

**HLA-A TYPING IN FORMALIN-FIXED PARAFFIN EMBEDDED TISSUE
SAMPLES: TOWARDS POTENTIAL RETROSPECTIVE ANALYSIS**

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DISCLAIMER

“Universidad del Rosario and Karolinska Institutet are not responsible for the emitted concepts by the researchers on their work, the mentioned institutions only ensure scientific, methodical and ethical rigor of this work in order to benefit the truth and the justice”

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CONTENTS.

1. Introduction	3
2. Objectives	7
2.1. General Objective	7
2.2. Specific Objective	7
3. Theoretical Framework	8
3.1. Human Leukocyte Antigen	8
3.2. HLA Typing	14
3.3. Formalin-fixed, paraffin embedded (FFPE) tissue as a DNA source	16
4. Rationale and Hypothesis Formation	19
5. Materials and Methods	20
5.1. Patients Description	20
5.2. DNA Extraction	20
5.3. Amplification Primers Design	20
5.4. Amplification Procedure	22
5.5. Sequencing Procedure	23
5.6. Sequence Analysis	24
6. Clinical Significance	26
7. Results	27
7.1. DNA Extraction	27
7.2. Amplification Procedure	27
7.3. Sequencing Procedure	30
7.4. Sequences Analysis	32
8. Discussion	36
9. Conclusions	43
10. Future Perspectives and Proposals	44
11. References	45
12. Annexes	49
12.1. Annex 1	50
12.2. Annex 2	62

TABLES INDEX.

Table 1. Detailed information about the primers for the different amplification reactions.	21
Table 2. List of positive amplification reactions and primers used in the performed amplification reaction.	28
Table 3. Sequencing Results from new method compared to PCR-SSP.	35

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ABSTRACT

Human Leukocyte Antigen (HLA) has been described in many cases as prognostic factor for cancer. The main feature of HLA genes, located on chromosome 6 (6p21.3), is their extensive polymorphism. Nucleotide sequence analysis of alleles shows that the variation is restricted predominantly to exons that encode the peptide-binding domain of the protein. Thus, HLA polymorphism defines the repertoire of peptides that bind to HLA allotypes and this fact defines an individual's ability to respond to exposure to many infections agents throughout his life. HLA typing has become an important analysis in the clinic. Formalin-fixed paraffin embedded (FFPE) tissue samples are routinely collected in the oncological clinic. This could be used as a good DNA source, since in past studies DNA collecting assays were not normally performed from almost any kind of tissue or sample on regular clinic procedures. Considering that the most important problem with FFPE DNA is fragmentation, we proposed a new method for HLA-A allele typing from FFPE samples based on the sequences of exons 2, 3 and 4. We designed a set of twelve primers: four for HLA-A exon 2, three for HLA-A exon 3 and five for HLA-A exon 4, each one according to the flanking sequences for their respective exon and the sequence variation between different alleles. 17 FFPE samples collected in Karolinska University Hospital, Stockholm Sweden, and 1 control blood sample underwent amplification reactions and the products were submitted to sequencing. Finally all the obtained sequences were analyzed and compared with IMGT-HLA database. The FFPE samples were previous to this HLA PCR-SSP typed in a certified laboratory and then compared to the results from our novel method. According to this, the samples could be correctly sequenced compared to the previous typing. With this procedure, we conclude that our study is the first Sequence Based Typing method which allows the analysis of damaged DNA samples. It opens the possibility to develop retrospective analysis in order to establish new relationships between HLA and different diseases as well cancer.

RESUMEN

El Antígeno Leucocitario Humano (HLA en inglés) ha sido descrito en muchos casos como factor de pronóstico para cáncer. La característica principal de los genes de HLA, localizados en el cromosoma 6 (6p21.3), son sus numerosos polimorfismos. Los análisis de secuencia de nucleótidos muestran que la variación está restringida predominantemente a los exones que codifican los dominios de unión a péptidos de la proteína. Por lo tanto, el polimorfismo del HLA define el repertorio de péptidos que se unen a los alotipos de HLA y este hecho define la habilidad de un individuo para responder a la exposición a muchos agentes infecciosos durante su vida. La tipificación de HLA se ha convertido en un análisis importante en clínica. Muestras de tejido embebidas en parafina y fijadas con formalina (FFPE en inglés) son recolectadas rutinariamente en oncología. Este procedimiento podría ser utilizado como una buena fuente de ADN, dado que en estudios en el pasado los ensayos de recolección de ADN no eran normalmente llevados a cabo de casi ningún tejido o muestra en procedimientos clínicos regulares. Teniendo en cuenta que el problema más importante con el ADN de muestras FFPE es la fragmentación, nosotros propusimos un nuevo método para la tipificación del alelo HLA-A desde muestras FFPE basado en las secuencias del exón 2, 3 y 4. Nosotros diseñamos un juego de 12 cebadores: cuatro para el exón 2 de HLA-A, tres para el exón 3 de HLA-A y cinco para el exón 4 de HLA-A, cada uno de acuerdo las secuencias flanqueantes de su respectivo exón y la variación en la secuencia entre diferentes alelos. 17 muestras FFPE colectadas en el Hospital Universitario de Karolinska en Estocolmo Suecia fueron sometidas a PCR y los productos fueron secuenciados. Finalmente todas las secuencias obtenidas fueron analizadas y comparadas con la base de datos del IMGT-HLA. Las muestras FFPE habían sido previamente tipificadas para HLA y los resultados fueron comparados con los de este método. De acuerdo con nuestros resultados, las muestras pudieron ser correctamente secuenciadas. Con este procedimiento, podemos concluir que nuestro estudio es el primer método de tipificación basado en secuencia que permite analizar muestras viejas de ADN de las cuales no se tiene otra fuente. Este estudio abre la posibilidad de desarrollar análisis para establecer nuevas relaciones entre HLA y diferentes enfermedades como el cáncer también.

1. INTRODUCTION

Human Leukocyte Antigen (HLA) has been described in many cases as prognostic factor for cancer (Little and Stern 1999). The HLA complex is located on chromosome 6 (6p21.31). This high polymorphic locus encodes peptide presentation proteins, which perform the first step on immune adaptive response against any foreign pathogen or any abnormality detected on the organism (Little and Stern 1999; The-MHC-Consortium 1999; Goldsby, Kindt et al. 2003). Classical HLA class I molecules (HLA-A, -B and -C) are expressed in most somatic cells and presents peptides of around nine residues long. These peptides are derived from intracellular proteins, including proteins from pathogens such as viruses. These proteins are proteolytically cleaved, and the fragments are joined with HLA in the endoplasmic reticulum. The HLA-Peptide complex is transported to the cell membrane and presented. When an appropriate cell (T cells, Natural killers) interacts with HLA class I complex, the antigen presenting cells are inhibited or lysated (Little and Stern 1999; Goldsby, Kindt et al. 2003).

The main feature of HLA genes is their extensive polymorphism. Nucleotide sequence analysis of alleles shows that variation is restricted predominantly to exons that encode the peptide-binding domain of the protein, i. e. exons 2 and 3. Thus, HLA polymorphism defines the repertoire of peptides that bind to HLA allotypes and individual's ability to respond to exposure to many infections agents throughout his life (Little and Stern 1999). At population level, the high polymorphism in this locus ensures that at least some members of the population could survive infection of any pathogenic agent. The heterozygosity of HLA is advantageous for the species survival. Studies have demonstrated that HIV patients have a better immune response when the person has a heterozygote HLA than a person with a homozygote HLA genotype (Turner 2004).

Cancer is a multistep process that is often characterized by the accumulation of multiple genetic events including several mechanisms that are considered necessary for cell transformation (Little and Stern 1999). In cancer events, the immune system can detect

defective cells and eliminate them (Chang and Ferrone 2007). Tumor cells often express new antigens as a result of multiple genetic alterations, and T cells can monitor these new antigens via presentation on HLA class I, but certain cancer types have developed mechanisms that evade this recognition. HLA loss has been seen on all types of tumor, irrespective of tissue origin. On the other hand, tumor cells evade recognition from the NK cells (Little and Stern 1999). The immune surveillance theory proposes that any defect on immune system leads to a tumor genesis. This theory has been deliberated along many studies with mixed results, but the majority of these suggest that the tumor genesis depends on the capacity of evading immune response (Chang and Ferrone 2007).

Indeed, HLA class I antigens have been studied according to association with a variety of cancer. In a study, an association between cancer and HLA-A*24 was found on Iranian patients, where exists an increased number of persons with esophageal cancer and HLA-A*24 allele (Eivazi-Ziaei, Dastgiri et al. 2006). Data obtained from melanoma German patients show an increased presence of the allele HLA-B*08 on health people. This study reflects the protective characteristic of this allele with a significative difference compared with melanoma stage IV patients (Fensterle, Trefzer et al. 2006). Previous studies found an overrepresentation of HLA-A*02 allele on ovarian cancer in Swedish patients. This allele is present in women who have advanced lesions of cancer (De Petris, Bergfeldt et al. 2004). In many cases, disease progress is so fast that many samples must be taken from tissue sample from already deceased women. So it is necessary to understand why a certain allele could be overrepresented or underrepresented. Furthermore, a detailed study showed a more interesting feature, HLA-A*02 allele was overrepresented in patients with advanced stages in ovary serous adenocarcinomas. The analysis in the total patient population did not find differences in the allele presence but in stratified patient population showed that HLA-A*02 may be related to patient outcome (Gamzatova, Villabona et al. 2006). Starting from these observations, the questions could be A) is there any kind of deregulation of the peptide presentation proteins? B) Does this machinery present peptides in a defective manner to immune system cells? C) Is there any kind of epigenetic mechanism that inhibits normal peptide presentation?

As the phenotype has cancer, presumably there is a genetic background. For example in lung cancers, there are several mutations on TP53 gene, but those that could generate new epitopes presented by HLA-A*02 are under-represented. Thus particular types of cancer could be associated with a population that has a low frequency of certain HLA types (Little and Stern 1999).

However, the high cost of HLA typing reagents makes it difficult for small laboratories to conduct large studies associating disease and HLA alleles (Abbott, Tukuitonga et al. 2006). Additionally, the complexity of HLA typing made large HLA screening problematic in past studies, for example it is not a common feature between studies from developing countries. In many cases, cancer patients have not been HLA typed and with the time they die, making blood samples unavailable. The absence of fresh DNA material makes it difficult to perform big retrospective studies on a large number of patients (Dubeau, Chandler et al. 1986). The development of rapid and cheap method is necessary and a sequence based typing could be this kind of method (Abbott, Tukuitonga et al. 2006).

Formalin-fixed paraffin embedded (FFPE) tissue samples have been collected for over 100 years (Klopfleisch, Weiss et al. 2011) for the majority of clinical trials in oncology (Sikora, Thibert et al. 2010). These samples have been collected in order to give patients correct diagnosis and then, give the patients a proper treatment. However the samples have been collected for clinical purposes, they are available for scientific purposes. Additionally FFPE tissues are accumulated worldwide along with clinical information or with information from elaborated and costly studies of great value (Klopfleisch, Weiss et al. 2011). This type of samples could be used as a good DNA source, since in past studies there were no DNA collecting assays. However, DNA samples from FFPE are characteristically chemically modified in ways that could limit genetic studies (Gilbert, Sanchez et al. 2007). The most important problem with FFPE DNA is fragmentation around 300bp to 400bp length (Lehmann and Kreipe 2001).

The main disadvantages for FFPE DNA are: the generation of DNA-Protein crosslinkages, presence of inhibiting substance remnants coming from the extraction reactions and contamination (Farrugia, Keyser et al. 2010). Another important issue is the fact that there is a lot of variation of fixation procedures, for example, a prolonged time since extraction from the tissue to the fixation could lead to DNA degradation (Lehmann and Kreipe 2001). Moreover, all-PCR based protocols have been designed for good quality DNA isolated from fresh cells (Sikora, Thibert et al. 2010).

This is why we proposed to develop a complete new HLA-A typing method based first, on DNA extraction from FFPE samples and then, amplification reaction and sequencing analysis of exons 2, 3 and 4. Our method amplifies exons leading PCR products up to 292 base pair long. The obtained sequences allow us to get HLA-A genotypes. These results compare to Sequence Specific Primers PCR (PCR-SSP) results.

2. OBJECTIVES

2.1.General Objective

- To develop a novel method for HLA-A typing in formalin-fixed paraffin embedded tissue samples in order to analyze HLA-A in this kind of samples.

2.2.Specific Objectives

- To evaluate formalin-fixed paraffin embedded tissue samples as DNA source for HLA-A typing.
- To design conserved sequence primers and amplification protocols in order to get HLA-A exon 2, 3 and 4 amplicons.
- To sequence and analyze HLA-A genes from tissue samples and compare to HLA-A genotypes established from PCR-SSP from the same patients.

3. THEOTERICAL FRAMEWORK

3.1.Human Leukocyte Antigen

The Major Histocompatibilty Complex (MHC) in Humans, coded by Human leukocyte antigen was described in 1936. It was discovered on leukocytes surfaces, and it was first associated to confer tolerance following tissue grafts and organ transplantation (Horton, Wilming et al. 2004). The HLA system has the highest diversity of any functional genetic system: some of its proteins have more than 200 allelic variants (The-MHC-Consortium 1999; Charron 2011). It has over 200 identified loci, so it is also, the densest region of the human genome (The-MHC-Consortium 1999).

The principal function of this complex is to supply protection against pathogens (Horton, Wilming et al. 2004). It is responsible to recognize and distinguish between the body's own and the alien or foreign, and trigger the body's immune response, either antibody-mediated humoral or cell type CTL-mediated (Goldsby, Kindt et al. 2003). This explains its polymorphism; the HLA has maintained a long-standing battle for the supremacy against the infectious pathogens (The-MHC-Consortium 1999).

HLA genes are arranged in a continuous stretch of DNA on chromosome 6 (6p21.31) in humans (Figures 1 and 2). The genes are organized within coding regions to three classes of molecules which are explained later on this section (The-MHC-Consortium 1999; Goldsby, Kindt et al. 2003; Horton, Wilming et al. 2004). The complete sequence has a 3.6 megabases length (The-MHC-Consortium 1999), but a new defined Extended Human MHC (xMHC) sequence has a 7.6 megabases length (Horton, Wilming et al. 2004).

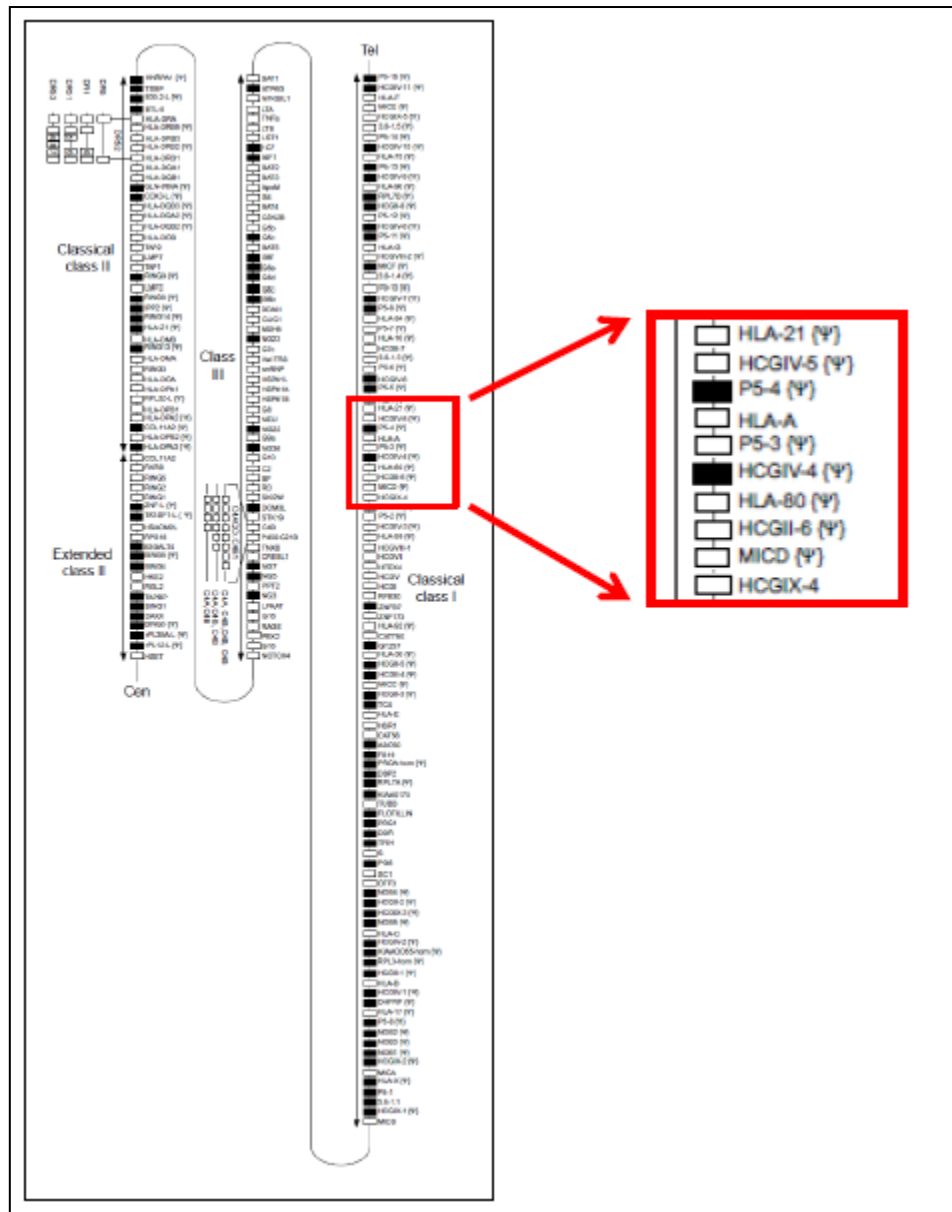


Figure 1. Complete gene map of the MHC. Genes are shown in order from telomere (tel) to centromere (cen) but not to scale. Gene loci that were discovered or located to the MHC as a direct result of the genomic sequence are indicated by filled boxes. The MHC reference sequence is a composite of different haplotypes. However, in regions with known differences in gene content (C4 region in class III and DR region in the classical class II region) only single haplotypes were sequenced (C4AQ0, C4B1 in the class III region and DR52 in the class II region). Red square shows in a bigger zoom HLA-A zone (The-MHC-Consortium 1999).

In summary, products from the HLA genes can be classified as: class I genes that encode glycoproteins on the surface of almost all cells which their function is to present intracellular antigens to Cytotoxic T Lymphocytes. Class II genes that encode glycoproteins only on the surface of presenting cells like macrophages, dendritic cells and B Lymphocytes, their function is to present antigens to T Helper Lymphocytes. Finally class III genes that encode several products that have immune functions, among these components of the complement system and molecules involved in inflammation process (Goldsby, Kindt et al. 2003). Class I genes are grouped on the HLA I supercluster. This region comprises the classical, non-classical class I genes (-A, -B, -C and -E, -F, -G respectively), and class I-like genes (MICA and MICB) (Horton, Wilming et al. 2004), (Figure 2).

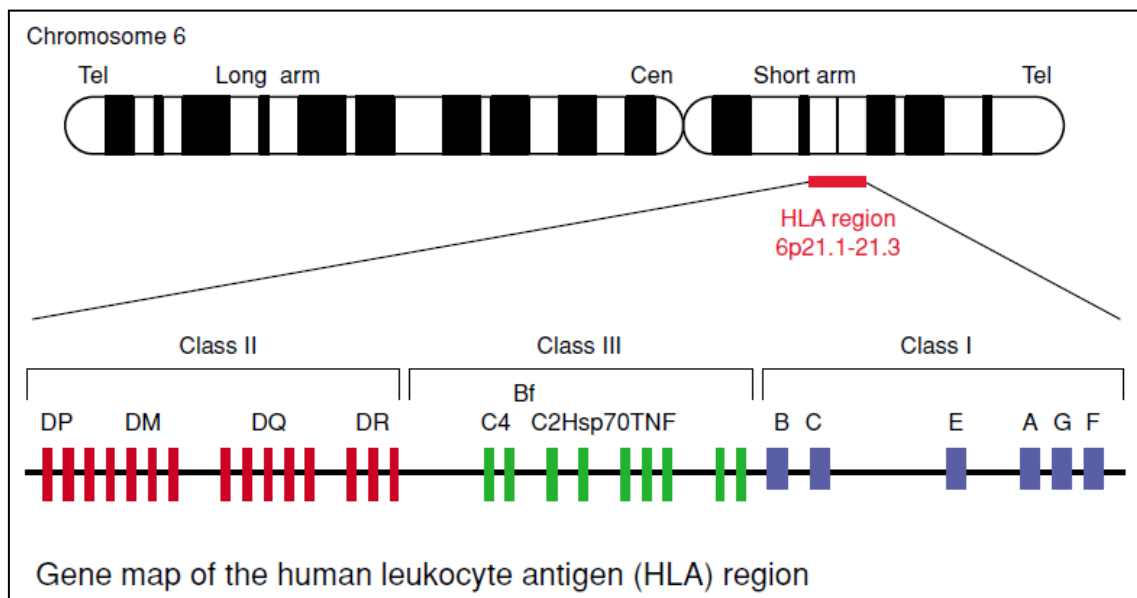


Figure 2. Gene map of the human leukocyte antigen (HLA) region. The HLA region spans 4×10^6 nucleotides on chromosome 6p21.1 to p21.3, with class II, class III and class I genes located from the centromeric (cen) to the telomeric (tel) end. HLA class I molecules restrict CD8⁺ cytotoxic T lymphocyte function and mediate immune responses against ‘endogenous’ antigens and virally infected targets, whereas HLA class II molecules are involved in the presentation of ‘exogenous’ antigens to T helper cells. The HLA class III region contains many genes encoding proteins that are unrelated to cell-mediated immunity but that nevertheless modulate or regulate immune responses in some way, including tumor necrosis factor (TNF), heat shock proteins (Hsps) and complement proteins (C2, C4) (fig001nmn) (Mehra and Kaur 2003).

HLA genes are highly polymorphic and this polymorphism is principally based on single nucleotide polymorphisms (SNPs), where the coding SNPs are very informative. The most polymorphic gene is HLA-B, with a high quantity of variants making it the most polymorphic human gene. Besides the SNPs, insertion/deletion polymorphism is important (Horton, Wilming et al. 2004). Nucleotide sequence analysis of alleles at a given locus shows that variation between alleles is restricted predominantly to the exons that encode the HLA peptide-binding domain. It implies that this high polymorphism on these alleles defines the repertoire of peptides that bind to HLA allotypes. Additionally, the expression of the different genes is co-dominant, which means that a heterozygous person can express six different classical class I and class II allotypes (Turner 2004). This kind of variety defines an individual's ability to respond to exposure to many infectious agents meaning that the HLA polymorphism is favorable to the species survival (Little and Stern 1999).

The MHC class I protein has a structure that consists of a transmembrane glycoprotein subunit, the heavy chain of 45kDa. This heavy chain is associated with a 12 kDa soluble light chain, known as β 2-microglobulin (Figure 3A, B), encoded in chromosome 15 (Heemels and Ploegh 1995). Furthermore the heavy chain is divided in three external segments named α 1, α 2 and α 3, each with 90 aminoacids in length; a transmembrane segment with 25 aminoacids in length; and finally a cytoplasmatic portion of 30 aminoacids in length (Goldsby, Kindt et al. 2003). The α 1 and α 2 segments comprise together the peptide binding domain, which is composed of two α helices supported by eight-stranded β -pleated sheet (Heemels and Ploegh 1995). This arrangement forms a small groove where the antigen is located, its dimensions are 25Å x 10Å x 11Å makes the maximum length of the peptide about 10 aminoacids (Figure 3C) (Goldsby, Kindt et al. 2003). This structure rests on the complex formed by the α 3 domain of the heavy chain and the β 2-microglobulin, which are quite similar. The α 3- β 2-microglobulin complex shows resemblance to the immunoglobulin constant-region (Heemels and Ploegh 1995; Goldsby, Kindt et al. 2003). When the structures are completely assembled with the antigenic peptide, the cells that are presenting the peptide interacts with a T cell CD8+, so the T cell receptor (TCR) connects with the α 1-2-peptide part, while the α 3- β 2-microglobulin part interact with the accessory molecule CD8 (Heemels and Ploegh 1995).

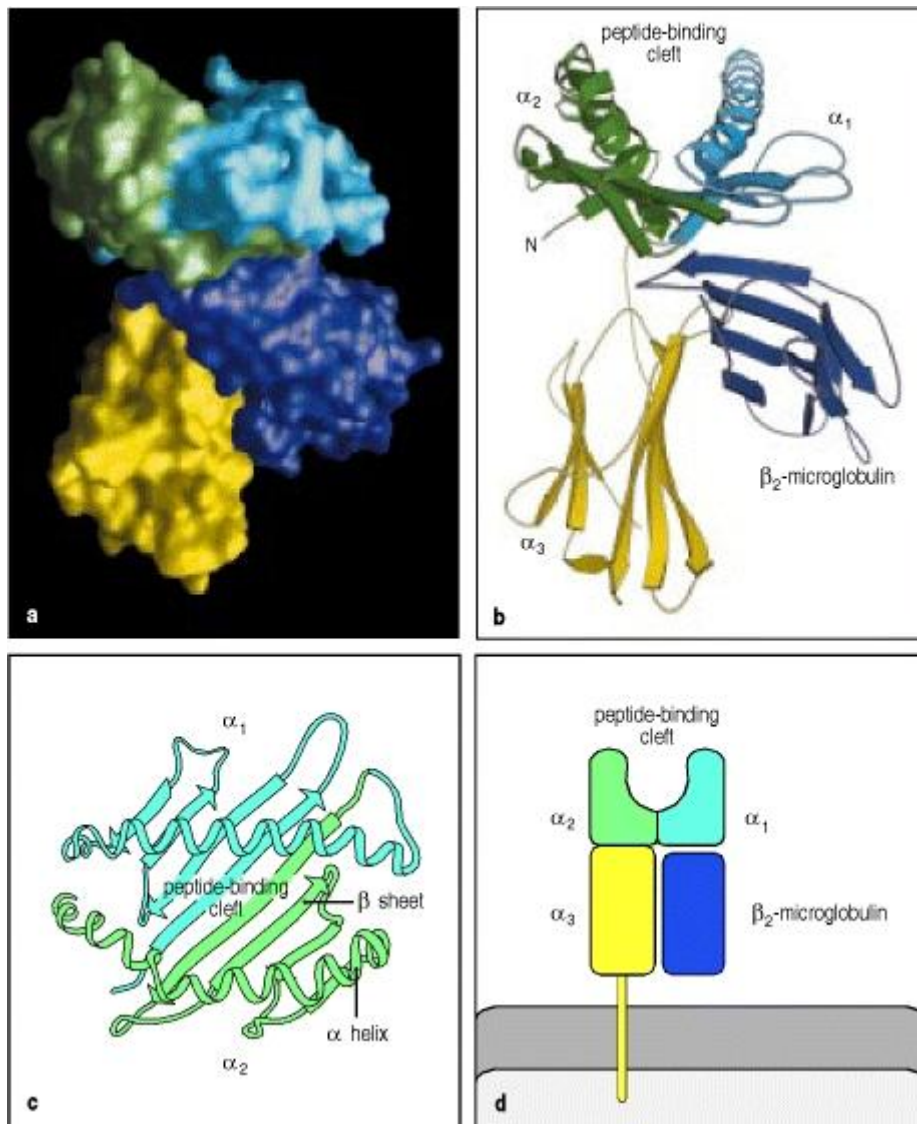


Figure 3. HLA class I structure determined by X-Ray crystallography. (A) 3D representation, (B) ribbon diagram showing different domains, (C) peptide-binding site Ribbon diagram, (D) schematic representation (Janeway, Travers et al. 2001).

HLA alleles have been associated with a high number of diseases. The importance of HLA in autoimmune disorders has been known and studied for many years. In disease where HLA association exist, it has been postulated that HLA-mediated thymic education of T-cells could affect the peripheral T-Cell repertoire that makes an individual more susceptible to a particular autoimmune disease or alternatively certain HLA types could present self peptides that could be recognized by T-cell previously activated in a event named molecular mimicry (Turner 2004). Associations between

cancer and HLA are now being determined. Interestingly, none of the HLA alleles have been demonstrated to be associated with an increased incidence per se of any cancer. However, individual alleles are known to be overrepresented in certain cancers or correlate with survival or prognosis (Masucci, Andersson et al. 2010).

The HLA-A*02 allele has been described as a negative prognostic factor for ovarian cancer. One study showed that the HLA-A*02 allele was similarly distributed between healthy and patients population however when the analysis were stratified showed an increased presence in advanced cancer stages, this finding showed the implication of HLA-A*02 presence and patient management according to the patients outcome presented in this particular study (Figure 4). Moreover the study was in concordance to the observations that pointed that the increase in ovarian cancer mortality in Europe was in concordance with HLA-A*02 frequency (Gamzatova, Villabona et al. 2006).

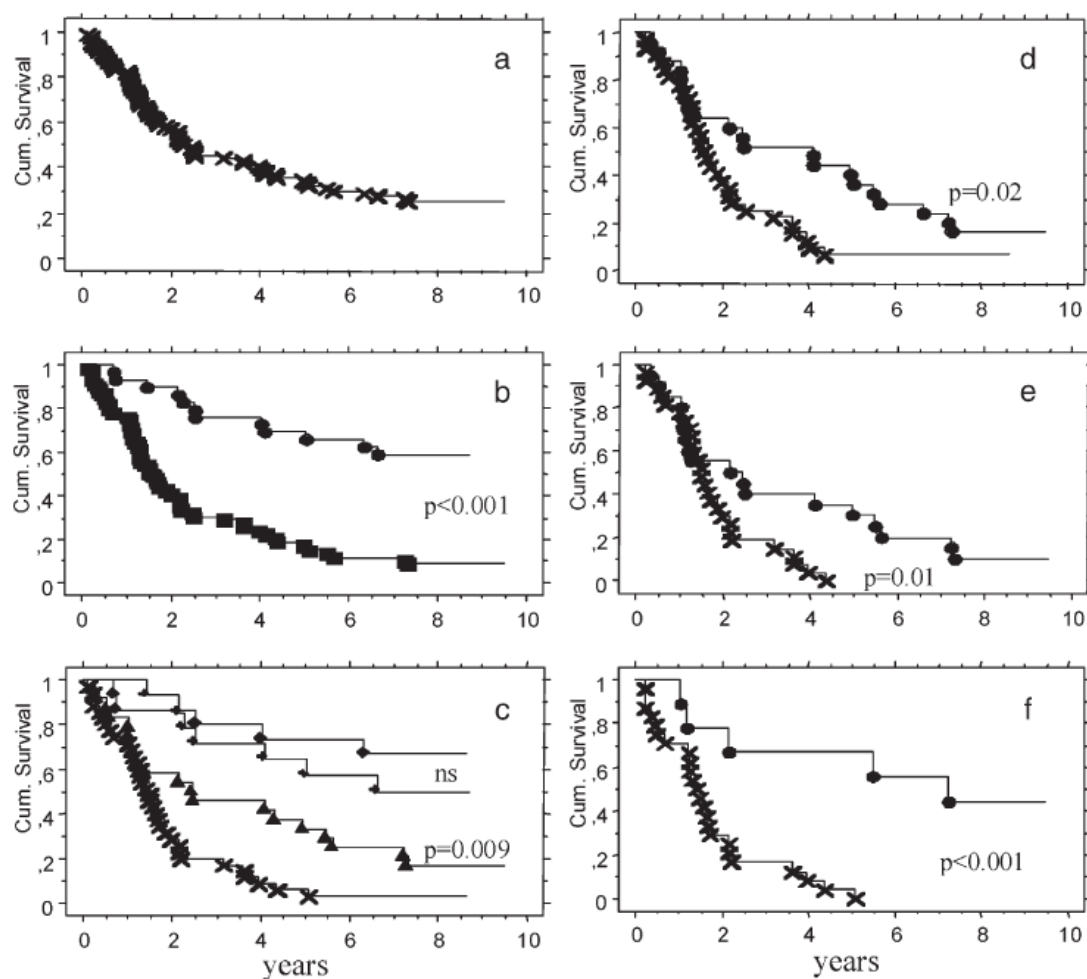


Figure 4. Kaplan–Meier analysis of survival, with log-rank Mantel–Cox test when applied. (a) All patients (n = 88); (b) merged stages I–II (n = 29) (●) and III–IV (n = 59) (▪); (c) stages I–II HLA-A2 positive (n = 15) (◆) and negative (n = 14) (●), stages III–IV HLA-A2 positive (n = 35) (x) and negative (n = 24) (▲); (d) grade 3 HLA-A2 positive (n = 32) (x) and negative n = (25) (●); (e) stages III–IV and grade 3 HLA-A2 positive (n = 27) (x) and negative n = (20) (●); (f) stages III–IV and serous HLA-A2 positive (n = 24) (x) and negative (n = 9) (●). Ns, not significant; P, probability. (Gamzatova, Villabona et al. 2006).

However, whatever the mechanism that causes disease-HLA associations, HLA typing can provide extra information in the diagnosis of certain diseases (Turner 2004). This association not only has to be determined in prospective studies, retrospective studies could be valuable in order to get more information of the HLA disease dependence or phenotype.

3.2.HLA typing

Besides this principal function, the HLA system displays a big variability. Survival from pathogen attacks has required a large investment in defense strategies. At a genomic level, more than 5% expressed genes are involved with immunity (Horton, Wilming et al. 2004).

As mentioned before, the function of HLA requires the gene to have high polymorphism. Historically HLA typing has evolved between different approaches, benefited from the many technological breakthroughs that have arisen in the two last decades (Itoh, Mizuki et al. 2005; Shaw, Arguello et al. 2010). HLA typing has become important since the discovery the role of specific HLA types. In clinic is routinely used for transplantation, since the mismatching has a large number of deleterious effects (Howell, Carter et al. 2010). In certain diseases, HLA could be related to patients outcome, for example ovarian cancer (Gamzatova, Villabona et al. 2006); HLA could be determinant for therapy intensisty (Masucci, Andersson et al. 2010).

The serological HLA typing method was the first approach to assess HLA type in patients. This particular technique was based on the detection of expressed Class I and II HLA molecules on the surface of T cells and B cells respectively. However, this kind of typing has a lot of drawbacks. For example, need of live lymphocytes and a big panel of antisera (Howell, Carter et al. 2010). Today, it is considered to lack the resolving power of DNA based methods and to be rather cumbersome and resource-intensive (Itoh, Mizuki et al. 2005).

DNA-based typing methods like sequence specific primer PCR (PCR-SSP), or sequence specific oligonucleotide probes PCR (PCR-SSOP) have a number of advantages over sera based methods. These new methods do not need live lymphocytes and could be used for any kind of nucleated cell. Peripheral blood is the most used source of DNA; it is easily extracted and stored (Howell, Carter et al. 2010). In the last years, the introduction of highly sensitive instruments and technologies has enabled the laboratories to perform more assays and manipulate a bigger number of samples (Shaw, Arguello et al. 2010). These DNA techniques are based on the same principle, first step is the amplification of specific DNA regions, corresponding to any of the HLA alleles, according to the method the primers can be designed in different ways. In some techniques, the method includes the use of oligonucleotide probes or a posterior sequencing protocol of amplified product (Howell, Carter et al. 2010). These DNA based methods could be grouped in three different groups or approaches.

Amplification methods with group specific primers are commonly applied. This is the first approach. The basis of this method is the use of specific primers with a polymorphic sequence. The determination of the presence of a certain allele is the combination of these primers and the amplification of product visualized in agarose gels (Howell, Carter et al. 2010; Shaw, Arguello et al. 2010). Disadvantages are the logistical considerations; this particular method is unsuited for typing a large number of samples (Howell, Carter et al. 2010) and it relies on a limited number of previously known polymorphisms (Shaw, Arguello et al. 2010). The appearance of a new allele could lead to a mistyping. The use of sequence specific oligonucleotide probes which detect the specific alleles by hybridization is another common method, and this is the second approach of this category. Modern techniques as LuminexTM have permitted to lead large studies with bigger numbers of patients, making successful HLA-A, -B, -C

and –DRB1 typing in only 5 hours (Itoh, Mizuki et al. 2005; Howell, Carter et al. 2010). As with the sequence specific primers, the main disadvantage is the use of probes limited to known polymorphisms and requires a large product for hybridization to attach the specific target DNA.

The third approach is the Sequence Based Typing (SBT). This particular method uses the amplified product as a template for a posterior sequence procedure. For different types of HLA, the sequences are obtained principally from the coding regions; exons 2 and 3 for HLA class I, and exon 2 for HLA class II (Howell, Carter et al. 2010). The polymorphism is relied on the peptide binding regions of the HLA molecules (Little and Stern 1999). Due to the high heterozygosity of the HLA alleles, after the procedure of samples sequencing, the obtained sequences has to be read with the help of bioinformatics tools. This method is not limited by the appearance of new alleles of new polymorphisms. One limitation is the arrangement of the different combinations which could lead to problems of genotype reading, this phenomenon is known as ambiguity (Adams, Barracchini et al. 2004; Shaw, Arguello et al. 2010). In the clinic this kind of technique is limited; it is not a high throughput screening method which is needed when typing before transplantation. However, it could be logistical feasible and low-cost and it is particularly important because it can be used by small laboratories to perform studies, and the results are comparable to commercial PCR-SSP (Abbott, Tukuitonga et al. 2006).

Almost all DNA methods are designed to use large bloodiness DNA as template. Blood is not always available, in some cases because in clinical studies the patients are already deceased and in other cases, many studies had not extracted and/or conserved DNA for further studies. Therefore there is the necessity of use another DNA source.

3.3. Formalin-fixed, paraffin embedded (FFPE) tissues as a DNA source

Tissues formalin fixation and posterior paraffin embedding has been a technique applied for over 100 years (Klopfleisch, Weiss et al. 2011). This kind of samples could constitute a valuable tool for molecular studies (Savage and Hostetter 2011). There is a big quantity of accumulated samples worldwide which contain valuable clinical

information that have been used for elaborated experiments in science (Klopfleisch, Weiss et al. 2011).

In many cases, the FFPE samples has been only used for histological and morphological studies, additionally in certain cases these samples has been used in experiments with immunohistochemical features (Klopfleisch, Weiss et al. 2011). However the use of these samples has been limited on molecular analysis because there are many adverse effects over nucleic acids with the fixation procedure.

With the appearance of molecular techniques, this particular DNA source has been studied for the applicability of theses procedures. However different kinds of fixation procedures, i.e. different methodologies could be important factors that affect DNA quality directly, that lead to poor results for PCR (Ben-Ezra, Johnson et al. 1991). For example, a prolonged time from tissue extraction to the fixation could lead to DNA degradation (Lehmann and Kreipe 2001). Moreover, DNA extraction protocols vary between different studies, so the fragment length obtained differs from <150bp (Gilbert, Sanchez et al. 2007) and up to 300 to 400bp (Lehmann and Kreipe 2001).

Additionally FFPE DNA has other disadvantages such as DNA-protein crosslinkages, presence of inhibiting substances coming from the extraction reactions and contamination that impede molecular reactions adequate performance (Farrugia, Keyser et al. 2010).

However, there are methodologies that could perform acceptable DNA quality extraction, in some cases for potential retrospective studies on gene amplification, deletion, DNA methylation, and restriction fragment length polymorphism on tumor behavior (Dubeau, Chandler et al. 1986). Moreover, these samples analyzed could be old, for example, samples with forty years of extraction and fixation could be suitable for studies (Shibata, Martin et al. 1988).

HLA typing became important according to the findings in the last years, principally, associations between specific HLA genotypes and a wide range of diseases (Horton, Wilming et al. 2004; Turner 2004). These studies are relatively new because it is really difficult to determinate HLA genotype. Until now, retrospective HLA studies have not

been described due to the lack of fresh DNA sources. Although FFPE tissue samples could be used as DNA source; there are few HLA typing studies based on FFPE DNA samples with mixed results (Bateman, Hemmatpour et al. 1997; Ota, Shimada et al. 2006).

Polymorphisms in HLA class I are mainly concentrated to Exon 2 and 3 (Little and Stern 1999; Shaw, Arguello et al. 2010). Using specific primers for HLA-A exon 2, 3, we propose the development of a new SBT HLA-A typing method using FFPE samples. In order to avoid certain kind of ambiguities, related to alleles differences defined outside mentioned exons (Adams, Barracchini et al. 2004), we also analyzed Exon 4. This method will be compared to the Swedish standard HLA typing procedure (PCR-SSP) in order to evaluate its accuracy. Our aim is to open a new opportunity to do retrospective HLA analysis in FFPE samples without any other fresh DNA source.

4. RATIONALE AND HYPOTHESIS FORMATION

The importance of HLA typing has become more important in modern studies and the availability of FFPE tissues samples has been increased during the last years. We propose that HLA-A SBT typing with DNA extracted from these kinds of samples has the same accuracy of normal HLA-A typing when using a standard HLA typing procedure in Sweden. With this method we could develop retrospective HLA studies with correct accuracy and high reliability.

5. MATERIALS AND METHODS

5.1. Patients Description

Seventeen unrelated Swedish women diagnosed with relapsing or progressive ovarian cancer and receiving treatment at the Karolinska University Hospital 2004-2005 were asked for a blood sample. These were analyzed for the genotypes at the HLA-A, HLA-B, HLA-Cw, and HLA-DRB1 loci by the PCR-SSP method by the certified immunological laboratory at Karolinska University Hospital, Huddinge. All women had undergone surgery previous to this study and their tissue material was routinely formalin fixed and paraffin embedded (2001 to 2002). The samples were coded as K and HZ with a number.

One healthy Swedish woman was asked for a blood sample for control. This woman has been previously PCR-SSP HLA typed. The sample was coded as VB1, and this sample was used to evaluate the new FFPE HLA-A typing method using fresh DNA.

5.2. DNA extraction

For extraction from FFPE samples, High Pure RNA extraction kit (RocheTM) was used. The step with DNase treatment was excluded. Extracted DNA was diluted in distilled water to reach a 30ng/μL concentration which was determined using NanodropTM.

5.3. Amplification Primers design

Amplification was designed to amplify exons 2, 3 and 4 from HLA-A. Sequences from all HLA-A alleles were obtained from IMGT-HLA database (Robinson, Mistry et al. 2011) and aligned into a document. We designed a complete set of primers from the conserved regions, for all the alleles. Each primer was designed using Gene RunnerTM Software version 3.05 (Hasting Software, Inc.). For exon 2, there were four primers, two forward and two reverse. For exon 3 we designed three primers, two forward and one reverse. For exon 4, we designed five primers, three forward and two reverse; in this case, we divided exon 4 in two parts for the amplification product so two forward

primers and one reverse were for the first half, and one forward primer and one reverse primer for the second half. For ambiguous results obtained with the sequences from the two first exon amplifications, exon 4 amplification procedure was performed (Adams, Barracchini et al. 2004). The distinct combination for the primers for each exon was determined according to sequence changes between different alleles. Detailed information on table 1 and figure 5.

Table 1. Detailed information about the primers for the different amplification reactions.

	Exon 2	Exon 3	Exon 4
Forward Primers.	A2-1F 5'-TCTCAGCCACTGCTCGCC-3' A2-2F 5'-TCTCAGCCACTCCTCGTC-3'	A3-1F 5'-GGTTCTCACACCGTCCAGA-3' A3-2F 5'-GGTTCTCACACCATCCAGA-3'	A4-1F 5'-GCGCCCCAAAACGCATATG-3' A4-2F 5'-CCCCCCAAGACACATATG-3' A4-3FH 5'-TTCTACCCTGCGGAGATCAC-3'
Reverse Primers.	A2-1R 5'-GTCCTCGCTCTGGTTGTAG-3' A2-2R 5'-GCCCTCGCTCTGGTTGTAG-3'	A3-2R 5'-CTTCCCGTTCTCCAGGTATC-3'	A4-1R 5'-CCATCTCAGGGTGAGGGG-3' A4-2RH 5'-ATCCCCTGCAGGCCTGGT-3'

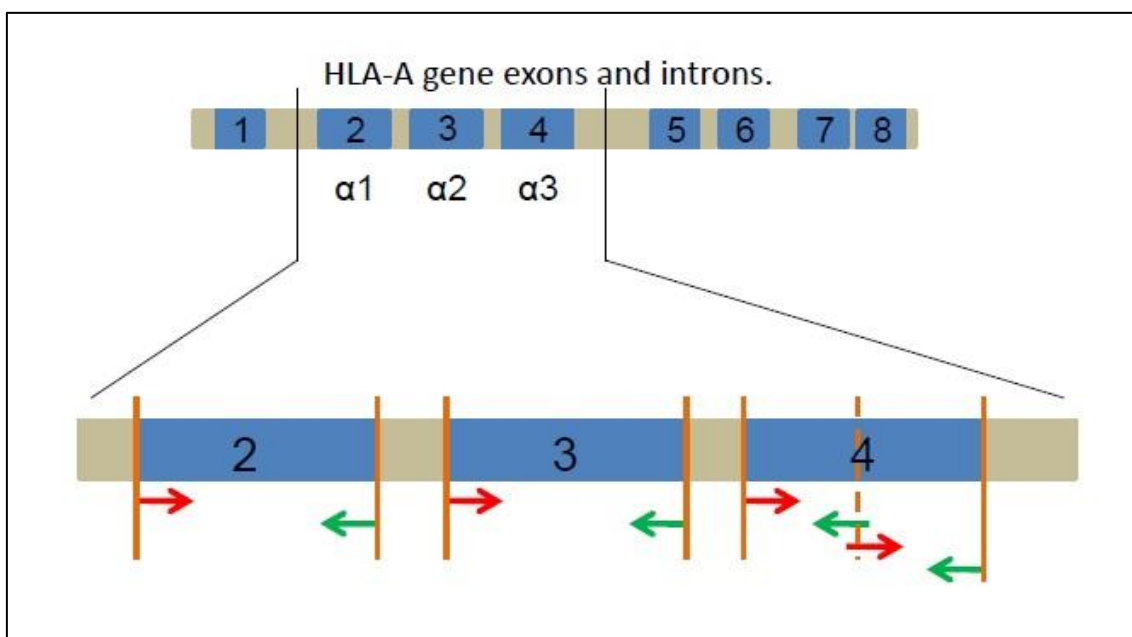


Figure 5. Schematic HLA-A gene representation. Exons are blue and introns are beige. Forward primers are red and Reverse primers are green, Exon 2 and exon 3 are fully amplified. Exon 4 is amplified in two halves. Primer sequences are listed in Table 1.

5.4. Amplification procedure

For all the amplification reactions, the mix and thermocycler program was the same; the unique difference was the primers utilized. The mix for the amplification was:

5.4.1. Amplification mix:

5.4.1.1.	10X amplification Buffer	5 μ L.
5.4.1.2.	DNTP (1.25mM)	8 μ L.
5.4.1.3.	MgCl ₂ (25mM)	3 μ L.
5.4.1.4.	Forward Primer (10pmol/ μ L)	3 μ L.
5.4.1.5.	Reverse Primer (10pmol/ μ L)	3 μ L.
5.4.1.6.	Distilled Water	22.8 μ L.
5.4.1.7.	Taq Polymerase	0.2 μ L.
5.4.1.8.	Sample DNA (150ng)	5 μ L.
5.4.1.9.	TOTAL	50 μ L.

For exon 2 amplification the primers utilized were A2-1F or A2-2F, and, A2-1R or A2-2R. For exon 3 the primers were A3-1F or A3-2F, and, A3-2R. And finally, for exon 4 the primers were used according for the two halves of exon 4. For the first half, the primers were A4-1F or A4-2F, and, A4-2RH; for the second half the primers were A4-3FH and A4-1R.

The thermocycler program for all amplification reactions was:

5.4.2. Program:

- 5.4.2.1. 94°C 5 minutes, 1 hold.
- 5.4.2.2. 94°C 30 seconds.
- 5.4.2.3. 60°C 30 seconds.
- 5.4.2.4. 72°C 45 seconds.
- 5.4.2.5. 40 times go to step 5.4.2.2.
- 5.4.2.6. 72°C 5 minutes, final hold.

All DNA samples performed all types of amplification, i. e. a total of 9 procedures per sample, the different primer combinations were: For exon 2 A2-1F & A2-1R, A2-2F & A2-2R, A2-1F & A2-2R, A2-2F & A2-1R; for exon 3 A3-1F & A3-2R, A3-2F & A3-2R; for exon 4 first half A4-1F & A4-2RH, A-42F & A4-2RH; and finally for exon 4 second half A4-3FH & A4-1R.

The products were run on a 2% agarose gel. For exon 2 the expected product is around 292 bp long, for exon 3 the expected product is around 258bp, and finally exon 4, for the first half reaction the expected product is around 166bp and the second half is around 201bp. All positive amplification products went to sequencing reaction.

5.5. Sequencing Procedure

All the amplification products were cleaned with ExoSAP-IT kitTM (Affymetrix Inc.). After that, all the products underwent sequencing program using Big DyeTM (Applied BiosystemsTM). Each amplification product was amplified twice, using forward and reverse primer separately. For this reaction, the mix and the programs were according to manufacturer's protocol:

5.5.1. SEKV amplification mix:

5.5.1.1.	Big Dye™ mix	3μL.
5.5.1.2.	Sequencing Buffer	2μL.
5.5.1.3.	Primer (1pmol/μL)	3μL.
5.5.1.4.	Amplification cleaned product	5μL.
5.5.1.5.	Distilled Water	6μL.

5.5.2. SEKV amplification program:

- 5.5.2.1. 96°C 10 seconds.
- 5.5.2.2. 50°C 5 seconds.
- 5.5.2.3. 60°C 4 minutes.
- 5.5.2.4. 25 times go to step 5.5.3.1.

After the SEKV amplification, the samples were diluted with 50μL 95% ethanol and 2μL sodium acetate pH 4.6 each one. The diluted products were then mixed with a vortex and left standing for 15 minutes. After this, the samples were centrifuged 13226 g for 30 minutes. Then, the supernatants were discarded, and the pellets were diluted with 250μL 70% ethanol. Again the samples were centrifuged 13226 g but only 10 minutes. Again, the supernatants were discarded. The pellet was air-dried, diluted with 15μL formamide, mixed with a vortex for 10 minutes, heated to 95°C for 2 minutes and then cooled down on ice for 2 minutes. The samples were placed on an Optical 96-well reaction plate, and read on an automatic sequencer (Applied Biosystems 7900 HT Real-Time System).

5.6. Sequence analysis

The obtained sequences were analyzed on Chromas Lite™ software version 2.01 (Technelysium Pty Ltd.). Each sample had two sequences corresponding to forward and

reverse sequence obtained according to the primer used in the sequencing reaction. Each sequence was exported to a FASTA format. Reverse sequences were translated into complementary strands using Gene RunnerTM Software version 3.05 (Hasting Software, Inc.). Using clustalw 2 tool (Thompson, Higgins et al. 1994) the two sequences were aligned. The remaining arms from the reverse and forward strands were added to a consensus sequence. This final sample sequence was analyzed using IMGT-HLA Blast searching tool (Robinson, Mistry et al. 2011). Heterozygosity was detected by looking for double peaks in each sequence graphic. By aligning the different sequences with known HLA-A alleles registered by the IMGT organization, the HLA-A type was determined.

6. CLINICAL SIGNIFICANCE

This new procedure will lead to research HLA types in FFPE samples which do not have any fresh DNA source. This advance could have a strong impact for HLA association studies.

Also this new procedure will allow typing HLA in samples from third world countries in order to look at new HLA associations with other diseases as well cancers in countries that don't have the capability to HLA type in clinical procedures. This new technique will allow researchers to perform retrospective studies in order to establish if certain risk HLA alleles could be found in studies in the developed countries.

The theory behind this method could be used for other polymorphic genes, i.e. KIR nonclassical HLA, etc.

7. RESULTS

7.1.DNA extraction

DNA of 17 patients was extracted from ten years old FFPE samples in order to be amplified with a set of primers, for HLA-A exon 2, 3 and 4. We had one Blood derived DNA sample for control. Extracted DNA was diluted on distilled water to a final concentration of 30ng/ μ L.

FFPE samples has been PCR-SSP typed in a certified laboratory, the results from this procedure will be used as control for the new method.

7.2.Amplification Procedure

From the extracted DNA, we yielded amplification products up to 292bp. In total, from the 162 different reactions: 9 for the each one of the different 17 FFPE DNA samples and 9 for the fresh blood sample, we obtained amplification product for 123 reactions.

From the 18 samples utilized in this study, for exon 2 were received product from 17 samples including the blood control sample. Almost all primer combinations i. e. from 72 possible products, 56 amplification products were obtained (Table 2). Products were around 295bp which were visualized on 2% agarose gel.

For exon 3, we obtained product from 16 samples including blood control sample. The obtained product, with a length of 258bp approximated, was visualized in 2% agarose gels. From 36 possible products it was obtained 30 amplification products (Table 2).

For Exon 4 amplification, we obtained product from fewer samples than the two first exons. For the first half, amplified with A4-1F/2RH and A4-2F/2RH primer combinations, from 36 possible products, 25 products were obtained, and for the second half obtained with A4-3FH/1R primers, 12 products were obtained from 18 possible products (Table 2).

Examples of the amplification agarose gels are listed on Figure 6. Only one sample (K13) did not amplify in any of the different reactions. Detailed information about PCR amplifications is described in Table 2.

Table 2: List of positive reactions and primers used in the performed amplification reaction.

	EXON 2				EXON 3		EXON 4		
Primers / samples	A2- 1F/1R	A2- 2F/2R	A2- 1F/2R	A2- 2F/1R	A3- 1F/2R	A3- 2F/2R	A4- 1F/2RH	A4- 2F/2RH	A4- 3FH/1R
VB1	+	+	+	+	+	+	+	+	+
HZ1	+	+	N	N	N	N	N	N	N
K1	+	+	+	-	+	-	+	+	+
K2	+	-	+	-	+	+	+	+	-
K3	-	+	+	+	+	+	+	+	-
K4	-	+	-	-	+	+	+	+	+
K5	+	+	+	+	+	+	+	+	+
K6	+	+	-	-	+	-	-	+	+
K8	+	+	+	+	+	+	-	-	-
K10	+	+	+	+	+	+	-	+	+
K11	+	+	+	-	+	+	-	-	-
K13	-	-	-	-	-	-	-	-	-
K14	+	+	+	+	+	+	+	+	+
K16	+	+	+	+	+	+	+	+	+
K17	+	+	+	+	+	+	+	+	+
K21	+	+	+	+	+	+	+	+	+
K23	+	+	+	+	+	+	-	+	+
K24	+	+	+	+	+	+	+	+	+
	15	16	14	11	16	14	11	14	12

N: Sample HZ1 did not perform these amplification reactions due to unavailability.

For all samples, except K8, K11 and K13, at least one amplification product was obtained for three different exons (Table 2). Sample HZ1 ran out for the analysis of exon 3 and 4. Additionally, K3 and K11 amplification products were obtained in a small

quantity compared with the 100bp ladder, and other amplification products from the same reaction mix (Figure 7).

The DNA quality was in general good; this quality was assessed according to the number of obtained amplification products. K13 could not be amplified probably due to too high DNA fragmentation below, 100bp length.

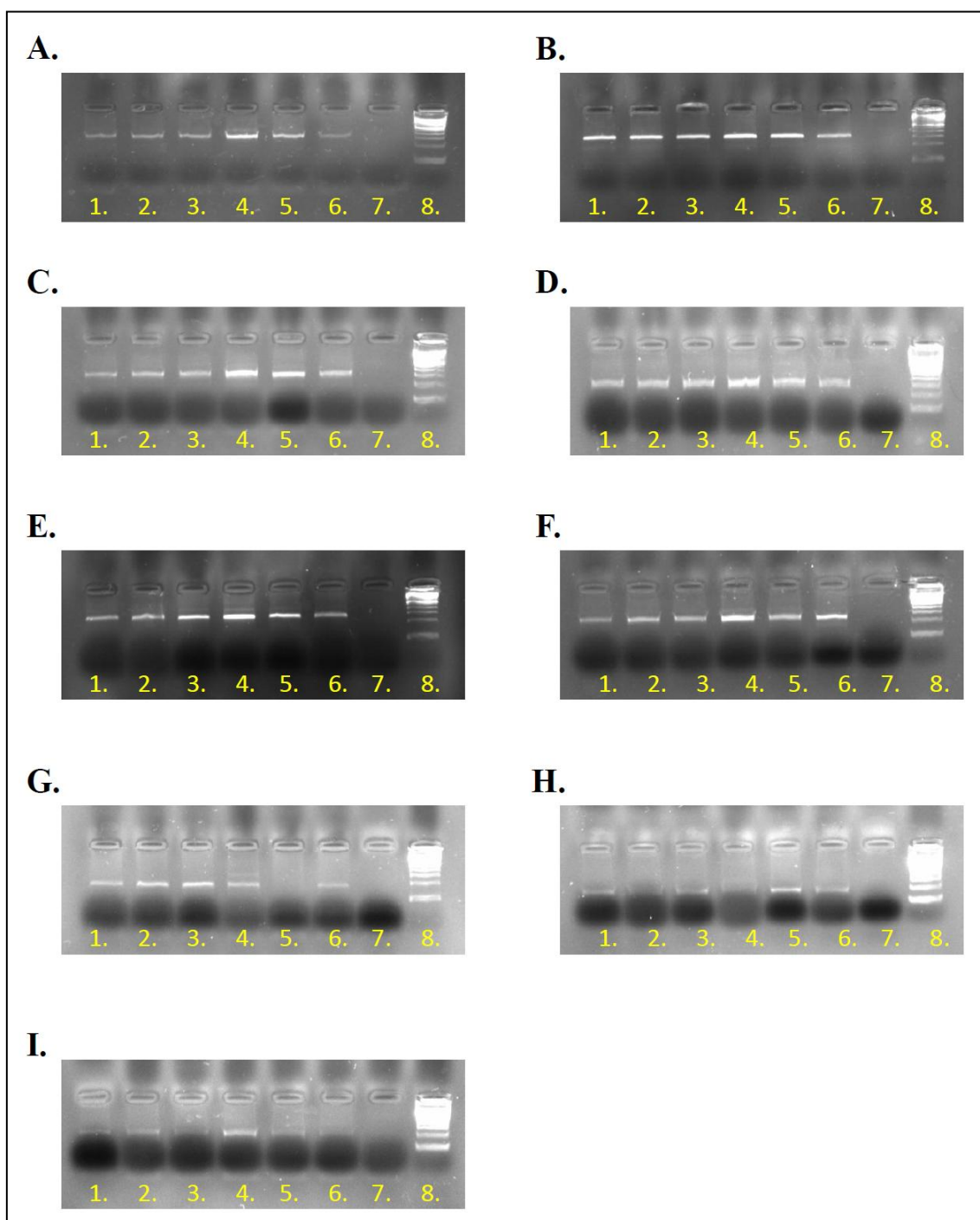


Figure 6: FFPE DNA amplification products. Lane 1 sample K14, lane 2 sample K16, lane 3 sample K17, lane 4 sample K21, lane 5 sample K23, lane 6 sample K24, lane 7 negative control, lane 8 100 bp ladder. The different Primer sets used on different protocols are listed as (A) A2-1F & A2-1R primers, (B) A2-2F & A2-2R primers, (C) A2-1F & A2-2R primers, (D) A2-2F & A2-1R primers, (E) A3-1F & A3-2R primers, (F) A3-2F & A3-2R primers, (G) A4-1F & A4-2RH primers, (H) A4-2F & A4-2RH primers, (I) A4-3FH and A4-1R primers.

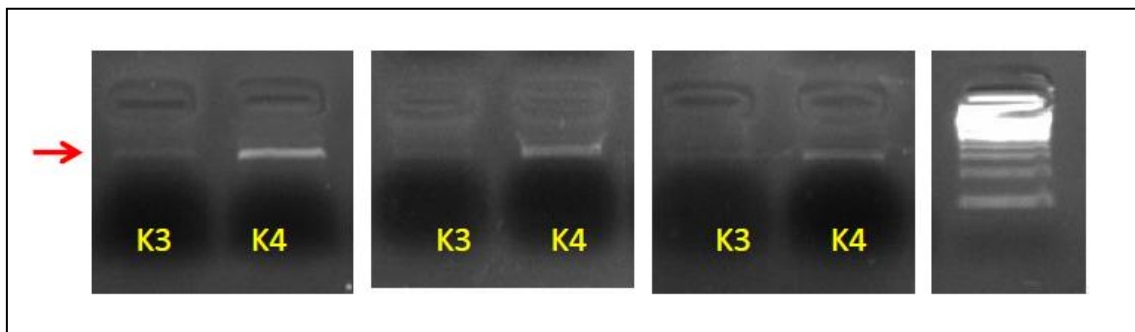


Figure 7. Comparison between different K3 and K4 amplification products. From left to right: A2-1F/2R reaction, A2-2F/1R reaction, A3-2F/2R reaction, 100bp ladder. K3 showed small quantity product compared to K4 and 100bp ladder lanes.

7.3. Sequencing Procedure

For exon 2, the obtained sequences were clearer and these sequence graphics were more easily read (Figure 8) than those from exon 3 and 4 (Figures 9 and 10). Exon 2 sequences had smaller background interference than exon 3 and 4 obtained sequences.

According to the gels (Figure 6 and Annex 1), it seems that exon 2 amplification gave a more specific product. The other exons, exon 3 and exon 4, seem to have given unspecific products. For exon 3, expected products were 258bp, but we got higher products (> 300bp) or smaller products (around 150bp) (Annex 1). This could explain why there was large background interference on these particular sequencing procedures.

However, the principal sequence that corresponds to the higher peaks showed in the sequence graphics (Figures 8, 9 and 10) and from which we obtained the reading that

was exported to the FASTA formats could be correctly assessed to HLA-A alleles in almost all samples. We assessed the allele when the alignment was at least 90% similar between the query sequence and the allele sequence on the database. In certain cases, amplified sequences did not correspond to HLA-A or any HLA sequence. FASTA formats were pasted into the IMGT-HLA database blast tool and we obtained the allele (Robinson, Mistry et al. 2011). But in all these cases, the obtained products with other amplification protocols i. e. different primers and sequencing results permitted us to asses the HLA-A genotype (Table3).

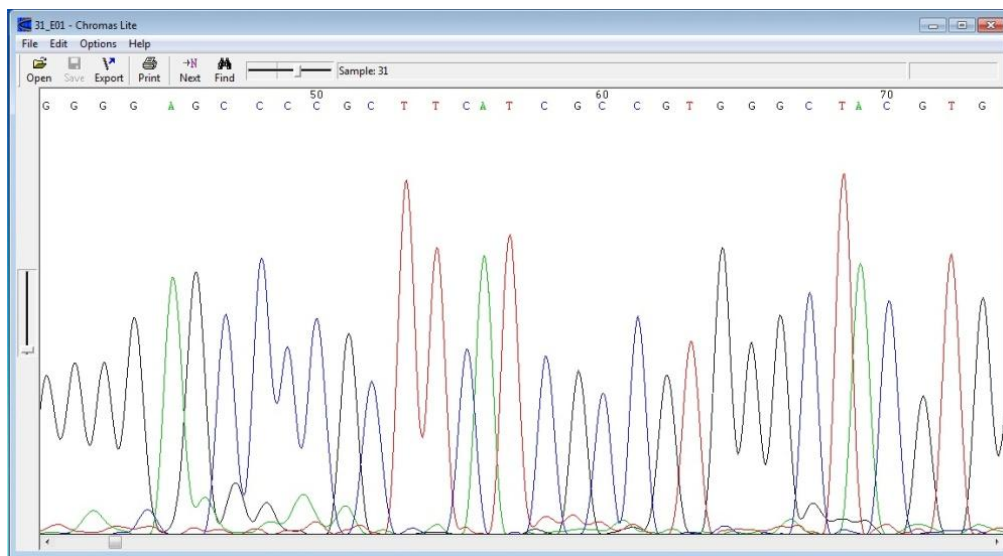


Figure 8: K23 HLA-A exon 2 Sequence graphic. Primers used were A2-1F and A2-1R.

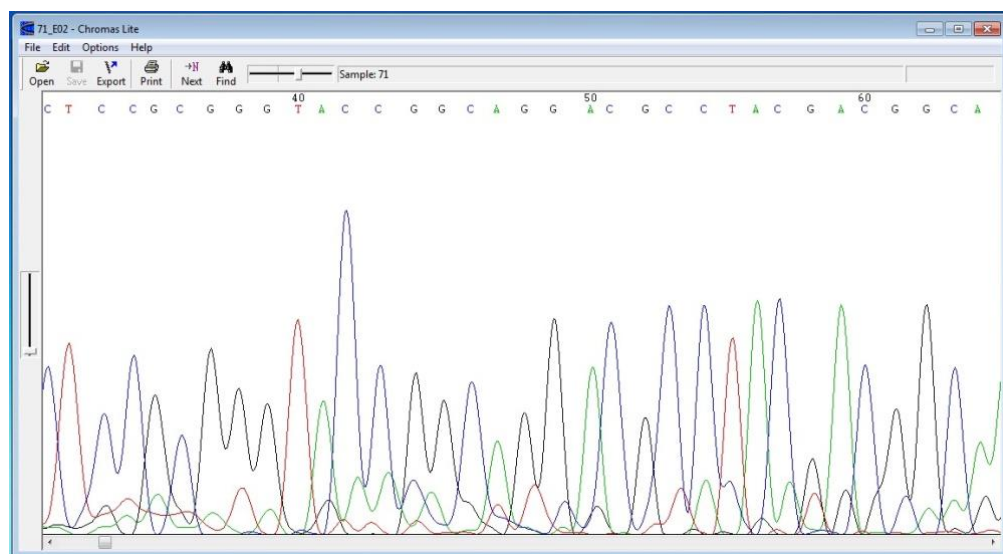


Figure 9: K23 HLA-A exon 3 Sequence graphic. Primers used were A3-1F and A3-2R. In this particular example, we can observe the background interference.

