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(54) Título: **MÉTODO PARA A PREDIÇÃO DO DESFECHO DO TRATAMENTO DE DOENÇAS HUMANAS UTILIZANDO FÁRMACOS METABOLIZADOS PELA N-ACETILTRANSFERASE 2 HUMANA (NAT2) COM BASE EM POLIMORFISMOS GENÉTICOS**

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(57) Resumo: Método para a predição do desfecho do tratamento de doenças humanas utilizando fármacos metabolizados pela N-acetiltransferase 2 humana (NAT2) com base em polimorfismos genéticos. A presente invenção está relacionada ao campo da Biologia Molecular e Genômica, especialmente a Farmacogenômica. A invenção descreve a presença de novos polimorfismos no gene que codifica para a enzima Arilamina N-acetiltransferase 2 humana (NAT2), a qual é responsável pela metabolização de fármacos importantes na terapêutica de várias doenças de etiologias diversas, bem como de inúmeras toxinas e carcinógenos presentes em alimentos, cigarro e no ambiente. A presente invenção inclui metodologia passível de utilização na terapêutica utilizando os polimorfismos descritos.



"Método para a predição do desfecho do tratamento de doenças humanas utilizando fármacos metabolizados pela N-acetiltransferase 2 humana (NAT2) com base em polimorfismos genéticos"

5 Campo da Invenção

A presente invenção está relacionada ao campo da Biologia Molecular e Genômica, especialmente a Farmacogenômica. Descreve a presença de novos polimorfismos no gene que codifica para a enzima Arilamina N-acetiltransferase 2 humana (NAT2), a qual é responsável pela metabolização de fármacos importantes na terapêutica de várias doenças de etiologias diversas, bem como de inúmeras toxinas e carcinógenos presentes em alimentos, cigarro e no ambiente. A presente invenção inclui metodologia passível de utilização na terapêutica utilizando os polimorfismos descritos.

Fundamentos e Estado da Arte

A análise de variações na seqüência de DNA para a compreensão dos diferentes fenótipos observados no ser humano tem sido o principal foco da pesquisa genética durante décadas. Diferentes testes têm sido extensivamente explorados através da análise de ligações, segundo os quais, mutações em um único gene podem ser suficientes não somente para explicar variações na suscetibilidade de diferentes indivíduos a uma ou mais doenças como também para explicar variações inter-individuais de resposta a um determinado fármaco. O tipo mais comum de variação encontrada no genoma humano é o polimorfismo de base única (*Single Nucleotide Polymorphism* - SNP). Tais variações têm

sido identificadas como marcadores genéticos para doenças de etiologias diversas sendo também relacionados com diferentes fenótipos de metabolização de xenobióticos.

Ingelman-Sundberg, J Int Med 250: 186-200 2001; Roses, 5 A.D Life Sciences 70:1471-1480 2002 e Prows & Prows, American Journal of Nursing 104:60-70 2004, através de estudos farmacogenéticos, nos quais foram avaliadas variações genéticas que causam diferentes respostas aos medicamentos, ao incluírem dados acerca das diferenças na 10 eficácia, interações fármaco-fármaco e o risco relativo de reações adversas, identificaram uma associação de vários SNPs com a expressão ou atividade de receptores farmacológicos, proteínas transportadoras, sinalizadoras e enzimas do metabolismo.

15 Um dos principais objetos de estudo da farmacogenética refere-se à análise de enzimas envolvidas na biotransformação de fármacos. Variações nos genes que codificam para essas enzimas podem resultar em uma diminuição de atividade destes fármacos, e favorecer o 20 aparecimento de reações adversas por toxicidade devido a uma baixa metabolização e conseqüente acúmulo do princípio ativo ou de metabólitos intermediários tóxicos (metabolizadores lentos). Por outro lado, segundo Ingelman-Sundberg, J Int Med 250: 186-200 2001, a presença de 25 variantes alélicas que não afetam a atividade enzimática, isto é, alelos funcionais (que caracterizam um fenótipo de metabolizadores rápidos) ou com múltiplas cópias (metabolizadores ultra-rápidos) pode estar associada a concentrações séricas subterapêuticas do fármaco.

Adicionalmente, de acordo com Kalow, *Pharmacological Reviews* 49:369-379 1997, nos casos de heterozigose onde os indivíduos sejam portadores de um alelo que caracterize baixa atividade enzimática e um alelo funcional, um
5 fenótipo de metabolização intermediária é originado.

A enzima N-acetiltransferase 2 humana (NAT2), codificada pelo gene *NAT2* está envolvida na metabolização de vários fármacos utilizados correntemente para o tratamento de: tuberculose (isoniazida), hipertensão
10 arterial (hidrazinas anti-hipertensivas), hanseníase (dapsona) e arritmia cardíaca (procainamida anti-arritmica) além de sulfametazina e outras sulfonamidas usadas para a terapia de outras desordens (Weber, *The Acetylator Genes and Drug Response*, Oxford University Press, N.Y. 1987).

15 Várias mutações pontuais na região codificante do gene *NAT2* são capazes de alterar a atividade de acetilação da enzima podendo resultar em três diferentes fenótipos: acetiladores lentos, intermediários e rápidos (Hein, *et al.*, 2000. *Cancer Epidemiology, Biomarkers and Prevention*, 9:29-42). O

20 fenótipo de acetilação lenta, caracterizado por determinados perfis genotípicos leva a um acúmulo do fármaco e conseqüentemente ao desenvolvimento de reações adversas, as quais são principalmente caracterizadas por neuropatias periféricas e hepatite. Já o fenótipo de

25 acetilação rápida leva a uma diminuição dos níveis séricos do fármaco, podendo alcançar níveis sub-terapêuticos com conseqüente falência terapêutica (Ingelman-Sundberg, *J Int Med* 250: 186-200 2001).

A enzima NAT2 participa também de vias de ativação de poluentes ambientais com potencial carcinogênico, tais como, 2-aminofluoreno, 4-aminobifenil, benzidina, beta-nafitilamina e algumas aminas heterocíclicas presentes em pirolisados protéicos (Kato, CRC Crit Ver.Toxicol. 16:307-348 1986; Weber, The Acetylator Genes and Drug Response, Oxford University Press, N.Y. 1987; Hein Biochim Biophys Acta, 948:37-66, 1988). Adicionalmente, a participação de NAT2 na detoxificação também tem sido associada à suscetibilidade a doenças induzidas por substâncias químicas, tais como neoplasia (Vatsis *et al.*, Pharmacogenetics, 5: 1-17 1995) quando da combinação de ingestão de carne vermelha com o fumo (Potter *et al* Câncer Epidem. Biomarkers & Prev., 8: 69-75 1999; Liu *et al.*, Canc Letters, 133: 115-123 1988).

Até o presente momento, já foram identificados 36 alelos diferentes para o gene NAT2 (<http://www.louisville.edu/medschool/pharmacology/NAT.html>), os quais consistem na combinação de até 4 mutações pontuais na região codificante do gene. Estudos funcionais realizados no início desta década demonstraram a existência de diferentes mecanismos que podem resultar no fenótipo de acetilação lenta dependendo dos polimorfismos presentes no gene NAT2. Dentre estes mecanismos estão: (i) diminuição da quantidade de proteína sintetizada, (SNPs C190T, T341C, A434C, G590A); (ii) diminuição da atividade enzimática (SNPs C190T, G191A, T341C, A434C e G59A) e (iii) diminuição da estabilidade da enzima NAT2 (SNPs G191A, A845C e G857A), (Fretland *et al.*, Pharmacogenetics, 11:207-215 2001; Zhu &

Hein, *Biol. Chem.*, 383: 983-987 2002). Por outro lado, outras mutações descritas na literatura como por exemplo T111C, C282T, C481T, C759T e A803G, não exercem nenhum efeito na atividade biológica da proteína, caracterizando um alelo funcional (Fretland *et al.*, *Pharmacogenetics*, 11:207-215 2001). Estudos adicionais que avaliaram a relação entre diferentes haplótipos e o desfecho de metabolização, baseados na expressão e atividade enzimática realizados com os alelos mais freqüentes de *NAT2*, possibilitaram a caracterização dos mesmos quanto ao perfil de acetilação. Os alelos dos clusters *NAT2* *5, *6, *7, *14 e *19 conferem um fenótipo de acetilação lenta enquanto os alelos *NAT2* *4 e dos clusters *12 e *13, conferem um fenótipo de acetilação rápida (Hein *et al.*, *Cancer Epidemiology, biomarkers and Prevention*, 9:29-42 2000; Hein, *Mutation Research*, 506-507:65-77. 2002).

As Reações Adversas a Drogas (ADRs) são causas comuns de hospitalização em todo o mundo e passíveis de promover o óbito de pacientes acometidos por tais situações. Recentemente, Bagheri *et al.*, *J. Clin. Pharmacol.* 50: 479-484 2000; Bissell *et al.*, *Hepatology* 33:1009-1013 2001; Larrey, *Seminars in Liver Disease* 22:145-155 2002, descobriram que, entre as reações adversas, a lesão hepática é o tipo mais freqüente. Segundo os autores, a doença hepática induzida por fármacos é uma das principais complicações durante o uso de antimicrobianos, uma vez que o fígado é o órgão central na biotransformação e excreção da maioria dos fármacos e substâncias xenobióticas.

Variações genéticas em enzimas que participam na geração destes bioprodutos tóxicos podem resultar em diferenças na reatividade metabólica a agentes específicos com variações de indivíduo para indivíduo. Assim, a
5 determinação dos perfis genotípicos individuais e seus fenótipos resultantes podem ser de grande valia para os médicos tanto na escolha do fármaco a ser indicado quanto na determinação da posologia e do esquema terapêutico a ser adotado, o qual deve encontrar um balanço adequado entre a
10 eficácia e a toxicidade. Adicionalmente, estas variações genéticas podem ser utilizadas como marcadores para identificar pré-disposição a cânceres.

Prince & Brookes, Expert Rev. Mol. Diagn. 1(3) 89-95,2001. "Towards high-throughput genotyping of SNPs by
15 dynamic allele-specific hybridization", descreveram a análise de SNPs como uma estratégia simples para a identificação de genes envolvidos em doenças complexas tais como Alzheimer, obesidade e diabetes melito e anteciparam que os SNPs teriam um papel muito importante na
20 farmacogenômica, onde a identificação de variações em genes específicos, relevantes na eficácia de determinada droga, toxicidade e metabolismo ajudariam a estabelecer estratégias terapêuticas ótimas para pacientes individuais. Refletindo estas expectativas, várias novas tecnologias têm
25 aparecido ao longo dos últimos anos, cada uma com vantagens particulares, mas todas com o objetivo único de simplificar a análise dos SNPs. Os autores descrevem uma técnica chamada "Hibridação dinâmica alelo-específica" (DASH), segundo eles, um método conveniente para a genotipagem de

SNPs e mutações do tipo *indel*, (inserção ou deleção), as quais possuem potencial de aplicação tanto na pesquisa básica como no diagnóstico clínico. Informam ainda que o DASH comercial está disponível, tornando a tecnologia
5 acessível para todos os laboratórios.

Garte, Cancer Epidemiology Biomarkers & Prevention Vol.10, 1233-1237, December 2001. "Metabolic Susceptibility Genes As Cancer Risk Factors" descrevem que polimorfismos em genes da via metabólica relacionada à ativação de
10 carcinógenos que conferem suscetibilidade ao câncer não mostraram uma associação consistente com o desenvolvimento de câncer quando somente os efeitos principais foram examinados. Isto realmente era esperado tendo em vista o limitado e específico papel bioquímico de tais genes no
15 processo carcinogênico. Contudo, quando grupos particulares de casos são examinados separadamente, a importância destes polimorfismos genéticos torna-se clara. Exemplos da literatura e um modelo hipotético são apresentados como suporte de que alelos de risco pertencentes à via
20 metabólica devem ser estudados em subgrupos de estudos do tipo caso-controle com maior casuística tendo como hipótese questões relacionadas à ação do produto gênico em função de variáveis demográficas, ambientais ou outras variáveis genéticas.

25 O pedido de patente US 20030096235 "Methods and products related to genotyping and DNA analysis", descreve métodos e produtos relacionados à genotipagem. Este método é baseado no uso de polimorfismos de base única (SNPs) para uma varredura ampla e de alta *performance* do genoma. O

método é realizado através da hibridização de oligonucleotídeos alelo específicos em um genoma de complexidade reduzida (RCG). A invenção também se relaciona com métodos de: preparo de oligonucleotídeos SNP-
5 específicos e RCGs, métodos de *fingerprinting*, determinação da frequência alélica para um determinado SNP, caracterização de tumores, geração de um código de classificação genômico para a identificação de SNPs desconhecidas, composições relacionadas e *kits*.

10 O pedido de patente US 20030049628 "Complexity Management of Genomic DNA", descreve métodos e *kits* para reduzir a complexidade de uma amostra de DNA através da disponibilização de métodos (não baseados em gel) para a amplificação de um subgrupo de seqüências em uma amostra
15 com sítios de restrição para duas ou mais enzimas, através da ligação de adaptadores aos fragmentos, de forma que somente um subgrupo de fragmentos possa ser amplificado. Esta invenção descreve adicionalmente procede a análise do produto amplificado acima por hibridação com um arranjo que
20 pode ser especificamente desenhado para características particulares dos fragmentos desejados, tais como, a presença ou ausência de um polimorfismo.

O pedido de patente US 20040053232 "Quantitative trait loci and somatostatin", relaciona-se ao uso de
25 características genéticas em gado para a determinação das características da progênie e para otimizar a manipulação do gado visando um aumento na performance de amamentação e qualidade da carne. O alvo especialmente estudado é o *locus* da somatostatina, o qual está associado com certos *loci* de

características quantitativas (QTLs). Os SNPs e haplótipos são preditivos do aumento ou decréscimo da quantidade de tecido no animal.

O pedido de patente US 20040081996 "Methods of
5 validating SNPs and compiling libraries of assays",
descreve bibliotecas de ensaios e métodos para a
compilação de dados em bibliotecas. Os ensaios podem
identificar polimorfismos de base única (SNPs).
Adicionalmente, métodos de validação de SNPs e construção
10 de mapas de desequilíbrio de ligação usando conjuntos ou
sub-conjuntos de SNPs são disponibilizados.

O pedido de patente US 20050042654 "Genotyping
Methods" descreve métodos para a amplificação do DNA
genômico e genotipagem das amostras amplificadas. Os
15 métodos de genotipagem utilizam arranjos de
oligonucleotídeos alelo específicos para polimorfismos de
base única (SNPs). Os métodos também relacionam técnicas
para a amplificação de múltiplas amostras de DNA de vários
indivíduos de maneira a minimizar a possibilidade de
20 contaminação das amostras por produtos amplificados
previamente (amplicons).

O pedido de patente US 20050153328 "Method and markers
for determining the genotype of horned/polled cattle",
descreve métodos para a descoberta e utilização de
25 polimorfismos de base única (SNPs) na determinação do
genótipo de ruminantes. Adicionalmente, a presente
invenção fornece seqüências específicas de ácidos
nucléicos, SNPs e perfis de SNPs que podem ser usados com
esta finalidade.

Chang-Claude *et al.*, *Cancer Epidemiology, Biomarkers & Prevention*, 11 698-704, 2002. "Differential Effect of NAT2 on the Association between Active and Passive Smoke Exposure and Breast Cancer Risk", em estudo caso-controle
5 realizado para avaliar o possível efeito diferencial do genótipo de NAT2 na relação entre fumantes ativos e passivos e o câncer de mama, descreveram que polimorfismos presentes no gene que codifica para a enzima N-acetyltransferase 2 (NAT2) influenciam na taxa de
10 metabolização de amins aromáticas heterocíclicas presentes no tabaco.

Anitha & Banerjee, *Int J Mol Med* Vol.11 125-131, 2003. "Arylamine N-acetyltransferase 2 polymorphism in the ethnic populations of South India ", mostraram que o
15 polimorfismo da N-acetilação é um tratto genético refletido fenotipicamente pelas diferenças na atividade da N-acetyltransferase 2 (NAT2) em agentes terapêuticos (acetiladores rápidos e lentos). Os autores relatam os resultados da genotipagem de NAT2 de comunidades
20 etnicamente diferentes do sul da Índia. Após a genotipagem de 8 diferentes comunidades étnicas, o fenótipo de acetilação lenta teve predominância de 74% nestas populações corroborando resultados encontrados em outras populações asiáticas onde esta predominância é de cerca de
25 60%. Os autores não encontraram associação entre o sexo e o fenótipo de acetilação.

Musbah *et al.*, *Squ Journal For Scientific Research: Medical Sciences* 2003 Vol 5, No. 1-2, 9-14. "Distribution of arylamine N-acetyltransferase 2 (NAT2) genotypes among

Omanis".descreve sistemas para a identificação da maioria dos polimorfismos conhecidos de NAT2, tais como: G191A, C282T, C341T, C481T, G590A, A803G e G857A usando a técnica de PCR-RFLP (Polymerase Chain Reaction-Restriction Fragment Length.Polymorphism).

Cavaco et al., Clin Chemical Lab Med ol.41(4) 606-609 2003 "CYP3A4*1B and NAT2 *14 Allele in a Native African Population", relatam polimorfismos de base única nos genes que codificam para o citocromo P450 3A4 (CYP3A4) e para a N-acetiltransferase 2 (NAT2), principais mediadores do metabolismo de uma grande variedade de drogas de uso terapêutico, bem como de xenobióticos.

Lash et al., Breast Cancer Research Vol: 7 N°3 R.385-393 2005. "A case-only analysis of the interaction between N-acetyltransferase haplotypes and tobacco smoke in breast cancer etiology", descreve haplótipos de N-acetyltransferase 2 envolvidos com câncer de mama. Mulheres que possuem alelos mutantes com um genótipo homozigoto possuem uma taxa de ativação metabólica mais baixa das arilaminas aromáticas, um dos constituintes do tabaco, identificado como carcinógeno. Os autores levantam a hipótese de que mulheres com câncer de mama com o fenótipo de acetilação lenta possuem um risco aumentado para o desenvolvimento deste tipo de carcinoma associado com o fumo ativo ou exposição passiva.

O pedido de patente US 20020128215. "Novel sequence variants of the human N-acetyltransferase 2 (NAT2) gene and use thereof", descreve novos polimorfismos no gene NAT2, os quais podem estar envolvidos no metabolismo de drogas

utilizadas para o tratamento de várias desordens bem como podem ser utilizados para a determinação de pré-disposição ao desenvolvimento de vários cânceres.

Em resumo, nenhum dos estudos já realizados e 5 documentos de patentes encontrados revelaram métodos similares, baseados nos SNPs aqui descritos, para predizer os efeitos hepatotóxicos provenientes da metabolização de drogas no organismo de um ser humano, através de variações na seqüência do gene codificador para a enzima Arilamina N- 10 acetiltransferase 2 (NAT2). Estes e outros aspectos vantajosos formam coletivamente os objetos da presente invenção, que serão descritos em mais detalhes a seguir.

Sumário da Invenção

A presente invenção inclui seqüências de ácidos 15 nucléicos mostradas nas FIGS. 1A-1B e Tabela 2, com destaque aos sítios polimórficos no gene que codifica para NAT2. A presente invenção relaciona-se ainda com oligonucleotídeos, mostrados na tabela 1, que hibridam especificamente com diferentes regiões da seqüência 20 mostrada nas FIGS. 1A-1B. Adicionalmente, a presente invenção descreve como os polimorfismos estão representados na população de duas regiões geográficas distintas do Brasil.

Métodos diagnósticos que utilizem toda ou parte das 25 seqüências contendo os SNPs identificados nesta invenção. Por exemplo, tais ácidos nucléicos ou especificamente os SNPs, podem ser utilizados como métodos para a identificação de polimorfismos no gene de NAT2 que estejam associados à predisposição a várias doenças incluindo, mas

não limitadas, a câncer de bexiga, câncer de colo e câncer de próstata.

Uma outra aplicação desta invenção inclui a possibilidade de criação de um protocolo de prognóstico para pacientes recebendo composições terapêuticas metabolizadas por NAT2, tais como: isoniazida, fenilzina, hidrazina, dapsona, procainamida, sulfametazina e outras sulfonamidas. O método inclui: a) identificação de pacientes recebendo uma destas drogas; b) determinação do fenótipo de acetilação (rápidos ou lentos) com base no genótipo; e c) conversão dos dados obtidos no passo (b) em um protocolo de prognóstico. O protocolo de prognóstico pode incluir a predição da eficácia da droga, a predição do prognóstico do paciente, a predição de interações entre drogas, e a predição de efeitos adversos.

A invenção também está relacionada com a identificação de diferenças entre indivíduos na metabolização de compostos exógenos, incluindo, mas não limitados a carcinógenos ou agentes mutagenicos, incluindo 2-aminofluoreno, 4-aminobifenil, benzidina, beta-nafitilamina, e certas arilaminas heterocíclicas presentes em pirolisados de proteínas.

Em outro contexto, a invenção descreve ainda a frequência dos polimorfismos de NAT2 em duas populações de regiões geográficas distintas do Brasil, permitindo, com base nestas informações, tanto a identificação de grupos étnicos mais suscetíveis a doenças ou desordens diversas, como também subsidiar os profissionais de saúde na elaboração e/ou redefinição de condutas terapêuticas em

especial na escolha do fármaco e sua dosagem a serem utilizados por um determinado grupo étnico.

Uma outra aplicabilidade desta invenção é a criação de um método para assistir no desenvolvimento de novos compostos terapêuticos através de ensaios clínicos. O método inclui: a) administração de um composto terapêutico a um indivíduo e avaliação de sua eficácia; b) determinação, através do genótipo incluindo os SNPs aqui descritos, se o indivíduo é um acetilador rápido ou lento; e c) determinar a partir dos passos (a) e (b), qual composição terapêutica será a mais efetiva para aquele genótipo em particular e qual estará mais associada aos efeitos adversos.

Descrição das Figuras

As Figuras 1A-1B mostram a seqüência do gene *NAT2* (alelo selvagem), (SEQ ID NO:1). Estas figuras contém a seqüência nucleotídica do tipo selvagem e a seqüência de aminoácidos (SEQ ID NO:2). O nucleotídeo de número 1 refere-se a adenosina do códon de iniciação "ATG", o qual encontra-se sublinhado. A posição das bases referente aos seis novos SNPs descobertos na região codificante do gene encontram-se sublinhadas e em negrito e correspondem as substituições de bases listadas na Tabela 2. O códon de terminação está indicado por um asterisco (*). Adicionalmente, as trocas de aminoácidos encontram-se sublinhadas e em negrito.

A seguir são apresentadas definições importantes para a perfeita compreensão do escopo da presente invenção.

"Amplificação de ácidos nucléicos" refere-se a métodos tais como a reação da polimerase em cadeia (PCR) e reação em cadeia da ligase (LCR). Estes métodos são bem conhecidos, amplamente disseminados e tanto os equipamentos como os reagentes para a execução da técnica de PCR estão comercialmente disponíveis. Os oligonucleotídeos utilizados para a amplificação de uma região específica do cromossomo são preferencialmente complementares e hibridam especificamente a seqüências na região cromossômica ou em regiões que flanqueiam a região alvo. As seqüências geradas por amplificação podem ser seqüenciadas diretamente ou ainda serem clonadas.

"Sequenciamento de DNA" refere-se a uma técnica utilizada para determinação exata da seqüência nucleotídica de um fragmento particular de DNA ou de um genoma inteiro. A ordem dos pares de bases na molécula de DNA fornece uma informação específica da seqüência de aminoácidos de uma proteína a ser produzida por um determinado gene.

"Condições de estringência" para hibridações referem-se às condições de temperatura e concentração de tampão que permite a hibridação de um ácido nucléico particular a outro ácido nucléico sendo que o primeiro ácido nucléico pode ser perfeitamente complementar ao segundo, ou pode somente compartilhar algum grau de complementariedade, menor que o perfeito. Por exemplo, algumas condições de alta estringência podem ser utilizadas, as quais distinguem perfeitamente ácidos nucléicos complementares daqueles com complementariedade menor.

"Clonagem" refere-se ao uso de técnicas de recombinação *in vitro* a fim de inserir um gene particular ou outra seqüência de DNA numa molécula que servirá como vetor. Para se obter sucesso na clonagem de um determinado gene, é necessário o uso de métodos para a geração de fragmentos de DNA, que sejam capazes de se ligar a moléculas vetores, com conseqüente introdução da molécula híbrida em uma célula hospedeira na qual poderá se replicar, para então proceder-se a seleção dos clones contendo o gene alvo.

"Veículo de clonagem" refere-se a um DNA de plasmídeo ou bacteriófago, ou outra seqüência de DNA, a qual seja capaz de se replicar numa célula hospedeira. O veículo (ou vetor de clonagem) é caracterizado pela presença de um ou mais sítios de restrição no qual cada seqüência de DNA pode ser cortada sem a perda da função biológica do DNA o qual pode conter um marcador útil para a identificação e seleção das células transformadas.

"Gene" refere-se a uma seqüência de DNA portando informação genética. Esta pode ser expressa através do RNA mensageiro, formando uma seqüência de aminoácidos característica de um peptídeo específico. O termo "gene" inclui regiões não codificantes (regulatórias), as quais não são transcritas, bem como regiões codificantes para RNAs que não serão posteriormente traduzidas na forma de proteínas.

A seqüência da presente invenção foi obtida a partir do DNA extraído de células humanas.

"Oligonucleotídeo" refere-se a um ácido nucléico de fita simples com tamanho variando entre 2 e 60 bases. Os oligonucleotídeos freqüentemente são sintéticos, mas podem também ser produzidos a partir de polinucleotídeos que ocorrem naturalmente. Uma sonda é um oligonucleotídeo utilizado, em experimentos laboratoriais, para detectar uma seqüência complementar em meio a uma mistura de moléculas de ácidos nucléicos. A sonda é capaz de se ligar ao ácido nucléico alvo com seqüência complementar através de um ou mais tipos de ligações químicas, usualmente através do pareamento complementar de bases via pontes de hidrogênio. As sondas oligonucleotídicas possuem freqüentemente de 5 a 60 nucleotídeos, variando mais freqüentemente entre 15 e 30 bases de tamanho. Um oligonucleotídeo pode incluir bases naturais (A, T, G, C) ou modificadas (7-deazaguanosina, iosina, etc). Além disto, as bases podem ser unidas por ligações outras que não a ligação fosfodiéster, tais como uma ligação fosfodiéster ou uma ligação fosforotioato.

"Farmacogenômica e Farmacogenética", Farmacogenômica é a aplicação de abordagens e tecnologias empregadas na Genômica e identificação de alvos para drogas. Em outras palavras, a farmacogenômica utiliza informação genética para predizer se uma droga irá contribuir positivamente ou negativamente no tratamento de um paciente. Farmacogenética é o estudo da variação da ação e reação às drogas e sua relação com o conteúdo genético do paciente. Os indivíduos respondem diferentemente aos tratamentos com drogas; alguns positivamente, outros sem modificações óbvias em sua condição e ainda outros com efeitos colaterais e/ou reações

alérgicas. A Farmacogenética é um subconjunto da farmacogenômica, empregando métodos e técnicas da Genômica e da Bioinformática para a identificação de correlações entre características genômicas, como por exemplo, SNPs, e perfis de resposta característicos.

"Polimorfismos", em termos gerais, a habilidade de algo aparecer em várias formas. Especificamente, a existência de duas ou mais formas alternativas (alelos) de um loco cromossomal diferindo na seqüência nucleotídica.

"Seqüência referência" é a seqüência nucleotídica do gene que codifica para a enzima NAT2 (SEQ ID NO:1) e a seqüência do aminoácido correspondente da proteína NAT2 (SEQ ID NO:2), como descrito por Rieder et al., 2003 (submissão direta) número de acesso no geneBank (AY331807).

"Polimorfismo de base única ou SNP" refere-se à substituição de um único nucleotídeo por outro com os dois ou mais estados sendo encontrados na população numa freqüência a partir de 1%.

"Hospedeiro" inclui procariotos e eucariotos, tais como, bactérias, leveduras e fungos filamentosos, bem como células vegetais e animais. O termo inclui um organismo ou célula que recebe um veículo de expressão ou de clonagem replicável.

"Promotor" refere-se a seqüência de DNA reconhecida por uma RNA polimerase. A presença de tal seqüência permite que a RNA polimerase se ligue ao DNA e inicie a transcrição de seqüências gênicas operacionalmente ligadas.

"Região promotora" é a região que inclui a seqüência promotora ou regulatória, bem como outras seqüências, as

quais, podem ser necessárias para a iniciação da transcrição. A presença da região promotora é necessária para levar a expressão de outras seqüências gênicas operacionalmente ligadas.

5 **"Fenótipo de acetilação rápida"** refere-se a características de metabolização de compostos por transferência de um grupamento acetil a partir da acetil-CoA, que em alguns indivíduos é rápida em comparação com outros indivíduos.

10 **"Fenótipo de acetilação lenta"** é a característica de um indivíduo, no qual, a acetilação de compostos por transferência de um grupamento acetil a partir da acetil-CoA, é lenta em comparação com outros indivíduos.

"Reações adversas" referem-se a efeitos não esperados
15 ou negativos induzidos por uma droga durante um tratamento quimioterápico. As reações adversas podem ser locais, sistêmicas ou alergênicas.

Descrição Detalhada da Invenção

 Esta invenção relata a identificação de seis novos
20 SNPs na região codificante do gene que codifica para a proteína N-acetiltransferase 2 (NAT2) humana em indivíduos residentes em duas diferentes regiões geográficas do Brasil. Os SNPs aqui descritos foram identificados através das técnicas de Reação em Cadeia da Polimerase (PCR) e
25 seqüenciamento dos produtos amplificados. A detecção de polimorfismos em seqüências específicas de DNA pode ser obtida por uma variedade de métodos incluindo, mas não limitada a i) polimorfismo de tamanho de fragmentos de restrição (PCR-RFLP) baseado na clivagem específica por uma

enzima de restrição de um sítio alelo específico, (kan e Dozy, Lancet ii:910-912, 1978); ii) hibridação com sondas oligonucleotídicas alelo específicas (Wallace *et al.*, Nucl Acids Res. 6:3543-3557 1978), incluindo oligonucleotídeos
5 imobilizados (Saiki *et al.*, Proc. Natl. Acad. Sci. USA 86:6230-6234 1989) ou arranjos de oligonucleotídeos (Maskos na Southern Nucl. Acids Res. 17:2503-2516 1993); iii) PCR alelo específico (Newton *et al.*, Nucl Acids Res 17:2503-2516 1989); iv) detecção e reparo de pareamento errôneo
10 "mismatch-repair detection" (MRD) (Faham & Cox, Genome Res. 5:474-482, 1995); v) gel de eletroforese desnaturante de gradiente "Denaturing-gradient gel electrophoresis" (DGGE) (Fisher *et al.*, Proc. Natl. Acad. Sci. USA 80:1579-1583 1983); vi) detecção de polimorfismo por conformação de fita
15 simples "Single strand conformation polymorphism" (SSCP) (Orita *et al.*, Genomics 5:874-879 1983); vii) clivagem de pareamento errôneo por RNase (Meyers *et al.*, Science 230:1242 1985); viii) método químico (Cotton *et al.*, Proc. Natl. Acad. Sci. USA 82:4397-440 1988) ou enzimático (Youil
20 *et al.*, Proc. Natl. Acad. Sci. USA 92:87-91 1995); ix) clivagem de DNA heteroduplex; x) métodos baseados na extensão de *primers* alelo específicos (Syvanen *et al.*, Genomics 8:684-692 1990); xi) ensaio de ligação de oligonucleotídeo "Oligonucleotide ligation Assay" (OLA)
25 (Landegren *et al.*, Science 241:1077 1988); xii) reação em cadeia de ligação alelo específica "allele-specific ligation chain reaction (LCR) (Barrany, Proc. Natl. Acad. Sci. USA. 88:189-193 1991); xiii) seqüenciamento radioativo ou fluorescente (Sambrook, J. & Russell, D. W. 2001;

Molecular cloning: a laboratory manual. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York).

Os 6 polimorfismos descritos nas FIGs. 1A-1B e Tabela 2 estão localizados na região codificante do gene *NAT2* e incluem as seguintes substituições (T → C na base 29, G → T na base 152, G → A na base 203, C → T na base 228, C → T na base 458, e A → G na base 600). Com exceção dos SNPs C228T e A600G que são silenciosos, todos os outros 4 SNPs modificam o aminoácido transcrito nas seguintes posições (SNP T 29 C troca de I → T no aminoácido 10, SNP G 152 T, troca de G → V no aminoácido 51, SNP G 203 A, troca de C → Y no aminoácido 68, SNP C 458 T, troca de T → I no aminoácido 153).

Como descrito acima, a presente invenção está relacionada a uma sequência de DNA compreendida na região codificante do gene *NAT2*, na qual foram identificados 6 novos SNPs. Variantes muito próximas também estão incluídas como parte desta invenção, bem como ácidos nucleicos recombinantes que contenham qualquer dos SNPs aqui descritos ou as regiões acima ou abaixo dos mesmos na sequência descrita nas FIGs. 1A-1B e reivindicações.

