

Mitofusin-2 modulates the epithelial to mesenchymal transition in thyroid cancer progression

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Running title: Mitofusin-2 deficiency elicits EMT in thyroid cancer

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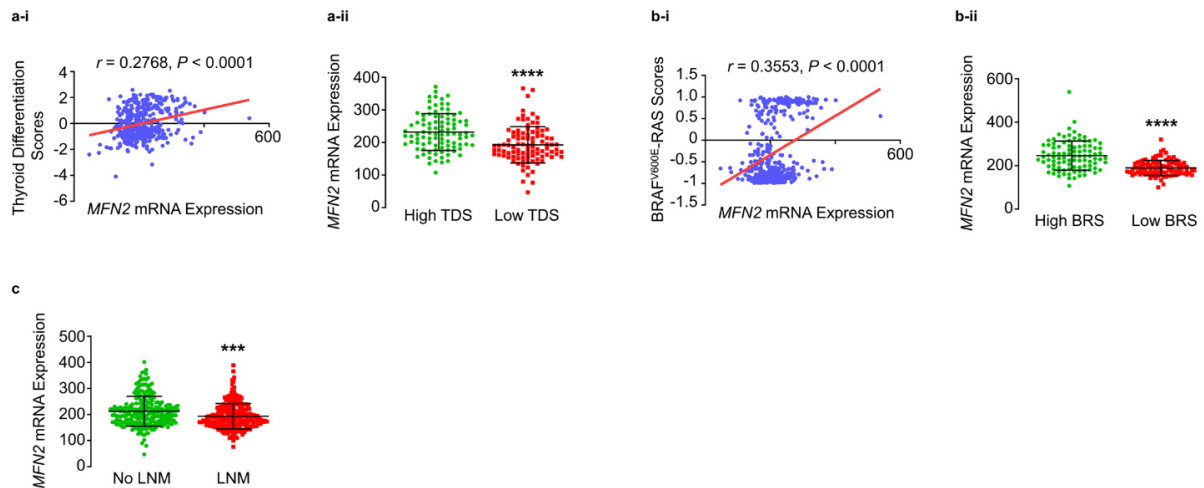
Supplementary Figure 1

MFN2 expression is a prognostic marker in human thyroid cancer.

(A-i) Relationship of *MFN2* expression with TDS. Correlation analysis using Pearson correlation coefficient and (A-ii) comparison of *MFN2* expression between high and low TDS tumors.

(B-i) Relationship of *MFN2* expression with BRS. Correlation analysis using Pearson correlation coefficient and (B-ii) comparison of *MFN2* expression between high and low BRS tumors.

(C) Comparison of *MFN2* expression between tumors without and with LNM. Data represent the mean \pm SD. Asterisks ($P < 0.001$ [***], $P < 0.0001$ [****]) indicate significant differences from the statistical analyses. Abbreviations: TDS, thyroid differentiation scores; BRS, BRAFV600E-RAS scores; LNM, lymph node metastasis.



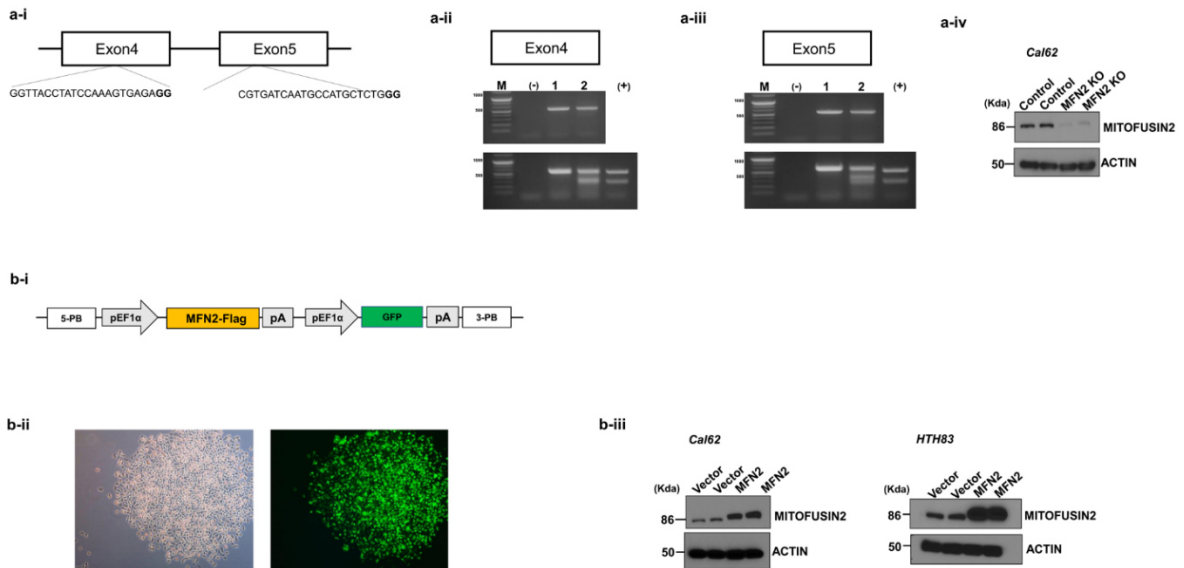
Supplementary Figure 2

(A) Knockout of MFN2 in the Cal 62 cell line. (A-i) Information on two guide RNAs on exon 4 and exon 5. Mutation assay with the T7E1 enzyme on exon 4 (A-ii) and exon 5 (A-iii); M: marker DNA ladder, (1): negative control, 1: wild-type genome, 2: transfected cells, (+): positive control. (A-iv) MFN2 knockout in the Cal62 cell line confirmed by western blotting.

(B-i) Illustration of the MFN2 and GFP expression vector.

(B-ii) Representative GFP-positive colony (left: brightness, right: fluorescence).

(B-iii) MFN2 overexpression in the Cal62 and HTH83 cell lines confirmed by western blotting.



Supplementary Figure 3

(A) Mitofusin-2 was not associated with the proliferation ability in Cal62 cells.

(A-i) Assay for comparing the proliferation ability of *MFN2* KO and control Cal62 cells (n.s; not significant).

(A-ii) Assay for comparing colony formation between *MFN2* KO and control Cal62 cells on day 7. (A-iii) Quantification of the colony forming assay (n.s; no significant difference).

(A-iv) Assay for comparing the proliferation ability of Cal62 Vector and *MFN2* groups.

(A-v) Image representing the colony formation by the Cal62 Vector and *MFN2* groups on day 7. (A-vi) Quantification of (A-v).

