Methods

Animal Husbandry, behavioral testing and behavioral measures

All behavioral methods have been previously published (*24*). C57BL/6J (stock number 000664) mice were obtained from Jackson Laboratory (Bar Harbor, ME). C57BL/6N were obtained from NCI-Frederick (Stock 01C55) **(*25*)**. All mice were housed in barrier SPF conditions with LD (12:12) according to University of Texas, Southwestern Medical Center (UTSW) IACUC guidelines. Only mice bred at UTSW were used in the study. Animals (10-14 weeks of age) were allowed to acclimate to the testing room for half an hour prior to behavioral testing. Mice were weighed and visually inspected for low body weight or any other developmental problems such as malocclusion. Any mouse deemed to be abnormal was removed from the screen. Mice were placed in a 55cm x 55cm x 36cm (Width x Length x Height) matrix for open field assay for 30 minutes followed by intraperitoneal injection with cocaine solution in 0.9% saline. Florescent light levels were measured at 700 lux +/- 56 lux (mean +/- SD of all 32 chambers in our testing facility). Ultrafine insulin syringes were used for injection of cocaine (3/10 mL BD Lo-Dose, Cat 328438). Following each test the test chamber was cleaned with dilute Quatricide solution. Testing was carried out between zeitgeber time (ZT) 4 and ZT10. Actimetrics LimeLight software was used for behavioral recording.

Velocity (mm/min) was measured during baseline (30 minutes before injection, referred to as -30 to 0) and post injection period (60 minutes of recording referred to as 0 to 60 minutes). The baseline measure is an average velocity over the 25 minutes (-30 to -5 minutes). The 30 minutes and 60 minute responses is a sum of 5-minute averages after injection. The net response was calculated by subtracting the average baseline velocity from the average velocity of 30 minutes post injection.

We tested C57BL/6J and C57BL/6N mice for sensitized responses to cocaine by injecting the mice with saline for 4 days, cocaine (10 or 15mg/kg) for 6 days, a saline challenge, and then a cocaine challenge at day 17 and 24

Cyfip2 knockout

The Cyfip2$^{tm1a(EUCOMM)Wtsi}$ (ID:33461) ES cells are derived from the C57BL/6N strain and were maintained in the same background through the course of our experiments. *Cyfip2* knockout ES cells were obtained from EUCOMM. Cyfip2$^{tm1a(EUCOMM)Wtsi}$ ES clones EPD0436_2_B03, EPD0436_2_H02, EPD0436_2_A04 were obtained after quality control testing. ES cells were expanded and microinjected into blastocysts by the UTSW core transgenic technology center. Chimeric mice were bred and germline transmission was obtained for two lines (A04 and H02). Data in this paper are from the A04 ES cell line. After intercrossing heterozygote carriers, we only recovered homozygous wild type and heterozygous knockouts. Genotyping of dead pups and E20 harvested embryos revealed knockouts were dying soon after birth or during gestation. We confirmed that *Cyfip2* mRNA is specifically reduced in homozygous and heterozygous knockout mice collected during gestation (fig. S16).

The knockout allele was genotyped by PCR with the following primers. Wild type allele was amplified with CyKO-1S and CyKO-1AS, yielding a 1.2 kb band. The knockout allele was amplified with CyKO-3S and CyKO-3AS yielding a 719 bp band.

CyKO-1S	AGC CTC ATG CTT CCT TAG GCC TCC CAC AGC TTC AGG
CyKO-1AS	AAT GCG GCC ACT GGG GTA ACT GGG GTA ATG TAT GCC
CyKO-3S	TGG AGT GCT GGG TCA CTT AGT GAA TGC ACC
CyKO-3AS	AGA CCT TGG GAC CAC CTC ATC AGA AGC AGG

DNA was prepared using phenol extraction and PCR was performed with HotStart Taq with the following cycles – 95°C 3min, 30 cycles of 95°C (15 sec), 64°C (15 sec), 72°C (2 min), 1 cycle of 72°C (10 min).

Discovery of C57BL/6N polymorphic markers

We searched for private C57BL/6J mutations reasoning that many of these would have arisen after C57BL/6J and C57BL/6N diverged through genetic drift. Laboratory strains of mice have genomes composed of limited number of mosaic haplotype blocks from progenitor species (*26*). Through the efforts of the mouse genetics community many strains have been genotyped at very high density and the data archived (*27*). If a SNP was ancestral then it would exist in multiple strains that share a haplotype block due to identity by descent. However, if a SNP is unique to C57BL/6J, then it must have arisen through genetic drift after C57BL/6J diverged from the other strains. We used two large datasets consisting of approximately 800,000 SNP genotypes from over 50 strains from the Broad Institute (Broad 2) (*28*) and the Center for Genome Dynamics (snp_cgd2_b37) (*29*) to find such SNPs (fig. S5). This approach is powerful and can be applied towards the discovery of private polymorphisms between any mouse substrains. For the experimental approach we genotyped C57BL/6N on the Mouse Diversity Array (*13*). Using these two approaches we constructed a panel of 93 polymorphic markers between C57BL/6N and C57BL/6J (Fig. 2B, Table S1). Of these 93 markers 23 were polymorphic between the current C57BL/6J mice and a stock of C57BL/6J DNA from 1984 (Table S2).

QTL analysis

QTL analysis was carried out using R/QTL (*30*). Interval mapping was performed using scanone function with Haley-Knott regression. Significance thresholds were established using 100,000 permutations tests. QTL effect was estimated using fitqtl command (*31*). We determined the QTL support interval by using 1.5 LOD drop (*32*) and Bayesian 95% confidence interval (*33*) (fig.S8). Because the 1.5 LOD was more conservative (larger), we used 21 cM-34 cM of chromosome 11 as the location of the QTL. The QTL support interval translates to a 22 Mb interval between 35 Mb-57 Mb of chromosome 11 (*12*)

SNP genotyping

Taqman probes were designed by ABI and tested on the Fluidigm platform and all C57BL/6J-C57BL/6N F2 DNA were genotyped on this platform using the 96.96 chip according to manufacturer instructions (*34, 35*). DNA from tails were prepared using phenol extraction. Mouse Diversity Array Array data can be downloaded here as a CEL file - http://cgd.jax.org/datasets/diversityarray/CELfiles.shtml.

Next Generation Sequence Analysis

The UTSW McDermott Sequencing Core Facility performed one mate pair and one paired end run on the ABI SOLiD platform. We obtained two C57BL/6NJ sequencing

datasets from the Sanger Centre (*14*). Chr 11 data was extracted from mapped bam files using samtools (*36*). We obtained chromosome 11 data from an unpublished dataset from the Sanger Centre (ftp://ftp-mouse.sanger.ac.uk/current_bams). For SNP and indel analysis, we used GATK (version 2.1.11) (*37*) for local realignment and calibration using the RealignerTargetCreator followed by IndelRealigner. Default settings were used to locally realign reads such that the number of mismatched bases are minimized across all reads using default settings. UnifiedGenotyper in GATK (version 2.1-11) was used to call SNP and indel variants. SNP and indel variants were called separately in separate runs with default settings except that "--max_alternate_alleles" was set to 2. The variants with GT setting "1/1" in .vcf file, i.e., the homozygous alternate, were selected for further analyses. snpEff (version 3.0) (*38*) was used to annotate the variants with coverage less than 5 removed ; the multiple same effects in transcript isoforms for the same "Gene_ID" were counted as one. Manual curation of the data revealed high levels of false positives on SNPs and indels that were unique to individual datasets. Therefore we only considered high confidence SNPs and indels that were present in at least two of the three datasets. Manual curation revealed little false positives in this data set.

We carried out structural variant (SV) analysis only with Sanger Centre data using SVmerge (*39*). The realigned data from GATK above were used for SV analyses with SVmerge (version 1.2r37) program suites from Sanger. BreakDancer (*40*), Pindel (*41*), SE Cluster, and CnD (*42*) SV calls were performed as suggested by SVmerge to make structural variant calls. The SV calls were then filtered, assembled, parsed, interpreted, and merged to get the final call set using the SVmerge default settings.

Analysis was performed using mm9 build of the mouse genome.

DNA Stock ID.

C57BL/6 substrain DNA were isolated from animals shipped from Jackson Laboratory, Charles River or Taconic. The following DNA were obtained from Jackson Labs Mouse DNA resource - C57BL/6NJ (37514), C57BL/6EiJ (37494), C57BL/6By (90664), C57BL/6Ei (32510), C57BL/6ByJ (40548), C57BL/6J (37688).

***Cyfip2* S968F mutation genotyping.**

Cyfip2 S968F mutation containing region was amplified and sequenced with the following primers.

Amplifying primers – 450bp Amplicon	
CYFIP-S	GAT ACT ACT GCT CAA AGG AAT TAC AGG
CYFIP-AS	ATC CCA CAT CTG TCA TAA AGT CTA CTC
Sequencing Primers	
CYFIP SEQ 5'	GAG CAC TCC TTT CCA TCC AC
CYFIP SEQ 3'	TAC CCC ACT GTG CCC TAC AT

PCR was performed using Accuprime polymerase as instructed. Amplification was done using 7 cycles of 95°C (30 sec), 66°C (30sec), 68°C (60sec), 7 cycles of 95°C (30 sec), 64°C (30sec), 68°C (60sec), 20 cycles of 95°C (30 sec), 62°C (30sec), 68°C (60sec). PCR products were purified and sequenced with both sequencing primers.

Protein Interaction Assays

Stable HEK293 cell lines expressing equivalent levels of FLAG-CYFIP2 wild type or S968F mutation were established according to standard protocols. All immunoprecipitation (IP) and proteomics studies were carried out in these cell lines.

Immunoprecipitations were performed as previously described (*43*). Cells were extracted with EB containing 20 mM HEPES, 150 mM NaCl, 0.1% Triton X-100, 5 mM sodium beta-glycerophosphate, 0.5 mM orthovanadate, 5 mM sodium fluoride, 1 mM EDTA, 1 mM PMSF, and Complete protease inhibitors. IPs were done using anti-FLAG M2 magnetic beads. Following binding the beads were washed with EB buffer. Western blots were carried out using the following antibodies HSPC300 (Abcam, ab87449), NAP1 (Sigma, N3788), DYKDDDK (Cell Signaling, 2368), FLAG (Sigma, M2, F1804), ABI2 (Epitomics, 5397-1), WAVE1 (NeuroMab, 75-048), beta-Tubulin (Li-Cor, 926-42211). Secondary IR conjugated anti-rabbit (827-11081) and anti-mouse (827-08364 (Li-Cor) were used according to instructions. All quantitative immunoprecipitation was quantitated out using the Li-Cor Odyssey imaging system.

Proteomics studies were carried out by immunoprecipitating FLAG-CYFIP2 WT or mutant from 30-15 cm plates of HEK293 stable cell lines. As control equivalent cells with no expression of FLAG CYFIP2 was used. Cells were extracted under mild conditions with EB and the extract was incubated with 1ml FLAG M2 magnetic beads. The beads were washed, boiled and loaded onto NuPAGE gels. After separation each lane was separated into 10 fractions and submitted for mass spectrometry according to standard techniques (UTSW spectrometry spec core). Proteins that were enriched at least 5 fold when compared to control IP were considered as true interactions.

Protein Stability Assays

FLAG-Cyfip2 wild type or mutant were transiently transfected into HEK293 cells plated in 12 well plates. 100 ng/well and 200 ng/well of expression plasmid was transfected using Effectene in triplicate. 32 hours later the transfected cells were treated with cycloheximide (100 ug/ml) for the indicated times and harvested. Following harvesting cells were lysed with EB and subjected to western blot with anti-FLAG M2 antibody (Sigma M2, F1804) and beta-tubulin (Li-Cor, 926-42211). Secondary IR conjugated antibody was used for quantitative western blots. The blots were scanned with Li-Cor Odyssey imaging system. The relative amount of signal (fraction of signal as compared with time 0) was calculated across all experiments and replicates to calculate the degradation curve. Statistical model for one phase exponential decay was used in Prism to calculate the $T_{1/2}$ (*44*).

Spine imaging

Ballistic "diolistic" labeling of nucleus accumbens (NAc) neurons were carried out in animals between 51 and 63 days as described previously (*45*) with the following modifications. Animals were anesthetized with Euthasol (0.1-0.3 ml) perfused with cold saline (20 mls) followed by cold 2% paraformaldehyde in PBS (40 mls). Brain was removed and post fixed for 2-3 hours in 2% paraformaldehyde at 4°C. The brains were rinsed with PBS and stored overnight in PBS containing 0.1% sodium azide. The following day the brain was sectioned into 200 μM coronal sections. Sections encompassing the NAc (+1.42 ± 0.25 mm anterior to bregma) were collected into PBS

with 0.1% sodium azide. The sections were shot with tungsten bullets coated with DiO and the dye was allowed to diffuse overnight at 4°C. The following day, the sections were post-fixed for 2 hour in 4% paraformaldehyde and mounted using Fluor-Save onto slides with 120 μM spacers. Individually isolated and well-labeled medium spiny neurons within the NAc shell or core were imaged within 48 hours of mounting using a confocal microscope with a 63X (NA1.4) oil immersion lens. Z-stacks of 0.3 μM steps were acquired with frame size of 512 x 512 pixel resolution. The images were deconvolved using AutoquantX3 and spines were classified using NeuronStudio (*46, 47*). In our analysis we attempted to use conditions and methods as described by the Morrison lab (*48, 49*). At least 6 animals were analyzed for each strain and at least 10 images from 3 independent cells were imaged for each animal.

Electrophysiology

Sagittal slices of the NAc shell (250 μm) were prepared as described previously (*50*). Slices recovered in a holding chamber for at least 1 h before use. During recording they were superfused with ACSF (31.5–32.5°C) saturated with 95% O2/5% CO_2 and containing (in mM) 119 NaCl, 2.5 KCl, 1.0 NaH_2PO_4, 1.3 $MgSO_4$, 2.5 $CaCl_2$, 26.2 $NaHCO_3$ and 11 glucose. Picrotoxin (100 μM) was added to block GABAA receptor-mediated IPSCs. Cells were visualized using infrared-differential interference contrast optics. Medium spiny neurons were identified by their morphology and high resting membrane potential (-75 to -85 mV). To assess excitatory synaptic transmission, miniature EPSCs (>200 per cell) were collected in the presence of TTX (0.5 μM). Neurons were voltage clamped at -80 mV using a Multiclamp 700B amplifier. Electrodes (2.5–3.5 MΩ) contained 117 mM cesium gluconate, 2.8 mM NaCl, 20 mM HEPES, 0.4 mM EGTA, 5 mM tetraethylammonium-Cl, 2 mM MgATP, and 0.3 mM MgGTP, pH 7.2–7.4 (285–295 mOsm). Series resistance (10–20 MΩ) and input resistance were monitored on-line with a 4 mV depolarizing step (100 ms) given with each sweep. Data were filtered at 2 kHz, digitized at 5 kHz, and collected with Clampex 10.3 software. Quantal events were analyzed using Minianalysis software and verified by eye. During the recording days, a similar amount of data was collected from B6J and B6N substrains. Results are presented as mean ± SEM. Statistical significance was assessed using two-tailed Student's t tests.

Supplementary Results and Discussion

Modeling of the CYFIP2 S968F mutation.

To estimate the change in stability of the mutant CYFIP2 protein we utilized FOLD-X software that uses the atomic coordinate data combined with experimentally derived force field measurements to predict a change in free energy of the variant protein (*51*). We modeled the S968F variant in the CYFIP1 crystal structure and CYFIP2 homology model, which calculated a free energy increase of 17.37 kcal/mol for CYFIP1 and 11.56 kcal/mol for CYFIP2, both predicted to severely destabilize the protein (fig. S14). Because S968 is highly conserved and a substitution of phenylalanine at this position destabilizes the protein we refer to this variant as a mutation.

CYFIP2 proteomic analysis

In addition to quantitative IPs with known CYFIP1/2 interacting proteins, we carried out unbiased proteomics analysis of the CYFIP2 interactome. We fractionated FLAG immunoaffinity purified complex and identified the proteins through mass spectrometry analysis. We identified 19 proteins that specifically interact with either WT or mutant CYFIP2 protein. Genemania (*52*) network analysis revealed that we specifically identified 19 of 38 known CYFIP2 interaction network components, including all components of the WAVE complex (fig. S15). Lack of significant difference between the interactome of WT and mutant protein led us to conclude that the mutant protein is less stable, but can still interact with its partners.

Supplementary Discussion.

CYFIP2 is a key regulator of cocaine response and a mutation in the C57BL/6N lineage leads to lowered acute and sensitized response to cocaine. CYFIP acts through at least two pathways – FMRP and the WAVE complex, both previously shown to regulate neuronal connectivity and behavior. Furthermore in zebrafish and *Drosophila, Cyfip* controls axon guidance, and haploinsufficiency of *Cyfip1* in mice leads to autism and schizophrenia like phenotypes (*53-55*). Recent data indicates that Rac1, which is upstream of WAVE signaling (*16, 56*), is an inhibitor of cocaine response through the cofillin pathway (*57*). The exact role of the cytoskeleton regulating enzymes in drug addiction remains elusive with contradictory evidence (*58*). These data argue that B6N has lower number of spines, the major sites of excitatory signaling, leading to compromised glutamate signaling. Glutamatergic signaling is inextricably linked with the dopaminergic pathways in cocaine response and addiction through regulation of plasticity (*59, 60*). Although CYFIP2 is a novel regulator of cocaine response, it remains to be seen if it translates to other classes of drugs or whether it has an effect in a true addiction paradigm test such as self-administration.

Supplemental Figure Legends

Fig S1: Cocaine response is lower in C57BL/6N (B6N) than in C57BL/6J (B6J) at multiple doses and measures. 30 minute post injection response for 5, 10, 15, and 20mg/kg dose (A). Sixty minutes post injection response for 5, 10, 15, and 20 mg/kg dose (B). Net Response at 5, 10, 15 and 20 mg/kg (C).

Fig S2: Breeding scheme of QTL cross to map the causative locus that regulates cocaine response difference between C57BL/6J and C57BL/6N. The parental and F1 generations are isogenic and the F2 is segregating. The three-generation cross generated 270 F2s that were genotyped and phenotyped. Animals from all three generations were phenotyped concurrently.

Fig S3: 30 minute post injection phenotype distribution of animals generated for QTL mapping.

Fig S4: Phenotype distribution of animals generated for QTL mapping separated by sex. There is no effect of sex.

Fig S5: Examples of private B6J SNPs. We used two large datasets consisting of approximately 800,000 SNP genotypes from over 50 strains from the Broad Institute (Broad 2) and the Center for Genome Dynamics (snp_cgd2_b37) to find such SNPs (fig. S6). Data were downloaded from http://phenome.jax.org/db/q?rtn=snp/chooseproj&handle=doc.

Fig S6: QTL scan of all measured phenotypes. 30 minute (A), 60 minute (B), net response (C), and baseline activity (D) are shown. The QTL on chromosome 11 is specific for cocaine response (A-C) and is not seen for baseline activity (D). All significance thresholds are based on 100,000 permutation tests.

Fig S7: Heritability and percent of total phenotypic variance accounted for by the Chr 11 QTL. The total variance in the F2 population is due to genetic and environmental effects. Modeling of the *Cyfip2* locus using *fitqtl* command in RQTL indicates that this the Chr11 QTL explains 11% of the total variance (genetic and non-genetic). We estimated the variance (environment) using the F1 and parental B6J and B6N population data shown in Figure 2A. Using the formulas below, the heritability of the phenotype is 18.1% and the *Cyfip2* locus explains 11/18 or 61% of the phenotypic variance due to genetics. All evidence suggests that the *Cyfip2* locus is the major genetic contributor to the trait under our experimental conditions.

Fig S8: QTL support interval. The 1.5LOD drop support interval (top) and 95% Bayesian support interval (bottom). Since the 1.5LOD support interval is larger, we used this as the location of the QTL.

Fig S9: Venn Diagrams showing overlaps in variant discovered through next generation sequencing. We used three datasets for a 100X coverage of chromosome 11, Sanger Center 17 strain sequence that is published (SangerOld), Sanger Center new unpublished sequence of B6NJ (SangerNew), and our own data generated at Univeristy of Texas, Southwestern Medical Center (UTSW). We considered any variant that is seen in at least two of the three datasets for SNP and Indel. All structural variants were considered. The exact locaton of each variant is provided in Table 4.

Fig S10: Next generation sequencing identifies a single nonsynonymous polymorphism in Cyfip2. C57BL/6N sequence data from three sources were combined to yield almost 100-fold coverage of chromosome 11. Classification of SNP (A), indels (B), and structural variants (C) from sequencing reveals only a single SNP (top row of A) in CYFIP2 (D) that changes Serine 968 to phenylalanine in C57BL/6N. Entire Chromosome 11 is shown.

Fig S11: PolyPhen-2 output indicating the S968F mutation is considered damaging.

Fig S12: *In situ* expression data from the Allen Brain Atlas of adult mouse brain. *Cyfip2* is broadly expressed throughout the brain where as *Cyfip1* is restricted to the hippocampus and cerebellum.

Fig S13: CYFIP2 S968F mutation occurs in a conserved residue and destabilizes the protein. (A) Serine 968 (red) of CYFIP2 is highly conserved in the CYFIP family. (B) S968 paralog in CYFIP1 (S969 red), shown using the WAVE complex crystal structure. CYFIP1 is shown in green with VDW surface rendering and NAP1 in white, and the inset shows helices 50, 51 and 39 that surround S968. (C) Molecular modeling to replace the S969 (left) with phenylalanine (right) leads to steric clashes with neighboring residues (pink).

Fig S14: FoldX prediction of free energy change caused by S969F mutation modeled in CYFIP1 (top) and S968F modeled in CYFIP2 (bottom).

Fig S15: Proteomics analysis of the CYFIP2 interactome. HEK293 cell lines expressing either the WT (B6J) , mutant (B6N) or neither (Control) were used for immunoprecipitation with anti FLAG antibody. The complex was separated on SDS-PAGE gel and cut into 10 fractions. Each fraction was subjected to mass-spectral analysis (left). The enriched proteins that specifically bound to CYFIP2 WT or mutant were analyzed using Genemania network analysis (right). The circles are known interactors of CYFIP, with the size of the circle representing the relative confidence of interaction. The colors represent the enrichment in WT (Blue) or mutant (Red) CYFIP2 (Green). For instance CYFIP1 is seen to equally interact with WT and mutant CYFIP2, but MYO18A is enriched more in WT than mutant pulldown. Analysis was carried out in Cytoscape using the Genemania plugin.

Cyfip1 - http://mouse.brain-map.org/experiment/show/69014410

Cyfip2 - http://mouse.brain-map.org/gene/show/52724

Fig S16: Quantitive rtPCR confirms lack of *Cyfip2* transcript in the knockout mice. Whole brain RNA was isolateed from embryos (e18 and e21). Two animals of each genotype were used in this assay. Taqman probes for *Med7* (Mm00502970), *Adam19* (Mm00477337), *Cyfip2* (Mm00460148), *GAPDH* (Mm99999915) were obtained from Life Technologies.

Fig S17: The rate of cocaine metabolism is identical in C57BL/6J and C57BL/6N. Cocaine metabolism was monitored by quantiating the production of benzoylecogonine after drug administration. Mice were intraperitoneally injected with Cocaine (20mg/kg) and blood was harvested by bleeding of the submandibular vein with Goldenrod Animal Lancet (Medipoint Inc) at the indicated times. Two mice were used from each strain for

each time point. Serum was used to quantitate benzoylecogonine using an ELISA kit (catalog number KA0929, Abnova).

Supplementary Tables Legends

Table 1: Polymorphic Markers used in QTL mapping.

Table 2: Polymorphic Markers between current C57BL/6J and DNA from 1984 stock of C57BL/6J.

Table 3: Next generation sequencing coverage statistics.

Table 4: Classification of all variants on chromosome 11 between C57BL/6N and C57BL/6J. There are three sheets that contain SNPs, indels and structural variants.

Table 5: Genome wide variant classification between C57BL/6N and C57BL/6J. There are three sheets that contain SNPs, indels and structural variants.

