



22 Computational secondary structure prediction (Chimera) for HGF PAN domain identifies the  
23 residues forming  $\beta$ -strands and  $\alpha$ -helix in PAN domain.

24

25 **Supplementary Figure 2.** The 3D conformation of four reported mutation sites located in the  
26 PAN domain of HGF.

27

28 **Supplementary Figure 3. Root-mean-square deviation (RMSD) time evolution plots from**  
29 **WT and 4Cys-4Ala MD simulations.** RMSD profiles and histograms for (a) Wild-type and (b)  
30 4Cys-4Ala mutant. For both datasets, the reference structure was the initial coordinates of the top  
31 WT model. RMSDs were calculated for all heavy atoms after alignment of all Ca atoms.

32

33 **Supplementary Figure 4. Representative structures of the WT and 4Cys-4Ala PAN domain**  
34 **from MD simulations.** (Left) Ca alignment of both structures to the initial coordinates of the top  
35 WT model. (Right) Close-up of the mutation positions for the two systems. In the absence of the  
36 disulfide pairs, the 4Cys-4Ala mutant maintained near equivalent positioning of the mutated  
37 residues.

38

39 **Supplementary Figure 5. The PAN domain of HGF is necessary for c-MET activation.** (a and  
40 b). HeLa cells were stimulated with HGF WT and HGF 4Cys-4Ala and expression of the proteins

41 related to c-MET signaling were examined by immunoblotting at the indicated times.  
42 Representative blot images from n=2 experiments.

43

44 **Supplementary Figure 6. Mutations of individual cysteines in the PAN domain abrogate**  
45 **downstream c-MET signaling.** 293T cells were stimulated with purified HGF WT, HGF C70A,  
46 HGF C74A, HGF C84A and HGF C96A mutants and phosphorylation of c-MET was examined  
47 by immunoblotting at the indicated times. Representative blot images from n=2 experiments.

48

49 **Supplementary Figure 7. Transfer of the biotin-tag from HGF into c-MET.** (a) *in vitro* cross-  
50 linking of purified HGF and purified c-MET. Purified 1 ug of Flag-HGF WT or Flag-HGF 4Cys-  
51 4Ala was activated by incubating with a biotin-containing trifunctional cross-linking reagent  
52 (Sulfo-SBED from Thermo). Activated HGF was then incubated with purified His-c-MET. After  
53 UV cross-linking (15 min), Sulfo-SBED biotin label transfer to His-c-MET from Flag-HGF WT  
54 or 4Cys-4Ala were analyzed by western blotting on reducing SDS-gels using anti-His, anti-Flag,  
55 and Streptavidin-HRP as a probe. Representative image of n=3 biological replicates. (b)  
56 Quantification of His-c-MET biotinylation in (a). Streptavidin band intensities for c-MET (a, top  
57 panel) were normalized to the streptavidin band intensities for labeled HGF protein (a, middle  
58 panel) before being cross-linked c-MET. Data are represented as mean  $\pm$  SEM, \*\*\*  $p < 0.0005$   
59 (Student's t test) and  $n = 3$  biological replicates. (c) Purified biotinylated HGF 4Cys- 4Ala could  
60 not cross-link with GFP-tagged c-MET expressed in 293T cells. The cross-linked complex was

61 immunoprecipitated on Streptavidin beads, and the amount of bound GFP-c-MET was confirmed  
62 following western blot using anti-GFP as a probe.

63

64 **Supplementary Figure 8. STAT3 phosphorylation is abrogated following HGF PAN**  
65 **mutation.** HeLa cells were treated with HGF WT and HGF 4Cys-4Ala for the indicated times,  
66 and immunoblotting was performed using anti-pSTAT3. Total STAT3 and actin were used as a  
67 loading control.

68

69 **Supplementary Figure 9. HGF stimulates cell proliferation and MMP9 expression in PAN**  
70 **domain dependent manner.** (a) Mutations on the conserved cysteines in HGF PAN domain  
71 downregulate cell proliferation. 293T and U-87 MG cells were plated in 96-well plates in serum-  
72 free medium for 24 hours. HGF WT and HGF 4Cys-4Ala were added to the cells where indicated  
73 and plates were incubated for 24 h. MTT reagents were added, and the absorbance was read at 492  
74 nm. A significant increase in the proliferation for both cells were observed when treated with HGF  
75 WT (\* $p < 0.05$ ). (b) Quantitative PCR analysis for MMP9 and MET mRNA expression. 293T and  
76 U-87 MG cells were serum starved before HGF treatment. Treatment was given for 24 hours and  
77 MMP9 and MET mRNA expressions were detected by conventional RT PCR. The graph  
78 represents the relative mRNA expression normalized to GAPDH control. Data (a and b) are  
79 represented as mean  $\pm$  SD,  $n=3$  independent biological replicates and \* $p < 0.05$  (Student's t test).

80

81 **Supplementary Figure 10.** (a) MTT cell proliferation assay. 293T cells were transfected with  
82 Flag-HGF WT and Flag-HGF 4Cys-4Ala. 24 hr post transfection cells were splitted and re-plated  
83 in 96-well plates in serum-free medium for 24 hours. Plates were incubated for the indicated time.  
84 MTT reagents were added, and the absorbance was read at 492 nm. A significant increase in the  
85 proliferation for cells was observed when transfected with HGF WT (\*p<0.05). (b) Heatmap of  
86 selected genes. Heat maps displaying pattern of expression for the candidates involved in Met  
87 signaling, cell cycle and invasion. Genes are depicted based on their expression ratios across three  
88 RNA seq comparison. Colors range from bright green (upregulation; log<sub>2</sub> ratio over control) to  
89 bright red (downregulation; log<sub>2</sub> ratio over control).

90

91 **Supplementary Figure 11.** Certificate of analysis of Flag tagged HGF WT, HGF C70A, HGF  
92 C74A, HGF C84A, HGF C96A and HGF 4Cys- 4Ala proteins using SDS PAGE and Western blot.

93

94 **Supplementary Figure 12. Uncropped gel scans for all presented Western blots.** (a)  
95 corresponds to Fig. 1a; (b) corresponds to Fig. 1c; (c) corresponds to Fig. 1d; (d-e) corresponds to  
96 Fig. 2a.

97

98 **Supplementary Figure 13. Uncropped gel scans for all presented Western blots.** (a)  
99 corresponds to Fig. 2b; (b) corresponds to Fig. 2e; (c) corresponds to Fig. 3a.

100

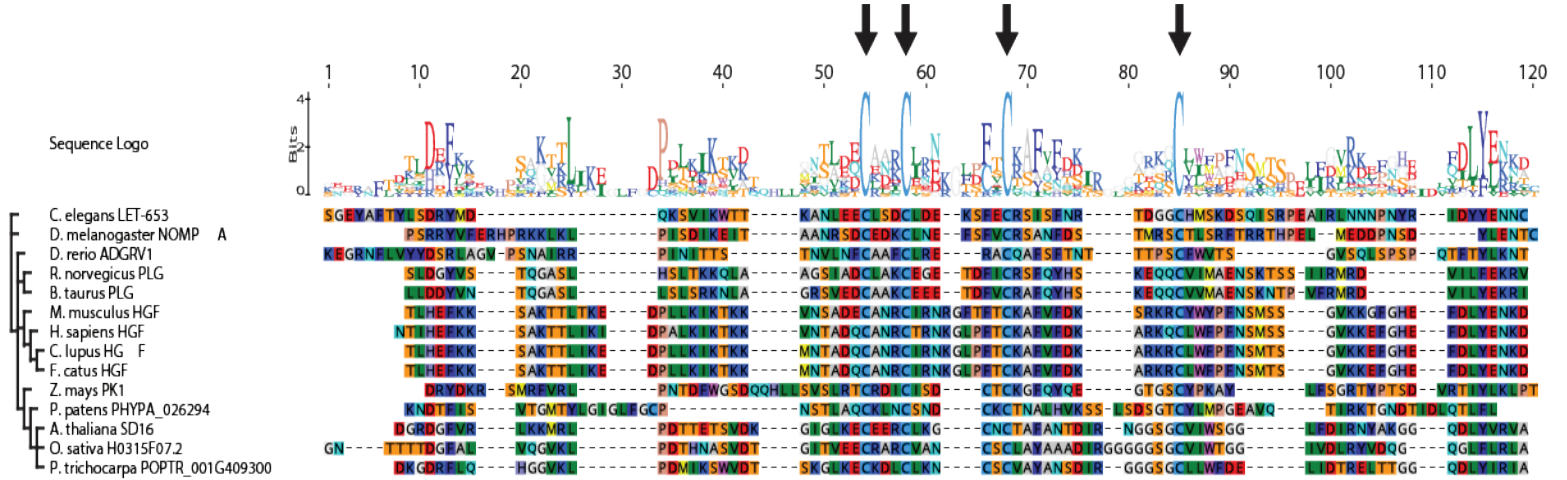
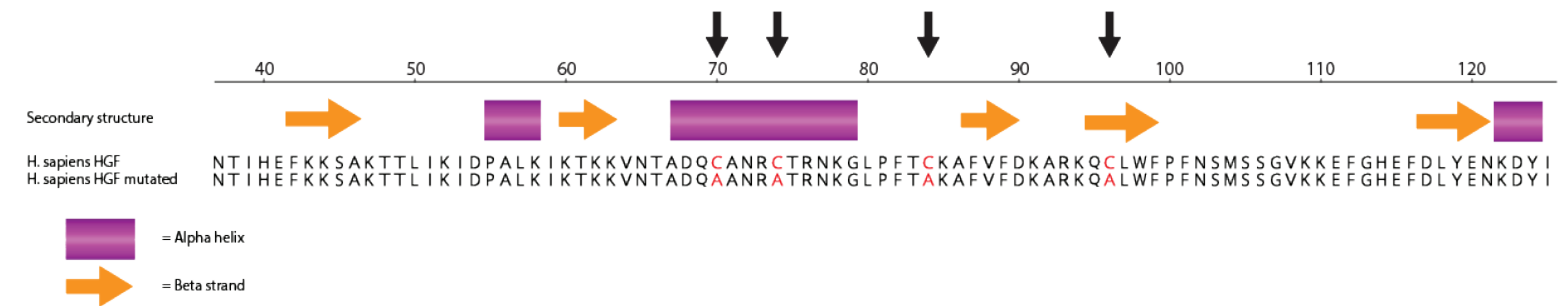
101 **Supplementary Figure 14. Uncropped gel scans for all presented Western blots.** (a)  
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103 corresponds to Supplementary Figure 6.

