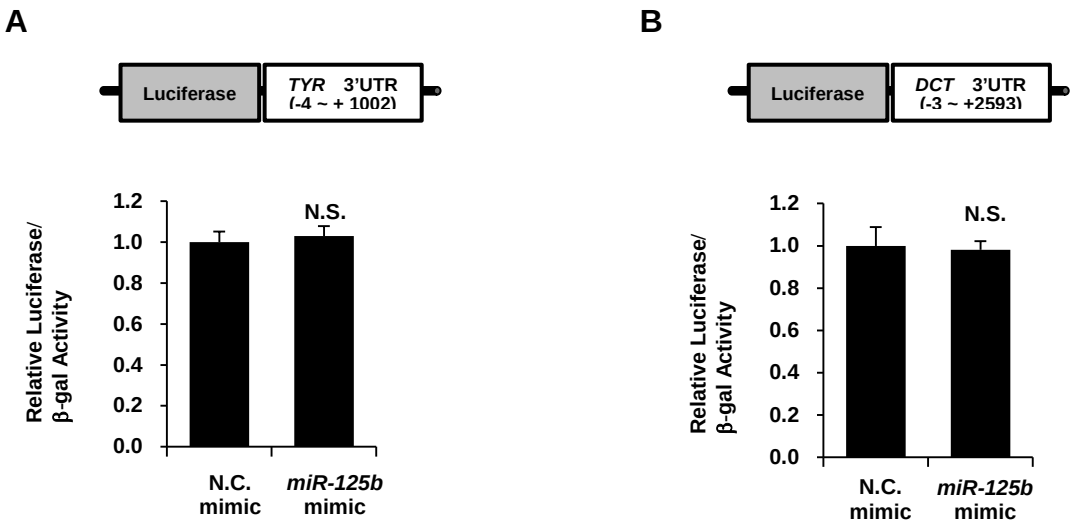
Supplementary Information

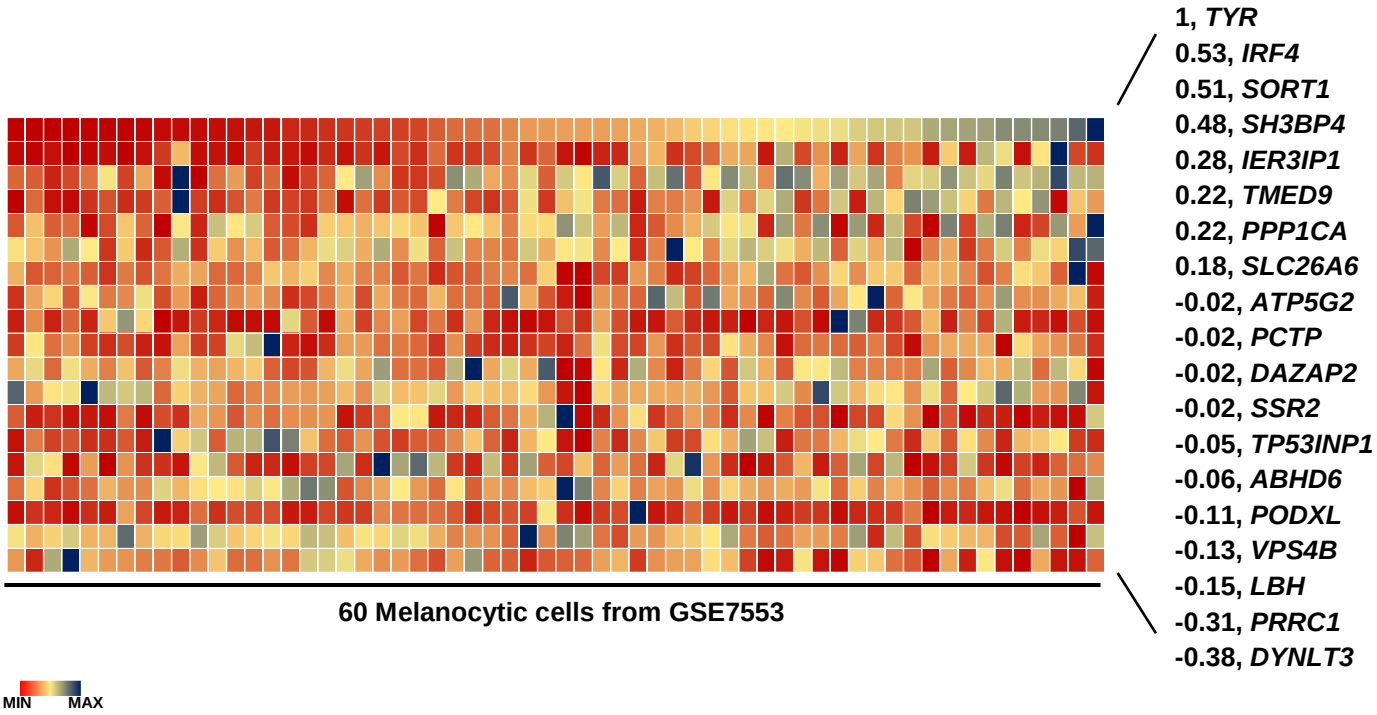
Supplementary Figures

Supplementary Figure S1.



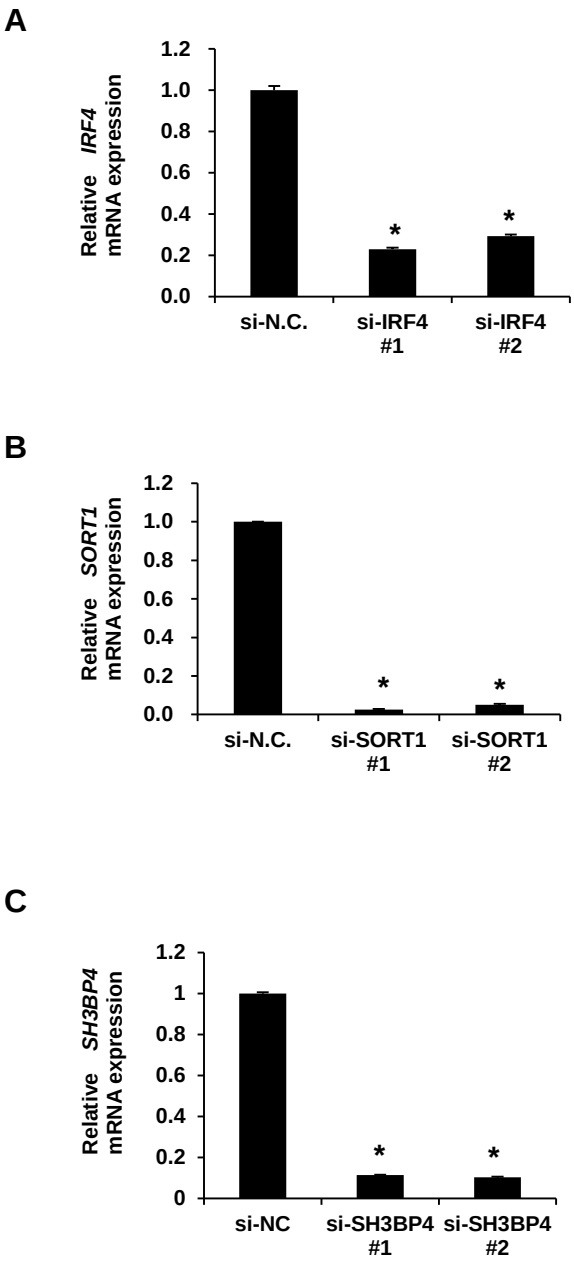
Supplementary Figure S1. The full 3′-UTRs of the *TYR* (A), and *DCT* (B) mRNAs were cloned into a luciferase reporter plasmid. The position of 3'UTR relative to the stop codon are indicated in brackets. WM266-4 cells transfected with 20 nM *miR-125b* mimic or the N.C. mimic were further transfected with a 3′-UTR luciferase construct for each gene and β-galactosidase expression vectors. Luciferase activity was measured after 24 h, and the level of luciferase activity was normalized to β-galactosidase activity. The data are presented as the mean ± SD of three independent experiments. **P* < 0.05, unpaired Student's *t*-tests.

Supplementary Figure S2.