Esta invenção também está relacionada à utilização de métodos que utilizem ácidos nucleicos (DNA ou RNA) isolados e/ou recombinantes que sejam caracterizados pela sua capacidade de hibridarem a um ácido nucleico que codifique uma proteína ou polipeptídeo, tal como um ácido nucleico que contenha a sequência descrita nas FIGs. 1A-1B ou parte de um DNA estranho que contenha o mínimo de nucleotídeos suficientes para codificar um polipeptídeo que contenha

parte da seqüência de aminoácidos descrita nas FIGs. 1A-1B e Tabela 2 ou que codifiquem para equivalentes funcionais, ou seja, um polipeptídeo que quando incorporado a uma célula hospedeira tenha toda ou parte da atividade da proteína NAT2. Um equivalente funcional da proteína NAT2 deve ter uma seqüência de aminoácido similar (no mínimo 65% de identidade) e características similares a proteína NAT2. Um ácido nucléico que hibrida com outro ácido nucléico que codifica para a proteína NAT2 ou polipeptídeo, tais como descrito nas FIGs. 1A-1B e Tabela 2 podem ser de fita dupla ou de fita simples. Hibridação com um DNA contendo toda ou parte da seqüência descrita nas FIGs. 1A-1B inclui hibridação tanto com a fita mostrada como com a sua fita complementar.

Ácidos nucléicos, incluindo DNA ou RNA, podem ser detectados e isolados por hibridação sob condições de estringência alta ou moderada, as quais são escolhidas de forma a não permitir a hibridação de seqüências nucleotídicas não complementares. "Condições de alta estringência" e "condições de estringência moderada" para a hibridação de ácidos nucléicos são exemplificadas em Sambrook, J. & Russell, D. W. 2001; *Molecular cloning: a laboratory manual*. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York. As condições exatas que determinam a estringência da hibridação dependem não somente da força iônica, temperatura e concentração de agentes desestabilizadores, tais como formamida, mais também de fatores tais como o tamanho da seqüência de ácido nucléico, a composição das bases, percentual de pareamento

errôneo entre as duas seqüências e a frequência de ocorrência. Assim, as condições de alta ou moderada estringência podem ser calculadas empiricamente.

A presente invenção também diz respeito ao uso da seqüência nucleotídica aqui descrita, ou parte da mesma, para a identificação de sondas de DNA específicas para o gene *NAT2* ou oligonucleotídeos para a amplificação (através de PCR) do gene *NAT2*.

A presente invenção também descreve, na Tabela 1, oligonucleotídeos para a amplificação de dois fragmentos, do gene de *NAT2*, que, juntos, compreendem toda a região codificante do respectivo gene contendo os polimorfismos descritos. Os seis novos SNPs presentes na região codificante do gene *NAT2* foram identificados a partir do seqüenciamento automático dos fragmentos gerados após a amplificação do DNA por PCR com os dois pares de oligonucleotídeos descritos na Tabela 1. Assim, estes oligonucleotídeos podem ser utilizados para detecção dos mesmos SNPs em quaisquer amostras de DNA provenientes de material biológico humano através do PCR e seqüenciamento.

Os seis novos SNPs descritos nas FIGs. 1A-1B e tabela 2 da presente invenção podem ser utilizados para a determinação de haplótipos, os quais, quando estendidos e associados aos SNPs já descritos, podem ser utilizados para a predição do fenótipo de acetilação (acetilador lento ou rápido) de um determinado indivíduo. Como descrito no exemplo 1, o DNA pode ser isolado de diferentes indivíduos e, através de técnicas de seqüenciamento de DNA, a seqüência do gene de *NAT2* de um indivíduo pode ser obtida.

Após a identificação dos polimorfismos, o genótipo é determinado permitindo assim a predição do fenótipo.

A invenção também está relacionada a um método de criação de um protocolo prognóstico para um paciente recebendo algum agente terapêutico metabolizado por NAT2 tais como, amonafida, isoniazida, fenilzina, hidrazina, dapsona, procainamida, sulfametazina e outras sulfonamidas. O método inclui: a) identificação de pacientes recebendo uma destas drogas; b) determinação do fenótipo de acetilação (rápidos ou lentos) com base no genótipo; e c) conversão dos dados obtidos no passo (b) em um protocolo prognóstico. O protocolo prognóstico pode incluir a prevenção da eficácia da droga, predição do prognóstico do paciente, predição de interações entre drogas, e predição de efeitos adversos. A combinação das seqüências de DNA geradas com o fenótipo de acetilação fornece um protocolo prognóstico específico para àquele indivíduo. Por exemplo, estudos têm mostrado que a isoniazida é mais tóxica em pacientes com fenótipo de acetiladores lentos que em pacientes com fenótipo de acetiladores rápidos. Portanto, a identificação destes pacientes usando as seqüências nucleotídicas fornecidas aqui pode auxiliar no desenho de esquemas terapêuticos balanceando eficácia e toxicidade.

Em outro exemplo, relacionado a protocolo prognóstico, pacientes identificados como acetiladores lentos estão sob risco de hipersensibilidade cutânea quando tratados com trimetoprin-sulfametoxazole (TMP-SMZ). Desta forma, antes de prescrever uma droga particular, tal como trimetoprin-sulfametoxazole (TMP-SMZ), o médico pode solicitar um teste

para a identificação do fenótipo de acetilação do paciente baseado no perfil genotípico e, uma vez o paciente sendo um acetilador lento o médico então pode prescrever uma terapêutica alternativa.

5 **Ensaio Clínico**

Esta invenção também relaciona-se a um método para auxiliar na avaliação de novos fármacos através de ensaios clínicos (*Clinical Trials*). O método inclui: a) administração de um agente terapêutico (metabolizado por NAT2) a um indivíduo e mensuração de sua eficácia; b) determinação do *status* de acetilação do indivíduo (rápido ou lento) baseado no genótipo ou haplótipo do gene de NAT2 incluindo os SNPs descritos na presente invenção e c) determinação a partir dos itens (a) e (b) do agente terapêutico seria mais eficaz para aquele genótipo em particular. Os ensaios clínicos geralmente baseiam-se em informações fornecidas pelo paciente, incluindo idade, sexo e histórico familiar. A invenção fornece uma seqüência de DNA do gene de NAT2 contendo novos SNPs os quais podem ser adicionados ao banco de SNPs e utilizados como fatores genéticos do paciente em um ensaio clínico. Como descrito aqui, um genótipo individual pode ser determinado por métodos de seqüenciamento de DNA descritos no exemplo 1 desde que seus haplótipos sejam de fase conhecida.

Após a administração da droga o genótipo do paciente pode então ser comparado com a eficácia da mesma e ocorrência de quaisquer efeitos adversos. Baseado nesta informação, fármacos podem ser desenvolvidos especificamente para genótipos individuais os quais estejam

relacionados com uma maior eficácia e/ou menor toxicidade. Genótipos de pacientes que não respondem ao fármaco podem ser agrupados e fármacos que utilizem vias alternativas de acetilação ser desenvolvidas.

5 **Freqüência dos dados**

A presente invenção também relata a freqüência dos novos SNPs em duas diferentes populações do Brasil, como descrito na Tabela 3. Os dados mostram que os SNPs identificados aparecem em diferentes freqüências e são
10 específicos nas duas populações estudadas, o que corrobora a hipótese de se tratarem de duas populações geneticamente distintas e conseqüentemente com fenótipos de acetilação também distintos. Os SNPs T29C, G152T, G203A, C458T e A600G ocorrem exclusivamente na amostra populacional do Rio de
15 Janeiro e o SNP C228T ocorre exclusivamente na amostra populacional de Goiás.

Como descrito anteriormente, a enzima NAT2 tem sido associada a uma variedade de doenças e desordens incluindo câncer de bexiga, câncer de colo, câncer de próstata,
20 carcinoma celular urotelial e doença de Gilbert's. Mais particularmente, a identificação de indivíduos mais suscetíveis a metabolização de compostos com potencial mutagênico e/ou carcinogênico incluindo 2-aminofluoreno, 4-aminobifenil, benzidina, beta-naftilamina e certas
25 arilaminas heterocíclicas presentes em pirolisados de proteínas, pode ser muito benéfica na prevenção, por parte do indivíduo, da utilização de tais compostos. Os inventores disponibilizam uma seqüência de DNA contendo novos SNPs, os quais podem ser úteis para a identificação

de indivíduos, com polimorfismos no gene *NAT2* que estão associados com estas doenças e afetam o metabolismo dos compostos descritos acima.

Ácidos nucleicos associados a doenças e úteis para métodos diagnósticos incluem oligonucleotídeos com um tamanho mínimo de 15 nucleotídeos, preferencialmente um tamanho mínimo de 20 nucleotídeos e mais preferencialmente um tamanho mínimo de 25 nucleotídeos que hibride especificamente com um ácido nucleico associado a doenças.

A amostra a ser analisada deve ser submetida a um processo de extração de DNA. Entende-se que o método de extração de DNA dependerá da natureza da amostra a ser analisada. O DNA resultante deverá ser submetido a PCR para amplificação da região contendo os SNPs e em seguida seqüenciados.

A seqüência polinucleotídica descrita na presente invenção (ou parte da mesma), principalmente aquela relacionada à identificação dos SNPs aqui descritos, representa uma valiosa fonte de informação para a caracterização de indivíduos em termos de haplótipos e outros subgrupos, como por exemplo na investigação de suscetibilidade ao tratamento com alguns fármacos particulares. Esta abordagem é ainda facilitada pelo armazenamento destas informações em uma base de dados informatizada e sua posterior análise por programas de bioinformática. Assim, a seqüência polinucleotídica da presente invenção é particularmente útil como componente de banco de dados utilizado para a identificação de seqüências e outras buscas. O estoque das informações da seqüência em

qualquer mídia e sua utilização em bancos de dados de seqüências com relação a "polinucleotídeo ou seqüência de polinucleotídeos da invenção" sobre qualquer característica química ou física do polinucleotídeo da presente invenção
5 que pode ser reduzido a, convertido em, ou estocado em alguma mídia, tais como, um disquete ou um CD, preferencialmente numa forma legível em um computador.

Exemplo 1

Amostras de sangue foram coletadas de 404 indivíduos
10 brasileiros consanguineamente não relacionados para a genotipagem de *NAT2*. As amostras utilizadas compreenderam indivíduos de duas regiões geograficamente distintas do Brasil (Rio de Janeiro e Goiás) e foram coletadas no Hospital Universitário Clementino Fraga Filho da
15 Universidade Federal do Rio de Janeiro (UFRJ) e no Hospital de Referência Anuar Auad do Estado de Goiás. O DNA genômico foi isolado deste material utilizando o kit comercial FlexiGene DNA Kit (Qiagen Inc., USA)

Os fragmentos de DNA cobrindo toda a região
20 codificante do gene *NAT2* para posterior seqüenciamento foram gerados a partir da amplificação pela técnica de "reação de polimerase em cadeia" (PCR), através da utilização de um par de oligonucleotídeos (*NAT2ED* e *NAT2ER*, Tabela 1). As condições para a reação de PCR foram as
25 seguintes: 100 ng de DNA genômico, 200 ng de cada oligonucleotídeo, 0,2 mM de dNTPs, 4.0 mM MgCl₂, 10% glicerol (Invitrogen Life Technologies, Gaithersburg, MD, USA), 10 mM Tris-HCl pH 9.0, 50 mM KCl, 0.1% Triton X-100, and 1.1 U da mistura de duas DNA polimerases (1 U de *Taq*

DNA polimerase e 0.1 U de *Tli* DNA polimerase - Promega Corporation, USA). Foram usados em um volume final de 50 µl para cada amostra. A amplificação foi realizada nas seguintes condições de ciclagem: uma desnaturação inicial a 94°C for 5 min, seguida de 35 ciclos de 94°C por 1 min. 57.5°C for 1 min e 72°C por 1 minuto. O passo de extensão final foi realizado a 72°C por 5 min. Após a amplificação, aproximadamente 20 % do produto amplificado foi examinado em gel de agarose. Antes da etapa de seqüenciamento do DNA, os produtos de PCR foram purificados com acetato de amônio 2.5 M.

Tabela 1

Seqüência dos oligonucleotídeos utilizados para a amplificação e/ou seqüenciamento da região codificante do gene *NAT2*

NAT2 ED	5' - TTA GTC ACA CGA GGA AAT CAA A - 3'
NAT2 ER	5' - AAA TGC TGA CAT TTT TAT GGA TGA - 3'
NAT2 ID	5' - ACC ATT GAC GGC AGG AAT TA - 3'
NAT2 IR	5' - TGG TCC AGG TAC CAG ATT CC - 3'

^{ED}- Externo direto; ^{ER}- Externo Reverso; ^{ID}- Interno direto; ^{IR}- Interno Reverso

Quatro reações de seqüenciamento foram realizadas para cada amostra utilizando o Kit ABI PRISM Big Dye Terminator v. 3.1 (PE Applied BioSystems), de acordo com as recomendações do fabricante em um seqüenciador de capilar "ABI PRISM 3730 DNA Analyzer" (PE Applied BioSystems). Em cada reação (10 µl de volume final), foram utilizados aproximadamente 20 ng de produto amplificado, 3,2 pmol do

iniciador, 0,5 μ l de Big Dye e 1,5 μ l de tampão 5X (fornecido no kit).

A análise das seqüências e identificação das SNPs presentes na região codificante de *NAT2* foi feita através do software SeqScape v. 2.5 (Applied Biosystems). (<http://www.appliedbiosystems.com/catalog/myab/StoreCatalog/products/CategoryDetails.jsp?hierarchyID=101&category3rd=111917&trail=no>). A seqüência AY331807 (<http://www.ncbi.nlm.nih.gov/GenBank>) foi usada como referência. As seqüências obtidas, referentes a cada amostra clínica individual, foram agrupadas sob forma de projeto de acordo com a utilização do SeqScape. As seqüências foram comparadas por alinhamento com a seqüência referência e os sítios polimórficos (SNPs), foram identificados.

As figuras 1A-1B mostram as seqüências nucleotídica e aminoacídica do tipo selvagem do gene *NAT2* descrita por Blum *et al.*, (*DNA and Cell Bio.*, 9:192-203, 1990), incluindo o sítio de iniciação da tradução "ATG". A posição dos seis novos SNPs descobertos estão sublinhadas e em negrito. Adicionalmente, as trocas aminoacídicas também estão sublinhadas e em negrito.

A Tabela 2 contém a lista dos polimorfismos de base única (SNPs) descobertos no gene *NAT2*. A posição do nucleotídeo de acordo com as FIGs. 1A-1B é listada na primeira coluna. A segunda coluna descreve as trocas de bases a partir do gene tipo selvagem. A posição do aminoácido afetado pela troca da base nucleotídica é listada na terceira coluna. As trocas de aminoácidos

decorrentes de 4 dos 6 SNPs adicionais (base 29, 152, 203, 228, 458 e 600) são listadas na quarta coluna.

Tabela 2

Posição dos SNPs	Troca de nucleotídeo	posição do aminoácido	Troca de aminoácido
29	T para C	10	I para T
152	G para T	51	G para V
203	G para A	68	C para Y
228	C para T	76	Não ocorre
458	C para T	153	T para I
600	A para G	158	Não ocorre

Significância dos novos SNPs

Nenhuma troca de aminoácido ocorre quando da presença do SNP na base 228 e 600 da seqüência descrita nas FIGs. 1A-1B. Trata-se de SNPs localizados no terceiro nucleotídeo dos códons 76 e 158 respectivamente.

Esta invenção fornece ainda quatro SNPs adicionais, não sinônimos, presentes na região codificante do gene de *NAT2*, os quais alteram a seqüência de aminoácidos da proteína.

A substituição no nucleotídeo 29 (T→C) na região codificante do gene *NAT2*, resulta numa troca de aminoácido No códon 10 (I→T: isoleucina para treonina). Neste caso temos a troca de um aminoácido cadeia lateral apolar, hidrofóbico por um polar. Tendo em vista a diferença entre as cadeias laterais destes aminoácidos, muito provavelmente esta substituição pode afetar a estrutura, flexibilidade, estabilidade e enovelamento da proteína *NAT2*.

A substituição no nucleotídeo 152 (G→T) na região codificante do gene *NAT2*, resulta numa troca de aminoácido

no códon 51 (G→V: glicina para valina). Aparentemente uma troca conservativa (aminoácidos com cadeias laterais similares). Contudo, se localizada em alguma região crítica (sítios de ligação do substrato ou co-fatores), esta troca
5 pode afetar a estrutura ou atividade da proteína.

A substituição no nucleotídeo 203 (G→A) na região codificante do gene *NAT2* resulta numa troca de aminoácido na posição 68 (C→Y: cisteína para tirosina). Neste caso temos a troca de um aminoácido apolar por um polar não
10 carregado. Tendo em vista a diferença entre as cadeias laterais destes aminoácidos, é provável que esta substituição afete a estrutura, flexibilidade, estabilidade e enovelamento da proteína *NAT2*. Adicionalmente, essa substituição ocorre no sítio catalítico da enzima podendo
15 alterar sua atividade.

A substituição no nucleotídeo 458 (C→T) na região codificante do gene *NAT2*, resulta numa troca de aminoácido na posição 153 (T→I: treonina para isoleucina). Neste caso temos a troca de um aminoácido polar não carregado por um
20 apolar. Tendo em vista a diferença entre as cadeias laterais destes aminoácidos, muito provavelmente esta substituição pode afetar a estrutura, flexibilidade, estabilidade e enovelamento da proteína *NAT2*.

A combinação de um ou todos os SNPs aqui descobertos
25 com aqueles já descritos na literatura pode ter efeitos adicionais na estrutura, atividade, dobramento e estabilidade da proteína. Evidências sugerem que o fenótipo metabólico seja gerado a partir da combinação de todos os SNPs presentes no indivíduo. Utilizando análises de

regressão linear múltipla, pesquisadores foram capazes de formular expressões matemáticas capazes de prever a capacidade metabólica da enzima NAT2 baseados no genótipo (Maisel *et al.*, Pharmacogenomics, 1997). De acordo com estas análises, todas as substituições de nucleotídeos, mesmo aquelas que não causam a troca de aminoácidos, afetam o fenótipo de alguma forma. Embora eles possam prever com razoável segurança o fenótipo da maioria dos indivíduos, se todos os SNPs conhecidos forem levados em consideração a precisão do modelo é consideravelmente maior. Uma vez que neste modelo os autores tiveram um indivíduo para o qual o fenótipo não pode ser predito, existe uma alta probabilidade da existência de SNPs adicionais no gene cujas análises realizadas não foram capazes de detectar.

Dados de Freqüência

A Tabela 3 mostra a freqüência alélica dos seis novos SNPs descritos na presente invenção em duas regiões distintas do Brasil. A primeira coluna lista os diferentes SNPs novos identificados nessa amostragem. A segunda, quinta e oitava colunas indicam as freqüências dos SNPs na amostra total, no Rio de Janeiro e em Goiás, respectivamente. As colunas 3, 4, 6, 7, 9 e 10 detalham se e quantos indivíduos foram homozigotos ou heterozigotos para o polimorfismo listado. A freqüência na segunda coluna refere-se ao número de alelos com polimorfismo dividido pelo número total de alelos na amostragem a troca de bases e posição referem-se às coordenadas das FIGS. 1A-1B.

A Tabela 4 lista a frequência dos SNPs descritos na invenção com os sítios polimórficos adicionais, suas respectivas frequências nas diferentes regiões estudadas e, para cada SNP, se a variante mutante foi encontrada em 5 homozigose ou heterozigose. A frequência é o número de alelos contendo o polimorfismo dividido pelo número total de alelos na amostragem. A troca de bases e a posição das bases, referem-se às coordenadas das FIGS. 1A-1B.

Tabela 3

**Frequência alélica dos SNPs da presente invenção no gene
NAT2 em duas diferentes regiões do Brasil**

SNPs	TOTAL		RIO DE JANEIRO		GOIÁS				
	% Heterozigotos	Homozigotos	% Heterozigotos	Homozigotos	% Heterozigotos	Homozigotos			
29C	0.1	01/404	0	0.1	01/298	0	0	0	0
152T	0.1	01/404	0	0.2	01/298	0	0	0	0
203 A	0.1	01/404	0	0.2	01/298	0	0	0	0
228 T	0.1	01/404	0	0	0	0	0.5	01/106	0
458 T	0.1	01/404	0	0.2	01/298	0	0	0	0
600G	0.1	01/404	0	0.1	01/298	0	0	0	0

Tabela 4

Frequência dos SNPs identificados no gene *NAT2* em duas diferentes regiões do Brasil

SNPs	TOTAL		RIO DE JANEIRO			GOIÁS			
	% Heterozigotos	Homozigotos	% Heterozigotos	Homozigotos	% Heterozigotos	Homozigotos	% Heterozigotos	Homozigotos	
29C	0.1	01/404	0	0.1	01/298	0	0	0	0
70A	0.1	01/404	0	0.2	01/298	0	0	0	0
152T	0.1	01/404	0	0.2	01/298	0	0	0	0
191A*	4.1	31/404	01/404	5	26/298	01/298	2	05/106	0
203A	0.1	01/404	0	0.2	01/298	0	0	0	0
228T	0.1	01/404	0	0	0	0	0.5	01/106	0
282T*	37	184/404	57/404	38	144/298	41/298	34	40/106	16/106
341C*	38	176/404	65/404	40	136/298	50/298	33	40/106	15/106
345T	0.3	02/404	0	0	0	0	1	02/106	0
403G	0.6	04/404	0	1	04/298	0	0.5	0	0
458T	0.1	01/404	0	0.2	01/298	0	0	0	0
472C	0.6	05/404	0	0.5	03/298	0	1	02/106	0
481T*	35	176/404	54/404	36	137/298	40/298	32	39/106	14/106
590A*	27	157/404	29/404	26	119/298	18/298	28	38/106	11/106
600G	0.1	01/404	0	0.1	01/298	0	0	0	0
609T	0.4	03/404	0	0.3	02/298	0	0.5	01/106	0
683T	0.2	02/404	0	0.3	02/298	0	0	0	0
766G	0.7	06/404	0	0.7	04/298	0	1	02/106	0
803G*	40	184/404	69/404	41	143/298	51/298	36	41/106	18/106
838A	0.5	04/404	0	0.5	03/298	0	0.5	01/106	0
G857A*	4.4	36/404	0	4.5	27/298	0	4.2	09/106	0

Apesar de ilustrada e descrita aqui com referência a determinadas representações específicas, a presente

invenção não tem, no entanto, a intenção de estar limitada aos detalhes mostrados. Várias modificações podem ser feitas nos detalhes dentro do âmbito e alcance de equivalentes sem se afastar do espírito da invenção.

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CTGTACTGGG CTCTGA

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TGTACTGGGC TCTGAC

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ACTTCTGTAC TGGGCTC

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CTGTACTGGG CTCTGAC

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GTACTGGGCT CTGACCA

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TACTGGGCTC TGACCAC

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ACTGGGCTCT GACCACA

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TCAATCAACT TCTGTACT

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AATCAACTTC TGTACTGG

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ATCAACTTCT GTACTGGG

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oligosPatNat2.txt

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TCAACTTCTG TACTGGGC

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ACTTCTGTAC TGGGCTCT

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GTACTGGGCT CTGACCAC

18

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<400> SEQUENCE: 64

TACTGGGCTC TGACCACA

18

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ACTGGGCTCT GACCACAA

18

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CTGGGCTCTG ACCACAAT

18

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GGTCAATCAA CTTCTGTAC

19

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GTCAATCAAC TTCTGTA

19

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TCAATCAACT TCTGTA

19

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CAATCAACTT CTGTA

19

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AATCAACTTC TGTACT

19

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ATCAACTTCT GTACT

19

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TCAACTTCTG TACTGGGCT

19

<210> SEQ ID NO 74

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CAACTTCTGT ACTGGGCTC

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AACTTCTGTA CTGGGCTCT

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ACTTCTGTAC TGGGCTCTG

19

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CTTCTGTACT GGGCTCTGA

19

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<211> LENGTH: 19

<212> TYPE: DNA

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TTCTGTACTG GGCTCTGAC 19

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TCTGTACTGG GCTCTGACC 19

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CTGTACTGGG CTCTGACCA 19

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TGTACTGGGC TCTGACCAC 19

<210> SEQ ID NO 82
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GTACTGGGCT CTGACCACA 19

<210> SEQ ID NO 83

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TACTGGGCTC TGACCACAA

19

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ACTGGGCTCT GACCACAAT

19

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CTGGGCTCTG ACCACAATC

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AGGTCAATCA ACTTCTGTAC

20

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<400> SEQUENCE: 87

GGTCAATCAA CTTCTGTACT

20

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GTCAATCAAC TTCTGTACTG 20

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TCAATCAACT TCTGTACTGG 20

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CAATCAACTT CTGTACTGGG 20

<210> SEQ ID NO 91
<211> LENGTH: 20
<212> TYPE: DNA
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AATCAACTTC TGTACTGGGC 20

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ATCAACTTCT GTACTGGGCT 20

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TCAACTTCTG TACTGGGCTC 20

<210> SEQ ID NO 94
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<400> SEQUENCE: 94

CAACTTCTGT ACTGGGCTCT 20

<210> SEQ ID NO 95
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<400> SEQUENCE: 95

AACTTCTGTA CTGGGCTCTG 20

<210> SEQ ID NO 96
<211> LENGTH: 20
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<400> SEQUENCE: 96

ACTTCTGTAC TGGGCTCTGA 20

<210> SEQ ID NO 97
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<400> SEQUENCE: 97

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CTTCTGACT GGGCTCTGAC

20

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<400> SEQUENCE: 98

TTCTGACTG GGCTCTGACC

20

<210> SEQ ID NO 99
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<212> TYPE: DNA
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TCTGACTGG GCTCTGACCA

20

<210> SEQ ID NO 100
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CTGTACTGGG CTCTGACCAC

20

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TGTACTGGGC TCTGACCACA

20

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<400> SEQUENCE: 102

GTACTGGGCT CTGACCACAA

20

<210> SEQ ID NO 103
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 <212> TYPE: DNA
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TACTGGGCTC TGACCACAAT

20

<210> SEQ ID NO 104
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<400> SEQUENCE: 104

ACTGGGCTCT GACCACAATC

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CTGGGCTCTG ACCACAATCG

20

<210> SEQ ID NO 106
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<400> SEQUENCE: 106

CAGGTCAATC AACTTCTGTA C

21

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<400> SEQUENCE: 107

AGGTCAATCA ACTTCTGTAC T

21

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<211> LENGTH: 21

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<400> SEQUENCE: 108

GGTCAATCAA CTTCTGTACT G

21

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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 109

GTCAATCAAC TTCTGTACTG G

21

<210> SEQ ID NO 110

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TCAATCAACT TCTGTACTGG G

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<212> TYPE: DNA

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CAATCAACTT CTGTACTGGG C

21

<210> SEQ ID NO 112

<211> LENGTH: 21

<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 112

AATCAACTTC TGTACTGGGC T 21

<210> SEQ ID NO 113
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ATCAACTTCT GTACTGGGCT C 21

<210> SEQ ID NO 114
<211> LENGTH: 21
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TCAACTTCTG TACTGGGCTC T 21

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CAACTTCTGT ACTGGGCTCT G 21

<210> SEQ ID NO 116
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AACTTCTGTA CTGGGCTCTG A 21

<210> SEQ ID NO 117

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<211> LENGTH: 21
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<400> SEQUENCE: 117

ACTTCTGTAC TGGGCTCTGA C

21

<210> SEQ ID NO 118
<211> LENGTH: 21
<212> TYPE: DNA
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<400> SEQUENCE: 118

CTTCTGTACT GGGCTCTGAC C

21

<210> SEQ ID NO 119
<211> LENGTH: 21
<212> TYPE: DNA
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TTCTGTACTG GGCTCTGACC A

21

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<212> TYPE: DNA
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TCTGTACTGG GCTCTGACCA C

21

<210> SEQ ID NO 121
<211> LENGTH: 21
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<400> SEQUENCE: 121

CTGTACTGGG CTCTGACCAC A

21

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TGTACTGGGC TCTGACCACA A

21

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GTACTGGGCT CTGACCACAA T

21

<210> SEQ ID NO 124
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TACTGGGCTC TGACCACAAT C

21

<210> SEQ ID NO 125
<211> LENGTH: 21
<212> TYPE: DNA
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ACTGGGCTCT GACCACAATC G

21

<210> SEQ ID NO 126
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<212> TYPE: DNA
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CTGGGCTCTG ACCACAATCG G

21

OligosPatNat2.txt

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<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
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<400> SEQUENCE: 127

CCAGGTCAAT CAACTTCTGT AC

22

<210> SEQ ID NO 128
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
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<400> SEQUENCE: 128

CAGGTCAATC AACTTCTGTA CT

22

<210> SEQ ID NO 129
<211> LENGTH: 22
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AGGTCAATCA ACTTCTGTAC TG

22

<210> SEQ ID NO 130
<211> LENGTH: 22
<212> TYPE: DNA
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<400> SEQUENCE: 130

GGTCAATCAA CTTCTGTACT GG

22

<210> SEQ ID NO 131
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<400> SEQUENCE: 131

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GTCAATCAAC TTCTGTACTG GG

22

<210> SEQ ID NO 132
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TCAATCAACT TCTGTACTGG GC

22

<210> SEQ ID NO 133
<211> LENGTH: 22
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CAATCAACTT CTGTACTGGG CT

22

<210> SEQ ID NO 134
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AATCAACTTC TGTACTGGGC TC

22

<210> SEQ ID NO 135
<211> LENGTH: 22
<212> TYPE: DNA
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<220> FEATURES:
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ATCAACTTCT GTACTGGGCT CT

22

<210> SEQ ID NO 136
<211> LENGTH: 22
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<400> SEQUENCE: 136

TCAACTTCTG TACTGGGCTC TG

22

<210> SEQ ID NO 137

<211> LENGTH: 22

<212> TYPE: DNA

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CAACTTCTGT ACTGGGCTCT GA

22

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AACTTCTGTA CTGGGCTCTG AC

22

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ACTTCTGTAC TGGGCTCTGA CC

22

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CTTCTGTACT GGGCTCTGAC CA

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TTCTGTACTG GGCTCTGACC AC

22

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TCTGTACTGG GCTCTGACCA CA

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CTGTACTGGG CTCTGACCAC AA

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TGTACTGGGC TCTGACCACA AT

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GTACTGGGCT CTGACCACAA TC

22

<210> SEQ ID NO 146

<211> LENGTH: 22

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TACTGGGCTC TGACCACAAT CG 22

<210> SEQ ID NO 147
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 <223> OTHER INFORMATION: cDNA for use as primers
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ACTGGGCTCT GACCACAATC GG 22

<210> SEQ ID NO 148
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CTGGGCTCTG ACCACAATCG GT 22

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TCCAGGTCAA TCAACTTCTG TAC 23

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CCAGGTCAAT CAACTTCTGT ACT 23

<210> SEQ ID NO 151

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<211> LENGTH: 23
<212> TYPE: DNA
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<400> SEQUENCE: 151

CAGGTCAATC AACTTCTGTA CTG

23

<210> SEQ ID NO 152
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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AGGTCAATCA ACTTCTGTAC TGG

23

<210> SEQ ID NO 153
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 153

GGTCAATCAA CTTCTGTACT GGG

23

<210> SEQ ID NO 154
<211> LENGTH: 23
<212> TYPE: DNA
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<220> FEATURES:
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<400> SEQUENCE: 154

GTCAATCAAC TTCTGTACTG GGC

23

<210> SEQ ID NO 155
<211> LENGTH: 23
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TCAATCAACT TCTGTACTGG GCT

23

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<210> SEQ ID NO 156
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CAATCAACTT CTGTACTGGG CTC 23

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AATCAACTTC TGTACTGGGC TCT 23

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ATCAACTTCT GTACTGGGCT CTG 23

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TCAACTTCTG TACTGGGCTC TGA 23

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CAACTTCTGT ACTGGGCTCT GAC 23

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AACTTCTGTA CTGGGCTCTG ACC

23

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ACTTCTGTAC TGGGCTCTGA CCA

23

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CTTCTGTACT GGGCTCTGAC CAC

23

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TTCTGTACTG GGCTCTGACC ACA

23

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TCTGTACTGG GCTCTGACCA CAA

23

<210> SEQ ID NO 166
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CTGTACTGGG CTCTGACCAC AAT

23

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TGTACTGGGC TCTGACCACA ATC

23

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GTACTGGGCT CTGACCACAA TCG

23

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TACTGGGCTC TGACCACAAT CGG

23

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ACTGGGCTCT GACCACAATC GGT

23

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CTGGGCTCTG ACCACAATCG GTT

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CTCCAGGTCA ATCAACTTCT GTAC

24

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TCCAGGTCAA TCAACTTCTG TACT

24

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CCAGGTCAAT CAACTTCTGT ACTG

24

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CAGGTCAATC AACTTCTGTA CTGG

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<210> SEQ ID NO 176

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AGGTCAATCA ACTTCTGTAC TGGG

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GGTCAATCAA CTTCTGTACT GGGC

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<400> SEQUENCE: 178

GTCAATCAAC TTCTGTACTG GGCT

24

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<211> LENGTH: 24

<212> TYPE: DNA

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<223> OTHER INFORMATION: cDNA for use as primers