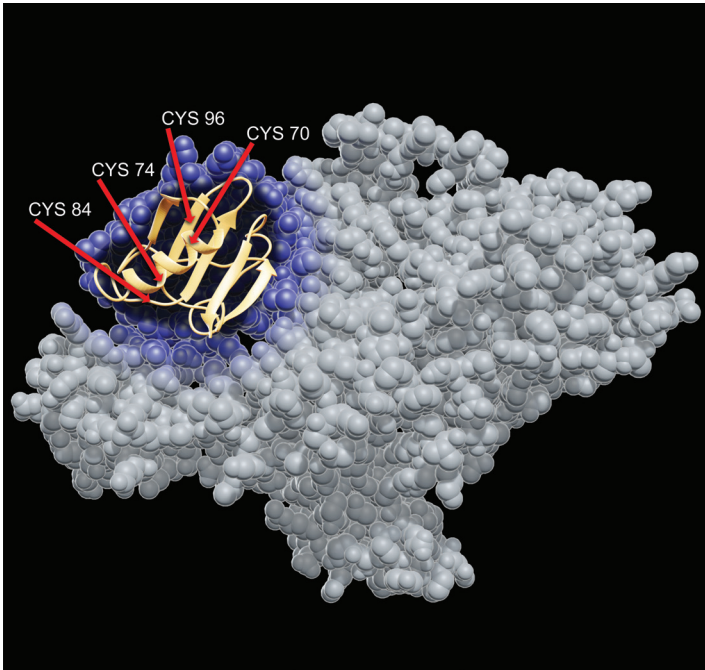
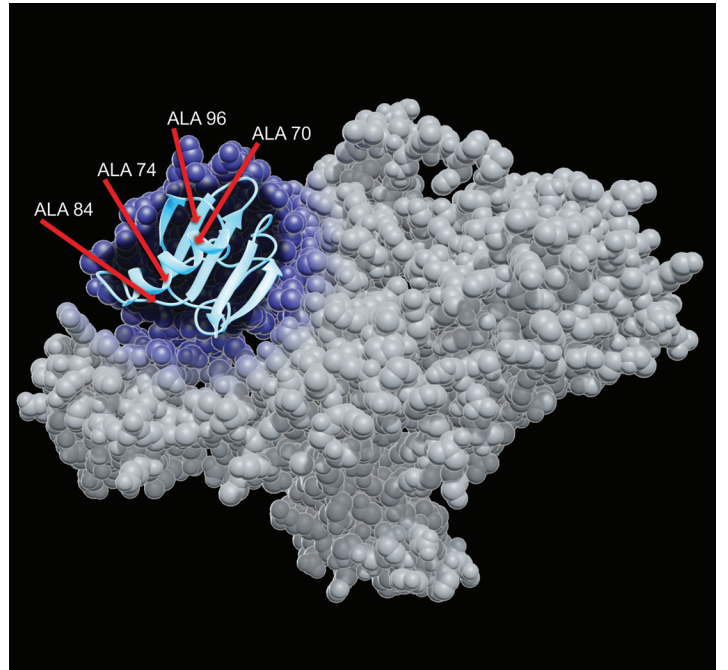
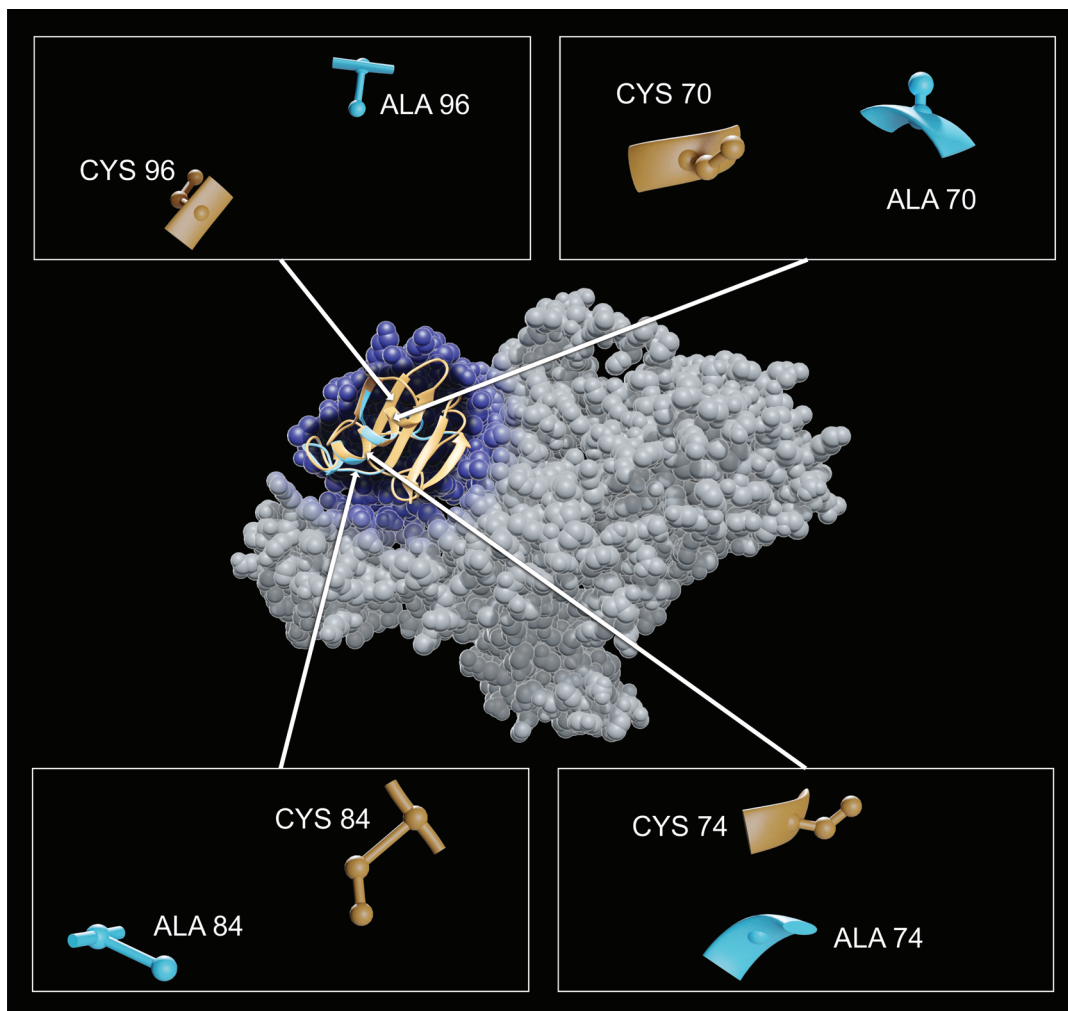
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105 **Supplementary Figure 15. Uncropped gel scans for all presented Western blots.** (a)  
106 corresponds to Supplementary Figure 7a; (b) corresponds to Supplementary Figure 7c.

