1/IL6/IL1B/IL2/IGF2/CD40LG	6
BP	GO:0062014	negative regulation of small molecule metabolic process	0.001278	AKT1/AKR1C3/SOD1/PPARA/ADIPOQ/PARP1	6
BP	GO:0051251	positive regulation of lymphocyte activation	0.001308	BCL2/AKT1/VCAM1/IL6/CAV1/IL1B/CCL2/IL2/IFNG/IGF2/CD40LG	11
BP	GO:0045923	positive regulation of fatty acid metabolic process	0.001308	PTGS2/PPARG/PPARA/ADIPOQ	4

BP	GO:0050892	intestinal absorption	0.001308	LDLR/SOAT2/AKR1C1/ADRA2A	4
BP	GO:0071470	cellular response to osmotic stress	0.001308	PTGS2/CASP3/SLC2A4/AKR1B1	4
BP	GO:0006874	cellular calcium ion homeostasis	0.001324	ADRA1A/ADRA1B/BCL2/BAX/GSTM2/ES R1/GOT1/CAV1/PTGER3/PRKCB/IL2/CX CL11/CXCL10	13
BP	GO:0019395	fatty acid oxidation	0.001341	PPARG/AKT1/PPARA/ADIPOQ/POR/PPA RD	6

BP	GO:0044773	mitotic DNA damage checkpoint	0.001341	BAX/CCND1/CDKN1A/CCNB1/CHEK2/E2F1	6
BP	GO:0022900	electron transport chain	0.001353	CYP1A2/GSR/AKR1B1/MAOB/POR/CCNB1/NCF1/NQO1	8
BP	GO:0045600	positive regulation of fat cell differentiation	0.001391	PTGS2/PPARG/AKT1/SULT1E1/PPARD	5
BP	GO:0043254	regulation of protein complex assembly	0.001403	BAX/JUN/MAP2/MMP1/ICAM1/ESR1/MMP3/VEGFA/RB1/RAF1/IFNG/PARP1/RASA1	13

BP	GO:0002027	regulation of heart rate	0.001403	KCNH2/SCN5A/ADRA1A/SREBF1/ADRB1/CAV1	6
BP	GO:0018958	phenol-containing compound metabolic process	0.001403	BCL2/ABAT/SLC6A3/AKR1B1/MAOB/MAOA	6
BP	GO:0031056	regulation of histone modification	0.001403	MAPK8/MAPK3/SREBF1/VEGFA/IL1B/CCNB1/IGF2	7
BP	GO:0070665	positive regulation of leukocyte proliferation	0.001403	BCL2/VCAM1/IL6/IL1B/IL2/IGF2/CD40LG	7

BP	GO:0002070	epithelial cell maturation	0.001403	PGR/CDKN1A/HIF1A	3
BP	GO:0009812	flavonoid metabolic process	0.001403	CYP1A1/UGT1A1/POR	3
BP	GO:0010875	positive regulation of cholesterol efflux	0.001403	PON1/ADIPOQ/NFKBIA	3
BP	GO:0030299	intestinal cholesterol absorption	0.001403	LDLR/SOAT2/AKR1C1	3

BP	GO:0030730	sequestering of triglyceride	0.001403	PPARG/PPARA/IL1B	3
BP	GO:0042447	hormone catabolic process	0.001403	ACHE/SULT1E1/SPP1	3
BP	GO:0051044	positive regulation of membrane protein ectodomain proteolysis	0.001403	ADRA2A/IL1B/IFNG	3
BP	GO:0006921	cellular component disassembly involved in execution phase of apoptosis	0.001431	BAX/CASP3/TOP2A/HSF1	4

BP	GO:0030212	hyaluronan metabolic process	0.001431	AKT1/HAS2/EGF/IL1B	4
BP	GO:1904037	positive regulation of epithelial cell apoptotic process	0.001431	AKR1C3/IL6/CCL2/CD40LG	4
BP	GO:0030308	negative regulation of cell growth	0.001431	BCL2/MAP2/PPARG/PPARA/CDKN1A/GJ A1/PPARD/SPP1	8
BP	GO:0034250	positive regulation of cellular amide metabolic process	0.001455	RXRA/MAPK3/MAPK1/EIF6/IL6/ERBB2/ NFE2L2	7

BP	GO:0060537	muscle tissue development	0.001463	RXRA/ADRA1A/BCL2/HMGCR/PPARA/VEGFA/FOS/RB1/CAV1/CCNB1/COL3A1/ERBB3	12
BP	GO:0010522	regulation of calcium ion transport into cytosol	0.001463	BCL2/BAX/GSTM2/CAV1/CXCL11/CXCL10	6
BP	GO:0034440	lipid oxidation	0.001463	PPARG/AKT1/PPARA/ADIPOQ/POR/PPARD	6
BP	GO:0046888	negative regulation of hormone secretion	0.001464	HMGCR/SREBF1/ADIPOQ/ADRA2A/IL1B	5

BP	GO:0030593	neutrophil chemotaxis	0.001539	IL1B/CCL2/CXCL8/CXCL11/CXCL2/CXCL10	6
BP	GO:0034766	negative regulation of ion transmembrane transport	0.001539	KCNH2/ AKT1/GSTM2/ ADRA2A/MMP9/CAV1	6
BP	GO:0014015	positive regulation of gliogenesis	0.001566	PPARG/RELA/IL6/IL1B/E2F1	5
BP	GO:0032677	regulation of interleukin-8 production	0.001566	ADIPOQ/IL10/IL1B/SERPINE1/CRP	5

BP	GO:1902107	positive regulation of leukocyte differentiation	0.001568	JUN/CASP8/PRKCA/FOS/RB1/IL2/IFNG	7
BP	GO:0006778	porphyrin-containi ng compound metabolic process	0.001568	HMOX1/CYP1A2/CYP1A1/UGT1A1	4
BP	GO:0010874	regulation of cholesterol efflux	0.001568	PON1/ADIPOQ/EGF/NFKBIA	4
BP	GO:0014037	Schwann cell differentiation	0.001568	RELA/AKT1/SOD1/ERBB3	4

BP	GO:0070741	response to interleukin-6	0.001568	RELA/STAT1/ICAM1/IL6	4
BP	GO:2000273	positive regulation of signaling receptor activity	0.001568	ADRB2/ADRA2A/EGF/NCF1	4
BP	GO:0038093	Fc receptor signaling pathway	0.001569	JUN/RELA/IKBKB/MAPK8/MAPK3/MAPK1/FOS/CHUK	8
BP	GO:0019233	sensory perception of pain	0.001606	PTGS2/OPRM1/MAPK3/MAPK1/IL10/ACPP	6

BP	GO:0035924	cellular response to vascular endothelial growth factor stimulus	0.001664	RELA/ AKT1/VCAM1/VEGFA/HSPB1	5
BP	GO:0055074	calcium ion homeostasis	0.001664	ADRA1A/ADRA1B/BCL2/BAX/GSTM2/ES R1/GOT1/CAV1/PTGER3/PRKCB/IL2/CX CL11/CXCL10	13
BP	GO:0017085	response to insecticide	0.001664	CYP1A1/CCNB1/HSF1	3
BP	GO:0030397	membrane disassembly	0.001664	PRKCA/PRKCB/CCNB1	3

BP	GO:0045986	negative regulation of smooth muscle contraction	0.001664	PTGS2/ ADRB2/SOD1	3
BP	GO:0051081	nuclear envelope disassembly	0.001664	PRKCA/PRKCB/CCNB1	3
BP	GO:0071380	cellular response to prostaglandin E stimulus	0.001664	PPARG/AKT1/ACACA	3
BP	GO:0098856	intestinal lipid absorption	0.001664	LDLR/SOAT2/AKR1C1	3

BP	GO:2001267	regulation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway	0.001664	BAX/CASP8/MMP9	3
BP	GO:0007219	Notch signaling pathway	0.001666	AKT1/STAT1/GOT1/EGFR/EGF/TP63/NF KBIA/MYC	8
BP	GO:0007517	muscle organ development	0.001707	RXRA/BCL2/ACHE/HMGCR/PPARA/FOS /RB1/CAV1/CCNB1/COL3A1/CXCL10/ER BB3	12
BP	GO:0019048	modulation by virus of host morphology or physiology	0.001714	RXRA/CASP8/INSR/BCL2L1	4

BP	GO:0045124	regulation of bone resorption	0.001714	PRKCA/EGFR/IL6/SPP1	4
BP	GO:0050805	negative regulation of synaptic transmission	0.00176	PTGS2/SLC6A4/ACHE/ADIPOQ/IL1B	5
BP	GO:0051592	response to calcium ion	0.001817	SCN5A/JUN/AKR1C3/EGFR/CCND1/FOS/CAV1	7
BP	GO:0006914	autophagy	0.001822	ADRA1A/ADRB2/BCL2/CASP3/AKT1/MA PK8/HMOX1/MAPK3/SREBF1/HIF1A/HSP B1/IFNG/HK2	13

BP	GO:0061919	process utilizing autophagic mechanism	0.001822	ADRA1A/ADRB2/BCL2/CASP3/AKT1/MA PK8/HMOX1/MAPK3/SREBF1/HIF1A/HSP B1/IFNG/HK2	13
BP	GO:0071479	cellular response to ionizing radiation	0.001876	BCL2L1/CDKN1A/ELK1/CHEK2/HSF1	5
BP	GO:0007210	serotonin receptor signaling pathway	0.001879	CHRM3/CHRM1/CHRM4/CHRM2	4
BP	GO:0033146	regulation of intracellular estrogen receptor signaling pathway	0.001879	AR/ESR1/TP63/PARP1	4

BP	GO:0042417	dopamine metabolic process	0.001879	ABAT/SLC6A3/MAOB/MAOA	4
BP	GO:0045746	negative regulation of Notch signaling pathway	0.001879	AKT1/EGFR/EGF/NFKBIA	4
BP	GO:0030278	regulation of ossification	0.001891	ADRB2/BCL2/MAPK3/MAPK1/IL6/TP63/ HIF1A/RUNX2	8
BP	GO:0019359	nicotinamide nucleotide biosynthetic process	0.001924	PTGS2/INSR/PPARA/EIF6/HIF1A/HK2	6

BP	GO:0019363	pyridine nucleotide biosynthetic process	0.001924	PTGS2/INSR/PPARA/EIF6/HIF1A/HK2	6
BP	GO:0043502	regulation of muscle adaptation	0.001924	SCN5A/ADRA1A/PRKCA/PPARA/NOS3/ PARP1	6
BP	GO:0071774	response to fibroblast growth factor	0.001947	MAPK3/MAPK1/ELK1/CCL2/CXCL8/COL 1A1/RUNX2	7
BP	GO:0060541	respiratory system development	0.001947	PGR/CYP1A2/MAPK3/MAPK1/SREBF1/E GFR/VEGFA/NOS3	8

BP	GO:0044241	lipid digestion	0.001957	LDLR/SOAT2/AKR1C1	3
BP	GO:0045725	positive regulation of glycogen biosynthetic process	0.001957	AKT1/INSR/IGF2	3
BP	GO:0045780	positive regulation of bone resorption	0.001957	PRKCA/EGFR/SPP1	3
BP	GO:0046852	positive regulation of bone remodeling	0.001957	PRKCA/EGFR/SPP1	3

BP	GO:0071605	monocyte chemotactic protein-1 production	0.001957	GSTP1/ADIPOQ/IL1B	3
BP	GO:0071637	regulation of monocyte chemotactic protein-1 production	0.001957	GSTP1/ADIPOQ/IL1B	3
BP	GO:1902644	tertiary alcohol metabolic process	0.001957	AKR1C3/AKR1C1/AKR1B1	3
BP	GO:0048678	response to axon injury	0.00197	BCL2/BAX/JUN/SOD1/SPP1	5

BP	GO:0031623	receptor internalization	0.001997	ACHE/SELE/VEGFA/EGF/CAV1/CXCL8	6
BP	GO:0048640	negative regulation of developmental growth	0.001997	ADRB2/SLC6A4/MAP2/PPARA/ADRB1/S PP1	6
BP	GO:0071156	regulation of cell cycle arrest	0.001997	BAX/CCND1/CDKN1A/CCNB1/CHEK2/E 2F1	6
BP	GO:0060402	calcium ion transport into cytosol	0.002004	ADRA1A/BCL2/BAX/GSTM2/CAV1/CXCL 11/CXCL10	7

BP	GO:0010828	positive regulation of glucose transmembrane transport	0.002026	AKT1/INSR/ADIPOQ/NFE2L2	4
BP	GO:0030810	positive regulation of nucleotide biosynthetic process	0.002026	NOS2/INSR/HIF1A/NOS3	4
BP	GO:0051281	positive regulation of release of sequestered calcium ion into cytosol	0.002026	BAX/GSTM2/CXCL11/CXCL10	4
BP	GO:0061028	establishment of endothelial barrier	0.002026	IKBKB/ICAM1/FASN/IL1B	4

BP	GO:0090311	regulation of protein deacetylation	0.002026	MAPK8/SREBF1/VEGFA/IFNG	4
BP	GO:1900373	positive regulation of purine nucleotide biosynthetic process	0.002026	NOS2/INSR/HIF1A/NOS3	4
BP	GO:0000187	activation of MAPK activity	0.002066	INSR/MAPK3/MAPK1/SOD1/EGF/IL1B/C D40LG	7
BP	GO:0031214	biomineral tissue development	0.002066	PTGS2/ADRB2/PPARA/HIF1A/NOS3/COL 1A1/SPP1	7

BP	GO:0048754	branching morphogenesis of an epithelial tube	0.002066	PGR/BCL2/ AR/ESR1/VEGFA/EGF/MYC	7
BP	GO:1903707	negative regulation of hemopoiesis	0.002066	ADIPOQ/NFKBIA/ERBB2/MYC/IL2/NFE2L2/IRF1	7
BP	GO:0046620	regulation of organ growth	0.002075	SLC6A4/ AKT1/SOD1/PPARA/POR/CCNB1	6
BP	GO:0005976	polysaccharide metabolic process	0.002174	AKT1/HAS2/INSR/EGF/MGAM/IGF2	6

BP	GO:0072525	pyridine-containing compound biosynthetic process	0.002174	PTGS2/INSR/PPARA/EIF6/HIF1A/HK2	6
BP	GO:0034341	response to interferon-gamma	0.002174	NOS2/PPARG/STAT1/ICAM1/VCAM1/CC L2/IFNG/IRF1	8
BP	GO:0070227	lymphocyte apoptotic process	0.002201	BAX/AKT1/IL10/HIF1A/IL2	5
BP	GO:1901616	organic hydroxy compound catabolic process	0.002201	AKR1C3/SLC6A3/MAOB/MAOA/SULT1E1	5

BP	GO:0002931	response to ischemia	0.002201	BCL2/CASP9/CAV1/HK2	4
BP	GO:0006110	regulation of glycolytic process	0.002201	INSR/PPARA/EIF6/HIF1A	4
BP	GO:0033574	response to testosterone	0.002201	AR/ELK1/HSF1/SPP1	4
BP	GO:0045861	negative regulation of proteolysis	0.002232	PTGS2/AKT1/SLPI/VEGFA/MMP9/IL10/P OR/RAF1/BIRC5/PLAT/SERPINE1	11

BP	GO:0010508	positive regulation of autophagy	0.002254	ADRB2/HMOX1/MAPK3/HIF1A/IFNG/HK2	6
BP	GO:0010951	negative regulation of endopeptidase activity	0.002254	PTGS2/AKT1/SLPI/VEGFA/MMP9/POR/RAF1/BIRC5/SERPINE1	9
BP	GO:0003085	negative regulation of systemic arterial blood pressure	0.002254	ADRA1A/ADRB2/ADRB1	3
BP	GO:0007252	I-kappaB phosphorylation	0.002254	IKBKB/AKT1/CHUK	3

BP	GO:0010224	response to UV-B	0.002254	BCL2/RELA/CDKN1A	3
BP	GO:0010544	negative regulation of platelet activation	0.002254	ABAT/NOS3/THBD	3
BP	GO:0030540	female genitalia development	0.002254	BAX/ESR1/TP63	3
BP	GO:0051023	regulation of immunoglobulin secretion	0.002254	IL6/IL2/CD40LG	3

BP	GO:0051767	nitric-oxide synthase biosynthetic process	0.002254	STAT1/GSTP1/CCL2	3
BP	GO:0051769	regulation of nitric-oxide synthase biosynthetic process	0.002254	STAT1/GSTP1/CCL2	3
BP	GO:0060252	positive regulation of glial cell proliferation	0.002254	IL6/IL1B/E2F1	3
BP	GO:0072401	signal transduction involved in DNA integrity checkpoint	0.002309	BAX/CDKN1A/CCNB1/CHEK2/E2F1	5

BP	GO:0072422	signal transduction involved in DNA damage checkpoint	0.002309	BAX/CDKN1A/CCNB1/CHEK2/E2F1	5
BP	GO:0002065	columnar/cuboidal epithelial cell differentiation	0.002348	RXRA/SOD1/CDKN1A/TP63/HIF1A/SERPINE1	6
BP	GO:0051783	regulation of nuclear division	0.002353	INSR/CCND1/EGF/RB1/IL1B/CCNB1/IL1A/IGF2	8
BP	GO:0006509	membrane protein ectodomain proteolysis	0.002373	ADRA2A/IL10/IL1B/IFNG	4

BP	GO:0010863	positive regulation of phospholipase C activity	0.002373	ADRA1A/SELE/ESR1/EGFR	4
BP	GO:0030811	regulation of nucleotide catabolic process	0.002373	INSR/PPARA/EIF6/HIF1A	4
BP	GO:0072503	cellular divalent inorganic cation homeostasis	0.002402	ADRA1A/ADRA1B/BCL2/BAX/GSTM2/ESR1/GOT1/CAV1/PTGER3/PRKCB/IL2/CXCL11/CXCL10	13
BP	GO:0000271	polysaccharide biosynthetic process	0.002433	AKT1/HAS2/INSR/EGF/IGF2	5

BP	GO:0006096	glycolytic process	0.002433	INSR/PPARA/EIF6/HIF1A/HK2	5
BP	GO:0072347	response to anesthetic	0.002433	OPRM1/F7/RELA/ABAT/SLC6A3	5
BP	GO:0072395	signal transduction involved in cell cycle checkpoint	0.002433	BAX/CDKN1A/CCNB1/CHEK2/E2F1	5
BP	GO:0071695	anatomical structure maturation	0.002433	PGR/BCL2/CDKN1A/MMP2/RB1/HIF1A/ CCNB1	7

BP	GO:0014013	regulation of gliogenesis	0.002435	PPARG/RELA/LDLR/IL6/IL1B/E2F1	6
BP	GO:1990266	neutrophil migration	0.002435	IL1B/CCL2/CXCL8/CXCL11/CXCL2/CXCL10	6
BP	GO:0043312	neutrophil degranulation	0.002477	ALOX5/GSTP1/PSMD3/SLPI/MAPK1/CAT/PLAU/LTA4H/MMP9/MGAM/MPO/ACP/CTSD	13
BP	GO:0045089	positive regulation of innate immune response	0.002542	CASP8/RELA/IKBKB/ESR1/APOB/NFKBIA/RAF1/CAV1/CHUK/IRF1	10

BP	GO:0010907	positive regulation of glucose metabolic process	0.002566	AKT1/INSR/PPARA/IGF2	4
BP	GO:0032965	regulation of collagen biosynthetic process	0.002566	PPARG/GOT1/IL6/PPARD	4
BP	GO:0006757	ATP generation from ADP	0.002566	INSR/PPARA/EIF6/HIF1A/HK2	5
BP	GO:0007422	peripheral nervous system development	0.002566	RELA/ AKT1/SOD1/ERBB2/ERBB3	5

BP	GO:0070664	negative regulation of leukocyte proliferation	0.002566	CASP3/GSTP1/IL10/ERBB2/IL2	5
BP	GO:0002902	regulation of B cell apoptotic process	0.002598	BAX/IL10/IL2	3
BP	GO:0051546	keratinocyte migration	0.002598	HAS2/MMP9/PPARD	3
BP	GO:0070875	positive regulation of glycogen metabolic process	0.002598	AKT1/INSR/IGF2	3

BP	GO:0002283	neutrophil activation involved in immune response	0.002599	ALOX5/GSTP1/PSMD3/SLPI/MAPK1/CAT/PLAU/LTA4H/MMP9/MGAM/MPO/ACP/CTSD	13
BP	GO:0016241	regulation of macroautophagy	0.002689	ADRB2/CASP3/AKT1/MAPK8/HMOX1/MAPK3/HIF1A	7
BP	GO:0031570	DNA integrity checkpoint	0.002689	BAX/CCND1/CDKN1A/CCNB1/TOP2A/CHK2/E2F1	7
BP	GO:2001020	regulation of response to DNA damage stimulus	0.002701	BCL2/CASP9/EGFR/BCL2L1/MYC/PARP1/CHK2/HSF1	8

BP	GO:0043407	negative regulation of MAP kinase activity	0.002704	GSTP1/HMGCR/ADIPOQ/CAV1/IL1B	5
BP	GO:0072332	intrinsic apoptotic signaling pathway by p53 class mediator	0.002704	BCL2/BAX/TP63/CHEK2/E2F1	5
BP	GO:0046850	regulation of bone remodeling	0.00277	PRKCA/EGFR/IL6/SPP1	4
BP	GO:1900274	regulation of phospholipase C activity	0.00277	ADRA1A/SELE/ESR1/EGFR	4

BP	GO:0044242	cellular lipid catabolic process	0.002775	AKT1/CYP1B1/AKR1C3/LDLR/APOB/PPARA/ADIPOQ/PPARD	8
BP	GO:0031334	positive regulation of protein complex assembly	0.002806	BAX/JUN/MMP1/ICAM1/ESR1/MMP3/VEGFA/IFNG/PARP1	9
BP	GO:0002718	regulation of cytokine production involved in immune response	0.002857	HMOX1/MAPK3/IL10/IL6/IL1B	5
BP	GO:0006754	ATP biosynthetic process	0.002868	INSR/PPARA/EIF6/HIF1A/PARP1/HK2	6

BP	GO:0051928	positive regulation of calcium ion transport	0.002868	BAX/GSTM2/CAV1/CCL2/CXCL11/CXCL10	6
BP	GO:0032409	regulation of transporter activity	0.002873	ADRB2/OPRM1/BCL2/PON1/PPARG/GSTM2/ADRA2A/MMP9/CAV1	9
BP	GO:0010466	negative regulation of peptidase activity	0.00295	PTGS2/AKT1/SLPI/VEGFA/MMP9/POR/RAF1/BIRC5/SERPINE1	9
BP	GO:0060401	cytosolic calcium ion transport	0.002969	ADRA1A/BCL2/BAX/GSTM2/CAV1/CXCL11/CXCL10	7

BP	GO:0016137	glycoside metabolic process	0.002976	AKR1C3/AKR1C1/AKR1B1	3
BP	GO:0019373	epoxygenase P450 pathway	0.002976	CYP1A2/CYP1A1/CYP1B1	3
BP	GO:0032682	negative regulation of chemokine production	0.002976	GSTP1/IL10/IL6	3
BP	GO:0042053	regulation of dopamine metabolic process	0.002976	ABAT/SLC6A3/MAOB	3

BP	GO:0042069	regulation of catecholamine metabolic process	0.002976	ABAT/SLC6A3/MAOB	3
BP	GO:0046697	decidualization	0.002976	PTGS2/PPARD/SPP1	3
BP	GO:0034198	cellular response to amino acid starvation	0.002976	MAPK8/MAPK3/MAPK1/CDKN1A	4
BP	GO:1904036	negative regulation of epithelial cell apoptotic process	0.002976	HMOX1/ICAM1/SERPINE1/NFE2L2	4

BP	GO:0042866	pyruvate biosynthetic process	0.002987	INSR/PPARA/EIF6/HIF1A/HK2	5
BP	GO:0051289	protein homotetramerization	0.002987	RXRA/CAT/TP63/ACACA/ACPP	5
BP	GO:1900182	positive regulation of protein localization to nucleus	0.002987	PTGS2/AKT1/MAPK1/IFNG/PARP1	5
BP	GO:0048762	mesenchymal cell differentiation	0.002996	BCL2/STAT1/HAS2/MAPK3/MAPK1/HIF1A/IL1B/COL1A1	8

BP	GO:0006733	oxidoreduction coenzyme metabolic process	0.003041	PTGS2/INSR/HMGCR/PPARA/EIF6/HIF1 A/HK2	7
BP	GO:0050680	negative regulation of epithelial cell proliferation	0.003041	AR/PPARG/STAT1/RB1/CAV1/CCL2/PPA RD	7
BP	GO:0055117	regulation of cardiac muscle contraction	0.003154	SCN5A/ADRA1A/ADRA1B/GSTM2/CAV1	5
BP	GO:0045732	positive regulation of protein catabolic process	0.003174	AKT1/LDLR/ADRA2A/EGF/CAV1/IL1B/I FNG/NFE2L2	8

BP	GO:0031952	regulation of protein autophosphorylation	0.003201	JUN/ADIPOQ/VEGFA/CAV1	4
BP	GO:0043330	response to exogenous dsRNA	0.003201	MAPK3/MAPK1/NFKBIA/CAV1	4
BP	GO:0044003	modification by symbiont of host morphology or physiology	0.003201	RXRA/CASP8/INSR/BCL2L1	4
BP	GO:0048806	genitalia development	0.003201	BAX/AR/ESR1/TP63	4

BP	GO:0016054	organic acid catabolic process	0.003218	PON1/NOS2/AKT1/PPARA/ADIPOQ/GOT 1/ABAT/NOS3/PPARD	9
BP	GO:0046395	carboxylic acid catabolic process	0.003218	PON1/NOS2/AKT1/PPARA/ADIPOQ/GOT 1/ABAT/NOS3/PPARD	9
BP	GO:0002695	negative regulation of leukocyte activation	0.003242	CASP3/HMOX1/LDLR/IL10/ERBB2/IL2/IR F1	7
BP	GO:0014706	striated muscle tissue development	0.003249	RXRA/ADRA1A/BCL2/HMGCR/PPARA/V EGFA/FOS/RB1/CAV1/CCNB1/ERBB3	11

