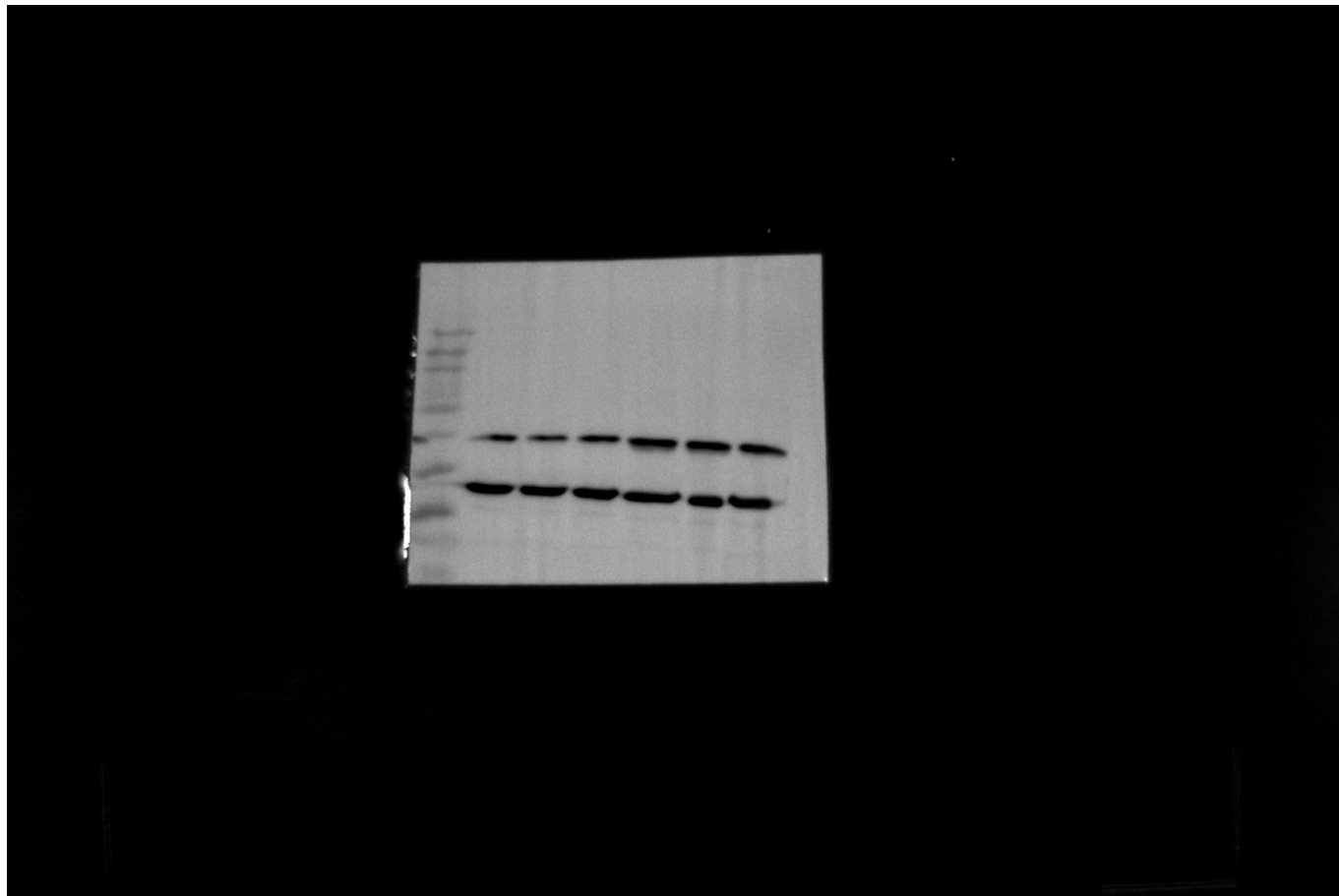


Supplementary information for Figure 2C

Source Western blot and documentation of image presentation

A Complete source image



The complete source image is shown in its original acquisition orientation. The marker lane is at the left. Sample lanes 1–3 are AS and lanes 4–6 are NC, from left to right. AS, asthenozoospermia; NC, normozoospermic controls.