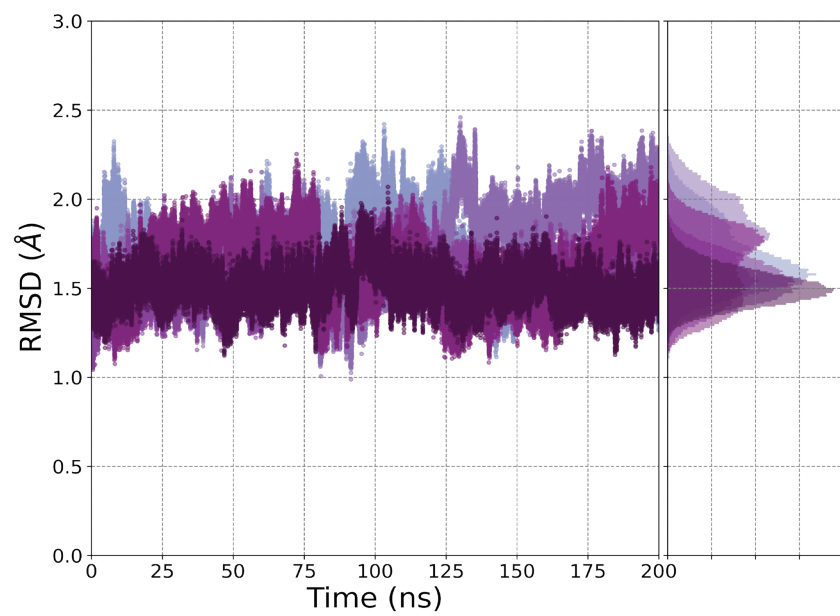
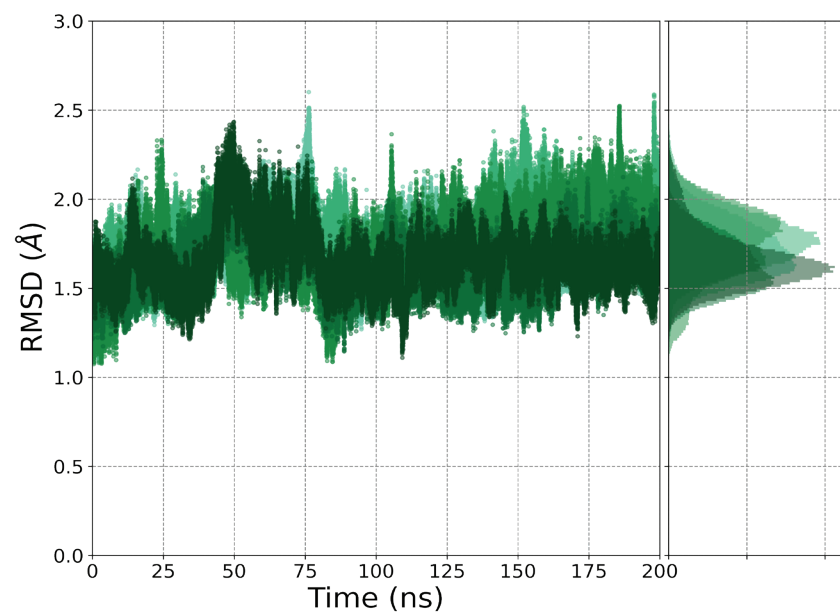
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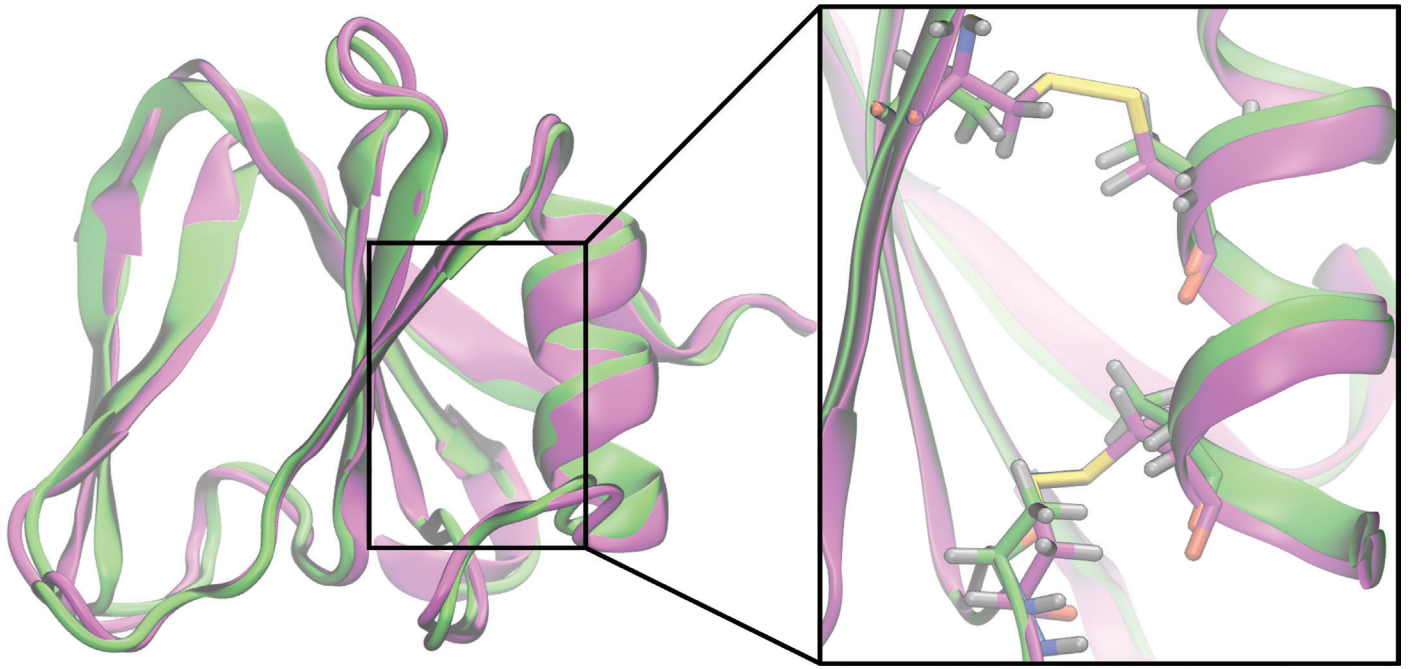
108 **Supplementary Figure 16. Uncropped gel scans for all presented Western blots.** Figure  
109 corresponds to Supplementary Figure 8.

