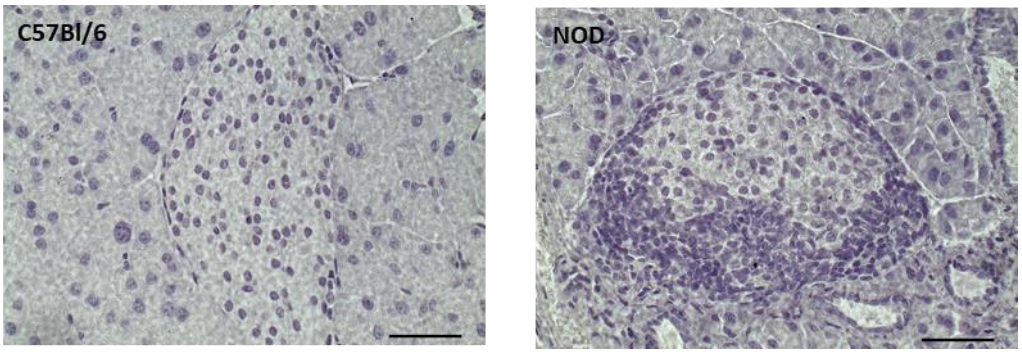
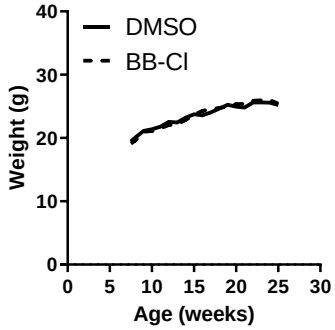
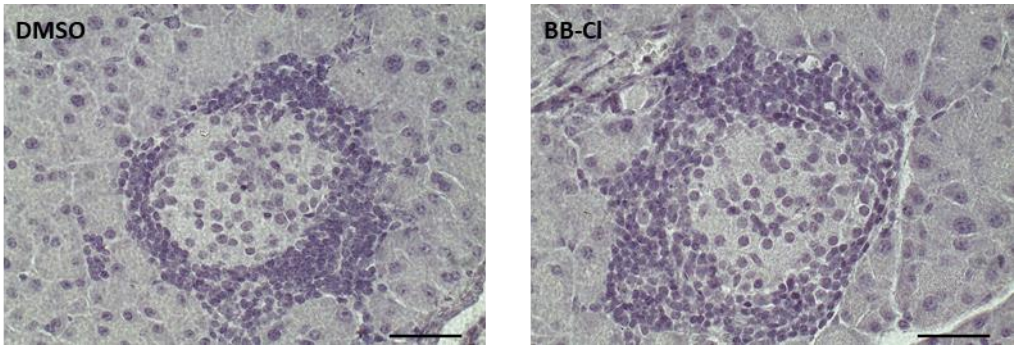
Supplementary Figure 1 – Negative staining controls for immunohistochemistry with anti-citrulline antibody. Representative immunohistochemistry images of the negative control staining. The negative control was performed by omitting the primary anti-citrulline antibody in pancreas sections of C57Bl/6 and NOD mice (shown in Figure 1 of the manuscript). All sections where mounted on one slide to enable good comparison (scale bar = 50µm).



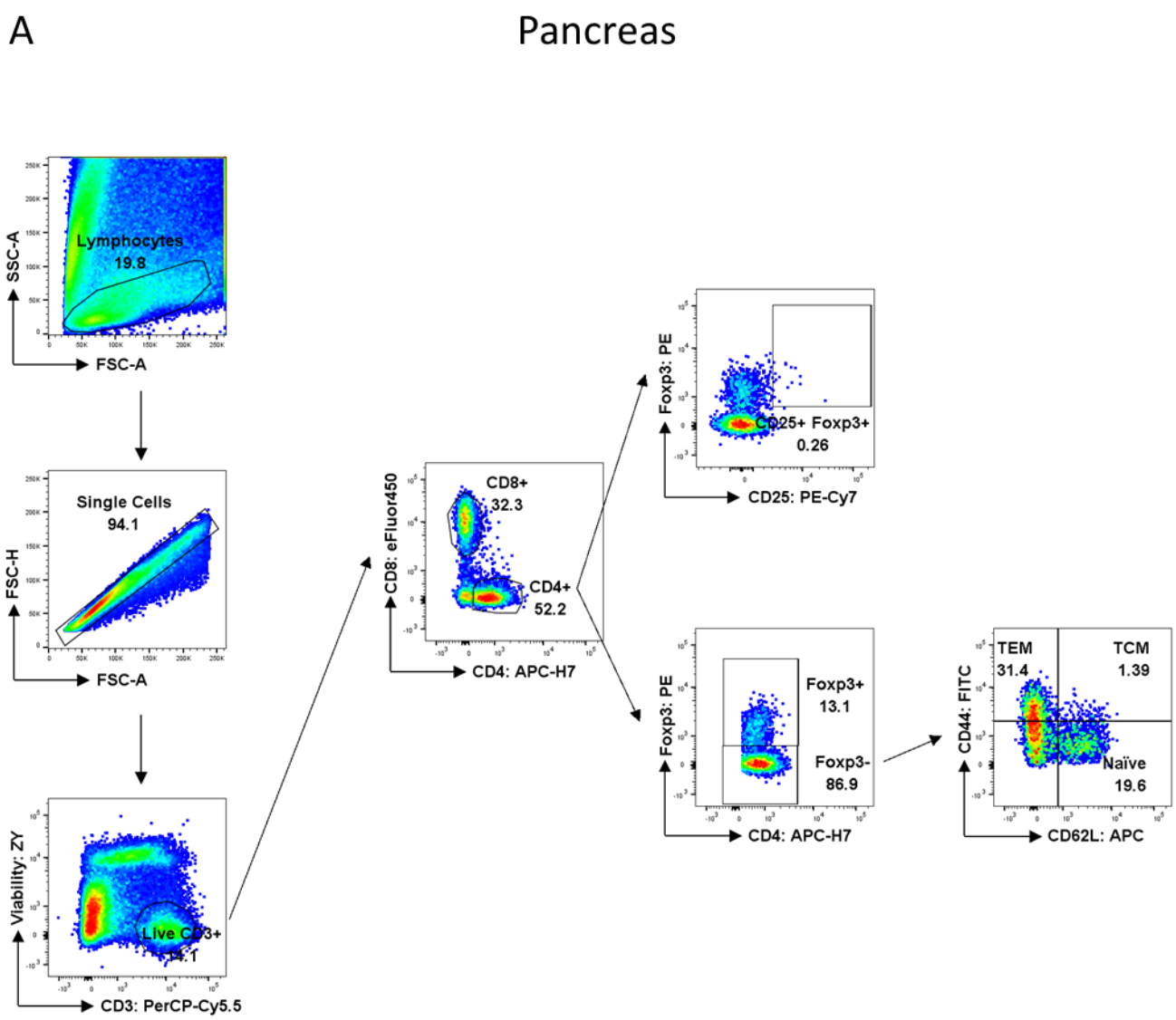
Supplementary Figure 2 – BB-Cl-amidine treatment does not alter body weight in NOD mice. Eight-week-old female littermate NOD mice were injected subcutaneously with vehicle (25% DMSO in PBS) or BB-Cl-amidine (1μg/g body weight) six times per week until 25 weeks of age. Body weight of NOD mice treated with DMSO or BB-Cl-amidine (n = 17-18 mice per group; 2 independent cohorts were performed with at least eight mice per group per experiment).



Supplementary Figure 3 – Negative staining controls for immunohistochemistry with anti-citrulline antibody. Representative immunohistochemistry images of the negative control staining. The negative control was performed by omitting the primary anti-citrulline antibody in pancreas sections of 13-week-old NOD mice treated with DMSO or BB-Cl-amidine from 8-13 weeks of age (shown in Figure 3 of the manuscript). All sections where mounted on one slide to enable good comparison (scale bar = 50µm).

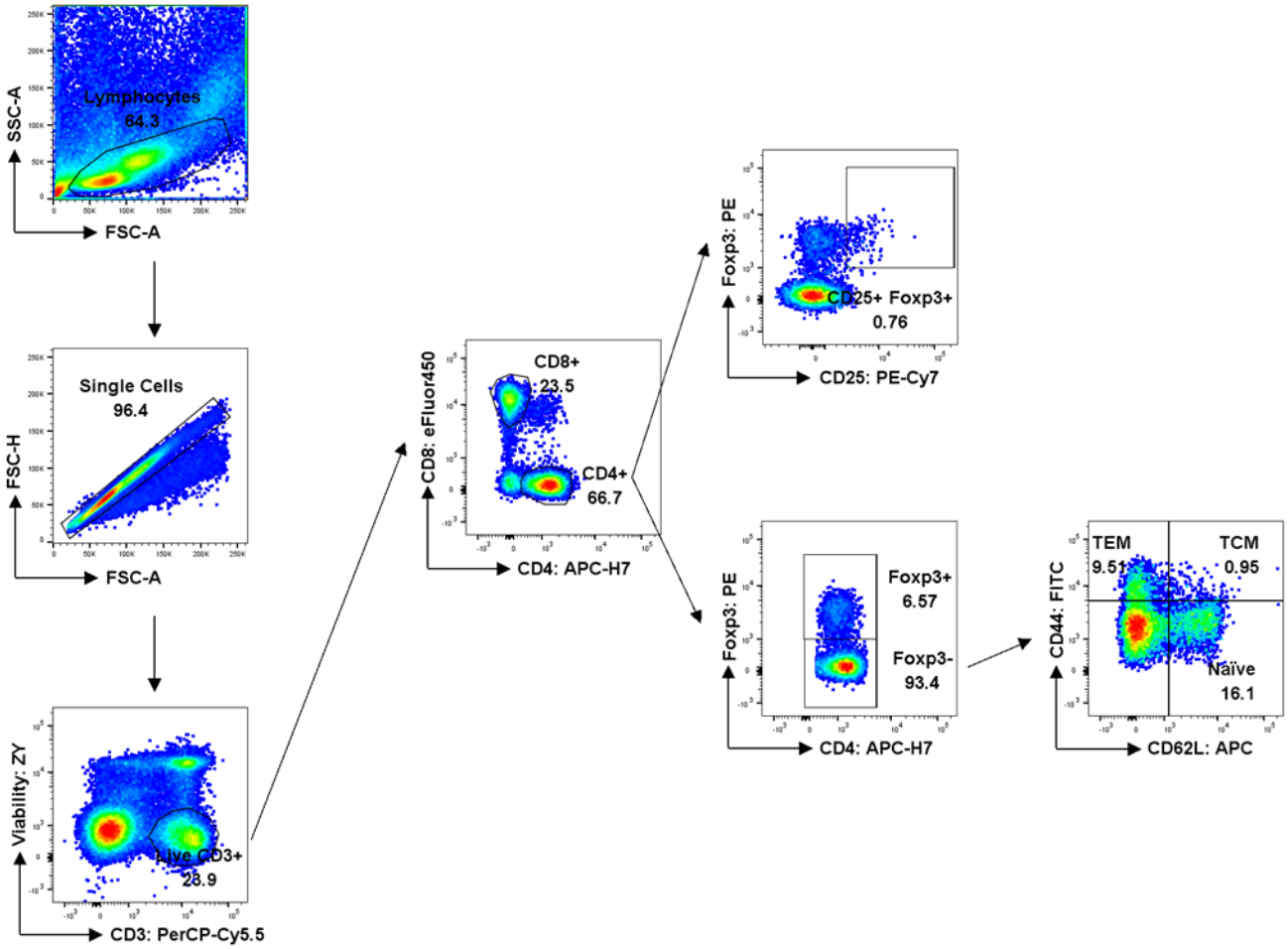


Supplementary Figure 4 – Gating strategy for T cell phenotyping. Gating strategy for T cell phenotyping in the pancreas (A), blood (B) and spleen (C). Left panels show the gating strategy for obtaining live $CD3^+$ T cells. Top right panel shows gating strategy for obtaining T_{reg} ($CD4^+$ $CD25^+$ $Foxp3^+$) cells. Bottom right panels show gating strategy for obtaining $CD4^+$ T_{EM} ($CD4^+$ $Foxp3^-$ $CD44^{HIGH}$ $CD62L^-$), $CD4^+$ T_{CM} ($CD4^+$ $Foxp3^-$ $CD44^{HIGH}$ $CD62L^+$) and $CD4^+$ $T_{naïve}$ ($CD4^+$ $Foxp3^-$ $CD44^{LOW}$ $CD62L^+$). $CD8^+$ T_{EM} ($CD8^+$ $Foxp3^-$ $CD44^{HIGH}$ $CD62L^-$), $CD8^+$ T_{CM} ($CD8^+$ $Foxp3^-$ $CD44^{HIGH}$ $CD62L^+$) and $CD8^+$ $T_{naïve}$ ($CD8^+$ $Foxp3^-$ $CD44^{LOW}$ $CD62L^+$) are obtained in the same way as $CD4^+$, but in the $CD8^+$ gate (not shown). Plots are representative of 2 independent experiments (n = 15-19), with at least six mice per group per experiment. ZY, Zombie Yellow; T_{reg}, regulatory T cells; T_{EM}, effector memory T cells; T_{CM}, central memory T cells.



