

Knock-out animal for TAAR1 function

Trace amines (TAs) are endogenous compounds related to biogenic amine neurotransmitters and present in the mammalian nervous system in trace amounts. The intense research efforts on the pharmacology and metabolism of trace amines during the last decades has been triggered by their tight link to a variety of highly prevalent

5 conditions such as depression, schizophrenia, anxiety disorders, bipolar disorder, attention deficit hyperactivity disorder, neurological diseases such as Parkinson's Disease, epilepsy, migraine, hypertension, substance abuse and metabolic disorders such as eating disorders, diabetes, obesity and dyslipidemia (Reviewed in: Lindemann & Höner, Trends Pharmacol Sci. 2005; 26(5):274-81 Branchek, T.A. and Blackburn, T.P. (2003) *Curr.*

10 *Opin. Pharmacol.* 3, 90-97; Premont, R.T., Gainetdinov, R.R., Caron, M.G. (2001) *Proc. Natl. Acad. Sci.* 98, 9474-9475.; Davenport, A.P. (2003) *Curr. Opin. Pharmacol.* 3,127-134.). However, a detailed understanding of the physiology of trace amines on the molecular level has only become possible with the recent identification of a novel family of G protein-coupled receptors termed Trace Amine Associated Receptors (TAARs;

15 Lindemann, L., Ebeling, M., Kratochwil, N.A., Bunzow J.R., Grandy, D.K., Hoener, M.C. (2005) *Genomics* 85, 372-385; Bunzow, et al. (2001) *Mol. Pharmacol.* 60, 1181-1188; Borowsky, B., et al., (2001). *Proc. Natl. Acad. Sci. U. S. A.* 98, 8966-8971). Some of these receptors display sensitivity to trace amines, and their unique pharmacology and expression pattern make these receptors prime candidates for targets in drug

20 development in the context of several diseases, some of which previously had been linked to trace amines. Progress in understanding the physiological relevance of Trace Amine Associated Receptors and their ligands on the systems level critically depends on a detailed knowledge of their expression pattern, their pharmacology and the modes of signal transduction. In this context, compounds acting as agonists, antagonists or positive

25 or negative modulators on TAARs, as well as transgenic animal models such as targeted "knock-out" mouse lines are essential tools for dissecting the molecular function of this receptor family and to fully understand their potential relevance as targets in drug development.

The present invention provides vector constructs and methods for producing non-

30 human knock-out animals comprising within their genome a targeted deletion of the *TAAR1* gene. Said *TAAR1* knock-out animals, as well as methods of producing them, are also provided. The invention also relates to the use of these animals as a tool for assessing

TAAR1 function and for identifying unknown ligands of TAAR1 as well as for the characterization of novel ligands of TAARs other than TAAR1, for analyzing the tissue distribution of TAAR1, for analyzing TAAR1 signal transduction mechanisms, for analyzing the physiological function of TAAR1 *in vivo*, and for identifying and testing for
5 the therapeutic effect of a compound in treating and preventing disorders comprising depression, anxiety disorders, bipolar disorder, attention deficit hyperactivity disorder, stress-related disorders, psychotic disorders such as schizophrenia, neurological diseases such as Parkinson's Disease, neurodegenerative disorders such as Alzheimer's disease, epilepsy, migraine, hypertension, substance abuse and metabolic disorders such as eating
10 disorders, diabetes, diabetic complications, obesity, dyslipidemia, disorders of energy consumption and assimilation, disorders and malfunction of body temperature homeostasis, disorders of sleep and circadian rhythm, and cardiovascular disorders.

The present invention therefore provides a vector construct comprising genomic sequences homologous to upstream and downstream regions flanking the single coding
15 exon of the TAAR1 gene suitable for homologous recombination and one or more selection marker genes.

The vector construct comprises genomic DNA sequences which are homologous to the sequences flanking the TAAR1 exon upstream and downstream on the chromosome. The lengths of the homologous sequences are chosen that it allows a targeted homologous
20 recombination with the TAAR1 allele. The homologous sequences may have a length of 2.5 up to 300 kb. Preferably, the homologous sequences have a length of 3 to 6 kb. Preferably, the homologous sequences comprise at least a part of the TAAR1 promoter.

Preferably, the vector construct comprise additionally a reporter gene. Said reporter gene is located between the homologous TAAR1 flanking sequences. Preferably, the
25 expression of said reporter gene is, after the integration into the genome, under the control of the TAAR1 promoter and optionally of other TAAR1 regulatory elements. The reporter gene may be selected of a group comprising LacZ or derivatives thereof, alkaline phosphatase, fluorescent proteins, luciferases, or other enzymes or proteins which may be specifically detected and quantified in tissue or cells of various kinds. Preferably, the
30 reporter gene is LacZ. Preferably, the reporter gene is at its N-terminus operably linked to a nuclear localization sequence (NLS). In a preferred embodiment, the reporter gene is inserted into the TAAR1 genomic sequence such that the endogenous start codon of the TAAR1 gene is preserved.

The selection marker gene may be a positive selection marker. The positive
35 selection marker may be selected from the group comprising a neomycin resistance gene, a hygromycin resistance gene, a puromycin resistance gene, a blasticidin S resistance gene,

a xanthine/guanine phosphoribosyl transferase gene or a zeomycin resistance gene. The positive selection marker may be framed by recognition sites for a recombinase, which allows for excision of the positive selection marker gene after selection of successful homologous recombination events. Thereby, any effect of the expression of the positive selection marker on the expression of the reporter gene may be avoided. The recognition sites for a recombinase may be selected from the group comprising *frt* sites for *flp* recombinase and *loxP* sites (including mutated *loxP* sites) for *cre* recombinase. Preferably, the positive selection marker is a neomycin resistance gene.

The selection marker gene may also be an negative selection marker. The negative selection marker may be selected from, but not limited to, the group consisting of a diphtheria toxin gene and an HSV-thymidine kinase gene. Preferably, the negative selection marker is a diphtheria toxin gene.

Preferably, the vector construct comprises positive selection marker and a negative selection marker. More preferably, the vector construct comprises a neomycin resistance gene and a diphtheria toxin gene.

In a preferred embodiment, the vector construct is the vector construct TAAR KO incorporated in the plasmid pSKDT-Tar1-NLS-PGK-Neo deposited under accession number DSMZ 17504 (Deposition date: 16.08.2005). Vector construct TAAR KO is depicted in Figure 1B.

The present invention further provides a method of producing a non-human knock-out animal, whose one or both alleles of *TAAR1* gene are mutated and/or truncated in a way that less or no active *TAAR1* protein is expressed comprising

- (a) introducing a vector construct as described above into the genome of an embryonic stem cell by means of homologous recombination,
- (b) generating a heterozygous and/or homozygous knock-out animal from the said embryonic stem cell, and thereby
- (c) producing a non-human knock-out animal, whose one or both alleles of the *TAAR1* gene are mutated and/or truncated in a way that less or no active *TAAR1* protein is expressed.

In a preferred embodiment, in step (c) of the described method, a non-human knock-out animal may be produced whose one or both alleles of a *TAAR1* gene comprise the *TAAR1*^{NLSlacZ} allele as depicted in Fig. 1A. In another preferred embodiment, in step (c) of the described method, a non-human knock-out animal may be produced whose one or both alleles of *TAAR1* gene comprise the construct TAAR1-KO (see Fig. 1B)

incorporated in the plasmid pSKDT-Tar1-NLS-PGK-Neo deposited under accession number DSMZ 17504 (Deposition date: 16.08.2005).

In a further embodiment, the above-described method additionally comprises
5 (d) further crossbreeding the knock-out animal produced in step (c) with an animal transgenic for the recombinase recognizing the recognition sites framing the positive selection marker gene.

Knock-out animals comprising targeted mutations are achieved routinely in the art as provided for example by the method by Joyner, A.L. (Gene Targeting. 1999, Second
10 Edition, The Practical Approach Series, Oxford University Press, New York) and Hogan, B., et al. (Manipulating the mouse embryo. 1994, Second Edition, Cold Spring Harbor Press, Cold Spring Harbor.).

For example, the heterozygous and/or homozygous knock-out animal of the above-described methods may be generated by selecting embryonic stem (ES) cell clones
15 carrying the targeted TAAR1 allele as described above, verifying the targeted mutation in the recombinant embryonic stem cell clones, injecting the verified recombinant embryonic stem cells into blastocysts of wild type animals, transferring these injected blastocysts into pseudo-pregnant foster mothers, breeding chimeras resulting from the blastocysts to wild type animals, testing the offspring resulting from these breedings for
20 the presence of the targeted mutation, breeding heterozygous animals, optionally to generate homozygous knock-out animals.

Embryonic stem cells used in the art which may also be used in the methods of this invention comprise for example embryonic stem cells derived from mouse strains such as C57BL/6, BALB/c, DBA/2, CBA/ and SV129. Preferably, embryonic stem cells derived
25 from C57BL/6 mice are used (Seong, E et al (2004) *Trends Genet.* 20, 59-62; Wolfer, D.P. et al., *Trends Neurosci.* 25 (2002): 336-340).

The present invention further provides the non-human knock-out animal produced by any of the above described methods.

30 In another embodiment of the invention, a non-human knock-out animal is provided, whose one or both alleles of *TAAR1* gene is mutated or truncated in a way that less or no active TAAR1 protein is expressed. Preferably, one or both alleles of the *TAAR1*

gene of the non-human knock-out animal are replaced with a reporter gene. Preferably, the reporter gene is LacZ.

In a preferred embodiment, a non-human knock-out animal is provided whose one or both alleles of a *TAAR1* gene comprise the *TAAR1*^{NLSlacZ} allele as depicted in Fig 1A. In
5 another preferred embodiment non-human knock-out animal whose one or both alleles of a *TAAR1* gene comprise the construct *TAAR1*-KO (see Fig. 1B) incorporated in the plasmid pSKDT-Tar1-NLS-PGK-Neo deposited under accession number DSM 17504 (Deposition date: 16.08.2005).

The non-human knock-out animal may be any animal known in the art, which may
10 be used for the methods of the invention. Preferably, the animal of the invention is a mammal, more preferred the knock-out animal of the invention is a rodent. The most preferred non-human knock-out animal is a mouse. Even more preferably, the non-human knock-out animal is a co-isogenic mutant mouse strain of C57BL/6.

The present invention also relates to descendants (= progeny) of the non-human
15 knock-out animals as provided by the invention, obtained by breeding with the same or with another genotype. Descendants may also be obtained by breeding with the same genetic background.

The knock-out animals can be used for preparing primary cell cultures, and for the preparation of secondary cell lines derived from primary cell preparations of these
20 animals. Furthermore, the knock-out animals can be used for the preparation of tissue or organ explants, and cultures thereof. In addition, the knock-out animal may be used for the preparation of tissue or cell extracts such as membrane or synaptosomal preparations.

The present invention further provides primary cell cultures, as well as secondary
25 cell lines derived from the non-human knock-out animals as provided by the invention or its descendants. In addition, the present invention provides tissue or organ explants and cultures thereof, as well as tissue or cell extracts derived from non-human knock-out animals as provided by the invention or its descendants. Tissue or cell extracts are for example membrane or synaptosomal preparations.

30 Integration of the genetic construct into the genome can be detected by various methods comprising genomic Southern blot and PCR analysis using DNA isolated e.g. from tail biopsies of the animals.

It will be apparent to the person skilled in the art that there are a large number of analytical procedures which may be used to detect the expression of the reporter gene comprising methods at the RNA level such as for example mRNA quantification by reverse transcriptase polymerase chain reaction (RT-PCR) or by Northern blot, *in situ* hybridization, as well as methods at the protein level comprising histochemistry, immunoblot analysis and *in vitro* binding studies. Quantification of the expression levels of the targeted gene can moreover be determined by the ELISA technology, which is common to those knowledgeable in the art.

Quantitative measurement can be accomplished using many standard assays. For example, transcript levels can be measured using RT-PCR and hybridization methods including RNase protection, Northern blot analysis, and RNA dot blot analysis. Protein levels can be assayed by ELISA, Western blot analysis, and by comparison of immunohistochemically or histochemically stained tissue sections. Immunohistochemical staining, enzymatic histochemical stainings as well as immunoelectron microscopy can also be used to assess the presence or absence of the TAAR1 protein. The TAAR1 expression may also be quantified making use of the NLSlacZ reporter in the TAAR1 non-human knock-out animal using immunohistochemical or histochemical lacZ stainings on tissue sections or quantitative enzymatic lacZ assays performed with tissue homogenates or tissue extracts. Specific examples of such assays are provided below.

The knock-out animals of the invention may be further characterized by methods known in the art, comprising immunohistochemistry, electron microscopy, Magnetic Resonance Imaging (MRI), Positron Emission Tomography (PET) and by behavioral and physiological studies addressing neurological, sensory, and cognitive functions as well as physiological (e.g. metabolic) parameters. Examples of behavioral tests and physiological examinations are: Spontaneous behavior, behavior related to cognitive functions, pharmacologically-disrupted behavior, grip strength test, horizontal wire test, forced swim test, rotarod test, locomotor activity test, Prepulse inhibition test, Morris water maze test, Y-maze test, light-dark preference test, passive and active avoidance tests, marble burying test, plus maze test, learned helplessness test, stress-induced hyperthermia, measuring food consumption and development of body weight over time, measuring body temperature and energy consumption under resting and basal conditions and during heat and cold exposure, determining the thermoneutral zone, determining the food assimilation coefficient (e.g. by bomb calorimetry), determining the energy assimilation and the energy content of feces, determining the respiratory coefficient e.g. for analysis of the carbohydrate and lipid metabolism, determining the substrate utilization and energy expenditure during food restriction, determining the oxygen

consumption, CO₂- and heat production e.g. by indirect calorimetry, measuring the heart rate and blood pressure under resting, basal and stress conditions (e.g. by telemetry), determining the body composition (e.g. regarding water content, fat amount and fat-free mass).

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“Oligonucleotide” and “nucleic acid” refer to single or double-stranded molecules which may be DNA, comprised of the nucleotide bases A, T, C and G, or RNA, comprised of the bases A, U (substitutes for T), C, and G. The oligonucleotide may represent a coding strand or its complement. Oligonucleotide molecules may be identical in sequence to the sequence, which is naturally occurring or may include alternative codons, which encode the same amino acid as that which is found in the naturally occurring sequence (see, Lewin "Genes V" Oxford University Press Chapter 7, 1994, 171-174). Furthermore, oligonucleotide molecules may include codons, which represent conservative substitutions of amino acids as described. The oligonucleotide may represent genomic DNA or cDNA.

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The term “allele” as used herein refers to any alternative form of a gene that can occupy a particular chromosomal locus.

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The term “promoter” of a gene as used herein refers to the regions of DNA which control the expression of the gene. The TAAR1 promoter is substantially the promoter which controls the expression of the *TAAR1* gene in a wildtype animal. Optionally, the genomic homologous sequences may comprise a part of the TAAR1 promoter or the whole TAAR1 promoter. The homologous sequences may optionally also comprise other TAAR1 regulatory elements.

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The term “knock-out animal” as used herein refers to non-human animals comprising a targeted null-mutation of a gene function.

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A further objective of the present invention is the use of the non-human knock-out animal as described, or a primary cell culture or secondary cell lines, tissue or organ explants and cultures thereof, or tissue or cell extracts derived from said animals, as a model for identifying and testing for a therapeutic effect of a compound in disorders comprising depression, anxiety disorders, bipolar disorder, attention deficit hyperactivity disorder, stress-related disorders, psychotic disorders such as schizophrenia, neurological diseases such as Parkinson’s Disease, neurodegenerative disorders such as Alzheimer’s Disease, epilepsy, migraine, hypertension, substance abuse and metabolic disorders such

as eating disorders, diabetes, diabetic complications, obesity, dyslipidemia, disorders of energy consumption and assimilation, disorders and malfunction of body temperature homeostasis, disorders of sleep and circadian rhythm, and cardiovascular disorders.

Additionally, these non-human knock-out animals as described above, these cell
5 cultures, cell lines, tissue or organ explants, cultures, or tissue or cell extracts derived from said animals, may be used as a model for studying the TAAR signaling pathway.