BP	GO:0042509	regulation of tyrosine phosphorylation of STAT protein	0.00331	IL6/CAV1/IL2/IFNG/HSF1	5
BP	GO:0007173	epidermal growth factor receptor signaling pathway	0.003329	AKT1/ADRA2A/EGFR/MMP9/EGF/NCF1	6
BP	GO:0034101	erythrocyte homeostasis	0.003329	CASP3/STAT1/HMOX1/VEGFA/RB1/HIF1A	6
BP	GO:0038061	NIK/NF-kappaB signaling	0.003329	RELA/AKT1/EGFR/NFKBIA/IL1B/CHUK	6

BP	GO:0045727	positive regulation of translation	0.003329	RXRA/MAPK3/MAPK1/EIF6/IL6/ERBB2	6
BP	GO:2001252	positive regulation of chromosome organization	0.003339	MAPK3/MAPK1/SREBF1/VEGFA/RB1/IL1B/CCNB1	7
BP	GO:0015980	energy derivation by oxidation of organic compounds	0.003353	NOS2/AKT1/CYP1A2/INSR/CAT/HIF1A/MYC/CCNB1/IGF2	9
BP	GO:0030728	ovulation	0.003353	PTGS2/PGR/NOS3	3

BP	GO:0032332	positive regulation of chondrocyte differentiation	0.003353	RELA/POR/RUNX2	3
BP	GO:0036499	PERK-mediated unfolded protein response	0.003353	CCL2/CXCL8/NFE2L2	3
BP	GO:0048305	immunoglobulin secretion	0.003353	IL6/IL2/CD40LG	3
BP	GO:0051900	regulation of mitochondrial depolarization	0.003353	BCL2/GOT1/PARP1	3

BP	GO:0071498	cellular response to fluid shear stress	0.003353	PTGS2/HAS2/NFE2L2	3
BP	GO:0090312	positive regulation of protein deacetylation	0.003353	SREBF1/VEGFA/IFNG	3
BP	GO:0022602	ovulation cycle process	0.003408	PGR/CASP3/ESR1/NOS3	4
BP	GO:0030850	prostate gland development	0.003408	RXRA/AR/ESR1/TP63	4

BP	GO:0090199	regulation of release of cytochrome c from mitochondria	0.003408	BAX/ AKT1/ BCL2L1/ MMP9	4
BP	GO:1990928	response to amino acid starvation	0.003408	MAPK8/ MAPK3/ MAPK1/ CDKN1A	4
BP	GO:0032088	negative regulation of NF-kappaB transcription factor activity	0.003447	CYP1B1/ CAT/ IL10/ NFKBIA/ CHUK	5
BP	GO:0002768	immune response-regulating cell surface receptor signaling pathway	0.003559	BCL2/ BAX/ JUN/ RELA/ IKBKB/ MAPK8/ MAPK3/ MAPK1/ FOS/ RAF1/ PRKCB/ CHUK	12

BP	GO:0009108	coenzyme biosynthetic process	0.003597	PTGS2/INSR/FASN/PPARA/EIF6/HIF1A/ ACACA/HK2	8
BP	GO:0071158	positive regulation of cell cycle arrest	0.003634	BAX/CDKN1A/CCNB1/CHEK2/E2F1	5
BP	GO:0003254	regulation of membrane depolarization	0.003662	SCN5A/BCL2/GOT1/PARP1	4
BP	GO:0010712	regulation of collagen metabolic process	0.003662	PPARG/GOT1/IL6/PPARD	4

BP	GO:0043470	regulation of carbohydrate catabolic process	0.003662	INSR/PPARA/EIF6/HIF1A	4
BP	GO:0051972	regulation of telomerase activity	0.003662	PPARG/MAPK3/MAPK1/MYC	4
BP	GO:1904707	positive regulation of vascular smooth muscle cell proliferation	0.003662	JUN/MMP2/MMP9/IL10	4
BP	GO:0072331	signal transduction by p53 class mediator	0.003683	BCL2/BAX/AKT1/CDKN1A/TP63/CCNB1/ CHEK2/E2F1	8

BP	GO:0006986	response to unfolded protein	0.003765	BAX/CCND1/CCL2/CXCL8/HSPB1/NFE2L 2/HSF1	7
BP	GO:0009235	cobalamin metabolic process	0.003784	PRSS1/ABCC1/CTRB1	3
BP	GO:0032373	positive regulation of sterol transport	0.003784	PON1/ADIPOQ/NFKBIA	3
BP	GO:0032376	positive regulation of cholesterol transport	0.003784	PON1/ADIPOQ/NFKBIA	3

BP	GO:0042573	retinoic acid metabolic process	0.003784	CYP1A1/AKR1C3/UGT1A1	3
BP	GO:0050995	negative regulation of lipid catabolic process	0.003784	AKT1/ADRA2A/IL1B	3
BP	GO:1901685	glutathione derivative metabolic process	0.003784	GSTP1/GSTM1/GSTM2	3
BP	GO:1901687	glutathione derivative biosynthetic process	0.003784	GSTP1/GSTM1/GSTM2	3

BP	GO:0007260	tyrosine phosphorylation of STAT protein	0.003786	IL6/CAV1/IL2/IFNG/HSF1	5
BP	GO:0046849	bone remodeling	0.003786	ADRB2/PRKCA/EGFR/IL6/SPP1	5
BP	GO:0048546	digestive tract morphogenesis	0.003919	BCL2/EGFR/TP63/HIF1A	4
BP	GO:0046031	ADP metabolic process	0.003982	INSR/PPARA/EIF6/HIF1A/HK2	5

BP	GO:0051781	positive regulation of cell division	0.003982	CAT/VEGFA/IL1B/IL1A/IGF2	5
BP	GO:0055072	iron ion homeostasis	0.003982	HMOX1/SOD1/HIF1A/MYC/ABCG2	5
BP	GO:0071482	cellular response to light stimulus	0.003982	PTGS2/BAX/CASP9/CDKN1A/MYC/PARP 1	6
BP	GO:0050769	positive regulation of neurogenesis	0.004061	OPRM1/BCL2/PPARG/RELA/NCOA1/VE GFA/IL6/HIF1A/IL1B/IL2/NFE2L2/E2F1	12

BP	GO:0034765	regulation of ion transmembrane transport	0.004134	KCNH2/SCN5A/ ADRB2/OPRM1/BAX/ AK T1/GSTM2/ ADRA2A/MMP9/CAV1/CXCL1 1/CXCL10	12
BP	GO:0045445	myoblast differentiation	0.004179	HMGCR/RB1/PPARD/CXCL10/IGFBP3	5
BP	GO:0071674	mononuclear cell migration	0.004179	MAPK3/IL6/CCL2/SERPINE1/CXCL10	5
BP	GO:1902803	regulation of synaptic vesicle transport	0.004179	ADRA1A/CHRM2/MAP2/SLC2A4/PRKCB	5

BP	GO:0140014	mitotic nuclear division	0.004198	INSR/CCND1/EGF/RB1/IL1B/CCNB1/IL1A/CHEK2/IGF2	9
BP	GO:0009110	vitamin biosynthetic process	0.004246	CYP3A4/IL1B/IFNG	3
BP	GO:0010640	regulation of platelet-derived growth factor receptor signaling pathway	0.004246	F7/ADIPOQ/F3	3
BP	GO:0034695	response to prostaglandin E	0.004246	PPARG/AKT1/ACACA	3

BP	GO:0051882	mitochondrial depolarization	0.004246	BCL2/GOT1/PARP1	3
BP	GO:0072215	regulation of metanephros development	0.004246	STAT1/ADIPOQ/MYC	3
BP	GO:1903649	regulation of cytoplasmic transport	0.004246	MAP2/MAPK3/MAPK1	3
BP	GO:1904031	positive regulation of cyclin-dependent protein kinase activity	0.004246	CCND1/CDKN1A/CCNB1	3

BP	GO:2000353	positive regulation of endothelial cell apoptotic process	0.004246	AKR1C3/CCL2/CD40LG	3
BP	GO:0009206	purine ribonucleoside triphosphate biosynthetic process	0.004268	INSR/PPARA/EIF6/HIF1A/PARP1/HK2	6
BP	GO:0051346	negative regulation of hydrolase activity	0.004402	PTGS2/MAP2/IKBKB/AKT1/SLPI/VEGFA/ MMP9/POR/RAF1/BIRC5/NOS3/SERPINE 1	12
BP	GO:0009145	purine nucleoside triphosphate biosynthetic process	0.004433	INSR/PPARA/EIF6/HIF1A/PARP1/HK2	6

BP	GO:0050709	negative regulation of protein secretion	0.004433	OPRM1/HMGCR/SREBF1/ADRA2A/IL10/IL1B	6
BP	GO:0048260	positive regulation of receptor-mediated endocytosis	0.004469	SELE/VEGFA/EGF/SERPINE1	4
BP	GO:0046486	glycerolipid metabolic process	0.004469	PON1/ACHE/ESR1/LDLR/CAT/APOB/SREBF1/EGFR/EGF/ERBB2/CAV1/ERBB3	12
BP	GO:1902275	regulation of chromatin organization	0.004473	MAPK8/MAPK3/SREBF1/VEGFA/IL1B/CCNB1/IGF2	7

BP	GO:0031589	cell-substrate adhesion	0.004542	BCL2/VCAM1/HAS2/PLAU/VEGFA/SERP1 NE1/COL1A1/COL3A1/PPARD/RASA1	10
BP	GO:0031058	positive regulation of histone modification	0.004568	MAPK3/SREBF1/VEGFA/IL1B/CCNB1	5
BP	GO:0042770	signal transduction in response to DNA damage	0.004712	BAX/CASP9/CDKN1A/CCNB1/CHEK2/E2 F1	6
BP	GO:0001516	prostaglandin biosynthetic process	0.004712	PTGS2/PTGS1/ AKR1C3	3

BP	GO:0001783	B cell apoptotic process	0.004712	BAX/IL10/IL2	3
BP	GO:0002092	positive regulation of receptor internalization	0.004712	SELE/VEGFA/EGF	3
BP	GO:0008210	estrogen metabolic process	0.004712	CYP1B1/UGT1A1/SULT1E1	3
BP	GO:0030878	thyroid gland development	0.004712	MAPK3/MAPK1/RAF1	3

BP	GO:0031639	plasminogen activation	0.004712	PLAU/PLAT/SERPINE1	3
BP	GO:0035666	TRIF-dependent toll-like receptor signaling pathway	0.004712	CASP8/IKBKB/CHUK	3
BP	GO:0042537	benzene-containing compound metabolic process	0.004712	GSTM1/GSTM2/UGT1A1	3
BP	GO:0042738	exogenous drug catabolic process	0.004712	CYP3A4/CYP1A2/NR1I2	3

BP	GO:0043457	regulation of cellular respiration	0.004712	NOS2/HIF1A/CCNB1	3
BP	GO:0046457	prostanoid biosynthetic process	0.004712	PTGS2/PTGS1/ AKR1C3	3
BP	GO:1900120	regulation of receptor binding	0.004712	ADIPOQ/MMP9/IL10	3
BP	GO:1903203	regulation of oxidative stress-induced neuron death	0.004712	IL10/HIF1A/PARP1	3

BP	GO:2000209	regulation of anoikis	0.004712	BCL2/CAV1/CHEK2	3
BP	GO:2000679	positive regulation of transcription regulatory region DNA binding	0.004712	RB1/IFNG/PARP1	3
BP	GO:0030199	collagen fibril organization	0.004712	CYP1B1/RB1/COL1A1/COL3A1	4
BP	GO:0031638	zymogen activation	0.004712	CASP8/PLAU/PLAT/SERPINE1	4

BP	GO:0032720	negative regulation of tumor necrosis factor production	0.004712	GSTP1/ADIPOQ/IL10/HSF1	4
BP	GO:0098930	axonal transport	0.004712	MAP2/SOD1/HIF1A/HSPB1	4
BP	GO:1903555	regulation of tumor necrosis factor superfamily cytokine production	0.004886	GSTP1/ADIPOQ/IL10/HSPB1/IFNG/HSF1	6
BP	GO:0009791	post-embryonic development	0.004961	BCL2/BAX/CYP1A2/APOB/VEGFA	5

BP	GO:1904063	negative regulation of cation transmembrane transport	0.004961	KCNH2/GSTM2/ADRA2A/MMP9/CAV1	5
BP	GO:0043331	response to dsRNA	0.00504	MAPK3/MAPK1/NFKBIA/CAV1	4
BP	GO:0043392	negative regulation of DNA binding	0.00504	JUN/HMOX1/NFKBIA/E2F1	4
BP	GO:0033157	regulation of intracellular protein transport	0.005189	PTGS2/CHRM1/MAPK1/SREBF1/ADIPOQ /ERBB2/IL1B/IFNG	8

BP	GO:0009201	ribonucleoside triphosphate biosynthetic process	0.005242	INSR/PPARA/EIF6/HIF1A/PARP1/HK2	6
BP	GO:0034620	cellular response to unfolded protein	0.005242	BAX/CCND1/CCL2/CXCL8/NFE2L2/HSF1	6
BP	GO:0006898	receptor-mediated endocytosis	0.005242	ADRB2/ACHE/SELE/LDLR/APOB/VEGFA/EGF/CAV1/CXCL8/SERPINE1	10
BP	GO:0006309	apoptotic DNA fragmentation	0.005242	BAX/CASP3/HSF1	3

BP	GO:0032461	positive regulation of protein oligomerization	0.005242	BAX/MMP1/MMP3	3
BP	GO:0034114	regulation of heterotypic cell-cell adhesion	0.005242	ADIPOQ/IL10/IL1B	3
BP	GO:0036475	neuron death in response to oxidative stress	0.005242	IL10/HIF1A/PARP1	3
BP	GO:0060330	regulation of response to interferon-gamma	0.005242	PPARG/STAT1/IFNG	3

BP	GO:0060334	regulation of interferon-gamma-mediated signaling pathway	0.005242	PPARG/STAT1/IFNG	3
BP	GO:0060444	branching involved in mammary gland duct morphogenesis	0.005242	PGR/ AR/ ESR1	3
BP	GO:0051224	negative regulation of protein transport	0.005258	OPRM1/HMGCR/SREBF1/ ADIPOQ/ ADRA 2A/IL10/IL1B	7
BP	GO:0045123	cellular extravasation	0.005339	ICAM1/SELE/VCAM1/CCL2	4

BP	GO:0090183	regulation of kidney development	0.005339	STAT1/ADIPOQ/VEGFA/MYC	4
BP	GO:1903556	negative regulation of tumor necrosis factor superfamily cytokine production	0.005339	GSTP1/ADIPOQ/IL10/HSF1	4
BP	GO:0019058	viral life cycle	0.005362	BCL2/ICAM1/SLPI/LDLR/EGFR/CAV1/CL2/CXCL8/TOP2A	9
BP	GO:1905330	regulation of morphogenesis of an epithelium	0.005393	RXRA/AR/STAT1/ESR1/VEGFA/CXCL10	6

BP	GO:0043409	negative regulation of MAPK cascade	0.005398	AKT1/GSTP1/HMGCR/ADIPOQ/CAV1/MYC/IL1B	7
BP	GO:0030217	T cell differentiation	0.005398	BCL2/SOD1/IL6/ERBB2/IL2/IFNG/RUNX2/IRF1	8
BP	GO:0006959	humoral immune response	0.005546	BCL2/SLPI/IL6/CCL2/CXCL8/IFNG/CXCL11/CXCL2/CRP/CXCL10	10
BP	GO:0002792	negative regulation of peptide secretion	0.005578	OPRM1/HMGCR/SREBF1/ADRA2A/IL10/IL1B	6

BP	GO:0071706	tumor necrosis factor superfamily cytokine production	0.005578	GSTP1/ADIPOQ/IL10/HSPB1/IFNG/HSF1	6
BP	GO:0006165	nucleoside diphosphate phosphorylation	0.005633	INSR/PPARA/EIF6/HIF1A/HK2	5
BP	GO:0032922	circadian regulation of gene expression	0.00567	NCOA2/AHR/PPARA/TOP1	4
BP	GO:0051196	regulation of coenzyme metabolic process	0.00567	INSR/PPARA/EIF6/HIF1A	4

BP	GO:1904950	negative regulation of establishment of protein localization	0.005711	OPRM1/HMGCR/SREBF1/ADIPOQ/ADRA2A/IL10/IL1B	7
BP	GO:0001654	eye development	0.005751	RXRA/BCL2/BAX/JUN/ACHE/CYP1A1/CYP1B1/EGFR/VEGFA/HIF1A	10
BP	GO:1904064	positive regulation of cation transmembrane transport	0.005764	KCNH2/ADRB2/BAX/GSTM2/CXCL11/CXCL10	6
BP	GO:0002053	positive regulation of mesenchymal cell proliferation	0.005778	STAT1/VEGFA/MYC	3

BP	GO:0031063	regulation of histone deacetylation	0.005778	MAPK8/SREBF1/VEGFA	3
BP	GO:0042953	lipoprotein transport	0.005778	PPARG/APOB/PRKCB	3
BP	GO:0044872	lipoprotein localization	0.005778	PPARG/APOB/PRKCB	3
BP	GO:0051194	positive regulation of cofactor metabolic process	0.005778	INSR/HIF1A/NFE2L2	3

BP	GO:0060669	embryonic placenta morphogenesis	0.005778	NCOA1/IL10/IGF2	3
BP	GO:0150063	visual system development	0.005836	RXRA/BCL2/BAX/JUN/ACHE/CYP1A1/C YP1B1/EGFR/VEGFA/HIF1A	10
BP	GO:0006942	regulation of striated muscle contraction	0.005843	SCN5A/ADRA1A/ADRA1B/GSTM2/CAV1	5
BP	GO:1903076	regulation of protein localization to plasma membrane	0.005843	AR/AKT1/EGFR/BCL2L1/IFNG	5

BP	GO:0010656	negative regulation of muscle cell apoptotic process	0.005991	HMOX1/HMGCR/NFE2L2/HSF1	4
BP	GO:0060688	regulation of morphogenesis of a branching structure	0.005991	RXRA/AR/ESR1/VEGFA	4
BP	GO:0086002	cardiac muscle cell action potential involved in contraction	0.005991	KCNH2/SCN5A/CAV1/GJA1	4
BP	GO:0009152	purine ribonucleotide biosynthetic process	0.006056	INSR/FASN/PPARA/EIF6/HIF1A/ACACA/PARP1/HK2	8

BP	GO:0046939	nucleotide phosphorylation	0.006097	INSR/PPARA/EIF6/HIF1A/HK2	5
BP	GO:1905269	positive regulation of chromatin organization	0.006097	MAPK3/SREBF1/VEGFA/IL1B/CCNB1	5
BP	GO:0000280	nuclear division	0.006103	INSR/CCND1/EGF/RB1/IL1B/CCNB1/IL1A/TOP2A/CHEK2/HSF1/IGF2	11
BP	GO:0071322	cellular response to carbohydrate stimulus	0.006124	ICAM1/HMGCR/ADRA2A/RAF1/HIF1A/PKCB	6

BP	GO:0046626	regulation of insulin receptor signaling pathway	0.006358	RELA/IL1B/PRKCB/IGF2	4
BP	GO:0070228	regulation of lymphocyte apoptotic process	0.006358	BAX/IL10/HIF1A/IL2	4
BP	GO:0002367	cytokine production involved in immune response	0.006358	HMOX1/MAPK3/IL10/IL6/IL1B	5
BP	GO:0060191	regulation of lipase activity	0.006358	ADRA1A/SELE/ESR1/EGFR/POR	5

BP	GO:0002756	MyD88-independent toll-like receptor signaling pathway	0.006361	CASP8/IKBKB/CHUK	3
BP	GO:0007176	regulation of epidermal growth factor-activated receptor activity	0.006361	ADRA2A/EGF/NCF1	3
BP	GO:0045932	negative regulation of muscle contraction	0.006361	PTGS2/ADRB2/SOD1	3
BP	GO:0071280	cellular response to copper ion	0.006361	CYP1A2/CYP1A1/HSF1	3

BP	GO:0048880	sensory system development	0.006374	RXRA/BCL2/BAX/JUN/ACHE/CYP1A1/CYP1B1/EGFR/VEGFA/HIF1A	10
BP	GO:0035966	response to topologically incorrect protein	0.006499	BAX/CCND1/CCL2/CXCL8/HSPB1/NFE2L2/HSF1	7
BP	GO:0072073	kidney epithelium development	0.006529	BCL2/STAT1/CAT/ADIPOQ/VEGFA/MYC	6
BP	GO:0009135	purine nucleoside diphosphate metabolic process	0.006611	INSR/PPARA/EIF6/HIF1A/HK2	5

BP	GO:0009179	purine ribonucleoside diphosphate metabolic process	0.006611	INSR/PPARA/EIF6/HIF1A/HK2	5
BP	GO:0001885	endothelial cell development	0.00671	IKBKB/ICAM1/FASN/IL1B	4
BP	GO:0010518	positive regulation of phospholipase activity	0.00671	ADRA1A/SELE/ESR1/EGFR	4
BP	GO:0030520	intracellular estrogen receptor signaling pathway	0.00671	AR/ESR1/TP63/PARP1	4

BP	GO:0007612	learning	0.00672	PTGS2/JUN/INSR/HMGCR/FOS/HIF1A	6
BP	GO:0009127	purine nucleoside monophosphate biosynthetic process	0.00672	INSR/PPARA/EIF6/HIF1A/PARP1/HK2	6
BP	GO:0009168	purine ribonucleoside monophosphate biosynthetic process	0.00672	INSR/PPARA/EIF6/HIF1A/PARP1/HK2	6
BP	GO:0051588	regulation of neurotransmitter transport	0.00672	ADRA1A/CHRM2/SLC6A4/ABAT/MAOB/ PRKCB	6

BP	GO:0021782	glial cell development	0.006876	AKT1/GSTP1/LDLR/SOD1/EGFR	5
BP	GO:0043010	camera-type eye development	0.006942	RXRA/BAX/JUN/ACHE/CYP1A1/CYP1B1/ EGFR/VEGFA/HIF1A	9
BP	GO:0001678	cellular glucose homeostasis	0.006942	ICAM1/HMGCR/ADRA2A/RAF1/HIF1A/ HK2	6
BP	GO:0044344	cellular response to fibroblast growth factor stimulus	0.006942	MAPK3/MAPK1/CCL2/CXCL8/COL1A1/R UNX2	6

BP	GO:0006790	sulfur compound metabolic process	0.006957	GSTP1/GSTM1/GSTM2/FASN/SOD1/GSR/ ACACA/SULT1E1/NFE2L2/ACPP	10
BP	GO:0005979	regulation of glycogen biosynthetic process	0.006957	AKT1/INSR/IGF2	3
BP	GO:0008209	androgen metabolic process	0.006957	CYP3A4/ESR1/SPP1	3
BP	GO:0009065	glutamine family amino acid catabolic process	0.006957	NOS2/GOT1/NOS3	3

BP	GO:0010962	regulation of glucan biosynthetic process	0.006957	AKT1/INSR/IGF2	3
BP	GO:0032647	regulation of interferon-alpha production	0.006957	STAT1/IL10/CHUK	3
BP	GO:0072678	T cell migration	0.007065	ICAM1/CCL2/CXCL11/CXCL10	4
BP	GO:0009185	ribonucleoside diphosphate metabolic process	0.007126	INSR/PPARA/EIF6/HIF1A/HK2	5

BP	GO:1902106	negative regulation of leukocyte differentiation	0.007126	ADIPOQ/ERBB2/MYC/IL2/IRF1	5
BP	GO:0010948	negative regulation of cell cycle process	0.007194	BCL2/BAX/CCND1/CDKN1A/RB1/CCL2/ CCNB1/CHEK2/E2F1	9
BP	GO:0008593	regulation of Notch signaling pathway	0.007432	AKT1/EGFR/EGF/TP63/NFKBIA	5
BP	GO:0044264	cellular polysaccharide metabolic process	0.007432	AKT1/HAS2/INSR/MGAM/IGF2	5

BP	GO:0009142	nucleoside triphosphate biosynthetic process	0.007621	INSR/PPARA/EIF6/HIF1A/PARP1/HK2	6
BP	GO:0019362	pyridine nucleotide metabolic process	0.007621	PTGS2/INSR/PPARA/EIF6/HIF1A/HK2	6
BP	GO:0046496	nicotinamide nucleotide metabolic process	0.007621	PTGS2/INSR/PPARA/EIF6/HIF1A/HK2	6
BP	GO:0007271	synaptic transmission, cholinergic	0.007631	CHRM3/ACHE/NQO1	3

BP	GO:0008299	isoprenoid biosynthetic process	0.007631	CYP1A1/AKR1C3/HMGCR	3
BP	GO:0032607	interferon-alpha production	0.007631	STAT1/IL10/CHUK	3
BP	GO:0046320	regulation of fatty acid oxidation	0.007631	PPARG/AKT1/PPARA	3
BP	GO:0000077	DNA damage checkpoint	0.007858	BAX/CCND1/CDKN1A/CCNB1/CHEK2/E 2F1	6

BP	GO:1900076	regulation of cellular response to insulin stimulus	0.0079	RELA/IL1B/PRKCB/IGF2	4
BP	GO:0006575	cellular modified amino acid metabolic process	0.00798	GSTP1/GSTM1/GSTM2/SOD1/GSR/POR/NFE2L2	7
BP	GO:0006641	triglyceride metabolic process	0.008035	LDLR/CAT/APOB/SREBF1/CAV1	5
BP	GO:0046632	alpha-beta T cell differentiation	0.008035	BCL2/IL6/IL2/IFNG/IRF1	5

