

Supplementary Figure legends:

Figure S1:

S1A: IHC results of pan-lysine lactylation based on TMA.

S1B: IHC results of H3K18la based on TMA.

S1C: Correlation between pan-lysine lactylation and H3K18la IHC scores for each sample based on TMA.

S1D: IHC results of H3K9la based on TMA.

S1E: Correlation between pan-lysine lactylation and H3K9la IHC scores for each sample based on TMA.

S1F: IHC results of H4K12la based on TMA.

S1G: Correlation between pan-lysine lactylation and H4K12la IHC scores for each sample based on TMA.

S1H and S1I: H4K12la IHC staining in PTC samples stratified by T stage (S1H) and N stage (S1I).

Figure S2:

S2A: IHC results of H3K18ac based on TMA.

S2B and S2C: H3K18ac IHC staining in PTC samples stratified by T stage (S2B) and N stage (S2C).

S2D: IHC results of H3K18cr based on TMA.

S2E and S2F: H3K18cr IHC staining in PTC samples stratified by T stage (S2E) and N stage (S2F).

Figure S3:

S3A: Proliferation levels of PTC cell lines following treatment with 2-DG and Shikonin.

S3B and S3C: Invasion levels of PTC cell lines following treatment with 2-DG and Shikonin.

S3D: Levels of H3K18la following EP300 knockdown.

S3E: mRNA and protein expression levels of EP300 in PTC cell lines after treatment with 2-DG and Shikonin.

S3F: Levels of H3K18la following KAT2A knockdown.

Figure S4:

S4A: Lactate production rate in PTC cell lines following treatment with 2-DG and Nala.

S4B: Proliferation levels of PTC cell lines following treatment with 2-DG and Nala.

S4C and S4D: Invasion levels of PTC cell lines following treatment with 2-DG and Nala.

S4E: Tumor images of subcutaneous xenografts in PTC cells following treatment with 2-DG and Nala.

Figure S5:

S5A: IHC results of H3K18la in subcutaneous PTC xenografts under 2-DG and Nala treatment;

S5B: IHC results of STAT1 in subcutaneous PTC xenografts under 2-DG and Nala treatment;

S5C: Dual-luciferase reporter assay showing suppressed STAT1 promoter activity under 2-DG treatment;

S5D: IHC results of STAT1 based on TMA.

Figure S6:

S6A: Proliferation levels of PTC cell lines with Sh-STAT1 and after Nala treatment;
S6B and S6C: Invasion levels of PTC cell lines with Sh-STAT1 and after Nala treatment.

Figure S7:

S7A: Proliferation levels of PTC cell lines with OE-STAT1 and after 2-DG treatment;
S6B and S6C: Invasion levels of PTC cell lines with OE-STAT1 and after 2-DG treatment.

Figure S8:

S8A: Expression levels of STAT family members other than STAT1 in PTC tumor tissues compared to p-tumor tissues based on the TCGA database.

S8B: Protein expression levels of STAT family members other than STAT1 in PTC cell lines compared with normal thyroid epithelial cells.

Figure S9:

S9A: IHC results of STAT1 in subcutaneous xenograft tumors derived from PTC cells with Sh-STAT1 or OE-STAT1.

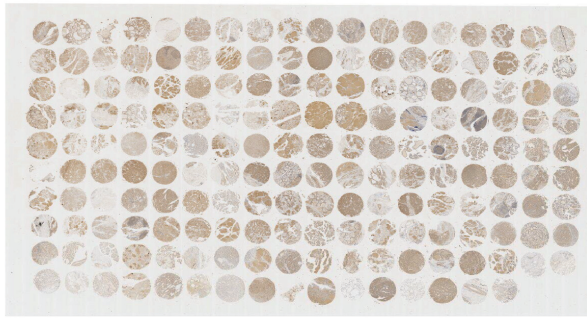
S9B: CUT&RUN-qPCR results of STAT1 binding at the GLUT1 promoter.

S9C: CUT&RUN-qPCR results of STAT1 binding at the LDHB promoter.

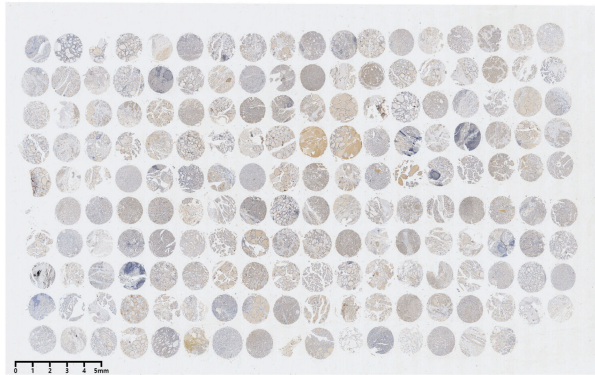
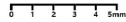
S9D: Gene co-expression analysis of STAT1 and LDHA based on the TCGA database.

S9E: Predicted potential interaction sites between STAT1 and LDHA based on AlphaFold3.

