

Supplementary data

Growth Hormone upregulates melanoma drug resistance and migration via melanoma derived exosomes

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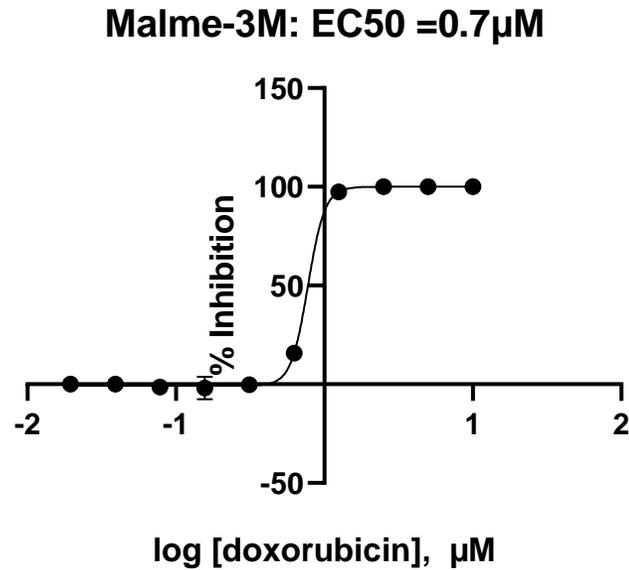
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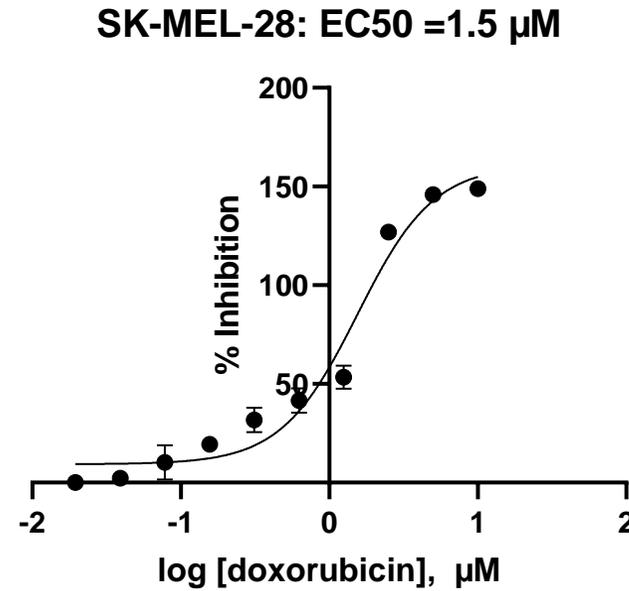
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Supplementary Figure 1.

A



B



C

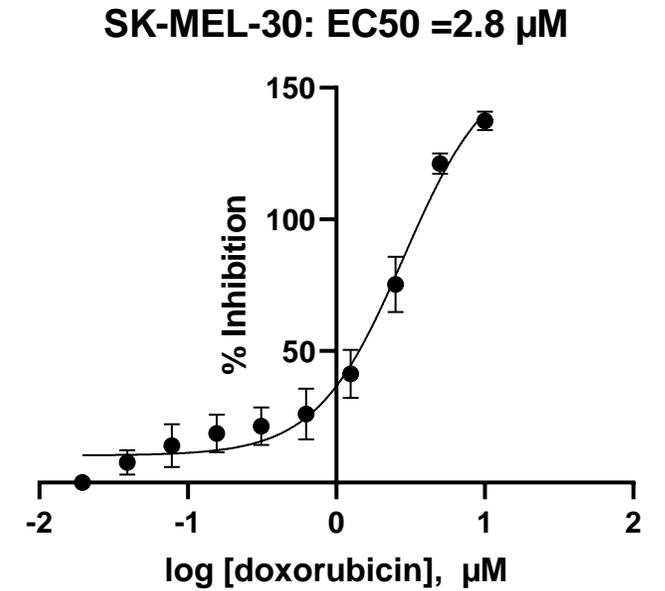
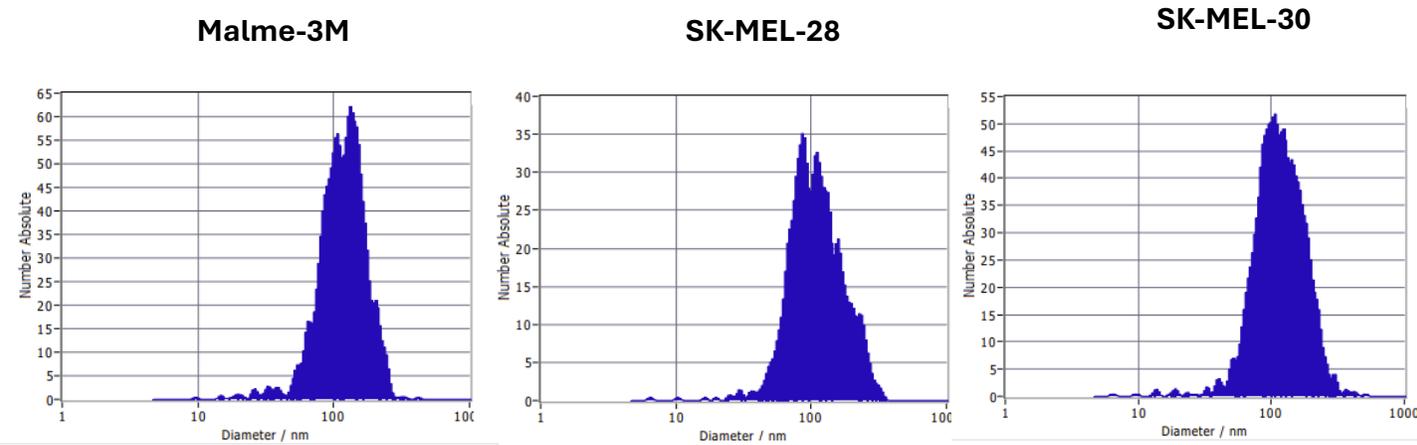