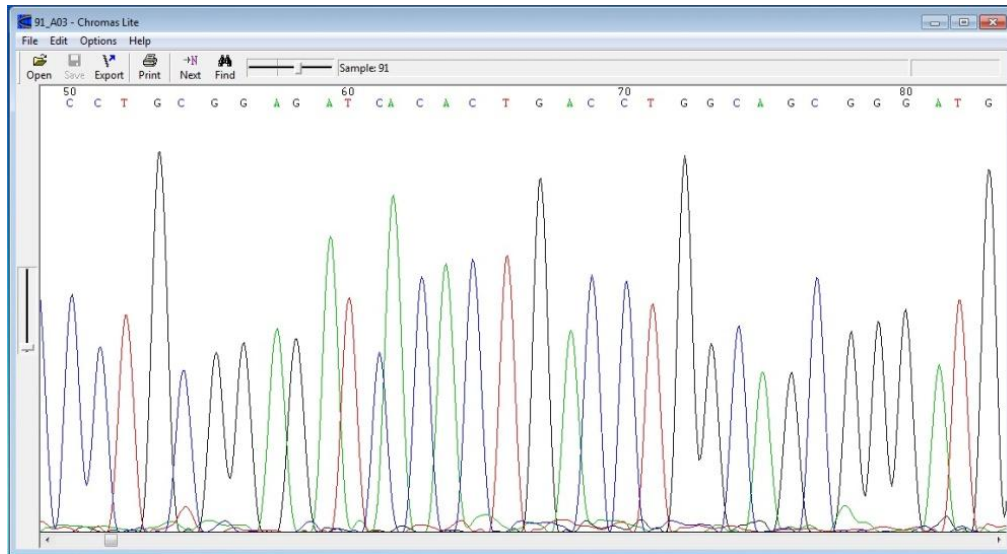


Figure 10: K23 Sequence graphic obtained for HLA-A exon 4 first half amplification. Primers used were A4-2F and A4-3RH.

7.4. Sequences analysis

The FFPE DNA amplification products underwent sequencing procedure according to the Big Dye™ protocol. For this study, FFPE samples belonged to patients that previously were HLA typed with PCR-SSP performed on blood-derived DNA.

All the samples typed displayed two different sequences according to the primer used in the amplification protocol. For each exon, different forward and reverse primers were used in order to amplify the different alleles that each sample could have. Each obtained sequence was exported to a FASTA format for further database analysis. The reverse primer sequences were translated to complementary strand and then aligned with the correspondent forward primer sequences using clustalw 2 tool (Thompson, Higgins et al. 1994). With these alignments we could obtain complete sequences that were used to determine the HLA-A allele (Figure 11).

A2-2/2

>K24FW

AGCTCACGCTGAGTATTTCTTCCATCCGTGTCCCGGCCCGGCCGCGGGGAGCCCC
GCTTCATCGCAGTGGGTACGTGGACGACACGCAGTTCGTGCGGTTCGACAGCGA
CGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGTCCG
GAGTATTGGGACGGGAGACACGGAAAGTGAAGGCCACTCACAGACTACCGAG
TGGACCTGGGGACCCTGCGCGGCTACTACAACAGAGCGAGGGCTA

>K24RV

GTCTCAGCCACTCCTCGTCCCCAGGCTCTCACTCCATGAGGTATTTCTTCACATC
CGTGTCCCGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCAGTGGGTACGTGGAC
GACACGCAGTTCGTGCGGTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGC
GGGCGCCGTGGATAGAGCAGGAGGGTCCGGAGTATTGGGACGGGAGACACGGAA
AGTGAAGGCCACTCACAGACTACCGAGGGAACCTCGCACTGCGCG

CLUSTAL 2.1 multiple sequence alignment

```

K24FW      -----AGCTCACGCT-----GAGTATTTCTTC-CATCCGTGT 31
K24RV      GTCTCAGCCACTCCTCGTCCCCAGGCTCTCACTCCATGAGGTATTTCTTCACATCCGTGT 60
              **** * ** *****
K24FW      CCCGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCAGTGGGTACGTGGACGACACGCAGT 91
K24RV      CCCGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCAGTGGGTACGTGGACGACACGCAGT 120
              *****
K24FW      TCGTGC GGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAG 151
K24RV      TCGTGC GGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAG 180
              *****
K24FW      AGCAGGAGGGTCCGGAGTATTGGGACGGGGAGACACGGAAAGTGAAGGCCACTCACAGA 211
K24RV      AGCAGGAGGGTCCGGAGTATTGGGACGGGGAGACACGGAAAGTGAAGGCCACTCACAGA 240
              *****
K24FW      CTCACCGAGTGGACCTGGGGACCCTGCGCGGCTACTACAACAGAGCGAGGGCTA 266
K24RV      CTCACCGAGGGAACCTCG---CACTGCGCG----- 267
              *****

```

>K24SeqCons

GTCTCAGCCACTCCTCGTCCCCAGGCTCTCACTCCATGAGGTATTTCTTCACA
TCCGTGTCCCGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCAGTGGGTACGT
GGACGACACGCAGTTCGTGCGGTTCGACAGCGACGCCGCGAGCCAGAGGATGG
AGCCGCGGGCGCCGTGGATAGAGCAGGAGGGTCCGGAGTATTGGGACGGGGAG
ACACGGAAAGTGAAGGCCACTCACAGACTACCGAGTGGACCTGGGGACCCT
GCGCGGCTACTACAACAGAGCGAGGGCTA

Figure 11: K24 forward and reverse sequence analysis from exon 2 A2-2F and A2-2R primers (A2-2/2). The obtained sequences were aligned, and the complementary sequence plus the outside arms was analyzed using clustalw 2 tool (Thompson, Higgins et al. 1994). (*) shows nucleotide identity and (-) shows gaps between both sequences.

The final sequence, consensus sequence plus external arms, was analyzed using the blast tool from IMGT-HLA database (Robinson, Mistry et al. 2011). The sequences on FASTA format were used as query. The different amplification protocols with different sets of primers used permitted us to get more than one different sequence for each sample. In certain cases in which the DNA quality was decreased, and we obtained only a few sequences, the genotype was determined by editing the FASTA sequence according to the graphics obtained from the sequencing protocol. In almost all cases there were different graphics that in certain positions displayed double peaks (Figure

12) that according to the sequences from the IMGT-HLA databases correspond to allele changes previously reported. The results were displayed on the webpage and permitted us to assess the allele (Figure 13), and with the different alleles the genotype (Table 3).

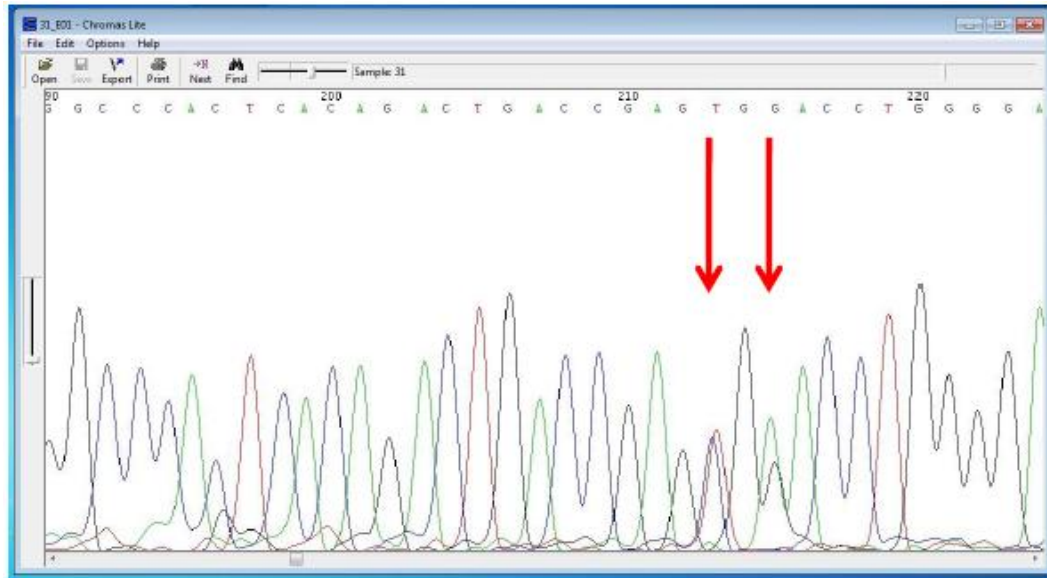


Figure 12: K23 exon 2 sequence graphic (A2-1F/1R). The two red arrows denote the double peaks which correspond to sequence changes. By editing FASTA formats with these changes we assessed the HLA-A genotype.

```
>IMGTHLA:HLA01718 A*03:01:01:02N 1163 bp
Length = 1163

Plus strand HSPs:

Score = 1342 (207.4 bits), Expect = 3.4e-57, P = 3.4e-57, Group = 1
Identities = 270/272 (99%), Positives = 270/272 (99%), Strand = Plus / Plus

Query:      20 CAGGCTCCCACTCCATGAGGTATTTCTTCACATCCGTGTCCTCCGGCCCGGCCGCGGGGAGC 79
             |||
Sbjct:      71 CGGGCTCCCACTCCATGAGGTATTTCTTCACATCCGTGTCCTCCGGCCCGGCCGCGGGGAGC 130

Query:      80 CCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTCGACAGCGACG 139
             |||
Sbjct:     131 CCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTCGACAGCGACG 190

Query:     140 CCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGGAGTATT 199
             |||
Sbjct:     191 CCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGGAGTATT 250

Query:     200 GGGACCAGGAGACACGGAATGTGAAGGCCAGTCACAGACTGACCGAGTGGACCTGGGGA 259
             |||
Sbjct:     251 GGGACCAGGAGACACGGAATGTGAAGGCCAGTCACAGACTGACCGAGTGGACCTGGGGA 310

Query:     260 CCCTGCGCGGCTACTACAACCAGAGCGAGGGC 291
             |||
Sbjct:     311 CCCTGCGCGGCTACTACAACCAGAGCGAGGCC 342
```

Figure 13: Result obtained from the IMGT-HLA database Blast tool. In this example, the sequence analyzed showed 99% HLA-A*03 allele nucleotides similitude. (|) shows equal nucleotides between analyzed and reference sequences.

For the 18 samples that were analyzed, we could genotype 16; from K11 we only got one allele. K13 sample could not be typed (Table 3). These results showed that we detected different alleles. From the different samples only K11 and K13 displayed problems with the analysis. The other samples could be typed, showing that this new method could be performed in a larger number of samples. The principle as well could be used for HLA-B, -C, -DQB, -DQR or -G.

Table 3. Sequencing Results from new method compared to PCR-SSP.

	EXON 2				EXON 3		EXON 4			HLA-A GENOTYPES	
Primers / samples	A2- 1F/1R	A2- 2F/2R	A2- 1F/2R	A2- 2F/1R	A3- 1F/2R	A3- 2F/2R	A4- 1F/2RH	A4- 2F/2RH	A4- 3FH/1R	FFPE method	PCR- SSP
VB1	NA	A*02/24	†	†	A*02/24	†	A*02	A*24	A*02	A*02/24	A*02/24
HZ1	A*02	A*02	N	N	N	N	N	N	N	A*02/02	A*02/02
K1	A*03/25	NA	A*25	NA	A*25	NA	A*25	A*03	NA	A*03/25	A*03/25
K2	A*03	NA	NA	NA	A*03	A*26	A*26	A*03	NA	A*03/26	A*03/26
K3	NA	A*02	A*01	A*02	A*02	A*01	A*02	NA	NA	A*01/02	A*01/02
K4	NA	NA	A*03	A*02	A*02	A*03	A*02	A*03	A*03	A*02/03	A*02/03
K5	A*03	A*02	A*03	A*02	A*02	NA	A*02	A*03	A*02	A*02/03	A*02/03
K6	A*01/24	A*24	NA	NA	A*01/24	NA	NA	A*24	NA	A*01/24	A*01/24
K8	A*01	A*02	A*01	A*01	A*02	A*01	NA	NA	NA	A*01/02	A*01/02
K10	A*01/03	NA	A*01/03	NA	A*01	A*01	NA	NA	A*03	A*01/03	A*01/03
K11	A*01	NA	A*01	NA	A*01	A*01	NA	NA	NA	A*01/--	A*01/26
K13	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	A*01/68
K14	A*11	A*02	A*11	A*02	A*02	A*11	A*02	A*11	A*02	A*02/11	A*02/11
K16	A*25	A*02	A*25	A*02	A*25	A*25	A*02	NA	NA	A*02/25	A*02/25
K17	A*26	A*02	A*26	A*02	A*02	A*26	A*02	NA	A*02	A*02/26	A*02/26
K21	A*01	A*02	A*01	A*02	A*01	A*01	A*02	NA	A*02	A*01/02	A*01/02
K23	A*01/03	NA	A*01/03	NA	A*01	A*01	NA	A*01	A*01	A*01/03	A*01/03
K24	A*03	A*02	A*03	A*02	A*03	A*03	A*02	A*03	NA	A*02/03	A*02/03

N: Sample HZ1 did not perform these amplification reactions due to unavailability.

NA: none or not HLA-A results or poor sequencing result.

† VB1 sample used in this case only as a positive control for amplification reactions, genotype established by editing FASTA formats.

Results in red correspond to genotypes established by editing FASTA formats according to double peaks in the sequences graphics (Figure 12).

8. DISCUSSION

The HLA complex supplies protection against pathogens. This particular function explains the high polymorphism. HLA genotype has been associated with hundreds of diseases, including autoimmune diseases (Horton, Wilming et al. 2004). It is important to study more associations between HLA types and different kinds of cancer around the world (The-MHC-Consortium 1999). In cancer, it has been observed that a common feature is the loss of HLA molecules (Little and Stern 1999). Moreover, the role of HLA molecules, genes and other related loci in the development and progression of neoplasia are becoming clearer. Different alleles have been proved to be associated with malignancies in different ethnic groups (Bateman and Howell 1999).

HLA typing has evolved with the technological advances and since its discovery, has had a large importance in the clinical world, for example in the transplantation procedures (Shaw, Arguello et al. 2010). The first approach was the serological typing method, with big disadvantages like the need for live lymphocytes and a large antisera panel. Next to the serological methods, molecular techniques were born. The new DNA based methods brought new opportunities to study the HLA types more in detail (Howell, Carter et al. 2010). One particular approach, the Sequence Based Typing (SBT) has a big advantage over other DNA based methods. This kind of procedures is not allele restricted (Howell, Carter et al. 2010; Shaw, Arguello et al. 2010), the appearance of a new allele or a rare allele does not limit one study performed with this method. However, molecular approaches use DNA extracted from peripheral blood as a template, it means, that most of these techniques uses DNA that has a good quality.

HLA typing and studies that establish association with cancer and other diseases could be previously only performed by analyzing good quality DNA samples. DNA extraction was not common in the past, so there are no available DNA sources for retrospective analysis. FFPE samples collected in past oncology studies with valuable clinical information, in our case collected ten years ago at Karolinska Hospital, could be a potential DNA source for HLA typing by amplification and sequencing. Until now, there are few HLA typing studies without concluding remarks using this particular DNA source (Bateman, Hemmatpour et al. 1997; Ota, Shimada et al. 2006).

In this study, we performed DNA extraction from 17 different 9 to 11 years old FFPE samples, and with a new method based on SBT we performed HLA-A typing. These samples were previously typed with PCR-SSP, a technique in which DNA used is extracted from fresh blood and the double strains are without alterations to the length and content. So in this particular study, the results were compared between DNA extracted from FFPE and DNA extracted from blood.

Complete sequences were analyzed on the IMGT-HLA blast tool (Robinson, Mistry et al. 2011), and we could establish directly the HLA genotype for the samples using the different sequences obtained from the different amplification protocols, except for samples K10, K11 and K23 (Table 3). For these three samples, we used the Chromas Lite graphics to observe the double peaks that correspond to nucleotide changes. Unlike the background, the double peaks were clearly higher and almost reached the intensity of the original peak. However, the real changes were also established according to the sequences from IMGT-HLA database, looking into the alignment files obtained from this database at http://hla.alleles.org/data/txt/a_nuc.txt (Robinson, Mistry et al. 2011). After this, the complete sequences were edited and reanalyzed with the Blast tool. For K10 and K23 samples the genotype could be correctly established. From K11 we could only establish one allele with the procedure. By observing the gels, this sample could not be amplified; the amplification product quantity was observed to be so low. This could be due to a bad extraction procedure. On the other hand, this sample is old and fixation protocol could be harder, causing more DNA damage. For this case, it is important to perform a new extraction with a new procedure, so we could estimate where the bad step is on this particular sample.

This new HLA-A typing method was compared to a standard procedure, in this case PCR-SSP, in order to evaluate its accuracy. In this study we used a panel of previously blood PCR-SSP typed patients' samples and a blood sample from a healthy volunteer as a control. When we finally concluded the typing with FFPE samples, our results showed large concordance with PCR-SSP results. K11 and K13 could not to be completely genotyped. This method detected 91% of alleles in FFPE studied samples.

This is the first study using HLA-A SBT with FFPE tissue samples. Our results suggest that our method is reliable, in the future it could be performed in a larger scale with more FFPE samples without previously HLA-A typing.

Using High Pure RNA extraction kit (RocheTM) omitting the step of DNase treatment, we extracted DNA from the samples. With this procedure we could only perform a DNA extraction and determine its concentration, NanodropTM did not permit us to evaluate the quality of DNA extracted. We already know that the DNA extracted from FFPE has a lower quality. DNA samples in 2% agarose gels shows smear patterns (Data not shown). This is because the DNA generates protein crosslinkages during the fixation procedure giving fragmentation of the strands (Farrugia, Keyser et al. 2010); the acidic environment induces protonation of purines that in this form are easy targets for cleavage by hydrolysis (Klopfleisch, Weiss et al. 2011). Despite of this issue, previous works have reported DNA extraction performance that was enough to develop different assays and analysis, DNA Methylation patterns (Dubeau, Chandler et al. 1986), PCR on old samples (Shibata, Martin et al. 1988), among others.

With extracted DNA, we proceeded with the new technique involving a new amplification and sequencing protocol in order to type HLA-A. For the amplification protocol we have considered the following points: DNA extracted from FFPE samples has been reported to be fragmented, segments have been described with various length from <150bp fragments (Gilbert, Sanchez et al. 2007) up to 400bp (Lehmann and Kreipe 2001); and the polymorphisms in HLA class I is mainly concentrated to Exon 2 and 3 (Little and Stern 1999; Shaw, Arguello et al. 2010).

Our amplification method includes the use of several sets of new designed primers for the exons 2 and 3. In order to avoid certain kind of ambiguities, related to alleles differences defined outside exons 2 and 3 (Adams, Barracchini et al. 2004), we also analyzed exon 4. For the FFPE DNA samples, a total of 9 different amplification reactions were performed for each sample according to the different set of primers used, four amplifications for exon 2, two for exon 3, and three for exon 4. We obtained amplification product for 123 reactions, distributed between exon 2, exon 3 and exon 4 amplification reactions (Table 2). In several cases, along with the blood sample, there were samples that amplified for all 9 different protocols.

In only one case, K13, we could not obtain any amplification product. For two samples, K8 and K11, we could not obtain product for the any of exon 4 amplification protocols. This could be associated to different fixation procedures; those could lead to different stage of damage in the DNA. The differences between fixation protocols as well laboratory organizations bring differences to the obtained DNA quality (Lehmann and Kreipe 2001; Gilbert, Sanchez et al. 2007). In this particular study, the fixation protocol was not controlled and the samples varied between different labs. This partially explains this part of the results. Other studies show the importance of different extraction protocols. Most studies uses commercial kits, and they obtain different DNA length (Klopfleisch, Weiss et al. 2011), in our case, we use only one commercial kit; so this method could fail for these samples. Using new extraction kits, it could be obtained enough DNA for future studies.

The primers in this study were designed according to the expected FFPE DNA fragmentation limitation. With this idea, we performed amplification using FFPE DNA and we got product from the majority of the reactions. Exon 2 and exon 3 primers were designed in order to yield a complete amplification product, and we got products up to 292bp long. However, this approach could not be applied to exon 4 amplification. Complete exon 4 product was not obtained (data not shown), so we divided the exon 4 reaction in order to obtain two fragments that could be amplified and analyzed. This study completed a new strategy, using old tissue material, amplifying the exons that we expect would be enough for HLA-A typing.

Immune genes have been under strong selection pressure, this is because they needed to diversify in order to cope with ever changing pathogenic epitopes. Duplication events could occur during this, so there are paralogous genes that could have similar sequences across all the genome (Horton, Wilming et al. 2004). We observed that some samples gave unspecific amplification products (Annex 1). Our primers were designed according to the sequences obtained from the IMGT-HLA database for different alleles. The primers had a low variability between them, because we selected conserved regions surrounding the different exons. They were tested in a Blast tool from de NCBI database in order to establish their specificity. Moreover we use the highest melting temperature possible for each amplification protocol (60°C for all procedures) to

increase the reactions specificity. With this, we could say that the obtained amplified unspecific product could correspond to one duplication event because, these unspecific products were found only in determined samples analysis. It can not be explained by sample contamination because negative controls did not display this product, so mixes were not contaminated. Although this result has to be analyzed more in detail in order to establish the source of this unspecific product.

Following amplification we performed a sequencing protocol for all the products from the amplification protocols. Sample K13 was discarded due to the negative results from amplification. For each positive sample, we used the different primers for the different protocols. Each primer, forward and reverse, were used separately according to the previous amplification reaction. After the reaction, the results were read in an automatic sequencer (Applied Biosystems 7900 HT Real-Time System). The sequences after this procedure were visualized on Chromas Lite software, and then, the sequences were exported to a FASTA format in order to be analyzed with the databases. Most of the graphics show specific peaks, only certain samples displayed big background peaks. These background peaks were most common in those amplifications protocols that showed unspecific products. DNA quality from FFPE samples is lower than fresh blood DNA; this could lead also to amplification of truncated products due to bad annealing. Further analysis is needed in order to try to eliminate these background peaks.

Despite of these unspecific products, we used the amplification mixes as the template for sequencing because DNA extraction from the agarose gels was not good enough for typing. The FASTA formats were saved, and for the Reverse primer sequencing results, the FASTA sequence was translated into the complementary strand using Gene Runner software. As mentioned before, primers were tested for their specificity using Blast tool in NCBI database. Background peaks as well unspecific amplification products could be assessed as duplication elements but further analysis is needed in order to establish their correct origin. However, the biggest peaks in the majority of cases permitted us to obtain HLA-A sequences which was analyzed (Table 3).

This is the first study where the strategy of different primer sets could obtain enough amplification products which have been sequenced and these sequences could be used for HLA-A analysis. Previous HLA studies on FFPE samples used other strategies for

typing. We must not forget that our restricted FFPE DNA samples number could be a limitation; however this is a good approach because these samples were in average ten years old and we had previous genotype information. This study showed the importance of FFPE samples as DNA source.

With the sequences exported and saved as FASTA formats, we proceeded to analyze the sequencing results using ClustalW2 (Thompson, Higgins et al. 1994) and EBI IMGT-HLA database Blast Tool (Robinson, Mistry et al. 2011). The first procedure was to obtain a complete sequence. For all the samples, forward and reverse sequences were aligned and the complete sequence was established using the consensus sequences plus the remaining arms that could be observed for each reaction, forward and reverse. Although some sequences could not be analyzed, the alignment in certain cases showed a big discrepancy between forward and reverse sequence so we could not perform the HLA typing. However, almost all the samples we got at least one complete sequence from the different Exons. For detailed information see annex 2. Our approach took into account, that our FFPE samples have different HLA-A genotypes. The used primers had different sequences which are present on different alleles, so the expected products correspond in many cases to the different alleles in the samples. Our 9 amplifications procedures were designed in order to type directly most of FFPE DNA samples, i. e. from different products we should get genotypes. For those samples where extracted DNA quality was not adequate, we edited FASTA formats according to double peaks showed on graphics.

In summary we could perform a DNA extraction from FFPE tissue samples; we obtained products up to 292bp in length. All amplification products sequences were analyzed with the IMGT-HLA database and for the majority of the samples we could determine the correct genotype. Compared to a blood derived DNA technique, our results showed that FFPE samples could be used as a DNA source in HLA typing. This method has the advantages of all SBT HLA typing approaches. More indeed, with this procedure we have done the first step toward a new era of HLA retrospective analysis. FFPE samples has been stored for more than a hundred years and for example, only the United States there are more than 300 million archival samples, and annually 20 million are added (Savage and Hostetter 2011). These samples are all around the world (Klopfleisch, Weiss et al. 2011). On other hand, this new approach is cheaper, and

logistically feasible. Previous methods are costly; many labs could not perform large studies (Abbott, Tukuitonga et al. 2006), which is why this is a large advance in order to perform more HLA analysis worldwide. The principle of this technique could be applied for the other HLA molecules, class I, II and III and also for other interesting genes.

9. CONCLUSIONS

1. The complete procedure permits us to extract enough DNA quantity in acceptable quality in order to amplify up to 292bp fragments.
2. The designed primers and amplification protocols were able to get exon2, exon 3 and exon 4 amplicons.
3. These fragments can be sequenced and thus genotype almost all the FFPE samples.
4. This is a new method that can be applied in order to perform retrospective HLA-A analysis using FFPE samples stored during past studies.
5. It is also a cost effective and feasible technique that small labs around the world could use for association studies with a big quantity of samples.
6. Finally this is an approach that be used for typing other polymorphic genes than HLA-A, for example HLA-B, -C, HLA class II, HLA class III, MICA, MICB and KIR. This is a new opportunity to develop retrospective association studies where none have been used so far.

10. FUTURE PERSPECTIVES AND PROPOSALS

This method could bring new opportunities in order to perform new association studies. However we need to collect more samples in order to demonstrate the accuracy of this new technique.

Despite of the feasibility of our method, a new proposal is to perform the use of probes and automated with the purpose of increasing the ease of the approach.

In order to evaluate the DNA quality we also propose to perform an additional DNA extraction procedure analysis. New extraction method could perform better DNA extractions, which could lead to increase the quality of these kinds of studies.

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ANNEXES

Annex 1

2% agarose gels from Amplification protocols.

Annex 2

Alignments and Blast results.

Annex 1

2% agarose gels from different amplification protocols and samples.

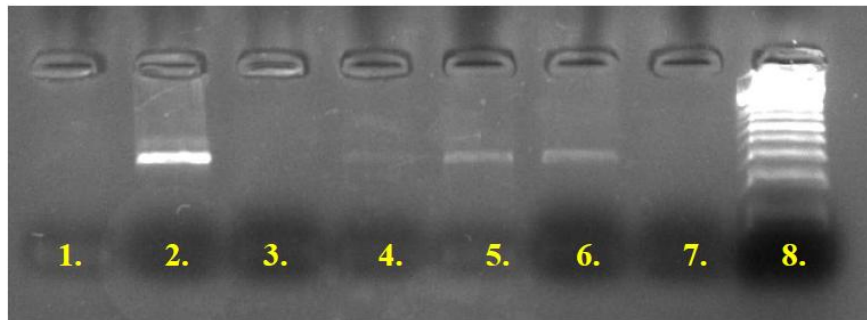


Figure A1: FFPE DNA amplification, A2-2F/2R. Lane 1, negative control; lane 2, VB1; lane 3, K2; lane 4, K3; lane 5, K4; lane 6, K6; lane 7, negative control; lane 8, 100bp ladder

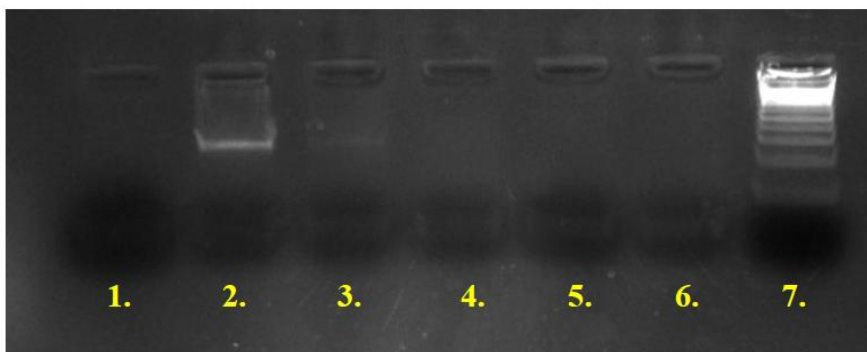


Figure A2: FFPE DNA amplification, A2-1F/1R. Lane 1, negative control; lane 2, VB1; lane 3, K1; lane 4, K2; lane 5, K3; lane 6, negative control; lane 7, 100bp ladder

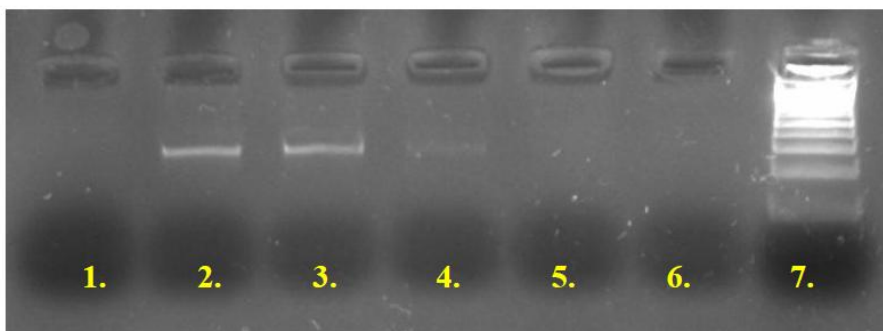


Figure A3: FFPE DNA amplification, A2-1F/2R. Lane 1, negative control; lane 2, VB1; lane 3, K1; lane 4, K2; lane 5, K3; lane 6, negative control; lane 7, 100bp ladder

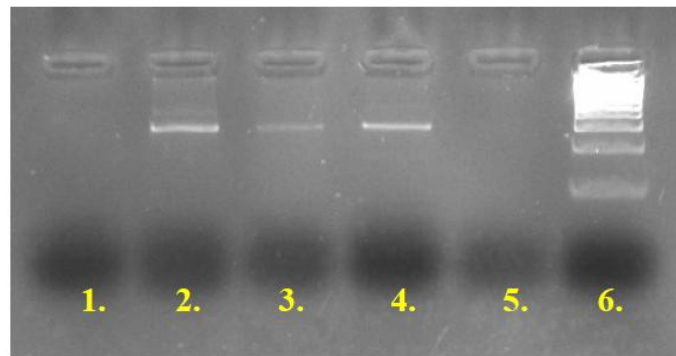


Figure A4: FFPE DNA amplification, A2-2F/1R. Lane 1, negative control; lane 2, VB1; lane 3, K2; lane 4, K3; lane 5, negative control; lane 6, 100bp ladder

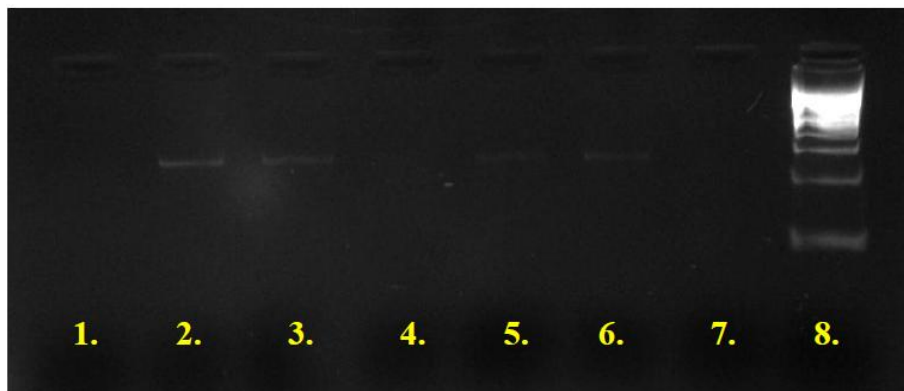


Figure A5: FFPE DNA amplification, A3-1F/2R. Lane 1, negative control; lane 2, VB1; lane 3, K1; lane 4, K3; lane 5, K4; lane 6, K6; lane 7, negative control; lane 8, 100bp ladder

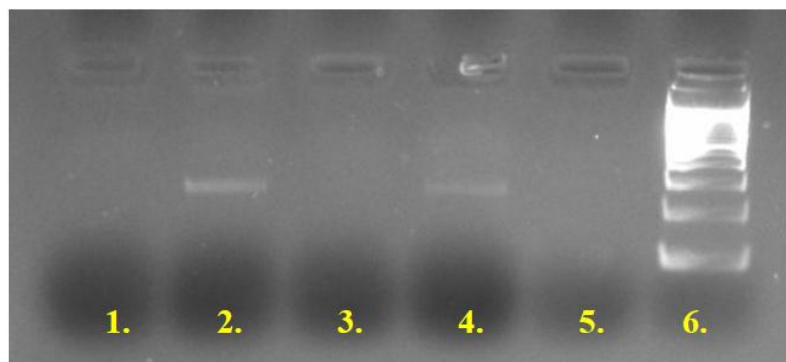


Figure A6: FFPE DNA amplification, A3-2F/2R. Lane 1, negative control; lane 2, VB1; lane 3, K3; lane 4, K4; lane 5, negative control; lane 6, 100bp ladder

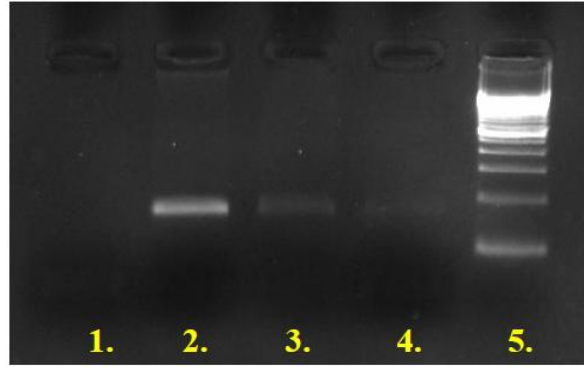


Figure A7: FFPE DNA amplification, A4-1F/2RH. Lane 1, negative control; lane 2, VB1; lane 3, K1; lane 4, K2; lane 5, 100bp ladder

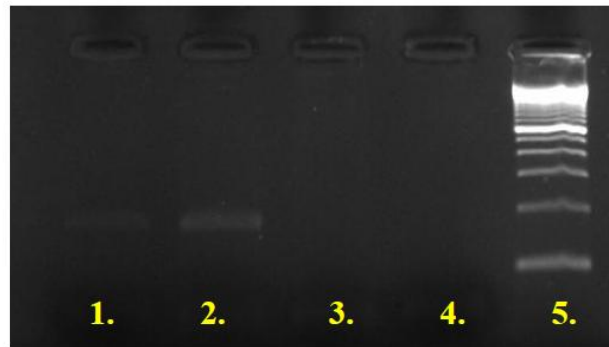


Figure A8: FFPE DNA amplification, A4-1F/2RH. Lane 1, K3; lane 2, K4; lane 3, K6; lane 4, negative control; lane 5, 100bp ladder

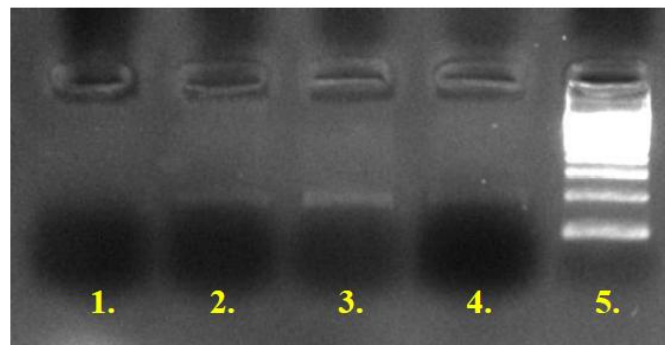


Figure A9: FFPE DNA amplification, A4-2F/2RH. Lane 1, negative control; lane 2, VB1; lane 3, K1; lane 4, K2; lane 5, 100bp ladder

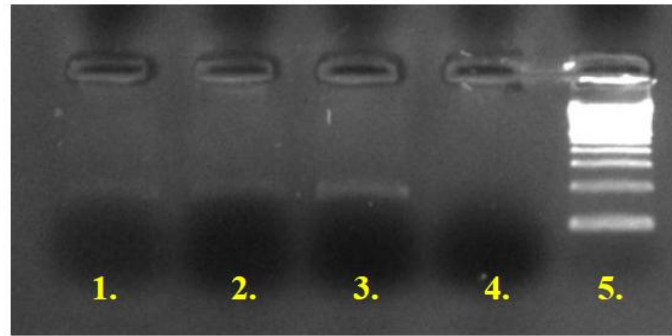


Figure A10: FFPE DNA amplification, A4-2F/2RH. Lane 1, K3; lane 2, K4; lane 3, K6; lane 4, negative control; lane 5, 100bp ladder

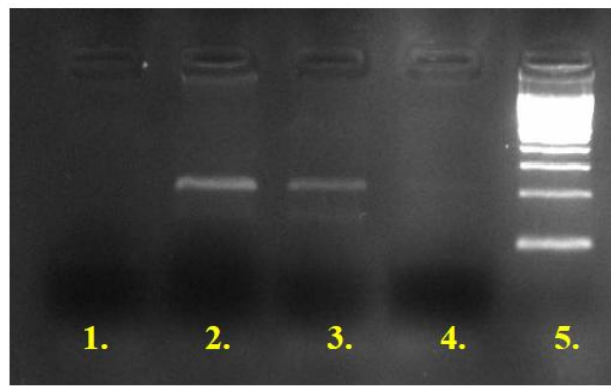


Figure A11: FFPE DNA amplification, A4-3FH/1R. Lane 1, negative control; lane 2, VB1; lane 3, K1; lane 4, K2; lane 5, 100bp ladder

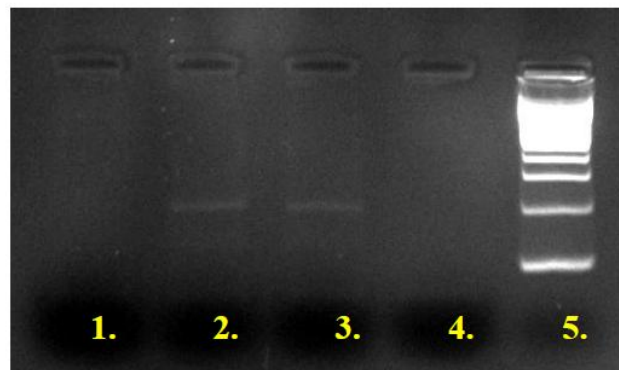


Figure A12: FFPE DNA amplification, A4-3FH/1R. Lane 1, K3; lane 2, K4; lane 3, K6; lane 4, negative control; lane 5, 100bp ladder

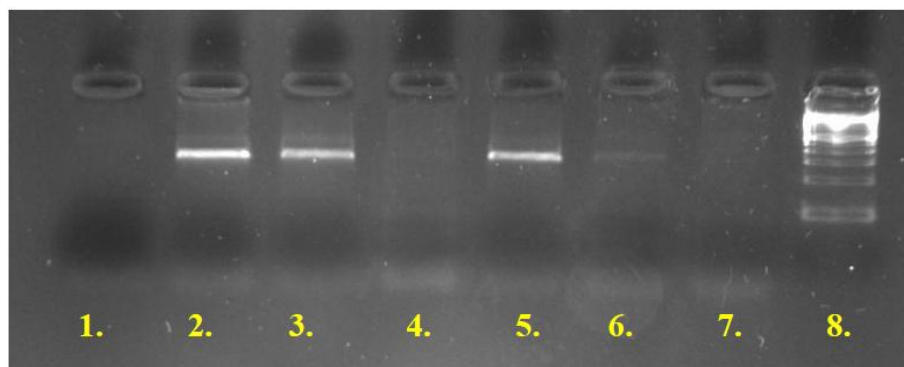


Figure A13: FFPE DNA amplification, A2-1F/1R. Lane 1, negative control; lane 2, VB1; lane 3, K5; lane 4, K8; lane 5, K10; lane 6, K11; lane 7, K13; lane 8, 100bp ladder

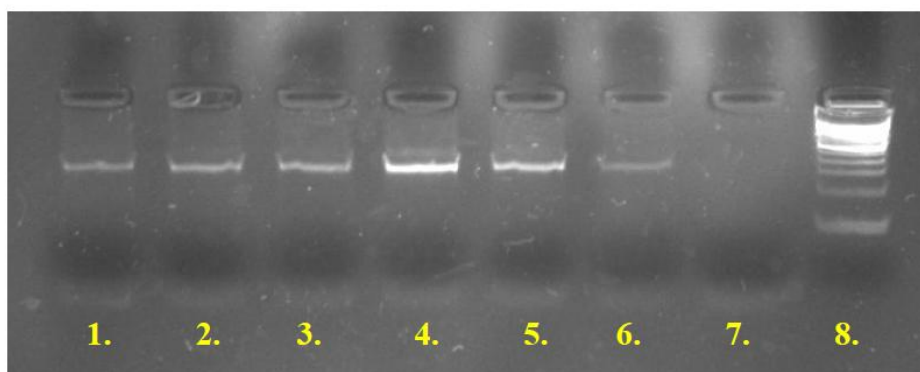


Figure A14: FFPE DNA amplification, A2-1F/1R. Lane 1, K14; lane 2, K16; lane 3, K17; lane 4, K21; lane 5, K23; lane 6, K24; lane 7, negative control; lane 8, 100bp ladder

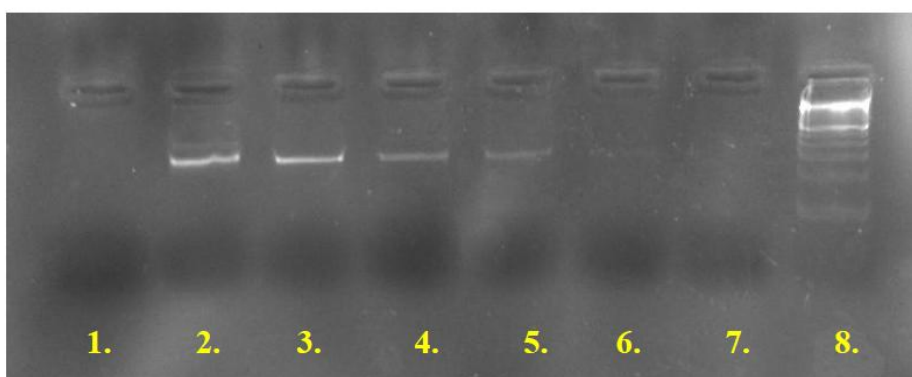


Figure A15: FFPE DNA amplification, A2-2F/2R. Lane 1, negative control; lane 2, VB1; lane 3, K5; lane 4, K8; lane 5, K10; lane 6, K11; lane 7, K13; lane 8, 100bp ladder

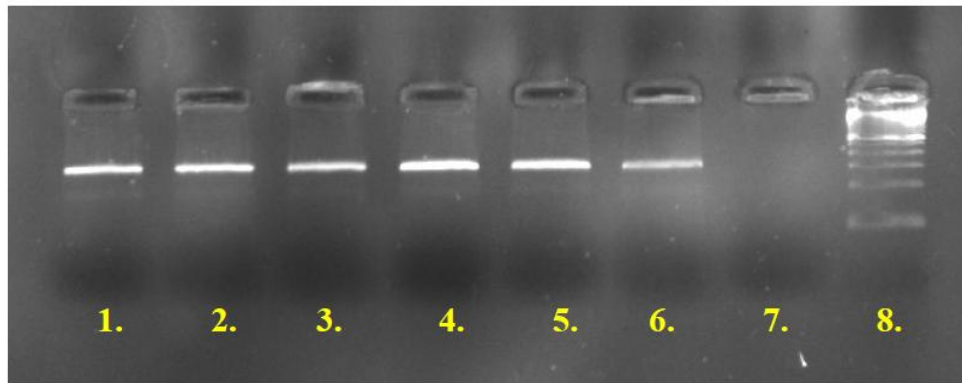


Figure A16: FFPE DNA amplification, A2-2F/2R. Lane 1, K14; lane 2, K16; lane 3, K17; lane 4, K21; lane 5, K23; lane 6, K24; lane 7, negative control; lane 8, 100bp ladder

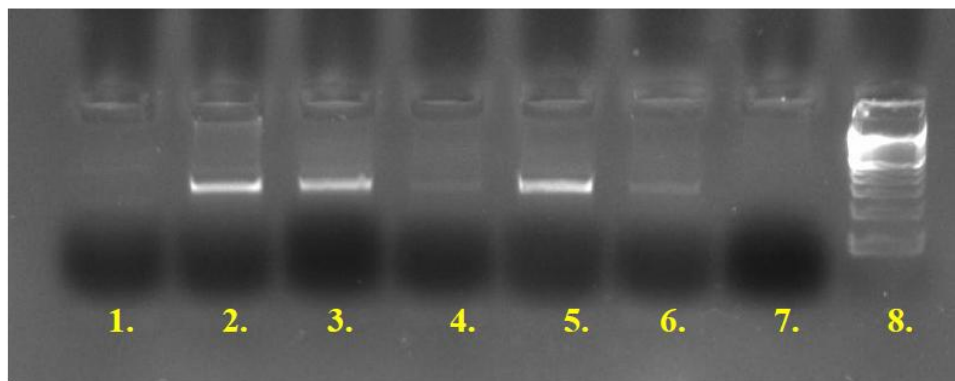


Figure A17: FFPE DNA amplification, A2-1F/2R. Lane 1, negative control; lane 2, VB1; lane 3, K5; lane 4, K8; lane 5, K10; lane 6, K11; lane 7, K13; lane 8, 100bp ladder

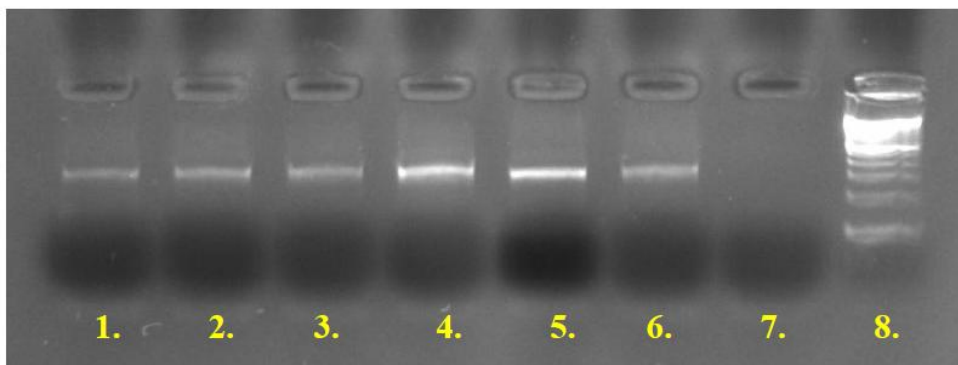


Figure A18: FFPE DNA amplification, A2-1F/2R. Lane 1, K14; lane 2, K16; lane 3, K17; lane 4, K21; lane 5, K23; lane 6, K24; lane 7, negative control; lane 8, 100bp ladder

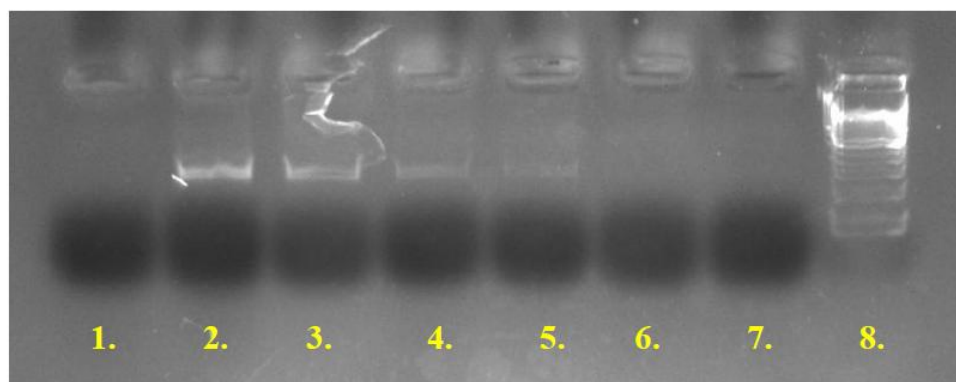


Figure A19: FFPE DNA amplification, A2-2F/1R. Lane 1, negative control; lane 2, VB1; lane 3, K5; lane 4, K8; lane 5, K10; lane 6, K11; lane 7, K13; lane 8, 100bp ladder

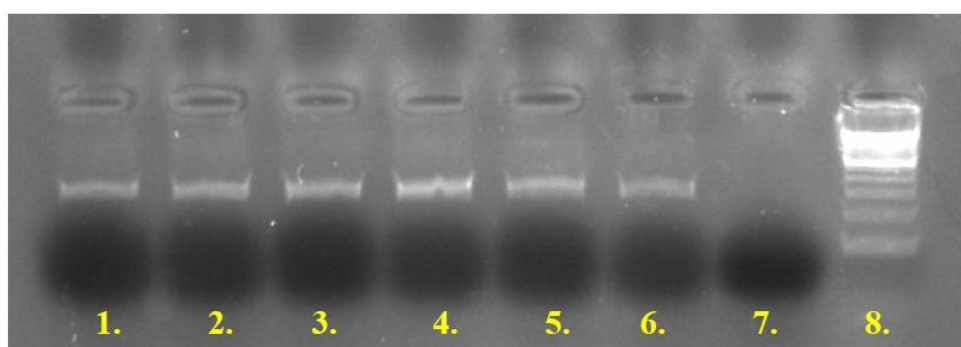


Figure A20: FFPE DNA amplification, A2-2F/1R. Lane 1, K14; lane 2, K16; lane 3, K17; lane 4, K21; lane 5, K23; lane 6, K24; lane 7, negative control; lane 8, 100bp ladder

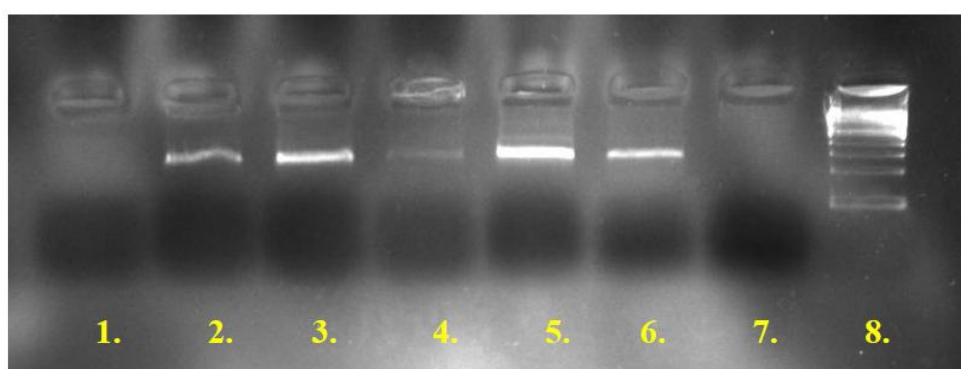


Figure A21: FFPE DNA amplification, A3-1F/2R. Lane 1, negative control; lane 2, VB1; lane 3, K5; lane 4, K8; lane 5, K10; lane 6, K11; lane 7, K13; lane 8, 100bp ladder

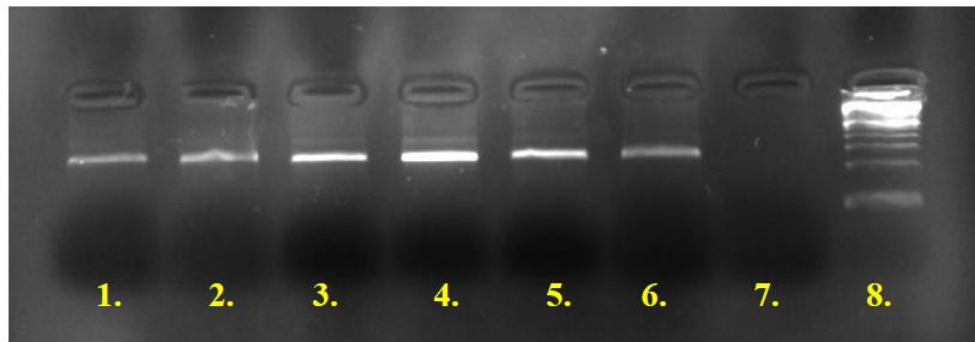


Figure A22: FFPE DNA amplification, A3-1F/2R. Lane 1, K14; lane 2, K16; lane 3, K17; lane 4, K21; lane 5, K23; lane 6, K24; lane 7, negative control; lane 8, 100bp ladder

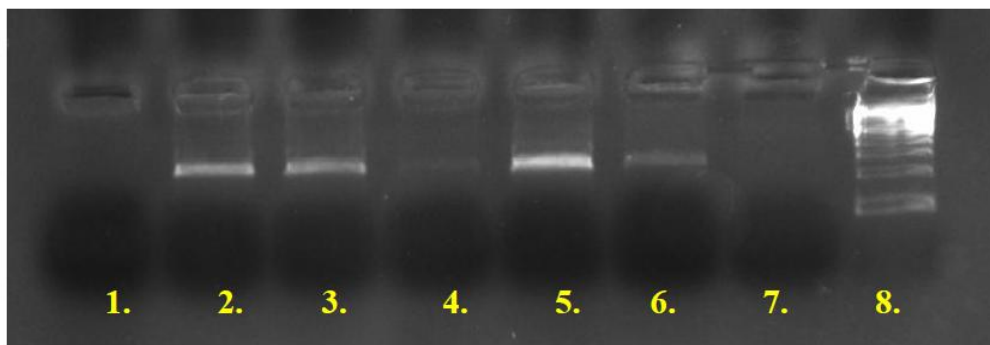


Figure A23: FFPE DNA amplification, A3-2F/2R. Lane 1, negative control; lane 2, VB1; lane 3, K5; lane 4, K8; lane 5, K10; lane 6, K11; lane 7, K13; lane 8, 100bp ladder

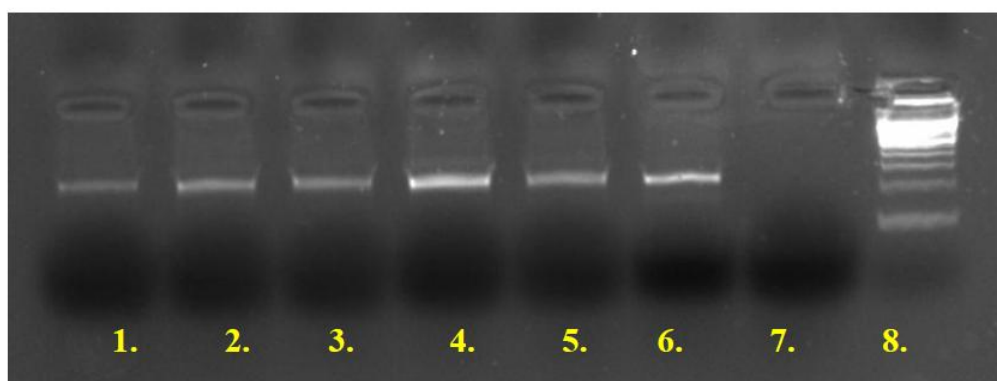


Figure A24: FFPE DNA amplification, A3-2F/2R. Lane 1, K14; lane 2, K16; lane 3, K17; lane 4, K21; lane 5, K23; lane 6, K24; lane 7, negative control; lane 8, 100bp ladder

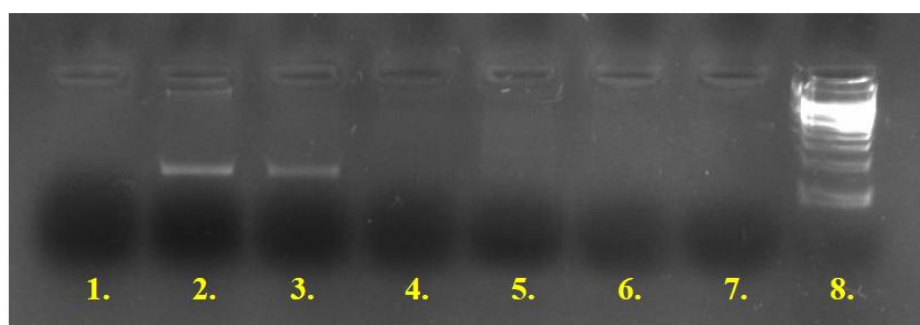


Figure A25: FFPE DNA amplification, A4-1F/2RH. Lane 1, negative control; lane 2, VB1; lane 3, K5; lane 4, K8; lane 5, K10; lane 6, K11; lane 7, K13; lane 8, 100bp ladder

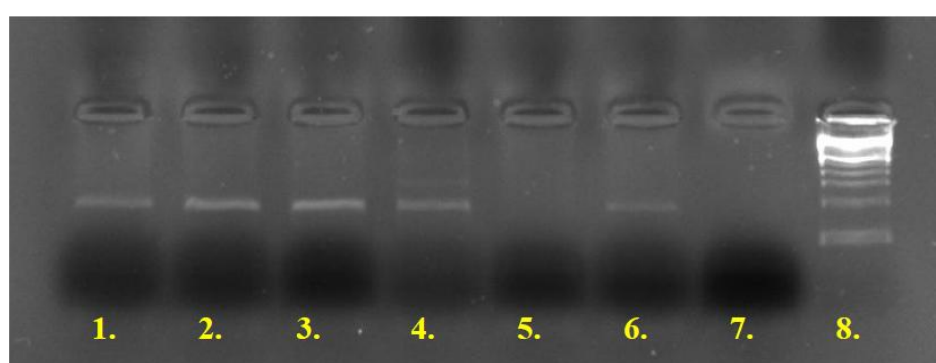


Figure A26: FFPE DNA amplification, A4-1F/2RH. Lane 1, K14; lane 2, K16; lane 3, K17; lane 4, K21; lane 5, K23; lane 6, K24; lane 7, negative control; lane 8, 100bp ladder

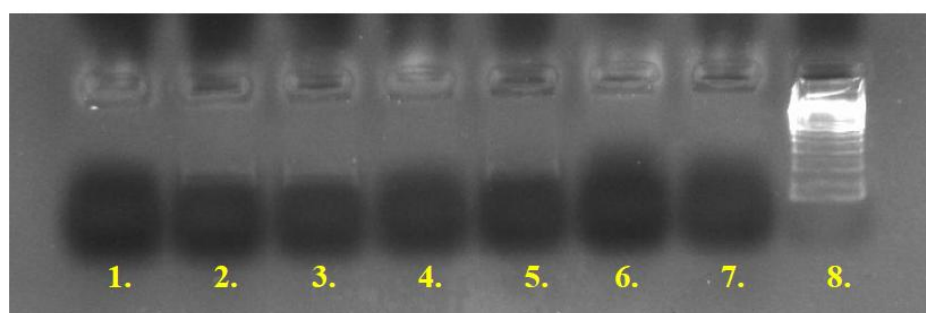


Figure A27: FFPE DNA amplification, A4-2F/2RH. Lane 1, negative control; lane 2, VB1; lane 3, K5; lane 4, K8; lane 5, K10; lane 6, K11; lane 7, K13; lane 8, 100bp ladder

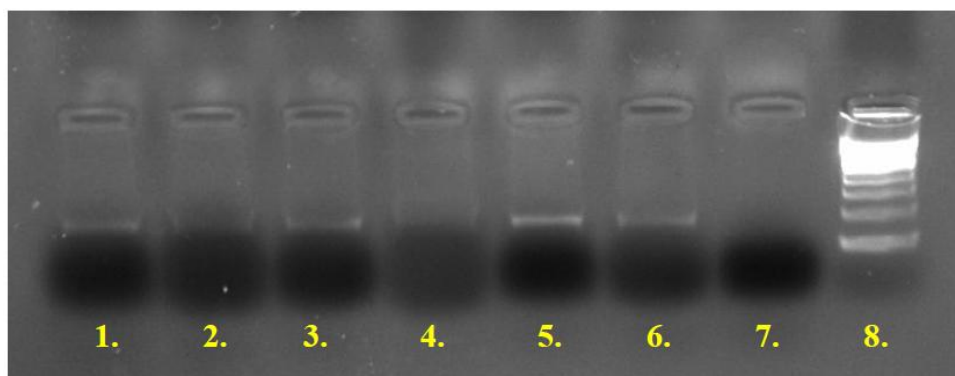


Figure A28: FFPE DNA amplification, A4-2F/2RH. Lane 1, K14; lane 2, K16; lane 3, K17; lane 4, K21; lane 5, K23; lane 6, K24; lane 7, negative control; lane 8, 100bp ladder

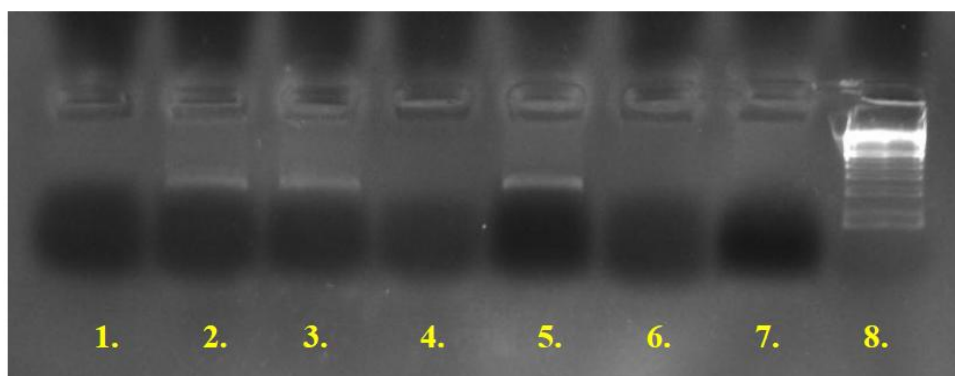


Figure A29: FFPE DNA amplification, A4-3FH/1R. Lane 1, negative control; lane 2, VB1; lane 3, K5; lane 4, K8; lane 5, K10; lane 6, K11; lane 7, K13; lane 8, 100bp ladder

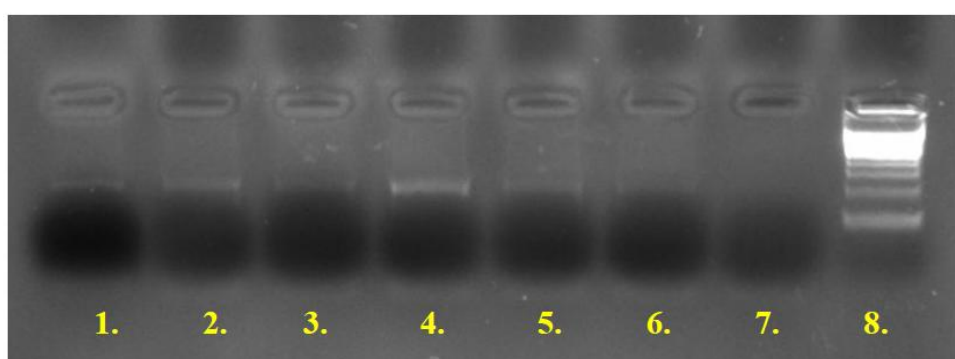


Figure A30: FFPE DNA amplification, A4-3FH/1R. Lane 1, K14; lane 2, K16; lane 3, K17; lane 4, K21; lane 5, K23; lane 6, K24; lane 7, negative control; lane 8, 100bp ladder

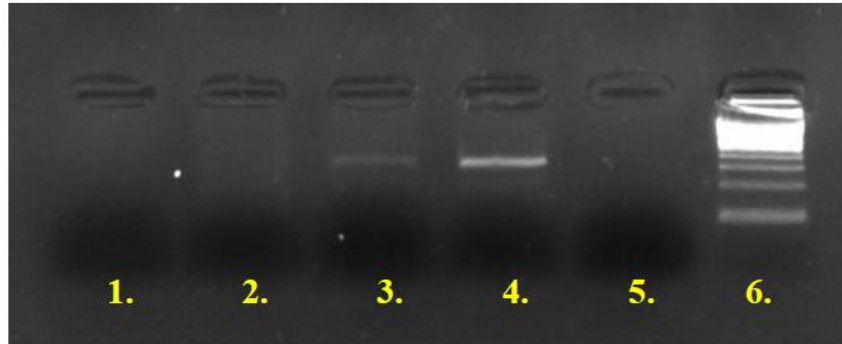


Figure A31: FFPE DNA amplification, A2-2F/2R. Lane 1, negative control; lane 2, K2; lane 3, K3; lane 4, K4; lane 5, negative control; lane 6, 100bp ladder

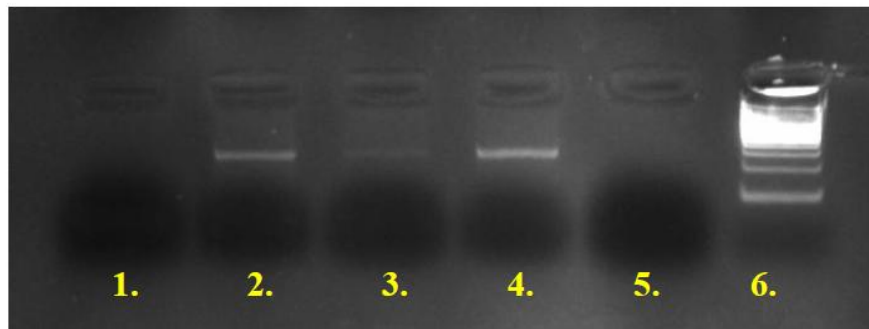


Figure A32: FFPE DNA amplification, A3-1F/2R. Lane 1, negative control; lane 2, K2; lane 3, K3; lane 4, K4; lane 5, negative control; lane 6, 100bp ladder

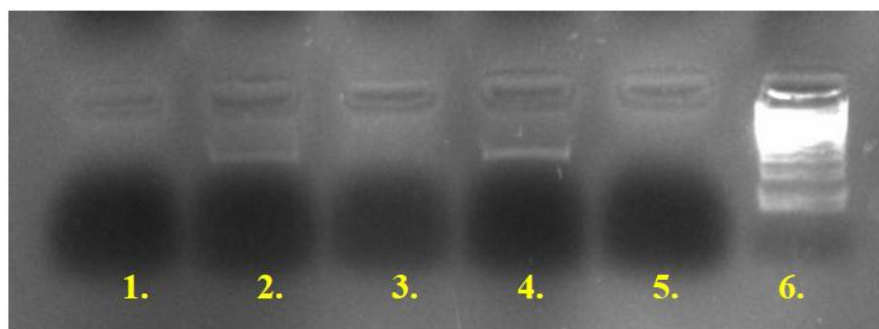


Figure A33: FFPE DNA amplification, A2-1F/1R. Lane 1, negative control; lane 2, K2; lane 3, K3; lane 4, K4; lane 5, negative control; lane 6, 100bp ladder

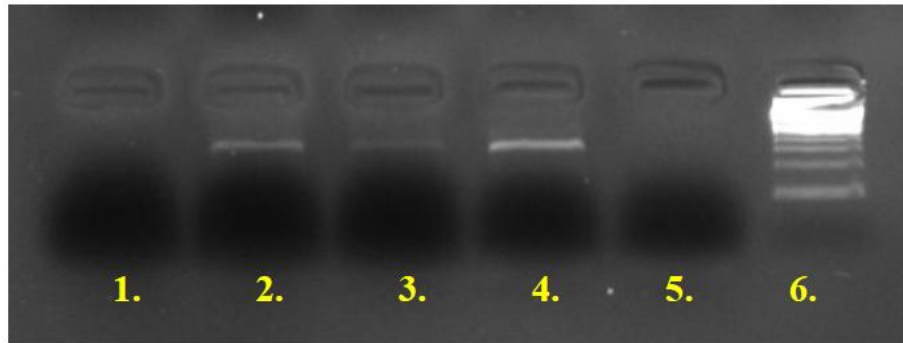


Figure A34: FFPE DNA amplification, A2-1F/2R. Lane 1, negative control; lane 2, K2; lane 3, K3; lane 4, K4; lane 5, negative control; lane 6, 100bp ladder

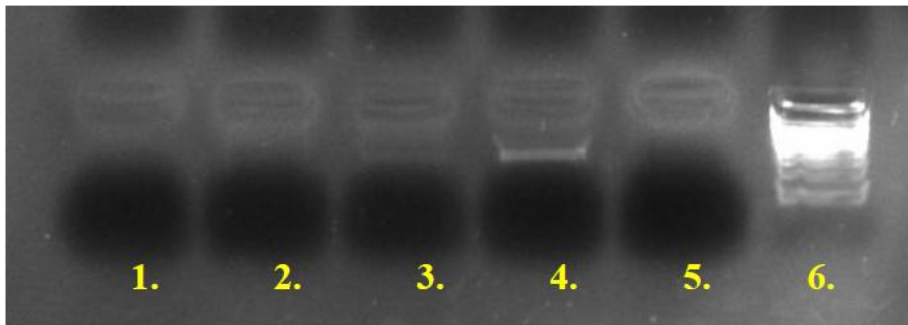


Figure A35: FFPE DNA amplification, A2-2F/1R. Lane 1, negative control; lane 2, K2; lane 3, K3; lane 4, K4; lane 5, negative control; lane 6, 100bp ladder

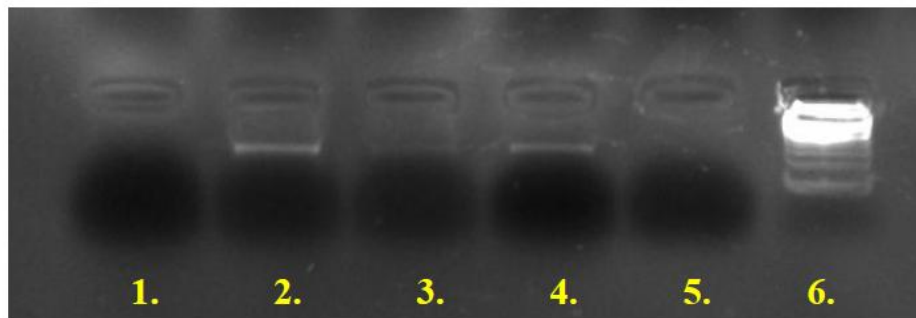


Figure A36: FFPE DNA amplification, A3-2F/2R. Lane 1, negative control; lane 2, K2; lane 3, K3; lane 4, K4; lane 5, negative control; lane 6, 100bp ladder

Annex 2

Alignments and Blast results.