BP	GO:0009260	ribonucleotide biosynthetic process	0.008271	INSR/FASN/PPARA/EIF6/HIF1A/ACACA/PARP1/HK2	8
BP	GO:0035773	insulin secretion involved in cellular response to glucose stimulus	0.008346	HMGCR/ADRA2A/RAF1/HIF1A	4
BP	GO:0048645	animal organ formation	0.008346	AR/MAPK3/MAPK1/TP63	4
BP	GO:0034767	positive regulation of ion transmembrane transport	0.008357	KCNH2/ADRB2/BAX/GSTM2/CXCL11/CXCL10	6

BP	GO:0007202	activation of phospholipase C activity	0.008357	ADRA1A/SELE/EGFR	3
BP	GO:0048863	stem cell differentiation	0.008392	ESR1/MAPK3/MAPK1/TP63/HIF1A/NFE2L2/RUNX2	7
BP	GO:0060562	epithelial tube morphogenesis	0.008605	PGR/BCL2/ AR/ESR1/VEGFA/EGF/HIF1A/MYC/CXCL10	9
BP	GO:0002673	regulation of acute inflammatory response	0.008617	PTGS2/PPARG/GSTP1/IL6/IL1B/PTGER3	6

BP	GO:1901990	regulation of mitotic cell cycle phase transition	0.008764	BCL2/BAX/CYP1A1/CCND1/CDKN1A/RB1/CCL2/CCNB1/CHEK2/E2F1	10
BP	GO:0002637	regulation of immunoglobulin production	0.008782	IL10/IL6/IL2/CD40LG	4
BP	GO:0008088	axo-dendritic transport	0.008782	MAP2/SOD1/HIF1A/HSPB1	4
BP	GO:0010676	positive regulation of cellular carbohydrate metabolic process	0.008782	AKT1/INSR/PPARA/IGF2	4

BP	GO:0050891	multicellular organismal water homeostasis	0.008782	HAS2/AKR1B1/TP63/CLDN4	4
BP	GO:0072524	pyridine-containin g compound metabolic process	0.008868	PTGS2/INSR/PPARA/EIF6/HIF1A/HK2	6
BP	GO:0030330	DNA damage response, signal transduction by p53 class mediator	0.009007	BAX/CDKN1A/CCNB1/CHEK2/E2F1	5
BP	GO:0045185	maintenance of protein location	0.009007	AKT1/IL10/NFKBIA/CAV1/HK2	5

BP	GO:2000278	regulation of DNA biosynthetic process	0.009007	PPARG/MAPK3/MAPK1/ADIPOQ/MYC	5
BP	GO:0001963	synaptic transmission, dopaminergic	0.00906	PTGS2/SLC6A4/SLC6A2	3
BP	GO:0006691	leukotriene metabolic process	0.00906	ALOX5/ABCC1/LTA4H	3
BP	GO:0007190	activation of adenylate cyclase activity	0.00906	ADRB2/ADRB1/RAF1	3

BP	GO:0045589	regulation of regulatory T cell differentiation	0.00906	IL2/IFNG/IRF1	3
BP	GO:0048873	homeostasis of number of cells within a tissue	0.00906	BCL2/BAX/NOS3	3
BP	GO:0055094	response to lipoprotein particle	0.00906	PPARG/AKT1/LDLR	3
BP	GO:1900745	positive regulation of p38MAPK cascade	0.00906	VEGFA/IL1B/NCF1	3

BP	GO:0035967	cellular response to topologically incorrect protein	0.00909	BAX/CCND1/CCL2/CXCL8/NFE2L2/HSF1	6
BP	GO:0002548	monocyte chemotaxis	0.009203	IL6/CCL2/SERPINE1/CXCL10	4
BP	GO:0016239	positive regulation of macroautophagy	0.009203	ADRB2/HMOX1/MAPK3/HIF1A	4
BP	GO:0090150	establishment of protein localization to membrane	0.009213	BCL2/BAX/CASP8/MAPK8/EGFR/TP63/E RBB2/NCF1/E2F1	9

BP	GO:0046434	organophosphate catabolic process	0.009213	PON1/INSR/LDLR/PPARA/EIF6/HIF1A/H K2	7
BP	GO:0032526	response to retinoic acid	0.00929	RXRA/SLC6A4/PPARG/SREBF1/COL1A1	5
BP	GO:0072676	lymphocyte migration	0.00929	AKT1/ICAM1/CCL2/CXCL11/CXCL10	5
BP	GO:0046390	ribose phosphate biosynthetic process	0.009327	INSR/FASN/PPARA/EIF6/HIF1A/ACACA /PARP1/HK2	8

BP	GO:0016052	carbohydrate catabolic process	0.009337	INSR/PPARA/EIF6/HIF1A/MGAM/HK2	6
BP	GO:0050868	negative regulation of T cell activation	0.009656	CASP3/IL10/ERBB2/IL2/IRF1	5
BP	GO:0002223	stimulatory C-type lectin receptor signaling pathway	0.009665	RELA/IKBKB/RAF1/CHUK	4
BP	GO:0032481	positive regulation of type I interferon production	0.009665	RELA/STAT1/CHUK/IRF1	4

BP	GO:0033627	cell adhesion mediated by integrin	0.009665	ICAM1/CYP1B1/PLAU/SERPINE1	4
BP	GO:0061036	positive regulation of cartilage development	0.009813	RELA/POR/RUNX2	3
BP	GO:0061418	regulation of transcription from RNA polymerase II promoter in response to hypoxia	0.009813	VEGFA/HIF1A/NFE2L2	3
BP	GO:0071549	cellular response to dexamethasone stimulus	0.009813	CASP9/ICAM1/EGFR	3

BP	GO:0050918	positive chemotaxis	0.010185	F7/VEGFA/F3/CXCL8	4
BP	GO:0009156	ribonucleoside monophosphate biosynthetic process	0.010214	INSR/PPARA/EIF6/HIF1A/PARP1/HK2	6
BP	GO:0034976	response to endoplasmic reticulum stress	0.010389	BCL2/BAX/JUN/CCND1/CAV1/CCL2/CX CL8/NFE2L2	8
BP	GO:0000737	DNA catabolic process, endonucleolytic	0.010621	BAX/CASP3/HSF1	3

BP	GO:0033028	myeloid cell apoptotic process	0.010621	BCL2/ADIPOQ/IL6	3
BP	GO:0033198	response to ATP	0.010621	PTGS2/SOD1/IL1B	3
BP	GO:0045066	regulatory T cell differentiation	0.010621	IL2/IFNG/IRF1	3
BP	GO:0045730	respiratory burst	0.010621	INSR/MPO/NCF1	3

BP	GO:0060251	regulation of glial cell proliferation	0.010621	IL6/IL1B/E2F1	3
BP	GO:0060603	mammary gland duct morphogenesis	0.010621	PGR/ AR/ ESR1	3
BP	GO:0070873	regulation of glycogen metabolic process	0.010621	AKT1/INSR/IGF2	3
BP	GO:0071402	cellular response to lipoprotein particle stimulus	0.010621	PPARG/ AKT1/ LDLR	3

BP	GO:0010810	regulation of cell-substrate adhesion	0.010621	BCL2/HAS2/PLAU/VEGFA/SERPINE1/CO L1A1/RASA1	7
BP	GO:0030104	water homeostasis	0.010621	HAS2/AKR1B1/TP63/CLDN4	4
BP	GO:0045454	cell redox homeostasis	0.010621	NOS2/GSR/NOS3/NFE2L2	4
BP	GO:0046824	positive regulation of nucleocytoplasmic transport	0.010621	PTGS2/MAPK1/IL1B/IFNG	4

BP	GO:0086003	cardiac muscle cell contraction	0.010621	KCNH2/SCN5A/CAV1/GJA1	4
BP	GO:1903672	positive regulation of sprouting angiogenesis	0.010621	PTGS2/HMOX1/VEGFA/IL10	4
BP	GO:0015696	ammonium transport	0.010674	SLC6A4/SLC6A2/ABAT/SLC6A3/MAOB	5
BP	GO:0046916	cellular transition metal ion homeostasis	0.010674	HMOX1/SOD1/HIF1A/MYC/ABCG2	5

BP	GO:0072009	nephron epithelium development	0.010674	BCL2/STAT1/ADIPOQ/VEGFA/MYC	5
BP	GO:0006606	protein import into nucleus	0.010721	PTGS2/AKT1/AKR1C3/MAPK1/NFKBIA/I FNG	6
BP	GO:0010721	negative regulation of cell development	0.010792	SLC6A4/BCL2/MAP2/LDLR/PPARA/IL6/I L1B/COL3A1/SPP1	9
BP	GO:0001820	serotonin secretion	0.010792	SLC6A4/MAOB	2

BP	GO:0010749	regulation of nitric oxide mediated signal transduction	0.010792	EGFR/VEGFA	2
BP	GO:0010838	positive regulation of keratinocyte proliferation	0.010792	HAS2/TP63	2
BP	GO:0016102	diterpenoid biosynthetic process	0.010792	CYP1A1/AKR1C3	2
BP	GO:0021924	cell proliferation in external granule layer	0.010792	SLC6A4/EGF	2

BP	GO:0021930	cerebellar granule cell precursor proliferation	0.010792	SLC6A4/EGF	2
BP	GO:0021936	regulation of cerebellar granule cell precursor proliferation	0.010792	SLC6A4/EGF	2
BP	GO:0031284	positive regulation of guanylate cyclase activity	0.010792	NOS2/NOS3	2
BP	GO:0033148	positive regulation of intracellular estrogen receptor signaling pathway	0.010792	AR/PARP1	2

BP	GO:0033240	positive regulation of cellular amine metabolic process	0.010792	ABAT/MAOB	2
BP	GO:0033327	Leydig cell differentiation	0.010792	AR/CCND1	2
BP	GO:0034378	chylomicron assembly	0.010792	MTTP/APOB	2
BP	GO:0035865	cellular response to potassium ion	0.010792	SOD1/HSF1	2

BP	GO:0045073	regulation of chemokine biosynthetic process	0.010792	HMOX1/IL6	2
BP	GO:0045713	low-density lipoprotein particle receptor biosynthetic process	0.010792	PPARG/ADIPOQ	2
BP	GO:0051918	negative regulation of fibrinolysis	0.010792	THBD/SERPINE1	2
BP	GO:0060068	vagina development	0.010792	BAX/ESR1	2

BP	GO:0060352	cell adhesion molecule production	0.010792	CAV1/IL1B	2
BP	GO:0060513	prostatic bud formation	0.010792	AR/TP63	2
BP	GO:0060736	prostate gland growth	0.010792	AR/ESR1	2
BP	GO:0072203	cell proliferation involved in metanephros development	0.010792	STAT1/MYC	2

BP	GO:0090205	positive regulation of cholesterol metabolic process	0.010792	SREBF1/POR	2
BP	GO:0090557	establishment of endothelial intestinal barrier	0.010792	ICAM1/FASN	2
BP	GO:0150065	regulation of deacetylase activity	0.010792	MAPK8/VEGFA	2
BP	GO:1902510	regulation of apoptotic DNA fragmentation	0.010792	BAX/HSF1	2

BP	GO:1904526	regulation of microtubule binding	0.010792	MAP2/HSF1	2
BP	GO:2001269	positive regulation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway	0.010792	BAX/CASP8	2
BP	GO:0090316	positive regulation of intracellular protein transport	0.010833	PTGS2/CHRM1/MAPK1/ERBB2/IL1B/IFNG	6
BP	GO:0002220	innate immune response activating cell surface receptor signaling pathway	0.01092	RELA/IKBKB/RAF1/CHUK	4

BP	GO:0033692	cellular polysaccharide biosynthetic process	0.01092	AKT1/HAS2/INSR/IGF2	4
BP	GO:0051187	cofactor catabolic process	0.01092	HMOX1/CAT/UGT1A1/MPO	4
BP	GO:0006836	neurotransmitter transport	0.010959	ADRA1A/CHRM2/SLC6A4/SLC6A2/ABAT /SLC6A3/MAOB/PRKCB	8
BP	GO:0050806	positive regulation of synaptic transmission	0.011133	PTGS2/ADRA1A/ADRB2/MAPK1/ABAT/E GFR	6

BP	GO:0034504	protein localization to nucleus	0.011156	PTGS2/AKT1/AKR1C3/MAPK1/NFKBIA/COL1A1/IFNG/PARP1	8
BP	GO:0010464	regulation of mesenchymal cell proliferation	0.011156	STAT1/VEGFA/MYC	3
BP	GO:0032148	activation of protein kinase B activity	0.011156	AKT1/INSR/ADRA2A	3
BP	GO:0046627	negative regulation of insulin receptor signaling pathway	0.011156	RELA/IL1B/PRKCB	3

BP	GO:0071868	cellular response to monoamine stimulus	0.011156	MAPK3/MAPK1/ADIPOQ	3
BP	GO:0071870	cellular response to catecholamine stimulus	0.011156	MAPK3/MAPK1/ADIPOQ	3
BP	GO:1900077	negative regulation of cellular response to insulin stimulus	0.011156	RELA/IL1B/PRKCB	3
BP	GO:2000352	negative regulation of endothelial cell apoptotic process	0.011156	ICAM1/SERPINE1/NFE2L2	3

BP	GO:0030218	erythrocyte differentiation	0.011158	CASP3/STAT1/VEGFA/RB1/HIF1A	5
BP	GO:0046854	phosphatidylinosit ol phosphorylation	0.011158	ESR1/EGFR/EGF/ERBB2/ERBB3	5
BP	GO:0099565	chemical synaptic transmission, postsynaptic	0.011158	ADRB2/CHRNA2/OPRM1/AKT1/ABAT	5
BP	GO:1904375	regulation of protein localization to cell periphery	0.011158	AR/AKT1/EGFR/BCL2L1/IFNG	5

BP	GO:0048285	organelle fission	0.011323	INSR/CCND1/EGF/RB1/IL1B/CCNB1/IL1A/TOP2A/CHEK2/HSF1/IGF2	11
BP	GO:0007254	JNK cascade	0.011323	AKT1/MAPK8/GSTP1/EGFR/IL1B/NCF1/CD40LG	7
BP	GO:0010517	regulation of phospholipase activity	0.011365	ADRA1A/SELE/ESR1/EGFR	4
BP	GO:0048708	astrocyte differentiation	0.011365	MAPK3/MAPK1/LDLR/EGFR	4

BP	GO:0051817	modification of morphology or physiology of other organism involved in symbiotic interaction	0.011553	RXRA/JUN/CASP8/INSR/BCL2L1	5
BP	GO:0032388	positive regulation of intracellular transport	0.011583	PTGS2/CHRM1/MAP2/MAPK1/ERBB2/IL1B/IFNG	7
BP	GO:0014068	positive regulation of phosphatidylinositol 3-kinase signaling	0.011878	CAT/NCF1/PPARD/ERBB3	4
BP	GO:0030521	androgen receptor signaling pathway	0.011878	AR/NR1I3/NCOA1/RB1	4

BP	GO:0032945	negative regulation of mononuclear cell proliferation	0.011878	CASP3/IL10/ERBB2/IL2	4
BP	GO:0042531	positive regulation of tyrosine phosphorylation of STAT protein	0.011878	IL6/IL2/IFNG/HSF1	4
BP	GO:0050672	negative regulation of lymphocyte proliferation	0.011878	CASP3/IL10/ERBB2/IL2	4
BP	GO:0060193	positive regulation of lipase activity	0.011878	ADRA1A/SELE/ESR1/EGFR	4

BP	GO:0070988	demethylation	0.011878	CYP3A4/CYP1A2/CYP1A1/POR	4
BP	GO:1904427	positive regulation of calcium ion transmembrane transport	0.011878	BAX/GSTM2/CXCL11/CXCL10	4
BP	GO:0006090	pyruvate metabolic process	0.011878	INSR/PPARA/EIF6/HIF1A/HK2	5
BP	GO:0032479	regulation of type I interferon production	0.011878	RELA/STAT1/IL10/CHUK/IRF1	5

BP	GO:0042303	molting cycle	0.011878	PTGS2/BCL2/RELA/EGFR/TP63	5
BP	GO:0042633	hair cycle	0.011878	PTGS2/BCL2/RELA/EGFR/TP63	5
BP	GO:0032365	intracellular lipid transport	0.011878	LDLR/CES1/ACACA	3
BP	GO:0033280	response to vitamin D	0.011878	PTGS2/CXCL10/SPP1	3

BP	GO:0045777	positive regulation of blood pressure	0.011878	ADRA1A/ADRA1B/ADRB1	3
BP	GO:0070423	nucleotide-binding oligomerization domain containing signaling pathway	0.011878	CASP8/RELA/NFKBIA	3
BP	GO:1905898	positive regulation of response to endoplasmic reticulum stress	0.011878	BAX/CAV1/NFE2L2	3
BP	GO:2001024	negative regulation of response to drug	0.011878	ABAT/IL10/NFE2L2	3

BP	GO:2001038	regulation of cellular response to drug	0.011878	NCOA1/IL10/NFE2L2	3
BP	GO:0043902	positive regulation of multi-organism process	0.011878	JUN/PRKCA/NOS2/MAPK3/IFNG/TOP2A	6
BP	GO:0030307	positive regulation of cell growth	0.01223	BCL2/AKT1/EGFR/VEGFA/ERBB2/IL2	6
BP	GO:0032606	type I interferon production	0.012259	RELA/STAT1/IL10/CHUK/IRF1	5

BP	GO:0015893	drug transport	0.012297	SLC6A2/NR1I2/ ABCC1/ ABAT/SLC6A3/MYC/ABCG2	7
BP	GO:0061844	antimicrobial humoral immune response mediated by antimicrobial peptide	0.012367	CXCL8/CXCL11/CXCL2/CXCL10	4
BP	GO:0006265	DNA topological change	0.012508	TOP1/TOP2A	2
BP	GO:0010269	response to selenium ion	0.012508	APOB/MAOB	2

BP	GO:0016264	gap junction assembly	0.012508	CAV1/GJA1	2
BP	GO:0021534	cell proliferation in hindbrain	0.012508	SLC6A4/EGF	2
BP	GO:0031442	positive regulation of mRNA 3'-end processing	0.012508	CCNB1/HSF1	2
BP	GO:0032494	response to peptidoglycan	0.012508	RELA/IL6	2

BP	GO:0033629	negative regulation of cell adhesion mediated by integrin	0.012508	CYP1B1/SERPINE1	2
BP	GO:0034115	negative regulation of heterotypic cell-cell adhesion	0.012508	ADIPOQ/IL10	2
BP	GO:0040015	negative regulation of multicellular organism growth	0.012508	ADRB2/ADRB1	2
BP	GO:0042033	chemokine biosynthetic process	0.012508	HMOX1/IL6	2

BP	GO:0045945	positive regulation of transcription by RNA polymerase III	0.012508	AR/ERBB2	2
BP	GO:0050755	chemokine metabolic process	0.012508	HMOX1/IL6	2
BP	GO:0051024	positive regulation of immunoglobulin secretion	0.012508	IL6/IL2	2
BP	GO:0060439	trachea morphogenesis	0.012508	MAPK3/MAPK1	2

BP	GO:0061307	cardiac neural crest cell differentiation involved in heart development	0.012508	MAPK3/MAPK1	2
BP	GO:0061308	cardiac neural crest cell development involved in heart development	0.012508	MAPK3/MAPK1	2
BP	GO:0070587	regulation of cell-cell adhesion involved in gastrulation	0.012508	ADIPOQ/IL10	2
BP	GO:0070673	response to interleukin-18	0.012508	AKT1/ALOX5	2

BP	GO:0071281	cellular response to iron ion	0.012508	HMOX1/CCNB1	2
BP	GO:0071639	positive regulation of monocyte chemotactic protein-1 production	0.012508	ADIPOQ/IL1B	2
BP	GO:0006692	prostanoid metabolic process	0.01261	PTGS2/PTGS1/ AKR1C3	3
BP	GO:0006693	prostaglandin metabolic process	0.01261	PTGS2/PTGS1/ AKR1C3	3

BP	GO:0035872	nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway	0.01261	CASP8/RELA/NFKBIA	3
BP	GO:0051973	positive regulation of telomerase activity	0.01261	MAPK3/MAPK1/MYC	3
BP	GO:1903580	positive regulation of ATP metabolic process	0.01261	INSR/HIF1A/CCNB1	3
BP	GO:0006635	fatty acid beta-oxidation	0.012773	AKT1/PPARA/ADIPOQ/PPARD	4

BP	GO:0009132	nucleoside diphosphate metabolic process	0.012931	INSR/PPARA/EIF6/HIF1A/HK2	5
BP	GO:0030968	endoplasmic reticulum unfolded protein response	0.012931	BAX/CCND1/CCL2/CXCL8/NFE2L2	5
BP	GO:0006081	cellular aldehyde metabolic process	0.013381	RELA/CYP1B1/AKR1C3/AKR1C1	4
BP	GO:0001952	regulation of cell-matrix adhesion	0.013381	BCL2/PLAU/VEGFA/SERPINE1/RASA1	5

BP	GO:0019079	viral genome replication	0.013381	BCL2/SLPI/CCL2/CXCL8/TOP2A	5
BP	GO:0009124	nucleoside monophosphate biosynthetic process	0.013431	INSR/PPARA/EIF6/HIF1A/PARP1/HK2	6
BP	GO:0048009	insulin-like growth factor receptor signaling pathway	0.013548	AR/AKT1/IGFBP3	3
BP	GO:0061756	leukocyte adhesion to vascular endothelial cell	0.013548	ICAM1/SELE/VCAM1	3

BP	GO:0007160	cell-matrix adhesion	0.013574	BCL2/VCAM1/PLAU/VEGFA/SERPINE1/ COL3A1/RASA1	7
BP	GO:0019730	antimicrobial humoral response	0.013823	SLPI/CXCL8/CXCL11/CXCL2/CXCL10	5
BP	GO:0006073	cellular glucan metabolic process	0.013951	AKT1/INSR/MGAM/IGF2	4
BP	GO:0010611	regulation of cardiac muscle hypertrophy	0.013951	ADRA1A/PRKCA/PPARA/PARP1	4

BP	GO:0044042	glucan metabolic process	0.013951	AKT1/INSR/MGAM/IGF2	4
BP	GO:0086001	cardiac muscle cell action potential	0.013951	KCNH2/SCN5A/CAV1/GJA1	4
BP	GO:0008207	C21-steroid hormone metabolic process	0.014413	AKR1C3/AKR1C1/AKR1B1	3
BP	GO:0010661	positive regulation of muscle cell apoptotic process	0.014413	PPARG/HMGCR/IFNG	3

BP	GO:0010664	negative regulation of striated muscle cell apoptotic process	0.014413	HMGCR/NFE2L2/HSF1	3
BP	GO:0046676	negative regulation of insulin secretion	0.014413	HMGCR/SREBF1/ADRA2A	3
BP	GO:0060306	regulation of membrane repolarization	0.014413	KCNH2/SCN5A/CAV1	3
BP	GO:0071867	response to monoamine	0.014413	MAPK3/MAPK1/ADIPOQ	3

BP	GO:0071869	response to catecholamine	0.014413	MAPK3/MAPK1/ADIPOQ	3
BP	GO:0086005	ventricular cardiac muscle cell action potential	0.014413	KCNH2/SCN5A/CAV1	3
BP	GO:0086091	regulation of heart rate by cardiac conduction	0.014413	KCNH2/SCN5A/CAV1	3
BP	GO:0090050	positive regulation of cell migration involved in sprouting angiogenesis	0.014413	PTGS2/HMOX1/VEGFA	3

BP	GO:1900117	regulation of execution phase of apoptosis	0.014413	BAX/BCL2L1/HSF1	3
BP	GO:0001937	negative regulation of endothelial cell proliferation	0.014413	PPARG/STAT1/CAV1/CCL2	4
BP	GO:0002674	negative regulation of acute inflammatory response	0.014413	PPARG/GSTP1	2
BP	GO:0006527	arginine catabolic process	0.014413	NOS2/NOS3	2

BP	GO:0010867	positive regulation of triglyceride biosynthetic process	0.014413	LDLR/SREBF1	2
BP	GO:0010889	regulation of sequestering of triglyceride	0.014413	PPARG/PPARA	2
BP	GO:0031282	regulation of guanylate cyclase activity	0.014413	NOS2/NOS3	2
BP	GO:0033160	positive regulation of protein import into nucleus, translocation	0.014413	MAPK1/IFNG	2

BP	GO:0045091	regulation of single stranded viral RNA replication via double stranded DNA intermediate	0.014413	CXCL8/TOP2A	2
BP	GO:0045760	positive regulation of action potential	0.014413	SCN5A/ADRA1A	2
BP	GO:0046541	saliva secretion	0.014413	CHRM3/CHRM1	2
BP	GO:0051549	positive regulation of keratinocyte migration	0.014413	HAS2/MMP9	2

BP	GO:0051712	positive regulation of killing of cells of other organism	0.014413	NOS2/IFNG	2
BP	GO:0060442	branching involved in prostate gland morphogenesis	0.014413	RXRA/ESR1	2
BP	GO:0061430	bone trabecula morphogenesis	0.014413	MMP2/COL1A1	2
BP	GO:0070486	leukocyte aggregation	0.014413	HAS2/IL1B	2

BP	GO:0070586	cell-cell adhesion involved in gastrulation	0.014413	ADIPOQ/IL10	2
BP	GO:0070989	oxidative demethylation	0.014413	CYP3A4/CYP1A2	2
BP	GO:0097284	hepatocyte apoptotic process	0.014413	BCL2L1/RB1	2
BP	GO:1901550	regulation of endothelial cell development	0.014413	IKBKB/IL1B	2

BP	GO:1903140	regulation of establishment of endothelial barrier	0.014413	IKBKB/IL1B	2
BP	GO:1903624	regulation of DNA catabolic process	0.014413	BAX/HSF1	2
BP	GO:1901987	regulation of cell cycle phase transition	0.014707	BCL2/BAX/CYP1A1/CCND1/CDKN1A/RB1/CCL2/CCNB1/CHEK2/E2F1	10
BP	GO:1900180	regulation of protein localization to nucleus	0.014956	PTGS2/AKT1/MAPK1/IFNG/PARP1	5

