SUPPLEMENTAL INFORMATION

Ethics Statement

The studies described here have been reviewed and approved by the Animal Care and Use Committees at The University of Chicago and Rutgers University which are both accredited by the Association for Assessment and Accreditation of Laboratory Animal Care (AAALAC).

SUPPLEMENTAL FIGURE LEGENDS

Figure. S1. Related to Figure 4. Characterization of *Ob*-deficient mice generated by CRISPR/Cas9 technology.

(**A**) Western blot analysis of lysates of B cells purified from $Ob^{-/-}$, $Ob^{+/-}$ and $Ob^{+/+}$ mice probed with antibodies against the Oβ luminal domain (top) and β-actin as a loading control (bottom). Purified $Ma^{-/-}$ B cells were used as a negative control. Numbers below strain names indicate individual mice. Two independent $Ob^{-/-}$ founder mice strains were analyzed. $Ob^{-/-}$ mice 1 and 2 were derived from founder mouse line 134 and mice 3 and 4 were from founder line 4905. Graphs at the bottom show quantification of Oβ levels normalized to the level obtained for $Ob^{+/+}$ B cells. Results show that $Ob^{-/-}$ mice express no detectable Oβ protein and that $\mathrm{Ob}^{+/-}$ mice express approximately half the level of $\mathrm{Ob}^{+/+}$ mice. Data are representative of two similar experiments. Significance was calculated using an unpaired *t* test.

(**B**) Representative FACS analysis of spleen cells from $Ob^{+/+}$, $Ob^{+/-}$ and $Ob^{-/-}$ mice (both 134 and 4905 lines were analyzed) showing the frequency of B cells (top plots, defined as B220^{+} CD19^{+}), total dendritic cells (DCs; middle plots, defined as CD11c^{+}) and two DC subsets (bottom plots), CD8α^{+} DCs (defined as CD11c^{+} MHC-II^{+} CD8α^{+} CD205^{+}) and CD8α^{-} DCs (defined as CD11c^{+} MHC-II^{+} CD8α^{-} CD205^{-}). Graphs to right of FACS plots show a summary of frequencies for all mice analyzed. Data are presented as the frequency of total spleen cells for B cells and total DCs or the frequency in the CD11c$^+$ DC gate for the CD8α DC subsets. Results show that *Ob*-deficiency does not alter antigen presenting cell development since all populations were present at similar frequencies in the spleens of *Ob*$^{+/+}$, *Ob*$^{+/-}$ and *Ob*$^{-/-}$ mice.

Figure S2. Related to Figure 4. MMTV-infected *Oa*- and *Ob*-deficient mice produce virus-neutralizing antibodies.

(**A**) Purified MMTV virions were incubated with the sera from MMTV-infected *Oa*$^{-/-}$ mice and injected i.p. into BALB/cJ mice. Five weeks after injection, mice were bled and peripheral T cells were analyzed by FACS for the percentage of SAg-cognate CD4$^+$T Vβ6$^+$ cells among CD4$^+$ T cells. Their deletion was used as an indicator of virus infectivity. Each dot is a mean of percent of CD4$^+$ Vβ6$^+$ T cells among CD4$^+$ T cells analyzed in three mice injected with the virus incubated with the same serum sample. n, numbers of sera used (combined data with calculated % of neutralization are shown in Figure 4A).

(**B**) Sera from infected *Ob*$^{-/-}$ mice were incubated with purified MMTV(LA) and injected into footpads of BALB/cJ mice. Four days after injection, cells isolated from the draining popliteal lymph node were analyzed by FACS for the percentage of CD4$^+$ Vβ6$^+$ T cells among CD4$^+$ T cells. The proliferation of SAg-cognate T cells was used as indicator of virus infectivity. Each dot is a mean of percent of CD4$^+$ Vβ6$^+$ T cells among CD4$^+$ T cells analyzed in nodes draining the sites of injection with the virus incubated with the same serum. n, number of the sera tested (combined data with calculated % of neutralization are shown in Figure 4B). Sera from infected B6$^{vic1i/i}$ and uninfected B6 (*Oa*$^{+/+}$ and *Ob*$^{+/+}$) were used as positive and negative controls, respectively. Significance was calculated using an unpaired *t* test.

(C) MMTV-neutralizing capacity of antibodies was also tested in the offspring produced by injected females (3 litters from each line). Females from infected *Ob*$^{-/-}$ and B6$^{vic1i/i}$ but not B6 females produced uninfected offspring. n, number of mice screened.

Figure S3. Related to Figure 6. Identification of human DOB variants with altered function.

(**A**) Approach used to measure MHCII-CLIP, DO, DM and MHCII levels after expression of DOB variants in HeLa.CIITA cells. HeLa cells stably expressing CIITA (MHCII+, DM+ and low levels of DOA) were transiently transfected with control vectors lacking inserts (IRES-mRuby / IRES-AcGFP) or with only DOA*0101 (most common DOA allele; DOA-IRES-mRuby /I RES-AcGFP) or only DOB*0101 (most common DOB allele; IRES-mRuby / DOB-IRES-AcGFP) or vectors expressing both DOA*0101 and DOB*0101 (DOA-IRES-mRuby / DOB-IRES-AcGFP) and 72 hours later cells were surface stained with Abs specific for MHCII and MHCII-CLIP or fixed, permeabilized and stained with Ab specific for the DO or DM heterodimers followed by flow cytometric analysis. Cells were gated for the expression of mRuby which reports DOA expression and AcGFP which reports DOB expression (Ruby+ GFP+) followed by gating for MHCII+ cells. MHCII-CLIP levels were then determined by measuring the gMFI for the Ruby+ GFP+ MHCII+ cells (top). For the determination of DO levels, cells were gated for mRuby and AcGFP followed by the selection of DM+ cells and the DO gMFI was determined in these cells (Ruby+ GFP+ DM+) (bottom). Fixation of cells results in decreased mRuby and AcGFP fluorescence. The gMFI fluorescence levels for MHCII-CLIP and DO are indicated on the left side of the respective histograms. DO expression and increased MHCII-CLIP levels were observed only after transfection of vectors expressing both DOA and DOB. Data is representative of 5 similar experiments.

(**B**) MHCII-CLIP, DO, DM and MHCII levels after expression of the 32 DOB variants in HeLa.CIITA cells. HeLa.CIITA cells were transiently transfected with a vector expressing DOA*0101 (DOA-IRES-mRuby) together with vectors expressing one of the 32 DOB variants and analyzed as in panel S3A. The gMFI for MHCII-CLIP, DO, DM and MHCII for each DOB variant were determined and normalized to the gMFI value obtained after transfection of DOA*0101 and DOB*0101. Seven of the DOB variants were frameshift and stop mutants and did not produce detectable DO (see also Figure S4A). Thus, the average gMFI obtained for MHCII-CLIP and DO was subtracted from the gMFI values obtained for the other 25 DOB variants to remove background staining prior to normalization with the gMFI obtained for DOB*0101. The DOB variant transfected is indicated on the Y-axis of each graph and the relative expression of MHCII-CLIP, DO, DM and MHCII is indicated on the X-axis. Open circles represent results from individual experiments and bars represent the mean +/- SD. Data was combined from 3-4 individual experiments.

Figure S4. Related to Figure 6. Frameshift and stop codon DOB variants do not make functional DOB protein and detailed analysis of DOB G77V.

(**A**) Western blot analysis of lysates from Hela.CIITA cells transiently transfected with vectors encoding for DOA*0101 and the indicated DOB alleles were probed with antibodies specific for the cytoplasmic tails of DOβ (top) and DMβ (middle) or β-actin as a loading control (bottom). Transfection with DOA*0101 and DOB*0101 was used as a positive control. Data are representative of 3 similar experiments.

(**B**) Differences in ability of DOB*0101 and DOB G77V to suppress DM function. HeLa.CIITA cells transfected with DOA*0101 and DOB*0101 or DOB G77V were surface stained for MHC-II and MHC-II-CLIP followed by analysis by flow cytometry. Resulting plots were analyzed by gating for mRuby expressing cells, which reports DOA expression and then for MHC-II (not shown). AcGFP levels (reports DOB expression) in the mRuby+ MHC-II+ cells were divided into bins (1-5) based upon fluorescence as indicated and the gMFI for MHCII-CLIP in each bin was determined and plotted in bar graphs below each FACs plot. To determine DO levels relative to AcGFP expression, transfected cells that had been fixed and permeablized prior to staining with Abs to DO and DM were analyzed by flow cytometry. Note that fixation of cells results in decreased mRuby and AcGFP fluorescence. Analysis was performed by gating on mRuby+ cells followed by selecting DM expressing cells (not shown). AcGFP levels in the mRuby+ DM+ cells were divided into bins (1-5) as described above and DO gMFI for each bin was plotted in bar graphs below each FACs plot. Staining is representative of 5 individual experiments.

Figure S5. Related to Figure 6. Amino acid alignment of DOB common alleles and variants.

Alignment of the five common DOB alleles to DOB*0101. Dashes indicate similarity. Missense, frameshift and stop mutations for the other 27 DOB variants are indicated below the amino acid sequences for the common variants. DOB alleles with altered function are highlighted in the same colors used in Figures 6, 7 and S3B. DOB protein domains are marked by colored frames.

Figure S6. Related to Figure 6. A heatmap of pairwise linkage disequilibrium (LD) statistics within the MHC class II region. Data from all populations in 1000 Genomes Project was used to calculate D’ scores, ranging from red indicating D’=1 to white indicating D’=0. Variants are ordered by genomic coordinates. Note that rs9276370, rs7756516, rs7453920, rs144814623, and rs2071469 all exhibit pairwise D' > .5, suggesting they are significantly associated with each other. rs9276370, rs7756516 and rs7453920 span the region linked to persistent HBV infection (Chang et al., 2014) whereas a 'C' allele in rs2071469 mapped to the 5' UTR of DOB was significantly associated with increased susceptibility to HCV infection (Huang et al., 2015). An 'A' allele in coding rs144814623 (resulting in G77V) was found in linkage disequilibrium with a 'C' in rs 4273729, the latter SNP was associated with HCV persistence (Duggal et al., 2013). Genes in the MHC class II region, their intron–exon structure, and genomic coordinates (in Mb, using the NCBI human genome sequence, Build 37, as reference) are shown at the bottom. Coding rs144814623 and non-coding 5'UTR-specific rs2071469 are within the DOB gene.

Figure S7. Related to Figure 7. I/LnJ Oβ is a full-length protein which is produced at normal levels and interacts with DM in the endosomal compartment.

(A) Quantification of Oβ and H2-Mα levels using western blotting (as shown in 7A). Normalization was performed relative to β-actin levels. Data are presented as the protein level relative to that obtained for B6 B cells. Data combined from 4 independent experiments. Significance was calculated using an unpaired *t* test. n, number of mice.

(B) Expression of C-terminal B6 or I/LnJ Oβ-YFP fusion proteins (YFP served as control) was measured 48 hrs after transfection in L cells expressing the class II transcriptional activator that allowed for endogenous expression of Mα, Mβ and Oα but not Oβ. Lysates were analyzed by western blotting with antibodies specific for the Oβ luminal domain (top), YFP (middle) or Mα (bottom). Data are representative of 5 independent experiments. *, a non-specific band.

(C) Western blot analysis of *in vitro* transcribed and translated (TnT) B6 and I/LnJ Oβ (left) or post-nuclear supernatants from B6 or I/LnJ splenocytes (right) separated by 10% SDS-PAGE (top) or by 10% SDS-PAGE containing 8M urea (bottom). Blots were probed with antibodies specific for the Oβ luminal domain. TnT of an empty vector (pTnT) and *Oa*$^{-/-}$ splenocytes were used as negative controls for the respective blots. Triangles indicate titrated doses of the TnT generated samples loaded on the gel.

(D) Left panel, I/LnJ Oβ traffics from the ER. H-2M and co-associated H-2O immunoprecipitated from the lysates of purified B6, I/LnJ, and *Ob*$^{-/-}$ (negative control) splenic B cells were released from the immunoprecipitation pellets and treated with Endo H (+Endo H) or Peptide-*N*-Glycosidase F (+PNGase F) prior to analysis by western blotting with antibodies specific for Oβ luminal domain. B6 and I/LnJ Ob were both resistant to digestion with EndoH but not PNGase F (which cleaves off immature and mature glycans). Thus, I/LnJ Oβ trafficked from the ER to post-golgi compartments. **Right panel**, H-2O is an obligate heterodimer: in the absence of Oα, Oβ never traffics from the ER and therefore remains sensitive to digestion with Endo H. We used the sensitivity of Oβ to Endo H digestion as a control to show that the Endo H used in experiments presented in the left panel was active. For these experiments, Oβ was immunoprecipitated from detergent lysates of *Oa*$^{-/-}$ or *Ob*$^{-/-}$ (negative control) B cells using a monoclonal antibody specific for Oβ. Oβ was released from the immunoprecipitation pellet and equal aliquots were treated with Endo H or PNGase F or mock treated (mock) prior to analysis by western blotting with antibodies specific for the Oβ luminal domain. As expected Oβ in *Oa*$^{-/-}$ B cells remained sensitive to Endo H digestion since Endo H- and PNGase F-digested Oβ migrated faster on SDS-PAGE than the mock treated Oβ. Oβ^{glycos}, glycosylated Oβ; Oβ^{deglycos}, deglycosylated Oβ. * and ** mark non-specific bands. Data are representative of 2 independent experiments.

Table S1. Nonsynonymous single nucleotide variants (SNV), deletions or insertions found in the *vic1* critical region. Comparison between the B6 and I/LnJ genomes. NT, nucleotide. The critical region is highlighted.

Table S2. Nonsynonymous single nucleotide variants (SNV), deletions or insertions found in the *vic1* critical region. Comparison between the B6 and BALB/cJ genomes. NT, nucleotide. The critical region is highlighted.

Table S3. Nonsynonymous single nucleotide variants (SNV), deletions or insertions found in the *vic1* critical region. Comparison between the B6 and C3H/HeN genomes. NT, nucleotide. The critical region is highlighted.

Table S4. Human DOB alleles. RSID, SNP ID. Highlighted are alleles which have been studied.

Table S5. Human DOA alleles. RSID, SNP ID

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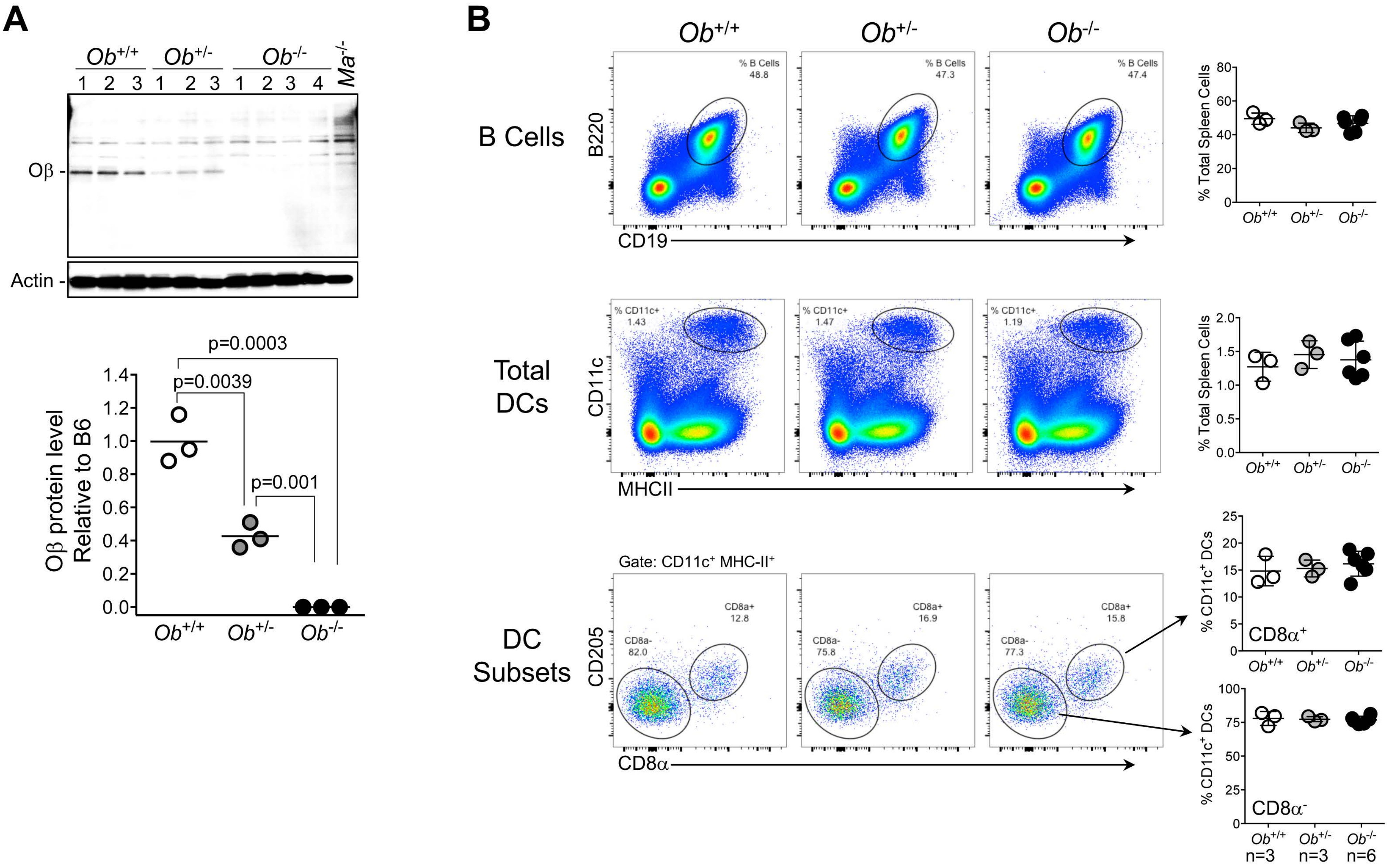
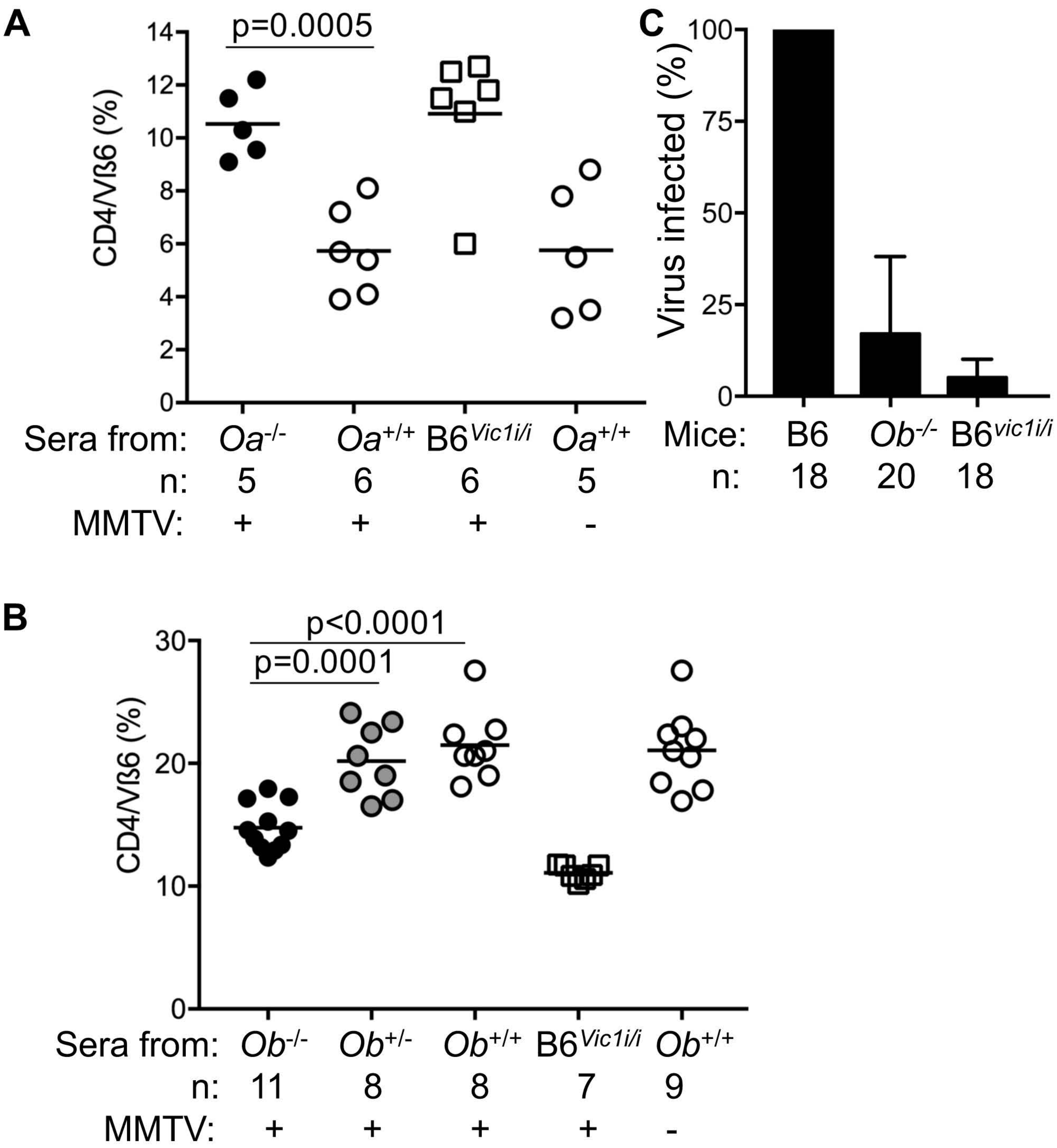


