DIANA - mirPath	Neg Ln (p-value)	Ingenuity Canonical Pathways	Neg Ln (p-value)
Pancreatic cancer	17.18	Pancreatic Adenocarcinoma Signaling	40.53
Chronic myeloid leukemia	18.7	Chronic Myeloid Leukemia Signaling	32.93
Colorectal cancer	18.39	Colorectal Cancer Metastasis Signaling	30.39
Bladder cancer	4.77	Bladder Cancer Signaling	28.55
p53 signaling pathway	3.6	**p53 Signaling**	27.63
TGF-β signaling pathway	16.33	**TGF-β Signaling**	24.41
Glioma	17.61	Glioma Signaling	23.95
Melanoma	8.09	Melanoma Signaling	21.92
Prostate cancer	9.22	Prostate Cancer Signaling	19.16
Acute myeloid leukemia	4.84	Acute Myeloid Leukemia Signaling	13.47
Endometrial cancer	3.81	Endometrial Cancer Signaling	12.04
MAPK signaling pathway	19.83	**ERK/MAPK Signaling**	11.49
Wnt signaling pathway	10.93	**Wnt/β-catenin Signaling**	11.10
mTOR signaling pathway	12.17	**mTOR Signaling**	10.96
Insulin signaling pathway	9.19	Insulin Receptor Signaling	10.34
Focal adhesion	10.32	**FAK Signaling**	10.11
Renal cell carcinoma	16.25	Renal Cell Carcinoma Signaling	9.88
VEGF signaling pathway	3.19	**VEGF Signaling**	9.86
T cell receptor signaling pathway	5.21	T Cell Receptor Signaling	5.89
Type II Diabetes Mellitus	5.88	Type II Diabetes Mellitus Signaling	3.29

Supplementary Table S4. We used the 25 microRNAs upregulated in CD114+ cells from 3 neuroblastoma cell lines (IMR-32, LA-N-5, NGP) for gene pathway prediction using two independent software tools. DIANA-mirPath (http://diana.cslab.ece.ntua.gr/) integrates 3 target prediction algorithms (Target scan5.0, DIANA micro-T, and PicTar). Ingenuity Pathway Analysis (http://www.ingenuity.com/) uses curated microRNA-gene interactions to independently associate microRNAs with gene pathways. There is very good agreement of the primary target pathways of the 25 microRNAs from Supplementary Table S3. Pathways in **bold** are either repressed in reprogrammed iPSCs, or activated in CD114- more mature neural crest cells.