

P-values and FDR values for the three “self-contained null hypothesis” and three “competitive null hypothesis” approaches

P-values for the genes sets with P-value $\leq$ 0.001 by any of the three “self-contained null hypothesis” in the analysis of the p53 dataset

Gene Set	Self-contained null hypothesis			Competitive null hypothesis		
	Global	Ancova	SAM-GS	SAFE [#]	GSEA [#]	Fisher [#]
ATM Pathway*	<0.001	0.002	<0.001	0.494	0.215	0.984
BAD Pathway**	<0.001	<0.001	<0.001	0.029	0.044	0.996
Calcineurin Pathway\$	0.007	0.002	<0.001	0.668	0.138	0.933
Cell cycle regulator†	0.002	0.001	<0.001	0.025	0.293	0.969
Hsp27Pathway**	<0.001	0.001	<0.001	0.027	<0.001	1.000
Mitochondria pathway***	0.007	0.007	<0.001	0.543	0.329	0.923
p53 signaling pathway*	0.003	0.003	0.001	0.289	0.013	0.994
P53_UP*	<0.001	<0.001	<0.001	0.413	<0.001	1.000
p53hypoxiaPathway*	<0.001	<0.001	<0.001	0.343	<0.001	1.000
p53Pathway*	<0.001	<0.001	<0.001	0.273	<0.001	1.000
Raccycd Pathway†	0.001	<0.001	<0.001	0.117	0.565	0.891
Radiation_sensitivity*	<0.001	<0.001	<0.001	0.204	0.002	0.998
SA_TRKA_RECEPTOR‡	0.001	<0.001	<0.001	0.362	0.347	0.792
bcl2family & reg. network**	0.001	0.005	<0.001	0.064	0.426	0.880
Cell cycle arrest†	0.027	0.018	0.005	0.074	0.491	0.521
Ceramide Pathway**	0.004	0.004	<0.001	0.421	0.308	0.891
CR_DEATH*	0.029	0.017	0.004	0.718	0.314	0.833

* pathway member

** apoptosis

\$ p53-induced proline oxidase mediates apoptosis via a calcineurin-dependent pathway

† cell cycle

‡ integrated negative feedback loop between Akt and p53

the only additional gene set identified with $p < 0.001$ by any of SAFE, GSEA, and Fisher was HUMAN_CD34_ENRICHED_TF_JP. For this gene set, Fisher p-value was <0.001 , but all the other five methods gave p-values > 0.37 .

FDR values for the genes sets with P-value $\leq$ 0.001 by any of the three

“self-contained null hypothesis” in the analysis of the p53 dataset

Gene Set	Self-contained null hypothesis			Competitive null hypothesis		
	Global	Ancova	SAM-GS	SAFE	GSEA	Fisher
ATM Pathway*	<0.0001	0.0036	<0.0001	0.5039	0.8734	1.0000
BAD Pathway**	<0.0001	<0.0001	<0.0001	0.4726	0.5750	1.0000
Calcineurin Pathway\$	0.0071	0.0036	<0.0001	0.5168	0.8424	1.0000
Cell cycle regulator†	0.0037	0.0026	<0.0001	0.4726	0.9066	1.0000
Hsp27Pathway**	<0.0001	0.0026	<0.0001	0.4726	<0.0001	1.0000
Mitochondria pathway**	0.0071	0.0071	<0.0001	0.5039	0.8860	1.0000
p53 signaling pathway*	0.0051	0.0046	<0.0001	0.5039	0.5132	1.0000
P53_UP*	<0.0001	<0.0001	<0.0001	0.5039	0.0131	1.0000
p53hypoxiaPathway*	<0.0001	<0.0001	<0.0001	0.5039	<0.0001	1.0000
p53Pathway*	<0.0001	<0.0001	<0.0001	0.5039	<0.0001	1.0000
Raccydc Pathway†	0.0020	<0.0001	<0.0001	0.4972	0.8373	1.0000
Radiation_sensitivity*	<0.0001	<0.0001	<0.0001	0.4972	0.0778	1.0000
SA_TRKA_RECEPTOR‡	0.0020	<0.0001	<0.0001	0.5039	0.8359	1.0000
bcl2family & reg. network**	0.0020	0.0066	0.0014	0.4920	0.8377	1.0000
Cell cycle arrest†	0.0137	0.0113	0.0014	0.4920	0.9810	1.0000
Ceramide Pathway**	0.0054	0.0058	0.0014	0.5039	0.8894	1.0000
CR_DEATH*	0.0140	0.0113	0.0063	0.5304	0.8615	1.0000

* pathway member

** apoptosis

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