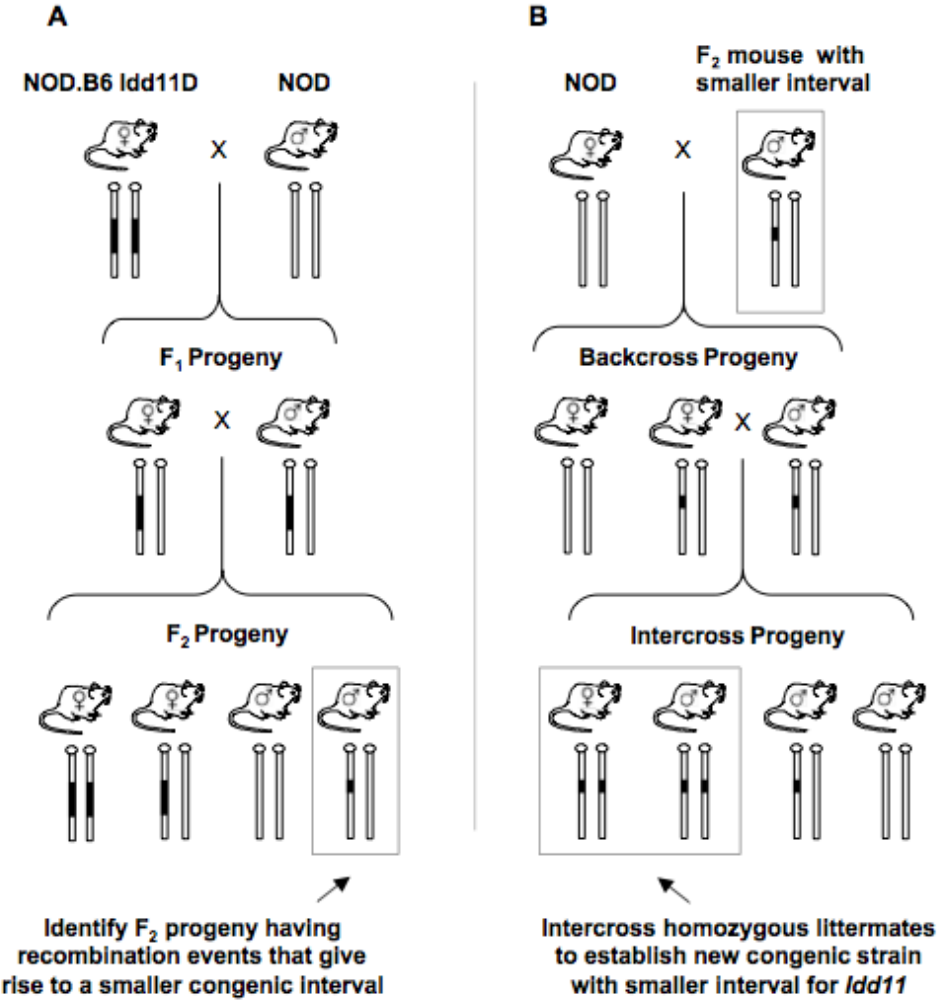