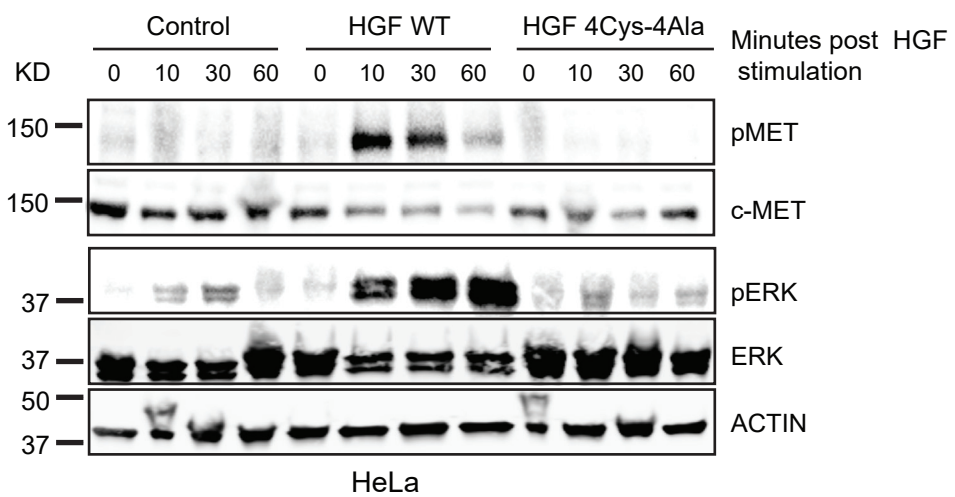
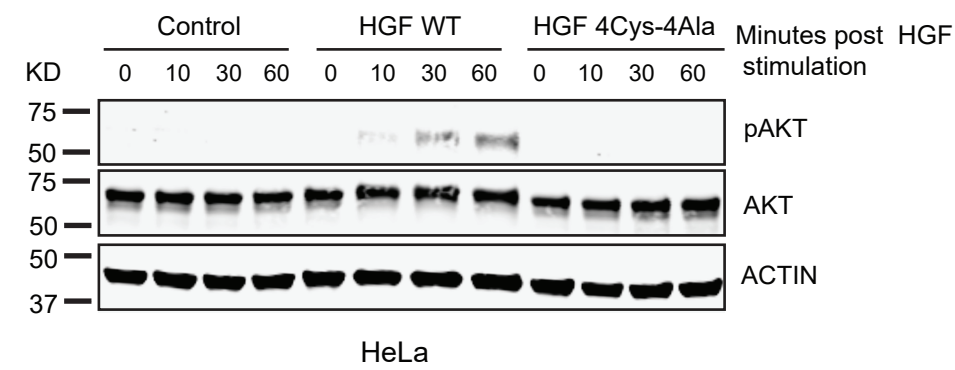
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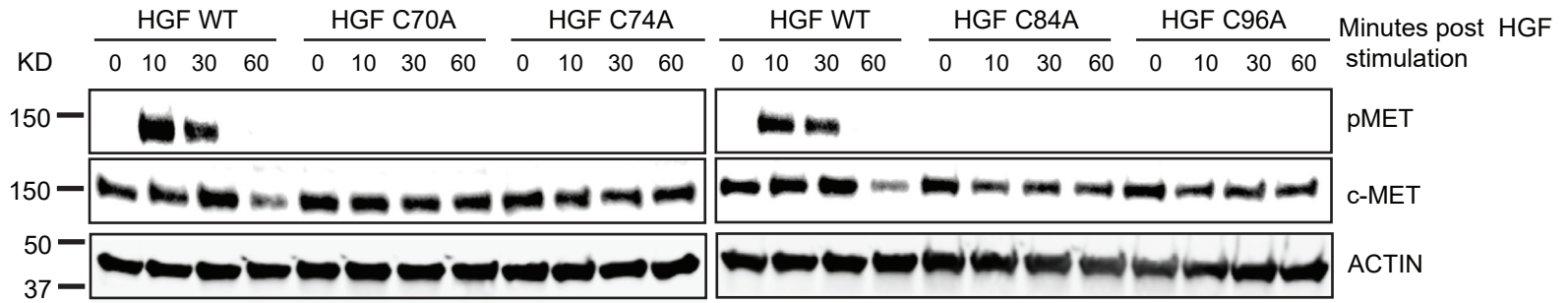
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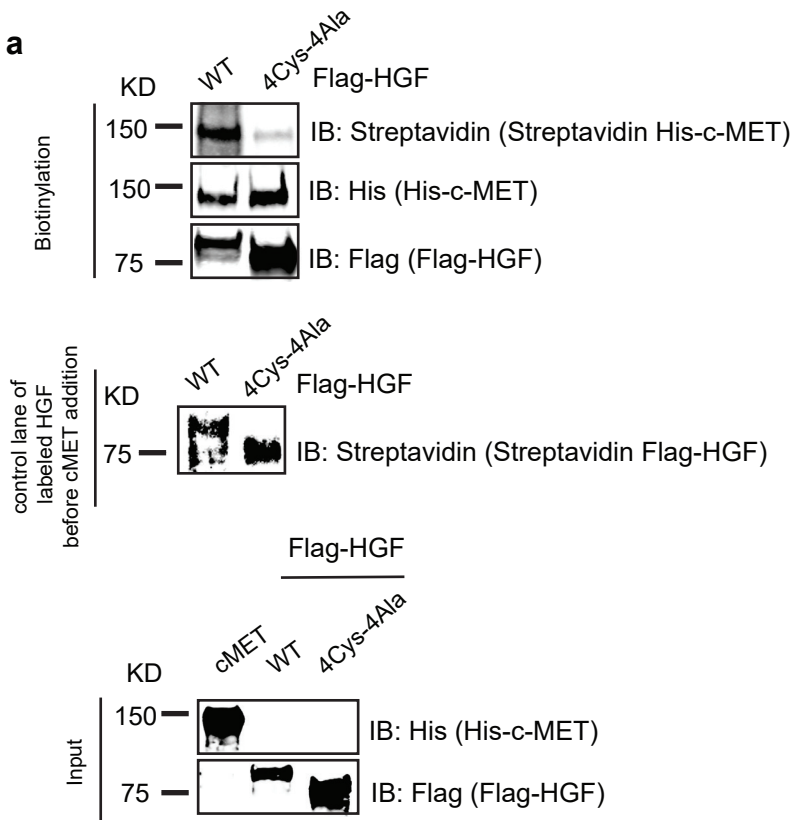
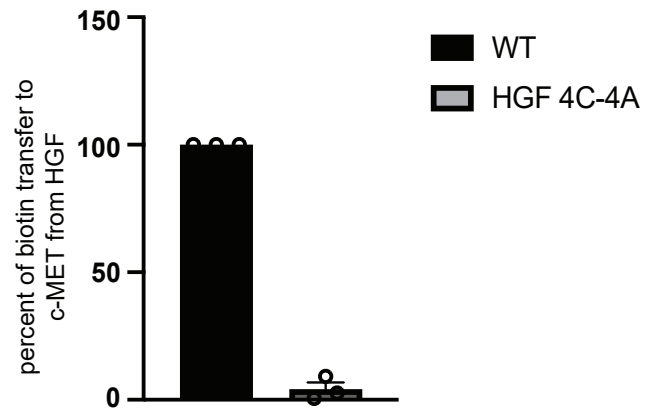
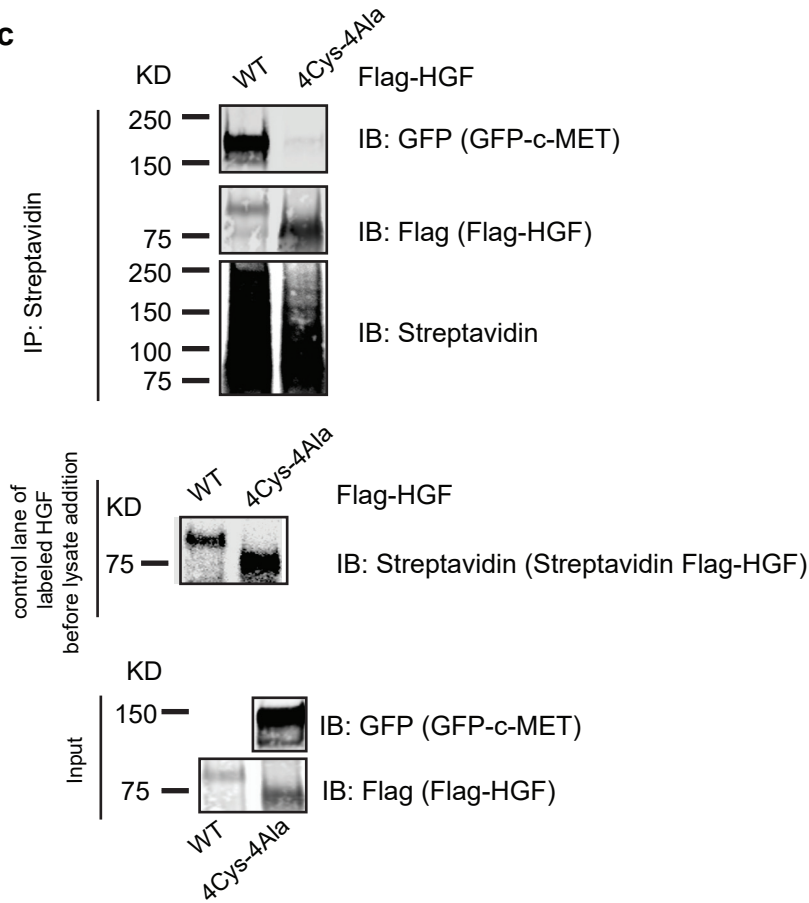
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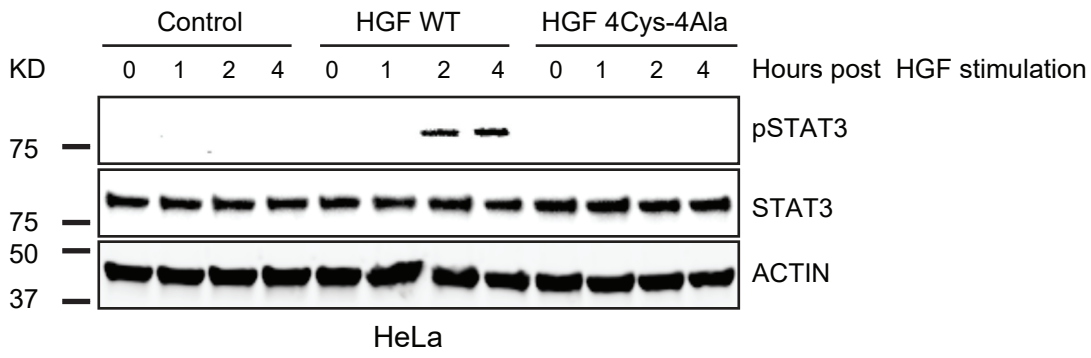


