

CORRECTION

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# Correction: PAX6 promotes neuroendocrine phenotypes of prostate cancer via enhancing MET/STAT5A mediated chromatin accessibility

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**Correction:** *J Exp Clin Cancer Res* 43, 144 (2024)  
<https://doi.org/10.1186/s13046-024-03064-1>

Following publication of the original article [1], an incorrect spelling was spotted in Fig. 6h of the published article. The tumor sample grouping as “PAX6 + shSTAT5A” should be corrected to “shPAX6 + STAT5A”.

Furthermore, errors were also spotted in the Supplementary Materials:

1. Supplement material 1: In the a-panel of Figure S3, the authors omitted to mark the significant difference of the qPCR result and now have added it according to the description in the text.

2. The “Additional information” file of this paper should be deleted because it is not the final version of the supporting data.
3. Supplement material 1: In the h-panel of Figure S5, the authors misspelled the name of the tumor sample grouping as “PAX6 + shSTAT5A”. The correct spelling should be “shPAX6 + STAT5A”.
4. Supplementary material 6 should be deleted because it is the response figure which is included in our response to the reviewers’ comments for argument and is also partially repeated to the supplementary material 1.
5. Supplementary material 7 should be deleted because it is actually the supplementary figure S7 and its relevant figure legend which have been included in the supplementary material 1.

The corrections do not affect the overall result or conclusion of the article. The original article has been corrected.