Furthermore, these non-human knock-out animals as described above, these cell cultures, cell lines, tissue or organ explant cultures, or tissue or cell extracts derived from said animals, may be used as a tool for assessing TAAR1 function, in particular for
10 assessing the TAAR1 function in disorders such as depression, anxiety disorders, bipolar disorder, attention deficit hyperactivity disorder, stress-related disorders, psychotic disorders such as schizophrenia, neurological diseases such as Parkinson's Disease, neurodegenerative disorders such as Alzheimer's Disease, epilepsy, migraine, hypertension, substance abuse and metabolic disorders such as eating disorders, diabetes,
15 diabetic complications, obesity, dyslipidemia, disorders of energy consumption and assimilation, disorders and malfunction of body temperature homeostasis, disorders of sleep and circadian rhythm, and cardiovascular disorders and disorders involving catecholamine neurotransmitters.

Furthermore, these non-human knock-out animals as described above, these cell
20 cultures, cell lines, tissue or organ explant cultures, or tissue or cell extracts derived from said animals, may also be used as a tool for determining the specificity of compounds acting on TAAR1.

In addition, these non-human knock-out animals as described above, these cell cultures, cell lines, tissue or organ explant cultures, or tissue or cell extracts derived from
25 said animals, may be used as a tool for the identification of so far unknown ligands of TAAR1, and for the characterization of novel ligands acting on TAARs other than TAAR1.

The present invention further provides a method of testing TAAR1 agonists, TAAR1 partial agonists, TAAR1 positive or negative modulators (e.g. TAAR1 enhancer)
30 or TAAR1 inhibitor compounds for effects other than TAAR1-specific effects which method comprises administering a TAAR1 agonist, a TAAR1 partial agonist, a TAAR1 positive or negative modulator (e.g. TAAR1 enhancer) or a TAAR1 inhibitor compound to a non-human knock-out animal as described above, or primary cell culture, or a secondary cell line, or a tissue or organ explant or a culture thereof, or tissue or organ
35 extracts derived from said non-human knock-out animals or its descendants, and

determining the effect of the compound comprising assessing neurological, sensory, and cognitive functions as well as physiological (e.g. metabolic) parameters and comparing these to the effect(s) of the same compound on wild type control animals. These neurological, sensory, and cognitive functions and physiological parameters are
5 determined by behavior and physiological studies addressing these functions and parameters.

Control may comprise any animal, primary cell culture, a secondary cell line, a tissue or organ explant or a culture thereof, or tissue or organ extracts, wherein the *TAAR1* gene is not mutated in a way, that less or no active TAAR1 protein is expressed, or
10 wherein the animal, primary cell culture, or a secondary cell line, or a tissue or organ explant or a culture thereof, or tissue or organ extracts comprises the native *TAAR1* gene. Preferably, the control is a wildtype animal.

Furthermore, the use of the non-human knock-out animal as described, or a primary cell culture, or a secondary cell line, or a tissue or organ explant or a culture
15 thereof, or tissue or organ extracts derived from said non-human animal or its descendants is provided for testing of TAAR1 agonists, TAAR1 partial agonists, TAAR1 positive and negative modulators (e.g. TAAR1 enhancer) or TAAR1 inhibitor compounds for effects other than TAAR1-specific effects.

Effects other than TAAR1-specific effects may be any side-effects of TAAR1
20 agonists, TAAR1 partial agonists, TAAR1 positive and negative modulators (e.g. TAAR1 enhancer) or TAAR1 inhibitor compounds produced by its interaction with any other molecule.

The term "Agonist" as used herein refers to a compound that binds to and forms a complex with a receptor and elicits a full pharmacological response which is specific to
25 the nature of the receptor involved.

The term "Partial agonist" as used herein refers to a compound that binds to and forms a complex with a receptor and elicits a pharmacological response, which unlike for a full agonist, does not reach the maximal response of the receptor.

The term "Antagonist" as used herein refers to a compound that binds to and forms
30 a complex with a receptor and acts inhibitory on the pharmacological response of the receptor to an agonist or partial agonist. Per definition the antagonist has no influence on receptor signaling in the absence of an agonist or partial agonist for that receptor.

The term "Modulator" as used herein, refers to a compound that binds to and forms a complex with a receptor, and that alters the pharmacological response of the receptor evoked by agonists or partial agonists in a quantitative manner.

5 The present invention further relates to a test system for testing TAAR1 agonists, TAAR1 partial agonists, TAAR1 positive and negative modulators (e.g. TAAR1 enhancer) or TAAR1 inhibitor compounds for effects other than TAAR1-specific effects comprising a non-human knock-out animal whose one or both alleles of a *TAAR1* gene are mutated and/or truncated in a way that less or no active TAAR1 protein is expressed, or a primary
10 cell culture, or a secondary cell line, or a tissue or organ explant or a culture thereof, or tissue or organ extracts derived from said non-human animal or its descendants, and a means for determining whether TAAR1 agonists, TAAR1 partial agonists, TAAR1 positive and negative modulators (e.g. TAAR1 enhancer) or TAAR1 inhibitor compounds exhibit effects other than TAAR1-specific effects.

15 In addition, the present invention provides a use of the non-human knock-out animal, whose one or both alleles of a TAAR1 gene are mutated and/or truncated in a way that less or no TAAR1 protein is expressed, or a primary cell culture, or a secondary cell line, or a tissue or organ explant or a culture thereof, or tissue or organ extracts derived from said non-human animal or its descendants for studying the intracellular trafficking
20 of TAARs or of other cellular components linked to TAARs.

 Furthermore, the present invention provides a use of the non-human knock-out animal, whose one or both TAAR1 alleles are replaced by a reporter gene for determining the TAAR1 expression profile. The expression profile can be readily analyzed because the reporter gene is expressed with the same spatiotemporal profile in the TAAR1 knock-out
25 as is TAAR1 in wild type animals.

 The invention further provides the knock-out animals, methods, compositions, kits, and uses substantially as described herein before especially with reference to the foregoing examples.

 Having now generally described this invention, the same will become better
30 understood by reference to the specific examples, which are included herein for purpose of illustration only and are not intended to be limiting unless otherwise specified, in connection with the following figures.

Figures

Figure 1A shows a schematic representation of the TAAR1 wildtype allele $TAAR^{+/+}$ allele (top) with a selection of restriction sites. Arrows represent oligonucleotides which were used for PCR amplification of the 5' arm and 3' arm of the targeting vector (bottom) from genomic DNA. The genomic sequence elements of the wildtype locus which were included into the targeting vector are indicated by dotted lines. The *NsiI* sites used to clone these genomic arms into the targeting vector are marked in bold lettering.

The resulting targeting vector pSKDT-Tar1-NLS-lacZ-PGK-Neo (bottom) comprises a genetic construct consisting of a genomic 5' arm (5' arm), the NLS-lacZ reporter-gene, a PGK-Neo resistance-gene and a 3' genomic arm (3' arm). The Diphtheria toxin gene (Dipht.) is placed at the 3' side of the construct.

Figure 1B shows a schematic representation of the TAAR1-KO construct.

Figure 2 shows the synthetic N-terminal NLS-signal of the lacZ reporter-gene. Oligonucleotides mTar1-29cA (underlined 5'-3' strand) and mTar1-30ncB (underlined 3'-5' strand) inserted in the *NsiI* sites and resulting amino acid of the NLS (PKKKRKV) sequence in single amino acid letter code. The start codon (ATG) of mTAAR1 is indicated with bold letters. The *StuI* site used to insert the lacZ-PGK-Neo cassette is indicated in the figure.

Figure 3 shows a PCR to identify clones with correct targeting at the 3' arm of the NLSlacZ construct. 0.8% agarose gel of PCR reactions with oligonucleotides IL4-neo and mTar26nc on ES-cell clones. Lane 1: DNA molecular weight marker IV (Roche Diagnostics, Mannheim, Germany), Lane 2: clone IIB1, Lane 3: clone IIB2, Lane 4: clone IIB3, Lane 5: clone IIB4, Lane 6: C57BL/6 ES-cell DNA (negative control), Lane 7: water control

Figure 4 shows a PCR to identify clones with correct targeting at the 5' arm. 0.8% agarose gel of PCR reactions with oligonucleotides IL4-rev and mTar24c on ES-cell clones. Lane 1: DNA molecular weight marker X (Roche Diagnostics, Mannheim, Germany), Lane 2: clone IIB1, Lane 3: clone IIB2, Lane 4: clone IIB3, Lane 5: clone IIB4, Lane 6: C57BL/6 ES-cell DNA (negative control). The arrow indicates the amplification product obtained from clone IIB1.

Figure 5 shows mice generated from Balb/c blastocysts and the mutant C57BL/6 mouse embryonic stem cell line as described above. The coat color can be used as an indicator for the degree of chimerism. The amount of black versus white hairs in the fur gives a rough quantitative measure for the degree of the overall chimerism.

Figure 6 shows a genotype analysis by means of PCR. Genomic DNA was analyzed for the presence of the $TAAR1^{+/+}$ or $TAAR1^{NLSlacZ}$ allele, indicating the respective genotypes of the animals. The 50 bp DNA ladder (Invitrogen) was used as molecular weight standard. M: 50 bp ladder, lane 1: $TAAR1^{NLSlacZ/NLSlacZ}$, lane 2: $TAAR1^{+/NLSlacZ}$, lane 3: $TAAR1^{+/+}$

Figure 7 shows a schematic structure of the $TAAR1^{+}$ (top) and $TAAR1^{NLSlacZ}$ allele (bottom). The PCR amplification and partial sequence analysis of the indicated DNA fragments (fragment 1-4; listing 1-9) confirmed the correct homologous recombination of the $TAAR1^{NLSlacZ}$ allele.

■ Sequenced stretches (listing 1 to 9)

Figure 8 shows an agarose gel of an electrophoresis of PCR amplified DNA fragments as summarized in Table 1.

A: Under the conditions of PCR protocol 5.1.1 (Table 1), a 2.72 kb PCR product (fragment 1, Fig. 7) was amplified from $TAAR1^{+/+}$ genomic DNA, and a 5.05 kb (fragment 3, Fig. 7) PCR product was amplified from $TAAR1^{NLSlacZ/NLSlacZ}$ genomic DNA. M: 1kb ladder, lane 1: Ø template (= without template), lane 2: $TAAR1^{+/+}$, lane 3: $TAAR1^{NLSlacZ/NLSlacZ}$.

B: Under the conditions of PCR protocol 5.1.2 (Table 1), a 7.33 kb PCR product (fragment 2, Fig. 7) was amplified from $TAAR1^{NLSlacZ/NLSlacZ}$ genomic DNA, while no product was obtained from $TAAR1^{+/+}$ genomic DNA. M: 1kb ladder, lane 1: Ø template (= without template), lane 2: $TAAR1^{+/+}$, lane 3: $TAAR1^{NLSlacZ/NLSlacZ}$.

C: Under the conditions of PCR protocol 5.1.3 (Table 1), a 2.86 kb PCR product (fragment 4, Fig. 7) was amplified from $TAAR1^{NLSlacZ/NLSlacZ}$ genomic DNA, while no

product was obtained from TAAR1^{+/+} genomic DNA.

M: 1kb ladder, lane 1: Ø template (= without template), lane 2: TAAR1^{+/+}, lane 3: TAAR1^{NLSlacZ/NLSlacZ}.

The 1 kb DNA ladder (Invitrogen) was used as molecular weight standard.

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Figure 9 shows an agarose gel of an electrophoresis of PCR products amplified from TAAR1^{+/+} and TAAR1^{NLSlacZ/NLSlacZ} mouse brain cDNA preparations, respectively, as summarized in Table 2.

10 A: PCR reactions specific for GAPDH (see above) on TAAR1^{+/+} and TAAR1^{NLSlacZ/NLSlacZ} mouse brain cDNA preparations. From both cDNAs a 452 bp PCR product was amplified.

M: 50bp ladder, lane 1: Ø template (= without template), lane 2: TAAR1^{NLSlacZ/NLSlacZ}, lane 3: TAAR1^{+/+}.

15 B: PCR reactions specific for NLSlacZ (see above) on TAAR1^{+/+} and TAAR1^{NLSlacZ/NLSlacZ} mouse brain cDNA preparations. A 631 bp PCR product was amplified from TAAR1^{NLSlacZ/NLSlacZ}, but not from TAAR1^{+/+} mouse brain cDNA.

M: 50bp ladder, lane 1: Ø template (= without template), lane 2: TAAR1^{NLSlacZ/NLSlacZ}, lane 3: TAAR1^{+/+}.

20 C: PCR reactions specific for TAAR1 (see above) on TAAR1^{+/+} and TAAR1^{NLSlacZ/NLSlacZ} mouse brain cDNA preparations. A 936 bp PCR product was amplified from TAAR1^{+/+}, but not from TAAR1^{NLSlacZ/NLSlacZ} mouse brain cDNA.

M: 1 kb ladder, lane 1: Ø template (= without template), lane 2: TAAR1^{NLSlacZ/NLSlacZ}, lane 3: TAAR1^{+/+}.

25 The 50 bp DNA ladder (Invitrogen; A, B) and the 1 kb DNA ladder (Invitrogen; C) were used as molecular weight standards.

30 Figure 10 shows an agarose gel of an electrophoresis of PCR products from the microsatellite analysis of 5 TAAR1^{+/NLSlacZ} mice of the F1 generation, the ES cell line used for generation of germline chimeras and samples of the mouse inbred strains C57BL/6, DBA and SV129 (result for the microsatellite marker D5MIT259). The match of the standard sample for C57BL/6 with all test samples provides evidence that the mutant mouse line carrying the TAAR1^{+/NLSlacZ} allele is on a C57BL/6 genetic background.

The 10 bp DNA ladder (Invitrogen) was used as molecular weight standard.

M: 10bp ladder, lane 1: C57BL/6, lane 2: DBA, lane 3:SV129, lane 4: ES TAAR1^{+/-NLSlacZ}, lane 5: F1 #1 TAAR1^{+/-NLSlacZ}, lane 6: F1 #2 TAAR1^{+/-NLSlacZ}, lane 7: F1 #3 TAAR1^{+/-NLSlacZ}, lane 8: F1 #4 TAAR1^{+/-NLSlacZ}, lane 9: F1 #5 TAAR1^{+/-NLSlacZ}.

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Figure 11 shows a LacZ staining of histological sections of adult TAAR1^{NLSlacZ/NLSlacZ} and TAAR1^{+/+} mouse brains. (A) The TAAR1^{NLSlacZ/NLSlacZ} mouse brain section displays a strong, specific staining; (B): higher magnification of boxed area in (A), (C): staining is absent from the TAAR1^{+/+} mouse brain section. Both sections were cut in sagittal orientation from equivalent brain regions (see D for schematic diagram of the brain regions from which the sections were cut).

Figure 12 show graphical representation of physical properties of the TAAR1^{LacZ} mouse mutant. Nest building behaviour (a) and development of body weight (b) of TAAR1^{+/+} (n = 22), TAAR1^{+/-LacZ} (n = 21) and TAAR1^{LacZ/LacZ} (n = 21) mice showed no differences between the genotypes. Rectal body temperature (c) of TAAR1^{+/+} (n = 22), TAAR1^{+/-LacZ} (n = 21) and TAAR1^{LacZ/LacZ} (n = 21) mice. No statistical significant difference in body temperature between genotypes was observed. Assessment of the physical strength of TAAR1^{+/+} (n = 22), TAAR1^{+/-LacZ} (n = 21) and TAAR1^{LacZ/LacZ} (n = 21) mice by means of the horizontal wire test (d) and grip strength (e) did not reveal any significant differences between genotypes. Motor coordination and balance revealed by the performance on the rotarod (f). No significant differences between the genotypes have been observed. (g) Locomotor activity of TAAR1^{+/+} and TAAR1^{LacZ/LacZ} mice after a single application of d-amphetamine (2.5 mg/kg i.p., n=12). The increase in locomotor activity triggered by the amphetamine challenge was significantly higher in TAAR1^{LacZ/LacZ} mice as compared to their wild type littermates (filled symbols, straight lines) while there were no significant differences between genotypes in vehicle treated animals (open symbols, dashed lines).