VB1 02-11-2010

A2-1/1

```
>VBFW
CGCGCGGCTGATAGCTATTTCGGTCGTCGTGCTGGGCTTGGCGTCAGTGTGTGCCGGT
CCCAATACTGCGGCCCTCTGTCTCCCCACGGCGCCCGGGCTCCATCCTCGGACTCGC
GGCGTCGCTGTGCAACCGCACGAATTGCGTGTCTGCCACGTACTCCACGGCGATGAAGCT
GGGCTCCCCCGCGGCCCGGGCCGGAACGGCGGTGCTGAAAATACCCTCATGGGAGTGGG
GAGCCTGGGGGGCGTGCAGGGCTTGAGAA
```

```
>VBRV
TGTCTCTGCTGGTTGTAGCGGCGGAGCAGGTTCCCTCAGGTTCACTCGGTCACTCTGTGC
GGGGCCTTGGAGTACCGTGTGTTCCAGTCCCAATACTCCGGCCCCCTTTGCTCCACCCAC
GGCGCCCGCGGCTCCATCCCTCGGACTCGCGGCGTCTGCTGCAACCGCAGGAACGCGT
GTCGTCCACGTAGCCACGGCAATGAAGCGGGGCTCCCCGCGGCCGGCCAGGACACGGC
GGTGCGAAATACTTAGCAGAGCG
```

CLUSTAL 2.1 multiple sequence alignment

```
VBFW      -----CGCGCGGCTGATAGC-----TATTTCGGTC-GTCTGTG 31
VBRV      TGTCTCTGCTGGTTG-TAGCGGCGGAGCAGGTTCCCTCAGGTTCACTCGGTCACTCTGTG 59
          **   **  **  ****                               *  *****  *****

VBFW      CCTGGGCTTGGCGT-CAGTGTGTGCCGGTCCCAATACTGCGGCCCTCTGTCTCC-CCC 89
VBRV      CG-GGGCCTTGGAGTACCGTGTGTTCCAGTCCCAATACTCCGGCCCCCTCTGTCTCCACCC 118
          *   *****  **  *  *****  **  *****  *****  *****  ***

VBFW      ACGGCGCCCGCGGCTCCATCC-TCGGACTCGCGGCGTCTGTCGAACCGCACGAATTGC 148
VBRV      ACGGCGCCCGCGGCTCCATCCCTCGGACTCGCGGCGTCTGTCGAACCGCAGGAAGTGC 178
          *****  *****  *****  *****  *****  *****  ***  ***

VBFW      GTGTCGTCCACGTACTCCACGGCGATGAAGCTGGGCTCCCCCGGGCCCGGGCCGGGA-A 207
VBRV      GTGTCGTCCACGTAGCCACGGCAATGAAGCGGGGCTCCCC-GCGGCC-GGGCCAGGACA 236
          *****  *****  *****  *****  *****  *****  ***  *

VBFW      CGGCGGTGCTGAAAATACCCTCATGGGAGTGGGGAGCCTGGGGGGCGTGCAGGGCTTGAG 267
VBRV      CGGCGGTGC--GAAATACTT-----AGC-----AGAGCG----- 263
          *****  *****                               ***   *  ***

VBFW      AA 269
VBRV      --
```

```
>VBSeqCons
TGTCTCTGCTGGTTGTAGCGGCGGAGCAGGTTCCCTCAGGTTGTCTGTGCTGGGCTTGG
GCGTCAGTGTGTGCCGGTCCCAATACTGCGGCCCTCTGTCTCCCCACGGCGCCCGCGG
CTCCATCCTCGGACTCGCGGCGTCTGTCGAACCGCACGAATTGCGTGTCTGTCACGTA
CTCCACGGCGATGAAGCTGGGCTCCCCCGGGCCCGGGCCGGGAACGGCGGTGCTGAAAA
TACCCTCAT
```

Not HLA-A result.

A2-2/2 23-11-2010

```
>VBFW
CCGCTAATCATGCGGTATTTCTTCCATGCCGTGTCCCGGCCCGCGCGGGGAGCCCCGC
TTCATCGCAGTGGGTACGTGGACGACACGAGTTCGTGCGGTTTCGACAGCGACGCGCG
AGTCCGAGGGGGAGCCGCGGGCGCGGTGGATAGAGCAGGAGGGGCGGAGTATTGGGAC
GGGAGACACGGAAGTGAAGGCCACTCACAGACTGACCGAGTGAACCTGCGGACCCCTG
CGCGGCTACTACAACCAGAGCGAGGG
```

```
>VBRV
TCTCAGCCACTCCTCGTCCCCAGGCTCCCACTCCATGAGGTATTTCTCCACATCCGTGTC
CCGGCCCCGGCCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGTT
CGTGCGGTTTCGACAGCGACGCCGCGAGCCCAAGGGGGGAGCCGCGGGCGCCGTGGATAGA
GCAGGAGGGGCCGGAGTATTGGGACGGGGAGACACGGAAGTCAAGGCCCACTCACAGAC
TCACCGAAGAACTGCGGACCTGCCCG
```

CLUSTAL 2.0.12 multiple sequence alignment

```
VBFW      -----CCGCTAATC-----ATGCGGTATTTCTTCCATGCCGTGTC 35
VBRV      TCTCAGCCACTCCTCGTCCCCAGGCTCCCACTCCATGAGGTATTTCTCCACATCCGTGTC 60
           **.*.*.*
           ***.***** *.:*****

VBFW      CCGGCCCCGGCCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGTT 95
VBRV      CCGGCCCCGGCCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGTT 120
           *****

VBFW      CGTGCGGTTTCGACAGCGACGCCGCGAGTCCGAGGGGGGAGCCGCGGGCGCCGTGGATAGA 155
VBRV      CGTGCGGTTTCGACAGCGACGCCGCGAGCCCAAGGGGGGAGCCGCGGGCGCCGTGGATAGA 180
           *****

VBFW      GCAGGAGGGGCCGGAGTATTGGGACGGGGAGACACGGAAGTGAAGGCCCACTCACAGAC 215
VBRV      GCAGGAGGGGCCGGAGTATTGGGACGGGGAGACACGGAAGTCAAGGCCCACTCACAGAC 240
           *****

VBFW      TGACCGAGTGAACCTGCGGACCCTGCGCGGCTACTACAACCAGAGCGAGGG 266
VBRV      TCACCGAAG--AACTGCGGACC-TGCCCG----- 266
           * ***** . *.***** *** **
```

```
>VBSecCons
ATGAGGTATTTCTCCACATCCGTGTCCCGGCCCGGCCGCGGGGAGCCCCGCTTCATCGC
AGTGGGCTACGTGGACGACACGCAGTTTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAA
GGGGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGGAGTATTGGGACGGGGAG
ACACGGAAGTCAAGGCCCACTCACAGACTACCGAAGAACTGCGGACCTGCCCG
```

```
>IMGTHLA:HLA05102 A*02:247 822 bp
Length = 822
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Plus Strand HSPs:

Score = 1040 (162.1 bits), Expect = 1.9e-43, P = 1.9e-43, Group = 1
Identities = 222/235 (94%), Positives = 222/235 (94%), Strand = Plus / Plus

```
Query:      1 ATGAGGTATTTCTCCACATCCGTGTCCCGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCA 60
             |||
Sbjct:     12 ATGAGGTATTTCTTCACATCCGTGTCCCGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCA 71

Query:     61 GTGGGCTACGTGGACGACACGCAGTTTCGTGCGGTTTCGACAGCGACGCCGCGAGCCCAAGG 120
             |||
Sbjct:     72 GTGGGCTACGTGGACGACACGCAGTTTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGG 131

Query:    121 GGGGAGCCCGGGCGCCGTGGATAGAGCAGGAGGGGCCGGAGTATTGGGACGGGGAGACA 180
             |||
Sbjct:    132 ATGGAGCCCGGGCGCCGTGGATAGAGCAGGAGGGTCCGGAGTATTGGGACGGGGAGACA 191

Query:    181 CGGAAAGTCAAGGCCCACTCACAGACTACCGA-AGAAC-TGCGGACC-TGCCCG 232
             |||
Sbjct:    192 CGGAAAGTGAAGGCCCACTCACAGACTGACCGAGAGAACCTGGGGACCCTGCGCG 246
```

```
>VBedit1
ATGAGGTATTTCTCCACATCCGTGTCCCGGCCCGGCCGCGG
GGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACGC
AGTTTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGACG
GAGCCCGGGGCGCCGTGGATAGAGCAGGAGGGGCCGGAGTA
TTGGGACGGGGAGACACGGAAGTCAAGGCCCACTCACAGA
CTCACCGAAGAACTGCGGACCTGCCCG
```

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>IMGTHLA:HLA01872 A*24:42 546 bp
Length = 546
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Score = 1075 (167.3 bits), Expect = 7.4e-45, P = 7.4e-45, Group = 1
Identities = 225/233 (96%), Positives = 225/233 (96%), Strand = Plus / Plus

A3-1/2 19-02-2011

>VBRV
TGGTTCTCACACCGTCCAGATGATGTTTGGCTGCGACGTGGGGTGGACGGGCGCTTCTCT
CCGCGGGTACCACAGTACGCCCTACGACGGCAAGGATTACATCGCCCTGAAGAGGACCT
CGCATTTGGACCGCGCGGACATGGCGGCTCAGATCACCAGCGAAGTGGGAGCGCGC
CATGTGGCGGAGCAGCAGAGAGCCTACCGGAGGGCACGGTGGGCCAGGGCCCCCA

```

VBFW      -----TGGCTGCAA-GTGGGGTCGGA-GGGCGCTTCCT  31
VBRV      TGGTTCTCACACCGTCCAGATGATGTTTGGCTGCGACGTGGGGTCGGACGGGCGCTTCCT  60
          ***** * *****
          *****

VBFW      CCGCGGGTACC-CCAGTACGCCTACGACGGCAAGGATTACATCGCCGTGAAAGAGGACCT  90
VBRV      CCGCGGGTACCACCACTACGCCTACGACGGCAAGGATTACATCGCCGTGAAAGAGGACCT  120
          *****
          *****

VBFW      GCGCTCTTGGACCGCGCGGACATGGCGGCTCAGATCACCAAGCGCAAGTGGGAGGCGGC  150
VBRV      GCGCTCTTGGACCGCGCGGACATGGCGGCTCAGATCACCAAGCGCAAGTGGGAGGCGGC  180
          *****
          *****

VBFW      CCATGTGGCGGAGCAGCGGAGAGCCTACCTGGAGGGCAGTGCCTGGAC--GGGCTCCGC  208
VBRV      CCATGTGGCGGAGCAGCAGAGAGCCTACC-GGAGGGCAGC--GTGGGCCAGGGCCCA-  235
          *****
          *****

VBFW      AGATACCTGGAGAACGGGAAG  229
VBRV      -----

```

```
>IMGTHLA:HLA03331 A*24:87 822 bp
      Length = 822
```

64

Score = 1227 (190.1 bits), Expect = 7.2e-52, P = 7.2e-52, Group = 1
Identities = 253/258 (98%), Positives = 253/258 (98%), Strand = Plus / Plus

```
Query:      2 GGTTCCTCACACCGTCCAGATGATGTTTGGCTGCAA-GTGGGGTCGGA-GGGCGCTTCCTC 59
            |||
Sbjct:    270 GGTTCCTCACACCTCCAGATGATGTTTGGCTGCGACGTGGGGTCGGACGGGCGCTTCCTC 329

Query:     60 CGCGGGTACC-CCAGTACGCCTACGACGGCAAGGATTACATCGCCCTGAAAGAGGACCTG 118
            |||
Sbjct:    330 CGCGGGTACCACCAGTACGCCTACGACGGCAAGGATTACATCGCCCTGAAAGAGGACCTG 389

Query:    119 CGCTCTTGGACCGCGGCGGACATGGCGGCTCAGATCACCAGCGCAAGTGGGAGGCGGCC 178
            |||
Sbjct:    390 CGCTCTTGGACCGCGGCGGACATGGCGGCTCAGATCACCAGCGCAAGTGGGAGGCGGCC 449

Query:    179 CATGTGGCGGAGCAGCGGAGAGCCTACCTGGAGGGCACGTGCGTGGACGGGCTCCGCAGA 238
            |||
Sbjct:    450 CATGTGGCGGAGCAGCGGAGAGCCTACCTGGAGGGCACGTGCGTGGACGGGCTCCGCAGA 509

Query:    239 TACCTGGAGAACGGGAAG 256
            |||
Sbjct:    510 TACCTGGAGAACGGGAAG 527
```

```
>VBSEdit1
TGGTTCTCACACCGTCCAGATGATGTTTGGCTGCAAGTGGGGTCGGAGGGCGCTT
CCTCCGCGGGTACCCAGTAGGCCCTACGACGGCAAGGATTACATCGCCCTGAAAG
AGGACCTGCGCTCTTGGACCGCGGCGGACATGGCAGCTCAGACCACCAAGCACAA
GTGGGAGGCGGCCATGTGGCGGAGCAGTAGAGAGCCTACCTGGAGGGCACGTGC
GTGGAGTGGCTCCGCAGATACCTGGAGAACGGGAAG
```

>IMGTHLA:HLA00015 A*02:10 1098 bp
Length = 1098

Plus Strand HSPs:

Score = 1209 (187.4 bits), Expect = 3.5e-51, P = 3.5e-51, Group = 1
Identities = 251/258 (97%), Positives = 251/258 (97%), Strand = Plus / Plus

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Query:      2 GGTTCCTCACACCGTCCAGATGATGTTTGGCTGCAA-GTGGGGTCGGA-GGGCGCTTCCTC 59
            |||
Sbjct:    343 GGTTCCTCACACCGTCCAGAGGATGTTTGGCTGCGACGTGGGGTCGGACGGGCGCTTCCTC 402

Query:     60 CGCGGGTACC-CCAGTAGGCCCTACGACGGCAAGGATTACATCGCCCTGAAAGAGGACCTG 118
            |||
Sbjct:    403 CGCGGGTACCACCAGTACGCCTACGACGGCAAGGATTACATCGCCCTGAAAGAGGACCTG 462

Query:    119 CGCTCTTGGACCGCGGCGGACATGGCAGCTCAGACCACCAAGCACAAAGTGGGAGGCGGCC 178
            |||
Sbjct:    463 CGCTCTTGGACCGCGGCGGACATGGCAGCTCAGACCACCAAGCACAAAGTGGGAGGCGGCC 522

Query:    179 CATGTGGCGGAGCAGTAGAGAGCCTACCTGGAGGGCACGTGCGTGGAGTGGCTCCGCAGA 238
            |||
Sbjct:    523 CATGTGGCGGAGCAGTTGAGAGCCTACCTGGAGGGCACGTGCGTGGAGTGGCTCCGCAGA 582

Query:    239 TACCTGGAGAACGGGAAG 256
            |||
Sbjct:    583 TACCTGGAGAACGGGAAG 600
```

A4-1/2H 29-03

```
>VBFW
TGCCGGTCAGTGTGATCTCCGACAGGCTAGAGCTCAGGGCCAGCACCTCAGGGTGGCTT
CATGGTCAGAGACAGCGTGGTGAGTCATATGCGTTTTGGGGGCGAA
```

```
>VBRV
TATCCCTGCAGGCCTGGTCTCCACGAGCTCCGTGTCCTGGGTCTGGTCTCCCATCCC
GCTGCCAGGTCAAGTGATCTCCGACAGGCTAGAGCTCAGGGCCAGCACCGCAGGGGGG
GCTTACACTGG
```

CLUSTAL 2.1 multiple sequence alignment

```

VBFW      ---TGCCGGTCAGTGTGATCTCCGCAGGGTAGAAGCTCAGGGCCCAGCAC-CTCAGGGTG  56
VBRV      TATCCCTGCAGGCCCTGGTCTCCACGAGCTCCGTGTCTGGGTCTGGTCTCCCATCCC  60
          ** *      * ** * * * * *      * * * * *      * * * *
VBFW      GCTTCATGGTCAGAG-----ACAGCGTGGTGAGTCATAT----GCGTTTTGGGGGCG  104
VBRV      GCTGCCAGGTCAAGTGTGATCTCCGCAGGGTAGAAGCTCAGGGCCCAGCACCGCAGGGGG  120
          *** *      * * * * *      *** ** *      ***      **      * * * *
VBFW      AA----- 106
VBRV      GCTTACACTGG 131

```

Score = 710 (112.6 bits), Expect = 1.2e-28, P = 1.2e-28, Group = 1
Identities = 150/157 (95%), Positives = 150/157 (95%), Strand = Plus / Plus

Query: 10 AAGACACATATGACCCACCACCCCATCTCTGACCATGAGGCCACTCTGCGGTGCTGGGCC 69
|||||
Sbjct: 628 AAGACACATATGACCCACCACCCCATCTCTGACCATGAGGCCACTCTGAGGTGCTGGGCC 687

Query: 70 CTGGGCTTCTACCTGCGGAGATC-CACTGACCTGGCAGCGGGATGGGGAGGACCAGACC 128
|||||
Sbjct: 688 CTGGGCTTCTACCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGACCAGACC 747

Query: 129 CAGGCACACGGGGTTTGTGGAAACCAGGCTTGCAGGG 165
|||||
Sbjct: 748 CAGG-ACACGGAGCTTGTGGAGACCAGGCCTGCAGGG 783

A4-3H/1 29-03

>VBFW
TGGACACCTCTGCTGGGGAGCCCGCCCGGCACACGGAGCTTGTGGACACCGGCCTGCAG
GGGATGGAACCTTCCAAAAGTGGGCGGCTGTGGTGGTGCCTTCTGGAAGGAGCAAAGATA
CACCTGCCATGTGCAGCATGAGGGTTTGCCCAAGCCCTCACCTGAGATGG

>VBRV
TTCTACCCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGACCAGACCAGGAC
ACGGAGCTCGTGGAGACCAGGCCTGCAGGGGATGGAACCTTCCAGAAGTGGGCGGCTGTG
GTGGTGCCTTCGGAGAGGAGCAGAGATACACCTGCCATGGCAGCAGAGGGGTGGCAA

CLUSTAL 2.1 multiple sequence alignment

```

VBFW      -----TGGACACC-----TCTGC-----TGGGGAG--CCCGGCCCGGCAC 33
VBRV      TTCTACCCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGACCAGACCAGGAC 60
           *** * *          ***          *
VBFW      ACGGAGCTTGTGGACACC-GGCCTGCAGGGGATGGAACCTTCCAAAAGTGGGCGGCTGTG 92
VBRV      ACGGAGCTCGTGGAGACCAGGCCTGCAGGGGATGGAACCTTCCAGAAGTGGGCGGCTGTG 120
           ***** *
VBFW      GTGGTGCCTTCTGGAAGGAGCAAAGATACACCTGCCATGTGCAGCATGAGGGTTTGCCCA 152
VBRV      GTGGTGCCTTTCGGAGAGGAGCAGAGATACACCTGCCATG-GCAGCA-GAGGGGTGGCAA 178
           ***** *
VBFW      AGCCCTCACCTGAGATGG 172
VBRV      -----

```

>VBSeqCons
TTCTACCCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGACCCGGCCCGGCACA
CGGAGCTTGTGGACACCGGCCTGCAGGGGATGGAACCTTCCAAAAGTGGGCGGCTGTGGT
GTGCCTTCTGGAAGGAGCAAAGATACACCTGCCATGTGCAGCATGAGGGTTTGCCCAAGCC
CCTCACCTGAGATGG

>IMGTHLA:HLA02509 A*02:97:01 822 bp
Length = 822

Plus Strand HSPs:

Score = 912 (142.9 bits), Expect = 1.2e-37, P = 1.2e-37, Group = 1
Identities = 192/201 (95%), Positives = 192/201 (95%), Strand = Plus / Plus

Query: 1 TTCTACCCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGACCCGGCCCGGCAC 60
|||||
Sbjct: 621 TTCTACCCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGACCAGACCAGGAC 680

Query: 61 ACGGAGCTTGTGGACACC-GGCCTGCAGGGGATGGAACCTTCCAAAAGTGGGCGGCTGTG 119
|||||
Sbjct: 681 ACGGAGCTCGTGGACACCAGGCCTGCAGGGGATGGAACCTTCCAGAAGTGGGCGGCTGTG 740

Query: 120 GTGGTGCCTTCTGGA-AGGAGCAAAGATACACCTGCCATGTGCAGCATGAGGGTTTGGCC 178
|||||
Sbjct: 741 GTGGTGCCTTCTGGACAGGAGCAGAGATACACCTGCCATGTGCAGCATGAGGGTTTGGCC 800

Query: 179 AAGCCCTCACCTGAGATGG 199

|||||
Sbjct: 801 AAGCCCCCTACCCTGAGATGG 821

HZ1 19-11-2010

A2-1/1

>HZFW
CTCGTCCAGGATTTCTACACCTCCGTGTCCCGGCCCGCGGGGAGCCCCGCTTC
ATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTCGACAGCGACCGCGGAGC
CAGAGGATGGAGCCGCGGGCGCGGTGGATAGAGCAGGAGGGCGCGAGTATTGGGACCAG
GAGACACGGAATGTGAAGGCCAGTCACAGACTGACCGAGTGGACCTGGGGACCCCTGCGC
GGCTACTACAACCAGAGCGAGGACA

>HZRV
TTTTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTATTCTACACCTCCGTGT
CCCCGGCCCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGT
TCGTGCGGTTCGACAGCGACGCCGCGAGCCAGAGATGGAGCCGCGGGCGCGGTGGATAG
AGCAGGAGGGCGCGAGTATTGGGACCAGGAGACACGGAATGGAAGGCCAGTCACAGAC
GACCGAGGGACCTG

CLUSTAL 2.1 multiple sequence alignment

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HZFW      -----CTCGTCC-----TGAGGTATTCTACACCTCCGTGT 31
HZRV      TTTTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTATTCTACACCTCCGTGT 60
          **** *
          *****

HZFW      CCGGCCCCGCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGT 91
HZRV      CCGGCCCCGCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGT 120
          *****

HZFW      TCGTGCGGTTCGACAGCGACGCCGCGAGCCAGAGATGGAGCCGCGGGCGCGGTGGATAG 151
HZRV      TCGTGCGGTTCGACAGCGACGCCGCGAGCCAGAGATGGAGCCGCGGGCGCGGTGGATAG 180
          *****

HZFW      AGCAGGAGGGCGCGAGTATTGGGACCAGGAGACACGGAATGTGAAGGCCAGTCACAGA 211
HZRV      AGCAGGAGGGCGCGAGTATTGGGACCAGGAGACACGGAATG-GAAGGCCAGTCACAGA 239
          *****

HZFW      CTGACCGAGTGGACCTGGGGACCCCTGCGCGGCTACTACAACCAGAGCGAGGACA 265
HZRV      C-GACCGAG-GGACCTG----- 254
          * *****

>HZSeqCons
TTTTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTATTCTACACCTCCGTGTTC
CCGCCCCGCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTC
GTGCGGTTCGACAGCGACGCCGCGAGCCAGAGATGGAGCCGCGGGCGCGGTGGATAGAGC
AGGAGGGCGCGAGTATTGGGACCAGGAGACACGGAATGTGAAGGCCAGTCACAGACTGA
CCGAGTGGACCTGGGGACCCCTGCGCGGCTACTACAACCAGAGCGAGGACA
```

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A02      GGGCCCCCTGGCGGGGGCGCAGGACCCGGGAAGCCGCGCCGGGAGGAGGGTCGGGCGGG 480
HZ      -----T 1

A02      TCTCAGCCACTCCTCGTCCCCAGGCTCTCACTCCATGAGGTATTCTTCACATCCGTGTC 540
HZ      TTTTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTATTCTACACCTCCGTGTC 61
          * *****

A02      CCGGCCCCGCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGTT 600
HZ      CCGGCCCCGCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTT 121
          *****

A02      CGTGCGGTTCGACAGCGACGCCGCGAGCCAGAGATGGAGCCGCGGGCGCGGTGGATAGA 660
HZ      CGTGCGGTTCGACAGCGACGCCGCGAGCCAGAGATGGAGCCGCGGGCGCGGTGGATAGA 181
          *****

A02      GCAGGAGGGTCCGGAGTATTGGGACGGGGAGACACGGAAGTGAAGGCCCACTCACAGAC 720
HZ      GCAGGAGGGCCCGAGTATTGGGACCAGGAGACACGGAATGTGAAGGCCCACTCACAGAC 241
          *****
```

A02 TCACCGAGTGGACCTGGGGACCCTGCGCGGCTACTACAACCAGAGCGAGGCCGGTGAGTG 780
 HZ TGACCGAGTGGACCTGGGGACCCTGCGCGGCTACTACAACCAGAGCGAGGACA----- 294
 * ***** *

A2-2/2

HZ1 A2-2 23-11

>HZFW
 CTTTCATACGAGGGGAATTTCTTCCATCCGTGTCCCGGCCCGCGGGGAGCCCCGCTT
 CATCGCAGTGGGTACGTGGACGACACGCAGTTCTGTGCGGTTTCGACAGCGACGCCGCGAG
 CCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGTCCGGAGTATTGGGACGG
 GGAGACACGGAAGTGAAGGCCACTCACAGACTCACCAGTGGACCTGGGGACCCTGCG
 CGGCTACTACAACCAGAGCGAGGGCA

>HZRV
 TCTCAGCCACTCCTCGTCCCCAGGCTCTCACTCCATGAGGTATTTCTTCACATCCGTGTC
 CCGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCAGTGGGTACGTGGACGACACGCAGTT
 CGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGA
 GCAGGAGGGTCCGGAGTATTGGGACGGGGAGACACGGAAGTGAAGGCCCACTCACAGAC
 TCACCGAGTGAACTTTGCCACCTCCCTCG

CLUSTAL 2.0.12 multiple sequence alignment

```

H2      -----CTTCATACGAGGGGAATTTCTTC-CATCCGTGTC 33
H3rev   TCTCAGCCACTCCTCGTCCCCAGGCTCTCACTCCATGAGGTATTTCTTCACATCCGTGTC 60
          ** .*.*.*:*.**:*****
H2      CCGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCAGTGGGTACGTGGACGACACGCAGTT 93
H3rev   CCGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCAGTGGGTACGTGGACGACACGCAGTT 120
          *****
H2      CGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGA 153
H3rev   CGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGA 180
          *****
H2      GCAGGAGGGTCCGGAGTATTGGGACGGGGAGACACGGAAGTGAAGGCCCACTCACAGAC 213
H3rev   GCAGGAGGGTCCGGAGTATTGGGACGGGGAGACACGGAAGTGAAGGCCCACTCACAGAC 240
          *****
H2      TCACCGAGTGGACCTGGGGACCCTGCGCGGCTACTACAACCAGAGCGAGGGCA 266
H3rev   TCACCGAGTGAACTT-----TGC-----CACCTCCCT---CG----- 269
          *****.*. *      ***      *:.*:.*:  **

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>HZSecCons
 ATTTCTTCACATCCGTGTCCCGGCCCGCGCGGGGAGCCCCGCTTCATCGCAGTGG
 GCTACGTGGACGACACGCAGTTCTGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGA
 TGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGTCCGGAGTATTGGGACGGGGAGA
 CACGGAAGTGAAGGCCCACTCACAGACTCACCAGTGAACCT

>IMGTHLA:HLA00005 A*02:01:01:01 1098 bp
 Length = 1098

Plus Strand HSPs:

Score = 1052 (163.9 bits), Expect = 4.0e-44, P = 4.0e-44, Group = 1
 Identities = 212/214 (99%), Positives = 212/214 (99%), Strand = Plus / Plus

```

Query:    1 ATTTCTTCACATCCGTGTCCCGGCCCGCGCGGGGAGCCCCGCTTCATCGCAGTGGGCT 60
          |||
Sbjct:   92 ATTTCTTCACATCCGTGTCCCGGCCCGCGCGGGGAGCCCCGCTTCATCGCAGTGGGCT 151

Query:    61 ACGTGGACGACACGCAGTTCTGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGC 120
          |||
Sbjct:   152 ACGTGGACGACACGCAGTTCTGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGC 211

Query:    121 CGCGGGCGCCGTGGATAGAGCAGGAGGGTCCGGAGTATTGGGACGGGGAGACACGGAAG 180
          |||
Sbjct:   212 CGCGGGCGCCGTGGATAGAGCAGGAGGGTCCGGAGTATTGGGACGGGGAGACACGGAAG 271

Query:    181 TGAAGGCCCACTCACAGACTCACCAGTGAACCT 214
          |||

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>K1SeqEdit1
GTCTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTATTCTACACCTCC
GTGTCCCGGGCCCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGA
CACGCAGTTCGTGCGGTTTCGACAGCGACGCCGCGAGCCGGAAGATGGAGCCGCGG
CGCCGTGGATAGAGCAGGAGAGGCCGAGTATTGGGAGCAGAAGACACGGAATATG
AAGGCCAGTCACAGACTGACCGAGTGAGCCTGCGGACCTGCTCCGCTACTACAA
CCAGACGAGGGGCA

>IMGTHLA:HLA01771 A*03:12 955 bp
    Length = 955

    Plus Strand HSPs:

    Score = 1227 (190.1 bits), Expect = 6.5e-52, P = 6.5e-52, Group = 1
    Identities = 257/270 (95%), Positives = 257/270 (95%), Strand = Plus / Plus

Query:    22 CAGGCTCCCACTCCATGAGGTATTCTACACCTCCGTGTCCCGGCCCGCGGGGAGC 81
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:    59 CGGGCTCCCACTCCATGAGGTATTCTACACCTCCGTGTCCCGGCCCGCGGGGAGC 118

Query:    82 CCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACG 141
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:    119 CCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACG 178

Query:    142 CCGCGAGCCGGAAGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGAGGCCGAGTATT 201
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:    179 CCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGAGTATT 238

Query:    202 GGGAGCAGAAGACACGGAATATGAAGGCCAGTCACAGACTGACCGAGTGAGCCTGCGGA 261
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:    239 GGGACCAGGAGACACGGAATGTGAAGGCCAGTCACAGACTGACCGAGTGAGCCTGCGGA 298

Query:    262 CCCTGCTCCGCTACTACAACCAGA-CGAGG 290
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:    299 CCCTGCGCGGCTACTACAACCAGAGCGAGG 328

A2-1/2 20-01-2011

>K1FW
CCACTAATGCCTGACTGTATTTCTACACCTCCGTGTCCCGGCCCGCGGGGAGCCCC
GCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACGCCG
CGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGAGTATTGGG
ACCGGAACACACGGAATGTGAAGGCCCACTACAGACTGACCGAGAGAGCCTGCGGATCG
CGCTCCGCTACTACAACCAGACGAGGGGCA

>K1RV
GTCTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTATTCTACACCTCCGTGT
CCCGGCCCGCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGT
TCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAG
AGCAGGAGGGGCCGAGTATTGGGACCGGAACACACGGAATGTGAAGGCCCACTACAG
ACTTACCGAGAGAGCAAACAACTACTCT

CLUSTAL 2.0.12 multiple sequence alignment

K1FW      -----CCACTAATG-----CCTGACT-----GTATTCTACACCTCCGTGT 36
K1RV      GTCTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTATTCTACACCTCCGTGT 60
          *****      **:*      *****

K1FW      CCCGGCCCGCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGT 96
K1RV      CCCGGCCCGCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGT 120
          *****

K1FW      TCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAG 156
K1RV      TCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAG 180
          *****

K1FW      AGCAGGAGGGGCCGAGTATTGGGACCGGAACACACGGAATGTGAAGGCCCA-CTCACAG 215
K1RV      AGCAGGAGGGGCCGAGTATTGGGACCGGAACACACGGAATGTGAAGGCCCACTCACAG 240
          *****

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K1FW ACTGACCGAGAGAGCCTGCGGATCGCGCTCCGCTACTACAACCAGACGAGGGGCA 270
 K1RV ACTTACCGAGAGAGCAAACTAAAC-AACTCT----- 270
 *** *****.:.*.:*..***

>K1SeqCons
 GTCTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTATTCTACACCTCCG
 TGTCCCGGGCCGCGCGGGGAGCCCCGCTTCATCGCCGTGGGTACGTGGACGACA
 CGCAGTTCTGTCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGC
 CGTGGATAGAGCAGGAGGGGCCGAGTATTGGGACCGGAACACACGGAATGTGAAGG
 CCCACTCACAGACTGACCGAGAGAGCCTGCGGATCGCGCTCCGCTACTACAACCAGA
 CGAGGGGCA

>IMGTHLA:HLA00071 A*25:01:01 1098 bp
 Length = 1098

Plus Strand HSPs:

Score = 1326 (205.0 bits), Expect = 1.8e-56, P = 1.8e-56, Group = 1
 Identities = 268/270 (99%), Positives = 268/270 (99%), Strand = Plus / Plus

Query: 22 CAGGCTCCCACTCCATGAGGTATTCTACACCTCCGTCGCCGCGCCGCGGGGAGC 81
 |
 Sbjct: 71 CGGGCTCCCACTCCATGAGGTATTCTACACCTCCGTCGCCGCGCCGCGGGGAGC 130
 Query: 82 CCCGCTTCATCGCCGTGGGCTACGTGGACGACACGAGTTCTGTCGGTTCGACAGCGACG 141
 |
 Sbjct: 131 CCCGCTTCATCGCCGTGGGCTACGTGGACGACACGAGTTCTGTCGGTTCGACAGCGACG 190
 Query: 142 CCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGCCGAGTATT 201
 |
 Sbjct: 191 CCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGCCGAGTATT 250
 Query: 202 GGGACCGGAACACACGGAATGTGAAGGCCCACTCACAGACTGACCGAGAGAGCCTGCGGA 261
 |
 Sbjct: 251 GGGACCGGAACACACGGAATGTGAAGGCCCACTCACAGACTGACCGAGAGAGCCTGCGGA 310
 Query: 262 TCGCGCTCCGCTACTACAACCAGA-CGAGG 290
 |
 Sbjct: 311 TCGCGCTCCGCTACTACAACCAGAGCGAGG 340

A3-1/2

>K1FW
 ATGGAATGCGAGTGGGGCCGGAGGGCGCTTCCTCCGCGGTACAGCAGGACGCTTACGAC
 GGCAGGATTACATCGCCCTGAACGAGGACCTGCGCTCTTGGACCGCGGACATGGCGG
 CTCAGATCACCCAGCGCAAGTGGGAGACGGCCATGAGGCGGAGCAGTGGAGAGCCTACC
 TGGAGGGCCGGTGCGTGAGTGCGTCCGCAGATACCTGGAGAACGGGAAG

>K1RV
 TGGTTCTCACACCGTCCAGAGGATGTATGGCTGCGACGTGGGGCCGGACGGGCGCTTCCT
 CCGCGGGTACCAGCAGGACGCTTACGACGCAAGGATTACATCGCCCTGAACGAGGACCT
 GCGCTCTTGGACCGCGGCGGACATGGCGGCTCAGATCACCCAGCGCAAGTGGGAGACGGC
 CCATGAGGCGGAGCAGTGGAGAGCCTAACCGGAGGTGCACGCTTGCTTCCAGCTCCGCA

CLUSTAL 2.1 multiple sequence alignment

K1FW -----ATG---GAATGCGA-GTGGGGCCGGA-GGGCGCTTCCT 33
 K1RV TGGTTCTCACACCGTCCAGAGGATGTATGGCTGCGACGTGGGGCCGGACGGGCGCTTCCT 60
 *** * *****
 K1FW CCGCGGGTAC-AGCAGGACGCTTACGACGGCA-GGATTACATCGCCCTGAACGAGGACCT 91
 K1RV CCGCGGGTACCAGCAGGACGCTTACGACGGCAAGGATTACATCGCCCTGAACGAGGACCT 120

 K1FW GCGCTCTTGGACCGCGGCGGACATGGCGGCTCAGATCACCCAGCGCAAGTGGGAGACGGC 151
 K1RV GCGCTCTTGGACCGCGGCGGACATGGCGGCTCAGATCACCCAGCGCAAGTGGGAGACGGC 180

 K1FW CCATGAGGCGGAGCAGTGGAGAGCCTACCTGGAGGGCCGGTGCGTGGAGTGGCTCCGAG 211
 K1RV CCATGAGGCGGAGCAGTGGAGAGCCTAACCGGAGG-----TGCACG--CTTGCTTCCAG 233

```

***** * *****
K1FW          ATACCTGGAGAACGGGAAG 230
K1RV          CT--CCGCA----- 240
              * * * *

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>K1SeqCons
TGGTTCTCACACCGTCCAGAGGATGTATGAATGCGAGTGGGGCCGAGGGCGCTTCCT
CCGCGGGTACAGCAGGACGCTTACGACGGCAGGATTACATCGCCCTGAACGAGGACCT
GCGCTCTTGGACCGCGGCGGACATGGCGGCTCAGATCACCAGCGCAAGTGGGAGACG
GCCCCATGAGGCGGAGCAGTGGAGAGCCTACCTGGAGGGCCGGTGCCTGGAGTGGCTCC
GCAGATACCTGGAGAACGGGAAG

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>IMGTHLA:HLA00071 A*25:01:01 1098 bp
Length = 1098

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Plus Strand HSPs:

```

Score = 1203 (186.5 bits), Expect = 6.5e-51, P = 6.5e-51, Group = 1
Identities = 251/258 (97%), Positives = 251/258 (97%), Strand = Plus / Plus

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```

Query:      2 GGTTCCTCACACCGTCCAGAGGATGTATGAATGCGA-GTGGGGCCGGA-GGGCGCTTCCTC 59
             |||||
Sbjct:     343 GGTTCCTCACACCATCCAGAGGATGTATGGCTGCGACGTGGGGCCGACGGGCGCTTCCTC 402
             |||||

Query:      60 CGCGGGTAC-AGCAGGACGCTTACGACGGCA-GGATTACATCGCCCTGAACGAGGACCTG 117
             |||||
Sbjct:     403 CGCGGGTACCAGCAGGACGCTTACGACGGCAAGGATTACATCGCCCTGAACGAGGACCTG 462
             |||||

Query:     118 CGCTCTTGGACCGCGGCGGACATGGCGGCTCAGATCACCAGCGCAAGTGGGAGACGGCC 177
             |||||
Sbjct:     463 CGCTCTTGGACCGCGGCGGACATGGCGGCTCAGATCACCAGCGCAAGTGGGAGACGGCC 522
             |||||

Query:     178 CATGAGGCGGAGCAGTGGAGAGCCTACCTGGAGGGCCGGTGCCTGGAGTGGCTCCGCAGA 237
             |||||
Sbjct:     523 CATGAGGCGGAGCAGTGGAGAGCCTACCTGGAGGGCCGGTGCCTGGAGTGGCTCCGCAGA 582
             |||||

Query:     238 TACCTGGAGAACGGGAAG 255
             |||||
Sbjct:     583 TACCTGGAGAACGGGAAG 60

```

A4-1/2H 29-03-2011

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>K1FW
GAACCCGCGGGCCGGCTGGCGCTGTAGCCCCCTGCAGTGTGGGCCCTGAGCTTCTACC
CTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGACCAGACCAGGACACGGAGC
TCGTGGAGACCAGGCCTGCAGGGGAT

```

```

>K1RV
TCGCCCCCAAACGCATATGACTCACCACGCTGTCTCTGACCATGAGGCCACCTGAGGT
GCTGGGCCCTGAGCTTCTACCTGCGGAGATCACACTGACCTGGCAGCGGGAGGGAGGA
CCAGACCCAGCCCCGAAACGCCT

```

CLUSTAL 2.1 multiple sequence alignment

```

K1FW          -----GAACCCG-----CGGGCCGGCT--GGCGCTGTAGCCCCCTGCAGT 39
K1RV          TCGCCCCCAAACGCATATGACTCACCACGCTGTCTCTGACCATGAGGCCACCTGAGGT 60
              *** *          * * * * * * * * * * * *

K1FW          GCTGGGCCCTGAGCTTCTACCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGG 99
K1RV          GCTGGGCCCTGAGCTTCTACCTGCGGAGATCACACTGACCTGGCAGCGGGA-GGGGAGG 119
              *****

K1FW          ACCAGACCCAGGACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGAT 146
K1RV          ACCAGACCCAGCCCCGAAAC-----GCCT----- 144
              ***** * * * *          *****

```

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>K1SeqCons
TCGCCCCCAAACGCATATGACTCACCACGCTGTCTCTGGCGCTGTAGCCCCCTGCAGT
GCTGGGCCCTGAGCTTCTACCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGG
ACCAGACCCAGGACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGAT

```

>IMGTHLA:HLA00071 A*25:01:01 1098 bp
Length = 1098

Plus Strand HSPs:

Score = 633 (101.0 bits), Expect = 3.8e-25, P = 3.8e-25, Group = 1
Identities = 135/144 (93%), Positives = 135/144 (93%), Strand = Plus / Plus

```
Query:      2 CGCCCCCAAACGCATATGACTCACCACGCTGTCTCTGACCATGAGGCCACCCTGAGGTG 61
             |||
Sbjct:     621 CGCCCCAAGACGCATATGACTCACCACGCTGTCTCTGACCATGAGGCCACCCTGAGGTG 680

Query:      62 CTGGGCCCTGAGCTTCTACCCGCGGAGATCACACTGACCTGGCAGCGGGA-GGGGAGGA 120
             |||
Sbjct:     681 CTGGGCCCTGAGCTTCTACCCGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGA 740

Query:     121 CCAGACCCAGCCCCGAAACGCCT 144
             |||
Sbjct:     741 CCAGACCCAGGACACGAGCTCGT 764
```

A4-2/2H 29-03-2011

>K1FW
GAGCCCCTGTCCCTCTGAAACAAGGAAGGCCCCCTGAGTGCTGGGCCCTGGGCTTCTACC
CTGCGGAGATCCACTGTATCTGGCAGCGGGATGGGGAGGACCAGCCACACACGGAGCT
CGTGGAGACCAGGCTGCAGGGGATA

>K1RV
CGTCCCCAAGAACACATATGACCCACCACCCCATCTCTGACCATGAGGCCACCCTGAGGT
GCTGGGCCCTGGGCTTCTACCCGCGGAGATCACACTAACCGGCAGCGGGAAGGGCAGGA
CCAGACCCCTCCGAAGACCTT

CLUSTAL 2.1 multiple sequence alignment

```
K1FW      -----GAGCCCCTGTCCC-TCTGAAACAAGGAAGGCCCCCTGAG-T 39
K1RV      CGTCCCCAAGAACACATATGACCCACCACCCCATCTCTGACCATGAGGCCACCCTGAGGT 60
             ** * * * * *

K1FW      GCTGGGCCCTGGGCTTCTACCCGCGGAGATCCACTGTATCTGGCAGCGGGATGGGGAGG 99
K1RV      GCTGGGCCCTGGGCTTCTACCCGCGGAGATC-ACACTAACCGGCAGCGGGAAGGGCAGG 119
             ***** ** * *

K1FW      ACCAGACCCACACGAGGCTCGTGGAGACCAGGCTGCAGGGGATA 146
K1RV      ACCAGACCCCTCTC-CTC-CGAAGACC-CTT----- 144
             ***** * * * * *
```

>K1SeqCons
CGTCCCCAAGAACACATATGACCCACCACCCCATCTCTGACCATGAGGCCACCCTGAGTG
CTGGGCCCTGGGCTTCTACCCGCGGAGATCCACTGTATCTGGCAGCGGGATGGGGAGGA
CCAGACCCACACGAGGCTCGTGGAGACCAGGCTGCAGGGGATA

Not HLA

>K1SeqEdit1
CGTCCCCAAGAACACATATGACCCACCACCCCATCTCTGACCATGAGGCCACCCTGAGG
TGCTGGGCCCTGGGCTTCTACCCGCGGAGATCACACTGACCTGGCAGCGGGATGGGGA
GGACCAGACCCAGGCACGGAGCTTGTGGAGACCAGGGCCGAGGGGATA

>IMGTHLA:HLA01718 A*03:01:01:02N 1163 bp
Length = 1163

Plus Strand HSPs:

Score = 763 (120.5 bits), Expect = 4.6e-31, P = 4.6e-31, Group = 1
Identities = 159/164 (96%), Positives = 159/164 (96%), Strand = Plus / Plus

```
Query:      4 CCCCCAAGAACACATATGACCCACCACCCCATCTCTGACCATGAGGCCACCCTGAGGTGCT 63
             |||
Sbjct:     624 CCCCCAAGA-CACATATGACCCACCACCCCATCTCTGACCATGAGGCCACCCTGAGGTGCT 682
```

Query: 64 GGGCCCTGGGCTTCTACCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGACC 123
 |||||
 Sbjct: 683 GGGCCCTGGGCTTCTACCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGACC 742

Query: 124 AGACCCAGG-CACGGAGCTTGTGGAGACCAGGGCCGAGGGGAT 166
 |||||
 Sbjct: 743 AGACCCAGGACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGAT 786

K2 30-05

A2-1/1

>K2FW

CCAGCCGACATAAATGCATGCGTTCTTGTTCATTACCGTGTGCCCCGCGCCGACGCGCGG
 GGCAGGGCAGCGTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGAC
 AGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGCGCCGTGGATAGAGCAGGAGGGGCGG
 GAGTATTGGGACCGGGACACACGGAATGTGAAAGCCCACTCACAGAACTGACCGAAGTGA
 ACCTGGGGACCTGGCGCGGGCTTCAACAAACAGGGCGAGGGACAC

>K2RV

TTCTCAGGCCCTGCACGCCCCAGGCTCCCACTCCATGAGGTTTTTCTTCACATCCGTGT
 CCGGCCCCGCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGT
 TTCGTGCGGTTTCACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATA
 GAGCAGGAGGGGCGGAGTATTGGACCGAGATACTACACCGCAATGTGTAAGGCCGCACT
 CGACAGCACGAGCGGAGGTGTAGCTCAGTGCAGTTGTTTTGTGGCGGT

CLUSTAL 2.1 multiple sequence alignment

K2FW	---CCAG--CCGACATA-----AATGCATGCG--TTCTTGTTCATTACCGTGT	41
K2RV	TTCTCAGGCCCTGCACGCCCCAGGCTCCCACTCCATGAGGTTTTTCTTCACATCCGTGT	60
	*** ** *	* * * * *
K2FW	GCCCGGCCCGGACGCGGGGGCAGGGCAGGCTTCATCGCCGTGGGCTACGTGGACGACAC	101
K2RV	-CCCGGCCCGGCCCGGGGAGC---CCCGCTTCATCGCCGTGGGCTACGTGGACGACAC	115
	***** ** *	* * * * *
K2FW	GCAGTT-CGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGT	160
K2RV	GCAGTTTCGTGCGGTTTCGACAGCGAGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGT	175

K2FW	GGATAGAGCAGGAGGGGCCGAGTATTGGGACCGGGACACA---CGGAATGTG-AAAGC	215
K2RV	GGATAGAGCAGGAGGGGCCGAGTATTGG-ACCGAGATACTACACCGCAATGTGTAAGGC	234
	***** ** *	** * * * *
K2FW	C-CACTC-ACAGAACTGACCGAAGTGAACCTGGGGACCTGGCGCGG--GCTTCAACAAAC	271
K2RV	CGCACTCGACAGCACGAGCGGAGGTGTA-----GCTCAGTGCAGTTGTTTGT-----	282
	* * * * *	* * * * *
K2FW	AGGGCGAGGGACAC	285
K2RV	--GGCGGT-----	288

>K2SeqCons

TTCTCAGGCCCTGCACGCCCCAGGCTCCCACTCCATGAGGTTTTTCTTCACATCCGT
 GTCCCGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACG
 CAGTTTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCG
 TGGATAGAGCAGGAGGGGCCGAGTATTGGACCGAGACACACGGAATGTGAAAGCCCA
 CTCACAGAACTGACCGAAGTGAACCTGGGGACCTGGCGCGGGCTTCAACAAACGCTTC
 AACAAAC

>IMGTHLA:HLA01718 A*03:01:01:02N 1163 bp
 Length = 1163

Plus Strand HSPs:

Score = 1133 (176.0 bits), Expect = 9.4e-48, P = 9.4e-48, Group = 1
 Identities = 247/265 (93%), Positives = 247/265 (93%), Strand = Plus / Plus

Query: 22 CAGGCTCCCACTCCATGAGGTTTTTCTTCACATCCGTGTCCCGGCCCGCGGGGAGC 81
 |
 Sbjct: 71 CGGGCTCCCACTCCATGAGGTTTTTCTTCACATCCGTGTCCCGGCCCGCGGGGAGC 130

Query: 82 CCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTTCGTGCGGTTTCGACAGCGAC 141
 |||||
 Sbjct: 131 CCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTT-CGTGCGGTTTCGACAGCGAC 189

Query: 142 GCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGGAGTAT 201
 |||||
 Sbjct: 190 GCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGGAGTAT 249

Query: 202 TGG-ACCGAGACACACGGAATGTGAAAGCCCACTCACAGAACTGACCGAAGTGAACCTGG 260
 |||||
 Sbjct: 250 TGGGACCAGGAGACACGGAATGTGAAGGCCAGTCACAGA-CTGACCGA-GTGGACCTGG 307

Query: 261 GGACCTGGCGCGGGCTTCAACAAAC 285
 |||||
 Sbjct: 308 GGACCTGCGCGG-CTACTACAACC 331

A2-1/2

>K2FW

CCCGACACAAGCATAACGAGCGACTTATTCACATCCGTGTCCCGCCCCGCGCGGGGA
 GCCCGCTTCATCGCCGTGGGCTACGTGGACGAACACGCAGTTTCGTGAGTTTGAAGCGAG
 CCGCGTGCAGAGAAAAACCGAAAGCGCCGTGGATAAGCAAGAAGGACCGAATATGGGA
 ACCAGAAAAACGGAAGTGAAAGCCAATCAAAAATGACCAATGAACCTGGGAACCTGGCGG
 T

>K2RV

TTAGGCATGTGCTCAGTCCATCATGAGGTATATCACAACCTCCGTGTCCCGCCCCGCGCGGG
 AGCCCGCATATCGCCGTGGGCTACGTGGACGACAGCAGTTTCGTGTCGACAGCGACGCGCG
 AGCAGAGATGAGCGCGCGCGGTGATAGAGCAGAGGGCGAGTATGACCAGAGACACGGAATG
 TGAAGGCCAGTCACAGACTGAGCGACGATACCGCTCCAGTCTAATACGTTGG

CLUSTAL 2.1 multiple sequence alignment

K2FW	CCCGACACAAGCATA---CAGCGAGCGACTTATTCACA--TCCGTGTCCCGCCCCGCGCGG	55
K2RV	TTAGGCATGTGCTCAGTCCATCATGAGGTATAT-CACAACCTCCGTGTCC--GCCCGCGCG	57
	* ** * * * * * * * * * * * * * * * *	
K2FW	CGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGAACACGCAGTTTCGTGAGTTTCG	115
K2RV	CGGGAG---CCCGCAT-ATCGCCGTGGGCTACGTGGACGA-CA-GCAGTTTCGT-CG--TCG	109
	**** * * * * * * * * * * * * * * * *	
K2FW	A-AGCGAGCCGCGTGCAGAGAAAAAACCGAAAGCGCCGTG-GATAAGCAAGAAGGACCG	173
K2RV	ACAGCGACGCGCGAGCAGAGA-----TGAGCGCGCGCGGTGATAGAGCAGAGGG--CG	160
	* * * * * * * * * * * * * * * * * * * *	
K2FW	AATATTGGGAACCGAAAAACGGAA-GTGAAGCC-AATCAAAA-TGACCAATGA-ACC	229
K2RV	AGTAT---GACCAGAGACACGGAATGTGAAGGCCAGTCACAGACTGAGCGACGATACC	216
	* * * * * * * * * * * * * * * * * * * *	
K2FW	TGGGAACCTGGCG-GT---	245
K2RV	GCTCCAGTCTAATACGTTGG	236
	* ** *	

Sequence not analyzed.

A3-1/2

>K2FW

CCGAGAAGTTCGGGCCCTACGGGTACGGCCGGGCGCTTCCTCCGCGGGTACCAGCAGGACG
 CTTACGACGGCAAGGATTACATCGCCCTGAACGAGGACCTGCGCTCTTGGACCGCGGCGGA
 CATGGCGGCTCAGATCACCAGCGCAAGTGGGAGGCGGCCCATGAGGCGGAGCAGTTGAGA
 GCCTACCTGGATGGCAGGTGCGTGGAGTGGGCTCCGCAGATACCTGGAAACGGGATGA

>K2RV

TGTTGTCTTTCCACGCTCAGAGATAAGTGTAGGGTTGAAACGTGGGCGGACCGGCGGCT
 CTCCTCCGCGGGTACCAGCAGGACGCTACGACGGCAAGGATACATCGCCTGAACGAGGAC
 TCGCTCTGGACCGCGGCGGACATGGCGGCTCAGATCACCCAGCGCAAGTGGGAGACGGCC
 CATGAGGCGGAGCAGTGGAGCAGCTCCCTGGTAGTGTCCGACACCGTCCGTATTGGACT
 G

CLUSTAL 2.1 multiple sequence alignment

```

K2FW      -----CCGAGA--AGT-TCGGGCCCTA---CGGGTCAGGCCCGGGCGC 36
K2RV      TGTGTGCTTTCCACGCTCAGAGATAAGTGTAGGGTTCGAACGTGGGCCGACCGGCGGC 60
              * **** * * * * * * * * * * * * * * * *

K2FW      T-TCCTCCGC-GGGTACCAGCAGGACGCTTACGACGGCAAGGATTACATCGCCCTGAACG 94
K2RV      TCCTCTCCGCCGGGTACCAGCAGGACGCT-ACGACGGCAAGGAT-ACATCGCC-TGAACG 117
              * **** * * * * * * * * * * * * * * * *

K2FW      AGGACCTGCGCTCTTGGACCGCGGCGGACATGGCGGCTCAGATCACCAAGCGCAAGTGGG 154
K2RV      AGGAC-TGCGCTCT-TGGACCGCGGCGGACATGGCGGCTCAGATCACCCAGCGCAAGTGGG 175
              *****

K2FW      AGGCGGCCCATGAGGCGGAGCAGTTGAG-AGCCTACCTGGATGGCAGGTGCGTGGAGTGG 213
K2RV      AGACGGCCCATGAGGCGGAGCAGTTGAGCAGCCTCCCC---TGGTAG-TGTCCGACACC 231
              ** ***** * * * * * * * * * * * * * * *

K2FW      GCTCCGAGATACCTGGAACGGGATGA 241
K2RV      --TCCGTA-----TTGGA--CTG----- 245
              **** *      **** * *

```

>K2SeqCons

```

TGTGTGCTTTCCACGCTCAGAGATAAGTGTAGGGTTCGAACGTGGGCCCTACGGGTACG
GCCGGGCGCTTCCTCCGCGGGTACCAGCAGGACGCTTACGACGGCAAGGATTACATCGCC
CTGAACGAGGACCTGCGCTCTTGGACCGCGGCGGACATGGCGGCTCAGATCACCAAGCGC
AAGTGGGAGGCGGCCCATGAGGCGGAGCAGTTGAGAGCCTACCTGGATGGCAGGTGCGTG
GAGTGGGCTCCGAGATACCTGGAACGGGATGA

```

>IMGTHLA:HLA05337 A*03:01:19 546 bp
Length = 546

Plus Strand HSPs:

Score = 1024 (159.7 bits), Expect = 1.7e-42, P = 1.7e-42, Group = 1
Identities = 214/221 (96%), Positives = 214/221 (96%), Strand = Plus / Plus

```

Query:    54 GGGTCAGGCCGGGCGCTTCCTCCGCGGTACCAGCAGGACGCTTACGACGGCAAGGATTA 113
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct:   309 GGGTC-GGACGGGCGCTTCCTCCGCGGTACCAGCAGGACGCTTACGACGGCAAGGATTA 367

Query:    114 CATCGCCCTGAACGAGGACCTGCGCTCTTGGACCGCGGCGGACATGGCGGCTCAGATCAC 173
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct:   368 CATCGCCCTGAACGAGGACCTGCGCTCTTGGACCGCGGCGGACATGGCGGCTCAGATCAC 427

Query:    174 CAAGCGCAAGTGGGAGGCGGCCCATGAGGCGGAGCAGTTGAGAGCCTACCTGGATGGCAG 233
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct:   428 CAAGCGCAAGTGGGAGGCGGCCCATGAGGCGGAGCAGTTGAGAGCCTACCTGGATGGCAG 487

Query:    234 GTGCGTGGAGTGGGCTCCGAGATACCTGGA-AACGGGATG 273
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct:   488 GTGCGTGGAGTGG-CTCCGAGATACCTGGAGAACGGGAAG 5

```

A3-2/2

>K2FW

```

CTTAGCATTACAGTCCCTGACACGGGTACGGATAGGGTCGCTTCCTCCGCGGTACCAG
CAGGGACGCTTACGACGGCAAGGATTACATCGCCCTGAACGAGGACCTGCGCTCTTGGA
CCGCGGCGGACATGGCGGCTCAGATCACCCAGCGCAAGTGGGAGACGGCCCATGAGGCG
GAGCAGTGGAGAGCCTACCTGGGAGGCCGTGCGTGGAGTGTCCGAGATCCTGGAGA
CCGGAAGA

```

>K2RV

```

CACCATCCAAGATGAAGTGATGGGCTGCGACGTGGGGTCGGGACGGGCGCTTCCTCCG
CCGGGTACCAGCAGGAACGCTTACGACGGCAAGGATTACATCGCCCTGAACGAGGACC
TGCGCTCTTGGACCGCGGCGGACATGGCGGTTAGATCACCCAGCGCAAGTGGGAGACG
GCCCATGAGGCGTAGCAGTGGAGAAACCTACCGGTACAGTCCAACCTAGCCTCACACAAG
AACGTG

```

CLUSTAL 2.1 multiple sequence alignment

K2RV TGTTCGCCCCAAAACGCATATGACTCACCACGCTGTCTCTGACCATGAGGCCACCCTG 60
 ** **

K2FW AGGTGCTGGGCCCTGAGCTTCTACCTGCGGAGATC-CACTGACCTGGCAGCGGGATGGG 66
 K2RV AGGTGCTGGGCCCTGAGCTTCTACCTGCGGAGATCACACTGACC-GGCAGCGGGA-GGG 118

K2FW GAGGACCAGACCCAGGACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGATA 118
 K2RV GAGTACCG--CCCTCGCTAAGCAG-TTATAG-----TTGC----- 150
 *** ** * * * * * ***

>K2SeqCons

TGTTCGCCCCAAAACGCATATGACTCACCACGCTGTCTCTGACCATGAGGCCACCCTG
 AGGTGCTGGGCCCTGAGCTTCTACCTGCGGAGATCCACTGACCTGGCAGCGGGATGGGG
 AGGACCAGACCCAGGACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGATA

>IMGTHLA:HLA00083 A*26:11N 1100 bp
 Length = 1100

Plus Strand HSPs:

Score = 806 (127.0 bits), Expect = 5.6e-33, P = 5.6e-33, Group = 1
 Identities = 164/166 (98%), Positives = 164/166 (98%), Strand = Plus / Plus

Query: 6 CGCCCCAAAACGCATATGACTCACCACGCTGTCTCTGACCATGAGGCCACCCTGAGGTG 65
 |||||
 Sbjct: 623 CGCCCCAAGACGCATATGACTCACCACGCTGTCTCTGACCATGAGGCCACCCTGAGGTG 682

Query: 66 CTGGGCCCTGAGCTTCTACCTGCGGAGATC-CACTGACCTGGCAGCGGGATGGGGAGGA 124
 |||||
 Sbjct: 683 CTGGGCCCTGAGCTTCTACCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGA 742

Query: 125 CCAGACCCAGGACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGAT 170
 |||||
 Sbjct: 743 CCAGACCCAGGACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGAT 78

A4-2/2H 29-03

>K2FW

GCACTGCAGGTGTGTGCGCGTGAGGTCCACCTGAGTGTGGGTCCCTGGGCTTCTACCC
 TCGCGAGATCACACTGACCTGGCAGCGGGATGGGGAGGACCAGACCCACGCACACGGGGC
 TCGGGGAGCCCAGGCCGGCAGGGAAT

>K2RV

TGCCGTTTCCCCAAACACATATTACCCACCACCCATTTTACCATTAGGCCACCCTTA
 GGTGGTGGGCCCTGGGGTTTACCTGCGGAGATCACAATTACCGCCACGGGGAAGGGC
 GGGACCAGCACTCCCTCCAGACCT

CLUSTAL 2.1 multiple sequence alignment

K2FW -GCA----CTGCAGGTGTGTGCG-----CGTGAGGTCCACCTG 34
 K2RV TGCCGTTTCCCCAAACACATATTACCCACCACCCATTTTACCATTAGGCCACCCTTA 60
 ** * ** *

K2FW AGTGCTGGGTCCCTGGGCTTCTACCTGCGGAGATCACACTGACCTGGCAGCGGGATGGG 94
 K2RV GGTGGTGGG-CCCTGGGGTTTACCTGCGGAGATCACAATTACCGGCCACGGGGAAGGG 119
 *** ** * * * * * * * * * *

K2FW GAGGACCAGACCCACGCACACGGGGCTCGGGGAGCCCAGGCCGGCAGGGAAT 146
 K2RV CGGGACCA-----GCACTC---CCC-----TCCAGACCT----- 146
 ***** ** * *

>K2SeqCons

TGCCGTTTCCCCAAACACATATTACCCACCACCCATTTTACCCTGAGGTCCACCTGA
 GTGCTGGGTCCCTGGGCTTCTACCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGA
 GGACCAGACCCACGCACACGGGGCTCGGGGAGCCCAGGCCGGCAGGGAAT

>IMGTHLA:HLA01718 A*03:01:01:02N 1163 bp
 Length = 1163

Plus Strand HSPs:

Score = 638 (101.8 bits), Expect = 2.0e-25, P = 2.0e-25, Group = 1
Identities = 148/166 (89%), Positives = 148/166 (89%), Strand = Plus / Plus