Figure S1 related to Figure 4



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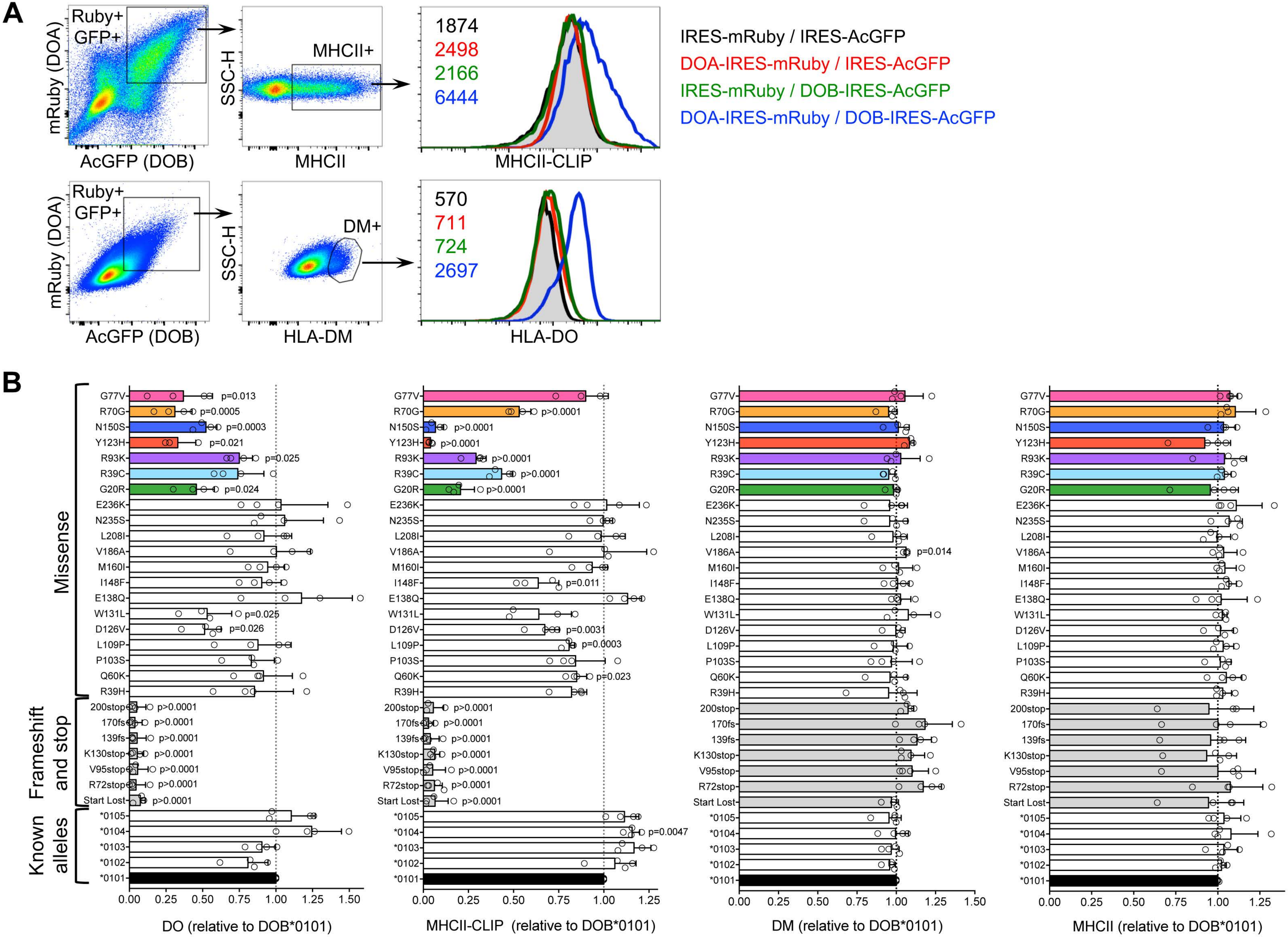

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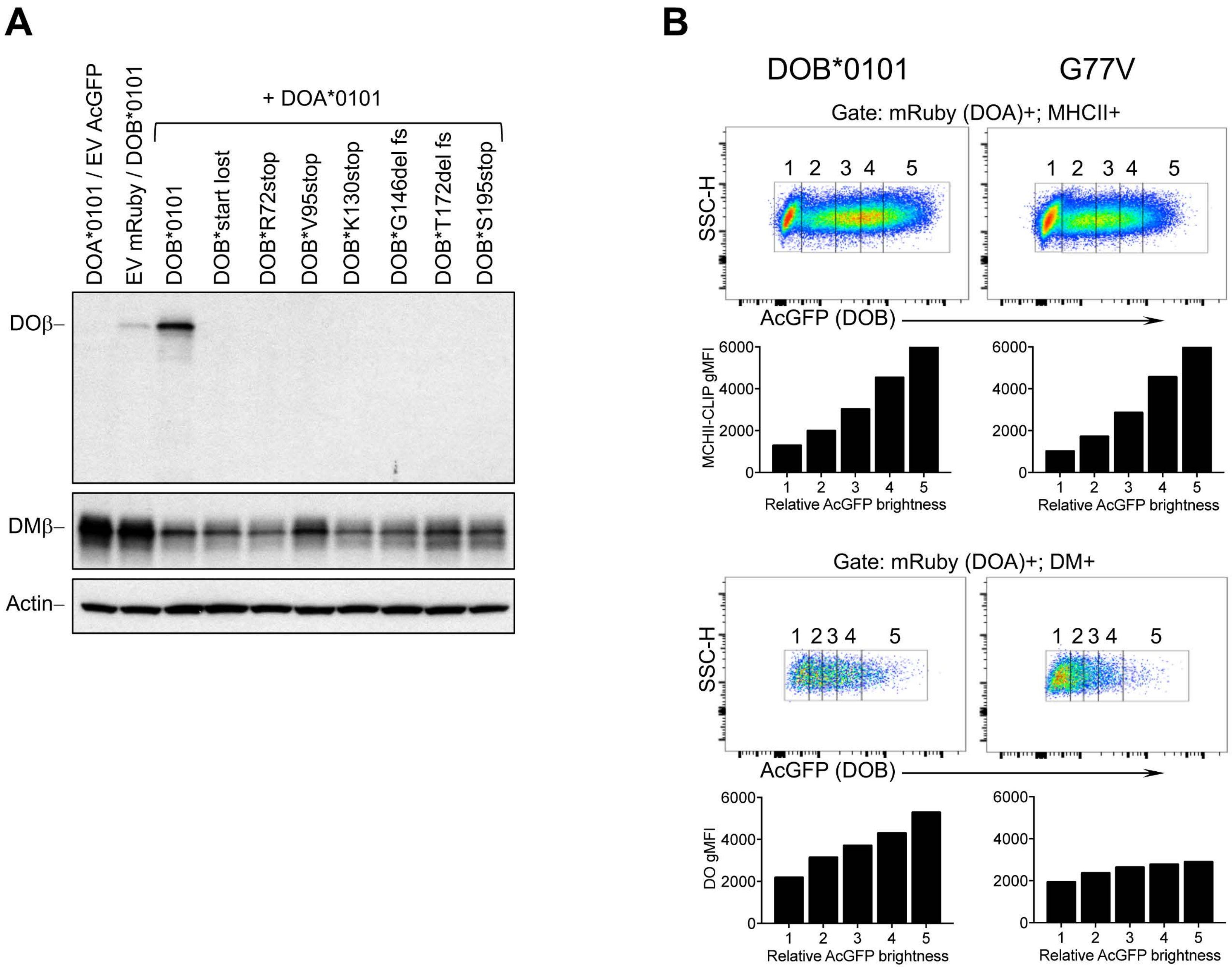

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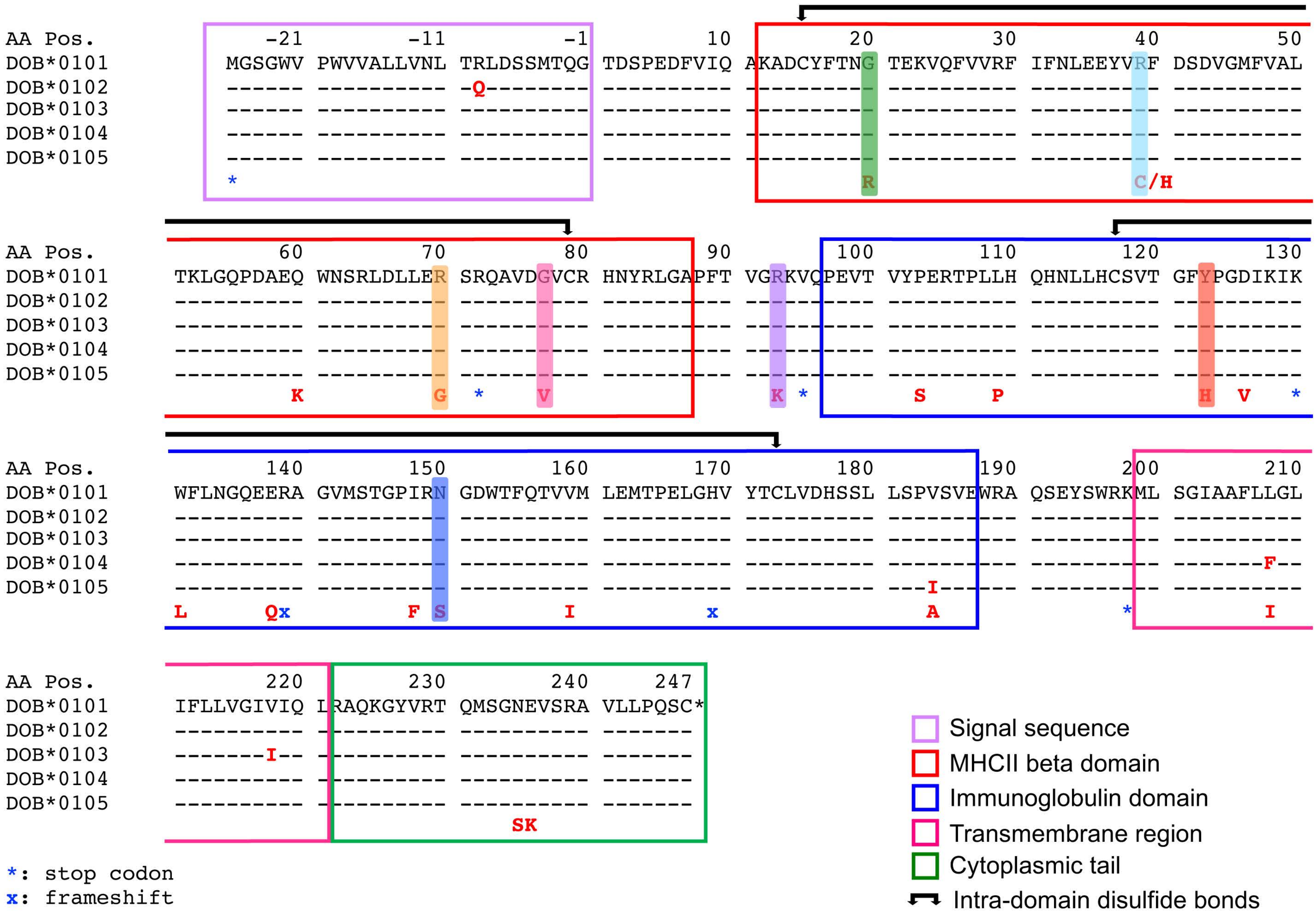

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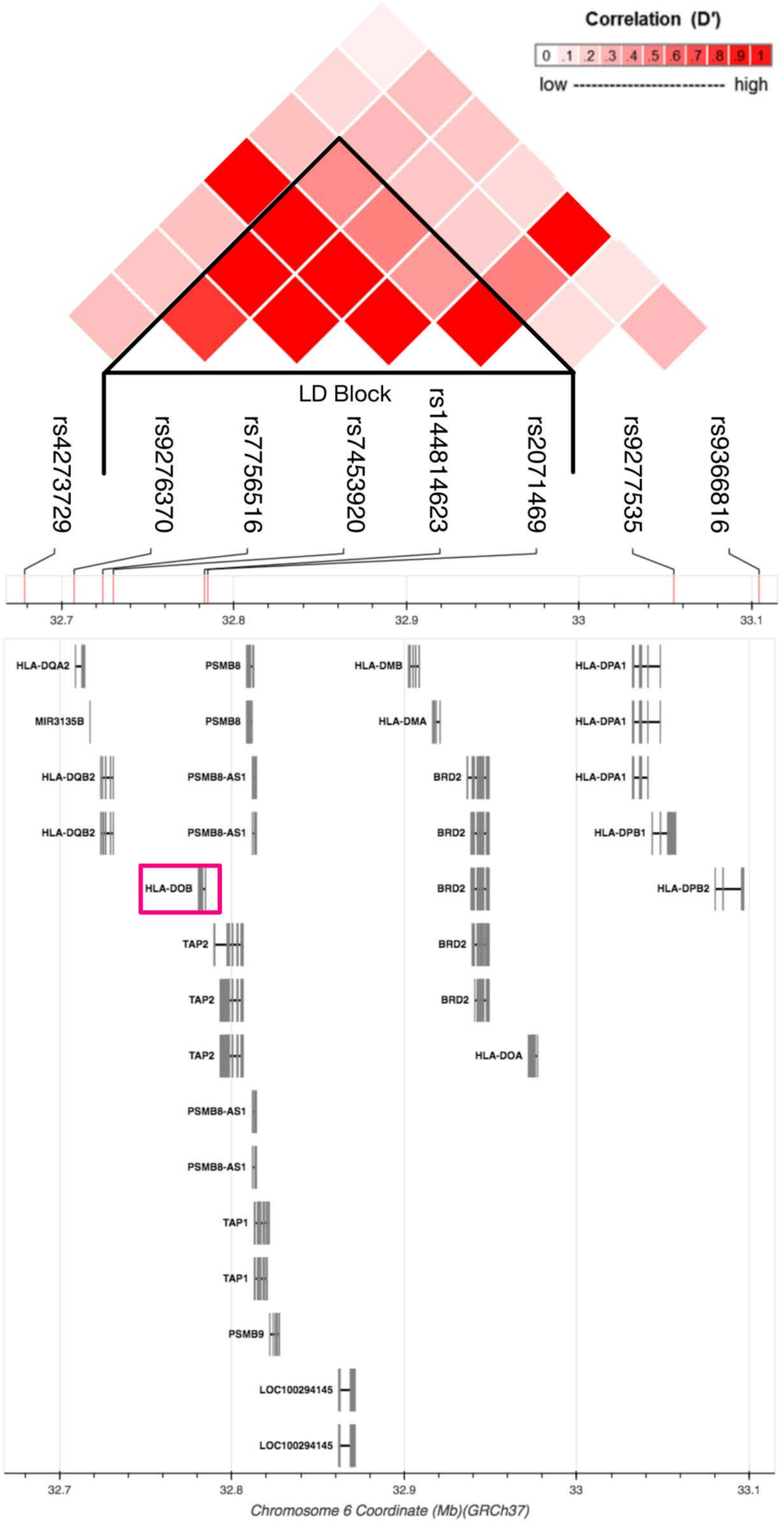

