

Figure S1. Kaplan-Meier survival analysis for patients with breast cancer according to the subcellular localization and differential expression of RAD51. (A) Disease-free survival and (B) overall survival of patients with breast cancer were analyzed for the four conditions that comprised low cytoplasmic RAD51 (cyto^{low}), high cytoplasmic RAD51 (cyto^{high}), low nuclear RAD51 (nu^{low}) and high nuclear RAD51 (nu^{high}). P-values were determined by two-sided log-rank tests. cyto, cytoplasm; nu, nucleus.

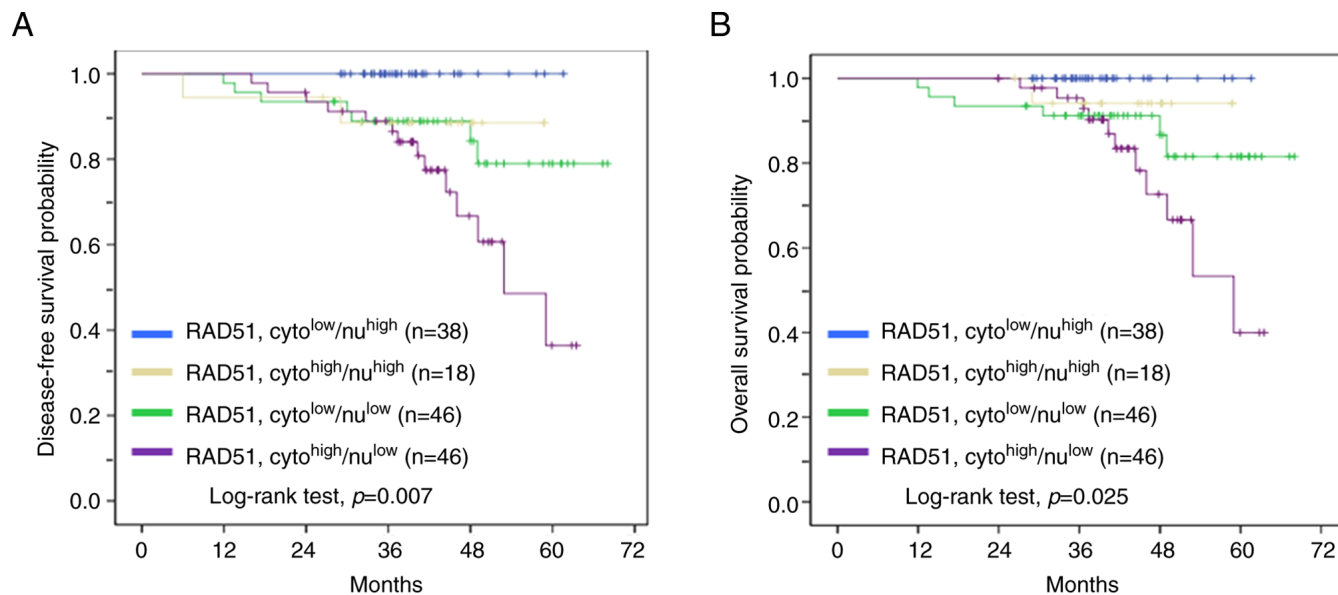
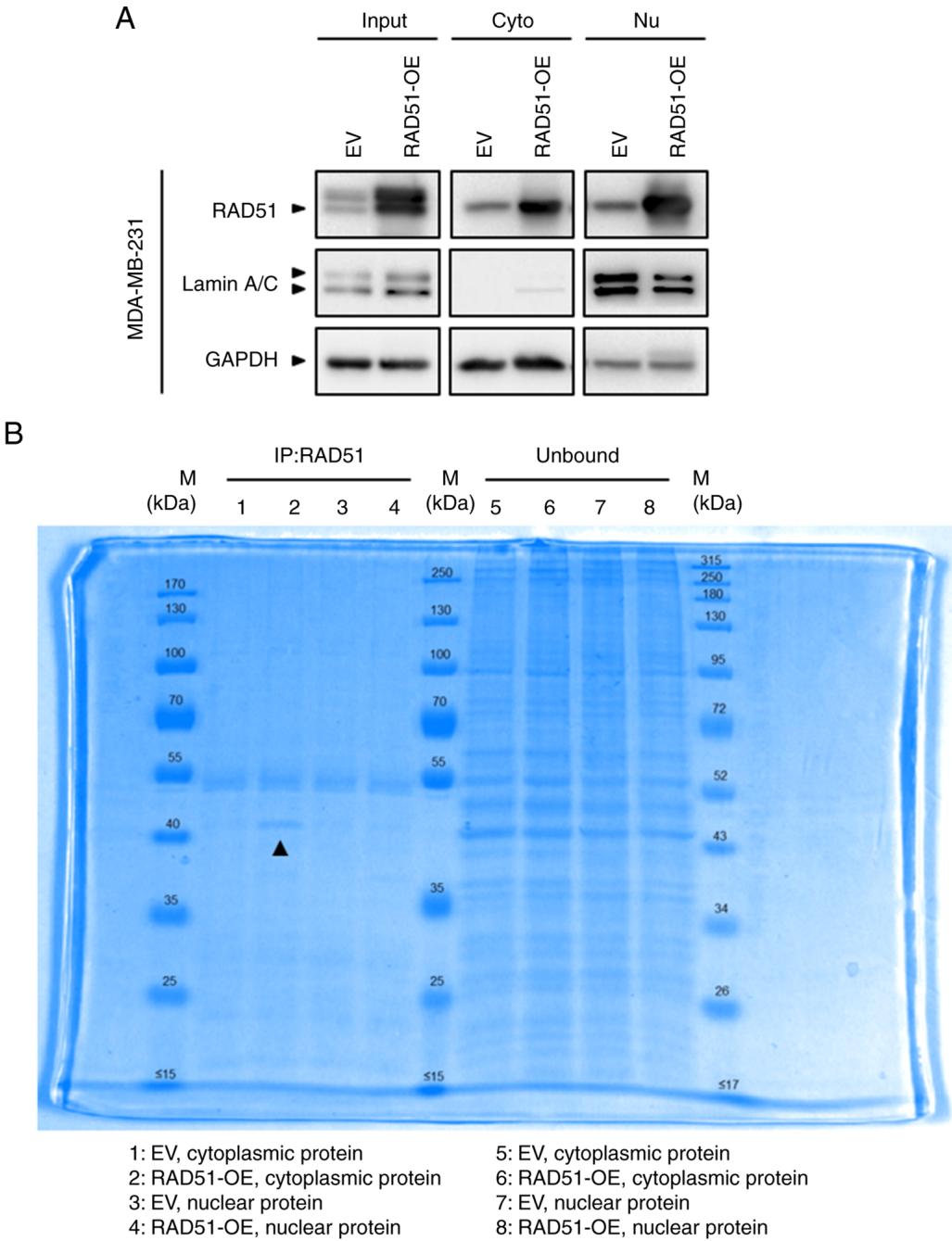