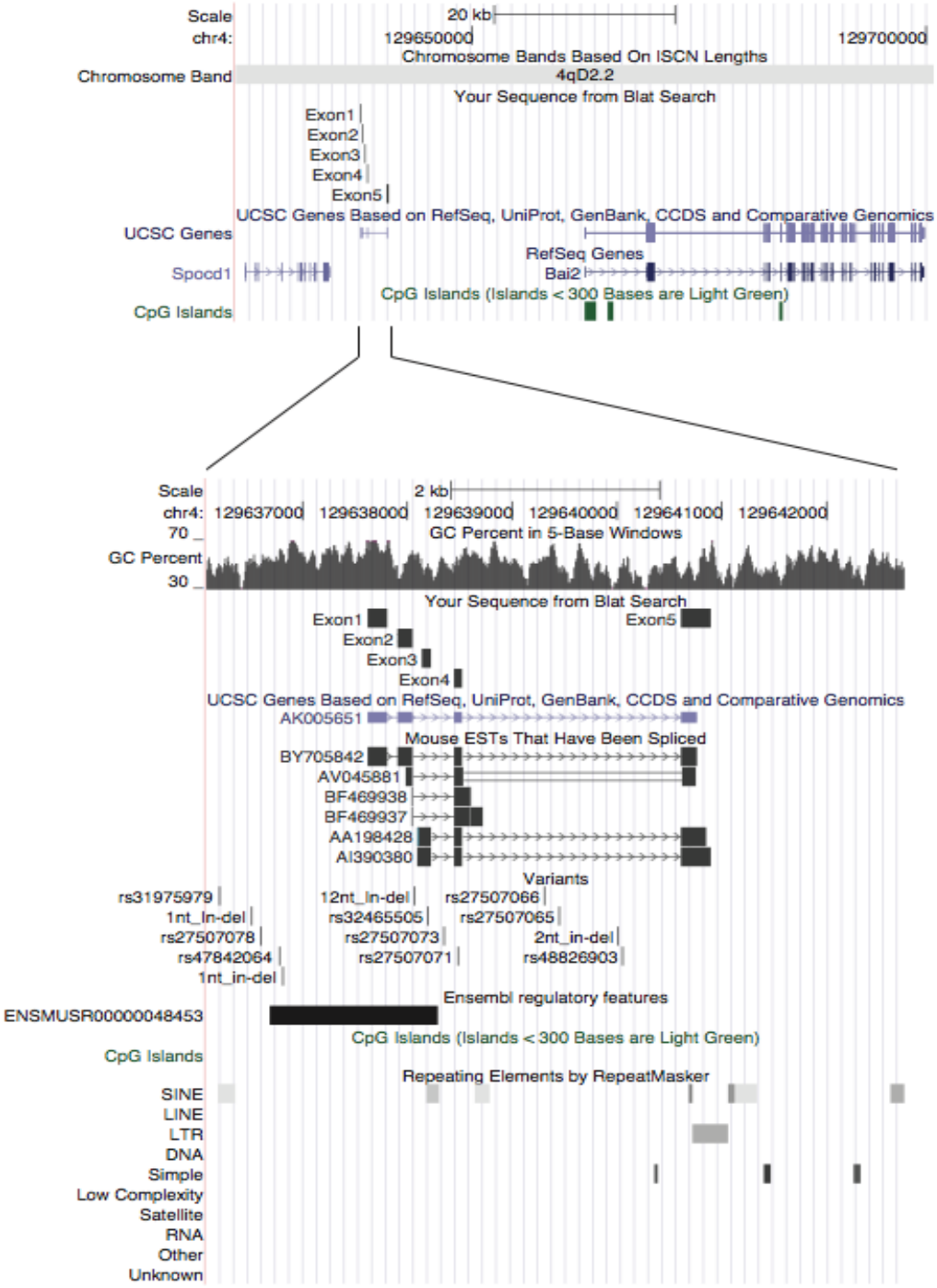
Tan *et al*. SUPPLEMENTAL DATA

