

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
4 April 2002 (04.04.2002)

PCT

(10) International Publication Number
WO 02/26815 A2

(51) International Patent Classification⁷: **C07K 14/47**

(21) International Application Number: PCT/EP01/11199

(22) International Filing Date:
27 September 2001 (27.09.2001)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
00870219.3 27 September 2000 (27.09.2000) EP

(71) Applicant (*for all designated States except US*):
**VLAAMS INTERUNIVERSITAIR INSTITUUT
VOOR BIOTECHNOLOGIE** [BE/BE]; Rijvisschestraat
120, B-9052 Zwijnaarde (BE).

(72) Inventors; and

(75) Inventors/Applicants (*for US only*): **VAN ROY, Frans**
[BE/BE]; Bijlokestraat 43, B-9070 Destelbergen (BE).
SPELEMAN, Frank [BE/BE]; Transvaalstraat 5, B-2600
Antwerpen (BE).

(74) Agent: **BRANTS, Johan, Philippe, Emile**; De Clercq,
Brants & Partners, E. Gevaertdreef 10 a, B-9830
Sint-Martens-Latem (BE).

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU,
AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU,
CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,
GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC,
LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW,
MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI,
SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU,
ZA, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM,
KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian
patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European
patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE,
IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF,
CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD,
TG).

Published:

- without international search report and to be republished
upon receipt of that report
- with sequence listing part of description published sepa-
rately in electronic form and available upon request from
the International Bureau

*For two-letter codes and other abbreviations, refer to the "Guid-
ance Notes on Codes and Abbreviations" appearing at the begin-
ning of each regular issue of the PCT Gazette.*

(54) Title: IDENTIFICATION OF NEUROBLASTOMA TUMOR SUPPRESSOR GENES

(57) Abstract: The present invention relates to a new tumor suppressor gene family. More specifically the present invention relates to a tumor suppressor involved in suppression of neuroblastoma. Said tumor suppressor is involved in the generation of micronuclei and in the removal of acentric chromosomal fragments that might contain amplified DNA.



WO 02/26815 A2

IDENTIFICATION OF NEUROBLASTOMA TUMOR SUPPRESSOR GENES

The present invention relates to a new tumor suppressor gene family. More specifically the present invention relates to a tumor suppressor involved in suppression of neuroblastoma. Said tumor suppressor is involved in the generation of micronuclei and in the removal of acentric chromosomal fragments that might contain amplified DNA.

Non-random structural rearrangements of the short arm of chromosome 1 (1p) are among the most common abnormalities in solid tumors as well as in hematological malignancies (for review, see Schwab et al. 1996). The most common structural rearrangements affecting 1p are deletions, thus suggesting the implication of tumor suppressor gene(s) located in this region. For several tumor types including neuroblastoma (Caron, 1995), meningioma (Cai et al., 2001), colorectal cancer (De Angelis et al., 2001), gastric carcinoma (Igarashi et al., 2000), and breast cancer (Ragnarsson et al., 1999), it has been shown that loss of 1p is correlated with poor prognosis or with tumor progression. The presence of a tumor suppressor gene on chromosome 1p is further supported by somatic cell fusion experiments. The delivery of chromosome 1p into the neuroblastoma cell line NGP by microcell-mediated chromosome transfer resulted in complete differentiation of the cells (Bader et al., 1991) and the introduction of the 1p36 chromosomal region in a colon carcinoma cell line suppressed tumorigenicity in nude mice (Tanaka et al., 1993). Deletion mapping in breast tumor cell lines has shown that one of the two SROs (shortest regions of overlaps) involving chromosome 1 overlaps with the consensus region of loss of heterozygosity (LOH) in neuroblastoma (Bieche et al., 1998). For malignant melanoma, frequent alterations of three evolutionary conserved regions on chromosome 1 (1p11-12, 1q21 and 1p36) were described (Zhang et al., 1999). Also metastatic retinoblastoma, which occasionally shows *MYCN* amplification, has been shown to have a recurrent LOH of chromosome 1p (Doz et al., 1996). Other LOH studies have identified several critical regions on 1p in various cancers including colon cancer, breast cancer, lung cancer, hepatocellular carcinoma, parathyroid adenoma, melanoma, and others. For different tumor types including neuroblastoma some SRO's (shortest regions of overlaps) for 1p deletions are overlapping indicating that the same tumor suppressor genes may be implicated in the different tumor types.

Tumor cells arise from normal tissues through the progressive accumulation of several mutations. These genetic changes consist of point mutations, deletions, inversions, translocations and DNA amplifications and result in the activation of proto-oncogenes

or the inactivation of tumor suppressor genes. Mutations in DNA repair genes can significantly speed up this process. DNA amplification is often detected in high-grade tumors where the amplified DNA is either incorporated in a chromosome and is apparent as a homogeneously staining region (HSR) or where it is present on double minute chromosomes (DMs). These DMs are small, acentric, paired structures that replicate autonomously. In many cases, it has been shown that these structures contain cellular proto-oncogenes.

The amplified genomic region is often tumor-specific and is correlated with a poor prognosis. For example, the *MYC* gene is amplified in several tumor types such as breast carcinoma, lung carcinoma and colon carcinoma. The related *MYCN* gene shows amplification in neuroblastoma and less frequently in retinoblastoma and small cell lung cancer (reviewed in Knuutila et al., 1998).

Double minutes are acentric and therefore they are not equally distributed between both daughter cells at mitosis. It has been shown that DMs are lost from cells if their presence does not result in a selective advantage (Shimizu et al., 1994). Several drugs such as hydroxyurea and etoposide lead to a significant drop in the number of DMs in several human cell lines (Von Hoff et al., 1991; Von Hoff et al., 1992, Canute et al., 1996) and elimination of DMs can lead to a reversion of a malignant phenotype or to cellular differentiation of Colo320DM cells (Von Hoff et al., 1992), HL-60 cells (Shimizu et al., 1994; Eckhardt et al., 1994) and a number of neuroblastoma cell lines (Ambros et al., 1997).

Micronuclei are small, sphere-like structures, which are detected in the cytoplasm and are surrounded by a nuclear membrane. They are generated around acentric chromosomal fragments, such as DMs, when the nuclear membrane is reformed after mitosis. DMs can avoid this encapsulation by what is known as the 'hitchhike' mechanism (Levan and Levan, 1978; Kanda et al., 2001). Recently, a new mechanism of micronucleation has been described, involving the generation of micronuclei through budding from the main nucleus during S phase (Shimizu et al., 1998). It was also shown that the DMs are preferentially located at the periphery of the nucleus. Since the contents of the formed micronuclei consist mostly of amplified DNA, located on DMs, this is a mechanism through which the cell can remove amplified DNA from the nucleus (Shimizu et al., 1998). The micronuclei are then removed via extrusion into the extracellular environment (Shimizu et al., 2000).

These results show that the elimination of DMs can be a new target in the development of tumor-selective chemotherapeutics. The treatment with hydroxyurea of patients with high-grade ovarian carcinomas led to a decrease in the number of DMs and to a better prognosis in several patients (Raymond et al., 2001).

5 Neuroblastoma is the most common extracranial solid tumor of childhood, originating from neuroectodermal cells. One of the hallmarks of neuroblastoma is the clinical and genetic heterogeneity. Brodeur et al. (1977) found that deletions of the short arm of chromosome 1 are a typical karyotypic finding in neuroblastoma cell lines and primary tumors. This observation has been extended by molecular genetic studies, which
10 demonstrated LOH in 27% of primary tumors (Fong et al., 1989; Fong et al., 1992). The majority of 1p deletions are large, and virtually all 1p deletions encompass a common region within chromosome band 1p36 (Brodeur, 1998). The finding of 1p deletions together with the fact that introduction of chromosome 1p sequences in a neuroblastoma cell line induces differentiation and/or cell death (Bader et al., 1991),
15 suggests that one or more tumor suppressor genes are located on the short arm of chromosome 1. Evidence for involvement of multiple tumor suppressor genes were provided by several studies. Schleiermacher et al. (1994) and Takeda et al. (1994) reported a case with interstitial deletions of the proximal part of 1p, suggesting the existence of a putative tumor suppressor gene in this proximal region. Furthermore,
20 Caron et al. (1993) found that tumors with amplification of the *MYCN* gene generally had large deletions, whereas in single-copy *MYCN* cases small terminal deletions were also observed. The latter tumors showed preferential deletion of the maternal allele, which is suggestive for the presence of an imprinted gene. Several genes have been analyzed as candidate tumor suppressor genes, but until now no mutations have been
25 found in the non-deleted allele of any of these candidate genes. The occurrence of tumor predisposing constitutional chromosome rearrangements may be helpful in positional cloning of tumor suppressor genes as was exemplified for retinoblastoma. In neuroblastoma, however, germline chromosomal abnormalities have been rarely described. Two neuroblastoma patients with constitutional interstitial deletions within
30 chromosome band 1p36 have been identified (Biegel et al., 1993; White et al, 2001). In addition, our research group (Laureys et al., 1990) described a neuroblastoma patient with a constitutional t(1;17)(p36.2;q11.2) chromosomal translocation. In addition to the well-established recurrent occurrence of 1p-deletions, more recently the possible role of 17q in neuroblastoma came into focus.

Recurrent abnormalities of the long arm of chromosome 17 were already reported by Gilbert et al. (1984), but were only confirmed with the advent of molecular cytogenetic techniques which showed that 17q gain is the most frequently occurring structural rearrangement in high stage neuroblastomas (Van Roy et al., 1994; Van Roy et al., 1995; Brinkschmidt et al., 1997; Lastowska et al., 1997; Plantaz et al., 1997; Van Roy et al., 1997a; Vandesompele et al., 1998). Gain of 17q was also shown to be the most important independent prognostic marker in neuroblastoma, indicating that 17q gain itself or tightly associated accompanying genetic changes have an important impact on the biological characteristics of neuroblastoma (Bown et al., 1999). These accompanying genetic changes may well be the partial losses in the partner chromosomes, which participate in the formation of the unbalanced 17q translocations. This lead us to suggest that both copy number gain of genes on 17q and loss of putative tumor suppressor genes on the partner chromosome could be of functional significance. In this respect, the frequent involvement of 1p in unbalanced 17q translocations (Savelyeva et al., 1994; Van Roy et al., 1994) is of relevance as 1p36 is the presumed location for one or more neuroblastoma tumor suppressor genes (Versteeg et al., 1995; Schwab et al., 1996). Molecular analyses in neuroblastoma cell lines and primary tumors revealed that 1p and 17q breakpoints were scattered over a region of several megabases on both chromosomes, thus excluding the possibility of the classical mechanism of recurrent activation of the same proto-oncogene or recurrent formation of a specific oncogenic hybrid gene (Van Roy et al., 1995; Van Roy et al., 1997b; Lastowska et al., 1998). In view of these observations, the finding of a constitutional t(1;17) translocation in a neuroblastoma patient is intriguing. In order to obtain insight into the role of this translocation in the development of neuroblastoma in this unique patient, positional cloning and sequence analysis of the regions covering both breakpoints was performed. The 1p breakpoint was previously mapped to 1p36.2 within a large cluster containing multiple copies of genes including snRNA and tRNAs (van der Drift et al., 1994; Laureys et al., 1995; van der Drift et al., 1995). Notwithstanding this substantial amount of research by several research groups, and although initial efforts allowed to locate the constitutional 17q breakpoint between the *NF1* gene and *SCYA7* gene (Van Roy et al., 1997b), up to now, no neuroblastoma tumor suppressor gene could be isolated.

Surprisingly, we were able to demonstrate that the breakpoint of the constitutional t(1;17) translocation is situated within the transcribed sequence of a novel gene on

chromosome 1. Analysis shows that this gene belongs to a highly conserved gene family, of which several members function as tumor suppressors. Even more surprisingly, these tumor suppressor genes were involved in the generation of micronuclei and the removal of amplified DNA. Gene disruption, caused by an event
5 such as chromosomal translocation, may lead to a gene product that is less active, or not able to induce micronuclei, and therefore losing its tumor suppressor activity.

It is a first aspect of the invention to provide an isolated tumor suppressor gene product, comprising SEQ ID N° 202 or a functional fragment, variant or fusion protein thereof. Preferentially, said tumor suppressor gene product is essentially consisting of

10 SEQ ID N° 202, more preferentially said tumor suppressor gene product is consisting of SEQ ID 202. One preferred embodiment is a tumor suppressor gene product fragment comprising SEQ ID N° 2, preferably essentially consisting of SEQ ID N° 2, more preferentially preferably consisting of SEQ ID N° 2. Another preferred embodiment is tumor suppressor gene product fragment comprising SEQ ID N° 161,

15 preferentially essentially consisting of SEQ ID N° 161, more preferentially consisting of SEQ ID N° 161. Still another preferred embodiment is a variant selected from the group of consisting of SEQ ID N° 175, 177, 181, 187, 189, 191 and 195, preferably essentially consisting of SEQ ID N° 175, 177, 181, 187, 189, 191 and 195, more preferably consisting of SEQ ID N° 175, 177, 181, 187, 189, 191 and 195. An even

20 more preferred embodiment is a variant selected from the group of consisting of SEQ ID N° 167, 169, 171, 179, 183 and 193, preferably essentially consisting of SEQ ID N° 167, 169, 171, 179, 183 and 193, more preferably consisting of SEQ ID N° 167, 169, 171, 179, 183 and 193. A most preferred embodiment is a variant selected from the group of consisting of SEQ ID N° 173, 185, 197, 198 and 200, preferably essentially
25 consisting of SEQ ID N° 173, 185, 197, 198 and 200, more preferably consisting of SEQ ID N° 173, 185, 197, 198 and 200. Still another preferred embodiment is a fusion protein of a tumor suppressor gene, consisting of SEQ ID N° 163 or SEQ ID N° 165

Preferentially, said tumor suppressor gene product is a tumor suppressor of meningioma, colorectal cancer, gastric carcinoma and/or breast cancer. Even more
30 preferentially, said tumor suppressor is a neuroblastoma tumor suppressor.

It is another aspect of the invention to provide a nucleic acid encoding a tumor suppressor gene product or a tumor suppressor gene product fragment, variant or fusion product according to the invention. Said nucleic acid can be, amongst others, mRNA, cDNA or genomic DNA. A preferred embodiment is a nucleic acid, comprising

SEQ ID N° 1, preferably essentially consisting of SEQ ID N°1, more preferably consisting of SEQ ID N°1. Another preferred embodiment is a nucleic acid, comprising SEQ ID N° 3, preferably essentially consisting of SEQ ID N°3, more preferably consisting of SEQ ID N°3. Still another preferred embodiment is a nucleic acid,
5 comprising SEQ ID N°4, preferably essentially consisting of SEQ ID N°4, more preferably consisting of SEQ ID N°4. Still another preferred embodiment is a nucleic acid, comprising SEQ ID N° 201, preferably essentially consisting of SEQ ID N° 201, more preferably consisting of SEQ ID N° 201. Still another preferred embodiment is a nucleic acid, comprising SEQ ID N° 203, preferably essentially consisting of SEQ ID N°
10 203, more preferably consisting of SEQ ID N° 203. Still another preferred embodiment is a nucleic acid, comprising the sequence selected from a group consisting of SEQ ID N° 174, 176, 180, 186, 188, 190 and 194, preferably essentially consisting of SEQ ID N° 174, 176, 180, 186, 188, 190 and 194, more preferably consisting of SEQ ID N° 174, 176, 180, 186, 188, 190 and 194. An even more preferred embodiment is a
15 variant selected from the group of consisting of SEQ ID N° 166, 168, 178, 182 and 192, preferably essentially consisting of SEQ ID N° 166, 168, 178, 182 and 192, more preferably consisting of SEQ ID N° 166, 168, 178, 182 and 192. A most preferred embodiment is a variant selected from the group of consisting of SEQ ID N°172, 184, 196, and 199, preferably essentially consisting of SEQ ID N° 172, 184, 196, and 199,
20 more preferably consisting of SEQ ID N° 172, 184, 196, and 199. Still another preferred embodiment is a nucleic acid, comprising the SEQ ID N°160, preferably essentially consisting of SEQ ID N° 160, more preferably consisting of SEQ ID N° 160. Still another preferred embodiment is a nucleic acid, consisting of SEQ ID N° 162 or SEQ ID N° 164.

25 Still another aspect of the invention is the use of a nucleic acid encoding a tumor suppressor gene product, or a functional fragment, variant or fusion product thereof according to the invention, or a nucleic acid with at least 60%, preferably 70%, more preferably 80%, most preferably 90% identity to said nucleic acid as measured by a BLASTN search (Altschul et al.,1997), or a functional fragment thereof in diagnosis of
30 cancer and/or prediction of the likelihood of developing cancer. A preferred embodiment is the use of said nucleic acid, whereby said cancer is meningioma, colorectal cancer, gastric carcinoma and/or breast cancer. An even more preferred embodiment is the use of said nucleic acid, whereby said cancer is neuroblastoma.

Said diagnosis and/or prediction can be based on the detection of mutations, comprising point mutations, deletions, insertions and rearrangements, in the tumor suppressor gene or in a translocation target sequence such as the translocation target sequence on chromosome 17, and/or by measuring the transcription level of the tumor suppressor gene. This analysis can be performed by techniques such as, as a non-limiting example, DNA/DNA hybridization, DNA/RNA hybridization, fluorescent in situ hybridization (FISH) or PCR reaction, all known to the person skilled in the art.

Another aspect of the invention is the use of a nucleic acid encoding a tumor suppressor gene product or a functional fragment or variant thereof, according to the invention, or a nucleic acid with at least 60%, preferably 70%, more preferably 80%, most preferably 90% identity to said nucleic acid as measured by a BLASTN search (Altschul et al., 1997), or a functional fragment thereof in the treatment of cancer. A preferred embodiment is the use of said nucleic acid in gene therapy, to restore the defective function of the tumor suppressor gene. Vectors for gene therapy are known to the person skilled in the art, and include, but are not limited, retroviral vectors, adenovirus-associated vectors and lentiviral vectors. Suitable vector systems have been described, amongst others, in WO9822143, WO9812338 and WO9817816. A preferred embodiment is said use, whereby said cancer is meningioma, colorectal cancer, gastric carcinoma and/or breast cancer. An even more preferred embodiment is said use, whereby said cancer is neuroblastoma.

Still another aspect of the invention is the use of a tumor suppressor gene product, or a functional fragment or variant thereof, according to the invention, or a protein with at least 60% identity, preferably 70% identity, more preferably 80% identity, most preferably 90% identity to said tumor suppressor, as measured by a BLASTP or TBLASTN search (Altschul et al., 1997) for the manufacture of a medicament to treat cancer. A preferred embodiment is said use, whereby said cancer is meningioma, colorectal cancer, gastric carcinoma and/or breast cancer. An even more preferred embodiment is said use, whereby said cancer is neuroblastoma.

Still another aspect of the invention is the use of a tumor suppressor gene product, or a functional fragment or variant thereof, according to the invention, or a protein with at least 60% identity, preferably 70% identity, more preferably 80% identity, most preferably 90% identity to said tumor suppressor, as measured by a BLASTP or TBLASTN search (Altschul et al., 1997), for the generation of micronuclei and/or the

removal of amplified DNA. Said generation of micronuclei may be useful in the suppression of different forms of cancer.

Still another aspect of the invention is a method to produce antibodies, using a tumor suppressor gene product or a functional fragment or variant or fusion protein thereof, according to the invention, or a protein with at least 60% identity, preferably 70% identity, more preferably 80% identity, most preferably 90% identity to said tumor suppressor, as measured by a BLASTP or TBLASTN search (Altschul et al., 1997), or using nucleic acid encoding such tumor suppressor gene product or a functional fragment or variant or fusion protein thereof, according to the invention, or a protein with at least 60% identity, preferably 70% identity, more preferably 80% identity, most preferably 90% identity to said tumor suppressor, as measured by a BLASTP or TBLASTN search (Altschul et al., 1997). Antibodies include polyclonal, monoclonal and synthetic antibodies. Methods to produce such antibodies are known to the person skilled in the art.

A further aspect of the invention is an antibody obtainable by said method.

Still a further aspect of the invention is the use of said antibody in diagnosis of cancer and/or prediction of likelihood of developing cancer. A preferred embodiment is said use whereby said cancer is meningioma, colorectal cancer, gastric carcinoma or breast cancer. An even more preferred embodiment is said use whereby said cancer is neuroblastoma. Said antibody may be used in assays such as, but not limited to, Western blot or ELISA, known to the person skilled in the art.

Another aspect of the invention is use of a tumor suppressor gene product, or a functional fragment, variant or fusion product thereof, according to the invention, or a protein with at least 60% identity, preferably 70% identity, more preferably 80% identity, most preferably 90% identity to said tumor suppressor, as measured by a BLASTP or TBLASTN search (Altschul et al., 1997), for the isolation of an interacting compound. Several methods have been described to detect protein – compound interactions and to select the interacting compound. These methods include, but are not limited to, phage display, yeast two-hybrid assay, coimmunoprecipitation, DNase protection assay, electrophoretic mobility shift assay, or mass spectrometric analyses, all known to the person skilled in the art, fluorescence resonance energy transfer (FRET, WO9918124) and bioluminescence resonance energy transfer (BRET, WO9966324).

Definitions

A *functional fragment of a tumor suppressor gene product*, means any proteinaceous molecule that retains its tumor suppression activity, and preferably its micronuclei inducing activity and/or the activity to remove amplified DNA.

- 5 A *variant of a tumor suppressor gene product* according to the invention is a gene product with at least 60% identity, preferably 70% identity, more preferably 80% identity, most preferably 90% identity to said tumor suppressor gene product, as measured by a BLASTP or TBLASTN search (Altschul et al., 1997), and retaining its tumor suppression activity, and preferably its micronuclei inducing activity and/or the
10 activity to remove amplified DNA.

- An isolated nucleic acid *encoding* a tumor suppressor gene product means that said nucleic acid comprises partly or totally the coding sequence of said tumor suppressor gene. The definition covers, but is not limited to genomic DNA and messenger RNA. It does however not implicate that said genomic DNA is transcribed and translated into
15 said tumor gene product.

A *functional fragment* of a nucleic acid for use in diagnosis of and/or prediction of the likelihood of means any fragment that can be used as specific probe in hybridization or as primer in PCR reactions.

- A *functional fragment* of a nucleic acid for use in the treatment of cancer means any
20 fragment that can be transcribed and/or translated into a functional tumor suppressor, which preferably retains its micronuclei inducing activity and or the activity to remove amplified DNA .

- A *functional fragment* of a tumor suppressor gene product for the manufacture of a medicament to treat cancer is any fragment of said tumor suppressor gene product
25 that retains its tumor suppression function and preferably its micronuclei inducing activity and or the activity to remove amplified DNA

A *functional fragment* of a tumor suppressor gene product in the production of antibodies is an immunogenic fragment that comprises at least one epitope and can be used for the production of antibodies against said tumor suppressor gene product.

- 30 A *functional fragment* of a tumor suppressor gene product in the isolation of an interacting compound is any fragment that can be used in an interaction screening assay, such as, but not limited to, a yeast two-hybrid assay, a phage display assay, coimmunoprecipitation, a DNase protection assay, an electrophoretic mobility shift assay, or mass spectrometric analyses.

The terms *protein* and *polypeptide* as used in this application are interchangeable. *Polypeptide* refers to a polymer of amino acids and does not refer to a specific length of the molecule. This term also includes post-translational modifications of the polypeptide, such as glycosylation, phosphorylation and acetylation

- 5 *Compound* as used here means any chemical or biological compound, including simple or complex organic or inorganic molecules, peptides, peptido-mimetics, proteins, antibodies, carbohydrates, nucleic acids or derivatives thereof.

Interacting compound with a protein means any compound that can bind, covalently or not, with said protein in a specific way.

10

Brief description of the figures

Figure 1

Physical map of PAC/BAC contig covering the constitutional 17q11.2 breakpoint based on fibre FISH, FIGE and content mapping of STS and EST clones. The orientation of
15 the map is centromere to telomere, left to right. Markers on the top row are cDNA/EST clones, polymorphic markers and STSs. Known genes are indicated by arrowheads. Partially sequenced BACs (with GenBank accession numbers) are indicated by dashed lines. Three breakpoint overlapping cosmid clones are shown, as indicated by ICRF numbers. The shaded bars indicate the approximate location of the 17q
20 breakpoint and the distal breakpoints of NF1 deletion patients UWA 155-1 and UWA 106-3 (for details on the latter two patients, see Dorschner et al., 2000).

Figure 2

Southern blot analysis of the t(1;17) translocation breakpoint by use of probe #6 (Table
25 4). Genomic DNAs extracted from a normal human placenta (normal) and from the Chinese hamster ovary cell line a3 served as controls in comparison to genomic DNAs from somatic cell hybrids 32-7A and 32-2F53VIII. Following exhaustive digestion with the restriction enzymes indicated on top, DNA fragments were subjected to Southern blot analysis. Probe #6 was prepared by PCR on the basis of the breakpoint-overlapping cosmid contig sequence (as described in Material and methods to the
30 examples). The bands corresponding to the normal, non-rearranged DNA are indicated by arrows, whereas the rearranged bands are indicated by arrowheads. Approximate sizes are indicated in bp.

Figure 3

Schematic representation of the normal and derivative chromosomal breakpoint region in the 32-2F53VIII somatic cell line hybrid. The location of the t(1;17) translocation breakpoint is indicated in each panel by a vertical double-pointed arrow. Restriction enzyme sites indicated are *Bam*HI (B), *Pvu*II (P), *Dra*I (D), *Stu*I (S) and *Eco*RV (E).

A. Schematic overview of the fragment of normal human chromosome 17 encompassing the chromosomal t(1;17) breakpoint. The horizontal bar represents the sequence (51,050 bp; GenBank Acc. No. AF148647) of a cosmid contig spanning the breakpoint in cell line 32-2F53VIII. The physical ends of the insert of cosmid ICRFc105F1060D1 were determined as indicated. An upward arrow shows the location of the SP6 end sequence of clone 841C13. Nine repeat-free probes (black boxes) were selected for use in the identification of the breakpoint by Southern hybridizations.

B. Schematic overview of a fragment of normal human chromosome 17. The breakpoint (Brkpt) in the chromosome-17 derivative of 32-2F53VIII cells was mapped to a 1,539-bp *Pvu*II fragment. The GenomeWalker PCR products extending from primer GSP1 to either *Stu*I, *Pvu*II or *Dra*I sites each comprise the location of the t(1;17) breakpoint as evidenced by a comparison with the scheme depicted in (C).

C. Schematic overview of a fragment of derivative chromosome 17, corresponding to the fragment of normal chromosome 17 depicted in (B). Cloned and sequenced GenomeWalker PCR products spanning the t(1;17) breakpoint are as indicated. The sequence of the (GSP-1 – *Eco*RV) fragment is shown in Fig. 5.

Figure 4

Cloning of the t(1;17) breakpoint of chromosome der17 by GenomeWalker PCR. Genomic DNA from the 32-2F53VIII cell line was digested as described in the text and summarized in Figure 3. GenomeWalker PCR was then performed using the following primer pairs (PR): either GSP1 + AP1 (four lanes at the left), or GSP1' plus AP1 (four lanes at the right). Restriction enzymes (RE) used are indicated on top: *Dra*I (D), *Eco*RV (E), *Pvu*II (P), and *Stu*I (S). M, Lambda *Bst*EII molecular weight marker. Bands were stained by ethidium bromide. The bands corresponding to normal chromosome 17 are indicated by *, whereas the bands rearranged by the t(1;17) translocation are

indicated by arrowheads. The latter were cloned and sequenced (Fig. 5). Fragment sizes (FS) are indicated at the bottom in bp.

Figure 5

5 Genomic DNA sequence (3,743 bp; GenBank Acc. No. AF379607) of the der17 chromosome overlapping the t(1;17)(p36.2;q11.2-q12.1) translocation breakpoint. Chromosome-17 specific sequences (602 bp) flanking the breakpoint are underlined. A spacer region of 7 bp (bold and underlined capitals) is of unknown origin. The remaining sequence of 3,134 bp represents chromosome-1 specific sequences
10 flanking the breakpoint. Three exons, two internal ones (designated x and y) and one 3' terminal (designated z), were predicted in the latter sequence. They are indicated by capitals; the predicted ORF is given in bold single-letter codes under the DNA sequence; the flanking splice donor and acceptor sites are underlined; a stop codon (indicated by *) in the 3' terminal exon z is in bold and underlined.

15

Figure 6

Sequence of a cDNA fragment (528 nucleotides) with corresponding amino acid sequence (175 amino acid residues), predicted to be encoded by the chromosome-1 specific genomic DNA sequence, flanking the t(1;17)(p36.2;q11.2-q12.1) translocation
20 breakpoint in the der17 chromosome (depicted in Fig. 5). A stop codon (indicated by *) is in bold and underlined.

Figure 7

Schematic overview of selected human cDNA (EST) sequences highly homologous or
25 identical to exons x to z (exons 11.1, 12.5 and 14.12), flanking the t(1;17)(p36.2;q11.2-q12.1) translocation breakpoint and depicted on top as Breakpoint der17. Sequences are identified by their respective cDNA code, as summarized in Tables 5 and 6. EST cDNA sequences as deposited in GenBank were confirmed, improved and often extended on the appropriate cDNA clones. The predicted protein fragments, encoded
30 by separate exons, were aligned as shown in Figs. 9 to 15. Asterisks refer to sequences corresponding to incomplete exons. Thin lines correspond either to sequences predicted to be intronic, or to sequences corresponding to the 3'UTR (size given in nucleotides). If the 3'UTR is thought to be complete, it is followed by AAAA. Dotted lines represent unfinished sequences. Sizes of separate exon-encoded

domains are indicated in amino acid residues (aa). Some sequence abnormalities (frameshift, internal deletion) are as indicated.

Figure 8

- 5 Schematic overview of selected human cDNA sequences highly homologous or identical to either exons A and B (exons 6.12 and 7.1) or exons x to z (exons 11.1, 12.5 and 14.12). These exons are flanking the t(1;17)(p36.2;q11.2-q12.1) translocation breakpoints of chromosomes der1 and der17 as depicted at the bottom. Sequences are identified by their respective GenBank Acc. No, as summarized in Table 5. The
- 10 predicted protein fragments were aligned as shown in Figs. 9 to 15. Sizes of separate exon-encoded domains are indicated in amino acid residues (aa). The double broken lines in the centre of the AB033071 molecule point at a single-nucleotide frameshift and an apparent deletion as compared to the other molecules depicted. Asterisks refer to sequences corresponding to incomplete exons. Thin lines in the scheme of cDNA
- 15 clone AI050141 correspond to sequences predicted to be intronic. The unlabeled black box (60 aa) in the scheme of cDNA clone AL136890 is of unknown origin.

Figures 9 to 15

- Alignments of protein fragments predicted to be encoded by exons identified in genomic and cDNA clones and belonging to a novel gene family, comprising exons
- 20 exons A, B and x to z, flanking the t(1;17)(p36.2;q11.2-q12.1) translocation breakpoints in chromosomes der1 or der17. The source of these sequences is summarized in Table 5 and partly depicted in Figs. 7, 8, 21, 22-25, 28 and 37. On top of each sequence alignment is a corresponding phylogenetic tree (scales indicate % of non-
- 25 similarity).

Fig. 9 represents exons of type 0, probably comprising highly conserved 5'UTR sequences, and exons of type 1, encoding both putative amino-terminal and internal domains (NBG proteins are probably starting with the highly conserved sequence MVVSAGP...).

- 30 Fig. 10 represents exons of types 2 and 3.

Fig. 11 represents exons of types 4, 5 and 6. Exon 6.12 corresponds to exon A.

Fig. 12 represents exons of types 7, 8 and 9. Exon 7.1 corresponds to exon B.

Fig. 13 represents exons of type 10 and 11. Exon 11.1 corresponds to exon x.

Fig. 14 represents exons of type 12 and 13. Exon 12.5 corresponds to exon y.

Fig. 15 represents exons of type 14, encoding carboxy-terminal protein domains. Exon 14.12 corresponds to exon z.

Figure 16

5 Southern blot analysis of the t(1;17) translocation breakpoint by use of probe #9 (Table 4). Genomic DNAs extracted from a normal human placenta (normal) and from the Chinese hamster ovary cell line a3 served as controls in comparison to genomic DNAs from somatic cell hybrids 32-2F53VIII and 32-7A. Following exhaustive digestion with the restriction enzymes indicated on top, DNA fragments were subjected to Southern
10 blot analysis. Probe #9 was prepared by PCR on the basis of the breakpoint-overlapping cosmid contig sequence (as described in Material and methods to the examples). Rearranged bands in the 32-7A genomic DNA are indicated by arrows. Size markers (DNA molecular weight marker II, Roche) are indicated in bp.

15 Figure 17

Schematic representation of the normal and derivative chromosomal breakpoint region in the 32-7A somatic cell line hybrid. The location of the t(1;17) translocation breakpoint is indicated in each panel by a vertical double-pointed arrow. Restriction enzyme sites indicated are *Bam*HI (B), *Pvu*II (P), *Dra*I (D), *Ssp*I (S) and *Eco*RV (E).

20 A. Schematic overview of the fragment of normal human chromosome 17 encompassing the chromosomal t(1;17) breakpoint. The horizontal bar represents the sequence (51,050 bp; GenBank Acc. No. AF148647) of a cosmid contig spanning the breakpoint in cell line 32-7A. The physical ends of the insert of cosmid ICRFc105F1060D1 were determined as indicated. An upward arrow shows the location of the SP6 end sequence of clone 841C13. Nine repeat-free
25 probes (black boxes) were selected for use in the identification of the breakpoint by Southern hybridizations.

B. Schematic overview of a fragment of normal human chromosome 17. The GenomeWalker PCR products extending from primer GSP1" to a *Dra*I site, or extending from primer GSP2 to *Pvu*II or *Ssp*I sites each comprise the location of
30 the t(1;17) breakpoint as evidenced by a comparison with the scheme depicted in (C).

C. Schematic overview of a fragment of derivative chromosome 1, corresponding to the fragment of normal chromosome 17 depicted in (B).

Cloned and sequenced GenomeWalker PCR products spanning the t(1;17) breakpoint are as indicated. The sequence of the (GSP1" – *Pvu*II) fragment is shown in Fig. 19.

5 Figure 18

Cloning of the t(1;17) breakpoint of chromosome der1 by GenomeWalker PCR. Genomic DNA from the 32-7A cell line was digested as described in the text and summarized in Figure 17 and GenomeWalker PCR was performed using the following primer pairs (PR): either GSP1" + AP1 (five lanes at the left), or GSP2 plus AP2 (five
10 lanes at the right). Restriction enzymes (RE) used are indicated on top: *Dra*I (D), *Eco*RV (E), *Pvu*II (P), *Sca*I (Sc) or *Ssp*I (S). M, Lambda *Bst*EII molecular weight marker. Bands were stained by ethidium bromide. The bands corresponding to normal chromosome 17 are indicated by *, whereas the bands rearranged by the t(1;17) translocation are indicated by arrowheads. The latter were cloned and sequenced (Fig.
15 19). Fragment sizes (FS) are indicated at the bottom in bp. Aspec, aspecifically amplified bands.

Figure 19

Genomic DNA sequence (4,512 bp; GenBank Acc. No. AF379606) of the der1
20 chromosome overlapping the t(1;17)(p36.2;q11.2-q12.1) translocation breakpoint. The sequence of the first 3,845 bp represents chromosome-1 specific sequences flanking the breakpoint. This is followed by a spacer region of 4 bp (bold and underlined capitals AAAG), which is of unknown origin. The remaining underlined sequence of 663 bp represents chromosome-17 specific sequences flanking the breakpoint. Two
25 exons (designated A and B) were predicted in the chromosome-1 sequence. They are indicated by capitals; the predicted ORF is given in bold single-letter codes under the DNA sequence; the flanking splice donor and acceptor sites are underlined.

Figure 20

30 Sequence of a cDNA fragment (258 nucleotides) with corresponding amino acid sequence (86 amino acid residues), predicted to be encoded by the chromosome-1 specific genomic DNA sequence, flanking the t(1;17)(p36.2;q11.2-q12.1) translocation breakpoint in the der1 chromosome (depicted in Fig. 19).

Figure 21

Schematic overview of selected human cDNA (EST) sequences highly homologous or identical to exons A and B (exons 6.12 and 7.1), flanking the t(1;17)(p36.2;q11.2-q12.1) translocation breakpoint and depicted on top as Breakpoint der1. Sequences are identified by their respective cDNA code, as summarized in Tables 5 and 6. EST cDNA sequences as deposited in GenBank were confirmed, improved and often extended on the appropriate cDNA clones. The predicted protein fragments, encoded by separate exons, were aligned as shown in Figs. 9 to 14. Asterisks refer to sequences corresponding to incomplete exons. Thin lines correspond to sequences predicted to be intronic. Sizes of separate exon-encoded domains are indicated in amino acid residues (aa). Some sequence abnormalities (frameshifts) are as indicated. The sequence of cDNA clone AE02 is homologous with the 5'-end of cDNA clone AG09. When domains of type 1 are preceded by one of type 0, they are predicted to contain the start codon.

Figure 22

Schematic overview of selected human cDNA (EST) sequences highly homologous or identical to exons x and y (exons 11.1 and 12.5), flanking the t(1;17)(p36.2;q11.2-q12.1) translocation breakpoint and depicted on top as Breakpoint der17. Sequences are identified by their respective cDNA code, as summarized in Tables 5 and 6. EST cDNA sequences as deposited in GenBank were confirmed, improved and often extended on the appropriate cDNA clones. The predicted protein fragments, encoded by separate exons, were aligned as shown in Figs. 13 and 14. Asterisks refer to sequences corresponding to incomplete exons. Thin lines correspond to sequences predicted to be intronic. Sizes of separate exon-encoded domains are indicated in amino acid residues (aa).

Figure 23

Schematic overview of selected human genomic sequences highly homologous or identical to either exons A and B (exons 6.12 and 7.1) or exons x to z (exons 11.1, 12.5 and 14.12). These exons are flanking the t(1;17)(p36.2;q11.2-q12.1) translocation breakpoints of chromosomes der1 and der17 as depicted at the top. Sequences are identified by their respective GenBank Acc. No, as summarized in Table 5. The predicted protein fragments were aligned as shown in Figs. 9 to 15. Sizes of separate

exon-encoded domains are indicated in amino acid residues (aa). The double-pointed horizontal arrows below the AL354666 and AL356581 molecules point at separate contigs of these unfinished genomic sequences (contigs are identified by #number). The exon types 4.1 and 5.1 between brackets were only detected in previous releases of sequence AL354666, but removed in release 5.

Figure 24

Schematic overview of the neuroblastoma breakpoint gene (NBG) gene structure at the t(1;17)(p36.2;q11.2-q12.1) translocation breakpoint. Idiograms of normal chromosome 1, normal chromosome 17 (shaded), and derivative chromosomes der1 and der17 are shown. The structure of the chromosome-1 NBG gene, interrupted by the translocation, is predicted on the basis of sequences of cDNA clone DKFZp434G2022 (clone AB25; Fig. 7) and sequences from unfinished genomic clones RP11-284O17 (GenBank Acc. No. AL355800) and RP11-45I3 (GenBank Acc. No. AC015618). Only exon sequences are represented (typing according to Table 5 and Figs. 9-15; sizes in aa, amino acid residues). Thin lines correspond to the 3'UTR sequence. Arrows denote the direction of transcription. Upon chromosomal translocation, a chromosome-1 region of about 20 kbp appears to be deleted (indicated by Del). After translocation, the gene on the der1 chromosome is expressed as chimeric transcripts (Figs. 25-27) as splicing occurs from exon 7.1 to chromosome-17 derived sequences X (as indicated in this figure) or Y (see also Fig. 25). Similar chimeric transcripts for the der17 chromosome are not yet identified.

Figure 25

Chimeric NBG-related transcripts. The chimera #1 and #2 transcripts were isolated by 3'-RACE on RNA from somatic cell hybrid 32-7A, containing the der1 chromosome (see Figs. 26 and 27 for the sequences of the 3'-RACE clones). Sequences X and Y are derived from chromosome 17. In addition, two tumor-derived cDNA clones contain NBG-related sequences fused to gene sequences from chromosome 1, as documented in the text.

Figure 26

Sequence of a chimeric cDNA fragment with corresponding amino acid sequence (GenBank Acc. No. AF420438), cloned by 3'-RACE on RNA from somatic cell hybrid

32-7A (see chimera #1 in Fig. 25). The sequence starts with gene-specific primer GSP2 located in NBG exon 6. Nucleotides from chromosome 1 (part of exon 6 plus exon 7.1) are put in capitals, and the encoded amino acid residues in bold capitals; nucleotides from chromosome 17 are put in lowercase and the encoded amino acid residues (ORF X) in underlined bold italics capitals. Asteriks, stop codon followed by 3'UTR and poly-A stretch.

Figure 27

Sequence of a chimeric cDNA fragment with corresponding amino acid sequence, (GenBank Acc. No. AF420439) cloned by 3'-RACE on RNA from somatic cell hybrid 32-7A (see chimera #2 in Fig. 25). The sequence starts with gene-specific primer GSP2 located in NBG exon 6. Nucleotides from chromosome 1 (part of exon 6 plus exon 7.1) are put in capitals, and the encoded amino acid residues in bold capitals; nucleotides from chromosome 17 are put in lowercase and the encoded amino acid residues (ORF Y) in underlined bold italics capitals. Asteriks, stop codon followed by 3'UTR and poly-A stretch.

Figure 28

Overview of cloned NBG-related 5'-RACE products. RNAs from four different cell lines were used as template, as indicated. Nested primers of these reactions were specific for type-11 exons but may anneal also to part of the type-10 exons. The predicted protein fragments, encoded by separate exons, were aligned as shown in Figs. 13 and 14. Asterisks refer to sequences corresponding to incomplete exons. Thin lines correspond to sequences predicted to be intronic. Sizes of separate exon-encoded domains are indicated in amino acid residues (aa). Double pointed arrows indicate the insert sizes of the fully overlapping shorter cDNA clones indicated.

Figure 29

Northern blot analysis of NBG-related transcripts in human tumor-derived cell lines as indicated, in somatic cell hybrid 32-7A and in mouse cell lines NMe and Neuro2A. Sequential hybridization was done with a 5' NBG probe followed by a 3' NBG probe (see Materials and methods to the examples). Loading of the mRNAs was estimated by hybridization with a mouse GAPDH probe. The graph shows the normalized relative amounts of the different bands (7.2 kb + 5.9 kb, 4.1 kb, 0.5 kb) as quantitated by

phosphor imaging. The 5' probe (5') allowed more efficient detection as compared to the 3' probe (3'). SH-SY5Y cells expressed the highest levels for all NBG transcripts, except for the 0.5 kb species that was expressed mainly by HCT8/R1 cells.

5 Figure 30

Flowchart of the construction of plasmid pBlue-KIAA-AB25, comprising a full-length NBG cDNA. cDNA/protein fragments, corresponding to separate exons, are labeled according to Table 5 and Figs. 9-15.

10 Figure 31

MCF7/AZ cells were transfected with different NBG constructs as indicated. Left panels show either the Myc-tag revealed by anti-Myc antibody (panels A and K) or fluorescence of the GFP-tag (panels C, E, G and I). Right panels show DNA staining by DAPI. Cells were transfected with a construct encoding a Myc-tagged aminoterminal fragment (A, B), a construct encoding a GFP-tagged aminoterminal fragment (C, D), a construct encoding a GFP-tagged carboxyterminal fragment (E-H), a GFP-tagged full-length construct (I, J), and a Myc-tagged full-length construct (K, L). Arrows point at micronuclei, which are particularly obvious in cells transfected with the full-length constructs (I and K).

20

Figure 32

MCF7/AZ cells were transfected with different NBG constructs as indicated. pCS2+MT-KIAA-AB25, a construct encoding a Myc-tagged full-length NBG protein, was used for cells in panels A-F. Cells were simultaneously stained with an anti-Myc antibody (A), a concanavalin-A conjugate to stain the endoplasmic reticulum (B), and with the DNA stain DAPI (C). This shows that the overexpressed protein is not localized in the endoplasmic reticulum. The arrows points at a micronucleus. Transfected cells were also simultaneously stained with the polyclonal NBG-specific antibody #31226 (D), with a mouse anti-lamin B antibody (E) and with DAPI (F). The 2 micronuclei in this cell (arrows) are clearly stained by the anti-lamin antibody and by DAPI, demonstrating that these structures are indeed micronuclei. Cells were also transfected with either the empty vector pEGFP-N3 (G, H) or the empty vector pEF6/Myc-His-A. GFP fluorescence is shown (G), staining with anti-Myc antibody (I) or DAPI staining (H, J).

30

Figure 33

HCT8/E8 cells were transfected with constructs encoding a Myc-tagged full-length NBG protein (A, B), a GFP-tagged aminoterminal fragment (C, D), a GFP-tagged carboxyterminal fragment (E, F), or with the empty vector pEGFP (G, H). Several
5 micronuclei are visible in the cytoplasm as indicated by arrows. GFP fluorescence is shown (C, E, G), staining with anti-Myc antibody (A) or DAPI staining (B, D, F, H).

Figure 34

HEK293T cells were transfected with constructs encoding a Myc-tagged full-length
10 NBG protein (A, B) or a GFP-tagged aminoterminal fragment (C, D). Micronuclei in the cytoplasm are indicated by arrows.

Colo320DM cells were transfected with a construct encoding a Myc-tagged full-length NBG protein (E, F), with the empty control vector (G, H), with a construct encoding a
15 GFP-tagged aminoterminal fragment (I, J), or with a construct encoding a GFP-tagged carboxyterminal fragment (K, L). The cell transfected with the full-length construct shows two micronuclei (arrows), the first one in the cytoplasm and the second still attached to the main nucleus.

GFP fluorescence is shown (C, I, K), staining with anti-Myc antibody (A, E, G) or DAPI staining (B, D, F, H, J, L).

Figure 35

Mouse NMe cells were transfected with several constructs as indicated. The latter encode a GFP-tagged full-length NBG protein (A, B), a GFP-tagged aminoterminal fragment (C, D), a Myc-tagged full-length NBG protein (E, F). In addition, empty vector
25 pEGFP (G, H) or empty vector pCS2+MT (I, J) were used. When the full-length protein was overexpressed, many micronucleus-like structures became visible (arrows in A and E), which stain negative for DAPI. Upon expression of the aminoterminal fragment, perinuclear fluorescence was apparent, but much less micronucleus-like cytoplasmic structures (C).

30 GFP fluorescence is shown (A, C, G), staining with anti-Myc antibody (E, I) or DAPI staining (B, D, F, H, J).

Figure 36

MCF7/AZ cells were transfected with two constructs expressing NBG-related chimeric transcripts as indicated. Chimeric cDNA fragments were cloned by 3'-RACE on mRNA of the 32-7A somatic cell hybrid, followed by ligation to a suitable fragment of plasmid pCS2+MT-KIAA-AB25. The transcripts encode an aminoterminal NBG fragment elongated by chromosome-17 sequences (see Fig. 25). Use of these constructs was featured by the generation of multiple vesicle-like structures in the cytoplasm (A, C). In addition, these cells contain some micronuclei as demonstrated by an arrow in (A). Staining was with anti-Myc antibody (A, C) or with DAPI staining (B, D).

Figure 37

RT-PCR was performed on RNA from either human fetal brain (HFB) or the somatic cell hybrid 32-2FVIII. Primers used in these experiments are denoted by FVR numbers under typical NBG exonic sequences. Sequences of cloned products are as depicted (see also Table 5 and Figs. 11-15 for the protein fragments, predicted to be encoded by separate exons). Several new exon subtypes were identified, including novel splice variants each time involving exon 8. Clone names with an asterisk contain a frameshift immediately before exon 9, as they either lack the complete exon 8 or parts of it (deletions indicated by dashed lines). In clones 27 and 28, domain 8 consists of the first 5 amino acid residues and the last 28 amino acid residues of a full-length exon-8 sequence (see also Fig. 12).

Figure 38

MCF7/AZ cells were transfected with a construct encoding a Myc-tagged full-length NBG protein followed by simultaneous staining with an anti-Myc antibody (A), polyclonal NBG-specific antibody #31226 (B) and DAPI (C). A transfected cell (centre) is stained by both the anti-Myc antibody and the polyclonal antibody, whereas nontransfected cells are not stained by anti-Myc antibody and only very lightly by the polyclonal antibody.

Examples

Material and methods to the examples

Library screening and DNA isolation

YAC- and PAC-end clones and selected STSs were used to screen for additional PAC clones. These clones were isolated by screening of a gridded RCPI-1 PAC library (Ioannou et al., 1994). Subsequently, breakpoint-overlapping PAC clones were used to screen a chromosome-17 specific cosmid library. The PAC and cosmid filters and clones were distributed by the Ressourcenzentrum Primärdatenbank in the Max Planck-Institut für Molekulare Genetik in Germany (RZPD) (Zehetner and Lehrach, 1994). In brief, 30 ng probe DNA (YAC- or PAC-end clone, STS) was randomly labeled using the Megaprime DNA labeling kit (AP Biotech) according to the supplier's protocol. Prehybridisation of filters, hybridization and washing steps were done according to standard procedures. BACs were obtained from the Children's Hospital Oakland Research Institute (C.H.O.R.I.) in Oakland, Ca., USA (<http://www.chori.org/bacpac>).

PACs, BACs and cosmids were cultured in LB-broth medium containing the appropriate antibiotics. DNA was isolated using a rapid alkaline lysis miniprep method (C.H.O.R.I.).

The following databases were consulted for identification of publicly available genetic markers and clones: Whitehead Institute for Biomedical Research (<http://www-genome.wi.mit.edu/>), Marshfield Medical Research Foundation Center for Medical Genetics (<http://www.marshmed.org/genetics>), CEPH-Généthon (<http://www.cephb.fr/ceph-genethon-map.html>), National Center for Biotechnology Information (NCBI, <http://www.ncbi.nlm.nih.gov/>) and the Human Genome Project Working Draft at UCSC (<http://genome.ucsc.edu/>).

YAC and PAC end isolation and generation of sequence-tagged sites

YAC end clones were isolated using an Alu-vector based method (Nelson et al., 1989). PAC end clones were obtained by vectorette PCR (Riley et al., 1990), or were obtained by direct sequencing and subsequent PCR amplification. For direct sequencing, PAC DNA was subjected to cycle sequencing using BigDye chemistry on an ABI377 automatic sequencer (Applied Biosystems) with the following vector based primers: T7 (5'-TAATACGACTCACTATAGGG-3') and SP6 (5'-CAAGCT

ATTTAGGTGACACTATAGA-3'). Screening for repetitive sequences was done using the program 'Repeat Masker'

(<http://ftp.genome.washington.edu/RM/RepeatMasker.html>). In total, 17 end

sequences were generated of which 9 were submitted as GGS to Genbank [SP6

5 RPCI-1 105C17 (acc. n° BH021100); SP6 RPCI-1 605A3 (acc. n° BH021101); T7

RPCI-1 1167N14 (acc. n° BH021102); SP6 RPCI-1 835C10 (acc. n° BH021103); T7

RPCI-1 835C10 (acc. n° BH021104); SP6 RPCI-1 55N16 (acc. n° BH021105); SP6

RPCI-1 266J21 (acc. n° BH021106); T7 RPCI-1 118B4 (acc. n° BH021107); T7 RPCI-1

266J21 (acc. n° BH021108)] and 8 were used to develop end STSs. Primers were

10 designed using the PrimerExpress software (Applied Biosystems). The novel STSs

and primer sequences have also been submitted to GenBank (see Table 1).

Fluorescence in situ hybridization (FISH)

PACs, BACs and cosmids were biotinylated (biotin-16-dUTP, Roche) or digoxigenated

15 (digoxigenin-11-dUTP, Roche) by standard nick translation. FISH was performed

according to Van Roy et al. (1994). Slides were mounted in Vectashield (Vector

laboratories) plus DAPI (4',6-diamidino-2'-phenylindole dihydrochloride, Roche) for

counterstaining and observed under a standard ZEISS epifluorescence microscope

equipped with a 100 W Hg lamp. FISH images were recorded using the ISIS digital

20 imaging system (MetaSystems). Verification of the chromosomal localization of the

isolated clones was done by hybridization to normal metaphase chromosomes.

Subsequently, the position of the probes with respect to the constitutional 17q

breakpoint was determined by FISH on hybrid cell lines containing either derivative

chromosome 1 or derivative chromosome 17 (Laureys et al., 1995). To facilitate the

25 detection of the respective derivative chromosomes, dual color hybridization was

performed with a chromosome-17 specific library pBS-17 (Collins et al., 1991) and a

chromosome-1p36 specific probe p1-79 (D1Z2) (Buroker et al., 1987).

Fiber FISH

30 Fiber FISH slides were prepared according to Speleman et al. (1997). Prior to

hybridization, fiber FISH slides were counterstained with DAPI and evaluated by

fluorescence microscopy. Probe order, degree of overlap and estimation of size of

gaps between probes was determined by dual color FISH experiments. Hybridization

on fiber FISH slides was performed according to Van Roy et al. (1994) with minor

35 modifications. Fiber slides were only pretreated with RNase A. Pepsin treatment and

postfixation were omitted. Antibody concentration for the immunohistochemical detection of biotin and digoxigenin labeled probes was doubled in comparison with the standard FISH procedure and incubation of antibodies was performed at 37°C for 30 min instead of 20 min at room temperature.

- 5 The lengths of probe signals, overlaps and gaps were measured from digitized images with the ISIS software program (MetaSystems, Atlussheim, Germany). The gap measurements were normalized based on the signal lengths of probes on both sides of the gap to compensate for the variation in the level of DNA stretching. For the purpose of probe ordering and length measurements, at least ten images were analyzed.

10

Estimation of clone insert sizes by Field Inversion Gel Electrophoresis (FIGE)

- PAC DNA (1 µg) was digested with restriction enzyme *NotI* according to the suppliers protocol (Gibco BRL). An agarose gel (1%) was run for 16 h, at 180 V forward and at 120 V reverse, at 20°C in 0.5xTBE buffer on a Biorad FIGE Mapper™. Insert fragment
15 sizes were determined by comparison with size standards (Lambda DNA-PFGE marker; Pharmacia Biotech) (Table 3).

Mapping of STSs and ESTs

- Mapping of STSs and ESTs was done by hybridization of PCR products on PAC dot
20 blots. PCR products were purified using a QIAquick PCR purification column (Qiagen). Purified PCR products were labeled using the Megaprime kit. Hybridization was performed according to standard procedures. Furthermore, STSs and ESTs were mapped by PCR on PAC and BAC clones or positions were inferred by BLAST query of the nr and htgs NCBI databases (<http://www.ncbi.nlm.nih.gov>).

25

Shotgun DNA sequencing

- Three overlapping cosmids (ICRFc105F1060D1, ICRFc105F1065D1, ICRFc105G3072D1), presumed to span the t(1;17) breakpoint on chromosome 17, were chosen for shotgun DNA sequencing. Cosmids were grown in LB with 25 µg/ml
30 kanamycin to late log phase. Cosmid DNA was isolated using columns (Qiagen) and sheared on ice using an ultrasound sonicator. Treated DNA was analyzed in an agarose gel. Fragments of 0.8 – 1.0 kbp were cut from the gel, extracted and the ends were polished using T4 DNA polymerase and Klenow polymerase. Fragments were ligated into the pUC18Srf plasmid. A shotgun-sequencing library was generated using

DH5 α competent cells and checked for insert size by digestion with *EcoRI* and *HindIII* enzymes. More than 313 shotgun clones were selected from the three different cosmid fragment libraries and plasmid DNA was prepared using a BioRobot 9600 (Qiagen, Valencia, CA, USA) and Qiagen Turbo kits. Clones were sequenced using universal M13 primers. In addition, specific walking primers were selected to fill the remaining gaps according to standard procedures.

DNA sequence analysis

Dye terminator sequencing (Sanger, 1981) was carried out by use of Big Dye chemistry (Perkin Elmer, Foster City, CA). The gels were run on a ABI Prism 377 DNA sequencer (Perkin Elmer, Foster City, CA). Nucleotide sequences were edited and assembled using GAP4 of the Staden software package (Bonfield et al., 1995) ([URL http://www.mrc-lmb.cam.uk/pubseq/](http://www.mrc-lmb.cam.uk/pubseq/)). RepeatMasker programs were used to screen DNA sequences for interspersed repeats known to exist in mammalian genomes ([URL http://ftp.genome.washington.edu/RM/RepeatMasker.html](http://ftp.genome.washington.edu/RM/RepeatMasker.html)).

All DNA sequences were analyzed using BLAST programs (Altschul et al., 1997) ([URL http://www.blast.genome.ad.jp](http://www.blast.genome.ad.jp)) to determine similarities or identities to known genes or EST sequences using non-redundant and EST compilation databases from Genbank and EMBL-EBI. Searches for amino-acid homologies were carried out using non-redundant Swiss-Prot and PIR databases with the BLASTP and FASTA programs. Exons were predicted by use of GENSCAN ([URL http://CCR-081.mit.edu/GENSCAN.html](http://CCR-081.mit.edu/GENSCAN.html)) and GeneMark software ([URL http://opal.biology.gatech.edu/GeneMark](http://opal.biology.gatech.edu/GeneMark)). Alignment of cDNA sequences to the genomic data (DNASTar software, Madison, WI) revealed exon-intron boundaries.

Southern blotting

Genomic DNA from normal human placenta, from the Chinese hamster ovary cell line a3, and from somatic cell hybrids 32-7A and 32-2F53VIII were restricted with *BglII*, *HindIII*, *SacI*, *XhoI*, *XbaI*, *McoI*, *PvuII*, *KpnI* or *HincII* restriction enzymes. The restricted DNA was ethanol-precipitated, washed, dissolved in 20 μ l, run on an 0.8 % agarose gel and transferred to Hybond N⁺ nylon membranes (Amersham) following the recommendations of the manufacturer. Membranes were hybridized, washed and revealed by autoradiography and phosphor imaging using a Molecular Imager Fx (BioRad, Herts, UK). Probes used for hybridization were labeled by incorporation of [α -

³²PjdCTP (Amersham) using a random priming kit (GibcoBRL). In order to generate probes adjacent to the t(1;17) breakpoint for Southern blot analysis, the cosmid contigs sequence spanning the breakpoint was screened with Repeatmasker (URL <http://ftp.genome.washington.edu/cgi-bin/RepeatMasker>) to select 9 repeat-free probes representative for the cosmid sequence contig (Table 4) (depicted in Figs. 3A and 17A). The resulting PCR products, probe #1 (516 bp), probe #2 (789 bp), probe #3 (465 bp), probe #4 (478 bp), probe #5 (678 bp), probe #6 (478 bp; also depicted in Figs. 3B, Fig. 3C and 17B); probe #7 (673 bp), probe #8 (761 bp) and probe #9 (567 bp; also depicted in Fig. B and 17C) were directly sequenced to confirm their identity.

GenomeWalker Libraries

Libraries were generated according to the manufacturer's instructions (Clontech Laboratories, Palo Alto, CA, USA). For the 32-2F53VIII somatic cell hybrid, 2.5 µg of genomic DNA was digested with blunt-end generating restriction enzymes *PvuII*, *DraI*, *StuI*, and *EcoRV*, for 2 h at 37 °C in a final reaction volume of 100 µl. After this incubation, the reaction was vortexed at low speed and returned to 37 °C for 16 h. DNA was purified by phenol-chloroform extraction and ethanol precipitation. Then, the digested DNA was dissolved in 20 µl.

Appropriate blunt-ended GenomeWalker adaptors (1.9 µl of 25µM) with sequence

5' -GTAATACGACTCACTATAGGGCACGCGTGGTTCGACGGCCCGGGCTGGT-3'

3' H₂N-CCCGACCA-PO₄-5'

(Clontech), 0.5 µl of T4 DNA ligase (1 U/µl) and 1.6 µl of 5X ligase buffer were added. The mixture was incubated at 16 °C for 16 h. TE (72 µl; pH 7.4) was added and the obtained libraries, designated 32-2F53VIII/*PvuII*, 32-2F53VIII/*StuI*, 32-2F53VIII/*EcoRV* and 32-2F53VIII/*DraI*, were stored at -20 °C in 10-µl aliquots until use.

For the 32-7A somatic cell hybrid, 2 µg of genomic DNA was digested with blunt-end generating restriction enzymes *DraI*, *EcoRV*, *PvuII*, *ScaI* and *SspI*, for 2 h at 37 °C in a final reaction volume of 80 µl. After this incubation, the reaction was vortexed at low speed and returned to 37 °C for 16 h. DNA was purified by phenol-chloroform extraction and ethanol precipitation. Then, the digested DNA was dissolved in 16 µl.

Appropriate blunt-ended GenomeWalker adaptors (1.9 µl of 25µM) with sequence

5' -GTAATACGACTCACTATAGGGGCACGCGTGGTCGACGGCCCGGGCTGGT-3'

3' H₂N-CCCGACCA-PO₄-5'

(Clontech), 0.5 µl of T4 DNA ligase (1 U/µl) and 0.8 µl of 10X ligase buffer were added to 4.8 µl of the digested DNA. The mixture was incubated at 16 °C for 16 h. TE (72 µl; pH 7.4) was added and the obtained libraries, designated 32-7A/*Dra*I, 32-7A/*Eco*RV, 32-7A/*Pvu*II, 32-7A/*Sca*I and 32-7A/*Ssp*I, were stored at -20 °C.

Long-range PCR amplification of GenomeWalker products

Takara LA TAQ mix (Takara) was used. Four µl dNTPs (2.5 mM), 5 µl 10X LA reaction buffer, 1 µl adaptor primer 1 (10 µM; 5'-GTAATACGACTCACTATAGGGC-3'), 1 µl Gene-specific primer (10 µM) and 1 µl GenomeWalker library DNA (see above) were mixed in a final volume of 50 µl. DNA was amplified using a two-step PCR with 7 cycles of denaturation at 94 °C for 2 sec plus extension at 72 °C for 3 min, followed by 35 cycles of denaturation at 94 °C for 2 sec plus extension at 67 °C for 3 min. After completion of the reaction, PCR products were analyzed on a 1 % agarose gel. For nested PCR reactions, 1/50 µl of the first PCR amplification mixture was used as a template in the next reaction.

For the 32-2F53VIII libraries, gene-specific primers (GSP) were selected on the basis of DNA sequence of probe #6 (Table 4):

GSP1: 5'-CCCCTCAGCTCTGTGCATTTTGTCTA-3'

GSP1': 5'-CCTCTTGCCCCCACCTAGTGTTTATTT-3'

For the 32-7A libraries, nested PCR reactions were done with adaptor primer 2 (5'-ACTATAGGGGCACGCGTGGT-3') and with gene-specific primers GSP1" and GSP2, which were selected on the basis of the DNA sequence of probe #9 (Table 4):

GSP1": 5'-CATAGTGGGGGACATCATGACAGTCAC-3'

GSP2: 5' ACACCACCAGCCTCCCTCCATTTCTGA-3' (probe #9 was elongated with 23 bp 5' to obtain GSP2).

Cloning of PCR products

PCR products were cloned by the TA cloning procedure in the pGEMTeasy vector (Promega). In the case of long-range PCR products (GenomeWalker experiment), PCR products were treated with normal TAQ polymerase after amplification in order to generate overhanging A ends to enable TA cloning.

Plasmid constructions

All enzymes were purchased from Promega, New England Biolabs, Roche, Invitrogen or Fermentas.

pBlueKIAA1245 (Fig. 30) stands for cDNA clone hg04073 (GenBank Acc No: AB033071 - GI:6330825; backbone vector pBluescriptII SK+); pSport-AB25 (Fig. 30) stands for cDNA clone DKFZp434G2022 (GenBank Acc No: AL042839 - GI:5935596; backbone vector pSport).

Construction of pBlue-KIAA-AB25 (Figure 30)

The pBlue-KIAA1245 plasmid was digested with *NofI* and *NcoI* and a fragment of 5,952 bp was isolated. Plasmid pSport-AB25 was digested with *NofI*, *NcoI* and *BstEII* and a *NofI*-*NcoI* fragment of 4,385 bp was isolated. These two fragments were ligated together with T4 DNA ligase, which produced pBlue-KIAA-AB25.

Construction of pEF6/Myc-His-A-KIAA-AT

Plasmid pEF6/Myc-His-A (Invitrogen) was digested with *Bam*HI and *Eco*RV and a fragment of 5,898 bp was isolated. Plasmid pBlue-KIAA1245 was cut with *NcoI*, blunted with *Pfu* DNA polymerase (Promega) and cut with *BclI* resulting in a fragment of 2,326 bp. These fragments were ligated with T4 DNA ligase, which produced plasmid pEF6/Myc-His A-KIAA-AT.

Construction of pCS2+MT-KIAA-AB25

Plasmid pCS2+MT (Roth et al., 1991) was linearized with *StuI* and dephosphorylated with CIP (calf intestinal phosphatase). Plasmid pBlue-KIAA-AB25 was cut with *BclI* and a fragment of 5,401 bp was isolated. This fragment was blunted using *Pfu* DNA polymerase. Vector and insert were ligated using T4 DNA ligase.

Construction of pEF6/Myc-His-B-KIAA-AB25

Plasmid pEF6/Myc-His-B (Invitrogen) was digested with *Bam*HI and *Eco*RV and a fragment of 5,902 bp was isolated. Plasmid pBlue-KIAA-AB25 was digested with *BclI* and *SapI*, which resulted in a fragment of 4,946 bp. PCR was used to mutate a stop codon using primers FVR2803 (5'-CGCATAGTGCGGTGTGCTGATGGAAGT-3') and FVR2804 (5'-GCGATATCGTACTGTGGGAATATGACTC-3'), which contains an *Eco*RV recognition site. 40 ng DNA (pSport-AB25) was used as a template in a PCR mix with VENT DNA polymerase. The DNA was denatured at 95°C for 5 min, followed by 35 cycles of denaturation at 95 °C for 30 sec, annealing at 56 °C for 30 sec and extension at 75 °C for 30 sec. The reaction had a final extension of 10 min at 75°C. After completion of the reaction, PCR products were analyzed on a 1 % agarose gel

and purified using Concert™ Rapid PCR Purification System (Invitrogen). Subsequently, the DNA was digested with *EcoRV* and *SapI*. The three fragments were ligated using T4 DNA ligase.

Construction of pEGFP-C3-AB25-CT

- 5 pEGFP-C3 (Clontech) was digested with *EcoRV* and *BamHI* and a fragment of 4,685 bp was isolated. Plasmid pSport-AB25 was cut with *NcoI*, blunted with *Pfu* DNA polymerase (Promega) and digested with *BclI*. A fragment of 3,079 bp was isolated. These fragments were ligated with T4 DNA ligase, which resulted in plasmid pEGFP-C3-AB25-CT.

10 *Construction of pEGFP-C3-KIAA-AB25*

Plasmid pEGFP-C3 (Clontech) was linearized with *BamHI* and dephosphorylated with calf intestinal phosphatase. Plasmid pBlue-KIAA-AB25 was cut with *BclI*, which resulted in a fragment of 5,401 bp. This was ligated with the linearized vector using T4 DNA ligase.

15 *Construction of pEGFP-N3-KIAA-AT*

Plasmid pEGFP-N3 (Clontech) was linearized with *EcoRV* and dephosphorylated with calf intestinal phosphatase, which resulted in a fragment of 4,729 bp. Plasmid pBlue-KIAA-AB25 was digested with *NcoI* and *BclI* and blunted with *Pfu* DNA polymerase resulting in a fragment of 2,326 bp. These fragments were ligated with T4 DNA ligase,
20 which resulted in plasmid pEGFP-N3-KIAA-AT.

Construction of pCS2+MT-chimera1

- Plasmid pCS2+MT-KIAA-AB25 was linearized with *XcmI* and blunted with T4 DNA polymerase. Subsequently, the DNA was cut with *BsrGI* and a fragment of 6,939 bp was isolated. Plasmid pGEM-T Easy-chimera1 (see further) was digested with *HincII*
25 and *BsrGI* and a fragment of 417 bp was isolated. The fragments were ligated using T4 DNA ligase.

Construction of pCS2+MT-chimera2

- Plasmid pCS2+MT-KIAA-AB25 was linearized with *XcmI* and blunted with T4 DNA polymerase. Subsequently, the DNA was cut with *BsrGI* and a fragment of 6,939 bp
30 was isolated. Plasmid pGEM-T Easy-chimera2 (see further) was linearized with *BstXI*, blunted with T4 DNA polymerase and cut with *BsrGI*. A fragment of 245 bp was isolated and ligated into the vector using T4 DNA ligase.

DNA Transfections

MCF7/AZ cells were maintained in DMEM, 10 % FCS, non-essential amino acids, sodium pyruvate and 6 ng/ml bovine insulin and transfected using Eugene6 Reagent (Roche) according to the manufacturer's instructions. Colo320DM cells were maintained in RPMI1640, 10 % FCS, L-Gln and penicillin/streptomycin and transfected using Lipofectamine (Invitrogen) according to the manufacturer's instructions. HEK293T cells were maintained in DMEM, 10 % FCS, L-Gln, penicillin/streptomycin, sodium pyruvate and non-essential amino acids and transfected using the calcium phosphate method. HCT8 cells were maintained in RPMI1640, 10 % FCS, L-Gln, penicillin/streptomycin and sodium pyruvate and transfected using Lipofectamine Plus (Roche) according to the manufacturer's instructions. Mouse NMe cells were maintained in DMEM, 10 % FCS, penicillin/streptomycin, L-Gln and 10 µg/ml insulin and transfected using Lipofectamine (Roche) according to the manufacturer's instructions.

Immunofluorescence

After transfection, cells were kept in culture for 48 h. After this period, cells were washed twice with PBS-A and fixed with ice-cold methanol. Incubation with primary antibody was during 1 h for anti-Myc (diluted 1/125) and anti-lamin B1 (diluted 1/60) antibodies (Calbiochem) or during 2 h for the polyclonal antibodies (diluted 1/100). As secondary antibodies anti-mouse IgG Alexa488, Alexa594, anti-rabbit IgG Alexa488 and Alexa594 (Molecular Probes) were used (diluted 1/300). The endoplasmic reticulum of MCF7/AZ cells was stained using 20 µg/ml Concanavalin A Alexa594 conjugate (Molecular Probes) in PBS-A for 30 min, followed by two washes with PBS-A.

Coverslips were mounted using Vectashield (Vector Laboratories) and observations were made through an Axiophot microscope (Zeiss). Images were obtained using MetaMorph software.

Northern analysis

Total RNA was isolated from cell lines using the RNeasy kit (Qiagen). 23 µg of RNA was loaded on a 1 % agarose gel and blotted on Hybond N⁺ Membrane (Amersham Pharmacia) using standard protocols (Sambrook et al., 1989). For generating a 5'-specific probe, PCR was performed on 2 ng of pCS2+MT-KIAA-AB25 DNA using

primers 5'-TGAGGAATGAGCGACAGT-3' and 5'-TTTGAGGCTTCTGAACTG-3' in a PCR mix with Taq DNA polymerase. The DNA was denatured at 94°C for 2 min, followed by 35 cycles of denaturation at 94 °C for 20 sec, annealing at 56 °C for 20 sec and extension at 72 °C for 1 min. The products were treated by a final extension of 10 min at 72°C. After completion of the reaction, PCR products were analyzed on a 1 % agarose gel and purified using Concert™ Rapid PCR Purification System (Invitrogen). For generation of a 3'-probe, cDNA clone DKFZp434M0628 (clone AB18, Table 6) was digested with *EcoRI* and *PstI* and a fragment of 691 bp was isolated. Probes were labelled using RadPrime Labelling Kit (Invitrogen) and alpha-³²P-dCTP (Amersham). Hybridisation was performed overnight in 1 % BSA, 7 % SDS, 0,5 M Na₂HPO₄, pH 7,2, 1 mM EDTA and 100 µg/ml ssDNA. After hybridisation, filters were washed at 65 °C with a final stringency of 0.1 M sodium phosphate, pH 7.2, 1% SDS and 1 mM EDTA. For detection and quantitation, a Phosphor Imager cassette (Molecular Dynamics, Sunnyvale, CA) was exposed and scanned with a Molecular Imager® FX using the Quantity One software (BioRad, Richmond, CA).

5'-RACE reactions

5'-RACE was performed using the 5'-RACE system for Rapid Amplification of cDNA Ends (Invitrogen) according to the manufacturer's instructions. Briefly, 2 µg total RNA, isolated from either 32-7A, or 32-2F53VIII, or SK-N-SH or TR-14 cells was first-strand transcribed using the gene-specific primers FVR2458 (5'-TTGTTCCCATCAAAGTAAGAAAC-3', located in type-14 exons) or FVR2457 (5'-ATTGACGGAGTCGAATAACATCTA-3, located in type-10, -11 or -14 exons). PCR was executed using the Abridged Anchor Primer (AAP) and a gene-specific primer FVR2456 (5'-CCCCTTCTCCTTCTTTTCTTCGT-3', located in exons 12.5, 12.6 and 12.7) or FVR2455 (5'-CTCCCACGTCAAGAGAAAAG-3', located in type-11 exons). Nested PCR was performed using the Unabridged Anchor Primer (UAP) and FVR2455 or FVR2454 (5'-CATAGGGCAGGCAGGAGTCAG-3', located in type-11 exons but with high homology to part of the type-10 exons). Products were separated on a 1% agarose gel, eluted using the Concert™ Rapid Gel Extraction Purification System (Invitrogen) and cloned into plasmid pGEM-T Easy (Promega).

3'-RACE

3'-RACE was performed using the 3'-RACE System for Rapid Amplification of cDNA Ends (Invitrogen) according to the manufacturer's instructions. Briefly, 2 µg of total RNA isolated from the 32-7A cell line was first-strand transcribed using the AP (Adapter Primer). Two PCRs (PCR A and PCR B) were set up using the UAP (Universal Anchor Primer) and a gene-specific primer (either GSP1 or GSP2):

PCR A: GSP1 (5'-GCCCTTATGACTCCAACCAG-3'),

PCR B: GSP2 (5'-ATTGGCTCATCCTCTCATGTT-3').

Nested PCRs were done using the Abridged Universal Anchor Primer (AUAP) and GSP2 (for nested PCR on PCR A), or the AUAP and GSP3 primer pair (for nested PCR on PCR B). GSP3: 5'-TCCCAGAAAATGAAAGTGATG-3'.

Products were separated on a 1% agarose gel and eluted using the Concert™ Rapid Gel Extraction Purification System (Invitrogen) and cloned in pGEM-T Easy (Promega). This yielded plasmids pGEM-T Easy-chimera1 and -chimera2 in the case of 32-7A RNA as template.

RT-PCR

RT-PCR was performed on RNA from the 32-2F53VIII somatic hybrid cell line and from human fetal brain (HFB). Total RNA was isolated from 32-2F53VIII cells using RNeasy RNA Extraction Kit (Qiagen), whereas HFB RNA was purchased (Clontech). First-strand synthesis was done using SuperScript II reverse transcriptase (Invitrogen) and oligo(dT) primers. Primers for RT-PCR on cDNA from 32-2F53VIII cells were FVR2457 (5'-ATTGACGGAGTCGAATAACATCTA-3') as reverse primer and FVR2511 (5'-TTGGCTCTTGACGTGGACAGAATTA-3') or FVR2512 (5'-AAGGACCAGGAAGAGGAAGAAGA-3') as forward primer. For RT-PCR on HFB cDNA, primers FVR2686 (5'-CTCAACTCTCATTGGCTCATC-3') and FVR2687 (5'-GTCCTCCTTTTCACTTGATC-3') were used. PCR fragments were separated on a 1% agarose gel and purified using the Concert™ Rapid Gel Extraction Purification System (Invitrogen) and cloned in pGEM-T Easy (Promega).

Antibodies

Antibodies specific for NBG proteins were raised by immunisation of rabbits with 200 µg of synthetic peptides with sequence NH₂-VGEIEKKGKGKKRRG-COOH (peptide #1059), NH₂-GEEDQNPPSPRLSGVLM-COOH (peptide #1060) or NH₂-

PEILQDSLDRSYSTPSM-COOH (peptide #1061). These peptides were coupled to keyhole limpet hemocyanin via an additional cysteine residue at the NH₂-terminal end using the Imject[®] Maleimide Activated mcKLH Kit (Pierce). Boosts were given with intervals of minimum two weeks. Sera were tested by ELISA on the peptides used for injection, using nonrelevant peptide as a negative control. Sera were also tested on lysates of HEK293 cells transfected with pEGFP-C3-AB25-CT encoding the GFP-tagged carboxyterminal part of the NBG protein. The specificity of the antibodies was also evaluated by use of immunofluorescence. To this end, MCF7/AZ cells were transfected with the pCS2+MT-KIAA-AB25 construct encoding the Myc-tagged full-length NBG-protein.

Example 1: Construction of a 1.4 Mb PAC/BAC contig covering the constitutional 17q breakpoint

Previous YAC mapping lead to the identification of apparently breakpoint overlapping clones (954-e-11 and 936-g-11) (Van Roy et al., 1997b). However, upon subsequent screening of a chromosome-17 specific cosmid library no breakpoint-overlapping cosmid clones could be identified suggesting that the region covering the breakpoint region was not present in any of the analyzed YAC clones. To overcome this problem, a PAC/BAC contig covering the 17q breakpoint region was constructed (Fig.1). The RCPI-1 PAC library was screened with end clones (Table 2) from YACs 725-g-2, 728-f-1, 15FD11, 776-d-7 and 681-c-3, cosmid clone cCI17-1079 (Van Roy et al., 1997b) and STS markers D17S1850, D17S1656 (WI-2906), D17S798 and PAC end clones to further close the remaining gaps. Additional STSs were generated from end sequences of the PACs, that covered the breakpoint or were located within its immediate vicinity (Table 1). BLAST searches with PAC end sequences allowed the identification of partially or completely sequenced BAC clones. Further analysis of the partial maps from the Map Viewer at NCBI (<http://www.ncbi.nlm.nih.gov/>) and from the Human Genome Project Working Draft at UCSC (<http://genome.ucsc.edu/>) allowed the identification of additional BACs in the breakpoint region. A 1.4 Mb contig was constructed by STS (including newly developed STSs) and EST content mapping by hybridization of PCR products on dot blots containing the PAC clones and/or PCR analyses of PAC and BAC clones. Further careful positioning of all clones was done by fiber FISH. The minimum tiling path of the contig was determined as: centromere * RPCI-11 29G21 * RPCI-11 421O15 * RPCI-11 205P19 * RPCI-1 105C17 * RPCI-1

733P21 * RCPI-1 880L8 * RPCI-1 952I18 * RPCI-1 243F6 * RPCI-1 682F9 * RPCI-1 194A10 * RPCI-1 55N16 * RPCI-1 257G22 * telomere (Fig. 1). PCR content mapping showed that the order of the markers assigned to BAC clone AC011824 had to be inversed. Despite the progress in the mapping of the human genome, inconsistencies exist with regard to the position of markers and genes within this region as reflected by the different and changing mapping information available at the NCBI and UCSC databases. Ordering of contigs and closing of gaps between contigs, as described here, will be crucial in the construction of the final human genome map.

10 ***Example 2: Identification of breakpoint overlapping clones***

The position of the PAC/BAC clones with respect to the constitutional 17q breakpoint, was analyzed using FISH on metaphases from somatic hybrid cell lines, containing the derivative chromosomes 1 and 17. A total of 21 and 18 PAC/BAC clones mapped to the derivative chromosome 1 or derivative chromosome 17, respectively. Using this FISH approach, four PACs and one BAC were shown to be breakpoint overlapping (RPCI-1 880L8, RPCI-1 624A6, RPCI-1 1020I1, RPCI-1 1167N14 and RPCI-1 118G23) (Table 2). PAC clone RPCI-1 880L8 was used to screen a chromosome 17 specific cosmid library. Eleven positive cosmid clones including three overlapping cosmids were identified (ICRFc105F1060D1, ICRFc105F1065D1 and ICRFc105G3072D1) (Table 2). The DNA of these three mutually overlapping cosmids was largely sequenced after shotgun subcloning (see Example 3).

Example 3: Shotgun sequencing of a cosmid contig on chromosome 17 overlapping the constitutional 17q breakpoint

After shotgun cloning and sequencing, we constructed a sequence contig of three chromosome-17 specific mutually overlapping cosmids (ICRFc105F1060D1, ICRFc105F1065D1, ICRFc105G3072D1) encompassing the translocation breakpoint. A total contiguous sequence of 51,050 bp was obtained (GenBank Acc. N° AF148647). Within this sequence, the end clone sequence SP6 841C3 was detected (position 13112-13806), but not these of SP6 829O10 or SP6 835C10 (Fig. 1 and Fig. 3A). Further, these cosmid sequences showed identity with one unfinished BAC sequences of the Human Genome Project (Genbank Acc. No. AC013739, version .2) and with two complete BAC sequences (GenBank Acc. No. AC011824, version .8 - GI:13940712; and AC024614, version .5 - GI:14575793).

So far, BLAST analysis did not show any evidence for the presence of exons or single-exon genes in these chromosome-17 sequences. However, the exon prediction algorithms GeneMark (URL <http://opal.biology.gatech.edu/GeneMark>) predicted several putative exons of which one was cloned by exon trapping (see annotation in GenBank Acc. No. AF148647). One EST cluster (stSG50857, Unigene cluster Hs.125747) was located at a maximum distance of ~180 kb proximal to the 17q breakpoint. Sequence analysis of 4 cDNA clones (IMAGE clones 742727, 2356570, 1471272, 1471196; Genbank Acc. No. AF381171-AF381174) showed alignment of three putative exons with the genomic sequence of BAC clone RPCI-11 31I22. On the basis of the stop codons observed, several possibilities can be proposed: either these ESTs represent a multi-exonic 3'UTR, or they represent a transcribed multi-exonic pseudogene with ORF disrupting mutations, or a short open reading frame starts in the second exon, encoding a polypeptide of 78 amino acid residues. The latter polypeptide does not show significant homology with hitherto known proteins or protein domains. BLAST analysis, without masking repeat sequences, of the breakpoint overlapping cosmid sequences against the human EST database showed the presence of two partially overlapping EST sequences (GenBank Acc No AI934614 and AI571839). Although both ESTs contained a LTR/MaLR repeat they show 100% sequence similarity to the cosmid sequence.

Example 4: Identification of rearranged genomic fragments comprising the constitutional t(1;17) breakpoint

To facilitate the identification and cloning of the t(1;17) breakpoint, genomic DNA from the somatic cell hybrids 32-7A and 32-2F53VIII, the Chinese hamster ovary cell line a3 and a normal human placenta were digested with a panel of restriction enzymes including *Bgl*II, *Hind*III, *Kpn*I, *Nco*I, *Pvu*II, *Xba*I, *Eco*RI, *Nsi*I and *Bgl*II. The somatic cell hybrids 32-7A and 32-2F53VIII contain, respectively, derivative chromosomes 1 and 17 from the original neuroblastoma patient. From the cosmid contig sequence, overspanning the translocation breakpoint, 9 DNA probes free of repetitive sequences were selected and PCR amplified. These probes are listed in Table 4. They were then used for hybridization to the digested genomic DNA in order to search for abnormal patient-specific hybridization bands. No aberrant migrating bands could be detected with probes #3, #4 or #5. However, upon using probe #6, additional bands were identified in the genomic DNA of 32-2F53VIII but not in any of the other DNAs,

indicating that these fragments spanned the breakpoint on chromosome 17q (Fig. 2). The smallest rearranged band detected with probe #6 was estimated to be approximately 4 kbp long and was found in the *PvuII* digested genomic DNA.

Upon use of probe #9, additional bands were identified in the genomic DNA of 32-7A but not in any of the other DNAs, indicating that these fragments spanned the breakpoint on chromosome 1p (Fig. 16). Rearranged bands detected with probe #9 were found in genomic DNA of 32-7A cells upon digestion with *EcoRI* (~19,500 bp instead of ~13,500 bp), *NsiI* (~8,800 bp instead of ~7,600 bp), *BglI* (~13,200 bp instead of ~7,950 bp), *HindIII* (~1,000 bp instead of ~3,300 bp) and *BglII* (~1,100 bp instead of ~3,300 bp).

Example 5: Cloning of the constitutional t(1;17) translocation breakpoint in the somatic cell hybrid 32-2F53VIII

GenomeWalker PCR (Siebert et al., 1995) was used to clone the unknown genomic chromosome-1 sequences that have been juxtaposed to known, chromosome-17 sequences as a result of the human t(1;17) chromosomal translocation in the somatic cell hybrid line 32-2F53VIII. In brief (Fig. 3), genomic DNA from cell line 32-2F53VIII was digested with blunt-end generating restriction enzymes *PvuII*, *StuI*, *EcoRV* and *DraI*, and the resulting DNA fragments were then separately ligated to compatible GenomeWalker adaptors to produce four libraries. PCR amplification was performed using gene-specific primers (GSP), localized in the probe #6 sequence in combination with a GenomeWalker adaptor-specific primer (AP1). As pointed out above, the chromosome-17 specific probe #6 hybridizes to a 4-kbp *PvuII* fragment encompassing the (1,17) breakpoint. During the first cycle of the PCR, the GSP primer anneals and one strand of the adaptor is copied. Due to the lack of the binding site for the AP1 primer in the 5'-extended adaptor in combination with the 3' end of the adaptor being blocked with an amine group to prevent extension, the AP1 primer anneals only to the newly synthesized strand and not to the adaptor-ligated primary template genomic DNA. If rare extension of the 3' end of the adaptor should occur, efficient panhandle formation suppresses nonspecific background amplification. In consequence, only the genomic DNA fragment containing the specific GSP sequence is amplified.

Primer pair GSP1 plus AP1 was used in a first round of amplification. Specific products of 1,457 bp and 3,575 bp were amplified from, respectively, the 32-2F53VIII/*StuI* and 32-2F53VIII/*PvuII* GenomeWalker libraries. With the GSP1' plus AP1 primer

combination, products of 1,029 bp and 3,459 bp were amplified from, respectively, the 32-2F53VIII/*Dra*I and 32-2F53VIII/*Eco*RV GenomeWalker libraries (Figures 3 and 4). All four 32-2F53VIII-specific products mentioned were cloned and fully sequenced. Overlapping novel sequences, derived from chromosome 1, were present in all clones. In total, a maximum of 3,141 bp of novel sequences were identified in the 32-2F53VIII/*Eco*RV clone (Figure 5; sequence deposited with GenBank under Acc N° AF379607). Of these, 3,134 bp were found to be chromosome-1 specific (Figure 3; see Example 7). As indicated in Fig. 3, the other clones contained shorter but completely overlapping sequences.

Example 6: Cloning of the constitutional t(1;17) translocation breakpoint in the somatic cell hybrid 32-7A

GenomeWalker PCR (Siebert et al., 1995) was used to clone the unknown genomic chromosome-1 sequences that have been juxtaposed to known, chromosome-17 sequences as a result of the human t(1;17) chromosomal translocation in the somatic cell hybrid line 32-7A. In brief (Fig. 17), genomic DNA from cell line 32-7A was digested with blunt-end generating restriction enzymes *Dra*I, *Eco*RV, *Pvu*II, *Sca*I and *Ssp*I, and the resulting DNA fragments were then separately ligated to compatible GenomeWalker adaptors to produce five libraries. PCR amplification was performed using gene-specific primers (GSP), localized in the probe #9 sequence in combination with a GenomeWalker adaptor-specific primer (AP1). As pointed out above (Fig. 16), the chromosome-17 specific probe #9 hybridizes to various restriction fragments encompassing the (1,17) breakpoint as their mobility is shifted in DNA digests of the 32-7A cell line as compared to the 32-2F53VIII cell line or normal human placenta.

Primer pair GSP1" plus AP1 was used in a first round of GenomeWalker amplification, as outlined above in Example 5. Specific products of 1,649 bp and 1,888 bp were amplified from, respectively, the 32-7A/*Dra*I and 32-7A/*Eco*RV GenomeWalker libraries. With the GSP2 plus AP2 primer combination, products of 1,268 bp and 4,355 bp was amplified from the 32-7A/*Ssp*I and 32-7A/*Pvu*II GenomeWalker libraries (Figures 17 and 18). All four 32-7A-specific products mentioned were cloned and fully sequenced. Overlapping novel sequences, derived from chromosome 1, were present in all clones. In total, a maximum of 3,853 bp of novel sequences were identified in the 32-7A/*Pvu*II clone (Figure 19; sequence deposited with GenBank under Acc. No. AF379606). Of these, 3,849 bp were found to be chromosome-1 specific (see Figure

17; Example 7). As indicated in Fig. 17, the other clones contained shorter but completely overlapping sequences.

Example 7: Analysis of sequences flanking the constitutional t(1;17) translocation breakpoint

Sequences generated from both sides of the t(1;17)(p36.2;q11.2-q12.1) breakpoint in the derivative chromosome-17 and derivative chromosome-1 were analyzed for the presence of putative protein-encoding gene sequences by using both BLASTN and BLASTX to search public databases. This demonstrated that the breakpoint-flanking sequence adjacent to the chromosome-17 sequences were chromosome-1 derived as they show almost perfect identity with several unfinished or finished sequences of BAC clones (Genbank Acc. N° AL354666, AL356581, AC015618, AL355149, AL355800, AL022240, AL049715, AL137798 and AL049742), all mapping to chromosome 1. Regarding chromosome-1 sequences on derivative chromosome 17 (der17), high to perfect homology was also found between parts of this genomic sequence and at least eleven EST sequences (GenBank Acc. N° AL040932, AL045522, AA322028, AL043132, AA609104, AA350323, AL042839, AL044108, AL043174, AL037724 and AW160820) (Tables 5 and 6, and Figure 7). This confirmed the prediction of three consecutive exons, designated x, y and z as indicated in Figures 3, 5 and 6. These exons x to z encode a carboxy-terminal fragment of a novel protein. This protein shows no identity with so far known gene products. The extended size of this particular protein, and of highly related new proteins, became apparent upon sequencing the full-size inserts of the cDNA clones represented by the EST sequences mentioned (summarized in Fig. 7, Tables 5 and 6). Corresponding nucleotide sequences were deposited with GenBank (Table 6). The predictable sequences of the protein domains, encoded by exons of the x, y or z type, are aligned in Figs. 13 to 15.

Regarding breakpoint-flanking chromosome-1 sequences on derivative chromosome-1, high to perfect homology was found between parts of this genomic sequence and the sequences of at least six cDNA clones (EST sequences deposited with GenBank under Acc. N° AI570017, AW173183, H06312, AW468059, AA704208, AI239884). Full-size insert sequences were determined and deposited with GenBank (summarized in Fig. 21, Tables 5 and 6). This confirmed the prediction of two consecutive exons, designated A and B as indicated in Figures 17, 19 and 20. The predictable sequences of the protein domains, encoded by exons of the A or B type, are aligned in Figs. 11

and 12. These exons A and B encode an internal fragment of a novel protein, belonging to the same family as the protein with the carboxy-terminal sequence encoded by exons x, y and z, discussed above. This is apparent both from cDNA sequences, notably the full-size sequences of the cDNA clones depicted in Fig. 7 and Fig. 21, and from genomic sequences (see Example 8).

Example 8: Chromosome-1 derived exons flanking the t(1;17) translocation breakpoint belong to a large and novel gene family NBG

High homology was found between on the one hand the exons x, y and z (Figures 5 and 6) and the exons A and B (Figures 19 and 20) and on the other hand many more EST sequences than the one mentioned in Example 7 (e.g. Genbank Acc. N° AL037724, AI909921, AA705685, AA701673, AI570017, AW173183, AA350323, AI372468, F11837, AI049567, AW238577, AI537172, AI953463, ...) (Tables 5 and 6). This became further clear upon sequencing the full-size inserts of cDNA clones represented by several of the additional EST sequences mentioned (summarized in Fig. 22, Tables 5 and 6). High homology was observed also between on the one hand exons A, B, x and y, and on the other hand two cDNA clones (Acc N° AK000726 and AB033071) and predictable exons of one genomic sequence AL049715 and this was particularly obvious upon comparison of the encoded protein fragments (Table 5, Figs. 8 and 23). High homology was also found between exons A, B, x and z and the cDNA sequence AB051480; between exons x+y and cDNA sequences AF161426 and AI050141; between exons y-z and cDNA sequence AF131738; and between exons A+B and predictable exons of genomic sequence AL137798 (Table 5, Figs. 8 and 23). High homology was also found between exons A, B and x to z and the cDNA sequence AL117237, predicted on the basis of the genomic sequence AL022240 (derived from clone 328E19), the cDNA sequence AL136890, and predictable exons of the genomic sequences AL354666, AL356581 and AL022240 (Table 5; Figs. 8 and 23). When the sequences of the predicted exons in various representative cDNA and genomic clones were aligned with each other, separate classes could be discerned, as shown in Table 5, Figures 7 to 15, and Figures 21 to 23 (overview in Figs. 7, 8, 21 to 23; alignments and pedigrees in Figs. 9 to 15). In these figures, the three exons x to z correspond to, respectively, exon 11.1, exon 12.5 and carboxy-terminal exon 14.12, whereas exons A and B correspond to exons 6.12 and 7.1. On the basis of sequences from cDNA clone DKFZp434G2022 (AB25; Table 6 and Fig. 7) and from genomic

clones RP11-284O17 and RP11-45I3 (GeneBank Acc. Nos. AL355800.5 and AC015618.3), we could predict the structure of the transcript interrupted by the chromosomal t(1;17) translocation (Fig. 24). By the translocation event, a genomic segment of about 20 kbp and comprising exons of the types 8 to 13 appears to be
5 deleted (Fig. 24).

Within this new gene family, designated NBG (Neuroblastoma Breakpoint Gene family), 5' exons of types 0 and 1 (Table 5) were represented by cDNA clone hg04073 (encoding protein KIAA1245; GenBank Acc. No. AB033071; Fig. 8), cDNA clone HEP17004 (GenBank Acc. No. AK000726; Fig. 8), IMAGE cDNA clone 2226413
10 (clone AG09; Table 6 and Fig. 21), IMAGE cDNA clone 341197 (clone AE02; Table 6 and Fig. 21), genomic clones RP11-87L17 and RP5-1020C22 (GenBank Acc. Nos. AL354666 and AL356581; Fig. 23). A likely start codon is situated in exon type 1 and yields proteins with starting sequence MVVSAG... (Fig. 9).

Upon comparison of exons A, B, and x to z, which were found to flank the cloned
15 breakpoints of the der1 and der17 chromosomes, with the cDNA and genomic sequences obtained so far, the transcript interrupted by the chromosomal t(1;17) translocation was predicted to have the structure depicted on top in Fig. 24. It corresponds to the sequence of cDNA clone DKFZp434G2022 (clone AB25; Fig. 7 and Table 6; exon types 6.3 and 6.12 are very closely related [cf. Fig. 11] as they differ by
20 only two out of 68 amino acid residues due to two nucleotide differences), completed at the 5' end by sequences from unfinished genomic clones RP11-284O17 (GenBank Acc. No. AL355800) and RP11-45I3 (GenBank Acc. No. AC015618). Upon chromosomal translocation, a genomic region covering one exon of type 8, one exon of type 9, and several exons of type 10, 11, 12 and 13 are lost (Fig. 24). The total
25 sequence that is predicted to be deleted is therefore as large as ~20 kbp.

The interrupted gene on the der1 chromosome is transcribed into chimeric molecules, as demonstrated by a 3'-RACE experiment on mRNA from the 32-7A somatic cell hybrid. Two chimeric transcripts were cloned in this way. The fusion partner is in both cases located on chromosome 17. In one chimeric transcript, represented by eight
30 distinct clones, the exon-7.1 sequence is spliced to chromosome-17 sequences at 338 nt from the breakpoint, and this yields a transcript extended by 295 additional nucleotides and an ORF extended by 34 additional codons in frame (represented by X in Figures 24 and 25; sequence depicted in Fig. 26; deposited with GenBank under Acc. No. AF420438). In a second chimeric transcript, represented by a single clone,

the exon-7.1 sequence is spliced to chromosome-17 sequences at 8,602 nt from the breakpoint according to the BAC sequence with GenBank Acc. No. AC024614.3. This yields a transcript extended by 325 additional nucleotides and an ORF extended by 11 additional codons in frame (represented by Y in Fig. 25; sequence depicted in Fig. 27; deposited with GenBank under Acc. No. AF420439). A reciprocal experiment aimed at identifying chimeric transcripts by 5'-RACE from somatic cell hybrid 32-2F53VIII and several more cell lines. Although many gene-specific fragments were detected illustrating the widespread expression of NBG family members (Fig. 28), no chimeric transcripts could be cloned so far from these 5'-RACE experiments.

Unusual features were also observed in several cDNA clones corresponding to this new NBG family: translation frameshifts (e.g. cDNA clones AG07 and AE01 in Fig. 7, cDNA clone AB033071 in Fig. 8, cDNA clones AG09 and AG10 in Fig. 21), and retention of intronic sequences (e.g. cDNA clones AD02 and AB06 in Fig. 7; cDNA clone AI050141 in Fig. 8, cDNA clone AB23 in Fig. 21; cDNA clones AB13 and AB14 in Fig. 22). Such intronic sequences were also found in 5'-RACE products of 32-2F53VIII, TR-14 and SK-N-SH cells (Fig. 28).

We addressed the number of different human NBG genes by checking the occurrence of nonidentical exon-7, -8 and -9 sequences in contiguous genomic sequences of the public-domain human genome resources. To our knowledge, these three exon types occur only once per transcript as exemplified in Figs. 7, 8 and 21. From the data, listed in Table 7, we conclude that there about 15 different NBG genes, mainly localized on chromosome arms 1p and 1q.