Figure 13 shows a graphical representation of increased amphetamine-triggered transmitter release in the striatum in absence of TAAR1 revealed by *in vivo* microdialysis. Extracellular levels of dopamine, 3,4-dihydroxyphenylacetic acid (DOPAC), noradrenaline and serotonin in the striatum of TAAR1^{+/+} and TAAR1^{LacZ/LacZ} mice after a single application of d-amphetamine (2.5 mg/kg i.p., n=7-8) as revealed by *in vivo* microdialysis. Dialysates of the same animals were analyzed for all four compounds.

- (a-b) The amphetamine-triggered increase in the extracellular dopamine levels is 2.3 fold as big in the striatum of $TAAR1^{LacZ/LacZ}$ mice as in their $TAAR1^{+/+}$ littermates, while there is only a marginal decrease in the levels of the dopamine catabolite DOPAC in both $TAAR1^{LacZ/LacZ}$ and $TAAR1^{+/+}$ animals in response to amphetamine with no significant differences between the genotypes. (c) The increase in the level of noradrenalin in response to the amphetamine challenge is 2.4-fold as big as in wild type animals. (d) A 2.5-fold increase in the serotonin level triggered by amphetamine was observed only in $TAAR1^{LacZ/LacZ}$ mice, but not in their $TAAR1^{+/+}$ littermates.

- Figure 14 shows a graphical representation of electrophysiological analysis of dopaminergic neurons in the VTA of $TAAR1^{LacZ/LacZ}$ and wild type mice. (a) The spontaneous firing rate of dopaminergic neurons is lower in the wild type (left panel) than in the $TAAR1^{LacZ/LacZ}$ mice (right). Cumulative probability histogram of spike intervals in the wild type (black trace) and $TAAR1^{LacZ/LacZ}$ mice (gray). In the $TAAR1^{LacZ/LacZ}$ mice, the distribution of interevent intervals is significantly shifted to the left, indicating an increase in the spontaneous spike frequency. (b) The $TAAR1$ agonist p-tyramine decreases the firing rate of dopaminergic neurons in the wild type but not in the $TAAR1^{LacZ/LacZ}$ mice, as shown by the shift in the cumulative probability histogram of interevent intervals in the wild type (left) but not in the $TAAR1^{LacZ/LacZ}$ mice (right).

Examples

Commercially available reagents referred to in the examples were used according to manufacturer's instructions unless otherwise indicated.

5 Example 1:

1) Strategy for gene replacement of the TAAR1 coding sequence by a synthetic NLS-lacZ coding sequence

To target TAAR1 in mouse embryonic stem cells (ES-cells) a gene-targeting vector was constructed and used to generate C57BL/6 mice with a deficiency of TAAR1. The
10 gene-targeting vector completely replaces the TAAR1 coding region as well as about 1,5 kb genomic sequence downstream of the coding sequence with a synthetic NLS-lacZ-PGK-Neo cassette.

It is a replacement type gene targeting vector allowing for positive selection of homogenously recombined ES-cells using the Neomycin-phosphotransferase-gene (Neo)
15 expressed under the control of the phosphoglycerate kinase promoter (PGK) (Galceran J, Miyashita-Lin E.M., Devaney E, Rubenstein J.L.R., Grosschedl R., Development 127 (2000): 469-482). To permit negative selection against ES clones carrying the targeting vector randomly integrated into the genome a diphtheria-toxin gene has been inserted into the vector outside of the TAAR1 genomic sequence (as described in Gabernet L.,
20 Pauly-Evers M., Schwerdel C., Lentz M., Bluethmann H., Vogt K., Alberati D., Mohler H., Boison D. Neurosci Lett. 373 (2005): 79-84).

At the same time the lacZ reporter-gene (Galceran J, Miyashita-Lin E.M., Devaney E, Rubenstein J.L.R., Grosschedl R., Development 127 (2000): 469-482) was fused to a nuclear signal sequence (NLS) and placed under the transcriptional control of the
25 putative TAAR1 promoter and regulatory elements. Hereby the start-codon of the synthetic reporter is identical to the start-codon of TAAR1. This allows the sensitive analysis of the expression pattern conferred by the endogenous TAAR1 control region in histochemical stainings for the product of the lacZ gene.

2) Cloning of a plasmid for targeting of the NLS-lacZ coding sequence to the TAAR1 gene by homologous recombination in ES-cells

2.1) Construction of the TAAR1 gene targeting vector

The resulting targeting vector consists of a genomic 5' arm (5'arm), the NLS-lacZ reporter-gene, a PGK-Neo resistance cassette and a 3' genomic arm. The Diphtheria toxin cassette (Dipht.) is placed at the 3' side of the targeting vector (see Fig. 1).

Oligonucleotides were designed based on the published genomic sequences of the mouse TAAR1 locus (Mouse genome sequence database, NCBI draft 34, May 2005) and obtained from a commercial supplier (Microsynth AG, Balgach, Switzerland). All molecular cloning techniques were carried out essentially according to Sambrook et. al. (Molecular Cloning: A laboratory manual. 1989, Cold Spring Harbor Laboratory Press, Cold Spring Harbor.) and the instructions of the suppliers of kits and enzymes.

The targeting vector pSKDT-Tar1-NLS-lacZ-PGK-Neo contains 4,0 kb genomic sequence 5' of the mouse TAAR1 coding sequence and 1,7kb genomic sequence 3' of the mouse TAAR1 coding sequence (Fig. 1).

These sequences were amplified from genomic C57BL/6 DNA using proofreading PCR and cloned into cloning vectors.

To clone the 5' arm oligonucleotide mTar1- 5'-KpnI-16c and oligonucleotide mTar1-755-nc were used in the following PCR reaction.

2 ng/ μ l genomic C57BL/6 DNA, 200 μ M dNTPs (PCR Nucleotide Mix, Roche Diagnostics, Mannheim, Germany), 0,5 μ M of each oligonucleotide, 1x PCR buffer (Promega, Madison, WI, USA), 0,06 U/ μ l Pfu Polymerase (Promega, Madison, WI, USA) in a total volume of 100 μ l were incubated with the following protocol: 95°C 2 min., 35 $\times$ (95°C 45 sec., 59°C 45 sec., 72°C 9 min.), 72°C 7 min, ∞ 4°C on a PCR Thermocycler MJ Research PTC-200 (MJ Research Inc., Watertown, USA). The resulting PCR product of 4,702kb contained the 5' arm of the TAAR1 locus and was cloned into the SrfI site of pPCR-Script Amp SK+ (Invitrogen-Gibco, Carlsbad, CA, USA).

Orientation and parts of the sequence were confirmed by sequencing using the BigDye Terminator v1.1 Cycle Sequencing Kit (Applied Biosystems) and an ABIPrism 310 Genetic Analyzer.

The resulting vector is pPCR-Script-5'Tar1.

To clone the 3' arm oligonucleotide mTar1-33c and oligonucleotide mTar1-SmaI-11nc were used in the following PCR reaction.

2ng/ μ l genomic C57BL/6 DNA, 200 μ M dNTPs (PCR Nucleotide Mix, Roche Diagnostics, Mannheim, Germany), 0,5 μ M of each oligonucleotide, 1x PCR buffer
5 (Promega, Madison, WI,USA), 0,06 U/ μ l Pfu Polymerase (Promega, Madison, WI,USA) in a total volume of 100 μ l were incubated with the following protocol: 95°C 2 min., 35 $\times$ (95°C 45 sec., 60°C 45 sec., 72°C 4 min.), 72°C 7 min, ∞ 4°C on a PCR Thermocycler MJ Research PTC-200 (MJ Research Inc., Watertown, USA).

The resulting PCR product of 1651kb was cloned into the SrfI site of pPCR-Script
10 Amp SK+ (Invitrogen-Gibco, Carlsbad, CA, USA).

Orientation and parts of the sequence were confirmed by sequencing using the BigDye Terminator v1.1 Cycle Sequencing Kit (Applied Biosystems) and an ABIPrism 310 Genetic Analyzer.

The resulting vector is pPCR-Script-3'Tar1.

15

The targeting vector was assembled in 3 steps.

Step 1: The 3' genomic arm and 5' genomic arm cloned as described above were assembled into the plasmid backbone pSK (Stratagene, La Jolla, CA, USA) which contains a diphtheria toxin cassette as described in Gabernet *et al.* (Enhancement of the NMDA
20 receptor function by reduction of glycine transporter-1 expression. Neurosci Lett. 373 (2005): 79-84). To this end, the 3' genomic arm was removed from the plasmid pPCR-Script-3'Tar1 by restriction digest with ClaI and NotI, and the resulting 1.7 kb genomic fragment was purified by agarose gel electrophoresis and gel extraction. Thereafter, the 1.7 kb genomic DNA fragment was ligated into the plasmid pSK, which previously had
25 been digested with ClaI and NotI. The resulting plasmid was called pSKDT-3'Tar1.

Subsequently, the 5' genomic arm cloned as described above was removed from the plasmid pPCR-Script-5'Tar1 by restriction digest with NsiI and KpnI and subsequent agarose gel electrophoresis and gel extraction. Following, the 4 kb genomic DNA fragment was ligated into the plasmid pSKDT-3'Tar1, which previously had been digested
30 with NsiI and KpnI, resulting in the plasmid pSKDT-5'-3'Tar1

Step2: A synthetic sequence harboring several restriction sites (see Fig. 2) as well as a NLS sequence was inserted into the plasmid pSKDT-5'-3'Tar1. To this end, the 5' phosphorylated oligonucleotides mTar1-29cA and mTar1-29cB were annealed. Plasmid

pSKDT-5'-3'Tar1 was digested with NsiI, and the annealed oligonucleotides were ligated into this plasmid, resulting in the plasmid pSKDT-5'-3'Tar1-NLS.

Step3: The NLS-lacZ-PGK-Neo cassette was inserted into the plasmid pSKDT-5'-3'Tar1-NLS. For this purpose plasmid pSKDT-5'-3'Tar1-NLS was linearized with a StuI restriction digest. The NLS-lacZ-PGK-Neo cassette was isolated from the plasmid C8 β gal (Galceran J, Miyashita-Lin E.M., Devaney E, Rubenstein J.L.R., Grosschedl R. Hippocampus development and generation of dentate gyrus granule cells is regulated by LEF1. Development 127 (2000): 469-482) with a SmaI restriction digest and subsequent agarose gel electrophoresis and gel extraction. The NLS-lacZ-PGK-Neo cassette DNA fragment was ligated into the StuI linearized plasmid pSKDT-5'-3'Tar1-NLS, resulting in the targeting vector pSKDT-Tar1-NLS-lacZ-PGK-Neo.

Deposition data: The plasmid pSKDT-Tar1-NLS-lacZ-PGK-Neo comprising the genetic construct TAAR1-KO (see Figure 1B) was deposited under the Budapest Treaty at the Deutsche Sammlung von Microorganismen und Zellkulturen GmbH (DSMZ), Mascheroder Weg 1 b, D-38124 Braunschweig, Germany, with an effective deposition date of 16.08.2005 under the accession number DSM 17504.

2.2) Gene targeting of the TAAR1 gene in mouse ES cells by homologous recombination

2.2.1) Culturing of C57BL/6 ES-cells

Handling of ES-cells was performed essentially as described in Joyner (Gene Targeting. 1999, Second Edition, The Practical Approach Series, Oxford University Press, New York). C57BL/6 ES-cells (Eurogentec, Seraing, Belgium) were grown on monolayers of mitotically inactivated primary mouse embryonic fibroblast (MEF) cells isolated from a mouse line CD1-Tg.neoR expressing the neomycin resistance gene (Stewart C.L., Schuetze S., Vanek M., Wagner E.F. Expression of retroviral vectors in transgenic mice obtained by embryo infection. EMBO J. 6 (1987): 383-8). MEFs were isolated as described in (Joyner, AL, eds.: Gene Targeting. A Practical Approach. 2000, Oxford University Press, New York) and mitotically inactivated by gamma radiation (18Sv in a Cs-137 irradiation source).

ES-cells were grown in ES-medium containing Dulbeccos's modified Eagle Medium (Invitrogen-Gibco, Carlsbad, CA, USA) supplemented with 15% FCS (Inotech/Biological Industries, Beit Haemek, Israel), 100 IU/ml Penicillin/Streptomycin (Invitrogen-Gibco,

Carlsbad, CA, USA), 0.5 mM β -Mercaptoethanol (Invitrogen-Gibco, Carlsbad, CA, USA), non essential amino acids MEM (1x, Invitrogen-Gibco, Carlsbad, CA, USA), 2 mM Glutamine (Invitrogen-Gibco, Carlsbad, CA, USA) and 1000 U/ml leukocyte inhibitory factor (Chemicon, Temecula, CA, USA).

5

2.2.2) Electroporation of the targeting vector into ES-cells

The SacII linearized targeting vector pSKDT-Tar1-NLS-lacZ-PGK-Neo (total amount: 30 μ g) was added to 30x10⁶ ES-cells in a buffer containing 137 mM NaCl, 2.7 mM KCl, 90 mM Na₂HPO₄, 1.5 mM KH₂PO₄, pH 7.4 (PBS) and electroporated with a
10 Bio-Rad Genepulzer with a capacity extender (Bio-Rad, Hercules, CA, USA; settings: 280 V, 500 μ F). Thereafter, ES-cells were plated on MEF mono cell layers and selected for the presence of the Neomycin gene in ES-medium supplemented with 350 μ g/ml G418 (geneticin, Sigma-Aldrich, St. Louis, MO, USA).

Individual, well separated ES-clones originating from the transfected cells were
15 transferred into 48 well culture dishes and grown for 10 days. 1/3 of the cells were used to isolate genomic DNA using the MagNAPure LC system (Roche Diagnostics, Basel, Switzerland; Laird, P.W., Zijderveld, A., Linders, K., Rudnicki, M.A., Jaenisch, R., Berns, A.: Simplified mammalian DNA isolation procedure. *Nucleic Acids Res.* 1991; 19 (15): 4293) and analyzed using PCR. The remaining 2/3 of the cells were eventually used for
20 further analysis and for blastocyst injections.

2.2.3) Screening of monoclonal ES-cells with PCR for correct targeting of TAAR1

In 62 clones the correct gene targeting event was assessed by PCR amplification of DNA fragments spanning the transition points between the genomic DNA included into
25 the targeting vector and surrounding genomic sequence.

To test for correct recombination at the 3' arm PCR clones were screened with PCRs using oligonucleotides IL4-neo and mTar26nc in the following protocol:

20-100 ng genomic DNA, 1x concentrated PCR buffer 3 (part of Expand High Fidelity PCR System; Roche Diagnostics, Mannheim, Germany), 500 μ M of each dNTP
30 (PCR Nucleotide Mix, Roche Diagnostics, Mannheim, Germany), 500 nM of each oligonucleotide (Microsynth AG) and 3.75 U/reaction Expand High Fidelity Enzyme Mix

(part of Expand High Fidelity PCR System; Roche Diagnostics). The PCR reactions were run with the following temperature protocol:

94°C 2min., 33× (94°C 15 sec., 62°C 30 sec., 68°C 3,5 min.), 68°C 20 min, ∞ 12°C

5 This PCR yields PCR products only in the presence of genomic DNA of ES-clones, in which the correct homologous recombination event between the 3' arm of the targeting vector and the chromosomal DNA as depicted in Fig. 1 has occurred. As negative control wildtype DNA (Fig. 3, Lane 6) as well as several ES-clones in which no homologous recombination has occurred (Fig. 3, Lane 3-5) were included into the analysis.

10 Importantly clone IIB1 gives amplification at the expected size of 3.2kb (Fig. 3., Lane 2).

To test for correct recombination at the 5' arm PCR clones were screened with PCRs using oligonucleotides IL4-rev and mTar24c in the following protocol:

15 20-100 ng genomic DNA, 1× concentrated PCR buffer 3 (part of Expand High Fidelity PCR System; Roche Diagnostics, Mannheim, Germany), 500 µM of each dNTP (PCR nucleotide Mix, Roche Diagnostics, Mannheim, Germany), 500 nM of each oligonucleotide (Microsynth AG) and 3.75 U/reaction Expand High Fidelity Enzyme Mix (part of Expand High Fidelity PCR System; Roche Diagnostics). The PCR reactions were run with the following temperature protocol:

20 94°C 2min., 33× (94°C 15 sec., 64°C 30 sec., 68°C 12 min.), 68°C 20 min, ∞ 12°C

25 This PCR yields PCR products only in the presence of genomic DNA of ES clones, in which the correct homologous recombination event between the 5' arm of the targeting vector and chromosomal DNA as depicted in Fig. 1 has occurred. As negative control wildtype DNA (Fig. 4, Lane 6) as well as several ES clones in which no homologous recombination has occurred (Fig. 4, Lane 3-5) were included into the analysis.

