

MicroRNA in combination with HER2-targeting drugs reduces breast cancer cell viability *in vitro*

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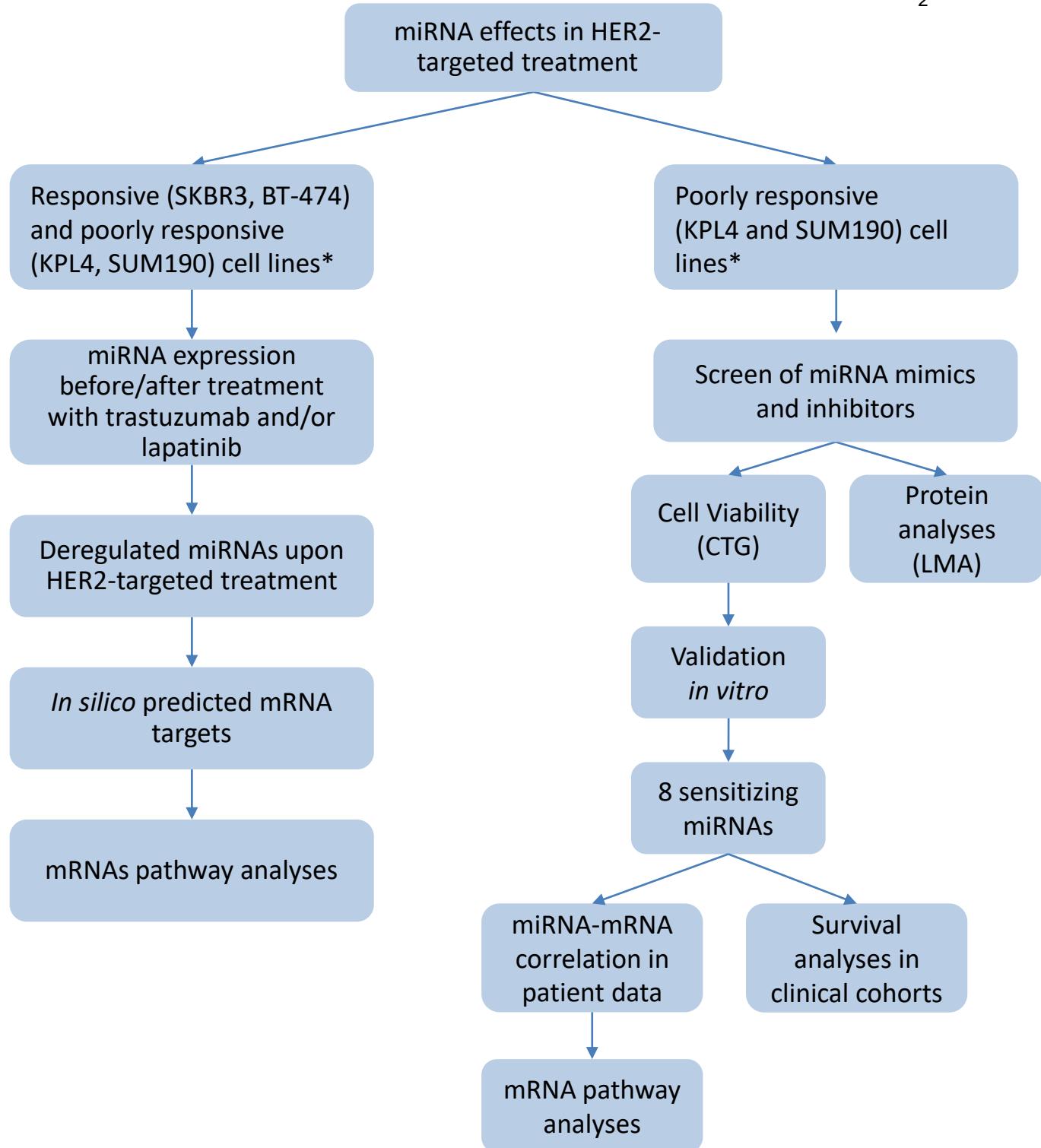
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Supplementary Figure S1

2



*Response to targeted treatment (trastuzumab and lapatinib).

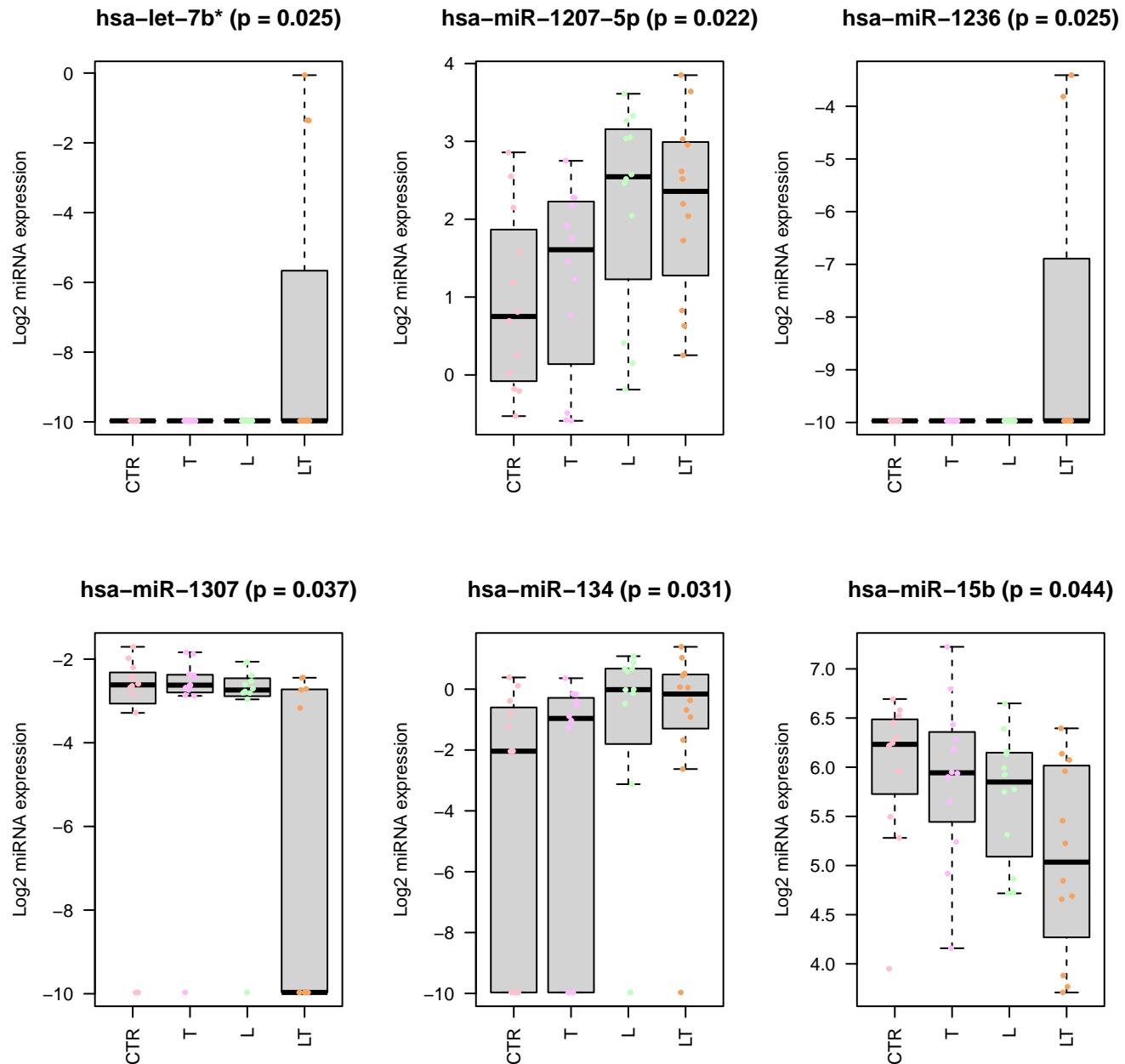
CTG = CellTiter-Glo. LMA = Protein Lysate Microarray

