SUPPLEMENTAL MATERIAL

Ge et al., http://www.jem.org/cgi/content/full/jem.20130731/DC1

Table S1. Serum IgM and IgG levels of NZM2328 and R27 at different ages

Strain (age)	IgM (mg/ml)	IgG (mg/ml)	IgG1 (mg/ml)	IgG2a (mg/ml)	IgG2b (mg/ml)
R27 (2–3 mo), *n* = 7	0.25 ± 0.046				
R27 (5–6 mo), *n* = 5	0.65 ± 0.20				
R27 (12 mo), *n* = 13	0.80 ± 0.45				
NZM2328 (6–7 mo), *n* = 4	0.79 ± 0.40				
R27 (2–3 mo), *n* = 7		1.08 ± 0.45	0.33 ± 0.57	0.17 ± 0.10	0.21 ± 0.039
R27 (5–6 mo), *n* = 5		3.62 ± 1.49	2.16 ± 2.04	0.32 ± 0.11	0.51 ± 0.18
R27 (8–9 mo), *n* = 7		8.12 ± 2.31	2.11 ± 1.89	0.67 ± 0.23	0.48 ± 0.13
R27 (12 mo), *n* = 15		7.36 ± 2.68	4.99 ± 2.47	0.56 ± 0.36	0.56 ± 0.27
NZM2328 (2 mo), *n* = 4		1.51 ± 0.46	0.13 ± 0.07	0.098 ± 0.057	0.096 ± 0.025
NZM2328 (5–6 mo), *n* = 5		5.7 ± 4.03	0.83 ± 0.64	0.87 ± 1.09	0.28 ± 0.21
NZM2328 (7–9 mo), *n* = 4		9.31 ± 4.22	1.82 ± 0.80*	1.37 ± 0.95*	0.59 ± 0.43

Serum levels of IgM, IgG, IgG1, IgG2a, and IgG2b were determined by ELISA. Values represent the mean ± SD. Student *t* tests were performed between 12-mo-old R27 and 7–9-mo-old NZM2328. *, $P < 0.05$.

Table S2. Percentages and activation status of $CD4^+$ T cells ($CD4^+CD3^+$), $CD8^+$ T cells ($CD8^+CD3^+$), and B cells ($CD19^+$) in spleens and kidney draining lymph nodes of 2–3-mo-old R27 and NZM2328 female mice were determined by flow cytometry

Cell subpopulation	R27 spleen	NZM2328 spleen	R27 LN	NZM2328 LN
$CD4^+$ T of total live cells (%)	41.14 ± 2.30 (*n* = 10)	39.71 ± 2.94 (*n* = 10)	62.19 ± 7.73 (*n* = 5)	60.15 ± 8.19 (*n* = 5)
$CD69^+$ of $CD4^+$ T cells (%)	7.16 ± 1.68 (*n* = 8)	7.50 ± 1.39 (*n* = 8)	10.30 ± 2.36 (*n* = 3)	10.36 ± 0.67 (*n* = 3)
$CD8^+$ T of total live cells (%)	9.29 ± 1.81 (*n* = 10)	9.47 ± 2.29 (*n* = 10)	11.69 ± 2.72 (*n* = 5)	10.08 ± 5.02 (*n* = 5)
$CD69^+$ of $CD8^+$ T cells (%)	2.47 ± 0.46 (*n* = 6)	2.72 ± 0.95 (*n* = 6)	3.88 ± 0.77 (*n* = 3)	3.60 ± 0.40 (*n* = 3)
B cells of total live cells (%)	36.13 ± 2.56 (*n* = 10)	38.75 ± 6.10 (*n* = 10)	15.52 ± 7.18 (*n* = 5)	16.48 ± 6.11 (*n* = 5)
CD86 on B cells (MFI)	22.11 ± 12.31 (*n* = 8)	21.08 ± 10.06 (*n* = 8)	8.85 ± 1.35 (*n* = 3)	11.93 ± 2.00 (*n* = 3)

Data represent mean ± SD. Two-tailed unpaired student *t* tests were performed to compare values of R27 and NZM2328 counterparts, and no significant differences were detected.