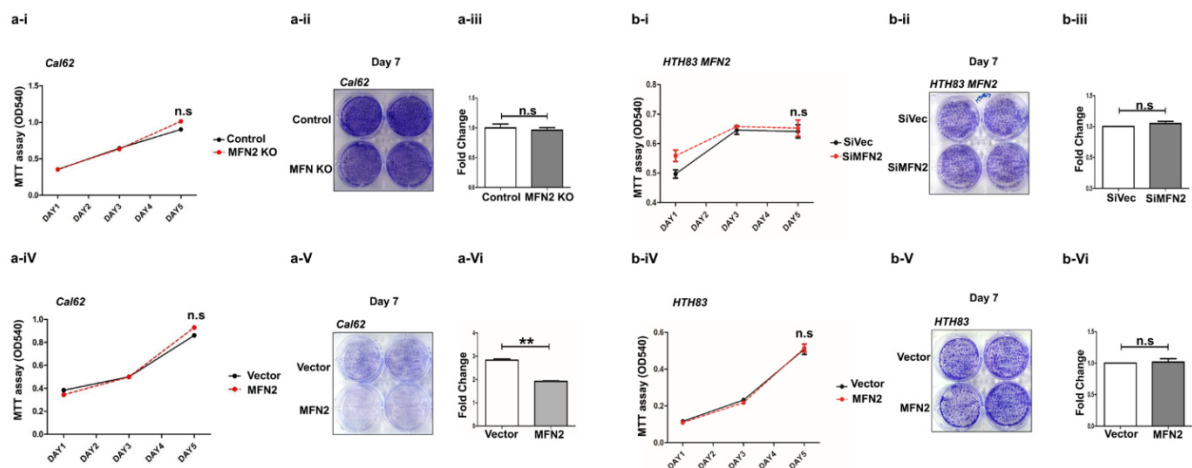
(B) Mitofusin-2 was also not associated with cell proliferation ability in HTH83 cells.

(B-i) Assay for comparing the proliferation ability of HTH83 *MFN2*-SiVector and SiMFN2 groups (n.s; not significant).

(B-ii) Image representing colony formation by the HTH83 *MFN2*-SiVector and SiMFN2 groups. (B-iii) Quantification of (B-ii) (n.s; no significant difference).

(B-iv) Assay for comparing the proliferation ability of the HTH83 Vector and *MFN2* groups. (B-v) Image representing colony formation by the HTH83 Vector and *MFN2* groups.

(B-vi) Quantification of (B-v) (n.s; no significant difference). Asterisks ($P < 0.01$ [**]) indicate significant differences from the statistical analyses. Each data point represents the mean \pm standard error of three independent experiments.



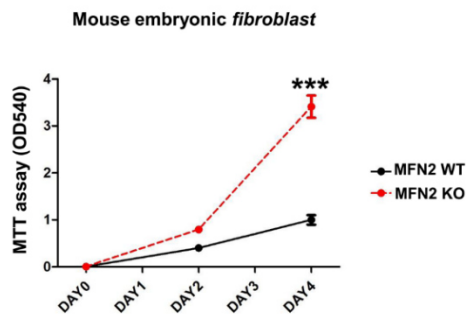
Supplementary Figure 4

(A) Mitofusin-2 was associated with proliferation ability of MEF cells. Assay for comparing the proliferation ability of the *MFN2* KO and MEF WT cells.

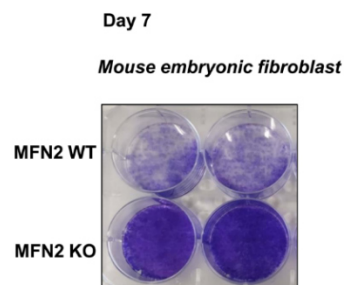
(B-i) Colony forming assay of *MFN2* KO and WT MEF cells on day 7.

(B-ii) Quantification of the colony forming assay. Asterisks ($P < 0.05$ [*], $P < 0.01$ [**], $P < 0.001$ [***]) indicate significant differences from the statistical analyses. Each data point represents the mean \pm standard error of three independent experiments.

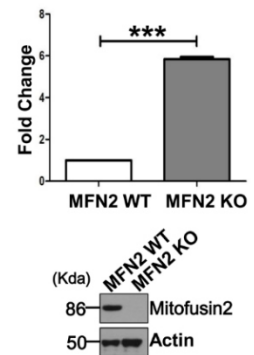
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b-i



b-ii



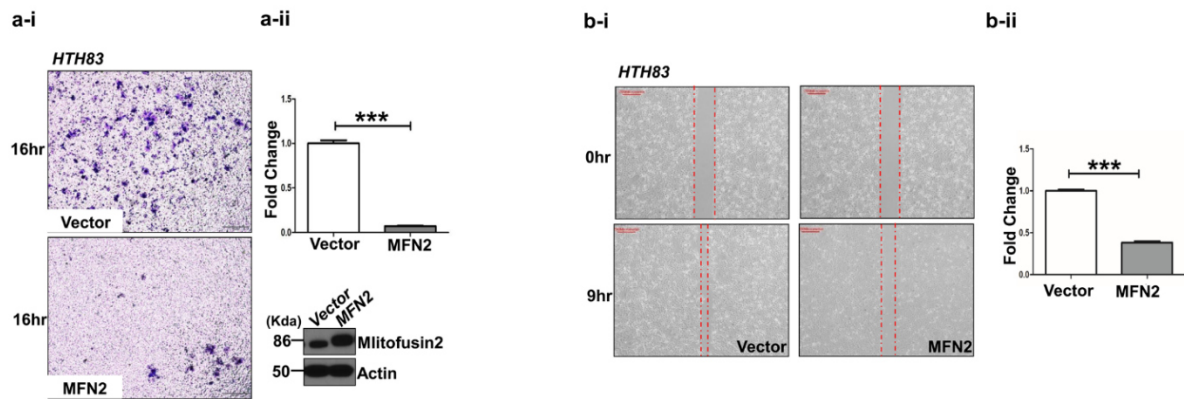
Supplementary Figure 5

(A-i) Transwell assays were performed in the HTH83 Vector and *MFN2* overexpression groups. A representative image was taken 12 h after the initial seeding (pore size 0.8 μm). (A-ii) Graph of the quantified results of (A-i).

(B-i) Wound-healing assays were performed to investigate the differences between the HTH83 Vector and HTH83 *MFN2* OE groups. We measured the gap distance 9 h after the initial scratching.

(B-ii) Graph of the quantified results of (B-i). Asterisks ($P < 0.05$ [*], $P < 0.01$ [**], $P < 0.001$ [***]) indicate significant differences from the statistical analyses. Each data point represents the mean

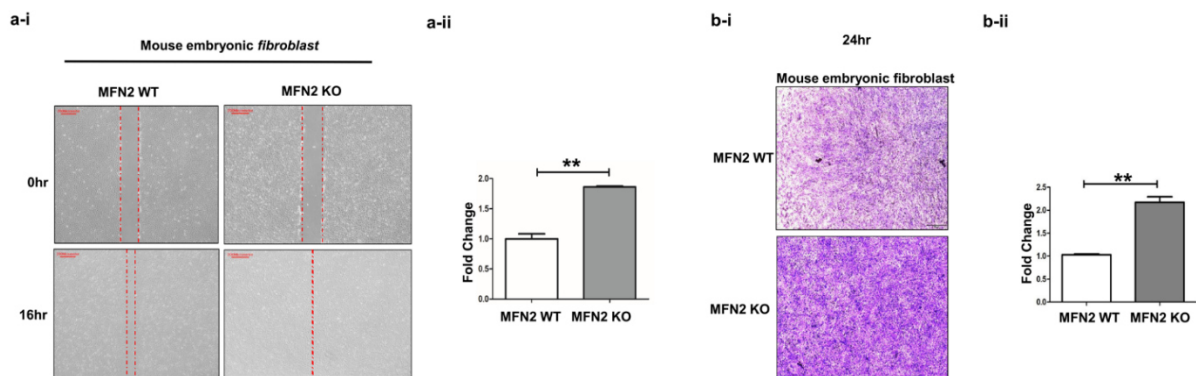
\pm standard error of three independent experiments.



