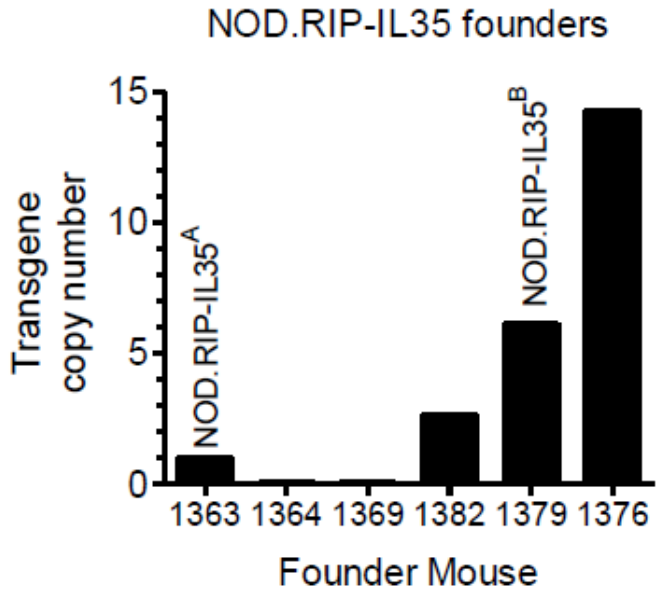
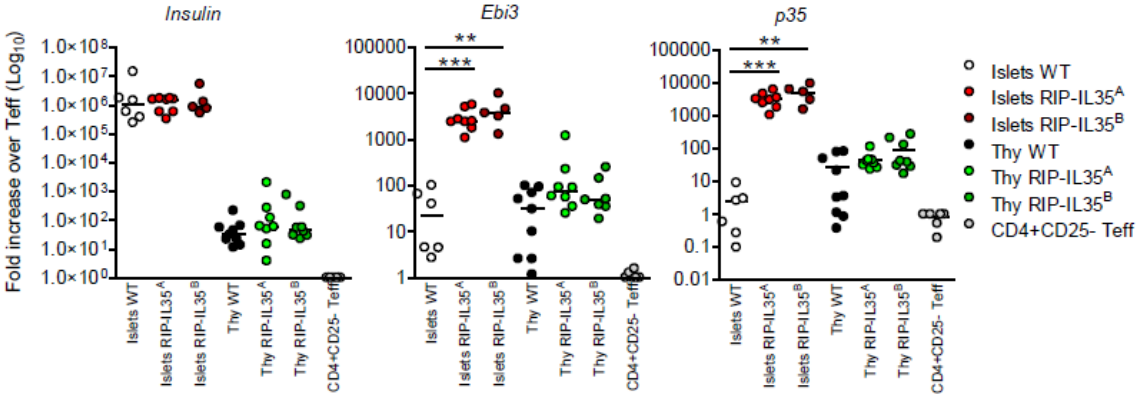
SUPPLEMENTARY DATA

Supplementary Figure 1. Selection of founders for the NOD.RIP-IL35^{A} and NOD.RIP-IL35^{B} strains. Genomic DNA was extracted from tailsnips by ProteinaseK (SigmaAldrich, St Louis, MO) digestion followed by isopropanol precipitation and spooling, then resuspended in water and purified with Phenol:Chloroform extraction. Following measurement of the concentration, standard curves of 2 ng, 1 ng and 0.5 ng were used as template for a Realtime PCR reaction with the following primers and probe: forward-CCT CTG CTA ACC ATG TTC ATG CCT T, reverse-AGG AGG TAG CGT GAT TGA CAC ATG C, and probe FAM-GGG CAA CGT GCT GGT TAT TGT GCT GTC TCA-BHQ1. The measurements for the 1ng samples were compared, using transgenic founder one as a normalizer, with a value of one. Samples where there was not a one CT difference between the 2 ng, 1ng and 0.5 ng measurements were discarded, as this indicates inhibitors in the genomic template. The reaction was run on an ABI 7900HT instrument, in a 15 ml reaction, using ABI 2xMasterMix (ABI, Foster City, CA).