BP	GO:0010507	negative regulation of autophagy	0.014956	ADRA1A/BCL2/AKT1/HMOX1	4
BP	GO:0014743	regulation of muscle hypertrophy	0.014956	ADRA1A/PRKCA/PPARA/PARP1	4
BP	GO:0051937	catecholamine transport	0.014956	SLC6A2/ABAT/ADRA2A/SLC6A3	4
BP	GO:0072088	nephron epithelium morphogenesis	0.014956	BCL2/STAT1/VEGFA/MYC	4

BP	GO:0051607	defense response to virus	0.015213	BCL2/RELA/STAT1/IL6/IFNG/CXCL10/IR F1	7
BP	GO:0006308	DNA catabolic process	0.015231	BAX/CASP3/HSF1	3
BP	GO:0051930	regulation of sensory perception of pain	0.015231	OPRM1/IL10/ACPP	3
BP	GO:0097300	programmed necrotic cell death	0.015231	BAX/CASP8/CAV1	3

BP	GO:0001570	vasculogenesis	0.015583	HAS2/VEGFA/CAV1/RASA1	4
BP	GO:0031016	pancreas development	0.015583	AKT1/INSR/IL6/IGF2	4
BP	GO:0032413	negative regulation of ion transmembrane transporter activity	0.015583	GSTM2/ADRA2A/MMP9/CAV1	4
BP	GO:0006732	coenzyme metabolic process	0.015583	PTGS2/INSR/FASN/HMGCR/PPARA/EIF6 /HIF1A/ACACA/HK2	9

BP	GO:0002285	lymphocyte activation involved in immune response	0.015774	ICAM1/IL10/IL6/IL2/IFNG/CD40LG	6
BP	GO:0072028	nephron morphogenesis	0.016228	BCL2/STAT1/VEGFA/MYC	4
BP	GO:0043616	keratinocyte proliferation	0.016228	HAS2/TP63/PPARD	3
BP	GO:0046006	regulation of activated T cell proliferation	0.016228	CASP3/IL2/IGF2	3

BP	GO:0051931	regulation of sensory perception	0.016228	OPRM1/IL10/ACPP	3
BP	GO:0061900	glial cell activation	0.016228	JUN/LDLR/EGFR	3
BP	GO:0090184	positive regulation of kidney development	0.016228	ADIPOQ/VEGFA/MYC	3
BP	GO:1903146	regulation of autophagy of mitochondrion	0.016228	SREBF1/HIF1A/HK2	3

BP	GO:0006639	acylglycerol metabolic process	0.016369	LDLR/CAT/APOB/SREBF1/CAV1	5
BP	GO:0009150	purine ribonucleotide metabolic process	0.016489	INSR/FASN/HMGCR/PPARA/EIF6/HIF1A /ACACA/SULT1E1/CCNB1/PARP1/HK2	11
BP	GO:0007171	activation of transmembrane receptor protein tyrosine kinase activity	0.016489	ADRB2/EGF	2
BP	GO:0009635	response to herbicide	0.016489	CYP1A1/HSF1	2

BP	GO:0032310	prostaglandin secretion	0.016489	NOS2/IL1B	2
BP	GO:0039692	single stranded viral RNA replication via double stranded DNA intermediate	0.016489	CXCL8/TOP2A	2
BP	GO:0042159	lipoprotein catabolic process	0.016489	LDLR/APOB	2
BP	GO:0043568	positive regulation of insulin-like growth factor receptor signaling pathway	0.016489	AR/IGFBP3	2

BP	GO:0044130	negative regulation of growth of symbiont in host	0.016489	IL10/MPO	2
BP	GO:0044849	estrous cycle	0.016489	OPRM1/HAS2	2
BP	GO:0045086	positive regulation of interleukin-2 biosynthetic process	0.016489	IL1B/IL1A	2
BP	GO:0060576	intestinal epithelial cell development	0.016489	CDKN1A/HIF1A	2

BP	GO:0060601	lateral sprouting from an epithelium	0.016489	AR/TP63	2
BP	GO:0060965	negative regulation of gene silencing by miRNA	0.016489	PPARG/ESR1	2
BP	GO:0061029	eyelid development in camera-type eye	0.016489	JUN/EGFR	2
BP	GO:0070208	protein heterotrimerization	0.016489	ADIPOQ/COL1A1	2

BP	GO:0070431	nucleotide-binding oligomerization domain containing 2 signaling pathway	0.016489	RELA/NFKBIA	2
BP	GO:1900119	positive regulation of execution phase of apoptosis	0.016489	BAX/HSF1	2
BP	GO:1902001	fatty acid transmembrane transport	0.016489	AKT1/ACACA	2
BP	GO:0003158	endothelium development	0.01669	IKBKB/ICAM1/FASN/IL1B/CXCL10	5

BP	GO:0006638	neutral lipid metabolic process	0.01669	LDLR/CAT/APOB/SREBF1/CAV1	5
BP	GO:0030183	B cell differentiation	0.01669	BCL2/BAX/VCAM1/IL10/CD40LG	5
BP	GO:0046834	lipid phosphorylation	0.01669	ESR1/EGFR/EGF/ERBB2/ERBB3	5
BP	GO:0032204	regulation of telomere maintenance	0.016697	MAPK3/MAPK1/MYC/PARP1	4

BP	GO:0033143	regulation of intracellular steroid hormone receptor signaling pathway	0.016697	AR/ESR1/TP63/PARP1	4
BP	GO:0050792	regulation of viral process	0.016753	BCL2/JUN/STAT1/SLPI/CXCL8/TOP2A	6
BP	GO:1990778	protein localization to cell periphery	0.016983	AR/IKBKB/AKT1/ADIPOQ/EGFR/BCL2L1/CAV1/IFNG	8
BP	GO:0043267	negative regulation of potassium ion transport	0.017083	KCNH2/CAV1/NOS3	3

BP	GO:0051170	import into nucleus	0.017174	PTGS2/ AKT1/ AKR1C3/ MAPK1/ NFKBIA/ I FNG	6
BP	GO:0050764	regulation of phagocytosis	0.017362	PPARG/ ADIPOQ/ IL1B/ CCL2	4
BP	GO:0051279	regulation of release of sequestered calcium ion into cytosol	0.017362	BAX/ GSTM2/ CXCL11/ CXCL10	4
BP	GO:0071277	cellular response to calcium ion	0.017362	SCN5A/ JUN/ AKR1C3/ FOS	4

BP	GO:2001021	negative regulation of response to DNA damage stimulus	0.017362	BCL2/BCL2L1/CHEK2/HSF1	4
BP	GO:0031644	regulation of neurological system process	0.01768	ADRB2/OPRM1/ABAT/IL10/ACPP	5
BP	GO:0032680	regulation of tumor necrosis factor production	0.01768	GSTP1/ADIPOQ/IL10/HSPB1/HSF1	5
BP	GO:0071333	cellular response to glucose stimulus	0.01768	ICAM1/HMGCR/ADRA2A/RAF1/HIF1A	5

BP	GO:0001504	neurotransmitter uptake	0.018113	SLC6A4/SLC6A2/SLC6A3	3
BP	GO:0002437	inflammatory response to antigenic stimulus	0.018113	OPRM1/ICAM1/IL10	3
BP	GO:0032459	regulation of protein oligomerization	0.018113	BAX/MMP1/MMP3	3
BP	GO:0042307	positive regulation of protein import into nucleus	0.018113	PTGS2/MAPK1/IFNG	3

BP	GO:0045581	negative regulation of T cell differentiation	0.018113	ERBB2/IL2/IRF1	3
BP	GO:0071675	regulation of mononuclear cell migration	0.018113	MAPK3/SERPINE1/CXCL10	3
BP	GO:0002576	platelet degranulation	0.018171	SOD1/VEGFA/EGF/SERPINE1/IGF2	5
BP	GO:0046887	positive regulation of hormone secretion	0.018171	ABAT/EGFR/HIF1A/PPARD/SPP1	5

BP	GO:0032640	tumor necrosis factor production	0.018396	GSTP1/ADIPOQ/IL10/HSPB1/HSF1	5
BP	GO:0055007	cardiac muscle cell differentiation	0.018396	RXRA/ADRA1A/PPARA/VEGFA/CCNB1	5
BP	GO:0071331	cellular response to hexose stimulus	0.018396	ICAM1/HMGCR/ADRA2A/RAF1/HIF1A	5
BP	GO:0072329	monocarboxylic acid catabolic process	0.018396	AKT1/PPARA/ADIPOQ/ABAT/PPARD	5

BP	GO:0014031	mesenchymal cell development	0.018396	BCL2/MAPK3/MAPK1/HIF1A	4
BP	GO:0110110	positive regulation of animal organ morphogenesis	0.018396	BAX/AR/VEGFA/MYC	4
BP	GO:0020027	hemoglobin metabolic process	0.018396	CAT/HIF1A	2
BP	GO:0030238	male sex determination	0.018396	AR/INSR	2

BP	GO:0033604	negative regulation of catecholamine secretion	0.018396	ABAT/ADRA2A	2
BP	GO:0034374	low-density lipoprotein particle remodeling	0.018396	APOB/MPO	2
BP	GO:0034433	steroid esterification	0.018396	SOAT2/SOAT1	2
BP	GO:0034434	sterol esterification	0.018396	SOAT2/SOAT1	2

BP	GO:0034435	cholesterol esterification	0.018396	SOAT2/SOAT1	2
BP	GO:0035112	genitalia morphogenesis	0.018396	AR/TP63	2
BP	GO:0035635	entry of bacterium into host cell	0.018396	CAV1/CXCL8	2
BP	GO:0036295	cellular response to increased oxygen levels	0.018396	PPARG/CAV1	2

BP	GO:0043217	myelin maintenance	0.018396	AKT1/SOD1	2
BP	GO:0043374	CD8-positive, alpha-beta T cell differentiation	0.018396	BCL2/IRF1	2
BP	GO:0044126	regulation of growth of symbiont in host	0.018396	IL10/MPO	2
BP	GO:0044146	negative regulation of growth of symbiont involved in interaction with host	0.018396	IL10/MPO	2

BP	GO:0045591	positive regulation of regulatory T cell differentiation	0.018396	IL2/IFNG	2
BP	GO:0048143	astrocyte activation	0.018396	LDLR/EGFR	2
BP	GO:0048308	organelle inheritance	0.018396	MAPK3/MAPK1	2
BP	GO:0048313	Golgi inheritance	0.018396	MAPK3/MAPK1	2

BP	GO:0050930	induction of positive chemotaxis	0.018396	VEGFA/CXCL8	2
BP	GO:0051547	regulation of keratinocyte migration	0.018396	HAS2/MMP9	2
BP	GO:0051709	regulation of killing of cells of other organism	0.018396	NOS2/IFNG	2
BP	GO:0051770	positive regulation of nitric-oxide synthase biosynthetic process	0.018396	STAT1/CCL2	2

BP	GO:0051917	regulation of fibrinolysis	0.018396	THBD/SERPINE1	2
BP	GO:0072216	positive regulation of metanephros development	0.018396	ADIPOQ/MYC	2
BP	GO:0090036	regulation of protein kinase C signaling	0.018396	ADRA1A/VEGFA	2
BP	GO:0106070	regulation of adenylate cyclase-activating G protein-coupled receptor signaling pathway	0.018396	OPRM1/PRKCA	2

BP	GO:0150078	positive regulation of neuroinflammatory response	0.018396	IL6/IL1B	2
BP	GO:1900121	negative regulation of receptor binding	0.018396	ADIPOQ/IL10	2
BP	GO:1903351	cellular response to dopamine	0.018396	MAPK3/MAPK1	2
BP	GO:1904294	positive regulation of ERAD pathway	0.018396	CAV1/NFE2L2	2

BP	GO:2000402	negative regulation of lymphocyte migration	0.018396	AKT1/CCL2	2
BP	GO:0007265	Ras protein signal transduction	0.018417	ADRA1A/JUN/ADRA2A/CDKN1A/RB1/RAF1/COL3A1/CHUK/RASSF1/RASA1	10
BP	GO:0010613	positive regulation of cardiac muscle hypertrophy	0.01881	ADRA1A/PRKCA/PARP1	3
BP	GO:0014009	glial cell proliferation	0.01881	IL6/IL1B/E2F1	3

BP	GO:0014742	positive regulation of muscle hypertrophy	0.01881	ADRA1A/PRKCA/PARP1	3
BP	GO:0042771	intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator	0.01881	BCL2/TP63/CHEK2	3
BP	GO:0071548	response to dexamethasone	0.01881	CASP9/ICAM1/EGFR	3
BP	GO:0045995	regulation of embryonic development	0.018841	AR/INSR/ADIPOQ/IL10/NFE2L2	5

BP	GO:0071326	cellular response to monosaccharide stimulus	0.018841	ICAM1/HMGCR/ADRA2A/RAF1/HIF1A	5
BP	GO:0050864	regulation of B cell activation	0.018847	BCL2/CASP3/AHR/IL10/IL6/IL2	6
BP	GO:0007009	plasma membrane organization	0.019049	AR/AKT1/SOD1/CAV1	4
BP	GO:0046328	regulation of JNK cascade	0.019311	AKT1/GSTP1/EGFR/IL1B/NCF1/CD40LG	6

BP	GO:0050777	negative regulation of immune response	0.019397	PPARG/HMOX1/IL10/IL2/COL3A1	5
BP	GO:0071560	cellular response to transforming growth factor beta stimulus	0.019466	JUN/GOT1/FOS/CAV1/COL1A1/PARP1/COL3A1	7
BP	GO:0045778	positive regulation of ossification	0.019798	ADRB2/IL6/TP63/RUNX2	4
BP	GO:2000177	regulation of neural precursor cell proliferation	0.019798	SLC6A4/VEGFA/EGF/HIF1A	4

BP	GO:0007157	heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules	0.019881	ICAM1/SELE/VCAM1	3
BP	GO:0008089	anterograde axonal transport	0.019881	MAP2/SOD1/HSPB1	3
BP	GO:0033628	regulation of cell adhesion mediated by integrin	0.019881	CYP1B1/PLAU/SERPINE1	3
BP	GO:0050798	activated T cell proliferation	0.019881	CASP3/IL2/IGF2	3

BP	GO:1904591	positive regulation of protein import	0.019881	PTGS2/MAPK1/IFNG	3
BP	GO:0072659	protein localization to plasma membrane	0.020222	AR/IKBKB/AKT1/ADIPOQ/EGFR/BCL2L1 /IFNG	7
BP	GO:0001508	action potential	0.020467	KCNH2/SCN5A/ADRA1A/CAV1/GJA1	5
BP	GO:0030260	entry into host cell	0.020467	ICAM1/LDLR/EGFR/CAV1/CXCL8	5

BP	GO:0044409	entry into host	0.020467	ICAM1/LDLR/EGFR/CAV1/CXCL8	5
BP	GO:0051806	entry into cell of other organism involved in symbiotic interaction	0.020467	ICAM1/LDLR/EGFR/CAV1/CXCL8	5
BP	GO:0051828	entry into other organism involved in symbiotic interaction	0.020467	ICAM1/LDLR/EGFR/CAV1/CXCL8	5
BP	GO:0002028	regulation of sodium ion transport	0.020467	SCN5A/ADRB2/AKT1/NOS3	4

BP	GO:1901992	positive regulation of mitotic cell cycle phase transition	0.020467	CYP1A1/CCND1/RB1/CCNB1	4
BP	GO:0022898	regulation of transmembrane transporter activity	0.020472	ADRB2/OPRM1/BCL2/GSTM2/ADRA2A/MMP9/CAV1	7
BP	GO:0031330	negative regulation of cellular catabolic process	0.020472	ADRA1A/BCL2/AKT1/HMOX1/PPARA/IL10/E2F1	7
BP	GO:0044272	sulfur compound biosynthetic process	0.020472	GSTP1/GSTM1/GSTM2/FASN/ACACA/NF E2L2	6

BP	GO:0006837	serotonin transport	0.020472	SLC6A4/MAOB	2
BP	GO:0015732	prostaglandin transport	0.020472	NOS2/IL1B	2
BP	GO:0016114	terpenoid biosynthetic process	0.020472	CYP1A1/AKR1C3	2
BP	GO:0030889	negative regulation of B cell proliferation	0.020472	CASP3/IL10	2

BP	GO:0034116	positive regulation of heterotypic cell-cell adhesion	0.020472	IL10/IL1B	2
BP	GO:0034310	primary alcohol catabolic process	0.020472	AKR1C3/SULT1E1	2
BP	GO:0035729	cellular response to hepatocyte growth factor stimulus	0.020472	RELA/IL10	2
BP	GO:0035864	response to potassium ion	0.020472	SOD1/HSF1	2

BP	GO:0044144	modulation of growth of symbiont involved in interaction with host	0.020472	IL10/MPO	2
BP	GO:0046321	positive regulation of fatty acid oxidation	0.020472	PPARG/PPARA	2
BP	GO:0048569	post-embryonic animal organ development	0.020472	BAX/VEGFA	2
BP	GO:0060149	negative regulation of posttranscriptional gene silencing	0.020472	PPARG/ESR1	2

BP	GO:0060967	negative regulation of gene silencing by RNA	0.020472	PPARG/ESR1	2
BP	GO:0072075	metanephric mesenchyme development	0.020472	STAT1/MYC	2
BP	GO:0090494	dopamine uptake	0.020472	SLC6A2/SLC6A3	2
BP	GO:1903350	response to dopamine	0.020472	MAPK3/MAPK1	2

BP	GO:1903358	regulation of Golgi organization	0.020472	MAPK3/MAPK1	2
BP	GO:2001028	positive regulation of endothelial cell chemotaxis	0.020472	VEGFA/HSPB1	2
BP	GO:2001170	negative regulation of ATP biosynthetic process	0.020472	PPARA/PARP1	2
BP	GO:0002686	negative regulation of leukocyte migration	0.020732	AKT1/HMOX1/CCL2	3

BP	GO:0010463	mesenchymal cell proliferation	0.020732	STAT1/VEGFA/MYC	3
BP	GO:0090278	negative regulation of peptide hormone secretion	0.020732	HMGCR/SREBF1/ADRA2A	3
BP	GO:1900034	regulation of cellular response to heat	0.020732	MAPK3/MAPK1/HSF1	3
BP	GO:0046631	alpha-beta T cell activation	0.020742	BCL2/IL6/IL2/IFNG/IRF1	5

BP	GO:0006767	water-soluble vitamin metabolic process	0.020935	PRSS1/ABCC1/CTRB1/ACPP	4
BP	GO:0045844	positive regulation of striated muscle tissue development	0.020935	BCL2/HMGCR/CCNB1/ERBB3	4
BP	GO:0048636	positive regulation of muscle organ development	0.020935	BCL2/HMGCR/CCNB1/ERBB3	4
BP	GO:0016485	protein processing	0.021493	CASP3/CASP8/F7/PLAU/F3/PLAT/SERPI NE1/PARP1	8

BP	GO:0000079	regulation of cyclin-dependent protein serine/threonine kinase activity	0.021698	CASP3/CCND1/CDKN1A/CCNB1	4
BP	GO:0001942	hair follicle development	0.021698	BCL2/RELA/EGFR/TP63	4
BP	GO:0006112	energy reserve metabolic process	0.021698	AKT1/INSR/MYC/IGF2	4
BP	GO:0055013	cardiac muscle cell development	0.021698	ADRA1A/PPARA/VEGFA/CCNB1	4

BP	GO:1901863	positive regulation of muscle tissue development	0.021698	BCL2/HMGCR/CCNB1/ERBB3	4
BP	GO:2000106	regulation of leukocyte apoptotic process	0.021698	BAX/IL10/HIF1A/IL2	4
BP	GO:0005978	glycogen biosynthetic process	0.021788	AKT1/INSR/IGF2	3
BP	GO:0006984	ER-nucleus signaling pathway	0.021788	CCL2/CXCL8/NFE2L2	3

BP	GO:0009250	glucan biosynthetic process	0.021788	AKT1/INSR/IGF2	3
BP	GO:0031103	axon regeneration	0.021788	BCL2/JUN/SPP1	3
BP	GO:0032757	positive regulation of interleukin-8 production	0.021788	ADIPOQ/IL1B/SERPINE1	3
BP	GO:1900744	regulation of p38MAPK cascade	0.021788	VEGFA/IL1B/NCF1	3

BP	GO:0071559	response to transforming growth factor beta	0.021788	JUN/GOT1/FOS/CAV1/COL1A1/PARP1/COL3A1	7
BP	GO:0055076	transition metal ion homeostasis	0.021788	HMOX1/SOD1/HIF1A/MYC/ABCG2	5
BP	GO:0072006	nephron development	0.021788	BCL2/STAT1/ADIPOQ/VEGFA/MYC	5
BP	GO:0046034	ATP metabolic process	0.022215	INSR/PPARA/EIF6/HIF1A/CCNB1/PARP1/HK2	7

BP	GO:0045580	regulation of T cell differentiation	0.022398	SOD1/ERBB2/IL2/IFNG/IRF1	5
BP	GO:0051250	negative regulation of lymphocyte activation	0.022398	CASP3/IL10/ERBB2/IL2/IRF1	5
BP	GO:0032410	negative regulation of transporter activity	0.022398	GSTM2/ADRA2A/MMP9/CAV1	4
BP	GO:0090596	sensory organ morphogenesis	0.022625	BCL2/BAX/MAPK3/MAPK1/SOD1/VEGFA/HIF1A	7

BP	GO:0002739	regulation of cytokine secretion involved in immune response	0.022729	MAPK3/IL10	2
BP	GO:0031000	response to caffeine	0.022729	PPARG/GSTM2	2
BP	GO:0032225	regulation of synaptic transmission, dopaminergic	0.022729	PTGS2/SLC6A4	2
BP	GO:0033158	regulation of protein import into nucleus, translocation	0.022729	MAPK1/IFNG	2

BP	GO:0036270	response to diuretic	0.022729	PPARG/GSTM2	2
BP	GO:0042448	progesterone metabolic process	0.022729	AKR1C3/AKR1C1	2
BP	GO:0048070	regulation of developmental pigmentation	0.022729	BCL2/BAX	2
BP	GO:0060572	morphogenesis of an epithelial bud	0.022729	AR/TP63	2

BP	GO:0090493	catecholamine uptake	0.022729	SLC6A2/SLC6A3	2
BP	GO:1903209	positive regulation of oxidative stress-induced cell death	0.022729	SOD1/MMP3	2
BP	GO:0002204	somatic recombination of immunoglobulin genes involved in immune response	0.022792	IL10/IL2/CD40LG	3
BP	GO:0002208	somatic diversification of immunoglobulins involved in immune response	0.022792	IL10/IL2/CD40LG	3

BP	GO:0002720	positive regulation of cytokine production involved in immune response	0.022792	MAPK3/IL6/IL1B	3
BP	GO:0006636	unsaturated fatty acid biosynthetic process	0.022792	PTGS2/PTGS1/ AKR1C3	3
BP	GO:0035722	interleukin-12-mediated signaling pathway	0.022792	SOD1/IL10/IFNG	3
BP	GO:0045190	isotype switching	0.022792	IL10/IL2/CD40LG	3

BP	GO:0051339	regulation of lyase activity	0.022792	OPRM1/NOS2/NOS3	3
BP	GO:1901185	negative regulation of ERBB signaling pathway	0.022792	EGFR/EGF/ERBB2	3
BP	GO:1903364	positive regulation of cellular protein catabolic process	0.0228	AKT1/LDLR/EGF/CAV1/NFE2L2	5
BP	GO:0007179	transforming growth factor beta receptor signaling pathway	0.022897	JUN/GOT1/FOS/CAV1/PARP1/COL3A1	6

BP	GO:0001656	metanephros development	0.02295	BCL2/STAT1/ADIPOQ/MYC	4
BP	GO:0022404	molting cycle process	0.02295	BCL2/RELA/EGFR/TP63	4
BP	GO:0022405	hair cycle process	0.02295	BCL2/RELA/EGFR/TP63	4
BP	GO:0098773	skin epidermis development	0.02295	BCL2/RELA/EGFR/TP63	4

BP	GO:0003007	heart morphogenesis	0.02323	RXRA/JUN/HAS2/INSR/VEGFA/HIF1A/N OS3	7
BP	GO:0019319	hexose biosynthetic process	0.023805	PPARA/ADIPOQ/GOT1/AKR1B1	4
BP	GO:0045069	regulation of viral genome replication	0.023805	BCL2/SLPI/CXCL8/TOP2A	4
BP	GO:0009166	nucleotide catabolic process	0.024041	INSR/PPARA/EIF6/HIF1A/HK2	5

BP	GO:0001818	negative regulation of cytokine production	0.024622	HMOX1/GSTP1/ADIPOQ/IL10/IL6/IFNG/HSF1	7
BP	GO:0002702	positive regulation of production of molecular mediator of immune response	0.024666	MAPK3/IL6/IL1B/IL2	4
BP	GO:1904029	regulation of cyclin-dependent protein kinase activity	0.024666	CASP3/CCND1/CDKN1A/CCNB1	4
BP	GO:0030809	negative regulation of nucleotide biosynthetic process	0.024972	PPARA/PARP1	2

BP	GO:0031065	positive regulation of histone deacetylation	0.024972	SREBF1/VEGFA	2
BP	GO:0033145	positive regulation of intracellular steroid hormone receptor signaling pathway	0.024972	AR/PARP1	2
BP	GO:0035728	response to hepatocyte growth factor	0.024972	RELA/IL10	2
BP	GO:0042994	cytoplasmic sequestering of transcription factor	0.024972	IL10/NFKBIA	2

