



(86) Date de dépôt PCT/PCT Filing Date: 1998/07/09
(87) Date publication PCT/PCT Publication Date: 1999/01/21
(45) Date de délivrance/Issue Date: 2008/10/07
(85) Entrée phase nationale/National Entry: 2000/01/07
(86) N° demande PCT/PCT Application No.: AU 1998/000530
(87) N° publication PCT/PCT Publication No.: 1999/002694
(30) Priorités/Priorities: 1997/07/09 (AUPO 7765);
1997/09/11 (AUPO 9467)

(51) Cl.Int./Int.Cl. *C12N 15/85* (2006.01),
C07K 14/025 (2006.01), *C12N 15/10* (2006.01),
C12N 15/37 (2006.01), *C12N 15/67* (2006.01),
C12N 7/00 (2006.01), *C12N 7/02* (2006.01)
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(54) Titre : SEQUENCE D'ACIDES NUCLEIQUES ET PROCEDE POUR EXPRIMER, DE MANIERE SELECTIVE, UNE
PROTEINE DANS UNE CELLULE OU UN TISSU CIBLE
(54) Title: NUCLEIC ACID SEQUENCE AND METHOD FOR SELECTIVELY EXPRESSING A PROTEIN IN A TARGET
CELL OR TISSUE

(57) **Abrégé/Abstract:**

A synthetic nucleic acid sequence and a method are disclosed for selectively expressing a protein in a target cell or tissue of a mammal. Selective expression is effected by replacing at least one existing codon of a parent nucleic acid sequence encoding a protein of interest with a synonymous codon to produce a synthetic nucleic acid sequence having altered translational kinetics compared to the parent nucleic acid sequence. The synonymous codon is selected such that it corresponds to an iso-tRNA which, when compared to an iso-tRNA corresponding to the at least one existing codon, is in higher abundance in the target cell or tissue relative to one or more other cells or tissues of the mammal.



**PCT**WORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C12N 15/37, C07K 14/025	A1	(11) International Publication Number: WO 99/02694 (43) International Publication Date: 21 January 1999 (21.01.99)
(21) International Application Number: PCT/AU98/00530 (22) International Filing Date: 9 July 1998 (09.07.98) (30) Priority Data: PO 7765 9 July 1997 (09.07.97) AU PO 9467 11 September 1997 (11.09.97) AU (71) Applicant (for all designated States except US): THE UNIVERSITY OF QUEENSLAND [AU/AU]; St. Lucia, QLD 4072 (AU). (72) Inventors; and (75) Inventors/Applicants (for US only): FRAZER, Ian [AU/AU]; 64 Eighth Avenue, St. Lucia, QLD 4067 (AU). ZHOU, Jian [AU/AU]; 21 Cooranga Street, Jindalee, QLD 4074 (AU). (74) Agent: HORSBURGH, Mark, Alexander; Fisher Adams Kelly, Level 13, 10 Eagle Street, Brisbane, QLD 4000 (AU).		(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>With international search report.</i>
(54) Title: NUCLEIC ACID SEQUENCE AND METHOD FOR SELECTIVELY EXPRESSING A PROTEIN IN A TARGET CELL OR TISSUE (57) Abstract A synthetic nucleic acid sequence and a method are disclosed for selectively expressing a protein in a target cell or tissue of a mammal. Selective expression is effected by replacing at least one existing codon of a parent nucleic acid sequence encoding a protein of interest with a synonymous codon to produce a synthetic nucleic acid sequence having altered translational kinetics compared to the parent nucleic acid sequence. The synonymous codon is selected such that it corresponds to an iso-tRNA which, when compared to an iso-tRNA corresponding to the at least one existing codon, is in higher abundance in the target cell or tissue relative to one or more other cells or tissues of the mammal.		

TITLE

"NUCLEIC ACID SEQUENCE AND METHOD FOR SELECTIVELY
EXPRESSING A PROTEIN IN A TARGET CELL OR TISSUE"

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FIELD OF THE INVENTION

THIS INVENTION relates generally to gene therapy. More particularly, the present invention relates to a synthetic nucleic acid sequence and to a method for selectively expressing a protein in a target cell or tissue in which at least one existing codon of a parent nucleic acid sequence encoding the protein has been replaced with a synonymous codon. The invention also relates to production of virus particles using one or more synthetic nucleic acid sequences and the method according to the invention.

10
15BACKGROUND OF THE INVENTION

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While gene therapy is of great clinical interest for treatment of gene defects, this therapy has not entered into mainstream clinical practice because selective delivery of genes to target tissues has proven extremely difficult. Currently, viral vectors are used, particularly retroviruses and adenovirus, which are to some extent selective. However, many vector systems are by their nature unable to produce stable integrants and some also invoke immune responses thereby preventing effective treatment. Alternatively, "naked" DNA is packaged in liposomes or other similar delivery systems. A major

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problem to be overcome is that such gene delivery systems themselves are not tissue selective, whereas selective targeting of genes to particular tissues would be desirable for many disorders (e.g., cancer therapy). While use of tissue specific promoters to target gene therapy has been effective in some animal models it has proven less so in man, and selective tissue specific promoters are not available for a wide range of tissues.

10 The current invention has arisen unexpectedly from recent investigations exploring why papillomavirus (PV) late gene expression is restricted to differentiated keratinocytes. In this regard, it is known that PV late genes L1 and L2 are only
15 expressed in non-dividing differentiated keratinocytes (KCs). Many investigators including the present inventors have been unable to detect significant PV L1 and L2 protein expression when these genes are transduced or transfected into undifferentiated
20 cultured cells, using a range of conventional constitutive viral promoters including retroviral long terminal repeats (LTRs) and the strong constitutive promoters of CMV and SV40.

 PV L1 mRNA can however be efficiently
25 translated *in vitro* using rabbit reticulocyte cell lysate, suggesting that there are no cellular inhibitors in the lysate interfering with translation of L1. The major difference between the *in vitro* and *in vivo* translation systems is that L1 comprises the
30 dominant L1 mRNA in *in vitro* translation reactions, while it constitutes a minor fraction among the cellular mRNAs in intact cells.

In vivo, PV late proteins are not produced in undifferentiated KC. However, they are expressed in large quantity in highly differentiated KC. The mechanism of this tight control of late gene expression has been poorly understood, and searches by many groups for KC specific PV gene transcriptional control proteins have been unrewarding.

Blockage to translation of L1 mRNA *in vivo* has been attributed to sequences within the L1 ORF (Tan et al. 1995, *J. Virol.* 69 5607-5620; Tan and Schwartz, 1995, *J. Virol.* 69 2932-2945). By using a Rev and Rev-responsive element of HIV, such inhibition could be overcome (Tan et al. 1995, *supra*). Accordingly, the inventors examined whether removal of putative "inhibitory sequences" in the L1 ORF would allow production of L1 protein in undifferentiated cells. Deletion mutagenesis of BPV L1 to remove putative inhibitory sequences and expression of resultant deletion mutants in CV-1 cells revealed surprisingly that despite expression of L1 mRNA, L1 protein could not be detected.

In view of the foregoing, it has been difficult hitherto to understand how papillomaviruses produce large amounts of L1 protein in the late stage of their life cycle using this apparently "untranslatable" gene.

Surprisingly, however, it has now been discovered that PV L1 protein can be produced at substantially enhanced levels in an undifferentiated host cell by replacing existing codons of a native L1 gene with synonymous codons used at relatively high frequency by genes of the undifferentiated host cell

compared to the existing codons. It has also been found unexpectedly that there are substantial differences in the relative abundance of particular isoaccepting transfer RNAs (tRNAs) in different cells or tissues and this plays a pivotal role in protein expression from a gene with a given codon usage or composition. This discovery has been reduced to practice in synthetic nucleic acid sequences and generic methods, which utilize codon alteration as a means for targeting expression of a protein to particular cells or tissues or alternatively, to cells in a specific state of differentiation.

OBJECT OF THE INVENTION

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It is therefore an object of the present invention to provide a synthetic nucleic acid sequence and a method for selectively expressing a protein in a target cell or tissue which sequence and method ameliorate at least some of the disadvantages associated with the prior art.

SUMMARY OF THE INVENTION

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Accordingly, in one aspect of the invention, there is provided a method of constructing a synthetic polynucleotide from which a protein is selectively expressible in a target cell or tissue of a mammal but from which said protein is substantially not expressible in one or more other cells or tissues of the mammal, said method including the step of replacing at least one existing codon of a parent

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polynucleotide with a synonymous codon to form said synthetic polynucleotide.

Suitably, the method further includes the step of selecting said synonymous codon such that it
5 corresponds to an iso-tRNA which, when compared to an iso-tRNA corresponding to the at least one existing codon, is in higher abundance in the target cell or tissue relative to said one or more other cells or tissues of the mammal.

10 Preferably, the step of selecting is further characterized by the steps of:-

- (a) measuring relative abundance of different iso-tRNAs in said target cell or tissue, and in said one or more other cells or tissues; and
- 15 (b) identifying said at least one existing codon and said synonymous codon based on said measurement, wherein said synonymous codon corresponds to an iso-tRNA which, when compared to an iso-tRNA corresponding to the existing codon, is in higher
20 abundance in said target cell or tissue relative to said one or more other cells or tissues.

Preferably, the step of selecting is further characterized in that said synonymous codon corresponds to an iso-tRNA which, when compared to an
25 iso-tRNA corresponding to the at least one existing codon, is in higher abundance in the target cell or tissue relative to a precursor cell or tissue of the target cell or tissue.

Alternatively, the step of selecting is
30 further characterized in that said synonymous codon corresponds to an iso-tRNA which, when compared to an iso-tRNA corresponding to the at least one existing

codon, is in higher abundance in the target cell or tissue relative to a cell or tissue derived from said target cell or tissue.

Advantageously, the step of selecting is
5 further characterized in that the corresponding iso-tRNA in said target cell or tissue is at a level which is at least 110%, preferably at least 200%, more preferably at least 500%, and most preferably at least 1000%, of that expressed in said one or more other
10 cells or tissues.

Alternatively, the method further includes the step of selecting said synonymous codon from the group consisting of (1) a codon used at relatively high frequency by genes, preferably highly expressed
15 genes, of the target cell or tissue, (2) a codon used at relatively high frequency by genes, preferably highly expressed genes, of said one or more other cells or tissues, (3) a codon used at relatively high frequency by genes, preferably highly expressed genes,
20 of the mammal, (4) a codon used at relatively low frequency by genes of the target cell or tissue, (5) a codon used at relatively low frequency by genes of said one or more other cells or tissues, (6) a codon used at relatively low frequency by genes of the
25 mammal, (7) a codon used at relatively high frequency by genes of another organism, and (8) a codon used at relatively low frequency by genes of another organism.

In a preferred embodiment, the method further includes the step of selecting the at least
30 one existing codon and the synonymous codon such that said protein is expressed from said synthetic polynucleotide in said target cell or tissue at a

level which is at least 110%, preferably at least 200%, more preferably at least 500%, and most preferably at least 1000%, of that expressed from said parent polynucleotide in said target cell or tissue.

5 In another aspect, the invention provides a synthetic polynucleotide constructed according to any one of the above methods.

10 Preferably, said synonymous codon(s) are selected from the group consisting of gca (Ala), cuu (Leu) and cua (Leu), and said target cell is a differentiated cell.

15 More preferably, said synonymous codon(s) are selected from the group consisting of gca (Ala), cuu (Leu) and cua (Leu), and said target cell is a differentiated keratinocyte.

In yet another aspect, the invention resides in a method for selectively expressing a protein in a target cell or tissue of a mammal, said method including the steps of:-

20 (a) replacing at least one existing codon of a parent polynucleotide encoding said protein with a synonymous codon to produce a synthetic polynucleotide having altered translational kinetics compared to said parent polynucleotide such that said
25 protein is selectively expressible in said target cell or tissue but such that said protein is not substantially expressible in one or more other cells or tissues of the mammal;

30 (b) administering to the mammal, and introducing into said target cell or tissue, or into a precursor cell or precursor tissue of said target cell or tissue, said synthetic polynucleotide operably

linked to one or more regulatory nucleotide sequences;
and

(c) selectively expressing said protein
in said target cell or tissue but not in said one or
5 more other cells or tissues.

Preferably, the method further includes,
prior to step (a):

(i) measuring relative abundance of
different iso-tRNAs in said target cell or tissue, and
10 in said one or more other cells or tissues; and

(ii) identifying said at least one
existing codon and said synonymous codon based on said
measurement, wherein said synonymous codon corresponds
to an iso-tRNA which, when compared to an iso-tRNA
15 corresponding to the existing codon, is in higher
abundance in said target cell or tissue relative to
said one or more other cells or tissues.

Suitably, step (ii) above is further
characterized in that said synonymous codon
20 corresponds to an iso-tRNA which, when compared to an
iso-tRNA corresponding to the at least one existing
codon, is in higher abundance in the target cell or
tissue relative to a precursor cell or tissue.

Alternatively, step (ii) above is further
25 characterized in that said synonymous codon
corresponds to an iso-tRNA which, when compared to an
iso-tRNA corresponding to the at least one existing
codon, is in higher abundance in the target cell or
tissue relative to a cell or tissue derived therefrom.