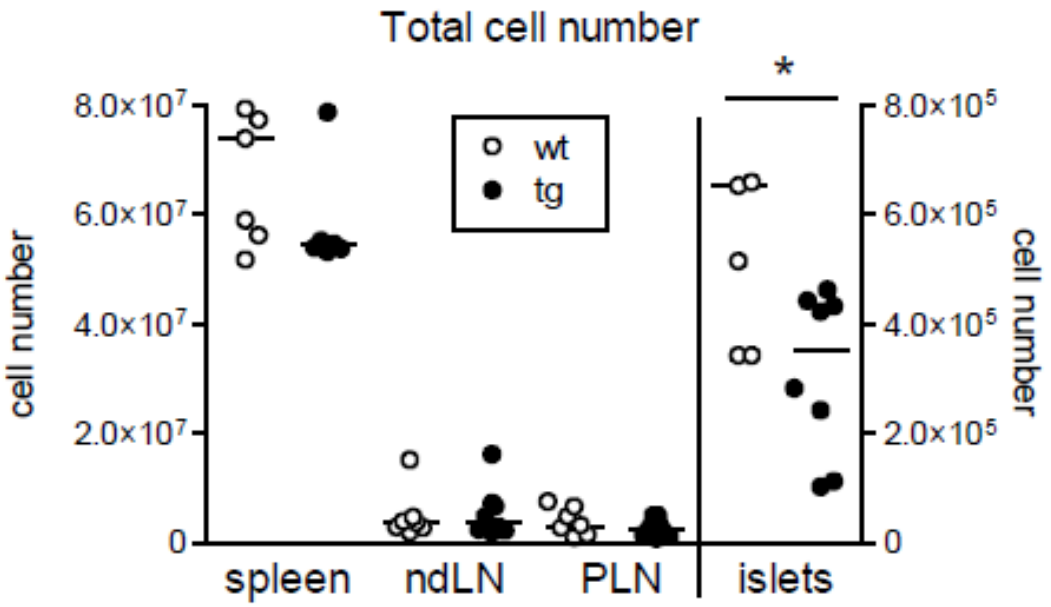


Supplementary Figure 2. Real time PCR quantification of *insulin*, *p35* and *Ebi3* expression in the islets and thymic epithelium of transgenic mice. Islets were isolated from pancreata as described in the methods section. Thymic mTEC enriched fraction was obtained by gently disrupting the thymi with frosted glass slides, then treating the remaining intact tissue with collagenase 4 (5000 u/mL) at 37°C for 1.5 hours, followed by depleting CD45+ cells via MACS separation. mRNA was isolated from CD45 negative fraction; cDNA was prepared using High Capacity cDNA Reverse Transcription Kit (Applied Biosystems). *Ebi3* primers for-AGC AGC AGC CTC CTA GCC T and rev-ACG CCT TCC GGA GGG TC, *p35* primers for-TGG CTA CTA GAG AGA CTT CTT CCA CAA and rev-GCA CAG GGT CAT CAT CAA AGA C, *insulin2* primers for-GAC CCA CAA GTG GCA CAA C and rev-TCT ACA ATG CCA CGC TTC TG, *cyclophillin* for-GGC CGA TGA CGA GCC C and rev-TGT CTT TGG AAC TTT GTC TGC AA were used in conjunction with SYBR Green (Applied Biosystems) on an ABI Prism 7900 Sequence Detection System instrument and relative expression was quantified by the comparative cycling threshold method. *Cyclophillin* expression was used as an endogenous control. Lines represent median, n = 6-9; $^{**}P$ = 0.0043, $^{***}P$ = 0.007 (Mann-Whitney two-tailed analysis).

SUPPLEMENTARY DATA



Supplementary Figure 3. Total islet infiltrating cell numbers are decreased in NOD.RIP-IL35B mice compared to littermate controls. Organs obtained from 10 week old mice were dissociated and counted. Lines represent median; *n* = 7-8 mice per group; **P* = 0.02, (Mann-Whitney two-tailed analysis).



SUPPLEMENTARY DATA

Supplementary Figure 4. Expression of endogenous *Ebi3* transcript in spleens and islets of NOD and NOD.RIP-IL-35^{B} mice. Teff ($CD4^{+}CD25^{-}$) and Treg ($CD4^{+}CD25^{+}$) cells were sorted from the islets and spleens of 10 week old transgenic or wild type littermates and mRNA was isolated with Trizol (Invitrogen). cDNA was prepared using High Capacity cDNA Reverse Transcription Kit (Applied Biosystems). *Ebi3*-UTR primers forward-CAG ACC CTG ATG TCG TCT ACT TGA and reverse-CCA GTA CAT GGA AAG TCA GTAT TCA GA were used in conjunction with SYBR Green (Applied Biosystems) to detect endogenous *Ebi3* message on an ABI Prism 7900 Sequence Detection System instrument and relative expression was quantified by the comparative cycling threshold method. Line represents the median.