No homologous or orthologous sequences for this novel gene family NBG were found in the genomes of either *Saccharomyces cerevisiae*, *Drosophila melanogaster* or *Caenorhabditis elegans*. The repetitive nature of the transcripts and proteins, encoded by this novel gene family, is particularly striking (Figs. 7, 8, 22 and 23). Nevertheless, upon screening various protein domain databases, no significant matches were found. These databases include: InterPro (URL <http://www.ebi.ac.uk/interpro/>), ProSite (URL <http://www.expasy.ch/prosite/>), Blocks (URL <http://www.blocks.fhcrc.org>), Prints (URL <http://www.biochem.ucl.ac.uk/bsm/dbbrowser/PRINTS/PRINTS.html>), PFAM (URL <http://genome.wustl.edu/Pfam>), and other databases. In conclusion, this failure to detect known protein domains points at a fully novel protein structure and innovative functions for the gene family members described above.

Example 9: Chimeric transcripts of the novel gene family in other tumor types besides neuroblastoma

Analysis of the non-redundant database and the EST-database at NCBI, resulted in the identification of two chimeric transcripts showing homology to the novel NBG gene family (Fig. 25). The first one, cDNA clone Y79AA1001711 (GenBank Acc. No. AK024044) was derived from the human retinoblastoma cell line Y79, and consists of 552 nucleotides of a NBG family member, followed by 5 unrelated nucleotides and 1,657 nucleotides of the SSA2 transcript (Sjogren syndrome antigen A2; 60-kDa ribonucleoprotein autoantigen SS-A/Ro) (nucleotides 1-1,657 of the GenBank sequence with Acc. No. XM_029851.1), encoded by the Sjogren syndrome gene SSA2 located at chromosome 1q31. The second chimeric transcript, cDNA clone IMAGE:3698601 (complement of sequence with GenBank Acc. No. BF478071.1) was derived from pooled germ cell tumors, and comprises some 75 NBG-specific nucleotides (encoding the exon-11 like peptide sequence TPTSCLEQPDSSQPYGSSFYALEEK), followed by a stretch of 9 A nucleotides, and 288 nucleotides of the 3' UTR of the transcript encoding human coatamer protein complex, subunit alpha (corresponding to nucleotides 4,735-5,022 of the GenBank sequence with Acc. No. XM_049690.1; gene LOC113148 on chromosome 1q).

Example 10: NBG mRNA expression analysis

A Northern blot was hybridized with two separate NBG-specific probes. In the first hybridisation, a 5'-specific probe was used. This resulted in a strong signal in the neuroblastoma cell lines SH-SY5Y, IMR-32, SK-N-AS and SK-N-SH, but no detectable signal in TR-14, which contains double minutes (Fig. 29, upper panel). Human non-neuroblastoma cell lines (MCF7/AZ, HEK293T, Colo320DM, and HCT8/R1) showed lower expression levels. No detectable signal was seen for mouse cell lines NMe and Neuro2A. When a 3'-specific probe was used, the signal resembled the signal from the 5' probe, but with an additional band of approximately 500 bp that was detected in HCT8/E8 (Fig. 29). The signal intensities were measured and normalized on the basis of the GAPDH transcript in the respective cell lines. The normalized values were graphically compared (Fig. 29, lower panel) and this emphasized the high expression level in SH-SY5Y.

The expression analysis of NBG family members was extended by RT-PCR experiments on either human fetal brain (HFB) RNA (using primers in exon 6 and exon

9) or on 32-2F53VIII RNA (using primers in exon 10 and exon 14). The cloned RT-PCR products were sequenced as depicted in Fig. 37. The products were specific for the NBG family but yielded also new exonic variants. Several splice variants of exon 8 were observed (exon 8.3, 8.14, 8.13, as well as removal of exon 8; Fig. 37), and this in line with the presence of a frameshift between exon 8 and exon 9 in cDNA clones AB033071 (Fig. 8) and Y79AA1001711 (see Example 9 and Fig. 25).

Example 11: NBG protein expression generates micronuclei

To study the function of this novel NBG gene family, several eukaryotic expression plasmids were constructed. To generate a representative full-length cDNA clone, sequences from two distinct cDNA clones were fused (Fig. 30). This full-length construct pBlueKIAA-AB25 was then tagged with either an aminoterminal Myc-epitope, or a carboxyterminal Myc-epitope, or an eGFP protein, yielding constructs pCS2+MT-KIAA-AB25, pEF6/Myc-His-B-KIAA-AB25 and pEGFP-C3-KIAA-AB25, respectively. The two distinct parts (aminoterminal and carboxyterminal half) were also separately coupled to eGFP (constructs pEGFP-N3-KIAA-AT and pEGFP-C3-AB25-CT, respectively), whereas the aminoterminal domain was also tagged with a Myc-epitope (construct pEF6/Myc-His-A-KIAA-AT).

These expression vectors were transfected into several human cell lines including mammary gland tumor cells MCF7/AZ (Figs. 31 and 32), colon tumor cells HCT8/E8 (Fig. 33), embryonic kidney cells HEK293T (Fig. 34, top panels), colon tumor cells Colo320DM (Fig. 34, middle and bottom panels), and also into the mouse mammary gland cell line NMe (Fig. 35). The ectopically expressed proteins were detected by use of an anti-Myc antibody or by GFP fluorescence. These proteins showed a preferential cytoplasmic localization with only 5% of the transfected cells showing nuclear staining (the latter exemplified in Fig. 31E). Comparable results were obtained for constructs expressing either GFP-tagged or Myc-tagged proteins. Staining of the endoplasmic reticulum did not show colocalization with the NBG product (Fig. 32A-C). Transfection of human cells with the full-size NBG constructs resulted in increased incidence of micronuclei-containing cells (illustrated by arrows in Fig. 31I-L; Fig. 32A-F; Fig. 33A,B; Fig. 34A,B,E,F). Staining of the nuclear lamina using an anti-lamin B1 antibody confirmed clearly the presence of micronuclei (Fig. 32,D-F), which were generally also detectable by DAPI-mediated DNA-staining (most right panels of each combination in Figs. 31-36). Transfections of backbone vectors served as negative controls and did

not yield high levels of micronuclei (Fig. 32G-J; Fig. 33G,H; Fig. 34G,H). Transfections of mouse NMe cells (Fig. 35) were particularly useful to demonstrate clearly the potential of the NBG proteins, as these cells lack endogenous NBG proteins. A high number of micronucleus-like structures was induced by full-size NBG protein in NMe cells (illustrated by the arrows Fig. 35A,B,E,F), whereas such structures were not detectable in control transfectants (Fig. 35G-J). According to DAPI staining, the NBG-induced cytoplasmic structures lacked DNA and this might point at molecules lacking in mouse and cooperating with NBG proteins in human cells in order to remove excessive DNA from the nucleus. Altogether, these data indicate that the NBG proteins can remove amplified DNA from human cells by inducing or enhancing micronuclei generation.

Transfections of plasmids encoding amino- or carboxyterminally truncated NBG proteins were also associated with micronuclei generation, although an aminoterminal fragment (illustrated in Fig. 31A-D; Fig. 33C,D; Fig. 34C,D; Fig. 34I,J; Fig. 35C,D) appeared to be less efficient than a carboxyterminal fragment (illustrated in Fig. 31E-H; Fig. 33E,F; Fig. 34K,L). Transfection into MCF7/AZ cells of plasmids encoding the two NBG chimeric cDNAs isolated by 3'-RACE from 32-7A cells (see Example 8) was featured by the formation of multiple vesicle-like structures in the cytoplasm, which were apparently lacking DNA (Fig. 36A,C). Some micronuclei were still visible in these transfected cells (Fig. 36A). From this, we conclude that these chimeric NBG transcripts are reorganizing the cytoplasmic organelles and interfere with the removal of excessive DNA such as amplified oncogenic DNA in cancer cells.

Example 12: NBG-specific antibodies

Polyclonal antibodies were raised against NBG-specific peptides. For example, rabbit polyclonal antibody #31226 was raised against peptide #1061 with sequence NH₂-PEILQDSLDRSYSTPSM-COOH. MCF7/AZ cells were transfected with a construct encoding a Myc-tagged full-length NBG protein. Fig. 38 illustrates that an anti-Myc antibody (A) and polyclonal antibody #31226 (B) produce overlapping staining patterns, pointing at the specificity of the polyclonal antibody. Non-transfected cells were not stained by anti-Myc antibody and only very lightly stained by polyclonal antibody #31226. The same polyclonal antibody was used in combination with anti-lamin B1 antibodies in order to allow identification of NBG-transfected cells (illustrated in Fig. 32D).

Table 1: Newly developed sequence-tagged sites (STS) obtained from sequenced PAC end clones: primer sequences, product size and annealing temperature

Marker (PAC clone end)	primer 1 (5'-3' sequence)	primer 2 (5'-3' sequence)	product size (bp)	annealing temperature
RPCI-1 880L8 SP6	GGCCATGTGAACCAATTCTG	GGAGAGCTGAGTGAGGAGGG	421	58°C
RPCI-1 243F6 SP6	CGCCTGGCCTATTTACATGT	TGCAGCCCATAAATACCCAC	451	55°C
RPCI-1 252F1 T7	CCTCGAGCTGAAGCCAAATT	TGGCCTCCATGCTGTAGGAT	151	56°C
RPCI-1 59J12 SP6	TCAAACCCCGACTTTCAGAT	TCTGTGCTGCCCTGGATTAC	501	58°C
RPCI-1 928F18 T7	GCCTGTTTCATCAAAATGCCTG	GGAGAAATGGCACAGAGGTGA	201	59°C
RPCI-1 841C13 T7	GAGACCAAGTTCTTTCCCGAG	GAGACCAAGTTCTTTCCCGAG	251	54°C
RPCI-1 841C13 SP6	ACAAGCAAGACTGTGAAGCCC	GGCTTCCTGTTTCTCCTCCAG	251	60°C
RPCI-1 605A3 T7	GCCTATCAGGCCATGATCCA	GGACTCCAGGACAGTGGCAT	151	58°C
RPCI-1 829O10 SP6	ACCCCATCTCTTTCCAGCAT	TTGCCTGGCATTTCATCTAGA	201	54°C
RPCI-1 829O10 T7	GGGTCCCTGGTAGTTAACGA	CCAACTCCTGACCCCCAGAA	481	56°C
RPCI-1 105C17 T7	ATGGATGGGTAAACTGAGGCC	GCTGACTTCCTGAGGGAGGC	151	60°C
RPCI-1 1167N14 SP6	CACCCAACTTTCCATGAGCTC	TGGTGGTGTACCCCTTGAC	301	59°C

Table 2: List of PAC and cosmid clones, screened by hybridization with the YAC, PAC, STS, and end clones indicated, and confirmed to be positive for hybridization (FISH) on chromosome band 17q11.2

Screening with	Clone type	Positive clones
cC117-1079	cosmid	RPCI-1 55N16, 118B4, 266J21
STS D17S1850	STS	RPCI-1 243F6
STS WI-2906	STS	RPCI-1 243F6, 107O9, 52F12, 59J12, 110I13, 107O9
4p728-f-1	YAC	RPCI-1 101G3, 194A10, 243F6, 107O9, 252F1
15FD11	YAC	RPCI-1 257G22
RPCI-1 266J21	PAC	RPCI-1 266J21, 257G22, 655N1, 163O13
776-d-7 (end clones)	YAC end	RPCI-1 201O9, 129G2
STS D17S798	STS	RPCI-1 32H9, 153M23
681-c-3 (end clones)	YAC end	RPCI-1 1027N14, 928F18, 1020I1, 880L8, 1167N14, 710N14, 841C13, 2H10, 863N19, 678O5, 624A6, 314I17
RPCI-1 243F6	PAC	RPCI-1 1188C15, 572L14, 1105H14, 952I18, 682F9, 921H21, 626M5
RPCI-1 880L8	PAC	ICRFc105F1060D1, ICRFc105E08156D1, ICRFc105B0832D1, ICRFc105C0471D1, ICRFc105B08115D1, ICRFc105F1065D1, ICRFc105B07149D1, ICRFc105H1244D1, ICRFc105G0372D1, ICRFc105C04161D1, ICRFc105F09116D1
RPCI-1 880L8 (end clones)	PAC end	RPCI-1 829O10, 733P21, 835C10, 758F20, 605A3, 758E20
RPCI-1 835C10	PAC	RPCI-1 79I2, 91O8, 105C17, 307B7, 542I11, 1167N14

Table 3: Determination of PAC clone insert sizes by FIGE

PAC clone	insert size
RPCI-1 257G22	~87 kb
RPCI-1 55N16	304 kb
RPCI-1 118B4	94 kb
RPCI-1 243F6	129 kb
RPCI-1 252F1	126 kb
RPCI-1 201O9	141kb
RPCI-1 129G2	141 kb
RPCI-1 1027N14	~ 130 kb
RPCI-1 928F18	170 kb
RPCI-1 1020I1	70 kb
RPCI-1 880L8	140 kb
RPCI-1 710N14	~ 155 kb
RPCI-1 841C13	~ 98 kb
RPCI-1 2H10	~ 98 kb
RPCI-1 863N19	~ 155 kb
RPCI-1 678O5	~ 100 kb
RPCI-1 624A6	112 kb
RPCI-1 572L14	~ 55-60 kb
RPCI-1 194A10	83 kb
RPCI-1 32H9	88 kb
RPCI-1 153M23	77 kb
RPCI-1 829O10	80 kb
RPCI-1 266J21	105 kb

Table 4. Sequences of 9 hybridization probes, specific for human chromosome 17 and generated by PCR on cosmid DNA template.

Probe N ^o .	# 1	
Primer ^a	(+) 5'-gaactgtcgccactcgtctg-3'	(-) 5'-acaccacagcgggatgatgt-3'
Position ^b	9,359	9,874

Probe sequence	gaactgtcgccactcgtctggatgtgcatcgcaagctgccctgcgagtgctgtcaattgcaaattcagcaattaggact cagcatcaggcagctggaatgacacttcctctagtgaagcctcagagagcttacttatgccactcattcagatggaga gcaaggggttgaaattgccccctctagagcccctgctgcactctgcaccgtatggcaaggttgatcaggcagagctt gtcctcaagaagcccgcagctcgtctggagagaggtgggcagtaaacacatgctccagctgtagccatgtccctgt ctggaccagttaactcaattcagttcaactgcagacagctcctcaagccaatcagacatcagagaaataaaaagg atgtgacaaaagagagtgaggtggagaacacagctcctcctctggacaaactgctctggaaagttgcacttgga ggtagatggggatgaagccaacacatcatcccgtgtgtgt	
Probe N ^o	# 2	
Primer ^a	(+) 5'-aaccccgagtgtgtctgaaa-3'	(-) 5'-ccattcccaagcacctcat-3'
Position ^b	14,748	15,536
Probe sequence	aaccocgagtgtgtgtaaataaaaaggctatgaagaagcagaagtcctgtgaaggtgtgttgggaaagagaattgtt cagatatgggtaagccactgaaaggtgtcttgatggttcactgaacatgggctgagaacctgaagcagatacagaaa gcaagatgaccatgctggaacaatgaggacagggaggatgggcagagtggctagggagaaggaggtcttgatg aacatctgagatagaaaatgccccctctggcggctcatgtgtgtcctctgatcacatgctctgacatggcaggccccag ccattctccttacgaacgacactgctgggaatccctactgggcacacacaaccagctacaagatagagtgtcc aaacccccatcctgggctgtgtgtggaagatgaacacaccgactggctacgctgcagtactgcattcttctggc tggttggaagcaaaactccactgccttctccccaggcctgacccattatgacaatggagccattgttctgaacagg ggcatgaggcagctgggactggccgaccctatgctggctcctcacatctcagaagcaagccctcagacagatcaa ggaaagtataaaattcagcgggaagcaggacagagtattggggctctgagccagcttctcctctcagttctgtatc gtgatgggaatgaataatcaccccaattacagagcaacctgaaggagacaaaataccttaactaaatgaggtgcttg gggaatgg	
Probe N ^o	# 3	
Primer ^a	(+) 5'-agagctgcacggcacttctc-3'	(-) 5'-cacgatgcaaaacgaactac-3'
Position ^b	18,773	19,237
Probe sequence	agagctgcacggcacttctcagcccacaagcccacttccatgcaccaagcccacccaccttacacttgccccctgg ctccttaaccttgagctcagcctccatcttaagggttcaccaagctgcccttcactatccggtctgttgagatttccagcta gactctgctagccacgctcgtactctgttgaccagctcccgaggagaagccaagccgactcccttcactcctctgc ccccgctgctgtcttacacagccgtaccttcttcttccccctctcttggtgtgtgagccacatttagcaccagcct ccaagagcaagcacccctgtgtaacttgggctcgtgtctgcgaagctaccaccctgatcttagaaacccgaagctcag aaaatagttcctatcttatgtgcgttatactctcaagaaggtagttcgttttgcacgtg	
Probe N ^o	# 4	
Primer ^a	(+) 5'-gtttggggagattttgagtgtg-3'	(-) 5'-gggcagcagaccttagcaact-3'
Position ^b	24,246	24,723

Probe sequence	gtttggggagattttgagtggtgggtggcagaaggcttttaggtgggtcacagtgcagcgggcccagaccacaa gcacagatattctagaactgggtttctacatcagactactactgtgagagccaagaggctcaaagccccagaggt gactcattttccagccctccgctcctcctgctgtccaggatcttgatcatccattatcagaactgctggaggaatc atctggaaggcttgaagtactggggggcatccgctgggtgtgagagctgctcggaggggtccctgtctgtccagtc acctctccacccaccttatgtgtgacccctgccaggactggacctccattcaactcttctgagcagaaggagcag aaaccatcctatctgactggcctggaatggacagtgtccccagcatggttctagggagttgctaaggctgtgtgcc c	
Probe N°	# 5	
Primer ^a	(+) 5'-tccaaaaggccagttcacac-3'	(-) 5'-tctcaggcgctctcatctcaac-3'
Position ^b	30,057	30,734
Probe sequence	tccaaaaggccagttcacacactccattaatgtgggtgccactgggacaattacagacagacagctttccatttg agcaacttctaaattaaaaagcaactgtgcaggaaggaaggagacatgtggctgtctactacagacctgtaaaa ggaggttcttctatgtattacccacccctccataccttctctaccacacacaagagctgaaataaaagttgcatt tcactgtgtgtggctgtattttttacactcctgttaaaaaaaaaaaaaagttctacttaaaaaaaaaatacatcacc caaacatgtctgagatttttgaaggcttgggtctgaaccagtcctttgataggggcattttcttagcctgtgtggcta aagatgggcatggtcggatttactcgcttgattagatggacttggccctaataatttttcttaattatttccaatttta agtgctccaagagatagctttgactttccacccagcctgtgtatgttcttcttaggaactgtacatctttaatacaac ctgtattcaagttctccttataggacctgagagattcaactggcagcatttaggactaccaggaatctccagctgtggcgttg agatgagacgcctgcaga	
Probe N°	# 6	
Primer ^a	(+) 5'-cccctcagctctgtgcat-3'	(-) 5'-tccctgctgaatgagtgttg-3'
Position ^b	36,914	37,391
Probe sequence	cccctcagctctgtgcatttgtctacaagcaagggtgactttgggttagtgtgtcatgtttcaacaagaatgtaagttggg atcagacatatgttaccctgttgatagtagctttgcaatcagctcttgcaaaaaatatccagaacaaggctagaacaa gggtgtacagaacaaataacacgtgttacagttacatatgagcttgattacctcctttatagaaggaagtggagacat ccttcagcagagatttaggatctctactagcactaacctcttgccccacctagtggtttattcaatcacccctgtgtcttt tatcaaatgaaagatacagatccacttttaagagtaaagaagagaggaagcacagttattaattaccattggtatccc aaggacttgtgtctccattatctcattgttttattcattcattaatccaaacactcattcagcagga	
Probe N°	# 7	
Primer ^a	(+) 5'-gaacctggtctacaaattatac-3'	(-) 5'-gactgggaccaattgttcttc-3'
Position ^b	42,102	42,774

Probe sequence	gaacctggtctacaaattatacaccctggcatgtccaaaagcaaatgctgcctacatctcctgaaaatgcaggaatgtcagaaaagctgctgaagtgggtggctaccaggagctccaggggcctagcaccactcccagcccagccctggggtg gggaggggtggtctcttcagagtggctcatttttagagctgactaccaagtcagaagaacaacgttttaatatatcg ggcagcagagcagctagatattaaggttcttcttgaggacatcatgaaatattgtcatgacgacctgacctgggtt ggcgcggggtgctcttcagagtggctcatttttagagctgacttccaagtcagaagaacaacttttaaatcgtcgg gtaacagagcagctagacattacggttcttcttgagaacatcatgaaatattgatgttaagctaaaacgaatataataa atgtatgattgctgctaaattggcattatcttttagattctggttgacagaaagtagcaggcccaatgggttaagaa agaaaggaaaaaatttttaattgaggaaatcatatccacgtcttttttaattgttgaaaagatgtccacagtcagattt cagaggaagaacaaattgtccagtc	
Probe N°	# 8	
Primer ^a	(+) 5'-gtacaccactcacctgtgat-3'	(-) 5'-tctaaggggaaaagtaaaca-3'
Position ^b	46,377	47,137
Probe sequence	gtacaccactcacctgtgatgtactaatggagcaggagggaacaggctgcatcaaagctaactcctggaaatga cctagaacccacagcctgtctcagccgtgctgcatgttcagcagggaaacaaagcgactgtgtattatgtaaattact tacctgataataaaatgtttgtggttgataaattgaacggatataattgttcttcaccccccccactagtggcaaaa gctgctctgtatgaatctgagtacatttctgtgacagtattcctcatatgtacagcattctatgtgaatcatctccaaaaattg ccatggggtcattatccccagttctaactagagaaactgagattctggaagtcctctgaatggccatacttcccagg tgtctctgcaggaaacaatgtggacaatcacagtagttggaaggacaatgactgacctaattggagttcaggacgctat gactgttgccacctgatgtgcacagctgctccatctgcgcagagagaatataaaggcagtgggcgtgaaacatctgc tgcttctcactccatcaagatggaactgactgtacatgcaagcaattttgatgaagagagtgatctcagagtgcgaa gataagttgttctcttgacacctaggaatgcacctggccaagaccctcagttgaaagacaatatcaataaatgcaa aatctaaatatccatgtgctgtttactttcccccttaga	
Probe N°.	# 9	
Primer ^a	(+) 5'-gtgtaccccccttgactca-3'	(-) 5'-gtgccagcaggagattcaat-3'
Position ^b	38,018	38,584
Probe sequence	gggtgaccccccttgacttcacctgaatgtcagggaaggccaggagcatgcaggaggctaaagattgggaacccct attctgggcttctcccatcttcttgagcaattggaagaggcccatgggaggagggtgactgtcatgatgtcccca ctatgaactatgggaatggctggagggtcactgggctggtgctccagctgctgacctgcagggaagtgttacctgc aggacctacagtgggagtggtgacaccctggctctgggaaggagctcatggaagtgggtgaacttctgttagac tacgcaggcttcagaagtgcattccatacggagtgggtggcctcccaggaggagcagagggcagccactgga acaagctacagctacaaaagaccacotttatccctctcaagttctccagggggccctgtgtctgctgtactagagga agtttcaaaggatttcttcccccaggatgaagaatgaggccacactgccaagcaagatctgtgctatgtgtgattg aatctcctgctgggcac	

a. The primers were designed on a genomic 51,050-bp sequence of human chromosome 17, obtained by shotgun cloning and DNA sequencing of three overlapping cosmids (Genbank Acc. No. AF148647).

b. Position refer to the location in the 51,050-bp sequence (Genbank Acc. No. AF148647).

Table 5: Overview of exons of a novel gene family, comprising tumor suppressor genes

Exon type ¹	Exon name ²	Size #aa	Source (clone name) ³			Remark
			Type4	Genbank Acc. No.	Clone No.	
ex0.1	B02AT09	11	BAC	AL356581.2	RP5-1020C22	
	B01AT14	11	BAC	AL354666.3	RP11-87L17	
	KIA-AT00	11	cDNA	AB033071	KIAA1245	
ex0.2	AK00AT00	13	cDNA	AK00726	HEP17004	
ex0.3	AE02AT01	11	EST checked	W58508	zd20d07.s1	
ex1.1	B01AT08	70	BAC	AL354666.3	RP11-87L17	
	B02AT14	70	BAC	AL356581.2	RP5-1020C22	
ex1.2	AK00AT05	70	cDNA	AK00726	HEP17004	
		70	BAC	AC060753.8	RP11-285C11	
ex1.3	KIA-AT06	70	cDNA	AB033071	KIAA1245	
	KIA-AT11	70	cDNA	AB033071	KIAA1245	
ex1.5		70	BAC	AL359176.4	RP11-47D6	
	AK00AT01	70	cDNA	AK00726	RP11-47D6	
		70	BAC	AL109937.4	HSJ322E17	
		70	BAC	AC060753.8	RP11-285C11	
ex1.6	KIA-AT01	70	cDNA	AB033071	KIAA1245	
		70	BAC	AL359176.4	RP11-47D6	
ex1.7	B01AT13	70	BAC	AL354666.3	RP11-87L17	
		70	BAC	AL355149	RP5-875O13	
		70	BAC	AL355800.5	RP11-284O17	

		70	BAC	AC084206.1	RP11-305B17	
		70	BAC	AC015618.3	RP11-45I3	
		70	BAC	AL137798.8	RP5-1182A14	
ex1.8	B02AT08	70	BAC	AL356581.2	RP5-1020C22	
ex1.9	AE02AT02	67	EST checked	W58508	zd20d07.s1	partial
ex1.10	ex1.A	70	BAC	AL109937.4	HSJ322E17	
		70	BAC	AL138796.3	RP4-791M13	
ex1.11	ex1.B	70	BAC	AL109937.4	HSJ322E17	
	AG10AT02	70	EST checked	AW173183	IMAGp998J126649Q2	
ex1.12	ex1.C	70	BAC	AL355149	RP5-875O13	
ex1.13	ex1.D	70	BAC	AL355800.5	RP11-284O17	
	ex1.E	70	BAC	AL355800.5	RP11-284O17	
	ex1.F	70	BAC	AC015618.3	RP11-45I3	
	ex1.G	70	BAC	AC015618.3	RP11-45I3	
		70	BAC	AL137798.8	RP5-1182A14	2 X in this BAC
		70	cDNA	AB051480	KIAA1693	
ex1.14	ex1.H	70	BAC	AC027727.3	RP11-18B10	
		70	BAC	AC026900.3	RP11-798G11	
ex1.15	ex1.I	70	BAC	AC027727.3	RP11-18B10	
		70	BAC	AC026900.3	RP11-798G11	
ex1.16	ex1.M	70	BAC	AC018381.3	RP11-5G21	
	ex1.O	70	BAC	AL359093.9	RP11-35B4	
	ex1.Q	70	BAC	AC018729.3	RP11-1F5	
	ex1.R	70	BAC	AC018729.3	RP11-1F5	stop codon!!
		70	BAC	AL049715.25	RP4-646P11	

ex1.17	ex1.J	70	BAC	AC027209.2	RP11-277H3	
	ex1.K	70	BAC	AL390296.3	RP11-555C20	
ex1.18	ex1.U	70	BAC	AC079074.1	CTD-2386B2	
ex1.19	ex1.L	70	BAC	AL390296.3	RP11-555C20	
ex1.20	ex1.N	70	BAC	AC018381.3	RP11-5G21	
		70	BAC	AC007734.3	RP11-44O1	
ex1.21	ex1.P	70	BAC	AL359093.9	RP11-35B4	
		70	BAC	AC024119.2	RP11-542J23	
		70	BAC	AC073223.4	RP11580F15	
ex1.22	ex1.S	70	BAC	AL391068.7	RP11-288L16	
	ex1.T	70	BAC	AC026565.3	RP11-702G12	
ex1.23	ex1.V	70	BAC	AC013673.2	RP11-20I21	
	ex1.W	70	BAC	AL356004.4	RP11-94I2	
		70	BAC	AL049742.7	RP4-565E6	
ex1.24	ex1.X	70	BAC	AL359752.7	RP5-1042I8	
ex1.25	ex1.Y	71	BAC	AC013627.3	RP11-11L4	71 AZ !!
	ex1.Z	71	BAC	AL359258.4	RP11-483I13	
	ex1.AA	71	BAC	AL356110.1	RP4-562N20	
	ex1.AB	71	BAC	AL390038.5	RP11-131J3	
ex1.26		70	BAC	AL049742.7	RP4-565E6	
ex1.27		70	BAC	AL049715.25	RP4-646P11	
ex2.1	KIA-AT07	35	cDNA	AB033071	KIAA1245	
	KIA-AT12	35	cDNA	AB033071	KIAA1245	
		35	BAC	AL359176.4	RP11-47D6	
ex2.2	AK00AT06	35	cDNA	AK00726	HEP17004	

ex2.3	AC01AT01	35	EST checked	AL042283	DKFZp434L1620	
		35	cDNA	AB051480	KIAA1693	
	KIA-AT02	35	cDNA	AB033071	KIAA1245	2 X in this cDNA
		35	BAC	AC015618.3	RP11-45I3	
		35	BAC	AL109937.4	RP3-322E17	
		35	BAC	AL355800.5	RP11284O17	
		35	BAC	AL356004.4	RP11-94I2	
		35	BAC	AC024119.2	RP11-542J23	
		35	BAC	AC023990.1	RP11-510K4	
		35	BAC	AC018729.3	RP11-1F5	
		35	BAC	AL138796.3	RP4-791M13	
		35	BAC	AC073223.4	RP11-580F15	
		35	BAC	AL359093.9	RP11-35B4	2X in this BAC
		35	BAC	AC018381.3	RP11-5G21	2X in this BAC
		35	BAC	AC027727.3	RP11-18B10	
		35	BAC	AL359176.4	RP11-47D6	
ex2.4		35	BAC	AC026900.3	RP11-798G11	2X in this BAC
		35	BAC	AL355149.4	RP5-875O13	
ex2.5	AL117AT1	29	pred. cDNA	AC007734.3	RP11-44O1	2X in this BAC
				AL117237	HS328E191	partial
ex2.5	B01AT07	35	BAC	AL354666.3	RP11-87L17	
	B02AT10	35	BAC	AL356581.2	RP5-1020C22	
		35	BAC	AC079074.1	CTD-2386B2	
		35	BAC	AC021397.3		
		35	BAC	AC015618.3	RP11-45I3	2X in this BAC

	35	BAC	AC060753.8	RP11-285C11	
	35	BAC	AL109937.4	RP3-322E17	
	35	BAC	AC084209.1	RP11-305B17	3X in this BAC
	35	BAC	AC027209.2	RP11-277H3	
	35	BAC	AL355800.5	RP11284O17	2X in this BAC
	35	BAC	AL356004.4	RP11-94I2	
	35	BAC	AL356581.4	RP5-1020C22	
	35	BAC	AL022240.8	RP3-328E19	
	35	BAC	AL049742.7	RP4-565E6	
	35	BAC	AL137798.8	RP5-1182A14	
	35	EST checked	AW173183	IMAGp998J126649Q2	
ex2.6	B01AT12	BAC	AL354666.3	RP11-87L17	
ex2.7	B02AT07	BAC	AL356581.2	RP5-1020C22	
		BAC	AL356581.4	RP5-1020C22	
ex2.8	ex2.A	BAC	AC060753.8	RP11-285C11	
		BAC	AL109937.4	RP3-322E17	
ex2.9	ex2.B	BAC	AC027209.2	RP11-277H3	
ex2.10	ex2.C	BAC	AL355149.4	RP5-875O13	
ex2.11	ex2.D	BAC	AL390296.3	RP11-555C20	
ex2.12	ex2.E	BAC	AL359752.7	RP5-1042I8	
ex2.13	ex2.F	BAC	AC024491.4	RP11-139D23	
ex2.14	ex2.G	BAC	AC053486.4	RP11-100A19	34 AZ !!!
ex2.15	ex2.H	BAC	AC026565.3	RP11-702G12	
	ex2.I	BAC	AL391068.7	RP11-288L16	
ex2.16	ex2.J	BAC	AC015706.3	RP11-325P15	

ex2.17	ex2.K	34	BAC	AL356110.1	RP4-562N20	34 AZ !!!
	ex2.L	34	BAC	AL359258.4	RP11-483I13	
	ex2.M	34	BAC	AL390038.5	RP131J3	
	ex2.N	34	BAC	AC013627.3	RP11-11L4	
ex2.18	ex2.O	35	BAC	AC024468.3	RP11-495P10	
	ex2.P	35	BAC	AC018593.3	RP11-21M21	
	ex2.Q	35	BAC	AL162612.3	RP4-691G10	
	ex2.S	35	BAC	AC025992.3	RP11-277L2	
	ex2.T	35	BAC	AL358813.4	RP11-353N4	
ex2.19	ex2.R	35	BAC	AC068979.9	RP11-134C18	
ex2.21		35	BAC	AL049715.25	RP4-646P11	2 X in this BAC
		35	BAC	AL137798.8	RP5-1182A14	
		35	BAC	AL049742.7	RP4-565E6	
ex2.22		35	BAC	AL137798.8	RP5-1182A14	
ex3.1	KIA-AT08	71	cDNA	AB033071	KIAA1245	
	KIA-AT13	71	cDNA	AB033071	KIAA1245	
		71	BAC	AL356004.4	RP11-94I2	2X in this BAC
		71	BAC	AL359093.9	RP11-35B4	
		71	BAC	AL359176.4	RP11-47D6	
		71	BAC	AL049742.7	RP4-565E6	2 X in this BAC
ex3.2	AK00AT02	71	cDNA	AK00726	HEP17004	
		71	BAC	AC060753.8	RP11-285C11	
		71	BAC	AL109937.4	HSJ322E17	
ex3.3	AK00AT07	71	cDNA	AK00726	HEP17004	
	AL117AT02	71	pred. cDNA	AL117237	HS328E191	

	AC01AT02	71	EST checked	AL042283	DKFZp434L1620	
		71	BAC	AC007734.3	RP11-44O1	
		71	BAC	AC060753.8	RP11-285C11	
		71	BAC	AC026900.3	RP11-798G11	
		71	BAC	AC018381.3	RP11-5G21	
		71	BAC	AL109937.4	HSJ322E17	2X in this BAC
		71	BAC	AC027727.3	RP11-18B10	
		71	BAC	AL138796.3	RP4-791M13	
		71	BAC	AL022240.8	RP3-328E19	
		71	cDNA	AB033071	KIAA1245	
ex3.4	KIA-AT03	71				
ex3.5	B01AT06	71	BAC	AL354666.5	RP11-87L17	
	B01AT11	71	BAC	AL354666.5	RP11-87L17	
	AE4AT01'	71	EST checked	AI239884	IMAGp998N074517	
	AB23AT01	71	EST checked	AI239884	IMAGp998N074517	
		71	BAC	AC015618.3	RP11-45I3	
ex3.6		71	BAC	AL355800.5	RP11-284O17	
	B02AT06	71	BAC	AL356581.4	RP5-1020C22	
	B02AT11	71	BAC	AL356581.4	RP5-1020C22	
		71	BAC	AL355149.4	RP5-875O13	2X in this BAC
	AG10AT04	71	EST checked	AW173183	IMAGp998J126649Q2	
ex3.7	AE03AT02	71	EST checked	H06312	IMAGp998I02268	
ex3.8	ex3.A	71	BAC	AC007734.3	RP11-44O1	
	ex3.D	71	BAC	AC018381.3	RP11-5G21	
ex3.9	ex3.B	71	BAC	AC026900.3	RP11-798G11	
	ex3.I	71	BAC	AC027727.3	RP11-18B10	

ex3.10	ex3.C	71	BAC	AL359176.4	RP11-47D6	
ex3.11	ex3.E	71	BAC	AC015618.3	RP11-45I3	
	ex3.G	71	BAC	AL355800.5	RP11-284O17	
		71	BAC	AL137798.8	RP5-1182A14	2 X in this BAC
		71	cDNA	AB051480	KIAA1693	
ex3.12	ex3.F	71	BAC	AC015618.3	RP11-45I3	
	ex3.H	71	BAC	AL355800.5	RP11-284O17	
ex3.13	ex3.J	71	BAC	AC027209.2	RP11-277H3	
	ex3.L	71	BAC	AL390296.3	RP11-555C20	
ex3.14	ex3.K	71	BAC	AC027209.2	RP11-277H3	
	ex3.M	71	BAC	AL390296.3	RP11-555C20	
ex3.16	ex3.N	71	BAC	AC073223.4	RP11580F15	
	ex3.O	71	BAC	AC024119.2	RP11-542J23	
ex3.17	ex3.P	71	BAC	AL359093.9	RP11-35B4	
		71	BAC	AL049715.25	RP4-646P11	
ex3.18	ex3.Q	71	BAC	AC023783.2	RP11-759I1	
		71	BAC	AL049715.25	RP4-646P11	
ex3.19	ex3.R	71	BAC	AC018729.3	RP11-1F5	
	ex3.S	71	BAC	AL391068.7	RP11-288L16	
ex3.20	ex3.T	71	BAC	AC026565.3	RP11-702G12	
	ex3.U	71	BAC	AL359752.7	RP5-1042I8	
ex3.22	ex3.V	71	BAC	AC013627.3	RP11-11L4	
	ex3.W	71	BAC	AL359258.4	RP11-483I13	
	ex3.X	71	BAC	AL356110.1	RP4-562N20	

	ex3.Y	71	BAC	AL390038.5	RP11-131J3	
ex3.23	ex3.Z	71	BAC	AC053486.4	RP11-100A19	3 stop codons
ex3.24	ex3.AA	71	BAC	AC024491.4	RP11-139D23	1 stop codon
ex3.25		71	BAC	AL137798.8	RP5-1182A14	
		71	cDNA	AB051480	KIAA1693	
ex4.1	B01AT10	25	BAC	AL354666.3	RP11-87L17	deleted in Vs.5
	B02AT12	25	BAC	AL356581.2	RP5-1020C22	
		25	BAC	AL355149.4	RP5-875O13	
		25	BAC	AC007734.3	RP11-44O1	
		25	BAC	AC018381.3	RP11-5G21	
		25	BAC	AL355800.5	RP11-284O17	2X in this BAC
		25	BAC	AC015618.3	RP11-45I3	2X in this BAC
		25	BAC	AC018729.3	RP11-1F5	
		25	BAC	AL359093.9	RP11-35B4	
		25	BAC	AL049715.25	RP4-646P11	
		25	BAC	AL137798.8	RP5-1182A14	2 X in this BAC
ex4.2	A117AT3	25	pred. cDNA	AL117237	HS328E191	
	B02AT05	25	BAC	AL356581.2	RP5-1020C22	
		25	BAC	AC024119.2		
		25	BAC	AC007734.3	RP11-44O1	
		25	BAC	AC018381.3	RP11-5G21	
		25	BAC	AL390296.4	RP11-555C20	
		25	BAC	AC073223.4	RP11-580F15	
		25	BAC	AC027727.3	RP11-18B10	
		25	BAC	AC026900.3	RP11-798G11	

	25	BAC	AC027209.2	RP11-277H3	
	25	BAC	AL022240.8	RP3-328E19	
	25	BAC	AL049715.25	RP4-646P11	
	25	BAC	AL137798.8	RP5-1182A14	
	25	EST checked	AI239884	IMAGp998N074517	
	25	EST checked	AL042283	DKFZp434L1620	
	25	EST checked	AI239884	IMAGp998N074517	
ex4.3	25	cDNA	AB033071	KIAA1245	
	25	EST checked	H06312	IMAGp998I02268	
	25	BAC	AL359176.4	RP11-47D6	
	25	BAC	AL356004.4	RP11-94I2	
ex4.4	25	cDNA	AK00726	HEP17004	
	25	BAC	AL109937.4	RP3-322E17	
	25	BAC	AC060753.8	RP11-285C11	
ex4.5	25	cDNA	AK00726	HEP17004	
	25	BAC	AL109937.4	RP3-322E17	
	25	BAC	AC060753.8	RP11-285C11	
ex4.6	25	cDNA	AB033071	KIAA1245	
	25	BAC	AC027727.3	RP11-18B10	
	25	BAC	AC026900.3	RP11-798G11	
	25	BAC	AC027209.2	RP11-277H3	
	25	BAC	AL359176.4	RP11-47D6	
	25	BAC	AL356004.4	RP11-94I2	
	25	BAC	AL049742.7	RP4-565E6	
ex4.7	25	cDNA	AB033071	KIAA1245	

ex4.8	B01AT05	25	BAC	AL354666.3	RP11-87L17	
		25	BAC	AL355149.4	RP5-875O13	
	AG10AT05	25	EST checked	AW173183	IMAGp998J126649Q2	
ex4.10	ex4.A	25	BAC	AL109937.4	RP3-322E17	
	ex4.E	25	BAC	AL138796.3	RP4-791M13	
ex4.11	ex4.B	25	BAC	AL390296.4	RP11-555C20	first a > g (from exon3)
ex4.12	ex4.C	25	BAC	AL355800.5	RP11-284O17	
	ex4.D	25	BAC	AC015618.3	RP11-45I3	
ex4.13	ex4.F	25	BAC	AC018729.3	RP11-1F5	
ex4.14	ex4.G	25	BAC	AC053486.4	RP11-100A19	
ex4.15	ex4.H	25	BAC	AC026565.3	RP11-702G12	
	ex4.I	25	BAC	AL391068.7	RP11-288L16	
ex4.16	ex4.J	25	BAC	AC024491.4	RP11-139D23	
ex4.17	AE01AT04	25	EST checked	AW160820	IMAGp998I196882	
		25	cDNA	AB051480	KIAA1693	
ex4.18	AG9AT04	25	EST checked	AI500017	IMAGp998E065507Q2	
		25	cDNA	AB051480	KIAA1693	
ex5.1	B01AT09	70	BAC	AL354666.3	RP11-87L17	deleted in Vs.5
	B02AT13	70	BAC	AL356581.4	RP5-1020C22	
		70	BAC	AC015618.3	RP11-45I3	
		70	BAC	AL355149.4	RP5-875O13	
		70	BAC	AL355800.5	RP11-284O17	2X in this BAC
		70	BAC	AL137798.8	RP5-1182A14	
ex5.2	KIA-AT10	70	cDNA	AB033071	KIAA1245	
ex5.3	AK00AT04	70	cDNA	AK00726	HEP17004	

		70	BAC	AC060753.8	RP11-285C11	
		70	BAC	AL109937.4	HSJ322E17	
ex5.4	KIA-AT05	70	cDNA	AB033071	KIAA1245	
		70	BAC	AL359176.4	RP11-47D6	
ex5.5	ex5+6.N	70	BAC	AC026900.3	RP11-798G11	
ex5.6	ex5+6.R	70	BAC	AC027727.3	RP11-18B10	1 stop codon
ex5.7	ex5+6.L	70	BAC	AC027209.2	RP11-277H3	
ex5.8	ex5+6.H	70	BAC	AC018729.3	RP11-1F5	
ex5.9	ex5+6.C	70	BAC	AC023990.1	RP11-510K4	
	ex5+6.D	70	BAC	AL390296.3	RP11-555C20	
	ex5+6.F	70	BAC	AL359093.9	RP11-35B4	
	ex5+6.G	70	BAC	AC018729.3	RP11-1F5	
	ex5+6.I	70	BAC	AC018381.3	RP11-5G21	
		70	BAC	AL049715.25	RP4-646P11	
ex5.10	ex5+6.B	70	BAC	AC015618.3	RP11-45I3	
ex5.11	ex5+6.K	70	BAC	AL356004.4	RP11-94I2	
		70	BAC	AL049742.7	RP4-565E6	
ex5.12	ex5+6.V	70	BAC	AL359752.7	RP5-1042I8	
ex5.13	ex5+6.U	70	BAC	AC015706.3	RP11-325P15	1 stop codon
ex5.14	ex5+6.Y	70	BAC	AL359258.4	RP11-483I13	
	ex5+6.Z	70	BAC	AL390038.5	RP11-131J3	
	ex5+6.AB	70	BAC	AC068979.9	RP11-134C18	
ex5.15	ex5+6.AA	70	BAC	AC013627.3	RP11-11L4	1 stop codon
ex5.16		70	cDNA	AB051480	KIAA1693	
		70	BAC	AL137798.8	RP5-1182A14	

ex6.1	AL117AT4	68	pred. cDNA	AL117237	HS328E191	
	KIA-AT15	68	cDNA	AB033071	KIAA1245	
	B02AT04	68	BAC	AL356581.2	RP5-1020C22	
	AC01AT04	68	EST checked	AL042283	DKFZp434L1620	
		68	BAC	AL359176.4	RP11-47D6	
		68	BAC	AL355149.4	RP5-875O13	
		68	BAC	AL356004.4	RP11-94I2	
		68	BAC	AL022240.8	RP3-328E19	
	AG10AT06	68	EST checked	AW173183	IMAGp998J126649Q2	
	AK00AT09	68	cDNA	AK00726	HEP17004	
ex6.2	AE05AT01	23	EST checked	AA704208	zj17a04.s1	partial
		68	BAC	AL109937.4	HSJ322E17	
ex6.3	B01AT04	68	BAC	AL354666.5	RP11-87L17	
	AE4AT02	68	EST checked	AI239884	IMAGp998N074517	
	AB23AT03	68	EST checked	AI239884	IMAGp998N074517	
		68	BAC	AC015618.3	RP11-45I3	
		68	BAC	AL355800.5	RP11-284O17	
		68	BAC	AL137798.8	RP5-1182A14	
	AG03AT02	68	EST checked	AW468059	IMAGp998B027200Q2	
		68	cDNA	AB051480	KIAA1693	
	AE03AT04	68	EST checked	H06312	IMAGp998I02268	
	ex5+6.J	68	BAC	AC018381.3	RP11-5G21	
ex6.5		68	BAC	AL049715.25	RP4-646P11	
	ex5+6.P	68	BAC	AC024119.2	RP11-542J23	
ex6.6	ex5+6.Q	68	BAC	AC073223.4	RP11580F15	
		68	BAC			

ex6.7	ex5+6.E	68	BAC	AL390296.3	RP11-555C20	
	ex5+6.M	68	BAC	AC027209.2	RP11-277H3	
ex6.8	ex5+6.A	68	BAC	AL109937.4	HSJ322E17	
	ex5+6.O	68	BAC	AC026900.3	RP11-798G11	
	ex5+6.S	68	BAC	AL138796.3	RP4-791M13	
ex6.9	ex5+6.T	68	BAC	AC053486.4	RP11-100A19	1 stop codon
ex6.10	ex5+6.W	68	BAC	AL391068.7	RP11-288L16	
	ex5+6.X	68	BAC	AC026565.3	RP11-702G12	
ex6.11		68	cDNA	Combination of KIAA1245 and AB25		
ex6.12	der_1AT01	68	genomic DNA			= exon A
ex7.1	B01AT03	18	BAC	AL354666.3	RP11-87L17	
	AK00AT10	18	cDNA	AK00726	HEP17004	
	AL117AT5	18	pred. cDNA	AL117237	HS328E191	
	KIA-AT16	18	cDNA	AB033071	KIAA1245	
	B02AT03	18	BAC	AL356581.2	RP5-1020C22	
	AE05AT02	18	EST checked	AA704208	zj17a04.s1	
	AC01AT05	18	EST checked	AL042283	DKFZp434L1620	
	AB25AT02	18	EST checked	AL042839	DKFZp434G2022	
	AE03AT05	18	EST checked	H06312	IMAGp998I02268	
		18	BAC	AL022240.8	RP3-328E19	
		18	BAC	AL049715.25	RP4-646P11	
		18	BAC	AL137798.8	RP5-1182A14	
		18	cDNA	AK024044	Y79AA1001711	
		18	RT-PCR HFB		pKNB11	
		18	RT-PCR HFB		pKNB16	

	18	RT-PCR HFB		pKNB21	
	18	RT-PCR HFB		pKNB26	
	18	RT-PCR HFB		pKNB20	
	18	RT-PCR HFB		pKNB23	
	18	RT-PCR HFB		pKNB27	
	18	RT-PCR HFB		pKNB28	
	AG03AT03	EST checked	AW468059	IMAGp998B027200Q2	
	der_1AT02	genomic DNA			= exon B
	AG10AT07	EST checked	AW173183	IMAGp998J126649Q2	
	18	cDNA	AB051480	KIAA1693	
ex7.2	18	BAC	AC026565.3	RP11-702G12	
	18	BAC	AL391068.7	RP11-288L16	
ex7.3	18	BAC	AC015706.3	RP11-325P15	
ex7.4	20	BAC	AC053486.4	RP11-100A19	
ex7.5	18	RT-PCR HFB		pKNB10	
ex8.1	54	cDNA	AK00726	HEP17004	
	54	BAC	AC018381.3	RP11-5G21	
	54	BAC	AC024119.2	RP11-542J23	
	54	BAC	AC109937.4	HSJ322E17	
	54	BAC	AL359093.9	RP11-35B4	
	54	BAC	AC060753.8	RP11-285C11	
	54	BAC	AL022240.8	RP3-328E19	
	AE03AT06	EST checked	H06312	IMAGp998I02268	
	AG03AT04	EST checked	AW468059	IMAGp998B027200Q2	
ex8.2	54	pred. cDNA	AL117237	HS328E191	

	AE05AT03	54	EST checked	AA704208	zj17a04.s1	
	AC01AT06	54	EST checked	AL042283	DKFZp434L1620	
		54	BAC	AC027209.2	RP11-277H3	
		54	BAC	AL049715.25	RP4-646P11	
ex8.3	KIA-AT17	27	cDNA	AB033071	KIAA1245	
		27	cDNA	AK024044	Y79AA1001711	
		27	RT-PCR HFB		pKNB16	
ex8.4	B01AT02	54	BAC	AL354666.5	RP11-87L17	
ex8.5	B02AT02	54	BAC	AL356581.4	RP5-1020C22	
		54	BAC	AL355149.4	RP5-875O13	
		54	BAC	AC015618.3	RP11-45I3	
		54	BAC	AL355800.5	RP11-284O17	
		54	BAC	AL137798.8	RP5-1182A14	
	AB25AT03	54	EST checked	AL042839	DKFZp434G2022	
		54	RT-PCR HFB		pKNB21	
	AG10AT08	54	EST checked	AW173183	IMAGp998J126649Q2	
		54	cDNA	AB051480	KIAA1693	
ex8.6	ex8.A	54	BAC	AL109937.4	HSJ322E17	
	ex8.B	54	BAC	AL138796.3	RP4-791M13	
	ex8.C	54	BAC	AC026900.3	RP11-798G11	
ex8.7	ex8.D	54	BAC	AL356004.4	RP11-94I2	
	ex8.E	54	BAC	AL359176.4	RP11-47D6	
		54	RT-PCR HFB		pKNB26	
ex8.8	ex8.F	54	BAC	AC027727.3	RP11-18B10	
ex8.9	ex8.G	54	BAC	AL390296.3	RP11-555C20	

ex8.10	ex8.H	54	BAC	AC053486.4	RP11-100A19	
ex8.11	ex8.I	54	BAC	AC026565.3	RP11-702G12	
	ex8.J	54	BAC	AL391068.7	RP11-288L16	
ex8.12	ex8.K	53	BAC	AC015706.3	RP11-325P15	
ex8.13		33	RT-PCR HFB		pKNB27	
		33	RT-PCR HFB		pKNB28	
ex8.14		27	RT-PCR HFB		pKNB10	
ex9.1	AK00AT12	18	cDNA	AK00726	HEP17004	
	KIA-AT18	18	cDNA	AB033071	KIAA1245	
		18	cDNA	AK024044	Y79AA1001711	
	AE03AT07	18	EST checked	H06312	IMAGp998I02268	
ex9.2	AL117AT7	18	pred. cDNA	AL117237	HS328E191	
	AE05AT04	18	EST	AA704208	zj17a04.s1	
	AC01AT07	18	EST checked	AL042283	DKFZp434L1620	
ex9.3	B01AT01	18	BAC	AL354666.5	RP11-87L17	
	B02AT01	18	BAC	AL356581.2	RP5-1020C22	
		18	BAC	AC015618.3	RP11-45I3	
		18	BAC	AC027727.3	RP11-18B10	
		18	BAC	AC026900.3	RP11-798G11	
		18	BAC	AL355147.2	RP11-78O9	
		18	BAC	AL356004.4	RP11-94I2	
		18	BAC	AL109937.4	HSJ322E17	
		18	BAC	AC018381.3	RP11-5G21	
		18	BAC	AL355800.5	RP11-284O17	
		18	BAC	AL355149.4	RP5-875O13	

	18	BAC	AC024119.2	RP11-542J23	
	18	BAC	AL138796.3	RP4-791M13	
	18	BAC	AL359176.4	RP11-47D6	
	18	BAC	AC060753.8	RP11-285C11	
	18	BAC	AC073223.4	RP11580F15	
	18	BAC	AC007734.3	RP11-44O1	
	18	BAC	AC079074.1	CTD-2386B2	2X in this BAC
	18	BAC	AL049715.25	RP4-646P11	
	18	BAC	AL137798.8	RP5-1182A14	
AB25AT04	18	EST checked	AL042839	DKFZp434G2022	
AG10AT09	18	EST checked	AW173183	IMAGp998J126649Q2	
	18	cDNA	AB051480	KIAA1693	
ex9.4	18	BAC	AC027209.2	RP11-277H3	
ex9.5	18	BAC	AC053486.4	RP11-100A19	
ex9.6	18	BAC	AC026565.3	RP11-702G12	
	18	BAC	AL391068.7	RP11-288L16	
ex9.7	18	BAC	AL022240.8	RP3-328E19	
ex9.8	18	EST checked	AW468059	IMAGp998B027200Q2	
ex9.9	18	cDNA	AL136890	DKFZp434D177	
ex10.1	57	cDNA	AB033071	KIAA1245	
	57	cDNA	AB033071	KIAA1245	
	57	cDNA	AB033071	KIAA1245	
	57	cDNA	AB033071	KIAA1245	
	57	cDNA	AB033071	KIAA1245	
	57	cDNA	AB033071	KIAA1245	
	57	cDNA	AB033071	KIAA1245	

ex10.2	KIAR1A	57	cDNA	AB033071	KIAA1245	
		57	cDNA	AK024044	Y79AA1001711	
ex10.3	AL117R1A	57	pred. cDNA	AL117237	HS328E191	
		57	BAC	AL022240.8	RP3-328E19	
ex10.4	AL117R4A	57	pred. cDNA	AL117237	HS328E191	
		57	BAC	AL022240.8	RP3-328E19	
ex10.5	E05R05SA	57	EST	AL037724	DKFZp564A057	
ex10.6	AL117R5A	57	pred. cDNA	AL117237	HS328E191	
		57	BAC	AL022240.8	RP3-328E19	
ex10.7	E02R02SA	57	EST checked	AL045522	DKFZp434J205	
	B01RA04	57	BAC	AL354666.3	RP11-87L17	
	B02RA02	57	BAC	AL356581.2	RP5-1020C22	
	B02RA06	57	BAC	AL356581.2	RP5-1020C22	
	1b9RA03	57	5'RACE 2F53VIII			
		57	BAC	AL137798.8	RP5-1182A14	
	R1d10ra2	57	RT-PCR 2F53VIII			
	R1a11ra2	57	RT-PCR 2F53VIII			
	AB06RA02	57	EST checked	AL045522	DKFZp434J205	
	AB25RA01	57	EST checked	AL042839	DKFZp434G2022	
	AB25RA04	57	EST checked	AL042839	DKFZp434G2022	
	AB25RA07	57	EST checked	AL042839	DKFZp434G2022	
	AG10RA01	57	EST checked	AW173183	IMAGp998J126649Q2	
		57	cDNA	AB051480	KIAA1493	
ex10.8	E03R04SA	56	EST	AL043132	DKFZp434D0623	
ex10.9	AL117R2A	57	pred. cDNA	AL117237	HS328E191	

	AL117R6A	57	pred. cDNA	AL117237	HS328E191	
	AC01RA02	57	EST checked	AL042283	DKFZp434L1620	
		57	BAC	AL022240.8	RP3-328E19	2 X in this BAC
ex10.10	E09R01A	57	EST	AA570017	nm48h10	
	2a1RA02	57	5'RACE TR14			
ex10.11	AC03RA01	57	EST checked	AL043132	DKFZp434D0623	
	AC03RA04	57	EST checked	AL043132	DKFZp434D0623	
	E10R02SA	57	EST	AW173183	xj84d06.x1	
	1b9RA02	57	5'RACE 2F53VIII			
	2g2Ra02	57	5'RACE 7A			
	2g7Ra02	57	5'RACE 7A			
	AB18RA01	57	EST checked	AL044108	DKFZp434M0628	
	2c4RA02	57	5'RACE SK-N-SH			
	AB25RA02	57	EST checked	AL042839	DKFZp434G2022	
	AB25RA05	57	EST checked	AL042839	DKFZp434G2022	
	AB25RA08	57	EST checked	AL042839	DKFZp434G2022	
	AG01RA02	57	EST checked	AL043174	DKFZp434F2323Q2	
	AG10RA02	57	EST checked	AW173183	IMAGp998J126649Q2	
		57	cDNA	AB051480	KIAA1693	
ex10.12	KIAR02A	57	cDNA	AB033071	KIAA1245	
	KIAR10A	57	cDNA	AB033071	KIAA1245	
	KIAR14A	57	cDNA	AB033071	KIAA1245	
	1b7RA02	57	5'RACE 2F53VIII			
	2b10RA02	57	5'RACE TR14			
ex10.13	KIAR06A	57	cDNA	AB033071	KIAA1245	

ex10.14	AK00R01A	57	cDNA	AK00726	HEP17004	
	AL050R2A	57	cDNA	AL050141	DKFZp586O031	
	AE05RA01	57	EST checked	AA704208	zj17a04.s1	
	AG01RA04	57	EST checked	AL043174	DKFZp434F2323Q2	
	AG04RA02	57	EST checked	AI049567	IMAGp998M024318Q2	
	AG02ra06	57	EST checked	AL037724	DKFZp564A057Q3	
	AG02ra09	57	EST checked	AL037724	DKFZp564A057Q3	
	AK00R02A	57	cDNA	AK00726	HEP17004	
	AL050R3A	57	cDNA	AL050141	DKFZp586O031	
ex10.15	1b3RA02	57	5'RACE 2F53VIII			
	1g1RA02	57	5'RACE 7A			
	1a8RA02	57	5'RACE 2F53VIII			
	1e2RA02	57	5'RACE 7A			
	1g1RA02	57	5'RACE 7A			
		57	BAC	AL049715.25	RP4-646P11	2 X in this BAC
	AG01RA02	57	EST checked	AL043174	DKFZp434F2323Q2	
	AG01RA05	57	EST checked	AL043174	DKFZp434F2323Q2	
	AG04RA03	57	EST checked	AI049567	IMAGp998M024318Q2	
	AG06RA04	57	EST checked	AI537172	IMAGp998E105403Q2	
	AG06RA010	57	EST checked	AI537172	IMAGp998E105403Q2	
	AG11RA03	57	EST checked	AI953463	IMAGp998F196353Q2	
ex10.16	AG11RA06	57	EST checked	AI953463	IMAGp998F196353Q2	
	B01RA01	57	BAC	AL354666.3	RP11-87L17	
ex10.17	B01RA03	57	BAC	AL354666.3	RP11-87L17	
	B02RA05	57	BAC	AL356581.2	RP5-1020C22	

	AB06RA03	57	EST checked	AL045522	DKFZp434J205	
ex10.18	AF16R2A	57	mRNA	AF161426	HSPC308	
	2f1RA02	57	5'RACE SK-N-SH			
ex10.19	1h5RA02	57	5'RACE TR14			
	AE03RA02	57	EST checked	H06312	IMAGp998I02268	
ex10.20	AB18RA01	57	EST checked	AL044108	DKFZp434M0628	
	AC03RA03	57	EST checked	AL043132	DKFZp434D0623	
ex10.21	2d5RA02	57	5'RACE SK-N-SH			
	AG06RA07	57	EST checked	AI537172	IMAGp998E105403Q2	
ex10.22	AC01RA01	57	EST checked	AL042283	DKFZp434L1620	
ex10.23		57	BAC	AL049715.25	RP4-646P11	
ex10.24		57	BAC	AL049715.25	RP4-646P11	
ex10.25		57	BAC	AL049715.25	RP4-646P11	
ex10.26	AE03RA01	57	EST checked	H06312	IMAGp998I02268	
ex10.27	AG01RA01	57	EST checked	AL043174	DKFZp434F2323Q2	
ex10.28	AG03RA01	57	EST checked	AW468059	IMAGp998B027200Q2	
ex10.29	AG08RA01	57	EST checked	AW238577	IMAGp998C056777Q2	
ex10.30	AG06RA03	57	EST checked	AI537172	IMAGp998E105403Q2	
	AG06RA06	57	EST checked	AI537172	IMAGp998E105403Q2	
	AG06RA09	57	EST checked	AI537172	IMAGp998E105403Q2	
	AG11RA02	57	EST checked	AI953463	IMAGp998F196353Q2	
	AG11RA05	57	EST checked	AI953463	IMAGp998F196353Q2	
ex10.31	AG02ra03	57	EST checked	AL037724	DKFZp564A057Q3	
ex10.32	AG02ra04	57	EST checked	AL037724	DKFZp564A057Q3	
ex10.34	AG02ra07	57	EST checked	AL037724	DKFZp564A057Q3	

ex10.35	AE1ra02	57	EST checked	AW160820	IMAGp998I196882	
ex10.36	AG9ra01	57	EST checked	AI570017	IMAGp998E065507Q2	
ex10.37		57	cDNA	AL136890	DKFZp434D177	
ex11.1	BRPEX1A	57	genomic DNA			= exon x
	AB06RA01	57	EST checked	AL045522	DKFZp434J205	
	AB13RA01	57	EST checked	AA705685	IMAGp998I041023	
	AB14RA01	57	EST checked	AA701673	IMAGp998H101019	
	AC03RA02	57	EST checked	AL043132	DKFZp434D0623	
	AC03RA05	57	EST checked	AL043132	DKFZp434D0623	
	AD02RA01	57	EST checked	AA322028	EST24684	
	B01RA02	57	BAC	AL354666.3	RP11-87L17	
	B02RA01	57	BAC	AL356581.2	RP5-1020C22	
	B02RA04	57	BAC	AL356581.2	RP5-1020C22	
	AB18RA03	57	EST checked	AL044108	DKFZp434M0628	
	2H2RA01	57	5'RACE TR14			
	RT1c6ra1	57	RT-PCR 2F53VIII			
	R1d10ra1	57	RT-PCR 2F53VIII			
	RT1a7ra1	57	RT-PCR 2F53VIII			
	RT1b2ra1	57	RT-PCR 2F53VIII			
	RT1b7ra1	57	RT-PCR 2F53VIII			
	R1a11ra1	57	RT-PCR 2F53VIII			
	RT1a1ra1	57	RT-PCR 2F53VIII			
	AB25RA03	57	EST checked	AL042839	DKFZp434G2022	
	AB25RA06	57	EST checked	AL042839	DKFZp434G2022	
	AB25RA09	57	EST checked	AL042839	DKFZp434G2022	

ex11.2	AG10RA03	57	EST checked	AW173183	IMAGp998J126649Q2	
		57	cDNA	AB051480	KIAA1693	
ex11.3	E10R03LA	57	EST	AW173183	xj84d06.x1	
	E05R02LA	57	EST	AL037724	zj17a04.s1	
	E09R02LA	57	EST	AA570017	nm48h10.s1	
	E11R02LA	57	EST	AI537172	tp01b05.x1	
	AL117R3A	57	pred. cDNA	AL117237	HS328E191	
	AL117R7A	57	pred. cDNA	AL117237	HS328E191	
	AK00R03A	57	cDNA	AK00726	HEP17004	
	AL050R1A	57	cDNA	AL050141	DKFZp586O031	
	AL050R4A	57	cDNA	AL050141	DKFZp586O031	
		57	BAC	AL022240.8	RP3-328E19	2 X in this BAC
		57	BAC	AL049715.25	RP4-646P11	2 X in this BAC
	AE03RA02	57	EST checked	H06312	IMAGp998I02268	
	AG01RA03	57	EST checked	AL043174	DKFZp434F2323Q2	
	AG01RA06	57	EST checked	AL043174	DKFZp434F2323Q2	
	AG03RA01	57	EST checked	AW468059	IMAGp998B027200Q2	
	AG04RA04	57	EST checked	AI049567	IMAGp998M024318Q2	
	AG08RA02	57	EST checked	AW238577	IMAGp998C056777Q2	
	AG06RA02	57	EST checked	AI537172	IMAGp998E105403Q2	
	AG06RA05	57	EST checked	AI537172	IMAGp998E105403Q2	
	AG06RA08	57	EST checked	AI537172	IMAGp998E105403Q2	
	AG06RA011	57	EST checked	AI537172	IMAGp998E105403Q2	
	AG11RA04	57	EST checked	AI953463	IMAGp998F196353Q2	
	AG11RA07	57	EST checked	AI953463	IMAGp998F196353Q2	

ex11.4	E06R02LA	57	EST	AI909921	IL-BT228-060599-008	
ex11.5	KIAR11A	57	cDNA	AB033071	KIAA1245	
	KIAR03A	57	cDNA	AB033071	KIAA1245	
	KIAR07A	57	cDNA	AB033071	KIAA1245	
	KIAR15A	57	cDNA	AB033071	KIAA1245	
	AF116R3A	57	mRNA	AF161426	HSPC308	
ex11.6	RT1a4ra1	57	RT-PCR 2F53VIII			
ex11.7	RT1a8ra1	57	RT-PCR 2F53VIII			
ex11.8	AB06RA04	57	EST checked	AL045522	DKFZp434J205	
ex11.9	AG02ra11	57	EST checked	AL037724	DKFZp564A057Q3	
ex11.10		57	cDNA	AL136890	DKFZp434D177	
ex11.11		57				
ex12.1	E17R01LB	35	EST	AW851278	IL3-CT0220-170200-067-E01	
	E06R02LB	35	EST	AI909921	IL-BT228-060599-008	
	KIAR03B	37	cDNA	AB033071	KIAA1245	
	KIAR07B	37	cDNA	AB033071	KIAA1245	
	KIAR11B	37	cDNA	AB033071	KIAA1245	
ex12.2	AF131R1B	37	mRNA	AF131738	24976	
	AG01RB07	37	EST checked	AL043174	DKFZp434F2323Q2	
	E05R02LB	37	EST	AL037724	zj17a04.s1	
	AL117R3B	37	pred. cDNA	AL117237	HS328E191	
	AL117R7B	37	pred. cDNA	AL117237	HS328E191	
ex12.3	AL050R1b	37	cDNA	AL050141	DKFZp586O031	
	2c3RB01	37	5'RACE SK-N-SH			
		37	BAC	AL022240.8	RP3-328E19	
		37	BAC	AL049715.25	RP4-646P11	2 X in this BAC
		37				

	AG01RB01	37	EST checked	AL043174	DKFZp434F2323Q2	
	AG01RB04	37	EST checked	AL043174	DKFZp434F2323Q2	
	AG04RB01	37	EST checked	AI049567	IMAGp998M024318Q2	
	AG06RB02	37	EST checked	AI537172	IMAGp998E105403Q2	
	AG06RB05	37	EST checked	AI537172	IMAGp998E105403Q2	
	AG06RB08	37	EST checked	AI537172	IMAGp998E105403Q2	
	AG11RB01	37	EST checked	AI953463	IMAGp998F196353Q2	
	AG11RB04	37	EST checked	AI953463	IMAGp998F196353Q2	
	E03R03LB	38	EST	AL043132	DKFZp434D0623	
	AB18RB04	38	EST checked	AL044108	DKFZp434M0628	
ex12.4	AC03RB03	38	EST checked	AL043132	DKFZp434D0623	
	AC03RB06	38	EST checked	AL043132	DKFZp434D0623	
	BRPEX2B	38	genomic DNA			= exon y
	AB06RB01	38	EST checked	AL045522	DKFZp434J205	
	AB03RB01	38	EST checked	AL040932	DKFZp434K1515	
	AD02RB01	38	EST checked	AA322028	EST24684	
	B01RB01L	38	BAC	AL354666.3	RP11-87L17	
	B02RB02L	38	BAC	AL356581.2	RP5-1020C22	
	RT1b2RB2	38	RT-PCR 2F53VIII			
	RT1a8RB2	38	RT-PCR 2F53VIII			
ex12.5	RT1a7RB2	38	RT-PCR 2F53VIII			
	RT1a4RB2	38	RT-PCR 2F53VIII			
	RT1a1RB2	38	RT-PCR 2F53VIII			
	R1d10RB2	38	RT-PCR 2F53VIII			
	R1a11RB2	38	RT-PCR 2F53VIII			

	AB25RA03	38	EST checked	AL042839	DKFZp434G2022	
	AB25RA06	38	EST checked	AL042839	DKFZp434G2022	
	AB25RA09	38	EST checked	AL042839	DKFZp434G2022	
ex12.6	B02RB01L	38	BAC	AL356581.2	RP5-1020C22	
	AB06RB04	38	EST checked	AL045522	DKFZp434J205	
ex12.7	AB13RB01	25	EST checked	AA705685	IMAGp998I041023	partial
	AB14RB01	25	EST checked	AA701673	IMAGp998H101019	partial
ex12.8	AG07RB01	37	EST checked	AA609104	IMAGp998B132576Q2	
ex12.9	AG02RB08	37	EST checked	AL037724	DKFZp564A057Q3	
ex12.10	AG02RB05	37	EST checked	AL037724	DKFZp564A057Q3	
ex13.1	E03R04SB	18	EST	AL043132	DKFZp434D0623	diff. From ESTchecked
ex13.2	E02R02SB	18	EST	AL045522	DKFZp434J205	
	E10R01SB	18	EST	AW173183	xj84d06.x1	
	KIAR13B	18	cDNA	AB033071	KIAA1245	
	KIAR12B	18	cDNA	AB033071	KIAA1245	
	KIAR09B	18	cDNA	AB033071	KIAA1245	
	KIAR08B	18	cDNA	AB033071	KIAA1245	
	KIAR05B	18	cDNA	AB033071	KIAA1245	
	AL117R5B	18	pred. cDNA	AL117237	HS328E191	
	KIAR01B	18	cDNA	AB033071	KIAA1245	
	AL117R1B	18	pred. cDNA	AL117237	HS328E191	
	AL117R4B	18	pred. cDNA	AL117237	HS328E191	
	KIAR04B	18	cDNA	AB033071	KIAA1245	
	AK00R1B	18	cDNA	AK00726	HEP17004	
	B01RB02S	18	BAC	AL354666.5	RP11-87L17	

B02RB04S	18	BAC	AL356581.2	RP5-1020C22	
AL050R2B	18	cDNA	AL050141	DKFZp586O031	
1b3RB02S	18	5'RACE 2F53VIII			
1b7RB02S	18	5'RACE 2F53VIII			
1b9RB02S	18	5'RACE 2F53VIII			
1e2rRB01	18	5'RACE 7A			
1f4RB01	18	5'RACE 7A			
2g2RB02	18	5'RACE 7A			
AB18RB02	18	EST checked	AL044108	DKFZp434M0628	
AC03RB04	18	EST checked	AL043132	DKFZp434D0623	
1h5RB02	18	5'RACE TR14			
2a8RB01	18	5'RACE TR14			
2a1RB02	18	5'RACE TR14			
2b10RB02	18	5'RACE TR14			
2c4RB02	18	5'RACE SK-N-SH			
2f1RB01	18	5'RACE SK-N-SH			
2d5RB02	18	5'RACE SK-N-SH			
	18	BAC	AL109937.4	HSJ322E17	
	18	BAC	AL390296.4	RP11-555C20	
	18	BAC	AC027727.3	RP11-18B10	
	18	BAC	AC023990.1	RP11-510K4	2 X in this BAC
	18	BAC	AL356581.4	RP5-1020C22	
	18	BAC	AC024119.2	RP11-542J23	3 X in this BAC
	18	BAC	AC018381.3	RP11-5G21	5 X in this BAC

	18	BAC	AL355800.5	RP11-284O17	2 X in this BAC
	18	BAC	AC026900.3	RP11-798G11	
	18	BAC	AL359093.9	RP11-35B4	8 X in this BAC
	18	BAC	AC079074.1	CTD-2386B2	
	18	BAC	AL355149.4	RP5-875O13	
	18	BAC	AL356004.4	RP11-94I2	
	18	BAC	AC073223.4	RP11580F15	2 X in this BAC
	18	BAC	AL138842.4	RP4-679C16	2 X in this BAC
	18	BAC	AL138796.3	RP4-791M13	
	18	BAC	AC018729.3	RP11-1F5	7 X in this BAC
	18	BAC	AC015618.3	RP11-45I3	
	18	BAC	AC007734.3	RP11-44O1	6 X in this BAC
	18	BAC	AL355505.7	RP4-634B11	7 X in this BAC
	18	BAC	AC084206.1	RP11-305B17	2 X in this BAC
	18	BAC	AL359176.4	RP11-47D6	3 X in this BAC
	18	BAC	AL139152.2	RP4-704D21	
	18	BAC	AC060753.8	RP11-285C11	5 X in this BAC
R1a11RB3	18	RT-PCR 2F53VIII			
R1d10Rb3	18	RT-PCR 2F53VIII			
AC01RB01	18	EST checked	AL042283	DKFZp434L1620	
	18	BAC	AL022240.8	RP3-328E19	3 X in this BAC
	18	BAC	AL049715.25	RP4-646P11	2 X in this BAC
	18	BAC	AL137798.8	RP5-1182A14	
R1a11rb3	18	RT-PCR 2F53VIII			

R1d10rb3	18	RT-PCR 2F53VIII			
AE03RB01	18	EST checked	H06312	IMAGp998J02268	
AB06RB02	18	EST checked	AL045522	DKFZp434J205	
AB25RA01	18	EST checked	AL042839	DKFZp434G2022	
AB25RA04	18	EST checked	AL042839	DKFZp434G2022	
AB25RA07	18	EST checked	AL042839	DKFZp434G2022	
AG01RB02	18	EST checked	AL043174	DKFZp434F2323Q2	
AG01RB05	18	EST checked	AL043174	DKFZp434F2323Q2	
AG03RB01	18	EST checked	AW468059	IMAGp998B027200Q2	
AG04RB02	18	EST checked	AI049567	IMAGp998M024318Q2	
AG06RB03	18	EST checked	AI537172	IMAGp998E105403Q2	
AG06RB06	18	EST checked	AI537172	IMAGp998E105403Q2	
AG06RB09	18	EST checked	AI537172	IMAGp998E105403Q2	
AG11RA02	18	EST checked	AI953463	IMAGp998F196353Q2	
AG11RA05	18	EST checked	AI953463	IMAGp998F196353Q2	
AG10RA01	18	EST checked	AW173183	IMAGp998J126649Q2	
	18	cDNA	AB051480	KIAA1693	
AC03RB02	18	EST checked	AL043132	DKFZp434D0623	
AC03RB05	18	EST checked	AL043132	DKFZp434D0623	
KIAR02SB	18	cDNA	AB033071	KIAA1245	
KIAR06B	18	cDNA	AB033071	KIAA1245	
KIAR10B	18	cDNA	AB033071	KIAA1245	
KIAR14B	18	cDNA	AB033071	KIAA1245	
E10R02SB	18	EST	AW173183	xj84d06.x1	
E11R01SB	18	EST	AI537172	tp01b05.x1	

ex13.3

AL117R2B	18	pred. cDNA	AL117237	HS328E191	
AL117R6B	18	pred. cDNA	AL117237	HS328E191	
E09R01SB	18	EST	AA570017	tr91b03.x1	
B01RB01'	18	BAC	AL354666.3	RP11-87L17	
AC03RB02	18	EST checked	AL043132	DKFZp434D0623	
AL050R3B	18	cDNA	AL050141	DKFZp586O031	
1b1RB01S	18	5'RACE 2F53VIII			
1b3RB01S	18	5'RACE 2F53VIII			
1b4RB01	18	5'RACE 2F53VIII			
1b7RB01S	18	5'RACE 2F53VIII			
1b9RB01S	18	5'RACE 2F53VIII			
1c11RB01S	18	5'RACE 2F53VIII			
1a8RB01	18	5'RACE 2F53VIII			
2g2RB01	18	5'RACE 7A			
2g7RB01	18	5'RACE 7A			
AB18RB03	18	EST checked	AL044108	DKFZp434M0628	
1h5RB01	18	5'RACE TR14			
1h3RB01	18	5'RACE TR14			
2b2RB01	18	5'RACE TR14			
2a1RB01	18	5'RACE TR14			
2c4RB01	18	5'RACE SK-N-SH			
RT1a4RB1	18	RT-PCR 2F53VIII			
RT1b7RB1	18	RT-PCR 2F53VIII			
RT1a8RB1	18	RT-PCR 2F53VIII			
RT1a7RB1	18	RT-PCR 2F53VIII			

RT1b2RB1	18	RT-PCR 2F53VIII			
RT1a1RB1	18	RT-PCR 2F53VIII			
R1a11RB1	18	RT-PCR 2F53VIII			
R1d10RB1	18	RT-PCR 2F53VIII			
AC01RB02	18	EST checked	AL042283	DKFZp434L1620	
AE03RB02	18	EST checked	H06312	IMAGp998I02268	
RT1a4rb1	18	RT-PCR 2F53VIII			
RT1b7rb1	18	RT-PCR 2F53VIII			
RT1a8r1b	18	RT-PCR 2F53VIII			
RT1a7rb1	18	RT-PCR 2F53VIII			
RT1b2rb1	18	RT-PCR 2F53VIII			
RT1a11rb1	18	RT-PCR 2F53VIII			
R1d10rb1	18	RT-PCR 2F53VIII			
AB25RA02	18	EST checked	AL042839	DKFZp434G2022	
AB25RA05	18	EST checked	AL042839	DKFZp434G2022	
AB25RA08	18	EST checked	AL042839	DKFZp434G2022	
AG03RB02	18	EST checked	AW468059	IMAGp998B027200Q2	
AG04RB01	18	EST checked	AI049567	IMAGp998M024318Q2	
AG08RB03	18	EST checked	AW238577	IMAGp998C056777Q2	
AG06RB01	18	EST checked	AI537172	IMAGp998E105403Q2	
AG06RB04	18	EST checked	AI537172	IMAGp998E105403Q2	
AG06RB07	18	EST checked	AI537172	IMAGp998E105403Q2	
AG06RB10	18	EST checked	AI537172	IMAGp998E105403Q2	
AG11RB03	18	EST checked	AI953463	IMAGp998F196353Q2	
AG11RB06	18	EST checked	AI953463	IMAGp998F196353Q2	

	AG10RB02	18	EST checked	AW173183	IMAGp998J126649Q2	
ex13.4	AK00R2B	18	cDNA	AK00726	HEP17004	
	1e10RB01	18	5'RACE 7A			
	1e2RB01	18	5'RACE 7A			
	AG01RB03	18	EST checked	AL043174	DKFZp434F2323Q2	
	AG01RB06	18	EST checked	AL043174	DKFZp434F2323Q2	
	B02RB03S	18	BAC	AL356581.2	RP5-1020C22	
ex13.5	1f10RB01	18	5'RACE 7A			
	AB06RB03	18	EST checked	AL045522	DKFZp434J205	
ex13.6	AF16R2B	18	mRNA	AF161426	HSPC308	
ex13.7	1e5RB01S	18	5'RACE 7A			
ex13.8	1g1RB01S	18	5'RACE 7A			
ex13.9	1g1RB02S	18	5'RACE 7A			
ex13.10		18	BAC	AL109937.4	HSJ322E17	
	2b10RB01	18	5'RACE TR14			
	1a8RB02S	18	5'RACE 2F53VIII			
		18	BAC	AC018381.3	RP11-5G21	
ex13.11		18	BAC	AC007734.3	RP11-44O1	2 X in this BAC
		18	BAC	AC053486.4	RP11-100A19	
	2g7RB02	18	5'RACE 7A			
ex13.12	2c11RB01	18	5'RACE SK-N-SH			
ex13.13	2d5RB01	18	5'RACE SK-N-SH			
ex13.14		18	cDNA	AB051480	KIAA1693	
	ex13.AD	18	BAC	AC007734.3	RP11-44O1	
ex13.15	ex13.AJ	18	BAC	AC026565.3	RP11-702G12	2 X in this BAC

	ex13.AM	18	BAC	AL391068.7	RP11-288L16	2 X in this BAC
ex13.17	ex13.AQ	18	BAC	AL359258.4	RP11-483I13	
	ex13.AR	18	BAC	AC013627.3	RP11-11L4	
	ex13.AS	18	BAC	AL390038.5	RP11-131J3	
	ex13.F	18	BAC	AC023990.1	RP11-510K4	
ex13.18	ex13.O	18	BAC	AC018381.3	RP11-5G21	
	ex13.Q	18	BAC	AL359093.9	RP11-35B4	
	ex13.U	18	BAC	AC073223.4	RP11580F15	2 X in this BAC
	ex13.W	18	BAC	AC018729.3	RP11-1F5	
ex13.19	ex13.AC	18	BAC	AC007734.3	RP11-44O1	2 X in this BAC
	ex13.AF	18	BAC	AL355505.7	RP4-634B11	
		18	BAC	AL049715.25	RP4-646P11	
	ex13.AK	18	BAC	AC026565.3	RP11-702G12	
ex13.20	ex13.AN	18	BAC	AL391068.7	RP11-288L16	
	ex13.AI	18	BAC	AC053486.4	RP11-100A19	
	ex13.AB	18	BAC	AC007734.3	RP11-44O1	1 stop codon
	ex13.G	18	BAC	AC023990.1	RP11-510K4	1 stop codon
ex13.21	ex13.AU	18	BAC	AC015706.3	RP11-325P15	
	ex13.L	18	BAC	AC024119.2	RP11-542J23	2 X in this BAC
	ex13.N	18	BAC	AC018381.3	RP11-5G21	2 X in this BAC
		18	BAC	AL049715.25	RP4-646P11	
ex13.22	ex13.AO	18	BAC	AC013673.2	RP11-20I21	
	ex13.B	18	BAC	AC027727.3	RP11-18B10	
	ex13.AT	18	BAC	AC015706.3	RP11-325P15	
	ex13.H	18	BAC	AC023990.1	RP11-510K4	

ex13.29	ex13.I	18	BAC	AL356581.4	RP5-1020C22	2 X in this BAC
ex13.30	ex13.C	18	BAC	AL109937.4	HSJ322E17	
ex13.31		18	BAC	AC060753.8	RP11-285C11	7 X in this BAC
	ex13.A	18	BAC	AL359176.4	RP11-47D6	2 X in this BAC
		18	BAC	AL139152.2	RP4-704D21	2 X in this BAC
		18	BAC	AL109937.4	HSJ322E17	2 X in this BAC
		18	BAC	AC027727.3	RP11-18B10	2 X in this BAC
		18	BAC	AC023990.1	RP11-510K4	4 X in this BAC
		18	BAC	AC024119.2	RP11-542J23	
		18	BAC	AC018381.3	RP11-5G21	5 X in this BAC
		18	BAC	AL355800.5	RP11-284O17	2 X in this BAC
		18	BAC	AL354666.5	RP11-87L17	
		18	BAC	AC026900.3	RP11-798G11	2 X in this BAC
		18	BAC	AL359093.9	RP11-35B4	5 X in this BAC
		18	BAC	AL356004.4	RP11-94I2	
		18	BAC	AC073223.4	RP11580F15	2 X in this BAC
		18	BAC	AL138842.4	RP4-679C16	
		18	BAC	AL138796.3	RP4-791M13	
		18	BAC	AC018729.3	RP11-1F5	4 X in this BAC
		18	BAC	AC015618.3	RP11-45I3	2 X in this BAC
		18	BAC	AC007734.3	RP11-44O1	6 X in this BAC
		18	BAC	AC084206.1	RP11-305B17	
		18	BAC	AC053486.4	RP11-100A19	
		18	BAC	AC026565.3	RP11-702G12	
AL050R0B		18	BAC	AL050141	DKFZp586O031	

		18	BAC	AL022240.8	RP3-328E19	
		18	BAC	AL022240.8	RP3-328E19	
ex13.32	ex13.M	18	BAC	AC024119.2	RP11-542J23	
ex13.33	ex13.X	18	BAC	AC018729.3	RP11-1F5	3 X in this BAC
ex13.34	ex13.S	18	BAC	AC079074.1	CTD-2386B2	
ex13.35	ex13.V	18	BAC	AC018729.3	RP11-1F5	1 stop codon
ex13.36	AG9rb01	18	EST checked	AI570017	IMAGp998E065507Q2	
ex13.37		18	cDNA	AL136890	DKFZp434D177	
ex14.1	E16CT	80	EST	C15842	GEN-181D02	
		80	BAC	AL138842.4	RP4-679C16	
		80	BAC	AL355505.7	RP4-634B11	
		80	BAC	AC018381.3	RP11-5G21	
		80	BAC	AL359093.9	RP11-35B4	
		80	BAC	AC007734.3	RP11-44O1	
	AG07CT	80	EST checked	AA609104	IMAGp998B132576Q2	
ex14.2	E18CT	80	EST	AA609104	af11c07.s1	
ex14.3	E21CT	80	EST	AA301198	EST14111	
	AE1CT	80	EST checked	AW160820	IMAGp998I96882	
		80	BAC	AL138796.3	RP4-791M13	
ex14.5	E24CT	80	EST	H29685	ym61b08	
ex14.6	AL117R8C	80	pred. cDNA	AL117237	HS328E191	
		80	BAC	AL022240.8	RP3-328E19	
ex14.7	E17CT	80	EST	AW851278	IL3-CT0220-170200-067-E01	
ex14.8	E19CT	80	EST	AA333188	EST37291	
ex14.9	AD01CT	80	EST checked	AA350323	EST57569	

	E14CT	80	EST	AI372468	EST175301	
	E15CT	80	EST	F11837	c-32c04	
ex14.10	E29CT	80	EST	T65179	yc74b04.r1	
ex14.11	AB03CT	80	EST checked	AL040932	DKFZp434K1515	
	B01CT01	80	BAC	AL354666.5	RP11-87L17	
		80	BAC	AC084206.1	RP11-305B17	
ex14.12	BRKPEX3L	80	genomic DNA			= exon z
	AB25CT	80	EST checked	AL042839	DKFZp434G2022	
ex14.13	E23CT	80	EST	AA315005	EST186812	
ex14.14	E27CT	80	EST	C17016	GEN-537A10	
ex14.15	AF131CT	80	mRNA	AF131738	24976	
		80	BAC	AL359176.4	RP11-47D6	
		80	BAC	AL139152.2	RP4-704D21	
ex14.16	B02CT01	80	BAC	AL356581.2	RP5-1020C22	
	AB06CT	80	EST checked	AL045522	DKFZp434J205	
ex14.17	AD02CT	80	EST checked	AA322028	EST24684	
ex14.18	AC03CT	80	EST checked	AL043132	DKFZp434D0623	
	AB18CT	80	EST checked	AL044108	DKFZp434M0628	
		80	BAC	AL355800.5	RP11-284O17	
		80	BAC	AL355149.4	RP5-875O13	
		80	BAC	AC015618.3	RP11-45I3	
ex14.19	ex14.A	80	BAC	AC027727.3	RP11-18B10	
ex14.20	ex14.B	80	BAC	AC060753.8	RP11-285C11	
	AG01CT	80	EST checked	AL043174	DKFZp434F2323Q2	
ex14.21	ex14.C	80	BAC	AC024119.2	RP11-542J23	

	ex14.D	80	BAC	AC073223.4	RP11580F15	
ex14.22	ex14.E	80	BAC	AC027209.2	RP11-277H3	
ex14.23	ex14.G	80	BAC	AL356004.4	RP11-94I2	
ex14.24	ex14.H	80	BAC	AC053486.4	RP11-100A19	
ex14.25	ex14.I	80	BAC	AL391068.7	RP11-288L16	
	ex14.J	80	BAC	AL391068.7	RP11-288L16	
	ex14.K	80	BAC	AC026565.3	RP11-702G12	
	ex14.L	80	BAC	AC026565.3	RP11-702G12	
ex14.26	AG02ct	80	EST-checked	AL037724	DKFZp564A057Q3	
		80	cDNA	AB051480	KIAA1693	

Footnotes to Table 5:

1. Exons are classified in types according to homologies at the protein level (Figs. 9 to 15)
2. Exon symbols refer to Laboratory Notebooks of the Dept. of Molecular Biology
3. Occurrence of exons in genomic and cDNA clones, as indicated (summarized in Figs. 7, 8, 21, 22, 23)
4. Among the clone types are expressed sequence tags (EST), whose sequence was either taken from the public domain or confirmed and completed in the authors' laboratory (labeled as 'EST-checked', see also Table 6).

Table 6: Sequenced NBG-related cDNA clones

DMB-VIB name	Depicted in Fig./ Sequence type	cDNA Clone Name(s)	GenBank Acc. No.	GenBank Acc. Nos. EST sequences	
AB01	3'-UTR	DKFZp434B235	AF379611	AL045343	AL045344
AB02	3'UTR + poly-A	DKFZp434J2318	AF379612	AL048907	
AB03	Fig. 7	DKFZp434K1515	AF379613	AL040932	
AB04	3'UTR + poly-A	IMAGp998O19822	AF379614	W95853	
		IMAGE : 385122			
AB05	3'UTR + poly-A	IMAGp998L06676	AF379615	W17223	
		IMAGE : 301973			
AB06	Fig. 7	DKFZp434J205	AF379616	AL045522	
AB10	3'UTR + poly-A	IMAGp998I18822	AF379617	W95142	
		IMAGE : 357977			
AB11	3'UTR + poly-A	IMAGp998I10824	AF379618	W94444	
		IMAGE : 358737			
AB13	Fig. 22	IMAGp998I041023	AF379619	AA705685	
		IMAGE : 435147			
AB14	Fig. 22	IMAGp998H101019	AF420437	AA701673	
		IMAGE : 433594			
AB16	3'UTR + poly-A	IMAGp998N141787	AF379621	AA398843	
		IMAGE : 728653			
AB18	Fig. 7	DKFZp434M0628	AF379622	AL044108	
AB23 = AE04	Fig. 21	IMAGp998N074517	AF379623	AI239884	
		IMAGE : 1846470			
AB25	Fig. 7	DKFZp434G2022	AF379624	AL042839	
AC02	Pseudogene?	DKFZp434K2231	AF379625	AL110415	
AC03	Fig. 7	DKFZp434D0623	AF379626	AL043132	
AD01	Fig. 7	EST57569	AF379627	AA350323	

AD02	Fig. 7	EST24684	AF379628	AA322028	
AE01	Fig. 7	IMAGp998I196882	5': AF419618	AW160820	
		IMAGE : 2782170	3': AF419619		
AE02	5'UTR + start codon	IMAGp9988N14778	AF379629	W58508	
		IMAGE : 341197			
AE03	Fig. 21	IMAGp998I02268	AF379630	H06312	
		IMAGE : 44185			
AE05	Fig. 21	IMAGp998I071063	AF379631	AA704208	
		IMAGE : 450510			
AG01	Fig. 7	DKFZp434F2323	AF380580	AL043174	
AG02	Fig. 7	DKFZp564A057	AF419616	AL037724	
AG03	Fig. 21	IMAGp998B027200	AF380581	AW468059	
		IMAGE : 2920609			
AG04	Fig. 22	IMAGp998M024318	AF379632	AI049567	
		IMAGE : 1700501			
AG06	Fig. 22	IMAGp998E105403	AF379633	AI537172	
		IMAGE : 2186481			
AG07	Fig. 7	IMAGp998B132576	AF379634	AA609104	
		IMAGE : 1031340			
AG08	Fig. 22	IMAGp998C056777	AF380582	AW238577	
		IMAGE:2741692			
AG09	Fig. 21	IMAGp998E065507	AF419617	AI570017	
		IMAGE:2226413			
AG10	Fig. 21	IMAGp998J126649	AF379635	AW173183	
		IMAGE : 2663915			
AG11	Fig. 22	IMAGp998F196353	AF379636	AI953463	
		IMAGE : 2550162			

Table 7: Human genomic contig sequences comprising NBG-related sequences

Contig	Size (bp)	Chromosomal localization	# of exon 7	# of exon 8	# of exon 9
NT_021932.4	1,279,026 bp	1q12	3	3	3
NT_004754.5	5,941,040 bp	1q12	5	6	5
NT_023400.4	373,558 bp	not placed (chr 6?)	1	1	1
NT_004644.5	1,210,659 bp	1q42.11	1	1	1
NT_028134.1	147,523 bp	not placed (chr3 ?)	1	1	1
NT_004434.5	1,108,112 bp	1q21	1	2	1
NT_004873.5	4,329,220 bp	1p36.13	2	2	2
NT_004576.5	1,278,015 bp	1p36.11	0	1	0
NT_004966.5	5,599,926 bp	1p13.1	0	0	0
NT_021907.5	1,184,925 bp	1q21.3	0	0	0
NT_019284.5	2,180,645 bp	1p21.3	0	0	1
NT_027019.2	493,854 bp	5q14	0	0	0
NT_005580.5	1,740,243 bp	3p22.1	0	0	0
Total			14	17	15

Result of a TBLASTN analysis (September 16, 2001) to the Human Genome Data using a typical NBG-protein as query. Thirteen contigs contained NBG-related sequences. Their GenBank accession numbers are given in the first column, their size (bp) in the second column, and their chromosomal localization as determined by MapView (NCBI: <http://www.ncbi.nlm.nih.gov>) in the third column. The occurrence (#) of different variants of the exon types 7, 8 and 9 (generally represented by a single copy in NBG transcripts) is also determined by BLAST analysis to the Human Genome Data.

References

- Altschul, S. F., Madden, T. L., Schaffer, A. A., Zhang, J. H., Zhang, Z., Miller, W., and Lipman, D. J. (1997). Gapped BLAST and PSI-BLAST: a new generation of protein database search programs, *Nucleic Acids Res.* 25, 3389-3402.
- 5 Ambros, I. M., Rumpler, S., Luegmayr, A., Hattinger, C. M., Strehl, S., Kovar, H., Gadner, H. and Ambros, P. F. (1997). Neuroblastoma cells can actively eliminate supernumerary MYCN gene copies by micronucleus formation--sign of tumour cell revertance? *Eur. J. Cancer* 33, 2043-9.
- Bader, S. A., Fasching, C., Brodeur, G. M., and Stanbridge, E. J. (1991). Dissociation
10 of suppression of tumorigenicity and differentiation in vitro effected by transfer of single human chromosomes into human neuroblastoma cells, *Cell Growth Differ.* 2, 245-55.
- Bieche, I., Khodja, A., and Lidereau, R. (1998). Deletion mapping in breast tumor cell lines points to two distinct tumor-suppressor genes in the 1p32-pter region, one of deleted regions (1p36.2) being located within the consensus region of LOH in
15 neuroblastoma, *Oncol. Rep.* 5, 267-272.
- Biegel, J. A., White, P. S., Marshall, H. N., Fujimori, M., Zackai, E. H., Scher, C. D., Brodeur, G. M., and Emanuel, B. S. (1993). Constitutional 1p36 deletion in a child with neuroblastoma, *Am. J. Hum. Genet.* 52, 176-82.
- Bonfield, J. K., Smith, K. F., and Staden, R. (1995). A new DNA sequence assembly
20 program, *Nucleic Acids Res.* 23, 4992-4999.
- Bown, N., Cotterill, S., Lastowska, M., O'Neill, S., Pearson, A. D., Plantaz, D., Meddeb, M., Danglot, G., Brinkschmidt, C., Christiansen, H., Laureys, G., and Speleman, F. (1999). Gain of chromosome arm 17q and adverse outcome in patients with neuroblastoma [see comments], *N. Engl. J. Med.* 340, 1954-61.
- 25 Brinkschmidt, C., Christiansen, H., Terpe, H. J., Simon, R., Boecker, W., Lampert, F., and Stoerkel, S. (1997). Comparative genomic hybridization (CGH) analysis of neuroblastomas--an important methodological approach in paediatric tumour pathology, *J. Pathol.* 181, 394-400.
- Brodeur, G. M. (1998). Clinical and biological aspects of neuroblastoma. In *The Genetic Basis of Human Cancer*, B. Vogelstein, and K. W. Kinzler, eds. (New York, NY, McGraw-Hill), pp. 691-711.
- 30 Brodeur, G. M., Sekhon, G., and Goldstein, M. N. (1977). Chromosomal aberrations in human neuroblastomas, *Cancer* 40, 2256-63.

Buroker N., Bestwick R., Haight G., Magenis R. E., and Litt M. (1987). A hypervariable repeated sequence on human chromosome 1p36, *Hum. Genet.* 77, 175-81.

Cai D .X., Banerjee R., Scheithauer B. W., Lohse C.M., Kleinschmidt-Demasters B.K., Perry A. (2001). Chromosome 1p and 14q FISH analysis in clinicopathologic subsets of meningioma: diagnostic and prognostic implications, *J. Neuropathol. Exp. Neurol.* 60, 628-636.

Canute, G. W., Longo, S. L., Longo, J. A., Winfield, J. A., Nevaldine, B. H. and Hahn, P. J. (1996). Hydroxyurea accelerates the loss of epidermal growth factor receptor genes amplified as double-minute chromosomes in human glioblastoma multiforme, *Neurosurgery* 39, 976-83.

Caron, H. (1995). Allelic loss of chromosome 1 and additional chromosome 17 material are both unfavourable prognostic markers in neuroblastoma, *Med. Pediatr. Oncol.* 24, 215-21.