30 Alternatively, the method further includes,
prior to step (a), identifying said at least one
existing codon and said synonymous codon based on

respective relative frequencies of particular codons used by genes selected from the group consisting of (I) genes of the target cell or tissue, (II) genes of the or each other cell or tissue, (III) genes of the mammal, and (IV) genes of another organism.

In yet another aspect, the invention provides a method for expressing a protein in a target cell or tissue from a first polynucleotide including the step of introducing into said target cell or tissue, or a precursor cell or precursor tissue thereof, a second polynucleotide encoding at least one isoaccepting transfer RNA wherein said second polynucleotide is operably linked to one or more regulatory nucleotide sequences, and wherein said at least one isoaccepting transfer RNA is normally in relatively low abundance in said target cell or tissue and corresponds to a codon of said first polynucleotide.

In a further aspect, the invention extends to a method for producing a virus particle in a cycling eukaryotic cell, said virus particle comprising at least one protein necessary for assembly of said virus particle, wherein said at least one protein is not expressed in said cell from a parent polynucleotide at a level sufficient to permit virus assembly therein, said method including the steps of:-

(a) replacing at least one existing codon of said parent polynucleotide with a synonymous codon to produce a synthetic polynucleotide having altered translational kinetics compared to said parent polynucleotide such that said at least one protein is expressible from said synthetic polynucleotide in said

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cell at a level sufficient to permit virus assembly therein;

(b) introducing into said cell or a precursor cell thereof said synthetic polynucleotide operably linked to one or more regulatory nucleotide sequences; and

(c) expressing said at least one protein in said cell in the presence of other viral proteins required for assembly of said virus particle to thereby produce said virus particle.

In yet a further aspect of the invention, there is provided a method for producing a virus particle in a cycling cell, said virus particle comprising at least one protein necessary for assembly of said virus particle, wherein said at least one protein is not expressed in said cell from a parent polynucleotide at a level sufficient to permit virus assembly therein, and wherein at least one existing codon of said parent polynucleotide is rate limiting for the production of said at least one protein to said level, said method including the step of introducing into said cell a polynucleotide capable of expressing therein an isoaccepting transfer RNA specific for said at least one codon.

According to an aspect of the present invention, there is provided a method of constructing a synthetic polynucleotide that encodes a polypeptide, the method comprising:

- selecting a first codon of a parent polynucleotide for replacement with a synonymous codon, wherein the synonymous codon is selected on the basis that it exhibits a higher translational efficiency in a first cell of a mammal than in a second cell of the mammal; and

9/1a

replacing the first codon with the synonymous codon to construct the synthetic polynucleotide.

According to another aspect of the present invention, there is provided a method of selectively
5 expressing a polypeptide in a first cell of a mammal, the method comprising:

selecting a first codon of a parent polynucleotide encoding the polypeptide for replacement with a synonymous codon, wherein the synonymous codon is selected on the
10 basis that it exhibits a higher translational efficiency in the first cell than in a second cell of the mammal;

replacing the first codon with the synonymous codon to construct a synthetic polynucleotide; and

introducing the synthetic polynucleotide into a cell
15 selected from the group consisting of the first cell and a precursor of the first cell, the synthetic polynucleotide being operably linked to a regulatory polynucleotide, whereby the polypeptide is selectively expressed in the first cell.

20 According to another aspect of the present invention, there is provided a method of expressing a polypeptide from a first polynucleotide in a mammalian cell, the method comprising:

- selecting an iso-tRNA on the basis that it is normally
25 in lower abundance in the cell than other iso-tRNAs and corresponds to a codon of the first polynucleotide;

- introducing into the cell a second polynucleotide that encodes the selected iso-tRNA and that is operably linked to a regulatory polynucleotide; and
30 expressing the second polynucleotide in the cell, whereby the polypeptide is expressed in the cell.

9/1b

According to another aspect of the present invention, there is provided a method of expressing a polypeptide from a first polynucleotide in a mammalian cell, the method comprising

- 5 - selecting an iso-tRNA on the basis that it is normally in lower abundance in the cell than other iso-tRNAs and corresponds to a codon of the first polynucleotide;

introducing into a precursor of the cell a second
10 polynucleotide that encodes the selected iso-tRNA and that is operably linked to a regulatory polynucleotide, wherein the precursor is exposed to conditions sufficient to produce the cell; and
expressing the second polynucleotide in the cell, whereby
15 the polypeptide is expressed in the cell.

According to another aspect of the present invention, there is provided a method of producing a virus particle in a cycling animal cell, wherein the virus particle comprises a polypeptide necessary for
20 assembly of the virus particle, and wherein the polypeptide is expressed in the cell from a parent polynucleotide, but not at a level sufficient to permit virus assembly therein, the method comprising:

providing a comparison of translational
25 efficiencies of individual codons in the cell;

- selecting from the comparison a first codon of the parent polynucleotide for replacement with a synonymous codon, wherein the synonymous codon is selected on the basis that it exhibits a higher translational
30 efficiency in the cell than the first codon; and

- replacing the first codon with the synonymous codon to construct a synthetic polynucleotide having enhanced translational kinetics compared to the parent

9/1c

polynucleotide, such that the polypeptide is expressible from the synthetic polynucleotide in the cell at a level sufficient to permit virus assembly therein; and

- introducing into the cell the synthetic
- 5 polynucleotide operably linked to a regulatory polynucleotide, whereby the polypeptide is expressed and the virus particle is produced in the cell.

According to another aspect of the present invention, there is provided a method of producing a virus particle in a cycling cell, wherein the virus particle comprises at least one polypeptide necessary for assembly of the virus particle, wherein the polypeptide is expressed in the cell from a first

10 polynucleotide, but not at a level sufficient to permit virus assembly therein, the method comprising:

- providing a comparison of translational efficiencies of individual codons in the cell;
 - selecting from the comparison a first codon of the
- 20 first polynucleotide that exhibits a lower translational efficiency in the cell than a synonymous codon;

introducing into the cell a second polynucleotide encoding an iso-tRNA specific for the first codon; and

25 expressing the second polynucleotide in the cell, whereby the virus particle is produced in the cycling cell.

According to another aspect of the present invention, there is provided a method of producing a virus particle in a cycling eukaryotic cell, wherein the virus

30 particle comprises a polypeptide necessary for assembly of the virus particle, and wherein the polypeptide is expressed in the cell from a parent polynucleotide, but not at a level sufficient to permit

9/1d

virus assembly therein, the method comprising:

- providing a comparison of translational efficiencies of individual codons in the cell;

- selecting from the comparison a first codon of the parent polynucleotide for replacement with a synonymous codon, wherein the synonymous codon is selected on the basis that it exhibits a higher translational efficiency in the cell than the first codon; and

- replacing the first codon with the synonymous codon to construct a synthetic polynucleotide having increased translational kinetics compared to the parent polynucleotide, such that the polypeptide is expressible from the synthetic polynucleotide in the cell at a level sufficient to permit virus assembly therein;

- introducing into a precursor of the cell the synthetic polynucleotide operably linked to a regulatory polynucleotide; and

- exposing the precursor to conditions sufficient to produce the cell, wherein the cell comprises the polypeptide necessary for assembly of the virus particle, whereby the polypeptide is expressed and the virus particle is produced in the cell.

According to another aspect of the present invention, there is provided a method of constructing a synthetic polynucleotide that encodes a polypeptide, the method comprising:

- selecting a first codon of a parent polynucleotide for replacement with a synonymous codon, wherein the synonymous codon is selected on the basis that it exhibits a lower translational efficiency in a first cell of a mammal than in a second cell of the mammal; and

9/1e

replacing the first codon with the synonymous codon to construct the synthetic polynucleotide.

According to another aspect of the present invention, there is provided a method of constructing a synthetic polynucleotide that encodes a polypeptide, the method comprising:

- providing a comparison of translational efficiencies of individual codons in a cell of a mammal;

selecting from the comparison a first codon of the parent polynucleotide for replacement with a synonymous codon, wherein the synonymous codon is selected on the basis that it exhibits a higher translational efficiency in the cell than the first codon; and

- replacing the first codon with the synonymous codon to construct the synthetic polynucleotide.

According to another aspect of the present invention, there is provided a method of constructing a synthetic polynucleotide encoding a polypeptide, the method comprising:

providing a comparison of translational efficiencies of individual codons in a cell of a mammal;

- selecting from the comparison a first codon of the parent polynucleotide for replacement with a synonymous codon, wherein the synonymous codon is selected on the basis that it exhibits a lower translational efficiency in the cell than the first codon; and

- replacing the first codon with the synonymous codon to construct the synthetic polynucleotide.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1A depicts the nucleotide sequence (SEQ ID NO:1) and deduced amino acid sequence (SEQ ID NO:2) of BPV1 L1. Amino acids (in single letter code) are presented below the second nucleotide of each codon. Mutations introduced into the genes are indicated above the corresponding nucleotides of the original sequence. Horizontal lines indicate the sites and enzymes used for cloning. This replacement of nucleotides resulted in a nucleic acid sequence encoding BPV-1 L1 polypeptide with an amino acid sequences identical to the wild type, but having synonymous codons that are frequently used by mammalian genes.

Figure 1B shows the nucleotide sequence (SEQ ID NO:5) and deduced amino acid sequence (SEQ ID NO:6) relating to BPV1 L2 ORF. Amino acids (in single letter code) are presented below the second nucleotide of each codon. Mutations introduced into the genes are indicated above the corresponding nucleotides of the original sequence. Horizontal lines indicate the sites and enzymes used for cloning. This replacement of nucleotides resulted in a nucleic acid sequence encoding BPV-1 L2 polypeptide with an amino acid sequences identical to the wild type, but having synonymous codons that are frequently used by mammalian genes.

Figure 1C depicts the nucleotide sequence (SEQ ID NO:9) and deduced amino acid sequence (SEQ ID NO:10) of green fluorescent protein (GFP). Amino acids (in single letter code) are presented below the

second nucleotide of each codon. Mutations introduced into the genes are indicated above the corresponding nucleotides of the original sequence. Horizontal lines indicate the sites and enzymes used for cloning.

5 This replacement of nucleotides resulted in a nucleic acid sequence encoding GFP polypeptide with an amino acid sequence identical to the native sequence modified for optimal expression in eukaryotic cells, but having synonymous codons that are frequently used
10 by papillomavirus genes.

Figure 2A shows detection of L1 protein expressed from synthetic and wild type BPV1 L1 genes. Cos-1 cells were transfected with a synthetic L1 expression plasmid pCDNA/HBL1, and a wild type L1
15 expression plasmid pCDNA/BPVL1wt. The expression of L1 was detected by immunofluorescent staining. Cells were fixed after 36 hrs and incubated with rabbit anti-BPV1 L1 antiserum, followed by FITC-conjugated goat anti-rabbit IgG antibody.

20 Figure 2B shows detection by Western blot of L1 protein from Cos-1 cells transfected with pCDNA/HBL1 and pCDNA/BPVL1wt.

Figure 2C shows a Northern blot in which L1 mRNA extracted from transfected cells was probed with
25 ³²P-labeled probes produced from wild type L1 sequence. The amount of mRNA loaded in respective lanes was examined by hybridization of the mRNA sample with a *gapdh* probe.

Figure 3A shows detection of L2 protein
30 expressed from synthetic and wild type BPV1 L2 genes. Cos-1 cells were transfected with a synthetic L2 expression plasmid pCDNA/HBL2, and a wild type L2

expression plasmid pCDNA/BPVL2wt. The expression of L2 was detected by immunofluorescent staining. Cells were fixed after 36 hrs and incubated with rabbit anti-BPV1 L2 antiserum, followed by FITC-conjugated goat anti-rabbit IgG antibody.

Figure 3B shows detection by Western blot of L2 protein from Cos-1 cells transfected with pCDNA/HBL2 and pCDNA/BPVL2wt.

Figure 3C shows a Northern blot in which L2 mRNA extracted from transfected cells was probed with ³²P-labeled probes produced from wild type L2 sequence. The amount of mRNA loaded in respective lanes was examined by hybridization of the mRNA sample with a *gapdh* probe.

Figure 4 shows *in vitro* translation of BPVL1 sequences, wild type BPVL1 (wt) or synthetic L1 (HB) using rabbit reticulocyte lysate or wheat germ extract in the presence of ³⁵S-methionine. In the top panel, wt L1 or HB L1 plasmid DNA was added to the T7 DNA polymerase-coupled *in vitro* translation system. L1 protein was detected by Western blot analysis. In the bottom panel, the translation efficiency of wt L1 or HB L1 sequences in the presence or absence of tRNA was compared. Translation was carried out in rabbit reticulocyte lysate (rabbit) or wheat germ extract (wheat), and samples were collected every two minutes starting from minute 8. Left side of lower panel indicates if 10⁻⁵ M bovine liver or yeast tRNA was supplied.