Supplementary Figure S1: Flowchart illustrating the main topics covered in the paper.

On the left side, the effects of HER2-targeted treatment on endogenous miRNA expression levels in HER2+ breast cancer cells are studied. On the right side, the effects of combinatorial treatment with HER2-targeted drugs and transfection of miRNAs in poorly responsive cell lines are explored.

Supplementary Figure S2: miRNA expression before and after targeted treatment in four cell lines (SKBR3, BT-474, KPL4, SUM190PT)

a

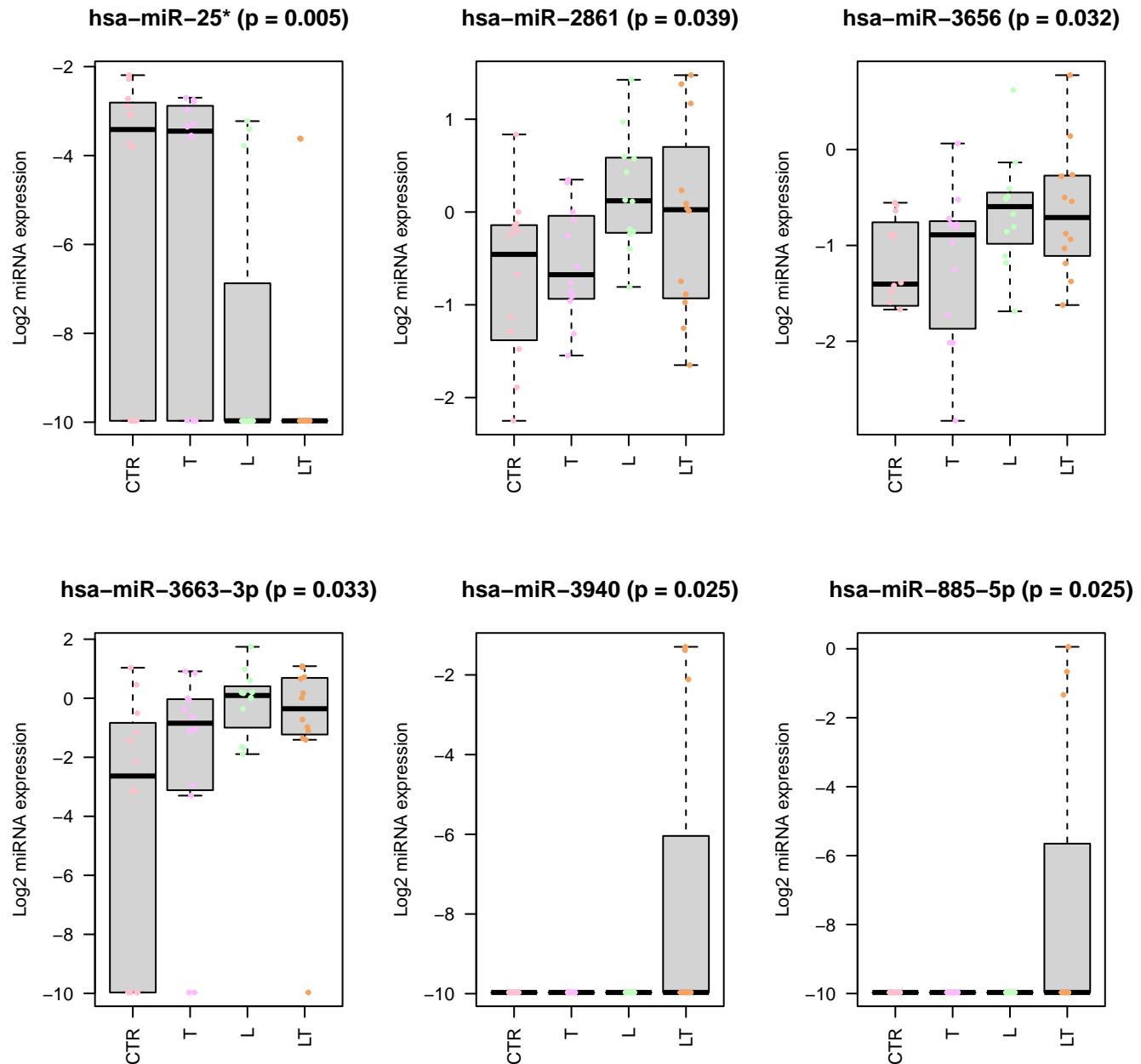


Supplementary Figure S2: miRNA expression after targeted treatment.

The cells were treated with trastuzumab (10 μ g/mL) or lapatinib (100 nM) alone and in combination for 24 hours before total RNA was extracted, and miRNA levels were measured using a one-color microarray Human miRNA Microarray Kit and scanned on Agilent Scanner G2565B. miRNAs with significant (Kruskal-Wallis test p -value < 0.05) expression regulations between any treatment groups are presented. The plots are presented for a-b: four HER2+ cell lines pooled together (SKBR3, BT-474, KPL4, SUM190PT); c-h: cell lines responsive to trastuzumab and lapatinib (SKBR3 and BT-474); and i: poorly responsive cell lines (KPL4 and SUM190PT). T = trastuzumab, L = lapatinib, TL = trastuzumab and lapatinib.

