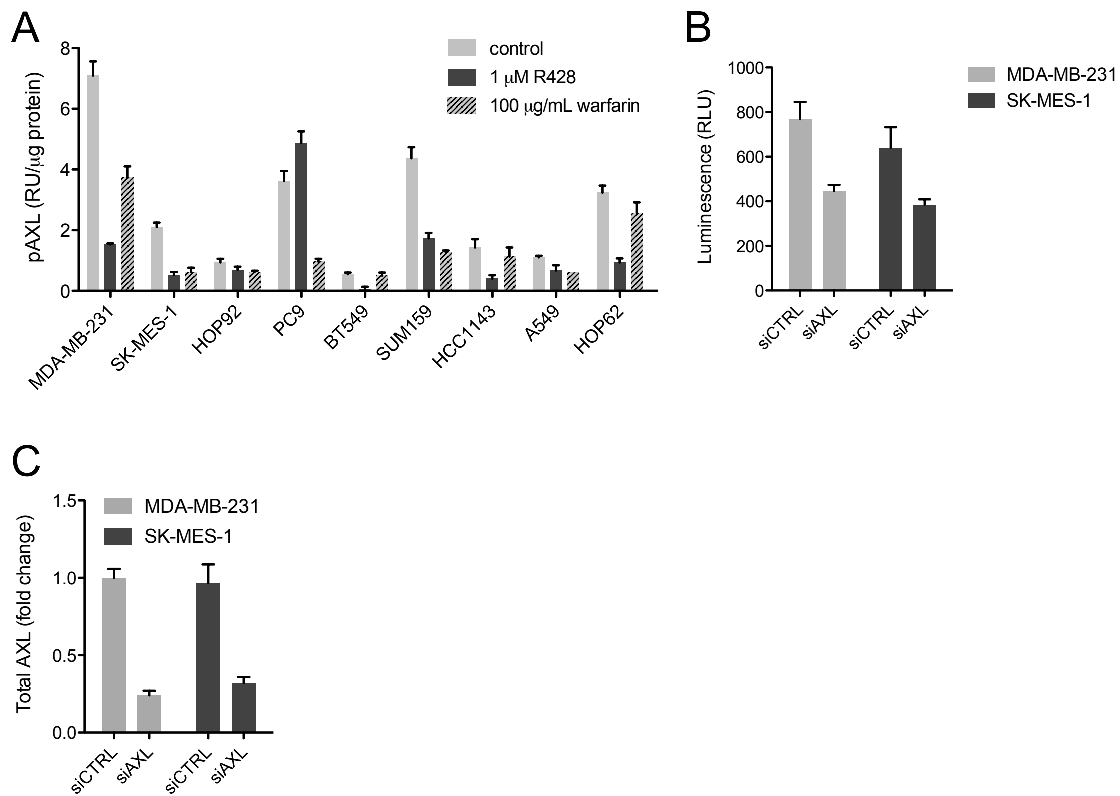
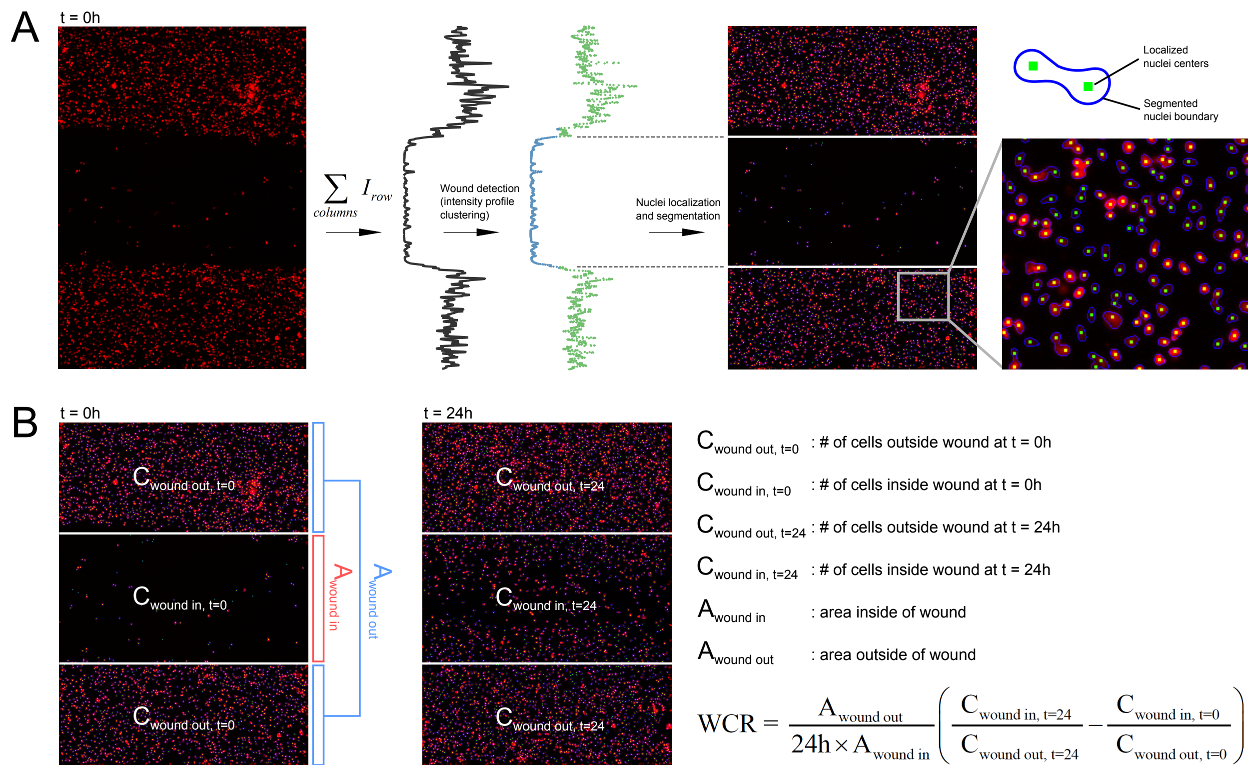


