

**Supplementary Table S2. KEGG pathways enriched by DEGs of different groups**

Group	KEGG_Name	Rich_factor	P_value	Input
Low.AF vs High.AF	AGE-RAGE signaling pathway in diabetic complications	0.040	0.000	<i>IL1B, NOS3, IL8, PIM1</i>
	NF-kappa B signaling pathway	0.040	0.000	<i>CCL19, IL1B, CCL4, IL8</i>
	Fluid shear stress and atherosclerosis	0.029	0.000	<i>NCF2, IL1B, NOS3, HMOX1</i>
	Malaria	0.061	0.000	<i>IL1B, CD36, IL8</i>
	Cytokine-cytokine receptor interaction	0.017	0.000	<i>CCL19, IL1B, BMP5, CCL4, IL8</i>
	Pathways in cancer	0.011	0.000	<i>IGF2, PIM1, HMOX1, KIT, FGF17, IL8</i>
	PI3K-Akt signaling pathway	0.014	0.000	<i>IGF2, DDIT4, NOS3, FGF17, KIT</i>
	Salmonella infection	0.036	0.000	<i>IL1B, CCL4, IL8</i>
	Hematopoietic cell lineage	0.031	0.000	<i>IL1B, CD36, KIT</i>
	Glycosaminoglycan degradation	0.105	0.000	<i>HYAL2, HPSE2</i>
	Viral protein interaction with cytokine and cytokine receptor	0.030	0.000	<i>CCL19, CCL4, IL8</i>
	Toll-like receptor signaling pathway	0.029	0.000	<i>IL1B, CCL4, IL8</i>
	MAPK signaling pathway	0.014	0.001	<i>IGF2, IL1B, FGF17, KIT</i>
	Phagosome	0.020	0.001	<i>NCF2, MARCO, CD36</i>
	Chemokine signaling pathway	0.016	0.002	<i>CCL19, CCL4, IL8</i>
	Legionellosis	0.036	0.003	<i>IL1B, IL8</i>
	Cytosolic DNA-sensing pathway	0.032	0.004	<i>IL1B, CCL4</i>
	Human cytomegalovirus infection	0.013	0.004	<i>IL1B, CCL4, IL8</i>
	Acute myeloid leukemia	0.030	0.004	<i>PIM1, KIT</i>
	Ras signaling pathway	0.013	0.004	<i>IGF2, FGF17, KIT</i>

Leishmaniasis	0.027	0.005	<i>NCF2, IL1B</i>
Pertussis	0.026	0.005	<i>IL1B, IL8</i>
Rheumatoid arthritis	0.022	0.007	<i>IL1B, IL8</i>
IL-17 signaling pathway	0.022	0.008	<i>IL1B, IL8</i>
TGF-beta signaling pathway	0.021	0.008	<i>BMP5, GREM1</i>
Amoebiasis	0.021	0.008	<i>IL1B, IL8</i>
MicroRNAs in cancer	0.010	0.008	<i>DDIT4, HMOX1, PIM1</i>
Chagas disease (American trypanosomiasis)	0.019	0.009	<i>IL1B, IL8</i>
Insulin resistance	0.019	0.010	<i>NOS3, CD36</i>
HIF-1 signaling pathway	0.018	0.010	<i>NOS3, HMOX1</i>
Neuroactive ligand-receptor interaction	0.009	0.012	<i>APEL, NPFF2, MC5R</i>
Yersinia infection	0.017	0.013	<i>IL1B, IL8</i>
Metabolic pathways	0.004	0.014	<i>NOS3, AMPD3, HYAL2, HMOX1, GADL1, HPSE2</i>
Osteoclast differentiation	0.016	0.014	<i>NCF2, IL1B</i>
Apelin signaling pathway	0.015	0.016	<i>NOS3, APEL</i>
Taurine and hypotaurine metabolism	0.091	0.016	<i>GADL1</i>
Breast cancer	0.014	0.018	<i>FGF17, KIT</i>
Phospholipase D signaling pathway	0.014	0.018	<i>IL8, KIT</i>
Non-alcoholic fatty liver disease (NAFLD)	0.013	0.018	<i>IL1B, IL8</i>
Influenza A	0.012	0.023	<i>IL1B, IL8</i>
Hepatocellular carcinoma	0.012	0.023	<i>IGF2, HMOX1</i>
NOD-like receptor signaling pathway	0.011	0.026	<i>IL1B, IL8</i>
Pantothenate and CoA biosynthesis	0.053	0.027	<i>GADL1</i>
Arginine biosynthesis	0.048	0.030	<i>NOS3</i>
Proteoglycans in cancer	0.010	0.032	<i>IGF2, HPSE2</i>
Rap1 signaling pathway	0.010	0.035	<i>FGF17, KIT</i>