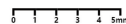
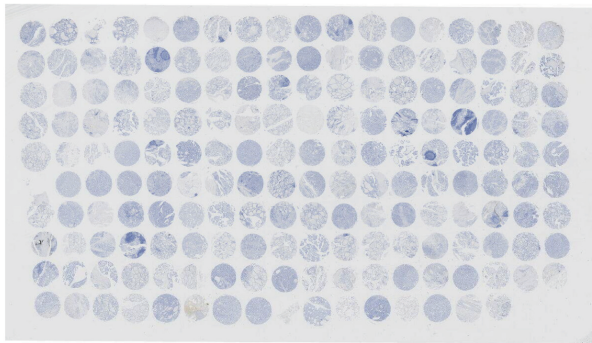
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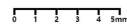
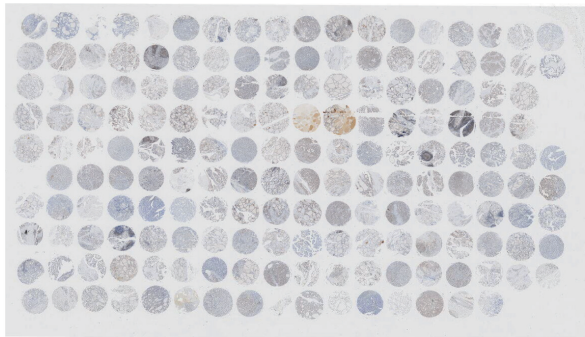
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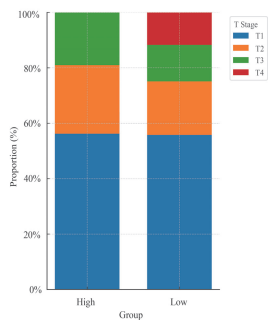
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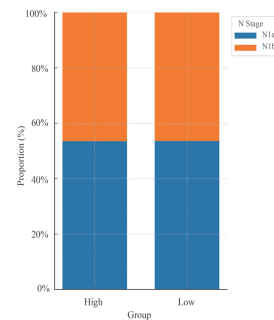
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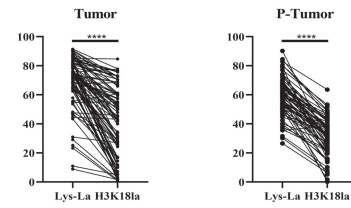
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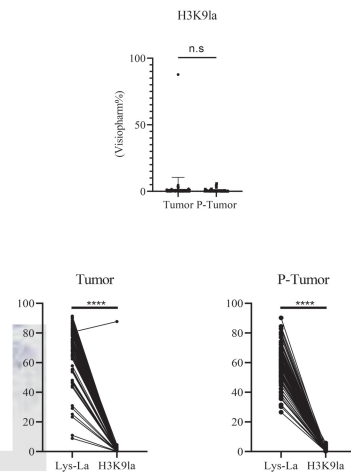
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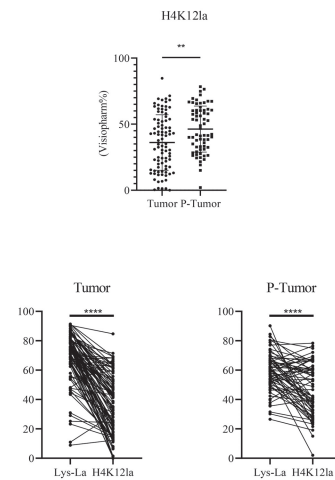
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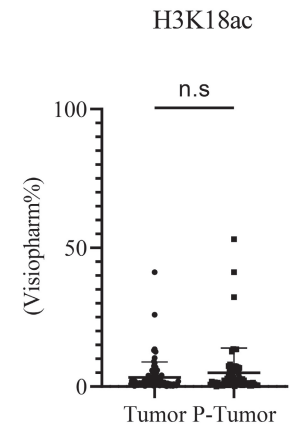
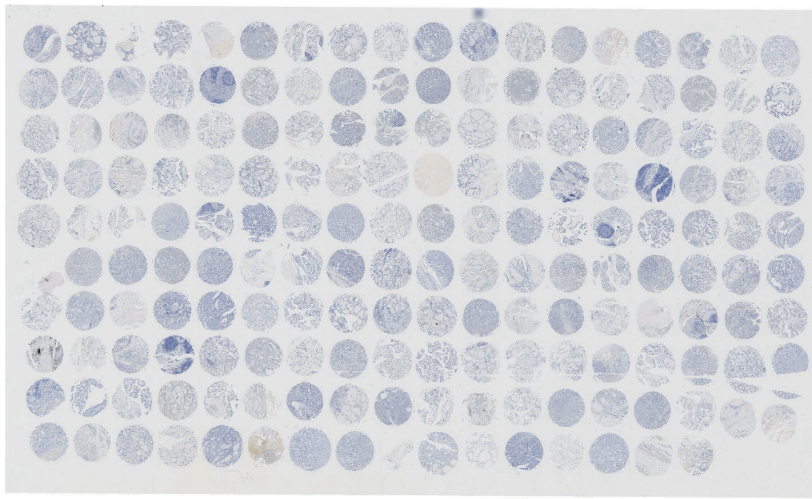
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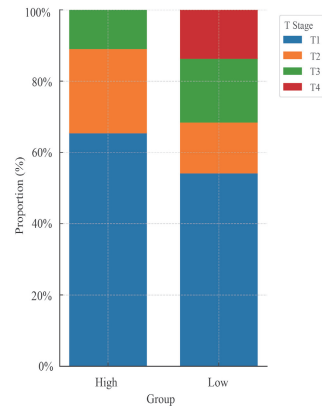


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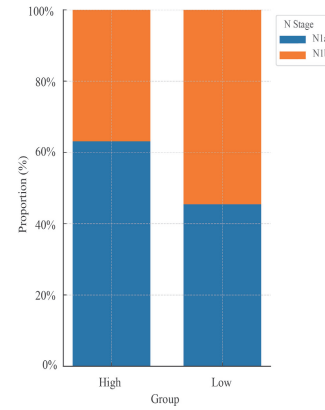


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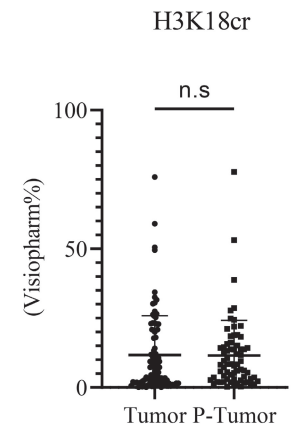
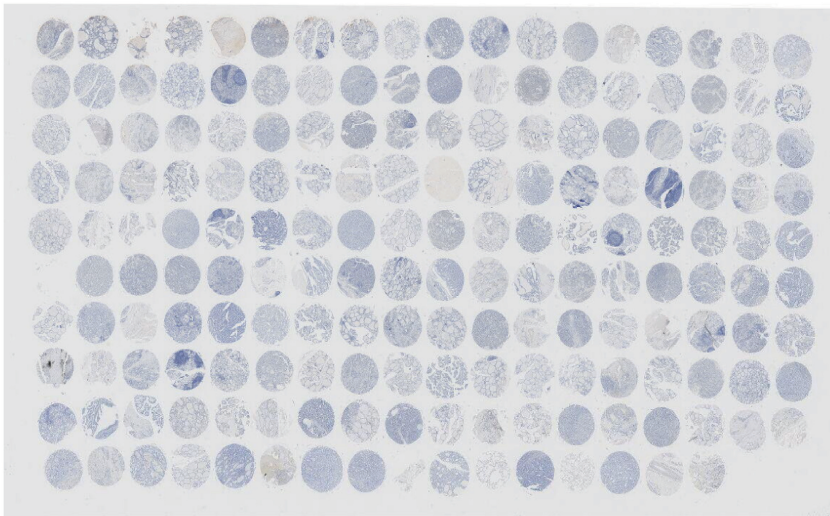
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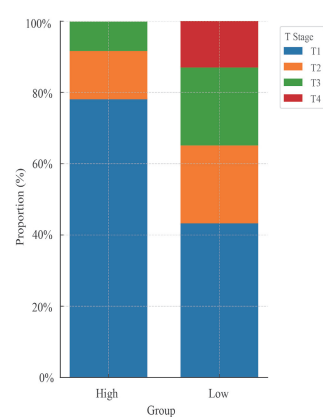


