Supplemental Material to:

Hua Zhu, Hao Wu, Xiuping Liu, Biao Li, Yun Chen, Xingcong Ren, Chang-Gong Liu and Jin-Ming Yang

Regulation of autophagy by a *beclin 1*-targeted microRNA, miR-30a, in cancer cells

Autophagy 2009; 5(6)

www.landesbioscience.com/journals/autophagy/article/9064

Figure S1

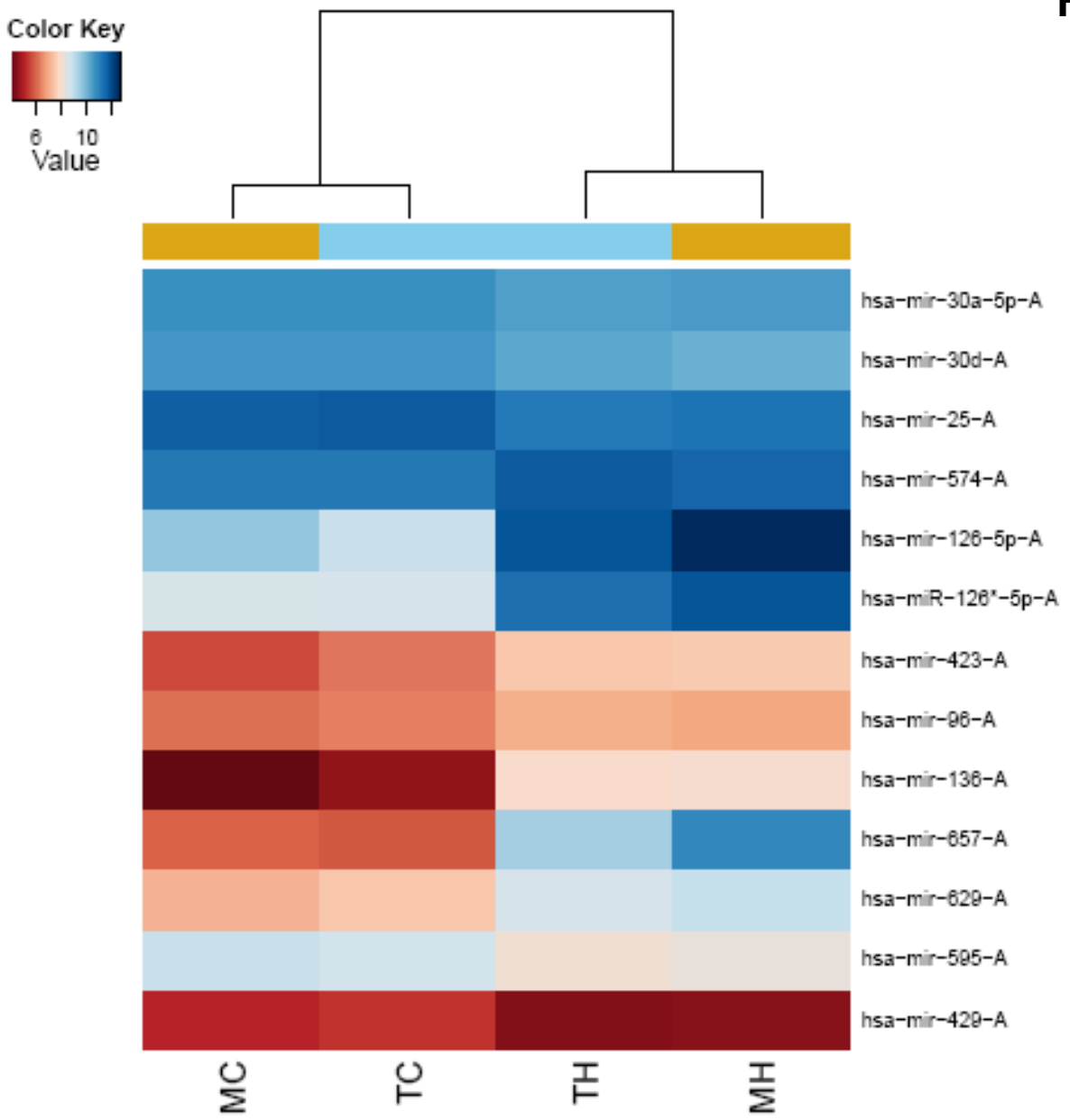
Color Key
6
10
Value
hsa-mir-30a-5p-A
hsa-mir-30d-A
hsa-mir-25-A
hsa-mir-574-A
hsa-mir-126-5p-A
hsa-miR-126*-5p-A
hsa-mir-423-A
hsa-mir-96-A
hsa-mir-136-A
hsa-mir-657-A
hsa-mir-628-A
hsa-mir-505-A
hsa-mir-429-A
MC
TC
TH
MH

Figure S1. Heat map of miRNAs expression profiles of the samples subjected to nutrient deprivation. Total RNAs from the treated cells were extracted using the TriZol Reagent, and 5 μg of total RNA from each sample was biotin-labeled by reverse transcription using 5′ biotin end-labeled random octomer oligo primer. Hybridization of biotin-labeled cDNA was carried out on miRNA microarray chip (OSU version 4.0, The Ohio State University, Columbus, OH), which contains 1600 miRNA oligo probes derived from 474 human and 373 mouse miRNA genes and printed in duplicates. Hybridization signals were detected by biotin binding of a Streptavidin–Alexa 647 conjugate using an Axon Scanner 4000B (Axon Instrument Inc., CA). The images were quantified using the GenePix 6.0 software (Axon Instrument Inc., CA). All analyses were carried out in R-Project (http://www.r-project.org) and BioConductor (http://www.bioconductor.org). Background adjustment was achieved by subtracting local median intensities from probe intensities. For the current analysis, only human active miRNA oligo probes with intensities at least 2 were considered. Replicated probes for the same miRNA were averaged and microarrays were normalized. Probe intensities were scaled on the log base 2 for statistical analysis. In the gene filter stage, probes with low variability across all arrays were removed and only probes with transformed values larger than log2(100) in at least 20 percent arrays and interquantile range more than 0.5 were retained, and this led to 133 probes for comparison. MC: MDA-MB-468 untreated control; TC: T98G untreated control; TH: T98G treated with HBSS; MH: MDA-MB-468 treated with HBSS.

Table S1. Alterations of miRNAs expression following nutrient depletion (numbers shown are percent change of each miRNA in cells treated with HBSS versus control)

ID	MDA-MB-468	T98G	P-value
hsa-mir-136-A	1431	870	0.005745852
hsa-miR-126*-5p-A	812	556	0.005916885
hsa-mir-25-A	-26	-34	0.018463077
hsa-mir-429-A	-34	-46	0.021818949
hsa-mir-629-A	253	123	0.023754234
hsa-mir-657-A	2925	1099	0.028652043
hsa-mir-126-5p-A	635	664	0.030104793
hsa-mir-30d-A	-26	-19	0.031463771
hsa-mir-595-A	-33	-34	0.031537263
hsa-mir-96-A	66	58	0.03323258
hsa-mir-30a-5p-A	-12	-15	0.034981848
hsa-mir-574-A	33	53	0.039253563
hsa-mir-423-A	282	126	0.043124315