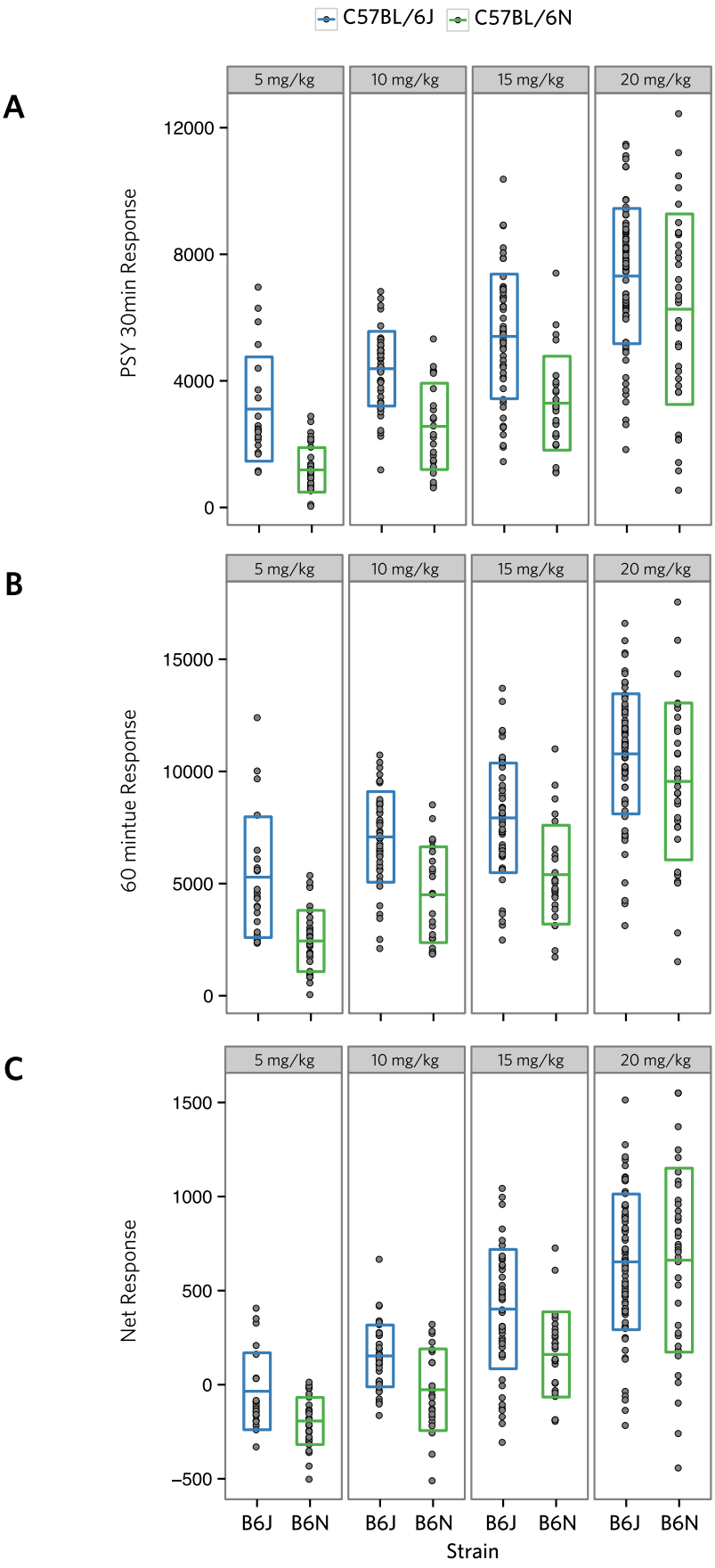
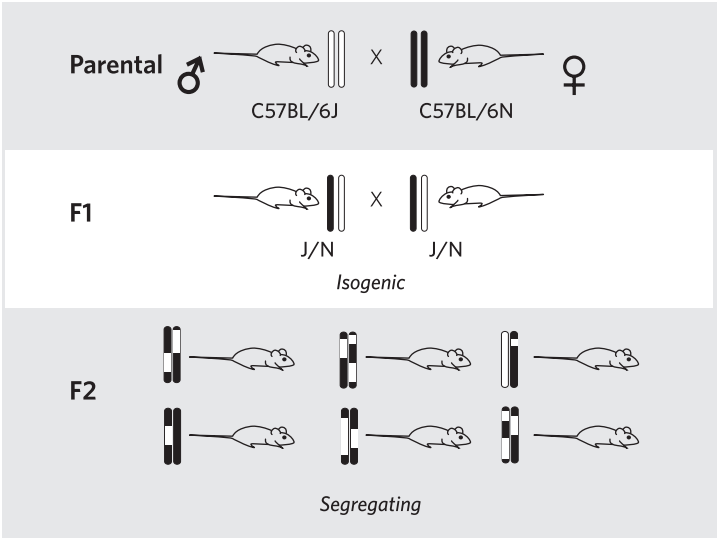


Fig S1: Cocaine response is lower in C57BL/6N (B6N) than in C57BL/6J (B6J) at multiple doses and measures. Thirty minute post injection response for 5, 10, 15, and 20mg/kg dose (A). Sixty minutes post injection response for 5, 10, 15, and 20 mg/kg dose (B). Net Response at 5, 10, 15 and 20 mg/kg (C). Boxes represent mean and 1SD range.



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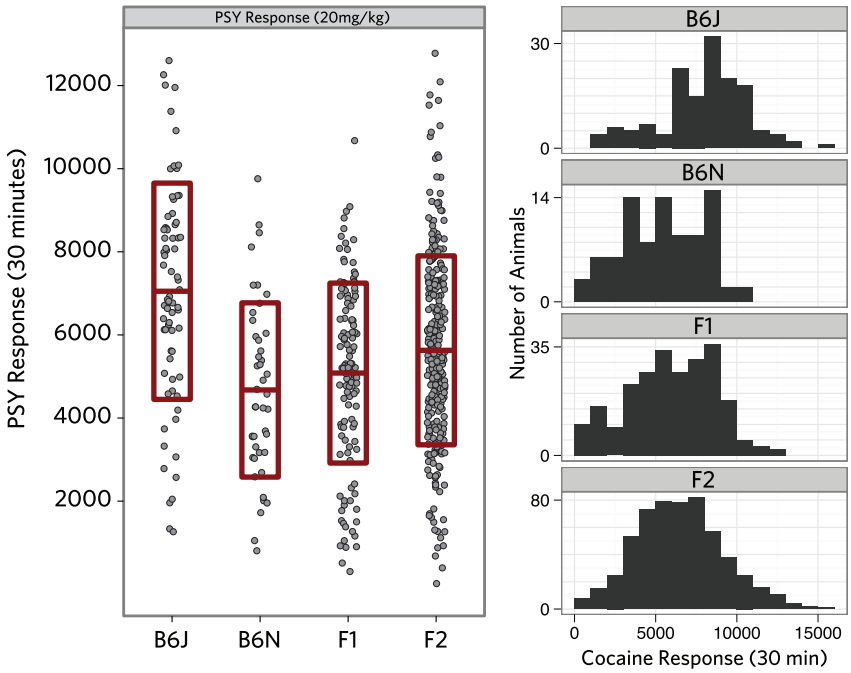


Fig S3: Thirty minute post injection response distribution of animals generated for QTL mapping.

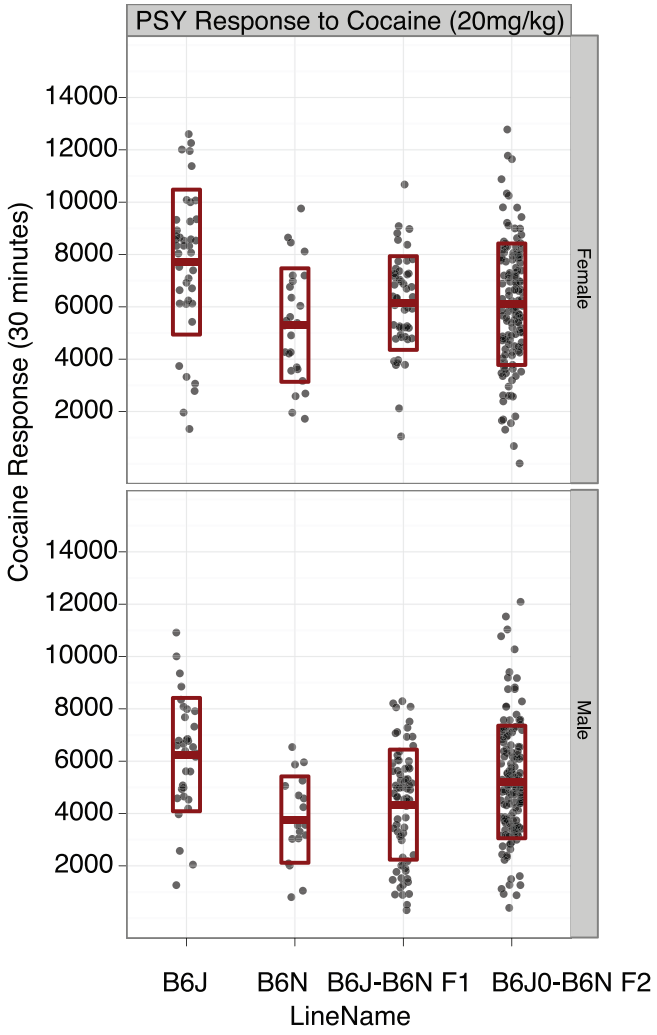
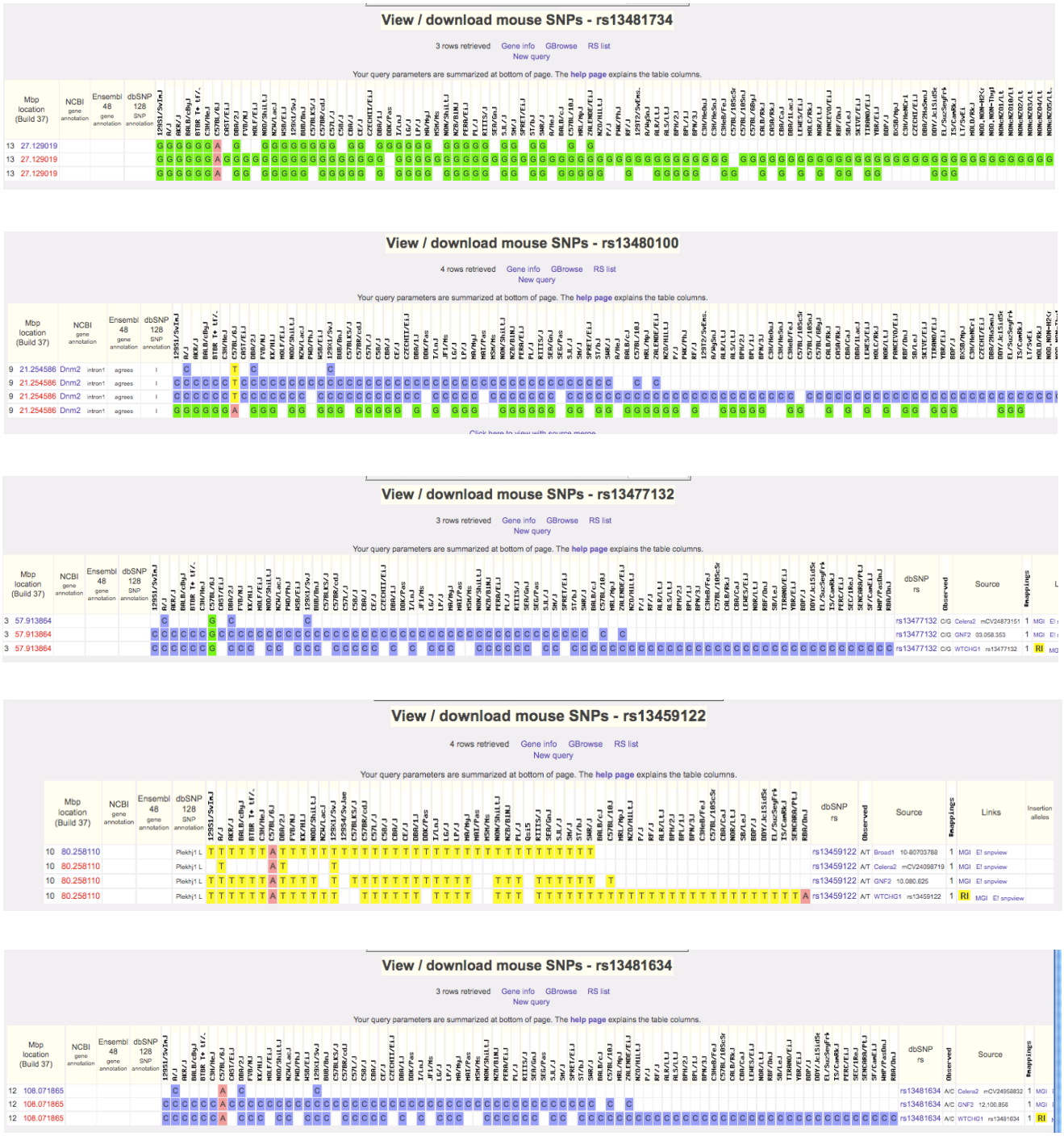


Fig S4: Phenotype distribution of animals generated for QTL mapping separated by sex.



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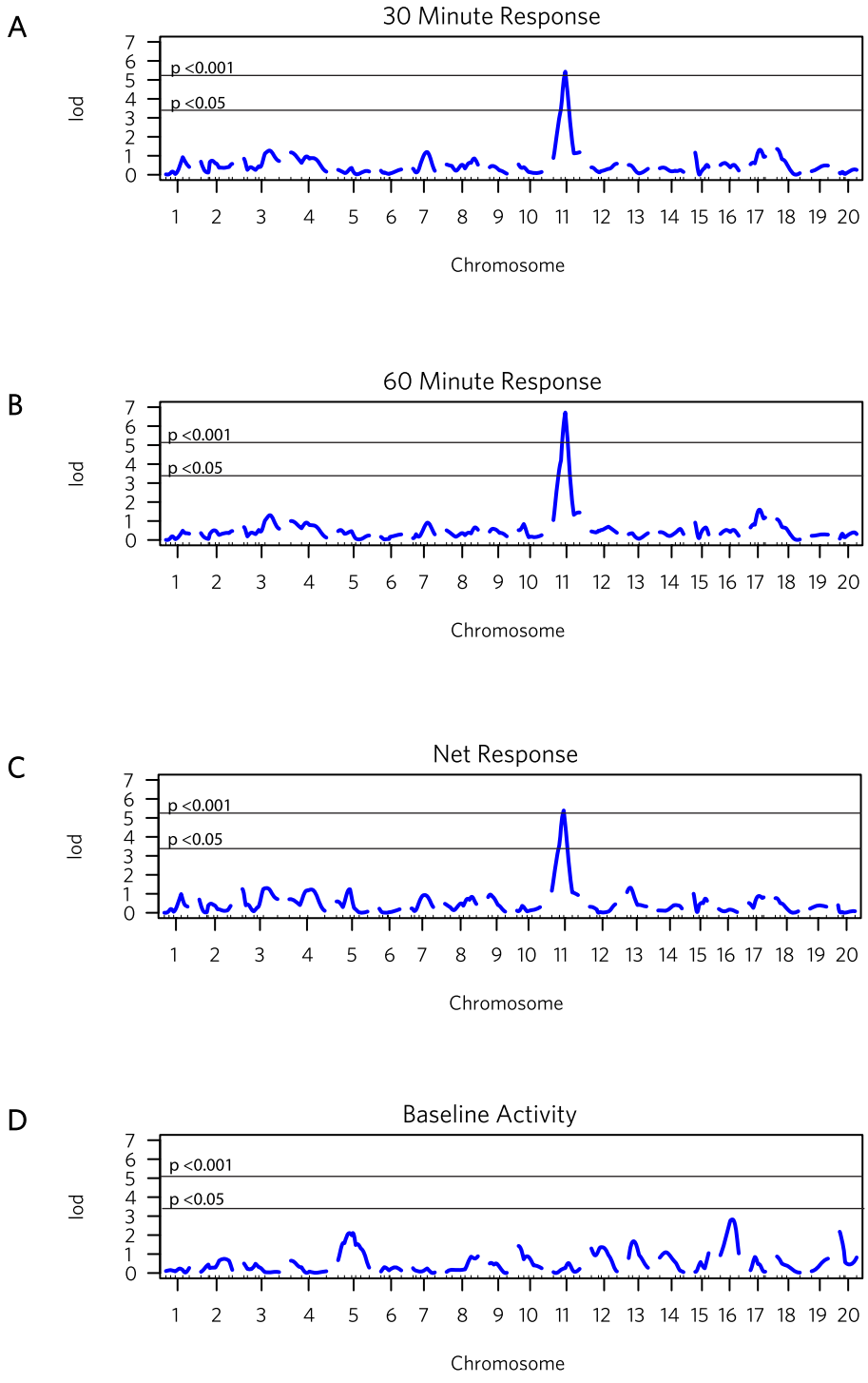

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$$h^2 = \frac{V_{Genetic}}{V_{Phenotype}} = \frac{\hat{\sigma}^2_{genetic}}{(\hat{\sigma}^2_{genetic} + \hat{\sigma}^2_{environment})}$$

$$\hat{\sigma}^2_{genetic} + \hat{\sigma}^2_{environment} = \hat{\sigma}^2_{F2}$$

$$\hat{\sigma}^2_{environment} = \frac{\hat{\sigma}^2_{F1} + \hat{\sigma}^2_{B6J} + \hat{\sigma}^2_{B6N}}{3}$$

$$\hat{\sigma}^2_{genetic} = \hat{\sigma}^2_{F2} - \hat{\sigma}^2_{environment}$$

Fig S7: Heritability and percent of total phenotypic variance accounted for by the Chr 11 QTL. The total variance in the F2 population is due to genetic and environmental effects. Modeling of the *Cyfip2* locus using *fitqtl* command in RQTL indicates that this the Chr11 QTL explains 11% of the total variance (genetic and non-genetic). We estimated the variance (environment) using the F1 and parental B6J and B6N population data shown in Figure 2A. Using the formulas below, the heritability of the phenotype is 18.1% and the *Cyfip2* locus explains 11/18 or 61% of the phenotypic variance due to genetics. All evidence suggests that the *Cyfip2* locus is the major genetic contributor to the trait under our experimental conditions.

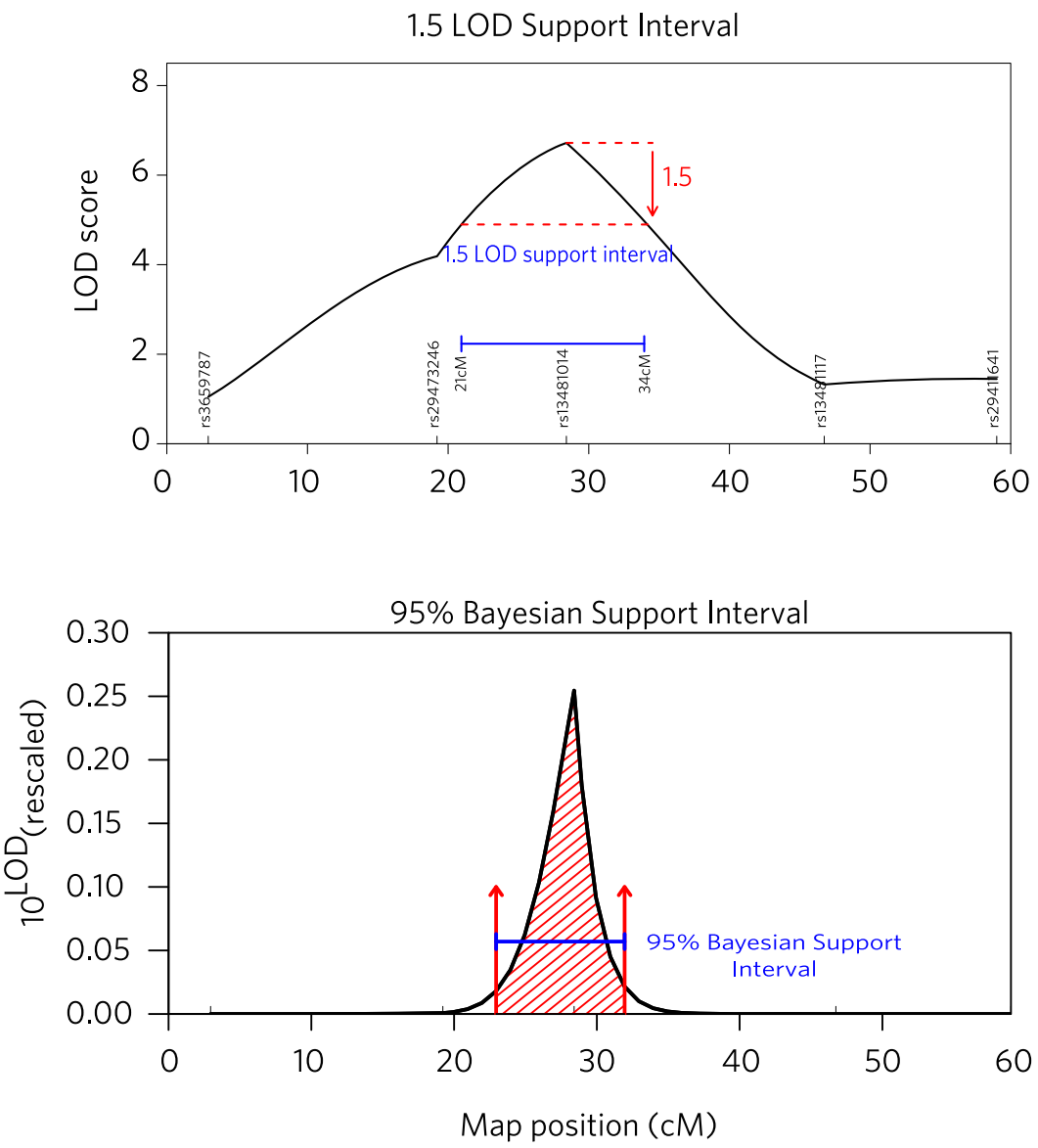


Fig S8: QTL support interval. The 1.5LOD drop support interval (top) and 95% Bayesian support interval (bottom). Since the 1.5LOD support interval is larger, we used this as the location of the QTL.

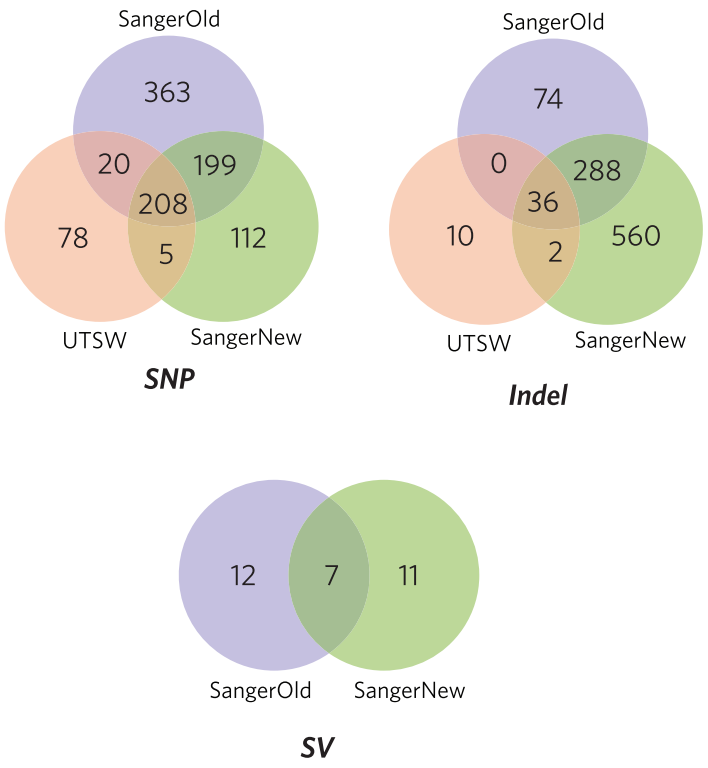


Fig S9: Venn Diagrams showing overlaps in variant discovered through next generation sequencing. We used three datasets for a 100X coverage of chromosome 11, Sanger Center 17 strain sequence that is published (SangerOld), Sanger Center new unpublished sequence of B6NJ (SangerNew), and our own data generated at University of Texas, Southwestern Medical Center (UTSW). We considered any variant that is seen in at least two of the three datasets for SNP and Indel. All structural variants were considered. The exact location of each variant is provided in Table 4.