BP	GO:0043651	linoleic acid metabolic process	0.024972	GSTP1/GSTM2	2
BP	GO:0044117	growth of symbiont in host	0.024972	IL10/MPO	2
BP	GO:0045019	negative regulation of nitric oxide biosynthetic process	0.024972	IL10/CAV1	2
BP	GO:0055012	ventricular cardiac muscle cell differentiation	0.024972	RXRA/CCNB1	2

BP	GO:0060544	regulation of necroptotic process	0.024972	CASP8/CAV1	2
BP	GO:0060644	mammary gland epithelial cell differentiation	0.024972	AKT1/HIF1A	2
BP	GO:0070102	interleukin-6-mediated signaling pathway	0.024972	STAT1/IL6	2
BP	GO:0090185	negative regulation of kidney development	0.024972	STAT1/ADIPOQ	2

BP	GO:0090330	regulation of platelet aggregation	0.024972	PRKCA/ABAT	2
BP	GO:1900372	negative regulation of purine nucleotide biosynthetic process	0.024972	PPARA/PARP1	2
BP	GO:1904355	positive regulation of telomere capping	0.024972	MAPK3/MAPK1	2
BP	GO:1904406	negative regulation of nitric oxide metabolic process	0.024972	IL10/CAV1	2

BP	GO:2000641	regulation of early endosome to late endosome transport	0.024972	MAPK3/MAPK1	2
BP	GO:2000811	negative regulation of anoikis	0.024972	BCL2/CAV1	2
BP	GO:0006998	nuclear envelope organization	0.024972	PRKCA/PRKCB/CCNB1	3
BP	GO:0032330	regulation of chondrocyte differentiation	0.024972	RELA/POR/RUNX2	3

BP	GO:0032873	negative regulation of stress-activated MAPK cascade	0.024972	AKT1/GSTP1/MYC	3
BP	GO:0035272	exocrine system development	0.024972	INSR/EGFR/IGF2	3
BP	GO:0045599	negative regulation of fat cell differentiation	0.024972	ADIPOQ/IL6/E2F1	3
BP	GO:0070303	negative regulation of stress-activated protein kinase signaling cascade	0.024972	AKT1/GSTP1/MYC	3

BP	GO:0071349	cellular response to interleukin-12	0.024972	SOD1/IL10/IFNG	3
BP	GO:0086009	membrane repolarization	0.024972	KCNH2/SCN5A/CAV1	3
BP	GO:0007605	sensory perception of sound	0.025012	CASP3/ICAM1/SOD1/BIRC5/COL1A1	5
BP	GO:0016570	histone modification	0.025032	PRKCA/MAPK8/MAPK3/SREBF1/NCOA1 /VEGFA/IL1B/PRKCB/CCNB1/IGF2	10

BP	GO:0050851	antigen receptor-mediated signaling pathway	0.025661	BCL2/BAX/RELA/IKBKB/MAPK1/PRKCB/ CHUK	7
BP	GO:0008544	epidermis development	0.025725	BCL2/CASP3/RELA/INSR/AKR1C3/SOD1/ PPARA/EGFR/TP63/PPARD	10
BP	GO:0055006	cardiac cell development	0.026056	ADRA1A/PPARA/VEGFA/CCNB1	4
BP	GO:0072080	nephron tubule development	0.026056	BCL2/STAT1/VEGFA/MYC	4

BP	GO:0090277	positive regulation of peptide hormone secretion	0.026056	ABAT/EGFR/HIF1A/PPARD	4
BP	GO:0016447	somatic recombination of immunoglobulin gene segments	0.026224	IL10/IL2/CD40LG	3
BP	GO:0042304	regulation of fatty acid biosynthetic process	0.026224	PTGS2/ADIPOQ/EIF6	3
BP	GO:0070231	T cell apoptotic process	0.026224	BAX/AKT1/HIF1A	3

BP	GO:0070671	response to interleukin-12	0.026224	SOD1/IL10/IFNG	3
BP	GO:0060993	kidney morphogenesis	0.02693	BCL2/STAT1/VEGFA/MYC	4
BP	GO:2000060	positive regulation of ubiquitin-dependent protein catabolic process	0.02693	AKT1/EGF/CAV1/NFE2L2	4
BP	GO:0008277	regulation of G protein-coupled receptor signaling pathway	0.026987	ADRB2/OPRM1/PRKCA/CXCL8/ACPP	5

BP	GO:1903169	regulation of calcium ion transmembrane transport	0.026987	BAX/GSTM2/ADRA2A/CXCL11/CXCL10	5
BP	GO:0061448	connective tissue development	0.027255	RELA/MAPK3/POR/HIF1A/COL1A1/PPARD/RUNX2	7
BP	GO:0045620	negative regulation of lymphocyte differentiation	0.027255	ERBB2/IL2/IRF1	3
BP	GO:0045744	negative regulation of G protein-coupled receptor signaling pathway	0.027255	ADRB2/OPRM1/CXCL8	3

BP	GO:2000677	regulation of transcription regulatory region DNA binding	0.027255	RB1/IFNG/PARP1	3
BP	GO:2001258	negative regulation of cation channel activity	0.027255	GSTM2/MMP9/CAV1	3
BP	GO:0002544	chronic inflammatory response	0.027255	VCAM1/IL10	2
BP	GO:0002726	positive regulation of T cell cytokine production	0.027255	IL6/IL1B	2

BP	GO:0006521	regulation of cellular amino acid metabolic process	0.027255	ODC1/NQO1	2
BP	GO:0031998	regulation of fatty acid beta-oxidation	0.027255	AKT1/PPARA	2
BP	GO:0032095	regulation of response to food	0.027255	OPRM1/PPARA	2
BP	GO:0033599	regulation of mammary gland epithelial cell proliferation	0.027255	BAX/CCND1	2

BP	GO:0044110	growth involved in symbiotic interaction	0.027255	IL10/MPO	2
BP	GO:0044116	growth of symbiont involved in interaction with host	0.027255	IL10/MPO	2
BP	GO:0045655	regulation of monocyte differentiation	0.027255	JUN/MYC	2
BP	GO:0061298	retina vasculature development in camera-type eye	0.027255	CYP1B1/HIF1A	2

BP	GO:0070230	positive regulation of lymphocyte apoptotic process	0.027255	BAX/IL10	2
BP	GO:0070242	thymocyte apoptotic process	0.027255	BAX/HIF1A	2
BP	GO:0071243	cellular response to arsenic-containing substance	0.027255	HMOX1/HSF1	2
BP	GO:0071318	cellular response to ATP	0.027255	PTGS2/SOD1	2

BP	GO:0090026	positive regulation of monocyte chemotaxis	0.027255	SERPINE1/CXCL10	2
BP	GO:1900409	positive regulation of cellular response to oxidative stress	0.027255	SOD1/MMP3	2
BP	GO:1903798	regulation of production of miRNAs involved in gene silencing by miRNA	0.027255	ESR1/EGFR	2
BP	GO:2000479	regulation of cAMP-dependent protein kinase activity	0.027255	ADRB2/ADIPOQ	2

BP	GO:2000696	regulation of epithelial cell differentiation involved in kidney development	0.027255	STAT1/ADIPOQ	2
BP	GO:1901292	nucleoside phosphate catabolic process	0.027356	INSR/PPARA/EIF6/HIF1A/HK2	5
BP	GO:0061326	renal tubule development	0.027483	BCL2/STAT1/VEGFA/MYC	4
BP	GO:0030902	hindbrain development	0.02808	SCN5A/SLC6A4/BCL2/ABAT/EGF	5

BP	GO:0017157	regulation of exocytosis	0.028196	ADRA1A/CHRM2/HMOX1/ADRA2A/PRKCB/IFNG	6
BP	GO:0001657	ureteric bud development	0.028396	BCL2/CAT/VEGFA/MYC	4
BP	GO:0046364	monosaccharide biosynthetic process	0.028396	PPARA/ADIPOQ/GOT1/AKR1B1	4
BP	GO:0048259	regulation of receptor-mediated endocytosis	0.028396	SELE/VEGFA/EGF/SERPINE1	4

BP	GO:0000186	activation of MAPKK activity	0.028501	EGFR/EGF/RAF1	3
BP	GO:0002090	regulation of receptor internalization	0.028501	SELE/VEGFA/EGF	3
BP	GO:0015872	dopamine transport	0.028501	SLC6A2/ ABAT/SLC6A3	3
BP	GO:0038066	p38MAPK cascade	0.028501	VEGFA/IL1B/NCF1	3

BP	GO:0042220	response to cocaine	0.028501	OPRM1/ ABAT/SLC6A3	3
BP	GO:0097366	response to bronchodilator	0.028501	ICAM1/SOD1/MMP3	3
BP	GO:2000179	positive regulation of neural precursor cell proliferation	0.028501	VEGFA/EGF/HIF1A	3
BP	GO:1903305	regulation of regulated secretory pathway	0.028659	ADRA1A/CHRM2/HMOX1/ADRA2A/PRK CB	5

BP	GO:0042752	regulation of circadian rhythm	0.029212	PPARG/MAPK8/PPARA/TOP2A	4
BP	GO:0072163	mesonephric epithelium development	0.029212	BCL2/CAT/VEGFA/MYC	4
BP	GO:0072164	mesonephric tubule development	0.029212	BCL2/CAT/VEGFA/MYC	4
BP	GO:0090263	positive regulation of canonical Wnt signaling pathway	0.029212	EGFR/EGF/CAV1/COL1A1	4

BP	GO:0051216	cartilage development	0.029212	RELA/MAPK3/POR/HIF1A/COL1A1/RUNX2	6
BP	GO:0016202	regulation of striated muscle tissue development	0.02934	BCL2/HMGCR/PPARA/CCNB1/ERBB3	5
BP	GO:0016569	covalent chromatin modification	0.029443	PRKCA/MAPK8/MAPK3/SREBF1/NCOA1/VEGFA/IL1B/PRKCB/CCNB1/IGF2	10
BP	GO:0002440	production of molecular mediator of immune response	0.029523	HMOX1/MAPK3/IL10/IL6/IL1B/IL2/CD40LG	7

BP	GO:0010665	regulation of cardiac muscle cell apoptotic process	0.029559	HMGCR/NFE2L2/HSF1	3
BP	GO:0045661	regulation of myoblast differentiation	0.029559	PPARD/CXCL10/IGFBP3	3
BP	GO:0070265	necrotic cell death	0.029559	BAX/CASP8/CAV1	3
BP	GO:0002076	osteoblast development	0.029559	ACHE/RUNX2	2

BP	GO:0002363	alpha-beta T cell lineage commitment	0.029559	BCL2/IL6	2
BP	GO:0002374	cytokine secretion involved in immune response	0.029559	MAPK3/IL10	2
BP	GO:0010523	negative regulation of calcium ion transport into cytosol	0.029559	BCL2/GSTM2	2
BP	GO:0010738	regulation of protein kinase A signaling	0.029559	ADRB2/ADIPOQ	2

BP	GO:0010829	negative regulation of glucose transmembrane transport	0.029559	IL1B/PRKCB	2
BP	GO:0034138	toll-like receptor 3 signaling pathway	0.029559	CASP8/CAV1	2
BP	GO:0042789	mRNA transcription by RNA polymerase II	0.029559	SREBF1/HIF1A	2
BP	GO:0045076	regulation of interleukin-2 biosynthetic process	0.029559	IL1B/IL1A	2

BP	GO:0045737	positive regulation of cyclin-dependent protein serine/threonine kinase activity	0.029559	CCND1/CCNB1	2
BP	GO:0045821	positive regulation of glycolytic process	0.029559	INSR/HIF1A	2
BP	GO:0060438	trachea development	0.029559	MAPK3/MAPK1	2
BP	GO:0072074	kidney mesenchyme development	0.029559	STAT1/MYC	2

BP	GO:0072111	cell proliferation involved in kidney development	0.029559	STAT1/MYC	2
BP	GO:0090201	negative regulation of release of cytochrome c from mitochondria	0.029559	AKT1/BCL2L1	2
BP	GO:0090208	positive regulation of triglyceride metabolic process	0.029559	LDLR/SREBF1	2
BP	GO:1903204	negative regulation of oxidative stress-induced neuron death	0.029559	IL10/HIF1A	2

BP	GO:1903599	positive regulation of autophagy of mitochondrion	0.029559	HIF1A/HK2	2
BP	GO:0010256	endomembrane system organization	0.030345	PRKCA/AR/AKT1/MAPK3/MAPK1/SOD1/CAV1/PRKCB/CCNB1	9
BP	GO:1901861	regulation of muscle tissue development	0.030515	BCL2/HMGCR/PPARA/CCNB1/ERBB3	5
BP	GO:0002699	positive regulation of immune effector process	0.030727	HMOX1/MAPK3/IL6/IL1B/IL2/IFNG	6

BP	GO:0002381	immunoglobulin production involved in immunoglobulin mediated immune response	0.030933	IL10/IL2/CD40LG	3
BP	GO:0031295	T cell costimulation	0.030933	AKT1/CAV1/CD40LG	3
BP	GO:0070206	protein trimerization	0.030933	ADIPOQ/COL1A1/HSF1	3
BP	GO:0098900	regulation of action potential	0.030933	SCN5A/ADRA1A/CAV1	3

BP	GO:0051053	negative regulation of DNA metabolic process	0.031221	PPARG/ADIPOQ/PARP1/CHEK2/HSF1	5
BP	GO:0050663	cytokine secretion	0.031292	NOS2/MAPK3/IL10/IL1A/CRP/CHUK	6
BP	GO:0055017	cardiac muscle tissue growth	0.031738	RXRA/ADRA1A/PPARA/CCNB1	4
BP	GO:1901989	positive regulation of cell cycle phase transition	0.031738	CYP1A1/CCND1/RB1/CCNB1	4

BP	GO:0048634	regulation of muscle organ development	0.031923	BCL2/HMGCR/PPARA/CCNB1/ERBB3	5
BP	GO:0010662	regulation of striated muscle cell apoptotic process	0.031923	HMGCR/NFE2L2/HSF1	3
BP	GO:0031102	neuron projection regeneration	0.031923	BCL2/JUN/SPP1	3
BP	GO:0031294	lymphocyte costimulation	0.031923	AKT1/CAV1/CD40LG	3

BP	GO:0061178	regulation of insulin secretion involved in cellular response to glucose stimulus	0.031923	HMGCR/ADRA2A/HIF1A	3
BP	GO:0006525	arginine metabolic process	0.031923	NOS2/NOS3	2
BP	GO:0007620	copulation	0.031923	SLC6A4/ABAT	2
BP	GO:0010866	regulation of triglyceride biosynthetic process	0.031923	LDLR/SREBF1	2

BP	GO:0019370	leukotriene biosynthetic process	0.031923	ALOX5/LTA4H	2
BP	GO:0030220	platelet formation	0.031923	CASP9/CASP3	2
BP	GO:0030813	positive regulation of nucleotide catabolic process	0.031923	INSR/HIF1A	2
BP	GO:0032098	regulation of appetite	0.031923	OPRM1/PPARA	2

BP	GO:0032495	response to muramyl dipeptide	0.031923	RELA/NFKBIA	2
BP	GO:0032891	negative regulation of organic acid transport	0.031923	AKT1/ABAT	2
BP	GO:0034393	positive regulation of smooth muscle cell apoptotic process	0.031923	PPARG/IFNG	2
BP	GO:0035458	cellular response to interferon-beta	0.031923	STAT1/IRF1	2

BP	GO:0042533	tumor necrosis factor biosynthetic process	0.031923	IL10/HSPB1	2
BP	GO:0042534	regulation of tumor necrosis factor biosynthetic process	0.031923	IL10/HSPB1	2
BP	GO:0046716	muscle cell cellular homeostasis	0.031923	SOD1/HIF1A	2
BP	GO:0051195	negative regulation of cofactor metabolic process	0.031923	PPARA/MMP3	2

BP	GO:0051197	positive regulation of coenzyme metabolic process	0.031923	INSR/HIF1A	2
BP	GO:0060575	intestinal epithelial cell differentiation	0.031923	CDKN1A/HIF1A	2
BP	GO:0060716	labyrinthine layer blood vessel development	0.031923	AKT1/MAPK1	2
BP	GO:0061436	establishment of skin barrier	0.031923	TP63/CLDN4	2

BP	GO:0070584	mitochondrion morphogenesis	0.031923	BAX/BCL2L1	2
BP	GO:0070920	regulation of production of small RNA involved in gene silencing by RNA	0.031923	ESR1/EGFR	2
BP	GO:0086014	atrial cardiac muscle cell action potential	0.031923	SCN5A/GJA1	2
BP	GO:0086026	atrial cardiac muscle cell to AV node cell signaling	0.031923	SCN5A/GJA1	2

BP	GO:0086066	atrial cardiac muscle cell to AV node cell communication	0.031923	SCN5A/GJA1	2
BP	GO:0097242	amyloid-beta clearance	0.031923	INSR/LDLR	2
BP	GO:1902884	positive regulation of response to oxidative stress	0.031923	SOD1/MMP3	2
BP	GO:0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	0.032085	JUN/MAPK3/GOT1/FOS/CAV1/PARP1/C OL3A1/RUNX2	8

BP	GO:0001823	mesonephros development	0.032164	BCL2/CAT/VEGFA/MYC	4
BP	GO:0002042	cell migration involved in sprouting angiogenesis	0.032164	PTGS2/AKT1/HMOX1/VEGFA	4
BP	GO:0002286	T cell activation involved in immune response	0.032164	ICAM1/IL6/IL2/IFNG	4
BP	GO:0006476	protein deacetylation	0.032164	MAPK8/SREBF1/VEGFA/IFNG	4

BP	GO:0048489	synaptic vesicle transport	0.032164	ADRA1A/CHRM2/MAP2/SLC2A4/PRKCB	5
BP	GO:0097480	establishment of synaptic vesicle localization	0.032164	ADRA1A/CHRM2/MAP2/SLC2A4/PRKCB	5
BP	GO:0016579	protein deubiquitination	0.032923	ADRB2/AR/PSMD3/ESR1/NFKBIA/HIF1A/MYC	7
BP	GO:1901222	regulation of NIK/NF-kappaB signaling	0.033181	RELA/EGFR/NFKBIA/IL1B	4

BP	GO:2001023	regulation of response to drug	0.033181	ABAT/NCOA1/IL10/NFE2L2	4
BP	GO:0017038	protein import	0.033197	PTGS2/AKT1/AKR1C3/MAPK1/NFKBIA/I FNG	6
BP	GO:0010659	cardiac muscle cell apoptotic process	0.033197	HMGCR/NFE2L2/HSF1	3
BP	GO:0032890	regulation of organic acid transport	0.033197	AKT1/ABAT/IL1B	3

BP	GO:0042130	negative regulation of T cell proliferation	0.033197	CASP3/IL10/ERBB2	3
BP	GO:0086065	cell communication involved in cardiac conduction	0.033197	SCN5A/CAV1/GJA1	3
BP	GO:1903078	positive regulation of protein localization to plasma membrane	0.033197	AKT1/EGFR/IFNG	3
BP	GO:0043588	skin development	0.033525	BCL2/CASP3/RELA/AKR1C3/EGFR/TP63/COL1A1/COL3A1/CLDN4	9

BP	GO:0060079	excitatory postsynaptic potential	0.034133	ADRB2/CHRNA2/OPRM1/AKT1	4
BP	GO:0002429	immune response-activating cell surface receptor signaling pathway	0.03434	BCL2/BAX/RELA/IKBKB/MAPK3/MAPK1/RAF1/PRKCB/CHUK	9
BP	GO:0002819	regulation of adaptive immune response	0.03434	IL10/IL6/IL1B/IL2/IRF1	5
BP	GO:0016236	macroautophagy	0.03434	ADRB2/CASP3/AKT1/MAPK8/HMOX1/MAPK3/HIF1A	7

BP	GO:0050768	negative regulation of neurogenesis	0.03434	SLC6A4/MAP2/LDLR/IL6/IL1B/COL3A1/S PP1	7
BP	GO:0002438	acute inflammatory response to antigenic stimulus	0.03434	OPRM1/ICAM1	2
BP	GO:0003180	aortic valve morphogenesis	0.03434	RB1/NOS3	2
BP	GO:0006067	ethanol metabolic process	0.03434	ADH1C/SULT1E1	2

BP	GO:0015874	norepinephrine transport	0.03434	SLC6A2/ADRA2A	2
BP	GO:0035162	embryonic hemopoiesis	0.03434	VEGFA/HIF1A	2
BP	GO:0035357	peroxisome proliferator activated receptor signaling pathway	0.03434	RXRA/PPARG	2
BP	GO:0035743	CD4-positive, alpha-beta T cell cytokine production	0.03434	IL6/IL1B	2

BP	GO:0035809	regulation of urine volume	0.03434	HAS2/ AKR1B1	2
BP	GO:0036344	platelet morphogenesis	0.03434	CASP9/ CASP3	2
BP	GO:0043369	CD4-positive or CD8-positive, alpha-beta T cell lineage commitment	0.03434	BCL2/IL6	2
BP	GO:0043496	regulation of protein homodimerization activity	0.03434	BCL2/BAX	2

BP	GO:0044346	fibroblast apoptotic process	0.03434	TP63/MYC	2
BP	GO:0050857	positive regulation of antigen receptor-mediated signaling pathway	0.03434	RELA/PRKCB	2
BP	GO:0051349	positive regulation of lyase activity	0.03434	NOS2/NOS3	2
BP	GO:0060713	labyrinthine layer morphogenesis	0.03434	NCOA1/IL10	2

BP	GO:0097709	connective tissue replacement	0.03434	HIF1A/IL1A	2
BP	GO:1904753	negative regulation of vascular associated smooth muscle cell migration	0.03434	ADIPOQ/NFE2L2	2
BP	GO:0002066	columnar/cuboidal epithelial cell development	0.03434	SOD1/CDKN1A/HIF1A	3
BP	GO:0050766	positive regulation of phagocytosis	0.03434	PPARG/IL1B/CCL2	3

BP	GO:0070527	platelet aggregation	0.03434	PRKCA/ ABAT/ HSPB1	3
BP	GO:0009205	purine ribonucleoside triphosphate metabolic process	0.034716	INSR/PPARA/EIF6/HIF1A/CCNB1/PARP1/ HK2	7
BP	GO:0017158	regulation of calcium ion-dependent exocytosis	0.034776	ADRA1A/CHRM2/ ADRA2A/PRKCB	4
BP	GO:0043266	regulation of potassium ion transport	0.035878	KCNH2/ ADRA2A/CAV1/NOS3	4

BP	GO:0010658	striated muscle cell apoptotic process	0.035881	HMGCR/NFE2L2/HSF1	3
BP	GO:0090287	regulation of cellular response to growth factor stimulus	0.035881	GOT1/VEGFA/HIF1A/CAV1/IL1B/PRKCB/RUNX2	7
BP	GO:0019722	calcium-mediated signaling	0.036892	SELE/VCAM1/GSTM2/EGFR/CXCL8/ERBB3	6
BP	GO:0009062	fatty acid catabolic process	0.036944	AKT1/PPARA/ADIPOQ/PPARD	4

BP	GO:0002052	positive regulation of neuroblast proliferation	0.037144	VEGFA/HIF1A	2
BP	GO:0007530	sex determination	0.037144	AR/INSR	2
BP	GO:0009651	response to salt stress	0.037144	BAX/AKR1B1	2
BP	GO:0010804	negative regulation of tumor necrosis factor-mediated signaling pathway	0.037144	GSTP1/ADIPOQ	2

BP	GO:0032469	endoplasmic reticulum calcium ion homeostasis	0.037144	BCL2/BAX	2
BP	GO:0032727	positive regulation of interferon-alpha production	0.037144	STAT1/CHUK	2
BP	GO:0033561	regulation of water loss via skin	0.037144	TP63/CLDN4	2
BP	GO:0042094	interleukin-2 biosynthetic process	0.037144	IL1B/IL1A	2

BP	GO:0051000	positive regulation of nitric-oxide synthase activity	0.037144	AKT1/HIF1A	2
BP	GO:0071677	positive regulation of mononuclear cell migration	0.037144	SERPINE1/CXCL10	2
BP	GO:0007519	skeletal muscle tissue development	0.037144	BCL2/HMGCR/FOS/RB1/CAV1	5
BP	GO:0050954	sensory perception of mechanical stimulus	0.037144	CASP3/ICAM1/SOD1/BIRC5/COL1A1	5

BP	GO:0061564	axon development	0.037144	BCL2/JUN/CASP3/PRKCA/MAP2/MAPK3 /MAPK1/VEGFA/ERBB2/SPP1	10
BP	GO:0002294	CD4-positive, alpha-beta T cell differentiation involved in immune response	0.037144	IL6/IL2/IFNG	3
BP	GO:0002562	somatic diversification of immune receptors via germline recombination within a single locus	0.037144	IL10/IL2/CD40LG	3
BP	GO:0016444	somatic cell DNA recombination	0.037144	IL10/IL2/CD40LG	3

BP	GO:0034113	heterotypic cell-cell adhesion	0.037144	ADIPOQ/IL10/IL1B	3
BP	GO:0046173	polyol biosynthetic process	0.037144	CYP3A4/GOT1/AKR1B1	3
BP	GO:2000401	regulation of lymphocyte migration	0.037144	AKT1/CCL2/CXCL10	3
BP	GO:0003300	cardiac muscle hypertrophy	0.0377	ADRA1A/PRKCA/PPARA/PARP1	4

BP	GO:0060419	heart growth	0.0377	RXRA/ADRA1A/PPARA/CCNB1	4
BP	GO:2001257	regulation of cation channel activity	0.037917	ADRB2/OPRM1/GSTM2/MMP9/CAV1	5
BP	GO:0009167	purine ribonucleoside monophosphate metabolic process	0.03794	INSR/PPARA/EIF6/HIF1A/CCNB1/PARP1 /HK2	7
BP	GO:0009199	ribonucleoside triphosphate metabolic process	0.03794	INSR/PPARA/EIF6/HIF1A/CCNB1/PARP1 /HK2	7