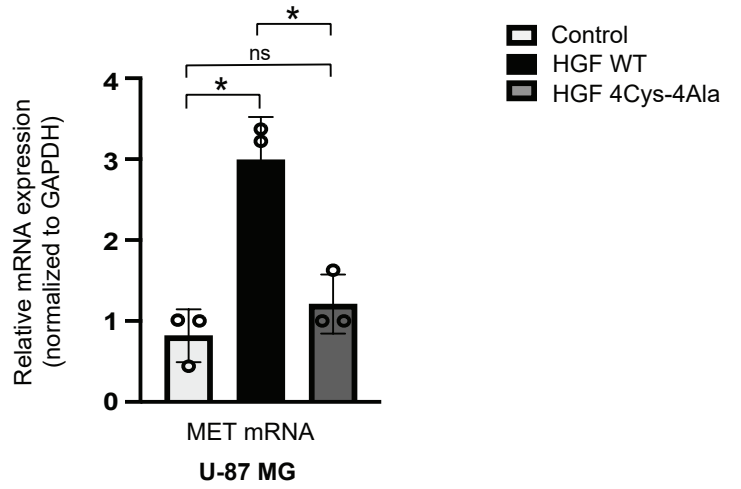
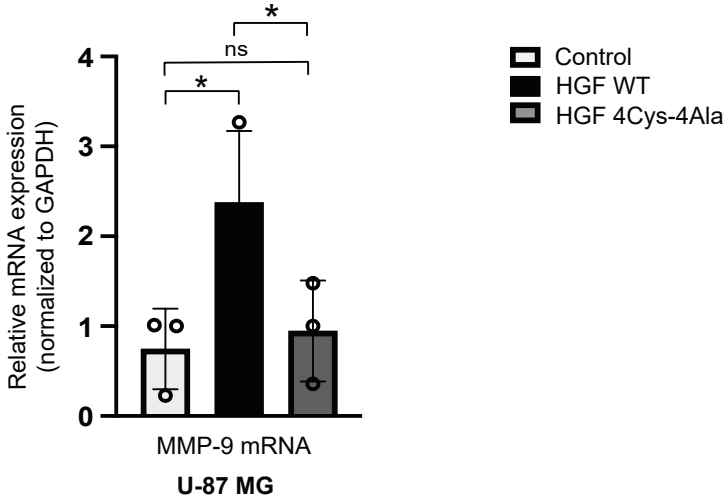
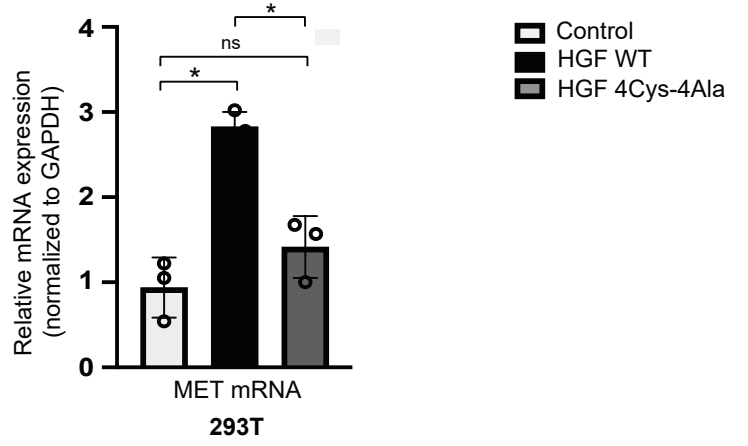
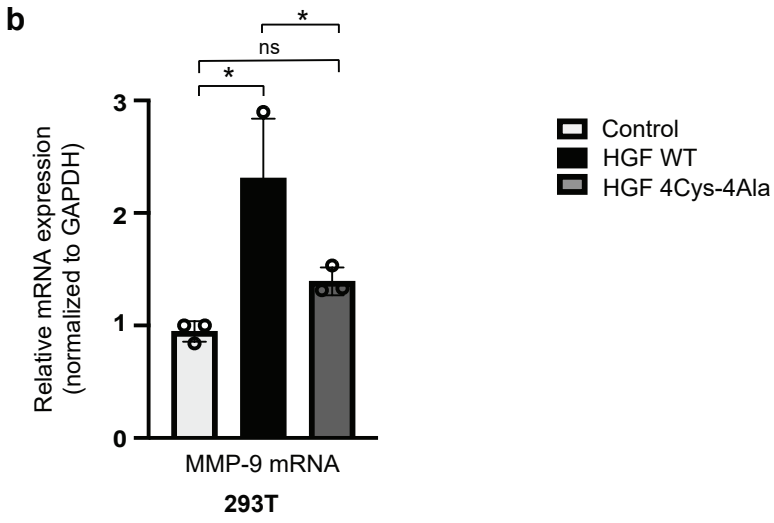
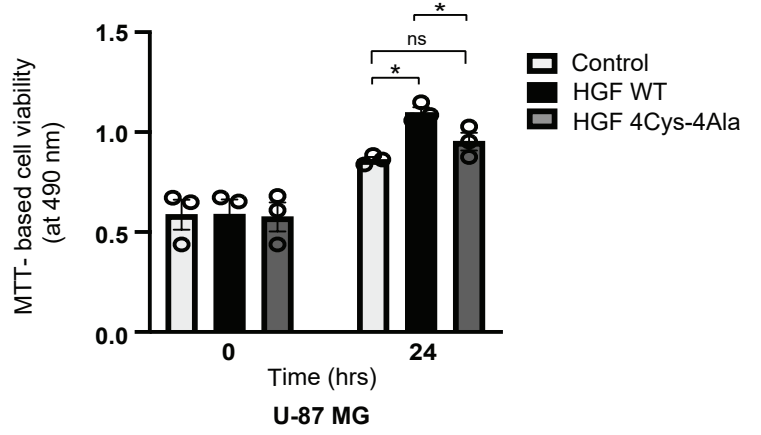
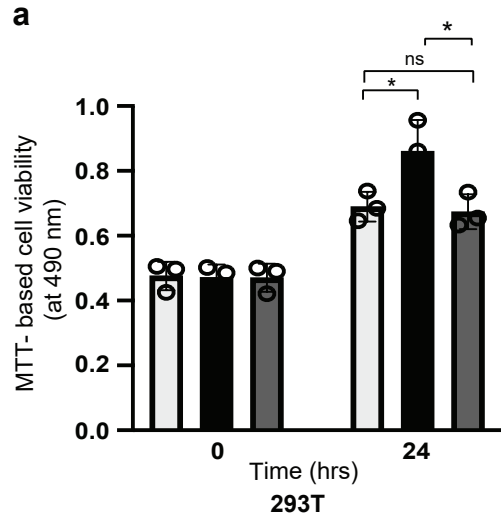
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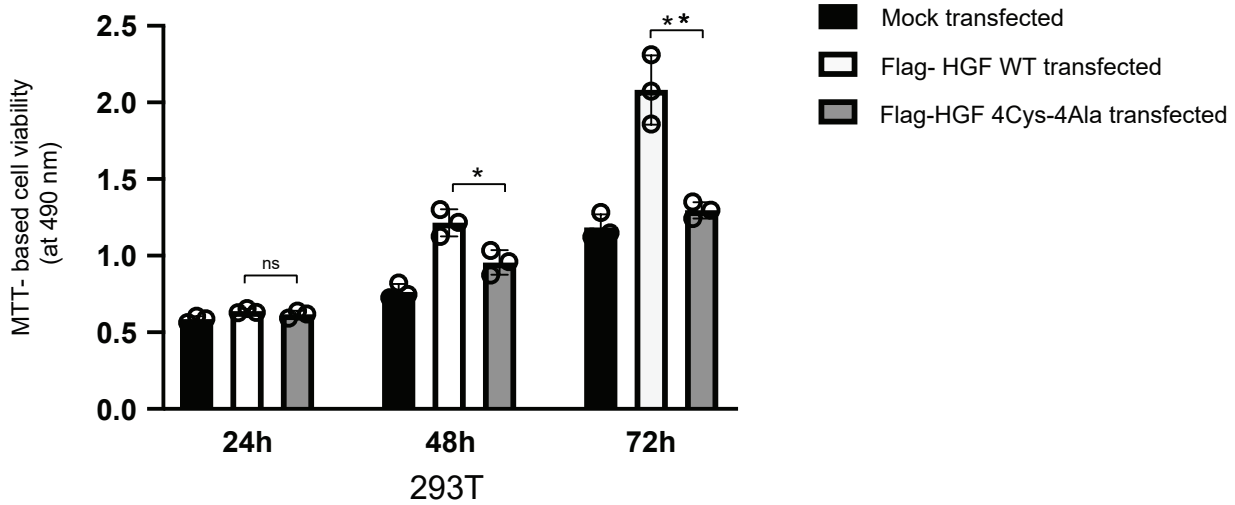
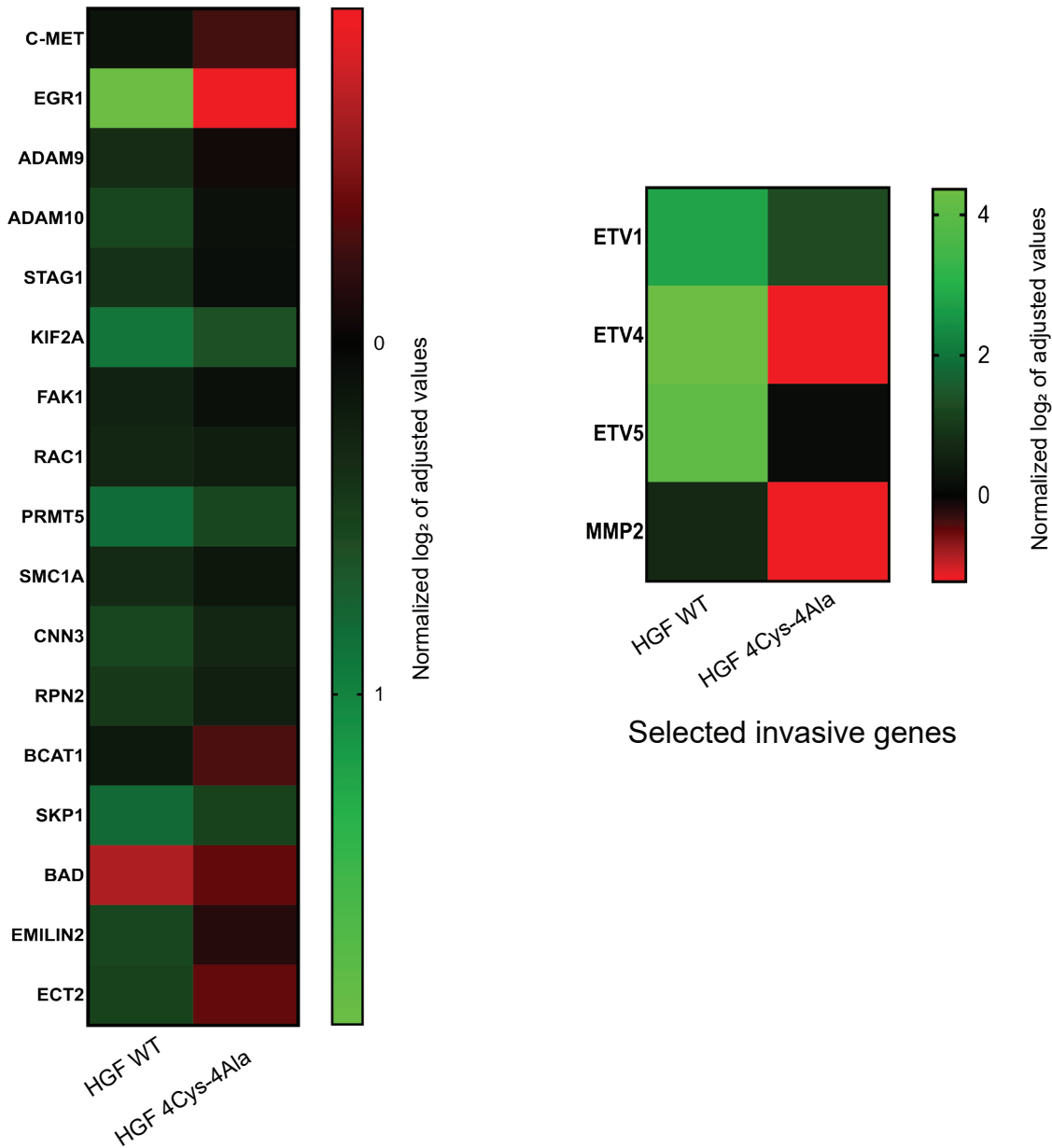


293T

**a****b****c**





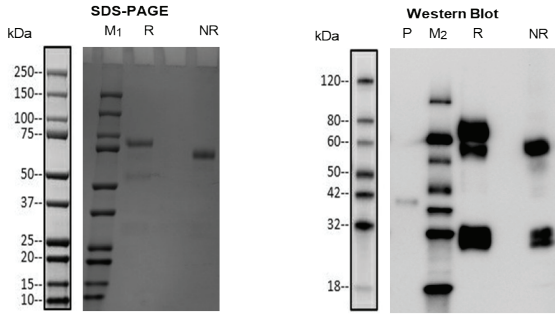
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Selected genes involve in MET signaling and cell cycle