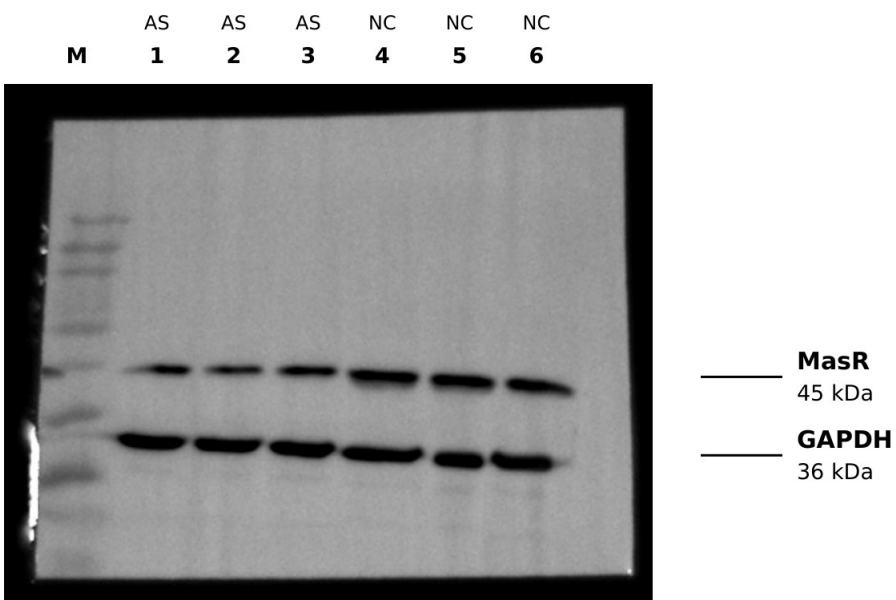
Image presentation

For Figure 2C, the blot image was horizontally flipped as a whole to display NC before AS. Consequently, the displayed sample lanes correspond to source lanes 6, 5, 4, 3, 2 and 1, from left to right. Individual lanes were not independently rearranged, and images from different sources were not merged.

The MasR and GAPDH regions were cropped and displayed as separate strips with white space between them. The complete source image above has not been flipped, cropped or subjected to intensity adjustment in preparing this supplementary document.

Figure 2C source annotation and displayed panel

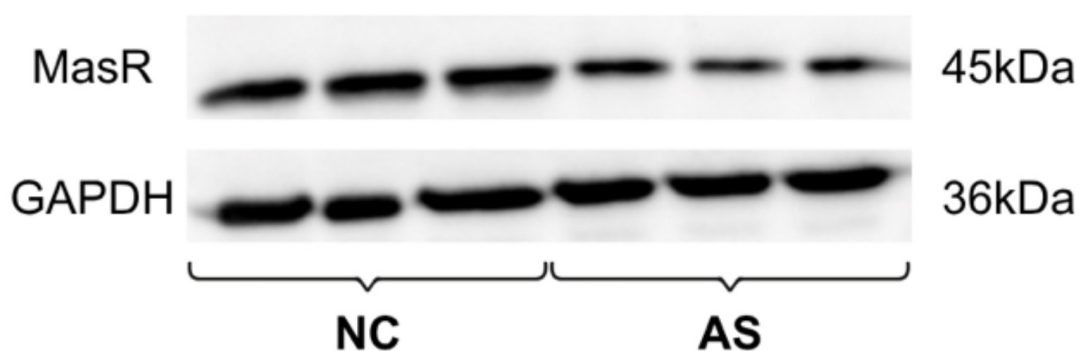
B Enlarged source view



M denotes the marker lane. Numbers 1–6 identify sample positions in the original image. Protein identities and nominal molecular masses follow Figure 2C: MasR, 45 kDa; GAPDH, 36 kDa.

