Xie *et al. Molecular Cancer* (2023) 22:173
https://doi.org/10.1186/s12943-023-01881-0

Molecular Cancer

CORRECTION

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Correction: CircSMARCC1 facilitates tumor progression by disrupting the crosstalk between prostate cancer cells and tumor-associated macrophages via miR-1322/CCL20/CCR6 signaling

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Correction: Mol Cancer 21, 173 (2022)
https://doi.org/10.1186/s12943-022-01630-9

Following publication of the original article [1], the authors requested to update the figures as stated below.

- We request to replace the misused image in C4-2 cells (sh-circ group) in Fig. 3H with the correct image which produced in May 26, 2021 when we conducted the experiment.
- We request to replace the misused images in C4-2 cells in Fig. 4J with the correct images which produced in June 2, 2021 when we conducted the experiment.
- We request to replace the misused image in the C4-2-sh-nc-CM group in Fig. 7F with the correct image which produced in April 14, 2021 when we conducted the experiment.
- We request to replace the misused image in the THP-1-Mø-CM group in Fig. 7H with the correct image which produced in June 3, 2021 when we conducted the experiment.

Published online: 23 October 2023

Reference

1. Xie T, Fu Dj, Li Zm, et al. CircSMARCC1 facilitates tumor progression by disrupting the crosstalk between prostate cancer cells and tumor-associated macrophages via miR-1322/CCL20/CCR6 signaling. Mol Cancer. 2022; 21: 173. https://doi.org/10.1186/s12943-022-01630-9.

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The original article can be found online at https://doi.org/10.1186/s12943-022-01630-9.

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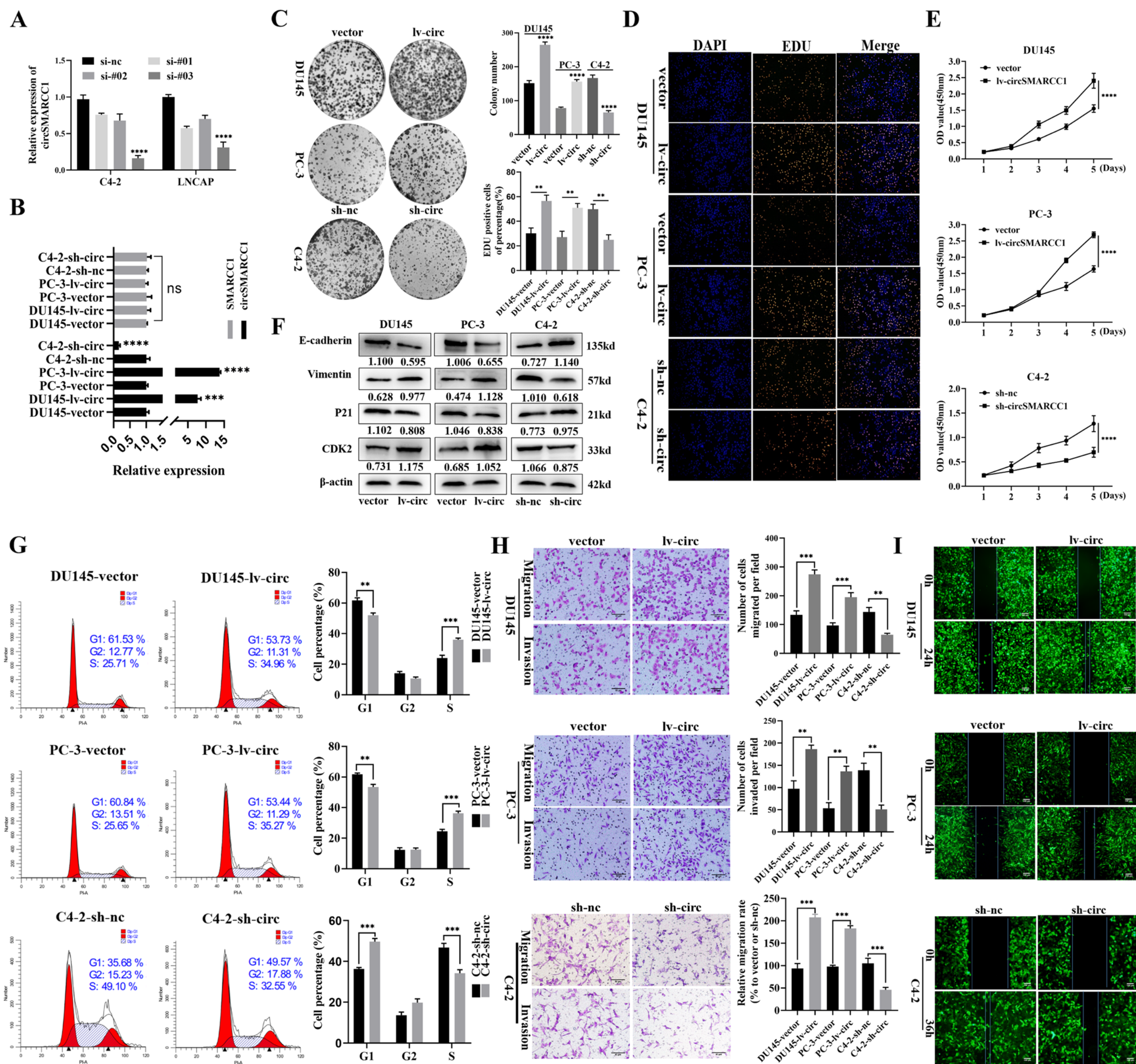