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TCAATCAACT TCTGTACTGG GCTC

24

<210> SEQ ID NO 180

<211> LENGTH: 24

<212> TYPE: DNA

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CAATCAACTT CTGTACTGGG CTCT 24

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AATCAACTTC TGTACTGGGC TCTG 24

<210> SEQ ID NO 182
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ATCAACTTCT GTACTGGGCT CTGA 24

<210> SEQ ID NO 183
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TCAACTTCTG TACTGGGCTC TGAC 24

<210> SEQ ID NO 184
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CAACTTCTGT ACTGGGCTCT GACC 24

<210> SEQ ID NO 185

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<211> LENGTH: 24
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AACTTCTGTA CTGGGCTCTG ACCA

24

<210> SEQ ID NO 186
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<400> SEQUENCE: 186

ACTTCTGTAC TGGGCTCTGA CCAC

24

<210> SEQ ID NO 187
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CTTCTGTACT GGGCTCTGAC CACA

24

<210> SEQ ID NO 188
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TTCTGTACTG GGCTCTGACC ACAA

24

<210> SEQ ID NO 189
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<400> SEQUENCE: 189

TCTGTACTGG GCTCTGACCA CAAT

24

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<210> SEQ ID NO 190
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<213> ORGANISM: Artificial Sequence
<220> FEATURES:
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<400> SEQUENCE: 190

CTGTACTGGG CTCTGACCAC AATC

24

<210> SEQ ID NO 191
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<400> SEQUENCE: 191

TGTACTGGGC TCTGACCACA ATCG

24

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GTACTGGGCT CTGACCACAA TCGG

24

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<400> SEQUENCE: 193

TACTGGGCTC TGACCACAAT CGGT

24

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<400> SEQUENCE: 194

ACTGGGCTCT GACCACAATC GGTT

24

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CTGGGCTCTG ACCACAATCG GTTT

24

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<400> SEQUENCE: 196

TCTCCAGGTC AATCAACTTC TGTAC

25

<210> SEQ ID NO 197
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<400> SEQUENCE: 197

CTCCAGGTCA ATCAACTTCT GTACT

25

<210> SEQ ID NO 198
<211> LENGTH: 25
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<400> SEQUENCE: 198

TCCAGGTCAA TCAACTTCTG TACTG

25

<210> SEQ ID NO 199
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<400> SEQUENCE: 199

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CCAGGTCAAT CAACTTCTGT ACTGG

25

<210> SEQ ID NO 200
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CAGGTCAATC AACTTCTGTA CTGGG

25

<210> SEQ ID NO 201
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AGGTCAATCA ACTTCTGTAC TGGGC

25

<210> SEQ ID NO 202
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GGTCAATCAA CTTCTGTACT GGGCT

25

<210> SEQ ID NO 203
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GTCAATCAAC TTCTGTACTG GGCTC

25

<210> SEQ ID NO 204
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<400> SEQUENCE: 204

TCAATCAACT TCTGTACTGG GCTCT

25

<210> SEQ ID NO 205

<211> LENGTH: 25

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CAATCAACTT CTGTACTGGG CTCTG

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AATCAACTTC TGTACTGGGC TCTGA

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ATCAACTTCT GTACTGGGCT CTGAC

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TCAACTTCTG TACTGGGCTC TGACC

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CAACTTCTGT ACTGGGCTCT GACCA

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ACTTCTGTAC TGGGCTCTGA CCACA

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CTTCTGTACT GGGCTCTGAC CACAA

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TTCTGTACTG GGCTCTGACC ACAAT

25

<210> SEQ ID NO 214

<211> LENGTH: 25

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<220> FEATURES:
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<400> SEQUENCE: 214

TCTGTACTGG GCTCTGACCA CAATC

25

<210> SEQ ID NO 215
<211> LENGTH: 25
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<400> SEQUENCE: 215

CTGTACTGGG CTCTGACCAC AATCG

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<400> SEQUENCE: 216

TGTACTGGGC TCTGACCACA ATCGG

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<400> SEQUENCE: 217

GTACTGGGCT CTGACCACAA TCGGT

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<400> SEQUENCE: 218

TACTGGGCTC TGACCACAAT CGGTT

25

<210> SEQ ID NO 219

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<211> LENGTH: 25
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<220> FEATURES:
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ACTGGGCTCT GACCACAATC GGTTT

25

<210> SEQ ID NO 220
<211> LENGTH: 25
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<220> FEATURES:
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CTGGGCTCTG ACCACAATCG GTTTT

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<210> SEQ ID NO 221
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GTACAGAAGT TGATT

15

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AGTACAGAAG TTGAT

15

<210> SEQ ID NO 223
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<223> OTHER INFORMATION: cDNA for use as primers
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CAGTACAGAA GTTGA

15

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<400> SEQUENCE: 224

CCAGTACAGA AGTTG 15

<210> SEQ ID NO 225
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CCCAGTACAG AAGTT 15

<210> SEQ ID NO 226
<211> LENGTH: 15
<212> TYPE: DNA
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<220> FEATURES:
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GCCCAGTACA GAAGT 15

<210> SEQ ID NO 227
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<212> TYPE: DNA
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<220> FEATURES:
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<400> SEQUENCE: 227

AGCCCAGTAC AGAAG 15

<210> SEQ ID NO 228
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GAGCCCAGTA CAGAA 15

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<210> SEQ ID NO 229
<211> LENGTH: 15
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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 229

AGAGCCCACT ACAGA

15

<210> SEQ ID NO 230
<211> LENGTH: 15
<212> TYPE: DNA
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<220> FEATURES:
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<400> SEQUENCE: 230

CAGAGCCCACT TACAG

15

<210> SEQ ID NO 231
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<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 231

TCAGAGCCCA GTACA

15

<210> SEQ ID NO 232
<211> LENGTH: 15
<212> TYPE: DNA
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<220> FEATURES:
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<400> SEQUENCE: 232

GTCAGAGCCC AGTAC

15

<210> SEQ ID NO 233
<211> LENGTH: 15
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<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 233

OligosPatNat2.txt

GGTCAGAGCC CAGTA

15

<210> SEQ ID NO 234
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<220> FEATURES:
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<400> SEQUENCE: 234

TGGTCAGAGC CAGT

15

<210> SEQ ID NO 235
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<220> FEATURES:
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<400> SEQUENCE: 235

GTGGTCAGAG CCCAG

15

<210> SEQ ID NO 236
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
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<400> SEQUENCE: 236

GTACAGAAGT TGATTG

16

<210> SEQ ID NO 237
<211> LENGTH: 16
<212> TYPE: DNA
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<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 237

AGTACAGAAG TTGATT

16

<210> SEQ ID NO 238
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<212> TYPE: DNA
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<400> SEQUENCE: 238

CAGTACAGAA GTTGAT

16

<210> SEQ ID NO 239
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CCAGTACAGA AGTTGA

16

<210> SEQ ID NO 240
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CCCAGTACAG AAGTTG

16

<210> SEQ ID NO 241
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GCCCAGTACA GAAGTT

16

<210> SEQ ID NO 242
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AGCCCAGTAC AGAAGT

16

<210> SEQ ID NO 243
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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 243

GAGCCAGTA CAGAAG

16

<210> SEQ ID NO 244

<211> LENGTH: 16

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<223> OTHER INFORMATION: cDNA for use as primers

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CAGAGCCAG TACAGA

16

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TCAGAGCCCA GTACAG

16

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16

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TGTGGTCAGA GCCCAG

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17

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AGTACAGAAG TTGATTG

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CAGTACAGAA GTTGATT

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17

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17

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TGGTCAGAGC CAGTAC

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TGTGGTCAGA GCCCAGT

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GTACAGAAGT TGATTGAC

18

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CAGTACAGAA GTTGATTG

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CCAGTACAGA AGTTGATT

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18

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18

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<223> OTHER INFORMATION: cDNA for use as primers

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18

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18

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18

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TGTGGTCAGA GCCCAGTA

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TTGTGGTCAG AGCCAGT

18

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ATTGTGGTCA GAGCCAG

18

<210> SEQ ID NO 287

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GTACAGAAGT TGATTGACC 19

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AGTACAGAAG TTGATTGAC 19

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CAGTACAGAA GTTGATTGA 19

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CCAGTACAGA AGTTGATTG 19

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GCCCAGTACA GAAGTTGAT

19

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AGCCCAGTAC AGAAGTTGA

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GAGCCCAGTA CAGAAGTTG

19

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CAGAGCCCAG TACAGAAGT

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<400> SEQUENCE: 297

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19

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<400> SEQUENCE: 298

GTCAGAGCCC AGTACAGAA

19

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19

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TGGTCAGAGC CAGTACAG

19

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GTGGTCAGAG CCCAGTACA 19

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TGTGGTCAGA GCCCAGTAC 19

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<212> TYPE: DNA
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<400> SEQUENCE: 303

TTGTGGTCAG AGCCAGTA 19

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ATTGTGGTCA GAGCCAGT 19

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<400> SEQUENCE: 305

GATTGTGGTC AGAGCCAG 19

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<400> SEQUENCE: 306

GTACAGAAGT TGATTGACCT

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<210> SEQ ID NO 307

<211> LENGTH: 20

<212> TYPE: DNA

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AGTACAGAAG TTGATTGACC

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CAGTACAGAA GTTGATTGAC

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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 310

CCCAGTACAG AAGTTGATTG

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<212> TYPE: DNA

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<223> OTHER INFORMATION: cDNA for use as primers

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GCCCAGTACA GAAGTTGATT

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CAGAGCCCAG TACAGAAGTT

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<210> SEQ ID NO 316

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TCAGAGCCCA GTACAGAAGT 20

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GTCAGAGCCC AGTACAGAAG 20

<210> SEQ ID NO 318
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GGTCAGAGCC CAGTACAGAA 20

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TGGTCAGAGC CAGTACAGA 20

<210> SEQ ID NO 320
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GTGGTCAGAG CCCAGTACAG 20

<210> SEQ ID NO 321

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<400> SEQUENCE: 321

TGTGGTCAGA GCCCAGTACA

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<210> SEQ ID NO 322
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TTGTGGTCAG AGCCAGTAC

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<210> SEQ ID NO 323
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<400> SEQUENCE: 323

ATTGTGGTCA GAGCCAGTA

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<400> SEQUENCE: 324

GATTGTGGTC AGAGCCAGT

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<210> SEQ ID NO 325
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<400> SEQUENCE: 325

CGATTGTGGT CAGAGCCAG

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GTACAGAAGT TGATTGACCT G

21

<210> SEQ ID NO 327
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AGTACAGAAG TTGATTGACC T

21

<210> SEQ ID NO 328
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CAGTACAGAA GTTGATTGAC C

21

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CCAGTACAGA AGTTGATTGA C

21

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CCCAGTACAG AAGTTGATTG A

21

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GCCCAGTACA GAAGTTGATT G

21

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AGCCCAGTAC AGAAGTTGAT T

21

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<400> SEQUENCE: 333

GAGCCCAGTA CAGAAGTTGA T

21

<210> SEQ ID NO 334
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AGAGCCCAGT ACAGAAGTTG A

21

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CAGAGCCCAG TACAGAAGTT G 21

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TCAGAGCCCA GTACAGAAGT T 21

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GTCAGAGCCC AGTACAGAAG T 21

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GGTCAGAGCC CAGTACAGAA G 21

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TGGTCAGAGC CAGTACAGA A 21

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GTGGTCAGAG CCCAGTACAG A

21

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21

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21

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GATTGTGGTC AGAGCCAGT A

21

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CGATTGTGGT CAGAGCCCAG T

21

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GTACAGAAGT TGATTGACCT GG

22

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AGTACAGAAG TTGATTGACC TG

22

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22

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CCCAGTACAG AAGTTGATTG AC 22

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GCCCAGTACA GAAGTTGATT GA 22

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AGCCCAGTAC AGAAGTTGAT TG 22

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22

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CAGAGCCCGT TACAGAAGTT GA

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TCAGAGCCCA GTACAGAAGT TG

22

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GTCAGAGCCC AGTACAGAAG TT

22

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22

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GTGGTCAGAG CCCAGTACAG AA

22

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TGTGGTCAGA GCCCAGTACA GA

22

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TTGTGGTCAG AGCCAGTAC AG

22

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ATTGTGGTCA GAGCCAGTA CA

22

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<400> SEQUENCE: 365

GATTGTGGTC AGAGCCAGT AC

22

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<400> SEQUENCE: 366

CGATTGTGGT CAGAGCCAG TA

22

<210> SEQ ID NO 367
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CCGATTGTGG TCAGAGCCCA GT

22

<210> SEQ ID NO 368
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ACCGATTGTG GTCAGAGCCC AG

22

<210> SEQ ID NO 369
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GTACAGAAGT TGATTGACCT GGA

23

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AGTACAGAAG TTGATTGACC TGG

23

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<400> SEQUENCE: 371

CAGTACAGAA GTTGATTGAC CTG

23

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<400> SEQUENCE: 372

CCAGTACAGA AGTTGATTGA CCT

23

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CCAGTACAG AAGTTGATTG ACC

23

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GCCCAGTACA GAAGTTGATT GAC

23

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AGCCCAGTAC AGAAGTTGAT TGA

23

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GAGCCAGTA CAGAAGTTGA TTG

23

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<400> SEQUENCE: 377

AGAGCCAGT ACAGAAGTTG ATT

23

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<400> SEQUENCE: 378

CAGAGCCAG TACAGAAGTT GAT

23

<210> SEQ ID NO 379
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TCAGAGCCCA GTACAGAAGT TGA

23

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<211> LENGTH: 23

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GTCAGAGCCC AGTACAGAAG TTG

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<400> SEQUENCE: 381

GGTCAGAGCC CAGTACAGAA GTT

23

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<220> FEATURES:

<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 382

TGGTCAGAGC CAGTACAGA AGT

23

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<220> FEATURES:

<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 383

GTGGTCAGAG CCCAGTACAG AAG

23

<210> SEQ ID NO 384

<211> LENGTH: 23

<212> TYPE: DNA

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TGTGGTCAGA GCCCAGTACA GAA

23

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TTGTGGTCAG AGCCCAGTAC AGA

23

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ATTGTGGTCA GAGCCCAGTA CAG

23

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GATTGTGGTC AGAGCCCAGT ACA

23

<210> SEQ ID NO 388
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CGATTGTGGT CAGAGCCCAG TAC

23

<210> SEQ ID NO 389

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<211> LENGTH: 23
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<220> FEATURES:
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<400> SEQUENCE: 389

CCGATTGTGG TCAGAGCCCA GTA

23

<210> SEQ ID NO 390
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ACCGATTGTG GTCAGAGCCC AGT

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<400> SEQUENCE: 391

AACCGATTGT GGTCAGAGCC CAG

23

<210> SEQ ID NO 392
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<212> TYPE: DNA
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<400> SEQUENCE: 392

GTACAGAAGT TGATTGACCT GGAG

24

<210> SEQ ID NO 393
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<212> TYPE: DNA
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<400> SEQUENCE: 393

AGTACAGAAG TTGATTGACC TGGA

24

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<212> TYPE: DNA
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<220> FEATURES:
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CAGTACAGAA GTTGATTGAC CTGG

24

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<220> FEATURES:
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CCAGTACAGA AGTTGATTGA CCTG

24

<210> SEQ ID NO 396
<211> LENGTH: 24
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<220> FEATURES:
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CCCAGTACAG AAGTTGATTG ACCT

24

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<220> FEATURES:
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GCCCAGTACA GAAGTTGATT GACC

24

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<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
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AGCCCAGTAC AGAAGTTGAT TGAC

24

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<220> FEATURES:
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<400> SEQUENCE: 399

GAGCCAGTA CAGAAGTTGA TTGA

24

<210> SEQ ID NO 400
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<212> TYPE: DNA
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<220> FEATURES:
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<400> SEQUENCE: 400

AGAGCCAGT ACAGAAGTTG ATTG

24

<210> SEQ ID NO 401
<211> LENGTH: 24
<212> TYPE: DNA
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<220> FEATURES:
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<400> SEQUENCE: 401

CAGAGCCAG TACAGAAGTT GATT

24

<210> SEQ ID NO 402
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
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<400> SEQUENCE: 402

TCAGAGCCCA GTACAGAAGT TGAT

24

<210> SEQ ID NO 403
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<220> FEATURES:
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<400> SEQUENCE: 403

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GTCAGAGCCC AGTACAGAAG TTGA

24

<210> SEQ ID NO 404
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GGTCAGAGCC CAGTACAGAA GTTG

24

<210> SEQ ID NO 405
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<212> TYPE: DNA
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TGGTCAGAGC CAGTACAGA AGTT

24

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<211> LENGTH: 24
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GTGGTCAGAG CCCAGTACAG AAGT

24

<210> SEQ ID NO 407
<211> LENGTH: 24
<212> TYPE: DNA
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<220> FEATURES:
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TGTGGTCAGA GCCCAGTACA GAAG

24

<210> SEQ ID NO 408
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<212> TYPE: DNA
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<220> FEATURES:
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<400> SEQUENCE: 408

TTGTGGTCAG AGCCAGTAC AGAA

24

<210> SEQ ID NO 409

<211> LENGTH: 24

<212> TYPE: DNA

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ATTGTGGTCA GAGCCAGTA CAGA

24

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GATTGTGGTC AGAGCCAGT ACAG

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CGATTGTGGT CAGAGCCAG TACA

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AACCGATTGT GGTCAGAGCC CAGT

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<400> SEQUENCE: 416

GTACAGAAGT TGATTGACCT GGAGA

25

<210> SEQ ID NO 417

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<212> TYPE: DNA

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AGTACAGAAG TTGATTGACC TGGAG

25

<210> SEQ ID NO 418

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence
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CAGTACAGAA GTTGATTGAC CTGGA 25

<210> SEQ ID NO 419
 <211> LENGTH: 25
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
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CCAGTACAGA AGTTGATTGA CCTGG 25

<210> SEQ ID NO 420
 <211> LENGTH: 25
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURES:
 <223> OTHER INFORMATION: cDNA for use as primers
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CCCAGTACAG AAGTTGATTG ACCTG 25

<210> SEQ ID NO 421
 <211> LENGTH: 25
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURES:
 <223> OTHER INFORMATION: cDNA for use as primers
 <400> SEQUENCE: 421

GCCAGTACA GAAGTTGATT GACCT 25

<210> SEQ ID NO 422
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 <212> TYPE: DNA
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 <223> OTHER INFORMATION: cDNA for use as primers
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AGCCAGTAC AGAAGTTGAT TGACC 25

<210> SEQ ID NO 423

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<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
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GAGCCCGTA CAGAAGTTGA TTGAC

25

<210> SEQ ID NO 424
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<212> TYPE: DNA
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AGAGCCCGT ACAGAAGTTG ATTGA

25

<210> SEQ ID NO 425
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: cDNA for use as primers
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CAGAGCCCG TACAGAAGTT GATTG

25

<210> SEQ ID NO 426
<211> LENGTH: 25
<212> TYPE: DNA
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TCAGAGCCCA GTACAGAAGT TGATT

25

<210> SEQ ID NO 427
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
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<400> SEQUENCE: 427

GTCAGAGCCC AGTACAGAAG TTGAT

25

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<210> SEQ ID NO 428
<211> LENGTH: 25
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<213> ORGANISM: Artificial Sequence
<220> FEATURES:
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GGTCAGAGCC CAGTACAGAA GTTGA

25

<210> SEQ ID NO 429
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
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TGGTCAGAGC CAGTACAGA AGTTG

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GTGGTCAGAG CCCAGTACAG AAGTT

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TGTGGTCAGA GCCCAGTACA GAAGT

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ATTGTGGTCA GAGCCAGTA CAGAA

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GATTGTGGTC AGAGCCAGT ACAGA

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CGATTGTGGT CAGAGCCAG TACAG

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ACCGATTGTG GTCAGAGCCC AGTAC

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AAAACCGATT GTGGTCAGAG CCCAG

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ATATTTTGAA AGAAT

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TTTTGAAAGA ATTGG

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TTGAAAGAAT TGGCT

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AGAATTGGCT ATAAG

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ATTGGCTATA AGAAC

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CATATTTTGA AAGAAT

16

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16

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TATTTTGAAA GAATTG

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16

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16

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TTTGAAAGAA TTGGCT

16

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TTGAAAGAAT TGGCTA

16

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TGAAAGAATT GGCTAT

16

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GAAAGAATTG GCTATA

16

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AAAGAATTGG CTATAA

16

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16

oligosPatNat2.txt

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AGAATTGGCT ATAAGA

16

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GAATTGGCTA TAAGAA

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AATTGGCTAT AAGAAC

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TTGGCTATAA GAACTC

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GCATATTTTG AAAGAAT

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CATATTTTGA AAGAATT

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ATATTTTGAA AGAATTG

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TATTTTGAAA GAATTGG

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ATTTTGAAAG AATTGGC

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TTTTGAAAGA ATTGGCT

17

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TTTGAAAGAA TTGGCTA

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TGAAAGAATT GGCTATA

17

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GAAAGAATTG GCTATAA

17

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GAATTGGCTA TAAGAAC

17

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AATTGGCTAT AAGAACT

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ATTGGCTATA AGAACTC

17

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TTGGCTATAA GAACTCT

17

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AGCATATTTT GAAAGAAT

18

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GCATATTTTG AAAGAATT

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<210> SEQ ID NO 491

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<211> LENGTH: 18
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CATATTTTGA AAGAATTG

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<400> SEQUENCE: 492

ATATTTTGAA AGAATTGG

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TATTTTGAAA GAATTGGC

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ATTTTGAAAG AATTGGCT

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TTTTGAAAGA ATTGGCTA

18

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TTTGAAAGAA TTGGCTAT

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TTGAAAGAAT TGGCTATA

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TGAAAGAATT GGCTATAA

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GAAAGAATTG GCTATAAG

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18

OligosPatNat2.txt

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<400> SEQUENCE: 502

AGAATTGGCT ATAAGAAC

18

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<400> SEQUENCE: 503

GAATTGGCTA TAAGAACT

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AATTGGCTAT AAGAACTC

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ATTGGCTATA AGAACTCT

18

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<400> SEQUENCE: 507

AAGCATATTT TGAAAGAAT

19

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AGCATATTTT GAAAGAATT

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GCATATTTTG AAAGAATTG

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CATATTTTGA AAGAATTGG

19

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ATATTTTGAA AGAATTGGC

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TATTTTGAAA GAATTGGCT

19

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ATTTTGAAAG AATTGGCTA

19

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TTTTGAAAGA ATTGGCTAT

19

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19

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AAAGAATTGG CTATAAGAA

19

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AAGAATTGGC TATAAGAAC 19

<210> SEQ ID NO 521
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AGAATTGGCT ATAAGAACT 19

<210> SEQ ID NO 522
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GAATTGGCTA TAAGAACTC 19

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AATTGGCTAT AAGAACTCT 19

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ATTGGCTATA AGAACTCTA 19

<210> SEQ ID NO 525

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TTGGCTATAA GAACTCTAG 19

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GAAGCATATT TTGAAAGAAT 20

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AAGCATATTT TGAAAGAATT 20

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AGCATATTTT GAAAGAATTG 20

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GCATATTTTG AAAGAATTGG 20

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CATATTTTGA AAGAATTGGC

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TATTTTGAAA GAATTGGCTA

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ATTTTGAAAG AATTGGCTAT

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TTTTGAAAGA ATTGGCTATA

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TTTGAAAGAA TTGGCTATAA

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TGAAAGAATT GGCTATAAGA

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AGAATTGGCT ATAAGAACTC

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GAATTGGCTA TAAGAACTCT

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AATTGGCTAT AAGAACTCTA

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TGAAGCATAT TTTGAAAGAA T

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<400> SEQUENCE: 547

GAAGCATATT TTGAAAGAAT T

21

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AAGCATATTT TGAAAGAATT G

21

<210> SEQ ID NO 549
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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 549

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<211> LENGTH: 21

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GCATATTTTG AAAGAATTGG C

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<223> OTHER INFORMATION: cDNA for use as primers

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CATATTTTGA AAGAATTGGC T

21

<210> SEQ ID NO 552

<211> LENGTH: 21

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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 552

ATATTTTGAA AGAATTGGCT A

21

<210> SEQ ID NO 553

<211> LENGTH: 21

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TATTTTGAAA GAATTGGCTA T

21

<210> SEQ ID NO 554

<211> LENGTH: 21

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ATTTTGAAAG AATTGGCTAT A

21

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TTTTGAAAGA ATTGGCTATA A

21

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TTTGAAAGAA TTGGCTATAA G

21

<210> SEQ ID NO 557
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TTGAAAGAAT TGGCTATAAG A

21

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TGAAAGAATT GGCTATAAGA A

21

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<211> LENGTH: 21
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GAAAGAATTG GCTATAAGAA C

21

<210> SEQ ID NO 560
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AAAGAATTGG CTATAAGAAC T

21

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AAGAATTGGC TATAAGAACT C

21

<210> SEQ ID NO 562
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AGAATTGGCT ATAAGAACTC T

21

<210> SEQ ID NO 563
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GAATTGGCTA TAAGAACTCT A

21

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<400> SEQUENCE: 564

AATTGGCTAT AAGAACTCTA G 21

<210> SEQ ID NO 565
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<400> SEQUENCE: 565

ATTGGCTATA AGAACTCTAG G 21

<210> SEQ ID NO 566
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<212> TYPE: DNA
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<400> SEQUENCE: 566

TTGGCTATAA GAACTCTAGG A 21

<210> SEQ ID NO 567
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<212> TYPE: DNA
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<400> SEQUENCE: 567

TTGAAGCATA TTTGAAAGA AT 22

<210> SEQ ID NO 568
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<212> TYPE: DNA
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<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 568

TGAAGCATAT TTTGAAAGAA TT 22

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<210> SEQ ID NO 569
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<400> SEQUENCE: 569

GAAGCATATT TTGAAAGAAT TG

22

<210> SEQ ID NO 570
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<400> SEQUENCE: 570

AAGCATATTT TGAAAGAATT GG

22

<210> SEQ ID NO 571
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AGCATATTTT GAAAGAATTG GC

22

<210> SEQ ID NO 572
<211> LENGTH: 22
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<400> SEQUENCE: 572

GCATATTTTG AAAGAATTGG CT

22

<210> SEQ ID NO 573
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<400> SEQUENCE: 573

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CATATTTTGA AAGAATTGGC TA

22

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ATATTTTGAA AGAATTGGCT AT

22

<210> SEQ ID NO 575
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TATTTTGAAA GAATTGGCTA TA

22

<210> SEQ ID NO 576
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ATTTTGAAAG AATTGGCTAT AA

22

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TTTTGAAAGA ATTGGCTATA AG

22

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TTTGAAAGAA TTGGCTATAA GA

22

<210> SEQ ID NO 579
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<400> SEQUENCE: 579

TTGAAAGAAT TGGCTATAAG AA

22

<210> SEQ ID NO 580
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<400> SEQUENCE: 580

TGAAAGAATT GGCTATAAGA AC

22

<210> SEQ ID NO 581
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<400> SEQUENCE: 581

GAAAGAATTG GCTATAAGAA CT

22

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AAAGAATTGG CTATAAGAAC TC

22

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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 583

AAGAATTGGC TATAAGAACT CT

22

<210> SEQ ID NO 584

<211> LENGTH: 22

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AGAATTGGCT ATAAGAACTC TA

22

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GAATTGGCTA TAAGAACTCT AG

22

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AATTGGCTAT AAGAACTCTA GG

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ATTGGCTATA AGAACTCTAG GA

22

<210> SEQ ID NO 588

<211> LENGTH: 22

<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: cDNA for use as primers
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TTGGCTATAA GAACTCTAGG AA 22

<210> SEQ ID NO 589
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: cDNA for use as primers
<400> SEQUENCE: 589

ATTGAAGCAT ATTTTGAAAG AAT 23

<210> SEQ ID NO 590
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<212> TYPE: DNA
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<223> OTHER INFORMATION: cDNA for use as primers
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TTGAAGCATA TTTTGAAAGA ATT 23

<210> SEQ ID NO 591
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TGAAGCATAT TTTGAAAGAA TTG 23

<210> SEQ ID NO 592
<211> LENGTH: 23
<212> TYPE: DNA
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GAAGCATATT TTGAAAGAAT TGG 23

<210> SEQ ID NO 593

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<211> LENGTH: 23
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AAGCATATTT TGAAAGAATT GGC

23

<210> SEQ ID NO 594
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AGCATATTTT GAAAGAATTG GCT

23

<210> SEQ ID NO 595
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GCATATTTTG AAAGAATTGG CTA

23

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CATATTTTGA AAGAATTGGC TAT

23

<210> SEQ ID NO 597
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ATATTTTGAA AGAATTGGCT ATA

23

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<210> SEQ ID NO 598
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<400> SEQUENCE: 598

TATTTTGAAA GAATTGGCTA TAA 23

<210> SEQ ID NO 599
<211> LENGTH: 23
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<400> SEQUENCE: 599

ATTTTGAAAG AATTGGCTAT AAG 23

<210> SEQ ID NO 600
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<400> SEQUENCE: 600

TTTTGAAAGA ATTGGCTATA AGA 23

<210> SEQ ID NO 601
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<212> TYPE: DNA
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<400> SEQUENCE: 601

TTTGAAAGAA TTGGCTATAA GAA 23

<210> SEQ ID NO 602
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<212> TYPE: DNA
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<400> SEQUENCE: 602

TTGAAAGAAT TGGCTATAAG AAC 23

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<210> SEQ ID NO 603
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<400> SEQUENCE: 603

TGAAAGAATT GGCTATAAGA ACT

23

<210> SEQ ID NO 604
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<400> SEQUENCE: 604

GAAAGAATTG GCTATAAGAA CTC

23

<210> SEQ ID NO 605
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<400> SEQUENCE: 605

AAAGAATTGG CTATAAGAAC TCT

23

<210> SEQ ID NO 606
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 606

AAGAATTGGC TATAAGAACT CTA

23

<210> SEQ ID NO 607
<211> LENGTH: 23
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<213> ORGANISM: Artificial Sequence
<220> FEATURES:
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<400> SEQUENCE: 607

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AGAATTGGCT ATAAGAACTC TAG

23

<210> SEQ ID NO 608
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GAATTGGCTA TAAGAACTCT AGG

23

<210> SEQ ID NO 609
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<213> ORGANISM: Artificial Sequence
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AATTGGCTAT AAGAACTCTA GGA

23

<210> SEQ ID NO 610
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ATTGGCTATA AGAACTCTAG GAA

23

<210> SEQ ID NO 611
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<212> TYPE: DNA
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<400> SEQUENCE: 611

TTGGCTATAA GAACTCTAGG AAC

23

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<220> FEATURES:
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<400> SEQUENCE: 612

CATTGAAGCA TATTTTGAAA GAAT

24

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TGAAGCATAT TTTGAAAGAA TTGG

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GAAGCATATT TTGAAAGAAT TGGC

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AGCATATTTT GAAAGAATTG GCTA

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24

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24

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TTTTGAAAGA ATTGGCTATA AGAA

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TTGAAAGAAT TGGCTATAAG AACT

24

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24

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GAAAGAATTG GCTATAAGAA CTCT

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AAAGAATTGG CTATAAGAAC TCTA

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AAGAATTGGC TATAAGAACT CTAG

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AGAATTGGCT ATAAGAACTC TAGG

24

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GAATTGGCTA TAAGAACTCT AGGA

24

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AATTGGCTAT AAGAACTCTA GGAA

24

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ATTGGCTATA AGAACTCTAG GAAC

24

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TTGGCTATAA GAACTCTAGG AACA

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ACATTGAAGC ATATTTTGAA AGAAT

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CATTGAAGCA TATTTTGAAA GAATT

25

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ATTGAAGCAT ATTTTGAAAG AATTG

25

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TTGAAGCATA TTTTGAAAGA ATTGG

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TGAAGCATAT TTTGAAAGAA TTGGC

25

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GAAGCATATT TTGAAAGAAT TGGCT

25

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AAGCATATTT TGAAAGAATT GGCTA

25

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AGCATATTTT GAAAGAATTG GCTAT

25

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GCATATTTTG AAAGAATTGG CTATA

25

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CATATTTTGA AAGAATTGGC TATAA

25

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25

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TATTTTGAAA GAATTGGCTA TAAGA

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ATTTTGAAAAG AATTGGCTAT AAGAA

25

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TTTTGAAAGA ATTGGCTATA AGAAC

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TTTGAAAGAA TTGGCTATAA GAACT

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TTGAAAGAAT TGGCTATAAG AACTC

25

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TGAAAGAATT GGCTATAAGA ACTCT

25

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GAAAGAATTG GCTATAAGAA CTCTA

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AAAGAATTGG CTATAAGAAC TCTAG

25

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AAGAATTGGC TATAAGAACT CTAGG

25

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GAATTGGCTA TAAGAACTCT AGGAA 25