### Flag-HGF-WT

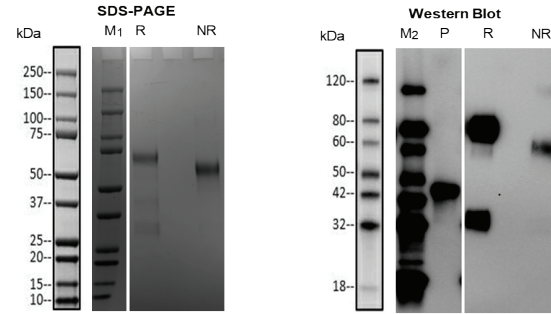
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 Lane M2: Protein Marker, GenScript, Cat. No. M00673, refer to annotated key on the left for size  
 R: Reducing condition  
 NR: Non-reducing condition  
 Lane P: Multiple-tag (GenScript, Cat.No. M0101) as positive control  
 Primary antibody: Rabbit anti-FLAG pAb (GenScript, Cat.No. A00170)

### Flag-HGF-C70A

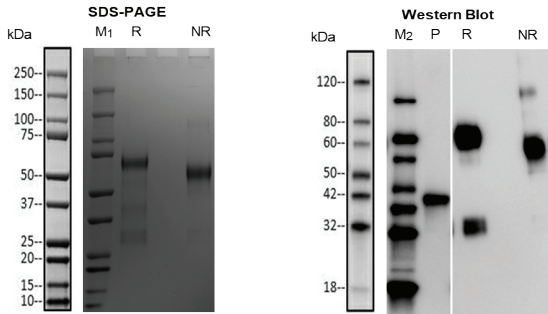
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### Flag-HGF-C74A

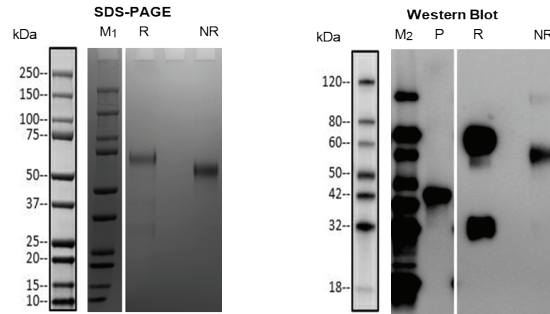
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### Flag-HGF-C84A

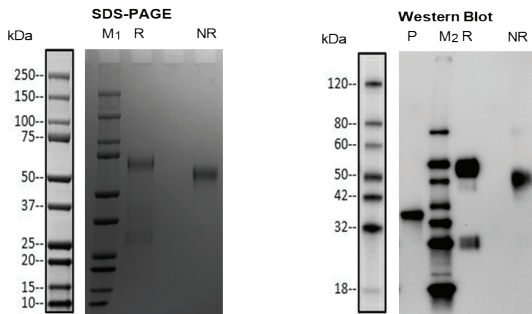
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### Flag-HGF-C96A

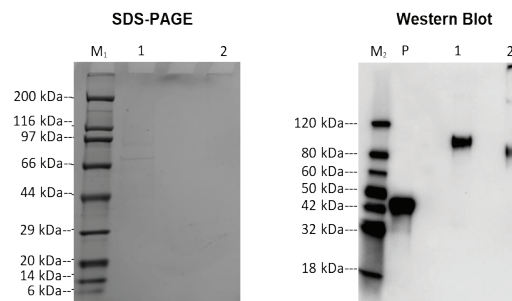
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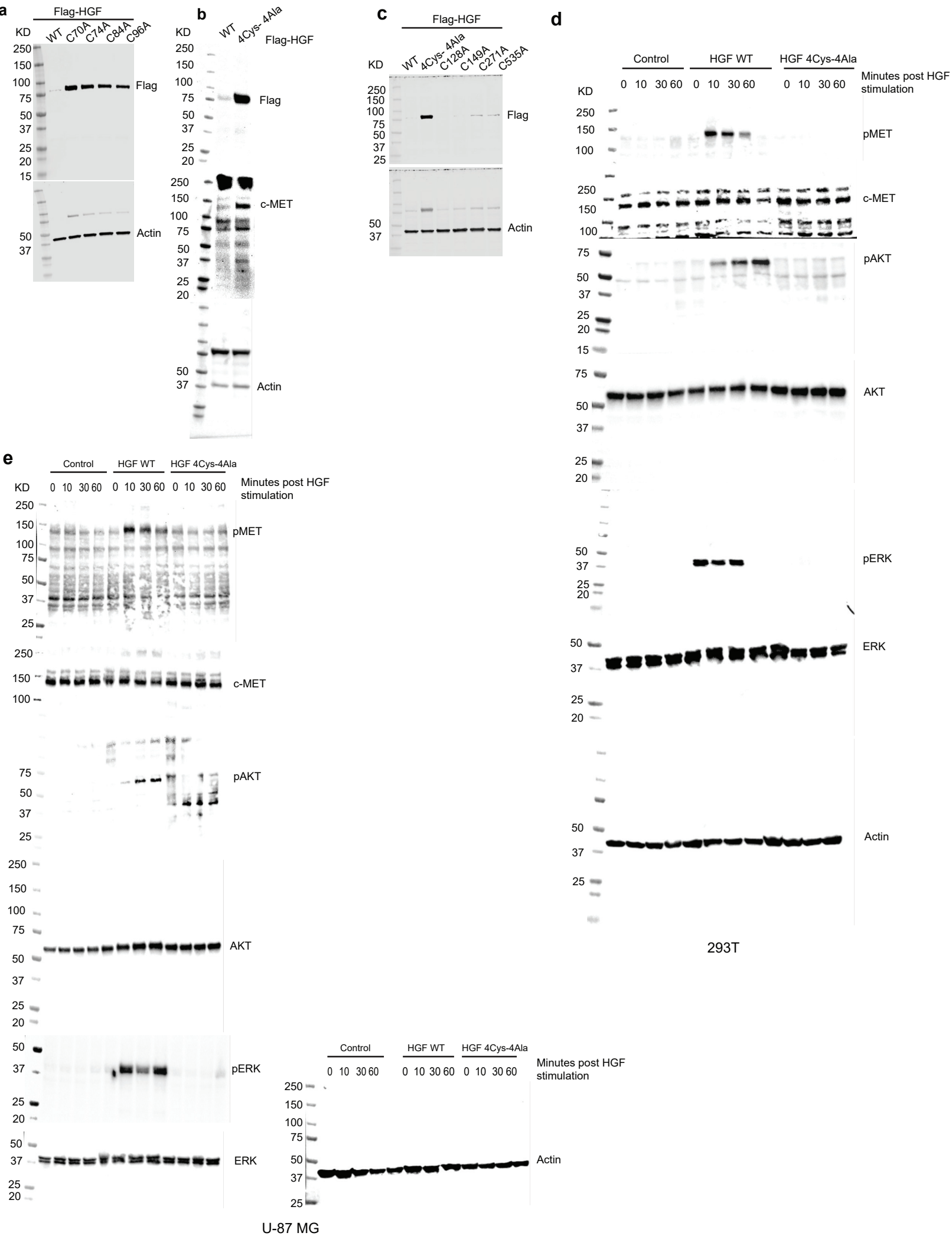
### Flag-HGF- 4C-4A

