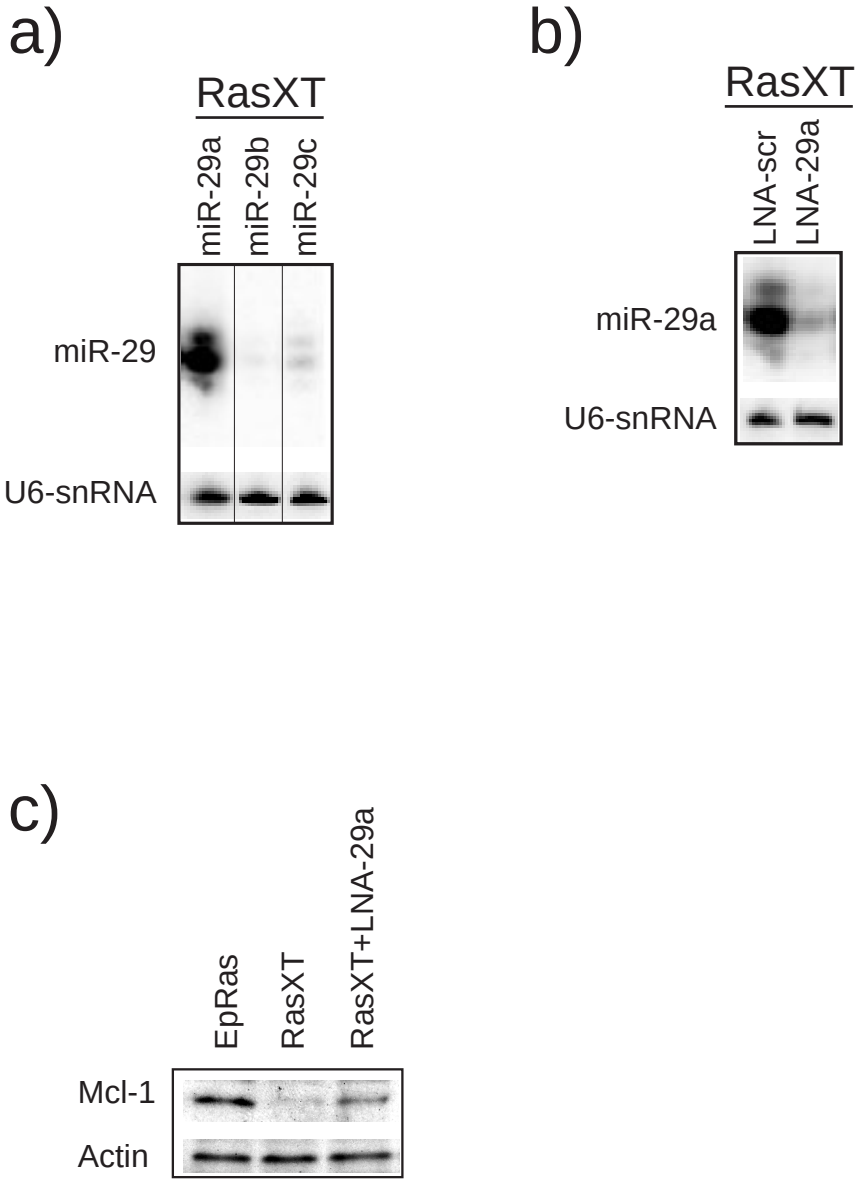
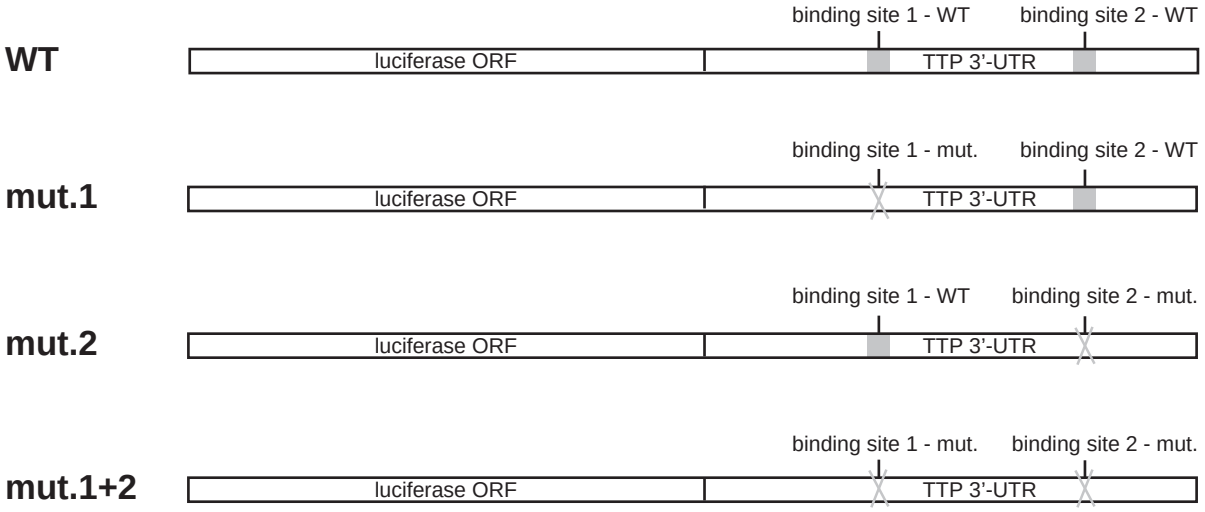
Gebeshuber et al., Figure S1