Caron, H., van Sluis, P., van Hoeve, M., de Kraker, J., Bras, J., Slater, R., Mannens, M., Voute, P. A., Westerveld, A., and Versteeg, R. (1993). Allelic loss of chromosome 1p36 in neuroblastoma is of preferential maternal origin and correlates with N-myc amplification [with published erratum in *Nat. Genet.* 1993 4:431], *Nat. Genet.* 4, 187-90.

Collins C., Kuo W. L., Segraves R., Fuscoe J., Pinkel D., and Gray J. W. (1991). Construction and characterization of plasmid libraries enriched in sequences from single human chromosomes, *Genomics* 11, 997-1006.

De Angelis, P. M., Stokke, T., Beigi, M., Mjaland, O., and Clausen, O. P. (2001). Prognostic significance of recurrent chromosomal aberrations detected by comparative genomic hybridization in sporadic colorectal cancer. *Int. J. Colorectal Dis.* 16, 38-45.

Dorschner M. O., Sybert V.P., Weaver M., Pletcher B. A., Stephens K. (2000). NF1 microdeletion breakpoints are clustered at flanking repetitive sequences, *Hum Mol Genet* 9, 35-46.

Doz, F., Peter, M., Schleiermacher, G., Vielh, P., Validire, P., Putterman, M., Blanquet, V., Desjardins, L., Dufier, J.L., Zucker, J.M., Mosseri, V., Thomas, G., Magdelenat, H., and Delattre, O. (1996). N-MYC amplification, loss of heterozygosity on the short arm of chromosome 1 and DNA ploidy in retinoblastoma, *Eur. J. Cancer* 32A, 645-649.

Eckhardt, S. G., Dai, A., Davidson, K. K., Forseth, B. J., Wahl, G. M. and Von Hoff, D. D. (1994). Induction of differentiation in HL60 cells by the reduction of extrachromosomally amplified c-myc, *Proc. Natl. Acad. Sci. U.S.A.* 91, 6674-8.

- Fong, C. T., Dracopoli, N. C., White, P. S., Merrill, P. T., Griffith, R. C., Housman, D. E., and Brodeur, G. M. (1989). Loss of heterozygosity for the short arm of chromosome 1 in human neuroblastomas: correlation with N-myc amplification, *Proc. Natl. Acad. Sci. U. S. A.* **86**, 3753-7.
- 5 Fong, C. T., White, P. S., Peterson, K., Sapienza, C., Cavenee, W. K., S.E., K., Vogelstein, B., Cantor, A. B., Look, A. T., and Brodeur, G. M. (1992). Loss of heterozygosity for chromosomes 1 or 14 defines subsets of advanced neuroblastomas, *Cancer Res.* **52**, 1780-1785.
- Gilbert, F., Feder, M., Balaban, G., Brangman, D., Lurie, D. K., Podolsky, R., Rinaldt, V., Vinikoor, N., and Weisband, J. (1984). Human neuroblastomas and abnormalities of chromosomes 1 and 17, *Cancer Res.* **44**, 5444-9.
- 10 Igarashi, J., Nimura, Y., Fujimori, M., Mihara, M., Adachi, W., Kageyama, H., and Nakagawara, A. (2000). Allelic loss of the region of chromosome 1p35-pter is associated with progression of human gastric carcinoma, *Jpn. J. Cancer Res.* **91**, 797-801.
- 15 Ioannou, P. A., Amemiya, C. T., Garnes, J., Kroisel, P. M., Shizuya, H., Chen, C., Batzer, M. A., and de Jong, P. J. (1994). A new bacteriophage P1-derived vector for the propagation of large human DNA fragments, *Nat. Genet.* **6**, 84-89.
- Kanda, T., Otter, M., and Wahl, G. M. (2001). Mitotic segregation of viral and cellular acentric extrachromosomal molecules by chromosome tethering, *J. Cell Sci.* **114**, 49-58.
- 20 Knuutila, S., Bjorkqvist, A. M., Autio, K., Tarkkanen, M., Wolf, M., Monni, O., Szymanska, J., Larramendy, M. L., Tapper, J., Pere, H. et al. (1998). DNA copy number amplifications in human neoplasms: review of comparative genomic hybridization studies, *Am. J. Pathol.* **152**, 1107-23.
- 25 Lastowska, M., Nacheva, E., McGuckin, A., Curtis, A., Grace, C., Pearson, A., and Bown, N. (1997). Comparative genomic hybridization study of primary neuroblastoma tumors. United Kingdom Children's Cancer Study Group, *Gene Chromosome Canc.* **18**, 162-9.
- 30 Lastowska, M., Van Roy, N., Brown, N., Speleman, F., Lunec, J., Strachan, T., Pearson, A. D. J., and Jackson, M. S. (1998). Molecular cytogenetic delineation of 17q translocation breakpoints in neuroblastoma cell lines, *Gene Chromosome Canc.* **23**, 116-122.

- Laureys, G., Speleman, F., Opdenakker, G., Benoit, Y., and Leroy, J. (1990). Constitutional translocation t(1;17)(p36;q12-21) in a patient with neuroblastoma, *Gene Chromosome Canc.* 2, 252-4.
- Laureys, G., Speleman, F., Versteeg, R., van der Drift, P., Chan, A., Leroy, J.,
5 Francke, U., Opdenakker, G., and Van Roy, N. (1995). Constitutional translocation t(1;17)(p36.31-p36.13; q11.2q12.1) in a neuroblastoma patient. establishment of somatic cell hybrids and identification of PND/a12m2 on chromosome 1 and NF1/SCYA7 on chromosome 17 as breakpoint flanking single copy markers, *Oncogene* 10, 1087-1093.
- 10 Levan, A. and Levan, G. (1978). Have double minutes functioning centromeres? *Hereditas* 88, 81-92.
- Nelson, D. L., Ledbetter, S. A., Corbo, L., Victoria, M. F., Ramirez-Solis, R., Webster, T. D., Ledbetter, D. H., and Caskey, C. T. (1989). Alu polymerase chain reaction: a method for rapid isolation of human-specific sequences from complex DNA sources,
15 *Proc. Natl. Acad. Sci. U. S. A.* 86, 6686-90.
- Plantaz, D., Mohapatra, G., Matthay, K. K., Pellarin, M., Seeger, R. C., and Feuerstein, B. G. (1997). Gain of chromosome 17 is the most frequent abnormality detected in neuroblastoma by comparative genomic hybridization, *Am. J. Pathol.* 150, 81-9.
- Ragnarsson, G., Eiriksdottir, G., Johannsdottir, J. T., Jonasson, J. G., Egilsson, V., and
20 Ingvarsson, S. (1999). Loss of heterozygosity at chromosome 1p in different solid human tumours: association with survival, *Br. J. Cancer* 79, 1468-1474.
- Raymond, E., Faivre, S., Weiss, G., McGill, J., Davidson, K., Izbicka, E., Kuhn, J. G., Allred, C., Clark, G. M. and Von Hoff, D. D. (2001). Effects of hydroxyurea on extrachromosomal DNA in patients with advanced ovarian carcinomas, *Clin. Cancer*
25 *Res.* 7, 1171-80.
- Riley, J., Butler, R., Ogilvie, D., Finniear, R., Jenner, D., Powell, S., Anand, R., Smith, J. C., and Markham, A. F. (1990). A novel, rapid method for the isolation of terminal sequences from yeast artificial chromosome (YAC) clones, *Nucleic Acid Res.* 18, 2887-2890.
- 30 Roth, M.B., Zahler, A. M. and Stolk, J. A. (1991). A conserved family of nuclear phosphoproteins localized to sites of polymerase II transcription, *J. Cell Biol.* 115, 587-596.
- Sambrook, J., Fritsch, E. F., and Maniatis, T. (1989). *Molecular Cloning. A Laboratory Manual* (Cold Spring Harbor, New York, Cold Spring Harbor Laboratory Press).

Sanger, F. (1981). Determination of nucleotide sequences in DNA, *Science* 214, 1205-1210.

Savelyeva, L., Corvi, R., and Schwab, M. (1994). Translocation involving 1p and 17q is a recurrent genetic alteration of human neuroblastoma cells, *Am. J. Hum. Genet.* 55, 334-40.

Schleiermacher, G., Peter, M., Michon, J., Hugot, J. P., Vielh, P., Zucker, J. M., Magdelenat, H., Thomas, G., and Delattre, O. (1994). Two distinct deleted regions on the short arm of chromosome 1 in neuroblastoma, *Gene Chromosome Canc.* 10, 275-81.

Schwab, M., Praml, C., and Amler, L. C. (1996). Genomic instability in 1p and human malignancies, *Gene Chromosome Canc.* 16, 211-29.

Shimizu, N., Nakamura, H., Kadota, T., Kitajima, K., Oda, T., Hirano, T. and Utiyama, H. (1994). Loss of amplified c-myc genes in the spontaneously differentiated HL-60 cells, *Cancer Res.* 54, 3561-7.

Shimizu, N., Itoh, N., Utiyama, H. and Wahl, G. M. (1998). Selective entrapment of extrachromosomally amplified DNA by nuclear budding and micronucleation during S phase, *J. Cell Biol.* 140, 1307-20.

Shimizu, N., Shimura, T. and Tanaka, T. (2000). Selective elimination of acentric double minutes from cancer cells through the extrusion of micronuclei, *Mutat. Res.* 448, 81-90.

Siebert, P. D., Chenchik, A., Kellogg, D. E., Lukyanov, K. A., and Lukyanov, S. A. (1995). An improved PCR method for walking in uncloned genomic DNA, *Nucleic Acids Res.* 23, 1087-1088.

Speleman, F., Van Gele, M., Maertens, L., and Van Roy, N. (1997). Improved protocol for chromatin fibre preparation from fixed cells. Technical Tips online, *Trends Genet.*, T01123.

Takeda, O., Homma, C., Maseki, N., Sakurai, M., Kanda, N., Schwab, M., Nakamura, Y., and Kaneko, Y. (1994). There may be two tumor suppressor genes on chromosome arm 1p closely associated with biologically distinct subtypes of neuroblastoma, *Gene Chromosome Canc.* 10, 30-9.

Tanaka, K., Yanoshita, R., Konishi, M., Oshimura, M., Maeda, Y., Mori, T., and Miyaki, M. (1993). Suppression of tumorigenicity in human colon carcinoma cells by introduction of normal chromosome 1p36 region, *Oncogene* 8, 2253-2258.

- van der Drift, P., Chan, A., Laureys, G., van Roy, N., Sickmann, G., den Dunnen, J., Westerveld, A., Speleman, F., and Versteeg, R. (1995). Balanced translocation in a neuroblastoma patient disrupts a cluster of small nuclear RNA U1 and tRNA genes in chromosomal band 1p36, *Gene Chromosome Canc.* **14**, 35-42.
- 5 van der Drift, P., Chan, A., van Roy, N., Laureys, G., Westerveld, A., Speleman, F., and Versteeg, R. (1994). A multimegabase cluster of snRNA and tRNA genes on chromosome 1p36 harbours an adenovirus/SV40 hybrid virus integration site, *Hum. Mol. Genet.* **3**, 2131-6.
- Von Hoff, D. D., Waddelow, T., Forseth, B., Davidson, K., Scott, J. and Wahl, G.
10 (1991). Hydroxyurea accelerates loss of extrachromosomally amplified genes from tumor cells. *Cancer Res.* **51**, 6273-9.
- Von Hoff, D. D., McGill, J. R., Forseth, B. J., Davidson, K. K., Bradley, T. P., Van Devanter, D. R. and Wahl, G. M. (1992). Elimination of extrachromosomally amplified MYC genes from human tumor cells reduces their tumorigenicity, *Proc. Natl. Acad. Sci.*
15 *U.S.A.* **89**, 8165-9.
- Van Roy, N., Cheng, N. C., Laureys, G., Opdenakker, G., and Speleman, F. (1995). Molecular cytogenetic analysis of 1;17 translocations in neuroblastoma, *Eur. J. Cancer* **31A**, 530-535.
- Van Roy, N., Jauch, A., Van Gele, M., Laureys, G., Versteeg, R., De Paepe, A.,
20 Cremer, T., and Speleman, F. (1997a). Comparative genomic hybridization analysis of human neuroblastomas: Detection of distal 1p deletions and further molecular genetic characterization of neuroblastoma cell lines, *Cancer Genet. Cytogenet.* **97**, 135-142.
- Van Roy, N., Laureys, G., Cheng, N. C., Willem, P., Opdenakker, G., Versteeg, R., and Speleman, F. (1994). 1;17 translocations and other chromosome 17 rearrangements in
25 human primary neuroblastoma tumors and cell lines, *Gene Chromosome Canc.* **10**, 103-114.
- Van Roy, N., Laureys, G., Van Gele, M., Opdenakker, G., Miura, R., vanderDrift, P., Chan, A., Versteeg, R., and Speleman, F. (1997b). Analysis of 1;17 translocation breakpoints in neuroblastoma: Implications for mapping of neuroblastoma genes, *Eur.*
30 *J. Cancer* **33**, 1974-1978.
- Vandesompele, J., Van Roy, N., Van Gele, M., Laureys, G., Ambros, P., Heimann, P., Devalck, C., Schuurin, E., Brock, P., Otten, J., Gyselinck, J., De Paepe, A., and Speleman, F. (1998). Genetic heterogeneity of neuroblastoma studied by comparative genomic hybridization, *Gene Chromosome Canc.* **23**, 141-152.

Versteeg, R., Caron, H., Cheng, N. C., Van der Drift, P., Slater, R., Westerveld, A., Voute, P. A., Delattre, O., Laureys, G., Van Roy, N., and Speleman, F. (1995). 1p36: every subband a suppressor?, *Eur. J. Cancer* 31A, 538-541.

White, P. S., Thompson, P. M., Seifreid, B. A., Sulman, E. P., Jensen, S. J., Guo, G.,
5 Maris, J. M., Hogarty, M. D., Allen, C., Biegel, J. A., Matise, T. C., Gregory, S. G.,
Reynolds, C. P., Brodeur, G. M. (2001). Detailed molecular analysis of 1p36 in
neuroblastoma, *Med Ped Oncol* 36, 37-41.

Zehetner, G., and Lehrach, H. (1994). The reference library system - sharing biological
material and experimental data, *Nature (London)* 367, 489-491.

10 Zhang, J., Glatfelter, A.A., Taetle, R., and Trent, J.M. (1999). Frequent alterations of
evolutionarily conserved regions of chromosome 1 in human malignant melanoma,
Cancer Genet Cytogenet. 111/119-123.

15

20

25

30

Claims

1. An isolated tumor suppressor gene product, comprising SEQ ID N° 202 or a functional fragment, variant or fusion protein thereof.
- 5 2. A functional fragment of a tumor suppressor gene product according to claim 1, whereby said functional fragment comprises at least SEQ ID N°2 or SEQ ID N° 161.
3. A variant of a tumor suppressor gene product according to claim 1, whereby said variant comprises at least a sequence selected from the group consisting of SEQ ID N° 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 198
10 and 200.
4. A fusion protein of a tumor suppressor gene product according to claim 1, whereby said fusion product comprises SEQ ID N° 163 or SEQ ID N° 165.
5. An isolated nucleic acid encoding a tumor suppressor gene product or a tumor suppressor gene product fragment, variant, or fusion product according to claim any of
15 the claims 1-4.
6. An isolated nucleic acid according to claim 5, comprising the sequence presented in SEQ ID N° 1.
7. An isolated nucleic acid according to claim 5, comprising the sequence presented in SEQ ID N° 3.
- 20 8. An isolated nucleic acid according to claim 5, comprising the sequence presented in SEQ ID N° 4.
9. An isolated nucleic acid according to claim 5, comprising the sequence presented in SEQ ID N° 201.
10. An isolated nucleic acid according to claim 5, comprising the sequence presented
25 in SEQ ID N° 203.
11. An isolated nucleic acid according to claim 5, comprising the sequence presented in SEQ ID N° 160.
12. An isolated nucleic acid according to claim 5, comprising the sequence selected from the group consisting of SEQ ID N° 166, 168, 172, 174, 176, 178, 180, 182, 184,
30 186, 188, 190, 192, 194, 196 and 199.
13. An isolated nucleic acid according to claim 5, comprising the sequence presented in SEQ ID N° 162 or SEQ ID N° 164.

14. The use of a nucleic acid according to any of the claims 5 - 13, or a nucleic acid with at least 60% identity to said nucleic acid, or a functional fragment thereof in diagnosis of cancer and/or prediction of the likelihood of developing cancer.

15. The use of a nucleic acid according to any of the claims 5 - 12, or a nucleic acid with at least 60% identity to said nucleic acid, or a functional fragment thereof in treatment of cancer.

16. The use of a tumor suppressor gene product, or a functional fragment or a variant thereof according to any of the claims 1 to 4, or a protein with at least 60% identity to said tumor suppressor gene product, for the manufacture of a medicament to treat cancer.

17. The use according to any of the claims 14 - 16, whereby said cancer is meningioma, colorectal cancer, gastric carcinoma and/or breast cancer.

18. The use according to any of the claims 14 - 16, whereby said cancer is neuroblastoma.

19. The use of a tumor suppressor gene product, or a functional fragment or a variant thereof according to any of the claims 1 to 4, or a protein with at least 60% identity to said tumor suppressor gene product for the generation of micronuclei and/or the removal of amplified DNA

20. A method for the production of antibodies against a tumor suppressor gene product, using a tumor suppressor gene product, or a functional fragment, variant or fusion product thereof according to any of the claims 1 - 4, or a protein with at least 60% identity to said tumor suppressor gene product, or an isolated nucleic acid encoding such polypeptide.

21. An antibody obtainable by the use according to claim 20.

22. The use of an antibody according to claim 21 in diagnosis of cancer and/or prediction of the likelihood of developing cancer.

23. The use of an antibody according to claim 22, whereby the cancer is meningioma, colorectal cancer, gastric carcinoma and/or breast cancer.

24. The use of an antibody according to claim 22, whereby the cancer is neuroblastoma

25. The use of a tumor suppressor gene product or a functional fragment, variant or fusion product thereof according to any of the claims 1 - 4, or a protein with at least 60% identity to said tumor suppressor gene product, for the isolation of an interacting compound.

Figure 1

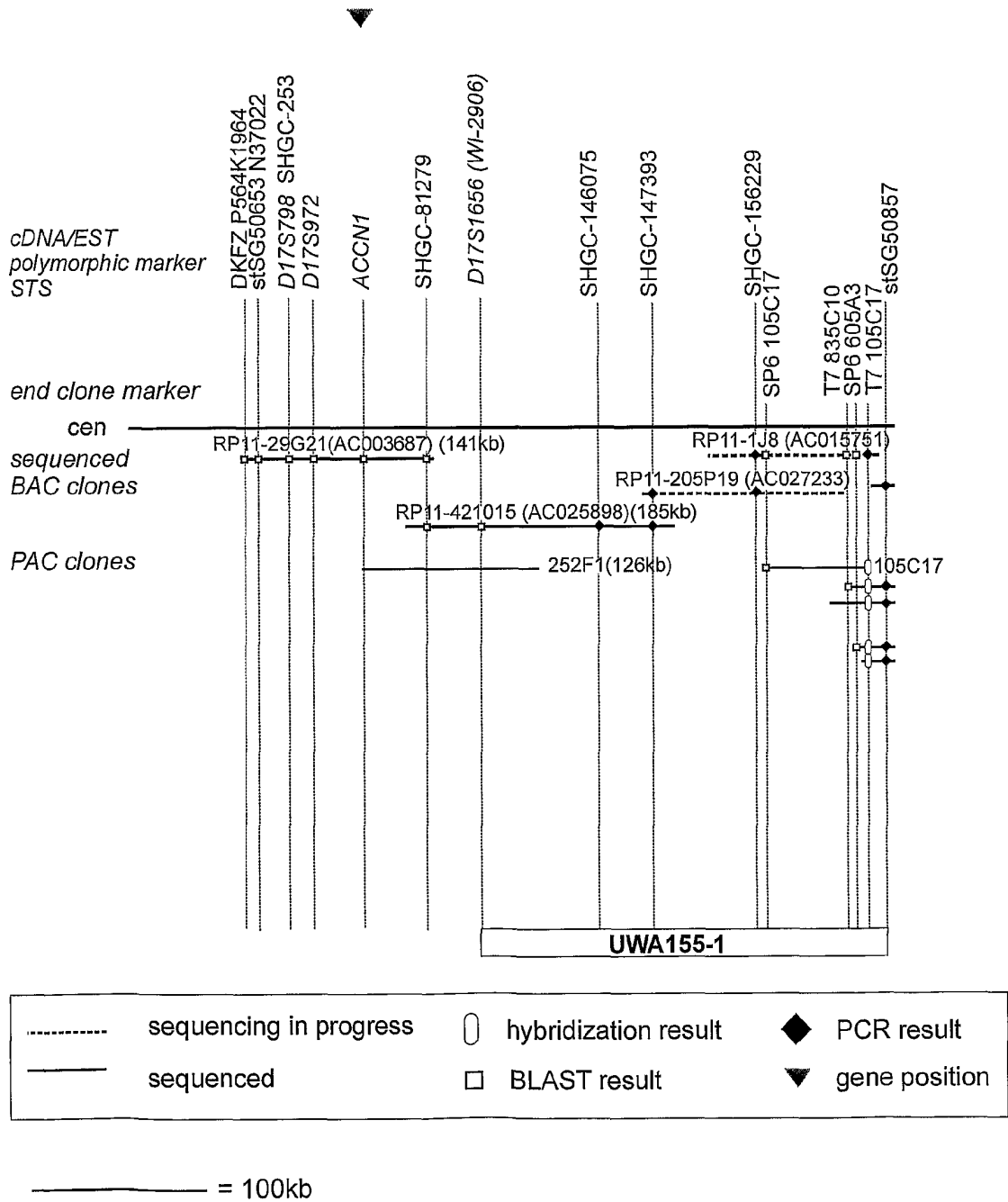
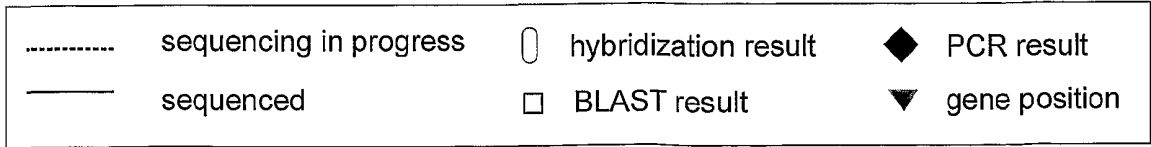
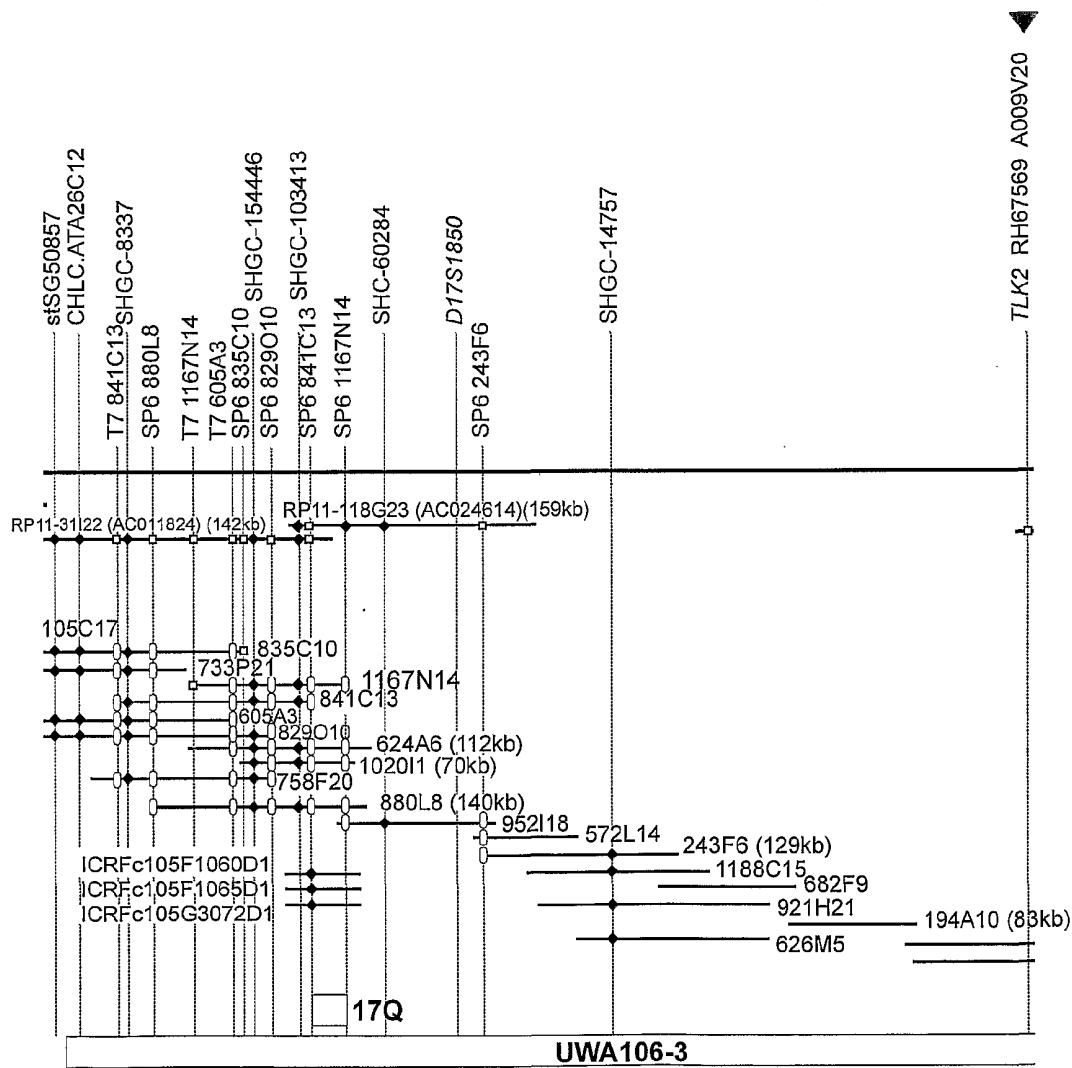
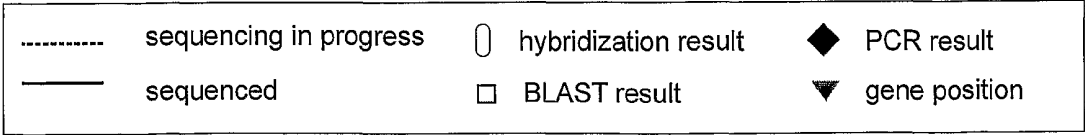
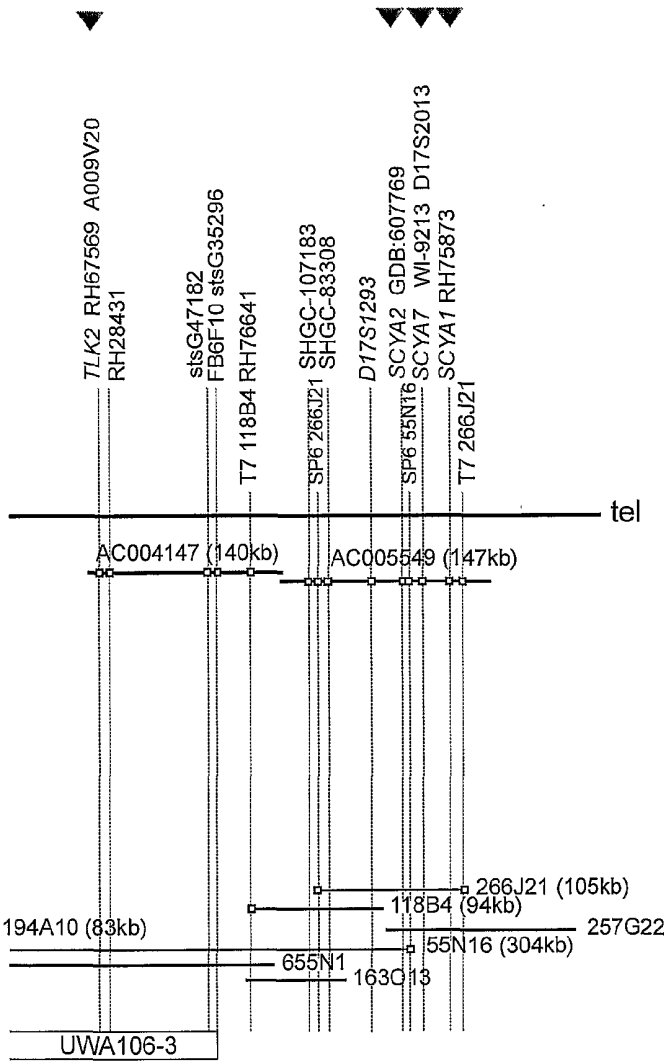


Figure 1 (cont.)



—— = 100kb

Figure 1 (cont.)



— = 100kb

Figure 2

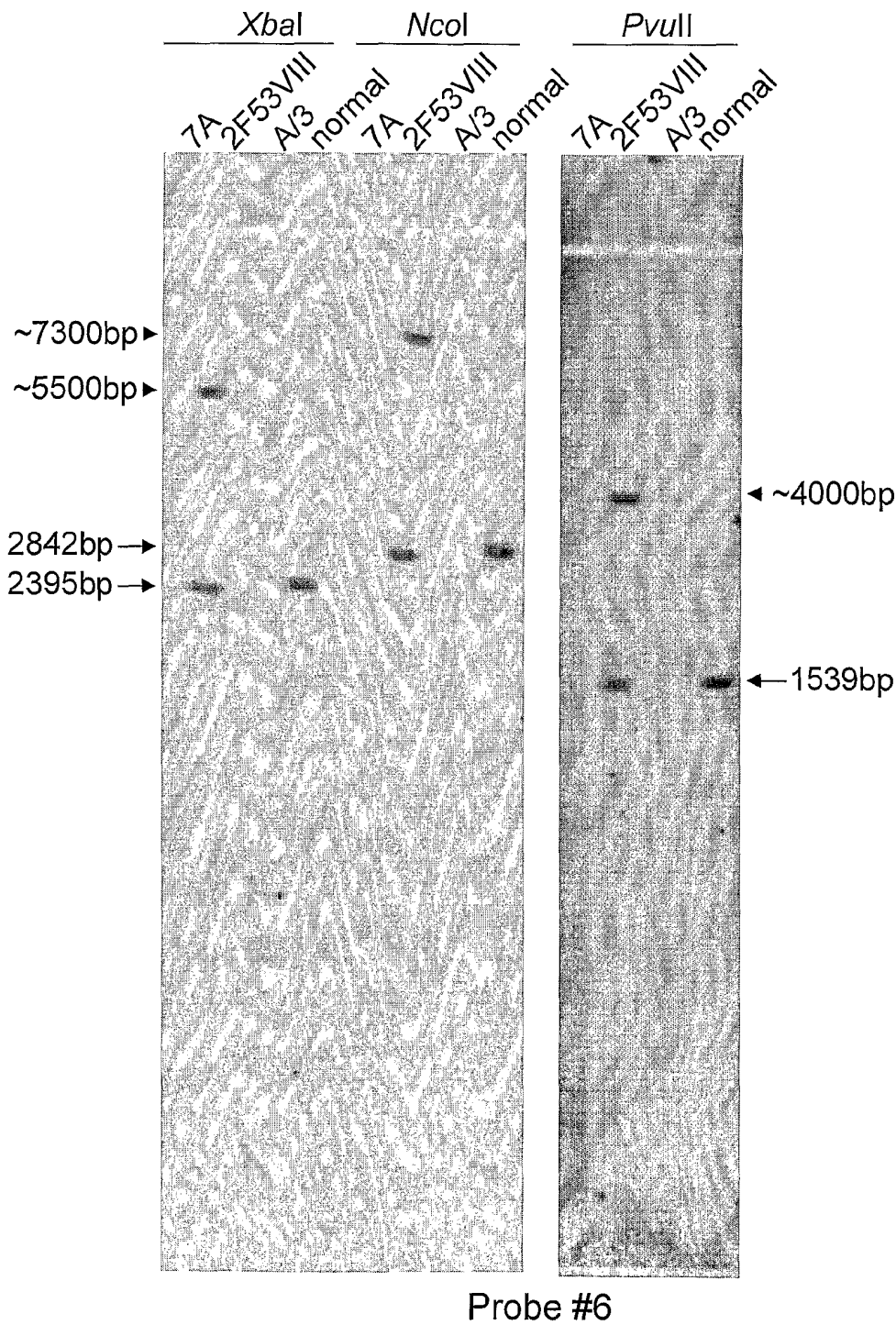


Figure 3 A - B

5/75

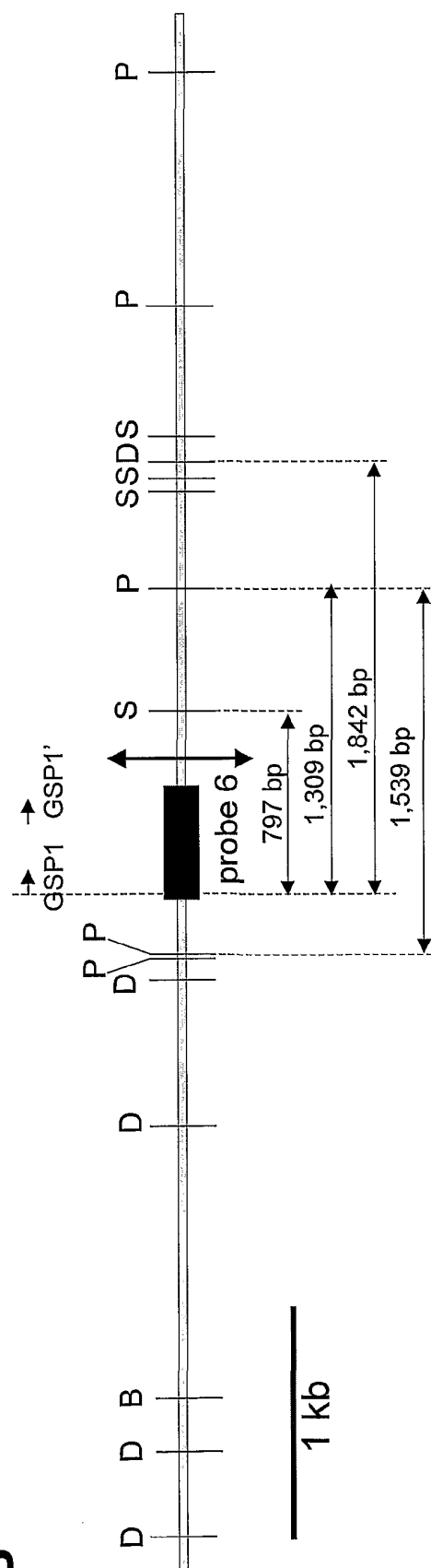
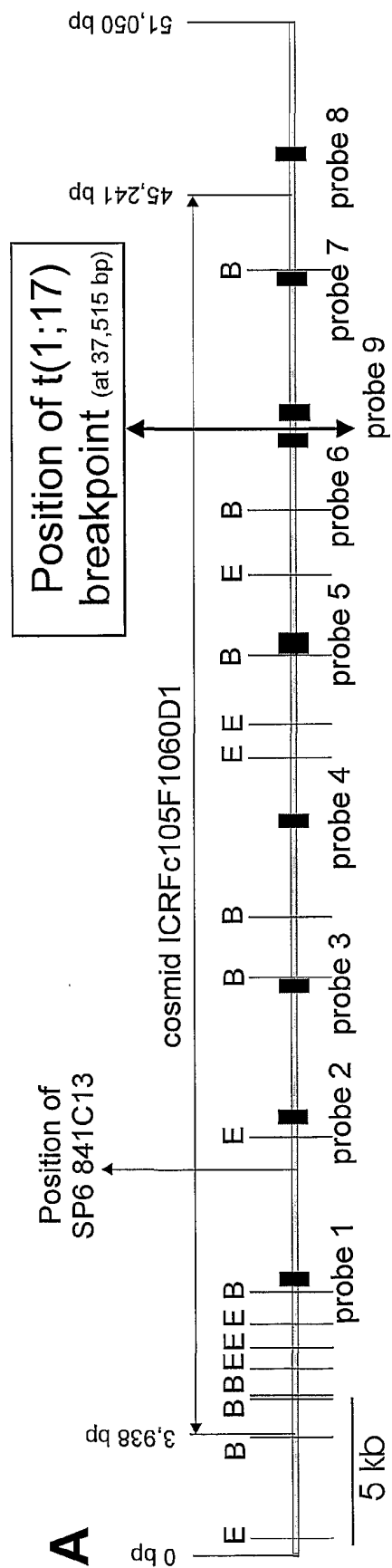
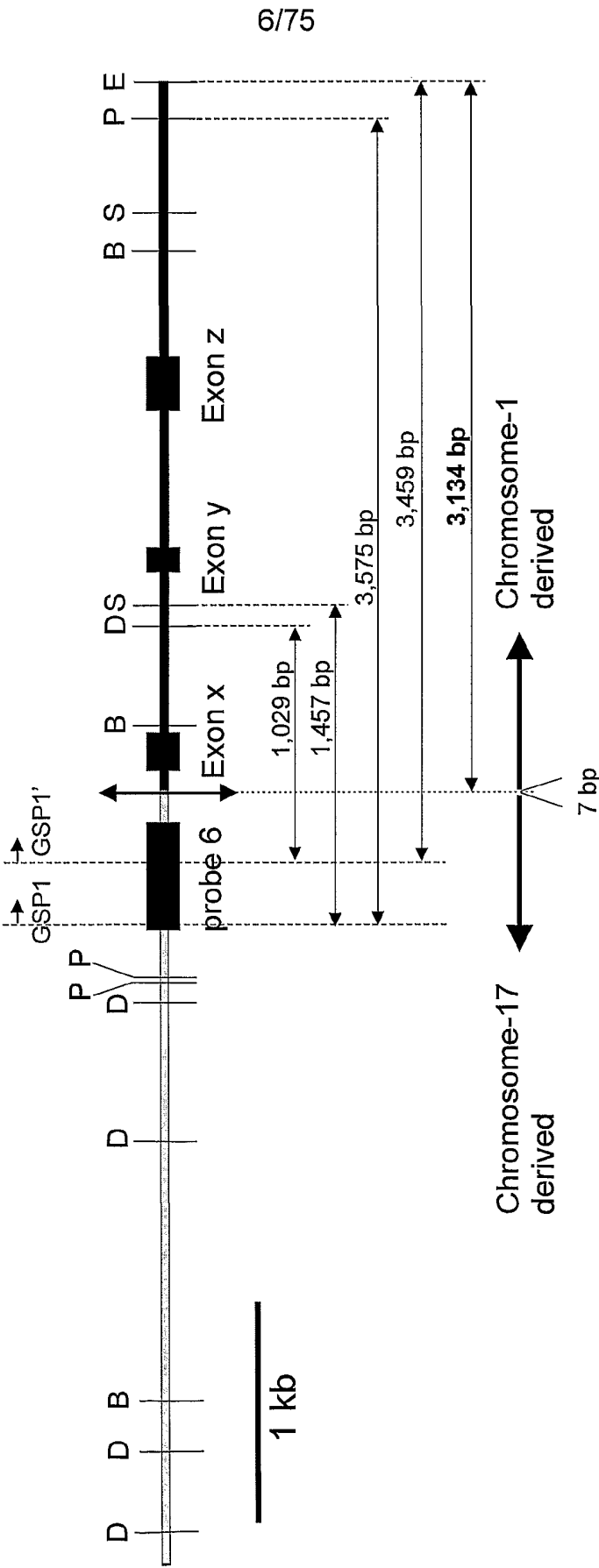


Figure 3 C



8/75

Figure 5 A

10	20	30	40	50	60	70
<u>cccctcagctctgtgcattttgtctacaagcaaggtagcttttgggttagtgtgttcatgtttcaacaag</u>						
80	90	100	110	120	130	140
<u>aatgtaagtttgggatacagacatatgttacccctgttgtagtagctttgcaatcagtcctttgcaaaaa</u>						
150	160	170	180	190	200	210
<u>atatccagaacaaggctagaacaaggtagggtacagaaaacaataaacacgtgttacagttacatatgagctt</u>						
220	230	240	250	260	270	280
<u>ggattacctcctttatagaagggaagtggagacatccttcacgcagagatttaggatctctcactagcact</u>						
290	300	310	320	330	340	350
<u>aaccctcttgccccacctaagtgtttatttcaatcacccctgttgctttttatcaaatgaaagatacaga</u>						
360	370	380	390	400	410	420
<u>tccacttttaagagtaaaagaagagaggaagcacagtttatttaattaccattgggtatcccaaggacttgt</u>						
430	440	450	460	470	480	490
<u>gcttccattatctcattgttttatttcatttaataatccaaacactcatcagcagggatttcttgggggc</u>						
500	510	520	530	540	550	560
<u>ctaccttgactgggctctgtggtcctgggagatgcagcaggggaatagatcacaggttgcaactcatag</u>						
570	580	590	600	610	620	630
<u>agagaaccttctagctggggagagacagacaacaatgacaaaaaGGAAAGTGctttttcaaccacttccttat</u>						

Figure 5 B

640	650	660	670	680	690	700
gctaccatgaaacctagttgggctctgtgtgtctgattccccctggcttattcttactttttccctc						
710	720	730	740	750	760	770
cctttccagGCTCAGCAGGGAGCTGCTGGAGGCAGTAGAGCCTGAAGTCTTGCAGGACTCACTGGATAGA						
L S R E L L E A V E P E V L Q D S L D R						
Exon x						
780	790	800	810	820	830	840
TGTTATTCAACTCCTTCCAGTTGTCTTGAACAGCCTGACTCCCTGCCCTATGGAAGTTCCTTTTATG						
C Y S T P S S C L E Q P D S C L P Y G S S F Y						
Exon x						
850	860	870	880	890	900	910
CATTGGAGGAAAAACATGTTGGCTTTTCTCTTGACGTGGGAGgtgagtacctttctatgaaggtgataag						
A L E E K H V G F S L D V G						
Exon x						
920	930	940	950	960	970	980
gatccactgagtcttccatataaagatcatattcctgctccaagtggccattactgagctgagagatgtc						
990	1000	1010	1020	1030	1040	1050
attgctgcagtgaggacctataggcacatgtaggttgaaatgaaactctagtcttaactggaagcccagac						
1060	1070	1080	1090	1100	1110	1120
atgggatgggtcagtgagcatggctctcttcctagtctcaggccatgcctgtggcactctgattctactc						
1130	1140	1150	1160	1170	1180	1190
tcatgacattggacctgggcagatgtgacaaaattcagagaactatgatttttgactcaagggtttgtagat						

Figure 5 C

1200	1210	1220	1230	1240	1250	1260
ttcctttttcactctctaatttcagtgctctaaagtcctcacaaacctgaacaatctgagtat						tttgatgagac
1270	1280	1290	1300	1310	1320	1330
agggtctaaatattgcagtttttctcctagaaaatcatttgagggtatttgcttttaaattgattgggaaaaat						
1340	1350	1360	1370	1380	1390	1400
atggcataactgtttgcacaaactcgggacaaaatgatattgggataacgatctactagaaatagggacatt						
1410	1420	1430	1440	1450	1460	1470
ttacccacagtttctgtggagaaaaaacccagggaatttctctatcatgaccagccttcaggcctcctgaaatat						
1480	1490	1500	1510	1520	1530	1540
atctctcacagtcctctattcttatgtctgaggagcctgaggtccctgtgtgagtagacagtggttg						
1550	1560	1570	1580	1590	1600	1610
ttatgtgtgtaggggaatcagccttaatgtgtctgtccatgtctgaatttattgcag						AAATTGAAAAAGAAAG
1620	1630	1640	1650	1660	1670	1680
GGGAAGGGGAAGAAAGGGGAAGAGATCAACGAAAGAAAAAGAGAGAGGGGAAAGAAAGAGGGG						
G K G K K R R G R R S T K K R R R R R G R K E G						Exon Y
1690	1700	1710	1720	1730	1740	1750
AAGAAGATCAAAACCCACCATGCCCCAGgttaactttcagcaattgtggatgcttaattctgtgttaacac						
E E D Q N P P C P R						Exon Y
1760	1770	1780	1790	1800	1810	1820
ctggaggccaacagatttcagggaaccagagtggtgttgatttcatgttttcaacgaaggctgaattactc						

Figure 5 D

1830	1840	1850	1860	1870	1880	1890
ctactgtcatgtgctgttgggttttcattgcagtagatgttttaggtttccattttcccttctcctcccttatcatt						
1900	1910	1920	1930	1940	1950	1960
tactaacgtaccataggaatgaccatacttcaaaagctgtactctcgtggtggccactgcacatcgaattttgagc						
1970	1980	1990	2000	2010	2020	2030
atatatttggaactattgagctcactcttttcatgatcgagtttgctgtgtgtcatgagggcacta						
2040	2050	2060	2070	2080	2090	2100
actcagagtgccttttactcccttaccagtatgtcacctggccaattcactagctcactttctctctgt						
2110	2120	2130	2140	2150	2160	2170
ctctgtctctgtctctctctgtcttttctctcttttcattgttttctacctggccctgttctatcccac						
2180	2190	2200	2210	2220	2230	2240
ataaaggcaataatttttttttacctcattaatggatctatcccttttcttttcttaccactttcctta						
2250	2260	2270	2280	2290	2300	2310
cgttacttctgaaatctagtggggctctgtggtgtctgattttccctggctgttctttagttttgtctg						
2320	2330	2340	2350	2360	2370	2380
cttttccagGCTCAGCGGTGTGCTGATGGAAGTGGAAGAGCCCTGAAATCTTGCAGGACTCACTGGATAGA						
<u>L S G V L M E V E E P E I L Q D S L D R</u>						
2390	2400	2410	2420	2430	2440	2450
TGTTATTCGACTCCGTCAATGTTCTTTGAACCTACCTGACTCATTCAGCACTACAGAAGTGTTTACT						
C Y S T P S M F F E L P D S F Q H Y R S V F Y Exon z						
2460	2470	2480	2490	2500	2510	2520
CATTGAGGAACAGCACATCAGCTTCGCCCTTGACGTGGACAATAGTTTCTTACTTTGATGGGAACAAG						
S F E E Q H I S F A L D V D N R R F L T L M G T S Exon z						

Figure 5 F

3230 3240 3250 3260 3270 3280 3290
aggagtcaggagccgctggcaggagacagcatgtcaccaggactctgccggtgcagaatatgaacaaacg
3300 3310 3320 3330 3340 3350 3360
ccatgttcttgcagaaaaacgcttagccctgagtttcataggaggtaatcacccagacaactgcagaatgttag
3370 3380 3390 3400 3410 3420 3430
aacactgagcaggacaactgacctgtctccttcacatagtcacataatcacacaacaaaaag
3440 3450 3460 3470 3480 3490 3500
gagaagagatatatttgggttcaaaaaagtaaaaagataataatagctgcatttctttagttattttgaac
3510 3520 3530 3540 3550 3560 3570
cccaaatatttcctcatctttttgttgttcattgattggtggatggacttggtttatatagaggacag
3580 3590 3600 3610 3620 3630 3640
gtcagctgtctggctcaatgatctacattctgaagtgtctgaaaatgtcttcatgattaaattcagcct
3650 3660 3670 3680 3690 3700 3710
aaacgttttgcggggaacactgcagagacaatgctgtgagtttccaaccttagcccatctgcggggcagag
3720 3730 3740
aaggctctagtttgtccatcagcattatcatgat

Figure 7 B

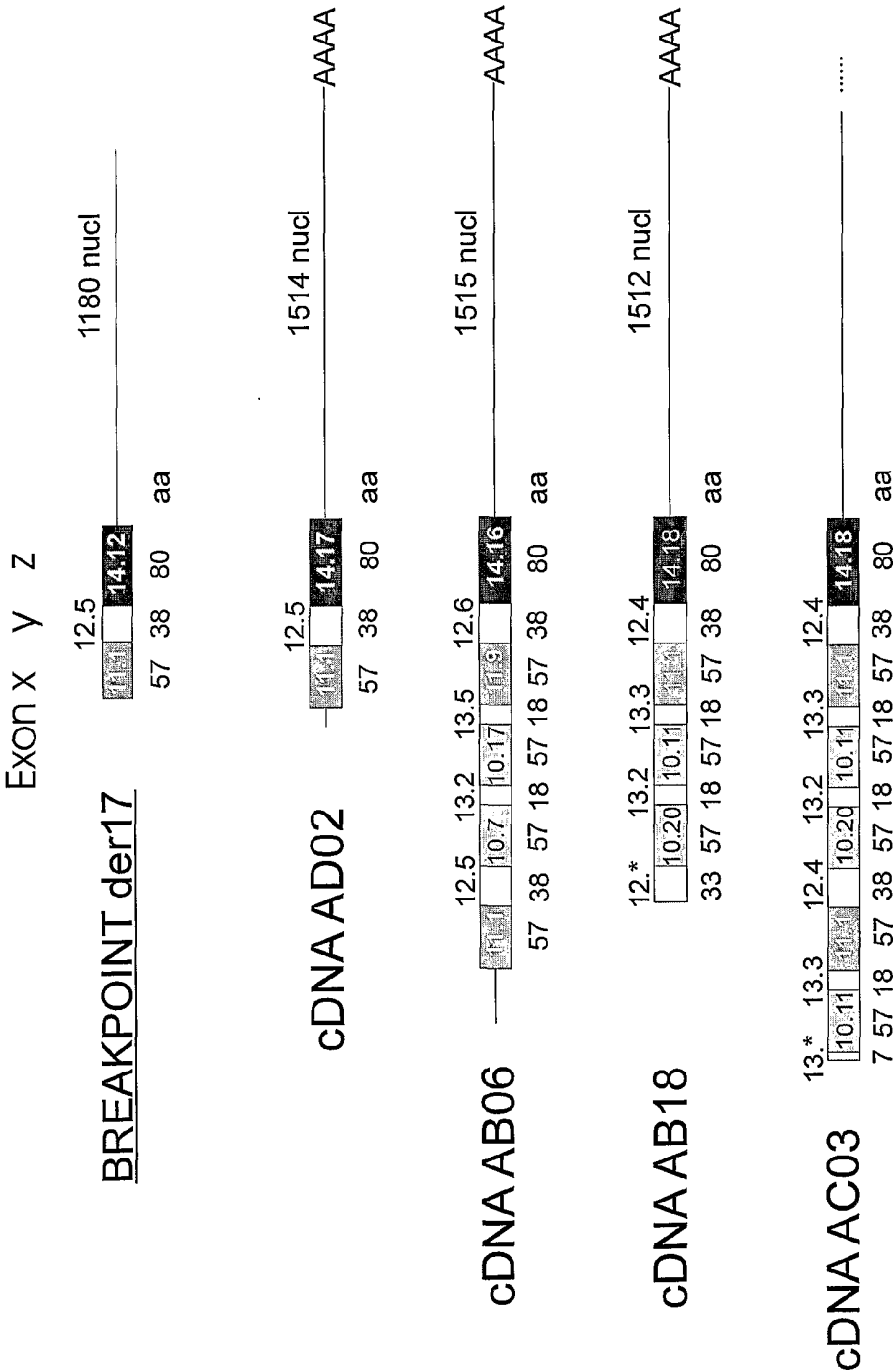


Figure 7 C

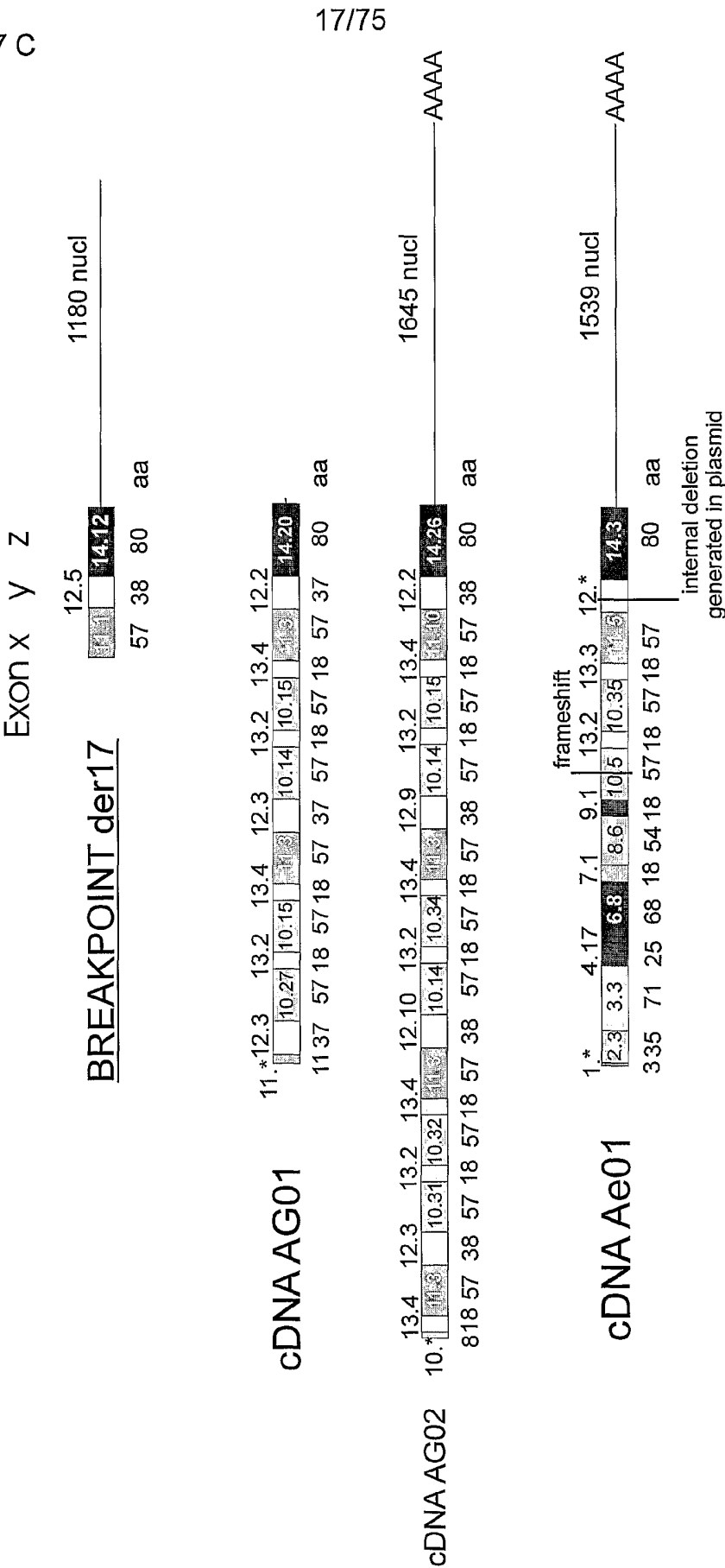


Figure 9 A

19/75

AT-exon0

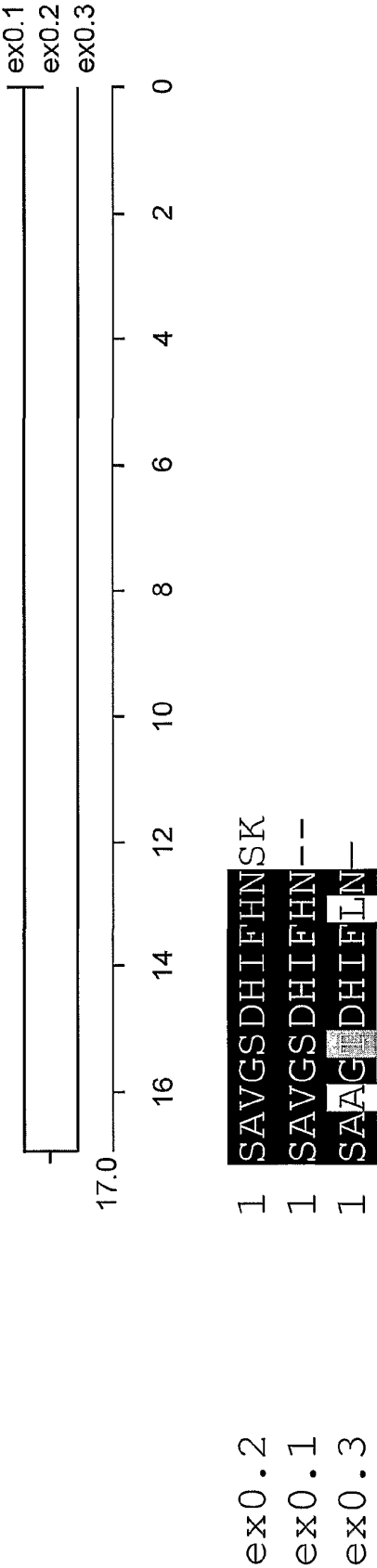


Figure 9 B

20/75

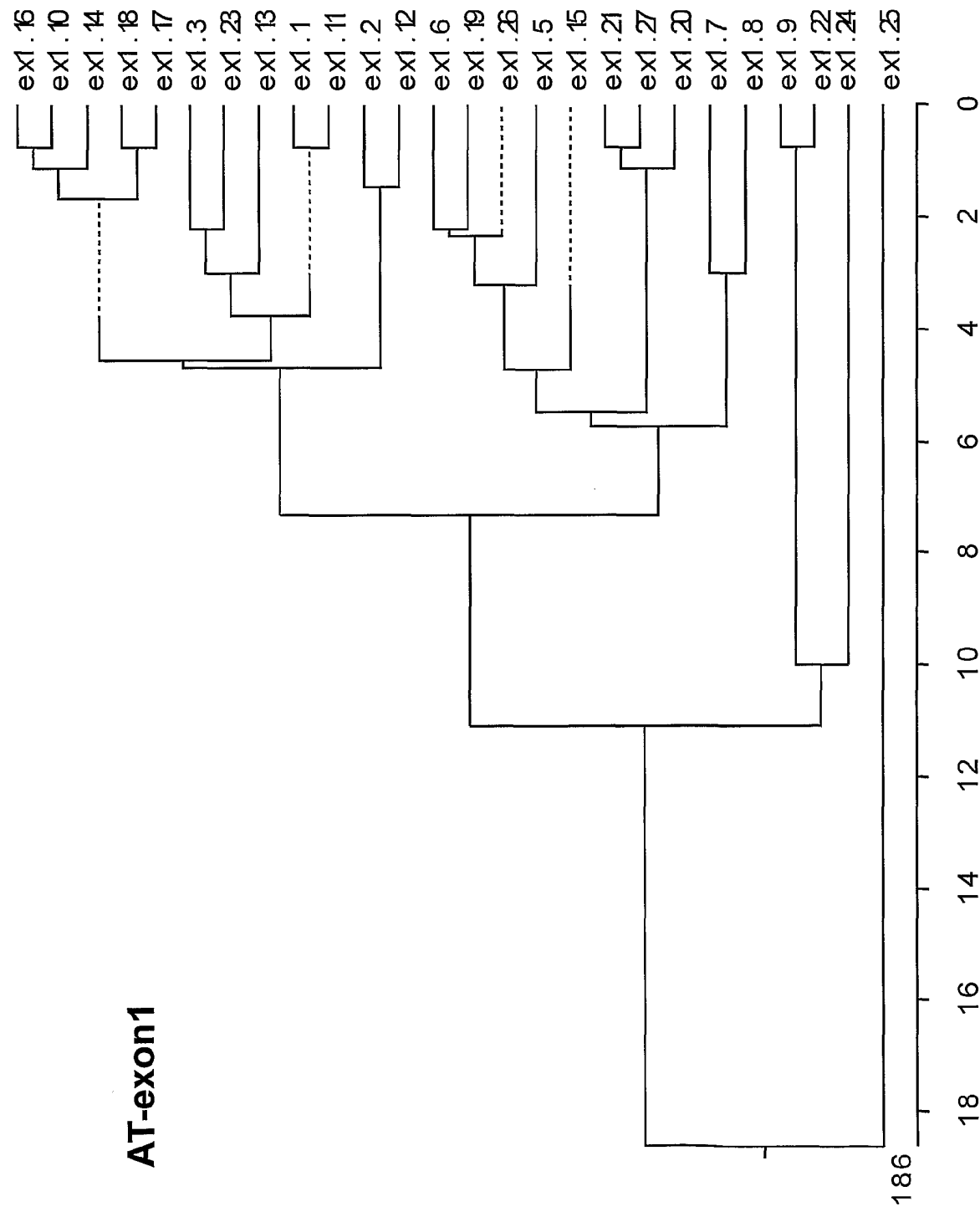
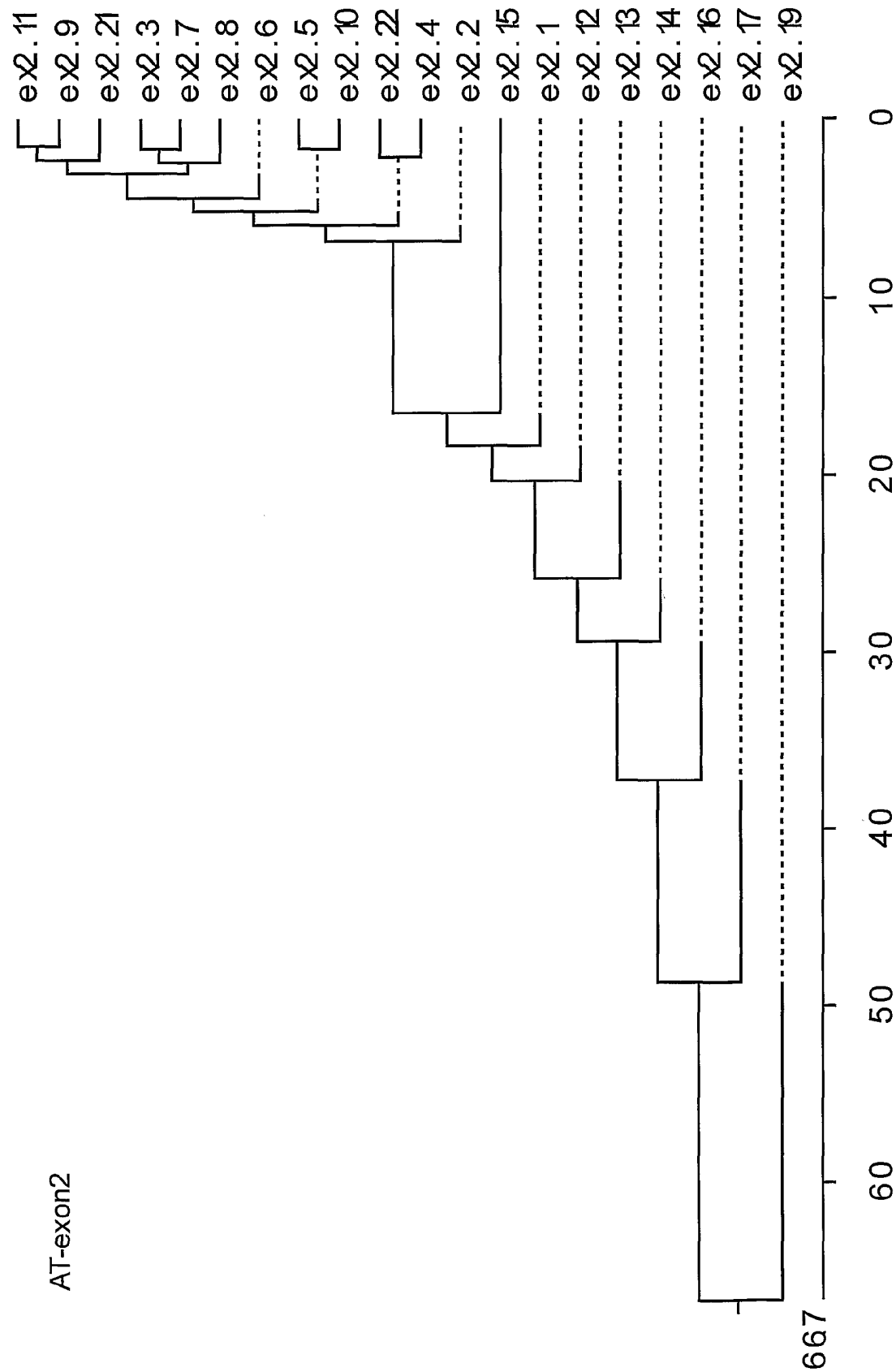


Figure 9 C

AT-exon1

ex1.16	1	VPGPTSSATNVSMVV	SAGP	LSSEKAEMNILEINEKLRPQ	LAEKKQQFRNLKEKCF	TQL	GF	LANQOKKY
ex1.10	1	VPGPTSSATNVSMVV	SAGP	LSSEKAEMNILEINEKLRPQ	LAEKKQQFRNLKEKCF	TQL	GF	LANQOKKY
ex1.14	1	VPGPTSSATNVSMVV	SAGP	LSSEKAEMNILEINEKLRPQ	LAEKKQQFRNLKEKCF	TQL	AGF	LANQOKKY
ex1.18	1	VPGPTSSATNVSMVV	SAGP	LSSEKAEMNILEINEKLRPQ	LAEKKQQFRNLKEKCF	TQL	AGF	LANRQOKKY
ex1.17	1	VPGPTSSATNVSMVV	SAGP	LSSEKAEMNILEINEKLRPQ	LAEKKQQFRNLKEKCF	TQL	AGF	LANQOKKY
ex1.3	1	VPGPTSSATNVSMVV	SAGP	LSSEKAEMNILEINEKLRPQ	LAEKKQQFRNLKEKCF	TQL	AGF	LAKQOKKY
ex1.23	1	VPGPTSSATNVSMVV	SAGP	LSSEKAEMNILEINEKLRPQ	LAEKKQQFRNLKEKCF	TQL	AGF	LAKQOKKY
ex1.13	1	VPGPTSSATNVSMVV	SAGP	LSSEKAEMNILEINEKLRPQ	LAEKKQQFRNLKEKCF	TQL	AGF	LANQOKKY
ex1.1	1	VPGPTSSATNVSMVV	SAGP	LSSEKAEMNILEINEKLRPQ	LAEKKQQFRNLKEKCF	TQL	AGF	LANQOKKY
ex1.11	1	VPGPTSSATNVSMVV	SAGP	LSSEKAEMNILEINEKLRPQ	LAEKKQQFRNLKEKCF	TQL	AGF	LANQOKKY
ex1.2	1	VPGPTSSATNVSMVV	SAGP	LSSEKAEMNILEINEKLRPQ	LAEKKQQFRNLKEKCF	TQL	AGF	LANQOKKY
ex1.12	1	VTGTTSSATNVSMVV	SAGP	LSSEKAEMNILEINEKLRPQ	LAEKKQQFRNLKEKCF	TQL	AGF	LANQOKKY
ex1.6	1	VPDSTSSATNVSMVV	SAGP	LSSEKAEMNILEINEKLRPQ	LAEKKQQFRNLKEKCF	TQL	AGF	LANRQOKKY
ex1.19	1	VPDSTSSATNVSMVV	SAGP	LSSEKAEMNILEINEKLRPQ	LAEKKQQFRNLKEKCF	TQL	AGF	LANRQOKKY
ex1.26	1	VPDSTSSATNVSMVV	SAGP	LSSEKAEMNILEINEKLRPQ	LAEKKQQFRNLKEKCF	TQL	AGF	LANRQOKKY
ex1.5	1	VPDSTSSATNVSMVV	SAGP	LSSEKAEMNILEINEKLRPQ	LAEKKQQFRNLKEKCF	TQL	AGF	LANQOKKY
ex1.15	1	VPDSTSSATNVSMVV	SAGP	LSSEKAEMNILEINEKLRPQ	LAEKKQQFRNLKEKCF	TQL	AGF	LANRQOKKY
ex1.21	1	VPDSTSSATNVSMVV	SAGP	LSSEKAEMNILEINEKLRPQ	LAEKKQQFRNLKEKCF	TQL	AGF	LANRQOKKY
ex1.27	1	VPDSTSSATNVSMVV	SAGP	LSSEKAEMNILEINEKLRPQ	LAEKKQQFRNLKEKCF	TQL	AGF	LANRQOKKY
ex1.20	1	VPDSTSSATNVSMVV	SAGP	LSSEKAEMNILEINEKLRPQ	LAEKKQQFRNLKEKCF	TQL	AGF	LANQOKKY
ex1.7	1	VPDSTSSATNVSMVV	SAGP	LSSEKAEMNILEINEKLRPQ	LAEKKQQFRNLKEKCF	TQL	AGF	LANRQOKKY
ex1.8	1	VPDSTSSATNVSMVV	SAGP	LSSEKAEMNILEINEKLRPQ	LAEKKQQFRNLKEKCF	TQL	AGF	LANRQOKKY
ex1.9	1	VPDSTSSATNVSMVV	SAGP	LSSEKAEMNILEINEKLRPQ	LAEKKQQFRNLKEKCF	TQL	AGF	LANRQOKKY
ex1.22	1	VPDSTSSATNVSMVV	SAGP	LSSEKAEMNILEINEKLRPQ	LAEKKQQFRNLKEKCF	TQL	AGF	LANRQOKKY
ex1.24	1	VPDSTSSATNVSMVV	SAGP	LSSEKAEMNILEINEKLRPQ	LAEKKQQFRNLKEKCF	TQL	AGF	LANQOKKY
ex1.25	1	VPDSTSSATNVSMVV	SAGP	LSSEKAEMNILEINEKLRPQ	LAEKKQQFRNLKEKCF	TQL	AGF	LANQOKKY

Figure 10 A

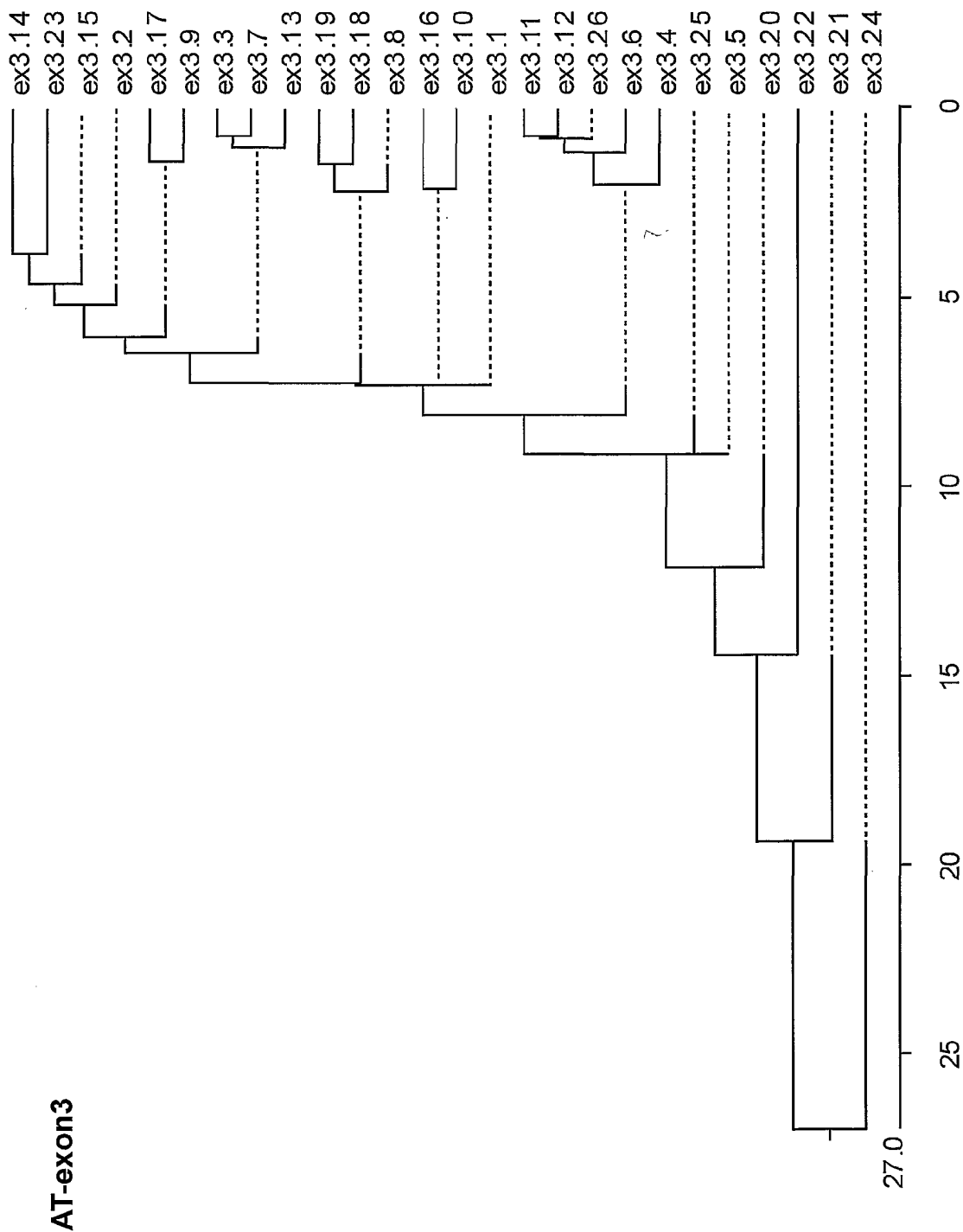


23/75

Figure 10 B
AT-exon2

ex2.11	1	EYEECKDLI	P	MLRNERQFKEEKLAEQ	LKQAEELR
ex2.9	1	EYEECKDLI	F	MLRNERQFKEEKLAEQ	LKQAEELR
ex2.21	1	EYEECKDLIK	F	MLRNERQFKEEKLAEQ	LKQAEELR
ex2.3	1	KYEECKDLIK	F	MLRNERQFKEEKLAEQ	LKQAEELR
ex2.7	1	KYEECKD	V	IKFMLRNERQFKEEKLAEQ	LKQAEELR
ex2.8	1	EYEECKDLIK	F	MLRNERQFKEEKLAEQ	LKQAEELR
ex2.6	1	EYEECKDLIK	M	LRNERQFKEEKLAEQ	LKQAEELR
ex2.5	1	EYEECKDLIK	S	MLRNERQFKEEKLAEQ	LKQAEELR
ex2.10	1	EYEECKDLIK	S	LRNERQFKEEKLAEQ	LKQAEELR
ex2.22	1	E	N	EECKDLIKSMLRNERQFKEEKLAEQ	LKQAEELR
ex2.4	1	-----	D	LIKSMLRNERQFKEEKLAEQ	LKQAEELR
ex2.2	1	KYEECKDLIK	S	MLRNERQFKEEKLAEQ	LKQAEELR
ex2.15	1	EYEECKDLIK	S	MLR	ERLLTEEKLAELGQAEELR
ex2.1	1	KYEECKDLIK	S	MLRNE	LOFKEEKLAEQ
ex2.12	1	EYEECKDLIK	S	MLREEL	QFKEEKLAEQ
ex2.13	1	EYEEFKDLIK	S	MLREEL	QFK
ex2.14	1	ECEECKDLIK	S	LRNELOFKE	-KLAEQLQAEELR
ex2.16	1	ECEECKDLIK	S	RRLRELOFKEEKLAEK	LQAGKLR
ex2.17	1	ECEEYKD	I	DSLRRELO	-SMEKLAEK
ex2.19	1	ECEEHKG	T	ESQLGEKM	QFKEEKLAEKSTQAEELR

Figure 10 C



25/75

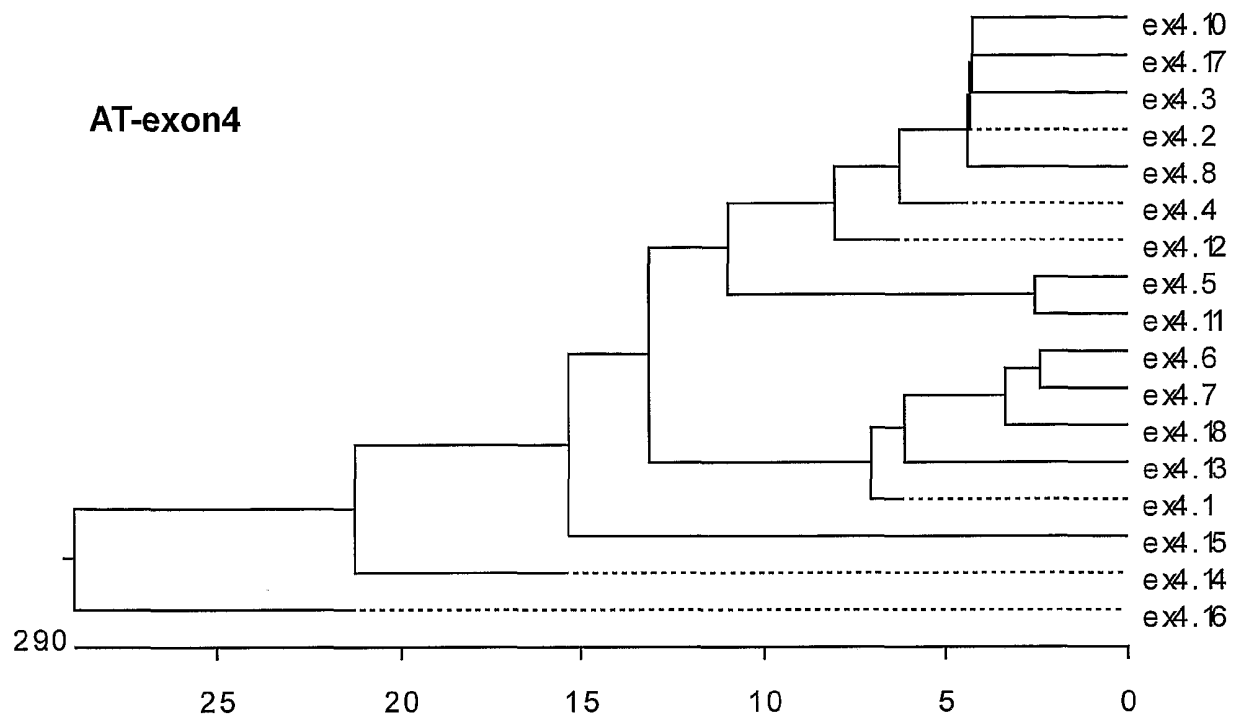
Figure 10 D

AT-exon3

ex3.14	1	QYKVLVHSQERELTQLEKLEGRDASRSLSNEHLQALLTLDEPDKSQGDLEQLAEGCRLAQHLVQKLS
ex3.23	1	.YKVPVHSQE.ELTQLEKLEGRDASRSLSNEHLQALLTLDEWDKS.GQDLEQLAEGCRLAQHLVQKLS
ex3.15	1	QYKVLVHSQERELTQLEKLEGRDASRSLSNEHLQALLTLDEPDKSQGDLEQLAEGCRLAQHLVQKLS
ex3.2	1	QYKVLVHSQERELTQLEKLEGRDASRSLSNEHLQALLTLDEPDKSQGDLEQLAEGCRLAQHLVQKLS
ex3.17	1	QYKVLVHQAQERELTQLEKLEGRDASRSLSNEHLQALLTPYEPDKSQGDLEQLAEGCRLAQHLVQKLS
ex3.9	1	QYKVLVHSQERELTQLEKLEGRDASRSLSNEHLQALLTPDEPDKSQGDLEQLAEGCRLAQHLVQKLS
ex3.3	1	QYKVLVHQAQERELTQLEKLEGRDASRSLSNEHLQALLTPDEPDKSQGDLEQLAEGCRLAQHLVQKLS
ex3.7	1	QYKVLVHQAQERELTQLEKLEGRDASRSLSNEHLQALLTPDEPDKSQGDLEQLAEGCRLAQHLVQKLS
ex3.13	1	QYKVLVHQAQERELTQLEKLEGRDASRSLSNEHLQALLTPDEPDKSQGDLEQLAEGCRLAQHLVQKLS
ex3.19	1	QYKVLVHSQERELTQLEKLEGRDASRSLSNEHLQALLTPDEPDKSQGDLEQLAEGCRLAQHLVQKLS
ex3.18	1	QYKVLVHSQERELTQLEKLEGRDASRSLSNEHLQALLTPDEPDKSQGDLEQLAEGCRLAQHLVQKLS
ex3.8	1	QYKVLVHSQERELTQLEKLEGRDASRSLSNEHLQALLTPYEPDKSQGDLEQLAEGCRLAQHLVQKLS
ex3.16	1	QYKVLVHSQERELTQLEKLEGRDASRSLSNEHLQALLTPDEPDKSQGDLEQLAEGCRLAQHLVQKLS
ex3.10	1	QYKVLVHSQERELTQLEKLEGRDASRSLSNEHLQALLTPDEPDKSQGDLEQLAEGCRLAQHLVQKLS
ex3.1	1	QYKVLVHSQERELTQLEKLEGRDASRSLSNEHLQALLTPDEPDKSQGDLEQLAEGCRLAQHLVQKLS
ex3.11	1	QYKVLVHSQERELTQLEKLEGRDASRSLSNEHLQALLTPDKPKSQGDLEQLAEGCRLAQHLVQKLS
ex3.12	1	QYKVLVHSQERELTQLEKLEGRDASRSLSNEHLQALLTPDKPKSQGDLEQLAEGCRLAQHLVQKLS
ex3.26	1	QYKVLVHSQERELTQLEKLEGRDASRSLSNEHLQALLTPDKPKSQGDLEQLAEGCRLAQHLVQKLS
ex3.6	1	QYKVLVHSQERELTQLEKLEGRDASRSLSNEHLQALLTPDEPDKSQGDLEQLAEGCRLAQHLVQKLS
ex3.4	1	QYKVLVHSQERELTQLEKLEGRDASRSLSNEHLQALLTPDEPDKSQGDLEQLAEGCRLAQHLVQKLS
ex3.25	1	QYKVLVHSQERELTQLEKLEGRDASRSLSNEHLQALLTPDEPDKSQGDLEQLAEGCRLAQHLVQKLS
ex3.5	1	QYKVLVHSQERELTQLEKLEGRDASRSLSNEHLQALLTPDEPDKSQGDLEQLAEGCRLAQHLVQKLS
ex3.20	1	QYKVLVHSQERELTQLEKLEGRDASRSLSNEHLQALLTPDEPDNSQGRDLREQLAEGCRLAQHLVQKLS
ex3.22	1	QYKALVHSQAELTQLEKLEGRDASRSLSNEHLQALLTPDKPKSQGDLEQLAEGCRLAQHLVQKLS
ex3.21	1	QYKVLVHSQERELTQLEKLEGRDASRSLSNEHLQALLTPDKHNSQGDLEQLAEGCRLAQHLVQKLS
ex3.24	1	QYKVLVHSQAARELAWLRKLEKLEGRDASRSLSNEHLQALLTPDEPDNSQGDLEQLAEGCRLAQHLVQKLS

26/75

Figure 11 A

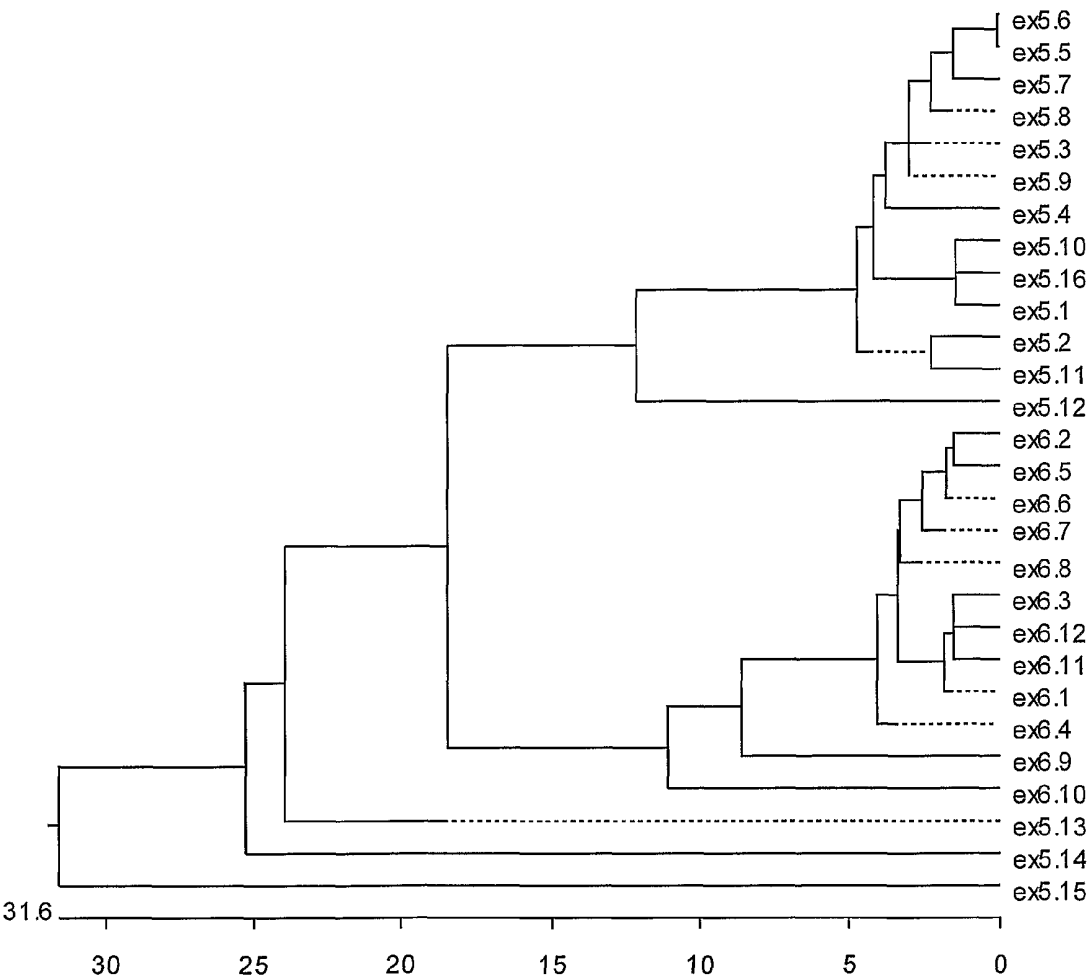


ex4.10	1	ENDNDDEDVQVEVAEKVQKSSAPR
ex4.17	1	ENDNDDEDVQVEVAEKVQKSSAPR
ex4.3	1	ENDNDDEDVQVEVAEKVQKSSAPR
ex4.2	1	ENDNDDEDVQVEVAEKVQKSSAPR
ex4.8	1	ENDNDHDEDVQVEVAEKVQKSSAPR
ex4.4	1	ENDNDDEDVQVELAEKVQKSSAPR
ex4.12	1	ENDNDDEDVQVEVAEKVQESSAPR
ex4.5	1	ENDEDEDEDVQVEEAEKVQKSSAPR
ex4.11	1	ENDEDEDEDVQVEEAEKVQKSSAPR
ex4.6	1	ENDEDEDEDVQVEEAEKVLESSAPR
ex4.7	1	ENDEDEDEDVQVEEAEKVLESSAPR
ex4.18	1	ENDKDEDEDVQVEEAEKVLESSAPR
ex4.13	1	ENKDEDEDVQVEEAEKVLESSAPR
ex4.1	1	ENDEDEDEDVQVEEAEKVLESSAPR
ex4.15	1	ENDDEDEDVKVEEAEKVQELYAPR
ex4.14	1	ENDEDEDKDVVEEAEKVQESCAPR
ex4.16	1	ENDEDVDVDVYVEEAEKVRESRAPR

27/75

Figure 11 B

AT-exon5-6



28/75

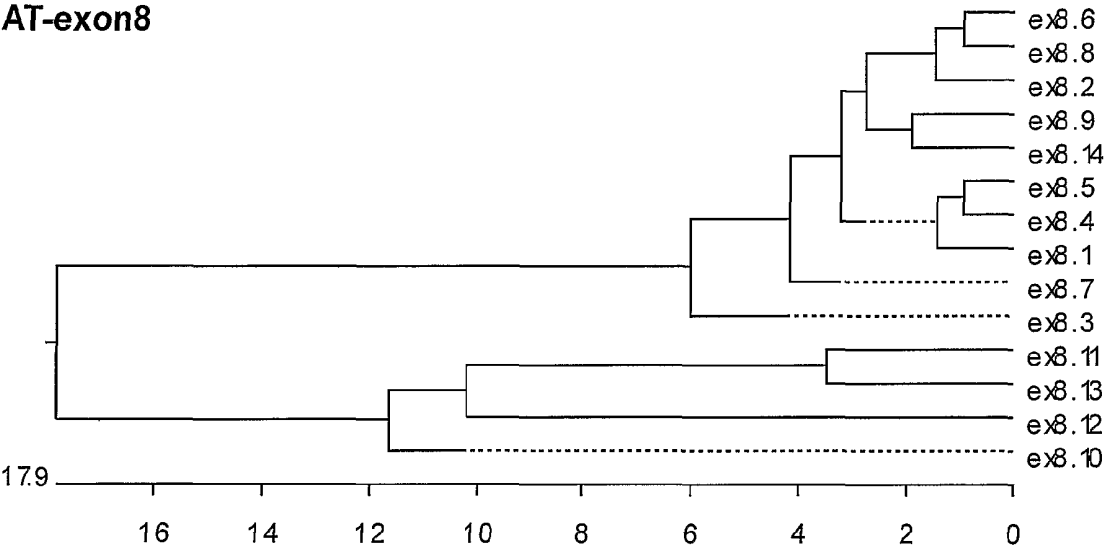
Figure 11 C

AT-exon5-6

ex5.6	1	EVQKAEESKVAEDSLEECALTCNSNSHGPCDSNQPHKNITKITF-EDEVNSTLVVDRESSH-DECCDAVNILP
ex5.5	1	EVQKAEESKVAEDSLEECALTCNSNSHGPCDSNQPHKNITKITFEEDEVNSTLVVDRESSH-DECCDAVNILP
ex5.7	1	EVQKAEVSKVPEDSLEECALTCNSNSHGPCDSNQPHKNITKITFEEDEVNSTLVVDRESSH-DECCDAVNILP
ex5.8	1	EVHKAEEESKVPEDSLEECALTCNSNSHGPCDSNQPHKNITKITFEEDEVNSTLVVDRESSH-DECCDAVNILP
ex5.3	1	EVQKTFEESKVPEDSLEECALTCNSNSHGPCDSNQPHKNITKITFEEDEVNSTLVVDRESSH-DECCDAVNILP
ex5.9	1	EVQKAEESKVPEDSLEECALTCNSNSHGPCDSNQPHKNITKITFEEDEVNSTLVVDRESSH-DECCDAVNILP
ex5.4	1	EVQKAEESKVPEDSLEECALTCNSNSHGPCDSNQPHKNITKITFEEDKVNSTLVVDKSSH-DECCDAVNILP
ex5.10	1	EVQKAEESKVPEDSLEECALTCNSNSHGPCDSNQPHKNITITFEEDKVNSTLVVDRESSH-DECCDAVNILP
ex5.16	1	EVQKAEESKVPEDSLEECALTCNSNSHGPCDSNQPHKNITITFEEDKVNSTLVVDRESSH-DECCDAVNILP
ex5.1	1	EVQKAEESKVPEDSLEECALTCNSNSHGPCDSNQPHKNITITFEEDKVSALVVDRESSH-DECCDAVNILP
ex5.2	1	EVQKAEESKVPEDSLEECALTCNSNSHGPCDSNQPHKNITITFEEDKVSALVVDRESSH-DECCDAVNILP
ex5.11	1	EVQKAEESKVPEDSLEECALTCNSNSHGPCDSNQPHKNITITFEEDKVSALVVDRESSH-DGCCDAVNILP
ex5.12	1	EEQKAEESKVPEDSLEECALTCNSNSHGPCDSNQPHKNITITSEEDKVSILVVDSESSQ-DEWCDANILL
ex6.2	1	EMQKAEESKVPEDSLEECALTCNSNSHGPGYDSNQPHKTKITITFEEDKVDSTLGS--SSH-VEWEDAVHIIP
ex6.5	1	EMQKAEESKVPEDSLEECALTCNSNSHGPGYDSNQPHKTKITITFEEDKVDSTLGS--SSH-VEWEDAVHIIP
ex6.6	1	EMQKAEESKVPEDSLEECALTCNSNSHGPGYDSNQPHKTKITITFEEDKVDSTLGS--SSH-VEWEDAVHIIP
ex6.7	1	EMQKAEESKVPEDSLEECALTCNSNSHGPGYDSNQPHKTKITITFEEDKVDSTLGS--SSH-VEWEDAVHIIP
ex6.8	1	EMQKAEESKVPEDSLEECALTCNSNSHGPGYDSNQPHKTKITITFEEDKVDSTLGS--SSH-VEREDAVHIIP
ex6.3	1	EMPQKAEESKVPEDSLEECALTCNSNSHGPGYDSNQPHKTKITITFEEDKVDSTLGS--SSH-VEWEDAVHIIP
ex6.12	1	DMQKAEESKVPEDSLEECALTCNSNSHGPGYDSNQPHKTKITITFEEDKVDSTLGS--SSH-VEWEDAVHIIP
ex6.11	1	EMQKAEESKVPEDSLEECALTCNSNSHGPGYDSNQPHKTKITITFEEDKVDSTLGS--SSH-VEWEDAVHIIP
ex6.1	1	EMQKAEESKVPEDSLEECALTCNSNSHGPGYDSNQPHKTKITITFEEDKVDSTLGS--SSH-VEWEDAVHIIP
ex6.4	1	EMQKAEESKVPEDSLEECALTCNSNSHGPGYDSNQPHKTKITITFEEDKVDSTLGS--SSH-VEWEDAVHIIP
ex6.9	1	EVQKAEESKVPEDSLEECALTCNSNSHGPGYDSNQPHKTKITITFEEDKVDSTLGS--SSH-VEWEDAVHIIP
ex6.10	1	EVQKAEESKVPEDSLEECALTCNSNSHGPGYDSNQPHKTKITITFEEDKVDSTLGS--SSH-DE-EDAVHIIP
ex5.13	1	EVQKAEESKVPEDSLEECALTCNSNSHGPGYDSNQPHKTKITITFEADKFDGLVDSSESSH-DEWEDAVHIIP
ex5.14	1	EVQKTFEESKVPEDSLEECALTCNSNSHGPGYDSNQPHKTKITITFEHEVDKVDSTLSEHPH-DEEAVNIPP
ex5.15	1	EVQKAEESKVPEDSLEECALTCNSNSHGPGYDSNQPHKTKITITFEESKVDKVDSTLSESSHYGEEVAVNIPP

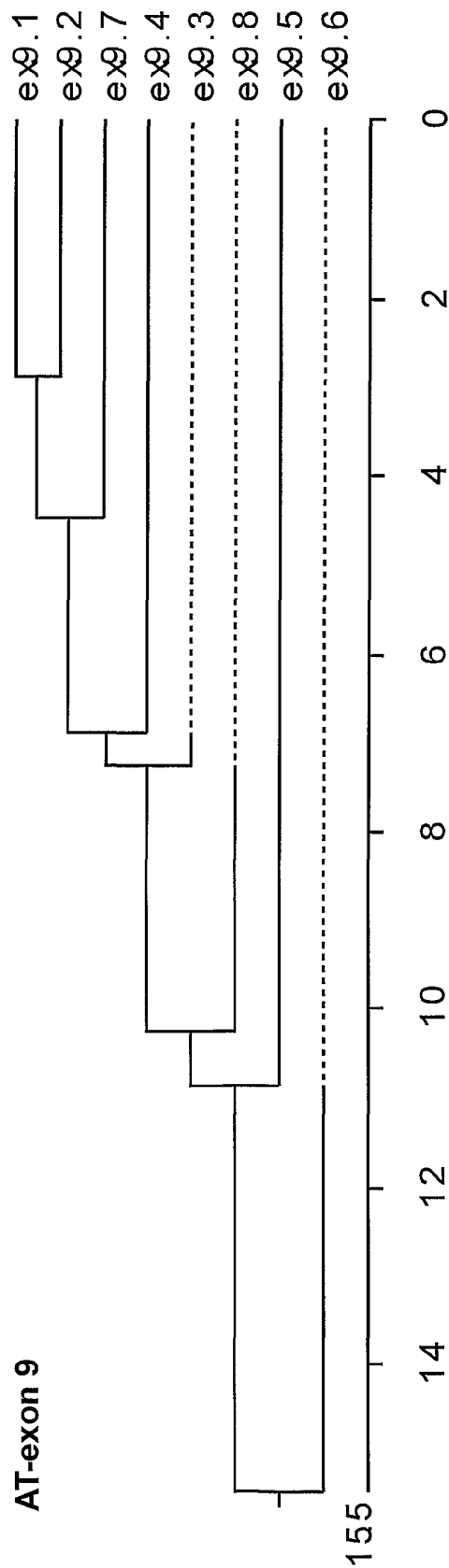
Figure 12 B

AT-exon8



ex8.6	1	NLQSEEEEEVPQESWDEGYSTPSIPPEMLASYKSYSSTFHSLEEQQVC	AVDIG
ex8.8	1	NLQSEEEEEVPQESWDEGYSTPSIPPEMLASYKSYSSTFHSLEEQQVC	AVDIG
ex8.2	1	NLQSEEEEEVPQESWDEGYSTLSIPPEMLASYKSYSSTFHSLEEQQVC	AVDIG
ex8.9	1	NLQSEEEEEVPQESWDEGYSTLSIPPEMLASNKFYSSTFHSLEEQQVC	AVDIG
ex8.14	1	NLQSEEEEEVPQESWDEGYSTLSIPPE-----	
ex8.5	1	NLQSEEEEEVPQESWDEGYSTLSIPPEMLASYQSYSGTFHSLEEQQVC	AVDIG
ex8.4	1	NLQSEEEEEVPQESWDEGYSTLSIPPEMLASYQSYSGTFHSLEEQQVC	AVDIG
ex8.1	1	NLQSEEEEEVPQESWDEGYSTLSIPPEMLASYQSYSTFHSLEEQQVC	AVDIG
ex8.7	1	NLQSEEEEEVPQESWDEGYSTLSIPPERLASYSSTFHSLEEQQVC	AVDIG
ex8.3	1	NLQSEEEEEVPQESWDEGYSTLSIPPE-----	
ex8.11	1	NLQSEEEEEAPQESWDEGDWTLSPPEMSASYQSDRSTFHSLEEQQVGLA	DIG
ex8.13	1	NLQES-----MSASYQSDRSTFHSLEEQQVGLA	DIG
ex8.12	1	NLQSEEEEEAPQESWDEGYSTLSIPPEMSALYQSYRSTFHSLEEQQVGLA	DIG
ex8.10	1	NLQSEEEEEAPQESWDEGYSTLSIPPEKMSASYQSYRSTFHSLEEQQVGLA	VIG