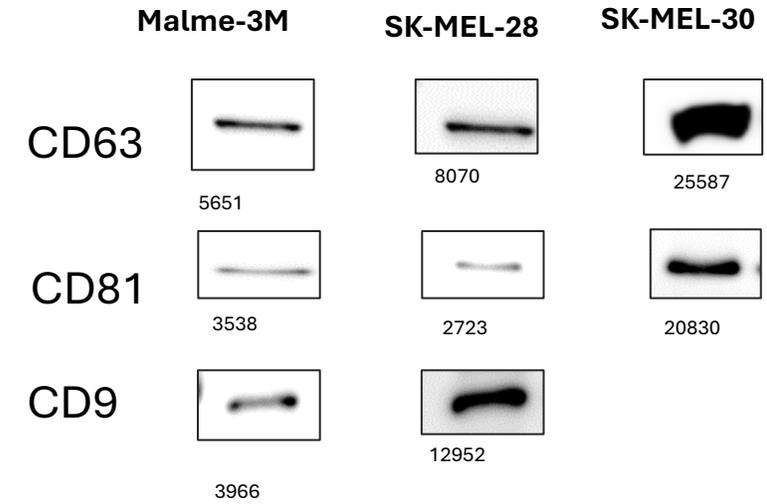
Figure. S1: EC₅₀s (in μM) of the doxorubicin chemotherapy in (A) Malme-3M, (B) SK-MEL-28, (C) SK-MEL-30 human melanoma cell lines. Resazurin-resorufin cell viability assay (48-hr) was employed for 10-dose EC₅₀ determination in 96-well plate format with 5000 cells/well. Percent inhibition was calculated and nonlinear regression (variable slope – four parameters) was used to calculate EC₅₀ in Graphpad Prizm.

Supplementary Figure 2.

A



B



FigureS2: Characterization of melanoma-derived exosomes. A. Nanoparticle Tracking Analysis of exosomes. B. Exosome markers CD63, CD9, CD81 as detected by western blot.

Supplementary Figure 3.