Supplementary Figure 6

(A-i) Transwell assays were performed in *MFN2* WT and KO MEF cells. A representative image was taken 24 h after the initial seeding (pore size 0.8 μm). (A-ii) Graph of the quantified results of (A-i). Significantly more cells migrated from *MFN2* KO MEFs than from the *MFN2* WT MEFs.

(B-i) Wound-healing assays were performed to investigate the differences between *MFN2* WT and KO MEFs. We measured the gap distance 16 h after the initial scratching. (B-ii) Quantification of (B-i) compared to the initial scratch size of the first gap distance after 16 h. Asterisks ($P < 0.05$ [*], $P < 0.01$ [**], $P < 0.001$ [***]) indicate significant differences from the statistical analyses. Each data point represents the mean \pm standard error of three independent experiments.



Supplementary Figure 7

MFN2 overexpression leads to pERK signal suppression.

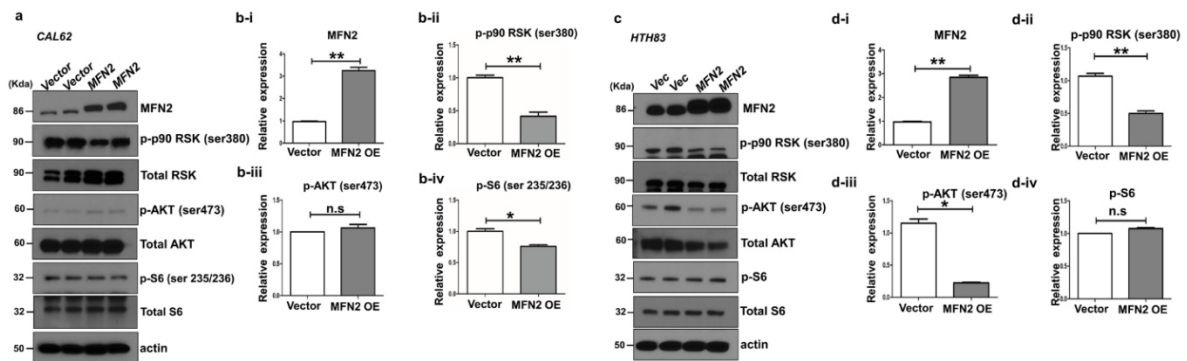
(A) Immunoblotting of MFN2, *p-p90* RSK (Ser380), *p*AKT (Ser473), and *p*-S6 (Ser235/236)

was conducted using lysates from Cal62 C and Cal62 MFN2 OE cells.

(B) Quantification of (B-i) MFN, (B-ii) *p-p90* RSK (Ser380), (B-iii) *p*-AKT (Ser473), and (B-iv) *p*-S6 (Ser235/236) levels.

(C) Immunoblotting for investigating the levels MFN2, *p-p90* RSK (Ser380), *p*AKT (Ser473), and *p*-S6 (Ser235/236) was performed using cell lysates from the HTH83 Vector and HTH83 MFN2 overexpression groups.

(D) Quantification of (D-i) *MFN2*, (D-ii) *p-p90* RSK (Ser380), (D-iii) *p*-AKT (Ser473), and (D-iv) *p*-S6 (Ser235/236). Asterisks ($P < 0.05$ [*], $P < 0.01$ [**], $P < 0.001$ [***]) indicate significant differences from the statistical analyses. Each data point represents the mean \pm standard error of three independent experiments.



Supplementary Table 1. Real-time q-RT-PCR primer sequences

Supplementary Table 1. Primers used for mRNA expression analysis

Gene	Primer	5'→3' sequence
E-Cadherin	Forward	GAACGCATTGCCACATACAC
	Reverse	GAATTCGGGCTTGTGTCAT
N-Cadherin	Forward	CCTGAGGGATCAAAGCCTGGAAC
	Reverse	TTGGAGCCTGAGACACGATTCTG
Snail	Forward	CTCCAGCAGCCCTACGAC
	Reverse	CGGTGGGGTTGAGGATCT

