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Correction to: Sunitinib-suppressed miR-452-5p facilitates renal cancer cell invasion and metastasis through modulating SMAD4/SMAD7 signals

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Following publication of the original article [1], a minor error was identified in the images presented in Fig. 1; specifically:

Fig. 1F: incorrect image used for representative image of invasive cells induced by transfection of miR-452-5p in OSRC-2 with treatment of 10 μ M Sunitinib (top left image); the image has been corrected.

The corrected figure is given here. The correction does not have any effect on the results or conclusions of the paper.

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(See figure on next page.)

Fig. 1 Sunitinib abrogates RCC cell invasion and metastasis via depressing miR-452-5p. a Presented are heatmap of the most differentially expressed miRNAs in peripheral blood under Sunitinib treatment (GSE32099) and between tumor tissue and pair-matched normal tissues(GSE37 989). b The above analysis showed 10 miRNAs were significantly differentially expressed both in GSE32099 and GSE37989. c qRT-PCR assays for miR-452-5p expression with 0, 5 and 10 µM Sunitinib treatment in OSRC-2 and SW839 cells. **d-e** Representative micrographs of wound-healing assay and decrease in wound width was induced by transfection of miR-452-5p in OSRC-2 and SW839 cells versus miR-NC cells with treatment of 10 µM Sunitinib. f-g Representative images and number of invasive cells per high-power field was induced by transfection of miR-452-5p in OSRC-2 and SW839 cells versus miR-NC cells with treatment of 10 μ M Sunitinib. h Orthotopic xenograft animal models were generated using miR-452-5p or miR-NC in OSRC-2 cells and mice treated with 10 µM Sunitinib. Presented are representative images (left) of abdominal metastasis viewed by IVIS system in each group 4 weeks after the orthotopic xenograft transplantation (n=8) and Quantitation of metastasis nodules shown at right. i Incidence of metastasis in orthotopic xenografts after 4 weeks. j TCGA cohort analysis of the differentially expressed levels of miR-452-5p in RCC tumor samples and pair-matched normal tissues. Each dot represents one sample. k Comparison of miR-452-5p expression in 20 paired RCC tumor tissues and adjacent normal tissues via qRT-PCR. I Relative miR-452-5p expression levels in RCC samples are presented as fold change=2(\Delta Ct normal-ΔCt tumor) of tumor versus matched normal tissues, 85% of which was upregulated in tumor tissues than adjacent normal tissues. **m** miR-452-5p expression in a series of RCC cell lines (SW839, A498, SN12-PM6 and OSRC-2) and human normal renal tubular epithelial cell line HK-2. n ROC analysis to assess the specificity and sensitivity of miR-452-5p to differentiate between RCC and normal tissues. • Kaplan–Meier analyses of the correlations between miR-452-5p expression level and overall survival of 806 patients with RCC through TCGA analysis. The median expression level was used as the cutoff. Data shown are mean \pm S.D. *p<0.05, **p<0.01

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