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ATTGGCTATA AGAACTCTAG GAACA 25

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15

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AATTCTTTCA AAATA

15

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CAATTCTTTC AAAAT

15

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CCAATTCTTT CAAAA

15

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GCCAATTCTT TCAAA

15

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AGCCAATTCT TTCAA

15

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TAGCCAATTC TTTCA

15

<210> SEQ ID NO 668
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ATAGCCAATT CTTTC

15

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TATAGCCAAT TCTTT

15

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TTATAGCCAA TTCTT

15

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CTTATAGCCA ATTCT

15

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TCTTATAGCC AATTC

15

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TTCTTATAGC CAATT

15

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GTTCTTATAG CCAAT

15

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AGTTCTTATA GCCAA

15

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ATTCTTTCAA AATATG

16

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AATTCTTTCA AAATAT

16

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CAATTCTTTC AAAATA

16

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CCAATTCTTT CAAAAT

16

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GCCAATTCTT TCAAAA

16

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TATAGCCAAT TCTTTC

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CTTATAGCCA ATTCTT

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TTCTTATAGC CAATTC

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GTTCTTATAG CCAATT

16

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<212> TYPE: DNA

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AGTTCTTATA GCCAAT

16

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GAGTTCTTAT AGCCAA

16

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ATTCTTTCAA AATATGC

17

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AATTCTTTCA AAATATG

17

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CAATTCTTTC AAAATAT

17

<210> SEQ ID NO 695

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<211> LENGTH: 17
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<400> SEQUENCE: 695

CCAATTCTTT CAAAATA

17

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GCCAATTCTT TCAAAT

17

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AGCCAATTCT TTCAAAA

17

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TAGCCAATTC TTTCAAA

17

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ATAGCCAATT CTTTCAA

17

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TATAGCCAAT TCTTTCA

17

<210> SEQ ID NO 701
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<400> SEQUENCE: 701

TTATAGCCAA TTCTTTC

17

<210> SEQ ID NO 702
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<400> SEQUENCE: 702

CTTATAGCCA ATTCTTT

17

<210> SEQ ID NO 703
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17

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17

oligosPatNat2.txt

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GAGTTCTTAT AGCCAAT

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AATTCTTTCA AAATATGC

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CAATTCTTTC AAAATATG

18

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CCAATTCTTT CAAAATAT

18

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GCCAATTCTT TCAAATA

18

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AGCCAATTCT TTCAAAAT

18

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TAGCCAATTC TTTCAAAA

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18

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AGTTCTTATA GCCAATTC

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GAGTTCTTAT AGCCAATT

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AGAGTTCTTA TAGCCAAT

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TAGAGTTCTT ATAGCCAA

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AATTCTTTCA AAATATGCT

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OligosPatNat2.txt

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CCAATTCTTT CAAAATATG

19

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GCCAATTCTT TCAAATAT

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AGCCAATTCT TTCAAATA

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TAGCCAATTC TTTCAAAT

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oligosPatNat2.txt

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ATAGCCAATT CTTTCAAAA 19

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TATAGCCAAT TCTTTCAA 19

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TTATAGCCAA TTCTTTCAA 19

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CTTATAGCCA ATTCTTTCA 19

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TCTTATAGCC AATTCTTTC 19

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TTCTTATAGC CAATTCTT

19

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GTTCTTATAG CCAATTCTT

19

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AGTTCTTATA GCCAATTCT

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GAGTTCTTAT AGCCAATTC

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AGAGTTCTTA TAGCCAATT 19

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TAGAGTTCTT ATAGCCAAT 19

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CTAGAGTTCT TATAGCCAA 19

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<210> SEQ ID NO 747
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AATTCTTTCA AAATATGCTT 20

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CAATTCTTTC AAAATATGCT

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CCAATTCTTT CAAAATATGC

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<400> SEQUENCE: 750

GCCAATTCTT TCAAATATG

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AGCCAATTCT TTCAAATAT

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TAGCCAATTC TTTCAAATA

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ATAGCCAATT CTTTCAAAT

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TATAGCCAAT TCTTTCAAAA

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<223> OTHER INFORMATION: cDNA for use as primers

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TTATAGCCAA TTCTTTCAAA

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CTTATAGCCA ATTCTTTCAA

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<400> SEQUENCE: 757

TCTTATAGCC AATTCTTTCA

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<210> SEQ ID NO 758

<211> LENGTH: 20

<212> TYPE: DNA

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TTCTTATAGC CAATTCTTTC

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GTTCTTATAG CCAATTCTTT

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AGTTCTTATA GCCAATTCTT

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GAGTTCTTAT AGCCAATTCT

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AGAGTTCTTA TAGCCAATTC

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<211> LENGTH: 20
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TAGAGTTCTT ATAGCCAATT

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CTAGAGTTCT TATAGCCAAT

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CCTAGAGTTC TTATAGCCAA

20

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<400> SEQUENCE: 766

ATTCTTTCAA AATATGCTTC A

21

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AATTCTTTCA AAATATGCTT C

21

oligosPatNat2.txt

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CAATTCTTTC AAAATATGCT T 21

<210> SEQ ID NO 769
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CCAATTCTTT CAAAATATGC T 21

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GCCAATTCTT TCAAAATATG C 21

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AGCCAATTCT TTCAAAATAT G 21

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TAGCCAATTC TTTCAAAATA T 21

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ATAGCCAATT CTTTCAAAT A

21

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TATAGCCAAT TCTTTCAAAA T

21

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TTATAGCCAA TTCTTTCAAA A

21

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CTTATAGCCA ATTCTTTCAA A

21

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oligosPatNat2.txt

TCTTATAGCC AATTCTTTCA A

21

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TTCTTATAGC CAATTCTTTC A

21

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GTTCTTATAG CCAATTCTTT C

21

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AGTTCTTATA GCCAATTCTT T

21

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GAGTTCTTAT AGCCAATTCT T

21

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<212> TYPE: DNA
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AGAGTTCTTA TAGCCAATTC T

21

<210> SEQ ID NO 783

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<212> TYPE: DNA

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TAGAGTTCTT ATAGCCAATT C

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CTAGAGTTCT TATAGCCAAT T

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CCTAGAGTTC TTATAGCCAA T

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TCCTAGAGTT CTTATAGCCA A

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ATTCTTTCAA AATATGCTTC AA

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AATTCTTTCA AAATATGCTT CA

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CAATTCTTTC AAAATATGCT TC

22

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CCAATTCTTT CAAAATATGC TT

22

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GCCAATTCTT TCAAATATG CT

22

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AGCCAATTCT TTCAAAATAT GC

22

<210> SEQ ID NO 793
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TAGCCAATTC TTTCAAATA TG

22

<210> SEQ ID NO 794
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ATAGCCAATT CTTTCAAAT AT

22

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22

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22

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OligosPatNat2.txt

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22

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22

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22

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22

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22

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23

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AATTCTTTCA AATATGCTT CAA

23

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CAATTCTTTC AAAATATGCT TCA

23

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CCAATTCTTT CAAAATATGC TTC

23

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23

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23

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TAGCCAATTC TTTCAAATA TGC

23

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23

<210> SEQ ID NO 817

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23

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<212> TYPE: DNA

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23

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CTAGAGTTCT TATAGCCAAT TCT

23

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CCTAGAGTTC TTATAGCCAA TTC

23

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TCCTAGAGTT CTTATAGCCA ATT

23

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23

<210> SEQ ID NO 831

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G TTCCTAGAG TTCTTATAGC CAA

23

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A TTCTTTCAA AATATGCTTC AATG

24

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A ATTCTTTCA AAATATGCTT CAAT

24

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C AATTCTTTC AAAATATGCT TCAA

24

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C CAATTCTTT CAAAATATGC TTCA

24

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AGCCAATTCT TTCAAAATAT GCTT 24

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TAGCCAATTC TTTCAAAATA TGCT 24

<210> SEQ ID NO 839
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<400> SEQUENCE: 839

ATAGCCAATT CTTTCAAAT ATGC 24

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<400> SEQUENCE: 840

TATAGCCAAT TCTTTCAAAA TATG 24

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TTATAGCCAA TTCTTTCAAA ATAT

24

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CTTATAGCCA ATTCTTTCAA AATA

24

<210> SEQ ID NO 843
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<400> SEQUENCE: 843

TCTTATAGCC AATTCTTTCA AAAT

24

<210> SEQ ID NO 844
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<400> SEQUENCE: 844

TTCTTATAGC CAATTCTTTC AAAA

24

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<400> SEQUENCE: 845

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GTTCTTATAG CCAATTCTTT CAAA

24

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<400> SEQUENCE: 846

AGTTCTTATA GCCAATTCTT TCAA

24

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GAGTTCTTAT AGCCAATTCT TTCA

24

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AGAGTTCTTA TAGCCAATTC TTTC

24

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<400> SEQUENCE: 849

TAGAGTTCTT ATAGCCAATT CTTT

24

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CTAGAGTTCT TATAGCCAAT TCTT

24

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<400> SEQUENCE: 851

CCTAGAGTTC TTATAGCCAA TTCT

24

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<400> SEQUENCE: 852

TCCTAGAGTT CTTATAGCCA ATTC

24

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24

<210> SEQ ID NO 854
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GTTCCCTAGAG TTCTTATAGC CAAT

24

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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 855

TGTTCTAGA GTTCTTATAG CCAA

24

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<220> FEATURES:

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<400> SEQUENCE: 856

ATTCTTTCAA AATATGCTTC AATGT

25

<210> SEQ ID NO 857

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURES:

<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 857

AATTCTTTCA AAATATGCTT CAATG

25

<210> SEQ ID NO 858

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CAATTCTTTC AAAATATGCT TCAAT

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CCAATTCTTT CAAAATATGC TTCAA

25

<210> SEQ ID NO 860

<211> LENGTH: 25

<212> TYPE: DNA

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<223> OTHER INFORMATION: cDNA for use as primers
<400> SEQUENCE: 860

GCCAATTCTT TCAAAATATG CTTC 25

<210> SEQ ID NO 861
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 861

AGCCAATTCT TTCAAAATAT GCTTC 25

<210> SEQ ID NO 862
<211> LENGTH: 25
<212> TYPE: DNA
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<223> OTHER INFORMATION: cDNA for use as primers
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TAGCCAATTC TTTCAAAATA TGCTT 25

<210> SEQ ID NO 863
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<223> OTHER INFORMATION: cDNA for use as primers
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ATAGCCAATT CTTTCAAAT ATGCT 25

<210> SEQ ID NO 864
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TATAGCCAAT TCTTTCAAAA TATGC 25

<210> SEQ ID NO 865

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<211> LENGTH: 25
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TTATAGCCAA TTCTTTCAAA ATATG

25

<210> SEQ ID NO 866
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CTTATAGCCA ATTCTTTCAA AATAT

25

<210> SEQ ID NO 867
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TCTTATAGCC AATTCTTTCA AAATA

25

<210> SEQ ID NO 868
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<212> TYPE: DNA
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TTCTTATAGC CAATTCTTTC AAAAT

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<210> SEQ ID NO 869
<211> LENGTH: 25
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GTTCTTATAG CCAATTCTTT CAAAA

25

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<400> SEQUENCE: 870

AGTTCTTATA GCCAATTCTT TCAAA 25

<210> SEQ ID NO 871
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
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<400> SEQUENCE: 871

GAGTTCTTAT AGCCAATTCT TTCAA 25

<210> SEQ ID NO 872
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<212> TYPE: DNA
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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 872

AGAGTTCTTA TAGCCAATTC TTTCA 25

<210> SEQ ID NO 873
<211> LENGTH: 25
<212> TYPE: DNA
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<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 873

TAGAGTTCTT ATAGCCAATT CTTTC 25

<210> SEQ ID NO 874
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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 874

CTAGAGTTCT TATAGCCAAT TCTTT 25

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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 875

CCTAGAGTTC TTATAGCCAA TTCTT

25

<210> SEQ ID NO 876
<211> LENGTH: 25
<212> TYPE: DNA
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<400> SEQUENCE: 876

TCCTAGAGTT CTTATAGCCA ATTCT

25

<210> SEQ ID NO 877
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TTCCTAGAGT TCTTATAGCC AATTC

25

<210> SEQ ID NO 878
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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 878

G TTCCTAGAG TTCTTATAGC CAATT

25

<210> SEQ ID NO 879
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 879

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TGTTCCCTAGA GTTCTTATAG CCAAT

25

<210> SEQ ID NO 880
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 880

TTGTTCCCTAG AGTTCTTATA GCCAA

25

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 881

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15

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 882

CGGGGTGGGT GGTGT

15

<210> SEQ ID NO 883
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GGGGTGGGTG GTGTC

15

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GGGTGGGTGG TGTCT

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GGTGGGTGGT GTCTC

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GTGGGTGGTG TCTCC

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TGGGTGGTGT CTCCA

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GGGTGGTGTC TCCAG

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GTGGTGTCTC CAGGT

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TGGTGTCTCC AGGTC

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GTGTCTCCAG GTCAA

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TGTCTCCAGG TCAAT

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GTCTCCAGGT CAATC

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ACCGGGGTGG GTGGTG

16

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CCGGGGTGGG TGGTGT

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GTGGGTGGTG TCTCCA

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16

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GGGTGGTGTC TCCAGG

16

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GTGGTGCTCTC CAGGTC

16

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TGGTGCTCTCC AGGTCA

16

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GGTGTCTCCA GGTCAA

16

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GTGTCTCCAG GTCAAT

16

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TGTCTCCAGG TCAATC

16

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GTCTCCAGGT CAATCA

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AACCGGGGTG GGTGGTG

17

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ACCGGGGTGG GTGGTGT

17

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CCGGGGTGGG TGGTGTC

17

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CGGGGTGGGT GGTGTCT

17

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GGGGTGGGTG GTGTCTC

17

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GGGTGGGTGG TGTCTCC

17

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GGTGGGTGGT GTCTCCA

17

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TGGGTGGTGT CTCCAGG

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GTGGTGTCTC CAGGTCA

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TGGTGTCTCC AGGTCAA

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GGTGTCTCCA GGTCAAT

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GTGTCTCCAG GTCAATC

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TGTCTCCAGG TCAATCA

17

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GTCTCCAGGT CAATCAA

17

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AAACCGGGGT GGGTGGTG

18

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AACCGGGGTG GGTGGTGT

18

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ACCGGGGTGG GTGGTGTC

18

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CCGGGGTGGG TGGTGTCT

18

<210> SEQ ID NO 933

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CGGGGTGGGT GGTGTCTC

18

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GGGGTGGGTG GTGTCTCC

18

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GGGTGGGTGG TGTCTCCA

18

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GGTGGGTGGT GTCTCCAG

18

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GTGGGTGGTG TCTCCAGG

18

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TGGGTGGTGT CTCCAGGT

18

<210> SEQ ID NO 939
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GGGTGGTGTC TCCAGGTC

18

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GGTGGTGTCT CCAGGTCA

18

<210> SEQ ID NO 941
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<400> SEQUENCE: 941

GTGGTGTCTC CAGGTCAA

18

<210> SEQ ID NO 942
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TGGTGTCTCC AGGTCAAT

18

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GGTGTCTCCA GGTCAATC

18

<210> SEQ ID NO 944
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<220> FEATURES:
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<400> SEQUENCE: 944

GTGTCTCCAG GTCAATCA

18

<210> SEQ ID NO 945
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TGTCTCCAGG TCAATCAA

18

<210> SEQ ID NO 946
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<400> SEQUENCE: 946

GTCTCCAGGT CAATCAAC

18

<210> SEQ ID NO 947
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GAAACCGGGG TGGGTGGTG 19

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<220> FEATURES:
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AAACCGGGGT GGGTGGTGT 19

<210> SEQ ID NO 949
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AACCGGGGTG GGTGGTGTC 19

<210> SEQ ID NO 950
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ACCGGGGTGG GTGGTGCT 19

<210> SEQ ID NO 951
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CCGGGGTGGG TGGTGCTC 19

<210> SEQ ID NO 952
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<400> SEQUENCE: 952

CGGGGTGGGT GGTGTCTCC

19

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<400> SEQUENCE: 953

GGGGTGGGTG GTGTCTCCA

19

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GGGTGGGTGG TGTCTCCAG

19

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GGTGGGTGGT GTCTCCAGG

19

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GTGGGTGGTG TCTCCAGGT

19

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<400> SEQUENCE: 957

TGGGTGGTGT CTCCAGGTC

19

<210> SEQ ID NO 958

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GTGGTGTCTC CAGGTCAAT

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TGGTGTCTCC AGGTCAATC

19

<210> SEQ ID NO 962

<211> LENGTH: 19

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence
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GGTGTCTCCA GGTCAATCA 19

<210> SEQ ID NO 963
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GTGTCTCCAG GTCAATCAA 19

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TGTCTCCAGG TCAATCAAC 19

<210> SEQ ID NO 965
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GTCTCCAGGT CAATCAACT 19

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AGAAACCGGG GTGGGTGGTG 20

<210> SEQ ID NO 967

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<211> LENGTH: 20
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GAAACCGGGG TGGGTGGTGT

20

<210> SEQ ID NO 968
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AAACCGGGGT GGGTGGTGTC

20

<210> SEQ ID NO 969
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AACCGGGGTG GGTGGTGCT

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<210> SEQ ID NO 970
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ACCGGGGTGG GTGGTGCTC

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<210> SEQ ID NO 971
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CCGGGGTGGG TGGTGTCTCC

20

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<210> SEQ ID NO 972
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<400> SEQUENCE: 972

CGGGGTGGGT GGTGTCTCCA

20

<210> SEQ ID NO 973
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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 973

GGGGTGGGTG GTGTCTCCAG

20

<210> SEQ ID NO 974
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GGGTGGGTGG TGTCTCCAGG

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GGTGGGTGGT GTCTCCAGGT

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GTGGGTGGTG TCTCCAGGTC

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TGGGTGGTGT CTCCAGGTCA

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GGGTGGTGT C CAGGTCAA

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GGTGGTGTCT CCAGGTCAAT

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GTGGTGTCTC CAGGTCAATC

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TGGTGTCTCC AGTCAATCA

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GGTGTCTCCA GGTCAATCAA

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GTGTCTCCAG GTCAATCAAC

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TGTCTCCAGG TCAATCAACT

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GTCTCCAGGT CAATCAACTT

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AAGAAACCGG GGTGGGTGGT G

21

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AGAAACCGGG GTGGGTGGTG T

21

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GAAACCGGGG TGGGTGGTGT C

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AAACCGGGGT GGGTGGTGTC T

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AACCGGGGTG GGTGGTGCT C

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ACCGGGGTGG GTGGTGTCTC C

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CCGGGGTGGG TGGTGTCTCC A

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CGGGGTGGGT GGTGTCTCCA G

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GGGGTGGGTG GTGTCTCCAG G

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GGGTGGGTGG TGTCTCCAGG T

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<213> ORGANISM: Artificial Sequence
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GGTGGGTGGT GTCTCCAGGT C

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<210> SEQ ID NO 997
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GTGGGTGGTG TCTCCAGGTC A

21

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TGGGTGGTGT CTCCAGGTCA A

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GGGTGGTGTC TCCAGGTCAA T

21

<210> SEQ ID NO 1000
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GGTGGTGTCT CCAGGTCAAT C

21

<210> SEQ ID NO 1001

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<211> LENGTH: 21
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GTGGTGTCTC CAGGTCAATC A

21

<210> SEQ ID NO 1002
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TGGTGTCTCC AGGTCAATCA A

21

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<400> SEQUENCE: 1003

GGTGTCTCCA GGTCAATCAA C

21

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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GTGTCTCCAG GTCAATCAAC T

21

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<211> LENGTH: 21
<212> TYPE: DNA
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<400> SEQUENCE: 1005

TGTCTCCAGG TCAATCAACT T

21

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<210> SEQ ID NO 1006
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<400> SEQUENCE: 1006

GTCTCCAGGT CAATCAACTT C 21

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<220> FEATURES:
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<400> SEQUENCE: 1007

GAAGAAACCG GGGTGGGTGG TG 22

<210> SEQ ID NO 1008
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
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<400> SEQUENCE: 1008

AAGAAACCGG GGTGGGTGGT GT 22

<210> SEQ ID NO 1009
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<212> TYPE: DNA
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AGAAACCGGG GTGGGTGGTG TC 22

<210> SEQ ID NO 1010
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<220> FEATURES:
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<400> SEQUENCE: 1010

GAAACCGGGG TGGGTGGTGT CT 22

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<210> SEQ ID NO 1011
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<400> SEQUENCE: 1011

AAACCGGGGT GGGTGGTGTC TC

22

<210> SEQ ID NO 1012
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AACCGGGGTG GGTGGTGTCT CC

22

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<400> SEQUENCE: 1013

ACCGGGGTGG GTGGTGTCTC CA

22

<210> SEQ ID NO 1014
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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CCGGGGTGGG TGGTGTCTCC AG

22

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<212> TYPE: DNA
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CGGGGTGGGT GGTGTCTCCA GG

22

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<212> TYPE: DNA
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<220> FEATURES:
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GGGGTGGGTG GTGTCTCCAG GT

22

<210> SEQ ID NO 1017
<211> LENGTH: 22
<212> TYPE: DNA
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<220> FEATURES:
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<400> SEQUENCE: 1017

GGGTGGGTGG TGTCTCCAGG TC

22

<210> SEQ ID NO 1018
<211> LENGTH: 22
<212> TYPE: DNA
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GGTGGGTGGT GTCTCCAGGT CA

22

<210> SEQ ID NO 1019
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GTGGGTGGTG TCTCCAGGTC AA

22

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<400> SEQUENCE: 1020

TGGGTGGTGT CTCCAGGTCA AT

22

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<400> SEQUENCE: 1021

GGGTGGTGTG TCCAGGTCAA TC

22

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<400> SEQUENCE: 1022

GGTGGTGTCT CCAGGTCAAT CA

22

<210> SEQ ID NO 1023
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<400> SEQUENCE: 1023

GTGGTGTCTC CAGGTCAATC AA

22

<210> SEQ ID NO 1024
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<400> SEQUENCE: 1024

TGGTGTCTCC AGGTCAATCA AC

22

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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1025

GGTGTCTCCA GGTCATCAA CT

22

<210> SEQ ID NO 1026

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GTGTCTCCAG GTCAATCAAC TT

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AGAAGAAACC GGGGTGGGTG GTG

23

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<211> LENGTH: 23

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GAAGAAACCG GGGTGGGTGG TGT 23

<210> SEQ ID NO 1031
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AAGAAACCGG GGTGGGTGGT GTC 23

<210> SEQ ID NO 1032
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AGAAACCGGG GTGGGTGGTG TCT 23

<210> SEQ ID NO 1033
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GAAACCGGGG TGGGTGGTGT CTC 23

<210> SEQ ID NO 1034
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AAACCGGGGT GGGTGGTGTC TCC 23

<210> SEQ ID NO 1035

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<211> LENGTH: 23
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AACCGGGGTG GGTGGTGTCT CCA

23

<210> SEQ ID NO 1036
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<400> SEQUENCE: 1036

ACCGGGGTGG GTGGTGTCTC CAG

23

<210> SEQ ID NO 1037
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<400> SEQUENCE: 1037

CCGGGGTGGG TGGTGTCTCC AGG

23

<210> SEQ ID NO 1038
<211> LENGTH: 23
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CGGGGTGGGT GGTGTCTCCA GGT

23

<210> SEQ ID NO 1039
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GGGGTGGGTG GTGTCTCCAG GTC

23

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<400> SEQUENCE: 1040

GGGTGGGTGG TGTCTCCAGG TCA 23

<210> SEQ ID NO 1041
<211> LENGTH: 23
<212> TYPE: DNA
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<400> SEQUENCE: 1041

GGTGGGTGGT GTCTCCAGGT CAA 23

<210> SEQ ID NO 1042
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
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<400> SEQUENCE: 1042

GTGGGTGGTG TCTCCAGGTC AAT 23

<210> SEQ ID NO 1043
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
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TGGGTGGTGT CTCCAGGTCA ATC 23

<210> SEQ ID NO 1044
<211> LENGTH: 23
<212> TYPE: DNA
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<400> SEQUENCE: 1044

GGGTGGTGTC TCCAGGTCAA TCA 23

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<210> SEQ ID NO 1045
<211> LENGTH: 23
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GGTGGTGTCT CCAGGTCAAT CAA

23

<210> SEQ ID NO 1046
<211> LENGTH: 23
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GTGGTGTCTC CAGGTCAATC AAC

23

<210> SEQ ID NO 1047
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TGGTGTCTCC AGGTCAATCA ACT

23

<210> SEQ ID NO 1048
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<223> OTHER INFORMATION: cDNA for use as primers
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GGTGTCTCCA GGTCAATCAA CTT

23

<210> SEQ ID NO 1049
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
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GTGTCTCCAG GTCAATCAAC TTC

23

<210> SEQ ID NO 1050
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
<400> SEQUENCE: 1050

TGTCTCCAGG TCAATCAACT TCT

23

<210> SEQ ID NO 1051
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
<400> SEQUENCE: 1051

GTCTCCAGGT CAATCAACTT CTG

23

<210> SEQ ID NO 1052
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
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<400> SEQUENCE: 1052

AAGAAGAAAC CGGGGTGGGT GGTG

24

<210> SEQ ID NO 1053
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
<400> SEQUENCE: 1053

AGAAGAAACC GGGGTGGGTG GTGT

24

<210> SEQ ID NO 1054
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
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<400> SEQUENCE: 1054

GAAGAAACCG GGGTGGGTGG TGTC

24

<210> SEQ ID NO 1055
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1055

AAGAAACCGG GGTGGGTGGT GTCT

24

<210> SEQ ID NO 1056
<211> LENGTH: 24
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<213> ORGANISM: Artificial Sequence
<220> FEATURES:
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<400> SEQUENCE: 1056

AGAAACCGGG GTGGGTGGTG TCTC

24

<210> SEQ ID NO 1057
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
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<400> SEQUENCE: 1057

GAAACCGGGG TGGGTGGTGT CTCC

24

<210> SEQ ID NO 1058
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1058

AAACCGGGGT GGGTGGTGTC TCCA

24

<210> SEQ ID NO 1059
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:

<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1059

AACCGGGGTG GGTGGTGTCT CCAG

24

<210> SEQ ID NO 1060

<211> LENGTH: 24

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ACCGGGGTGG GTGGTGTCTC CAGG

24

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CCGGGTGGG TGGTGTCTCC AGGT

24

<210> SEQ ID NO 1062

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CGGGGTGGGT GGTGTCTCCA GGTC

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<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURES:

<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1063

GGGGTGGGTG GTGTCTCCAG GTCA

24

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GGGTGGGTGG TGTCTCCAGG TCAA

24

<210> SEQ ID NO 1065
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GGTGGGTGGT GTCTCCAGGT CAAT

24

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GTGGGTGGTG TCTCCAGGTC AATC

24

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TGGGTGGTGT CTCCAGGTCA ATCA

24

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GGGTGGTGTC TCCAGGTCAA TCAA

24

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GGTGGTGTCT CCAGGTCAAT CAAC

24

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GTGGTGTCTC CAGGTCAATC AACT

24

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TGGTGTCTCC AGGTCAATCA ACTT

24

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GGTGTCTCCA GGTCATCAA CTTC

24

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GTGTCTCCAG GTCAATCAAC TTCT

24

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TGTCTCCAGG TCAATCAACT TCTG 24

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GTCTCCAGGT CAATCAACTT CTGT 24

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TAAGAAGAAA CCGGGGTGGG TGGTG 25

<210> SEQ ID NO 1077
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AAGAAGAAAC CGGGGTGGGT GGTGT 25

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AGAAGAAACC GGGGTGGGTG GTGTC 25

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GAAGAAACCG GGGTGGGTGG TGTCT

25

<210> SEQ ID NO 1080
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AAGAAACCGG GGTGGGTGGT GTCTC

25

<210> SEQ ID NO 1081
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AGAAACCGGG GTGGGTGGTG TCTCC

25

<210> SEQ ID NO 1082
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GAAACCGGGG TGGGTGGTGT CTCCA

25

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AAACCGGGGT GGGTGGTGTC TCCAG 25

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AACCGGGGTG GGTGGTGTCT CCAGG 25

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ACCGGGGTGG GTGGTGTCTC CAGGT 25

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CCGGGGTGGG TGGTGTCTCC AGGTC 25

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CGGGGTGGGT GGTGTCTCCA GGTCA 25

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GGGGTGGGTG GTGTCTCCAG GTCAA

25

<210> SEQ ID NO 1089
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<400> SEQUENCE: 1089

GGGTGGGTGG TGTCTCCAGG TCAAT

25

<210> SEQ ID NO 1090
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GGTGGGTGGT GTCTCCAGGT CAATC

25

<210> SEQ ID NO 1091
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GTGGGTGGTG TCTCCAGGTC AATCA

25

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TGGGTGGTGT CTCCAGGTCA ATCAA

25

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<400> SEQUENCE: 1093

GGGTGGTGTC TCCAGGTCAA TCAAC

25

<210> SEQ ID NO 1094

<211> LENGTH: 25

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GGTGGTGTCT CCAGGTCAAT CAACT

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<400> SEQUENCE: 1095

GTGGTGTCTC CAGGTCAATC AACTT

25

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<400> SEQUENCE: 1096

TGGTGTCTCC AGGTCAATCA ACTTC

25

<210> SEQ ID NO 1097

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GGTGTCTCCA GGTCAATCAA CTTCT

25

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<212> TYPE: DNA

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<220> FEATURES:
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<400> SEQUENCE: 1098

GTGTCTCCAG GTCAATCAAC TTCTG

25

<210> SEQ ID NO 1099
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<212> TYPE: DNA
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TGTCTCCAGG TCAATCAACT TCTGT

25

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GTCTCCAGGT CAATCAACTT CTGTA

25

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<400> SEQUENCE: 1101

CACCACCCAC CCCGG

15

<210> SEQ ID NO 1102
<211> LENGTH: 15
<212> TYPE: DNA
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ACACCACCCA CCCCCG

15

<210> SEQ ID NO 1103

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<211> LENGTH: 15
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GACACCACCC ACCCC

15

<210> SEQ ID NO 1104
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<212> TYPE: DNA
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AGACACCACC CACCC

15

<210> SEQ ID NO 1105
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GAGACACCAC CCACC

15

<210> SEQ ID NO 1106
<211> LENGTH: 15
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GGAGACACCA CCCAC

15

<210> SEQ ID NO 1107
<211> LENGTH: 15
<212> TYPE: DNA
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TGGAGACACC ACCCA

15

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<210> SEQ ID NO 1108
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<400> SEQUENCE: 1108

CTGGAGACAC CACCC

15

<210> SEQ ID NO 1109
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<400> SEQUENCE: 1109

CCTGGAGACA CCACC

15

<210> SEQ ID NO 1110
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ACCTGGAGAC ACCAC

15

<210> SEQ ID NO 1111
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GACCTGGAGA CACCA

15

<210> SEQ ID NO 1112
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TGACCTGGAG ACACC

15

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<210> SEQ ID NO 1113
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TTGACCTGGA GACAC

15

<210> SEQ ID NO 1114
<211> LENGTH: 15
<212> TYPE: DNA
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ATTGACCTGG AGACA

15

<210> SEQ ID NO 1115
<211> LENGTH: 15
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GATTGACCTG GAGAC

15

<210> SEQ ID NO 1116
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CACCACCCAC CCCGGT

16

<210> SEQ ID NO 1117
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ACACCACCCA CCCC GG

16

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GACACCACCC ACCCG

16

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AGACACCACC CACCCC

16

<210> SEQ ID NO 1120
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GAGACACCAC CCACCC

16

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GGAGACACCA CCCACC

16

<210> SEQ ID NO 1122
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<400> SEQUENCE: 1122

TGGAGACACC ACCCAC

16

<210> SEQ ID NO 1123
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<400> SEQUENCE: 1123

CTGGAGACAC CACCCA

16

<210> SEQ ID NO 1124
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CCTGGAGACA CCACCC

16

<210> SEQ ID NO 1125
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<212> TYPE: DNA
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<400> SEQUENCE: 1125

ACCTGGAGAC ACCACC

16

<210> SEQ ID NO 1126
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GACCTGGAGA CACCAC

16

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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1127

TGACCTGGAG ACACCA

16

<210> SEQ ID NO 1128

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TTGACCTGGA GACACC

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ATTGACCTGG AGACAC

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GATTGACCTG GAGACA

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TGATTGACCT GGAGAC

16

<210> SEQ ID NO 1132

<211> LENGTH: 17

<212> TYPE: DNA

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 <220> FEATURES:
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CACCACCCAC CCCGGTT 17

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 <211> LENGTH: 17
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ACACCACCCA CCCCAGT 17

<210> SEQ ID NO 1134
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GACACCACCC ACCCCGG 17

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AGACACCACC CACCCCG 17

<210> SEQ ID NO 1136
 <211> LENGTH: 17
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GAGACACCAC CCACCCC 17

<210> SEQ ID NO 1137

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<211> LENGTH: 17
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<400> SEQUENCE: 1137

GGAGACACCA CCCACCC

17

<210> SEQ ID NO 1138
<211> LENGTH: 17
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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TGGAGACACC ACCCACC

17

<210> SEQ ID NO 1139
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CTGGAGACAC CACCCAC

17

<210> SEQ ID NO 1140
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CCTGGAGACA CCACCCA

17

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<211> LENGTH: 17
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<220> FEATURES:
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ACCTGGAGAC ACCACCC

17

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<210> SEQ ID NO 1142
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<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers.