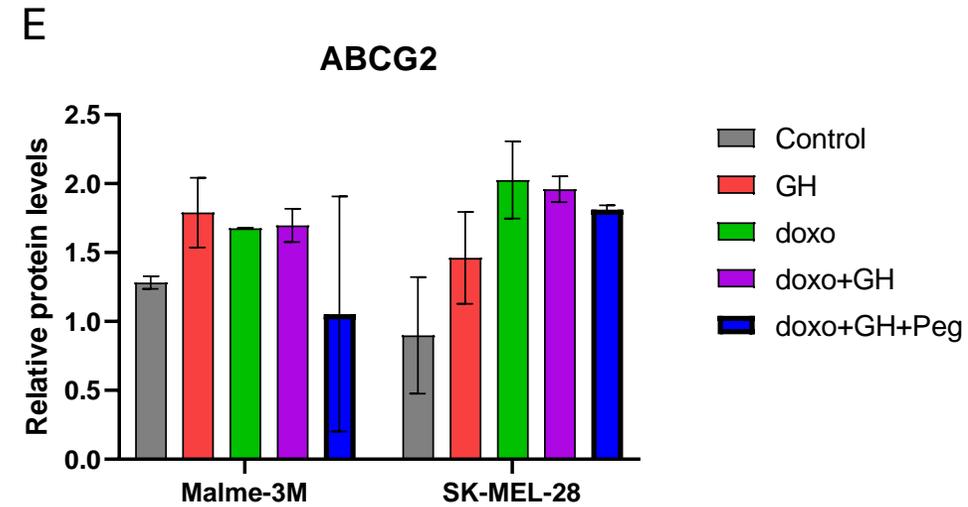
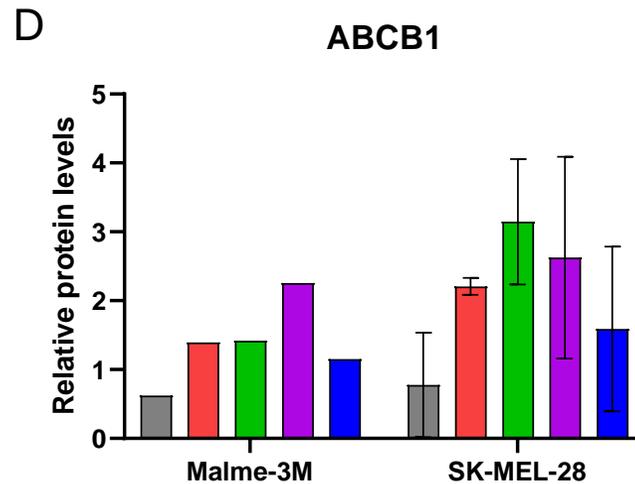
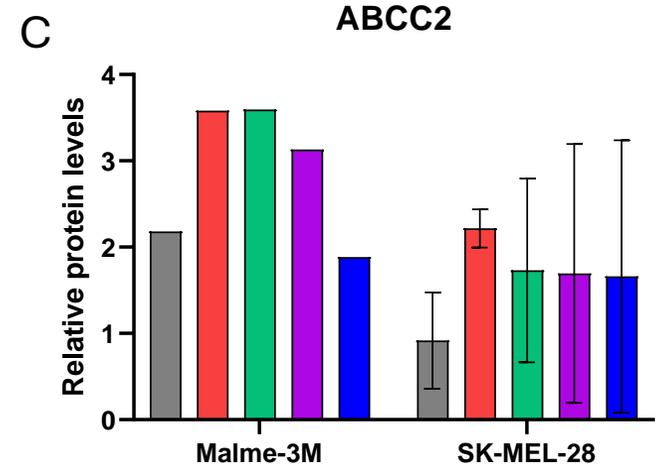
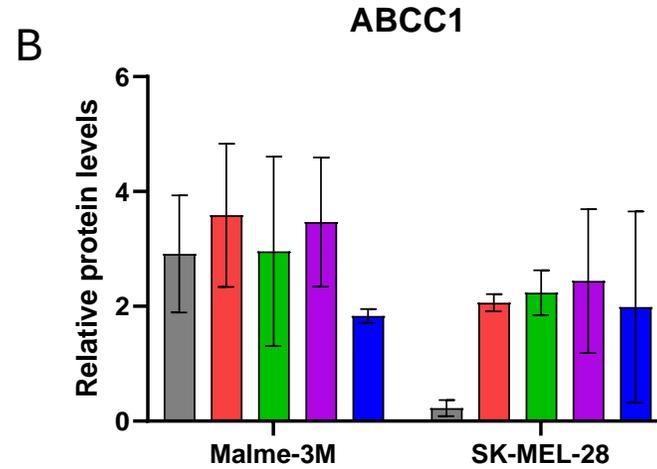
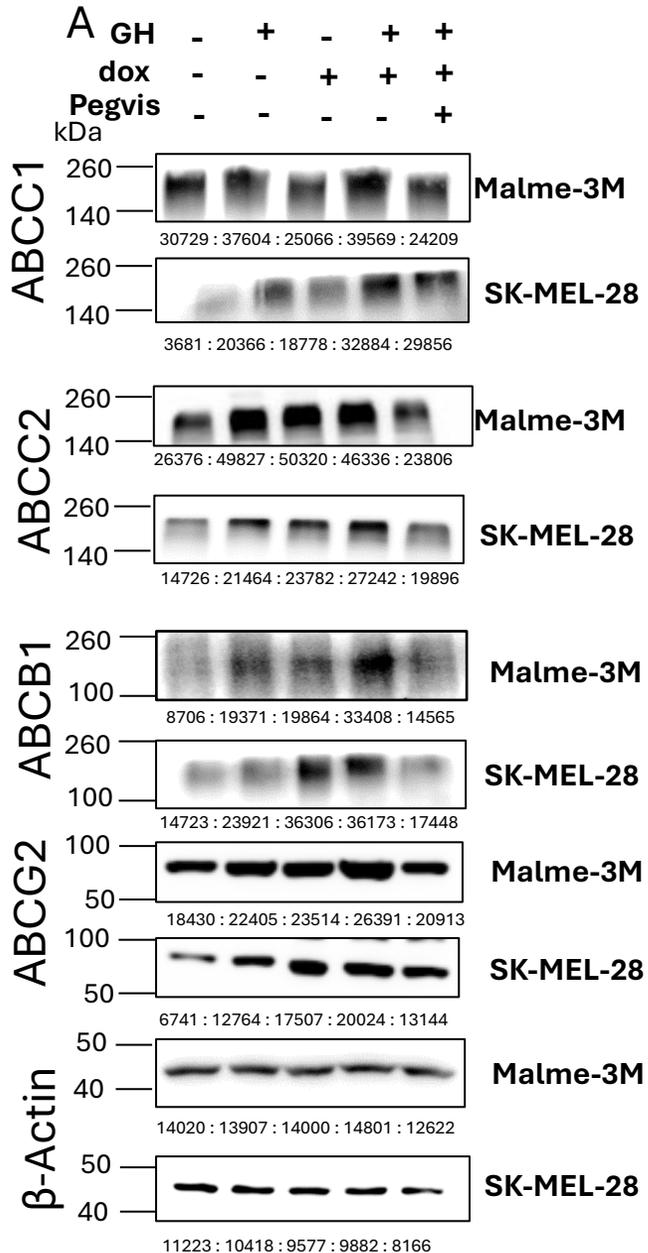


