Figure S1. The prognostic impact of *ELP6* expression levels in patients with SKCM. (A) Kaplan-Meier plotter analysis of disease-free survival between ELP6^{high} and ELP6^{low} patients with SKCM according to Gene Expression Profiling Interactive Analysis data. (B-E) The Kaplan-Meier analysis of survival probability was performed for (B) stage 0, I and II patients with SKCM (n=220), (C) stage III and IV patients with SKCM (n=191), (D) female patients with SKCM (n=174) and (E) male patients with SKCM (n=284), compared with that of the OS-ELP6 ^{high} (yellow) and OS-ELP6 ^{low} (blue) groups based on data from The Cancer Genome Atlas database. ELP6, elongator acetyltransferase complex subunit 6; SKCM, skin cutaneous melanoma; OS, overall survival.

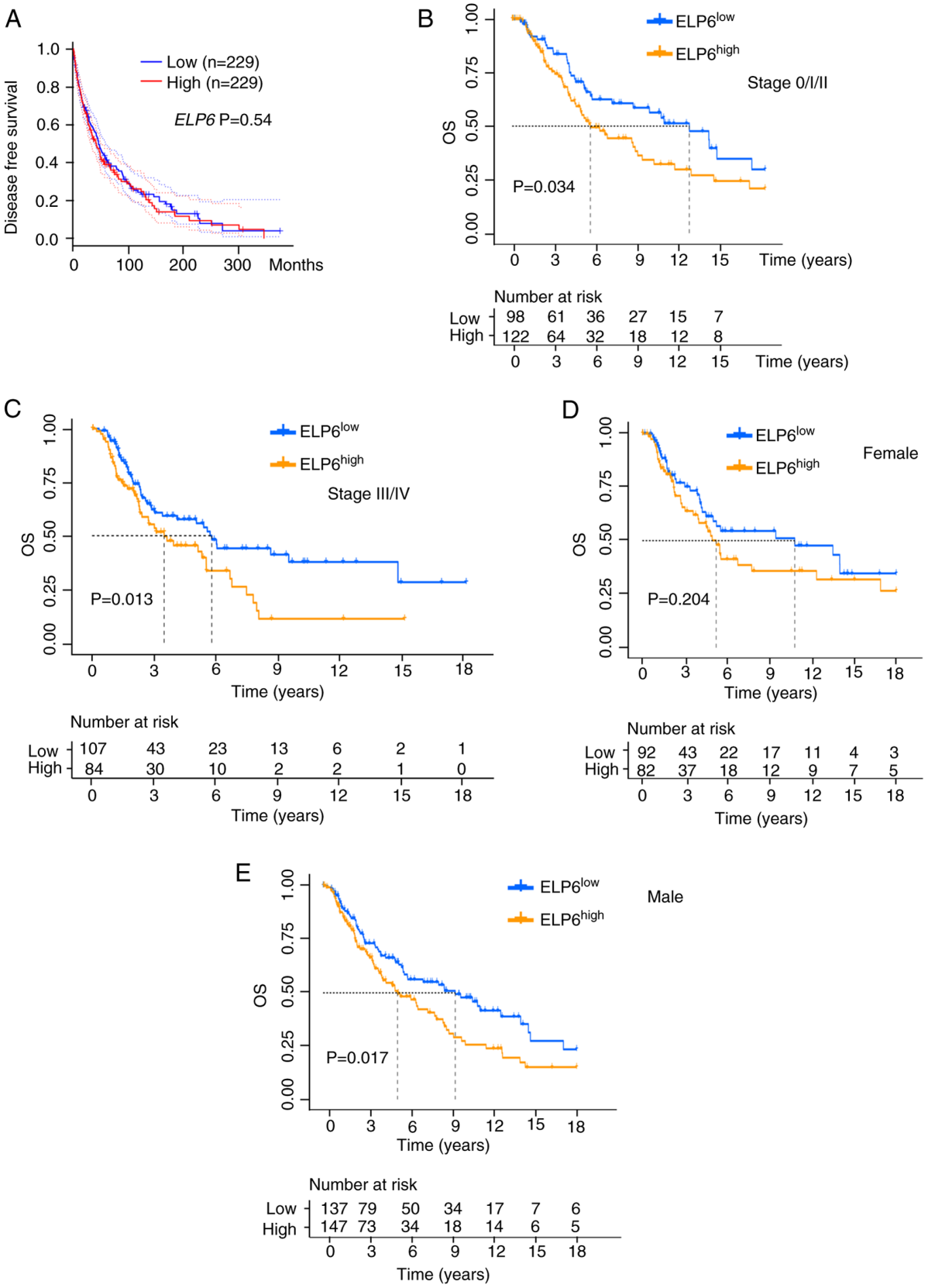

Figure S2. Analysis of *ELP* mutations and demographic factors in patients with SKCM. (A) The distribution of mutations in *ELP1*, *ELP2*, *ELP3*, *ELP4*, *ELP5* and *ELP6*, including missense mutation, splice mutation, truncating mutation, structural variant, amplification and deep deletion, was analysed in SKCM samples using data from cBioPortal. The dataset utilized comprised samples from the TCGA PanCancer Atlas, totalling 363 patients with mutation and copy number alteration data. (B) Patients with SKCM (n=468) with ELP6^{high} (left bar) or ELP6^{low} groups (right bar) were analysed according to age composition; percentage of individuals aged ≥50 (red) or <50 years (blue) relative to the total number of individuals in each group. (C) Using TCGA data, patients with SKCM (n=458) were grouped by age, ≥50 (red) or <50, and *ELP6* expression levels compared using the Wilcoxon test. (D) Patients with SKCM (n=458) were divided into ELP6^{high} (left bar) or ELP6^{low} groups and the sex distribution was analysed; percentage of males (red) or females (blue) relative to the total number of individuals in each group. (E) Patients with SKCM (n=458) into two groups based on sex, male (red) or female (blue) according to the TCGA database, and *ELP6* expression levels were compared between the two groups using the Wilcoxon test. TCGA, The Cancer Genome Atlas database; ELP6, elongator acetyltransferase complex subunit 6; SKCM, skin cutaneous melanoma.