<400> SEQUENCE: 1142

GACCTGGAGA CACCACC

17

<210> SEQ ID NO 1143
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<212> TYPE: DNA
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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1143

TGACCTGGAG ACACCAC

17

<210> SEQ ID NO 1144
<211> LENGTH: 17
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<400> SEQUENCE: 1144

TTGACCTGGA GACACCA

17

<210> SEQ ID NO 1145
<211> LENGTH: 17
<212> TYPE: DNA
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<400> SEQUENCE: 1145

ATTGACCTGG AGACACC

17

<210> SEQ ID NO 1146
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<400> SEQUENCE: 1146

GATTGACCTG GAGACAC

17

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<210> SEQ ID NO 1147
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<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1147

TGATTGACCT GGAGACA

17

<210> SEQ ID NO 1148
<211> LENGTH: 17
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1148

TTGATTGACC TGGAGAC

17

<210> SEQ ID NO 1149
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1149

CACCACCCAC CCCGGTTT

18

<210> SEQ ID NO 1150
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1150

ACACCACCCA CCCC GGTT

18

<210> SEQ ID NO 1151
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1151

GACACCACC ACCCCGGT

18

<210> SEQ ID NO 1152
<211> LENGTH: 18
<212> TYPE: DNA
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<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
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AGACACCACC CACCCCGG

18

<210> SEQ ID NO 1153
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<212> TYPE: DNA
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GAGACACCAC CCACCCCG

18

<210> SEQ ID NO 1154
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GGAGACACCA CCCACCCC

18

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TGGAGACACC ACCCACCC

18

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18

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CCTGGAGACA CCACCCAC

18

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ACCTGGAGAC ACCACCCA

18

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18

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18

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ATTGACCTGG AGACACCA

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TTGATTGACC TGGAGACA

18

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GTTGATTGAC CTGGAGAC

18

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CACCACCCAC CCCGGTTTC

19

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19

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GACACCACC ACCCCGGTT

19

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19

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GAGACACCAC CCACCCCGG

19

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GGAGACACCA CCCACCCCG

19

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TGGAGACACC ACCCACCC

19

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19

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CCTGGAGACA CCACCCACC

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ACCTGGAGAC ACCACCCAC 19

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GACCTGGAGA CACCACCA 19

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TGACCTGGAG ACACCACCC 19

<210> SEQ ID NO 1179
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ATTGACCTGG AGACACCAC 19

<210> SEQ ID NO 1181
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GATTGACCTG GAGACACCA

19

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<400> SEQUENCE: 1182

TGATTGACCT GGAGACACC

19

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TTGATTGACC TGGAGACAC

19

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GTTGATTGAC CTGGAGACA

19

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ACACCACCCA CCCCGGTTTC 20

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GACACCACCC ACCCGGTTT 20

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<400> SEQUENCE: 1189

AGACACCACC CACCCGGTT 20

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GAGACACCAC CCACCCCGGT

20

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GGAGACACCA CCCACCCCGG

20

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<400> SEQUENCE: 1192

TGGAGACACC ACCCACCCCG

20

<210> SEQ ID NO 1193
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<400> SEQUENCE: 1193

CTGGAGACAC CACCCACCCC

20

<210> SEQ ID NO 1194
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CCTGGAGACA CCACCCACCC

20

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ACCTGGAGAC ACCACCCACC

20

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GACCTGGAGA CACCACCCAC

20

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TGACCTGGAG ACACCACCCA

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TTGACCTGGA GACACCACCC

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ATTGACCTGG AGACACCACC

20

<210> SEQ ID NO 1200

<211> LENGTH: 20

<212> TYPE: DNA

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GATTGACCTG GAGACACCAC 20

<210> SEQ ID NO 1201
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TGATTGACCT GGAGACACCA 20

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 <212> TYPE: DNA
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TTGATTGACC TGGAGACACC 20

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GTTGATTGAC CTGGAGACAC 20

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AGTTGATTGA CCTGGAGACA 20

<210> SEQ ID NO 1205

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AAGTTGATTG ACCTGGAGAC

20

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CACCACCCAC CCCGGTTTCT T

21

<210> SEQ ID NO 1207
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ACACCACCCA CCCCGGTTTC T

21

<210> SEQ ID NO 1208
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GACACCACCC ACCCGGTTT C

21

<210> SEQ ID NO 1209
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AGACACCACC CACCCCGGTT T

21

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GAGACACCAC CCACCCCGGT T 21

<210> SEQ ID NO 1211
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GGAGACACCA CCCACCCCGG T 21

<210> SEQ ID NO 1212
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TGGAGACACC ACCCACCCCG G 21

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CTGGAGACAC CACCCACCCC G 21

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ACCTGGAGAC ACCACCCACC C

21

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GACCTGGAGA CACCACCCAC C

21

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TGACCTGGAG ACACCACCCA C

21

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TTGACCTGGA GACACCACCC A

21

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ATTGACCTGG AGACACCACC C

21

<210> SEQ ID NO 1220
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GATTGACCTG GAGACACCAC C

21

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TGATTGACCT GGAGACACCA C

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TTGATTGACC TGGAGACACC A

21

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GTTGATTGAC CTGGAGACAC C

21

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AGTTGATTGA CCTGGAGACA C

21

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AAGTTGATTG ACCTGGAGAC A

21

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GAAGTTGATT GACCTGGAGA C

21

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CACCACCCAC CCCGTTTCT TC

22

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ACACCACCCA CCCCGTTTC TT

22

<210> SEQ ID NO 1229
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GACACCACCC ACCCCGGTTT CT

22

<210> SEQ ID NO 1230

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TGGAGACACC ACCCACCCCG GT

22

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CTGGAGACAC CACCCACCCC GG 22

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CCTGGAGACA CCACCCACCC CG 22

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ACCTGGAGAC ACCACCCACC CC 22

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GACCTGGAGA CACCACCCAC CC 22

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TGACCTGGAG ACACCACCCA CC 22

<210> SEQ ID NO 1239

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TTGACCTGGA GACACCACCC AC

22

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ATTGACCTGG AGACACCACC CA

22

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GATTGACCTG GAGACACCAC CC

22

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TGATTGACCT GGAGACACCA CC

22

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TTGATTGACC TGGAGACACC AC

22

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<400> SEQUENCE: 1244

GTTGATTGAC CTGGAGACAC CA 22

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: cDNA for use as primers

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AGTTGATTGA CCTGGAGACA CC 22

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AAGTTGATTG ACCTGGAGAC AC 22

<210> SEQ ID NO 1247
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GAAGTTGATT GACCTGGAGA CA 22

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AGAAGTTGAT TGACCTGGAG AC 22

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<210> SEQ ID NO 1249
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CACCACCCAC CCCGGTTTCT TCT

23

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ACACCACCCA CCCC GGTTTC TTC

23

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GACACCACCC ACCCGGTTT CTT

23

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AGACACCACC CACCCCGGTT TCT

23

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GAGACACCAC CCACCCCGGT TTC

23

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GGAGACACCA CCCACCCCGG TTT

23

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TGGAGACACC ACCACCCCG GTT

23

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CTGGAGACAC CACCCACCC GGT

23

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CCTGGAGACA CCACCCACCC CGG

23

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ACCTGGAGAC ACCACCCACC CCG

23

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GACCTGGAGA CACCACCCAC CCC

23

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TGACCTGGAG ACACCACCCA CCC

23

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TTGACCTGGA GACACCACCC ACC

23

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ATTGACCTGG AGACACCACC CAC

23

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GATTGACCTG GAGACACCAC CCA

23

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TGATTGACCT GGAGACACCA CCC

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TTGATTGACC TGGAGACACC ACC

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GTTGATTGAC CTGGAGACAC CAC

23

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AGTTGATTGA CCTGGAGACA CCA

23

<210> SEQ ID NO 1268

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AAGTTGATTG ACCTGGAGAC ACC 23

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GAAGTTGATT GACCTGGAGA CAC 23

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AGAAGTTGAT TGACCTGGAG ACA 23

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CAGAAAGTTGA TTGACCTGGA GAC 23

<210> SEQ ID NO 1272
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<210> SEQ ID NO 1273

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ACACCACCCA CCCC GGTTTC TTCT

24

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GACACCACCC ACCC GGTTT CTTC

24

<210> SEQ ID NO 1275
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AGACACCACC CACCC GGTT TCTT

24

<210> SEQ ID NO 1276
<211> LENGTH: 24
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GAGACACCAC CCACCC GGTT TTCT

24

<210> SEQ ID NO 1277
<211> LENGTH: 24
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GGAGACACCA CCCACCC GG TTTC

24

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<210> SEQ ID NO 1278
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<400> SEQUENCE: 1278

TGGAGACACC ACCCACCCG GTTT

24

<210> SEQ ID NO 1279
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<212> TYPE: DNA
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<400> SEQUENCE: 1279

CTGGAGACAC CACCCACCC GGTT

24

<210> SEQ ID NO 1280
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
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<400> SEQUENCE: 1280

CCTGGAGACA CCACCCACCC CGGT

24

<210> SEQ ID NO 1281
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
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<400> SEQUENCE: 1281

ACCTGGAGAC ACCACCCACC CCGG

24

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GACCTGGAGA CACCCACCC CCGG

24

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<400> SEQUENCE: 1283

TGACCTGGAG ACACCACCCA CCCC

24

<210> SEQ ID NO 1284
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 1284

TTGACCTGGA GACACCACCC ACCC

24

<210> SEQ ID NO 1285
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<212> TYPE: DNA
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<400> SEQUENCE: 1285

ATTGACCTGG AGACACCACC CACC

24

<210> SEQ ID NO 1286
<211> LENGTH: 24
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<400> SEQUENCE: 1286

GATTGACCTG GAGACACCAC CCAC

24

<210> SEQ ID NO 1287
<211> LENGTH: 24
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<400> SEQUENCE: 1287

TGATTGACCT GGAGACACCA CCCA

24

<210> SEQ ID NO 1288
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TTGATTGACC TGGAGACACC ACCC

24

<210> SEQ ID NO 1289
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GTTGATTGAC CTGGAGACAC CACC

24

<210> SEQ ID NO 1290
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 <400> SEQUENCE: 1290

AGTTGATTGA CCTGGAGACA CCAC

24

<210> SEQ ID NO 1291
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 <400> SEQUENCE: 1291

AAGTTGATTG ACCTGGAGAC ACCA

24

<210> SEQ ID NO 1292
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 <212> TYPE: DNA
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<400> SEQUENCE: 1292

GAAGTTGATT GACCTGGAGA CACC

24

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<400> SEQUENCE: 1293

AGAAGTTGAT TGACCTGGAG ACAC

24

<210> SEQ ID NO 1294
 <211> LENGTH: 24
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<400> SEQUENCE: 1294

CAGAAGTTGA TTGACCTGGA GACA

24

<210> SEQ ID NO 1295
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 1295

ACAGAAGTTG ATTGACCTGG AGAC

24

<210> SEQ ID NO 1296
 <211> LENGTH: 25
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 <213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 1296

CACCACCCAC CCCGGTTTCT TCTTA

25

<210> SEQ ID NO 1297
 <211> LENGTH: 25
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<400> SEQUENCE: 1297

ACACCACCCA CCCCGGTTTC TTCTT

25

<210> SEQ ID NO 1298

<211> LENGTH: 25

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GACACCACC ACCCGGTTT CTTCT

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GAGACACCAC CCACCCCGGT TTCTT

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GGAGACACCA CCCACCCCGG TTTCT

25

<210> SEQ ID NO 1302

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence
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 <400> SEQUENCE: 1302

TGGAGACACC ACCCACCCCG GTTTC 25

<210> SEQ ID NO 1303
 <211> LENGTH: 25
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
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 <400> SEQUENCE: 1303

CTGGAGACAC CACCCACCCC GGTTT 25

<210> SEQ ID NO 1304
 <211> LENGTH: 25
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 <213> ORGANISM: Artificial Sequence
 <220> FEATURES:
 <223> OTHER INFORMATION: cDNA for use as primers
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CCTGGAGACA CCACCCACCC CGGTT 25

<210> SEQ ID NO 1305
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 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
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ACCTGGAGAC ACCACCCACC CCGGT 25

<210> SEQ ID NO 1306
 <211> LENGTH: 25
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
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GACCTGGAGA CACCACCCAC CCCGG 25

<210> SEQ ID NO 1307

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<211> LENGTH: 25
<212> TYPE: DNA
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TGACCTGGAG ACACCACCCA CCCC

25

<210> SEQ ID NO 1308
<211> LENGTH: 25
<212> TYPE: DNA
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TTGACCTGGA GACACCACCC ACCC

25

<210> SEQ ID NO 1309
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
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ATTGACCTGG AGACACCACC CACCC

25

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<211> LENGTH: 25
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GATTGACCTG GAGACACCAC CCACC

25

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<223> OTHER INFORMATION: cDNA for use as primers
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TGATTGACCT GGAGACACCA CCCAC

25

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<210> SEQ ID NO 1312
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<400> SEQUENCE: 1312

TTGATTGACC TGGAGACACC ACCCA 25

<210> SEQ ID NO 1313
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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GTTGATTGAC CTGGAGACAC CACCC 25

<210> SEQ ID NO 1314
<211> LENGTH: 25
<212> TYPE: DNA
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AGTTGATTGA CCTGGAGACA CCACC 25

<210> SEQ ID NO 1315
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AAGTTGATTG ACCTGGAGAC ACCAC 25

<210> SEQ ID NO 1316
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<400> SEQUENCE: 1316

GAAGTTGATT GACCTGGAGA CACCA 25

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<210> SEQ ID NO 1317
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<400> SEQUENCE: 1317

AGAAGTTGAT TGACCTGGAG ACACC

25

<210> SEQ ID NO 1318
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1318

CAGAAGTTGA TTGACCTGGA GACAC

25

<210> SEQ ID NO 1319
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 1319

ACAGAAGTTG ATTGACCTGG AGACA

25

<210> SEQ ID NO 1320
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<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1320

TACAGAAGTT GATTGACCTG GAGAC

25

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<220> FEATURES:
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<400> SEQUENCE: 1321

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CCTCGAACAA TTGAA

15

<210> SEQ ID NO 1322
<211> LENGTH: 15
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
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CTCGAACAAAT TGAAG

15

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<211> LENGTH: 15
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
<400> SEQUENCE: 1323

TCGAACAATT GAAGA

15

<210> SEQ ID NO 1324
<211> LENGTH: 15
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
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CGAACAATTG AAGAT

15

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<211> LENGTH: 15
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
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<223> OTHER INFORMATION: cDNA for use as primers
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GAACAATTGA AGATT

15

<210> SEQ ID NO 1326
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AACAATTGAA GATTT

15

<210> SEQ ID NO 1327
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 <212> TYPE: DNA
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<400> SEQUENCE: 1327

ACAATTGAAG ATTTT

15

<210> SEQ ID NO 1328
 <211> LENGTH: 15
 <212> TYPE: DNA
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 <220> FEATURES:
 <223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1328

CAATTGAAGA TTTTG

15

<210> SEQ ID NO 1329
 <211> LENGTH: 15
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
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 <223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1329

AATTGAAGAT TTTGA

15

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 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURES:
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<400> SEQUENCE: 1330

ATTGAAGATT TTGAG

15

<210> SEQ ID NO 1331
 <211> LENGTH: 15
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1331

TTGAAGATTT TGAGT

15

<210> SEQ ID NO 1332

<211> LENGTH: 15

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TGAAGATTTT GAGTC

15

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GAAGATTTTG AGTCT

15

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AAGATTTTGA GTCTA

15

<210> SEQ ID NO 1335

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AGATTTTGAG TCTAT

15

<210> SEQ ID NO 1336

<211> LENGTH: 16

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ACCTCGAACA ATTGAA

16

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CCTCGAACAA TTGAAG

16

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CTCGAACAAT TGAAGA

16

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TCGAACAATT GAAGAT

16

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CGAACAATTG AAGATT

16

<210> SEQ ID NO 1341

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GAACAATTGA AGATTT

16

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AACAATTGAA GATTTT

16

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ACAATTGAAG ATTTTG

16

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CAATTGAAGA TTTTGA

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AATTGAAGAT TTTGAG

16

oligosPatNat2.txt

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ATTGAAGATT TTGAGT

16

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TTGAAGATTT TGAGTC

16

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<400> SEQUENCE: 1348

TGAAGATTTT GAGTCT

16

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GAAGATTTTG AGTCTA

16

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AAGATTTTGA GTCTAT

16

oligosPatNat2.txt

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AGATTTTGAG TCTATG

16

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AACCTCGAAC AATTGAA

17

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ACCTCGAACA ATTGAAG

17

<210> SEQ ID NO 1354
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<400> SEQUENCE: 1354

CCTCGAACAA TTGAAGA

17

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CTCGAACAAAT TGAAGAT

17

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TCGAACAATT GAAGATT

17

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CGAACAATTG AAGATTT

17

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GAACAATTGA AGATTTT

17

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AACAATTGAA GATTTTG

17

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ACAATTGAAG ATTTTGA

17

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CAATTGAAGA TTTTGAG

17

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AATTGAAGAT TTTGAGT

17

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ATTGAAGATT TTGAGTC

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TTGAAGATTT TGAGTCT

17

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TGAAGATTTT GAGTCTA

17

<210> SEQ ID NO 1366

<211> LENGTH: 17

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GAAGATTTTG AGTCTAT

17

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AAGATTTTGA GTCTATG

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<212> TYPE: DNA

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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1368

AGATTTTGAG TCTATGA

17

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<212> TYPE: DNA

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<400> SEQUENCE: 1369

GAACCTCGAA CAATTGAA

18

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<212> TYPE: DNA

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AACCTCGAAC AATTGAAG

18

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ACCTCGAACA ATTGAAGA

18

<210> SEQ ID NO 1372
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CCTCGAACAA TTGAAGAT

18

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<400> SEQUENCE: 1373

CTCGAACAA TGAAGATT

18

<210> SEQ ID NO 1374
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TCGAACAATT GAAGATTT

18

<210> SEQ ID NO 1375

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<211> LENGTH: 18
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CGAACAATTG AAGATTTT

18

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GAACAATTGA AGATTTTG

18

<210> SEQ ID NO 1377
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AACAATTGAA GATTTTGA

18

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ACAATTGAAG ATTTTGAG

18

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CAATTGAAGA TTTTGAGT

18

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AATTGAAGAT TTTGAGTC

18

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ATTGAAGATT TTGAGTCT

18

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TTGAAGATTT TGAGTCTA

18

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TGAAGATTTT GAGTCTAT

18

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GAAGATTTTG AGTCTATG

18

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AAGATTTTGA GTCTATGA

18

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AGATTTTGAG TCTATGAA

18

<210> SEQ ID NO 1387
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TGAACCTCGA ACAATTGAA

19

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GAACCTCGAA CAATTGAAG

19

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 <211> LENGTH: 19
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 <213> ORGANISM: Artificial Sequence
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AACCTCGAAC AATTGAAGA 19

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ACCTCGAACA ATTGAAGAT 19

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CCTCGAACAA TTGAAGATT 19

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<211> LENGTH: 19
<212> TYPE: DNA
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<400> SEQUENCE: 1392

CTCGAACAAT TGAAGATTT 19

<210> SEQ ID NO 1393
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 1393

TCGAACAATT GAAGATTTT 19

<210> SEQ ID NO 1394
<211> LENGTH: 19
<212> TYPE: DNA
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<400> SEQUENCE: 1394

CGAACAATTG AAGATTTTG

19

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<211> LENGTH: 19
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<400> SEQUENCE: 1395

GAACAATTGA AGATTTTGA

19

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<400> SEQUENCE: 1396

AACAATTGAA GATTTTGAG

19

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<400> SEQUENCE: 1397

ACAATTGAAG ATTTTGAGT

19

<210> SEQ ID NO 1398
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<212> TYPE: DNA
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CAATTGAAGA TTTTGAGTC

19

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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1399

AATTGAAGAT TTTGAGTCT

19

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ATTGAAGATT TTGAGTCTA

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TTGAAGATTT TGAGTCTAT

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TGAAGATTTT GAGTCTATG

19

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GAAGATTTTG AGTCTATGA

19

<210> SEQ ID NO 1404

<211> LENGTH: 19

<212> TYPE: DNA

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AAGATTTTGA GTCTATGAA

19

<210> SEQ ID NO 1405
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<223> OTHER INFORMATION: cDNA for use as primers
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AGATTTTGAG TCTATGAAT

19

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TTGAACCTCG AACCAATTGAA

20

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TGAACCTCGA ACAATTGAAG

20

<210> SEQ ID NO 1408
<211> LENGTH: 20
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GAACCTCGAA CAATTGAAGA

20

<210> SEQ ID NO 1409

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<211> LENGTH: 20
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<400> SEQUENCE: 1409

AACCTCGAAC AATTGAAGAT

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<210> SEQ ID NO 1410
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<400> SEQUENCE: 1410

ACCTCGAACA ATTGAAGATT

20

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<212> TYPE: DNA
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<223> OTHER INFORMATION: cDNA for use as primers
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CCTCGAACAA TTGAAGATTT

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CTCGAACAAT TGAAGATTTT

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<210> SEQ ID NO 1413
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<213> ORGANISM: Artificial Sequence
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TCGAACAATT GAAGATTTTG

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<220> FEATURES:
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<400> SEQUENCE: 1414

CGAACAATTG AAGATTTTGA

20

<210> SEQ ID NO 1415
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<213> ORGANISM: Artificial Sequence
<220> FEATURES:
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<400> SEQUENCE: 1415

GAACAATTGA AGATTTTGAG

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<210> SEQ ID NO 1416
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 1416

AACAATTGAA GATTTTGAGT

20

<210> SEQ ID NO 1417
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1417

ACAATTGAAG ATTTTGAGTC

20

<210> SEQ ID NO 1418
<211> LENGTH: 20
<212> TYPE: DNA
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<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1418

CAATTGAAGA TTTTGAGTCT

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<210> SEQ ID NO 1419
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<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 1419

AATTGAAGAT TTTGAGTCTA

20

<210> SEQ ID NO 1420
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ATTGAAGATT TTGAGTCTAT

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<210> SEQ ID NO 1421
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<212> TYPE: DNA
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<220> FEATURES:
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<400> SEQUENCE: 1421

TTGAAGATTT TGAGTCTATG

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<400> SEQUENCE: 1422

TGAAGATTTT GAGTCTATGA

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<210> SEQ ID NO 1423
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<213> ORGANISM: Artificial Sequence
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GAAGATTTTG AGTCTATGAA

20

<210> SEQ ID NO 1424
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AAGATTTTGA GTCTATGAAT

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<210> SEQ ID NO 1425
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AGATTTTGAG TCTATGAATA

20

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CTTGAACCTC GAACAATTGA A

21

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TTGAACCTCG AACAATTGAA G

21

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TGAACCTCGA ACAATTGAAG A

21

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GAACCTCGAA CAATTGAAGA T

21

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ACCTCGAACA ATTGAAGATT T

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CCTCGAACAA TTGAAGATTT T

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CTCGAACAAAT TGAAGATTTT G

21

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21

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GAACAATTGA AGATTTTGAG T

21

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AACAATTGAA GATTTTGAGT C

21

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ACAATTGAAG ATTTTGAGTC T 21

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CAATTGAAGA TTTTGAGTCT A 21

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ATTGAAGATT TTGAGTCTAT G 21

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TTGAAGATTT TGAGTCTATG A 21

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TGAAGATTTT GAGTCTATGA A

21

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GAAGATTTTG AGTCTATGAA T

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AGATTTTGAG TCTATGAATA C

21

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GCTTGAACCT CGAACAATTG AA

22

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CTTGAACCTC GAACAATTGA AG 22

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GAACCTCGAA CAATTGAAGA TT 22

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ACCTCGAACA ATTGAAGATT TT

22

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CCTCGAACAA TTGAAGATTT TG

22

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CTCGAACAAT TGAAGATTTT GA

22

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TCGAACAATT GAAGATTTTG AG

22

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CGAACAATTG AAGATTTTGA GT

22

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GAACAATTGA AGATTTTGAG TC

22

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AACAATTGAA GATTTTGAGT CT

22

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ACAATTGAAG ATTTTGAGTC TA

22

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CAATTGAAGA TTTTGAGTCT AT

22

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AATTGAAGAT TTTGAGTCTA TG

22

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<400> SEQUENCE: 1463

ATTGAAGATT TTGAGTCTAT GA

22

<210> SEQ ID NO 1464
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<400> SEQUENCE: 1464

TTGAAGATTT TGAGTCTATG AA

22

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<400> SEQUENCE: 1465

TGAAGATTTT GAGTCTATGA AT

22

<210> SEQ ID NO 1466
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<212> TYPE: DNA
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<400> SEQUENCE: 1466

GAAGATTTTG AGTCTATGAA TA

22

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<223> OTHER INFORMATION: cDNA for use as primers

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AAGATTTTGA GTCTATGAAT AC

22

<210> SEQ ID NO 1468

<211> LENGTH: 22

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AGATTTTGAG TCTATGAATA CA

22

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CGCTTGAACC TCGAACAATT GAA

23

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GCTTGAACCT CGAACAATTG AAG

23

<210> SEQ ID NO 1471

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CTTGAACCTC GAACAATTGA AGA

23

<210> SEQ ID NO 1472

<211> LENGTH: 23

<212> TYPE: DNA

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TTGAACCTCG AACCAATTGAA GAT 23

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TGAACCTCGA ACAATTGAAG ATT 23

<210> SEQ ID NO 1474
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GAACCTCGAA CAATTGAAGA TTT 23

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AACCTCGAAC AATTGAAGAT TTT 23

<210> SEQ ID NO 1476
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ACCTCGAACA ATTGAAGATT TTG 23

<210> SEQ ID NO 1477

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<211> LENGTH: 23
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CCTCGAACAA TTGAAGATTT TGA 23

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CTCGAACAA TGAAGATTTT GAG 23

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TCGAACAATT GAAGATTTTG AGT 23

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CGAACAAATTG AAGATTTTGA GTC 23

<210> SEQ ID NO 1481
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GAACAATTGA AGATTTTGAG TCT 23

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<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 1482

AACAATTGAA GATTTTGAGT CTA

23

<210> SEQ ID NO 1483
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<400> SEQUENCE: 1483

ACAATTGAAG ATTTTGAGTC TAT

23

<210> SEQ ID NO 1484
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CAATTGAAGA TTTTGAGTCT ATG

23

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AATTGAAGAT TTTGAGTCTA TGA

23

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ATTGAAGATT TTGAGTCTAT GAA

23

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TTGAAGATTT TGAGTCTATG AAT

23

<210> SEQ ID NO 1488
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<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

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TGAAGATTTT GAGTCTATGA ATA

23

<210> SEQ ID NO 1489
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 1489

GAAGATTTTG AGTCTATGAA TAC

23

<210> SEQ ID NO 1490
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 1490

AAGATTTTGA GTCTATGAAT ACA

23

<210> SEQ ID NO 1491
<211> LENGTH: 23
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AGATTTTGAG TCTATGAATA CAT

23

<210> SEQ ID NO 1492
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ACGCTTGAAC CTCGAACAAT TGAA

24

<210> SEQ ID NO 1493
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CGCTTGAACC TCGAACAATT GAAG

24

<210> SEQ ID NO 1494
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GCTTGAACCT CGAACAATTG AAGA

24

<210> SEQ ID NO 1495
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CTTGAACCTC GAACAATTGA AGAT

24

<210> SEQ ID NO 1496
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TTGAACCTCG AACAAATTGAA GATT

24

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<400> SEQUENCE: 1497

TGAACCTCGA ACAATTGAAG ATTT

24

<210> SEQ ID NO 1498
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<400> SEQUENCE: 1498

GAACCTCGAA CAATTGAAGA TTTT

24

<210> SEQ ID NO 1499
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AACCTCGAAC AATTGAAGAT TTTG

24

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ACCTCGAACA ATTGAAGATT TTGA

24

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CCTCGAACAA TTGAAGATTT TGAG

24

<210> SEQ ID NO 1502

<211> LENGTH: 24

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CTCGAACAA TGAAGATTTT GAGT

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TCGAACAATT GAAGATTTTG AGTC

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CGAACAAATTG AAGATTTTGA GTCT

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GAACAATTGA AGATTTTGAG TCTA

24

<210> SEQ ID NO 1506

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<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence
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ACAATTGAA GATTTTGAGT CTAT

24

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ACAATTGAAG ATTTTGAGTC TATG

24

<210> SEQ ID NO 1508
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CAATTGAAGA TTTTGAGTCT ATGA

24

<210> SEQ ID NO 1509
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AATTGAAGAT TTTGAGTCTA TGAA

24

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ATTGAAGATT TTGAGTCTAT GAAT

24

<210> SEQ ID NO 1511

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<211> LENGTH: 24
<212> TYPE: DNA
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TTGAAGATTT TGAGTCTATG AATA

24

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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TGAAGATTTT GAGTCTATGA ATAC

24

<210> SEQ ID NO 1513
<211> LENGTH: 24
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<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: cDNA for use as primers
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GAAGATTTTG AGTCTATGAA TACA

24

<210> SEQ ID NO 1514
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<213> ORGANISM: Artificial Sequence
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AAGATTTTGA GTCTATGAAT ACAT

24

<210> SEQ ID NO 1515
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24

oligosPatNat2.txt

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oligosPatNat2.txt

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GAACCTCGAA CAATTGAAGA TTTTG

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AACCTCGAAC AATTGAAGAT TTTGA

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ACCTCGAACA ATTGAAGATT TTGAG

25

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CTCGAACAAT TGAAGATTTT GAGTC

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ACAATTGAAG ATTTTGAGTC TATGA

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CAATTGAAGA TTTTGAGTCT ATGAA

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TTGAAGATTT TGAGTCTATG AATAC

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AGATTTTGAG TCTATGAATA CATAC

25

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TTCAATTGTT CGAGG

15

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CTTCAATTGT TCGAG

15

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TCTTCAATTG TTCGA

15

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ATCTTCAATT GTTCG

15

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AATCTTCAAT TG TTC

15

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AAATCTTCAA TTGTT

15

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AAAATCTTCA ATTGT

15

<210> SEQ ID NO 1548
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CAAAATCTTC AATTG

15

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TCAAAATCTT CAATT

15

OligosPatNat2.txt

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CTCAAATCT TCAAT

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ACTCAAATC TTCAA

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GACTCAAAT CTTC

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AGACTCAAAA TCTTC

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TAGACTCAAA ATCTT

15

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ATAGACTCAA AATCT

15

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TTCAATTGTT CGAGGT

16

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<400> SEQUENCE: 1557

CTTCAATTGT TCGAGG

16

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TCTTCAATTG TTCGAG

16

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ATCTTCAATT GTTCGA

16

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16

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AAATCTTCAA TTGTTC

16

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AAAATCTTCA ATTGTT

16

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<400> SEQUENCE: 1563

CAAAATCTTC AATTGT

16

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<400> SEQUENCE: 1564

TCAAAATCTT CAATTG

16

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CTCAAAATCT TCAATT

16

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ACTCAAAATC TTCAAT

16

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GACTCAAAAT CTTCAA

16

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TAGACTCAAA ATCTTC

16

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CATAGACTCA AAATCT

16

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CTTCAATTGT TCGAGGT

17

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<212> TYPE: DNA

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TCTTCAATTG TTCGAGG

17

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17

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AATCTTCAAT TGTTCGA

17

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AAATCTTCAA TTGTTCG

17

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AAAATCTTCA ATTGTTC

17

<210> SEQ ID NO 1579

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CAAAATCTTC AATTGTT

17

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TCAAAATCTT CAATTGT

17

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CTCAAAATCT TCAATTG

17

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ACTCAAAATC TTCAATT

17

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GACTCAAAAT CTTCAAT

17

oligosPatNat2.txt

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<400> SEQUENCE: 1584

AGACTCAAAA TCTTCAA

17

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<400> SEQUENCE: 1585

TAGACTCAAA ATCTTCA

17

<210> SEQ ID NO 1586
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ATAGACTCAA AATCTTC

17

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<400> SEQUENCE: 1587

CATAGACTCA AAATCTT

17

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TCATAGACTC AAAATCT

17

oligosPatNat2.txt

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<400> SEQUENCE: 1589

TTCAATTGTT CGAGGTTC

18

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<400> SEQUENCE: 1590

CTTCAATTGT TCGAGGTT

18

<210> SEQ ID NO 1591
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TCTTCAATTG TTCGAGGT

