

Table S8

layer1	layer2	layer3	ID	Input.num	Backgrou	pvalue	FDR	Input	Hyperlink
5. Organism	5.2 Endocrinology	PPAR signaling	ko03320	14	69	2.16E-07	3.97E-05	ACAA1 AC	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabolism	1.3 Lipid metabolism	Fatty acid	ko00071	9	36	5.26E-06	0.000484	ACAA1 AC	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabolism	1.0 Global metabolism	Fatty acid	ko01212	11	59	1.03E-05	0.00063	ACAA1 AC	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabolism	1.3 Lipid metabolism	Fatty acid	ko00061	6	20	6.72E-05	0.00309	ACACA AC	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabolism	1.0 Global metabolism	Biosynthesis	ko01130	18	204	0.000691	0.025433	ACAA1 AC	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabolism	1.3 Lipid metabolism	Steroid biosynthesis	ko00100	5	20	0.000709	0.021743	DHCR24 C	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabolism	1.0 Global metabolism	Biosynthesis	ko01110	29	406	0.000714	0.018761	ACAA1 AC	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabolism	1.9 Metabolism	Sesquiterpene	ko00909	2	2	0.001405	0.032325	FDFT1 SQ	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabolism	1.1 Carbohydrate	Pyruvate	ko00620	6	36	0.002027	0.041444	ACACA AC	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabolism	1.5 Amino acid	Valine, leucine	ko00280	7	49	0.002206	0.040581	AACS AC	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabolism	1.1 Carbohydrate	Propanoate	ko00640	5	31	0.005531	0.092511	ACACA AC	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabolism	1.3 Lipid metabolism	Glycerolipid	ko00561	7	61	0.00762	0.116846	AGPAT2 A	http://www.genome.jp/kegg-bin/show_pathway?koC
4. Cellular process	4.2 Cell growth	Cell cycle	ko04110	10	118	0.013303	0.188285	BUB1 CCN	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organism	5.2 Endocrinology	Glucagon	ko04922	7	78	0.02689	0.353412	ACACA AC	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabolism	1.3 Lipid metabolism	Biosynthesis	ko01040	4	31	0.02765	0.339179	ACAA1 AC	http://www.genome.jp/kegg-bin/show_pathway?koC
4. Cellular process	4.1 Transport	Peroxisome	ko04146	7	79	0.028588	0.328762	ACAA1 AC	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organism	5.2 Endocrinology	Adipocyte	ko04920	6	66	0.036995	0.400421	ACACB AC	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabolism	1.0 Global metabolism	Carbon metabolism	ko01200	8	106	0.045835	0.468532	ACOX1 AC	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabolism	1.0 Global metabolism	Metabolic	ko01100	64	1385	0.046764	0.45287	AACS AC	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organism	5.5 Excretion	Collecting duct	ko04966	3	23	0.053308	0.490438	ATP6V0D2	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabolism	1.1 Carbohydrate	Butanoate	ko00650	3	23	0.053308	0.467083	AACS EH	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organism	5.4 Digestion	Cholesterol	ko04979	5	55	0.054692	0.457425	ANGPTL3	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabolism	1.1 Carbohydrate	Glycolysis	ko00010	5	56	0.058287	0.466295	ACSS1B A	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabolism	1.11 Xenobiotic	Drug metabolism	ko00983	5	56	0.058287	0.446866	CES1L2 G	http://www.genome.jp/kegg-bin/show_pathway?koC