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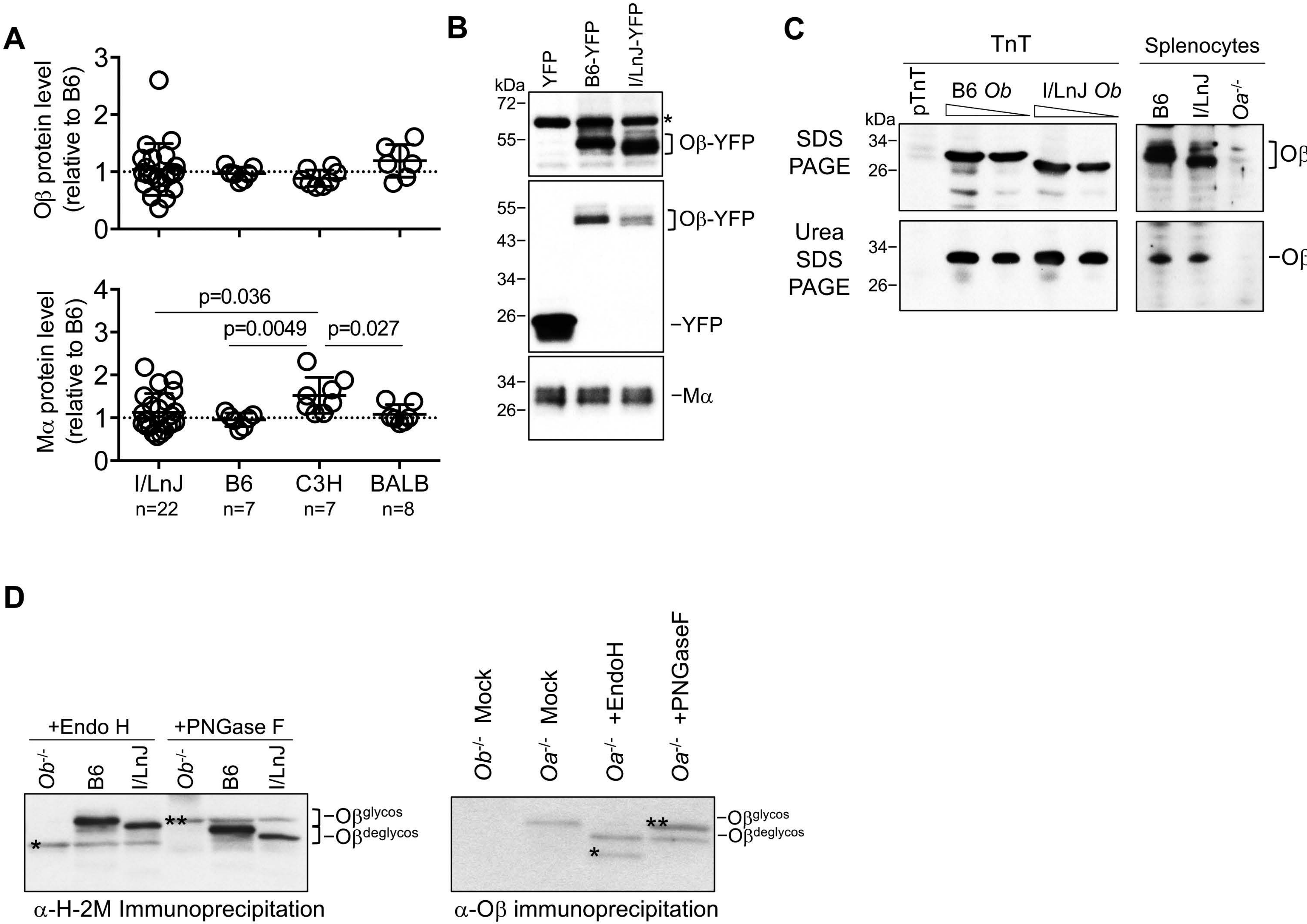

Figure S7 related to Figure 7

Supplemental Table 1a

Type	Gene	RefSeq ID	EXON	NT change	AA change	CHROM	POS	C57BL/6J	I/LnJ
nonsynonymous SNV	Tap2	NM_011530	exon2	c.A170G	p.E57G,	chr17	34205464	A	G
nonsynonymous SNV	Tap2	NM_011530	exon2	c.T326C	p.V109A,	chr17	34205620	T	C
nonsynonymous SNV	Tap2	NM_011530	exon6	c.A1058G	p.H353R,	chr17	34211985	A	G
nonsynonymous SNV	Tap2	NM_011530	exon8	c.A1271G	p.N424S,	chr17	34214016	A	G
nonsynonymous SNV	Tap2	NM_011530	exon8	c.A1346G	p.K449R,	chr17	34214091	A	G
nonsynonymous SNV	Tap2	NM_011530	exon10	c.A1754C	p.D585A,	chr17	34214767	A	C
nonsynonymous SNV	H2-Ob	NM_010389	exon3	c.G461A	p.S154N,	chr17	34242536	G	A
nonsynonymous SNV	H2-Ob	NM_010389	exon3	c.G520A	p.V174I,	chr17	34242595	G	A
nonsynonymous SNV	H2-Ob	NM_010389	exon3	c.T578A	p.L193H,	chr17	34242653	T	A
nonsynonymous SNV	H2-Ob	NM_010389	exon4	c.T692C	p.V231A,	chr17	34243516	T	C
nonsynonymous SNV	H2-Ob	NM_010389	exon6	c.G793A	p.E265K,	chr17	34244098	G	A
nonsynonymous SNV	H2-Ob	NM_010389	exon6	c.A796C	p.S266R,	chr17	34244101	A	C
nonsynonymous SNV	H2-Ob	NM_010389	exon6	c.G797T	p.S266I,	chr17	34244102	G	T

nonsynonymous single nucleotide variants (SNVs) in I/LnJ coding exons. **Type** = indicates a nonsynonymous single nucleotide variant (SNV) identified; **Gene** = gene name**; RefSeq ID** = reference annotated gene ID; **EXON** = exon number containing SNV in the annotated gene; **NT change** = change in base; **AA change** = change in amino acid; **CHROM** = chromosomal location of SNV; **POS** = genomic location of SNV; **C57BL/6J** = reference; **I/LnJ** = alternative nucleotide.

Supplemental Table 1b

Type	Gene	RefSeq ID	EXON	NT change	AA change	CHROM	POS	C57BL/6J	I/LnJ
nonframeshift insertion	Tap2	NM_011530	exon2	c.404_405insACT	p.T135delinsTL,	chr17	34205698	-	ACT

Structural variant (deletion or insertion) in I/LnJ coding exons coding exons**.** **Type** = indicates structural variant identified; **Gene** = gene name**;** **RefSeq ID** = reference annotated gene ID; **EXON** = exon number containing SNV in the annotated gene; **NT change** = change in base; **AA change** = change in amino acid; **CHROM** = chromosomal location of SNV; **POS** = genomic location of SNV; **C57BL/6J** = reference; **I/LnJ** = insertion. ACT, 3-nt insertion.

Supplemental Table 1c

Type	Gene (distance)	CHROM	POS	C57BL/6J	I/LnJ
intergenic	Psmb8(dist=1218),Tap2(dist=1807)	chr17	34202672	C	G
intergenic	Psmb8(dist=1338),Tap2(dist=1687)	chr17	34202792	G	T
intergenic	Psmb8(dist=1344),Tap2(dist=1681)	chr17	34202798	G	A
intergenic	Psmb8(dist=1373),Tap2(dist=1652)	chr17	34202827	G	A
intergenic	Psmb8(dist=1457),Tap2(dist=1568)	chr17	34202911	G	A
intergenic	Psmb8(dist=1474),Tap2(dist=1551)	chr17	34202928	T	G
intergenic	Psmb8(dist=1547),Tap2(dist=1478)	chr17	34203001	A	G
intergenic	Psmb8(dist=1593),Tap2(dist=1432)	chr17	34203047	A	T
intergenic	Psmb8(dist=1602),Tap2(dist=1423)	chr17	34203056	A	G
intergenic	Psmb8(dist=1609),Tap2(dist=1416)	chr17	34203063	A	G
intergenic	Psmb8(dist=1959),Tap2(dist=1066)	chr17	34203413	C	T
intergenic	Psmb8(dist=1973),Tap2(dist=1052)	chr17	34203427	C	T
upstream	Tap2	chr17	34203503	A	G
upstream	Tap2	chr17	34203551	T	A
upstream	Tap2	chr17	34203782	G	T
upstream	Tap2	chr17	34203948	T	C
upstream	Tap2	chr17	34204141	C	T
upstream	Tap2	chr17	34204147	A	C
upstream	Tap2	chr17	34204227	A	G
upstream	Tap2	chr17	34204246	C	A
upstream	Tap2	chr17	34204297	T	A
upstream	Tap2	chr17	34204300	T	G
upstream	Tap2	chr17	34204344	T	C
intronic	Tap2	chr17	34204830	C	T
intronic	Tap2	chr17	34204924	C	A
intronic	Tap2	chr17	34204972	A	G
intronic	Tap2	chr17	34205059	T	A
intronic	Tap2	chr17	34205142	C	T
intronic	Tap2	chr17	34205238	A	G
intronic	Tap2	chr17	34205273	C	T
exonic	Tap2	chr17	34205464	A	G
exonic	Tap2	chr17	34205537	T	C
exonic	Tap2	chr17	34205570	C	G
exonic	Tap2	chr17	34205603	G	A
exonic	Tap2	chr17	34205620	T	C
exonic	Tap2	chr17	34205621	T	C
intronic	Tap2	chr17	34205793	A	G
exonic	Tap2	chr17	34205937	C	T

intronic	Tap2	chr17	34206130	C	T
intronic	Tap2	chr17	34206200	T	C
intronic	Tap2	chr17	34206348	C	T
intronic	Tap2	chr17	34206406	T	C
intronic	Tap2	chr17	34206426	G	A
intronic	Tap2	chr17	34206745	A	G
intronic	Tap2	chr17	34206821	G	T
intronic	Tap2	chr17	34207182	G	A
intronic	Tap2	chr17	34207259	T	C
intronic	Tap2	chr17	34208195	G	T
intronic	Tap2	chr17	34208303	T	G
intronic	Tap2	chr17	34208621	T	C
intronic	Tap2	chr17	34208922	T	C
intronic	Tap2	chr17	34209341	G	A
intronic	Tap2	chr17	34209540	C	T
intronic	Tap2	chr17	34209614	C	T
intronic	Tap2	chr17	34210055	G	T
intronic	Tap2	chr17	34210146	G	C
intronic	Tap2	chr17	34210352	T	C
intronic	Tap2	chr17	34210638	T	C
intronic	Tap2	chr17	34210659	C	T
intronic	Tap2	chr17	34210791	A	G
intronic	Tap2	chr17	34210838	G	A
intronic	Tap2	chr17	34211100	C	T
intronic	Tap2	chr17	34211123	A	G
intronic	Tap2	chr17	34211645	T	C
intronic	Tap2	chr17	34211799	T	C
intronic	Tap2	chr17	34211836	T	C
intronic	Tap2	chr17	34211866	T	C
exonic	Tap2	chr17	34211985	A	G
intronic	Tap2	chr17	34212368	G	A
intronic	Tap2	chr17	34212739	T	C
intronic	Tap2	chr17	34212740	A	C
intronic	Tap2	chr17	34212741	A	G
intronic	Tap2	chr17	34212753	C	T
intronic	Tap2	chr17	34212761	C	G
intronic	Tap2	chr17	34212889	C	A
intronic	Tap2	chr17	34212901	T	G
intronic	Tap2	chr17	34212962	C	T
intronic	Tap2	chr17	34213098	G	A
intronic	Tap2	chr17	34213138	T	A

intronic	Tap2	chr17	34213169	A	C
intronic	Tap2	chr17	34213210	C	T
intronic	Tap2	chr17	34213343	C	T
intronic	Tap2	chr17	34213364	T	C
intronic	Tap2	chr17	34213404	C	A
intronic	Tap2	chr17	34213460	T	A
intronic	Tap2	chr17	34213491	A	G
intronic	Tap2	chr17	34213541	G	A
intronic	Tap2	chr17	34213542	T	C
intronic	Tap2	chr17	34213553	T	C
intronic	Tap2	chr17	34213558	A	G
intronic	Tap2	chr17	34213579	T	C
intronic	Tap2	chr17	34213611	G	C
intronic	Tap2	chr17	34213633	C	A
intronic	Tap2	chr17	34213656	G	A
intronic	Tap2	chr17	34213677	A	G
intronic	Tap2	chr17	34213689	T	G
intronic	Tap2	chr17	34213727	T	C
intronic	Tap2	chr17	34213751	T	C
intronic	Tap2	chr17	34213975	C	A
exonic	Tap2	chr17	34214016	A	G
exonic	Tap2	chr17	34214091	A	G
exonic	Tap2	chr17	34214143	C	T
intronic	Tap2	chr17	34214230	G	C
intronic	Tap2	chr17	34214519	T	A
intronic	Tap2	chr17	34214549	C	A
intronic	Tap2	chr17	34214582	T	C
intronic	Tap2	chr17	34214585	G	T
exonic	Tap2	chr17	34214767	A	C
intronic	Tap2	chr17	34214809	C	T
intronic	Tap2	chr17	34214874	A	G
intronic	Tap2	chr17	34214929	T	A
intronic	Tap2	chr17	34215036	G	A
intronic	Tap2	chr17	34215050	C	G
intronic	Tap2	chr17	34215071	C	A
intronic	Tap2	chr17	34215115	T	A
intronic	Tap2	chr17	34215272	C	A
intronic	Tap2	chr17	34215297	G	T
exonic	Tap2	chr17	34215338	C	T
exonic	Tap2	chr17	34215464	A	G
intronic	Tap2	chr17	34215495	A	G

intronic	Tap2	chr17	34215550	A	G
intronic	Tap2	chr17	34215571	C	G
intronic	Tap2	chr17	34215708	A	G
exonic	Tap2	chr17	34216042	G	A
UTR3	Tap2(NM_011530:c.*36C>A)	chr17	34216129	C	A
downstream	Tap2	chr17	34216428	G	A
downstream	Tap2	chr17	34216482	T	C
downstream	Tap2	chr17	34216641	C	T
downstream	Tap2	chr17	34216707	T	C
downstream	Tap2	chr17	34216712	A	G
downstream	Tap2	chr17	34216716	A	G
downstream	Tap2	chr17	34216811	C	T
downstream	Tap2	chr17	34217048	T	C
intergenic	Tap2(dist=1466),H2-Ob(dist=21118)	chr17	34217787	C	T
intergenic	Tap2(dist=1503),H2-Ob(dist=21081)	chr17	34217824	T	C
intergenic	Tap2(dist=1562),H2-Ob(dist=21022)	chr17	34217883	C	T
intergenic	Tap2(dist=1563),H2-Ob(dist=21021)	chr17	34217884	A	C
intergenic	Tap2(dist=1642),H2-Ob(dist=20942)	chr17	34217963	C	T
intergenic	Tap2(dist=1752),H2-Ob(dist=20832)	chr17	34218073	G	A
intergenic	Tap2(dist=1765),H2-Ob(dist=20819)	chr17	34218086	C	T
intergenic	Tap2(dist=2156),H2-Ob(dist=20428)	chr17	34218477	A	G
intergenic	Tap2(dist=2398),H2-Ob(dist=20186)	chr17	34218719	G	A
intergenic	Tap2(dist=2453),H2-Ob(dist=20131)	chr17	34218774	A	C
intergenic	Tap2(dist=2575),H2-Ob(dist=20009)	chr17	34218896	T	C
intergenic	Tap2(dist=2715),H2-Ob(dist=19869)	chr17	34219036	C	A
intergenic	Tap2(dist=2771),H2-Ob(dist=19813)	chr17	34219092	T	A
intergenic	Tap2(dist=2843),H2-Ob(dist=19741)	chr17	34219164	A	G
intergenic	Tap2(dist=2906),H2-Ob(dist=19678)	chr17	34219227	A	G
intergenic	Tap2(dist=3647),H2-Ob(dist=18937)	chr17	34219968	C	T
intergenic	Tap2(dist=8164),H2-Ob(dist=14420)	chr17	34224485	A	G
intergenic	Tap2(dist=8201),H2-Ob(dist=14383)	chr17	34224522	T	C
intergenic	Tap2(dist=8381),H2-Ob(dist=14203)	chr17	34224702	C	T
intergenic	Tap2(dist=8521),H2-Ob(dist=14063)	chr17	34224842	A	G
intergenic	Tap2(dist=8642),H2-Ob(dist=13942)	chr17	34224963	T	G
intergenic	Tap2(dist=8952),H2-Ob(dist=13632)	chr17	34225273	G	A
intergenic	Tap2(dist=9177),H2-Ob(dist=13407)	chr17	34225498	A	G
intergenic	Tap2(dist=9178),H2-Ob(dist=13406)	chr17	34225499	A	C
intergenic	Tap2(dist=9223),H2-Ob(dist=13361)	chr17	34225544	A	G
intergenic	Tap2(dist=9228),H2-Ob(dist=13356)	chr17	34225549	T	C
intergenic	Tap2(dist=9260),H2-Ob(dist=13324)	chr17	34225581	G	A
intergenic	Tap2(dist=9282),H2-Ob(dist=13302)	chr17	34225603	C	T

intergenic	Tap2(dist=9312),H2-Ob(dist=13272)	chr17	34225633	T	C
intergenic	Tap2(dist=9399),H2-Ob(dist=13185)	chr17	34225720	T	C
intergenic	Tap2(dist=16780),H2-Ob(dist=5804)	chr17	34233101	C	A
intergenic	Tap2(dist=16833),H2-Ob(dist=5751)	chr17	34233154	C	T
intergenic	Tap2(dist=17164),H2-Ob(dist=5420)	chr17	34233485	C	T
intergenic	Tap2(dist=17184),H2-Ob(dist=5400)	chr17	34233505	T	C
intergenic	Tap2(dist=17190),H2-Ob(dist=5394)	chr17	34233511	T	G
intergenic	Tap2(dist=17373),H2-Ob(dist=5211)	chr17	34233694	T	G
intergenic	Tap2(dist=17407),H2-Ob(dist=5177)	chr17	34233728	G	A
intergenic	Tap2(dist=17736),H2-Ob(dist=4848)	chr17	34234057	C	T
intergenic	Tap2(dist=17955),H2-Ob(dist=4629)	chr17	34234276	G	T
intergenic	Tap2(dist=18050),H2-Ob(dist=4534)	chr17	34234371	C	T
intergenic	Tap2(dist=18090),H2-Ob(dist=4494)	chr17	34234411	T	G
intergenic	Tap2(dist=18091),H2-Ob(dist=4493)	chr17	34234412	T	G
intergenic	Tap2(dist=18421),H2-Ob(dist=4163)	chr17	34234742	T	C
intergenic	Tap2(dist=18771),H2-Ob(dist=3813)	chr17	34235092	C	T
intergenic	Tap2(dist=18994),H2-Ob(dist=3590)	chr17	34235315	C	T
intergenic	Tap2(dist=19123),H2-Ob(dist=3461)	chr17	34235444	T	C
intergenic	Tap2(dist=19484),H2-Ob(dist=3100)	chr17	34235805	G	T
intergenic	Tap2(dist=19590),H2-Ob(dist=2994)	chr17	34235911	G	A
intergenic	Tap2(dist=19990),H2-Ob(dist=2594)	chr17	34236311	A	C
intergenic	Tap2(dist=20535),H2-Ob(dist=2049)	chr17	34236856	A	C
intergenic	Tap2(dist=20542),H2-Ob(dist=2042)	chr17	34236863	C	T
intergenic	Tap2(dist=20704),H2-Ob(dist=1880)	chr17	34237025	A	T
intergenic	Tap2(dist=21306),H2-Ob(dist=1278)	chr17	34237627	T	C
intergenic	Tap2(dist=21343),H2-Ob(dist=1241)	chr17	34237664	G	A
intergenic	Tap2(dist=21350),H2-Ob(dist=1234)	chr17	34237671	C	T
intergenic	Tap2(dist=21363),H2-Ob(dist=1221)	chr17	34237684	G	A
intergenic	Tap2(dist=21366),H2-Ob(dist=1218)	chr17	34237687	T	C
intergenic	Tap2(dist=21400),H2-Ob(dist=1184)	chr17	34237721	T	C
intergenic	Tap2(dist=21502),H2-Ob(dist=1082)	chr17	34237823	T	A
upstream	H2-Ob	chr17	34237922	G	A
upstream	H2-Ob	chr17	34238194	T	A
upstream	H2-Ob	chr17	34238210	T	C
upstream	H2-Ob	chr17	34238237	T	C
upstream	H2-Ob	chr17	34238420	C	T
upstream	H2-Ob	chr17	34238452	C	T
upstream	H2-Ob	chr17	34238511	C	T
upstream	H2-Ob	chr17	34238713	C	T
upstream	H2-Ob	chr17	34238722	C	T
upstream	H2-Ob	chr17	34238735	C	T

