

Supplementary table 5 GO enrichment analysis of the thirteen prognostic genes derived from the predictive signature in COAD.

ONTOLOGY	ID	Description	Count	p-value	q-value	Gene ID
BP	GO:071466	cellular response to xenobiotic stimulus	4	0.000	0.004	EPHX2/NAT1/NAT2/PPARGC1A
BP	GO:009410	response to xenobiotic stimulus	4	0.000	0.013	EPHX2/NAT1/NAT2/PPARGC1A
BP	GO:006805	xenobiotic metabolic process	3	0.000	0.015	EPHX2/NAT1/NAT2
BP	GO:0042759	long-chain fatty acid biosynthetic process	2	0.000	0.024	EPHX2/HPGD
BP	GO:0072330	monocarboxylic acid biosynthetic process	3	0.002	0.068	EPHX2/HPGD/PPARGC1A
BP	GO:0048661	positive regulation of smooth muscle cell proliferation	2	0.003	0.068	HPGD/PPARGC1A
BP	GO:006631	fatty acid metabolic process	3	0.003	0.068	EPHX2/HPGD/PPARGC1A
BP	GO:0001676	long-chain fatty acid metabolic process	2	0.003	0.068	EPHX2/HPGD
BP	GO:0033559	unsaturated fatty acid metabolic process	2	0.003	0.068	EPHX2/HPGD
BP	GO:006690	icosanoid metabolic process	2	0.004	0.068	EPHX2/HPGD
BP	GO:0019218	regulation of steroid metabolic process	2	0.004	0.068	EPHX2/PPARGC1A
BP	GO:0032355	response to estradiol	2	0.005	0.068	HPGD/PPARGC1A
BP	GO:0007586	digestion	2	0.005	0.068	PLS1/PPARGC1A

BP	GO:0 0463 94	carboxylic acid biosynthetic process	3	0.005	0.068	EPHX2/HPGD/PPARGC1A
BP	GO:0 0160 53	organic acid biosynthetic process	3	0.006	0.068	EPHX2/HPGD/PPARGC1A
BP	GO:0 0352 96	regulation of tube diameter	2	0.006	0.068	EPHX2/CHGA
BP	GO:0 0508 80	regulation of blood vessel size	2	0.006	0.068	EPHX2/CHGA
BP	GO:0 0977 46	regulation of blood vessel diameter	2	0.006	0.068	EPHX2/CHGA
BP	GO:0 0351 50	regulation of tube size	2	0.006	0.068	EPHX2/CHGA
BP	GO:0 0066 33	fatty acid biosynthetic process	2	0.007	0.068	EPHX2/HPGD
BP	GO:1 9015 68	fatty acid derivative metabolic process	2	0.008	0.068	EPHX2/HPGD
BP	GO:0 0486 60	regulation of smooth muscle cell proliferation	2	0.008	0.068	HPGD/PPARGC1A
BP	GO:0 0358 65	cellular response to potassium ion	1	0.008	0.068	PPARGC1A
BP	GO:0 0713 13	cellular response to caffeine	1	0.008	0.068	PPARGC1A
BP	GO:0 0486 59	smooth muscle cell proliferation	2	0.008	0.068	HPGD/PPARGC1A
BP	GO:0 0030 18	vascular process in circulatory system	2	0.008	0.068	EPHX2/CHGA
BP	GO:0 0508 21	protein stabilization	2	0.009	0.068	TSPAN1/PPARGC1A
BP	GO:0 0468	positive regulation of hormone biosynthetic process	1	0.009	0.068	PPARGC1A