Table S3. Genes that are located within the refined Cgnz1 region

Gene (abbreviation)
Fc receptor, IgG, low affinity IV (Fcgr4 [partial]*)
Fc receptor, IgG, low affinity III (Fcgr3*)
RIKEN cDNA 1700009P17 gene (1700009P17Rik)
succinate dehydrogenase complex, subunit C, integral membrane protein (Sdhc)
myelin protein zero (Mpz)
Purkinje cell protein 4-like 1 (Pcp4l1)
nuclear receptor subfamily 1, group I, member 3 (Nr1i3)
translocase of outer mitochondrial membrane 40 homolog-like (yeast) (Tomm40l)
apolipoprotein A-II (Apoa2)
Fc receptor, IgE, high affinity I, gamma polypeptide (Fcer1g)
NADH dehydrogenase (ubiquinone) Fe-S protein 2 (Ndufs2)
a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 4 (Adamts4)
betaGlcNAc beta 1,4-galactosyltransferase, polypeptide (B4galt3)
protoporphyrinogen oxidase (Ppox)
ubiquitin specific peptidase 21 (Usp21)
ubiquitin-fold modifier conjugating enzyme 1 (Ufc1)
death effector domain-containing (Dedd)
nitrilase 1 (Nit1)
prefoldin 2 (Pfdn2)
kelch domain containing 9 (Klhdc9)
poliovirus receptor-related 4 (Pvrl4)
Rho GTPase activating protein 30 (Arhgap30)
upstream transcription factor 1 (Usf1)
F11 receptor (F11r)
RNA and export factor binding protein 2 (Refbp2)
intelectin 1 (galactofuranose binding) (Itln1)
CD244 natural killer cell receptor 2B4 (Cd244)
lymphocyte antigen 9 (Ly9)
SLAM family member 7 (Slamf7)
CD48 antigen (Cd48)
signaling lymphocytic activation molecule family member 1 (Slamf1)
CD84 antigen (Cd84)
SLAM family member 6 (Slamf6)
vang-like 2 (van gogh, *Drosophila*) (Vangl2)
nescient helix loop helix 1 (Nhlh1)
nicastrin (Ncstn)
peroxisomal biogenesis factor 19 (Pex19)
WD repeat domain 42A (Wdr42a)
phosphoprotein enriched in astrocytes 15A (Pea15a)
calsequestrin 1 (Casq1)
ATPase, Na^+/K+ transporting, alpha 4 polypeptide (Atp1a4)
ATPase, Na^+/K+ transporting, alpha 2 polypeptide (Atp1a2)
immunoglobulin superfamily, member 8 (Igsf8)
potassium inwardly rectifying channel, subfamily J, member 9 (Kcnj9)
potassium inwardly rectifying channel, subfamily J, member 10 (Kcnj10 [partial]*)

*, genes located within the boundaries of the recombination sites.

Table S4. Nine candidate genes for Cgnz1 with nucleotide replacements in promoter, exon, and intro regions

