

Additional file 2: Validation of microarray results by quantitative RT-PCR

Category	Gene symbol	Description	Fold-change*	
			microarray	RT-PCR
IEGs	<i>EGR-1</i>	early growth response 1	13.30	9.59
	<i>c-FOS</i>	FBJ osteosarcoma oncogene	10.80	13.01
	<i>FOSB</i>	FBJ osteosarcoma oncogene B	10.72	9.01
	<i>CEBPD</i>	CCAAT/enhancer binding protein (C/EBP), delta	8.84	5.82
	<i>B3GALT2</i>	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2	4.67	3.56
	<i>KLF4</i>	Kruppel-like factor 4 (gut)	3.67	2.95
	<i>IRS1</i>	insulin receptor substrate 1	3.40	3.56
	<i>MAN2A1</i>	mannosidase 2, alpha 1	2.41	2.18
	<i>FOXA1</i>	forkhead box A1	2.14	1.88
	<i>FOXA2</i>	forkhead box A2	2.03	2.47
targets	<i>SRXN1</i>	sulfiredoxin (neoplastic progression 3)	5.49	7.99
	<i>DUSP4</i>	dual specificity phosphatase 4	2.56	2.19
	<i>SIAT8E</i>	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 5	2.00	2.34
	<i>MGAT2</i>	mannoside acetylglucosaminyltransferase 2	1.94	1.83
	<i>ARL6IP5</i>	ADP-ribosylation factor-like 6 interacting protein 5	1.70	1.61
	<i>TTR</i>	transthyretin	1.69	2.07
	<i>ANXA5</i>	annexin A5	1.69	1.55
	<i>SLC35A2</i>	solute carrier family 35 (UDP-galactose transporter), member 2	1.60	1.53
	<i>DAD1</i>	defender against cell death 1	1.58	1.50
	<i>NDUFA4</i>	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4	1.55	1.60
	<i>TRP53</i>	transformation related protein 53 (p53)	-1.85	-1.91
	<i>NGLY1</i>	N-glycanase 1	-1.91	-2.08
	<i>BBC3</i>	Bcl-2 binding component 3 (PUMA)	-2.28	-2.75
	non-regulated gene	<i>JUND1</i>	Jun proto-oncogene related gene d1	-1.19

*For genes with more than one probe set on the microarray, the mean fold-change value is shown. RT-PCR results as mean of fold-change after normalization with 18S rRNA content in each sample (n =5).