Figure 5A is a schematic representation of plasmids used to determine L2 expression from BPV cryptic promoter(s). The wild type L1 sequence and

most of the wild type L2 sequence were deleted from the BPV1 genome by *Bam*HI and *Hind*III digestion and the remaining BPV1 sequence (in yellow) was cloned into pUC18. Wild type or synthetic humanized L2 sequences (in red) were inserted into the *Bam*HI site of the BPV1 genome. The position of the inserted SV40 *ori* sequence (in white) is indicated. The plasmid in which modified L2 was used but without SV40 *ori* sequence was also used as a control. The plasmids were transfected into Cos-1 cells and the expression of L2 protein was determined using BPV1 L2-specific polyclonal antiserum followed by FITC-linked anti rabbit IgG.

Figure 5B shows expression of L2 protein from native papillomavirus promoter. The plasmids shown in Figure 5A were used to transfect Cos-1 cells and the expression of L2 protein was determined using BPV1 L2-specific polyclonal antiserum followed by FITC-linked anti rabbit IgG. A mock transfection in which the cells did not receive plasmid was used as control.

Figure 6 shows expression of GFP in Cos-1 cells transfected with wild-type *gfp* (wt) or a synthetic *gfp* gene carrying codons used at relatively high frequency by papillomavirus genes (p). The mRNA extracted from cells transfected with *gfp* or P *gfp* was probed with ³²P-labeled *gfp* probe and is shown on the right panel, using *gapdh* as a reference gene.

Figure 7 shows the expression pattern of GFP *in vivo* from wild-type *gfp* gene, or a synthetic *gfp* gene carrying codons used at relatively high frequency by papillomavirus genes. Using a gene gun,

mice were shot with PGFP (left panel) and GFP (right panel) expression plasmids encoding GFP protein. A transverse section of the mouse skin section shows where the *gfp* gene is expressed. Bright-field
5 photographs of the same section where dermis (D) epidermis (E) are highlighted are shown to identify the location of fluorescence in the epidermis. Arrows indicate fluorescent signals.

10

DETAILED DESCRIPTION

The present invention arises from the unexpected discovery that the relative abundance of different isoaccepting transfer RNAs varies in
15 different cells or tissues, or alternatively in cells or tissues in different states of differentiation or in different stages of the cell cycle, and that such differences may be exploited together with codon composition of a gene to regulate and direct
20 expression of a protein to a particular cell or tissue, or alternatively to a cell or tissue in a specific state of differentiation or in a specific stage of the cell cycle. According to the present invention, this selective targeting is effected by
25 replacing at least one existing codon of a parent nucleic acid sequence encoding the protein with a synonymous codon.

Replacement of synonymous codons for existing codons is not new per se. In this regard, we
30 refer to International Application Publication No WO 96/09378 which utilizes such substitution to provide a method of expressing proteins of eukaryotic and viral

origin at high levels in in vitro mammalian cell culture systems, the main thrust of the method being the harvesting of such proteins. In distinct contrast, the present invention utilizes substitution of one or more codons in a gene for targeting expression of the gene to particular cells or tissues with the ultimate aim of facilitating gene therapy as described herein.

The term "synonymous codon" as used herein refers to a codon having a different nucleotide sequence to an existing codon but encoding the same amino acid as the existing codon.

By "isoaccepting transfer RNA" is meant one or more transfer RNA molecules that differ in their anticodon structure but are specific for the same amino acid.

Throughout this specification, unless the context requires otherwise, the words "comprise", "comprises" and "comprising" will be understood to imply the inclusion of a stated integer or group of integers but not the exclusion of any other integer or group of integers.

Selection of synonymous codons

Determination of relative abundance of different tRNA species in different cells

Advantageously, the synonymous codon corresponds to an iso-tRNA (iso-tRNA) which, when compared to an iso-tRNA corresponding to the at least one existing codon, is in higher abundance in the

target cell or tissue relative to one or more other cells or tissues of the mammal.

Any method for determining the relative abundance of an iso-tRNA in two or more cells or tissues may be employed. For example, such method may include isolating two or more particular cells or tissues from a mammal, preparing an RNA extract from each cell or tissue which extract includes tRNA, and probing each extract respectively with different nucleic acid sequences each being specific for a particular iso-tRNA to determine the relative abundance of an iso-tRNA between the two or more cells or tissues.

Suitable methods for isolating particular cells or tissues are well known to those of skill in the art. For example, one can take advantage of one or more particular characteristics of a cell or tissue to specifically isolate the cell or tissue from a heterogeneous population. Such characteristics include, but are not limited to, anatomical location of a tissue, cell density, cell size, cell morphology, cellular metabolic activity, cell uptake of ions such as Ca^{2+} , K^+ , and H^+ ions, cell uptake of compounds such as stains, markers expressed on the cell surface, cytokine expression, protein fluorescence, and membrane potential. Suitable methods that may be used in this regard include surgical removal of tissue, flow cytometry techniques such as fluorescence-activated cell sorting (FACS), immunoaffinity separation (e.g., magnetic bead separation such as Dynabead™ separation), density separation (e.g., metrizamide, Percoll™, or Ficoll™ gradient

centrifugation), and cell-type specific density separation (e.g., LymphoprepTM). For example, dividing cells or blast cells may be separated from non-dividing cells or resting cells according to cell size by
5 FACS or metrizamide gradient separation.

Any suitable method for isolating total RNA from a cell or tissue may be used. Typical procedures contemplated by the invention are described in CURRENT PROTOCOLS IN MOLECULAR BIOLOGY (Ausubel, et al., eds) (John
10 Wiley & Sons, Inc. 1997) at page 4.2.1 through page 4.2.7. Preferably, techniques which favor isolation of tRNA are employed as, for example, described in Brunngraber, E.F. (1962, *Biochem. Biophys. Res. Commun.* 8:1-3).

The probing of an RNA extract is suitably
15 effected with different oligonucleotide sequences each being specific for a particular iso-tRNA. Of course it will be appreciated that for a given mammal, oligonucleotide sequences would need to be selected which hybridize specifically with particular iso-tRNA
20 sequences expressed by the mammal. Such selection is well within the realm of one of ordinary skill in the art based a known iso-tRNA sequence. For example, in the case of a mouse, exemplary oligonucleotide sequences which may be used include those described in
25 Gauss and Sprinzel (1983, *Nucleic Acids Res.* 11 (1)). In this respect, the oligonucleotide sequences may be selected from the group consisting of:

	5'-TAAGGACTGTAAGACTT-3'	(SEQ ID NO:13)	for Ala ^{GCA}
	5'-CGAGCCAGCCAGGAGTC-3'	(SEQ ID NO:14)	for Arg ^{CGA}
	5'-CTAGATTGGCAGGAATT-3'	(SEQ ID NO:15)	for Asn ^{AAC}
5	5'-TAAGATATATAGATTAT-3'	(SEQ ID NO:16)	for Asp ^{GAC}
	5'-AAGTCTTAGTAGAGATT-3'	(SEQ ID NO:17)	for Cys ^{TGC}
	5'-TATTTCTACACAGCATT-3'	(SEQ ID NO:18)	for Glu ^{GAA}
	5'-CTAGGACAATAGGAATT-3'	(SEQ ID NO:19)	for Gln ^{CAA}
	5'-TACTCTCTTCTGGGTTT-3'	(SEQ ID NO:20)	for Gly ^{GGA}
10	5'-TGCCGTGACTCGGATTC-3'	(SEQ ID NO:21)	for His ^{CAC}
	5'-TAGAAATAAGAGGGCTT-3'	(SEQ ID NO:22)	for Ile ^{ATC}
	5'-TACTTTTATTTGGATTT-3'	(SEQ ID NO:23)	for Leu ^{CTA}
	5'-TATTAGGGAGAGGATTT-3'	(SEQ ID NO:24)	for Leu ^{CTT}
	5'-TCACTATGGAGATTTTA-3'	(SEQ ID NO:25)	for Lys ^{AAA}
15	5'-CGCCCAACGTGGGGCTC-3'	(SEQ ID NO:26)	for Lys ^{AAG}
	5'-TAGTACGGGAAGGATTT-3'	(SEQ ID NO:27)	for Met ^{elong}
	5'-TGTTTATGGGATACAAT-3'	(SEQ ID NO:28)	for Phe ^{TTC}
	5'-TCAAGAAGAAGGAGCTA-3'	(SEQ ID NO:29)	for Pro ^{CCA}
	5'-GGGCTCGTCCGGGATTT-3'	(SEQ ID NO:30)	for Pro ^{CCI}
20	5'-ATAAGAAAGGAAGATCG-3'	(SEQ ID NO:31)	for Ser ^{AGC}
	5'-TGTCTTGAGAAGAGAAG-3'	(SEQ ID NO:32)	for Thr ^{ACA}
	5'-TGGTAAAAAGAGGATTT-3'	(SEQ ID NO:33)	for Tyr ^{TAC}
	5'-TCAGAGTGTTTCATTGGT-3'	(SEQ ID NO:34)	for Val ^{GTA}

25 Typically, the relative abundance of iso-
tRNA species may be determined by blotting techniques
that include a step whereby sample RNA or tRNA extract
is immobilized on a matrix (preferably a synthetic
membrane such as nitrocellulose), a hybridization
30 step, and a detection step. Northern blotting may be
used to identify an RNA sequence that is complementary
to a nucleic acid probe. Alternatively, dot blotting

and slot blotting can be used to identify complementary DNA/RNA or RNA/RNA nucleic acid sequences. Such techniques are well known by those skilled in the art, and have been described in
5 Ausubel, et al (supra) at pages 2.9.1 through 2.9.20.

According to such methods, a sample of tRNA immobilized on a matrix is hybridized under stringent conditions to a complementary nucleotide sequence (such as those mentioned above) which is labeled, for
10 example, radioactively, enzymatically or fluorochromatically.

"Stringency" as used herein, refers to the temperature and ionic strength conditions, and presence or absence of certain organic solvents,
15 during hybridization. The higher the stringency, the higher will be the degree of complementarity between the immobilized nucleotide sequences (i.e., iso-tRNA) and the labeled oligonucleotide sequence. For a discussion of typical stringent conditions that may be
20 used, see CURRENT PROTOCOLS IN MOLECULAR BIOLOGY supra at pages 2.10.1 to 2.10.16, and Sambrook et al in MOLECULAR CLONING.

While stringent washes are typically carried out at temperatures from about 42°C to 68°C, one
25 skilled in the art will appreciate that other temperatures may be suitable for stringent conditions. Maximum hybridization typically occurs at about 20° to 25° below the T_m for formation of a DNA-DNA hybrid. It is well known in the art that the T_m is the melting temperature, or
30 temperature at which two complementary

nucleic acid sequences dissociate. Methods for estimating T_m are well known in the art (see CURRENT PROTOCOLS IN MOLECULAR BIOLOGY *supra* at page 2.10.8). Maximum hybridization typically occurs at about 10° to
5 15° below the T_m for a DNA-RNA hybrid.

Other stringent conditions are well known in the art. A skilled addressee will recognize that various factors can be manipulated to optimize the specificity of the hybridization. Optimization of the
10 stringency of the final washes can serve to ensure a high degree of hybridization.

Methods for detecting labeled nucleotide sequences hybridized to an immobilized nucleotide sequence are well known to practitioners in the art.
15 Such methods include autoradiography, chemiluminescent, fluorescent and colorimetric detection.

Advantageously, the relative abundance of an iso-tRNA in two or more cells or tissues may be
20 determined by comparing the respective levels of binding of a labeled nucleotide sequence specific for the iso-tRNA to equivalent amounts of immobilized RNA obtained from the two or more cells or tissues. Similar comparisons are suitably carried out to
25 determine the respective relative abundance of other iso-tRNAs in the two or more cells or tissues. One of ordinary skill in the art will thereby be able to determine a relative tRNA abundance table (see for example TABLE 2) for different cells or tissues. From
30 such comparisons, one or more synonymous codons may be selected such that the or each synonymous codon corresponds to an iso-tRNA which, when compared to an

iso-tRNA corresponding to an existing codon of the parent nucleic acid sequence, is in higher abundance in the target cell or tissue relative to other cells or tissues of the mammal.

5 Advantageously, a synonymous codon is selected such that its corresponding iso-tRNA in the target cell or tissue is at a level which is at least 110%, preferably at least 200%, more preferably at least 500%, and most preferably at least 1000%, of
10 that expressed in the or each other cell or tissue of the mammal.

 Suitably, synonymous codons for selective expression of a protein in a differentiated cell, preferably a differentiated keratinocyte, are selected
15 from the group consisting of gca (Ala), cuu (Leu) and cua (Leu).

 Synonymous codons for selective expression of a protein in an undifferentiated cell, preferably an undifferentiated keratinocyte, are suitably
20 selected from the group consisting of cga (Arg), cci (Pro) and aac (Asn).

Analysis of codon usage

 Alternatively, synonymous codons may be
25 selected by analyzing the frequency at which codons are used by genes expressed in (i) particular cells or tissues, (ii) substantially all cells or tissues of the mammal, or (iii) an organism which may infect particular cells or tissues of the mammal.

30 Codon frequency tables as well as suitable methods for determining frequency of codon usage in an organism are described, for example, in an article by

Sharp et al (1988, *Nucleic Acids Res.* 16 8207-8211).

