## The resident pathobiont *Staphylococcus xylosus* in *Nfkbiz*-deficient skin accelerates spontaneous skin inflammation

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Fig E1. Accumulation of immune cells in skin of  $Nfkbiz^{-/-}$  mice with dermatitis is reduced by ABX treatment. (A) FACS analysis of CD45<sup>+</sup> cells and CD45<sup>+</sup>MHCII<sup>+</sup>CD11c<sup>+</sup> cells in the skin of  $Nfkbiz^{+/-}$  and  $Nfkbiz^{-/-}$  mice. (B) FACS analysis of CD45<sup>+</sup> cells and CD45<sup>+</sup>MHCII<sup>+</sup>CD11c<sup>+</sup> cells in the skin of untreated and ABX-treated  $Nfkbiz^{-/-}$  mice. Data are representative of three independent experiments. \*p < 0.05, \*\*p < 0.01.



Fig E2. The level of IFN- $\gamma$  in the skin of *Nfkbiz*<sup>-/-</sup> mice remains unchanged after ABX treatments. FACS analysis of IFN- $\gamma$  production by CD4<sup>+</sup> and CD8<sup>+</sup> cells in the skin of *Nfkbiz*<sup>+/-</sup>, untreated, and ABX-treated *Nfkbiz*<sup>-/-</sup> mice. Data are representative of three independent experiments. \*p < 0.05, \*\*p < 0.01.



**Fig E3.** Gene expression related to inflammation is upregulated in the skin of  $Nfkbiz^{-/-}$  mice. (A) Microarray analysis of the skin from  $Nfkbiz^{+/-}$  and  $Nfkbiz^{-/-}$  mice (n = 3 per group). Genes exhibiting significant change in expression (fold change > 1.0 and p < 0.05) between  $Nfkbiz^{+/-}$  and  $Nfkbiz^{-/-}$  mice were clustered in a heatmap. (B) A gene interaction network, associated with spontaneous dermatitis in  $Nfkbiz^{-/-}$  mice, was established using Ingenuity Pathway Analysis (IPA) software. Solid lines indicate direct interaction, while dashed lines indicate indirect interaction.



Fig E4. Colonization pattern of *S. xylosus* after its topical application is shown. CFUs of *Staphylococcus* species of skin swabs from *Nfkbiz<sup>-/-</sup>* and *Nfkbiz<sup>+/-</sup>* mice upon the inoculation of PBS, heat-killed *S. xylosus* (HK-*S.x*), and *S. xylosus* (*S.x*). Data are mean  $\pm$  s.e.m. Data are representative of two independent experiments. \*p < 0.05, \*\*p < 0.01.



Fig E5. Inoculation of *S. xylosus* triggered the differentiation of Th17 cells and the production of cytokines and chemokines in *Nfkbiz*<sup>+/-</sup> mice. (A) FACS analysis of the IL-17A production by CD4<sup>+</sup> cells in the skin of *Nfkbz*<sup>+/-</sup> mice with the inoculation of PBS, heat-killed *S. xylosus* (HK-*S.x*), and *S. xylosus* (*S.x*). (B) Cytokine and chemokine levels in skin homogenate from *Nfkbiz*<sup>+/-</sup> mice with the inoculation of PBS, HK-*S.x*, and *S.x*. Data are mean  $\pm$  s.e.m. Data are representative of three independent experiments. \*p < 0.05, \*\*p < 0.01.



Fig E6. Cells in skin draining lymph nodes (sdLNs) from  $Nfkbiz^{-/-}$  and  $Nfkbiz^{+/-}$  mice were increased after the inoculation of *S. xylosus*. (A) FACS analysis of CD45<sup>+</sup> cells and CD45<sup>+</sup>MHCII<sup>+</sup>CD11c<sup>+</sup> cells in sdLNs from  $Nfkbiz^{+/-}$  mice with the inoculation of PBS, HK-*S.x*, and *S.x*. (B) CD45<sup>+</sup> cells and CD45<sup>+</sup>MHCII<sup>+</sup>CD11c<sup>+</sup> cells in sdLNs from  $Nfkbiz^{-/-}$  mice with the inoculation of PBS, HK-*S.x*, and *S.x*. (B) CD45<sup>+</sup> cells and CD45<sup>+</sup>MHCII<sup>+</sup>CD11c<sup>+</sup> cells in sdLNs from  $Nfkbiz^{-/-}$  mice with the inoculation of PBS, HK-*S.x*, and *S.x*. (B) CD45<sup>+</sup> cells and CD45<sup>+</sup>MHCII<sup>+</sup>CD11c<sup>+</sup> cells in sdLNs from  $Nfkbiz^{-/-}$  mice with the inoculation of PBS, HK-*S.x*, and *S.x*. (B) CD45<sup>+</sup> cells and CD45<sup>+</sup>MHCII<sup>+</sup>CD11c<sup>+</sup> cells in sdLNs from  $Nfkbiz^{-/-}$  mice with the inoculation of PBS, HK-*S.x*, and *S.x*. (B) CD45<sup>+</sup> cells and CD45<sup>+</sup>MHCII<sup>+</sup>CD11c<sup>+</sup> cells in sdLNs from  $Nfkbiz^{-/-}$  mice with the inoculation of PBS, HK-*S.x*, and *S.x*. Data are representative of three independent experiments. \*p < 0.05, \*\*p < 0.01.