18

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ATCTTCAATT GTTCGAGG

18

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AATCTTCAAT TGTTGAG

18

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AAATCTTCAA TTGTTGGA

18

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AAAATCTTCA ATTGTTG

18

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CAAAATCTTC AATTGTT

18

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TCAAAATCTT CAATTGTT

18

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CTCAAAATCT TCAATTGT

18

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ACTCAAAATC TTCAATTG

18

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GACTCAAAAT CTTCAATT

18

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<400> SEQUENCE: 1601

AGACTCAAAA TCTTCAAT

18

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<400> SEQUENCE: 1602

TAGACTCAAA ATCTTCAA

18

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<212> TYPE: DNA
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<400> SEQUENCE: 1603

ATAGACTCAA AATCTTCA

18

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<212> TYPE: DNA

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CATAGACTCA AAATCTTC

18

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<220> FEATURES:

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TCATAGACTC AAAATCTT

18

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TTCATAGACT CAAAATCT

18

<210> SEQ ID NO 1607

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TTCAATTGTT CGAGGTCA

19

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CTTCAATTGT TCGAGGTTC 19

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TCTTCAATTG TTCGAGGTT 19

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ATCTTCAATT GTTCGAGGT 19

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AATCTTCAAT TGTTGAGG 19

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AAATCTTCAA TTGTTGAG 19

<210> SEQ ID NO 1613

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<211> LENGTH: 19
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AAAATCTTCA ATTGTTCA

19

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CAAAATCTTC AATTGTTTCG

19

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TCAAAATCTT CAATTGTTT

19

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CTCAAAATCT TCAATTGTT

19

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ACTCAAAATC TTCAATTGT

19

oligosPatNat2.txt

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GACTCAAAAT CTTCAATTG 19

<210> SEQ ID NO 1619
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AGACTCAAAA TCTTCAATT 19

<210> SEQ ID NO 1620
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TAGACTCAAA ATCTTCAAT 19

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ATAGACTCAA AATCTTCAA 19

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CATAGACTCA AAATCTTCA 19

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TCATAGACTC AAAATCTTC

19

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19

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20

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20

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AATCTTCAAT TGTTGAGGT

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AAATCTTCAA TTGTTGAGG

20

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AAAATCTTCA ATTGTTGAG

20

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CAAAATCTTC AATTGTTGGA

20

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TCAAAATCTT CAATTGTTG

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CTCAAAATCT TCAATTGTTG

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ACTCAAAATC TTCAATTGTT

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<210> SEQ ID NO 1637
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GACTCAAAAT CTTCAATTGT

20

<210> SEQ ID NO 1638

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TAGACTCAAA ATCTTCAATT

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ATAGACTCAA AATCTTCAAT

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<213> ORGANISM: Artificial sequence

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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1641

CATAGACTCA AAATCTTCAA

20

<210> SEQ ID NO 1642

<211> LENGTH: 20

<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURES:
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<400> SEQUENCE: 1642

TCATAGACTC AAAATCTTCA 20

<210> SEQ ID NO 1643
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<223> OTHER INFORMATION: cDNA for use as primers
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TTCATAGACT CAAAATCTTC 20

<210> SEQ ID NO 1644
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ATTCATAGAC TCAAAATCTT 20

<210> SEQ ID NO 1645
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TATTCATAGA CTCAAAATCT 20

<210> SEQ ID NO 1646
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TTCAATTGTT CGAGGTTCAA G 21

<210> SEQ ID NO 1647

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<211> LENGTH: 21
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CTTCAATTGT TCGAGGTTCA A

21

<210> SEQ ID NO 1648
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TCTTCAATTG TTCGAGGTTCA A

21

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ATCTTCAATT GTTCGAGGTT C

21

<210> SEQ ID NO 1650
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<212> TYPE: DNA
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AATCTTCAAT TGTCGAGGT T

21

<210> SEQ ID NO 1651
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21

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<210> SEQ ID NO 1652
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<400> SEQUENCE: 1652

AAAATCTTCA ATTGTTGAG G 21

<210> SEQ ID NO 1653
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<400> SEQUENCE: 1653

CAAAATCTTC AATTGTTGGA G 21

<210> SEQ ID NO 1654
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TCAAAATCTT CAATTGTTG A 21

<210> SEQ ID NO 1655
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<212> TYPE: DNA
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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1655

CTCAAAATCT TCAATTGTTG G 21

<210> SEQ ID NO 1656
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<400> SEQUENCE: 1656

ACTCAAAATC TTCAATTGTT C 21

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<210> SEQ ID NO 1657
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<400> SEQUENCE: 1657

GACTCAAAAT CTTCAATTGT T

21

<210> SEQ ID NO 1658
<211> LENGTH: 21
<212> TYPE: DNA
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<400> SEQUENCE: 1658

AGACTCAAAA TCTTCAATTG T

21

<210> SEQ ID NO 1659
<211> LENGTH: 21
<212> TYPE: DNA
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TAGACTCAAA ATCTTCAATT G

21

<210> SEQ ID NO 1660
<211> LENGTH: 21
<212> TYPE: DNA
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<400> SEQUENCE: 1660

ATAGACTCAA AATCTTCAAT T

21

<210> SEQ ID NO 1661
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 1661

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CATAGACTCA AAATCTTCAA T

21

<210> SEQ ID NO 1662
<211> LENGTH: 21
<212> TYPE: DNA
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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1662

TCATAGACTC AAAATCTTCA A

21

<210> SEQ ID NO 1663
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<212> TYPE: DNA
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<220> FEATURES:
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TTCATAGACT CAAAATCTTC A

21

<210> SEQ ID NO 1664
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<212> TYPE: DNA
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<400> SEQUENCE: 1664

ATTCATAGAC TCAAATCTT C

21

<210> SEQ ID NO 1665
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
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<400> SEQUENCE: 1665

TATTCATAGA CTCAAATCT T

21

<210> SEQ ID NO 1666
<211> LENGTH: 21
<212> TYPE: DNA
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<400> SEQUENCE: 1666

GTATTCATAG ACTCAAATC T

21

<210> SEQ ID NO 1667
 <211> LENGTH: 22
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 1667

TTCAATTGTT CGAGGTCAA GC

22

<210> SEQ ID NO 1668
 <211> LENGTH: 22
 <212> TYPE: DNA
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<400> SEQUENCE: 1668

CTTCAATTGT TCGAGGTCA AG

22

<210> SEQ ID NO 1669
 <211> LENGTH: 22
 <212> TYPE: DNA
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TCTTCAATTG TTCGAGGTTC AA

22

<210> SEQ ID NO 1670
 <211> LENGTH: 22
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<400> SEQUENCE: 1670

ATCTTCAATT GTTCGAGGTT CA

22

<210> SEQ ID NO 1671
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<223> OTHER INFORMATION: cDNA for use as primers

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AATCTTCAAT TGTTGAGGT TC

22

<210> SEQ ID NO 1672

<211> LENGTH: 22

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AAATCTTCAA TTGTTGAGG TT

22

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AAAATCTTCA ATTGTTGAG GT

22

<210> SEQ ID NO 1674

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CAAAATCTTC AATTGTTGGA GG

22

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TCAAAATCTT CAATTGTTG AG

22

<210> SEQ ID NO 1676

<211> LENGTH: 22

<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURES:
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CTCAAAATCT TCAATTGTTG GA

22

<210> SEQ ID NO 1677
<211> LENGTH: 22
<212> TYPE: DNA
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ACTCAAAATC TTCAATTGTT CG

22

<210> SEQ ID NO 1678
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
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GACTCAAAAT CTTCAATTGT TC

22

<210> SEQ ID NO 1679
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: cDNA for use as primers
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AGACTCAAAA TCTTCAATTG TT

22

<210> SEQ ID NO 1680
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<212> TYPE: DNA
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TAGACTCAAA ATCTTCAATT GT

22

<210> SEQ ID NO 1681

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<211> LENGTH: 22
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ATAGACTCAA AATCTTCAAT TG

22

<210> SEQ ID NO 1682
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<223> OTHER INFORMATION: cDNA for use as primers
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CATAGACTCA AAATCTTCAA TT

22

<210> SEQ ID NO 1683
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<223> OTHER INFORMATION: cDNA for use as primers
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TCATAGACTC AAAATCTTCA AT

22

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<212> TYPE: DNA
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TTCATAGACT CAAAATCTTC AA

22

<210> SEQ ID NO 1685
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<212> TYPE: DNA
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<223> OTHER INFORMATION: cDNA for use as primers
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ATTCATAGAC TCAAATCTT CA

22

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<210> SEQ ID NO 1686
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<212> TYPE: DNA
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<400> SEQUENCE: 1686

TATTCATAGA CTCAAAATCT TC 22

<210> SEQ ID NO 1687
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<212> TYPE: DNA
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<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1687

GTATTCATAG ACTCAAAATC TT 22

<210> SEQ ID NO 1688
<211> LENGTH: 22
<212> TYPE: DNA
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<220> FEATURES:
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TGTATTCATA GACTCAAAAT CT 22

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<212> TYPE: DNA
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<220> FEATURES:
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TTCAATTGTT CGAGGTTCAG GCG 23

<210> SEQ ID NO 1690
<211> LENGTH: 23
<212> TYPE: DNA
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<400> SEQUENCE: 1690

CTTCAATTGT TCGAGGTTCAG AGC 23

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<210> SEQ ID NO 1691
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TCTTCAATTG TTCGAGGTT C AAG

23

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ATCTTCAATT GTTCGAGGTT CAA

23

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<212> TYPE: DNA
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AATCTTCAAT TGTCGAGGT TCA

23

<210> SEQ ID NO 1694
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 1694

AAATCTTCAA TTGTCGAGG TTC

23

<210> SEQ ID NO 1695
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<212> TYPE: DNA
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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1695

AAAATCTTCA ATTGTTGAG GTT

23

<210> SEQ ID NO 1696
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CAAAATCTTC AATTGTTGGA GGT

23

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TCAAAATCTT CAATTGTTG AGG

23

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CTCAAAATCT TCAATTGTTG GAG

23

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ACTCAAAATC TTCAATTGTT CGA

23

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GACTCAAAAT CTTCAATTGT TCG

23

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AGACTCAAAA TCTTCAATTG TTC

23

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TAGACTCAAA ATCTTCAATT GTT

23

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ATAGACTCAA AATCTTCAAT TGT

23

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CATAGACTCA AAATCTTCAA TTG

23

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TCATAGACTC AAAATCTTCA ATT

23

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23

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GTATTCATAG ACTCAAATC TTC

23

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ATGTATTCAT AGACTCAAAA TCT 23

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TTCAATTGTT CGAGGTCAA GCGT 24

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CTTCAATTGT TCGAGGTCA AGCG 24

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<210> SEQ ID NO 1715

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ATCTTCAATT GTTCGAGGTT CAAG

24

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AATCTTCAAT TGTCGAGGT TCAA

24

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AAATCTTCAA TTGTCGAGG TTCA

24

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AAAATCTTCA ATTGTCGAG GTTC

24

<210> SEQ ID NO 1719
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CAAAATCTTC AATTGTCGA GGTT

24

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TCAAAATCTT CAATTGTTTCG AGGT 24

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CTCAAAATCT TCAATTGTTC GAGG 24

<210> SEQ ID NO 1722
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ACTCAAAATC TTCAATTGTT CGAG 24

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GACTCAAAAT CTTCAATTGT TCGA 24

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AGACTCAAAA TCTTCAATTG TTCG 24

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TAGACTCAA ATCTTCAATT GTTC

24

<210> SEQ ID NO 1726
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ATAGACTCAA AATCTTCAAT TGTT

24

<210> SEQ ID NO 1727
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CATAGACTCA AAATCTTCAA TTGT

24

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TCATAGACTC AAAATCTTCA ATTG

24

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TTCATAGACT CAAAATCTTC AATT

24

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ATTCATAGAC TCAAAATCTT CAAT

24

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TATTCATAGA CTCAAAATCT TCAA

24

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GTATTCATAG ACTCAAAATC TTCA

24

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TGTATTCATA GACTCAAAAT CTTC

24

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ATGTATTCAT AGACTCAAAA TCTT

24

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TATGTATTCA TAGACTCAAA ATCT

24

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TTCAATTGTT CGAGGTTCAA GCGTA

25

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CTTCAATTGT TCGAGGTTCA AGCGT

25

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<400> SEQUENCE: 1738

TCTTCAATTG TTCGAGGTTCA AAGCG

25

<210> SEQ ID NO 1739
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ATCTTCAATT GTTCGAGGTT CAAGC

25

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AATCTTCAAT TGTTGAGGTT TCAAG

25

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AAATCTTCAA TTGTTGAGG TTCAA

25

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AAAATCTTCA ATTGTTGAG GTTCA

25

<210> SEQ ID NO 1743

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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1743

CAAAATCTTC AATTGTTGGA GGTTC

25

<210> SEQ ID NO 1744

<211> LENGTH: 25

<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURES:
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<400> SEQUENCE: 1744

TCAAAATCTT CAATTGTTTCG AGGTT 25

<210> SEQ ID NO 1745
<211> LENGTH: 25
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CTCAAAATCT TCAATTGTTC GAGGT 25

<210> SEQ ID NO 1746
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ACTCAAAATC TTCAATTGTT CGAGG 25

<210> SEQ ID NO 1747
<211> LENGTH: 25
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<223> OTHER INFORMATION: cDNA for use as primers
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GACTCAAAAT CTTCAATTGT TCGAG 25

<210> SEQ ID NO 1748
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<212> TYPE: DNA
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AGACTCAAAA TCTTCAATTG TTCGA 25

<210> SEQ ID NO 1749

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<211> LENGTH: 25
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<400> SEQUENCE: 1749

TAGACTCAA ATCTTCAATT GTTCG

25

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<400> SEQUENCE: 1750

ATAGACTCAA AATCTTCAAT TGTTG

25

<210> SEQ ID NO 1751
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<400> SEQUENCE: 1751

CATAGACTCA AAATCTTCAA TTGTT

25

<210> SEQ ID NO 1752
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<400> SEQUENCE: 1752

TCATAGACTC AAAATCTTCA ATTGT

25

<210> SEQ ID NO 1753
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<400> SEQUENCE: 1753

TTCATAGACT CAAAATCTTC AATTG

25

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<400> SEQUENCE: 1754

ATTCATAGAC TCAAATCTT CAATT

25

<210> SEQ ID NO 1755
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TATTCATAGA CTCAAATCT TCAAT

25

<210> SEQ ID NO 1756
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<400> SEQUENCE: 1756

GTATTCATAG ACTCAAATC TCAA

25

<210> SEQ ID NO 1757
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<400> SEQUENCE: 1757

TGTATTCATA GACTCAAAT CTCA

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<210> SEQ ID NO 1758
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<400> SEQUENCE: 1758

ATGTATTCAT AGACTCAAAA TCTTC

25

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<210> SEQ ID NO 1759
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<213> ORGANISM: Artificial Sequence
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TATGTATTCA TAGACTCAAA ATCTT

25

<210> SEQ ID NO 1760
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
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GTATGTATTG ATAGACTCAA AATCT

25

<210> SEQ ID NO 1761
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 1761

AGCCATGGAG TTGGG

15

<210> SEQ ID NO 1762
<211> LENGTH: 15
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
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GCCATGGAGT TGGGC

15

<210> SEQ ID NO 1763
<211> LENGTH: 15
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 1763

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CCATGGAGTT GGGCT

15

<210> SEQ ID NO 1764
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<223> OTHER INFORMATION: cDNA for use as primers
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CATGGAGTTG GGCTT

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<210> SEQ ID NO 1765
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<223> OTHER INFORMATION: cDNA for use as primers
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ATGGAGTTGG GCTTA

15

<210> SEQ ID NO 1766
<211> LENGTH: 15
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TGGAGTTGGG CTTAG

15

<210> SEQ ID NO 1767
<211> LENGTH: 15
<212> TYPE: DNA
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<223> OTHER INFORMATION: cDNA for use as primers
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GGAGTTGGGC TTAGA

15

<210> SEQ ID NO 1768
<211> LENGTH: 15
<212> TYPE: DNA
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<400> SEQUENCE: 1768

GAGTTGGGCT TAGAG

15

<210> SEQ ID NO 1769
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<212> TYPE: DNA
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<400> SEQUENCE: 1769

AGTTGGGCTT AGAGG

15

<210> SEQ ID NO 1770
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<212> TYPE: DNA
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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1770

GTTGGGCTTA GAGGC

15

<210> SEQ ID NO 1771
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<212> TYPE: DNA
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<400> SEQUENCE: 1771

TTGGGCTTAG AGGCT

15

<210> SEQ ID NO 1772
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<212> TYPE: DNA
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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1772

TGGGCTTAGA GGCTA

15

<210> SEQ ID NO 1773
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<212> TYPE: DNA
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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1773

GGGCTTAGAG GCTAT

15

<210> SEQ ID NO 1774

<211> LENGTH: 15

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GGCTTAGAGG CTATT

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GCTTAGAGGC TATTT

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AAGCCATGGA GTTGGG

16

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AGCCATGGAG TTGGGC

16

<210> SEQ ID NO 1778

<211> LENGTH: 16

<212> TYPE: DNA

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<223> OTHER INFORMATION: cDNA for use as primers
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GCCATGGAGT TGGGCT

16

<210> SEQ ID NO 1779
<211> LENGTH: 16
<212> TYPE: DNA
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CCATGGAGTT GGGCTT

16

<210> SEQ ID NO 1780
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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CATGGAGTTG GGCTTA

16

<210> SEQ ID NO 1781
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<212> TYPE: DNA
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ATGGAGTTGG GCTTAG

16

<210> SEQ ID NO 1782
<211> LENGTH: 16
<212> TYPE: DNA
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<223> OTHER INFORMATION: cDNA for use as primers
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TGGAGTTGGG CTTAGA

16

<210> SEQ ID NO 1783

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<211> LENGTH: 16
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1783

GGAGTTGGGC TTAGAG

16

<210> SEQ ID NO 1784
<211> LENGTH: 16
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 1784

GAGTTGGGCT TAGAGG

16

<210> SEQ ID NO 1785
<211> LENGTH: 16
<212> TYPE: DNA
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AGTTGGGCTT AGAGGC

16

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GTTGGGCTTA GAGGCT

16

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TTGGGCTTAG AGGCTA

16

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GCTTAGAGGC TATTTT 16

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CAAGCCATGG AGTTGGG 17

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17

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AGCCATGGAG TTGGGCT

17

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GCCATGGAGT TGGGCTT

17

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CCATGGAGTT GGGCTTA

17

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17

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17

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TGGAGTTGGG CTTAGAG

17

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GGAGTTGGGC TTAGAGG

17

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GAGTTGGGCT TAGAGGC

17

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17

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GTTGGGCTTA GAGGCTA

17

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TTGGGCTTAG AGGCTAT

17

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TGGGCTTAGA GGCTATT

17

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GGGCTTAGAG GCTATTT

17

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17

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<211> LENGTH: 17

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GCTTAGAGGC TATTTT

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18

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18

<210> SEQ ID NO 1812

<211> LENGTH: 18

<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
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AGCCATGGAG TTGGGCTT

18

<210> SEQ ID NO 1813
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GCCATGGAGT TGGGCTTA

18

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18

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CATGGAGTTG GGCTTAGA

18

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18

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<211> LENGTH: 18
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TGGAGTTGGG CTTAGAGG

18

<210> SEQ ID NO 1818
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<400> SEQUENCE: 1818

GGAGTTGGGC TTAGAGGC

18

<210> SEQ ID NO 1819
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<212> TYPE: DNA
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GAGTTGGGCT TAGAGGCT

18

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<400> SEQUENCE: 1820

AGTTGGGCTT AGAGGCTA

18

<210> SEQ ID NO 1821
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<400> SEQUENCE: 1821

GTTGGGCTTA GAGGCTAT

18

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<400> SEQUENCE: 1822

TTGGGCTTAG AGGCTATT

18

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<400> SEQUENCE: 1823

TGGGCTTAGA GGCTATTT

18

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GGGCTTAGAG GCTATTTT

18

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GGCTTAGAGG CTATTTT

18

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<400> SEQUENCE: 1826

GCTTAGAGGC TATTTTGG

18

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GGCAAGCCAT GGAGTTGGG

19

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GCAAGCCATG GAGTTGGGC

19

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CAAGCCATGG AGTTGGGCT

19

<210> SEQ ID NO 1830
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AAGCCATGGA GTTGGGCTT

19

<210> SEQ ID NO 1831
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AGCCATGGAG TTGGGCTTA 19

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GCCATGGAGT TGGGCTTAG 19

<210> SEQ ID NO 1833
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CCATGGAGTT GGGCTTAGA 19

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CATGGAGTTG GGCTTAGAG 19

<210> SEQ ID NO 1835
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ATGGAGTTGG GCTTAGAGG 19

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<400> SEQUENCE: 1836

TGGAGTTGGG CTTAGAGGC

19

<210> SEQ ID NO 1837
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<212> TYPE: DNA
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<400> SEQUENCE: 1837

GGAGTTGGGC TTAGAGGCT

19

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<400> SEQUENCE: 1838

GAGTTGGGCT TAGAGGCTA

19

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<212> TYPE: DNA
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<400> SEQUENCE: 1839

AGTTGGGCTT AGAGGCTAT

19

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<212> TYPE: DNA
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<400> SEQUENCE: 1840

GTTGGGCTTA GAGGCTATT

19

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<212> TYPE: DNA
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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1841

TTGGGCTTAG AGGCTATTT

19

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<211> LENGTH: 19

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<400> SEQUENCE: 1842

TGGGCTTAGA GGCTATTTT

19

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GGGCTTAGAG GCTATTTT

19

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19

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<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: cDNA for use as primers
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GGGCAAGCCA TGGAGTTGGG

20

<210> SEQ ID NO 1847
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GGCAAGCCAT GGAGTTGGGC

20

<210> SEQ ID NO 1848
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: cDNA for use as primers
<400> SEQUENCE: 1848

GCAAGCCATG GAGTTGGGCT

20

<210> SEQ ID NO 1849
<211> LENGTH: 20
<212> TYPE: DNA
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<223> OTHER INFORMATION: cDNA for use as primers
<400> SEQUENCE: 1849

CAAGCCATGG AGTTGGGCTT

20

<210> SEQ ID NO 1850
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<212> TYPE: DNA
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AAGCCATGGA GTTGGGCTTA

20

<210> SEQ ID NO 1851

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<211> LENGTH: 20
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<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 1851

AGCCATGGAG TTGGGCTTAG

20

<210> SEQ ID NO 1852
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<400> SEQUENCE: 1852

GCCATGGAGT TGGGCTTAGA

20

<210> SEQ ID NO 1853
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CCATGGAGTT GGGCTTAGAG

20

<210> SEQ ID NO 1854
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CATGGAGTTG GGCTTAGAGG

20

<210> SEQ ID NO 1855
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ATGGAGTTGG GCTTAGAGGC

20

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 1856

TGGAGTTGGG CTTAGAGGCT

20

<210> SEQ ID NO 1857
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1857

GGAGTTGGGC TTAGAGGCTA

20

<210> SEQ ID NO 1858
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
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<400> SEQUENCE: 1858

GAGTTGGGCT TAGAGGCTAT

20

<210> SEQ ID NO 1859
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1859

AGTTGGGCTT AGAGGCTATT

20

<210> SEQ ID NO 1860
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1860

GTTGGGCTTA GAGGCTATTT

20

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<210> SEQ ID NO 1861
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1861

TTGGGCTTAG AGGCTATTTT

20

<210> SEQ ID NO 1862
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1862

TGGGCTTAGA GGCTATTTT

20

<210> SEQ ID NO 1863
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1863

GGGCTTAGAG GCTATTTTGT

20

<210> SEQ ID NO 1864
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
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<400> SEQUENCE: 1864

GGCTTAGAGG CTATTTTGA

20

<210> SEQ ID NO 1865
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
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<400> SEQUENCE: 1865

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GCTTAGAGGC TATTTTGGAT

20

<210> SEQ ID NO 1866
 <211> LENGTH: 21
 <212> TYPE: DNA
 <213> ORGANISM: Artificial sequence
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 <400> SEQUENCE: 1866

TGGGCAAGCC ATGGAGTTGG G

21

<210> SEQ ID NO 1867
 <211> LENGTH: 21
 <212> TYPE: DNA
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GGGCAAGCCA TGGAGTTGGG C

21

<210> SEQ ID NO 1868
 <211> LENGTH: 21
 <212> TYPE: DNA
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GGCAAGCCAT GGAGTTGGGC T

21

<210> SEQ ID NO 1869
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 <212> TYPE: DNA
 <213> ORGANISM: Artificial sequence
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 <400> SEQUENCE: 1869

GCAAGCCATG GAGTTGGGCT T

21

<210> SEQ ID NO 1870
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 <213> ORGANISM: Artificial sequence
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<400> SEQUENCE: 1870

CAAGCCATGG AGTTGGGCTT A

21

<210> SEQ ID NO 1871

<211> LENGTH: 21

<212> TYPE: DNA

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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1871

AAGCCATGGA GTTGGGCTTA G

21

<210> SEQ ID NO 1872

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AGCCATGGAG TTGGGCTTAG A

21

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GCCATGGAGT TGGGCTTAGA G

21

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<212> TYPE: DNA

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<220> FEATURES:

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<400> SEQUENCE: 1874

CCATGGAGTT GGGCTTAGAG G

21

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<212> TYPE: DNA

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CATGGAGTTG GGCTTAGAGG C

21

<210> SEQ ID NO 1876

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<220> FEATURES:

<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1876

ATGGAGTTGG GCTTAGAGGC T

21

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<211> LENGTH: 21

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<400> SEQUENCE: 1877

TGGAGTTGGG CTTAGAGGCT A

21

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<211> LENGTH: 21

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<220> FEATURES:

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<400> SEQUENCE: 1878

GGAGTTGGGC TTAGAGGCTA T

21

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<220> FEATURES:

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<400> SEQUENCE: 1879

GAGTTGGGCT TAGAGGCTAT T

21

<210> SEQ ID NO 1880

<211> LENGTH: 21

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence
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AGTTGGGCTT AGAGGCTATT T 21

<210> SEQ ID NO 1881
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GTTGGGCTTA GAGGCTATTT T 21

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TTGGGCTTAG AGGCTATTTT T 21

<210> SEQ ID NO 1883
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TGGGCTTAGA GGCTATTTTT G 21

<210> SEQ ID NO 1884
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GGGCTTAGAG GCTATTTTTG A 21

<210> SEQ ID NO 1885

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<211> LENGTH: 21
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GGCTTAGAGG CTATTTTGA T 21

<210> SEQ ID NO 1886
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GCTTAGAGGC TATTTTGGAT C 21

<210> SEQ ID NO 1887
 <211> LENGTH: 22
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GTGGGCAAGC CATGGAGTTG GG 22

<210> SEQ ID NO 1888
 <211> LENGTH: 22
 <212> TYPE: DNA
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 <223> OTHER INFORMATION: cDNA for use as primers
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TGGGCAAGCC ATGGAGTTGG GC 22

<210> SEQ ID NO 1889
 <211> LENGTH: 22
 <212> TYPE: DNA
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 <223> OTHER INFORMATION: cDNA for use as primers
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GGGCAAGCCA TGGAGTTGGG CT 22

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<210> SEQ ID NO 1890
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<212> TYPE: DNA
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<220> FEATURES:
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<400> SEQUENCE: 1890

GGCAAGCCAT GGAGTTGGGC TT 22

<210> SEQ ID NO 1891
<211> LENGTH: 22
<212> TYPE: DNA
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<220> FEATURES:
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<400> SEQUENCE: 1891

GCAAGCCATG GAGTTGGGCT TA 22

<210> SEQ ID NO 1892
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1892

CAAGCCATGG AGTTGGGCTT AG 22

<210> SEQ ID NO 1893
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1893

AAGCCATGGA GTTGGGCTTA GA 22

<210> SEQ ID NO 1894
<211> LENGTH: 22
<212> TYPE: DNA
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<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1894

AGCCATGGAG TTGGGCTTAG AG 22

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<210> SEQ ID NO 1895
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
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<400> SEQUENCE: 1895

GCCATGGAGT TGGGCTTAGA GG

22

<210> SEQ ID NO 1896
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1896

CCATGGAGTT GGGCTTAGAG GC

22

<210> SEQ ID NO 1897
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1897

CATGGAGTTG GGCTTAGAGG CT

22

<210> SEQ ID NO 1898
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1898

ATGGAGTTGG GCTTAGAGGC TA

22

<210> SEQ ID NO 1899
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1899

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TGGAGTTGGG CTTAGAGGCT AT

22

<210> SEQ ID NO 1900
 <211> LENGTH: 22
 <212> TYPE: DNA
 <213> ORGANISM: Artificial sequence
 <220> FEATURES:
 <223> OTHER INFORMATION: cDNA for use as primers
 <400> SEQUENCE: 1900

GGAGTTGGGC TTAGAGGCTA TT

22

<210> SEQ ID NO 1901
 <211> LENGTH: 22
 <212> TYPE: DNA
 <213> ORGANISM: Artificial sequence
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 <223> OTHER INFORMATION: cDNA for use as primers
 <400> SEQUENCE: 1901

GAGTTGGGCT TAGAGGCTAT TT

22

<210> SEQ ID NO 1902
 <211> LENGTH: 22
 <212> TYPE: DNA
 <213> ORGANISM: Artificial sequence
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 <223> OTHER INFORMATION: cDNA for use as primers
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AGTTGGGCTT AGAGGCTATT TT

22

<210> SEQ ID NO 1903
 <211> LENGTH: 22
 <212> TYPE: DNA
 <213> ORGANISM: Artificial sequence
 <220> FEATURES:
 <223> OTHER INFORMATION: cDNA for use as primers
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GTTGGGCTTA GAGGCTATTT TT

22

<210> SEQ ID NO 1904
 <211> LENGTH: 22
 <212> TYPE: DNA
 <213> ORGANISM: Artificial sequence
 <220> FEATURES:
 <223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1904

TTGGGCTTAG AGGCTATTTT TG

22

<210> SEQ ID NO 1905
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1905

TGGGCTTAGA GGCTATTTT GA

22

<210> SEQ ID NO 1906
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
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<400> SEQUENCE: 1906

GGGCTTAGAG GCTATTTT TG AT

22

<210> SEQ ID NO 1907
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1907

GGCTTAGAGG CTATTTTGA TC

22

<210> SEQ ID NO 1908
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1908

GCTTAGAGGC TATTTT GAT CA

22

<210> SEQ ID NO 1909
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:

<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1909

TGTGGGCAAG CCATGGAGTT GGG

23

<210> SEQ ID NO 1910

<211> LENGTH: 23

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<220> FEATURES:

<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1910

GTGGGCAAGC CATGGAGTTG GGC

23

<210> SEQ ID NO 1911

<211> LENGTH: 23

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURES:

<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1911

TGGGCAAGCC ATGGAGTTGG GCT

23

<210> SEQ ID NO 1912

<211> LENGTH: 23

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURES:

<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1912

GGGCAAGCCA TGGAGTTGGG CTT

23

<210> SEQ ID NO 1913

<211> LENGTH: 23

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURES:

<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1913

GGCAAGCCAT GGAGTTGGGC TTA

23

<210> SEQ ID NO 1914

<211> LENGTH: 23

<212> TYPE: DNA

<213> ORGANISM: Artificial sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
<400> SEQUENCE: 1914

GCAAGCCATG GAGTTGGGCT TAG

23

<210> SEQ ID NO 1915
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
<400> SEQUENCE: 1915

CAAGCCATGG AGTTGGGCTT AGA

23

<210> SEQ ID NO 1916
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
<400> SEQUENCE: 1916

AAGCCATGGA GTTGGGCTTA GAG

23

<210> SEQ ID NO 1917
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
<400> SEQUENCE: 1917

AGCCATGGAG TTGGGCTTAG AGG

23

<210> SEQ ID NO 1918
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
<400> SEQUENCE: 1918

GCCATGGAGT TGGGCTTAGA GGC

23

<210> SEQ ID NO 1919

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<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1919

CCATGGAGTT GGGCTTAGAG GCT

23

<210> SEQ ID NO 1920
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1920

CATGGAGTTG GGCTTAGAGG CTA

23

<210> SEQ ID NO 1921
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1921

ATGGAGTTGG GCTTAGAGGC TAT

23

<210> SEQ ID NO 1922
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1922

TGGAGTTGGG CTTAGAGGCT ATT

23

<210> SEQ ID NO 1923
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1923

GGAGTTGGGC TTAGAGGCTA TTT

23

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<210> SEQ ID NO 1924
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1924

GAGTTGGGCT TAGAGGCTAT TTT 23

<210> SEQ ID NO 1925
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1925

AGTTGGGCTT AGAGGCTATT TTT 23

<210> SEQ ID NO 1926
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1926

GTTGGGCTTA GAGGCTATTT TTG 23

<210> SEQ ID NO 1927
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1927

TTGGGCTTAG AGGCTATTTT TGA 23

<210> SEQ ID NO 1928
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1928

TGGGCTTAGA GGCTATTTT GAT 23

<210> SEQ ID NO 1929
 <211> LENGTH: 23
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURES:
 <223> OTHER INFORMATION: cDNA for use as primers
 <400> SEQUENCE: 1929