The above PCR conducted with genomic DNA of Clone IIB1 gives an amplification at the expected size of 9.8kb (Fig. 4, Lane 2, arrow).

Clone IIB1 was chosen for injection into blastocysts as described in chapter 3.

30 Following Oligonucleotides (all sequences in 5'→3' orientation) were used:

Name	Sequence	SEQ. ID NO:
mTar1-5'-KpnI-16c	CGGGTACCTGTCACTCACCGGCATTTCGG	10
mTar1-755-nc	CCTTGCTTGTCTTTAGCTATG	11
mTar1-33c	CCCATGTGACCAATTTGTTACAC	12
mTar1-3'-SmaI-11nc	CTGCTGCCCCGGGATTCAAGCTCTTCTTGACTCTGG	13
mTar1-29cA	TCCAAAGAAGAAGAGAAAGGTTTCGGAGGCCTATGCA	14
mTar1-30ncB	TTGGCCTCCGAAACCTTTCTCTTCTTTGGATGCA	15
IL4-neo	GCGCATCGCCTTCTATCGCC	16
mTar1-26nc	GAGCTTCACACATGAACACACC	17
mTar1-24c	GTGGGCTAAGATCTAGGAACG	18
IL4-rev	GGCGATAGAAGGCGATGCGC	19

3) Generation of a TAAR1 – NLSlacZ knock-in mouse line from a mutant ES cell line

- 5 All handling of animals was carried out in compliance with Swiss Federal and Cantonal laws on animal research, and permission for the generation and handling of the mutant mouse line was specifically granted from the Kantonale Veterinäräm of Basel City with the Tierversuchgenehmigung No. 2055 as of August 23rd 2004.

- 10 A mutant mouse line which carries an inheritable targeted mutation of the TAAR1 gene as described in chapter 1) in all cells was generated following standard procedures essentially as described in Hogan et al. (Manipulating the mouse embryo. 1994, Second Edition, Cold Spring Harbor Press, Cold Spring Harbor.) by Polygene AG (Rümlang, Switzerland). For the generation of chimeric animals, the monoclonal mutant ES cells (clone IIB1, as described in chapter 2) were injected into embryonic day 3.5 – 4.5 (E3.5 – 4.5) Balb/c blastocysts and transferred into pseudo-pregnant C57BL/6 x CBA F1 females.
- 15 Offspring delivered by these females were judged for the degree of chimerism (i.e. the degree of overall contribution of ES cells to the chimeric animals). The employed breeding paradigm allowed to use the coat color as parameter for estimating the degree of chimerism, with the percentage of black hairs in the fur reflecting the degree of chimerism.

- 20 Male high percentage chimeras were naturally mated with C57BL/6 females, and all offspring with purely black coat color was analyzed for the presence of the TAAR1^{NLSlacZ}

allele. To this end, genomic DNA was isolated from tail biopsies of adult animals with a MagNAPure LC system for nucleic acid purification (Roche Applied Science, Rotkreuz, Switzerland) according to the instructions of the manufacturer and analyzed for the presence of the TAAR1 wild type allele (TAAR1⁺; indicating the presence of the
5. undisrupted TAAR1 gene) as well as the neomycin phosphotransferase coding sequence (indicating the presence of the TAAR1^{NLSlacZ} allele) by means of PCR.

PCR reactions were performed on a GenAmp 9700 thermocycler (Applied Biosystems, Rotkreuz, Switzerland) in a total volume of 50 µl per reaction composed as follows (final concentrations/amounts):

10 20 - 100 ng genomic DNA, 20 mM Tris-HCl (pH8.4), 50 mM KCl, 1.5 mM MgCl₂, 200 nM of each oligonucleotide (Microsynth AG, Balgach, Switzerland), 200 mM of each dNTP (Amersham), 5 U/reaction recombinant Taq DNA polymerase (Invitrogen). The targeted or undisrupted TAAR1 alleles were detected simultaneously in the same PCR reaction by the following oligonucleotides:

15 TAAR1⁺ allele:

TAAR1 31c: 5'-gaaggtggaattctaactgac-3' (SEQ. ID NO: 20)

TAAR1 D8: 5'-ccttgctgtccttagctatg-3' (SEQ. ID NO: 21)

TAAR1^{NLSlacZ} allele:

NEO U1: 5'-cttgggtggagaggctattc-3' (SEQ. ID NO: 22)

20 Neo D1: 5'-aggtgagatgacaggagatc-3' (SEQ. ID NO: 23)

The PCR reactions were run with the following temperature profile: 95°C 2min., 35× (95°C 30 sec., 57°C 30 sec., 72°C 1 min.), 72°C 5 min, ∞ 4°C. The PCR products were analyzed by standard agarose gel electrophoresis as described in Sambrook et al. (Molecular Cloning: A laboratory manual. 1989, Cold Spring Harbor Laboratory Press,
25 Cold Spring Harbor.), and the expected DNA fragment sizes were 755 bp for the undisrupted TAAR1 allele and 280 bp for the TAAR1^{NLSlacZ} allele.

4) Characterization of the TAAR1 – NLSlacZ knock-out

4.1) Analysis of the TAAR1 – NLSlacZ gene replacement inherited in the TAAR1 – NLSlacZ knock-out mouse line

30 In order to proof that the TAAR1^{NLSlacZ} allele equals the designed mutant gene as described in 2 the targeted gene locus was analyzed based on genomic DNA derived from homozygous mutants of the F2 generation. The correct gene targeting event was verified by PCR amplification and DNA sequence analysis of DNA fragments spanning the

transition points between the genomic DNA included into the targeting vector and surrounding genomic sequence (see Figure 7).

The DNA fragments 1-4 (see Fig. 7) were amplified by PCR from genomic DNA as
5 template. The genomic DNA was extracted with a MagNAPure LC system for nucleic acid
purification (Roche Diagnostics, Basel, Switzerland) from tail biopsies of adult animals
carrying either two TAAR1⁺ alleles (genotype: TAAR1^{+/+}) or two TAAR1^{NLSlacZ} alleles
(genotype: TAAR1^{NLSlacZ/NLSlacZ}). PCR reactions were performed on a GenAmp 9700
thermocycler (Applied Biosystems, Rotkreuz, Switzerland) in a total volume of 50 µl per
10 reaction composed as follows (final concentrations/amounts):

20 - 100 ng genomic DNA, 1× concentrated PCR buffer 3 (part of Expand High
Fidelity PCR System; Roche Diagnostics, Mannheim, Germany), 500 µM of each dNTP
(Amersham), 300 nM of each oligonucleotide (Microsynth AG) and 3.75 U/reaction
Expand High Fidelity Enzyme Mix (part of Expand High Fidelity PCR System; Roche
15 Diagnostics). The PCR reactions were run using the combinations of genomic DNA
template, oligonucleotide and PCR protocols as summarized in Table 1.

The PCR reactions were run with one of the following temperature protocols:

Protocol 5.1.1:

94°C 2min., 35× (94°C 15 sec., 62°C 30 sec., 68°C 10 min.), 68°C 20 min, ∞ 4°C

20 Protocol 5.1.2:

94°C 2min., 35× (94°C 15 sec., 63°C 30 sec., 68°C 10 min.), 68°C 20 min, ∞ 4°C

Protocol 5.1.3:

94°C 2min., 35× (94°C 15 sec., 62°C 30 sec., 68°C 3.5 min.), 68°C 20 min, ∞ 4°C

25 The PCR products were analyzed by standard agarose gel electrophoresis (Fig. 8) as
described in Sambrook et al. (Molecular Cloning: A laboratory manual. 1989, Cold
Spring Harbor Laboratory Press, Cold Spring Harbor.). The size and partial sequence
proves the expected identity of the DNA fragments and provides evidence that the
homologous recombination of the targeting vector with the chromosomal TAAR1 gene
30 locus occurred in a precise manner for the 5' as well as the 3' genomic arm of the
targeting vector. The DNA sequencing results summarized in listing 1-9 proves
furthermore, that the homologous recombination occurred without undesired side events
such as the chromosomal integration of tandem repeats of the vector constructs or parts

thereof or a loss of the NLSlacZ coding sequence included in the targeting vector. In addition, the DNA sequence analysis of DNA fragments 1 – 3 (listing 1, 4 and 5) demonstrates that the NLSlacZ coding sequence was targeted to the *TAAR1* gene locus such that the NLSlacZ open reading frame starts with the endogenous start codon of the *TAAR1* gene and that the structure of the surrounding genomic sequence including putative promotor and other elements involved in transcriptional regulation of the *TAAR1* gene from the *TAAR1*⁺ allele is preserved in the *TAAR1*^{NLSlacZ} allele. Consequently, the NLSlacZ transcript shall be expressed from the *TAAR1*^{NLSlacZ} allele with the same spatio-temporal profile as the *TAAR1* transcript from the *TAAR1*⁺ allele, and NLSlacZ expression in animals carrying the mutant allele shall reflect the endogenous expression profile of *TAAR1* in wild type animals. An example for the use of the NLSlacZ expression from the *TAAR1*^{NLSlacZ} allele as tool for analyzing the *TAAR1* expression will be provided below.

For DNA sequence analysis DNA fragments 1-4 were amplified from genomic DNA by PCR and subjected to agarose gel electrophoresis as described above. PCR products of the expected sizes were cut out from the gels with sterile scalpels (Bayha, Tuttlingen, Germany) and extracted from the agarose gel slices using the QIAquick Gel Extraction Kit (QIAGEN AG, Basel, Switzerland) following the instructions of the manufacturer. The extracted PCR products were adjusted to a defined concentration with cold ethanol/sodium acetate DNA precipitation (Sambrook, J., Fritsch, E.F., und Maniatis, T.: Molecular Cloning: A laboratory manual. 1989, Cold Spring Harbor Laboratory Press, Cold Spring Harbor.) and subsequently dissolving the DNA pellets in the required volume of 10 mM Tris/HCl pH 7.5. DNA sequence analysis of the PCR products was carried out at Microsynth AG employing BigDye chemistry and a 3730 capillary DNA analyzer (Applied Biosystems), and the oligonucleotides used for the individual sequence analysis reactions as well the sequence analysis results are summarized in listing 1-9 (see below). The sequence listings are limited to those parts of the sequence analysis results which were judged as reliable based on the chromatograms.

PCR reaction	Oligonucleotide combination	Template <i>TAAR1</i> ^{+/+} genomic DNA	Template <i>TAAR1</i> ^{NLSlacZ} genomic DNA
PCR protocol 5.1.1	mTAR31c (5'-gaaggtggaattctaactgac-3') mTAR32nc (5'-ctcatgtgaatcagtagcacag-3')	<ul style="list-style-type: none"> • PCR product: DNA fragment 1 (2.72 kb, see Fig. 7 & 8) • DNA sequence analysis (listing 1) fits expected sequence 	<ul style="list-style-type: none"> • PCR product: DNA fragment 3 (5.05 kb; see Fig. 7 & 8) • DNA sequence analysis (listing 2) fits expected sequence
PCR protocol 5.1.2	mTAR24c (5'-gtgggctaagatctaggaacg-3') lacZ10 (5'-ggaacaggtattcgctgtgcac-3')	<ul style="list-style-type: none"> • No PCR product (as expected, see Fig. 7 & 8) 	<ul style="list-style-type: none"> • PCR product: DNA fragment 2 (7.33 kb; see Fig. 7 & 8) • Sequence analysis (listing 2-4) fits expected sequence

PCR protocol 5.1.3	PGK1 (5'- gtgggctctatggctctgag-3') mTAR25nc (5'- aggtccaactctgtgtgatgg-3')	• No PCR product (as expected, see Fig. 7 & 8)	• PCR product: DNA fragment 4 (2.86 kb; see Fig. 7 & 8) • Sequence analysis (listing 7- 9) fits expected sequence
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Table 1: PCR amplification of DNA fragments 1-4 (see Fig. 7) from genomic DNA derived from tail biopsies of TAAR1^{+/+} and TAAR1^{NLSlacZ/NLSlacZ} mice. The obtained pattern of PCR products supported by the results of partial DNA sequence analysis of the DNA fragments confirms the correct targeting of the TAAR1 gene in the TAAR1^{NLSlacZ} allele.

Listing 1 (SEQ. ID NO: 1): Result of DNA sequence analysis of DNA fragment 1 (Fig. 7/ Table 1) with oligonucleotide mTAR31c (Table 1)

```

10      1 GAGGGAAAGC CCAGCCTGTG TCTAGTTCTC TGCAGTGATG CATCTTTGCC
      51 ACCTATCAC AAACATTTCC CACAGAAACA GCGACTGGTC AAGAGAAGTC
101 CAAGCTTCCC TGTACAGCTT AATGTCACTC ATAATCCTGG CCACTCTGGT
151 TGGCAACTTA ATAGTAATAA TTTCCATATC CCATTTCAAG CAACTTCATA
201 CACCCACCAA CTGGCTCCTT CACTCCATGG CCATTGTCTGA CTTTCTGCTG
251 GGCTGTCTGA TAATGCCCTG CAGCATGGTG AGAACTGTTG AGCGCTGTTG
15      301 GTATTTTGGG GAAATCCTCT GTAAAGTTCA CACCAGCACC GATATCATGC
351 TGAGCTCCGC CTCATTTTTC CACTTAGCTT TCATTTCCAT TGACCGCTAC
401 TGTGCTGTGT GTGACCCTTT GAGATACAAA GCCAAGATCA ATATCTCCAC
451 TATTCTTGTG ATGATCCTCG TTAGTTGGAG CCTTCTGCT GTTTATGCAT
501 TTGGGATGAT CTTCTGGAA CTGAACCTAA AAGGAGTGGA AGAGCT
20

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Listing 2 (SEQ. ID NO: 2): Result of DNA sequence analysis of DNA fragment 2 (Fig. 7/ Table 1) with oligonucleotide mTAR24c (Table 1)

```

25      1 GACATTTTAT TTACAGGCAC AGAGTCTCCT GGACAGGCTG GTGAAGGTGA
      51 ACTCTGATTC AAAGACCGTG TGAGGGGTAT CCACCAGAGA AGACCGCTGG
101 GACCAGGGCT TAAGTCTTTA TTAGCAGGTC GGTGTCTACA CTGGGTGTTT
151 GGGATCCCAG TGTAGTCCCG AGCCTTTCTT TGAGCCTTTA AGCACAAAAA
201 AAAACCAAAA AACTAGTTTC AGGGTTGACA TACTTCAGTT ACCAAGAACA
251 GTTAGCCAGA AGTGGAACCTA TAAAGCCAA ATAGTAAGGT TAATACATTT
30      301 GGAAACTTTC CCAGGCCTTT GATGGATTAG GTCTGTGTTT TAGTTTGGC
351 AGCCAGTGCT ATGTGCTGAG TTTGGCAGCC TGAGTGATGT GTCTATCATG
401 GAGTCCATCA TGCTAAGGTG TCAGGGTCTA CTAAAGTCTG TGGGGCTGTT
451 ACAAGGCCAT ATTATGTAA AACCTACACA AACGTGCCAT TCTATAAAAG
501 ACGGTTACAT AACAGGTATA TCATGATTTA CTTTCGGGTT CTCTAGATAT
551 CTGGTGTCTG TCATTTTGTG CTGACTCATG GTGGTCCTGA AAAAGTATAA
35      601 CGTAAAAGCA AAATCTAGG CTTTATAGCC CAGGCTTGAG AATGTGACCT
651 CTGTGACTCA ATGCTCCAAG GTATGCTAAT CATAAAACAG ATAGCGACAT
701 TCCTCCACCC ACCCTCTTCC TGGGTTCAAG GAGTGTTTCT TT

```

Listing 3 (SEQ. ID NO:3): Result of DNA sequence analysis of DNA fragment 2 (Fig. 7/ Table 1) with oligonucleotide mTAR39c (5'- cactcttacatccagccttagc-3')