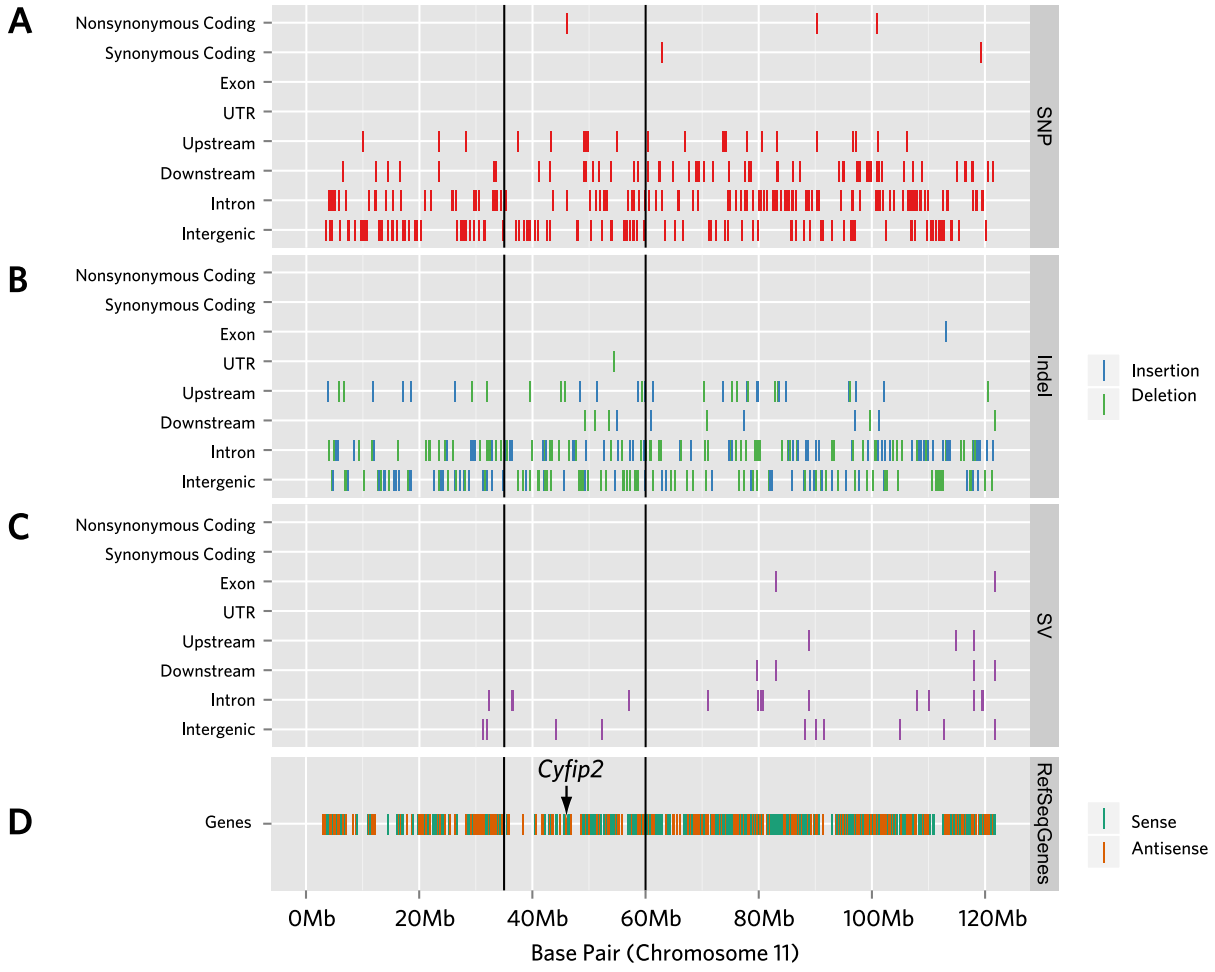


Fig S10: Next generation sequencing identifies a single nonsynonymous polymorphism in *Cyfip2*. C57BL/6N sequence data from three sources were combined to yield almost 100-fold coverage of chromosome 11. Classification of SNP (A), indels (B), and structural variants (C) from sequencing reveals only a single SNP (top row of A) in CYFIP2 (D) that changes Serine 968 to phenylalanine in C57BL/6N. Entire Chromosome 11 is shown. The black lines represent QTL interval shown in Fig. 3.

PolyPhen-2

PolyPhen-2 report for Q5SQX6 S968F

Query

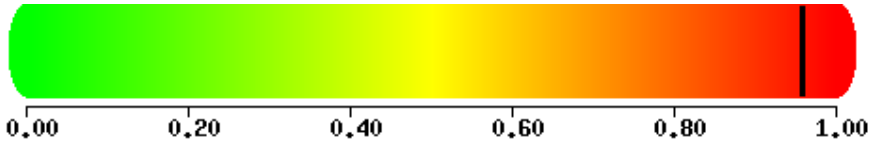
Protein Acc	Position	AA 1	AA 2	Description
Q5SQX6	968	S	F	Cytoplasmic FMR1-interacting protein 2 OS=Mus musculus GN=Cyfip2 PE=1 SV=2

Results

Prediction/Confidence PolyPhen-2 v2.2.2r395

HumDiv

This mutation is predicted to be PROBABLY DAMAGING with a score of 0.957
(sensitivity: 0.78 ; specificity: 0.95)



HumVar

Details

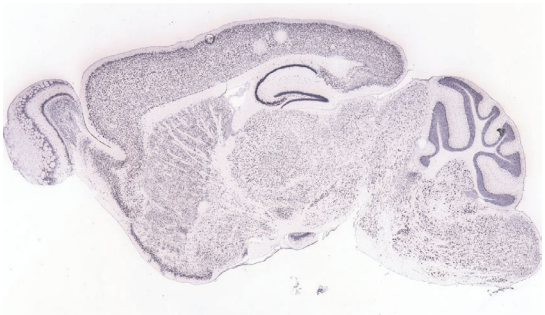
Multiple sequence alignment UniProtKB/UniRef100 Release 2011_12 (14-Dec-2011)

```
sp|F6SLX2#1                VVKSL----LQGTILQYVKTLMEVMPKICRLPRHEYGSPGILEFFHHQLKDIVEYAELK
sp|UPI00022578A6#1         VVKSL----LQGTILQYVKTLMEVMPKICRLPRHEYGSPGILEFFHHQLKDIVEYAELK
sp|F7E7A5#1                VVKSL----LQGTILQYVKTLMEVMPKICRLPRHEYGSPGILEFFHHQLKDIVEYAELK
sp|UPI0001CE16D0#1         VVKSL----LQGTILQYVKTLMEVMPKICRLPRHEYGSPGILEFFHHQLKDIVEYAELK
sp|F1PDQ4#1                VVKSL----LQGTILQYVKTLMEVMPKICRLPRHEYGSPGILEFFHHQLKDIVEYAELK
sp|Q7TMB8-2#1              VVKSL----LQGTILQYVKTLMEVMPKICRLPRHEYGSPGILEFFHHQLKDIVEYAELK
sp|D4A524#1                VVKSL----LQGTILQYVKTLMEVMPKICRLPRHEYGSPGILEFFHHQLKDIVEYAELK
sp|UPI00022B37E2#1         VVKSL----LQGTILQYVKTLMEVMPKICRLPRHEYGSPGILEFFHHQLKDIVEYAELK
sp|UPI0001D6018E#1         VVKSL----LQGTILQYVKTLMEVMPKICRLPRHEYGSPGILEFFHHQLKDIVEYAELK
sp|UPI00022F5204#1         VVKSL----LQGTILQYVKTLMEVMPKICRLPRHEYGSPGILEFFHHQLKDIVEYAELK
sp|F7ATN4#1                VVKSL----LQGTILQYVKTLMEVMPKICRLPRHEYGSPGILEFFHHQLKDIVEYAELK
sp|F7ATP3#1                VVKSL----LQGTILQYVKTLMEVMPKICRLPRHEYGSPGILEFFHHQLKDIVEYAELK
sp|F7A5M9#1                ITLSF---NLQGTILQYVKTLMEVMPKICRLPRHEYGSPGILEFFHHQLKDIVEYAELK
sp|G3QIA7#1                VVKSL----LQGTILQYVKTLMEVMPKICRLPRHEYGSPGILEFFHHQLKDIVEYAELK
sp|G5AZH3#1                VVKSL----LQGTILQYVKTLMEVMPKICRLPRHEYGSPGILEFFHHQLKDIVEYAELK
sp|UPI0001D55D95#1         VVKSL----LQGTILQYVKTLMEVMPKICRLPRHEYGSPGILEFFHHQLKDIVEYAELK
sp|F7ATM6#1                VVKSL----LQGTILQYVKTLMEVMPKICRLPRHEYGSPGILEFFHHQLKDIVEYAELK
```

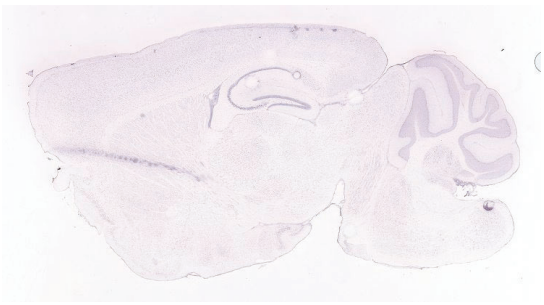
Figure S11

Cyfip2 mRNA expression

data from Allen Brain Atlas



Cyfip2



Cyfip1

Image credit: Allen Institute for Brain Science

Fig S12: *In situ* expression data from the Allen Brain Atlas of adult mouse brain. *Cyfip2* is broadly expressed throughout the brain whereas *Cyfip1* is restricted to the hippocampus and cerebellum. *Cyfip2* saggital-93 is shown. *Cyfip1* saggital-91 is shown.

Cyfip1 - http://mouse.brain-map.org/experiment/show/69014410
Cyfip2 - http://mouse.brain-map.org/experiment/show/68919922

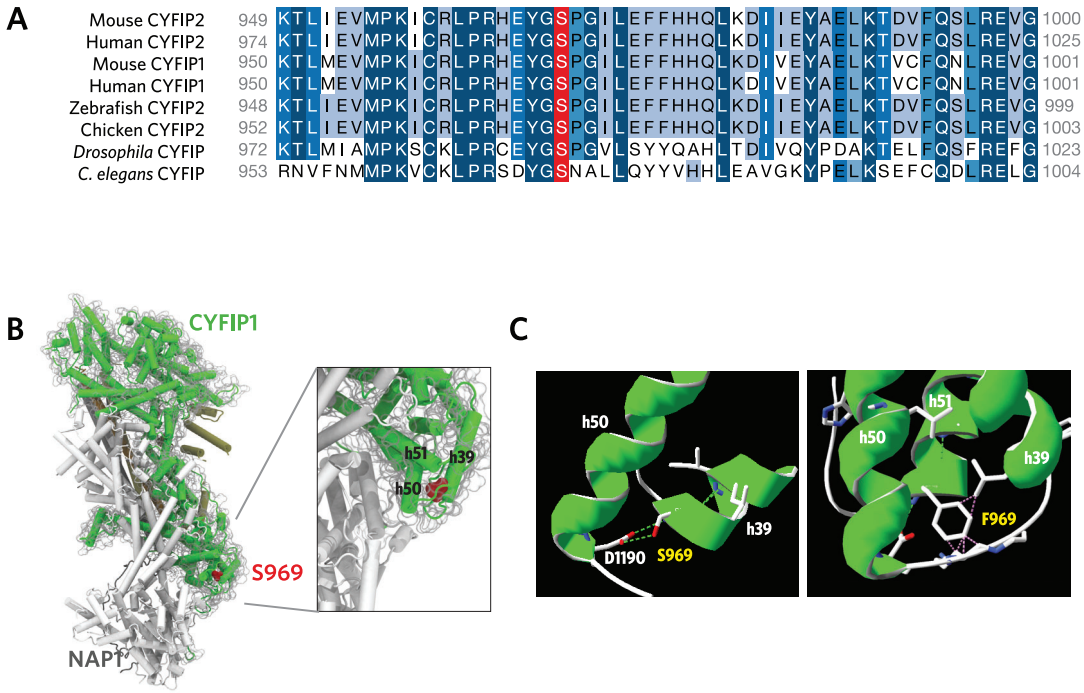
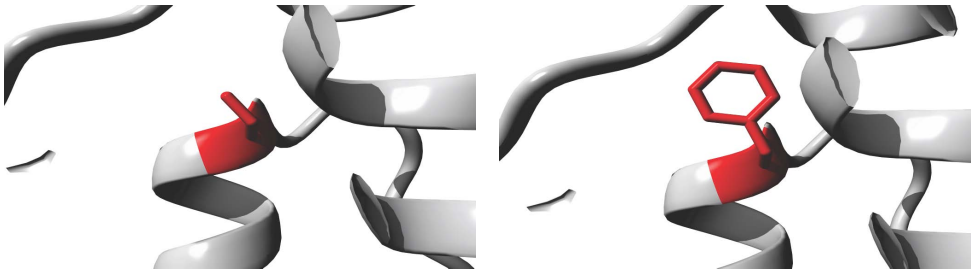


Fig S13: CYFIP2 S968F mutation occurs in a conserved residue and destabilizes the protein. (A) Serine 968 (red) of CYFIP2 is highly conserved in the CYFIP family. (B) S968 paralog in CYFIP1 (S969 red), shown using the WAVE complex crystal structure. CYFIP1 is shown in green with VDW surface rendering and NAP1 in white, and the inset shows helices 50, 51 and 39 that surround S968. (C) Molecular modeling to replace the S969 (left) with phenylalanine (right) leads to steric clashes with neighboring residues (pink).

CYFIP1 S969F FoldX prediction

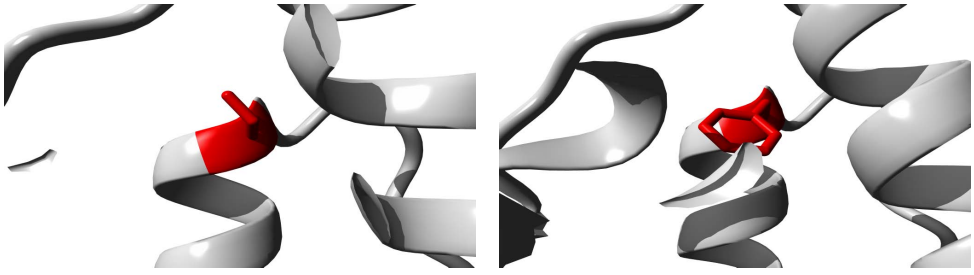
The empirical protein design forcefield FoldX is used to calculate the difference in free energy of the mutation: ddG (delta delta G). If the mutation destabilizes the structure, ddG is increased, whereas stabilizing mutations decrease the ddG. Since the FoldX error margin is around 0.5 kcal/mol, changes in this range are considered insignificant.
3p8c has 99.91 percent homology with the submitted sequence. Using FoldX, we build a homology model starting from this PDB.This pdb is then used to get some more information on the structural effect.The mutation from SER to PHE at position 969 results in a ddG of 17.37 kcal/mol. This implies that the mutation severely reduces the protein stability.



Molecular visualization of the WT (left) and variant (right) amino acid.
The residues colored in red represents the wild type (SER) and variant residue (PHE).

CYFIP2 S968F FoldX prediction

The empirical protein design forcefield FoldX is used to calculate the difference in free energy of the mutation: ddG (delta delta G). If the mutation destabilizes the structure, ddG is increased, whereas stabilizing mutations decrease the ddG. Since the FoldX error margin is around 0.5 kcal/mol, changes in this range are considered insignificant.
3p8c has 88.51 percent homology with the submitted sequence. Using FoldX, we build a homology model starting from this PDB.This pdb is then used to get some more information on the structural effect.The mutation from SER to PHE at position 969 results in a ddG of 11.56 kcal/mol. This implies that the mutation severely reduces the protein stability.



Molecular visualization of the WT (left) and variant (right) amino acid.
The residues colored in red represents the wild type (SER) and variant residue (PHE).

Fig S14

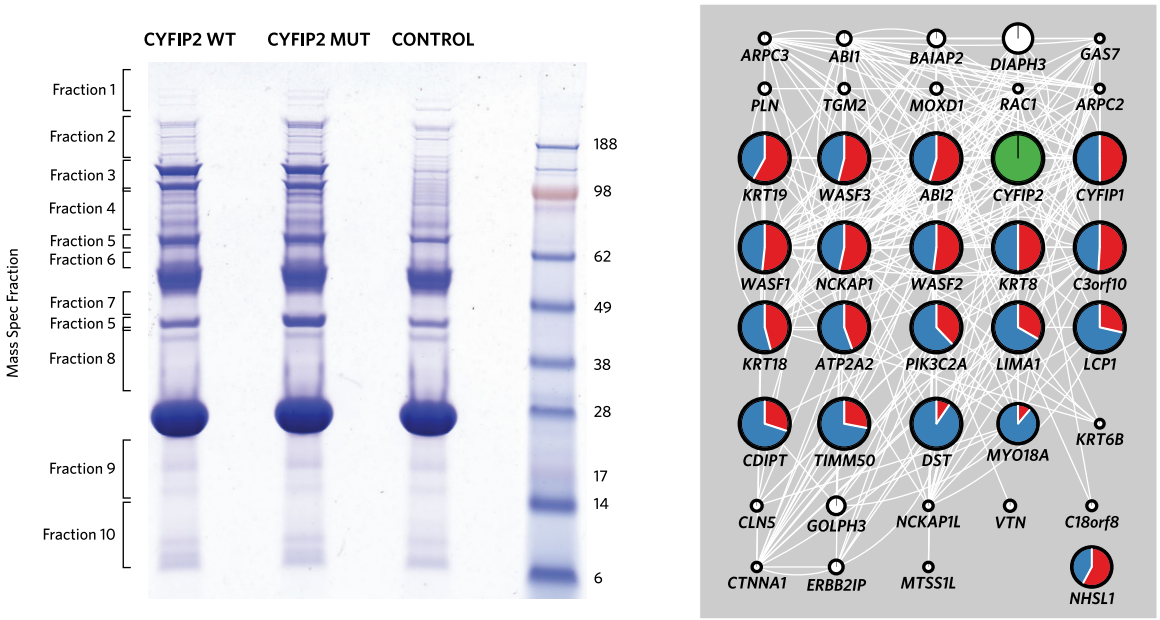


Fig S15: Proteomics analysis of the CYFIP2 interactome. HEK293 cell lines expressing either the WT (B6J) , mutant (B6N) or neither (Control) CYFIP2 were used for immunoprecipitation with anti FLAG antibody. The complex was separated on SDS-PAGE gel which was cut into 10 fractions. Each fraction was subjected to mass spectrometry analysis (left). The enriched proteins that specifically bound to CYFIP2 WT or mutant were analyzed using Genemania network analysis(right). The circles are known interactors of CYFIP, with the size of the circle representing the relative confidence of interaction. The colors represent the enrichment in WT (Blue) or mutant (Red) CYFIP2 (Green). For instance CYFIP1 equally interacts with WT and mutant CYFIP2, but MYO18A is enriched more in WT than mutant pulldown. Analysis was carried out in Cytoscape using the Genemania plugin.

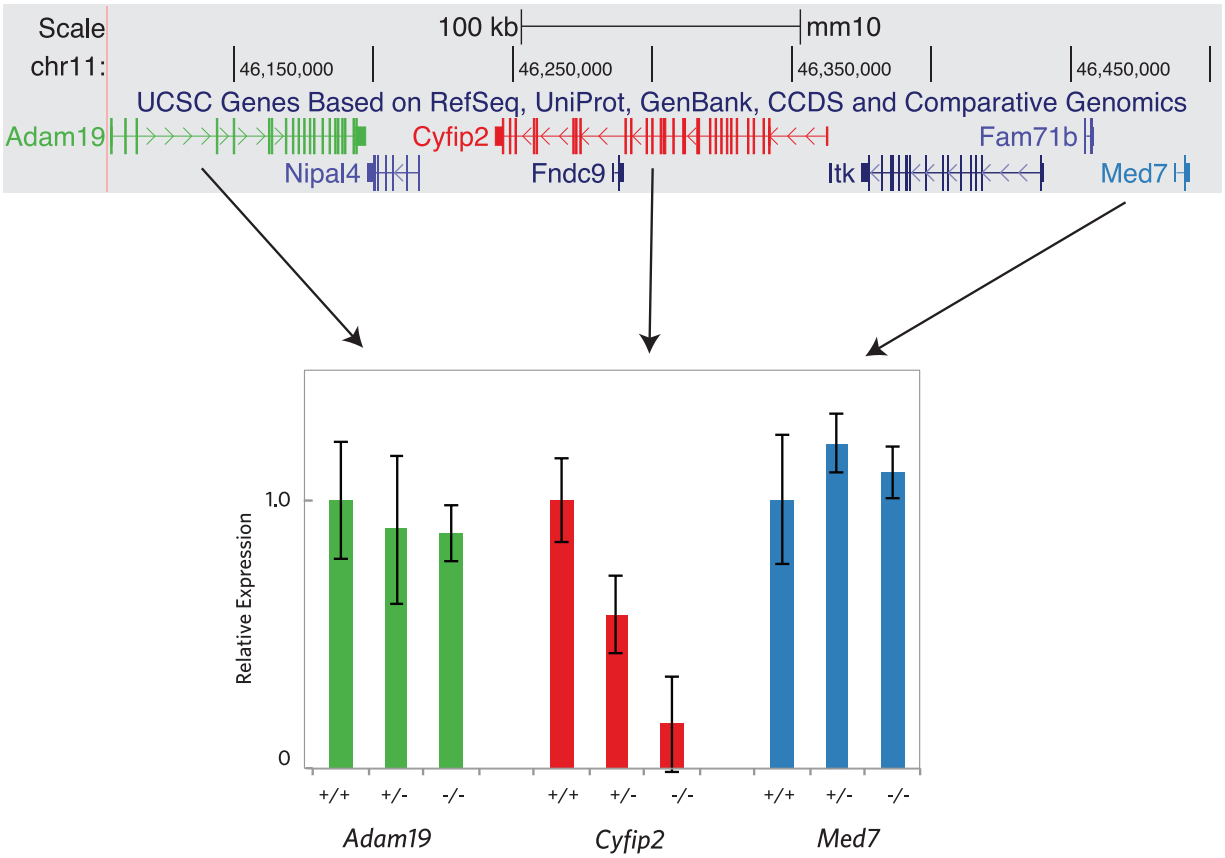


Fig S16: Quantitative rtPCR confirms lack of *Cyfip2* transcript in the knockout mice. Whole brain RNA was isolated from embryos (E18 and E21). Two animals of each genotype were used in this assay. As control expression levels of neighboring genes were also quantitated. Taqman probes for *Med7* (Mm00502970), *Adam19* (Mm00477337), *Cyfip2* (Mm00460148), *GAPDH* (Mm99999915) were obtained from Life Technologies.

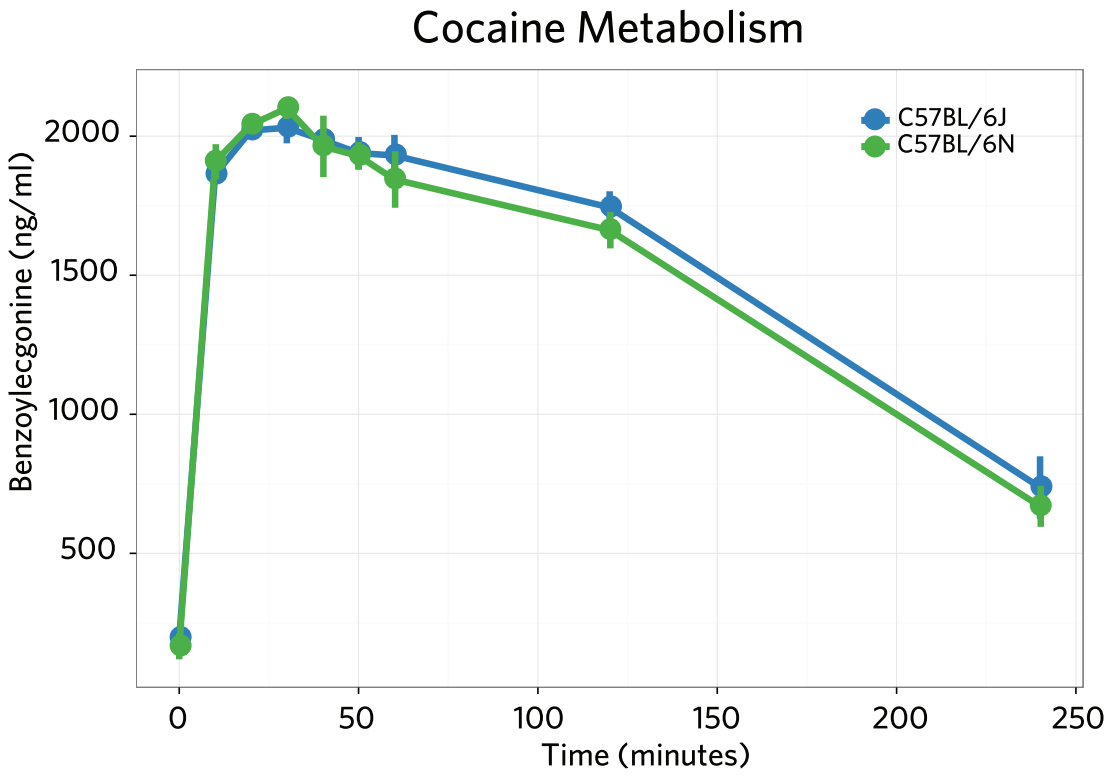


Fig S17: The rate of cocaine metabolism is identical in C57BL/6J and C57BL/6N. Cocaine metabolism was monitored by quantifying the production of benzoylecogonine after drug administration. Mice were intraperitoneally injected with Cocaine (20mg/kg) and blood was harvested by bleeding of the submandibular vein with Goldenrod Animal Lancet (Medipoint Inc) at the indicated times. Two mice were used from each strain for each time point. Serum was used to quantitate benzoylecogonine using an ELISA kit (catalog number KA0929, Abnova).

