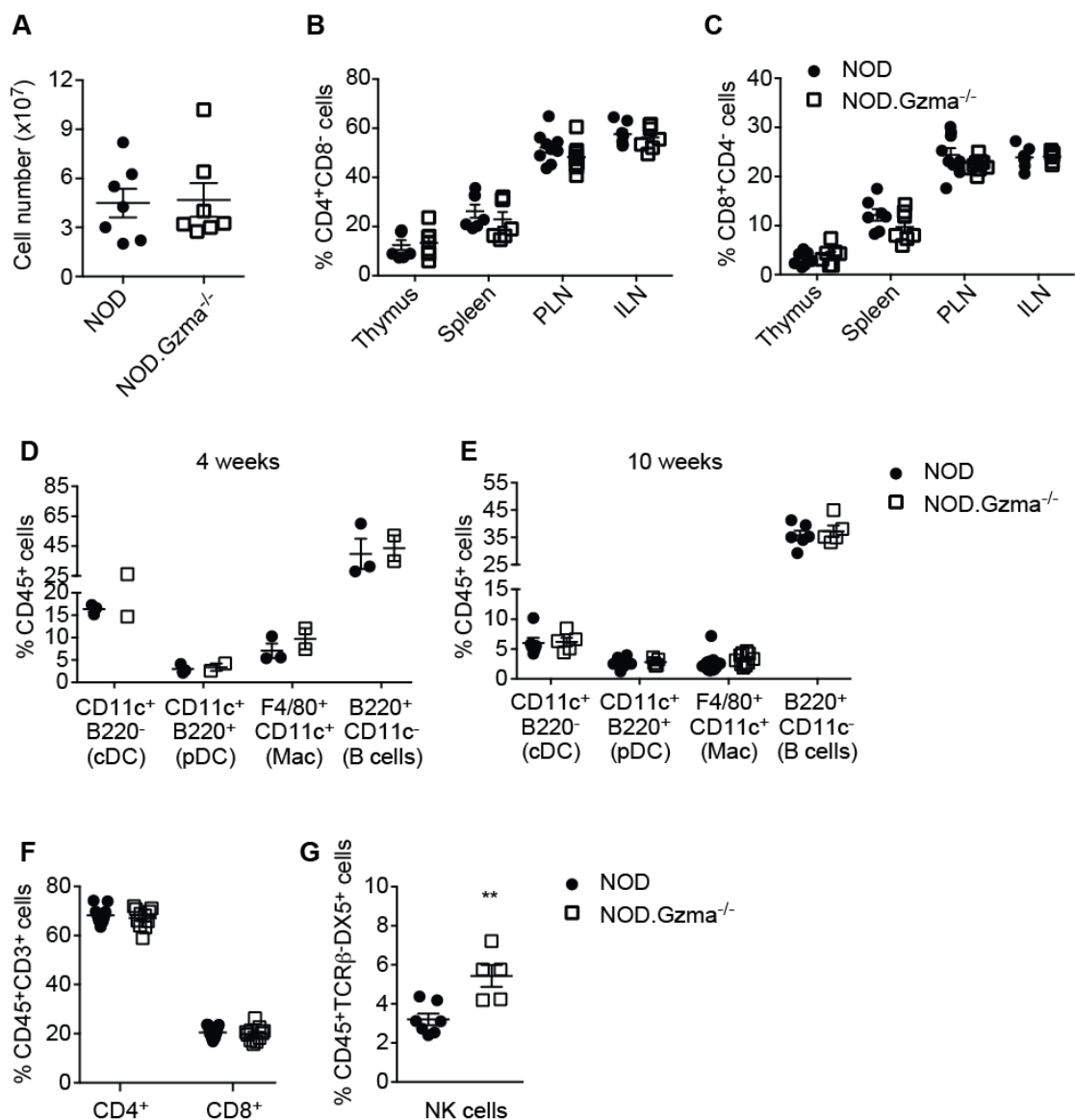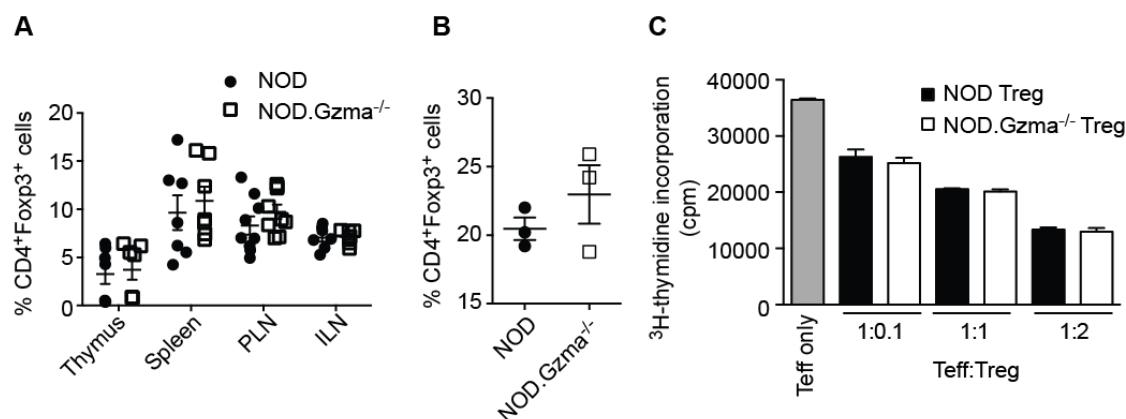SUPPLEMENTARY DATA