GGGCTTAGAG GCTATTTTGG ATC

23

<210> SEQ ID NO 1930
 <211> LENGTH: 23
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURES:
 <223> OTHER INFORMATION: cDNA for use as primers
 <400> SEQUENCE: 1930

GGCTTAGAGG CTATTTTGA TCA

23

<210> SEQ ID NO 1931
 <211> LENGTH: 23
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURES:
 <223> OTHER INFORMATION: cDNA for use as primers
 <400> SEQUENCE: 1931

GCTTAGAGGC TATTTTGGAT CAC

23

<210> SEQ ID NO 1932
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURES:
 <223> OTHER INFORMATION: cDNA for use as primers
 <400> SEQUENCE: 1932

TTGTGGGCAA GCCATGGAGT TGGG

24

<210> SEQ ID NO 1933
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURES:
 <223> OTHER INFORMATION: cDNA for use as primers
 <400> SEQUENCE: 1933

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TGTGGGCAAG CCATGGAGTT GGGC

24

<210> SEQ ID NO 1934
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1934

GTGGGCAAGC CATGGAGTTG GGCT

24

<210> SEQ ID NO 1935
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1935

TGGGCAAGCC ATGGAGTTGG GCTT

24

<210> SEQ ID NO 1936
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1936

GGGCAAGCCA TGGAGTTGGG CTTA

24

<210> SEQ ID NO 1937
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1937

GGCAAGCCAT GGAGTTGGGC TTAG

24

<210> SEQ ID NO 1938
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1938

GCAAGCCATG GAGTTGGGCT TAGA

24

<210> SEQ ID NO 1939
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1939

CAAGCCATGG AGTTGGGCTT AGAG

24

<210> SEQ ID NO 1940
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1940

AAGCCATGGA GTTGGGCTTA GAGG

24

<210> SEQ ID NO 1941
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1941

AGCCATGGAG TTGGGCTTAG AGGC

24

<210> SEQ ID NO 1942
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1942

GCCATGGAGT TGGGCTTAGA GGCT

24

<210> SEQ ID NO 1943
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:

<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1943

CCATGGAGTT GGGCTTAGAG GCTA

24

<210> SEQ ID NO 1944

<211> LENGTH: 24

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURES:

<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1944

CATGGAGTTG GGCTTAGAGG CTAT

24

<210> SEQ ID NO 1945

<211> LENGTH: 24

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURES:

<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1945

ATGGAGTTGG GCTTAGAGGC TATT

24

<210> SEQ ID NO 1946

<211> LENGTH: 24

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURES:

<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1946

TGGAGTTGGG CTTAGAGGCT ATTT

24

<210> SEQ ID NO 1947

<211> LENGTH: 24

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURES:

<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1947

GGAGTTGGGC TTAGAGGCTA TTTT

24

<210> SEQ ID NO 1948

<211> LENGTH: 24

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence
 <220> FEATURES:
 <223> OTHER INFORMATION: cDNA for use as primers
 <400> SEQUENCE: 1948

GAGTTGGGCT TAGAGGCTAT TTTT

24

<210> SEQ ID NO 1949
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURES:
 <223> OTHER INFORMATION: cDNA for use as primers
 <400> SEQUENCE: 1949

AGTTGGGCTT AGAGGCTATT TTTG

24

<210> SEQ ID NO 1950
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURES:
 <223> OTHER INFORMATION: cDNA for use as primers
 <400> SEQUENCE: 1950

GTTGGGCTTA GAGGCTATTT TTGA

24

<210> SEQ ID NO 1951
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURES:
 <223> OTHER INFORMATION: cDNA for use as primers
 <400> SEQUENCE: 1951

TTGGGCTTAG AGGCTATTTT TGAT

24

<210> SEQ ID NO 1952
 <211> LENGTH: 24
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURES:
 <223> OTHER INFORMATION: cDNA for use as primers
 <400> SEQUENCE: 1952

TGGGCTTAGA GGCTATTTT GATC

24

<210> SEQ ID NO 1953

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<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
<400> SEQUENCE: 1953

GGGCTTAGAG GCTATTTTGG ATCA

24

<210> SEQ ID NO 1954
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
<400> SEQUENCE: 1954

GGCTTAGAGG CTATTTTGA TCAC

24

<210> SEQ ID NO 1955
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
<400> SEQUENCE: 1955

GCTTAGAGGC TATTTTGGAT CACA

24

<210> SEQ ID NO 1956
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
<400> SEQUENCE: 1956

ATTGTGGGCA AGCCATGGAG TTGGG

25

<210> SEQ ID NO 1957
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
<400> SEQUENCE: 1957

TTGTGGGCAA GCCATGGAGT TGGGC

25

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<210> SEQ ID NO 1958
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1958

TGTGGGCAAG CCATGGAGTT GGGCT

25

<210> SEQ ID NO 1959
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1959

GTGGGCAAGC CATGGAGTTG GGCTT

25

<210> SEQ ID NO 1960
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1960

TGGGCAAGCC ATGGAGTTGG GCTTA

25

<210> SEQ ID NO 1961
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1961

GGGCAAGCCA TGGAGTTGGG CTTAG

25

<210> SEQ ID NO 1962
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1962

GGCAAGCCAT GGAGTTGGGC TTAGA

25

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<210> SEQ ID NO 1963
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1963

GCAAGCCATG GAGTTGGGCT TAGAG

25

<210> SEQ ID NO 1964
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1964

CAAGCCATGG AGTTGGGCTT AGAGG

25

<210> SEQ ID NO 1965
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1965

AAGCCATGGA GTTGGGCTTA GAGGC

25

<210> SEQ ID NO 1966
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

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AGCCATGGAG TTGGGCTTAG AGGCT

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<212> TYPE: DNA
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<400> SEQUENCE: 1967

oligosPatNat2.txt

GCCATGGAGT TGGGCTTAGA GGCTA

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<210> SEQ ID NO 1968
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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CCATGGAGTT GGGCTTAGAG GCTAT

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<210> SEQ ID NO 1969
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CATGGAGTTG GGCTTAGAGG CTATT

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<220> FEATURES:
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ATGGAGTTGG GCTTAGAGGC TATTT

25

<210> SEQ ID NO 1971
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TGGAGTTGGG CTTAGAGGCT ATTTT

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<210> SEQ ID NO 1972
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GGAGTTGGGC TTAGAGGCTA TTTT

25

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<400> SEQUENCE: 1973

GAGTTGGGCT TAGAGGCTAT TTTTG

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<210> SEQ ID NO 1974
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AGTTGGGCTT AGAGGCTATT TTTGA

25

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GTTGGGCTTA GAGGCTATTT TTGAT

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TTGGGCTTAG AGGCTATTTT TGATC

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<210> SEQ ID NO 1978

<211> LENGTH: 25

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CCCAACTCCA TGGCT

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<211> LENGTH: 15

<212> TYPE: DNA

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<210> SEQ ID NO 1983
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 <213> ORGANISM: Artificial Sequence
 <220> FEATURES:
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<210> SEQ ID NO 1984
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AAGCCCAACT CCATG

15

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TAAGCCCAAC TCCAT

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CTAAGCCCAA CTCCA

15

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<211> LENGTH: 15
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TCTAAGCCCA ACTCC

15

<210> SEQ ID NO 1988
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CTCTAAGCCC AACTC

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<210> SEQ ID NO 1989
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<220> FEATURES:
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CCTCTAAGCC CAACT

15

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<212> TYPE: DNA
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<220> FEATURES:
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GCCTCTAAGC CCAAC

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<210> SEQ ID NO 1991
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
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AGCCTCTAAG CCAA

15

OligosPatNat2.txt

<210> SEQ ID NO 1992
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<400> SEQUENCE: 1992

TAGCCTCTAA GCCCA

15

<210> SEQ ID NO 1993
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<212> TYPE: DNA
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<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1993

ATAGCCTCTA AGCCC

15

<210> SEQ ID NO 1994
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<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1994

AATAGCCTCT AAGCC

15

<210> SEQ ID NO 1995
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1995

AAATAGCCTC TAAGC

15

<210> SEQ ID NO 1996
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1996

CCCAACTCCA TGGCTT

16

oligosPatNat2.txt

<210> SEQ ID NO 1997
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<213> ORGANISM: Artificial Sequence
<220> FEATURES:
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<400> SEQUENCE: 1997

GCCCAACTCC ATGGCT

16

<210> SEQ ID NO 1998
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1998

AGCCCAACTC CATGGC

16

<210> SEQ ID NO 1999
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<212> TYPE: DNA
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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 1999

AAGCCCAACT CCATGG

16

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<212> TYPE: DNA
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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2000

TAAGCCCAAC TCCATG

16

<210> SEQ ID NO 2001
<211> LENGTH: 16
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2001

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CTAAGCCCAA CTCCAT

16

<210> SEQ ID NO 2002
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<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
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TCTAAGCCCA ACTCCA

16

<210> SEQ ID NO 2003
<211> LENGTH: 16
<212> TYPE: DNA
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<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
<400> SEQUENCE: 2003

CTCTAAGCCC AACTCC

16

<210> SEQ ID NO 2004
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
<400> SEQUENCE: 2004

CCTCTAAGCC CAACTC

16

<210> SEQ ID NO 2005
<211> LENGTH: 16
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
<400> SEQUENCE: 2005

GCCTCTAAGC CCAACT

16

<210> SEQ ID NO 2006
<211> LENGTH: 16
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2006

AGCCTCTAAG CCCAAC

16

<210> SEQ ID NO 2007
<211> LENGTH: 16
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2007

TAGCCTCTAA GCCCAA

16

<210> SEQ ID NO 2008
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2008

ATAGCCTCTA AGCCCA

16

<210> SEQ ID NO 2009
<211> LENGTH: 16
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2009

AATAGCCTCT AAGCCC

16

<210> SEQ ID NO 2010
<211> LENGTH: 16
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2010

AAATAGCCTC TAAGCC

16

<210> SEQ ID NO 2011
<211> LENGTH: 16
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:

<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2011

AAAATAGCCT CTAAGC

16

<210> SEQ ID NO 2012

<211> LENGTH: 17

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURES:

<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2012

CCCAACTCCA TGGCTTG

17

<210> SEQ ID NO 2013

<211> LENGTH: 17

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURES:

<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2013

GCCCAACTCC ATGGCTT

17

<210> SEQ ID NO 2014

<211> LENGTH: 17

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURES:

<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2014

AGCCCAACTC CATGGCT

17

<210> SEQ ID NO 2015

<211> LENGTH: 17

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURES:

<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2015

AAGCCCAACT CCATGGC

17

<210> SEQ ID NO 2016

<211> LENGTH: 17

<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
<400> SEQUENCE: 2016

TAAGCCCAAC TCCATGG 17

<210> SEQ ID NO 2017
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<212> TYPE: DNA
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<220> FEATURES:
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CTAAGCCCAA CTCCATG 17

<210> SEQ ID NO 2018
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<212> TYPE: DNA
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TCTAAGCCCA ACTCCAT 17

<210> SEQ ID NO 2019
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
<400> SEQUENCE: 2019

CTCTAAGCCC AACTCCA 17

<210> SEQ ID NO 2020
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
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CCTCTAAGCC CAACTCC 17

<210> SEQ ID NO 2021

oligosPatNat2.txt

<211> LENGTH: 17
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<220> FEATURES:
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GCCTCTAAGC CCAACTC

17

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
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AGCCTCTAAG CCCAACT

17

<210> SEQ ID NO 2023
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: cDNA for use as primers
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TAGCCTCTAA GCCCAAC

17

<210> SEQ ID NO 2024
<211> LENGTH: 17
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
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ATAGCCTCTA AGCCCAA

17

<210> SEQ ID NO 2025
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
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AATAGCCTCT AAGCCCA

17

oligosPatNat2.txt

<210> SEQ ID NO 2026
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2026

AAATAGCCTC TAAGCCC

17

<210> SEQ ID NO 2027
<211> LENGTH: 17
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2027

AAAATAGCCT CTAAGCC

17

<210> SEQ ID NO 2028
<211> LENGTH: 17
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2028

AAAAATAGCC TCTAAGC

17

<210> SEQ ID NO 2029
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2029

CCCAACTCCA TGGCTTGC

18

<210> SEQ ID NO 2030
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2030

GCCCAACTCC ATGGCTTG

18

OligosPatNat2.txt

<210> SEQ ID NO 2031
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2031

AGCCCAACTC CATGGCTT

18

<210> SEQ ID NO 2032
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2032

AAGCCCAACT CCATGGCT

18

<210> SEQ ID NO 2033
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2033

TAAGCCCAAC TCCATGGC

18

<210> SEQ ID NO 2034
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2034

CTAAGCCCAA CTCCATGG

18

<210> SEQ ID NO 2035
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2035

OligosPatNat2.txt

TCTAAGCCCA ACTCCATG

18

<210> SEQ ID NO 2036
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
<400> SEQUENCE: 2036

CTCTAAGCCC AACTCCAT

18

<210> SEQ ID NO 2037
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<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
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CCTCTAAGCC CAACTCCA

18

<210> SEQ ID NO 2038
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<212> TYPE: DNA
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<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
<400> SEQUENCE: 2038

GCCTCTAAGC CCAACTCC

18

<210> SEQ ID NO 2039
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<212> TYPE: DNA
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<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
<400> SEQUENCE: 2039

AGCCTCTAAG CCAACTC

18

<210> SEQ ID NO 2040
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2040

TAGCCTCTAA GCCCAACT

18

<210> SEQ ID NO 2041
<211> LENGTH: 18
<212> TYPE: DNA
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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2041

ATAGCCTCTA AGCCCAAC

18

<210> SEQ ID NO 2042
<211> LENGTH: 18
<212> TYPE: DNA
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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2042

AATAGCCTCT AAGCCCAA

18

<210> SEQ ID NO 2043
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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2043

AAATAGCCTC TAAGCCCA

18

<210> SEQ ID NO 2044
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2044

AAAATAGCCT CTAAGCCC

18

<210> SEQ ID NO 2045
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:

<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2045

AAAAATAGCC TCTAAGCC

18

<210> SEQ ID NO 2046

<211> LENGTH: 18

<212> TYPE: DNA

<213> ORGANISM: Artificial sequence

<220> FEATURES:

<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2046

CAAAAATAGC CTCTAAGC

18

<210> SEQ ID NO 2047

<211> LENGTH: 19

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURES:

<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2047

CCCAACTCCA TGGCTTGCC

19

<210> SEQ ID NO 2048

<211> LENGTH: 19

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURES:

<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2048

GCCCAACTCC ATGGCTTGC

19

<210> SEQ ID NO 2049

<211> LENGTH: 19

<212> TYPE: DNA

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<223> OTHER INFORMATION: cDNA for use as primers

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AGCCCAACTC CATGGCTTG

19

<210> SEQ ID NO 2050

<211> LENGTH: 19

<212> TYPE: DNA

OligosPatNat2.txt

<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
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AAGCCCAACT CCATGGCTT

19

<210> SEQ ID NO 2051
<211> LENGTH: 19
<212> TYPE: DNA
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<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
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TAAGCCCAAC TCCATGGCT

19

<210> SEQ ID NO 2052
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<223> OTHER INFORMATION: cDNA for use as primers
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CTAAGCCCAA CTCCATGGC

19

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
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TCTAAGCCCA ACTCCATGG

19

<210> SEQ ID NO 2054
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: cDNA for use as primers
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CTCTAAGCCC AACTCCATG

19

<210> SEQ ID NO 2055

OligosPatNat2.txt

<211> LENGTH: 19
<212> TYPE: DNA
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<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2055

CCTCTAAGCC CAACTCCAT

19

<210> SEQ ID NO 2056
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2056

GCCTCTAAGC CCAACTCCA

19

<210> SEQ ID NO 2057
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2057

AGCCTCTAAG CCAACTCC

19

<210> SEQ ID NO 2058
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2058

TAGCCTCTAA GCCCAACTC

19

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<400> SEQUENCE: 2059

ATAGCCTCTA AGCCCAACT

19

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<212> TYPE: DNA
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<400> SEQUENCE: 2060

AATAGCCTCT AAGCCCAAC

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AAATAGCCTC TAAGCCCAA

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AAAATAGCCT CTAAGCCCA

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AAAAATAGCC TCTAAGCCC

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<400> SEQUENCE: 2064

CAAAAATAGC CTCTAAGCC

19

OligosPatNat2.txt

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<400> SEQUENCE: 2065

TCAAAAATAG CCTCTAAGC

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<210> SEQ ID NO 2066
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<212> TYPE: DNA
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<400> SEQUENCE: 2066

CCCAACTCCA TGGCTTGCCC

20

<210> SEQ ID NO 2067
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GCCCAACTCC ATGGCTTGCC

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<210> SEQ ID NO 2068
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AGCCCAACTC CATGGCTTGC

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<210> SEQ ID NO 2069
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AAGCCCAACT CCATGGCTTG

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TAAGCCCAAC TCCATGGCTT

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CTAAGCCCAA CTCCATGGCT

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TCTAAGCCCA ACTCCATGGC

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CTCTAAGCCC AACTCCATGG

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CCTCTAAGCC CAACTCCATG

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<210> SEQ ID NO 2075
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GCCTCTAAGC CCAACTCCAT

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<211> LENGTH: 20
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AGCCTCTAAG CCAACTCCA

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<210> SEQ ID NO 2077
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TAGCCTCTAA GCCCAACTCC

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<210> SEQ ID NO 2078
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AATAGCCTCT AAGCCCAACT

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AAATAGCCTC TAAGCCCAAC

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AAAATAGCCT CTAAGCCCAA

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<210> SEQ ID NO 2084

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TCAAAAATAG CCTCTAAGCC

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ATCAAAAATA GCCTCTAAGC

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CCCAACTCCA TGGCTTGCCC A

21

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GCCCAACTCC ATGGCTTGCC C

21

<210> SEQ ID NO 2088
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AGCCCAACTC CATGGCTTGC C

21

<210> SEQ ID NO 2089

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<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 2089

AAGCCCAACT CCATGGCTTG C

21

<210> SEQ ID NO 2090
<211> LENGTH: 21
<212> TYPE: DNA
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<400> SEQUENCE: 2090

TAAGCCCAAC TCCATGGCTT G

21

<210> SEQ ID NO 2091
<211> LENGTH: 21
<212> TYPE: DNA
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CTAAGCCCAA CTCCATGGCT T

21

<210> SEQ ID NO 2092
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<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

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TCTAAGCCCA ACTCCATGGC T

21

<210> SEQ ID NO 2093
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
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<400> SEQUENCE: 2093

CTCTAAGCCC AACTCCATGG C

21

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<210> SEQ ID NO 2094
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<212> TYPE: DNA
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CCTCTAAGCC CAACTCCATG G 21

<210> SEQ ID NO 2095
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GCCTCTAAGC CCAACTCCAT G 21

<210> SEQ ID NO 2096
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AGCCTCTAAG CCCAACTCCA T 21

<210> SEQ ID NO 2097
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 2097

TAGCCTCTAA GCCCAACTCC A 21

<210> SEQ ID NO 2098
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<212> TYPE: DNA
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ATAGCCTCTA AGCCCAACTC C 21

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AATAGCCTCT AAGCCCAACT C

21

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21

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AAAATAGCCT CTAAGCCCAA C

21

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<400> SEQUENCE: 2102

AAAAATAGCC TCTAAGCCCA A

21

<210> SEQ ID NO 2103
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<400> SEQUENCE: 2103

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CAAAAATAGC CTCTAAGCCC A

21

<210> SEQ ID NO 2104
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TCAAAAATAG CCTCTAAGCC C

21

<210> SEQ ID NO 2105
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ATCAAAAATA GCCTCTAAGC C

21

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GATCAAAAAT AGCCTCTAAG C

21

<210> SEQ ID NO 2107
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<212> TYPE: DNA
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<400> SEQUENCE: 2107

CCCAACTCCA TGGCTTGCCC AC

22

<210> SEQ ID NO 2108
<211> LENGTH: 22
<212> TYPE: DNA
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<400> SEQUENCE: 2108

GCCCAACTCC ATGGCTTGCC CA

22

<210> SEQ ID NO 2109
<211> LENGTH: 22
<212> TYPE: DNA
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<400> SEQUENCE: 2109

AGCCCAACTC CATGGCTTGC CC

22

<210> SEQ ID NO 2110
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<400> SEQUENCE: 2110

AAGCCCAACT CCATGGCTTG CC

22

<210> SEQ ID NO 2111
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<212> TYPE: DNA
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TAAGCCCAAC TCCATGGCTT GC

22

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<400> SEQUENCE: 2112

CTAAGCCCAA CTCCATGGCT TG

22

<210> SEQ ID NO 2113
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<223> OTHER INFORMATION: cDNA for use as primers
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TCTAAGCCCA ACTCCATGGC TT 22

<210> SEQ ID NO 2114
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CTCTAAGCCC AACTCCATGG CT 22

<210> SEQ ID NO 2115
<211> LENGTH: 22
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<223> OTHER INFORMATION: cDNA for use as primers
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CCTCTAAGCC CAACTCCATG GC 22

<210> SEQ ID NO 2116
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<212> TYPE: DNA
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GCCTCTAAGC CCAACTCCAT GG 22

<210> SEQ ID NO 2117
<211> LENGTH: 22
<212> TYPE: DNA
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AGCCTCTAAG CCCAACTCCA TG 22

<210> SEQ ID NO 2118
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<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: cDNA for use as primers
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TAGCCTCTAA GCCCAACTCC AT

22

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<211> LENGTH: 22
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<223> OTHER INFORMATION: cDNA for use as primers
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ATAGCCTCTA AGCCCAACTC CA

22

<210> SEQ ID NO 2120
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AATAGCCTCT AAGCCCAACT CC

22

<210> SEQ ID NO 2121
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AAATAGCCTC TAAGCCCAAC TC

22

<210> SEQ ID NO 2122
<211> LENGTH: 22
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AAAATAGCCT CTAAGCCCAA CT

22

<210> SEQ ID NO 2123

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<211> LENGTH: 22
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AAAAATAGCC TCTAAGCCCA AC

22

<210> SEQ ID NO 2124
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CAAAAATAGC CTCTAAGCCC AA

22

<210> SEQ ID NO 2125
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TCAAAAATAG CCTCTAAGCC CA

22

<210> SEQ ID NO 2126
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ATCAAAAATA GCCTCTAAGC CC

22

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<223> OTHER INFORMATION: cDNA for use as primers
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GATCAAAAAT AGCCTCTAAG CC

22

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<210> SEQ ID NO 2128
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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2128

TGATCAAAAA TAGCCTCTAA GC

22

<210> SEQ ID NO 2129
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<400> SEQUENCE: 2129

CCCAACTCCA TGGCTTGCCC ACA

23

<210> SEQ ID NO 2130
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2130

GCCCAACTCC ATGGCTTGCC CAC

23

<210> SEQ ID NO 2131
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2131

AGCCCAACTC CATGGCTTGC CCA

23

<210> SEQ ID NO 2132
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<212> TYPE: DNA
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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2132

AAGCCCAACT CCATGGCTTG CCC

23

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<210> SEQ ID NO 2133
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: cDNA for use as primers
<400> SEQUENCE: 2133

TAAGCCCAAC TCCATGGCTT GCC

23

<210> SEQ ID NO 2134
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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CTAAGCCCAA CTCCATGGCT TGC

23

<210> SEQ ID NO 2135
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<223> OTHER INFORMATION: cDNA for use as primers
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TCTAAGCCCA ACTCCATGGC TTG

23

<210> SEQ ID NO 2136
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CTCTAAGCCC AACTCCATGG CTT

23

<210> SEQ ID NO 2137
<211> LENGTH: 23
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<223> OTHER INFORMATION: cDNA for use as primers
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CCTCTAAGCC CAACTCCATG GCT

23

<210> SEQ ID NO 2138
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GCCTCTAAGC CCAACTCCAT GGC

23

<210> SEQ ID NO 2139
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AGCCTCTAAG CCCAACTCCA TGG

23

<210> SEQ ID NO 2140
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TAGCCTCTAA GCCCAACTCC ATG

23

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ATAGCCTCTA AGCCCAACTC CAT

23

<210> SEQ ID NO 2142
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<400> SEQUENCE: 2142

AATAGCCTCT AAGCCCAACT CCA

23

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AAATAGCCTC TAAGCCCAAC TCC

23

<210> SEQ ID NO 2144
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<400> SEQUENCE: 2144

AAAATAGCCT CTAAGCCCAA CTC

23

<210> SEQ ID NO 2145
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<400> SEQUENCE: 2145

AAAAATAGCC TCTAAGCCCA ACT

23

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<400> SEQUENCE: 2146

CAAAAATAGC CTCTAAGCCC AAC

23

<210> SEQ ID NO 2147
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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2147

TCAAAAATAG CCTCTAAGCC CAA

23

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ATCAAAAATA GCCTCTAAGC CCA

23

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GATCAAAAAT AGCCTCTAAG CCC

23

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23

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GTGATCAAAA ATAGCCTCTA AGC

23

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CCCAACTCCA TGGCTTGCCC ACAA

24

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GCCCAACTCC ATGGCTTGCC CACA

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AGCCCAACTC CATGGCTTGC CCAC

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AAGCCCAACT CCATGGCTTG CCCA

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CTAAGCCCAA CTCCATGGCT TGCC

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TCTAAGCCCA ACTCCATGGC TTGC

24

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CTCTAAGCCC AACTCCATGG CTTG

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CCTCTAAGCC CAACTCCATG GCTT

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GCCTTAAGC CCAACTCCAT GGCT

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AGCCTCTAAG CCCAACTCCA TGGC

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TAGCCTCTAA GCCCAACTCC ATGG

24

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ATAGCCTCTA AGCCCAACTC CATG

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AATAGCCTCT AAGCCCAACT CCAT

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AAAATAGCCT CTAAGCCCAA CTCC

24

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AAAAATAGCC TCTAAGCCCA ACTC

24

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24

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TCAAAAATAG CCTCTAAGCC CAAC

24

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ATCAAAAATA GCCTCTAAGC CCAA

24

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GATCAAAAAT AGCCTCTAAG CCCA

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TGATCAAAAA TAGCCTCTAA GCCC

24

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GTGATCAAAA ATAGCCTCTA AGCC

24

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TGTGATCAAA AATAGCCTCT AAGC

24

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CCCAACTCCA TGGCTTGCCC ACAAT

25

<210> SEQ ID NO 2177
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GCCCAACTCC ATGGCTTGCC CACAA

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AGCCCAACTC CATGGCTTGC CCACA

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AAGCCCAACT CCATGGCTTG CCCAC

25

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TAAGCCCAAC TCCATGGCTT GCCCA

25

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CTAAGCCCAA CTCCATGGCT TGCCC

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<210> SEQ ID NO 2182

<211> LENGTH: 25

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TCTAAGCCCA ACTCCATGGC TTGCC

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CTCTAAGCCC AACTCCATGG CTTGC

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CCTCTAAGCC CAACTCCATG GCTTG

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GCCTCTAAGC CCAACTCCAT GGCTT

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AGCCTCTAAG CCCAACTCCA TGGCT

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TAGCCTCTAA GCCCAACTCC ATGGC

25

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ATAGCCTCTA AGCCCAACTC CATGG

25

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AATAGCCTCT AAGCCCAACT CCATG

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AAATAGCCTC TAAGCCCAAC TCCAT

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<210> SEQ ID NO 2191

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AAAATAGCCT CTAAGCCCAA CTCCA

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AAAAATAGCC TCTAAGCCCA ACTCC

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CAAAAATAGC CTCTAAGCCC AACTC

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TCAAAAATAG CCTCTAAGCC CAACT

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ATCAAAAATA GCCTCTAAGC CCAAC

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<400> SEQUENCE: 2196

GATCAAAAAT AGCCTCTAAG CCCAA

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TGATCAAAAA TAGCCTCTAA GCCCA

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TGTGATCAAA AATAGCCTCT AAGCC

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25

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CATTTTCTGC TTGAC

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<213> ORGANISM: Artificial Sequence
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ATTTTCTGCT TGACA

15

<210> SEQ ID NO 2203
<211> LENGTH: 15
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TTTTCTGCTT GACAG

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TTTCTGCTTG ACAGA

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TTCTGCTTGA CAGAA

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TCTGCTTGAC AGAAG

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CTGCTTGACA GAAGA

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TGCTTGACAG AAGAG

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<220> FEATURES:
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GCTTGACAGA AGAGA

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15

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15

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TGACAGAAGA GAGAG

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<210> SEQ ID NO 2213
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GACAGAAGAG AGAGG

15

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ACAGAAGAGA GAGGA

15

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GCATTTTCTG CTTGAC

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CATTTTCTGC TTGACA

16

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ATTTTCTGCT TGACAG

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16

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<211> LENGTH: 16

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TTTCTGCTTG ACAGAA

16

<210> SEQ ID NO 2221
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TTCTGCTTGA CAGAAG

16

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TCTGCTTGAC AGAAGA

16

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<223> OTHER INFORMATION: cDNA for use as primers
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CTGCTTGACA GAAGAG

16

<210> SEQ ID NO 2224
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TGCTTGACAG AAGAGA

16

<210> SEQ ID NO 2225

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GCTTGACAGA AGAGAG

16

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CTTGACAGAA GAGAGA

16

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TTGACAGAAG AGAGAG

16

<210> SEQ ID NO 2228
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TGACAGAAGA GAGAGG

16

<210> SEQ ID NO 2229
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GACAGAAGAG AGAGGA

16

OligosPatNat2.txt

<210> SEQ ID NO 2230
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<400> SEQUENCE: 2230

ACAGAAGAGA GAGGAA

16

<210> SEQ ID NO 2231
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<220> FEATURES:
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<400> SEQUENCE: 2231

CAGAAGAGAG AGGAAT

16

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TGCATTTTCT GCTTGAC

17

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GCATTTTCTG CTTGACA

17

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CATTTTCTGC TTGACAG

17

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ATTTTCTGCT TGACAGA

17

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<400> SEQUENCE: 2236

TTTTCTGCTT GACAGAA

17

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TTTCTGCTTG ACAGAAG

17

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TTCTGCTTGA CAGAAGA

17

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TCTGCTTGAC AGAAGAG

17

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CTGCTTGACA GAAGAGA

17

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TGCTTGACAG AAGAGAG

17

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GCTTGACAGA AGAGAGA

17

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CTTGACAGAA GAGAGAG

17

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TTGACAGAAG AGAGAGG

17

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TGACAGAAGA GAGAGGA

17

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GACAGAAGAG AGAGGAA

17

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ACAGAAGAGA GAGGAAT

17

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CAGAAGAGAG AGGAATC

17

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TTGCATTTTC TGCTTGAC

18

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CATTTTCTGC TTGACAGA

18

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TTTTCTGCTT GACAGAAG 18

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TTTCTGCTTG ACAGAAGA 18

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TTCTGCTTGA CAGAAGAG 18

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TCTGCTTGAC AGAAGAGA 18

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TGCTTGACAG AAGAGAGA

18

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GCTTGACAGA AGAGAGAG

18

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CTTGACAGAA GAGAGAGG

18

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TTGACAGAAG AGAGAGGA

18

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TGACAGAAGA GAGAGGAA

18

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GACAGAAGAG AGAGGAAT

18

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ACAGAAGAGA GAGGAATC

18

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CAGAAGAGAG AGGAATCT

18

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CTTGCAATTT CTGCTTGAC

19

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TTGCATTTTC TGCTTGACA

19

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TGCATTTTCT GCTTGACAG

19

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GCATTTTCTG CTTGACAGA

19

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CATTTTCTGC TTGACAGAA

19

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ATTTTCTGCT TGACAGAAG

19

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TTTTCTGCTT GACAGAAGA

19

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TTTCTGCTTG ACAGAAGAG

19

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TTCTGCTTGA CAGAAGAGA

19

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TCTGCTTGAC AGAAGAGAG

19

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CTGCTTGACA GAAGAGAGA

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TGCTTGACAG AAGAGAGAG

19

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GCTTGACAGA AGAGAGAGG

19

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CTTGACAGAA GAGAGAGGA

19

<210> SEQ ID NO 2281
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<400> SEQUENCE: 2281

TTGACAGAAG AGAGAGGAA

19

<210> SEQ ID NO 2282
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<400> SEQUENCE: 2282

TGACAGAAGA GAGAGGAAT

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<210> SEQ ID NO 2283
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<400> SEQUENCE: 2283

GACAGAAGAG AGAGGAATC

19

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<211> LENGTH: 19

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ACAGAAGAGA GAGGAATCT

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CAGAAGAGAG AGGAATCTG

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CTTGCAATTTT CTGCTTGACA

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TTGCATTTTC TGCTTGACAG

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TGCATTTTCT GCTTGACAGA

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GCATTTTCTG CTTGACAGAA

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CATTTTCTGC TTGACAGAAG

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ATTTTCTGCT TGACAGAAGA

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<400> SEQUENCE: 2293

TTTTCTGCTT GACAGAAGAG

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<210> SEQ ID NO 2294
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TTTCTGCTTG ACAGAAGAGA