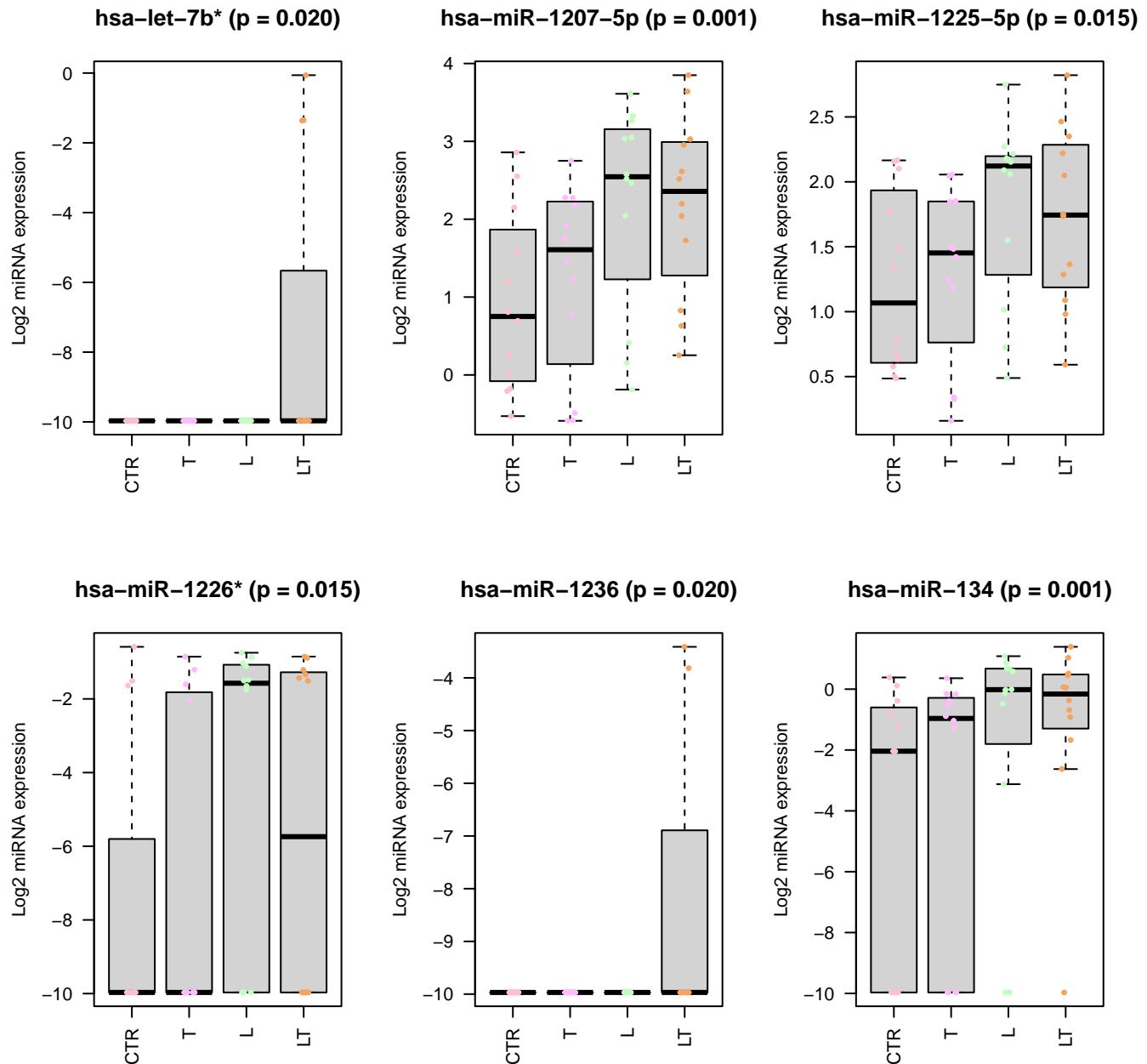
Supplementary Figure S2: miRNA expression before and after targeted treatment in four cell lines (SKBR3, BT-474, KPL4, SUM190PT)

b



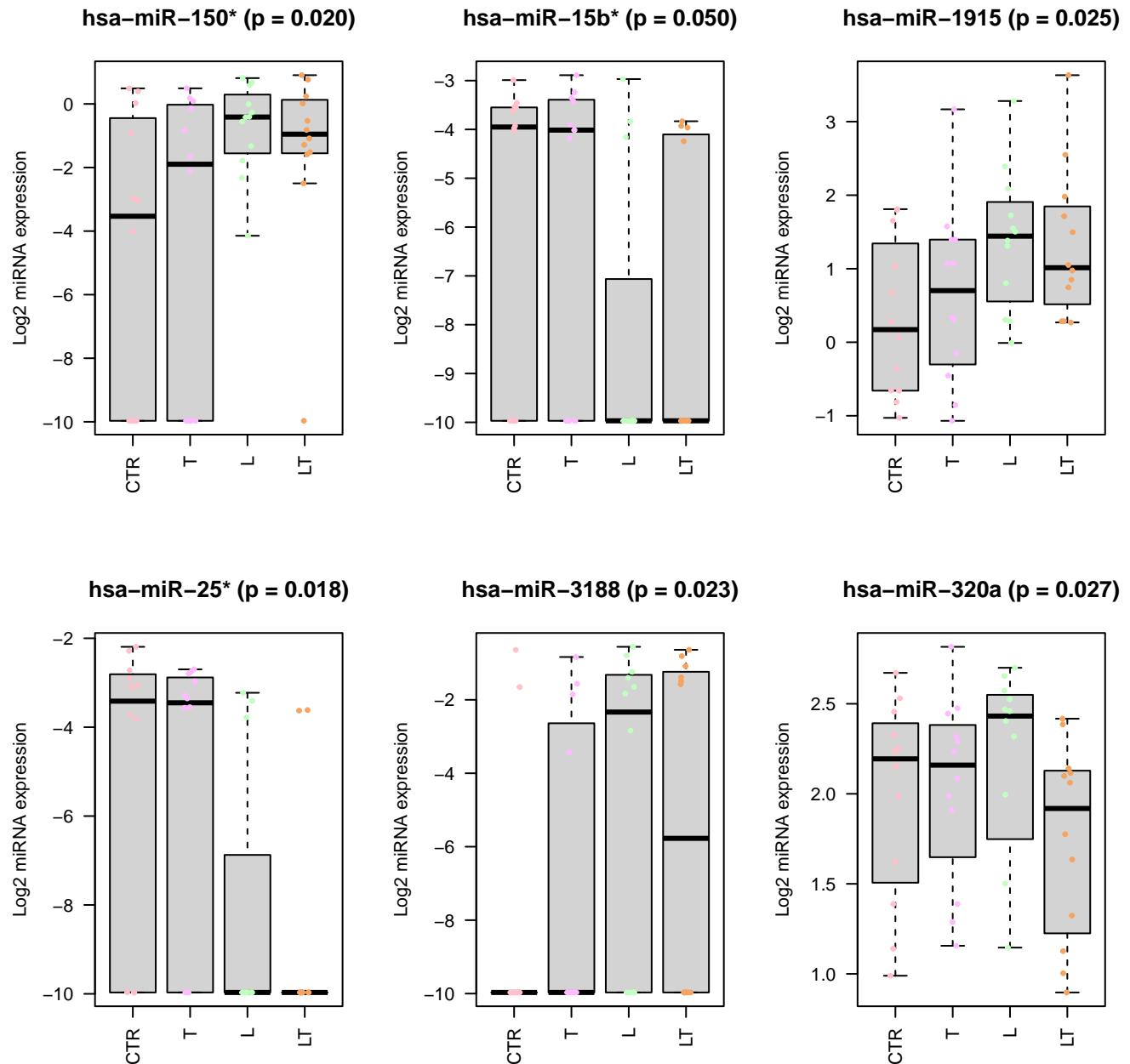
Supplementary Figure S2: miRNA expression before and after targeted treatment in responsive cell lines (SKBR3, BT-474)