3. Environment	3.2 Signal transduction	AMPK signaling	ko04152	8	112	0.059748	0.439747	ACACA AC	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabolism	1.8 Metabolism	Retinol metabolism	ko00830	4	40	0.061877	0.437897	CYP3A5 L	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabolism	1.11 Xenobiotic	Toluene degradation	ko00623	1	2	0.073635	0.501808	CMBL	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabolism	1.11 Xenobiotic	Fluorobenzene	ko00364	1	2	0.073635	0.483887	CMBL	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabolism	1.1 Carbohydrate	C5-Branch	ko00660	1	2	0.073635	0.467201	ACOD1	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabolism	1.11 Xenobiotic	Chlorocyclohexane	ko00361	1	2	0.073635	0.451628	CMBL	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabolism	1.6 Metabolism	beta-Alanine	ko00410	3	28	0.0861	0.511047	ACOX1 AL	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabolism	1.1 Carbohydrate	Amino sugar	ko00520	4	46	0.093054	0.53506	GALE HKD	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabolism	1.3 Lipid metabolism	Primary bile acid	ko00120	2	15	0.106964	0.596406	CYP7A1 C	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabolism	1.1 Carbohydrate	Ascorbate	ko00053	2	15	0.106964	0.578865	ALDH1A3	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabolism	1.1 Carbohydrate	Glyoxylate	ko00630	3	31	0.108985	0.572948	ACSS1B G	http://www.genome.jp/kegg-bin/show_pathway?koC
2. Genetic information	2.4 Replication	DNA replication	ko03030	3	32	0.117084	0.598428	MCM3 MC	http://www.genome.jp/kegg-bin/show_pathway?koC

1. Metabo 1.11 Xeno Drug metabolis	3	32	0.117084	0.582255	GSTK1 GS	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabo 1.11 Xeno Metabolis	3	34	0.133921	0.64846	GSTK1 GS	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabo 1.9 Metab Geraniol d	1	4	0.141856	0.669271	HMGCL	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabo 1.11 Xeno Caprolact	1	4	0.141856	0.652539	EHHADH	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabo 1.5 Amino Phenylalar	1	4	0.141856	0.636624	IL4I1	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabo 1.9 Metab Limonene	1	4	0.141856	0.621466	ALDH1A3	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabo 1.1 Carbol Galactose	3	36	0.151534	0.648425	GALE HKD	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabo 1.3 Lipid n Glyceroph	6	98	0.162391	0.679089	AGPAT2 C	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organıs 5.2 Endocı Insulin sigı	7	120	0.164776	0.673753	ACACA A	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organıs 5.4 Digest Mineral at	3	38	0.169831	0.679323	MT3 MT4	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabo 1.9 Metab Insect horı	1	5	0.174062	0.681436	ALDH1A3	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabo 1.11 Xeno Aminoben	1	5	0.174062	0.667239	EHHADH	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabo 1.3 Lipid n Steroid hc	3	39	0.179207	0.672941	CYP3A5 C	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabo 1.1 Carbol Pentose aı	2	21	0.185289	0.681863	LOC12111	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabo 1.11 Xeno Chloroalk	1	6	0.205062	0.739831	ALDH1A3	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabo 1.5 Amino Tryptopha	3	42	0.208114	0.736403	ALDH1A3	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabo 1.6 Metab Glutathion	3	45	0.237961	0.826129	GSTK1 GS	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabo 1.5 Amino Arginine a	3	46	0.248071	0.845279	ALDH1A3	http://www.genome.jp/kegg-bin/show_pathway?koC
4. Cellular 4.2 Cell gr Cellular se	8	160	0.253045	0.846551	CCNB3 C	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabo 1.2 Energy Methane r	2	26	0.254999	0.837853	ACSS1B F	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabo 1.3 Lipid n Fatty acid	2	27	0.26908	0.86861	ELOVL2 H	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabo 1.8 Metab Folate bioı	2	27	0.26908	0.853634	ALPI FPGS	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organıs 5.2 Endocı Thyroid hc	3	50	0.289055	0.901459	CREB3L3 F	http://www.genome.jp/kegg-bin/show_pathway?koC