Supplemental Figure 1 Schematic diagram of breeding strategy for *Idd11* congenic mouse strains



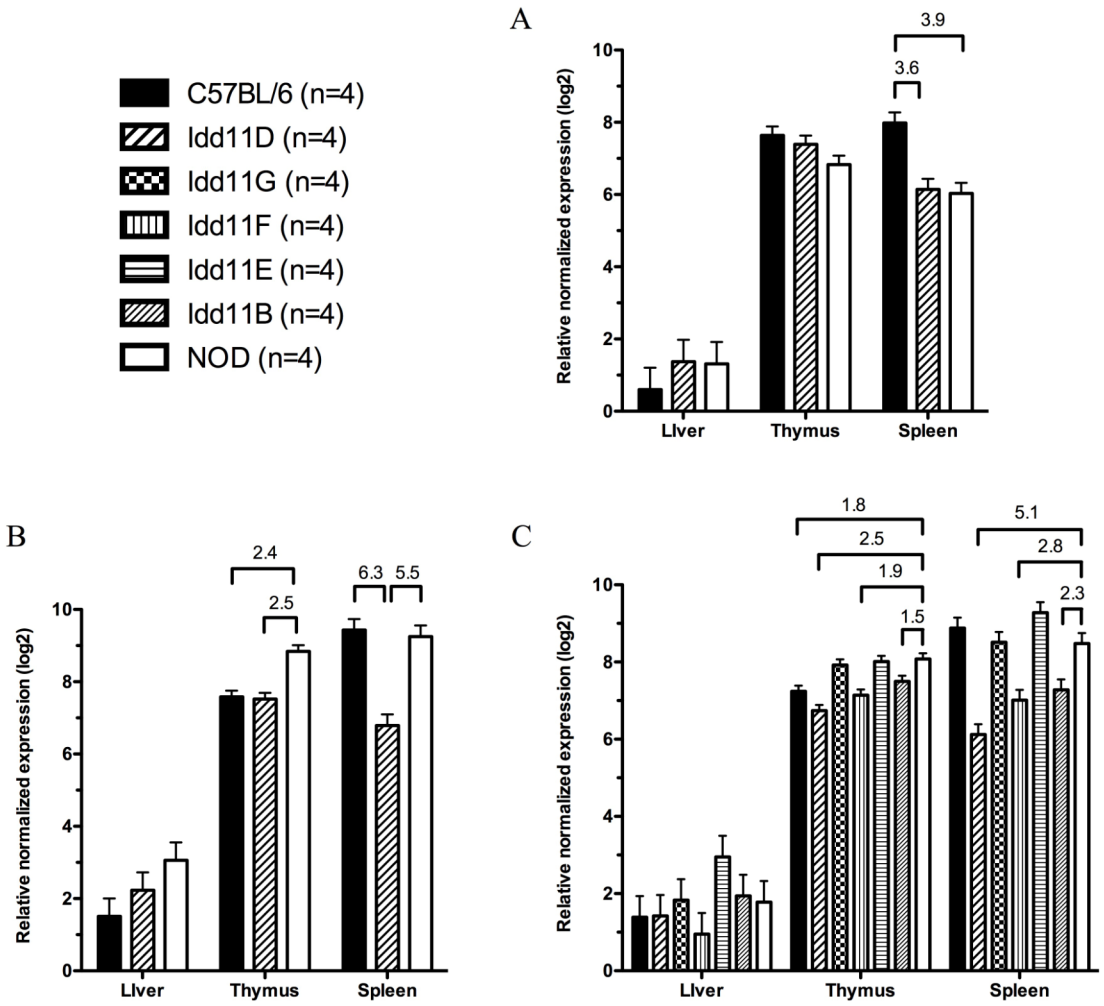
Our series of congenic mouse strains was generated using a conventional breeding approach. The NOD.B6Idd11B (Idd11B) and NOD.B6Idd11D (Idd11D) congenic strains were established as previously described (Brodnicki *et al*. 200 Immunogenetics 51:37; Brodnicki *et al.* 2005 Diabetes 54:3453). Briefly, NOD and C57BL/6 mice were crossed to generate (NOD x C57BL/6)F_1 females, which were then backcrossed to NOD males. Nine subsequent backcrosses were then performed using NOD males or females and appropriate backcross progeny based on genotyping results. C57BL/6-derived Chr4 intervals (e.g. Idd11B or Idd11D) were fixed to homozygosity on the NOD background by brother-sister matings using the tenth backcross generation (note: a 10cM averaged genome-wide marker panel detected no B6-derived alleles outside the defined congenic intervals). Idd11E, Idd11F, and Idd11G congenic mouse strains were derived from the Idd11D congenic strain as follows: (A) Idd11D mice were crossed to NOD mice to generate (Idd11D x NOD)F_1 progeny. These F_1 progeny were then intercrossed to generate F_2 progeny, which were genotyped for genetic markers across the Idd11D C57BL/6-derived interval. (B) F_2 mice having smaller congenic intervals due to recombination events were then backcrossed to NOD mice. Backcross progeny that were heterozygous for the identical smaller congenic interval, based on genotyping, were intercrossed. Intercross progeny were genotyped and homozygous littermates for the defined interval were mated to establish a new congenic mouse strain (e.g. Idd11E, Idd11F, Idd11G).

Supplemental Figure 2 Genomic interval on mouse Chr4 encompassing *Idd11*



This schematic diagram is adapted from snapshots provided by the UCSC Genome Bioinformatics genome browser (NCBI Build 37/mm9: http://genome.ucsc.edu). Repeat masker analysis detected some homology between *AK005651* genomic sequence and repetitive elements, but it is not clear what effect this sequence has upon *AK005651* regulation or function. Neither GC-content, CpG-island, nor GC-skew (not shown) analyses pointed to obvious regulatory features in or around *AK005651*. Other genomic features presented in this figure (e.g. Ensembl regulatory features - release 57 Mar 2010, ESTs) and potential effects of sequence variation are described in the main text.

Supplemental Figure 3 Expression analysis of *Spocd1* and *Bai2*.