C



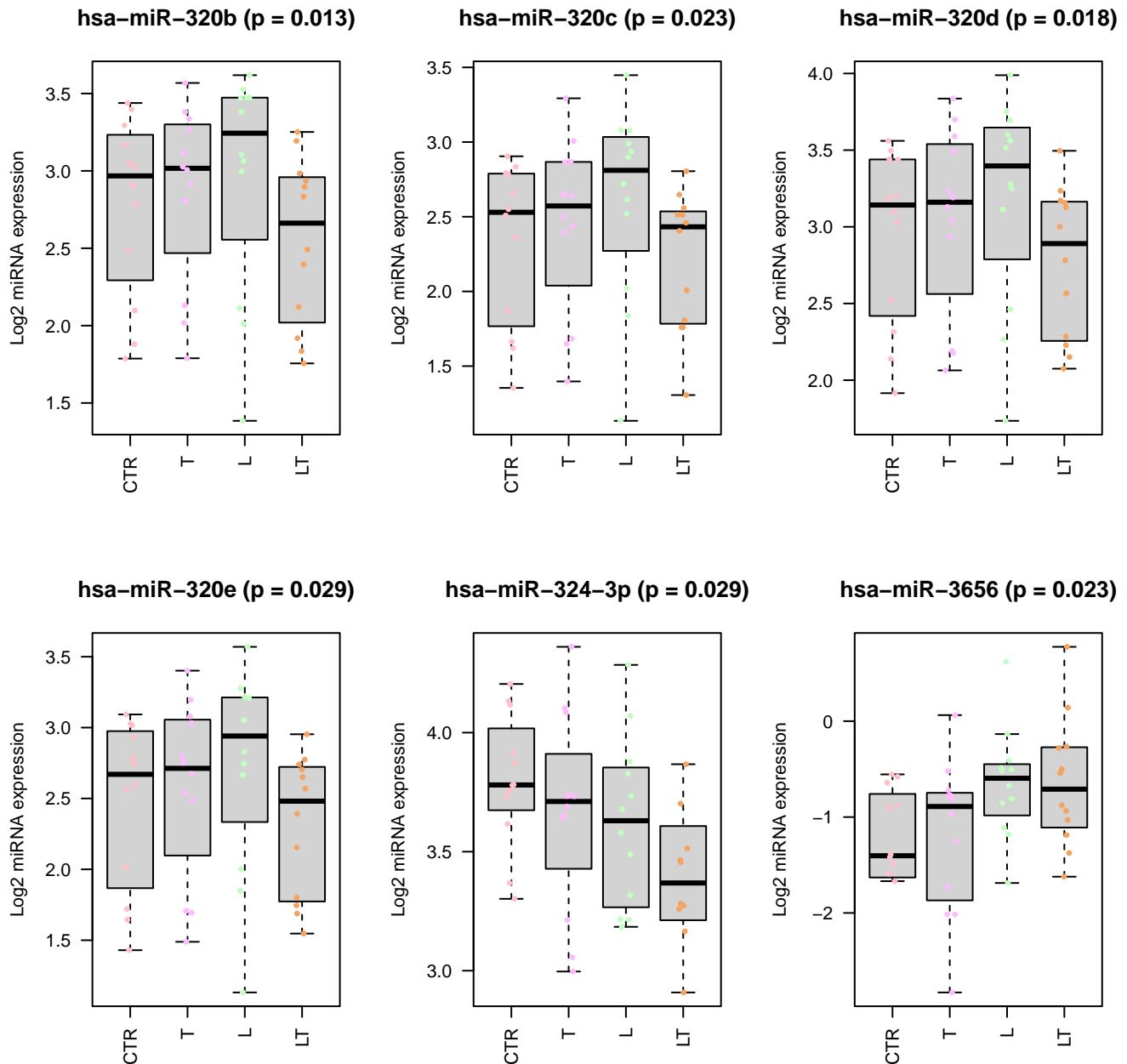
Supplementary Figure S2: miRNA expression before and after targeted treatment in responsive cell lines (SKBR3, BT-474)

d



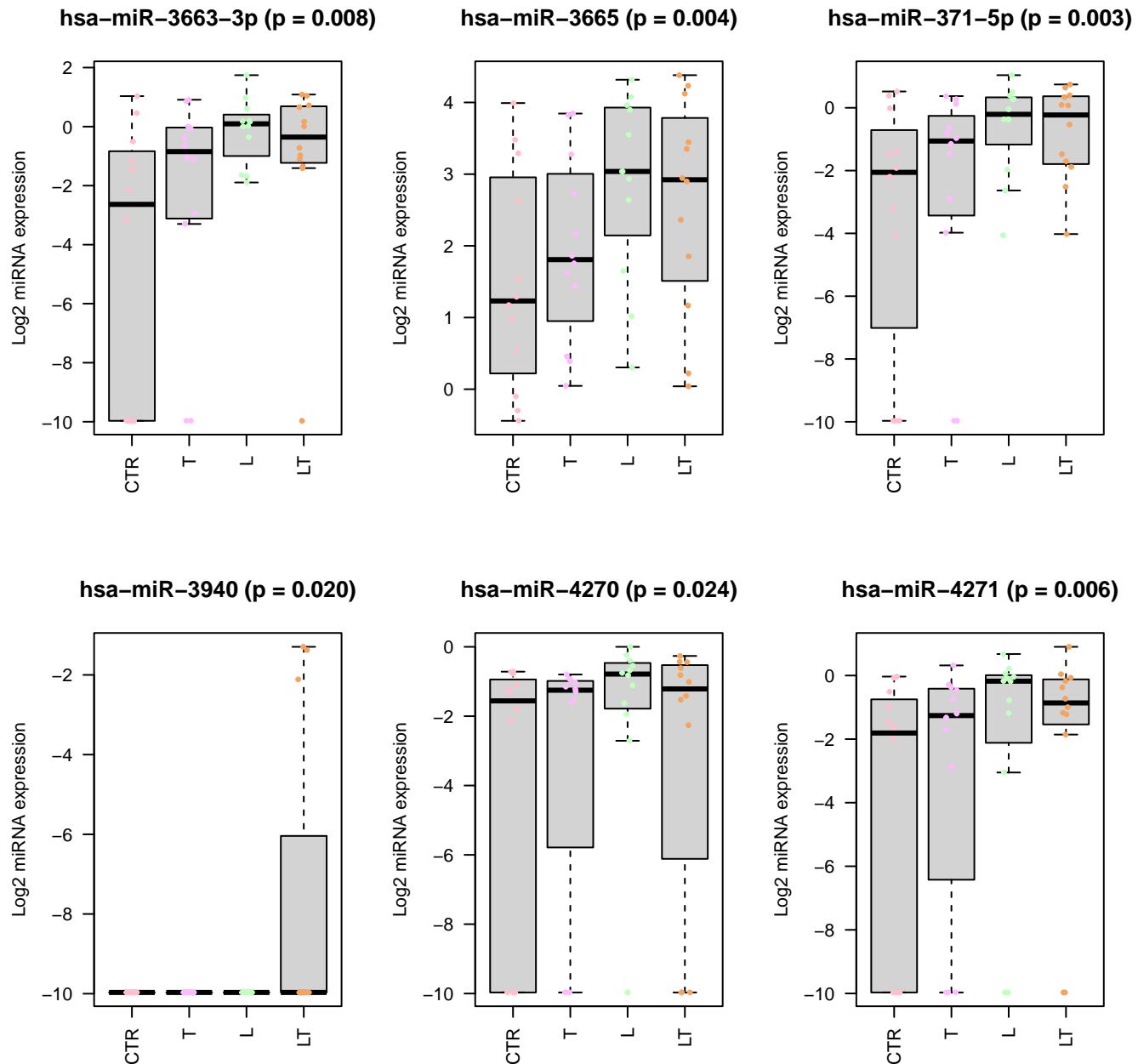
Supplementary Figure S2: miRNA expression before and after targeted treatment in responsive cell lines (SKBR3, BT-474)