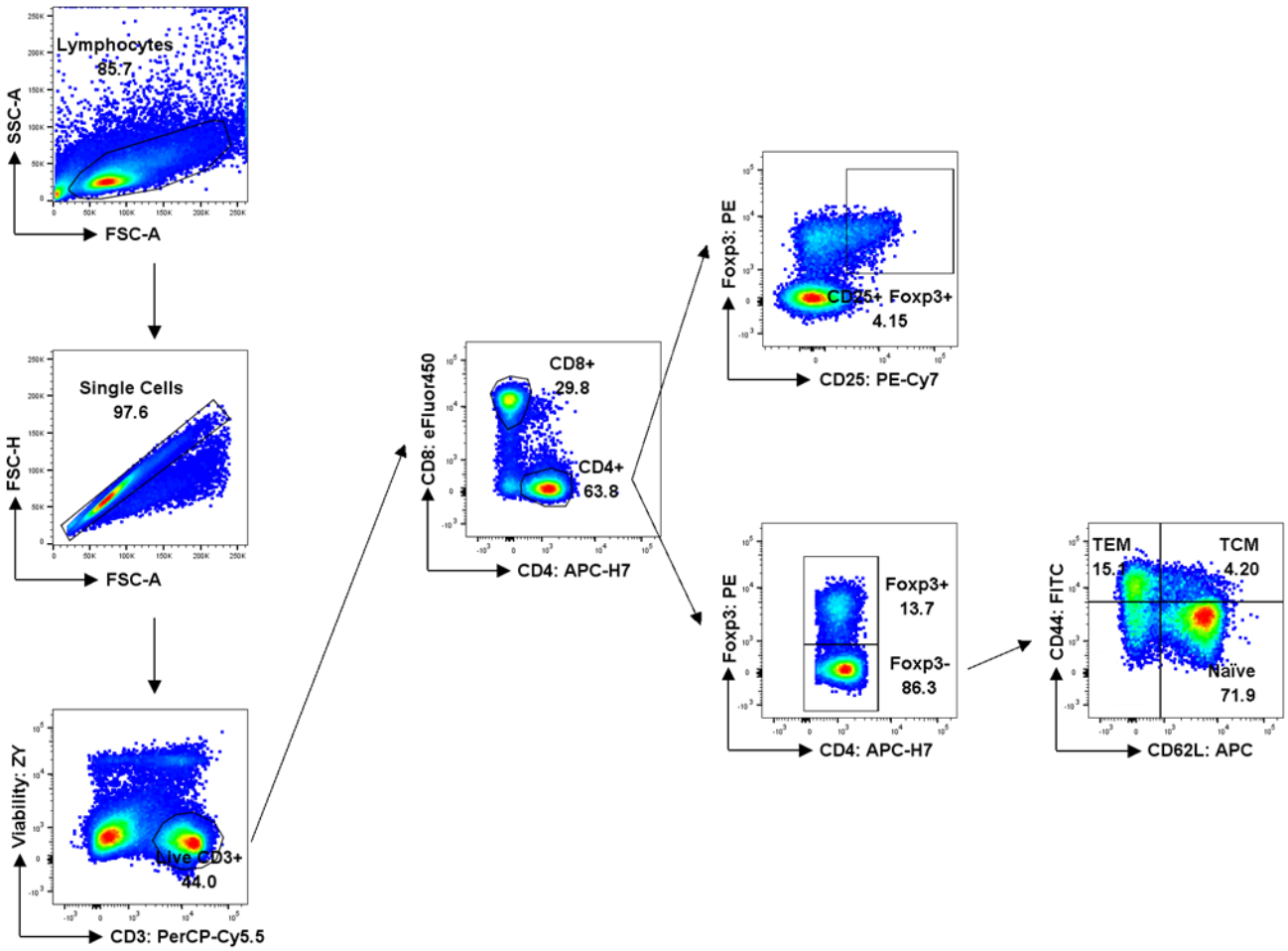
B

Blood

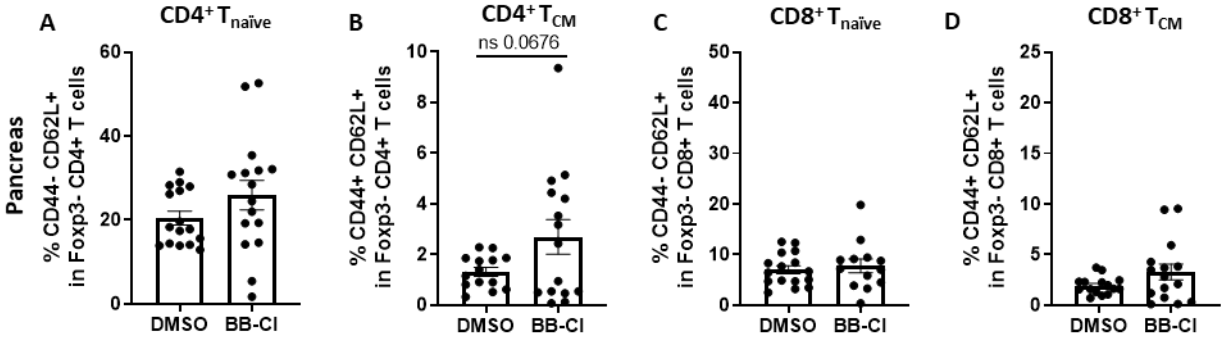

SSC-A
Lymphocytes
64.3
FSC-A
FSC-H
Single Cells
96.4
FSC-A
Viability: ZY
Live CD3+
28.9
CD3: PerCP-Cy5.5
CD8: eFluor450
CD8+
23.5
CD4+
66.7
CD4: APC-H7
Foxp3: PE
CD25+ Foxp3+
0.76
CD25: PE-Cy7
Foxp3: PE
Foxp3+
6.57
Foxp3-
93.4
CD4: APC-H7
CD44: FITC
TEM
9.51
TCM
0.95
Naïve
16.1
CD62L: APC

C

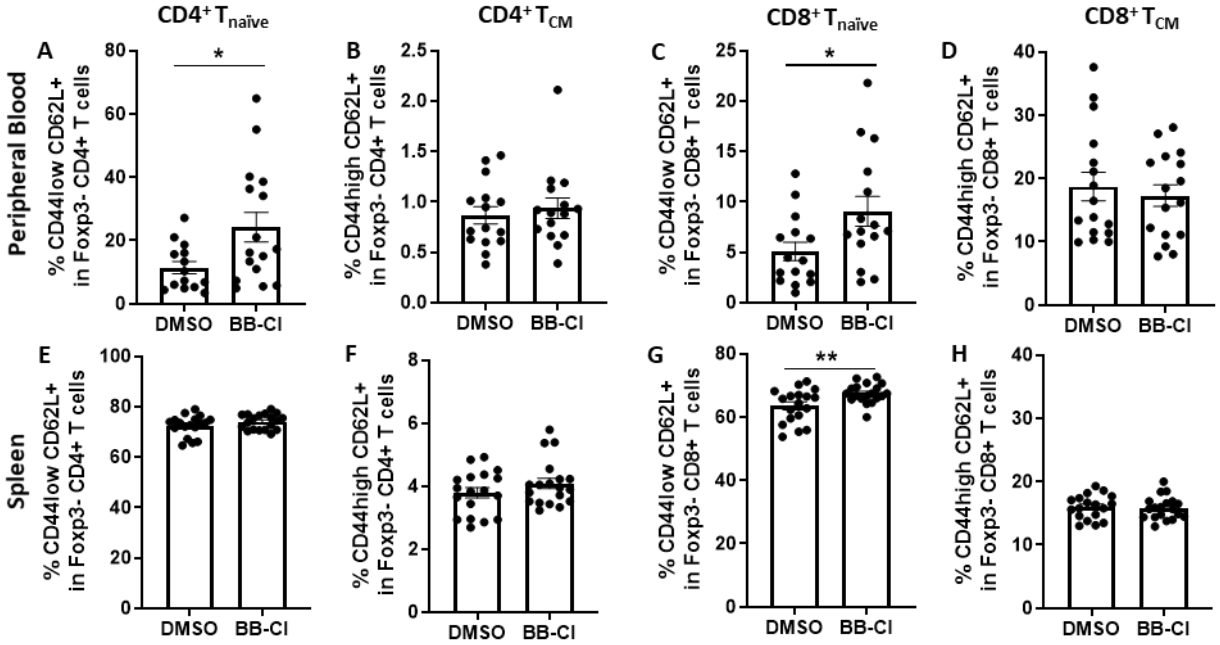
Spleen


Lymphocytes
85.7
SSC-A
FSC-A
Single Cells
97.6
FSC-H
FSC-A
Viability: ZY
Live CD3+
44.0
CD3: PerCP-Cy5.5
CD8: eFluor450
CD8+
29.8
CD4+
63.8
CD4: APC-H7
Foxp3: PE
CD25+ Foxp3+
4.15
CD25: PE-Cy7
Foxp3: PE
Foxp3+
13.7
Foxp3-
86.3
CD4: APC-H7
CD44: FITC
TEM
15.
TCM
4.20
Naïve
71.9
CD62L: APC

Supplementary Figure 5 – Phenotype of pancreatic T cells. A-D: Percentage of $CD4^+$ $T_{naïve}$ ($CD4^+$ $Foxp3^-$ $CD44^{LOW}$ $CD62L^+$) (A), $CD4^+$ T_{CM} ($CD4^+$ $Foxp3^-$ $CD44^{HIGH}$ $CD62L^+$) (B), $CD8^+$ $T_{naïve}$ ($CD8^+$ $Foxp3^-$ $CD44^{LOW}$ $CD62L^+$) (C) and $CD8^+$ T_{CM} ($CD8^+$ $Foxp3^-$ $CD44^{HIGH}$ $CD62L^+$) (D) in the pancreas of 13-week-old NOD mice treated with DMSO or BB-Cl-amidine (n = 15-16 mice per group; two independent experiments were performed with at least six mice per group per experiment). T_{CM}, central memory T cell.



Supplementary Figure 6 – Phenotype of peripheral T cells. Percentage of $CD4^+$ $T_{naïve}$ ($CD4^+$ $Foxp3^-$ $CD44^{LOW}$ $CD62L^+$), $CD4^+$ T_{CM} ($CD4^+$ $Foxp3^-$ $CD44^{HIGH}$ $CD62L^+$), $CD8^+$ $T_{naïve}$ ($CD8^+$ $Foxp3^-$ $CD44^{LOW}$ $CD62L^+$) and $CD8^+$ T_{CM} ($CD8^+$ $Foxp3^-$ $CD44^{HIGH}$ $CD62L^+$) in different organs of 13-week-old NOD mice treated with DMSO or BB-Cl-amidine (n = 15-19 mice per group; two independent experiments were performed with at least six mice per group per experiment). A-D: Frequency of $CD4^+$ $T_{naïve}$ (A), $CD4^+$ T_{CM} (B), $CD8^+$ $T_{naïve}$ (C) and $CD8^+$ T_{CM} (D) in peripheral blood. E-H: Frequency of $CD4^+$ $T_{naïve}$ (E), $CD4^+$ T_{CM} (F), $CD8^+$ $T_{naïve}$ (G) and $CD8^+$ T_{CM} (H) in spleen. *P<0.05 and **P<0.01. T_{CM}, central memory T cell.



Isolation of pancreatic islets

For isolation of NOD adult islets 0.5mg/ml collagenase P (Sigma) diluted in HBSS (Thermo Fisher) was injected in the main pancreatic duct while the ampulla of Vater was clamped. Next, the pancreas was collected and incubated in 0.5mg/ml collagenase P at 37°C for 11min. Islets were handpicked and cultured overnight in RPMI 1640 (Thermo Fisher) supplemented with 10% (vol/vol) Fetal Bovine Serum (FBS) (Biowest).

Flow cytometry sorting

Islets were dispersed into single-cell suspensions by incubation for 90sec at 37°C in 0.025% trypsin-EDTA (Thermo Fisher). Similarly as previously described (1), for cell surface staining, cells were incubated with antibodies at 4°C for 15min in the dark in FACS medium (HBSS + 2% FBS), rinsed in FACS medium and resuspended in FACS medium with propidium iodide (1/4000, Sigma) before FACS acquisition and sorting. The following antibodies were used: EpCam-BV605 (G8.8, Biolegend BLE118227), CD31-PercpCy5.5 (MEC13.3, Biolegend BLE102522), CD45-PercpCy5.5 (30-F11, Biolegend BLE103132), CD24-APC-Fire 750 (MA/69, Biolegend BLE101840), CD49f-PE (GoH3, Biolegend BLE313612), CD71-FITC (RI7217, Biolegend BLE113806), TER-119-PercpCy5.5 (TER-119, Biolegend BLE116228), TCRb-PECy7 (H57-597, Biolegend BLE109222), CD4-APC (GK1.5, Biolegend BLE100412), CD44-BV421 (IM7, BD Biosciences # 563970). For each antibody, optimal dilution was determined by titration. Cell sorting was carried out using a FACSAria III (BD). Data were analyzed using FlowJo 9.9.4 (RRID: SCR_008520). Dead cells were excluded from analyses using propidium iodide (fluorescence in both PE-A and PercpCy5.5-A channels, exclusion of the diagonal) and non-pancreatic lineages were excluded using the pan-hematopoietic marker CD45, the erythroid marker TER119, and the endothelial marker CD31. Pancreatic alpha- and beta-enriched fractions were isolated as described previously. As we determined that more than 95% of Lin+ cells are CD45+, sorted Lin+ were considered as CD45+ cells. For qPCR cells were collected directly in Buffer RLT for qPCR (Qiagen).

Quantitative RT-PCR

RNA was isolated with the RNeasy Micro Kit (Qiagen) and RNA sample was reverse-transcribed using the Maxima First Strand cDNA Synthesis Kit (Thermo Fisher) and a Biometra T3 Thermocycler (Analytik Jena). All kits were used per the manufacturer's instructions. SYBR green qPCR was performed on a QuantStudio 3 (Thermo Fisher) per the manufacturer's instructions.

Proteomic analysis making use of biotin-phenylglyoxal labeling

DMSO (n=4) and BB-Cl-amidine treated (n=4) mice pancreata were pooled in buffer (50mM HEPES pH 7.6, 0.5% NP40 and 1mM PMSF) and homogenized using a tissue homogenizer (20sec with maximum speed with 10min time interval three times). The lysed tissue samples were centrifuged (12,000rpm, 30min) at 4°C. The supernatants were isolated, and the protein concentration was determined using the DC™ (detergent compatible) assay. Equal protein

concentrations from DMSO and BB-Cl-amidine treated samples were labeled with biotin-phenylglyoxal (biotin-PG) in quadruplicate as previously described (2). Briefly, supernatants from DMSO and BB-Cl-amidine treated samples (300µg) were diluted in buffer (100mM HEPES pH 7.6) to a final concentration of 1µg/µL in a reaction volume of 300µL and incubated with 20% trichloroacetic acid (60µL of 100% TCA) and 0.5mM biotin-PG (5µL of 5mM stock) for 30min at 37°C. After a 30min incubation, the reaction was quenched with 60µL of 0.1M citrulline dissolved in 50mM HEPES pH 7.6. Proteins were precipitated by placing the reaction mixtures on ice for 30min followed by centrifugation (13,500rpm, 15min) at 4°C. The supernatants were discarded, and the protein pellet was washed twice with cold acetone and dried.

Protein pellets were then resuspended in 1.2% SDS in PBS, boiled for 10min and sonicated for 12-15min. Once dissolved, samples were diluted in PBS buffer (0.2% final SDS concentration) and incubated with streptavidin agarose slurry (170µL) overnight at 4°C, and a further 3h at 25°C. Streptavidin beads were then washed with PBS containing 0.2% SDS (1X), with PBS alone (3X), and water (3X) in order to remove any unbound proteins. Streptavidin beads were heated in a buffer containing 500µL of 6M urea in PBS and 10mM DTT (65°C, 20min) followed by iodoacetamide (20mM) addition and further incubation for 30min at 37°C. The beads were pelleted by centrifugation (1,400 x g for 3min), resuspended in a premixed solution of 2M urea, 1mM $CaCl_2$ and 2µg trypsin in PBS and incubated overnight at 37°C. The beads were then pelleted by centrifugation and the supernatant, containing the peptide digests, was collected. The pellet was washed twice with water (50µL) and the collected supernatant fractions were combined. Formic acid (15µL) was added to the peptide mixture.