Quantitative real-time PCR was performed to detect expression differences between mouse strains at ~50 days of age for *Spocd1* (A) and *Bai2* (B, C) as described in the Methods. Approximate fold change is shown only for significant pair-wise comparison between NOD and the other mouse strains ($p<0.05$, adjusted for multiple testing). Bars represent mean expression ($\pm$ pooled SEM for each tissue). See Supplemental Table 9 for oligonucleotides used for real-time PCR.

Results: (A) Thymic expression of *Spocd1*, based on the spliced product of the last two exons, was not significantly different between NOD, C57BL/6 or Idd11D. Splenic expression of *Spocd1* was significantly greater in C57BL/6 mice, but expression in Idd11D was not significantly different to that in NOD. These results indicate that *Spocd1* is not likely to be affected by sequence variation within *AK005651*. (B) In contrast to *Spocd1*, thymic and splenic expression of *Bai2*, based on the spliced product of the last two exons, was significantly decreased in Idd11D mice compared to NOD mice. (C) Further analysis of new cohorts of NOD, B6 and congenic strains, which dissect the Idd11D interval, indicated that regulation of *Bai2* expression mapped distal to sequence variant #4 within the *Idd11* haplotype – Idd11G, and Idd11E do not harbor B6-derived intervals for *Bai2* and lack decreased *Bai2* expression as observed in Idd11B, Idd11D and Idd11F. While these experiments do not conclusively eliminate the possibility that sequence variation within *AK005651* can affect *Bai2* expression, it seems unlikely that *Bai2* expression, due to *AK005651* sequence variation, is contributing to diabetes susceptibility in our series of congenic mouse strains. The simplest interpretation of our data for *AK005651*, *Spocd1* and *Bai2* is that sequence variation within *AK005651* affects expression of *AK005651* and susceptibility to T1D.

Supplemental Table 1 Novel nucleotide-repeat markers polymorphic between NOD and B6 mice

Marker	PUID[a]	Chr4 coordinates[b]	Forward Oligonucleotide	Reverse Oligonucleotide
D4Wehi1	10544425	129,422,665	CCAAAGACAGGGCTTTCAATAA	TGAGTACACTGTAGCTGGGAATTGA
D4Wehi2	10544436	129,521,871	TCAGCAGTGATCAGGAAGTTG	ATTAAAGGCATGAGCCACCA
D4Wehi3	10544440	129,610,665	TGGAGGTGATAGAGGGTGACA	ATGAACGGCAGTCTCAAAGG
D4Wehi4	10544441	129,614,246	TCCACAATTTTGCGTTTCTT	CGGGGAATTACCGTCTGATA
D4Wehi5	10544442	129,633,461	CCCACCTCAGTGTCAGGAAG	TTCAAGGCCTGAAAAGAGGA
D4Wehi6	10544443	129,640,320	TCATGTGCTTGGGTCTGGTA	CAGCCCCATAGAGAGACAGG
D4Wehi7	10544444	129,641,347	CAAGCAGAACCCACAATGAA	TGGGTGTGGATAGTTTTGGAG
D4Wehi8	10544445	129,641,346	CCAAGCAGAACCCACAATG	TGGAGTGGGAGCAGTATTCA
D4Wehi9	10544446	129,642,226	TCCGGCCTAGTCTTTGTGAG	ATCCAGAAGAAGCAGGGTCA
D4Wehi10	10544426	129,645,417	AGCACTGGAGGGGGAATATC	GGGGGAGAGGAGCTATACCA
D4Wehi11	10544427	129,656,433	GGGTGCAGTCTTTGTGTGTG	TGGCGTTGTACACATATGCTC
D4Wehi12	10544428	129,657,159	GGAAGAGGATCCACATTGAG	AGAGAAGGGCCCAATGAAAC
D4Wehi13	10544429	129,666,984	ATGCATGTGTGCCTGTTCAT	TGGGCCCAGAGACATATACA
D4Wehi14	10544430	129,708,644	TCCAAGCATCACAGATGACAG	CCAGCTTGACTTCTCCATGTT
D4Wehi15	10544431	129,709,644	CAGGTGGATAGGGAAGTTGG	AAGGCATTTGCCACTACACC
D4Wehi16	10544432	129,709,898	GTGGCAAATGCCTTTAATCA	CTCTGCAGACCAAGGTAGCC
D4Wehi17	10544433	129,711,291	AAGGGATGCTGAGGTCACAC	TCTTCTCCCGAGGCTGTATC
D4Wehi18	10544434	129,746,066	CACGGAGCTGATGCTTCTGT	GCTGCTCTTCCAAAGGACTG
D4Wehi19	10544435	129,838,431	AGCAGGAAGCAGGATGCTC	CTGCTACCAGCATCCCAATA
D4Wehi20	10544437	129,945,779	AGGGAGAGGGGATGGTTTTA	CATCTGATCACCCACCCAAG
D4Wehi21	10544438	130,392,752	AAACATTTACTTTCTGAGTGTG	CAGGAAAAACAAGGGGCTCT
D4Wehi22	10544439	132,008,637	GGAAAGCCACAGAGAAGACC	CAAGGCAAGGTCTGATGCTT