a)



b)

TTP 3'-UTR binding site 1

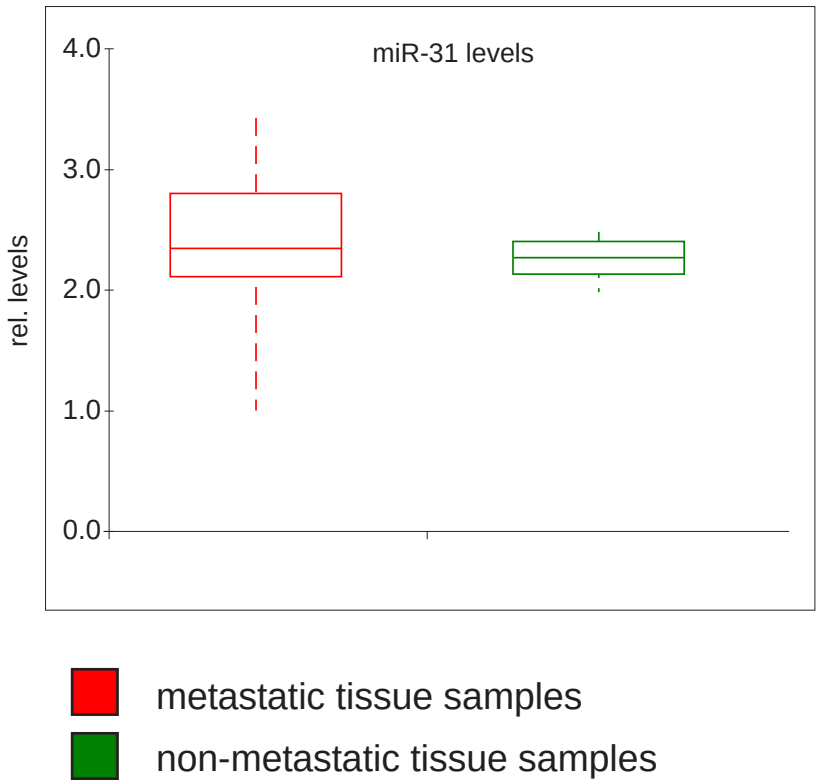
```
miR-29a   3' AUUGGCUAAAGUCUACCACGAU 5'
WT        5' AUAACCCAUUUCCCUGGUGCUG 3'
mut.      5' AUAACCCAUUUCCCUGGUCGUG 3'
```