	86					
BP	GO:0 0713 72	cellular response to follicle-stimulating hormone stimulus	1	0.009	0.068	PPARGC1A
BP	GO:0 0860 23	adenylate cyclase-activating adrenergic receptor signaling pathway involved in heart process	1	0.009	0.068	CHGA
BP	GO:1 9010 77	regulation of relaxation of muscle	1	0.009	0.068	CHGA
BP	GO:0 0082 17	regulation of blood pressure	2	0.009	0.068	EPHX2/CHGA
BP	GO:0 0434 01	steroid hormone mediated signaling pathway	2	0.009	0.068	NR3C2/PPARGC1A
BP	GO:0 0025 51	mast cell chemotaxis	1	0.010	0.068	CHGA
BP	GO:0 0148 89	muscle atrophy	1	0.010	0.068	PPARGC1A
BP	GO:0 0454 72	response to ether	1	0.010	0.068	PPARGC1A
BP	GO:0 0704 93	thrombin-activated receptor signaling pathway	1	0.010	0.068	HPGD
BP	GO:0 0975 31	mast cell migration	1	0.010	0.068	CHGA
BP	GO:0 0063 67	transcription initiation from RNA polymerase II promoter	2	0.010	0.068	NR3C2/PPARGC1A
BP	GO:0 0453 33	cellular respiration	2	0.010	0.068	SUCLG2/PPARGC1A
BP	GO:0 0060 12	galactose metabolic process	1	0.010	0.068	PPARGC1A
BP	GO:0 0325 30	regulation of microvillus organization	1	0.010	0.068	PLS1

	GO:0					
BP	0325	regulation of cell projection size	1	0.010	0.068	PLS1
	36					
	GO:0					
BP	0432	response to leucine	1	0.010	0.068	PPARGC1A
	01					
	GO:0					
BP	0458	negative regulation of glycolytic process	1	0.010	0.068	PPARGC1A
	20					
	GO:0					
BP	0714	cellular response to purine-containing compound	1	0.010	0.068	PPARGC1A
	15					
	GO:0					
BP	0604	positive regulation of cardiac muscle contraction	1	0.011	0.068	CHGA
	52					
	GO:1					
BP	9012	negative regulation of neuron death	2	0.012	0.068	CHGA/PPARGC1A
	15					
	GO:0					
BP	0098	flavonoid metabolic process	1	0.012	0.068	PPARGC1A
	12					
	GO:0					
BP	0148	response to stimulus involved in regulation of muscle adaptation	1	0.012	0.068	PPARGC1A
	74					
	GO:0					
BP	0308	negative regulation of nucleotide catabolic process	1	0.012	0.068	PPARGC1A
	12					
	GO:0					
BP	0323	positive regulation of hormone metabolic process	1	0.012	0.068	PPARGC1A
	52					
	GO:0					
BP	0336	negative regulation of catecholamine secretion	1	0.012	0.068	CHGA
	04					
	GO:0					
BP	0358	response to potassium ion	1	0.012	0.068	PPARGC1A
	64					
	GO:0					
BP	0463	positive regulation of fatty acid oxidation	1	0.012	0.068	PPARGC1A
	21					
	GO:0					
BP	0511	negative regulation of coenzyme metabolic process	1	0.012	0.068	PPARGC1A
	98					
	GO:0					
BP	0075	parturition	1	0.013	0.068	HPGD

	67					
BP	GO:0105	regulation of ketone biosynthetic process	1	0.013	0.068	PPARGC1A
	66					
BP	GO:0193	lipoxygenase pathway	1	0.013	0.068	HPGD
	72					
BP	GO:0323	response to follicle-stimulating hormone	1	0.013	0.068	PPARGC1A
	54					
BP	GO:0424	progesterone metabolic process	1	0.013	0.068	PPARGC1A
	48					
BP	GO:0457	positive regulation of gluconeogenesis	1	0.013	0.068	PPARGC1A
	22					
BP	GO:0459	positive regulation of striated muscle contraction	1	0.013	0.068	CHGA
	89					
BP	GO:0551	relaxation of cardiac muscle	1	0.013	0.068	CHGA
	19					
BP	GO:0718	response to epinephrine	1	0.013	0.068	PPARGC1A
	71					
BP	GO:0861	G protein-coupled receptor signaling pathway involved in heart process	1	0.013	0.068	CHGA
	03					
BP	GO:0970	cellular response to thyroid hormone stimulus	1	0.013	0.068	PPARGC1A
	67					
BP	GO:20011	negative regulation of ATP biosynthetic process	1	0.013	0.068	PPARGC1A
	70					
BP	GO:0189	ether metabolic process	1	0.014	0.070	EPHX2
	04					
BP	GO:0310	response to caffeine	1	0.014	0.070	PPARGC1A
	00					
BP	GO:0362	response to diuretic	1	0.014	0.070	PPARGC1A
	70					
BP	GO:0	negative regulation of nucleotide	1	0.014	0.071	PPARGC1A