Genes	Amino acid mutations	Nuclear acid mutations		
		Promoter region	Exon	Intron
Apoa2	43D>E, 49M>V, 61A>V	−262T>C, −296T>C, -424A>T, −520C>T, -638T>C, -670G>A, -746T>G, -961C>G	635A>G, 644G>A, 668A>G, **689T>A**, **705A>G**, **742C>T**, 922T>C	468T>C, 491G>C, 499C>A, 591A>G, 812C>A, 837A>G, 923G>A, 966T>C, 1062T>C, 1064T>C, 1080C>T
1700009P17Rik	—	−308C>T, −490A>G, −491C>T, −775T>C, −785T>C, −829G>A, −848G>T, −863T>C, −904G>C, −934T>A, −961C>T	1408A>G, 5107T>G	190T>C, 284C>T, 304T>C, 366G>C, 545A>T, 548T>A, 549C>G, 551G>A, 554T>C, 586C>T, 978T>C, 1072A>G, 1107G>A, 1185C>A, 1187G>A, 1214G>T, 1240C>A, 1356C>T, 1549T>G, 1833T>C, 1942T>C, 2272A>C, 2438C>T, 2498A>G, 3014G>A, 3074C>T, 3275G>C, 3440T>A, 3936A>G, 4110T>C, 4205C>T, 4208T>C, 4213T>G
Tomm40l	—	−164G>A, −183T>C, −221T>G, −259T>C, −293A>G, −530G>C, −792C>T	529A>C	180C>A, 224G>A, 405G>A, 725G>C, 735T>C, 786C>T, 833T>G, 834A>G, 1101C>T, 1211T>C, 1543G>C, 2589G>A, 2765G>A, 2811G>A, 3022T>G, 3164C>G
Ndufs2	8R>G	−1138G>A, −1259G>A, −1426T>C	**46G>C**, 105T>C, 919A>G, 964C>G, 7820A>G, 8782G>A, 9109G>A, 9142G>A, 9166A>G, 9928C>T	210T>C, 492T>C, 647A>G, 739T>C, 874G>A, 895T>C, 1129T>C, 1241C>T, 1323G>A, 1348C>T, 1874G>T, 1938G>C, 1939T>C, 1940G>C, 1982T>C, 2053C>T, 2079A>C, 2110G>A, 2459C>G, 2489C>T, 2496T>G, 2711A>G, 2804A>T, 2805A>G, 2806C>T, 2877C>T, 2915A>G, 2916A>T, 2917A>G, 2940A>G, 2965A>C, 2968A>C, 2971A>C, 3152G>T, 3201G>A, 3226C>T, 3229T>C, 3261T>C, 3284A>G, 3439C>G, 3534A>G, 3540G>A, 3585A>G, 3665T>C, 3763A>G, 4200C>T, 4225T>G, 4538T>C, 4551T>C, 4572A>C, 4590C>T, 4620C>T, 4674A>G, 4935T>C, 4990T>C, 5139C>T, 5143C>A, 5150G>C, 5197C>T, 5255G>A, 5370A>C, 5372C>T, 5843A>G, 5887T>C, 6272G>A, 6284C>G, 7058T>A, 7106G>A, 7190G>A, 7218G>C, 7242C>G, 7273G>C, 7289C>G, 7361G>C, 7569A>C, 7637C>G, 7649A>G, 7929A>G, 7931T>(DEL), 7932A>(DEL), 7987T>C, 8002T>C, 8037C>T, 8159T>G, 8496C>T, 8619T>C, 8675C>T, 8729C>G, 8733C>T, 8978C>T, 9179A>T, 9198T>C, 9218T>A, 9278G>C, 9348T>C, 9535G>A, 9595C>A, 9616T>C, 9665G>A, 9986C>T, 9994C>T, 9996C>G, 9999C>(DEL), 10000C>T, 10033T>G, 10035A>G, 10042G>C, 10045T>C, 10108T>A, 10114G>A, 10115T>C, 10166T>(DEL), 10270T>G, 10278A>T, 10834G>A, 10839A>C, 10861A>C, 11033C>T, 11153A>G, 11216A>T, 11301C>A, 11517G>A, 11738A>G, 11755A>T, 11902C>T
Pex19	55P>S	−47G>A, −75A>G	**1969C>T**, 6381A>G	174A>G, 311C>A, 1140A>G, 1145C>A, 1209A>G, 1350G>T, 1825G>A, 2197C>A, 2286C>T, 2643A>G, 2689G>C, 2852G>C, 3236A>G, 3484A>G, 3489A>G, 3490C>G, 3516T>C, 3567T>C, 3725T>C, 4204T>C, 4463T>G, 4582C>T, 4710G>C, 4996A>G, 5012A>C, 5081T>C, 5117G>A, 5878G>A, 6074A>G, 6075A>T, 6078A>(DEL), 6198C>G, 6231C>T, 6248T>A, 6589C>T, 6856G>A, 6934A>G, 6980A>G, 7027C>G, 7158T>C

Table S4. Nine candidate genes for Cgnz1 with nucleotide replacements in promoter, exon, and intro regions *(Continued)*

