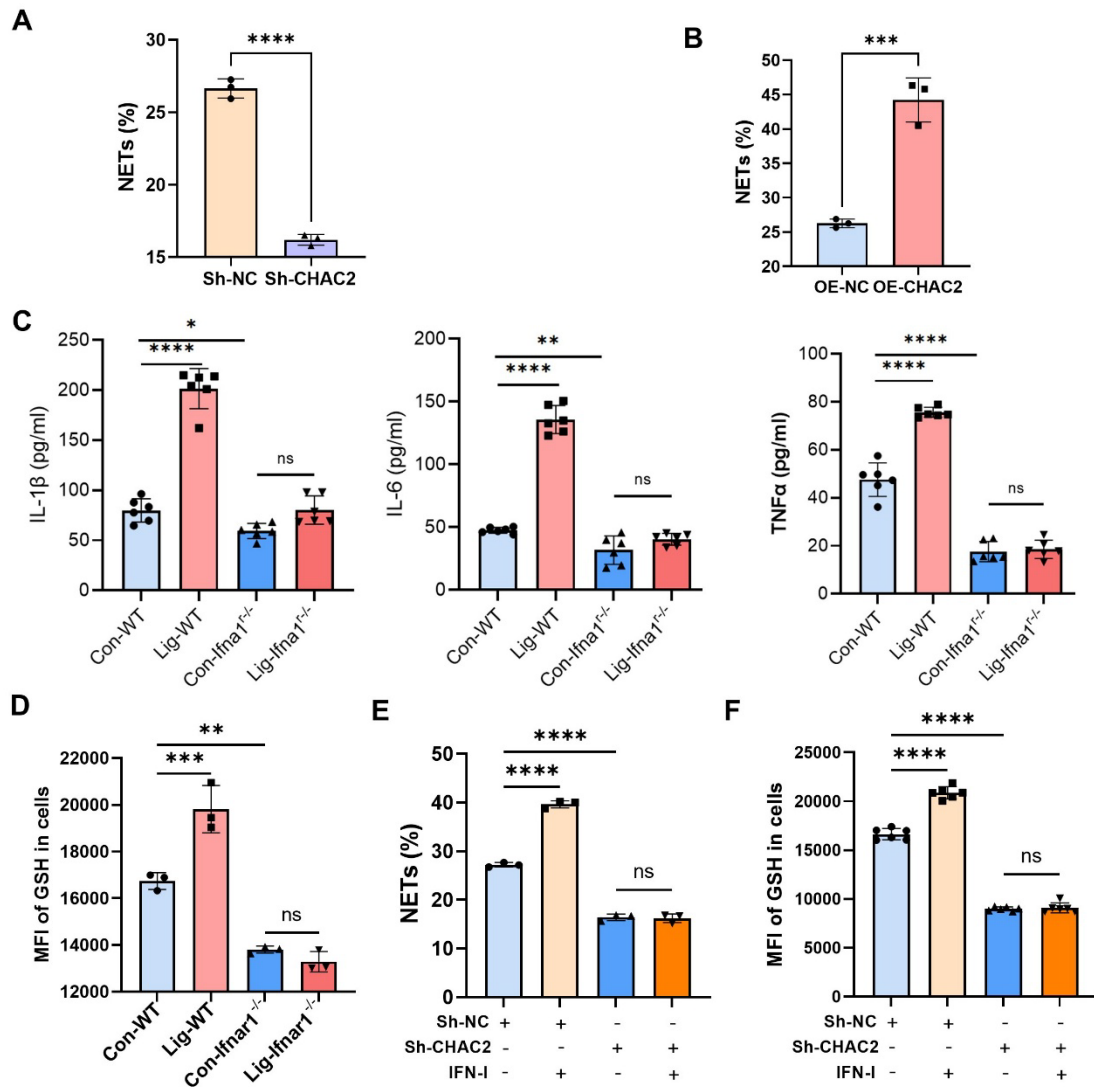


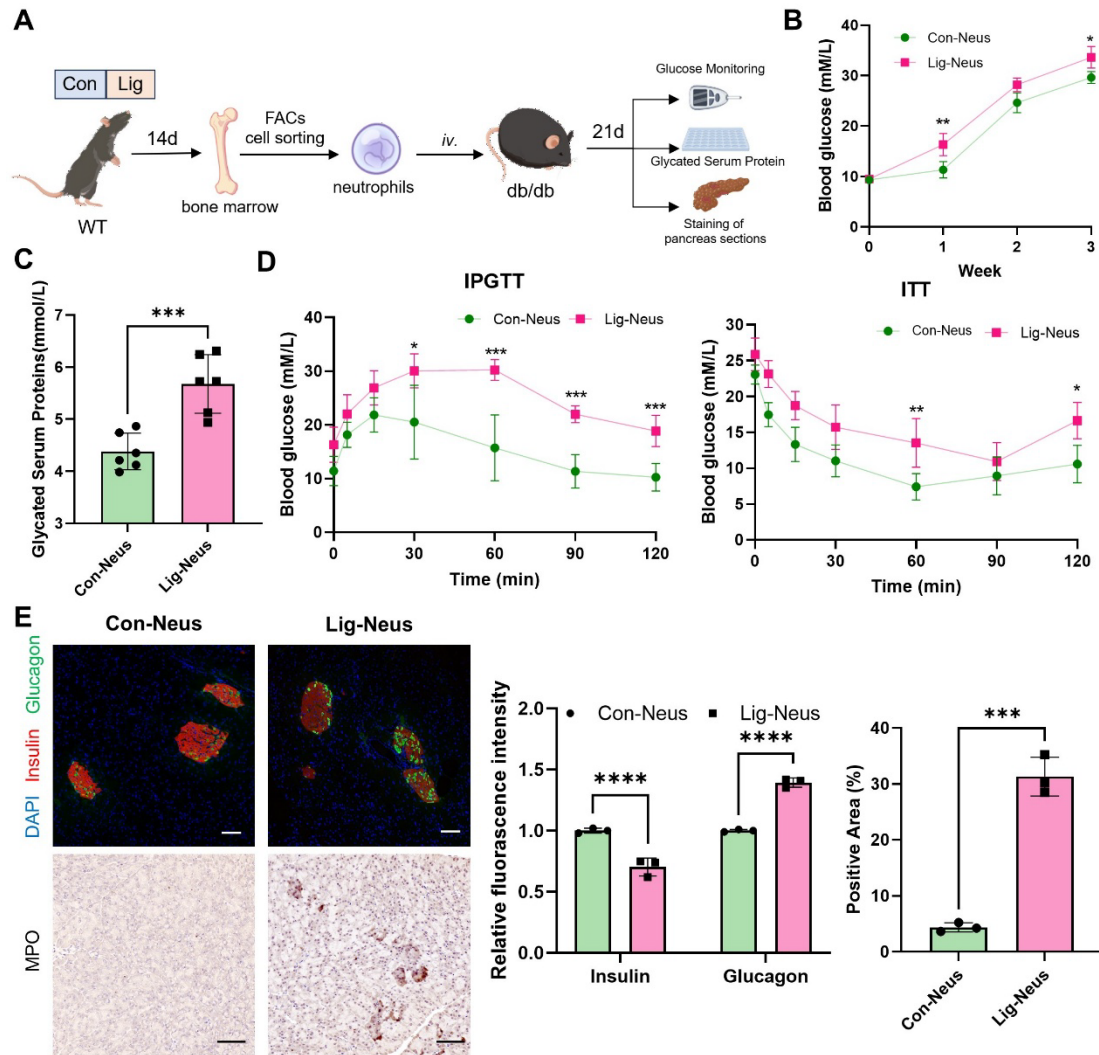
**Figure S1**

**(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-I 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 glycation 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.**

<b>Gene</b>	<b>Primer sequence (5' to 3') -Forward</b>	<b>Primer sequence (5' to 3')-Reverse</b>
<i>Gapdh</i>	CCATCACCATCTTCCAGG	AGACTCCACGACATACTCA
<i>Chac2</i>	GTGACCCTTGTTGAAGATCCTGG	GACTGTCGTAGTTCTGTAGCCTC
<i>Chac1</i>	TGACCCTCCTTGAAGACCGTGA	AGTGTCATAGCCACCAAGCACG
<i>Gsr</i>	GTTTACCGCTCCACACATCCTG	GCTGAAAGAAGCCATCACTGGTG
<i>Gclc</i>	ACACCTGGATGATGCCAACGAG	CCTCCATTGGTCGGAACCTCTAC
<i>Gclm</i>	TCCTGCTGTGTGATGCCACCAG	GCTTCCTGGAAACTTGCCTCAG
<i>Gss</i>	CCAGGAAGTTGCTGTGGTGTAC	GCTGTATGGCAATGTCTGGACAC
<i>Anpep</i>	CGAACACCGTTTATCTGGACCTG	AGCCCATCTGTAGAATCCAGCG