	0308	biosynthetic process				
	09					
	GO:0					
BP	0713	cellular response to gonadotropin stimulus	1	0.014	0.071	PPARGC1A
	71					
	GO:1					
BP	9003	negative regulation of purine nucleotide biosynthetic process	1	0.014	0.071	PPARGC1A
	72					
	GO:0					
BP	0097	hormone-mediated signaling pathway	2	0.015	0.071	NR3C2/PPARGC1A
	55					
	GO:1					
BP	9021	cellular response to reactive nitrogen species	1	0.015	0.071	PPARGC1A
	70					
	GO:0					
BP	0302	lipid modification	2	0.015	0.071	EPHX2/PPARGC1A
	58					
	GO:0					
BP	0330	muscle cell proliferation	2	0.015	0.071	HPGD/PPARGC1A
	02					
	GO:0					
BP	0193	epoxygenase P450 pathway	1	0.016	0.071	EPHX2
	73					
	GO:0					
BP	0320	mitochondrial DNA metabolic process	1	0.016	0.071	PPARGC1A
	42					
	GO:0					
BP	0063	DNA-templated transcription, initiation	2	0.017	0.071	NR3C2/PPARGC1A
	52					
	GO:0					
BP	0715	cellular response to transforming growth factor beta stimulus	2	0.017	0.071	HPGD/PPARGC1A
	60					
	GO:0					
BP	0713	cellular response to steroid hormone stimulus	2	0.017	0.071	NR3C2/PPARGC1A
	83					
	GO:0					
BP	0108	positive regulation of steroid biosynthetic process	1	0.017	0.071	PPARGC1A
	93					
	GO:0					
BP	0307	ovulation	1	0.017	0.071	HPGD
	28					
	GO:0					
BP	0080	regulation of heart contraction	2	0.017	0.071	FXYD3/CHGA
	16					

BP	GO:0 0715 59	response to transforming growth factor beta	2	0.017	0.073	HPGD/PPARGC1A
BP	GO:0 0511 95	negative regulation of cofactor metabolic process	1	0.018	0.073	PPARGC1A
BP	GO:0 0902 57	regulation of muscle system process	2	0.018	0.073	CHGA/PPARGC1A
BP	GO:0 0324 12	regulation of ion transmembrane transporter activity	2	0.018	0.073	FXYD3/PPARGC1A
BP	GO:0 0901 40	regulation of mitochondrial fission	1	0.018	0.073	PPARGC1A
BP	GO:0 0228 98	regulation of transmembrane transporter activity	2	0.019	0.074	FXYD3/PPARGC1A
BP	GO:0 0148 50	response to muscle activity	1	0.019	0.074	PPARGC1A
BP	GO:0 0325 28	microvillus organization	1	0.019	0.074	PLS1
BP	GO:0 0600 47	heart contraction	2	0.021	0.074	FXYD3/CHGA
BP	GO:0 0067 00	C21-steroid hormone biosynthetic process	1	0.021	0.074	PPARGC1A
BP	GO:0 0970 66	response to thyroid hormone	1	0.021	0.074	PPARGC1A
BP	GO:1 9035 79	negative regulation of ATP metabolic process	1	0.021	0.074	PPARGC1A
BP	GO:0 0324 09	regulation of transporter activity	2	0.021	0.074	FXYD3/PPARGC1A
BP	GO:0 0316 47	regulation of protein stability	2	0.021	0.074	TSPAN1/PPARGC1A
BP	GO:0 0159	energy derivation by oxidation of organic compounds	2	0.021	0.074	SUCLG2/PPARGC1A