TTP 3'-UTR binding site 2

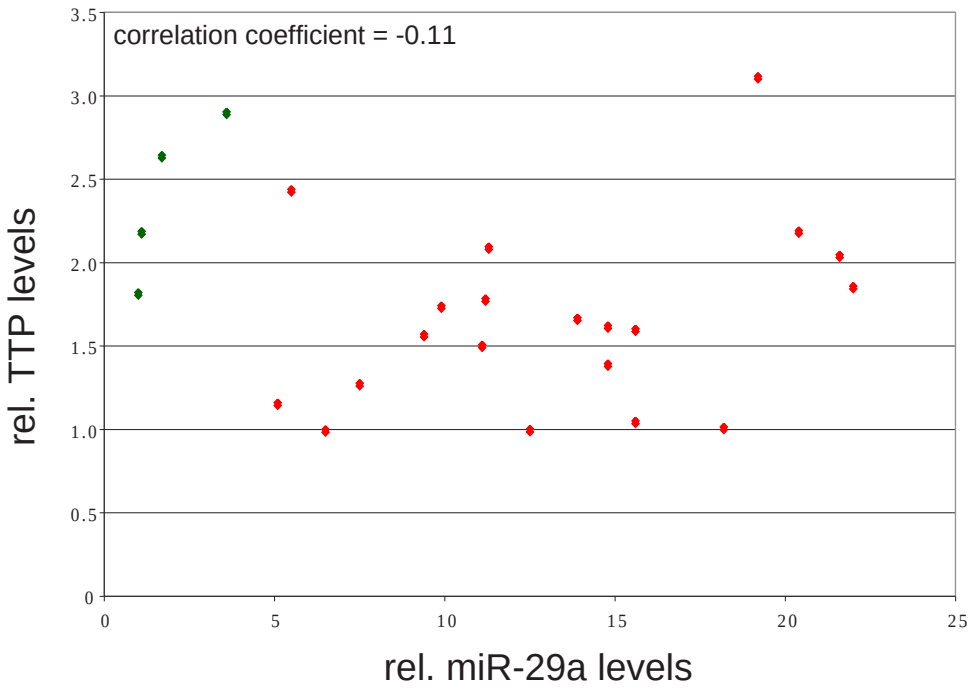
```
miR-29a   3' AUUGGCUAAAGUCUACCACGAU 5'
WT        5' UCUCCUGAGAAUCCUGGUGCUC 3'
mut.      5' UCUCCUGAGAAUCCUGGUCGUC 3'
```

Gebeshuber et al., Figure S3

a)



b)



Supplementary Figure legends

S1a) Northern blot analysis using total RNA extracted from RasXT cells was performed to monitor the expression levels of miR-29a, miR-29b and miR-29c. The relative expression of miR-29b and miR-29c was much weaker than that of miR-29a. Thus, for this study we focused on miR-29a.

S1b) Northern blot analysis using total RNA extracted from RasXT cells transfected with LNA-scr or LNA complementary to miR-29a was performed to monitor the expression levels of miR-29a.

S1c) Western blot analysis using whole cell extracts of RasXT cells transfected with LNA-scr or LNA complementary to miR-29a (LNA-29a) was performed to monitor the expression of Mcl-1. EpRas cells are shown as a control. Expression of the anti-apoptotic protein Mcl-1 - a known target for the miR-29 family - was enhanced upon transfection of LNA complementary to miR-29a potentially counteracting tumour-suppressive effects.

Therefore, the finding that inhibition of miR-29a does not reduce metastasis is not unexpected and might be a consequence of up-regulation of Mcl-1 and other oncogenic miR-29 targets.

S2a) Constructs used for the reporter gene assay (Fig. 2) are shown.

S2b) The putative binding sites for miR-29a within the sequence of the TTP 3'-UTR are depicted. The underlined region represents the seed of miR-29a, the grey background indicates perfect matches, the white background mismatches.

S3a) Total RNA was extracted from patient samples with invasive breast carcinomas (red) or non-invasive hyperplasias (green). Levels of miR-31 were determined in a padlock assay followed by detection with a ^{32}P-labelled probe. Results are shown as a box plot.

S3b) Scatter plot depicting relative miR-29a and TTP levels in individual human breast cancer patient samples.

Supplement Table 1

sample ID	sex	type	ER	PR
65	F	DC, I	neg	neg
68	F	DC, I	neg	neg
176	F	DC, I	low	med
200	F	DC, I	n.d.	n.d.
216	F	DC, I	high	low
240	F	DC, I	n.d.	n.d.
249	F	DC, I	n.d.	n.d.
278	F	DC, I	n.d.	n.d.
285	M	DC, I	low	low
319	F	DC, I	neg	neg
326	F	DC, I	neg	neg
409	F	DC, I	low	low
425	F	DC, I	low	low
426	F	DC, I	low	low
648	F	DC, I	low	low
771	F	DC, I	neg	neg
925	F	DC, I	med	med
967	F	DC, I	high	high
1308	F	DC, I	n.d.	n.d.
3375	F	DC, I	neg	neg
11374	F	MH, NI	n.d.	n.d.
12018	F	MH, NI	n.d.	n.d.
13025	F	MH, NI	n.d.	n.d.
13215	F	MH, NI	n.d.	n.d.

legend

DC: ductal carcinoma
I: invasive
MH: mamma hyperplasia, benign
NI: non-invasive
ER: estrogen receptor levels
PR: progesterone receptor levels
n.d.: not determined