4. Cellular 4.4 Cellula Quorum s	1	9	0.291263	0.893205	ACSL1	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabo 1.3 Lipid n alpha-Lin	2	29	0.297206	0.896489	ACAA1 A	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabo 1.10 Biosy Isoquinolir	1	10	0.31787	0.943356	IL4I1	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabo 1.3 Lipid n Synthesis i	1	10	0.31787	0.928382	HMGCL	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabo 1.5 Amino Lysine deç	3	53	0.320113	0.920326	ALDH1A3	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabo 1.1 Carbol Starch anc	2	31	0.325159	0.92045	HKDC1 U	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabo 1.5 Amino Tyrosine n	2	33	0.352813	0.9836	DCT IL4I1	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organıs 5.1 Immur Toll and Ir	2	35	0.380061	0.999979	ANK1 DUC	http://www.genome.jp/kegg-bin/show_pathway?koC
3. Environı 3.2 Signal Two-comı	1	13	0.391857	0.999979	ALPI	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabo 1.8 Metab Thiamine i	1	13	0.391857	0.999979	ALPI	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organıs 5.2 Endocı Melanoge	4	86	0.404493	0.999979	ASIP CREB	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabo 1.1 Carbol Fructose a	2	37	0.406812	0.999979	FBP2 HKD	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organıs 5.4 Digest Fat digesti	2	37	0.406812	0.999979	AGPAT2 F	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabo 1.5 Amino Phenylalar	1	14	0.414694	0.999979	IL4I1	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabo 1.7 Glycan Various tyı	2	40	0.445849	0.999979	ALG12 M	http://www.genome.jp/kegg-bin/show_pathway?koC

1. Metabo 1.8 Metab One carb	ko00670	1	16	0.457831	0.999979	ATIC	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organ 5.2 Endoc Renin-ang	ko04614	1	16	0.457831	0.999979	ENPEP	http://www.genome.jp/kegg-bin/show_pathway?koC
3. Environ 3.2 Signal FoxO sign	ko04068	5	120	0.470524	0.999979	CCNB3 CC	http://www.genome.jp/kegg-bin/show_pathway?koC
4. Cellular 4.2 Cell gr p53 signal	ko04115	3	68	0.472261	0.999979	CDK6 GAC	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabo 1.2 Energy Nitrogen r	ko00910	1	17	0.478194	0.999979	CA5A	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabo 1.8 Metab Pantothen	ko00770	1	17	0.478194	0.999979	PANK1	http://www.genome.jp/kegg-bin/show_pathway?koC
2. Genetic 2.3 Folding Protein pr	ko04141	6	152	0.508347	0.999979	DNAJB11	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organ 5.6 Nervoi Synaptic v	ko04721	3	73	0.519712	0.999979	ATP6V0D2	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabo 1.7 Glycan N-Glycan	ko00510	2	48	0.542368	0.999979	ALG12 MA	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organ 5.8 Develc Dorso-ver	ko04320	1	21	0.552292	0.999979	SPIRE2	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabo 1.9 Metab Terpenoid	ko00900	1	21	0.552292	0.999979	FDPS	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organ 5.2 Endoc Regulatio	ko04923	2	49	0.553586	0.999979	FABP4 PN	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organ 5.2 Endoc GnRH secr	ko04929	2	49	0.553586	0.999979	ARR3 CAC	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organ 5.2 Endoc Cortisol sy	ko04927	2	49	0.553586	0.999979	CACNA1H	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabo 1.5 Amino Histidine r	ko00340	1	22	0.569113	0.999979	ALDH1A3	http://www.genome.jp/kegg-bin/show_pathway?koC
2. Genetic 2.3 Folding Protein ex	ko03060	1	22	0.569113	0.999979	HSPA5	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabo 1.4 Nuclec Pyrimidine	ko00240	2	51	0.575433	0.999979	RRM2 TK1	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organ 5.4 Digest Bile secret	ko04976	2	51	0.575433	0.999979	CYP7A1 SI	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabo 1.7 Glycan Glycosami	ko00534	1	23	0.585303	0.999979	HS6ST3	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organ 5.2 Endoc Parathyroi	ko04928	3	83	0.607125	0.999979	ARR3 CAS	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organ 5.4 