No.AF vs Low.AF	Antifolate resistance	0.032	0.043	<i>IL1B</i>
	beta-Alanine metabolism	0.030	0.046	<i>GADL1</i>
	Prion diseases	0.029	0.048	<i>IL1B</i>
	Metabolic pathways	0.010	0.000	<i>ECHA, GPX2, DGAT2, KBL, ADCY3, KMO, LIPH, HAOX2, QCR10, HAOX1, GYS2, QCR7, HGD, ALDOB, DGKG</i>
	Cholesterol metabolism	0.080	0.000	<i>LIPH, PCSK9, APOB, APOA2</i>
	Complement and coagulation cascades	0.051	0.000	<i>MBL, KNG1, MASP1, AIAT</i>
	Peroxisome	0.048	0.000	<i>HAOX1, HAOX2, PEX5, ALS</i>
	Fat digestion and absorption	0.073	0.000	<i>FABPL, DGAT2, APOB</i>
	Carbon metabolism	0.034	0.000	<i>HAOX1, ECHA, ALDOB, HAOX2</i>
	Glycerolipid metabolism	0.049	0.001	<i>LIPH, DGAT2, DGKG</i>
	Longevity regulating pathway - multiple species	0.048	0.001	<i>FOXA2, ALS, ADCY3</i>
	Bile secretion	0.042	0.001	<i>NR0B2, OSTA, ADCY3</i>
	Huntington disease	0.021	0.002	<i>CYC, QCR10, QCR7, ALS</i>
	Vitamin digestion and absorption	0.083	0.002	<i>APOB, IF</i>
	Viral protein interaction with cytokine and cytokine receptor	0.030	0.003	<i>CCL19, CSF1R, CCL4</i>
	Glyoxylate and dicarboxylate metabolism	0.067	0.003	<i>HAOX1, HAOX2</i>
	Tryptophan metabolism	0.048	0.006	<i>KMO, ECHA</i>
	Parkinson disease	0.021	0.007	<i>CYC, QCR10, QCR7</i>
	Non-alcoholic fatty liver disease (NAFLD)	0.020	0.008	<i>CYC, QCR10, QCR7</i>
	Amyotrophic lateral sclerosis (ALS)	0.039	0.009	<i>CYC, ALS</i>
	cGMP-PKG signaling pathway	0.018	0.011	<i>KNG1, GARI, ADCY3</i>
	Alzheimer disease	0.018	0.012	<i>CYC, QCR10, QCR7</i>
	Pathways in cancer	0.009	0.016	<i>CYC, CSF1R, KNG1, MMP2, ADCY3</i>

No.AF vs High.AF	Staphylococcus aureus infection	0.029	0.016	<i>MBL, MASP1</i>
	Chemokine signaling pathway	0.016	0.016	<i>CCL19, CCL4, ADCY3</i>
	p53 signaling pathway	0.028	0.017	<i>CYC, SESN2</i>
	Thyroid hormone synthesis	0.027	0.018	<i>GPX2, ADCY3</i>
	PPAR signaling pathway	0.026	0.019	<i>FABPL, APOA2</i>
	Cardiac muscle contraction	0.023	0.024	<i>QCR10, QCR7</i>
	Human cytomegalovirus infection	0.013	0.025	<i>CYC, CCL4, ADCY3</i>
	Longevity regulating pathway	0.022	0.026	<i>SESN2, ADCY3</i>
	Thermogenesis	0.013	0.026	<i>QCR10, QCR7, ADCY3</i>
	GnRH signaling pathway	0.022	0.028	<i>MMP2, ADCY3</i>
	TGF-beta signaling pathway	0.021	0.028	<i>THSD4, LTBP1</i>
	Endocrine resistance	0.020	0.031	<i>MMP2, ADCY3</i>
	Inflammatory mediator regulation of TRP channels	0.020	0.032	<i>KNG1, ADCY3</i>
	NF-kappa B signaling pathway	0.020	0.032	<i>CCL19, CCL4</i>
	Leukocyte transendothelial migration	0.018	0.039	<i>MMP2, JAM1</i>
	Cytokine-cytokine receptor interaction	0.010	0.048	<i>CCL19, CSF1R, CCL4</i>
	Cholesterol metabolism	0.140	0.000	<i>LIPC, APOB, ABCG5, ABCG8, LIPH, CD36, APOA2</i>
	Metabolic pathways	0.019	0.000	<i>GAMT, AMPD3, HAOX2, P4HA3, GADL1, RGN, CERS4, KYNU, KBL, DHRS9, DGAT2, KMO, SERA, TCB, LIPC, GPAT4, AADAT, LIPH, ADA2, GYS2, PLB1, ALDOB, ADCY2, G6PC, ACSL5, RDH11, EKI2</i>
	Fat digestion and absorption	0.146	0.000	<i>APOB, ABCG5, ABCG8, MTP, DGAT2, CD36</i>
	Complement and coagulation cascades	0.089	0.000	<i>MBL, F13A, KNG1, EPCR, TFP11, A1AT, VWF</i>
	Hematopoietic cell lineage	0.072	0.000	<i>TFR1, CD34, CD36, KIT, CD2, IL1B, CD9</i>
	Bile secretion	0.083	0.000	<i>ABCG5, ADCY2, ABCG8, NR0B2, OSTA, NR1H4</i>