C Figure 2C as displayed in the manuscript

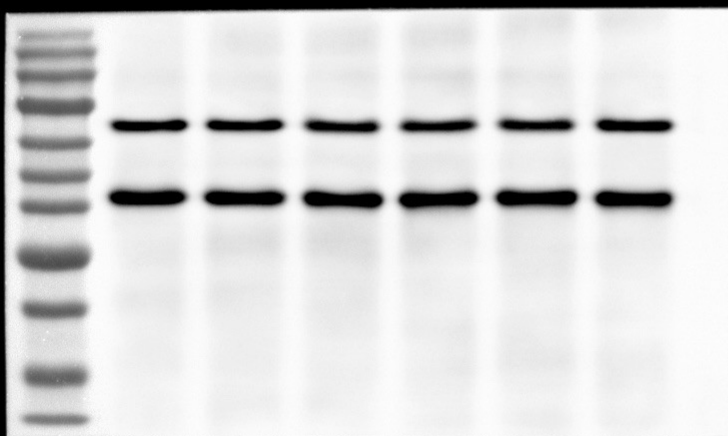
C



Both protein strips share the same horizontally flipped orientation. The three NC samples are displayed on the left and the three AS samples on the right. The full source image and lane assignments are provided in panels A and B.

Supplementary information for Figure 4A

A Complete AKT source image



The complete source image is reproduced in its original orientation. The leftmost lane contains the molecular-weight marker. Sample lanes 1–3 are Vehicle; sample lanes 4–6 are AVE0991 0.1 nM. The sample order is the same as in Figure 4A.

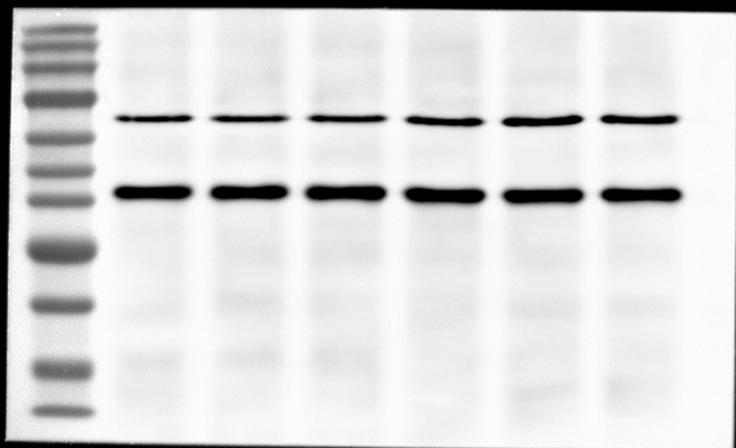
The upper band region corresponds to AKT, nominally 60 kDa, and the lower region to GAPDH, nominally 36 kDa.

No cropping, horizontal flipping, lane rearrangement or intensity adjustment was applied to this complete source image in preparing this supplementary document.

The AKT/GAPDH and p-AKT/GAPDH data are supplied as two separate source images. Figure 4A presents their cropped band regions in separate blocks with white space between them; each target is shown with its corresponding GAPDH region.

Supplementary information for Figure 4A

B Complete p AKT source image



The complete source image is reproduced in its original orientation. The leftmost lane contains the molecular-weight marker. Sample lanes 1–3 are Vehicle; sample lanes 4–6 are AVE0991 0.1 nM. The sample order is the same as in Figure 4A.

