

A

Sum threshold

	0	1	2	3	4	5	6
0.01	0.525971	1.67E-05	0.188794	1	1	1	1
0.05	0.525971	6.91E-06	7.27E-06	0.292627	1	1	1
0.1	0.525971	0.000209	3.03E-06	2.56E-05	0.022711	0.027533	1
0.15	0.525971	0.00267	2.88E-08	2.48E-05	0.142231	0.097275	1
0.2	0.525971	0.012907	1.50E-08	2.46E-07	0.130738	0.209256	1
0.25	0.525971	0.01349	1.52E-07	5.66E-07	0.321113	1	1
0.3	0.525971	0.099369	0.000115	1.74E-05	0.276062	1	1

B

Sum threshold

	0	1	2	3	4	5	6
0.01	118	23	1	0	0	0	0
0.05	118	62	14	1	0	0	0
0.1	118	78	25	9	2	1	0
0.15	118	84	39	13	2	1	0
0.2	118	88	48	20	3	1	0
0.25	118	94	53	23	3	0	0
0.3	118	88	50	23	4	0	0

C

gene_symbol	hypertension	COPD	diabetes	smoke	cancer	sex	age	sum
cav1	-1	-1	-1	-1	-1	0	0	-5
ube2i	0	-1	-1	-1	-1	0	0	-4
jun	-1	1	-1	-1	-1	-1	0	-4
atp6v1a	-1	-1	-1	1	-1	0	0	-3
irf1	-1	0	1	-1	-1	0	-1	-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
dis3	-1	0	0	-1	-1	0	1	-2
myc	-1	1	0	0	0	-1	-1	-2
akap8l	0	-1	-1	0	0	-1	1	-2
foxa3	-1	0	0	0	0	0	-1	-2
stx4	-1	-1	0	0	0	0	0	-2
junb	-1	1	0	0	-1	-1	0	-2
srf	-1	1	0	-1	-1	0	0	-2
sox12	0	-1	0	-1	0	0	0	-2
mef2a	0	0	0	-1	-1	0	0	-2
stat6	0	0	-1	-1	-1	0	1	-2
clu	1	-1	-1	-1	-1	0	1	-2
nr2f1	0	-1	0	-1	-1	0	1	-2
sox10	0	1	1	1	-1	0	0	2
sympk	0	0	0	0	0	1	1	2
ep300	0	0	1	-1	0	1	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
rif1	0	1	0	0	-1	1	1	2
ptrj	-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
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
onecut1	0	1	-1	1	1	0	1	3
sox2	1	-1	1	1	1	0	0	3
zc3h18	0	1	0	0	0	1	1	3
plau	0	0	0	1	1	1	0	3
itch	0	1	0	1	0	0	1	3
csnk2b	1	1	0	0	1	0	0	3
pdia3	0	1	-1	0	1	1	1	3

D

GO biological process complete	raw P value	FDR
positive regulation of nitrogen compound metabolic process	3.34E-17	5.31E-13
positive regulation of cellular metabolic process	2.03E-16	1.61E-12
positive regulation of macromolecule metabolic process	9.69E-16	5.13E-12
positive regulation of cellular biosynthetic process	4.28E-15	1.70E-11
positive regulation of biosynthetic process	6.49E-15	2.06E-11
positive regulation of transcription by RNA polymerase II	8.40E-15	2.23E-11
positive regulation of metabolic process	1.33E-14	2.64E-11
positive regulation of macromolecule biosynthetic process	1.22E-14	2.77E-11
positive regulation of cellular process	1.76E-14	3.10E-11
positive regulation of nucleobase-containing compound metabolic process	1.24E-13	1.79E-10
positive regulation of transcription, DNA-templated	1.18E-13	1.87E-10
positive regulation of gene expression	1.88E-13	2.49E-10
positive regulation of RNA biosynthetic process	3.90E-13	4.43E-10
regulation of transcription by RNA polymerase II	4.30E-13	4.56E-10
positive regulation of nucleic acid-templated transcription	3.85E-13	4.70E-10
regulation of macromolecule biosynthetic process	5.23E-13	5.20E-10
regulation of nucleobase-containing compound metabolic process	6.35E-13	5.61E-10
regulation of RNA metabolic process	6.21E-13	5.81E-10
positive regulation of biological process	7.03E-13	5.88E-10
regulation of nitrogen compound metabolic process	7.51E-13	5.97E-10
regulation of cellular metabolic process	1.09E-12	8.24E-10
positive regulation of RNA metabolic process	1.25E-12	9.02E-10
regulation of cellular macromolecule biosynthetic process	1.52E-12	1.05E-09
regulation of cellular biosynthetic process	1.59E-12	1.06E-09
regulation of primary metabolic process	2.43E-12	1.54E-09