# Supplementary Information

**Interleukin 32 exacerbates vitiligo by promoting inflammation and oxidative stress-induced injury in melanocytes**

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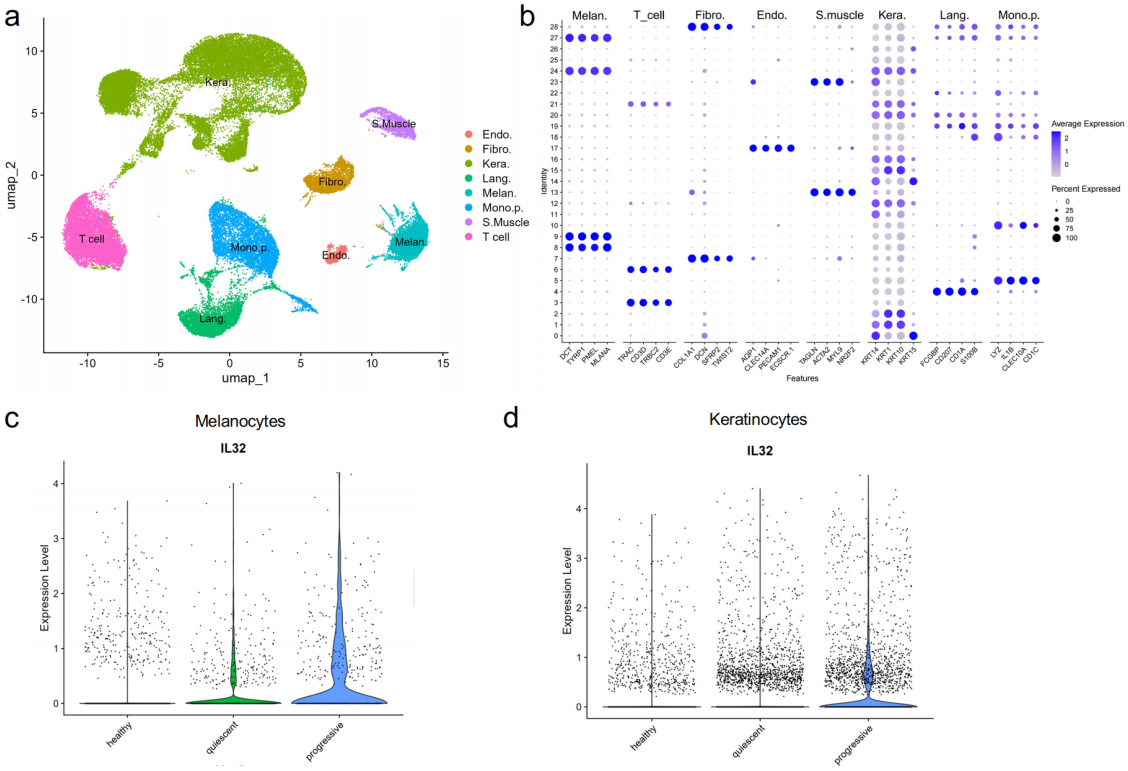
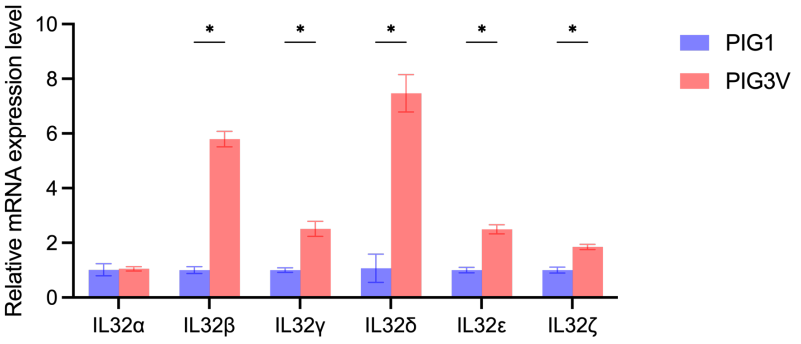
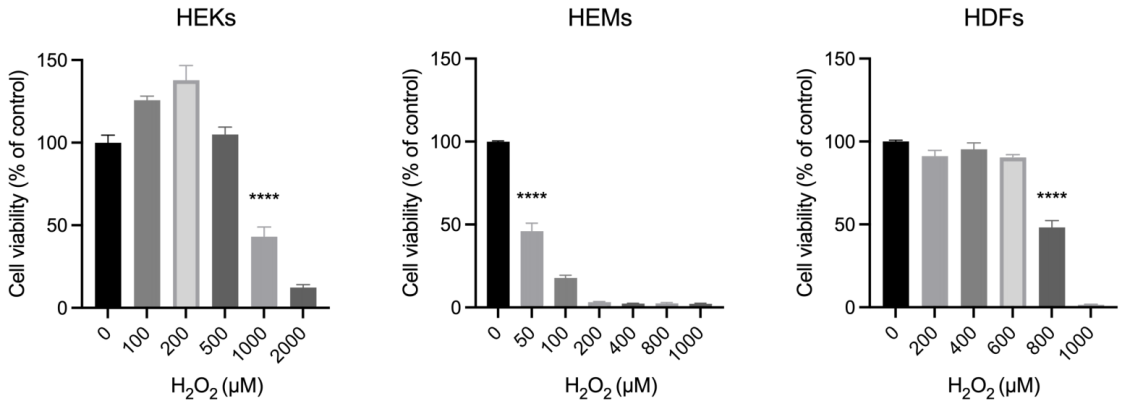
**Supplementary Figure S1** Single-cell RNA-seq profiling of skin cells from vitiligo and healthy control samples. (a) UMAP plot of all cells after quality control and unsupervised clustering. Each dot represents a single cell, colored according to the assigned cell type. A total of eight major cell populations were identified: keratinocytes (Kera.), dermal fibroblasts (Fibro.), endothelial cells (Endo.), melanocytes (Melan.), smooth muscle cells (S. Muscle), monocyte/macrophages (Mono. p.), T cells, and Langerhans cells (Lang.). (b) Feature plots showing marker genes used for annotation in each cell type. (c-d) Violin plot of IL32 expression in the melanocytes (Melan.) and keratinocytes (Kera.) of healthy controls and different stages of vitiligo patients. Green represents stable vitiligo and blue represents progressive vitiligo.