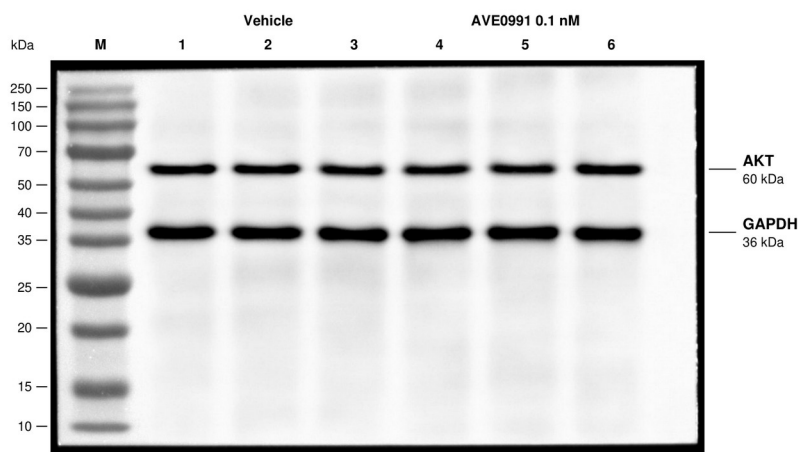
The upper band region corresponds to p-AKT, nominally 60 kDa, and the lower region to GAPDH, nominally 36 kDa.

No cropping, horizontal flipping, lane rearrangement or intensity adjustment was applied to this complete source image in preparing this supplementary document.

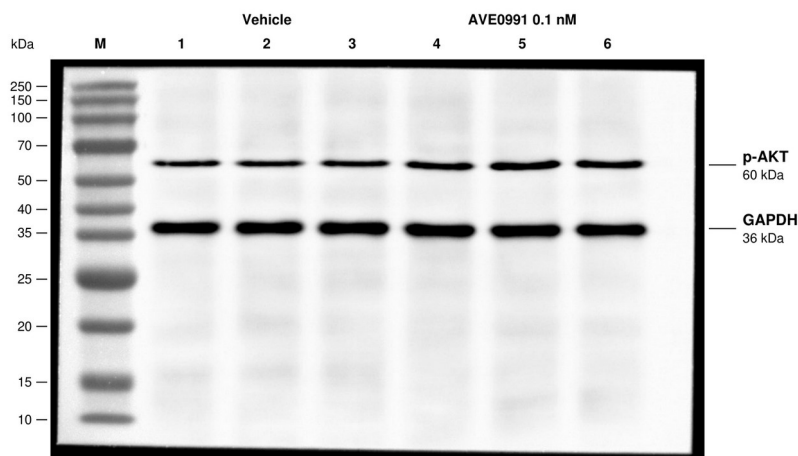
The AKT/GAPDH and p-AKT/GAPDH data are supplied as two separate source images. Figure 4A presents their cropped band regions in separate blocks with white space between them; each target is shown with its corresponding GAPDH region.

Figure 4A source annotations

C AKT source view



D p AKT source view



M, molecular-weight marker. Marker bands are labelled using the corrected reference supplied by the authors: 250, 150, 100, 70, 50, 40, 35, 25, 20, 15 and 10 kDa, from top to bottom. Protein labels at the right indicate nominal target masses.