```
Query:      9  CCCCAC-ACACATATTACCCACACCCCATTTTACCGTGAGGTCCCACCTGAG-TGCT 66
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:     624 CCCCAGACACATATGACCCACACCCCATCTCTGACCATGAGGCCAC-CCTGAGGTGCT 682

Query:     67  GGGTCCCTGGGCTTCTACCCCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGAC 126
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:    683  GGG-CCCTGGGCTTCTACCCCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGAC 741

Query:    127  CAGACCCACGCACACGGGGCTCGGGGAGCCCAGGCCGCGCAGGGAAT 172
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:    742  CAGACCCAGG-ACACGAGCTCGTGGAGACCAGGCCTGCAGGGGAT 786
```

K3 30-05

A2-2/2

>K3FW

CAGCAAGTAAATAAACTACCACGCATGTACTTCCACATCCGTGTCTCGGCCCGGCCGCG
GGGAGCCCCGCTTTATCGCAGTGGGCTACGTGGACGACACGAGTTCGTGCGGTTTCGACA
CGCAGCCCGCAGTCAAAGAATGGAGCCGCGGGCGCCGTGGGTAGAGCAGGAGGGTCCGG
AGTATTGGGACGGGGAGACACGGAAGTGAAGGCCCACTCACAGACTCACCGAGTGGACC
TGGGGACACTGCGCGGCTACTACAACCAGACCGAGGGCA

>K3RV

TCTCAGCCACTCCTCGTCCCCAGGCTCTCACTCCATGAGGTATTTCTTCACATCCGTGTC
CCGGCCCCGCGCGGGGAGCCCCGCTTTCATCGCAGTGGGCTACGTGGACGACACGAGTT
CGTGCGGTTTCGACAGCGACGCCGCGAGCCAAAGGGGGAGCCGCGGGAGCCGTGGGTAGA
GCAGGAGGGGCCGGAGTATTGGGACGGGGAGACACGGAAGTGAAGGCCACGCGCACAG
ACGCACCGTAGGGAACCGACGACAGTATTGTAGGTTAGGGT

CLUSTAL 2.1 multiple sequence alignment

```
K3FW      ---CAGCAA-----GTAAATAAACTACCACGC----ATGTACTTC--CACATCCGTGTC 45
K3RV      TCTCAGCCACTCCTCGTCCCCAGGCTCTCACTCCATGAGGTATTTCTTCACATCCGTGTC 60
          **** *      ** * * * * * * * * * * * * * * * * * * * * * * * *

K3FW      CTCGGCCCCGCGCGGGGAGCCCCGCTTTATCGCAGTGGGCTACGTGGACGACACGAGT 105
K3RV      C-CGGCCCCGCGCGGGGAGCCCCGCTTTCATCGCAGTGGGCTACGTGGACGACACGAGT 119
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

K3FW      TCGTGCGGTTTCGACAGCGACGCCGCGAGTCAAAGAATGGAGCCGCGGGCGCCGTGGGTAG 165
K3RV      TCGTGCGGTTTCGACAGCGACGCCGCGAGCCAAAGGGGGAGCCGCGGGAGCCGTGGGTAG 179
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

K3FW      AGCAGGAGGTCGGAGTATTGGGACGGGGAGACACGGAAGTG-AAGGCCCA-CTCACA 223
K3RV      AGCAGGAGGGCCGGAGTATTGGGACGGGGAGACACGGAAGTGAAGGCCAGCGCACAC 239
          * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

K3FW      GACTCACCGAGTGGACCTGGGGACACTGCGCGGCTACTACAACCAGACCGAGGGCA 279
K3RV      GACGCACCG-----TAGGGAACCGACGACAGTTTGTA----GGTT-AGGGT- 281
          *** * * * *      * * * * * * * * * * * * * * * * * * * * * * * *
```

>K3SeqCons

TCTCAGCCACTCCTCGTCCCCAGGCTCTCACTCCATGAGGTATTTCTTCACATCCGTG
TCCTCGGCCCGCGCGGGGAGCCCCGCTTTATCGCAGTGGGCTACGTGGACGACACG
CAGTTTCGTGCGGTTTCGACAGCGACGCCGCGAGTCAAAGAATGGAGCCGCGGGCGCCGT
GGGTAGAGCAGGAGGTCGGAGTATTGGGACGGGGAGACACGGAAGTGAAGGCCCA
CTCAGACTCACCGAGTGGACCTGGGGACACTGCGCGGCTACTACAACCAGACCGAG
GGCA

>IMGTHLA:HLA00005 A*02:01:01:01 1098 bp
Length = 1098

Plus Strand HSPs:

Score = 1269 (196.5 bits), Expect = 7.2e-54, P = 7.2e-54, Group = 1
Identities = 263/273 (96%), Positives = 263/273 (96%), Strand = Plus / Plus


```

Query:      21  CAGGCTCCCACTCCATGAGGTATTTCTTCACATCCGTGTCCCGGCCCGGCCGCGGGGCGC  80
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:      71  CGGGCTCCCACTCCATGAGGTATTTCTTCACATCCGTGTCCCGGCCCGGCCGCGGGGAGC  130

Query:      81  CCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACG  140
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     131  CCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACG  190

Query:     141  CCGCGAGCCAGAAGGTGGAGCCGCGGGCGCCGTGGATAGGAGCAGGAGGGGCCGGAGTAT  200
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     191  CCGCGAGCCAGAAGATGGAGCCGCGGGCGCCGTGGATAG-AGCAGGAGGGGCCGGAGTAT  249

Query:     201  TGGGACCAGGAGACACGGAATATGAAGGCCCACTCACAGACTGACCGAGCGAACCTGGGG  260
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     250  TGGGACCAGGAGACACGGAATATGAAGGCCCACTCACAGACTGACCGAGCGAACCTGGGG  309

Query:     261  ACCCTGCGCGGCTACTACAACAGAGCGAGGGC  293
            | | | | | | | | | | | | | | | |
Sbjct:     310  ACCCTGCGCGGCTACTACAACAGAGCGAGGAC  342

```

>K3FW
TTGATTTTTATAGCTGATGGTCAGTTATTTCACATTCGTGTCCCGGCCCGGC
CGCGGGGAGCCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGTTCGT
GCGGTTTCGACAGCGACGCCCGAGTCCAAGGGGGGAGCCCGGGCGCCGTGGG
TAGAGCAGGAGGTCGCCGAGTATTGGGACGGGGAGACACGAAAGTGAAGCGC
CACTCACAGACTCACCGAGTGGACCTGGGGACACTGCGCGGCTACTACAACCA
GAGCGAGGACCCG

CLUSTAL 2.1 multiple sequence alignment

>K3SeqCons
TAGTCTCAGCCACTCCTCGTCCCCAGGCTCTCACTCCATGAGGTATTTCTTCA
CATCCGTFGTCCCGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCAGTGGGGCTAC
GTGGACGACAGCAGCATTCGTGCGGTTTCGACAGCGACGCCGCGAGTCCAAGGGG
GGAGCGCGCGGGCGCCGTGGGTAGACAGGAGGGTCCGGATATTGGGACGGGG

TCCTCCGCGGCTACCACCAGTACGCCTACTACGGCAGGATTACATCGCCCTGA
 ACGAGACCTGCGCTCTTGGACCGCGGCGGACATGGCAGCTCATATCACCAGC
 ACAGTGGGAGGCGGCCCATGTGGCGGAGCAGCTGAGAGTCTACCTGGAGGGCA
 CGTTGCGTGGGAGTGGCTCCGCAATACCTGGAGACCGGGAAGAC

>IMGTHLA:HLA00009 A*02:04 1098 bp
 Length = 1098

Plus Strand HSPs:

Score = 1078 (167.8 bits), Expect = 3.1e-45, P = 3.1e-45, Group = 1
 Identities = 242/260 (93%), Positives = 242/260 (93%), Strand = Plus / Plus

Query: 3 GGTTCTCACACCGTCCAGATGATGTA-GG-TGCGACG-GGGGTCTGGAC-GGCGCTTCCTC 58
 |||||
 Sbjct: 343 GGTTCTCACACCGTCCAGATGATGATGGCTGCGACGTGGGGTCTGGACTGGCGCTTCCTC 402
 Query: 59 CGCGGTACCACCAGTACGCCTACTACGGCA-GGATTACATCGCCCTGAACGAG-ACCTG 116
 |||||
 Sbjct: 403 CGCGGTACCACCAGTACGCCTACGACGGCAAGGATTACATCGCCCTGAAAGAGGACCTG 462
 Query: 117 CGCTCTTGGACCGCGGCGGACATGGCAGCTCATATCACCAGCACA-GTGGGAGGCGGCC 175
 |||||
 Sbjct: 463 CGCTCTTGGACCGCGGCGGACATGGCAGCTCAGACCACCAAGCACAAGTGGGAGGCGGCC 522
 Query: 176 CATGTGGCGGAGCAGCTGAGAGTCTACCTGGAGGGCACGTTGCGTGGGAGTGGCTCCGCA 235
 |||||
 Sbjct: 523 CATGTGGCGGAGCAGTTGAGAGCTACCTGGAGGGCACGT-GCGTGG-AGTGGCTCCGCA 580
 Query: 236 -ATACCTGGAGACCGGGAAG 254
 |||||
 Sbjct: 581 GATACCTGGAGAACGGGAAG 600

A3-2/2

>K3FW

CAGGAGTACGGGTGTATCATGGGCCATGTCACTGCGACGACATGGCCTAC
 ACGCGGGTACACGGCAGGACGCTACGACGGCAAGGATTACATCGCCCTG
 AACGAGGACCTGCGCTCTTGGACCGCGGCGGACATGGCAGCTCAGATCAC
 CAAGCGCAAGTGGGAGGCGGTCCATGCGGCGGAGCAGCGGAGAGTCTACC
 TGGAGGGCCGGTGCCTGGACGGGCTCCGCAGATACCTGGAGACCGGGAAG
 A

>K3RV

TTCTTTTTTTTCCCCCGAACAAAAAAGAGTGCAGTTCCCAAAAAA
 GGGGGGTTTTTCCCCCCCCCAAAAAAAGTTAAAGGGGGCGAAGGGGCTT
 TCCCCGGGGACGCGGAAGCAAGCAGATAAACGCCGAAAAGACTGGCTCG
 AAGGGCGAAGCGCAGTCAATCACAGCGCAAGTAGAAAGGCCAGCGCCTAG
 ACCAGTATGTCCCTATGCCGGATGTGAAGGTGGTCTCAACAACCTCCCC
 T

CLUSTAL 2.1 multiple sequence alignment

```

K3FW      -----CAGGAGTACGGGTGTATCAT-----GGGCCA 26
K3RV      TTCTTTTTTTTCCCCCGAACAAAAAAGAGTGCAGT-TCCCAAAAAAGGGGGTTT 59
              ** *** * ** * **      ***

K3FW      TGCTACTGCGACGACATGGCCTACACGGGGTACACGGC-----AGGACGCCTACGA 78
K3RV      TCCCCCCCCCAAAAAAAGTTAAAGGGGGCGAAGGGGCTTCCCCGGGGACGC----GG 115
              * * * * * * *      * * * * *      * * * * *      *

K3FW      CGGCAAGGATTACATCGCCCTGAACGAGGACCTGCGCTCTTGGACCGGGCGGACATGGC 138
K3RV      AAGCAAAGCAGATAA-ACGCCGAA--AAGACTGGC----TCGAA---GGGCGAAC--GGC 163
              **** *  * *  * * * *  * * * *  * * *  * * * *  * * *

K3FW      AGCTCAGATCACCAAGCGCAAGTGGGAGGCGGTCCATGCGGCGGAGCAGCGGAGAGTCTA 198
K3RV      AG-TCA-ATCAC--AGCGCAAGTAGAAA--GGCCAGCGCC-TAGACCAGT---ATGTCC- 212
              ** *** ***** ***** * *  ** *  **      ** ***      ***

K3FW      CCTGGAGGGCCGGTGCCTGGACGGGCTCCGCAGATACCTGGAGACCGGGAAGA 251
K3RV      CCT--ATGCCGGATGTGAAGGTGGTCTCAACAACCTCCC-----CT----- 251
              *** * * * * * * *  * * * *  * *  * *      *

```

Sequence cons not Analyzed. Only FW.

>IMGTHLA:HLA02537 A*01:20 1098 bp
Length = 1098

Plus Strand HSPs:

Score = 981 (153.2 bits), Expect = 7.3e-41, P = 7.3e-41, Group = 1
Identities = 221/243 (90%), Positives = 221/243 (90%), Strand = Plus / Plus

```
Query:    10 GGGTGTATCA-TGGGCCATGTCACTGCGACGA-CATGGCCTACACGCGGGTACACGGCAG 67
           || |||||  || | |||  || |||||  || || ||||| |||||
Sbjct:   362 GGATGTATGGCTGCGACGTGGGGCCG-GACGGGCGCTTCCT-C-CGCGGGTAC-CGGCAG 417

Query:    68 GACGCCTACGACGGCAAGGATTACATCGCCCTGAACGAGGACCTGCGCTCTTGGACCGCG 127
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:   418 GACGCCTACGACGGCAAGGATTACATCGCCCTGAACGAGGACCTGCGCTCTTGGACCGCG 477

Query:   128 GCGGACATGGCAGCTCAGATCACCAAGCGCAAGTGGGAGGCGGTCCATGCGGCGGAGCAG 187
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:   478 GCGGACATGGCAGCTCAGATCACCAAGCGCAAGTGGGAGGCGGTCCATGCGGCGGAGCAG 537

Query:   188 CGGAGAGTCTACCTGGAGGGCCGGTGCCTGGACGGGCTCCGCAGATACCTGGAGACCGGG 247
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:   538 CGGAGAGTCTACCTGGAGGGCCGGTGCCTGGACGGGCTCCGCAGATACCTGGAGAACGGG 597

Query:   248 AAG 250
           |||
Sbjct:   598 AAG 600
```

A4-1/2H 29-03

>K3FW

CCGCACTGCACCTGCTGGCGTGTACTCCCCCTGAGTGCTGGGCCCTGAGCTTCTACCCCTG
CGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGACCAGACCCAGGACACGGAGCTCG
TGGAGACCAGGCCTGCAGGGGATA

>K3RV

CTCGCCCCCAAACGCATATGACTCACCACGCTGTCTCTGACCATGAAGCCACCCTGAGG
TGCTGGGCCCTGAGCTTCTACCCCTGCGGAGATCGACACGACCGGCAGCGGGAGGGGGGA
ACGAGACCTAAAATGAAATTGT

CLUSTAL 2.1 multiple sequence alignment

```
K3FW      -----CCGCACTGCACCTG-----CTGGC-GTGTACTCCCCCTGAG- 35
K3RV      CTCGCCCCCAAACGCATATGACTCACCACGCTGTCTCTGACCATGAAGCCACCCTGAGG 60
           ** * *** **                *** * * * * *

K3FW      TGCTGGGCCCTGAGCTTCTACCCCTGCGGAGATC-ACACTGACCTGGCAGCGGGATGGGGA 94
K3RV      TGCTGGGCCCTGAGCTTCTACCCCTGCGGAGATCGACAC-GACC-GGCAGCGGGAGGGGGG 118
           ***** *****

K3FW      GGACCAGACCCAGGACACGGAGCTCGTGAGACCAGGCCTGCAGGGGATA 144
K3RV      GAACGAGACCTAAAAT--GAAATTGT----- 144
           * ** ***** * * * * *
```

>K3SeqCons

CTCGCCCCCAAACGCATATGACTCACCACGCTGTCTCTGACCATGAAGCCACCCTGAGT
GCTGGGCCCTGAGCTTCTACCCCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGG
ACCAGACCCAGGACACGGAGCTCGTGAGACCAGGCCTGCAGGGGATA

>IMGTHLA:HLA00005 A*02:01:01:01 1098 bp
Length = 1098

Plus Strand HSPs:

Score = 815 (128.3 bits), Expect = 2.2e-33, P = 2.2e-33, Group = 1
Identities = 165/166 (99%), Positives = 165/166 (99%), Strand = Plus / Plus

```
Query:    3 CGCCCCCAAACGCATATGACTCACCACGCTGTCTCTGACCATGAAGCCACCCTGAG-TG 61
```

```

Sbjct: 621 |||||CGCCCCAAAACGCATATGACTCACCACGCTGTCTCTGACCATGAAGCCACCCTGAGGTG 680
Query: 62 CTGGGCCCTGAGCTTCTACCCGCGGAGATCACAACCTGGCAGCGGGATGGGGAGGA 121
Sbjct: 681 |||||CTGGGCCCTGAGCTTCTACCCGCGGAGATCACAACCTGGCAGCGGGATGGGGAGGA 740
Query: 122 CCAGACCCAGGACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGAT 167
Sbjct: 741 |||||CCAGACCCAGGACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGAT 786

```

A4-2/2H 29-03

```

>K3FW
AGTGCTGGGCCCTGGGCTTCTACCCGCGGAATCACAACCTGGCAGCGGGATGGGGA
GGACCAGACCCACGCACCGGGCTTGGGGAAACCCAGGCTGGAGGGGGT

```

```

>K3RV
CCCCCCCCCAAAAAAATATAACCCACCACCCATTTTTTAACATTAAGGCCACCTTAAGG
TGTTGGGCCCTGGGTTTTTACCTTGGGAAGATCACATTAACGGGAAGCGGAAGGGCAGG
ACCCAAAACCCCTCACAAAACCCG

```

CLUSTAL 2.1 multiple sequence alignment

```

K3FW      -----AG 2
K3RV      CCCCCCAAAAAAATATAACCCACCACCCATTTTTTAACATTAAGGCCACCTTAAGG 60
          *

K3FW      TGCTGGGCCCTGGGCTTCTACCCGCGGA-ATCACAACCTGGCAGCGGGATGGGGAG 61
K3RV      TGTTGGGCCCTGGGTTTTTACCTTGGGAAGATCACATTAACG-GGAAGCGGAAGGGCAG 119
          ** ***** ** * * * * * * * * * * * * * * * * * * * *

K3FW      GACC--AGACCCACGCACCGGGCTTGGGGAAACCCAGGCTGGAGGGGGT 108
K3RV      GACCAAAACCCCT-----CTCACAACCAACCCG----- 147
          **** * * * * * * * * * * * * * * * *

```

Sequence could not be analyzed.

K4 30-05

A2-1/1

```

>K4FW
TACACACCATTTCTGCGTTTACAGCGACGCCGAGCGAAGGTGGAGCCCCGGCGCCTGGT
AGACAGGAGGGGCCGAGTATTGGACCAAAAACACGAATGTGAAGCCCATCACAGACTGA
CCAGTGGACCTGGGACCTCGCGCTACTACAACCAAGCGAGGACA

```

```

>K4RV
TTCTCAGACATGCTCGCCCCAGGCTCCACCCATGAGGTATTTTTTACATCGTGTCCGGCC
GGCCGGGGGAGCCAGTTATCGCGTGGGCTACGTGCACGACACGAGTTGGTGGGTGGAA
GGACGCGGAGTCAGAGGATGGAGACGGGGCGCCGTGGATAGAGAGGAGGGCGGACTATT
GGAGA

```

CLUSTAL 2.1 multiple sequence alignment

```

K4FW      TACACAC-CATTCTGCGTTTACAGCGACGCCGAGCGAAGGTGGAGCCCCGG--GCGCCT 57
K4RV      TTCTCAGACATGCT-CGCCCCAGGCTCCACCCATG---AGGTATTTTTTACATCGTGTCC 56
          * * * * * * * * * * * * * * * * * * * *

K4FW      GGTAGACAGGAGGGGCCGAGTAT---TGGACCAAAAACACGAATGTGAAGCCCATCA- 112
K4RV      GGCCGGCCGGGGGAGCCAGT-TATCGCGTGGGCTACGTGCACGA-CACGCAGTTGGTGGG 114
          ** * * * * * * * * * * * * * * * * * * *

K4FW      -CAGACTGAC-----CAGTGGACCTGGGACCCTCGCGCTAC---TACAACCAAGCGA- 160
K4RV      TTGGAAGGACGCGGAGTCAGAGGA--TGGAGACGGGGCGCCGTGGATAGAGAGGAGGGGC 172
          ** *** * * * * * * * * * * * * * * *

K4FW      GGACA----- 165

```

K4RV GGACTATTGGAGA 185

Sequence not analyzed.

A2-2/2

>K4FW
GCAGTATTTGTCCCATCCGTGTCTGGCCCGGCCGCGGGGAGCCCCCTTCATCGCAGT
GGGCTACGTGGACGACACGCGAGTCGTGCGTTACAGCGACGCCGCGAGTGCAAGAAGG
GAGCCCGGGAGCCTGGTGGGGGGGGGGGGGGGGTATTGGACCGGGAACACAGAAA
TACAAGGCCCACTCACAGACTACCGAGTGAACCTGCGGAAACTGCGCGGCTACTACA
ACGA

>K4RV
TTCTCAGCCACTCCTCGTCCCCAGGCTCCCACTCCATGAGGTATTTCTCCACATCCGT
GTCCTGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACG
CAGTTCGTGCGGTTTCGACAGCGACGCCGCGAGCCCAAGAGGGGAGCCGCGGGAGCCGT
GGGTGGAGCAGGAGGGCCGAGTATTGGGACCGGGAGACACAGAAGACAAGCGCCAG
GCACAGGCTCACCAGGAACCGCGGAACCTGT

CLUSTAL 2.1 multiple sequence alignment

```
K4FW      -----GCAGTATTTGTCC-CATCCGTGT 22
K4RV      TTCTCAGCCACTCCTCGTCCCCAGGCTCCCACTCCATGAGGTATTTCTCCACATCCGTGT 60
              *  *****  ***  *****

K4FW      CCTGGCCCGGCCGCGGGGAGCCCC-CTTCATCGCAGTGGGCTACGTGGACGACACGCGAGT 81
K4RV      CCTGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCGAGT 120
              *****

K4FW      -CGTGCG-TTC-ACAGCGACGCCGCGAGTGCAAGAAGGGAGCC-CGGGAGCCT--GGTGG 135
K4RV      TCGTGCGGTTTCGACAGCGACGCCGCGAGCCCAAGAGGGGAGCCGCGGGAGCCGTGGGTGG 180
              *****  ***  *****  *****  *****

K4FW      GGGGGGGGGGGGGGGGTATTGG-ACCGGGA-ACACAGAAATACAAGGCCCACTCACAGA 193
K4RV      AGCAGGAGGGGCCGAGTATTGGGACCGGGAGACACAGAAG-ACAAGCGCCAGGCACAGG 239
              *  **  ****  *  *****  *****  *****  *****  ***  *****

K4FW      CTCACCGAGTGAACCTGCGGAAACTGCGCGGCTACTACAACGA 236
K4RV      CTCACCGAG-GAACC-GCGGAACCTGT----- 264
              *****  *****  *****  ***
```

>K4SeqCons
TTCTCAGCCACTCCTCGTCCCCAGGCTCCCACTCCATGAGGTATTTCTCCACATCC
GTGTCCTGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGA
CACGCGAGTTCGTGCGGTTTCGACAGCGACGCCGCGAGCCCAAGAGGGGAGCCGCGGG
AGCCGTGGGTGGAGCAGGAGGGGCCGAGTATTGGGACCGGGAGACACAGAAGACA
AGCGCCAGGCACAGGCTCACCGAGGAACCGCGGAACCTGTGCGGCTACTACAACGA

Not HLA-A result.

A2-1/2

>K4FW
TCCGTGTCCGTGCCCCGCCGCGGGGGCCCCGCTTCATCGCCGTGGGGTACGTGGA
CACACGCGAGTCTGCGGTTCCACAGCGACGCCGCGAGCGAAGGAGGGAGCCCCGGGC
GCCTGGGTAGAGCAGGAGGGGCCGGGTATTGGGACCGAGGACACGGAATGTGAA
GGCCCGAGTCACAGACTGACCGAGTGGACCTGGGGACCTGCGCGGCTACTACAAC
AGAGGGAGGGGCA

>K4RV
TTCTCAGCCACTCCTCGCCCCAGGCTCTCACCCATGAGGTATTTCTTCACATCGG
TGTCCTGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACCAC
ACGCGAGTTGGTGCGGTTGGACAGGGACGCCGAGCCAGAGGATGGAGCCCGGGGC
CCGTGGATAGAGCAGGAAAGGCCCCCACTTTGGGGCGGGACGGGGAATTAAAAAAC
ACTCAC

CLUSTAL 2.1 multiple sequence alignment

```

K4FW      -----TCCGTGTC 8
K4RV      TTCTCAGCCACTCCTCGCCCCAGGCTCTCACCCATGAGGTATTTCTTCACATCGGTGTC 60
          ** *****

K4FW      CGTGCCCGGCCGCGGGGGGCCCCGCTTCATCGCCGTGGGGTACGTGGAC-ACACGCAGTC 67
K4RV      CCGGCCCCGCGCGGGGAGCCCCGCTTCATCGCCGTGGGGTACGTGGACCACACGCAGTT 120
          * *****

K4FW      --TGCGGTTCCACAGCGACGCCGCGAGCGAAGGAGGGAGCCCCGGGCGCC-TGGGTAGAG 124
K4RV      GGTGCGGTTGGACAGGGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAG 180
          ***** **** ***** * **** ***** ***** *** *****

K4FW      CAGGAGGGGCCGGGTATTGGGACCAGGAGACACGGAATGTGAAGGCCCAGTCACAGACT 184
K4RV      CAGGAAAGGCCCCCACTTTGGGGC--GGGACGGGAATTAAAAAACAC--TCAC----- 230
          ***** **** ***** * * *** ***** ** * * *****

K4FW      GACCGAGTGGACCTGGGGACCCTGCGCGGCTACTACAACCAGAGGGAGGGGCA 237
K4RV      -----

```

>K4SeqCons

```

TTCTCAGCCACTCCTCGCCCCAGGCTCTCACCCATGAGGTATTTCTTCACATC
CGTGTCCGTGCCCGGCCGCGGGGGGCCCCGCTTCATCGCCGTGGGGTACGTGGA
CACACGCAGTCTGCGGTTCCACAGCGACGCCGCGAGCGAAGGAGGGAGCCCCGG
GCGCCTGGGTAGAGCAGGAGGGGCGGGGTATTGGGACCAGGAGACACGGAATG
TGAAGGCCCAGTCACAGACTGACCGAGTGGACCTGGGGACCCTGCGCGGCTACT
ACAACCAGAGGGAGGGGCA

```

>IMGTHLA:HLA01718 A*03:01:01:02N 1163 bp
Length = 1163

Plus Strand HSPs:

Score = 1143 (177.5 bits), Expect = 3.3e-48, P = 3.3e-48, Group = 1
Identities = 251/270 (92%), Positives = 251/270 (92%), Strand = Plus / Plus

```

Query:    22 CAGGCTCTCAC-CCATGAGGTATTTCTTCACATCCGTGTCCGTGCCCGGCCGCGGGGGGC 80
          | ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:    71 CGGGCTCCCACTCCATGAGGTATTTCTTCACATCCGTGTCCCGGCCCGGCCGCGGGGAGC 130

Query:    81 CCCGCTTCATCGCCGTGGGGTACGTGGAC-ACACGCAGT-C-TGCGGTTCCACAGCGACG 137
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:    131 CCCGCTTCATCGCCGTGGGGTACGTGGACGACACGCAGTTTCGTGCGGTTTCGACAGCGACG 190

Query:    138 CCGCGAGCGA-AGGAGGGAGCCCCGGGCGCC-TGGGTAGAGCAGGAGGGGCGGGGTATT 195
          ||||| ||| |||| ||||| ||||| ||| ||||| ||||| ||||| ||||| |||||
Sbjct:    191 CCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCGGAGTATT 250

Query:    196 GGGACCAGGAGACACGGAATGTGAAGGCCCAGTCACAGACTGACCGAGTGGACCTGGGGA 255
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:    251 GGGACCAGGAGACACGGAATGTGAAGGCCCAGTCACAGACTGACCGAGTGGACCTGGGGA 310

Query:    256 CCCTGCGCGGCTACTACAACCAGAGGGAGG 285
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:    311 CCCTGCGCGGCTACTACAACCAGAGCGAGG 340

```

A2-2/1

>K4FW

```

GATTTCTTCCATCCTGTCCGGGCGCGGGGAGCCCCCTTCATCGCAGTGG
GCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACGCCGAGCGAAAGA
ATGGAGCCCCGGGCGCCCTGGTGGAGCAGGAGGGGGCGGAGTATTGAGACCGGGA
AACACAGAAATTGAAGGGCCACTCACAGACTCACCGAGTGAACCTGGGGACACTG
CGCGGGTACTACAACCAGAGGGAGGGACA

```

>K4RV

```

GTCTCACCAACCCCTGGTCCCCAGGCTCTCACCCCATGAGGTATTTCTTCACATCC
GTGCCCTGGCCCGGCCGCGGGGAGCCCCGCTTATCGCAGTGGGCTACGTGGACGA
CACGCAGTTGGTGGGGTTGGACAGGACGCCGGGAGCCAAAGGATGGAGCCGGGGA
GCCGTGGCTACGACGAGGACTCCGGAGTATTTGGGACGGGGAGACACGGAAGGAAG
GCCCAGGCACAGA

```

CLUSTAL 2.1 multiple sequence alignment

```

K4FW      -----GATTCTTC-CATCC-TGTC 18
K4RV      GTCTCACCACCCCTGGTCCCCAGGCTCTCACCCTAGAGTATTTCTTCACATCCGTGCC 60
              *****  *****  ** *

K4FW      CGGCCCCGCGCCGCGGGAGCCCCCTTCATCGCAGTGGGCTACGTGGACGACACGCAGTTC 78
K4RV      CTGGCCCCGCGCCGCGGGAGCCCCGCTTATCGCAGTGGGCTACGTGGACGACACGCAGTTG 120
              * *****  * *****

K4FW      GTGCGGTTTCGACAGCGACGCCCG-AGCGAAAGAATGGAGCCCCGGCGCCCTGGTGGAGC 137
K4RV      GTGGGGTTGGACAG-GACGCCGGGAGCCAAAGGATGGAGCCG-GGGAGCCGTGGCTACGC 178
              ***  ****  *****  *  ***  ****  *****  ***  ***  ***  **

K4FW      AGGAGGGGGCGGAGTATTGAGACCGGAAACACAGAAATTGAAGGGCCACTCACAGACTC 197
K4RV      AGGAGCTC-CGGAGTATTGGGACGGGAGACACGAAAG-GAAGGCCAGGCACAGA--- 233
              *****  *****  ***  ****  ****  *****  *****  ***  *****

K4FW      ACCGAGTGAACCTGGGGACACTGCGCGGGTACTACAACCAGAGGGAGGGACA 249
K4RV      -----

```

>K4SeqCons

```

GTCTCACCACCCCTGGTCCCCAGGCTCTCACCCTAGAGTATTTCTTCACATC
CGTGCCCTGGCCCGCCGCGGGAGCCCCGCTTATCGCAGTGGGCTACGTGGAC
GACACGCAGTTGGTGGGTTGGACAGGACGCCGGGAGCCAAAGGATGGAGCCGG
GGAGCCGTGGCTACGCAGGAGCTCCGGAGTATTGGGACGGGGAGACACGGAAG
GAAGGCCAGGCACAGACTCACCGAGTGAACCTGGGGACACTGCGCGGGTACTA
CAACCAGAGGGAGGGACA

```

>IMGTHLA:HLA01034 A*02:34 822 bp
Length = 822

Plus Strand HSPs:

Score = 1092 (169.9 bits), Expect = 9.5e-46, P = 9.5e-46, Group = 1
Identities = 244/267 (91%), Positives = 244/267 (91%), Strand = Plus / Plus

```

Query:    24  GCTCTCACCCTAGAGTATTTCTTCACATCCGTGCCCTGGCCCCGCGCGGGAGCCCC 83
           |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct:    1   GCTCTCACTCCATGAGTATTTCTTCACATCCGTGTCCCGCCCGCCGCGGGAGCCCC 60

Query:    84  GCTT-ATCGCAGTGGGCTACGTGGACGACACGCAGTTGGTGGGTTGGACAG-GACGCCG 141
           |||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct:    61  GCTTCATCGCAGTGGGCTACGTGGACGACACGCAGTTCTGTCGGTTCGACAGCAGCCG 120

Query:    142 GGAGCCAAAGGATGGAGCCG-GGGAGCCGTGGCTAC-GCAGGAGC-TCCGGAGTATTGGG 198
           |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct:    121 CGAGCCAGAGGATGGAGCCGCGCGCGCTGGATAGAGCAGGAGGTCGGAGTATTGGG 180

Query:    199 ACGGGGAGACACGGAAG-GAAGGCCAGGCACAGACTCACCGAGTGAACCTGGGGACAC 257
           |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct:    181 ACGGGGAGACACGGAAGTGAAGGCCAGTCACAGACTCACCGAGTGGACTGGGGACCC 240

Query:    258 TGCGCGGGTACTACAACCAGAGGGAGG 284
           |||||  |||||  |||||  |||||
Sbjct:    241 TGCGCGGTACTACAACCAGAGCGAGG 267

```

A3-1/2

>K4FW

```

TTGTAGTTCGGGTGTACGGGTAGGAATGGCGCTTCCTCCGCGGTACCACCAG
TACGCCCTACGACGGCAGGATTACATCGCCCTGAAGAGGACCTGCGCTCTTGA
CCGCGGCGGACATGGCAGCTCAATCACCAGCACAAAGTGGGAGGCGGCCCATG
TGGCGGACATTGAGAGCTTACCTGGAGGCACGTGCGTGGAGTGGCTCCGCAAT
ACCTGGAAACGGGAAGAC

```

>K4RV

```

GTTCTCAACCGTCCAGAGGATGTATGGCTGCGACGTGGGGTTCGGACTGGCGCA
ACCTCCGCGGGTACCACCACTACGCTACGACGGCAAGGATTACATCGCCTCA
GAAAGAGGACCTGCGCTCTTGGACCGCGCGGACATGGCAGGCCAGACCACC
ACAGCACAAAGTGGGAGAGCGGCCCATAGTGGCGGAGCAGTTGAGAGCCTACCG

```

GTAGTGACACCTAGCGTCCACGAACA

CLUSTAL 2.1 multiple sequence alignment

```
K4FW      --TTGTA---G TTC---GGGTGTACGG-----GTAGGAATGGCGCTTCCTCCG 40
K4RV      GTTCTCAACCGTCCAGAGGATGTATGGCTGCGACGTGGGGTCGGACTGGCGCAACCTCCG 60
          *   *   ** *   **   ***   **           **   **   *****   *****

K4FW      CGGGTACCACCACTACGCCTACGACGGCA-GGATTACATCGCCCTG--AAGAGGACCTGC 97
K4RV      CGGGTACCACCACTACGCCTACGACGGCAAGGATTACATCGCCTCAGAAAGAGGACCTGC 120
          *****

K4FW      GCTCTTGGACCGCGCGGACATGGCAG-CTCA-ATCACCA-AGCACAAGTGGGAG-GCGG 153
K4RV      GCTCTTGGACCGCGCGGACATGGCAGGCCAGACCACCACAGCACAAGTGGGAGAGCGG 180
          ***** *   *   *   *   *   *   *   *   *   *   *   *   *

K4FW      CCCAT-GTGGCGGA-CA-TTGAGAGCCTACCTGGAGGCACGTGCGTGGAGTGGCTCCGCA 210
K4RV      CCCATAGTGGCGGAGCAGTTGAGAGCCTACC---GGTA-----GTGACACC-TA 225
          ***** **   *****   **   *           ***   *   *   *

K4FW      ATACCTGGAAACGGGAAGAC 230
K4RV      GCGTCC----ACACGAACA- 240
          *       **   ***   *
```

>K4SeqCons

GTTCTCAACCGTCCAGAGGATGTATGGCTGCGACGTGGGGTCGGACTGGCGC
AACCTCCGCGGTACCACCACTACGCCTACGACGGCAAGGATTACATCGCCT
CAGAAAGAGGACCTGCGCTCTTGGACCGCGCGGACATGGCAGGCCAGACC
ACCACAGCACAAGTGGGAGAGCGGCCCATAGTGGCGGAGCAGTTGAGAGCCT
ACCTGGAGGCACGTGCGTGGAGTGGCTCCGCAATACCTGGAAACGGGAAGAC

>IMGTHLA:HLA00005 A*02:01:01:01 1098 bp
Length = 1098

Plus Strand HSPs:

Score = 1139 (176.9 bits), Expect = 5.4e-48, P = 5.4e-48, Group = 1
Identities = 249/262 (95%), Positives = 249/262 (95%), Strand = Plus / Plus

```
Query:      1 GTTCTCA-ACCGTCCAGAGGATGTATGGCTGCGACGTGGGGTCGGACTGGCGCAACCTCC 59
             |||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||
Sbjct:     344 GTTCTCACACCGTCCAGAGGATGTATGGCTGCGACGTGGGGTCGGACTGGCGCTTCCTCC 403

Query:      60 GCGGGTACCACCACTACGCCTACGACGGCAAGGATTACATCGCCTCAGAAAGAGGACCTG 119
             |||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||
Sbjct:     404 GCGGGTACCACCACTACGCCTACGACGGCAAGGATTACATCGCC-CTGAAAGAGGACCTG 462

Query:     120 CGCTCTTGGACCGCGCGGACATGGCAGGCCAGACCACCACAGCACAAGTGGGAGAGCG 179
             |||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||
Sbjct:     463 CGCTCTTGGACCGCGCGGACATGGCAG-CTCAGACCACCA-AGCACAAGTGGGAG-GCG 519

Query:     180 GCCCATAGTGGCGGAGCAGTTGAGAGCCTACCTGGAGG-CACGTGCGTGGAGTGGCTCCG 238
             |||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||
Sbjct:     520 GCCCAT-GTGGCGGAGCAGTTGAGAGCCTACCTGGAGGGCACGTGCGTGGAGTGGCTCCG 578

Query:     239 CA-ATACCTGGA-AACGGGAAG 258
             ||  |||||||  |||||||
Sbjct:     579 CAGATACCTGGAGAACGGGAAG 600
```

A3-2/2

>K4FW

ATCAGGGGTAGAAGCTGTAGATGTAGAATGGGGTCGCATTGCTACCGCGG
GTACCGGCAGGACGCCTACGACGGCATGGATTAACATCGCCCTGAACGAG
GACCTGCGCTCTTGGACCGCGCGGACATGGCGGCTCTGATCACCAAGCG
CATGTGGGAGGCGGCCATGAGGCGGAGCAGTTGAGAGCCTACCTGGATG
GCACGTGCGTGGAGTGGCTCCGCAATACCTGGAAACGGGAAGA

>K4RV

GATGGATCTCCAACCATCCAGATAATGTATGGCTGCGACGTGGGGTCGGA
CGGGCGCAACCTCCGCGGTACCGGACGACGCCTACGACGGCAAGGATT

ACATCGCCAGAACGAGGACCTGCGCTCTTGGACCGCGGCGGACATGGCG
GCTCAGATCACCAAGCGCAAGTGGGAGGCGGCCCATGCAGCCCTGAGCCG
AGTTAAGGGCCCATCGCAGGCATGCCACTACCACCGCTACAACGA

CLUSTAL 2.1 multiple sequence alignment

```

K4FW      -----ATC---AGGGGT--AGAAGCTGTA--GATGTAGAATGGGGTCGCATTG-----C 42
K4RV      GATGGATCTCCAACCATCCAGATAATGTATGGCTGCGACGTGGGGTCGGACGGGCGCAAC 60
          ***      *      *      ***      ***      *      *      *      *      *
K4FW      TACCGCGGGTACCGGCAGGACGCCTACGACGGCATGGATTAAACATCGCCCTGAACGAGGA 102
K4RV      CTCGCGGGTACCGGCAGGACGCCTACGACGGCAAGGATTA-CATCGCCAGAACGAGGA 119
          *****
K4FW      CCTGCGCTCTTGGACCGCGCGGACATGGCGGCTCTGATCACCAAGCGCATGTGGGAGGC 162
K4RV      CCTGCGCTCTTGGACCGCGCGGACATGGCGGCTCAGATCACCAAGCGCAAGTGGGAGGC 179
          *****
K4FW      GGCCCATGAGGCG--GAGC--AGTTGAGAGCCTACCTGGATGGCACGTGCGTGGAGTGGC 218
K4RV      GGCCCATGCGCCCTGAGCCGAGTTAAGGGCCCATC--GCAGGCATGCC-----ACTACC 232
          ***** **      ***      ***      *      *      *      *      *
K4FW      TCCGCAATACCTGGAACGGAAGA 243
K4RV      ACCGC--TAC-----AACGA----- 245
          ****      ***      ****

```

>K4SeqCons
GATGGATCTCCAACCATCCAGATAATGTATGGCTGCGACGTGGGGTCGG
ACGGGCGCAACCTCCGCGGGTACCGGCAGGACGCCTACGACGGCAAGGA
TTACATCGCCAGAACGAGGACCTGCGCTCTTGGACCGCGCGGACATG
GCGGCTCAGATCACCAAGCGCAAGTGGGAGGCGGCCATGAGGCGGAGC
AGTTGAGAGCCTACCTGGATGGCACGTGCGTGGAGTGGCTCCGCAATAC
CTGGAACGGAAGA

>IMGTHLA:HLA01718 A*03:01:01:02N 1163 bp
Length = 1163

Plus Strand HSPs:

Score = 1206 (187.0 bits), Expect = 4.8e-51, P = 4.8e-51, Group = 1
Identities = 250/258 (96%), Positives = 250/258 (96%), Strand = Plus / Plus

```

Query:      4 GGATCTCCAACCATCCAGATAATGTATGGCTGCGACGTGGGGTCGGACGGGCGCAACCTC 63
            || |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     343 GGTCTCTACACCATCCAGATAATGTATGGCTGCGACGTGGGGTCGGACGGGCGCTTCCTC 402

Query:      64 CGCGGGTACCGGCAGGACGCCTACGACGGCAAGGATTACATCGCCAGAACGAGGACCTG 123
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     403 CGCGGGTACCGGCAGGACGCCTACGACGGCAAGGATTACATCGCCCTGAACGAGGACCTG 462

Query:     124 CGCTCTTGGACCGCGGCGGACATGGCGGCTCAGATCACCAAGCGCAAGTGGGAGGCGGCC 183
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     463 CGCTCTTGGACCGCGGCGGACATGGCGGCTCAGATCACCAAGCGCAAGTGGGAGGCGGCC 522

Query:     184 CATGAGGCGGAGCAGTTGAGAGCCTACCTGGATGGCACGTGCGTGGAGTGGCTCCGCA-A 242
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     523 CATGAGGCGGAGCAGTTGAGAGCCTACCTGGATGGCACGTGCGTGGAGTGGCTCCGAGA 582

Query:     243 TACCTGGA-AACGGAAG 259
            | | | | | | | | | | | | | |
Sbjct:     583 TACCTGGAGAACGGAAG 600

```

A4-1/2H 29-03

>K4FW
TGCTGGGCGCTGACTTCTACCTGCGGAATCACACTGACCTGGCAGCGGGATGGGGAGGA
CCAGACCCAGGACACGGAGCTCGTGGAGACGAGCCTGCAGGGGATA

>K4RV
TCGCCCCAAAACGCATATGACTCACCACGCTGTCTCTGACCATGAAGCCACCCTGAGGT
GCTGGGCGCTGAGCTTCTACCTGCGGAGATCACACTGACCGGCAGCGGGAGGGGAGGTA
CCAGCCCACGCAACCGAAATCAG

CLUSTAL 2.1 multiple sequence alignment

```

K4FW      -----T 1
K4RV      TCGCCCCAAAACGCATATGACTCACCACGCTGTCTCTGACCATGAAGCCACCCTGAGGT 60
                                         *

K4FW      GCTGGGCCCTGA-CTTCTACCCTGCGGA-ATCACACTGACCTGGCAGCGGGATGGGGAGG 59
K4RV      GCTGGGCCCTGAGCTTCTACCCTGCGGAGATCACACTGACC-GGCAGCGGGAGGGGAGGT 119
          *****
          *****
          *****

K4FW      ACCAGACCCAGGACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGATA 107
K4RV      ACCAGCCC-----ACGCAACC-----GAAATCAG----- 143
          *****
          *****
          *****

```

>K4SeqCons

```

TCGCCCCAAAACGCATATGACTCACCACGCTGTCTCTGACCATGAAGCCACCCTGAGGT
GCTGGGCCCTGAGCTTCTACCCTGCGGAATCACACTGACCTGGCAGCGGGATGGGGAGGAC
CAGACCCAGGACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGATA

```

>IMGTHLA:HLA00005 A*02:01:01:01 1098 bp
Length = 1098

Plus Strand HSPs:

Score = 800 (126.1 bits), Expect = 1.0e-32, P = 1.0e-32, Group = 1
Identities = 164/166 (98%), Positives = 164/166 (98%), Strand = Plus / Plus

```

Query:      2 CGCCCCAAAACGCATATGACTCACCACGCTGTCTCTGACCATGAAGCCACCCTGAGGTG 61
             |||
Sbjct:     621 CGCCCCAAAACGCATATGACTCACCACGCTGTCTCTGACCATGAAGCCACCCTGAGGTG 680

Query:      62 CTGGGCCCTGA-CTTCTACCCTGCGGA-ATCACACTGACCTGGCAGCGGGATGGGGAGGA 119
             |||
Sbjct:     681 CTGGGCCCTGAGCTTCTACCCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGA 740

Query:     120 CCAGACCCAGGACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGAT 165
             |||
Sbjct:     741 CCAGACCCAGGACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGAT 786

```

A4-2/2H 29-03

>K4FW

```

CAACCCCTGTAGCTGAGCCAGGGGTGCTGGGCCCTGGGCTTCTACCCTGCGGAGAT
CACACTGACCTGGCAGCGGGATGGGGAGGACCAGACCCAGGCACACGGAGCTCGTGGAGC
ACCAGGCCTGCAGGGGATA

```

>K4RV

```

CCCCCCCCAAGACACATATGACCCACCACCCATCTCTGACCATGAGGCCACCCTGAGGT
GCTGGGCCCTGGGCTTCTACCCTGCGGAGATCACACTGACCGG

```

CLUSTAL 2.1 multiple sequence alignment

```

K4FW      -----CAACCCCTGT-TAGC--TGAGCCCAG---GGGGT 29
K4RV      CCCCCCAAGACACATATGACCCACCACCCATCTCTGACCATGAGGCCACCCTGAGGT 60
                                         * * * * *
                                         * * * * *

K4FW      GCTGGGCCCTGGGCTTCTACCCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGG 89
K4RV      GCTGGGCCCTGGGCTTCTACCCTGCGGAGATCACACTGACC-GGC----- 104
          *****
          *****
          *****

K4FW      ACCAGACCCAGGCACACGGAGCTCGTGGAGCACCAGGCCTGCAGGGGATA 139
K4RV      -----

```

>K4SeqCons

```

CCCCCCCCAAGACACATATGACCCACCACCCATCTCTGACCATGAGGCCACCCTGGGGT
GCTGGGCCCTGGGCTTCTACCCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGG
ACCAGACCCAGGCACACGGAGCTCGTGGAGCACCAGGCCTGCAGGGGATA

```

>IMGTHLA:HLA01718 A*03:01:01:02N 1163 bp
Length = 1163

Plus Strand HSPs:

Score = 766 (121.0 bits), Expect = 3.4e-31, P = 3.4e-31, Group = 1
Identities = 158/161 (98%), Positives = 158/161 (98%), Strand = Plus / Plus

```
Query:      9 AAGACACATATGACCCACCCACCCATCTCTGACCATGAGGCCACCCCTGGGGTGCTGGGCC 68
|||||
Sbjct:    628 AAGACACATATGACCCACCCACCCATCTCTGACCATGAGGCCACCCCTGAGGTGCTGGGCC 687

Query:     69 CTGGGCTTCTACCCCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGACCAGACC 128
|||||
Sbjct:    688 CTGGGCTTCTACCCCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGACCAGACC 747

Query:    129 CAGGCACACGGAGCTCGTGGAGCACCAGGCCCTGCAGGGGAT 169
||||
Sbjct:    748 CAGG-ACACGGAGCTCGTGGAG-ACCAGGCCCTGCAGGGGAT 786
```

A4-3H/1 29-03

>K4FW

GTGGCACCCGGCCTGCAGGGGATGGAACCTTCCAAAAGTGGGCGGCTGTGGTGGTGCCTT
CTGGAGAGGAGCAGAGATACACCTGCCATGTGCAGCATGAGGGTCTGCCCAAGCCCTCA
CCCTGAGATGG

>K4RV

TTCTACCCCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGACCAGACCCAGGAC
ACGGAGCTCGTGGAGACCAGGCCCTGCAGGGGATGGAACCTTCCAGAAGTGGGCGGCTGTG
GTGGTGCCTTTCGGAGAGGAGCAGACTATACGGGATAAGCATGTGTGTTAAGAAGGGGAGA
AGG

CLUSTAL 2.1 multiple sequence alignment

```
K4FW      -----
K4RV      TTCTACCCCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGACCAGACCCAGGAC 60

K4FW      -----GTGGC-ACCCGGCCTGCAGGGGATGGAACCTTCCAAAAGTGGGCGGCTGTG 50
K4RV      ACGGAGCTCGTGGAGACCAGGCCCTGCAGGGGATGGAACCTTCCAGAAGTGGGCGGCTGTG 120
          ****  ***  *****

K4FW      GTGGTGCCTTCTGGAGAGGAGCAGAGATACACCTGCCATGTGCAGCATGAGGGTCTGCCC 110
K4RV      GTGGTGCCTTC-GGAGAGGAGCAGAC-TATACGGGATA-----AGCATGTGTGTT----- 168
          *****  *****  **  *  *  *  *****  *  **

K4FW      AAGCCCTCACCTGAGATGG 131
K4RV      AAG-----AAGGGGAGAAGG 183
          ***      *      ****  **
```

>K4SeqCons

TTCTACCCCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGACCAGACCCAGGA
CACGGAGCTCGTGGAGACCCGGCCTGCAGGGGATGGAACCTTCCAAAAGTGGGCGGCTG
TGGTGGTGCCTTCTGGAGAGGAGCAGAGATACACCTGCCATGTGCAGCATGAGGGTCTG
CCCAAGCCCTCACCTGAGATGG

>IMGTHLA:HLA01718 A*03:01:01:02N 1163 bp
Length = 1163

Plus Strand HSPs:

Score = 987 (154.1 bits), Expect = 3.5e-41, P = 3.5e-41, Group = 1
Identities = 199/201 (99%), Positives = 199/201 (99%), Strand = Plus / Plus

```
Query:      1 TTCTACCCCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGACCAGACCCAGGAC 60
|||||
Sbjct:    694 TTCTACCCCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGACCAGACCCAGGAC 753

Query:     61 ACGGAGCTCGTGGAGACCCGGCCTGCAGGGGATGGAACCTTCCAAAAGTGGGCGGCTGTG 120
|||||
Sbjct:    754 ACGGAGCTCGTGGAGACCAGGCCCTGCAGGGGATGGAACCTTCCAGAAGTGGGCGGCTGTG 813
```

Query: 121 GTGGTGCCTTCTGGAGAGGAGCAGAGATACACCTGCCATGTGCAGCATGAGGGTCTGCCC 180
 ||
 Sbjct: 814 GTGGTGCCTTCTGGAGAGGAGCAGAGATACACCTGCCATGTGCAGCATGAGGGTCTGCCC 873

Query: 181 AAGCCCCCTACCCTGAGATGG 201
 ||||||||||||||||
 Sbjct: 874 AAGCCCCCTACCCTGAGATGG 894

K5 26-04

A2-1/1

>K5FW
 CGACTGAGTGCCCTCTAGTATTTCTTCACATGCCGTGTCCTGGCCCCGGCCGCGGGGAGCCC
 CGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTCGACAGCGACGCC
 GCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATGGAGCAGGAGGGGCGGAGTATTGG
 GACCGGGAGACACGAATGTGAAGGCCAGTCACAGACTGACCGAGTGGACCTGGGGACC
 CTGCGCGGCTACTACAACCAGAGCGAGGACA

>K5RV
 ATTCTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTATTTCTTCACATCCGTG
 TCCCGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAG
 TTCGTGCGGTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATA
 GAGCAGGAGGGGCGGAGTATTGGGACCAGGAGACACGGAATGCAAGGCCACGACACAG
 ACGACTGCTGGCACTCGGATCTTCCCG

CLUSTAL 2.1 multiple sequence alignment

K5FW	-----CGACTGAGTGCCCTCTAG-----TATTTCTTCACATGCCGT	35
K5RV	ATTCTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTATTTCTTCACAT-CCGT	59
	* **** * * *	***** *
K5FW	GTCTGGCCCCGGCCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCA	95
K5RV	GTCCCGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCA	119
	**** *	
K5FW	GTTCTGTCGGTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGAT	155
K5RV	GTTCTGTCGGTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGAT	179

K5FW	GGAGCAGGAGGGGCGGAGTATTGGGACCGGAGACACGGAATGTGAAGGCCCA-GTCAC	214
K5RV	AGAGCAGGAGGGGCGGAGTATTGGGACCAGGAGACACGGAATGC-AAGGCCACGACAC	238
	***** *	
K5FW	AGACTGACCGAGTGGACCTGGGGACCCTGCGCGGCTACTACAACCAGAGCGAGGACA	271
K5RV	AGAC-GACTG-----CTGG-----CACTCGGATCTT-----CCCG-----	267
	*** * * **** * * * *	

>K5SeqCons
 ATTCTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTATTTCTTCACATGCC
 GTGTCCTGGCCCCGGCCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACA
 CGCAGTTCGTGCGGTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCC
 GTGGATGGAGCAGGAGGGGCGGAGTATTGGGACCGGAGACACGGAATGTGAAGGCC
 CAGTCACAGACTGACCGAGTGGACCTGGGGACCCTGCGCGGCTACTACAACCAGAGCG
 AGGACA

>IMGTHLA:HLA01718 A*03:01:01:02N 1163 bp
 Length = 1163

Plus Strand HSPs:

Score = 1305 (201.9 bits), Expect = 1.6e-55, P = 1.6e-55, Group = 1
 Identities = 267/273 (97%), Positives = 267/273 (97%), Strand = Plus / Plus

Query: 23 CAGGCTCCCACTCCATGAGGTATTTCTTCACATGCCGTGTCCTGGCCCCGGCCGCGGGGAG 82
 | ||||||||||||||||||||||||| ||||| |||||||||||||
 Sbjct: 71 CGGGCTCCCACTCCATGAGGTATTTCTTCACAT-CCGTGTCGCCGCGCCGCGGGGAG 129

Query: 83 CCCCCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTCGACAGCGAC 142
 |||

Sbjct: 130 CCCCCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGAC 189

Query: 143 GCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATGGAGCAGGAGGGGCCGGAGTAT 202
 |||

Sbjct: 190 GCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGGAGTAT 249

Query: 203 TGGGACCGGGAGACACGGAATGTGAAGGCCAGTCACAGACTGACCGAGTGGACCTGGGG 262
 |||

Sbjct: 250 TGGGACCGAGGAGACACGGAATGTGAAGGCCAGTCACAGACTGACCGAGTGGACCTGGGG 309

Query: 263 ACCCTGCGCGGCTACTACAACCAGAGCGAGGAC 295
 |||

Sbjct: 310 ACCCTGCGCGGCTACTACAACCAGAGCGAGGCC 342

A2-2/2

>K5FW
 AGCCCTTCCTCCTGCGGTATTTCTTCCATCCGTGTCCCGGCCCGCGCGGGGAGC
 CCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGC
 GACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGTCC
 GGAGTATTGGGACGGGGAGACACGGAAGTGAAGGCCACTCACAGACTCACCGAG
 TGGACCTGGGGACCTGCGCGGCTACTACAACCAGACGAGGGTGT

>K5RV
 TCTCAGCCACTCCTCGTCCCCAGGCTCTCACTCCATGAGGTATTTCTTCACATCCG
 TGTCCCGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGAC
 ACGCAGTTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGC
 GCCGTGGATAGAGCAGGAGGGTCCGGAGTATTGGGACGGGGAGACACGGAAGTGA
 AGGCCCCTCACAGACTCACCGAGTGACCGGCACCTGCGCGGA

CLUSTAL 2.1 multiple sequence alignment

K5FW	-----AGCCCTTCCTCC--TGC	GGTATTTCTTC--CATCCGTGTC	36
K5RV	TCTCAGCCACTCCTCGTCCCCAGGCTCTCACTCCATGAGGTATTTCTTCACATCCGTGTC		60
	** ** **** ** ***** *****		
K5FW	CCGCCCCGCGCCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGTT		96
K5RV	CCGCCCCGCGCCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGTT		120

K5FW	CGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGA		156
K5RV	CGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGA		180

K5FW	GCAGGAGGGTCCGGAGTATTGGGACGGGGAGACACGGAAGTGAAGGCCCACTCACAGAC		216
K5RV	GCAGGAGGGTCCGGAGTATTGGGACGGGGAGACACGGAAGTGAAGGCCCACTCACAGAC		240

K5FW	TCACCGAGTGGACCTGGGGACCTGCGCGGCTACTACAACCAGACGAGGGTGT		269
K5RV	TCACCGAGTG-ACC---GGCACCTGCGCGGA-----		267
	***** ** ** *****		

>K5SeqCons
 TCTCAGCCACTCCTCGTCCCCAGGCTCTCACTCCATGAGGTATTTCTTCCATCC
 GTGTCCCGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGAC
 GACACGCAGTTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCG
 CGGGCGCCGTGGATAGAGCAGGAGGGTCCGGAGTATTGGGACGGGGAGACACGG
 AAAGTGAAGGCCCACTCACAGACTCACCGAGTGGACCTGGGGACCTGCGCGGC
 TACTACAACCAGACGAGGGTGT

>IMGTHLA:HLA01218 A*02:43N 1099 bp
 Length = 1099

Plus Strand HSPs:

Score = 1311 (202.8 bits), Expect = 9.1e-56, P = 9.1e-56, Group = 1
 Identities = 267/270 (98%), Positives = 267/270 (98%), Strand = Plus / Plus

Query: 21 CAGGCTCTCACTCCATGAGGTATTTCTTC--CATCCGTGTCCCGGCCCGCGGGGAGC 79
 | |||

Sbjct: 71 CGGGCTCTCACTCCATGAGGTATTTCTTCACATCCGTGTCCCGGCCCGCGGGGAGC 130

Query: 80 CCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACG 139

```

Sbjct: 131 ||||| CCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTCGACAGCGACG 190
Query: 140 CCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGTCCGGAGTATT 199
Sbjct: 191 ||||| CCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGTCCGGAGTATT 250
Query: 200 GGGACGGGGAGACACGGAAGTGAAGGCCCACTCACAGACTCACCGAGTGGACCTGGGGA 259
Sbjct: 251 GGGACGGGGAGACACGGAAGTGAAGGCCCACTCACAGACTCACCGAGTGGACCTGGGGA 310
Query: 260 CCCTGCGCGGCTACTACAACCAGA-CGAGG 288
Sbjct: 311 ||||| CCCTGCGCGGCTACTACAACCAGAGCGAGG 340

```

A2-1/2

```

>K5FW
ACACCCTGGTGGAGGTATATTCTCACATGCCGTGTCCCGGCCCGCGGGGAGCCCCG
CTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACCCGC
GAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGCGCGGAGTATTGGGA
CCGGGAGACACGGAATGTGAAGGCCCACTCACAGACTGACCGAGTGGACCTGGGGACCTT
GCGCGGCTACTACAACCAGAGCGAGGGCA

```

```

>K5RV
TCTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTATTTCTTCACATCCGTGTC
CCGGCCCGCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTT
CGTGCGGTTTCGACAGCGACCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGA
GCAGGAGGGCGCGGAGTATTGGGACCGAGGAGACACGGAATGCAAGGCCAGACACAGACG
ACGATGTCAGCCGCATCCCCCG

```

CLUSTAL 2.1 multiple sequence alignment

```

K5FW      -----ACACCCTGGTG-----GAGGTATATTCTCACATGCCGTGT 35
K5RV      TCTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTATTTCTTCACAT-CCGTGT 59
              *  **  *
K5FW      CCGGCCCGCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGT 95
K5RV      CCGGCCCGCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGT 119
              *****
K5FW      TCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAG 155
K5RV      TCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAG 179
              *****
K5FW      AGCAGGAGGGGCGGAGTATTGGGACCGGAGACACGGAATGTGAAGGCCAGTCACAGA 215
K5RV      AGCAGGAGGGGCGGAGTATTGGGACCGAGGAGACACGGAATGC-AAGGCCAGACACAGA 238
              *****
K5FW      CTGACCGAGTGGACCTGGGGACCTGCGCGGCTACTACAACCAGAGCGAGGGCA 269
K5RV      C-GACGATGTCAGC---GCATCCCCCG----- 264
              *  **  *  *  *  *  *

```

```

>K5SeqCons
TCTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTATATTCTCACATGCCGTGT
CCCGCCCCGCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGT
TCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAG
AGCAGGAGGGGCGGAGTATTGGGACCGGAGACACGGAATGTGAAGGCCAGTCACAGA
CTGACCGAGTGGACCTGGGGACCTGCGCGGCTACTACAACCAGAGCGAGGGCA

```

>IMGTHLA:HLA01718 A*03:01:01:02N 1163 bp
Length = 1163

Plus Strand HSPs:

Score = 1298 (200.8 bits), Expect = 3.3e-55, P = 3.3e-55, Group = 1
Identities = 268/274 (97%), Positives = 268/274 (97%), Strand = Plus / Plus

```

Query: 21 CAGGCTCCCACTCCATGAGGTATATTCT-CACATGCCGTGTCCCGGCCCGCGGGGA 79
      | |||||
Sbjct: 71 CGGGCTCCCACTCCATGAGGTAT-TTCTTCACAT-CCGTGTCCCGGCCCGCGGGGA 128

```



```

Query:      81 CCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGTTTCGTGCGGTTCGACAGCGACG 140
           |||
Sbjct:     131 CCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGTTTCGTGCGGTTCGACAGCGACG 190

Query:     141 CCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGTCGCGAGTATT 200
           |||
Sbjct:     191 CCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGTCGCGAGTATT 250

Query:     201 GGGACGGGGAGACACGGAAGTGAAGGCCACTCACAGACTCACCGAGTGGACCTGGGGA 260
           |||
Sbjct:     251 GGGACGGGGAGACACGGAAGTGAAGGCCACTCACAGACTCACCGAGTGGACCTGGGGA 310

Query:     261 CCCTGCGCGGCTACTACAACCAGAGCGAGGAC 292
           |||
Sbjct:     311 CCCTGCGCGGCTACTACAACCAGAGCGAGGCC 342

```

A3-1/2

```

>K5FW
TCCTAATGGCCTGCCCGTGAGGCCGAGGGCGCTTCCTCCGCGGGTACCCAGTACGCCT
ACGACGGCAAGGATTACATCGCCCTGAAGAGGACCTGCGCTCTTGGACCGCGGCGGACAT
GGCAGCTCAAACCACCAAGCACAAAGTGGGAGGCGGCCATGTGGCGGAGCAGTTGAGAGC
CTACCTGGGGGCACGTGCGTGGAGTGGCTCCGCAAATACCTGGAGAACGGGAAGA

```

```

>K5RV
TGGTTCTCACACCGTCCAAAGGATGTATGGCTGCGACGTGGGGTCGGACTGGCGCTTCCT
CCGCGGGTACCACAGTACGCCTACGACGGCAAGGATTACATCGCCCTGAAAGAGGACCT
GCGCTCTTGGACCGCGGCGGACATGGCAGCTCAGATCACCAGCACAAAGTGGGAGGCGGC
CCATGGGCGGAGCAGTTAAAGCCTACCTGAGGGCACGGGTGTGCGACCCCA

```

CLUSTAL 2.1 multiple sequence alignment

```

K5FW      -----TCCTAATGGC-----CTGCC-CGTGAGGCCGGAG-GGCGCTTCCT 38
K5RV      TGGTTCTCACACCGTCCAAAGGATGTATGGCTGCGACGTGGGGTCGGACTGGCGCTTCCT 60
           ***  * *          ****  ****  * *  * *  * *  * *  * *  * *

K5FW      CCGCGGGTACC-CCAGTACGCCTACGACGGCAAGGATTACATCGCCCTGAA-GAGGACCT 96
K5RV      CCGCGGGTACCACAGTACGCCTACGACGGCAAGGATTACATCGCCCTGAAAGAGGACCT 120
           *****

K5FW      GCGCTCTTGGACCGCGGCGGACATGGCAGCTCAAACCACCAAGCACAAAGTGGGAGGCGGC 156
K5RV      GCGCTCTTGGACCGCGGCGGACATGGCAGCTCAGATCACCAGCACAAAGTGGGAGGCGGC 180
           ***** * *****

K5FW      CCATGTGGCGGAGCAGTTGAGAGCCTACCTGGGGGCACGTGCGTGGAGTGGCTCCGCAA 216
K5RV      CCATG-GGCGGAGCAGTTAA-AGCCTACCTGAGGGCACGGGTGTGCG---GACCCCA---- 231
           ***** * ***** * * * * * * * * * *

K5FW      TACCTGGAGAACGGGAAGA 235
K5RV      -----

```

```

>K5SeqCons
TGGTTCTCACACCGTCCAAAGGATGTATGGCTGCGACGTGGGGTCGGACTGGCGCTTCCT
TCCGCGGGTACCCAGTACGCCTACGACGGCAAGGATTACATCGCCCTGAAGAGGACCT
GCGCTCTTGGACCGCGGCGGACATGGCAGCTCAAACCACCAAGCACAAAGTGGGAGGCGG
CCCATGTGGCGGAGCAGTTGAGAGCCTACCTGGGGGCACGTGCGTGGAGTGGCTCCGCA
AATACCTGGAGAACGGGAAGA

```

>IMGTHLA:HLA01218 A*02:43N 1099 bp
Length = 1099

Plus Strand HSPs:

Score = 1218 (188.8 bits), Expect = 1.4e-51, P = 1.4e-51, Group = 1
Identities = 252/258 (97%), Positives = 252/258 (97%), Strand = Plus / Plus