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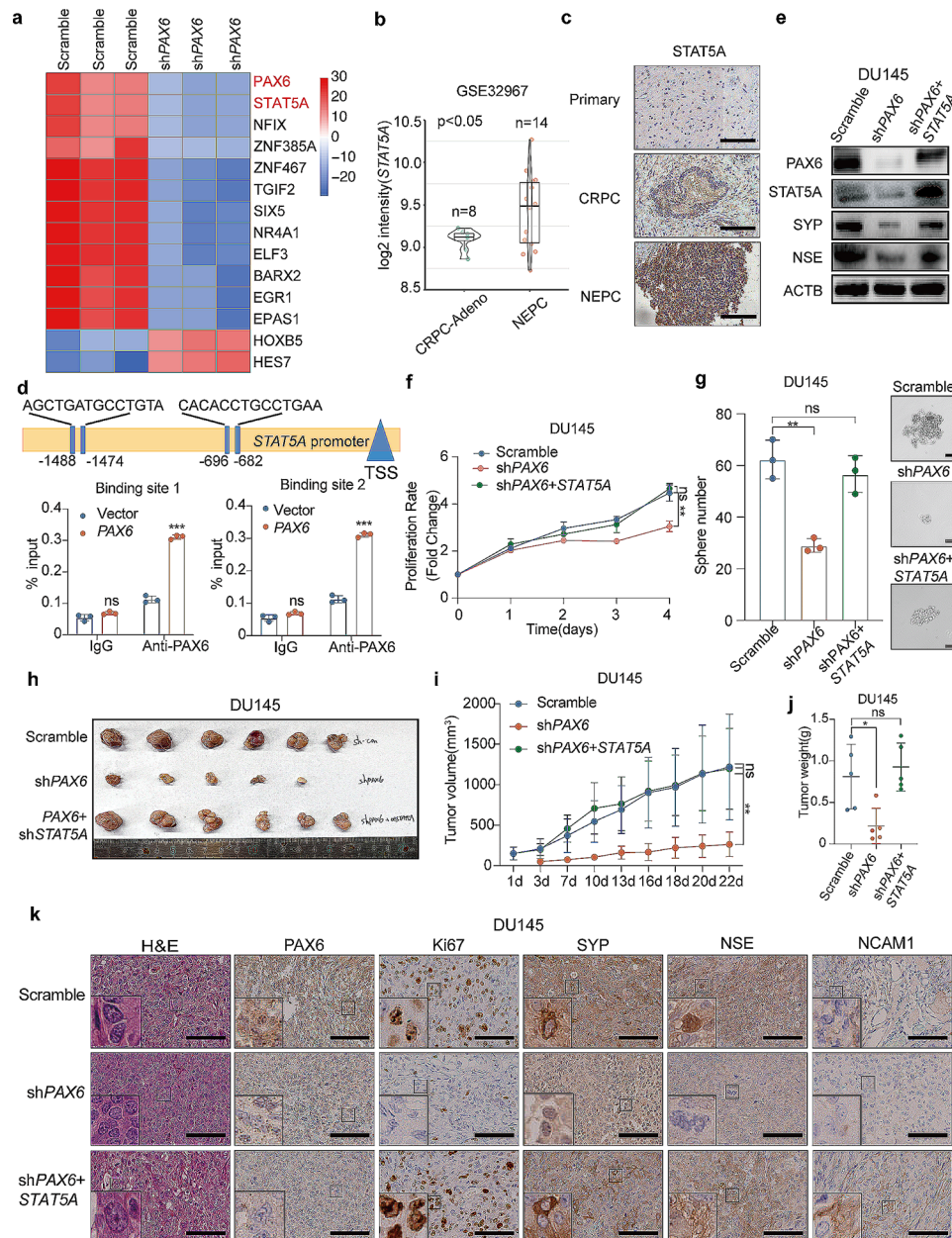
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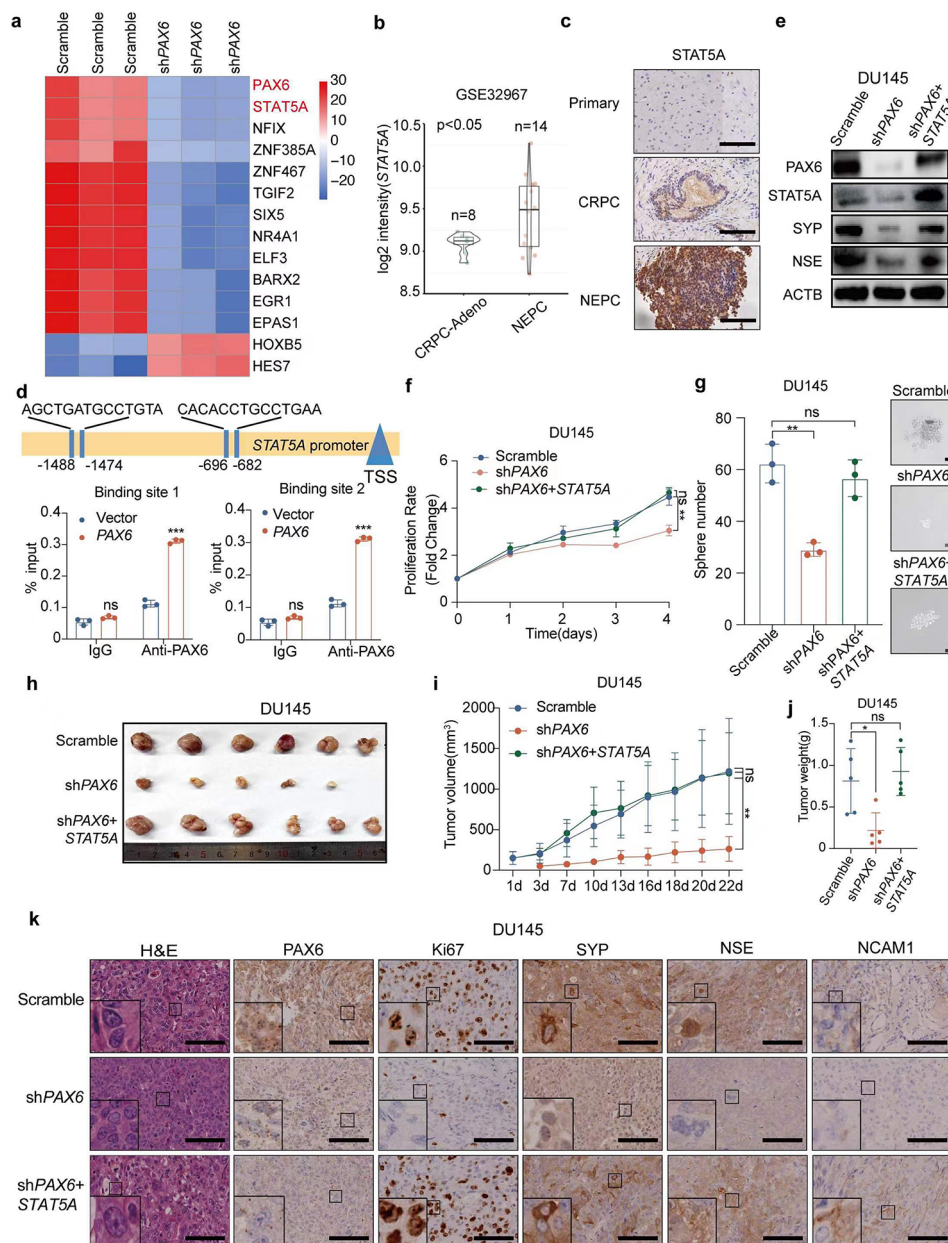