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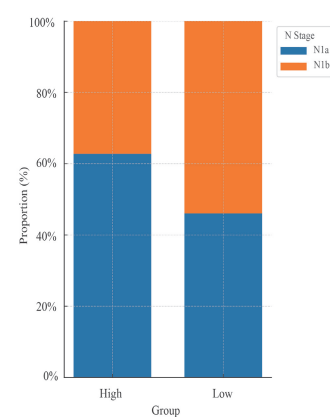


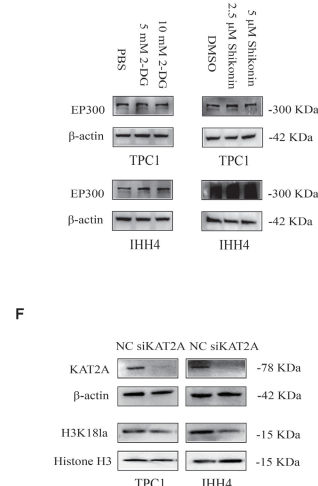
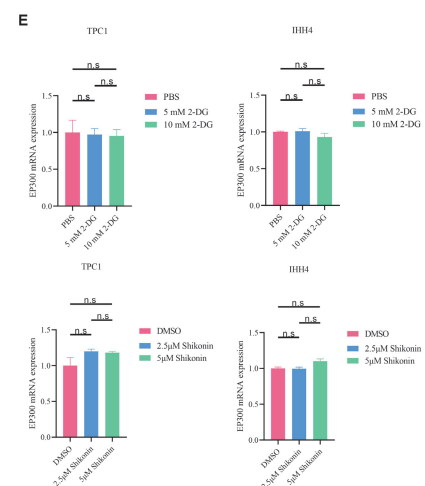
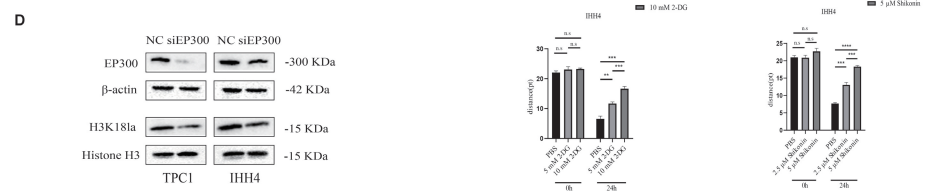
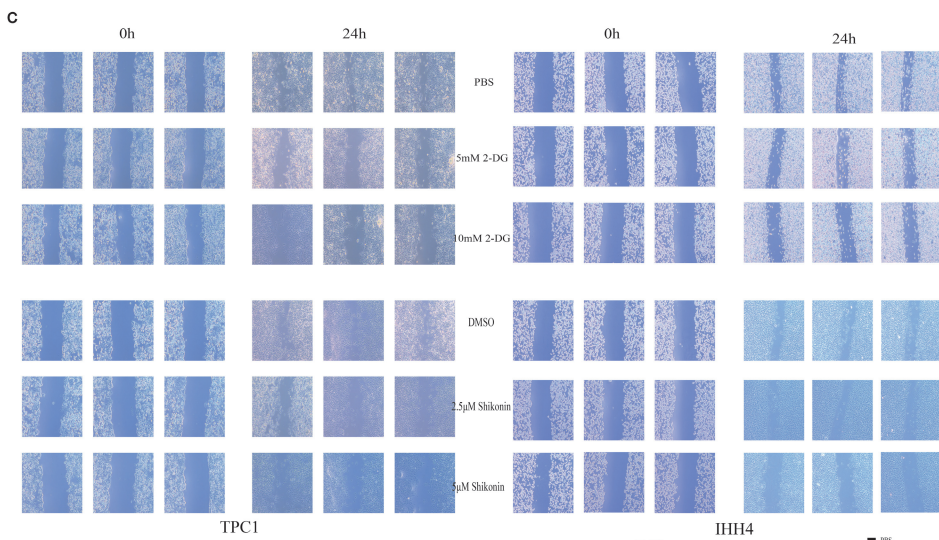
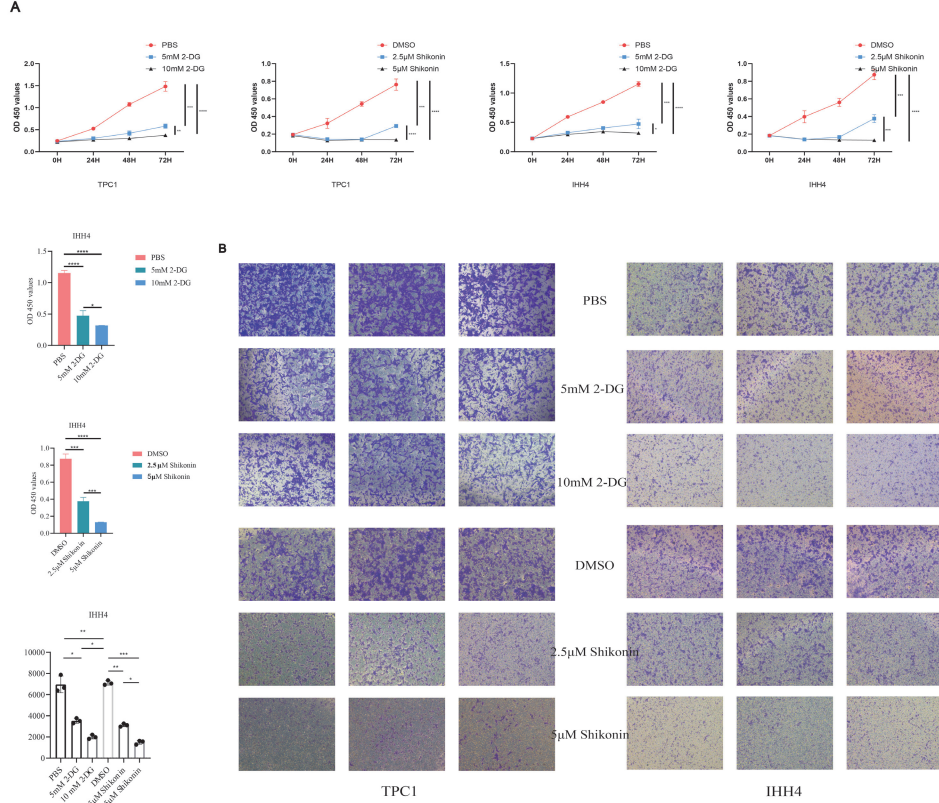
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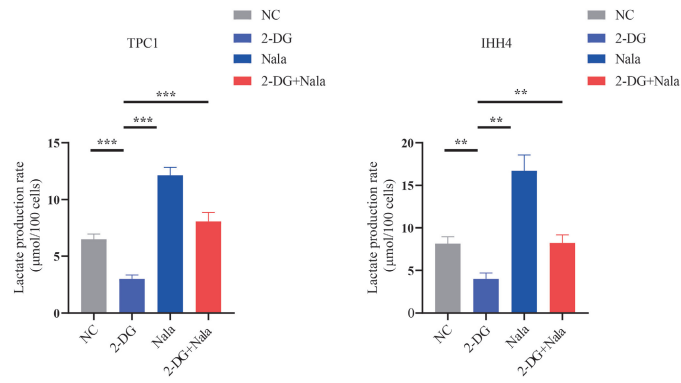


