## Stromal cell extracellular vesicular cargo mediated regulation of breast cancer cell metastasis via Ubiquitin Conjugating Enzyme E2 N pathway

## SUPPLEMENTARY MATERIALS



Supplementary Figure 1:  $5 \times 10^5$  MDA-MB-231 cells and hMSC-EV-primed MDA-MB-231 cells were intracardially injected into nude mice. At the endpoint, mice were sacrificed and the total photon of lungs, liver, adrenals, legs, brain, and ovaries were measured, n = 8.



Supplementary Figure 2: Representative images of hematoxylin and eosin staining of tumor sections showing higher grade of tumors (arrows) in mice that received untreated cells compared with the hMSC-s-EV-primed cancer cells.



**Supplementary Figure 3:** (A) Schematic overview of the in silico procedures used to shortlist the miRNAs in metastasis. The experimental approach used to validate the shortlisted miRNAs is also depicted. (B) The panel of 36 miRNAs that have a known role in metastasis.

miR-99a

5sRNA

18sRNA

**RNU6-2** 

SNORD68

miR-9

miR-34c

miR-379

miR-497

miR-517a



**Supplementary Figure 4: Microarray clustering analysis of GEO datasets.** A heat map was generated for the 27 genes out of 281 that were significantly up- or downregulated in the metastatic sublines compared with parental cells (MDA-MB-231).



Supplementary Figure 5: Real- time PCR data showing the significant down-regulation of the target genes upon expression of miR-205 and miR-31 by lentiviral transductions.





**Supplementary Figure 6:** (A) Schematic representation of the UBE2N 3'-UTR with binding sites for miR-205 and miR-31 and sequence alignment of predicted miR-205 and 31 binding sites on UBE2N 3'-UTR. Complementary sequences of miR-205 and 31 to mammalian UBE2N 3'-UTR are shaded red. (B) MDA-MB-231, 231-BM, 231-BrM, and 231-LM cells were treated with hMSC-EVs, and the UBE2N/Ubc13 levels were measured by RT-PCR.