```

1 TGTCTTCTC TAAGAGCCTG TCACTCACCG GCATTCGGCA ACCTTCATCG
51 TTGTTGGTTT GTAAACAAGT GTGGGGATGC TCTTTGACAT TTTCATTTCT
101 ATAATGTTTA GTACGTTTAC TGTCCATCAG ATCAGTATGA TATTTAGTCA

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151 CGATTTCATT ATTCGCTTTT GTACTTTCCT GGAGAAATTA AAACACCACA
201 TACCATTTCT TTAGACCATT CACATTTATC TTCTTAGTTA GTGTGCTTTA
251 TCTGTTTTTG GCTTTAGATT TTCATTTCTC TGTCTCCACA GTCCTTCTCT
301 ATTTGACTTG GCTTCTGTCT GCTGTCATTC CACATTGCTA ATGGTGTFTT
5 351 AATGTTTCTT GGCAACACAT CTCAGGAGCA CGGGATTGG AGCATCTCTA
401 AGATTCTGCT ATCGGGGTCT CTTCAGTAGA TTCTCTTTCA CTGACAAAGC
451 TTACTGTCAG TGCTTGAGAG CTCACTCCAC ACTTGGTTGT TACACATGCA
501 GCTCTCCCGT AATTGCATTT GTATTTTAAG GCAGAACTTG TTGCAATTAT
551 TGAAACACAA TTCTCTTTGA TTTGCATAGA ATTAATTATT TGGTTTTGTT
10 601 TAGAACCCAG TTCTCAACAT CTTAATTTTC CTGTCTTCTT CAAGCAATAA
651 AGGACACATA GGTGTTGTAT CTTGTGATTC CTTGATTCTG AGAGACATCT
701 TTCACACTTA CACAAAGACA TTTCTTTGTT CTTTGTAAAT TATTCTTACA
751 TTTAACATTC TCTTGTTTTA AACAAGTTCC TTGTAGCTCT CTATGTTGTT
801 TCTTATTAAA TGAAAGGCTC AGCATTCCTG AGACATTAA GGCTATGTGA
15 851 CTCTGGGAAA ACACATTAAT TAA

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Listing 4: (SEQ. ID NO: 4) Result of DNA sequence analysis of DNA fragment 2 (Fig. 7/ Table 1) with oligonucleotide mTAR31c (Table 1)

```

1 GGGAAAGCCC AGCCTGTGTC TAGTTCTCTG CAGTGATGCA TCCAAAGAAG
20 51 AAGAGAAAGG TTTCGGAGGG GGGGAGCTTG ATGATCTGTG ACATGGCGGA
101 TCCCGTCGTT TTACAACGTC GTGACTGGGA AAACCCTGGC GTTACCCAAC
151 TTAATCGCCT TGCAGCACAT CCCCCTTTCG CCAGCTGGCG TAATAGCGAA
201 GAGGCCCGCA CCGATCGCCC TTCCCAACAG TTGCGCAGCC TGAATGGCGA
251 ATGGCGCTTT GCCTGGTTTC CGGCACCAGA AGCGGTGCCG GAAAGCTGGC
25 301 TGGAGTGCGA TCTTCCTGAG GCCGATACTG TCGTCGTCCC CTCAAACCTGG
351 CAGATGCACG GTTACGATGC GCCCATCTAC ACCAACGTGA CCTATCCCAT
401 TACGGTCAAT CCGCCGTTTG TTCCCACGGA GAATCCGACG GGTGTTACT
451 CGCTCACATT TAATGTTGAT GAAAGCTGGC TACAGGAAGG CCAGACGCGA
501 ATTATTTTTG ATGGCGTTAA CTCGGCGTTT CATCTGTGGT GCAACGG
30

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Listing 5 (SEQ. ID NO: 5): Result of DNA sequence analysis of DNA fragment 3 (Fig. 7/ Table 1) with oligonucleotide mTAR31c (Table 1)

```

1 GAGGGAAAGC CCAGCCTGTG TCTAGTTCTC TGCAGTGATG CATCCAAAGA
51 AGAAGAGAAA GGTTCGGAG GGGGGAGCT TGATGATCTG TGACATGGCG
35 101 GATCCCGTCG TTTTACAACG TCGTGACTGG GAAAACCCTG GCGTTACCCA
151 ACTTAATCGC CTTGCAGCAC ATCCCCCTTT CGCCAGCTGG CGTAATAGCG
201 AAGAGGCCCG CACCGATCGC CCTTCCCAAC AGTTGCGCAG CCTGAATGGC
251 GAATGGCGCT TTGCCTGGTT TCCGGCACC

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Listing 6 (SEQ. ID NO: 6): Result of DNA sequence analysis of DNA fragment 3 (Fig. 7/ Table 1). The listed sequence represents a contig assembled from sequence analyses of DNA fragment 3 with oligonucleotides mTAR32nc (Table 1) and IL4rev (5'-ggcgatagaaggcgatgcgc-3')

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1 TCATCTCCGG GCCTTTCGAC CTGCAGCCAA TATGGGATCG GCCATTGAAC
45 51 AAGATGGATT GCACGCAGGT TCTCCGCCCC CTTGGGTGGA GAGGCTATTC
101 GGCTATGACT GGGCACAACA GACAATCGGC TGCTCTGATG CCGCCGTGTT
151 CCGGCTGTCA GCGCAGGGGC GCCCGGTTCT TTTTGTCAAG ACCGACCTGT
201 CCGGTGCCCT GAATGAACTG CAGGACGAGG CAGCGCGGCT ATCGTGGCTG
251 GCCACGACGG GCGTTCCTTG CGCAGCTGTG CTGACGTTG TCACTGAAGC

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301 GGAAGGGAC TGGCTGCTAT TGGGCGAAGT GCCGGGGCAG GATCTCCTGT
351 CATCTCACCT TGCTCCTGCC GAGAAAGTAT CCATCATGGC TGATGCAATG
401 CGGCGGCTGC ATACGCTTGA TCCGGCTACC TGCCCATTCTG ACCACCAAGC
451 GAAACATCGC ATCGAGCGAG CACGTACTCG GATGGAAGCC GGTCTTGTCTG
5 501 ATCAGGATGA TCTGGACGAA GAGCATCAGG GGCTCGCGCC AGCCGAAGT
551 TTCGCCAGGC TCAAGGCGCG CATGCCCGAC GGCGATGATC TCGTCGTGAC
601 CCATGGCGAT GCCTGCTTGC CGAATATCAT GGTGGAAAAT GGCCGCTTTT
651 CTGGATTTCAT CGACTGTGGC CGGCTGGGTG TGGCGGACCG CTATCAGGAC
701 ATAGCGTTGG CTACCCGTGA TATTGCTGAA GAGCTTGGCG GCGAATGGGC
10 751 TGACCGCTTC CTCGTGCTTT ACGGTATCGC CGCTCCCGAT TCGCAGCGCA
801 TCGCCTTCTA TCGCCTTCTT GACGAGTTCT TCTGAGGGGA TCAATTCTCT
851 AGAGCTCGCT GATCAGCCTC GACTGTGCCT TCTAGTTGCC AGCCATCTGT
901 TGTTTGCCCC TCCCCCGTGC CTTCCCTTGAC CCTGGAAGGT GCCACTCCCA
951 CTGTCCTTTC CTAATAAAAT GAGGAAATTG CATCGCATG TCTGAGTAGG
15 1001 TGTCATTCTA TTCTGGGGGG TGGGGTGGGG CAGGACAGCA AGGGGGAGGA
1051 TTGGGAAGAC AATAGCAGGC ATGCTGGGGA TGCGGTGGGC TCTATGGCTT
1101 CTGAGGCGGA AAGAACCAGC TGGGGCTCGA TCCTCTAGAG TCGATCGACC
1151 TCGACCCCCC CTATGCATTT TTGGAGAATC ATCTATACTT TACAGTGAGT
1201 TTCTGTGGCT TTATTTATTT CAAGATCTTC CTTACAGATT ATT
20

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Listing 7 (SEQ. ID NO: 7): Result of DNA sequence analysis of DNA fragment 4 (Fig. 7/ Table 1) with oligonucleotide PGK1 (Table 1)

```

1 CGATCGACCT CGACCCCCCC TATGCATTTT TGGAGAATCA TCTATACTTT
51 ACAGTGAGTT TCTGTGGCTT TATTTATTTT AAGATCTTCC TTACAGATTA
25 101 TTTCCAGATG TTGTATAAAT CTTTAAATAA CTGTGGTACT GATTACATG
151 AGAAAAAAGG CTCTAGAAAT GAAGAGCCCA AGATCCAGAA ATAAGTGTCT
201 GGGTTTATGA GCAGTTGTGT AGCTGTGTGA TCAGAGGTTG ATTATGTACA
251 GTCTAAGGGG AGTAGCTGAG TGAAAAGGAA AAAGACTAGT TTTTAATGTA
301 ACCATTATTG CCACTATTAT ATATGTTATA TAAACAAGGT TATGTATAAA
30 351 CAATAAAGTT TATATTATAT TTTCACCTGT TTTGTTTCTT GTTTTATAAT
401 ATATAGGCAT ATTAACTTTT ACATTGTTTT AACTTTTTTT AAATAATTGC
451 TATTATTTTT TTGAGACAGG GTCCTAGTAT ATAGCTTGAC TAGCCCAGAA
501 GTCTCTGTGA AGACTAGGAT GGTCTCAGAC TCAGAGAGAT TTGCCTGCCC
551 CTGCTGCCCC AGTGCTGAGA TTAAAGTATT TAGTCATTAA GGTGTGTATA
35 601 TACATTATGT CTAGCCATTG AGGTTTTTAT ATTACCACA TCCAGATGTT
651 AAGGTTTCTA GGCACACATC CATTCTTAC TCTATTAGTC AGAATTTCTA
701 GAACAATACT GATATTAAGG ATGGATCTTA TTACTTGG

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Listing 8 (SEQ. ID NO: 8): Result of DNA sequence analysis of DNA fragment 4 (Fig. 3/ Table 1) with oligonucleotide mTAR1D11 (5'- atagggaacttttgggatagc-3')

```

1 CCTACCTCTG GCCTCTGGCC TTTCCCTTTA ACTCCACAGA TAAGTGCATA
51 AGCTCCTTTA AAAATTTT CAG AAGATTTTTT TTCCAGAATC TTTATAAATG
101 TAAGCAGGCA GTGATCCTTC ACATTATCAT TAGGAGGGAC TAGCCAAAGG
151 GTGTAGAGTT CCAGTTTGCA CAAGGGCTAA GGTCATGGTC AGACAGCTCC
45 201 CTCTATGTCC ATTTCCAATG TGAGTTACGA AACTTCTTAC CAAGTTCATG
251 AGTTCCAGAC AGCCTTCCAA GAAAAGTTTT TAGTTACATC AATGGAAAAG
301 ATAGAATCTG GTTGTGCAA GAAAAACAGT TACAACAACA TCAATACTTA
351 TTTCTAAGTC AATTTGTGGC AAAAATAATT TCATTTTCGA GGTCTACTG
401 AAAATATTCA TATAAATGTT CATTTTCATAT CAAGTAGTAA TGTGTTGGTC
50 451 AGGACTTTTT TGTGGAAATG GATTATTAAC AACGGTGCTT TCTTAAGAGG
501 TTAGTGAGCT AGGAGGTTC ATCATGATTT TAGACTATAT CTGGAAGTCA
551 ACAATCCAGT CTTGGCAAAC TCACACATAT TTGTCAGAAA GTAGGACAAA

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601GTGGGTAATC TCCAATCCAC TGAGAATTTT GGTAAGTCAC AGTTTCTGCT
651TAGCTGAACC AGAGTCAAGA AGAGCTTGAA TATTAAGGGT AGAAAGATGC
701ATGAAGAATG GTGGATTGG TTTTCTAAA ACAGTTTGCT TTGAATATTT
751 ATTTTAGTTA TTTTGGGG GGAGGAAAGT TTATTTAGCT TACACT
```

5

Listing 9 (SEQ. ID NO: 9): Result of DNA sequence analysis of DNA fragment 4 (Fig. 7/ Table 1) with oligonucleotide mTAR25nc (Table 1)

