

A

Sum threshold

quantile	0	1	2	3	4	5	6
0.01	0.521784	3.41E-09	0.257172	1	1	1	1
0.05	0.521784	1.12E-09	7.47E-05	0.087696	1	1	1
0.1	0.521784	5.46E-06	6.72E-10	1.28E-05	0.042956	0.038893	1
0.15	0.521784	0.001791	1.06E-09	5.79E-08	0.015509	0.13533	1
0.2	0.521784	0.003871	1.11E-10	5.77E-09	0.00053	0.283653	1
0.25	0.521784	0.012143	5.80E-10	1.56E-10	0.009083	0.125431	1
0.3	0.521784	0.02944	6.04E-07	1.09E-08	0.005948	0.29093	0.216887

B

Sum threshold

quantile	0	1	2	3	4	5	6
0.01	168	37	1	0	0	0	0
0.05	168	96	15	2	0	0	0
0.1	168	113	39	11	2	1	0
0.15	168	114	52	20	4	1	0
0.2	168	125	66	27	8	1	0
0.25	168	128	75	35	8	2	0
0.3	168	130	75	36	10	2	1

C

gene_symbol	hypertension	COPD	diabetes	smoke	cancer	sex	age	sum
cav1	-1	-1	-1	-1	-1	0	0	-5
rtn4	-1	-1	-1	0	-1	0	0	-4
b4gat1	0	0	0	-1	-1	-1	-1	-4
wwp2	0	-1	-1	-1	-1	0	0	-4
ube2i	0	-1	-1	-1	-1	0	0	-4
jun	-1	1	-1	-1	-1	-1	0	-4
stom	-1	-1	1	-1	-1	0	0	-3
tgfb2	0	0	-1	-1	-1	0	0	-3
erbb2	1	-1	0	-1	-1	0	-1	-3
fos	-1	0	1	-1	-1	0	-1	-3
raly	0	0	-1	-1	0	-1	0	-3
acat1	0	-1	-1	0	0	-1	0	-3
hsf1	-1	0	0	-1	0	-1	0	-3
ctnna1	0	-1	0	-1	-1	0	0	-3
brd2	-1	1	-1	-1	-1	-1	1	-3
nfe2l2	-1	-1	1	0	-1	0	0	-2
myc	-1	1	0	0	0	-1	-1	-2
aar2	-1	0	0	-1	0	-1	1	-2
akap8l	0	-1	-1	0	0	-1	1	-2
nubp2	0	0	-1	-1	0	0	0	-2
stx4	-1	-1	0	0	0	0	0	-2
junb	-1	1	0	0	-1	-1	0	-2
snx17	0	-1	1	-1	-1	0	0	-2
jak2	-1	1	0	-1	-1	0	0	-2
ctnna2	0	0	-1	0	-1	1	-1	-2
epha2	-1	1	-1	0	0	-1	0	-2
srf	-1	1	0	-1	-1	0	0	-2
dnajb2	0	-1	0	-1	0	0	0	-2
clu	1	-1	-1	-1	-1	0	1	-2
plat	-1	0	0	-1	0	-1	1	-2
ints1	0	0	1	0	1	0	0	2
sympk	0	0	0	0	0	1	1	2
ep300	0	0	1	-1	0	1	1	2
il6st	0	1	1	1	-1	0	0	2
rab1a	0	1	0	-1	1	0	1	2
cul2	0	1	0	0	0	0	1	2
atm	1	1	0	1	-1	0	0	2
atr	1	0	0	0	1	0	0	2
g3bp1	0	0	-1	1	1	0	1	2
cd70	0	1	0	0	1	0	0	2
os9	0	0	0	-1	1	1	1	2
ints2	1	1	0	0	0	0	0	2
irak1	0	0	0	0	1	1	0	2
cs	0	0	1	0	1	0	0	2
lox	-1	0	1	0	0	1	1	2
ptprj	-1	1	1	0	0	1	0	2
prpf40a	0	0	0	1	1	-1	1	2
oat	1	0	-1	0	1	1	0	2
mpzl1	0	1	-1	1	1	0	0	2
fgb	-1	0	1	1	1	1	-1	2
rad18	1	0	0	0	0	0	1	2
smad3	0	-1	1	-1	1	1	1	2
foxm1	1	0	0	0	1	0	0	2
larp1	0	0	1	-1	1	0	1	2
brca1	1	0	0	1	1	0	0	3
sox2	1	-1	1	1	1	0	0	3
serpine2	1	0	0	0	1	0	1	3
zc3h18	0	1	0	0	0	1	1	3
plau	0	0	0	1	1	1	0	3
ctsb	1	1	0	1	-1	1	0	3
itch	0	1	0	1	0	0	1	3
csnk2b	1	1	0	0	1	0	0	3
pfkp	0	1	0	0	1	1	0	3
pdia3	0	1	-1	0	1	1	1	3
nup93	0	1	0	0	1	1	1	4
neu1	-1	1	1	1	1	0	1	4

D

	raw P value	▲ FDR
GO biological process complete		
regulation of protein metabolic process	1.24E-13	1.97E-09
regulation of cellular protein metabolic process	9.37E-13	4.97E-09
response to stress	1.31E-12	5.22E-09
symbiotic process	2.09E-12	5.55E-09
positive regulation of protein metabolic process	7.24E-13	5.75E-09
positive regulation of cellular process	1.84E-12	5.84E-09
response to organic substance	2.69E-11	3.29E-08
regulation of cell population proliferation	1.72E-11	3.42E-08
primary metabolic process	1.98E-11	3.49E-08
regulation of cell communication	2.68E-11	3.56E-08
response to hypoxia	1.60E-11	3.62E-08
viral process	2.63E-11	3.80E-08
response to decreased oxygen levels	2.56E-11	4.06E-08
regulation of signaling	3.71E-11	4.21E-08
response to oxygen levels	6.02E-11	6.38E-08
positive regulation of cellular protein metabolic process	6.79E-11	6.74E-08
positive regulation of biological process	9.46E-11	8.36E-08
regulation of signal transduction	9.32E-11	8.71E-08
positive regulation of cellular metabolic process	1.26E-10	1.06E-07
positive regulation of nitrogen compound metabolic process	1.37E-10	1.09E-07
organic substance metabolic process	1.46E-10	1.11E-07
response to abiotic stimulus	2.07E-10	1.50E-07
positive regulation of metabolic process	2.20E-10	1.52E-07
regulation of protein modification process	2.42E-10	1.60E-07
regulation of cell adhesion	3.01E-10	1.91E-07
regulation of cell motility	3.41E-10	2.09E-07
apoptotic signaling pathway	3.65E-10	2.15E-07
positive regulation of macromolecule metabolic process	4.87E-10	2.77E-07
response to chemical	5.46E-10	2.99E-07