	80					
	GO:0					
BP	0020	response to dietary excess	1	0.021	0.074	PPARGC1A
	21					
	GO:0					
BP	0020	regulation of the force of heart contraction	1	0.021	0.074	CHGA
	26					
	GO:0					
BP	0468	regulation of hormone biosynthetic process	1	0.021	0.074	PPARGC1A
	85					
	GO:0					
BP	0519	negative regulation of amine transport	1	0.021	0.074	CHGA
	53					
	GO:0					
BP	0030	heart process	2	0.022	0.074	FXYP3/CHGA
	15					
	GO:0					
BP	0082	androgen metabolic process	1	0.022	0.074	PPARGC1A
	09					
	GO:0					
BP	0346	response to gonadotropin	1	0.022	0.074	PPARGC1A
	98					
	GO:0					
BP	0435	skeletal muscle adaptation	1	0.022	0.074	PPARGC1A
	01					
	GO:1					
BP	9005	negative regulation of purine nucleotide metabolic process	1	0.022	0.074	PPARGC1A
	43					
	GO:0					
BP	0459	negative regulation of nucleotide metabolic process	1	0.023	0.074	PPARGC1A
	80					
	GO:1					
BP	9035	regulation of blood circulation	2	0.023	0.074	FXYP3/CHGA
	22					
	GO:0					
BP	0000	mitochondrial genome maintenance	1	0.024	0.074	PPARGC1A
	02					
	GO:0					
BP	0350	positive regulation of histone acetylation	1	0.024	0.074	PPARGC1A
	66					
	GO:0					
BP	0459	positive regulation of steroid metabolic process	1	0.024	0.074	PPARGC1A
	40					
BP	GO:0	regulation of fatty acid oxidation	1	0.024	0.074	PPARGC1A

	0463					
	20					
	GO:0					
BP	0610	myeloid leukocyte cytokine production	1	0.024	0.074	CHGA
	82					
	GO:0					
BP	0400	positive regulation of multicellular organism growth	1	0.025	0.074	PLS1
	18					
	GO:0					
BP	0434	regulation of cellular respiration	1	0.025	0.074	PPARGC1A
	57					
	GO:0					
BP	0718	adenylate cyclase-activating adrenergic receptor signaling pathway	1	0.025	0.074	CHGA
	80					
	GO:0					
BP	0900	relaxation of muscle	1	0.025	0.074	CHGA
	75					
	GO:0					
BP	0457	positive regulation of G protein-coupled receptor signaling pathway	1	0.025	0.075	CHGA
	45					
	GO:1					
BP	9012	regulation of neuron death	2	0.025	0.075	CHGA/PPARGC1A
	14					
	GO:2					
BP	0007	positive regulation of peptidyl-lysine acetylation	1	0.026	0.075	PPARGC1A
	58					
	GO:0					
BP	0060	tricarboxylic acid cycle	1	0.027	0.075	SUCLG2
	99					
	GO:0					
BP	0718	adrenergic receptor signaling pathway	1	0.027	0.075	CHGA
	75					
	GO:0					
BP	0970	energy homeostasis	1	0.027	0.075	PPARGC1A
	09					
	GO:0					
BP	0002	mitochondrial fission	1	0.028	0.075	PPARGC1A
	66					
	GO:0					
BP	0061	citrate metabolic process	1	0.028	0.075	SUCLG2
	01					
	GO:0					
BP	0713	cellular response to alkaloid	1	0.028	0.075	PPARGC1A
	12					