UTR5	H2-Ob(NM_010389:c.-42T>G)	chr17	34238930	T	G
intronic	H2-Ob	chr17	34239199	A	G
intronic	H2-Ob	chr17	34239357	A	C
intronic	H2-Ob	chr17	34239691	G	A
intronic	H2-Ob	chr17	34239693	G	T
intronic	H2-Ob	chr17	34239694	A	T
intronic	H2-Ob	chr17	34239780	A	G
intronic	H2-Ob	chr17	34239788	C	T
intronic	H2-Ob	chr17	34239912	C	A
intronic	H2-Ob	chr17	34239969	G	A
intronic	H2-Ob	chr17	34240076	A	T
intronic	H2-Ob	chr17	34240093	G	A
intronic	H2-Ob	chr17	34240267	C	T
intronic	H2-Ob	chr17	34240292	T	C
intronic	H2-Ob	chr17	34240302	A	C
intronic	H2-Ob	chr17	34240325	G	T
intronic	H2-Ob	chr17	34240326	T	C
intronic	H2-Ob	chr17	34240328	T	C
intronic	H2-Ob	chr17	34240409	A	C
intronic	H2-Ob	chr17	34240456	T	C
intronic	H2-Ob	chr17	34240590	C	T
intronic	H2-Ob	chr17	34240721	C	G
intronic	H2-Ob	chr17	34240749	C	T
intronic	H2-Ob	chr17	34240764	G	A
intronic	H2-Ob	chr17	34240785	T	C
intronic	H2-Ob	chr17	34240786	G	A
intronic	H2-Ob	chr17	34240801	T	C
intronic	H2-Ob	chr17	34240868	G	A
intronic	H2-Ob	chr17	34240951	C	A
intronic	H2-Ob	chr17	34240970	G	C
intronic	H2-Ob	chr17	34241469	A	T
intronic	H2-Ob	chr17	34241550	G	C
intronic	H2-Ob	chr17	34241612	G	T
intronic	H2-Ob	chr17	34241630	G	T
intronic	H2-Ob	chr17	34241928	C	T
intronic	H2-Ob	chr17	34241943	T	C
intronic	H2-Ob	chr17	34241976	A	G
intronic	H2-Ob	chr17	34242015	T	C
intronic	H2-Ob	chr17	34242023	A	C
intronic	H2-Ob	chr17	34242031	G	A
intronic	H2-Ob	chr17	34242032	C	T

intronic	H2-Ob	chr17	34242080	C	T
intronic	H2-Ob	chr17	34242110	G	A
intronic	H2-Ob	chr17	34242155	T	C
intronic	H2-Ob	chr17	34242212	G	A
intronic	H2-Ob	chr17	34242348	C	T
intronic	H2-Ob	chr17	34242356	G	C
intronic	H2-Ob	chr17	34242386	C	T
intronic	H2-Ob	chr17	34242397	G	C
exonic	H2-Ob	chr17	34242459	T	C
exonic	H2-Ob	chr17	34242474	G	A
exonic	H2-Ob	chr17	34242536	G	A
exonic	H2-Ob	chr17	34242595	G	A
exonic	H2-Ob	chr17	34242653	T	A
exonic	H2-Ob	chr17	34242687	C	T
intronic	H2-Ob	chr17	34242742	C	T
intronic	H2-Ob	chr17	34242833	G	T
intronic	H2-Ob	chr17	34242905	C	T
intronic	H2-Ob	chr17	34242971	C	A
intronic	H2-Ob	chr17	34242985	G	T
intronic	H2-Ob	chr17	34242998	A	G
intronic	H2-Ob	chr17	34243037	C	G
intronic	H2-Ob	chr17	34243054	C	G
intronic	H2-Ob	chr17	34243080	C	T
intronic	H2-Ob	chr17	34243137	T	C
intronic	H2-Ob	chr17	34243181	G	T
intronic	H2-Ob	chr17	34243217	A	G
intronic	H2-Ob	chr17	34243246	T	C
intronic	H2-Ob	chr17	34243256	G	C
intronic	H2-Ob	chr17	34243278	A	G
intronic	H2-Ob	chr17	34243283	T	C
intronic	H2-Ob	chr17	34243297	C	T
intronic	H2-Ob	chr17	34243329	C	T
intronic	H2-Ob	chr17	34243401	A	G
exonic	H2-Ob	chr17	34243516	T	C
intronic	H2-Ob	chr17	34243582	A	G
intronic	H2-Ob	chr17	34243731	A	G
intronic	H2-Ob	chr17	34243754	C	T
intronic	H2-Ob	chr17	34243785	G	A
intronic	H2-Ob	chr17	34243789	T	C
intronic	H2-Ob	chr17	34243814	G	A
intronic	H2-Ob	chr17	34243827	C	G

intronic	H2-Ob	chr17	34243871	G	A
intronic	H2-Ob	chr17	34243997	A	C
intronic	H2-Ob	chr17	34244018	C	G
intronic	H2-Ob	chr17	34244076	A	G
exonic	H2-Ob	chr17	34244098	G	A
exonic	H2-Ob	chr17	34244101	A	C
exonic	H2-Ob	chr17	34244102	G	T
UTR3	H2-Ob(NM_010389:c.*116C>T)	chr17	34244237	C	T
UTR3	H2-Ob(NM_010389:c.*192C>T)	chr17	34244313	C	T
UTR3	H2-Ob(NM_010389:c.*233G>A)	chr17	34244354	G	A
UTR3	H2-Ob(NM_010389:c.*309A>G)	chr17	34244430	A	G
UTR3	H2-Ob(NM_010389:c.*314G>A)	chr17	34244435	G	A
UTR3	H2-Ob(NM_010389:c.*352C>T)	chr17	34244473	C	T
UTR3	H2-Ob(NM_010389:c.*440C>T)	chr17	34244561	C	T
UTR3	H2-Ob(NM_010389:c.*646A>G)	chr17	34244767	A	G
UTR3	H2-Ob(NM_010389:c.*647T>C)	chr17	34244768	T	C
UTR3	H2-Ob(NM_010389:c.*664T>C)	chr17	34244785	T	C
UTR3	H2-Ob(NM_010389:c.*679C>A)	chr17	34244800	C	A
UTR3	H2-Ob(NM_010389:c.*687C>T)	chr17	34244808	C	T
UTR3	H2-Ob(NM_010389:c.*688T>G)	chr17	34244809	T	G
UTR3	H2-Ob(NM_010389:c.*691C>G)	chr17	34244812	C	G
UTR3	H2-Ob(NM_010389:c.*815T>C)	chr17	34244936	T	C
UTR3	H2-Ob(NM_010389:c.*1004T>C)	chr17	34245125	T	C
UTR3	H2-Ob(NM_010389:c.*1019G>A)	chr17	34245140	G	A
UTR3	H2-Ob(NM_010389:c.*1044C>T)	chr17	34245165	C	T
UTR3	H2-Ob(NM_010389:c.*1208G>A)	chr17	34245329	G	A
UTR3	H2-Ob(NM_010389:c.*1250G>A)	chr17	34245371	G	A
UTR3	H2-Ob(NM_010389:c.*1324A>G)	chr17	34245445	A	G
UTR3	H2-Ob(NM_010389:c.*1491T>C)	chr17	34245612	T	C
UTR3	H2-Ob(NM_010389:c.*1537G>A)	chr17	34245658	G	A
UTR3	H2-Ob(NM_010389:c.*1578A>T)	chr17	34245699	A	T
UTR3	H2-Ob(NM_010389:c.*1581T>C)	chr17	34245702	T	C
UTR3	H2-Ob(NM_010389:c.*1646C>T)	chr17	34245767	C	T
UTR3	H2-Ob(NM_010389:c.*1668T>C)	chr17	34245789	T	C
downstream	H2-Ob	chr17	34245990	A	G
downstream	H2-Ob	chr17	34246368	A	G
downstream	H2-Ob	chr17	34246433	T	C
downstream	H2-Ob	chr17	34246449	T	C
downstream	H2-Ob	chr17	34246464	G	A
downstream	H2-Ob	chr17	34246666	A	G
downstream	H2-Ob	chr17	34246678	T	C

All single nucleotide variants (SNVs) in I/LnJ. **Type** = indicates a single nucleotide variant (SNV) identified relative to a known gene; **Gene (distance)**= gene containing SNV, or distance to nearest genes in 3’ and 5’ direction**; CHROM** = chromosomal location of SNV; **POS** = genomic location of SNV; **C57BL/6J** = reference; **I/LnJ** = detected nucleotide. The *vic1* critical region is highlighted in yellow.

Supplemental Table 2a

Type	Gene	RefSeq ID	EXON	NT change	AA change	CHROM	POS	C57BL/6J	BALB/cJ
nonsynonymous SNV	Tap2	NM_011530	exon2	c.G169A	p.E57K,	chr17	34205463	G	A
nonsynonymous SNV	Tap2	NM_011530	exon2	c.A170G	p.E57G,	chr17	34205464	A	G
nonsynonymous SNV	Tap2	NM_011530	exon2	c.T326C	p.V109A,	chr17	34205620	T	C
nonsynonymous SNV	Tap2	NM_011530	exon6	c.A1058G	p.H353R,	chr17	34211985	A	G
nonsynonymous SNV	Tap2	NM_011530	exon8	c.A1346G	p.K449R,	chr17	34214091	A	G
nonsynonymous SNV	Tap2	NM_011530	exon10	c.G1765C	p.G589R,	chr17	34214778	G	C
nonsynonymous SNV	H2-Ob	NM_010389	exon1	c.G14T	p.R5M,	chr17	34238985	G	T
nonsynonymous SNV	H2-Ob	NM_010389	exon1	c.G16T	p.A6S,	chr17	34238987	G	T
nonsynonymous SNV	H2-Ob	NM_010389	exon2	c.A329G	p.K110R,	chr17	34241245	A	G
nonsynonymous SNV	H2-Ob	NM_010389	exon4	c.T692C	p.V231A,	chr17	34243516	T	C
nonsynonymous SNV	H2-Ob	NM_010389	exon6	c.A796C	p.S266R,	chr17	34244101	A	C
nonsynonymous SNV	H2-Ob	NM_010389	exon6	c.G797T	p.S266I,	chr17	34244102	G	T

Nonsynonymous single nucleotide variants (SNVs) in BALB/cJ coding exons. **Type** = indicates a nonsynonymous single nucleotide variant (SNV) identified; **Gene** = gene name**; RefSeq ID** = reference annotated gene ID; **EXON** = exon number containing SNV in the annotated gene; **NT change** = change in base; **AA change** = change in amino acid; **CHROM** = chromosomal location of SNV; **POS** = genomic location of SNV; **C57BL/6J** = reference; **BALB/cJ** = alternative nucleotide.

Supplemental Table 2b

Type	Gene	RefSeq ID	EXON	NT change	AA change	CHROM	POS	C57BL/6J	BALB/cJ
nonframeshift insertion	Tap2	NM_011530	exon2	c.404_405insACT	p.T135delinsTL,	chr17	34205698	-	ACT

Structural variant (deletion or insertion) in BALB/cJ coding exons coding exons**. Type** = indicates structural variant identified; **Gene** = gene name**; RefSeq ID** = reference annotated gene ID; **EXON** = exon number containing SNV in the annotated gene; **NT change** = change in base; **AA change** = change in amino acid; **CHROM** = chromosomal location of SNV; **POS** = genomic location of SNV; **C57BL/6J** = reference; **BALB/cJ** = insertion. ACT, 3-nt insertion.

Supplemental Table 2c

Type	Gene (distance)	CHROM	POS	C57BL/6J	BALB/cJ
upstream	Tap2	chr17	34204147	A	C
upstream	Tap2	chr17	34204217	C	T
upstream	Tap2	chr17	34204294	T	G
upstream	Tap2	chr17	34204300	T	G
upstream	Tap2	chr17	34204305	T	G
upstream	Tap2	chr17	34204306	G	T
exonic	Tap2	chr17	34205463	G	A
exonic	Tap2	chr17	34205464	A	G
exonic	Tap2	chr17	34205537	T	C
exonic	Tap2	chr17	34205570	C	G
exonic	Tap2	chr17	34205603	G	A
exonic	Tap2	chr17	34205620	T	C
exonic	Tap2	chr17	34205621	T	C
intronic	Tap2	chr17	34205793	A	G
exonic	Tap2	chr17	34205937	C	T
intronic	Tap2	chr17	34206130	C	T
intronic	Tap2	chr17	34206200	T	C
intronic	Tap2	chr17	34206348	C	T
intronic	Tap2	chr17	34206406	T	C
intronic	Tap2	chr17	34206426	G	A
intronic	Tap2	chr17	34206745	A	T
intronic	Tap2	chr17	34206821	G	T
intronic	Tap2	chr17	34206949	G	A
intronic	Tap2	chr17	34207182	G	A
intronic	Tap2	chr17	34207259	T	C
intronic	Tap2	chr17	34207823	G	C
intronic	Tap2	chr17	34207878	A	C
intronic	Tap2	chr17	34208137	A	G
intronic	Tap2	chr17	34208139	A	G
intronic	Tap2	chr17	34208195	G	T
intronic	Tap2	chr17	34208303	T	G
intronic	Tap2	chr17	34208329	C	T
intronic	Tap2	chr17	34208489	G	T
intronic	Tap2	chr17	34208497	G	A
intronic	Tap2	chr17	34208621	T	C
intronic	Tap2	chr17	34208677	C	T
intronic	Tap2	chr17	34208740	C	T
intronic	Tap2	chr17	34208922	T	C

intronic	Tap2	chr17	34209341	G	A
intronic	Tap2	chr17	34209540	C	T
intronic	Tap2	chr17	34210055	G	T
intronic	Tap2	chr17	34210146	G	C
intronic	Tap2	chr17	34210352	T	C
intronic	Tap2	chr17	34210638	T	C
intronic	Tap2	chr17	34210791	A	G
intronic	Tap2	chr17	34211354	G	C
intronic	Tap2	chr17	34211661	T	C
intronic	Tap2	chr17	34211836	T	C
exonic	Tap2	chr17	34211985	A	G
intronic	Tap2	chr17	34212187	G	C
exonic	Tap2	chr17	34212289	T	C
intronic	Tap2	chr17	34212601	A	G
intronic	Tap2	chr17	34212889	C	A
intronic	Tap2	chr17	34212962	C	T
intronic	Tap2	chr17	34213039	G	A
intronic	Tap2	chr17	34213169	A	C
intronic	Tap2	chr17	34213193	G	A
intronic	Tap2	chr17	34213210	C	T
intronic	Tap2	chr17	34213343	C	T
intronic	Tap2	chr17	34213364	T	C
intronic	Tap2	chr17	34213404	C	A
intronic	Tap2	chr17	34213460	T	A
intronic	Tap2	chr17	34213491	A	G
intronic	Tap2	chr17	34213541	G	A
intronic	Tap2	chr17	34213542	T	C
intronic	Tap2	chr17	34213553	T	C
intronic	Tap2	chr17	34213558	A	G
intronic	Tap2	chr17	34213579	T	C
intronic	Tap2	chr17	34213592	G	A
intronic	Tap2	chr17	34213597	G	A
intronic	Tap2	chr17	34213633	C	A
intronic	Tap2	chr17	34213656	G	A
intronic	Tap2	chr17	34213677	A	G
intronic	Tap2	chr17	34213689	T	G
intronic	Tap2	chr17	34213727	T	C
intronic	Tap2	chr17	34213751	T	C
intronic	Tap2	chr17	34213843	A	T
intronic	Tap2	chr17	34213975	C	A
exonic	Tap2	chr17	34214091	A	G

exonic	Tap2	chr17	34214143	C	T
intronic	Tap2	chr17	34214239	C	T
intronic	Tap2	chr17	34214264	C	G
exonic	Tap2	chr17	34214442	G	A
intronic	Tap2	chr17	34214519	T	A
intronic	Tap2	chr17	34214549	C	A
intronic	Tap2	chr17	34214567	C	A
intronic	Tap2	chr17	34214612	G	T
exonic	Tap2	chr17	34214778	G	C
intronic	Tap2	chr17	34214874	A	G
intronic	Tap2	chr17	34214928	T	A
intronic	Tap2	chr17	34214962	A	G
intronic	Tap2	chr17	34214982	G	A
intronic	Tap2	chr17	34214985	T	C
intronic	Tap2	chr17	34215049	T	A
intronic	Tap2	chr17	34215071	C	A
intronic	Tap2	chr17	34215272	C	A
intronic	Tap2	chr17	34215297	G	T
exonic	Tap2	chr17	34215338	C	T
exonic	Tap2	chr17	34215395	G	A
intronic	Tap2	chr17	34215495	A	G
intronic	Tap2	chr17	34215550	A	G
intronic	Tap2	chr17	34215571	C	G
intronic	Tap2	chr17	34215684	G	A
intronic	Tap2	chr17	34215708	A	G
intronic	Tap2	chr17	34215894	C	A
exonic	Tap2	chr17	34216042	G	A
exonic	Tap2	chr17	34216067	C	T
exonic	Tap2	chr17	34216090	A	G
UTR3	Tap2(NM_011530:c.*7C>T)	chr17	34216100	C	T
downstream	Tap2	chr17	34216372	G	A
downstream	Tap2	chr17	34216457	T	C
downstream	Tap2	chr17	34216482	T	C
downstream	Tap2	chr17	34216562	A	T
downstream	Tap2	chr17	34216667	T	C
downstream	Tap2	chr17	34216707	T	C
downstream	Tap2	chr17	34216712	A	G
downstream	Tap2	chr17	34216903	T	C
downstream	Tap2	chr17	34216904	G	A
downstream	Tap2	chr17	34216908	A	G
downstream	Tap2	chr17	34217016	C	A

