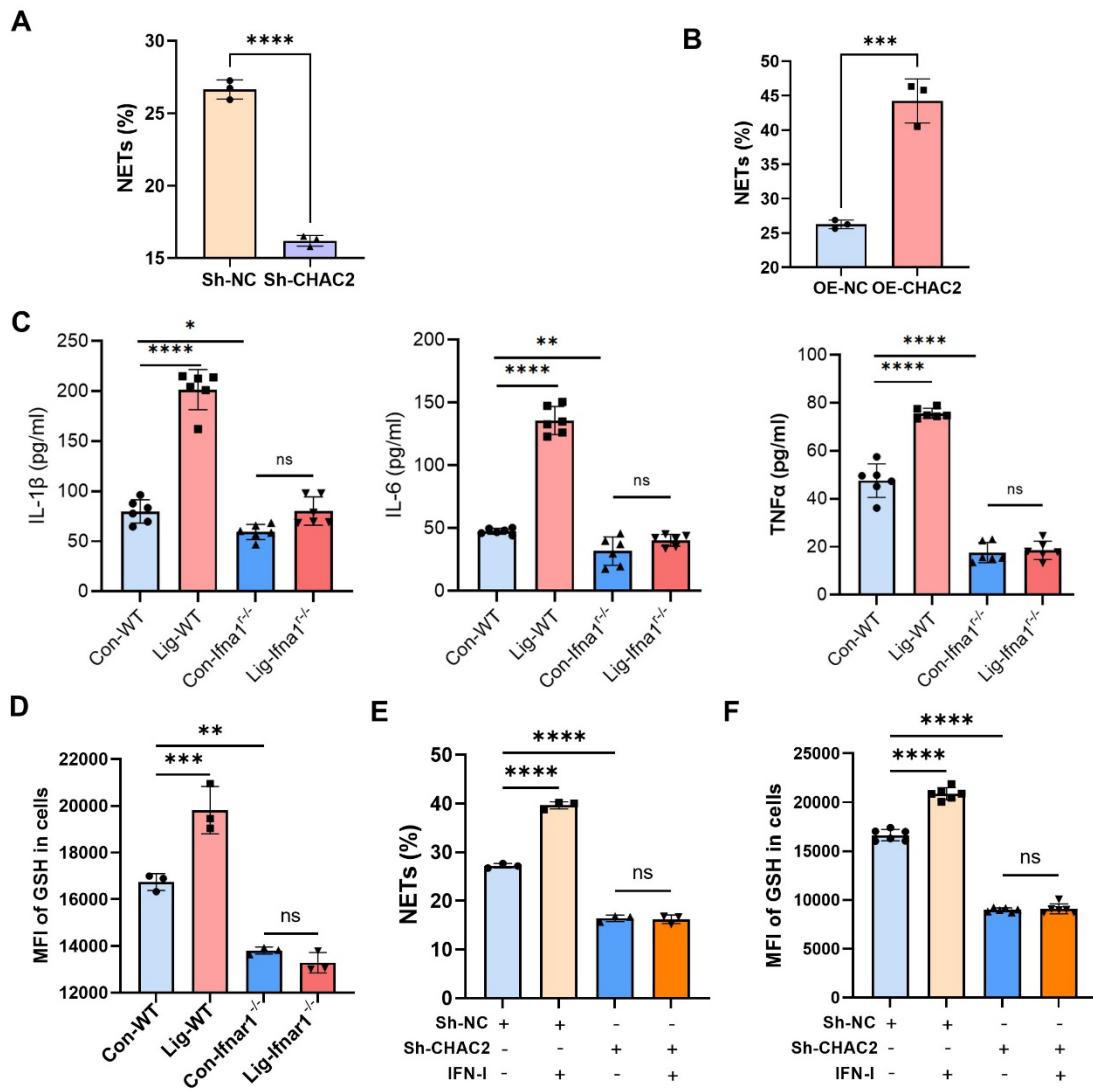


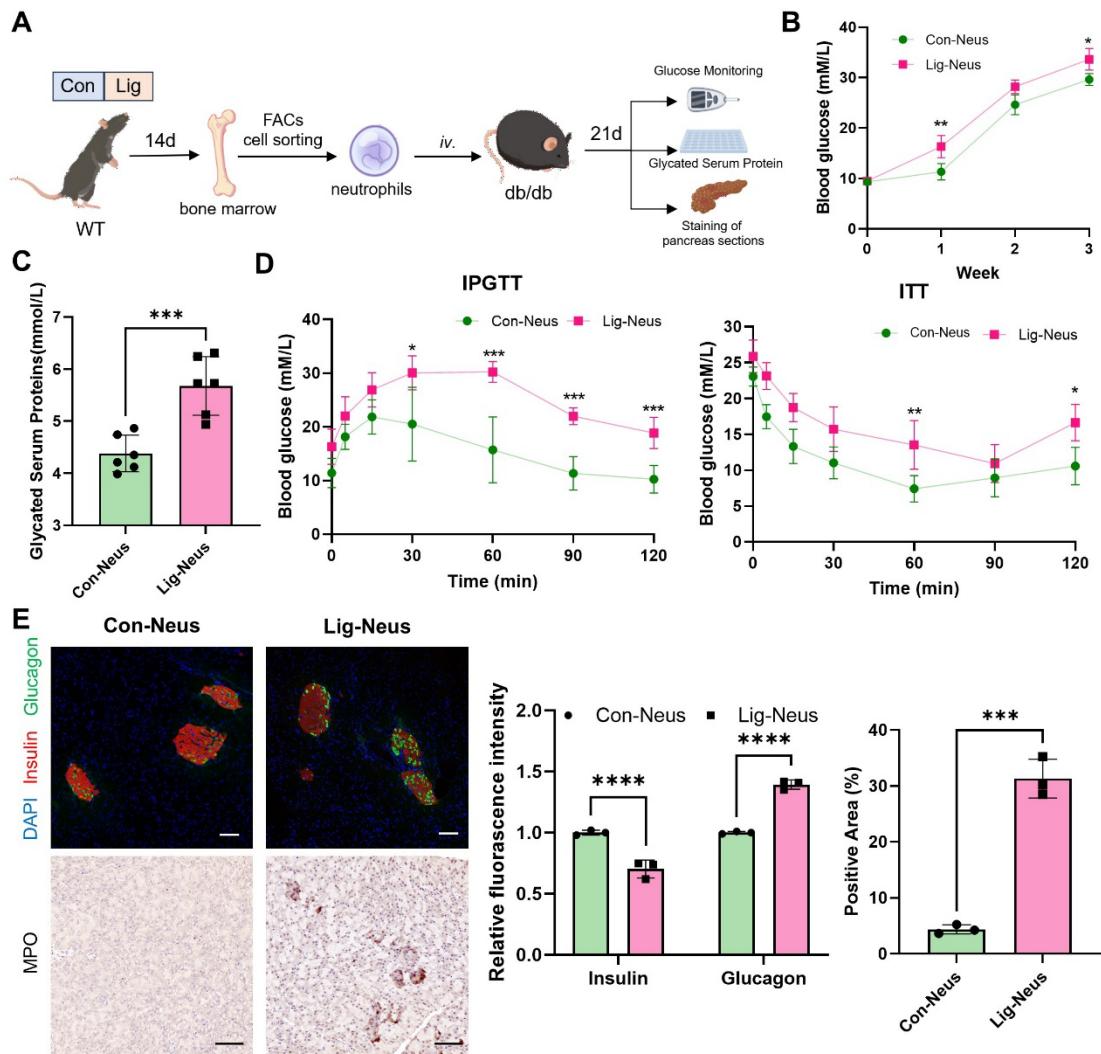
**Figure S1**

**(A)** Heat map of metabolites normalized concentration of BM neutrophils the Con group and Lig group. **(B)** Quantification of total GSH concentrations in BM neutrophils from the Con and Lig mice. **(C)** Overlay histogram of GSH concentration in Con, GDE and L-BSO neutrophils. **(D)** Percentage of NETs area in the Con, GDE and L-BSO neutrophils normalized to an MPO-citH3 positive signal. Data are presented as the mean  $\pm$  SD from at least three independent experiments. P values were calculated using two-tailed Student's t test; \*P < 0.05, \*\*P < 0.01, \*\*\*P < 0.001.