Supplementary Figure S1. T cell development is similar in NOD and NOD.Gzma$^{-/-}$ mice. (**A**) Absolute cell number after lysis of red blood cells in spleens isolated from NOD and NOD.Gzma$^{-/-}$ mice at 10 weeks of age (n=7). (**B**) The percentage of CD4$^+$CD8$^-$ T cells and (**C**) CD8$^+$CD4$^-$ T cells in thymus (n=7), spleen (n=7), pancreatic lymph nodes (n=9) and inguinal lymph nodes (n=7) from 10 week-old mice. Data for individual mice are shown with mean±SEM. (**D, E**) The percentage of CD45$^+$ cells in the islets of 4 week (D) and 10 week (E) old mice that were cDC, pDC, macrophages (mac) and B cells. Data for individual mice are shown (n=2-6) with mean±SEM. (**F, G**) The percentage of CD45$^+$ cells in the islets of 10 week-old mice that were CD3$^+$CD4$^+$ or CD3$^+$CD8$^+$ T cells (F) or NK cells (G). Data for individual mice are shown (n=5-7) with mean±SEM. No significant differences were observed except **p<0.01 for NK cells (G), unpaired two-tailed Student's t-test.
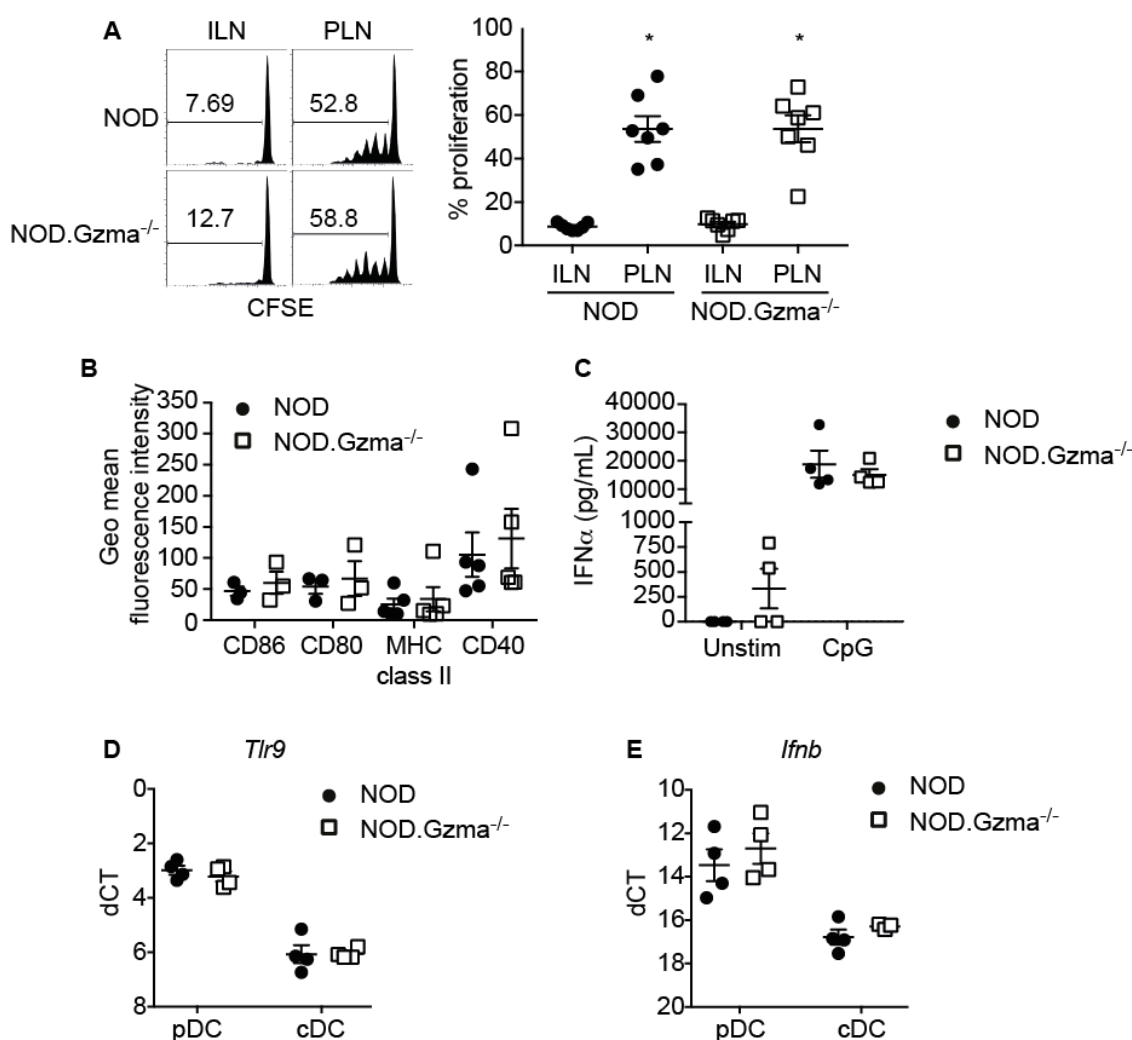
SUPPLEMENTARY DATA