TMT labeling of tryptic digest

A total of eight peptide digests were obtained from quadruplicate labeling of the DMSO and BB-Cl-amidine treated samples. These samples were subjected to desalting using commercially available Pierce C18 Spin columns (Thermo Fisher) to remove buffer components that may interfere with TMT labeling. The desalting procedure followed the manufacturer's protocol. Peptide concentration was determined before as well as after desalting using the commercially available Pierce Quantitative Colorimetric Peptide Assay kit (Thermo Fisher) to ensure that the peptides were not lost during the desalting procedure. The samples were then evaporated to dryness in a Speedvac. The eight peptide digests were then labeled using a commercially available TMT labeling system (Thermo Fisher). Briefly, the samples were resuspended in 100mM HEPES pH 8.6 (100µL) in eight different Eppendorf tubes and treated with 8µL of TMT10plex labeling reagent. The samples were incubated for 1h at RT. The reaction was further quenched using 2.5µL of 5% hydroxylamine and samples were further incubated for 15min at RT. After quenching excess TMT reagent, the TMT-labeled samples (90µL) from each tube were mixed together in a separate Eppendorf tube. The combined sample were evaporated to dryness in a Speedvac and then stored at -80°C until mass spectrometry (MS) analysis.

LC-MS/MS and Data Processing

Liquid chromatography tandem mass spectrometry (LC-MS/MS) was performed on a NanoAcquity UPLC (Waters Corporation) coupled to an Orbitrap Fusion Lumos Tribrid (Thermo Fisher) mass spectrometer, operating in the positive ion mode (1.4kV, applied by liquid junction). Mobile phases were A (0.1% (v/v) formic acid in water) and B (0.1% (v/v)

formic acid in acetonitrile). The peptides were reconstituted in 35µL of 5% (v/v) acetonitrile, 0.1% (v/v) formic acid in water, and 3.8µL was injected in 5% B at 4µL/min for 4min to a 100µm ID fused-silica pre-column (Kasil frit) packed with 2cm of ProntoSIL C18 AQ (Bischoff Chromatography, 200Å, 5µm) particles. Peptides were then separated and eluted at 300nL/min by an *in-house* packed fused silica analytical column (gravity-pulled tip) packed with 25cm Magic C18AQ (Bruker-Michrom, 100Å, 3µm) particles. In brief, the gradient was 10-35% B (0-100min); 35-65% B (100-120min); 95% B (121-126min), 5% B (127-140min). Mass spectra were acquired in the Orbitrap mass analyzer using a resolution of 60,000 (*m/z* 200), an ion target population of $7e^5$, and maximum ion injection time of 30msec. Tandem mass spectra were acquired using data dependent acquisition using the following parameters: cycle time, 2sec; intensity threshold, $2e^4$; isolation width, 0.8Da; HCD collision energy, 38%; resolution, 30,000; ion population, $1e^5$; maximum ion injection time,110 msec.

The raw data were processed using Proteome Discoverer (Thermo Fisher, version 2.1.1.21) and searched against SwissProt murine (downloaded 07/2019) database using Mascot (Matrix Science, version 2.6.2). The mass tolerance was 10ppm for precursor and 0.05Da for the fragment ions. Full tryptic cleavages were considered along with static modifications of carbamidomethylation (cysteine), TMT labelling (peptide N-terminal and lysine) and dynamic modifications of acetylation (protein N-terminal), oxidation (methionine) and glutamine to pyroglutamate conversion (peptide N-terminal). Peptides were assembled to proteins using Scaffold (Proteome Software, version 4.11.0) and were filtered to a 1% FDR using Peptide Prophet (3). The protein threshold was set to 99% probability using Protein Prophet (4) and only proteins with 2 or more filtered peptides were considered. The data was further processed by Scaffold Q+S (4.11.0) for quantitative analysis.

References:

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3. Keller A, Nesvizhskii AI, Kolker E, Aebersold R. Empirical statistical model to estimate the accuracy of peptide identifications made by MS/MS and database search. Anal Chem. 2002;74(20):5383–92.

4. Nesvizhskii AI, Keller A, Kolker E, Aebersold R. A statistical model for identifying proteins by tandem mass spectrometry. Anal Chem. 2003;75(17):4646–58.

Supplementary Table 1. Differentially regulated citrullinated proteins in pancreas of BB-Cl-amidine treated versus DMSO treated NOD mice

* P<0.05 (Log_{10}p-value = 1.122)

	Log_2Ratio	Log_{10}p-value (*)	Accession
1	-1.606163	1.3050913	sp|Q8BU14|SEC62_MOUSE
2	-1.5756054	2.4036503	sp|Q8CAQ8-2|MIC60_MOUSE
3	-1.5686817	2.758175	sp|P47915|RL29_MOUSE
4	-1.5622921	3.109283	sp|P35564|CALX_MOUSE
5	-1.5391521	1.3050913	sp|Q9ERG0-2|LIMA1_MOUSE
6	-1.5389996	3.4577034	sp|Q9D0F3|LMAN1_MOUSE
7	-1.5316582	15.25562	sp|P08113|ENPL_MOUSE
8	-1.5246878	4.14842	sp|Q60997-2|DMBT1_MOUSE
9	-1.5179377	11.206782	sp|Q64285|CEL_MOUSE
10	-1.5131435	1.6794106	sp|Q9Z0Y2|PA21B_MOUSE
11	-1.5123882	1.6794106	sp|Q6ZQ58|LARP1_MOUSE
12	-1.5034275	3.109283	sp|P47963|RL13_MOUSE
13	-1.4920053	5.8520784	sp|P27659|RL3_MOUSE
14	-1.4888325	2.4036503	sp|Q8BKC5|IPO5_MOUSE
15	-1.4820528	1.3050913	sp|Q8C0D5|EFL1_MOUSE
16	-1.4796295	1.3050913	sp|Q3U0V1|FUBP2_MOUSE
17	-1.4736061	1.6794106	sp|P13020-2|GELS_MOUSE
18	-1.4711285	14.724141	sp|Q78PY7|SND1_MOUSE
19	-1.4627047	1.3050913	sp|P26043|RADI_MOUSE
20	-1.460556	2.044628	sp|Q8BI84-3|TGO1_MOUSE
21	-1.45401	11.539065	sp|Q9JKR6|HYOU1_MOUSE
22	-1.4527073	9.2091	sp|Q9D8E6|RL4_MOUSE
23	-1.4449883	4.8330717	sp|Q8BM55|TM214_MOUSE
24	-1.4447136	5.17366	sp|Q9Z1Z0|USO1_MOUSE
25	-1.4443893	3.8039558	sp|Q8VEK3-2|HNRPU_MOUSE
26	-1.4433832	1.6794106	sp|Q9CQX2|CYB5B_MOUSE
27	-1.4416866	14.778499	sp|Q8VDJ3|VIGLN_MOUSE
28	-1.4405212	10.541792	sp|P08003|PDIA4_MOUSE
29	-1.4388752	1.3050913	sp|P62911|RL32_MOUSE
30	-1.4383736	5.8520784	sp|P62754|RS6_MOUSE
31	-1.4367504	3.8039558	sp|Q8R1B4|EIF3C_MOUSE
32	-1.4338951	6.527502	sp|Q99PL5|RRBP1_MOUSE
33	-1.4318275	7.5362897	sp|Q8VDD5|MYH9_MOUSE
34	-1.4302464	3.109283	sp|P84099|RL19_MOUSE
35	-1.4291286	2.4036503	sp|Q7TPR4|ACTN1_MOUSE
36	-1.4274426	4.4913836	sp|P47911|RL6_MOUSE
37	-1.4266815	6.527502	sp|Q7TPZ8|CBPA1_MOUSE

38	-1.4237385	2.758175	sp|Q91ZV0-3|MIA2_MOUSE
39	-1.4216404	5.5132895	sp|P12970|RL7A_MOUSE
40	-1.4201832	1.3050913	sp|Q4PJX1|ODR4_MOUSE
41	-1.420105	1.6794106	sp|Q99LM2|CK5P3_MOUSE
42	-1.4167576	3.8039558	sp|Q8VIJ6|SFPQ_MOUSE
43	-1.416626	3.109283	sp|P41105|RL28_MOUSE
44	-1.4158173	1.6794106	sp|Q9Z1D1|EIF3G_MOUSE
45	-1.4133005	10.541792	sp|P23116|EIF3A_MOUSE
46	-1.4126663	2.758175	sp|Q9D733|GP2_MOUSE
47	-1.4123726	1.3050913	sp|P61514|RL37A_MOUSE
48	-1.4122839	13.544657	sp|D3Z6P0-2|PDIA2_MOUSE
49	-1.4114666	>20	sp|P20029|BIP_MOUSE
50	-1.4096727	1.6794106	sp|Q8VE88-2|F1142_MOUSE
51	-1.4092903	1.3050913	sp|Q9JHU9|INO1_MOUSE
52	-1.4076557	6.527502	sp|Q99MR8|MCCA_MOUSE
53	-1.407486	9.2091	sp|P14211|CALR_MOUSE
54	-1.4055767	1.3050913	sp|Q64514-2|TPP2_MOUSE
55	-1.4040947	2.758175	sp|Q9DB77|QCR2_MOUSE
56	-1.4026165	1.6794106	sp|Q3U1J4|DDB1_MOUSE
57	-1.4025726	4.4913836	sp|Q8BMA6|SRP68_MOUSE
58	-1.4007816	3.109283	sp|Q6ZQ38|CAND1_MOUSE
59	-1.4003506	4.14842	sp|Q61035|SYHC_MOUSE
60	-1.39781	1.3050913	sp|O08553|DPYL2_MOUSE
61	-1.3975468	2.4036503	sp|P70168|IMB1_MOUSE
62	-1.3956604	1.3050913	sp|P97449|AMPN_MOUSE
63	-1.3956413	1.6794106	sp|P97379-2|G3BP2_MOUSE
64	-1.3956404	2.044628	sp|Q8VCT4|CES1D_MOUSE
65	-1.3933754	2.044628	sp|Q3TXS7|PSMD1_MOUSE
66	-1.3922386	3.4577034	sp|Q9CZM2|RL15_MOUSE
67	-1.3906231	1.3050913	sp|Q9CYA0|CREL2_MOUSE
68	-1.3901138	2.044628	sp|O08795-2|GLU2B_MOUSE
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70	-1.387639	1.3050913	sp|Q8VDM4|PSMD2_MOUSE
71	-1.3873711	3.4577034	sp|P62918|RL8_MOUSE
72	-1.3868294	3.4577034	sp|Q8K2B3|SDHA_MOUSE
73	-1.3841171	4.8330717	sp|Q60864|STIP1_MOUSE
74	-1.3825274	11.870765	sp|Q8K009|AL1L2_MOUSE
75	-1.3819504	1.3050913	sp|P19783|COX41_MOUSE
76	-1.3817673	5.8520784	sp|O55029|COPB2_MOUSE
77	-1.3795776	4.8330717	sp|Q61941|NNTM_MOUSE
78	-1.3793259	11.870765	sp|Q02053|UBA1_MOUSE
79	-1.3792286	5.8520784	sp|Q6P5E4|UGGG1_MOUSE
80	-1.3786354	6.864285	sp|Q91YW3|DNJC3_MOUSE
81	-1.3778496	>20	sp|P58252|EF2_MOUSE
82	-1.3770294	3.4577034	sp|Q60597-2|ODO1_MOUSE

83	-1.3759804	4.8330717	sp|Q8VDN2|AT1A1_MOUSE
84	-1.3738422	1.6794106	sp|Q69ZS7-2|HBS1L_MOUSE
85	-1.3731365	1.6794106	sp|Q9CY27|TECR_MOUSE
86	-1.3721466	7.2005315	sp|P62242|RS8_MOUSE
87	-1.3701077	4.14842	sp|P57780|ACTN4_MOUSE
88	-1.3683395	2.044628	sp|Q61937|NPM_MOUSE
89	-1.3667011	4.4913836	sp|Q504N0|CBPA2_MOUSE
90	-1.3636742	2.044628	sp|Q8R146-2|APEH_MOUSE
91	-1.3631992	1.3050913	sp|P45700|MA1A1_MOUSE
92	-1.3621225	4.4913836	sp|Q61316|HSP74_MOUSE
93	-1.3612518	2.044628	sp|Q8BWW4|LARP4_MOUSE
94	-1.3611755	2.758175	sp|Q6P1B1|XPP1_MOUSE
95	-1.360982	1.6794106	sp|P46935|NEDD4_MOUSE
96	-1.3584862	4.14842	sp|P42932|TCPQ_MOUSE
97	-1.3582964	2.758175	sp|Q9WVE8|PACN2_MOUSE
98	-1.3576298	7.2005315	sp|O55143|AT2A2_MOUSE
99	-1.3571434	1.6794106	sp|P34022|RANG_MOUSE
100	-1.3570337	1.3050913	sp|Q8R010|AIMP2_MOUSE
101	-1.3560905	9.2091	sp|P29341|PABP1_MOUSE
102	-1.3555489	8.20651	sp|Q922D8|C1TC_MOUSE
103	-1.3548622	3.4577034	sp|Q99K01-2|PDXD1_MOUSE
104	-1.3539143	5.17366	sp|Q9ER72-2|SYCC_MOUSE
105	-1.3538799	5.8520784	sp|Q9Z1Q9|SYVC_MOUSE
106	-1.3524313	3.8039558	sp|Q921G7|ETFD_MOUSE
107	-1.350872	2.4036503	sp|Q9WUM5|SUCA_MOUSE
108	-1.3487844	5.17366	sp|Q9DBG7|SRPRA_MOUSE
109	-1.3481827	1.3050913	sp|P10630-2|IF4A2_MOUSE
110	-1.3480272	1.3050913	sp|O08529|CAN2_MOUSE
111	-1.3476143	5.17366	sp|P07901|HS90A_MOUSE
112	-1.3463306	1.3050913	sp|P62900|RL31_MOUSE
113	-1.3462315	2.758175	sp|Q9Z2I9|SUCB1_MOUSE
114	-1.3461132	9.875973	sp|P63017|HSP7C_MOUSE
115	-1.3459053	4.14842	sp|P19253|RL13A_MOUSE
116	-1.3458977	5.5132895	sp|Q99K67|AASS_MOUSE
117	-1.3458471	1.3050913	sp|P62960|YBOX1_MOUSE
118	-1.3456907	2.044628	sp|P19096|FAS_MOUSE
119	-1.3452873	3.109283	sp|Q80X90|FLNB_MOUSE
120	-1.3451614	2.4036503	sp|P46460|NSF_MOUSE
121	-1.3440971	5.17366	sp|P50580|PA2G4_MOUSE
122	-1.3432941	2.758175	sp|Q60854|SPB6_MOUSE
123	-1.3426933	2.758175	sp|Q93092|TALDO_MOUSE
124	-1.3426638	1.3050913	sp|Q6NZC7|S23IP_MOUSE
125	-1.3417797	5.5132895	sp|Q08642|PADI2_MOUSE
126	-1.3408585	9.2091	sp|P63038|CH60_MOUSE
127	-1.3408566	1.3050913	sp|Q99KB8-2|GLO2_MOUSE