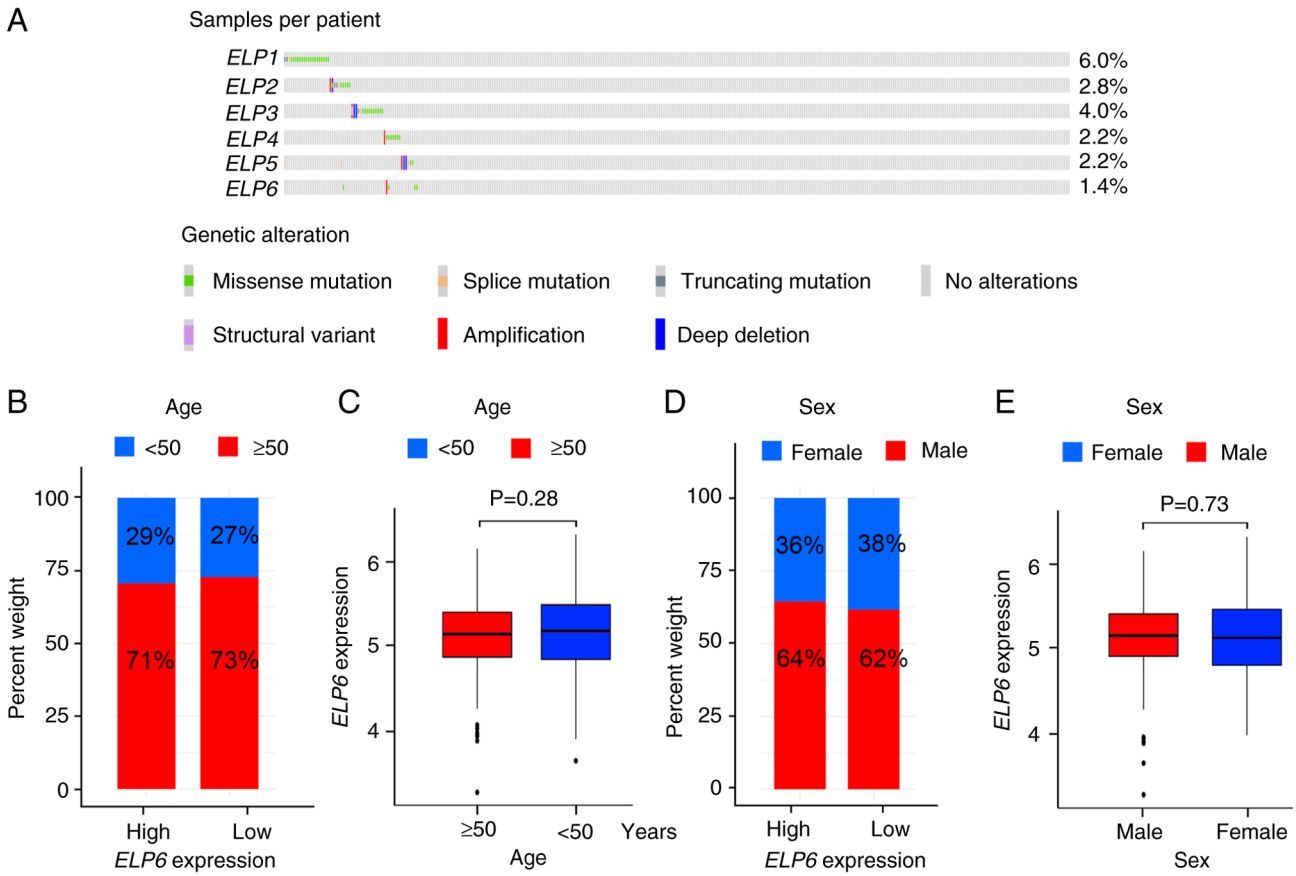

Figure S3. Effects of ELP6 knockdown on melanoma cell proliferation and related molecular expression. (A) mRNA expression levels of ELP6 to assess ELP6 knockdown efficiencies in SK-MEL-2 cells. (B) The viability of shCtrl and shELP6 SK-MEL-2 cells was measured at 24, 48 and 72 h. (C) The expression levels of PCNA mRNA were evaluated in A375 or shELP6 A375 cells after transfection with either the pEGFP-C2 or pEGFP-*ELP6* plasmid. (D) Protein expression levels of p42 MAPK in from shCtrl and shELP6 SK-MEL-2 cell lines. *P<0.05. ns, not significant; ELP6, elongator acetyltransferase complex subunit 6; SKCM, skin cutaneous melanoma; Ctrl, control; mRNA, messenger; PCNA, proliferating cell nuclear antigen.

