

Figure S1. Relative miRNA-302b levels in the four *in vivo* groups. Data are presented as mean and SD of all tumors from each mice group.

Figure S2. Western Blot analysis of Integrin Subunit Alpha 6 (ITGA6) protein expression in mice tumors treated with miR-302b mimic alone and cel-miR-67 alone. Upper figure shows specific ITGA6 bands and vinculin bands as housekeeping; lower histogram represents ITGA6 densitometric quantification.

Figure S3. BT549 cell count after small interfering-ITGA6 (si-ITGA6) transfection and cisplatin treatment compared with their negative controls. Data are representative of three independent experiments performed at least by triplicate (* $p \leq 0.05$ Student's *t* test).

Figure S4. Venn diagram showing the overlap of enriched Transcription Factors (TFs) whose binding sites are overrepresented in the promoter of the differentially expressed genes in *in vivo* assay (miR-302b+cisplatin *versus* cel-miR-67 negative control+cisplatin). Identification of enriched transcription factors using oPOSSUM and PASTAA algorithms.

Figure S5. Densitometric protein quantifications of figure 7 performed with QuantiyOne tool.

Figure S6. Correlation matrix of Yin Yang 1 (YY1) and human TFs in TNBC cases of ITAL-MEX and TCGA cohorts computed by Spearman correlation. Purple areas indicate strong positive correlation. Only genes with a significant correlation (BH adjusted $p < 0.05$) were colored.

Figure S7. Normalized expression profiles of E2F/ITAG6/YY1 *axis on* TCGA and METABRIC cohorts.

Table S1: Gene expression profiles of in-vivo assay evaluated by microarray analysis

Table S2: Summary of the TFs in silico analysis including oPOSSUM, PASTAA and miRwalk results

Table S3: Summary of in-silico JASPAR analysis of the selected TFs.