Table S1. Polymorphic Markers used in QTL mapping

ID	chr	cM	bp	Class
rs31362610	1	20.60	42,424,440	SNP
rs13475886	1	30.64	61,228,463	SNP
rs32481241	1	40.55	78,483,338	SNP
rs6327099	1	56.61	131,282,938	SNP
rs6341208	1	70.42	165,062,830	SNP
rs13476348	2	8.42	11,092,478	SNP
rs33064547	2	24.42	38,802,132	SNP
rs33488914	2	27.33	44,998,528	SNP
rs13476554	2	39.32	67,080,320	SNP
rs33162749	2	47.11	78,639,333	SNP
rs13476801	2	68.38	138,305,756	SNP
rs29818510	2	75.41	152,936,750	SNP
rs13476956	3	1.96	5,370,727	SNP
rs13477019	3	9.25	23,723,842	SNP
rs30557586	3	26.64	55,568,652	SNP
rs31154737	3	33.61	73,922,455	SNP
rs31321678	3	46.83	107,273,295	SNP
rs31594267	3	77.06	151,882,540	SNP
rs13477622	4	11.78	28,249,560	SNP
rs13477746	4	34.61	65,605,269	SNP
rs3680956	4	51.37	109,547,100	SNP
rs6397070	4	87.66	155,284,926	SNP
rs33367397	5	8.37	18,216,206	SNP
rs33508711	5	22.00	41,153,028	SNP
rs13478320	5	37.42	71,133,300	SNP
rs33249065	5	45.91	92,510,104	SNP
rs3662161	5	56.88	117,909,356	SNP
rs13478542	5	74.86	135,358,216	SNP
rs30032909	6	11.65	25,337,386	SNP
rs30314218	6	18.83	40,029,337	SNP
rs13478783	6	29.10	60,541,373	SNP
rs6157367	6	30.80	67,237,174	SNP
rs13478995	6	55.16	117,420,898	SNP
rs31221380	7	24.48	38,216,957	SNP
rs13479233	7	31.01	55,071,694	SNP
rs32060039	7	41.08	78,961,795	SNP
7-110121823	7	54.85	110,121,823	SNP
rs13479522	7	71.15	136,179,208	SNP
rs13479605	8	4.97	10,521,755	SNP
rs13479672	8	16.56	30,207,547	SNP

rs32729089	8	35.56	77,477,256	SNP
rs33601490	8	44.39	94,031,516	SNP
rs33219858	8	57.42	112,622,271	SNP
rs32577205	8	72.10	126,154,896	SNP
rs13480100	9	7.80	21,254,586	SNP
rs13480122	9	16.67	30,964,211	SNP
rs29644859	9	29.12	52,593,224	SNP
rs29934845	9	44.50	81,281,343	SNP
rs29332012	10	7.55	17,969,433	SNP
rs13480575	10	18.70	33,372,829	SNP
rs13480619	10	29.24	57,472,268	SNP
rs13459122	10	39.72	80,258,110	SNP
rs13480759	10	57.01	108,815,683	SNP
rs3659787	11	2.94	4,408,733	SNP
rs29473246	11	19.21	33,448,367	SNP
rs13481014	11	28.41	47,930,884	SNP
rs13481117	11	46.74	79,065,732	SNP
rs29411641	11	59.01	94,820,571	SNP
rs29158719	12	2.80	5,967,934	SNP
rs13481403	12	18.06	40,215,580	SNP
rs6385807	12	24.14	56,859,360	SNP
rs13481569	12	39.76	86,986,287	SNP
rs13481634	12	57.49	108,071,865	SNP
rs13481734	13	12.24	27,129,019	SNP
rs3722313	13	20.49	41,538,155	SNP
13-66355394	13	34.52	66,355,394	SNP
rs3702296	13	53.59	101,979,187	SNP
rs31187642	14	5.80	10,769,899	SNP
rs30264676	14	39.28	74,815,528	SNP
rs31059846	14	49.62	100,024,215	SNP
rs31273189	14	56.62	109,059,068	SNP
rs13459145	15	3.48	7,117,980	SNP
rs31810918	15	14.99	37,392,168	SNP
rs3702158	15	23.86	56,992,041	SNP
rs31858887	15	32.24	71,462,981	SNP
rs4165065	16	10.79	17,412,172	SNP
rs4186435	16	31.96	51,172,069	SNP
rs4214728	16	50.08	87,819,874	SNP
rs4137196	17	3.10	5,332,903	SNP
rs29512740	17	12.53	25,523,395	SNP
rs33334258	17	19.16	39,307,300	SNP
rs13483055	17	31.31	60,459,368	SNP
rs13483071	17	34.71	65,343,195	SNP

rs13483221	18	8.58	15,408,257	SNP
rs13483296	18	18.94	35,366,160	SNP
rs13483369	18	29.22	54,774,495	SNP
rs29690544	18	57.53	84,686,237	SNP
rs30709918	19	11.68	16,676,708	SNP
rs30608930	19	46.76	52,433,860	SNP
rs6368704	20	32.29	55,120,804	SNP
rs6275359	20	41.30	90,945,246	SNP
rs31259892	20	43.84	98,418,215	SNP
rs31266096	20	68.46	147,904,667	SNP

Table S2. Polymorphic Markers between current C57BL/6J and DNA from 1984 stock of C57BL/6J

chromosome	position	rsid
17	39,307,300	rs33334258
2	78,639,333	rs33162749
6	40,029,337	rs30314218
10	17,969,433	rs29332012
1	78,483,338	rs32481241
12	5,967,934	rs29158719
19	16,676,708	rs30709918
15	37,392,168	rs31810918
20	98,418,215	rs31259892
11	33,448,367	rs29473246
6	25,337,386	rs30032909
2	11,092,478	rs13476348
2	67,080,320	rs13476554
3	23,723,842	rs13477019
6	30,872,499	rs13478690
8	119,637,332	rs13480010
12	40,215,580	rs13481403
12	56,859,360	rs6385807
12	108,071,865	rs13481634
15	7,117,980	rs13459145
16	51,172,069	rs4186435
18	54,774,495	rs13483369
19	52,433,860	rs30608930

Table S3: Next generation sequencing coverage statistics

Column1	Target	total_coverage	average_coverage	C57BL_total_cvg	C57BL_mean_cvg	C57BL_granular_Q1	C57BL_granular_median	C57BL_granular_Q3	C57BL_%_above_15
SangerOld	11:1-121843856	3,678,350,283	30.98	3,678,350,283	30.98	24	31	38	93
SangerNew	11:1-121843856	6,310,333,098	53.14	6,310,333,098	53.14	46	54	61	99.2
UTSW	chr11:1-1218438	1,847,499,298	15.56	1,847,499,298	15.56	12	17	21	57
Summary		11,836,182,679	99.68	11,836,182,679	99.68				

Table S4. Classification of all variants on chromosome 11 between C57BL/6N and C57BL/6J. There are three sections that contain SNPs, indels and structural variants.

SNP variants

Chromosome	Position	Reference	Change	Change_type	Homozygous	Quality	Coverage	Warnings	Gene_ID	Gene_nam	Bio_type	Exon_ID	Exon_Rank	Effect
11	3487233	C	A	SNP	Hom	411	14	NA					NA	INTERGENIC
11	3936845	C	T	SNP	Hom	153.13	9	NA	ENSMUSG00000019368	Sec14l4	protein_coding		NA	INTRON
11	4148231	C	A	SNP	Hom	226.03	9	NA					NA	INTERGENIC
11	4408733	G	A	SNP	Hom	394	11	NA	ENSMUSG00000034354	Mtmr3	protein_coding		NA	INTRON
11	4595965	C	A	SNP	Hom	191.13	8	NA					NA	INTERGENIC
11	4676225	A	G	SNP	Hom	272.03	9	NA	ENSMUSG00000009073	Nf2	protein_coding		NA	INTRON
11	5125634	A	C	SNP	Hom	362	14	NA	ENSMUSG00000020393	Kremen1	protein_coding		NA	INTRON
11	5837251	G	T	SNP	Hom	569	22	NA	ENSMUSG00000041798	Gck	protein_coding		NA	INTRON
11	5984921	A	G	SNP	Hom	329.01	9	NA					NA	INTERGENIC
11	6404420	T	C	SNP	Hom	587	16	NA	ENSMUSG00000020437	Myo1g	protein_coding		NA	DOWNSTREAM
11	7019754	G	T	SNP	Hom	238.13	8	NA	ENSMUSG00000020431	Adcy1	protein_coding		NA	INTRON
11	7030169	G	A	SNP	Hom	574	15	NA	ENSMUSG00000020431	Adcy1	protein_coding		NA	INTRON
11	7338077	T	C	SNP	Hom	468	15	NA					NA	INTERGENIC
11	7386861	C	A	SNP	Hom	454	20	NA					NA	INTERGENIC
11	7456145	A	C	SNP	Hom	289.03	10	NA					NA	INTERGENIC
11	8655605	C	T	SNP	Hom	59.97	16	NA					NA	INTERGENIC
11	9626981	T	C	SNP	Hom	518	15	NA					NA	INTERGENIC
11	9728793	T	A	SNP	Hom	237.06	8	NA					NA	INTERGENIC
11	9734998	G	T	SNP	Hom	263.06	8	NA					NA	INTERGENIC
11	10022561	C	T	SNP	Hom	315.01	27	NA					NA	INTERGENIC
11	10097494	C	T	SNP	Hom	37.76	18	NA	ENSMUSG00000084091	Gm11995	pseudogene		NA	UPSTREAM
11	10335959	T	C	SNP	Hom	298	17	NA					NA	INTERGENIC
11	10729450	T	G	SNP	Hom	394	13	NA					NA	INTERGENIC
11	11018623	A	C	SNP	Hom	315	16	NA	ENSMUSG00000050830	Vwc2	protein_coding		NA	INTRON
11	12153006	A	T	SNP	Hom	548	16	NA	ENSMUSG00000020173	Cobl	protein_coding		NA	INTRON
11	12163894	G	T	SNP	Hom	689	20	NA	ENSMUSG00000020173	Cobl	protein_coding		NA	INTRON
11	12241453	C	A	SNP	Hom	157.26	7	NA	ENSMUSG00000086584	Gm12002	processed_transcript		NA	DOWNSTREAM
11	12331253	G	A	SNP	Hom	176.13	8	NA	ENSMUSG00000020173	Cobl	protein_coding		NA	INTRON
11	12934353	A	G	SNP	Hom	285.03	9	NA					NA	INTERGENIC
11	12944508	A	G	SNP	Hom	206.13	9	NA					NA	INTERGENIC
11	13413099	T	C	SNP	Hom	666	21	NA					NA	INTERGENIC
11	14072930	G	T	SNP	Hom	98.51	5	NA	ENSMUSG00000085452	4930554G2	processed_transcript		NA	INTRON
11	14392914	T	C	SNP	Hom	526	14	NA	ENSMUSG00000080734	Gm12006	pseudogene		NA	DOWNSTREAM
11	14512346	A	T	SNP	Hom	407	33	NA					NA	INTERGENIC
11	14512404	C	T	SNP	Hom	220.13	6	NA					NA	INTERGENIC
11	15065667	C	T	SNP	Hom	667	20	NA					NA	INTERGENIC
11	15276479	A	C	SNP	Hom	77.97	6	NA					NA	INTERGENIC
11	15386631	A	G	SNP	Hom	486.01	51	NA	ENSMUSG00000083292	Gm12010	pseudogene		NA	INTRON
11	15977997	C	A	SNP	Hom	332	10	NA					NA	INTERGENIC
11	16628346	T	C	SNP	Hom	1147	34	NA	ENSMUSG00000064831	U6.145	snRNA		NA	DOWNSTREAM
11	16703877	G	A	SNP	Hom	419	12	NA	ENSMUSG00000020122	Egfr	protein_coding		NA	INTRON
11	17142200	T	A	SNP	Hom	253.03	12	NA					NA	INTERGENIC
11	17277912	C	T	SNP	Hom	559	17	NA					NA	INTERGENIC
11	17420444	T	A	SNP	Hom	326	13	NA					NA	INTERGENIC
11	17499495	A	G	SNP	Hom	425	12	NA					NA	INTERGENIC
11	18214202	G	A	SNP	Hom	596	18	NA					NA	INTERGENIC
11	19183398	T	C	SNP	Hom	80.97	7	NA					NA	INTERGENIC
11	19632927	G	C	SNP	Hom	601.01	20	NA					NA	INTERGENIC
11	20357467	C	T	SNP	Hom	408	13	NA					NA	INTERGENIC
11	21040136	A	G	SNP	Hom	425	11	NA	ENSMUSG00000020134	Peli1	protein_coding		NA	INTRON
11	21982867	T	A	SNP	Hom	539	16	NA	ENSMUSG00000042302	Ehbp1	protein_coding		NA	INTRON
11	23527127	C	A	SNP	Hom	412	12	NA	ENSMUSG00000042208	0610010F0	protein_coding		NA	DOWNSTREAM
11	23538532	G	A	SNP	Hom	99.51	7	NA	ENSMUSG00000042208	0610010F0	protein_coding		NA	UPSTREAM
11	25757134	G	A	SNP	Hom	358	13	NA	ENSMUSG00000032985	5730522E0	protein_coding		NA	INTRON
11	25910068	T	C	SNP	Hom	788	22	NA	ENSMUSG00000032985	5730522E0	protein_coding		NA	INTRON
11	26453484	C	A	SNP	Hom	136.51	6	NA	ENSMUSG00000064090	Vrk2	protein_coding		NA	INTRON
11	26657109	C	T	SNP	Hom	203.06	12	NA					NA	INTERGENIC
11	26705708	G	A	SNP	Hom	47.76	9	NA					NA	INTERGENIC
11	27433378	G	T	SNP	Hom	225.54	9	NA					NA	INTERGENIC
11	27535012	C	A	SNP	Hom	571	28	NA					NA	INTERGENIC
11	27662333	G	T	SNP	Hom	278.01	16	NA					NA	INTERGENIC
11	28108412	C	T	SNP	Hom	291.03	10	NA					NA	INTERGENIC
11	28232032	G	C	SNP	Hom	240.03	18	NA					NA	INTERGENIC
11	28239853	C	T	SNP	Hom	466	27	NA	ENSMUSG00000032889	Gm6685	protein_coding		NA	UPSTREAM
11	28932065	A	G	SNP	Hom	466	20	NA					NA	INTERGENIC
11	29003036	A	C	SNP	Hom	375	12	NA					NA	INTERGENIC
11	29572869	C	A	SNP	Hom	295	17	NA					NA	INTERGENIC
11	29679482	T	A	SNP	Hom	250.06	8	NA	ENSMUSG00000044072	Eml6	protein_coding		NA	INTRON
11	30055673	T	A	SNP	Hom	428.13	17	NA	ENSMUSG00000020315	Spnb2	protein_coding		NA	INTRON
11	30452213	T	C	SNP	Hom	730	19	NA	ENSMUSG00000060923	Acyp2	protein_coding		NA	INTRON
11	30568835	C	A	SNP	Hom	235.54	8	NA					NA	INTERGENIC
11	30575691	A	C	SNP	Hom	343	13	NA					NA	INTERGENIC
11	31482524	T	G	SNP	Hom	497.51	15	NA					NA	INTERGENIC
11	31677676	A	G	SNP	Hom	347.01	9	NA					NA	INTERGENIC
11	32973589	G	A	SNP	Hom	359.97	17	NA	ENSMUSG00000087318	Gm12114	processed_transcript		NA	INTRON
11	32973593	G	A	SNP	Hom	424	17	NA	ENSMUSG00000087318	Gm12114	processed_transcript		NA	INTRON
11	32973597	G	A	SNP	Hom	389.51	17	NA	ENSMUSG00000087318	Gm12114	processed_transcript		NA	INTRON
11	33123249	G	A	SNP	Hom	541	17	NA	ENSMUSG00000087501	Gm12116	lincRNA		NA	DOWNSTREAM
11	33254090	T	G	SNP	Hom	386	19	NA	ENSMUSG00000040594	Ranbp17	protein_coding		NA	INTRON
11	33448367	A	G	SNP	Hom	602	16	NA	ENSMUSG00000020159	Gabrp	protein_coding		NA	DOWNSTREAM
11	33595529	A	C	SNP	Hom	492	16	NA	ENSMUSG00000053519	Kcnip1	protein_coding		NA	INTRON
11	33663208	A	G	SNP	Hom	428	14	NA	ENSMUSG00000053519	Kcnip1	protein_coding		NA	INTRON
11	34442982	C	A	SNP	Hom	238.06	10	NA	ENSMUSG00000020143	Dock2	protein_coding		NA	INTRON
11	34443000	C	T	SNP	Hom	316	11	NA	ENSMUSG00000020143	Dock2	protein_coding		NA	INTRON
11	34443006	C	A	SNP	Hom	294.01	12	NA	ENSMUSG00000020143	Dock2	protein_coding		NA	INTRON
11	34443020	C	A	SNP	Hom	383	13	NA	ENSMUSG00000020143	Dock2	protein_coding		NA	INTRON
11	34443030	C	A	SNP	Hom	234.06	7	NA	ENSMUSG00000020143	Dock2	protein_coding		NA	INTRON
11	34443081	C	G	SNP	Hom	470	16	NA	ENSMUSG00000020143	Dock2	protein_coding		NA	INTRON
11	34443092	C	A	SNP	Hom	431	16	NA	ENSMUSG00000020143	Dock2	protein_coding		NA	INTRON
11	34443104	C	G	SNP	Hom	488	17	NA	ENSMUSG00000020143	Dock2	protein_coding		NA	INTRON
11	34443125	C	A	SNP	Hom	45.76	5	NA	ENSMUSG00000020143	Dock2	protein_coding		NA	INTRON

11	34443235	C	A	SNP	Hom	67.97	6	NA	ENSMUSG00000020143	Dock2	protein_coding	NA	INTRON
11	34443245	C	A	SNP	Hom	434	16	NA	ENSMUSG00000020143	Dock2	protein_coding	NA	INTRON
11	34443270	C	A	SNP	Hom	326	12	NA	ENSMUSG00000020143	Dock2	protein_coding	NA	INTRON
11	34443294	C	A	SNP	Hom	300.01	11	NA	ENSMUSG00000020143	Dock2	protein_coding	NA	INTRON
11	34443322	C	G	SNP	Hom	337	11	NA	ENSMUSG00000020143	Dock2	protein_coding	NA	INTRON
11	34443342	C	A	SNP	Hom	453	16	NA	ENSMUSG00000020143	Dock2	protein_coding	NA	INTRON
11	34443345	C	G	SNP	Hom	477	16	NA	ENSMUSG00000020143	Dock2	protein_coding	NA	INTRON
11	34443908	A	T	SNP	Hom	420	13	NA	ENSMUSG00000020143	Dock2	protein_coding	NA	INTRON
11	34443909	A	G	SNP	Hom	336.03	13	NA	ENSMUSG00000020143	Dock2	protein_coding	NA	INTRON
11	34443910	A	G	SNP	Hom	409	14	NA	ENSMUSG00000020143	Dock2	protein_coding	NA	INTRON
11	34495164	T	A	SNP	Hom	1371	44	NA	ENSMUSG00000020143	Dock2	protein_coding	NA	INTRON
11	34495166	C	A	SNP	Hom	1390	46	NA	ENSMUSG00000020143	Dock2	protein_coding	NA	INTRON
11	34780294	G	T	SNP	Hom	347	17	NA				NA	INTERGENIC
11	35234632	A	G	SNP	Hom	427	11	NA	ENSMUSG00000056427	Slit3	protein_coding	NA	INTRON
11	37115943	G	A	SNP	Hom	387	14	NA				NA	INTERGENIC
11	37116114	T	G	SNP	Hom	308.01	9	NA				NA	INTERGENIC
11	37468487	C	T	SNP	Hom	79.97	5	NA	ENSMUSG00000087388	Gm12128	processed_transcript	NA	UPSTREAM
11	37561095	G	A	SNP	Hom	448	13	NA				NA	INTERGENIC
11	38401072	T	C	SNP	Hom	589	17	NA				NA	INTERGENIC
11	38401120	T	G	SNP	Hom	547	15	NA				NA	INTERGENIC
11	38494133	T	G	SNP	Hom	461	12	NA				NA	INTERGENIC
11	38964770	A	C	SNP	Hom	204.13	8	NA				NA	INTERGENIC
11	39222314	G	A	SNP	Hom	718	19	NA				NA	INTERGENIC
11	39598862	T	C	SNP	Hom	301.01	9	NA				NA	INTERGENIC
11	40411018	G	A	SNP	Hom	371	10	NA				NA	INTERGENIC
11	41025615	T	G	SNP	Hom	494	13	NA				NA	INTERGENIC
11	41192910	T	C	SNP	Hom	234.03	11	NA	ENSMUSG00000081112	Gm12140	pseudogene	NA	DOWNSTREAM
11	42611956	C	A	SNP	Hom	179.13	6	NA				NA	INTERGENIC
11	42612003	A	G	SNP	Hom	239.01	29	NA				NA	INTERGENIC
11	42612009	A	G	SNP	Hom	191.06	31	NA				NA	INTERGENIC
11	42612056	G	A	SNP	Hom	800	44	NA				NA	INTERGENIC
11	43076671	T	C	SNP	Hom	358	12	NA	ENSMUSG00000055415	Atp10b	protein_coding	NA	DOWNSTREAM
11	43171964	A	G	SNP	Hom	475	13	NA				NA	INTERGENIC
11	43340333	G	T	SNP	Hom	376	15	NA	ENSMUSG00000044707	Ccnjl	protein_coding	NA	UPSTREAM
11	43654559	T	C	SNP	Hom	294.01	13	NA	ENSMUSG00000050541	Adra1b	protein_coding	NA	INTRON
11	46036117	G	A	SNP	Hom	219.06	8	NA	ENSMUSG00000020340	Cyfip2	protein_coding	exon_11_46(	26 NS_CODING
11	46084671	T	C	SNP	Hom	266.01	10	NA	ENSMUSG00000020340	Cyfip2	protein_coding	NA	INTRON
11	47930884	T	C	SNP	Hom	329.01	11	NA				NA	INTERGENIC
11	48065799	T	C	SNP	Hom	508	14	NA				NA	INTERGENIC
11	49015265	G	C	SNP	Hom	385.19	25	NA	ENSMUSG00000046311	Zfp62	protein_coding	NA	UPSTREAM
11	49110483	T	C	SNP	Hom	206.13	12	NA	ENSMUSG00000050959	Olfr1392	protein_coding	NA	DOWNSTREAM
11	49408579	T	C	SNP	Hom	437.04	17	NA	ENSMUSG00000081791	Gm12190	pseudogene	NA	DOWNSTREAM
11	49475509	G	A	SNP	Hom	609	36	NA	ENSMUSG00000064057	Scgb3a1	protein_coding	NA	UPSTREAM
11	49475518	G	A	SNP	Hom	422	35	NA	ENSMUSG00000064057	Scgb3a1	protein_coding	NA	UPSTREAM
11	49530193	C	A	SNP	Hom	315	15	NA	ENSMUSG00000020362	Cnot6	protein_coding	NA	UPSTREAM
11	49838455	T	G	SNP	Hom	741	27	NA	ENSMUSG00000020376	Rnf130	protein_coding	NA	UPSTREAM
11	50232547	C	A	SNP	Hom	650	22	NA	ENSMUSG00000020375	Rufy1	protein_coding	NA	INTRON
11	50314369	A	G	SNP	Hom	325.01	11	NA				NA	INTERGENIC
11	50776124	A	G	SNP	Hom	597	20	NA	ENSMUSG00000083542	Olfr1379-ps	pseudogene	NA	DOWNSTREAM
11	51150239	C	T	SNP	Hom	438	13	NA	ENSMUSG00000063564	Col23a1	protein_coding	NA	INTRON
11	51835312	G	T	SNP	Hom	31.77	5	NA	ENSMUSG00000020389	Cdkl3	protein_coding	NA	DOWNSTREAM
11	51878742	T	C	SNP	Hom	260.03	10	NA	ENSMUSG00000087101	Gm16953	lincRNA	NA	INTRON
11	52247258	C	A	SNP	Hom	193.13	10	NA				NA	INTERGENIC
11	52263223	G	T	SNP	Hom	571	22	NA				NA	INTERGENIC
11	52725097	G	A	SNP	Hom	565	16	NA	ENSMUSG00000036264	Fstl4	protein_coding	NA	INTRON
11	52831098	A	G	SNP	Hom	236.06	7	NA	ENSMUSG00000036264	Fstl4	protein_coding	NA	INTRON
11	52831203	A	G	SNP	Hom	916	25	NA	ENSMUSG00000036264	Fstl4	protein_coding	NA	INTRON
11	52831257	T	G	SNP	Hom	202.13	6	NA	ENSMUSG00000036264	Fstl4	protein_coding	NA	INTRON
11	52834380	A	G	SNP	Hom	439	15	NA	ENSMUSG00000036264	Fstl4	protein_coding	NA	INTRON
11	53109728	A	G	SNP	Hom	574	18	NA	ENSMUSG00000020361	Hspa4	protein_coding	NA	INTRON
11	53793075	T	C	SNP	Hom	667	33	NA	ENSMUSG00000020334	Slc22a4	protein_coding	NA	DOWNSTREAM
11	53850694	C	T	SNP	Hom	241.06	8	NA				NA	INTERGENIC
11	53954080	G	A	SNP	Hom	7219.01	250	NA				NA	INTERGENIC
11	53954118	A	T	SNP	Hom	7052.01	250	NA				NA	INTERGENIC
11	53954121	C	T	SNP	Hom	7293.01	250	NA				NA	INTERGENIC
11	54048103	T	C	SNP	Hom	508	14	NA				NA	INTERGENIC
11	54909259	C	A	SNP	Hom	176.13	8	NA	ENSMUSG00000000594	Gm2a	protein_coding	NA	UPSTREAM
11	56184043	G	T	SNP	Hom	451	16	NA				NA	INTERGENIC
11	56446472	G	C	SNP	Hom	1013	50	NA				NA	INTERGENIC
11	56467321	A	G	SNP	Hom	1153	31	NA				NA	INTERGENIC
11	56704748	C	T	SNP	Hom	132.51	6	NA				NA	INTERGENIC
11	56881782	A	G	SNP	Hom	496	15	NA	ENSMUSG00000020524	Gria1	protein_coding	NA	INTRON
11	57150478	G	A	SNP	Hom	132.26	5	NA				NA	INTERGENIC
11	57611712	C	A	SNP	Hom	496.21	22	NA	ENSMUSG00000087165	2010001A1	lincRNA	NA	INTRON
11	57621311	A	T	SNP	Hom	173.26	6	NA	ENSMUSG00000020519	Sap30l	protein_coding	NA	INTRON
11	57739193	G	T	SNP	Hom	779	28	NA				NA	INTERGENIC
11	57845997	G	A	SNP	Hom	423	11	NA	ENSMUSG00000037331	Larp1	protein_coding	NA	INTRON
11	57893450	G	T	SNP	Hom	495	18	NA				NA	INTERGENIC
11	57994103	G	T	SNP	Hom	160.26	6	NA	ENSMUSG00000020514	Mrpl22	protein_coding	NA	DOWNSTREAM
11	58000175	G	T	SNP	Hom	320.01	14	NA	ENSMUSG00000082292	Gm12250	pseudogene	NA	INTRON
11	58508180	A	G	SNP	Hom	220.13	6	NA				NA	INTERGENIC
11	58595831	T	A	SNP	Hom	510	15	NA	ENSMUSG00000056959	Olfr315	protein_coding	NA	DOWNSTREAM
11	58595832	G	C	SNP	Hom	481	14	NA	ENSMUSG00000056959	Olfr315	protein_coding	NA	DOWNSTREAM
11	58912550	T	C	SNP	Hom	266.03	12	NA	ENSMUSG00000061462	Obscn	protein_coding	NA	INTRON
11	59727055	C	T	SNP	Hom	241.06	9	NA				NA	INTERGENIC
11	59975491	C	T	SNP	Hom	164.26	7	NA	ENSMUSG00000062115	Rai1	protein_coding	NA	INTRON
11	60471403	C	A	SNP	Hom	217.06	34	NA	ENSMUSG00000084335	Gm12619	pseudogene	NA	UPSTREAM
11	60490168	G	C	SNP	Hom	35.77	28	NA	ENSMUSG00000082748	Gm12616	pseudogene	NA	DOWNSTREAM
11	60669079	A	T	SNP	Hom	432	13	NA	ENSMUSG00000042569	Dhrs7b	protein_coding	NA	INTRON
11	61902241	C	T	SNP	Hom	248.12	14	NA	ENSMUSG00000042331	Specc1	protein_coding	NA	INTRON
11	62335824	T	G	SNP	Hom	585	15	NA	ENSMUSG00000018509	Cenpv	protein_coding	NA	DOWNSTREAM
11	62559152	T	C	SNP	Hom	350	12	NA	ENSMUSG00000084020	Gm12282	pseudogene	NA	DOWNSTREAM
11	62814700	G	C	SNP	Hom	714	27	NA	ENSMUSG00000087604	4930452L0;	processed_transcript	NA	INTRON
11	62881422	A	G	SNP	Hom	506	14	NA	ENSMUSG00000042189	Tekt3	protein_coding	NA	INTRON
11	62886983	T	C	SNP	Hom	433	12	NA	ENSMUSG00000042189	Tekt3	protein_coding	exon_11_628	3 SYN_CODING