Digest Vitamin di	ko04977	1	26	0.630319	0.999979	TCN2	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabo 1.1 Carbol Citrate cyc	ko00020	1	26	0.630319	0.999979	PDHA2	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabo 1.1 Carbol Pentose p	ko00030	1	28	0.657586	0.999979	FBP2	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organ 5.6 Nervoi Cholinergi	ko04725	3	90	0.661667	0.999979	CHRNA3 C	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organ 5.5 Excret Aldosteror	ko04960	1	29	0.670456	0.999979	SGK1	http://www.genome.jp/kegg-bin/show_pathway?koC
2. Genetic 2.4 Replic Base excis	ko03410	1	31	0.694767	0.999979	UNG	http://www.genome.jp/kegg-bin/show_pathway?koC
4. Cellular 4.2 Cell gr Ferroptosi	ko04216	1	32	0.706242	0.999979	ACSL1	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organ 5.2 Endoc Insulin sec	ko04911	2	65	0.706391	0.999979	CREB3L3 F	http://www.genome.jp/kegg-bin/show_pathway?koC
4. Cellular 4.1 Transp Phagosom	ko04145	5	159	0.716781	0.999979	ATP6V0D2	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabo 1.5 Amino Alanine, a	ko00250	1	33	0.717287	0.999979	IL4I1	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabo 1.3 Lipid n Linoleic ac	ko00591	1	33	0.717287	0.999979	CYP3A5	http://www.genome.jp/kegg-bin/show_pathway?koC
4. Cellular 4.1 Transp Endocytos	ko04144	8	252	0.733687	0.999979	ARR3 DNM	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organ 5.4 Digest Carbohydi	ko04973	1	35	0.738148	0.999979	HKDC1	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organ 5.1 Immur Antigen p	ko04612	3	103	0.74791	0.999979	LOC1211C	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organ 5.2 Endoc Aldosteror	ko04925	2	71	0.751304	0.999979	CACNA1H	http://www.genome.jp/kegg-bin/show_pathway?koC
2. Genetic 2.1 Transc Basal tran	ko03022	1	37	0.757472	0.999979	TAF10	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organ 5.2 Endoc Progester	ko04914	2	73	0.764904	0.999979	BUB1 CCN	http://www.genome.jp/kegg-bin/show_pathway?koC
3. Environ 3.1 Memb ABC trans	ko02010	1	38	0.766594	0.999979	ABCA12	http://www.genome.jp/kegg-bin/show_pathway?koC

5. Organism 5.5 Excretory Endocrine ko04961	1	39	0.775373	0.999979	DNM1	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabolic 1.5 Amino Glycine, serine ko00260	1	39	0.775373	0.999979	GLDC	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organism 5.2 Endocrine Thyroid hormone ko04919	3	111	0.791645	0.999979	MED13 RC3H1	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabolic 1.5 Amino Cysteine and Methionine ko00270	1	43	0.807314	0.999979	IL4I1	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organism 5.7 Sensor Taste Transduction ko04742	1	43	0.807314	0.999979	TRPM5	http://www.genome.jp/kegg-bin/show_pathway?koC
3. Environment 3.3 Signaling ECM-receptor interaction ko04512	2	80	0.807529	0.999979	ITGB6 LANA1	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organism 5.3 Circulatory Adrenergic ko04261	3	115	0.811037	0.999979	CREB3L3 HTR7	http://www.genome.jp/kegg-bin/show_pathway?koC
3. Environment 3.2 Signaling TNF signaling ko04668	2	82	0.818377	0.999979	CREB3L3 FOSL1	http://www.genome.jp/kegg-bin/show_pathway?koC
3. Environment 3.2 Signaling MAPK signaling ko04010	7	247	0.823844	0.999979	ARR3 CACNA1H	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organism 5.9 Aging Longevity ko04211	2	84	0.828674	0.999979	CREB3L3 FOSL1	http://www.genome.jp/kegg-bin/show_pathway?koC
3. Environment 3.2 Signaling Hedgehog ko04340	1	47	0.834719	0.999979	ARR3	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organism 5.8 Development Axon regeneration ko04361	2	86	0.838443	0.999979	DUSP4 PSD95	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organism 5.4 Digestion Protein digestion ko04974	2	86	0.838443	0.999979	DPP4 KCNK10	http://www.genome.jp/kegg-bin/show_pathway?koC