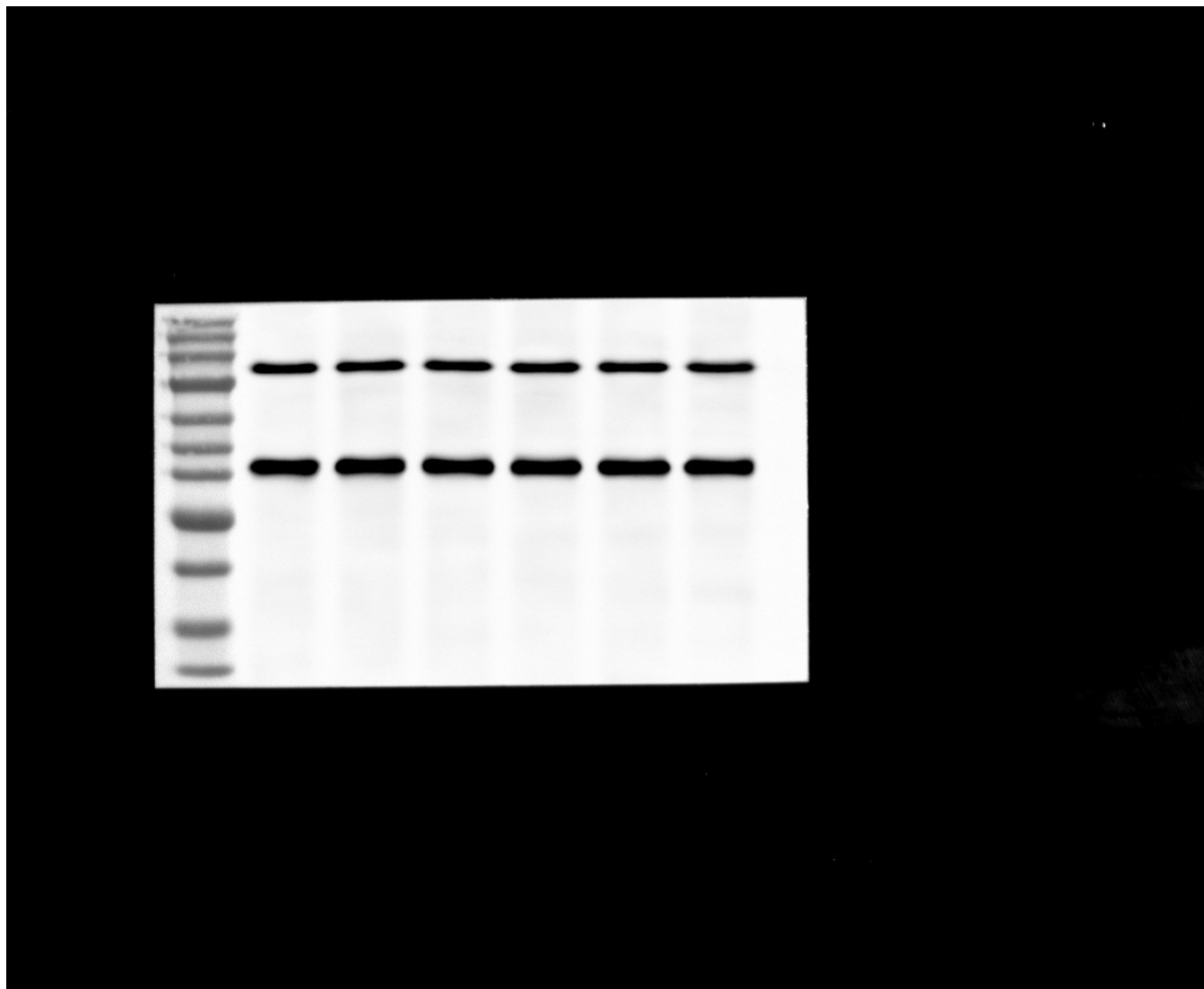
E Figure 4A as displayed in the manuscript

A



Supplementary information for Figure 4D

A Complete PI3K source image



The complete source image is reproduced in its original orientation. The leftmost lane contains the molecular-weight marker. Sample lanes 1–3 are Vehicle; sample lanes 4–6 are AVE0991 0.1 nM. The sample order is the same as in Figure 4D.