128	-1.3404121	1.3050913	sp|P99024|TBB5_MOUSE
129	-1.3401604	2.044628	sp|P09405|NUCL_MOUSE
130	-1.3398399	2.044628	sp|Q8BJ64|CHDH_MOUSE
131	-1.3393288	4.8330717	sp|Q91VD9|NDUS1_MOUSE
132	-1.3380337	3.109283	sp|Q922Q1|MARC2_MOUSE
133	-1.3370905	1.3050913	sp|Q99J99|THTM_MOUSE
134	-1.3368435	7.2005315	sp|Q99MN1|SYK_MOUSE
135	-1.3365211	7.5362897	sp|P25444|RS2_MOUSE
136	-1.3362446	8.541041	sp|Q8BH04|PCKGM_MOUSE
137	-1.3361301	4.14842	sp|P62717|RL18A_MOUSE
138	-1.3357277	4.14842	sp|Q76MZ3|2AAA_MOUSE
139	-1.3349895	6.1901226	sp|P11499|HS90B_MOUSE
140	-1.3349838	6.1901226	sp|Q8C1A5|THOP1_MOUSE
141	-1.3348017	1.3050913	sp|Q8BH24|TM9S4_MOUSE
142	-1.3339005	2.044628	sp|Q8BHN3-2|GANAB_MOUSE
143	-1.3320112	7.2005315	sp|Q921I1|TRFE_MOUSE
144	-1.3313932	1.3050913	sp|Q9CXI5|MANF_MOUSE
145	-1.3310795	1.3050913	sp|Q6IRU5-2|CLCB_MOUSE
146	-1.3307247	4.4913836	sp|Q8JZQ9|EIF3B_MOUSE
147	-1.329732	5.17366	sp|Q9CZ13|QCR1_MOUSE
148	-1.3291674	2.044628	sp|Q8BJW6|EIF2A_MOUSE
149	-1.3288612	4.14842	sp|Q9DBG6|RPN2_MOUSE
150	-1.3288498	1.3050913	sp|P47757-2|CAPZB_MOUSE
151	-1.3287697	4.8330717	sp|P61222|ABCE1_MOUSE
152	-1.3275337	2.044628	sp|Q91WD5|NDUS2_MOUSE
153	-1.3272305	1.6794106	sp|Q3V3R1|C1TM_MOUSE
154	-1.3262081	11.206782	sp|P27773|PDIA3_MOUSE
155	-1.3258724	3.109283	sp|Q9JKF1|IQGA1_MOUSE
156	-1.325594	3.4577034	sp|P62267|RS23_MOUSE
157	-1.3255043	5.5132895	sp|Q9Z110-2|P5CS_MOUSE
158	-1.3244228	2.4036503	sp|Q9R111|GUAD_MOUSE
159	-1.3243294	5.17366	sp|P16331|PH4H_MOUSE
160	-1.323288	10.209015	sp|Q05920|PYC_MOUSE
161	-1.3188515	3.8039558	sp|E9PVA8|GCN1_MOUSE
162	-1.3182621	3.109283	sp|P16332|MUTA_MOUSE
163	-1.318121	4.14842	sp|Q61768|KINH_MOUSE
164	-1.3170776	3.109283	sp|Q91VR5|DDX1_MOUSE
165	-1.3169403	4.14842	sp|Q8VE47|UBA5_MOUSE
166	-1.3169346	1.3050913	sp|P13439|UMPS_MOUSE
167	-1.3159828	1.3050913	sp|Q8R4N0|CLYBL_MOUSE
168	-1.3152256	2.044628	sp|Q8CGK3|LONM_MOUSE
169	-1.3147907	1.3050913	sp|O35295|PURB_MOUSE
170	-1.314601	1.3050913	sp|Q3THS6|METK2_MOUSE
171	-1.3144493	3.4577034	sp|Q8BP67|RL24_MOUSE
172	-1.3129902	5.5132895	sp|Q8BU30|SYIC_MOUSE

173	-1.3128166	1.3050913	sp|Q8R081|HNRPL_MOUSE
174	-1.312418	9.875973	sp|P40142|TKT_MOUSE
175	-1.3121223	5.8520784	sp|Q9QZE5|COPG1_MOUSE
176	-1.312088	1.3050913	sp|Q5FWK3|RHG01_MOUSE
177	-1.3116188	5.17366	sp|P17892|LIPR2_MOUSE
178	-1.3114376	1.3050913	sp|Q60931|VDAC3_MOUSE
179	-1.3113327	3.109283	sp|Q64727|VINC_MOUSE
180	-1.311204	2.758175	sp|P56399|UBP5_MOUSE
181	-1.310852	3.8039558	sp|Q8BGD9|IF4B_MOUSE
182	-1.3106852	3.109283	sp|Q9D8U3|ERP27_MOUSE
183	-1.3085461	5.8520784	sp|Q8R2E9|ERO1B_MOUSE
184	-1.3082428	2.758175	sp|Q9R0N0|GALK1_MOUSE
185	-1.3080387	13.879043	sp|Q8CGC7|SYEP_MOUSE
186	-1.3077297	8.87523	sp|Q99KI0|ACON_MOUSE
187	-1.3073292	1.3050913	sp|Q9EQH3|VPS35_MOUSE
188	-1.3064976	1.6794106	sp|Q99K23|UFSP2_MOUSE
189	-1.3062477	2.4036503	sp|O08807|PRDX4_MOUSE
190	-1.3061066	5.17366	sp|Q6ZWX6|IF2A_MOUSE
191	-1.3054523	3.8039558	sp|Q9CPR4|RL17_MOUSE
192	-1.3040752	8.20651	sp|Q8BGQ7|SYAC_MOUSE
193	-1.3038893	1.3050913	sp|A2ALS5-3|RPGP1_MOUSE
194	-1.3038769	1.3050913	sp|Q61712|DNJC1_MOUSE
195	-1.3026886	1.6794106	sp|Q62433|NDRG1_MOUSE
196	-1.301486	5.8520784	sp|Q8BMJ2|SYLC_MOUSE
197	-1.3014832	1.6794106	sp|Q9EPJ9-2|ARFG1_MOUSE
198	-1.3013763	5.5132895	sp|P10852|4F2_MOUSE
199	-1.3013611	4.14842	sp|Q9WU78-3|PDC6I_MOUSE
200	-1.300457	3.109283	sp|P31230|AIMP1_MOUSE
201	-1.3002872	3.109283	sp|P50136|ODBA_MOUSE
202	-1.3000164	3.4577034	sp|Q9Z0X1|AIFM1_MOUSE
203	-1.2996407	1.6794106	sp|P45952|ACADM_MOUSE
204	-1.2996159	3.109283	sp|P46978|STT3A_MOUSE
205	-1.2995377	4.8330717	sp|P80313|TCPH_MOUSE
206	-1.2984924	>20	sp|P09103|PDIA1_MOUSE
207	-1.2976894	2.044628	sp|Q99JY9|ARP3_MOUSE
208	-1.2975521	6.527502	sp|P80318|TCPG_MOUSE
209	-1.2969227	1.3050913	sp|Q64324|STXB2_MOUSE
210	-1.2958546	2.4036503	sp|Q9CR57|RL14_MOUSE
211	-1.2954254	5.5132895	sp|Q6NZJ6|IF4G1_MOUSE
212	-1.2949848	3.8039558	sp|Q7TSV4|PGM2_MOUSE
213	-1.2946405	5.17366	sp|Q7TMK9-2|HNRPQ_MOUSE
214	-1.2941017	7.2005315	sp|Q8R0Y6|AL1L1_MOUSE
215	-1.2937813	2.4036503	sp|Q8VCT3|AMPB_MOUSE
216	-1.2937784	4.14842	sp|P80316|TCPE_MOUSE
217	-1.2931099	15.4774685	sp|Q01853|TERA_MOUSE

218	-1.2930288	1.3050913	sp|Q9CXR1|DHRS7_MOUSE
219	-1.291956	5.17366	sp|Q91WT9-2|CBS_MOUSE
220	-1.291832	4.4913836	sp|Q9JK88|SPI2_MOUSE
221	-1.2915516	9.875973	sp|Q6P8U6|LIPP_MOUSE
222	-1.2909584	3.4577034	sp|Q5SUR0|PUR4_MOUSE
223	-1.2907934	4.4913836	sp|P28271|ACOC_MOUSE
224	-1.2906647	4.8330717	sp|Q9CWJ9|PUR9_MOUSE
225	-1.2903461	1.6794106	sp|Q9DB25|ALG5_MOUSE
226	-1.2898369	4.8330717	sp|O70194|EIF3D_MOUSE
227	-1.2889051	5.17366	sp|Q91V92|ACLY_MOUSE
228	-1.2882395	5.5132895	sp|P80314|TCPB_MOUSE
229	-1.2875557	3.8039558	sp|Q8CHT0|AL4A1_MOUSE
230	-1.28619	5.17366	sp|Q9JHU4|DYHC1_MOUSE
231	-1.2860632	9.875973	sp|Q03265|ATPA_MOUSE
232	-1.2860603	4.8330717	sp|Q9D8S3|ARFG3_MOUSE
233	-1.2857866	2.4036503	sp|Q9DCX2|ATP5H_MOUSE
234	-1.2849884	1.6794106	sp|O88487|DC1I2_MOUSE
235	-1.2849503	1.6794106	sp|P68372|TBB4B_MOUSE
236	-1.2847481	6.527502	sp|Q5XJY5|COPD_MOUSE
237	-1.2844143	2.044628	sp|Q9Z1Z2|STRAP_MOUSE
238	-1.2842455	7.5362897	sp|P26638|SYSC_MOUSE
239	-1.2839375	1.3050913	sp|Q8VBV7|CSN8_MOUSE
240	-1.2835426	6.864285	sp|P38647|GRP75_MOUSE
241	-1.2834921	2.044628	sp|Q9CY58-2|PAIRB_MOUSE
242	-1.2819977	5.17366	sp|Q68FD5|CLH1_MOUSE
243	-1.2819004	5.5132895	sp|Q9JIF7|COPB_MOUSE
244	-1.2816324	3.8039558	sp|Q8CCJ3|UFL1_MOUSE
245	-1.2815514	8.87523	sp|P26443|DHE3_MOUSE
246	-1.2805405	3.4577034	sp|P26039|TLN1_MOUSE
247	-1.2801208	1.3050913	sp|Q9CPX6|ATG3_MOUSE
248	-1.2797565	2.4036503	sp|Q00PI9|HNRL2_MOUSE
249	-1.2796917	3.109283	sp|Q8BH59|CMC1_MOUSE
250	-1.2796316	1.6794106	sp|Q9WUM3|COR1B_MOUSE
251	-1.2790489	9.2091	sp|Q3UPL0-2|SC31A_MOUSE
252	-1.2786016	2.758175	sp|Q8VCA8|SCRN2_MOUSE
253	-1.2774887	3.109283	sp|Q9CQA3|SDHB_MOUSE
254	-1.27707	6.864285	sp|Q99MN9|PCCB_MOUSE
255	-1.2770615	1.3050913	sp|Q9WVJ2|PSD13_MOUSE
256	-1.2764082	8.541041	sp|Q91YQ5|RPN1_MOUSE
257	-1.2756062	3.109283	sp|Q9Z2I8-2|SUCB2_MOUSE
258	-1.2742653	1.6794106	sp|P29758|OAT_MOUSE
259	-1.2741928	2.044628	sp|P81117|NUCB2_MOUSE
260	-1.2736826	1.3050913	sp|P20357|MTAP2_MOUSE
261	-1.2730732	1.6794106	sp|Q3UM45|PP1R7_MOUSE
262	-1.2729797	1.3050913	sp|Q80UU9|PGRC2_MOUSE

263	-1.2727833	1.3050913	sp|Q61792|LASP1_MOUSE
264	-1.2726507	5.8520784	sp|Q8BMS1|ECHA_MOUSE
265	-1.2719345	1.3050913	sp|O70503-2|DHB12_MOUSE
266	-1.2717094	2.044628	sp|O54724|CAVN1_MOUSE
267	-1.2707272	2.758175	sp|P24527|LKHA4_MOUSE
268	-1.2707233	2.4036503	sp|Q9DBC7|KAP0_MOUSE
269	-1.2700119	4.4913836	sp|P80317|TCPZ_MOUSE
270	-1.268858	6.864285	sp|P20152|VIME_MOUSE
271	-1.2685776	1.3050913	sp|P97855|G3BP1_MOUSE
272	-1.268301	3.109283	sp|Q8VCR2-2|DHB13_MOUSE
273	-1.2682877	4.4913836	sp|O08749|DLDH_MOUSE
274	-1.2681694	3.4577034	sp|Q99L88|SNTB1_MOUSE
275	-1.266922	1.6794106	sp|P61982|1433G_MOUSE
276	-1.2664375	8.20651	sp|P14148|RL7_MOUSE
277	-1.266159	2.758175	sp|Q8K0C9|GMDS_MOUSE
278	-1.2659197	1.3050913	sp|Q9D8S4|ORN_MOUSE
279	-1.2655277	3.8039558	sp|P68368|TBA4A_MOUSE
280	-1.2654095	13.544657	sp|Q61753|SERA_MOUSE
281	-1.2650509	4.14842	sp|Q99LF4|RTCB_MOUSE
282	-1.2646408	5.5132895	sp|Q91WQ3|SYYC_MOUSE
283	-1.263113	7.5362897	sp|Q922R8|PDIA6_MOUSE
284	-1.2624445	1.3050913	sp|Q921F4|HNRLL_MOUSE
285	-1.2621841	12.202081	sp|Q91VI7|RINI_MOUSE
286	-1.261591	5.8520784	sp|Q9CZD3|GARS_MOUSE
287	-1.2613306	4.8330717	sp|P11983|TCPA_MOUSE
288	-1.261198	2.758175	sp|O09167|RL21_MOUSE
289	-1.2602272	1.3050913	sp|O35129|PHB2_MOUSE
290	-1.2596807	12.202081	sp|Q8CIE6|COPA_MOUSE
291	-1.2593307	2.758175	sp|Q60932-2|VDAC1_MOUSE
292	-1.2590218	6.527502	sp|P47962|RL5_MOUSE
293	-1.2587128	2.044628	sp|Q9D7S7-2|RL22L_MOUSE
294	-1.2579155	2.758175	sp|Q8C0C7|SYFA_MOUSE
295	-1.2578335	2.044628	sp|Q8VCK7|SYCN_MOUSE
296	-1.2575798	1.3050913	sp|O70310|NMT1_MOUSE
297	-1.2570591	2.758175	sp|Q8BG32|PSD11_MOUSE
298	-1.256978	1.3050913	sp|Q99JX3-2|GORS2_MOUSE
299	-1.2556381	1.3050913	sp|Q68FL4|SAHH3_MOUSE
300	-1.2545471	4.14842	sp|Q9JMH6-2|TRXR1_MOUSE
301	-1.2544708	5.5132895	sp|Q91YI0|ARLY_MOUSE
302	-1.254446	2.044628	sp|P62264|RS14_MOUSE
303	-1.2543488	6.864285	sp|Q9CR35|CTRB1_MOUSE
304	-1.2530174	12.533645	sp|Q91ZA3|PCCA_MOUSE
305	-1.252924	2.044628	sp|Q9CXF4|TBC15_MOUSE
306	-1.2526445	1.3050913	sp|Q8K1M6-2|DNM1L_MOUSE
307	-1.2522888	2.4036503	sp|Q91W90|TXND5_MOUSE