BP	GO:0009126	purine nucleoside monophosphate metabolic process	0.038553	INSR/PPARA/EIF6/HIF1A/CCNB1/PARP1 /HK2	7
BP	GO:0009144	purine nucleoside triphosphate metabolic process	0.038553	INSR/PPARA/EIF6/HIF1A/CCNB1/PARP1 /HK2	7
BP	GO:0001658	branching involved in ureteric bud morphogenesis	0.038601	BCL2/VEGFA/MYC	3
BP	GO:0002287	alpha-beta T cell activation involved in immune response	0.038601	IL6/IL2/IFNG	3

BP	GO:0002293	alpha-beta T cell differentiation involved in immune response	0.038601	IL6/IL2/IFNG	3
BP	GO:0002753	cytoplasmic pattern recognition receptor signaling pathway	0.038601	CASP8/RELA/NFKBIA	3
BP	GO:0016445	somatic diversification of immunoglobulins	0.038601	IL10/IL2/CD40LG	3
BP	GO:0055002	striated muscle cell development	0.038635	ADRA1A/BCL2/PPARA/VEGFA/CCNB1	5

BP	GO:0048738	cardiac muscle tissue development	0.03925	RXRA/ADRA1A/PPARA/VEGFA/CCNB1/ ERBB3	6
BP	GO:0014897	striated muscle hypertrophy	0.039658	ADRA1A/PRKCA/PPARA/PARP1	4
BP	GO:0002021	response to dietary excess	0.039658	ADRB2/ADRB1	2
BP	GO:0019400	alditol metabolic process	0.039658	GOT1/AKR1B1	2

BP	GO:0032366	intracellular sterol transport	0.039658	LDLR/CES1	2
BP	GO:0032367	intracellular cholesterol transport	0.039658	LDLR/CES1	2
BP	GO:0032799	low-density lipoprotein receptor particle metabolic process	0.039658	PPARG/ADIPOQ	2
BP	GO:0034505	tooth mineralization	0.039658	PPARA/COL1A1	2

BP	GO:0036037	CD8-positive, alpha-beta T cell activation	0.039658	BCL2/IRF1	2
BP	GO:0050996	positive regulation of lipid catabolic process	0.039658	PPARA/IL1B	2
BP	GO:0051220	cytoplasmic sequestering of protein	0.039658	IL10/NFKBIA	2
BP	GO:0051589	negative regulation of neurotransmitter transport	0.039658	ABAT/MAOB	2

BP	GO:0071157	negative regulation of cell cycle arrest	0.039658	CCND1/CHEK2	2
BP	GO:0071404	cellular response to low-density lipoprotein particle stimulus	0.039658	PPARG/LDLR	2
BP	GO:0072243	metanephric nephron epithelium development	0.039658	STAT1/ADIPOQ	2
BP	GO:1903306	negative regulation of regulated secretory pathway	0.039658	HMOX1/ADRA2A	2

BP	GO:1903579	negative regulation of ATP metabolic process	0.039658	PPARA/PARP1	2
BP	GO:1903589	positive regulation of blood vessel endothelial cell proliferation involved in sprouting angiogenesis	0.039658	HMOX1/VEGFA	2
BP	GO:0006913	nucleocytoplasmic transport	0.039658	PTGS2/AKT1/AKR1C3/MAPK1/EIF6/NFKBIA/IL1B/IFNG	8
BP	GO:0045669	positive regulation of osteoblast differentiation	0.039882	IL6/TP63/RUNX2	3

BP	GO:1904356	regulation of telomere maintenance via telomere lengthening	0.039882	MAPK3/MAPK1/PARP1	3
BP	GO:0006338	chromatin remodeling	0.04003	ESR1/RB1/TP63/TOP1/MYC	5
BP	GO:0097479	synaptic vesicle localization	0.04003	ADRA1A/CHRM2/MAP2/SLC2A4/PRKCB	5
BP	GO:1903510	mucopolysaccharide metabolic process	0.040564	AKT1/HAS2/EGF/IL1B	4

BP	GO:0045619	regulation of lymphocyte differentiation	0.04093	SOD1/ERBB2/IL2/IFNG/IRF1	5
BP	GO:0070646	protein modification by small protein removal	0.041262	ADRB2/AR/PSMD3/ESR1/NFKBIA/HIF1A/MYC	7
BP	GO:0051169	nuclear transport	0.041294	PTGS2/AKT1/AKR1C3/MAPK1/EIF6/NFKBIA/IL1B/IFNG	8
BP	GO:0045685	regulation of glial cell differentiation	0.041483	PPARG/RELA/LDLR	3

BP	GO:0014896	muscle hypertrophy	0.041575	ADRA1A/PRKCA/PPARA/PARP1	4
BP	GO:0021987	cerebral cortex development	0.041575	BAX/EGFR/HIF1A/COL3A1	4
BP	GO:0035601	protein deacylation	0.041575	MAPK8/SREBF1/VEGFA/IFNG	4
BP	GO:0045446	endothelial cell differentiation	0.041575	IKBKB/ICAM1/FASN/IL1B	4

BP	GO:0060349	bone morphogenesis	0.041575	HAS2/POR/COL1A1/RUNX2	4
BP	GO:0061337	cardiac conduction	0.041575	KCNH2/SCN5A/CAV1/GJA1	4
BP	GO:0002719	negative regulation of cytokine production involved in immune response	0.042359	HMOX1/IL10	2
BP	GO:0003176	aortic valve development	0.042359	RB1/NOS3	2

BP	GO:0006359	regulation of transcription by RNA polymerase III	0.042359	AR/ERBB2	2
BP	GO:0010288	response to lead ion	0.042359	PTGS2/CAT	2
BP	GO:0032104	regulation of response to extracellular stimulus	0.042359	OPRM1/PPARA	2
BP	GO:0032107	regulation of response to nutrient levels	0.042359	OPRM1/PPARA	2

BP	GO:0033081	regulation of T cell differentiation in thymus	0.042359	SOD1/ERBB2	2
BP	GO:0034110	regulation of homotypic cell-cell adhesion	0.042359	PRKCA/ABAT	2
BP	GO:0043567	regulation of insulin-like growth factor receptor signaling pathway	0.042359	AR/IGFBP3	2
BP	GO:0045672	positive regulation of osteoclast differentiation	0.042359	FOS/IFNG	2

BP	GO:0086064	cell communication by electrical coupling involved in cardiac conduction	0.042359	CAV1/GJA1	2
BP	GO:0090025	regulation of monocyte chemotaxis	0.042359	SERPINE1/CXCL10	2
BP	GO:0098810	neurotransmitter reuptake	0.042359	SLC6A4/SLC6A2	2
BP	GO:2000191	regulation of fatty acid transport	0.042359	AKT1/IL1B	2

BP	GO:2001026	regulation of endothelial cell chemotaxis	0.042359	VEGFA/HSPB1	2
BP	GO:0007613	memory	0.04241	PTGS2/SLC6A4/INSR/LDLR	4
BP	GO:0046717	acid secretion	0.04241	NOS2/ABAT/IL1B/PTGER3	4
BP	GO:0046822	regulation of nucleocytoplasmic transport	0.04241	PTGS2/MAPK1/IL1B/IFNG	4

BP	GO:0098732	macromolecule deacylation	0.04241	MAPK8/SREBF1/VEGFA/IFNG	4
BP	GO:0002532	production of molecular mediator involved in inflammatory response	0.04267	NOS2/ALOX5/SERPINE1	3
BP	GO:0048247	lymphocyte chemotaxis	0.04267	CCL2/CXCL11/CXCL10	3
BP	GO:1904377	positive regulation of protein localization to cell periphery	0.04267	AKT1/EGFR/IFNG	3

BP	GO:0021543	pallium development	0.043128	BAX/CASP3/EGFR/HIF1A/COL3A1	5
BP	GO:0043901	negative regulation of multi-organism process	0.043128	JUN/STAT1/SLPI/IL10/MPO	5
BP	GO:0060538	skeletal muscle organ development	0.044088	BCL2/HMGCR/FOS/RB1/CAV1	5
BP	GO:0042306	regulation of protein import into nucleus	0.044381	PTGS2/MAPK1/IFNG	3

BP	GO:0051961	negative regulation of nervous system development	0.044703	SLC6A4/MAP2/LDLR/IL6/IL1B/COL3A1/SPP1	7
BP	GO:0070252	actin-mediated cell contraction	0.044703	KCNH2/SCN5A/CAV1/GJA1	4
BP	GO:0098693	regulation of synaptic vesicle cycle	0.044703	ADRA1A/CHRM2/SLC2A4/PRKCB	4
BP	GO:0006650	glycerophospholipid metabolic process	0.044877	PON1/ACHE/ESR1/LDLR/EGFR/EGF/ERBB2/ERBB3	8

BP	GO:0032874	positive regulation of stress-activated MAPK cascade	0.044951	HMGCR/VEGFA/IL1B/NCF1/CD40LG	5
BP	GO:0002697	regulation of immune effector process	0.04514	STAT1/HMOX1/MAPK3/IL10/IL6/IL1B/IL2/IFNG/CD40LG	9
BP	GO:0010460	positive regulation of heart rate	0.04514	ADRA1A/ADRB1	2
BP	GO:0019054	modulation by virus of host process	0.04514	CASP8/BCL2L1	2

BP	GO:0031069	hair follicle morphogenesis	0.04514	BCL2/TP63	2
BP	GO:0045662	negative regulation of myoblast differentiation	0.04514	PPARD/CXCL10	2
BP	GO:0050901	leukocyte tethering or rolling	0.04514	SELE/VCAM1	2
BP	GO:0060343	trabecula formation	0.04514	MMP2/COL1A1	2

BP	GO:1900543	negative regulation of purine nucleotide metabolic process	0.04514	PPARA/PARP1	2
BP	GO:1901032	negative regulation of response to reactive oxygen species	0.04514	IL10/NFE2L2	2
BP	GO:1903206	negative regulation of hydrogen peroxide-induced cell death	0.04514	IL10/NFE2L2	2
BP	GO:1905208	negative regulation of cardiocyte differentiation	0.04514	PPARA/EGFR	2

BP	GO:2001039	negative regulation of cellular response to drug	0.04514	IL10/NFE2L2	2
BP	GO:0070304	positive regulation of stress-activated protein kinase signaling cascade	0.045669	HMGCR/VEGFA/IL1B/NCF1/CD40LG	5
BP	GO:0009161	ribonucleoside monophosphate metabolic process	0.045746	INSR/PPARA/EIF6/HIF1A/CCNB1/PARP1/HK2	7
BP	GO:0034121	regulation of toll-like receptor signaling pathway	0.045746	ESR1/CAV1/IRF1	3

BP	GO:0060675	ureteric bud morphogenesis	0.045746	BCL2/VEGFA/MYC	3
BP	GO:0007272	ensheathment of neurons	0.04681	AKT1/SOD1/ERBB2/PPARD	4
BP	GO:0008366	axon ensheathment	0.04681	AKT1/SOD1/ERBB2/PPARD	4
BP	GO:0051209	release of sequestered calcium ion into cytosol	0.04681	BAX/GSTM2/CXCL11/CXCL10	4

BP	GO:0002292	T cell differentiation involved in immune response	0.047419	IL6/IL2/IFNG	3
BP	GO:0010812	negative regulation of cell-substrate adhesion	0.047419	SERPINE1/COL1A1/RASA1	3
BP	GO:0015909	long-chain fatty acid transport	0.047419	PPARG/AKT1/ACACA	3
BP	GO:0072171	mesonephric tubule morphogenesis	0.047419	BCL2/VEGFA/MYC	3

BP	GO:2000573	positive regulation of DNA biosynthetic process	0.047419	MAPK3/MAPK1/MYC	3
BP	GO:0001958	endochondral ossification	0.047885	COL1A1/RUNX2	2
BP	GO:0002360	T cell lineage commitment	0.047885	BCL2/IL6	2
BP	GO:0002479	antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent	0.047885	IKBKB/CHUK	2

BP	GO:0022011	myelination in peripheral nervous system	0.047885	AKT1/SOD1	2
BP	GO:0032292	peripheral nervous system axon ensheathment	0.047885	AKT1/SOD1	2
BP	GO:0033137	negative regulation of peptidyl-serine phosphorylation	0.047885	BAX/CAV1	2
BP	GO:0036075	replacement ossification	0.047885	COL1A1/RUNX2	2

BP	GO:0045736	negative regulation of cyclin-dependent protein serine/threonine kinase activity	0.047885	CASP3/CDKN1A	2
BP	GO:0045980	negative regulation of nucleotide metabolic process	0.047885	PPARA/PARP1	2
BP	GO:0051953	negative regulation of amine transport	0.047885	ABAT/ADRA2A	2
BP	GO:0060307	regulation of ventricular cardiac muscle cell membrane repolarization	0.047885	KCNH2/SCN5A	2

BP	GO:0060706	cell differentiation involved in embryonic placenta development	0.047885	CASP8/ AKT1	2
BP	GO:0070168	negative regulation of biomineral tissue development	0.047885	HIF1A/NOS3	2
BP	GO:0070528	protein kinase C signaling	0.047885	ADRA1A/VEGFA	2
BP	GO:0071168	protein localization to chromatin	0.047885	ESR1/RB1	2

BP	GO:0072202	cell differentiation involved in metanephros development	0.047885	STAT1/ADIPOQ	2
BP	GO:0072539	T-helper 17 cell differentiation	0.047885	IL6/IL2	2
BP	GO:1901623	regulation of lymphocyte chemotaxis	0.047885	CCL2/CXCL10	2
BP	GO:1904353	regulation of telomere capping	0.047885	MAPK3/MAPK1	2

BP	GO:0032412	regulation of ion transmembrane transporter activity	0.048378	ADRB2/OPRM1/GSTM2/ADRA2A/MMP9/ CAV1	6
BP	GO:0034329	cell junction assembly	0.048378	BCL2/PRKCA/IKBKB/VEGFA/CAV1/GJA1	6
BP	GO:0030900	forebrain development	0.048413	SCN5A/BAX/CASP3/SLC6A3/EGFR/HIF1 A/COL3A1/E2F1	8
BP	GO:1904589	regulation of protein import	0.048707	PTGS2/MAPK1/IFNG	3

BP	GO:0009063	cellular amino acid catabolic process	0.048707	NOS2/GOT1/ABAT/NOS3	4
BP	GO:0043488	regulation of mRNA stability	0.048707	PRKCA/AKT1/HSPB1/E2F1	4
BP	GO:0051283	negative regulation of sequestering of calcium ion	0.048707	BAX/GSTM2/CXCL11/CXCL10	4
BP	GO:1903052	positive regulation of proteolysis involved in cellular protein catabolic process	0.048707	AKT1/EGF/CAV1/NFE2L2	4

BP	GO:0035637	multicellular organismal signaling	0.048845	KCNH2/SCN5A/SOD1/CAV1/GJA1	5
BP	GO:0045333	cellular respiration	0.048845	NOS2/CYP1A2/CAT/HIF1A/CCNB1	5
BP	GO:0055001	muscle cell development	0.048845	ADRA1A/BCL2/PPARA/VEGFA/CCNB1	5
CC	GO:0045121	membrane raft	5.19E-13	PTGS2/SCN5A/ADRA1A/ADRA1B/SLC6A 4/OPRM1/CASP3/CASP8/SLC6A2/IKBKB/ HMOX1/ICAM1/SELE/SLC2A4/INSR/MA PK3/MAPK1/SLC6A3/EGFR/CAV1/GJA1/ NOS3/CTSD	23

CC	GO:0098857	membrane microdomain	5.19E-13	PTGS2/SCN5A/ADRA1A/ADRA1B/SLC6A4/OPRM1/CASP3/CASP8/SLC6A2/IKBKB/HMOX1/ICAM1/SELE/SLC2A4/INSR/MAPK3/MAPK1/SLC6A3/EGFR/CAV1/GJA1/NOS3/CTSD	23
CC	GO:0098589	membrane region	7.43E-13	PTGS2/SCN5A/ADRA1A/ADRA1B/SLC6A4/OPRM1/CASP3/CASP8/SLC6A2/IKBKB/HMOX1/ICAM1/SELE/SLC2A4/INSR/MAPK3/MAPK1/SLC6A3/EGFR/CAV1/GJA1/NOS3/CTSD	23
CC	GO:0005901	caveola	2.60E-10	PTGS2/SCN5A/ADRA1A/ADRA1B/HMOX1/SELE/INSR/MAPK3/MAPK1/SLC6A3/CAV1/NOS3	12
CC	GO:0044853	plasma membrane raft	6.31E-09	PTGS2/SCN5A/ADRA1A/ADRA1B/HMOX1/SELE/INSR/MAPK3/MAPK1/SLC6A3/CAV1/NOS3	12

CC	GO:0043235	receptor complex	7.45E-07	RXRA/ADRB2/CHRNA2/GABRA1/IKBKB/AHR/INSR/LDLR/MTTP/NR3C2/ADRA2A/EGFR/EGF/IL6/ERBB2/ABCG2/CHUK/ERBB3	18
CC	GO:0090575	RNA polymerase II transcription factor complex	8.56E-06	RXRA/JUN/PPARG/NR1I2/NR1I3/PPARA/FOS/RB1/HIF1A/PPARD/E2F1	11
CC	GO:0005667	transcription factor complex	2.49E-05	RXRA/JUN/PPARG/RELA/NR1I2/AHR/NR1I3/PPARA/FOS/RB1/HIF1A/PARP1/PPARD/RUNX2/E2F1	15
CC	GO:0099055	integral component of postsynaptic membrane	3.30E-05	CHRM3/CHRM1/ADRA1A/CHRM2/SLC6A4/OPRM1/GABRA1/SLC6A3/ADRB1	9

CC	GO:0098936	intrinsic component of postsynaptic membrane	4.23E-05	CHRM3/CHRM1/ADRA1A/CHRM2/SLC6A4/OPRM1/GABRA1/SLC6A3/ADRB1	9
CC	GO:0044798	nuclear transcription factor complex	4.28E-05	RXRA/JUN/PPARG/NR1I2/NR1I3/PPARA/FOS/RB1/HIF1A/PPARD/E2F1	11
CC	GO:0031012	extracellular matrix	4.29E-05	PRSS1/ACHE/MMP1/ICAM1/SLPI/SOD1/ADIPOQ/MMP3/VEGFA/MMP2/MMP9/F3/SERPINE1/COL1A1/COL3A1/CTSD/PCOLCE	17
CC	GO:0031983	vesicle lumen	4.66E-05	ALOX5/GSTP1/PSMD3/SLPI/MAPK1/CAT/APOB/EGFR/VEGFA/EGF/SERPINE1/MPO/CTSD/IGF2	14

CC	GO:0099056	integral component of presynaptic membrane	9.80E-05	CHRM3/CHRM1/ADRA1A/CHRM2/SLC6A4/OPRM1/SLC6A3	7
CC	GO:0000790	nuclear chromatin	0.000108	RXRA/JUN/AR/RELA/STAT1/ESR1/NCOA1/RB1/TP63/MYC/PPARD/RUNX2/E2F1/IRF1	14
CC	GO:0062023	collagen-containing extracellular matrix	0.000158	PRSS1/ACHE/ICAM1/SLPI/ADIPOQ/MMP2/MMP9/F3/SERPINE1/COL1A1/COL3A1/CTSD/PCOLCE	13
CC	GO:0099699	integral component of synaptic membrane	0.000162	CHRM3/CHRM1/ADRA1A/CHRM2/SLC6A4/OPRM1/GABRA1/SLC6A3/ADRB1	9

CC	GO:0098889	intrinsic component of presynaptic membrane	0.000162	CHRM3/CHRM1/ADRA1A/CHRM2/SLC6A4/OPRM1/SLC6A3	7
CC	GO:0060205	cytoplasmic vesicle lumen	0.000162	ALOX5/GSTP1/PSMD3/SLPI/MAPK1/CAT/APOB/VEGFA/EGF/SERPINE1/MPO/CTSD/IGF2	13
CC	GO:1904813	ficolin-1-rich granule lumen	0.000224	ALOX5/GSTP1/PSMD3/MAPK1/CAT/LTA4H/MMP9/CTSD	8
CC	GO:0099240	intrinsic component of synaptic membrane	0.000251	CHRM3/CHRM1/ADRA1A/CHRM2/SLC6A4/OPRM1/GABRA1/SLC6A3/ADRB1	9

CC	GO:0034774	secretory granule lumen	0.000409	ALOX5/GSTP1/PSMD3/SLPI/MAPK1/CAT/VEGFA/EGF/SERPINE1/MPO/CTSD/IGF2	12
CC	GO:0005741	mitochondrial outer membrane	0.000435	PGR/BCL2/BAX/CASP8/MAOB/MAOA/BCL2L1/RAF1/HK2	9
CC	GO:0101002	ficolin-1-rich granule	0.000517	ALOX5/GSTP1/PSMD3/MAPK1/CAT/LTA4H/MMP9/MGAM/CTSD	9
CC	GO:1902911	protein kinase complex	0.00057	IKBKB/INSR/CCND1/CDKN1A/RB1/CCNB1/CHUK	7

CC	GO:0120111	neuron projection cytoplasm	0.000973	OPRM1/MAP2/MAPK1/SOD1/HIF1A/HSP B1	6
CC	GO:0031968	organelle outer membrane	0.000978	PGR/BCL2/BAX/CASP8/MAOB/MAOA/B CL2L1/RAF1/HK2	9
CC	GO:0019867	outer membrane	0.000998	PGR/BCL2/BAX/CASP8/MAOB/MAOA/B CL2L1/RAF1/HK2	9
CC	GO:0042734	presynaptic membrane	0.000998	CHRM3/CHRM1/ADRA1A/CHRM2/SLC6 A4/OPRM1/SLC6A2/SLC6A3	8

CC	GO:0043025	neuronal cell body	0.001042	CHRM2/OPRM1/CASP3/MAP2/SLC6A2/INSR/MAPK1/SOD1/APOB/SLC6A3/ELK1/TOP1/NCF1/NQO1	14
CC	GO:0016323	basolateral plasma membrane	0.001178	CHRM3/LDLR/MTTP/ABCC1/ADRA2A/EGFR/ERBB2/CLDN4/ERBB3	9
CC	GO:1902554	serine/threonine protein kinase complex	0.001178	IKBKB/CCND1/CDKN1A/RB1/CCNB1/CHUK	6
CC	GO:0045211	postsynaptic membrane	0.001314	CHRM3/CHRM1/CHRM4/ADRA1A/CHRM2/CHRNA2/SLC6A4/OPRM1/GABRA1/SLC6A3/ADRB1	11

CC	GO:0009925	basal plasma membrane	0.001973	EGFR/ERBB2/CLDN4/ERBB3	4
CC	GO:0032839	dendrite cytoplasm	0.001973	OPRM1/MAP2/MAPK1/SOD1	4
CC	GO:0005635	nuclear envelope	0.002018	ADRA1A/ADRA1B/BCL2/BAX/ALOX5/IN SR/MAPK3/SREBF1/EGFR/BCL2L1/PTGER 3/SULT1E1/PARP1	13
CC	GO:0005788	endoplasmic reticulum lumen	0.002932	PTGS2/F7/MTTP/APOB/CES1/IL6/COL1A 1/COL3A1/SPP1/IGFBP3	10

CC	GO:0098793	presynapse	0.002932	CHRM3/CHRM1/ADRA1A/CHRM2/SLC6A4/OPRM1/SLC6A2/SLC2A4/GOT1/SLC6A3/BCL2L1/ELK1/PRKCB	13
CC	GO:0030665	clathrin-coated vesicle membrane	0.002993	CHRM2/ADRB2/LDLR/APOB/EGFR/EGF	6
CC	GO:0031143	pseudopodium	0.003286	MAPK3/MAPK1/RAF1	3
CC	GO:0097060	synaptic membrane	0.003423	CHRM3/CHRM1/CHRM4/ADRA1A/CHRM2/CHRNA2/SLC6A4/OPRM1/GABRA1/SLC6A2/SLC6A3/ADRB1	12

CC	GO:0000307	cyclin-dependent protein kinase holoenzyme complex	0.003423	CCND1/CDKN1A/RB1/CCNB1	4
CC	GO:0043679	axon terminus	0.004995	CHRM3/CHRM1/CHRM2/GOT1/ELK1/PR KCB	6
CC	GO:0030662	coated vesicle membrane	0.006438	CHRM2/ADRB2/LDLR/APOB/SREBF1/EG FR/EGF	7
CC	GO:0045178	basal part of cell	0.007363	EGFR/ERBB2/CLDN4/ERBB3	4

CC	GO:0030136	clathrin-coated vesicle	0.007503	CHRM2/ADRB2/SLC2A4/LDLR/APOB/EGFR/EGF	7
CC	GO:0042383	sarcolemma	0.007811	SCN5A/ADRA1A/OPRM1/VCAM1/SLC2A4/CAV1	6
CC	GO:0044306	neuron projection terminus	0.009246	CHRM3/CHRM1/CHRM2/GOT1/ELK1/PRKCB	6
CC	GO:0033267	axon part	0.011037	CHRM3/CHRM1/CHRM2/MAP2/SOD1/GOT1/ELK1/HIF1A/PRKCB/HSPB1	10

CC	GO:0045177	apical part of cell	0.011037	ADRB2/VCAM1/LDLR/EGFR/ERBB2/MGAM/PLAT/ABCG2/CLDN4/ERBB3	10
CC	GO:0032838	plasma membrane bounded cell projection cytoplasm	0.011037	OPRM1/MAP2/MAPK1/SOD1/AKR1B1/HIF1A/HSPB1	7
CC	GO:0031093	platelet alpha granule lumen	0.017528	VEGFA/EGF/SERPINE1/IGF2	4
CC	GO:0005925	focal adhesion	0.018119	OPRM1/ICAM1/MAPK3/MAPK1/CAT/PLAU/EGFR/CAV1/GJA1/HSPB1	10