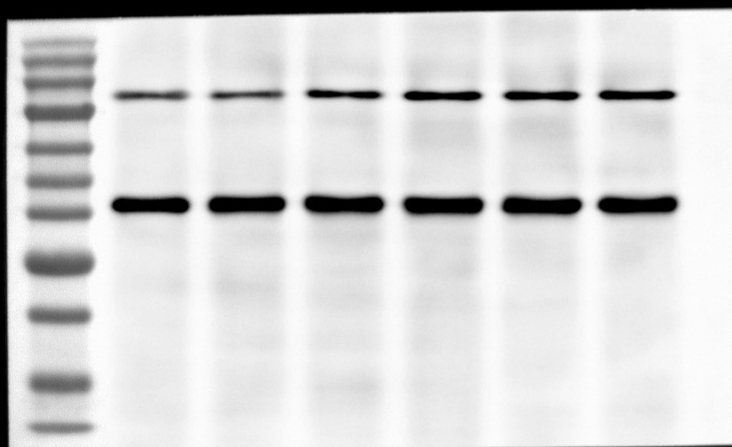
The upper band region corresponds to PI3K, nominally 85 kDa, and the lower region to GAPDH, nominally 36 kDa.

No cropping, horizontal flipping, lane rearrangement or intensity adjustment was applied to this complete source image in preparing this supplementary document.

The PI3K/GAPDH and p-PI3K/GAPDH data are supplied as two separate source images. Figure 4D presents their cropped band regions in separate blocks with white space between them; each target is shown with its corresponding GAPDH region.

Supplementary information for Figure 4D

B Complete p PI3K source image



The complete source image is reproduced in its original orientation. The leftmost lane contains the molecular-weight marker. Sample lanes 1–3 are Vehicle; sample lanes 4–6 are AVE0991 0.1 nM. The sample order is the same as in Figure 4D.

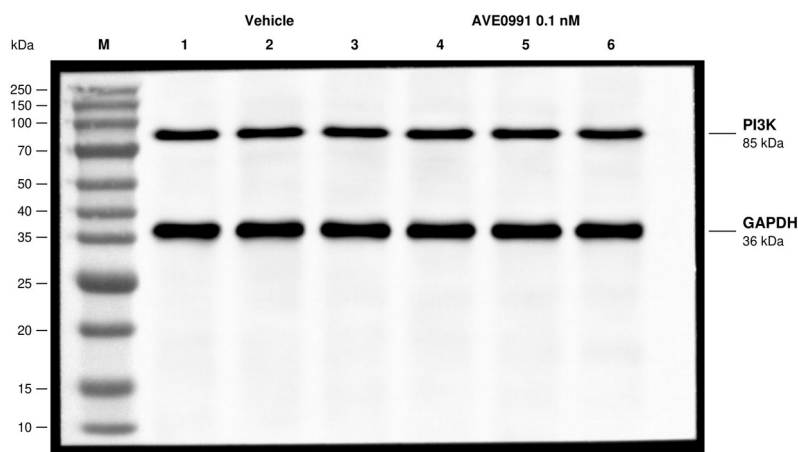
The upper band region corresponds to p-PI3K, nominally 85 kDa, and the lower region to GAPDH, nominally 36 kDa.

No cropping, horizontal flipping, lane rearrangement or intensity adjustment was applied to this complete source image in preparing this supplementary document.

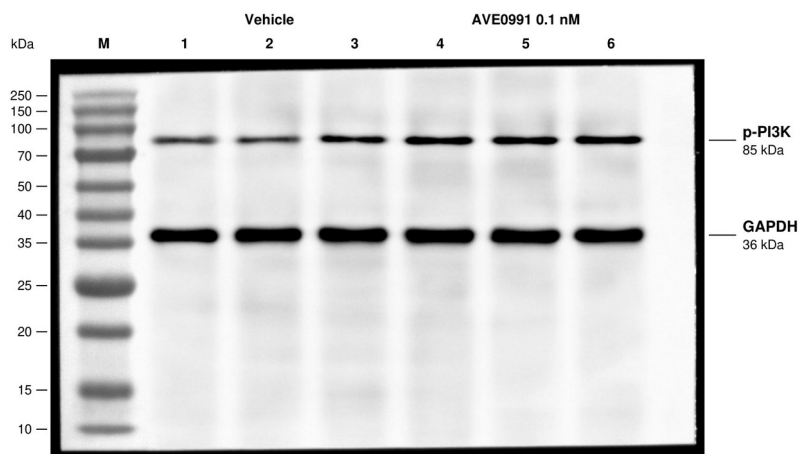
The PI3K/GAPDH and p-PI3K/GAPDH data are supplied as two separate source images. Figure 4D presents their cropped band regions in separate blocks with white space between them; each target is shown with its corresponding GAPDH region.