308	-1.2520561	2.044628	sp|P30999-2|CTND1_MOUSE
309	-1.2511292	1.3050913	sp|Q9QXK3-4|COPG2_MOUSE
310	-1.2510643	2.758175	sp|P14115|RL27A_MOUSE
311	-1.2509689	1.3050913	sp|Q61749-2|EI2BD_MOUSE
312	-1.2500534	7.871603	sp|Q9CPY7-2|AMPL_MOUSE
313	-1.2498074	2.044628	sp|Q9D1R9|RL34_MOUSE
314	-1.2494869	9.542674	sp|P00688|AMYP_MOUSE
315	-1.2493353	2.044628	sp|Q921F2|TADBP_MOUSE
316	-1.2482071	4.4913836	sp|P97429|ANXA4_MOUSE
317	-1.2477598	1.3050913	sp|Q3UW53|NIBAN_MOUSE
318	-1.2468872	7.5362897	sp|P14206|RSSA_MOUSE
319	-1.245183	4.8330717	sp|Q9D662|SC23B_MOUSE
320	-1.2451668	4.8330717	sp|Q8QZT1|THIL_MOUSE
321	-1.2449217	4.14842	sp|P05201|AATC_MOUSE
322	-1.2442493	2.044628	sp|O55234|PSB5_MOUSE
323	-1.2440205	1.3050913	sp|Q91W50|CSDE1_MOUSE
324	-1.2438259	1.6794106	sp|Q9D1M7|FKB11_MOUSE
325	-1.2428455	1.6794106	sp|P50544|ACADV_MOUSE
326	-1.2422352	4.14842	sp|P17563|SBP1_MOUSE
327	-1.2422047	6.527502	sp|Q9D0R2|SYTC_MOUSE
328	-1.2420607	2.4036503	sp|P40124|CAP1_MOUSE
329	-1.242033	3.4577034	sp|Q9EP69|SAC1_MOUSE
330	-1.2414513	1.3050913	sp|P68037|UB2L3_MOUSE
331	-1.2410183	2.4036503	sp|Q9JMD3|STA10_MOUSE
332	-1.2408857	13.879043	sp|P07724|ALBU_MOUSE
333	-1.2403259	1.6794106	sp|P61620|S61A1_MOUSE
334	-1.2402878	7.871603	sp|Q5BKQ4|LIPR1_MOUSE
335	-1.2398195	2.4036503	sp|Q501J6|DDX17_MOUSE
336	-1.2398071	2.4036503	sp|P43137|LIT1_MOUSE
337	-1.2398014	2.4036503	sp|Q80UM7|MOGS_MOUSE
338	-1.2397232	2.4036503	sp|Q9DBT5|AMPD2_MOUSE
339	-1.2394905	1.3050913	sp|P63085|MK01_MOUSE
340	-1.2394314	1.6794106	sp|Q61655|DD19A_MOUSE
341	-1.2394104	3.109283	sp|P07759|SPA3K_MOUSE
342	-1.2393808	2.044628	sp|P26040|EZRI_MOUSE
343	-1.2392197	1.3050913	sp|Q9D8W5|PSD12_MOUSE
344	-1.2390957	2.4036503	sp|Q9D1D4|TMEDA_MOUSE
345	-1.2390442	3.109283	sp|Q8R050-2|ERF3A_MOUSE
346	-1.2390137	8.541041	sp|Q9EQ20|MMSA_MOUSE
347	-1.2386875	2.044628	sp|P16546-2|SPTN1_MOUSE
348	-1.2385035	2.4036503	sp|P50516|VATA_MOUSE
349	-1.2384434	4.4913836	sp|Q3ULD5|MCCB_MOUSE
350	-1.2383823	1.6794106	sp|Q9Z2M7|PMM2_MOUSE
351	-1.2382393	3.109283	sp|Q9D0E1-2|HNRPM_MOUSE
352	-1.2381363	3.8039558	sp|Q9CQ52|CEL3B_MOUSE

353	-1.2380524	5.17366	sp|Q61656|DDX5_MOUSE
354	-1.2374115	2.044628	sp|Q64737|PUR2_MOUSE
355	-1.2358093	2.4036503	sp|P62821|RAB1A_MOUSE
356	-1.2353916	1.6794106	sp|Q8BWF0|SSDH_MOUSE
357	-1.2348747	4.4913836	sp|Q922Q8|LRC59_MOUSE
358	-1.2344933	7.2005315	sp|Q9D8N0|EF1G_MOUSE
359	-1.2338982	5.5132895	sp|P32921-2|SYWC_MOUSE
360	-1.233263	4.4913836	sp|P53395|ODB2_MOUSE
361	-1.2329149	1.6794106	sp|Q62318|TIF1B_MOUSE
362	-1.2329006	1.3050913	sp|O70378|EMC8_MOUSE
363	-1.2326508	2.758175	sp|P46471|PRS7_MOUSE
364	-1.232357	6.864285	sp|P14152|MDHC_MOUSE
365	-1.2322598	2.4036503	sp|Q9WTP7|KAD3_MOUSE
366	-1.2322226	6.864285	sp|P51881|ADT2_MOUSE
367	-1.2318592	3.8039558	sp|P60229|EIF3E_MOUSE
368	-1.2318182	2.044628	sp|Q64105|SPRE_MOUSE
369	-1.2316704	2.758175	sp|Q9D6R2|IDH3A_MOUSE
370	-1.2314072	2.044628	sp|Q8CC86|PNCB_MOUSE
371	-1.2311535	3.8039558	sp|Q8BWT1|THIM_MOUSE
372	-1.230875	2.4036503	sp|Q9D1M0|SEC13_MOUSE
373	-1.2305536	2.044628	sp|P51150|RAB7A_MOUSE
374	-1.2305307	1.6794106	sp|Q00612|G6PD1_MOUSE
375	-1.2305117	4.4913836	sp|Q8BFR5|EFTU_MOUSE
376	-1.2304802	3.109283	sp|O08547|SC22B_MOUSE
377	-1.2302799	2.4036503	sp|O09131|GSTO1_MOUSE
378	-1.230217	2.4036503	sp|P07146|TRY2_MOUSE
379	-1.2294235	5.5132895	sp|P62702|RS4X_MOUSE
380	-1.2292967	8.87523	sp|Q9DBF1-2|AL7A1_MOUSE
381	-1.2286272	3.109283	sp|Q9DBE8|ALG2_MOUSE
382	-1.228198	1.3050913	sp|Q8K268|ABCF3_MOUSE
383	-1.2280216	2.4036503	sp|Q9EPU0-2|RENT1_MOUSE
384	-1.2277203	3.4577034	sp|P35980|RL18_MOUSE
385	-1.2275372	4.8330717	sp|Q9DCS3|MECR_MOUSE
386	-1.2258224	2.044628	sp|P67984|RL22_MOUSE
387	-1.2256184	2.044628	sp|P46638|RB11B_MOUSE
388	-1.2253809	1.6794106	sp|Q61699-2|HS105_MOUSE
389	-1.2244892	1.6794106	sp|Q99KJ8|DCTN2_MOUSE
390	-1.224266	3.109283	sp|Q9WUQ2|PREB_MOUSE
391	-1.2236204	1.3050913	sp|P63330|PP2AA_MOUSE
392	-1.2234249	1.6794106	sp|Q9DBE0|CSAD_MOUSE
393	-1.2232704	1.3050913	sp|O35639|ANXA3_MOUSE
394	-1.2221279	2.044628	sp|Q9DBJ1|PGAM1_MOUSE
395	-1.2198334	4.14842	sp|Q91X79|CELA1_MOUSE
396	-1.2187748	3.4577034	sp|Q9CZN7-2|GLYM_MOUSE
397	-1.2182426	2.044628	sp|P47955|RLA1_MOUSE

398	-1.2181587	1.3050913	sp|Q8VDL4-3|ADPGK_MOUSE
399	-1.21809	1.3050913	sp|P22892|AP1G1_MOUSE
400	-1.2178001	5.5132895	sp|Q9JHI5|IVD_MOUSE
401	-1.2174044	1.3050913	sp|Q8BTY8-2|SCFD2_MOUSE
402	-1.2172241	3.109283	sp|P16460|ASSY_MOUSE
403	-1.2171345	1.6794106	sp|P62897|CYC_MOUSE
404	-1.2166939	1.6794106	sp|Q9WV32|ARC1B_MOUSE
405	-1.2147427	3.109283	sp|O08663|MAP2_MOUSE
406	-1.2141209	2.044628	sp|P60766|CDC42_MOUSE
407	-1.2137928	1.3050913	sp|Q62087|PON3_MOUSE
408	-1.2136002	5.5132895	sp|P06745|G6PI_MOUSE
409	-1.2135181	7.2005315	sp|Q8BML9|SYQ_MOUSE
410	-1.2135086	2.044628	sp|P10639|THIO_MOUSE
411	-1.2134705	2.758175	sp|O35945|AL1A7_MOUSE
412	-1.213131	7.5362897	sp|Q9D154|ILEUA_MOUSE
413	-1.2126694	7.5362897	sp|P97351|RS3A_MOUSE
414	-1.2123632	3.4577034	sp|P67778|PHB_MOUSE
415	-1.2122631	4.8330717	sp|Q8QZS1|HIBCH_MOUSE
416	-1.2121181	6.864285	sp|P14869|RLA0_MOUSE
417	-1.2116718	6.1901226	sp|Q61598|GDIB_MOUSE
418	-1.2113695	3.109283	sp|O88685|PRS6A_MOUSE
419	-1.2113047	1.3050913	sp|Q9DBG3-2|AP2B1_MOUSE
420	-1.2110729	2.4036503	sp|Q9DB29|IAH1_MOUSE
421	-1.2109756	4.8330717	sp|Q922B2|SYDC_MOUSE
422	-1.2109451	2.044628	sp|Q6PDI5-2|ECM29_MOUSE
423	-1.2104816	2.044628	sp|P62814|VATB2_MOUSE
424	-1.2103176	1.3050913	sp|Q00623|APOA1_MOUSE
425	-1.2098598	1.6794106	sp|P52480|KPYM_MOUSE
426	-1.2095823	2.044628	sp|Q60605-2|MYL6_MOUSE
427	-1.2094078	4.4913836	sp|Q68FL6|SYMC_MOUSE
428	-1.2086239	1.3050913	sp|P17225|PTBP1_MOUSE
429	-1.2081375	3.109283	sp|P59325|IF5_MOUSE
430	-1.2079468	2.758175	sp|Q61425|HCDH_MOUSE
431	-1.2077026	4.14842	sp|P63101|1433Z_MOUSE
432	-1.2072868	2.044628	sp|P16254|SRP14_MOUSE
433	-1.2065659	2.4036503	sp|Q9DBL1|ACDSB_MOUSE
434	-1.20607	2.4036503	sp|Q60928|GGT1_MOUSE
435	-1.2052937	5.17366	sp|Q99LB7|SARDH_MOUSE
436	-1.2052326	1.6794106	sp|P22599|A1AT2_MOUSE
437	-1.2049294	3.109283	sp|P62830|RL23_MOUSE
438	-1.2048836	2.044628	sp|Q9DB20|ATPO_MOUSE
439	-1.20401	2.044628	sp|Q9QUR6|PPCE_MOUSE
440	-1.2036858	2.758175	sp|P15947|KLK1_MOUSE
441	-1.2035866	3.4577034	sp|P19001|K1C19_MOUSE
442	-1.2031517	1.3050913	sp|Q6PB66|LPPRC_MOUSE

443	-1.202982	1.3050913	sp|P50096|IMDH1_MOUSE
444	-1.2026825	3.8039558	sp|Q9CYR6|AGM1_MOUSE
445	-1.2026491	2.044628	sp|Q9CZ30|OLA1_MOUSE
446	-1.2025928	2.4036503	sp|P62245|RS15A_MOUSE
447	-1.2021599	2.758175	sp|Q8K0C5|ZG16_MOUSE
448	-1.2017212	2.758175	sp|Q91X83|METK1_MOUSE
449	-1.2005901	1.6794106	sp|Q922W5|P5CR1_MOUSE
450	-1.2005043	7.2005315	sp|P47856-2|GFPT1_MOUSE
451	-1.200057	2.4036503	sp|Q9DCL9|PUR6_MOUSE
452	-1.1999035	12.202081	sp|P05784|K1C18_MOUSE
453	-1.1997299	3.8039558	sp|Q99JR1|SFXN1_MOUSE
454	-1.199727	3.8039558	sp|P24549|AL1A1_MOUSE
455	-1.1993027	8.87523	sp|P14824|ANXA6_MOUSE
456	-1.199131	7.871603	sp|Q8BP47|SYNC_MOUSE
457	-1.1989794	3.8039558	sp|Q9D1A2|CNDP2_MOUSE
458	-1.1985054	1.6794106	sp|Q9CQM9|GLRX3_MOUSE
459	-1.1983871	1.6794106	sp|Q9JMA1|UBP14_MOUSE
460	-1.1983643	2.044628	sp|P47740|AL3A2_MOUSE
461	-1.1980343	2.4036503	sp|P60867|RS20_MOUSE
462	-1.1972475	4.14842	sp|P97807-2|FUMH_MOUSE
463	-1.1962757	1.3050913	sp|P62874|GBB1_MOUSE
464	-1.1960812	2.4036503	sp|P00687|AMY1_MOUSE
465	-1.1949425	2.758175	sp|O54734|OST48_MOUSE
466	-1.1939955	2.4036503	sp|P54775|PRS6B_MOUSE
467	-1.1938419	5.8520784	sp|O88844|IDHC_MOUSE
468	-1.1938324	5.5132895	sp|Q64442|DHSO_MOUSE
469	-1.1936865	1.3050913	sp|A3KMP2|TTC38_MOUSE
470	-1.1935654	1.3050913	sp|P62855|RS26_MOUSE
471	-1.1931896	6.1901226	sp|P56480|ATPB_MOUSE
472	-1.1927719	9.2091	sp|Q9D0I9|SYRC_MOUSE
473	-1.1926117	3.4577034	sp|Q9JII6|AK1A1_MOUSE
474	-1.19244	1.6794106	sp|P97364|SPS2_MOUSE
475	-1.1923447	1.3050913	sp|O88342|WDR1_MOUSE
476	-1.1920319	1.6794106	sp|P70349|HINT1_MOUSE
477	-1.1919155	1.6794106	sp|Q9QXB9|DRG2_MOUSE
478	-1.191803	2.4036503	sp|P12787|COX5A_MOUSE
479	-1.1913805	5.17366	sp|P57776-2|EF1D_MOUSE
480	-1.1909008	2.758175	sp|Q3UGC7|EI3JA_MOUSE
481	-1.1903687	2.4036503	sp|Q9DCD0|6PGD_MOUSE
482	-1.1902828	1.3050913	sp|Q9ESP1|SDF2L_MOUSE
483	-1.1898289	1.6794106	sp|Q9DCC4|P5CR3_MOUSE
484	-1.189579	1.6794106	sp|Q505F5|LRC47_MOUSE
485	-1.1889296	1.3050913	sp|P31786|ACBP_MOUSE
486	-1.1883411	4.14842	sp|P45376|ALDR_MOUSE
487	-1.1882343	4.8330717	sp|Q6ZWV3|RL10_MOUSE