PI3K-Akt signaling pathway	0.031	0.000	<i>FOXO3, DDIT4, SGK2, COMP, G6PC, KIT, TLR2, GYS2, VWF, LPAR1, FGFR2</i>
Malaria	0.102	0.000	<i>TLR2, COMP, IL1B, CD36, IL8</i>
Pathways in cancer	0.021	0.000	<i>KNG1, ADCY2, PIMI, WNT2, RXRG, MMP2, KIT, RARB, LPAR1, FGFR2, IL8</i>
Glycerolipid metabolism	0.066	0.001	<i>LIPH, LIPC, GPAT4, DGAT2</i>
Longevity regulating pathway - multiple species	0.065	0.001	<i>FOXO3, FOXA2, ALS, ADCY2</i>
Carbon metabolism	0.043	0.001	<i>HAOX2, TCB, RGN, ALDOB, SERA</i>
Adipocytokine signaling pathway	0.058	0.001	<i>RXRG, G6PC, CD36, ACSL5</i>
PPAR signaling pathway	0.053	0.001	<i>RXRG, APOA2, CD36, ACSL5</i>
Salmonella infection	0.048	0.002	<i>IL1B, RHOG, CCL4, IL8</i>
Cytokine-cytokine receptor interaction	0.024	0.002	<i>CCL4, IL16, INHBC, CCR7, GDF15, IL1B, IL8</i>
Glycine, serine and threonine metabolism	0.075	0.002	<i>GAMT, KBL, SERA</i>
Phagosome	0.033	0.002	<i>TLR2, COMP, MBL, CD36, TFR1</i>
Tryptophan metabolism	0.071	0.002	<i>KMO, KYNU, AADAT</i>
ABC transporters	0.067	0.003	<i>ABCG8, ABCG5, ABCC9</i>
AGE-RAGE signaling pathway in diabetic complications	0.040	0.003	<i>IL1B, MMP2, IL8, PIMI</i>
NF-kappa B signaling pathway	0.040	0.003	<i>IL1B, CCL4, IL8, ZAP70</i>
Chagas disease (American trypanosomiasis)	0.039	0.003	<i>TLR2, IL1B, KNG1, IL8</i>
Toll-like receptor signaling pathway	0.038	0.003	<i>TLR2, IL1B, CCL4, IL8</i>
Glucagon signaling pathway	0.038	0.004	<i>TCB, GYS2, G6PC, ADCY2</i>
Th17 cell differentiation	0.037	0.004	<i>RORG, IL1B, RXRG, ZAP70</i>
Legionellosis	0.055	0.004	<i>TLR2, IL1B, IL8</i>
Chemokine signaling pathway	0.026	0.005	<i>FOXO3, ADCY2, CCL4, IL8, CCR7</i>