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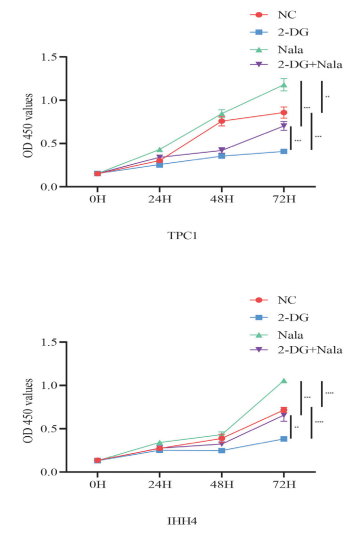




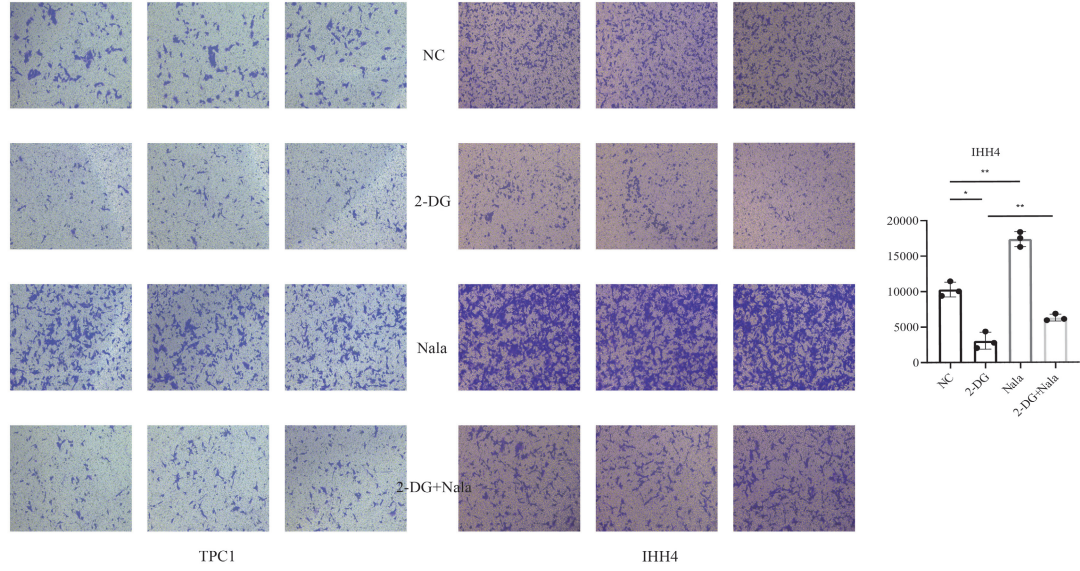
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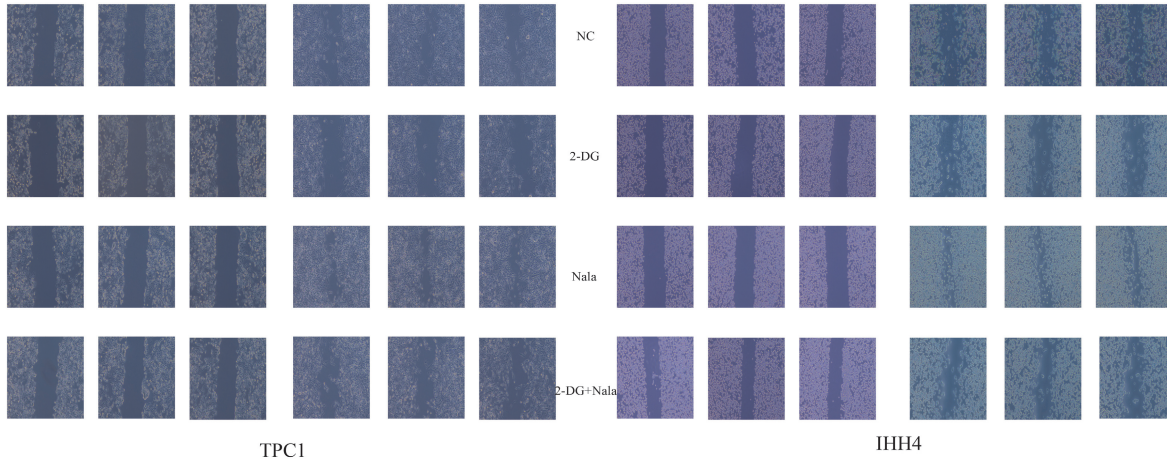
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