Incorrect Figure 6



**Fig. 6** PAX6 promotes NE characteristics via STAT5A. **a** The heatmap of candidate TFs with significant expressional difference in DU145-shPAX6 cells and DU145-Scramble cells. **b** Comparisons of *STAT5A* mRNA expression in CRPC-Adeno vs. NEPC based on the GSE32967 dataset (CRPC-Adeno, n=8; NEPC, n=14). **c** Representative IHC staining of *STAT5A* in tissues from patient with Primary PCa, CRPC or NEPC (Scale Bar: 100 μm). **d** ChIP assay of PAX6 binding at the promoter region of *STAT5A* in LNCaP-PAX6 cells. **e** Protein expression of PAX6, *STAT5A*, SYP and NSE in DU145-shPAX6 cells with or without *STAT5A* overexpression. **f** Cell proliferation assay in DU145-shPAX6 cells with or without *STAT5A* overexpression. **g** Representative image and quantification assay of tumorsphere formation in DU145-shPAX6 cells with or without *STAT5A* over-expression. **h** Anatomic tumor images and tumor weight analysis of DU145-shPAX6 cells inoculated xenografts with or without *STAT5A* overexpression (n=6). **i** Tumor volume analysis of DU145-Scramble, DU145-shPAX6 or DU145-shPAX6+*STAT5A* cells inoculated xenografts respectively (n=6). **j** Tumor weights analysis of DU145-shPAX6 and DU145-shPAX6+*STAT5A* cells inoculated xenografts respectively (n=6). **k** Representative staining H&E and IHC staining of PAX6, Ki67, SYP, NSE, NCAM1 in DU145-shPAX6 and DU145-shPAX6+*STAT5A* cells inoculated xenograft samples (Scale Bar: 100 μm, with the boxed region enlarged and shown on the left, n=6). All the experiments were repeated for three times. Data represents the mean ± SD. ns: no significance, \*p < 0.05, \*\*\*p < 0.001

Correct Figure 6



**Fig. 6** *PAX6* promotes NE characteristics via *STAT5A*. **a** The heatmap of candidate TFs with significant expressional difference in DU145-shPAX6 cells and DU145-Scramble cells. **b** Comparisons of *STAT5A* mRNA expression in CRPC-Adeno vs. NEPC based on the GSE32967 dataset (CRPC-Adeno,  $n=8$ ; NEPC,  $n=14$ ). **c** Representative IHC staining of *STAT5A* in tissues from patient with Primary PCa, CRPC or NEPC (Scale Bar: 100  $\mu$ m). **d** ChIP assay of PAX6 binding at the promoter region of *STAT5A* in LNCaP-PAX6 cells. **e** Protein expression of PAX6, *STAT5A*, SYP and NSE in DU145-shPAX6 cells with or without *STAT5A* overexpression. **f** Cell proliferation assay in DU145-shPAX6 cells with or without *STAT5A* overexpression. **g** Representative image and quantification assay of tumorsphere formation in DU145-shPAX6 cells with or without *STAT5A* over-expression. **h** Anatomic tumor images and tumor weight analysis of DU145-shPAX6 cells inoculated xenografts with or without *STAT5A* overexpression ( $n=6$ ). **i** Tumor volume analysis of DU145-Scramble, DU145-shPAX6 or DU145-shPAX6+*STAT5A* cells inoculated xenografts respectively ( $n=6$ ). **j** Tumor weights analysis of DU145-shPAX6 and DU145-shPAX6+*STAT5A* cells inoculated xenografts respectively ( $n=6$ ). **k** Representative staining H&E and IHC staining of PAX6, Ki67, SYP, NSE, NCAM1 in DU145-shPAX6 and DU145-shPAX6+*STAT5A* cells inoculated xenograft samples (Scale Bar: 100  $\mu$ m, with the boxed region enlarged and shown on the left,  $n=6$ ). All the experiments were repeated for three times. Data represents the mean  $\pm$  SD. ns: no significance, \* $p < 0.05$ , \*\*\* $p < 0.001$

## Supplementary Information

The online version contains supplementary material available at <https://doi.org/10.1186/s13046-024-03084-x>.

Supplementary Material 1

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## References

1. Jing N, Du X, Liang Y, et al. PAX6 promotes neuroendocrine phenotypes of prostate cancer via enhancing MET/STAT5A-mediated chromatin accessibility. *J Exp Clin Cancer Res.* 2024;43:144. <https://doi.org/10.1186/s13046-024-03064-1>.

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