Uncropped Gels shown as representative blots in Main& Supplementary Figures

Figure 2

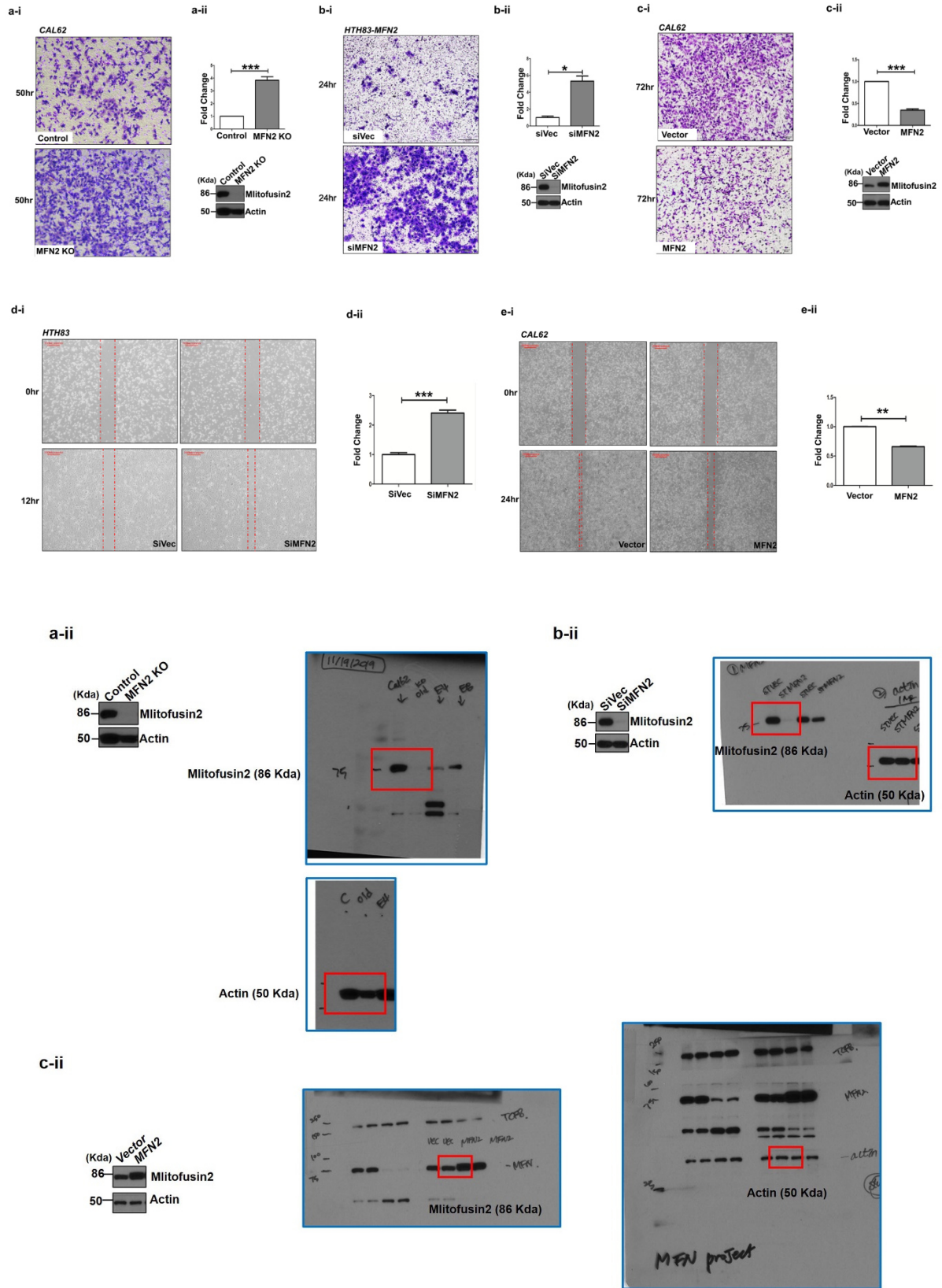
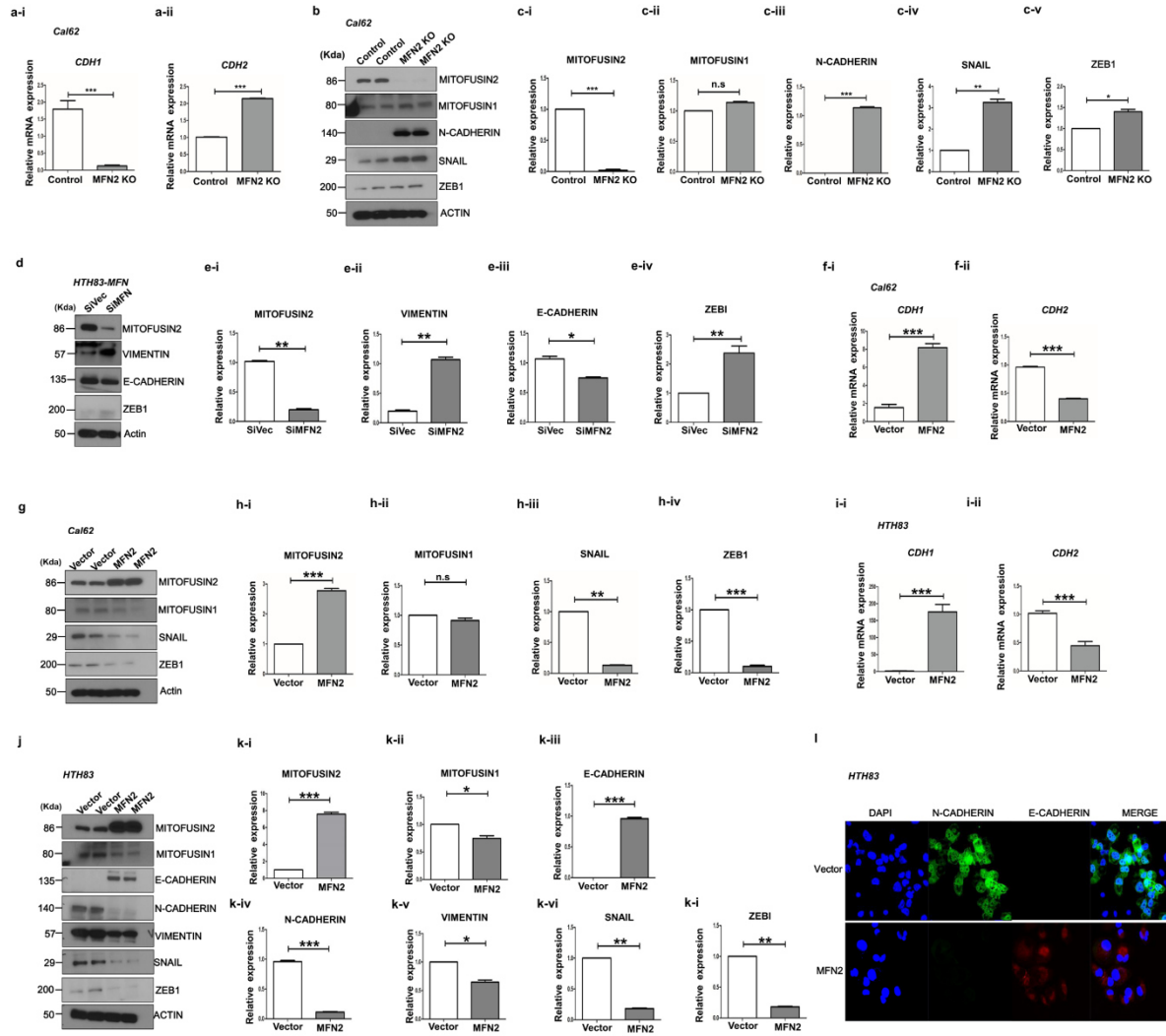
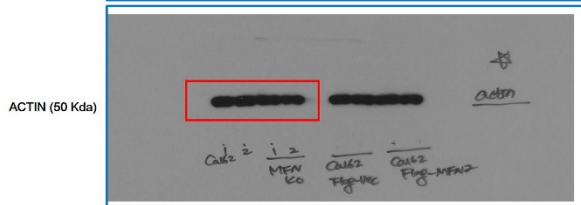
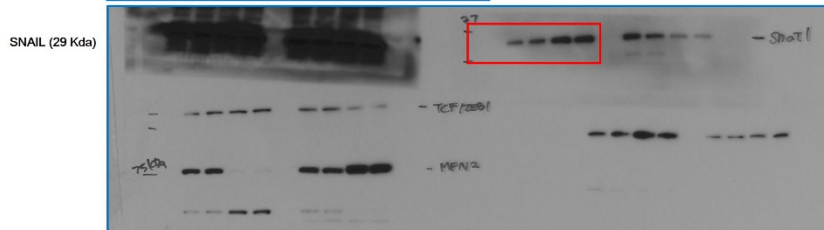
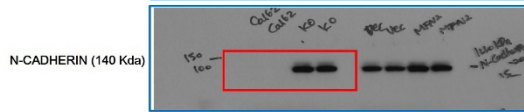
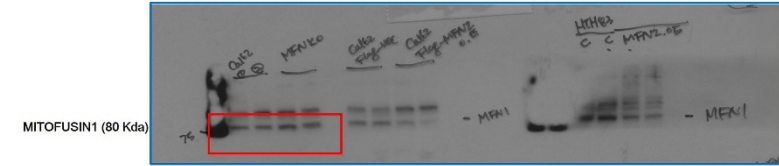
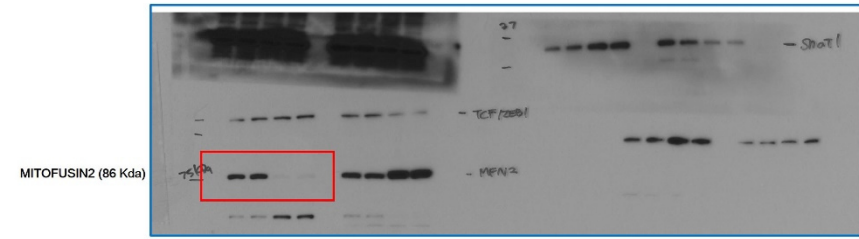
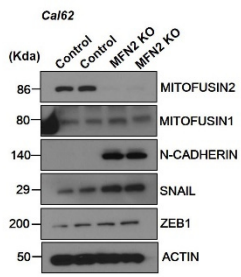