downstream	Tap2	chr17	34217048	T	C
downstream	Tap2	chr17	34217073	T	C
downstream	Tap2	chr17	34217116	G	A
intergenic	Tap2(dist=1046),H2-Ob(dist=21538)	chr17	34217367	C	G
intergenic	Tap2(dist=1075),H2-Ob(dist=21509)	chr17	34217396	A	T
intergenic	Tap2(dist=1109),H2-Ob(dist=21475)	chr17	34217430	C	A
intergenic	Tap2(dist=1194),H2-Ob(dist=21390)	chr17	34217515	A	C
intergenic	Tap2(dist=1381),H2-Ob(dist=21203)	chr17	34217702	T	C
intergenic	Tap2(dist=1503),H2-Ob(dist=21081)	chr17	34217824	T	C
intergenic	Tap2(dist=1557),H2-Ob(dist=21027)	chr17	34217878	C	T
intergenic	Tap2(dist=1575),H2-Ob(dist=21009)	chr17	34217896	T	G
intergenic	Tap2(dist=1586),H2-Ob(dist=20998)	chr17	34217907	C	A
intergenic	Tap2(dist=1640),H2-Ob(dist=20944)	chr17	34217961	T	G
intergenic	Tap2(dist=1718),H2-Ob(dist=20866)	chr17	34218039	A	G
intergenic	Tap2(dist=1752),H2-Ob(dist=20832)	chr17	34218073	G	A
intergenic	Tap2(dist=1873),H2-Ob(dist=20711)	chr17	34218194	A	G
intergenic	Tap2(dist=1902),H2-Ob(dist=20682)	chr17	34218223	C	A
intergenic	Tap2(dist=1945),H2-Ob(dist=20639)	chr17	34218266	T	C
intergenic	Tap2(dist=2021),H2-Ob(dist=20563)	chr17	34218342	C	T
intergenic	Tap2(dist=2100),H2-Ob(dist=20484)	chr17	34218421	A	C
intergenic	Tap2(dist=2156),H2-Ob(dist=20428)	chr17	34218477	A	G
intergenic	Tap2(dist=2160),H2-Ob(dist=20424)	chr17	34218481	C	T
intergenic	Tap2(dist=2165),H2-Ob(dist=20419)	chr17	34218486	T	C
intergenic	Tap2(dist=2230),H2-Ob(dist=20354)	chr17	34218551	T	C
intergenic	Tap2(dist=2240),H2-Ob(dist=20344)	chr17	34218561	C	T
intergenic	Tap2(dist=2241),H2-Ob(dist=20343)	chr17	34218562	A	G
intergenic	Tap2(dist=2246),H2-Ob(dist=20338)	chr17	34218567	C	T
intergenic	Tap2(dist=2332),H2-Ob(dist=20252)	chr17	34218653	C	T
intergenic	Tap2(dist=2398),H2-Ob(dist=20186)	chr17	34218719	G	A
intergenic	Tap2(dist=2583),H2-Ob(dist=20001)	chr17	34218904	G	T
intergenic	Tap2(dist=2687),H2-Ob(dist=19897)	chr17	34219008	C	G
intergenic	Tap2(dist=2701),H2-Ob(dist=19883)	chr17	34219022	A	G
intergenic	Tap2(dist=2709),H2-Ob(dist=19875)	chr17	34219030	G	A
intergenic	Tap2(dist=2789),H2-Ob(dist=19795)	chr17	34219110	C	T
intergenic	Tap2(dist=2843),H2-Ob(dist=19741)	chr17	34219164	A	G
intergenic	Tap2(dist=2848),H2-Ob(dist=19736)	chr17	34219169	C	A
intergenic	Tap2(dist=2864),H2-Ob(dist=19720)	chr17	34219185	C	T
intergenic	Tap2(dist=2906),H2-Ob(dist=19678)	chr17	34219227	A	G
intergenic	Tap2(dist=7841),H2-Ob(dist=14743)	chr17	34224162	T	A
intergenic	Tap2(dist=7890),H2-Ob(dist=14694)	chr17	34224211	T	C
intergenic	Tap2(dist=8066),H2-Ob(dist=14518)	chr17	34224387	A	T

intergenic	Tap2(dist=8103),H2-Ob(dist=14481)	chr17	34224424	A	G
intergenic	Tap2(dist=8201),H2-Ob(dist=14383)	chr17	34224522	T	C
intergenic	Tap2(dist=8264),H2-Ob(dist=14320)	chr17	34224585	C	T
intergenic	Tap2(dist=8381),H2-Ob(dist=14203)	chr17	34224702	C	T
intergenic	Tap2(dist=8441),H2-Ob(dist=14143)	chr17	34224762	C	T
intergenic	Tap2(dist=8521),H2-Ob(dist=14063)	chr17	34224842	A	G
intergenic	Tap2(dist=8621),H2-Ob(dist=13963)	chr17	34224942	G	A
intergenic	Tap2(dist=8642),H2-Ob(dist=13942)	chr17	34224963	T	G
intergenic	Tap2(dist=8663),H2-Ob(dist=13921)	chr17	34224984	G	A
intergenic	Tap2(dist=8967),H2-Ob(dist=13617)	chr17	34225288	G	C
intergenic	Tap2(dist=9017),H2-Ob(dist=13567)	chr17	34225338	C	T
intergenic	Tap2(dist=9034),H2-Ob(dist=13550)	chr17	34225355	T	C
intergenic	Tap2(dist=9062),H2-Ob(dist=13522)	chr17	34225383	T	G
intergenic	Tap2(dist=9086),H2-Ob(dist=13498)	chr17	34225407	C	T
intergenic	Tap2(dist=9100),H2-Ob(dist=13484)	chr17	34225421	C	T
intergenic	Tap2(dist=9106),H2-Ob(dist=13478)	chr17	34225427	C	T
intergenic	Tap2(dist=9113),H2-Ob(dist=13471)	chr17	34225434	A	T
intergenic	Tap2(dist=9170),H2-Ob(dist=13414)	chr17	34225491	G	T
intergenic	Tap2(dist=9177),H2-Ob(dist=13407)	chr17	34225498	A	G
intergenic	Tap2(dist=9178),H2-Ob(dist=13406)	chr17	34225499	A	C
intergenic	Tap2(dist=9180),H2-Ob(dist=13404)	chr17	34225501	T	C
intergenic	Tap2(dist=9223),H2-Ob(dist=13361)	chr17	34225544	A	G
intergenic	Tap2(dist=9228),H2-Ob(dist=13356)	chr17	34225549	T	C
intergenic	Tap2(dist=9312),H2-Ob(dist=13272)	chr17	34225633	T	C
intergenic	Tap2(dist=9399),H2-Ob(dist=13185)	chr17	34225720	T	C
intergenic	Tap2(dist=9422),H2-Ob(dist=13162)	chr17	34225743	C	A
intergenic	Tap2(dist=9434),H2-Ob(dist=13150)	chr17	34225755	C	T
intergenic	Tap2(dist=16688),H2-Ob(dist=5896)	chr17	34233009	C	T
intergenic	Tap2(dist=16703),H2-Ob(dist=5881)	chr17	34233024	A	C
intergenic	Tap2(dist=16706),H2-Ob(dist=5878)	chr17	34233027	A	T
intergenic	Tap2(dist=16718),H2-Ob(dist=5866)	chr17	34233039	T	A
intergenic	Tap2(dist=16757),H2-Ob(dist=5827)	chr17	34233078	A	G
intergenic	Tap2(dist=16758),H2-Ob(dist=5826)	chr17	34233079	G	T
intergenic	Tap2(dist=16808),H2-Ob(dist=5776)	chr17	34233129	A	T
intergenic	Tap2(dist=16810),H2-Ob(dist=5774)	chr17	34233131	A	C
intergenic	Tap2(dist=16811),H2-Ob(dist=5773)	chr17	34233132	G	T
intergenic	Tap2(dist=16885),H2-Ob(dist=5699)	chr17	34233206	C	T
intergenic	Tap2(dist=16891),H2-Ob(dist=5693)	chr17	34233212	G	C
intergenic	Tap2(dist=16894),H2-Ob(dist=5690)	chr17	34233215	A	G
intergenic	Tap2(dist=16922),H2-Ob(dist=5662)	chr17	34233243	A	C
intergenic	Tap2(dist=16927),H2-Ob(dist=5657)	chr17	34233248	A	G

intergenic	Tap2(dist=16931),H2-Ob(dist=5653)	chr17	34233252	A	C
intergenic	Tap2(dist=16951),H2-Ob(dist=5633)	chr17	34233272	G	A
intergenic	Tap2(dist=17078),H2-Ob(dist=5506)	chr17	34233399	C	T
intergenic	Tap2(dist=17116),H2-Ob(dist=5468)	chr17	34233437	T	C
intergenic	Tap2(dist=17148),H2-Ob(dist=5436)	chr17	34233469	C	T
intergenic	Tap2(dist=17164),H2-Ob(dist=5420)	chr17	34233485	C	T
intergenic	Tap2(dist=17184),H2-Ob(dist=5400)	chr17	34233505	T	C
intergenic	Tap2(dist=17190),H2-Ob(dist=5394)	chr17	34233511	T	G
intergenic	Tap2(dist=17200),H2-Ob(dist=5384)	chr17	34233521	C	T
intergenic	Tap2(dist=17295),H2-Ob(dist=5289)	chr17	34233616	A	T
intergenic	Tap2(dist=17371),H2-Ob(dist=5213)	chr17	34233692	C	T
intergenic	Tap2(dist=17373),H2-Ob(dist=5211)	chr17	34233694	T	G
intergenic	Tap2(dist=17386),H2-Ob(dist=5198)	chr17	34233707	T	C
intergenic	Tap2(dist=17593),H2-Ob(dist=4991)	chr17	34233914	A	G
intergenic	Tap2(dist=17602),H2-Ob(dist=4982)	chr17	34233923	C	T
intergenic	Tap2(dist=17646),H2-Ob(dist=4938)	chr17	34233967	A	G
intergenic	Tap2(dist=17730),H2-Ob(dist=4854)	chr17	34234051	T	C
intergenic	Tap2(dist=17737),H2-Ob(dist=4847)	chr17	34234058	G	A
intergenic	Tap2(dist=17948),H2-Ob(dist=4636)	chr17	34234269	A	G
intergenic	Tap2(dist=18009),H2-Ob(dist=4575)	chr17	34234330	C	T
intergenic	Tap2(dist=18043),H2-Ob(dist=4541)	chr17	34234364	G	T
intergenic	Tap2(dist=18082),H2-Ob(dist=4502)	chr17	34234403	A	G
intergenic	Tap2(dist=18090),H2-Ob(dist=4494)	chr17	34234411	T	G
intergenic	Tap2(dist=18091),H2-Ob(dist=4493)	chr17	34234412	T	G
intergenic	Tap2(dist=18143),H2-Ob(dist=4441)	chr17	34234464	A	C
intergenic	Tap2(dist=18166),H2-Ob(dist=4418)	chr17	34234487	T	C
intergenic	Tap2(dist=18178),H2-Ob(dist=4406)	chr17	34234499	C	T
intergenic	Tap2(dist=18216),H2-Ob(dist=4368)	chr17	34234537	A	G
intergenic	Tap2(dist=18221),H2-Ob(dist=4363)	chr17	34234542	G	T
intergenic	Tap2(dist=18421),H2-Ob(dist=4163)	chr17	34234742	T	C
intergenic	Tap2(dist=18484),H2-Ob(dist=4100)	chr17	34234805	A	G
intergenic	Tap2(dist=18583),H2-Ob(dist=4001)	chr17	34234904	T	C
intergenic	Tap2(dist=18599),H2-Ob(dist=3985)	chr17	34234920	G	A
intergenic	Tap2(dist=18632),H2-Ob(dist=3952)	chr17	34234953	C	T
intergenic	Tap2(dist=18690),H2-Ob(dist=3894)	chr17	34235011	C	T
intergenic	Tap2(dist=18746),H2-Ob(dist=3838)	chr17	34235067	T	C
intergenic	Tap2(dist=18771),H2-Ob(dist=3813)	chr17	34235092	C	G
intergenic	Tap2(dist=18887),H2-Ob(dist=3697)	chr17	34235208	T	C
intergenic	Tap2(dist=18994),H2-Ob(dist=3590)	chr17	34235315	C	T
intergenic	Tap2(dist=19026),H2-Ob(dist=3558)	chr17	34235347	T	A
intergenic	Tap2(dist=19120),H2-Ob(dist=3464)	chr17	34235441	C	T

intergenic	Tap2(dist=19281),H2-Ob(dist=3303)	chr17	34235602	A	G
intergenic	Tap2(dist=19301),H2-Ob(dist=3283)	chr17	34235622	A	G
intergenic	Tap2(dist=19318),H2-Ob(dist=3266)	chr17	34235639	A	G
intergenic	Tap2(dist=19337),H2-Ob(dist=3247)	chr17	34235658	C	T
intergenic	Tap2(dist=19427),H2-Ob(dist=3157)	chr17	34235748	T	C
intergenic	Tap2(dist=19589),H2-Ob(dist=2995)	chr17	34235910	C	A
intergenic	Tap2(dist=19815),H2-Ob(dist=2769)	chr17	34236136	G	A
intergenic	Tap2(dist=19836),H2-Ob(dist=2748)	chr17	34236157	A	G
intergenic	Tap2(dist=19843),H2-Ob(dist=2741)	chr17	34236164	T	C
intergenic	Tap2(dist=19880),H2-Ob(dist=2704)	chr17	34236201	A	G
intergenic	Tap2(dist=19882),H2-Ob(dist=2702)	chr17	34236203	G	T
intergenic	Tap2(dist=19885),H2-Ob(dist=2699)	chr17	34236206	C	T
intergenic	Tap2(dist=19899),H2-Ob(dist=2685)	chr17	34236220	G	A
intergenic	Tap2(dist=19912),H2-Ob(dist=2672)	chr17	34236233	C	T
intergenic	Tap2(dist=19917),H2-Ob(dist=2667)	chr17	34236238	C	T
intergenic	Tap2(dist=19963),H2-Ob(dist=2621)	chr17	34236284	T	C
intergenic	Tap2(dist=20002),H2-Ob(dist=2582)	chr17	34236323	G	A
intergenic	Tap2(dist=20035),H2-Ob(dist=2549)	chr17	34236356	T	A
intergenic	Tap2(dist=20063),H2-Ob(dist=2521)	chr17	34236384	C	T
intergenic	Tap2(dist=20123),H2-Ob(dist=2461)	chr17	34236444	C	G
intergenic	Tap2(dist=20159),H2-Ob(dist=2425)	chr17	34236480	A	G
intergenic	Tap2(dist=20166),H2-Ob(dist=2418)	chr17	34236487	A	G
intergenic	Tap2(dist=20168),H2-Ob(dist=2416)	chr17	34236489	T	C
intergenic	Tap2(dist=20321),H2-Ob(dist=2263)	chr17	34236642	C	T
intergenic	Tap2(dist=20366),H2-Ob(dist=2218)	chr17	34236687	A	G
intergenic	Tap2(dist=20404),H2-Ob(dist=2180)	chr17	34236725	A	G
intergenic	Tap2(dist=20441),H2-Ob(dist=2143)	chr17	34236762	G	A
intergenic	Tap2(dist=20443),H2-Ob(dist=2141)	chr17	34236764	T	G
intergenic	Tap2(dist=20460),H2-Ob(dist=2124)	chr17	34236781	C	T
intergenic	Tap2(dist=20475),H2-Ob(dist=2109)	chr17	34236796	T	C
intergenic	Tap2(dist=20535),H2-Ob(dist=2049)	chr17	34236856	A	C
intergenic	Tap2(dist=20601),H2-Ob(dist=1983)	chr17	34236922	T	C
intergenic	Tap2(dist=20612),H2-Ob(dist=1972)	chr17	34236933	A	G
intergenic	Tap2(dist=20704),H2-Ob(dist=1880)	chr17	34237025	A	C
intergenic	Tap2(dist=20798),H2-Ob(dist=1786)	chr17	34237119	G	T
intergenic	Tap2(dist=20869),H2-Ob(dist=1715)	chr17	34237190	G	T
intergenic	Tap2(dist=20955),H2-Ob(dist=1629)	chr17	34237276	A	G
intergenic	Tap2(dist=20959),H2-Ob(dist=1625)	chr17	34237280	C	T
intergenic	Tap2(dist=20978),H2-Ob(dist=1606)	chr17	34237299	T	A
intergenic	Tap2(dist=21018),H2-Ob(dist=1566)	chr17	34237339	C	T
intergenic	Tap2(dist=21046),H2-Ob(dist=1538)	chr17	34237367	G	A

intergenic	Tap2(dist=21101),H2-Ob(dist=1483)	chr17	34237422	C	T
intergenic	Tap2(dist=21120),H2-Ob(dist=1464)	chr17	34237441	T	C
intergenic	Tap2(dist=21398),H2-Ob(dist=1186)	chr17	34237719	T	C
intergenic	Tap2(dist=21400),H2-Ob(dist=1184)	chr17	34237721	T	C
upstream	H2-Ob	chr17	34238000	C	T
upstream	H2-Ob	chr17	34238263	G	A
upstream	H2-Ob	chr17	34238292	G	A
upstream	H2-Ob	chr17	34238346	G	T
upstream	H2-Ob	chr17	34238425	T	C
upstream	H2-Ob	chr17	34238487	C	T
upstream	H2-Ob	chr17	34238512	G	A
upstream	H2-Ob	chr17	34238725	G	A
upstream	H2-Ob	chr17	34238777	C	T
upstream	H2-Ob	chr17	34238882	C	G
UTR5	H2-Ob(NM_010389:c.-42T>G)	chr17	34238930	T	G
exonic	H2-Ob	chr17	34238985	G	T
exonic	H2-Ob	chr17	34238987	G	T
intronic	H2-Ob	chr17	34239149	C	G
intronic	H2-Ob	chr17	34239199	A	G
intronic	H2-Ob	chr17	34239207	T	C
intronic	H2-Ob	chr17	34239403	A	T
intronic	H2-Ob	chr17	34239454	T	C
intronic	H2-Ob	chr17	34239466	T	G
intronic	H2-Ob	chr17	34239517	A	G
intronic	H2-Ob	chr17	34239744	T	C
intronic	H2-Ob	chr17	34239748	G	A
intronic	H2-Ob	chr17	34239780	A	G
intronic	H2-Ob	chr17	34239807	C	T
intronic	H2-Ob	chr17	34239912	C	A
intronic	H2-Ob	chr17	34239921	G	T
intronic	H2-Ob	chr17	34239934	C	T
intronic	H2-Ob	chr17	34239969	G	A
intronic	H2-Ob	chr17	34240049	A	G
intronic	H2-Ob	chr17	34240053	G	C
intronic	H2-Ob	chr17	34240161	C	T
intronic	H2-Ob	chr17	34240258	A	C
intronic	H2-Ob	chr17	34240292	T	C
intronic	H2-Ob	chr17	34240302	A	C
intronic	H2-Ob	chr17	34240325	G	T
intronic	H2-Ob	chr17	34240326	T	C
intronic	H2-Ob	chr17	34240328	T	C

