

Figure S1 Genes ordered by drug response score (DRS). Pharmacotranscriptomic correlations of each gene to 481 drugs from the Cancer Therapeutics Response Portal (CTRP) were calculated and converted to DRS(0.3). The DRS for all drugs, all kinase inhibitors, and inhibitors against PI3K β , ALK, and MET are comparatively shown.

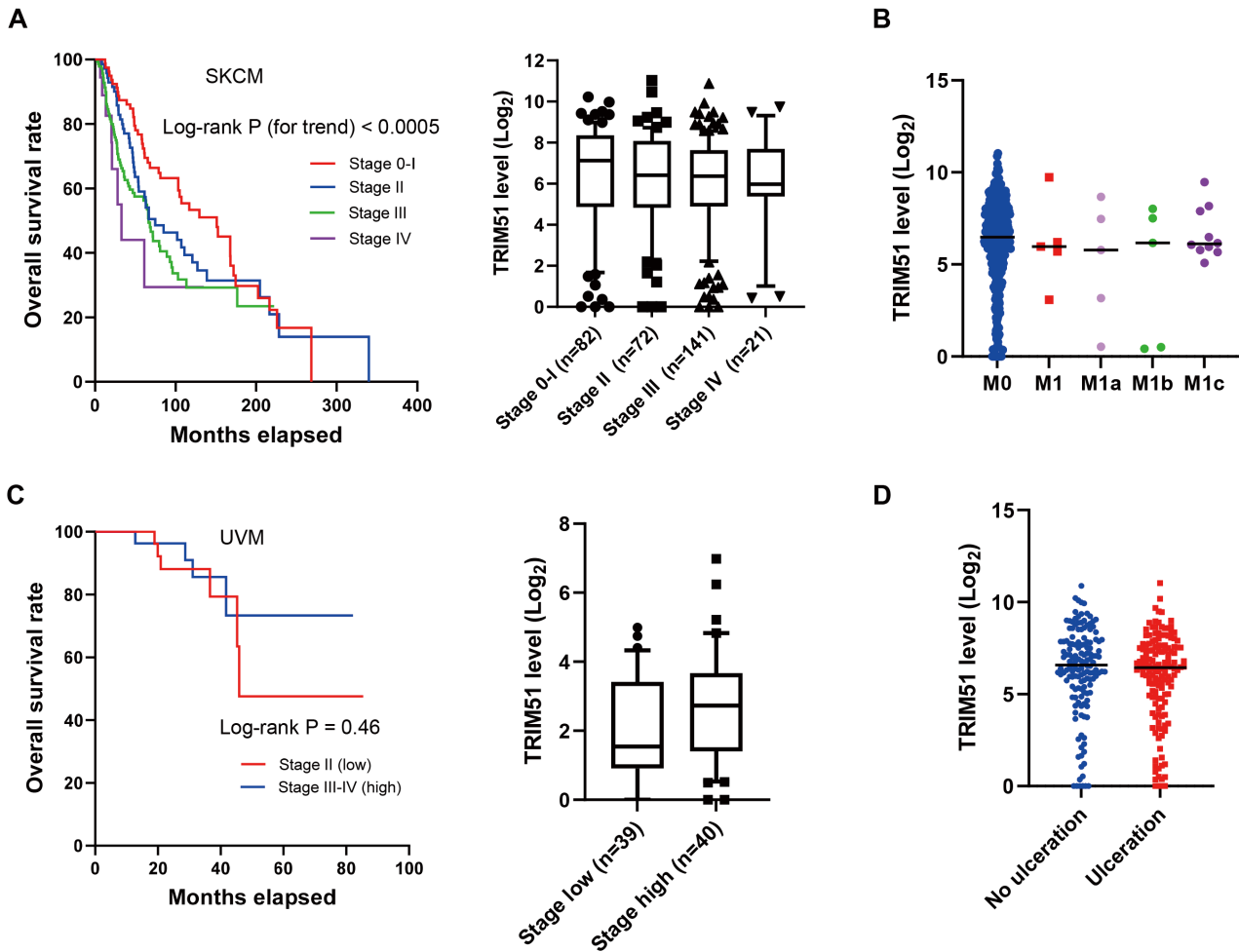
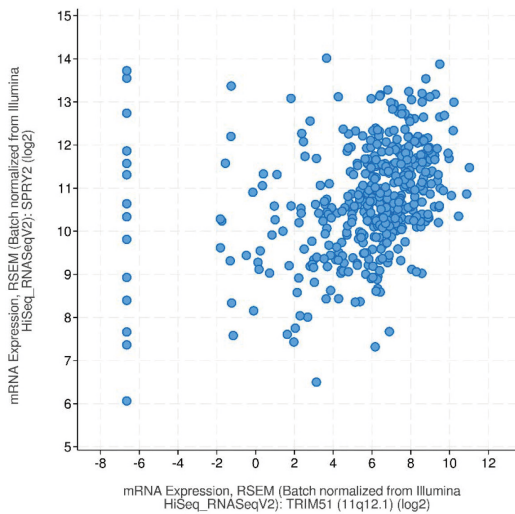


Figure S2 Kaplan-Meier curves showing overall survival rates and boxplots showing the mRNA level of *TRIM51*. (A-C) Using The Cancer Genome Atlas (TCGA) data, overall survival rates and the *TRIM51* mRNA levels were examined by disease stage (A) and metastasis subgroups in skin cutaneous melanoma (SKCM) (B) and in uveal melanoma (UVM) (C). (D) *TRIM51* mRNA levels examined by the presence of ulceration.

A

Products	Interactant	Other Gene	Complex	Source	Pubs	Description
TRIM51	P43364	MAGEA11		HPRD	PubMed	
TRIM51	Q75150	RNF40		HPRD	PubMed	
TRIM51	Q43597	SPRY2		HPRD	PubMed	
BioGRID:124248	BioGRID_110284	MAGEA11		BioGRID	PubMed	Two-hybrid
BioGRID:124248	BioGRID_115149	RNF40		BioGRID	PubMed	Two-hybrid
BioGRID:124248	BioGRID_115547	SPRY2		BioGRID	PubMed	Two-hybrid

B

Spearman: 0.39
($p = 1.33e-17$)
Pearson: 0.31
($p = 2.45e-11$)

C

Human Protein Atlas

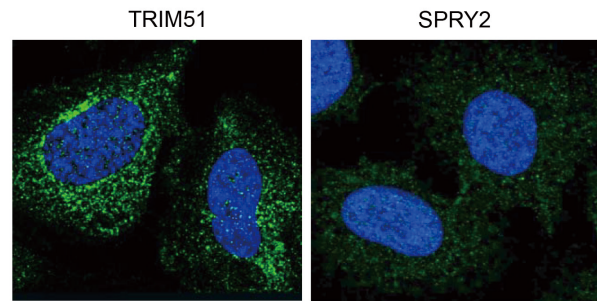


Figure S3 Evidences suggesting a functional relationship between TRIM51 and the BRAF-MEK-MAPK signaling pathway. (A) SPRY2 acting as a putative binding partner of TRIM51 shown in the NCBI webpage. (B) Analysis of the expression correlation between *TRIM51* and *SPRY2* in melanoma using the cBioPortal. (C) The subcellular localization pattern of TRIM51 and SPRY2 shown in the Human Protein Atlas.