Figure 3



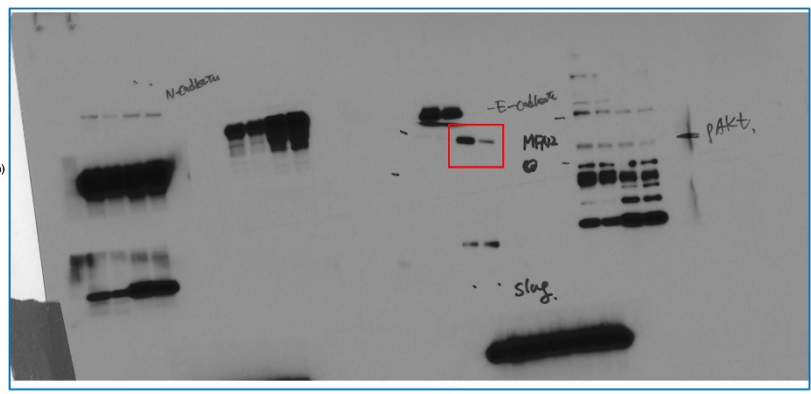
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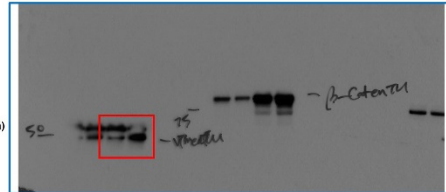
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HTH83-MFN
(Kda) SVEC SW620
86 - MITOFUSIN2
57 - VIMENTIN
135 - E-CADHERIN
200 - ZEB1
50 - Actin

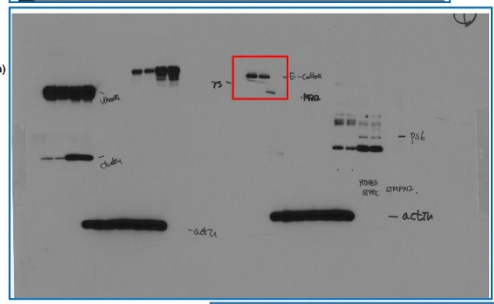
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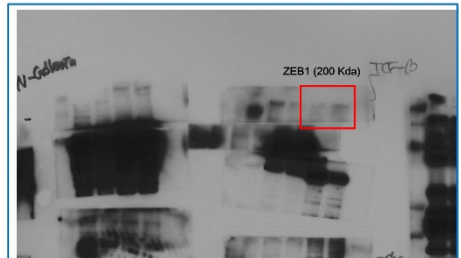
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E-CADHERIN (135 Kda)



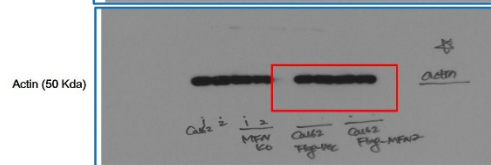
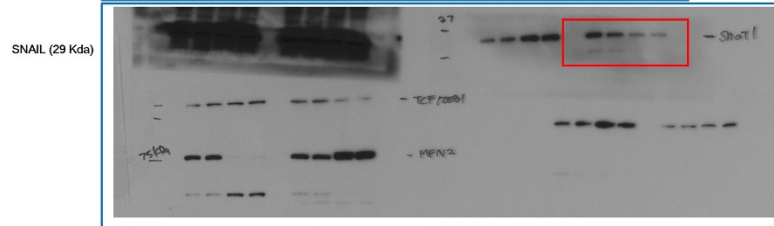
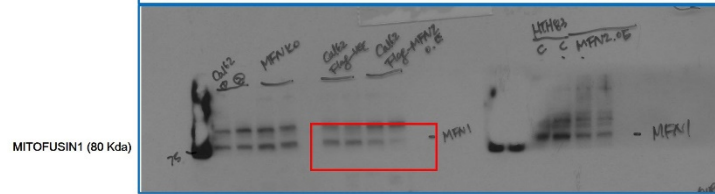
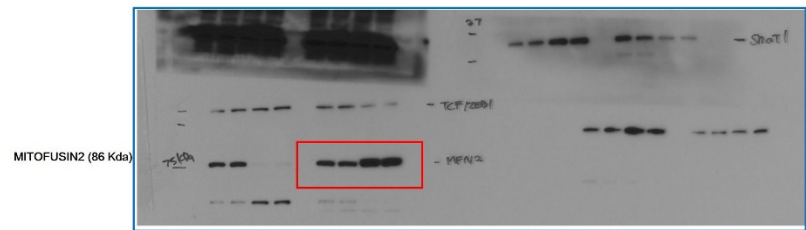
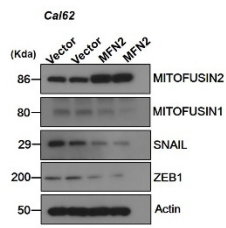
ZEB1 (200 Kda)



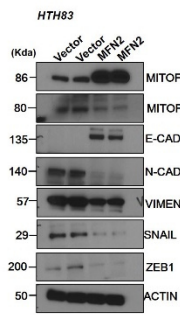
Actin (50 Kda)