intronic	H2-Ob	chr17	34240408	G	T
intronic	H2-Ob	chr17	34240409	A	C
intronic	H2-Ob	chr17	34240456	T	C
intronic	H2-Ob	chr17	34240721	C	G
intronic	H2-Ob	chr17	34240749	C	T
intronic	H2-Ob	chr17	34240785	T	C
intronic	H2-Ob	chr17	34240801	T	C
intronic	H2-Ob	chr17	34240868	G	A
exonic	H2-Ob	chr17	34241033	G	A
exonic	H2-Ob	chr17	34241245	A	G
intronic	H2-Ob	chr17	34241469	A	T
intronic	H2-Ob	chr17	34241550	G	C
intronic	H2-Ob	chr17	34241561	A	C
intronic	H2-Ob	chr17	34241612	G	T
intronic	H2-Ob	chr17	34241753	C	T
intronic	H2-Ob	chr17	34241908	C	T
intronic	H2-Ob	chr17	34241943	T	C
intronic	H2-Ob	chr17	34241952	T	C
intronic	H2-Ob	chr17	34241976	A	G
intronic	H2-Ob	chr17	34242098	A	T
intronic	H2-Ob	chr17	34242110	G	A
intronic	H2-Ob	chr17	34242155	T	C
intronic	H2-Ob	chr17	34242356	G	C
intronic	H2-Ob	chr17	34242397	G	C
intronic	H2-Ob	chr17	34242404	C	T
exonic	H2-Ob	chr17	34242459	T	C
exonic	H2-Ob	chr17	34242474	G	A
intronic	H2-Ob	chr17	34242742	C	T
intronic	H2-Ob	chr17	34242750	C	T
intronic	H2-Ob	chr17	34242856	C	T
intronic	H2-Ob	chr17	34242861	C	T
intronic	H2-Ob	chr17	34243274	G	A
intronic	H2-Ob	chr17	34243275	T	C
intronic	H2-Ob	chr17	34243283	T	C
intronic	H2-Ob	chr17	34243303	C	T
intronic	H2-Ob	chr17	34243307	C	T
intronic	H2-Ob	chr17	34243360	C	T
intronic	H2-Ob	chr17	34243370	C	T
exonic	H2-Ob	chr17	34243472	T	C
exonic	H2-Ob	chr17	34243516	T	C
exonic	H2-Ob	chr17	34243541	C	T

exonic	H2-Ob	chr17	34243550	G	C
intronic	H2-Ob	chr17	34243582	A	G
intronic	H2-Ob	chr17	34243674	A	G
intronic	H2-Ob	chr17	34243686	A	G
intronic	H2-Ob	chr17	34243730	G	A
intronic	H2-Ob	chr17	34243731	A	G
intronic	H2-Ob	chr17	34243732	A	G
intronic	H2-Ob	chr17	34243737	C	T
intronic	H2-Ob	chr17	34243789	T	A
intronic	H2-Ob	chr17	34243821	A	C
intronic	H2-Ob	chr17	34243828	A	C
intronic	H2-Ob	chr17	34243832	T	C
intronic	H2-Ob	chr17	34243870	C	T
intronic	H2-Ob	chr17	34243945	T	C
intronic	H2-Ob	chr17	34243971	T	C
intronic	H2-Ob	chr17	34243995	A	G
intronic	H2-Ob	chr17	34244012	T	C
intronic	H2-Ob	chr17	34244013	G	A
intronic	H2-Ob	chr17	34244018	C	G
intronic	H2-Ob	chr17	34244036	G	C
intronic	H2-Ob	chr17	34244076	A	G
exonic	H2-Ob	chr17	34244101	A	C
exonic	H2-Ob	chr17	34244102	G	T
UTR3	H2-Ob(NM_010389:c.*309A>G)	chr17	34244430	A	G
UTR3	H2-Ob(NM_010389:c.*314G>A)	chr17	34244435	G	A
UTR3	H2-Ob(NM_010389:c.*646A>G)	chr17	34244767	A	G
UTR3	H2-Ob(NM_010389:c.*647T>C)	chr17	34244768	T	C
UTR3	H2-Ob(NM_010389:c.*664T>C)	chr17	34244785	T	C
UTR3	H2-Ob(NM_010389:c.*760A>G)	chr17	34244881	A	G
UTR3	H2-Ob(NM_010389:c.*815T>C)	chr17	34244936	T	C
UTR3	H2-Ob(NM_010389:c.*1324A>G)	chr17	34245445	A	G
UTR3	H2-Ob(NM_010389:c.*1359C>T)	chr17	34245480	C	T
UTR3	H2-Ob(NM_010389:c.*1491T>C)	chr17	34245612	T	C
UTR3	H2-Ob(NM_010389:c.*1578A>T)	chr17	34245699	A	T
UTR3	H2-Ob(NM_010389:c.*1581T>C)	chr17	34245702	T	C
downstream	H2-Ob	chr17	34245929	G	A
downstream	H2-Ob	chr17	34245974	G	A
downstream	H2-Ob	chr17	34245985	T	G
downstream	H2-Ob	chr17	34245998	G	T
downstream	H2-Ob	chr17	34246026	C	G
downstream	H2-Ob	chr17	34246130	T	C

downstream	H2-Ob	chr17	34246175	C	T
downstream	H2-Ob	chr17	34246249	A	G
downstream	H2-Ob	chr17	34246301	G	A
downstream	H2-Ob	chr17	34246433	T	C
downstream	H2-Ob	chr17	34246464	G	A
downstream	H2-Ob	chr17	34246511	C	T
downstream	H2-Ob	chr17	34246678	T	C
downstream	H2-Ob	chr17	34246681	C	A
downstream	H2-Ob	chr17	34246683	A	G
downstream	H2-Ob	chr17	34246794	G	A
downstream	H2-Ob	chr17	34246808	T	G
downstream	H2-Ob	chr17	34246818	C	T
downstream	H2-Ob	chr17	34246844	G	C
downstream	H2-Ob	chr17	34246858	A	C
downstream	H2-Ob	chr17	34246876	G	A
downstream	H2-Ob	chr17	34246901	A	T

All single nucleotide variants (SNVs) in BALB/cJ. **Type** = indicates a single nucleotide variant (SNV) identified relative to a known gene; **Gene (distance)**= gene containing SNV, or distance to nearest genes in 3' and 5' direction**; CHROM** = chromosomal location of SNV; **POS** = genomic location of SNV; **C57BL/6J** = reference; **BALB/cJ** = detected nucleotide. The *vic1* critical region is highlighted in yellow.

Supplemental Table 3a

Type	Gene	RefSeq ID	EXON	NT change	AA change	CHROM	POS	C57BL/6J	C3H/HeN
nonsynonymous SNV	Tap2	NM_011530	exon2	c.A170G	p.E57G,	chr17	34205464	A	G
nonsynonymous SNV	Tap2	NM_011530	exon2	c.G259A	p.A87T,	chr17	34205553	G	A
nonsynonymous SNV	Tap2	NM_011530	exon6	c.A1058G	p.H353R,	chr17	34211985	A	G
nonsynonymous SNV	Tap2	NM_011530	exon8	c.A1346G	p.K449R,	chr17	34214091	A	G
nonsynonymous SNV	H2-Ob	NM_010389	exon2	c.G216A	p.M72I,	chr17	34241132	G	A
nonsynonymous SNV	H2-Ob	NM_010389	exon4	c.G645T	p.M215I,	chr17	34243469	G	T
nonsynonymous SNV	H2-Ob	NM_010389	exon4	c.T692C	p.V231A,	chr17	34243516	T	C
nonsynonymous SNV	H2-Ob	NM_010389	exon6	c.A796C	p.S266R,	chr17	34244101	A	C
nonsynonymous SNV	H2-Ob	NM_010389	exon6	c.G797T	p.S266I,	chr17	34244102	G	T

Nonsynonymous single nucleotide variants (SNVs) in C3H/HeN coding exons. **Type** = indicates a nonsynonymous single nucleotide variant (SNV) identified; **Gene** = gene name**; RefSeq ID** = reference annotated gene ID; **EXON** = exon number containing SNV in the annotated gene; **NT change** = change in base; **AA change** = change in amino acid; **CHROM** = chromosomal location of SNV; **POS** = genomic location of SNV; **C57BL/6J** = reference; **C3H/HeN** = alternative nucleotide.

Supplemental Table 3b

Type	Gene	RefSeq ID	EXON	NT change	AA change	CHROM	POS	C57BL/6J	C3H/HeN
nonframeshift insertion	Tap2	NM_011530	exon2	c.404_405insACT	p.T135delinsTL,	chr17	34205698	-	ACT

Structural variant (deletion or insertion) in C3H/HeN coding exons coding exons**. Type** = indicates structural variant identified; **Gene** = gene name**; RefSeq ID** = reference annotated gene ID; **EXON** = exon number containing SNV in the annotated gene; **NT change** = change in base; **AA change** = change in amino acid; **CHROM** = chromosomal location of SNV; **POS** = genomic location of SNV; **C57BL/6J** = reference; **C3H/HeN** = insertion. ACT, 3–nt insertion.

Supplemental Table 3c

Type	Gene (distance)	CHROM	POS	C57BL/6J	C3H/HeN
intergenic	Psmb8(dist=1218),Tap2(dist=1807)	chr17	34202672	C	G
intergenic	Psmb8(dist=1338),Tap2(dist=1687)	chr17	34202792	G	T
intergenic	Psmb8(dist=1344),Tap2(dist=1681)	chr17	34202798	G	A
intergenic	Psmb8(dist=1367),Tap2(dist=1658)	chr17	34202821	G	A
intergenic	Psmb8(dist=1380),Tap2(dist=1645)	chr17	34202834	C	T
intergenic	Psmb8(dist=1474),Tap2(dist=1551)	chr17	34202928	T	G
intergenic	Psmb8(dist=1531),Tap2(dist=1494)	chr17	34202985	A	G
intergenic	Psmb8(dist=1593),Tap2(dist=1432)	chr17	34203047	A	G
intergenic	Psmb8(dist=1711),Tap2(dist=1314)	chr17	34203165	A	G
intergenic	Psmb8(dist=1718),Tap2(dist=1307)	chr17	34203172	A	T
upstream	Tap2	chr17	34203688	C	A
upstream	Tap2	chr17	34203930	G	A
upstream	Tap2	chr17	34204147	A	C
upstream	Tap2	chr17	34204297	T	A
upstream	Tap2	chr17	34204337	G	C
upstream	Tap2	chr17	34204344	T	C
UTR5	Tap2(NM_011530:c.-814C>G)	chr17	34204481	C	G
intronic	Tap2	chr17	34204639	T	C
intronic	Tap2	chr17	34204806	C	T
intronic	Tap2	chr17	34204847	C	T
intronic	Tap2	chr17	34204874	C	T
intronic	Tap2	chr17	34204892	C	A
intronic	Tap2	chr17	34204972	A	G
intronic	Tap2	chr17	34205059	T	A
intronic	Tap2	chr17	34205238	A	G
exonic	Tap2	chr17	34205396	G	A
exonic	Tap2	chr17	34205464	A	G
exonic	Tap2	chr17	34205474	A	G
exonic	Tap2	chr17	34205537	T	C
exonic	Tap2	chr17	34205553	G	A
exonic	Tap2	chr17	34205621	T	C
intronic	Tap2	chr17	34205793	A	G
exonic	Tap2	chr17	34205877	A	G
intronic	Tap2	chr17	34206250	G	A
intronic	Tap2	chr17	34206446	C	T
intronic	Tap2	chr17	34206621	T	G
intronic	Tap2	chr17	34206821	G	T
intronic	Tap2	chr17	34206882	C	G

intronic	Tap2	chr17	34207233	A	G
intronic	Tap2	chr17	34207259	T	C
intronic	Tap2	chr17	34207571	C	T
intronic	Tap2	chr17	34207609	T	C
intronic	Tap2	chr17	34207651	G	A
intronic	Tap2	chr17	34207858	T	C
intronic	Tap2	chr17	34207878	A	G
intronic	Tap2	chr17	34208068	A	T
intronic	Tap2	chr17	34208069	T	G
intronic	Tap2	chr17	34208138	C	A
intronic	Tap2	chr17	34208200	C	A
intronic	Tap2	chr17	34208303	T	G
intronic	Tap2	chr17	34208329	C	T
intronic	Tap2	chr17	34208391	C	T
intronic	Tap2	chr17	34208456	A	G
intronic	Tap2	chr17	34208497	G	A
intronic	Tap2	chr17	34208576	G	T
intronic	Tap2	chr17	34208621	T	C
exonic	Tap2	chr17	34208790	C	T
intronic	Tap2	chr17	34208919	C	T
intronic	Tap2	chr17	34208922	T	C
intronic	Tap2	chr17	34209051	A	G
exonic	Tap2	chr17	34209104	A	C
intronic	Tap2	chr17	34209341	G	A
intronic	Tap2	chr17	34209413	C	T
intronic	Tap2	chr17	34209476	A	G
intronic	Tap2	chr17	34209525	A	G
intronic	Tap2	chr17	34209540	C	T
intronic	Tap2	chr17	34209550	C	A
intronic	Tap2	chr17	34209613	G	A
intronic	Tap2	chr17	34209686	C	A
intronic	Tap2	chr17	34209827	C	A
intronic	Tap2	chr17	34209914	G	T
intronic	Tap2	chr17	34209923	G	A
intronic	Tap2	chr17	34210055	G	T
intronic	Tap2	chr17	34210100	C	T
intronic	Tap2	chr17	34210146	G	C
intronic	Tap2	chr17	34210352	T	C
intronic	Tap2	chr17	34210446	A	G
intronic	Tap2	chr17	34210485	A	G
intronic	Tap2	chr17	34210546	C	T

intronic	Tap2	chr17	34210552	C	T
intronic	Tap2	chr17	34210621	T	C
intronic	Tap2	chr17	34210638	T	C
intronic	Tap2	chr17	34210643	T	G
intronic	Tap2	chr17	34210675	A	G
intronic	Tap2	chr17	34210725	T	C
intronic	Tap2	chr17	34210775	T	C
intronic	Tap2	chr17	34210793	C	A
intronic	Tap2	chr17	34211015	T	G
intronic	Tap2	chr17	34211084	C	T
intronic	Tap2	chr17	34211086	G	C
intronic	Tap2	chr17	34211117	G	A
intronic	Tap2	chr17	34211154	T	G
intronic	Tap2	chr17	34211156	T	C
intronic	Tap2	chr17	34211295	T	G
intronic	Tap2	chr17	34211356	G	C
intronic	Tap2	chr17	34211522	C	T
intronic	Tap2	chr17	34211645	T	C
intronic	Tap2	chr17	34211799	T	C
intronic	Tap2	chr17	34211836	T	C
intronic	Tap2	chr17	34211866	T	C
exonic	Tap2	chr17	34211951	C	A
exonic	Tap2	chr17	34211985	A	G
intronic	Tap2	chr17	34212147	G	A
intronic	Tap2	chr17	34212739	T	C
intronic	Tap2	chr17	34212740	A	C
intronic	Tap2	chr17	34212741	A	G
intronic	Tap2	chr17	34212753	C	T
intronic	Tap2	chr17	34213098	G	A
intronic	Tap2	chr17	34213169	A	C
intronic	Tap2	chr17	34213210	C	T
intronic	Tap2	chr17	34213332	G	A
intronic	Tap2	chr17	34213343	C	T
intronic	Tap2	chr17	34213364	T	C
intronic	Tap2	chr17	34213404	C	A
intronic	Tap2	chr17	34213422	T	A
intronic	Tap2	chr17	34213751	T	C
exonic	Tap2	chr17	34214091	A	G
intronic	Tap2	chr17	34214519	T	A
intronic	Tap2	chr17	34214549	C	A
intronic	Tap2	chr17	34214874	A	G

intronic	Tap2	chr17	34214929	T	A
intronic	Tap2	chr17	34215049	T	A
intronic	Tap2	chr17	34215071	C	A
intronic	Tap2	chr17	34215272	C	A
intronic	Tap2	chr17	34215495	A	G
intronic	Tap2	chr17	34215550	A	G
intronic	Tap2	chr17	34215571	C	G
intronic	Tap2	chr17	34215708	A	G
intronic	Tap2	chr17	34215905	C	A
exonic	Tap2	chr17	34216042	G	A
UTR3	Tap2(NM_011530:c.*7C>T)	chr17	34216100	C	T
downstream	Tap2	chr17	34216343	G	C
downstream	Tap2	chr17	34216428	G	A
downstream	Tap2	chr17	34216482	T	C
downstream	Tap2	chr17	34216641	C	T
downstream	Tap2	chr17	34216707	T	C
downstream	Tap2	chr17	34216712	A	G
downstream	Tap2	chr17	34216829	G	T
downstream	Tap2	chr17	34216908	A	G
downstream	Tap2	chr17	34216949	C	T
downstream	Tap2	chr17	34217048	T	C
downstream	Tap2	chr17	34217118	C	A
downstream	Tap2	chr17	34217125	C	T
downstream	Tap2	chr17	34217193	G	A
intergenic	Tap2(dist=1075),H2-Ob(dist=21509)	chr17	34217396	A	T
intergenic	Tap2(dist=1141),H2-Ob(dist=21443)	chr17	34217462	G	A
intergenic	Tap2(dist=1229),H2-Ob(dist=21355)	chr17	34217550	C	A
intergenic	Tap2(dist=1370),H2-Ob(dist=21214)	chr17	34217691	A	G
intergenic	Tap2(dist=1503),H2-Ob(dist=21081)	chr17	34217824	T	C
intergenic	Tap2(dist=1718),H2-Ob(dist=20866)	chr17	34218039	A	G
intergenic	Tap2(dist=1752),H2-Ob(dist=20832)	chr17	34218073	G	A
intergenic	Tap2(dist=1755),H2-Ob(dist=20829)	chr17	34218076	C	A
intergenic	Tap2(dist=1945),H2-Ob(dist=20639)	chr17	34218266	T	C
intergenic	Tap2(dist=1972),H2-Ob(dist=20612)	chr17	34218293	C	T
intergenic	Tap2(dist=2021),H2-Ob(dist=20563)	chr17	34218342	C	T
intergenic	Tap2(dist=2100),H2-Ob(dist=20484)	chr17	34218421	A	C
intergenic	Tap2(dist=2156),H2-Ob(dist=20428)	chr17	34218477	A	G
intergenic	Tap2(dist=2230),H2-Ob(dist=20354)	chr17	34218551	T	C
intergenic	Tap2(dist=2241),H2-Ob(dist=20343)	chr17	34218562	A	G
intergenic	Tap2(dist=2452),H2-Ob(dist=20132)	chr17	34218773	G	T
intergenic	Tap2(dist=2468),H2-Ob(dist=20116)	chr17	34218789	G	A