Genes	Amino acid mutations	Nuclear acid mutations		
		Promoter region	Exon	Intron
Casq1	—	−543A>G, −749C>T	364G>A, 430G>A, 4861G>C, 6558G>A, 9395G>C	135C>T, 495T>C, 658G>A, 804G>A, 823T>C, 1180A>G, 1224G>A, 1268A>G, 1305T>C, 1312C>A, 1415T>A, 1516T>C, 1551G>A, 1691A> G, 1812G>A, 2452G>T, 2575C>G, 2646A>C, 2671C>A, 2939T>C, 3151C>G, 3249G>A, 3369C>T, 3623G>A, 4075C>A, 4076G>A, 4226G>A, 4235C>T, 4887C>T, 5110A>C, 5305G>A, 5431G>A, 5473G>A, 5640A>G, 6295G>A, 6710T>C, 7148G>A, 7518A>G, 7855A>G, 7975G>A, 8047T>C, 8096A>G, 8124C>T, 8195G>A, 8201A>G, 8213T>A, 8267A>G, 8291T>C, 8299G>C, 8365G>A, 8518C>T, 8743C>T, 8872C>T, 9315C>T, 9321C>T, 9557C>A
Dedd	—	−223T>C, −299T>C, −621C>T, −678G>A, −684T>C	9420C>T, 9492A>C	109C>A, 1000G>T, 1668G>T, 1741T>C, 2213A>G, 2222A>T, 2379A>G, 2433C>G, 2445G>T, 2478C>(DEL), 2488C>T, 2505G>C, 2681C>T, 3094A>G, 3134C>5, 3255G>A, 3279G>T, 3687T>C, 3897G>A, 4465C>G, 5117C>T, 5209T>A, 5337C>A, 5481G>C, 5740A>G, 5790G>T, 6147G>C, 6148G>A, 6355G>A, 6384G>A, 6421G>T, 6439G>A, 6519G>A, 7353T>C, 7696G>A, 7808A>G, 7837T>A, 7838G>A, 8007G>A, 8411G>A, 8700A>G, 8836T>C, 8840G>(DEL), 8853G>T, 9072G>(DEL), 9073C(DEL), 9868G>A, 10234T>C, 10352G>A, 10356A>G, 10491C>A, 10541G>A, 10597C>T, 10910T>T, 11218A>G, 11219C>A, 11432G>A, 11540A>G
Itln1	207L>V, 289D>N, 295N>T, 302K>E	−45G>A, −51A>G, −96A>G, −191A>T, −752G>C	519A>C, 3681G>T, 4150G>A, 4689T>C, **4735A>C**, 16961A>G, **16977C>T**, **16996T>G**, **17016T>C**	27G>A, 86A>C, 365A>T, 805T>G, 1119A>C, 1137C>T, 1273A>G, 1306T>C, 1384A>G, 1512T>G, 1518G>A, 1576T>G, 1604A>T, 1646G>A, 1647C>T, 1661T>G, 1706C>T, 1960A>T, 2054C>T, 2262A>G, 2264C>G, 2293C>T, 2327C>G, 2349A>T, 2369G>A, 2505G>A, 2528T>C, 2600A>G, 2714C>T, 2777C>A, 2781G>A, 2813C>G, 2864C>G, 2907A>G, 3151T>G, 3194G>A, 3222C>T, 3272A>G, 3273A>G, 3289T>C, 3336A>C, 3394T>A, 3401T>G, 3415T>A, 3440C>G, 3442T>G, 3444A>C, 3452A>C, 3476C>T, 3477G>A, 3501T>G, 3516T>C, 4273T>A, 4331G>C, 4334A>T, 4409C>T, 4843C>T, 5098G>T, 5246T>C, 5301C>A, 5718G>A, 5929G>C, 6044T>C, 6243A>G, 6405A>G, 6548A>G, 6827T>C, 6840C>A, 6994A>G, 7014C>G, 7030C>T, 7034C>T, 7066G>T, 7067G>C, 7675T>G, 7695G>A, 7906C>A, 8001T>C, 8075C>G, 8182A>T, 8187C>A, 8311T>G, 8408A>T, 8725T>C, 8807C>A, 8895G>T, 8927G>C, 8951C>T, 9053A>G, 9094G>A, 9176A>T, 9355T>C, 9365T>C, 9391A>T, 9451C>T, 9500T>G, 9554T>C, 9596A>C, 9725G>A, 9794C>A, 9839T>C, 9928A>G, 9979C>T, 9988C>G, 10015C>A, 10033T>A, 10039T>C, 10066G>A, 10068T>C, 10093T>C, 10098T>C, 10253C>T, 10303T>C, 10457T>A, 15835A>(DEL), 16121C>T, 16626T>C, 16672A>G, 16729A>T, 16754C>T, 16775A>G, 16779A>G, 16868C>G, 16891T>C, 17126C>T, 17127C>G
Pea15a	—	−237C>G, −262A>G, −297T>C, −316T>C, −575A>T, −670A>G, −753T>C, −775C>T, −846A>G, −859G>T, −891A>G, −946A>T	6331A>G, 7532A>T	321T>C, 595G>T, 712A>C, 733C>G, 839T>C, 1523C>T, 1651T>G, 1797T>C, 1859C>G, 1860T>A, 2252A>G, 2326C>T, 2342G>T, 2402G>T, 2883C>G, 3105G>C, 3193C>T, 3336A>G, 3737G>C, 3800A>G, 3851G>A, 5288T>C, 5353G>A, 5367G>A, 5922C>A, 6181A>C, 7104T>G, 8053C>T, 8381C>T, 8388T>A, 8690A>G, 9191A>G, 9702G>A

Bolding and underlining indicate that the nucleotide change would change the amino acid to be coded. This means that the point mutation is nonsilent mutation.