The relative level of gene expression (e.g., detectable protein expression vs no detectable protein expression) can provide an indirect measure of the relative abundance of specific iso-tRNAs expressed in different cells or tissues. For example, a virus may be capable of propagating within a first cell or tissue (which may include a cell or tissue at specific stage of differentiation) but may be substantially incapable of propagating in a second cell or tissue (which may include a cell or tissue at another stage of differentiation). Comparison of the pattern of codon usage by genes of the virus with the pattern of codon usage by genes expressed in the second cell or tissue may thus provide indirectly a set of synonymous codons which correspond to iso-tRNAs expressed at relatively high abundance in the first cell or tissue relative to the second cell or tissue and vice versa. Simultaneously, the above comparison may also provide indirectly a set of synonymous codons which correspond to iso-tRNAs expressed at relatively high abundance in the second cell or tissue relative to the first cell or tissue.

From the foregoing, a synonymous codon according to the invention may correspond to a codon including, but not limited to, (1) a codon used at relatively high frequency by genes, preferably highly expressed genes, of the target cell or tissue, (2) a codon used at relatively high frequency by genes, preferably highly expressed genes, of the or each other cell or tissue, (3) a codon used at relatively

high frequency by genes, preferably highly expressed genes, of the mammal, (4) a codon used at relatively low frequency by genes of the target cell or tissue, (5) a codon used at relatively low frequency by genes of the or each other cell or tissue, (6) a codon used at relatively low frequency by genes of the mammal, (7) a codon used at relatively high frequency by genes of another organism, and (8) a codon used at relatively low frequency by genes of another organism.

For example, codons used at a relatively high frequency by genes, preferably highly expressed genes, of the mammal may be selected from the group consisting of: cuc (Leu), cuu, (Leu), cug (Leu), uua (Leu), uug (Leu); cgg (Arg), cgc (Arg), aga (Arg), agg (Arg); agu (Ser), agc (Ser), ucu (Ser), ucc (Ser), and uca (Ser). Alternatively, such codons may include auu (Ile), auc (Ile); guu (Val), guc (Val), gug (Val); acu (Thr), acc (Thr), aca (Thr); gcu (Ala), gcc (Ala), gca (Ala); cag (Glu); ggc (Gly), gga (Gly), ggg (Gly).

Codons used at a relatively low frequency by genes of the mammal are described, for example, in Sharp et al (1988, *supra*). Such codons may comprise cua (Leu); cga (Arg), cgu (Arg); ucg (Ser). Alternatively, such codons may include aua (Ile); gua (Val); acg (Thr); gcg (Ala); caa (Glu); ggu (Gly).

Construction of synthetic nucleic acid sequences

The step of replacing synonymous codons for existing codons may be effected by any suitable technique. For example, in vitro mutagenesis methods may be employed which are well known to those of skill in the art. Suitable mutagenesis methods are

described for example in the relevant sections of Ausubel, et al. (supra) and of Sambrook, et al., (supra).

Alternatively, suitable methods for altering DNA are set forth, for example, in U.S. Patent Nos 4,184,917, 4,321,365 and 4,351,901. Instead of in vitro mutagenesis, the second nucleic acid sequence may be synthesized *de novo* using readily available machinery. Sequential synthesis of DNA is described, for example, in U.S. Patent No 4,293,652. However, it should be noted that the present invention is not dependent on and not directed to any one particular technique for replacing synonymous codons for existing codons.

It is not necessary to replace all the existing codons of the parent nucleic acid sequence with synonymous codons each corresponding to a iso-tRNA expressed in relatively high abundance in the target cell compared to other cells. Increased expression may be accomplished even with partial replacement. Preferably, the replacing step affects 5%, 10%, 15%, 20%, 25%, 30%, more preferably 35%, 40%, 50%, 60%, 70% or more of the existing codons of the parent nucleic acid sequence.

The parent nucleic acid sequence is preferably a natural gene. By "natural gene" is meant a gene that naturally encodes the protein. However, it is possible that the parent nucleic acid sequence encodes a protein that is not naturally-occurring but has been engineered using recombinant techniques.

The parent nucleic acid sequence need not be obtained from the mammal but may be obtained from any suitable source such as from a eukaryotic or prokaryotic organism. For example, the parent nucleic acid
5 sequence may be obtained from another mammal or other animal. Alternatively, the parent nucleic acid sequence may be obtained from a pathogenic organism. In such a case, a natural host of the pathogenic organism is preferably a mammal. For example, the pathogenic
10 organism may be a yeast, bacterium or virus.

For example, suitable proteins which may be used for selective expression in accordance with the invention include, but are not limited to the cystic fibrosis transmembrane conductance regulator (CFTR)
15 protein, and adenosine deaminase (ADA). In the case of CFTR, a parent nucleic acid sequence encoding the CFTR protein which may be utilized to produce the synthetic nucleic acid sequence is described, for example, in Riordan et al (1989, Science 245 1066-
20 1073), and in the GenBank database under Accession No. HUMCFTRM.

The term "nucleic acid sequence" as used herein designates mRNA, RNA, cRNA, cDNA or DNA.

Regulatory nucleotide sequences which may be
25 utilized to regulate expression of the synthetic nucleic acid sequence include, but are not limited to, a promoter, an enhancer, and a transcriptional terminator. Such regulatory sequences are well known to those of skill in the art.

30 Synthetic nucleic acid sequences according to the invention may be operably linked to one or more

regulatory sequences in the form of an expression vector. By "vector" is meant a nucleic acid molecule, preferably a DNA molecule derived, for example, from a plasmid, bacteriophage, or mammalian or insect virus, into
5 which a synthetic nucleic acid sequence may be inserted or cloned. A vector preferably contains one or more unique restriction sites and may be capable of autonomous replication in a defined host cell including the target cell or tissue or a precursor cell or precursor
10 tissue thereof, or be integratable with the genome of the defined host such that the cloned sequence is reproducible. Thus, by "expression vector" is meant any autonomous element capable of directing the synthesis of a protein. Such expression vectors are well known by
15 practitioners in the art.

The term "precursor cell" as used herein refers to a cell that gives rise to the target cell.

The invention also contemplates synthetic nucleic acid sub-sequences encoding desired portions of
20 the protein. A nucleic acid sub-sequence encodes a domain of the protein having a function associated therewith and preferably encodes at least 10, 20, 50, 100, 150, or 500 contiguous amino acids of the protein.

The step of introducing the synthetic
25 nucleic acid sequence into a target cell will differ depending on the intended use and or species, and may involve non-viral and viral vectors, cationic liposomes, retroviruses and adenoviruses such as, for example, described in Mulligan, R.C., (1993 Science 260
30 926-932). Such methods may include:

(i) Local application of the synthetic nucleic acid sequence by injection (Wolff et al., 1990, *Science* 247 1465-1468, surgical implantation, instillation or any other means. This method may also be
5 used in combination with local application by injection, surgical implantation, instillation or any other means, of cells responsive to the protein encoded by the synthetic nucleic acid sequence so as to increase the effectiveness of that treatment. This method
10 may also be used in combination with local application by injection, surgical implantation, instillation or any other means, of another factor or factors required for the activity of said protein.

(ii) General systemic delivery by
15 injection of DNA, (Calabretta et al., 1993, *Cancer Treat. Rev.* 19 169-175, or RNA, alone or in combination with liposomes (Zhu et al., 1993, *Science* 261 209-212, viral capsids or nanoparticles (Bertling et al., 1991, *Biotech. Appl. Biochem.* 13 390-405 or any other
20 mediator of delivery. Improved targeting might be achieved by linking the synthetic nucleic acid sequence to a targeting molecule (the so-called "magic bullet" approach employing for example, an antibody), or by local application by injection,
25 surgical implantation or any other means, of another factor or factors required for the activity of the protein produced from said synthetic nucleic acid sequence, or of cells responsive to said protein.

(iii) Injection or implantation or delivery by any means, of cells that have been modified ex vivo by transfection (for example, in the presence of calcium phosphate: Chen et al., 1987, *Mole. Cell Biochem.* 7 2745-2752, or of cationic lipids and polyamines: Rose et al., 1991, *BioTech.* 10 520-525, infection, injection, electroporation (Shigekawa et al., 1988, *BioTech.* 6 742-751 or any other way so as to increase the expression of said synthetic nucleic acid sequence in those cells. The modification may be mediated by plasmid, bacteriophage, cosmid, viral (such as adenoviral or retroviral; Mulligan, 1993, *Science* 260 926-932; Miller, 1992, *Nature* 357 455-460; Salmons et al., 1993, *Hum. Gen. Ther.* 4 129-141, or other vectors, or other agents of modification such as liposomes (Zhu et al., 1993, *Science* 261 209-212, viral capsids or nanoparticles (Bertling et al., 1991, *Biotech. Appl. Biochem.* 13 390-405, or any other mediator of modification. The use of cells as a delivery vehicle for genes or gene products has been described by Barr et al., 1991, *Science* 254 1507-1512 and by Dhawan et al., 1991, *Science* 254 1509-1512. Treated cells may be delivered in combination with any nutrient, growth factor, matrix or other agent that will promote their survival in the treated subject.

In yet another aspect, the invention provides a pharmaceutical composition comprising the synthetic nucleic sequences of the invention and a pharmaceutically acceptable carrier.

5 By "pharmaceutically-acceptable carrier" is meant a solid or liquid filler, diluent or encapsulating substance that may be safely used in systemic administration. Depending upon the particular route of administration, a variety of
10 pharmaceutically acceptable carriers, well known in the art may be used. These carriers may be selected from a group including sugars, starches, cellulose and its derivatives, malt, gelatin, talc, calcium sulfate, vegetable oils, synthetic oils, polyols, alginic acid,
15 phosphate buffered solutions, emulsifiers, isotonic saline, and pyrogen-free water.

Any suitable technique may be employed for determining expression of the protein from said synthetic nucleic acid sequence in a particular cell
20 or tissue. For example, expression can be measured using an antibody specific for the protein of interest or portion thereof. Such antibodies and measurement techniques are well known to those skilled in the art.

Applications

25 In one embodiment of the present invention, the target cell is suitably a differentiated cell. Advantageously, the protein which is desired to be selectively expressed in the differentiated cell is not expressible in a precursor cell thereof (such as
30 an undifferentiated or less differentiated cell of the mammal) from a parent nucleic acid sequence at a level

sufficient to effect a particular function associated with said protein. In this embodiment, the step of replacing at least one existing codon with a synonymous codon is characterized in that the
5 synonymous codon corresponds to an iso-tRNA which, when compared to the iso-tRNA corresponding to the at least one existing codon, is in relatively higher abundance in the differentiated cell compared to the precursor cell. Accordingly, a synthetic nucleic acid
10 sequence is produced having altered translational kinetics compared to the parent nucleic acid sequence wherein the protein is expressible in the differentiated cell at a level sufficient to effect a particular function associated with said protein, but
15 wherein the protein is not expressible in the precursor cell at a level sufficient to effect said function.

As used herein, the term "function" refers to a biological, or therapeutic function.

20 The above embodiment may be utilized advantageously for somatic gene therapy where overexpression of a protein in undifferentiated cells such as stems cells has undesirable consequences including death or differentiation of the stem cells.
25 In such a case, a suitable protein may include cystic fibrosis transmembrane conductance regulator (CFTR) protein, and adenosine deaminase (ADA).

The differentiated cell may comprise a cell of any lineage including a cell of epithelial,
30 hemopoetic or neural origin. For example, the differentiated cell may be a mature differentiated keratinocyte.

Targeting expression of a protein to progeny of a stem cell but not to the stem cell itself

The synthetic nucleic acid sequence produced above may be transfected directly into the differentiated cell for the desired function or alternatively, transfected into the precursor cell. For example, in the case of ADA deficiency, expression of ADA in stem cells may result in loss of stem phenotype which is undesirable. However, an advantageous therapy may reside in transducing autologous marrow stem cells with a synthetic nucleic acid sequence operably linked to one or more regulatory sequences, wherein existing codons of the wild type ADA gene have been replaced with synonymous codons each corresponding to an iso-tRNA expressed in relatively high abundance in differentiated lymphocytes compared to the marrow stem cells. The transduced stem cells may then be reinfused into the patient. This approach will result in transduced marrow stem cells which are not capable of expressing ADA themselves, but which are able to give rise to a renewable population of differentiated lymphocytes which are capable of expressing ADA at levels sufficient to permit a therapeutic effect. In this regard, a suitable cell source for this purpose may comprise stem cells isolated as CD34 positive cells from a patient's peripheral blood or marrow. For gene delivery, a suitable vector may include a retrovirus or Adeno associated virus.