AMPK signaling pathway	0.033	0.005	<i>FOXO3, GYS2, G6PC, CD36</i>
Pantothenate and CoA biosynthesis	0.105	0.006	<i>GADL1, VNN1</i>
Proteoglycans in cancer	0.025	0.007	<i>TLR2, WNT2, IHH, MMP2, ANK1</i>
Inflammatory bowel disease (IBD)	0.046	0.007	<i>TLR2, RORG, IL1B</i>
Non-small cell lung cancer	0.045	0.007	<i>FOXO3, RARB, RXRG</i>
Purine metabolism	0.031	0.007	<i>AMPD3, ADA2, TCB, ADCY2</i>
Glycolysis / Gluconeogenesis	0.044	0.008	<i>TCB, ALDOB, G6PC</i>
Central carbon metabolism in cancer	0.043	0.008	<i>TCB, FGFR2, KIT</i>
Vitamin digestion and absorption	0.083	0.009	<i>APOB, PLB1</i>
Biosynthesis of amino acids	0.040	0.010	<i>ALDOB, TCB, SERA</i>
Phospholipase D signaling pathway	0.027	0.011	<i>LPAR1, ADCY2, IL8, KIT</i>
Gastric cancer	0.027	0.011	<i>RARB, WNT2, RXRG, FGFR2</i>
EGFR tyrosine kinase inhibitor resistance	0.038	0.011	<i>FOXO3, NRG2, FGFR2</i>
Peroxisome	0.036	0.013	<i>HAOX2, ALS, ACSL5</i>
Pentose phosphate pathway	0.067	0.014	<i>ALDOB, RGN</i>
ECM-receptor interaction	0.035	0.014	<i>COMP, VWF, CD36</i>
Antifolate resistance	0.065	0.015	<i>IL1B, FOLR1</i>
Circadian rhythm	0.065	0.015	<i>RORG, RORB</i>
Longevity regulating pathway	0.034	0.015	<i>FOXO3, SESN2, ADCY2</i>
Rheumatoid arthritis	0.033	0.016	<i>TLR2, IL1B, IL8</i>
TGF-beta signaling pathway	0.032	0.018	<i>THSD4, INHBC, FBN1</i>
Amoebiasis	0.032	0.018	<i>TLR2, IL1B, IL8</i>
Prion diseases	0.057	0.018	<i>IL1B, ALS</i>
Glycerophospholipid metabolism	0.031	0.019	<i>EKI2, GPAT4, PLB1</i>
Starch and sucrose metabolism	0.056	0.019	<i>GYS2, G6PC</i>
Primary immunodeficiency	0.054	0.020	<i>C2TA, ZAP70</i>

Low.L vs High.L	African trypanosomiasis	0.054	0.020	<i>IL1B, KNG1</i>
	Inflammatory mediator regulation of TRP channels	0.030	0.021	<i>IL1B, KNG1, ADCY2</i>
	Viral protein interaction with cytokine and cytokine receptor	0.030	0.021	<i>CCL4, IL8, CCR7</i>
	Melanogenesis	0.030	0.021	<i>WNT2, ADCY2, KIT</i>
	Ferroptosis	0.050	0.023	<i>TFR1, ACSL5</i>
	Bladder cancer	0.049	0.024	<i>MMP2, IL8</i>
	Insulin resistance	0.028	0.025	<i>GYS2, G6PC, CD36</i>
	Ether lipid metabolism	0.043	0.031	<i>ENPP6, PLB1</i>
	Yersinia infection	0.025	0.033	<i>IL1B, ZAP70, IL8</i>
	Rap1 signaling pathway	0.019	0.033	<i>LPAR1, FGFR2, ADCY2, KIT</i>
	Arginine and proline metabolism	0.040	0.035	<i>P4HA3, GAMT</i>
	Relaxin signaling pathway	0.023	0.040	<i>RXFP1, MMP2, ADCY2</i>
	Human cytomegalovirus infection	0.018	0.041	<i>IL1B, CCL4, IL8, ADCY2</i>
	FoxO signaling pathway	0.023	0.041	<i>FOXO3, G6PC, SGK2</i>
	Human papillomavirus infection	0.015	0.042	<i>WNT2, VWF, TCB, MFNG, COMP</i>
	Insulin signaling pathway	0.022	0.045	<i>G6PC, GYS2, SH2B2</i>
	Estrogen signaling pathway	0.022	0.046	<i>MMP2, KCNJ6, ADCY2</i>
	Signaling pathways regulating pluripotency of stem cells	0.021	0.047	<i>WNT2, INHBC, FGFR2</i>
	Glycerolipid metabolism	0.049	0.000	<i>DGAT1, LPIN2, LPIN1</i>
	Signaling pathways regulating pluripotency of stem cells	0.021	0.000	<i>TBX3, FZD5, WNT9A</i>
	mTOR signaling pathway	0.020	0.000	<i>FZD5, WNT9A, LPIN1</i>
	Proteoglycans in cancer	0.015	0.001	<i>TLR2, FZD5, WNT9A</i>