[a]The PUIDs (Probe Unique ID) are for these markers in the NCBI Probe Database. [b] Genomic coordinates were obtained from the UCSC Genome Bioinformatics browser (NCBI Build 37/mm9: http://genome.ucsc.edu), based on the genomic coordinates of the forward oligonucleotide. These oligonucleotides flank nucleotide repeats that are polymorphic between NOD and C57BL/6 mouse strains. Note: *D4Wehi7* and *D4Wehi8* represent different forward and reverse oligonucleotides to amplify the same nucleotide repeat.

Supplemental Table 2 Primer pairs for genomic PCR products spanning the *Idd11* critical interval

Forward Oligo	Reverse Oligo	Chr4: Start - End (bp[a])	Product Size
ACCACAGCCTGTAAGCCACT	GAGACGCTCTCTCCATATCCAA	129,635,820 – 129,636,702	883 bp
GGATAGGTCAGGCAGGGATT	GGAAGGGCAAACTGAACCTCTA	129,636,437 – 129,637,351	915 bp
CTGGAGCCCCTCTTTCTACC	CGCAGTTCGCTAAAACCCTTT	129,636,849 – 129,637,668	820 bp
CAACTTGGGTGGCTTTCCTAAC	GCAAAGCCAGGAGAACTGTC	129,637,188 – 129,638,015	828 bp
TCACCCTATTGCTCCCAAAG	TGCTTGCATAGTCCCAAGAA	129,637,888 – 129,638,895	1008 bp
GTGTCCGGATCCCTTGTATTCT	CCGGTGGTTGACAGTCGTAT	129,638,581 – 129,639,619	1039 bp
GGGGCCAATTAAGTCTCTATCC	CAGCCCCATAGAGAGACAGG	129,639,419 – 129,640,471	1053 bp
TGTGTTCTTCATGTGCTTGG	GGCTAGCCCTAGGCTCACTT	129,640,312 – 129,641,729	1418 bp
GAGCAAAACCAAGCAGAACC	GACCAGCATCCAGAAGAAGC	129,641,338 – 129,642,414	1077 bp

[a] Genomic coordinates were obtained from the UCSC Genome Bioinformatics browser (NCBI Build 37/mm9: http://genome.ucsc.edu).

Supplemental Table 3 Oligonucleotides for genotyping *Idd11* sequence variants

Marker	Forward Oligo (5' – 3')	Reverse Oligo (5' – 3')	Probe (VIC)[a]	Probe (FAM)[a]
Variant #1 (ss262803379)	GACTGCGCATGCGTGAGT	CGGCCACCGTCAAAAGTCT	CCTCTCGGTGTTCTC	CCACCTCAAACCGAGCA
Variant #2 (rs32465505)	TCCTAACCGAAGACTCAGTTCCTT	CCTAAGACGACACAGCCAGAAAA	TTGTTGGACCTCAGTTCT	TTGGACCCCAGTTCT
Variant #3 (rs27507073)	CTTTGGCGCACACTCGTT	AGGCAGAAAACAACCACACACT	CTGTGCACCAGGACAT	TGTGCACCGGGACAT
Variant #4 (rs27507071)	GGCAGGAGAAACTTCCAGATGT	GGTCTGGCCAATATTTCTCATCTCA	CAGGGCAGACCGGATT	CAGGGCAAACCGGATT
Variant #5 (rs27507066)	CATACCTTGTGGTTGTCACTCTGA	GCTACAGAGAAGGGACTGATCTACT	CCAGCAGAGAGCAGT	CCAGCAGAAAGCAGT
Variant #6 (rs27507065)	GGCTGGCCTGCCTGTGT	CAGGTGTTTGCTGCCTTATTAGC	CTAGCTGCGCTGAT	CTAGCTGCGCCGAT
Variant #7 (ss262803405)	CCCATGTCACACAGAGCTAGAAAT	TGGCAAACATGGTATGTATGCA	CTTCATACACATGAGGTCAT	AGCTTCATACACATGGTCA
Variant #8 (rs48826903)	GTCATATTTGCATACATACCATGTTTGCC	CCTCACTAAGATGACCCTAAGCAA	TGGCCATCGGGAGAT	TGGCCATCAGGAGAT