Figure S3. GH elevates ABC efflux pump levels in melanoma cells. A. Protein levels of ABCC1, ABCC2, ABCB1, and ABCG2 in human melanoma cells, Malme-3M, SK-Mel-28, and SK-MEL30, 96-hour post treatment with 50 ng/ml GH independently or in combination with 150 nM doxorubicin, 250nM pegvi-somant. B-E. Blots were quantified using ImageJ and expressions were normalized using β -actin as a control and presented as relative protein expression.

Supplementary Figure 4.

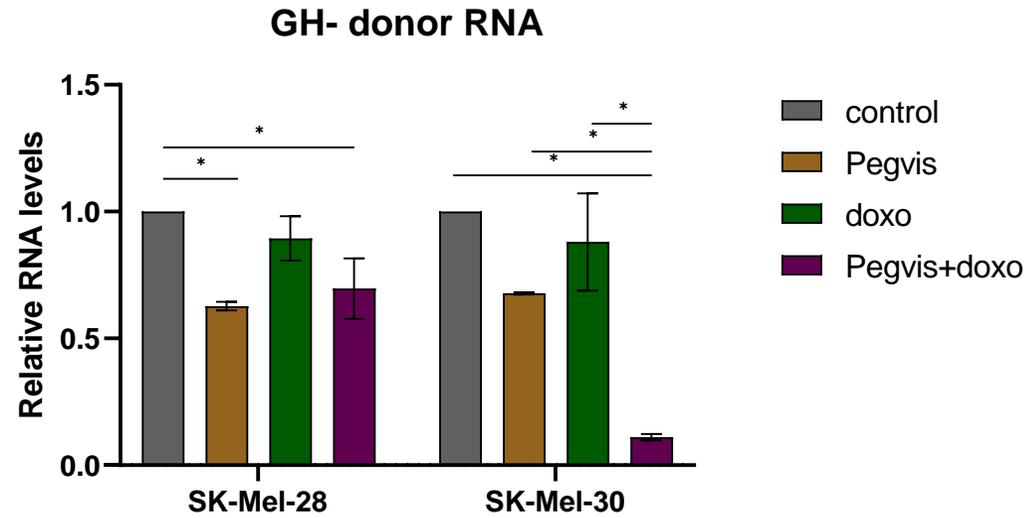


Figure S4. Pegvisomant downregulates basal levels of GH in human melanoma cells in SK-Mel-28, and SK-MEL30, 24-hour post treatment with EC50 dosage of doxorubicin or in combination with 250nM pegvisomant.

Supplementary Figure 5.

