

Top 100 genes + TFs analysis for scRNA-seq SDREM model with protein phosphorylation data integrated

A

		Sum threshold						
		0	1	2	3	4	5	6
quantile	0.01	0.525038	6.33E-06	0.201545	1	1	1	1
	0.05	0.525038	1.56E-07	1.56E-05	0.310931	1	1	1
	0.1	0.525038	8.51E-07	1.03E-10	0.000248	0.002088	0.029587	1
	0.15	0.525038	0.000188	1.19E-09	2.79E-06	0.006142	0.104244	1
	0.2	0.525038	0.00477	1.36E-09	6.93E-07	0.012293	0.22319	1
	0.25	0.525038	0.007227	2.11E-11	1.28E-08	0.170602	0.079134	1
	0.3	0.525038	0.03262	1.56E-07	8.06E-07	0.009743	0.195827	1

B

		Sum threshold						
		0	1	2	3	4	5	6
quantile	0.01	127	25	1	0	0	0	0
	0.05	127	72	14	1	0	0	0
	0.1	127	96	35	8	3	1	0
	0.15	127	98	44	15	4	1	0
	0.2	127	98	53	20	5	1	0
	0.25	127	103	67	27	4	2	0
	0.3	127	101	64	27	8	2	0

C

gene_symbol	hypertension	COPD	diabetes	smoke	cancer	sex	age	sum
nr3c1	-1	-1	-1	-1	-1	0	0	-5
cav1	-1	-1	-1	-1	-1	1	0	-4
jun	-1	1	-1	-1	-1	-1	0	-4
hspa8	-1	-1	0	0	0	-1	0	-3
erbb2	1	-1	0	-1	-1	0	-1	-3
srf	-1	1	-1	-1	-1	0	0	-3
fos	-1	0	1	-1	-1	0	-1	-3
acat1	0	-1	-1	-1	0	-1	1	-3
apc	0	-1	-1	0	-1	0	0	-3
mafk	-1	0	0	-1	0	0	-1	-3
ctnna1	1	-1	0	-1	-1	-1	0	-3
mzf1	0	-1	0	-1	-1	1	-1	-3
brd2	-1	1	-1	-1	-1	-1	1	-3
mcm3ap	0	-1	0	-1	0	-1	0	-3
myc	-1	1	0	0	0	-1	-1	-2
akap8l	0	-1	-1	0	0	-1	1	-2
atf3	-1	1	0	0	-1	0	-1	-2
rxra	0	-1	0	-1	-1	0	1	-2
stx4	-1	-1	0	0	0	0	0	-2
creb1	0	-1	1	1	-1	-1	-1	-2
junb	-1	1	0	0	-1	-1	0	-2
bach1	-1	-1	0	0	0	0	0	-2
jak2	-1	1	0	-1	-1	0	0	-2
ccdc8	0	-1	-1	0	0	0	0	-2
crebbp	0	-1	-1	-1	0	0	1	-2
ctnna2	0	0	-1	0	-1	1	-1	-2
irf1	-1	0	1	-1	-1	1	-1	-2
stat6	0	0	-1	-1	-1	0	1	-2
rela	-1	0	0	0	-1	1	-1	-2
stip1	-1	1	1	1	0	0	0	2
cul2	0	1	0	0	0	0	1	2
maf	-1	1	1	0	0	1	0	2
atm	1	1	0	1	-1	0	0	2
fancg	0	1	0	0	1	0	0	2
mxd1	-1	1	0	1	0	0	1	2
g3bp1	0	0	-1	1	1	0	1	2
esrra	0	1	-1	1	1	0	0	2
sumo1	1	1	0	-1	1	0	0	2
cebp	0	0	1	1	0	0	0	2
fam20c	0	1	1	0	0	0	0	2
hes1	1	1	1	1	-1	0	-1	2
elk1	-1	-1	1	1	1	0	1	2
irf6	1	-1	1	-1	1	1	0	2
arfgef2	1	0	-1	1	1	-1	1	2
prpf40a	0	0	0	1	1	-1	1	2
hmg1	-1	1	0	1	1	0	0	2
bclaf1	0	-1	1	1	0	1	0	2
tfdp1	1	-1	0	0	1	0	1	2
hnf4a	0	1	-1	1	0	1	0	2
smad3	0	-1	1	-1	1	1	1	2
dsp	1	1	-1	-1	1	1	0	2
nr1h3	0	0	1	0	0	0	1	2
larp1	0	0	1	-1	1	0	1	2
arid5b	0	1	0	1	0	0	0	2
emd	0	1	1	0	1	0	0	3
sympk	0	0	0	0	1	1	1	3
ep300	0	1	1	-1	0	1	1	3
irak1	0	0	1	-1	1	1	1	3
ptprj	-1	1	1	0	0	1	1	3
egfr	0	1	1	1	1	-1	0	3
neu1	-1	1	1	1	1	-1	1	3
fosl2	-1	1	0	1	0	1	1	3
csnk2a2	0	1	1	-1	1	0	1	3
zc3h18	0	1	0	0	0	1	1	3
itch	0	1	0	1	0	0	1	3
irf5	0	1	0	1	0	0	1	3
csnk2a1	0	1	1	1	1	0	1	5

D

GO biological process complete	raw P value	▲ FDR
positive regulation of transcription by RNA polymerase II	1.51E-21	2.39E-17
positive regulation of nitrogen compound metabolic process	4.95E-21	3.93E-17
positive regulation of gene expression	1.06E-20	4.19E-17
positive regulation of macromolecule biosynthetic process	9.05E-21	4.80E-17
positive regulation of cellular biosynthetic process	5.22E-20	1.18E-16
positive regulation of RNA metabolic process	4.73E-20	1.25E-16
positive regulation of biosynthetic process	9.15E-20	1.32E-16
positive regulation of macromolecule metabolic process	4.24E-20	1.35E-16
positive regulation of RNA biosynthetic process	8.88E-20	1.41E-16
positive regulation of nucleic acid-templated transcription	8.71E-20	1.54E-16
regulation of transcription by RNA polymerase II	8.49E-20	1.69E-16
regulation of transcription, DNA-templated	1.44E-19	1.90E-16
positive regulation of transcription, DNA-templated	1.70E-19	1.93E-16
positive regulation of metabolic process	1.58E-19	1.93E-16
regulation of cellular macromolecule biosynthetic process	3.67E-19	3.43E-16
regulation of RNA biosynthetic process	3.53E-19	3.50E-16
regulation of nucleic acid-templated transcription	3.33E-19	3.53E-16
regulation of RNA metabolic process	8.55E-19	7.55E-16
positive regulation of nucleobase-containing compound metabolic process	1.01E-18	8.48E-16
regulation of macromolecule biosynthetic process	1.41E-18	1.12E-15
positive regulation of cellular metabolic process	3.80E-18	2.87E-15
regulation of cellular biosynthetic process	6.84E-18	4.94E-15
regulation of biosynthetic process	1.54E-17	1.02E-14
regulation of nucleobase-containing compound metabolic process	1.49E-17	1.03E-14
positive regulation of cellular process	2.05E-17	1.31E-14
positive regulation of biological process	3.21E-16	1.96E-13
response to stress	4.61E-16	2.61E-13
cellular response to chemical stimulus	4.60E-16	2.71E-13