Basal cell carcinoma	0.032	0.002	<i>FZD5, WNT9A</i>
Metabolic pathways	0.004	0.002	<i>AOC3, LPIN2, LPIN1, DGAT1, ACSF3, G6PC2</i>
Glycerophospholipid metabolism	0.021	0.004	<i>LPIN2, LPIN1</i>
Melanogenesis	0.020	0.005	<i>FZD5, WNT9A</i>
PI3K-Akt signaling pathway	0.008	0.005	<i>TLR2, FOXO3, G6PC2</i>
AMPK signaling pathway	0.017	0.006	<i>FOXO3, G6PC2</i>
FoxO signaling pathway	0.015	0.007	<i>FOXO3, G6PC2</i>
Breast cancer	0.014	0.009	<i>FZD5, WNT9A</i>
Gastric cancer	0.013	0.009	<i>FZD5, WNT9A</i>
Hippo signaling pathway	0.013	0.010	<i>FZD5, WNT9A</i>
Cushing syndrome	0.013	0.010	<i>FZD5, WNT9A</i>
Wnt signaling pathway	0.013	0.011	<i>FZD5, WNT9A</i>
Hepatocellular carcinoma	0.012	0.012	<i>FZD5, WNT9A</i>
Pathways in cancer	0.006	0.015	<i>FZD5, WNT9A, CXCR4</i>
Chemokine signaling pathway	0.011	0.015	<i>FOXO3, CXCR4</i>
Phenylalanine metabolism	0.059	0.017	<i>AOC3</i>
Fatty acid biosynthesis	0.056	0.018	<i>ACSF3</i>
Human immunodeficiency virus 1 infection	0.009	0.018	<i>TLR2, CXCR4</i>
Vitamin digestion and absorption	0.042	0.024	<i>RBP2</i>
Maturity onset diabetes of the young	0.038	0.026	<i>NR5A2</i>
Galactose metabolism	0.032	0.031	<i>G6PC2</i>
beta-Alanine metabolism	0.030	0.032	<i>AOC3</i>
Tyrosine metabolism	0.028	0.035	<i>AOC3</i>
Starch and sucrose metabolism	0.028	0.035	<i>G6PC2</i>
Glycine, serine and threonine metabolism	0.025	0.039	<i>AOC3</i>
Fat digestion and absorption	0.024	0.040	<i>DGAT1</i>

No.L vs Low.L	Human papillomavirus infection	0.006	0.041	<i>FZD5, WNT9A</i>
	Carbohydrate digestion and absorption	0.023	0.043	<i>G6PC2</i>
	ABC transporters	0.022	0.044	<i>ABCA4</i>
	Valine, leucine and isoleucine degradation	0.021	0.046	<i>ACSF3</i>
	Intestinal immune network for IgA production	0.020	0.047	<i>CXCR4</i>
	Malaria	0.020	0.047	<i>TLR2</i>
	Tuberculosis	0.017	0.000	<i>MOT2, CRI, SPHK1</i>
	Circadian rhythm	0.065	0.000	<i>PER3, NPAS2</i>
	VEGF signaling pathway	0.034	0.000	<i>SPHK1, NOS3</i>
	Circadian entrainment	0.021	0.001	<i>PER3, RASD1</i>
	Insulin resistance	0.019	0.001	<i>PTPRF, NOS3</i>
	Sphingolipid signaling pathway	0.017	0.001	<i>SPHK1, NOS3</i>
	Apelin signaling pathway	0.015	0.001	<i>SPHK1, NOS3</i>
	Calcium signaling pathway	0.010	0.002	<i>SPHK1, NOS3</i>
	Synthesis and degradation of ketone bodies	0.100	0.004	<i>BDH</i>
	Arginine biosynthesis	0.048	0.008	<i>NOS3</i>
	Butanoate metabolism	0.036	0.011	<i>BDH</i>
	Metabolic pathways	0.002	0.016	<i>SPHK1, NOS3, BDH</i>
	Sphingolipid metabolism	0.021	0.018	<i>SPHK1</i>
	Malaria	0.020	0.019	<i>CRI</i>
	Arginine and proline metabolism	0.020	0.019	<i>NOS3</i>
	Mineral absorption	0.019	0.020	<i>COPT1</i>
	Legionellosis	0.018	0.021	<i>CRI</i>
	Renal cell carcinoma	0.014	0.026	<i>PRCC</i>
	Adherens junction	0.014	0.028	<i>PTPRF</i>
	Platinum drug resistance	0.014	0.028	<i>COPT1</i>