intergenic	Tap2(dist=2715),H2-Ob(dist=19869)	chr17	34219036	C	A
intergenic	Tap2(dist=2824),H2-Ob(dist=19760)	chr17	34219145	C	T
intergenic	Tap2(dist=2843),H2-Ob(dist=19741)	chr17	34219164	A	G
intergenic	Tap2(dist=2906),H2-Ob(dist=19678)	chr17	34219227	A	G
intergenic	Tap2(dist=3008),H2-Ob(dist=19576)	chr17	34219329	A	T
intergenic	Tap2(dist=3647),H2-Ob(dist=18937)	chr17	34219968	C	T
intergenic	Tap2(dist=7945),H2-Ob(dist=14639)	chr17	34224266	C	T
intergenic	Tap2(dist=8201),H2-Ob(dist=14383)	chr17	34224522	T	C
intergenic	Tap2(dist=8381),H2-Ob(dist=14203)	chr17	34224702	C	T
intergenic	Tap2(dist=8400),H2-Ob(dist=14184)	chr17	34224721	C	T
intergenic	Tap2(dist=8521),H2-Ob(dist=14063)	chr17	34224842	A	G
intergenic	Tap2(dist=8546),H2-Ob(dist=14038)	chr17	34224867	T	A
intergenic	Tap2(dist=8575),H2-Ob(dist=14009)	chr17	34224896	G	A
intergenic	Tap2(dist=8642),H2-Ob(dist=13942)	chr17	34224963	T	G
intergenic	Tap2(dist=8967),H2-Ob(dist=13617)	chr17	34225288	G	C
intergenic	Tap2(dist=9017),H2-Ob(dist=13567)	chr17	34225338	C	T
intergenic	Tap2(dist=9034),H2-Ob(dist=13550)	chr17	34225355	T	C
intergenic	Tap2(dist=9062),H2-Ob(dist=13522)	chr17	34225383	T	G
intergenic	Tap2(dist=9086),H2-Ob(dist=13498)	chr17	34225407	C	T
intergenic	Tap2(dist=9113),H2-Ob(dist=13471)	chr17	34225434	A	T
intergenic	Tap2(dist=9172),H2-Ob(dist=13412)	chr17	34225493	G	A
intergenic	Tap2(dist=9177),H2-Ob(dist=13407)	chr17	34225498	A	G
intergenic	Tap2(dist=9178),H2-Ob(dist=13406)	chr17	34225499	A	C
intergenic	Tap2(dist=9223),H2-Ob(dist=13361)	chr17	34225544	A	G
intergenic	Tap2(dist=9228),H2-Ob(dist=13356)	chr17	34225549	T	C
intergenic	Tap2(dist=9312),H2-Ob(dist=13272)	chr17	34225633	T	C
intergenic	Tap2(dist=9351),H2-Ob(dist=13233)	chr17	34225672	C	T
intergenic	Tap2(dist=9399),H2-Ob(dist=13185)	chr17	34225720	T	C
intergenic	Tap2(dist=9403),H2-Ob(dist=13181)	chr17	34225724	C	T
intergenic	Tap2(dist=16643),H2-Ob(dist=5941)	chr17	34232964	C	T
intergenic	Tap2(dist=16780),H2-Ob(dist=5804)	chr17	34233101	C	A
intergenic	Tap2(dist=16833),H2-Ob(dist=5751)	chr17	34233154	C	T
intergenic	Tap2(dist=17116),H2-Ob(dist=5468)	chr17	34233437	T	C
intergenic	Tap2(dist=17164),H2-Ob(dist=5420)	chr17	34233485	C	T
intergenic	Tap2(dist=17184),H2-Ob(dist=5400)	chr17	34233505	T	C
intergenic	Tap2(dist=17190),H2-Ob(dist=5394)	chr17	34233511	T	G
intergenic	Tap2(dist=17371),H2-Ob(dist=5213)	chr17	34233692	C	T
intergenic	Tap2(dist=17373),H2-Ob(dist=5211)	chr17	34233694	T	G
intergenic	Tap2(dist=17386),H2-Ob(dist=5198)	chr17	34233707	T	C
intergenic	Tap2(dist=17461),H2-Ob(dist=5123)	chr17	34233782	C	T
intergenic	Tap2(dist=17529),H2-Ob(dist=5055)	chr17	34233850	G	A

intergenic	Tap2(dist=17562),H2-Ob(dist=5022)	chr17	34233883	T	A
intergenic	Tap2(dist=17593),H2-Ob(dist=4991)	chr17	34233914	A	G
intergenic	Tap2(dist=17595),H2-Ob(dist=4989)	chr17	34233916	G	T
intergenic	Tap2(dist=17646),H2-Ob(dist=4938)	chr17	34233967	A	G
intergenic	Tap2(dist=17948),H2-Ob(dist=4636)	chr17	34234269	A	G
intergenic	Tap2(dist=17954),H2-Ob(dist=4630)	chr17	34234275	C	A
intergenic	Tap2(dist=18043),H2-Ob(dist=4541)	chr17	34234364	G	T
intergenic	Tap2(dist=18089),H2-Ob(dist=4495)	chr17	34234410	G	C
intergenic	Tap2(dist=18090),H2-Ob(dist=4494)	chr17	34234411	T	G
intergenic	Tap2(dist=18091),H2-Ob(dist=4493)	chr17	34234412	T	G
intergenic	Tap2(dist=18143),H2-Ob(dist=4441)	chr17	34234464	A	C
intergenic	Tap2(dist=18166),H2-Ob(dist=4418)	chr17	34234487	T	C
intergenic	Tap2(dist=18178),H2-Ob(dist=4406)	chr17	34234499	C	T
intergenic	Tap2(dist=18196),H2-Ob(dist=4388)	chr17	34234517	C	T
intergenic	Tap2(dist=18216),H2-Ob(dist=4368)	chr17	34234537	A	G
intergenic	Tap2(dist=18421),H2-Ob(dist=4163)	chr17	34234742	T	C
intergenic	Tap2(dist=18583),H2-Ob(dist=4001)	chr17	34234904	T	C
intergenic	Tap2(dist=18746),H2-Ob(dist=3838)	chr17	34235067	T	C
intergenic	Tap2(dist=18771),H2-Ob(dist=3813)	chr17	34235092	C	G
intergenic	Tap2(dist=18994),H2-Ob(dist=3590)	chr17	34235315	C	T
intergenic	Tap2(dist=19123),H2-Ob(dist=3461)	chr17	34235444	T	C
intergenic	Tap2(dist=20048),H2-Ob(dist=2536)	chr17	34236369	C	T
intergenic	Tap2(dist=20404),H2-Ob(dist=2180)	chr17	34236725	A	G
intergenic	Tap2(dist=20535),H2-Ob(dist=2049)	chr17	34236856	A	C
intergenic	Tap2(dist=20601),H2-Ob(dist=1983)	chr17	34236922	T	C
intergenic	Tap2(dist=20607),H2-Ob(dist=1977)	chr17	34236928	C	T
intergenic	Tap2(dist=20612),H2-Ob(dist=1972)	chr17	34236933	A	G
intergenic	Tap2(dist=20704),H2-Ob(dist=1880)	chr17	34237025	A	C
intergenic	Tap2(dist=21120),H2-Ob(dist=1464)	chr17	34237441	T	C
intergenic	Tap2(dist=21350),H2-Ob(dist=1234)	chr17	34237671	C	T
intergenic	Tap2(dist=21361),H2-Ob(dist=1223)	chr17	34237682	A	G
intergenic	Tap2(dist=21400),H2-Ob(dist=1184)	chr17	34237721	T	C
intergenic	Tap2(dist=21502),H2-Ob(dist=1082)	chr17	34237823	T	A
intergenic	Tap2(dist=21558),H2-Ob(dist=1026)	chr17	34237879	G	T
upstream	H2-Ob	chr17	34237922	G	A
upstream	H2-Ob	chr17	34237984	C	T
upstream	H2-Ob	chr17	34238023	G	A
upstream	H2-Ob	chr17	34238109	G	T
upstream	H2-Ob	chr17	34238125	C	A
upstream	H2-Ob	chr17	34238451	T	G
upstream	H2-Ob	chr17	34238452	C	T

upstream	H2-Ob	chr17	34238717	C	T
upstream	H2-Ob	chr17	34238898	T	C
upstream	H2-Ob	chr17	34238899	T	C
UTR5	H2-Ob(NM_010389:c.-42T>G)	chr17	34238930	T	G
intronic	H2-Ob	chr17	34239199	A	G
intronic	H2-Ob	chr17	34239357	A	C
intronic	H2-Ob	chr17	34239403	A	T
intronic	H2-Ob	chr17	34239517	A	G
intronic	H2-Ob	chr17	34239545	G	A
intronic	H2-Ob	chr17	34239547	C	T
intronic	H2-Ob	chr17	34239572	C	G
intronic	H2-Ob	chr17	34239691	G	A
intronic	H2-Ob	chr17	34239693	G	T
intronic	H2-Ob	chr17	34239694	A	T
intronic	H2-Ob	chr17	34239710	G	A
intronic	H2-Ob	chr17	34239744	T	C
intronic	H2-Ob	chr17	34239780	A	G
intronic	H2-Ob	chr17	34239912	C	A
intronic	H2-Ob	chr17	34240043	G	A
intronic	H2-Ob	chr17	34240261	T	C
intronic	H2-Ob	chr17	34240280	G	A
intronic	H2-Ob	chr17	34240289	C	T
intronic	H2-Ob	chr17	34240304	A	C
intronic	H2-Ob	chr17	34240409	A	C
intronic	H2-Ob	chr17	34240683	G	A
intronic	H2-Ob	chr17	34240698	A	G
intronic	H2-Ob	chr17	34240713	G	A
intronic	H2-Ob	chr17	34240721	C	G
intronic	H2-Ob	chr17	34240785	T	C
intronic	H2-Ob	chr17	34240801	T	C
intronic	H2-Ob	chr17	34240868	G	A
intronic	H2-Ob	chr17	34240905	C	T
exonic	H2-Ob	chr17	34241132	G	A
exonic	H2-Ob	chr17	34241204	G	A
intronic	H2-Ob	chr17	34241469	A	T
intronic	H2-Ob	chr17	34241526	A	G
intronic	H2-Ob	chr17	34241550	G	C
intronic	H2-Ob	chr17	34241561	A	C
intronic	H2-Ob	chr17	34241612	G	T
intronic	H2-Ob	chr17	34241630	G	T
intronic	H2-Ob	chr17	34241807	C	T

intronic	H2-Ob	chr17	34241976	A	G
intronic	H2-Ob	chr17	34242098	A	T
intronic	H2-Ob	chr17	34242110	G	A
intronic	H2-Ob	chr17	34242135	C	T
intronic	H2-Ob	chr17	34242155	T	C
intronic	H2-Ob	chr17	34242356	G	C
intronic	H2-Ob	chr17	34242380	C	T
intronic	H2-Ob	chr17	34242397	G	C
exonic	H2-Ob	chr17	34242459	T	C
exonic	H2-Ob	chr17	34242522	C	T
intronic	H2-Ob	chr17	34242742	C	T
intronic	H2-Ob	chr17	34242814	A	G
intronic	H2-Ob	chr17	34242863	C	T
intronic	H2-Ob	chr17	34242882	A	T
intronic	H2-Ob	chr17	34242963	C	T
intronic	H2-Ob	chr17	34242999	G	T
intronic	H2-Ob	chr17	34243048	C	T
intronic	H2-Ob	chr17	34243112	G	A
intronic	H2-Ob	chr17	34243277	C	T
intronic	H2-Ob	chr17	34243278	A	G
intronic	H2-Ob	chr17	34243283	T	C
intronic	H2-Ob	chr17	34243394	G	A
exonic	H2-Ob	chr17	34243469	G	T
exonic	H2-Ob	chr17	34243516	T	C
intronic	H2-Ob	chr17	34243582	A	G
intronic	H2-Ob	chr17	34243674	A	G
intronic	H2-Ob	chr17	34243686	A	G
intronic	H2-Ob	chr17	34243730	G	A
intronic	H2-Ob	chr17	34243731	A	G
intronic	H2-Ob	chr17	34243732	A	G
intronic	H2-Ob	chr17	34243737	C	T
intronic	H2-Ob	chr17	34243789	T	C
intronic	H2-Ob	chr17	34243831	C	T
intronic	H2-Ob	chr17	34243971	T	C
intronic	H2-Ob	chr17	34243980	G	A
intronic	H2-Ob	chr17	34243995	A	G
intronic	H2-Ob	chr17	34244012	T	C
intronic	H2-Ob	chr17	34244018	C	G
intronic	H2-Ob	chr17	34244076	A	G
exonic	H2-Ob	chr17	34244101	A	C
exonic	H2-Ob	chr17	34244102	G	T

UTR3	H2-Ob(NM_010389:c.*91C>T)	chr17	34244212	C	T
UTR3	H2-Ob(NM_010389:c.*139C>T)	chr17	34244260	C	T
UTR3	H2-Ob(NM_010389:c.*144G>A)	chr17	34244265	G	A
UTR3	H2-Ob(NM_010389:c.*169T>G)	chr17	34244290	T	G
UTR3	H2-Ob(NM_010389:c.*195C>A)	chr17	34244316	C	A
UTR3	H2-Ob(NM_010389:c.*255C>T)	chr17	34244376	C	T
UTR3	H2-Ob(NM_010389:c.*327A>C)	chr17	34244448	A	C
UTR3	H2-Ob(NM_010389:c.*328C>T)	chr17	34244449	C	T
UTR3	H2-Ob(NM_010389:c.*330G>A)	chr17	34244451	G	A
UTR3	H2-Ob(NM_010389:c.*375C>T)	chr17	34244496	C	T
UTR3	H2-Ob(NM_010389:c.*381T>C)	chr17	34244502	T	C
UTR3	H2-Ob(NM_010389:c.*398C>T)	chr17	34244519	C	T
UTR3	H2-Ob(NM_010389:c.*399A>G)	chr17	34244520	A	G
UTR3	H2-Ob(NM_010389:c.*404G>A)	chr17	34244525	G	A
UTR3	H2-Ob(NM_010389:c.*424C>A)	chr17	34244545	C	A
UTR3	H2-Ob(NM_010389:c.*469C>T)	chr17	34244590	C	T
UTR3	H2-Ob(NM_010389:c.*556C>T)	chr17	34244677	C	T
UTR3	H2-Ob(NM_010389:c.*647T>C)	chr17	34244768	T	C
UTR3	H2-Ob(NM_010389:c.*664T>C)	chr17	34244785	T	C
UTR3	H2-Ob(NM_010389:c.*688T>G)	chr17	34244809	T	G
UTR3	H2-Ob(NM_010389:c.*689G>T)	chr17	34244810	G	T
UTR3	H2-Ob(NM_010389:c.*691C>G)	chr17	34244812	C	G
UTR3	H2-Ob(NM_010389:c.*729A>G)	chr17	34244850	A	G
UTR3	H2-Ob(NM_010389:c.*739A>C)	chr17	34244860	A	C
UTR3	H2-Ob(NM_010389:c.*740T>C)	chr17	34244861	T	C
UTR3	H2-Ob(NM_010389:c.*753T>C)	chr17	34244874	T	C
UTR3	H2-Ob(NM_010389:c.*760A>G)	chr17	34244881	A	G
UTR3	H2-Ob(NM_010389:c.*767A>G)	chr17	34244888	A	G
UTR3	H2-Ob(NM_010389:c.*815T>C)	chr17	34244936	T	C
UTR3	H2-Ob(NM_010389:c.*832T>C)	chr17	34244953	T	C
UTR3	H2-Ob(NM_010389:c.*838C>T)	chr17	34244959	C	T
UTR3	H2-Ob(NM_010389:c.*899G>T)	chr17	34245020	G	T
UTR3	H2-Ob(NM_010389:c.*912C>T)	chr17	34245033	C	T
UTR3	H2-Ob(NM_010389:c.*1039G>A)	chr17	34245160	G	A
UTR3	H2-Ob(NM_010389:c.*1055G>C)	chr17	34245176	G	C
UTR3	H2-Ob(NM_010389:c.*1250G>A)	chr17	34245371	G	A
UTR3	H2-Ob(NM_010389:c.*1324A>G)	chr17	34245445	A	G
UTR3	H2-Ob(NM_010389:c.*1472G>A)	chr17	34245593	G	A
UTR3	H2-Ob(NM_010389:c.*1476A>G)	chr17	34245597	A	G
UTR3	H2-Ob(NM_010389:c.*1491T>C)	chr17	34245612	T	C
UTR3	H2-Ob(NM_010389:c.*1578A>T)	chr17	34245699	A	T

UTR3	H2-Ob(NM_010389:c.*1581T>C)	chr17	34245702	T	C
downstream	H2-Ob	chr17	34245985	T	G
downstream	H2-Ob	chr17	34245989	C	T
downstream	H2-Ob	chr17	34245990	A	G
downstream	H2-Ob	chr17	34245998	G	T
downstream	H2-Ob	chr17	34246249	A	G
downstream	H2-Ob	chr17	34246355	C	T
downstream	H2-Ob	chr17	34246357	C	T
downstream	H2-Ob	chr17	34246433	T	C
downstream	H2-Ob	chr17	34246438	G	A
downstream	H2-Ob	chr17	34246464	G	A
downstream	H2-Ob	chr17	34246666	A	G
downstream	H2-Ob	chr17	34246816	T	C
downstream	H2-Ob	chr17	34246844	G	C
downstream	H2-Ob	chr17	34246901	A	T

All single nucleotide variants (SNVs) in C3H/HeN. **Type** = indicates a single nucleotide variant (SNV) identified relative to a known gene; **Gene (distance)**= gene containing SNV, or distance to nearest genes in 3’ and 5’ direction**; CHROM** = chromosomal location of SNV; **POS** = genomic location of SNV; **C3H/HeN** = reference; **BALB/cJ** = detected nucleotide. The *vic1* critical region is highlighted in yellow.

Supplemental Table 4. DOB alleles.