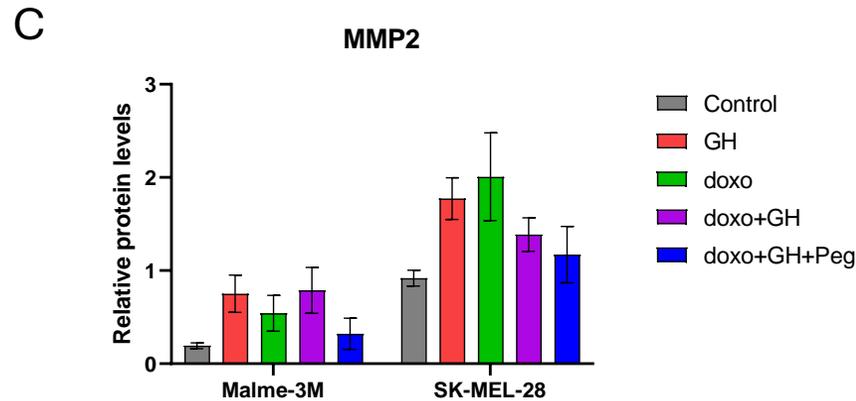
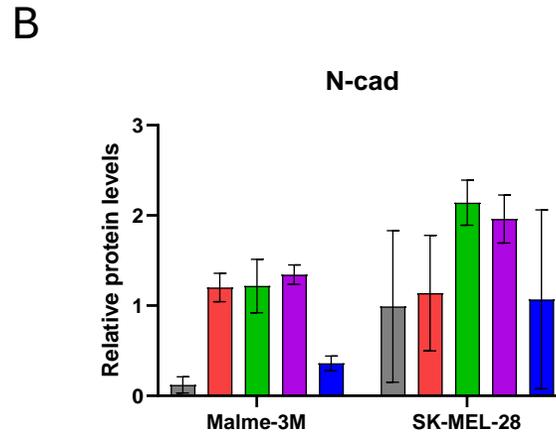
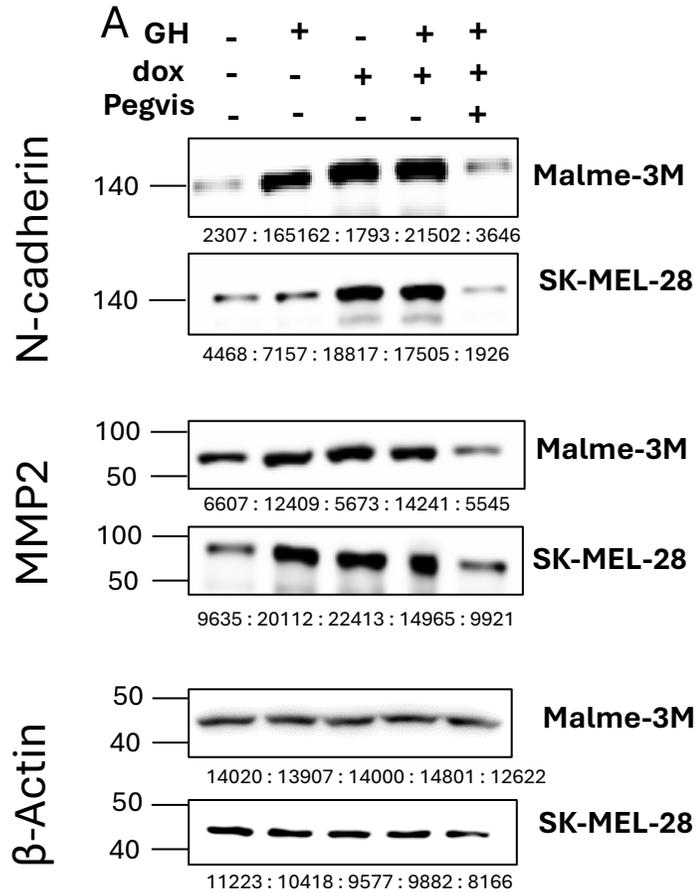


Figure S5. GH elevates ABC efflux pump levels in melanoma cells. A. Protein levels of ABCC1, ABCC2, ACCB1, and ABCG2 in human melanoma cells, Malme-3M, SK-Mel-28, and SK-MEL30, 96-hour post treatment with 50 ng/ml GH independently or in combination with EC50 dosage of doxorubicin, 250nM pegvi-somant. B-E. Blots were quantified using ImageJ and expressions were normalized using β -actin as a control and presented as relative protein expression.

Supplementary Figure 6.