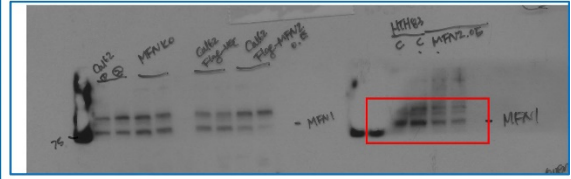
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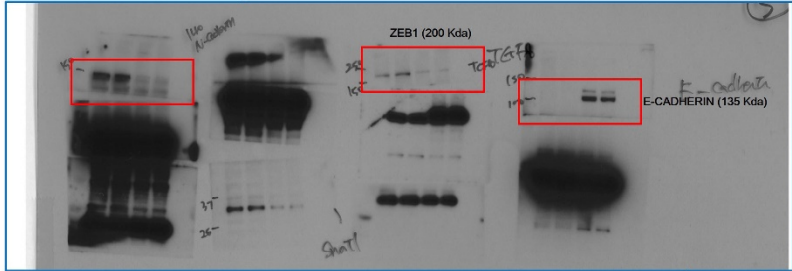


MITOFUSIN2 (86 Kda)

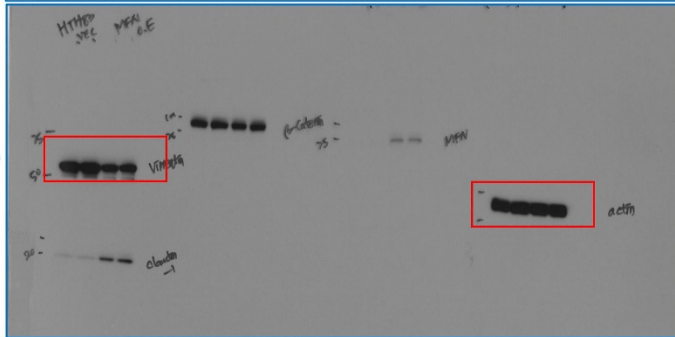


MITOFUSIN1 (80 Kda)

N-CADHERIN (140 Kda)



VIMENTIN (57 Kda)



ACTIN (50 Kda)

SNAIL (29 Kda)

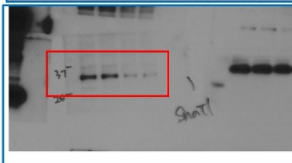


Figure 4

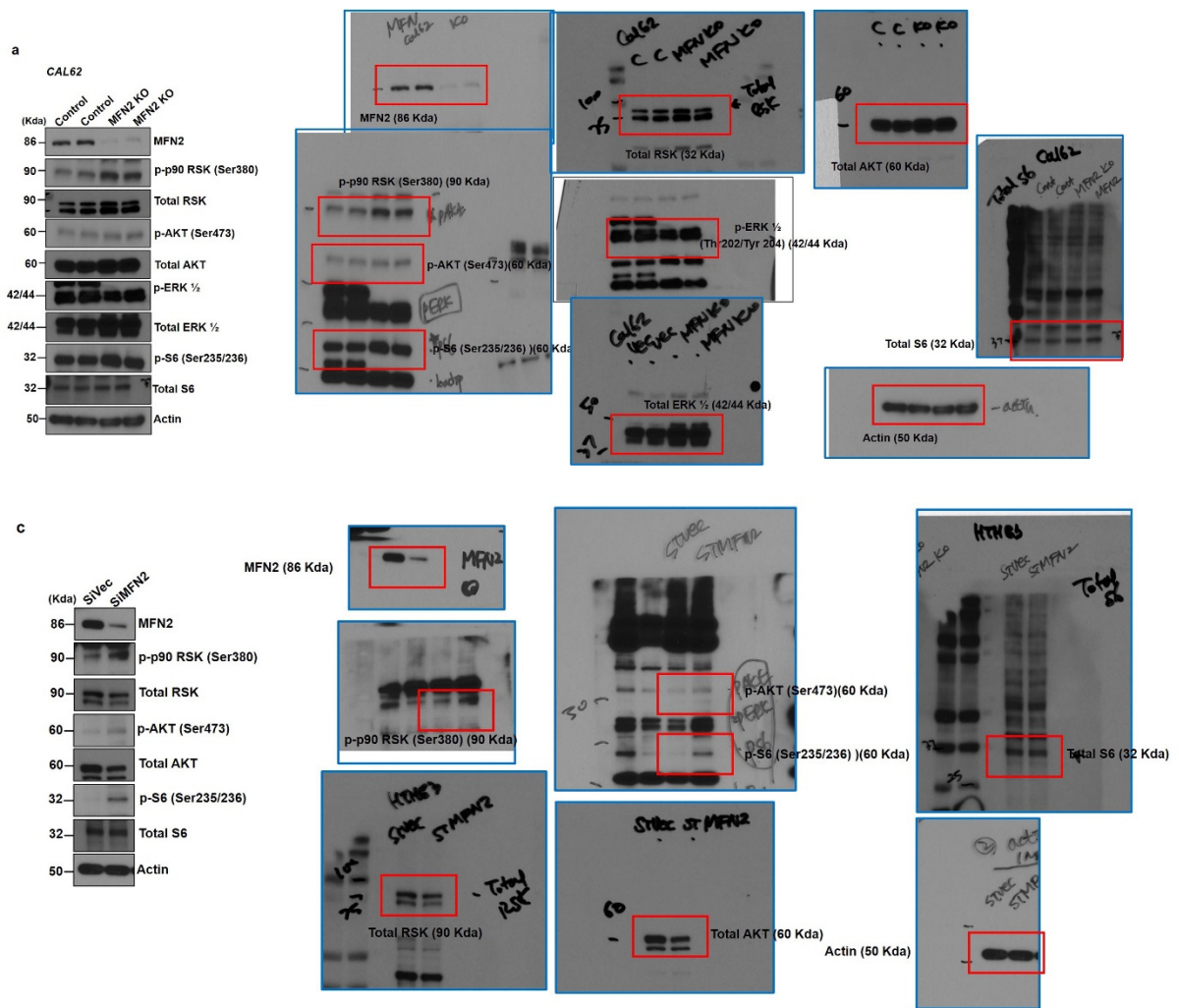
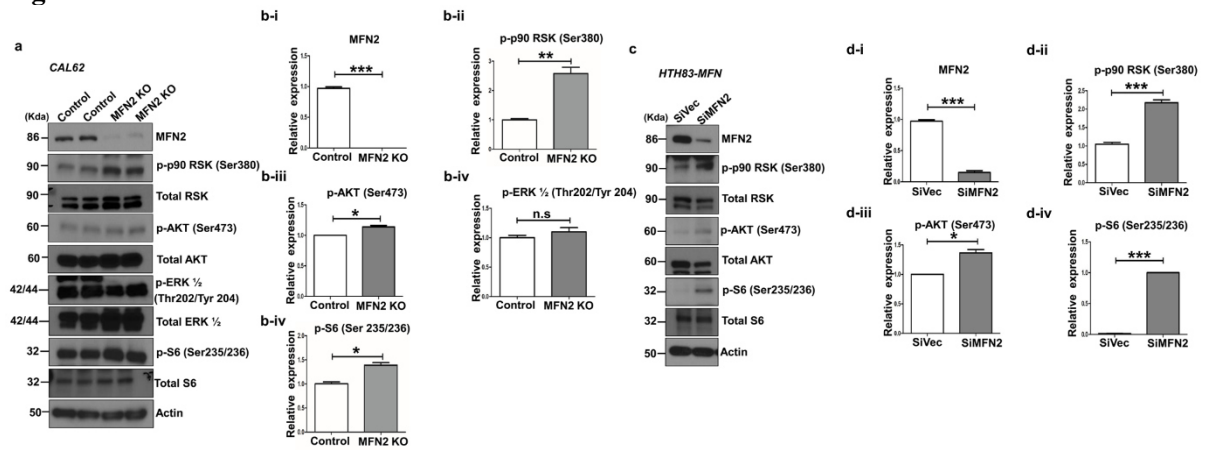
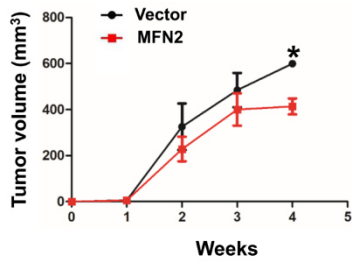
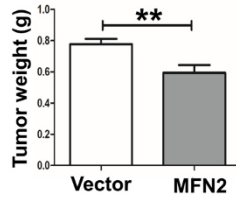