[a]VIC Taqman probes detect C57BL/6 sequence variant, FAM Taqman probes detect NOD sequence variant

Supplemental Table 4 Sequence variants for inbred mouse strains within the critical interval (6.9kb) for *Idd11*

Sequence Variant (accession #)	Chr4 Position [a]	C57BL/6	NOD	129/Sv	WSB	SJL	SWR	FVB	NON	A/J	CBAN	C3H	DBA/2	ALR	ALS	AKR	CTS	BALB/c	NZW	NZO	CAST	PWD	NZB	DBA/1	NOR	MOLF	C57BL/10
rs31975979	129,636,201	A	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	A	A	A	A	A	A
ss262803370	129,636,514	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	G	G	G	G	G	G
rs27507078	129,636,594	A	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	A	A	A	A	A	A
ss262803372	129,636,773	C	C	C	C	C	C	C	T	T	T	T	T	T	T	T	T	T	T	T	C	C	C	C	C	C	C
rs47842064	129,636,778	T	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	T	T	T	T	T
ss262803374	129,636,801	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	T	T	T	?	T
rs32717076	129,636,955	G	G	G	G	G	G	G	C	C	C	C	C	C	C	C	C	C	C	C	?	G	G	G	?	G	G
ss262803376	129,637,001	-	-	-	-	-	-	-	G	G	G	G	G	G	G	G	G	G	G	G	-	-	-	-	?	-	-
rs27507077	129,637,195	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	A	G	G	G	G	G
rs27507076	129,637,947	G	G	T	T	T	T	T	G	G	G	G	G	G	G	G	G	G	G	G	T	G	G	G	G	G	G
ss262803379 [b]	129,638,063	ins	del	ins	ins	ins	ins	ins	ins	ins	ins	ins	ins	ins	ins	ins	ins	ins	ins	ins	ins	ins	ins	ins	ins	ins	ins
rs27507075	129,638,113	G	G	G	G	G	G	G	A	A	A	A	A	A	A	A	A	A	A	A	G	G	G	G	G	G	G
rs27507074	129,638,129	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	T	C	C	C	C	C	C
ss262803382	129,638,175	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	G	G	C	C	C	C	C
rs32465505	129,638,192	T	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	T	C	T	T	T	T	T
rs32897619	129,638,211	C	C	T	T	T	T	T	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C
ss262803385 [c]	129,638,266	ins	ins	ins	ins	ins	ins	ins	ins	ins	ins	ins	ins	ins	ins	ins	ins	ins	ins	ins	del	ins	ins	ins	ins	ins	ins
rs27507073	129,638,344	T	C	C	C	T	T	T	C	C	C	C	C	C	C	C	C	C	C	C	T	T	T	T	T	T	T
rs27507072	129,638,364	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	A	G	G	G	G	G	G
ss262803388 [d]	129,638,415	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	ins	del	del	del	del	del	del
rs27507071	129,638,482	G	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	G	G	G	G	G	G	G
ss262803390 [e]	129,638,607	ins	ins	del	del	ins	ins	ins	ins	ins	ins	ins	ins	ins	ins	ins	ins	ins	ins	ins	ins	ins	ins	ins	ins	ins	ins
ss262803391	129,638,812	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	C	T	T	T	T	T	T
ss262803392	129,638,833	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	A	G	G	G	G	G	G
rs27507070	129,638,904	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	A	G	G	G	G	G	G
ss262803394	129,638,958	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	G	C	C	C	C	C	C
rs27507069	129,638,974	T	T	T	C	C	C	C	T	T	T	T	T	T	T	T	T	T	T	T	C	T	T	T	T	T	T
rs27507068	129,639,182	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	C	G	G	G	G	G	G
ss262803397	129,639,284	G	G	G	G	T	T	T	G	G	G	G	G	G	G	G	G	G	G	G	T	G	G	G	G	G	G
rs27507067	129,639,290	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	C	T	T	T	T	T	T
rs27507066	129,639,302	C	T	T	T	C	C	C	T	T	T	T	T	T	T	T	T	T	T	T	C	C	C	C	C	C	C
ss262803400	129,639,448	C	C	C	C	T	T	T	C	C	C	C	C	C	C	C	C	C	C	C	T	C	C	C	C	C	C
rs27507065	129,639,451	T	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	T	T	T	T	T
ss262803402	129,639,812	CC	CC	CC	CC	CC	CC	CC	CC	CC	CC	CC	CC	CC	CC	CC	CC	CC	CC	CC	GA	CC	CC	CC	CC	CC	CC
ss262803403	129,639,873	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	T	C	C	C	C	C	C
ss262803404 [f]	129,639,913	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	del	ins	del	del	del	del	del	del
ss262803405	129,640,008	AG	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	AG	AG	AG	AG	AG	AG	AG
rs48826903	129,640,045	C	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	C	C	C	C	C	C

