





Supplementary Fig. 1: Genes belonging to the Olfactory Transduction pathway (KEGG 4659, **A**) and GO term 4984 (Olfactory receptor activity, **B**) that are differentially expressed in the islets of 4 week old NOD vs. NOD.B10 mice. **C**) RT-PCR results showing the expression of *OR51S1, OR5B21, OR3A2, OR4D6, OR6C74*, and *OR2C1* in human islets from 2 donors (1: R271; 2: R314; L:100 bp ladder). Donor information is shown on Supplementary Table 1, and similar results for donor R274 are shown in **Fig. 5G**. Specific bands for the expected size are indicated by the arrowheads. Panels **A** and **B** were generated using iPathwayGuide (AdvaitaBio.com).

KEGG 4659: Th17 Cell differentiation ($P = 1.12 \times 10^{-8}$)



А

KEGG 4650: Natural killer cell-mediated cytotoxicity (P = 1.12x10⁻⁸)



В

KEGG 4660: T cell receptor signaling pathway ($P = 6.61 \times 10^{-7}$)



Supplementary Fig. 2: Genes in KEGG pathways 4659 (Th17 Cell differentiation; **A**), 4650 (Natural killer cell-mediated cytotoxicity; **B**), and 4660 (T cell receptor signaling; **C**) that are significantly changed in the islets of 12 week old NOD vs. NOD.B10 mice. Figures were generated using iPathwayGuide (AdvaitaBio.com).



Supplementary Fig. 3: Microarray data showing the expression of various iron regulatory genes and iron responsive element (IRE)-containing genes in 12 week old NOD vs. NOD.B10 islets. Only *Hamp* levels were changed by >2-fold, while *Zip14, Fth1*, and *Mrcka* levels were changed by >1.5-fold (indicated by red dotted lines). Corrected p-value < 0.05*; < 0.001**.

Supplementary Fig. 4



Supplementary Fig. 4: Iron chelation on disease progression in NOD mice. NOD mice were maintained on the standard 5P04 diet and given free access to water or water containing 0.2 mg/ml of the iron chelator deferiprone (~40 mg/kg/day, based on daily drinking volumes of 5 ml/25 g mouse). Deferiprone treatment had no significant effect on disease progression.