488	-1.1880875	2.4036503	sp|Q9CQ60|6PGL_MOUSE
489	-1.1876583	1.6794106	sp|Q9JHH9|COPZ2_MOUSE
490	-1.1874218	1.3050913	sp|P70404|IDHG1_MOUSE
491	-1.1870861	4.14842	sp|Q9WUA2|SYFB_MOUSE
492	-1.1869183	1.3050913	sp|P70372|ELAV1_MOUSE
493	-1.1869135	1.6794106	sp|Q99KV1|DJB11_MOUSE
494	-1.1862221	1.3050913	sp|P97315|CSRP1_MOUSE
495	-1.1851444	3.4577034	sp|Q8BRF7|SCFD1_MOUSE
496	-1.1847076	1.6794106	sp|P10107|ANXA1_MOUSE
497	-1.1841087	4.8330717	sp|Q8VCN5|CGL_MOUSE
498	-1.1839962	3.109283	sp|Q91Z53|GRHPR_MOUSE
499	-1.1836319	1.3050913	sp|Q8BJY1|PSMD5_MOUSE
500	-1.1835632	3.8039558	sp|P35979|RL12_MOUSE
501	-1.1831312	6.1901226	sp|P17751|TPIS_MOUSE
502	-1.1825371	1.6794106	sp|Q9EPE9|AT131_MOUSE
503	-1.1824512	5.8520784	sp|P05208|CEL2A_MOUSE
504	-1.182064	1.3050913	sp|Q99LD9|EI2BB_MOUSE
505	-1.1816406	1.3050913	sp|P63073|IF4E_MOUSE
506	-1.1809025	3.109283	sp|P41216|ACSL1_MOUSE
507	-1.1803513	1.3050913	sp|Q9CQC6|BZW1_MOUSE
508	-1.180027	2.044628	sp|Q02248|CTNB1_MOUSE
509	-1.1800194	4.8330717	sp|Q9JLJ2|AL9A1_MOUSE
510	-1.1799641	3.109283	sp|P47758|SRPRB_MOUSE
511	-1.1795483	2.4036503	sp|Q99KK7|DPP3_MOUSE
512	-1.1788673	6.864285	sp|P47738|ALDH2_MOUSE
513	-1.1785793	1.6794106	sp|P63005-2|LIS1_MOUSE
514	-1.1780281	1.6794106	sp|Q99KR7|PPIF_MOUSE
515	-1.1776447	3.4577034	sp|Q3TW96|UAP1L_MOUSE
516	-1.1773138	2.044628	sp|Q99020|ROAA_MOUSE
517	-1.1772804	2.758175	sp|Q3ULJ0-2|GPD1L_MOUSE
518	-1.1771526	5.8520784	sp|P09411|PGK1_MOUSE
519	-1.176693	1.3050913	sp|Q9WUP7-2|UCHL5_MOUSE
520	-1.1761904	5.8520784	sp|P06151|LDHA_MOUSE
521	-1.1761398	4.4913836	sp|P62281|RS11_MOUSE
522	-1.1751757	3.8039558	sp|Q99L04|DHRS1_MOUSE
523	-1.1737366	2.4036503	sp|Q99PT1|GDIR1_MOUSE
524	-1.1736565	2.758175	sp|Q3UPH1|PRRC1_MOUSE
525	-1.1735573	6.1901226	sp|P05202|AATM_MOUSE
526	-1.1734276	1.6794106	sp|P61089|UBE2N_MOUSE
527	-1.1726398	2.4036503	sp|Q9QUM9|PSA6_MOUSE
528	-1.1719694	3.109283	sp|P60843|IF4A1_MOUSE
529	-1.1717148	1.3050913	sp|Q60692|PSB6_MOUSE
530	-1.1711302	3.109283	sp|P35505|FAAA_MOUSE
531	-1.1709566	5.8520784	sp|O88986|KBL_MOUSE
532	-1.170826	3.4577034	sp|P14576|SRP54_MOUSE

533	-1.1706753	2.4036503	sp|Q9CQR2|RS21_MOUSE
534	-1.17066	6.1901226	sp|Q6ZWN5|RS9_MOUSE
535	-1.1703405	11.539065	sp|Q61024|ASNS_MOUSE
536	-1.1703348	2.044628	sp|Q8BWY3|ERF1_MOUSE
537	-1.1702461	5.5132895	sp|P51410|RL9_MOUSE
538	-1.16922	1.6794106	sp|Q9Z1N5|DX39B_MOUSE
539	-1.1691589	1.6794106	sp|P62751|RL23A_MOUSE
540	-1.166542	1.3050913	sp|P35293|RAB18_MOUSE
541	-1.1659575	2.044628	sp|Q8K183|PDXK_MOUSE
542	-1.1644859	1.3050913	sp|B2RSH2|GNAI1_MOUSE
543	-1.1639977	2.044628	sp|Q99L47|F10A1_MOUSE
544	-1.1637392	2.758175	sp|Q9Z204-2|HNRPC_MOUSE
545	-1.1633167	3.4577034	sp|P35486|ODPA_MOUSE
546	-1.16325	9.2091	sp|P17182|ENOA_MOUSE
547	-1.1630039	2.4036503	sp|P68254-2|1433T_MOUSE
548	-1.1629868	1.6794106	sp|P42669|PURA_MOUSE
549	-1.1629524	1.3050913	sp|Q99JT9|MTND_MOUSE
550	-1.1629381	1.6794106	sp|Q8BFY9-2|TNPO1_MOUSE
551	-1.1622543	2.044628	sp|Q8BVI4|DHPR_MOUSE
552	-1.1620283	1.3050913	sp|Q8R059|GALE_MOUSE
553	-1.1615868	1.3050913	sp|P61924|COPZ1_MOUSE
554	-1.160984	4.14842	sp|Q9Z0N1|IF2G_MOUSE
555	-1.1597481	2.4036503	sp|Q9QZD9|EIF3I_MOUSE
556	-1.1596756	2.044628	sp|Q62465|VAT1_MOUSE
557	-1.1595402	2.044628	sp|Q99JY0|ECHB_MOUSE
558	-1.1595078	1.3050913	sp|Q9QYJ0|DNJA2_MOUSE
559	-1.1592178	1.3050913	sp|B2RQC6-2|PYR1_MOUSE
560	-1.1588058	3.8039558	sp|P62082|RS7_MOUSE
561	-1.1584663	3.109283	sp|Q91YT0|NDUV1_MOUSE
562	-1.1580219	2.758175	sp|Q9CZU6|CISY_MOUSE
563	-1.1574211	2.758175	sp|Q8VEM8|MPCP_MOUSE
564	-1.1571522	2.044628	sp|Q9CQ62|DECR_MOUSE
565	-1.1565971	1.6794106	sp|Q9Z2U0|PSA7_MOUSE
566	-1.156208	1.3050913	sp|Q63932|MP2K2_MOUSE
567	-1.1557693	2.4036503	sp|P07356|ANXA2_MOUSE
568	-1.1547451	4.4913836	sp|Q9CZX8|RS19_MOUSE
569	-1.1545506	1.3050913	sp|Q9Z0L8-2|GGH_MOUSE
570	-1.154439	8.87523	sp|Q9D964|GATM_MOUSE
571	-1.1544151	1.3050913	sp|Q9CPQ8|ATP5L_MOUSE
572	-1.1543827	2.4036503	sp|Q9D2G2-2|ODO2_MOUSE
573	-1.1542625	2.758175	sp|Q9CPV4|GLOD4_MOUSE
574	-1.1527195	2.044628	sp|P49312-2|ROA1_MOUSE
575	-1.1526899	1.6794106	sp|Q9WUM4|COR1C_MOUSE
576	-1.1514435	1.3050913	sp|Q9D358-2|PPAC_MOUSE
577	-1.1514091	2.044628	sp|P13707|GPDA_MOUSE

578	-1.1512756	1.6794106	sp|Q99L13|3HIDH_MOUSE
579	-1.1506748	1.3050913	sp|P54822|PUR8_MOUSE
580	-1.1505117	2.044628	sp|Q91V41|RAB14_MOUSE
581	-1.1504059	4.14842	sp|O70251|EF1B_MOUSE
582	-1.1497898	4.4913836	sp|P62270|RS18_MOUSE
583	-1.1495504	3.109283	sp|Q9WUK2-2|IF4H_MOUSE
584	-1.1489086	1.6794106	sp|Q9EQP2|EHD4_MOUSE
585	-1.1481438	2.758175	sp|Q8BTZ7|GMPPB_MOUSE
586	-1.1479921	1.3050913	sp|P12367|KAP2_MOUSE
587	-1.1472387	1.3050913	sp|Q9Z1Q5|CLIC1_MOUSE
588	-1.146718	1.6794106	sp|P35276|RAB3D_MOUSE
589	-1.146718	4.14842	sp|Q9R0P3|ESTD_MOUSE
590	-1.1466923	1.6794106	sp|Q62186|SSRD_MOUSE
591	-1.145338	2.758175	sp|Q8CG76|ARK72_MOUSE
592	-1.1451931	7.5362897	sp|P10126|EF1A1_MOUSE
593	-1.1447754	1.6794106	sp|O08605|MKNK1_MOUSE
594	-1.1446972	1.3050913	sp|Q8K3J1|NDUS8_MOUSE
595	-1.1445351	6.527502	sp|P54071|IDHP_MOUSE
596	-1.1444817	1.6794106	sp|Q9DB05|SNAA_MOUSE
597	-1.1439724	5.8520784	sp|Q71RI9-2|KAT3_MOUSE
598	-1.1431608	3.4577034	sp|O89079|COPE_MOUSE
599	-1.142704	1.6794106	sp|Q60759|GCDH_MOUSE
600	-1.1425323	1.6794106	sp|P03336|GAG_MLVAV
601	-1.1424065	3.109283	sp|P63325|RS10_MOUSE
602	-1.1409607	3.109283	sp|P63242|IF5A1_MOUSE
603	-1.1404762	5.8520784	sp|P16858|G3P_MOUSE
604	-1.1403866	13.879043	sp|P11679|K2C8_MOUSE
605	-1.1400976	1.3050913	sp|Q3THK7|GUAA_MOUSE
606	-1.1398773	4.14842	sp|P62259|1433E_MOUSE
607	-1.1394539	3.8039558	sp|P55264-2|ADK_MOUSE
608	-1.1384506	2.758175	sp|Q07417|ACADS_MOUSE
609	-1.1378603	3.4577034	sp|P97461|RS5_MOUSE
610	-1.1370087	1.3050913	sp|Q9JHR7|IDE_MOUSE
611	-1.1349316	1.3050913	sp|Q8VCW8|ACSF2_MOUSE
612	-1.1329117	1.6794106	sp|O55022|PGRC1_MOUSE
613	-1.1324539	9.875973	sp|Q62167|DDX3X_MOUSE
614	-1.1315155	2.4036503	sp|P60335|PCBP1_MOUSE
615	-1.1312065	1.6794106	sp|P16045|LEG1_MOUSE
616	-1.1303768	5.5132895	sp|P05064|ALDOA_MOUSE
617	-1.1301899	2.758175	sp|P52825|CPT2_MOUSE
618	-1.1299324	2.044628	sp|Q8QZY1|EIF3L_MOUSE
619	-1.1297264	1.6794106	sp|Q9DBZ5|EIF3K_MOUSE
620	-1.1294155	2.044628	sp|P10518|HEM2_MOUSE
621	-1.1289959	4.14842	sp|Q9Z2W0|DNPEP_MOUSE
622	-1.1285181	1.6794106	sp|P62880|GBB2_MOUSE

623	-1.1283092	2.4036503	sp|Q8BMF4|ODP2_MOUSE
624	-1.1281643	1.6794106	sp|P99027|RLA2_MOUSE
625	-1.1278677	5.5132895	sp|Q99K85|SERC_MOUSE
626	-1.1272163	1.6794106	sp|Q64471|GSTT1_MOUSE
627	-1.1268978	1.3050913	sp|Q61510|TRI25_MOUSE
628	-1.1265507	2.4036503	sp|Q9D172|GAL3A_MOUSE
629	-1.1265383	3.109283	sp|Q04447|KCRB_MOUSE
630	-1.1263762	3.109283	sp|P80315|TCPD_MOUSE
631	-1.126358	3.109283	sp|O35969-2|GAMT_MOUSE
632	-1.1262836	2.044628	sp|Q9R1P4|PSA1_MOUSE
633	-1.1249123	8.20651	sp|P50247|SAHH_MOUSE
634	-1.1245079	4.4913836	sp|P24369|PPIB_MOUSE
635	-1.1243048	3.109283	sp|Q9R0P5|DEST_MOUSE
636	-1.1225996	1.6794106	sp|Q62393-2|TPD52_MOUSE
637	-1.1221457	1.6794106	sp|Q8BP48|MAP11_MOUSE
638	-1.1221275	3.4577034	sp|O08709|PRDX6_MOUSE
639	-1.1220894	2.044628	sp|Q9JJI8|RL38_MOUSE
640	-1.1220264	3.8039558	sp|O35855|BCAT2_MOUSE
641	-1.1214447	1.6794106	sp|Q99KC8|VMA5A_MOUSE
642	-1.120224	4.4913836	sp|Q9D051|ODPB_MOUSE
643	-1.1194305	1.3050913	sp|P47791-2|GSHR_MOUSE
644	-1.1193085	1.6794106	sp|Q9JLZ3|AUHM_MOUSE
645	-1.1181297	1.3050913	sp|Q8QZR5|ALAT1_MOUSE
646	-1.1180878	1.3050913	sp|Q9DCH4|EIF3F_MOUSE
647	-1.1177883	2.044628	sp|P49722|PSA2_MOUSE
648	-1.1174593	2.044628	sp|Q9CQ65|MTAP_MOUSE
649	-1.1165123	1.3050913	sp|Q9QUI0|RHOA_MOUSE
650	-1.1159191	2.758175	sp|Q9WTP6-2|KAD2_MOUSE
651	-1.115036	2.758175	sp|Q9DCS2|MTL26_MOUSE
652	-1.1111603	2.044628	sp|Q9DCN2-2|NB5R3_MOUSE
653	-1.110589	1.3050913	sp|Q91V76|CK054_MOUSE
654	-1.1104412	2.044628	sp|Q9Z0S1|BPNT1_MOUSE
655	-1.1097298	2.044628	sp|P57759|ERP29_MOUSE
656	-1.1096573	1.6794106	sp|Q8CHP8|PGP_MOUSE
657	-1.1084394	1.6794106	sp|Q9CPP6|NDUA5_MOUSE
658	-1.1083565	2.044628	sp|Q6P3A8-2|ODBB_MOUSE
659	-1.1078281	2.4036503	sp|P23591|FCL_MOUSE
660	-1.1077929	2.044628	sp|Q99JW2|ACY1_MOUSE
661	-1.1074533	2.4036503	sp|Q8CDN6|TXNL1_MOUSE
662	-1.1061687	1.3050913	sp|P62334|PRS10_MOUSE
663	-1.1043339	2.4036503	sp|O08756|HCD2_MOUSE
664	-1.1033707	5.8520784	sp|Q99LC5|ETFA_MOUSE
665	-1.1031055	1.6794106	sp|P70296|PEBP1_MOUSE
666	-1.1027069	1.6794106	sp|Q9CQC2|COL_MOUSE
667	-1.1026287	1.3050913	sp|Q9CYN2|SPCS2_MOUSE