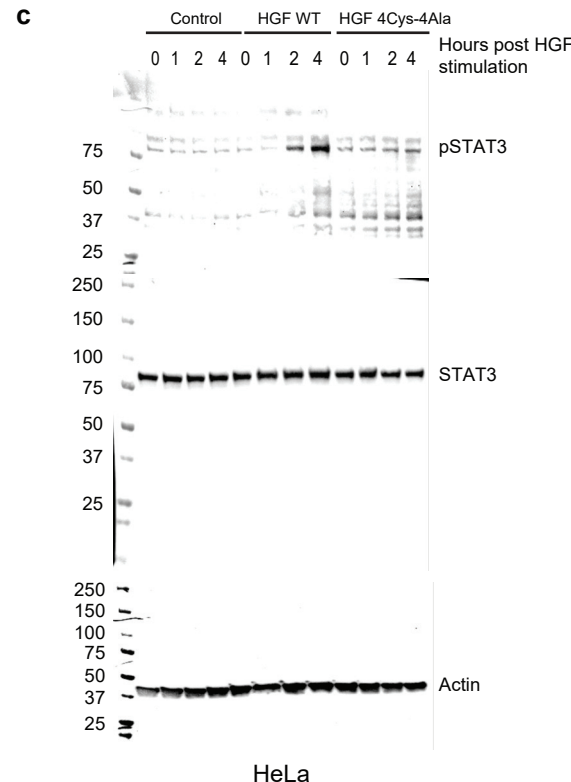
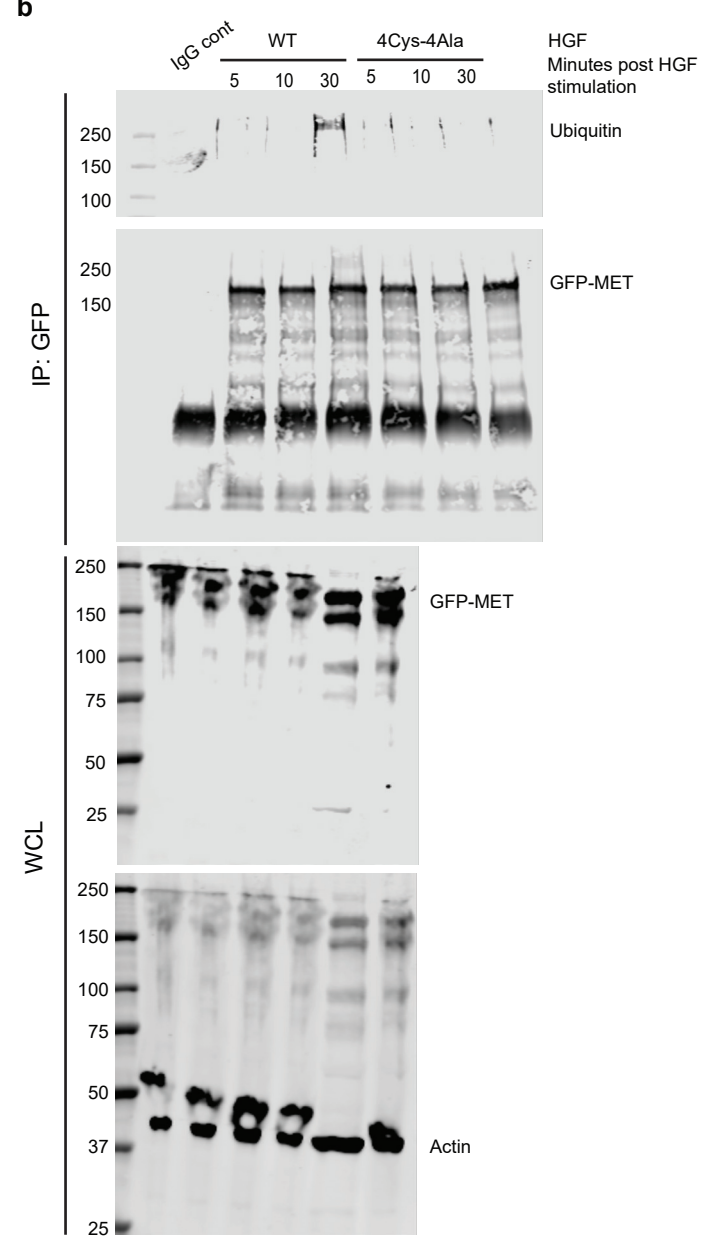
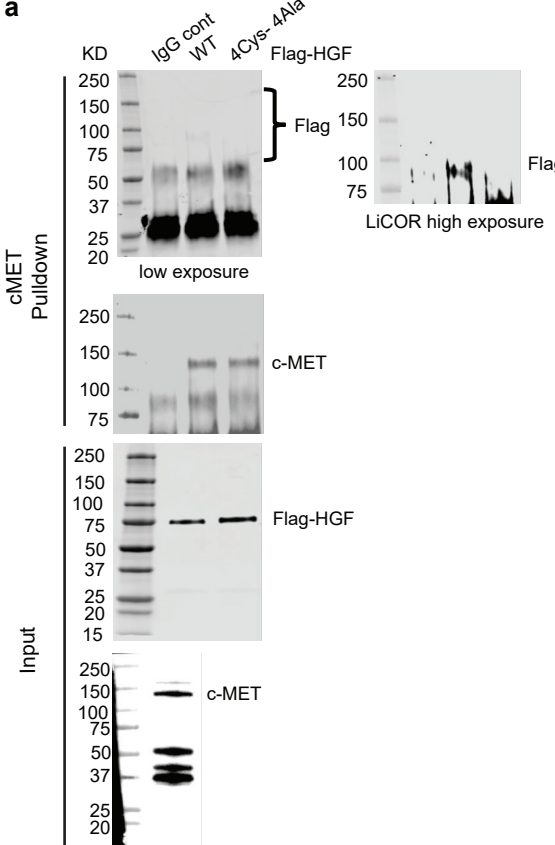
SDS-PAGE & Western Blot Analysis:

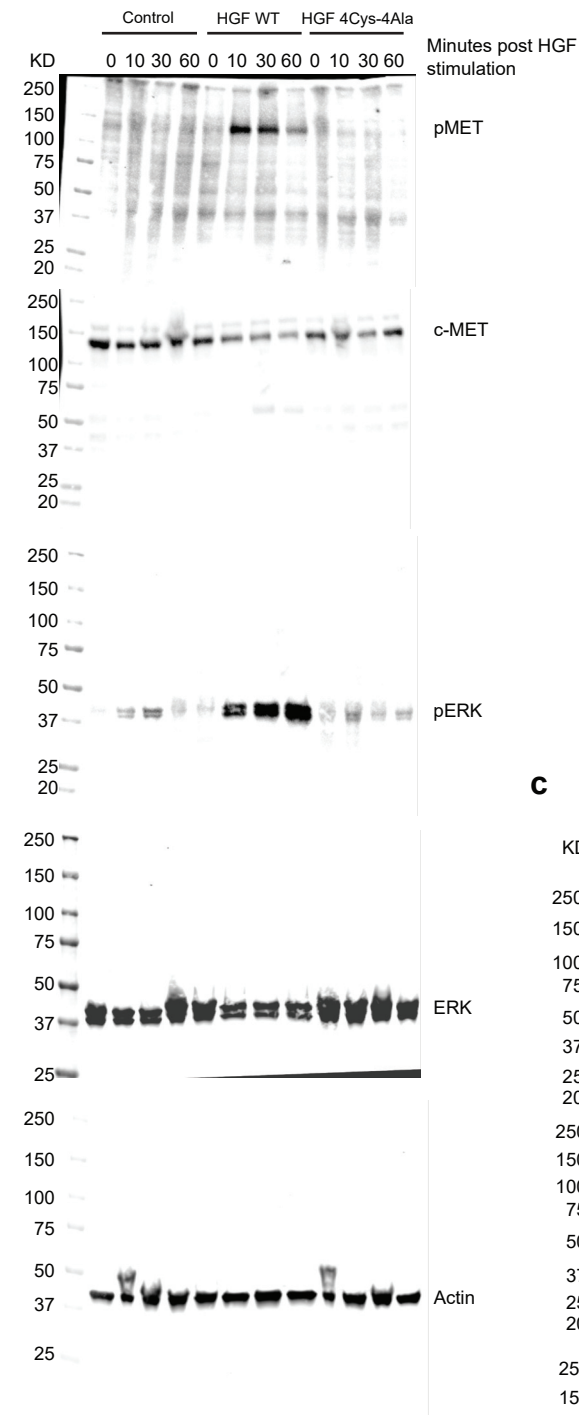


**Fig.1 SDS-PAGE and Western blot analysis of 4 Cys to Ala HGF**

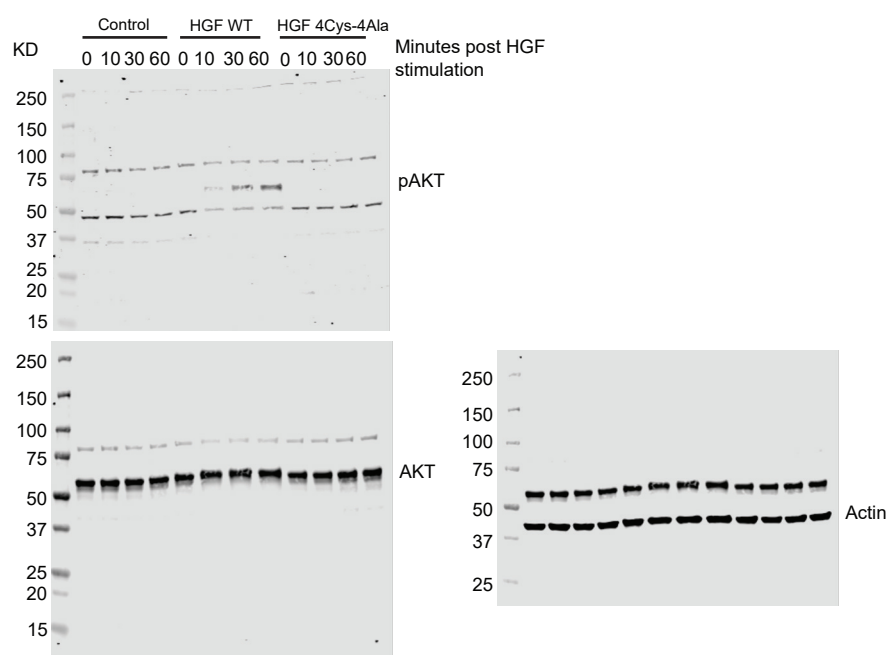
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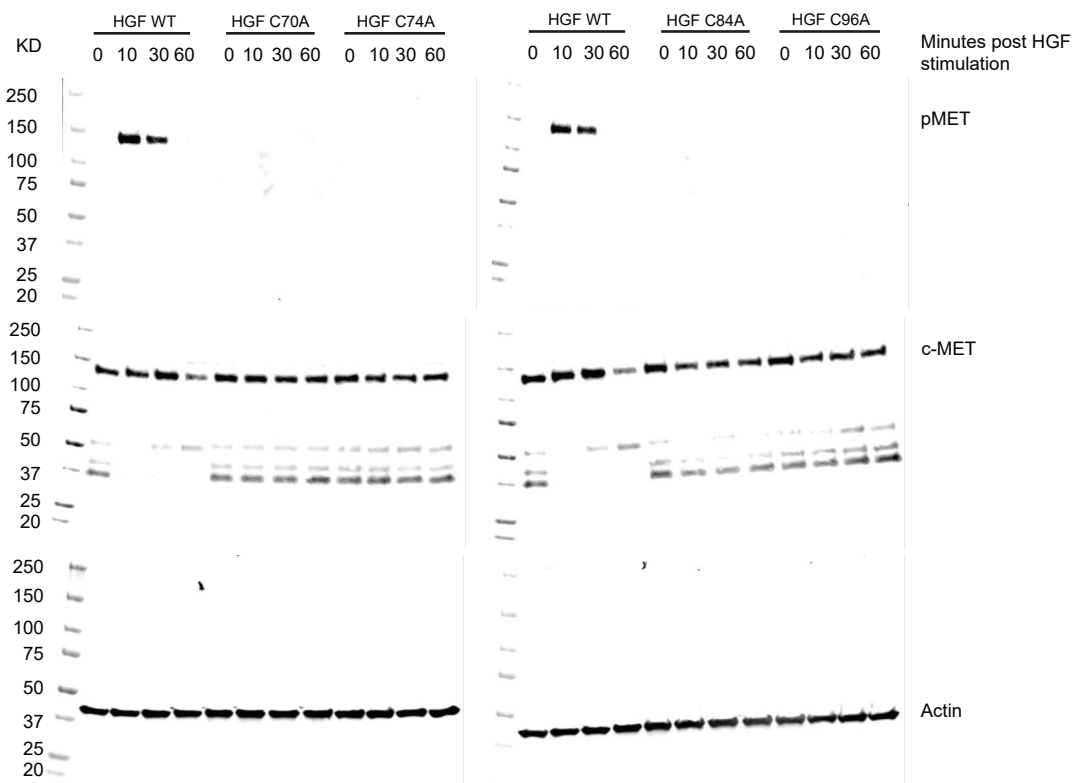