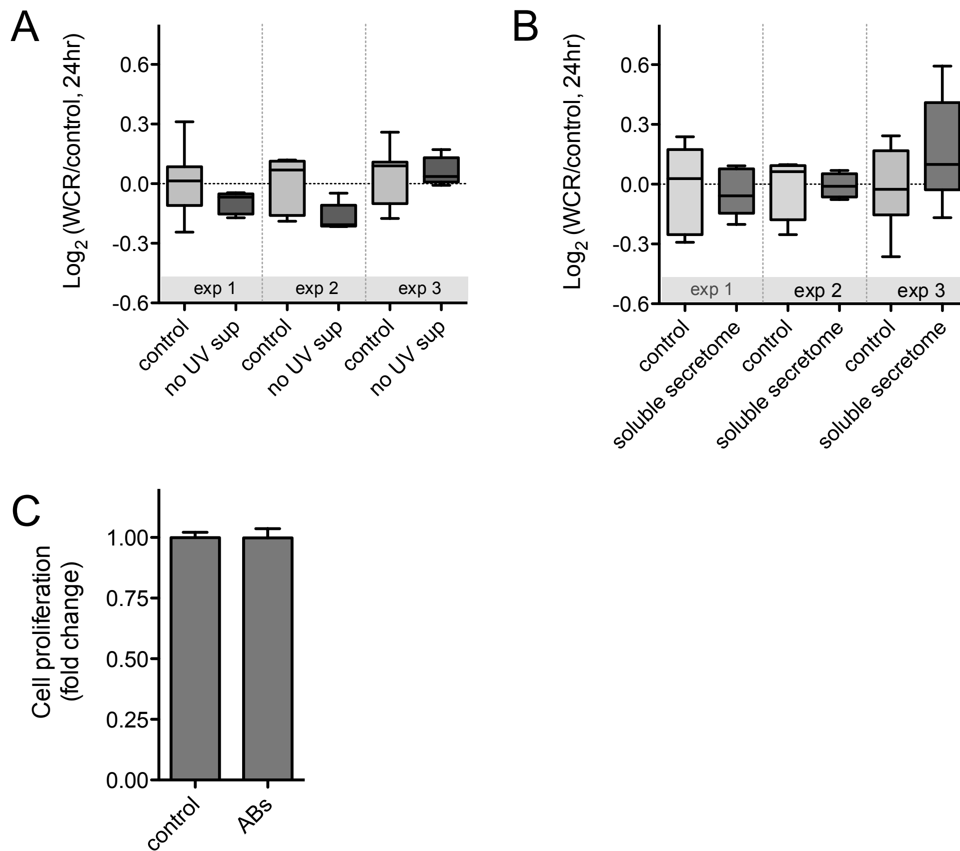

**Supplementary Fig. S1**

(A) AXL phosphorylation (pAXL) levels after 24 hrs of treatment with 1 µM R428 or 100 µg/mL warfarin, measured by ELISA. Data are means ± SEM of three biological replicates. (B) Cell proliferation measured in a Cell Titer Glo assay after 72 hrs of treatment with siAXL or non-targeting siCTRL. (C) AXL expression (tAXL) levels after 24 hrs of treatment with siAXL, measured by ELISA. Data are means ± SEM of three biological replicates. Cells were transfected with 25 nM of nontargeting siRNA or siRNA targeting AXL using DharmaFECT 1 (SK-MES-1) or DharmaFECT 4 (MDA-MB-231) transfection reagent.