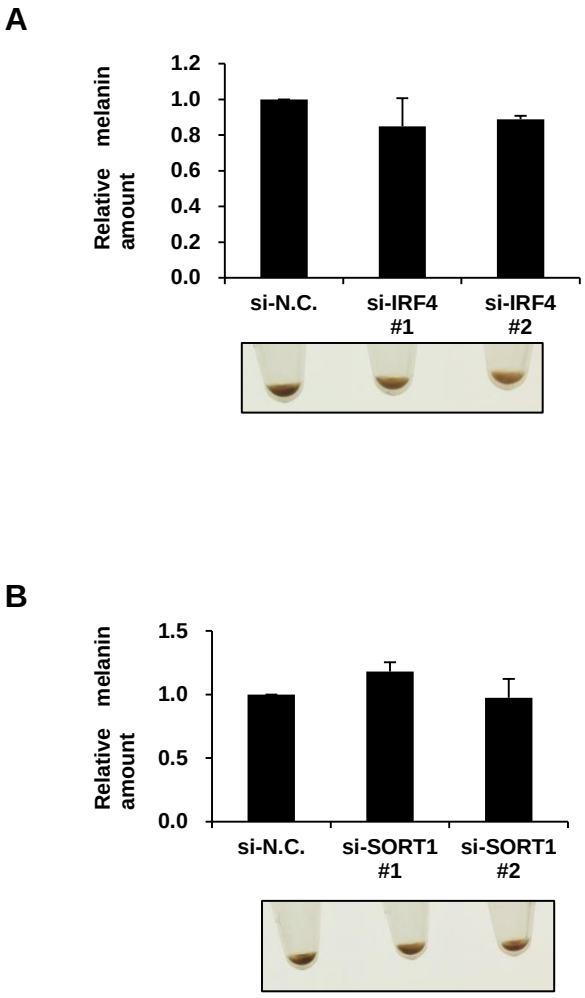
Supplementary Figure S2. Comparison of the mRNA expression levels of *miR-125b* targets with that of *TYR* in 60 melanocytic cells (GSE7553). Pearson's *r* values are shown on the left of each gene.

Supplementary Figure S3.



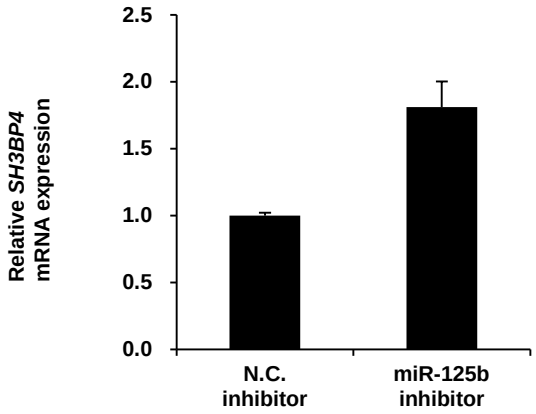
Supplementary Figure S3. WM266-4 cells were transfected with siRNAs against IRF4 (A), SORT1 (B), or SH3BP4 (C). RNAs were extracted, and the expression of each mRNA was analyzed by RT-qPCR. The data are presented as the mean ± SD of three independent experiments. *$P < 0.05$, unpaired Student's *t*-tests.

Supplementary Figure S4.



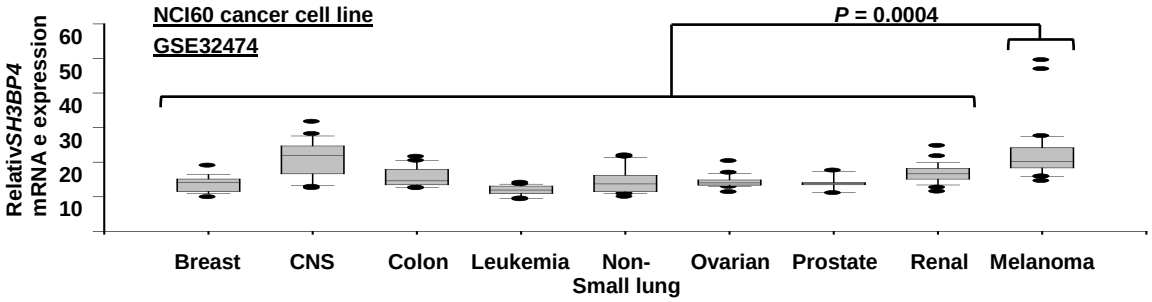
Supplementary Figure S4. Human melanocytes were transfected with siRNAs against IRF4 (A) or SORT1 (B) for 7 days. Images of cell pellets were obtained following centrifugation of equal cell numbers (2×10^4 cells). The data are presented as the mean ± SD of three independent experiments. *$P < 0.05$, unpaired Student's *t*-test.