Fig. 3 CircSMARCC1 promotes proliferation, migration and invasion of PCa cells. **A** three siRNAs (si-#01,02,03) targeting circSMARCC1 were constructed to silence its expression and confirmed by qRT-PCR. **B** The relative expression of circSMARCC1 and SMARCC1 in PCa cells transfected with circSMARCC1 overexpressing or knockdown lentivirus by qRT-PCR. **C**-**E** Assessment of cell proliferation capacity by colony formation, EdU assay (scale bar, 100 μm) and CCK-8 assay. **F** Western blot analysis evaluated expression of cell cycle-associated proteins and EMT biomarkers following overexpression or knockdown of circSMARCC1. **G** Flow cytometric analysis of changes in the cell cycle profile of PCa cells stably transfected with circSMARCC1. **H**, **I** Transwell assays and wound healing assays assessed the migration and invasion abilities of PCa cells stably transfected with circSMARCC1 (Scalebar, 50 μm). The data are presented as the mean ± SD, ***p* < 0.01, ****p* < 0.001, *****p* < 0.0001

(See figure on next page.)

Fig. 4 CircSMARCC1 acts as a sponge for miR-1322 and miR-1322 reverses the oncogenic effects of circSMARCC1 on proliferation, invasion and migration in PCa cells. **A** Schematic diagram of circSMARCC1 luciferase reporter vectors carrying wild-type (Wt) or mutant (Mut) miR-1322 binding sites. **B** Luciferase reporter assay to analyze the effects of 9 candidate miRNAs on the luciferase activity of circSMARCC1. **C** The RNA pull-down assay performed in DU145 cells using circSMARCC1 and negative control probes. **D** The relative expression of miR-1322 in PCa cells after transfection of circSMARCC1 was detected by qRT-PCR. **E** The relative luciferase activities measured in 293 T cells co-transfected with circSMARCC1-Wt or circSMARCC1-Mut and miR-1322 mimics or miR-nc by luciferase reporter assay. **F** The co-localization of circSMARCC1 and miR-1322 observed using RNA-FISH in DU145 cells (scale bar, 5 μm). The nuclei were stained with DAPI. **G-I** The viability of PCa cells in miR-1322 rescue experiments was analyzed by colony formation assay, EdU assay (scale bar, 100 μm) and CCK8 assay, respectively. **J**, **K** The migration and invasion capacity of PCa cells in the miR-1322 rescue experiment was analyzed by transwell assays (scale bar, 50 μm) and wound healing (scale bar, 100 μm) assays. The data are presented as the mean ± SD, *$p < 0.05$, **$p < 0.01$, ***$p < 0.001$, ****$p < 0.0001$