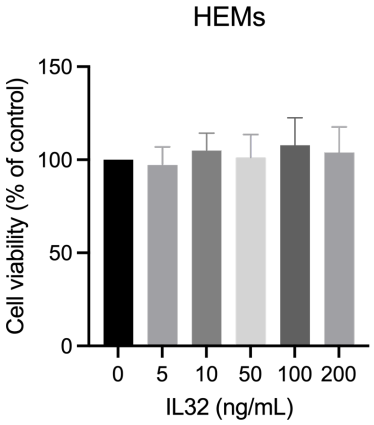

**Supplementary Figure S2** Expression level of different *IL32* isoforms in PIG1 and PIG3V cells. Blue bars represent PIG1 cells and red bars represent PIG3V cells. Data were presented as mean ± SD. **P* < 0.05. (two-way ANOVA).



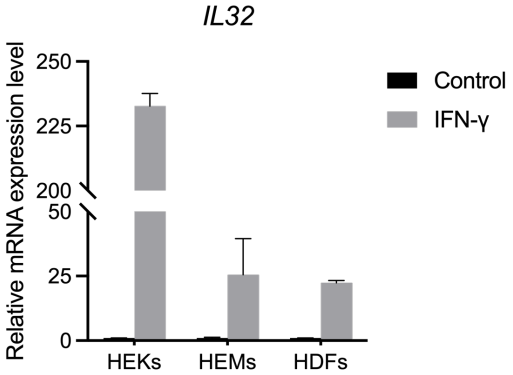
**Supplementary Figure S3** Cell viability of different cells treated with $H_2O_2$ for 24h. Bar plots with different shades of gray represent cell viability of HEKs, HEMs, and HDFs after being treated with different concentrations of $H_2O_2$. Data were presented as mean ± SD. ****$P <$ 0.0001. (one-way ANOVA).




**Supplementary Figure S4** Cell viability of HEMs treated with rhIL32β for 24h. Different shades of gray represent cell viabilities of HEMs under different rhIL32β concentrations. There was no significant change ($P > 0.05$). Data were presented as mean ± SD. (one-way ANOVA).




**Supplementary Figure S5** RT-qPCR analysis of IL32 in HEKs, HEMs, and HDFs treated with 20 ng/mL of IFN-γ for 24h compared to the control group.



**Supplementary Table S1** Knockdown sequences for *IL32*.

| small interfering RNA | | |
|---|---|---|
| siIL32-1 | sense | GAAUGCACCAGGCCAUAGATT |
| | antisense | UCUAUGGCCUGGUGCAUUCTT |
| siIL32-2 | sense | GCUCACUCCUCUACUUGAATT |
| | antisense | UUCAAGUAGAGGAGUGAGCTT |

**Supplementary Table S2** Primer sequences used for qPCR.

| Gene name | | |
|---|---|---|
| *β-actin* | F | CCATCGTCCACCGCAAAT |
| | R | GCTGTCACCTTCACCGTTCC |
| *GAPDH* | F | TGCACCACCAACTGCTTA |
| | R | GGCATGGACTGTGGTCAT |
| *CXCL9* | F | CCAGTAGTGAGAAAGGGTCGC |
| | R | AGGGCTTGGGGCAAATTGTT |
| *CXCL10* | F | GTGGCATTCAAGGAGTACCTC |
| | R | TGATGGCCTTCGATTCTGGATT |
| *IL-32* | F | GACAGTGGCGGCTTATTATGAG |
| | R | CCTCGGCACCGTAATCCAT |
| *IL-32α* | F | GACAGTGGCGGCTTATTATGAG |
| | R | GCTCCGTAGGACTTGTCACAAA |
| *IL-32β* | F | GAAGACTGCGTGCAGAAGGT |
| | R | CTTTCTATGGCCTGGTGCAT |
| *IL-32γ* | F | AGGCCCGAATGGTAATGCT |
| | R | CCACAGTGTCCTCAGTGTCACA |
| *IL-32ζ* | F | GACGTGGACAGGACGACTTCA |
| | R | CCTCGGCACCGTAATCCAT |
| *IL-32ε* | F | AGGCCCGAATGGTGATGT |
| | R | GGCACCGTAATCCATCTCTT |
| *IL-32δ* | F | TCTGTCTCTCTCGGGTCCTCTCT |
| | R | TGTCTCCAGGTAGCCCTCTTTG |