Figure 5

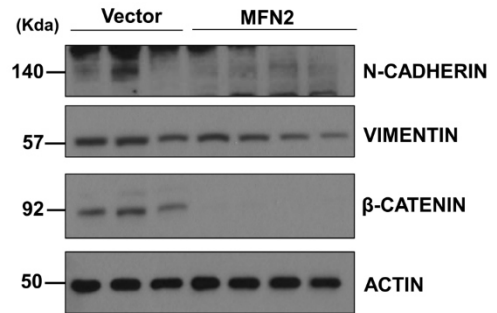
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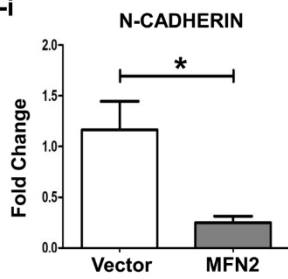
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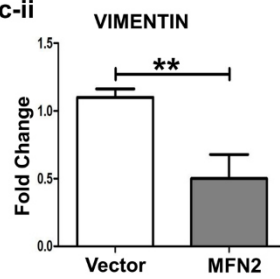
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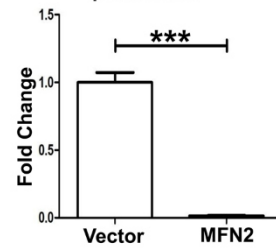
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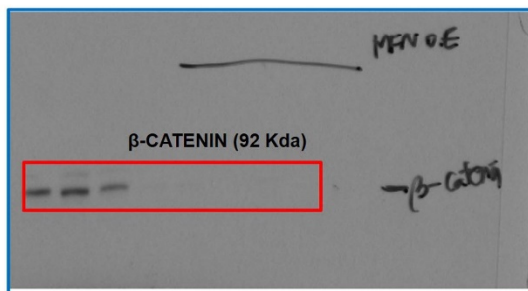
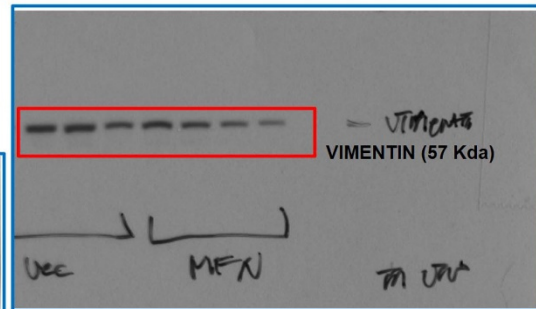
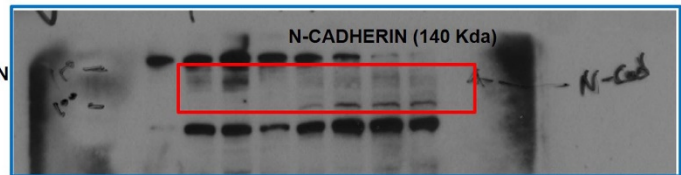
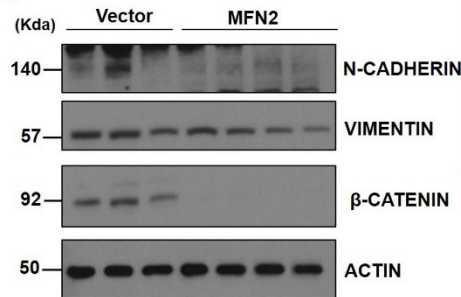
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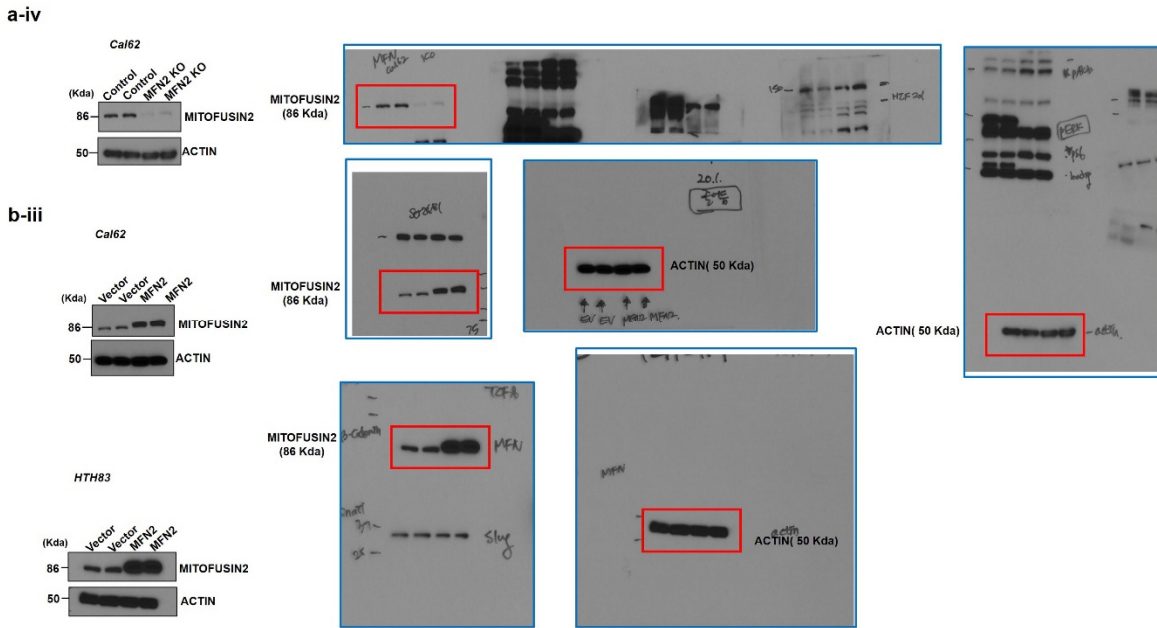
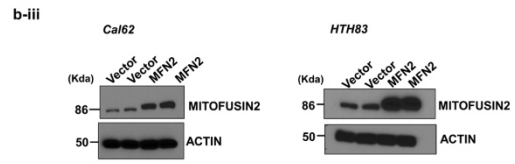
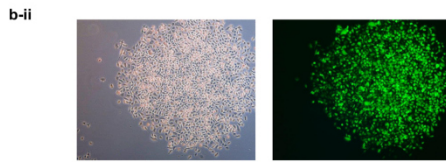
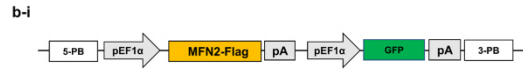
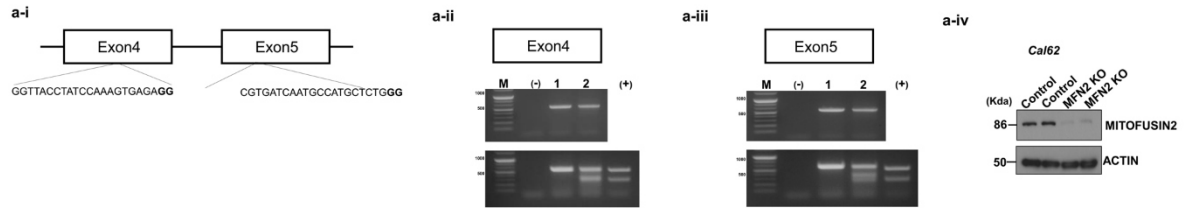
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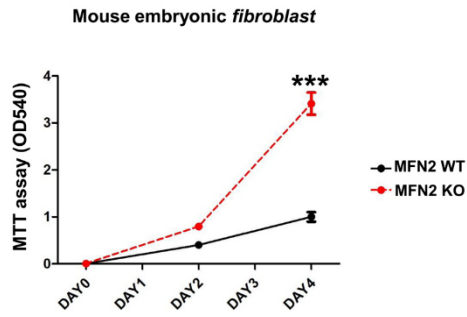