Supplementary Figure S2. Regulatory T cell development and function are intact in NOD.Gzma$^{-/-}$ mice. The percentage of Foxp3$^+$CD4$^+$ T cells in (**A**) thymus (n=7), spleen (n=7), pancreatic lymph node (n=9), inguinal lymph node (n=7) and (**B**) islets (n=3) from NOD and NOD.Gzma$^{-/-}$ at 10-14 weeks of age. Data for individual mice are shown with mean±SEM. No significant differences using unpaired two-tailed Student's t-test. (**C**) Foxp3$^+$CD4$^+$ regulatory T cell function measured by ^{3}H-thymidine incorporation. Effector T cells from NOD mice were mixed with regulatory T cells from either NOD or NOD.Gzma$^{-/-}$ mice at ratios of 1:0.1, 1:1 or 1:2. One experiment performed in triplicate is shown.
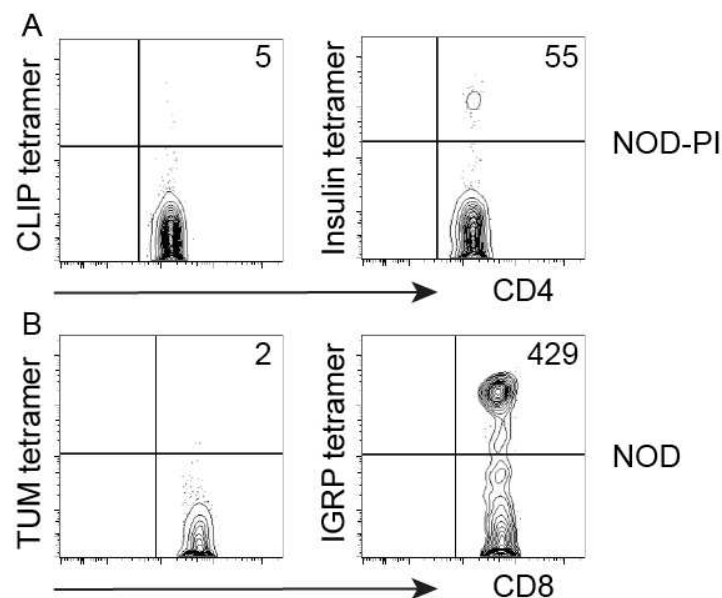
SUPPLEMENTARY DATA