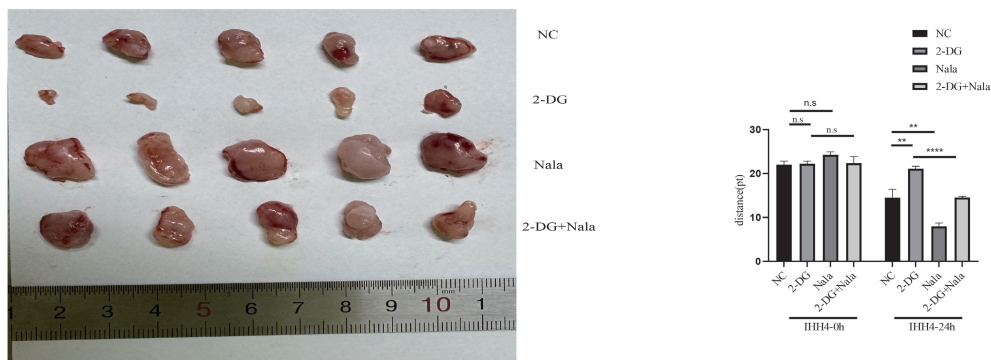
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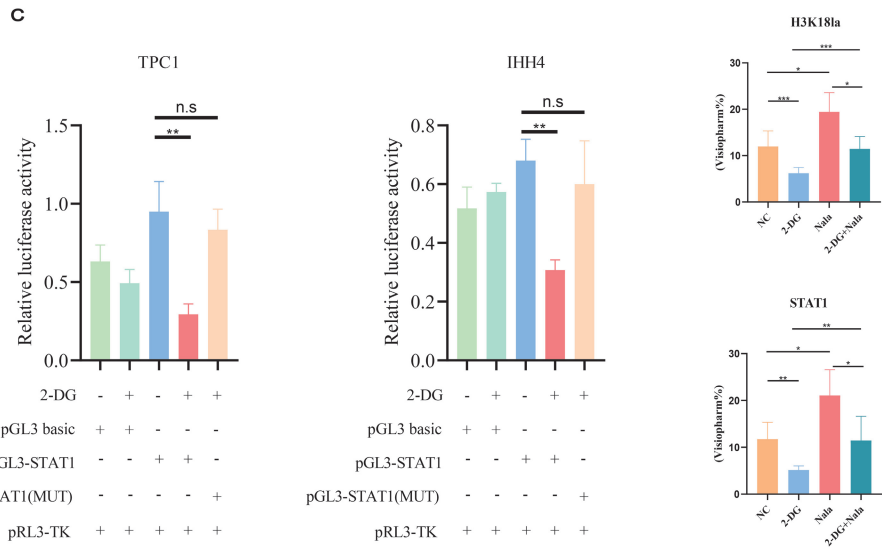
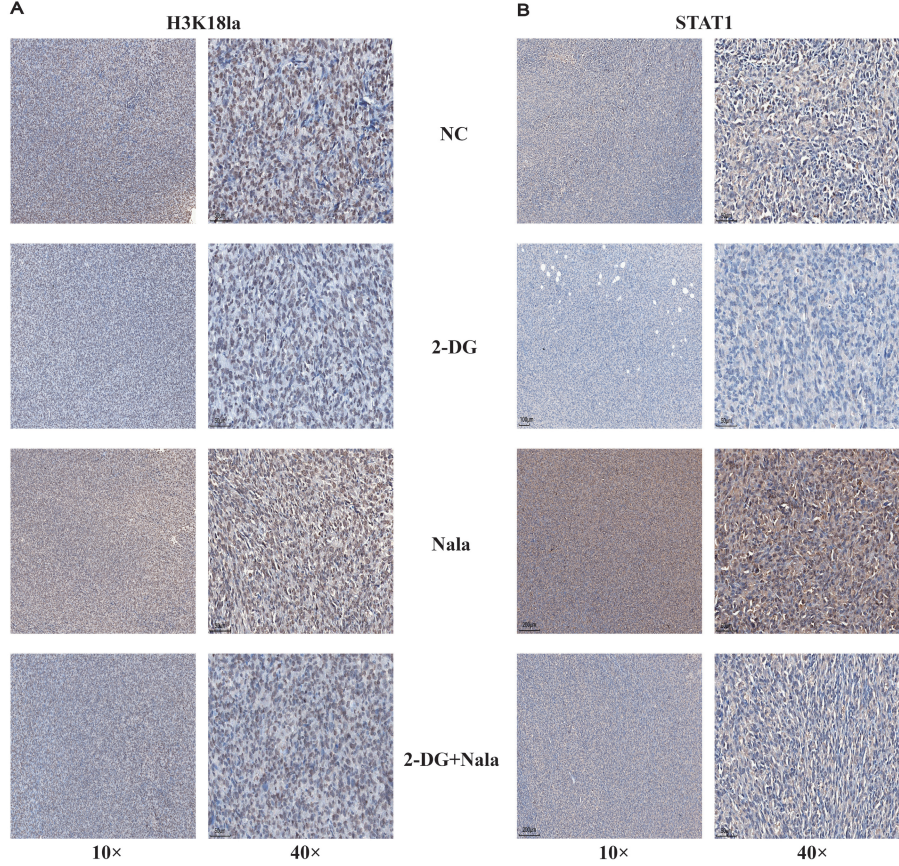


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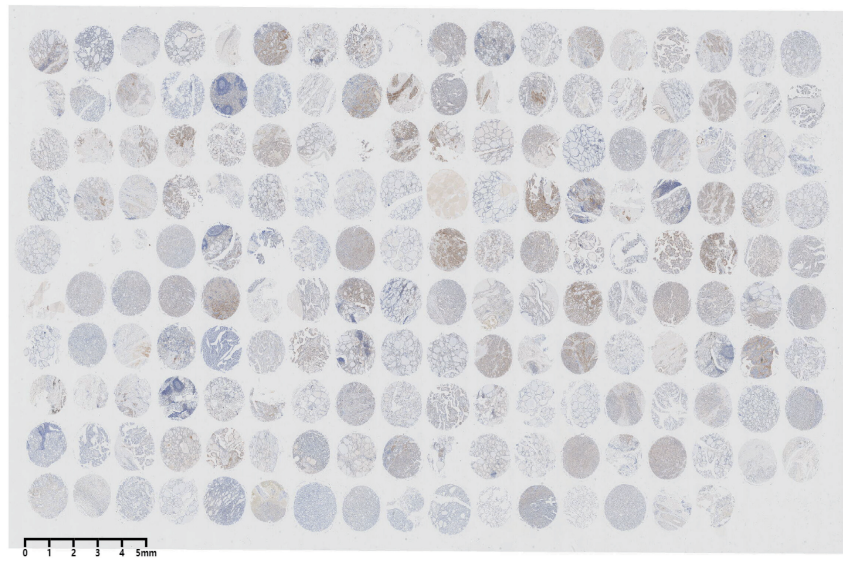