	GO:0					
BP	0324	response to lipopolysaccharide	2	0.028	0.075	HPGD/PPARGC1A
	96					
	GO:0					
BP	0082	steroid metabolic process	2	0.028	0.075	EPHX2/PPARGC1A
	02					
	GO:0					
BP	0713	cellular response to estradiol stimulus	1	0.029	0.075	PPARGC1A
	92					
	GO:2					
BP	0003	regulation of NMDA receptor activity	1	0.029	0.075	PPARGC1A
	10					
	GO:2					
BP	0011	positive regulation of ATP biosynthetic process	1	0.029	0.075	PPARGC1A
	71					
	GO:0					
BP	0149	negative regulation of smooth muscle cell migration	1	0.029	0.075	PPARGC1A
	12					
	GO:0					
BP	0459	positive regulation of fatty acid metabolic process	1	0.029	0.075	PPARGC1A
	23					
	GO:0					
BP	0468	phospholipid dephosphorylation	1	0.029	0.075	EPHX2
	39					
	GO:1					
BP	9040	regulation of cation transmembrane transport	2	0.030	0.075	FXYD3/PPARGC1A
	62					
	GO:0					
BP	0323	regulation of hormone metabolic process	1	0.030	0.075	PPARGC1A
	50					
	GO:0					
BP	0466	negative regulation of insulin secretion	1	0.030	0.075	CHGA
	76					
	GO:0					
BP	0508	intestinal absorption	1	0.030	0.075	PLS1
	92					
	GO:0					
BP	0718	response to monoamine	1	0.030	0.075	PPARGC1A
	67					
	GO:0					
BP	0718	response to catecholamine	1	0.030	0.075	PPARGC1A
	69					
	GO:1					
BP	9040	positive regulation of epithelial cell apoptotic process	1	0.030	0.075	PPARGC1A

	37					
BP	GO:002237	response to molecule of bacterial origin	2	0.030	0.075	HPGD/PPARGC1A
BP	GO:008207	C21-steroid hormone metabolic process	1	0.031	0.076	PPARGC1A
BP	GO:007235	tricarboxylic acid metabolic process	1	0.031	0.076	SUCLG2
BP	GO:007099	neuron death	2	0.031	0.076	CHGA/PPARGC1A
BP	GO:0045823	positive regulation of heart contraction	1	0.032	0.076	CHGA
BP	GO:0050832	defense response to fungus	1	0.032	0.076	CHGA
BP	GO:0050873	brown fat cell differentiation	1	0.032	0.077	PPARGC1A
BP	GO:0010677	negative regulation of cellular carbohydrate metabolic process	1	0.033	0.077	PPARGC1A
BP	GO:0010907	positive regulation of glucose metabolic process	1	0.033	0.077	PPARGC1A
BP	GO:0042181	ketone biosynthetic process	1	0.033	0.077	PPARGC1A
BP	GO:0006692	prostanoid metabolic process	1	0.034	0.077	HPGD
BP	GO:0006693	prostaglandin metabolic process	1	0.034	0.077	HPGD
BP	GO:0003086	cortical actin cytoskeleton organization	1	0.034	0.077	PLS1
BP	GO:0005160	response to electrical stimulus	1	0.034	0.077	PPARGC1A
BP	GO:000202	adipose tissue development	1	0.034	0.077	PPARGC1A

	0606					
	12					
	GO:1					
BP	9019	positive regulation of protein acetylation	1	0.034	0.077	PPARGC1A
	85					
	GO:0					
BP	0902	negative regulation of peptide hormone secretion	1	0.036	0.080	CHGA
	78					
	GO:0					
BP	0308	positive regulation of nucleotide biosynthetic process	1	0.036	0.080	PPARGC1A
	10					
	GO:0					
BP	0713	cellular response to interleukin-6	1	0.036	0.080	PPARGC1A
	54					
	GO:1					
BP	9003	positive regulation of purine nucleotide biosynthetic process	1	0.036	0.080	PPARGC1A
	73					
	GO:0					
BP	0433	mast cell degranulation	1	0.037	0.080	CHGA
	03					
	GO:1					
BP	9035	positive regulation of ATP metabolic process	1	0.037	0.080	PPARGC1A
	80					
	GO:0					
BP	0485	response to steroid hormone	2	0.037	0.080	NR3C2/PPARGC1A
	45					
	GO:0					
BP	0022	mast cell activation involved in immune response	1	0.038	0.080	CHGA
	79					
	GO:0					
BP	0061	regulation of gluconeogenesis	1	0.038	0.080	PPARGC1A
	11					
	GO:0					
BP	0308	cortical cytoskeleton organization	1	0.038	0.080	PLS1
	65					
	GO:0					
BP	0459	negative regulation of carbohydrate metabolic process	1	0.038	0.080	PPARGC1A
	12					
	GO:0					
BP	0459	positive regulation of muscle contraction	1	0.038	0.080	CHGA
	33					
	GO:0					
BP	0024	mast cell mediated immunity	1	0.039	0.080	CHGA
	48					