Alternatively, in the case of inducing cell mediated immunity, dendritic cells are important

antigen presenting cells (APC) but have a very limited life span for antigen presentation once activated of between 14 to 21 days. Consequently, dendritic cells provide relatively short-term immune stimulation that
5 may not be optimal. However, in accordance with the present invention, a long-term immune stimulation may be provided by transducing autologous bone marrow-derived CD34 positive dendritic cell precursors with a synthetic nucleotide sequence encoding an antigen.
10 such as the melanoma antigen MART-1, wherein the synthetic sequence is operably linked to one or more regulatory sequences, and wherein existing codons of a wild type nucleotide sequence encoding MART-1 have been replaced with synonymous codons each
15 corresponding to an iso-tRNA expressed in relatively high abundance in dendritic cells compared to the dendritic cell precursors. The transduced dendritic cell precursors may then be reinfused into the patient. This approach will result in transduced
20 dendritic cell precursors which are not capable of expressing MART-1 themselves, but which are able to give rise to a renewable population of dendritic cells which are capable of expressing MART-1 at levels sufficient to permit a lifelong intermittent
25 restimulation of a cytotoxic T lymphocyte (CTL) response to the MART-1 antigen.

Targeting expression of a protein to a stem cell but not to progeny of the stem cell

30 In an alternate embodiment, the target cell may be an undifferentiated cell wherein the protein is not expressible in said undifferentiated cell, from a

parent nucleic acid sequence encoding the protein, at a level sufficient to effect a particular function associated with the protein. In such a case, at least one existing codon of the parent nucleic acid sequence is replaced with a synonymous codon corresponding to an iso-tRNA which, when compared to the iso-tRNA corresponding to the at least one existing codon, is in relatively higher abundance in the undifferentiated cell compared to a differentiated cell. This results in a synthetic nucleic acid sequence having altered translational kinetics compared to said parent nucleic acid sequence wherein the protein is expressible in the undifferentiated cell at a level sufficient to effect a particular function associated with the protein, but wherein the protein is not expressible in differentiated cells derived from the undifferentiated cell at a level sufficient to effect said function.

This alternate embodiment may, by way of example, be used to permit expression of a transcriptional regulatory protein which when expressed in a particular undifferentiated cell or stem cell facilitates differentiation of the stem cell along a particular cell lineage. It will be appreciated that in such a case, the regulatory protein is normally expressed from a gene in which the existing codons correspond to iso-tRNAs which are in relatively low abundance in the stem cell compared to other iso-tRNAs and that therefore the protein is not capable of being expressed at levels sufficient for commitment of the stem cell to differentiate along a particular cell lineage. It will also be apparent that such commitment to differentiate along a

particular cell lineage may be utilized to prevent production of a particular lineage of cells such as cancer cells.

Alternatively, the method according to this embodiment may be used to express a transcriptional regulatory protein that is involved in the production of a therapeutic agent or agents. Such a protein may include, for example, NF-kappa-B transcription factor p65 subunit (NF-kappa-B p65) which is involved in the production of interleukin-2 (IL-2), interleukin-3 (IL-3) and granulocyte and macrophage colony stimulating factor (GM-CSF). NF-kappa-B p65 is encoded naturally by a nucleotide sequence comprising a number of existing codons each corresponding to an iso-tRNA expressed in relatively low abundance in stem cells. Accordingly, such sequence may be used as the parent nucleic acid sequence according to this embodiment. A suitable nucleotide sequence encoding this protein is described, for example, in Lyle et al (1994, Gene 138 265-266) and in the EMBL database under Accession No HSNFKB65A.

A suitable undifferentiated cell which may be utilized in accordance with the present embodiment includes but is not limited to a stem cell, such as a CD34 positive hemopoietic stem cell.

The present embodiment may also be used advantageously for gene therapy where ongoing regulated expression of a transgene is desirable. For example, secure but reversible regulation of fertility is desirable in veterinary practice and in humans. Such regulation may be effected by transducing autologous breast ductal epithelial cells with a

synthetic nucleic acid encoding a leutinising hormone (LH) antagonist or a leutinising hormone releasing hormone (LHRH) antagonist under the control of one or more regulatory sequences. The synthetic nucleic acid
5 may be produced by replacing existing codons of a parent nucleic acid with synonymous codons corresponding to iso-tRNAs expressed in relatively high abundance in resting breast ductal epithelial cells compared to differentiated cells arising
10 therefrom. Once the transduced cells are implanted back into the patient, expression may be switched off by oral administration of progestagen, forcing the differentiation of the majority of the stem cells and loss of expression of the antagonist. Once pregnancy
15 is established, the suppression would be self sustaining by the naturally produced progestagen. The iso-tRNA composition of resting and oestrogen driven breast epithelial cells may be established by first obtaining resting cells from reduction mammoplasty,
20 and determining the cellular tRNA composition in the presence and absence of oestrogen. The synthetic nucleic acid sequence may be introduced into autologous resting epithelial cells by cell electroporation ex vivo, and the transduced cells may
25 be subsequently transplanted subcutaneously into the patient. Progestagen may be administered as required to reverse regulation of fertility.

*Targeting expression of a toxin to a tumor
30 cell but not to any other cells of the mammal*

Many toxins and drugs are available that can kill tumor cells. However, these toxins and drugs

are generally toxic for all dividing cells. This problem may be nevertheless ameliorated by establishing the isoacceptor tRNA composition in a tumor clone, and constructing a synthetic toxin gene (e.g., ricin gene) or a synthetic anti-proliferation gene (e.g., the tumor supressor p53) using synonymous codons corresponding to iso-tRNAs expressed at relatively high abundance in the tumor clone compared to normal dividing cells of the mammal. The synthetic gene is then introduced into the patient by suitable means to selectively express the synthetic genes in tumor cells.

Alternatively, a chemotherapy enhancing product gene (i.e., a drug resistance gene e.g., the multi-drug resistance gene) using a codon pattern unlikely to be expressed in the tumor efficiently may be employed.

Targeting gene therapy to control body fat

Leptins are proteins known to control satiety. By analogy with animal data, however, if too much leptin is administered to a patient, leptin-induced starvation might occur. Advantageously, a synthetic gene encoding leptin may be constructed including synonymous codons corresponding to iso-tRNAs expressed at relatively high levels in activated adipocytes compared to non-activated adipocytes. The synthetic gene may then be introduced into the patient by suitable means such that leptin is only expressed substantially in activated adipocytes as opposed to non-activated adipocytes. As body fat turnover diminishes under the influence of leptin reduced

appetite, the metabolic activity of the adipocytes falls and the leptin production decreases correspondingly.

5 *Targeting expression of a protein to a stage of the cell cycle*

 In another embodiment of the invention, the target cell may be a non-cycling cell. In this case, the protein which is desired to be selectively
10 expressed in the non-cycling cell is expressible in a cycling cell of the mammal from a parent nucleic acid sequence at a level sufficient to effect a particular function associated with the protein. The synonymous codons are selected such that each corresponds to an
15 iso-tRNA which, when compared to the iso-tRNA corresponding to the at least one existing codon, is in higher abundance in the non-cycling cell compared to the cycling cell. Accordingly, a synthetic nucleic acid sequence is produced having altered translational
20 kinetics compared to the parent nucleic acid sequence wherein the protein is expressible in the non-cycling cell at a level sufficient to effect a particular function associated with said protein, but wherein the protein is not expressible in the non-cycling cell to
25 effect said function.

 The term "non-cycling cell" as used herein refers to a cell that has withdrawn from the cell cycle and has entered the G0 state. In this state, it is well known that transcription of endogenous genes
30 and protein translation are at substantially reduced levels compared to phases of the cell cycle, namely G1, S, G2 and M.

By "cycling cell" is meant a cell which is in one of the above phases of the cell cycle.

Expressing a protein in a target cell or
5 tissue by in vivo expression of iso-tRNAs in the target cell or tissue

In another aspect, the invention extends to a method wherein a protein may be selectively expressed in a target cell by introducing into the
10 cell an auxiliary nucleic acid sequence capable of expressing therein one or more isoaccepting transfer RNAs which are not expressed in relatively high abundance in the cell but which are rate limiting for expression of the protein from a parent nucleic acid
15 sequence to a level sufficient for effecting a function associated with the protein. In this embodiment, introduction of the auxiliary nucleic acid sequence in the cell changes the translational kinetics of the parent nucleic acid sequence such that
20 said protein is expressed at a level sufficient to effect a function associated with the protein.

The step of introducing the auxiliary nucleic acid sequence into the target cell or a tissue comprising a plurality of these cells may be effected
25 by any suitable means. For example, analogous methodologies for introduction of the synthetic nucleic acid sequence referred to above may be employed for delivery of the auxiliary nucleic acid sequence into said cycling cell.

30

Assembly of virus particles in cells which do not normally permit assembly of virus particles

In yet another aspect, the invention extends to a method for producing a virus particle in a cycling eukaryotic cell. The virus particle will comprise at least one protein necessary for virus assembly, wherein the at least one protein is not expressed in the cell from a parent nucleic acid sequence at a level sufficient to permit virus assembly therein. This method is characterized by replacing at least one existing codon of the parent nucleic acid sequence with a synonymous codon to produce a synthetic nucleic acid sequence having altered translational kinetics compared to the parent nucleic acid sequence such that the at least one protein is expressible from the synthetic nucleic acid sequence in the cell at a level sufficient to permit virus assembly therein. The synthetic nucleic acid sequence so produced is operably linked to one or more regulatory nucleotide sequences and is then introduced into the cell or a precursor cell thereof. The at least one protein is expressed subsequently in the cell in the presence of other viral proteins required for assembly of the virus particle to thereby produce the virus particle.

Advantageously, the synonymous codon corresponds to an iso-tRNA expressed at relatively high level in the cell compared to the iso-tRNAs corresponding to the existing codons.

The cycling cell may be any cell in which the virus is capable of replication. Suitably, the cycling cell is a eukaryotic cell. Preferably, the

cycling cell for production of the virus particle is a eukaryotic cell line capable of being grown in vitro such as, for example, CV-1 cells, COS cells, yeast or spodoptera cells.

5 Suitably, the at least one protein of the virus particle are viral capsid proteins. Preferably, the viral capsid proteins comprise L1 and/or L2 proteins of papillomavirus.

10 The other viral proteins required for assembly of the virus particle in the cell may be expressed from another nucleic acid sequence(s) which suitably contain the rest of the viral genome. In the case of the at least one protein comprising L1 and/or L2 of papillomavirus, said other nucleic acid
15 sequence(s) preferably comprises the papillomavirus genome without the nucleotide sequences encoding L1 and/or L2.

 In yet a further aspect of the invention, there is provided a method for producing a virus
20 particle in a cycling cell, said virus particle comprising at least one protein necessary for assembly of said virus particle, wherein said at least one protein is not expressed in said cell from a parent nucleic acid sequence at a level sufficient to permit
25 virus assembly therein, and wherein at least one existing codon of said parent nucleic acid sequence is rate limiting for the production said at least one protein to said level, said method including the step of introducing into said cell a nucleic acid sequence
30 capable of expressing therein an isoaccepting transfer RNA specific for said at least one codon.

In yet a further aspect, the invention resides in virus particles resulting from the above methods.

5 The invention further contemplates cells or tissues containing therein the synthetic nucleic acid sequences of the invention, or alternatively, cells or tissues produced from the methods of the invention.

The invention is further described with reference to the following non-limiting examples.

10

EXAMPLE 1

Expression of synthetic L1 and L2 protein in undifferentiated cells.

15 Materials and Methods

Codon replacements in the bovine PV (BPV) L1 and L2 genes

20 The DNA and amino acid sequences of the wild-type L1 (SEQ ID NOS:1,2) and L2 genes (SEQ ID NOS:5,6) are shown respectively in Figures 1A and 1B. To determine whether the presence of rare codons in wild-type L1 (SEQ ID NO:1) and L2 (SEQ ID NO:5) genes (Table 1) inhibited translation, we synthesized the L1 (SEQ ID NO:3) and L2 (SEQ ID NO:7) genes by using
25 synonymous substitutions as shown. To construct the synthetic sequences, we synthesized 11 pairs of oligonucleotides for L1 and 10 pairs of oligonucleotides for L2. Each pair of oligonucleotides has restriction sites incorporated to
30 facilitate subsequent cloning (Figures 1A and 1B). The degenerate oligonucleotides were used to amplify

L1 and L2 sequences by PCR using a plasmid with BPV1 genome as the template. The amplified fragments were cut with appropriate enzymes and sequentially ligated to pUC18 vector, producing pUCHBL1 and pUCHBL2. The
5 synthetic L1 (SEQ ID NO:3) and L2 (SEQ ID NO:7) sequences were sequenced and found to be error-free, and then sub-cloned into the mammalian expression vector pCDNA3 containing SV40 ori (Invitrogen), giving expression plasmids pCDNA/HBL1 and pCDNA/HBL2. To
10 compare expression of L1 and L2 with that of the original sequences, the wild type L1 (SEQ ID NO:1) and L2 (SEQ ID NO:5) genes were cloned into the pCDNA3 vector, resulting in pCDNA/BPVL1wt and pCDNA/BPVL2wt.