No.L vs High.L	Leishmaniasis	0.014	0.028	<i>CRI</i>
	RNA degradation	0.013	0.030	<i>MOT2</i>
	Complement and coagulation cascades	0.013	0.030	<i>CRI</i>
	Fc gamma R-mediated phagocytosis	0.011	0.036	<i>SPHK1</i>
	Hematopoietic cell lineage	0.010	0.037	<i>CRI</i>
	AGE-RAGE signaling pathway in diabetic complications	0.010	0.038	<i>NOS3</i>
	HIF-1 signaling pathway	0.009	0.041	<i>NOS3</i>
	Platelet activation	0.008	0.047	<i>NOS3</i>
	Relaxin signaling pathway	0.008	0.049	<i>NOS3</i>
				<i>AOC3, AOC2, HCD2, SPHK1, G6PC2, LPIN2, CGT, LPIN1, HKDC1, XDH, FAHD1, TKT, P5CS, NRK2, SUOX, RIFK, GALT, BDH, SCD5, ALG12, EKII, ACOT1, ACYP1, GCSP, HEXD, TKFC, AZIN2, OPLA, CANT1, PDE4B, CHAC1, AGT2</i>
	Metabolic pathways	0.022	0.000	
	TGF-beta signaling pathway	0.074	0.000	<i>BMP6, INHBC, THSD4, INHBA, CHRD, FST, MIS</i>
	Glycine, serine and threonine metabolism	0.100	0.000	<i>AOC3, AOC2, AGT2, GCSP</i>
	Cholesterol metabolism	0.080	0.000	<i>LRP2, APOA4, PLTP, LCAT</i>
	Glycerophospholipid metabolism	0.052	0.000	<i>PLPP5, LCAT, LPIN2, EKII, LPIN1</i>
	Cytokine-cytokine receptor interaction	0.027	0.000	<i>BMP6, EDA, IL2RG, FAS, INHBA, INHBC, CXCR4, MIS</i>
	Glycerolipid metabolism	0.066	0.000	<i>PLPP5, LPIN2, TKFC, LPIN1</i>
	Maturity onset diabetes of the young	0.115	0.001	<i>HNF4G, FOXA2, NR5A2</i>
	Inflammatory bowel disease (IBD)	0.062	0.001	<i>TLR2, RORG, TLR5, IL2RG</i>
	Galactose metabolism	0.097	0.001	<i>GALT, HKDC1, G6PC2</i>
	Calcium signaling pathway	0.031	0.001	<i>TPC1, ERBB2, SPHK1, CXCR4, P2RX2, P2RX5</i>
	Pathways in cancer	0.019	0.001	<i>ERBB2, STAT2, IL2RG, FAS, TRXR1, GLII, WNT9A, CXCR4, PML, FGF22</i>

PPAR signaling pathway	0.053	0.001	<i>SCD5, FABPI, PLTP, PLIN1</i>
Proteoglycans in cancer	0.030	0.001	<i>ERBB2, FAS, SDC4, TLR2, IHH, WNT9A</i>
Tyrosine metabolism	0.083	0.001	<i>FAHD1, AOC3, AOC2</i>
Signaling pathways regulating pluripotency of stem cells	0.036	0.001	<i>TBX3, KLF4, INHBC, WNT9A, INHBA</i>
Hedgehog signaling pathway	0.064	0.003	<i>LRP2, IHH, GLI1</i>
Legionellosis	0.055	0.004	<i>TLR2, CR1, TLR5</i>
Carbon metabolism	0.034	0.005	<i>HKDC1, TKT, TKFC, GCSP</i>
Phenylalanine metabolism	0.118	0.005	<i>AOC3, AOC2</i>
AMPK signaling pathway	0.033	0.005	<i>STK11, SCD5, ULK1, G6PC2</i>
Human immunodeficiency virus 1 infection	0.024	0.008	<i>TLR2, PAK5, FAS, CCNB3, CXCR4</i>
Measles	0.029	0.009	<i>TLR2, FAS, STAT2, IL2RG</i>
Platinum drug resistance	0.041	0.009	<i>ERBB2, FAS, COPT1</i>
Biosynthesis of unsaturated fatty acids	0.074	0.011	<i>SCD5, ACOT1</i>
mTOR signaling pathway	0.026	0.012	<i>STK11, ULK1, WNT9A, LPIN1</i>
Neuroactive ligand-receptor interaction	0.018	0.013	<i>NPY4R, H3, VIPR2, P2RX2, P2RX5, APEL</i>
Endocytosis	0.020	0.013	<i>PML, TRFR, IL2RG, GBF1, CXCR4</i>
Circadian rhythm	0.065	0.015	<i>RORG, NPAS2</i>
PI3K-Akt signaling pathway	0.017	0.016	<i>ERBB2, IL2RG, STK11, G6PC2, TLR2, FGF22</i>
Fructose and mannose metabolism	0.061	0.016	<i>HKDC1, TKFC</i>
Base excision repair	0.061	0.016	<i>NEIL1, OGG1</i>
beta-Alanine metabolism	0.061	0.016	<i>AOC3, AOC2</i>
Starch and sucrose metabolism	0.056	0.019	<i>HKDC1, G6PC2</i>
Progesterone-mediated oocyte maturation	0.030	0.020	<i>CCNB3, CPEB3, KIF22</i>
Tuberculosis	0.022	0.020	<i>TLR2, MRC1, SPHK1, CR1</i>
Axon guidance	0.022	0.021	<i>PAK5, SLIT1, FPS, CXCR4</i>