Figure 12 C



ex9.1	1	RHRWDQVKKEDQEATGPR
ex9.2	1	RHRWDQVKKEDHEATGPR
ex9.7	1	GHRWDQVKKEDHEATGPR
ex9.4	1	GHRWDQVKKEDQEATGPR
ex9.3	1	GHRWDQVKKEDQEATGPR
ex9.8	1	GHRWDQVKKEDQEATGPR
ex9.5	1	GHRWDQVKKEDQEATDPR
ex9.6	1	GHRWDQVKKEDQEATSPR

Figure 13 A

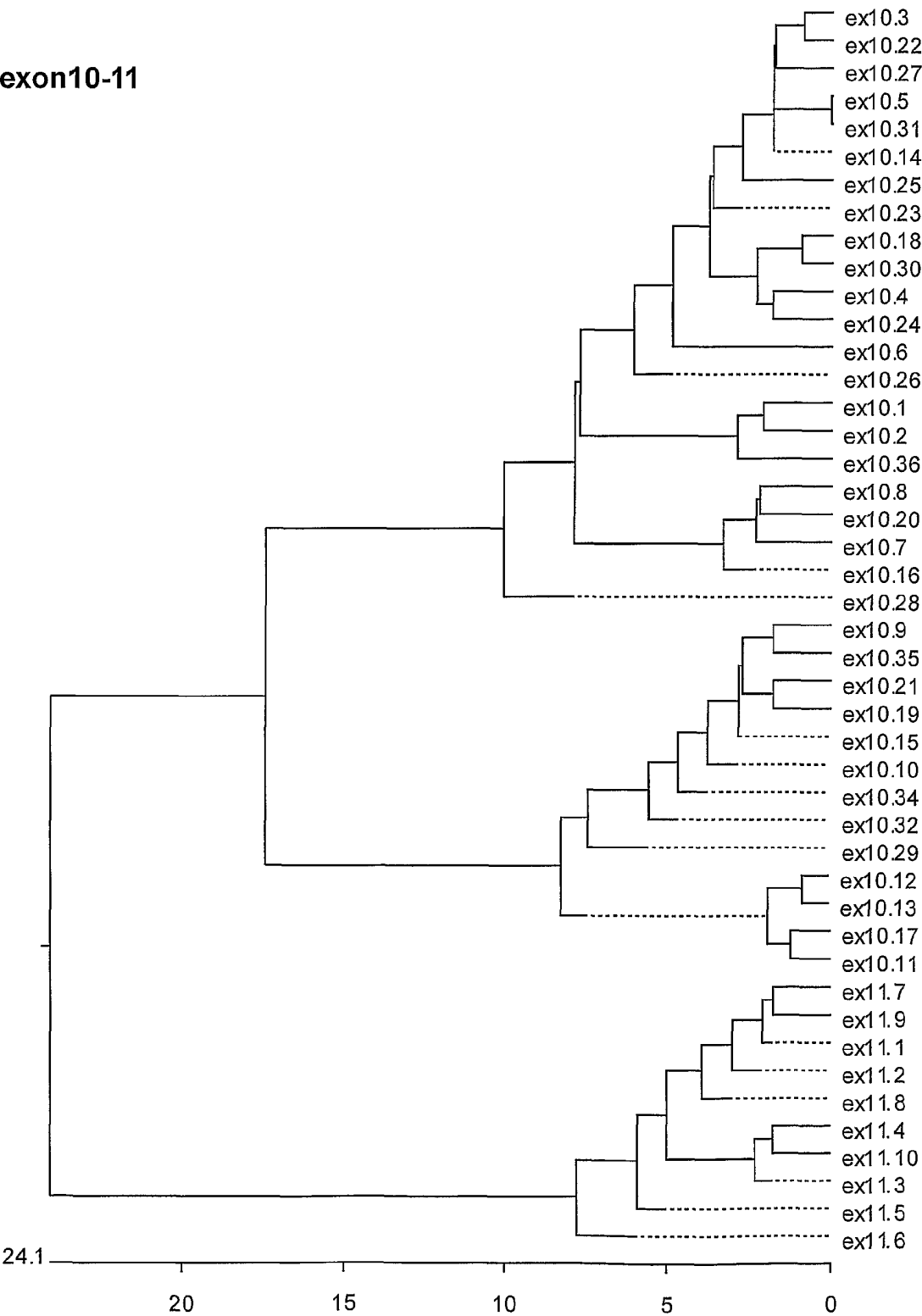


Figure 13 B

exon10-11

1	ex10.3	LSRELLDEKGP	EV	LQ	DSL	DR	CYST	PS	GC	LE	L	T	D	S	C	Q	P	Y	R	S	A	F	V	L	E	Q	V	G	L	A	N	M	D			
1	ex10.22	LSRELLDEKGP	EV	LQ	DSL	DR	CYST	PS	GC	LE	L	T	D	S	C	Q	P	Y	R	S	A	F	V	L	E	Q	V	G	L	A	H	M	D			
1	ex10.27	LSRELLDEKGP	EV	LQ	DSL	DR	S	YST	PS	GC	LE	L	T	D	S	C	Q	P	Y	R	S	A	F	V	L	E	Q	V	G	L	A	D	M			
1	ex10.5	LSRELLDEKGP	EV	LQ	DSL	DR	CYST	PS	GC	LE	L	T	D	S	C	Q	P	Y	R	S	A	F	V	L	E	X	Q	V	G	L	A	D	M			
1	ex10.31	LSRELLDEEGP	EV	LQ	DSL	DR	CYST	PS	GC	LE	L	T	D	S	C	Q	P	Y	R	S	A	F	V	L	E	Q	V	G	L	A	D	M	D			
1	ex10.14	LSRELLDEKGP	EV	LQ	DSL	DR	CYST	PS	GC	LE	L	T	D	S	C	Q	P	Y	R	S	A	F	V	L	E	Q	V	G	L	A	D	M	D			
1	ex10.25	LSRELLDEKGP	EV	LQ	DSL	DR	CYST	PS	GC	LE	L	T	D	S	C	Q	P	Y	R	S	A	F	V	L	E	Q	V	G	L	A	D	M	D			
1	ex10.23	LSRELLDEKGP	EV	LQ	DSL	DR	CYST	PS	GC	LE	L	T	D	S	C	Q	P	Y	R	S	A	F	V	L	E	Q	V	G	L	A	D	M	D			
1	ex10.18	LSRELLDEKGP	EV	LQ	DSL	DR	CYST	PS	GC	LE	L	T	D	S	C	Q	P	Y	R	S	A	V	I	L	E	Q	C	V	G	L	A	D	M			
1	ex10.30	LSRELLDEKGP	EV	LQ	DSL	DR	CYST	PS	GC	LE	L	T	D	S	C	Q	P	Y	R	S	A	F	I	L	E	Q	C	V	G	L	A	D	M			
1	ex10.4	LSRELLDEKGP	EV	LQ	DSL	DR	CYST	PS	GC	LE	L	T	D	S	C	Q	P	Y	R	S	A	F	I	L	E	Q	V	G	L	A	D	M	D			
1	ex10.24	LSRELLDEKGP	EV	LQ	DSL	DR	CYST	PS	GC	LE	L	T	D	S	C	Q	P	Y	R	S	A	F	I	L	E	Q	V	G	L	A	D	M	D			
1	ex10.6	LSGELLDEKEP	EV	LQ	DSL	DR	CYST	PS	GC	LE	L	T	D	S	C	Q	P	Y	R	S	A	F	I	L	E	Q	V	G	L	A	D	M	D			
1	ex10.26	LSRELLDEKEP	EV	LQ	DSL	DR	CYST	PS	GC	LE	L	T	D	S	C	Q	P	Y	R	S	A	F	V	L	E	Q	V	G	L	A	D	M	D			
1	ex10.1	LSRELLAEKEP	EV	LQ	DSL	DR	W	YST	PS	V	Y	L	G	L	T	D	P	C	P	Y	R	S	A	F	V	L	E	Q	V	G	L	A	D	M		
1	ex10.2	LSRELLAEKEP	EV	LQ	DSL	DR	CYST	PS	V	Y	L	G	L	T	D	S	C	Q	P	Y	R	S	A	F	V	L	E	Q	V	G	L	A	D	M		
1	ex10.36	LSRELLDEKEP	EV	LQ	DSL	DR	CYST	PS	V	Y	L	G	L	T	D	S	C	Q	P	Y	R	S	A	F	V	L	E	Q	V	G	L	A	D	M		
1	ex10.8	LNRELLDEKGP	EV	LQ	DSL	DR	CYST	X	S	G	Y	L	-	L	T	D	S	C	Q	P	Y	R	S	A	F	I	L	E	Q	V	G	A	L	D	I	V
1	ex10.20	LNRELLDEKGP	EV	LQ	DSL	DR	CYST	PS	G	Y	L	E	L	T	D	S	C	Q	P	Y	R	S	A	F	I	L	E	Q	V	G	A	L	D	M	D	
1	ex10.7	LSRELLDEKGP	EV	LQ	DSL	DR	CYST	PS	G	Y	L	E	L	T	D	S	C	Q	P	Y	R	S	A	F	I	L	E	Q	V	G	A	L	D	M	D	
1	ex10.16	LSRELLDEKGP	EV	LQ	DSL	DR	CYST	PS	G	Y	L	E	L	T	D	S	C	Q	P	Y	R	S	A	F	I	L	E	Q	V	G	A	L	D	M	D	
1	ex10.28	LSRELLDEKGP	EV	LQ	DSL	DR	CYST	PS	G	Y	L	E	L	T	D	S	C	Q	P	Y	R	S	A	F	I	L	E	Q	V	G	A	L	D	M	D	
1	ex10.9	LSRELLDEKEP	EV	LQ	DSL	GR	CYST	PS	G	Y	L	E	L	P	D	S	C	Q	P	Y	R	S	A	F	V	L	E	Q	V	G	L	T	L	D	M	
1		LSRELLDEKEP	EV	LQ	DSL	GR	CYST	PS	G	Y	L	E	L	P	D	L	G	Q	P	Y	S	A	V	I	S	E	E	Q	V	G	L	A	D	M	D	

Figure 13 C

exon10-11

ex10.35	1	LSRELLDEKEPEVLQDSLGRWYSTPSGYLELPDLGQPYSSAVYSLEEQYGLALD	D
ex10.21	1	LSRELLDEKEPEVLQDSLDRCYSLPSGYLELPDLGQPYSSAVYSLEEQYGLALD	D
ex10.19	1	LSRELLDEKEPEVLQDSLDRCYSTPSDYLELPDLGQPYSSAVYSLEEQYGLALD	D
ex10.15	1	LSRELLDEKEPEVLQDSLDRCYSTPSGYLELPDLGQPYSSAVYSLEEQYGLALD	D
ex10.10	1	LSRELLAEKEPEVLQDSLDRCYSTPSGYLELPDLGQPYSSAVYSLEEQYGLALD	D
ex10.34	1	LSRELLDEKEPEVLQDSLDRCYSTPSGYLELPDLGQPYSSAEYSLEEQYGLALD	D
ex10.32	1	LSRELLDEKEPEVLQDSLDRCYSTPSGCLLPDLGQPYSSAVYSLEEQYGLALD	D
ex10.29	1	LSRELLDEKEPEVLQDSLDRCYSTPSGYLELPDLGQPYSSAVYSLEEQYGLALD	D
ex10.12	1	LSRELLAEKEPEVLQDSLDRCYSTPSGYLELPDLGQPYSSAVYSLEEQYGLALD	D
ex10.13	1	LSRELLAEKEPEVLQDSLDRCYSTPSGYLELPDLGQPYSSAVYSLEEQYGLALD	D
ex10.17	1	LSRELLDEKEPEVLQDSLDRCYSTPSGYLELPDLGQPYSSAVHSLEEQYGLALD	D
ex10.11	1	LSRELLDEKEPEVLQDSLDRCYSTPSGYLELPDLGQPYSSAVYSLEEQYGLALD	D
ex11.7	1	LSRELLAVEPEVLQDSLDRCYSTPSSCLEQPDSCLPYGSFYALEEKHAGFSLDV	G
ex11.9	1	LSRELLAVEPEVLQDSLDRCYSTPSSCLEQPDSCLPYGSFYALEEKHAGFSLDV	G
ex11.1	1	LSRELLAVEPEVLQDSLDRCYSTPSSCLEQPDSCLPYGSFYALEEKHAGFSLDV	G
ex11.2	1	LSRELLRAVEPEVLQDSLDRCYSTPSSCLEQPDSCLPYGSFYALEEKHAGFSLDV	G
ex11.8	1	LSRELLRAVEPEVLQDSLDRCYSTPSSCLEQPDSCLPYGSFYALEEKHAGFSLDV	G
ex11.4	1	LSRELLRAVEPEVLQDSLDRCYSTPSSCLEQPDSCLPYGSFYALEEKHAGFSLDV	G
ex11.10	1	LSRELLRAVEPEVLQDSLDRCYSTPSSCLEQPDSCLPYGSFYALEEKHAGFSLDV	G
ex11.3	1	LSRELLRAVEPEVLQDSLDRCYSTPSSCLEQPDSCLPYGSFYALEEKHAGFSLDV	G
ex11.5	1	LSRELLRAVEPEVLQDSLDRCYSTPSSCLEQPDSCLPYGSFYALEEKHAGFSLDV	G
ex11.6	1	LSRELLRAVEPEVLQDSLDRCYSTPSSCLEQPDSCLPYGSFYALEEKHAGFSLDV	G

35/75

Figure 14 A

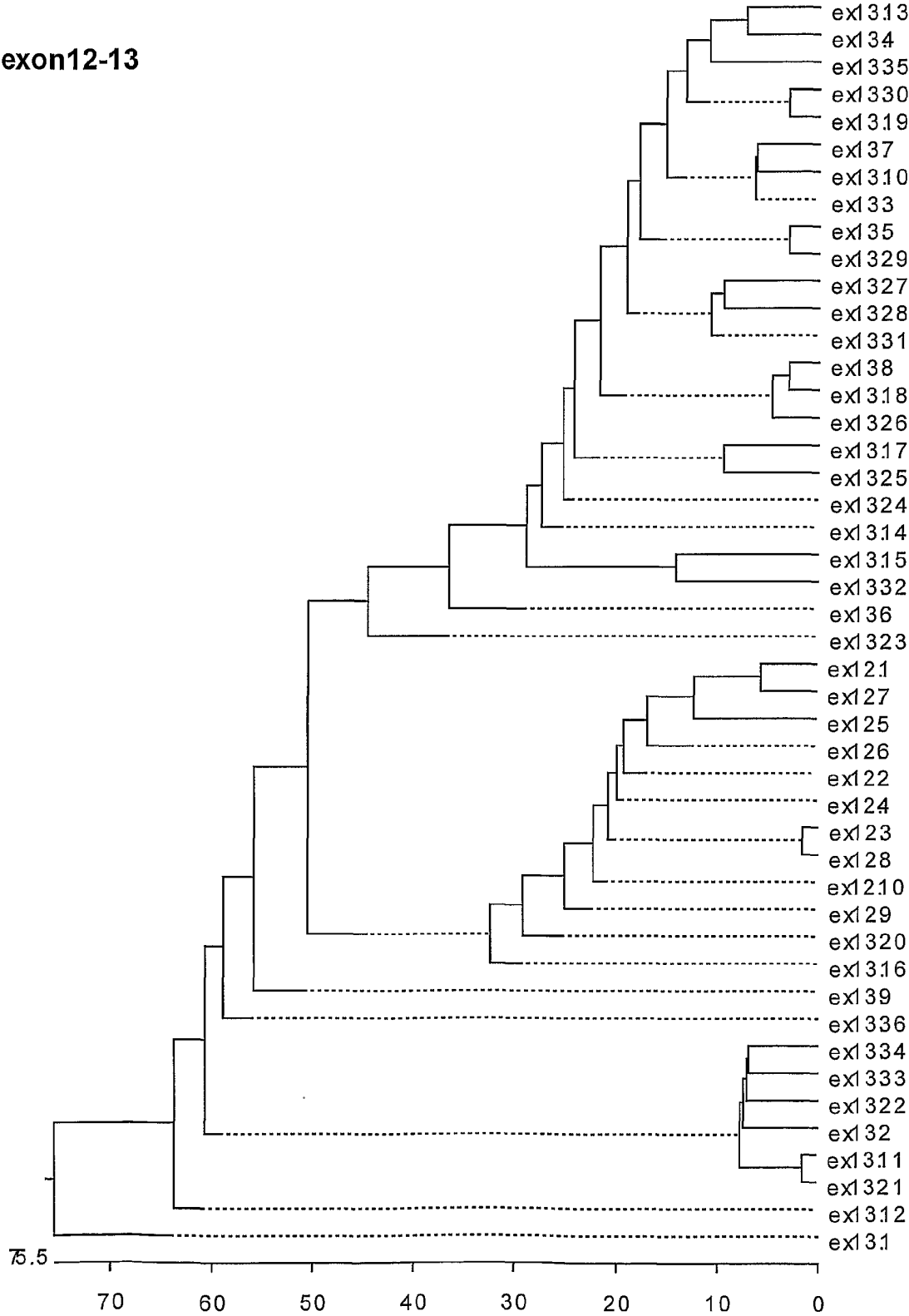


Figure 14 B

36/75

ex13.13	1	RTKKD-----	QEEEEEDQGPPSCP--
ex13.4	1	RTKKD-----	QEEEEEDQGPPCPR--
ex13.35	1	RS-KD-----	QEEEEEDQGPPCPR--
ex13.30	1	GTKKD-----	QEEEEEDQGPPCPR--
ex13.19	1	GKKKD-----	QEEEEEDQGPPCPR--
ex13.7	1	RIKKD-----	QEEEEEDQGPPCPR--
ex13.10	1	RIKQD-----	QEEEEEDQGPPCPR--
ex13.3	1	RIKKD-----	QEEEEEDQGPPCPR--
ex13.5	1	RIKKD-----	QEEEEEDQGPPCSR--
ex13.29	1	GIKKD-----	QEEEEEDQGPPCSR--
ex13.27	1	GIKKD-----	QEEEEEDQGPPGPG--
ex13.28	1	GIKKD-----	QEEEEEDQCPPCPT--
ex13.31	1	GIKKD-----	QEEEEEDQGPPCPR--
ex13.8	1	RIKKD-----	EEEEEDQDPCCPR--
ex13.18	1	GIKKD-----	EEEEEDQDPCCPR--
ex13.26	1	GIKKD-----	EEEEEDQGPPCPR--
ex13.17	1	EIKKD-----	QEEIIEDQSPPCPR--
ex13.25	1	GIKKD-----	QEEEEEDPSPPCPR--
ex13.24	1	GIKKD-----	QEEEEEDQDPCCPR--
ex13.14	1	RIKKD-----	QEEEEEDQDPCCPR--
ex13.15	1	EIKKT-----	KXEEEEEDQGPPCPR--
ex13.32	1	EIKSV-----	QEEEEEDQDPCCPR--
ex13.6	1	EIKKY-----	QEEEEEDQDPSCPR--
ex13.23	1	EIEKN-----	QEEEEEDQDPQCPR--
ex12.1	1	EIEKKGKGKKRRGRRS-KKKRRRGRKE	EGEED-NPPCP--
ex12.7	1	EIEKKGKGKKRRGRRSTKERRRRGR--	
ex12.5	1	EIEKKGKGKKRRGRRSTKKRRRRGRKE	EGEEDQNPPCPR--
ex12.6	1	EIEKKGKGKKRRGRRSTKKRRRRGSKE	EGEEDQNPPCPR--
ex12.2	1	EIEKKGKGKKRRGRRS-KKKRRRGRKE	EGEEDQNPPCPR--
ex12.4	1	EIEKKGKGKKRRGRRSMKKRRRRGRKE	EGEEDQNPPCPR--
ex12.3	1	EIEKKGKGKKRRGRRS-KKERRRGRKE	EGEEDQNPPCPR--
ex12.8	1	KIEKKGKGKKRRGRRS-KKERRRGRKE	EGEEDQNPPCPR--
ex12.10	1	EIEKKGKGKKRRGRRS-KKERRRGRKE	EGEEDQNPPCPR--
ex12.9	1	EIEKKGKGKKRGGRRS-EKERRRGRKE	EGEEDQNPPCPR--
ex13.20	1	EIEKY-----	QEGEEDQNPPCPR--
ex13.16	1	EIEKY-----	QEGEEDQKPPCPR--
ex13.9	1	EIEKY-----	QEVEREEDQGPSCPR--
ex13.36	1	EIEKC-----	QEVEREEDQDPSCPR--
ex13.34	1	EXEKY-----	QEVEREEDQDPSCRR--
ex13.33	1	EIEKY-----	QEVGEDQDPSCAX--
ex13.22	1	ENEKY-----	Q-VEEDQDPSCPR--
ex13.2	1	EIEKY-----	QEVEREEDQDPSCPR--
ex13.11	1	EIEKY-----	KEVEREEDQDPSCPR--
ex13.21	1	-IEKY-----	KEVEREEDQDPSCPR--
ex13.12	1	EIEKY-----	QEVEREEDQNPS CPR--
ex13.1	1	EIEKSQKWKK--	-TQNPSCPR--

37/75

Figure 15 A

Carboxy-terminal exon14

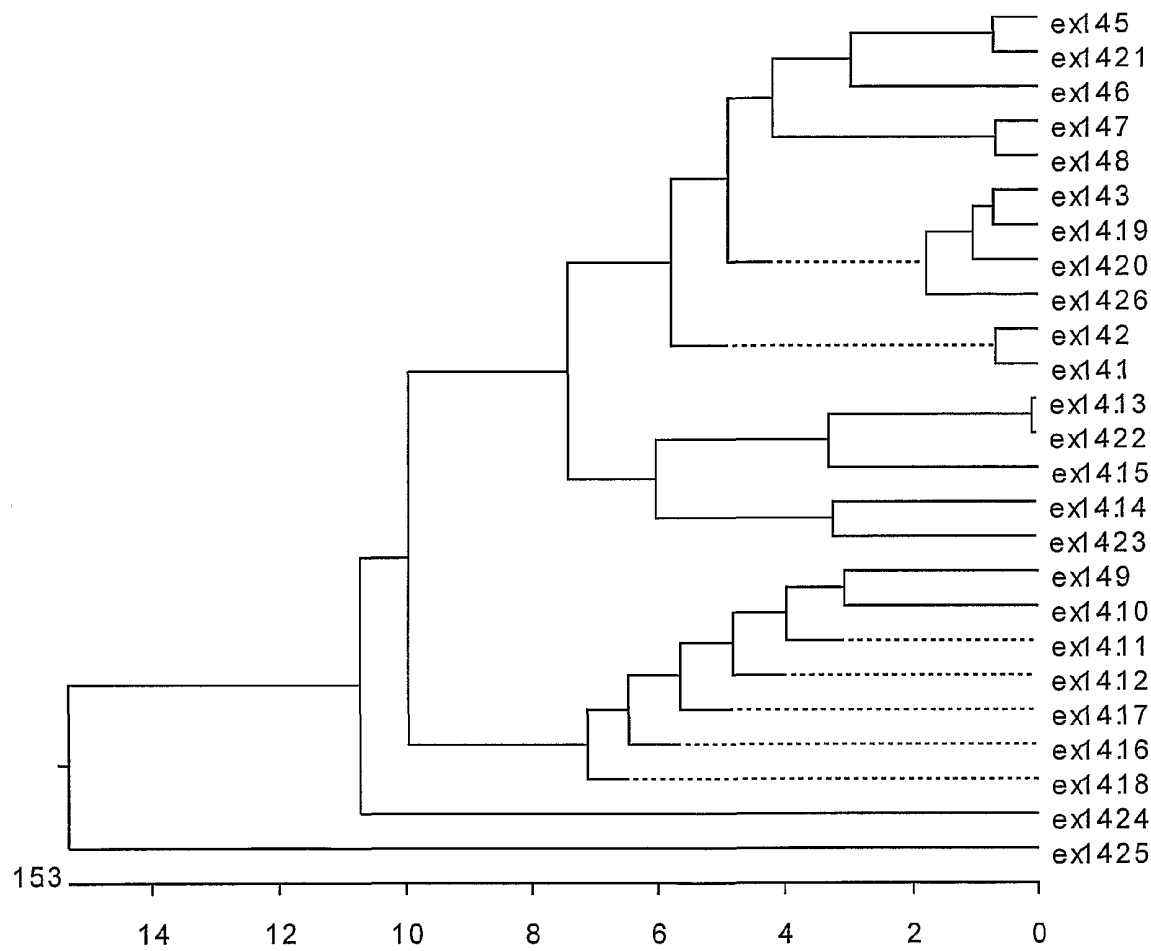


Figure 15 B

38/75

Carboxy-terminal exon14

ex14.5	1	LN	SV	ME	VE	EE	PE	VL	QD	SL	DG	CY	ST	PS	MY	FE	LP	DS	FQ	HY	RS	VF	YS	FE	EE	HI	SF	AL	Y	DN	RF	FT	LT	VT	SL	HL	VF	QMG	VI	FP	Q					
ex14.21	1	LN	SV	ME	VE	EE	PE	VL	QD	SL	DG	CY	ST	PS	MY	FE	LP	DS	FQ	HY	RS	VF	YS	FE	EE	HI	SF	AL	Y	DN	RF	FT	LT	VT	SL	HL	VF	QMG	VI	FP	Q					
ex14.6	1	LN	SV	ME	VE	EE	PE	VL	QD	SL	DG	IC	Y	ST	PS	MY	FE	LP	DS	FQ	HY	RS	VF	YS	FE	EE	HI	SF	AL	Y	DN	RF	FT	LT	VT	SL	HL	VF	QMG	VI	FP	Q				
ex14.7	1	LY	GV	ME	VE	EE	PE	VL	QD	SL	DR	CY	ST	PS	MY	FE	Q	PD	SF	FQ	HY	RS	VF	YS	FE	EE	HI	SF	AL	Y	DN	RF	FT	LT	VT	SL	HL	VF	QMG	VI	FP	Q				
ex14.8	1	SY	GV	ME	VE	EE	PE	VL	QD	SL	DR	CY	ST	PS	MY	FE	Q	PD	SF	FQ	HY	RS	VF	YS	FE	EE	HI	SF	AL	Y	DN	RF	FT	LT	VT	SL	HL	VF	QMG	VI	FP	Q				
ex14.3	1	LN	GV	ME	VE	EE	PE	VL	QD	SL	DG	CY	ST	PS	MY	FE	LP	DS	FQ	HY	RS	VF	YS	FE	EE	HI	SF	AL	Y	DN	RF	FT	LT	VT	SL	HL	VF	QMG	VI	FP	Q					
ex14.19	1	LN	GV	ME	VE	EE	PE	VL	QD	SL	DG	CY	ST	PS	MY	FE	LP	DS	FQ	HY	RS	VF	YS	FE	EE	HI	SF	AL	Y	DN	RF	FT	LT	VT	SL	HL	VF	QMG	VI	FP	Q					
ex14.20	1	LN	GV	ME	VE	EE	PE	VL	QD	SL	DG	CY	ST	PS	MY	FE	LP	DS	FQ	HY	RS	VF	YS	FE	EE	HI	SF	AL	Y	DN	RF	FT	LT	VT	SL	HL	VF	QMG	VI	FP	Q					
ex14.26	1	P	NG	VI	ME	VE	G	PE	VL	QD	SL	DG	CY	ST	PS	MY	FE	LP	DS	FQ	HY	RS	VF	YS	FE	EE	HI	SF	AL	Y	DN	RF	FT	LT	VT	SL	HL	VF	QMG	VI	FP	Q				
ex14.2	1	LN	GV	ME	VE	EE	PE	VL	QD	SL	DR	CY	ST	PS	MY	FE	LP	DS	FQ	HY	RS	VF	YS	FE	EE	HI	SF	AL	Y	DN	RF	FT	LT	VT	SL	HL	VF	QMG	VI	FP	Q					
ex14.1	1	LN	GV	ME	VE	EE	PE	VL	QD	SL	DR	CY	ST	PS	MY	FE	LP	DS	FQ	HY	RS	VF	YS	FE	EE	HI	SF	AL	Y	DN	RF	FT	LT	VT	SL	HL	VF	QMG	VI	FP	Q					
ex14.13	1	LN	SV	ME	VE	EE	PE	VL	QD	SL	DR	CY	ST	PS	MY	CE	LR	DS	FQ	HY	RS	VF	YS	FE	EE	HI	SF	AL	D	Y	DN	RF	FT	LT	VT	SL	Y	LV	FQ	MG	VI	FP	Q			
ex14.22	1	LN	SV	ME	VE	EE	PE	VL	QD	SL	DR	CY	ST	PS	MY	CE	LR	DS	FQ	HY	RS	VF	YS	FE	EE	HI	SF	AL	D	Y	DN	RF	FT	LT	VT	SL	Y	LV	FQ	MG	VI	FP	Q			
ex14.15	1	LN	SV	ME	VE	EE	PE	VL	QD	SL	DR	CY	ST	PS	MY	FE	LP	DS	FQ	HY	RS	VF	YS	FE	EE	HI	SF	AL	D	Y	DN	RF	FT	LT	VT	SL	HL	VF	QMG	VI	FP	Q				
ex14.14	1	L	SS	VI	ME	VE	V	PE	VL	QD	SL	DR	Y	Y	ST	PS	MY	FE	LP	DS	FQ	HY	RS	VF	YS	FE	EE	HI	SF	AL	T	W	T	I	G	F	FT	LT	VR	SL	HL	VF	QMG	VI	FP	Q
ex14.23	1	L	SS	VI	ME	VE	V	PE	VL	QD	SL	DR	Y	Y	ST	PS	MY	FE	LP	DS	FQ	HY	RS	VF	YS	FE	EE	HI	SF	AL	D	Y	DN	RF	FT	LT	VR	SL	HL	VF	QMG	VI	FP	Q		
ex14.9	1	L	SG	VI	ME	VE	EE	PE	L	QD	SL	DR	CY	ST	LS	LS	FE	LP	DS	FQ	HY	RS	VF	YS	FE	EE	HI	SF	AL	D	Y	DN	RF	FT	LT	MG	T	SL	HL	VF	QMG	VI	FP	Q		
ex14.10	1	F	SG	VI	ME	VE	EE	PE	L	QD	SL	DR	CY	ST	LS	LS	FE	LP	DS	FQ	HY	RS	VF	YS	FE	EE	HI	SF	AL	D	Y	DN	RF	FT	LT	MG	T	SL	HR	G	F	X	MG	VI	FP	Q
ex14.11	1	L	SG	VI	ME	VE	EE	PE	L	QD	SL	DR	CY	ST	PS	PS	FE	LP	DS	FQ	HY	RS	VF	YS	FE	EE	HI	SF	AL	D	Y	DN	RF	FT	LT	MG	T	SL	HL	VF	QMG	VI	FP	Q		
ex14.12	1	L	SG	VI	ME	VE	EE	PE	L	QD	SL	DR	CY	ST	PS	PS	FE	LP	DS	FQ	HY	RS	VF	YS	FE	EE	HI	SF	AL	D	Y	DN	RF	FT	LT	MG	T	SL	HL	VF	QMG	VI	FP	Q		
ex14.17	1	L	SG	VI	ME	VE	EE	PE	VL	QD	SL	DR	CY	ST	PS	PS	FE	LP	DS	FQ	HY	RS	VF	YS	FE	EE	HI	SF	AL	D	Y	DN	RF	FT	LT	MG	T	SL	HL	VF	QMG	VI	FP	Q		
ex14.16	1	L	SG	VI	ME	VE	EE	PE	VL	QD	SL	DR	CY	ST	PS	PS	FE	LP	DS	FQ	HY	RS	VF	YS	FE	EE	HI	SF	AL	D	Y	DN	RF	FT	LT	MG	T	SL	HL	VF	QMG	VI	FP	Q		
ex14.18	1	L	SG	VI	ME	VE	EE	PE	VL	QD	SL	DR	CY	ST	PS	PS	FE	LP	DS	FQ	HY	RS	VF	YS	FE	EE	HI	SF	AL	D	Y	DN	RF	FT	LT	MG	T	SL	HL	VF	QMG	VI	FP	Q		
ex14.24	1	LN	GV	ME	VE	EE	PE	VL	QD	SL	DR	CY	ST	PT	Y	FE	LP	DS	FQ	HY	RS	VF	YS	FE	EE	HI	SF	AL	E	Y	DN	RF	FT	LT	MG	T	SL	HL	VF	QMG	VI	FP	Q			
ex14.25	1	LN	EV	ME	AE	EE	PE	VL	QD	SL	DR	CY	ST	TS	Y	FE	LP	DS	FQ	HY	RS	VF	YS	FE	EE	HI	SF	AL	D	Y	DN	RF	FT	LT	VR	SL	HL	VF	QMG	VI	FP	Q				

Figure 16

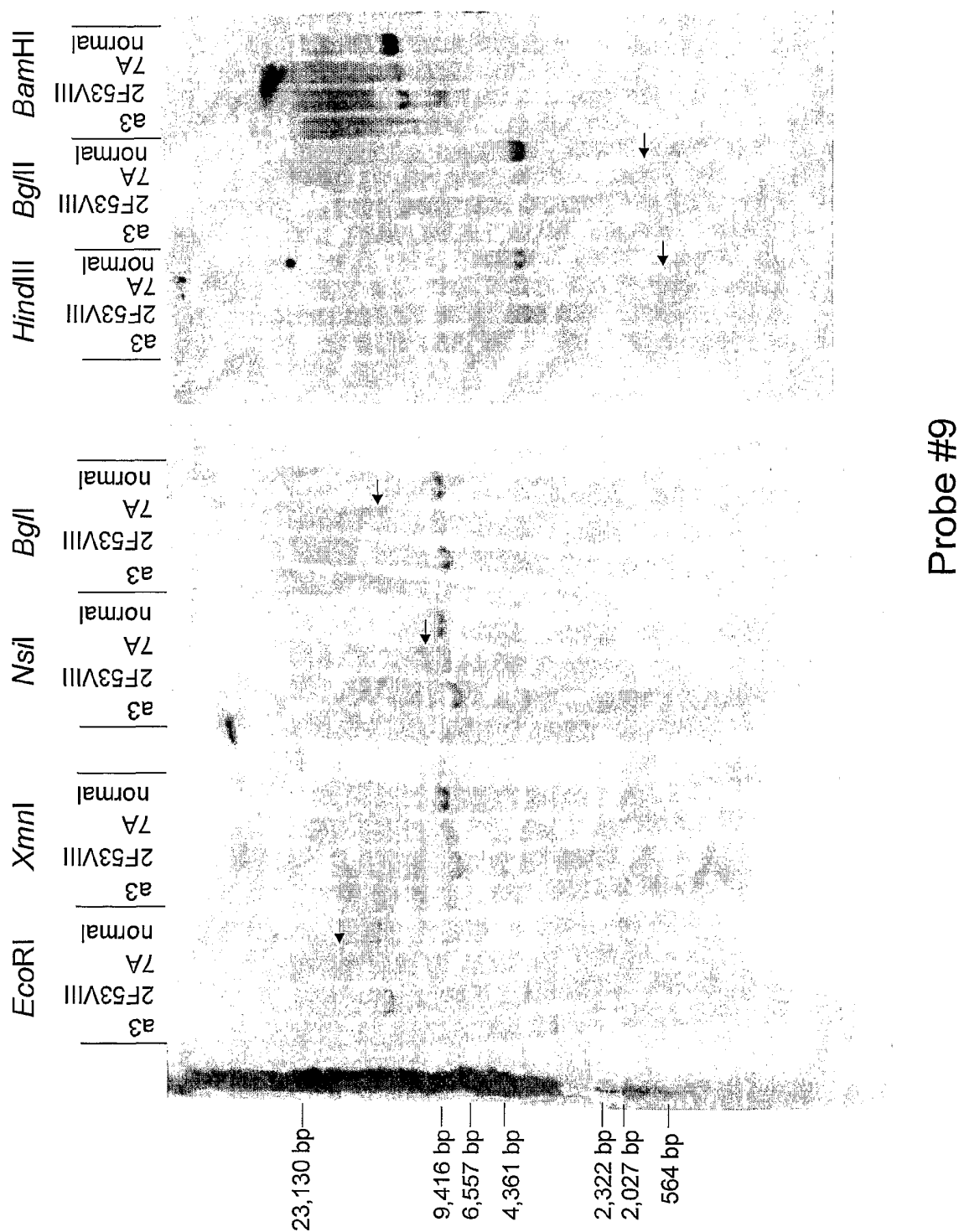


Figure 17 A - B

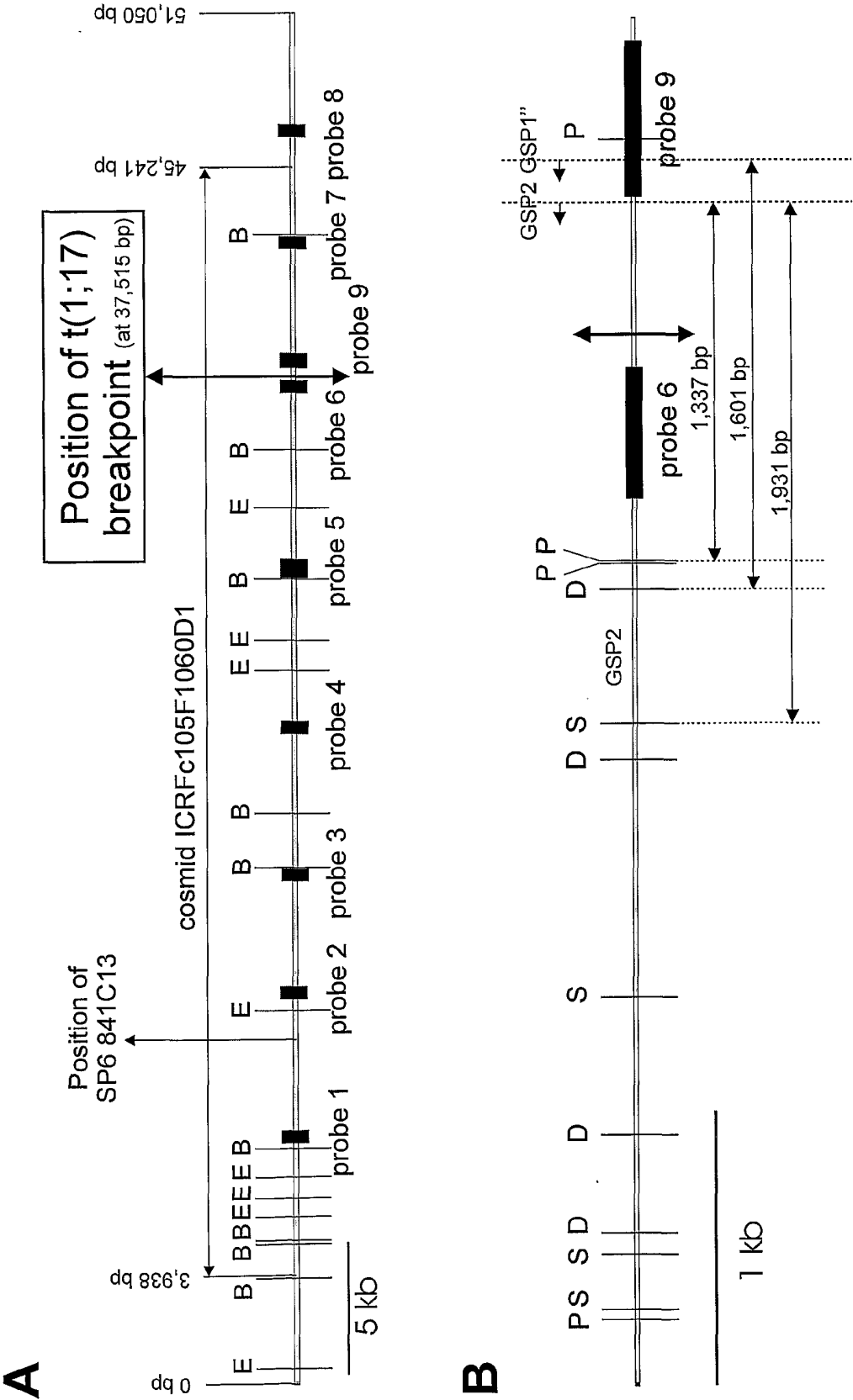


Figure 17 C

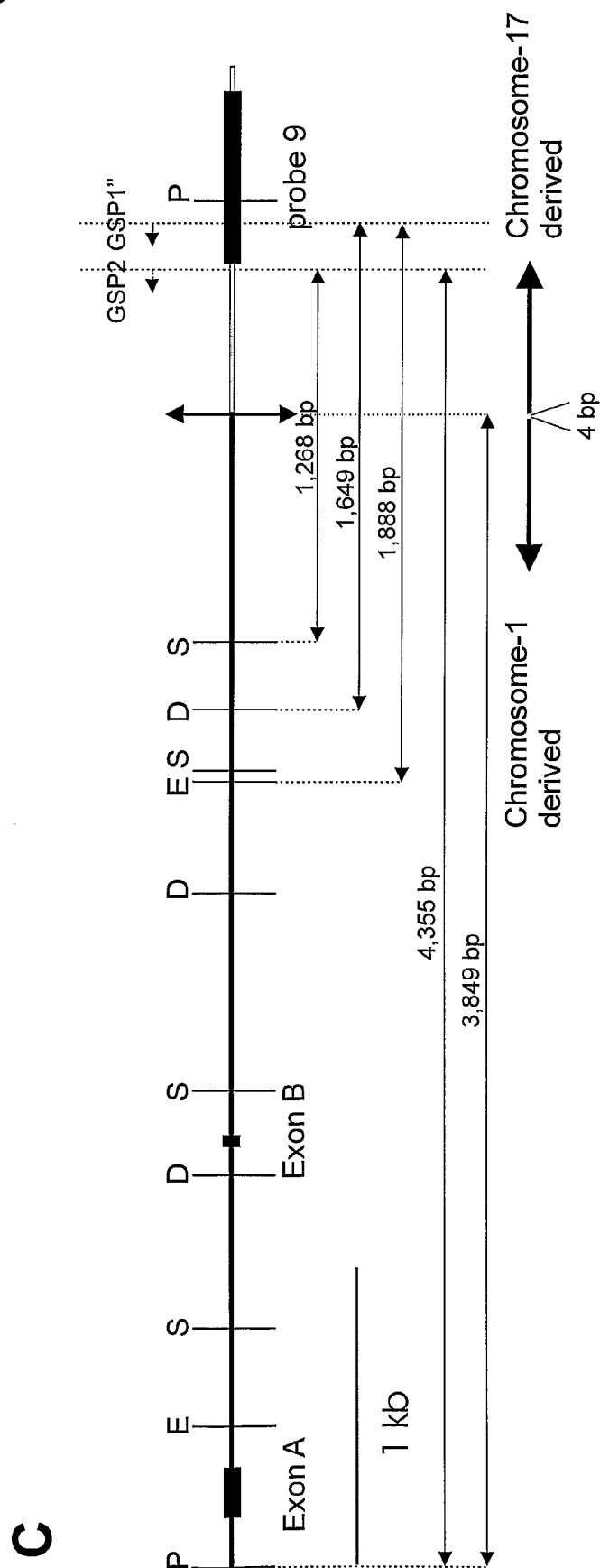


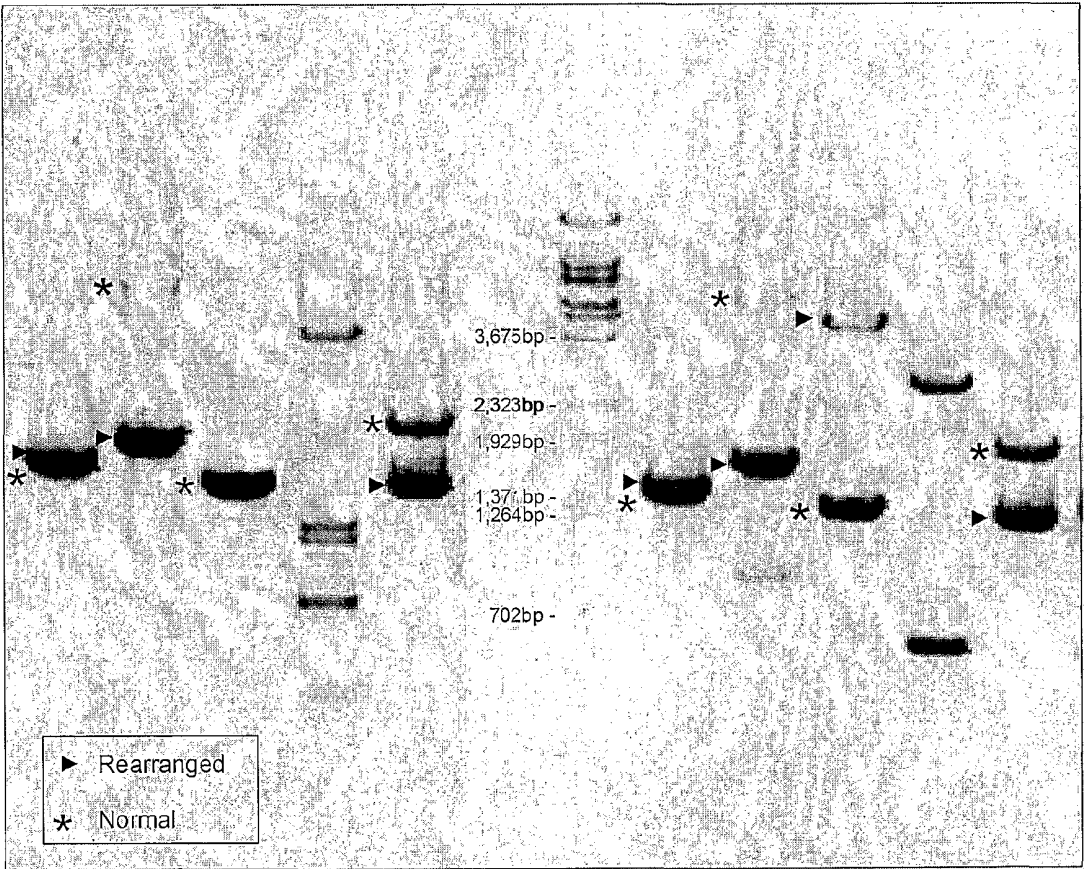
Figure 18

PR : GSP1'' + AP1

RE : D E P Sc S

GSP2 + AP2

M D E P Sc S



FS : ▶ 1649 1888 4512 aspec 1425

* 1601 5537 1495 >5000 2088

1492 1731 4355 aspec 1268

1444 5379 1337 >5000 1931

Figure 19 A

10	20	30	40	50	60	70
ctgctctctctctctggttcccatggcagccatgctctgttgagagagaacaggattgcatgtaccc						
80	90	100	110	120	130	140
tcttaatgggaacctccagtttgctttctgggaccactctcttaatgccgcctgtcaaaaccagctagga						
150	160	170	180	190	200	210
ctccctgggtcccaatccctctgtgtttaatcttctgtcatctctgttcccacctgggtcatcagGGACAT						
						<u>D M</u>
220	230	240	250	260	270	280
GCAGAGGCTGAAGAAAAGGAAGTCCCTGAGGACTCACTGGAGGAATGTGCCATCACTTGTCAAATAGC						
<u>Q K A E E K E V P E D S L E E C A I T C S N S</u>						<u>Exon A</u>
290	300	310	320	330	340	350
CATGGCCCTTATGACTCCAAACCGCACATAGGAAAACCAAAATCACATTTGAGGAAGACAAAGTCGACT						
<u>H G P Y D S N Q P H R K T K I T F E E D K V D</u>						<u>Exon A</u>
360	370	380	390	400	410	420
CAACTCTCATTTGGCTCATCCTCTCATGTTGAATGGGAGGATGCTGTACACATATCCCAGgtagcctctg						
<u>S T L I G S S S H V E W E D A V H I I P</u>						<u>Exon A</u>
430	440	450	460	470	480	490
ttttcccttggtctcatcacctctctctaggtgaggaagataaaactctgaagacagggtctataaacaca .						
500	510	520	530	540	550	560
aattcatttgaataaaaaactatgatgggtttctaaacagatatatcaggggaggttttttgccttctcagc						
570	580	590	600	610	620	630
taatgtcatgcctttgtctgccagtccccagtatcaagttactcgaacccaggcaaggtgtgacaatctca						

Figure 19 B

640 650 660 670 680 690 700
tagtcacctgagtgacaggaggtgcacagggcagtatctgtcaggcctcctagcttcgattcagtatctctt
710 720 730 740 750 760 770
gtcatctgtgattaaagtcatctgtccctgaacaaatgtccatggagtttctctatgcctgtttcaggaaagctg
780 790 800 810 820 830 840
gcagccttgccctttgtatttggaataattgttccccaggcttcactgctctcagctttcatctggatctc
850 860 870 880 890 900 910
ctttaagtcagcttgcttagctgcacagtcaccctgaaatcaggatggaaaacttttctcttactttgc
920 930 940 950 960 970 980
tgatatatttccataaagcaaggctggaccctggttctccaccctgtcaatgcaatggctgatccaatgt
990 1000 1010 1020 1030 1040 1050
ttctttgtagcatcgtggattttttttttttttttttttttttttttttttttttttttttttgcat
1060 1070 1080 1090 1100 1110 1120
ggagtccttgctctgtcaccaggctagagtgagtgccacctcttggtggtgcaacctctgcctccc
1130 1140 1150 1160 1170 1180 1190
agattcaagtgattctcctgcctcagcctcctgagttgctgggaccacaggtgcacaacatcacatctgg
1200 1210 1220 1230 1240 1250 1260
ctaattttgtatttttagtagagacagtggttcccccatattggccagggtagtcctgaactcatgacct
1270 1280 1290 1300 1310 1320 1330
caaatgattcacctgtcttggcctcccaaatcacagattctttttaagcaagagttgttcaaatattatc

Figure 19 C

45/75

1340	1350	1360	1370	1380	1390	1400
tatcagtcgtgtttcatgtatagatgcctctaaacatttaatgtccatgttatctctggatataagtccg						
1410	1420	1430	1440	1450	1460	1470
tattgcagcaacactcttagaaaaatggaccaatttttggagattttttgggaaaaaattttgtttaac						
1480	1490	1500	1510	1520	1530	1540
tttgactcaggcagggaatatggcattatggtctacacgtagaggagatttttggcctgtgggtctggaa						
1550	1560	1570	1580	1590	1600	1610
agcagggtcatctaatctcaccaaaagttaatctagggcaccctagaaatattcctgtcagaatccttatt						
1620	1630	1640	1650	1660	1670	1680
cttgcaactgagaatagttatgtccttgtgctatgactggacagtgatttggtcatatgtgaagtatgaat						
1690	1700	1710	1720	1730	1740	1750
tgcttaatgtgacctgcttctctgaattttattacagAAAAATGAAAGTGATGATGAGGAAGGAAGAAA						
E N E S D D E E E E E						Exon B
1760	1770	1780	1790	1800	1810	1820
AAGGGCCAGTGCTCCAGgtaatgtgtggaattgttggctgttaattcagtagtgacatctggagatt						
K G P V S P R						Exon B
1830	1840	1850	1860	1870	1880	1890
gtagatttagggaaaaatgaggaaagtgatgaatagaaactatttcttccattcaccagctacaaattgtgc						
1900	1910	1920	1930	1940	1950	1960
tgattttacaatgttgtatgttattttgtgacacttgtattgggttttaatttcatatagtcctctcaagatagg						

Figure 19 D

1970	1980	1990	2000	2010	2020	2030
aacttgccatcagatgagccaggtagaactagccaacagggttttcttgttgatcttttcaaaaaaccag						
2040	2050	2060	2070	2080	2090	2100
ccctggattcattgatatttttgaagggtttttgtgtctctatctcttagttctgtctctgatcttagt						
2110	2120	2130	2140	2150	2160	2170
tacttctgtcttctgctagcttttgaatttgtgtgtctctcttagttattttaattgtgatgtta						
2180	2190	2200	2210	2220	2230	2240
gggtgtcaatttttagatcttttctgtcttctgtgggcatttagtgctataaattttccctctacacat						
2250	2260	2270	2280	2290	2300	2310
tgctttaaattgtgtccagagattctggtagttgtgtctttgttctcattggtttcaagaacaatcttt						
2320	2330	2340	2350	2360	2370	2380
atctctgccttcattttgttattttccagtagtcatttcaggagcaggtgttcagtttcccatgtagttg						
2390	2400	2410	2420	2430	2440	2450
tgcgggttttgagtgagttccttaatcctgagtttctaatttgactgcactgtggtctgacagtttgttgtg						
2460	2470	2480	2490	2500	2510	2520
gtttccattcttttacatttgctgaggagtgctttacctccaactatgtggtcaattttggaataagtgt						
2530	2540	2550	2560	2570	2580	2590
gatgtggtgctgagaagaatgtatatctgtgtgatttgggggtggagagttctgtagatgtcttttaggtc						
2600	2610	2620	2630	2640	2650	2660
tgcttggtggagagctgagttcaagtcctggatatccttgtaaagcttctgtctcattgatctgtcta						

Figure 19 E

2670 2680 2690 2700 2710 2720 2730
attgacagtgggtgttaaagtctcccatattgattgtgtggagtctaaatctctttgtaggtctctcag
2740 2750 2760 2770 2780 2790 2800
gacttgctttatgaatctgggtgctcctgtatataggtgcataataatttaggatagttaactcttcttgt
2810 2820 2830 2840 2850 2860 2870
tgaattgatccctttaccattatgtagtggccttctttgtctctcttttgatctttgttggtttaaaagtctg
2880 2890 2900 2910 2920 2930 2940
ttttatcagagactaggaattgcaacccctgcatttttttgctttccatttgcttggtagatcttcctcca
2950 2960 2970 2980 2990 3000 3010
tccctttatttgagcctatgtgtctctctgcattgtgagatgggtttcctgagtacagcacactgatggg
3020 3030 3040 3050 3060 3070 3080
tcttgactctttgtccaatttgccattctgtgtttttaactggggcatttagcccatttacatttaagg
3090 3100 3110 3120 3130 3140 3150
ttaatatgttatgtgtgaatttgagcctgtcgttatgatgttagctggttatttcgcccgtagttgat
3160 3170 3180 3190 3200 3210 3220
gcagtttcttcctagcgtcaatggcttttacagtttggcatgtttttgcagtggtggtaccgggtgttc
3230 3240 3250 3260 3270 3280 3290
ctttcccatgttttagtgcttccctttaggagctcttgtaaaggcaggcctggtggtgacaaaaatctctcagca
3300 3310 3320 3330 3340 3350 3360
tttgcttctctgttaaaggatttatttctccttcacttatgaagctttgtttggctggatatgaaattctg

48/75

Figure 19 F

3370 3380 3390 3400 3410 3420 3430
 ggttgaaaaattcttctttaaagaatgttgaagatgctggagaggatgtggagaaataggaacactttta
 3440 3450 3460 3470 3480 3490 3500
 cactgttggtgagagtgtaaactagtccaacgattgtggaaggcagtggtggaattcctcagggatctag
 3510 3520 3530 3540 3550 3560 3570
 aactagaaatagcatttgacccagccatcccattactgggtgtatacccaaggattataaatcatgctg
 3580 3590 3600 3610 3620 3630 3640
 ctgtaagacacatgcacacatatgtttattgcgggcactattcacaaatagcaaaagacttggaaaccaagcc
 3650 3660 3670 3680 3690 3700 3710
 aaatatccagcaatgatagactggattaagaaaaatgtggcacgtatacacccatgggaatactatgcagcta
 3720 3730 3740 3750 3760 3770 3780
 taaaaaatgatgagttcatgtcctttttaggggcatggatgaagctggaaaaccatcattctcagcaaat
 3790 3800 3810 3820 3830 3840 3850
 atcgcaaggacaaaaaaccaagtaccgcatgttcttactcacagggtggaaatgaacaaatgagaaa**AAAGc**
 3860 3870 3880 3890 3900 3910 3920
 acatagcactaggaaggagccagtagaatttcagggtgaagagtaatgggagatgggaacctacacaac
 3930 3940 3950 3960 3970 3980 3990
 tggagagacccaggaaagccctctgagaagggtcctttaagatgagctgtgagggccaaggaaagagcaggcc
 4000 4010 4020 4030 4040 4050 4060
 aggcgaaggcagaggggacagcccttccagtgagtggaaacacagcaaaatgcaaggcctcgaggcggggcag

Figure 19 G

4070 4080 4090 4100 4110 4120 4130
ggcttgctctttgggagcagaaaaaggtcacggaaaaaacagcgtgattcatggagagagggcca

4140 4150 4160 4170 4180 4190 4200
gggctgaaaaaggagagggcaggagtggggctcatggtctctagaaaaacagactgggtttgagtttggtgta

4210 4220 4230 4240 4250 4260 4270
atagcctggtgaggacggtattatttctgcttccattttacagttacagaaacagagggcagcatat

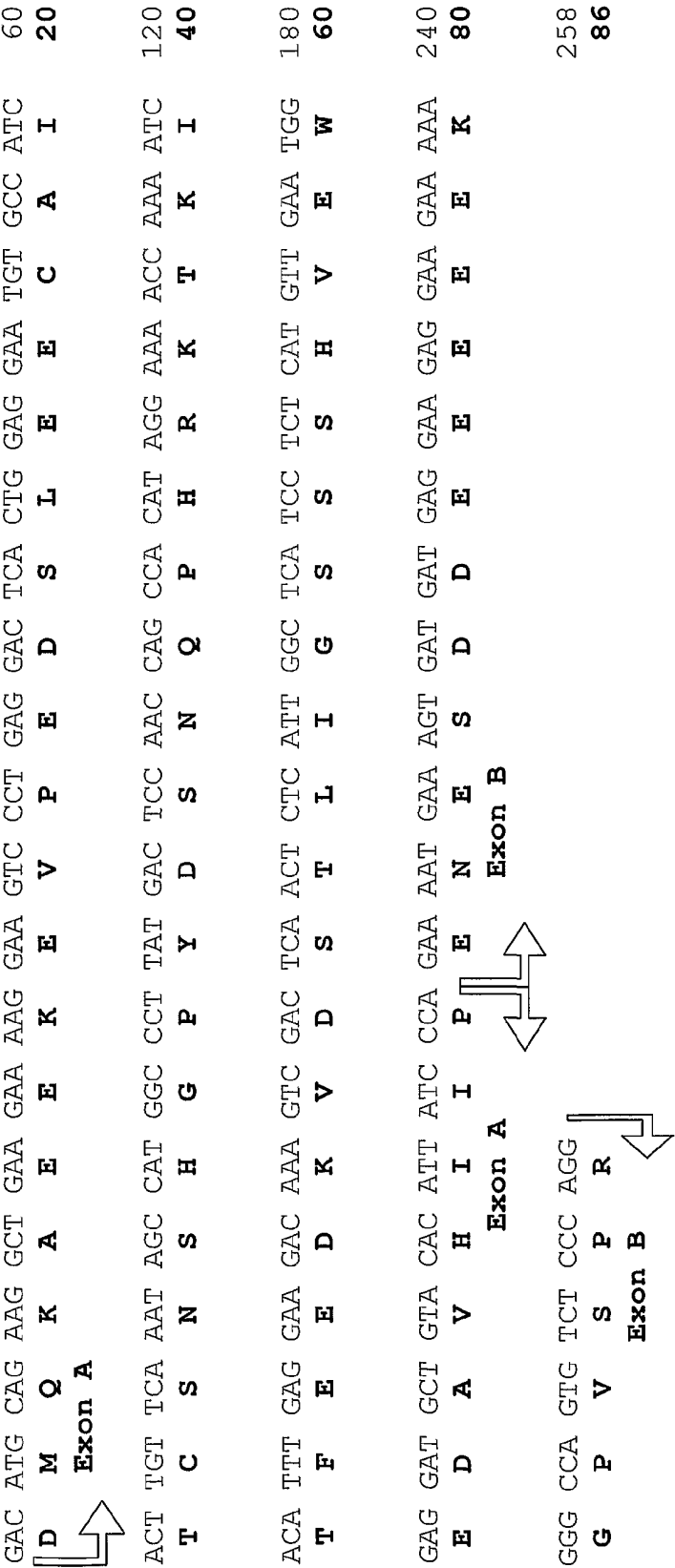
4280 4290 4300 4310 4320 4330 4340
gatactgggggtactgggatatagggtgtgttattgattgatgggggacacctttgacgggtcagaaaatggag

4350 4360 4370 4380 4390 4400 4410
ggaggctggtggtgtaccccccttgacttcacctgaatgtcagggcaaggccaggagcatgcaggaggctt

4420 4430 4440 4450 4460 4470 4480
aaagattgggaacccctattcttgggccttctccccattcttctgagagcaattggaagagggcccatggg

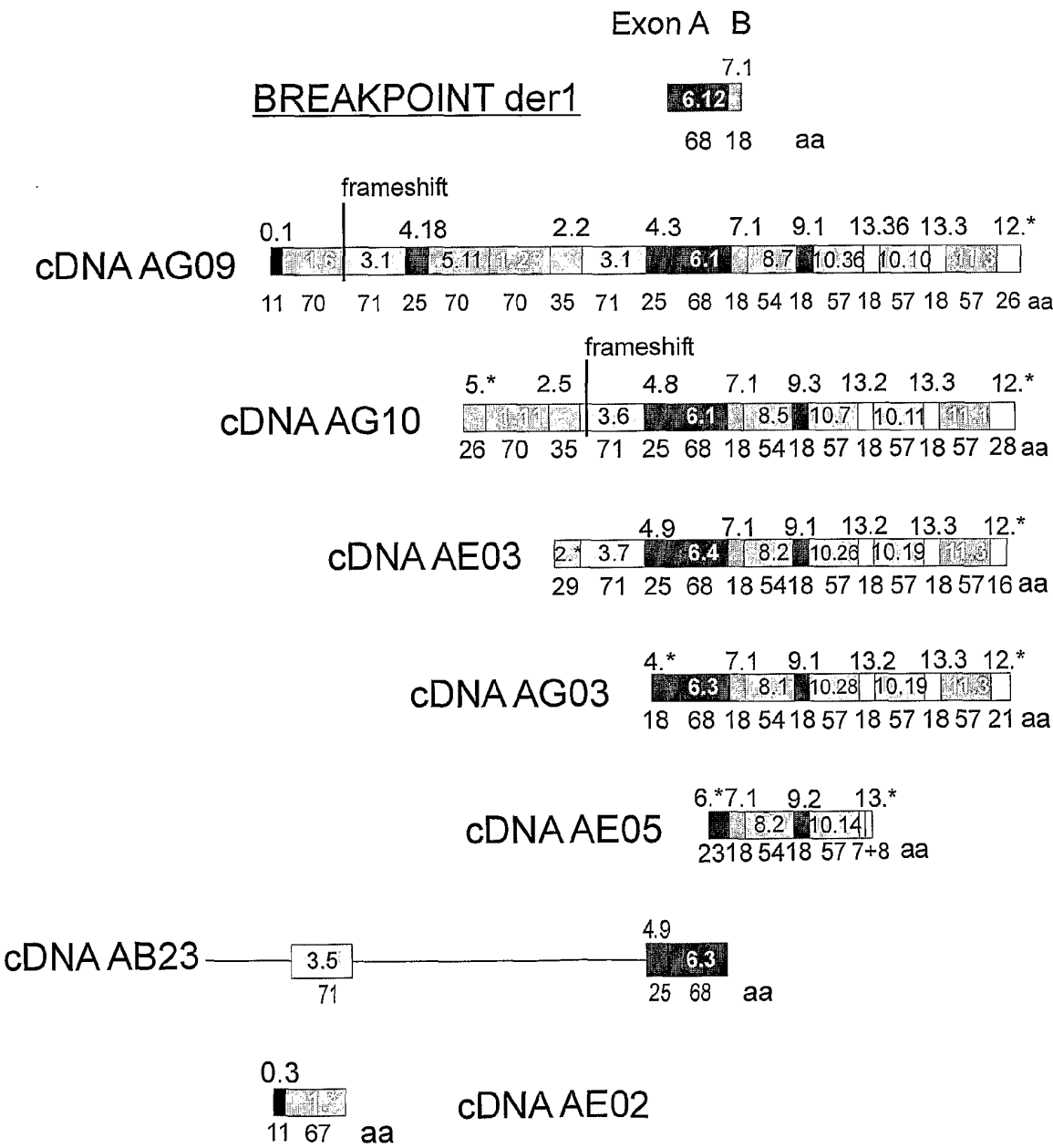
4490 4500 4510
agggaggtgactgtcatgtatgtccccactat

Figure 20



51/75

Figure 21



52/75

Figure 22

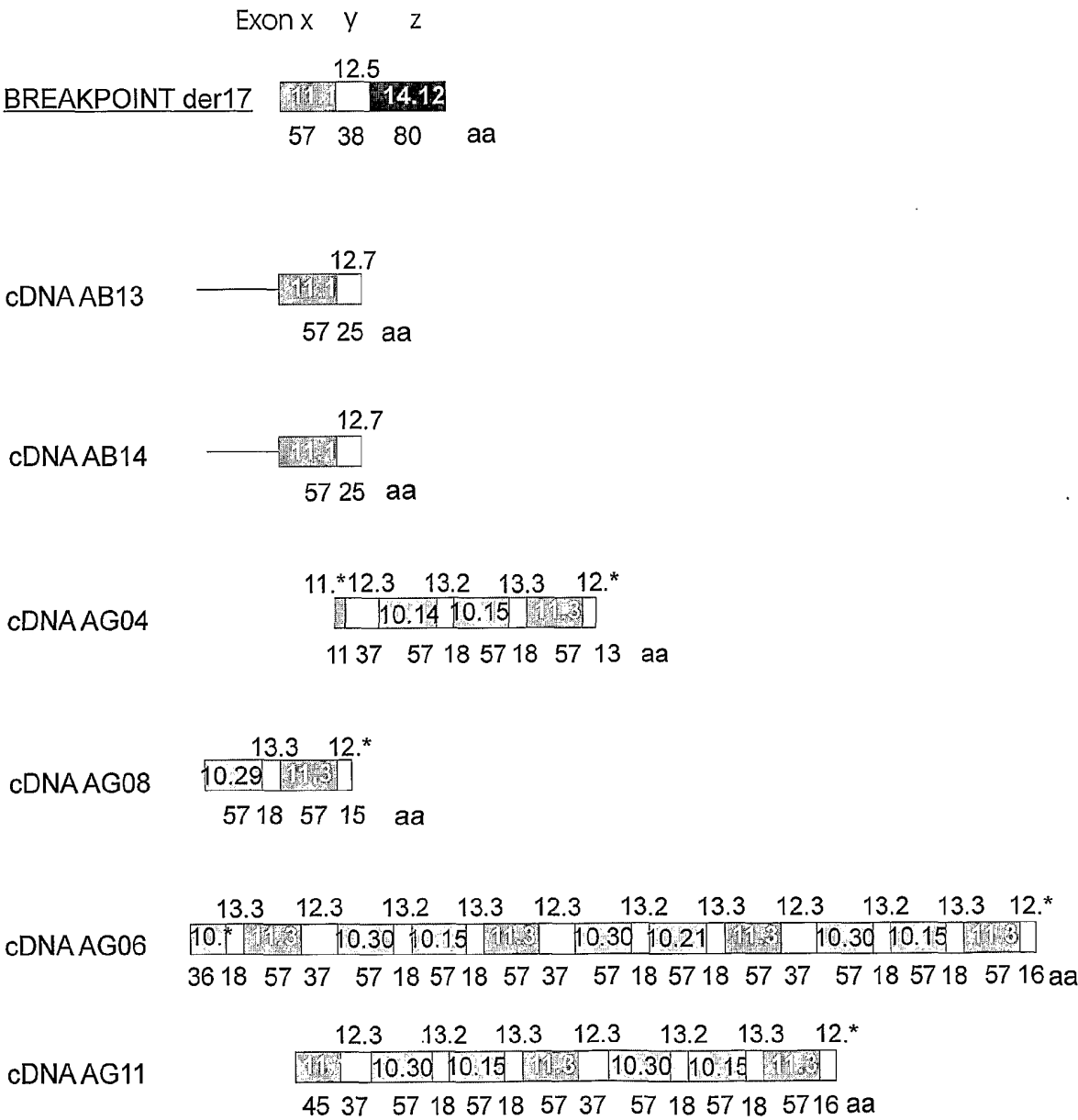


Figure 23

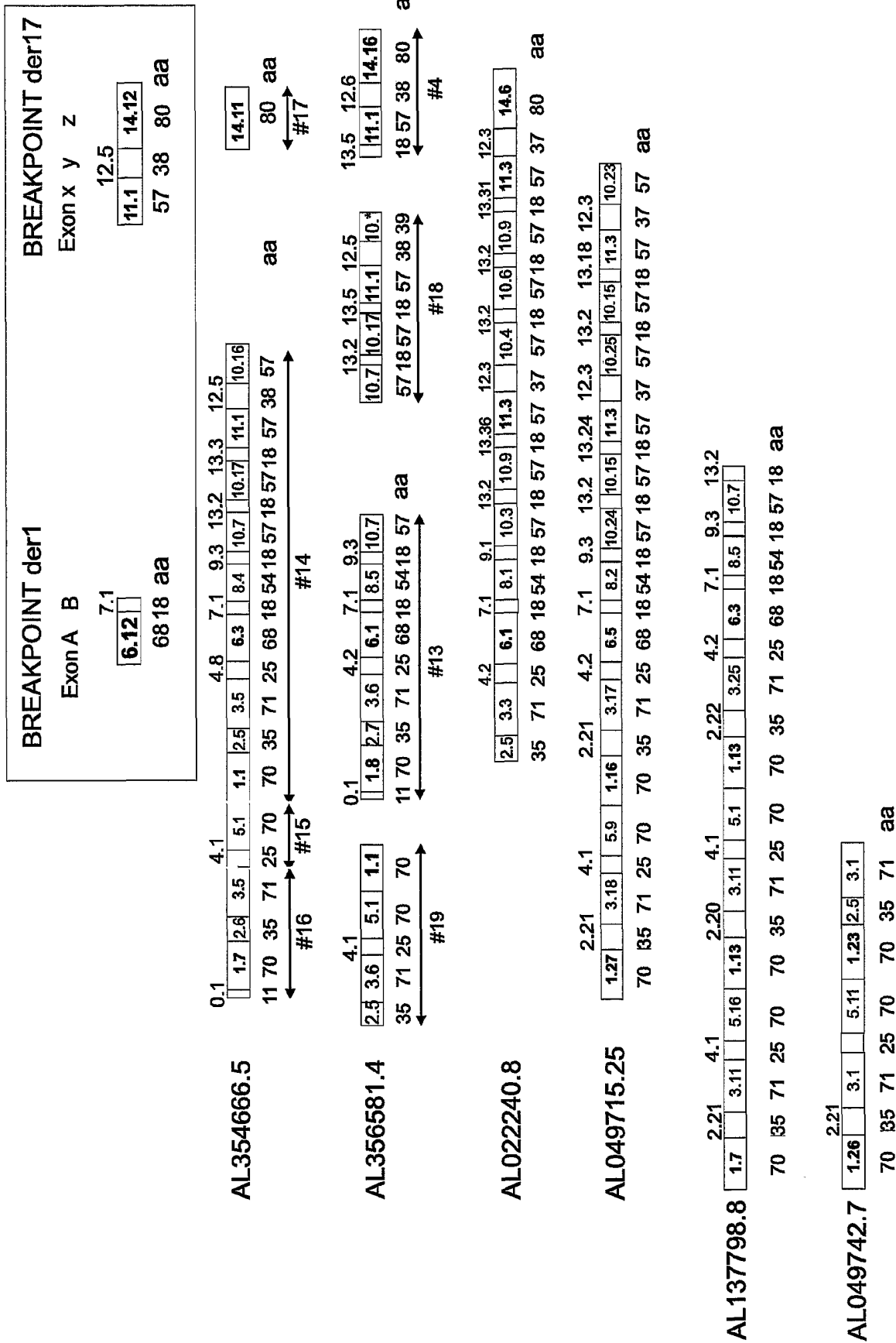


Figure 24 B

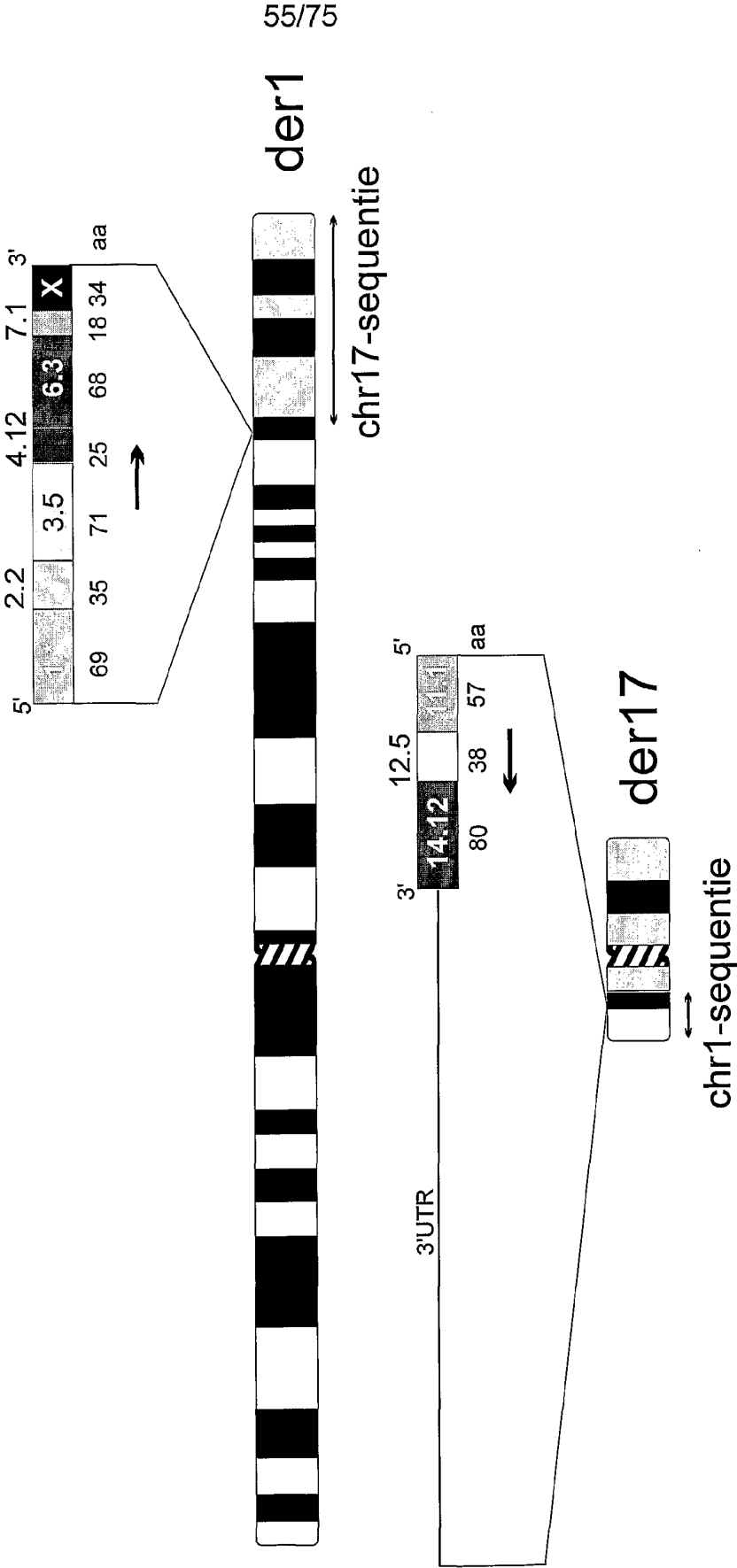


Figure 25

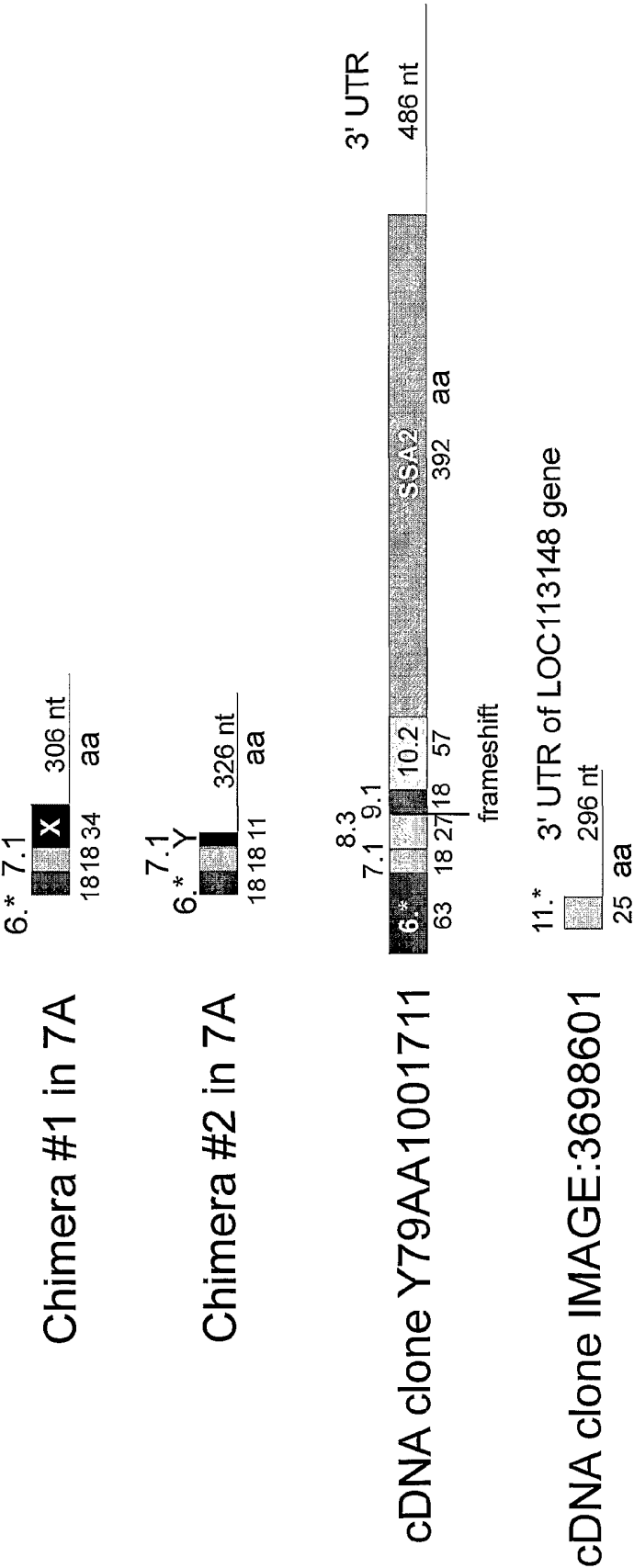


Figure 26

10	20	30	40	50	60	70
ATTGGCTCATCCTCTCATGTTGAATGGGAGGATGCTGTACACATTATCCAGAAAATGAAAGTGATGATG						
I G S S S H V E W E D A V H I I P E N E S D D						
Exon 6.*-7.1						
80	90	100	110	120	130	140
AGGAAAGAGGAAAGAAAAGGCCAGTGTCTCCAGGatgaagaatgagggccacactgccaagcaagatatct						
E E E E E K G P V S P R M K N E A T L P K Q D L						
Exon 7.1 + X						
150	160	170	180	190	200	210
cgtgctatgtgtgattgaatctcctgctggcgccaagcagggaatctcatcatttccccacaggccctga						
V L C V I E S P A G R Q A G I S S F P H R P *						
220	230	240	250	260	270	280
gagcacacaggcctcatccccaccacacacagtgcagtgcactcactgcagagccaatgaggcctgagc						
290	300	310	320	330	340	350
tcagggtctgcgtctgcctgcattcgtgcattggccacttccatctgtggtactgtgttagttattttaaatg						
360	370	380	390	400	410	420
tgcgattttggttgcatctttctccttctaaatatacacagtagtttttgcacaaaaaaaaaaaaaaaa						

Figure 27

10 20 30 40 50 60 70
 ATGGCTCATCCTCTCATGTTGAATGGGAGGATGCTGTACACATTATCCCAGAAAATGAAAGTGATGATG
 I G S S S H V E W E D A V H I I P E N E S D D **Exon 6.*-7.1**
 80 90 100 110 120 130 140
 AGGAAGAGGAAAGAAAAAGGCCAGTGTCTCCAGGtgctctctgcaggaaacaatgtggacaatcacag**ta**
 E E E E K G G P V S P R C L C R K Q C G Q S Q * **Ex 7 + ORF Y**
 150 160 170 180 190 200 210
 gttggaaggacaatgactgacctaatggagttcaggacgctatgactgttggcacctgatgtgcacagct
 220 230 240 250 260 270 280
 gctcccatctgcgcagagagaataataaaggcagtggcgctgaaacatctgctgcttccactcaccatcaa
 290 300 310 320 330 340 350
 gatggaactgactgtacatgcaagcaaatTTTgatgaagagagtgatctcagagtgcggaagataaagtTgt
 360 370 380 390 400 410 420
 ttctccttgacacctaggaatgcacctggcccaagaccctcagttgaaagacaatatcaataataatggcaaa
 430 440 450 457
 .attgtaaatcaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa

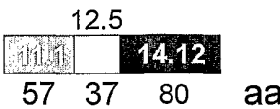
59/75

Figure 28 A

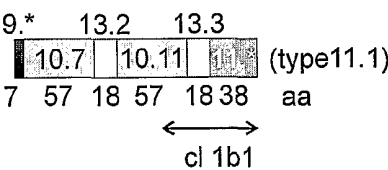
5'RACE
templates

2F53VIII

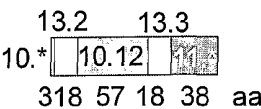
BREAKPT (t1;17)



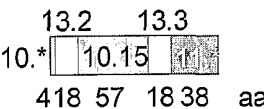
cl 1b9



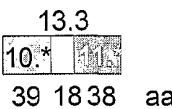
cl 1b7



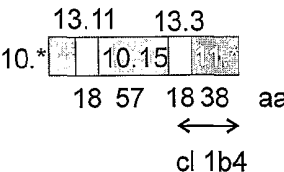
cl 1b3



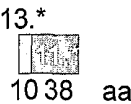
cl 1c11



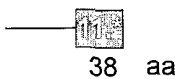
cl 1a8



cl 1a4 =1c12



cl 1a2



cl 1a1

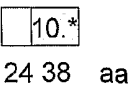
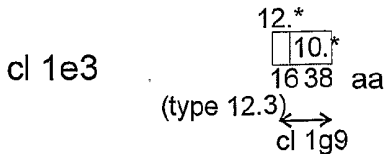
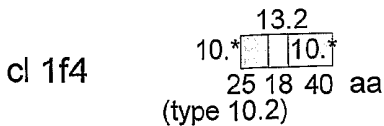
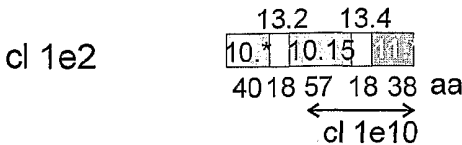
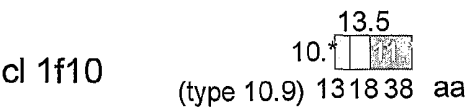
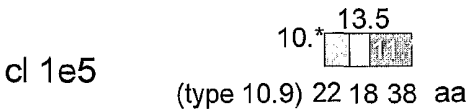
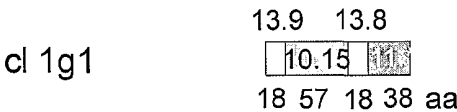
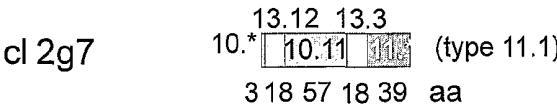
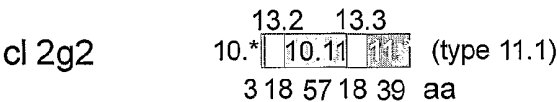
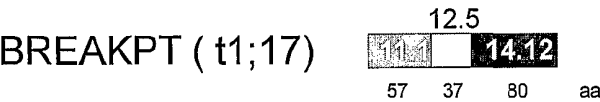


Figure 28 B 60/75

5'RACE
templates

7 A

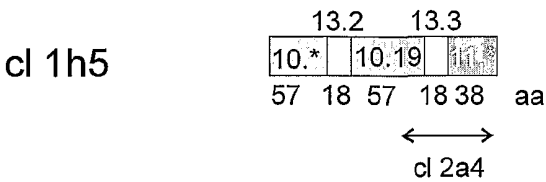
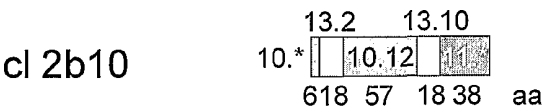
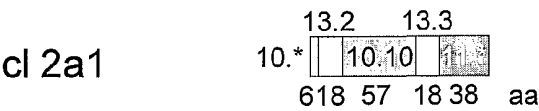


61/75

Figure 28 C

5'RACE
templates

7TR-14



62/75

Figure 28 D

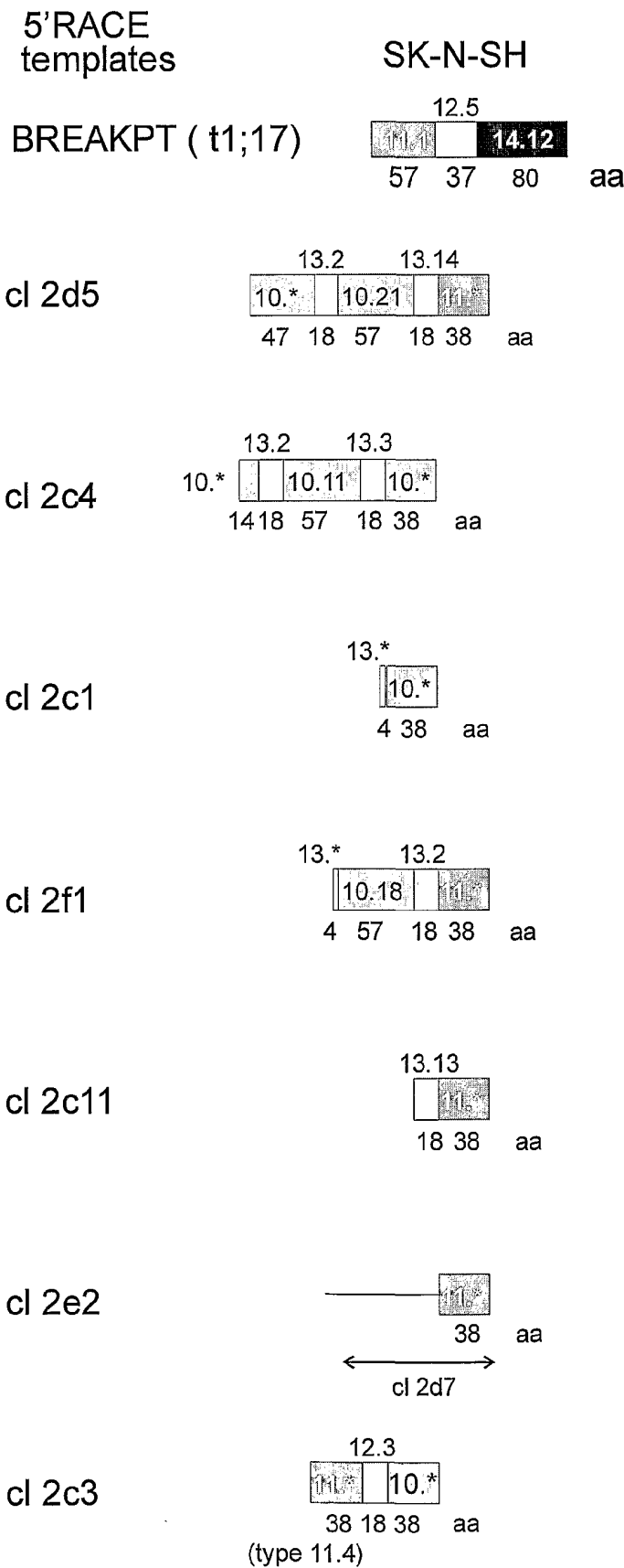
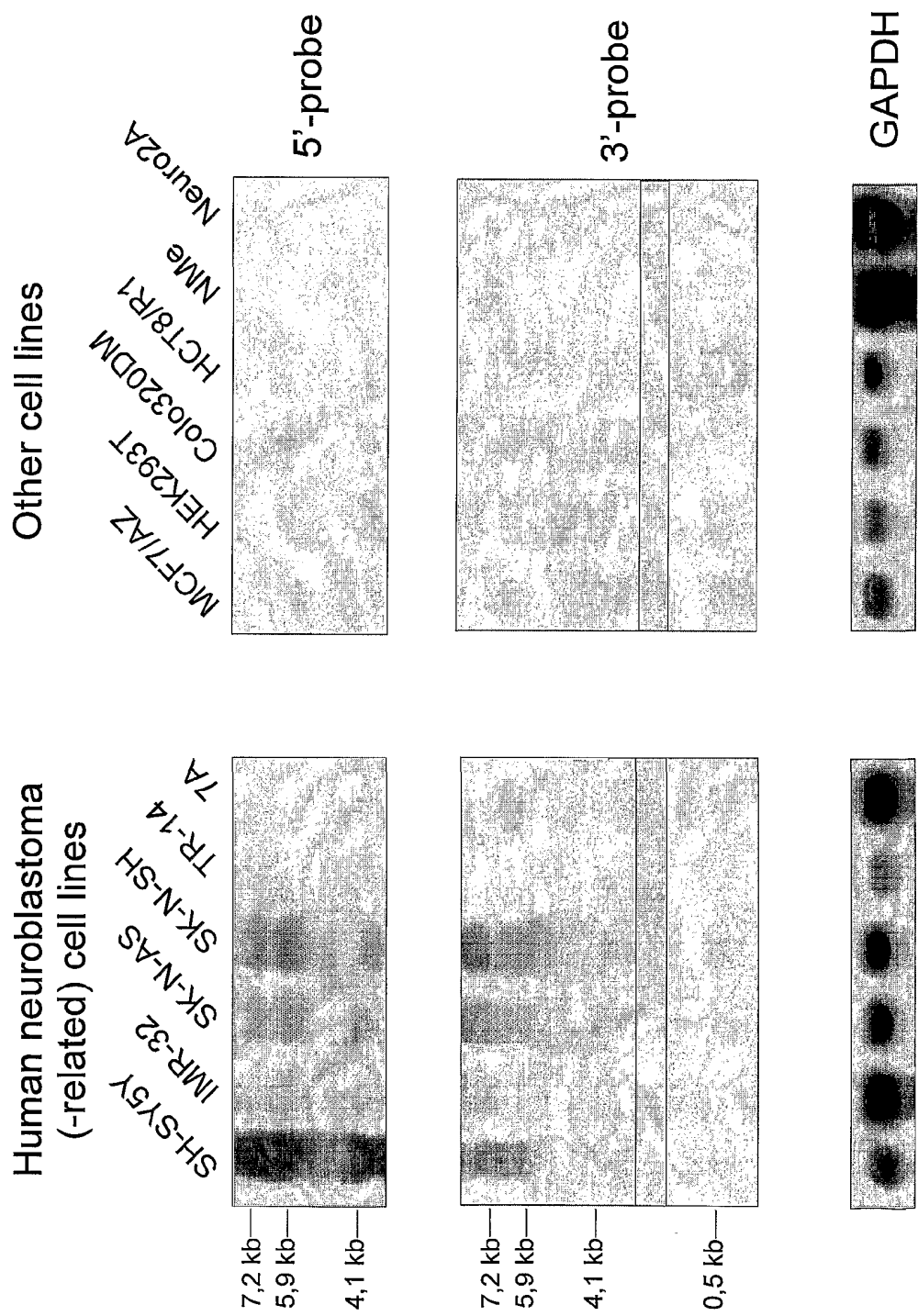


