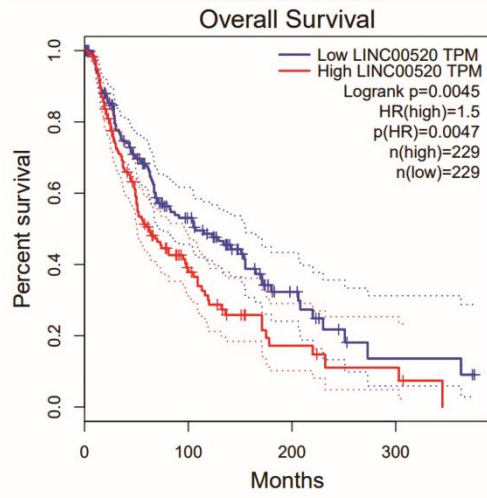
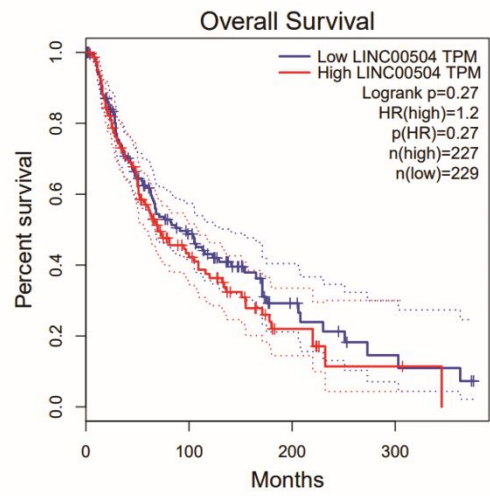
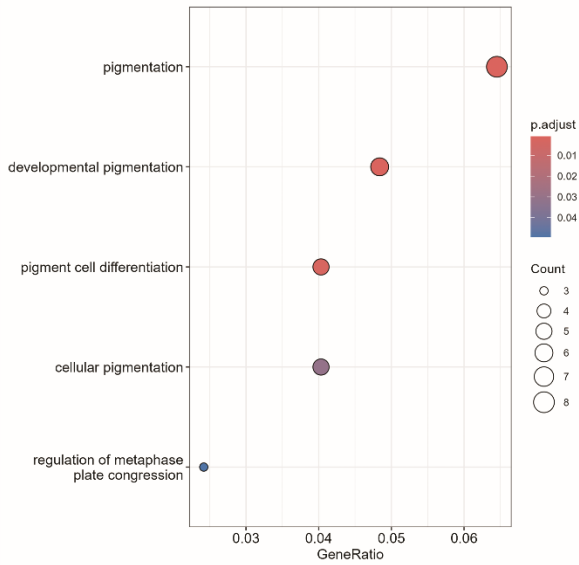


Supplementary information

Supplementary Figure S1. Prognostic value of *LINC00504* and *LINC00520* in melanoma patients. Kaplan-Meier survival curves showing the association between lincRNA expression levels and Overall Survival (OS) in the TCGA-SKCM cohort. Patients were stratified into high (red) and low (blue) expression groups based on the median TPM (Transcripts Per Million) values. **(A)** High expression of *LINC00520* is significantly associated with poorer overall survival (Log-rank $p=0.0045$; HR=1.5). **(B)** A consistent trend is observed for *LINC00504*. Dashed lines represent the 95% confidence intervals.

Supplementary Figure S2: Functional characterization of the *MITF*-regulated gene network. Dot plots representing Gene Ontology (GO) enrichment analysis for biological processes (BP) associated with genes regulated by *MITF*. **(A)** Biological processes associated with genes activated by *MITF*, highlighting pathways related to melanocyte identity, including pigmentation, melanin biosynthetic processes, and developmental differentiation. **(B)** Biological processes associated with genes repressed by *MITF*, showing a predominance of pathways linked to cell-substrate adhesion, mesenchymal development, and extracellular matrix organization. The x-axis represents the Gene Ratio (the percentage of genes from each GO category that were identified in our analysis), while the y-axis lists the enriched Biological Processes. The size of the dots represents the Count (number of genes associated with the biological process), and the colour gradient indicates the statistical significance expressed as $p.adjust$.

A**B****A****B**