Supplementary Figure S5.



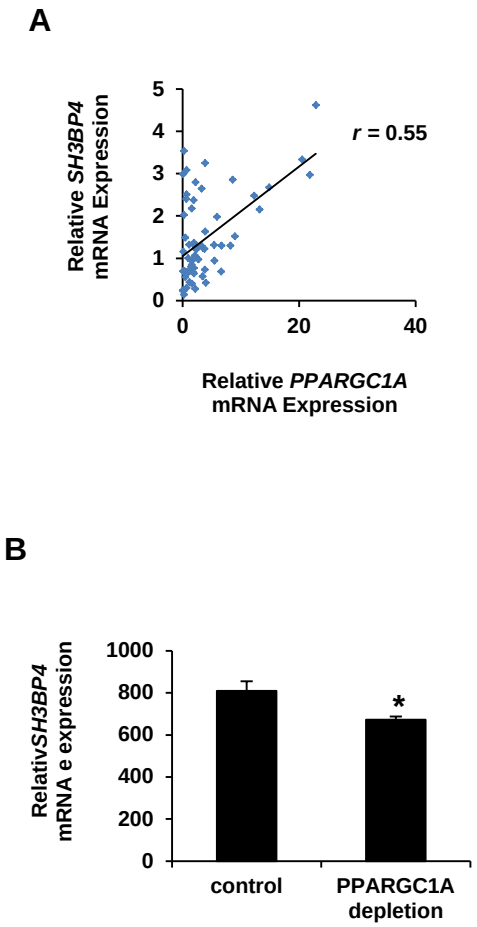
Supplementary Figure S5. WM266-4 melanoma cells were transfected with miR-125b inhibitors or negative control (N.C.) inhibitors for 3 days. RNAs were extracted, and the expression of SH3BP4 mRNA was analyzed by RT-qPCR. The data are presented as the mean ± SD of three independent experiments. *$P < 0.05$, unpaired Student's *t*-tests.

Supplementary Figure S6.



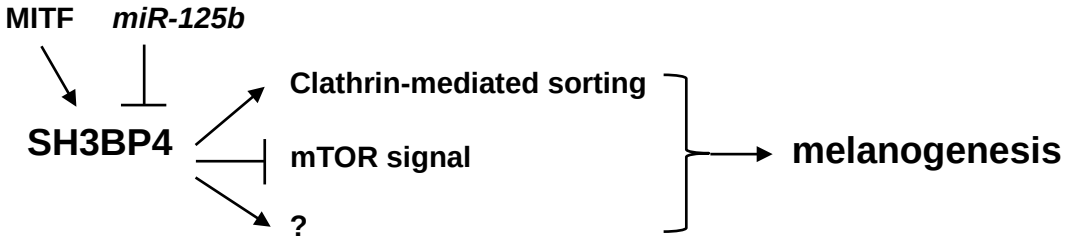
Supplementary Figure S6. Box plot showing the relative *SH3BP4* mRNA level across various cancer cell lines.

Supplementary Figure S7.



Supplementary Figure S7. (A) The relative mRNA expression of *PPARGC1A* was plotted against that of *SH3BP4* from 60 melanomas (microarray dataset: GSE7553). The Pearson's *r* value is indicated. (B) *SH3BP4* mRNA levels were analyzed from the microarray data for the control versus PPARGC1A-depleted cells (GSE36879). **P* < 0.05, unpaired Student's *t*-tests.

Supplementary Figure S8.



Supplementary Figure S8. Model of *SH3BP4* function as a pigmentary gene. *SH3BP4* is negatively regulated by *miR-125b*, which inhibits melanogenesis. In contrast, *SH3BP4* is positively regulated by MITF, a transcription factor affecting melanocytic lineage-specific expression. Furthermore, SH3BP4 may be involved in melanogenesis through mediation of clathrin-mediated sorting or the mTOR signal pathway, resulting in melanogenesis.