Figure 29 A



Northern blot analysis

Figure 29 B

64/75

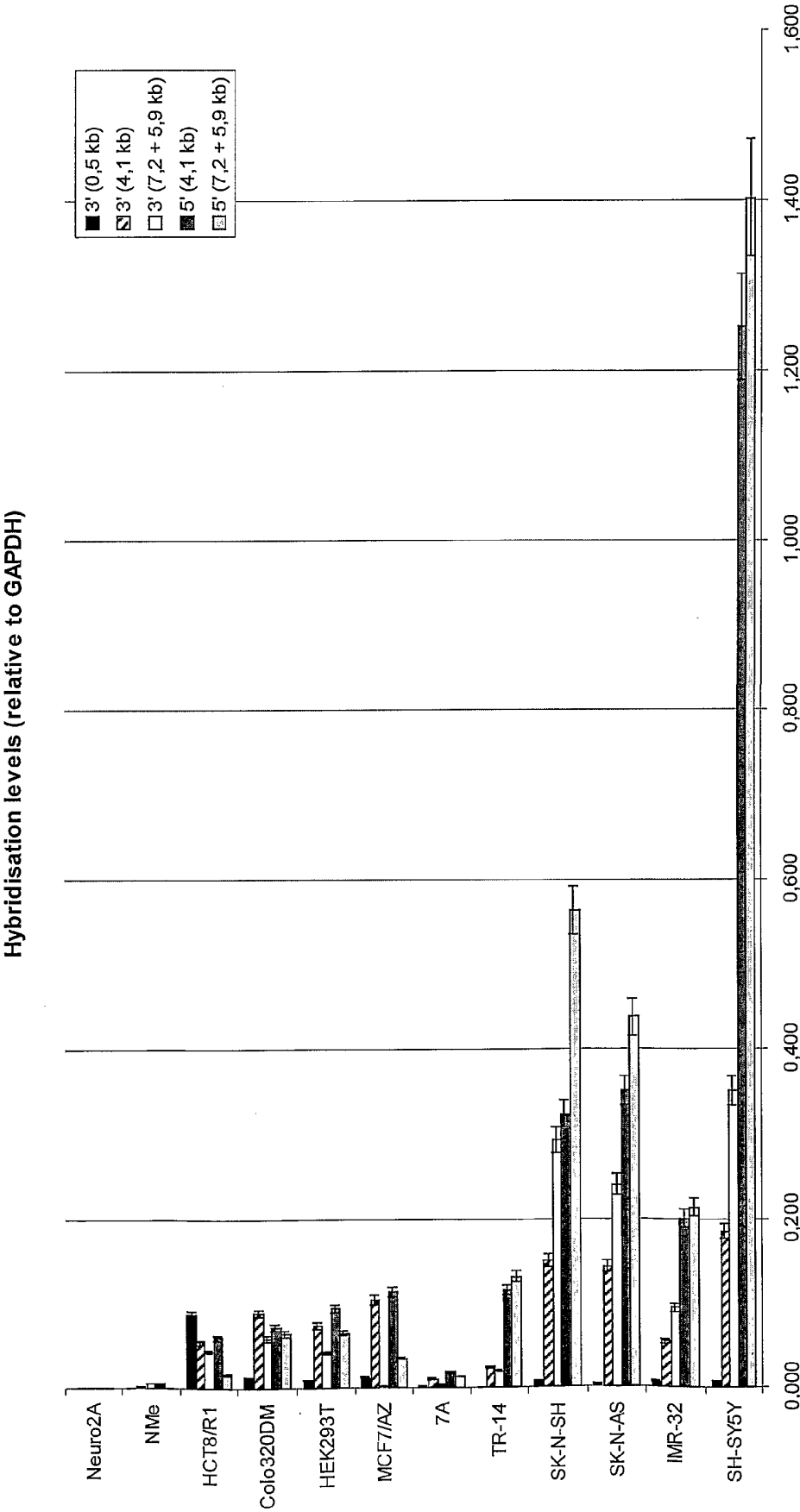


Figure 30 A

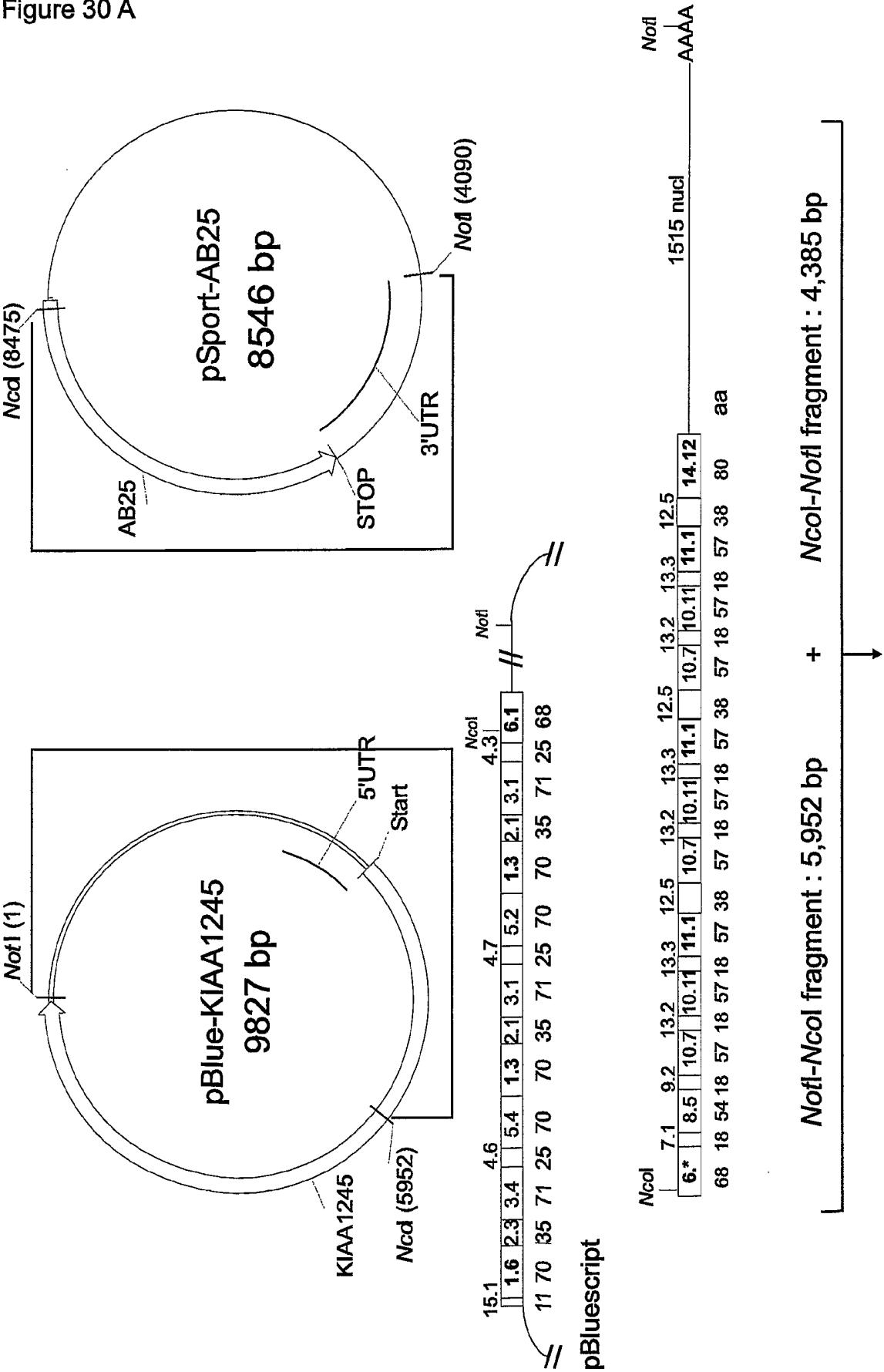


Figure 30 B

66/75

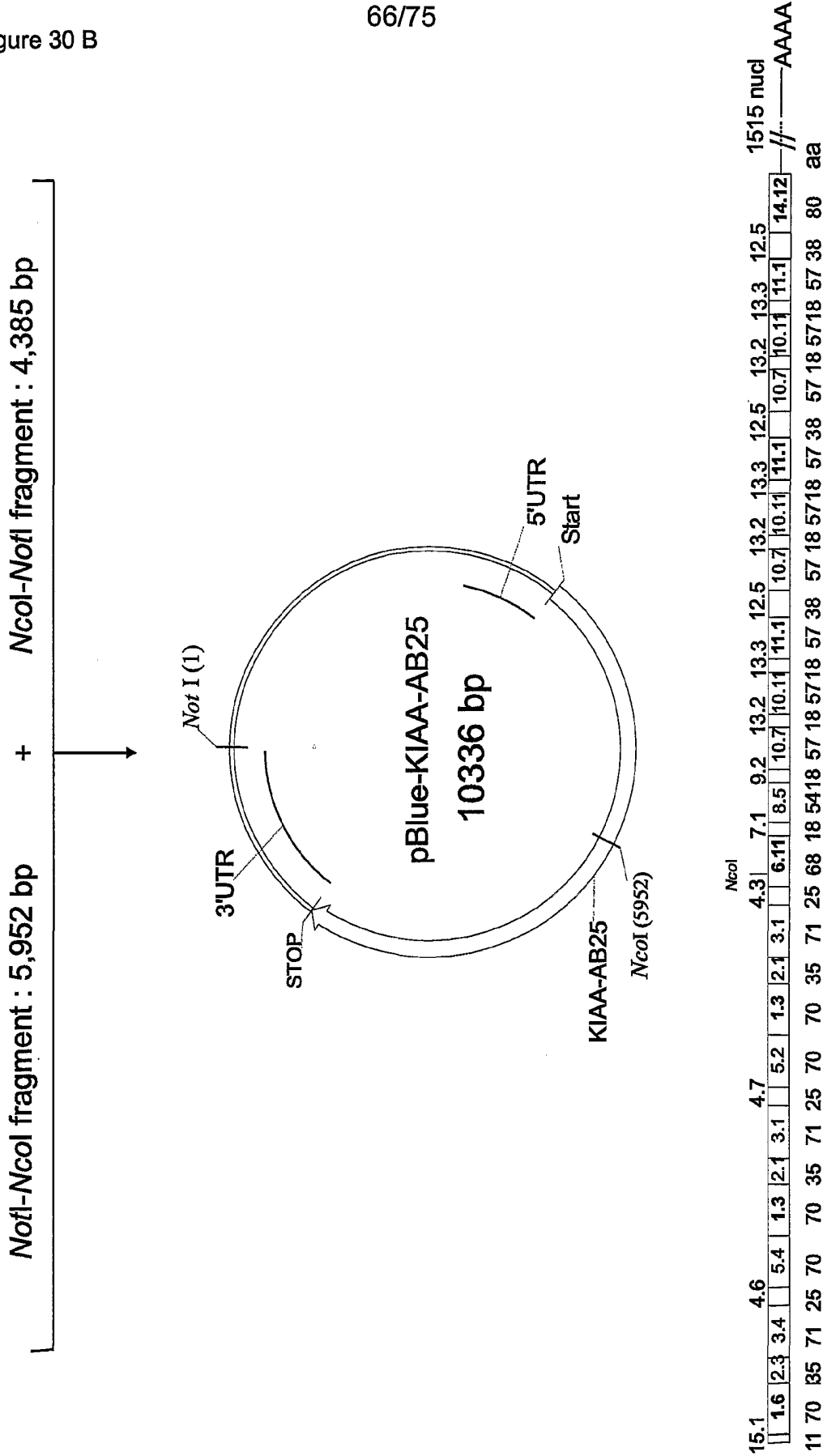
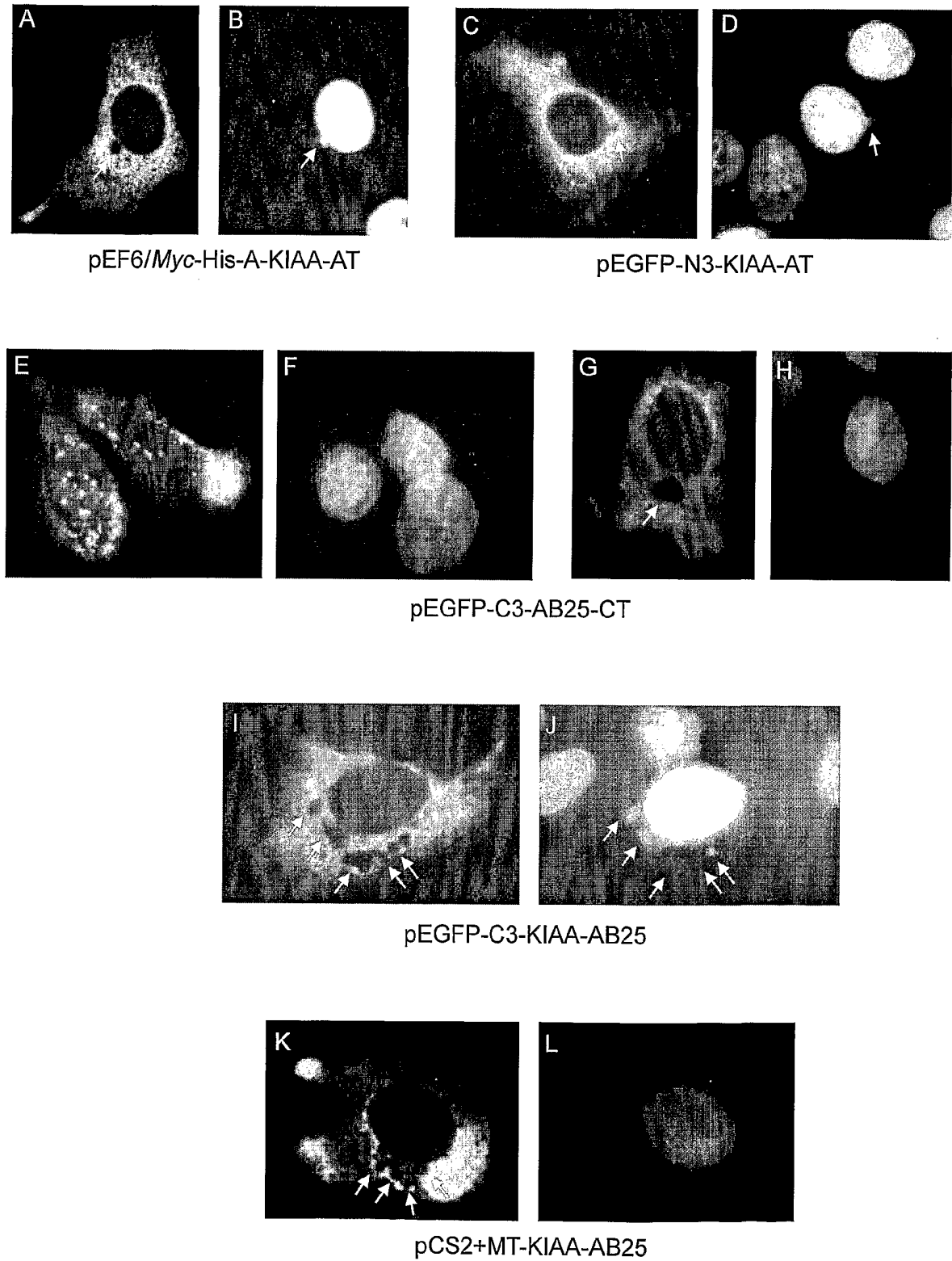


Figure 31

67/75

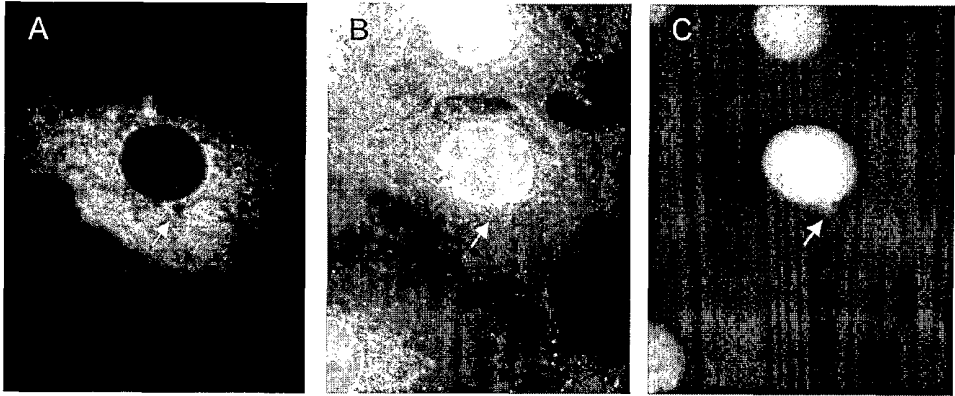
MCF7/AZ



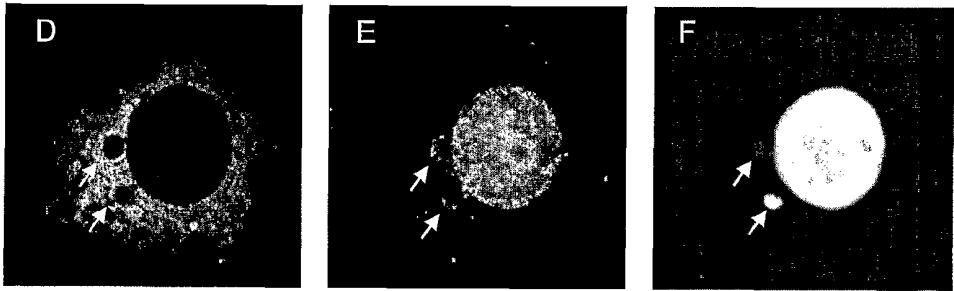
68/75

Figure 32

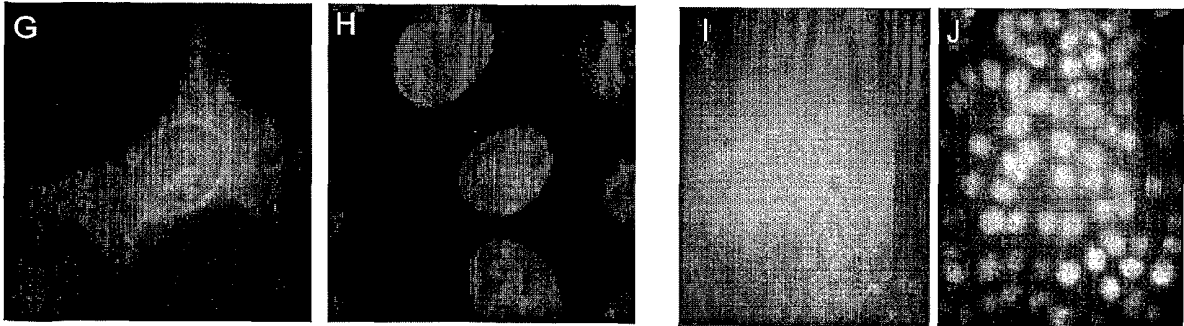
MCF7/AZ



ER staining
pCS2+MT-KIAA-AB25



Lamin B staining
pCS2+MT-KIAA-AB25

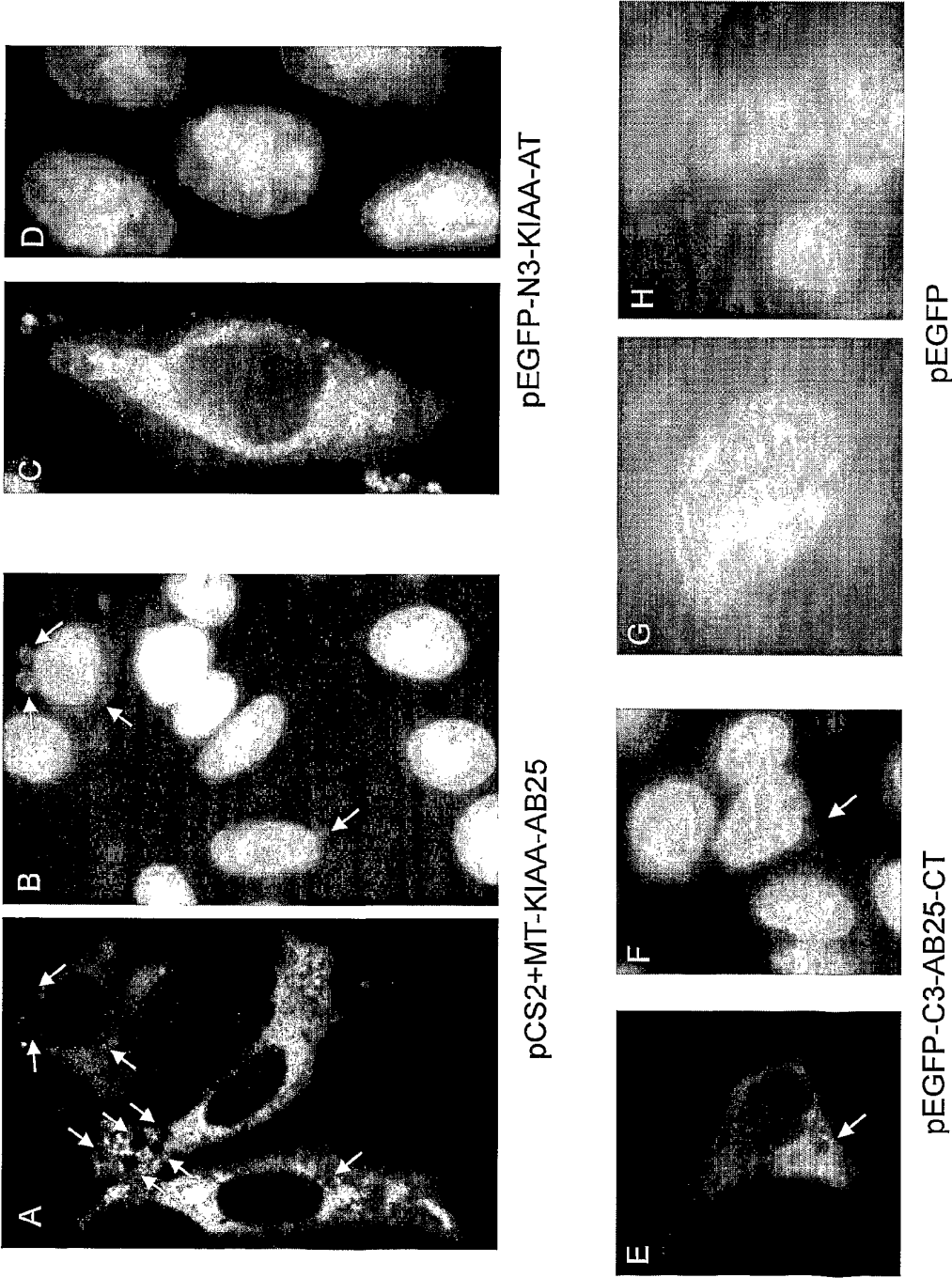


pEGFP

pEF6/Myc-His-A

Figure 33

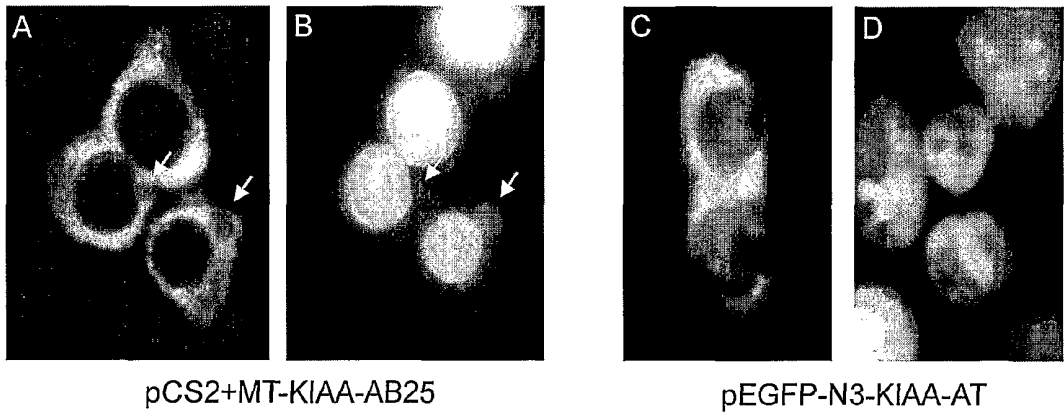
HCT8/E8



70/75

Figure 34

HEK293T



Colo320DM

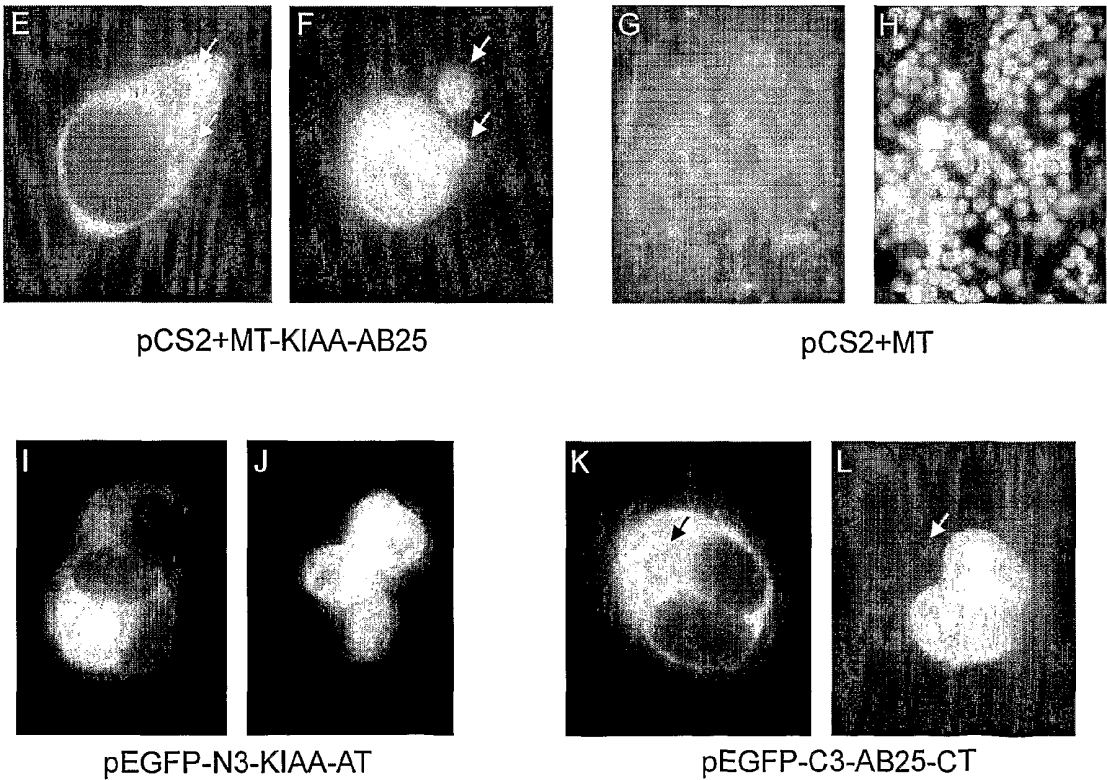


Figure 35

NMe

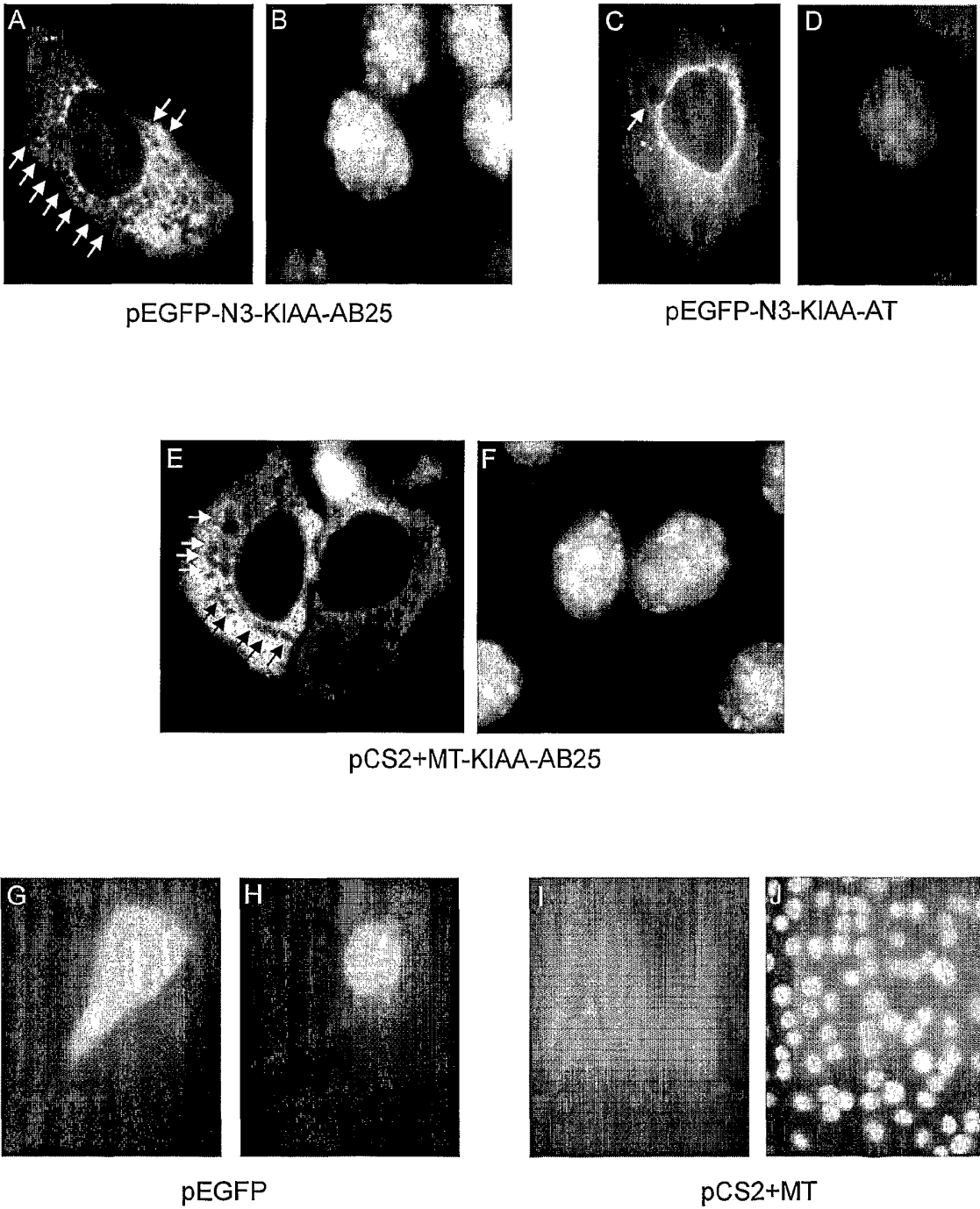
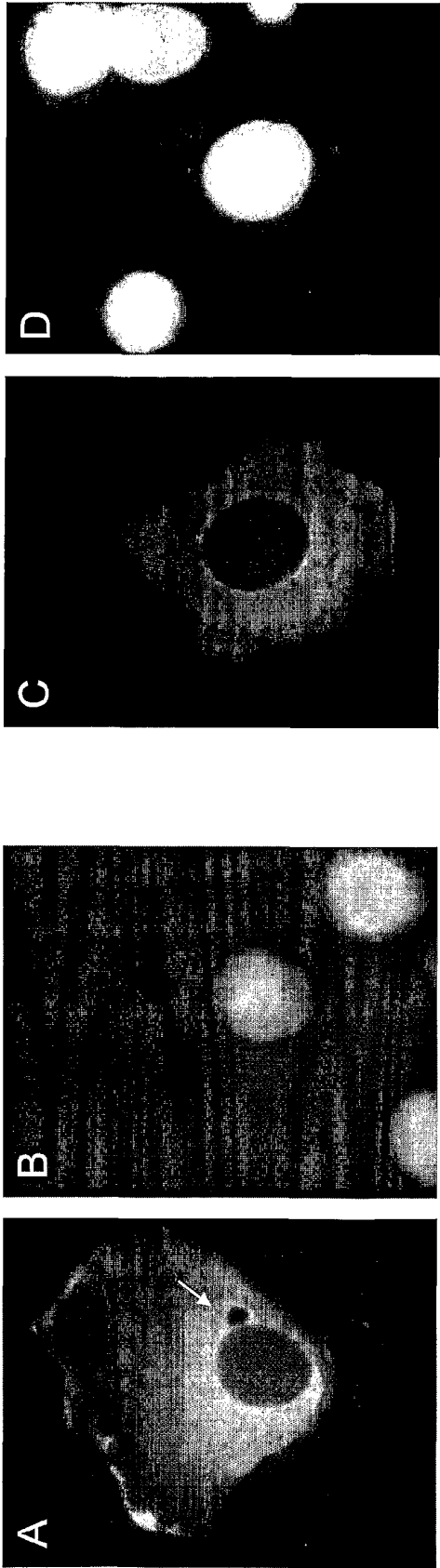


Figure 36

MCF7/AZ



pCS2+MT-chimera2

pCS2+MT-chimera1

Figure 37 A

RT-PCR products on human fetal brain (HFB) RNA template

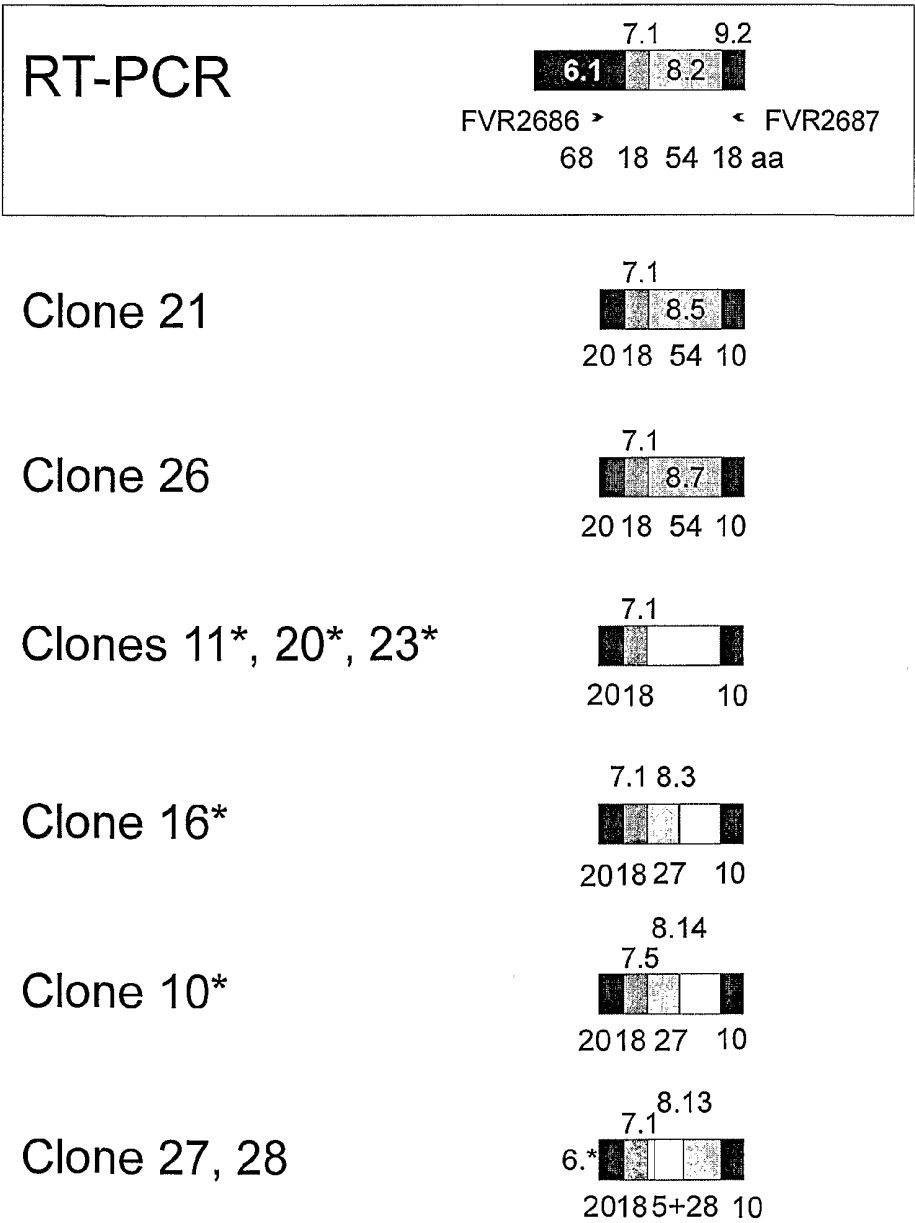
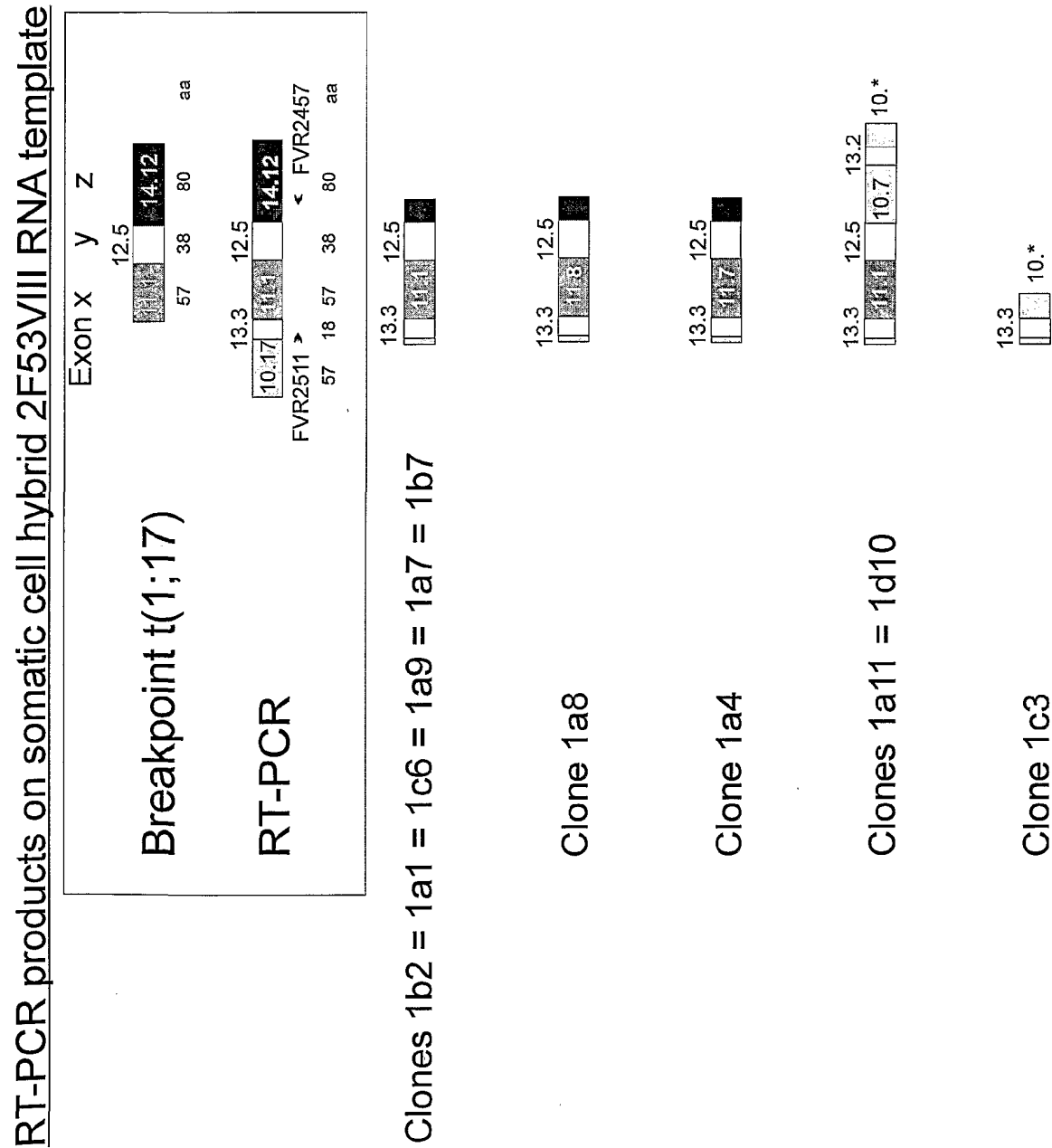


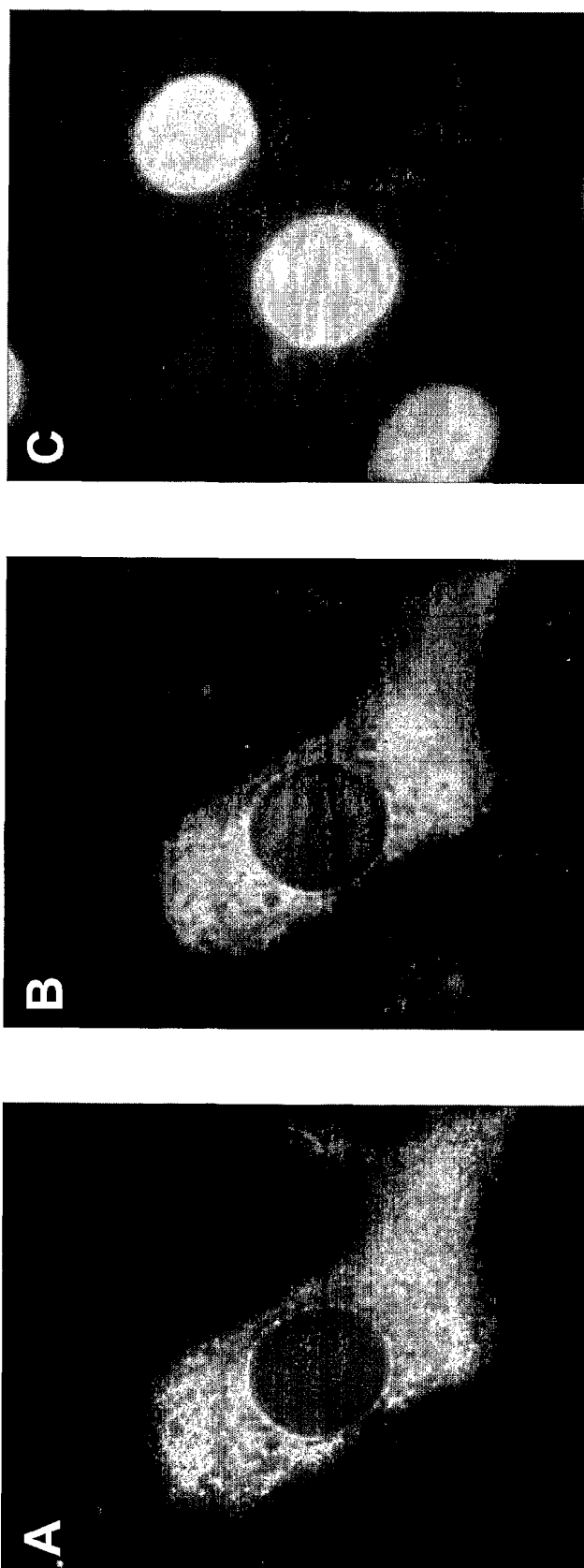
Figure 37 B

74/75



75/75

Figure 38



SEQUENCE LISTING

<110> VLAAMS INTERUNIVERSITAIR INSTITUUT VOOR BIOTECHNOL

<120> IDENTIFICATION OF NEUROBLASTOMA TUMOR SUPPRESSOR GENES

<130> FVR/RUG/V072

<140>

<141>

<150> EP 00870219.3

<151> 2000-09-27

<160> 203

<170> PatentIn Ver. 2.1

<210> 1

<211> 528

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(528)

<400> 1

ctc	agc	agg	gag	ctg	ctg	gag	gca	gta	gag	cct	gaa	gtc	ttg	cag	gac	48
Leu	Ser	Arg	Glu	Leu	Leu	Glu	Ala	Val	Glu	Pro	Glu	Val	Leu	Gln	Asp	
1				5					10					15		

tca	ctg	gat	aga	tgt	tat	tca	act	cct	tcc	agt	tgt	ctt	gaa	cag	cct	96
Ser	Leu	Asp	Arg	Cys	Tyr	Ser	Thr	Pro	Ser	Ser	Cys	Leu	Glu	Gln	Pro	
			20					25					30			

gac	tcc	tgc	ctg	ccc	tat	gga	agt	tcc	ttt	tat	gca	ttg	gag	gaa	aaa	144
Asp	Ser	Cys	Leu	Pro	Tyr	Gly	Ser	Ser	Phe	Tyr	Ala	Leu	Glu	Glu	Lys	
		35					40					45				

cat	gtt	ggc	ttt	tct	ctt	gac	gtg	gga	gaa	att	gaa	aag	aag	ggg	aag	192
His	Val	Gly	Phe	Ser	Leu	Asp	Val	Gly	Glu	Ile	Glu	Lys	Lys	Gly	Lys	
	50					55				60						

ggg	aag	aaa	aga	agg	gga	aga	aga	tca	acg	aag	aaa	aga	agg	aga	agg	240
Gly	Lys	Lys	Arg	Arg	Gly	Arg	Arg	Ser	Thr	Lys	Lys	Arg	Arg	Arg	Arg	
65					70					75					80	

gga aga aaa gaa ggg gaa gaa gat caa aac cca cca tgc ccc agg ctc 288
 Gly Arg Lys Glu Gly Glu Glu Asp Gln Asn Pro Pro Cys Pro Arg Leu
 85 90 95

agc ggt gtg ctg atg gaa gtg gaa gag cct gaa atc ttg cag gac tca 336
 Ser Gly Val Leu Met Glu Val Glu Glu Pro Glu Ile Leu Gln Asp Ser
 100 105 110

ctg gat aga tgt tat tcg act ccg tca atg ttc ttt gaa cta cct gac 384
 Leu Asp Arg Cys Tyr Ser Thr Pro Ser Met Phe Phe Glu Leu Pro Asp
 115 120 125

tca ttc cag cac tac aga agt gtg ttt tac tca ttt gag gaa cag cac 432
 Ser Phe Gln His Tyr Arg Ser Val Phe Tyr Ser Phe Glu Glu Gln His
 130 135 140

atc agc ttc gcc ctt gac gtg gac aat agg ttt ctt act ttg atg gga 480
 Ile Ser Phe Ala Leu Asp Val Asp Asn Arg Phe Leu Thr Leu Met Gly
 145 150 155 160

aca agt ctc cac ctg gtc ttc cag atg gga gtc ata ttc cca cag taa 528
 Thr Ser Leu His Leu Val Phe Gln Met Gly Val Ile Phe Pro Gln
 165 170 175

<210> 2

<211> 175

<212> PRT

<213> Homo sapiens

<400> 2

Leu Ser Arg Glu Leu Leu Glu Ala Val Glu Pro Glu Val Leu Gln Asp
 1 5 10 15
 Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Ser Cys Leu Glu Gln Pro
 20 25 30
 Asp Ser Cys Leu Pro Tyr Gly Ser Ser Phe Tyr Ala Leu Glu Glu Lys
 35 40 45
 His Val Gly Phe Ser Leu Asp Val Gly Glu Ile Glu Lys Lys Gly Lys
 50 55 60
 Gly Lys Lys Arg Arg Gly Arg Arg Ser Thr Lys Lys Arg Arg Arg Arg
 65 70 75 80
 Gly Arg Lys Glu Gly Glu Glu Asp Gln Asn Pro Pro Cys Pro Arg Leu
 85 90 95
 Ser Gly Val Leu Met Glu Val Glu Glu Pro Glu Ile Leu Gln Asp Ser
 100 105 110
 Leu Asp Arg Cys Tyr Ser Thr Pro Ser Met Phe Phe Glu Leu Pro Asp
 115 120 125
 Ser Phe Gln His Tyr Arg Ser Val Phe Tyr Ser Phe Glu Glu Gln His

130		135		140	
Ile Ser Phe Ala Leu Asp Val Asp Asn Arg Phe Leu Thr Leu Met Gly					
145		150		155	160
Thr Ser Leu His Leu Val Phe Gln Met Gly Val Ile Phe Pro Gln					
	165		170		175

<210> 3
 <211> 3033
 <212> DNA
 <213> Homo sapiens

<220>
 <221> exon
 <222> (1)..(171)

<220>
 <221> exon
 <222> (886)..(999)
 <223> exon y

<220>
 <221> exon
 <222> (1611)..(1853)
 <223> exon z

<400> 3
 ctc agc agg gag ctg ctg gag gca gta gag cct gaa gtc ttg cag gac 48
 tca ctg gat aga tgt tat tca act cct tcc agt tgt ctt gaa cag cct 96
 gac tcc tgc ctg ccc tat gga agt tcc ttt tat gca ttg gag gaa aaa 144
 cat gtt ggc ttt tct ctt gac gtg gga ggtgagtacc tttctatgaa 191
 ggtgataagg atccactgag tcttccatat aaagatcata ttcttgctcc aagtggccat 251
 tactgagctg agagatgtca ttgctgcagt gaggacctat aggcacatgt aggttgaatg 311
 aaactctagt tctaactgga agcccagaca tgggatgggt cagtgagcat ggctctcttc 371
 ctagtctcag gccatgcctg tggcactctg attctactct catgacattg gacctgggca 431
 gatgtgacaa attcagagaa ctatgatttt gactcaaggg tttgtagatt tcctttttca 491
 ctctaatttc agtgtctaaa gtccctcaca ccatgaacaa tctgagtatt tgatgagaca 551

gggctaaata ttgcagtttt tctcctagaa atcatttgag ggtatttgct ttaaattgat 611
tggaataata tggcataact gtttgcacaa actcgggaca aatgatattg ggataacgat 671
ctactagaat agggacattt taccacagt ttctgggaga aaaaccgagg aatttctatc 731
atgaccagcc ttcaggcctc ctgaaatata tctctcacag tctcctattc ttatgctgag 791
gagcctgagg tccctgtgtg aggattagac agtggattgt tatgtgtgta ggggaatcag 851
cttaatgtgt ctgtccatgt ctgaatttat tgca gaa att gaa aag aag ggg aag 906
ggg aag aaa aga agg gga aga aga tca acg aag aaa aga agg aga agg 954
gga aga aaa gaa ggg gaa gaa gat caa aac cca cca tgc ccc agg 999
taactttcag caattgtgga tgcttaattc tgtgttaaca cctggaggca acagattcag 1059
ggaaaccaga gtgtgtttga tttcatgttt tcaacgaagg ctgaattact cctactgtca 1119
ttgctgttgg ttttcattgc agtagatgtt taggtttcca tttcttcctc cccttatcat 1179
ttactaacgt accataggat gaccatactt caaaagctgt actctcgtgg ccaactgcac 1239
gaattttgag catattttat ggaaaactat tgagctcact cttttcatga tcgcagtttg 1299
ctgtgtgtca tgagggcact aactcagagt gtccttttac tcccttacca gtatgtcacc 1359
tggccaattc actagctcac tttctctctg tctctgtctc tgtctctgtc tctctgtott 1419
tctctttcat tgtttttctac ctggccctgt tctatcccaa cataaaggca ataatttttt 1479
ttttttacct cattaatgga totatccttt tcttttctta ccaattcctt acgttacttc 1539
tgaaatctag tggggctctg tgggtgtctga ttttccctgg ctgcttcttt agttttgtct 1599
gcttttccag g ctc agc ggt gtg ctg atg gaa gtg gaa gag cct gaa atc 1649
ttg cag gac tca ctg gat aga tgt tat tcg act ccg tca atg ttc ttt 1697
gaa cta cct gac tca ttc cag cac tac aga agt gtg ttt tac tca ttt 1745
gag gaa cag cac atc agc ttc gcc ctt gac gtg gac aat agg ttt ctt 1793
act ttg atg gga aca agt ctc cac ctg gtc ttc cag atg gga gtc ata 1841
ttc cca cag taa gcagccctta ctaagccgag agatgtcatt cctgcaggca 1893

ggacctatag gcacgtgaag atttgaatga aactatagtt ccatttggaa gcccagacat 1953
aggatgggtc agtgggcatg gctctattcc tattctcaga ccatgccagt ggcaacctgt 2013
gctcagtttg aagacaatgg acccaagtta ggtgtgacac gttcacataa ctgtgcagca 2073
catgcogggga gtgatcagtc agacatttta atttgaacca cgtatctctg ggtagctaca 2133
aagttcctca gggatttcat tttgcaggca tgtctctgag cttctataacc tgctcaaggt 2193
cagtgtcatc tttgtgttta gctcatccaa aggtgttacc ctggtttcaa tgaacctaac 2253
ctcattcttt gtatcttcag tgttgaattg ttttagctga tccatcttta acacaggagg 2313
gatccttggc tgaggattgt atttcagaac caccaactgc tcttgacaat tgtaaaccog 2373
ctaggctcct ttggtttagag aagccacagt ccttcagcct ccaattgggtg tcagtactta 2433
ggaagaccac agctagatgg acaaacagca ttgggaggcc ttagccctgc tcctctogat 2493
tccatcctgt agagaacagg agtcaggagc cgctggcagg agacagcatg tcaccagga 2553
ctctgccggt gcagaatatg aacaacgcca tgttcttgca gaaaacgctt agcctgagtt 2613
tcataggagg taatcaccag acaactgcag aatgtagaac actgagcagg acaactgacc 2673
tgtctccttc acatagtcca tatcaccaca aatcacacaa caaaaaggag aagagatatt 2733
ttgggttcaa aaaaagtaaa aagataatat agctgcattt ctttagttat tttgaacccc 2793
aaatatttcc tcatcttttt gttgttgtca ttgatgggtg tgacatggac ttgtttatag 2853
aggacaggtc agctgtctgg ctcaatgatc tacattctga agttgtctga aaatgtcttc 2913
atgattaaat tcagcctaaa cgttttgccg ggaacactgc agagacaatg ctgtgagttt 2973
ccaaccttag cccatctgcg ggcagagaag gtctagtttg tccatcagca ttatcatgat 3033

<210> 4

<211> 3743

<212> DNA

<213> Homo sapiens

<220>

<221> exon

<222> (711)..(881)

<223> Exon x

<220>

<221> exon

<222> (1596)..(1709)

<223> Exon y

<220>

<221> exon

<222> (2321)..(2563)

<223> Exon z

<400> 4

```

cccctcagct ctgtgcattt tgtctacaag caaggtgact ttgggttttag tgtgttcatg 60
tttcaacaag aatgtaagtt tgggatcaga catatgttac ccctgttgga tagtagcttt 120
gcaatcagtc tttgcaaaaa atatccagaa caaggctaga acaaggtggg acagaaacaa 180
ataacacgtg ttacagttac atatgagctt ggattacctc ctttatagaa ggaagtggag 240
acatccttca tgcagagatt taggatctct cactagcact aaccctcttg ccccccaccta 300
gtgtttatatt caatcacccc tgttgctttt tatcaaatga aagatacaga tccactttta 360
agagtaaaga agagaggaag cacagtttat taattaccca ttggtatccc aaggacttgt 420
gcttccatta totcattggt ttattcattc attaatccaa acactcattc agcagggatt 480
tottgggggc ctaccttgta ctgggctctg tggtcctggg agatgcagca gggaaatagag 540
tcacaggctt gcaactcatag agagaacctt ctagctgggg agacagacaa caatgacaaa 600
aaggaagtgc tttttcaacc acttccttat gctacccatg aaacctagtt ggggctctgt 660
tgtgtctgat ttcccctggc ttattcttta ctttttcctc cttttccagg ctc agc 716
agg gag ctg ctg gag gca gta gag cct gaa gtc ttg cag gac tca ctg 764
gat aga tgt tat tca act cct tcc agt tgt ctt gaa cag cct gac tcc 812
tgc ctg ccc tat gga agt tcc ttt tat gca ttg gag gaa aaa cat gtt 860
ggc ttt tct ctt gac gtg gga ggtgagtacc tttctatgaa ggtgataagg 911
atccactgag tottccatat aaagatcata ttctgctcc aagtggccat tactgagctg 971
agagatgtca ttgctgcagt gaggacctat aggcacatgt aggttgaatg aaactctagt 1031

```

tctaactgga agcccagaca tgggatgggt cagtgagcat ggctctcttc ctagtctcag 1091
gccatgcctg tggcactctg attctactct catgacattg gacctgggca gatgtgacaa 1151
attcagagaa ctatgatttt gactcaaggg tttgtagatt tcctttttca ctotaatttc 1211
agtgtctaaa gtcttcacaa ccatgaacaa tctgagtatt tgatgagaca gggctaaata 1271
ttgcagtttt tctcctagaa atcatttgag ggtatttgct ttaaattgat tggaaaaata 1331
tggcataact gtttgcacaa actcgggaca aatgatattg ggataacgat ctactagaat 1391
agggacattt taccacagt ttctgggaga aaaaccgagg aatttctatc atgaccagcc 1451
ttcaggcctc ctgaaatata tctctcacag tctcctattc ttatgctgag gagcctgagg 1511
tcctgtgtg aggattagac agtggattgt tatgtgtgta ggggaatcag cttaatgtgt 1571
ctgtccatgt ctgaatttat tgca gaa att gaa aag aag ggg aag ggg aag 1622
aaa aga agg gga aga aga tca acg aag aaa aga agg aga agg gga aga 1670
aaa gaa ggg gaa gaa gat caa aac cca cca tgc ccc agg taactttcag 1719
caattgtgga tgcttaattc tgtgttaaca cctggaggca acagattcag ggaaaccaga 1779
gtgtgtttga tttcatgttt tcaacgaagg ctgaattact cctactgtca ttgctgttg 1839
ttttcattgc agtagatgtt taggtttcca tttcttctc cccttatcat ttactaacgt 1899
accataggat gaccatactt caaaagctgt actctcgtgg ccactgcac gaattttgag 1959
catattttat ggaaaactat tgagctcact cttttcatga tcgcagtttg ctgtgtgtca 2019
tgagggcact aactcagagt gtccctttac tcccttacca gtatgtcacc tggccaattc 2079
actagctcac tttctctctg tctctgtctc tgtctctgtc tctctgtctt tctctttcat 2139
tgttttctac ctggccctgt tctatcccaa cataaaggca ataatttttt ttttttacct 2199
cattaatgga tctatccttt tcttttctta ccacttcctt acgttacttc tgaaatctag 2259
tggggctctg tgggtgtctga tttccctgg ctgcttcttt agttttgtct gcttttccag 2319
g ctc agc ggt gtg ctg atg gaa gtg gaa gag cct gaa atc ttg cag gac 2368
tca ctg gat aga tgt tat tcg act ccg tca atg ttc ttt gaa cta cct 2416

gac tca ttc cag cac tac aga agt gtg ttt tac tca ttt gag gaa cag 2464
 cac atc agc ttc gcc ctt gac gtg gac aat agg ttt ctt act ttg atg 2512
 gga aca agt ctc cac ctg gtc ttc cag atg gga gtc ata ttc cca cag 2560
 taa gcagccctta ctaagccgag agatgtcatt cctgcaggca ggacctatag 2613
 gcacgtgaag atttgaatga aactatagtt ccatttggaa gccagacat aggatgggtc 2673
 agtgggcatg gctctattcc tattctcaga ccatgccagt ggcaacctgt gctcagtctg 2733
 aagacaatgg acccaagtta ggtgtgacac gttcacataa ctgtgcagca catgccggga 2793
 gtgatcagtc agacatttta atttgaacca cgtatctctg ggtagctaca aagttcctca 2853
 gggatttcat tttgcaggca tgtctctgag cttctatacc tgctcaaggt cagtgtcatc 2913
 tttgtgttta gctcatccaa aggtgttacc ctggtttcaa tgaacctaac ctcatctttt 2973
 gtatcttcag tgttgaattg ttttagctga tccatcttta acacaggagg gatccttggc 3033
 tgaggattgt atttcagaac caccaactgc tcttgacaat tgtaaccgcg ctaggctcct 3093
 ttggttagag aagccacagt ccttcagcct ccaattgggtg tcagtactta ggaagaccac 3153
 agctagatgg acaaacagca ttgggaggcc ttagccctgc tcctctcgat tccatcctgt 3213
 agagaacagg agtcaggagc cgctggcagg agacagcatg tcaccagga ctctgcoggt 3273
 gcagaatatg aacaacgcca tgttcttgca gaaaacgctt agcctgagtt tcataggagg 3333
 taatcaccag acaactgcag aatgtagaac actgagcagg acaactgacc tgtctccttc 3393
 acatagtcca tatcaccaca aatcacacaa caaaaaggag aagagatatt ttgggttcaa 3453
 aaaaagtaaa aagataatat agctgcattt ctttagttat tttgaacccc aaatatttcc 3513
 tcatcttttt gttgttgtca ttgatgggtg tgacatggac ttgtttatag aggacaggtc 3573
 agctgtctgg ctcaatgac tacattctga agttgtctga aaatgtcttc atgattaaat 3633
 tcagcctaaa cgttttgccc ggaacactgc agagacaatg ctgtgagttt ccaaccttag 3693
 cccatctgcg ggcagagaag gtctagtttg tccatcagca ttatcatgat 3743

<210> 5

<211> 48

<212> DNA

<213> Homo sapiens

<220>

<223> GenomeWalker adaptor

<400> 5

gtaatacgac tcactatagg gcacgcgtgg tcgacggccc gggctggt 48

<210> 6

<211> 22

<212> DNA

<213> Homo sapiens

<400> 6

gtaatacgac tcactatagg gc 22

<210> 7

<211> 26

<212> DNA

<213> Homo sapiens

<400> 7

cccctcagct ctgtgcattt tgtcta 26

<210> 8

<211> 27

<212> DNA

<213> Homo sapiens

<400> 8

cctcttgccc ccacctagtg tttattt 27

<210> 9

<211> 20

<212> DNA

<213> Homo sapiens

<400> 9

ggccatgtga accaattctg 20

<210> 10
<211> 20
<212> DNA
<213> Homo sapiens

<400> 10
ggagagctga gtgaggaggg 20

<210> 11
<211> 20
<212> DNA
<213> Homo sapiens

<400> 11
cgccctggcct atttacctgt 20

<210> 12
<211> 20
<212> DNA
<213> Homo sapiens

<400> 12
tgcagcccat aaatacccac 20

<210> 13
<211> 20
<212> DNA
<213> Homo sapiens

<400> 13
cctcgagctg aagccaaatt 20

<210> 14
<211> 20
<212> DNA
<213> Homo sapiens

<400> 14
tggcctccat gctgtaggat 20

<210> 15
<211> 20

<212> DNA

<213> Homo sapiens

<400> 15

tcaaaccgccg actttcagat

20

<210> 16

<211> 20

<212> DNA

<213> Homo sapiens

<400> 16

tctgtgctgc ctggattcac

20

<210> 17

<211> 21

<212> DNA

<213> Homo sapiens

<400> 17

gcctgtttca tcaaatgcct g

21

<210> 18

<211> 21

<212> DNA

<213> Homo sapiens

<400> 18

ggagaaatgg cacagaggtg a

21

<210> 19

<211> 20

<212> DNA

<213> Homo sapiens

<400> 19

gagaccaagt tctttcccag

20

<210> 20

<211> 20

<212> DNA

<213> Homo sapiens

<400> 20
gagaccaagt tctttcccag

20

<210> 21
<211> 21
<212> DNA
<213> Homo sapiens

<400> 21
acaagcaaga ctgtgaagcc c

21

<210> 22
<211> 21
<212> DNA
<213> Homo sapiens

<400> 22
ggcttctctgt ttctcctcca g

21

<210> 23
<211> 20
<212> DNA
<213> Homo sapiens

<400> 23
gcctatcagg ccatgatcca

20

<210> 24
<211> 20
<212> DNA
<213> Homo sapiens

<400> 24
ggactccagg acagtggcat

20

<210> 25
<211> 20
<212> DNA
<213> Homo sapiens

<400> 25
accccatctc ttccagcat

20

<210> 26
<211> 20
<212> DNA
<213> Homo sapiens

<400> 26
ttgcctggca ttcactctaga 20

<210> 27
<211> 20
<212> DNA
<213> Homo sapiens

<400> 27
gggtccctgg tagttaacga 20

<210> 28
<211> 19
<212> DNA
<213> Homo sapiens

<400> 28
ccaactcctg accccagaa 19

<210> 29
<211> 21
<212> DNA
<213> Homo sapiens

<400> 29
atggatgggt aaactgaggc c 21

<210> 30
<211> 20
<212> DNA
<213> Homo sapiens

<400> 30
gctgacttcc tgagggaggc 20

<210> 31
<211> 21

<212> DNA

<213> Homo sapiens

<400> 31

caccacaatt tccatgagct c

21

<210> 32

<211> 20

<212> DNA

<213> Homo sapiens

<400> 32

tggtggtgta ccccttgac

20

<210> 33

<211> 20

<212> DNA

<213> Homo sapiens

<400> 33

gaactgtcgc cactcgtctg

20

<210> 34

<211> 20

<212> DNA

<213> Homo sapiens

<400> 34

acaccacagc gggatgatgt

20

<210> 35

<211> 516

<212> DNA

<213> Homo sapiens

<400> 35

gaactgtcgc cactcgtctg gatgtgcatt cgcaagctgc cctgcgagtg ctgtcaattg 60
 caaattcagt caattaggac tcagcatcag gcagctggaa tgacacttcc tctagtgaag 120
 cctcagagag cttacttatg ccactcattt cagatggaga gcaagggttt gaatttgccc 180
 cctctagagc ccatgctcgc acttctgcac cgtatggcaa ggttgagtca ggcagagctt 240
 gtctctcaaga agcccgagc ctgctgtgga gagaggtggg cagtataaca catgctccag 300
 ctgtagccat gtccctgtct ggaccagtta actcaattca gtttcaactt gcagacagct 360
 ccttcaagcc aatcagacat cagagaaata aaaaggatgt gacaaaagag agtgaggtgg 420
 agaacacagt ctccctctcc tggacaaact gctctgggaa agtttgcact tggaggtaga 480

tggggatgaa gccaacacat catcccgctg tgggtg 516

<210> 36

<211> 20

<212> DNA

<213> Homo sapiens

<400> 36

aaccccgagt gttgctgaaa 20

<210> 37

<211> 20

<212> DNA

<213> Homo sapiens

<400> 37

ccattcccca agcacctcat 20

<210> 38

<211> 789

<212> DNA

<213> Homo sapiens

<400> 38

aaccccgagt gttgctgaaa tcaaaaggct atgaagaagc agaagtcttg tgaagggtgtt 60
 gttgggaaag agaattgttc agatatgggt aagccactga aagggtgtctt gatgggttcat 120
 ctgaacatgg gctgagaacc tgaagcagat acagaaagca agatgaccat gctggaacaa 180
 tgaaggacagg gaggatgggc agagtggcta gggagaagga ggtcttggat gaacatctga 240
 gatagaaaat gcccctcttg cggctcatgt gtgctctcct gatcacatgc tctgacatgg 300
 caggccccag ccattctctc ttaogaacga cacttgctgg gaatccctac tgggcacaca 360
 caaccagtc tacaagatag agtgggtccaa acccccctc ctgggctgtg gtgcttggaa 420
 gatgcaacac accgactggc taogctgcag ttactgcac tttctggctg gctggcaagc 480
 aaacttccca ctgcctttct cccagggcct gacccatta tgacaatgga gccattgttc 540
 tgaacagggg ccatgaggca gctgggactg gccgacccta tgctggctcc tcacatctca 600
 gaagtcaagc cctcagacag atcaaggaaa gtgataaaat tcagcgggaa gcaggacaga 660
 gtattggggg tcctgagcca gcttcttcct ctgagttctg tatcgtgatg ggaatgaata 720
 atcaccccaa ttacagagca acctgaagga gacaaaatca cttaactaaa tgagggtgctt 780
 gggaatgg 789

<210> 39

<211> 20

<212> DNA

<213> Homo sapiens

<400> 39

agagctgcac ggcactttctc

20

<210> 40

<211> 20

<212> DNA

<213> Homo sapiens

<400> 40

cacgatgcaa aacgaactac

20

<210> 41

<211> 465

<212> DNA

<213> Homo sapiens

<400> 41

```

agagctgcac ggcactttctc agcccacaag cccactttcc atgcaccaag cccaccccccac 60
cttacacttg gcccctgggt ccttaacctt gagctcagcc tccatcttaa ggtttcacca 120
agctgccctt cactatccgg tctgttggag atttccagc tagactctgc tagccacgct 180
ctgactctgt ttgaccagc tcccggggag aagccaagcc gactcccttc cactccctct 240
gccccgctg ctgtcttaca cagccgtacc ttcctttcct ttgccccctc tcttggtctg 300
tgtgagcca catttagcac cagcctccaa gagcaagcac cctgtgctaa cttgggctcg 360
tgtctcgcaa gctaccaccc tgatcttaga aaccggaagc tcagaaaata gttcctatct 420
tatgtgcgtt atactcttca agaaggtagt tcgttttgca tcgtg 465

```

<210> 42

<211> 22

<212> DNA

<213> Homo sapiens

<400> 42

gtttggggag attttgagtg tg

22

<210> 43

<211> 21

<212> DNA

<213> Homo sapiens

<400> 43

gggcagcaga ccttagcaac t

21

<210> 44

<211> 478

<212> DNA

<213> Homo sapiens

<400> 44

```

gtttggggag attttgagtg tgtgggtggc agaaggtact tttagggttg ggtcacagtg 60
cagcgggccc agcaccaaag cacagatatt ctagaactgg ggttctacat cagactacta 120
ctgtgagagc caagaggctc aaagccccc gagggtgact cattcttcca gccctccgcc 180
tcctcctgcc tgtccaggtc atcttgatca tcccattatc agaactgctg gaggaatcat 240
ctggaaggct tgaagtgact ggggggcatc cgctgggttg tgagagctgc tcggaggggc 300
ccttgctctgt ccaggtccac ctctccacc caccttatgc tgtcaccccc tgcccaggac 360
tggacctcca ttcaactctt ctgagcagaa ggagcagaaa ccatcctatc tctgcactgg 420
cctggaatgg acagtgtcc ccagcatggt tctaggagtg tgctaaggtc tgctgccc 478

```

<210> 45

<211> 22

<212> DNA

<213> Homo sapiens

<400> 45

```

tccccaaaagg ccagtttcac ac 22

```

<210> 46

<211> 22

<212> DNA

<213> Homo sapiens

<400> 46

```

tctgcaggcg tctcatctca ac 22

```

<210> 47

<211> 678

<212> DNA

<213> Homo sapiens

<400> 47

```

tccccaaaagg ccagtttcac aactccatt aatgctggct gccactggga caattacaga 60
cagacagctt ttccatttg agcaacttct taaatttaaa aagcaactgt gcaggaagga 120
aggagacatg tggtgtctct actacagacc ttgtaaaagg aggttcttct atgctattac 180
ccacccctc ccatacctac ctttcctacc acacacaaga gctgaaataa aagttgcatt 240
tcaacttgtgt tgtggctgtt attttatttt aactccttg cttaaaaaaa aaaaagtct 300
tcaacttaaaa aaaaatacat caccacaaca tgtctgagat tttttgcaag gcttgggtct 360
gaaccagtg cctttgatag gggcattttt cttagcctgc tgtggctaaa gatgggcatg 420
gtcggatttc actcgttgg attaggatgg acttggcctt aatatatttg ttcttaatga 480
ttcttccaat ttttaagtgt cccaagagat agctttgact ttccaccca gcctgctgat 540

```

gttatctttcc taggaactgc tacatctttt aatacaacct gtattcaagt tctccttata 600
 ggacctgaga gattcaactg gcagcattta ggactaccag gaatctccag tctggcggtg 660
 agatgagacg cctgcaga 678

<210> 48
 <211> 20
 <212> DNA
 <213> Homo sapiens

<400> 48
 cccctcagct ctgtgcattt 20

<210> 49
 <211> 21
 <212> DNA
 <213> Homo sapiens

<400> 49
 tccctgctga atgagtgttt g 21

<210> 50
 <211> 478
 <212> DNA
 <213> Homo sapiens

<400> 50
 cccctcagct ctgtgcattt tgtctacaag caagggtgact ttgggttttag tgtgttcatg 60
 tttcaacaag aatgtaagtt tgggatcaga catatgttac ccctgttgga tagtagcttt 120
 gcaatcagtc tttgcaaaaa atatccagaa caaggctaga acaagggtgg acagaaacaa 180
 ataacacgtg ttacagttac atatgagctt ggattacctc ctttatagaa ggaagtggag 240
 acatccttca tgcagagatt taggatctct cactagcact aaccctcttg cccccacct 300
 gtgtttatatt caatcacccc tgttgctttt tatcaaatga aagatacaga tccactttta 360
 agagtaaaga agagaggaag cacagtttat taattacca ttggtatccc aaggacttgt 420
 gcttccatta tctcattgtt ttattcattc attaatccaa acactcattc agcaggga 478

<210> 51
 <211> 22
 <212> DNA
 <213> Homo sapiens

<400> 51
 gaacctggtc taaaaattat ac 22

<210> 52
 <211> 22
 <212> DNA
 <213> Homo sapiens

<400> 52
 gactgggacc aatttgttct tc 22

<210> 53
 <211> 673
 <212> DNA
 <213> Homo sapiens

<400> 53
 gaacctgggc tacaaattat acaccctggc atgtccaaaa gcaaaatgct gcctacatct 60
 cctgaaaatg caggaatgtc agaaaagctg ctgaagtggc ggctaccagg agctccagg 120
 gcctagcacc cactcccagc ccgaccctgg ggtggggagg gtggtgctct tcagagtggc 180
 tcatttttaga gctgactacc caagtgcaga agaaacaacg ttttaaatat atcgggcagc 240
 agagcagcta gatattaagg ttcttctttg caggacatca tgaaatattg ttcattgacga 300
 ccctgaccct ggggttggcg cgggtgctct tcagagtggc tcatttttaga gctgacttcc 360
 caagtgcaga agaaacaact ttttaaatac gtcgggtaac agagcagcta gacattacgg 420
 ttcttctttg cagaacatca tgaaatattg atgttaagct aaaacgaata taataaatgt 480
 atgattgcct gctaaattgg tcattatctt ttttagattc tggctttgac agaaagtagc 540
 aggccccaat ggtttaagaa agaaaggaaa aaattttttt aattgaggaa atcatatcca 600
 cgtctttttt tttttaattg ttgaaaagat gtccacagtc agatttcaga ggaagaacaa 660
 attggtccca gtc 673

<210> 54
 <211> 21
 <212> DNA
 <213> Homo sapiens

<400> 54
 gtacacccac tcacctgtga t 21

<210> 55
 <211> 22
 <212> DNA
 <213> Homo sapiens

<400> 55
 tctaaggggg aaaagtaaac aa 22

<210> 56

<211> 761
 <212> DNA
 <213> Homo sapiens

<400> 56
 gtacacccac tcacctgtga tgtacttaat ggagcaggag ggaacaggct gccatcaaag 60
 ctaactcctg gaaatgacct agaaccaca gcctgtctca gccgtgctgc atgttccagc 120
 agggacaaca gcgactgttg tattatgtaa aattacttac ctgataataa aatgtttgtg 180
 gattggataa atttgaacgg atatattgtt tccttcaccc cccccccact agtggcaaaa 240
 gctgctctgt atgaatctga gtacatttct gtgacagtat tcctcatatg tacagcattc 300
 tatgtgaatc atctcccaaa aattgccatg gggtcattat cccagttct taactagaga 360
 aactgagatt ctggaagtcc ctctgaatgg ccatacttc ccaggtgtc tctgcaggaa 420
 acaatgtgga caatcacagt agttggaagg acaatgactg acctaataa gttcaggacg 480
 ctatgactgt tggcacctga tgtgcacagc tgctcccatc tgccgagaga gaataaaag 540
 gcagtggcgc tgaaacatct gctgctttca ctcaccatca agatggaact gactgtacat 600
 gcaagcaaat ttgatgaag agagtgatct cagagtgcga agataagttg tttctccttg 660
 acacctagga atgcacctgg ccaagacct cagttgaaag acaatatcaa ataaatgcaa 720
 aatctaaata tccatgtgct tgtttacttt tcccccttag a 761

<210> 57
 <211> 11
 <212> PRT
 <213> Homo sapiens

<400> 57
 Ser Ala Val Gly Ser Asp His Ile Phe His Asn
 1 5 10

<210> 58
 <211> 13
 <212> PRT
 <213> Homo sapiens

<400> 58
 Ser Ala Val Gly Ser Asp His Ile Phe His Asn Ser Lys
 1 5 10

<210> 59
 <211> 11
 <212> PRT
 <213> Homo sapiens

<400> 59
 Ser Ala Ala Gly Thr Asp His Ile Phe Leu Asn
 1 5 10

<210> 60

<211> 70

<212> PRT

<213> Homo sapiens

<400> 60

Val Pro Gly Pro Thr Ser Ser Ala Thr Asn Val Ser Met Val Val Ser
 1 5 10 15

Ala Gly Pro Leu Ser Ser Glu Lys Ala Glu Met Asn Ile Leu Glu Met
 20 25 30

Asn Glu Lys Leu Arg Pro Gln Leu Ala Glu Lys Lys Gln Gln Phe Arg
 35 40 45

Asn Leu Lys Glu Lys Cys Phe Val Thr Gln Leu Ala Gly Phe Leu Ala
 50 55 60

Asn Gln Gln Asn Lys Tyr
 65 70

<210> 61

<211> 70

<212> PRT

<213> Homo sapiens

<400> 61

Val Pro Gly Pro Thr Ser Ser Ala Thr Asn Val Ser Met Val Val Ser
 1 5 10 15

Ala Gly Pro Leu Ser Ser Glu Lys Ala Glu Met Asn Ile Leu Glu Ile
 20 25 30

Asn Glu Lys Leu His Pro Gln Leu Ala Glu Lys Lys Gln Gln Phe Arg
 35 40 45

Asn Leu Lys Glu Arg Cys Phe Val Thr Gln Leu Ala Gly Phe Leu Ala
 50 55 60

Asn Gln Gln Lys Lys Tyr
 65 70

<210> 62

<211> 70

<212> PRT

<213> Homo sapiens

<400> 62

Val Pro Gly Pro Thr Ser Ser Ala Thr Asn Val Ser Met Val Val Ser
1 5 10 15

Ala Gly Pro Leu Ser Ser Glu Lys Ala Glu Met Asn Ile Leu Glu Ile
20 25 30

Asn Glu Lys Leu Arg Pro Gln Leu Ala Glu Lys Lys Gln Gln Phe Arg
35 40 45

Ser Leu Lys Glu Lys Cys Phe Val Thr Gln Leu Ala Gly Phe Leu Ala
50 55 60

Lys Gln Gln Asn Lys Tyr
65 70

<210> 63

<211> 70

<212> PRT

<213> Homo sapiens

<400> 63

Val Pro Asp Ser Thr Ser Ser Ala Thr Asn Val Ser Met Val Val Ser
1 5 10 15

Ala Gly Pro Trp Ser Ser Glu Lys Ala Glu Met Asn Ile Leu Glu Ile
20 25 30

Asn Glu Lys Leu Arg Pro Gln Leu Ala Glu Asn Lys Gln Gln Phe Gly
35 40 45

Asn Leu Lys Glu Arg Cys Phe Val Thr Gln Leu Ala Gly Phe Leu Ala
50 55 60

Asn Gln Gln Lys Lys Tyr
65 70

<210> 64

<211> 70

<212> PRT

<213> Homo sapiens

<400> 64

Ile Pro Asp Ser Thr Ser Ser Ala Thr Asn Val Ser Met Val Val Ser
 1 5 10 15

Ala Gly Pro Trp Ser Ser Glu Lys Ala Glu Met Asn Ile Leu Glu Ile
 20 25 30

Asn Glu Lys Leu Arg Pro Gln Leu Ala Glu Asn Lys Gln Gln Phe Arg
 35 40 45

Asn Leu Lys Glu Arg Cys Phe Leu Thr Gln Leu Ala Gly Phe Leu Ala
 50 55 60

Asn Arg Gln Lys Lys Tyr
 65 70

<210> 65

<211> 70

<212> PRT

<213> Homo sapiens

<400> 65

Val Pro Gly Ser Thr Ser Ser Ala Thr Asn Val Ser Met Val Val Ser
 1 5 10 15

Ala Gly Pro Trp Ser Ser Glu Lys Ala Glu Thr Asn Ile Leu Glu Ile
 20 25 30

Asn Glu Lys Leu Arg Pro Gln Leu Ala Glu Asn Lys Gln Gln Phe Arg
 35 40 45

Asn Leu Lys Glu Lys Cys Phe Val Thr Gln Leu Ala Gly Phe Leu Ala
 50 55 60

Asn Arg Gln Lys Lys Tyr
 65 70

<210> 66

<211> 70

<212> PRT

<213> Homo sapiens

<400> 66

Ile Pro Gly Ser Thr Ser Ser Ala Thr Asn Val Ser Met Val Val Ser
 1 5 10 15

Ala Gly Pro Trp Ser Ser Glu Lys Ala Glu Thr Asn Ile Leu Lys Met

```

                20                      25                      30
Asn Glu Lys Leu Arg Pro Gln Leu Ala Glu Lys Lys Gln Gln Phe Arg
          35                      40                      45

Asn Leu Lys Glu Lys Cys Phe Val Thr Gln Leu Ala Gly Phe Leu Ala
          50                      55                      60

Asn Arg Gln Lys Lys Tyr
          65                      70

```

```
<210> 67
<211> 67
<212> PRT
<213> Homo sapiens
```

<400> 67
Ile Pro Gly Pro Thr Ser Ser Ala Thr Asn Val Ser Met Val Val Ser
1 5 10 15

Ala Gly Pro Trp Ser Gly Glu Lys Ala Glu Met Asn Ile Leu Glu Ile
20 25 30

Asn Lys Lys Ser Arg Pro Gln Leu Ala Glu Asn Lys Gln Gln Phe Arg
35 40 45

Asn Leu Lys Gln Lys Cys Leu Val Thr Gln Val Ala Tyr Phe Leu Ala
50 55 60

Asn Arg Gln
65

```
<210> 68
<211> 35
<212> PRT
<213> Homo sapiens
```

<400> 68
Lys Tyr Glu Glu Cys Lys Asp Leu Ile Lys Ser Met Leu Arg Asn Glu
1 5 10 15

Leu Gln Phe Lys Glu Glu Lys Leu Ala Glu Gln Leu Lys Gln Ala Glu
20 25 30

Glu Leu Arg
35

<210> 69

<211> 35

<212> PRT

<213> Homo sapiens

<400> 69

Lys Tyr Glu Glu Cys Lys Asp Leu Ile Lys Ser Met Leu Arg Asn Glu
1 5 10 15

Arg Gln Phe Lys Glu Glu Lys Leu Ala Glu Gln Leu Lys Gln Ala Glu
20 25 30

Glu Leu Arg
35

<210> 70

<211> 35

<212> PRT

<213> Homo sapiens

<400> 70

Lys Tyr Glu Glu Cys Lys Asp Leu Ile Lys Phe Met Leu Arg Asn Glu
1 5 10 15

Arg Gln Phe Lys Glu Glu Lys Leu Ala Glu Gln Leu Lys Gln Ala Glu
20 25 30

Glu Leu Arg
35

<210> 71

<211> 29

<212> PRT

<213> Homo sapiens

<400> 71

Asp Leu Ile Lys Ser Met Leu Arg Asn Glu Arg Gln Phe Lys Glu Glu
1 5 10 15

Lys Leu Ala Glu Gln Leu Lys Gln Ala Glu Glu Leu Arg
20 25

<210> 72

<211> 35

<212> PRT

<213> Homo sapiens

<400> 72

Glu Tyr Glu Glu Cys Lys Asp Leu Ile Lys Ser Met Leu Arg Asn Glu

1

5

10

15

Arg Gln Phe Lys Glu Glu Lys Leu Ala Glu Gln Leu Lys Gln Ala Glu

20

25

30

Glu Leu Arg

35

<210> 73

<211> 35

<212> PRT

<213> Homo sapiens

<400> 73

Glu Tyr Glu Glu Cys Lys Asp Leu Ile Lys Cys Met Leu Arg Asn Glu

1

5

10

15

Arg Gln Phe Lys Glu Glu Lys Leu Ala Glu Gln Leu Lys Gln Ala Glu

20

25

30

Glu Leu Arg

35

<210> 74

<211> 35

<212> PRT

<213> Homo sapiens

<400> 74

Lys Tyr Glu Glu Cys Lys Asp Val Ile Lys Phe Met Leu Arg Asn Glu

1

5

10

15

Arg Gln Phe Lys Glu Glu Lys Leu Ala Glu Gln Leu Lys Gln Ala Glu

20

25

30

Glu Leu Arg

35

<210> 75

<211> 71

<212> PRT

<213> Homo sapiens

<400> 75

Gln Tyr Lys Val Leu Val His Ser Gln Glu Arg Glu Leu Thr Gln Leu

1

5

10

15

Arg Glu Lys Leu Arg Glu Gly Arg Asp Ala Ser Arg Ser Leu Asn Glu

20

25

30

His Leu Gln Ala Leu Leu Thr Pro Asp Glu Pro Asp Lys Ser Gln Gly

35

40

45

Gln Asp Leu Gln Glu Gln Leu Ala Glu Gly Cys Arg Leu Ala Gln His

50

55

60

Leu Val Gln Lys Leu Ser Pro

65

70

<210> 76

<211> 71

<212> PRT

<213> Homo sapiens

<400> 76

Gln Tyr Lys Val Leu Val His Ser Gln Glu Arg Glu Leu Thr Gln Leu

1

5

10

15

Arg Glu Lys Leu Arg Glu Gly Arg Asp Ala Ser Arg Ser Leu Asn Glu

20

25

30

His Leu Gln Ala Leu Leu Thr Leu Asp Glu Pro Asp Lys Ser Gln Gly

35

40

45

Gln Asp Leu Gln Glu Gln Leu Ala Glu Gly Cys Arg Leu Ala Gln His

50

55

60

Leu Val Gln Lys Leu Ser Pro

65

70

<210> 77

<211> 71

<212> PRT

<213> Homo sapiens

<400> 77

Gln Tyr Lys Val Leu Val His Ala Gln Glu Arg Glu Leu Thr Gln Leu
 1 5 10 15

Arg Glu Lys Leu Arg Glu Gly Arg Asp Ala Ser Arg Ser Leu Asn Glu
 20 25 30

His Leu Gln Ala Leu Leu Thr Pro Asp Glu Pro Asp Lys Ser Gln Gly
 35 40 45

Gln Asp Leu Gln Glu Gln Leu Ala Glu Gly Cys Arg Leu Ala Gln His
 50 55 60

Leu Val Gln Lys Leu Ser Pro
 65 70

<210> 78

<211> 71

<212> PRT

<213> Homo sapiens

<400> 78

Gln Tyr Lys Val Leu Val His Ser Gln Glu Arg Glu Leu Thr Gln Leu
 1 5 10 15

Arg Glu Lys Leu Arg Glu Gly Arg Asp Ala Ser Arg Ser Leu Asn Glu
 20 25 30

His Leu Gln Ala Leu Leu Thr Pro Asp Glu Pro Asp Lys Ser Gln Gly
 35 40 45

Gln Asp Leu Gln Glu Gln Leu Ala Glu Gly Cys Arg Leu Ala Gln Gln
 50 55 60

Leu Val Gln Lys Leu Ser Pro
 65 70

<210> 79

<211> 71

<212> PRT

<213> Homo sapiens

<400> 79

Gln Tyr Lys Val Leu Val His Ser Gln Glu Arg Glu Leu Thr Gln Leu
 1 5 10 15

Arg Glu Lys Leu Arg Glu Gly Arg Asp Ala Ser Arg Ser Leu Asn Gln
 20 25 30

His Leu Gln Ala Leu Leu Thr Pro Asp Glu Pro Asp Lys Ser Gln Gly
 35 40 45

Gln Asp Leu Gln Glu Gln Leu Ala Glu Gly Cys Arg Leu Ala Gln His
 50 55 60

Leu Val Gln Lys Leu Ser Pro
 65 70

<210> 80

<211> 71

<212> PRT

<213> Homo sapiens

<400> 80

Gln Tyr Lys Val Leu Val His Ser Gln Glu Arg Glu Leu Thr Gln Leu
 1 5 10 15

Arg Glu Lys Leu Arg Glu Gly Arg Asp Ala Ser Arg Ser Leu Asn Gln
 20 25 30

His Leu Gln Ala Leu Leu Thr Pro Asp Glu Pro Asp Lys Ser Gln Gly
 35 40 45

Gln Asp Leu Gln Glu Gln Leu Ala Glu Gly Cys Arg Leu Ala Gln Gln
 50 55 60

Leu Phe Gln Lys Leu Ser Pro
 65 70

<210> 81

<211> 25

<212> PRT

<213> Homo sapiens

<400> 81

Glu Asn Asp Glu Asp Glu Asp Glu Asp Val Gln Val Glu Glu Ala Glu
 1 5 10 15

Lys Val Leu Glu Ser Ser Ala Pro Arg
 20 25

<210> 82
<211> 25
<212> PRT
<213> Homo sapiens

<400> 82
Glu Asn Asp Asn Asp Asp Asp Glu Asp Val Gln Val Glu Val Ala Glu
1 5 10 15
Lys Val Gln Lys Ser Ser Ala Pro Arg
20 25

<210> 83
<211> 25
<212> PRT
<213> Homo sapiens

<400> 83
Glu Asn Asp Asn Asp Asp Asp Glu Asp Val Gln Val Glu Val Ala Glu
1 5 10 15
Lys Val Gln Lys Ser Ser Ser Pro Arg
20 25

<210> 84
<211> 25
<212> PRT
<213> Homo sapiens

<400> 84
Glu Asn Asp Asn Asp Asp Asp Glu Asp Val Gln Val Glu Leu Ala Glu
1 5 10 15
Lys Val Gln Lys Ser Ser Ala Pro Arg
20 25

<210> 85
<211> 25
<212> PRT
<213> Homo sapiens

<400> 85
Glu Asn Asp Glu Asp Glu Asp Glu Asp Val Gln Val Glu Glu Ala Glu
1 5 10 15

Lys Val Gln Lys Ser Ser Ala Pro Arg
20 25

<210> 86

<211> 25

<212> PRT

<213> Homo sapiens

<400> 86

Glu Asn Asp Glu Asp Glu Asp Glu Asp Val Gln Val Glu Glu Asp Glu
1 5 10 15

Lys Val Leu Glu Ser Ser Ala Pro Arg
20 25

<210> 87

<211> 25

<212> PRT

<213> Homo sapiens

<400> 87

Glu Asn Asp Glu Asp Glu Asp Glu Asp Val Gln Val Glu Glu Asp Glu
1 5 10 15

Lys Val Leu Glu Ser Ser Ser Pro Arg
20 25

<210> 88

<211> 25

<212> PRT

<213> Homo sapiens

<400> 88

Glu Asn Asp Asn Asp His Asp Glu Asp Val Gln Val Glu Val Ala Glu
1 5 10 15

Lys Val Gln Lys Ser Ser Ala Pro Arg
20 25

<210> 89

<211> 70

<212> PRT

<213> Homo sapiens

<400> 89

Glu Val Gln Lys Ala Glu Glu Ser Lys Val Pro Glu Asp Ser Leu Glu
 1 5 10 15

Glu Cys Ala Ile Thr Cys Ser Asn Ser His Gly Pro Cys Asp Ser Asn
 20 25 30

Gln Pro His Lys Asn Ile Asn Ile Thr Phe Glu Glu Asp Lys Val Asn
 35 40 45

Ser Ala Leu Val Val Asp Arg Glu Ser Ser His Asp Glu Cys Gln Asp
 50 55 60

Ala Val Asn Ile Leu Pro
 65 70

<210> 90

<211> 70

<212> PRT.