15 *Immunofluorescence and Western blot staining*

For immunoblotting assays, Cos-1 cells in 6-well plates were transfected with 2 μ g L1 or L2 expression plasmids using lipofectamine (Gibco). 36
20 hrs after transfection, cells were washed with 0.15M phosphate buffered 0.9% NaCl (PBS) and lysed in SDS loading buffer. The cellular proteins were separated by 10% SDS PAGE and blotted onto nitrocellulose membrane. The L1 or L2 proteins were identified by
25 electrochemiluminescence (Amersham, UK), using BPV1 L1 (DAKO) or L2-specific (17) antisera. For immunofluorescent staining, Cos-1 cells were grown on 8-chamber slides, transfected with plasmids, and fixed and permeabilised with 85% ethanol 36hr after
30 transfection. The slides were blocked with 5% milk-PBS and probed with L1 or L2-specific antisera, followed by FITC-conjugated anti-rabbit IgG (Sigma). For GFP or

PGFP plasmid transfected cells, the cell were fixed with 4% buffered formaldehyde and viewed by epi-fluorescence microscopy.

5 *Northern blotting*

Cos cells transfected with various plasmids were used to extract cytoplasmic or total RNA using the QIAGEN RNeasy mini kit according to the supplier's handbook. Briefly, for cytoplasmic RNA
10 purification, buffer RLN (50 mM Tris, pH 8.0, 140 mM NaCl, 1.5 mM MgCl₂ and 0.5% NP40) was directly added to monolayer cells and cells were lysed in 4 °C for 5 min. After the nuclei were removed by centrifugation, cytoplasmic RNAs were purified by column. For total
15 RNA extraction, the monolayer cells were lysed using buffer RLT supplied by the kit and RNA was purified by spin column. The purified RNAs were separated by 1.5% agarose gel in the presence of formaldehyde. The RNAs were then blotted onto nylon membrane and probed with
20 (a) 1:1 mixed 5'-end labelled L1 wt and HBL1 fragments; (b) 1:1 mixed 5'-end labelled L2 wt and HBL2 fragments; (c) 1:1 mixed 5'end labelled GFP and PGFP fragments or (d) randomly labelled PAGDH fragment. The blots were washed extensively at 65 °C
25 and exposed to X-ray films for three days.

Results

To test the hypothesis that the codon composition of the genes encoding the L1 and L2 capsid
30 proteins of papillomavirus (PV) contributes to their preferential expression in differentiated epithelial

cells, we produced synthetic BPV1 L1 (SEQ ID NO:3) and L2 (SEQ ID NO:7) genes, substituting codons preferentially used in mammalian genes for the codons frequently present in the wild type BPV1 L1 and L2 sequences which are rare in eukaryotic genes (Figures 1A, 1B).

For the L1 gene, a total of 202 base substitutions were made in 196 codons, without changing the encoded amino acid sequence (Figure 1A). This synthetic "humanized" BPV L1 gene (SEQ ID NO:3) was designated HBL1. In a similarly modified BPV1 L2 gene (SEQ ID NO:7) designated HBL2, 303 bases were changed to substitute 290 less frequently used codons with the corresponding preferentially used codons. Using the synthetic HBL1 (SEQ ID NO:3) and HBL2 (SEQ ID NO:7) genes, we constructed two eukaryotic expression plasmids based on pCDNA3, and designated pCDNA/HBL1 and pCDNA/HBL2. Similar expression plasmids, constructed with the wild type BPV1 L1 (SEQ ID NO:1) and BPV1 L2 (SEQ ID NO:5) genes, were designated pCDNA/BPVL1wt and pCDNA/BPVL2wt, respectively. In each of these plasmids the SV40 ori allowed replication in Cos-1 cells, and the L1 or L2 gene was driven by a strong constitutive CMV promoter.

To compare the expression of the synthetic humanized and the wild type BPV1 L1 or BPV1 L2 genes, we separately transfected Cos-1 cells with each of the L1 and L2 plasmids described above. Transfected cells were analyzed for expression of L1 (SEQ ID NO:2,4) or L2 (SEQ ID NO:6,8) protein by immunofluorescence 36 hr after transfection (Figures 2A and 3A). Cells transfected with the pCDNA3 expression plasmid

containing the synthetic humanized L1 (SEQ ID NO:3) or L2 (SEQ ID NO:7) genes were observed to produce large amounts of the corresponding protein, while cells transfected with expression plasmids with the wild type L1 (SEQ ID NO:1) or L2 (SEQ ID NO:5) sequences produced no detectable L1 or L2 protein (Figures 2A and 3A, see nuclear staining of L1 and L2 proteins). To compare more accurately the expression of the different L1 and L2 constructs, L1 and L2 protein expression was assessed by immunoblot in Cos-1 cells transfected with the wild type or synthetic humanized BPV1 L1 or L2 pCDNA3 expression constructs (Figures 2B and 3B). Large amounts of immunoreactive L1 and L2 proteins were expressed from the synthetic humanized L1 (SEQ ID NO:3) and L2 (SEQ ID NO:7) sequences, but no L1 or L2 protein was expressed from the wild type L1 and L2 sequences (SEQ ID NO:1,5).

To establish whether the alterations to the primary sequence of the L1 and L2 mRNA which resulted from the codon alterations also affected steady state expression of the corresponding message, mRNA was prepared from Cos-1 cells transfected with the various capsid protein gene constructs. Using GAPDH as an internal standard it was established by Northern blot that two to three times more modified than wild type L1 mRNA, and similar levels of wild type and modified L2 mRNA were present in the cytoplasm of transfected cells (Figures 2C and 3C). The amount of L1 or L2 protein expressed per arbitrary unit of L1 or L2 mRNA was at least 100 fold higher for the humanized gene constructs than for the natural gene constructs.

EXAMPLE 2Papillomavirus late protein translation *in vitro*5 Materials and Methods*In vitro translation assay*

One microgram of each plasmid was incubated with 20 μCi ^{35}S -methionine (Amersham) and 40 μL T7 coupled rabbit reticulocyte or wheat germ lysates (Promega). Translation was performed at 30 °C and stopped by adding SDS loading buffer. The L1 proteins were separated by 10% SDS PAGE and examined by autoradiography.

15 *Production of aminoacyl-tRNA*

2.5 x 10⁻⁴ M tRNA (Boehringer) was added to a 20 μL reaction containing 10 mM Tris-acetate, pH.7.8, 44 mM KCl, 12 mM MgCl₂, 9 mM -mercaptoethanol, 38 mM ATP, 0.25 mM GTP and 7 μL rabbit reticulocyte extract. The reaction was carried out at 25 °C for 20 min, and 30 μL H₂O was added to the reaction to dilute the tRNAs to 1 x 10⁻⁴ M. The aminoacyl-tRNAs were then aliquoted and stored at -70 °C.

25 Results

As the major limitation to expression of the wild type BPV L1 and L2 genes appeared to be translational in our system we wished to test whether this limitation reflected a limited availability of the appropriate tRNA species for gene translation. As transient expression of the synthetic genes within

intact cells may be regulated by many factors, we tested our hypothesis in a cell free system using rabbit reticulocyte lysate (RRL) or wheat germ lysate to examine gene translation. Similar amounts of plasmids expressing the wild type or synthetic humanized BPV1 L1 gene were added to a T7-DNA polymerase coupled RRL transcription/translation system in the presence of ³⁵S-methionine. After 20 minutes, translated proteins were separated by SDS PAGE and visualized by autoradiography. Efficient translation of the modified L1 gene was observed (Figure 4, top panel, lane 2), while translation of the wild type BPV1 L1 sequence resulted in a weak 55 kDa L1 band (Figure 4, upper panel, lane 1). We reasoned that although the wild type sequence was not optimized for translation in RRL, some translation would occur as there would be no cellular mRNA species competing for the 'rare' codons present in the wild type L1 sequence. The above data suggest that the observed difference in efficiency of translation of the wild type and synthetic humanized L1 genes is a consequence of limited availability of the tRNAs required for translation of the rare codons present in the wild type gene. We therefore expected that addition of excess tRNA to the in vitro translation system would overcome the inhibition of translation of the wild type L1 gene. To address this question, 10⁻⁵ M aminoacyl-tRNAs from yeast were added into the RRL translation system, and L1 protein synthesis was assessed. Introduction of exogenous tRNAs resulted in a dramatic improvement in translation of the wild type L1 sequence, which now gave a yield of L1 protein

comparable to that observed with the synthetic humanized L1 sequence (SEQ ID NO:3) (Figure 4, top panel). Enhancement of translation of the wild type L1 gene (SEQ ID NO:1) by aminoacyl-tRNA was dose-dependent, with an optimum efficiency at 10^{-5} M tRNA. As addition of exogenous tRNA improved the yield of L1 protein translated from the wild type L1 gene sequence (SEQ ID NO:1), we assessed the speed of translation of wild type and humanized L1 mRNA. Samples were collected from the translation mixture every 2 minutes, starting at the 8th minute. Translation of L1 (SEQ ID NO:2,4) from the wild type sequence (SEQ ID NO:1) was much slower than from the humanized L1 sequence (SEQ ID NO:3) (Figure 4 bottom panel), and the retardation of translation could be completely overcome by adding exogenous tRNA from commercially available yeast tRNA. Yeast tRNA was chosen in the above analysis because the codon usage in yeast is similar to that of papillomavirus (Table 1). Addition of exogenous tRNA did not significantly improve the translation of the humanized L1 gene (SEQ ID NO:3), indicating that this sequence was optimized with regard to codon usage for the rabbit reticulocyte translation machinery (Figure 4, bottom panel). In separate experiments we established that wt L1 translation could also be enhanced by liver tRNA (Figure 4), and by tRNAs extracted from bovine skin epidermis, which presumably constitutes a mixture of tRNAs from differentiated and undifferentiated cells (data not shown).

EXAMPLE 3

Translation of wild type L1 is efficient in wheat germ
5 extract.

To further test our hypothesis that tRNA
availability is a determinant of expression of the
wild type BPV1 L1 gene (SEQ ID NO:1), we examined the
translation of L1 in a cell type in which a quite
10 different set of tRNAs would be available. In a wheat
germ translation system, wild type L1 mRNA was
translated as efficiently as humanized L1 mRNA, and
addition of exogenous aminoacyl-tRNAs did not improve
the translation efficiency of either wild type or
15 humanized sequences (Figure 4 bottom panel). This
indicated that in wheat germ there are sufficient of
the tRNAs which are limiting for translation of wild
type L1 sequence in RRL to allow efficient L1
translation.

20

EXAMPLE 4

Modified late genes can be expressed in
undifferentiated cells from papillomavirus promoter(s)

25 While our data presented above indicates
that translation is limiting for the production of
BPV1 capsid proteins in our test system, these
experiments were conducted in systems which are not
truly representative of the viral late gene
30 transcription from the BPV genome, in part because the
genes were driven by a strong CMV promoter. We
therefore wished to establish whether synthetic

humanized BPV capsid protein mRNA would be translated more efficiently than the wild type mRNA, if transcribed from the natural BPV1 promoter. This would establish whether translation was indeed one of the limiting factors for expression of BPV1 late genes driven from the natural cryptic late gene promoter in an undifferentiated cell. The BPV genome was cleaved at nt 4450 and 6958 with *Bam*HI/*Hind*III and the original L1 (nt 4186-5595) and L2 (5068-7095) ORFs were removed. The synthetic humanized L2 gene (SEQ ID NO:7), together with an SV40 ori sequence to allow plasmid replication in eukaryotic cells, were inserted into the BPV genome lacking L1/L2 ORF sequences. This plasmid (Figure 5A) was designated pCICR1. A similar plasmid was constructed with wild type (SEQ ID NO:5) rather than synthetic humanized L2 and designated pCICR2. Cos-1 cells were transfected with these plasmids and L2 protein expression examined by immunofluorescence of transfected cells. Synthetic humanized L2 (SEQ ID NO:7), driven by the natural BPV-1 promoter, was efficiently expressed, whereas the wild type L2 sequence (SEQ ID NO:5), driven from a similar construct, produced no immunoreactive L2 protein (SEQ ID NO:6,8) (Figure 5B). As undifferentiated cells supported the expression of the humanized L2 gene (SEQ ID NO:7) but not the wild type L2 (SEQ ID NO:5) expressed from the cryptic late BPV promoter, the results confirmed our earlier observations from experiments using the CMV promoter. However, the plasmids tested here contained SV40 ori, designed to replicate the DNA in Cos cells. The increased copy number of the BPV1 L2 plasmids or the

transcriptional enhancing activity of the SV40 ori might explain in part the increased efficiency of expression of L2 in this experimental system when compared with infected skin. However, the marked
5 difference in expression between the natural and humanized genes seen with a CMV promoter construct is still observed with the natural promoter.

EXAMPLE 5

10

Substitution of papillomavirus-preferred codons prevents translation but not transcription of a non-papillomavirus gene in undifferentiated cells.

Materials and Methods

15

Codon replacement in gfp gene

To construct a modified gfp gene (SEQ ID NO:11) using papillomavirus preferred codons (PGFP), 6 pairs of oligonucleotides were synthesized. Each pair of oligonucleotides has restriction sites incorporated
20 and was used to amplify gfp using a humanized gfp gene (SEQ ID NO:9) (GIBCO) as template. The PCR fragments were ligated into the pUC18 vector to produce pUCPGFP. The PGFP gene was sequenced, and cloned into *Bam*HI site of the same mammalian expression vector, pCDNA3,
25 under the CMV promoter. The DNA and deduced amino acid sequences of the humanized GFP gene are shown in Figures 1C. Mutations introduced into the wild type gfp gene (SEQ ID NO:9) to produce the Pgfp gene (SEQ ID NO:11) are indicated above the corresponding
30 nucleotides of the wild-type sequence.