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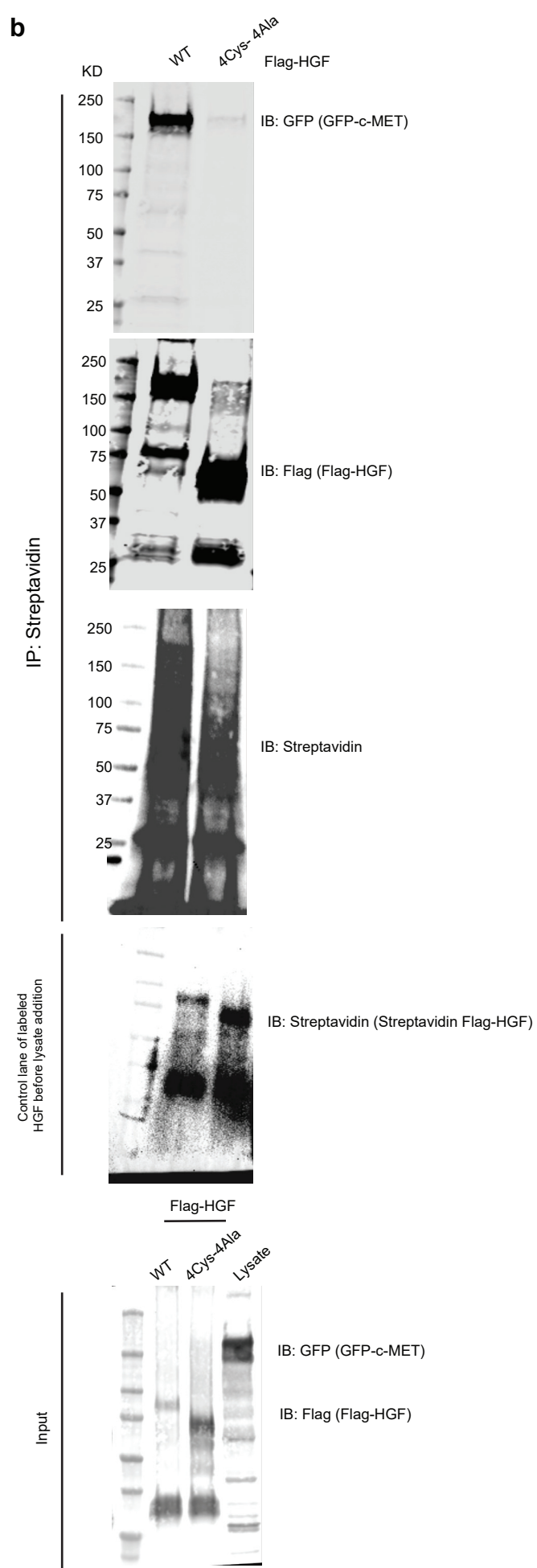
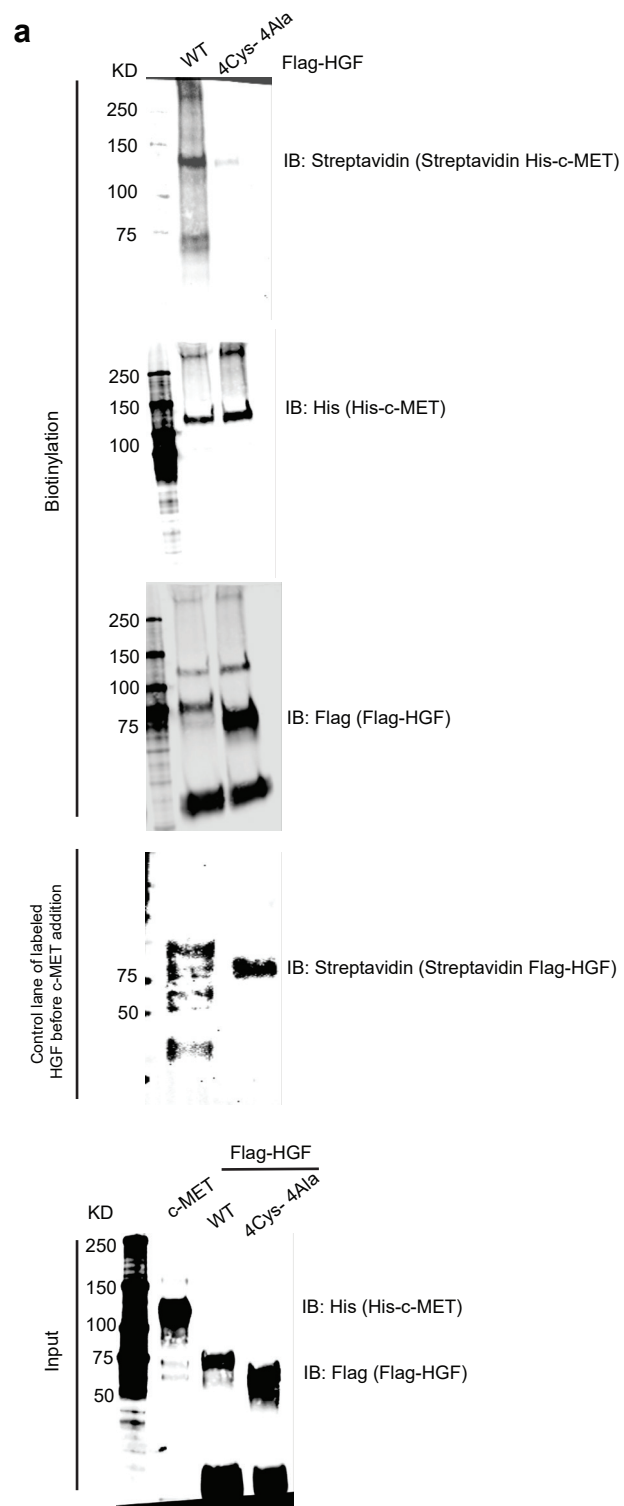
HeLa

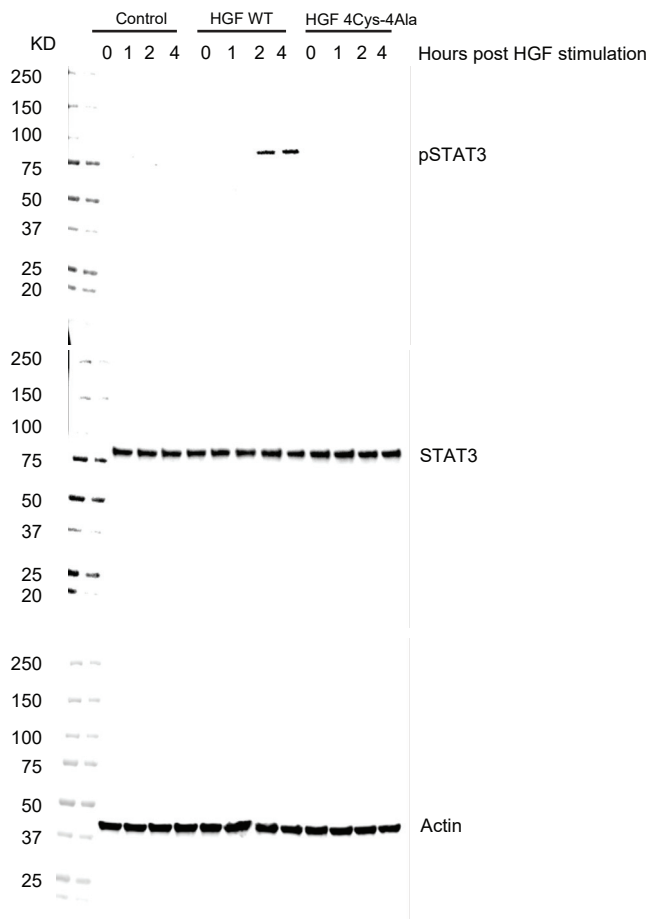
**b**

HeLa

**c**

293T





HeLa