Figure 4D source annotations

C PI3K source view



D p PI3K source view



M, molecular-weight marker. Marker bands are labelled using the WJ103 prestained protein marker reference: 250, 150, 100, 70, 50, 40, 35, 25, 20, 15 and 10 kDa, from top to bottom. Protein labels at the right indicate nominal target masses.

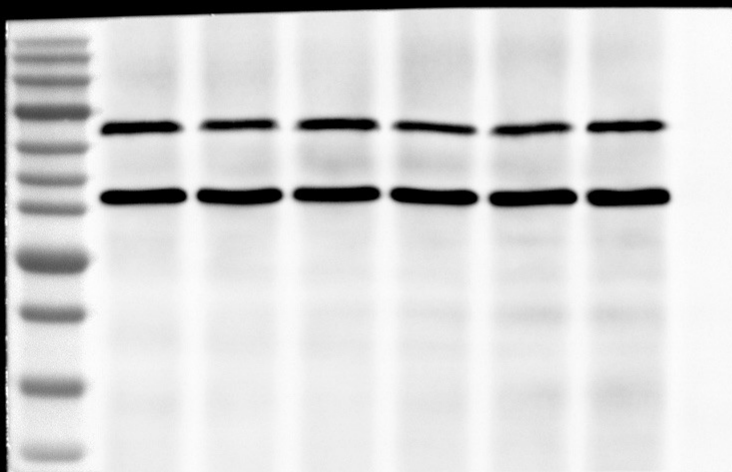
E Figure 4D as displayed in the manuscript

D



Supplementary information for Figure 6I

A Complete AKT source image



The complete source image is reproduced in its original orientation. The leftmost lane contains the molecular-weight marker. Sample lanes 1–6 are NC, T1DM, T1DM + AVE0991, T1DM + AVE0991 + LY294002, KO and KO + AVE0991, respectively. The sample order is the same as in Figure 6I.

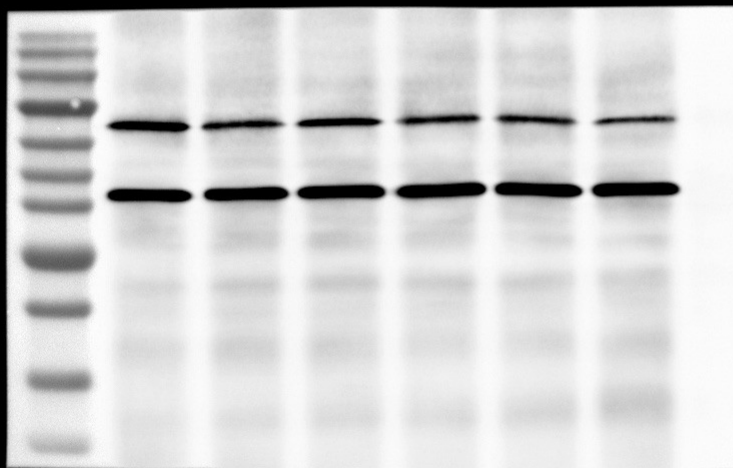
The upper band region corresponds to AKT, nominally 60 kDa, and the lower region to GAPDH, nominally 36 kDa.

No cropping, horizontal flipping, lane rearrangement or intensity adjustment was applied to this complete source image in preparing this supplementary document.

The AKT/GAPDH and p-AKT/GAPDH data are supplied as two separate source images. Figure 6I presents their cropped band regions in separate blocks with white space between them; each target is shown with its corresponding GAPDH region.