[a]Genomic coordinates were obtained from the UCSC Genome Bioinformatics browser (NCBI Build 37/mm9: http://genome.ucsc.edu). [b]ins/del = CCTCTCGGTGTT. [c]ins/del = TAGGTG. [d]ins/del = CCCCCCCC. [e]ins/del = CCGGCA. [f]ins/del = GTGTCACA. nd – sequence variant not described previously. No shading = NOD and C57BL/6 have identical sequence, Grey shading = C57BL/6 sequence, Orange shading = NOD sequence, Pink shading = sequence not identical to NOD or C57BL/6 sequence.

Supplemental Table 5 Genomic structure of *AK005651*

Genomic element	Chr4 Start – End (bp[a])	Size
Exon 1	129,637,618 – 129,637,805	188
Intron 1	129,637,806 – 129,637,907	102
Exon 2	129,637,908 – 129,638,052	145
Intron 2	129,638,053 – 129,638,139	87
Exon 3[b]	129,638,140 – 129,638,224	85
Intron 3	129,638,225 – 129,638,442	218
Exon 4	129,638,443 – 129,638,524	82
Intron 4	129,638,525 – 129,640,615	2091
Exon 5	129,640,616 – 129,640,901	286

[a] Genomic coordinates were obtained from the UCSC Genome Bioinformatics browser (NCBI Build 37/mm9: http://genome.ucsc.edu).

[b] Note: Exon 3 size is alternatively spliced as detected by RT-PCR and sequence analysis (data not shown).

Supplemental Table 6 Summary of Bioinformatic Analysis

Method[a]	Result Summary
UCSC genome browser	The proposed *Idd11* haplotype and recombination hotspot are encompassed by *AK005651*, an uncharacterized GenBank mRNA, located at chr4:129637618-129640764 (NCBI Build 37) and supported by a number of mouse ESTs including BY705842, AV045881, AA198428, AI390380.
BLAT sequence alignment	All *AK005651* exon sequences align within Chr4:129,637,618-129,640,901 of the mouse genome (NCBI Build 37). This interval is contained within a syntenic block, Chr4:102,986,087-155,610,416, that is orthologous to the human genomic interval on Chr1:884,178-58,785,354 (NCBI Build 36.1). The orthologous transcript maps approximately to human Chr1:32,023,718-32,026,832. This region contains unspliced human ESTs (CV390389, BF351649, DA803845) that overlap with the alignment of *AK005651* to the human genome.
Multiz/phastCons	The mouse locus shows strong sequence conservation across eutherian mammals and more limited conservation to marsupials. Sequence conservation overlaps with exon 1, 2 and 5 of *AK005651*. Additional sequence conservation can be found upstream of exon 1 and within the last intron between exon 4 and 5.
BLASTX and BLASTN	The BLASTX search of the NR protein database revealed significant matches (E-value<10^{-5}) to only five hypothetical mouse peptide sequences (EDL30156, EDL30157, EDL30155, XP_001473403, XP_001475645). None of these represent complete or convincing gene models. The BLASTN search of the NCBI EST database revealed significant matches (E-value<10^{-5}) to nine mouse ESTs (BY705842, AV045881, AI390380, AA198428, AV039251, AV046306, CJ150532, BF469938, BF469937), two human ESTs (CV390389, DA803845), and one rat EST (CB726336). Of these ESTs, only the mouse ESTs represent spliced transcripts.
PFAM	The six-frame translation of *AK005651*, including both splice variants, revealed no significant alignments (E-value<10) to known domains.
RFAM	Neither of the two splice variants demonstrates matches with non-coding RNA families (E-value<10).
miRBase	The BLASTN search of miRBase revealed no significant matches (E-value<0.1) to mature miRNAs or stem-loop sequences.