Results

To further confirm that codon usage can alter gene expression in mammalian cells, we made a further variant on a synthetic *gfp* gene modified for optimal expression in eukaryotic cells (Zolotukhin, et al., 1996. *J. Virol.* 70:4646-4654). In our variant, codons optimized for expression in eukaryotic cells were substituted by those preferentially used in papillomavirus late genes. Of 240 codons in the humanized *gfp* gene (SEQ ID NO:9), which expresses high levels of fluorescent protein in cultured cells, 156 were changed to the corresponding papillomavirus late gene-preferred codons to produce a new *gfp* gene (SEQ ID NO:11) designated *Pgfp*. Expression of *Pgfp* (SEQ ID NO:11) in undifferentiated cells was compared with that of humanized *gfp* (SEQ ID NO:9). Cos-1 cells transfected with the humanized *gfp* (SEQ ID NO:9) produced a bright fluorescent signal after 24 hrs, while cells transfected with *Pgfp* (SEQ ID NO:11) produced only a faint fluorescent signal (Figure 6A). To confirm that this difference reflected differing translational efficacy, *gfp* specific mRNA was tested in both transfections and found not to be significantly different (Figure 6B.). Thus, codon usage and corresponding tRNA availability apparently determines the observed restriction of expression of PV late genes, and modification of codon usage in other genes similarly prevents their expression in undifferentiated cells.

EXAMPLE 6

PGFP with papillomavirus-preferred codons is
5 efficiently expressed in vivo in differentiated mouse
keratinocytes.

Materials and Methods

*Delivery of plasmid DNA into mouse skin by
gene gun*

10 Fifty microgram of DNA was coated onto 25
µg gold micro-carriers by calcium precipitation,
following the manufacturer's instructions (Bio-Rad).
C57/bl mouse skin was bombarded with gold particles
coated with DNA plasmid at a pressure of 600 psi.
15 Serial sections were taken from the skin and examined
for distribution of the particles, confirming that a
pressure of 600 psi could deliver particles throughout
the epidermis.

Results

20 Mice were shot with gold beads carrying
PGFP DNA plasmid and, 24 hrs later, skin samples were
cut from the site of DNA delivery and examined for
expression of GFP protein (SEQ ID NO:10,12).
Fluorescence was detected mostly in upper keratinocyte
25 layers, representing the differentiated epithelium,
and was not seen in undifferentiated basal cells. In
contrast, skin sections shot with the humanized GFP
plasmid showed fluorescence in cells randomly
distributed throughout the whole epidermis (Figure 7).
30 Although GFP-positive cells were rare in both PGFP-
(SEQ ID NO:11) and GFP-inoculated (SEQ ID NO:9) mouse

skin, fluorescence was observed only in differentiated strata in the PGFP sample (SEQ ID NO:11), whereas fluorescence was observed throughout the epidermis in GFP-inoculated (SEQ ID NO:9) mouse skin. This result
5 confirmed that the use of papillomavirus-preferred codons resulted in the protein being expressed in an epithelial differentiation-dependent manner.

EXAMPLE 7

10

Microinjection of yeast tRNA and wild type L1 gene into cultured cells

To test if yeast tRNA could facilitate expression of wild type BPV-1 L1 (SEQ ID NO:1) (as
15 yeast uses a similar set of codons to those observed in papillomavirus for its own genes), 2 pL of mixtures containing tRNA (2 mg/mL) (purified yeast tRNA (Boehringer Mannheim) or bovine liver tRNA - control) and BPV L1 DNA (2 µg/mL) can be injected into CV-1
20 cells (Lu and Campisi, 1992, *Proc. Natl. Acad. Sci. U. S. A.* 89 3889-3893). The injected cells can then be cultured for 48 hrs at 37 °C and examined for expression of L1 gene by standard immunofluorescence methods using BPV L1-specific antibody and quantified
25 by FACS analysis (Qi et al 1996, *Virology* 216 35-45).

EXAMPLE 8

*Establishment of a cell line which can
30 continuously produce HPV virus particles*

To produce infectious PV, various methods have been tried including the epithelial raft culture

system (Dollard et al 1992, *Genes Dev* 6 1131-1142), and cell lines containing BPV-1 episomal DNA, and infected by BPV-1 L1/L2 recombinant vaccinia (Zhou et al 1993, *J. Gen. Virol.* 74 763-768) or transfected by SFV RNA (Roden et al 1996, *J. Virol.* 70 5875-5883). The yield of particles is in each case low. In a reduction to practice of our discovery, synthetic BPV L1 (SEQ ID NO:3) and L2 genes (SEQ ID NO:7) (as described in Example 1) can be used to produce infectious BPV in a cell line containing BPV-1 episomal DNA. Fibroblast cell lines (CON/BPV) containing BPV-1 episomal DNA (Zhou et al 1993, *J. Gen. Virol.* 74 763-768) can be used for transfection of the synthetic BPV-1 L1 (SEQ ID NO:3) and L2 genes (SEQ ID NO:7) under control of CMV promoter. BPV particles may then be purified from the cell lysate and the purified particles examined for the presence of BPV-1 genome. Standard methods such as transfection with lipofectamine (BRL) and G418 selection of transfected cells can be utilized to generate suitable transfectants expressing humanized L1 (SEQ ID NO:3) and L2 (SEQ ID NO:7) in the background of BPV-1 episomal DNA. Examination of L1 and L2 protein expression can be performed using rabbit anti-BPV L1 or rabbit anti-BPV L2 polyclonal antibodies. BPV particles can then be purified using our published methods (Zhou et al 1995, *Virology* 214 167-176) and can be characterized by electron microscopy and DNA blotting. The infectivity of BPV particles isolated from the cultured cells may be tested in focus formation assays using C127 fibroblasts.

EXAMPLE 9

Method for extracting and measuring tRNA from tissues

Tissue(100g) is homogenized in a Waring
5 Blender with 150 mL of phenol (Mallinckrodt,
Analytical Reagent, 88%) saturated with water (15:3)
and 150 mL of 1.0 M NaCl, 0.005 M EDTA in 0.1 M Tris-
chloride buffer, pH 7.5. The homogenate was spun
for ten minutes at top speed in the International
10 clinical centrifuge and the upper layer was carefully
decanted off. To this aqueous layer, three volumes of
95% ethanol were added. The resultant precipitate was
spun down at top speed in the International clinical
centrifuge and resuspended in 250 mL of 0.1 M
15 Tris/chloride buffer, pH 7.5. This solution was added
(flow rate of 15-20 drops per minute) to a column (2 x
10 cm) of 2 g of DEAE-cellulose previously
equilibrated with cold 0.1 M Tris-chloride buffer pH
7.5. The column was then washed with 1 L of Tris-
20 chloride buffer, pH 7.5 and the RNA eluted with 1.0 M
NaCl in 0.1 M Tris-chloride buffer, pH 7.5. The first
10 mL of NaCl solution were discarded as "hold-up."
Sufficient salt solution (60-80 mL) was then collected
until the optical density of the effluent was less
25 than three at 260 nm. This solution was extracted
twice with an equal volume of phenol saturated with
water and twice with ether. To the aqueous solution
containing the RNA, three volumes of 95% ethanol were
added and the solution was allowed to stand overnight
30 in the cold. The precipitate was spun down and washed
first with 80% and then twice with 95% ethanol and

dried in a vacuum. Approximately 60 mg of soluble RNA were obtained from a 100-g lot of rat liver.

Quantitating tRNAs

5 The following nylon membranes are used:
Biodine A and B (PALL). For the preparation of dot
blots, the tRNA samples (from 1 pg to 5 ng) are
denatured at 60 °C for 15 min in 1-5 µL of 15%
formaldehyde. 10x SSC (SSC is NaCl 0.3 M, tri-sodium
10 citrate 0.03 M). The samples are spotted in 1 µL
aliquots onto the membranes that have been soaked for
15 min in deionized water and slightly dried between
two sheets of 3MM Whatman paper prior to the
application of the samples. The tRNAs are fixed
15 covalently (in the membranes by ultraviolet-
irradiation (10 mm using an ultraviolet lamp at 254
nm and 100 W strength at a distance of 20 cm) and the
membranes are baked for 2-3 h at 80 °C.

 A 5' end labelled synthetic deoxyribo-
20 oligonucleotide complementary to the A54-A73 sequence
of the tRNA is used as a probe for the hybridization
experiments. Labelling of the oligonucleotide is
performed by direct phosphorylation of the 5' OH'
ended probe.

25 For hybridisation experiments, the UV-
irradiated membranes are first preincubated for 5 h at
50 °C in 50% deionized formamide, 5 x SSC, 1% SDS,
0.04% Ficoll 0.04% polyvinylpyrrolidone and 250 µL/mL
of sonicated salmon sperm DNA using 5 mL of buffer for
30 100 cm² of membrane. Hybridization is finally
performed overnight at 50 °C in the above solution
(2.5 mL/100 cm²) where the labeled probe has been

added. After hybridization, the membranes are washed twice in 2 x SSC, 0.1% SDS for 5 min at room temperature, twice in 2 x SSC, 1% SDS for 30 min at 60 °C and finally in 0.1 x SSC. 0.1% SDS for 30 min at room temperature. To detect the hybridized probes the membranes are exposed for 16 h to Fuji XR film at 70 °C with an intensifying screen.

Sequence of tRNA probes

The sequences of the tRNA probes are as follows:

	Ala ^{GCA} :	5' -TAAGGACTGTAAGACTT	(SEQ ID NO:13)
	Arg ^{CGA} :	5' -CGAGCCAGCCAGGAGTC	(SEQ ID NO:14)
	Asn ^{AAC} :	5' -CTAGATTGGCAGGAATT	(SEQ ID NO:15)
15	Asp ^{GAC} :	5' -TAAGATATATAGATTAT	(SEQ ID NO:16)
	Csy ^{TGC} :	5' -AAGTCTTAGTAGAGATT	(SEQ ID NO:17)
	Glu ^{GAA} :	5' -TATTTCTACACAGCATT	(SEQ ID NO:18)
	Gln ^{CAA} :	5' -CTAGGACAATAGGAATT	(SEQ ID NO:19)
	Gly ^{GGA} :	5' -TACTCTCTTCTGGGTTT	(SEQ ID NO:20)
20	His ^{CAC} :	5' -TGCCGTGACTCGGATTC	(SEQ ID NO:21)
	Ile ^{ATC} :	5' -TAGAAATAAGAGGGCTT	(SEQ ID NO:22)
	Leu ^{CTA} :	5' -TACTTTTATTTGGATTT	(SEQ ID NO:23)
	Leu ^{CTT} :	5' -TATTAGGGAGAGGATTT	(SEQ ID NO:24)
	Lys ^{AAA} :	5' -TCACTATGGAGATTTTA	(SEQ ID NO:25)
25	Lys ^{AAG} :	5' -CGCCCAACGTGGGGCTC	(SEQ ID NO:26)
	Met ^{elong} :	5' -TAGTACGGGAAGGATTT	(SEQ ID NO:27)
	Phe ^{TTC} :	5' -TGTTTATGGGATACAAT	(SEQ ID NO:28)
	Pro ^{CCA} :	5' -TCAAGAAGAAGGAGCTA	(SEQ ID NO:29)
	Pro ^{CCI} :	5' -GGGCTCGTCCGGGATTT	(SEQ ID NO:30)
30	Ser ^{AGC} :	5' -ATAAGAAAGGAAGATCG	(SEQ ID NO:31)
	Thr ^{ACA} :	5' -TGTCTTGAGAAGAGAAG	(SEQ ID NO:32)
	Tyr ^{TAC} :	5' -TGGTAAAAAGAGGATTT	(SEQ ID NO:33)

Val^{GTA}: 5'-TCAGAGTGTTTCATTGGT (SEQ ID NO:34)

EXAMPLE 10

- 5 Comparison of the relative abundance of tRNA species
in undifferentiated and differentiated keratinocytes

Materials and Methods

Isolation of epidermal cells

- 2-day old mice were killed and their skins
10 removed. The skins were digested with 0.25% trypsin
PBS at 4 °C overnight. The epidermis was separated
from the dermis using forceps and minced with scissors
in 10% FCS DMEM medium. The cell suspension was first
filtered through a 1 mm and then a 0.2 mm nylon net.
15 The cell suspension was then pelleted and washed twice
with PBS.

Density gradient centrifugation

- The keratinocytes were resuspended in 30%
20 Percoll and separated by centrifugation through a
discontinuous Percoll gradient (1.085, 1.075 and 1.050
g/mL) at 1200 x g at room temperature for 25 min. The
cells were then washed with PBS and used to extract
tRNA.