11	63445159	T	C	SNP	Hom	525	37	NA				NA	NA	INTERGENIC
11	64808045	T	C	SNP	Hom	541	14	NA	ENSMUSG00000020549	Elac2	protein_coding	NA	NA	DOWNSTREAM
11	65237281	A	G	SNP	Hom	454	14	NA				NA	NA	INTERGENIC
11	65765558	G	T	SNP	Hom	273.01	23	NA	ENSMUSG00000056752	Dnahc9	protein_coding	NA	NA	INTRON
11	65886145	A	C	SNP	Hom	461	13	NA	ENSMUSG00000056752	Dnahc9	protein_coding	NA	NA	INTRON
11	66667847	T	C	SNP	Hom	439.41	16	NA				NA	NA	INTERGENIC
11	66937684	G	T	SNP	Hom	523	15	NA	ENSMUSG00000087410	2310065F0	processed_transcript	NA	NA	UPSTREAM
11	67741335	T	A	SNP	Hom	1239	33	NA	ENSMUSG00000055134	9130017K1	lincRNA	NA	NA	DOWNSTREAM
11	68409281	C	T	SNP	Hom	212.03	42	NA	ENSMUSG00000045915	Ccdc42	protein_coding	NA	NA	INTRON
11	68910076	G	T	SNP	Hom	99.51	6	NA	ENSMUSG00000020894	Vamp2	protein_coding	NA	NA	DOWNSTREAM
11	69109927	C	T	SNP	Hom	687	24	NA	ENSMUSG00000087003	1700067G0	processed_transcript	NA	NA	DOWNSTREAM
11	69253975	A	G	SNP	Hom	445	13	NA	ENSMUSG00000005237	Dnahc2	protein_coding	NA	NA	INTRON
11	69316112	G	T	SNP	Hom	334.97	11	NA	ENSMUSG00000005237	Dnahc2	protein_coding	NA	NA	INTRON
11	69405425	G	A	SNP	Hom	444	13	NA	ENSMUSG00000059552	Trp53	protein_coding	NA	NA	DOWNSTREAM
11	69447165	T	C	SNP	Hom	907	32	NA	ENSMUSG00000080573	Mir467f	miRNA	NA	NA	DOWNSTREAM
11	70338563	A	C	SNP	Hom	964	32	NA	ENSMUSG00000046811	Gltpd2	protein_coding	NA	NA	DOWNSTREAM
11	71190336	C	A	SNP	Hom	1160	30	NA				NA	NA	INTERGENIC
11	71491881	G	T	SNP	Hom	282.01	9	NA				NA	NA	INTERGENIC
11	71836925	T	G	SNP	Hom	448	14	NA	ENSMUSG00000080577	U6atac.16	snRNA	NA	NA	DOWNSTREAM
11	72370465	A	C	SNP	Hom	166.13	12	NA				NA	NA	INTERGENIC
11	73666274	C	T	SNP	Hom	684	19	NA	ENSMUSG00000064228	Olfr393	protein_coding	NA	NA	UPSTREAM
11	73740508	A	T	SNP	Hom	372	11	NA	ENSMUSG00000086011	Olfr396-ps1	pseudogene	NA	NA	UPSTREAM
11	73914573	C	T	SNP	Hom	758	21	NA	ENSMUSG00000081162	Olfr400-ps1	pseudogene	NA	NA	UPSTREAM
11	73986864	A	G	SNP	Hom	197.06	17	NA				NA	NA	INTERGENIC
11	74151395	A	C	SNP	Hom	663	18	NA	ENSMUSG00000063116	Olfr410	protein_coding	NA	NA	UPSTREAM
11	74493173	T	C	SNP	Hom	694	21	NA	ENSMUSG00000020745	Pafah1b1	protein_coding	NA	NA	INTRON
11	74576813	G	T	SNP	Hom	1234	37	NA				NA	NA	INTERGENIC
11	74723885	T	A	SNP	Hom	1430	37	NA	ENSMUSG00000001323	Srr	protein_coding	NA	NA	DOWNSTREAM
11	74797307	G	T	SNP	Hom	888	32	NA	ENSMUSG00000038290	Smg6	protein_coding	NA	NA	INTRON
11	75000595	A	C	SNP	Hom	295.97	19	NA	ENSMUSG00000078789	Dph1	protein_coding	NA	NA	INTRON
11	75900596	A	G	SNP	Hom	433	16	NA	ENSMUSG00000017288	Vps53	protein_coding	NA	NA	INTRON
11	76817264	A	G	SNP	Hom	592	17	NA	ENSMUSG00000020838	Slc6a4	protein_coding	NA	NA	INTRON
11	77011233	A	G	SNP	Hom	263.06	8	NA				NA	NA	INTERGENIC
11	77553016	G	A	SNP	Hom	84.97	11	NA	ENSMUSG00000037857	Nufip2	protein_coding	NA	NA	INTRON
11	77557175	A	G	SNP	Hom	1195	36	NA	ENSMUSG00000037857	Nufip2	protein_coding	NA	NA	DOWNSTREAM
11	77762346	A	C	SNP	Hom	1032	29	NA	ENSMUSG00000000632	Sez6	protein_coding	NA	NA	INTRON
11	77762477	C	T	SNP	Hom	138.26	6	NA	ENSMUSG00000000632	Sez6	protein_coding	NA	NA	INTRON
11	77857230	C	A	SNP	Hom	517.02	22	NA	ENSMUSG00000061981	Flot2	protein_coding	NA	NA	INTRON
11	77904686	G	T	SNP	Hom	1459	40	NA	ENSMUSG00000037750	BC017647	protein_coding	NA	NA	UPSTREAM
11	78011962	C	T	SNP	Hom	891.06	29	NA	ENSMUSG00000044122	Proca1	protein_coding	NA	NA	INTRON
11	78284601	G	T	SNP	Hom	220.13	8	NA	ENSMUSG00000050132	Sarm1	protein_coding	NA	NA	DOWNSTREAM
11	78559023	A	G	SNP	Hom	513	15	NA	ENSMUSG00000049489	Fam58b	protein_coding	NA	NA	DOWNSTREAM
11	79003241	C	T	SNP	Hom	1816	99	NA				NA	NA	INTERGENIC
11	79003303	G	A	SNP	Hom	2797	101	NA				NA	NA	INTERGENIC
11	79065732	G	T	SNP	Hom	364	15	NA	ENSMUSG00000017677	Wsb1	protein_coding	NA	NA	INTRON
11	79800827	G	T	SNP	Hom	1093	36	NA				NA	NA	INTERGENIC
11	80044019	G	T	SNP	Hom	642.54	31	NA	ENSMUSG00000017686	Rhot1	protein_coding	NA	NA	INTRON
11	80178710	G	T	SNP	Hom	1059	36	NA	ENSMUSG00000057181	5730455P1	protein_coding	NA	NA	INTRON
11	80388301	C	A	SNP	Hom	235.01	10	NA	ENSMUSG00000035441	Myo1d	protein_coding	NA	NA	INTRON
11	80622422	A	C	SNP	Hom	951	30	NA	ENSMUSG00000035413	Tmem98	protein_coding	NA	NA	UPSTREAM
11	80999859	G	C	SNP	Hom	1244	33	NA	ENSMUSG00000020704	Accn1	protein_coding	NA	NA	INTRON
11	81000565	C	A	SNP	Hom	1435	39	NA	ENSMUSG00000020704	Accn1	protein_coding	NA	NA	INTRON
11	81434038	C	A	SNP	Hom	647	21	NA	ENSMUSG00000020704	Accn1	protein_coding	NA	NA	INTRON
11	81476471	A	C	SNP	Hom	619	16	NA	ENSMUSG00000020704	Accn1	protein_coding	NA	NA	INTRON
11	82601520	A	G	SNP	Hom	247.06	7	NA	ENSMUSG00000020697	Lig3	protein_coding	NA	NA	INTRON
11	82694980	C	T	SNP	Hom	465	13	NA	ENSMUSG00000018841	Rad51l3	protein_coding	NA	NA	INTRON
11	82931735	G	A	SNP	Hom	419	13	NA	ENSMUSG00000078763	Slfn1	protein_coding	NA	NA	INTRON
11	83143024	T	C	SNP	Hom	624	16	NA	ENSMUSG00000035152	Ap2b1	protein_coding	NA	NA	INTRON
11	83220064	G	T	SNP	Hom	219.13	7	NA	ENSMUSG00000035152	Ap2b1	protein_coding	NA	NA	DOWNSTREAM
11	83286412	G	C	SNP	Hom	1456	38	NA	ENSMUSG00000020680	Taf15	protein_coding	NA	NA	UPSTREAM
11	83479502	A	G	SNP	Hom	1613	43	NA	ENSMUSG00000018930	Ccl4	protein_coding	NA	NA	DOWNSTREAM
11	83956143	C	A	SNP	Hom	163.26	5	NA	ENSMUSG00000020532	Acaca	protein_coding	NA	NA	INTRON
11	84674773	G	A	SNP	Hom	1514	42	NA	ENSMUSG00000020530	Ggnbp2	protein_coding	NA	NA	INTRON
11	84992909	T	C	SNP	Hom	90.11	5	NA	ENSMUSG00000018479	1700125H2	protein_coding	NA	NA	INTRON
11	85043220	T	C	SNP	Hom	822	30	NA	ENSMUSG00000018481	Appbp2	protein_coding	NA	NA	INTRON
11	85359123	A	C	SNP	Hom	862.41	32	NA	ENSMUSG00000059439	Bcas3	protein_coding	NA	NA	INTRON
11	85679835	A	C	SNP	Hom	565	15	NA				NA	NA	INTERGENIC
11	85823915	T	G	SNP	Hom	1621	42	NA				NA	NA	INTERGENIC
11	85964653	C	G	SNP	Hom	1607	43	NA	ENSMUSG00000034329	Brip1	protein_coding	NA	NA	INTRON
11	86084721	T	A	SNP	Hom	1040	35	NA	ENSMUSG00000034297	Med13	protein_coding	NA	NA	DOWNSTREAM
11	86136234	G	A	SNP	Hom	667	22	NA	ENSMUSG00000034297	Med13	protein_coding	NA	NA	INTRON
11	86553266	G	T	SNP	Hom	910.04	31	NA	ENSMUSG00000047126	Cltc	protein_coding	NA	NA	INTRON
11	86637186	G	A	SNP	Hom	305.01	11	NA				NA	NA	INTERGENIC
11	86637760	C	T	SNP	Hom	615	30	NA				NA	NA	INTERGENIC
11	87288833	G	T	SNP	Hom	386	15	NA	ENSMUSG00000070168	U3.5	snoRNA	NA	NA	DOWNSTREAM
11	88048269	T	G	SNP	Hom	1222	38	NA				NA	NA	INTERGENIC
11	88309445	T	C	SNP	Hom	420	14	NA	ENSMUSG00000069769	Msi2	protein_coding	NA	NA	INTRON
11	88408825	G	T	SNP	Hom	1002	45	NA	ENSMUSG00000069769	Msi2	protein_coding	NA	NA	INTRON
11	88459680	C	A	SNP	Hom	300.03	9	NA	ENSMUSG00000069769	Msi2	protein_coding	NA	NA	INTRON
11	88459682	A	G	SNP	Hom	300.03	9	NA	ENSMUSG00000069769	Msi2	protein_coding	NA	NA	INTRON
11	88459719	C	A	SNP	Hom	1316	41	NA	ENSMUSG00000069769	Msi2	protein_coding	NA	NA	INTRON
11	88459722	C	T	SNP	Hom	1271	40	NA	ENSMUSG00000069769	Msi2	protein_coding	NA	NA	INTRON
11	88459741	C	G	SNP	Hom	886	29	NA	ENSMUSG00000069769	Msi2	protein_coding	NA	NA	INTRON
11	88459745	C	A	SNP	Hom	851	27	NA	ENSMUSG00000069769	Msi2	protein_coding	NA	NA	INTRON
11	88460027	T	G	SNP	Hom	521	17	NA	ENSMUSG00000069769	Msi2	protein_coding	NA	NA	INTRON
11	88903368	C	A	SNP	Hom	390	11	NA	ENSMUSG00000000276	Dgke	protein_coding	NA	NA	INTRON
11	89021216	C	A	SNP	Hom	606.54	24	NA				NA	NA	INTERGENIC
11	89377944	T	C	SNP	Hom	1254	37	NA	ENSMUSG00000047773	Ankfn1	protein_coding	NA	NA	INTRON
11	90231349	G	T	SNP	Hom	1671	46	NA	ENSMUSG00000003949	Hlf	protein_coding	NA	NA	INTRON
11	90252994	A	G	SNP	Hom	385	12	NA	ENSMUSG00000003949	Hlf	protein_coding	NA	NA	UPSTREAM
11	90341985	C	T	SNP	Hom	448	13	NA	ENSMUSG00000020546	Stxbp4	protein_coding	exon_11_90	18	NS_CODING
11	90674802	G	C	SNP	Hom	928	27	NA	ENSMUSG00000085940	4930405D1	processed_transcript	NA	NA	INTRON
11	90951742	T	C	SNP	Hom	445.17	16	NA				NA	NA	INTERGENIC
11	91408581	T	G	SNP	Hom	505	17	NA				NA	NA	INTERGENIC
11	92892753	G	T	SNP	Hom	1739	46	NA				NA	NA	INTERGENIC

11	94225110	T	C	SNP	Hom	585	23	NA	ENSMUSG00000020865	Abcc3	protein_coding		NA	DOWNSTREAM
11	94541624	C	A	SNP	Hom	1132	31	NA	ENSMUSG00000085051	Gm11542	lincRNA		NA	INTRON
11	94541664	C	T	SNP	Hom	1265	36	NA	ENSMUSG00000085051	Gm11542	lincRNA		NA	INTRON
11	94820611	T	G	SNP	Hom	629	17	NA	ENSMUSG00000001508	Sgca	protein_coding		NA	DOWNSTREAM
11	95065932	A	G	SNP	Hom	539	23	NA					NA	INTERGENIC
11	95101851	A	G	SNP	Hom	1260	35	NA					NA	INTERGENIC
11	95144676	T	A	SNP	Hom	457	14	NA	ENSMUSG00000038909	Myst2	protein_coding		NA	DOWNSTREAM
11	96299684	C	T	SNP	Hom	948	29	NA					NA	INTERGENIC
11	96460587	A	T	SNP	Hom	358	14	NA	ENSMUSG00000057058	Skap1	protein_coding		NA	INTRON
11	96614971	T	C	SNP	Hom	786	29	NA	ENSMUSG00000057058	Skap1	protein_coding		NA	INTRON
11	96648966	G	T	SNP	Hom	848	33	NA	ENSMUSG00000018666	Cbx1	protein_coding		NA	UPSTREAM
11	96705229	G	C	SNP	Hom	750	25	NA					NA	INTERGENIC
11	96950730	A	G	SNP	Hom	558	16	NA					NA	INTERGENIC
11	97275072	C	G	SNP	Hom	1698	67	NA	ENSMUSG00000049807	Arhgap23	protein_coding		NA	UPSTREAM
11	97411534	T	C	SNP	Hom	1789	48	NA	ENSMUSG00000038453	Srcin1	protein_coding		NA	DOWNSTREAM
11	97698092	A	G	SNP	Hom	1787	46	NA	ENSMUSG00000038366	Lasp1	protein_coding		NA	DOWNSTREAM
11	97827556	G	A	SNP	Hom	947	27	NA	ENSMUSG00000017417	Plxdc1	protein_coding		NA	INTRON
11	97849250	T	C	SNP	Hom	1758	47	NA	ENSMUSG00000038352	Arl5c	protein_coding		NA	DOWNSTREAM
11	99083237	T	C	SNP	Hom	299.01	11	NA	ENSMUSG00000037935	Smarce1	protein_coding		NA	DOWNSTREAM
11	99553667	T	A	SNP	Hom	1019.21	48	NA	ENSMUSG00000078275	Gm14192	protein_coding		NA	DOWNSTREAM
11	99827570	A	G	SNP	Hom	386	11	NA	ENSMUSG00000081547	Gm11553	pseudogene		NA	DOWNSTREAM
11	100779233	A	G	SNP	Hom	1565	42	NA	ENSMUSG00000004040	Stat3	protein_coding		NA	INTRON
11	100937788	C	G	SNP	Hom	1902	51	NA	ENSMUSG00000001751	Naglu	protein_coding	exon_11_10(	3	NS_CODING
11	100989377	G	T	SNP	Hom	203.13	7	NA	ENSMUSG00000035198	Tubg1	protein_coding		NA	DOWNSTREAM
11	101090632	A	G	SNP	Hom	1808	47	NA	ENSMUSG00000006920	Ezh1	protein_coding		NA	UPSTREAM
11	101117446	C	A	SNP	Hom	1938	51	NA	ENSMUSG00000001240	Ramp2	protein_coding		NA	INTRON
11	101182979	C	G	SNP	Hom	160.26	7	NA	ENSMUSG00000078652	Psme3	protein_coding		NA	DOWNSTREAM
11	101419827	A	G	SNP	Hom	437	15	NA	ENSMUSG00000017119	Nbr1	protein_coding		NA	INTRON
11	101825288	C	G	SNP	Hom	428	23	NA	ENSMUSG00000071818	4930417O2	processed_transcript		NA	DOWNSTREAM
11	101961787	T	A	SNP	Hom	1077.05	46	NA	ENSMUSG00000017316	Ppy	protein_coding		NA	INTRON
11	102428238	A	G	SNP	Hom	705	34	NA					NA	INTERGENIC
11	103207136	T	C	SNP	Hom	355	10	NA	ENSMUSG00000034255	Arhgap27	protein_coding		NA	INTRON
11	103837151	A	G	SNP	Hom	1526	43	NA	ENSMUSG00000062421	Arf2	protein_coding		NA	INTRON
11	103837152	C	A	SNP	Hom	1603	43	NA	ENSMUSG00000062421	Arf2	protein_coding		NA	INTRON
11	105537692	G	T	SNP	Hom	158.26	5	NA	ENSMUSG00000053580	Tanc2	protein_coding		NA	INTRON
11	105642290	C	T	SNP	Hom	1300	38	NA	ENSMUSG00000053580	Tanc2	protein_coding		NA	DOWNSTREAM
11	106136423	G	A	SNP	Hom	1744	50	NA	ENSMUSG00000020712	Tcam1	protein_coding		NA	UPSTREAM
11	106332890	A	C	SNP	Hom	1453	38	NA	ENSMUSG00000020715	Ern1	protein_coding		NA	INTRON
11	106378404	T	G	SNP	Hom	88.97	6	NA	ENSMUSG00000040548	Tex2	protein_coding		NA	INTRON
11	106580491	C	A	SNP	Hom	218.13	6	NA	ENSMUSG00000020717	Pecam1	protein_coding		NA	INTRON
11	106914006	T	C	SNP	Hom	467	15	NA	ENSMUSG00000040481	Bptf	protein_coding		NA	INTRON
11	107012799	G	T	SNP	Hom	327	14	NA					NA	INTERGENIC
11	107059653	C	A	SNP	Hom	206.06	9	NA					NA	INTERGENIC
11	107162311	A	C	SNP	Hom	1923	53	NA	ENSMUSG00000040430	Pitpnc1	protein_coding		NA	INTRON
11	107365972	G	T	SNP	Hom	779	28	NA	ENSMUSG00000020720	Psmd12	protein_coding		NA	DOWNSTREAM
11	107399176	T	G	SNP	Hom	868	24	NA	ENSMUSG00000059706	A830035A1	processed_transcript		NA	INTRON
11	107399181	T	G	SNP	Hom	857	24	NA	ENSMUSG00000059706	A830035A1	processed_transcript		NA	INTRON
11	107682856	A	C	SNP	Hom	1467	41	NA					NA	INTERGENIC
11	107750347	C	T	SNP	Hom	342.01	15	NA	ENSMUSG00000040373	Cacng5	protein_coding		NA	INTRON
11	107967175	G	A	SNP	Hom	160.26	5	NA	ENSMUSG00000050965	Prkca	protein_coding		NA	INTRON
11	108564316	A	T	SNP	Hom	2004	55	NA	ENSMUSG00000020728	Ccdc46	protein_coding		NA	INTRON
11	108695766	A	T	SNP	Hom	2069	54	NA	ENSMUSG00000020728	Ccdc46	protein_coding		NA	INTRON
11	108873084	T	C	SNP	Hom	4534.01	250	NA	ENSMUSG00000081392	Gm11668	pseudogene		NA	DOWNSTREAM
11	108873097	A	G	SNP	Hom	5578.01	250	NA	ENSMUSG00000081392	Gm11668	pseudogene		NA	DOWNSTREAM
11	108873098	T	C	SNP	Hom	5838.01	250	NA	ENSMUSG00000081392	Gm11668	pseudogene		NA	DOWNSTREAM
11	108873117	T	G	SNP	Hom	4538.01	250	NA	ENSMUSG00000081392	Gm11668	pseudogene		NA	DOWNSTREAM
11	108873129	A	G	SNP	Hom	243	19	NA	ENSMUSG00000081392	Gm11668	pseudogene		NA	DOWNSTREAM
11	108873250	T	C	SNP	Hom	5930.01	248	NA	ENSMUSG00000081392	Gm11668	pseudogene		NA	DOWNSTREAM
11	108873256	T	C	SNP	Hom	5204.01	250	NA	ENSMUSG00000081392	Gm11668	pseudogene		NA	DOWNSTREAM
11	108873278	C	T	SNP	Hom	4851.01	249	NA	ENSMUSG00000081392	Gm11668	pseudogene		NA	DOWNSTREAM
11	108873282	A	G	SNP	Hom	4858.01	250	NA	ENSMUSG00000081392	Gm11668	pseudogene		NA	DOWNSTREAM
11	108873313	A	G	SNP	Hom	4853.01	250	NA	ENSMUSG00000081392	Gm11668	pseudogene		NA	DOWNSTREAM
11	108873333	A	G	SNP	Hom	5355.01	250	NA	ENSMUSG00000081392	Gm11668	pseudogene		NA	DOWNSTREAM
11	108873349	T	C	SNP	Hom	6365.01	250	NA	ENSMUSG00000081392	Gm11668	pseudogene		NA	DOWNSTREAM
11	108873364	T	C	SNP	Hom	6644.01	250	NA	ENSMUSG00000081392	Gm11668	pseudogene		NA	DOWNSTREAM
11	109377958	C	T	SNP	Hom	511	15	NA	ENSMUSG00000020604	Arsg	protein_coding		NA	INTRON
11	109739141	C	A	SNP	Hom	2430	94	NA					NA	INTERGENIC
11	109739170	A	C	SNP	Hom	1502	49	NA					NA	INTERGENIC
11	109739238	A	C	SNP	Hom	1748	100	NA					NA	INTERGENIC
11	109739241	C	G	SNP	Hom	1931	57	NA					NA	INTERGENIC
11	109765669	A	C	SNP	Hom	1159	35	NA					NA	INTERGENIC
11	109774772	T	C	SNP	Hom	1531	47	NA					NA	INTERGENIC
11	110018684	G	T	SNP	Hom	280.03	8	NA	ENSMUSG00000041797	Abca9	protein_coding		NA	INTRON
11	110543045	A	C	SNP	Hom	2203	55	NA					NA	INTERGENIC
11	110900584	T	A	SNP	Hom	2032	52	NA					NA	INTERGENIC
11	111345478	A	C	SNP	Hom	193.13	6	NA					NA	INTERGENIC
11	111405296	A	G	SNP	Hom	799	24	NA					NA	INTERGENIC
11	111405343	G	A	SNP	Hom	894	26	NA					NA	INTERGENIC
11	111405349	G	A	SNP	Hom	844	26	NA					NA	INTERGENIC
11	111405358	G	A	SNP	Hom	698	21	NA					NA	INTERGENIC
11	111405377	G	A	SNP	Hom	549	17	NA					NA	INTERGENIC
11	111405392	G	A	SNP	Hom	394	14	NA					NA	INTERGENIC
11	111405427	G	A	SNP	Hom	400	14	NA					NA	INTERGENIC
11	111405435	G	A	SNP	Hom	527	17	NA					NA	INTERGENIC
11	111405447	G	A	SNP	Hom	668	21	NA					NA	INTERGENIC
11	111405455	G	A	SNP	Hom	622	21	NA					NA	INTERGENIC
11	111405461	G	A	SNP	Hom	595	20	NA					NA	INTERGENIC
11	111405467	G	A	SNP	Hom	514	19	NA					NA	INTERGENIC
11	111405477	G	A	SNP	Hom	559	19	NA					NA	INTERGENIC
11	111405486	G	A	SNP	Hom	689	24	NA					NA	INTERGENIC
11	111405494	G	A	SNP	Hom	613	22	NA					NA	INTERGENIC
11	111405516	G	A	SNP	Hom	614	22	NA					NA	INTERGENIC
11	111405528	G	A	SNP	Hom	739	24	NA					NA	INTERGENIC
11	111405534	G	A	SNP	Hom	617	22	NA					NA	INTERGENIC
11	111405546	G	A	SNP	Hom	699	22	NA					NA	INTERGENIC