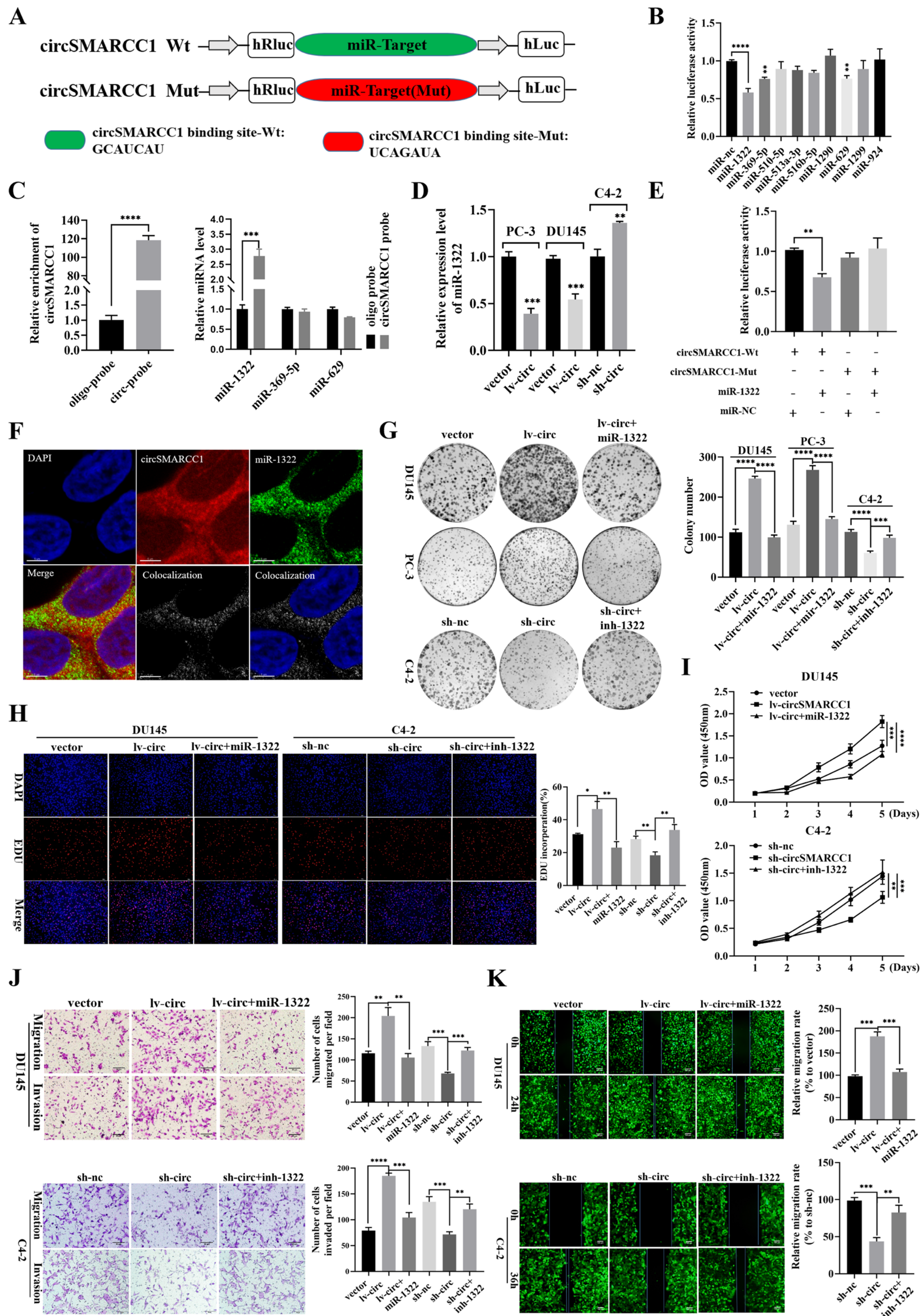

Fig. 4 (See legend on previous page.)

(See figure on next page.)

Fig. 7 circSMARCC1 promotes M2 macrophage polarization and recruitment via the CCL20-CCR6 axis. **A** IHC detected the infiltration of $CD68^+$/ $CD163^+$/ $CD206^+$ macrophages in human PCa tissue and Para-cancerous tissues (scale bar, 100 μm and 20 μm). **B** IHC detected the infiltration of $CD68^+$/ $CD163^+$/ $CD206^+$ macrophages in mouse xenograft tumors (scale bar, 100 μm and 20 μm). **C**, **D** The expression of M1 phenotype (TNF-a, CD80 and CD86) and M2 phenotype (IL-10, ARG-1 and CD163) markers were detected by qRT-PCR in THP-1 cells, THP-1-Mø and THP-1-M2 cells. **E** The proportion of CD68 and CD163 positive cells detected by flow cytometry. **F** The CM prepared from lv-circSMARCC1 or vector and sh-circSMARCC1 or sh-nc tumor cells was used to evaluate the migration ability of macrophages through transwell experiments (scale bar, 50 μm). **G** The migration ability of TAM was detected by transwell assay using CCL20 recombinant protein and CCR6 neutralizing antibody (scale bar, 50 μm). **H** The CM prepared from THP-1-Mø or THP-1-M2 cells for PCa cells migration experiments (scale bar, 50 μm). **I**, **J** qRT-PCR tested the expression of M2 phenotypes marker (IL-10, ARG-1, CD68 and CD163) when co-cultured with DU145-lv-circSMARCC1 cells or vector cells or using CCL20 recombinant protein, with IL-4 and IL-3 polarization as the reference. **K** The expression of CD68, CD163 and CCR6 in THP-1 cells, THP-1-Mø cells stimulated by CCL20 recombinant protein, and THP-1-Mø cells (with and without co-culture) were detected by Western blotting. **L** The expression of CD68, CD163 and CCR6 in THP-1-Mø cells and THP-1-M2 cells (with and without anti-CCR6) were detected by Western blotting. $^*p < 0.05$, $^{**}p < 0.01$, $^{***}p < 0.001$, $^{****}p < 0.0001$.