Chrom	Position	RSID	Ref	Alt	Protein Consequence	Transcript Consequence	Annotation	Number of Homozygotes	Allele Frequency
6	32782883	.	G	A	p.Ala100Val	c.299C>T	missense	0	0.00002472
6	32782931	.	G	A	p.Ala84Val	c.251C>T	missense	0	0.000008237
6	32782827	.	T	C	p.Arg119Gly	c.355A>G	missense	0	0.00001656
6	32782826	rs143319753	C	T	p.Arg119Lys	c.356G>A	missense	0	0.001093
6	32782246	.	C	A	p.Arg165Ile	c.494G>T	missense	0	0.000008579
6	32784676	rs2071554	C	T	p.Arg18Gln	c.53G>A	missense	343	0.06776
6	32781586	.	C	T	p.Arg223Lys	c.668G>A	missense	0	0.00003937
6	32782989	rs147835586	G	A	p.Arg65Cys	c.193C>T	missense	0	0.00002471
6	32782988	rs144504518	C	T	p.Arg65His	c.194G>A	missense	0	0.00003295
6	32782913	.	C	T	p.Arg90Gln	c.269G>A	missense	0	0.000008238
6	32782913	.	C	A	p.Arg90Leu	c.269G>T	missense	0	0.000008238
6	32782914	.	G	A	p.Arg90Trp	c.268C>T	missense	0	0.00001648
6	32782896	.	T	C	p.Arg96Gly	c.286A>G	missense	0	0.00004119
6	32782325	rs139684832	T	G	p.Asn139His	c.415A>C	missense	0	0.000008605
6	32782213	.	T	C	p.Asn176Ser	c.527A>G	missense	0	0.0001543
6	32781221	rs143706496	T	C	p.Asn261Ser	c.782A>G	missense	0	0.00000859
6	32782877	.	T	A	p.Asp102Val	c.305A>T	missense	0	0.00001648
6	32782285	.	T	A	p.Asp152Val	c.455A>T	missense	0	0.00005158
6	32784646	.	T	C	p.Asp28Gly	c.83A>G	missense	0	0.000008614
6	32782983	.	C	T	p.Asp67Asn	c.199G>A	missense	0	0.000008237
6	32782935	.	C	A	p.Asp83Tyr	c.247G>T	missense	0	0.000008237
6	32780998	.	A	G	p.Cys273Arg	c.817T>C	missense	0	0.000008601
6	32782376	.	G	A	p.Gln122Ter	c.364C>T	stop gained	0	0.000008656
6	32782330	.	T	C	p.Gln137Arg	c.410A>G	missense	0	0.000008606
6	32782255	.	T	C	p.Gln162Arg	c.485A>G	missense	0	0.000008583
6	32781234	.	G	C	p.Gln257Glu	c.769C>G	missense	0	0.000008592
6	32784655	.	T	C	p.Gln25Arg	c.74A>G	missense	0	0.000008611
6	32782924	.	C	A	p.Gln86His	c.258G>T	missense	0	0.000008237
6	32782926	rs142229094	G	T	p.Gln86Lys	c.256C>A	missense	0	0.0005437
6	32782885	.	C	A	p.Gln99His	c.297G>T	missense	0	0.000008239
6	32782887	.	G	A	p.Gln99Ter	c.295C>T	stop gained	0	0.00001648
6	32782251	.	C	A	p.Glu163Asp	c.489G>T	missense	0	0.00002574
6	32782250	rs142148406	C	G	p.Glu164Gln	c.490G>C	missense	0	0.0001201
6	32782102	.	T	C	p.Glu213Gly	c.638A>G	missense	0	0.000008624
6	32781219	.	C	T	p.Glu262Lys	c.784G>A	missense	0	0.00004295
6	32783001	.	C	T	p.Glu61Lys	c.181G>A	missense	0	0.000008237
6	32782929	.	C	T	p.Glu85Lys	c.253G>A	missense	0	0.000008238
6	32782874	rs144814623	C	A	p.Gly103Val	c.308G>T	missense	1	0.0003791
6	32782224	.	GC	G	p.Gly172AlafsTer14	c.515delG	frameshift	0	0.0004802

6	32781500	.	C	T	p.Gly252Arg	c.754G>A	missense	0	0.00004295
6	32783046	.	C	T	p.Gly46Arg	c.136G>A	missense	0	0.00005767
6	32783045	.	C	T	p.Gly46Glu	c.137G>A	missense	0	0.000008238
6	32782863	.	G	T	p.His107Asn	c.319C>A	missense	0	0.000008243
6	32782334	.	G	A	p.His136Tyr	c.406C>T	missense	0	0.000008608
6	32782316	.	G	A	p.His142Tyr	c.424C>T	missense	0	0.000008603
6	32782276	.	A	G	p.Ile155Thr	c.464T>C	missense	0	0.000008593
6	32782220	.	T	A	p.Ile174Phe	c.520A>T	missense	0	0.00001715
6	32782219	.	A	G	p.Ile174Thr	c.521T>C	missense	0	0.0000343
6	32782336	.	A	G	p.Leu135Pro	c.404T>C	missense	0	0.0001549
6	32782318	.	A	G	p.Leu141Pro	c.422T>C	missense	0	0.00001721
6	32782142	.	G	T	p.Leu200Ile	c.598C>A	missense	0	0.000008589
6	32781554	rs2070121	G	T	p.Leu234Ile	c.700C>A	missense	0	0.0009835
6	32781554	rs2070121	G	A	p.Leu234Phe	c.700C>T	missense	143	0.114
6	32782904	.	A	T	p.Leu93His	c.278T>A	missense	0	0.000008238
6	32782279	.	T	C	p.Lys154Arg	c.461A>G	missense	0	0.000008594
6	32784728	.	T	C	p.Met1?	c.1A>G	start lost	0	0.00001729
6	32782182	.	C	A	p.Met186Ile	c.558G>T	missense	0	0.00001715
6	32782182	.	C	T	p.Met186Ile	c.558G>A	missense	0	0.00001715
6	32782183	.	A	G	p.Met186Thr	c.557T>C	missense	0	0.000008573
6	32782173	.	C	T	p.Met189Ile	c.567G>A	missense	0	0.000008576
6	32784662	.	T	C	p.Met23Val	c.67A>G	missense	0	0.00002583
6	32782298	.	A	T	p.Phe148Ile	c.442T>A	missense	0	0.0000086
6	32783028	.	A	G	p.Phe52Leu	c.154T>C	missense	0	0.000008237
6	32782355	.	G	A	p.Pro129Ser	c.385C>T	missense	0	0.00003448
6	32784710	.	G	C	p.Pro7Ala	c.19C>G	missense	0	0.00001724
6	32784664	.	G	A	p.Ser22Phe	c.65C>T	missense	0	0.00006027
6	32781227	.	G	C	p.Ser259Cys	c.776C>G	missense	0	0.00000859
6	32782836	.	T	C	p.Thr116Ala	c.346A>G	missense	0	0.000008267
6	32782304	.	T	A	p.Thr146Ser	c.436A>T	missense	0	0.000008601
6	32784679	.	G	A	p.Thr17Ile	c.50C>T	missense	0	0.00001722
6	32782146	.	GGT	G	p.Thr198LeufsTer21	c.592_593delAC	frameshift	0	0.000008587
6	32781236	.	G	T	p.Thr256Lys	c.767C>A	missense	0	0.000008593
6	32781236	.	G	A	p.Thr256Met	c.767C>T	missense	0	0.00001719
6	32782270	rs146350950	C	A	p.Trp157Leu	c.470G>T	missense	0	0.00006872
6	32782270	rs146350950	C	T	p.Trp157Ter	c.470G>A	stop gained	0	0.00000859
6	32781588	.	C	T	p.Trp222Ter	c.666G>A	stop gained	0	0.00003966
6	32782922	.	C	A	p.Trp87Leu	c.260G>T	missense	0	0.000008237
6	32784707	.	A	G	p.Trp8Arg	c.22T>C	missense	0	0.000008619
6	32782295	.	A	G	p.Tyr149His	c.445T>C	missense	0	0.0000344
6	32782832	.	A	G	p.Val117Ala	c.350T>C	missense	0	0.000008273
6	32782832	.	A	C	p.Val117Gly	c.350T>G	missense	0	0.000008273
6	32782833	.	C	G	p.Val117Leu	c.349G>C	missense	0	0.00002481
6	32782367	.	C	T	p.Val125Met	c.373G>A	missense	0	0.000008634

6	32782189	.	A	G	p.Val184Ala	c.551T>C	missense	0	0.000008573
6	32782186	.	A	G	p.Val185Ala	c.554T>C	missense	0	0.000008573
6	32782153	.	A	T	p.Val196Asp	c.587T>A	missense	0	0.000008581
6	32782112	rs150697393	C	T	p.Val210Ile	c.628G>A	missense	80	0.02834
6	32782105	.	A	G	p.Val212Ala	c.635T>C	missense	0	0.00004309
6	32781524	rs148095098	C	T	p.Val244Ile	c.730G>A	missense	25	0.03823
6	32783025	.	C	G	p.Val53Leu	c.157G>C	missense	0	0.000008237
6	32782096	.	C	A		c.643+1G>T	splice donor	0	0.000008648
6	32781030	.	T	C		c.787-2A>G	splice acceptor	0	0.0000086
6	32783091	.	C	T		c.92-1G>A	splice acceptor	0	0.000008256

All single nucleotide variants found in human HLA-DOB from ExAC. http://exac.broadinstitute.org/gene/ENSG00000241106.
Ref, DOB*0101 common allele. RSID, SNP. Highlighed, alleles used in Figures 6 and S3).

Supplemental Table 5. DOA alleles.

Chrom	Position	RSID	Ref	Alt	Protein Consequence	Transcript Consequence	Annotation	Number of Homozygotes	Allele Frequency
6	32975808	rs11575906	G	A	p.Arg105Cys	c.313C>T	missense	23	0.01242
6	32977298	rs144931749	C	T	p.Gly6Arg	c.16G>A	missense	19	0.008975
6	32975286	rs34987694	A	G	p.Phe139Leu	c.415T>C	missense	7	0.004471
6	32974914	rs141887419	C	A	p.Gly231Val	c.692G>T	missense	0	0.001788
6	32975885	rs148303384	C	T	p.Arg79His	c.236G>A	missense	1	0.001655
6	32974897	rs114742371	C	T	p.Val237Ile	c.709G>A	missense	0	0.0007655
6	32975177	rs150939187	T	C	p.His175Arg	c.524A>G	missense	0	0.0006018
6	32974966	rs144962928	C	T	p.Asp214Asn	c.640G>A	missense	0	0.000554
6	32976012	rs41541116	CG	C	p.Ala37ProfsTer26	c.108delC	frameshift	0	0.0003387
6	32975163	rs142562508	C	T	p.Val180Met	c.538G>A	missense	0	0.0002033
6	32975945	.	G	A	p.Ser59Phe	c.176C>T	missense	0	0.0001465
6	32974980	rs147947959	G	A	p.Pro209Leu	c.626C>T	missense	0	0.00008402
6	32975284	.	G	T	p.Phe139Leu	c.417C>A	missense	0	0.0000777
6	32975187	.	G	A	p.Arg172Cys	c.514C>T	missense	0	0.00007089
6	32975250	.	C	G	p.Gly151Arg	c.451G>C	missense	0	0.00006983
6	32977258	.	C	T	p.Ser19Asn	c.56G>A	missense	0	0.00005399
6	32975352	.	C	T	p.Val117Met	c.349G>A	missense	0	0.00005237
6	32975255	.	C	T	p.Arg149His	c.446G>A	missense	0	0.00005225
6	32975319	.	G	T	p.Pro128Thr	c.382C>A	missense	0	0.00005187
6	32975845	.	G	C	p.Ile92Met	c.276C>G	missense	0	0.0000431
6	32975874	.	G	A	p.Gln83Ter	c.247C>T	stop gained	0	0.00004309
6	32975151	.	C	T	p.Glu184Lys	c.550G>A	missense	0	0.0000352
6	32975337	.	G	A	p.Arg122Trp	c.364C>T	missense	0	0.00003474
6	32974906	.	C	T	p.Val234Met	c.700G>A	missense	0	0.00003359
6	32975207	.	G	A	p.Ser165Phe	c.494C>T	missense	0	0.00002651
6	32975360	.	C	T	p.Arg114Gln	c.341G>A	missense	0	0.00002628
6	32975336	.	C	T	p.Arg122Gln	c.365G>A	missense	0	0.00002602
6	32975994	rs139861642	C	T	p.Gly43Ser	c.127G>A	missense	0	0.00002599
6	32975315	.	T	C	p.Asn129Ser	c.386A>G	missense	0	0.00002592
6	32975934	.	T	C	p.Lys63Glu	c.187A>G	missense	0	0.00002585
6	32974883	rs142612904	C	T	p.Met241Ile	c.723G>A	missense	0	0.00002532
6	32977230	.	A	T		c.82+2T>A	splice donor	0	0.00001935
6	32975196	.	G	A	p.His169Tyr	c.505C>T	missense	0	0.0000177
6	32975145	.	C	T	p.Val186Ile	c.556G>A	missense	0	0.00001757
6	32975232	.	C	T	p.Gly157Arg	c.469G>A	missense	0	0.00001756
6	32975144	.	A	G	p.Val186Ala	c.557T>C	missense	0	0.00001755
6	32976024	.	A	G	p.Ser33Pro	c.97T>C	missense	0	0.0000174
6	32976012	rs41541116	C	A	p.Ala37Ser	c.109G>T	missense	0	0.00001737
6	32975264	.	G	T	p.Thr146Asn	c.437C>A	missense	0	0.00001729
6	32975278	.	AG	A	p.Pro141LeufsTer2	c.422delC	frameshift	0	0.00001727

6	32975280	.	G	C	p.Pro141Ala	c.421C>G	missense	0	0.00001727
6	32975298	.	C	T	p.Val135Met	c.403G>A	missense	0	0.00001727
6	32975850	.	C	A	p.Ala91Ser	c.271G>T	missense	0	0.00001724
6	32975958	rs140147098	C	T	p.Glu55Lys	c.163G>A	missense	0	0.00001724
6	32975931	.	T	C	p.Lys64Glu	c.190A>G	missense	0	0.00001723
6	32977310	.	C	T	p.Ala2Thr	c.4G>A	missense	0	0.00001345
6	32977311	.	C	T	p.Met1?	c.3G>A	start lost	0	0.00001344
6	32977309	.	G	T	p.Ala2Asp	c.5C>A	missense	0	0.00001336
6	32977276	.	G	T	p.Thr13Asn	c.38C>A	missense	0	0.00001252
6	32975186	.	C	T	p.Arg172His	c.515G>A	missense	0	0.000008875
6	32975175	.	A	G	p.Tyr176His	c.526T>C	missense	0	0.000008849
6	32975222	.	T	C	p.Gln160Arg	c.479A>G	missense	0	0.000008802
6	32975223	.	G	A	p.Gln160Ter	c.478C>T	stop gained	0	0.000008802
6	32975790	.	C	G	p.Val111Leu	c.331G>C	missense	0	0.000008797
6	32975369	.	A	T	p.Val111Glu	c.332T>A	missense	0	0.000008794
6	32975148	.	C	T	p.Asp185Asn	c.553G>A	missense	0	0.000008787
6	32975364	.	G	T	p.Pro113Thr	c.337C>A	missense	0	0.00000878
6	32975142	rs145505686	A	G	p.Tyr187His	c.559T>C	missense	0	0.000008769
6	32975141	.	T	C	p.Tyr187Cys	c.560A>G	missense	0	0.000008765
6	32975237	.	G	C	p.Thr155Ser	c.464C>G	missense	0	0.000008761
6	32975361	.	G	A	p.Arg114Trp	c.340C>T	missense	0	0.000008757
6	32976038	.	G	C	p.Ala28Gly	c.83C>G	missense	0	0.000008737
6	32975250	.	C	T	p.Gly151Ser	c.451G>A	missense	0	0.000008728
6	32975124	.	G	T	p.His193Asn	c.577C>A	missense	0	0.000008723
6	32976030	.	T	C	p.Met31Val	c.91A>G	missense	0	0.000008715
6	32975120	.	C	T	p.Trp194Ter	c.581G>A	stop gained	0	0.000008713
6	32975800	.	T	A	p.Arg107Ser	c.321A>T	missense	0	0.000008708
6	32975256	.	G	A	p.Arg149Cys	c.445C>T	missense	0	0.000008703
6	32976018	.	C	T	p.Gly35Arg	c.103G>A	missense	0	0.000008694
6	32975108	.	G	A	p.Ala198Val	c.593C>T	missense	0	0.000008684
6	32975807	.	C	T	p.Arg105His	c.314G>A	missense	0	0.000008673
6	32975099	.	A	G	p.Leu201Pro	c.602T>C	missense	0	0.000008657
6	32975986	.	CGA	C	p.Ser45GlyfsTer6	c.133_134delTC	frameshift	0	0.000008654
6	32975987	.	G	C	p.Ser45Trp	c.134C>G	missense	0	0.000008654
6	32975985	.	C	G	p.Gly46Arg	c.136G>C	missense	0	0.000008653
6	32975260	.	C	T	p.Trp147Ter	c.441G>A	stop gained	0	0.00000865
6	32975320	.	C	A	p.Gln127His	c.381G>T	missense	0	0.000008646
6	32975320	.	C	G	p.Gln127His	c.381G>C	missense	0	0.000008646
6	32975980	rs145654970	C	A	p.Gln47His	c.141G>T	missense	0	0.000008645
6	32975318	.	G	A	p.Pro128Leu	c.383C>T	missense	0	0.000008643
6	32975978	.	A	G	p.Phe48Ser	c.143T>C	missense	0	0.000008642
6	32975817	.	G	A	p.Arg102Cys	c.304C>T	missense	0	0.00000864
6	32975091	.	A	G	p.Trp204Arg	c.610T>C	missense	0	0.000008635
6	32975279	rs115076830	G	A	p.Pro141Leu	c.422C>T	missense	0	0.000008635

6	32975280	.	G	T	p.Pro141Thr	c.421C>A	missense	0	0.000008634
6	32975302	.	G	T	p.Cys133Ter	c.399C>A	stop gained	0	0.000008632
6	32975286	rs34987694	A	T	p.Phe139Ile	c.415T>A	missense	0	0.000008631
6	32975970	.	C	G	p.Glu51Gln	c.151G>C	missense	0	0.000008631
6	32975823	.	C	G	p.Val100Leu	c.298G>C	missense	0	0.00000863
6	32975825	.	A	G	p.Leu99Pro	c.296T>C	missense	0	0.000008627
6	32975859	.	C	G	p.Gly88Arg	c.262G>C	missense	0	0.00000862
6	32975886	.	G	A	p.Arg79Cys	c.235C>T	missense	0	0.000008618
6	32975895	.	C	T	p.Asp76Asn	c.226G>A	missense	0	0.000008616
6	32975913	.	G	A	p.Arg70Cys	c.208C>T	missense	0	0.000008616
6	32975897	.	C	G	p.Gly75Ala	c.224G>C	missense	0	0.000008615
6	32975897	.	C	T	p.Gly75Asp	c.224G>A	missense	0	0.000008615
6	32975912	.	C	G	p.Arg70Pro	c.209G>C	missense	0	0.000008615
6	32975914	.	C	T	p.Trp69Ter	c.207G>A	stop gained	0	0.000008615
6	32975927	.	C	G	p.Ser65Thr	c.194G>C	missense	0	0.000008615
6	32974857	.	C	G	p.Arg250Thr	c.749G>C	missense	0	0.000008604
6	32974873	.	C	T	p.Val245Met	c.733G>A	missense	0	0.000008486
6	32974873	.	CAT	C	p.Tyr244CysfsTer43	c.731_732delAT	frameshift	0	0.000008486
6	32974887	.	A	G	p.Ile240Thr	c.719T>C	missense	0	0.000008427
6	32974891	.	T	C	p.Ile239Val	c.715A>G	missense	0	0.000008418
6	32974986	.	T	A	p.Gln207Leu	c.620A>T	missense	0	0.000008406
6	32974985	.	C	A	p.Gln207His	c.621G>T	missense	0	0.000008405
6	32974978	.	T	C	p.Ile210Val	c.628A>G	missense	0	0.000008399
6	32974963	.	C	A	p.Ala215Ser	c.643G>T	missense	0	0.000008394
6	32974954	.	T	A	p.Thr218Ser	c.652A>T	missense	0	0.000008392

All single nucleotide variants found in human HLA-DOA from ExAC. http://exac.broadinstitute.org/gene/ENSG00000204252.
Ref, DOA*0101 common allele. RSID, SNP.