

Supplementary Table IX. Transcriptional regulators inferred to be active in RTs, based on IPA analysis of downstream target gene expression, using genes dysregulated in all 3 RT groups compared to normal.

Upstream Regulator	Fold Change of Upstream Regulator*	Predicted Activation State	Activation z-score	P-value of overlap
MYC		Activated	5.71	1.60E-21
HGF		Activated	4.91	2.43E-16
Vegf		Activated	4.76	2.02E-17
TBX2		Activated	4.43	3.10E-22
FOXO1		Activated	3.94	2.18E-05
E2F1		Activated	3.66	4.07E-22
FOXM1	30.3	Activated	3.50	8.41E-13
EP400		Activated	3.43	1.65E-12
CCND1		Activated	3.21	1.90E-16
EIF4E		Activated	3.11	2.00E-03
E2F2		Activated	2.83	1.13E-13
ERBB2		Activated	2.74	1.79E-19
S100A6		Activated	2.71	1.62E-10
CD24		Activated	2.53	2.80E-04
CD40LG		Activated	2.49	1.25E-02
MYCN		Activated	2.48	5.33E-08
SATB1		Activated	2.43	9.84E-02
Hdac		Activated	2.37	1.92E-01
SMOC2		Activated	2.24	5.17E-07
TFDP1		Activated	2.21	5.07E-05
E2F3		Activated	2.20	5.38E-15
E2f		Activated	2.18	2.20E-13
ANGPT2		Activated	2.06	7.30E-03
CD247		Activated	2.00	1.31E-01
NFYA		Activated	2.00	4.49E-04
AGA		Inhibited	-2.00	4.18E-06
SLC13A1		Inhibited	-2.00	3.08E-01
SMARCE1		Inhibited	-2.00	2.11E-04
HNF4A		Inhibited	-2.13	9.56E-06
IKBKB		Inhibited	-2.18	1.27E-03
SPI1		Inhibited	-2.20	9.95E-02
UXT		Inhibited	-2.22	1.96E-03

ESR2		Inhibited	-2.22	1.32E-01
PTEN		Inhibited	-2.39	5.52E-07
STAT5A		Inhibited	-2.41	1.78E-01
MXI1		Inhibited	-2.41	1.91E-06
FOXO3		Inhibited	-2.44	1.26E-04
ADCYAP1		Inhibited	-2.50	2.69E-02
TREM1		Inhibited	-2.50	5.40E-03
PPARG		Inhibited	-2.50	2.50E-02
TOB1		Inhibited	-2.53	7.85E-07
PPARGC1A		Inhibited	-2.61	8.12E-02
TCF3	4.47	Inhibited	-2.75	2.46E-07
SMARCB1		Inhibited	-2.99	5.82E-10
BNIP3L		Inhibited	-3.15	3.85E-06
RBL2		Inhibited	-3.28	1.43E-08
CD28		Inhibited	-3.43	1.72E-05
Rb		Inhibited	-3.43	7.08E-13
KDM5B		Inhibited	-3.44	7.89E-16
RBL1		Inhibited	-3.59	6.52E-12
CDKN1A		Inhibited	-3.61	4.81E-40
IRGM		Inhibited	-3.74	1.79E-11
TP53	20.2	Inhibited	-3.95	2.92E-36
CDKN2A		Inhibited	-4.24	5.60E-21
RB1		Inhibited	-4.40	3.81E-19

*Fold change shown if the upstream regulator was itself among the 610 dysregulated genes input to IPA