```
1 GGCATTCCCC TGTACTGGGG CATATAAAGT TTGCAATACC AAAGGTCCTC
51 TCCTCCCAGT GATGGCCGAT TAGGCCATCT TCTGCTACAT ATGCAGCTAG
10 101 AGATATGAAG TCATTAGATA TGCACCTACT GATAAGTGGA TATTAGCCCA
151 GAAACATAGA ACACCCAAGA TACAATTTGC AAAACACAAG AAAATCAAGA
201 AGAAGGAAGA CCAATGGATG GATACTTCAT TCCTCCTTAG AATAGGGAAC
251 AAAATACCCA TGAAAGGAGT TACAGAGACA AAGTTTGGAG CTAAGACAAA
301 AGGATGGACT ATCCAGAGAC TAGCCCTCCC AGGGATCCAT CCCATAATCA
15 351 GCCACCAAAC CTAGACACTA TTGCATATGC CAGAAAGATT TTGCTGAAGG
401 GACCCTGTTA TAGCTGTCTC GTATGAGGCT ATGCCAGTGC CTGGCAAACA
451 CAGAAGTGGA TGCTCACAGT CATCTATAAG ATGGAACCTA GGGCCCCCAA
501 TGGAGGAGCA AGAGAAAGCA CCCAAGAAGA TGAAGGGGTC TGCAACCCTA
551 TAGGTGGAAC AACAATATGA ACTAACCAGT ACCCCAGAG CTCATATCTC
20 601 TAGCTGCATA TATTAGTTAT TTAAAGTTG TGTGTGCATG CATGTGTGTG
651 CACGTGGGAA CAGAAGTGTG GGTGCCAGTA GAGGAATTC AATCCCTTGC
701 AGCTAGAATT ACAGGGAGAC TTGAATTGCC CACAAGATTG CTGGGAACCTG
751 ACTCTGGGTC CTCAGTAAGA GCTGCATTT
```

25 In order to confirm the successful gene replacement on the transcript level cDNA derived from whole brains of juvenile TAAR1^{+/+} or TAAR1^{NLSlacZ/NLSlacZ} mice were prepared as described below.

RNA was prepared from tissue samples essentially according to Chomczynski and Sacchi (Single-step method of RNA isolation by acid guanidinium thiocyanate-phenol-
30 chloroform extraction, Anal. Biochem. 162 (1987) 156-159.). In brief, mouse pups of day 11 after birth were sacrificed, and total brains were removed and homogenized in the 10× volume of Trizol Reagent (Invitrogen, Paisley, UK) in a glass douncer (Inotech AG, Dottikon, Switzerland). Total RNA was isolated according to the instructions of the manufacturer. Raw RNA was dissolved in 10 mM Tris/HCl pH 7.0 and treated with 25
35 U/μl DNase I (Roche Diagnostics, Rotkreuz, Switzerland) in 10 mM Tris/HCl pH 7.0 with 10 mM MgCl₂ for 1 hr. The DNase I was removed by phenol/chloroform extraction according to (Sambrook, J., Fritsch, E.F., und Maniatis, T.: Molecular Cloning: A laboratory manual. 1989, Cold Spring Harbor Laboratory Press, Cold Spring Harbor.). RNA was precipitated, dissolved to a final concentration of 1 mg/ml in 10 mM Tris/HCl
40 pH 7.0 and used for first strand synthesis.

For cDNA synthesis Superscript II RNase H⁻ Reverse Transcriptase (Invitrogen, Paisley, UK) was used according to the instructions of the manufacturer. Briefly, 4 μg total RNA were mixed with 1 μg oligo (dT)₁₂₋₁₈ (Invitrogen, Paisley, UK) in H₂O in a total

volume of 23 μ l, incubated at 70°C for 10 min. and chilled on ice. The following components were added on ice (final concentrations): 50 mM Tris-HCl (pH8.3), 75 mM KCl, 3 mM MgCl₂, 10 mM DTT, 0.5 mM of each dNTP (Amersham, Otelfingen, Switzerland), 1 U/ μ l RNase Out RNase inhibitor (Invitrogen) and 10 U/ μ l reverse transcriptase. The reaction was incubated for 1 hr at 42°C, stopped by incubation at 70°C for 10 min. and diluted to a total volume of 100 μ l with 10 mM Tris/HCl pH 7.0.

PCR amplification of transcripts was carried out essentially as described in 4, but with the following modifications: PCR reactions were carried out in a total volume of 50 μ l per reaction composed as follows (final concentrations/amounts): 1 μ l of cDNA preparation (equivalent to a total amount of 40 ng whole brain total RNA), 20 mM Tris-HCl (pH8.4), 50 mM KCl, 1.5 mM MgCl₂, 200 nM of each oligonucleotide (Microsynth AG, Balgach, Switzerland), 200 mM of each dNTP (Amersham), 5 U/reaction recombinant Taq DNA polymerase (Invitrogen). For the detection of individual mRNA transcripts the following oligonucleotides and temperature profiles were used:

15 Glyceraldehyde-3-phosphate dehydrogenase (GAPDH):

Oligonucleotides:

GAPDH U: 5'-accacagtccatgccatcac-3' (SEQ. ID NO: 24);

GAPDH D: 5'-tccaccacctgttgctgta-3' (SEQ. ID NO: 25)

Temperature profile:

20 94°C 2min., 22 $\times$ (94°C 15 sec., 64°C 30 sec., 72°C 1 min.), 72°C 5 min, ∞ 4°C

TAAR1:

Oligonucleotides:

mTAAR1 U1: 5'-atgcatctttgccacgctatc-3' (SEQ. ID NO: 26);

mTAAR1 D2: 5'-caaggctcttctgaaccagg-3' (SEQ. ID NO: 27)

25 Temperature profile: 94°C 2min., 40 $\times$ (94°C 15 sec., 53°C 30 sec., 72°C 1 min.), 72°C 5 min, ∞ 4°C

NLSlacZ:

Oligonucleotides:

VN12taulacZ U1: 5'- ggtggcgctggatggtaa-3' (SEQ. ID NO: 28);

30 VN12taulacZ D1: 5'- cgccatttgaccactacc-3' (SEQ. ID NO: 29)

Temperature profile: 94°C 2min., 40 $\times$ (94°C 15 sec., 60°C 30 sec., 72°C 1 min.), 72°C 5 min, ∞ 4°C

As expected, the GAPDH transcript was detected in both cDNA preparations from TAAR1^{+/+} and TAAR1^{NLSlacZ/NLSlacZ} mouse brain indicating that the cDNA preparations per se were successful. While the PCR analysis detected TAAR1 transcript only in

35

TAAR1^{+/+}, but not in TAAR1^{NLSlacZ/NLSlacZ} mouse brain cDNA, the NLSlacZ transcript was detected only in TAAR1^{NLSlacZ/NLSlacZ}, but not in TAAR1^{+/+} mouse brain cDNA.

These data reveal that there is no TAAR1 expression in TAAR1^{NLSlacZ/NLSlacZ} mouse brain which is in agreement with the deletion of the TAAR1 coding sequence in the TAAR1^{NLSlacZ/NLSlacZ} mouse line. The presence of NLSlacZ mRNA transcript in TAAR1^{NLSlacZ/NLSlacZ} mouse brain provides evidence for the expression of NLSlacZ in TAAR1^{NLSlacZ/NLSlacZ} mutants from the endogenous TAAR1 gene locus. The absence of NLSlacZ transcript from TAAR1^{+/+} mouse brain as apparent from Fig. 9 C is in line with the fact that NLSlacZ does not naturally occur in mammalian species and supports the specificity of the PCR conditions.

PCR specific for transcript	cDNA used as PCR template	
	TAAR1 ^{+/+} brain cDNA	TAAR1 ^{NLSlacZ/NLSlacZ} brain cDNA
GAPDH	452 bp fragment	452 bp fragment
TAAR1	936 bp fragment	no PCR product
NLSlacZ	no PCR product	631 bp fragment

Table 2: Results of the analysis of cDNAs derived from TAAR1^{+/+} and TAAR1^{NLSlacZ/NLSlacZ} mouse brain for the presence of GAPDH, TAAR1 and NLSlacZ mRNA transcripts.

15

4.2) Analysis of the genetic background of the TAAR1 – NLSlacZ knock-in mouse line

The genetic background of genetically modified mouse lines has a profound impact on their phenotype, and the variability of the genetic background between individual animals of a mouse line caused e.g. by a so-called mixed genetic background can complicate or even make impossible the meaningful and consistent phenotypical characterization of a mutant mouse line or its use e.g. in behavioral pharmacology (Gerlai, R., Gene-targeting studies of mammalian behavior: is it the mutation or the background genotype? Trends Neurosci. 19 (1996) 177-181.; Bucan and Abel, The mouse: genetics meets behaviour. Nat. Rev. Genet. 3 (2002) 114-123; Banburry Conference on Genetic Background in Mice (1997): Mutant Mice and Neuroscience:

25

Recommendations Concerning Genetic Background. Neuron 19, 755-759). For historical and practical reasons, targeted mouse mutants are most frequently generated using ES cells derived from one of the various SV129 inbred mouse lines (Hogan, B., Beddington, R., Costantini, F., und Lacy, E.: Manipulating the mouse embryo. 1994, Second Edition, Cold Spring Harbor Press, Cold Spring Harbor.; Threadgill, D.W., Yee, D., Matin, A., Nadeau, J.H., Magnuson, T., Genealogy of the 129 inbred strains: 129/SvJ is a contaminated inbred strain. Mamm Genome. 8 (1997) 390-393). Because of the unfavorable properties of the SV129 mouse lines related to neuroanatomy, breeding performance and behavior mice generated using SV129 ES cells need to be transferred to a homogenous and more favorable genetic background by backcrossing with mice of the desired genetic background for at least 10 generations requiring several years of work (Silver, L.M.: Mouse Genetics. 1995, Oxford University Press, New York).

The use of ES cells derived from C57BL/6 mice (Kontgen, F., Suss, G., Stewart, C., Steinmetz, M., Bluethmann H., Targeted disruption of the MHC class II Aa gene in C57BL/6 mice. Int Immunol. 5 (1993) 957-964) in combination with an appropriate breeding scheme allowed us to generate a mutant mouse line carrying the TAAR1^{NLSlacZ} allele on a pure C57BL/6 genetic background. The homogeneity of the genetic background was experimentally confirmed by means of microsatellite analysis on 5 heterozygous mutants of the F1 generation as well as for the ES cell line used for the generation of germline chimeras.

For this analysis genomic DNA was isolated from tail biopsies of 5 mice of the F1 generation carrying the TAAR1^{NLSlacZ} allele, as well as from a sample of ES cells used for the generation of the germline chimeras, with the MagNAPure LC system for nucleic acid purification (Roche Diagnostics, Basel, Switzerland). Genomic DNA of congenic C57BL/6, DBA and SV129 mice were used as standard and were analyzed in parallel by PCR; the genomic DNA of the congenic inbred mouse strains C57BL/6, DBA and SV129 were purchased from Jackson Laboratory (Bar harbor, Maine, USA).

PCR reactions were performed on a GenAmp 9700 thermocycler (Applied Biosystems) in a total volume of 20 µl per reaction composed as follows (final concentrations/amounts):

10-20 ng genomic DNA, 67 mM Tris-HCl pH 8.8, 16.6 mM (NH₄)₂SO₄, 0.1 mg/ml BSA, 2 mM MgCl₂, 200 µM of each dNTP (Amersham), 200 nM of each oligonucleotide (Microsynth AG) and 1U/reaction Taq DNA polymerase (Invitrogen). All microsatellite PCR reactions were run with the following temperature profile:

94°C 2min., 35× (94°C 15 sec., 55°C 45 sec., 72°C 1 min.), 72°C 5 min, ∞ 4°C. PCR products were analyzed using an Elchrom electrophoresis unit (Elchrom Scientific AG, Cham, Switzerland).

For confirming the homogeneity of the genetic background of the mutant mouse line carrying the TAAR1^{NLSlacZ} allele a density of about 2 markers pro chromosome were used, and the following microsatellites were included into the analysis: D1MIT217, D1MIT291, D2MIT312, D2MIT285, D3MIT22, D3MIT45, D4MIT149, D4MIT166, D5MIT259, D5MIT95, D6MIT86, D6MIT188, D7MIT76, D7MIT246, D8MIT155, D8MIT248, D9MIT191, D9MIT182, D10MIT35, D10MIT83, D11MIT149, D11MIT99, D12MIT136, D12MIT99, D13MIT16, D13MIT35, D14MIT203, D14MIT165, D15MIT193, D16MIT131, D16MIT4, D17MIT93, D17MIT155, D18MIT19, D18MIT152, D19MIT71, DxMIT64 (oligonucleotide sequences were chosen according to Jaxon Lab Mouse Informatics Database; Eppig, J.T. *et al.* The Mouse Genome Database (MGD): from genes to mice - a community resource for mouse biology. *Nucleic Acids Res.* 33, D471-D475 2005).

The microsatellite analysis revealed that the mutant mouse line carrying the TAAR1^{NLSlacZ} allele matches with wild type C57BL/6 mice for all microsatellites tested (see Fig. 10 for example), confirming that the mutant mouse carrying the TAAR1^{NLSlacZ} allele possesses a pure C57BL/6 genetic background and harbors no potential contaminations from either DBA or SV129.

4.3) Proof of concept: Use of TAAR1 – NLSlacZ gene replacement as tool for analyzing the tissue distribution of TAAR1 expression

The TAAR1^{NLSlacZ} mutant mouse line was generated using a gene replacement strategy as described in chapter 1). As a consequence, the histological marker NLSlacZ has been targeted to the TAAR1 gene locus such that its expression reflects the spatio-temporal tissue distribution of TAAR1 expression in wild type animals. To this end, the TAAR1^{NLSlacZ} mutant mouse line serves as a powerful tool which allows for detailed TAAR1 expression studies without the need to generate and validate TAAR1-specific probes such as specific antibodies or radioligands.

The expression of a synthetic coding sequence from a chromosomal locus can be potentially compromised e.g. by gene silencing events or by insufficient expression levels, both of which are difficult to predict without experimental data derived from the actual mutant of interest. In order to proof the functionality of the NLSlacZ coding sequence targeted to the TAAR1 gene locus in the TAAR1^{NLSlacZ} mutant mouse as histological

marker a lacZ staining was carried out on tissue sections of adult TAAR1^{NLSlacZ/NLSlacZ} and TAAR1^{+/+} mouse brains.

Adult TAAR1^{NLSlacZ/NLSlacZ} and TAAR1^{+/+} mice were transcardially perfused under terminal isoflurane anesthesia essentially as described in Romeis (Mikroskopische
5 Technik. 1989, 17., neubearbeitete Auflage, Urban and Schwarzenberg; München, Wien, Baltimore). The animals were perfused consecutively with 10 ml phosphate buffered saline (PBS; 137 mM NaCl, 2.7 mM KCl, 90 mM Na₂HPO₄, 1,5 mM KH₂PO₄, pH 7.4) and 15 ml fixative (2% w/v paraformaldehyde and 0.2% w/v glutaraldehyde in PBS). The
10 brains were removed from the skull, post-fixed for 4 hours in fixative at 4°C and immersed into 0.5 M sucrose in PBS over night at 4°C. Brains were embedded in OCT compound (Medite Medizintechnik, Nunningen, Switzerland) in Peel-A-Way tissue embedding molds (Polysciences Inc., Warrington, USA) and frozen on liquid nitrogen. Brains were cut in parasagittal orientation on a cryomicrotome (Leica Microsystems AG, Glatbrugg, Switzerland) at 50 µm and thaw mounted on gelatin coated glass slides
15 (Fisher Scientific, Wohlen, Switzerland). Tissue sections were air dried at room temperature for 2 h, washed 5 times for 10 min each in PBS at room temperature (RT) and incubated for 16-24 h in lacZ staining solution (1 mg/ml 5-bromo-4-chloro-3-indolyl-beta-D-galactopyranoside, 5 mM K₃Fe(CN)₆, 5 mM K₄Fe(CN)₆, 2 mM MgCl₂ in PBS) in a light tight container at 37°C on a horizontal shaker. The staining process was
20 stopped by washing the tissue sections 5 times for 10 min each in PBS at RT. Tissue sections were dehydrated through an ascending ethanol series, equilibrated to xylene and coverslipped with DePex (Serva GmbH, Heidelberg, Germany). Tissue sections were analyzed on an Axioplan I microscope (Carl Zeiss AG, Feldbach, Switzerland) equipped with an AxioCam CCD camera system (Carl Zeiss AG).

25 The lacZ staining of the tissue sections revealed a strong and specific staining in TAAR1^{NLSlacZ/NLSlacZ} mouse brain sections, which was absent from a tissue section of an equivalent region of a TAAR1^{+/+} mouse brain. This result confirms, that NLSlacZ expression from the *TAAR1* gene locus in TAAR1^{NLSlacZ} mutant mice functions as histological marker for analyzing TAAR1 expression in mouse (Figure 11).

30 In order to exclude potential deficits in the spontaneous behavior or sensory capabilities and the physiological conditions of the TAAR1^{NLSlacZ} mutant mouse line, which could arise through the mere presence of the targeted mutation of the *TAAR1* gene. The baseline conditions were analyzed in adult animals 3 months of age of all three genotypes and both genders.

To this end, the physical state of animals was examined regarding gain of body weight in the first three months of postnatal age, regarding rectal temperature, and nest building behavior. The neurological state of the animals was analyzed regarding the potential occurrence of catalepsy, ataxia, tremor, lacrimation and salivation and the degree of arousal in response to transfer of the animals to a novel environment. The dexterity and coordination of the animals was examined by analyzing grip strength and spontaneous horizontal locomotor activity as well as in the so-called rotarod and horizontal wire tests (e.g. Crawley, J.N. (2000) *What's Wrong With My Mouse?* 1. Edition, Wiley & Sons, ISBN 0471316393; Irwin, S. *Comprehensive observational assessment: Ia. A systematic, quantitative procedure for assessing the behavioral and physiologic state of the mouse. Psychopharmacologia* 13, 222-257, 1968).

None of the tests and examinations revealed a significant difference in comparison of the genotypes, demonstrating that there are no deficits in spontaneous behavior, sensory capabilities or physiological state which could impact the characterization of the mutant mouse line in behavioral models directed towards dissecting the potential role of TAAR1 in disease models or towards the characterization of pharmacological compounds.