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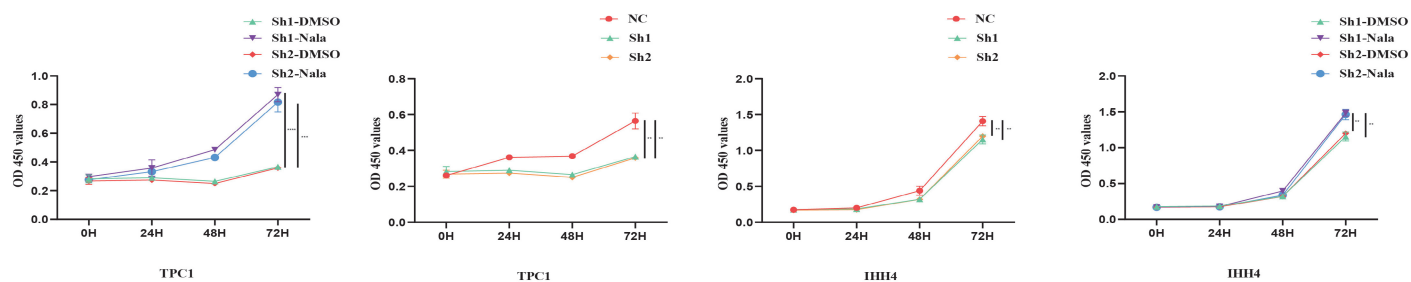