e



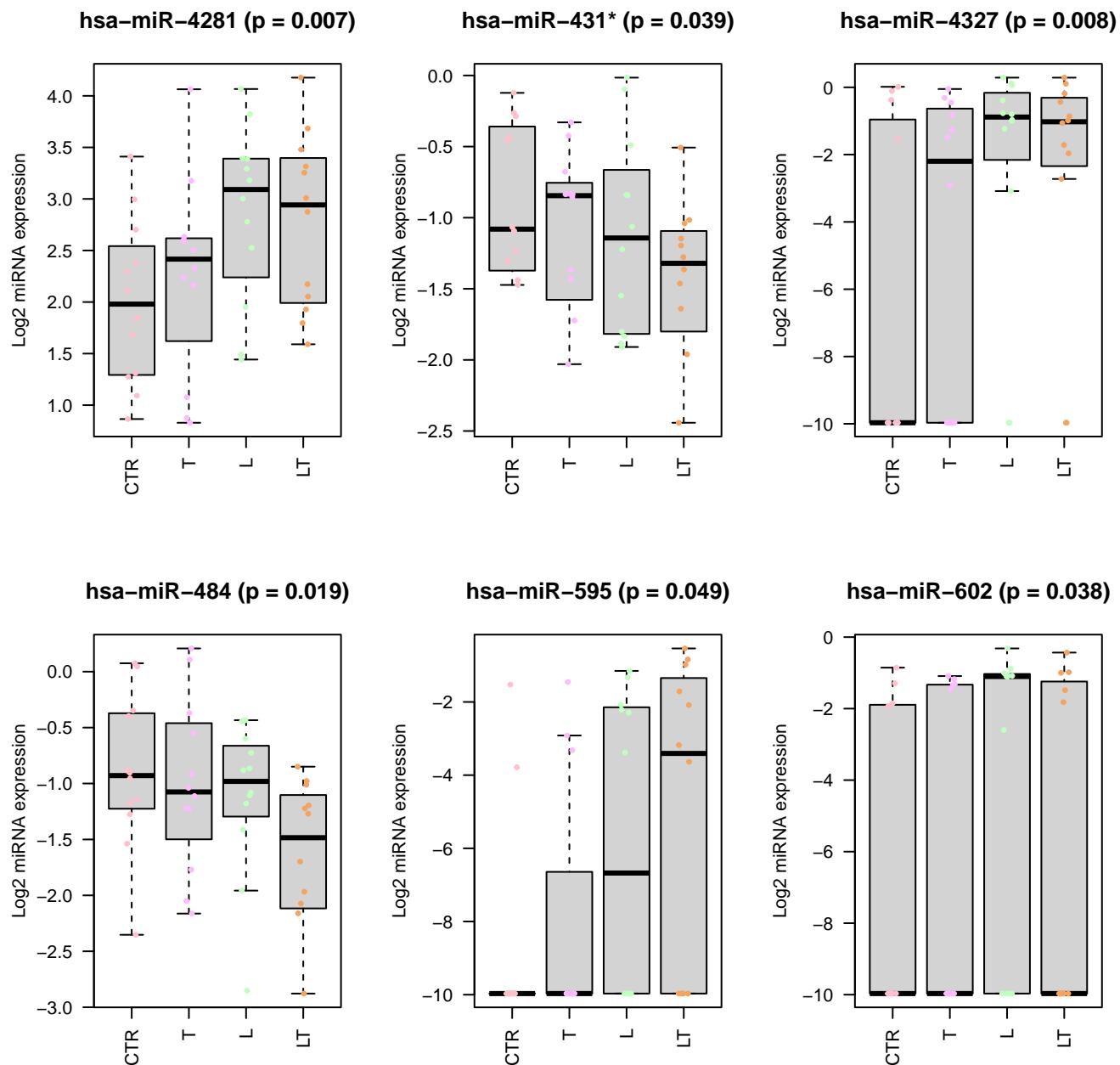
Supplementary Figure S2: miRNA expression before and after targeted treatment in responsive cell lines (SKBR3, BT-474)