2. Genetic 2.4 Replication Fanconi anemia ko03460	1	49	0.846926	0.999979	RMI2	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabolic 1.3 Lipid metabolism Sphingolipid metabolism ko00600	1	50	0.852688	0.999979	SGPP2	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organism 5.6 Nervous Long-term ko04720	1	51	0.858233	0.999979	GRIN2C	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organism 5.2 Endocrine Growth hormone ko04935	3	127	0.86027	0.999979	CREB3L3 C/EBPβ	http://www.genome.jp/kegg-bin/show_pathway?koC
4. Cellular 4.2 Cell growth Oocyte maturation ko04114	2	93	0.868785	0.999979	BUB1 PTTG1	http://www.genome.jp/kegg-bin/show_pathway?koC
3. Environment 3.2 Signaling PI3K-Akt signaling ko04151	8	297	0.87307	0.999979	CDK6 CREB1	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organism 5.4 Digestion Gastric acid ko04971	1	55	0.878406	0.999979	KCNQ1	http://www.genome.jp/kegg-bin/show_pathway?koC
4. Cellular 4.1 Transport Lysosome ko04142	3	133	0.880385	0.999979	ATP6V0D2	http://www.genome.jp/kegg-bin/show_pathway?koC
3. Environment 3.2 Signaling Phospholipid signaling ko04072	3	133	0.880385	0.999979	AGPAT2 DCX	http://www.genome.jp/kegg-bin/show_pathway?koC
3. Environment 3.2 Signaling Notch signaling ko04330	1	57	0.887391	0.999979	RBPJ	http://www.genome.jp/kegg-bin/show_pathway?koC
3. Environment 3.2 Signaling HIF-1 signaling ko04066	2	99	0.89053	0.999979	HKDC1 PCNA	http://www.genome.jp/kegg-bin/show_pathway?koC
3. Environment 3.3 Signaling Cell adhesion ko04514	4	173	0.893422	0.999979	LOC121110	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organism 5.6 Nervous Dopamine ko04728	2	100	0.893812	0.999979	ARR3 CREB1	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organism 5.10 Environment Circadian rhythm ko04713	2	100	0.893812	0.999979	CACNA1H	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organism 5.2 Endocrine Estrogen signaling ko04915	2	101	0.897002	0.999979	CREB3L3 HTR7	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organism 5.2 Endocrine Relaxin signaling ko04926	2	104	0.906045	0.999979	ARR3 CREB1	http://www.genome.jp/kegg-bin/show_pathway?koC
3. Environment 3.2 Signaling cAMP signaling ko04024	5	217	0.913892	0.999979	ACOX1 CFEB	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organism 5.2 Endocrine Prolactin signaling ko04917	1	66	0.920293	0.999979	SOCS3	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organism 5.1 Immune Natural killer ko04650	1	67	0.923297	0.999979	FASLG	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organism 5.1 Immune IL-17 signaling ko04657	1	69	0.928969	0.999979	HSP90B1	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organism 5.4 Digestion Salivary secretion ko04970	1	71	0.934222	0.999979	LOC101750	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organism 5.1 Immune Toll-like receptor ko04620	1	72	0.936701	0.999979	TLR5	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabolic 1.2 Energy Oxidative phosphorylation ko00190	2	120	0.942956	0.999979	ATP6V0D2	http://www.genome.jp/kegg-bin/show_pathway?koC
4. Cellular 4.3 Cellular Gap junctions ko04540	1	76	0.94572	0.999979	GJA1	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organism 5.1 Immune Th1 and T helper ko04658	1	77	0.947767	0.999979	RBPJ	http://www.genome.jp/kegg-bin/show_pathway?koC

5. Organism 5.10 Environmental Thermogenesis	ko04714	5	241	0.950815	0.999979	ACSL1 CP	http://www.genome.jp/kegg-bin/show_pathway?koC
2. Genetic 2.3 Folding Ubiquitin	ko04120	2	125	0.951326	0.999979	SOCS3 UB	http://www.genome.jp/kegg-bin/show_pathway?koC
3. Environmental 3.2 Signal NF-kappa	ko04064	1	80	0.953456	0.999979	CARD10	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organism 5.1 Immune NOD-like	ko04621	2	127	0.954335	0.999979	CASR LOC	http://www.genome.jp/kegg-bin/show_pathway?koC