CC	GO:0005924	cell-substrate adherens junction	0.018337	OPRM1/ICAM1/MAPK3/MAPK1/CAT/PL AU/EGFR/CAV1/GJA1/HSPB1	10
CC	GO:0005769	early endosome	0.018337	ADRB2/VCAM1/MAPK3/MAPK1/LDLR/A POB/ADRB1/EGFR/CAV1	9
CC	GO:0008385	IkappaB kinase complex	0.018337	IKBKB/CHUK	2
CC	GO:0098981	cholinergic synapse	0.018337	CHRM1/CHRM2	2

CC	GO:0030135	coated vesicle	0.018395	CHRM2/ADRB2/SLC2A4/LDLR/APOB/SR EBF1/EGFR/EGF	8
CC	GO:0030055	cell-substrate junction	0.018395	OPRM1/ICAM1/MAPK3/MAPK1/CAT/PL AU/EGFR/CAV1/GJA1/HSPB1	10
CC	GO:0005583	fibrillar collagen trimer	0.020486	COL1A1/COL3A1	2
CC	GO:0035631	CD40 receptor complex	0.020486	IKBKB/CHUK	2

CC	GO:0098643	banded collagen fibril	0.020486	COL1A1/COL3A1	2
CC	GO:0099060	integral component of postsynaptic specialization membrane	0.020712	CHRM3/CHRM1/GABRA1/ADRB1	4
CC	GO:0034358	plasma lipoprotein particle	0.021909	PON1/LDLR/APOB	3
CC	GO:1990777	lipoprotein particle	0.021909	PON1/LDLR/APOB	3

CC	GO:0009897	external side of plasma membrane	0.022095	ICAM1/VCAM1/SLC2A4/INSR/LDLR/GSR /F3/CXCL10/CD40LG	9
CC	GO:0098948	intrinsic component of postsynaptic specialization membrane	0.022445	CHRM3/CHRM1/GABRA1/ADRB1	4
CC	GO:0032590	dendrite membrane	0.023864	OPRM1/GABRA1/INSR	3
CC	GO:0032994	protein-lipid complex	0.023864	PON1/LDLR/APOB	3

CC	GO:0098691	dopaminergic synapse	0.025437	ADRA1A/SLC6A3	2
CC	GO:0034362	low-density lipoprotein particle	0.02909	LDLR/APOB	2
CC	GO:0061695	transferase complex, transferring phosphorus-containing groups	0.035743	IKBKB/INSR/CCND1/CDKN1A/RB1/CCNB1/CHUK	7
CC	GO:0031091	platelet alpha granule	0.036512	VEGFA/EGF/SERPINE1/IGF2	4

CC	GO:1905368	peptidase complex	0.036512	F7/PSMD3/F3/HSPB1	4
CC	GO:0005819	spindle	0.039875	AKT1/MAPK1/RB1/BIRC5/HSPB1/CCNB1/HSF1/RASSF1	8
CC	GO:0099568	cytoplasmic region	0.041473	OPRM1/MAP2/NOS2/SELE/MAPK1/SOD1/AKR1B1/HIF1A/CAV1/HSPB1	10
CC	GO:0030315	T-tubule	0.041473	SCN5A/ADRA1A/SLC2A4	3

CC	GO:0099061	integral component of postsynaptic density membrane	0.041473	CHRM3/CHRM1/ADRB1	3
CC	GO:0016327	apicolateral plasma membrane	0.042419	THBD/CLDN4	2
CC	GO:0046930	pore complex	0.042419	BCL2/BAX	2
CC	GO:1904115	axon cytoplasm	0.044356	SOD1/HIF1A/HSPB1	3

CC	GO:0098644	complex of collagen trimers	0.045542	COL1A1/COL3A1	2
CC	GO:0099146	intrinsic component of postsynaptic density membrane	0.045542	CHRM3/CHRM1/ADRB1	3
CC	GO:0150034	distal axon	0.045713	CHRM3/CHRM1/CHRM2/MAP2/GOT1/E LK1/PRKCB	7
CC	GO:1904724	tertiary granule lumen	0.046389	LTA4H/MMP9/CTSD	3

CC	GO:0099634	postsynaptic specialization membrane	0.046389	CHRM3/CHRM1/GABRA1/ADRB1	4
CC	GO:0016328	lateral plasma membrane	0.047942	SCN5A/CLDN4/ERBB3	3
CC	GO:0032589	neuron projection membrane	0.049712	OPRM1/GABRA1/INSR	3
MF	GO:0004879	nuclear receptor activity	4.27E-10	RXRA/PGR/AR/PPARG/NR1I2/AHR/NR1I3/ESR1/PPARA/SREBF1/PPARD	11

MF	GO:0098531	transcription factor activity, direct ligand regulated sequence-specific DNA binding	4.27E-10	RXRA/PGR/AR/PPARG/NR1I2/AHR/NR1I3/ESR1/PPARA/SREBF1/PPARD	11
MF	GO:0003707	steroid hormone receptor activity	1.44E-08	RXRA/PGR/AR/PPARG/NR1I2/NR1I3/ESR1/PPARA/NR3C2/PPARD	10
MF	GO:0048037	cofactor binding	1.44E-08	PTGS2/PTGS1/NOS2/HMOX1/CYP3A4/CYP1A2/CYP1A1/CYP1B1/GSTP1/GSTM1/GSTM2/FASN/CAT/HMGCR/GSR/SOAT2/GOT1/ABAT/SOAT1/MAOB/POR/NOS3/MPO/PARP1	24
MF	GO:0005125	cytokine activity	4.66E-07	ADIPOQ/VEGFA/IL10/IL6/IL1B/CCL2/CXCL8/IL2/IFNG/IL1A/CXCL11/CXCL2/CXCL10/SPP1/CD40LG	15

MF	GO:0008227	G protein-coupled amine receptor activity	5.08E-07	CHRM3/CHRM1/CHRM4/ADRA1A/CHRM2/ADRA1B/ADRB2/ADRA2A/ADRB1	9
MF	GO:0005496	steroid binding	1.09E-06	PGR/AR/CYP3A4/ESR1/UGT1A1/SOAT2/SOAT1/NR3C2/CAV1/SULT1E1	10
MF	GO:0000982	transcription factor activity, RNA polymerase II proximal promoter sequence-specific DNA binding	1.09E-06	PGR/JUN/AR/PPARG/RELA/STAT1/ESR1/PPARA/SREBF1/FOS/RB1/TP63/ELK1/HIF1A/MYC/PPARD/HSF1/RUNX2/E2F1/IRF1	20
MF	GO:0005126	cytokine receptor binding	1.09E-06	CASP3/CASP8/STAT1/VEGFA/IL10/IL6/IL1B/CCL2/CXCL8/IL2/IFNG/IL1A/CXCL11/CXCL2/CXCL10/CD40LG	16

MF	GO:0016705	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	3.32E-06	PTGS2/PTGS1/NOS2/HMOX1/CYP3A4/CYP1A2/CYP1A1/CYP1B1/AKR1C3/AKR1C1/POR/NOS3	12
MF	GO:0020037	heme binding	3.32E-06	PTGS2/PTGS1/NOS2/HMOX1/CYP3A4/CYP1A2/CYP1A1/CYP1B1/CAT/NOS3/MPO	11
MF	GO:0001228	DNA-binding transcription activator activity, RNA polymerase II-specific	4.24E-06	PGR/JUN/AR/RELA/NR1I2/NR1I3/ESR1/PPARA/SREBF1/FOS/TP63/ELK1/HIF1A/MYC/NFE2L2/PARP1/RUNX2/E2F1/IRF1	19
MF	GO:0001085	RNA polymerase II transcription factor binding	5.56E-06	JUN/AR/PPARG/AHR/ESR1/PPARA/FOS/RB1/ELK1/NFE2L2/PPARD	11

MF	GO:0046906	tetrapyrrole binding	5.56E-06	PTGS2/PTGS1/NOS2/HMOX1/CYP3A4/CYP1A2/CYP1A1/CYP1B1/CAT/NOS3/MPO	11
MF	GO:0016209	antioxidant activity	5.93E-06	PTGS2/PTGS1/GSTP1/GSTM2/SOD1/CAT/GSR/MPO/NQO1	9
MF	GO:0019902	phosphatase binding	6.47E-06	BCL2/PPARG/AKT1/STAT1/MAPK3/MAPK1/SOD1/HMGCR/PPARA/SLC6A3/EGFR/ERBB2	12
MF	GO:0001077	proximal promoter DNA-binding transcription activator activity, RNA polymerase II-specific	7.75E-06	PGR/JUN/AR/RELA/ESR1/PPARA/SREBF1/FOS/TP63/ELK1/HIF1A/MYC/RUNX2/IRF1	15

MF	GO:0030374	nuclear receptor transcription coactivator activity	7.75E-06	NCOA2/PPARG/NR1I2/NR1I3/PPARA/NC OA1/PRKCB/PPARD	8
MF	GO:0044389	ubiquitin-like protein ligase binding	8.28E-06	KCNH2/SCN5A/BCL2/JUN/CASP8/RELA /STAT1/EGFR/CDKN1A/RB1/NFKBIA/HI F1A/CCNB1/CHEK2/ERBB3	15
MF	GO:0004935	adrenergic receptor activity	1.30E-05	ADRA1A/ADRA1B/ADRB2/ADRA2A/ADR B1	5
MF	GO:0050661	NADP binding	1.40E-05	NOS2/FASN/CAT/HMGCR/GSR/POR/NO S3	7

MF	GO:0097110	scaffold protein binding	3.75E-05	KCNH2/SCN5A/CASP8/IKBKB/MAPK3/NOS3/CHUK	7
MF	GO:0015464	acetylcholine receptor activity	5.80E-05	CHRM3/CHRM1/CHRM4/CHRM2/CHRNA2	5
MF	GO:0035257	nuclear hormone receptor binding	5.80E-05	RXRA/NCOA2/PPARG/STAT1/ESR1/NCOA1/RB1/HIF1A/PRKCB/PARP1	10
MF	GO:0099528	G protein-coupled neurotransmitter receptor activity	5.98E-05	CHRM3/CHRM1/CHRM4/CHRM2/OPRM1/ADRB1	6

MF	GO:0031406	carboxylic acid binding	6.47E-05	RXRA/NOS2/PPARG/SELE/UGT1A1/PPARA/ADIPOQ/AKR1C1/GOT1/NOS3/PPARD	11
MF	GO:0050662	coenzyme binding	9.50E-05	NOS2/FASN/CAT/HMGCR/GSR/SOAT2/GOT1/ABAT/SOAT1/MAOB/POR/NOS3/PARP1	13
MF	GO:0048018	receptor ligand activity	9.50E-05	ADIPOQ/VEGFA/IL10/EGF/IL6/IL1B/CCL2/CXCL8/IL2/IFNG/IL1A/CXCL11/CXCL2/CXCL10/SPP1/IGF2/CD40LG	17
MF	GO:0031625	ubiquitin protein ligase binding	9.50E-05	KCNH2/SCN5A/BCL2/JUN/CASP8/RELA/EGFR/CDKN1A/RB1/NFKBIA/HIF1A/HEK2/ERBB3	13

MF	GO:0004497	monooxygenase activity	9.72E-05	NOS2/CYP3A4/CYP1A2/CYP1A1/CYP1B1/AKR1C3/AKR1C1/NOS3	8
MF	GO:0043177	organic acid binding	9.72E-05	RXRA/NOS2/PPARG/SELE/UGT1A1/PPARA/ADIPOQ/AKR1C1/GOT1/NOS3/PPARD	11
MF	GO:0016653	oxidoreductase activity, acting on NAD(P)H, heme protein as acceptor	0.000101	NOS2/POR/NOS3/NQO1	4
MF	GO:0019903	protein phosphatase binding	0.000107	BCL2/PPARG/AKT1/STAT1/SOD1/HMGCR/SLC6A3/EGFR/ERBB2	9

MF	GO:0019207	kinase regulator activity	0.000107	CASP3/GSTP1/CCND1/CDKN1A/EGF/HS PB1/IL2/CCNB1/CXCL10/IGF2/ERBB3	11
MF	GO:0070491	repressing transcription factor binding	0.000124	PPARG/RELA/STAT1/PPARA/MYC/PPAR D/RUNX2	7
MF	GO:0051721	protein phosphatase 2A binding	0.000126	BCL2/AKT1/STAT1/HMGCR/SLC6A3	5
MF	GO:0033218	amide binding	0.00013	RXRA/ADRB2/OPRM1/PPARG/ACHE/GS TP1/INSR/GSTM1/GSTM2/FASN/LDLR/S OAT2/SOAT1/NFKBIA	14

MF	GO:0033613	activating transcription factor binding	0.000136	JUN/PPARG/RELA/FOS/RB1/MYC/NFE2L2	7
MF	GO:0016651	oxidoreductase activity, acting on NAD(P)H	0.000144	NOS2/AKR1C3/GSR/AKR1C1/POR/NOS3/NCF1/NQO1	8
MF	GO:0004601	peroxidase activity	0.000155	PTGS2/PTGS1/GSTP1/GSTM2/CAT/MPO	6
MF	GO:0051427	hormone receptor binding	0.000194	RXRA/NCOA2/PPARG/STAT1/ESR1/NCOA1/RB1/HIF1A/PRKCB/PARP1	10

MF	GO:0016684	oxidoreductase activity, acting on peroxide as acceptor	0.000227	PTGS2/PTGS1/GSTP1/GSTM2/CAT/MPO	6
MF	GO:0017171	serine hydrolase activity	0.000241	PRSS1/ACHE/F7/MMP1/PLAU/CTRB1/MMP3/MMP2/MMP9/F3/PLAT/CTSD	12
MF	GO:0030594	neurotransmitter receptor activity	0.000246	CHRM3/CHRM1/CHRM4/CHRM2/CHRNA2/OPRM1/GABRA1/ADRB1	8
MF	GO:1901681	sulfur compound binding	0.000332	GSTP1/GSTM1/GSTM2/APOB/SOAT2/SOAT1/VEGFA/MPO/CXCL11/CXCL10/PCOLCE	11

MF	GO:0002020	protease binding	0.00038	BCL2/CASP3/LDLR/SLC6A3/F3/SERPINE1 /COL1A1/COL3A1	8
MF	GO:0004252	serine-type endopeptidase activity	0.000414	PRSS1/F7/MMP1/PLAU/CTRB1/MMP3/M MP2/MMP9/F3/PLAT/CTSD	11
MF	GO:0016709	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of one atom of oxygen	0.000414	NOS2/CYP1A1/AKR1C3/AKR1C1/NOS3	5

MF	GO:0033293	monocarboxylic acid binding	0.000414	RXRA/PPARG/UGT1A1/PPARA/AKR1C1/ PPARD	6
MF	GO:1901338	catecholamine binding	0.000414	ADRB2/ADRA2A/SLC6A3/ADRB1	4
MF	GO:0004674	protein serine/threonine kinase activity	0.000464	PRKCA/IKBKB/AKT1/MAPK8/MAPK3/M APK1/EGFR/CCND1/CDKN1A/TOP1/RAF 1/PRKCB/CCNB1/CHEK2/CHUK	15
MF	GO:0042379	chemokine receptor binding	0.000474	STAT1/CCL2/CXCL8/CXCL11/CXCL2/CX CL10	6

MF	GO:0019838	growth factor binding	0.000635	SCN5A/INSR/EGFR/ERBB2/COL1A1/COL3A1/IGFBP3/ERBB3	8
MF	GO:0019887	protein kinase regulator activity	0.000727	CASP3/CCND1/CDKN1A/EGF/HSPB1/CENB1/CXCL10/IGF2/ERBB3	9
MF	GO:0008236	serine-type peptidase activity	0.00081	PRSS1/F7/MMP1/PLAU/CTRB1/MMP3/MMP2/MMP9/F3/PLAT/CTSD	11
MF	GO:0070405	ammonium ion binding	0.000841	CHRM3/CHRNA2/SLC6A4/ACHE/SLC6A3/CRP	6

MF	GO:0015378	sodium:chloride symporter activity	0.000969	SLC6A4/SLC6A2/SLC6A3	3
MF	GO:0051400	BH domain binding	0.000969	BCL2/BAX/BCL2L1	3
MF	GO:0070513	death domain binding	0.000969	BCL2/BAX/BCL2L1	3
MF	GO:0008009	chemokine activity	0.001039	CCL2/CXCL8/CXCL11/CXCL2/CXCL10	5

MF	GO:0042277	peptide binding	0.001069	RXRA/ADRB2/OPRM1/PPARG/ACHE/GS TP1/INSR/GSTM1/GSTM2/LDLR/NFKBIA	11
MF	GO:0009055	electron transfer activity	0.001151	CYP1A2/GSR/AKR1B1/MAOB/POR/NCF1 /NQO1	7
MF	GO:0030235	nitric-oxide synthase regulator activity	0.001201	AKT1/ESR1/EGFR	3
MF	GO:0043295	glutathione binding	0.001201	GSTP1/GSTM1/GSTM2	3

MF	GO:0045236	CXCR chemokine receptor binding	0.001201	CXCL8/CXCL11/CXCL10	3
MF	GO:1900750	oligopeptide binding	0.001566	GSTP1/GSTM1/GSTM2	3
MF	GO:0042165	neurotransmitter binding	0.001618	CHRM3/CHRNA2/SLC6A4/ACHE/CRP	5
MF	GO:0019209	kinase activator activity	0.0017	CDKN1A/EGF/IL2/CCNB1/IGF2/ERBB3	6

MF	GO:0005178	integrin binding	0.001905	PRKCA/ICAM1/VCAM1/EGFR/IL1B/COL3A1/IGF2	7
MF	GO:0015373	anion:sodium symporter activity	0.001905	SLC6A4/SLC6A2/SLC6A3	3
MF	GO:0035258	steroid hormone receptor binding	0.001948	PPARG/ESR1/NCOA1/RB1/PRKCB/PARP1	6
MF	GO:0016712	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced flavin or flavoprotein as one	0.001948	CYP3A4/CYP1A2/CYP1A1/CYP1B1	4

donor, and
incorporation of
one atom of
oxygen

MF	GO:0004032	alditol:NADP+ 1-oxidoreductase activity	0.002277	AKR1C3/AKR1C1/AKR1B1	3
MF	GO:0004707	MAP kinase activity	0.002277	MAPK8/MAPK3/MAPK1	3
MF	GO:0070851	growth factor receptor binding	0.002313	VEGFA/IL10/EGF/IL6/IL1B/IL2/IL1A	7

MF	GO:0004993	G protein-coupled serotonin receptor activity	0.002313	CHRM3/CHRM1/CHRM4/CHRM2	4
MF	GO:0099589	serotonin receptor activity	0.002313	CHRM3/CHRM1/CHRM4/CHRM2	4
MF	GO:0003713	transcription coactivator activity	0.002336	RXRA/NCOA2/JUN/PPARG/NR1I2/NR1I3 /PPARA/NCOA1/RB1/PRKCB/PPARD	11
MF	GO:0010181	FMN binding	0.002582	NOS2/POR/NOS3	3

MF	GO:0050998	nitric-oxide synthase binding	0.002582	SCN5A/SLC6A4/CAV1	3
MF	GO:0097153	cysteine-type endopeptidase activity involved in apoptotic process	0.002582	CASP9/CASP3/CASP8	3
MF	GO:0015377	cation:chloride symporter activity	0.003079	SLC6A4/SLC6A2/SLC6A3	3
MF	GO:0016641	oxidoreductase activity, acting on the CH-NH2 group of donors, oxygen as acceptor	0.003079	VCAM1/MAOB/MAOA	3

MF	GO:0051879	Hsp90 protein binding	0.003274	AHSA1/ AHR/ HIF1A/ HSF1	4
MF	GO:0046934	phosphatidylinositol-4,5-bisphosphate 3-kinase activity	0.00345	ESR1/ EGFR/ EGF/ ERBB2/ ERBB3	5
MF	GO:0042562	hormone binding	0.003501	CHRM3/ CHRNA2/ AR/ ACHE/ INSR/ EGFR	6
MF	GO:0035173	histone kinase activity	0.003501	PRKCA/ PRKCB/ CCNB1	3

MF	GO:0042166	acetylcholine binding	0.003501	CHRM3/CHRNA2/ACHE	3
MF	GO:0030331	estrogen receptor binding	0.003768	PPARG/ESR1/NCOA1/PARP1	4
MF	GO:0052813	phosphatidylinositol bisphosphate kinase activity	0.003974	ESR1/EGFR/EGF/ERBB2/ERBB3	5
MF	GO:0001221	transcription cofactor binding	0.004052	AHR/ESR1/PPARA/NFE2L2	4

MF	GO:0015296	anion:cation symporter activity	0.004653	SLC6A4/SLC6A2/SLC6A3	3
MF	GO:0016922	nuclear receptor binding	0.004653	RXRA/NCOA2/NCOA1	3
MF	GO:0042826	histone deacetylase binding	0.004765	RELA/MAPK8/CCND1/HIF1A/TOP2A/PARP1	6
MF	GO:0001102	RNA polymerase II activating transcription factor binding	0.005086	JUN/FOS/RB1/NFE2L2	4

MF	GO:0001091	RNA polymerase II basal transcription factor binding	0.005265	AR/AHR/ESR1	3
MF	GO:0050660	flavin adenine dinucleotide binding	0.005338	NOS2/GSR/MAOB/POR/NOS3	5
MF	GO:0099529	neurotransmitter receptor activity involved in regulation of postsynaptic membrane potential	0.00537	CHRM1/CHRNA2/GABRA1/ADRB1	4
MF	GO:0032813	tumor necrosis factor receptor superfamily binding	0.005739	CASP3/CASP8/STAT1/CD40LG	4

MF	GO:0035004	phosphatidylinositol 3-kinase activity	0.005739	ESR1/EGFR/EGF/ERBB2/ERBB3	5
MF	GO:0001223	transcription coactivator binding	0.005739	AHR/ESR1/PPARA	3
MF	GO:0016638	oxidoreductase activity, acting on the CH-NH2 group of donors	0.005739	VCAM1/MAOB/MAOA	3
MF	GO:0030295	protein kinase activator activity	0.005966	CDKN1A/EGF/CCNB1/IGF2/ERBB3	5

MF	GO:0098960	postsynaptic neurotransmitter receptor activity	0.005966	CHRM1/CHRNA2/GABRA1/ADRB1	4
MF	GO:0016616	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	0.006289	AKR1C3/FASN/HMGCR/AKR1C1/ADH1C /AKR1B1	6
MF	GO:0016538	cyclin-dependent protein serine/threonine kinase regulator activity	0.006289	CASP3/CCND1/CDKN1A/CCNB1	4
MF	GO:0070330	aromatase activity	0.006289	CYP1A2/CYP1A1/CYP1B1	3

MF	GO:0051219	phosphoprotein binding	0.006365	MAPK3/MAPK1/RB1/PLAT/RASA1	5
MF	GO:0005080	protein kinase C binding	0.00666	AKT1/PRKCB/HSPB1/TOP2A	4
MF	GO:0001078	proximal promoter DNA-binding transcription repressor activity, RNA polymerase II-specific	0.00686	PPARG/RELA/PPARA/RB1/PPARD/HSF1/E2F1	7
MF	GO:0008106	alcohol dehydrogenase (NADP+) activity	0.00686	AKR1C3/AKR1C1/AKR1B1	3

MF	GO:0070412	R-SMAD binding	0.00686	JUN/FOS/PARP1	3
MF	GO:0070888	E-box binding	0.00693	PPARG/AHR/HIF1A/MYC	4
MF	GO:0001664	G protein-coupled receptor binding	0.007421	STAT1/ADRA2A/ADRB1/CCL2/CXCL8/IL 2/CXCL11/CXCL2/CXCL10	9
MF	GO:0004364	glutathione transferase activity	0.008553	GSTP1/GSTM1/GSTM2	3

MF	GO:0016614	oxidoreductase activity, acting on CH-OH group of donors	0.009001	AKR1C3/FASN/HMGCR/AKR1C1/ADH1C/AKR1B1	6
MF	GO:0016628	oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor	0.009436	AKR1C3/FASN/AKR1C1	3
MF	GO:0005328	neurotransmitter:sodium symporter activity	0.01045	SLC6A4/SLC6A2/SLC6A3	3
MF	GO:0051059	NF-kappaB binding	0.011426	RELA/NFKBIA/PPARD	3

MF	GO:1901567	fatty acid derivative binding	0.011426	PPARG/SOAT2/SOAT1	3
MF	GO:0004033	aldo-keto reductase (NADP) activity	0.012549	AKR1C3/AKR1C1/AKR1B1	3
MF	GO:0001540	amyloid-beta binding	0.013381	ADRB2/ACHE/INSR/LDLR	4
MF	GO:0015108	chloride transmembrane transporter activity	0.013393	SLC6A4/GABRA1/SLC6A2/SLC6A3/CLDN 4	5

MF	GO:0005164	tumor necrosis factor receptor binding	0.014849	CASP8/STAT1/CD40LG	3
MF	GO:0004714	transmembrane receptor protein tyrosine kinase activity	0.015544	INSR/EGFR/ERBB2/ERBB3	4
MF	GO:0008519	ammonium transmembrane transporter activity	0.01601	SLC6A4/SLC6A2/SLC6A3	3
MF	GO:0005504	fatty acid binding	0.01686	PPARG/PPARA/PPARD	3

MF	GO:0030291	protein serine/threonine kinase inhibitor activity	0.01686	CASP3/CDKN1A/HSPB1	3
MF	GO:0001162	RNA polymerase II intronic transcription regulatory region sequence-specific DNA binding	0.01686	NCOA2/HSF1	2
MF	GO:0004954	prostanoid receptor activity	0.01686	PPARG/PTGER3	2
MF	GO:0016725	oxidoreductase activity, acting on CH or CH2 groups	0.01686	CYP3A4/CYP1A2	2