11	111405558	G	A	SNP	Hom	877	29	NA				NA	INTERGENIC
11	111957770	C	T	SNP	Hom	622	22	NA				NA	INTERGENIC
11	111957780	C	T	SNP	Hom	587	21	NA				NA	INTERGENIC
11	111957811	T	C	SNP	Hom	673	23	NA				NA	INTERGENIC
11	111957820	C	T	SNP	Hom	649	22	NA				NA	INTERGENIC
11	111957826	T	A	SNP	Hom	625	21	NA				NA	INTERGENIC
11	111957833	C	A	SNP	Hom	624	21	NA				NA	INTERGENIC
11	111957838	A	T	SNP	Hom	655	22	NA				NA	INTERGENIC
11	111957846	C	T	SNP	Hom	708	25	NA				NA	INTERGENIC
11	111957853	A	T	SNP	Hom	727	25	NA				NA	INTERGENIC
11	111957873	A	C	SNP	Hom	749	25	NA				NA	INTERGENIC
11	111957881	T	A	SNP	Hom	600	27	NA				NA	INTERGENIC
11	111957894	T	C	SNP	Hom	780	25	NA				NA	INTERGENIC
11	111957898	T	C	SNP	Hom	851	27	NA				NA	INTERGENIC
11	111957902	T	C	SNP	Hom	791	25	NA				NA	INTERGENIC
11	111957914	T	C	SNP	Hom	724	24	NA				NA	INTERGENIC
11	111957928	C	T	SNP	Hom	820	26	NA				NA	INTERGENIC
11	111957932	C	T	SNP	Hom	745	24	NA				NA	INTERGENIC
11	111957943	C	T	SNP	Hom	602	20	NA				NA	INTERGENIC
11	111957947	C	T	SNP	Hom	535.03	19	NA				NA	INTERGENIC
11	111957951	C	T	SNP	Hom	468.13	17	NA				NA	INTERGENIC
11	111957955	C	T	SNP	Hom	432.26	16	NA				NA	INTERGENIC
11	111957959	C	T	SNP	Hom	408.05	15	NA				NA	INTERGENIC
11	111957963	C	T	SNP	Hom	336.76	13	NA				NA	INTERGENIC
11	111957967	C	T	SNP	Hom	334.76	13	NA				NA	INTERGENIC
11	112069870	A	G	SNP	Hom	1772	51	NA				NA	INTERGENIC
11	112112015	A	G	SNP	Hom	1076	35	NA				NA	INTERGENIC
11	112475911	A	G	SNP	Hom	1942	50	NA				NA	INTERGENIC
11	112613541	T	G	SNP	Hom	1441	42	NA	ENSMUSG00000041674	BC006965	lincRNA	NA	INTRON
11	112626720	G	T	SNP	Hom	791	22	NA	ENSMUSG00000041674	BC006965	lincRNA	NA	INTRON
11	112762294	A	G	SNP	Hom	580.03	23	NA				NA	INTERGENIC
11	113221444	C	G	SNP	Hom	1624	45	NA	ENSMUSG00000041654	Slc39a11	protein_coding	NA	INTRON
11	113483695	A	T	SNP	Hom	741	19	NA	ENSMUSG00000041654	Slc39a11	protein_coding	NA	INTRON
11	114002627	T	C	SNP	Hom	2130	65	NA				NA	INTERGENIC
11	114141419	C	A	SNP	Hom	841	25	NA				NA	INTERGENIC
11	114979024	G	A	SNP	Hom	2009	53	NA	ENSMUSG00000047798	Cd300lf	protein_coding	NA	DOWNSTREAM
11	115413007	C	A	SNP	Hom	158.26	5	NA				NA	INTERGENIC
11	116458399	C	T	SNP	Hom	2050	58	NA	ENSMUSG00000020806	Rhbdf2	protein_coding	NA	DOWNSTREAM
11	116738570	C	T	SNP	Hom	1513	49	NA	ENSMUSG00000020818	Mfsd11	protein_coding	NA	DOWNSTREAM
11	117643494	T	G	SNP	Hom	1653	46	NA	ENSMUSG00000087486	Gm11723	processed_transcript	NA	DOWNSTREAM
11	117886744	A	T	SNP	Hom	1963	56	NA	ENSMUSG00000017715	Pgs1	protein_coding	NA	DOWNSTREAM
11	117886745	G	A	SNP	Hom	1993	57	NA	ENSMUSG00000017715	Pgs1	protein_coding	NA	DOWNSTREAM
11	117960667	A	C	SNP	Hom	1141	35	NA	ENSMUSG00000033987	Dnahc17	protein_coding	NA	INTRON
11	118502730	A	G	SNP	Hom	1675	49	NA	ENSMUSG00000025576	D11Bwg051	protein_coding	NA	INTRON
11	118622410	T	C	SNP	Hom	1514	42	NA	ENSMUSG00000025576	D11Bwg051	protein_coding	NA	INTRON
11	119307505	C	T	SNP	Hom	2188	59	NA	ENSMUSG00000070327	Rnf213	protein_coding	exon_11_11	30 SYN_CODING
11	119560388	A	G	SNP	Hom	219.06	7	NA	ENSMUSG00000025583	Rptor	protein_coding	NA	INTRON
11	119605099	T	C	SNP	Hom	2461	65	NA	ENSMUSG00000025583	Rptor	protein_coding	NA	INTRON
11	120168102	T	C	SNP	Hom	2344	63	NA				NA	INTERGENIC
11	120179505	G	T	SNP	Hom	672	26	NA				NA	INTERGENIC
11	120199241	G	T	SNP	Hom	1372	45	NA				NA	INTERGENIC
11	120564230	G	T	SNP	Hom	1052	36	NA	ENSMUSG00000025142	Aspscr1	protein_coding	NA	DOWNSTREAM
11	121454566	T	C	SNP	Hom	1174	34	NA	ENSMUSG00000039230	Tbcd	protein_coding	NA	DOWNSTREAM

Indels

Chromosome	Start	Stop	Reference	Change	LenIndel	Change_type	Homozygous	Quality	Coverage	Warnings	Gene_ID	Gene_name	Bio_type	Exon_ID
11	3832372	3832374	*	+TC	2	INS	Hom	148.98	12	NA	ENSMUSG00000020432	Tcn2	protein_coding	UPSTREAM
11	3931573	3931574	*	-A	1	DEL	Hom	697.96	24	NA	ENSMUSG00000019368	Sec14l4	protein_coding	INTRON
11	4591840	4591845	*	+AAAGG	5	INS	Hom	964.23	37	NA				INTERGENIC
11	4593731	4593735	*	-CTTT	4	DEL	Hom	368.98	24	NA				INTERGENIC
11	4754934	4754935	*	+T	1	INS	Hom	610.96	21	NA				INTERGENIC
11	4914193	4914195	*	-CA	2	DEL	Hom	626.96	44	NA	ENSMUSG00000009090	Ap1b1	protein_coding	INTRON
11	5204450	5204456	*	+ACACAC	6	INS	Hom	236.23	16	NA	ENSMUSG00000041961	Znrf3	protein_coding	INTRON
11	5573084	5573092	*	-AAACAAAC	8	DEL	Hom	1622.96	22	NA	ENSMUSG00000020481	Ankrd36	protein_coding	INTRON
11	5661175	5661179	*	+TCTT	4	INS	Hom	493.97	19	NA	ENSMUSG00000049680	Urgcp	protein_coding	INTRON
11	5720088	5720092	*	-GATA	4	DEL	Hom	310.1	14	NA	ENSMUSG00000080904	Gm11966	pseudogene	UPSTREAM
11	5854708	5854712	*	-TCTT	4	DEL	Hom	209.23	27	NA	ENSMUSG00000041798	Gck	protein_coding	UPSTREAM
11	6739469	6739474	*	-TTTTC	5	DEL	Hom	384.98	13	NA	ENSMUSG00000081213	Gm11983	pseudogene	UPSTREAM
11	6775844	6775848	*	-TGTG	4	DEL	Hom	258.1	22	NA				INTERGENIC
11	6826472	6826477	*	-TTTGT	5	DEL	Hom	565.13	29	NA				INTERGENIC
11	7149652	7149653	*	-G	1	DEL	Hom	162.99	9	NA				INTERGENIC
11	7335641	7335642	*	+G	1	INS	Hom	1625.96	41	NA				INTERGENIC
11	8449180	8449181	*	+G	1	INS	Hom	1202.96	35	NA	ENSMUSG00000020422	Tns3	protein_coding	INTRON
11	9292242	9292246	*	-ATCT	4	DEL	Hom	216.23	18	NA	ENSMUSG00000004668	Abca13	protein_coding	INTRON
11	10204913	10204914	*	+A	1	INS	Hom	529.96	15	NA				INTERGENIC
11	10248919	10248923	*	-GTGT	4	DEL	Hom	302.03	15	NA				INTERGENIC
11	11588476	11588484	*	-ATAGATAG	8	DEL	Hom	1258.96	22	NA	ENSMUSG00000018654	Ikzf1	protein_coding	INTRON
11	11799182	11799186	*	+TGTG	4	INS	Hom	959.97	32	NA	ENSMUSG00000020182	Ddc	protein_coding	UPSTREAM
11	11910782	11910783	*	-A	1	DEL	Hom	491.96	37	NA	ENSMUSG00000020176	Grb10	protein_coding	INTRON
11	11927436	11927440	*	-ACAC	4	DEL	Hom	777.96	28	NA	ENSMUSG00000020176	Grb10	protein_coding	INTRON
11	11931011	11931012	*	+G	1	INS	Hom	59.48	13	NA	ENSMUSG00000020176	Grb10	protein_coding	INTRON
11	12747803	12747805	*	-TG	2	DEL	Hom	309.17	33	NA				INTERGENIC
11	12827308	12827312	*	+AGAG	4	INS	Hom	263.1	28	NA				INTERGENIC
11	12827900	12827905	*	-AAAAC	5	DEL	Hom	916.96	22	NA				INTERGENIC
11	12915462	12915463	*	+T	1	INS	Hom	243.16	18	NA				INTERGENIC
11	13235735	13235736	*	-A	1	DEL	Hom	143.1	9	NA				INTERGENIC
11	13699250	13699251	*	+T	1	INS	Hom	150.05	15	NA				INTERGENIC
11	13831158	13831162	*	+TTTC	4	INS	Hom	693.96	25	NA				INTERGENIC
11	14559067	14559068	*	-A	1	DEL	Hom	146.1	7	NA				INTERGENIC
11	15420856	15420860	*	-GAAG	4	DEL	Hom	311.03	17	NA				INTERGENIC
11	15423923	15423925	*	+CT	2	INS	Hom	160.48	8	NA				INTERGENIC
11	15892460	15892461	*	+G	1	INS	Hom	563.96	16	NA				INTERGENIC
11	16236393	16236397	*	-AGAA	4	DEL	Hom	194.23	17	NA	ENSMUSG00000048834	Vstm2a	protein_coding	INTRON
11	16395209	16395210	*	+A	1	INS	Hom	625.96	30	NA				INTERGENIC
11	16442280	16442281	*	+T	1	INS	Hom	1005.96	28	NA				INTERGENIC
11	16443059	16443060	*	+T	1	INS	Hom	181.99	10	NA				INTERGENIC
11	17154685	17154689	*	+TCTA	4	INS	Hom	428.98	27	NA	ENSMUSG00000000581	C1d	protein_coding	UPSTREAM
11	17987749	17987751	*	-CA	2	DEL	Hom	145.03	17	NA				INTERGENIC
11	18346489	18346494	*	+CTTTT	5	INS	Hom	543.97	27	NA				INTERGENIC
11	18427060	18427061	*	+A	1	INS	Hom	694.96	19	NA				INTERGENIC
11	18479080	18479084	*	+AATT	4	INS	Hom	589.96	25	NA	ENSMUSG00000081101	Gm12024	pseudogene	UPSTREAM
11	21235151	21235157	*	-AAGAAG	6	DEL	Hom	399.1	7	NA	ENSMUSG00000001891	Ugp2	protein_coding	INTRON
11	21692620	21692621	*	-A	1	DEL	Hom	358.99	28	NA	ENSMUSG00000020319	AV249152	protein_coding	INTRON
11	21929933	21929937	*	-TCTA	4	DEL	Hom	151.48	14	NA	ENSMUSG00000042302	Ehbp1	protein_coding	INTRON
11	22614917	22614922	*	+TTTTG	5	INS	Hom	963.96	29	NA				INTERGENIC
11	23406424	23406425	*	-C	1	DEL	Hom	144	25	NA				INTERGENIC
11	23486952	23486960	*	-AGGCAGAG	8	DEL	Hom	478.03	22	NA	ENSMUSG00000042208	0610010F05I	protein_coding	INTRON
11	23888911	23888912	*	+T	1	INS	Hom	507.96	27	NA				INTERGENIC
11	23941245	23941246	*	+A	1	INS	Hom	427.5	22	NA				INTERGENIC
11	24079749	24079753	*	+AAAC	4	INS	Hom	608.96	28	NA				INTERGENIC
11	24542220	24542224	*	-TATC	4	DEL	Hom	704.96	28	NA	ENSMUSG00000087085	Gm12068	processed_transc	INTRON
11	24825565	24825566	*	+A	1	INS	Hom	603.96	30	NA	ENSMUSG00000087145	Gm12665	processed_transc	INTRON
11	24965757	24965761	*	-CCTT	4	DEL	Hom	241.23	14	NA				INTERGENIC
11	25918072	25918076	*	-TGTG	4	DEL	Hom	668.96	42	NA	ENSMUSG00000032985	5730522E02I	protein_coding	INTRON
11	26217627	26217628	*	+G	1	INS	Hom	296.99	12	NA				INTERGENIC
11	26241603	26241604	*	+C	1	INS	Hom	1388.96	40	NA	ENSMUSG00000065889	U1.105	snRNA	UPSTREAM
11	26519450	26519454	*	-CTAT	4	DEL	Hom	253.1	32	NA				INTERGENIC
11	27110540	27110541	*	+A	1	INS	Hom	365.96	19	NA				INTERGENIC
11	27132297	27132298	*	+A	1	INS	Hom	77.05	16	NA				INTERGENIC
11	27843082	27843083	*	+A	1	INS	Hom	154.03	8	NA				INTERGENIC
11	27844190	27844194	*	+TCTT	4	INS	Hom	251.23	15	NA				INTERGENIC
11	28023623	28023625	*	-TG	2	DEL	Hom	485.42	24	NA				INTERGENIC
11	28844396	28844397	*	+A	1	INS	Hom	649.96	19	NA				INTERGENIC
11	29036202	29036214	*	+AAGGAAGGA	12	INS	Hom	1039.99	14	NA	ENSMUSG00000020464	Pnpt1	protein_coding	INTRON
11	29250061	29250067	*	-ACAGAC	6	DEL	Hom	447.97	29	NA	ENSMUSG00000082721	Gm12087	pseudogene	UPSTREAM
11	29358723	29358724	*	+A	1	INS	Hom	110.1	12	NA	ENSMUSG00000032740	Ccdc88a	protein_coding	INTRON
11	29634339	29634340	*	+G	1	INS	Hom	346.98	9	NA	ENSMUSG00000020458	Rtn4	protein_coding	INTRON
11	29763616	29763617	*	+A	1	INS	Hom	966.96	33	NA	ENSMUSG00000044072	Eml6	protein_coding	INTRON
11	30674740	30674743	*	-TTA	3	DEL	Hom	161.48	10	NA	ENSMUSG00000040850	Psme4	protein_coding	INTRON
11	31279119	31279120	*	+G	1	INS	Hom	704.97	40	NA				INTERGENIC
11	31551184	31551190	*	-TGTGTG	6	DEL	Hom	346.03	27	NA				INTERGENIC
11	31898074	31898080	*	-TTGTTG	6	DEL	Hom	737.96	18	NA	ENSMUSG00000020297	Nsg2	protein_coding	UPSTREAM
11	31918103	31918108	*	-TTTTG	5	DEL	Hom	469.05	31	NA	ENSMUSG00000020297	Nsg2	protein_coding	INTRON
11	31966875	31966879	*	+TCCT	4	INS	Hom	1602.96	29	NA				INTERGENIC
11	32258990	32258994	*	-TCTT	4	DEL	Hom	343.99	18	NA	ENSMUSG00000040711	Sh3pxd2b	protein_coding	INTRON
11	32488480	32488483	*	-TTG	3	DEL	Hom	649.96	17	NA	ENSMUSG00000020272	Stk10	protein_coding	INTRON
11	32821528	32821529	*	+T	1	INS	Hom	582.96	31	NA	ENSMUSG00000085402	Gm12111	processed_transc	INTRON
11	32891271	32891272	*	+C	1	INS	Hom	945.96	29	NA				INTERGENIC
11	33610837	33610841	*	-CTTT	4	DEL	Hom	374.99	19	NA	ENSMUSG00000053519	Kcnip1	protein_coding	INTRON
11	34352779	34352785	*	-TCTCTG	6	DEL	Hom	377.98	29	NA	ENSMUSG00000020143	Dock2	protein_coding	INTRON
11	34442842	34442843	*	-C	1	DEL	Hom	182.23	5	NA	ENSMUSG00000020143	Dock2	protein_coding	INTRON
11	34846927	34846928	*	+A	1	INS	Hom	636.96	18	NA				INTERGENIC
11	35175481	35175489	*	+GATAGATA	8	INS	Hom	300.23	19	NA	ENSMUSG00000056427	Slit3	protein_coding	INTRON
11	35424726	35424730	*	-AGAT	4	DEL	Hom	500.97	32	NA	ENSMUSG00000056427	Slit3	protein_coding	INTRON
11	36003803	36003804	*	+A	1	INS	Hom	155.05	14	NA	ENSMUSG00000049336	Odz2	protein_coding	INTRON
11	36300826	36300842	*	+TGTGTGTGTG	16	INS	Hom	2074.96	20	NA	ENSMUSG00000049336	Odz2	protein_coding	INTRON
11	37465329	37465335	*	-TGTGTG	6	DEL	Hom	523.99	16	NA				INTERGENIC
11	38342738	38342739	*	-G	1	DEL	Hom	1624.96	42	NA				INTERGENIC