BP	GO:1 9047 07	positive regulation of vascular smooth muscle cell proliferation	1	0.039	0.080	HPGD
BP	GO:0 0029 31	response to ischemia	1	0.039	0.081	PPARGC1A
BP	GO:0 0094 09	response to cold	1	0.039	0.081	PPARGC1A
BP	GO:0 0707 41	response to interleukin-6	1	0.039	0.081	PPARGC1A
BP	GO:0 0193 69	arachidonic acid metabolic process	1	0.040	0.082	EPHX2
BP	GO:0 0067 32	coenzyme metabolic process	2	0.041	0.082	SUCLG2/PPARGC1A
BP	GO:0 0096 20	response to fungus	1	0.041	0.082	CHGA
BP	GO:2 0006 49	regulation of sodium ion transmembrane transporter activity	1	0.041	0.082	FXYD3
BP	GO:0 0350 65	regulation of histone acetylation	1	0.042	0.083	PPARGC1A
BP	GO:0 0192 16	regulation of lipid metabolic process	2	0.042	0.083	EPHX2/PPARGC1A
BP	GO:0 0066 36	unsaturated fatty acid biosynthetic process	1	0.043	0.084	HPGD
BP	GO:0 0108 23	negative regulation of mitochondrion organization	1	0.043	0.084	PPARGC1A
BP	GO:0 0464 56	icosanoid biosynthetic process	1	0.043	0.084	HPGD
BP	GO:1 9030 78	positive regulation of protein localization to plasma membrane	1	0.044	0.085	PLS1
BP	GO:0 0148	striated muscle adaptation	1	0.045	0.085	PPARGC1A

	88					
BP	GO:0 0459 81	positive regulation of nucleotide metabolic process	1	0.045	0.085	PPARGC1A
BP	GO:0 0713 98	cellular response to fatty acid	1	0.045	0.085	PPARGC1A
BP	GO:1 9005 44	positive regulation of purine nucleotide metabolic process	1	0.045	0.085	PPARGC1A
BP	GO:2 0002 72	negative regulation of signaling receptor activity	1	0.045	0.085	PPARGC1A
BP	GO:0 0977 55	positive regulation of blood vessel diameter	1	0.046	0.087	EPHX2
BP	GO:2 0007 56	regulation of peptidyl-lysine acetylation	1	0.046	0.087	PPARGC1A
BP	GO:0 0455 76	mast cell activation	1	0.047	0.087	CHGA
BP	GO:0 0305 21	androgen receptor signaling pathway	1	0.048	0.087	PPARGC1A
BP	GO:0 0106 76	positive regulation of cellular carbohydrate metabolic process	1	0.049	0.087	PPARGC1A
BP	GO:0 0316 40	killing of cells of other organism	1	0.049	0.087	CHGA
BP	GO:0 0329 22	circadian regulation of gene expression	1	0.049	0.087	PPARGC1A
BP	GO:0 0443 64	disruption of cells of other organism	1	0.049	0.087	CHGA
BP	GO:0 0504 33	regulation of catecholamine secretion	1	0.049	0.087	CHGA
BP	GO:1 9023 05	regulation of sodium ion transmembrane transport	1	0.049	0.087	FXYP3
BP	GO:0	regulation of cholesterol	1	0.049	0.088	EPHX2