```

Query:      2 GGTTCCTCACACCGTCCAAAGGATGTATGGCTGCGACGTGGGGTCGGACTGGCGCTTCCTC 61
           |||
Sbjct:     343 GGTTCCTCACACCGTCCAGAGGATGTATGGCTGCGACGTGGGGTCGGACTGGCGCTTCCTC 402

Query:     62 CGCGGGTACC-CCAGTACGCCTACGACGGCAAGGATTACATCGCCCTGAA-GAGGACCTG 119
           |||

```

Sbjct: 403 CGCGGGTACCACCAGTACGCCTACGACGGCAAGGATTACATCGCCCTGAAAGAGGACCTG 462

Query: 120 CGCTCTTGGACCGCGCGGACATGGCAGCTCAAACCACCAAGCACAAGTGGGAGGCGGCC 179
 |||

Sbjct: 463 CGCTCTTGGACCGCGCGGACATGGCAGCTCAGACCACCAAGCACAAGTGGGAGGCGGCC 522

Query: 180 CATGTGGCGGAGCAGTTGAGAGCCTACCTGG-GGGCAGCTGCGTGGAGTGGCTCCGCAA 238
 |||

Sbjct: 523 CATGTGGCGGAGCAGTTGAGAGCCTACCTGGAGGGCAGCTGCGTGGAGTGGCTCCGAGA 582

Query: 239 TACCTGGAGAACGGGAAG 256
 |||

Sbjct: 583 TACCTGGAGAACGGGAAG 600

A3-2/2

>K5FW
 CGCAAGGCTGCGCGTGGGGCCGACGGGCGCTTTCTCCTGTGTACAACTTGACGCCCAC
 TAGCGCGGATAATACATCGCCCTGAAAGGACCCTGCTCTTGGACCGCGGCAACACATG
 GGCTCACATATCCCAAACACGTGTGAAACGCGCACCTTCTGGCAGAACGTTGGGACTA
 TATCTGGGCGGGTCTTGGTGTGGCGGCTCCGATACTTCTGAACAACGGGAAGACCA

>K5RV
 CATCCTCTCTGATTGGTTTCCCCCCCACCCAAAGAAAGCATGGTTGCAAGTTGGGCCC
 ACAGGCGCTTCTCCGAGGTATGAACAGTTTCGCCTACGATGGCAAGGATTACATCGCC
 CTGAACGAGGACCTGCACTCTTGGACCGCGCGAACAACAGGGCTCAGATCACCAAGCAA
 ATGGAAGGGCCCAATGTCTAGCAGGAAGGCCCTACCTGTGTGCAACGCAGCAGACCCT

CLUSTAL 2.1 multiple sequence alignment

K5FW	-----CGCAAGGCTGCGCGTGGGGCCGGA	24
K5RV	CATCCTCTCTGATTGGTTTCCCCCCCACCCAAAGAAAGCATGGTTGCAAGTTGGGCCC	60
	*** ** *	
K5FW	CGGGCGCTTCTCC-----TGTTGTACAACTTGACGCCCAC--TAGCGCGGATAATACATC	77
K5RV	CAGGCGCTTCTCCGAGGTATGAACAGTT--CGCCTACGATGGCAAGGAT--TACATC	115
	* **** * * * * * * * * * * * * * * *	
K5FW	GCCCTGAA--AGGACCC-TGCTCTTGGACCGCGGCAACACATGGGCTCACATATCCCAA	134
K5RV	GCCCTGAACGAGGACCTGCACTCTTGGACCGCGCGAACAACA-GGGCTCAGAT-CACCAA	173
	***** * * * * * * * * * * * * * * *	
K5FW	ACACGTGTGAAACGCGCACCTTCTGGCAGAACGTTTGGGACTATATCTGGGCGGGTGCTT	194
K5RV	GCAATG-GAAGGGCCCAATGTCTAGCAGGG-----AAGGCCCTACCTG-----	216
	* * * * * * * * * * * * * * *	
K5FW	GGTGTGGCGGCTCCGATACTTCTGAACAACG-GGAAGACCA-	235
K5RV	--TGTG-----CAACGCAGCAGACCCT	236
	**** * ****	

Sequence not analyzed.

A4-1/2H

>K5FW
 AAGCCGCGCGTGCCTGAATGTAGCCCCCTGAGTGTGGGCCCTGAGCTTCTACCC
 TGGGAGATCACACTGGCAGCGGGATGGGGAGGACAGACCAGGACACGGA
 GCTCGTGGAGACCAGGCTGCAGGGATAGA

>K5RV
 TCTCGCCCCAAAACGCATATGACTCACCACGCTGTCTCTGACCATGAAGCCACCCT
 GAGGTGTGGGCCCTGAGCTTCTACCTGCGGAGATCACACTGACCGGCAGCGGGAG
 GGGAGGACCAGACTAGCACAAGGAGCTGGTT

CLUSTAL 2.1 multiple sequence alignment

K5FW	-----AAGC-----CCGCGCGTGCCTGA--ATGTAGCC-CCCTGAG	34
K5RV	TCTCGCCCCAAAACGCATATGACTCACCACGCTGTCTCTGACCATGAAGCCACCCTGAG	60
	* * * * * * * * * * * * * * *	
K5FW	-TGTTGGGCCCTGAGCTTCTACCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGA	93
K5RV	GTGTGGGCCCTGAGCTTCTACCTGCGGAGATCACACTGACC-GGCAGCGGA-GGGGA	118

```

*****
K5FW      GGACCAGACCCAGGACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGATAGA 145
K5RV      GGACCAGACT-AGCACAAGGAGCTGGTT----- 145
*****  ** *** ***** **

```

```

>K5SeqCons
TCTCGCCCCCAAACGCATATGACTCACCACGCTGTCTCTGACCATGTAGCCCCCT
GAGTGCTGGGCCCCGAGCTTCTACCCTGCGGAGATCACACTGACCTGGCAGCGGGA
TGGGAGGACCAGACCCAGGACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGATA
GA

```

```

>IMGTHLA:HLA00005 A*02:01:01:01 1098 bp
Length = 1098

```

Plus Strand HSPs:

```

Score = 797 (125.6 bits), Expect = 1.5e-32, P = 1.5e-32, Group = 1
Identities = 165/169 (97%), Positives = 165/169 (97%), Strand = Plus / Plus

```

```

Query:      4 CGCCCCCAAACGCATATGACTCACCACGCTGTCTCTGACCATGTAGCC-CCCTGAG-TG 61
             |||
Sbjct:     621 CGCCCCCAAACGCATATGACTCACCACGCTGTCTCTGACCATGAAGCCACCCTGAGGTG 680
             |||

Query:      62 CTGGGCCCTGAGCTTCTACCCGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGA 121
             |||
Sbjct:     681 CTGGGCCCTGAGCTTCTACCCGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGA 740
             |||

Query:     122 CCAGACCCAGGACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGATAGA 170
             |||
Sbjct:     741 CCAGACCCAGGACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGATGGA 789
             |||

```

A4-2/2H

```

>K5FW
ACGACCTGCGGGGGTGGACCTGAGGCCCTTGAGTGCTGGGCCCTGGGCTTCTACC
CTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGACCAGACCCAGGCCACG
GAGCTCGTGGAGCCCAGGCCTGCAGGGGATATT

>K5RV
CCCCCCCCAAGACACATATGCCCCCACCCATTCTGACCATAAGGCCACCCTGA
GGTGGTGGGCCCTGGGGTTCTACCCCTATGAGATCACACTGACCTAGCCAGCAGG
AGGGGAGGACCAGATCCCCCACGGGGCCCTG

```

CLUSTAL 2.1 multiple sequence alignment

```

K5FW      ACGACCTGCGGGG-----GTG-----GACC-TGAGGCC-CCCTGAG-T 35
K5RV      -CCCCCCAAGACACATATGCCCCCACCCATTCTGACCATAAGGCCACCCTGAGGT 59
             *  ** *  *          **          ***** * ***** *
K5FW      GCTGGGCCCTGGGCTTCTACCCGCGGAGATCAC-ACTGACCTGGC-AGCGGGATGGGGA 93
K5RV      GGTGGGCCCTGGGGTTCTACCCCTATGAGATCACACTGACCTAGCCAGCAGGA-GGGGA 118
             * ***** * ***** * ***** * * * * * *
K5FW      GGACCAGACCCAGGCCACGGAGCTCGTGGAGCCCAGGCCTGCAGGGGATATT 145
K5RV      GGACCAGATCCCC-CCACGGGGC-----CCTG----- 144
             ***** **          ***** **          ****

```

```

>K5SeqCons
CCCCCCCCAAGACACATATGCCCCCACCCATTCTGACCTGAGGCCCTTGAGT
GCTGGGCCCTGGGCTTCTACCCGCGGAGATCACACTGACCTGGCAGCGGGATGGG
GAGGACCAGACCCAGGCCACGGAGCTCGTGGAGCCCAGGCCTGCAGGGGATATT

```

```

>IMGTHLA:HLA02369 A*03:21N 1099 bp
Length = 1099

```

Plus Strand HSPs:

```

Score = 603 (96.5 bits), Expect = 8.7e-24, P = 8.7e-24, Group = 1
Identities = 129/135 (95%), Positives = 129/135 (95%), Strand = Plus / Plus

```

```

Query:      32 ATTTCTGACC-TGAGGCC-CCCTGAG-TGCTGGGCCCTGGGCTTCTACCTGCGGAGATC 88
           || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:     653 ATCTCTGACCATGAGGCCACCCTGAGGTGCTGGGCCCTGGGCTTCTACCTGCGGAGATC 712

Query:      89 ACACTGACCTGGCAGCGGGATGGGGAGGACCAGACCCAGGCCACGGAGCTCGTGGAGCCC 148
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:     713 ACACTGACCTGGCAGCGGGATGGGGAGGACCAGACCCAGGACACGGAGCTCGTGGAGACC 772

Query:     149 AGGCCTGCAGGGGAT 163
           ||||| ||||| |||||
Sbjct:     773 AGGCCTGCAGGGGAT 787

```

A4-3H/1

```

>K5FW
CGGACTGCCCCCGGCTGGGTGGGCCAAGGCCCGGCACACTGTGTTCGTGGACCCG
GCTTGCGGGGATGGAACCTTCCAATTGGGCGGTTGTGGTGGTGCCTTTGGAGGGA
GCAAAAACCACTGCCATGTGCAGAATGAGGGTTTGCCCAACCCCTTAACCTGAA
ATGGAC

```

```

>K5RV
TTTTTACCCTGCGGAGATCACACTGACCTGGCAACGGGATGGGGAGGACCAGACCC
AGGACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGATGGAACCTTCCAGAAGTGG
GCGGCTGTGGTGGCTTCTGAGAGGAGCAGAGATACACCTGCCATGTGCAGGC
ATAGGTGCTGCG

```

CLUSTAL 2.1 multiple sequence alignment

```

K5FW      -----CGGA-----CTGCCCC-----CCGGCTGGGTGGGCCAAGGCCCGGCA 37
K5RV      TTTTACCCTGCGGAGATCACACTGACCTGGCAACGGGATGGGGAGGACCAGACCAGGA 60
           ****          *** *          * * * * * * * * * * * *

K5FW      CACTGTGTTCGTGGA--CCCGCTTGC-GGGGATGGAACCTTCCA--ATTGGGCGGTTGT 92
K5RV      CACGGAGCTCGTGGAGACCAGGCCTGCAGGGGATGGAACCTTCCAGAAGTGGGCGGCTGT 120
           *** * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

K5FW      GGTGGTGCCTTTGGAG-GGAGCAAAAC-CACCTGCCATGTGCAGAATGAGGGTTTGCC 150
K5RV      GGTGGTGCCTTCTGGAGAGGAGCAGAGATACACCTGCCATGTGCAGGCATAGGTGCTGCG 180
           ***** * * * * * * * * * * * * * * * * * * * * * * * * *

K5FW      CAACCCCTTAACCTGAAATGGAC 174
K5RV      -----

```

```

>K5SeqCons
TTTTTACCCTGCGGAGATCACACTGACCTGGCAACCGGCTGGGTGGGCCAAGG
CCCGGCACACTGTGTTCGTGGACCCGGCTTGCAGGGGATGGAACCTTCCAATG
GGCGGTTGTGGTGGCTTCTGGAGGGAGCAAAAACCACTGCCATGTGCAG
AATGAGGGTTTGCCCAACCCCTTAACCTGAAATGGAC

```

>IMGTHLA:HLA06077 A*02:291 822 bp
Length = 822

Plus Strand HSPs:

Score = 657 (104.6 bits), Expect = 4.2e-26, P = 4.2e-26, Group = 1
Identities = 167/201 (83%), Positives = 167/201 (83%), Strand = Plus / Plus

```

Query:      2 TTTTACCCTGCGGAGATCACACTGACCTGGCAACCGGCTGGGTGGGCCAAGGCCCGGCAC 61
           || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:     621 TTCTACCCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGACCAGACCCAGGAC 680

Query:      62 ACTGTGTTCGTGGAC-CC-GGCTTGC-GGGGATGGAACCTTCCA--ATTGGGCGGTTGTG 116
           || | | ||||| || ||| ||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:     681 ACGGAGCTCGTGGAGACCAGGCCTGCAGGGGATGGAACCTTCCAGAAGTGGGCGGCTGTG 740

Query:     117 GTGGTGCCTTTTGGAG-GGAGCAAAAC-CACCTGCCATGTGCAGAATGAGGGTTTGCCC 174
           ||||| ||||| ||||| | | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:     741 GTGGTGCCTTCTGGACAGGAGCAGAGATACACCTGCCATGTGCAGCATGAGGGTTTGCCC 800

Query:     175 AACCCCTTAACCTGAAATGG 195
           || ||||| ||||| |||||

```

Sbjct: 801 AAGCCCTTCACCCTGAGATGG 821

K6

A2-1/1 7-12

>K6FW

CACCGCTCCCTTCCCTCCACTTCTTCCATCCGTGTCCCGGCCCGGCCGGGGAGCCCCG
CTTCATCGCGGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACGCCGC
GAGCCAGAAGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCGGAGTATTGGGA
CCAGGAGACACGGAATATGAAGGCCCACTACAGACTGACCGAGCGAACCTGGGGACCCT
GCGCGGCTACTACAACCAGACGAGGAC

>K6RV

CTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTATTTCTTCACATCCGTGTCC
CGGCCCCGGCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTC
GTGCGGTTTCGACAGCGACGCCGCGAGCCAGAAGATGGAGCCGCGGGCGCGGTGGATAGAG
CAGGAGGGGCGGAGTATTGGGACCAGGAGACACGGAATATGAAGGCCCACTACAGACG
ACCGAGCGTACAGTATTATGGTTTATTT

CLUSTAL 2.0.12 multiple sequence alignment

```
K6FW      -----CAC----CGTCCCT---TCCCTCCACTT-----CTTC-CATCCGTGTCC 37
K6RV      CTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTATTTCTTCACATCCGTGTCC 60
          ***      ***   *:   *:   *:   *:   *:   *:   *:   *:   *:   *:
          ****      *****

K6FW      CGGCCCCGGCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTC 97
K6RV      CGGCCCCGGCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTC 120
          *****

K6FW      GTGCGGTTTCGACAGCGACGCCGCGAGCCAGAAGATGGAGCCGCGGGCGCGGTGGATAGAG 157
K6RV      GTGCGGTTTCGACAGCGACGCCGCGAGCCAGAAGATGGAGCCGCGGGCGCGGTGGATAGAG 180
          *****

K6FW      CAGGAGGGGCGGAGTATTGGGACCAGGAGACACGGAATATGAAGGCCCACTACAGACT 217
K6RV      CAGGAGGGGCGGAGTATTGGGACCAGGAGACACGGAATATGAAGGCCCACTACAGAC- 239
          *****

K6FW      GACCGAGCGAACCTGGGGACCCTGCGCGGCTACTACAACCAGACGAGGAC 267
K6RV      GACCGAGCGTACA--GGTATTATG---GTTTATTT----- 269
          *****:*.  ** * .** * ** *:
          *****
```

>K6SecCons

CATCCGTGTCCCGGCCCGGCCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGA
CGACACGCAGTTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAAGATGGAGCCGCGG
GCGCGGTGGATAGACAGGAGGGGCGGAGTATTGGGACCAGGAGACACGGAATATGA
AGGCCCACTACAGACTGACCGAGCG

>IMGTHLA:HLA00004 A*01:04N 1099 bp
Length = 1099

Plus Strand HSPs:

Score = 1000 (156.1 bits), Expect = 9.0e-42, P = 9.0e-42, Group = 1
Identities = 200/200 (100%), Positives = 200/200 (100%), Strand = Plus / Plus

```
Query:      1 CATCCGTGTCCCGGCCCGGCCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACG 60
             |||
Sbjct:     101 CATCCGTGTCCCGGCCCGGCCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACG 160

Query:      61 ACACGCAGTTTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAAGATGGAGCCGCGGGCGC 120
             |||
Sbjct:     161 ACACGCAGTTTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAAGATGGAGCCGCGGGCGC 220

Query:     121 CGTGGATAGAGCAGGAGGGGCGGAGTATTGGGACCAGGAGACACGGAATATGAAGGCCC 180
             |||
Sbjct:     221 CGTGGATAGAGCAGGAGGGGCGGAGTATTGGGACCAGGAGACACGGAATATGAAGGCCC 280

Query:     181 ACTCACAGACTGACCGAGCG 200
             |||
```

```
>K6SecEdit1
CATCCGTGTCCCGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGA
CGACACGCAGTTCGTGCGGTTTCGACACGCACGCCCGAGCCAGAGGATGGAGCCCGCG
GCGCCGTGGATAGACGAGGAGGGGCCGAGTATTGGGACCAGGAGACACGGAATATGA
AGGCCCACTCACAGACTGACCGAGCG

>IMGTHLA:HLA04871 A*24:129 1098 bp
      Length = 1098

      Plus Strand HSPs:

      Score = 1000 (156.1 bits), Expect = 9.0e-42, P = 9.0e-42, Group = 1
      Identities = 200/200 (100%), Positives = 200/200 (100%), Strand = Plus / Plus

Query:      1  CATCCGTGTCCCGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACG  60
             |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:     101 CATCCGTGTCCCGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACG  160

Query:      61  ACACGCAGTTCGTGCGGTTTCGACACGCACGCCCGAGCCAGAGGATGGAGCCCGCGGGCGC  120
             |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:     161 ACACGCAGTTCGTGCGGTTTCGACACGCACGCCCGAGCCAGAGGATGGAGCCCGCGGGCGC  220

Query:     121  CGTGGATAGAGCAGGAGGGGCCGAGTATTGGGACCAGGAGACACGGAATATGAAGGCC  180
             |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:     221 CGTGGATAGAGCAGGAGGGGCCGAGTATTGGGACCAGGAGACACGGAATATGAAGGCC  280

Query:     181  ACTCACAGACTGACCGAGCG  200
             |||||||||||||||
Sbjct:     281 ACTCACAGACTGACCGAGCG  300
```

A2-2/2

>K6FW
ACTGCTGTCTCCTCTATGGGCTCCCATCCGTGTCCCGGCCCGGCCGCGGGGAAGCCCCGC
TTCATCGCCGTGGGTACGTGGACGACACGCAGTTCTGTGCGGTTTCGACAGCGACGCCCGC
AGCCAGAGGATGGAGCCGCGGCCCGCTGGATAGACAGGAGGGGCCGGAGTATTGGGAC
GAGGAGACAGGGAAAGTGAAGGCCCACTCACAGACTGACCGAGAGAACCTGCGGATCGCG
CTCCGCTACTACAACCAGACGAGGGCA

>K6RV
TCTCAGCCACTCCTCGTCCCCAGGCTCCCACTCCATGAGGTATTTCTCCACATCCGTGTC
CCGGCCCGGCCCGGGGAGCCCCGCTTCATCGCCGTGGGTACGTGGACGACACGCAGTT
CGTGCGGTTTCGACGCGACGCCCGCAGGACAGGATGGAGCCGCGGGCGCCGTGGATAGA
GCAGGAGGGGCCGGAGTATTGGGACGAGGAGACAGGGAAGGAAGGCCCACTCACAGACG
ACCGAGACAACGGGGATTTTTTTGAGG

CLUSTAL 2.0.12 multiple sequence alignment

K6FW	-----ACTGCT-GTCTCCT-----CTATGGG-----CTCC-CATCCGTGTC	34
K6RV	TCTCAGCCACTCCTCGTCCCAGGCTCCCACTCCATGAGGTATTTCTCFCACATCCGTGTC	60
	*** ** ***: * **.* **** *	
K6FW	CCGGCCCCGGCCGGGGGAAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGT	94
K6RV	CCGGCCCCGGCCGGGGG-AGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGT	119

K6FW	TCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAG	154
K6RV	TCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAG	179

K6FW	AGCAGGAGGGGCCGGAGTATTGGGACGAGGAGACAGGGAAAGTGAAGGCCCACTCACAGA	214
K6RV	AGCAGGAGGGGCCGGAGTATTGGGACGAGGAGACAGGGAAAG-GAAGGCCCACTCACAGA	238

K6FW	CTGACCGAGAGAACCTGCGGATCGCGTCCGCTACTACAACCGACGAGGGCA	267
K6RV	C-GACCGAGACAAC--GGGGATT-----TTTGAGG---	266
	* ***** * * * * * . * ****	

```

>K6SeqCons
TCTCAGCCACTCCTCGTCCCCAGGCTCCCACTCCATGAGGTATTTCTCCCATCCGTGTCC
CGGCCCCGGCCGCGGGGAAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTT
CGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGA
GCAGGAGGGGCCGGAGTATTGGGACGAGGAGACAGGGAAGTGAAGGCCCACTCACAGAC
TGACCGAGAGAACCTGCGGATCGCGCTCCGCTACTACAACCAGACGAGGGCA

>IMGTHLA:HLA03251 A*24:86N 1115 bp
      Length = 1115

      Plus Strand HSPs:

      Score = 1311 (202.8 bits), Expect = 8.5e-56, P = 8.5e-56, Group = 1
      Identities = 269/273 (98%), Positives = 269/273 (98%), Strand = Plus / Plus

Query:    21 CAGGCTCCCACTCCATGAGGTATTTCTCC-CATCCGTGTCCCGCCCCGGCCGCGGGGAAG 79
          |||
Sbjct:    71 CAGGCTCCCACTCCATGAGGTATTTCTCCACATCCGTGTCCCGCCCCGGCCGCGGGGA-G 129

Query:    80 CCCCCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGAC 139
          |||
Sbjct:    130 CCCCCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGAC 189

Query:    140 GCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGGAGTAT 199
          |||
Sbjct:    190 GCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGGAGTAT 249

Query:    200 TGGGACGAGGAGACAGGGAAGTGAAGGCCCACTCACAGACTGACCGAGAGAACCTGCGG 259
          |||
Sbjct:    250 TGGGACGAGGAGACAGGGAAGTGAAGGCCCACTCACAGACTGACCGAGAGAACCTGCGG 309

Query:    260 ATCGCGCTCCGCTACTACAACCAGA-CGAGGGC 291
          |||
Sbjct:    310 ATCGCGCTCCGCTACTACAACCAGAGCGAGGCC 342

K6 A3-1-2 19-02

>K6FW
AGAGTGGCCGCGCAATAAGGGCCGCGAGGGCGCTTCCTCCGCGGGTACCGGCAGGACGCCT
ACGACGGCAAGGATTACATCGCCCTGAACGAGGACCTGCGCTCTTGGACCGCGCGGACA
TGGCAGCTCAGATCACCAGCGCAAGTGGGAGGCGGTCCATGCGGCGGAGCAGCAGAGAG
TCTACCTGGAGGGCCGGTGCGTGACGGGCTCCGCAGATACCTGGAGAACGGGAAGA

>K6RV
TGGTTCTCACACCGTCCAGATAATGTATGGCTGCGACGTGGGGTCGGACGGGCGCTTCCT
CCGCGGGTACCGGCAGGACGCCTACGACGGCAAGGATTACATCGCCCTGAACGAGGACCT
GCGCTCTTGGACCGCGGCGGACATGGCAGCTCAGATCACCAGCGCAAGTGGGAGGCGGT
CCATGTGGCGGAGCATCGTCAAGCCTACCGGATTGACAGAGATCCACGCACACGCCA

CLUSTAL 2.1 multiple sequence alignment

K6FW      -----AGAGTGGCCGCGCAATA-AGGGCCGCA-----GGGCGCTTCCT 37
K6RV      TGGTTCTCACACCGTCCAGATAATGTATGGCTGCGACGTGGGGTCGGACGGGCGCTTCCT 60
          * * * * *
          * * * * *

K6FW      CCGCGGGTACCGGCAGGACGCCTACGACGGCAAGGATTACATCGCCCTGAACGAGGACCT 97
K6RV      CCGCGGGTACCGGCAGGACGCCTACGACGGCAAGGATTACATCGCCCTGAACGAGGACCT 120
          *****

K6FW      GCGCTCTTGGACCGCGGCGGACATGGCAGCTCAGATCACCAGCGCAAGTGGGAGGCGGT 157
K6RV      GCGCTCTTGGACCGCGGCGGACATGGCAGCTCAGATCACCAGCGCAAGTGGGAGGCGGT 180
          *****

K6FW      CCATGCGGCGGAGCAGCAGAGAGTCTACCTGGAGGGCCGGTGCGTGACGGGCTCCGCAG 217
K6RV      CCATGTGGCGGAGCATCGTCAAGCCTACC---GGATTGACA-----GAGATCCACGC 229
          *****

K6FW      ATACCTGGAGAACGGGAAGA 237
K6RV      ACACGCCA----- 237
          * *

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>K6SeqCons
TGGTTCTCACACCGTCCAGATAATGTATGGCTGCGACGTGGGGTCGGACGGGCGCTTC
CTCCGCGGGTACCGGCAGGACGCCCTACGACGGCAAGGATTACATCGCCCTGAACGAGG
ACCTGCGCTCTTGGACCGCGGGCGGACATGGCAGCTCAGATCACCAGCGCAAGTGGGA
GGCGGTCCATGCGGCGGAGCAGCAGAGAGTCTACCTGGAGGGCCGGTGCGTGGACGGG
CTCCGAGATACTGGAGAACGGGAAGA

>IMGTHLA:HLA02897 A*01:25 546 bp
      Length = 546

      Plus Strand HSPs:

      Score = 1272 (196.9 bits), Expect = 1.0e-53, P = 1.0e-53, Group = 1
      Identities = 256/258 (99%), Positives = 256/258 (99%), Strand = Plus / Plus

Query:      2  GGTTCCTCACACCGTCCAGATAATGTATGGCTGCGACGTGGGGTCGGACGGGCGCTTCCTC 61
      |||
Sbjct:     270  GGTTCCTCACACCATCCAGATAATGTATGGCTGCGACGTGGGGCCGGACGGGCGCTTCCTC 329

Query:      62  CGCGGGTACCGGCAGGACGCCCTACGACGGCAAGGATTACATCGCCCTGAACGAGGACCTG 121
      |||
Sbjct:     330  CGCGGGTACCGGCAGGACGCCCTACGACGGCAAGGATTACATCGCCCTGAACGAGGACCTG 389

Query:     122  CGCTCTTGGACCGCGGGCGGACATGGCAGCTCAGATCACCAGCGCAAGTGGGAGGCGGTC 181
      |||
Sbjct:     390  CGCTCTTGGACCGCGGGCGGACATGGCAGCTCAGATCACCAGCGCAAGTGGGAGGCGGTC 449

Query:     182  CATGCGGCGGAGCAGCAGAGAGTCTACCTGGAGGGCCGGTGCGTGGACGGGCTCCGCAGA 241
      |||
Sbjct:     450  CATGCGGCGGAGCAGCAGAGAGTCTACCTGGAGGGCCGGTGCGTGGACGGGCTCCGCAGA 509

Query:     242  TACCTGGAGAACGGGAAG 259
      |||
Sbjct:     510  TACCTGGAGAACGGGAAG 527

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>K6SeqEdit1
TGGTTCTCACACCGTCCAGATAATGTATGGCTGCGACGTGGGGTCGGACGGGCGCTTCC
TCCGCGGGTACCACCAGTACGCCCTACGACGGCAAGGATTACATCGCCCTGAAAGAGGAC
CTGCGCTCTTGGACCGCGGGCGGACATGGCGGCTCAGATCACCAGCACAAAGTGGGAGGC
GGCCCATGTGGCGGAGCAGCGGAGAGCCTACCTGGAGGGCAGGTGCGTGGAGGGGCTCC
GCAGATAACCTGGAGAACGGGAAGA

>IMGTHLA:HLA02198 A*24:53 895 bp
      Length = 895

      Plus Strand HSPs:

      Score = 1236 (191.5 bits), Expect = 2.6e-52, P = 2.6e-52, Group = 1
      Identities = 252/258 (97%), Positives = 252/258 (97%), Strand = Plus / Plus

Query:      2  GGTTCCTCACACCGTCCAGATAATGTATGGCTGCGACGTGGGGTCGGACGGGCGCTTCCTC 61
      |||
Sbjct:     343  GGTTCCTCACACCTCCAGATGATGTATGGCTGCGACGTGGGGTCGGACGGGCGCTTCCTC 402

Query:      62  CGCGGGTACCACCAGTACGCCCTACGACGGCAAGGATTACATCGCCCTGAAAGAGGACCTG 121
      |||
Sbjct:     403  CGCGGGTACCACCAGTACGCCCTACGACGGCAAGGATTACATCGCCCTGAAAGAGGACCTG 462

Query:     122  CGCTCTTGGACCGCGGGCGGACATGGCGGCTCAGATCACCAGCACAAAGTGGGAGGCGGCC 181
      |||
Sbjct:     463  CGCTCTTGGACCGCGGGCGGACATGGCGGCTCAGATCACCAGCGCAAGTGGGAGGCGGCC 522

Query:     182  CATGTGGCGGAGCAGCGGAGAGCCTACCTGGAGGGCAGGTGCGTGGAGGGGCTCCGCAGA 241
      |||
Sbjct:     523  CATGTGGCGGAGCAGCAGAGAGCCTACCTGGAGGGCAGGTGCGTGGACGGGCTCCGCAGA 582

Query:     242  TACCTGGAGAACGGGAAG 259
      |||
Sbjct:     583  TACCTGGAGAACGGGAAG 600

```

A4-2/2H 29-03

>K6FW

GCCCCGGTTCATCGCGAAGGAGTACTTGGACGACACGCAGTTCGTGCGGTTAGACAGCGA
CGCCGCGAGTCCGAGGATGGAGCCGCGGGCGCCGTGGGTGGAGCAGGAGGGGCCGAGTA
TTGGGACCGGGAGACACGGAATTTCAAGGCCACGCACAGACTGACCGAGTGAACCTGGG
GAACCTGCTCGGCTACTACAACCAGAGCGAGGAC

>IMGTHLA:HLA03131 A*01:01:05 822 bp
Length = 822

Plus Strand HSPs:

Score = 1060 (165.1 bits), Expect = 2.7e-44, P = 2.7e-44, Group = 1
Identities = 236/263 (89%), Positives = 236/263 (89%), Strand = Plus / Plus

Query: 13 CCCCAGGCGGTATTTCTTTA-ATGTTGTGTCCCGGCCGCGGGGAGCCCCGGTTCA 71
| ||| | ||||| || | || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 8 CTCCATGAGGTATTTCTTCACATCC-GTGTCCCGGCCGCGGGGAGCCCCGCTTCA 66
Query: 72 TCGCGAAGGAGTACTTGGACGACACGCAGTTCGTGCGGTTAGACAGCGACGCCGCGAGTC 131
|||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 67 TCGCGGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTGACAGCGACGCCGCGAGCC 126
Query: 132 CGAGGATGGAGCCGCGGGCGCCGTGGGTGGAGCAGGAGGGGCCGAGTATTGGGACCGGG 191
|||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 127 AGAAGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGAGTATTGGGACCGAG 186
Query: 192 AGACACGGAATTTCAAGGCCACGCACAGACTGACCGAGTGAACCTGGGGAACCTGCTCG 251
|||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 187 AGACACGGAATATGAAGGCCACTCACAGACTGACCGAGCGAACCTGGGGACCTGCGCG 246
Query: 252 GCTACTACAACCAGAGCGAGGAC 274
|||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 247 GCTACTACAACCAGAGCGAGGAC 269

A2-2/2

>K8FW

TTCATTGCTTTTGTGCTACGTGGCCCCCAGCTGTTCGTGCGGTTTCGACAGCGACGC
CCCGAGCCAAAGGATGGAGCCGCGGGCGCCGTGGATGGAGCAGGAGGGGCCGAGTAT
TGGGACGGGGAGACACGGAAGTGAAGGGCCCTCACAGACTGACCGAGTGAACCTGCG
GACCGTGCGCCGCTACTAAAACCAGAGCCAGGGCACCCG

>K8RV

TTCTCAGCCACTCCTCGTCCCCAGGCTCTCACTCCATGAGGTATTTCTTCACATCCGT
GTCCCGGCCCGGCCGCGGGGAGACCCGCTTTAAATCACATTGGGCTACGTGGACGACA
CGCAGTTCTGTGCGGTTTCGACAGCGACGCCGCGAGTCAGAGGATGGAGCCGCGGGCGCC
GTGGATAGAGCAGGAGGTCCGAGTATTGGGACGGGGAGACACGGAAGGAAGGCC
ACTCACAGACTCACTGAACGAACCGCGGAGCTGCCA

CLUSTAL 2.1 multiple sequence alignment

```

K8FW      -----TTCAT----- 5
K8RV      TTCTCAGCCACTCCTCGTCCCCAGGCTCTCACTCCATGAGGTATTTCTTCACATCCGTGT 60
              ****

K8FW      -----TGTGCTACGTGGCCCCCAGC 33
K8RV      CCCGGCCCCGCGCGGGGAGACCCGCTTTAAATCACATTGGGCTACGTGGACGAC-ACGC 119
              *****          ****

K8FW      TGTTCGTGCGGTTTCGACAGCGACGCCAGCCAAAGGATGGAGCCGCGGGCGCCGTGGA 93
K8RV      AGTTCGTGCGGTTTCGACAGCGACGCCGCGAGTCAGAGGATGGAGCCGCGGGCGCCGTGGA 179
              *****          ****

K8FW      TGGAGCAGGAGGGCGCGGAGTATTGGGACGGGGAGACACGGAAGTGAAGGGCC-CTCAC 152
K8RV      TAGAGCAGGAGGTCGCGGAGTATTGGGACGGGGAGACACGGAAG-GAAGGCCCACTCAC 238
              * *****          ****

K8FW      AGACTGACCGAGTGAACCTGCGGACCGTGCGCCGCTACTAAAACCAGAGCCAGGGCACCC 212
K8RV      AGACTCACTGAACGAACC-GCGGA-----GCTGCCA----- 268
              *****          ** *

K8FW      G 213
K8RV      -

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>K8SeqCons
TTCTCAGCCACTCCTCGTCCCCAGGCTCTCACTCCATGAGGTATTTCTTCACATCC
GTGTCCCGGCCCGGCCGCGGGGAGACCCGCTTTAAATCACATTGGGCTACGTGGAC
GACACGCAGTTCTGTCGGTTCGACAGCGACGCCGCGAGTCAGAGGATGGAGCCGCG
GGCGCCGTGGATAGAGCAGGAGGGTCCGGAGTATTGGGACGGGGAGACACGAAAG
GAAGGCCACTCACAGACTGACCGAGTGAACCTGCGGACCGTGCGCCGCTACTAAA
ACCAGAGCCAGGGCACCC

>IMGTHLA:HLA02840 A*02:112 822 bp
      Length = 822

      Plus Strand HSPs:

      Score = 1202 (186.4 bits), Expect = 1.0e-50, P = 1.0e-50, Group = 1
      Identities = 256/271 (94%), Positives = 256/271 (94%), Strand = Plus / Plus

Query:    25 GCTCTCACTCCATGAGGTATTTCTTCACATCCGTGTCCCGGCCCGGCCGCGGGGAGACCC 84
           |||||
Sbjct:    1  GCTCTCACTCCATGAGGTATTTCTTCACATCCGTGTCCCGGCCCGGCCGCGGGGAGCCCC 60

Query:    85 GCTTTAAATCACATTGGGCTACGTGGACGACACGCAGTTCTGTCGGTTCGACAGCGACGC 144
           |||||
Sbjct:    61 GCTTCA--TCGCAGTGGGCTACGTGGACGACACGCAGTTCTGTCGGTTCGACAGCGACGC 118

Query:    145 CGCGAGTCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGTCCGGAGTATTG 204
           |||||
Sbjct:    119 CGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGTCCGGAGTATTG 178

Query:    205 GGACGGGGAGACACGGAAG--GAAGGCCACTCACAGACTGACCGAGTGAACCTGCGGAC 263
           |||||
Sbjct:    179 GGACGGGGAGACACGGAAGTGAAGGCCACTCACAGACTGACCGAGAGAACCTGCGGAT 238

Query:    264 CGTGCGCCGCTACTAAAACCAGAGCCAGGGC 294
           |||||
Sbjct:    239 CGCGCTCCGCTACTACAACCAGAGCGAGGCC 269

A2-1/2

>K8FW
ACTAGCCAGGACGAGGGCACTATGTACTTACCTTTTAGTTTCTTACAACGAGGGGAAGGG
CACTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCTGTCGGTTCGACAGCGACGCC
GCGAGCCAGAAGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGAGTATTGG
GACCAGGAGACACGGAATATGAAGGCCACTCACAGACTGACCGAGCGAACCTGGGGACC
CTGCGCGGCTACTACAACCAGAGCGAGGGCA

>K8RV
TTTTTCAGCCACTGCTCGCCCCAGGGTCCCCTTCCATTAGGGATTTTCTTCACATCCG
TGTCGCCGCCCGGCCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGC
AGTTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAAGATGGAGCCGCGGGCGCCGTGGA
TAGAGCAGGAGGGGCCGAGTATTGGGACCAGGTGTGAGCCACTGCTACCCGCACTAGG
CACACCGTGCGATGTCAGCCATCGTGCACTCG

CLUSTAL 2.1 multiple sequence alignment

K8FW      ---ACTAGCCA--GGACG-----AGGG-----CACTATGTACTTACCTTTTA--G 38
K8RV      TTTTTCAGCCACTGCTCGCCCCAGGGTCCCCTTCCATTAGGGATTTTCTTCACATCCG 60
           ***** * **          ***** ** * * * * * * * *

K8FW      TTTCCCTA--CAAC-GAGGGGAAGGGCACTTCATCGCCGTGGGCTACGTGGACGACACGC 94
K8RV      TGTCGCCGCCCGGCCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGC 120
           * ***      * * * * * * * * * * * * * * * * * * * * * *

K8FW      AGTTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAAGATGGAGCCGCGGGCGCCGTGGA 154
K8RV      AGTTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAAGATGGAGCCGCGGGCGCCGTGGA 180
           *****

K8FW      TAGAGCAGGAGGGGCCGAGTATTGGGACCAGGAGACACGGAATATGAAGGCCCACTCAC 214
K8RV      TAGAGCAGGAGGGGCCGAGTATTGGGACCAGGTGTCA-----GCCACTGCTACCCGC 234
           ***** * **          * * * * * *

K8FW      AGACTGACCGAGCGAACCTGGGGACCTGCGCGGCTACTACAACCAGAGCGAGGGCA 271
K8RV      -----ACTAGGCACACCGTGCGATGTCA-GCCATCGCTGCACTCG----- 273
           **      ** * * * * * * * * * * * *

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>K8SeqCons
TTTTTCAGCCACTGCTCGCCCCCAGGGTCCCCTTCCATTAGGGATTTTCTTCACATC
CGTGTCCCGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGAC
ACGCAGTTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAAGATGGAGCCGCGGGGCGC
CGTGGATAGAGCAGGAGGGGCGGAGTATTGGGACCAGGAGACACGGAATATGAAGGC
CCACTCACAGACTGACCGAGCGAACCTGGGGACCCTGCGCGGCTACTACAACCAGAGC
GAGGGCA

>IMGTHLA:HLA00004 A*01:04N 1099 bp
    Length = 1099

    Plus Strand HSPs:

    Score = 1295 (200.4 bits), Expect = 4.8e-55, P = 4.8e-55, Group = 1
    Identities = 267/274 (97%), Positives = 267/274 (97%), Strand = Plus / Plus

Query:    23 CAGGGTCCCCTTCCATTAGGGATTTTCTTCACATCCGTGTCCCGGCCCGGCCGCGGGGA 82
          | || ||||| ||| || ||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:    71 CGGGTCCCCT-CCATGAGGTATTT-CTTCACATCCGTGTCCCGGCCCGGCCGCGGGGA 128

Query:    83 GCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGA 142
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:    129 GCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGA 188

Query:    143 CGCCGCGAGCCAGAAGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGAGTA 202
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:    189 CGCCGCGAGCCAGAAGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGAGTA 248

Query:    203 TTGGGACCAGGAGACACGGAATATGAAGGCCCTCACAGACTGACCGAGCGAACCTGGG 262
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:    249 TTGGGACCAGGAGACACGGAATATGAAGGCCCTCACAGACTGACCGAGCGAACCTGGG 308

Query:    263 GACCCTGCGCGGCTACTACAACCAGAGCGAGGGC 296
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:    309 GACCCTGCGCGGCTACTACAACCAGAGCGAGGGAC 342

A2-2/1

>K8FW
TCCCTTCTGCTGAGTATTTCTTCCATCCGTGTCCCGGCCCGGCCGCGGGGAGCCCC
GCTTCATCGCAGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGAC
GCCGCGAGCCCGAGGGGGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGGA
GTATTGGGACGGGAGACACGGAAGTGAAGGCCCTCACAGACTGACCGAGTGA
ACCTGGGGACCTGCGCGGCTACTACAACCAGAGCGAGGACAG

>K8RV
TCTCAGCCACTCCTCGTCCCCAGGCTCCCCTCCATGAGGTATTTCTTCACATCCG
TGTCCCGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGAC
ACGCAGTTCGTGCGGTTTCGACAGCGACGCCGCGAGCCCAAGGTTGGAGCCGCGGGC
GCCGTGGATAGAGCAGGAGGGTCCGAGTATTGGGACGGGGAGACACGGAAGGAA
GGCCACGCACAGACTCACCGAAGAACTGGGGAATCCGT

CLUSTAL 2.1 multiple sequence alignment

K8FW      -----TCCC-----TTCTGCT-----GAGTATTTCTTC-CATCCGTGTC 33
K8RV      TCTCAGCCACTCCTCGTCCCCAGGCTCCCCTCCATGAGGTATTTCTTCACATCCGTGTC 60
          ****          *  *  *          *****

K8FW      CCGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGTT 93
K8RV      CCGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGTT 120
          *****

K8FW      CGTGCGGTTTCGACAGCGACGCCGCGAGCCCAAGGTTGGAGCCGCGGGCGCCGTGGATAGA 153
K8RV      CGTGCGGTTTCGACAGCGACGCCGCGAGCCCAAGGTTGGAGCCGCGGGCGCCGTGGATAGA 180
          *****

K8FW      GCAGGAGGGGCCGAGTATTGGGACGGGGAGACACGGAAGTGAAGGCCCTCACAGAC 213
K8RV      GCAGGAGGGTCCGAGTATTGGGACGGGGAGACACGGAAG-GAAGGCCACGCACAGAC 239
          *****

K8FW      TGACCGAGTGAACCTGGGGACCCTGCGCGGCTACTACAACCAGAGCGAGGACAG 267

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K8RV          TCACCGAA-GAACTGGGGAAGTCCGT----- 264
              * * * * * * * * * *

>K8SeqCons
TCTCAGCCACTCCTCGTCCCCAGGCTCCCACTCCATGAGGTATTTCTTCCATCC
GTGTCGCGGCGCGGCGCGGGGAGCCCCGCTTCATCGCAGTGGGTACGTGGAC
GACACGCAGTTCGTGCGGTTCGACAGCGACGCCGCGAGCCGAGGGGGAGCCG
CGGGCGCGGTGGATAGAGCAGGAGGGGCGGAGTATTGGGACGGGAGACACGG
AAAGTGAAGGCCCACTCACAGACTGACCGAGTGAACCTGGGGACCCTGCGCGGC
TACTACAACCAGAGCGAGGACAG

>IMGTHLA:HLA05978 A*01:83 546 bp
      Length = 546

      Plus Strand HSPs:

      Score = 1277 (197.7 bits), Expect = 6.3e-54, P = 6.3e-54, Group = 1
      Identities = 263/271 (97%), Positives = 263/271 (97%), Strand = Plus / Plus

Query:      24 GCTCCCACTCCATGAGGTATTTCTTC-CATCCGTGTCCCGGCCCGCGGGGAGCCCC 82
      |||
Sbjct:      1 GCTCCCACTCCATGAGGTATTTCTTCACATCCGTGTCCCGGCCCGCGGGGAGCCCC 60

Query:      83 GCTTCATCGCAGTGGGTACGTGGACGACACGAGTTCGTGCGGTTCGACAGCGACGCCG 142
      |||
Sbjct:      61 GCTTCATCGCGGTGGGTACGTGGACGACACGAGTTCGTGCGGTTCGACAGCGACGCCG 120

Query:     143 CGAGCCCGAGGGGGAGCCGCGGGCGCGGTGGATAGAGCAGGAGGGGCCGAGTATTGGG 202
      |||
Sbjct:     121 CGAGCCAGAAGATGGAGCCGCGGGCGCGGTGGATAGAGCAGGAGGGGCCGAGTATTGGG 180

Query:     203 ACGGGGAGACACGGAAGTGAAGGCCCACTCACAGACTGACCGAGTGAACCTGGGGACCC 262
      |||
Sbjct:     181 ACGGGGAGACACGGAAGTGAAGGCCCACTCACAGACTGACCGAGCGAACCTGGGGACCC 240

Query:     263 TGC GCGGCTACTACAACCAGAGCGAGGACAG 293
      |||
Sbjct:     241 TGC GCGGCTACTACAACCAGAGCGAGGACGG 271

A3-1/2

>K8FW
CTAACGCCTCCTAGCAGGGGTACGCATGGCGCTTCCGACGCGGTACCACCAGTACGCCT
ACGACGGCAAGGATTACATCGCCCTGAAAGAGGACCTGCGCTCTTGGACCGCGCGGACA
TGGCAGCTCAGACCACCAAGCACAAAGTGGGAGGCGGCCATGTGGCGGAGCAGTTGAGAG
CTTACCTGGAGGGCAGTGCCTGGAGTGGCTCCGCAGATACCTGGAGAACGGGAAGA

>K8RV
ATTTTCTCACACCGTCCAGAGGATGTATGGCTGCGACGTGGGGTTCGACTGGCGCTTCCT
CCGCGGGTACCACCAGTACGCCTACGACGGCAAGGATTACATCGCCCTGAAAGAGGACCT
GCGCTCTTGGACCGCGGCGGACATGGCAGCTCAGACCACCAAGCACAAAGTGGGAGGCGGC
CCATGTGGCGGAGCGAGTTCGAGCCTACCGGAGGGCACCTCGCGCAGACTGGCT

CLUSTAL 2.1 multiple sequence alignment

K8FW          -----CTAACGCCTCCTAGCAGGGGTACG-----CATGG-----CGCTTCCG 37
K8RV          ATTTTCTCACACCGTCCAGAGGATGTATGGCTGCGACGTGGGGTTCGACTGGCGCTTCCT 60
              * * * * * * * * * * * * * * * * * * * * * * * *

K8FW          ACGCGGGTACCACCAGTACGCCTACGACGGCAAGGATTACATCGCCCTGAAAGAGGACCT 97
K8RV          CCGCGGGTACCACCAGTACGCCTACGACGGCAAGGATTACATCGCCCTGAAAGAGGACCT 120
              * * * * * * * * * * * * * * * * * * * * * * * *

K8FW          GCGCTCTTGGACCGCGGCGGACATGGCAGCTCAGACCACCAAGCACAAAGTGGGAGGCGGC 157
K8RV          GCGCTCTTGGACCGCGGCGGACATGGCAGCTCAGACCACCAAGCACAAAGTGGGAGGCGGC 180
              * * * * * * * * * * * * * * * * * * * * * * * *

K8FW          CCATGTGGCGGAGCAGTTGAGAGCCTACCTGGAGGGCACGT-GCGTGGAGTGGCTCCGCA 216
K8RV          CCATGTGGCGGAGCAGTTGAGAGCCTACC-GGAGGGCACCTCGCGCAGACTGGCT----- 234
              * * * * * * * * * * * * * * * * * * * * * * * *

K8FW          GATACCTGGAGAACGGGAAGA 237
K8RV          -----

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>K8SeqCons
ATTTTCTCACACCGTCCAGAGGATGTATGGCTGCGACGTGGGGTCGGAAGGCTTC
CGACGCGGGTACCACCAAGTACGCTACGACGGCAAGGATTACATCGCCCTGAAAGAGG
ACCTGCGCTCTTGGACCGCGGGCGGACATGGCAGCTCAGACCACCAAGCACAAGTGGGA
GGCGGCCCATGTGGCGGAGCAGTTGAGAGCCTACCTGGAGGGCACGTGCGTGGAGTGG
CTCCGCAGATACCTGGAGAACGGGAAGA

>IMGTHLA:HLA01218 A*02:43N 1099 bp
    Length = 1099

    Plus Strand HSPs:

    Score = 1262 (195.4 bits), Expect = 1.5e-53, P = 1.5e-53, Group = 1
    Identities = 254/256 (99%), Positives = 254/256 (99%), Strand = Plus / Plus

Query:      4 TTCTCACACCGTCCAGAGGATGTATGGCTGCGACGTGGGGTCGGAAGGCTTCCTCCAGC 63
            |||
Sbjct:     345 TTCTCACACCGTCCAGAGGATGTATGGCTGCGACGTGGGGTCGGAAGGCTTCCTCCG 404

Query:      64 CGGGTACCACCAAGTACGCTACGACGGCAAGGATTACATCGCCCTGAAAGAGGACCTGCG 123
            |||
Sbjct:     405 CGGGTACCACCAAGTACGCTACGACGGCAAGGATTACATCGCCCTGAAAGAGGACCTGCG 464

Query:     124 CTCTTGGACCGCGGGCGGACATGGCAGCTCAGACCACCAAGCACAAGTGGGAGGCGGCCCA 183
            |||
Sbjct:     465 CTCTTGGACCGCGGGCGGACATGGCAGCTCAGACCACCAAGCACAAGTGGGAGGCGGCCCA 524

Query:     184 TGTGGCGGAGCAGTTGAGAGCCTACCTGGAGGGCACGTGCGTGGAGTGGCTCCGCAGATA 243
            |||
Sbjct:     525 TGTGGCGGAGCAGTTGAGAGCCTACCTGGAGGGCACGTGCGTGGAGTGGCTCCGCAGATA 584

Query:     244 CCTGGAGAACGGGAAG 259
            |||
Sbjct:     585 CCTGGAGAACGGGAAG 600

A3-2/2

>K8FW
CCGCGGTACTGTAGTACGGGCGAGCCGGGCACACGGGAAGAGGGTACCGGCAGGA
CGCCTACGACGGCAAGGATTACATCGCCCTGAACGAGGACCTGCGCTCTTGGAC
CGCGGCGGACATGGCAGCTCAGATCACCAGCGCAAGTGGGAGGCGGTCCATGC
GGCGGAGCAGCGGAGAGTCTACCTGGAGGGCCGGTGCGTGACGGGCTCCGCAG
ATACCTGGAGAACGGGAAGATC

>K8RV
TGATGGTTCTCACACCATCCAGATAATGTATGGCTGCGACGTGGGGCCGGACGG
GCGCTTCTCCGCGGGTACCGGCAGGACGCCTACGACGGCAAGGATTACATCGC
CCTGAACGAGGACCTGCGCTCTTGGACCGCGGGCGGACATGGCAGCTCAGATCAC
CAAGCGCAAGTGGGAGACGGCCCATGGCCTGCGCCACGATCTCCCCCGGCCAG
GTGCTACGCTATCACAGACT

CLUSTAL 2.1 multiple sequence alignment

K8FW      CCGCGGTACT-----GTA--GTACGG--GCAGC--CGGG--CACACGGGAA--- 38
K8RV      TGATGGTTCTCACACCATCCAGATAATGTATGGCTGCGACGTGGGGCCGGACGGGCGCTT 60
            ***  **                **  **  **  **  *  ***  *  *****

K8FW      -----GAGGGTACCGGCAGGACGCCTACGACGGCAAGGATTACATCGCCCTGAACGAGGA 93
K8RV      CCTCCGCGGGTACCGGCAGGACGCCTACGACGGCAAGGATTACATCGCCCTGAACGAGGA 120
            *  *****

K8FW      CCTGCGCTCTTGGACCGCGGGCGGACATGGCAGCTCAGATCACCAGCGCAAGTGGGAGGC 153
K8RV      CCTGCGCTCTTGGACCGCGGGCGGACATGGCAGCTCAGATCACCAGCGCAAGTGGGAGAC 180
            *****

K8FW      GGTCCATGCGGCGGAGCAGCGGAGAGTCTACCTGGAGGGCCGGTGCGTGGACGGGCTC-C 212
K8RV      GGCCCATG--GCCTGCGCCACG----ATCTCCCC--CCGCCAGGTG-----CTCAC 224
            **  *****  *  *  *  **  **  **  **  ***  ***  ***  *

K8FW      GCAGATACCTGGAGAACGGGAAGATC 238
K8RV      GC---TATC-----AC---ACGACT 238

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K10FW GCAGGAGGGGCGGAGTATTGGGACCAGGAGACACGGAATATGAAGGCCCACTCACAGAC 214
 K10RV GCAGGAGGGGCGGAGTATTGGGACCAGGAGACACGGAATG-GAAGGCCCACTCACAGAC 239

K10FW TGACCGAGTGAACCTGGGGACCTGCGCGGCTACTACAACCAGACGAGGACT 266
 K10RV -GACCGAGCGAACC--GGGATCT--GCCGCT----- 265
 ***** ** *

>K10SeqCons

TCTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTATTTCTTCCATCCGTGTC
 CCGGCCCCGGCCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGT
 TCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAAGATGGAGCCGCGGGCGCCGTGGATA
 GAGCAGGAGGGGCGGAGTATTGGGACCAGGAGACACGGAATATGAAGGCCCACTCACA
 GACTGACCGAGTGAACCTGGGGACCTGCGCGGCTACTACAACCAGACGAGGACT

>IMGTHLA:HLA00004 A*01:04N 1099 bp
 Length = 1099

Plus Strand HSPs:

Score = 1312 (202.9 bits), Expect = 8.2e-56, P = 8.2e-56, Group = 1
 Identities = 268/272 (98%), Positives = 268/272 (98%), Strand = Plus / Plus

Query: 21 CAGGCTCCCACTCCATGAGGTATTTCTTTC-CATCCGTGTCCCGCCCCGGCCGGGGAGC 79
 | |||||
 Sbjct: 71 CGGGCTCCCACTCCATGAGGTATTTCTTTCACATCCGTGTCCCGCCCCGGCCGGGGAGC 130
 Query: 80 CCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACG 139
 |||||
 Sbjct: 131 CCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACG 190
 Query: 140 CCGCAGCCAGAAGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGCCGGAGTATT 199
 |||||
 Sbjct: 191 CCGCAGCCAGAAGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGCCGGAGTATT 250
 Query: 200 GGGACCAGGAGACACGGAATATGAAGGCCCACTCACAGACTGACCGAGTGAACCTGGGGA 259
 |||||
 Sbjct: 251 GGGACCAGGAGACACGGAATATGAAGGCCCACTCACAGACTGACCGAGCGAACCTGGGGA 310
 Query: 260 CCCTGCGCGGCTACTACAACCAGA-CGAGGAC 290
 |||||
 Sbjct: 311 CCCTGCGCGGCTACTACAACCAGAGCGAGGAC 342

A2-2/2

>K10FW

TTCTTCCTGAGGAATGTGAGAACACGCCCAGTACAGGCGCTCCGCCTGGAGACCCTATTC
 ATCTAACTAGGGACAGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACGCCGCGAGT
 CCGAGGGAGGAGCCGCGGGCGCGGTGGATAGAGCAGGAGGGGCCGGAGTATTGGGACCGG
 AACACACAGAATTCAAGACCAACACACAGACTGACCGAGAGAGCCTGCGGAACCTGCGC
 GGCTACTACAACCAGAGCGAGGGC

>K10RV

TCTCAGCCACTCCTCGTCCCCAGGCTCCCACTCCATGAGGTATTTTCGACACCGCCATGTC
 CCGGCCCCGGCCGGGGAGCCCCGCTTTCATCTCAGTGGGCTACGTGGACGACACGCAGT
 TCGTGCGGTTTCGACAGCGACGCCGCGGATTCCGAGAGAGGAGCCGCGGGCGCCGTGGATAG
 AGCAGGAGGGGCCGGAGTATCGGGACTGGTACACACGGCAGGCAAGGCCCGCCACACT
 TCCGACGACAGCTCGTACTCCTCG

CLUSTAL 2.1 multiple sequence alignment

K10FW -----TTCTTCCTGAGG-----AAT--GTGAGA-----ACACGCCCA-GTA 33
 K10RV TCTCAGCCACTCCTCGTCCCCAGGCTCCCACTCCATGAGGTATTTTCGACACCGCCATGTC 60
 * * * * *
 K10FW CAGGCGCT-CCGCCTGGAGACCC-TATTCATCTAACTAGGGACAGTGGACGACACGCAGT 91
 K10RV CCGGCCCCGGCCGGGGAGCCCCGCTTTCATCTCAGTGGGCTACGTGGACGACACGCAGT 120
 * * * * *
 K10FW TCGTGCGGTTTCGACAGCGACGCCGCGAGTCCGAGGGAGGAGCCGCGGGCGCCGTGGATAG 151
 K10RV TCGTGCGGTTTCGACAGCGACGCCGCGGATTCCGAGAGAGGAGCCGCGGGCGCCGTGGATAG 180

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*****
K10FW      AGCAGGAGGGGCCGAGTATTGGGACCGGAACACACAGAACTTCAAGACCAACACACAGA 211
K10RV      AGCAGGAGGGGCCGAGTATCGGGACTGGTACACACGGCAGG-CAAGGCCC-CGCCACACA 238
*****

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K10FW      CTGACCGAGAGAGCCTGCGGAACCTGCGCGGCTACTACAACCAGAGCGAGGGC 264
K10RV      CTT-CCG-----CAGCAGA-----CGTCGCTACTCC--TCG----- 266
**   ***           *   *   *   **   *   *   *   *

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>K10SeqCons
TCTCAGCCACTCCTCGTCCCCAGGCTCCCACTCCATGAGGTATTTTCGACACCGCCATGTCC
CGGCCCCGGCCGCGGGGAGCCCCGCTTTCATCTCAGTGGGTACGTGGACGACACGCAGTTC
GTGCGGTTTCGACAGCGACGCCGCGAGTCCGAGGGAGGAGCCGCGGGCGCCGTGGATAGAGC
AGGAGGGGCCGAGTATTGGGACCGGAACACACAGAACTTCAAGACCAACACACAGACTGA
CCGAGAGAGCCTGCGGAACCTGCGCGGCTACTACAACCAGAGCGAGGGC

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Not HLA-A result.