Supplementary Figure S3. Dendritic cell function is normal in NOD.Gzma$^{-/-}$ mice. (**A**) Inguinal (ILN) and pancreatic lymph nodes (PLN) were harvested from 6 week old NOD or NOD.Gzma$^{-/-}$ mice 5 days after transfer of CFSE-labeled NOD8.3 CD8$^+$ T cells. Representative FACS plots showing the proportion of proliferated CD8$^+$ T cells (left), and pooled data from n=7 mice per group showing mean±SEM (right). *p<0.0001 comparing ILN to PLN, unpaired Student's t-test. (**B**) Geometric mean fluorescence intensity of staining for CD80, CD86, MHC class II and CD40 on splenic CD11c$^+$ DC cultured for 48 hours. N=4-5 mice/genotype showing mean±SEM. No significant differences between genotypes, unpaired Student's t-test. (**C**) IFNα production by splenic pDC cultured for 18 hours in the absence (unstim) or presence of CpG$_{2216}$, measured by flow cytometry. N=4 mice per genotype showing mean±SEM. No significant differences between genotypes, unpaired Student's t-test. (**D, E**) Quantitative real time PCR of *Tlr9* (D) or *Ifnb* (E) gene expression from pDC or cDC isolated from wild-type NOD (n=4) or NOD.Gzma$^{-/-}$ (n=4) mice. Data show delta CT values for individual mice with mean±SEM. No significant differences between groups, unpaired Student's t-test. (C-E) Each data point represents cells pooled from the spleens of two mice.

Supplementary Figure S4. Control tetramer staining. Representative FACS plots showing absolute number of (**A**) CLIP control or insulin$_{B10-23}$-specific CD4$^+$ T cells or (**B**) TUM control or IGRP$_{206-214}$-specific CD8$^+$ T cells in the peripheral lymphoid organs from NOD.PI (A) or NOD (B) mice. Top right quadrant shows absolute number of tetramer$^+$ T cells.

SUPPLEMENTARY DATA

Supplementary Table S1. Oligonucleotides used in the generation of 3' flap substrate for nuclease activity. Complementary sequences are color coded.

Xom1	5'ACGCTGCCGAATTCTACCAGTGCCTTGCTAGGACATCTTTGCCCACCTGCAGGTT CACCC3'
Xo3	5'CATGGAGCTGTCTAGAGGATCCGACTATCG3'
Xo4	5'CGATAGTCGGATCCTCTAGACAGCTCCATGTAGCAAGGCACTGGTAGAATTCGG CAGCGT3'

Supplementary Table S2. Fold-change of IFN-regulated gene expression in islets from 4- and 10-12-week old NOD (n=6-9) and NOD.Gzma$^{-/-}$ (n=6-8) mice, calculated relative to gene expression in islets from 4-week old NOD.Gzma$^{-/-}$Ifnar1$^{-/-}$ (n=7) mice using the $\Delta\Delta$CT method with *Actin-b* as a housekeeping gene. Mean and SEM are shown. P values calculated by t-test between NOD and NOD.Gzma$^{-/-}$ for each gene.

Gene	4-weeks of age			10-12-weeks of age		
	NOD	**NOD.Gzma**	**P value**	**NOD**	**NOD.Gzma**	**P value**
Mx1	1.67±0.45	4.85±1.05	0.011	12.21±2.09	17.89±1.99	0.078
Isg15	3.94±0.81	8.54±2.03	0.044	10.27±2.01	22.42±5.10	0.051
Ifit1	0.81±0.16	2.89±0.79	0.016	5.18±0.84	12.23±2.79	0.036
Oas1a	9.06±2.59	25.55±6.94	0.034	11.02±2.33	25.61±8.00	0.111