Low.O vs High.O	Transcriptional misregulation in cancer	0.022	0.022	<i>PML, PRCC, KLF3, LIPO</i>
	Th17 cell differentiation	0.028	0.024	<i>RORG, IRF4, IL2RG</i>
	Fat digestion and absorption	0.049	0.024	<i>APOA4, FABPI</i>
	HIF-1 signaling pathway	0.028	0.025	<i>HKDC1, ERBB2, TRFR</i>
	Carbohydrate digestion and absorption	0.045	0.027	<i>HKDC1, G6PC2</i>
	Epstein-Barr virus infection	0.020	0.029	<i>TLR2, FAS, STAT2, SUH</i>
	Sphingolipid metabolism	0.043	0.031	<i>SPHK1, CGT</i>
	Notch signaling pathway	0.042	0.032	<i>LFNG, SUH</i>
	Amino sugar and nucleotide sugar metabolism	0.042	0.032	<i>GALT, HKDC1</i>
	Valine, leucine and isoleucine degradation	0.042	0.032	<i>HCD2, AGT2</i>
	Caffeine metabolism	0.200	0.033	<i>XDH</i>
	Neomycin, kanamycin and gentamicin biosynthesis	0.200	0.033	<i>HKDC1</i>
	Malaria	0.041	0.033	<i>TLR2, CR1</i>
	Arginine and proline metabolism	0.040	0.034	<i>P5CS, AZIN2</i>
	cAMP signaling pathway	0.019	0.035	<i>PDE4B, GLII, VIPR2, MIS</i>
	Purine metabolism	0.023	0.039	<i>PDE4B, CANT1, XDH</i>
	FoxO signaling pathway	0.023	0.041	<i>CCNB3, STK11, G6PC2</i>
	Human papillomavirus infection	0.015	0.041	<i>FAS, LFNG, STAT2, WNT9A, SUH</i>
	Glutathione metabolism	0.036	0.042	<i>CHAC1, OPLA</i>
	Insulin signaling pathway	0.022	0.044	<i>HKDC1, SH2B2, G6PC2</i>
	Apelin signaling pathway	0.022	0.044	<i>SPHK1, APEL, PLIN1</i>
	Riboflavin metabolism	0.125	0.049	<i>RIFK</i>
	Regulation of actin cytoskeleton	0.019	0.000	<i>DIAP3, PAK6, FGF17, FGF16</i>
	Melanoma	0.042	0.000	<i>FGF17, FGF16, E2F1</i>
	Breast cancer	0.020	0.000	<i>FGF17, FGF16, E2F1</i>

No.O vs High.O	Gastric cancer	0.020	0.000	<i>FGF17, FGF16, E2F1</i>
	Ras signaling pathway	0.013	0.000	<i>PAK6, FGF17, FGF16</i>
	Pathways in cancer	0.006	0.004	<i>FGF17, FGF16, E2F1</i>
	Rap1 signaling pathway	0.010	0.007	<i>FGF17, FGF16</i>
	MAPK signaling pathway	0.007	0.013	<i>FGF17, FGF16</i>
	PI3K-Akt signaling pathway	0.006	0.018	<i>FGF17, FGF16</i>
	Circadian rhythm	0.032	0.019	<i>RORB</i>
	Bladder cancer	0.024	0.024	<i>E2F1</i>
	ABC transporters	0.022	0.027	<i>ABCC9</i>
	Ovarian steroidogenesis	0.020	0.029	<i>BMP15</i>
	Mitophagy - animal	0.015	0.038	<i>E2F1</i>
	Non-small cell lung cancer	0.015	0.039	<i>E2F1</i>
	Renal cell carcinoma	0.014	0.040	<i>PAK6</i>
	Adherens junction	0.014	0.042	<i>SNAI2</i>
	Pancreatic cancer	0.013	0.044	<i>E2F1</i>
	Glioma	0.013	0.044	<i>E2F1</i>
	Chronic myeloid leukemia	0.013	0.044	<i>E2F1</i>
	ErbB signaling pathway	0.012	0.049	<i>PAK6</i>
	Cardiac muscle contraction	0.012	0.050	<i>QCR7</i>
	ECM-receptor interaction	0.012	0.050	<i>SV2C</i>
	Rap1 signaling pathway	0.024	0.000	<i>EFNA3, RHOA, ADCY8, FGF17, FGF16</i>
	cAMP signaling pathway	0.023	0.000	<i>PTC1, RHOA, GRIA1, ADCY8, GARI</i>
	Regulation of actin cytoskeleton	0.023	0.000	<i>DIAP3, FGF17, PAK6, RHOA, FGF16</i>
	Ras signaling pathway	0.022	0.000	<i>RHOA, EFNA3, PAK6, FGF17, FGF16</i>
	Pathways in cancer	0.011	0.000	<i>E2F1, ADCY8, PTC1, RHOA, FGF17, FGF16</i>
	Axon guidance	0.022	0.000	<i>PTC1, PAK6, EFNA3, RHOA</i>