Chromosome	Start	Stop	Reference	Change	LenIndel	Change_type	Homozygous	Quality	Coverage	Warnings	Gene_ID	Gene_name	Bio_type	Exon_ID
11	38815738	38815739	*	+T	1	INS	Hom	1407.96	40	NA				INTERGENIC
11	38846405	38846406	*	+A	1	INS	Hom	48.5	8	NA				INTERGENIC
11	39544073	39544074	*	-T	1	DEL	Hom	458.96	24	NA	ENSMUSG00000083806	Gm12131	pseudogene	UPSTREAM
11	39548273	39548275	*	-TG	2	DEL	Hom	450.09	22	NA				INTERGENIC
11	39868123	39868124	*	-G	1	DEL	Hom	366.98	10	NA	ENSMUSG00000085301	Gm12132	processed_transc	INTRON
11	39920010	39920011	*	-G	1	DEL	Hom	282.99	18	NA	ENSMUSG00000085301	Gm12132	processed_transc	INTRON
11	40973428	40973432	*	-ATCT	4	DEL	Hom	291.1	19	NA				INTERGENIC
11	40976418	40976440	*	-TCTCTCTCTCT	22	DEL	Hom	818.03	16	NA				INTERGENIC
11	41120107	41120108	*	-C	1	DEL	Hom	50.48	12	NA				INTERGENIC
11	41800265	41800266	*	+T	1	INS	Hom	167.73	18	NA	ENSMUSG00000020436	Gabrg2	protein_coding	INTRON
11	42089665	42089666	*	+T	1	INS	Hom	1164.96	32	NA				INTERGENIC
11	42162791	42162795	*	-TTTC	4	DEL	Hom	390.98	23	NA				INTERGENIC
11	42259888	42259889	*	-A	1	DEL	Hom	349.96	18	NA	ENSMUSG00000007653	Gabrb2	protein_coding	INTRON
11	42371197	42371198	*	+A	1	INS	Hom	380.01	19	NA	ENSMUSG00000007653	Gabrb2	protein_coding	INTRON
11	42541340	42541341	*	-G	1	DEL	Hom	104.5	16	NA				INTERGENIC
11	43004957	43004960	*	-AAG	3	DEL	Hom	123.48	20	NA	ENSMUSG00000055415	Atp10b	protein_coding	INTRON
11	43087407	43087411	*	-AGAT	4	DEL	Hom	129.93	16	NA	ENSMUSG00000086791	Gm12147	processed_transc	INTRON
11	43219067	43219068	*	-A	1	DEL	Hom	177.98	13	NA				INTERGENIC
11	43224632	43224642	*	-TCTCTCTCTC	10	DEL	Hom	471.1	13	NA				INTERGENIC
11	43411640	43411648	*	-ATAGATAG	8	DEL	Hom	664.98	16	NA	ENSMUSG00000020405	Fabp6	protein_coding	INTRON
11	44636159	44636163	*	-TATC	4	DEL	Hom	455.97	29	NA	ENSMUSG00000057098	Ebf1	protein_coding	INTRON
11	44971474	44971475	*	-A	1	DEL	Hom	116.1	16	NA	ENSMUSG00000087089	Gm12160	processed_transc	UPSTREAM
11	45518054	45518056	*	-GC	2	DEL	Hom	994.96	27	NA				INTERGENIC
11	45518739	45518743	*	-TTTG	4	DEL	Hom	506.97	22	NA				INTERGENIC
11	45532704	45532705	*	+G	1	INS	Hom	81.48	10	NA				INTERGENIC
11	45771302	45771303	*	+A	1	INS	Hom	458.96	18	NA	ENSMUSG00000011254	Thg1l	protein_coding	UPSTREAM
11	45791496	45791500	*	-CACA	4	DEL	Hom	912.96	25	NA	ENSMUSG00000040489	Sox30	protein_coding	UPSTREAM
11	46396588	46396589	*	-T	1	DEL	Hom	250.75	38	NA	ENSMUSG00000046974	BC053393	protein_coding	INTRON
11	47136187	47136189	*	+AA	2	INS	Hom	168.03	14	NA	ENSMUSG00000020354	Sgcd	protein_coding	INTRON
11	47387328	47387333	*	+GATAT	5	INS	Hom	233.48	11	NA	ENSMUSG00000020354	Sgcd	protein_coding	INTRON
11	47767916	47767920	*	-ATCT	4	DEL	Hom	346.03	22	NA	ENSMUSG00000020354	Sgcd	protein_coding	INTRON
11	48202928	48202929	*	+C	1	INS	Hom	315.37	22	NA				INTERGENIC
11	48294976	48294977	*	-C	1	DEL	Hom	179.17	22	NA				INTERGENIC
11	48305787	48305791	*	-GATA	4	DEL	Hom	503.96	22	NA				INTERGENIC
11	48377869	48377870	*	+T	1	INS	Hom	257.37	23	NA	ENSMUSG00000083159	Gm12180	pseudogene	UPSTREAM
11	48529142	48529146	*	-GTGT	4	DEL	Hom	450.1	33	NA				INTERGENIC
11	48692792	48692800	*	-AATAAATA	8	DEL	Hom	394.23	12	NA				INTERGENIC
11	49042740	49042744	*	-TTCC	4	DEL	Hom	244.1	32	NA				INTERGENIC
11	49222486	49222487	*	-A	1	DEL	Hom	88.1	13	NA	ENSMUSG00000084278	Gm12189	pseudogene	DOWNSTREAM
11	49357553	49357554	*	+A	1	INS	Hom	400.96	23	NA				INTERGENIC
11	49521283	49521285	*	+TT	2	INS	Hom	671.96	16	NA	ENSMUSG00000020362	Cnot6	protein_coding	INTRON
11	49818152	49818153	*	-A	1	DEL	Hom	377.96	17	NA				INTERGENIC
11	51052299	51052300	*	-C	1	DEL	Hom	524.96	22	NA	ENSMUSG00000061469	Gm12569	processed_transc	DOWNSTREAM
11	51065625	51065628	*	-ACA	3	DEL	Hom	1188.96	23	NA	ENSMUSG00000045942	BC049762	protein_coding	DOWNSTREAM
11	51464621	51464622	*	+G	1	INS	Hom	309.98	18	NA	ENSMUSG00000001053	N4bp3	protein_coding	UPSTREAM
11	52117523	52117524	*	-A	1	DEL	Hom	802.96	25	NA				INTERGENIC
11	52604326	52604334	*	-CTATCTAT	8	DEL	Hom	982.96	34	NA	ENSMUSG00000036264	Fstl4	protein_coding	INTRON
11	52608698	52608702	*	+CTGT	4	INS	Hom	571.96	34	NA	ENSMUSG00000036264	Fstl4	protein_coding	INTRON
11	53028056	53028058	*	-AC	2	DEL	Hom	262.99	30	NA				INTERGENIC
11	53535176	53535177	*	+A	1	INS	Hom	242.6	21	NA	ENSMUSG00000086595	Gm12214	processed_transc	DOWNSTREAM
11	53583671	53583672	*	-G	1	DEL	Hom	312.97	20	NA	ENSMUSG00000091191	AL596182.1	protein_coding	DOWNSTREAM
11	53813037	53813038	*	-G	1	DEL	Hom	2558.96	74	NA	ENSMUSG00000020334	Slc22a4	protein_coding	INTRON
11	54330429	54330433	*	-AAGA	4	DEL	Hom	455.99	12	NA	ENSMUSG00000035992	Fnip1	protein_coding	UTR
11	54613865	54613869	*	+TTGG	4	INS	Hom	488.97	36	NA				INTERGENIC
11	55004409	55004413	*	+TCTA	4	INS	Hom	308.03	18	NA	ENSMUSG00000084980	4921508A21	processed_transc	DOWNSTREAM
11	55101765	55101767	*	-GT	2	DEL	Hom	371.96	48	NA	ENSMUSG00000055333	Fat2	protein_coding	INTRON
11	55108619	55108624	*	+AGAAG	5	INS	Hom	476.97	15	NA	ENSMUSG00000055333	Fat2	protein_coding	INTRON
11	55737142	55737146	*	-TCTA	4	DEL	Hom	187.48	14	NA	ENSMUSG00000086020	Gm12239	processed_transc	INTRON
11	56034332	56034335	*	-TAC	3	DEL	Hom	489.96	21	NA				INTERGENIC
11	56242865	56242869	*	-CTAT	4	DEL	Hom	417.98	25	NA				INTERGENIC
11	56678570	56678574	*	-AGAT	4	DEL	Hom	434.99	18	NA				INTERGENIC
11	57214798	57214800	*	-GT	2	DEL	Hom	461.96	28	NA				INTERGENIC
11	57315649	57315653	*	+ATAC	4	INS	Hom	318.03	18	NA	ENSMUSG00000020523	Fam114a2	protein_coding	INTRON
11	57851560	57851564	*	+ATTG	4	INS	Hom	993.97	38	NA	ENSMUSG00000037331	Larp1	protein_coding	INTRON
11	58080547	58080551	*	-TCTA	4	DEL	Hom	104.93	13	NA				INTERGENIC
11	58401328	58401329	*	-A	1	DEL	Hom	570.96	34	NA				INTERGENIC
11	58622601	58622605	*	-TCTA	4	DEL	Hom	234.23	15	NA				INTERGENIC
11	58718179	58718189	*	+TGTGTGTGTG	10	INS	Hom	699.97	18	NA	ENSMUSG00000037001	Zfp39	protein_coding	UPSTREAM
11	59239447	59239448	*	-C	1	DEL	Hom	1020.96	35	NA	ENSMUSG00000009894	Snap47	protein_coding	INTRON
11	59388242	59388250	*	-TATCTATC	8	DEL	Hom	806.96	25	NA	ENSMUSG00000059610	Olfr222	protein_coding	UPSTREAM
11	59670708	59670709	*	+T	1	INS	Hom	381.97	27	NA	ENSMUSG00000032615	Nt5m	protein_coding	INTRON
11	59864504	59864508	*	+AGAA	4	INS	Hom	367.98	20	NA	ENSMUSG00000000301	Pemt	protein_coding	UPSTREAM
11	59871389	59871393	*	+GAAA	4	INS	Hom	554.97	17	NA				INTERGENIC
11	60115132	60115133	*	-T	1	DEL	Hom	697.96	28	NA	ENSMUSG00000000538	Tom1l2	protein_coding	INTRON
11	60737599	60737603	*	-TCTT	4	DEL	Hom	347.01	16	NA	ENSMUSG00000042549	Gm16516	processed_transc	INTRON
11	60949082	60949086	*	-TTTC	4	DEL	Hom	213.37	28	NA	ENSMUSG00000010142	Tnfrsf13b	protein_coding	INTRON
11	60962982	60962983	*	+A	1	INS	Hom	196.97	16	NA	ENSMUSG00000010142	Tnfrsf13b	protein_coding	DOWNSTREAM
11	61285479	61285483	*	-GAAG	4	DEL	Hom	698.96	38	NA				INTERGENIC
11	61308078	61308079	*	+G	1	INS	Hom	149.23	8	NA	ENSMUSG00000001034	Mapk7	protein_coding	UPSTREAM
11	62305131	62305135	*	-AAGA	4	DEL	Hom	359.03	17	NA	ENSMUSG00000014245	Pigl	protein_coding	INTRON
11	62576604	62576605	*	-A	1	DEL	Hom	103.07	11	NA	ENSMUSG00000047342	Zfp286	protein_coding	INTRON
11	62781779	62781780	*	-C	1	DEL	Hom	221.23	18	NA	ENSMUSG00000042200	Cdrt4	protein_coding	INTRON
11	62825904	62825908	*	-TATC	4	DEL	Hom	222.23	10	NA				INTERGENIC
11	62979963	62979964	*	+G	1	INS	Hom	416.96	23	NA				INTERGENIC
11	63652173	63652174	*	+A	1	INS	Hom	1811.96	51	NA				INTERGENIC
11	64568184	64568186	*	-AC	2	DEL	Hom	120.07	31	NA				INTERGENIC
11	65188813	65188814	*	-C	1	DEL	Hom	405.96	28	NA				INTERGENIC
11	66002685	66002686	*	+A	1	INS	Hom	275.96	15	NA	ENSMUSG00000084967	Gm12296	lincRNA	INTRON
11	66230244	66230248	*	-TCTA	4	DEL	Hom	362.97	22	NA	ENSMUSG00000053930	Shisa6	protein_coding	INTRON
11	67243056	67243060	*	-CACA	4	DEL	Hom	322.17	25	NA				INTERGENIC
11	68003648	68003649	*	+G	1	INS	Hom	1131.96	34	NA	ENSMUSG00000020903	Stx8	protein_coding	INTRON
11	68381800	68381801	*	-T	1	DEL	Hom	121.98	14	NA				INTERGENIC
11	70349062	70349063	*	-C	1	DEL	Hom	148.73	26	NA	ENSMUSG00000020828	Pld2	protein_coding	UPSTREAM
11	70416609	70416610	*	-G	1	DEL	Hom	497.96	34	NA	ENSMUSG00000020827	Mink1	protein_coding	INTRON

11	70593561	70593565	*	-CTTC	4	DEL	Hom	355.05	21	NA				INTERGENIC
11	70869695	70869699	*	-ATCT	4	DEL	Hom	526.97	25	NA	ENSMUSG00000083171	Gm12321	pseudogene	DOWNSTREAM
11	70998894	70998898	*	-AGAG	4	DEL	Hom	1085.96	27	NA	ENSMUSG00000070390	Nlrp1b	protein_coding	INTRON
11	71770449	71770453	*	+TGTG	4	INS	Hom	366.99	24	NA				INTERGENIC
11	73664384	73664385	*	+A	1	INS	Hom	164.03	7	NA	ENSMUSG00000064228	Olfr393	protein_coding	UPSTREAM
11	74807449	74807450	*	+A	1	INS	Hom	482.96	25	NA	ENSMUSG00000038290	Smg6	protein_coding	INTRON
11	75153381	75153382	*	-T	1	DEL	Hom	109.05	8	NA	ENSMUSG00000000751	Rpa1	protein_coding	INTRON
11	75298320	75298324	*	-TCTT	4	DEL	Hom	278.1	23	NA	ENSMUSG00000020850	Prpf8	protein_coding	UPSTREAM
11	75362054	75362055	*	+T	1	INS	Hom	224.09	20	NA	ENSMUSG00000038178	Slc43a2	protein_coding	INTRON
11	75919212	75919216	*	-AGCA	4	DEL	Hom	469.98	29	NA	ENSMUSG00000017288	Vps53	protein_coding	INTRON
11	75959481	75959482	*	-A	1	DEL	Hom	154.16	11	NA	ENSMUSG00000017286	Glod4	protein_coding	INTRON
11	76215843	76215844	*	-C	1	DEL	Hom	457.96	19	NA	ENSMUSG00000020843	Timm22	protein_coding	UPSTREAM
11	76526301	76526305	*	-ATAG	4	DEL	Hom	310.1	23	NA				INTERGENIC
11	76926268	76926272	*	-TCTA	4	DEL	Hom	449.98	31	NA	ENSMUSG00000050944	Efcab5	protein_coding	INTRON
11	77306131	77306132	*	+A	1	INS	Hom	166.98	14	NA	ENSMUSG00000091461	AL607072.1	lincRNA	DOWNSTREAM
11	77464220	77464224	*	-TTGG	4	DEL	Hom	482.97	18	NA				INTERGENIC
11	77789400	77789402	*	-AC	2	DEL	Hom	432.96	31	NA	ENSMUSG00000000632	Sez6	protein_coding	INTRON
11	77999502	77999506	*	+AGAT	4	INS	Hom	1028.96	31	NA	ENSMUSG00000064540	Snord42a	snoRNA	UPSTREAM
11	78062401	78062403	*	-GT	2	DEL	Hom	501.99	33	NA	ENSMUSG00000002064	Sdf2	protein_coding	UPSTREAM
11	78685327	78685329	*	+AA	2	INS	Hom	161.1	10	NA				INTERGENIC
11	79000415	79000417	*	-TG	2	DEL	Hom	670.96	41	NA				INTERGENIC
11	79410147	79410151	*	-GGAA	4	DEL	Hom	467.98	26	NA	ENSMUSG00000017639	Rab11fip4	protein_coding	INTRON
11	79632939	79632943	*	-TCTT	4	DEL	Hom	178.73	12	NA	ENSMUSG00000086474	9130204K15I	processed_transc	INTRON
11	79696431	79696433	*	-AG	2	DEL	Hom	205.6	27	NA				INTERGENIC
11	79715750	79715754	*	+AGAT	4	INS	Hom	818.96	25	NA	ENSMUSG00000082252	Gm11204	pseudogene	UPSTREAM
11	79802854	79802862	*	+GTGTGTGT	8	INS	Hom	344.03	13	NA	ENSMUSG00000017548	Suz12	protein_coding	UPSTREAM
11	79825289	79825293	*	-CTAT	4	DEL	Hom	420.99	23	NA	ENSMUSG00000017548	Suz12	protein_coding	INTRON
11	80138078	80138080	*	-CA	2	DEL	Hom	198.05	24	NA	ENSMUSG00000017692	Rhbdl3	protein_coding	INTRON
11	81819340	81819344	*	-TGTG	4	DEL	Hom	340.99	27	NA				INTERGENIC
11	81970364	81970368	*	+GTAT	4	INS	Hom	814.96	22	NA				INTERGENIC
11	82275003	82275004	*	+C	1	INS	Hom	989.96	32	NA				INTERGENIC
11	82854557	82854565	*	-TCTATCTA	8	DEL	Hom	479.1	17	NA	ENSMUSG00000072621	Slfn10 -ps	protein_coding	UPSTREAM
11	83473408	83473409	*	-T	1	DEL	Hom	153.6	23	NA	ENSMUSG00000018930	Ccl4	protein_coding	UPSTREAM
11	83612145	83612148	*	+GTT	3	INS	Hom	923.96	24	NA	ENSMUSG00000081342	Gm11434	pseudogene	UPSTREAM
11	84108843	84108847	*	-ATAG	4	DEL	Hom	132.93	13	NA	ENSMUSG00000020532	Acaca	protein_coding	INTRON
11	84766456	84766457	*	+G	1	INS	Hom	705.96	23	NA	ENSMUSG00000000805	Car4	protein_coding	UPSTREAM
11	85141434	85141438	*	+ATGT	4	INS	Hom	464.98	23	NA	ENSMUSG00000020525	Ppm1d	protein_coding	INTRON
11	85142107	85142111	*	-ATCT	4	DEL	Hom	200.23	23	NA	ENSMUSG00000020525	Ppm1d	protein_coding	INTRON
11	85359116	85359117	*	+T	1	INS	Hom	671.96	28	NA	ENSMUSG00000059439	Bcas3	protein_coding	INTRON
11	85609048	85609049	*	-C	1	DEL	Hom	197.97	28	NA	ENSMUSG00000059439	Bcas3	protein_coding	INTRON
11	85813179	85813181	*	+TT	2	INS	Hom	588.96	23	NA				INTERGENIC
11	86032789	86032790	*	+A	1	INS	Hom	487.96	16	NA	ENSMUSG00000085208	4632419I22R	processed_transc	INTRON
11	86763615	86763616	*	-T	1	DEL	Hom	137.09	30	NA	ENSMUSG00000018427	Ypel2	protein_coding	INTRON
11	86955794	86955795	*	+T	1	INS	Hom	107.03	11	NA	ENSMUSG00000018548	Trim37	protein_coding	INTRON
11	88043015	88043019	*	-ATCT	4	DEL	Hom	352	21	NA				INTERGENIC
11	88043178	88043182	*	+CTAT	4	INS	Hom	262.03	10	NA				INTERGENIC
11	88082413	88082414	*	+G	1	INS	Hom	428.96	20	NA				INTERGENIC
11	88099189	88099193	*	-ATGA	4	DEL	Hom	270.1	25	NA				INTERGENIC
11	88295325	88295326	*	+C	1	INS	Hom	62.48	12	NA	ENSMUSG00000069769	Msi2	protein_coding	INTRON
11	88711747	88711749	*	+CA	2	INS	Hom	245.97	14	NA	ENSMUSG00000018428	Akap1	protein_coding	INTRON
11	89090018	89090022	*	+ATTC	4	INS	Hom	480.98	32	NA				INTERGENIC
11	89755686	89755690	*	+GATA	4	INS	Hom	423.99	22	NA				INTERGENIC
11	89788961	89788962	*	+C	1	INS	Hom	381.97	10	NA				INTERGENIC
11	90084380	90084384	*	+TCTA	4	INS	Hom	332.03	24	NA	ENSMUSG00000003948	Mmd	protein_coding	INTRON
11	90177428	90177432	*	-ATCT	4	DEL	Hom	284.03	24	NA				INTERGENIC
11	90704953	90704959	*	+CACACA	6	INS	Hom	576.98	31	NA	ENSMUSG00000085940	4930405D11	processed_transc	INTRON
11	91058759	91058760	*	-G	1	DEL	Hom	191.1	7	NA				INTERGENIC
11	91234885	91234886	*	+T	1	INS	Hom	319.99	9	NA				INTERGENIC
11	91813746	91813747	*	+C	1	INS	Hom	486.96	15	NA				INTERGENIC
11	91881454	91881458	*	-AGAA	4	DEL	Hom	371.07	15	NA				INTERGENIC
11	92879168	92879169	*	+T	1	INS	Hom	221.96	17	NA				INTERGENIC
11	93035172	93035173	*	-C	1	DEL	Hom	183.93	16	NA	ENSMUSG00000056158	Car10	protein_coding	INTRON
11	93268499	93268504	*	-GTAGT	5	DEL	Hom	627.96	36	NA	ENSMUSG00000056158	Car10	protein_coding	INTRON
11	94040497	94040501	*	-TCTG	4	DEL	Hom	445.96	26	NA				INTERGENIC
11	95516727	95516735	*	+TGTGTGCA	8	INS	Hom	1111.97	31	NA				INTERGENIC
11	95941443	95941444	*	+G	1	INS	Hom	242.03	11	NA	ENSMUSG00000006057	Atp5g1	protein_coding	UPSTREAM
11	96223826	96223830	*	-AGGA	4	DEL	Hom	840.96	19	NA	ENSMUSG00000018973	Hoxb1	protein_coding	UPSTREAM
11	96439375	96439379	*	+CCAC	4	INS	Hom	2301.96	42	NA	ENSMUSG00000057058	Skap1	protein_coding	INTRON
11	96595651	96595657	*	-GAAAAG	6	DEL	Hom	395.98	24	NA	ENSMUSG00000057058	Skap1	protein_coding	INTRON
11	96962231	96962235	*	+ATGG	4	INS	Hom	484.98	34	NA	ENSMUSG00000084068	Gm11573	pseudogene	DOWNSTREAM
11	96983399	96983403	*	-TCTG	4	DEL	Hom	911.96	43	NA				INTERGENIC
11	97274905	97274907	*	+TG	2	INS	Hom	788.96	36	NA	ENSMUSG00000049807	Arhgap23	protein_coding	UPSTREAM
11	97762707	97762711	*	+GGAT	4	INS	Hom	873.96	84	NA				INTERGENIC
11	98356329	98356331	*	-TC	2	DEL	Hom	239.97	41	NA	ENSMUSG00000018168	Ikzf3	protein_coding	INTRON
11	99157362	99157367	*	-CTTTC	5	DEL	Hom	270.1	27	NA				INTERGENIC
11	99296362	99296372	*	+CACACACAC/	10	INS	Hom	1315.96	26	NA	ENSMUSG00000035775	Krt20	protein_coding	INTRON
11	99649692	99649696	*	+TGGA	4	INS	Hom	402.99	22	NA	ENSMUSG00000090037	Krtap4 -9	pseudogene	DOWNSTREAM
11	99657836	99657840	*	-CTTC	4	DEL	Hom	318.01	22	NA	ENSMUSG00000078260	Gm11569	protein_coding	DOWNSTREAM
11	100170851	100170855	*	-TGAA	4	DEL	Hom	440.98	20	NA				INTERGENIC
11	100598895	100598896	*	-C	1	DEL	Hom	31.75	12	NA	ENSMUSG00000019173	Rab5c	protein_coding	INTRON
11	100897003	100897007	*	-TATC	4	DEL	Hom	682.96	30	NA	ENSMUSG00000019302	Atp6v0a1	protein_coding	INTRON
11	101027060	101027064	*	+TTCC	4	INS	Hom	358.96	20	NA	ENSMUSG00000035172	Plekhh3	protein_coding	INTRON
11	101338383	101338388	*	+AAAAG	5	INS	Hom	618.96	21	NA	ENSMUSG00000080839	Gm11625	pseudogene	DOWNSTREAM
11	101741513	101741517	*	+ATGT	4	INS	Hom	926.96	56	NA	ENSMUSG00000001493	Meox1	protein_coding	INTRON
11	102129034	102129037	*	+CTC	3	INS	Hom	848.96	20	NA	ENSMUSG00000034768	Asb16	protein_coding	UPSTREAM
11	102194986	102194996	*	+AAACCAAACA	10	INS	Hom	1367.96	29	NA				INTERGENIC
11	102281472	102281473	*	-T	1	DEL	Hom	627.96	31	NA				INTERGENIC
11	102346642	102346646	*	+CTAT	4	INS	Hom	515.97	22	NA	ENSMUSG00000034621	Gpatch8	protein_coding	INTRON
11	102652759	102652761	*	-TG	2	DEL	Hom	309.93	38	NA				INTERGENIC
11	103208748	103208752	*	+ACAC	4	INS	Hom	929.97	57	NA	ENSMUSG00000034255	Arhgap27	protein_coding	INTRON
11	103805447	103805451	*	-AGAT	4	DEL	Hom	283.1	17	NA	ENSMUSG00000034187	Nsf	protein_coding	INTRON
11	104477183	104477187	*	-TATC	4	DEL	Hom	311.03	25	NA	ENSMUSG00000020689	Itgb3	protein_coding	INTRON
11	104687272	104687275	*	-GAA	3	DEL	Hom	225.03	15	NA				INTERGENIC
11	105283098	105283102	*	-TCCA	4	DEL	Hom	592.96	34	NA	ENSMUSG00000078627	40978	protein_coding	INTRON
11	107134486	107134490	*	+CAAC	4	INS	Hom	1308.96	47	NA	ENSMUSG00000040430	Pitpnc1	protein_coding	INTRON

11	107145009	107145013	*	+ATCC	4	INS	Hom	1191.96	51	NA	ENSMUSG00000040430	Pitpnc1	protein_coding	INTRON
11	107936817	107936833	*	-CAGACATCCA	16	DEL	Hom	602.99	26	NA	ENSMUSG00000050965	Prkca	protein_coding	INTRON
11	108291735	108291736	*	+T	1	INS	Hom	287.37	24	NA	ENSMUSG00000020728	Ccdc46	protein_coding	INTRON
11	108646294	108646295	*	+T	1	INS	Hom	425.96	16	NA	ENSMUSG00000020728	Ccdc46	protein_coding	INTRON
11	109300681	109300683	*	+GA	2	INS	Hom	611.96	21	NA	ENSMUSG00000020610	Amz2	protein_coding	INTRON
11	109494401	109494405	*	-ATCT	4	DEL	Hom	304.1	33	NA	ENSMUSG00000086733	Gm11685	processed_transc	INTRON
11	109956173	109956177	*	+AAAT	4	INS	Hom	250.23	12	NA	ENSMUSG00000041828	Abca8a	protein_coding	INTRON
11	110689103	110689107	*	-ACAC	4	DEL	Hom	236.29	24	NA				INTERGENIC
11	110845331	110845332	*	+C	1	INS	Hom	339.98	12	NA	ENSMUSG00000051497	Kcnj16	protein_coding	INTRON
11	110849465	110849471	*	+ACACAC	6	INS	Hom	1106.96	32	NA	ENSMUSG00000051497	Kcnj16	protein_coding	INTRON
11	111414735	111414737	*	-GA	2	DEL	Hom	70.42	16	NA				INTERGENIC
11	111642294	111642296	*	-GG	2	DEL	Hom	204.23	8	NA				INTERGENIC
11	112077462	112077463	*	-A	1	DEL	Hom	158.23	7	NA				INTERGENIC
11	112231672	112231674	*	-TG	2	DEL	Hom	359.96	29	NA				INTERGENIC
11	112516261	112516266	*	-TTGTT	5	DEL	Hom	443.99	31	NA				INTERGENIC
11	112555908	112555910	*	+AC	2	INS	Hom	758.99	32	NA	ENSMUSG00000041674	BC006965	lincRNA	INTRON
11	113064653	113064654	*	+T	1	INS	Hom	172.98	15	NA	ENSMUSG00000085421	4732490B19I	processed_transc	EXON
11	113172733	113172737	*	-CACA	4	DEL	Hom	381.98	29	NA	ENSMUSG00000041654	Slc39a11	protein_coding	INTRON
11	113264775	113264778	*	-GTT	3	DEL	Hom	557.96	15	NA	ENSMUSG00000041654	Slc39a11	protein_coding	INTRON
11	113319762	113319773	*	+CCACCCCACC	11	INS	Hom	1327.96	22	NA	ENSMUSG00000041654	Slc39a11	protein_coding	INTRON
11	113510714	113510715	*	+A	1	INS	Hom	535.96	25	NA	ENSMUSG00000041654	Slc39a11	protein_coding	INTRON
11	113863597	113863605	*	+TCTATCTA	8	INS	Hom	1148.96	26	NA	ENSMUSG00000041592	Sdk2	protein_coding	INTRON
11	115841777	115841782	*	-AAAGA	5	DEL	Hom	304.99	17	NA	ENSMUSG00000020758	Itgb4	protein_coding	INTRON
11	116234009	116234013	*	-CACA	4	DEL	Hom	130.93	15	NA	ENSMUSG00000052949	Rnf157	protein_coding	INTRON
11	116877501	116877505	*	+GATG	4	INS	Hom	724.96	38	NA				INTERGENIC
11	117417848	117417851	*	-TTG	3	DEL	Hom	410.97	48	NA				INTERGENIC
11	117487508	117487509	*	-G	1	DEL	Hom	196.99	17	NA				INTERGENIC
11	117812100	117812102	*	+GC	2	INS	Hom	454.98	11	NA				INTERGENIC
11	117975037	117975039	*	-CA	2	DEL	Hom	1368.96	37	NA	ENSMUSG00000033987	Dnahc17	protein_coding	INTRON
11	118100325	118100327	*	+AG	2	INS	Hom	356.23	30	NA	ENSMUSG00000017132	Cyth1	protein_coding	INTRON
11	118302942	118302945	*	-TGC	3	DEL	Hom	5493	113	NA	ENSMUSG00000017446	C1qtnf1	protein_coding	INTRON
11	118354789	118354790	*	+A	1	INS	Hom	208.98	11	NA	ENSMUSG00000025576	D11Bwg0517	protein_coding	INTRON
11	118356862	118356866	*	-CCTT	4	DEL	Hom	464.96	40	NA	ENSMUSG00000025576	D11Bwg0517	protein_coding	INTRON
11	118562726	118562730	*	-GGGA	4	DEL	Hom	470.97	17	NA	ENSMUSG00000025576	D11Bwg0517	protein_coding	INTRON
11	118674767	118674768	*	+G	1	INS	Hom	903.96	22	NA	ENSMUSG00000025576	D11Bwg0517	protein_coding	INTRON
11	118679262	118679266	*	+GATA	4	INS	Hom	385.99	23	NA	ENSMUSG00000025576	D11Bwg0517	protein_coding	INTRON
11	118748600	118748604	*	+ATAC	4	INS	Hom	780.96	41	NA	ENSMUSG00000025576	D11Bwg0517	protein_coding	INTRON
11	118817657	118817658	*	+C	1	INS	Hom	775.96	33	NA				INTERGENIC
11	119094805	119094809	*	+TTGG	4	INS	Hom	625.96	30	NA	ENSMUSG00000039963	Ccdc40	protein_coding	INTRON
11	120063905	120063913	*	-GATAGATA	8	DEL	Hom	638.97	24	NA				INTERGENIC
11	120353578	120353579	*	+C	1	INS	Hom	496.96	16	NA	ENSMUSG00000025792	Slc25a10	protein_coding	INTRON
11	120574195	120574196	*	-C	1	DEL	Hom	39.48	17	NA	ENSMUSG00000025145	Lrrc45	protein_coding	UPSTREAM
11	121256614	121256615	*	-G	1	DEL	Hom	103.23	16	NA				INTERGENIC
11	121338637	121338638	*	+C	1	INS	Hom	157.03	16	NA	ENSMUSG00000039230	Tbcd	protein_coding	INTRON
11	121724800	121724802	*	-CA	2	DEL	Hom	235.99	20	NA	ENSMUSG00000084401	Gm12586	pseudogene	DOWNSTREAM

