

Supplementary Table S6. The results of a TOX analysis in Ingenuity Pathway Analysis carried out for the complete transcriptome of fibroblasts treated with PDGF2 ($p \leq 0.05$) in comparison to that of parallel controls untreated with PDGF2

Categories: Cancer, Organismal Injury and Abnormalities Cancer, Cellular Development, Cellular Growth and Proliferation, Organismal Injury and Abnormalities, Tumor Morphology

Diseases or Functions Annotation	p	Predicted Activation State	Activation z-Score	Number of Molecules Involved in the Process
Cancer	3.64E-05		-1.207	754
Malignant solid tumor	8.78E-05		-0.557	750
Nonhematological malignant neoplasm	3.52E-06		-0.492	744
Nonmelanoma solid tumor	1.89E-05		-0.445	737
Nonhematological solid tumor	5.95E-06		-0.436	745
Extracranial solid tumor	9.78E-04		-0.391	745
Solid tumor	2.63E-04		-0.274	752
Cytotoxic reaction of tumor cell lines	2.27E-02		0.555	5
Colony formation of tumor cells	1.86E-02		0.000	4
Solid tumor	2.63E-04		-0.274	752
Extracranial solid tumor	9.78E-04		-0.391	745
Nonhematological solid tumor	5.95E-06		-0.436	745
Nonmelanoma solid tumor	1.89E-05		-0.445	737
Nonhematological malignant neoplasm	3.52E-06		-0.492	744
Malignant solid tumor	8.78E-05		-0.557	750
Cancer	3.64E-05		-1.207	754
<i>Category: Cell Death and Survival</i>				
Cell death of tumor cell lines	3.16E-02		0.821	106
Apoptosis of tumor cell lines	7.94E-03		0.553	90
Necrosis	1.16E-02		0.259	132
Apoptosis	2.67E-03		-0.485	129

The z-score is an algorithm in the IPA software designed to reduce the chance that random data will produce a significant prediction. It identifies functions with the strongest prediction for an increase (positive z-score) or a decrease (negative z-score). p -Score values <0.05 and z-score values ≤ -2 or ≥ 2 were considered significant.

SUPPLEMENTARY REFERENCE

S1. Edgar RC. MUSCLE: multiple sequence alignment with high accuracy and high throughput. *Nucleic Acids Res* 2004;32:1792–1797.