<213> Homo sapiens

<400> 90

Glu Met Gln Lys Ala Glu Glu Ser Lys Val Pro Glu Asp Ser Leu Glu
 1 5 10 15

Glu Cys Ala Ile Thr Cys Ser Asn Ser His Gly Pro Cys Asp Ser Asn
 20 25 30

Gln Pro His Lys Asn Ile Lys Ile Thr Phe Glu Glu Asp Lys Val Asn
 35 40 45

Ser Ser Leu Val Val Asp Arg Glu Ser Ser His Asp Glu Cys Gln Asp
 50 55 60

Ala Leu Asn Ile Leu Pro
 65 70

<210> 91

<211> 70

<212> PRT

<213> Homo sapiens

<400> 91

Glu Val Gln Lys Thr Glu Glu Ser Lys Val Pro Glu Asp Ser Leu Glu
 1 5 10 15

Glu Cys Ala Ile Thr Cys Ser Asn Ser His Gly Pro Cys Asp Ser Asn
 20 25 30

Gln Pro His Lys Asn Ile Lys Ile Thr Phe Glu Glu Asp Glu Val Asn
 35 40 45

Ser Thr Leu Val Val Asp Arg Glu Ser Ser His Asp Glu Cys Gln Asp
 50 55 60

Ala Leu Asn Ile Leu Pro
 65 70

<210> 92

<211> 70

<212> PRT

<213> Homo sapiens

<400> 92

Glu Val Gln Lys Ala Glu Glu Ser Lys Val Pro Glu Asp Ser Leu Glu
 1 5 10 15

Glu Cys Ala Ile Thr Cys Ser Asn Ser His Gly Pro Cys Asp Ser Asn
 20 25 30

Gln Pro His Lys Asn Ile Lys Ile Thr Phe Glu Glu Asp Lys Val Asn
 35 40 45

Ser Thr Val Val Val Asp Arg Lys Ser Ser His Asp Glu Cys Gln Asp
 50 55 60

Ala Leu Asn Ile Leu Pro
 65 70

<210> 93

<211> 68

<212> PRT

<213> Homo sapiens

<400> 93

Glu Met Gln Lys Ala Glu Glu Lys Glu Val Pro Glu Asp Ser Leu Glu
 1 5 10 15

Glu Cys Ala Ile Thr Cys Ser Asn Ser His Gly Pro Tyr Asp Ser Asn
 20 25 30

Gln Pro His Arg Lys Thr Lys Ile Thr Phe Glu Glu Asp Lys Val Asp

35 40 45
 Ser Thr Leu Ile Gly Ser Ser Ser His Val Glu Trp Glu Asp Ala Val
 50 55 60

 His Ile Ile Pro
 65

<210> 94
 <211> 68
 <212> PRT
 <213> Homo sapiens

<400> 94
 Glu Met Gln Lys Ala Glu Glu Lys Glu Val Pro Glu Asp Ser Gln Glu
 1 5 10 15

 Glu Cys Ala Ile Thr Tyr Ser Asn Ser His Gly Pro Tyr Asp Ser Asn
 20 25 30

Gln Pro His Arg Lys Thr Lys Ile Thr Phe Glu Glu Asp Lys Val Asp
 35 40 45

Ser Thr Leu Ile Gly Ser Ser Ser His Val Glu Trp Glu Asp Ala Val
 50 55 60

 His Ile Ile Pro
 65

<210> 95
 <211> 68
 <212> PRT
 <213> Homo sapiens

<400> 95
 Glu Met Pro Lys Ala Glu Glu Lys Glu Val Pro Glu Asp Ser Leu Glu
 1 5 10 15

 Glu Cys Ala Ile Thr Cys Ser Asn Ser His Gly Pro Tyr Asp Ser Asn
 20 25 30

Gln Pro His Arg Lys Thr Lys Ile Thr Phe Glu Glu Asp Lys Val Asp
 35 40 45

Ser Thr Leu Ile Gly Ser Ser Ser His Val Glu Trp Glu Asp Ala Val
 50 55 60

His Ile Ile Pro
65

<210> 96
<211> 18
<212> PRT
<213> Homo sapiens

<400> 96
Glu Asn Glu Ser Asp Asp Glu Glu Glu Glu Glu Lys Gly Pro Val Ser
1 5 10 15

Pro Arg

<210> 97
<211> 54
<212> PRT
<213> Homo sapiens

<400> 97
Asn Leu Gln Glu Ser Glu Glu Glu Glu Val Pro Gln Glu Ser Trp Asp
1 5 10 15

Glu Gly Tyr Ser Thr Leu Ser Ile Pro Pro Glu Met Leu Ala Ser Tyr
20 25 30

Gln Ser Tyr Ser Ser Thr Phe His Ser Leu Glu Glu Gln Gln Val Cys
35 40 45

Met Ala Val Asp Ile Gly
50

<210> 98
<211> 54
<212> PRT
<213> Homo sapiens

<400> 98
Asn Leu Gln Glu Ser Glu Glu Glu Glu Val Pro Gln Glu Ser Trp Asp
1 5 10 15

Glu Gly Tyr Ser Thr Leu Ser Ile Pro Pro Glu Met Leu Ala Ser Tyr
20 25 30

Lys Ser Tyr Ser Ser Thr Phe His Ser Leu Glu Glu Gln Gln Val Cys
 35 40 45

Met Ala Val Asp Ile Gly
 50

<210> 99

<211> 27

<212> PRT

<213> Homo sapiens

<400> 99

Asn Leu Gln Glu Ser Glu Glu Glu Glu Val Pro Gln Glu Ser Trp Asp
 1 5 10 15

Glu Gly Tyr Ser Thr Leu Ser Ile Pro Pro Glu
 20 25

<210> 100

<211> 54

<212> PRT

<213> Homo sapiens

<400> 100

Asn Leu Gln Glu Ser Glu Glu Glu Glu Val Pro Gln Glu Ser Trp Asp
 1 5 10 15

Glu Gly Tyr Ser Thr Leu Ser Ile Pro Pro Glu Met Leu Ala Ser Tyr
 20 25 30

Gln Ser Tyr Ser Gly Thr Phe His Ser Leu Glu Glu Gln Gln Val Cys
 35 40 45

Val Ala Val Asp Ile Gly
 50

<210> 101

<211> 54

<212> PRT

<213> Homo sapiens

<400> 101

Asn Leu Gln Glu Ser Glu Glu Glu Glu Val Pro Gln Glu Ser Trp Asp
 1 5 10 15

Glu Gly Tyr Ser Thr Leu Ser Ile Pro Pro Glu Met Leu Ala Ser Tyr
20 25 30

Gln Ser Tyr Ser Gly Thr Phe His Ser Leu Glu Glu Gln Gln Val Cys
35 40 45

Met Ala Val Asp Ile Gly
50

<210> 102

<211> 18

<212> PRT

<213> Homo sapiens

<400> 102

Arg His Arg Trp Asp Gln Val Lys Lys Glu Asp Gln Glu Ala Thr Gly
1 5 10 15

Pro Arg

<210> 103

<211> 18

<212> PRT

<213> Homo sapiens

<400> 103

Arg His Arg Trp Asp Gln Val Lys Lys Glu Asp His Glu Ala Thr Gly
1 5 10 15

Pro Arg

<210> 104

<211> 18

<212> PRT

<213> Homo sapiens

<400> 104

Gly His Arg Trp Asp Gln Val Lys Lys Glu Asp Gln Glu Ala Thr Gly
1 5 10 15

Pro Arg

<210> 105

<211> 57

<212> PRT

<213> Homo sapiens

<400> 105

Leu Ser Arg Glu Leu Leu Ala Glu Lys Glu Pro Glu Val Leu Gln Asp
 1 5 10 15

Ser Leu Asp Arg Trp Tyr Ser Thr Pro Ser Val Tyr Leu Gly Leu Thr
 20 25 30

Asp Pro Cys Gln Pro Tyr Arg Ser Ala Phe Tyr Val Leu Glu Gln Gln
 35 40 45

Arg Val Gly Leu Ala Val Asp Met Asp
 50 55

<210> 106

<211> 57

<212> PRT

<213> Homo sapiens

<400> 106

Leu Ser Arg Glu Leu Leu Ala Glu Lys Glu Pro Glu Val Leu Gln Asp
 1 5 10 15

Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Val Tyr Leu Gly Leu Thr
 20 25 30

Asp Ser Cys Gln Pro Tyr Arg Ser Ala Phe Tyr Val Leu Glu Gln Gln
 35 40 45

Arg Val Gly Leu Ala Val Asp Met Asp
 50 55

<210> 107

<211> 57

<212> PRT

<213> Homo sapiens

<400> 107

Leu Ser Arg Glu Leu Leu Asp Glu Lys Gly Pro Glu Val Leu Gln Asp
 1 5 10 15

Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Cys Leu Glu Leu Thr
 20 25 30

Asp Ser Cys Gln Pro Tyr Arg Ser Ala Phe Tyr Val Leu Glu Gln Gln
 35 40 45

Arg Val Gly Leu Ala Val Asn Met Asp
 50 55

<210> 108

<211> 57

<212> PRT

<213> Homo sapiens

<400> 108

Leu Ser Arg Glu Leu Leu Asp Glu Lys Gly Pro Glu Val Leu Gln Asp
 1 5 10 15

Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Cys Leu Glu Leu Thr
 20 25 30

Asp Ser Cys Gln Pro Tyr Arg Ser Ala Phe Tyr Ile Leu Glu Gln Gln
 35 40 45

Arg Val Gly Leu Ala Val Asp Met Asp
 50 55

<210> 109

<211> 57

<212> PRT

<213> Homo sapiens

<400> 109

Leu Ser Arg Glu Leu Leu Asp Glu Glu Gly Pro Glu Val Leu Gln Asp
 1 5 10 15

Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Cys Leu Glu Leu Thr
 20 25 30

Asp Ser Cys Gln Pro Tyr Arg Ser Ala Phe Tyr Val Leu Glu Xaa Gln
 35 40 45

Arg Val Gly Leu Ala Val Asp Met Asp
 50 55

<210> 110

<211> 57

<212> PRT

<213> Homo sapiens

<400> 110

Leu Ser Gly Glu Leu Leu Asp Glu Lys Glu Pro Glu Val Leu Gln Glu
 1 5 10 15

Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Cys Leu Glu Leu Thr
 20 25 30

Asp Ser Cys Gln Pro Tyr Arg Ser Ala Phe Tyr Ile Leu Glu Gln Gln
 35 40 45

Arg Val Gly Leu Ala Val Asp Met Asp
 50 55

<210> 111

<211> 57

<212> PRT

<213> Homo sapiens

<400> 111

Leu Ser Arg Glu Leu Leu Asp Glu Lys Gly Pro Glu Val Leu Gln Asp
 1 5 10 15

Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Tyr Leu Glu Leu Thr
 20 25 30

Asp Ser Cys Gln Pro Tyr Arg Ser Ala Phe Tyr Ile Leu Glu Gln Gln
 35 40 45

Arg Val Gly Trp Ala Leu Asp Met Asp
 50 55

<210> 112

<211> 56

<212> PRT

<213> Homo sapiens

<400> 112

Leu Asn Arg Glu Leu Leu Asp Glu Lys Gly Pro Glu Val Leu Gln Asp
 1 5 10 15

Ser Leu Asp Arg Cys Tyr Ser Thr Xaa Ser Gly Tyr Leu Leu Thr Asp
20 25 30

Ser Cys Gln Pro Tyr Arg Ser Ala Phe Tyr Ile Leu Glu Gln Gln Arg
35 40 45

Val Gly Trp Ala Leu Asp Leu Val
50 55

<210> 113

<211> 57

<212> PRT

<213> Homo sapiens

<400> 113

Leu Ser Arg Glu Leu Leu Asp Glu Lys Glu Pro Glu Val Leu Gln Asp
1 5 10 15

Ser Leu Gly Arg Cys Tyr Ser Thr Pro Ser Gly Tyr Leu Glu Leu Pro
20 25 30

Asp Leu Gly Gln Pro Tyr Ser Ser Ala Val Tyr Ser Leu Glu Glu Gln
35 40 45

Tyr Leu Gly Leu Ala Leu Asp Val Asp
50 55

<210> 114

<211> 57

<212> PRT

<213> Homo sapiens

<400> 114

Leu Ser Arg Glu Leu Leu Ala Glu Lys Glu Pro Glu Val Leu Gln Asp
1 5 10 15

Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Tyr Leu Glu Leu Pro
20 25 30

Asp Leu Gly Gln Pro Tyr Ser Ser Ala Val Tyr Ser Leu Glu Glu Gln
35 40 45

Tyr Leu Gly Leu Ala Leu Asp Val Asp
50 55

<210> 115
 <211> 57
 <212> PRT
 <213> Homo sapiens

<400> 115
 Leu Ser Arg Glu Leu Leu Asp Glu Lys Glu Pro Glu Val Leu Gln Asp
 1 5 10 15
 Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Tyr Leu Glu Leu Pro
 20 25 30
 Asp Leu Gly Gln Pro Tyr Arg Ser Ala Val Tyr Ser Leu Glu Glu Gln
 35 40 45
 Tyr Leu Gly Leu Ala Leu Asp Val Asp
 50 55

<210> 116
 <211> 57
 <212> PRT
 <213> Homo sapiens

<400> 116
 Leu Ser Arg Glu Leu Leu Ala Glu Lys Glu Pro Glu Val Leu Gln Asp
 1 5 10 15
 Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Tyr Leu Glu Leu Pro
 20 25 30
 Asp Leu Gly Gln Pro Tyr Arg Ser Ala Val Tyr Ser Leu Glu Glu Gln
 35 40 45
 Tyr Leu Gly Leu Ala Leu Asp Val Asp
 50 55

<210> 117
 <211> 57
 <212> PRT
 <213> Homo sapiens

<400> 117
 Leu Ser Arg Glu Leu Leu Ala Glu Lys Glu Pro Glu Val Leu Gln Asp
 1 5 10 15
 Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Tyr Leu Glu Leu Pro

20 25 30
 Asp Leu Gly Gln Pro Tyr Arg Ser Ala Ala Tyr Ser Leu Glu Glu Gln
 35 40 45

Tyr Leu Gly Leu Ala Leu Asp Val Asp
 50 55

<210> 118
 <211> 57
 <212> PRT
 <213> Homo sapiens

<400> 118
 Leu Ser Arg Glu Leu Leu Asp Glu Lys Gly Pro Glu Val Leu Gln Asp
 1 5 10 15

Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Cys Leu Glu Leu Thr
 20 25 30

Asp Ser Cys Gln Pro Tyr Arg Ser Ala Phe Tyr Val Leu Glu Gln Gln
 35 40 45

Arg Val Gly Leu Ala Val Asp Met Asp
 50 55

<210> 119
 <211> 57
 <212> PRT
 <213> Homo sapiens

<400> 119
 Leu Ser Arg Glu Leu Leu Asp Glu Lys Gly Pro Glu Val Leu Gln Asp
 1 5 10 15

Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Tyr Leu Glu Leu Pro
 20 25 30

Asp Leu Gly Gln Pro Tyr Ser Ser Ala Val Tyr Ser Leu Glu Glu Gln
 35 40 45

Tyr Leu Gly Leu Ala Leu Asp Val Asp
 50 55

<210> 120

<211> 57

<212> PRT

<213> Homo sapiens

<400> 120

Leu Ser Arg Glu Leu Leu Asp Glu Lys Gly Pro Glu Val Leu Gln Asp

1

5

10

15

Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Tyr Leu Glu Leu Thr

20

25

30

Asp Ser Cys Gln Pro Tyr Arg Ser Ala Cys Tyr Ile Leu Glu Gln Gln

35

40

45

Arg Val Gly Trp Ala Leu Asp Met Asp

50

55

<210> 121

<211> 57

<212> PRT

<213> Homo sapiens

<400> 121

Leu Ser Arg Glu Leu Leu Asp Glu Lys Gly Pro Glu Val Leu Gln Asp

1

5

10

15

Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Tyr Leu Glu Leu Pro

20

25

30

Asp Leu Gly Gln Pro Tyr Arg Ser Ala Val His Ser Leu Glu Glu Gln

35

40

45

Tyr Leu Gly Leu Ala Leu Asp Val Asp

50

55

<210> 122

<211> 57

<212> PRT

<213> Homo sapiens

<400> 122

Leu Ser Arg Glu Leu Leu Asp Glu Lys Gly Pro Glu Val Leu Gln Asp

1

5

10

15

Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Cys Leu Glu Leu Thr

20

25

30

Asp Ser Cys Gln Pro Tyr Arg Ser Ala Val Tyr Ile Leu Glu Gln Gln
 35 40 45

Cys Val Gly Leu Ala Val Asp Met Asp
 50 55

<210> 123

<211> 57

<212> PRT

<213> Homo sapiens

<400> 123

Leu Ser Arg Glu Leu Leu Glu Ala Val Glu Pro Glu Val Leu Gln Asp
 1 5 10 15

Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Ser Cys Leu Glu Gln Pro
 20 25 30

Asp Ser Cys Leu Pro Tyr Gly Ser Ser Phe Tyr Ala Leu Glu Glu Lys
 35 40 45

His Val Gly Phe Ser Leu Asp Val Gly
 50 55

<210> 124

<211> 57

<212> PRT

<213> Homo sapiens

<400> 124

Leu Ser Arg Glu Leu Leu Arg Ala Val Glu Pro Glu Val Leu Gln Asp
 1 5 10 15

Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Ser Cys Leu Glu Gln Pro
 20 25 30

Asp Ser Cys Leu Pro Tyr Gly Ser Ser Phe Tyr Ala Leu Glu Glu Lys
 35 40 45

His Val Gly Phe Ser Leu Asp Val Gly
 50 55

<210> 125

<211> 57

<212> PRT

<213> Homo sapiens

<400> 125

Leu Ser Arg Glu Leu Leu Glu Val Val Glu Pro Glu Val Leu Gln Asp
 1 5 10 15

Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Ser Cys Leu Glu Gln Pro
 20 25 30

Asp Ser Cys Gln Pro Tyr Gly Ser Ser Phe Tyr Ala Leu Glu Glu Lys
 35 40 45

His Val Gly Phe Ser Leu Asp Val Gly
 50 55

<210> 126

<211> 57

<212> PRT

<213> Homo sapiens

<400> 126

Leu Ser Arg Glu Leu Leu Glu Val Val Glu Pro Glu Val Leu Gln Gly
 1 5 10 15

Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Ser Cys Leu Glu Gln Pro
 20 25 30

Asp Ser Cys Gln Pro Tyr Gly Ser Ser Phe Tyr Ala Leu Glu Glu Lys
 35 40 45

His Val Gly Phe Ser Leu Asp Val Gly
 50 55

<210> 127

<211> 57

<212> PRT

<213> Homo sapiens

<400> 127

Leu Ser Arg Glu Leu Leu Glu Val Val Glu Pro Glu Val Leu Gln Asp
 1 5 10 15

Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Ser Cys Leu Glu Gln Pro
 20 25 30

Asp Ser Cys Gln Pro Tyr Arg Ser Ser Phe Tyr Ala Leu Glu Glu Lys
 35 40 45

His Val Gly Phe Ser Leu Asp Val Gly
 50 55

<210> 128

<211> 57

<212> PRT

<213> Homo sapiens

<400> 128

Leu Ser Arg Glu Leu Leu Glu Val Val Glu Pro Glu Val Leu Gln Asp
 1 5 10 15

Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Ser Tyr Leu Glu Leu Pro
 20 25 30

Asp Ser Cys Gln Pro Tyr Gly Ser Ser Phe Tyr Ala Leu Glu Glu Lys
 35 40 45

His Val Gly Phe Ser Leu Asp Val Gly
 50 55

<210> 129

<211> 35

<212> PRT

<213> Homo sapiens

<400> 129

Glu Ile Glu Lys Lys Gly Lys Gly Lys Lys Arg Arg Gly Arg Arg Ser
 1 5 10 15

Lys Lys Lys Arg Arg Arg Gly Arg Lys Glu Gly Glu Asp Asp Asn Pro
 20 25 30

Pro Cys Pro
 35

<210> 130

<211> 37

<212> PRT

<213> Homo sapiens

<400> 130

Glu Ile Glu Lys Lys Gly Lys Gly Lys Lys Arg Arg Gly Arg Arg Ser
1 5 10 15

Lys Lys Lys Arg Arg Arg Gly Arg Lys Glu Gly Glu Glu Asp Gln Asn
20 25 30

Pro Pro Cys Pro Arg
35

<210> 131

<211> 37

<212> PRT

<213> Homo sapiens

<400> 131

Glu Ile Glu Lys Lys Gly Lys Gly Lys Lys Arg Arg Gly Arg Arg Ser
1 5 10 15

Lys Lys Glu Arg Arg Arg Gly Arg Lys Glu Gly Glu Glu Asp Gln Asn
20 25 30

Pro Pro Cys Pro Arg
35

<210> 132

<211> 38

<212> PRT

<213> Homo sapiens

<400> 132

Glu Ile Glu Lys Lys Gly Lys Gly Lys Lys Arg Arg Gly Arg Arg Ser
1 5 10 15

Met Lys Lys Arg Arg Arg Arg Gly Arg Lys Glu Gly Glu Glu Asp Gln
20 25 30

Asn Pro Pro Cys Pro Arg
35

<210> 133

<211> 38

<212> PRT

<213> Homo sapiens

<400> 133

Glu Ile Glu Lys Lys Gly Lys Gly Lys Lys Arg Arg Gly Arg Arg Ser
1 5 10 15

Thr Lys Lys Arg Arg Arg Arg Gly Arg Lys Glu Gly Glu Glu Asp Gln
20 25 30

Asn Pro Pro Cys Pro Arg
35

<210> 134

<211> 38

<212> PRT

<213> Homo sapiens

<400> 134

Glu Ile Glu Lys Lys Gly Lys Gly Lys Lys Arg Arg Gly Arg Arg Ser
1 5 10 15

Thr Lys Lys Arg Arg Arg Arg Gly Ser Lys Glu Gly Glu Glu Asp Gln
20 25 30

Asn Pro Pro Cys Pro Arg
35

<210> 135

<211> 25

<212> PRT

<213> Homo sapiens

<400> 135

Glu Ile Glu Lys Lys Gly Lys Gly Lys Lys Arg Arg Gly Arg Arg Ser
1 5 10 15

Thr Lys Glu Arg Arg Arg Arg Gly Arg
20 25

<210> 136

<211> 18

<212> PRT

<213> Homo sapiens

<400> 136

Glu Ile Glu Lys Ser Gln Lys Trp Lys Lys Thr Gln Asn Pro Ser Cys
1 5 10 15

Pro Arg

<210> 137

<211> 18

<212> PRT

<213> Homo sapiens

<400> 137

Glu	Ile	Glu	Lys	Tyr	Gln	Glu	Val	Glu	Glu	Asp	Gln	Asp	Pro	Ser	Cys
1				5				10					15		

Pro Arg

<210> 138

<211> 18

<212> PRT

<213> Homo sapiens

<400> 138

Arg	Ile	Lys	Lys	Asp	Gln	Glu	Glu	Glu	Glu	Asp	Gln	Gly	Pro	Pro	Cys
1				5				10					15		

Pro Arg

<210> 139

<211> 18

<212> PRT

<213> Homo sapiens

<400> 139

Arg	Thr	Lys	Lys	Asp	Gln	Glu	Glu	Glu	Glu	Asp	Gln	Gly	Pro	Pro	Cys
1				5				10					15		

Pro Arg

<210> 140

<211> 18

<212> PRT

<213> Homo sapiens

<400> 140

Arg Ile Lys Lys Asp Gln Glu Glu Glu Glu Asp Gln Gly Pro Pro Cys
 1 5 10 15

Ser Arg

<210> 141

<211> 23

<212> PRT

<213> Homo sapiens

<400> 141

Glu Xaa Ser Glu Gln Glu Ile Lys Lys Tyr Gln Glu Glu Glu Glu Asp
 1 5 10 15

Gln Asp Pro Ser Cys Pro Arg
 20

<210> 142

<211> 80

<212> PRT

<213> Homo sapiens

<400> 142

Leu Asn Gly Val Leu Met Glu Val Glu Glu Arg Glu Val Leu Gln Asp
 1 5 10 15

Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Met Tyr Phe Glu Leu Pro
 20 25 30

Asp Ser Phe Gln His Tyr Arg Ser Val Phe Tyr Ser Phe Glu Glu Gln
 35 40 45

His Ile Ser Phe Ala Leu Tyr Val Asp Asn Arg Phe Phe Thr Leu Thr
 50 55 60

Val Thr Ser Leu His Leu Val Phe Gln Met Gly Val Ile Phe Pro Gln
 65 70 75 80

<210> 143

<211> 80

<212> PRT

<213> Homo sapiens

<400> 143

Leu Asn Gly Val Leu Met Glu Val Glu Glu Arg Glu Val Leu Gln Asp
 1 5 10 15

Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Met Tyr Phe Glu Leu Pro
 20 25 30

Asp Ser Phe Gln His Tyr Arg Ser Val Phe Tyr Ser Phe Glu Glu Gln
 35 40 45

His Ile Thr Phe Ala Leu Tyr Val Asp Asn Arg Phe Phe Thr Leu Thr
 50 55 60

Val Thr Ser Leu His Leu Val Phe Gln Met Gly Val Ile Phe Pro Gln
 65 70 75 80

<210> 144

<211> 80

<212> PRT

<213> Homo sapiens

<400> 144

Leu Asn Gly Val Leu Met Glu Val Glu Glu Pro Glu Val Leu Gln Asp
 1 5 10 15

Ser Leu Asp Gly Cys Tyr Ser Thr Pro Ser Met Tyr Phe Glu Leu Pro
 20 25 30

Asp Ser Phe Gln His Tyr Arg Ser Val Phe Tyr Ser Phe Glu Glu Gln
 35 40 45

His Ile Ser Phe Ala Leu Tyr Val Asp Asn Arg Phe Phe Thr Leu Thr
 50 55 60

Val Thr Ser Leu His Leu Val Phe Gln Met Glu Val Ile Phe Pro Gln
 65 70 75 80

<210> 145

<211> 80

<212> PRT

<213> Homo sapiens

<400> 145

Leu Asn Ser Val Leu Met Glu Val Glu Glu Pro Glu Val Leu Gln Asp
 1 5 10 15

Ser Leu Asp Gly Cys Tyr Ser Thr Pro Ser Met Tyr Phe Glu Leu Pro
 20 25 30

Asp Ser Phe Gln His Tyr Arg Ser Val Phe Tyr Ser Phe Glu Glu Glu
 35 40 45

His Ile Ser Phe Ala Leu Tyr Leu Asp Asn Arg Phe Phe Thr Leu Thr
 50 55 60

Val Thr Ser Leu His Leu Val Phe Gln Met Leu Val Ile Phe Pro Gln
 65 70 75 80

<210> 146

<211> 80

<212> PRT

<213> Homo sapiens

<400> 146

Leu Asn Ser Met Leu Met Glu Val Glu Glu Pro Glu Val Leu Gln Asp
 1 5 10 15

Ser Leu Asp Ile Cys Tyr Ser Thr Pro Ser Met Tyr Phe Glu Leu Pro
 20 25 30

Asp Ser Phe Gln His Tyr Arg Ser Val Phe Tyr Ser Phe Glu Glu Glu
 35 40 45

His Ile Ser Phe Ala Leu Tyr Val Asp Asn Arg Phe Phe Thr Leu Thr
 50 55 60

Val Thr Ser Leu His Leu Val Phe Gln Met Gly Val Ile Phe Pro Gln
 65 70 75 80

<210> 147

<211> 80

<212> PRT

<213> Homo sapiens

<400> 147

Leu Tyr Gly Val Leu Met Glu Val Glu Glu Pro Glu Val Leu Gln Asp
 1 5 10 15

Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Met Tyr Phe Glu Gln Pro
 20 25 30

Asp Ser Phe Gln His Tyr Arg Ser Val Phe Tyr Ser Phe Glu Glu Glu
 35 40 45

His Ile Ser Phe Ala Leu Tyr Val Asp Asn Arg Phe Phe Thr Leu Thr
 50 55 60

Val Thr Ser Leu His Leu Val Phe Gln Met Gly Val Ile Phe Pro Gln
 65 70 75 80

<210> 148

<211> 80

<212> PRT

<213> Homo sapiens

<400> 148

Ser Tyr Gly Val Leu Met Glu Val Glu Glu Pro Glu Val Leu Gln Asp
 1 5 10 15

Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Met Tyr Phe Glu Gln Pro
 20 25 30

Asp Ser Phe Gln His Tyr Arg Ser Val Phe Tyr Ser Phe Glu Glu Glu
 35 40 45

His Ile Ser Phe Ala Leu Tyr Val Asp Asn Arg Phe Phe Thr Leu Thr
 50 55 60

Val Thr Ser Leu His Leu Val Phe Gln Met Gly Val Ile Phe Pro Gln
 65 70 75 80

<210> 149

<211> 80

<212> PRT

<213> Homo sapiens

<400> 149

Leu Ser Gly Val Leu Met Glu Val Glu Glu Pro Glu Ile Leu Gln Asp
 1 5 10 15

Ser Leu Asp Arg Cys Tyr Ser Thr Leu Ser Leu Phe Phe Glu Leu Pro
 20 25 30

Asp Ser Phe Gln His Tyr Arg Ser Val Phe Tyr Ser Phe Glu Glu Gln
 35 40 45

His Ile Ser Phe Ala Leu Asp Val Asp Asn Arg Phe Leu Thr Leu Met
 50 55 60

Gly Thr Ser Leu His Leu Val Phe Gln Met Gly Val Ile Phe Pro Gln
 65 70 75 80

<210> 150

<211> 80

<212> PRT

<213> Homo sapiens

<400> 150

Phe Ser Gly Val Leu Met Glu Val Glu Glu Pro Glu Ile Leu Gln Asp
 1 5 10 15

Ser Leu Asp Arg Cys Tyr Ser Thr Leu Ser Leu Phe Phe Glu Leu Pro
 20 25 30

Asp Ser Phe Gln His Tyr Arg Ser Val Phe Tyr Ser Phe Glu Xaa Gln
 35 40 45

His Ile Ser Phe Ala Leu Xaa Val Asp Asn Arg Val Leu Thr Leu Met
 50 55 60

Gly Thr Ser Leu His Arg Gly Phe Xaa Met Gly Val Ile Phe Pro Gln

65

70

75

80

<210> 151

<211> 80

<212> PRT

<213> Homo sapiens

<400> 151

Leu Ser Gly Val Leu Met Glu Val Glu Glu Pro Glu Ile Leu Gln Asp
 1 5 10 15

Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Leu Phe Phe Glu Leu Pro
 20 25 30

Asp Ser Phe Gln His Tyr Arg Ser Val Phe Tyr Ser Phe Glu Glu Gln
 35 40 45

His Ile Ser Phe Ala Leu Asp Val Asp Asn Arg Phe Leu Thr Leu Met
 50 55 60

Gly Thr Ser Leu His Leu Val Phe Gln Met Gly Val Ile Phe Pro Gln
 65 70 75 80

<210> 152

<211> 80

<212> PRT

<213> Homo sapiens

<400> 152

Leu Ser Gly Val Leu Met Glu Val Glu Glu Pro Glu Ile Leu Gln Asp
 1 5 10 15

Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Met Phe Phe Glu Leu Pro
 20 25 30

Asp Ser Phe Gln His Tyr Arg Ser Val Phe Tyr Ser Phe Glu Glu Gln
 35 40 45

His Ile Ser Phe Ala Leu Asp Val Asp Asn Arg Phe Leu Thr Leu Met
 50 55 60

Gly Thr Ser Leu His Leu Val Phe Gln Met Gly Val Ile Phe Pro Gln
 65 70 75 80

<210> 153

<211> 80

<212> PRT

<213> Homo sapiens

<400> 153

Leu Asn Ser Val Leu Met Glu Val Glu Glu Pro Glu Val Leu Gln Asp
 1 5 10 15

Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Met Tyr Cys Glu Leu Arg
 20 25 30

Asp Ser Phe Gln His Tyr Arg Ser Val Phe Tyr Ser Phe Glu Glu Gln
 35 40 45

His Ile Ser Phe Ala Leu Asp Met Asp Asn Arg Phe Phe Thr Leu Thr
 50 55 60

Val Thr Ser Leu Tyr Leu Val Phe Gln Met Gly Val Ile Phe Pro Gln
 65 70 75 80

<210> 154

<211> 80

<212> PRT

<213> Homo sapiens

<400> 154

Leu Ser Ser Val Leu Met Glu Val Glu Val Pro Glu Val Leu Gln Asp
 1 5 10 15

Ser Leu Asp Arg Tyr Tyr Ser Thr Pro Ser Met Tyr Phe Glu Leu Pro
 20 25 30

Asp Ser Phe Gln His Tyr Arg Ser Val Phe Tyr Ser Phe Glu Glu Gln
 35 40 45

His Ile Ser Phe Ala Leu Thr Trp Thr Ile Gly Phe Phe Thr Leu Thr
50 55 60

Val Arg Ser Leu His Leu Val Phe Gln Met Gly Val Ile Phe Pro Gln
65 70 75 80

<210> 155

<211> 80

<212> PRT

<213> Homo sapiens

<400> 155

Leu Asn Ser Val Leu Met Glu Val Glu Glu Pro Glu Val Leu Gln Asp
1 5 10 15

Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Met Tyr Phe Glu Leu Pro
20 25 30

Asp Ser Phe Gln His Tyr Arg Ser Val Phe Tyr Ser Phe Glu Glu Gln
35 40 45

His Ile Thr Phe Ala Leu Asp Met Asp Asn Ser Phe Phe Thr Leu Thr
50 55 60

Val Thr Ser Leu His Leu Val Phe Gln Met Gly Val Ile Phe Pro Gln
65 70 75 80

<210> 156

<211> 80

<212> PRT

<213> Homo sapiens

<400> 156

Leu Ser Gly Val Leu Met Glu Val Glu Glu Pro Glu Val Leu Gln Asp
1 5 10 15

Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Met Tyr Phe Glu Leu Pro
20 25 30

Asp Ser Phe Gln His Tyr Arg Ser Val Phe Tyr Ser Phe Glu Glu Gln

	35		40		45										
His	Ile	Ser	Phe	Ala	Leu	Asp	Val	Asp	Asn	Arg	Phe	Leu	Thr	Leu	Met
	50						55					60			
Gly	Thr	Ser	Leu	His	Leu	Val	Phe	Gln	Met	Gly	Val	Ile	Phe	Pro	Gln
	65				70					75				80	

<210> 157

<211> 20

<212> DNA

<213> Homo sapiens

<400> 157

gttgtacccc cttgacttca

20

<210> 158

<211> 21

<212> DNA

<213> Homo sapiens

<400> 158

gtgcccagca ggagattcaa t

21

<210> 159

<211> 568

<212> DNA

<213> Homo sapiens

<400> 159

```

ggtgtacccc cttgacttca cctgaatgtc agggcaaggc caggagcatg caggaggctt 60
aaagattggg aaccctatt cttgggcctt ctccccattc tttctggagc aattggaaga 120
ggcccatggg agggagggtga ctgtcatgat gtccccact atgaactatg ggaatggctg 180
gagggtcact gggcctggtg ctccagctgc ctgacctgca gggaagtggg acctgcagga 240
octacagtga gggagtgttg acaccctggc tctgggaagg agctcatgga aagttgggtg 300
aacttcttgt tagactacgc aggctttcag aagtgcattc catacggagt ggggtggcct 360
ccccagggag gagcagaggg cagccactgg aacaagctac agctacaaaa gaccaccttt 420
atccctctca agttctccca ggggccctg tgtctgcctg tactagagga agtttccaaa 480
ggattttcct ttccccagga tgaagaatga ggccacactg ccaaagcaag atctcgtgct 540
atgtgtgatt gaatctcctg ctgggcac                                568

```

<210> 160
 <211> 4512
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (206)..(409)

<220>
 <221> CDS
 <222> (1717)..(1770)

<220>
 <223> der1 breakpoint-overlapping; Genbank AF379606

<400> 160
 ctgctctctt cctctctggg tcccatggca gccatgctct gttgcagaga gaacaggatt 60
 gcatgtaccc tcttaatggg aacctccagt ttgctttctg ggaccactct cttaatgccg 120
 cctgtcaaaa ccagctagga ctccctgggg tccaatccct ctgtgtttta tcttctgtca 180
 tctctgtccc acctgggtca tcagg gac atg cag aag gct gaa gaa aag gaa 232
 Asp Met Gln Lys Ala Glu Glu Lys Glu
 1 5
 gtc cct gag gac tca ctg gag gaa tgt gcc atc act tgt tca aat agc 280
 Val Pro Glu Asp Ser Leu Glu Glu Cys Ala Ile Thr Cys Ser Asn Ser
 10 15 20 25
 cat ggc cct tat gac tcc aac cag cca cat agg aaa acc aaa atc aca 328
 His Gly Pro Tyr Asp Ser Asn Gln Pro His Arg Lys Thr Lys Ile Thr
 30 35 40
 ttt gag gaa gac aaa gtc gac tca act ctc att ggc tca tcc tct cat 376
 Phe Glu Glu Asp Lys Val Asp Ser Thr Leu Ile Gly Ser Ser Ser His
 45 50 55
 gtt gaa tgg gag gat gct gta cac att atc cca ggtagcctct gttttccttg 429
 Val Glu Trp Glu Asp Ala Val His Ile Ile Pro
 60 65
 tgtctcatat ctctctctag gctgaggaag ataaactctg aagacaggct ctataaacac 489
 aaattcattt gaataaaaaa ctatgatggg tttctaaaca gatatcaggg agtttttttg 549
 tccttctcag ctaatgtcat gcctttgtct gccagtcccc agtatcaagt tactcgaccc 609

caggcaagtg tgacaatctc atagtcacct gagtgcagga ggtgcacagg cagtatctgt 669
 caggcctcct agcttcgatt cagtatctct tgtcatctgt gattaagtca tctgtccctg 729
 aacaatgtcc atggagtttc tatgcctgtt tcaggaagct ggcagccttg cctttgtatt 789
 tggaaatatt gttccccagg cttcaactgct ctcagctttc atctggatct cctttaagtc 849
 agcttgctta gctgcacagt caccctgaaa tcaggatgga aacttttctt ctttactttg 909
 ctgatatatt tccataaagc aaggctggac cctggttctc caccctgtca atgcaatggc 969
 tgatccaatg tttctttgta gcatcgtgga tttttttttt tttttttttt tttttttttt 1029
 tttttttttt ttttttgoga tggagtcttg ctctgtcacc caggctagag tgcagttgca 1089
 ccatcttggc ttggtgcaac ctctgcctcc cagattcaag tgattctcct gcctcagcct 1149
 cctgagttgc tgggaccaca ggtgcacaac atcacatctg gctaattttt gtattttttag 1209
 tagagacagt gtttcccat attggccagg gtagtcctga actcatgacc tcaaattgatt 1269
 cacctgtctt ggccctccaa atcacagatt ctttttaaag caagagttgt tcaaatttat 1329
 ctatcagtcg tgtttcatgt atagatgcct ctaaacattt aatgtccatg ttatctgggtg 1389
 atataagtcc gtattgcagc aacactctta gaaaatggac caatttttgg agattttttt 1449
 ggggaaaaaa ttttgtttaa ctttgactca ggcagggaat atggcattat ggtctacacg 1509
 tagagggaga ttttggcctg tgggtctgga aagcagggtc atctaattct caccaaagtt 1569
 aatctagggc accctagaat attcctgtca gaatccttat tcttgcaactg agaatagtta 1629
 tgtccttggtg ctatgactgg acagtgattt ggtcatatgt gaagtatgaa ttgcttaatg 1689
 tgacctgctt ctctgaattt atttaca gaa aat gaa agt gat gat gag gaa gag 1743
 Glu Asn Glu Ser Asp Asp Glu Glu Glu
 70 75
 gaa gaa aaa ggg cca gtg tct ccc agg taatgttgtg gaattgttgg 1790
 Glu Glu Lys Gly Pro Val Ser Pro Arg
 80 85
 ctgttaattc agtagtgaca tctggagatt gtagatttag ggaaaatgag gaagtgatga 1850
 atagaactat ttcttccatt caccagcta caaattgtgc tgatttaciaa tgttgtatgt 1910

tatttgtgac acttgtattg gttttaattt catagtcctc tcaagatagg aacttgccat 1970
cagatgagcc aggtgaacta gccaaacagg gttttcttgt tgatcttttc aaaaaaccag 2030
ccctggattc attgattttt tgaagggttt tttgtgtctc tatctccttt agttctgctc 2090
tgatcttagt taacttcttgt cttctgctag cttttgaatt tgtttgcttt gcttctctag 2150
ttattttaat tgtgatgtta ggggtgtcaat tttagatctt ttctgctttc tcttggtggc 2210
athtagtgct ataattttcc ctctacacat tgctttaaat gtgtcccaga gattctggta 2270
tgttgtgtct ttgttctcat tggtttcaaa gaacatcttt atttctgcct tcattttgtt 2330
attttccag tagtcattca ggagcagggt gttcagtttc catgtagttg tgcggttttg 2390
agtgagttcc ttaatcctga gttctaattt gactgcactg tggctctgaca gtttgttgtg 2450
gtttccattc ttttacattt gctgaggagt gctttacctc caactatgtg gtcaattttg 2510
gaataagtgt gatgtggtgc tgagaagaat gtatatctctg ttgatttggg gtggagagtt 2570
ctgtagatgt cttttaggtc tgcttgggtg agagctgagt tcaagtcctg gatatccttg 2630
taaagcttct gtctcattga tctgtctaatt attgacagtg ggggtgttaa gtctcccatt 2690
atgattgtgt ggagtctaaa tctctttgta ggtctctcag gacttgcttt atgaatctgg 2750
gtgctcctgt ataggggtgca tatatatatta ggatagttaa ctcttcttgt tgaattgatc 2810
cctttaccat tatgtagtgg ccttctttgt ctcttttgat ctttgttggt ttaaagtctg 2870
ttttatcaga gactaggatt gcaacccctg ctttttttg ctttccattt gcttggtaga 2930
tcttctcca tccctttatt ttgagcctat gtgtgtctct gcattgtgaga taggtttcct 2990
gagtacagca cactgatggg tcttgactct ttgtccaatt tgccattctg tgttttttaa 3050
ctggggcatt tagcccattht acatttaagg ttaatatgtt tatgtgtgaa tttgagcctg 3110
tcgttatgat gttagctggg tatttgcgcc gttagttgat gcagtttctt cctagcgtca 3170
atggtcttta cagtttgcca tgtttttgca gtggctggta ccggttgctt ctttccatgt 3230
ttagtgcttc ctttaggagc tcttgtaagg caggcctggg ggtgacaaaa tctctcagca 3290
tttgcttctc tgtaaaggat ttatttctcc ttcacttatg aagctttgtt tggctggata 3350

tgaaaattctg ggttgaaaat tcttttcttt aagaatgttg aagatgctgg agaggatgtg 3410
gagaaatagg aacactttta cactgttggg gagagtgtaa actagttcaa cgattgtgga 3470
aggcagtgtg gcaattcctc agggatctag aactagaaat agcatttgac ccagccatcc 3530
cattactggg tgtataccca aaggattata aatcatgctg ctgtaaagac acatgcacac 3590
atatgtttat tgcggaacta ttcacaatag caaagacttg gaaccaagcc aaatatccag 3650
caatgataga ctggattaag aaaatgtggc acgtatacac catggaatac tatgcagcta 3710
taaaaaatga tgagttcatg tcctttgtag gggcatggat gaagctggaa accatcattc 3770
tcagcaaact atcgcaagga caaaaaacca agtaccgcat gttcttactc acaggtggaa 3830
attgaacaat gagaaaaagc acatagcact aggaaggagg ccagtagaat ttcaggtgaa 3890
gagtaatggg agatgggaac ctacacaaac tggagagacc caggaaagcc tcctgagaag 3950
gtcctttaag atgagctgtg aggccaagga agagcaggcc aggcgaaggc agagggggaca 4010
gccttccagt gagtggaaac agcaaagca aaggcctcga ggcggggcag ggcttgtgct 4070
tttggggagc agaaagaagg tcacggaaaa aaaacagcgt gattcatgga gagaggccca 4130
gggctgaaaa gggagaggca ggagtggggc tcatggtctc tagaaaacag actggggttg 4190
agtttgtgta atagcctggg gaggacggta ttattatttc tgcttcatt ttacagttac 4250
agaaacagag ggcagcatat gatactgggg ggtactggga tagggctgtg ttattgattg 4310
atgggggacc tttgacggtc agaaatggag ggaggctggg ggtgtacccc cttgacttca 4370
cctgaatgtc agggcaaggc caggagcatg caggaggctt aaagattggg aaccctatt 4430
cttgggcctt ctccccattc tttctggagc aattggaaga ggcccatggg agggaggtga 4490
ctgtcatgat gtccccact at 4512

<210> 161

<211> 86

<212> PRT

<213> Homo sapiens

<223> der1 breakpoint-overlapping; Genbank AF379606

<400> 161

Asp Met Gln Lys Ala Glu Glu Lys Glu Val Pro Glu Asp Ser Leu Glu
 1 5 10 15

Glu Cys Ala Ile Thr Cys Ser Asn Ser His Gly Pro Tyr Asp Ser Asn
 20 25 30

Gln Pro His Arg Lys Thr Lys Ile Thr Phe Glu Glu Asp Lys Val Asp
 35 40 45

Ser Thr Leu Ile Gly Ser Ser Ser His Val Glu Trp Glu Asp Ala Val
 50 55 60

His Ile Ile Pro Glu Asn Glu Ser Asp Asp Glu Glu Glu Glu Glu Lys
 65 70 75 80

Gly Pro Val Ser Pro Arg
 85

<210> 162

<211> 420

<212> DNA

<213> Homo sapiens

<220>

<223> chimera 1; Genbank AF420438

<220>

<221> CDS

<222> (1)..(207)

<400> 162

att ggc tca tcc tct cat gtt gaa tgg gag gat gct gta cac att atc 48
 Ile Gly Ser Ser Ser His Val Glu Trp Glu Asp Ala Val His Ile Ile
 1 5 10 15

cca gaa aat gaa agt gat gat gag gaa gag gaa gaa aaa ggg cca gtg 96
 Pro Glu Asn Glu Ser Asp Asp Glu Glu Glu Glu Glu Lys Gly Pro Val
 20 25 30

tct ccc agg atg aag aat gag gcc aca ctg cca aag caa gat ctc gtg 144
 Ser Pro Arg Met Lys Asn Glu Ala Thr Leu Pro Lys Gln Asp Leu Val
 35 40 45

cta tgt gtg att gaa tct cct gct ggg cgc caa gca gga atc tca tca 192
 Leu Cys Val Ile Glu Ser Pro Ala Gly Arg Gln Ala Gly Ile Ser Ser

50 55 60
ttt ccc cac agg ccc tgagagcaca caggcctcat cccaccccca ccacagtga 247
Phe Pro His Arg Pro
65
gtgcactcac tgcagagcca atgaggcctg agctcagggt ctgcgtctgc ctgcatctgc 307
atggccactt ccactctgtgg tacttggttag tttattttaa atgtgcgatt tgtttggttg 367
cattttctcc ttctaaatat acagtagttt ttgcaaaaaa aaaaaaaaaa aaa 420

<210> 163
<211> 69
<212> PRT
<213> Homo sapiens
<223> chimera 1; Genbank AF420438

<400> 163
Ile Gly Ser Ser Ser His Val Glu Trp Glu Asp Ala Val His Ile Ile
1 5 10 15
Pro Glu Asn Glu Ser Asp Asp Glu Glu Glu Glu Glu Lys Gly Pro Val
20 25 30
Ser Pro Arg Met Lys Asn Glu Ala Thr Leu Pro Lys Gln Asp Leu Val
35 40 45
Leu Cys Val Ile Glu Ser Pro Ala Gly Arg Gln Ala Gly Ile Ser Ser
50 55 60
Phe Pro His Arg Pro
65

<210> 164
<211> 457
<212> DNA
<213> Homo sapiens

<220>
<223> chimera 2; Genbank AF420439

<220>
<221> CDS
<222> (1)..(138)

<400> 164

att ggc tca tcc tct cat gtt gaa tgg gag gat gct gta cac att atc 48
 Ile Gly Ser Ser Ser His Val Glu Trp Glu Asp Ala Val His Ile Ile
 1 5 10 15

cca gaa aat gaa agt gat gat gag gaa gag gaa gaa aaa ggg cca gtg 96
 Pro Glu Asn Glu Ser Asp Asp Glu Glu Glu Glu Glu Lys Gly Pro Val
 20 25 30

tct ccc agg tgt ctc tgc agg aaa caa tgt gga caa tca cag 138
 Ser Pro Arg Cys Leu Cys Arg Lys Gln Cys Gly Gln Ser Gln
 35 40 45

tagttggaag gacaatgact gacctaatgg agttcaggac gctatgactg ttggcacctg 198

atgtgcacag ctgctcccat ctgcgcagag agaataataaa ggcagtggcg ctgaaacatc 258

tgctgctttc actcaccatc aagatggaac tgactgtaca tgcaagcaaa ttttgatgaa 318

gagagtgatc tcagagtgcg aagataagtt gtttctcctt gacacctagg aatgcacctg 378

gccaagacccc tcagttgaaa gacaatatca aataaatgca aaattgtaaa tcaaaaaaaaa 438

aaaaaaaaaa aaaaaaaaaa 457

<210> 165

<211> 46

<212> PRT

<213> Homo sapiens

<223> chimera 2; Genbank AF420439

<400> 165

Ile Gly Ser Ser Ser His Val Glu Trp Glu Asp Ala Val His Ile Ile
 1 5 10 15

Pro Glu Asn Glu Ser Asp Asp Glu Glu Glu Glu Glu Lys Gly Pro Val
 20 25 30

Ser Pro Arg Cys Leu Cys Arg Lys Gln Cys Gly Gln Ser Gln
 35 40 45

<210> 166

<211> 1677

<212> DNA

<213> Homo sapiens

<220>

<223> image: 2550162; Genbank AF379636; cDNA clone AG11

<220>

<221> CDS

<222> (1)..(1647)

<400> 166

gtc ttg cag gac tca ctg gat aga tgt tat tca act cct tcc agt tgt 48

Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Ser Cys

1

5

10

15

ctt gaa cag cct gac tcc tgc cag ccc tat gga agt tcc ttt tat gca 96

Leu Glu Gln Pro Asp Ser Cys Gln Pro Tyr Gly Ser Ser Phe Tyr Ala

20

25

30

ttg gag gaa aaa cat gtt ggc ttt tct ctt gac gtg gga gaa att gaa 144

Leu Glu Glu Lys His Val Gly Phe Ser Leu Asp Val Gly Glu Ile Glu

35

40

45

aag aag ggg aag ggg aag aaa aga agg gga aga aga tca aag aag gaa 192

Lys Lys Gly Lys Gly Lys Lys Arg Arg Gly Arg Arg Ser Lys Lys Glu

50

55

60

aga aga agg gga aga aaa gaa ggg gaa gaa gat caa aac cca cca tgc 240

Arg Arg Arg Gly Arg Lys Glu Gly Glu Glu Asp Gln Asn Pro Pro Cys

65

70

75

80

ccc agg ctc agc agg gag ctg ctg gat gag aaa ggg cct gaa gtc ttg 288

Pro Arg Leu Ser Arg Glu Leu Leu Asp Glu Lys Gly Pro Glu Val Leu

85

90

95

cag gac tca ctg gat aga tgt tat tca act cct tca ggt tgt ctt gaa 336

Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Cys Leu Glu

100

105

110

ctg act gac tca tgc cag ccc tac aga agt gcc ttt tac ata ttg gag 384

Leu Thr Asp Ser Cys Gln Pro Tyr Arg Ser Ala Phe Tyr Ile Leu Glu

115

120

125

caa cag tgt gtt ggc ttg gct gtt gac atg gat gaa att gaa aag tac 432

Gln Gln Cys Val Gly Leu Ala Val Asp Met Asp Glu Ile Glu Lys Tyr

130

135

140

caa gaa gtg gaa gaa gac caa gac cca tca tgc ccc agg ctc agc agg 480

Gln Glu Val Glu Glu Asp Gln Asp Pro Ser Cys Pro Arg Leu Ser Arg

145	150	155	160	
gag ctg ctg gat gag aaa gag cct gaa gtc ttg cag gac tca ctg gat				528
Glu Leu Leu Asp Glu Lys Glu Pro Glu Val Leu Gln Asp Ser Leu Asp				
	165	170	175	
aga tgt tat tcg act cct tca ggt tat ctt gaa ctg cct gac tta ggc				576
Arg Cys Tyr Ser Thr Pro Ser Gly Tyr Leu Glu Leu Pro Asp Leu Gly				
	180	185	190	
cag ccc tac agc agt gct gtt tac tca ttg gag gaa cag tac ctt ggc				624
Gln Pro Tyr Ser Ser Ala Val Tyr Ser Leu Glu Glu Gln Tyr Leu Gly				
	195	200	205	
ttg gct ctt gac gtg gac aga att aaa aag gac caa gaa gag gaa gaa				672
Leu Ala Leu Asp Val Asp Arg Ile Lys Lys Asp Gln Glu Glu Glu Glu				
	210	215	220	
gac caa ggc cca cca tgc ccc agg ctc agc agg gag ctg ctg gag gta				720
Asp Gln Gly Pro Pro Cys Pro Arg Leu Ser Arg Glu Leu Leu Glu Val				
225	230	235	240	
gta gag cct gaa gtc ttg cag gac tca ctg gat aga tgt tat tca act				768
Val Glu Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr				
	245	250	255	
cct tcc agt tgt ctt gaa cag cct gac tcc tgc cag ccc tat gga agt				816
Pro Ser Ser Cys Leu Glu Gln Pro Asp Ser Cys Gln Pro Tyr Gly Ser				
	260	265	270	
tcc ttt tat gca ttg gag gaa aaa cat gtt ggc ttt tct ctt gac gtg				864
Ser Phe Tyr Ala Leu Glu Glu Lys His Val Gly Phe Ser Leu Asp Val				
	275	280	285	
gga gaa att gaa aag aag ggg aag ggg aag aaa aga agg gga aga aga				912
Gly Glu Ile Glu Lys Lys Gly Lys Gly Lys Lys Arg Arg Gly Arg Arg				
	290	295	300	
tca aag aag gaa aga aga agg gga aga aaa gaa ggg gaa gaa gat caa				960
Ser Lys Lys Glu Arg Arg Arg Gly Arg Lys Glu Gly Glu Glu Asp Gln				
305	310	315	320	
aac cca cca tgc ccc agg ctc agc agg gag ctg ctg gat gag aaa ggg				1008
Asn Pro Pro Cys Pro Arg Leu Ser Arg Glu Leu Leu Asp Glu Lys Gly				
	325	330	335	
cct gaa gtc ttg cag gac tca ctg gat aga tgt tat tca act cct tca				1056
Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser				

340	345	350	
ggc tgc cag ccc tac aga agt gcc ttt	1104		
Gly Cys Leu Glu Leu Thr Asp Ser Cys Gln Pro Tyr Arg Ser Ala Phe			
355	360	365	
tac ata ttg gag caa cag tgt gtt ggc ttg gct gtt gac atg gat gaa	1152		
Tyr Ile Leu Glu Gln Gln Cys Val Gly Leu Ala Val Asp Met Asp Glu			
370	375	380	
att gaa aag tac caa gaa gtg gaa gaa gac caa gac cca tca tgc ccc	1200		
Ile Glu Lys Tyr Gln Glu Val Glu Glu Asp Gln Asp Pro Ser Cys Pro			
385	390	395	400
agg ctc agc agg gag ctg ctg gat gag aaa gag cct gaa gtc ttg cag	1248		
Arg Leu Ser Arg Glu Leu Leu Asp Glu Lys Glu Pro Glu Val Leu Gln			
405	410	415	
gac tca ctg gat aga tgt tat tcg act cct tca ggt tat ctt gaa ctg	1296		
Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Tyr Leu Glu Leu			
420	425	430	
cct gac tta ggc cag ccc tac agc agt gct gtt tac tca ttg gag gaa	1344		
Pro Asp Leu Gly Gln Pro Tyr Ser Ser Ala Val Tyr Ser Leu Glu Glu			
435	440	445	
cag tac ctt ggc ttg gct ctt gac gtg gac aga att aaa aag gac caa	1392		
Gln Tyr Leu Gly Leu Ala Leu Asp Val Asp Arg Ile Lys Lys Asp Gln			
450	455	460	
gaa gag gaa gaa gac caa ggc cca cca tgc ccc agg ctc agc agg gag	1440		
Glu Glu Glu Glu Asp Gln Gly Pro Pro Cys Pro Arg Leu Ser Arg Glu			
465	470	475	480
ctg ctg gag gta gta gag cct gaa gtc ttg cag gac tca ctg gat aga	1488		
Leu Leu Glu Val Val Glu Pro Glu Val Leu Gln Asp Ser Leu Asp Arg			
485	490	495	
tgt tat tca act cct tcc agt tgt ctt gaa cag cct gac tcc tgc cag	1536		
Cys Tyr Ser Thr Pro Ser Ser Cys Leu Glu Gln Pro Asp Ser Cys Gln			
500	505	510	
ccc tat gga agt tcc ttt tat gca ttg gag gaa aaa cat gtt ggc ttt	1584		
Pro Tyr Gly Ser Ser Phe Tyr Ala Leu Glu Glu Lys His Val Gly Phe			
515	520	525	
tct ctt gac gtg gga gaa att gaa aag aag ggg aag ggg aag aaa aga	1632		
Ser Leu Asp Val Gly Glu Ile Glu Lys Lys Gly Lys Gly Lys Lys Arg			

530 535 540
 agg gga aga aga tca aagaaggaaa gaaaaaaaaa aaaaaaaaaa 1677
 Arg Gly Arg Arg Ser
 545

 <210> 167
 <211> 549
 <212> PRT
 <213> Homo sapiens
 <223> image: 2550162; Genbank AF379636; cDNA clone AG11

 <400> 167
 Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Ser Cys
 1 5 10 15

 Leu Glu Gln Pro Asp Ser Cys Gln Pro Tyr Gly Ser Ser Phe Tyr Ala
 20 25 30

 Leu Glu Glu Lys His Val Gly Phe Ser Leu Asp Val Gly Glu Ile Glu
 35 40 45

 Lys Lys Gly Lys Gly Lys Lys Arg Arg Gly Arg Arg Ser Lys Lys Glu
 50 55 60

 Arg Arg Arg Gly Arg Lys Glu Gly Glu Glu Asp Gln Asn Pro Pro Cys
 65 70 75 80

 Pro Arg Leu Ser Arg Glu Leu Leu Asp Glu Lys Gly Pro Glu Val Leu
 85 90 95

 Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Cys Leu Glu
 100 105 110

 Leu Thr Asp Ser Cys Gln Pro Tyr Arg Ser Ala Phe Tyr Ile Leu Glu
 115 120 125

 Gln Gln Cys Val Gly Leu Ala Val Asp Met Asp Glu Ile Glu Lys Tyr
 130 135 140

 Gln Glu Val Glu Glu Asp Gln Asp Pro Ser Cys Pro Arg Leu Ser Arg
 145 150 155 160

 Glu Leu Leu Asp Glu Lys Glu Pro Glu Val Leu Gln Asp Ser Leu Asp
 165 170 175

 Arg Cys Tyr Ser Thr Pro Ser Gly Tyr Leu Glu Leu Pro Asp Leu Gly

180	185	190
Gln Pro Tyr Ser Ser Ala Val Tyr Ser Leu Glu Glu Gln Tyr Leu Gly		
195	200	205
Leu Ala Leu Asp Val Asp Arg Ile Lys Lys Asp Gln Glu Glu Glu Glu		
210	215	220
Asp Gln Gly Pro Pro Cys Pro Arg Leu Ser Arg Glu Leu Leu Glu Val		
225	230	235
Val Glu Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr		
245	250	255
Pro Ser Ser Cys Leu Glu Gln Pro Asp Ser Cys Gln Pro Tyr Gly Ser		
260	265	270
Ser Phe Tyr Ala Leu Glu Glu Lys His Val Gly Phe Ser Leu Asp Val		
275	280	285
Gly Glu Ile Glu Lys Lys Gly Lys Gly Lys Lys Arg Arg Gly Arg Arg		
290	295	300
Ser Lys Lys Glu Arg Arg Arg Gly Arg Lys Glu Gly Glu Glu Asp Gln		
305	310	315
Asn Pro Pro Cys Pro Arg Leu Ser Arg Glu Leu Leu Asp Glu Lys Gly		
325	330	335
Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser		
340	345	350
Gly Cys Leu Glu Leu Thr Asp Ser Cys Gln Pro Tyr Arg Ser Ala Phe		
355	360	365
Tyr Ile Leu Glu Gln Gln Cys Val Gly Leu Ala Val Asp Met Asp Glu		
370	375	380
Ile Glu Lys Tyr Gln Glu Val Glu Glu Asp Gln Asp Pro Ser Cys Pro		
385	390	395
Arg Leu Ser Arg Glu Leu Leu Asp Glu Lys Glu Pro Glu Val Leu Gln		
405	410	415
Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Tyr Leu Glu Leu		
420	425	430
Pro Asp Leu Gly Gln Pro Tyr Ser Ser Ala Val Tyr Ser Leu Glu Glu		

435 440 445
 Gln Tyr Leu Gly Leu Ala Leu Asp Val Asp Arg Ile Lys Lys Asp Gln
 450 455 460
 Glu Glu Glu Glu Asp Gln Gly Pro Pro Cys Pro Arg Leu Ser Arg Glu
 465 470 475 480
 Leu Leu Glu Val Val Glu Pro Glu Val Leu Gln Asp Ser Leu Asp Arg
 485 490 495
 Cys Tyr Ser Thr Pro Ser Ser Cys Leu Glu Gln Pro Asp Ser Cys Gln
 500 505 510
 Pro Tyr Gly Ser Ser Phe Tyr Ala Leu Glu Glu Lys His Val Gly Phe
 515 520 525
 Ser Leu Asp Val Gly Glu Ile Glu Lys Lys Gly Lys Gly Lys Lys Arg
 530 535 540
 Arg Gly Arg Arg Ser
 545

<210> 168

<211> 1865

<212> DNA

<213> Homo sapiens

<220>

<223> image: 2663915; Genbank AF379635; cDNA clone AG10;
before frameshift

<220>

<221> CDS

<222> (3)..(416)

<400> 168

ac aaa gtc aac tca gct ctg gtt gta gac aga gaa tcc tct cat gat 47
 Lys Val Asn Ser Ala Leu Val Val Asp Arg Glu Ser Ser His Asp
 1 5 10 15
 gaa tgt cag gat gct gta aac att ctc cca gtc cct ggc ccc acc tct 95
 Glu Cys Gln Asp Ala Val Asn Ile Leu Pro Val Pro Gly Pro Thr Ser
 20 25 30
 tct gcc aca aac gtc agc atg gtg gta tca gcc ggc cct ttg tcc agc 143

Ser Ala Thr Asn Val Ser Met Val Val Ser Ala Gly Pro Leu Ser Ser
 35 40 45
 gag aag gca gag atg aac att cta gaa atg aat gag aaa ttg cgc ccc 191
 Glu Lys Ala Glu Met Asn Ile Leu Glu Met Asn Glu Lys Leu Arg Pro
 50 55 60
 cag ctg gca gag aag aaa cag cag ttc aga aac ctc aaa gag aaa tgt 239
 Gln Leu Ala Glu Lys Lys Gln Gln Phe Arg Asn Leu Lys Glu Lys Cys
 65 70 75
 ttt gta act caa ctg gcc tgc ttc ctg gcc aac cag cag aac aaa tac 287
 Phe Val Thr Gln Leu Ala Cys Phe Leu Ala Asn Gln Gln Asn Lys Tyr
 80 85 90 95
 aaa tat gaa gag tgc aaa gac ctc ata aaa tct gtg ctg agg aat gag 335
 Lys Tyr Glu Glu Cys Lys Asp Leu Ile Lys Ser Val Leu Arg Asn Glu
 100 105 110
 cga cag ttc aag gag gag aag ctt gca gag cag ctc aag caa gct gag 383
 Arg Gln Phe Lys Glu Glu Lys Leu Ala Glu Gln Leu Lys Gln Ala Glu
 115 120 125
 gag ctc agg caa tat aaa gtc ctg gtt cac tca ggaacgagag ctgacccagt 436
 Glu Leu Arg Gln Tyr Lys Val Leu Val His Ser
 130 135
 taaggagaaa gttacgggaa gggagagatg cctcccgctc attgaatcag catctccagg 496
 ccctcctcac tcoggatgag ccagacaagt ccaggggca ggacctccaa gaacagctgg 556
 ctgaggggtg tagactggca cagcaacttt tccaaaagct cagcccagaa aatgacaatg 616
 atcacgatga agatgttcaa gttgaggtgg ctgagaaagt gcagaaatcg tctgccccca 676
 gggagatgca gaaggctgaa gaaaaggaag tccctgagga ctcaactggag gaatgtgcca 736
 tcaattgttc aaatagccat ggcccttatg actccaacca gccacatagg aaaacaaaaa 796
 tcacatttga ggaagacaaa gtcgactcaa ctctcattgg ctcatcctct catgttgaat 856
 gggaggatgc tgtacacatt atcccagaaa atgaaagtga tgatgaggaa gaggaagaaa 916
 aagggccagt gtctcccagg aatctgcagg agtctgaaga ggaggaagtc ccccaggagt 976
 cctgggatga aggttattcg actctctcaa ttctctctga aatgttggcc tcgtaccagt 1036
 cttacagcgg cacatttcac tcattagagg aacagcaagt ctgcatggct gttgacatag 1096

gcgacatcg gtgggatcaa gtgaaaaagg aggaccaaga ggcaacaggt cccagggtca 1156
 gcagggagct gctggatgag aaagggcctg aagtcttgca ggactcactg gatagatggt 1216
 attcaactcc ttcaggttat ctggaactga ctgactcatg ccagccctac agaagtgcct 1276
 ttacatatt ggagcaacag cgtgttggtt gggctcttga catggatgaa attgaaaagt 1336
 accaagaagt ggaagaagac caagacccat catgcccag gctcagcagg gagctgctgg 1396
 atgagaaaga gctgaagtc ttgcaggact cactggatag atgttattcg actccttcag 1456
 gttatcttga actgcctgac ttaggccagc cctacagaag tgctgtttac tcattggagg 1516
 aacagtacct tggtttggct ctgacgtgg acagaattaa aaaggaccag gaagaggaag 1576
 aagaccaagg cccaccatgc cccagggtca gcagggagct gctggaggca gtagagcctg 1636
 aagtcttgca ggactcactg gatagatggt attcaactcc ttccagttgt ctggaacagc 1696
 ctgactcctg cctgccctat ggaagttcct tttatgcatt ggaggaaaaa catgttggct 1756
 tttctcttga cgtgggagaa attgaaaaga aggggaaggg gaagaaaaga aggggaagaa 1816
 gatcaacgaa gaaaagaagg agaaggggaa gaaaagaaaa aaaaaaaaaa 1865

<210> 169

<211> 138

<212> PRT

<213> Homo sapiens

<223> image: 2663915; Genbank AF379635; cDNA clone AG10;
 before frameshift

<400> 169

Lys Val Asn Ser Ala Leu Val Val Asp Arg Glu Ser Ser His Asp Glu
 1 5 10 15

Cys Gln Asp Ala Val Asn Ile Leu Pro Val Pro Gly Pro Thr Ser Ser
 20 25 30

Ala Thr Asn Val Ser Met Val Val Ser Ala Gly Pro Leu Ser Ser Glu
 35 40 45

Lys Ala Glu Met Asn Ile Leu Glu Met Asn Glu Lys Leu Arg Pro Gln
 50 55 60

Leu Ala Glu Lys Lys Gln Gln Phe Arg Asn Leu Lys Glu Lys Cys Phe
 65 70 75 80

Val Thr Gln Leu Ala Cys Phe Leu Ala Asn Gln Gln Asn Lys Tyr Lys
 85 90 95

Tyr Glu Glu Cys Lys Asp Leu Ile Lys Ser Val Leu Arg Asn Glu Arg
 100 105 110

Gln Phe Lys Glu Glu Lys Leu Ala Glu Gln Leu Lys Gln Ala Glu Glu
 115 120 125

Leu Arg Gln Tyr Lys Val Leu Val His Ser
 130 135

<210> 170

<211> 1865

<212> DNA

<213> Homo sapiens

<220>

<223> image: 2663915; Genbank AF379635; cDNA clone AG10;
 after frameshift

<220>

<221> CDS

<222> (415)..(1863)

<400> 170

acaaagtcaa ctcagctctg gttgtagaca gagaatcctc tcatgatgaa tgtcaggatg 60

ctgtaaacad tctcccagtc cctggcccca cctcttctgc cacaaacgtc agcatgggtg 120

tatcagccgg ccctttgtcc agcgagaagg cagagatgaa cattctagaa atgaatgaga 180

aattgcgccc ccagctggca gagaagaaac agcagttcag aaacctcaaa gagaaatgtt 240

ttgtaactca actggcctgc ttctggcca accagcagaa caaatacaaa tatgaagagt 300

gcaaagacct cataaaatct gtgctgagga atgagcgaca gttcaaggag gagaagcttg 360

cagagcagct caagcaagct gaggagctca ggcaatataa agtcctgggt cact cag 417
 Gln

1

gaa cga gag ctg acc cag tta agg gag aag tta cgg gaa ggg aga gat 465

Glu Arg Glu Leu Thr Gln Leu Arg Glu Lys Leu Arg Glu Gly Arg Asp	
5 10 15	
gcc tcc cgc tca ttg aat cag cat ctc cag gcc ctc ctc act cgc gat	513
Ala Ser Arg Ser Leu Asn Gln His Leu Gln Ala Leu Leu Thr Pro Asp	
20 25 30	
gag cca gac aag tcc cag ggg cag gac ctc caa gaa cag ctg gct gag	561
Glu Pro Asp Lys Ser Gln Gly Gln Asp Leu Gln Glu Gln Leu Ala Glu	
35 40 45	
ggg tgt aga ctg gca cag caa ctt ttc caa aag ctc agc cca gaa aat	609
Gly Cys Arg Leu Ala Gln Gln Leu Phe Gln Lys Leu Ser Pro Glu Asn	
50 55 60 65	
gac aat gat cac gat gaa gat gtt caa gtt gag gtg gct gag aaa gtg	657
Asp Asn Asp His Asp Glu Asp Val Gln Val Glu Val Ala Glu Lys Val	
70 75 80	
cag aaa tcg tct gcc ccc agg gag atg cag aag gct gaa gaa aag gaa	705
Gln Lys Ser Ser Ala Pro Arg Glu Met Gln Lys Ala Glu Glu Lys Glu	
85 90 95	
gtc cct gag gac tca ctg gag gaa tgt gcc atc act tgt tca aat agc	753
Val Pro Glu Asp Ser Leu Glu Glu Cys Ala Ile Thr Cys Ser Asn Ser	
100 105 110	
cat ggc cct tat gac tcc aac cag cca cat agg aaa acc aaa atc aca	801
His Gly Pro Tyr Asp Ser Asn Gln Pro His Arg Lys Thr Lys Ile Thr	
115 120 125	
ttt gag gaa gac aaa gtc gac tca act ctc att ggc tca tcc tct cat	849
Phe Glu Glu Asp Lys Val Asp Ser Thr Leu Ile Gly Ser Ser Ser His	
130 135 140 145	
gtt gaa tgg gag gat gct gta cac att atc cca gaa aat gaa agt gat	897
Val Glu Trp Glu Asp Ala Val His Ile Ile Pro Glu Asn Glu Ser Asp	
150 155 160	
gat gag gaa gag gaa gaa aaa ggg cca gtg tct ccc agg aat ctg cag	945
Asp Glu Glu Glu Glu Glu Lys Gly Pro Val Ser Pro Arg Asn Leu Gln	
165 170 175	
gag tct gaa gag gag gaa gtc ccc cag gag tcc tgg gat gaa ggt tat	993
Glu Ser Glu Glu Glu Glu Val Pro Gln Glu Ser Trp Asp Glu Gly Tyr	
180 185 190	
tcg act ctc tca att cct cct gaa atg ttg gcc tcg tac cag tct tac	1041

Ser Thr Leu Ser Ile Pro Pro Glu Met Leu Ala Ser Tyr Gln Ser Tyr	
195	200 205
agc ggc aca ttt cac tca tta gag gaa cag caa gtc tgc atg gct gtt	1089
Ser Gly Thr Phe His Ser Leu Glu Glu Gln Gln Val Cys Met Ala Val	
210	215 220 225
gac ata ggc gga cat cgg tgg gat caa gtg aaa aag gag gac caa gag	1137
Asp Ile Gly Gly His Arg Trp Asp Gln Val Lys Lys Glu Asp Gln Glu	
	230 235 240
gca aca ggt ccc agg ctc agc agg gag ctg ctg gat gag aaa ggg cct	1185
Ala Thr Gly Pro Arg Leu Ser Arg Glu Leu Leu Asp Glu Lys Gly Pro	
	245 250 255
gaa gtc ttg cag gac tca ctg gat aga tgt tat tca act cct tca ggt	1233
Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly	
	260 265 270
tat ctt gaa ctg act gac tca tgc cag ccc tac aga agt gcc ttt tac	1281
Tyr Leu Glu Leu Thr Asp Ser Cys Gln Pro Tyr Arg Ser Ala Phe Tyr	
	275 280 285
ata ttg gag caa cag cgt gtt ggc tgg gct ctt gac atg gat gaa att	1329
Ile Leu Glu Gln Gln Arg Val Gly Trp Ala Leu Asp Met Asp Glu Ile	
	290 295 300 305
gaa aag tac caa gaa gtg gaa gaa gac caa gac cca tca tgc ccc agg	1377
Glu Lys Tyr Gln Glu Val Glu Glu Asp Gln Asp Pro Ser Cys Pro Arg	
	310 315 320
ctc agc agg gag ctg ctg gat gag aaa gag cct gaa gtc ttg cag gac	1425
Leu Ser Arg Glu Leu Leu Asp Glu Lys Glu Pro Glu Val Leu Gln Asp	
	325 330 335
tca ctg gat aga tgt tat tog act cct tca ggt tat ctt gaa ctg cct	1473
Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Tyr Leu Glu Leu Pro	
	340 345 350
gac tta ggc cag ccc tac aga agt gct gtt tac tca ttg gag gaa cag	1521
Asp Leu Gly Gln Pro Tyr Arg Ser Ala Val Tyr Ser Leu Glu Glu Gln	
	355 360 365
tac ctt ggc ttg gct ctt gac gtg gac aga att aaa aag gac cag gaa	1569
Tyr Leu Gly Leu Ala Leu Asp Val Asp Arg Ile Lys Lys Asp Gln Glu	
	370 375 380 385
gag gaa gaa gac caa ggc cca cca tgc ccc agg ctc agc agg gag ctg	1617

Glu Glu Glu Asp Gln Gly Pro Pro Cys Pro Arg Leu Ser Arg Glu Leu
 390 395 400

 ctg gag gca gta gag cct gaa gtc ttg cag gac tca ctg gat aga tgt 1665
 Leu Glu Ala Val Glu Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys
 405 410 415

 tat tca act cct tcc agt tgt ctt gaa cag cct gac tcc tgc ctg ccc 1713
 Tyr Ser Thr Pro Ser Ser Cys Leu Glu Gln Pro Asp Ser Cys Leu Pro
 420 425 430

 tat gga agt tcc ttt tat gca ttg gag gaa aaa cat gtt ggc ttt tct 1761
 Tyr Gly Ser Ser Phe Tyr Ala Leu Glu Glu Lys His Val Gly Phe Ser
 435 440 445

 ctt gac gtg gga gaa att gaa aag aag ggg aag ggg aag aaa aga agg 1809
 Leu Asp Val Gly Glu Ile Glu Lys Lys Gly Lys Gly Lys Lys Arg Arg
 450 455 460 465

 gga aga aga tca acg aag aaa aga agg aga agg gga aga aaa gaa aaa 1857
 Gly Arg Arg Ser Thr Lys Lys Arg Arg Arg Arg Gly Arg Lys Glu Lys
 470 475 480

 aaa aaa aa 1865
 Lys Lys

 <210> 171
 <211> 483
 <212> PRT
 <213> Homo sapiens
 <223> image: 2663915; Genbank AF379635; cDNA clone AG10;
 after frameshift

 <400> 171
 Gln Glu Arg Glu Leu Thr Gln Leu Arg Glu Lys Leu Arg Glu Gly Arg
 1 5 10 15

 Asp Ala Ser Arg Ser Leu Asn Gln His Leu Gln Ala Leu Leu Thr Pro
 20 25 30

 Asp Glu Pro Asp Lys Ser Gln Gly Gln Asp Leu Gln Glu Gln Leu Ala
 35 40 45

 Glu Gly Cys Arg Leu Ala Gln Gln Leu Phe Gln Lys Leu Ser Pro Glu
 50 55 60

 Asn Asp Asn Asp His Asp Glu Asp Val Gln Val Glu Val Ala Glu Lys

65		70		75		80									
Val	Gln	Lys	Ser	Ser	Ala	Pro	Arg	Glu	Met	Gln	Lys	Ala	Glu	Glu	Lys
				85					90					95	
Glu	Val	Pro	Glu	Asp	Ser	Leu	Glu	Glu	Cys	Ala	Ile	Thr	Cys	Ser	Asn
			100					105					110		
Ser	His	Gly	Pro	Tyr	Asp	Ser	Asn	Gln	Pro	His	Arg	Lys	Thr	Lys	Ile
		115					120					125			
Thr	Phe	Glu	Glu	Asp	Lys	Val	Asp	Ser	Thr	Leu	Ile	Gly	Ser	Ser	Ser
	130					135					140				
His	Val	Glu	Trp	Glu	Asp	Ala	Val	His	Ile	Ile	Pro	Glu	Asn	Glu	Ser
145					150					155					160
Asp	Asp	Glu	Glu	Glu	Glu	Glu	Lys	Gly	Pro	Val	Ser	Pro	Arg	Asn	Leu
				165					170					175	
Gln	Glu	Ser	Glu	Glu	Glu	Glu	Val	Pro	Gln	Glu	Ser	Trp	Asp	Glu	Gly
			180					185					190		
Tyr	Ser	Thr	Leu	Ser	Ile	Pro	Pro	Glu	Met	Leu	Ala	Ser	Tyr	Gln	Ser
		195					200					205			
Tyr	Ser	Gly	Thr	Phe	His	Ser	Leu	Glu	Glu	Gln	Gln	Val	Cys	Met	Ala
		210				215					220				
Val	Asp	Ile	Gly	Gly	His	Arg	Trp	Asp	Gln	Val	Lys	Lys	Glu	Asp	Gln
225					230					235					240
Glu	Ala	Thr	Gly	Pro	Arg	Leu	Ser	Arg	Glu	Leu	Leu	Asp	Glu	Lys	Gly
				245					250				255		
Pro	Glu	Val	Leu	Gln	Asp	Ser	Leu	Asp	Arg	Cys	Tyr	Ser	Thr	Pro	Ser
			260					265					270		
Gly	Tyr	Leu	Glu	Leu	Thr	Asp	Ser	Cys	Gln	Pro	Tyr	Arg	Ser	Ala	Phe
		275					280					285			
Tyr	Ile	Leu	Glu	Gln	Gln	Arg	Val	Gly	Trp	Ala	Leu	Asp	Met	Asp	Glu
		290				295					300				
Ile	Glu	Lys	Tyr	Gln	Glu	Val	Glu	Glu	Asp	Gln	Asp	Pro	Ser	Cys	Pro
305					310					315					320
Arg	Leu	Ser	Arg	Glu	Leu	Leu	Asp	Glu	Lys	Glu	Pro	Glu	Val	Leu	Gln

```
<210> 172
<211> 2594
<212> DNA
<213> Homo sapiens
```

<220>
<223> image: 2186481; Genbak AF379633; cDNA clone AG06

```
<220>  
<221> CDS  
<222> (3)..(2579)
```

```
<400> 172
gt tat tgc act cct tca ggt tat ctt gaa ctg cct gac tta ggc cag 47
```

Tyr	Ser	Thr	Pro	Ser	Gly	Tyr	Leu	Glu	Leu	Pro	Asp	Leu	Gly	Gln		
1				5					10					15		
ccc	tac	agc	agt	gct	gtt	tac	tca	ttg	gag	gaa	cag	tac	ctt	ggc	ttg	95
Pro	Tyr	Ser	Ser	Ala	Val	Tyr	Ser	Leu	Glu	Glu	Gln	Tyr	Leu	Gly	Leu	
				20				25					30			
gct	ctt	gac	gtg	gac	aga	att	aaa	aag	gac	caa	gaa	gag	gaa	gaa	gac	143
Ala	Leu	Asp	Val	Asp	Arg	Ile	Lys	Lys	Asp	Gln	Glu	Glu	Glu	Glu	Asp	
			35				40					45				
caa	ggc	cca	cca	tgc	ccc	agg	ctc	agc	agg	gag	ctg	ctg	gag	gta	gta	191
Gln	Gly	Pro	Pro	Cys	Pro	Arg	Leu	Ser	Arg	Glu	Leu	Leu	Glu	Val	Val	
	50						55				60					
gag	cct	gaa	gtc	ttg	cag	gac	tca	ctg	gat	aga	tgt	tat	tca	act	cct	239
Glu	Pro	Glu	Val	Leu	Gln	Asp	Ser	Leu	Asp	Arg	Cys	Tyr	Ser	Thr	Pro	
	65				70				75							
tcc	agt	tgt	ctt	gaa	cag	cct	gac	tcc	tgc	cag	ccc	tat	gga	agt	tcc	287
Ser	Ser	Cys	Leu	Glu	Gln	Pro	Asp	Ser	Cys	Gln	Pro	Tyr	Gly	Ser	Ser	
80					85				90						95	
ttt	tat	gca	ttg	gag	gaa	aaa	cat	gtt	ggc	ttt	tct	ctt	gac	gtg	gga	335
Phe	Tyr	Ala	Leu	Glu	Glu	Lys	His	Val	Gly	Phe	Ser	Leu	Asp	Val	Gly	
			100					105					110			
gaa	att	gaa	aag	aag	ggg	aag	ggg	aag	aaa	aga	agg	gga	aga	aga	tca	383
Glu	Ile	Glu	Lys	Lys	Gly	Lys	Gly	Lys	Lys	Arg	Arg	Gly	Arg	Arg	Ser	
			115				120					125				
aag	aag	gaa	aga	aga	agg	gga	aga	aaa	gaa	ggg	gaa	gaa	gat	caa	aac	431
Lys	Lys	Glu	Arg	Arg	Arg	Gly	Arg	Lys	Glu	Gly	Glu	Glu	Asp	Gln	Asn	
	130					135					140					
cca	cca	tgc	ccc	agg	ctc	agc	agg	gag	ctg	ctg	gat	gag	aaa	ggg	cct	479
Pro	Pro	Cys	Pro	Arg	Leu	Ser	Arg	Glu	Leu	Leu	Asp	Glu	Lys	Gly	Pro	
	145				150						155					
gaa	gtc	ttg	cag	gac	tca	ctg	gat	aga	tgt	tat	tca	act	cct	tca	ggt	527
Glu	Val	Leu	Gln	Asp	Ser	Leu	Asp	Arg	Cys	Tyr	Ser	Thr	Pro	Ser	Gly	
160				165					170					175		
tgt	ctt	gaa	ctg	act	gac	tca	tgc	cag	ccc	tac	aga	agt	gcc	ttt	tac	575
Cys	Leu	Glu	Leu	Thr	Asp	Ser	Cys	Gln	Pro	Tyr	Arg	Ser	Ala	Phe	Tyr	
				180				185					190			
ata	ttg	gag	caa	cag	tgt	gtt	ggc	ttg	gct	gtt	gac	atg	gat	gaa	att	623

Ile Leu Glu Gln Gln Cys Val Gly Leu Ala Val Asp Met Asp Glu Ile	
195	200 205
gaa aag tac caa gaa gtg gaa gaa gac caa gac cca tca tgc ccc agg	671
Glu Lys Tyr Gln Glu Val Glu Glu Asp Gln Asp Pro Ser Cys Pro Arg	
210	215 220
ctc agc agg gag ctg ctg gat gag aaa gag cct gaa gtc ttg cag gac	719
Leu Ser Arg Glu Leu Leu Asp Glu Lys Glu Pro Glu Val Leu Gln Asp	
225	230 235
tca ctg gat aga tgt tat tcg act cct tca ggt tat ctt gaa ctg cct	767
Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Tyr Leu Glu Leu Pro	
240	245 250 255
gac tta ggc cag ccc tac agc agt gct gtt tac tca ttg gag gaa cag	815
Asp Leu Gly Gln Pro Tyr Ser Ser Ala Val Tyr Ser Leu Glu Glu Gln	
260	265 270
tac ctt ggc ttg gct ctt gac gtg gac aga att aaa aag gac caa gaa	863
Tyr Leu Gly Leu Ala Leu Asp Val Asp Arg Ile Lys Lys Asp Gln Glu	
275	280 285
gag gaa gaa gac caa ggc cca cca tgc ccc agg ctc agc agg gag ctg	911
Glu Glu Glu Asp Gln Gly Pro Pro Cys Pro Arg Leu Ser Arg Glu Leu	
290	295 300
ctg gag gta gta gag cct gaa gtc ttg cag gac tca ctg gat aga tgt	959
Leu Glu Val Val Glu Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys	
305	310 315
tat tca act cct tcc agt tgt ctt gaa cag cct gac tcc tgc cag ccc	1007
Tyr Ser Thr Pro Ser Ser Cys Leu Glu Gln Pro Asp Ser Cys Gln Pro	
320	325 330 335
tat gga agt tcc ttt tat gca ttg gag gaa aaa cat gtt ggc ttt tct	1055
Tyr Gly Ser Ser Phe Tyr Ala Leu Glu Glu Lys His Val Gly Phe Ser	
340	345 350
ctt gac gtg gga gaa att gaa aag aag ggg aag ggg aag aaa aga agg	1103
Leu Asp Val Gly Glu Ile Glu Lys Lys Gly Lys Gly Lys Lys Arg Arg	
355	360 365
gga aga aga tca aag aag gaa aga aga agg gga aga aaa gaa ggg gaa	1151
Gly Arg Arg Ser Lys Lys Glu Arg Arg Arg Gly Arg Lys Glu Gly Glu	
370	375 380
gaa gat caa aac cca cca tgc ccc agg ctc agc agg gag ctg ctg gat	1199

Glu Asp Gln Asn Pro Pro Cys Pro Arg Leu Ser Arg Glu Leu Leu Asp	
385	390 395
gag aaa ggg cct gaa gtc ttg cag gac tca ctg gat aga tgt tat tca 1247	
Glu Lys Gly Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser	
400	405 410 415
act cct tca ggt tgt ctt gaa ctg act gac tca tgc cag ccc tac aga 1295	
Thr Pro Ser Gly Cys Leu Glu Leu Thr Asp Ser Cys Gln Pro Tyr Arg	
	420 425 430
agt gcc ttt tac ata ttg gag caa cag tgt gtt ggc ttg gct gtt gac 1343	
Ser Ala Phe Tyr Ile Leu Glu Gln Gln Cys Val Gly Leu Ala Val Asp	
	435 440 445
atg gat gaa att gaa aag tac caa gaa gtg gaa gaa gac caa gac cca 1391	
Met Asp Glu Ile Glu Lys Tyr Gln Glu Val Glu Glu Asp Gln Asp Pro	
	450 455 460
tca tgc ccc agg ctc agc agg gag ctg ctg gat gag aaa gag cct gaa 1439	
Ser Cys Pro Arg Leu Ser Arg Glu Leu Leu Asp Glu Lys Glu Pro Glu	
	465 470 475
gtc ttg cag gac tca ctg gat aga tgt tat tcg att cct tca ggt tat 1487	
Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Ile Pro Ser Gly Tyr	
480	485 490 495
ctt gaa ctg cct gac tta ggc cag ccc tac agc agt gct gtt tac tca 1535	
Leu Glu Leu Pro Asp Leu Gly Gln Pro Tyr Ser Ser Ala Val Tyr Ser	
	500 505 510
ttg gag gaa cag tac ctt ggc ttg gct ctt gac gtg gac aga att aaa 1583	
Leu Glu Glu Gln Tyr Leu Gly Leu Ala Leu Asp Val Asp Arg Ile Lys	
	515 520 525
aag gac caa gaa gag gaa gaa gac caa ggc cca cca tgc ccc agg ctc 1631	
Lys Asp Gln Glu Glu Glu Glu Asp Gln Gly Pro Pro Cys Pro Arg Leu	
	530 535 540
agc agg gag ctg ctg gag gta gta gag cct gaa gtc ttg cag gac tca 1679	
Ser Arg Glu Leu Leu Glu Val Val Glu Pro Glu Val Leu Gln Asp Ser	
	545 550 555
ctg gat aga tgt tat tca act cct tcc agt tgt ctt gaa cag cct gac 1727	
Leu Asp Arg Cys Tyr Ser Thr Pro Ser Ser Cys Leu Glu Gln Pro Asp	
560	565 570 575
tcc tgc cag ccc tat gga agt tcc ttt tat gca ttg gag gaa aaa cat 1775	

Ser Cys Gln Pro Tyr Gly Ser Ser Phe Tyr Ala Leu Glu Glu Lys His	
580 585 590	
gtt ggc ttt tct ctt gac gtg gga gaa att gaa aag aag ggg aag ggg	1823
Val Gly Phe Ser Leu Asp Val Gly Glu Ile Glu Lys Lys Gly Lys Gly	
595 600 605	
aag aaa aga agg gga aga aga tca aag aag gaa aga aga agg gga aga	1871
Lys Lys Arg Arg Gly Arg Arg Ser Lys Lys Glu Arg Arg Arg Gly Arg	
610 615 620	
aaa gaa ggg gaa gaa gat caa aac cca cca tgc ccc agg ctc agc agg	1919
Lys Glu Gly Glu Glu Asp Gln Asn Pro Pro Cys Pro Arg Leu Ser Arg	
625 630 635	
gag ctg ctg gat gag aaa ggg cct gaa gtc ttg cag gac tca ctg gat	1967
Glu Leu Leu Asp Glu Lys Gly Pro Glu Val Leu Gln Asp Ser Leu Asp	
640 645 650 655	
aga tgt tat tca act cct tca ggt tgt ctt gaa ctg act gac tca tgc	2015
Arg Cys Tyr Ser Thr Pro Ser Gly Cys Leu Glu Leu Thr Asp Ser Cys	
660 665 670	
cag ccc tac aga agt gcc ttt tac ata ttg gag caa cag tgt gtt ggc	2063
Gln Pro Tyr Arg Ser Ala Phe Tyr Ile Leu Glu Gln Gln Cys Val Gly	
675 680 685	
ttg gct gtt gac atg gat gaa att gaa aag tac caa gaa gtg gaa gaa	2111
Leu Ala Val Asp Met Asp Glu Ile Glu Lys Tyr Gln Glu Val Glu Glu	
690 695 700	
gac caa gac cca tca tgc ccc agg ctc agc agg gag ctg ctg gat gag	2159
Asp Gln Asp Pro Ser Cys Pro Arg Leu Ser Arg Glu Leu Leu Asp Glu	
705 710 715	
aaa gag cct gaa gtc ttg cag gac tca ctg gat aga tgt tat tgc act	2207
Lys Glu Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr	
720 725 730 735	
cct tca ggt tat ctt gaa ctg cct gac tta ggc cag ccc tac agc agt	2255
Pro Ser Gly Tyr Leu Glu Leu Pro Asp Leu Gly Gln Pro Tyr Ser Ser	
740 745 750	
gct gtt tac tca ttg gag gaa cag tac ctt ggc ttg gct ctt gac gtg	2303
Ala Val Tyr Ser Leu Glu Glu Gln Tyr Leu Gly Leu Ala Leu Asp Val	
755 760 765	
gac aga att aaa aag gac caa gaa gag gaa gaa gac caa ggc cca cca	2351

Asp Arg Ile Lys Lys Asp Gln Glu Glu Glu Asp Gln Gly Pro Pro
 770 775 780

 tgc ccc agg ctc agc agg gag ctg ctg gag gta gta gag cct gaa gtc 2399
 Cys Pro Arg Leu Ser Arg Glu Leu Leu Glu Val Val Glu Pro Glu Val
 785 790 795

 ttg cag gac tca ctg gat aga tgt tat tca act cct tcc agt tgt ctt 2447
 Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Ser Cys Leu
 800 805 810 815

 gaa cag cct gac tcc tgc cag ccc tat gga agt tcc ttt tat gca ttg 2495
 Glu Gln Pro Asp Ser Cys Gln Pro Tyr Gly Ser Ser Phe Tyr Ala Leu
 820 825 830

 gag gaa aaa cat gtt ggc ttt tct ctt gac gtg gga gaa att gaa aag 2543
 Glu Glu Lys His Val Gly Phe Ser Leu Asp Val Gly Glu Ile Glu Lys
 835 840 845

 aag ggg aag ggg aag aaa aga agg gga aga aga tca aaaaaaaaaa aaaaa 2594
 Lys Gly Lys Gly Lys Lys Arg Arg Gly Arg Arg Ser
 850 855

<210> 173

<211> 859

<212> PRT

<213> Homo sapiens

<223> image: 2186481; Genbak AF379633; cDNA clone AG06

<400> 173

Tyr Ser Thr Pro Ser Gly Tyr Leu Glu Leu Pro Asp Leu Gly Gln Pro
 1 5 10 15

Tyr Ser Ser Ala Val Tyr Ser Leu Glu Glu Gln Tyr Leu Gly Leu Ala
 20 25 30

Leu Asp Val Asp Arg Ile Lys Lys Asp Gln Glu Glu Glu Glu Asp Gln
 35 40 45

Gly Pro Pro Cys Pro Arg Leu Ser Arg Glu Leu Leu Glu Val Val Glu
 50 55 60

Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser
 65 70 75 80

Ser Cys Leu Glu Gln Pro Asp Ser Cys Gln Pro Tyr Gly Ser Ser Phe
 85 90 95

Tyr Ala Leu Glu Glu Lys His Val Gly Phe Ser Leu Asp Val Gly Glu
 100 105 110
 Ile Glu Lys Lys Gly Lys Gly Lys Lys Arg Arg Gly Arg Arg Ser Lys
 115 120 125
 Lys Glu Arg Arg Arg Gly Arg Lys Glu Gly Glu Glu Asp Gln Asn Pro
 130 135 140
 Pro Cys Pro Arg Leu Ser Arg Glu Leu Leu Asp Glu Lys Gly Pro Glu
 145 150 155 160
 Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Cys
 165 170 175
 Leu Glu Leu Thr Asp Ser Cys Gln Pro Tyr Arg Ser Ala Phe Tyr Ile
 180 185 190
 Leu Glu Gln Gln Cys Val Gly Leu Ala Val Asp Met Asp Glu Ile Glu
 195 200 205
 Lys Tyr Gln Glu Val Glu Glu Asp Gln Asp Pro Ser Cys Pro Arg Leu
 210 215 220
 Ser Arg Glu Leu Leu Asp Glu Lys Glu Pro Glu Val Leu Gln Asp Ser
 225 230 235 240
 Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Tyr Leu Glu Leu Pro Asp
 245 250 255
 Leu Gly Gln Pro Tyr Ser Ser Ala Val Tyr Ser Leu Glu Glu Gln Tyr
 260 265 270
 Leu Gly Leu Ala Leu Asp Val Asp Arg Ile Lys Lys Asp Gln Glu Glu
 275 280 285
 Glu Glu Asp Gln Gly Pro Pro Cys Pro Arg Leu Ser Arg Glu Leu Leu
 290 295 300
 Glu Val Val Glu Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr
 305 310 315 320
 Ser Thr Pro Ser Ser Cys Leu Glu Gln Pro Asp Ser Cys Gln Pro Tyr
 325 330 335
 Gly Ser Ser Phe Tyr Ala Leu Glu Glu Lys His Val Gly Phe Ser Leu
 340 345 350

Asp Val Gly Glu Ile Glu Lys Lys Gly Lys Gly Lys Lys Arg Arg Gly
 355 360 365
 Arg Arg Ser Lys Lys Glu Arg Arg Arg Gly Arg Lys Glu Gly Glu Glu
 370 375 380
 Asp Gln Asn Pro Pro Cys Pro Arg Leu Ser Arg Glu Leu Leu Asp Glu
 385 390 395 400
 Lys Gly Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr
 405 410 415
 Pro Ser Gly Cys Leu Glu Leu Thr Asp Ser Cys Gln Pro Tyr Arg Ser
 420 425 430
 Ala Phe Tyr Ile Leu Glu Gln Gln Cys Val Gly Leu Ala Val Asp Met
 435 440 445
 Asp Glu Ile Glu Lys Tyr Gln Glu Val Glu Glu Asp Gln Asp Pro Ser
 450 455 460
 Cys Pro Arg Leu Ser Arg Glu Leu Leu Asp Glu Lys Glu Pro Glu Val
 465 470 475 480
 Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Ile Pro Ser Gly Tyr Leu
 485 490 495
 Glu Leu Pro Asp Leu Gly Gln Pro Tyr Ser Ser Ala Val Tyr Ser Leu
 500 505 510
 Glu Glu Gln Tyr Leu Gly Leu Ala Leu Asp Val Asp Arg Ile Lys Lys
 515 520 525
 Asp Gln Glu Glu Glu Glu Asp Gln Gly Pro Pro Cys Pro Arg Leu Ser
 530 535 540
 Arg Glu Leu Leu Glu Val Val Glu Pro Glu Val Leu Gln Asp Ser Leu
 545 550 555 560
 Asp Arg Cys Tyr Ser Thr Pro Ser Ser Cys Leu Glu Gln Pro Asp Ser
 565 570 575
 Cys Gln Pro Tyr Gly Ser Ser Phe Tyr Ala Leu Glu Glu Lys His Val
 580 585 590
 Gly Phe Ser Leu Asp Val Gly Glu Ile Glu Lys Lys Gly Lys Gly Lys
 595 600 605

Lys Arg Arg Gly Arg Arg Sér Lys Lys Glu Arg Arg Arg Gly Arg Lys
 610 615 620

Glu Gly Glu Glu Asp Gln Asn Pro Pro Cys Pro Arg Leu Ser Arg Glu
 625 630 635 640

Leu Leu Asp Glu Lys Gly Pro Glu Val Leu Gln Asp Ser Leu Asp Arg
 645 650 655

Cys Tyr Ser Thr Pro Ser Gly Cys Leu Glu Leu Thr Asp Ser Cys Gln
 660 665 670

Pro Tyr Arg Ser Ala Phe Tyr Ile Leu Glu Gln Gln Cys Val Gly Leu
 675 680 685

Ala Val Asp Met Asp Glu Ile Glu Lys Tyr Gln Glu Val Glu Glu Asp
 690 695 700

Gln Asp Pro Ser Cys Pro Arg Leu Ser Arg Glu Leu Leu Asp Glu Lys
 705 710 715 720

Glu Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro
 725 730 735

Ser Gly Tyr Leu Glu Leu Pro Asp Leu Gly Gln Pro Tyr Ser Ser Ala
 740 745 750

Val Tyr Ser Leu Glu Glu Gln Tyr Leu Gly Leu Ala Leu Asp Val Asp
 755 760 765

Arg Ile Lys Lys Asp Gln Glu Glu Glu Glu Asp Gln Gly Pro Pro Cys
 770 775 780

Pro Arg Leu Ser Arg Glu Leu Leu Glu Val Val Glu Pro Glu Val Leu
 785 790 795 800

Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Ser Cys Leu Glu
 805 810 815

Gln Pro Asp Ser Cys Gln Pro Tyr Gly Ser Ser Phe Tyr Ala Leu Glu
 820 825 830

Glu Lys His Val Gly Phe Ser Leu Asp Val Gly Glu Ile Glu Lys Lys
 835 840 845

Gly Lys Gly Lys Lys Arg Arg Gly Arg Arg Ser
 850 855

<210> 174

<211> 915

<212> DNA

<213> Homo sapiens

<220>

<223> image: 1700501; Genbank AF379632; cDNA clone AG04

<220>

<221> CDS

<222> (1)..(897)

<400> 174

ggg gaa aaa cat gtt ggc ttt tct ctt gac gtg gga gaa att gaa aag 48

Gly Glu Lys His Val Gly Phe Ser Leu Asp Val Gly Glu Ile Glu Lys

1

5

10

15

aag ggg aag ggg aag aaa aga agg gga aga aga tca aag aag gaa aga 96

Lys Gly Lys Gly Lys Lys Arg Arg Gly Arg Arg Ser Lys Lys Glu Arg

20

25

30

aga agg gga aga aaa gaa ggg gaa gaa gat caa aac cca cca tgc ccc 144

Arg Arg Gly Arg Lys Glu Gly Glu Glu Asp Gln Asn Pro Pro Cys Pro

35

40

45

agg ctc agc agg gag ctg ctg gat gag aaa ggg cct gaa gtc ttg cag 192

Arg Leu Ser Arg Glu Leu Leu Asp Glu Lys Gly Pro Glu Val Leu Gln

50

55

60

gac tca ctg gat aga tgt tat tca act cct tca ggt tgt ctt gaa ctg 240

Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Cys Leu Glu Leu

65

70

75

80

act gac tca tgc cag ccc tac aga agt gcc ttt tat gta ttg gag caa 288

Thr Asp Ser Cys Gln Pro Tyr Arg Ser Ala Phe Tyr Val Leu Glu Gln

85

90

95

cag cgt gtt ggc ttg gct gtt gac atg gat gaa att gaa aag tac caa 336

Gln Arg Val Gly Leu Ala Val Asp Met Asp Glu Ile Glu Lys Tyr Gln

100

105

110

gaa gtg gaa gaa gac caa gac cca tca tgc ccc agg ctc agc agg gag 384

Glu Val Glu Glu Asp Gln Asp Pro Ser Cys Pro Arg Leu Ser Arg Glu

115

120

125

ctg ctg gat gag aaa gag cct gaa gtc ttg cag gac tca ctg gat aga 432
 Leu Leu Asp Glu Lys Glu Pro Glu Val Leu Gln Asp Ser Leu Asp Arg
 130 135 140

tgt tat tcg act cct tca ggt tat ctt gaa ctg cct gac tta ggc cag 480
 Cys Tyr Ser Thr Pro Ser Gly Tyr Leu Glu Leu Pro Asp Leu Gly Gln
 145 150 155 160

ccc tac agc agt gct gtt tac tca ttg gag gaa cag tac ctt ggc ttg 528
 Pro Tyr Ser Ser Ala Val Tyr Ser Leu Glu Glu Gln Tyr Leu Gly Leu
 165 170 175

gct ctt gac gtg gac aga att aaa aag gac caa gaa gag gaa gaa gac 576
 Ala Leu Asp Val Asp Arg Ile Lys Lys Asp Gln Glu Glu Glu Glu Asp
 180 185 190

caa ggc cca cca tgc ccc agg ctc agc agg gag ctg ctg gag gta gta 624
 Gln Gly Pro Pro Cys Pro Arg Leu Ser Arg Glu Leu Leu Glu Val Val
 195 200 205

gag cct gaa gtc ttg cag gac tca ctg gat aga tgt tat tca act cct 672
 Glu Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro
 210 215 220

tcc agt tgt ctt gaa cag cct gac tcc tgc cag ccc tat gga agt tcc 720
 Ser Ser Cys Leu Glu Gln Pro Asp Ser Cys Gln Pro Tyr Gly Ser Ser
 225 230 235 240

ttt tat gca ttg gag gaa aaa cat gtt ggc ttt tct ctt gac gtg gga 768
 Phe Tyr Ala Leu Glu Glu Lys His Val Gly Phe Ser Leu Asp Val Gly
 245 250 255

gaa att gaa aag aag ggg aag ggg aag aaa aga agg gga aga aga tca 816
 Glu Ile Glu Lys Lys Gly Lys Gly Lys Lys Arg Arg Gly Arg Arg Ser
 260 265 270

aag aag atc aaa gaa gaa ggg gaa gaa aaa aag ggg aag aaa aga agg 864
 Lys Lys Ile Lys Glu Glu Gly Glu Glu Lys Lys Gly Lys Lys Arg Arg
 275 280 285

gga aga aga tca aag aag gaa aga aga agg gga agaaaaaaaa aaaaaaaa 915
 Gly Arg Arg Ser Lys Lys Glu Arg Arg Arg Gly
 290 295

<210> 175

<211> 299

<212> PRT

<213> Homo sapiens

<223> image: 1700501; Genbank AF379632; cDNA clone AG04

<400> 175

Gly Glu Lys His Val Gly Phe Ser Leu Asp Val Gly Glu Ile Glu Lys
 1 5 10 15

Lys Gly Lys Gly Lys Lys Arg Arg Gly Arg Arg Ser Lys Lys Glu Arg
 20 25 30

Arg Arg Gly Arg Lys Glu Gly Glu Glu Asp Gln Asn Pro Pro Cys Pro
 35 40 45

Arg Leu Ser Arg Glu Leu Leu Asp Glu Lys Gly Pro Glu Val Leu Gln
 50 55 60

Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Cys Leu Glu Leu
 65 70 75 80

Thr Asp Ser Cys Gln Pro Tyr Arg Ser Ala Phe Tyr Val Leu Glu Gln
 85 90 95

Gln Arg Val Gly Leu Ala Val Asp Met Asp Glu Ile Glu Lys Tyr Gln
 100 105 110

Glu Val Glu Glu Asp Gln Asp Pro Ser Cys Pro Arg Leu Ser Arg Glu
 115 120 125

Leu Leu Asp Glu Lys Glu Pro Glu Val Leu Gln Asp Ser Leu Asp Arg
 130 135 140

Cys Tyr Ser Thr Pro Ser Gly Tyr Leu Glu Leu Pro Asp Leu Gly Gln
 145 150 155 160

Pro Tyr Ser Ser Ala Val Tyr Ser Leu Glu Glu Gln Tyr Leu Gly Leu
 165 170 175

Ala Leu Asp Val Asp Arg Ile Lys Lys Asp Gln Glu Glu Glu Glu Asp
 180 185 190

Gln Gly Pro Pro Cys Pro Arg Leu Ser Arg Glu Leu Leu Glu Val Val
 195 200 205

Glu Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro
 210 215 220

Ser Ser Cys Leu Glu Gln Pro Asp Ser Cys Gln Pro Tyr Gly Ser Ser
 225 230 235 240

Phe Tyr Ala Leu Glu Glu Lys His Val Gly Phe Ser Leu Asp Val Gly
 245 250 255

Glu Ile Glu Lys Lys Gly Lys Gly Lys Lys Arg Arg Gly Arg Arg Ser
 260 265 270

Lys Lys Ile Lys Glu Glu Gly Glu Glu Lys Lys Gly Lys Lys Arg Arg
 275 280 285

Gly Arg Arg Ser Lys Lys Glu Arg Arg Arg Gly
 290 295

<210> 176

<211> 582

<212> DNA

<213> Homo sapiens

<220>

<223> image: 450510; Genbank AF379631; cDNA clone AE05

<220>

<221> CDS

<222> (1)..(522)