Example 2:

METHODS

Behavioral phenotyping

Animals were maintained under conditions of constant temperature (22 ± 2 °C) and humidity (55–65%), and all mice were singly housed for the duration of study. Food and water were available *ad libitum*. All experiments were conducted during the light phase of the light/dark cycle (lights on: 6 a.m. – 6 p.m.). All animal procedures were conducted in strict adherence to the Swiss federal regulations on animal protection and to the rules of the Association for Assessment and Accreditation of Laboratory Animal Care International (AAALAC), and with the explicit approval of the local veterinary authority.

Behavioral assessment. Mice were assessed for standard physiological parameters (body temperature, evolution of body weight), and in several neurological and behavioral tests, including grip strength (g), horizontal wire test, rotarod test, and locomotor activity.

Body temperature was measured to the nearest 0.1 °C by a HANNA instruments thermometer (Ronchi di Villafranca, Italy) by inserting a lubricated thermistor probe (2 mm diameter) 20 mm into the rectum; the mouse was hand held at the base of the tail during this determination and the thermistor probe was left in place until steady readings were obtained (~15 s).

Body weight (g) was checked at various time points in mice aged from 12 to 24 weeks.

Horizontal wire test: mice were held by the tail and required to grip and hang from a 1.5 mm in diameter bar fixed in a horizontal position at a height of 30 cm above the surface for a maximum period of 1 min. The latency for the mice to fall was measured, and a cut-off of either 60 sec or the highest fall latency score from three attempts was used.

Rotarod test: The apparatus consisted of a fixed speed rotarod (Ugo Basile, Biological Research Apparatus, Varese, Italy) rotating at either 16 or 32 rpm. Bar is 10 cm wide, 3 cm in diameter, and 25 cm above the bench. Motor incoordination on the rotating rod translates into animals falling off the bar. On the test day, subjects were placed on the rotarod and their latency to fall measured. All mice were tested at both 16 and 32 rpm, and in both tests a cut-off of either 120 s or the highest fall latency score from three attempts was used.

Locomotor activity. A computerized Digiscan 16 Animal Activity Monitoring System (Omnitech Electronics, Columbus, OH) was used to quantitate spontaneous locomotor activity. Data were obtained simultaneously from eight Digiscan activity chambers placed in a soundproof room with a 12 hr light/dark cycle. All tests were performed during the light phase (6 a.m. to 6 p.m.). Each activity monitor consisted of a Plexiglas box (20 x 20 x 30.5 cm) with sawdust bedding on the floor surrounded by invisible horizontal and vertical infrared sensor beams. The cages were connected to a Digiscan Analyzer linked to a PC that constantly collected the beam status information. With this system, different behavioral parameters could be measured, such as horizontal and vertical activity, total distance travelled (in cm), and stereotypies. The mice were tested via a pseudo-Latin squares design twice weekly with at least a 10-day interval between two consecutive test sessions. Vehicle (saline 0.9%) or d-amphetamine (0.4, 1, 2.5, 5 mg/kg, i.p.) was administered to wild-type (n=16) and TAAR-1 KO (n=12) mice just prior to testing. Locomotor activity was recorded for 90 min starting immediately after the mice were placed in the cages.

Statistics. Behavioral observations were recorded as mean values $\pm$ SE and analyzed with an unpaired t test. Locomotor activity data (total distance) were analyzed with a two-factor (Genotype and Dose) ANOVA with repeated measures. Comparisons of dose effects in each genotype were undertaken with a repeated measures ANOVA, followed in significant cases by paired t tests. A p value of 0.05 was accepted as statistically significant.

Assessment of extracellular levels of biogenic amines

Four months old male mice were used for these experiments. The procedures used for the experiments described in this report received prior approval from the City of Basel Cantonal Animal Protection Committee based on adherence to federal and local regulations on animal maintenance and testing.

Surgery and implantation of the microdialysis probe

Forty-five minutes before anesthesia mice received subcutaneously 0.075 mg/kg of buprenorphine. Mice were then anesthetized with isoflurane and placed in a stereotaxic device equipped with dual manipulators arms and an anesthetic mask. Anesthesia was maintained with isoflurane 0.8-1.2% (v/v; support gas oxygen/air, 2:1). The head was shaved and the skin was cut along the midline to expose the skull. A small bore hole was made in the skull to allow the stereotaxical insertion of the microdialysis probe (vertical probe carrying a 2 mm polyacrylonitrile dialysis membrane; Brains On-line, Groningen, The Netherlands) in the striatum (coordinates: A 0.9 mm, L -1.8 mm, V -4.6 mm). The probe was cemented into place using binary dental cement. Once the cement was firm, the wound was closed with silk thread for suture (Silkam) the animal was removed from the stereotaxic instrument and returned to its cage. At the end of the surgery and 24 hrs later mice were treated with Meloxicam 1 mg/kg sc. The body weight of the animals was measured before the surgery and in the following days to monitor the recovery of the animal from surgery.

Microdialysis experiments

All microdialysis experiments were carried out 3-4 days after surgery in awake, freely moving mice. The day of the experiment, the inlet of the implanted dialysis probe was connected to a micro-perfusion pump (CMA/Microdialysis, Sweden) and the outlet was connected to a fraction collector. The microdialysis probe was then perfused with Ringer solution (NaCl 147 mM, KCl 3 mM, CaCl₂ 1.2 mM, MgCl₂ 1.2 mM) at a constant flow rate of 1.5 μ l/min and dialyzates were collected in 15 min aliquots in plastic vial containing 37.5 μ l of acetic acid 0.02 M. Four samples of dialysates were collected before

pharmacological treatment to determine the baseline levels of biogenic amines and their metabolites. Mice were then treated intraperitoneally with 2.5 mg/kg of amphetamine and dialysate samples collected for further 2.5 hrs. Dialysate samples were stored frozen at -80 °C until analysis.

5 *Analysis of microdialysate*

Frozen dialysate samples were shipped in dry ice to Brains On-Line for assay of monoamines and their metabolites. The concentrations of dopamine, DOPAC, serotonin, 5-HIAA and noradrenaline were measured by use an HPLC equipped with an electrochemical detector according to the procedure of van der Vegt et al. (2003).

10

In vivo microdialysis assessment of biogenic amine neurotransmitter levels

Concentrations of norepinephrine, dopamine, and serotonin were determined within the same samples by HPLC separation and electrochemical detection. Samples were split into two aliquots; one used for simultaneous analysis of norepinephrine and
15 dopamine, the other for analysis of serotonin.

Norepinephrine and Dopamine

Aliquots (20 µL) were injected onto the HPLC column by a refrigerated micro-sampler system, consisting of a syringe pump (Gilson, model 402), a multi-column injector (Gilson, model 233 XL), and a temperature regulator (Gilson, model 832).
20 Chromatographic separation was performed on a reverse-phase 150 x 2.1 mm (3 µm) C18 Thermo BDS Hypersil column (Keystone Scientific). The mobile phase (isocratic) consisted of a sodium acetate buffer (4.1 g/L Na acetate) with 2.5 % v/v methanol, 150 mg/L Titriplex (EDTA), 150 mg/L 1-octanesulfonic acid, and 150 mg/L tetramethylammonium chloride (pH = 4.1 adjusted with glacial acetic acid). Mobile
25 phase was run through the system at a flow rate of 0.35 mL/min by an HPLC pump (Shimadzu, model LC-10AD vp).

Norepinephrine and dopamine were detected electrochemically using a potentiostat (Antec Leyden, model Intro) fitted with a glassy carbon electrode set at +500 mV vs. Ag/AgCl (Antec Leyden). Data were analyzed by Chromatography Data
30 System (Shimadzu, class-vp) software. Concentrations of monoamines were quantitated by external standard method.

Serotonin

Aliquots (20 μ L) were injected onto the HPLC column as described for norepinephrine and dopamine. Chromatographic separation was performed on a reverse-phase 100 x 2 mm (3 μ m) C18 ODS Hypersil column (Phenomenex). The mobile phase (isocratic) consisted of a sodium acetate buffer (4.1 g/L Na acetate) with 4.5 % v/v methanol, 500 mg/L Titriplex (EDTA), 50 mg/L 1-heptanesulfonic acid, and 30 μ L/L tetraethylammonium (pH = 4.74 adjusted with glacial acetic acid). Mobile phase was run through the system at a flow rate of 0.4 mL/min by an HPLC pump (Shimadzu, model LC-10AD vp). Serotonin was detected electrochemically using the same method as described for norepinephrine and dopamine.

10

Slice electrophysiology in the ventral tegmental area (VTA).

Horizontal slices (250 μ m thick, VT1000 vibratome, Leica) of the midbrain were prepared from TAAR1 knock-out and littermate wild-type mice 25-60 days of age. Slices were cooled in artificial cerebrospinal fluid (ACSF) containing in mM: 119 NaCl, 2.5 KCl, 1.3 MgCl₂, 2.5 CaCl₂, 1.0 NaH₂PO₄, 26.2 NaHCO₃ and 11 glucose. Slices were continuously bubbled with 95% O₂ and 5% CO₂ and transferred after 1 h to the recording chamber superfused (1.5 ml/min) with ACSF at 32-34 °C. The VTA was identified as the region medial to the medial terminal nucleus of the accessory optical tract. Visualized whole-cell current-clamp recording techniques were used to measure the spontaneous firing rate and holding currents of neurons. All cells used for the statistical analysis displayed a stable firing activity for more than 30 minutes. Dopaminergic neurons were identified by a large I_h current. The internal solution contained in mM: 140 potassium gluconate, 4 NaCl, 2 MgCl₂, 1.1 EGTA, 5 HEPES, 2 Na₂ATP, 5 sodium creatine phosphate and 0.6 Na₂GTP; the pH was adjusted to 7.3 with KOH. Data were obtained with an Axopatch 200B (Axon Instruments, Union City, CA, USA), filtered at 2kHz and digitized at 10kHz, acquired and analyzed with pClamp9 (Axon Instruments, Union City, CA, USA). Values are expressed as mean $\pm$ sem. For statistical comparisons we used the Kolmogorov-Smirnov test. The level of significance was set at P=0.05.

RESULTS

Physical and behavioral properties of TAAR1^{LacZ/LacZ} mice

The general health, physical state and sensory functions of the TAAR1^{LacZ/LacZ} mouse line was examined according to a modified version of standard procedures used for behavioral phenotyping of genetically modified mice (Irwin, S. Comprehensive observational assessment: Ia. A systematic, quantitative procedure for assessing the behavioral and physiologic state of the mouse. *Psychopharmacologia* 13, 222-257 (1968); Hatcher, J.P. *et al.* Development of SHIRPA to characterise the phenotype of gene-targeted mice. *Behav. Brain Res.* 125, 43-47 (2001)). The comparison of TAAR1^{+/LacZ} and TAAR1^{LacZ/LacZ} mice to their wild-type siblings did not reveal any significant differences regarding their general state of health, their viability, fertility, lifespan, nest building behaviour (Fig. 12a), body weight (Fig. 12b) as well as their body temperature (Fig. 12c). Regarding general motor functions and behavior no significant differences between genotypes were observed analyzing dexterity and motor coordination (Fig. 12d-f) as well as spontaneous locomotor activity (Fig. 12g).

TAAR1^{LacZ/LacZ} mice display elevated sensitivity to psychostimulants

Recent observations indicate that at least part of the pharmacological effects of trace amines are due to modulation of catecholamine neurotransmission (Berry, M.D. Mammalian central nervous system trace amines. Pharmacologic amphetamines, physiologic neuromodulators. *J. Neurochem.* 90, 275-271 (2004); Geracitano, R., Federici, M., Prisco, S., Bernardi, G. & Mercuri N.B. Inhibitory effects of trace amines on rat midbrain dopaminergic neurons. *Neuropharmacol.* 46, 807-814 (2004)). In addition, TAAR1 has been found to be localized in brain areas with pronounced dopaminergic and serotonergic neurotransmission (Borowsky, B. *et al.* Trace amines: identification of a family of mammalian G protein-coupled receptors. *Proc. Natl. Acad. Sci. USA* 98, 8966-8971 (2001)). Amphetamines are known to act as indirect catecholamine agonists that achieve their pharmacological effects by inducing the release of cytosolic dopamine and norepinephrine (King, G.R. & Ellinwood, E.H. Amphetamines and other stimulants. In Lowinson, J.H., Ruiz, P., Millman, R.B. & Langrod, J.G., editors. Substance abuse: a comprehensive textbook, Williams & Wilkins., Baltimore, 1992). Increased extracellular levels of these neurotransmitters, in turn, produce hyperlocomotor activity. The effect of d-amphetamine (2.5 mg/kg i.p.) on locomotor function was therefore compared between TAAR1^{LacZ/LacZ} and TAAR1^{+/+} mice. Whereas the locomotor activity decreased in wild type mice after d-amphetamine injection regarding total distance moved TAAR1^{LacZ/LacZ}

mice were first more active and then moved significantly more than wild type littermates (Fig. 12g). Similar results were obtained looking at horizontal activity and stereotypic (results not shown). Basal locomotor activity before amphetamine application was comparable between both genotypes (Fig. 12g).

5 The behavioural changes were further investigated in microdialysis studies. The effect of d-amphetamine on the extracellular levels of catecholamines in the striatum revealed 2.3 fold increased levels of dopamine and norepinephrine in $TAAR1^{LacZ/LacZ}$ compared to wild type mice (Fig. 13a and 13c). No significant differences in basal levels of dopamine ($2.23 \pm 0.65 \mu M$ and $2.27 \pm 0.68 \mu M$ in $TAAR1^{+/+}$ and $TAAR1^{LacZ/LacZ}$,
10 respectively) and norepinephrine ($0.30 \pm 0.12 \mu M$ and $0.38 \pm 0.18 \mu M$ in $TAAR1^{+/+}$ and $TAAR1^{LacZ/LacZ}$, respectively) were seen. In $TAAR1^{LacZ/LacZ}$ mice dopamine and norepinephrine levels increased by 11 and 4.9 fold, respectively. Whereas no significant changes in the basal level of the dopamine metabolite DOPAC have been seen in $TAAR1^{LacZ/LacZ}$ mice (basal level: $148 \pm 36 \mu M$), DOPAC levels were significantly
15 decreased versus wild-type control 45 min after d-amphetamine administration and returned to basal levels after 135 minutes in $TAAR1^{LacZ/LacZ}$ mice (Fig. 13b; basal level: $132 \pm 44 \mu M$). Serotonin levels remained unchanged after d-amphetamine application in wild type animals (basal level: $0.35 \mu M$), but increased by 2.5 fold in $TAAR1^{LacZ/LacZ}$ mice. No significant changes were seen in levels of the 5-HT metabolite 5-HIAA in both
20 genotypes (basal levels: $124 \pm 19 \mu M$ in $TAAR1^{+/+}$ and $119 \pm 18 \mu M$ in $TAAR1^{LacZ/LacZ}$).

TAAR1 activity decreases the spontaneous firing rate of dopaminergic neurons in the VTA

25 The spontaneous firing rate of dopaminergic neurons in the VTA was determined under current clamp conditions. The mean spike frequency in $TAAR1^{+/+}$ ($n = 22$) and in $TAAR1^{LacZ/LacZ}$ ($n = 25$) was 2.3 ± 0.8 Hz and 17.2 ± 1.2 Hz ($p < 0.0001$, Fig. 14a), respectively, thus revealing a significantly increased firing rate in $TAAR1^{LacZ/LacZ}$ neurons. The data suggest that in wild type mice TAAR1 is tonically activated by ambient