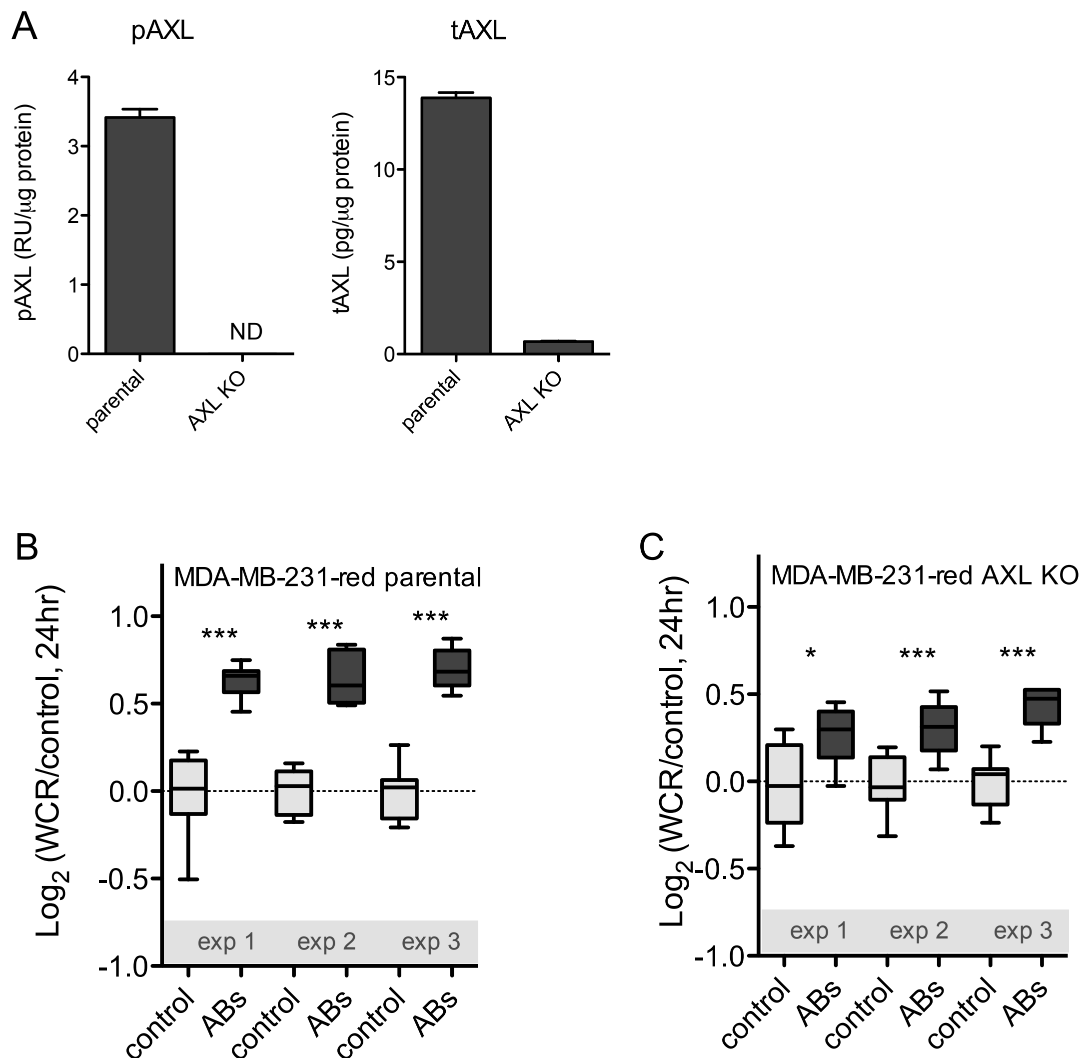

**Supplementary Fig. S2**

Image processing and quantification workflow for cell migration analysis. (A) A monolayer of cells expressing a red nuclear fluorescent reporter is scratched to create a wound region at time point t = 0h. Pixel intensities of nuclei are summed across columns for each row to generate a vertical image intensity profile. The wound region is automatically identified in each image via k-means clustering of the intensity profile to delineate a transition between the low intensity cluster (blue profile region = wound region) and high intensity cluster (green profile region = regions outside the wound). A 2D Gaussian filter-based convolution is used to segment nuclei and detect nuclei centers in each image and time point. (B) For each image a Wound Closure Rate (WCR) metric is computed for a given time point (e.g. 24h after wound scratching and treatment addition) to quantify cell migration into the wound over time. The WCR takes into account the number of cells and image areas both inside and outside of the wound to control for changes in cell number and differences in wound areas between images.



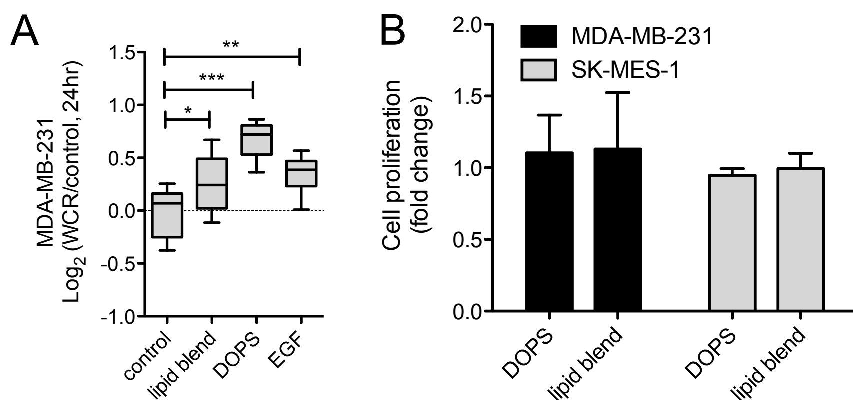

**Supplementary Fig. S3**

(A+B) Wound closure rate (WCR) of MDA-MB-231-red cells upon addition of the supernatant of non-UV irradiated HCC827 cells (A) or the soluble secretome of UV-irradiated HCC827 cells that was collected after centrifugation at 16500xg (B). Data of three independent experiments is presented as Log2 of the median with whiskers representing the 5 to 95 percentile of at least six measurements per condition. (C) Cell proliferation measured in a Cell Titer Glo assay after 72 hrs of treatment with apoptotic bodies (ABs). Data are means ± SEM of three biological replicates.