<400> 176

ggc acg agc aaa gtc gac tca act ctc att ggc tca tcc tct cat gtt 48

Gly Thr Ser Lys Val Asp Ser Thr Leu Ile Gly Ser Ser Ser His Val
 1 5 10 15

gaa tgg gag gat gct gta cac att att cca gaa aat gaa agt gat gat 96

Glu Trp Glu Asp Ala Val His Ile Ile Pro Glu Asn Glu Ser Asp Asp
 20 25 30

gag gaa gag gaa gaa aaa gga cca gtg tct ccc agg aat ctg cag gag 144

Glu Glu Glu Glu Glu Lys Gly Pro Val Ser Pro Arg Asn Leu Gln Glu
 35 40 45

tct gaa gag gag gaa gtc ccc cag gag tcc tgg gat gaa ggt tat tcg 192

Ser Glu Glu Glu Glu Val Pro Gln Glu Ser Trp Asp Glu Gly Tyr Ser
 50 55 60

act ctc tca att cct cct gaa atg ttg gcc tcg tac aag tct tac agc 240

Thr Leu Ser Ile Pro Pro Glu Met Leu Ala Ser Tyr Lys Ser Tyr Ser
 65 70 75 80

agc aca ttt cac tca tta gag gaa cag caa gtc tgc atg gct gtt gac 288
 Ser Thr Phe His Ser Leu Glu Glu Gln Gln Val Cys Met Ala Val Asp
 85 90 95

ata ggc aga cat cgg tgg gat caa gtg aaa aag gag gac cac gag gca 336
 Ile Gly Arg His Arg Trp Asp Gln Val Lys Lys Glu Asp His Glu Ala
 100 105 110

aca ggt ccc agg ctc agc aga gag ctg ctg gat gag aaa ggg cct gaa 384
 Thr Gly Pro Arg Leu Ser Arg Glu Leu Leu Asp Glu Lys Gly Pro Glu
 115 120 125

gtc ttg cag gac tca ctg gat aga tgt tat tca act cct tca ggt tgt 432
 Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Cys
 130 135 140

ctt gaa ctg act gac tca tgc cag ccc tac aga agt gcc ttt tac gta 480
 Leu Glu Leu Thr Asp Ser Cys Gln Pro Tyr Arg Ser Ala Phe Tyr Val
 145 150 155 160

ttg gag caa cag cgt gtt ggc ttg gct gtt gac atg gat gaa 522
 Leu Glu Gln Gln Arg Val Gly Leu Ala Val Asp Met Asp Glu
 165 170

attgaaaagt accaagaaat aaactogtaa ccctgtcctt caaaaaaaaaa aaaaaaaaaa 582

<210> 177

<211> 174

<212> PRT

<213> Homo sapiens

<223> image: 450510; Genbank AF379631; cDNA clone AE05

<400> 177

Gly Thr Ser Lys Val Asp Ser Thr Leu Ile Gly Ser Ser Ser His Val
 1 5 10 15

Glu Trp Glu Asp Ala Val His Ile Ile Pro Glu Asn Glu Ser Asp Asp
 20 25 30

Glu Glu Glu Glu Glu Lys Gly Pro Val Ser Pro Arg Asn Leu Gln Glu
 35 40 45

Ser Glu Glu Glu Glu Val Pro Gln Glu Ser Trp Asp Glu Gly Tyr Ser
 50 55 60

Thr Leu Ser Ile Pro Pro Glu Met Leu Ala Ser Tyr Lys Ser Tyr Ser
 65 70 75 80

Ser Thr Phe His Ser Leu Glu Glu Gln Gln Val Cys Met Ala Val Asp
 85 90 95

Ile Gly Arg His Arg Trp Asp Gln Val Lys Lys Glu Asp His Glu Ala
 100 105 110

Thr Gly Pro Arg Leu Ser Arg Glu Leu Leu Asp Glu Lys Gly Pro Glu
 115 120 125

Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Cys
 130 135 140

Leu Glu Leu Thr Asp Ser Cys Gln Pro Tyr Arg Ser Ala Phe Tyr Val
 145 150 155 160

Leu Glu Gln Gln Arg Val Gly Leu Ala Val Asp Met Asp Glu
 165 170

<210> 178

<211> 1555

<212> DNA

<213> Homo sapiens

<220>

<223> image: 44185; Genbank AF379630; cDNA clone AE03

<220>

<221> CDS

<222> (3)..(1520)

<400> 178

aa gat ctc ata aaa ttt atg ctg agg aat gag cga cag ttc aag gag 47
 Asp Leu Ile Lys Phe Met Leu Arg Asn Glu Arg Gln Phe Lys Glu
 1 5 10 15

gag aag ctt gca gag cag ctc aag caa gct gag gag ctc agg caa tat 95
 Glu Lys Leu Ala Glu Gln Leu Lys Gln Ala Glu Glu Leu Arg Gln Tyr
 20 25 30

aaa gtc ctg gtt cac gct cag gaa cga gag ctg acc cag tta agg gag 143
 Lys Val Leu Val His Ala Gln Glu Arg Glu Leu Thr Gln Leu Arg Glu
 35 40 45

aag tta cgg gaa ggg aga gat gcc tcc cgc tca ttg aat gag cat ctc 191
 Lys Leu Arg Glu Gly Arg Asp Ala Ser Arg Ser Leu Asn Glu His Leu

50	55	60	
cag gcc ctc ctc act ccg gat gag ccg gac aag tcc cag ggg cag gac			239
Gln Ala Leu Leu Thr Pro Asp Glu Pro Asp Lys Ser Gln Gly Gln Asp			
65	70	75	
ctc caa gaa cag ctg gct gag ggg tgt aga ctg aca cag cac ctt gtc			287
Leu Gln Glu Gln Leu Ala Glu Gly Cys Arg Leu Thr Gln His Leu Val			
80	85	90	95
caa aag ctc agc cca gaa aat gac aac gat gac gat gaa gat gtt caa			335
Gln Lys Leu Ser Pro Glu Asn Asp Asn Asp Asp Asp Glu Asp Val Gln			
100	105	110	
gtt gag gtg gct gag aaa gtg cag aaa tcg tct gcc ccc agg gag atg			383
Val Glu Val Ala Glu Lys Val Gln Lys Ser Ser Ala Pro Arg Glu Met			
115	120	125	
cag aag gct gaa gaa aag gaa gtc cct gag gac tca ctg gag gaa tgt			431
Gln Lys Ala Glu Glu Lys Glu Val Pro Glu Asp Ser Leu Glu Glu Cys			
130	135	140	
gcc atc act tgt tca aat agc cat ggc cct tat gac tcc aac cag cca			479
Ala Ile Thr Cys Ser Asn Ser His Gly Pro Tyr Asp Ser Asn Gln Pro			
145	150	155	
cat aag aaa acc aaa atc aca ttt gag gaa gac aaa gtc gac tca act			527
His Lys Lys Thr Lys Ile Thr Phe Glu Glu Asp Lys Val Asp Ser Thr			
160	165	170	175
ctc att ggc tca tcc tct cat gtt gaa tgg gag gat gct gta cac att			575
Leu Ile Gly Ser Ser Ser His Val Glu Trp Glu Asp Ala Val His Ile			
180	185	190	
att cca gaa aat gaa agt gat gat gag gaa gag gaa gaa aaa ggg cca			623
Ile Pro Glu Asn Glu Ser Asp Asp Glu Glu Glu Glu Glu Lys Gly Pro			
195	200	205	
gtg tct ccc agg aat ctg cag gag tct gaa gag gag gaa gtc ccc cag			671
Val Ser Pro Arg Asn Leu Gln Glu Ser Glu Glu Glu Glu Val Pro Gln			
210	215	220	
gag tcc tgg gat gaa ggt tat tcg act ctc tca att cct cct gaa atg			719
Glu Ser Trp Asp Glu Gly Tyr Ser Thr Leu Ser Ile Pro Pro Glu Met			
225	230	235	
ttg gcc tcg tac cag tct tac agc agc aca ttt cac tca tta gag gaa			767
Leu Ala Ser Tyr Gln Ser Tyr Ser Ser Thr Phe His Ser Leu Glu Glu			

240	245	250	255	
cag caa gtc tgc atg gct gtt gac ata ggc aga cat cgg tgg gat caa				815
Gln Gln Val Cys Met Ala Val Asp Ile Gly Arg His Arg Trp Asp Gln				
	260	265	270	
gtg aaa aag gag gac caa gag gca aca ggt ccc agg ctc agc agg gag				863
Val Lys Lys Glu Asp Gln Glu Ala Thr Gly Pro Arg Leu Ser Arg Glu				
	275	280	285	
ctg ctg gat gag aaa gag cct gaa gtc ttg cag gac tca ctg gat aga				911
Leu Leu Asp Glu Lys Glu Pro Glu Val Leu Gln Asp Ser Leu Asp Arg				
	290	295	300	
tgt tat tca act cct tca ggt tgt ctt gaa ctg act gac tca tgc cag				959
Cys Tyr Ser Thr Pro Ser Gly Cys Leu Glu Leu Thr Asp Ser Cys Gln				
	305	310	315	
ccc tac aga agt gcc ttt tac gta ttg gag caa cag cgt gtt ggc ttg				1007
Pro Tyr Arg Ser Ala Phe Tyr Val Leu Glu Gln Gln Arg Val Gly Leu				
	320	325	330	335
gct att gac atg gat gaa att gaa aag tac caa gaa gtg gaa gaa gac				1055
Ala Ile Asp Met Asp Glu Ile Glu Lys Tyr Gln Glu Val Glu Glu Asp				
	340	345	350	
caa gac cca tca tgc ccc agg ctc agc agg gag ctg ctg gat gag aaa				1103
Gln Asp Pro Ser Cys Pro Arg Leu Ser Arg Glu Leu Leu Asp Glu Lys				
	355	360	365	
gag cct gaa gtc ttg cag gac tca ctg gat aga tgt tat tca act cct				1151
Glu Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro				
	370	375	380	
tca gat tat ctt gaa ctg cct gac tta ggc cag ccc tac agc agt gct				1199
Ser Asp Tyr Leu Glu Leu Pro Asp Leu Gly Gln Pro Tyr Ser Ser Ala				
	385	390	395	
gtt tac tca ttg gag gaa cag tac ctt ggc ttg gct ctt gac gtg gac				1247
Val Tyr Ser Leu Glu Glu Gln Tyr Leu Gly Leu Ala Leu Asp Val Asp				
	400	405	410	415
aga att aaa aag gac caa gaa gag gaa gaa gac caa ggc cca cca tgc				1295
Arg Ile Lys Lys Asp Gln Glu Glu Glu Glu Asp Gln Gly Pro Pro Cys				
	420	425	430	
ccc agg ctc agc agg gag ctg ctg gag gta gta gag cct gaa gtc ttg				1343
Pro Arg Leu Ser Arg Glu Leu Leu Glu Val Val Glu Pro Glu Val Leu				

```

                435                      440                      445
cag gac tca ctg gat aga tgt tat tca act cct tcc agt tgt ctt gaa 1391
Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Ser Cys Leu Glu
                450                      455                      460

cag cct gac tcc tgc cag ccc tat gga agt tcc ttt tat gca ttg gag 1439
Gln Pro Asp Ser Cys Gln Pro Tyr Gly Ser Ser Phe Tyr Ala Leu Glu
                465                      470                      475

gaa aaa cat gtt ggc ttt tct ctt gac gtg gga gaa att gaa aag aag 1487
Glu Lys His Val Gly Phe Ser Leu Asp Val Gly Glu Ile Glu Lys Lys
280                      485                      490                      495

ggg aag ggg aag aaa aga agg gga aga aga tca aaaaaaaaaa aaaaaaaaaa 1540
Gly Lys Gly Lys Lys Arg Arg Gly Arg Arg Ser
                500                      505

aaaaaaaaaa aaaaaa 1555

```

<210> 179

<211> 506

<212> PRT

<213> Homo sapiens

<223> image: 44185; Genbank AF379630; cDNA clone AE03

<400> 179

```

Asp Leu Ile Lys Phe Met Leu Arg Asn Glu Arg Gln Phe Lys Glu Glu
  1                      5                      10                      15

```

```

Lys Leu Ala Glu Gln Leu Lys Gln Ala Glu Glu Leu Arg Gln Tyr Lys
                20                      25                      30

```

```

Val Leu Val His Ala Gln Glu Arg Glu Leu Thr Gln Leu Arg Glu Lys
                35                      40                      45

```

```

Leu Arg Glu Gly Arg Asp Ala Ser Arg Ser Leu Asn Glu His Leu Gln
                50                      55                      60

```

```

Ala Leu Leu Thr Pro Asp Glu Pro Asp Lys Ser Gln Gly Gln Asp Leu
                65                      70                      75                      80

```

```

Gln Glu Gln Leu Ala Glu Gly Cys Arg Leu Thr Gln His Leu Val Gln
                85                      90                      95

```

```

Lys Leu Ser Pro Glu Asn Asp Asn Asp Asp Asp Glu Asp Val Gln Val
                100                      105                      110

```

Glu Val Ala Glu Lys Val Gln Lys Ser Ser Ala Pro Arg Glu Met Gln
 115 120 125

Lys Ala Glu Glu Lys Glu Val Pro Glu Asp Ser Leu Glu Glu Cys Ala
 130 135 140

Ile Thr Cys Ser Asn Ser His Gly Pro Tyr Asp Ser Asn Gln Pro His
 145 150 155 160

Lys Lys Thr Lys Ile Thr Phe Glu Glu Asp Lys Val Asp Ser Thr Leu
 165 170 175

Ile Gly Ser Ser Ser His Val Glu Trp Glu Asp Ala Val His Ile Ile
 180 185 190

Pro Glu Asn Glu Ser Asp Asp Glu Glu Glu Glu Glu Lys Gly Pro Val
 195 200 205

Ser Pro Arg Asn Leu Gln Glu Ser Glu Glu Glu Glu Val Pro Gln Glu
 210 215 220

Ser Trp Asp Glu Gly Tyr Ser Thr Leu Ser Ile Pro Pro Glu Met Leu
 225 230 235 240

Ala Ser Tyr Gln Ser Tyr Ser Ser Thr Phe His Ser Leu Glu Glu Gln
 245 250 255

Gln Val Cys Met Ala Val Asp Ile Gly Arg His Arg Trp Asp Gln Val
 260 265 270

Lys Lys Glu Asp Gln Glu Ala Thr Gly Pro Arg Leu Ser Arg Glu Leu
 275 280 285

Leu Asp Glu Lys Glu Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys
 290 295 300

Tyr Ser Thr Pro Ser Gly Cys Leu Glu Leu Thr Asp Ser Cys Gln Pro
 305 310 315 320

Tyr Arg Ser Ala Phe Tyr Val Leu Glu Gln Gln Arg Val Gly Leu Ala
 325 330 335

Ile Asp Met Asp Glu Ile Glu Lys Tyr Gln Glu Val Glu Glu Asp Gln
 340 345 350

Asp Pro Ser Cys Pro Arg Leu Ser Arg Glu Leu Leu Asp Glu Lys Glu
 355 360 365

Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser
 370 375 380
 Asp Tyr Leu Glu Leu Pro Asp Leu Gly Gln Pro Tyr Ser Ser Ala Val
 385 390 395 400
 Tyr Ser Leu Glu Glu Gln Tyr Leu Gly Leu Ala Leu Asp Val Asp Arg
 405 410 415
 Ile Lys Lys Asp Gln Glu Glu Glu Glu Asp Gln Gly Pro Pro Cys Pro
 420 425 430
 Arg Leu Ser Arg Glu Leu Leu Glu Val Val Glu Pro Glu Val Leu Gln
 435 440 445
 Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Ser Cys Leu Glu Gln
 450 455 460
 Pro Asp Ser Cys Gln Pro Tyr Gly Ser Ser Phe Tyr Ala Leu Glu Glu
 465 470 475 480
 Lys His Val Gly Phe Ser Leu Asp Val Gly Glu Ile Glu Lys Lys Gly
 485 490 495
 Lys Gly Lys Lys Arg Arg Gly Arg Arg Ser
 500 505

<210> 180

<211> 444

<212> DNA

<213> Homo sapiens

<220>

<223> image: 341197; Genbank AF379629; cDNA clone AE02

<220>

<221> CDS

<222> (269)..(433)

<400> 180

ggcacgagga ttgatccagt cctccttcct tcactaccac atgaatgctg ggcagcccag 60

gatcacactc actgcaccct caactcagac cgttacctgg cacactggcc tcactcttgt 120

cggagactga gctattggca gtgccttcag ctctgagctc aggcacctcg aacattgttt 180

ttgtcggttaa ggatcctaaa gtgctgoggg gactgatcac atttttctca acatccctgg 240

ccccacctct tctgccacaa acgtcagc atg gtg gta tct gcc ggc cct tgg 292

Met Val Val Ser Ala Gly Pro Trp

1

5

tcc ggt gag aag gca gag atg aac att cta gaa atc aac aag aaa tcg 340

Ser Gly Glu Lys Ala Glu Met Asn Ile Leu Glu Ile Asn Lys Lys Ser

10

15

20

cgc ccc cag ctg gca gag aac aaa cag cag ttc aga aac ctc aaa cag 388

Arg Pro Gln Leu Ala Glu Asn Lys Gln Gln Phe Arg Asn Leu Lys Gln

25

30

35

40

aaa tgt ctt gta act caa gtg gcc tac ttc ctg gcc aac cgg caa 433

Lys Cys Leu Val Thr Gln Val Ala Tyr Phe Leu Ala Asn Arg Gln

45

50

55

aaaaaaaaa a

444

<210> 181

<211> 55

<212> PRT

<213> Homo sapiens

<223> image: 341197; Genbank AF379629; cDNA clone AE02

<400> 181

Met Val Val Ser Ala Gly Pro Trp Ser Gly Glu Lys Ala Glu Met Asn

1

5

10

15

Ile Leu Glu Ile Asn Lys Lys Ser Arg Pro Gln Leu Ala Glu Asn Lys

20

25

30

Gln Gln Phe Arg Asn Leu Lys Gln Lys Cys Leu Val Thr Gln Val Ala

35

40

45

Tyr Phe Leu Ala Asn Arg Gln

50

55

<210> 182

<211> 2630

<212> DNA

<213> Homo sapiens

<220>

<223> DKFZp434D0623; Genbank AF379626; cDNA clone AC03

<220>

<221> CDS

<222> (2)..(1507)

<400> 182

c caa gac cca tca tgc ccc agg ctc agc agg gag ctg ctg gat gag aaa 49

Gln Asp Pro Ser Cys Pro Arg Leu Ser Arg Glu Leu Leu Asp Glu Lys

1

5

10

15

gag cct gaa gtc ttg cag gac tca ctg gat aga tgt tat tcg act cct 97

Glu Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro

20

25

30

tca ggt tat ctt gaa ctg cct gac tta ggc cag ccc tac aga agt gct 145

Ser Gly Tyr Leu Glu Leu Pro Asp Leu Gly Gln Pro Tyr Arg Ser Ala

35

40

45

gtt tac tca ttg gag gaa cag tac ctt ggc ttg gct ctt gac gtg gac 193

Val Tyr Ser Leu Glu Glu Gln Tyr Leu Gly Leu Ala Leu Asp Val Asp

50

55

60

aga att aaa aag gac caa gaa gag gaa gaa gac caa ggc cca cca tgc 241

Arg Ile Lys Lys Asp Gln Glu Glu Glu Glu Asp Gln Gly Pro Pro Cys

65

70

75

80

ccc agg ctc agc agg gag ctg ctg gag gca gta gag cct gaa gtc ttg 289

Pro Arg Leu Ser Arg Glu Leu Leu Glu Ala Val Glu Pro Glu Val Leu

85

90

95

cag gac tca ctg gat aga tgt tat tca act cct tcc agt tgt ctt gaa 337

Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Ser Cys Leu Glu

100

105

110

cag cct gac tcc tgc ctg ccc tat gga agt tcc ttt tat gca ttg gag 385

Gln Pro Asp Ser Cys Leu Pro Tyr Gly Ser Ser Phe Tyr Ala Leu Glu

115

120

125

gaa aaa cat gtt ggc ttt tct ctt gac gtg gga gaa att gaa aag aag 433

Glu Lys His Val Gly Phe Ser Leu Asp Val Gly Glu Ile Glu Lys Lys

130

135

140

ggg aag ggg aag aaa aga agg gga aga aga tca atg aag aaa aga agg 481

Gly Lys Gly Lys Lys Arg Arg Gly Arg Arg Ser Met Lys Lys Arg Arg

145

150

155

160

aga agg gga aga aaa gaa ggg gaa gaa gat caa aac cca cca tgc ccc	529
Arg Arg Gly Arg Lys Glu Gly Glu Glu Asp Gln Asn Pro Pro Cys Pro	
165 170 175	
agg ctc aac agg gag ctg ctg gat gag aaa ggg cct gaa gtc ttg cag	577
Arg Leu Asn Arg Glu Leu Leu Asp Glu Lys Gly Pro Glu Val Leu Gln	
180 185 190	
gac tca ctg gat aga tgt tat tca act cct tca ggt tat ctt gaa ctg	625
Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Tyr Leu Glu Leu	
195 200 205	
act gac tca tgc cag ccc tac aga agt gcc ttt tac ata ttg gag caa	673
Thr Asp Ser Cys Gln Pro Tyr Arg Ser Ala Phe Tyr Ile Leu Glu Gln	
210 215 220	
cag cgt gtt ggc tgg gct ctt gac atg gat gaa att gaa aag tac caa	721
Gln Arg Val Gly Trp Ala Leu Asp Met Asp Glu Ile Glu Lys Tyr Gln	
225 230 235 240	
gaa gtg gaa gaa gac caa gac cca tca tgc ccc agg ctc agc agg gag	769
Glu Val Glu Glu Asp Gln Asp Pro Ser Cys Pro Arg Leu Ser Arg Glu	
245 250 255	
ctg ctg gat gag aaa gag cct gaa gtc ttg cag gac tca ctg gat aga	817
Leu Leu Asp Glu Lys Glu Pro Glu Val Leu Gln Asp Ser Leu Asp Arg	
260 265 270	
tgt tat tcg act cct tca ggt tat ctt gaa ctg cct gac tta ggc cag	865
Cys Tyr Ser Thr Pro Ser Gly Tyr Leu Glu Leu Pro Asp Leu Gly Gln	
275 280 285	
ccc tac aga agt gct gtt tac tca ttg gag gaa cag tac ctt ggc ttg	913
Pro Tyr Arg Ser Ala Val Tyr Ser Leu Glu Glu Gln Tyr Leu Gly Leu	
290 295 300	
gct ctt gac gtg gac aga att aaa aag gac caa gaa gag gaa gaa gac	961
Ala Leu Asp Val Asp Arg Ile Lys Lys Asp Gln Glu Glu Glu Glu Asp	
305 310 315 320	
caa ggc cca cca tgc ccc agg ctc agc agg gag ctg ctg gag gca gta	1009
Gln Gly Pro Pro Cys Pro Arg Leu Ser Arg Glu Leu Leu Glu Ala Val	
325 330 335	
gag cct gaa gtc ttg cag gac tca ctg gat aga tgt tat tca act cct	1057
Glu Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro	
340 345 350	

```

tcc agt tgt ctt gaa cag cct gac tcc tgc ctg ccc tat gga agt tcc 1105
Ser Ser Cys Leu Glu Gln Pro Asp Ser Cys Leu Pro Tyr Gly Ser Ser
      355                      360                      365

ttt tat gca ttg gag gaa aaa cat gtt ggc ttt tct ctt gac gtg gga 1153
Phe Tyr Ala Leu Glu Glu Lys His Val Gly Phe Ser Leu Asp Val Gly
      370                      375                      380

gaa att gaa aag aag ggg aag ggg aag aaa aga agg gga aga aga tca 1201
Glu Ile Glu Lys Lys Gly Lys Gly Lys Lys Arg Arg Gly Arg Arg Ser
385                      390                      395                      400

atg aag aaa aga agg aga agg gga aga aaa gaa ggg gaa gaa gat caa 1249
Met Lys Lys Arg Arg Arg Arg Gly Arg Lys Glu Gly Glu Glu Asp Gln
      405                      410                      415

aac cca cca tgc ccc agg ctc agc ggc atg ctg atg gaa gtg gaa gag 1297
Asn Pro Pro Cys Pro Arg Leu Ser Gly Met Leu Met Glu Val Glu Glu
      420                      425                      430

cct gaa gtc ttg cag gac tca ctg gat aga tgt tat tcg act ccg tca 1345
Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser
      435                      440                      445

atg tac ttt gaa cta cct gac tca ttc cag cac tac aga agt gtg ttt 1393
Met Tyr Phe Glu Leu Pro Asp Ser Phe Gln His Tyr Arg Ser Val Phe
      450                      455                      460

tac tca ttt gag gaa cag cac atc agc ttc gcc ctt gac gtg gac aat 1441
Tyr Ser Phe Glu Glu Gln His Ile Ser Phe Ala Leu Asp Val Asp Asn
465                      470                      475                      480

agg ttt ctt act ttg atg gga aca agt ctc cac ctg gtc ttc cag atg 1489
Arg Phe Leu Thr Leu Met Gly Thr Ser Leu His Leu Val Phe Gln Met
      485                      490                      495

gga gtc ata ttc cca cag taagcagccc ttactaagcc gagagatgtc 1537
Gly Val Ile Phe Pro Gln
      500

attcctgcag gcaggaccta taggcacgtg aagatttgaa tgaaactata gttccatttg 1597

gaagcccaga cataggatgg gtcagtgggc atggctctat tcctattctc agaccatgcc 1657

agtggcaacc tgtgctcagt ctgaagacaa tggaccaag ttaggtgtga cacgttcaca 1717

taactgtgca gcacatgccg ggagtgatca gtcagacatt ttaatttgaa ccacttatct 1777

```

ctgggtagct acaaagttcc tcagggattt cattttgcag tcatgtctct gagcttctat 1837
 acctgctcaa ggtcagtgtc atctttgtgt ttagctcatc caaagggtgtt accctgggtt 1897
 caatgaacct aacctcattc tttgtatctt cagtgttgaa ttgttttagc tgatccatct 1957
 ttaacacagg agggatcctt ggctgaggat tgtatttcag aaccaccaac tgctcttgac 2017
 aattgttaac ccgctaggct cctttgggta gagaagccag tccttcagcc tccaattggg 2077
 gtcagtactt aggaagacca cagctagatg gacaaacagc attgggaggc cttagccctg 2137
 ctctctcga ttccatcctg tagagaacag gagtcaggag ccgctggcag gagacagcat 2197
 gtcacccagg actctgccg tgcagaatat gaacaacgcc atgttcttgc agaaaacgct 2257
 tagcctgagt ttcataggag gtaattacca gacaactgca gaatgtagaa cactgagcag 2317
 gacaactgac ctgtctcctt cacatagtcc atatcaccac aaatcacaca aaaaaagga 2377
 gaagagatat tttgggttca aaaaaagtaa aaagataata tagctgcatt tctttagtta 2437
 ttttgaaccc caaatatttc ctcatctttt tgttgttgc attgatggtg gtgacatgga 2497
 cttgtttata gaggacaggc cagctgtctg gctcaatgat ctacattctg aagttgtctg 2557
 aaaatgtctt catgattaaa ttcagcctaa acgttttgcc gggaacactg cagaagacaa 2617
 tgctgtgagt ttc 2630

<210> 183

<211> 502

<212> PRT

<213> Homo sapiens

<223> DKFZp434D0623; Genbank AF379626; cDNA clone AC03

<400> 183

Gln	Asp	Pro	Ser	Cys	Pro	Arg	Leu	Ser	Arg	Glu	Leu	Leu	Asp	Glu	Lys
1				5					10					15	

Glu	Pro	Glu	Val	Leu	Gln	Asp	Ser	Leu	Asp	Arg	Cys	Tyr	Ser	Thr	Pro
			20						25				30		

Ser	Gly	Tyr	Leu	Glu	Leu	Pro	Asp	Leu	Gly	Gln	Pro	Tyr	Arg	Ser	Ala
			35					40					45		

Val	Tyr	Ser	Leu	Glu	Glu	Gln	Tyr	Leu	Gly	Leu	Ala	Leu	Asp	Val	Asp

50		55		60	
Arg Ile Lys Lys Asp Gln Glu Glu Glu Glu Asp Gln Gly Pro Pro Cys					
65		70		75	80
Pro Arg Leu Ser Arg Glu Leu Leu Glu Ala Val Glu Pro Glu Val Leu					
	85		90		95
Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Ser Cys Leu Glu					
	100		105		110
Gln Pro Asp Ser Cys Leu Pro Tyr Gly Ser Ser Phe Tyr Ala Leu Glu					
	115		120		125
Glu Lys His Val Gly Phe Ser Leu Asp Val Gly Glu Ile Glu Lys Lys					
	130		135		140
Gly Lys Gly Lys Lys Arg Arg Gly Arg Arg Ser Met Lys Lys Arg Arg					
145		150		155	160
Arg Arg Gly Arg Lys Glu Gly Glu Glu Asp Gln Asn Pro Pro Cys Pro					
	165		170		175
Arg Leu Asn Arg Glu Leu Leu Asp Glu Lys Gly Pro Glu Val Leu Gln					
	180		185		190
Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Tyr Leu Glu Leu					
	195		200		205
Thr Asp Ser Cys Gln Pro Tyr Arg Ser Ala Phe Tyr Ile Leu Glu Gln					
	210		215		220
Gln Arg Val Gly Trp Ala Leu Asp Met Asp Glu Ile Glu Lys Tyr Gln					
225		230		235	240
Glu Val Glu Glu Asp Gln Asp Pro Ser Cys Pro Arg Leu Ser Arg Glu					
	245		250		255
Leu Leu Asp Glu Lys Glu Pro Glu Val Leu Gln Asp Ser Leu Asp Arg					
	260		265		270
Cys Tyr Ser Thr Pro Ser Gly Tyr Leu Glu Leu Pro Asp Leu Gly Gln					
	275		280		285
Pro Tyr Arg Ser Ala Val Tyr Ser Leu Glu Glu Gln Tyr Leu Gly Leu					
	290		295		300
Ala Leu Asp Val Asp Arg Ile Lys Lys Asp Gln Glu Glu Glu Glu Asp					

<220>
<223> DKFZp434G2022

<220>

<221> CDS

<222> (3)..(2903)

<400> 184

```

aa gaa aag gaa gtc cct gag gac tca ctg gag gaa tgt gcc atc act      47
   Glu Lys Glu Val Pro Glu Asp Ser Leu Glu Glu Cys Ala Ile Thr
      1              5              10              15

tgt tca aat agc cat ggc cct tat tac tcc aac cag cca cat agg aaa      95
   Cys Ser Asn Ser His Gly Pro Tyr Tyr Ser Asn Gln Pro His Arg Lys
                20              25              30

acc aaa atc aca ttt gag gaa gac aaa gtc gac tca act ctc att ggc      143
   Thr Lys Ile Thr Phe Glu Glu Asp Lys Val Asp Ser Thr Leu Ile Gly
                35              40              45

tca tcc tct cat gtt gaa tgg gag gat gct gta cac att atc cca gaa      191
   Ser Ser Ser His Val Glu Trp Glu Asp Ala Val His Ile Ile Pro Glu
                50              55              60

aat gaa agt gat gat gag gaa gag gaa gaa aaa ggg cca gtg tct ccc      239
   Asn Glu Ser Asp Asp Glu Glu Glu Glu Glu Lys Gly Pro Val Ser Pro
                65              70              75

agg aat ctg cag gag tct gaa gag gag gaa gtc ccc cag gag tcc tgg      287
   Arg Asn Leu Gln Glu Ser Glu Glu Glu Glu Val Pro Gln Glu Ser Trp
      80              85              90              95

gat gaa ggt tat tcg act ctc tca att cct cct gaa atg ttg gcc tcg      335
   Asp Glu Gly Tyr Ser Thr Leu Ser Ile Pro Pro Glu Met Leu Ala Ser
                100              105              110

tac cag tct tac agc ggc aca ttt cac tca tta gag gaa cag caa gtc      383
   Tyr Gln Ser Tyr Ser Gly Thr Phe His Ser Leu Glu Glu Gln Gln Val
                115              120              125

tgc atg gct gtt gac ata ggc gga cat cgg tgg gat caa gtg aaa aag      431
   Cys Met Ala Val Asp Ile Gly Gly His Arg Trp Asp Gln Val Lys Lys
                130              135              140

gag gac caa gag gca aca ggt ccc agg ctc agc agg gag ctg ctg gat      479
   Glu Asp Gln Glu Ala Thr Gly Pro Arg Leu Ser Arg Glu Leu Leu Asp
                145              150              155

gag aaa ggg cct gaa gtc ttg cag gac tca ctg gat aga tgt tat tca      527
   Glu Lys Gly Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser
      160              165              170              175

```

act cct tca ggt tat ctt gaa ctg act gac tca tgc cag ccc tac aga	575
Thr Pro Ser Gly Tyr Leu Glu Leu Thr Asp Ser Cys Gln Pro Tyr Arg	
180 185 190	
agt gcc ttt tac ata ttg gag caa cag cgt gtt ggc tgg gct ctt gac	623
Ser Ala Phe Tyr Ile Leu Glu Gln Gln Arg Val Gly Trp Ala Leu Asp	
195 200 205	
atg gat gaa att gaa aag tac caa gaa gtg gaa gaa gac caa gac cca	671
Met Asp Glu Ile Glu Lys Tyr Gln Glu Val Glu Glu Asp Gln Asp Pro	
210 215 220	
tca tgc ccc agg ctc agc agg gag ctg ctg gat gag aaa gag cct gaa	719
Ser Cys Pro Arg Leu Ser Arg Glu Leu Leu Asp Glu Lys Glu Pro Glu	
225 230 235	
gtc ttg cag gac tcc ctg gat aga tgt tat tcg act cct tca ggt tat	767
Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Tyr	
240 245 250 255	
ctt gaa ctg cct gac tta ggc cag ccc tac aga agt gct gtt tac tca	815
Leu Glu Leu Pro Asp Leu Gly Gln Pro Tyr Arg Ser Ala Val Tyr Ser	
260 265 270	
ttg gag gaa cag tac ctt ggc ttg gct ctt gac gtg gac aga att aaa	863
Leu Glu Glu Gln Tyr Leu Gly Leu Ala Leu Asp Val Asp Arg Ile Lys	
275 280 285	
aag gac caa gaa gag gaa gaa gac caa ggc cca cca tgc ccc agg ctc	911
Lys Asp Gln Glu Glu Glu Glu Asp Gln Gly Pro Pro Cys Pro Arg Leu	
290 295 300	
agc agg gag ctg ctg gag gca gta gag cct gaa gtc ttg cag gac tca	959
Ser Arg Glu Leu Leu Glu Ala Val Glu Pro Glu Val Leu Gln Asp Ser	
305 310 315	
ctg gat aga tgt tat tca act cct tcc agt tgt ctt gaa cag cct gac	1007
Leu Asp Arg Cys Tyr Ser Thr Pro Ser Ser Cys Leu Glu Gln Pro Asp	
320 325 330 335	
tcc tgc ctg ccc tat gga agt tcc ttt tat gca ttg gag gaa aaa cat	1055
Ser Cys Leu Pro Tyr Gly Ser Ser Phe Tyr Ala Leu Glu Glu Lys His	
340 345 350	
gtt ggc ttt tct ctt gac gtg gga gaa att gaa aag aag ggg aag ggg	1103
Val Gly Phe Ser Leu Asp Val Gly Glu Ile Glu Lys Lys Gly Lys Gly	
355 360 365	

aag aaa aga agg gga aga aga tca acg aag aaa aga agg aga agg gga	1151
Lys Lys Arg Arg Gly Arg Arg Ser Thr Lys Lys Arg Arg Arg Arg Gly	
370 375 380	
aga aaa gaa ggg gaa gaa gat caa aac cca cca tgc ccc agg ctc agc	1199
Arg Lys Glu Gly Glu Glu Asp Gln Asn Pro Pro Cys Pro Arg Leu Ser	
385 390 395	
agg gag ctg ctg gat gag aaa ggg cct gaa gtc ttg cag gac tca ctg	1247
Arg Glu Leu Leu Asp Glu Lys Gly Pro Glu Val Leu Gln Asp Ser Leu	
400 405 410 415	
gat aga tgt tat tca act cct tca ggt tat ctt gaa ctg act gac tca	1295
Asp Arg Cys Tyr Ser Thr Pro Ser Gly Tyr Leu Glu Leu Thr Asp Ser	
420 425 430	
tgc cag ccc tac aga agt gcc ttt tac ata ttg gag caa cag cgt gtt	1343
Cys Gln Pro Tyr Arg Ser Ala Phe Tyr Ile Leu Glu Gln Gln Arg Val	
435 440 445	
ggc tgg gct ctt gac atg gat gaa att gaa aag tac caa gaa gtg gaa	1391
Gly Trp Ala Leu Asp Met Asp Glu Ile Glu Lys Tyr Gln Glu Val Glu	
450 455 460	
gaa gac caa gac cca tca tgc ccc agg ctc agc agg gag ctg ctg gat	1439
Glu Asp Gln Asp Pro Ser Cys Pro Arg Leu Ser Arg Glu Leu Leu Asp	
465 470 475	
gag aaa gag cct gaa gtc ttg cag gac tcc ctg gat aga tgt tat tcg	1487
Glu Lys Glu Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser	
480 485 490 495	
act cct tca ggt tat ctt gaa ctg cct gac tta ggc cag ccc tac aga	1535
Thr Pro Ser Gly Tyr Leu Glu Leu Pro Asp Leu Gly Gln Pro Tyr Arg	
500 505 510	
agt gct gtt tac tca ttg gag gaa cag tac ctt ggc ttg gct ctt gac	1583
Ser Ala Val Tyr Ser Leu Glu Glu Gln Tyr Leu Gly Leu Ala Leu Asp	
515 520 525	
gtg gac aga att aaa aag gac cag gaa gag gaa gaa gac caa ggc cca	1631
Val Asp Arg Ile Lys Lys Asp Gln Glu Glu Glu Glu Asp Gln Gly Pro	
530 535 540	
cca tgc ccc agg ctc agc agg gag ctg ctg gag gca gta gag cct gaa	1679
Pro Cys Pro Arg Leu Ser Arg Glu Leu Leu Glu Ala Val Glu Pro Glu	
545 550 555	

gtc ttg cag gac tca ctg gat aga tgt tat tca act cct tcc agt tgt	1727
Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Ser Cys	
560 565 570 575	
ctt gaa cag cct gac tcc tgc ctg ccc tat gga agt tcc ttt tat gca	1775
Leu Glu Gln Pro Asp Ser Cys Leu Pro Tyr Gly Ser Ser Phe Tyr Ala	
580 585 590	
ttg gag gaa aaa cat gtt ggc ttt tct ctt gac gtg gga gaa att gaa	1823
Leu Glu Glu Lys His Val Gly Phe Ser Leu Asp Val Gly Glu Ile Glu	
595 600 605	
aag aag ggg aag ggg aag aaa aga agg gga aga aga tca acg aag aaa	1871
Lys Lys Gly Lys Gly Lys Lys Arg Arg Gly Arg Arg Ser Thr Lys Lys	
610 615 620	
aga agg aga agg gga aga aaa gaa ggg gaa gaa gat caa aac cca cca	1919
Arg Arg Arg Arg Gly Arg Lys Glu Gly Glu Glu Asp Gln Asn Pro Pro	
625 630 635	
tgc ccc agg ctc agc agg gag ctg ctg gat gag aaa ggg cct gaa gtc	1967
Cys Pro Arg Leu Ser Arg Glu Leu Leu Asp Glu Lys Gly Pro Glu Val	
640 645 650 655	
ttg cag gac tca ctg gat aga tgt tat tca act cct tca ggt tat ctt	2015
Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Tyr Leu	
660 665 670	
gaa ctg act gac tca tgc cag ccc tac aga agt gcc ttt tac ata ttg	2063
Glu Leu Thr Asp Ser Cys Gln Pro Tyr Arg Ser Ala Phe Tyr Ile Leu	
675 680 685	
gag caa cag cgt gtt ggc tgg gct ctt gac atg gat gaa att gaa aag	2111
Glu Gln Gln Arg Val Gly Trp Ala Leu Asp Met Asp Glu Ile Glu Lys	
690 695 700	
tac caa gaa gtg gaa gaa gac caa gac cca tca tgc ccc agg ctc agc	2159
Tyr Gln Glu Val Glu Glu Asp Gln Asp Pro Ser Cys Pro Arg Leu Ser	
705 710 715	
agg gag ctg ctg gat gag aaa gag cct gaa gtc ttg cag gac tcc ctg	2207
Arg Glu Leu Leu Asp Glu Lys Glu Pro Glu Val Leu Gln Asp Ser Leu	
720 725 730 735	
gat aga tgt tat tcg act cct tca ggt tat ctt gaa ctg cct gac tta	2255
Asp Arg Cys Tyr Ser Thr Pro Ser Gly Tyr Leu Glu Leu Pro Asp Leu	
740 745 750	

ggc cag ccc tac aga agt gct gtt tac tca ttg gag gaa cag tac ctt	2303
Gly Gln Pro Tyr Arg Ser Ala Val Tyr Ser Leu Glu Glu Gln Tyr Leu	
755 760 765	
ggc ttg gct ctt gac gtg gac aga att aaa aag gac cag gaa gag gaa	2351
Gly Leu Ala Leu Asp Val Asp Arg Ile Lys Lys Asp Gln Glu Glu Glu	
770 775 780	
gaa gac caa ggc cca cca tgc ccc agg ctc agc agg gag ctg ctg gag	2399
Glu Asp Gln Gly Pro Pro Cys Pro Arg Leu Ser Arg Glu Leu Leu Glu	
785 790 795	
gca gta gag cct gaa gtc ttg cag gac tca ctg gat aga tgt tat tca	2447
Ala Val Glu Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser	
800 805 810 815	
act cct tcc agt tgt ctt gaa cag cct gac tcc tgc ctg ccc tat gga	2495
Thr Pro Ser Ser Cys Leu Glu Gln Pro Asp Ser Cys Leu Pro Tyr Gly	
820 825 830	
agt tcc ttt tat gca ttg gag gaa aaa cat gtt ggc ttt tct ctt gac	2543
Ser Ser Phe Tyr Ala Leu Glu Glu Lys His Val Gly Phe Ser Leu Asp	
835 840 845	
gtg gga gaa att gaa aag aag ggg aag ggg aag aaa aga agg gga aga	2591
Val Gly Glu Ile Glu Lys Lys Gly Lys Gly Lys Lys Arg Arg Gly Arg	
850 855 860	
aga tca acg aag aaa aga agg aga agg gga aga aaa gaa ggg gaa gaa	2639
Arg Ser Thr Lys Lys Arg Arg Arg Arg Gly Arg Lys Glu Gly Glu Glu	
865 870 875	
gat caa aac cca cca tgc ccc agg ctc agc ggt gtg ctg atg gaa gtg	2687
Asp Gln Asn Pro Pro Cys Pro Arg Leu Ser Gly Val Leu Met Glu Val	
880 885 890 895	
gaa gag cct gaa atc ttg cag gac tca ctg gat aga tgt tat tcg act	2735
Glu Glu Pro Glu Ile Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr	
900 905 910	
ccg tca atg ttc ttt gaa cta cct gac tca ttc cag cac tac aga agt	2783
Pro Ser Met Phe Phe Glu Leu Pro Asp Ser Phe Gln His Tyr Arg Ser	
915 920 925	
gtg ttt tac tca ttt gag gaa cag cac atc agc ttc gcc ctt gac gtg	2831
Val Phe Tyr Ser Phe Glu Glu Gln His Ile Ser Phe Ala Leu Asp Val	
930 935 940	

gac aat agg ttt ott act ttg atg gga aca agt ctc cac ctg gtc ttc 2879
 Asp Asn Arg Phe Leu Thr Leu Met Gly Thr Ser Leu His Leu Val Phe
 945 950 955

cag atg gga gtc ata ttc cca cag taagcagccc ttactaagcc gagagatgtc 2933
 Gln Met Gly Val Ile Phe Pro Gln
 960 965

attcctgcag gcaggaccta taggcacatg aagatttgaa tgaaactata gttccatttg 2993
 gaagcccaga cataggatgg gtcagtgggc atggctctat tcctattctc agaccatgcc 3053
 agtggcaacc tgtgctcagt ctgaagacaa tggaccaag ttaggtgtga cacgttcaca 3113
 taactgtgca gcacatgccg ggagtgatca gtcagacatt tcaatttgaa ccacgtatct 3173
 ctgggtagct acaaagttcc tcagggattt cattttgcag gcatgtctct gagcttctat 3233
 acctgctcaa ggtcagtgtc atctttgtgt ttagctcatc caaagggtt accctgggtt 3293
 caatgaacct aacctattc tttgtatctt cagtgttgaa ttgttttagc tgatccatct 3353
 ttaacacagg agggatcctt ggctgaggat tgtatttcag aaccaccaac tgctcttgac 3413
 aattgttaac cgcctaggct cctttgggta gagaagccac agtccttcag cctccaattg 3473
 gtgtcagtac ttaggaagac cacagctaga tggacaaaca gcattgggag gccttagccc 3533
 tgctcctctc gattccatcc tgtagagaac aggagtcagg agccgctggc aggagacagc 3593
 atgtcaccca ggactctgcc ggtgcagaat atgaacaacg ccatgttctt gcagaaaacg 3653
 cttagcctga gtttcatagg aggtaatcac cagacaactg cggaatgtag agcactgagc 3713
 aggacagctg gcctgtctcc ttcacatagt ccatgtcaac cacaatcac acaacaaaaa 3773
 ggagaggaga tattttgggt tcaaaaaag taaaaagata atgtagctgc atttctttgg 3833
 ttattttggg ccccaaatat ttctcatct tttgtgtgt gtcattgatg gtggtgacat 3893
 ggacttgttt atagaggaca ggtcagctgt ctggctcagt gatctacatt ctgaagttgt 3953
 ctgaaaatgt cttcatgatt aaattcagcc taaacgtttt gccgggaaca ctgcagagac 4013
 aatgctgtga gtttccaacc ttagcccatc tgcgggcaga gaaggctag tttgtccatc 4073
 agcattatca tgatatcagg actggttact tggttaagga ggggtctagg agatctgtcc 4133

ctttttagaga caccttactt ataatgaagt atttgggagg gtggttttca aaagtagaaa 4193
 tgtcctgtat tccgatgac atcctgtaaa cattttatca tttattaatc atccctgcct 4253
 gtgtctatta ttatattcat atctctacgc tggaaacttt ctgcctcaat gtttactgtg 4313
 cctttgtttt tgctagtgtg tgttggtgaa aaaaaaaaca ttctctgcct gagttttaat 4373
 ttttgtccaa agttatttta atctatacaa ttaaaagctt ttgcctatca aaaaaaaaaa 4433
 aaaaaaa 4440

<210> 185

<211> 967

<212> PRT

<213> Homo sapiens

<223> DKFZp434G2022

<400> 185

Glu	Lys	Glu	Val	Pro	Glu	Asp	Ser	Leu	Glu	Glu	Cys	Ala	Ile	Thr	Cys
1				5					10					15	
Ser	Asn	Ser	His	Gly	Pro	Tyr	Tyr	Ser	Asn	Gln	Pro	His	Arg	Lys	Thr
			20					25					30		
Lys	Ile	Thr	Phe	Glu	Glu	Asp	Lys	Val	Asp	Ser	Thr	Leu	Ile	Gly	Ser
		35					40					45			
Ser	Ser	His	Val	Glu	Trp	Glu	Asp	Ala	Val	His	Ile	Ile	Pro	Glu	Asn
	50					55				60					
Glu	Ser	Asp	Asp	Glu	Glu	Glu	Glu	Glu	Lys	Gly	Pro	Val	Ser	Pro	Arg
65				70					75					80	
Asn	Leu	Gln	Glu	Ser	Glu	Glu	Glu	Glu	Val	Pro	Gln	Glu	Ser	Trp	Asp
			85					90						95	
Glu	Gly	Tyr	Ser	Thr	Leu	Ser	Ile	Pro	Pro	Glu	Met	Leu	Ala	Ser	Tyr
			100					105					110		
Gln	Ser	Tyr	Ser	Gly	Thr	Phe	His	Ser	Leu	Glu	Glu	Gln	Gln	Val	Cys
		115					120					125			
Met	Ala	Val	Asp	Ile	Gly	Gly	His	Arg	Trp	Asp	Gln	Val	Lys	Lys	Glu
	130						135								140

Asp	Gln	Glu	Ala	Thr	Gly	Pro	Arg	Leu	Ser	Arg	Glu	Leu	Leu	Asp	Glu	145	150	155	160
Lys	Gly	Pro	Glu	Val	Leu	Gln	Asp	Ser	Leu	Asp	Arg	Cys	Tyr	Ser	Thr	165	170	175	
Pro	Ser	Gly	Tyr	Leu	Glu	Leu	Thr	Asp	Ser	Cys	Gln	Pro	Tyr	Arg	Ser	180	185	190	
Ala	Phe	Tyr	Ile	Leu	Glu	Gln	Gln	Arg	Val	Gly	Trp	Ala	Leu	Asp	Met	195	200	205	
Asp	Glu	Ile	Glu	Lys	Tyr	Gln	Glu	Val	Glu	Glu	Asp	Gln	Asp	Pro	Ser	210	215	220	
Cys	Pro	Arg	Leu	Ser	Arg	Glu	Leu	Leu	Asp	Glu	Lys	Glu	Pro	Glu	Val	225	230	235	240
Leu	Gln	Asp	Ser	Leu	Asp	Arg	Cys	Tyr	Ser	Thr	Pro	Ser	Gly	Tyr	Leu	245	250	255	
Glu	Leu	Pro	Asp	Leu	Gly	Gln	Pro	Tyr	Arg	Ser	Ala	Val	Tyr	Ser	Leu	260	265	270	
Glu	Glu	Gln	Tyr	Leu	Gly	Leu	Ala	Leu	Asp	Val	Asp	Arg	Ile	Lys	Lys	275	280	285	
Asp	Gln	Glu	Glu	Glu	Glu	Asp	Gln	Gly	Pro	Pro	Cys	Pro	Arg	Leu	Ser	290	295	300	
Arg	Glu	Leu	Leu	Glu	Ala	Val	Glu	Pro	Glu	Val	Leu	Gln	Asp	Ser	Leu	305	310	315	320
Asp	Arg	Cys	Tyr	Ser	Thr	Pro	Ser	Ser	Cys	Leu	Glu	Gln	Pro	Asp	Ser	325	330	335	
Cys	Leu	Pro	Tyr	Gly	Ser	Ser	Phe	Tyr	Ala	Leu	Glu	Glu	Lys	His	Val	340	345	350	
Gly	Phe	Ser	Leu	Asp	Val	Gly	Glu	Ile	Glu	Lys	Lys	Gly	Lys	Gly	Lys	355	360	365	
Lys	Arg	Arg	Gly	Arg	Arg	Ser	Thr	Lys	Lys	Arg	Arg	Arg	Arg	Gly	Arg	370	375	380	
Lys	Glu	Gly	Glu	Glu	Asp	Gln	Asn	Pro	Pro	Cys	Pro	Arg	Leu	Ser	Arg	385	390	395	400

Glu Leu Leu Asp Glu Lys Gly Pro Glu Val Leu Gln Asp Ser Leu Asp
 405 410 415
 Arg Cys Tyr Ser Thr Pro Ser Gly Tyr Leu Glu Leu Thr Asp Ser Cys
 420 425 430
 Gln Pro Tyr Arg Ser Ala Phe Tyr Ile Leu Glu Gln Gln Arg Val Gly
 435 440 445
 Trp Ala Leu Asp Met Asp Glu Ile Glu Lys Tyr Gln Glu Val Glu Glu
 450 455 460
 Asp Gln Asp Pro Ser Cys Pro Arg Leu Ser Arg Glu Leu Leu Asp Glu
 465 470 475 480
 Lys Glu Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr
 485 490 495
 Pro Ser Gly Tyr Leu Glu Leu Pro Asp Leu Gly Gln Pro Tyr Arg Ser
 500 505 510
 Ala Val Tyr Ser Leu Glu Glu Gln Tyr Leu Gly Leu Ala Leu Asp Val
 515 520 525
 Asp Arg Ile Lys Lys Asp Gln Glu Glu Glu Glu Asp Gln Gly Pro Pro
 530 535 540
 Cys Pro Arg Leu Ser Arg Glu Leu Leu Glu Ala Val Glu Pro Glu Val
 545 550 555 560
 Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Ser Cys Leu
 565 570 575
 Glu Gln Pro Asp Ser Cys Leu Pro Tyr Gly Ser Ser Phe Tyr Ala Leu
 580 585 590
 Glu Glu Lys His Val Gly Phe Ser Leu Asp Val Gly Glu Ile Glu Lys
 595 600 605
 Lys Gly Lys Gly Lys Lys Arg Arg Gly Arg Arg Ser Thr Lys Lys Arg
 610 615 620
 Arg Arg Arg Gly Arg Lys Glu Gly Glu Glu Asp Gln Asn Pro Pro Cys
 625 630 635 640
 Pro Arg Leu Ser Arg Glu Leu Leu Asp Glu Lys Gly Pro Glu Val Leu
 645 650 655

Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Tyr Leu Glu
 660 665 670
 Leu Thr Asp Ser Cys Gln Pro Tyr Arg Ser Ala Phe Tyr Ile Leu Glu
 675 680 685
 Gln Gln Arg Val Gly Trp Ala Leu Asp Met Asp Glu Ile Glu Lys Tyr
 690 695 700
 Gln Glu Val Glu Glu Asp Gln Asp Pro Ser Cys Pro Arg Leu Ser Arg
 705 710 715 720
 Glu Leu Leu Asp Glu Lys Glu Pro Glu Val Leu Gln Asp Ser Leu Asp
 725 730 735
 Arg Cys Tyr Ser Thr Pro Ser Gly Tyr Leu Glu Leu Pro Asp Leu Gly
 740 745 750
 Gln Pro Tyr Arg Ser Ala Val Tyr Ser Leu Glu Glu Gln Tyr Leu Gly
 755 760 765
 Leu Ala Leu Asp Val Asp Arg Ile Lys Lys Asp Gln Glu Glu Glu Glu
 770 775 780
 Asp Gln Gly Pro Pro Cys Pro Arg Leu Ser Arg Glu Leu Leu Glu Ala
 785 790 795 800
 Val Glu Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr
 805 810 815
 Pro Ser Ser Cys Leu Glu Gln Pro Asp Ser Cys Leu Pro Tyr Gly Ser
 820 825 830
 Ser Phe Tyr Ala Leu Glu Glu Lys His Val Gly Phe Ser Leu Asp Val
 835 840 845
 Gly Glu Ile Glu Lys Lys Gly Lys Gly Lys Lys Arg Arg Gly Arg Arg
 850 855 860
 Ser Thr Lys Lys Arg Arg Arg Arg Gly Arg Lys Glu Gly Glu Glu Asp
 865 870 875 880
 Gln Asn Pro Pro Cys Pro Arg Leu Ser Gly Val Leu Met Glu Val Glu
 885 890 895
 Glu Pro Glu Ile Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro
 900 905 910

Ser Met Phe Phe Glu Leu Pro Asp Ser Phe Gln His Tyr Arg Ser Val
 915 920 925

Phe Tyr Ser Phe Glu Glu Gln His Ile Ser Phe Ala Leu Asp Val Asp
 930 935 940

Asn Arg Phe Leu Thr Leu Met Gly Thr Ser Leu His Leu Val Phe Gln
 945 950 955 960

Met Gly Val Ile Phe Pro Gln
 965

<210> 186

<211> 2647

<212> DNA

<213> Homo sapiens

<220>

<223> DKFZp434M0628; Genbank AF379622; cDNA clone AB18

<220>

<221> CDS

<222> (1)..(1074)

<400> 186

```

ggg aag ggg aag aaa aga agg gga aga aga tca atg aag aaa aga agg      48
Gly Lys Gly Lys Lys Arg Arg Gly Arg Arg Ser Met Lys Lys Arg Arg
  1             5             10             15

aga agg gga aga aaa gaa ggg gaa gaa gat caa aac cca cca tgc ccc      96
Arg Arg Gly Arg Lys Glu Gly Glu Glu Asp Gln Asn Pro Pro Cys Pro
          20             25             30

agg ctc aac agg gag ctg ctg gat gag aaa ggg cct gaa gtc ttg cag     144
Arg Leu Asn Arg Glu Leu Leu Asp Glu Lys Gly Pro Glu Val Leu Gln
          35             40             45

gac tca ctg gat aga tgt tat tca act cct tca ggt tat ctt gaa ctg     192
Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Tyr Leu Glu Leu
          50             55             60

act gac tca tgc cag ccc tac aga agt gcc ttt tac ata ttg gag caa     240
Thr Asp Ser Cys Gln Pro Tyr Arg Ser Ala Phe Tyr Ile Leu Glu Gln
          65             70             75             80

cag cgt gtt ggc tgg gct ctt gac atg gat gaa att gaa aag tac caa     288
```

Gln	Arg	Val	Gly	Trp	Ala	Leu	Asp	Met	Asp	Glu	Ile	Glu	Lys	Tyr	Gln	
				85					90						95	
gaa gtg gaa gaa gac caa gac cca tca tgc ccc agg ctc agc agg gag 336																
Glu	Val	Glu	Glu	Asp	Gln	Asp	Pro	Ser	Cys	Pro	Arg	Leu	Ser	Arg	Glu	
			100					105					110			
ctg ctg gat gag aaa gag cct gaa gtc ttg cag gac tca ctg gat aga 384																
Leu	Leu	Asp	Glu	Lys	Glu	Pro	Glu	Val	Leu	Gln	Asp	Ser	Leu	Asp	Arg	
			115					120					125			
tgt tat tcg act cct tca ggt tat ctt gaa ctg cct gac tta ggc cag 432																
Cys	Tyr	Ser	Thr	Pro	Ser	Gly	Tyr	Leu	Glu	Leu	Pro	Asp	Leu	Gly	Gln	
			130					135					140			
ccc tac aga agt gct gtt tac tca ttg gag gaa cag tac ctt ggc ttg 480																
Pro	Tyr	Arg	Ser	Ala	Val	Tyr	Ser	Leu	Glu	Glu	Gln	Tyr	Leu	Gly	Leu	
			145					150					155			160
gct ctt gac gtg gac aga att aaa aag gac caa gaa gag gaa gaa gac 528																
Ala	Leu	Asp	Val	Asp	Arg	Ile	Lys	Lys	Asp	Gln	Glu	Glu	Glu	Glu	Asp	
				165					170						175	
caa ggc cca cca tgc ccc agg ctc agc agg gag ctg ctg gag gca gta 576																
Gln	Gly	Pro	Pro	Cys	Pro	Arg	Leu	Ser	Arg	Glu	Leu	Leu	Glu	Ala	Val	
				180					185						190	
gag cct gaa gtc ttg cag gac tca ctg gat aga tgt tat tca act cct 624																
Glu	Pro	Glu	Val	Leu	Gln	Asp	Ser	Leu	Asp	Arg	Cys	Tyr	Ser	Thr	Pro	
			195					200							205	
tcc agt tgt ctt gaa cag cct gac tcc tgc ctg ccc tat gga agt tcc 672																
Ser	Ser	Cys	Leu	Glu	Gln	Pro	Asp	Ser	Cys	Leu	Pro	Tyr	Gly	Ser	Ser	
			210					215							220	
ttt tat gca ttg gag gaa aaa cat gtt ggc ttt tct ctt gac gtg gga 720																
Phe	Tyr	Ala	Leu	Glu	Glu	Lys	His	Val	Gly	Phe	Ser	Leu	Asp	Val	Gly	
			225					230					235			240
gaa att gaa aag aag ggg aag ggg aag aaa aga agg gga aga aga tca 768																
Glu	Ile	Glu	Lys	Lys	Gly	Lys	Gly	Lys	Lys	Arg	Arg	Gly	Arg	Arg	Ser	
				245					250						255	
atg aag aaa aga agg aga agg gga aga aaa gaa ggg gaa gaa gat caa 816																
Met	Lys	Lys	Arg	Arg	Arg	Arg	Gly	Arg	Lys	Glu	Gly	Glu	Glu	Asp	Gln	
				260					265						270	
aac cca cca tgc ccc agg ctc agc ggc atg ctg atg gaa gtg gaa gag 864																

```

Asn Pro Pro Cys Pro Arg Leu Ser Gly Met Leu Met Glu Val Glu Glu
      275                      280                      285

cct gaa gtc ttg cag gac tca ctg gat aga tgt tat tcg act ccg tca   912
Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser
      290                      295                      300

atg tac ttt gaa cta cct gac tca ttc cag cac tac aga agt gtg ttt   960
Met Tyr Phe Glu Leu Pro Asp Ser Phe Gln His Tyr Arg Ser Val Phe
305                      310                      315                      320

tac tca ttt gag gaa cag cac atc agc ttc gcc ctt gac gtg gac aat   1008
Tyr Ser Phe Glu Glu Gln His Ile Ser Phe Ala Leu Asp Val Asp Asn
      325                      330                      335

agg ttt ctt act ttg atg gga aca agt ctc cac ctg gtc ttc cag atg   1056
Arg Phe Leu Thr Leu Met Gly Thr Ser Leu His Leu Val Phe Gln Met
      340                      345                      350

gga gtc ata ttc cca cag taagcagccc ttactaagcc gagagatgtc       1104
Gly Val Ile Phe Pro Gln
      355

attcctgcag gcaggaccta taggcacgtg aagatttgaa tgaaactata gttccatttg 1164

gaagcccaga cataggatgg gtcagtgggc atggctctat tcctattctc agaccatgcc 1224

agtggcaacc tgtgctcagt ctgaagacaa tggaccaag ttaggtgtga cacgttcaca 1284

taactgtgca gcacatgccg ggagtgatca gtcagacatt ttaatttgaa ccaattatct 1344

ctgggtagct acaaagttcc tcagggattt cattttgcag tcatgtctct gagcttctat 1404

acctgctcaa ggtcagtgtc atcttttgtt ttagctcatc caaagggtgtt acctgggttt 1464

caatgaacct aacctcatc tttgtatctt cagtgttgaa ttgttttagc tgatccatct 1524

ttaacacagg agggatcctt ggctgaggat tgtatttcag aaccaccaac tgctcttgac 1584

aattgttaac ccgctaggct cctttggtta gagaagccag tccttcagcc tccaattggg 1644

gtcagtactt aggaagacca cagctagatg gacaaacagc attgggaggc cttagccctg 1704

ctcctctcga ttccatcctg tagagaacag gagtcaggag ccgctggcag gagacagcat 1764

gtcaccacagg actctgccg tgcagaatat gaacaacgcc atgttcttgc agaaaacgct 1824

tggcctgagt ttcataggag gtaattacca gacaactgca gaatgtagaa cactgagcag 1884

```

gacaactgac ctgtctcctt cacatagtc ataccacac aaatcacaca aaaaaaagga 1944
gaagagatat tttgggttca aaaaaagtaa aaagataata tagctgcatt tcttttagtta 2004
ttttgaaccc caaatatttc ctcatctttt tgttggtgtc attgatgggtg gtgacatgga 2064
cttgtttata gaggacaggt cagctgtctg gctcaatgat ctacattctg aagttgtctg 2124
aaaatgtctt catgattaaa ttcagcctaa acgttttgcc gggaacactg cagagacaat 2184
gctgtgagtt tccaacctta gcccatctgc gggcagagaa ggtctagttt gtccatcagc 2244
attatcatga tatcaggact gggtacttgg ttaaggaggg gtctaggaga tctgtccctt 2304
ttagagacac cttacttata atgaagtatt tgggaggggtg gttttcaaaa gtagaaatgt 2364
cctgtattcc gatgatcatc ctgtaaacad tttatcattt attaatacatc cctgcctgtg 2424
tctattatta tattcatatc tctacgttg aaactttctg cctcaatgtt tactgtgcct 2484
ttgtttttgc tagtgtgtgt tgttgaaaaa aaaaacattc tctgcctgag ttttaatttt 2544
tgtccaaagt tattttaatc tatacaatta aaagcttttg cctatcaaaa aaaaaaaaaa 2604
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 2647

<210> 187

<211> 358

<212> PRT

<213> Homo sapiens

<223> DKFZp434M0628; Genbank AF379622; cDNA clone AB18

<400> 187

Gly Lys Gly Lys Lys Arg Arg Gly Arg Arg Ser Met Lys Lys Arg Arg
1 5 10 15

Arg Arg Gly Arg Lys Glu Gly Glu Glu Asp Gln Asn Pro Pro Cys Pro
20 25 30

Arg Leu Asn Arg Glu Leu Leu Asp Glu Lys Gly Pro Glu Val Leu Gln
35 40 45

Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Tyr Leu Glu Leu
50 55 60

Thr Asp Ser Cys Gln Pro Tyr Arg Ser Ala Phe Tyr Ile Leu Glu Gln

65					70						75				80
Gln	Arg	Val	Gly	Trp	Ala	Leu	Asp	Met	Asp	Glu	Ile	Glu	Lys	Tyr	Gln
				85					90					95	
Glu	Val	Glu	Glu	Asp	Gln	Asp	Pro	Ser	Cys	Pro	Arg	Leu	Ser	Arg	Glu
			100					105					110		
Leu	Leu	Asp	Glu	Lys	Glu	Pro	Glu	Val	Leu	Gln	Asp	Ser	Leu	Asp	Arg
			115					120					125		
Cys	Tyr	Ser	Thr	Pro	Ser	Gly	Tyr	Leu	Glu	Leu	Pro	Asp	Leu	Gly	Gln
			130					135					140		
Pro	Tyr	Arg	Ser	Ala	Val	Tyr	Ser	Leu	Glu	Glu	Gln	Tyr	Leu	Gly	Leu
					150					155					160
Ala	Leu	Asp	Val	Asp	Arg	Ile	Lys	Lys	Asp	Gln	Glu	Glu	Glu	Glu	Asp
					165					170					175
Gln	Gly	Pro	Pro	Cys	Pro	Arg	Leu	Ser	Arg	Glu	Leu	Leu	Glu	Ala	Val
					180					185				190	
Glu	Pro	Glu	Val	Leu	Gln	Asp	Ser	Leu	Asp	Arg	Cys	Tyr	Ser	Thr	Pro
					195					200				205	
Ser	Ser	Cys	Leu	Glu	Gln	Pro	Asp	Ser	Cys	Leu	Pro	Tyr	Gly	Ser	Ser
								215					220		
Phe	Tyr	Ala	Leu	Glu	Glu	Lys	His	Val	Gly	Phe	Ser	Leu	Asp	Val	Gly
						230				235					240
Glu	Ile	Glu	Lys	Lys	Gly	Lys	Gly	Lys	Lys	Arg	Arg	Gly	Arg	Arg	Ser
					245					250				255	
Met	Lys	Lys	Arg	Arg	Arg	Arg	Gly	Arg	Lys	Glu	Gly	Glu	Glu	Asp	Gln
					260					265				270	
Asn	Pro	Pro	Cys	Pro	Arg	Leu	Ser	Gly	Met	Leu	Met	Glu	Val	Glu	Glu
					275					280				285	
Pro	Glu	Val	Leu	Gln	Asp	Ser	Leu	Asp	Arg	Cys	Tyr	Ser	Thr	Pro	Ser
								295				300			
Met	Tyr	Phe	Glu	Leu	Pro	Asp	Ser	Phe	Gln	His	Tyr	Arg	Ser	Val	Phe
					310					315					320
Tyr	Ser	Phe	Glu	Glu	Gln	His	Ile	Ser	Phe	Ala	Leu	Asp	Val	Asp	Asn

```

          325              330              335
Arg Phe Leu Thr Leu Met Gly Thr Ser Leu His Leu Val Phe Gln Met
          340              345              350

Gly Val Ile Phe Pro Gln
          355

<210> 188
<211> 2982
<212> DNA
<213> Homo sapiens

<220>
<223> DKFZp434J205; Genbank AF379616; cDNA clone AB06

<220>
<221> CDS
<222> (152)..(1411)

<400> 188
ccaacatgaa ggcaataatt tgttacctca ttaatggatc tctcctttta ctttttcaac 60

cacttcctta tgctaccat gaaacctagt tggggctctg ttgtgtotga tttcccttg 120

cttattcttt acttttttct ccttttccag g ctc agc agg gag ctg ctg gag      172
                        Leu Ser Arg Glu Leu Leu Glu
                        1              5

gca gta gag cct gaa gtc ttg cag gac tca ctg gat aga tgt tat tca      220
Ala Val Glu Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser
          10              15              20

act cct tcc agt tgt ctt gaa cag cct gac tcc tgc ctg ccc tat gga      268
Thr Pro Ser Ser Cys Leu Glu Gln Pro Asp Ser Cys Leu Pro Tyr Gly
          25              30              35

agt tcc ttt tat gca ttg gag gaa aaa cat gtt ggc ttt tct ctt gac      316
Ser Ser Phe Tyr Ala Leu Glu Glu Lys His Val Gly Phe Ser Leu Asp
          40              45              50              55

gtg gga gaa att gaa aag aag ggg aag ggg aag aaa aga agg gga aga      364
Val Gly Glu Ile Glu Lys Lys Gly Lys Gly Lys Lys Arg Arg Gly Arg
          60              65              70

aga tca acg aag aaa aga agg aga agg gga aga aaa gaa ggg gaa gaa      412

```

Arg	Ser	Thr	Lys	Lys	Arg	Arg	Arg	Arg	Gly	Arg	Lys	Glu	Gly	Glu	Glu		
			75					80					85				
gat	caa	aac	cca	cca	tgc	ccc	agg	ctc	agc	agg	gag	ctg	ctg	gat	gag	460	
Asp	Gln	Asn	Pro	Pro	Cys	Pro	Arg	Leu	Ser	Arg	Glu	Leu	Leu	Asp	Glu		
			90				95					100					
aaa	ggg	cct	gaa	gtc	ttg	cag	gac	tca	ctg	gat	aga	tgt	tat	tca	act	508	
Lys	Gly	Pro	Glu	Val	Leu	Gln	Asp	Ser	Leu	Asp	Arg	Cys	Tyr	Ser	Thr		
	105					110					115						
cct	tca	ggt	tat	ctt	gaa	ctg	act	gac	tca	tgc	cag	ccc	tac	aga	agt	556	
Pro	Ser	Gly	Tyr	Leu	Glu	Leu	Thr	Asp	Ser	Cys	Gln	Pro	Tyr	Arg	Ser		
120					125				130					135			
gcc	ttt	tac	ata	ttg	gag	caa	cag	cgt	gtt	ggc	tgg	gct	ctt	gac	atg	604	
Ala	Phe	Tyr	Ile	Leu	Glu	Gln	Gln	Arg	Val	Gly	Trp	Ala	Leu	Asp	Met		
			140					145					150				
gat	gaa	att	gaa	aag	tac	caa	gaa	gtg	gaa	gaa	gac	caa	gac	cca	tca	652	
Asp	Glu	Ile	Glu	Lys	Tyr	Gln	Glu	Val	Glu	Glu	Asp	Gln	Asp	Pro	Ser		
			155				160					165					
tgc	ccc	agg	ctc	agc	agg	gag	ctg	ctg	gat	gag	aaa	gag	cct	gaa	gtc	700	
Cys	Pro	Arg	Leu	Ser	Arg	Glu	Leu	Leu	Asp	Glu	Lys	Glu	Pro	Glu	Val		
			170			175						180					
ttg	cag	gac	tca	ctg	gat	aga	tgt	tat	tcg	act	cct	tca	ggt	tat	ctt	748	
Leu	Gln	Asp	Ser	Leu	Asp	Arg	Cys	Tyr	Ser	Thr	Pro	Ser	Gly	Tyr	Leu		
	185					190					195						
gaa	ctg	cct	gac	tta	ggc	cag	ccc	tac	aga	agt	gct	gtt	cac	tca	ttg	796	
Glu	Leu	Pro	Asp	Leu	Gly	Gln	Pro	Tyr	Arg	Ser	Ala	Val	His	Ser	Leu		
200				205				210				215					
gag	gaa	cag	tac	ctt	ggc	ttg	gct	ctt	gac	gtg	gac	aga	att	aaa	aag	844	
Glu	Glu	Gln	Tyr	Leu	Gly	Leu	Ala	Leu	Asp	Val	Asp	Arg	Ile	Lys	Lys		
			220					225				230					
gac	cag	gaa	gag	gaa	gaa	gac	caa	ggc	cca	cca	tgc	tcc	agg	ctc	agc	892	
Asp	Gln	Glu	Glu	Glu	Glu	Asp	Gln	Gly	Pro	Pro	Cys	Ser	Arg	Leu	Ser		
			235				240					245					
agg	gag	ctg	ctg	gag	gca	gta	gag	cct	gaa	gtc	ttg	ctg	gac	tca	ctg	940	
Arg	Glu	Leu	Leu	Glu	Ala	Val	Glu	Pro	Glu	Val	Leu	Leu	Asp	Ser	Leu		
			250				255					260					
gat	aga	tgt	tat	tca	act	cct	tcc	agt	tgt	ctt	gaa	cag	cct	gac	tcc	988	

Asp Arg Cys Tyr Ser Thr Pro Ser Ser Cys Leu Glu Gln Pro Asp Ser
 265 270 275
 tgc ctg ccc tat gga agt tcc ttt tat gca ttg gag gaa aaa cat gtt 1036
 Cys Leu Pro Tyr Gly Ser Ser Phe Tyr Ala Leu Glu Glu Lys His Val
 280 285 290 295
 ggc ttt tct ctt gac gtg gga gaa att gaa aag aag ggg aag ggg aag 1084
 Gly Phe Ser Leu Asp Val Gly Glu Ile Glu Lys Lys Gly Lys Gly Lys
 300 305 310
 aaa aga agg gga aga aga tca acg aag aaa aga agg aga agg gga agt 1132
 Lys Arg Arg Gly Arg Arg Ser Thr Lys Lys Arg Arg Arg Arg Gly Ser
 315 320 325
 aaa gaa ggg gaa gaa gat caa aac cca cca tgc ccc agg ctc agc ggt 1180
 Lys Glu Gly Glu Glu Asp Gln Asn Pro Pro Cys Pro Arg Leu Ser Gly
 330 335 340
 gtg ctg atg gaa gtg gaa gag cct gaa gtc tta cag gac tca ctg gat 1228
 Val Leu Met Glu Val Glu Glu Pro Glu Val Leu Gln Asp Ser Leu Asp
 345 350 355
 aga tgt tat tcg act ccg tca atg tac ttt gaa cta cct gac tca ttc 1276
 Arg Cys Tyr Ser Thr Pro Ser Met Tyr Phe Glu Leu Pro Asp Ser Phe
 360 365 370 375
 cag cac tac aga agt gtg ttt tac tca ttt gag gaa cag cac atc agc 1324
 Gln His Tyr Arg Ser Val Phe Tyr Ser Phe Glu Glu Gln His Ile Ser
 380 385 390
 ttc gcc ctt gac gtg gac aat agg ttt ctt act ttg atg gga aca agt 1372
 Phe Ala Leu Asp Val Asp Asn Arg Phe Leu Thr Leu Met Gly Thr Ser
 395 400 405
 ctc cac ctg gtc ttc cag atg gga gtc ata ttc cca cag taagcagccc 1421
 Leu His Leu Val Phe Gln Met Gly Val Ile Phe Pro Gln
 410 415 420
 tttctaagcc gagagatgtc attcctgcag gcaggaccta taggcacgtg aagatttgaa 1481
 tgaaactata gttccatttg gaagcccaga cataggatgg gtcagtgggc gtggctctat 1541
 tcctattctc agaccatgcc agtggcaacc tgtgctcagt ctgaagacaa tggacccaag 1601
 ttaggtgtga cacgttcaca taactgtgca gcacatgccg ggagtgatca gtcagacatt 1661
 ttaatttgaa ccacgtatct ctgggtagct acaaagttcc tcagggattt cattttgcag 1721

gcattgtctct gagctttctat acctgctcaa ggtcagtgtc atcttttgtgt ttagctcatc 1781
caaagggtgtt accctgggttt caatgaacct aacctcattc tttgtatctt cagtgttgaa 1841
ttgttttttagc tgatccatct ttaacacagg agggatcctt ggctgaggat tgtatttcag 1901
aaccaccaac tgctcttgac aattgttaac ccgctaggct cctttgggtta gagaagccac 1961
agtccctcag cctccaattg gtgttagtac ttaagaagac cacagctaga tggacaaaca 2021
gcattgggag gccttagccc tgctcctctc gattccatcc tgtagagaac aggagtcagg 2081
agccgctggc aggagacagc atgtcaccca ggactctgcc ggtgcagaat atgaacaacg 2141
ccatgttctt gcagaaaacg cttagcctga gtttcatagg aggtaatcac cagacaactg 2201
cagaatgtgg aacctgagc aggacaactg acctgtctcc ttcacatagt ccatatcacc 2261
acaaatcaca caacagaaag gagaagagat attttgggtt caaaaaaagt aaaaagataa 2321
tatagctgca tttcttttagt tattttgaac cccaaatatt tctcatctt tttgttggtg 2381
tcattgatgg tggtgacatg gacttgttta tagaggacag gtcagctgtc tggctcagtg 2441
atctacattc tgaagttgtc tgaaaatgtc ttcattgatta aattcagcct aaacgttttg 2501
ccgggaacac tgcagagaca atgctgtgag tttccaacct tagcccatct gcgggcagag 2561
aagggtctagt ttgtccatca gcattatcat gatatcagga ctggttactt ggtaaggag 2621
gggtctagga gatgtgtccc ttttagagac accttactta taatgaagta tttgggaggg 2681
tggttttcaa aagtagaaat gtcctgtatt ccgatgatca tctgttaaac attttatcat 2741
ttattaatca tccctgcctg tgtctattat tatattcata tctctacgct ggaaactttc 2801
tgccctctatg tttactgtgc ctttgttttt gctagtgtgt gttgttgaaa aaaaaaacat 2861
tctctgcctg agttttaatt tttgtccaaa gttattttta tctatacaat taaaagcttt 2921
tgccctatcaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2981
a 2982

<210> 189

<211> 420

<212> PRT

<213> Homo sapiens

<223> DKFZp434J205; Genbank AF379616; cDNA clone AB06

<400> 189

Leu Ser Arg Glu Leu Leu Glu Ala Val Glu Pro Glu Val Leu Gln Asp

1

5

10

15

Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Ser Cys Leu Glu Gln Pro

20

25

30

Asp Ser Cys Leu Pro Tyr Gly Ser Ser Phe Tyr Ala Leu Glu Glu Lys

35

40

45

His Val Gly Phe Ser Leu Asp Val Gly Glu Ile Glu Lys Lys Gly Lys

50

55

60

Gly Lys Lys Arg Arg Gly Arg Arg Ser Thr Lys Lys Arg Arg Arg Arg

65

70

75

80

Gly Arg Lys Glu Gly Glu Glu Asp Gln Asn Pro Pro Cys Pro Arg Leu

85

90

95

Ser Arg Glu Leu Leu Asp Glu Lys Gly Pro Glu Val Leu Gln Asp Ser

100

105

110

Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Tyr Leu Glu Leu Thr Asp

115

120

125

Ser Cys Gln Pro Tyr Arg Ser Ala Phe Tyr Ile Leu Glu Gln Gln Arg

130

135

140

Val Gly Trp Ala Leu Asp Met Asp Glu Ile Glu Lys Tyr Gln Glu Val

145

150

155

160

Glu Glu Asp Gln Asp Pro Ser Cys Pro Arg Leu Ser Arg Glu Leu Leu

165

170

175

Asp Glu Lys Glu Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr

180

185

190

Ser Thr Pro Ser Gly Tyr Leu Glu Leu Pro Asp Leu Gly Gln Pro Tyr

195

200

205

Arg Ser Ala Val His Ser Leu Glu Glu Gln Tyr Leu Gly Leu Ala Leu

210

215

220

Asp Val Asp Arg Ile Lys Lys Asp Gln Glu Glu Glu Glu Asp Gln Gly

<223> image: 2920609; Genbank AF380581; cDNA clone AG03

<220>

<221> CDS

<222> (2)..(1201)

<400> 190

t gaa gat gtt caa gtt gag gtg gct gag aaa gtg cag aaa tcg tct gcc 49

Glu Asp Val Gln Val Glu Val Ala Glu Lys Val Gln Lys Ser Ser Ala

1

5

10

15

ccc agg gag atg ccg aag gct gaa gaa aag gaa gtc cct gag gac tca 97

Pro Arg Glu Met Pro Lys Ala Glu Glu Lys Glu Val Pro Glu Asp Ser

20

25

30

ctg gag gaa tgt gcc atc act tgt tca aat agc cat ggc cct tat gac 145

Leu Glu Glu Cys Ala Ile Thr Cys Ser Asn Ser His Gly Pro Tyr Asp

35

40

45

tcc aac cag cca cat agg aaa acc aaa atc aca ttt gag gaa gac aaa 193

Ser Asn Gln Pro His Arg Lys Thr Lys Ile Thr Phe Glu Glu Asp Lys

50

55

60

gtc gac tca act ctc att ggc tca tcc tct cat gtt gaa tgg gag gat 241

Val Asp Ser Thr Leu Ile Gly Ser Ser Ser His Val Glu Trp Glu Asp

65

70

75

80

gct gta cac att atc cca gaa aat gaa agt gat gat gag gaa gag gaa 289

Ala Val His Ile Ile Pro Glu Asn Glu Ser Asp Asp Glu Glu Glu Glu

85

90

95

gaa aaa ggg cca gtg tct ccc agg aat ctg cag gag tct gaa gag gag 337

Glu Lys Gly Pro Val Ser Pro Arg Asn Leu Gln Glu Ser Glu Glu Glu

100

105

110

gaa gtc ccc cag gag tcc tgg gat gaa ggt tat tcg act ctc tca att 385

Glu Val Pro Gln Glu Ser Trp Asp Glu Gly Tyr Ser Thr Leu Ser Ile

115

120

125

cct cct gaa atg ttg gcc tcg tac cag tct tac agc agc aca ttt cac 433

Pro Pro Glu Met Leu Ala Ser Tyr Gln Ser Tyr Ser Ser Thr Phe His

130

135

140

tca tta gag gaa cag caa gtc tgc atg gct gtt gac ata ggc gga cat 481

Ser Leu Glu Glu Gln Gln Val Cys Met Ala Val Asp Ile Gly Gly His

145

150

155

160

cag tgg gat caa gtg aaa aag gag gac caa gag gca aca ggt ccc agg 529

Gln Trp Asp Gln Val Lys Lys Glu Asp Gln Glu Ala Thr Gly Pro Arg

165

170

175

ctc agc agg gag ctg ctg gat gag aaa ggg cct gaa gtc ttg cag gac	577
Leu Ser Arg Glu Leu Leu Asp Glu Lys Gly Pro Glu Val Leu Gln Asp	
180 185 190	
tca ctg gat aga tgt tat tca act cct tca ggt tat ctt gaa ctg cct	625
Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Tyr Leu Glu Leu Pro	
195 200 205	
gac tca tgc cag ccc tac aga agt gcc ttt tac gta ttg gag caa cag	673
Asp Ser Cys Gln Pro Tyr Arg Ser Ala Phe Tyr Val Leu Glu Gln Gln	
210 215 220	
cgt gtt ggc ttg act ctt gac atg gat gaa att gaa aag tac caa gaa	721
Arg Val Gly Leu Thr Leu Asp Met Asp Glu Ile Glu Lys Tyr Gln Glu	
225 230 235 240	
gtg gaa gaa gac caa gac cca tca tgc ccc agg ctc agc agg gag ctg	769
Val Glu Glu Asp Gln Asp Pro Ser Cys Pro Arg Leu Ser Arg Glu Leu	
245 250 255	
ctg gat gag aaa gag cct gaa gtc ttg cag gac tcc ctg gat aga tgt	817
Leu Asp Glu Lys Glu Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys	
260 265 270	
tat tcg act cct tca ggt tat ctt gaa ctg cct gac tta ggc cag ccc	865
Tyr Ser Thr Pro Ser Gly Tyr Leu Glu Leu Pro Asp Leu Gly Gln Pro	
275 280 285	
tac aga agt gct gtt tac tca ttg gag gaa cag tac ctt ggc ttg gct	913
Tyr Arg Ser Ala Val Tyr Ser Leu Glu Glu Gln Tyr Leu Gly Leu Ala	
290 295 300	
ctt gac gtg gat aga att aaa aag gac caa gaa gag gaa gaa gac cag	961
Leu Asp Val Asp Arg Ile Lys Lys Asp Gln Glu Glu Glu Glu Asp Gln	
305 310 315 320	
ggc cca cca tgc ccc agg ctc agc agg gag ctg ctg gag gta gta gag	1009
Gly Pro Pro Cys Pro Arg Leu Ser Arg Glu Leu Leu Glu Val Val Glu	
325 330 335	
cct gaa gtc ttg cag gac tca ctg gat aga tgt tat tca act cct tcc	1057
Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser	
340 345 350	
agt tgt ctt gaa cag cct gac tcc tgc cag ccc tat gga agt tcc ttt	1105
Ser Cys Leu Glu Gln Pro Asp Ser Cys Gln Pro Tyr Gly Ser Ser Phe	
355 360 365	

tat gca ttg gag gaa aaa cat gtt ggc ttt tct ctt gac gtg gga gaa 1153
 Tyr Ala Leu Glu Glu Lys His Val Gly Phe Ser Leu Asp Val Gly Glu
 370 375 380

att gaa aag aag ggg aag ggg aag aaa aga agg gga aga aga tca acg 1201
 Ile Glu Lys Lys Gly Lys Gly Lys Lys Arg Arg Gly Arg Arg Ser Thr
 385 390 395 400

aaaaaaaaaa aaaaaa 1217

<210> 191

<211> 400

<212> PRT

<213> Homo sapiens

<223> image: 2920609; Genbank AF380581; cDNA clone AG03

<400> 191

Glu Asp Val Gln Val Glu Val Ala Glu Lys Val Gln Lys Ser Ser Ala
 1 5 10 15

Pro Arg Glu Met Pro Lys Ala Glu Glu Lys Glu Val Pro Glu Asp Ser
 20 25 30

Leu Glu Glu Cys Ala Ile Thr Cys Ser Asn Ser His Gly Pro Tyr Asp
 35 40 45

Ser Asn Gln Pro His Arg Lys Thr Lys Ile Thr Phe Glu Glu Asp Lys
 50 55 60

Val Asp Ser Thr Leu Ile Gly Ser Ser Ser His Val Glu Trp Glu Asp
 65 70 75 80

Ala Val His Ile Ile Pro Glu Asn Glu Ser Asp Asp Glu Glu Glu Glu
 85 90 95

Glu Lys Gly Pro Val Ser Pro Arg Asn Leu Gln Glu Ser Glu Glu Glu
 100 105 110

Glu Val Pro Gln Glu Ser Trp Asp Glu Gly Tyr Ser Thr Leu Ser Ile
 115 120 125

Pro Pro Glu Met Leu Ala Ser Tyr Gln Ser Tyr Ser Ser Thr Phe His
 130 135 140

Ser Leu Glu Glu Gln Gln Val Cys Met Ala Val Asp Ile Gly Gly His
 145 150 155 160

Gln	Trp	Asp	Gln	Val	Lys	Lys	Glu	Asp	Gln	Glu	Ala	Thr	Gly	Pro	Arg	
				165					170					175		
Leu	Ser	Arg	Glu	Leu	Leu	Asp	Glu	Lys	Gly	Pro	Glu	Val	Leu	Gln	Asp	
			180					185					190			
Ser	Leu	Asp	Arg	Cys	Tyr	Ser	Thr	Pro	Ser	Gly	Tyr	Leu	Glu	Leu	Pro	
		195					200					205				
Asp	Ser	Cys	Gln	Pro	Tyr	Arg	Ser	Ala	Phe	Tyr	Val	Leu	Glu	Gln	Gln	
		210				215					220					
Arg	Val	Gly	Leu	Thr	Leu	Asp	Met	Asp	Glu	Ile	Glu	Lys	Tyr	Gln	Glu	
225					230				235						240	
Val	Glu	Glu	Asp	Gln	Asp	Pro	Ser	Cys	Pro	Arg	Leu	Ser	Arg	Glu	Leu	
				245				250						255		
Leu	Asp	Glu	Lys	Glu	Pro	Glu	Val	Leu	Gln	Asp	Ser	Leu	Asp	Arg	Cys	
			260					265					270			
Tyr	Ser	Thr	Pro	Ser	Gly	Tyr	Leu	Glu	Leu	Pro	Asp	Leu	Gly	Gln	Pro	
		275					280					285				
Tyr	Arg	Ser	Ala	Val	Tyr	Ser	Leu	Glu	Glu	Gln	Tyr	Leu	Gly	Leu	Ala	
		290				295					300					
Leu	Asp	Val	Asp	Arg	Ile	Lys	Lys	Asp	Gln	Glu	Glu	Glu	Glu	Asp	Gln	
305					310				315						320	
Gly	Pro	Pro	Cys	Pro	Arg	Leu	Ser	Arg	Glu	Leu	Leu	Glu	Val	Val	Glu	
				325					330					335		
Pro	Glu	Val	Leu	Gln	Asp	Ser	Leu	Asp	Arg	Cys	Tyr	Ser	Thr	Pro	Ser	
			340					345					350			
Ser	Cys	Leu	Glu	Gln	Pro	Asp	Ser	Cys	Gln	Pro	Tyr	Gly	Ser	Ser	Phe	
		355					360					365				
Tyr	Ala	Leu	Glu	Glu	Lys	His	Val	Gly	Phe	Ser	Leu	Asp	Val	Gly	Glu	
		370				375					380					
Ile	Glu	Lys	Lys	Gly	Lys	Gly	Lys	Lys	Arg	Arg	Gly	Arg	Arg	Ser	Thr	
385					390				395						400	

<210> 192
 <211> 1885
 <212> DNA
 <213> Homo sapiens

<220>
 <223> DKFZp434F2323; Genbank AF380580; cDNA clone AG01

<220>
 <221> CDS
 <222> (3)..(1847)

<400> 192
 aa aaa cat gtt ggc ttt tct ctt gac gtg gga gaa att gaa aag aag 47
 Lys His Val Gly Phe Ser Leu Asp Val Gly Glu Ile Glu Lys Lys
 1 5 10 15
 ggg aag ggg aag aaa aga agg gga aga aga tca aag aag gaa aga aga 95
 Gly Lys Gly Lys Lys Arg Arg Gly Arg Arg Ser Lys Lys Glu Arg Arg
 20 25 30
 agg gga aga aaa gaa ggg gaa gaa gat caa aac cca cca tgc ccc agg 143
 Arg Gly Arg Lys Glu Gly Glu Glu Asp Gln Asn Pro Pro Cys Pro Arg
 35 40 45
 ctc agc agg gag ctg ctg gat gag aaa ggg cct gaa gtc ttg cag gac 191
 Leu Ser Arg Glu Leu Leu Asp Glu Lys Gly Pro Glu Val Leu Gln Asp
 50 55 60
 tca ctg gat aga agt tat tca act cct tca ggt tgt ctt gaa ctg act 239
 Ser Leu Asp Arg Ser Tyr Ser Thr Pro Ser Gly Cys Leu Glu Leu Thr
 65 70 75
 gac tca tgc cag ccc tac aga agt gcc ttt tac gta ttg gag caa cag 287
 Asp Ser Cys Gln Pro Tyr Arg Ser Ala Phe Tyr Val Leu Glu Gln Gln
 80 85 90 95
 cgt gtt ggc ttg gct gtt gac atg gat gaa att gaa aag tac caa gaa 335
 Arg Val Gly Leu Ala Val Asp Met Asp Glu Ile Glu Lys Tyr Gln Glu
 100 105 110
 gtg gaa gaa gac caa gac cca tca tgc ccc agg ctc agc agg gag ctg 383
 Val Glu Glu Asp Gln Asp Pro Ser Cys Pro Arg Leu Ser Arg Glu Leu
 115 120 125
 ctg gat gag aaa gag cct gaa gtc ttg cag gac tca ctg gat aga tgt 431
 Leu Asp Glu Lys Glu Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys
 130 135 140

tat tcg act cct tca ggt tat ctt gaa ctg cct gac tta ggc cag ccc	479
Tyr Ser Thr Pro Ser Gly Tyr Leu Glu Leu Pro Asp Leu Gly Gln Pro	
145 150 155	
tac agc agt gct gtg tac tca ttg gag gaa cag tac ctt ggc ttg gct	527
Tyr Ser Ser Ala Val Tyr Ser Leu Glu Glu Gln Tyr Leu Gly Leu Ala	
160 165 170 175	
ctt gac gtg gac aga act aaa aag gac caa gaa gag gaa gaa gac caa	575
Leu Asp Val Asp Arg Thr Lys Lys Asp Gln Glu Glu Glu Glu Asp Gln	
180 185 190	
ggc cca cca tgc ccc agg ctc agc agg gag ctg ctg gag gta gta gag	623
Gly Pro Pro Cys Pro Arg Leu Ser Arg Glu Leu Leu Glu Val Val Glu	
195 200 205	
cct gaa gtc ttg cag gac tca ctg gat aga tgt tat tca act cct tcc	671
Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser	
210 215 220	
agt tgt ctt gaa cag cct gac tcc tgc cag ccc tat gga agt tcc ttt	719
Ser Cys Leu Glu Gln Pro Asp Ser Cys Gln Pro Tyr Gly Ser Ser Phe	
225 230 235	
tat gca ttg gag gaa aaa cat gtt ggc ttt tct ctc gac gtg gga gaa	767
Tyr Ala Leu Glu Glu Lys His Val Gly Phe Ser Leu Asp Val Gly Glu	
240 245 250 255	
att gaa aag aag ggg aag ggg aag aaa aga agg gga aga aga tca aag	815
Ile Glu Lys Lys Gly Lys Gly Lys Lys Arg Arg Gly Arg Arg Ser Lys	
260 265 270	
aag gaa aga aga agg gga aga aaa gaa ggg gaa gaa gat caa aac cca	863
Lys Glu Arg Arg Arg Gly Arg Lys Glu Gly Glu Glu Asp Gln Asn Pro	
275 280 285	
cca tgc ccc agg ctc agc agg gag ctg ctg gat gag aaa ggg cct gaa	911
Pro Cys Pro Arg Leu Ser Arg Glu Leu Leu Asp Glu Lys Gly Pro Glu	
290 295 300	
gtc ttg cag gac tca ctg gat aga tgt tat tca act cct tca ggt tgt	959
Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Cys	
305 310 315	
ctt gaa ctg act gac tca tgc cag ccc tac aga agt gcc ttt tac gta	1007
Leu Glu Leu Thr Asp Ser Cys Gln Pro Tyr Arg Ser Ala Phe Tyr Val	
320 325 330 335	

ttg gag caa cag cgt gtt ggc ttg gct gtt gac atg gat gaa att gaa	1055
Leu Glu Gln Gln Arg Val Gly Leu Ala Val Asp Met Asp Glu Ile Glu	
340 345 350	
aag tac caa gaa gtg gaa gaa gac caa gac cca tca tgc ccc agg ctc	1103
Lys Tyr Gln Glu Val Glu Glu Asp Gln Asp Pro Ser Cys Pro Arg Leu	
355 360 365	
agc agg gag ctg ctg gat gag aaa gag cct gaa gtc ttg cag gac tca	1151
Ser Arg Glu Leu Leu Asp Glu Lys Glu Pro Glu Val Leu Gln Asp Ser	
370 375 380	
ctg gat aga tgt tat tcg act cct tca ggt tat ctt gaa ctg cct gac	1199
Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Tyr Leu Glu Leu Pro Asp	
385 390 395	
tta ggc cag ccc tac agc agt gct gtt tac tca ttg gag gaa cag tac	1247
Leu Gly Gln Pro Tyr Ser Ser Ala Val Tyr Ser Leu Glu Glu Gln Tyr	
400 405 410 415	
ctt ggc ttg gct ctt gac gtg gac aga act aaa aag gac caa gaa gag	1295
Leu Gly Leu Ala Leu Asp Val Asp Arg Thr Lys Lys Asp Gln Glu Glu	
420 425 430	
gaa gaa gac caa ggc cca cca tgc ccc agg ctc agc agg gag ctg ctg	1343
Glu Glu Asp Gln Gly Pro Pro Cys Pro Arg Leu Ser Arg Glu Leu Leu	
435 440 445	
gag gta gta gag cct gaa gtc ttg cag gac tca ctg gat aga tgt tat	1391
Glu Val Val Glu Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr	
450 455 460	
tca act cct tcc agt tgt ctt gaa cag cct gac tcc tgc cag ccc tat	1439
Ser Thr Pro Ser Ser Cys Leu Glu Gln Pro Asp Ser Cys Gln Pro Tyr	
465 470 475	
gga agt tcc ttt tat gca ttg gag gaa aaa cat gtt ggc ttt tct ctt	1487
Gly Ser Ser Phe Tyr Ala Leu Glu Glu Lys His Val Gly Phe Ser Leu	
480 485 490 495	
gac gtg gga gaa att gaa aag aag ggg aag ggg aag aaa aga agg gga	1535
Asp Val Gly Glu Ile Glu Lys Lys Gly Lys Gly Lys Lys Arg Arg Gly	
500 505 510	
aga aga tca aag aag aaa aga aga agg gga aga aaa gaa ggg gaa gaa	1583
Arg Arg Ser Lys Lys Lys Arg Arg Arg Gly Arg Lys Glu Gly Glu Glu	
515 520 525	

gat caa aac cca cca tgc ccc agg ctc aac ggc gtg ctg atg gaa gtg 1631
 Asp Gln Asn Pro Pro Cys Pro Arg Leu Asn Gly Val Leu Met Glu Val
 530 535 540

gaa gag cct gaa gtc tta cag gac tca ctg gat gga tgt tat tct act 1679
 Glu Glu Pro Glu Val Leu Gln Asp Ser Leu Asp Gly Cys Tyr Ser Thr
 545 550 555

ccg tca atg tac ttt gaa cta cct gac tca ttc cag cac tac aga agt 1727
 Pro Ser Met Tyr Phe Glu Leu Pro Asp Ser Phe Gln His Tyr Arg Ser
 560 565 570 575

gtg ttt tac tca ttt gag gaa cag cac atc agc ttc gcc ctt tac gtg 1775
 Val Phe Tyr Ser Phe Glu Glu Gln His Ile Ser Phe Ala Leu Tyr Val
 580 585 590

gac aat agg ttt ttt act ttg acg gtg aca agt ctc cac ctg gtg ttc 1823
 Asp Asn Arg Phe Phe Thr Leu Thr Val Thr Ser Leu His Leu Val Phe
 595 600 605

cag atg gga gtc ata ttc cca caa taaacagccc ttactaaaaa aaaaaaaaaa 1877
 Gln Met Gly Val Ile Phe Pro Gln
 610 615

aaaaaaaa 1885

<210> 193

<211> 615

<212> PRT

<213> Homo sapiens

<223> DKFZp434F2323; Genbank AF380580; cDNA clone AG01

<400> 193

Lys His Val Gly Phe Ser Leu Asp Val Gly Glu Ile Glu Lys Lys Gly
 1 5 10 15

Lys Gly Lys Lys Arg Arg Gly Arg Arg Ser Lys Lys Glu Arg Arg Arg
 20 25 30

Gly Arg Lys Glu Gly Glu Glu Asp Gln Asn Pro Pro Cys Pro Arg Leu
 35 40 45

Ser Arg Glu Leu Leu Asp Glu Lys Gly Pro Glu Val Leu Gln Asp Ser
 50 55 60

Leu Asp Arg Ser Tyr Ser Thr Pro Ser Gly Cys Leu Glu Leu Thr Asp

65		70		75		80									
Ser	Cys	Gln	Pro	Tyr	Arg	Ser	Ala	Phe	Tyr	Val	Leu	Glu	Gln	Gln	Arg
				85					90					95	
Val	Gly	Leu	Ala	Val	Asp	Met	Asp	Glu	Ile	Glu	Lys	Tyr	Gln	Glu	Val
			100					105					110		
Glu	Glu	Asp	Gln	Asp	Pro	Ser	Cys	Pro	Arg	Leu	Ser	Arg	Glu	Leu	Leu
		115					120					125			
Asp	Glu	Lys	Glu	Pro	Glu	Val	Leu	Gln	Asp	Ser	Leu	Asp	Arg	Cys	Tyr
	130					135					140				
Ser	Thr	Pro	Ser	Gly	Tyr	Leu	Glu	Leu	Pro	Asp	Leu	Gly	Gln	Pro	Tyr
145					150					155					160
Ser	Ser	Ala	Val	Tyr	Ser	Leu	Glu	Glu	Gln	Tyr	Leu	Gly	Leu	Ala	Leu
				165					170					175	
Asp	Val	Asp	Arg	Thr	Lys	Lys	Asp	Gln	Glu	Glu	Glu	Glu	Asp	Gln	Gly
			180					185					190		
Pro	Pro	Cys	Pro	Arg	Leu	Ser	Arg	Glu	Leu	Leu	Glu	Val	Val	Glu	Pro
		195					200					205			
Glu	Val	Leu	Gln	Asp	Ser	Leu	Asp	Arg	Cys	Tyr	Ser	Thr	Pro	Ser	Ser
	210					215					220				
Cys	Leu	Glu	Gln	Pro	Asp	Ser	Cys	Gln	Pro	Tyr	Gly	Ser	Ser	Phe	Tyr
225					230					235					240
Ala	Leu	Glu	Glu	Lys	His	Val	Gly	Phe	Ser	Leu	Asp	Val	Gly	Glu	Ile
				245				250						255	
Glu	Lys	Lys	Gly	Lys	Gly	Lys	Lys	Arg	Arg	Gly	Arg	Arg	Ser	Lys	Lys
			260					265					270		
Glu	Arg	Arg	Arg	Gly	Arg	Lys	Glu	Gly	Glu	Glu	Asp	Gln	Asn	Pro	Pro
		275					280					285			
Cys	Pro	Arg	Leu	Ser	Arg	Glu	Leu	Leu	Asp	Glu	Lys	Gly	Pro	Glu	Val
	290					295					300				
Leu	Gln	Asp	Ser	Leu	Asp	Arg	Cys	Tyr	Ser	Thr	Pro	Ser	Gly	Cys	Leu
305					310					315					320
Glu	Leu	Thr	Asp	Ser	Cys	Gln	Pro	Tyr	Arg	Ser	Ala	Phe	Tyr	Val	Leu