A2-1/2

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>K10FW
AGGCACCATCATGAGGTATTTCTTCCATCCGTGTCCCGGCCCGGGCCGCGGGGAGCCCCGCT
TCATCGCCGTGGGTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACGCCGCGAG
CCAGAAGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGAGTATTGGGACCAG
GAGACACGGAATATGAAGGCCCACTCACAGACTGACCGAGCGAACCTGGGGACCCTGCGCG
GCTACTACAACCAGAGCGAGGG

```

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>K10RV
CACAAACCCGTGTCCCGGGCCGCGGGGAGCCCCGCTTCATCGCCGTGGGTACGTGG
ACGACACGCAGTTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAAGATGGAGCCGCGGGC
GCCGTGGATAGAGCAGGAGGGGCCGAGTATTGGGACCAGGAGACACGGAATATGAAGGCC
CACTCACAGACGAGCGAGCGAACCGGGGACCTGCGG

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CLUSTAL 2.1 multiple sequence alignment

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K10FW      AGGCACCATCATGAGGTATTTCTTCCATCCGTGTCCCGGCCCGG-CCGCGGGGAGCCCCG 59
K10RV      -----CACAA-----CCCGTGTCCCGGCCCGGGCCGCGGGGAGCCCCG 38
              **   *               *****   ****   *****
K10FW      CTTATCGCCGTGGGTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACGCCG 119
K10RV      CTTATCGCCGTGGGTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACGCCG 98
*****
K10FW      GAGCCAGAAGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGAGTATTGGGA 179
K10RV      GAGCCAGAAGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGAGTATTGGGA 158
*****
K10FW      CCAGGAGACACGGAATATGAAGGCCCACTCACAGACTGACCGAGCGAACCTGGGGACCCT 239
K10RV      CCAGGAGACACGGAATATGAAGGCCCACTCACAGAC-GACGGAGCGAAC-GGGGACC-- 214
*****
K10FW      GCGCGGCTACTACAACCAGAGCGAGGG 266
K10RV      -TGGG----- 219
              ****

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>K10SeqCons
AGGCACCATCATGAGGTATTTCTTCCATCCGTGTCCCGGCCCGGGCCGCGGGGAGCCCCGCT
TCATCGCCGTGGGTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACGCCGCGAG
CCAGAAGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGAGTATTGGGACCAG
GAGACACGGAATATGAAGGCCCACTCACAGACTGACCGAGCGAACCTGGGGACCCTGCGCG
GCTACTACAACCAGAGCGAGGG

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>IMGTHLA:HLA00004 A*01:04N 1099 bp
Length = 1099

Plus Strand HSPs:

Score = 1271 (196.8 bits), Expect = 5.8e-54, P = 5.8e-54, Group = 1
Identities = 263/268 (98%), Positives = 263/268 (98%), Strand = Plus / Plus

Query: 2 GGCACC-A-TC-ATGAGGTATTTCTTC-CATCCGTGTCCCGGCCCGGGGAGCCC 57


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>K10RV
TGGTTCTCACACCGTCCAGATAATGTATGGCTGCGACGTGGGGCCGGACGGGCGCTTCCT
CCGCGGGTACCGGCAGGACGCCCTACGACGGCAAGGATTACATCGCCCTGAACGAGGACCT
GCGCTCTTGGACCGCGGCGGACATGGCAGCTCAGATCACCAAGCGCAAGTGGGAGGCGGC
CCATGCGGCGGAGCAGCGGAGATCTACCTAGGCAAGGCGAT
```

CLUSTAL 2.1 multiple sequence alignment

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K10FW      TTGG-----AATG-----CGA-GTGGGGCCGA-GGGCGCTTCC 32
K10RV      -TGGTTCTCACACCGTCCAGATAATGTATGGCTGCGACGTGGGGCCGGACGGGCGCTTCC 59
          ***                ****                *** *****

K10FW      TCCGCGGGTACCGGCAGGACGCCCTACGACGGCA-GGATTACATCGCCCTGAACGAGGACC 91
K10RV      TCCGCGGGTACCGGCAGGACGCCCTACGACGGCAAGGATTACATCGCCCTGAACGAGGACC 119
          *****

K10FW      TGGCTCTTGGACCGCGGCGGACATGGCAGCTCAGATCACCAAGCGCAAGTGGGAGGCGG 151
K10RV      TGGCTCTTGGACCGCGGCGGACATGGCAGCTCAGATCACCAAGCGCAAGTGGGAGGCGG 179
          *****

K10FW      TCCATGCGGCGGAGCAGCGGAGAGTCTACCTGGAGGGCCGGTGCGTGACGGGCTCCGCA 211
K10RV      CCCATGCGGCGGAGCAGCGGAGA-TCTACCTAG-----GCA 214
          ***** *

K10FW      AATACCTGGAGAACGGGAAGA 233
K10RV      A-----GGCGAT----- 221
          *      ** **
```

```
>K10SeqCons
TGGTTCTCACACCGTCCAGATAATGTATGGCTGCGACGTGGGGCCGGAGGGCGCTTCCT
CCGCGGGTACCGGCAGGACGCCCTACGACGGCAGGATTACATCGCCCTGAACGAGGACCT
GCGCTCTTGGACCGCGGCGGACATGGCAGCTCAGATCACCAAGCGCAAGTGGGAGGCGG
TCCATGCGGCGGAGCAGCGGAGAGTCTACCTGGAGGGCCGGTGCGTGACGGGCTCCGC
AAATACCTGGAGAACGGGAAGA
```

```
>IMGTHLA:HLA00004 A*01:04N 1099 bp
Length = 1099
```

Plus Strand HSPs:

```
Score = 1234 (191.2 bits), Expect = 2.7e-52, P = 2.7e-52, Group = 1
Identities = 254/260 (97%), Positives = 254/260 (97%), Strand = Plus / Plus
```

```
Query:      2 GGTTCCTCACACCGTCCAGATAATGTATGGCTGCGACGTGGGGCCGA-GGGCGCTTCCTC 60
             ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     343 GGTTCCTCACACCATCCAGATAATGTATGGCTGCGACGTGGGGCCGGACGGGCGCTTCCTC 402

Query:      61 CGCGGGTACCGGCAGGACGCCCTACGACGGCA-GGATTACATCGCCCTGAACGAGGACCTG 119
             ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     403 CGCGGGTACCGGCAGGACGCCCTACGACGGCAAGGATTACATCGCCCTGAACGAGGACCTG 462

Query:     120 CGCTCTTGGACCGCGGCGGACATGGCAGCTCAGATCACCAAGCGCAAGTGGGAGGCGGTC 179
             ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     463 CGCTCTTGGACCGCGGCGGACATGGCAGCTCAGATCACCAAGCGCAAGTGGGAGGCGGTC 522

Query:     180 CATGCGGCGGAGCAGCGGAGAGTCTACCTGGAGGGCCGGTGCGTGACGGGCTCCGCAAA 239
             ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     523 CATGCGGCGGAGCAGCGGAGAGTCTACCTGGAGGGCCGGTGCGTGACGGGCTCCGCGAGA 582

Query:     240 TACCTGGAGAACGGGAAGA 259
             ||| | | | | | | | | | | |
Sbjct:     583 TACCTGGAGAACGGGAAGGA 602
```

A3-2/2

```
>K10FW
CGGCTGGAGTGGGGCCGGAGGGCGCTTCCTCCGCGGGTACCGGCAGGACGCCCTACGACG
GCAGGATTACATCGCCCTGAACGAGGACCTGCGCTCTTGGACCGCGGCGGACATGGCAG
CTCATATACCAAGCGCAAGTGGGAGGCGGTCCATGCGGCGGAGCAGCGGAGAGTCTAC
CTGGAGGGCCGGTGCGTGACGGGCTCCGCGAGATACCTGGAGAACGGGAAGA
```

>K10RV

TGATGGTTCTCACACCATCCAGATAATGTATGGCTGCGACGTGGGGCCGGACGGGCGCT
 TCCTCCGCGGGTACCGGCAGGACGCCTACGACGGCAAGGATTACATCGCCCTGAACGAG
 GACCTGCGCTCTTGGACCGCGGCGGACATGGCAGCTCAGATCACCAAGCGCAAGTGGAG
 GCGGTCCATGCGGCGGAGCAGCGGAGAGCCTACCGGAGGGCCAGGCTCCAGTCCT

CLUSTAL 2.1 multiple sequence alignment

```

K10FW      -----CGGCTG-GA-GTGGGGCCGGA-GGGCGCTT  27
K10RV      TGATGGTTCTCACACCATCCAGATAATGTATGGCTGCGACGTGGGGCCGGACGGGCGCTT  60
              ***** ** *****
K10FW      CCTCCGCGGGTACCGGCAGGACGCCTACGACGGCA-GGATTACATCGCCCTGAACGAGGA  86
K10RV      CCTCCGCGGGTACCGGCAGGACGCCTACGACGGCAAGGATTACATCGCCCTGAACGAGGA 120
              *****
K10FW      CCTGCGCTCTTGGACCGCGGCGGACATGGCAGCTCATATCACCAAGCGCAAGTGGGAGGC 146
K10RV      CCTGCGCTCTTGGACCGCGGCGGACATGGCAGCTCAGATCACCAAGCGCAAGTGG-AGGC 179
              *****
K10FW      GGTCCATGCGGCGGAGCAGCGGAGAGTCTACCTGGAGGGCCGGTGCCTGGACGGGCTCCG 206
K10RV      GGTCCATGCGGCGGAGCAGCGGAGAGCCTACC-GGAGGGCCAG-----GCTCC- 226
              *****
K10FW      CAGATACCTGGAGAACGGGAAGA 229
K10RV      ---AGTCCT----- 232
              *  ***
  
```

>K10SeqCons

TGATGGTTCTCACACCATCCAGATAATGTATGGCTGGAGTGGGGCCGGAGGGCGCTT
 CCTCCGCGGGTACCGGCAGGACGCCTACGACGGCAGGATTACATCGCCCTGAACGAG
 GACCTGCGCTCTTGGACCGCGGCGGACATGGCAGCTCATATCACCAAGCGCAAGTGG
 GAGGCGGTCCATGCGGCGGAGCAGCGGAGAGTCTACCTGGAGGGCCGGTGCCTGGAC
 GGGCTCCGCAGATACCTGGAGAACGGGAAGA

>IMGTHLA:HLA00004 A*01:04N 1099 bp
 Length = 1099

Plus Strand HSPs:

Score = 1227 (190.1 bits), Expect = 5.7e-52, P = 5.7e-52, Group = 1
 Identities = 255/261 (97%), Positives = 255/261 (97%), Strand = Plus / Plus

```

Query:      2  GATGGTTCTCACACCATCCAGATAATGTATGGCTG-GA-GTGGGGCCGGA-GGGCGCTTC  58
              || |||||
Sbjct:     340 GACGGTTCTCACACCATCCAGATAATGTATGGCTGCGACGTGGGGCCGGACGGGCGCTTC 399

Query:      59  CTCCGCGGGTACCGGCAGGACGCCTACGACGGCA-GGATTACATCGCCCTGAACGAGGAC 117
              |||||
Sbjct:     400 CTCCGCGGGTACCGGCAGGACGCCTACGACGGCAAGGATTACATCGCCCTGAACGAGGAC 459

Query:     118  CTGCGCTCTTGGACCGCGGCGGACATGGCAGCTCATATCACCAAGCGCAAGTGGGAGGCG 177
              |||||
Sbjct:     460 CTGCGCTCTTGGACCGCGGCGGACATGGCAGCTCAGATCACCAAGCGCAAGTGGGAGGCG 519

Query:     178  GTCCATGCGGCGGAGCAGCGGAGAGTCTACCTGGAGGGCCGGTGCCTGGACGGGCTCCGC 237
              |||||
Sbjct:     520 GTCCATGCGGCGGAGCAGCGGAGAGTCTACCTGGAGGGCCGGTGCCTGGACGGGCTCCGC 579

Query:     238  AGATACCTGGAGAACGGGAAG 258
              |||||
Sbjct:     580 AGATACCTGGAGAACGGGAAG 600
  
```

A4-2/2H

>K10FW

CACCATGAGCGAGTTAACTCGAGAGCTTTATTTTTGTAGTCTGTAGCTGAGCCCA
 GCTGAGTGCTGGGCCCTGGGCTTCTACCCTGCGGAGATCACACTGACCTGGCAGCGG
 GATGGGGAGGACCAGACCCAGGCACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGA
 TAT

>K10RV

ATACCCTCAGACTCGTGTCCACGAGCTCCGTGTCTGGGGTCTTGGCCCCGCAAGG

ACACATATGACCCCCACCTCATTTTTTACCATTAGGCCACCCTGAGGTGGTTGGAA
CCTTGGCTTCTACCCTTGGGAGATCACAC

CLUSTAL 2.1 multiple sequence alignment

```

K10FW      -CACCATGAG---CGAGTTAACTCGAGAGCTTTATTTTTTGTAGTCTGTTAGCTGAGCCC 56
K10RV      ATACCCTCAGACTCGTGTCCAC----GAGCTCCGTGTCTGG-GGTCC-TTGGCC---CCC 51
           *** * **  ** **  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
K10FW      AGCTGAGTGC--TGGGCCCTGGGCTTCTACCCTGCGG--AGATCACACTGACCTGGCAG 111
K10RV      GCAAGGACACATATGACCCCCACCTCATTTTTTACCATTAGGCCACCCTGA---GGTGG 108
           *  *  **  ***  **  *  *  *  *  **  ***  *  *  *
K10FW      CGGGATGGGGAGGACCAGACCCAGGCACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGA 171
K10RV      TTGGA-----ACCTTGGC-TTCTACCCTTG-GGAGATCACAC----- 143
           ***          ***  ***  *  *  *  *  *  *  *  *
K10FW      TAT 174
K10RV      ---

```

Not analyzed.

A4-3H/1

```

>K10FW
TGGCTGGCGCGGCTGGGGAGGACCGGCCCGGCACACGGAGCTCGTGGACACAGGC
CTGCAGGGGATGGAACCTTCCAAAATTGGGCGGTTGTGGTGGTGCCTTTTGAAA
GGAGCAAAGTTACACCTGCCATGTGCAGCATGAGGGTTTGCCCAAGCCCTCACC
CTGAAATGGACG

```

```

>K10RV
TTTTTTACCCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGACCAGAC
CCAGGACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGATGGAACCTTCCAGAAG
TGGGCGCGCTGTGGTGGTGCCTTCGGAGAGGAGCAGAGATACACCTGCCATGTGC
AGCATAGTGCTGCG

```

CLUSTAL 2.1 multiple sequence alignment

```

K10FW      -----TGGC-TGGC-GCGGC-TGGGGAGGACCGG-CCCGGC 32
K10RV      TTTTTTACCCTGCGGAGATCACACTGGCTGGCAGCGGGATGGGGAGGACCAGACCAG 60
           *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
K10FW      ACACGGAGCTCGTGGACAC-AGGCCTGCAGGGGATGGAACCTTCCAAAATTGGGCG-GTT 90
K10RV      ACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGATGGAACCTTCCAGAAGTGGGCGCGCT 120
           *****  *  *****  *  *****  *  *****  *  *
K10FW      GTGGTGGTGCCTTTTGAAAGGAGCAAAGTTACACCTGCCATGTGCAGCATGAGGGTTTG 150
K10RV      GTGGTGGTGCCTTC-GGAGAGGAGCAGAGATACACCTGCCATGTGCAGCAT-AGTGCT-- 176
           *****  ***  *****  *  *****  *  *  *  *
K10FW      CCCAAGCCCCTCACCTGAAATGGACG 177
K10RV      -----GCG 179
           **

```

```

>K10SeqCons
TTTTTTACCCTGCGGAGATCACACTGGCTGGCGCGGCTGGGGAGGACCGGCCCGG
CACACGGAGCTCGTGGACACAGGCCTGCAGGGGATGGAACCTTCCAAAATTGGGC
GGTTGTGGTGGTGCCTTTTGAAAGGAGCAAAGTTACACCTGCCATGTGCAGCAT
GAGGGTTTGCCCAAGCCCTCACCTGAAATGGACG

```

>IMGTHLA:HLA02509 A*02:97:01 822 bp
Length = 822

Plus Strand HSPs:

Score = 804 (126.7 bits), Expect = 9.7e-33, P = 9.7e-33, Group = 1
Identities = 182/201 (90%), Positives = 182/201 (90%), Strand = Plus / Plus

```

Query:      3 TTTTACCCTGCGGAGATCACACTGGC-TGGC-GCGGC-TGGGGAGGACCGG-CCCGGCAC 58
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```



```

Sbjct: 133 |||||CGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACGCC 192
Query: 118 GCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGGAGTATTGG 177
Sbjct: 193 |||||GCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGGAGTATTGG 252
Query: 178 GACCAGGAGACACGGAATGTGAAGGCCAGTCACAGACTGACCGAGCGGACCTGGGGACC 237
Sbjct: 253 |||||GACCAGGAGACACGGAATGTGAAGGCCAGTCACAGACTGACCGAGTGGACCTGGGGACC 312
Query: 238 CTGCGCGGCTACTACAACCAGAGCGAGG 265
Sbjct: 313 |||||CTGCGCGGCTACTACAACCAGAGCGAGG 340

```

K11 26-04

A2-1/1

```

>K11FW
AAACGCGTACTACAGGTTCCCTTACTCACTTCCGTGTATCCGTCTACAACGAGGAGGAAG
CCACACTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGAC
GCCGCGAGCCAGAAGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGGAGTAT
TGGGACCAGGACACACGGAATATGAAGGCCCACTCACAGACTGACCGAGCGAACCTGGGG
ACCCTGCGCGGCTACTACAACCAGAGCGAGGACA

```

```

>K11RV
TCTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTATTTCTTCACATCCGTGTC
CCGGCCCGGCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTT
CGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAAGATGGAGCCGCGGGCGCCGTGGATAGA
GCAGGAGGGGCCGGAGTATTGGGACCAGGTCTCAGCCACTACTCAGCCGCTCTCGACAT
TTTTGCGCTCGTTAGATACTGTGTTTTTTGTGT

```

CLUSTAL 2.1 multiple sequence alignment

```

K11FW      ----AAACGCGTACTA-----CAGGTTCCCTTACTC-----ACTTCCGTGTATCCGTC 43
K11RV      TCTCAGCCAC-TGCTCGCCCCAGGCTCCC-ACTCCATGAGGTATTTCTTCACATCCGTG 58
           * * * * *      * * * * *      * * *      * * * * *

K11FW      CTACAACGAGG----AGGAAGCCACACTTCATCGCCGTGGGCTACGTGGACGACACGCAG 99
K11RV      TCCGGCCCGGCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAG 118
           * * *      * * * * * * * * * * * * * * * * * * * * * * *

K11FW      TTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAAGATGGAGCCGCGGGCGCCGTGGATA 159
K11RV      TTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAAGATGGAGCCGCGGGCGCCGTGGATA 178
           * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

K11FW      GAGCAGGAGGGGCCGGAGTATTGGGACCAGGACACGGAATATGAAGGCCCACTCACAG 219
K11RV      GAGCAGGAGGGGCCGGAGTATTGGGACCAGGTCTCAGCCACTACTCAG-CCCGCTCTC-- 235
           * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

K11FW      ACTGACCGAGCGAACCTGGGGACCTGCGCGGCTACTACAACCAGAGCGAGGACA 274
K11RV      ---GAC-----ATTTTTCGCTCGT---TAGATACTGTGTTTTTTGTGT----- 273
           * * *      * * * * * * *      * * * * *      * *

```

```

>K11SeqCons
TCTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTATTTCTTCACATCCGT
GTCCCGGCCCGGCGCGGGGAGCCACACTTCATCGCCGTGGGCTACGTGGACGACAC
GCAGTTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAAGATGGAGCCGCGGGCGCC
GTGGATAGAGCAGGAGGGGCCGGAGTATTGGGACCAGGACACGGAATATGAAGGC
CCACTCACAGACTGACCGAGCGAACCTGGGGACCTGCGCGGCTACTACAACCAGAG
CGAGGACA

```

>IMGTHLA:HLA00004 A*01:04N 1099 bp
Length = 1099

Plus Strand HSPs:

Score = 1324 (204.7 bits), Expect = 2.4e-56, P = 2.4e-56, Group = 1
Identities = 268/272 (98%), Positives = 268/272 (98%), Strand = Plus / Plus


```
>K11RV
TCTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTATTTCTTCACATCCGTGTC
CCGGCCCCGGCCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTT
CGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAAGATGGAGCCGCGGGCGCCGTGGATAGA
GCAGGAGGGGCCGAGTATTGGGACCAGGAGTCAGCCACTGCTCAGCCCCACTAGACAC
ATGAGCGCTGTCACATCACGACCGACCGCGG
```

CLUSTAL 2.1 multiple sequence alignment

```
K11FW      ---ACGAACTGTATCG----AGGG---CATTT-----GCACTTCCTTGTA---GTTT  40
K11RV      TCTCAGCCACTGC-TCGCCCCAGGCTCCCACTCCATGAGGTATTTCTTCACATCCGTGT  59
              *  ***  ***      *  *  *      *  *  *  *  *  *  *

K11FW      CCTACAACGAGGGCAAGGG---CACTTCATCGCCGTGGGCTACGTGGACGACACGCAGT  96
K11RV      CCGGCCCCGGCCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGT 119
              **      *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

K11FW      TCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAAGATGGAGCCGCGGGCGCCGTGGATAG 156
K11RV      TCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAAGATGGAGCCGCGGGCGCCGTGGATAG 179
              *****

K11FW      AGCAGGAGGGGCCGAGTATTGGGACCAGGAGACACGGAATATGAAGGCCCACT-CACAG 215
K11RV      AGCAGGAGGGGCCGAGTATTGGGACCAGGAGTCAG-----CCACTGCTCAG 226
              *****  *  *  *

K11FW      ACTG-ACCGAGCGAACCTGGGGACCTGCGCGGCTACTACAACCAGAGCGAGGGCA 270
K11RV      CCCGCACTAGAC--ACATGAGCGTGT-CAC----ATCAGACC-GACCGCGG--- 271
              *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
```

```
>K11SeqCons
TCTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTATTTCTTCACATCCGTGT
CCCGCCCCGGCCGCGGGGAGCCCCACTTCATCGCCGTGGGCTACGTGGACGACACGCAG
TTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAAGATGGAGCCGCGGGCGCCGTGGAT
AGAGCAGGAGGGGCCGAGTATTGGGACCAGGAGACACGGAATATGAAGGCCCACTCAC
AGACTGACCGAGCGAACCTGGGGACCTGCGCGGCTACTACAACCAGAGCGAGGGCA
```

```
>IMGTHLA:HLA00004 A*01:04N 1099 bp
Length = 1099
```

Plus Strand HSPs:

Score = 1333 (206.1 bits), Expect = 9.3e-57, P = 9.3e-57, Group = 1
Identities = 269/272 (98%), Positives = 269/272 (98%), Strand = Plus / Plus

```
Query:      21 CAGGCTCCCACTCCATGAGGTATTTCTTCACATCCGTGTCCCGCCCCGGCCGCGGGGAGC  80
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:      71 CGGGTCCCACTCCATGAGGTATTTCTTCACATCCGTGTCCCGCCCCGGCCGCGGGGAGC 130

Query:      81 CCCACTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTTCGTGCGGTTTCGACAGCGACG 140
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     131 CCCGTTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTTCGTGCGGTTTCGACAGCGACG 190

Query:     141 CCGCGAGCCAGAAGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGAGTATT 200
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     191 CCGCGAGCCAGAAGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGAGTATT 250

Query:     201 GGGACCAGGAGACACGGAATATGAAGGCCCACTCACAGACTGACCGAGCGAACCTGGGGA 260
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     251 GGGACCAGGAGACACGGAATATGAAGGCCCACTCACAGACTGACCGAGCGAACCTGGGGA 310

Query:     261 CCCTGCGCGGCTACTACAACCAGAGCGAGGGC 292
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     311 CCCTGCGCGGCTACTACAACCAGAGCGAGGAC 342
```

A3-1/2

```
>K11FW
CTGAGGCCGGGCAGTAGGGGGCCCCCGGGCGCTTCCTCCGCGGGTACCGGCAGGACGCC
TACGACGGCAAGGATTACATCGCCCTGAACGAGGACCTGCGCTCTTGGACCGCGCGGAC
ATGGCAGCTCAGATCACCAAGCGCAAGTGGGAGGCGGTCCATGCGGCGGAGCAGCGGAGA
GTCTACCTGGAGGGCCGTCGCTGGACGGGCTCCGCAGATACCTGGAGAACGGGAA
```

CLUSTAL 2.1 multiple sequence alignment

```
>K11SeqCons
```

```
>IMGTHLA:HLA00004 A*01:04N 1099 bp
      Length = 1099
```

Score = 1249 (193.4 bits), Expect = 5.8e-53, P = 5.8e-53, Group = 1
Identities = 253/257 (98%), Positives = 253/257 (98%), Strand = Plus / Plus

A3-2/2

>K11RV

>IMGTHLA:HLA03435 A*03:41 546 bp
Length = 546

Plus Strand HSPs:

Score = 1327 (205.2 bits), Expect = 3.5e-56, P = 3.5e-56, Group = 1
Identities = 267/269 (99%), Positives = 267/269 (99%), Strand = Plus / Plus

```
Query:      24 GCTCCCACTCCATGAGGTATTTCTTCACATCCGTGTCCCGGCCCGGCCGCGGGGAGCCAC 83
             |||
Sbjct:      1 GCTCCCACTCCATGAGGTATTTCTTCACATCCGTGTCCCGGCCCGGCCGCGGGGAGCCCC 60

Query:      84 ACTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACGCCG 143
             |||
Sbjct:      61 GCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACGCCG 120

Query:     144 CGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGAGTATTGGG 203
             |||
Sbjct:     121 CGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGAGTATTGGG 180

Query:     204 ACCAGGAGACACGGAATGTGAAGGCCCACTCACAGACTGACCGAGCGAACCTGGGGACCC 263
             |||
Sbjct:     181 ACCAGGAGACACGGAATGTGAAGGCCCACTCACAGACTGACCGAGCGAACCTGGGGACCC 240

Query:     264 TCGCGGGCTACTACAACCAGAGCGAGGAC 292
             |||
Sbjct:     241 TCGCGGGCTACTACAACCAGAGCGAGGAC 269
```

>K11SeqEdit2

TCTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTATTTCTTCAC
ATCCGTGTCCCGGCCCGGCCGCGGGGAGCCCCACTTCATCGCCGTGGGCTA
CGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAG
GATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGAGTATTGGGA
CCAGGACACACGGAATGTGAAGGCCCACTCACAGACTGACCGAGCGAACCT
GGGGACCCCTGCGCGGGCTACTACAACCAGAGCGAGGGCA

>IMGTHLA:HLA03435 A*03:41 546 bp
Length = 546

Plus Strand HSPs:

Score = 1318 (203.8 bits), Expect = 8.9e-56, P = 8.9e-56, Group = 1
Identities = 266/269 (98%), Positives = 266/269 (98%), Strand = Plus / Plus

```
Query:      24 GCTCCCACTCCATGAGGTATTTCTTCACATCCGTGTCCCGGCCCGGCCGCGGGGAGCCCC 83
             |||
Sbjct:      1 GCTCCCACTCCATGAGGTATTTCTTCACATCCGTGTCCCGGCCCGGCCGCGGGGAGCCCC 60

Query:      84 ACTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACGCCG 143
             |||
Sbjct:      61 GCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACGCCG 120

Query:     144 CGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGAGTATTGGG 203
             |||
Sbjct:     121 CGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGAGTATTGGG 180

Query:     204 ACCAGGACACACGGAATGTGAAGGCCCACTCACAGACTGACCGAGCGAACCTGGGGACCC 263
             |||
Sbjct:     181 ACCAGGAGACACGGAATGTGAAGGCCCACTCACAGACTGACCGAGCGAACCTGGGGACCC 240

Query:     264 TCGCGGGCTACTACAACCAGAGCGAGGGC 292
             |||
Sbjct:     241 TCGCGGGCTACTACAACCAGAGCGAGGAC 269
```

K14 27-04

A2-1/1

>K14FW

ATGGGCGAGGTATCAACTACACTCTCCGTGTACTGGCCTACAACGAGGGGAAGCCCACTT
CATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACGCCGCGAG

CCAGAGGATGGAGCCGCGGGCGCCCGTGGATAGAGCAGGAGGGGCCGGAGTATTGGGACCA
GGAGACACGGAATGTGAAGGCCAGTACAGACTGACCGAGTGGACCTGGGGACCTGCG
CGCTACTACAACCAGAGCGAGGACA

>K14RV
CTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTATTTCTACACCTCCGTGTCC
CGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTC
GTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAG
CAGGAGGGGCCGGAGTATTGGGACCAGGAGTCAGGGAATGCTAAGGCCAGAGACAGAAC
GTGTGCACGGCACCGAACATCCCGCG

CLUSTAL 2.1 multiple sequence alignment

```
K14FW      -----ATGGGC-----GAGGTATCAACTACACTCTCCGTGT 31
K14RV      CTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTATTT-CTACAC-CTCCGTGT 58
              ***          *****          *****          *****

K14FW      ACTGGCCTACAACGAGGGGAAGCCCACTTCATCGCCGTGGGCTACGTGGACGACACGCAG 91
K14RV      CCCGGCCCG-GCCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAG 117
              *  ****          **  *****          *****          *****

K14FW      TTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATA 151
K14RV      TTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATA 177
              *****

K14FW      GAGCAGGAGGGGCCGGAGTATTGGGACCAGGAGACACGGAATGTGAAGGCCAGTCACAG 211
K14RV      GAGCAGGAGGGGCCGGAGTATTGGGACCAGGAGTCAGGGAATGCTAAGGCCAG----AG 233
              *****          **  *****          *****          **

K14FW      ACTGACCGAGTGGACCTGGGGACCTGCGCGGCTACTACAACCAGAGCGAGGACA 266
K14RV      ACAGAACGTGTGCAC---GGCAC-----CGA-----ACATCCCGCG----- 266
              **  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
```

>K14SeqCons
CTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTATTTCTACACCTCCGT
GTCCCGGCCCGCGCCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACA
CGCAGTTTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCG
CCGTGGATAGAGCAGGAGGGGCCGGAGTATTGGGACCAGGAGACACGGAATGTGAA
GGCCAGTACAGACTGACCGAGTGGACCTGGGGACCTGCGCGGCTACTACAACC
AGAGCGAGGACA

>IMGTHLA:HLA00043 A*11:01:01 1098 bp
Length = 1098

Plus Strand HSPs:

Score = 1351 (208.8 bits), Expect = 1.4e-57, P = 1.4e-57, Group = 1
Identities = 271/272 (99%), Positives = 271/272 (99%), Strand = Plus / Plus

```
Query:      20 CAGGCTCCCACTCCATGAGGTATTTCTACACCTCCGTGTCCCGGCCCGCGCGGGGAGC 79
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:      71 CGGGCTCCCACTCCATGAGGTATTTCTACACCTCCGTGTCCCGGCCCGCGCGGGGAGC 130

Query:      80 CCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACG 139
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     131 CCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACG 190

Query:     140 CCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGGAGTATT 199
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     191 CCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGGAGTATT 250

Query:     200 GGGACCAGGAGACACGGAATGTGAAGGCCAGTCACAGACTGACCGAGTGGACCTGGGGA 259
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     251 GGGACCAGGAGACACGGAATGTGAAGGCCAGTCACAGACTGACCGAGTGGACCTGGGGA 310

Query:     260 CCCTGCGCGGCTACTACAACCAGAGCGAGGAC 291
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     311 CCCTGCGCGGCTACTACAACCAGAGCGAGGAC 342
```

A2-2/2

>K14FW

CTCATGAGGTATTTCTTCCATCCGTGTCCCGGCCCGGCCGCGGGAGCCCCGCTTCATCG
 CAGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGA
 GGATGGAGCCGCGGCGCCGTGGATAGAGCAGGAGGGTCCGGAGTATTGGGACGGGGAGA
 CACGGAAGTGAAGGCCACTCACAGACTACCGAGTGGACCTGGGGACCCTGCGCGGCT
 ACTACAACCAGAGCGAGGGCA

>K14RV

GTGCTCAGCCACTCCTCGTCCCCAGGCTCTCACTCCATGAGGTATTTCTTCACATCCGTG
 TCCCGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAG
 TTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATA
 GAGCAGGAGGGTCCGGAGTATTGGGACGGGGAGACACGGAAGGAAGGCCCACTCACAGA
 CTCACCGAGTGACCGGCACTGCGGG

CLUSTAL 2.1 multiple sequence alignment

```

K14FW      -----CTCATGAGGTATTTCTTC-CATCCGTG  26
K14RV      GTGCTCAGCCACTCCTCGTCCCCAGGCTCTCACTCCATGAGGTATTTCTTCACATCCGTG  60
                        *****

K14FW      TCCCGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAG  86
K14RV      TCCCGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAG  120
                        *****

K14FW      TTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATA  146
K14RV      TTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATA  180
                        *****

K14FW      GAGCAGGAGGGTCCGGAGTATTGGGACGGGGAGACACGGAAGTGAAGGCCCACTCACAG  206
K14RV      GAGCAGGAGGGTCCGGAGTATTGGGACGGGGAGACACGGAAG-GAAGGCCCACTCACAG  239
                        *****

K14FW      ACTCACCGAGTGGACCTGGGGACCCTGCGCGGCTACTACAACCAGAGCGAGGGCA  261
K14RV      ACTCACCGAGTG-ACC-----GGCACTGCGGG-----  265
                        *****  ***      * *  *****

```

>K14SeqCons

GTGCTCAGCCACTCCTCGTCCCCAGGCTCTCACTCCATGAGGTATTTCTTCCATCCGT
 GTCCCGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACG
 CAGTTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGT
 GGATAGAGCAGGAGGGTCCGGAGTATTGGGACGGGGAGACACGGAAGTGAAGGCCCA
 CTCACAGACTCACCGAGTGGACCTGGGGACCCTGCGCGGCTACTACAACCAGAGCGAG
 GGCA

>IMGTHLA:HLA01218 A*02:43N 1099 bp
 Length = 1099

Plus Strand HSPs:

Score = 1327 (205.2 bits), Expect = 1.7e-56, P = 1.7e-56, Group = 1
 Identities = 269/272 (98%), Positives = 269/272 (98%), Strand = Plus / Plus

```

Query:      23 CAGGCTCTCACTCCATGAGGTATTTCTTC-CATCCGTGTCCCGGCCCGGCCGCGGGGAGC  81
             | |||||
Sbjct:      71 CGGGCTCTCACTCCATGAGGTATTTCTTCACATCCGTGTCCCGGCCCGGCCGCGGGGAGC  130

Query:      82 CCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACG  141
             |||||
Sbjct:      131 CCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACG  190

Query:      142 CCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGTCCGGAGTATT  201
             |||||
Sbjct:      191 CCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGTCCGGAGTATT  250

Query:      202 GGGACGGGGAGACACGGAAGTGAAGGCCCACTCACAGACTCACCGAGTGGACCTGGGGA  261
             |||||
Sbjct:      251 GGGACGGGGAGACACGGAAGTGAAGGCCCACTCACAGACTCACCGAGTGGACCTGGGGA  310

Query:      262 CCCTGCGCGGCTACTACAACCAGAGCGAGGGC  293
             |||||
Sbjct:      311 CCCTGCGCGGCTACTACAACCAGAGCGAGGCC  342

```

A2-1/2

>K14FW
 CTGGTCGGAGGTACATTACTACACTCTCCGTGTCCCGGCCCGGCCGGGGAGCCCCGCT
 TCATCGCCGTGGGCTACGTGGACGACACGCAGTTTCGTGCGGTTTCGACAGCGACGCCGCGA
 GCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCGGAGTATTGGGACC
 AGGAGACACGGAATGTGAAGGCCAGTACAGACTGACCGAGTGGACCTGGGGACCCTGC
 CGCGCTACTACAACCAGAGCGAGGGCA

>K14RV
 TCTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTATTTCTACACCTCCGTGTTC
 CCGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTT
 CGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGA
 GCAGGAGGGGCCGAGTATTGGGACCAGGAGACACGGACATGTTAAGGCCAGACACAGA
 CGTGCTGCTGGCAGCCGCGATGCATGCG

CLUSTAL 2.1 multiple sequence alignment

```

K14FW      -----CTGGTCG-----GAGGTACATTACTACACTCTCCGT 31
K14RV      TCTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGT--ATTCTACAC-CTCCGT 57
              ***   *               *****   *   *   *   *   *

K14FW      GTCCCGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCA 91
K14RV      GTCCCGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCA 117
              *****

K14FW      GTTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGAT 151
K14RV      GTTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGAT 177
              *****

K14FW      AGAGCAGGAGGGGCCGAGTATTGGGACCAGGAGACACGGA-ATGTGAAGGCCAGTCAC 210
K14RV      AGAGCAGGAGGGGCCGAGTATTGGGACCAGGAGACACGGACATGTTAAGGCCAGACAC 237
              *****   *   *   *   *   *

K14FW      AGACTGACCGAGTGGACCTGGGGACCCTGCGCGGCTACTACAACCAGAGCGAGGGCA 267
K14RV      AGAC-----GTG-----CTGC-TGGCAGCCGCGATGCATGCG----- 268
              ***       **       ****   *   *   *   *   *

```

>K14SeqCons
 TCTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTATTTCTACACCTCCGTGTTC
 CGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTTCG
 TGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCA
 GGAGGGGCCGAGTATTGGGACCAGGAGACACGGAATGTGAAGGCCAGTACAGACTGAC
 CGAGTGGACCTGGGGACCCTGCGCGGCTACTACAACCAGAGCGAGGGCA

>IMGTHLA:HLA00043 A*11:01:01 1098 bp
 Length = 1098

Plus Strand HSPs:

Score = 1342 (207.4 bits), Expect = 3.6e-57, P = 3.6e-57, Group = 1
 Identities = 270/272 (99%), Positives = 270/272 (99%), Strand = Plus / Plus

```

Query:      21 CAGGCTCCCACTCCATGAGGTATTTCTACACCTCCGTGTCCCGGCCCGGCCGGGGAGC 80
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:      71 CGGGCTCCCACTCCATGAGGTATTTCTACACCTCCGTGTCCCGGCCCGGCCGGGGAGC 130

Query:      81 CCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTTCGTGCGGTTTCGACAGCGACG 140
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     131 CCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTTCGTGCGGTTTCGACAGCGACG 190

Query:     141 CCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGAGTATT 200
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     191 CCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGAGTATT 250

Query:     201 GGGACCAGGAGACACGGAATGTGAAGGCCAGTACAGACTGACCGAGTGGACCTGGGGA 260
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     251 GGGACCAGGAGACACGGAATGTGAAGGCCAGTACAGACTGACCGAGTGGACCTGGGGA 310

Query:     261 CCCTGCGCGGCTACTACAACCAGAGCGAGGGC 292
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     311 CCCTGCGCGGCTACTACAACCAGAGCGAGGAC 342

```

A2-2/1

>K14FW

TCTGAGGTATTTCTCCATCCGTGTCCCGCCCCGCCGCGGGGAGCCCCGCTTCATCGCA
GTGGGCTACGTGGACGACACGCAGTTTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGG
ATGGAGCCGCGGGCCCGTGGATAGAGCAGGAGGGTCCCGAGTATTGGGACGGGGAGACA
CGGAAAGTGAAGGCCACTCACAGACTCACCAGTGGACCTGGGGACCCTGCGCGGCTAC
TACAACCAGAGCGAGGACAA

>K14RV

GTTCTCAGCCACTCCTCGTCCCCAGGCTCTCACTCCATGAGGTATTTCTTCACATCCGTG
TCCCGCCCCGCCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAG
TTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATA
GAGCAGGAGGGTCCGGAGTATTGGGACGGGGAGACACGGAAGTGAAGGCCACTCACAG
ACTCACCATTGACCTGGCAGCTGCCGC

CLUSTAL 2.1 multiple sequence alignment

```
K14FW      -----TC--TGAGGTATTTCTTC-CATCCGTG  24
K14RV      GTTCTCAGCCACTCCTCGTCCCCAGGCTCTCACTCCATGAGGTATTTCTTCACATCCGTG  60
                        **  *****  *****

K14FW      TCCCGCCCCGCCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAG  84
K14RV      TCCCGCCCCGCCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAG 120
                        *****

K14FW      TTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATA 144
K14RV      TTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATA 180
                        *****

K14FW      GAGCAGGAGGGTCCGGAGTATTGGGACGGGGAGACACGGAAGTGAAGGCCACTCACAG  204
K14RV      GAGCAGGAGGGTCCGGAGTATTGGGACGGGGAGACACGGAAGTGAAGGCCACTCACAG  240
                        *****

K14FW      ACTCACCAGTGGACCTGGGGACCCTGCGCGGCTACTACAACCAGAGCGAGGACAA  260
K14RV      ACTACCGA-TTGACCTGG-----CAGCTGCCGC-----  268
                        ***** * ***** * * * *
```

>K14SeqCons

GTTCTCAGCCACTCCTCGTCCCCAGGCTCTCACTCCATGAGGTATTTCTTCATCCGTG
TCCCGCCCCGCCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCA
GTTTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGA
TAGAGCAGGAGGGTCCGGAGTATTGGGACGGGGAGACACGGAAGTGAAGGCCACTCA
CAGACTCACCAGTGGACCTGGGGACCCTGCGCGGCTACTACAACCAGAGCGAGGACAA

>IMGTHLA:HLA01218 A*02:43N 1099 bp
Length = 1099

Plus Strand HSPs:

Score = 1327 (205.2 bits), Expect = 1.7e-56, P = 1.7e-56, Group = 1
Identities = 269/272 (98%), Positives = 269/272 (98%), Strand = Plus / Plus

```
Query:      23 CAGGCTCTCACTCCATGAGGTATTTCTTC-CATCCGTGTCCCGCCCCGCCGCGGGGAGC  81
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:      71 CGGGCTCTCACTCCATGAGGTATTTCTTCACATCCGTGTCCCGCCCCGCCGCGGGGAGC 130

Query:      82 CCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGTTTCGTGCGGTTTCGACAGCGACG 141
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     131 CCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGTTTCGTGCGGTTTCGACAGCGACG 190

Query:     142 CCGCAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGTCCGGAGTATT 201
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     191 CCGCAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGTCCGGAGTATT 250

Query:     202 GGGACGGGGAGACACGGAAGTGAAGGCCACTCACAGACTCACCAGTGGACCTGGGGA 261
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     251 GGGACGGGGAGACACGGAAGTGAAGGCCACTCACAGACTCACCAGTGGACCTGGGGA 310

Query:     262 CCCTGCGCGGCTACTACAACCAGAGCGAGGAC 293
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     311 CCCTGCGCGGCTACTACAACCAGAGCGAGGCC 342
```

A3-1/2

>K14FW

CTGAGCATGGTAGTGGGCCGGAGGCGCTTCTCCGCGGGTACCCAGTCGCCTACACGG
CAGGATTACATCGCCCTGAAAGAGGACCTGCGCTCTTGGACCGCGCGGACATGGCAGCT
CAAATCACCACAGCACAAGTGGGAGCGGCCATGTGGCGGAGCAGCAGAGAGCCTACCTG
GAGGGCACGTGCGTGGAGTGGCTCCGCAGATACCTGGAGAACGGGAAG

>K14RV

CTGGTTCTCACACCGTCCAGAGGATGTATGGCTGCGACGTGGGGTCGGACTGGCGCTTCC
TCCGCGGGTACCACCAGTACGCCTACGACGGCAAGGATTACATCGCCCTGAAAGAGGACC
TGCGCTCTTGGACCGCGCGGACATGGCAGCTCAGACCACCAAGCACAAGTGGAGACGGC
CCATGGGCGGAGCAGTTAGAGCCTACCGGAGGGCACATGGCCACACGCA

CLUSTAL 2.1 multiple sequence alignment

```
K14FW      CTGA-----GCATGGTAGTG-----GGCCGGAG-GGCGCTTCC 32
K14RV      CTGGTTCTCACACCGTCCAGAGGATGTATGGCTGCGACGTGGGGTCGGACTGGCGCTTCC 60
          ***                      *  ****  *  *      **  ****  *****

K14FW      TCCGCGGGTACC-CCAGT-CGCCTAC-ACGGCA-GGATTACATCGCCCTGAAAGAGGACC 88
K14RV      TCCGCGGGTACCACCAGTACGCCTACGACGGCAAGGATTACATCGCCCTGAAAGAGGACC 120
          *****  *****  *****  *****  *****

K14FW      TGCGCTCTTGGACCGCGCGGACATGGCAGCTCAAATCACCACCAAGCACAAGTGGGAGGCGG 148
K14RV      TGCGCTCTTGGACCGCGCGGACATGGCAGCTCAGACCACCAAGCACAAGTGG-AGACGG 179
          *****  *****  *****  *****  *****  *  *****  *  *  *

K14FW      CCCATGTGGCGGAGCAGCAGAGAGCCTACCTGGAGGGCACGTGCGTGGAGTGGCTCCGCA 208
K14RV      CCCATG-GGCGGAGCAGTT-AGAGCCTACC-GGAGGGCACAT-----GGCCACACG 227
          *****  *****  *****  *****  *  *      ***  *  *

K14FW      GATACCTGGAGAACGGGAAG 228
K14RV      CA----- 229
```

>K14SeqCons

CTGGTTCTCACACCGTCCAGAGGATGTATGGCTGCGACGTGGGGTCGGACTGGCGCT
TCCTCCGCGGGTACCACCAGTACGCCTACGACGGCAAGGATTACATCGCCCTGAAAG
AGGACCTGCGCTCTTGGACCGCGCGGACATGGCAGCTCAGACCACCAAGCACAAGT
GGAGACGGCCCATGTGGCGGAGCAGCAGAGAGCCTACCTGGAGGGCACGTGCGTGGGA
GTGGCTCCGCAGATACCTGGAGAACGGGAAG

>IMGTHLA:HLA00017 A*02:12 1098 bp
Length = 1098

Plus Strand HSPs:

Score = 1267 (196.2 bits), Expect = 8.9e-54, P = 8.9e-54, Group = 1
Identities = 257/260 (98%), Positives = 257/260 (98%), Strand = Plus / Plus

```
Query:      1 CTGGTTCTCACACCGTCCAGAGGATGTATGGCTGCGACGTGGGGTCGGACTGGCGCTTCC 60
             | |||||
Sbjct:     341 CCGGTTCTCACACCGTCCAGAGGATGTATGGCTGCGACGTGGGGTCGGACTGGCGCTTCC 400

Query:      61 TCCGCGGGTACCACCAGTACGCCTACGACGGCAAGGATTACATCGCCCTGAAAGAGGACC 120
             | |||||
Sbjct:     401 TCCGCGGGTACCACCAGTACGCCTACGACGGCAAGGATTACATCGCCCTGAAAGAGGACC 460

Query:     121 TGCGCTCTTGGACCGCGCGGACATGGCAGCTCAGACCACCAAGCACAAGTGG-AGACGG 179
             | |||||
Sbjct:     461 TGCGCTCTTGGACCGCGCGGACATGGCAGCTCAGACCACCAAGCACAAGTGGGAGGCGG 520

Query:     180 CCCATGTGGCGGAGCAGCAGAGAGCCTACCTGGAGGGCACGTGCGTGGAGTGGCTCCGCA 239
             | |||||
Sbjct:     521 CCCATGTGGCGGAGCAGCAGAGAGCCTACCTGGAGGGCACGTGCGTGGAGTGGCTCCGCA 580

Query:     240 GATACCTGGAGAACGGGAAG 259
             | |||||
Sbjct:     581 GATACCTGGAGAACGGGAAG 600
```

A3-2/2

```
>K14FW
ATGAGTACTGGCCGGACGGGCGCTTCTCCACGGGTACCGGCAGGACGCCTACT
ACGGCAAGGATTACATCGCCCTGAAAGAGGACCTGCGCTCTTGGACCGGCGCG
ACATGGCAGCTCATATCACCAAGCGCAAGTGGGAGGCGGACCATGCGGCGGAAC
ATCAGAGAGCCTACCTGGAGGGCCGGTGCGTGGGGTGGCTCCGCAACTACCTGG
ACAACGGGAAGAC
```

```
>K14RV
GGATGGTTCTCACACCATCCAAATAATGTATGGCTGCGACGTGGGGCCGGACGG
GCGCTTCTCCGCGGTACCGGCAGGACGCCTACGACGGCAAGGATTACATCGC
CCTGAACGAGGACCTGCGCTCTTGGACCGGCGGCGGACATACAGCTCAGATCAC
AAGGCGAAATGGAGACGGCCATACGGCGGAACACGGATAGCCACCGGGGT
GCTCACGGCGACCA
```

CLUSTAL 2.1 multiple sequence alignment

```
K14FW      -----ATGA-GTA---CTG-----GCCGGACGGGCGCTT  25
K14RV      GGATGGTTCTCACACCATCCAAATAATGTATGGCTGCGACGTGGGGCCGGACGGGCGCTT  60
              ** * ***   ***               *****

K14FW      TCTCCACGGGTACCGGCAGGACGCCTACTACGGCAAGGATTACATCGCCCTGAAAGAGGA  85
K14RV      CCTCCGCGGTACCGGCAGGACGCCTACGACGGCAAGGATTACATCGCCCTGAACGAGGA  120
              **** *****

K14FW      CCTGCGCTCTTGGACCGCGGCGGACATGGCAGCTCATATCACCAAGCGCAAGTGGGAGGC  145
K14RV      CCTGCGCTCTTGGACCGCGGCGGACATA-CAGCTCAGATCACCAAGGGCAAATTGGAGAC  179
              *****

K14FW      GGACCATGCGGCGGAACATCAGAGAGCCTACCTGGAGGGCCGGTGCGTGGGGTGGCTCCG  205
K14RV      GGCCCATACGGCGGAACACGGATAGCCACC-----GGGGTG--CTCA  221
              ** ***** * ** ***** ***               ***** *

K14FW      CAACTACCTGGACAACGGGAAGAC  229
K14RV      CGGCGACCA-----  230
              * * ***
```

```
>K14SeqCons
GGATGGTTCTCACACCATCCAAATAATGTATGGCTGCGACGTGGGGCCGGAC
GGGCGCTTTCTCCACGGGTACCGGCAGGACGCCTACTACGGCAAGGATTACA
TCGCCCTGAAAGAGGACCTGCGCTCTTGGACCGCGGCGGACATGGCAGCTCA
TATACCAAGCGCAAGTGGGAGGCGGACCATGCGGCGGAACATCAGAGAGCC
TACCTGGAGGGCCGGTGCGTGGGGTGGCTCCGCAACTACCTGGACAACGGGA
AGAC
```

>IMGTHLA:HLA05450 A*11:66 546 bp
Length = 546

Plus Strand HSPs:

Score = 1193 (185.0 bits), Expect = 3.9e-50, P = 3.9e-50, Group = 1
Identities = 249/262 (95%), Positives = 249/262 (95%), Strand = Plus / Plus

```
Query:      1 GGATGGTTCTCACACCATCCAAATAATGTATGGCTGCGACGTGGGGCCGGACGGGCGCTT  60
              ||| ||||||||||||||| |||||||||||||||||||||||||||||||
Sbjct:     266 GGACGGTTCTCACACCATCCAGATAATGTATGGCTGCGACGTGGGGCCGGACGGGCGCTT  325

Query:      61 TCTCCACGGGTACCGGCAGGACGCCTACTACGGCAAGGATTACATCGCCCTGAAAGAGGA  120
              |||| ||||||||||||||| |||||||||||||||||||||||||||||
Sbjct:     326 CCTCCGCGGTACCGGCAGGACGCCTACTACGGCAAGGATTACATCGCCCTGAACGAGGA  385

Query:     121 CCTGCGCTCTTGGACCGCGGCGGACATGGCAGCTCATATCACCAAGCGCAAGTGGGAGGC  180
              ||||||||||||||||||| |||||||||||||||||||||||||||||
Sbjct:     386 CCTGCGCTCTTGGACCGCGGCGGACATGGCAGCTCAGATCACCAAGCGCAAGTGGGAGGC  445

Query:     181 GGACCATGCGGCGGAACATCAGAGAGCCTACCTGGAGGGCCGGTGCGTGGGGTGGCTCCG  240
              || |||||||||||| || ||||||||||||||||||||||||||| |||||||
Sbjct:     446 GGCCCATGCGGCGGAGCAGCAGAGAGCCTACCTGGAGGGCCGGTGCGTGGAGTGGCTCCG  505

Query:     241 CAACTACCTGGACAACGGGAAG  262
              || ||||||| |||||||
```

Sbjct: 506 CAGATACCTGGAGAACGGGAAG 527

A4-1/2H

>K14FW
CCCTGCTGTGAAGCGCTTAGCCCCCTGAGTGCTGGGCCCTGAGCTTCTACCT
GCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGACCAGACCCAGGACAC
GGAGCTCGTGGAGACCAGGCCTGCAGGGGATAA

>K14RV
TCGCCCCCAAACGCATATGACTCACCACGCTGTCTCTGACCATGAAGCCACC
CTGAGGTGCTGGGCCCTGAGCTTCTACCTGCGGAGATCACACTGACCGGCAG
CGGGAGGGGAGGACCAGACTCAGCAACCAAACGCA

CLUSTAL 2.1 multiple sequence alignment

```
K14FW      -----CCC----TGC-TGTGAA-----GCGCT-----TAGCC-----CCCTGAG-T 30
K14RV      TCGCCCCCAAACGCATATGACTCACCACGCTGTCTCTGACCATGAAGCCACCCTGAGGT 60
              ***      ** * ***      ****      * **      *
K14FW      GCTGGGCCCTGAGCTTCTACCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGG 90
K14RV      GCTGGGCCCTGAGCTTCTACCTGCGGAGATCACACTGACC-GGCAGCGGGA-GGGGAGG 118
              *****
K14FW      ACCAGACCCAGGACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGATAA 139
K14RV      ACCAGACTCAGCA-----ACCAAAC-GCA----- 142
              ***** ** *      ****      * ***
```

>K14SeqCons
TCGCCCCCAAACGCATATGACTCACCACGCTGTCTCTGACCATGAAGCCAC
CCTGAGTGCTGGGCCCTGAGCTTCTACCTGCGGAGATCACACTGACCTGGC
AGCGGGATGGGGAGGACCAGACCCAGGACACGGAGCTCGTGGAGACCAGGCC
TCAGGGGATAA

>IMGTHLA:HLA00005 A*02:01:01:01 1098 bp
Length = 1098

Plus Strand HSPs:

Score = 815 (128.3 bits), Expect = 2.3e-33, P = 2.3e-33, Group = 1
Identities = 165/166 (99%), Positives = 165/166 (99%), Strand = Plus / Plus

```
Query:      2 CGCCCCCAAACGCATATGACTCACCACGCTGTCTCTGACCATGAAGCCACCCTGAG-TG 60
              |||
Sbjct:      621 CGCCCCCAAACGCATATGACTCACCACGCTGTCTCTGACCATGAAGCCACCCTGAGGTG 680
Query:      61 CTGGGCCCTGAGCTTCTACCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGA 120
              |||
Sbjct:      681 CTGGGCCCTGAGCTTCTACCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGA 740
Query:      121 CCAGACCCAGGACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGAT 166
              |||
Sbjct:      741 CCAGACCCAGGACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGAT 786
```

A4-2/2H

>K14FW
CGCCCTGCAGTGTGGCCCTTCGGCCCCCTGAGTGCTGGGCCCTGGGCTTCT
ACCTGCGGAGATCCACTGACCTGGCAGCGGGATGGGGAGGACCAGACCCA
GGACACGGAGCTTGTGGAGACCAGGCCTGCAGGGGATA

>K14RV
CCCCCCCCAAGACACATATGACCCACCATTCATCTCTGACCATAAGGCCA
CCCTGAGGTGCTGGGCCCTGGGCTTCTACCTTGGGAGATCACACTGACCG
GCAGCAGGAGGAAAGGAACAAGATCAGCAACAAGCACG

CLUSTAL 2.1 multiple sequence alignment

```
K14FW      CGCCCTGCAG-----TGTGGCCC---TTC-----GGCC-CCCTGAG-T 33
```

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K14RV          CCCCCCAAGACACATATGACCCACCATTCATCTCTGACCATAAGGCCACCCTGAGGT 60
                *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
K14FW          GCTGGGCCCTGGGCTTCTACCCTGCGGAGATC-CACTGACCTGGCAGCGGGATGGGGAGG 92
K14RV          GCTGGGCCCTGGGCTTCTACCCTTGGGAGATCACAAGTACC-GGCAGCAGGAGGAAAGGA 119
                *****  *****  *****  *****  *****  *
K14FW          ACCAGACCCAGGACACGGAGCTTGTGGAGACCAGGCCTGCAGGGGATA 140
K14RV          ACAAGATC-----AGC-----AACAAGCACG----- 140
                **  *  *  *  *  *  *  *  *  *  *  *  *  *

```

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>K14SeqCons
CCCCCAAGACACATATGACCCACCATTCATCTCTGACCATAAGGC
CCCCTGAGTGCTGGGCCCTGGGCTTCTACCCTGCGGAGATCCACTGACC
TGGCAGCGGGATGGGGAGGACCAGACCCAGGACACGGAGCTTGTGGAGA
CCAGGCCTGCAGGGGATA

```

```

>IMGTHLA:HLA00043 A*11:01:01 1098 bp
    Length = 1098

```

Plus Strand HSPs:

```

Score = 714 (113.2 bits), Expect = 8.4e-29, P = 8.4e-29, Group = 1
Identities = 152/159 (95%), Positives = 152/159 (95%), Strand = Plus / Plus

```

```

Query:      9 AAGACACATATGACCCACCATTCATCTCTGACCATAAGGCC-CCCTGAG-TGCTGGGCC 66
             |||
Sbjct:     628 AAGACACATATGACCCACCATTCATCTCTGACCATGAGGCCACCCTGAGGTGCTGGGCC 687
             |||
Query:     67 CTGGGCTTCTACCCTGCGGAGATC-CACTGACCTGGCAGCGGGATGGGGAGGACCAGACC 125
             |||
Sbjct:     688 CTGGGCTTCTACCCTGCGGAGATCACAAGTACC-GGCAGCAGGAGTGGGGAGGACCAGACC 747
             |||
Query:    126 CAGGACACGGAGCTTGTGGAGACCAGGCCTGCAGGGGAT 164
             |||
Sbjct:    748 CAGGACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGAT 786
             |||

```

A4-3H/1

```

>K14FW
AGACCTGGGGGGGCTGGGGCGGCCCCCGCCGAAGTCACGGAGCTCGT
GGACACCGGCCTGCAGGGGATGGAACCTTCCAAAAGTGGGCGGCTGT
GGTGGTGCCCTTCTGGAGAGGAGCAAAGATACACCTGCCATGTGCAGC
ATGAGGGTTTGCCCAAGCCCCTCACCTGAGATGGACG

```

```

>K14RV
CTACCCTGCGGAGATCACAAGTACCTGGCAGCGGGATGGGGAGGACC
AGACCCAGGACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGATGGA
ACCTTCCAGAAGTGGGCGGCTGTGGTGGTGCCTTCGGAGAGGAGCAG
AGCATAACGGGGGCCATGTGCAGTCAGACTTACGGACGG

```

CLUSTAL 2.1 multiple sequence alignment

```

K14FW          -----AGACCTGG--GGGGGCTGGGGCGGCCCCCGCCGAAGTCAC 38
K14RV          CTACCCTGCGGAGATCACAAGTACCTGGCAGCGGGATGGGGAGGACCAGACCCAGGACAC 60
                *****  *  *  *  *  *  *  *  *  *  *  *
K14FW          GGAGCTCGTGGACACC-GGCTGCAGGGGATGGAACCTTCCAAAAGTGGGCGGCTGTGGT 97
K14RV          GGAGCTCGTGGAGACCAGGCCTGCAGGGGATGGAACCTTCCAGAAGTGGGCGGCTGTGGT 120
                *****  *  *  *  *  *  *  *  *  *  *  *
K14FW          GGTGCCTTCTGGAGAGGAGCAAAG-ATACACCTG-CCATGTGCAGCATGAGGGTTTGCCC 155
K14RV          GGTGCCTTC-GGAGAGGAGCAGACATACGGGGGGCCATGTGCAGTCAGA----- 169
                *****  *  *  *  *  *  *  *  *  *  *  *
K14FW          AAGCCCCTCACCTGAGATGGACG 179
K14RV          -----CTTAC-----GGACGG--- 180
                **  **  *  *  *  *  *  *  *  *  *  *  *

```

```

>K14SeqCons
CTACCCTGCGGAGATCACAAGTACCTGGCAGCGGGATGGGGAGGA
CCAGACCCAGGACACGGAGCTCGTGGACACCGGCCTGCAGGGGAT

```

GGAACCTTCCAAAAGTGGGCGGCTGTGGTGGTGCCTTCTGGAGAG
 GAGCAAAGATACACCTGCCATGTGCAGCATGAGGGTTTGCCCAAG
 CCCCTCACCTGAGATGGACG

>IMGTHLA:HLA06081 A*02:294 822 bp
 Length = 822

Plus Strand HSPs:

Score = 953 (149.0 bits), Expect = 1.8e-39, P = 1.8e-39, Group = 1
 Identities = 195/199 (97%), Positives = 195/199 (97%), Strand = Plus / Plus

Query: 1 CTACCCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGACCAGACCCAGGACAC 60
 ||
 Sbjct: 623 CTACCCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGACCAGACCCAGGACAC 682

Query: 61 GGAGCTCGTGGACACC-GGCCTGCAGGGGATGGAACCTTCCAAAAGTGGGCGGCTGTGGT 119
 |||||||||||| || ||||||||||||||||||||||||||||||||||||||
 Sbjct: 683 GGAGCTCGTGGAGACCAGGCCTGCAGGGGATGGAACCTTCCAGAAGTGGGCGGCTGTGGT 742

Query: 120 GGTGCCTTCTGGAGAGGAGCAAAGATACACCTGCCATGTGCAGCATGAGGGTTTGCCCAA 179
 |||||||||||| ||||||||||||||||||||||||||||||||||||||
 Sbjct: 743 GGTGCCTTCTGGAGAGGAGCAGAGATACACCTGCCATGTGCAGCATGAGGGTTTGCCCAA 802

Query: 180 GCCCCTCACCTGAGATGG 198
 ||||||||||||||||||
 Sbjct: 803 GCCCCTCACCTGAGATGG 821

K16 27-04

A2-1/1

>K16FW
 GAAACCCCAACCAGGTTGACCACGAAGCTCCGGTACTTCTAACCTCCGTGTCCTGGCCCG
 GCCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGT
 TCGACAGCGAGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGG
 GGCCGAGTATTGGGACCGGAACACACGGAATGTGAAGGCCCACTCACAGACTGACCGAG
 AGAGCCTGCGGATCGCGCTCCGCTACTACAACCAGAGCGAGGACA

>K16RV
 TGTCTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTATTTCTACACCTCCGTG
 TCCCGGCCCCGCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAG
 TTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATA
 GAGCAGGAGGGGCGGAGTATTGGGACCGGAACACACGGAATGTAAGGCCCACTCACAGA
 CGACCGATAGAGACCCGCACCTCCT

CLUSTAL 2.1 multiple sequence alignment

K16FW	GAAACCCCAACCAG-GTTGACCACGAAGCTCC-----GGTACTTCTA-ACCTCCG	48
K16RV	--TGTTCTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTATTTCTACACCTCCG	58
	* * * * *	
K16FW	TGTCTTGGCCCCGCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGC	108
K16RV	TGTCCCGGCCCCGCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGC	118

K16FW	AGTTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGA	168
K16RV	AGTTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGA	178

K16FW	TAGAGCAGGAGGGGCCGAGTATTGGGACCGGAACACACGGAATGTGAAGGCCCACTCAC	228
K16RV	TAGAGCAGGAGGGGCCGAGTATTGGGACCGGAACACACGGAATGT-AAGGCCCACTCAC	237

K16FW	AGACTGACCGAGAGAGCCTGCGGATCGCGCTCCGCTACTACAACCAGAGCGAGGACA	285
K16RV	AGAC-GACCGATAGAGACC-----CGCACCTC-CT-----	265
	*** * * * *	

>K16SeqCons
 TGTCTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTACTTCTAACCTCCG
 TGTCTTGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACA
 CGCAGTTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGC

CGTGGATAGAGCAGGAGGGGCCGAGTATTGGGACCGGAACACACGGAATGTGAAGG
 CCCACTCACAGACTGACCGAGAGAGCCTGCGGATCGCGCTCCGCTACTACAACCAGA
 GCGAGGACA

>IMGTHLA:HLA00071 A*25:01:01 1098 bp
 Length = 1098

Plus Strand HSPs:

Score = 1318 (203.8 bits), Expect = 4.4e-56, P = 4.4e-56, Group = 1
 Identities = 268/272 (98%), Positives = 268/272 (98%), Strand = Plus / Plus

Query: 23 CAGGCTCCCACTCCATGAGGTACTTCTA-ACCTCCGTGTCTGGCCCGCGCGGGGAGC 81
 | |||||
 Sbjct: 71 CGGGCTCCCACTCCATGAGGTATTTCTACACCTCCGTGTCCCGGCCCGCGCGGGGAGC 130
 Query: 82 CCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTCGACACGCACG 141
 | |||||
 Sbjct: 131 CCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTCGACACGCACG 190
 Query: 142 CCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGAGTATT 201
 | |||||
 Sbjct: 191 CCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGAGTATT 250
 Query: 202 GGGACCGGAACACACGGAATGTGAAGGCCCACTCACAGACTGACCGAGAGAGCCTGCGGA 261
 | |||||
 Sbjct: 251 GGGACCGGAACACACGGAATGTGAAGGCCCACTCACAGACTGACCGAGAGAGCCTGCGGA 310
 Query: 262 TCGCGCTCCGCTACTACAACCAGAGCGAGGAC 293
 | |||||
 Sbjct: 311 TCGCGCTCCGCTACTACAACCAGAGCGAGGAC 342

A2-2/2

>K16FW

TCTGAGGTATTTCTTCCATCCGTGTCCCGGCCCGCGCGGGGTGCCCGCTTCATCGCA
 GTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTCGACAGCGACGCCGCGAGCCAGAGG
 ATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGTCCGGAGTATTGGGACGGGGAAACA
 CGGAAAGTGAAGGCCCACTCACAGACTCACCGAGTGGACCTGGGGACCCTGCGCGGCTAC
 TACAACCAGAGCGAGGGCA

>K16RV

GTTCTCAGCCACTCCTCGTCCCCAGGCTCTCACTCCATGAGGTATTTCTTCACATCCGTG
 TCCCGGCCCGCGCGGGGAGCCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAG
 TTCGTGCGGTTTCGACAGCGAGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATA
 GAGCAGGAGGTTCCGGAGTATTGGGACGGGAGACACGGAAGGAAGGCCCACTCACAGA
 CTCACCGAGGACCGGGACTGAG

CLUSTAL 2.1 multiple sequence alignment

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K16FW      -----TC--TGAGGTATTTCTTC-CATCCGTG  24
K16RV      GTTCTCAGCCACTCCTCGTCCCCAGGCTCTCACTCCATGAGGTATTTCTTCACATCCGTG  60
              **  *****

K16FW      TCCCGGCCCGCGCGGGGTGCCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAG  84
K16RV      TCCCGGCCCGCGCGGGGAGCCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAG 120
              *****

K16FW      TTCGTGCGGTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATA 144
K16RV      TTCGTGCGGTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATA 180
              *****

K16FW      GAGCAGGAGGGTCCGGAGTATTGGGACGGGGAAACACGGAAGTGAAGGCCCACTCACAG 204
K16RV      GAGCAGGAGGGTCCGGAGTATTGGGACGGGGAGACACGGAAG-GAAGGCCCACTCACAG 239
              *****

K16FW      ACTCACCGAGTGGACCTGGGGACCCTGCGCGGCTACTACAACCAGAGCGAGGGCA  259
K16RV      ACTCACCGAG-GGACC--GGGACT-----GAG-----  263
              *****
  
```

>K16SeqCons

GTTCTCAGCCACTCCTCGTCCCCAGGCTCTCACTCCATGAGGTATTTCTTCCATCCG
 TGTCCCGGGCCGCGGGGGTCCCCGCTTCATCGCAGTGGGCTACGTGGACGACA
 CGCAGTTTCGTGCGGTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGC
 CGTGGATAGAGCAGGAGGGTCCGGAGTATTGGGACGGGGAACACGGAAGTGAAGG
 CCCACTCACAGACTACCGAGTGGACCTGGGGACCTGCGCGGCTACTACAACCAGA
 GCGAGGGCA

>IMGTHLA:HLA01218 A*02:43N 1099 bp
 Length = 1099

Plus Strand HSPs:

Score = 1309 (202.5 bits), Expect = 1.1e-55, P = 1.1e-55, Group = 1
 Identities = 267/272 (98%), Positives = 267/272 (98%), Strand = Plus / Plus

Query: 23 CAGGCTCTCACTCCATGAGGTATTTCTTC-CATCCGTGTCCCGCCCCGCGGGGTGC 81
 | |||||
 Sbjct: 71 CGGGCTCTCACTCCATGAGGTATTTCTTCACATCCGTGTCCCGCCCCGCGGGGAGC 130

 Query: 82 CCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTCGACAGCGACG 141
 | |||||
 Sbjct: 131 CCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTCGACAGCGACG 190

 Query: 142 CCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGTCCGGAGTATT 201
 | |||||
 Sbjct: 191 CCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGTCCGGAGTATT 250

 Query: 202 GGGACGGGGAACACGGAAGTGAAGGCCACTCACAGACTACCGAGTGGACCTGGGGA 261
 | |||||
 Sbjct: 251 GGGACGGGAGACACGGAAGTGAAGGCCACTCACAGACTACCGAGTGGACCTGGGGA 310

 Query: 262 CCCTGCGCGGCTACTACAACCAGAGCGAGGGC 293
 | |||||
 Sbjct: 311 CCCTGCGCGGCTACTACAACCAGAGCGAGGCC 342

A2-1/2

>K16FW
 ACTACCTGCTCGAGGTATATTCTACACCTCCGTGTCCCGCCCCGCGGGGGA
 GCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTCGA
 CAGCGACGCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGA
 GGGGCCGAGTATTGGGACCGGAACACACGAATGTGAAGGCCACTCACAGAC
 TGACCGAGAGAGCCTGCGGATCGCGCTCCGCTACTACAACCAGAGCGAGGGCC

>K16RV
 TCTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTATTTCTACACCTC
 CGTGTCCCGCCCCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGA
 CGACACGCAGTTCGTGCGGTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCC
 GCGGGCGCCGTGGATAGAGCAGGAGGGGCCGAGTATTGGGACCGGAACACACG
 GAATGTGAAGGCCACTCACAGACACCGATAGACACCCGCACGCCGCG

CLUSTAL 2.1 multiple sequence alignment

K16FW	-----ACTACCTGCTC-----GAGGTATATTCTACACCTCCGTGT	35
K16RV	TCTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTAT-TTCTACACCTCCGTGT	59
	*** * ** *	*****
K16FW	CCCGCCCCGCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGT	95
K16RV	CCCGCCCCGCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGT	119

K16FW	TCGTGCGGTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAG	155
K16RV	TCGTGCGGTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAG	179

K16FW	AGCAGGAGGGGCCGAGTATTGGGACCGGAACACACGAATGTGAAGGCCCACTCACAGA	215
K16RV	AGCAGGAGGGGCCGAGTATTGGGACCGGAACACACGAATGTGAAGGCCCACTCACAGA	239

K16FW	CTGACCGAGAGA-GCCTGCGGATCGCGCTCCGCTACTACAACCAGAGCGAGGGCC	269
K16RV	C-GACCGATAGACACCCGCACGCCGCG-----	265
	* ***** ** ** *	****

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>K16SeqCons
TCTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTATTTCTACACC
TCCGTGTCCCGGCCCGGCCGCGGGAGCCCCGCTTCATCGCCGTGGGCTACG
TGGACGACACGCAGTTTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGAT
GGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGAGTATTGGGACCGG
AACACACGGAATGTGAAGGCCCACTCACAGACTGACCGAGAGAGCCTGCGGA
TCGCGCTCCGCTACTACAACCAGAGCGAGGGCC

>IMGTHLA:HLA00071 A*25:01:01 1098 bp
    Length = 1098

    Plus Strand HSPs:

    Score = 1342 (207.4 bits), Expect = 3.6e-57, P = 3.6e-57, Group = 1
    Identities = 270/272 (99%), Positives = 270/272 (99%), Strand = Plus / Plus

Query:      21 CAGGCTCCCACTCCATGAGGTATTTCTACACCTCCGTGTCCCGGCCCGGCCGCGGGGAGC  80
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:      71 CGGGCTCCCACTCCATGAGGTATTTCTACACCTCCGTGTCCCGGCCCGGCCGCGGGGAGC 130

Query:      81 CCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTTCGTGCGGTTTCGACAGCGACG 140
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     131 CCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTTCGTGCGGTTTCGACAGCGACG 190

Query:     141 CCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGAGTATT 200
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     191 CCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGAGTATT 250

Query:     201 GGGACCGGAACACACGGAATGTGAAGGCCCACTCACAGACTGACCGAGAGAGCCTGCGGA 260
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     251 GGGACCGGAACACACGGAATGTGAAGGCCCACTCACAGACTGACCGAGAGAGCCTGCGGA 310

Query:     261 TCGCGCTCCGCTACTACAACCAGAGCGAGGGC 292
             | | | | | | | | | | | | | | | | | | | |
Sbjct:     311 TCGCGCTCCGCTACTACAACCAGAGCGAGGAC 342


A2-2/1

>K16FW
AACCTTCTGTGAGTATTTCTTCCATCCGTGTCCCGGCCCGGCCGCGGGAGCCCCGCTT
CATCGCAGTGGGTACGTGGACGACACGCAGTTTCGTGCGGTTTCGACAGCGACGCCGCGAG
CCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGTCCGGAGTATTGGGACGG
GGAGACACGGAAAGTGAAGGCCCACTCACAGACTCACCGAGTGGACCTGGGGACCCCTGCG
CGGCTACTACAACCAGAGCGAGGACA

>K16RV
TCTCAGCCACTCCTCGTCCCCAGGCTCTCACTCCATGAGGTATTTCTTCACATCCGTGTC
CCGGCCCCGCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGTT
CGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGA
GCAGGAGGGTCCGGAGTATTGGGACGGGGAGACACGGAAGTGAAGGCCCACTCACAGAC
TCACCGAGTGACCTGGCAGTG

CLUSTAL 2.1 multiple sequence alignment

K16FW      ----AACC--TTCT-----GCT-----GAGTATTTCTTC-CATCCGTGTC 33
K16RV      TCTCAGCCACTCCTCGTCCCCAGGCTCTCACTCCATGAGGTATTTCTTCACATCCGTGTC 60
             *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

K16FW      CCGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGTT 93
K16RV      CCGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGTT 120
             *****

K16FW      CGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGA 153
K16RV      CGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGA 180
             *****

K16FW      GCAGGAGGGTCCGGAGTATTGGGACGGGGAGACACGGAAGTGAAGGCCCACTCACAGAC 213
K16RV      GCAGGAGGGTCCGGAGTATTGGGACGGGGAGACACGGAAGTGAAGGCCCACTCACAGAC 240
             *****

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K16FW          TCACCGAGTGGACCTGGGGACCCTGCGCGGCTACTACAACCAGAGCGAGGACA 266
K16RV          TCACCGAGTG-ACCTGG-----CAGTG----- 261
                *****
                ***

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>K16SeqCons
TCTCAGCCACTCCTCGTCCCCAGGCTCTCACTCCATGGAGTATTTCTTCCATCCGTGT
CCCCGGCCCGCCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCA
GTTTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGG
ATAGAGCAGGAGGGTCCGGAGTATTGGGACGGGGAGACACGGAAGTGAAGGCCCACT
CACAGACTACCGAGTGGACCTGGGGACCCTGCGCGGCTACTACAACCAGAGCGAGGA
CA

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>IMGTHLA:HLA01218 A*02:43N 1099 bp
    Length = 1099