f



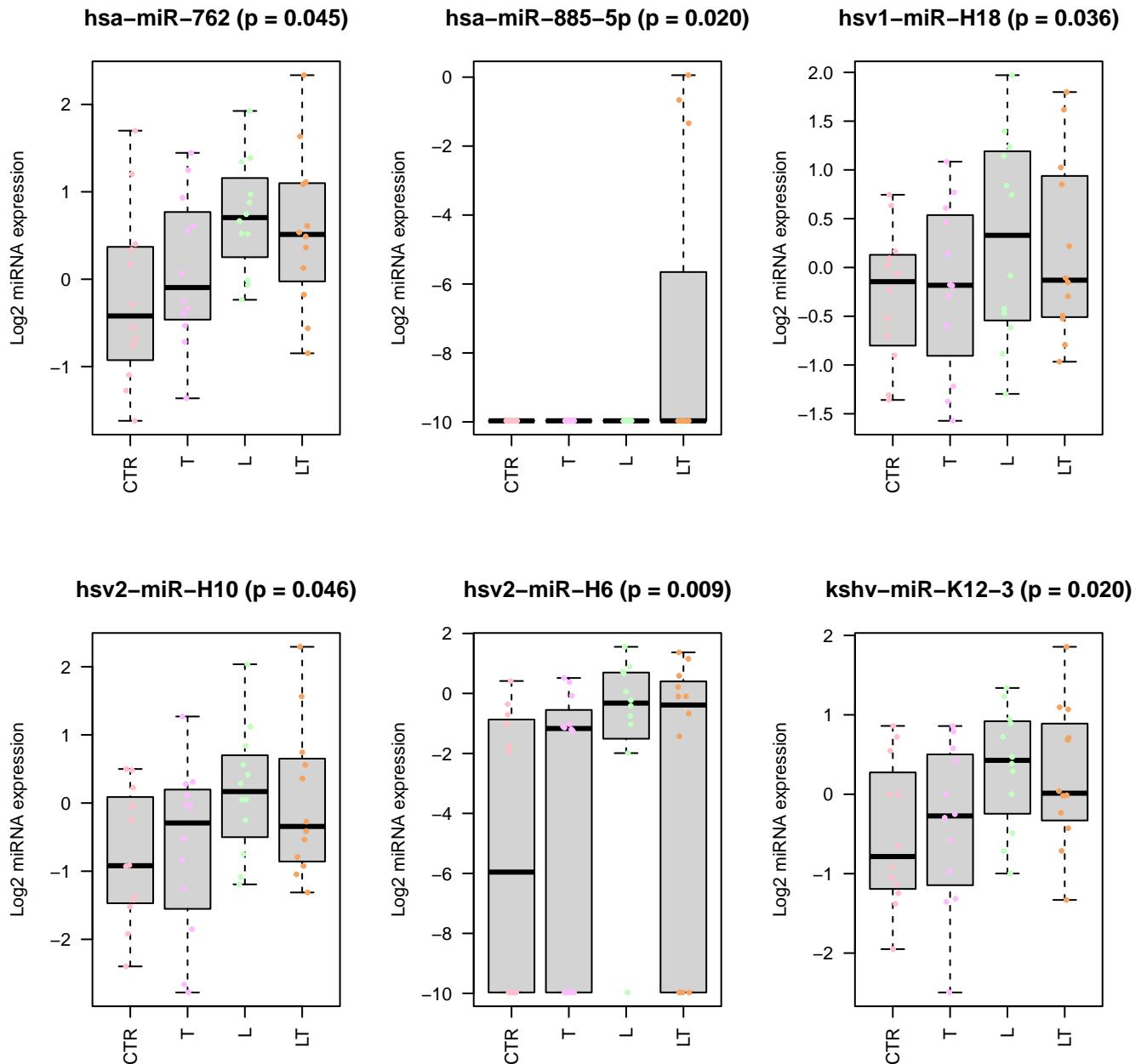
Supplementary Figure S2: miRNA expression before and after targeted treatment in responsive cell lines (SKBR3, BT-474)

g



Supplementary Figure S2: miRNA expression before and after targeted treatment in responsive cell lines (SKBR3, BT-474)

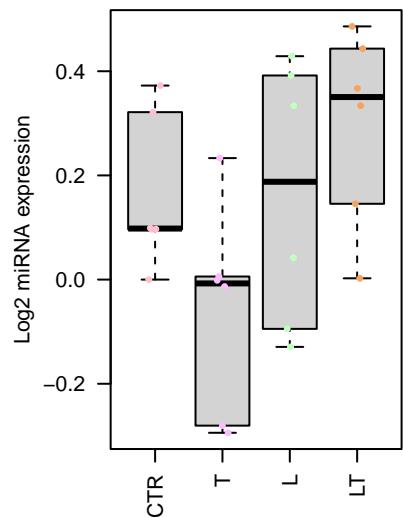
h



Supplementary Figure S2: miRNA expression before and after targeted treatment in poorly responsive cell lines (KPL4. SUM190PT)