	0901	metabolic process				
	81					
	GO:1					
BP	9043	positive regulation of protein localization to cell periphery	1	0.049	0.088	PLS1
	77					
	GO:0					
CC	0425	zymogen granule membrane	1	0.009	0.119	ZG16
	89					
	GO:0					
CC	0425	zymogen granule	1	0.012	0.119	ZG16
	88					
	GO:0					
CC	0452	tricarboxylic acid cycle enzyme complex	1	0.012	0.119	SUCLG2
	39					
	GO:0					
CC	0974	apical dendrite	1	0.015	0.119	PPARGC1A
	40					
	GO:0					
CC	0426	mast cell granule	1	0.019	0.123	CHGA
	29					
	GO:0					
CC	0057	nuclear euchromatin	1	0.026	0.139	PPARGC1A
	19					
	GO:0					
CC	0007	euchromatin	1	0.032	0.150	PPARGC1A
	91					
	GO:0					
CC	0057	peroxisomal matrix	1	0.043	0.156	EPHX2
	82					
	GO:0					
CC	0319	microbody lumen	1	0.043	0.156	EPHX2
	07					
	GO:0					
MF	0080	N-acetyltransferase activity	2	0.003	0.046	NAT1/NAT2
	80					
	GO:0					
MF	0164	acetyltransferase activity	2	0.004	0.046	NAT1/NAT2
	07					
	GO:0					
MF	0164	N-acyltransferase activity	2	0.004	0.046	NAT1/NAT2
	10					
	GO:0					
MF	0049	prostaglandin receptor activity	1	0.008	0.046	HPGD
	55					

	GO:0					
MF	016803	ether hydrolase activity	1	0.008	0.046	EPHX2
	GO:0					
MF	004954	prostanoid receptor activity	1	0.009	0.046	HPGD
	GO:0					
MF	015643	toxic substance binding	1	0.009	0.046	EPHX2
	GO:0					
MF	016801	hydrolase activity, acting on ether bonds	1	0.009	0.046	EPHX2
	GO:0					
MF	042577	lipid phosphatase activity	1	0.009	0.046	EPHX2
	GO:0					
MF	042975	peroxisome proliferator activated receptor binding	1	0.010	0.046	PPARGC1A
	GO:0					
MF	070403	NAD+ binding	1	0.012	0.048	HPGD
	GO:0					
MF	004953	icosanoid receptor activity	1	0.013	0.048	HPGD
	GO:0					
MF	000287	magnesium ion binding	2	0.014	0.048	SUCLG2/EPHX2
	GO:0					
MF	016747	transferase activity, transferring acyl groups other than amino-acyl groups	2	0.016	0.051	NAT1/NAT2
	GO:0					
MF	016922	nuclear receptor binding	1	0.017	0.051	PPARGC1A
	GO:0					
MF	072509	divalent inorganic cation transmembrane transporter activity	1	0.020	0.055	SLC41A2
	GO:0					
MF	016746	transferase activity, transferring acyl groups	2	0.020	0.055	NAT1/NAT2
	GO:0					
MF	016878	acid-thiol ligase activity	1	0.025	0.063	SUCLG2
	GO:0					
MF	0011	RNA polymerase II repressing transcription factor binding	1	0.029	0.067	MIER3

	03					
	GO:0					
MF	0170	sodium channel regulator activity	1	0.030	0.067	FXYD3
	80					
	GO:0					
MF	0430	alpha-tubulin binding	1	0.031	0.067	PPARGC1A
	14					
	GO:0					
MF	0168	ligase activity, forming carbon-sulfur bonds	1	0.033	0.069	SUCLG2
	77					
	GO:0					
MF	0303	estrogen receptor binding	1	0.035	0.069	PPARGC1A
	31					
	GO:0					
MF	0506	androgen receptor binding	1	0.037	0.069	PPARGC1A
	81					
	GO:1					
MF	9908	promoter-specific chromatin binding	1	0.040	0.072	PPARGC1A
	41					
	GO:0					
MF	0037	steroid hormone receptor activity	1	0.046	0.078	NR3C2
	07					
	GO:0					
MF	0512	NAD binding	1	0.046	0.078	HPGD
	87					