Structural variants

Chromosome	Start	Finish	Svsize	Reference	Change	Change_type	Homozygous	Quality	Coverage	Warnings	Gene_ID	Gene_name	Bio_type	Exon_ID
11	31245663	31246147	484	NA	NA	Interval	NA	0	0	NA				INTERGENIC
11	32022724	32022917	193	NA	NA	Interval	NA	0	0	NA				INTERGENIC
11	32385719	32385721	2	NA	NA	Interval	NA	0	0	NA	ENSMUSG00000044949	Ubtd2	protein_coding	INTRON
11	36442060	36442062	2	NA	NA	Interval	NA	0	0	NA	ENSMUSG00000049336	Odz2	protein_coding	INTRON
11	36612388	36612402	14	NA	NA	Interval	NA	0	0	NA	ENSMUSG00000049336	Odz2	protein_coding	INTRON
11	44162255	44162257	2	NA	NA	Interval	NA	0	0	NA				INTERGENIC
11	52273086	52273088	2	NA	NA	Interval	NA	0	0	NA				INTERGENIC
11	57000397	57000399	2	NA	NA	Interval	NA	0	0	NA	ENSMUSG00000020524	Gria1	protein_coding	INTRON
11	57000402	57000404	2	NA	NA	Interval	NA	0	0	NA	ENSMUSG00000020524	Gria1	protein_coding	INTRON
11	71039987	71039989	2	NA	NA	Interval	NA	0	0	NA	ENSMUSG00000070390	Nlrp1b	protein_coding	INTRON
11	79723116	79723120	4	NA	NA	Interval	NA	0	0	NA	ENSMUSG00000082252	Gm11204	pseudogene	DOWNSTREAM
11	79809573	79809676	103	NA	NA	Interval	NA	0	0	NA	ENSMUSG00000017548	Suz12	protein_coding	INTRON
11	80381796	80381798	2	NA	NA	Interval	NA	0	0	NA	ENSMUSG00000035441	Myo1d	protein_coding	INTRON
11	80733734	80733879	145	NA	NA	Interval	NA	0	0	NA	ENSMUSG00000020704	Accn1	protein_coding	INTRON
11	83088917	83088919	2	NA	NA	Interval	NA	0	0	NA	ENSMUSG00000082101	Slfn14-ps	pseudogene	EXON
11	83088917	83088919	2	NA	NA	Interval	NA	0	0	NA	ENSMUSG00000082101	Slfn14-ps	pseudogene	DOWNSTREAM
11	88119979	88120232	253	NA	NA	Interval	NA	0	0	NA				INTERGENIC
11	88832157	88832159	2	NA	NA	Interval	NA	0	0	NA	ENSMUSG00000033983	Coil	protein_coding	INTRON
11	88832157	88832159	2	NA	NA	Interval	NA	0	0	NA	ENSMUSG00000033983	Coil	protein_coding	UPSTREAM
11	90156751	90156753	2	NA	NA	Interval	NA	0	0	NA				INTERGENIC
11	91590387	91590389	2	NA	NA	Interval	NA	0	0	NA				INTERGENIC
11	104906404	104906618	214	NA	NA	Interval	NA	0	0	NA				INTERGENIC
11	107967159	107973827	6668	NA	NA	Interval	NA	0	0	NA	ENSMUSG00000050965	Prkca	protein_coding	INTRON
11	107967186	107973850	6664	NA	NA	Interval	NA	0	0	NA	ENSMUSG00000050965	Prkca	protein_coding	INTRON
11	110083360	110083362	2	NA	NA	Interval	NA	0	0	NA	ENSMUSG00000044749	Abca6	protein_coding	INTRON
11	112699097	112699099	2	NA	NA	Interval	NA	0	0	NA				INTERGENIC
11	114800287	114800289	2	NA	NA	Interval	NA	0	0	NA	ENSMUSG00000063193	Cd300lb	protein_coding	UPSTREAM
11	117989080	117989082	2	NA	NA	Interval	NA	0	0	NA	ENSMUSG00000033987	Dnahc17	protein_coding	INTRON
11	117989080	117989082	2	NA	NA	Interval	NA	0	0	NA	ENSMUSG00000033987	Dnahc17	protein_coding	UPSTREAM
11	117989080	117989082	2	NA	NA	Interval	NA	0	0	NA	ENSMUSG00000017132	Cyth1	protein_coding	DOWNSTREAM
11	119560384	119566877	6493	NA	NA	Interval	NA	0	0	NA	ENSMUSG00000025583	Rptor	protein_coding	INTRON
11	119674456	119674460	4	NA	NA	Interval	NA	0	0	NA	ENSMUSG00000025583	Rptor	protein_coding	INTRON
11	121794737	121794739	2	NA	NA	Interval	NA	0	0	NA				INTERGENIC
11	121798837	121798839	2	NA	NA	Interval	NA	0	0	NA	ENSMUSG00000078564	Gm9631	protein_coding	DOWNSTREAM
11	121830166	121830168	2	NA	NA	Interval	NA	0	0	NA	ENSMUSG00000082831	Gm12591	pseudogene	EXON

ENSMUST00000033207	549	A	V	P20239	549	A	V	benign	neutral	0	1	1	0.575
ENSMUST00000033154	364	R	W	Q07832	364	R	W	possiblydamaging	deleterious	0.849	0.0674	0.834	0.0988
ENSMUST00000062451	1951	T	K	F8WIM6	1951	T	K	benign	neutral	0	1	1	0.575
ENSMUST00000171124	1948	T	K	E9Q471	1948	T	K	benign	neutral	0	1	1	0.575
ENSMUST00000026590	1166	Y	C	E9QAR7	1166	Y	C	benign	neutral	0	1	1	0.575
ENSMUST00000151376	41	Q	H	F6VLK5	41	Q	H	benign	neutral	0	1	1	0.575
ENSMUST00000115743	184	V	F	D3YZD5	184	V	F	benign	neutral	0	1	1	0.575
ENSMUST00000099051	64	L	S	F6QDW5	64	L	S	benign	neutral	0	1	1	0.575
ENSMUST00000099051	66	T	S	F6QDW5	66	T	S	benign	neutral	0	1	1	0.575
ENSMUST00000099051	67	A	G	F6QDW5	67	A	G	benign	neutral	0	1	1	0.575
ENSMUST00000099050	6	N	H	D3Z1I5	6	N	H	benign	neutral	0	1	1	0.575
ENSMUST00000099050	84	L	M	D3Z1I5	84	L	M	benign	neutral	0.001	0.852	0.994	0.514
ENSMUST00000099050	152	T	K	D3Z1I5	152	T	K	benign	neutral	0	1	1	0.575
ENSMUST00000099049	73	T	K	D3Z1I6	73	T	K	benign	neutral	0	1	1	0.575
ENSMUST00000099046	76	T	S	D3Z1I7	76	T	S	benign	neutral	0	1	1	0.575
ENSMUST00000099042	23	R	P	F6QHK0	23	R	P	benign	neutral	0	1	1	0.575
ENSMUST00000099042	25	L	F	F6QHK0	25	L	F	benign	neutral	0	1	1	0.575
ENSMUST00000099042	73	T	S	F6QHK0	73	T	S	benign	neutral	0	1	1	0.575
ENSMUST00000008573	85	V	L	Q9JJC9	85	V	L	probablydamaging	deleterious	0.978	0.0417	0.756	0.0695
ENSMUST00000054925	305	H	R	Q8BI38	305	H	R	benign	neutral	0	1	1	0.575
ENSMUST00000120329	305	H	R	Q3UWS5	305	H	R	benign	neutral	0	1	1	0.575
ENSMUST00000111635	970	Q	P	E9QQ93	970	Q	P	benign	neutral	0	1	1	0.575
ENSMUST00000047687	120	F	V	E9PYV0	120	F	V	benign	neutral	0	1	1	0.575
ENSMUST00000051446	1715	L	P	Q69ZK6	1715	L	P	benign	neutral	0	1	1	0.575
ENSMUST00000095573	1715	L	P	E9QPL3	1715	L	P	benign	neutral	0	1	1	0.575
ENSMUST00000165834	316	N	S	E9Q1L0	316	N	S	benign	neutral	0.164	0.132	0.92	0.162
ENSMUST00000048621	132	I	T	Q9D220	132	I	T	benign	neutral	0.011	0.222	0.959	0.239
ENSMUST00000101649	1079	E	G	Q5NBZ9	1079	E	G	benign	neutral	0	1	1	0.575
ENSMUST00000101655	1099	E	G	E9QJT8	1099	E	G	benign	neutral	0	1	1	0.575
ENSMUST00000081318	1110	E	G	Q3UZY0	1110	E	G	benign	neutral	0	1	1	0.575
ENSMUST00000140846	1018	E	G	E9Q799	1018	E	G	benign	neutral	0	1	1	0.575
ENSMUST00000153425	1068	E	G	E9Q8V3	1068	E	G	benign	neutral	0	1	1	0.575
ENSMUST00000101649	991	T	M	Q5NBZ9	991	T	M	benign	neutral	0.001	0.852	0.994	0.514
ENSMUST00000101655	1011	T	M	E9QJT8	1011	T	M	benign	neutral	0.001	0.852	0.994	0.514
ENSMUST00000081318	1022	T	M	Q3UZY0	1022	T	M	benign	neutral	0	1	1	0.575
ENSMUST00000140846	930	T	M	E9Q799	930	T	M	benign	neutral	0	1	1	0.575
ENSMUST00000153425	980	T	M	E9Q8V3	980	T	M	benign	neutral	0	1	1	0.575
ENSMUST00000101649	792	L	F	Q5NBZ9	792	L	F	benign	neutral	0.001	0.852	0.994	0.514
ENSMUST00000101655	823	L	F	E9QJT8	823	L	F	benign	neutral	0.001	0.852	0.994	0.514
ENSMUST00000081318	823	L	F	Q3UZY0	823	L	F	benign	neutral	0	1	1	0.575
ENSMUST00000093407	563	L	F	H7BX67	563	L	F	benign	neutral	0.005	0.26	0.968	0.267
ENSMUST00000140846	742	L	F	E9Q799	742	L	F	benign	neutral	0	1	1	0.575
ENSMUST00000066391	791	L	F	Q3UZY0	791	L	F	probablydamaging	deleterious	0.999	0.00574	0.136	0.0192
ENSMUST00000153425	792	L	F	E9Q8V3	792	L	F	benign	neutral	0	1	1	0.575
ENSMUST00000101649	765	S	G	Q5NBZ9	765	S	G	benign	neutral	0.011	0.222	0.959	0.239
ENSMUST00000101655	796	S	G	E9QJT8	796	S	G	benign	neutral	0.006	0.253	0.967	0.262
ENSMUST00000081318	796	S	G	Q3UZY0	796	S	G	benign	neutral	0.006	0.253	0.967	0.262
ENSMUST00000093407	536	S	G	H7BX67	536	S	G	benign	neutral	0.014	0.212	0.956	0.231
ENSMUST00000140846	715	S	G	E9Q799	715	S	G	benign	neutral	0	1	1	0.575
ENSMUST00000153425	765	S	G	E9Q8V3	765	S	G	benign	neutral	0.006	0.253	0.967	0.262
ENSMUST00000101649	728	H	R	Q5NBZ9	728	H	R	benign	neutral	0	1	1	0.575
ENSMUST00000101655	759	H	R	E9QJT8	759	H	R	benign	neutral	0	1	1	0.575
ENSMUST00000081318	759	H	R	Q3UZY0	759	H	R	benign	neutral	0	1	1	0.575
ENSMUST00000093407	499	H	R	H7BX67	499	H	R	benign	neutral	0.001	0.852	0.994	0.514
ENSMUST00000140846	678	H	R	E9Q799	678	H	R	benign	neutral	0	1	1	0.575
ENSMUST00000066391	727	H	R	Q3UZY0	727	R	H	probablydamaging	deleterious	1	0.00026	0.00018	0.0109
ENSMUST00000153425	728	H	R	E9Q8V3	728	H	R	benign	neutral	0	1	1	0.575
ENSMUST00000101649	719	Q	R	Q5NBZ9	719	Q	R	benign	neutral	0.011	0.222	0.959	0.239
ENSMUST00000101655	750	Q	R	E9QJT8	750	Q	R	benign	neutral	0.053	0.164	0.94	0.191
ENSMUST00000081318	750	Q	R	Q3UZY0	750	Q	R	benign	neutral	0.053	0.164	0.94	0.191
ENSMUST00000093407	490	Q	R	H7BX67	490	Q	R	benign	neutral	0.014	0.212	0.956	0.231
ENSMUST00000140846	669	Q	R	E9Q799	669	Q	R	benign	neutral	0	1	1	0.575
ENSMUST00000153425	719	Q	R	E9Q8V3	719	Q	R	benign	neutral	0.053	0.164	0.94	0.191
ENSMUST00000101649	680	R	Q	Q5NBZ9	680	R	Q	possiblydamaging	deleterious	0.754	0.0773	0.852	0.109
ENSMUST00000101655	711	R	Q	E9QJT8	711	R	Q	possiblydamaging	deleterious	0.786	0.0742	0.847	0.106
ENSMUST00000081318	711	R	Q	Q3UZY0	711	R	Q	possiblydamaging	deleterious	0.867	0.066	0.828	0.0974
ENSMUST00000093407	451	R	Q	H7BX67	451	R	Q	possiblydamaging	deleterious	0.943	0.0548	0.797	0.0852

ENSMUST00000140846	630	R	Q	E9Q799	630	R	Q	probablydamaging	deleterious	0.958	0.0492	0.783	0.0785
ENSMUST00000153425	680	R	Q	E9Q8V3	680	R	Q	possiblydamaging	deleterious	0.867	0.066	0.828	0.0974
ENSMUST00000101649	667	V	I	Q5NBZ9	667	V	I	possiblydamaging	neutral	0.492	0.0975	0.885	0.13
ENSMUST00000101655	698	V	I	E9QJT8	698	V	I	benign	neutral	0.204	0.124	0.915	0.156
ENSMUST00000081318	698	V	I	Q3UZY0	698	V	I	benign	neutral	0.204	0.124	0.915	0.156
ENSMUST00000093407	438	V	I	H7BX67	438	V	I	benign	neutral	0.225	0.121	0.913	0.152
ENSMUST00000140846	617	V	I	E9Q799	617	V	I	possiblydamaging	deleterious	0.805	0.0722	0.842	0.104
ENSMUST00000153425	667	V	I	E9Q8V3	667	V	I	benign	neutral	0.204	0.124	0.915	0.156
ENSMUST00000101649	587	A	V	Q5NBZ9	587	A	V	probablydamaging	deleterious	1	0.00026	0.00018	0.0109
ENSMUST00000101655	618	A	V	E9QJT8	618	A	V	probablydamaging	deleterious	1	0.00026	0.00018	0.0109
ENSMUST00000081318	618	A	V	Q3UZY0	618	A	V	probablydamaging	deleterious	1	0.00026	0.00018	0.0109
ENSMUST00000140846	537	A	V	E9Q799	537	A	V	probablydamaging	deleterious	0.991	0.0326	0.711	0.0584
ENSMUST00000153425	587	A	V	E9Q8V3	587	A	V	probablydamaging	deleterious	1	0.00026	0.00018	0.0109
ENSMUST00000101649	565	R	W	Q5NBZ9	565	R	W	benign	neutral	0	1	1	0.575
ENSMUST00000101655	596	R	W	E9QJT8	596	R	W	benign	neutral	0	1	1	0.575
ENSMUST00000081318	596	R	W	Q3UZY0	596	R	W	benign	neutral	0	1	1	0.575
ENSMUST00000093407	368	R	W	H7BX67	368	R	W	benign	neutral	0.006	0.253	0.967	0.262
ENSMUST00000140846	515	R	W	E9Q799	515	R	W	benign	neutral	0	1	1	0.575
ENSMUST00000066391	596	R	W	Q3UZY0	596	R	W	benign	neutral	0	1	1	0.575
ENSMUST00000153425	565	R	W	E9Q8V3	565	R	W	benign	neutral	0	1	1	0.575
ENSMUST00000101649	561	Q	R	Q5NBZ9	561	Q	R	benign	neutral	0	1	1	0.575
ENSMUST00000101655	592	Q	R	E9QJT8	592	Q	R	benign	neutral	0	1	1	0.575
ENSMUST00000081318	592	Q	R	Q3UZY0	592	Q	R	benign	neutral	0	1	1	0.575
ENSMUST00000093407	364	Q	R	H7BX67	364	Q	R	benign	neutral	0.006	0.253	0.967	0.262
ENSMUST00000140846	511	Q	R	E9Q799	511	Q	R	benign	neutral	0	1	1	0.575
ENSMUST00000066391	592	Q	R	Q3UZY0	592	Q	R	benign	neutral	0	1	1	0.575
ENSMUST00000153425	561	Q	R	E9Q8V3	561	Q	R	benign	neutral	0	1	1	0.575
ENSMUST00000101649	413	Q	R	Q5NBZ9	413	Q	R	benign	neutral	0	1	1	0.575
ENSMUST00000101655	444	Q	R	E9QJT8	444	Q	R	benign	neutral	0	1	1	0.575
ENSMUST00000081318	444	Q	R	Q3UZY0	444	Q	R	benign	neutral	0	1	1	0.575
ENSMUST00000093407	216	Q	R	H7BX67	216	Q	R	benign	neutral	0.001	0.852	0.994	0.514
ENSMUST00000140846	363	Q	R	E9Q799	363	Q	R	benign	neutral	0	1	1	0.575
ENSMUST00000066391	444	Q	R	Q3UZY0	444	Q	R	benign	neutral	0	1	1	0.575
ENSMUST00000153425	413	Q	R	E9Q8V3	413	Q	R	benign	neutral	0	1	1	0.575
ENSMUST00000101649	403	R	K	Q5NBZ9	403	R	K	benign	neutral	0.035	0.177	0.945	0.202
ENSMUST00000101655	434	R	K	E9QJT8	434	R	K	benign	neutral	0.009	0.233	0.961	0.247
ENSMUST00000081318	434	R	K	Q3UZY0	434	R	K	benign	neutral	0.009	0.233	0.961	0.247
ENSMUST00000093407	206	R	K	H7BX67	206	R	K	benign	neutral	0.017	0.205	0.954	0.225
ENSMUST00000140846	353	R	K	E9Q799	353	R	K	benign	neutral	0.001	0.852	0.994	0.514
ENSMUST00000066391	434	R	K	Q3UZY0	434	R	K	benign	neutral	0.009	0.233	0.961	0.247
ENSMUST00000153425	403	R	K	E9Q8V3	403	R	K	benign	neutral	0.016	0.207	0.955	0.227
ENSMUST00000101649	393	Y	H	Q5NBZ9	393	Y	H	benign	neutral	0.056	0.163	0.939	0.19
ENSMUST00000101655	424	Y	H	E9QJT8	424	Y	H	benign	neutral	0.032	0.18	0.946	0.205
ENSMUST00000081318	424	Y	H	Q3UZY0	424	Y	H	benign	neutral	0.032	0.18	0.946	0.205
ENSMUST00000140846	343	Y	H	E9Q799	343	Y	H	probablydamaging	deleterious	0.993	0.0301	0.696	0.0553
ENSMUST00000066391	424	Y	H	Q3UZY0	424	Y	H	benign	neutral	0.032	0.18	0.946	0.205
ENSMUST00000153425	393	Y	H	E9Q8V3	393	Y	H	benign	neutral	0.056	0.163	0.939	0.19
ENSMUST00000101649	381	V	E	Q5NBZ9	381	V	E	benign	neutral	0.002	0.704	0.987	0.452
ENSMUST00000101655	412	V	E	E9QJT8	412	V	E	benign	neutral	0.002	0.704	0.987	0.452
ENSMUST00000081318	412	V	E	Q3UZY0	412	V	E	benign	neutral	0.001	0.852	0.994	0.514
ENSMUST00000140846	331	V	E	E9Q799	331	V	E	benign	neutral	0.001	0.852	0.994	0.514
ENSMUST00000066391	412	V	E	Q3UZY0	412	V	E	benign	neutral	0.001	0.852	0.994	0.514
ENSMUST00000153425	381	V	E	E9Q8V3	381	V	E	benign	neutral	0.002	0.704	0.987	0.452
ENSMUST00000101649	371	Q	L	Q5NBZ9	371	Q	L	possiblydamaging	deleterious	0.778	0.075	0.848	0.107
ENSMUST00000101655	402	Q	L	E9QJT8	402	Q	L	possiblydamaging	deleterious	0.95	0.0527	0.791	0.0828
ENSMUST00000081318	402	Q	L	Q3UZY0	402	Q	L	possiblydamaging	deleterious	0.913	0.0604	0.813	0.0915
ENSMUST00000140846	321	Q	L	E9Q799	321	Q	L	possiblydamaging	deleterious	0.766	0.0764	0.851	0.108
ENSMUST00000066391	402	Q	L	Q3UZY0	402	Q	L	possiblydamaging	deleterious	0.913	0.0604	0.813	0.0915
ENSMUST00000153425	371	Q	L	E9Q8V3	371	Q	L	possiblydamaging	deleterious	0.95	0.0527	0.791	0.0828
ENSMUST00000101649	368	N	H	Q5NBZ9	368	N	H	probablydamaging	deleterious	0.993	0.0301	0.696	0.0553
ENSMUST00000101655	399	N	H	E9QJT8	399	N	H	probablydamaging	deleterious	0.997	0.0167	0.409	0.0357
ENSMUST00000081318	399	N	H	Q3UZY0	399	N	H	probablydamaging	deleterious	0.987	0.036	0.731	0.0626
ENSMUST00000140846	318	N	H	E9Q799	318	N	H	probablydamaging	deleterious	0.993	0.0301	0.696	0.0553
ENSMUST00000066391	399	N	H	Q3UZY0	399	N	H	probablydamaging	deleterious	0.987	0.036	0.731	0.0626
ENSMUST00000153425	368	N	H	E9Q8V3	368	N	H	probablydamaging	deleterious	0.993	0.0301	0.696	0.0553
ENSMUST00000101655	380	T	I	E9QJT8	380	T	I	benign	neutral	0.002	0.704	0.987	0.452
ENSMUST00000081318	380	T	I	Q3UZY0	380	T	I	benign	neutral	0.001	0.852	0.994	0.514

ENSMUST00000140846	299	T	I	E9Q799	299	T	I	benign	neutral	0	1	1	0.575
ENSMUST00000066391	380	T	I	Q3UZY0	380	T	I	benign	neutral	0.001	0.852	0.994	0.514

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