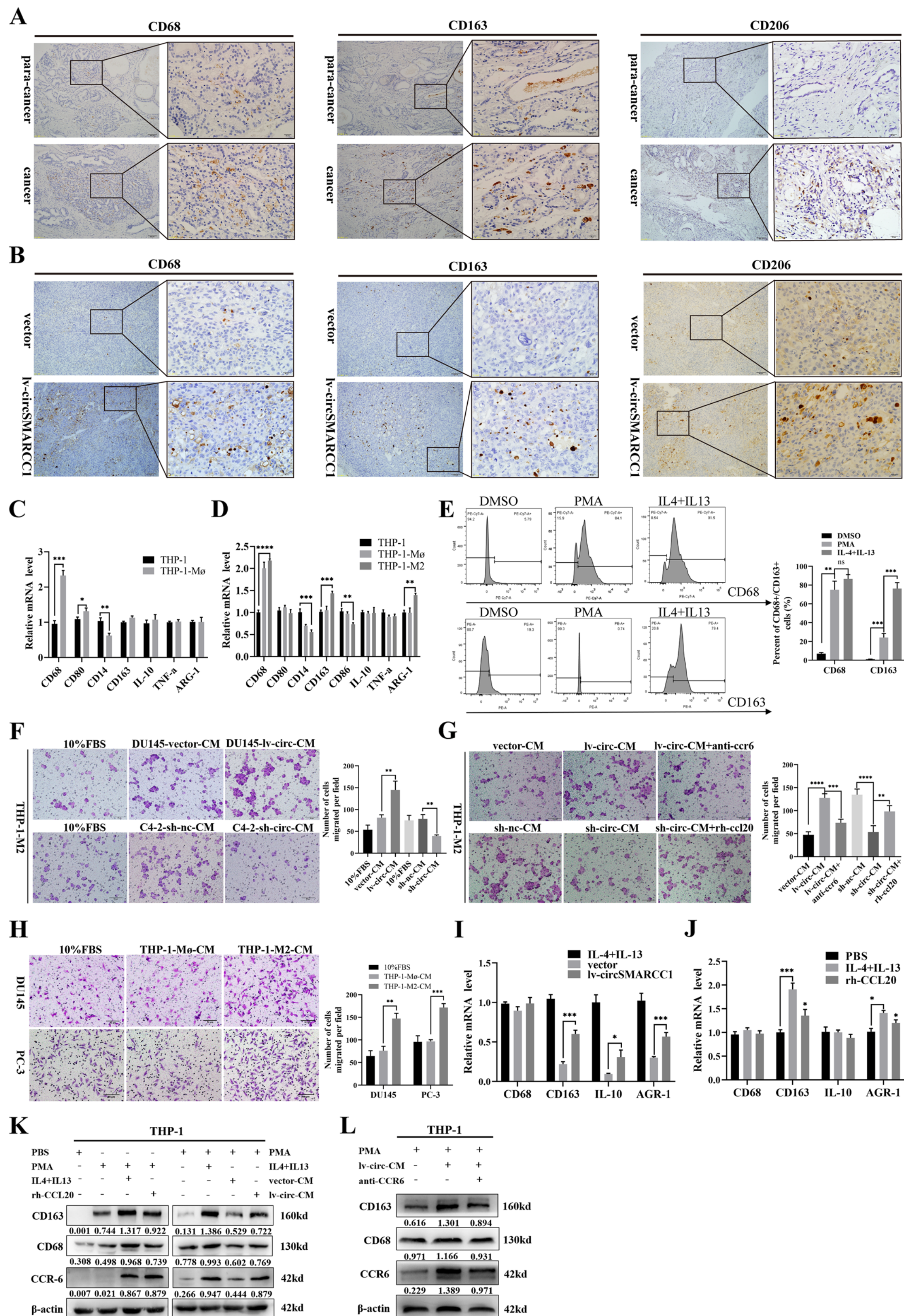

Fig. 7 (See legend on previous page.)