<i>Gstk1</i>	AAGCTCCTGAGACACCATCTCC	CTCTGGATGCTCCAAGTTCACG
<i>Gstm1</i>	TGTTTGAGCCCAAGTGCCTGGA	TAGGTGTTGCGATGTAGCGGCT
<i>Gsto1</i>	CGAACCTAAGGGAAGCGTTGGA	TTCCAGTCGCTGAAACCAAGGC
<i>Mgst1</i>	TGCGACCGCATTCAGAGGATA	TCCACCTTCTCGTCAGTGCGAA
<i>Gpx4</i>	CCTCTGCTGCAAGAGCCTCCC	CTTATCCAGGCAGACCATGTGC
<i>Pgd</i>	CATCGCTGCAAAAGTGGGAACC	AGCCTCACAGATGAGCTGCATG
<i>Idh1</i>	CAGGCTCATAGATGACATGGTGG	CACTGGTCATCATGCCAAGGGA
<i>G6pdx</i>	GACCAAGAAGCCTGGCATGTTC	AGACATCCAGGATGAGGCGTTC
<i>GAPDH</i>	GTCTCCTCTGACTTCAACAGCG	ACCACCCTGTTGCTGTAGCCAA
<i>CHAC1</i>	GTGGTGACGCTCCTTGAAGATC	GAAGGTGACCTCCTTGGTATCG
<i>CHAC2</i>	ACATCACCAACTACAGCAGGCG	CTGGCAATCTGTAAGCAACACCC
<i>IL-6</i>	AGACAGCCACTCACCTCTTCAG	TTCTGCCAGTGCCTCTTTGCTG
<i>IL-1B</i>	CCACAGACCTTCCAGGAGAATG	GTGCAGTTCAGTGATCGTACAGG
<i>TNF-A</i>	CTCTTCTGCCTGCTGCACTTTG	ATGGGCTACAGGCTTGTCACCTC