	325		330		335
Glu Gln Gln Arg Val Gly Leu Ala Val Asp Met Asp Glu Ile Glu Lys					
	340		345		350
Tyr Gln Glu Val Glu Glu Asp Gln Asp Pro Ser Cys Pro Arg Leu Ser					
	355		360		365
Arg Glu Leu Leu Asp Glu Lys Glu Pro Glu Val Leu Gln Asp Ser Leu					
	370		375		380
Asp Arg Cys Tyr Ser Thr Pro Ser Gly Tyr Leu Glu Leu Pro Asp Leu					
	385		390		395
Gly Gln Pro Tyr Ser Ser Ala Val Tyr Ser Leu Glu Glu Gln Tyr Leu					
	405		410		415
Gly Leu Ala Leu Asp Val Asp Arg Thr Lys Lys Asp Gln Glu Glu Glu					
	420		425		430
Glu Asp Gln Gly Pro Pro Cys Pro Arg Leu Ser Arg Glu Leu Leu Glu					
	435		440		445
Val Val Glu Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser					
	450		455		460
Thr Pro Ser Ser Cys Leu Glu Gln Pro Asp Ser Cys Gln Pro Tyr Gly					
	465		470		475
Ser Ser Phe Tyr Ala Leu Glu Glu Lys His Val Gly Phe Ser Leu Asp					
	485		490		495
Val Gly Glu Ile Glu Lys Lys Gly Lys Gly Lys Lys Arg Arg Gly Arg					
	500		505		510
Arg Ser Lys Lys Lys Arg Arg Arg Gly Arg Lys Glu Gly Glu Glu Asp					
	515		520		525
Gln Asn Pro Pro Cys Pro Arg Leu Asn Gly Val Leu Met Glu Val Glu					
	530		535		540
Glu Pro Glu Val Leu Gln Asp Ser Leu Asp Gly Cys Tyr Ser Thr Pro					
	545		550		555
Ser Met Tyr Phe Glu Leu Pro Asp Ser Phe Gln His Tyr Arg Ser Val					
	565		570		575
phe Tyr Ser Phe Glu Glu Gln His Ile Ser Phe Ala Leu Tyr Val Asp					

580 585 590
 Asn Arg Phe Phe Thr Leu Thr Val Thr Ser Leu His Leu Val Phe Gln
 595 600 605
 Met Gly Val Ile Phe Pro Gln
 610 615

 <210> 194
 <211> 1528
 <212> DNA
 <213> Homo sapiens

 <220>
 <223> image: 2782170 (5' end); Genbank AF419618; cDNA
 clone AE01

 <220>
 <221> CDS
 <222> (2)..(964)

 <400> 194
 g aac aaa tac aag tat gaa gag tgt aaa gac ctc ata aaa ttt atg ctg 49
 Asn Lys Tyr Lys Tyr Glu Glu Cys Lys Asp Leu Ile Lys Phe Met Leu
 1 5 10 15
 agg aat gag cga cag ttc aag gag gag aag ctt gca gag cag ctg aag 97
 Arg Asn Glu Arg Gln Phe Lys Glu Glu Lys Leu Ala Glu Gln Leu Lys
 20 25 30
 caa gct gag gag ctc agg caa tat aaa gtc ctg gtt cac gct cag gaa 145
 Gln Ala Glu Glu Leu Arg Gln Tyr Lys Val Leu Val His Ala Gln Glu
 35 40 45
 cga gag ctg acc cag tta agg gag aag ttg cgg gaa ggg aga gat gcc 193
 Arg Glu Leu Thr Gln Leu Arg Glu Lys Leu Arg Glu Gly Arg Asp Ala
 50 55 60
 tcc cgc tca ttg aat gag cat ctc cag gcc ctc ctc act ccg gat gag 241
 Ser Arg Ser Leu Asn Glu His Leu Gln Ala Leu Leu Thr Pro Asp Glu
 65 70 75 80
 ccg gac aag tcc cag ggg cag gac ctc caa gaa cag ctg gct gag ggg 289
 Pro Asp Lys Ser Gln Gly Gln Asp Leu Gln Glu Gln Leu Ala Glu Gly
 85 90 95

tgt aga ctg gca cag cac ctt gtc caa aag ctc agc cca gaa aat gac	337
Cys Arg Leu Ala Gln His Leu Val Gln Lys Leu Ser Pro Glu Asn Asp	
100 105 110	
aac gat gac gat gaa gat gtt caa att gag gtg gct gag aaa gtg cag	385
Asn Asp Asp Asp Glu Asp Val Gln Ile Glu Val Ala Glu Lys Val Gln	
115 120 125	
aaa tcg tct gcc ccc agg gag atg cag aag gct gaa gaa aag gaa gtc	433
Lys Ser Ser Ala Pro Arg Glu Met Gln Lys Ala Glu Glu Lys Glu Val	
130 135 140	
cct gag gac tca ctg gag gaa tgt gcc atc act tat tca aat agc cat	481
Pro Glu Asp Ser Leu Glu Glu Cys Ala Ile Thr Tyr Ser Asn Ser His	
145 150 155 160	
ggc cct tat gac tcc aac cag cca cat agg aaa acc aaa atc aca ttt	529
Gly Pro Tyr Asp Ser Asn Gln Pro His Arg Lys Thr Lys Ile Thr Phe	
165 170 175	
gag gaa gac aaa gtc gac tca act ctc att ggc tca tcc tct cat gtt	577
Glu Glu Asp Lys Val Asp Ser Thr Leu Ile Gly Ser Ser Ser His Val	
180 185 190	
gaa cgg gaa gat gct gta cac att att cca gaa aat gaa agt gat gat	625
Glu Arg Glu Asp Ala Val His Ile Ile Pro Glu Asn Glu Ser Asp Asp	
195 200 205	
gag gaa gag gaa gaa aaa ggg cca gtg tct ccc agg aat ctg cag gag	673
Glu Glu Glu Glu Glu Lys Gly Pro Val Ser Pro Arg Asn Leu Gln Glu	
210 215 220	
tct gaa gag gag gaa gtc ccc cag gag tcc tgg gat gaa ggt tat tcg	721
Ser Glu Glu Glu Glu Val Pro Gln Glu Ser Trp Asp Glu Gly Tyr Ser	
225 230 235 240	
act ccc tca att cct cct gaa atg ttg gcc tcg tac aag tct tac agc	769
Thr Pro Ser Ile Pro Pro Glu Met Leu Ala Ser Tyr Lys Ser Tyr Ser	
245 250 255	
agc aca ttt cac tca tta gag gaa cag caa gtc tgc atg gct gtt gac	817
Ser Thr Phe His Ser Leu Glu Glu Gln Gln Val Cys Met Ala Val Asp	
260 265 270	
ata ggc aga cat cgg tgg gat caa gtg aaa aag gag gac caa gag gca	865
Ile Gly Arg His Arg Trp Asp Gln Val Lys Lys Glu Asp Gln Glu Ala	
275 280 285	

aca ggt ccc agg ctc agc agg gag ctg ctg gat gag aaa ggg cct gaa 913
 Thr Gly Pro Arg Leu Ser Arg Glu Leu Leu Asp Glu Lys Gly Pro Glu
 290 295 300

gtc ttg cag gac tca ctg gat aga tgt tta ttc aac tcc ttc agg ttg 961
 Val Leu Gln Asp Ser Leu Asp Arg Cys Leu Phe Asn Ser Phe Arg Leu
 305 310 315 320

tct tgaactgact gactcatgcc agccctacag aagtccttt tacgtattgg 1014
 Ser

agcaacacgcg tgttggcttg gctgttgaca tggatgaaat tgaaaagtac caagaagtgg 1074

aagaagacca agacccatca tgccccaggc tcagcaggga gctgctggat gagaaagagc 1134

ctgaagtctt gcaggactca ctgggtagat ggtattcgac tccttcaggt tatcttgaac 1194

tgcttgactt aggccagccc tacagcagtg ctgtttactc attggaggaa cagtaccttg 1254

gcttggctct tgacttggac agaattaaaa aggaccaaga agaggaagaa gaccaaggcc 1314

caccatgccc caggctcagc agggagctgc tggaggtagt agagcctgaa gtcttgcagg 1374

actcactgga tagatgttat tcaactcctt ccagttgtct tgaacagcct gactcctgcc 1434

agccctatgg aagttccttt tatgcattgg aggaaaaaca tgttggcttt tctcttgacg 1494

tgggagaaaat tgaaaagaag ggggaagggga agaa 1528

<210> 195

<211> 321

<212> PRT

<213> Homo sapiens

<223> image: 2782170 (5' end); Genbank AF419618; cDNA

clone AE01

<400> 195

Asn Lys Tyr Lys Tyr Glu Glu Cys Lys Asp Leu Ile Lys Phe Met Leu
 1 5 10 15

Arg Asn Glu Arg Gln Phe Lys Glu Glu Lys Leu Ala Glu Gln Leu Lys
 20 25 30

Gln Ala Glu Glu Leu Arg Gln Tyr Lys Val Leu Val His Ala Gln Glu
 35 40 45

Arg Glu Leu Thr Gln Leu Arg Glu Lys Leu Arg Glu Gly Arg Asp Ala

50		55		60	
Ser Arg Ser Leu Asn Glu His Leu Gln Ala Leu Leu Thr Pro Asp Glu					
65		70		75	80
Pro Asp Lys Ser Gln Gly Gln Asp Leu Gln Glu Gln Leu Ala Glu Gly					
	85		90		95
Cys Arg Leu Ala Gln His Leu Val Gln Lys Leu Ser Pro Glu Asn Asp					
	100		105		110
Asn Asp Asp Asp Glu Asp Val Gln Ile Glu Val Ala Glu Lys Val Gln					
	115		120		125
Lys Ser Ser Ala Pro Arg Glu Met Gln Lys Ala Glu Glu Lys Glu Val					
	130		135		140
Pro Glu Asp Ser Leu Glu Glu Cys Ala Ile Thr Tyr Ser Asn Ser His					
145		150		155	160
Gly Pro Tyr Asp Ser Asn Gln Pro His Arg Lys Thr Lys Ile Thr Phe					
	165		170		175
Glu Glu Asp Lys Val Asp Ser Thr Leu Ile Gly Ser Ser Ser His Val					
	180		185		190
Glu Arg Glu Asp Ala Val His Ile Ile Pro Glu Asn Glu Ser Asp Asp					
	195		200		205
Glu Glu Glu Glu Glu Lys Gly Pro Val Ser Pro Arg Asn Leu Gln Glu					
	210		215		220
Ser Glu Glu Glu Glu Val Pro Gln Glu Ser Trp Asp Glu Gly Tyr Ser					
225		230		235	240
Thr Pro Ser Ile Pro Pro Glu Met Leu Ala Ser Tyr Lys Ser Tyr Ser					
	245		250		255
Ser Thr Phe His Ser Leu Glu Glu Gln Gln Val Cys Met Ala Val Asp					
	260		265		270
Ile Gly Arg His Arg Trp Asp Gln Val Lys Lys Glu Asp Gln Glu Ala					
	275		280		285
Thr Gly Pro Arg Leu Ser Arg Glu Leu Leu Asp Glu Lys Gly Pro Glu					
	290		295		300
Val Leu Gln Asp Ser Leu Asp Arg Cys Leu Phe Asn Ser Phe Arg Leu					

305

310

315

320

Ser

<210> 196

<211> 2991

<212> DNA

<213> Homo sapiens

<220>

<223> image: 2226413; Genbank AF419617; cDNA clone AG09

<220>

<221> CDS

<222> (542)..(715)

<220>

<221> CDS

<222> (718)..(2979)

<400> 196

attgataaca gtaaagccac actcctcaag tgcctgaaat acccctcatt gtctttcttca 60

ggtggcaagg gctctggaac agccacataa agcccttgaa gataaggatg gtcaaacaaa 120

ataatatcat acctggagaa actcagatct tgctaagatt tactggttgg gaatccaaag 180

ttaatgccaa gaagcagctg ccagttggga tcaaagtga gcctatggat caaggaatgt 240

ctggacacag tagacaaagg tttttcaact ggatgcctta ggatacatgc ttccaaaaac 300

aaagtagcca aaaagaaacc agagtcacag aatatcagag ccagaggaac atttggagac 360

ggttacctgg cacgctggcc acaatctacc tcactcttat cagagtctga gcagtgcctt 420

cagctctgag ttgaggcacc tcgaaccttg tttttgtggt gaaggatcct aaagtgcctgt 480

ggggagtgat cacatctttc acaacatccc tgactccacc tcttctgccaa caaacgtcag 540

c atg gtg gta tca gcc ggc cct tgg tcc agc gag aag gca gag atg aac 589

Met Val Val Ser Ala Gly Pro Trp Ser Ser Glu Lys Ala Glu Met Asn

1

5

10

15

att cta gaa atc aac gag aaa ttg cgc ccc cag ttg gca gag aac aaa 637

Ile Leu Glu Ile Asn Glu Lys Leu Arg Pro Gln Leu Ala Glu Asn Lys

20	25	30	
cag cag ttc aga aac ctc aaa gag aga tgt ttt cta act caa ctg gcc			685
Gln Gln Phe Arg Asn Leu Lys Glu Arg Cys Phe Leu Thr Gln Leu Ala			
35	40	45	
ggc ttc ctg gcc aac cga cag aag aaa tac ag caa tat aaa gtc ctg			732
Gly Phe Leu Ala Asn Arg Gln Lys Lys Tyr Gln Tyr Lys Val Leu			
50	55	60	
gtt cac tct cag gaa cga gag ctg acc cag tta agg gag aag tta cgg			780
Val His Ser Gln Glu Arg Glu Leu Thr Gln Leu Arg Glu Lys Leu Arg			
65	70	75	
gaa ggg aga gat gcc tcc cgc tca ttg aat gag cat ctc cag gcc ctc			828
Glu Gly Arg Asp Ala Ser Arg Ser Leu Asn Glu His Leu Gln Ala Leu			
80	85	90	95
ctc act ccg gat gag ccg gac aag tcc cag ggg cag gac ctc caa gaa			876
Leu Thr Pro Asp Glu Pro Asp Lys Ser Gln Gly Gln Asp Leu Gln Glu			
100	105	110	
cag ctg gct gag ggg tgt aga ctg gca cag cac ctt gtc caa aag ctc			924
Gln Leu Ala Glu Gly Cys Arg Leu Ala Gln His Leu Val Gln Lys Leu			
115	120	125	
agc cca gaa aat gac aaa gat gag gat gaa gat gtt caa gtt gag gag			972
Ser Pro Glu Asn Asp Lys Asp Glu Asp Glu Asp Val Gln Val Glu Glu			
130	135	140	
gat gag aaa gta ctg gaa tca tct gcc ccc agg gag gtg cag aag gct			1020
Asp Glu Lys Val Leu Glu Ser Ser Ala Pro Arg Glu Val Gln Lys Ala			
145	150	155	
gaa gag agc aaa gtc cct gag gac tca ctg gag gaa tgt gcc atc act			1068
Glu Glu Ser Lys Val Pro Glu Asp Ser Leu Glu Glu Cys Ala Ile Thr			
160	165	170	175
tgt tca aat agc cac ggc cct tgt gac tcc atc cag cct cac aag aac			1116
Cys Ser Asn Ser His Gly Pro Cys Asp Ser Ile Gln Pro His Lys Asn			
180	185	190	
atc aaa atc aca ttt gag gaa gac aaa gtc aac tca tct ctg gtt gta			1164
Ile Lys Ile Thr Phe Glu Glu Asp Lys Val Asn Ser Ser Leu Val Val			
195	200	205	
gac aga gaa tcc tct cat gat gga tgt cag gat gct cta aac att ctc			1212
Asp Arg Glu Ser Ser His Asp Gly Cys Gln Asp Ala Leu Asn Ile Leu			

210	215	220	
cca gtc cct ggc ccc acc tct tct gcc aca aac gtc agc atg gtg gta			1260
Pro Val Pro Gly Pro Thr Ser Ser Ala Thr Asn Val Ser Met Val Val			
225	230	235	
tca gcc ggc cct ttg tcc agc gag aag gca gag atg aac att cta gaa			1308
Ser Ala Gly Pro Leu Ser Ser Glu Lys Ala Glu Met Asn Ile Leu Glu			
240	245	250	255
atc aat gag aaa ttg tgc ccc cag ctg gca gag aag aaa cag cag ttc			1356
Ile Asn Glu Lys Leu Cys Pro Gln Leu Ala Glu Lys Lys Gln Gln Phe			
260	265	270	
aga agc ctc aaa gag aaa tgt ttt gta act caa gtg gcc tgc ttc ctg			1404
Arg Ser Leu Lys Glu Lys Cys Phe Val Thr Gln Val Ala Cys Phe Leu			
275	280	285	
gcc aag cag cag aac aaa tac aaa tat gaa gag tgc aaa gac ctc ata			1452
Ala Lys Gln Gln Asn Lys Tyr Lys Tyr Glu Glu Cys Lys Asp Leu Ile			
290	295	300	
aaa tct atg ctg agg aat gag cga cag ttc aag gag gag aag ctt gca			1500
Lys Ser Met Leu Arg Asn Glu Arg Gln Phe Lys Glu Glu Lys Leu Ala			
305	310	315	
gag cag ctg aag caa gct gag gag ctc agg caa tat aaa gtc ctg gtt			1548
Glu Gln Leu Lys Gln Ala Glu Glu Leu Arg Gln Tyr Lys Val Leu Val			
320	325	330	335
cac tct cag gaa cga gag ctg acc cag tta agg gag aag tta cgg gaa			1596
His Ser Gln Glu Arg Glu Leu Thr Gln Leu Arg Glu Lys Leu Arg Glu			
340	345	350	
ggg aga gat gcc tcc cgc tca ttg aat gag cat ctc cag gcc ctc ctc			1644
Gly Arg Asp Ala Ser Arg Ser Leu Asn Glu His Leu Gln Ala Leu Leu			
355	360	365	
act ccg gat gag ccg gac aag tcc cag ggg cag gac ctc caa gaa cag			1692
Thr Pro Asp Glu Pro Asp Lys Ser Gln Gly Gln Asp Leu Gln Glu Gln			
370	375	380	
ctg gct gag ggg tgt aga ctg gca cag cac ctt gtc caa aag ctc agc			1740
Leu Ala Glu Gly Cys Arg Leu Ala Gln His Leu Val Gln Lys Leu Ser			
385	390	395	
cca gaa aat gat aac gat gac gat gaa gat gtt caa gtt gag gtg gct			1788
Pro Glu Asn Asp Asn Asp Asp Asp Glu Asp Val Gln Val Glu Val Ala			

400	405	410	415	
gag aaa gtg cag aaa tcg tct tcc ccc agg gag atg cag aag gct gaa 1836				
Glu Lys Val Gln Lys Ser Ser Ser Pro Arg Glu Met Gln Lys Ala Glu				
	420	425	430	
gaa aag gaa gtc cct gag gac tca ctg gag gag tgt gcc atc act tgt 1884				
Glu Lys Glu Val Pro Glu Asp Ser Leu Glu Glu Cys Ala Ile Thr Cys				
	435	440	445	
tca aat agc cat ggc cct tat gac tcc aac cag cca cat aga aaa acc 1932				
Ser Asn Ser His Gly Pro Tyr Asp Ser Asn Gln Pro His Arg Lys Thr				
	450	455	460	
aaa atc aca ttt gag gaa gac aaa gtc gac tca act ctc att ggc tca 1980				
Lys Ile Thr Phe Glu Glu Asp Lys Val Asp Ser Thr Leu Ile Gly Ser				
	465	470	475	
tcc tct cat gtt gaa tgg gag gat gct gta cac att atc cca gaa aat 2028				
Ser Ser His Val Glu Trp Glu Asp Ala Val His Ile Ile Pro Glu Asn				
480	485	490	495	
gaa agt gat gat gag gaa gag gaa gaa aaa ggg cca gtg tct ccc agg 2076				
Glu Ser Asp Asp Glu Glu Glu Glu Glu Lys Gly Pro Val Ser Pro Arg				
	500	505	510	
aat ctg cag gag tct gaa gag gag gaa gtc ccc cag gag tcc tgg gat 2124				
Asn Leu Gln Glu Ser Glu Glu Glu Glu Val Pro Gln Glu Ser Trp Asp				
	515	520	525	
gaa ggt tat tcg act ctc tca att cct cct gaa agg ttg gcc tcg tac 2172				
Glu Gly Tyr Ser Thr Leu Ser Ile Pro Pro Glu Arg Leu Ala Ser Tyr				
	530	535	540	
cag tct tac agc agc aca ttt cac tca tta gag gaa cag caa gtc tgc 2220				
Gln Ser Tyr Ser Ser Thr Phe His Ser Leu Glu Glu Gln Gln Val Cys				
	545	550	555	
atg gct gtt gac ata ggc aga cat cgg tgg gat caa gtg aaa aag gag 2268				
Met Ala Val Asp Ile Gly Arg His Arg Trp Asp Gln Val Lys Lys Glu				
560	565	570	575	
gac caa gag gca aca ggt ccc agg ctc agc agg gag ctg ctg gat gag 2316				
Asp Gln Glu Ala Thr Gly Pro Arg Leu Ser Arg Glu Leu Leu Asp Glu				
	580	585	590	
aaa gag cct gaa gtc ttg cag gac tca ctg gat aga tgt tat tca act 2364				
Lys Glu Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr				

595	600	605	
cct tca gtt tat ctt gga ctg act gac tca tgc cag ccc tac aga agt			2412
Pro Ser Val Tyr Leu Gly Leu Thr Asp Ser Cys Gln Pro Tyr Arg Ser			
610	615	620	
gcc ttt tac gta ttg gag caa cag cgt att ggc ttg gct gtt gac atg			2460
Ala Phe Tyr Val Leu Glu Gln Gln Arg Ile Gly Leu Ala Val Asp Met			
625	630	635	
gat gaa att gaa aag tgc caa gaa gtg gaa gaa gac caa gac cca tca			2508
Asp Glu Ile Glu Lys Cys Gln Glu Val Glu Glu Asp Gln Asp Pro Ser			
640	645	650	655
tgc ccc agg ctc agc agg gag ctg ctg gct gag aaa gag cct gaa gtc			2556
Cys Pro Arg Leu Ser Arg Glu Leu Leu Ala Glu Lys Glu Pro Glu Val			
660	665	670	
ttg cag gac tca ctg gat aga tgt tat tcg act cct tca ggt tat ctt			2604
Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Tyr Leu			
675	680	685	
gaa ctg cct gac tta ggc cag ccc tac agc agt gct gtt tac tca ttg			2652
Glu Leu Pro Asp Leu Gly Gln Pro Tyr Ser Ser Ala Val Tyr Ser Leu			
690	695	700	
gag gaa cag tac ctt ggc ttg gct ctt gac gtg gac aga att aaa aag			2700
Glu Glu Gln Tyr Leu Gly Leu Ala Leu Asp Val Asp Arg Ile Lys Lys			
705	710	715	
gac caa gaa gag gaa gaa gac caa ggc cca ccg tgc ccc agg ctc agc			2748
Asp Gln Glu Glu Glu Glu Asp Gln Gly Pro Pro Cys Pro Arg Leu Ser			
720	725	730	735
agg gag ctg ctg gag gta gta gag cct gaa gtc ttg cag gac tca ctg			2796
Arg Glu Leu Leu Glu Val Val Glu Pro Glu Val Leu Gln Asp Ser Leu			
740	745	750	
gat aga tgt tat tca act cct tcc agt tgt ctt gaa cag cct gac tcc			2844
Asp Arg Cys Tyr Ser Thr Pro Ser Ser Cys Leu Glu Gln Pro Asp Ser			
755	760	765	
tgc cag ccc tac gga agt tcc ttt tat gca ttg gag gaa aaa cat gtt			2892
Cys Gln Pro Tyr Gly Ser Ser Phe Tyr Ala Leu Glu Glu Lys His Val			
770	775	780	
ggc ttt tct ctt gac gtg gga gaa att gaa aag aag ggg aag ggg aag			2940
Gly Phe Ser Leu Asp Val Gly Glu Ile Glu Lys Lys Gly Lys Gly Lys			

785

790

795

aaa aga agg gga aga aga tca aag aag aaa aga aga aaa aaaaaaaaaa aa 2991
 Lys Arg Arg Gly Arg Arg Ser Lys Lys Lys Arg Arg Lys
 800 805 810

<210> 197

<211> 58

<212> PRT

<213> Homo sapiens

<223> image: 2226413; Genbank AF419617; cDNA clone AG09

<400> 197

Met Val Val Ser Ala Gly Pro Trp Ser Ser Glu Lys Ala Glu Met Asn
 1 5 10 15
 Ile Leu Glu Ile Asn Glu Lys Leu Arg Pro Gln Leu Ala Glu Asn Lys
 20 25 30
 Gln Gln Phe Arg Asn Leu Lys Glu Arg Cys Phe Leu Thr Gln Leu Ala
 35 40 45
 Gly Phe Leu Ala Asn Arg Gln Lys Lys Tyr
 50 55

<210> 198

<211> 754

<212> PRT

<213> Homo sapiens

<223> image: 2226413; Genbank AF419617; cDNA clone AG09

<400> 198

Gln Tyr Lys Val Leu Val His Ser Gln Glu Arg Glu Leu Thr Gln Leu
 1 5 10 15
 Arg Glu Lys Leu Arg Glu Gly Arg Asp Ala Ser Arg Ser Leu Asn Glu
 20 25 30
 His Leu Gln Ala Leu Leu Thr Pro Asp Glu Pro Asp Lys Ser Gln Gly
 35 40 45
 Gln Asp Leu Gln Glu Gln Leu Ala Glu Gly Cys Arg Leu Ala Gln His
 50 55 60
 Leu Val Gln Lys Leu Ser Pro Glu Asn Asp Lys Asp Glu Asp Glu Asp
 65 70 75 80
 Val Gln Val Glu Glu Asp Glu Lys Val Leu Glu Ser Ser Ala Pro Arg
 85 90 95
 Glu Val Gln Lys Ala Glu Glu Ser Lys Val Pro Glu Asp Ser Leu Glu
 100 105 110
 Glu Cys Ala Ile Thr Cys Ser Asn Ser His Gly Pro Cys Asp Ser Ile
 115 120 125
 Gln Pro His Lys Asn Ile Lys Ile Thr Phe Glu Glu Asp Lys Val Asn

130	135	140
Ser Ser Leu Val Val Asp Arg Glu Ser Ser His Asp Gly Cys Gln Asp		
145	150	155
Ala Leu Asn Ile Leu Pro Val Pro Gly Pro Thr Ser Ser Ala Thr Asn		
165	170	175
Val Ser Met Val Val Ser Ala Gly Pro Leu Ser Ser Glu Lys Ala Glu		
180	185	190
Met Asn Ile Leu Glu Ile Asn Glu Lys Leu Cys Pro Gln Leu Ala Glu		
195	200	205
Lys Lys Gln Gln Phe Arg Ser Leu Lys Glu Lys Cys Phe Val Thr Gln		
210	215	220
Val Ala Cys Phe Leu Ala Lys Gln Gln Asn Lys Tyr Lys Tyr Glu Glu		
225	230	235
Cys Lys Asp Leu Ile Lys Ser Met Leu Arg Asn Glu Arg Gln Phe Lys		
245	250	255
Glu Glu Lys Leu Ala Glu Gln Leu Lys Gln Ala Glu Glu Leu Arg Gln		
260	265	270
Tyr Lys Val Leu Val His Ser Gln Glu Arg Glu Leu Thr Gln Leu Arg		
275	280	285
Glu Lys Leu Arg Glu Gly Arg Asp Ala Ser Arg Ser Leu Asn Glu His		
290	295	300
Leu Gln Ala Leu Leu Thr Pro Asp Glu Pro Asp Lys Ser Gln Gly Gln		
305	310	315
Asp Leu Gln Glu Gln Leu Ala Glu Gly Cys Arg Leu Ala Gln His Leu		
325	330	335
Val Gln Lys Leu Ser Pro Glu Asn Asp Asn Asp Asp Asp Glu Asp Val		
340	345	350
Gln Val Glu Val Ala Glu Lys Val Gln Lys Ser Ser Ser Pro Arg Glu		
355	360	365
Met Gln Lys Ala Glu Glu Lys Glu Val Pro Glu Asp Ser Leu Glu Glu		
370	375	380
Cys Ala Ile Thr Cys Ser Asn Ser His Gly Pro Tyr Asp Ser Asn Gln		
385	390	395
Pro His Arg Lys Thr Lys Ile Thr Phe Glu Glu Asp Lys Val Asp Ser		
405	410	415
Thr Leu Ile Gly Ser Ser Ser His Val Glu Trp Glu Asp Ala Val His		
420	425	430
Ile Ile Pro Glu Asn Glu Ser Asp Asp Glu Glu Glu Glu Lys Gly		
435	440	445
Pro Val Ser Pro Arg Asn Leu Gln Glu Ser Glu Glu Glu Glu Val Pro		
450	455	460
Gln Glu Ser Trp Asp Glu Gly Tyr Ser Thr Leu Ser Ile Pro Pro Glu		
465	470	475
Arg Leu Ala Ser Tyr Gln Ser Tyr Ser Ser Thr Phe His Ser Leu Glu		
485	490	495
Glu Gln Gln Val Cys Met Ala Val Asp Ile Gly Arg His Arg Trp Asp		
500	505	510
Gln Val Lys Lys Glu Asp Gln Glu Ala Thr Gly Pro Arg Leu Ser Arg		


```

      515              520              525
Glu Leu Leu Asp Glu Lys Glu Pro Glu Val Leu Gln Asp Ser Leu Asp
      530              535              540
Arg Cys Tyr Ser Thr Pro Ser Val Tyr Leu Gly Leu Thr Asp Ser Cys
545              550              555              560
Gln Pro Tyr Arg Ser Ala Phe Tyr Val Leu Glu Gln Gln Arg Ile Gly
      565              570              575
Leu Ala Val Asp Met Asp Glu Ile Glu Lys Cys Gln Glu Val Glu Glu
      580              585              590
Asp Gln Asp Pro Ser Cys Pro Arg Leu Ser Arg Glu Leu Leu Ala Glu
      595              600              605
Lys Glu Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr
      610              615              620
Pro Ser Gly Tyr Leu Glu Leu Pro Asp Leu Gly Gln Pro Tyr Ser Ser
625              630              635              640
Ala Val Tyr Ser Leu Glu Glu Gln Tyr Leu Gly Leu Ala Leu Asp Val
      645              650              655
Asp Arg Ile Lys Lys Asp Gln Glu Glu Glu Glu Asp Gln Gly Pro Pro
      660              665              670
Cys Pro Arg Leu Ser Arg Glu Leu Leu Glu Val Val Glu Pro Glu Val
      675              680              685
Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Ser Cys Leu
      690              695              700
Glu Gln Pro Asp Ser Cys Gln Pro Tyr Gly Ser Ser Phe Tyr Ala Leu
705              710              715              720
Glu Glu Lys His Val Gly Phe Ser Leu Asp Val Gly Glu Ile Glu Lys
      725              730              735
Lys Gly Lys Gly Lys Lys Arg Arg Gly Arg Arg Ser Lys Lys Lys Arg
      740              745              750
Arg Lys

```

<210> 199

<211> 4444

<212> DNA

<213> Homo sapiens

<220>

<223> DKFZp564A057; Genbank AF419616; cDNA clone AG02

<220>

<221> CDS

<222> (1)..(2796)

<400> 199

```

ctt ggc ttg gct cct gac gtg gac aga act aaa aag gac caa gaa gag   48
Leu Gly Leu Ala Pro Asp Val Asp Arg Thr Lys Lys Asp Gln Glu Glu

```

1	5	10	15	
gaa gaa gac caa ggc cca cca tgc ccc agg ctc agc agg gag ctg ctg				96
Glu Glu Asp Gln Gly Pro Pro Cys Pro Arg Leu Ser Arg Glu Leu Leu				
20	25	30		
gag gta gta gag cct gaa gtc ttg cag gac tca ctg gat aga tgt tat				144
Glu Val Val Glu Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr				
35	40	45		
tca act cct tcc agt tgt ctt gaa cag cct gac tcc tgc cag ccc tat				192
Ser Thr Pro Ser Ser Cys Leu Glu Gln Pro Asp Ser Cys Gln Pro Tyr				
50	55	60		
gga agt tcc ttt tat gca ttg gag gaa aaa cat gtt ggc ttt tct ctc				240
Gly Ser Ser Phe Tyr Ala Leu Glu Glu Lys His Val Gly Phe Ser Leu				
65	70	75	80	
gac gtg gga gaa att gaa aag aag ggg aag ggg aag aaa aga agg gga				288
Asp Val Gly Glu Ile Glu Lys Lys Gly Lys Gly Lys Lys Arg Arg Gly				
85	90	95		
aga aga tca aag aag gaa aga aga agg gga aga aaa gaa ggg gaa gaa				336
Arg Arg Ser Lys Lys Glu Arg Arg Arg Gly Arg Lys Glu Gly Glu Glu				
100	105	110		
gat caa aac cca cca tgc ccc agg ctc agc agg gag ctg ctg gat gag				384
Asp Gln Asn Pro Pro Cys Pro Arg Leu Ser Arg Glu Leu Leu Asp Glu				
115	120	125		
gaa ggg cct gaa gtc ttg cag gac tca ctg gat aga tgt tat tca act				432
Glu Gly Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr				
130	135	140		
cct tca ggt tgt ctt gaa ctg act gac tca tgc cag ccc tac aga agt				480
Pro Ser Gly Cys Leu Glu Leu Thr Asp Ser Cys Gln Pro Tyr Arg Ser				
145	150	155	160	
gcc ttt tac gta ttg gag caa cag cgt gtt ggc ttg gct gtt gac atg				528
Ala Phe Tyr Val Leu Glu Gln Gln Arg Val Gly Leu Ala Val Asp Met				
165	170	175		
gat gaa att gaa aag tac caa gaa gtg gaa gaa gac caa gac cca tca				576
Asp Glu Ile Glu Lys Tyr Gln Glu Val Glu Glu Asp Gln Asp Pro Ser				
180	185	190		
tgc ccc agg ctc agc agg gag ctg ctg gat gag aaa gag cct gaa gtc				624
Cys Pro Arg Leu Ser Arg Glu Leu Leu Asp Glu Lys Glu Pro Glu Val				

195	200	205	
ttg cag gac tca ctg gat aga tgt tat tcg act cct tca ggt tgt ctt			672
Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Cys Leu			
210	215	220	
gaa ctg cct gac tta ggc cag ccc tac agc agt gct gtt tac tca ttg			720
Glu Leu Pro Asp Leu Gly Gln Pro Tyr Ser Ser Ala Val Tyr Ser Leu			
225	230	235	240
gag gaa cag tac ctt ggc ttg gct ctt gac gtg gac aga act aaa aag			768
Glu Glu Gln Tyr Leu Gly Leu Ala Leu Asp Val Asp Arg Thr Lys Lys			
245	250	255	
gac caa gaa gag gaa gaa gac caa ggc cca cca tgc ccc agg ctc agc			816
Asp Gln Glu Glu Glu Glu Asp Gln Gly Pro Pro Cys Pro Arg Leu Ser			
260	265	270	
agg gag ctg ctg gag gta gta gag cct gaa gtc ttg cag gac tca ctg			864
Arg Glu Leu Leu Glu Val Val Glu Pro Glu Val Leu Gln Asp Ser Leu			
275	280	285	
gat aga tgt tat tca act cct tcc agt tgt ctt gaa cag cct gac tcc			912
Asp Arg Cys Tyr Ser Thr Pro Ser Ser Cys Leu Glu Gln Pro Asp Ser			
290	295	300	
tgc cag ccc tat gga agt tcc ttt tat gca ttg gag gaa aaa cat gtt			960
Cys Gln Pro Tyr Gly Ser Ser Phe Tyr Ala Leu Glu Glu Lys His Val			
305	310	315	320
ggc ttt tct ctt gac gtg gga gaa att gaa aag aag ggg aag ggg aag			1008
Gly Phe Ser Leu Asp Val Gly Glu Ile Glu Lys Lys Gly Lys Gly Lys			
325	330	335	
aaa aga agg gga aga aga tca aag aag gaa aga aga ggg gga aga aaa			1056
Lys Arg Arg Gly Arg Arg Ser Lys Lys Glu Arg Arg Gly Gly Arg Lys			
340	345	350	
gaa ggg gaa gaa gat caa aac cca cca tgc ccc agg ctc agc agg gag			1104
Glu Gly Glu Glu Asp Gln Asn Pro Pro Cys Pro Arg Leu Ser Arg Glu			
355	360	365	
ctg ctg gat gag aaa ggg cct gaa gtc ttg cag gac tca ctg gat aga			1152
Leu Leu Asp Glu Lys Gly Pro Glu Val Leu Gln Asp Ser Leu Asp Arg			
370	375	380	
tgt tat tca act cct tca ggt tgt ctt gaa ctg act gac tca tgc cag			1200
Cys Tyr Ser Thr Pro Ser Gly Cys Leu Glu Leu Thr Asp Ser Cys Gln			

385	390	395	400
ccc tac aga agt gcc ttt tac gta ttg gag caa cag cgt gtt ggc ttg	1248		
Pro Tyr Arg Ser Ala Phe Tyr Val Leu Glu Gln Gln Arg Val Gly Leu			
405	410	415	
gct gtt gac atg gat gaa att gaa aag tac caa gaa gtg gaa gaa gac	1296		
Ala Val Asp Met Asp Glu Ile Glu Lys Tyr Gln Glu Val Glu Glu Asp			
420	425	430	
caa gac cca tca tgc ccc agg ctc agc agg gag ctg ctg gat gag aaa	1344		
Gln Asp Pro Ser Cys Pro Arg Leu Ser Arg Glu Leu Leu Asp Glu Lys			
435	440	445	
gag cct gaa gtc ttg cag gac tca ctg gat aga tgt tat tcg act cct	1392		
Glu Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro			
450	455	460	
tca ggt tat ctt gaa ctg cct gac tta ggc cag ccc tac agc agt gct	1440		
Ser Gly Tyr Leu Glu Leu Pro Asp Leu Gly Gln Pro Tyr Ser Ser Ala			
465	470	475	480
gag tac tca ttg gag gaa cag tac ctt ggc ttg gct ctt gac gtg gac	1488		
Glu Tyr Ser Leu Glu Glu Gln Tyr Leu Gly Leu Ala Leu Asp Val Asp			
485	490	495	
aga act aaa aag gac caa gaa gag gaa gaa gac caa ggc cca cca tgc	1536		
Arg Thr Lys Lys Asp Gln Glu Glu Glu Glu Asp Gln Gly Pro Pro Cys			
500	505	510	
ccc agg ctc agc agg gag ctg ctg gag gta gta gag cct gaa gtc ttg	1584		
Pro Arg Leu Ser Arg Glu Leu Leu Glu Val Val Glu Pro Glu Val Leu			
515	520	525	
cag gac tca ctg gat aga tgt tat tca act cct tcc agt tgt ctt gaa	1632		
Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Ser Cys Leu Glu			
530	535	540	
cag cct gac tcc tgc cag ccc tat gga agt tcc ttt tat gca ttg gag	1680		
Gln Pro Asp Ser Cys Gln Pro Tyr Gly Ser Ser Phe Tyr Ala Leu Glu			
545	550	555	560
gaa aaa cat gtt ggc ttt tct ctc gac gtg gga gaa att gaa aag aag	1728		
Glu Lys His Val Gly Phe Ser Leu Asp Val Gly Glu Ile Glu Lys Lys			
565	570	575	
ggg aag ggg aag aaa aga ggg gga aga aga tca gag aag gaa aga aga	1776		
Gly Lys Gly Lys Lys Arg Gly Gly Arg Arg Ser Glu Lys Glu Arg Arg			

580	585	590	
agg gga aga aaa gaa ggg gaa gaa gat caa aac cca cca tgc ccc agg			1824
Arg Gly Arg Lys Glu Gly Glu Glu Asp Gln Asn Pro Pro Cys Pro Arg			
595	600	605	
ctc agc agg gag ctg ctg gat gag aaa ggg cct gaa gtc ttg cag gac			1872
Leu Ser Arg Glu Leu Leu Asp Glu Lys Gly Pro Glu Val Leu Gln Asp			
610	615	620	
tca ctg gat aga tgt tat tca act cct tca ggt tgt ctt gaa ctg act			1920
Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Cys Leu Glu Leu Thr			
625	630	635	640
gac tca tgc cag ccc tac aga agt gcc ttt tac gta ttg gag caa cag			1968
Asp Ser Cys Gln Pro Tyr Arg Ser Ala Phe Tyr Val Leu Glu Gln Gln			
645	650	655	
cgt gtt ggc ttg gct gtt gac atg gat gaa att gaa aag tac caa gaa			2016
Arg Val Gly Leu Ala Val Asp Met Asp Glu Ile Glu Lys Tyr Gln Glu			
660	665	670	
gtg gaa gaa gac caa gac cca tca tgc ccc agg ctc agc agg gag ctg			2064
Val Glu Glu Asp Gln Asp Pro Ser Cys Pro Arg Leu Ser Arg Glu Leu			
675	680	685	
ctg gat gag aaa gag cct gaa gtc ttg cag gac tca ctg gat aga tgt			2112
Leu Asp Glu Lys Glu Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys			
690	695	700	
tat tcg act cct tca ggt tat ctt gaa ctg cct gac tta ggc cag ccc			2160
Tyr Ser Thr Pro Ser Gly Tyr Leu Glu Leu Pro Asp Leu Gly Gln Pro			
705	710	715	720
tac agc agt gct gtt tac tcatttg gag gaa cag tac ctt ggc ttg gct			2208
Tyr Ser Ser Ala Val Tyr Ser Leu Glu Glu Gln Tyr Leu Gly Leu Ala			
725	730	735	
ctt gac gtg gac aga act aaa aag gac caa gaa gag gaa gaa gac caa			2256
Leu Asp Val Asp Arg Thr Lys Lys Asp Gln Glu Glu Glu Glu Asp Gln			
740	745	750	
ggc cca cca tgc ccc agg ctc agc agg gag ctg ctg gag gta gta gag			2304
Gly Pro Pro Cys Pro Arg Leu Ser Arg Glu Leu Leu Glu Val Val Glu			
755	760	765	
cct gaa gtc ttg cag gac tca ctg aat aga tgt tat tca act cct tcc			2352
Pro Glu Val Leu Gln Asp Ser Leu Asn Arg Cys Tyr Ser Thr Pro Ser			

770	775	780	
agt tgt ctt gaa cag cct gac tcc tgc cag ccc tat gga agt tcc ttt			2400
Ser Cys Leu Glu Gln Pro Asp Ser Cys Gln Pro Tyr Gly Ser Ser Phe			
785	790	795	800
tat gca ttg gag gaa aaa cat gtt ggc ttt tct ctt gac gtg gga gaa			2448
Tyr Ala Leu Glu Glu Lys His Val Gly Phe Ser Leu Asp Val Gly Glu			
	805	810	815
att gaa aag aag ggg aag ggg aag aaa aga agg gga aga aga tca aag			2496
Ile Glu Lys Lys Gly Lys Gly Lys Lys Arg Arg Gly Arg Arg Ser Lys			
	820	825	830
aag aaa aga aga agg gga aga aaa gaa ggg gaa gaa gat caa aac cca			2544
Lys Lys Arg Arg Arg Gly Arg Lys Glu Gly Glu Glu Asp Gln Asn Pro			
	835	840	845
cca tgc ccc agg ccc aac ggc gtg ctg atg gaa gtg gaa ggg cct gaa			2592
Pro Cys Pro Arg Pro Asn Gly Val Leu Met Glu Val Glu Gly Pro Glu			
	850	855	860
gtc tta cag gac tca ctg gat gga tgt tat tct act ccg tca atg tac			2640
Val Leu Gln Asp Ser Leu Asp Gly Cys Tyr Ser Thr Pro Ser Met Tyr			
865	870	875	880
ttt gaa cta cct gac tca ttc cag cac tac aga agt gtg ttt tac tca			2688
Phe Glu Leu Pro Asp Ser Phe Gln His Tyr Arg Ser Val Phe Tyr Ser			
	885	890	895
ttt gag gaa cag cac atc agc ttc gcc ctt tac gtg gac aat agg ttt			2736
Phe Glu Glu Gln His Ile Ser Phe Ala Leu Tyr Val Asp Asn Arg Phe			
	900	905	910
ttt act ttg acg gtg aca agt ctc cac ctg gtg ttc cag atg gga gtc			2784
Phe Thr Leu Thr Val Thr Ser Leu His Leu Val Phe Gln Met Gly Val			
	915	920	925
ata ttc cca caa taaacagccc ttactaagcc gagagatgtc attcctgcag			2836
Ile Phe Pro Gln			
930			
gcaggaccta taggcacgtg aagatttgaa tgaaagtaca gttccatttg gaagcccaga			2896
cataggatgg gtcagtgggc atggctgtat tcctattctc aaaccatgcc agtggcaacc			2956
tgtgctcagt ctgaagacaa tggaccacg ttaggtgtga cacgttcaca taactgtgca			3016

gcacatgccg ggagtgatca gtcagacatt ttaatttgaa ccacgtatct ctgggtagct 3076
acaaaattcc tcagggatth ctttttgag gcatgtctct gagcttctat acctgtctaa 3136
ggtcattgtc atctttgtgt ttagctcatc caaagggtgt accctgggtt caatgaacct 3196
aacctcatc tttgtgtctt cagtgttggc ttgttttagc tgatccatct gtaacacagg 3256
agggatccct ggttgaggat tgtatttcag aaccaccaac tgctcttgac aattgttaac 3316
ccgctaggct cctttgggta gagaagccac agtccttcag cctccaattg gtgtcagtac 3376
ttaggaagac cacagctaga tggacaaaaca gcattgggag gccttagccc tgctctctc 3436
aattccatcc ttagagaaac aggagtcagg agccgctggc aggagacagc atgtcaccca 3496
ggactctgcc ggtgcagaat atgaacagt ccatgttctt gcagaaaacg cttagcctga 3556
gtttcatagg aggtaatcac cagacaactg cagaatgtgg aacctgagc gggacagctg 3616
acctgtctcc ttcacatagt ccatgtcacc acaaatacaca caacaaaaag gagaagagat 3676
atthtgggtt caaaaaacgt aaaaagataa ttagctgca tttctttagt tathhtgggc 3736
cccaaatatt tctcatctt tttgtttgtg tcatggatgg tggtagatg gacttgttta 3796
tagaggacag gtcagctgtc tggctcagt atctacattc tgaagttgtc tgaaaatgtc 3856
ttcatgatta aattcagcct aaacgttttg ccgggaacac tgcagagaca atgtctgtgag 3916
tttccaacct cagcccatct gcgggcagag aaggctagt ttgtccatca ccattatgat 3976
atcaggactg gttacttggg taaggagggg tctaggagat ctgtcccttt tagagacacc 4036
ttacttataa tgaagaagta ctgggaaag cggttttcaa gagtataaat atcctgtatt 4096
ctaatgatca tctctaaac atthtatcat ttattaatcc tccctgctg tgtctattat 4156
tatattcata tctctacact gcaaattttg ggtctcaatt tttactgtgc ctttgtttt 4216
actagtgtct gctgttgcaa aaagaaggag acattctctg cctgagtttt aathhtgtc 4276
caaagttaat tttaatctat acaattaaaa cttttgcct atcactctgg acttctggat 4336
tgttttttac attcagtgtt ataataattg attatgctga ttggttttgg tgggtactga 4396
tgogaattaa taaaaacatt tcatttccaa aaaaaaaaaa aaaaaaaa 4444

<210> 200

<211> 932

<212> PRT

<213> Homo sapiens

<223> DKFZp564A057; Genbank AF419616; cDNA clone AG02

<400> 200

Leu Gly Leu Ala Pro Asp Val Asp Arg Thr Lys Lys Asp Gln Glu Glu
 1 5 10 15

Glu Glu Asp Gln Gly Pro Pro Cys Pro Arg Leu Ser Arg Glu Leu Leu
 20 25 30

Glu Val Val Glu Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr
 35 40 45

Ser Thr Pro Ser Ser Cys Leu Glu Gln Pro Asp Ser Cys Gln Pro Tyr
 50 55 60

Gly Ser Ser Phe Tyr Ala Leu Glu Glu Lys His Val Gly Phe Ser Leu
 65 70 75 80

Asp Val Gly Glu Ile Glu Lys Lys Gly Lys Gly Lys Lys Arg Arg Gly
 85 90 95

Arg Arg Ser Lys Lys Glu Arg Arg Arg Gly Arg Lys Glu Gly Glu Glu
 100 105 110

Asp Gln Asn Pro Pro Cys Pro Arg Leu Ser Arg Glu Leu Leu Asp Glu
 115 120 125

Glu Gly Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr
 130 135 140

Pro Ser Gly Cys Leu Glu Leu Thr Asp Ser Cys Gln Pro Tyr Arg Ser
 145 150 155 160

Ala Phe Tyr Val Leu Glu Gln Gln Arg Val Gly Leu Ala Val Asp Met
 165 170 175

Asp Glu Ile Glu Lys Tyr Gln Glu Val Glu Glu Asp Gln Asp Pro Ser
 180 185 190

Cys Pro Arg Leu Ser Arg Glu Leu Leu Asp Glu Lys Glu Pro Glu Val
 195 200 205

Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Cys Leu

210	215	220
Glu Leu Pro Asp Leu Gly Gln Pro Tyr Ser Ser Ala Val Tyr Ser Leu		
225	230	235 240
Glu Glu Gln Tyr Leu Gly Leu Ala Leu Asp Val Asp Arg Thr Lys Lys		
245	250	255
Asp Gln Glu Glu Glu Glu Asp Gln Gly Pro Pro Cys Pro Arg Leu Ser		
260	265	270
Arg Glu Leu Leu Glu Val Val Glu Pro Glu Val Leu Gln Asp Ser Leu		
275	280	285
Asp Arg Cys Tyr Ser Thr Pro Ser Ser Cys Leu Glu Gln Pro Asp Ser		
290	295	300
Cys Gln Pro Tyr Gly Ser Ser Phe Tyr Ala Leu Glu Glu Lys His Val		
305	310	315 320
Gly Phe Ser Leu Asp Val Gly Glu Ile Glu Lys Lys Gly Lys Gly Lys		
325	330	335
Lys Arg Arg Gly Arg Arg Ser Lys Lys Glu Arg Arg Gly Gly Arg Lys		
340	345	350
Glu Gly Glu Glu Asp Gln Asn Pro Pro Cys Pro Arg Leu Ser Arg Glu		
355	360	365
Leu Leu Asp Glu Lys Gly Pro Glu Val Leu Gln Asp Ser Leu Asp Arg		
370	375	380
Cys Tyr Ser Thr Pro Ser Gly Cys Leu Glu Leu Thr Asp Ser Cys Gln		
385	390	395 400
Pro Tyr Arg Ser Ala Phe Tyr Val Leu Glu Gln Gln Arg Val Gly Leu		
405	410	415
Ala Val Asp Met Asp Glu Ile Glu Lys Tyr Gln Glu Val Glu Glu Asp		
420	425	430
Gln Asp Pro Ser Cys Pro Arg Leu Ser Arg Glu Leu Leu Asp Glu Lys		
435	440	445
Glu Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro		
450	455	460
Ser Gly Tyr Leu Glu Leu Pro Asp Leu Gly Gln Pro Tyr Ser Ser Ala		

465 470 475 480
 Glu Tyr Ser Leu Glu Glu Gln Tyr Leu Gly Leu Ala Leu Asp Val Asp
 485 490 495
 Arg Thr Lys Lys Asp Gln Glu Glu Glu Glu Asp Gln Gly Pro Pro Cys
 500 505 510
 Pro Arg Leu Ser Arg Glu Leu Leu Glu Val Val Glu Pro Glu Val Leu
 515 520 525
 Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Ser Cys Leu Glu
 530 535 540
 Gln Pro Asp Ser Cys Gln Pro Tyr Gly Ser Ser Phe Tyr Ala Leu Glu
 545 550 555 560
 Glu Lys His Val Gly Phe Ser Leu Asp Val Gly Glu Ile Glu Lys Lys
 565 570 575
 Gly Lys Gly Lys Lys Arg Gly Gly Arg Arg Ser Glu Lys Glu Arg Arg
 580 585 590
 Arg Gly Arg Lys Glu Gly Glu Glu Asp Gln Asn Pro Pro Cys Pro Arg
 595 600 605
 Leu Ser Arg Glu Leu Leu Asp Glu Lys Gly Pro Glu Val Leu Gln Asp
 610 615 620
 Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Cys Leu Glu Leu Thr
 625 630 635 640
 Asp Ser Cys Gln Pro Tyr Arg Ser Ala Phe Tyr Val Leu Glu Gln Gln
 645 650 655
 Arg Val Gly Leu Ala Val Asp Met Asp Glu Ile Glu Lys Tyr Gln Glu
 660 665 670
 Val Glu Glu Asp Gln Asp Pro Ser Cys Pro Arg Leu Ser Arg Glu Leu
 675 680 685
 Leu Asp Glu Lys Glu Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys
 690 695 700
 Tyr Ser Thr Pro Ser Gly Tyr Leu Glu Leu Pro Asp Leu Gly Gln Pro
 705 710 715 720
 Tyr Ser Ser Ala Val Tyr Ser Leu Glu Glu Gln Tyr Leu Gly Leu Ala

```
<210> 201
<211> 5166
<212> DNA
<213> Homo sapiens
```

<220>

<223> Full-size DNA sequence of representative NBG gene

<220>

<221> CDS

<222> (55)..(5166)

<400> 201

```

gatcacattt ttccacaacat ccctgactcc acctcttctg ccacaaacgt cagc atg      57
                                           Met
                                           1

gtg gta tca gcc ggc cct tgg tcc agc gag aag gca gag atg aac att      105
Val Val Ser Ala Gly Pro Trp Ser Ser Glu Lys Ala Glu Met Asn Ile
           5                      10                      15

cta gaa atc aac gag aaa ttg cgc ccc cag ttg gca gag aac aaa cag      153
Leu Glu Ile Asn Glu Lys Leu Arg Pro Gln Leu Ala Glu Asn Lys Gln
           20                      25                      30

cag ttc aga aac ctc aaa gag aga tgt ttt cta act caa ctg gcc ggc      201
Gln Phe Arg Asn Leu Lys Glu Arg Cys Phe Leu Thr Gln Leu Ala Gly
           35                      40                      45

ttc ctg gcc aac cga cag aag aaa tac aag tat gaa gag tgt aaa gac      249
Phe Leu Ala Asn Arg Gln Lys Lys Tyr Lys Tyr Glu Glu Cys Lys Asp
           50                      55                      60                      65

ctc ata aaa ttt atg ctg agg aat gag cga cag ttc aag gag gag aag      297
Leu Ile Lys Phe Met Leu Arg Asn Glu Arg Gln Phe Lys Glu Glu Lys
           70                      75                      80

ctt gca gag cag ctg aaa caa gct gag gag ctc agg caa tat aaa gtc      345
Leu Ala Glu Gln Leu Lys Gln Ala Glu Glu Leu Arg Gln Tyr Lys Val
           85                      90                      95

ctg gtt cac tct cag gaa cga gag ctg acc cag tta agg gag aag tta      393
Leu Val His Ser Gln Glu Arg Glu Leu Thr Gln Leu Arg Glu Lys Leu
           100                     105                     110

cgg gaa ggg aga gat gcc tcc cgc tca ttg aat gag cat ctc cag gcc      441
Arg Glu Gly Arg Asp Ala Ser Arg Ser Leu Asn Glu His Leu Gln Ala
           115                     120                     125

ctc ctc act ccg gat gag ccg gac aag tcc cag ggg cag gac ctc caa      489
Leu Leu Thr Pro Asp Glu Pro Asp Lys Ser Gln Gly Gln Asp Leu Gln
           130                     135                     140                     145

```

gaa cag ctg gct gag ggg tgt aga ctg gca cag caa ctt gtc caa aag	537
Glu Gln Leu Ala Glu Gly Cys Arg Leu Ala Gln Gln Leu Val Gln Lys	
150 155 160	
ctc agc cca gaa aat gat gaa gat gag gat gaa gat gtt caa gtt gag	585
Leu Ser Pro Glu Asn Asp Glu Asp Glu Asp Glu Asp Val Gln Val Glu	
165 170 175	
gag gat gag aaa gta ctg gaa tca tct gcc ccc agg gag gtg cag aag	633
Glu Asp Glu Lys Val Leu Glu Ser Ser Ala Pro Arg Glu Val Gln Lys	
180 185 190	
gct gaa gag agc aaa gtc cct gag gac tca ctg gag gaa tgt gcc atc	681
Ala Glu Glu Ser Lys Val Pro Glu Asp Ser Leu Glu Glu Cys Ala Ile	
195 200 205	
act tgt tca aat agc cac ggc cct tgt gac tcc aac cag cct cac aag	729
Thr Cys Ser Asn Ser His Gly Pro Cys Asp Ser Asn Gln Pro His Lys	
210 215 220 225	
aac atc aaa atc aca ttt gag gaa gac aaa gtc aac tca act gtg gtt	777
Asn Ile Lys Ile Thr Phe Glu Glu Asp Lys Val Asn Ser Thr Val Val	
230 235 240	
gta gac aga aaa tcc tct cat gat gaa tgt cag gat gct cta aac att	825
Val Asp Arg Lys Ser Ser His Asp Glu Cys Gln Asp Ala Leu Asn Ile	
245 250 255	
ctc cca gtc cct ggc ccc acc tct tct gcc aca aac gtc agc atg gtg	873
Leu Pro Val Pro Gly Pro Thr Ser Ser Ala Thr Asn Val Ser Met Val	
260 265 270	
gta tca gcc ggc cct ttg tcc agc gag aag gca gag atg aac att cta	921
Val Ser Ala Gly Pro Leu Ser Ser Glu Lys Ala Glu Met Asn Ile Leu	
275 280 285	
gaa atc aat gag aag ttg cgc ccc cag ctg gca gag aag aaa cag cag	969
Glu Ile Asn Glu Lys Leu Arg Pro Gln Leu Ala Glu Lys Lys Gln Gln	
290 295 300 305	
ttc aga agc ctc aaa gag aaa tgt ttt gta act caa ctg gcc ggc ttc	1017
Phe Arg Ser Leu Lys Glu Lys Cys Phe Val Thr Gln Leu Ala Gly Phe	
310 315 320	
ctg gcc aag cag cag aac aaa tac aaa tat gaa gag tgc aaa gac ctc	1065
Leu Ala Lys Gln Gln Asn Lys Tyr Lys Tyr Glu Glu Cys Lys Asp Leu	
325 330 335	

ata aaa tct atg ctg agg aat gag cta cag ttc aag gag gag aag ctt	1113
Ile Lys Ser Met Leu Arg Asn Glu Leu Gln Phe Lys Glu Glu Lys Leu	
340 345 350	
gca gag cag ctg aag caa gct gag gag ctc agg caa tat aaa gtc ctg	1161
Ala Glu Gln Leu Lys Gln Ala Glu Glu Leu Arg Gln Tyr Lys Val Leu	
355 360 365	
gtt cac tct cag gaa cga gag ctg acc cag tta agg gag aag tta cgg	1209
Val His Ser Gln Glu Arg Glu Leu Thr Gln Leu Arg Glu Lys Leu Arg	
370 375 380 385	
gaa ggg aga gat gcc tcc cgc tca ttg aat gag cat ctc cag gcc ctc	1257
Glu Gly Arg Asp Ala Ser Arg Ser Leu Asn Glu His Leu Gln Ala Leu	
390 395 400	
ctc act ccg gat gag ccg gac aag tcc cag ggg cag gac ctc caa gaa	1305
Leu Thr Pro Asp Glu Pro Asp Lys Ser Gln Gly Gln Asp Leu Gln Glu	
405 410 415	
cag ctg gct gag ggg tgt aga ctg gca cag cac ctt gtc caa aag ctc	1353
Gln Leu Ala Glu Gly Cys Arg Leu Ala Gln His Leu Val Gln Lys Leu	
420 425 430	
agc cca gaa aat gat gaa gat gag gat gaa gat gtt caa gtt gag gag	1401
Ser Pro Glu Asn Asp Glu Asp Glu Asp Glu Asp Val Gln Val Glu Glu	
435 440 445	
gat gag aaa gtg ctg gaa tca tct tcc ccc agg gag atg cag aag gct	1449
Asp Glu Lys Val Leu Glu Ser Ser Ser Pro Arg Glu Met Gln Lys Ala	
450 455 460 465	
gaa gaa agc aaa gtc cct gag gac tca ctg gag gaa tgt gcc atc act	1497
Glu Glu Ser Lys Val Pro Glu Asp Ser Leu Glu Glu Cys Ala Ile Thr	
470 475 480	
tgt tca aat agc cac ggc cct tgt gac tcc aac cag cct cac aag aac	1545
Cys Ser Asn Ser His Gly Pro Cys Asp Ser Asn Gln Pro His Lys Asn	
485 490 495	
atc aaa atc aca ttt gag gaa gac aaa gtc aac tca tct ctg gtt gta	1593
Ile Lys Ile Thr Phe Glu Glu Asp Lys Val Asn Ser Ser Leu Val Val	
500 505 510	
gac aga gaa tcc tct cat gat gaa tgt cag gat gct cta aac att ctc	1641
Asp Arg Glu Ser Ser His Asp Glu Cys Gln Asp Ala Leu Asn Ile Leu	
515 520 525	

cca gtc cct ggc ccc acc tct tct gcc aca aac gtc agc atg gtg gta	1689
Pro Val Pro Gly Pro Thr Ser Ser Ala Thr Asn Val Ser Met Val Val	
530 535 540 545	
tca gcc ggc cct ttg tcc agc gag aag gca gag atg aac att cta gaa	1737
Ser Ala Gly Pro Leu Ser Ser Glu Lys Ala Glu Met Asn Ile Leu Glu	
550 555 560	
atc aat gag aag ttg cgc ccc cag ctg gca gag aag aaa cag cag ttc	1785
Ile Asn Glu Lys Leu Arg Pro Gln Leu Ala Glu Lys Lys Gln Gln Phe	
565 570 575	
aga agc ctc aaa gag aaa tgt ttt gta act caa gtg gcc tgc ttc ctg	1833
Arg Ser Leu Lys Glu Lys Cys Phe Val Thr Gln Val Ala Cys Phe Leu	
580 585 590	
gcc aag cag cag aac aaa tac aaa tat gaa gag tgc aaa gac ctc ata	1881
Ala Lys Gln Gln Asn Lys Tyr Lys Tyr Glu Glu Cys Lys Asp Leu Ile	
595 600 605	
aaa tct atg ctg agg aat gag cta cag ttc aag gag gag aag ctt gca	1929
Lys Ser Met Leu Arg Asn Glu Leu Gln Phe Lys Glu Glu Lys Leu Ala	
610 615 620 625	
gag cag ctg aag caa gct gag gag ctc agg caa tat aaa gtc ctg gtt	1977
Glu Gln Leu Lys Gln Ala Glu Glu Leu Arg Gln Tyr Lys Val Leu Val	
630 635 640	
cac tct cag gaa cga gag ctg acc cag tta agg gag aag tta cgg gaa	2025
His Ser Gln Glu Arg Glu Leu Thr Gln Leu Arg Glu Lys Leu Arg Glu	
645 650 655	
ggg aga gat gcc tcc cgc tca ttg aat gag cat ctc cag gcc ctc ctc	2073
Gly Arg Asp Ala Ser Arg Ser Leu Asn Glu His Leu Gln Ala Leu Leu	
660 665 670	
act ccg gat gag ccg gac aag tcc cag ggg cag gac ctc caa gaa cag	2121
Thr Pro Asp Glu Pro Asp Lys Ser Gln Gly Gln Asp Leu Gln Glu Gln	
675 680 685	
ctg gct gag ggg tgt aga ctg gca caa cac ctt gtc caa aag ctc agc	2169
Leu Ala Glu Gly Cys Arg Leu Ala Gln His Leu Val Gln Lys Leu Ser	
690 695 700 705	
cca gaa aat gat aac gat gac gat gaa gat gtt caa gtt gag gtg gct	2217
Pro Glu Asn Asp Asn Asp Asp Asp Glu Asp Val Gln Val Glu Val Ala	
710 715 720	

gag aaa gtg cag aaa tcg tct tcc ccc agg gag atg cag aag gct gaa	2265
Glu Lys Val Gln Lys Ser Ser Ser Pro Arg Glu Met Gln Lys Ala Glu	
725 730 735	
gaa aag gaa gtc cct gag gac tca ctg gag gag tgt gcc atc act tgt	2313
Glu Lys Glu Val Pro Glu Asp Ser Leu Glu Glu Cys Ala Ile Thr Cys	
740 745 750	
tca aat agc cat ggc cct tat tac tcc aac cag cca cat agg aaa acc	2361
Ser Asn Ser His Gly Pro Tyr Tyr Ser Asn Gln Pro His Arg Lys Thr	
755 760 765	
aaa atc aca ttt gag gaa gac aaa gtc gac tca act ctc att ggc tca	2409
Lys Ile Thr Phe Glu Glu Asp Lys Val Asp Ser Thr Leu Ile Gly Ser	
770 775 780 785	
tcc tct cat gtt gaa tgg gag gat gct gta cac att atc cca gaa aat	2457
Ser Ser His Val Glu Trp Glu Asp Ala Val His Ile Ile Pro Glu Asn	
790 795 800	
gaa agt gat gat gag gaa gag gaa gaa aaa ggg cca gtg tct ccc agg	2505
Glu Ser Asp Asp Glu Glu Glu Glu Glu Lys Gly Pro Val Ser Pro Arg	
805 810 815	
aat ctg cag gag tct gaa gag gag gaa gtc ccc cag gag tcc tgg gat	2553
Asn Leu Gln Glu Ser Glu Glu Glu Glu Val Pro Gln Glu Ser Trp Asp	
820 825 830	
gaa ggt tat tcg act ctc tca att cct cct gaa atg ttg gcc tcg tac	2601
Glu Gly Tyr Ser Thr Leu Ser Ile Pro Pro Glu Met Leu Ala Ser Tyr	
835 840 845	
cag tct tac agc ggc aca ttt cac tca tta gag gaa cag caa gtc tgc	2649
Gln Ser Tyr Ser Gly Thr Phe His Ser Leu Glu Glu Gln Gln Val Cys	
850 855 860 865	
atg gct gtt gac ata ggc gga cat cgg tgg gat caa gtg aaa aag gag	2697
Met Ala Val Asp Ile Gly Gly His Arg Trp Asp Gln Val Lys Lys Glu	
870 875 880	
gac caa gag gca aca ggt ccc agg ctc agc agg gag ctg ctg gat gag	2745
Asp Gln Glu Ala Thr Gly Pro Arg Leu Ser Arg Glu Leu Leu Asp Glu	
885 890 895	
aaa ggg cct gaa gtc ttg cag gac tca ctg gat aga tgt tat tca act	2793
Lys Gly Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr	
900 905 910	

cct tca ggt tat ctt gaa ctg act gac tca tgc cag ccc tac aga agt	2841
Pro Ser Gly Tyr Leu Glu Leu Thr Asp Ser Cys Gln Pro Tyr Arg Ser	
915 920 925	
gcc ttt tac ata ttg gag caa cag cgt gtt ggc tgg gct ctt gac atg	2889
Ala Phe Tyr Ile Leu Glu Gln Gln Arg Val Gly Trp Ala Leu Asp Met	
930 935 940 945	
gat gaa att gaa aag tac caa gaa gtg gaa gaa gac caa gac cca tca	2937
Asp Glu Ile Glu Lys Tyr Gln Glu Val Glu Glu Asp Gln Asp Pro Ser	
950 955 960	
tgc ccc agg ctc agc agg gag ctg ctg gat gag aaa gag cct gaa gtc	2985
Cys Pro Arg Leu Ser Arg Glu Leu Leu Asp Glu Lys Glu Pro Glu Val	
965 970 975	
ttg cag gac tcc ctg gat aga tgt tat tcg act cct tca ggt tat ctt	3033
Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Tyr Leu	
980 985 990	
gaa ctg cct gac tta ggc cag ccc tac aga agt gct gtt tac tca ttg	3081
Glu Leu Pro Asp Leu Gly Gln Pro Tyr Arg Ser Ala Val Tyr Ser Leu	
995 1000 1005	
gag gaa cag tac ctt ggc ttg gct ctt gac gtg gac aga att aaa aag	3129
Glu Glu Gln Tyr Leu Gly Leu Ala Leu Asp Val Asp Arg Ile Lys Lys	
1010 1015 1020 1025	
gac caa gaa gag gaa gaa gac caa ggc cca cca tgc ccc agg ctc agc	3177
Asp Gln Glu Glu Glu Glu Asp Gln Gly Pro Pro Cys Pro Arg Leu Ser	
1030 1035 1040	
agg gag ctg ctg gag gca gta gag cct gaa gtc ttg cag gac tca ctg	3225
Arg Glu Leu Leu Glu Ala Val Glu Pro Glu Val Leu Gln Asp Ser Leu	
1045 1050 1055	
gat aga tgt tat tca act cct tcc agt tgt ctt gaa cag cct gac tcc	3273
Asp Arg Cys Tyr Ser Thr Pro Ser Ser Cys Leu Glu Gln Pro Asp Ser	
1060 1065 1070	
tgc ctg ccc tat gga agt tcc ttt tat gca ttg gag gaa aaa cat gtt	3321
Cys Leu Pro Tyr Gly Ser Ser Phe Tyr Ala Leu Glu Glu Lys His Val	
1075 1080 1085	
ggc ttt tct ctt gac gtg gga gaa att gaa aag aag ggg aag ggg aag	3369
Gly Phe Ser Leu Asp Val Gly Glu Ile Glu Lys Lys Gly Lys Gly Lys	
1090 1095 1100 1105	

aaa aga agg gga aga aga tca acg aag aaa aga agg aga agg gga aga	3417
Lys Arg Arg Gly Arg Arg Ser Thr Lys Lys Arg Arg Arg Arg Gly Arg	
1110 1115 1120	
aaa gaa ggg gaa gaa gat caa aac cca cca tgc ccc agg ctc agc agg	3465
Lys Glu Gly Glu Glu Asp Gln Asn Pro Pro Cys Pro Arg Leu Ser Arg	
1125 1130 1135	
gag ctg ctg gat gag aaa ggg cct gaa gtc ttg cag gac tca ctg gat	3513
Glu Leu Leu Asp Glu Lys Gly Pro Glu Val Leu Gln Asp Ser Leu Asp	
1140 1145 1150	
aga tgt tat tca act cct tca ggt tat ctt gaa ctg act gac tca tgc	3561
Arg Cys Tyr Ser Thr Pro Ser Gly Tyr Leu Glu Leu Thr Asp Ser Cys	
1155 1160 1165	
cag ccc tac aga agt gcc ttt tac ata ttg gag caa cag cgt gtt ggc	3609
Gln Pro Tyr Arg Ser Ala Phe Tyr Ile Leu Glu Gln Gln Arg Val Gly	
1170 1175 1180 1185	
tgg gct ctt gac atg gat gaa att gaa aag tac caa gaa gtg gaa gaa	3657
Trp Ala Leu Asp Met Asp Glu Ile Glu Lys Tyr Gln Glu Val Glu Glu	
1190 1195 1200	
gac caa gac cca tca tgc ccc agg ctc agc agg gag ctg ctg gat gag	3705
Asp Gln Asp Pro Ser Cys Pro Arg Leu Ser Arg Glu Leu Leu Asp Glu	
1205 1210 1215	
aaa gag cct gaa gtc ttg cag gac tcc ctg gat aga tgt tat tcg act	3753
Lys Glu Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr	
1220 1225 1230	
cct tca ggt tat ctt gaa ctg cct gac tta ggc cag ccc tac aga agt	3801
Pro Ser Gly Tyr Leu Glu Leu Pro Asp Leu Gly Gln Pro Tyr Arg Ser	
1235 1240 1245	
gct gtt tac tca ttg gag gaa cag tac ctt ggc ttg gct ctt gac gtg	3849
Ala Val Tyr Ser Leu Glu Glu Gln Tyr Leu Gly Leu Ala Leu Asp Val	
1250 1255 1260 1265	
gac aga att aaa aag gac cag gaa gag gaa gaa gac caa ggc cca cca	3897
Asp Arg Ile Lys Lys Asp Gln Glu Glu Glu Glu Asp Gln Gly Pro Pro	
1270 1275 1280	
tgc ccc agg ctc agc agg gag ctg ctg gag gca gta gag cct gaa gtc	3945
Cys Pro Arg Leu Ser Arg Glu Leu Leu Glu Ala Val Glu Pro Glu Val	
1285 1290 1295	

ttg cag gac tca ctg gat aga tgt tat tca act cct tcc agt tgt ctt	3993
Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Ser Cys Leu	
1300 1305 1310	
 gaa cag cct gac tcc tgc ctg ccc tat gga agt tcc ttt tat gca ttg	4041
Glu Gln Pro Asp Ser Cys Leu Pro Tyr Gly Ser Ser Phe Tyr Ala Leu	
1315 1320 1325	
 gag gaa aaa cat gtt ggc ttt tct ctt gac gtg gga gaa att gaa aag	4089
Glu Glu Lys His Val Gly Phe Ser Leu Asp Val Gly Glu Ile Glu Lys	
1330 1335 1340 1345	
 aag ggg aag ggg aag aaa aga agg gga aga aga tca acg aag aaa aga	4137
Lys Gly Lys Gly Lys Lys Arg Arg Gly Arg Arg Ser Thr Lys Lys Arg	
1350 1355 1360	
 agg aga agg gga aga aaa gaa ggg gaa gaa gat caa aac cca cca tgc	4185
Arg Arg Arg Gly Arg Lys Glu Gly Glu Glu Asp Gln Asn Pro Pro Cys	
1365 1370 1375	
 ccc agg ctc agc agg gag ctg ctg gat gag aaa ggg cct gaa gtc ttg	4233
Pro Arg Leu Ser Arg Glu Leu Leu Asp Glu Lys Gly Pro Glu Val Leu	
1380 1385 1390	
 cag gac tca ctg gat aga tgt tat tca act cct tca ggt tat ctt gaa	4281
Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Tyr Leu Glu	
1395 1400 1405	
 ctg act gac tca tgc cag ccc tac aga agt gcc ttt tac ata ttg gag	4329
Leu Thr Asp Ser Cys Gln Pro Tyr Arg Ser Ala Phe Tyr Ile Leu Glu	
1410 1415 1420 1425	
 caa cag cgt gtt ggc tgg gct ctt gac atg gat gaa att gaa aag tac	4377
Gln Gln Arg Val Gly Trp Ala Leu Asp Met Asp Glu Ile Glu Lys Tyr	
1430 1435 1440	
 caa gaa gtg gaa gaa gac caa gac cca tca tgc ccc agg ctc agc agg	4425
Gln Glu Val Glu Glu Asp Gln Asp Pro Ser Cys Pro Arg Leu Ser Arg	
1445 1450 1455	
 gag ctg ctg gat gag aaa gag cct gaa gtc ttg cag gac tcc ctg gat	4473
Glu Leu Leu Asp Glu Lys Glu Pro Glu Val Leu Gln Asp Ser Leu Asp	
1460 1465 1470	
 aga tgt tat tcg act cct tca ggt tat ctt gaa ctg cct gac tta ggc	4521
Arg Cys Tyr Ser Thr Pro Ser Gly Tyr Leu Glu Leu Pro Asp Leu Gly	
1475 1480 1485	

cag ccc tac aga agt gct gtt tac tca ttg gag gaa cag tac ctt ggc	4569
Gln Pro Tyr Arg Ser Ala Val Tyr Ser Leu Glu Glu Gln Tyr Leu Gly	
1490 1495 1500 1505	
ttg gct ctt gac gtg gac aga att aaa aag gac cag gaa gag gaa gaa	4617
Leu Ala Leu Asp Val Asp Arg Ile Lys Lys Asp Gln Glu Glu Glu Glu	
1510 1515 1520	
gac caa ggc cca cca tgc ccc agg ctc agc agg gag ctg ctg gag gca	4665
Asp Gln Gly Pro Pro Cys Pro Arg Leu Ser Arg Glu Leu Leu Glu Ala	
1525 1530 1535	
gta gag cct gaa gtc ttg cag gac tca ctg gat aga tgt tat tca act	4713
Val Glu Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr	
1540 1545 1550	
cct tcc agt tgt ctt gaa cag cct gac tcc tgc ctg ccc tat gga agt	4761
Pro Ser Ser Cys Leu Glu Gln Pro Asp Ser Cys Leu Pro Tyr Gly Ser	
1555 1560 1565	
tcc ttt tat gca ttg gag gaa aaa cat gtt ggc ttt tct ctt gac gtg	4809
Ser Phe Tyr Ala Leu Glu Glu Lys His Val Gly Phe Ser Leu Asp Val	
1570 1575 1580 1585	
gga gaa att gaa aag aag ggg aag ggg aag aaa aga agg gga aga aga	4857
Gly Glu Ile Glu Lys Lys Gly Lys Gly Lys Lys Arg Arg Gly Arg Arg	
1590 1595 1600	
tca acg aag aaa aga agg aga agg gga aga aaa gaa ggg gaa gaa gat	4905
Ser Thr Lys Lys Arg Arg Arg Arg Gly Arg Lys Glu Gly Glu Glu Asp	
1605 1610 1615	
caa aac cca cca tgc ccc agg ctc agc ggt gtg ctg atg gaa gtg gaa	4953
Gln Asn Pro Pro Cys Pro Arg Leu Ser Gly Val Leu Met Glu Val Glu	
1620 1625 1630	
gag cct gaa atc ttg cag gac tca ctg gat aga tgt tat tcg act ccg	5001
Glu Pro Glu Ile Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro	
1635 1640 1645	
tca atg ttc ttt gaa cta cct gac tca ttc cag cac tac aga agt gtg	5049
Ser Met Phe Phe Glu Leu Pro Asp Ser Phe Gln His Tyr Arg Ser Val	
1650 1655 1660 1665	
ttt tac tca ttt gag gaa cag cac atc agc ttc gcc ctt gac gtg gac	5097
Phe Tyr Ser Phe Glu Glu Gln His Ile Ser Phe Ala Leu Asp Val Asp	
1670 1675 1680	

aat agg ttt ctt act ttg atg gga aca agt ctc cac ctg gtc ttc cag 5145
 Asn Arg Phe Leu Thr Leu Met Gly Thr Ser Leu His Leu Val Phe Gln
 1685 1690 1695

atg gga gtc ata ttc cca cag 5166
 Met Gly Val Ile Phe Pro Gln
 1700

<210> 202

<211> 1704

<212> PRT

<213> Homo sapiens

<223> Full-size DNA sequence of representative NBG gene

<400> 202

Met Val Val Ser Ala Gly Pro Trp Ser Ser Glu Lys Ala Glu Met Asn
 1 5 10 15

Ile Leu Glu Ile Asn Glu Lys Leu Arg Pro Gln Leu Ala Glu Asn Lys
 20 25 30

Gln Gln Phe Arg Asn Leu Lys Glu Arg Cys Phe Leu Thr Gln Leu Ala
 35 40 45

Gly Phe Leu Ala Asn Arg Gln Lys Lys Tyr Lys Tyr Glu Glu Cys Lys
 50 55 60

Asp Leu Ile Lys Phe Met Leu Arg Asn Glu Arg Gln Phe Lys Glu Glu
 65 70 75 80

Lys Leu Ala Glu Gln Leu Lys Gln Ala Glu Glu Leu Arg Gln Tyr Lys
 85 90 95

Val Leu Val His Ser Gln Glu Arg Glu Leu Thr Gln Leu Arg Glu Lys
 100 105 110

Leu Arg Glu Gly Arg Asp Ala Ser Arg Ser Leu Asn Glu His Leu Gln
 115 120 125

Ala Leu Leu Thr Pro Asp Glu Pro Asp Lys Ser Gln Gly Gln Asp Leu
 130 135 140

Gln Glu Gln Leu Ala Glu Gly Cys Arg Leu Ala Gln Gln Leu Val Gln
 145 150 155 160

Lys Leu Ser Pro Glu Asn Asp Glu Asp Glu Asp Glu Asp Val Gln Val
 165 170 175

Glu Glu Asp Glu Lys Val Leu Glu Ser Ser Ala Pro Arg Glu Val Gln
 180 185 190

Lys Ala Glu Glu Ser Lys Val Pro Glu Asp Ser Leu Glu Glu Cys Ala
 195 200 205

Ile Thr Cys Ser Asn Ser His Gly Pro Cys Asp Ser Asn Gln Pro His
 210 215 220

Lys Asn Ile Lys Ile Thr Phe Glu Glu Asp Lys Val Asn Ser Thr Val
 225 230 235 240

Val Val Asp Arg Lys Ser Ser His Asp Glu Cys Gln Asp Ala Leu Asn
 245 250 255

Ile Leu Pro Val Pro Gly Pro Thr Ser Ser Ala Thr Asn Val Ser Met
 260 265 270

Val Val Ser Ala Gly Pro Leu Ser Ser Glu Lys Ala Glu Met Asn Ile
 275 280 285

Leu Glu Ile Asn Glu Lys Leu Arg Pro Gln Leu Ala Glu Lys Lys Gln
 290 295 300

Gln Phe Arg Ser Leu Lys Glu Lys Cys Phe Val Thr Gln Leu Ala Gly
 305 310 315 320

Phe Leu Ala Lys Gln Gln Asn Lys Tyr Lys Tyr Glu Glu Cys Lys Asp
 325 330 335

Leu Ile Lys Ser Met Leu Arg Asn Glu Leu Gln Phe Lys Glu Glu Lys
 340 345 350

Leu Ala Glu Gln Leu Lys Gln Ala Glu Glu Leu Arg Gln Tyr Lys Val
 355 360 365

Leu Val His Ser Gln Glu Arg Glu Leu Thr Gln Leu Arg Glu Lys Leu
 370 375 380

Arg Glu Gly Arg Asp Ala Ser Arg Ser Leu Asn Glu His Leu Gln Ala
 385 390 395 400

Leu Leu Thr Pro Asp Glu Pro Asp Lys Ser Gln Gly Gln Asp Leu Gln
 405 410 415

Glu Gln Leu Ala Glu Gly Cys Arg Leu Ala Gln His Leu Val Gln Lys
 420 425 430

Leu Ser Pro Glu Asn Asp Glu Asp Glu Asp Glu Asp Val Gln Val Glu
 435 440 445
 Glu Asp Glu Lys Val Leu Glu Ser Ser Ser Pro Arg Glu Met Gln Lys
 450 455 460
 Ala Glu Glu Ser Lys Val Pro Glu Asp Ser Leu Glu Glu Cys Ala Ile
 465 470 475 480
 Thr Cys Ser Asn Ser His Gly Pro Cys Asp Ser Asn Gln Pro His Lys
 485 490 495
 Asn Ile Lys Ile Thr Phe Glu Glu Asp Lys Val Asn Ser Ser Leu Val
 500 505 510
 Val Asp Arg Glu Ser Ser His Asp Glu Cys Gln Asp Ala Leu Asn Ile
 515 520 525
 Leu Pro Val Pro Gly Pro Thr Ser Ser Ala Thr Asn Val Ser Met Val
 530 535 540
 Val Ser Ala Gly Pro Leu Ser Ser Glu Lys Ala Glu Met Asn Ile Leu
 545 550 555 560
 Glu Ile Asn Glu Lys Leu Arg Pro Gln Leu Ala Glu Lys Lys Gln Gln
 565 570 575
 Phe Arg Ser Leu Lys Glu Lys Cys Phe Val Thr Gln Val Ala Cys Phe
 580 585 590
 Leu Ala Lys Gln Gln Asn Lys Tyr Lys Tyr Glu Glu Cys Lys Asp Leu
 595 600 605
 Ile Lys Ser Met Leu Arg Asn Glu Leu Gln Phe Lys Glu Glu Lys Leu
 610 615 620
 Ala Glu Gln Leu Lys Gln Ala Glu Glu Leu Arg Gln Tyr Lys Val Leu
 625 630 635 640
 Val His Ser Gln Glu Arg Glu Leu Thr Gln Leu Arg Glu Lys Leu Arg
 645 650 655
 Glu Gly Arg Asp Ala Ser Arg Ser Leu Asn Glu His Leu Gln Ala Leu
 660 665 670
 Leu Thr Pro Asp Glu Pro Asp Lys Ser Gln Gly Gln Asp Leu Gln Glu
 675 680 685

Gln Leu Ala Glu Gly Cys Arg Leu Ala Gln His Leu Val Gln Lys Leu
 690 695 700
 Ser Pro Glu Asn Asp Asn Asp Asp Asp Glu Asp Val Gln Val Glu Val
 705 710 715 720
 Ala Glu Lys Val Gln Lys Ser Ser Ser Pro Arg Glu Met Gln Lys Ala
 725 730 735
 Glu Glu Lys Glu Val Pro Glu Asp Ser Leu Glu Glu Cys Ala Ile Thr
 740 745 750
 Cys Ser Asn Ser His Gly Pro Tyr Tyr Ser Asn Gln Pro His Arg Lys
 755 760 765
 Thr Lys Ile Thr Phe Glu Glu Asp Lys Val Asp Ser Thr Leu Ile Gly
 770 775 780
 Ser Ser Ser His Val Glu Trp Glu Asp Ala Val His Ile Ile Pro Glu
 785 790 795 800
 Asn Glu Ser Asp Asp Glu Glu Glu Glu Glu Lys Gly Pro Val Ser Pro
 805 810 815
 Arg Asn Leu Gln Glu Ser Glu Glu Glu Glu Val Pro Gln Glu Ser Trp
 820 825 830
 Asp Glu Gly Tyr Ser Thr Leu Ser Ile Pro Pro Glu Met Leu Ala Ser
 835 840 845
 Tyr Gln Ser Tyr Ser Gly Thr Phe His Ser Leu Glu Glu Gln Gln Val
 850 855 860
 Cys Met Ala Val Asp Ile Gly Gly His Arg Trp Asp Gln Val Lys Lys
 865 870 875 880
 Glu Asp Gln Glu Ala Thr Gly Pro Arg Leu Ser Arg Glu Leu Leu Asp
 885 890 895
 Glu Lys Gly Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser
 900 905 910
 Thr Pro Ser Gly Tyr Leu Glu Leu Thr Asp Ser Cys Gln Pro Tyr Arg
 915 920 925
 Ser Ala Phe Tyr Ile Leu Glu Gln Gln Arg Val Gly Trp Ala Leu Asp
 930 935 940

Met Asp Glu Ile Glu Lys Tyr Gln Glu Val Glu Glu Asp Gln Asp Pro
 945 950 955 960
 Ser Cys Pro Arg Leu Ser Arg Glu Leu Leu Asp Glu Lys Glu Pro Glu
 965 970 975
 Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Tyr
 980 985 990
 Leu Glu Leu Pro Asp Leu Gly Gln Pro Tyr Arg Ser Ala Val Tyr Ser
 995 1000 1005
 Leu Glu Glu Gln Tyr Leu Gly Leu Ala Leu Asp Val Asp Arg Ile Lys
 1010 1015 1020
 Lys Asp Gln Glu Glu Glu Asp Gln Gly Pro Pro Cys Pro Arg Leu
 1025 1030 1035 1040
 Ser Arg Glu Leu Leu Glu Ala Val Glu Pro Glu Val Leu Gln Asp Ser
 1045 1050 1055
 Leu Asp Arg Cys Tyr Ser Thr Pro Ser Ser Cys Leu Glu Gln Pro Asp
 1060 1065 1070
 Ser Cys Leu Pro Tyr Gly Ser Ser Phe Tyr Ala Leu Glu Glu Lys His
 1075 1080 1085
 Val Gly Phe Ser Leu Asp Val Gly Glu Ile Glu Lys Lys Gly Lys Gly
 1090 1095 1100
 Lys Lys Arg Arg Gly Arg Arg Ser Thr Lys Lys Arg Arg Arg Arg Gly
 1105 1110 1115 1120
 Arg Lys Glu Gly Glu Glu Asp Gln Asn Pro Pro Cys Pro Arg Leu Ser
 1125 1130 1135
 Arg Glu Leu Leu Asp Glu Lys Gly Pro Glu Val Leu Gln Asp Ser Leu
 1140 1145 1150
 Asp Arg Cys Tyr Ser Thr Pro Ser Gly Tyr Leu Glu Leu Thr Asp Ser
 1155 1160 1165
 Cys Gln Pro Tyr Arg Ser Ala Phe Tyr Ile Leu Glu Gln Gln Arg Val
 1170 1175 1180
 Gly Trp Ala Leu Asp Met Asp Glu Ile Glu Lys Tyr Gln Glu Val Glu
 1185 1190 1195 1200

Glu Asp Gln Asp Pro Ser Cys Pro Arg Leu Ser Arg Glu Leu Leu Asp
 1205 1210 1215
 Glu Lys Glu Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser
 1220 1225 1230
 Thr Pro Ser Gly Tyr Leu Glu Leu Pro Asp Leu Gly Gln Pro Tyr Arg
 1235 1240 1245
 Ser Ala Val Tyr Ser Leu Glu Glu Gln Tyr Leu Gly Leu Ala Leu Asp
 1250 1255 1260
 Val Asp Arg Ile Lys Lys Asp Gln Glu Glu Glu Glu Asp Gln Gly Pro
 265 1270 1275 1280
 Pro Cys Pro Arg Leu Ser Arg Glu Leu Leu Glu Ala Val Glu Pro Glu
 1285 1290 1295
 Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Ser Cys
 1300 1305 1310
 Leu Glu Gln Pro Asp Ser Cys Leu Pro Tyr Gly Ser Ser Phe Tyr Ala
 1315 1320 1325
 Leu Glu Glu Lys His Val Gly Phe Ser Leu Asp Val Gly Glu Ile Glu
 1330 1335 1340
 Lys Lys Gly Lys Gly Lys Lys Arg Arg Gly Arg Arg Ser Thr Lys Lys
 345 1350 1355 1360
 Arg Arg Arg Arg Gly Arg Lys Glu Gly Glu Glu Asp Gln Asn Pro Pro
 1365 1370 1375
 Cys Pro Arg Leu Ser Arg Glu Leu Leu Asp Glu Lys Gly Pro Glu Val
 1380 1385 1390
 Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Gly Tyr Leu
 1395 1400 1405
 Glu Leu Thr Asp Ser Cys Gln Pro Tyr Arg Ser Ala Phe Tyr Ile Leu
 1410 1415 1420
 Glu Gln Gln Arg Val Gly Trp Ala Leu Asp Met Asp Glu Ile Glu Lys
 425 1430 1435 1440
 Tyr Gln Glu Val Glu Glu Asp Gln Asp Pro Ser Cys Pro Arg Leu Ser
 1445 1450 1455

Arg Glu Leu Leu Asp Glu Lys Glu Pro Glu Val Leu Gln Asp Ser Leu
 1460 1465 1470

Asp Arg Cys Tyr Ser Thr Pro Ser Gly Tyr Leu Glu Leu Pro Asp Leu
 1475 1480 1485

Gly Gln Pro Tyr Arg Ser Ala Val Tyr Ser Leu Glu Glu Gln Tyr Leu
 1490 1495 1500

Gly Leu Ala Leu Asp Val Asp Arg Ile Lys Lys Asp Gln Glu Glu Glu
 505 1510 1515 1520

Glu Asp Gln Gly Pro Pro Cys Pro Arg Leu Ser Arg Glu Leu Leu Glu
 1525 1530 1535

Ala Val Glu Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser
 1540 1545 1550

Thr Pro Ser Ser Cys Leu Glu Gln Pro Asp Ser Cys Leu Pro Tyr Gly
 1555 1560 1565

Ser Ser Phe Tyr Ala Leu Glu Glu Lys His Val Gly Phe Ser Leu Asp
 1570 1575 1580

Val Gly Glu Ile Glu Lys Lys Gly Lys Gly Lys Lys Arg Arg Gly Arg
 585 1590 1595 1600

Arg Ser Thr Lys Lys Arg Arg Arg Arg Gly Arg Lys Glu Gly Glu Glu
 1605 1610 1615

Asp Gln Asn Pro Pro Cys Pro Arg Leu Ser Gly Val Leu Met Glu Val
 1620 1625 1630

Glu Glu Pro Glu Ile Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr
 1635 1640 1645

Pro Ser Met Phe Phe Glu Leu Pro Asp Ser Phe Gln His Tyr Arg Ser
 1650 1655 1660

Val Phe Tyr Ser Phe Glu Glu Gln His Ile Ser Phe Ala Leu Asp Val
 665 1670 1675 1680

Asp Asn Arg Phe Leu Thr Leu Met Gly Thr Ser Leu His Leu Val Phe
 1685 1690 1695

Gln Met Gly Val Ile Phe Pro Gln
 1700

<210> 203

<211> 263

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: cDNA of exon A
and B

<400> 203

```
tcagggacat gcagaaggct gaagaaaagg aagtcacctga ggactcactg gaggaatgtg 60
ccatcaacttg ttcaaatagc catggccctt atgactccaa ccagccacat aggaaaacca 120
aaatcacatt tgaggaagac aaagtcgact caactctcat tggctcatcc tctcatgttg 180
aatgggagga tgctgtacac attatcccag aaaatgaaag tgatgatgag gaagaggaag 240
aaaaagggcc agtgtctccc agg                                     263
```