668	-1.1007032	1.3050913	sp|P61082|UBC12_MOUSE
669	-1.0978203	5.5132895	sp|P48758|CBR1_MOUSE
670	-1.0973434	2.758175	sp|Q99J77|SIAS_MOUSE
671	-1.0968475	3.8039558	sp|P62301|RS13_MOUSE
672	-1.0965519	3.8039558	sp|Q64674|SPEE_MOUSE
673	-1.0955677	1.6794106	sp|Q05816|FABP5_MOUSE
674	-1.0951557	2.758175	sp|Q9D7B6|ACAD8_MOUSE
675	-1.09441	2.758175	sp|P35700|PRDX1_MOUSE
676	-1.0940285	2.044628	sp|P08228|SODC_MOUSE
677	-1.0935612	1.3050913	sp|Q99JX4|EIF3M_MOUSE
678	-1.0930023	1.6794106	sp|Q922H4|GMPPA_MOUSE
679	-1.0929871	1.3050913	sp|Q60668-2|HNRPD_MOUSE
680	-1.0912857	3.8039558	sp|P63276|RS17_MOUSE
681	-1.0904655	3.109283	sp|P28474|ADHX_MOUSE
682	-1.0902042	1.6794106	sp|P62835|RAP1A_MOUSE
683	-1.0896196	1.3050913	sp|P62849-2|RS24_MOUSE
684	-1.0894089	1.3050913	sp|P56391|CX6B1_MOUSE
685	-1.0887585	1.3050913	sp|Q9R062|GLYG_MOUSE
686	-1.0879536	2.044628	sp|Q9JK38|GNA1_MOUSE
687	-1.0871983	4.4913836	sp|P18760|COF1_MOUSE
688	-1.086916	1.6794106	sp|O70400|PDLI1_MOUSE
689	-1.0858173	2.758175	sp|Q61171|PRDX2_MOUSE
690	-1.0835028	1.3050913	sp|Q61490|CD166_MOUSE
691	-1.0825024	1.3050913	sp|O08691|ARGI2_MOUSE
692	-1.0819969	1.3050913	sp|P52760|RIDA_MOUSE
693	-1.0818291	3.109283	sp|Q60930|VDAC2_MOUSE
694	-1.0809746	4.8330717	sp|Q9DCW4|ETFB_MOUSE
695	-1.0768194	2.044628	sp|Q8VC28|AK1CD_MOUSE
696	-1.0767021	1.3050913	sp|P18242|CATD_MOUSE
697	-1.0762653	8.87523	sp|P08249|MDHM_MOUSE
698	-1.0760937	7.5362897	sp|P68040|RACK1_MOUSE
699	-1.0760603	2.044628	sp|P53994|RAB2A_MOUSE
700	-1.075716	2.044628	sp|Q9CPU0|LGUL_MOUSE
701	-1.0754766	1.6794106	sp|Q91ZJ5-2|UGPA_MOUSE
702	-1.0735226	1.6794106	sp|P62827|RAN_MOUSE
703	-1.0692596	1.6794106	sp|Q61990-2|PCBP2_MOUSE
704	-1.0691986	1.3050913	sp|Q9Z2U1|PSA5_MOUSE
705	-1.0689297	3.109283	sp|Q9D819|IPYR_MOUSE
706	-1.0689259	2.044628	sp|O35215|DOPD_MOUSE
707	-1.0682068	1.3050913	sp|P30115|GSTA3_MOUSE
708	-1.0657978	2.044628	sp|Q3SYP2|CTRC_MOUSE
709	-1.0642433	2.758175	sp|P52196|THTR_MOUSE
710	-1.0620289	2.758175	sp|Q99L20|GSTT3_MOUSE
711	-1.0597897	2.044628	sp|P62196|PRS8_MOUSE
712	-1.0595093	4.8330717	sp|Q8BH95|ECHM_MOUSE

713	-1.0560722	2.758175	sp|Q9WVA4|TAGL2_MOUSE
714	-1.0556202	4.14842	sp|P63323|RS12_MOUSE
715	-1.0548668	4.8330717	sp|P10649|GSTM1_MOUSE
716	-1.0540771	10.209015	sp|P62908|RS3_MOUSE
717	-1.0534363	2.758175	sp|P68369|TBA1A_MOUSE
718	-1.0515995	1.6794106	sp|Q91V64|ISOC1_MOUSE
719	-1.0514774	2.044628	sp|Q8R164|BPHL_MOUSE
720	-1.0509663	2.4036503	sp|P61458|PHS_MOUSE
721	-1.0502453	1.6794106	sp|P85094|ISC2A_MOUSE
722	-1.0480881	1.6794106	sp|P59999|ARPC4_MOUSE
723	-1.0436516	1.3050913	sp|Q9CQE8|RTRAF_MOUSE
724	-1.0411072	1.3050913	sp|Q9D6J6|NDUV2_MOUSE
725	-1.040082	3.109283	sp|Q9DBP5|KCY_MOUSE
726	-1.0398941	1.3050913	sp|P62852|RS25_MOUSE
727	-1.038868	2.758175	sp|P42125|ECI1_MOUSE
728	-1.0380573	3.109283	sp|P53026|RL10A_MOUSE
729	-1.0365582	3.8039558	sp|P48036|ANXA5_MOUSE
730	-1.0364647	1.3050913	sp|O54984|ASNA_MOUSE
731	-1.0322914	1.3050913	sp|Q91VR2|ATPG_MOUSE
732	-1.0300941	1.3050913	sp|P56959|FUS_MOUSE
733	-1.0268536	1.3050913	sp|P38060|HMGCL_MOUSE
734	-1.0248852	4.4913836	sp|P17742|PPIA_MOUSE
735	-1.024353	2.044628	sp|O55142|RL35A_MOUSE
736	-1.0221062	1.3634305	sp|P30416|FKBP4_MOUSE
737	-1.0180988	1.6794106	sp|P63028|TCTP_MOUSE
738	-1.0178442	3.109283	sp|P62962|PROF1_MOUSE
739	-1.0130997	2.4036503	sp|Q9CXW4|RL11_MOUSE
740	-1.0070839	4.4913836	sp|O88569-2|ROA2_MOUSE
741	-1.0063515	1.6794106	sp|P62858|RS28_MOUSE
742	-1.0013771	5.17366	sp|P19157|GSTP1_MOUSE
743	-0.9943714	2.758175	sp|P99029-2|PRDX5_MOUSE
744	-0.9920082	3.4577034	sp|Q9QXF8|GNMT_MOUSE
745	-0.9902792	1.3050913	sp|O35658|C1QBP_MOUSE
746	-0.98579407	3.109283	sp|P14131|RS16_MOUSE
747	-0.9848137	1.3050913	sp|Q07076|ANXA7_MOUSE
748	-0.98314095	2.758175	sp|P62889|RL30_MOUSE
749	-0.97930527	2.044628	sp|Q9CQM5|TXD17_MOUSE
750	-0.9738865	3.8039558	sp|P15626|GSTM2_MOUSE
751	-0.96040344	1.3050913	sp|P00329|ADH1_MOUSE
752	-0.95006275	1.6794106	sp|Q91X72|HEMO_MOUSE
753	-0.94696236	1.3050913	sp|Q9WVL0|MAAI_MOUSE
754	-0.9423332	1.6794106	sp|P02535-2|K1C10_MOUSE
755	-0.9328289	1.3050913	sp|Q9R1P1|PSB3_MOUSE
756	-0.9205513	1.6794106	sp|Q01768|NDKB_MOUSE
757	-0.918993	1.3050913	sp|P16125|LDHB_MOUSE

758	-0.91344833	3.109283	sp|P01942|HBA_MOUSE
759	-0.8999491	1.3050913	sp|Q64010-2|CRK_MOUSE
760	-0.8672409	1.6794106	sp|P04117|FABP4_MOUSE
761	-0.85577774	1.3050913	sp|Q9JKB1|UCHL3_MOUSE
762	-0.80261326	1.3050913	sp|P15532|NDKA_MOUSE
763	-0.76784515	2.4036503	sp|P02088|HBB1_MOUSE
764	-0.6644497	1.3050913	sp|P02798|MT2_MOUSE
765	-0.57154083	1.3050913	sp|P02802|MT1_MOUSE

Supplementary Table 2. Citrullinated proteins in pancreas of BB-Cl-amidine treated versus DMSO treated NOD mice not significantly altered by the treatment

** P≥0.05 (Log_{10}p-value = 1.122)

	Log_2Ratio	**Log_{10}p-value (**)**	**Accession**
1	-1.7894802	0.49851555	sp|P23953|EST1C_MOUSE
2	-1.6683903	0.91601306	sp|O08786|CCKAR_MOUSE
3	-1.6681643	0.49851555	sp|P53996|CNBP_MOUSE
4	-1.6120167	0.91601306	sp|P83882|RL36A_MOUSE
5	-1.580823	0.91601306	sp|Q9JKB3-2|YBOX3_MOUSE
6	-1.5767965	0.49851555	sp|P48774|GSTM5_MOUSE
7	-1.5470638	0.49851555	sp|O35643|AP1B1_MOUSE
8	-1.5351009	0.91601306	sp|Q8CHW4|EI2BE_MOUSE
9	-1.5293589	0.91601306	sp|Q9CQJ6|DENR_MOUSE
10	-1.5259628	0.91601306	sp|P70441|NHRF1_MOUSE
11	-1.519249	0.91601306	sp|P63328-2|PP2BA_MOUSE
12	-1.4998703	0.91601306	sp|Q6GQT9|NOMO1_MOUSE
13	-1.4967995	0.91601306	sp|Q99LE6|ABCF2_MOUSE
14	-1.4886131	0.91601306	sp|O54692|ZW10_MOUSE
15	-1.4832001	0.91601306	sp|Q9ERK4|XPO2_MOUSE
16	-1.4829292	0.91601306	sp|Q791V5|MTCH2_MOUSE
17	-1.481122	0.49851555	sp|Q8BFZ3|ACTBL_MOUSE
18	-1.4794674	0.91601306	sp|Q9D281|NXP20_MOUSE
19	-1.4741497	0.91601306	sp|Q11136|PEPD_MOUSE
20	-1.4740906	0.91601306	sp|Q60598|SRC8_MOUSE
21	-1.472992	0.91601306	sp|Q91XE8|TM205_MOUSE
22	-1.4608564	0.91601306	sp|P14685|PSMD3_MOUSE
23	-1.4468403	0.91601306	sp|A2ALW5|DJC25_MOUSE
24	-1.4434948	0.91601306	sp|Q6PB93-2|GALT2_MOUSE
25	-1.4420519	0.49851555	sp|P48722-2|HS74L_MOUSE
26	-1.4326811	0.91601306	sp|O88543|CSN3_MOUSE

27	-1.4253664	0.91601306	sp|Q9QXX4|CMC2_MOUSE
28	-1.4231462	0.91601306	sp|Q9Z1W9|STK39_MOUSE
29	-1.4202251	0.49851555	sp|Q9D2M8-2|UB2V2_MOUSE
30	-1.414794	0.91601306	sp|P35235-2|PTN11_MOUSE
31	-1.4048777	0.91601306	sp|P17918|PCNA_MOUSE
32	-1.4022331	0.49851555	sp|P84084|ARF5_MOUSE
33	-1.3996744	0.91601306	sp|Q62448-2|IF4G2_MOUSE
34	-1.3991852	0.49851555	sp|P61205|ARF3_MOUSE
35	-1.3975315	0.49851555	sp|Q8R5C5|ACTY_MOUSE
36	-1.3934231	0.91601306	sp|P08752|GNAI2_MOUSE
37	-1.3886375	0.49851555	sp|P63094-2|GNAS2_MOUSE
38	-1.3862152	0.91601306	sp|Q9D379|HYEP_MOUSE
39	-1.3848953	0.91601306	sp|Q8BMP6|GCP60_MOUSE
40	-1.3750544	0.91601306	sp|P70195|PSB7_MOUSE
41	-1.3742962	0.91601306	sp|P47964|RL36_MOUSE
42	-1.3739471	0.91601306	sp|Q9CR62|M2OM_MOUSE
43	-1.3707561	0.49851555	sp|P21107|TPM3_MOUSE
44	-1.368391	0.91601306	sp|P32067|LA_MOUSE
45	-1.3655033	0.91601306	sp|Q9R099|TBL2_MOUSE
46	-1.3651772	0.91601306	sp|Q8BW75|AOFB_MOUSE
47	-1.3639383	0.91601306	sp|P36536|SAR1A_MOUSE
48	-1.3636379	0.91601306	sp|Q9DC51|GNAI3_MOUSE
49	-1.3608398	0.91601306	sp|Q62446|FKBP3_MOUSE
50	-1.3594933	0.91601306	sp|Q9D8V0-3|HM13_MOUSE
51	-1.3579845	0.91601306	sp|Q9D2R4|TMD11_MOUSE
52	-1.3569355	0.91601306	sp|Q8R1F6-2|HID1_MOUSE
53	-1.3559589	0.91601306	sp|O08788-2|DCTN1_MOUSE
54	-1.3549404	0.91601306	sp|Q9CR68|UCRI_MOUSE
55	-1.3546295	0.91601306	sp|Q8BVE3|VATH_MOUSE
56	-1.3509512	0.91601306	sp|Q9CWK8|SNX2_MOUSE
57	-1.3440714	0.91601306	sp|Q9D5V6|SYAP1_MOUSE
58	-1.3432989	0.49851555	sp|P53996-2|CNBP_MOUSE
59	-1.3417873	0.91601306	sp|Q9JIZ0|CMLO1_MOUSE
60	-1.3416767	0.49851555	sp|P26041|MOES_MOUSE
61	-1.3410187	0.91601306	sp|Q8BX90|FND3A_MOUSE
62	-1.3388853	0.91601306	sp|P47226-2|TES_MOUSE
63	-1.3375111	0.91601306	sp|Q8BLF1|NCEH1_MOUSE
64	-1.3332996	0.91601306	sp|Q9CQF9|PCYOX_MOUSE
65	-1.3274622	0.91601306	sp|Q920E5|FPPS_MOUSE
66	-1.3102036	0.91601306	sp|P19536|COX5B_MOUSE
67	-1.3058357	0.91601306	sp|P60670-2|NPL4_MOUSE
68	-1.3058205	0.91601306	sp|P10853|H2B1F_MOUSE
69	-1.3057585	0.91601306	sp|Q99K28-2|ARFG2_MOUSE
70	-1.3037853	0.91601306	sp|O88544|CSN4_MOUSE
71	-1.3005562	0.91601306	sp|Q9JII5-2|DAZP1_MOUSE