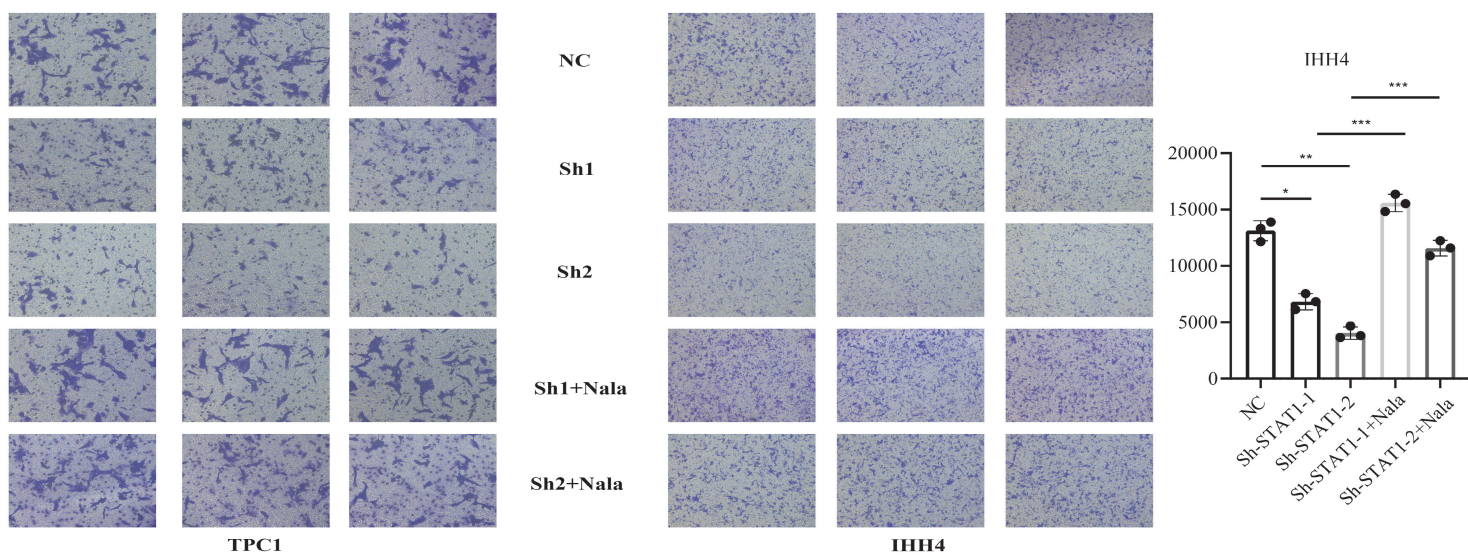
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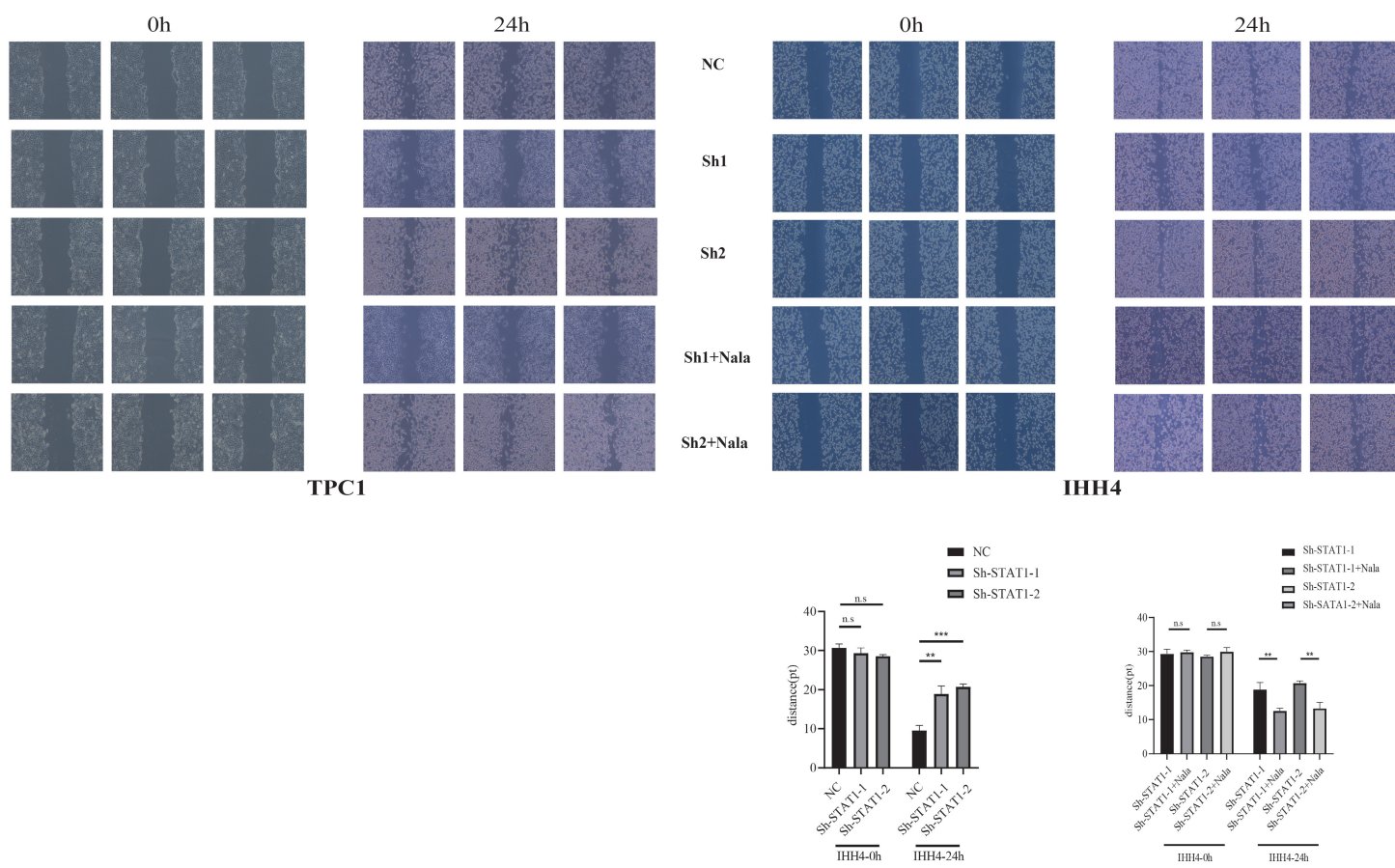
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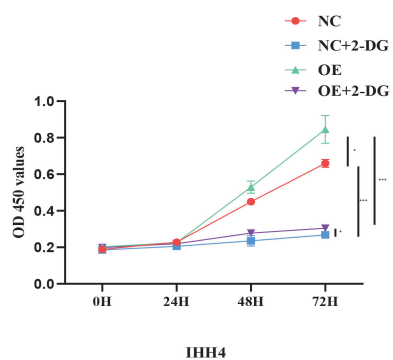
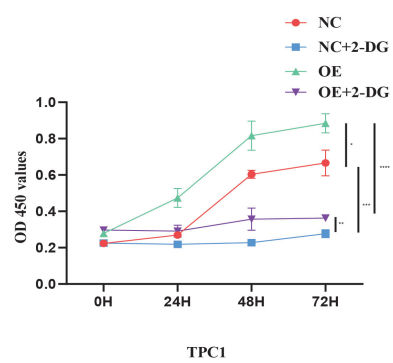
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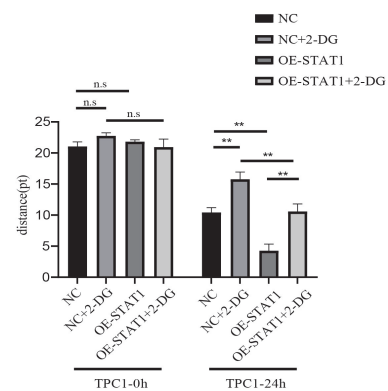