**Figure S2**

**(A)** Percentage of NETs area in the Sh-NC and Sh-Chac2 neutrophils normalized to an MPO-citH3 positive signal. **(B)** Percentage of NETs area in the OE-NC and OE-Chac2 neutrophils normalized to an MPO-citH3 positive signal. **(C)** Quantitative statistical analysis of reactive cytokines IL-6, IL-1 $\beta$ , and TNF- $\alpha$  produced by mice BM neutrophils in response to LPS stimulation. **(D)** Corresponding mean FCS fluorescence intensity of GSH concentration in mice BM neutrophils. **(E)** Percentage of NETs area in the Sh-NC and Sh-Chac2 neutrophils treated with or without IFN-1 normalized to an MPO-citH3 positive signal. **(F)** Corresponding mean FCS fluorescence intensity of GSH concentration in neutrophils. Data are presented as the mean  $\pm$  SD from at least three independent experiments. P values were calculated using two-tailed Student's t test; \*P < 0.05, \*\*P < 0.01, \*\*\*P < 0.001.



**Figure S3**

**(A)** Schematic illustration of the experimental design for the transfer BM neutrophils from Con or Lig wild-type mice to db/db mice. **(B)** Statistical curves of random blood glucose measurements in the Con-Neus and Lig-Neus groups. **(C)** Quantitative analysis of serum glycated protein content. **(D)** Statistical curves of blood glucose measurements during IPGTT and ITT. **(E)** Representative immunofluorescent staining of glucagon (green), insulin (red), and cell nuclei (DAPI, blue), together with immunohistochemical staining of MPO in pancreas tissue sections. Scale bar = 100  $\mu$ m. Data are presented as the mean  $\pm$  SD from at least three independent experiments. P values were calculated using two-tailed Student's t test; \*P < 0.05, \*\*P < 0.01, \*\*\*P < 0.001.

**Table S1: The primers used for RT-qPCR.**

Gene	Primer sequence (5' to 3') -Forward	Primer sequence (5' to 3')-Reverse
<i>Gapdh</i>	CCATCACCATCTTCCAGG	AGACTCCACGACATACTCA
<i>Chac2</i>	GTGACCCTTGTGAAGATCCTGG	GACTGTCGTAGTTCTGTAGCCTC
<i>Chac1</i>	TGACCCTCCTGAAGACCGTGA	AGTGTCATAGCCACCAAGCACG
<i>Gsr</i>	GTTCACCGCTCCACACATCCTG	GCTGAAAGAAGCCATCACTGGTG
<i>Gclc</i>	ACACCTGGATGATGCCAACGAG	CCTCCATTGGTCGGAACCTCTAC
<i>Gclm</i>	TCCTGCTGTGTGATGCCACCAAG	GCTTCCTGGAAACTTGCCTCAG
<i>Gss</i>	CCAGGAAGTTGCTGTGGTGTAC	GCTGTATGGCAATGTCTGGACAC
<i>Anpep</i>	CGAACACCGTTATCTGGACCTG	AGCCCATCTGTAGAATCCAGCG
<i>Gstk1</i>	AAGCTCCTGAGACACCATCTCC	CTCTGGATGCTCCAAGTTCACG
<i>Gstm1</i>	TGTTTAGGCCAAGTGCCTGGA	TAGGTGTTGCGATGTAGCGGCT
<i>Gsto1</i>	CGAACCTAAGGGAAAGCGTTGGA	TTCCAGTCGCTGAAACCAAGGC
<i>Mgst1</i>	TGCGACCCTGATTCCAGAGGATA	TCCACCTCTCGTCAGTGCAGAA
<i>Gpx4</i>	CCTCTGCTGCAAGAGCCTCCC	CTTATCCAGGCAGACCATGTGC
<i>Pgd</i>	CATCGCTGCAAAAGGGAAACC	AGCCTCACAGATGAGCTGCATG
<i>Idh1</i>	CAGGCTCATAGATGACATGGTGG	CACTGGTCATCATGCCAAGGGA
<i>G6pdx</i>	GACCAAGAACCTGGCATGTT	AGACATCCAGGATGAGGCGTT
<i>GAPDH</i>	GTCTCCTCTGACTTCAACAGCG	ACCACCTGTTGCTGTAGCCAA
<i>CHAC1</i>	GTGGTGACGCTCCTGAAGATC	GAAGGTGACCTCCTGGTATCG
<i>CHAC2</i>	ACATCACCAACTACAGCAGGCG	CTGGCAATCTGTAAGCAACACCC
<i>IL-6</i>	AGACAGCCACTCACCTCTCAG	TTCTGCCAGTGCCTCTTGCTG
<i>IL-1B</i>	CCACAGACCTCCAGGAGAATG	GTGCAGTTCACTGATCGTACAGG
<i>TNF-A</i>	CTCTTCTGCCTGCTGCACTTG	ATGGGCTACAGGCTTGTCACTC