```

Plus Strand HSPs:

```

Score = 1309 (202.5 bits), Expect = 1.1e-55, P = 1.1e-55, Group = 1
Identities = 267/272 (98%), Positives = 267/272 (98%), Strand = Plus / Plus

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```

Query:    21 CAGGCTCTCACTCCATGGAGTATTTCTTC-CATCCGTGTCCCGGCCCGCGGGGAGC 79
          | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:    71 CGGGCTCTCACTCCATGAGGTATTTCTTCACATCCGTGTCCCGGCCCGCGGGGAGC 130

Query:    80 CCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGTTTCGTGCGGTTTCGACAGCGACG 139
          | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:    131 CCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGTTTCGTGCGGTTTCGACAGCGACG 190

Query:    140 CCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGTCCGGAGTATT 199
          | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:    191 CCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGTCCGGAGTATT 250

Query:    200 GGGACGGGGAGACACGGAAGTGAAGGCCCACTCACAGACTCACCGAGTGGACCTGGGGA 259
          | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:    251 GGGACGGGGAGACACGGAAGTGAAGGCCCACTCACAGACTCACCGAGTGGACCTGGGGA 310

Query:    260 CCCTGCGCGGCTACTACAACCAGAGCGAGGAC 291
          | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:    311 CCCTGCGCGGCTACTACAACCAGAGCGAGGCC 342

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A3-1/2

```

>K16FW
ATGGTAGTGC GGCCGAGGGCGCTTCCTCCGCGGGTACACCAGGACGCTTACGACGGCAA
GGATTACATCGCCCTGAACGAGGACCTGCGCTCTTGGACCGCGCGGACATGGCAGCTCA
AATACCCAGCACAATGGGGAGGCGGACCATGTGCGGGAGCAGTGGGGAGCCTACCTGGG
GGGACGGTGCGTGGAGTGGTCCGCAAATACCTGGACAACGGGAAGAC

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>K16RV
TGGTTCTCACACCGTCCAGAGGATGTATGGCTGCGACGTGGGGCCGGACGGGCGCTTCCT
CCGCGGGTACCACAGTACGCTTACGACGGCAAGGATTACATCGCCCTGAAAGAGGACCT
GCGCTCTTGGACCGCGCGGACATGGCAGCTCAGACCACCAAGCGCAAGTGGGAGCGGCC
CATAGGCGGAGCAGTGAGAGCCTACCGAGGGCAGGGGGCCAGCGCT

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CLUSTAL 2.1 multiple sequence alignment

```

K16FW          -----ATGGTAG-----TGCGGCCGGA-GGGCGCTTCCT 28
K16RV          TGGTTCTCACACCGTCCAGAGGATGTATGGCTGCGACGTGGGGCCGGACGGGCGCTTCCT 60
                **** *      ** *****
                ****

K16FW          CCGCGGGTAC-ACCAGGACGCTTACGACGGCAAGGATTACATCGCCCTGAACGAGGACCT 87
K16RV          CCGCGGGTACCACAGTACGCTTACGACGGCAAGGATTACATCGCCCTGAAAGAGGACCT 120
                *****

K16FW          GCGCTCTTGGACCGCGCGGACATGGCAGCTCAAATCACCAGCACAATGGGGAGGCGGA 147
K16RV          GCGCTCTTGGACCGCGCGGACATGGCAGCTCAGACCACCAAGCGCAAGTGGGAG-CGGC 179
                ***** * **** *

K16FW          CCATGTGGCGGAGCAGTGGGGAGCCTACCTGGGGGACGGTGCGTGGAGTGGTCCGCAA 207
K16RV          CCATA-GGCGGAGCAGTGAG-AGCCTACCGGAGGCAAGGGGC-----CAGCGCT---- 227
                **** ***** * ***** * * * * *

```


CCCCCTGAGTGCTGGGCCCTGAGCTTCTACCTGCGGAGATCCACTGACCTGG
CAGCGGGATGGGGAGGACCAGACCCAGGACACGGAGCTCGTGAGACCAGGCC
TGCAGGGGATA

>IMGTHLA:HLA00005 A*02:01:01:01 1098 bp
Length = 1098

Plus Strand HSPs:

Score = 791 (124.7 bits), Expect = 2.8e-32, P = 2.8e-32, Group = 1
Identities = 165/169 (97%), Positives = 165/169 (97%), Strand = Plus / Plus

Query: 4 GGTGCCCCCAAACGCATATGACTCACCACGCTGTCTCTGACCATGAAGCC-CCCTGAG 62
|| |||||
Sbjct: 618 GGACGCCCCCAAACGCATATGACTCACCACGCTGTCTCTGACCATGAAGCCACCCTGAG 677

Query: 63 -TGCTGGGCCCTGAGCTTCTACCTGCGGAGATC-CACTGACCTGGCAGCGGGATGGGGA 120
|| |||||
Sbjct: 678 GTGCTGGGCCCTGAGCTTCTACCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGA 737

Query: 121 GGACCAGACCCAGGACACGGAGCTCGTGAGACCAGGCCTGCAGGGGAT 169
|| |||||
Sbjct: 738 GGACCAGACCCAGGACACGGAGCTCGTGAGACCAGGCCTGCAGGGGAT 786

A4-2/2H

>K16FW
CACCTGTCTGTTACCTGAGGCCCCCTGAGTGCTGGGCCCTGGGCTTCTACCT
GCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGACCAGACCCACACG
AGCTCGGGGAGACCAGGCCTGCAGGGGAT

>K16RV
CCCCCCCCAAGACACATATGACCCACCACCCATCTCTGACCATGAGGCCACC
TTGAGGTGTTGGGCCCTGGGTTTCTACCTGCGGAGATCAGATGACCGGCAGCG
GGAGGGGAGGACCAGATCCACCGAGGCCG

CLUSTAL 2.1 multiple sequence alignment

```
K16FW      -----CACCTGTCTGTTACC-TGAGGCC-CCCTGAG- 30
K16RV      CCCCCCCAAGACACATATGACCCACCACCCATCTCTGACCATGAGGCCACCTTGAGG 60
                        *****  *** *  ***  *****  **  ****

K16FW      TGCTGGGCCCTGGGCTTCTACCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAG 90
K16RV      TGTGGGCCCTGGGTTTCTACCTGCGGAGATCACA-TGACC-GGCAGCGGGA-GGGGAG 117
      **  *****  *****  *****  *****  *****  *****

K16FW      GACCAGACCCACACACGGAGCTCGGGGAGACCAGGCCTGCAGGGGAT 137
K16RV      GACCAGATCC---CACCGAGGCCG----- 138
      *****  **    ***  ***  **
```

>K16SeqCons
CCCCCCCCAAGACACATATGACCCACCACCCATCTCTGACCATGAGGCCAC
CTTGAGGTGCTGGGCCCTGGGCTTCTACCTGCGGAGATCACACTGACCTGGC
AGCGGGATGGGGAGGACCAGACCCACACACGGAGCTCGGGGAGACCAGGCCTG
CAGGGGAT

>IMGTHLA:HLA02878 A*01:22N 821 bp
Length = 821

Plus Strand HSPs:

Score = 772 (121.9 bits), Expect = 2.7e-31, P = 2.7e-31, Group = 1
Identities = 156/158 (98%), Positives = 156/158 (98%), Strand = Plus / Plus

Query: 10 AAGACACATATGACCCACCACCCATCTCTGACCATGAGGCCACCTTGAGGTGCTGGGCC 69
|| |||||
Sbjct: 555 AAGACACATATGACCCACCACCCATCTCTGACCATGAGGCCACCTTGAGGTGCTGGGCC 614

Query: 70 CTGGGCTTCTACCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGACCAGACC 129
|| |||||
Sbjct: 615 CTGGGCTTCTACCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGACCAGACC 674

Query: 130 CACACACGGAGCTCGGGGAGACCAGGCCTGCAGGGGAT 167
 |||||
 Sbjct: 675 CACACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGAT 712

A4-3H/1

>K16FW
 TGA CTGCTTGGTCGGGCGGCCCTGCCGATGACGGGGCTTGAACCCGG
 CTTGCGGGAATGAACTTTAAAATGGGCGGGTGTGGGGGGCCTTTTGA
 AAGAACAAAAACCACTGGCATTGTCCACATGAGGGTTTTGCCCAACCCCT
 TAACCTGGAATGGCCC

>K16RV
 TTTTTCCTGCGGAAATCCCCATTACCCGGGAACGGGAATGGGAGGGCCA
 AAACCAGCACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGATGGAACCTT
 CCAGAAGTGGGCGTGTGTGGTGGTGCCTTCGGACAGGAGCAGAGATACAC
 CTGACCATGTGCAGAAGACGTGTACAG

CLUSTAL 2.1 multiple sequence alignment

```

K16FW      -----TG-----ACTGCTTGGT-----CGGGGCGGCCCTGCCGATG 32
K16RV      TTTTTCCTGCGGAAATCCCCATTACCCGGGAACGGGAATGGGAGGGCCAAACAGCA 60
              **          * * * * *          ***   ****   **

K16FW      -ACGGGGCTT-TGGA-ACCCGGCTTGC-GGGAATGAACTTT---AAAATGGGCGGG-TG 84
K16RV      CACGGAGCTCGTGGAGACCAGGCCTGCAGGGGATGGAACCTTCCAGAAGTGGGCGTGTG 120
              ****   *  ****   *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

K16FW      TGGGGGGGCCTTTTGAAGAACAACCAACAC-TGGCATTGTCCACATGAGGGTTTTG 143
K16RV      TGGTGGTGCCTTCG-GACAGGAGCAGAGATACACCTGACCATGTGCAGAAGACG----TG 175
              ***  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

K16FW      CCCAACCCCTTAACCTGGAATGGCCC 170
K16RV      TACAG----- 180
              **
  
```

Not Analyzed.

K17 28-04

A2-1/1

>K17FW
 GGATAGAGGTATTACGACACTCTCCGTGTCTGTCCCGCCGCGGGGTAGCCCGCTTCA
 TCGCCGTGGGCTACGTGGAGCACGACGAGTTCGTGCGGTTTCGACAGCGACGCCGCGAGCC
 AGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCGGAGTATTGGGACCGGA
 ACACACGGAATGTGAAGGCCCACTCACAGACTGACCGAGCGAACCTGGGGACCCTGCGCG
 GCTACTACAACACGACGAGGACA

>K17RV
 TTCTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTATTCTACACCTCCGTGT
 CCCGGCCCGCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGAGT
 TCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAG
 AGCAGGAGGGGCGGAGTATTGGGACCGGAACACACGGAATGGAAGGCCCACTCACAGAC
 GACCGAGCGAACCGGCACTCGCG

CLUSTAL 2.1 multiple sequence alignment

```

K17FW      -----GGATA-----GAGGTATTACGACACTCTCCGT 28
K17RV      TTCTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTATTT-CTACAC-CTCCGT 58
              ** *          ***** *  *  *  *  *  *

K17FW      GTCCTGTCCCGGCCGCGGGGTAGCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCA 88
K17RV      GTCCCGGCCCGCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCA 118
              ****  *  *****  *****  *****  *****

K17FW      GTTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGAT 148
K17RV      GTTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGAT 178
  
```

```

*****
K17FW      AGAGCAGGAGGGGCGGAGTATTGGGACCGGAACACACGGAATGTGAAGGCCCACTCACA 208
K17RV      AGAGCAGGAGGGGCGGAGTATTGGGACCGGAACACACGGAATG-GAAGGCCCACTCACA 237
*****

```

```

K17FW      GACTGACCGAGCGAACCTGGGGACCTGCGCGGCTACTACAACCAGACGAGGACA 263
K17RV      GAC-GACCGAGCGAAC--GGCACTC-GCG----- 263
*** ***** ** * * **

```

```

>K17SeqCons
TTCTCAGCCACTGTCGCCCCAGGCTCCCACTCCATGAGGTATTTCTACACCTCCG
TGTCCCGGGCCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACA
CGCAGTTTCGTGCGGTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGCGC
CGTGGATAGAGCAGGAGGGGCGGAGTATTGGGACCGGAACACACGGAATGTGAAGG
CCCACTCACAGACTGACCGAGCGAACCTGGGGACCTGCGCGGCTACTACAACCAGA
CGAGGACA

```

```

>IMGTHLA:HLA00083 A*26:11N 1100 bp
Length = 1100

```

Plus Strand HSPs:

```

Score = 1336 (206.5 bits), Expect = 6.8e-57, P = 6.8e-57, Group = 1
Identities = 270/272 (99%), Positives = 270/272 (99%), Strand = Plus / Plus

```

```

Query:      22 CAGGCTCCCACTCCATGAGGTATTTCTACACCTCCGTGTCCCGGCCCGCGGGGAGC 81
|
Sbjct:      71 CGGGCTCCCACTCCATGAGGTATTTCTACACCTCCGTGTCCCGGCCCGCGGGGAGC 130

Query:      82 CCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTTCGTGCGGTTCGACAGCGACG 141
|
Sbjct:     131 CCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTTCGTGCGGTTCGACAGCGACG 190

Query:     142 CCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGCCGGAGTATT 201
|
Sbjct:     191 CCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGCCGGAGTATT 250

Query:     202 GGGACCGGAACACACGGAATGTGAAGGCCCACTCACAGACTGACCGAGCGAACCTGGGGA 261
|
Sbjct:     251 GGGACCGGAACACACGGAATGTGAAGGCCCACTCACAGACTGACCGAGCGAACCTGGGGA 310

Query:     262 CCCTGCGCGGCTACTACAACCAGA-CGAGGAC 292
|
Sbjct:     311 CCCTGCGCGGCTACTACAACCAGAGCGAGGAC 342

```

A2-2/2

```

>K17FW
CGCTTCTCTGAGTATTTCTTCCATCCGTGTCCCGGCCCGCGGGGAGCCCCGCTTC
ATCGCAGTGGGCTACGTGGACGACACGCAGTTTCGTGCGGTTCGACAGCGACGCCGAGC
CAGAGGATGGAGCCGCGGGGCGCGTGGATAGAGCAGGAGGTCGGGAGTATTGGGACGGG
GAGACACGGAAGTGAAGGCCCACTCACAGACTCACCGAGTGACCTGGGGACCCTGCGC
GGCTACTACAACCAGAGCGAGGGC

```

```

>K17RV
TCTCAGCCACTCCTCGTCCCCAGGCTCTCACTCCATGAGGTATTTCTTACATCCGTGTC
CCGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGTT
CGTGCGGTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGA
GCAGGAGGGTCCGGAGTATTGGGACGGGGAGACACGGAAGTGAAGGCCCACTCACAGAC
TCACCGAGGGACCTGGGACTGGC

```

CLUSTAL 2.1 multiple sequence alignment

```

K17FW      -----CGCTTCTCCT-----GAGTATTTCTTC-CATCCGTGTC 32
K17RV      TCTCAGCCACTCCTCGTCCCCAGGCTCTCACTCCATGAGGTATTTCTTACATCCGTGTC 60
          *  *  *  *
          *****

K17FW      CCGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGTT 92
K17RV      CCGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGTT 120
          *****

```

```

K17FW          CGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGA 152
K17RV          CGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGA 180
                *****

K17FW          GCAGGAGGGTCCGGAGTATTGGGACGGGGAGACACGGAAAGTGAAGGCCCACTCACAGAC 212
K17RV          GCAGGAGGGTCCGGAGTATTGGGACGGGGAGACACGGAAAGTGAAGGCCCACTCACAGAC 240
                *****

K17FW          TCACCGAGTGGACCTGGGGACCTGCGCGGCTACTACAACCAGAGCGAGGGC 264
K17RV          TCACCGAG--GGACCTGGG-----ACT-----GGC 263
                *****          **          **

```



```

K17FW      CCGGCCCCGGCCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGTT 88
K17RV      CCGGCCCCGGCCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGTT 120
          *****

K17FW      CGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGA 148
K17RV      CGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGA 180
          *****

K17FW      GCAGGAGGGTCCGGAGTATTGGGACGGGGAGACACGGAAGTGAAGGCCCACTCACAGAC 208
K17RV      GCAGGAGGGTCCGGAGTATTGGGACGGGGAGACACGGAAG-GAAGGCCCACTCACAGAC 239
          *****

K17FW      TCACCGAGTGGACCTGGGGACCCTGCGCGGCTACTACAACCAGACGAGGACA 260
K17RV      TCACCGAG-GGAC--GGAC--TGCGCG----- 263
          *****

```

>K17SeqCons

```

TCTCAGCCACTCCTCGTCCCCAGGCTCTCACTCCATGAGGTATTTCTTCACATCCGTGTC
CCGGCCCCGGCCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGTT
CGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGA
GCAGGAGGGTCCGGAGTATTGGGACGGGGAGACACGGAAGTGAAGGCCCACTCACAGAC
TCACCGAGTGGACCTGGGGACCCTGCGCGGCTACTACAACCAGACGAGGACA

```

>IMGTHLA:HLA01218 A*02:43N 1099 bp
Length = 1099

Plus Strand HSPs:

Score = 1327 (205.2 bits), Expect = 1.7e-56, P = 1.7e-56, Group = 1
Identities = 269/272 (98%), Positives = 269/272 (98%), Strand = Plus / Plus

```

Query:      21 CAGGCTCTCACTCCATGAGGTATTTCTTCACATCCGTGTCCCGCCCCGCGCGGGGAGC 80
             | |||||
Sbjct:      71 CGGGCTCTCACTCCATGAGGTATTTCTTCACATCCGTGTCCCGCCCCGCGCGGGGAGC 130

Query:      81 CCGGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGTTTCGTGCGGTTTCGACAGCGACG 140
             | |||||
Sbjct:      131 CCGGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGTTTCGTGCGGTTTCGACAGCGACG 190

Query:      141 CCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGTCCGGAGTATT 200
             | |||||
Sbjct:      191 CCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGTCCGGAGTATT 250

Query:      201 GGGACGGGGAGACACGGAAGTGAAGGCCCACTCACAGACTCACCGAGTGGACCTGGGGA 260
             | |||||
Sbjct:      251 GGGACGGGGAGACACGGAAGTGAAGGCCCACTCACAGACTCACCGAGTGGACCTGGGGA 310

Query:      261 CCCTGCGCGGCTACTACAACCAGA-CGAGGAC 291
             | |||||
Sbjct:      311 CCCTGCGCGGCTACTACAACCAGAGCGAGGCC 342

```

A3-1/2

>K17FW

```

CAGGGATGCTAGTGGGCCGGAGGGCGCTTCCTCCGCGGGTACCCAGGACGCT
TACGACGGCAAGGATTACATCGCCCTGAACGAGGACCTGCGCTCTTGGACCGC
GGCGGACATGGCAGCTCAAATCACCAAGCACAATTGGGAGGCGGCCCATGTGG
CGGAGCAGTGGAGAGCCTACCTGGAGGGCACGGTGCGTGGGGTGGCTCCGCAA
ATACCTGGACAACGGGAAGA

```

>K17RV

```

TGGTTCTCACACCGTCCAGAGGATGTATGGCTGCGACGTGGGGCCGGACGGGC
GCTTCCTCCGCGGGTACCACAGTACGCTTACGACGGCAAGGATTACATCGCC
CTGAAAGAGGACCTGCGCTCTTGGACCGCGCGGACATGGCAGCTCAGACCAC
CCAGCGCAAGTGGGAGCGGCCCATAGGCGGAGCAGTGAGAGCCTACCGGAGGG
CACGGCTGTACACGCA

```

CLUSTAL 2.1 multiple sequence alignment

```

K17FW      -----CAG-GGATGC-TAGT-----GGGCCGGA-GGGCGCTTCCT 32
K17RV      TGGTTCTCACACCGTCCAGAGGATGTATGGCTGCGACGTGGGGCCGGACGGGCGCTTCCT 60
              ***  *****  *  *  *****  *****

K17FW      CCGCGGGTACC-CCAGGACGCTTACGACGGCAAGGATTACATCGCCCTGAACGAGGACCT 91
K17RV      CCGCGGGTACCACCAGTACGCTTACGACGGCAAGGATTACATCGCCCTGAAAGAGGACCT 120
              *****  ****  *****

K17FW      GCGCTCTTGGACCGCGGCGGACATGGCAGCTCAAATCACCAAGCACAATTGGGAGGCGGC 151
K17RV      GCGCTCTTGGACCGCGGCGGACATGGCAGCTCAGACCACCCAGCGCAAGTGGGAG-CGGC 179
              *****  *****  *  ****  ***  ****  ****

K17FW      CCATGTGGCGGAGCAGTGGAGAGCCTACCTGGAGGGCACGGTGCCTGGGGTGGCTC-CGC 210
K17RV      CCATA-GGCGGAGCAGTG-AGAGCCTACC-GGAGGGCACGGC-----TGTCACACGC 228
              ****  *****  *****  *****  *****  **  *  *  ***

K17FW      AAATACCTGGACAACGGGAAGA 232
K17RV      A----- 229
              *

```

```

>K17SeqCons
TGGTTCTCACACCGTCCAGAGGATGTATGGCTGCGACGTGGGGCCGGACGGG
CGCTTCCTCCGCGGGTACCCAGGACGCTTACGACGGCAAGGATTACATCGC
CCTGAACGAGGACCTGCGCTCTTGGACCGCGGCGGACATGGCAGCTCAAATC
ACCAAGCACAATTGGGAGGCGGCCCATGTGGCGGAGCAGTGGAGAGCCTACC
TGGAGGGCACGGTGCGTGGGGTGGCTCCGCAAATACCTGGACAACGGGAAGA

```

```

>IMGTHLA:HLA05801 A*02:279 1098 bp
      Length = 1098

```

Plus Strand HSPs:

```

Score = 1175 (182.3 bits), Expect = 1.3e-49, P = 1.3e-49, Group = 1
Identities = 247/259 (95%), Positives = 247/259 (95%), Strand = Plus / Plus

```

```

Query:      2  GGTTCCTCACACCGTCCAGAGGATGTATGGCTGCGACGTGGGGCCGGACGGGCGCTTCCTC 61
      |||
Sbjct:     343 GGTTCCTCACACCGTCCAGAGGATGTATGGCTGCGACGTGGGGCCGGACGGGCGCTTCCTC 402

Query:      62  CGCGGGTACCC-CAGGACGCTTACGACGGCAAGGATTACATCGCCCTGAACGAGGACCTG 120
      |||
Sbjct:     403 CGCGGGTACCGGCAGGACGCCATACGACGGCAAGGATTACATCGCCCTGAAAGAGGACCTG 462

Query:     121  CGCTCTTGGACCGCGGCGGACATGGCAGCTCAAATCACCAAGCACAATTGGGAGGCGGCC 180
      |||
Sbjct:     463 CGCTCTTGGACCGCGGCGGACATGGCAGCTCAGACCACCAAGCACAAGTGGGAGGCGGCC 522

Query:     181  CATGTGGCGGAGCAGTGGAGAGCCTACCTGGAGGGCACGGTGCCTGGGGTGGCTCCGCAA 240
      |||
Sbjct:     523 CATGTGGCGGAGCAGTTGAGAGCCTACCTGGAGGGCACG-TGCGTGGAGTGGCTCCGCAG 581

Query:     241  ATACCTGGACAACGGGAAG 259
      |||
Sbjct:     582 ATACCTGGAGAACGGGAAG 600

```

A3-2/2

```

>K17FW
GGGGCCGGTGTACGGCAGGAAGGGCGCTTCCTCCGCGGGTACAACAGGACGCT
TACGACGGCAGGATTACATCGCCCTGAACGAGGACCTGCGCTCTTGGACCGCG
GCGGACATGGCGGCTCATATCAGGAGCGCAAGTGGGAGACGGCCCATGAGGC
GGAGCAGTGGAGAGCCTACCTGGAGGGCCGGTGCCTGGAGTGGCTCCGCAGAT
ACCTGGAGAACGGGAAGA

```

```

>K17RV
GATGGTTCTCACACCATCCAGAGGATGTATGGCTGCGACGTGGGGCCGGACGG
GCGCTTCCTCCGCGGGTACCAGCAGGACGCTTACGACGGCAAGGATTACATCG
CCCTGAACGAGGACCTGCGCTCTTGGACCGCGGCGGACATGGCGGCTCAGATC
ACCCAGCGCAAGTGGGAGACGGCCCATGAGGCGGAGCAGGAGAGCCTACCGG
AGTGCCAGGCTACCAGCAC

```

CLUSTAL 2.1 multiple sequence alignment

```

K17FW      -----GG-----GGC--CGGTGTACGGCAGGAAGGGCGCTTC 30
K17RV      GATGGTTCTCACACCATCCAGAGGATGTATGGCTGCGACGTGGGGCCGGACGGGCGCTTC 60
              **      ***  **  *  ***  ***  *****

K17FW      CTCCGCGGGTAC-AACAGGACGCTTACGACGGCA-GGATTACATCGCCCTGAACGAGGAC 88
K17RV      CTCCGCGGGTACCAGCAGGACGCTTACGACGGCAAGGATTACATCGCCCTGAACGAGGAC 120
              ***** * *****

K17FW      CTGCGCTCTTGGACCGCGCGGACATGGCGGCTCATATCAGCGCAAGTGGGAGACG 148
K17RV      CTGCGCTCTTGGACCGCGCGGACATGGCGGCTCAGATCAGCGCAAGTGGGAGACG 180
              *****

K17FW      GCCCATGAGGCGGAGCAGTGGAGAGCCTACCTGGAGGGCCGGTGCGTGGAGTGGCTCCGC 208
K17RV      GCCCATGAGGCGGAGCAG-GGAGAGCCTACC-GGAGTGCCAG----- 220
              ***** **** *

K17FW      AGATACCTGGAGAACGGGAAGA 230
K17RV      -GCTACC---AGCACA----- 232
              * ****  ** **

```

```

>K17SeqCons
GATGGTTCTCACACCATCCAGAGGATGTATGGCTGCGACGTGGGGCCGGACG
GGCGCTTCTCCGCGGGTACAACAGGACGCTTACGACGGCAGGATTACATCG
CCCTGAACGAGGACCTGCGCTCTTGGACCGCGCGGACATGGCGGCTCATAT
CAGCGCGCAAGTGGGAGACGCGCCATGAGGCGGAGCAGTGGAGAGCCTAC
CTGGAGGGCCGGTGCGTGGAGTGGCTCCGAGATACCTGGAGAACGGGAAGA

```

```

>IMGTHLA:HLA00073 A*26:01:01 1098 bp
      Length = 1098

```

Plus Strand HSPs:

```

Score = 1248 (193.3 bits), Expect = 6.4e-53, P = 6.4e-53, Group = 1
Identities = 256/261 (98%), Positives = 256/261 (98%), Strand = Plus / Plus

```

```

Query:      1 GATGGTTCTCACACCATCCAGAGGATGTATGGCTGCGACGTGGGGCCGGACGGGCGCTTC 60
             || |||||
Sbjct:     340 GACGGTTCTCACACCATCCAGAGGATGTATGGCTGCGACGTGGGGCCGGACGGGCGCTTC 399

Query:      61 CTCCGCGGGTACAA-CAGGACGCTTACGACGGCA-GGATTACATCGCCCTGAACGAGGAC 118
             |||||
Sbjct:     400 CTCCGCGGGTACCAGCAGGACGCTTACGACGGCAAGGATTACATCGCCCTGAACGAGGAC 459

Query:     119 CTGCGCTCTTGGACCGCGCGGACATGGCGGCTCATATCAGCGCAAGTGGGAGACG 178
             |||||
Sbjct:     460 CTGCGCTCTTGGACCGCGCGGACATGGCGGCTCAGATCAGCGCAAGTGGGAGACG 519

Query:     179 GCCCATGAGGCGGAGCAGTGGAGAGCCTACCTGGAGGGCCGGTGCGTGGAGTGGCTCCGC 238
             |||||
Sbjct:     520 GCCCATGAGGCGGAGCAGTGGAGAGCCTACCTGGAGGGCCGGTGCGTGGAGTGGCTCCGC 579

Query:     239 AGATACCTGGAGAACGGGAAG 259
             |||||
Sbjct:     580 AGATACCTGGAGAACGGGAAG 600

```

A4-1/2H

```

>K17FW
CACTGTGTAATGCGCTAGGCTGTACGCCCCCTGAGTGCTGGGCCCTGAGCTTCTACCCCTG
CGGAGATCACTGACCTGGCAGCGGGATGGGGAGGACCAGACCCAGGACACGGAGCTCG
TGGAGACCAGGCCTGCAGGGGAT

```

```

>K17RV
ATCGCCCCAAAACGCATATGACTCACCACGCTGTCTCTGACCATGAAGCCACCCCTGAGG
TGCTGGGCCCTGAGCTTCTACCTGCGGAGATCAGCTGACCGGCAGCGGGAGGGGAGGA
CCAGACTCAGCAACCCAGAGTTGCAA

```

CLUSTAL 2.1 multiple sequence alignment

```

K17FW      --CACT-----GTGTAATGCGCTAGGCTGT-----ACGCC-CCCTGAG- 35
K17RV      ATCGCCCCAAAACGCATATGACTCACCACGCTGTCTCTGACCATGAAGCCACCCTGAGG 60
           * *                * * * * * * * * * * * * * * * *

```

```

K17FW      TGCTGGGCCCTGAGCTTCTACCCCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAG 95
K17RV      TGCTGGGCCCTGAGCTTCTACCCCTGCGGAGATCACACTGACC-GGCAGCGGGA-GGGGAG 118
           *****

```

```

K17FW      GACCAGACCCAGGACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGAT 143
K17RV      GACCAGACTCAGCA-AC-----CCAGAGTTGCAA----- 146
           ***** * * * *

```

```

>K17SeqCons
ATCGCCCCAAAACGCATATGACTCACCACGCTGTCTCTGACCATGAAGCCACCCTGAG
GTGCTGGGCCCTGAGCTTCTACCCCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGG
AGGACCAGACCCAGGACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGAT

```

```

>IMGTHLA:HLA00005 A*02:01:01:01 1098 bp
      Length = 1098

```

Plus Strand HSPs:

```

Score = 830 (130.6 bits), Expect = 4.9e-34, P = 4.9e-34, Group = 1
Identities = 166/166 (100%), Positives = 166/166 (100%), Strand = Plus / Plus

```

```

Query:      3 CGCCCCAAAACGCATATGACTCACCACGCTGTCTCTGACCATGAAGCCACCCTGAGGTG 62
             |||
Sbjct:     621 CGCCCCAAAACGCATATGACTCACCACGCTGTCTCTGACCATGAAGCCACCCTGAGGTG 680

Query:      63 CTGGGCCCTGAGCTTCTACCCCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGA 122
             |||
Sbjct:     681 CTGGGCCCTGAGCTTCTACCCCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGA 740

Query:     123 CCAGACCCAGGACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGAT 168
             |||
Sbjct:     741 CCAGACCCAGGACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGAT 786

```

A4-2/2H

```

>K17FW
CCGCCCTGCTGCTGTGTACCTGAGGCCCTGAGTGTGGGCCCTGGGCTTCTACCCCTGCG
GAGATCACACTGACCTGGCAGCGGGATGGGGAGGACCAGACCCACACAGGGGCTCGGGGA
AACCAGGCCTGCAGGGGATAA

```

```

>K17RV
CCCCCCCCAAGACACATATGACCCACCACCCATCTCTGACCATGAGGCCACCCTGAGGTG
CTGGGCCCTGGGCTTCTACCCCTGCGGAGATCACATGACCGGCAGCAGGAGGGGAGGACCAG
ATCACACCAAGACCG

```

CLUSTAL 2.1 multiple sequence alignment

```

K17FW      -CCGCCCTG---CTCGTGTG---TACC-----TGAGGCC-CCCTGAG-T 35
K17RV      CCCCCCCAAGACACATATGACCCACCACCCATCTCTGACCATGAGGCCACCCTGAGGT 60
           ** ** * * * * *

```

```

K17FW      GCTGGGCCCTGGGCTTCTACCCCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGG 95
K17RV      GCTGGGCCCTGGGCTTCTACCCCTGCGGAGATCACA-TGACC-GGCAGCAGGA-GGGGAGG 117
           *****

```

```

K17FW      ACCAGACCCACACAGGGGCTCGGGGAAACCAGGCCTGCAGGGGATAA 143
K17RV      ACCAGATC-----ACACCAAGACCG----- 137
           ***** * * * *

```

```

>K17SeqCons
CCCCCCCCAAGACACATATGACCCACCACCCATCTCTGACCATGAGGCCACCCTGAGGTG
CTGGGCCCTGGGCTTCTACCCCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGAC
CAGACCCACACAGGGGCTCGGGGAAACCAGGCCTGCAGGGGATAA

```

Not HLA-A result.

A4-3/1

```
>K17FW
TGGACTGTGTGGTCTGGGGGGGCCCTGGTGAAGACGGGGCTTTGTGAACCCGGCTTGGGG
GAATGGAACCTTTAAATGGGGGGTGGTGGGGGGCCTTTTGGAAAAGAACAAAATTACAC
TTGCATGGTCAACATGAGGGTTTTGCCCAACCCCTTAACCTGGAATTGGA
```

```
>K17RV
TTTTTCCCTGCGGAGATCACCATTACCTGGCAACGGGATGGGGAGGGCCAAAACCAGCAC
ACGGAGCTCGTGGAGACCAGGCCTGCAGGGGATGGAACCTTCCAGAAGTGGGCGGCTGTGG
TGGTGCCTTCGGACAGGAGCAGAGATACACCTGACCATGTGCATTACAGGTGTTGCGG
```

CLUSTAL 2.1 multiple sequence alignment

```
K17FW      -----TGGA-----CTGTGTGGTC-----TGGGGGGGCCCTGGTGA--A 33
K17RV      TTTTTCCCTGCGGAGATCACCATTACCTGGCAACGGGATGGGGAGGGCCAAAACCAGCA 60
              ***          *      ***          ***** ** *      *  *

K17FW      GACGGGGCCTT-TGTGAACCCGGCTTG-GGGGAATGGAACCTT---AAAATGGGGGGTGG 88
K17RV      CACGGAGCTCGTGGAGACCAGGCCTGCAGGGGATGGAACCTTCCAGAAGTGGGCGGCTG- 119
              **** **  **      *** **  **      *** ***** **      ** ***** **  *

K17FW      TGGGGGGCCTTTTGGAAAAGAACAAAATTACACTTGCATGGTCAACATGAGGGTTTGC 148
K17RV      TGGTGGTGCCTTCGGACAGGAGCAGAGAT-ACACCTG-----ACCATGTGCATT---C 168
              *** **  *  ** **  *  **  *  *  *  *  *  *  *  *  *  *  *  *  *

K17FW      CCAACCCCTTAACCTGGAATTGGA- 172
K17RV      ACA-----GGTGTGCGG 181
              **          **      ***
```

Sequence not analyzed. Reverse sequence corresponds to HLA-A*02 (90%).

Reverse strand

```
>IMGTHLA:HLA02960 A*02:124 1098 bp
      Length = 1098
```

Plus Strand HSPs:

Score = 723 (114.5 bits), Expect = 3.3e-29, P = 3.3e-29, Group = 1
Identities = 163/180 (90%), Positives = 163/180 (90%), Strand = Plus / Plus

```
Query:      2 TTTTTCCCTGCGGAGATCACCATTACCTGGCAACGGGATGGGGAGGGCCAAAACCAGCAC 61
              || | ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:     694 TTCTACCTGCGGAGATCACACTGGCAGCGGGATGGGGAGGACCAGACCCAGGAC 753

Query:      62 ACGGAGCTCGTGGAGACCAGGCCTGCAGGGGATGGAACCTTCCAGAAGTGGGCGGCTGTG 121
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:     754 ACGGAGCTCGTGGAGACCAGGCCTGCAGGGGATGGAACCTTCCAGAAGTGGGCGGCTGTG 813

Query:     122 GTGGTGCCTTTC-GGACAGGAGCAGAGATACACCTGACCATGTGCATTAC-AGGTGTTGC 179
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:     814 GTGGTGCCTTCTGGACAGGAGCAGAGATACACCTG-CCATGTGCAG-CATGAGGTTTTGC 871
```

K21 28-04

A2-1/1

```
>K21FW
TCCTGAGGTATTTCTTCCATCCGTGTCCCGGCCCGCGCGGGGAGCCCCGCTTCATCGC
CGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTCGACAGCGACGCCGCGAGCCAGAA
GATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGAGTATTGGGACCAGGAGAC
ACGGAATATGAAGGCCCACTCACAGACTGACCGAGCGAACCTGGGGACCCCTGC GCGGCTA
CTACAACCAGAGCGAGGACC
```

```
>K21RV
TTCTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTATTTCTTCACATCCGTGT
CCCCGCCCGCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGT
TCGTGCGGTTCGACAGCGACGCCGCGAGCCAGAAGATGGAGCCGCGGGCGCCGTGGATAG
AGCAGGAGGGGCCGAGTATTGGGACCAGGAGACCGGAATAGAAGGCCCACTCACAGAC
GACCGAGCGAACC GGCACCTGCGCG
```

K21FW	-----TCC-TGAGGATATTTCTTC-CATCCGTGT	26
K21RV	TTCTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTATTTCTTCACATCCGTGT	60
	*** *****	
K21FW	CCCGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCCGTGGGTACGTGGACGACACGCAGT	86
K21RV	CCCGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCCGTGGGTACGTGGACGACACGCAGT	120

K21FW	TCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAAGATGGAGCCGCGGGCGCCGTGGATAG	146
K21RV	TCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAAGATGGAGCCGCGGGCGCCGTGGATAG	180

K21FW	AGCAGGAGGGGCGGAGTATTGGGACCAGGAGACACGGAATATGAAGGCCCACTCACAGA	206
K21RV	AGCAGGAGGGGCGGAGTATTGGGACCAGGAGACACGGAATA-GAAGGCCCACTCACAGA	239

K21FW	CTGACCGAGCGAACCTGGGGACCTGCGCGGCTACTACAACCAGAGCGAGGACC	260
K21RV	C-GACCGAGCGAAC---GGCACTGCGCG-----	264
	* ***** * *	

TTCTCAGCAGCTGCTCGCCCCAGGCTCCCACTCCATGAGGTATTCTTCACATCCGTGT
CCCGGCCCGGCCGCGGGGAGCCCGCTTATCGCCGTGGGCTACGTGGACGACACGCAGT
TCGTGCGGTTTCGACGACGACGCGCGAGCCAGAAGATGGAACGCCGGCGCGCTGGATAG
AGCAGGAGGGGGCCGGAGTATTGGGACAGGAGACCGGAATATGAAGGCCCACTCACAGA
CTGACCGAGCGAACCTGGGGACCTCGCGCGGCTACTACACAGGACGAGGAGACC

Plus Strand HSPs:

```

Query:      22 CAGGCTCCCACTCCATGAGGTATTTCTTCACATCCGTGTCCCGGCCCGCCGCGGGGAGC 81
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:      71 CGGGCTCCCACTCCATGAGGTATTTCTTCACATCCGTGTCCCGGCCCGCCGCGGGGAGC 130

Query:      82 CCCGCTTCATCGCGGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACG 141
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     131 CCCGCTTCATCGCGGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACG 190

Query:     142 CCGCGAGCCAGAAGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGAGTATT 201
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     191 CCGCGAGCCAGAAGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGAGTATT 250

Query:     202 GGGACCAGGAGACACGGAATATGAAGGCCCACTCACAGACTGACCGAGCGAACCTGGGGA 261
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     251 GGGACCAGGAGACACGGAATATGAAGGCCCACTCACAGACTGACCGAGCGAACCTGGGGA 310

Query:     262 CCCTGCGCGGCTACTACAACCAGAGCGAGGAC 293
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     311 CCCTGCGCGGCTACTACAACCAGAGCGAGGAC 342

```

>K21FW

>K21RV
GGTTCTCAGCCACTCTCTCGTCCCAGGCTCTCACTCCATGAGGTATTTCTTCACATCCGT
GTCCCGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCAGTGGGTACGTGGACGACACGCA
TCTCGTCCGGTTTCAGACGCACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGAT
AGAGCAGGAGGGGTCGGAGTATTGGGACGGGGAGACACGGAAGTGAAGGCCCACTCACA

CLUSTAL 2.1 multiple sequence alignment

K21FW	-----TCC-TGAGGTATTCTTC-CATCCGT	24
K21RV	GGTTCTCAGCCACTCCTCGTCCCCAGGCTCTCACTCCATGAGGTATTCTTCACATCCGT	60
	*** *****	
K21FW	GTCCCGCCCGCCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCA	84
K21RV	GTCCCGCCCGCCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCA	120

K21FW	GTTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGAT	144
K21RV	GTTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGAT	180

K21FW	AGAGCAGGAGGGTCCGGAGTATTGGGACGGGGAGACACGAAAGTGAAGGCCCACTCACA	204
K21RV	AGAGCAGGAGGGTCCGGAGTATTGGGACGGGGAGACACGAAAGTGAAGGCCCACTCACA	240

K21FW	GACTCACCGAGTGGACCTGGGGACCTGCGCGGCTACTACAACCAGAGCGAGGGC	259
K21RV	GACTCACCGAGTG-----ACCG-----GCAGCTGCC-----GGCG-----	270

>K21SeqCons
GGTTTCTCAGCCACTCCTCGTCCCTCAGGCTCTCACTCCATGAGGTATTCTTTCACATCCG
TGTCGCCGCCCGGCCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACG
CAGTTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTG
GATAGAGCAGGAGGGTTCGGAGTATTGGGACGGGGAGACACGGAAGTGAAGGCCCACT
CAGACACTCACCGAGTGGCACTTGGGAGCCCTCGCGCGCTACTACAACAGAGCGAGGGC

```
>IMGTHLA:HLA01218 A*02:43N 1099 bp
      Length = 1099
```

Plus Strand HSPs:

Score = 1342 (207.4 bits), Expect = 3.6e-57, P = 3.6e-57, Group = 1
Identities = 270/272 (99%), Positives = 270/272 (99%), Strand = Plus / Plus

Query:	24	CAGGCTCTCACTCCATGAGGTATTTCTTCACATCCGTGTCCCGGCCCGGCCGCGGGGAGC	83
Sbjct:	71	CGGGCTCTCACTCCATGAGGTATTTCTTCACATCCGTGTCCCGGCCCGGCCGCGGGGAGC	130
Query:	84	CCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACG	143
Sbjct:	131	CCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACG	190
Query:	144	CCGCAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGTCCGGAGTATT	203
Sbjct:	191	CCGCAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGTCCGGAGTATT	250
Query:	204	GGGACGGGGAGACACGAAAGTGAAGGCCCACTCACAGACTCACCGAGTGGACCTGGGGA	263
Sbjct:	251	GGGACGGGGAGACACGAAAGTGAAGGCCCACTCACAGACTCACCGAGTGGACCTGGGGA	310
Query:	264	CCCTGCGCGGCTACTACAACCAGAGCGAGGGC	295
Sbjct:	311	CCCTGCGCGGCTACTACAACCAGAGCGAGGGC	342

A2-1/2

>K21FW
CTGCATCGGAGGTATATCTTCCATCCGTGTCCCGGCCCGGCCGCGGGGAGCCCCGCTTCAT
CGCGTGGGGTACGTGGACGACACGCAGTTCTGTGCGGTTGCACAGCGACGCCGCGAGCCAGA
AGATGGAGCCCGGGGCGCCGTGGATAGAGCAGGAGGGGCCGGAGTATTGGGACCAGGAGACA
CGGAATATGAAGGCCCACTCACAGACTGACCGAGCGAACCTGGGGACCCCTGCGCGGCTACTA
CAACCAGAGCGAGGGCC

>K21RV
GTTTCTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTATTTCTTCACATCCGTGTC
CCGGCCCCGGCCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAAGTTCG

CLUSTAL 2.1 multiple sequence alignment

```
>K21SeqCons
```

```
>IMGTHLA:HLA00004 A*01:04N 1099 bp
      Length = 1099
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Plus Strand HSPs:

Score = 1342 (207.4 bits), Expect = 3.6e-57, P = 3.6e-57, Group = 1
Identities = 270/272 (99%), Positives = 270/272 (99%), Strand = Plus / Plus

```

Query:      23  CAGGCTCCCACTCCATGAGGTATTTCTTCACATCCGTGTCCGGCCCCGGCCGCGGGGAGC  82
            | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:      71  CGGGCTCCCACTCCATGAGGTATTTCTTCACATCCGTGTCCGGCCCCGGCCGCGGGGAGC  130

Query:      83  CCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACG  142
            | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     131  CCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACG  190

Query:     143  CCGCGAGCCAGAAGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGGAGTATT  202
            | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     191  CCGCGAGCCAGAAGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGGAGTATT  250

Query:     203  GGGACCAGGAGACACGGAATATGAAGGCCCACTCACAGACTGACCAGCGAACCTGGGGA  262
            | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     251  GGGACCAGGAGACACGGAATATGAAGGCCCACTCACAGACTGACCAGCGAACCTGGGGA  310

Query:     263  CCCTGCGCGGCTACTACAACCAGAGCGAGGGC  294
            | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:     311  CCCTGCGCGGCTACTACAACCAGAGCGAGGAC  34

```

A2-2/1

>K21FW

TCATGAGGTTATTTCTTCCATCCGTGTCGCCGCCGCCGCCGGGGAGCCCCGCTTCATCGC
AGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCACAGCGACGCCCGGAGCCAGAG
GATGGAGCCCGGGCGCGCTGGATAGAGCAGGAGGGTCCGGAGTATTGGGACGGGGAGAC
ACGGAAAGTGAAAGCCCCACTACAGACTCACCAGTGGACCTGGGGACCTGCGCGGCTA
CTACAACGACGAGGGAGCTA

>K21RV

GTCTCAGCCACTCCTCGTCCCCAGGCTCTCACTCCATGAGGTATTTCTTCACATCCGTGT

```

CCCCGCCCCGCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGT
TCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAG
AGCAGGAGGGTCCGGAGTATTGGGACGCGGGAGACACGGAAGGAAGGCCCACTCACAGAC
TCACCGATGACCGGCACTGCGCG

```

CLUSTAL 2.1 multiple sequence alignment

```

K21FW      -----TCATGAGGTATTTCTTC-CATCCGTGT 26
K21RV      GTCTCAGCCACTCCTCGTCCCCAGGCTCTCACTCCATGAGGTATTTCTTCACATCCGTGT 60
              *****

K21FW      CCGGCCCCGCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGT 86
K21RV      CCGGCCCCGCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGT 120
              *****

K21FW      TCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAG 146
K21RV      TCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAG 180
              *****

K21FW      AGCAGGAGGGTCCGGAGTATTGGGACGCGGGAGACACGGAAGTGAAGGCCCACTCACAGA 206
K21RV      AGCAGGAGGGTCCGGAGTATTGGGACGCGGGAGACACGGAAG-GAAGGCCCACTCACAGA 239
              *****

K21FW      CTCACCGAGTGGACCTGGGGACCCTGCGCGGCTACTACAACCAGAGGGAGGACA 260
K21RV      CTCACCGAT--GACC----GGCACTGCGCG----- 263
              *****      * * *****

```

>K21SeqCons

```

GTCTCAGCCACTCCTCGTCCCCAGGCTCTCACTCCATGAGGTATTTCTTCACATCCGTGT
CCCCGCCCCGCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGT
TCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAG
AGCAGGAGGGTCCGGAGTATTGGGACGCGGGAGACACGGAAGTGAAGGCCCACTCACAGA
CTCACCGAGTGGACCTGGGGACCCTGCGCGGCTACTACAACCAGAGGGAGGACA

```

>IMGTHLA:HLA01218 A*02:43N 1099 bp
Length = 1099

Plus Strand HSPs:

Score = 1333 (206.1 bits), Expect = 9.3e-57, P = 9.3e-57, Group = 1
Identities = 269/272 (98%), Positives = 269/272 (98%), Strand = Plus / Plus

```

Query:      22 CAGGCTCTCACTCCATGAGGTATTTCTTCACATCCGTGTCCCGCCCCGCGCGGGGAGC 81
              | |||||
Sbjct:      71 CGGGCTCTCACTCCATGAGGTATTTCTTCACATCCGTGTCCCGCCCCGCGCGGGGAGC 130

Query:      82 CCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACG 141
              |||||
Sbjct:     131 CCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACG 190

Query:     142 CCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGTCCGGAGTATT 201
              |||||
Sbjct:     191 CCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGTCCGGAGTATT 250

Query:     202 GGGACGGGGAGACACGGAAGTGAAGGCCCACTCACAGACTCACCGAGTGGACCTGGGGA 261
              |||||
Sbjct:     251 GGGACGGGGAGACACGGAAGTGAAGGCCCACTCACAGACTCACCGAGTGGACCTGGGGA 310

Query:     262 CCCTGCGCGGCTACTACAACCAGAGGGAGGAC 293
              |||||
Sbjct:     311 CCCTGCGCGGCTACTACAACCAGAGCGAGGCC 342

```

A3-1/2

>K21FW

```

TGGTATGCTAGTGGGGCCGGAGGGCGCTTCTCCGCGGTTACCGGCAGGACGCCTACG
ACGGCAGGATTACATCGCCCTGAACGAGGACCTGCGCTCTTGGACCGCGGCGGACATG
GCAGCTCATATACCAAGCGCAAGTGGGAGGCGGTCCATGCGGCGGAGCAGCGGAGAG
TCTACCTGGAGGGCCGGTTCGTGGACGGGCTCCGAAAATACCTGGGAGAACGGGAAG

```

>K21RV

TGGTTCTCACACCGTCCAGATAATGTATGGCTGCGACGTGGGGCCGGACGGGCGCTTC
 CTCGCGGGTACCGGCAGGACGCCTACGACGGCAAGGATTACATCGCCCTGAACGAGG
 ACCTGCGCTCTTGGACCGCGCGGACATGGCAGCTCAGATCACCAGCGCAAGTGGAG
 ACGGTCCATGCGGCGGAGCAACGGAGAGTCTACCGGAGGGCCGGGCGCCAGTCGCA

CLUSTAL 2.1 multiple sequence alignment

```

K21FW      TGGT-----ATG-----CTA---GTGGGGCCGGA-GGGCGCTTCCT 32
K21RV      TGGTCTCACACCGTCCAGATAATGTATGGCTGCGACGTGGGGCCGGACGGGCGCTTCCT 60
          ****                      **      *****
K21FW      CCGCGGGTACCGGCAGGACGCCTACGACGGCA-GGATTACATCGCCCTGAACGAGGACCT 91
K21RV      CCGCGGGTACCGGCAGGACGCCTACGACGGCAAGGATTACATCGCCCTGAACGAGGACCT 120
          *****
K21FW      GCGCTCTTGGACCGCGGCGGACATGGCAGCTCATATCACCAGCGCAAGTGGGAGGCGGT 151
K21RV      GCGCTCTTGGACCGCGGCGGACATGGCAGCTCAGATCACCAGCGCAAGTGG-AGACGGT 179
          ***** **
K21FW      CCATGCGGCGGAGCAGCGGAGAGTCTACCTGGAGGGCCGGTGCGTGGACGGGCTCCGAAA 211
K21RV      CCATGCGGCGGAGCAACGAGAGTCTACC-GGAGGGCCGG-GCGC---CAG--TCGCA- 230
          ***** **
K21FW      ATACCTGGAGAACGGGAAG 230
K21RV      -----

```

>K21SeqCons
 TGGTTCTCACACCGTCCAGATAATGTATGGCTGCGACGTGGGGCCGGACGGGCGCTTCC
 TCCGCGGGTACCGGCAGGACGCCTACGACGGCAGGATTACATCGCCCTGAACGAGGACC
 TGGCGTCTTGGACCGCGGCGGACATGGCAGCTCATATCACCAGCGCAAGTGGGAGGCG
 GTCCATGCGGCGGAGCAGCGGAGAGTCTACCTGGAGGGCCGGTGCGTGGACGGGCTCCG
 AAAATACCTGGAGAACGGGAAG

>IMGTHLA:HLA00004 A*01:04N 1099 bp
 Length = 1099

Plus Strand HSPs:

Score = 1239 (191.9 bits), Expect = 1.6e-52, P = 1.6e-52, Group = 1
 Identities = 253/258 (98%), Positives = 253/258 (98%), Strand = Plus / Plus

```

Query:      2 GGTCTCTCACACCGTCCAGATAATGTATGGCTGCGACGTGGGGCCGGACGGGCGCTTCCTC 61
             |||
Sbjct:     343 GGTCTCTCACACCATCCAGATAATGTATGGCTGCGACGTGGGGCCGGACGGGCGCTTCCTC 402
K21FW      62 CGCGGGTACCGGCAGGACGCCTACGACGGCA-GGATTACATCGCCCTGAACGAGGACCTG 120
             |||
Sbjct:     403 CGCGGGTACCGGCAGGACGCCTACGACGGCAAGGATTACATCGCCCTGAACGAGGACCTG 462
K21FW      121 CGCTCTTGGACCGCGGCGGACATGGCAGCTCATATCACCAGCGCAAGTGGGAGGCGGTC 180
             |||
Sbjct:     463 CGCTCTTGGACCGCGGCGGACATGGCAGCTCAGATCACCAGCGCAAGTGGGAGGCGGTC 522
K21FW      181 CATGCGGCGGAGCAGCGGAGAGTCTACCTGGAGGGCCGGTGCGTGGACGGGCTCCGAAAA 240
             |||
Sbjct:     523 CATGCGGCGGAGCAGCGGAGAGTCTACCTGGAGGGCCGGTGCGTGGACGGGCTCCGCAGA 582
K21FW      241 TACCTGGAGAACGGGAAG 258
             |||
Sbjct:     583 TACCTGGAGAACGGGAAG 600

```

A3-2/2

>K21FW
 TGATGGCTGCGCGTGGGGCCGGCAGGGCGCTTCTCCGCGGGTACCGGCAGGACGCCTA
 CTACGGCAAGGATTACATCGCCCTGAACGAGGACCTGCGCTCTTGGACCGCGCGGACA
 TGGCAGCTCATATCACCAGCGCAAGTGGGAGGCGGTCCATGCGGCGGAACAGCGGAGA
 GTCTACCTGGAGGGCCGGTGCGTGGACGGGCTCCGAAAAACCTGGAGAACGGGAAG

>K21RV
 ATGGTTCTCACACCATCCAAATAATGTATGGCTGCGACGTGGGGCCGGACGGGCGCTTCC

TCCGCGGGTACCGGCAGGACGCCTACGACGGCAAGGATTACATCGCCCTGAACGAGGACC
 TGCCTCTTGGACCGCGCGGACATGGCAGCTCAGATCACCAAGCGCAAGTGGGAGACGG
 TCCATGCGGCGGAGCAGCGGAGAGTCTACCGGAGGTGCCACTGCTTCG

CLUSTAL 2.1 multiple sequence alignment

```

K21FW      -----TG-ATGGCTGCG-CGTGGGGCCGGCAGGGCGCTTCC 34
K21RV      ATGGTTCTCACACCATCCAAATAATGTATGGCTGCGACGTGGGGCCGGACGGGCGCTTCC 60
              ** *****
K21FW      TCCGCGGGTACCGGCAGGACGCCTACTACGGCAAGGATTACATCGCCCTGAACGAGGACC 94
K21RV      TCCGCGGGTACCGGCAGGACGCCTACTACGGCAAGGATTACATCGCCCTGAACGAGGACC 120
              *****
K21FW      TGCCTCTTGGACCGCGCGGACATGGCAGCTCATATCACCAAGCGCAAGTGGGAGGCGG 154
K21RV      TGCCTCTTGGACCGCGCGGACATGGCAGCTCAGATCACCAAGCGCAAGTGGGAGACGG 180
              *****
K21FW      TCCATGCGGCGGAACAGCGGAGAGTCTACCTGGAGGGCCGGTGCCTGGACGGGCTCCGAA 214
K21RV      TCCATGCGGCGGAGCAGCGGAGAGTCTACCGGAGGTGCCACTGC-----TTCG-- 228
              ***** * * * * *
K21FW      AATACCTGGAGAACGGGAAG 234
K21RV      -----
  
```

>K21SeqCons
 ATGGTTCTCACACCATCCAAATAATGTATGGCTGCGACGTGGGGCCGGCAGGGCGCTTCC
 TCCGCGGGTACCGGCAGGACGCCTACTACGGCAAGGATTACATCGCCCTGAACGAGGACC
 TGCCTCTTGGACCGCGCGGACATGGCAGCTCATATCACCAAGCGCAAGTGGGAGGCGG
 TCCATGCGGCGGAACAGCGGAGAGTCTACCTGGAGGGCCGGTGCCTGGACGGGCTCCGAA
 AATACCTGGAGAACGGGAAG

>IMGTHLA:HLA00004 A*01:04N 1099 bp
 Length = 1099

Plus Strand HSPs:

Score = 1219 (188.9 bits), Expect = 1.3e-51, P = 1.3e-51, Group = 1
 Identities = 251/260 (96%), Positives = 251/260 (96%), Strand = Plus / Plus

```

Query:      1 ATGGTTCTCACACCATCCAAATAATGTATGGCTGCGACGTGGGGCCGGCAGGGCGCTTCC 60
             | |||||
Sbjct:     341 ACGTTCTCACACCATCCAGATAATGTATGGCTGCGACGTGGGGCCGGACGGGCGCTTCC 400
             |||||
Query:      61 TCCGCGGGTACCGGCAGGACGCCTACTACGGCAAGGATTACATCGCCCTGAACGAGGACC 120
             |||||
Sbjct:     401 TCCGCGGGTACCGGCAGGACGCCTACTACGGCAAGGATTACATCGCCCTGAACGAGGACC 460
             |||||
Query:     121 TGCCTCTTGGACCGCGCGGACATGGCAGCTCATATCACCAAGCGCAAGTGGGAGGCGG 180
             |||||
Sbjct:     461 TGCCTCTTGGACCGCGCGGACATGGCAGCTCAGATCACCAAGCGCAAGTGGGAGGCGG 520
             |||||
Query:     181 TCCATGCGGCGGAACAGCGGAGAGTCTACCTGGAGGGCCGGTGCCTGGACGGGCTCCGAA 240
             |||||
Sbjct:     521 TCCATGCGGCGGAGCAGCGGAGAGTCTACCTGGAGGGCCGGTGCCTGGACGGGCTCCGCA 580
             |||||
Query:     241 AATACCTGGAGAACGGGAAG 260
             |||||
Sbjct:     581 GATACCTGGAGAACGGGAAG 600
  
```

A4-1/2H

>K21FW
 CCCTGATGTGCTGGGCTGAAGCCCCCTGAGTGCTGGGCCCTGAGCTTCTACCTGCGGAGA
 TCACACTGACCTGGCAGGGATGGGGAGGACCAGACCCAGGACACGGAGCTCGTGGAGAC
 CAGGCCTGCAGGGGATA

>K21RV
 CGCCCCAAAACGCATATGACTCACACGCTGTCTTGACCATGAAGCCACCCTGAGGTGC
 TGGGCCCTGAGCTTCTACCTGCGGAGATCACACACCGGCAGCGGGAGGGAGGACCAGC
 CCTAGCAACCGCAAATGA

CLUSTAL 2.1 multiple sequence alignment

```

K21FW      ---CCCTGA-----TGTG-----CTGGGC-TGAAGCC-CCCTGAG-TG 32
K21RV      CGCCCCAAAACGCATATGACTCACCACGCTGTCTCTGACCATGAAGCCACCCTGAGGTG 60
           *** * * * * * * * * * * * * * * * * * * * * * * *
K21FW      CTGGGCCCTGAGCTTCTACCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGA 92
K21RV      CTGGGCCCTGAGCTTCTACCTGCGGAGATCACAC-GACC-GGCAGCGGGA-GGGGAGGA 117
           ***** * * * * * * * * * * * * * * * * * * * * *
K21FW      CCAGACCCAGGACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGATA 139
K21RV      CCAGCCCTAGCA-----ACC-----GCAATGA-- 140
           **** * * * * * * * * * * * * * * * * * * * * *

```

>K21SeqCons

```

CGCCCCAAAACGCATATGACTCACCACGCTGTCTCTGACCATGAAGCCACCCTGAGGTG
CTGGGCCCTGAGCTTCTACCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGA
CCAGACCCAGGACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGATA

```

>IMGTHLA:HLA00005 A*02:01:01:01 1098 bp
Length = 1098

Plus Strand HSPs:

Score = 830 (130.6 bits), Expect = 4.9e-34, P = 4.9e-34, Group = 1
Identities = 166/166 (100%), Positives = 166/166 (100%), Strand = Plus / Plus

```

Query:      1 CGCCCCAAAACGCATATGACTCACCACGCTGTCTCTGACCATGAAGCCACCCTGAGGTG 60
             |||
Sbjct:      621 CGCCCCAAAACGCATATGACTCACCACGCTGTCTCTGACCATGAAGCCACCCTGAGGTG 680
             |||
Query:      61 CTGGGCCCTGAGCTTCTACCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGA 120
             |||
Sbjct:      681 CTGGGCCCTGAGCTTCTACCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGA 740
             |||
Query:      121 CCAGACCCAGGACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGAT 166
             |||
Sbjct:      741 CCAGACCCAGGACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGAT 786
             |||

```

----- 29-04 -----

A4-2/2H

>K21FW

```

CCCCGGGCTTCCTGAGGCCCTGAGTGCTGGGCCCTGGGCTTCTACCTGCGGAGATAC
ACTGACCTGGCAGCGGGATGGGGAGGACCAGACCCAGGAACGGAGCTAGGGAAGCCAGG
CCTGCAGGGGAT

```

>K21RV

```

CCCCCCCCAAGACAGGGGAACCCCACTCCCATTTTTGACCATAAGGCCCCCTGAGGTG
ATTGCCCCATGGGTTTACCTTGGGAGATCACACTACCGGCAACAGGATGGGAGGACCAG
ATCGCACACAAGGCCG

```

CLUSTAL 2.1 multiple sequence alignment

