

# A tiny RNA with a big role in melanoma

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will emerge as a better therapeutic option to treat [melanoma](#) patients," said senior author Narendra Wajapeyee, assistant professor of pathology at Yale School of Medicine and a member of Yale Cancer Center.

Provided by Yale University

Credit:

A Yale-led study has identified a key mechanism in the regulation of gene expression that promotes the proliferation of melanoma cells. The finding opens a possible avenue for development of treatments that target this mechanism. The study appears online Feb. 18 in the journal *eLife*.

Melanoma is the deadliest form of skin cancer. BRAF and NRAS genetic mutations are known to occur in a very large proportion of melanomas. But although scientists have identified the oncogenic mutations that trigger [melanoma cells](#) and their proliferation, the mechanism that causes [normal cells](#) to transform into cancerous melanoma cells and cause their spread has not been well defined.

The Yale team identified a microRNA called miR-146a that accelerates in activity in the presence of these oncogenes by activating a cancer promoting signaling pathway called Notch.

The authors suggest that Notch and another signaling pathway called MAP kinase, which is activated by these same oncogenes, represent a valuable drug development target. "Our study has identified a new genetic vulnerability in melanoma, and it is likely that simultaneous inhibition of MAP Kinase pathway and NOTCH [signaling pathway](#)

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