[a]See Methods section for description and references.

Supplemental Table 7 Exon codons affected by *Idd11* haplotype variants #2 and #4

SNP Location	Exon	C57BL/6 codons	NOD codons
Chr4: 129,638,192	3	CC**T**CA	CC**C**CA
Variant #2	ORF 1	P	P
rs32465505	ORF 2	L	P
	ORF 3	S	P
Chr4: 129,638,482	4	CA**G**AC	CA**A**AC
Variant #4	ORF1	Q	Q
rs27507071	ORF2	R	K
	ORF3	D	N

Nucleotides that are bolded and underlined are the sequence differences between C57BL/6 and NOD mouse strains for these variants.

Supplemental Table 8 Transcription factor binding site predictions

Variant	TRANSFAC predictions[ab]
Intron 2 Variant 1 ss262803379	1 ----><u>V$KID3_01</u>(1.00) ----------><u>V$SPZ1_01</u>(0.96) 2 ----------><u>V$PAX8_01</u>(0.91) <----<u>V$KID3_01</u>(1.00) 3 <----<u>V$KID3_01</u>(1.00) CGATGGCCACCTGGACTGCGCATGCGTGAGTTTTG**<u>CCTCTCGGTGTT</u>**CTCGGTTTGAGGTGGGTGGGAGAC 71
Exon 3 Variant #2 rs32465505	1 <----------<u>V$PAX3_B</u>(0.96) ACTCAGTTCCTTAAACAACCGTGACTTGTTGGACC**<u>T</u>**CAGTTCTGCCTTTTCTGGCTGTGTCGTCTTAGGTT 71
Intron 3 Variant #3 rs27507073	1 <----------<u>V$E2F_Q6_01</u>(0.95) 2 ----------><u>V$E2F_03</u>(0.96) TGGACTGCAACTTTGGCGCACACTCGTTGATGTCC**<u>T</u>**GGTGCACAGTAGGCAGTGTGTGGTTGTTTTCTGCC 71
Exon 4 Variant #4 rs27507071	1 <----------<u>V$HAND1E47_01</u>(0.94) AGACATGGCAGGAGAAACTTCCAGATGTCAGGGCA**<u>G</u>**ACCGGATTCCAGCCGTGAGATGAGAAATATTGGCC 71
Intron4 Variant #5 rs27507066	No TRANSFAC TFBS predicted TGGTTGTCACTCTGACCGCTGTATACCGGACTGCT**<u>C</u>**TCTGCTGGCAGTAGATCAGTCCCTTCTCTGTAGCC

[a] Sequence variants are shown in bold underlined red font (B6 sequence is provided)
[b] Match scores are shown in parentheses.
Note: dashes indicate the transcription factor binding site above the sequence, the arrows indicate strand

Supplemental Table 9 Oligonucleotides for real-time PCR

Gene	Forward Oligo (5' – 3')	Reverse Oligo (5' – 3')	Probe (FAM-labelled)
Hprt1	TCCTCCTCAGACCGCTTTT	CCTGGTTCATCATCGCTAATC	AGTCCCAG
Hprt1	Taqman Gene Expression Assay - Mm01545399_m1		
Hmbs	TCCCTGAAGGATGTGCCTAC	AAGGGTTTTCCCGTTTGC	CCTCCTGG
Hmbs	Taqman Gene Expression Assay - Mm01143545_m1		
AK005651 (Exon 2 & 3)	TCTCCTGGCTTTGCTTTCATC	TGTTTAAGGAACTGAGTCTTCGGTTAG	CGCATGCAAACAT
AK005651 (Exon 2 & 4)	TCTCCTGGCTTTGCTTTCATC	GCCCTGACATCTGGAAGTTTCT	CGCATGCCTCCAGAC
AK005651 (Exon 4 & 5)	GATGAGAAATATTGGCCAGACC	AGATAGCATTCTCCTGCCTCA	ACTGGGAA
AK005651 (Exon 4 & 5)	AGCCGTGAGATGAGAAATATTGG	GAACCTTCAGGTCCATTTCTTTAGAG	ACCAGGGTCTTCCATC
Spocd1 (Exon 9 & 10)	CTGCCTTTGAGCCTCTGC	AGGCTCGTGTGAGTAATTTCAAG	CCAGGCTG
Bai2 (Exon 29 & 30)	CACACTTTCGACCGCTACC	CCTCCTGTGCTGGGACAA	TCCTCAGC