MF	GO:0015103	inorganic anion transmembrane transporter activity	0.018683	SLC6A4/GABRA1/SLC6A2/ ABCC1/SLC6A3 /CLDN4	6
MF	GO:0001227	DNA-binding transcription repressor activity, RNA polymerase II-specific	0.019721	PPARG/RELA/PPARA/RB1/MYC/PPARD/ HSF1/E2F1	8
MF	GO:0009931	calcium-dependent protein serine/threonine kinase activity	0.019721	PRKCA/PRKCB	2
MF	GO:0033691	sialic acid binding	0.019721	SELE/ADIPOQ	2

MF	GO:0048407	platelet-derived growth factor binding	0.019721	COL1A1/COL3A1	2
MF	GO:0004693	cyclin-dependent protein serine/threonine kinase activity	0.020449	CCND1/CDKN1A/CCNB1	3
MF	GO:0019825	oxygen binding	0.020449	CYP3A4/CYP1A1/CYP1B1	3
MF	GO:0008201	heparin binding	0.021258	APOB/VEGFA/MPO/CXCL11/CXCL10/PC OLCE	6

MF	GO:0031072	heat shock protein binding	0.021335	BAX/ AHSA1/ AHR/ HIF1A/ HSF1	5
MF	GO:0097472	cyclin-dependent protein kinase activity	0.021625	CCND1/ CDKN1A/ CCNB1	3
MF	GO:0004861	cyclin-dependent protein serine/threonine kinase inhibitor activity	0.022207	CASP3/ CDKN1A	2
MF	GO:0010857	calcium-dependent protein kinase activity	0.022207	PRKCA/ PRKCB	2

MF	GO:0031994	insulin-like growth factor I binding	0.022207	INSR/IGFBP3	2
MF	GO:0008083	growth factor activity	0.022236	VEGFA/IL10/EGF/IL6/IL2/IGF2	6
MF	GO:0001103	RNA polymerase II repressing transcription factor binding	0.02236	PPARG/PPARA/PPARD	3
MF	GO:0016248	channel inhibitor activity	0.02236	BCL2/CAV1/RASA1	3

MF	GO:0016504	peptidase activator activity	0.023888	CASP3/CAV1/PCOLCE	3
MF	GO:0001161	intronic transcription regulatory region sequence-specific DNA binding	0.024704	NCOA2/HSF1	2
MF	GO:0008179	adenylate cyclase binding	0.024704	ADRB2/RAF1	2
MF	GO:0036041	long-chain fatty acid binding	0.024704	PPARG/PPARD	2

MF	GO:0044213	intronic transcription regulatory region DNA binding	0.024704	NCOA2/HSF1	2
MF	GO:0001784	phosphotyrosine residue binding	0.024803	MAPK3/MAPK1/RASA1	3
MF	GO:0046332	SMAD binding	0.027655	JUN/FOS/PARP1/COL3A1	4
MF	GO:0051117	ATPase binding	0.027655	PGR/AR/ESR1/CAV1	4

MF	GO:0004953	icosanoid receptor activity	0.027725	PPARG/PTGER3	2
MF	GO:0070402	NADPH binding	0.027725	FASN/HMGCR	2
MF	GO:0019199	transmembrane receptor protein kinase activity	0.028325	INSR/EGFR/ERBB2/ERBB3	4
MF	GO:0004712	protein serine/threonine/tyrosine kinase activity	0.029181	AKT1/MAPK3/MAPK1	3

MF	GO:0015485	cholesterol binding	0.030428	SOAT2/SOAT1/CAV1	3
MF	GO:0050681	androgen receptor binding	0.030428	NCOA1/RB1/PRKCB	3
MF	GO:1901618	organic hydroxy compound transmembrane transporter activity	0.030428	SLC6A4/SLC6A2/SLC6A3	3
MF	GO:0005149	interleukin-1 receptor binding	0.030428	IL1B/IL1A	2

MF	GO:0030169	low-density lipoprotein particle binding	0.030428	LDLR/CRP	2
MF	GO:0072341	modified amino acid binding	0.033343	GSTP1/GSTM1/GSTM2/FASN	4
MF	GO:0004697	protein kinase C activity	0.03373	PRKCA/PRKCB	2
MF	GO:0004708	MAP kinase kinase activity	0.03373	MAPK3/MAPK1	2

MF	GO:0005159	insulin-like growth factor receptor binding	0.03373	INSR/IGF2	2
MF	GO:0005123	death receptor binding	0.037758	CASP3/CASP8	2
MF	GO:0045309	protein phosphorylated amino acid binding	0.039043	MAPK3/MAPK1/RASA1	3
MF	GO:0016247	channel regulator activity	0.0402	ADRB2/BCL2/CAV1/PRKCB/RASA1	5

MF	GO:0051213	dioxygenase activity	0.040234	PTGS2/PTGS1/ ALOX5/POR	4
MF	GO:0032934	sterol binding	0.040526	SOAT2/SOAT1/CAV1	3
MF	GO:0004745	retinol dehydrogenase activity	0.040759	AKR1C3/ADH1C	2
MF	GO:0030296	protein tyrosine kinase activator activity	0.040759	EGF/ERBB3	2

MF	GO:0015459	potassium channel regulator activity	0.044252	ADRB2/CAV1/RASA1	3
MF	GO:0001972	retinoic acid binding	0.044252	RXRA/UGT1A1	2
MF	GO:0017127	cholesterol transporter activity	0.044252	APOB/ABCG2	2
MF	GO:0031690	adrenergic receptor binding	0.044252	ADRA2A/ADRB1	2

MF	GO:0005326	neurotransmitter transporter activity	0.047912	SLC6A4/SLC6A2/SLC6A3	3
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BP: Biological process; CC: Cellular component; GO: Gene ontology; FDR: False discovery rate; MF: Molecular function.

Supplementary Table 4 Kyoto encyclopedia of genes and genomes enrichment analysis results (False discovery rate < 0.05)

ID	Description	FDR	geneID	Count
hsa04668	TNF signaling pathway	4.77E-17	PTGS2/JUN/CASP3/CASP8/RELA/IKBKB/AKT1/MAPK8/ICAM1/SELE/VCAM1/MAPK3/MAPK1/MMP3/FOS/MMP9/IL6/NFKBIA/IL1B/CCL2/CXCL2/CXCL10/CHUK/IRF1	24
hsa04657	IL-17 signaling pathway	1.93E-16	PTGS2/JUN/CASP3/CASP8/RELA/IKBKB/MAPK8/MMP1/MAPK3/MAPK1/MMP3/FOS/MMP9/IL6/NFKBIA/IL1B/CCL2/CXCL8/IFNG/CXCL2/CXCL10/CHUK	22
hsa04066	HIF-1 signaling pathway	1.01E-14	BCL2/PRKCA/NOS2/RELA/AKT1/HMOX1/INSR/MAPK3/MAPK1/EGFR/VEGFA/CDKN1A/EGF/IL6/HIF1A/ERBB2/PRKCB/NOS3/SERPINE1/IFNG/HK2	21
hsa01522	Endocrine resistance	1.08E-11	BCL2/BAX/JUN/AKT1/MAPK8/ESR1/MAPK3/MAPK1/EGFR/CCND1/FOS/CDKN1A/MMP2/MMP9/RB1/RAF1/ERBB2/E2F1	18
hsa04620	Toll-like receptor signaling pathway	2.44E-11	JUN/CASP8/RELA/IKBKB/AKT1/MAPK8/STAT1/MAPK3/MAPK1/FOS/IL6/NFKBIA/IL1B/CXCL8/CXCL11/CXCL10/CHUK/SPP1	18
hsa04625	C-type lectin receptor signaling	2.44E-11	PTGS2/JUN/CASP8/RELA/IKBKB/AKT1/MAPK8/STAT1/MAPK3/MAPK1/IL10/IL6/NFKBIA/RAF1/IL1B/IL2/CHUK/IRF1	18

pathway				
hsa04210	Apoptosis	2.94E-11	BCL2/BAX/CASP9/JUN/CASP3/CASP8/RELA/IKBKB/AKT1/MAPK8/MAPK3/MAPK1/BCL2L1/FOS/NFKBIA/RAF1/BIRC5/PARP1/CHUK/CTSD	20
hsa04926	Relaxin signaling pathway	1.11E-10	JUN/PRKCA/NOS2/RELA/AKT1/MAPK8/MMP1/MAPK3/MAPK1/EGFR/VEGFA/FOS/MMP2/MMP9/NFKBIA/RAF1/NOS3/COL1A1/COL3A1	19
hsa04659	Th17 cell differentiation	3.39E-10	RXRA/JUN/RELA/IKBKB/MAPK8/STAT1/AHR/MAPK3/MAPK1/FOS/IL6/NFKBIA/HIF1A/IL1B/IL2/IFNG/CHUK	17
hsa01521	EGFR tyrosine kinase inhibitor resistance	3.50E-10	BCL2/BAX/PRKCA/AKT1/MAPK3/MAPK1/EGFR/VEGFA/BCL2L1/EGF/IL6/RAF1/ERBB2/PRKCB/ERBB3	15
hsa04064	NF-kappa B signaling pathway	4.94E-10	PTGS2/BCL2/RELA/IKBKB/ICAM1/VCAM1/PLAU/BCL2L1/NFKBIA/IL1B/CXCL8/PRKCB/PARP1/CXCL2/CHUK/CD40LG	16
hsa04151	PI3K-Akt signaling pathway	6.81E-10	RXRA/CHRM1/CHRM2/BCL2/CASP9/PRKCA/RELA/IKBKB/AKT1/INSR/MAPK3/MAPK1/EGFR/VEGFA/CCND1/BCL2L1/CDKN1A/EGF/IL6/RAF1/ERBB2/MYC/NOS3/IL2/COL1A1/CHUK/SPP1/IGF2/ERBB3	29

hsa04012	ErbB signaling pathway	8.69E-10	JUN/PRKCA/AKT1/MAPK8/MAPK3/MAPK1/EGFR/CDKN1A/EGF/ELK1/RAF1/ERBB2/MYC/PRKCB/ERBB3	15
hsa04010	MAPK signaling pathway	1.36E-09	JUN/CASP3/PRKCA/RELA/IKBKB/AKT1/MAPK8/INSR/MAPK3/MAPK1/EGFR/VEGFA/FOS/EGF/ELK1/RAF1/ERBB2/MYC/IL1B/PRKCB/HSPB1/IL1A/CHUK/IGF2/ERBB3/RASA1	26
hsa04068	FoxO signaling pathway	7.10E-09	IKBKB/AKT1/MAPK8/SLC2A4/INSR/MAPK3/MAPK1/CAT/EGFR/CCND1/CDKN1A/IL10/EGF/IL6/RAF1/CCNB1/CHUK	17
hsa04915	Estrogen signaling pathway	1.39E-08	PGR/NCOA2/OPRM1/BCL2/JUN/AKT1/ESR1/MAPK3/MAPK1/NCOA1/EGFR/FOS/MMP2/MMP9/RAF1/NOS3/CTSD	17
hsa04380	Osteoclast differentiation	3.19E-08	JUN/PPARG/RELA/IKBKB/AKT1/MAPK8/STAT1/MAPK3/MAPK1/FOS/NFKBIA/IL1B/IFNG/IL1A/NCF1/CHUK	16
hsa04919	Thyroid hormone signaling pathway	5.74E-08	RXRA/NCOA2/CASP9/PRKCA/AKT1/STAT1/ESR1/MAPK3/MAPK1/NCOA1/CCND1/RAF1/HIF1A/MYC/PRKCB	15
hsa04660	T cell receptor signaling pathway	7.17E-08	JUN/RELA/IKBKB/AKT1/MAPK3/MAPK1/FOS/IL10/NFKBIA/RAF1/IL2/IFNG/CHUK/CD40LG	14

hsa04115	p53 signaling pathway	9.32E-08	BCL2/BAX/CASP9/CASP3/CASP8/CCND1/BCL2L1/CDKN1A/CCNB1/SERPINE1/CHEK2/IGFBP3	12
hsa04370	VEGF signaling pathway	1.07E-07	PTGS2/CASP9/PRKCA/AKT1/MAPK3/MAPK1/VEGFA/RAF1/PRKCB/NOS3/HSPB1	11
hsa04218	Cellular senescence	1.07E-07	RELA/AKT1/MAPK3/MAPK1/CCND1/CDKN1A/RB1/IL6/RAF1/MYC/CXCL8/CCNB1/SERPINE1/IL1A/CHEK2/E2F1/IGFBP3	17
hsa04510	Focal adhesion	4.47E-07	BCL2/JUN/PRKCA/AKT1/MAPK8/MAPK3/MAPK1/EGFR/VEGFA/CND1/EGF/ELK1/RAF1/ERBB2/CAV1/PRKCB/COL1A1/SPP1	18
hsa04621	NOD-like receptor signaling pathway	4.61E-07	BCL2/JUN/CASP8/RELA/IKBKB/MAPK8/STAT1/MAPK3/MAPK1/BCL2L1/IL6/NFKBIA/IL1B/CCL2/CXCL8/CXCL2/CHUK	17
hsa04917	Prolactin signaling pathway	5.76E-07	RELA/AKT1/MAPK8/STAT1/ESR1/MAPK3/MAPK1/CCND1/FOS/RAF1/IRF1	11
hsa04662	B cell receptor signaling pathway	6.59E-07	JUN/RELA/IKBKB/AKT1/MAPK3/MAPK1/FOS/NFKBIA/RAF1/PRKCB/CHUK	11

hsa04014	Ras signaling pathway	8.50E-07	PRKCA/RELA/IKBKB/ AKT1/MAPK8/INSR/MAPK3/MAPK1/EGFR/V EGFA/BCL2L1/EGF/ELK1/RAF1/PRKCB/CHUK/RASSF1/IGF2/RASA1	19
hsa04215	Apoptosis - multiple species	8.85E-07	BCL2/BAX/CASP9/CASP3/CASP8/MAPK8/BCL2L1/BIRC5	8
hsa04658	Th1 and Th2 cell differentiation	1.16E-06	JUN/RELA/IKBKB/MAPK8/STAT1/MAPK3/MAPK1/FOS/NFKBIA/IL2 /IFNG/CHUK	12
hsa04071	Sphingolipid signaling pathway	2.77E-06	BCL2/BAX/PRKCA/RELA/ AKT1/MAPK8/MAPK3/MAPK1/ABCC1/R AF1/PRKCB/NOS3/CTSD	13
hsa04920	Adipocytokine signaling pathway	3.85E-06	RXRA/RELA/IKBKB/ AKT1/MAPK8/SLC2A4/PPARA/ ADIPOQ/NFKBI A/CHUK	10
hsa04062	Chemokine signaling pathway	4.79E-06	RELA/IKBKB/ AKT1/STAT1/MAPK3/MAPK1/NFKBIA/RAF1/CCL2/C XCL8/PRKCB/NCF1/CXCL11/CXCL2/CXCL10/CHUK	16
hsa04931	Insulin resistance	5.83E-06	RELA/IKBKB/ AKT1/MAPK8/SLC2A4/INSR/PPARA/SREBF1/IL6/NFK BIA/PRKCB/NOS3	12

hsa01523	Antifolate resistance	7.30E-06	RELA/IKBKB/ABCC1/IL6/IL1B/ABCG2/CHUK	7
hsa04725	Cholinergic synapse	8.39E-06	CHRM3/CHRM1/CHRM4/CHRM2/BCL2/PRKCA/ACHE/AKT1/MAPK3/MAPK1/FOS/PRKCB	12
hsa00980	Metabolism of xenobiotics by cytochrome P450	8.97E-06	CYP3A4/CYP1A2/CYP1A1/CYP1B1/GSTP1/GSTM1/GSTM2/UGT1A1/AKR1C1/ADH1C	10
hsa04726	Serotonergic synapse	1.07E-05	PTGS2/PTGS1/SLC6A4/CASP3/PRKCA/ALOX5/MAPK3/MAPK1/MAOB/MAOA/RAF1/PRKCB	12
hsa04910	Insulin signaling pathway	1.20E-05	IKBKB/AKT1/MAPK8/SLC2A4/INSR/MAPK3/MAPK1/FASN/SREBF1/ELK1/RAF1/ACACA/HK2	13
hsa04630	JAK-STAT signaling pathway	1.50E-05	BCL2/AKT1/STAT1/EGFR/CCND1/BCL2L1/CDKN1A/IL10/EGF/IL6/RAF1/MYC/IL2/IFNG	14
hsa04020	Calcium signaling pathway	1.75E-05	CHRM3/CHRM1/ADRA1A/CHRM2/ADRA1B/ADRB2/PRKCA/NOS2/ADRB1/EGFR/ERBB2/PTGER3/PRKCB/NOS3/ERBB3	15

hsa04928	Parathyroid hormone synthesis, secretion and action	2.66E-05	RXRA/BCL2/PRKCA/MAPK3/MAPK1/EGFR/FOS/CDKN1A/RAF1/PRKCB/RUNX2	11
hsa04921	Oxytocin signaling pathway	3.69E-05	PTGS2/JUN/PRKCA/MAPK3/MAPK1/EGFR/CCND1/FOS/CDKN1A/ELK1/RAF1/PRKCB/NOS3	13
hsa00982	Drug metabolism - cytochrome P450	3.82E-05	CYP3A4/CYP1A2/GSTP1/GSTM1/GSTM2/UGT1A1/ADH1C/MAOB/MAOA	9
hsa04912	GnRH signaling pathway	4.85E-05	JUN/PRKCA/MAPK8/MAPK3/MAPK1/EGFR/MMP2/ELK1/RAF1/PRKCB	10
hsa04024	cAMP signaling pathway	6.95E-05	CHRM1/CHRM2/ADRB2/JUN/RELA/AKT1/MAPK8/MAPK3/MAPK1/PPARA/ADRB1/FOS/NFKBIA/RAF1/PTGER3	15
hsa00140	Steroid hormone biosynthesis	6.99E-05	CYP3A4/CYP1A2/CYP1A1/CYP1B1/AKR1C3/UGT1A1/AKR1C1/SULT1E1	8
hsa04722	Neurotrophin signaling pathway	7.54E-05	BCL2/BAX/JUN/RELA/IKBKB/AKT1/MAPK8/MAPK3/MAPK1/NFKBIA/RAF1	11

hsa04152	AMPK signaling pathway	8.07E-05	ADRA1A/PPARG/AKT1/SLC2A4/INSR/FASN/HMGCR/SREBF1/ADIP OQ/CCND1/ACACA	11
hsa04913	Ovarian steroidogenesis	0.000138	PTGS2/CYP1A1/CYP1B1/ALOX5/INSR/AKR1C3/LDLR	7
hsa04540	Gap junction	0.000177	PRKCA/MAPK3/MAPK1/ADRB1/EGFR/EGF/RAF1/GJA1/PRKCB	9
hsa04622	RIG-I-like receptor signaling pathway	0.000198	CASP8/RELA/IKBKB/MAPK8/NFKBIA/CXCL8/CXCL10/CHUK	8
hsa04960	Aldosterone-regulated sodium reabsorption	0.000218	PRKCA/INSR/MAPK3/MAPK1/NR3C2/PRKCB	6
hsa04923	Regulation of lipolysis in adipocytes	0.000275	PTGS2/PTGS1/ADRB2/AKT1/INSR/ADRB1/PTGER3	7
hsa00380	Tryptophan metabolism	0.00044	CYP1A2/CYP1A1/CYP1B1/CAT/MAOB/MAOA	6

hsa04623	Cytosolic DNA-sensing pathway	0.000636	RELA/IKBKB/IL6/NFKBIA/IL1B/CXCL10/CHUK	7
hsa04664	Fc epsilon RI signaling pathway	0.001005	PRKCA/AKT1/MAPK8/ALOX5/MAPK3/MAPK1/RAF1	7
hsa05031	Amphetamine addiction	0.001005	JUN/PRKCA/SLC6A3/MAOB/MAOA/FOS/PRKCB	7
hsa04371	Apelin signaling pathway	0.00106	NOS2/AKT1/MAPK3/MAPK1/CCND1/RAF1/NOS3/PLAT/SERPINE1/ SPP1	10
hsa00330	Arginine and proline metabolism	0.001114	NOS2/GOT1/MAOB/MAOA/ODC1/NOS3	6
hsa04022	cGMP-PKG signaling pathway	0.001245	ADRA1A/ADRA1B/ADRB2/AKT1/INSR/MAPK3/MAPK1/ADRA2A/A DRB1/RAF1/NOS3	11
hsa04261	Adrenergic signaling in cardiomyocytes	0.001614	SCN5A/ADRA1A/ADRA1B/ADRB2/BCL2/PRKCA/AKT1/MAPK3/MA PK1/ADRB1	10

hsa00983	Drug metabolism - other enzymes	0.002385	CYP3A4/GSTP1/GSTM1/GSTM2/UGT1A1/CES1/MPO	7
hsa04140	Autophagy - animal	0.002545	BCL2/ AKT1/MAPK8/MAPK3/MAPK1/BCL2L1/RAF1/HIF1A/CTSD	9
hsa04670	Leukocyte transendothelial migration	0.004235	PRKCA/ICAM1/VCAM1/MMP2/MMP9/PRKCB/NCF1/CLDN4	8
hsa04137	Mitophagy - animal	0.004241	JUN/RELA/MAPK8/BCL2L1/HIF1A/E2F1	6
hsa04211	Longevity regulating pathway	0.004586	BAX/PPARG/RELA/ AKT1/INSR/CAT/ADIPOQ	7
hsa04970	Salivary secretion	0.004849	CHRM3/ADRA1A/ADRA1B/ADRB2/PRKCA/ADRB1/PRKCB	7
hsa04666	Fc gamma R-mediated phagocytosis	0.005123	PRKCA/ AKT1/MAPK3/MAPK1/RAF1/PRKCB/NCF1	7

hsa05030	Cocaine addiction	0.00622	JUN/RELA/SLC6A3/MAOB/MAOA	5
hsa04072	Phospholipase D signaling pathway	0.006431	PRKCA/AKT1/INSR/MAPK3/MAPK1/EGFR/EGF/RAF1/CXCL8	9
hsa03320	PPAR signaling pathway	0.007734	RXRA/PPARG/MMP1/PPARA/ADIPOQ/PPARD	6
hsa04150	mTOR signaling pathway	0.007847	PRKCA/IKBKB/AKT1/INSR/MAPK3/MAPK1/RAF1/PRKCB/CHUK	9
hsa04914	Progesterone-mediated oocyte maturation	0.007847	PGR/AKT1/MAPK8/MAPK3/MAPK1/RAF1/CCNB1	7
hsa00360	Phenylalanine metabolism	0.008877	GOT1/MAOB/MAOA	3
hsa04650	Natural killer cell mediated cytotoxicity	0.009962	CASP3/PRKCA/ICAM1/MAPK3/MAPK1/RAF1/PRKCB/IFNG	8

hsa04728	Dopaminergic synapse	0.009962	PRKCA/AKT1/MAPK8/SLC6A3/MAOB/MAOA/FOS/PRKCB	8
hsa04610	Complement and coagulation cascades	0.01012	F7/PLAU/F3/PLAT/THBD/SERPINE1	6
hsa00480	Glutathione metabolism	0.010293	GSTP1/GSTM1/GSTM2/GSR/ODC1	5
hsa04217	Necroptosis	0.010793	BCL2/BAX/CASP8/MAPK8/STAT1/IL1B/IFNG/IL1A/PARP1	9
hsa00350	Tyrosine metabolism	0.010931	GOT1/ADH1C/MAOB/MAOA	4
hsa00220	Arginine biosynthesis	0.015305	NOS2/GOT1/NOS3	3
hsa00590	Arachidonic acid metabolism	0.016112	PTGS2/PTGS1/ALOX5/AKR1C3/LTA4H	5

hsa04080	Neuroactive ligand-receptor interaction	0.016112	CHRM3/CHRM1/CHRM4/ADRA1A/CHRM2/ADRA1B/ADRB2/CHRNA2/OPRM1/GABRA1/PRSS1/ADRA2A/ADRB1/PTGER3	14
hsa04015	Rap1 signaling pathway	0.016603	PRKCA/AKT1/INSR/MAPK3/MAPK1/EGFR/VEGFA/EGF/RAF1/PRKCB	10
hsa00830	Retinol metabolism	0.02013	CYP3A4/CYP1A2/CYP1A1/UGT1A1/ADH1C	5
hsa04720	Long-term potentiation	0.02013	PRKCA/MAPK3/MAPK1/RAF1/PRKCB	5
hsa04973	Carbohydrate digestion and absorption	0.020706	AKT1/PRKCB/MGAM/HK2	4
hsa04110	Cell cycle	0.022547	CCND1/CDKN1A/RB1/MYC/CCNB1/CHEK2/E2F1	7
hsa04611	Platelet activation	0.022547	PTGS1/AKT1/MAPK3/MAPK1/NOS3/COL1A1/COL3A1	7

hsa04520	Adherens junction	0.026008	INSR/MAPK3/MAPK1/EGFR/ERBB2	5
hsa04976	Bile secretion	0.026008	RXRA/CYP3A4/LDLR/HMGCR/ABCG2	5
hsa04060	Cytokine-cytokine receptor interaction	0.02818	IL10/IL6/IL1B/CCL2/CXCL8/IL2/IFNG/IL1A/CXCL11/CXCL2/CXCL10/CD40LG	12
hsa04672	Intestinal immune network for IgA production	0.028716	IL10/IL6/IL2/CD40LG	4
hsa04270	Vascular smooth muscle contraction	0.029868	ADRA1A/ADRA1B/PRKCA/MAPK3/MAPK1/RAF1/PRKCB	7
hsa04979	Cholesterol metabolism	0.030333	LDLR/APOB/SOAT2/SOAT1	4
hsa00052	Galactose metabolism	0.040032	AKR1B1/MGAM/HK2	3

hsa00061	Fatty acid biosynthesis	0.04489	FASN/ACACA	2
hsa04810	Regulation of actin cytoskeleton	0.049409	CHRM3/CHRM1/CHRM4/CHRM2/MAPK3/MAPK1/EGFR/EGF/RAF1	9

FDR: False discovery rate; KEGG: Kyoto encyclopedia of genes and genomes.