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TTCTGCTTGA CAGAAGAGAG

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TCTGCTTGAC AGAAGAGAGA

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<400> SEQUENCE: 2297

CTGCTTGACA GAAGAGAGAG

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TGCTTGACAG AAGAGAGAGG 20

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GCTTGACAGA AGAGAGAGGA 20

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CTTGACAGAA GAGAGAGGAA 20

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<400> SEQUENCE: 2301

TTGACAGAAG AGAGAGGAAT 20

<210> SEQ ID NO 2302
<211> LENGTH: 20
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<400> SEQUENCE: 2302

TGACAGAAGA GAGAGGAATC 20

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GACAGAAGAG AGAGGAATCT

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<210> SEQ ID NO 2304
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ACAGAAGAGA GAGGAATCTG

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<210> SEQ ID NO 2305
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CAGAAGAGAG AGGAATCTGG

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GCCTTGCATT TTCTGCTTGA C

21

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<400> SEQUENCE: 2307

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CCTTGCAATTT TCTGCTTGAC A 21

<210> SEQ ID NO 2308
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CTTGCAATTT CTGCTTGACA G 21

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TTGCAATTTTC TGCTTGACAG A 21

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TGCAATTTTCT GCTTGACAGA A 21

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CATTTTCTGC TTGACAGAAG A

21

<210> SEQ ID NO 2313
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ATTTTCTGCT TGACAGAAGA G

21

<210> SEQ ID NO 2314
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TTTTCTGCTT GACAGAAGAG A

21

<210> SEQ ID NO 2315
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TTTCTGCTTG ACAGAAGAGA G

21

<210> SEQ ID NO 2316
 <211> LENGTH: 21
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TTCTGCTTGA CAGAAGAGAG A

21

<210> SEQ ID NO 2317
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 <213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2317

TCTGCTTGAC AGAAGAGAGA G

21

<210> SEQ ID NO 2318

<211> LENGTH: 21

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CTGCTTGACA GAAGAGAGAG G

21

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TGCTTGACAG AAGAGAGAGG A

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GCTTGACAGA AGAGAGAGGA A

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21

<210> SEQ ID NO 2322

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<213> ORGANISM: Artificial Sequence
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TTGACAGAAG AGAGAGGAAT C

21

<210> SEQ ID NO 2323
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TGACAGAAGA GAGAGGAATC T

21

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GACAGAAGAG AGAGGAATCT G

21

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ACAGAAGAGA GAGGAATCTG G

21

<210> SEQ ID NO 2326
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CAGAAGAGAG AGGAATCTGG T

21

<210> SEQ ID NO 2327

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TGCCTTGCAT TTTCTGCTTG AC

22

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GCCTTGCATT TTCTGCTTGA CA

22

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CCTTGCATTT TCTGCTTGAC AG

22

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CTTGCATTTT CTGCTTGACA GA

22

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TTGCATTTTC TGCTTGACAG AA

22

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TGCATTTTCT GCTTGACAGA AG

22

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GCATTTTCTG CTTGACAGAA GA

22

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CATTTTCTGC TTGACAGAAG AG

22

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ATTTTCTGCT TGACAGAAGA GA

22

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TTTTCTGCTT GACAGAAGAG AG

22

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TTTCTGCTTG ACAGAAGAGA GA

22

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TTCTGCTTGA CAGAAGAGAG AG

22

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TCTGCTTGAC AGAAGAGAGA GG

22

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CTGCTTGACA GAAGAGAGAG GA

22

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TGCTTGACAG AAGAGAGAGG AA

22

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GCTTGACAGA AGAGAGAGGA AT

22

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CTTGACAGAA GAGAGAGGAA TC

22

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TTGACAGAAG AGAGAGGAAT CT

22

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TGACAGAAGA GAGAGGAATC TG

22

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GACAGAAGAG AGAGGAATCT GG

22

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ACAGAAGAGA GAGGAATCTG GT

22

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CAGAAGAGAG AGGAATCTGG TA

22

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GTGCCTTGCA TTTTCTGCTT GAC

23

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TGCCTTGCAT TTTCTGCTTG ACA

23

<210> SEQ ID NO 2351
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GCCTTGCA TTCTGCTTGA CAG

23

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<220> FEATURES:

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<400> SEQUENCE: 2352

CCTTGCA TTT TCTGCTT GAC AGA

23

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<220> FEATURES:

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<400> SEQUENCE: 2353

CTTGCA TTTT CTGCTT GACA GAA

23

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<400> SEQUENCE: 2354

TTGCAT TTTT TGCTT GACAG AAG

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TGCAT TTTTCT GCTT GACAGA AGA

23

<210> SEQ ID NO 2356

<211> LENGTH: 23

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence
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GCATTTTCTG CTTGACAGAA GAG 23

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CATTTTCTGC TTGACAGAAG AGA 23

<210> SEQ ID NO 2358
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ATTTTCTGCT TGACAGAAGA GAG 23

<210> SEQ ID NO 2359
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TTTTCTGCTT GACAGAAGAG AGA 23

<210> SEQ ID NO 2360
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TTTCTGCTTG ACAGAAGAGA GAG 23

<210> SEQ ID NO 2361

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<211> LENGTH: 23
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TTCTGCTTGA CAGAAGAGAG AGG

23

<210> SEQ ID NO 2362
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TCTGCTTGAC AGAAGAGAGA GGA

23

<210> SEQ ID NO 2363
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CTGCTTGACA GAAGAGAGAG GAA

23

<210> SEQ ID NO 2364
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<400> SEQUENCE: 2364

TGCTTGACAG AAGAGAGAGG AAT

23

<210> SEQ ID NO 2365
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<400> SEQUENCE: 2365

GCTTGACAGA AGAGAGAGGA ATC

23

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<210> SEQ ID NO 2366
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<400> SEQUENCE: 2366

CTTGACAGAA GAGAGAGGAA TCT 23

<210> SEQ ID NO 2367
<211> LENGTH: 23
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<400> SEQUENCE: 2367

TTGACAGAAG AGAGAGGAAT CTG 23

<210> SEQ ID NO 2368
<211> LENGTH: 23
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<400> SEQUENCE: 2368

TGACAGAAGA GAGAGGAATC TGG 23

<210> SEQ ID NO 2369
<211> LENGTH: 23
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<400> SEQUENCE: 2369

GACAGAAGAG AGAGGAATCT GGT 23

<210> SEQ ID NO 2370
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<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2370

ACAGAAGAGA GAGGAATCTG GTA 23

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<210> SEQ ID NO 2371
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<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2371

CAGAAGAGAG AGGAATCTGG TAC

23

<210> SEQ ID NO 2372
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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 2372

GGTGCCTTGC ATTTTCTGCT TGAC

24

<210> SEQ ID NO 2373
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
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<400> SEQUENCE: 2373

GTGCCTTGCA TTTTCTGCTT GACA

24

<210> SEQ ID NO 2374
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2374

TGCCTTGCAT TTTCTGCTTG ACAG

24

<210> SEQ ID NO 2375
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<400> SEQUENCE: 2375

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GCCTTGCAATT TTCTGCTTGA CAGA

24

<210> SEQ ID NO 2376
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 <400> SEQUENCE: 2376

CCTTGCAATTT TCTGCTTGAC AGAA

24

<210> SEQ ID NO 2377
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CTTGCAATTTT CTGCTTGACA GAAG

24

<210> SEQ ID NO 2378
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TTGCATTTTC TGCTTGACAG AAGA

24

<210> SEQ ID NO 2379
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TGCATTTTCT GCTTGACAGA AGAG

24

<210> SEQ ID NO 2380
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 <213> ORGANISM: Artificial Sequence
 <220> FEATURES:
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<400> SEQUENCE: 2380

GCATTTTCTG CTTGACAGAA GAGA

24

<210> SEQ ID NO 2381
<211> LENGTH: 24
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<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2381

CATTTTCTGC TTGACAGAAG AGAG

24

<210> SEQ ID NO 2382
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2382

ATTTTCTGCT TGACAGAAGA GAGA

24

<210> SEQ ID NO 2383
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2383

TTTTCTGCTT GACAGAAGAG AGAG

24

<210> SEQ ID NO 2384
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2384

TTTCTGCTTG ACAGAAGAGA GAGG

24

<210> SEQ ID NO 2385
<211> LENGTH: 24
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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2385

TTCTGCTTGA CAGAAGAGAG AGGA

24

<210> SEQ ID NO 2386

<211> LENGTH: 24

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<400> SEQUENCE: 2386

TCTGCTTGAC AGAAGAGAGA GGAA

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<213> ORGANISM: Artificial Sequence

<220> FEATURES:

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CTGCTTGACA GAAGAGAGAG GAAT

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TGCTTGACAG AAGAGAGAGG AATC

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<211> LENGTH: 24

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

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<400> SEQUENCE: 2389

GCTTGACAGA AGAGAGAGGA ATCT

24

<210> SEQ ID NO 2390

<211> LENGTH: 24

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: cDNA for use as primers
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CTTGACAGAA GAGAGAGGAA TCTG

24

<210> SEQ ID NO 2391
<211> LENGTH: 24
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<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
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TTGACAGAAG AGAGAGGAAT CTGG

24

<210> SEQ ID NO 2392
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
<400> SEQUENCE: 2392

TGACAGAAGA GAGAGGAATC TGGT

24

<210> SEQ ID NO 2393
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
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<400> SEQUENCE: 2393

GACAGAAGAG AGAGGAATCT GGTA

24

<210> SEQ ID NO 2394
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: cDNA for use as primers
<400> SEQUENCE: 2394

ACAGAAGAGA GAGGAATCTG GTAC

24

<210> SEQ ID NO 2395

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<211> LENGTH: 24
<212> TYPE: DNA
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<400> SEQUENCE: 2395

CAGAAGAGAG AGGAATCTGG TACC

24

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<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
<400> SEQUENCE: 2396

AGGTGCCTTG CATTTTCTGC TTGAC

25

<210> SEQ ID NO 2397
<211> LENGTH: 25
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<400> SEQUENCE: 2397

GGTGCCTTGC ATTTTCTGCT TGACA

25

<210> SEQ ID NO 2398
<211> LENGTH: 25
<212> TYPE: DNA
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<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
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GTGCCTTGCA TTTTCTGCTT GACAG

25

<210> SEQ ID NO 2399
<211> LENGTH: 25
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<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
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TGCCTTGCAT TTTCTGCTTG ACAGA

25

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<210> SEQ ID NO 2400
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
<400> SEQUENCE: 2400

GCCTTGCAAT TTCTGCTTGA CAGAA

25

<210> SEQ ID NO 2401
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
<400> SEQUENCE: 2401

CCTTGCAATTT TCTGCTTGAC AGAAG

25

<210> SEQ ID NO 2402
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
<400> SEQUENCE: 2402

CTTGCAATTTT CTGCTTGACA GAAGA

25

<210> SEQ ID NO 2403
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
<400> SEQUENCE: 2403

TTGCATTTTC TGCTTGACAG AAGAG

25

<210> SEQ ID NO 2404
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
<400> SEQUENCE: 2404

TGCATTTTCT GCTTGACAGA AGAGA

25

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<210> SEQ ID NO 2405
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2405

GCATTTTCTG CTTGACAGAA GAGAG

25

<210> SEQ ID NO 2406
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2406

CATTTTCTGC TTGACAGAAG AGAGA

25

<210> SEQ ID NO 2407
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2407

ATTTTCTGCT TGACAGAAGA GAGAG

25

<210> SEQ ID NO 2408
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2408

TTTTCTGCTT GACAGAAGAG AGAGG

25

<210> SEQ ID NO 2409
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
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<400> SEQUENCE: 2409

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TTTCTGCTTG ACAGAAGAGA GAGGA

25

<210> SEQ ID NO 2410
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<223> OTHER INFORMATION: cDNA for use as primers
<400> SEQUENCE: 2410

TTCTGCTTGA CAGAAGAGAG AGGAA

25

<210> SEQ ID NO 2411
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<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
<400> SEQUENCE: 2411

TCTGCTTGAC AGAAGAGAGA GGAAT

25

<210> SEQ ID NO 2412
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<212> TYPE: DNA
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<223> OTHER INFORMATION: cDNA for use as primers
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CTGCTTGACA GAAGAGAGAG GAATC

25

<210> SEQ ID NO 2413
<211> LENGTH: 25
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<213> ORGANISM: Artificial sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
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TGCTTGACAG AAGAGAGAGG AATCT

25

<210> SEQ ID NO 2414
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2414

GCTTGACAGA AGAGAGAGGA ATCTG

25

<210> SEQ ID NO 2415
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OligosPatNat2.txt

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GTCAAGCAGA AAATGC 16

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TGTCAAGCAG AAAATG 16

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TCTGTCAAGC AGAAAA

16

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TTCTGTCAAG CAGAAA

16

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<212> TYPE: DNA
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CTTCTGTCAA GCAGAA

16

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<212> TYPE: DNA
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TCTTCTGTCA AGCAGA

16

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CTCTTCTGTC AAGCAG

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TCTCTTCTGT CAAGCA

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<210> SEQ ID NO 2445
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CTCTCTTCTG TCAAGC

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TCTCTCTTCT GTCAAG

16

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CTCTCTCTTC TGTCAA

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CCTCTCTCTT CTGTCA

16

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TCCTCTCTCT TCTGTC

16

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TTCTCTCTC TTCTGT

16

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ATTCCTCTCT CTTCTG

16

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GTCAAGCAGA AAATGCA

17

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<400> SEQUENCE: 2453

TGTC AAGCAG AAAATGC

17

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<211> LENGTH: 17

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<400> SEQUENCE: 2457

CTTCTGTCAA GCAGAAA

17

<210> SEQ ID NO 2458

<211> LENGTH: 17

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence
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TCTTCTGTCA AGCAGAA 17

<210> SEQ ID NO 2459
 <211> LENGTH: 17
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CTCTTCTGTC AAGCAGA 17

<210> SEQ ID NO 2460
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TCTCTTCTGT CAAGCAG 17

<210> SEQ ID NO 2461
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CTCTCTTCTG TCAAGCA 17

<210> SEQ ID NO 2462
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TCTCTCTTCT GTCAAGC 17

<210> SEQ ID NO 2463

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CTCTCTCTTC TGTC AAG

17

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CCTCTCTCTT CTGTCAA

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17

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<400> SEQUENCE: 2466

TTCCTCTCTC TTCTGTC

17

<210> SEQ ID NO 2467
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<400> SEQUENCE: 2467

ATTCCTCTCT CTTCTGT

17

OligosPatNat2.txt

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<400> SEQUENCE: 2468

GATTCCTCTC TCTTCTG

17

<210> SEQ ID NO 2469
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18

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TGTCAAGCAG AAAATGCA

18

<210> SEQ ID NO 2471
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<400> SEQUENCE: 2471

CTGTCAAGCA GAAAATGC

18

<210> SEQ ID NO 2472
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TCTGTCAAGC AGAAAATG

18

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<400> SEQUENCE: 2473

TTCTGTCAAG CAGAAAAT

18

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<400> SEQUENCE: 2474

CTTCTGTCAA GCAGAAAA

18

<210> SEQ ID NO 2475
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<400> SEQUENCE: 2475

TCTTCTGTCA AGCAGAAA

18

<210> SEQ ID NO 2476
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<212> TYPE: DNA
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<400> SEQUENCE: 2476

CTCTTCTGTC AAGCAGAA

18

<210> SEQ ID NO 2477
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<400> SEQUENCE: 2477

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TCTCTTCTGT CAAGCAGA

18

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<400> SEQUENCE: 2478

CTCTCTTCTG TCAAGCAG

18

<210> SEQ ID NO 2479
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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TCTCTTTCT GTCAAGCA

18

<210> SEQ ID NO 2480
<211> LENGTH: 18
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<223> OTHER INFORMATION: cDNA for use as primers
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CTCTCTTTC TGCAAGC

18

<210> SEQ ID NO 2481
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CCTCTCTTT CTGTCAAG

18

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TCCTCTCTCT TCTGTCAA

18

<210> SEQ ID NO 2483
<211> LENGTH: 18
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<400> SEQUENCE: 2483

TTCCTCTCTC TTCTGTCA

18

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<212> TYPE: DNA
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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2484

ATTCCTCTCT CTTCTGTC

18

<210> SEQ ID NO 2485
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<212> TYPE: DNA
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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2485

GATTCCTCTC TCTTCTGT

18

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<212> TYPE: DNA
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<400> SEQUENCE: 2486

AGATTCCTCT CTCTTCTG

18

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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2487

GTCAAGCAGA AAATGCAAG

19

<210> SEQ ID NO 2488

<211> LENGTH: 19

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TGTCAAGCAG AAAATGCAA

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CTGTCAAGCA GAAAATGCA

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TTCTGTCAAG CAGAAAATG

19

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<211> LENGTH: 19

<212> TYPE: DNA

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CTTCTGTCAA GCAGAAAAT

19

<210> SEQ ID NO 2493
<211> LENGTH: 19
<212> TYPE: DNA
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<223> OTHER INFORMATION: cDNA for use as primers
<400> SEQUENCE: 2493

TCTTCTGTCA AGCAGAAAA

19

<210> SEQ ID NO 2494
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<212> TYPE: DNA
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<223> OTHER INFORMATION: cDNA for use as primers
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CTCTTCTGTC AAGCAGAAA

19

<210> SEQ ID NO 2495
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TCTCTTCTGT CAAGCAGAA

19

<210> SEQ ID NO 2496
<211> LENGTH: 19
<212> TYPE: DNA
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CTCTCTTCTG TCAAGCAGA

19

<210> SEQ ID NO 2497

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<211> LENGTH: 19
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<400> SEQUENCE: 2497

TCTCTCTTCT GTCAAGCAG 19

<210> SEQ ID NO 2498
<211> LENGTH: 19
<212> TYPE: DNA
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CTCTCTCTTC TGTCAGCA 19

<210> SEQ ID NO 2499
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CCTCTCTCTT CTGTCAAGC 19

<210> SEQ ID NO 2500
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<210> SEQ ID NO 2501
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<212> TYPE: DNA
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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2502

ATTCCTCTCT CTTCTGTCA 19

<210> SEQ ID NO 2503
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<212> TYPE: DNA
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<400> SEQUENCE: 2503

GATTCCTCTC TCTTCTGTC 19

<210> SEQ ID NO 2504
<211> LENGTH: 19
<212> TYPE: DNA
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<400> SEQUENCE: 2504

AGATTCCTCT CTCTTCTGT 19

<210> SEQ ID NO 2505
<211> LENGTH: 19
<212> TYPE: DNA
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<400> SEQUENCE: 2505

CAGATTCCTC TCTCTTCTG 19

<210> SEQ ID NO 2506
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<212> TYPE: DNA
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TCTTCTGTCA AGCAGAAAAT G

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21

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CCTCTCTCTT CTGTCAAGCA G

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TTCTCTCTC TTCTGTCAAG C

21

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21

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AGATTCCTCT CTCTTCTGTC A

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CAGATTCCTC TCTCTTCTGT C

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CCAGATTCCT CTCTCTTCTG T

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22

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TGTCAAGCAG AAAATGCAAG GC

22

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CTGTCAAGCA GAAAATGCAA GG

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TCTTCTGTCA AGCAGAAAAT GC

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CTCTTCTGTC AAGCAGAAAA TG

22

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TCTCTTCTGT CAAGCAGAAA AT

22

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CTCTCTCTTC TGTCAGCAG AA

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22

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<210> SEQ ID NO 2562
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ATTCCTCTCT CTTCTGTCAA GC 22

<210> SEQ ID NO 2563
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GATTCCTCTC TCTTCTGTCA AG 22

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<211> LENGTH: 22
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CAGATTCCTC TCTCTTCTGT CA

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<210> SEQ ID NO 2566
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CCAGATTCCT CTCTCTTCTG TC

22

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<400> SEQUENCE: 2567

ACCAGATTCC TCTCTTCT GT

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<210> SEQ ID NO 2568
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<400> SEQUENCE: 2568

TACCAGATTC CTCTCTTCTC TG

22

<210> SEQ ID NO 2569
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<212> TYPE: DNA
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<400> SEQUENCE: 2569

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23

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TGTCAAGCAG AAAATGCAAG GCA

23

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CTGTCAAGCA GAAAATGCAA GGC

23

<210> SEQ ID NO 2572
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<400> SEQUENCE: 2572

TCTGTCAAGC AGAAAATGCA AGG

23

<210> SEQ ID NO 2573
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TTCTGTCAAG CAGAAAATGC AAG

23

<210> SEQ ID NO 2574
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<212> TYPE: DNA
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CTTCTGTCAA GCAGAAAATG CAA

23

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<210> SEQ ID NO 2575
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<400> SEQUENCE: 2575

TCTTCTGTCA AGCAGAAAAT GCA

23

<210> SEQ ID NO 2576
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<400> SEQUENCE: 2576

CTCTTCTGTC AAGCAGAAAA TGC

23

<210> SEQ ID NO 2577
<211> LENGTH: 23
<212> TYPE: DNA
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TCTCTTCTGT CAAGCAGAAA ATG

23

<210> SEQ ID NO 2578
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<400> SEQUENCE: 2578

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23

<210> SEQ ID NO 2579
<211> LENGTH: 23
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<220> FEATURES:
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<400> SEQUENCE: 2579

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TCTCTCTTCT GTCAAGCAGA AAA

23

<210> SEQ ID NO 2580
<211> LENGTH: 23
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<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
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CTCTCTCTTC TGTCAAGCAG AAA

23

<210> SEQ ID NO 2581
<211> LENGTH: 23
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CCTCTCTCTT CTGTCAAGCA GAA

23

<210> SEQ ID NO 2582
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: cDNA for use as primers
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TCCTCTCTCT TCTGTCAAGC AGA

23

<210> SEQ ID NO 2583
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURES:
<223> OTHER INFORMATION: cDNA for use as primers
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TTCCTCTCTC TTCTGTCAAG CAG

23

<210> SEQ ID NO 2584
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<212> TYPE: DNA
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ATTCCTCTCT CTTCTGTCAA GCA

23

<210> SEQ ID NO 2585
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<400> SEQUENCE: 2585

GATTCCTCTC TCTTCTGTCA AGC

23

<210> SEQ ID NO 2586
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<400> SEQUENCE: 2586

AGATTCCTCT CTCTTCTGTC AAG

23

<210> SEQ ID NO 2587
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CAGATTCCTC TCTCTTCTGT CAA

23

<210> SEQ ID NO 2588
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CCAGATTCCT CTCTCTTCTG TCA

23

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23

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GTCAAGCAGA AAATGCAAGG CACC

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24

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CTGTCAAGCA GAAAATGCAA GGCA

24

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TCTGTCAAGC AGAAAATGCA AGGC

24

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<213> ORGANISM: Artificial sequence
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TTCTGTCAAG CAGAAAATGC AAGG

24

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CTTCTGTCAA GCAGAAAATG CAAG

24

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TCTTCTGTCA AGCAGAAAAT GCAA

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CTCTTCTGTC AAGCAGAAAA TGCA

24

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TCTCTTCTGT CAAGCAGAAA ATGC

24

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CTCTCTTCTG TCAAGCAGAA AATG

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TCTCTTCTGT GTCAAGCAGA AAAT

24

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CTCTCTCTTC TGCAAGCAG AAAA

24

oligosPatNat2.txt

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CCTCTCTCTT CTGTCAAGCA GAAA

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TCCTCTCTCT TCTGTCAAGC AGAA

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TTCCTCTCTC TTCTGTCAAG CAGA

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ATTCCTCTCT CTTCTGTCAA GCAG

24

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GATTCCTCTC TCTTCTGTCA AGCA

24

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AGATTCCTCT CTCTTCTGTC AAGC

24

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CAGATTCCTC TCTCTTCTGT CAAG

24

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CCAGATTCCT CTCTCTTCTG TCAA

24

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ACCAGATTCC TCTCTTCTCT GTCA

24

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TACCAGATTC CTCTCTCTTC TGTC

24

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GTACCAGATT CCTCTCTCTT CTGT

24

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GGTACCAGAT TCCTCTCTCT TCTG

24

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GTCAAGCAGA AAATGCAAGG CACCT

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TGCAAGCAG AAAATGCAAG GCACC

25

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CTGTCAAGCA GAAAATGCAA GGCAC

25

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TCTGTCAAGC AGAAAATGCA AGGCA

25

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TTCTGTCAAG CAGAAAATGC AAGGC

25

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CTTCTGTCAA GCAGAAAATG CAAGG

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TCTTCTGTCA AGCAGAAAAT GCAAG

25

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CTCTTCTGTC AAGCAGAAAA TGCAA

25

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<211> LENGTH: 25

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TCTCTTCTGT CAAGCAGAAA ATGCA

25

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<212> TYPE: DNA

<213> ORGANISM: Artificial sequence

<220> FEATURES:

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CTCTCTTCTG TCAAGCAGAA AATGC

25

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<220> FEATURES:

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TCTCTTCTCT GTCAAGCAGA AAATG

25

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<213> ORGANISM: Artificial sequence

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<212> TYPE: DNA

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CCTCTCTCTT CTGTCAAGCA GAAAA

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TCCTCTCTCT TCTGTCAAGC AGAAA

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TTCCTCTCTC TTCTGTCAAG CAGAA

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ATTCCTCTCT CTTCTGTCAA GCAGA

25

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GATTCCTCTC TCTTCTGTCA AGCAG

25

<210> SEQ ID NO 2633

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AGATTCCTCT CTCTTCTGTC AAGCA

25

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<211> LENGTH: 25
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<223> OTHER INFORMATION: cDNA for use as primers
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CAGATTCCTC TCTCTTCTGT CAAGC

25

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<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
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<223> OTHER INFORMATION: cDNA for use as primers
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CCAGATTCCT CTCTCTTCTG TCAAG

25

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ACCAGATTCC TCTCTTTCT GTCAA

25

<210> SEQ ID NO 2637
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<223> OTHER INFORMATION: cDNA for use as primers
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TACCAGATTC CTCTCTTCT TGTC A

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<211> LENGTH: 25
<212> TYPE: DNA
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<400> SEQUENCE: 2638

GTACCAGATT CCTCTCTCTT CTGTC

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<210> SEQ ID NO 2639
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GGTACCAGAT TCCTCTCTCT TCTGT

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<212> TYPE: DNA
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<223> OTHER INFORMATION: cDNA for use as primers

<400> SEQUENCE: 2640

AGGTACCAGA TTCCTCTCTC TTCTG

25

REIVINDICAÇÕES

1. Ácido nucléico isolado compreendendo pelo menos 15 bases nucleotídicas incluindo o sítio polimórfico caracterizado por ser selecionado de um grupo consistindo

5 de:

(a) uma substituição T → C no nucleotídeo 29 da SEQ ID NO:1

(b) uma substituição G → T no nucleotídeo 152 da SEQ ID NO:1

10 (c) uma substituição G → A no nucleotídeo 203 da SEQ ID NO:1

(d) uma substituição C → T no nucleotídeo 228 da SEQ ID NO:1

15 (e) uma substituição C → T no nucleotídeo 458 da SEQ ID NO:1

(f) uma substituição A → G no nucleotídeo 600 da SEQ ID NO:1.

2. Ácido nucléico isolado de acordo com a reivindicação 1 caracterizado por compreender um DNA.

20 3. Sonda específica para um alelo isolado caracterizado por ser capaz de detectar um sítio polimórfico da SEQ ID NO:1 da reivindicação 1.

4. Oligonucleotídeo específico para um alelo isolado caracterizado por ser capaz de detectar um sítio

25 polimórfico da SEQ ID NO:1 da reivindicação 1.

5. Kit diagnóstico caracterizado por utilizar a sonda alelo específica conforme reivindicação 3 ou um oligonucleotídeo alelo específico conforme a reivindicação 4.

6. Método de identificação de qualquer polimorfismo da SEQ ID NO:1 em mamíferos caracterizado por compreender as seguintes etapas:

5 (a) preparo de amostras de células ou tecidos de mamíferos;

(b) identificação de tecidos ou células contendo todos ou parte dos polimorfismos da SEQ ID NO:1 da reivindicação 1, em condições onde o DNA hibridado possa ser produzido;

(c) identificação do DNA hibridado;

10 (d) clonagem e seqüenciamento do DNA hibridado para a identificação do gene *NAT2* em mamíferos.

7. Método de identificação individual em um ensaio clínico caracterizado por compreender:

15 (a) produção de uma biblioteca de SNPs incluindo os sítios polimórficos da SEQ ID NO:1 conforme a reivindicação 1 e seu respectivo fenótipo;

(b) seqüenciamento individual do gene *NAT2*;

(c) conjugação do genótipo obtido no Ítem (b) com o fenótipo obtido em (a).

20 8. Método de identificação de composições terapêuticas as quais são eficazes em indivíduos caracterizado por compreender:

(a) administração de composição terapêutica para um indivíduo e mensuração de sua eficácia;

25 (b) determinação de genótipos individuais e de sítios polimórficos da SEQ ID NO:1 da reivindicação 1 que indiquem se o indivíduo é um acetilador rápido ou lento;

(c) determinação a partir das etapas (a) e (b) de quais composições terapêuticas serão as mais efetivas para um genótipo particular e quais terão efeitos adversos.

-50

TGCTAAAGTATGATATGTTTTATGTTTTGTTTTCTTGCTTAGGGGATCATGGACATTG
 M D I

11

T29C

AAGCATATTTTCAAAGAATTGGCTATAAGAACTCTAGGAACAAATTGGACTTGAAACAT
 E A Y F E R I G Y K N S R N K L D L E T

71

TAAGTACATTCTTGAGCACCAGATCCGGGCTGTTCCCTTTGAGAACCTTAACATGCATT
 L T D I L E H Q I R A V P F E N L N M H

131

G152T

GTGGGCAAGCCATGGAGTTGGGCTTAGAGGCTATTTTTGATCACATTGTAAGAAGAAACC
 C G Q A M E L G L E A I F D H I V R R N

191

G203A**C228T**

GGGGTGGGTGGTGTCTCCAGGTCAATCAACTTCTGTACTGGGGCTCTGACCACAATCGGT
 R G G W C L Q V N Q L L Y W A L T T I G

251

TTCAGACCACAATGTTAGGAGGGTATTTTTACATCCCTCCAGTTAACAAATACAGCACTG
 F Q T T M L G G Y F Y I P P V N K Y S T

311

GCATGGTTCACCTTCTCCTGCAGGTGACCATTGACGGCAGGAATTACATTGTCGATGCTG
 G M V H L L L Q V T I D G R N Y I V D A

371

GGTCTGGAAGCTCCTCCCAGATGTGGCAGCCTCTAGAATTAATTTCTGGGAAGGATCAGC
 G S G S S S Q M W Q P L E L I S G K D Q

431

C458T

CTCAGGTGCCTTGCATTTTCTGCTTGACAGAAAGAGAGGAATCTGGTACCTGGACCAA
 P Q V P C I F C L T E E R G I W Y L D Q

491

TCAGGAGAGAGCAGTATATTACAAACAAAGAATTTCTTAATTCTCATCTCCTGCCAAAGA
 I R R E Q Y I T N K E F L N S H L L P K

551

A600G

AGAAACACCAAAAAATATACTTATTTACGCTTGAACCTCGAACAATTGAAGATTTTGAGT
 K K H Q K I Y L F T L E P R T I E D F E

FIGURA 1A

611

CTATGAATACATACCTGCAGACGTCTCCAACATCTTCATTTATAACCACATCATTTTGT
S M N T Y L Q T S P T S S F I T T S F C

671

CCTTGCAGACCCCAGAAGGGGTTTACTGTTTGGTGGGCTTCATCCTCACCTATAGAAAAT
S L Q T P E G V Y C L V G F I L T Y R K

731

TCAATTATAAAGACAATACAGATCTGGTTCGAGTTTAAACTCTCACTGAGGAAGAGGTTG
F N Y K D N T D L V E F K T L T E E E V

791

AAGAAGTGCTGAAAAATATATTTAAGATTTTCCTTGGGGAGAAATCTCGTGCCCAAACCTG
E E V L K N I F K I S L G R N L V P K P

851

GTGATGGATCCCTTACTATTTAG
G D G S L T I *

FIGURA 1B

RESUMO

"Método para a predição do desfecho do tratamento de doenças humanas utilizando fármacos metabolizados pela N-acetiltransferase 2 humana (NAT2) com base em polimorfismos genéticos"

A presente invenção está relacionada ao campo da Biologia Molecular e Genômica, especialmente a Farmacogenômica. A invenção descreve a presença de novos polimorfismos no gene que codifica para a enzima Arilamina N-acetiltransferase 2 humana (NAT2), a qual é responsável pela metabolização de fármacos importantes na terapêutica de várias doenças de etiologias diversas, bem como de inúmeras toxinas e carcinógenos presentes em alimentos, cigarro e no ambiente. A presente invenção inclui metodologia passível de utilização na terapêutica utilizando os polimorfismos descritos.