72	-1.2993164	0.91601306	sp|Q6ZPJ3|UBE2O_MOUSE
73	-1.2982349	0.91601306	sp|O70435|PSA3_MOUSE
74	-1.2982273	0.91601306	sp|P28656|NP1L1_MOUSE
75	-1.2957315	0.91601306	sp|Q8K4F5|ABHDB_MOUSE
76	-1.2951851	0.49851555	sp|Q8BG05-2|ROA3_MOUSE
77	-1.2950277	0.91601306	sp|P61079|UB2D3_MOUSE
78	-1.2935734	0.49851555	sp|Q9DCG6|PBLD1_MOUSE
79	-1.2907848	0.91601306	sp|P97328|KHK_MOUSE
80	-1.2887697	0.91601306	sp|Q8BWG8-2|ARRB1_MOUSE
81	-1.2876129	0.91601306	sp|Q60872|IF1A_MOUSE
82	-1.2811394	0.49851555	sp|Q6IFX2|K1C42_MOUSE
83	-1.2802505	0.91601306	sp|Q9CXT8|MPPB_MOUSE
84	-1.2752724	0.91601306	sp|Q8VDM6-2|HNRL1_MOUSE
85	-1.2748566	0.91601306	sp|Q4VAA2-2|CDV3_MOUSE
86	-1.2747765	0.91601306	sp|Q9WVP1-2|AP1M2_MOUSE
87	-1.2743025	0.91601306	sp|P62737|ACTA_MOUSE
88	-1.273632	0.91601306	sp|P61161|ARP2_MOUSE
89	-1.272152	0.91601306	sp|Q922Q4|P5CR2_MOUSE
90	-1.2720823	0.91601306	sp|Q8R1Q8|DC1L1_MOUSE
91	-1.2703238	0.91601306	sp|Q9JJK5|HERP1_MOUSE
92	-1.2654572	0.91601306	sp|Q9CZY3|UB2V1_MOUSE
93	-1.2645807	0.91601306	sp|Q6ZPE2-2|MTMR5_MOUSE
94	-1.2635231	0.91601306	sp|Q60710-2|SAMH1_MOUSE
95	-1.262888	0.91601306	sp|P50431|GLYC_MOUSE
96	-1.2597857	0.91601306	sp|Q3TZM9-2|ALG11_MOUSE
97	-1.2529278	0.91601306	sp|Q9CXN7|PBLD2_MOUSE
98	-1.2518997	0.49851555	sp|P62137|PP1A_MOUSE
99	-1.2499361	0.91601306	sp|Q8VI75|IPO4_MOUSE
100	-1.2495613	0.91601306	sp|Q99LB2|DHRS4_MOUSE
101	-1.2485752	0.91601306	sp|P22907-2|HEM3_MOUSE
102	-1.2483006	0.91601306	sp|P56395|CYB5_MOUSE
103	-1.2480507	0.49851555	sp|P21107-2|TPM3_MOUSE
104	-1.2457695	0.91601306	sp|Q9DCJ5|NDUA8_MOUSE
105	-1.243103	0.91601306	sp|Q9D0F9|PGM1_MOUSE
106	-1.2426987	0.91601306	sp|Q91X52|DCXR_MOUSE
107	-1.2419586	0.49851555	sp|Q8R180|ERO1A_MOUSE
108	-1.238163	0.91601306	sp|P27046|MA2A1_MOUSE
109	-1.2355175	0.91601306	sp|P00405|COX2_MOUSE
110	-1.2326698	0.91601306	sp|Q922B1|MACD1_MOUSE
111	-1.2316475	0.49851555	sp|Q9D6F9|TBB4A_MOUSE
112	-1.2304764	0.91601306	sp|Q61081|CDC37_MOUSE
113	-1.2287579	0.91601306	sp|P58281-2|OPA1_MOUSE
114	-1.2281294	0.91601306	sp|Q3B7Z2|OSBP1_MOUSE
115	-1.2280521	0.91601306	sp|Q8R1F1|NIBL1_MOUSE
116	-1.2269764	0.91601306	sp|Q6Y7W8|GGYF2_MOUSE

117	-1.2266569	0.91601306	sp|Q9Z0U1|ZO2_MOUSE
118	-1.2253742	0.91601306	sp|Q6PA06-2|ATLA2_MOUSE
119	-1.2230349	0.91601306	sp|Q3UMF0-2|COBL1_MOUSE
120	-1.2195797	0.91601306	sp|P49442|INPP_MOUSE
121	-1.219389	0.91601306	sp|Q9DCF9-2|SSRG_MOUSE
122	-1.2190657	0.49851555	sp|P61164|ACTZ_MOUSE
123	-1.2168465	0.91601306	sp|Q9DC16|ERGI1_MOUSE
124	-1.2116909	0.91601306	sp|O55028|BCKD_MOUSE
125	-1.2110748	0.49851555	sp|P53810|PIPNA_MOUSE
126	-1.2081051	0.91601306	sp|P53811|PIPNB_MOUSE
127	-1.2073975	0.91601306	sp|Q91WK2|EIF3H_MOUSE
128	-1.2065105	0.49851555	sp|Q80SW1|SAHH2_MOUSE
129	-1.2050934	0.91601306	sp|Q9WUL7|ARL3_MOUSE
130	-1.2028103	0.91601306	sp|Q8C181-2|MBNL2_MOUSE
131	-1.2007256	0.91601306	sp|Q9D1Q6|ERP44_MOUSE
132	-1.2003794	0.91601306	sp|P47857-2|PFKAM_MOUSE
133	-1.1973591	0.91601306	sp|Q8CIM3|D2HDH_MOUSE
134	-1.1967716	0.91601306	sp|P45878|FKBP2_MOUSE
135	-1.1963501	0.91601306	sp|Q8VCM8|NCLN_MOUSE
136	-1.1960773	0.91601306	sp|Q9DCS9|NDUBA_MOUSE
137	-1.1942635	0.91601306	sp|Q9D8C2|TSN13_MOUSE
138	-1.1915073	0.91601306	sp|Q05144|RAC2_MOUSE
139	-1.1868706	0.91601306	sp|Q6ZWQ7|SPCS3_MOUSE
140	-1.184555	0.91601306	sp|P62983|RS27A_MOUSE
141	-1.1835709	0.91601306	sp|Q64310|SURF4_MOUSE
142	-1.1805344	0.91601306	sp|Q9R112|SQOR_MOUSE
143	-1.1790028	0.91601306	sp|Q9DCT2|NDUS3_MOUSE
144	-1.1763353	0.49851555	sp|P70333|HNRH2_MOUSE
145	-1.1745644	0.91601306	sp|Q9CQZ5|NDUA6_MOUSE
146	-1.171978	0.91601306	sp|P99026|PSB4_MOUSE
147	-1.1718845	0.91601306	sp|Q9DBH5|LMAN2_MOUSE
148	-1.171689	0.49851555	sp|Q61133|GSTT2_MOUSE
149	-1.1700516	0.91601306	sp|P68510|1433F_MOUSE
150	-1.1697206	0.91601306	sp|Q9CZ44-3|NSF1C_MOUSE
151	-1.1675911	0.91601306	sp|Q9JM14|NT5C_MOUSE
152	-1.1669292	0.91601306	sp|P24547|IMDH2_MOUSE
153	-1.165226	0.91601306	sp|Q921X9|PDIA5_MOUSE
154	-1.16292	0.91601306	sp|Q80UM3|NAA15_MOUSE
155	-1.162157	0.91601306	sp|Q8JZU2|TXTP_MOUSE
156	-1.1541367	0.91601306	sp|Q9CYZ2|TPD54_MOUSE
157	-1.151825	0.91601306	sp|Q924M7|MPI_MOUSE
158	-1.1503906	0.49851555	sp|O35737|HNRH1_MOUSE
159	-1.1486397	0.91601306	sp|Q5YD48-2|A1CF_MOUSE
160	-1.1478958	0.91601306	sp|P60824|CIRBP_MOUSE
161	-1.1461182	0.49851555	sp|Q3UV17|K22O_MOUSE

162	-1.1445503	0.91601306	sp|Q9D892|ITPA_MOUSE
163	-1.1439457	0.91601306	sp|Q3TJZ6|FA98A_MOUSE
164	-1.1354609	0.91601306	sp|Q9D0K2|SCOT1_MOUSE
165	-1.1338282	0.91601306	sp|P62141|PP1B_MOUSE
166	-1.1316261	0.91601306	sp|Q99J39-2|DCMC_MOUSE
167	-1.1280613	0.91601306	sp|P32233|DRG1_MOUSE
168	-1.1258507	0.91601306	sp|Q8R0X7|SGPL1_MOUSE
169	-1.1228218	0.91601306	sp|P62274|RS29_MOUSE
170	-1.1226807	0.91601306	sp|Q9JM76|ARPC3_MOUSE
171	-1.1201134	0.91601306	sp|Q9R1P0|PSA4_MOUSE
172	-1.1139317	0.91601306	sp|P47754|CAZA2_MOUSE
173	-1.1125727	0.91601306	sp|P28658|ATX10_MOUSE
174	-1.1081991	0.91601306	sp|Q01405|SC23A_MOUSE
175	-1.1076202	0.91601306	sp|P48193-2|41_MOUSE
176	-1.1073151	0.91601306	sp|Q9DC69|NDUA9_MOUSE
177	-1.1060591	0.49851555	sp|Q78ZA7|NP1L4_MOUSE
178	-1.0976181	0.91601306	sp|P61750|ARF4_MOUSE
179	-1.0975285	0.91601306	sp|Q9CQC9|SAR1B_MOUSE
180	-1.0948553	0.91601306	sp|Q9Z2X1-2|HNRPF_MOUSE
181	-1.0947847	0.91601306	sp|Q9JHW2|NIT2_MOUSE
182	-1.0917206	0.91601306	sp|Q9QYJ3|DNJB1_MOUSE
183	-1.0882874	0.91601306	sp|P51174|ACADL_MOUSE
184	-1.083662	0.91601306	sp|Q7TQI3|OTUB1_MOUSE
185	-1.0804901	0.91601306	sp|P70695|F16P2_MOUSE
186	-1.0790787	0.91601306	sp|Q6ZWU9|RS27_MOUSE
187	-1.0770531	0.91601306	sp|Q99LX0|PARK7_MOUSE
188	-1.076642	0.91601306	sp|Q8K1E0-2|STX5_MOUSE
189	-1.0762386	0.91601306	sp|Q99LC8|EI2BA_MOUSE
190	-1.0753365	0.91601306	sp|Q99KR3|LACB2_MOUSE
191	-1.072854	0.91601306	sp|Q9D1G1|RAB1B_MOUSE
192	-1.071846	0.91601306	sp|P61202-2|CSN2_MOUSE
193	-1.0705929	0.49851555	sp|Q9WV02-2|RBMX_MOUSE
194	-1.0703392	0.91601306	sp|P29391|FRIL1_MOUSE
195	-1.067997	0.49851555	sp|P55258|RAB8A_MOUSE
196	-1.0677948	0.91601306	sp|Q8K310|MATR3_MOUSE
197	-1.0526981	0.91601306	sp|Q9CR16|PPID_MOUSE
198	-1.047514	0.91601306	sp|Q91VF2|HNMT_MOUSE
199	-1.044919	0.91601306	sp|Q8VC30|TKFC_MOUSE
200	-1.0421238	0.91601306	sp|O88696|CLPP_MOUSE
201	-1.0341625	0.91601306	sp|P56380|AP4A_MOUSE
202	-1.0339527	0.91601306	sp|P61979-2|HNRPK_MOUSE
203	-1.0335789	0.91601306	sp|Q99LB6-2|MAT2B_MOUSE
204	-1.0331154	0.91601306	sp|Q9CPT4|MYDGF_MOUSE
205	-1.0248833	0.91601306	sp|Q9CQS8|SC61B_MOUSE
206	-1.0220718	0.49851555	sp|Q6IFZ6|K2C1B_MOUSE

207	-1.0210285	0.91601306	sp|Q9DCT8|CRIP2_MOUSE
208	-1.0209751	0.91601306	sp|Q8VCR7|ABHEB_MOUSE
209	-1.0161228	0.91601306	sp|P63260|ACTG_MOUSE
210	-1.0129232	0.91601306	sp|Q6P8X1|SNX6_MOUSE
211	-1.0076065	0.91601306	sp|P61358|RL27_MOUSE
212	-0.9983959	0.91601306	sp|P27048|RSMB_MOUSE
213	-0.9941635	0.91601306	sp|P07758|A1AT1_MOUSE
214	-0.9922199	0.91601306	sp|Q9D7A6|SRP19_MOUSE
215	-0.98636055	0.91601306	sp|Q9QXT0|CNPY2_MOUSE
216	-0.98517704	0.91601306	sp|Q8BH64|EHD2_MOUSE
217	-0.98493385	0.91601306	sp|P97823-2|LYPA1_MOUSE
218	-0.98397064	0.49851555	sp|Q9CZ42-3|NNRD_MOUSE
219	-0.9828243	0.91601306	sp|Q64133|AOFA_MOUSE
220	-0.98198223	0.91601306	sp|Q6ZWR4-2|2ABB_MOUSE
221	-0.9791479	0.49851555	sp|Q9DCV7|K2C7_MOUSE
222	-0.9758949	0.49851555	sp|Q91VM5|RMXL1_MOUSE
223	-0.9753418	0.91601306	sp|Q9R1P3|PSB2_MOUSE
224	-0.96315384	0.91601306	sp|P34884|MIF_MOUSE
225	-0.9358063	0.49851555	sp|P17426-2|AP2A1_MOUSE
226	-0.9327469	0.91601306	sp|Q3UGR5|HDHD2_MOUSE
227	-0.93006516	0.91601306	sp|P60710|ACTB_MOUSE
228	-0.923213	0.49851555	sp|P17427|AP2A2_MOUSE
229	-0.8823776	0.91601306	sp|P23492|PNPH_MOUSE
230	-0.8738289	0.91601306	sp|P50543|S10AB_MOUSE
231	-0.872838	0.91601306	sp|P20108|PRDX3_MOUSE
232	-0.8728094	0.49851555	sp|Q922U2|K2C5_MOUSE
233	-0.8593445	0.91601306	sp|Q78XF5|OSTC_MOUSE
234	-0.83586407	0.49851555	sp|P61027|RAB10_MOUSE
235	-0.8286371	0.91601306	sp|P52480-2|KPYM_MOUSE
236	-0.7517929	0.91601306	sp|P00920|CAH2_MOUSE
237	-0.6766529	0.49851555	sp|Q8VED5|K2C79_MOUSE
238	-0.1389122	0.39426914	sp|P16015|CAH3_MOUSE