Supplementary information for Figure 6I

B Complete p AKT source image



The complete source image is reproduced in its original orientation. The leftmost lane contains the molecular-weight marker. Sample lanes 1–6 are NC, T1DM, T1DM + AVE0991, T1DM + AVE0991 + LY294002, KO and KO + AVE0991, respectively. The sample order is the same as in Figure 6I.

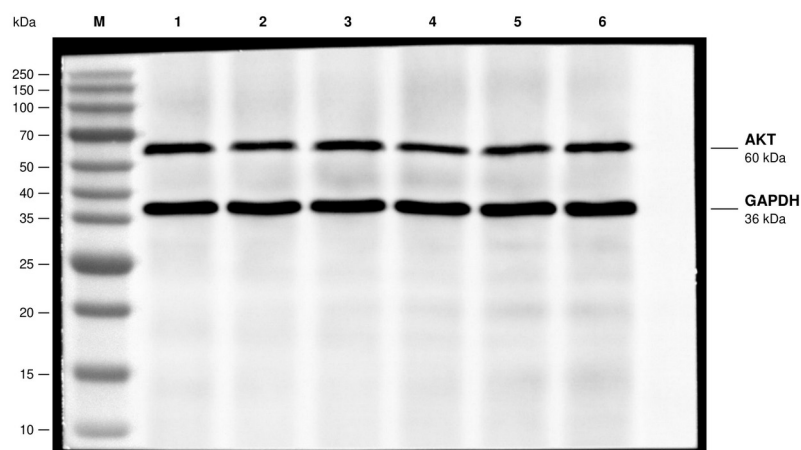
The upper band region corresponds to p-AKT, nominally 60 kDa, and the lower region to GAPDH, nominally 36 kDa.

No cropping, horizontal flipping, lane rearrangement or intensity adjustment was applied to this complete source image in preparing this supplementary document.

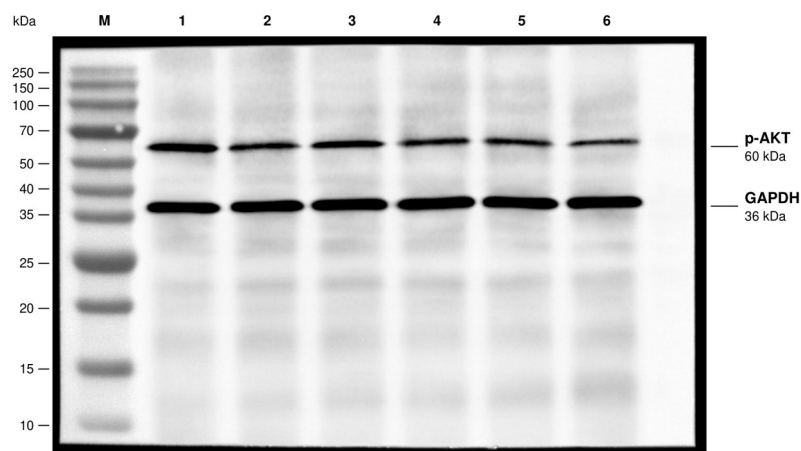
The AKT/GAPDH and p-AKT/GAPDH data are supplied as two separate source images. Figure 6I presents their cropped band regions in separate blocks with white space between them; each target is shown with its corresponding GAPDH region.

Figure 6I source annotations

C AKT source view



D p AKT source view



M, molecular-weight marker. Marker bands are labelled using the WJ103 prestained protein marker reference: 250, 150, 100, 70, 50, 40, 35, 25, 20, 15 and 10 kDa, from top to bottom. Protein labels at the right indicate nominal target masses.

Sample lanes: 1, NC; 2, T1DM; 3, T1DM + AVE0991; 4, T1DM + AVE0991 + LY294002; 5, KO; 6, KO + AVE0991. LY in the manuscript panel denotes LY294002.

Figure 6I panel correspondence

E Figure 6I as displayed in the manuscript