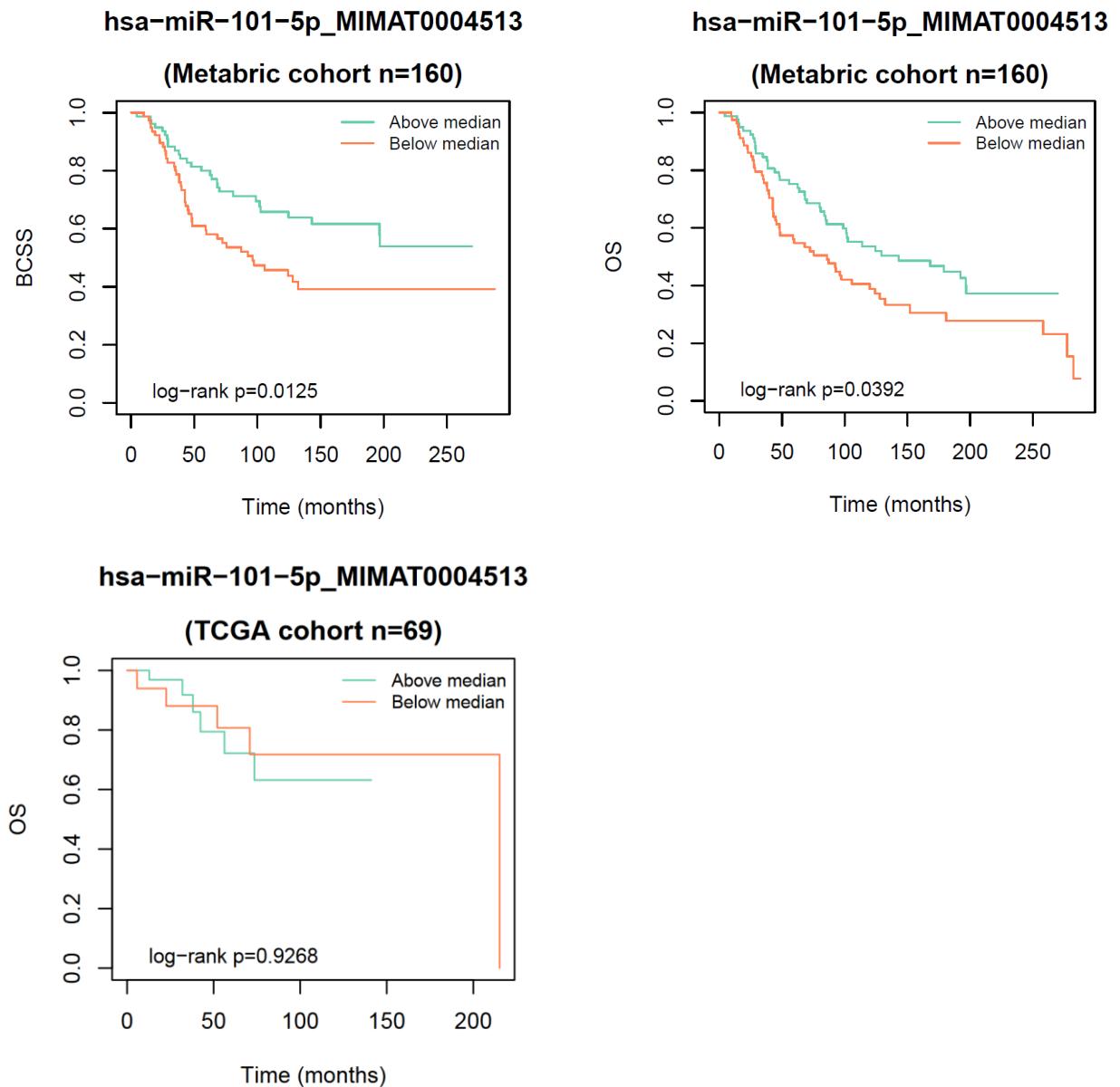
i

hsa-miR-1268 (p=0.020)



Supplementary Figure S3

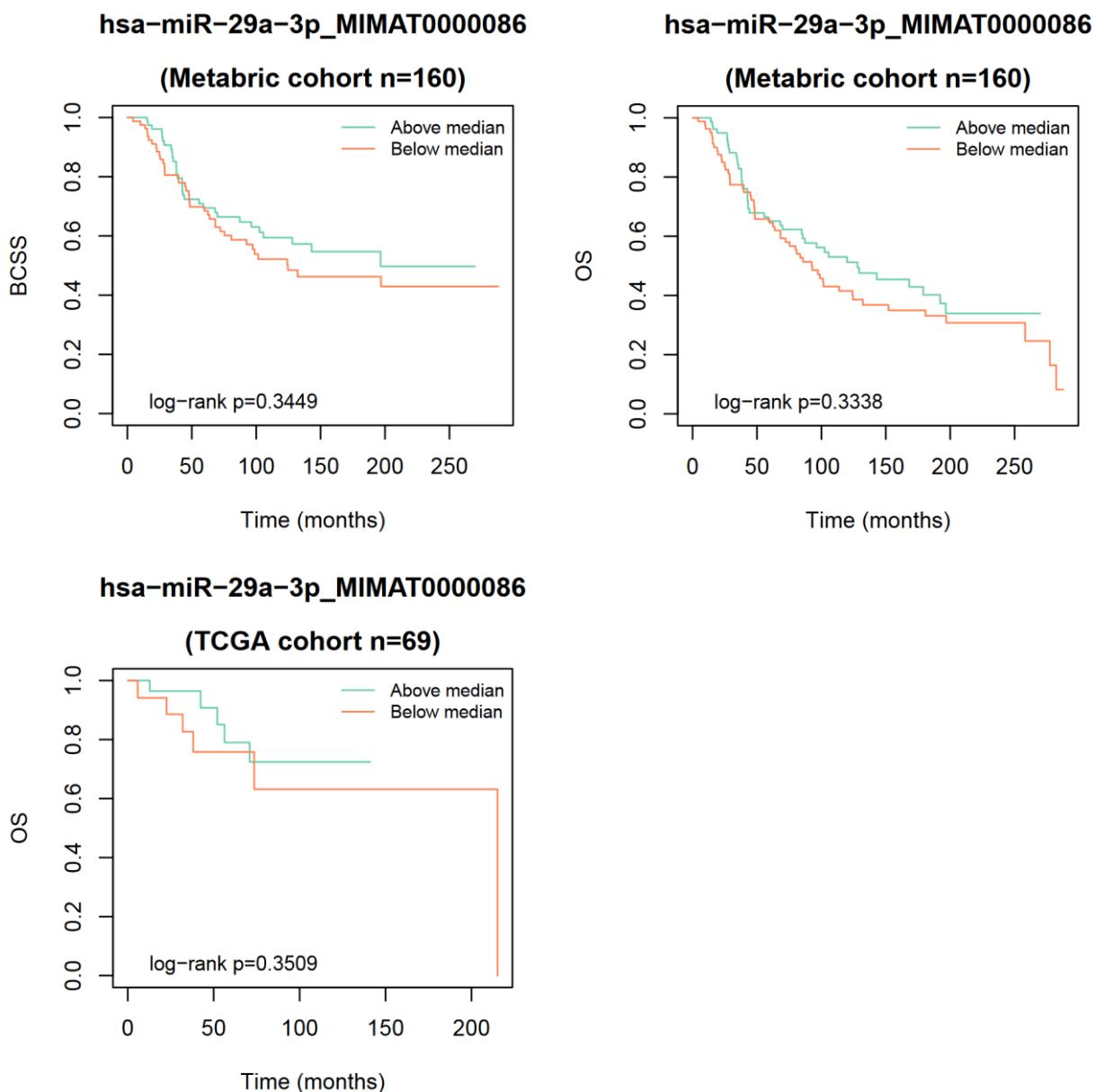
a



Supplementary Figure S3: The clinical significance of sensitizing miRNAs in breast cancer patients.