30 concentrations of an endogenous ligand. We further observed that the resting membrane potential in the $TAAR1^{LacZ/LacZ}$ mice (-33.53 ± 0.55 mV, $n = 26$) was depolarized compared to wild-type mice (-47.82 ± 0.66 mV, $n = 22$). The depolarized resting membrane potential may to some extent underlie the increased firing rate but alternatively could also be a consequence of the increased firing rate. We next tested
35 whether application of p-tyramine decreases the spontaneous firing rate of dopaminergic neurons in the VTA of wild type mice. Bath application of p-tyramine ($10 \mu M$) caused a

significant decrease in the spike frequency in TAAR^{+/+} (control: $F = 2.1 \pm 0.3$ Hz, p-tyramine: $F = 0.63 \pm 0.04$ Hz, $n = 19$, $p < 0.0001$) but not in the TAAR1^{LacZ/LacZ} mice (control: $F = 16.73 \pm 1.15$ Hz, p-tyramine: $F = 16.57 \pm 1.35$ Hz, $n = 15$, $p > 0.05$; Fig. 14b). This directly shows that TAAR1 activity can inhibit the spontaneous firing of

5 dopaminergic neurons in the VTA.

Claims

1. A vector construct comprising genomic sequences homologous to upstream and downstream regions flanking the single coding exon of the TAAR1 gene suitable for homologous recombination and one or more selection marker genes.
5
2. A vector construct according to claim 1 wherein the vector construct comprises additionally a reporter gene, and wherein the reporter gene is located between the homologous TAAR1 flanking sequences.
3. The vector construct according to claim 2 wherein the reporter gene encodes LacZ.
10
4. The vector construct according to any one of claims 2 to 3 wherein the reporter gene is operably linked to a NLS sequence.
5. The vector construct according to any one of claims 1 to 4, wherein the selection marker gene is a neomycin resistance gene.
6. The vector construct according to any one of claims 1 to 5, wherein the selection marker gene is a diphtheria toxin gene.
15
7. The vector construct according to any one of claims 1 to 6, wherein said selection marker genes are a neomycin resistance gene and a diphtheria toxin gene.
8. The vector construct according to any one of claims 1 to 7 wherein the homologous sequences comprise at least a part of the TAAR1 promoter.
20
9. A vector construct TAAR-KO incorporated in the plasmid pSKDT-Tar1-NLS-PGK-Neo deposited under the accession number DSM 17504.
10. A method of producing a non-human knock-out animal, whose one or both alleles of *TAAR1* gene are mutated and/or truncated in a way that less or no active TAAR1 protein is expressed comprising
25
 - (a) introducing a vector construct according to any one of claims 1 to 9 into an embryonic stem cell by means of homologous recombination,
 - (b) generating a heterozygous and/or homozygous knock-out animal from the said embryonic stem cell, and thereby
30
 - (c) producing a non-human knock-out animal, whose one or both alleles

of a *TAAR1* gene are mutated and/or truncated in a way that less or no active TAAR1 protein is expressed.

11. The method according to claim 10, wherein the embryonic stem cell of a) is derived from the mouse strain C57BL/6.
- 5 12. A non-human knock-out animal produced by the method according to any one of claims 10 to 11.
13. A non-human knock-out animal whose one or both alleles of a *TAAR1* gene are mutated and/or truncated in a way that less or no active TAAR1 protein is expressed.
- 10 14. The non-human knock-out animal according to claim 13 wherein one or both alleles of a *TAAR1* gene are replaced by a reporter gene.
15. The non-human knock-out animal according to claim 14, wherein the reporter gene encodes LacZ.
- 15 16. The non-human knock-out animal according to any one of claims 12 to 15, wherein the animal is a rodent.
17. The non-human knock-out animal according to claim 16, wherein the rodent is a mouse.
18. The non-human knock-out animal according to claim 17, wherein the mouse is a co-isogenic C57BL/6 mouse.
- 20 19. Descendant of the non-human knock-out animal according to any one of claims 12 to 18, obtained by breeding with animals of the same or another genotype.
20. A primary cell culture or a secondary cell line derived from a non-human knock-out animal or its descendants according to any one of claims 12 to 25 19.
21. A tissue or organ explant or culture thereof, derived from a non-human knock-out animal or its descendants according to claims 12 to 19.
22. A tissue or cell extract derived from a non-human knock-out animal or its descendants according to claims 12 to 19.

23. Use of a non-human knock-out animal according to claims 12 to 19, or primary cell culture or secondary cell line according to claim 20, or a tissue or organ explant or culture thereof according to claim 21, or a tissue or cell extract according claim 22 as a model for identifying and testing the therapeutic effect of a compound in disorders comprising depression, anxiety disorders, bipolar disorder, attention deficit hyperactivity disorder, stress-related disorders, psychotic disorders such as schizophrenia, neurological diseases such as Parkinson's Disease, neurodegenerative disorders such as Alzheimer's Disease, epilepsy, migraine, hypertension, substance abuse and metabolic disorders such as eating disorders, diabetes, diabetic complications, obesity, dyslipidemia, disorders of energy consumption and assimilation, disorders and malfunction of body temperature homeostasis, disorders of sleep and circadian rhythm, and cardiovascular disorders.
24. Use of a non-human knock-out animal according to claims 12 to 19, or a primary cell culture or secondary cell line according to claim 20, or a tissue or organ explant or culture thereof according to claim 21, or a tissue or cell extract according claim 22 as a tool for assessing TAAR1 function.
25. Use of a non-human knock-out animal according to claims 12 to 19, or primary cell culture or secondary cell line according to claim 20, or a tissue or organ explant or culture thereof according to claim 21, or a tissue or cell extract according claim 22 as a tool for identifying unknown ligands of TAAR1 and for the characterization of ligands to TAARs other than TAAR1.
26. A method of testing TAAR1 inhibitor compounds for effects other than TAAR1-specific effects which method comprises administering a TAAR1 agonist, a TAAR1 partial agonist, a TAAR1 modulator or a TAAR1 inhibitor compound to a non-human knock-out animal according to claims 12 to 19, or primary cell culture or secondary cell line according to claim 20, or a tissue or organ explant or culture thereof according to claim 21, or a tissue or cell extract according claim 22, and determining the effect of the compound by behavior and physiological studies addressing neurological, sensory, and cognitive functions as well as physiological parameters and comparing these to the effect(s) of the same compound on wild type control animals.

- 5 27. Use of a non-human knock-out animal according to claims 12 to 19, or a primary cell culture or secondary cell line according to claim 20, or a tissue or organ explant or culture thereof according to claim 21, or a tissue or cell extract according claim 22 as a tool for testing a TAAR1 agonist, a TAAR1 partial agonist, a TAAR1 modulator or a TAAR1 inhibitor compounds for effects other than TAAR1-specific effects.
- 10 28. Use of a non-human knock-out animal according to claims 12 to 19, or a primary cell culture or secondary cell line according to claim 20, or a tissue or organ explant or culture thereof according to claim 21, or a tissue or cell extract according claim 22 as a tool for determining the specificity of compounds acting on TAAR1.
- 15 29. Use of a non-human knock-out animal according to claims 12 to 19, or a primary cell culture or secondary cell line according to claim 20, or a tissue or organ explant or culture thereof according to claim 21, or a tissue or cell extract according claim 22 for studying the intracellular trafficking of TAARs or of other cellular components linked to TAARs.
- 20 30. Use of the non-human knock-out animal, according to any one of the claims 14 to 19 for determining the TAAR1 expression profile.
- 25 31. A test system for testing TAAR1 agonists, TAAR1 partial agonists, TAAR1 positive and negative modulators or TAAR1 inhibitor compounds for effects other than TAAR1-specific effects comprising non-human knock-out animal according to claims 12 to 19, or a primary cell culture or secondary cell line according to claim 20, or a tissue or organ explant or culture thereof according to claim 21, or a tissue or cell extract according claim 22, and a means for determining whether TAAR1 agonists, TAAR1 partial agonists, TAAR1 positive and negative modulators or TAAR1 inhibitor compounds exhibit effects other than TAAR1-specific effects.
- 30 32. The vector constructs, methods, knock-out animals, test systems and uses substantially as described herein before especially with reference to the foregoing examples.

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 40 atcgtggctg gccacgacgg gcgttccttg cgcagctgtg ctcgacgttg tctactgaagc 300
 gggaagggac tggctgctat tgggcgaagt gccggggcag gatctcctgt catctcacct 360
 tgctcctgcc gagaaagtat ccatcatggc tgatgcaatg cggcggctgc atacgcttga 420
 45 tccggctacc tgcccattcg accaccaagc gaaacatcgc atcgagcgag cacgtactcg 480
 gatggaagcc ggtcttgctg atcaggatga tctggacgaa gagcatcagg ggctcgcgcc 540
 50 agccgaactg ttcgccaggc tcaaggcgcg catgcccagc ggcgatgatc tcgtcgtgac 600
 ccatggcgat gcctgcttgc cgaatatcat ggtggaaaat ggccgctttt ctggattcat 660
 cgactgtggc cggctgggtg tggcggaccg ctatcaggac atagcgttgg ctaccctgta 720
 55 tattgtgaa gagcttggcg gcgaatgggc tgaccgcttc ctcgtgcttt acggtatcgc 780
 cgctcccgat tcgcagcgca tcgccttcta tcgccttctt gacgagttct tctgagggga 840
 60 tcaattctct agagctcgct gatcagcctc gactgtgcct tctagttgcc agccatctgt 900
 tgtttgcccc tcccccgctc cttccttgac cctggaaggt gccactccca ctgtcctttc 960
 ctaataaaat gaggaaattg catcgcatgt tctgagtagg tgtcattcta ttctgggggg 1020
 65 tgggggtggg caggacagca agggggagga ttgggaagac aatagcaggc atgctgggga 1080
 tgcggtgggc tctatggctt ctgaggcgga aagaaccagc tggggctcga tcctctagag 1140
 70 tcgatcgacc tcgaccccc ctatgcattt ttggagaatc atctatactt tacagtgagt 1200

ttctgtggct ttatttattt caagatcttc cttacagatt att

243

5 <210> 7
<211> 738
<212> DNA
<213> Artificial

10 <220>
<223> Description of Artificial Sequence: Sequence contains murine sequence and part of PGK-NEO-Resistance cassette.

<400> 7
15 cgatcgacct cgaccccccc tatgcatttt tggagaatca tctatacttt acagtgagtt 60
tctgtggctt tatttatttc aagatcttcc ttacagatta tttccagatg ttgtataaat 120
cttttaaaaa ctgtggtact gattcacatg agaaaaaagg ctctagaaat gaagagccca 180
20 agatccagaa ataactgtct gggtttatga gcagtttgtt agctgtgtga tcagagggtg 240
attatgtaca gtctaagggg agtagctgag tgaaaaggaa aaagactagt ttttaagtga 300
25 accattattg ccactattat atatgttata taaacaaggt tatgtataaa caataaagtt 360
tatattatat tttcacttgt tttgtttctt gttttataat atatagggcat attaaacttt 420
acattgtttt aacttttttt aaataattgc tattattttt ttgagacagg gtcttagtat 480
30 atagcttgac tagcccagaa gtctctgtga agactaggat ggtctcagac tcagagagat 540
ttgcctgccc ctgctgccc agtgctgaga ttttaagtatt tagtcattaa ggtttgtata 600
35 tacattatgt ctagccattg aggtttttat attcaccaca tccagatgtt aagggtttcta 660
ggcacacatc catttcttac tctattagtc agaatttcta gaacaatact gatattaagg 720
atggatctta ttacttgg 738

40
<210> 8
<211> 796
<212> DNA
45 <213> Mus musculus

<400> 8
cctacctctg gcctctggcc tttcccttta actccacaga taagtgcata agctccttta 60
50 aaaatttcag aagatttttt ttccagaatc ttataaatg taagcaggca gtgatccttc 120
acattatcat taggaggggac tagccaaagg gtgtagagtt ccagtttgca caagggctaa 180
ggatcatggc agacagctcc ctctatgtcc atttccaatg tgagttacga aacttcttac 240
55 caagttcatg agttccagac agccttccaa gaaaagtttt tagttacatc aatggaaaag 300
atagaatctg gttgttgcaa gaaaaacagt tacaacaaca tcaatactta tttctaagtc 360
60 aatttgtggc aaaaataatt tcatttcgca ggttctactg aaaatattca tataaatgtt 420
catttcatat caagtagtaa tgtgttggtc aggacttttt tgtggaaatg gattattaac 480
aacggtgctt tcttaagagg ttagtgagct aggaggttcc atcatgattt tagactatat 540
65 ctggaagtca acaatccagt cttggcaaac tcacacatat ttgtcagaaa gtaggacaaa 600
gtgggtaatc tccaatccac tgagaatttt ggtaagtcac agtttctgct tagctgaacc 660
70 agagtcaaga agagcttgaa tattaagggt agaaagatgc atgaagaatg gtggatttgg 720

tttttctaaa acagtttgct ttgaatattt atttttagtta ttttttgggg ggaggaaagt 780
 ttatttagct tacact 796
 5
 <210> 9
 <211> 779
 <212> DNA
 10 <213> Mus musculus
 <400> 9
 ggcattcccc tgtactgggg catataaagt ttgcaatacc aaaggctctc tcctcccagt 60
 15 gatggccgat taggccatct tctgctacat atgcagctag agatatgaag tcattagata 120
 tgcactcact gataagtgga tattagccca gaaacataga acaccaaga tacaatttgc 180
 20 aaaacacaag aaaatcaaga agaaggaaga ccaatggatg gatacttcac tcctccttag 240
 aataggaac aaaataccca tgaaaggagt tacagagaca aagtttggag ctaagacaaa 300
 aggatggact atccagagac tagccctccc agggatccat ccataatca gccaccaaac 360
 25 ctagacacta ttgcatatgc cagaaagatt ttgctgaagg gaccctgtta tagctgtctc 420
 gtatgaggct atgccagtgc ctggcaaaca cagaagtgga tgctcacagt catctataag 480
 atggaactca gggcccccaa tggaggagca agagaaagca cccaagaaga tgaaggggtc 540
 30 tgcaacccta taggtggaac aacaatatga actaaccagt acccccagag ctcatatctc 600
 tagctgcata tattagttat tttaaagttg tgtgtgcatg catgtgtgtg cacgtgggaa 660
 35 cagaagtgtg ggtgccagta gaggaatttc aatcccttgc agctagaatt acagggagac 720
 ttgaattgcc cacaagattg ctgggaactg actctgggtc ctcaagtaaga gctgcattt 779
 40 <210> 10
 <211> 28
 <212> DNA
 <213> Artificial
 45 <220>
 <223> Description of Artificial Sequence: Oligonucleotide derived from
 TAAR1 (mus musculus) genomic sequence, additional restriction
 site inserted.
 50 <400> 10 28
 cgggtacctg tcaactcaccg gcattcgg
 55 <210> 11
 <211> 22
 <212> DNA
 <213> Mus musculus
 60 <400> 11 22
 ccttgcttgt ccttttagcta tg
 65 <210> 12
 <211> 23
 <212> DNA
 <213> Mus musculus
 <400> 12 23
 cccatgtgac caatttggtc acc
 70

<210> 13
 <211> 35
 <212> DNA
 5 <213> Artificial

 <220>
 <223> Description of Artificial Sequence: derived from TAAR1 genomic
 sequence (mus musculus), additional restriction site inserted.
 10
 <400> 13
 ctgctgccg ggattcaagc tcttcttgac tctgg 35

 15 <210> 14
 <211> 37
 <212> DNA
 <213> Artificial

 20 <220>
 <223> Description of Artificial Sequence: oligonucleotide for
 introducing NLS and cloning site StuI in vector construct

 <400> 14
 25 tccaaagaag aagagaaagg tttcggaggc ctatgca 37

 <210> 15
 <211> 37
 30 <212> DNA
 <213> Artificial

 <220>
 <223> Description of Artificial Sequence: oligonucleotide for
 35 introducing NLS and cloning site StuI in vector construct.

 <400> 15
 ttggcctccg aaacctttct cttcttcttt ggatgca 37

 40
 <210> 16
 <211> 20
 <212> DNA
 <213> Escherichia coli
 45
 <400> 16
 gcgcatcgcc ttctatcgcc 20

 50 <210> 17
 <211> 22
 <212> DNA
 <213> Mus musculus

 55 <400> 17
 gagcttcaca catgaacaca cc 22

 60 <210> 18
 <211> 21
 <212> DNA
 <213> Mus musculus

 <400> 18
 65 gtgggctaag atctaggaac g 21

 <210> 19
 <211> 20
 70 <212> DNA

	<213>	Escherichia coli	
	<400>	19	20
5		ggcgatagaa ggcgatgcgc	
	<210>	20	
	<211>	22	
	<212>	DNA	
10	<213>	Mus musculus	
	<400>	20	22
		gaaggtggaa ttctaacctg ac	
15	<210>	21	
	<211>	22	
	<212>	DNA	
	<213>	Mus musculus	
20	<400>	21	22
		ccttgcttgt cctttagcta tg	
25	<210>	22	
	<211>	20	
	<212>	DNA	
	<213>	Escherichia coli	
30	<400>	22	20
		cttgggtgga gaggctattc	
35	<210>	23	
	<211>	20	
	<212>	DNA	
	<213>	Escherichia coli	
40	<400>	23	20
		aggtgagatg acaggagatc	
45	<210>	24	
	<211>	20	
	<212>	DNA	
	<213>	Mus musculus	
50	<400>	24	20
		accacagtcc atgccatcac	
55	<210>	25	
	<211>	20	
	<212>	DNA	
	<213>	Mus musculus	
60	<400>	25	20
		tccaccaccc tgttgctgta	
65	<210>	26	
	<211>	21	
	<212>	DNA	
	<213>	Mus musculus	
70	<400>	26	21
		atgcatcttt gccacgctat c	
	<210>	27	

	<211> 20	
	<212> DNA	
	<213> Mus musculus	
5	<400> 27	
	caaggctctt ctgaaccagg	20
<hr/>		
	<210> 28	
10	<211> 18	
	<212> DNA	
	<213> Escherichia coli	
	<400> 28	
15	ggtggcgctg gatggtaa	18
	<210> 29	
	<211> 18	
20	<212> DNA	
	<213> Escherichia coli	
	<400> 29	
	cgccatttga ccactacc	18
25		