Supplementary Figure 2

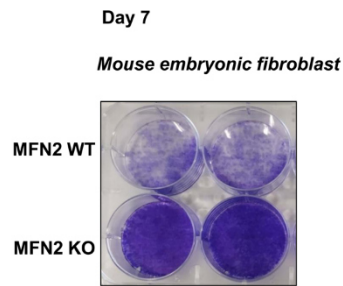


Supplementary Figure 4

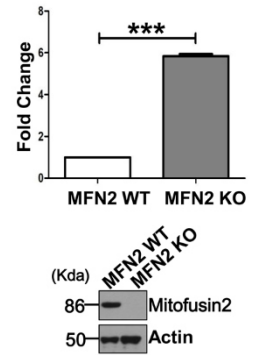
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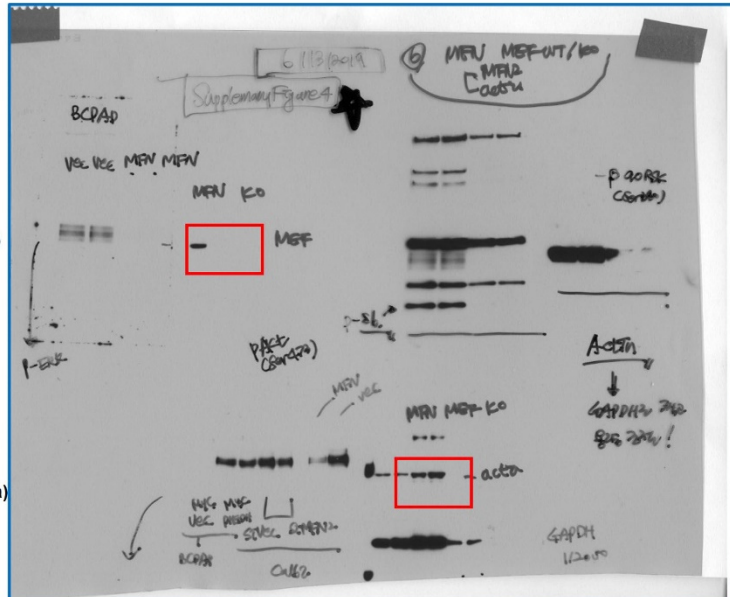
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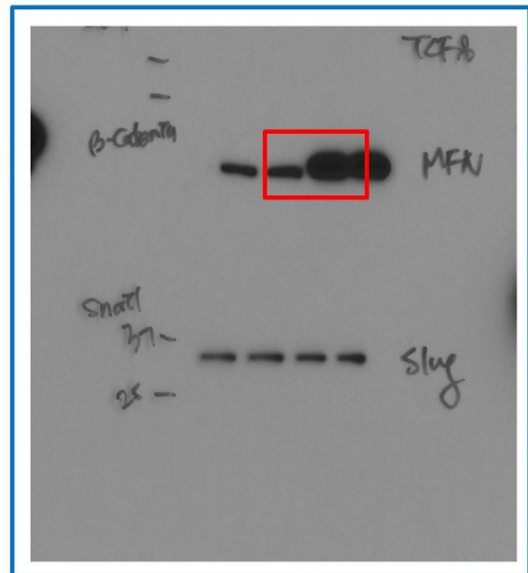
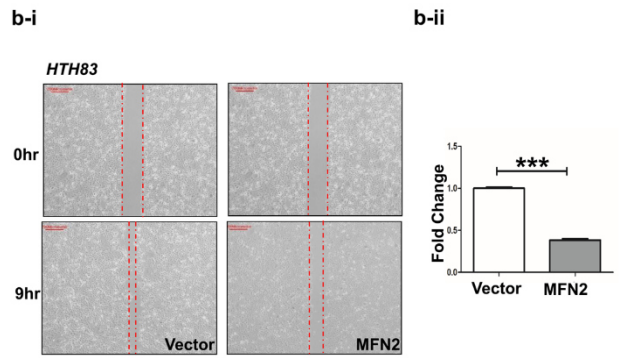
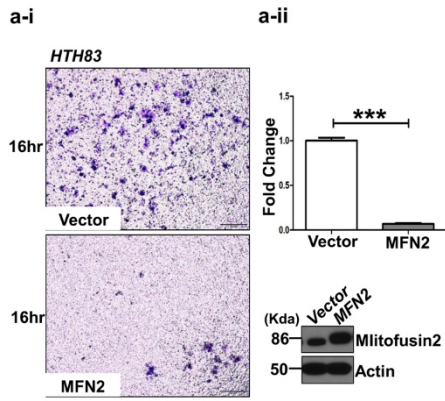
b-ii



b-ii



Supplementary Figure 5



Actin (50 Kda)



Supplementary Figure 7