Melanoma	0.042	0.000	<i>FGF17, FGF16, E2F1</i>
Human cytomegalovirus infection	0.018	0.000	<i>CCL2, RHOA, ADCY8, E2F1</i>
Breast cancer	0.020	0.002	<i>FGF17, FGF16, E2F1</i>
Gastric cancer	0.020	0.002	<i>FGF17, FGF16, E2F1</i>
cGMP-PKG signaling pathway	0.018	0.002	<i>RHOA, ADCY8, GARI</i>
Ovarian steroidogenesis	0.041	0.003	<i>ADCY8, BMP15</i>
Chemokine signaling pathway	0.016	0.004	<i>CCL2, RHOA, ADCY8</i>
Human T-cell leukemia virus 1 infection	0.014	0.005	<i>CDS1, ADCY8, E2F1</i>
Long-term potentiation	0.030	0.005	<i>GRI1, ADCY8</i>
p53 signaling pathway	0.028	0.006	<i>CDS1, SESN2</i>
ECM-receptor interaction	0.023	0.009	<i>AGRIN, SV2C</i>
Longevity regulating pathway	0.022	0.009	<i>ADCY8, SESN2</i>
Circadian entrainment	0.021	0.011	<i>GRI1, ADCY8</i>
Pancreatic secretion	0.020	0.011	<i>RHOA, ADCY8</i>
Endocrine resistance	0.020	0.011	<i>ADCY8, E2F1</i>
MAPK signaling pathway	0.010	0.012	<i>EFNA3, FGF17, FGF16</i>
T cell receptor signaling pathway	0.019	0.012	<i>PAK6, RHOA</i>
MicroRNAs in cancer	0.010	0.012	<i>RHOA, EFNA3, E2F1</i>
Parathyroid hormone synthesis, secretion and action	0.019	0.013	<i>RHOA, ADCY8</i>
Glutamatergic synapse	0.018	0.015	<i>GRI1, ADCY8</i>
Yersinia infection	0.017	0.016	<i>CCL2, RHOA</i>
Cell cycle	0.016	0.017	<i>CDS1, E2F1</i>
Platelet activation	0.016	0.017	<i>RHOA, ADCY8</i>
PI3K-Akt signaling pathway	0.008	0.019	<i>EFNA3, FGF17, FGF16</i>
Vascular smooth muscle contraction	0.015	0.019	<i>RHOA, ADCY8</i>

Fluid shear stress and atherosclerosis	0.014	0.021	<i>CCL2, RHOA</i>
Phospholipase D signaling pathway	0.014	0.024	<i>RHOA, ADCY8</i>
Retrograde endocannabinoid signaling	0.014	0.024	<i>GRI1, ADCY8</i>
mTOR signaling pathway	0.013	0.025	<i>RHOA, SESN2</i>
Oxytocin signaling pathway	0.013	0.025	<i>RHOA, ADCY8</i>
Cushing syndrome	0.013	0.026	<i>ADCY8, E2F1</i>
Cellular senescence	0.013	0.027	<i>CDS1, E2F1</i>
Jak-STAT signaling pathway	0.012	0.028	<i>GFAP, CISH</i>
NOD-like receptor signaling pathway	0.011	0.033	<i>CCL2, RHOA</i>
Calcium signaling pathway	0.010	0.038	<i>ADCY8, P2RX5</i>
Vitamin digestion and absorption	0.042	0.039	<i>APOA4</i>
Focal adhesion	0.010	0.040	<i>PAK6, RHOA</i>
Epstein-Barr virus infection	0.010	0.041	<i>CR2, E2F1</i>
Proteoglycans in cancer	0.010	0.042	<i>PTC1, RHOA</i>
Phototransduction	0.036	0.045	<i>GAR1</i>

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