**Supplementary Fig. S4**

(A) AXL phosphorylation (pAXL) and total AXL (tAXL) expression levels in MDA-MB-231-red parental and MDA-MB-231-red AXL knockout cells measured by ELISA. Data are means ± SEM of three biological replicates. pAXL levels in the AXL knockout cell line were not detectable (ND). (B+C) Wound closure rate (WCR) of MDA-MB-231-red parental cells (B) and AXL knock out (KO) cells (C) upon addition of apoptotic bodies (ABs). Data of three independent experiments is presented as Log2 of median with whiskers representing the 5 to 95 percentile of at least eight measurements per condition (*p < 0.05, **p < 0.01, ***p < 0.001, Student's *t* test).




**Supplementary Fig. S5**

(A) Wound closure rate (WCR) of MDA-MB-231-red cells upon addition of SUVs composed of DOPS alone, a 5:3:2 w/w lipid blend of DOPE:DOPS:DOPC, or 200 ng/mL EGF. All lipids were present at a concentration of 50 μg/mL. Data of a representative experiment is presented as Log2 of the median with whiskers representing the 5 to 95 percentile of at least six measurements per condition (*$p < 0.05$, **$p < 0.01$, ***$p < 0.001$, Student's *t* test). (B) Cell proliferation of MDA-MB-231 and SK-MES-1 cells measured in a Cell Titer Glo assay after 72 hrs of treatment with SUVs of DOPS or the lipid blend. Data are means ± SEM of three biological replicates.