

Text S2: Computing the Fisher's Exact Test to Assess Overenrichment

For the 10 stimulus-induced genes by ATRA or DMSO (PTEN, Akt1, p27, RXR- α , p21, CITED2, RARRES3, MBN, CD38, SMYD5), 9 out of 10 were classified as transient genes.

	Stimulus-Induced Genes	Non-Stimulus Induced Genes	
Transient Genes	$X = 9$	1461	$k = 1462$
Core Genes	1	1419	$N - k = 1428$
	$M = 10$		$N = 2890$

The quantity X can be modeled as a hypergeometric random variable:

$$P(X = x) = \frac{\binom{M}{x} \binom{N-M}{k-x}}{\binom{N}{k}}$$

The statistical significance of seeing 9 out of 10 stimulus-induced genes represented in the transient group of genes corresponds to calculating the sum of probabilities greater than equal to what we observed.

$$P(X \geq 9) = \sum_{x=9}^{10} \frac{\binom{M}{x} \binom{N-M}{k-x}}{\binom{N}{k}} = 0.0117.$$

For the sixteen genes identified by [15, 16], thirteen were classified as core genes.

	Myeloid-Specific Differentiation Genes	Non-Myeloid-Specific Differentiation Genes	
Core Genes	$X = 13$	1415	$k = 1428$
Transient Genes	3	1459	$N - k = 1462$
	$M = 16$		$N = 2890$

The statistical significance of seeing 13 out of 16 myeloid-specific differentiation genes represented in the core group of genes corresponds to calculating the sum of probabilities greater than equal to what we observed.

$$P(X \geq 13) = \sum_{x=13}^{16} \frac{\binom{M}{x} \binom{N-M}{k-x}}{\binom{N}{k}} = 0.00924.$$

Similarly, for the apoptosis-related genes:

	Apoptosis-Related Genes	Non-Apoptosis-Related Genes	
Core Genes	$X = 10$	1418	$k = 1428$
Transient Genes	3	1459	$N - k = 1462$
	$M = 13$		$N = 2890$

$$P(X \geq 10) = \sum_{x=10}^{13} \frac{\binom{M}{x} \binom{N-M}{k-x}}{\binom{N}{k}} = 0.0418.$$