4. Cellular 4.2 Cell growth Apoptosis	ko04210	2	128	0.955771	0.999979	FASLG GA	http://www.genome.jp/kegg-bin/show_pathway?koC
3. Environmental 3.2 Signal Jak-STAT	ko04630	2	132	0.961098	0.999979	IL22RA1 S	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organism 5.4 Digestive Pancreatic	ko04972	1	85	0.961596	0.999979	KCNQ1	http://www.genome.jp/kegg-bin/show_pathway?koC
3. Environmental 3.2 Signal TGF-beta	ko04350	1	87	0.96444	0.999979	CDKN2B	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organism 5.6 Nervous Glutamate	ko04724	1	88	0.965781	0.999979	GRIN2C	http://www.genome.jp/kegg-bin/show_pathway?koC
1. Metabolic 1.4 Nucleic Purine	me ko00230	2	141	0.970925	0.999979	ATIC RRM	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organism 5.1 Immune Th17 cell	ko04659	1	93	0.971769	0.999979	AHR1B	http://www.genome.jp/kegg-bin/show_pathway?koC
3. Environmental 3.2 Signal mTOR	sign ko04150	2	144	0.973633	0.999979	SGK1 WN	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organism 5.8 Development Osteoclast	ko04380	1	97	0.975797	0.999979	SOCS3	http://www.genome.jp/kegg-bin/show_pathway?koC
3. Environmental 3.2 Signal Sphingolipid	ko04071	1	106	0.982884	0.999979	SGPP2	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organism 5.8 Development Axon	guid ko04360	2	160	0.984431	0.999979	DPYSL2 EF	http://www.genome.jp/kegg-bin/show_pathway?koC
3. Environmental 3.2 Signal Calcium	sign ko04020	2	161	0.98494	0.999979	CACNA1H	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organism 5.6 Nervous Neurotrophin	ko04722	1	110	0.985328	0.999979	FASLG	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organism 5.1 Immune Leukocyte	ko04670	1	112	0.986416	0.999979	RAPGEF4	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organism 5.6 Nervous Retrograde	ko04723	1	120	0.99002	0.999979	ABHD6	http://www.genome.jp/kegg-bin/show_pathway?koC
4. Cellular 4.2 Cell growth Necroptosis	ko04217	1	124	0.991446	0.999979	FASLG	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organism 5.1 Immune T cell	receptor ko04660	1	125	0.991769	0.999979	PDCD1	http://www.genome.jp/kegg-bin/show_pathway?koC
3. Environmental 3.3 Signaling Neuroactive	ko04080	5	313	0.992263	0.999979	CHRNA3 C	http://www.genome.jp/kegg-bin/show_pathway?koC
4. Cellular 4.5 Cell membrane Regulation	ko04810	2	183	0.992801	0.999979	FGF19 ITG	http://www.genome.jp/kegg-bin/show_pathway?koC
4. Cellular 4.3 Cellular Signaling	ko04550	1	129	0.992946	0.999979	WNT11	http://www.genome.jp/kegg-bin/show_pathway?koC
4. Cellular 4.3 Cellular Focal adhesion	ko04510	2	186	0.993497	0.999979	ITGB6 LAN	http://www.genome.jp/kegg-bin/show_pathway?koC
3. Environmental 3.2 Signal Rap1	sign ko04015	2	188	0.993923	0.999979	FGF19 RAI	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organism 5.1 Immune Chemokine	ko04062	1	133	0.993954	0.999979	ARR3	http://www.genome.jp/kegg-bin/show_pathway?koC
3. Environmental 3.2 Signal Apelin	sign ko04371	1	139	0.995204	0.999979	PPARGC1	http://www.genome.jp/kegg-bin/show_pathway?koC
3. Environmental 3.3 Signaling Cytokine	ko04060	2	195	0.995212	0.999979	FASLG IL2	http://www.genome.jp/kegg-bin/show_pathway?koC
3. Environmental 3.2 Signal cGMP-PK	ko04022	1	140	0.995385	0.999979	CREB3L3	http://www.genome.jp/kegg-bin/show_pathway?koC
3. Environmental 3.2 Signal Ras	sign ko04014	2	199	0.995824	0.999979	FASLG FGI	http://www.genome.jp/kegg-bin/show_pathway?koC
3. Environmental 3.2 Signal Wnt	sign ko04310	1	151	0.996982	0.999979	WNT11	http://www.genome.jp/kegg-bin/show_pathway?koC
3. Environmental 3.2 Signal Hippo	sign ko04390	1	157	0.997607	0.999979	WNT11	http://www.genome.jp/kegg-bin/show_pathway?koC
5. Organism 5.7 Sensor Olfactory	ko04740	1	279	0.999979	0.999979	ARR3	http://www.genome.jp/kegg-bin/show_pathway?koC

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