Figure S2. Subcellular fractionation, immunoprecipitation and results of LC-MS/MS for the identification of RAD51-interacting proteins. (A) The cytoplasmic and nuclear protein fractions of MDA-MB-231 cells were extracted, followed by western blot analysis for protein expression. (B) The subcellular protein fractions of MDA-MB-231 cells with overexpression of RAD51 or their controls were immunoprecipitated with anti-RAD51 antibodies (lanes 1-4), and the corresponding unbound flowthrough was loaded in parallel (lanes 5-8), followed by one-dimensional SDS-PAGE and Coomassie blue staining for the separated proteins. (C) The protein band visualized by Coomassie blue staining as indicated by a solid arrowhead was excised for in-gel digestion, followed by LC-MS/MS for protein identification. The results showed the highest spectral count of 104 compared to others, and that matched the protein identity of β -actin. EV, empty vector; RAD51-OE, overexpression of RAD51; shLuc, knockdown of firefly luciferase; shRAD51, knockdown of RAD51; cyto, cytoplasm; nu, nucleus; IP, immunoprecipitation; M, MW marker; MW, molecular weight; LC-MS/MS, liquid chromatography tandem mass spectrometry.



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UniProt ID	Protein name	Length (amino acids)	Predicted MW (Da)	LC-MS/MS Spectral count	Description
P60709 • ACTB_HUMAN	β -actin	375	41,737	104	Protein was identified from the excised gel slice indicated with "▲"