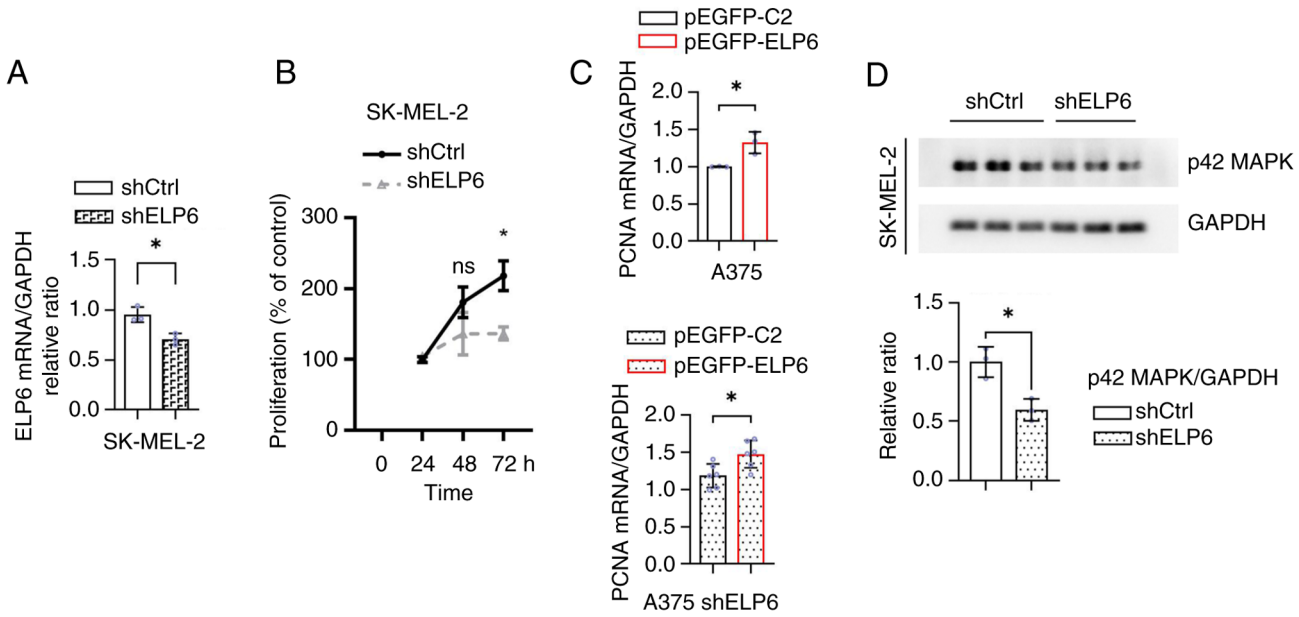

Figure S4. Fluorescence microscopy and western blot analysis of A375 and 293T cells transfected with pEGFP-C2 or pEGFP-ELP6 plasmids. (A) A375 and (B) 293T cells were transfected with either pEGFP-C2 or pEGFP-ELP6 plasmids for 48 h and representative fluorescent images presented. White arrows denote A375 cells successfully transfected with plasmids. Scale bar, 200 μm. (C and D) ELP6 mRNA expression levels and (E and F) p42 MAPK protein expression levels were also assessed. *P<0.05; **P<0.01. ELP6, elongator acetyltransferase complex subunit 6; mRNA, messenger RNA.

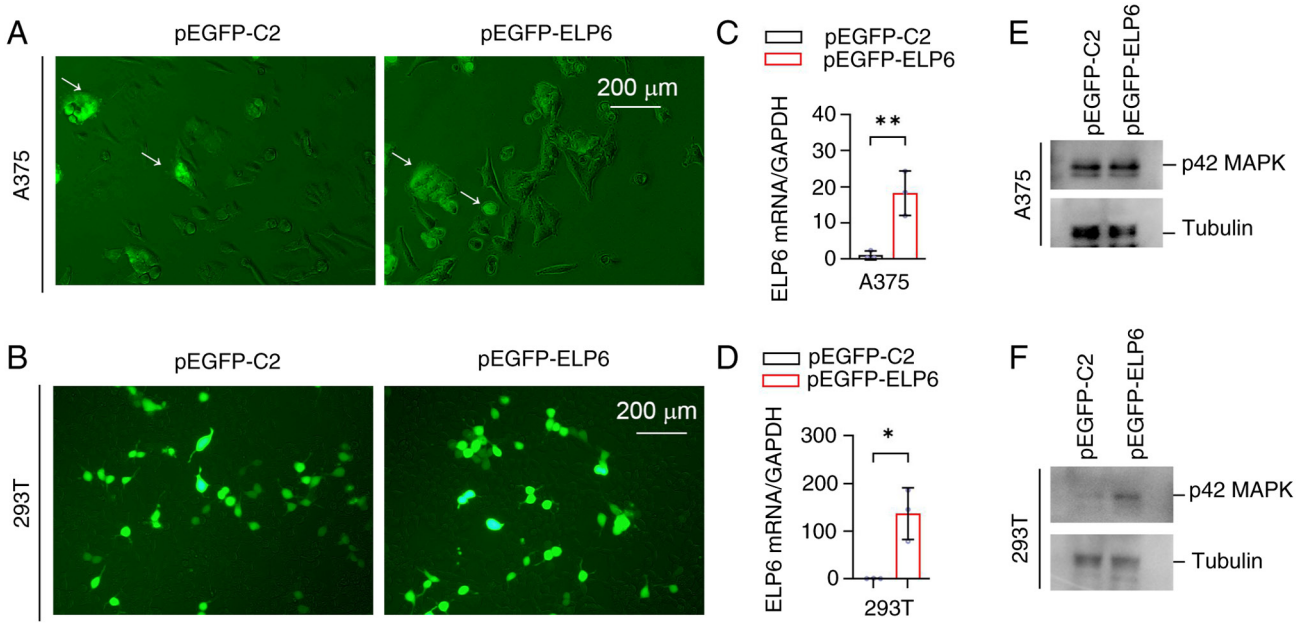

Figure S5. Overview of BRAF alterations in patients with SKCM with high and low *ELP6* expression levels using The Cancer Genome Atlas database. The frequency of *BRAF* alterations was widely and non-uniformly distributed between patients with SKCM with high (A) and low *ELP6* (B) expression levels. *BRAF* alterations occurred in 51% of the ELP6^{high} and 50% of the ELP6^{low} group, with the types of mutations observed including missense mutation, in-frame deletion, frame shift deletion, nonsense mutation, frame shift insertion, multi-hit mutation and in-frame insertion. Fustat refers to patient survival status. SKCM, skin cutaneous melanoma; TMB, tumour mutational burden.