```

K21FW      ---CCCC-----GGG-----CTTCC-----TGAGGCCCCC-TGAG-TG 28
K21RV      CCCCCCAAAGACAGGGGAACCCCACTCCCATTTTTGACCATAAGGCCCCCTGAGGTG 60
           *** * * * * * * * * * * * * * * * * * * * * *
K21FW      CTGGGCCCTGGGCTTCTACCTGCGGAGAT-ACACTGACCTGGCAGCGGGATGGGGAGGA 87
K21RV      ATTGCCCCATGGGTTTACCTTG-GGAGATCACACTA--CCGGCAACAGGATGGG-AGGA 116
           * * * * * * * * * * * * * * * * * * * * * * * *
K21FW      CCAGACCCAGGAACGGAGCTAGGGAAGCCAGGCCTGCAGGGGAT 132
K21RV      CCAGATC---GCACA-----CAAGGCCG----- 136
           ***** * * * * * * * * * * * * * * * * * *

```

Sequence not analyzed.

A4-3H/1

>K21FW

TGCCTGCGCGGGCTGGGGAGGCCCGTCCCCGCACACGGACTTGGTGGACACAGGCTTGCA
GGGAATGGAACCTTCCAAAATTGGGCGGTGGGGGGGGCTTTTGAAGAAGCAAAAAT
TCCACTGGCATGGTCCAGATGGGGGTTTGTCCCAACCCCTTAACCCGGAATTGGAC

>K21RV

TTTTTAACCTGCGGAGATCACAATTACCCGGGAACGGGATGGGGAGGGCCCAAACCAGGA
CACGGAGCTCGTGGAGACCAGGCCTGCAGGGGATGGAACCTTCCAGAAGTGGGCGGCTGT
GGTGGTGCCTTCTGGAGAGGAGCAGAGATACACCTGCCATGTGCAGCATACGTACTGCAG

CLUSTAL 2.1 multiple sequence alignment

```
K21FW      -----TGCCTGCG-----CGGGCTGGGGAGG-CCCGTCCCCGCA 33
K21RV      TTTTAACTGCGGAGATCACAATTACCCGGGAACGGGATGGGGAGGGCCCAAACCAGGA 60
              *****                      **** *
K21FW      CACGGACTTGGTGGACAC-AGGCTTGCAGGGAATGGAACCTTCCAAAATTGGGCGGTGG 92
K21RV      CACGGAGCTCGTGGAGACCAGGCCTGCAGGGGATGGAACCTTCCAGAAGTGGGCGGCTGT 120
              ***** *
K21FW      GGGGGGGCTTTTGAAGAAGAA-CAAAAATTCCACTGGCATGGTCCAGATGGGGGTTTTCG 151
K21RV      GGTGGTGCCTTCTGGAGAGGAGCAGAGATACACCTGCCATG-TGCAG-CATACGTACTGC 178
              ** *
K21FW      CCAACCCCTTAACCCGGAATTGGAC 176
K21RV      --AG----- 180
              *
```

>K21SeqCons

TTTTTAACCTGCGGAGATCACAATTACCCGGGAACGGGATGGGGAGGGCCCAAACCAGGA
CACGGAGCTCGTGGAGACCAGGCCTGCAGGGGATGGAACCTTCCAGAAGTGGGCGGCTGT
GGTGGTGCCTTCTGGAGAGGAGCAGAGATACACCTGCCATGGTCCAGATGGGGGTTTTCG
CCAACCCCTTAACCCGG

>IMGTHLA:HLA06077 A*02:291 822 bp
Length = 822

Plus Strand HSPs:

Score = 787 (124.1 bits), Expect = 5.7e-32, P = 5.7e-32, Group = 1
Identities = 177/197 (89%), Positives = 177/197 (89%), Strand = Plus / Plus

```
Query:      2 TTTTAACCTGCGGAGATCACAATTACCCGGGAACGGGATGGGGAGGGCCCAAACCAGGAC 61
              || || ||||| ||||| || || || ||||| ||||| || || |||||
Sbjct:     621 TTCTACCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGACCAGACCCAGGAC 680

Query:      62 ACGGAGCTCGTGGAGACCAGGCCTGCAGGGGATGGAACCTTCCAGAAGTGGGCGGCTGTG 121
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:     681 ACGGAGCTCGTGGAGACCAGGCCTGCAGGGGATGGAACCTTCCAGAAGTGGGCGGCTGTG 740

Query:     122 GTGGTGCCTTCTGGAGAGGAGCAGAGATACACCTGCCATGGTCCAG-ATGGGGGTTTTCG 180
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct:     741 GTGGTGCCTTCTGGACAGGAGCAGAGATACACCTGCCATG-TGCAGCATGAGGGTTT-GC 798

Query:     181 CCAACCCCTTAACCCGG 197
              |||| |||| |||| |
Sbjct:     799 CCAAGCCCTTCACCCTG 815
```

K23 29-04

A2-1/1

>K23FW

TCCTGAGGTATTTCTTCCATCCGTGTCCCCGCCCGCCGCGGGGAGCCCCGCTTCATCGC
CGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTACGCAACCCGGGCCACAAGATGG

AGCCGCGGCGCCGCGGTGGATAGAGCAGGAGGGGCGGATTATTGGGACCAGGAGACACG
GAATGTGAAGGCCACTCACAGACTGACCGAGTGGACCTGGGGACCCTGCGCGGCTACTA
CAACCAGACGAGGACCCG

>K23RV

TTCTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTATTTCTTCACATCCGTGT
CCCGGCCCGCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGT
TCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCGCTGGATAG
AGCAGGAGGGGCGGAGTATTGGGACCAGGAGACCGGAATATGAAGGCCACTCACAGA
CGACGATCGAACCTGGTACCTG

CLUSTAL 2.1 multiple sequence alignment

```

K23FW      -----TCC-TGAGGTATTTCTTC-CATCCGTGT 26
K23RV      TTCTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTATTTCTTCACATCCGTGT 60
              *** *****

K23FW      CCCGGCCCCGCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGT 86
K23RV      CCCGGCCCCGCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGT 120
              *****

K23FW      TCGTGCGGTTC-AC-GCAACCC---GGGCCACAAGATGGAGCCGCGGCGCGCGGTGGAT 141
K23RV      TCGTGCGGTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGG--CGCCGTGGAT 178
              *****  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

K23FW      AGAGCAGGAGGGGCGGATTATTGGGACCAGGAGACACGGAATGTGAAGGCCCACTCACA 201
K23RV      AGAGCAGGAGGGGCGGAGTATTGGGACCAGGAGACACGGAATATGAAGGCCCACTCACA 238
              *****

K23FW      GACTGACCGAGTGGACCTGGGGACCCTGCGCGGCTACTACAACCAGACGAGGACCCG 258
K23RV      GAC-GAC-GATCGAACCTGGTA--CCTG----- 262
              ***  ***  *  *  *  *  *  *  *  *

```

>K23SeqCons

TTCTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTATTTCTTCACATCCGTGT
CCCGGCCCGCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGT
TCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCGCTGGATAG
AGCAGGAGGGGCGGAGTATTGGGACCAGGAGACCGGAATATGAAGGCCCACTCACATG
ACCAGTGGACCTGGGGACCTGCGCGGCTACTACAACCAGACGAGGACCCG

>IMGTHLA:HLA02985 A*01:28 546 bp
Length = 546

Plus Strand HSPs:

Score = 1276 (197.5 bits), Expect = 7.0e-54, P = 7.0e-54, Group = 1
Identities = 264/269 (98%), Positives = 264/269 (98%), Strand = Plus / Plus

```

Query:      25 GCTCCCACTCCATGAGGTATTTCTTCACATCCGTGTCCCGGCCCGCGCGGGGAGCCCC 84
              |||
Sbjct:      1  GCTCCCACTCCATGAGGTATTTCTTCACATCCGTGTCCCGGCCCGCGCGGGGAGCCCC 60

Query:      85 GCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCTGTGCGGTTTCGACAGCGACGCCG 144
              |||
Sbjct:      61 GCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCTGTGCGGTTTCGACAGCGACGCCG 120

Query:      145 CGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCGGAGTATTGGG 204
              |||
Sbjct:      121 CGAGCCAGAAGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCGGAGTATTGGG 180

Query:      205 ACCAGGAGACACGGAATATGAAGGCCCACTCACA---TGACCGAGTGGACCTGGGGACCC 261
              |||
Sbjct:      181 ACCAGGAGACACGGAATATGAAGGCCCACTCACAGACTGACCGAGTGGACCTGGGGACCC 240

Query:      262 TCGCGGGCTACTACAACCAGA-CGAGGAC 289
              |||
Sbjct:      241 TCGCGGGCTACTACAACCAGAGCGAGGAC 269

```

A2-2/2

>K23FW

TCATGAGGTATTTCTCCCATCCGTGTCCTGGCCCCGCGCGGGGAGCCCCGCTTCATCGC
 AGTGGGCTACGTGGACGACACGCGAGTTCGTGCGGTTCGACAGCGACGCCGCGAGTCCAAG
 AGGGGAGCCGCGGGAGCCGTGGGTGGAGCAGGAGGGGCCGAGTATTGGGACCGGGAGAC
 ACAGAAGTACAAGCGCCAGGCACAGGCTGACCGAGTGAACCTGCGGAACTGCGCGGCTA
 CTACAACCAGAGGAGGGCA

>K23RV
 TCTCAGCCACTCCTCGTCCCCAGGCTCCCACTCCATGAGGTATTTCTCCACATCCGTGTC
 CTGCCCCGCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCGAGTT
 CGTGCGGTTCGACAGCGACGCCGCGAGTCCAAGAGGGGAGCCGCGGGAGCCGTGGGTGGA
 GCAGGAGGGGCCGAGTATTGGGACCGGGAGACACAGAAGTACAAGCGCCAGGCACAGGC
 GACCGAGTAACTGCGGAAACGTA

CLUSTAL 2.1 multiple sequence alignment

```

K23FW      -----TCATGAGGTATTTCTCC-CATCCGTGTC  27
K23RV      TCTCAGCCACTCCTCGTCCCCAGGCTCCCACTCCATGAGGTATTTCTCCACATCCGTGTC  60
                        *****

K23FW      CTGCCCCGCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCGAGTT  87
K23RV      CTGCCCCGCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCGAGTT  120
                        *****

K23FW      CGTGCGGTTCGACAGCGACGCCGCGAGTCCAAGAGGGGAGCCGCGGGAGCCGTGGGTGGA  147
K23RV      CGTGCGGTTCGACAGCGACGCCGCGAGTCCAAGAGGGGAGCCGCGGGAGCCGTGGGTGGA  180
                        *****

K23FW      GCAGGAGGGGCCGAGTATTGGGACCGGGAGACACAGAAGTACAAGCGCCAGGCACAGGC  207
K23RV      GCAGGAGGGGCCGAGTATTGGGACCGGGAGACACAGAAGTACAAGCGCCAGGCACAGGC  240
                        *****

K23FW      TGACCGAGTGAACCTGCGGAAACTGCGCGGCTACTACAACCAGAGGAGGGCA  259
K23RV      -GACCGAGTAA--CTGCGGAAAC-----GTA  263
                        ***** *

```

>K23SeqCons
 TCTCAGCCACTCCTCGTCCCCAGGCTCCCACTCCATGAGGTATTTCTCCACATCCGTGTC
 CTGCCCCGCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCGAGTT
 CGTGCGGTTCGACAGCGACGCCGCGAGTCCAAGAGGGGAGCCGCGGGAGCCGTGGGTGGA
 GCAGGAGGGGCCGAGTATTGGGACCGGGAGACACAGAAGTACAAGCGCCAGGCACAGGC
 TGACCGAGTGAACCTGCGGAAACTGCGCGGCTACTACAACCAGAGGAGGGCA

Not HLA-A result.

A2-1/2

>K23FW
 CATACCCCCTACCTCCCAGGTATATTCTTCCATCCGTGTCCTGGCCCCGCGCGGGGAGCC
 CCGCTTCATCGCCGTGGGCTACGTGGACGACACGCGAGTTCGTGCGGTTCGACAGCGACGC
 CGCGAGCCAGAAGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGAGTATTG
 GGACCAGGAGACACGGAATGTGAAGGCCCACTCACAGACTGACCGAGCGAACCTGGGGAC
 CCTGCGCGGCTACTACAACCAGAGCGAGGGCA

>K23RV
 TCTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTATTTCTTCACATCCGTGTC
 CCGCCCCGCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCGAGTT
 CGTGCGGTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGA
 GCAGGAGGGGCCGAGTATTGGGACCAGGAGACACGGAATGGAAGGCCCACTCACAGACG
 ATGGAAGAAAGCCTCCATCCAGGAGGGGG

CLUSTAL 2.1 multiple sequence alignment

```

K23FW      -----CATACCCCCTAC-CTCCCA-----GGTATATTCTTC-CATCCGTGT  38
K23RV      TCTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTAT-TTCTTCACATCCGTGT  59
                        *   *** *   *****   *****

K23FW      CCGGCCCCGCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCGAGT  98
K23RV      CCGGCCCCGCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCGAGT  119
                        *****

```

K23FW TCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAAGATGGAGCCGCGGGCGCCGTGGATAG 158
 K23RV TCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAAGATGGAGCCGCGGGCGCCGTGGATAG 179

K23FW AGCAGGAGGGGCCGGAGTATTGGGACCAGGAGACACGGAATGTGAAGGCCCACTCACAGA 218
 K23RV AGCAGGAGGGGCCGGAGTATTGGGACCAGGAGACACGGAATG-GAAGGCCCACTCACAGA 238

K23FW CTGACCGAGCGAACCTGGGGACCTGCGCGGCTACTACAACCAGAGCGAGGGCA 272
 K23RV C-GATGGAAGAAAAGC-----CTCCATCCAGGGAGGGGG-- 270
 *

>K23SeqCons
 TCTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTATTTCTTCACATCCGTGT
 CCCGGCCCCGCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAG
 TTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAAGATGGAGCCGCGGGCGCCGTGGAT
 AGAGCAGGAGGGGCCGGAGTATTGGGACCAGGAGACACGGAATGTGAAGGCCCACTCAC
 AGACTGACCGAGCGAACCTGGGGACCTGCGCGGCTACTACAACCAGAGCGAGGGCA

>IMGTHLA:HLA00004 A*01:04N 1099 bp
 Length = 1099

Plus Strand HSPs:

Score = 1333 (206.1 bits), Expect = 9.3e-57, P = 9.3e-57, Group = 1
 Identities = 269/272 (98%), Positives = 269/272 (98%), Strand = Plus / Plus

Query: 21 CAGGCTCCCACTCCATGAGGTATTTCTTCACATCCGTGTCCCGCCCCGCGCGGGGAGC 80
 | |||||
 Sbjct: 71 CGGGCTCCCACTCCATGAGGTATTTCTTCACATCCGTGTCCCGCCCCGCGCGGGGAGC 130
 Query: 81 CCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACG 140
 |||||
 Sbjct: 131 CCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACG 190
 Query: 141 CCGCGAGCCAGAAGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGGAGTATT 200
 |||||
 Sbjct: 191 CCGCGAGCCAGAAGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGGAGTATT 250
 Query: 201 GGGACCAGGAGACACGGAATGTGAAGGCCCACTCACAGACTGACCGAGCGAACCTGGGGA 260
 |||||
 Sbjct: 251 GGGACCAGGAGACACGGAATATGAAGGCCCACTCACAGACTGACCGAGCGAACCTGGGGA 310
 Query: 261 CCCTGCGCGGCTACTACAACCAGAGCGAGGGC 292
 |||||
 Sbjct: 311 CCCTGCGCGGCTACTACAACCAGAGCGAGGAC 3

A2-2/1

>K23FW
 CGACCCTACCTGGAAGGTATTTCTCCCATCCGTGTTCTGGGCCCGCGGGGAGGCC
 CCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGA
 CGCCGCGAGTCCAAGAGGGGAGCCGCGGGAGCCGTGGGTGGAGCAGGAGGGGCCGGA
 GTATTGGGACCGGGAGACACAGAAGTACAAGCGCCAGGCACAGGCTGACCGAGTGAA
 CCTGCGGAAACTGCGCGGCTACTACAACCAGAGCGAGGACAT

>K23RV
 TTCTCAGCCACTCCTCGTCCCCAGGCTCCCACTCCATGAGGTATTTCTCCACATCCG
 TGTCTGGCCCGCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACA
 CGCAGTTTCGTGCGGTTTCGACAGCGACGCCGCGAGTCCAAGAGGGGAGCCGCGGGAGC
 CGTGGGTGGAGCAGGAGGGGCCGGAGTATTGGGACCGGGAGACACAGAAGTACAAGC
 GCCAGGCACAGGCGACCGAGTAAGTGTAGGTCTTATGTTTGT

CLUSTAL 2.1 multiple sequence alignment

K23FW -----CGACCCTA-----CCTGGAAGGTATTTCTCC-CATCCGTGT 35
 K23RV TTCTCAGCCACTCCTCGTCCCCAGGCTCCCACTCCATGAGGTATTTCTCCACATCCGTGT 60
 *
 K23FW TCGGGCCCCGCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGT 95
 K23RV CCTGGCCCCGCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGT 120

```

* ****
K23FW      TCGTGCGGTTTCGACAGCGACGCCGCGAGTCCAAGAGGGGAGCCGCGGGAGCCGTGGGTGG 155
K23RV      TCGTGCGGTTTCGACAGCGACGCCGCGAGTCCAAGAGGGGAGCCGCGGGAGCCGTGGGTGG 180
          ****

K23FW      AGCAGGAGGGGCCGGAGTATTGGGACCGGGAGACACAGAAGTACAAGCGCCAGGCACAGG 215
K23RV      AGCAGGAGGGGCCGGAGTATTGGGACCGGGAGACACAGAAGTACAAGCGCCAGGCACAGG 240
          ****

K23FW      CTGACCGAGTGAACCTGCGGAAACTGCGCGGCTACTACAACCAGAGCGAGGACAT 270
K23RV      C-GACCGAGTAA--CTGTTAGGTCT-TATGTTTGT----- 271
          * **** * ** ** *

```

```

>K23SeqCons
TTCTCAGCCACTCCTCGTCCCCAGGCTCCCACTCCATGAGGTATTTCTCCACATC
CGTGTTCCGGCCCCGCCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGAC
GACACGCAAGTTCGTGCGGTTTCGACAGCGACGCCGCGAGTCCAAGAGGGGAGCCGC
GGGAGCCGTGGGTGGAGCAGGAGGGGCCGGAGTATTGGGACCGGGAGACACAGAA
GTACAAGCGCCAGGCACAGGTGACCGAGTGAACCTGCGGAACTGCGCGGCTAC
TACAACCAGAGCGAGGACAT

```

Not HLA-A result.

A3-1/2

```

>K23FW
CTTGCTGCTCGTGCGGCCGGAGGGCGCTTCTCCGCGGTACCGGCAGGACGCCT
ACGACGGCAAGGATTACATCGCCCTGAACGAGGACCTGCGCTCTTGACCGCGGC
GGACATGGCGGCTCAGATCACCAGCGCAAGTGGGAGCGGCCCATGCGCGGGAG
CAGCTGAGAGTCTACCTGGATGGCCGGTGCGTGAGGGGCTCCGAGATACCTGG
AGAACGGGAAG

```

```

>K23RV
GTGGGTTCTCACACCGTCCAGATAATGTATGGCTGCGACGTGGGGCCGGACGGGC
GCTTCTCCGCGGGTACCGGCAGGACGCCTACGACGGCAAGGATTACATCGCCCT
GAACGAGGACCTGCGCTCTTGACCGCGCGGACATGGCAGCTCAGATCACCAG
CGCAAGTGGGAGGCGGCCCATGAGGCGGAGCAGGGAGAGCCTACCGAGTGCACC
GCTCTCAG

```

CLUSTAL 2.1 multiple sequence alignment

```

K23FW      -----CTT-----GCTGCT-CGTGGGGCCGGA-GGGCGCTTC 30
K23RV      GTGGGTTCTCACACCGTCCAGATAATGTATGGCTGCGACGTGGGGCCGGACGGGCGCTTC 60
          **          *****

K23FW      CTCCGCGGGTACCGGCAGGACGCCTACGACGGCAAGGATTACATCGCCCTGAACGAGGAC 90
K23RV      CTCCGCGGGTACCGGCAGGACGCCTACGACGGCAAGGATTACATCGCCCTGAACGAGGAC 120
          ****

K23FW      CTGCGCTCTTGACCGCGCGGACATGGCGGCTCAGATCACCAGCGCAAGTGGGAGGCG 150
K23RV      CTGCGCTCTTGACCGCGCGGACATGGCAGCTCAGATCACCAGCGCAAGTGGGAGGCG 180
          ****

K23FW      GCCCATGCGGCGGAGCAGCTGAGAGTCTACCTGGATGGCCGGTGCGTGAGGGGCTCCGC 210
K23RV      GCCCATGAGGCGGAGCAGG-GAGAGCCTACC-GGA-----GTGCAC-----CGCTCT-C 226
          ***** ** ** ** **

K23FW      AGATACCTGGAGAACGGGAAG 231
K23RV      AG----- 228
          **

```

```

>K23SeqCons
GTGGGTTCTCACACCGTCCAGATAATGTATGGCTGCGACGTGGGGCCGGACGG
GCGCTTCCTCCGCGGGTACCGGCAGGACGCCTACGACGGCAAGGATTACATCG
CCCTGAACGAGGACCTGCGCTCTTGACCGCGCGGACATGGCGGCTCAGATC
ACCAAGCGCAAGTGGGAGGCGGCCCATGCGGCGGAGCAGCTGAGAGTCTACCT
GGATGGCCGGTGCGTGAGGGGCTCCGAGATACCTGGAGAACGGGAAG

```

>IMGTHLA:HLA05907 A*01:01:26 822 bp
Length = 822

Plus Strand HSPs:

Score = 1245 (192.8 bits), Expect = 1.2e-52, P = 1.2e-52, Group = 1
Identities = 253/258 (98%), Positives = 253/258 (98%), Strand = Plus / Plus

```
Query:      4  GGTTCCTCACACCGTCCAGATAATGTATGGCTGCGACGTGGGGCCGGACGGGCGCTTCCTC 63
      |||
Sbjct:    270  GGTTCCTCACACCATCCAGATAATGTATGGCTGCGACGTGGGGCCGGACGGGCGCTTCCTC 329

Query:     64  CGCGGGTACCGGCAGGACGCCTACGACGGCAAGGATTACATCGCCCTGAACGAGGACCTG 123
      |||
Sbjct:    330  CGCGGGTACCGGCAGGACGCCTACGACGGCAAGGATTACATCGCCCTGAACGAGGACCTG 389

Query:    124  CGCTCTTGGACCGCGGCGGACATGGCGGCTCAGATCACCAAGCGCAAGTGGGAGGCGGCC 183
      |||
Sbjct:    390  CGCTCTTGGACCGCGGCGGACATGGCGGCTCAGATCACCAAGCGCAAGTGGGAGGCGGTC 449

Query:    184  CATGCGCGGAGCAGCTGAGAGTCTACCTGGATGGCCGGTGCCTGGAGGGGTCCGCAGA 243
      |||
Sbjct:    450  CATGCGCGGAGCAGCGGAGAGTCTACCTGGAGGGCCGGTGCCTGGACGGGTCCGCAGA 509

Query:    244  TACCTGGAGAACGGGAAG 261
      |||
Sbjct:    510  TACCTGGAGAACGGGAAG 527
```

A3-2/2

>K23FW

TGCCGGAGTGGGGCCGGACGGGCGCTTCCTCCGCGGGTACCGGCAGGACGCCT
ACGACGGCAAGGATTACATCGCCCTGAACGAGGACCTGCGCTCTTGGACCGCG
GCGGACATGGCAGCTCAGATCACCAAGCGCAAGTGGGAGGCGGCCATGCGGC
GGAGCAGCTGAGAGTCTACCTGGATGGCCGGTGCCTGGACGGGTCCGCAGAT
ACCTGGAGAACGGGAAGA

>K23RV

GATGGTTCTCACACCATCCAGATAATGTATGGCTGCGACGTGGGGCCGGACGG
GCGCTTCCTCCGCGGGTACCGGCAGGACGCCTACGACGGCAAGGATTACATCG
CCCTGAACGAGGACCTGCGCTCTTGGACCGCGGCGGACATGGCAGCTCAGATC
ACCAAGCGCAAGTGGGAGGCGGCCATGCGGCGGAGCAGCGGAGAGCCTACCG
GGGTGCCACGCTATCAGACACT

CLUSTAL 2.1 multiple sequence alignment

```
K23FW      --TG-----CCGGA-----GTGGGCGCGGACGGGCGCTTC 28
K23RV      GATGGTTCTCACACCATCCAGATAATGTATGGCTGCGACGTGGGGCCGGACGGGCGCTTC 60
          **                * * * * *

K23FW      CTCCGCGGGTACCGGCAGGACGCCTACGACGGCAAGGATTACATCGCCCTGAACGAGGAC 88
K23RV      CTCCGCGGGTACCGGCAGGACGCCTACGACGGCAAGGATTACATCGCCCTGAACGAGGAC 120
          *****

K23FW      CTGCGCTCTTGGACCGCGGCGGACATGGCAGCTCAGATCACCAAGCGCAAGTGGGAGGCG 148
K23RV      CTGCGCTCTTGGACCGCGGCGGACATGGCAGCTCAGATCACCAAGCGCAAGTGGGAGGCG 180
          *****

K23FW      GCCCATGCGGCGGAGCAGCTGAGAGTCTACCTGGATGGCCGGTGCCTGGACGGGTCCGC 208
K23RV      GCCCATGCGGCGGAGCAGCGGAGAGCCTACCGGGGTGCC-----AC--GCTAT-C 227
          ***** * * * * * * * * * * * * * * *

K23FW      AGATACCTGGAGAACGGGAAGA 230
K23RV      AGACACT----- 234
          *** **
```

>K23SeqCons

GATGGTTCTCACACCATCCAGATAATGTATGGCTGCGACGTGGGGCCGGAC
GGGCGCTTCCTCCGCGGGTACCGGCAGGACGCCTACGACGGCAAGGATTAC
ATCGCCCTGAACGAGGACCTGCGCTCTTGGACCGCGGCGGACATGGCAGCT
CAGATCACCAAGCGCAAGTGGGAGGCGGCCATGCGGCGGAGCAGCTGAGA
GTCTACCTGGATGGCCGGTGCCTGGACGGGTCCGCAGATACCTGGAGAAC
GGGAAGA

>IMGTHLA:HLA02920 A*01:26 546 bp
Length = 546

Plus Strand HSPs:

Score = 1278 (197.8 bits), Expect = 5.7e-54, P = 5.7e-54, Group = 1
Identities = 258/261 (98%), Positives = 258/261 (98%), Strand = Plus / Plus

```
Query:      1 GATGGTTCTCACACCATCCAGATAATGTATGGCTGCGACGTGGGGCCGGACGGGCGCTTC 60
||| |||||
Sbjct:    267 GACGGTTCTCACACCATCCAGATAATGTATGGCTGCGACGTGGGGCCGGACGGGCGCTTC 326

Query:     61 CTCCGCGGGTACCGGCAGGACGCCTACGACGGCAAGGATTACATCGCCCTGAACGAGGAC 120
||| |||||
Sbjct:    327 CTCCGCGGGTACCGGCAGGACGCCTACGACGGCAAGGATTACATCGCCCTGAACGAGGAC 386

Query:    121 CTGCGCTCTTGGACCGCGGCGGACATGGCAGCTCAGATCACCAAGCGCAAGTGGGAGGCG 180
||| |||||
Sbjct:    387 CTGCGCTCTTGGACCGCGGCGGACATGGCAGCTCAGATCACCAAGCGCAAGTGGGAGGCG 446

Query:    181 GCCCATGCGGCGGAGCAGCTGAGAGTCTACCTGGATGGCCGGTGCCTGGACGGGCTCCGC 240
||| |||||
Sbjct:    447 GCCCATGCGGCGGAGCAGCGGAGAGTCTACCTGGAGGGCCGGTGCCTGGACGGGCTCCGC 506

Query:    241 AGATACCTGGAGAACGGGAAG 261
||| |||||
Sbjct:    507 AGATACCTGGAGAACGGGAAG 527
```

A4-2/2H

>K23FW
CCCCCGTCTGTTCTGAGGCCCCCTGAGTGCTGGGCCCTGGGCTTCTAC
CTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGACCAAGCC
AGGACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGATAG

>K23RV
CCCCCCCCAAGACACATATGACCCACCACCCATCTCTGACCATGAGGC
CACCTGAGGTGCTGGGCCCTGGGCTTTTACCCTGCGGAGATCACACTA
CCGGCAGCGGGAGGGGAGGACCAACCCGCACCGAGCCG

CLUSTAL 2.1 multiple sequence alignment

```
K23FW      ---CCCCG-----TCTGTCTCTGAGGCC-CCCTGAG-T 29
K23RV      CCCCCCAAGACACATATGACCCACCACCCATCTCTGACCATGAGGCCACCCTGAGGT 60
          *****                      ***** *

K23FW      GCTGGGCCCTGGGCTTCTACCCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGG 89
K23RV      GCTGGGCCCTGGGCTTTTACCCTGCGGAGATCACACTA--CCGGCAGCGGGAGGGGAGGG 118
          *****                      * ***** **

K23FW      ACCAGACCCAGGACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGATAG 138
K23RV      ACCAAACCG---CACCGAGC-CG----- 138
          ****  ****      *** *****
```

>K23SeqCons
CCCCCCCCAAGACACATATGACCCACCACCCATCTCTGACCATGAGGC
CACCTGAGGGCCCCCTGAGTGCTGGGCCCTGGGCTTCTACCCTGCGGA
GATCACACTGACCTGGCAGCGGGATGGGGAGGACCAAGACCCAGGACACG
GAGTCTCGTGGAGACCAGGCCTGCAGGGGATAG

>IMGTHLA:HLA00004 A*01:04N 1099 bp
Length = 1099

Plus Strand HSPs:

Score = 599 (95.9 bits), Expect = 1.3e-23, P = 1.3e-23, Group = 1
Identities = 125/130 (96%), Positives = 125/130 (96%), Strand = Plus / Plus

```
Query:     51 ACCCTGAGGGCCCCCTGAG-TGCTGGGCCCTGGGCTTCTACCCTGCGGAGATCACACTGA 109
||| |||||
Sbjct:    660 ACCATGAGGCCACCCTGAGGTGCTGGGCCCTGGGCTTCTACCCTGCGGAGATCACACTGA 719
```

```

Query:   110 CCTGGCAGCGGGATGGGGAGGACCAGACCCAGGACACGGAGCTCGTGGAGACCAGGCCTG 169
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   720 CCTGGCAGCGGGATGGGGAGGACCAGACCCAGGACACGGAGCTCGTGGAGACCAGGCCTG 779

Query:   170 CAGGGGATAG 179
          |||||||||
Sbjct:   780 CAGGGGATGG 789

```

A4-3H/1

```

>K23FW
CTGTGCTGGTGTGGGGTAGGCATCCTGCCGATCACACGGAGCTCGTGGA
GACAGGCCTGCAGGGGATGGAACCTTCCAAAAGTGGGCGGCTGTGGTGG
TGCCTTCTGGAAGGAGCAAAGATACACCTGCCATGTGCAGCATGAGGG
TCTGCCCAAGCCCCCTCACCTGAGATGGAC

```

```

>K23RV
TTTTACCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGACC
AGACCCAGGACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGATGGAAC
CTTCCAGAAGTGGGCGGCTGTGGTGGTGCCTTCGGAGAGGAGCAGAGAT
ACACCTGACCATGTGCAGAAGAGGACTACAG

```

CLUSTAL 2.1 multiple sequence alignment

```

K23FW      -----CTGTG-----CTGGT-GTGGGGTAGGCA---TCCTGCCGATCAC 35
K23RV      TTTTACCCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGACCAGACCCAGGAC 60
          *** *          * * * * * * * * * * * * * * *

K23FW      ACGGAGCTCGTGGAGAC-AGGCCTGCAGGGGATGGAACCTTCCAAAAGTGGGCGGCTGTG 94
K23RV      ACGGAGCTCGTGGAGACCAGGCCTGCAGGGGATGGAACCTTCCAGAAGTGGGCGGCTGTG 120
          *****

K23FW      GTGGTGCCTTCTGGAAGGAGCAAAGATACACCTG-CCATGTGCAGCATGAGGGTCTGCC 153
K23RV      GTGGTGCCTTC-GGAGAGGAGCAGAGATACACCTGACCATGTGCAG-AAGAGGA-CTAC- 176
          ***** * * * * * * * * * * * * * * * * * * *

K23FW      CAAGCCCCTCACCTGAGATGGAC 177
K23RV      --AG----- 178
          **

```

```

>K23SeqCons
TTTTACCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGAC
CAGACCCAGGACACGGAGCTCGTGGAGACAGGCCTGCAGGGGATGGA
CCTTCCAAAAGTGGGCGGCTGTGGTGGTGCCTTCTGGAAGGAGCAA
GATACACCTGCCATGTGCAGCATGAGGGTCTGCCCAAGCCCCTCACCC
TGAGATGGAC

```

>IMGTHLA:HLA00004 A*01:04N 1099 bp
Length = 1099

Plus Strand HSPs:

Score = 954 (149.2 bits), Expect = 1.2e-39, P = 1.2e-39, Group = 1
Identities = 196/201 (97%), Positives = 196/201 (97%), Strand = Plus / Plus

```

Query:     1 TTTTACCCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGACCAGACCCAGGAC 60
          || |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   695 TTCTACCCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGACCAGACCCAGGAC 754

Query:     61 ACGGAGCTCGTGGAGAC-AGGCCTGCAGGGGATGGAACCTTCCAAAAGTGGGCGGCTGTG 119
          ||||||||||||||| ||||||||||||||||||||||||||| |||||||||||
Sbjct:   755 ACGGAGCTCGTGGAGACCAGGCCTGCAGGGGATGGAACCTTCCAGAAGTGGGCGGCTGTG 814

Query:    120 GTGGTGCCTTCTGGAAGGAGCAAAGATACACCTGCCATGTGCAGCATGAGGGTCTGCCC 179
          ||||||||||||||| ||||| ||||||||||||||||||||||| |||||||
Sbjct:   815 GTGGTGCCTTCTGGAGAGGAGCAGAGATACACCTGCCATGTGCAGCATGAGGGTCTGCCC 874

Query:    180 AAGCCCCTCACCTGAGATGG 200
          |||||||||||||||
Sbjct:   875 AAGCCCCTCACCTGAGATGG 895

```

Edited sequences

>K23Edit1

```

TTCTCAGCCACTGCTCGCCCCCAGGCTCCCACTCCATGAGGTATTTC
TTCACATCCGTGTCCCGGCCCGGCCGCGGGGAGCCCCGCTTCATCGC
CGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACG
CCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAG
GGGCCGGAGTATTGGGACCAGGAGACACGGAATGTGAAGGCCCACTC
ACATGACCGAGCGAACCTGGGGACCCTGCGCGGCTACTACAACCAGA
CGAGGACCCG

```

>IMGTHLA:HLA03435 A*03:41 546 bp
Length = 546

Plus Strand HSPs:

Score = 1285 (198.9 bits), Expect = 2.7e-54, P = 2.7e-54, Group = 1
Identities = 265/269 (98%), Positives = 265/269 (98%), Strand = Plus / Plus

```

Query:      25 GCTCCCACTCCATGAGGTATTTCTTCACATCCGTGTCCCGGCCCGGCCGCGGGGAGCCCC 84
              |||
Sbjct:      1  GCTCCCACTCCATGAGGTATTTCTTCACATCCGTGTCCCGGCCCGGCCGCGGGGAGCCCC 60

Query:      85 GCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACGCCG 144
              |||
Sbjct:      61 GCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACGCCG 120

Query:     145 CGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGAGTATTGGG 204
              |||
Sbjct:     121 CGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGAGTATTGGG 180

Query:     205 ACCAGGAGACACGGAATGTGAAGGCCCACTCACA---TGACCGAGCGAACCTGGGGACCC 261
              |||
Sbjct:     181 ACCAGGAGACACGGAATGTGAAGGCCCACTCAGAGTACCGAGCGAACCTGGGGACCC 240

Query:     262 TCGCGCGGCTACTACAACCAGA-CGAGGAC 289
              |||
Sbjct:     241 TCGCGCGGCTACTACAACCAGAGCGAGGAC 269

```

>K23Edit2

```

TCTCAGCCACTGCTCGCCCCCAGGCTCCCACTCCATGAGGTATTTCT
TCACATCCGTGTCCCGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCC
GTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACGC
CGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGG
GGCCGGAGTATTGGGACCAGGAGACACGGAATATGAAGGCCCACTCA
CAGACTGACCGAGTGCACCTGGGGACCCTGCGCGGCTACTACAACCA
GAGCGAGGGCA

```

>IMGTHLA:HLA01718 A*03:01:01:02N 1163 bp
Length = 1163

Plus Strand HSPs:

Score = 1315 (203.4 bits), Expect = 5.7e-56, P = 5.7e-56, Group = 1
Identities = 267/272 (98%), Positives = 267/272 (98%), Strand = Plus / Plus

```

Query:      21 CAGGCTCCCACTCCATGAGGTATTTCTTCACATCCGTGTCCCGGCCCGGCCGCGGGGAGC 80
              |
Sbjct:      71 CGGGCTCCCACTCCATGAGGTATTTCTTCACATCCGTGTCCCGGCCCGGCCGCGGGGAGC 130

Query:      81 CCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACG 140
              |||
Sbjct:     131 CCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACG 190

Query:     141 CCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGAGTATT 200
              |||
Sbjct:     191 CCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGAGTATT 250

Query:     201 GGGACCAGGAGACACGGAATATGAAGGCCCACTCAGAGTACCGAGTGCACCTGGGGA 260
              |||

```

Sbjct: 251 GGGACCAGGAGACACGGAATGTGAAGGCCAGTCACAGACTGACCGAGTGGACCTGGGGA 310

Query: 261 CCCTGCGCGGCTACTACAACCAGAGCGAGGCC 292
 |||||

Sbjct: 311 CCCTGCGCGGCTACTACAACCAGAGCGAGGCC 342

K24 29-04

A2-1/1

>K24FW
 CGCGTACTAGAGTATTTCTTCCATCCGTGTCCCGGCCCGGCCGCGGGAGCCCCGCTTCA
 TCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGCGCCCCGAGGCC
 AAAGGTGGGAGCCGCGGGCGCCGTGTATAGAGCAGGAGGGCGCGGAGTATTGGGACCGGG
 AGACACGGAATGTGAAGGCCAGTCACAGACTGACCGAGTGGACCTGGGGACCCTGCGCG
 GCTACTACAACCAGAGCGAGGACA

>K24RV
 CTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTATTTCTTCACATCCGTGTCC
 CGGCCCCGCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTC
 GTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAG
 CAGGAGGGGCGGAGTATTGGGACCAGGAGACACGGAATGTGAAGGCCAGTCACAGACG
 ACCGAGGGTACCAGCACTGTACG

CLUSTAL 2.1 multiple sequence alignment

K24FW	-----CGCGTACT----AGAGTATTTCTTC-CATCCGTGTCC	32
K24RV	CTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTATTTCTTCACATCCGTGTCC	60
	* * * *	
K24FW	CGGCCCCGCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTC	92
K24RV	CGGCCCCGCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTC	120

K24FW	GTGCGGTTTCGACAGCG-CGCCCCGAGGCCAAAGGTGGGAGCCGCGGGCGCCGTGTATAGA	151
K24RV	GTGCGGTTTCGACAGCGACGCCGCGAG-CCAGAGGATGGAGCCGCGGGCGCCGTGGATAGA	179
	***** * * * * *	
K24FW	GCAGGAGGGGCGGAGTATTGGGACCGGGAGACACGGAATGTGAAGGCCAGTCACAGAC	211
K24RV	GCAGGAGGGGCGGAGTATTGGGACCAGGAGACACGGAATGTGAAGGCCAGTCACAGAC	239

K24FW	TGACCGAGTGGACCTGGGGACCCTGCGCGGCTACTACAACCAGAGCGAGGACA	264
K24RV	-GACCGAGGTACCAG----CACTGTACG-----	263
	***** * * * * * * * * *	

>K24SeqCons
 CTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTATTTCTTCACATCCGTG
 TCCCGGCCCGCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACAG
 CAGTTCGTGCGGTTTCGACAGCGCCCCGAGGCCAAAGGTGGGAGCCGCGGGCGCCG
 TGTATAGAGCAGGAGGGGCGGAGTATTGGGACCGGGAGACACGGAATGTGAAGGCC
 CAGTCACAGACTGACCGAGTGGACCTGGGGACCCTGCGCGGCTACTACAACCAGAGC
 GAGGACA

>IMGTHLA:HLA01718 A*03:01:01:02N 1163 bp
 Length = 1163

Plus Strand HSPs:

Score = 1263 (195.6 bits), Expect = 1.3e-53, P = 1.3e-53, Group = 1
 Identities = 263/273 (96%), Positives = 263/273 (96%), Strand = Plus / Plus

Query: 20 CAGGCTCCCACTCCATGAGGTATTTCTTCACATCCGTGTCCCGGCCCGCGGGGAGC 79
 | |||||

Sbjct: 71 CGGGCTCCCACTCCATGAGGTATTTCTTCACATCCGTGTCCCGGCCCGCGGGGAGC 130

Query: 80 CCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCG-CG 138
 |||||

Sbjct: 131 CCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACG 190

Query: 139 CCCCAGGGCCAAAGGTGGGAGCCGCGGGCGCCGTGTATAGAGCAGGAGGGGCGGAGTAT 198

```

Sbjct: 191 CCGCGAG-CCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGGAGTAT 249
Query: 199 TGGGACCGGGAGACACGGAATGTGAAGGCCAGTCACAGACTGACCGAGTGGACCTGGGG 258
Sbjct: 250 TGGGACCAGGAGACACGGAATGTGAAGGCCAGTCACAGACTGACCGAGTGGACCTGGGG 309
Query: 259 ACCCTGCGCGGCTACTACAACCAGAGCGAGGAC 291
Sbjct: 310 ACCCTGCGCGGCTACTACAACCAGAGCGAGGCC 342

```

>K24FW
AGCTCACGCTGAGTATTCTTCCATCCGTGTCCCGGCCCGGCCGCGGGAGCCCC
GTTTCATCGAGTGGGCTACGTGACGACACGCAAGTTCGTGCGGTTTCGACAGCGA
CGCCCGAGCCAGAGGATGAGCCGCGGGCCCGTGGATAGACAGAGAGGGTCCG
GAGTATTGGGACGGGGAGACACGGAAAGTGAAGGCCCATCACAGACTCACCGAG
TGGACCTGGGGACCTGCGCGGCTACTACAACGACGAGCGAGGGCTA

CLUSTAL 2.1 multiple sequence alignment

>K24SeqCons
GTCCTACGCCACTCCTCGTCCCCAGGCTCTCACTCCATGAGGTATTCTTCACA
TCCGTGTCCCGGCCCGGCCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGT
GGACGACACGCAAGTTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGGATGG
AGCCGCGGGCGCGGTGGATAGACAGGAGGGTCCGGAGTATTGGGACGGGGAG
ACACGGAAAGTGAAGGCCCATCACAGACTACCGAGTGGACCTGGGGACCCCT
CGCGGGCTACTACAACACAGCGAGGGGCTA

Plus Strand HSPs:

```

Query:      22  CAGGCTCTCACTCCATGAGGTATTTCTTCACATCCGTGTCCCGGCCCGGCCGCGGGGAGC   81
             | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct:      71  CGGGCTCTCACTCCATGAGGTATTTCTTCACATCCGTGTCCCGGCCCGGCCGCGGGGAGC   130

Query:      82  CCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACG   141

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Sbjct: 131 CCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACG 190

Query: 142 CCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGTCCGAGTATT 201
 |||

Sbjct: 191 CCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGTCCGAGTATT 250

Query: 202 GGGACGGGGAGACACGGAAGTGAAGGCCACTCACAGACTCACCGAGTGGACCTGGGGA 261
 |||

Sbjct: 251 GGGACGGGGAGACACGGAAGTGAAGGCCACTCACAGACTCACCGAGTGGACCTGGGGA 310

Query: 262 CCCTGCGCGGCTACTACAACCAGAGCGAGGGC 293
 |||||||||||||||||||||||||

Sbjct: 311 CCCTGCGCGGCTACTACAACCAGAGCGAGGCC 342

A2-1/2

>K24FW
 CGCGTCGGAGGTACATTCTTCCATCCGTGTCCCGGCCCGGCCGCGGGGAGCCCCGCTTCA
 TCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACGCCGCGAGCC
 AGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGGCCGAGTATTGGGACCAGG
 AGACACGGAATGTGAAGGCCAGTCACAGACTGACCGAGTGGACCTGGGGACCCCTGCGCG
 GCTACTACAACCAGAGCGAGGGCA

>K24RV
 CTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTATTTCTTCACATCCGTGTCC
 CGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTC
 GTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAG
 CAGGAGGGGCCGAGTATTGGGACCAGGAGACACGGAATGTGAAGGCCAGTCACAGACG
 ACCGATGTGCACCCATCATCCGCCTCG

CLUSTAL 2.1 multiple sequence alignment

K24FW	-----CGCGTCG-GAGGTACATTCTTC-CATCCGTGTC	31
K24RV	CTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTAT-TTCTTCACATCCGTGTC	59
	* * * * *	
K24FW	CCGCCCCGCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTT	91
K24RV	CCGCCCCGCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTT	119

K24FW	CGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGA	151
K24RV	CGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGA	179

K24FW	GCAGGAGGGGCCGAGTATTGGGACCAGGAGACACGGAATGTGAAGGCCAGTCACAGAC	211
K24RV	GCAGGAGGGGCCGAGTATTGGGACCAGGAGACACGGAATGTGAAGGCCAGTCACAGAC	239

K24FW	TGACCGA-GTGGACCTGGGGACCTGCGCGGCTACTACAACCAGAGCGAGGGCA	264
K24RV	-GACCGATGTGACCC---ATCATCCGC--CT-----CG-----	267
	***** * * * * *	

>K24SeqCons
 CTCAGCCACTGCTCGCCCCAGGCTCCCACTCCATGAGGTATTTCTTCACATCCGTGTC
 CCGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGT
 TCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATA
 GAGCAGGAGGGGCCGAGTATTGGGACCAGGAGACACGGAATGTGAAGGCCAGTCACA
 GACTGACCGAGTGGACCTGGGGACCTGCGCGGCTACTACAACCAGAGCGAGGGCA

>IMGTHLA:HLA01718 A*03:01:01:02N 1163 bp
 Length = 1163

Plus Strand HSPs:

Score = 1342 (207.4 bits), Expect = 3.4e-57, P = 3.4e-57, Group = 1
 Identities = 270/272 (99%), Positives = 270/272 (99%), Strand = Plus / Plus

Query: 20 CAGGCTCCCACTCCATGAGGTATTTCTTCACATCCGTGTCCCGGCCCGCGGGGAGC 79
 | |||

Sbjct: 71 CGGGCTCCCACTCCATGAGGTATTTCTTCACATCCGTGTCCCGGCCCGCGGGGAGC 130

Query: 80 CCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACG 139
 |||||
 Sbjct: 131 CCCGCTTCATCGCCGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACG 190

Query: 140 CCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGCCGGAGTATT 199
 |||||
 Sbjct: 191 CCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGCCGGAGTATT 250

Query: 200 GGGACCAGGAGACACGGAATGTGAAGGCCAGTCACAGACTGACCGAGTGGACCTGGGGA 259
 |||||
 Sbjct: 251 GGGACCAGGAGACACGGAATGTGAAGGCCAGTCACAGACTGACCGAGTGGACCTGGGGA 310

Query: 260 CCCTGCGCGGCTACTACAACCAGAGCGAGGGC 291
 |||||
 Sbjct: 311 CCCTGCGCGGCTACTACAACCAGAGCGAGGCC 342

A2-2/1

>K24FW
 ACTCCTGACGTATTTCTTCCATCCGTGTCCCGGCCGCGCGGGGAGCCCCGCTTCATC
 GCAGTGGGCTACGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAG
 AGGATGGAGCCGCGGGCGCCGTGGATAGAGCAGGAGGGTCCGGAGTATTGGGACGGGGAG
 ACACGGAAAGTGAAGGCCCACTCACAGACTCACCGAGTGGACCTGGGGACCCTGCGCGGC
 TACTACAACCAGAGCGAGGAC

>K24RV
 TTCTCAGCCACTCCTCGTCCCCAGGCTCTCACTCCATGAGGTATTTCTTCACATCCGTGT
 CCCGGCCCCGCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGT
 TCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAG
 AGCAGGAGGGTCCGGAGTATTGGGACGGGGAGACACGGAAAGTGAAGGCCCACTCACAGA
 CTCACCGAGGGTACCTGGCACTGTA

CLUSTAL 2.1 multiple sequence alignment

K24FW	-----ACTCC-TGACGTATTTCTTC-CATCCGTGT	28
K24RV	TTCTCAGCCACTCCTCGTCCCCAGGCTCTCACTCCATGAGGTATTTCTTCACATCCGTGT	60
	***** **	
K24FW	CCCGGCCCGCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGT	88
K24RV	CCCGGCCCGCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCAGT	120

K24FW	TCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAG	148
K24RV	TCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGATAG	180

K24FW	AGCAGGAGGGTCCGGAGTATTGGGACGGGGAGACACGGAAAGTGAAGGCCCACTCACAGA	208
K24RV	AGCAGGAGGGTCCGGAGTATTGGGACGGGGAGACACGGAAAGTGAAGGCCCACTCACAGA	240

K24FW	CTCACCGAGTGGACCTGGGGACCCTGCGCGGCTACTACAACCAGAGCGAGGAC	261
K24RV	CTCACCGAGGTACCTGG-----CACTGTA-----	265
	***** * ***** ** *	

>K24SeqCons
 TTCTCAGCCACTCCTCGTCCCCAGGCTCTCACTCCATGAGGTATTTCTTCACATCCGTG
 TCCCGGCCCGCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACGACACGCA
 GTTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGGA
 TAGAGCAGGAGGGTCCGGAGTATTGGGACGGGGAGACACGGAAAGTGAAGGCCCACTCA
 CAGACTCACCGAGTGGACCTGGGGACCCTGCGCGGCTACTACAACCAGAGCGAGGAC

>IMGTHLA:HLA01218 A*02:43N 1099 bp
 Length = 1099

Plus Strand HSPs:

Score = 1342 (207.4 bits), Expect = 3.6e-57, P = 3.6e-57, Group = 1
 Identities = 270/272 (99%), Positives = 270/272 (99%), Strand = Plus / Plus

Query: 22 CAGGCTCTCACTCCATGAGGTATTTCTTCACATCCGTGTCCCGGCCCGCGCGGGGAGC 81
 | |||||

Sbjct: 343 GGTTCCTCACACCATCCAGATAATGTATGGCTGCGACGTGGGGTCGGACGGGCGCTTCCTC 402

Query: 62 CGCGGGTACCGGCAGGACGCCCTACGACGGCAAGGATTACATCGCCCTGAACGAGGACCTG 121
 |||

Sbjct: 403 CGCGGGTACCGGCAGGACGCCCTACGACGGCAAGGATTACATCGCCCTGAACGAGGACCTG 462

Query: 122 CGCTCTTGGACCGCGGCGGACATGGCGGCTCATATCACCAGCGCAAGTGGGAGGCGGCC 181
 |||

Sbjct: 463 CGCTCTTGGACCGCGGCGGACATGGCGGCTCAGATCACCAGCGCAAGTGGGAGGCGGCC 522

Query: 182 CATGAGGCGGAGCAGTTGAGAGCCTACCTGGATGGCACGTGCGTGGAGTGGCTCCGCAGA 241
 |||

Sbjct: 523 CATGAGGCGGAGCAGTTGAGAGCCTACCTGGATGGCACGTGCGTGGAGTGGCTCCGCAGA 582

Query: 242 TACCTGGAGAACGGGAAG 259
 |||

Sbjct: 583 TACCTGGAGAACGGGAAG 600

A3-2/2

>K24FW
 CCGGTCCTGCGTAGCTGCGCGTCGGCAGGGCGCTTCCTCCGCGGGTACCGGCAGGACG
 CCTACGACGGCAAGGATTACATCGCCCTGAACGAGGACCTGCGCTCTTGGACCGCGGC
 GGACATGGCGGCTCATATCACCAGCGCAAGTGGGAGGCGGCCCATGAGGCGGAGCAG
 TTGAGAGCCTACCTGGATGGCACGTGCGTGGAGTGGCTCCGCAGATACCTGGAGAACG
 GGAAGA

>K24RV
 TGATGGTTCTCACACCATCCAAATAATGTATGGGTGCGACGTGGGGTCGGACGGGCGC
 TTCCTCCGCGGGTACCGGCAGGACGCCCTACGACGGCAAGGATTACATCGCCCTGAACG
 AGGACCTGCGCTCTTGGACCGCGGCGGACATGGCGGCTCAGATCACCAGCGCAAGTG
 GGAGGCGGCCCATGAGGCGGAGCAGTTAGAGCCTACCTGTAGTGCAACGGTACCAGAC
 GACT

CLUSTAL 2.1 multiple sequence alignment

K24FW	--CCGGTCCT-----GCGTAGCTGCGC-----GTCGGCAGGGCGCTT	35
K24RV	TGATGGTTCTCACACCATCCAAATAATGTATGGGTGCGACGTGGGGTCGGACGGGCGCTT	60
	*** ** * * * *	
K24FW	CCTCCGCGGGTACCGGCAGGACGCCCTACGACGGCAAGGATTACATCGCCCTGAACGAGGA	95
K24RV	CCTCCGCGGGTACCGGCAGGACGCCCTACGACGGCAAGGATTACATCGCCCTGAACGAGGA	120

K24FW	CCTGCGCTCTTGGACCGCGGCGGACATGGCGGCTCATATCACCAGCGCAAGTGGGAGGC	155
K24RV	CCTGCGCTCTTGGACCGCGGCGGACATGGCGGCTCAGATCACCAGCGCAAGTGGGAGGC	180

K24FW	GGCCCATGAGGCGGAGCAGTTGAGAGCCTACCTGGATGGCACGTGCGTGGAGTGGCTCCG	215
K24RV	GGCCCATGAGGCGGAGCAGTT-AGAGCCTACCTGTA-----GTGCAACGGTAC--	227
	***** * **** * * *	
K24FW	CAGATACCTGGAGAACGGGAAGA	238
K24RV	CAGACGACT-----	236
	**** **	

>K24SeqCons
 TGATGGTTCTCACACCATCCAAATAATGTATGGGTGCGACGTGGGGTCGGCAGGGCG
 CTTCTCCGCGGGTACCGGCAGGACGCCCTACGACGGCAAGGATTACATCGCCCTGAA
 CGAGGACCTGCGCTCTTGGACCGCGGCGGACATGGCGGCTCATATCACCAGCGCAA
 GTGGGAGGCGGCCATGAGGCGGAGCAGTTGAGAGCCTACCTGGATGGCACGTGCGT
 GGAGTGGCTCCGCAGATACCTGGAGAACGGGAAGA

>IMGTHLA:HLA06559 A*03:121 546 bp
 Length = 546

Plus Strand HSPs:

Score = 1254 (194.2 bits), Expect = 6.9e-53, P = 6.9e-53, Group = 1
 Identities = 254/258 (98%), Positives = 254/258 (98%), Strand = Plus / Plus

```

Query:      5 GGTTCCTCACACCATCCAAATAATGTATGGGTGCGACGTGGGGTCGGCAGGGCGCTTCCTC 64
            |||
Sbjct:     270 GGTTCCTCACACCATCCAGATAATGTATGGCTGCGACGTGGGGTCGGAAGGGCGCTTCCTC 329

Query:      65 CGCGGGTACCGGCAGGACGCCCTACGACGGCAAGGATTACATCGCCCTGAACGAGGACCTG 124
            |||
Sbjct:     330 CGCGGGTACCGGCAGGACGCCCTACGACGGCAAGGATTACATCGCCCTGAACGAGGACCTG 389

Query:     125 CGCTCTTGGACCGCGCGGACATGGCGGCTCATATCACCAGCGCAAGTGGGAGGCGGCC 184
            |||
Sbjct:     390 CGCTCTTGGACCGCGCGGACATGGCGGCTCAGATCACCAGCGCAAGTGGGAGGCGGCC 449

Query:     185 CATGAGGCGGAGCAGTTGAGAGCCTACCTGGATGGCAGCTGCGTGGAGTGGCTCCGCAGA 244
            |||
Sbjct:     450 CATGAGGCGGAGCAGTTGAGAGCCTACCTGGATGGCAGCTGCGTGGAGTGGCTCCGCAGA 509

Query:     245 TACCTGGAGAACGGGAAG 262
            |||
Sbjct:     510 TACCTGGAGAACGGGAAG 527

```

A4-1/2H

```

>K24FW
CGCCTGTATCTCCTCCGCTGGAGCCCCCTGAGTGTGGGCCCTGAGCTTCTACCT
GCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGACCAGACCAGGACACGGA
GCTCGTGGAGACCAGGCCTGCAGGGGATA

```

```

>K24RV
TCGCCCCCAAACGCATATGACTCACCACGCTGTCTCTGACCATGAAGCCACCCTG
AGGTGCTGGGCCCTGAGCTTCTACCTGCGGAGATCACACGACCGGCAGCGGGAGG
GGAGGACTAGCCCTCAAAAAGCATCTGAT

```

CLUSTAL 2.1 multiple sequence alignment

```

K24FW      -----CGCCTGTATCTCCTC-CGCTG-----GAGCC-CCCTGAG-T 33
K24RV      TCGCCCCCAAACGCATATGACTCACCACGCTGTCTCTGACCATGAAGCCACCCTGAGGT 60
            *** * *   *** *   *****          **** * * * * * *

K24FW      GCTGGGCCCTGAGCTTCTACCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGG 93
K24RV      GCTGGGCCCTGAGCTTCTACCTGCGGAGATCACAC-GACC-GGCAGCGGGA-GGGGAGG 117
            *****

K24FW      ACCAGACCCAGGACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGATA 141
K24RV      ACTAGCCCT----CAAAAAGC-----ATCTG-----AT- 141
            ** * * *   **   ***          ***      **

```

```

>K24SeqCons
TCGCCCCCAAACGCATATGACTCACCACGCTGTCTCTGACCATGAAGCCACCC
TGAGTGCTGGGCCCTGAGCTTCTACCTGCGGAGATCACACTGACCTGGCAGCG
GGATGGGGAGGACCAGACCCAGGACACGGAGCTCGTGGAGACCAGGCCTGCAGG
GGATA

```

>IMGTHLA:HLA00005 A*02:01:01:01 1098 bp
Length = 1098

Plus Strand HSPs:

Score = 815 (128.3 bits), Expect = 2.3e-33, P = 2.3e-33, Group = 1
Identities = 165/166 (99%), Positives = 165/166 (99%), Strand = Plus / Plus

```

Query:      2 CGCCCCCAAACGCATATGACTCACCACGCTGTCTCTGACCATGAAGCCACCCTGAG-TG 60
            |||
Sbjct:     621 CGCCCCCAAACGCATATGACTCACCACGCTGTCTCTGACCATGAAGCCACCCTGAGGTG 680

Query:      61 CTGGGCCCTGAGCTTCTACCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGA 120
            |||
Sbjct:     681 CTGGGCCCTGAGCTTCTACCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGA 740

Query:     121 CCAGACCCAGGACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGAT 166
            |||
Sbjct:     741 CCAGACCCAGGACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGAT 786

```

A4-2/2H

```
>K24FW
GCCGTCGTGTGTACCTGAGGCCCTGAGTGCTGGGCCCTGGGCTTCTACCTG
CGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGACCAGACCAGGACACGG
AGCTCGTGGAGACCAGGCCTGCAGGGGATA
```

```
>K24RV
CCCCCAAGACACATATGACCCACCACCCCATCTCTGACCATGAGGCCACCTT
GAGGTGCTGGGCCCTGGGCTTCTACCTGCGGAGATCACACGACCGGCAGCGGG
AGGGGAGGACCAGCACCAGCACCAGACCG
```

CLUSTAL 2.1 multiple sequence alignment

```
K24FW      -----GCCGTCGTGTGT---ACC-TGAGGCC-CCCTGAG-TG 31
K24RV      CCCCCCAAGACACATATGACCCACCACCCCATCTCTGACCATGAGGCCACCTGAGGTG 60
              * * * * *
K24FW      CTGGGCCCTGGGCTTCTACCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGA 91
K24RV      CTGGGCCCTGGGCTTCTACCTGCGGAGATCACAC-GACC-GGCAGCGGGA-GGGGAGGA 117
              *****
K24FW      CCAGACCCAGGACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGATA 138
K24RV      CCAGCACCAG--CACCAAGACCG----- 138
              **** * * *
```

```
>K24SeqCons
CCCCCAAGACACATATGACCCACCACCCCATCTCTGACCATGAGGCCACCC
TGAGGTGCTGGGCCCTGGGCTTCTACCTGCGGAGATCACACTGACCTGGCAG
CGGGATGGGGAGGACCAGACCCAGGACACGGAGCTCGTGGAGACCAGGCCTGC
AGGGGATA
```

>IMGTHLA:HLA01718 A*03:01:01:02N 1163 bp
Length = 1163

Plus Strand HSPs:

Score = 830 (130.6 bits), Expect = 4.6e-34, P = 4.6e-34, Group = 1
Identities = 166/166 (100%), Positives = 166/166 (100%), Strand = Plus / Plus

```
Query:      1 CCCCCCAAGACACATATGACCCACCACCCCATCTCTGACCATGAGGCCACCTGAGGTG 60
              |||
Sbjct:     621 CCCCCCAAGACACATATGACCCACCACCCCATCTCTGACCATGAGGCCACCTGAGGTG 680
Query:      61 CTGGGCCCTGGGCTTCTACCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGA 120
              |||
Sbjct:     681 CTGGGCCCTGGGCTTCTACCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGA 740
Query:     121 CCAGACCCAGGACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGAT 166
              |||
Sbjct:     741 CCAGACCCAGGACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGAT 786
```

A4-3H/1

```
>K24FW
CGAACTGGGTGGGCTCTGGGCATTATCCTGCTGTTGTACGGAGCTCGTGGAG
ACCGCCTGCAGGGGATGGAACCTTCCAGAAGTGGGCGGCTGTGGTGGTGCCT
TCTGGAGAGGAGCAGAGATACACCTGCCATGTGCAGCATGAGGGTCTGCCCAA
GCCCTCACCTGAGATGGA
```

```
>K24RV
TTCTACCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGACCAGAC
CCAGGACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGATGGAACCTTCCAGA
AGTGGGCGGCTGTGGTGGTGCCTTCGGAGAGGAGCAGACTATACACATAGCAT
ATGTACAGCAGATAGACAGACATG
```

CLUSTAL 2.1 multiple sequence alignment

```

K24FW      -----CGAACTGG--GTGGGCTCTGGGCATTATCCTGCTGTTG 36
K24RV      TTCTACCCTGCGGAGATCACACTGACCTGGCAGCGGGA--TGGGGAGGACCAGACCCAGG 58
              **  ***  *  ***  ***  *  *  *  *  *
              *  *  *  *  *  *  *  *  *  *  *  *  *

K24FW      TCACGGAGCTCGTGGAGACC-GGCCTGCAGGGGATGGAACCTTCCAGAAGTGGGCGGCTG 95
K24RV      ACACGGAGCTCGTGGAGACCAGGCCTGCAGGGGATGGAACCTTCCAGAAGTGGGCGGCTG 118
              *****
              *  *  *  *  *  *  *  *  *  *  *  *  *

K24FW      TGGTGGTGCCTTCTGGAGAGGAGCAGAG-ATACACCTGCCATGTGCAGCATGAGGGTCTG 154
K24RV      TGGTGGTGCCTTC-GGAGAGGAGCAGACTATACATAGCATATGTA-CAGCAGA----- 171
              *****  *  ***  *  *  *  *  *  *  *

K24FW      CCCAAGCCCCTCACCTGAGATGGA 179
K24RV      -----TAGACAGACATG-- 183
              *  *  *  *  *

```

```

>K24SeqCons
TGGGGAGGACCAGACCCAGGTTCTACCCTGCGGAGATCACACTGACCTGGC
AGCGGGATCACGGAGCTCGTGGAGACCGGCCTGCAGGGGATGGAACCTTCC
AGAAGTGGGCGGCTGTGGTGGTGCCTTCTGGAGAGGAGCAGAGATACACCT
GCCATGTGCAGCATGAGGGTCTGCCCAAGCCCCTCACCTGAGATGGA

```

Not HLA-A single result.

FIGURES INDEX.

Figure 1. Complete gene map of the MHC. (The-MHC-Consortium 1999)	9
Figure 2. Gene map of the human leukocyte antigen (HLA) region. (Mehra and Kaur 2003)	10
Figure 3. HLA class I structure determined by X-Ray crystallography. (Janeway, Travers et al. 2001)	12
Figure 4. Kaplan–Meier analysis of survival in ovarian cancer patients. (Gamzatova, Villabona et al. 2006)	13
Figure 5. Schematic HLA-A gene representation.	21
Figure 6. FFPE DNA amplification products in 2% agarose gels.	29
Figure 7. Comparison between different K3 and K4 amplification products.	30
Figure 8. K23 Sequence graphic obtained for a HLA-A exon 2 amplification.	31
Figure 9. K23 Sequence graphic obtained for a HLA-A exon 3 amplification.	31
Figure 10. Sequence graphic obtained for a HLA-A exon 4 first half amplification.	32
Figure 11. K24 forward and reverse sequences analysis from exon 2 A2-2F and A2-2R primers (A2-2/2).	33
Figure 12. K23 exon 2 sequence graphic (A2-1F/1R).	34
Figure 13. Result obtained from the IMGT-HLA database Blast tool.	34