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**Fig. S1.** Consensus clustering for immune-infiltrating immune cells.

**(A-G)** Consensus matrices (k = 3-9) of the SKCM cohort. **(E-H)** Tracking plot (k = 2-9) of the SKCM cohort. **(L)** Stacked heatmap of immune-infiltrating immune cells in different clusters.



**Fig. S2.** Landscape of TMB, single gene mutation visualization, transition and transversion situations.

**(A)** Landscape of mutations across all samples. **(B-D)** Single gene mutation visualization for DNAH7 **(B)**, ADGRV1 **(C)**, and BRAF **(D)**. **(E)** The transition and transversion situations in high-risk groups. (F) The transition and transversion situations in low-risk groups.



**Fig. S3.** The distribution of 6 prognostic genes in different TME cell subsets.

**(A)** The 21 cell clusters in the GSE123139 dataset. **(B)** The 8 cell types were identified. **(C-H)** The expression of prognostic genes in cell subsets, with the red box highlighting cells exhibiting perceptible expression of these genes.



**Fig. S4.** The cell markers, proportion and the interaction analysis.

**(A)** Markers of the annotated cells. **(B)** The proportion of various cells. **(C)** The heatmap of interaction counts between clusters. **(D)** The significant ligand-receptor pairs between mono/macro\_C5 and other cell clusters. The edge width is proportional to the indicated number of ligand-receptor pairs.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Target | Regulation | Action | Citation | |
| CXCL12 | ↑ | Circ\_0020710 could upregulate the CXCL12 expression to enhance melanoma cell proliferation, migration and invasion *in vitro* as well as tumor growth *in vivo*.  AMD11070 abrogated melanoma cell migration through inhibition of CXCR4-CXCL12 chemotaxis. | | [1]  [2] |
| PLAU | ↓ | Glutamate release inhibitor riluzole, with the ability to inhibit melanoma cell xenograft growth, could upregulate the expression of PLAU. | | [3] |
| LAP3 | ↓  ↑ | Interferon-α is therapeutic in some melanoma patients, it induces proteins that respond to type I interferon, including leucine aminopeptidase.  Bestatin, the inhibitor of LAP3, could inhibit the angiogenesis induced by B16-BL6 melanoma cells. | | [4]  [5] |
| PIM1 | ↑ | MiR-542-3p could suppress the invasion and metastasis of melanoma by decreasing PIM1 expression. | | [6] |
| PTK2B | ↓  ↑ | FES, the gene encodes the tyrosine kinase, is highly expressed in normal human melanocytes, whereas strongly decreased in human melanomas.  The expression of MERTK, a tyrosine kinase, correlates with the advancement of melanoma, with its highest expression observed in metastatic melanoma. | | [7]  [8] |
| CCL8 | ↓  ↑ | In a subcutaneous transplantation model of B16F10 melanoma cells, mice with high CCL8 expression showed anti-tumor metastatic effect and survived longer.  CCL8 contributed to melanoma cell proliferation *in vitro* and enhanced tumor growth, metastasis *in vivo*. | | [9]  [10] |

**Table S9**

The abnormal expression of 6 prognostic genes for SKCM.

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