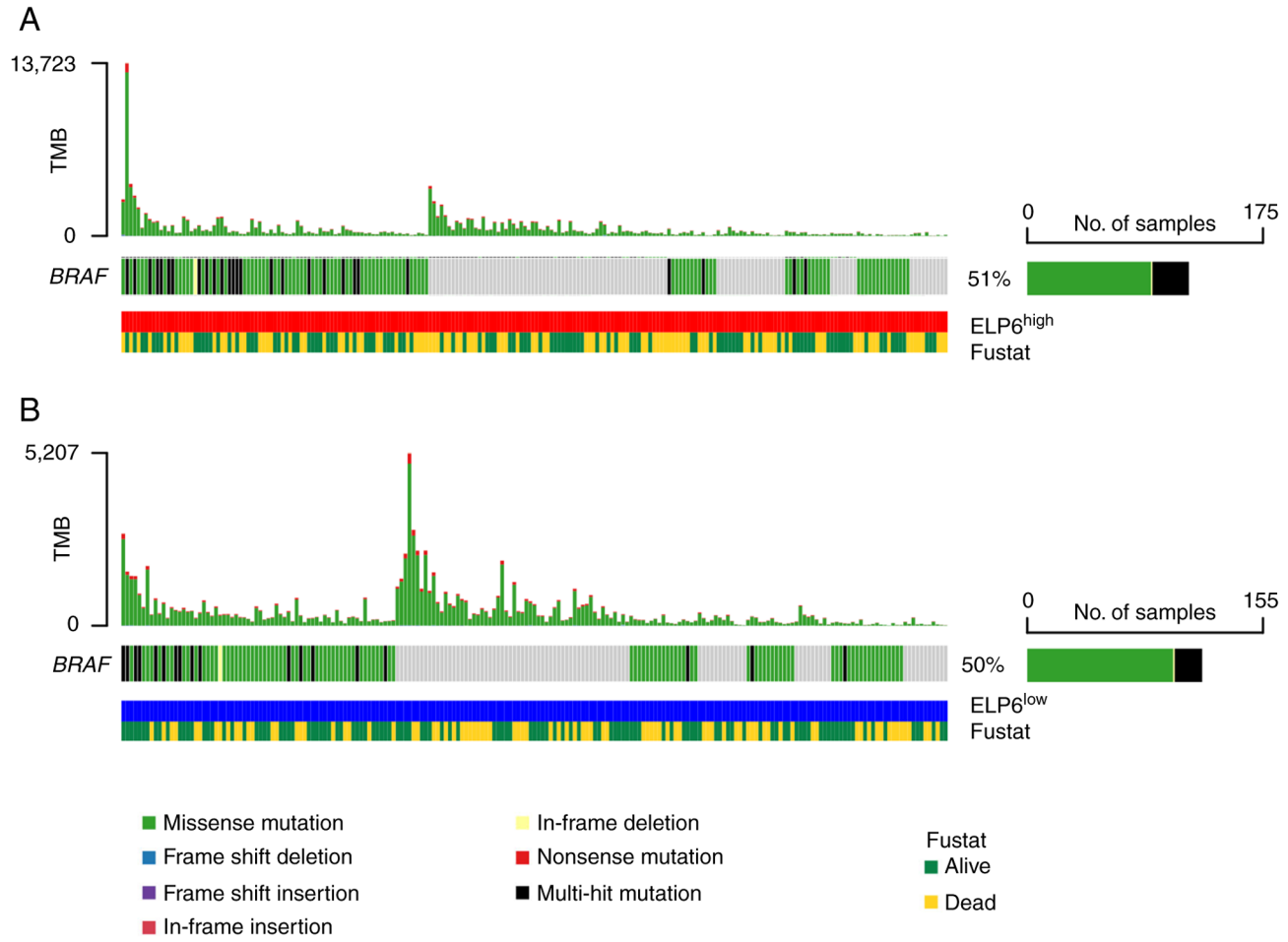

Figure S6. *ELP6* knockdown alters sensitivity of SK-MEL-2 cells to U0126. shCtrl and shELP6 SK-MEL-2 cells were treated with for 48 h, followed by a CCK-8 assay to assess cell viability; normalized viability inhibited by U0126 in each cell line depicted. *P<0.05; ns, not significant.