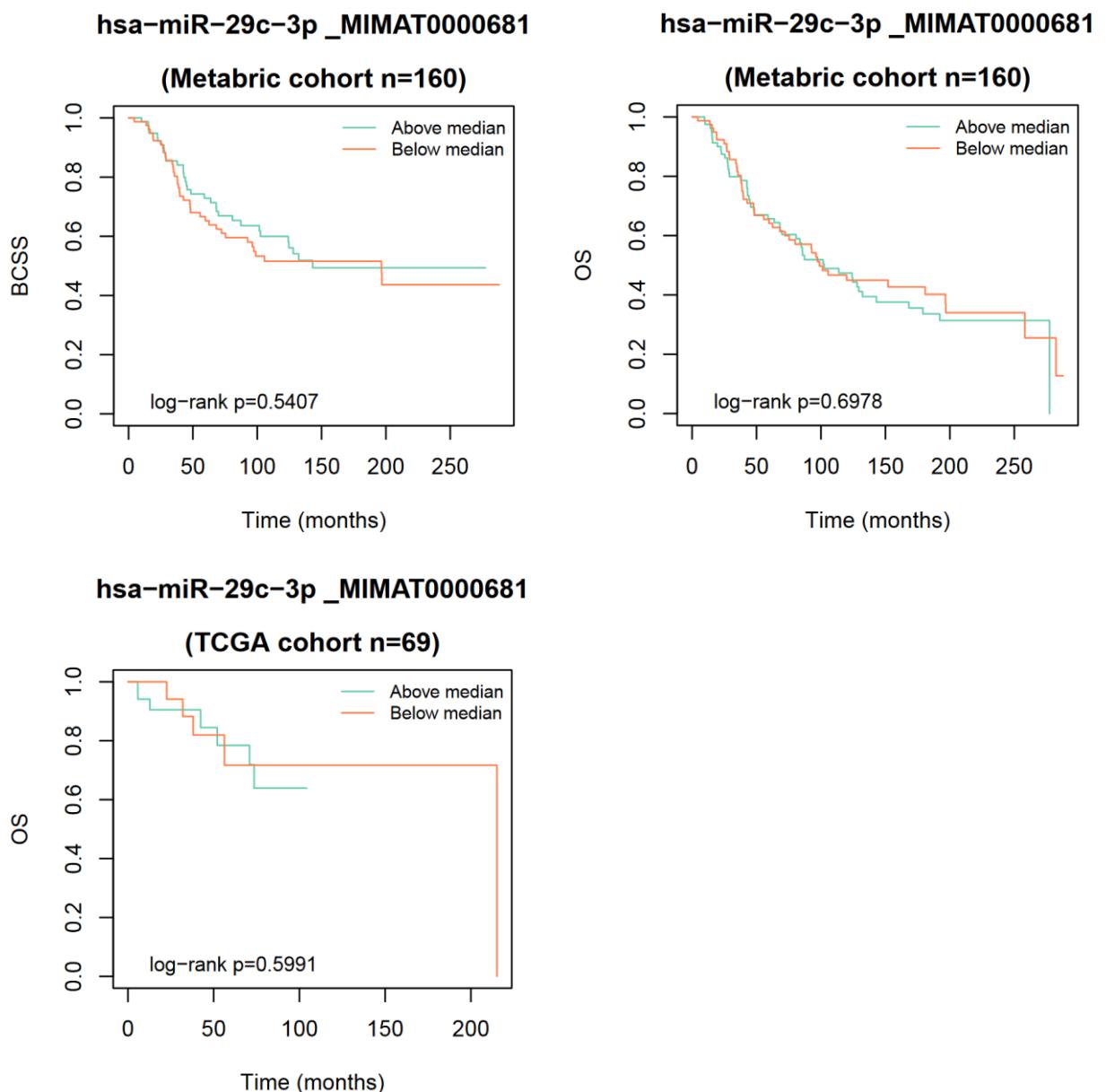
The survival curves are prepared for HER2+ breast cancer patients in the METABRIC ($n = 160$) and the TCGA($n = 69$) datasets. For the METABRIC data, breast cancer specific survival (BCSS) and overall survival (OS) of four miRNAs are presented (miR-101-5p (a), miR-29a-3p (b), miR29c-3p (c) and miR-744-3p (d)). For the TCGA data, OS for five miRNAs are presented (miR-101-5p (a), miR-29a-3p (b), miR29c-3p (c), miR-744-3p (d) and mir-106a-5p (e)). Log-rank p -values are significant ($p < 0.05$) only for miR-101-5p in the METABRIC dataset.

Supplementary Figure S3

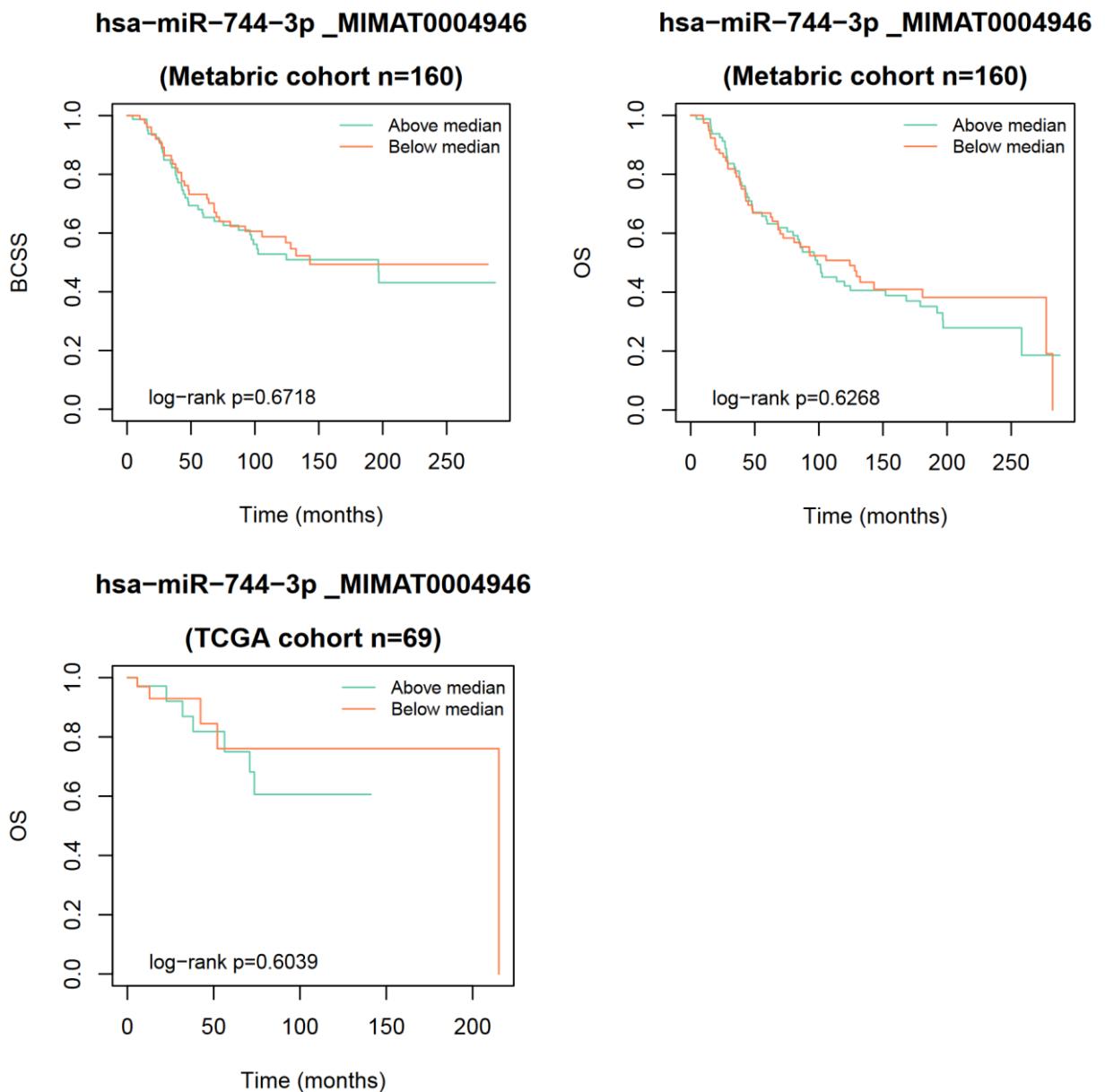
b

Supplementary Figure S3

C



Supplementary Figure S3

d

Supplementary Figure S3

e**hsa-miR-106a-5p_MIMAT0000103**

(TCGA cohort n=69)