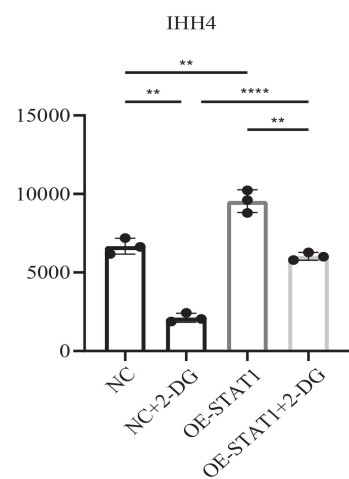
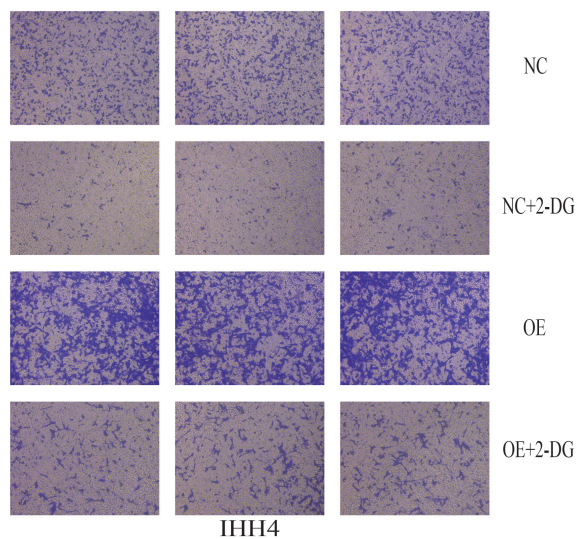
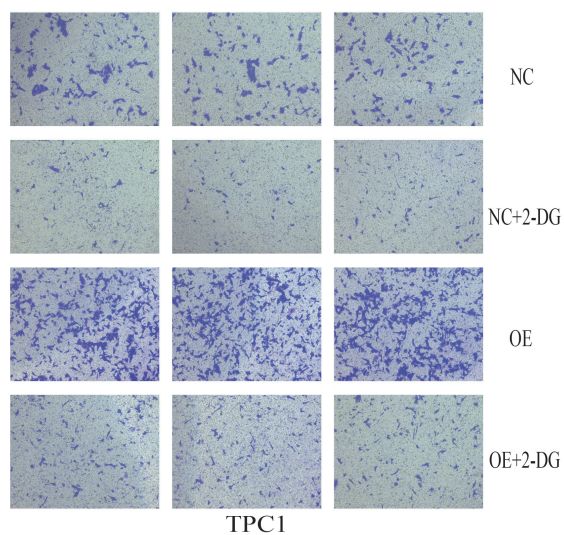
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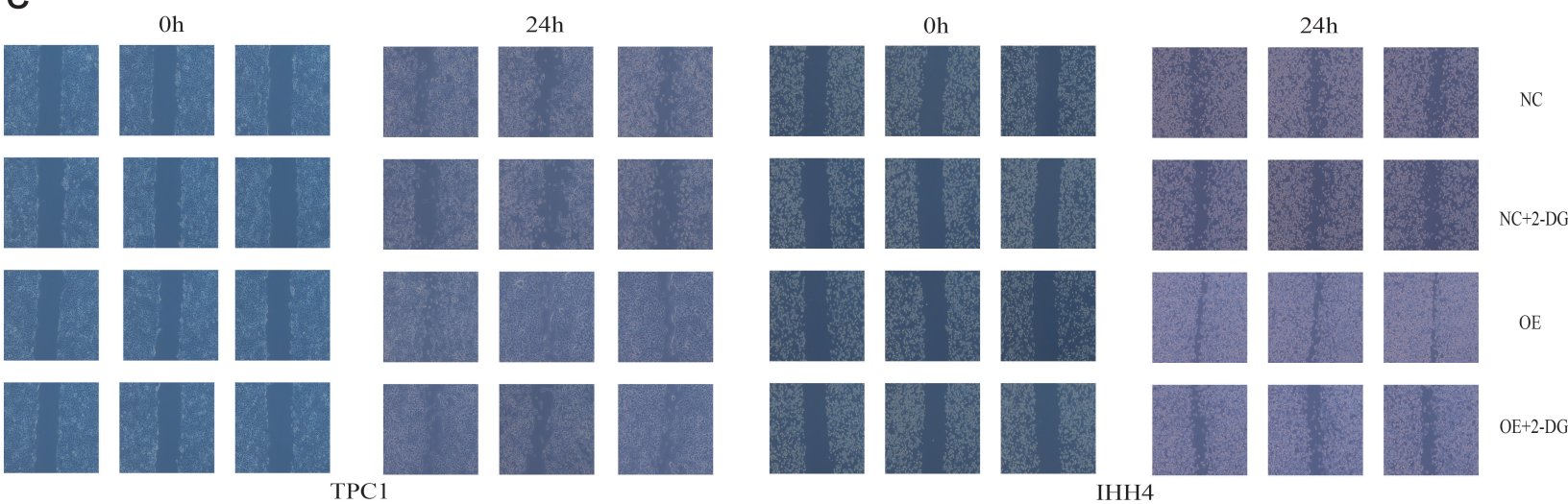
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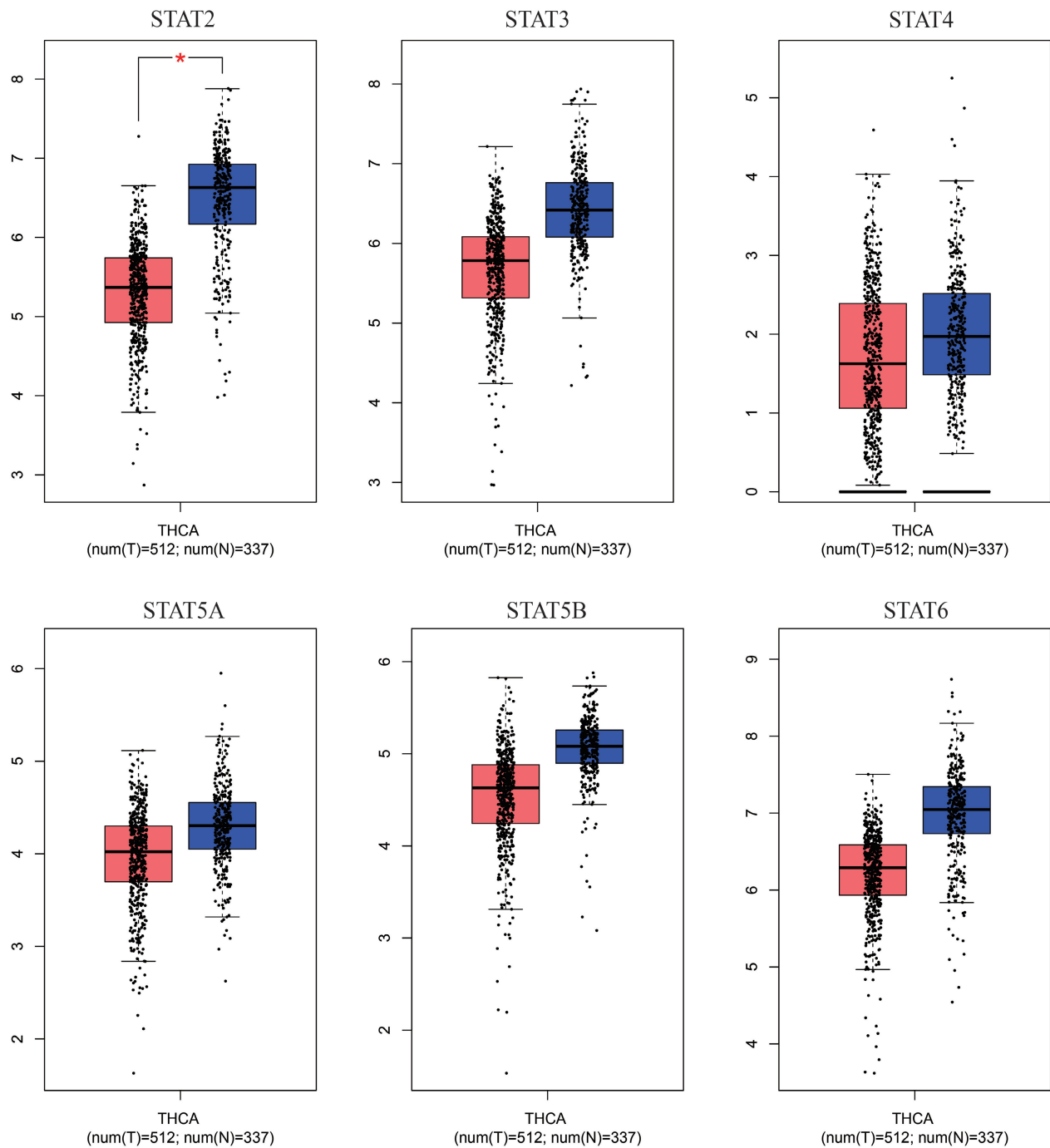


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