25

tRNA purification

- The cells were lysed in 5 mL of lysis
buffer (0.2 M NaOH, 1% SDS) for 10 min at room
temperature. The lysate was neutralized with 5 mL of
30 3.0 M potassium acetate (pH 5.5). After
centrifugation, the supernatant was diluted with 3

volumes of 100 mM Tris (pH 7.5) and added to a DEAE column equilibrated with 100 mM Tris (pH 7.5). An equal volume of isopropanol was added to the aqueous solution containing tRNA, and the solution was allowed to stand overnight at 4 °C. The tRNA was spun down and washed with 75% ethanol, then dissolved in RNase-free water.

tRNA blotting

10 ng of each tRNA sample in 1 µL was denatured in 60°C for 15 min in 4 µL formaldehyde and 5 µL 20 x SSC. The samples were spotted in 1 µL aliquots onto charged nylon membrane (Amersham), and the tRNAs were fixed with UV and probed with ³²P-oligonucleotides.

Results

Comparison of the abundance of the tRNA species in undifferentiated and differentiated keratinocytes showed that the levels of some tRNA populations changed dramatically. For example, the levels of tRNAs specific for Ala^{GCA}, Leu^{CTT}, Leu^{CTA} were increased in differentiated cells while tRNAs for Arg^{CGA}, Pro^{CCG}, Asn^{AAC} were more abundant in undifferentiated keratinocytes (see Table 2).

GENERAL DISCUSSION

In the present specification the inventors have confirmed that one determinant of the efficiency of translation of a gene in mammalian cells is its codon composition. This observation has commonly been

made when genes from prokaryotic organisms have been expressed in eukaryotic cells (Smith, D. W., 1996, *Biotechnol. Prog.* 12:417-422). The present inventors have also presented evidence that mRNA encoding the capsid genes of papillomavirus are not effectively translated in cultured eukaryotic cells, apparently because tRNA availability is rate limiting for translation, and that the block to PV late gene translation in eukaryotic cells in culture can be overcome by altering the codon usage of the late genes to match the consensus for mammalian genes, or alternatively by providing exogenous tRNAs. Alterations to mRNA secondary structure or protein binding (Sokolowski, et al., 1998, *J. Virol.* 72:1504-1515) as a consequence of the changes to the primary sequence of the PV capsid genes might contribute to the observed differences in efficiency of translation of the natural and modified PV capsid gene mRNAs in cultured cells. However, the enhancement of translation of the natural but not the modified mRNA that was observed after addition of tRNA in a mammalian in vitro translation system, which was not observed in a plant translation system, strengthens the argument that tRNA availability is rate limiting for translation of the natural gene in mammalian cells. A shortage of critical tRNAs could result in slowed elongation of the nascent peptide or premature termination of translation (Oba, et al., 1991, *Biochimie* 73:1109-1112). Slowed elongation appears to be the major consequence for the PV late gene. Analysis of codon usage in the PV genome shows that PV late genes use many codons that mammalian cells rarely

use. For example, PV frequently uses UUA for leucine, CGU for arginine, ACA for threonine, and AUA for isoleucine, whereas these codons are significantly less often used in mammalian genes. In contrast, papillomavirus late genes can be expressed efficiently in yeast (Jansen, et al., 1995, *Vaccine* 13:1509-1514) (Sasagawa, et al., 1995, *Virology* 206:126-135) and the codon composition of yeast and papillomavirus genes are similar (Table 1). An apparent exception is that PV L1 genes can be efficiently expressed in insect cells (Kirnbauer, et al., 1992, *Proc. Natl. Acad. Sci. USA* 89:12180-12184) using recombinant baculovirus, or in various undifferentiated mammalian cells using recombinant vaccinia (Zhou, et al., 1991, *Virology* 185:251-257). As infection with vaccinia or baculovirus down regulates cellular protein synthesis, the efficient expression of the L1 capsid proteins under these circumstances may occur because less cellular mRNA is available in a virus infected cell to compete with the L1 mRNA for the rarer tRNAs.

Codon composition could be a more general determinant of gene expression within different stages of differentiation of the same tissue. Although the genetic code is essentially universal, different organisms show differences in codon composition of their genes, while the codon composition of genes tends to be relatively similar for all genes within each organism, and matched to the population of iso-tRNAs for that organism (Ikemura, T., 1981, *J. Mol. Biol.* 146:1-21). However, populations of tRNAs in differentiating and neoplastic cells are different (Kanduc, D., 1997, *Arch. Biochem. Biophys.* 342:1-6;

Yang, and Comb, 1968, *J. Mol. Biol.* 31:138-142; Yang, and Novelli, 1968, *Biochem. Biophys. Res. Commun.* 31: 534-539) and the tRNA populations also vary in cells growing under different growth conditions (Doi, et al., 1968, *J. Biol. Chem.* 243:945-951). Accordingly, the inventors believe that codon composition and tRNA availability together provide a primitive mechanism for spatial and/or temporal regulation of gene expression. It is well recognized that the G+C content of many dsDNA viruses, a crude marker for viral gene codon composition, is markedly different from the G+C content of the DNA of the cells they infect (Strauss, et al., 1995, "Virus Evolution" in *Virology* (eds. Fields, B. N., et al.), Lipipincott-Raven, Philadelphia, pp 153-171). Viruses may therefore have evolved to take advantage of codon composition to regulate their own program of gene expression, perhaps to avoid expression of lethal quantities of viral proteins in undifferentiated cells where the virus utilizes the cellular machinery to replicate its genome.

As the inventors' observations represent an apparently novel mechanism of regulation of gene translation within a single tissue, it is relevant to consider how this relates to previously proposed hypotheses for the restriction of expression of PV late genes to differentiated epithelium. A number of explanations have been proposed for the observation that PV late genes are only effectively expressed in differentiated epithelium. Reduced late gene transcription may reflect dependence of transcription from the late promoter on transcription factors

expressed only in differentiated epithelium, or may alternatively be due to suppression of late promoter transcription by viral (Stubenrauch, et al., 1996, *J. Virol.* 70:119-126) or cellular gene products expressed in undifferentiated cells. The "late" promoters of HPV31b and of HPV5 (Haller, et al., 1995, *Virology* 214:245-255; Hummel, et al., 1992, *J. Virol.* 66:6070-6080) are described as differentiation dependent, although the search for relevant transcription control factors in differentiated keratinocytes by conventional footprinting and DNA binding studies has to date been unrewarding. Our data show that capsid proteins are not translated from PV L1 and L2 mRNAs in cells transfected with CMV promoter-based expression vectors (Fig. 2), suggesting that in addition to any transcriptional controls that may exist that there is a post-transcriptional block to capsid protein synthesis in undifferentiated cells. Sequences resembling 5' splice donor sites exist within L1 or L2 mRNA or within flanking untranslated message which are inhibitory to transcription of genes with which they are associated (Kennedy, et al., 1991, *J. Virol.* 65:2093-2097) (Furth, et al., 1994, *Mol. Cell. Biol.* 14:5278-5289). Other AU rich sequences in L1 or L2 mRNA promote mRNA degradation (Sokolowski, et al., 1997, *Oncogene* 15:2303-2319). These mechanisms inhibiting L1 and L2 expression in undifferentiated cells have yet to be shown to be inactive in differentiated epithelium, to explain the successful translation of late genes in this tissue.

Because inhibitory RNA sequences within the L1 coding sequence could have been rendered non-

functional by the systematic codon substitution employed in the experiments described herein and the untranslated inhibitory sequences were not included in the inventors' test system, the respective roles of inhibitory sequences and codon mismatch in suppression of PV late gene expression in cultured mammalian cells cannot be determined. However, regulatory sequences promoting RNA degradation or inhibiting translation are presumed to act through interaction with nuclear or cytoplasmic proteins (Sokolowski, et al., 1998, *J. Virol.* 72:1504-1515), and inefficient translation of native sequence L1 mRNA was observed in a cell free translation system from anucleate cells, demonstrating that codon composition of the PV late genes must play some role in regulation of PV late gene translation.

Further evidence supporting the hypothesis that codon composition is an important determinant of PV capsid gene expression was gathered from an analysis of the 84 PV L1 sequences currently available in Genbank. The codon composition of the L1 genes, and particularly the frequency of usage of the rarer codons, was essentially the same across all the published sequences (data not shown) as would be predicted by the similar G+C content of the papillomavirus genomes. The PV L1 gene is relatively conserved at the amino acid level, showing 60 - 80% amino acid homology between PV genotypes, as might be expected by the constraints on capsid protein function. There are, however, no obvious constraining influences on the codon composition of the PV late genes beyond those of the inventors' hypothesis, as the late gene region does not code for other genes,

either in other reading frames or on the complementary DNA strand, and has no known *cis* acting regulatory functions. If codon composition of the capsid genes were not important for PV function, a considerable
5 heterogeneity of codon usage might therefore be expected, given the evolutionary diversity of PVs (Chan, et al. 1995, *J. Virol.* 69:3074-3083).

Taken together, the data and evidence outlined herein makes a strong case that codon usage
10 is a significant determinant of expression of PV late genes in undifferentiated and differentiated epithelial cells, and that this observation is generalizable. The relative role of message instability and codon mismatch in determining
15 expression in differentiated tissues will require comparisons of transcriptional activity and translation of the L1 or L2 genes driven from strong constitutive promoters in differentiated and undifferentiated epithelium. Such work should now be
20 feasible using either transgenic technology or keratinocyte raft cultures.

Although mechanisms of transcriptional regulation of PV L1 or L2 gene expression in the superficial layer of differentiated epithelium have
25 been proposed (Zeltner et al., 1994, *J. Virol.* 68:3620; Brown, et al., 1995, *Virology* 214:259; Stoler et al., 1992, *Hum. Pathol.* 23:117; Hummel et al., 1995, *J. Virol.* 69:3381; Haller et al., 1995, *Virology* 214:245; Barksdale and Baker, 1993, *J. Virol.* 67:5605), measurable PV late gene mRNA is not always
30 associated with production of late proteins (Zeltner et al., 1994, *supra*; Ozbun and Meyers, 1997, *J. Virol.*

71:5161), and the data presented here suggest that translation regulation may play a major part in controlling PV late gene expression. This observation has implications as herein described for the regulation of expression of genes related to the specialised functions of any differentiated tissue, and also for targeting of expression of therapeutic genes to such tissue while avoiding the potentially deleterious consequences of expression of the exogenous gene in a self renewing stem cell population.

The present invention has been described in terms of particular embodiments found or proposed by the present inventors to comprise preferred modes for the practice of the invention. Those of skill in the art will appreciate that, in light of the present disclosure, numerous modifications and changes may be made in the particular embodiments exemplified without departing from the scope of the invention. All such modifications are intended to be included within the scope of the appended claims.

TABLE LEGENDS

TABLE 1

The codon usage data for human, cow yeast and wheat proteins are derived from published results(18). The BPV1 data are from the sequences in the Genbank database.

TABLE 2

Each iso-acceptor tRNA with anticodon shown as superscript are shown on top row. The "+" indicates the abundance of tRNA wherein each "+" indicates about 10 fold increase.

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TABLESTABLE 1

Frequency (per one thousand) of codon usage for individual organisms.

5

Amino acids	Codons	Human	Cow	Yeast	Wheat	BPVL1/L2
ARG	CGA	5.4	5.5	2.3	2.3	7.2
	CGC	11.3	12.2	2.0	7.5	4.1
	CGG	10.4	11.2	1.1	4.6	5.1
	CGU	4.7	3.7	7.5	1.1	10.4
	AGA	9.9	9.9	24.0	4.1	14.4
	AGG	11.1	11.4	7.5	7.1	9.3
LEU	CUA	6.2	4.9	11.8	12.1	18.6
	CUC	19.9	21.2	4.1	18.6	6.2
	CUG	42.5	46.6	8.3	15.5	15.5
	CUU	10.7	10.6	9.6	6.5	20.7
	UUA	5.3	4.0	24.5	1.8	14.5
	UUG	11.0	9.6	32.1	15.3	15.5
SER	UCA	9.3	7.6	15.6	14.6	16.6
	UCC	17.7	17.6	14.4	10.1	11.4
	UCG	4.2	4.5	6.5	9.6	6.2
	UCU	13.2	11.2	24.6	14.8	15.5
	AGC	18.7	18.7	7.1	12.8	12.4
	AGU	9.4	8.6	11.7	12.9	21.7
THR	ACA	14.4	11.4	15.6	4.6	37.3
	ACC	23.0	21.1	13.9	15.9	19.7
	ACG	6.7	7.8	6.7	4.5	4.1
	ACU	12.7	9.6	22.0	11.8	28.0

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Amino acids	Codons	Human	Cow	Yeast	Wheat	BPVL1/ L2
PRO	CCA	14.6	12.0	21.4	71.2	22.8
	CCC	20.0	19.2	5.9	11.1	15.5
	CCG	6.5	7.9	4.1	19.4	0.0
	CCU	15.5	14.6	12.8	10.3	33.1
ALA	GCA	14.0	13.1	15.3	11.2	33.1
	GCC	29.1	35.8	15.5	19.5	17.6
	GCG	7.2	9.3	5.1	13.8	4.1
	GCU	19.6	19.1	28.3	9.6	13.5
GLY	GGA	17.1	16.2	8.9	25.9	22.8
	GGC	25.4	28.1	8.9	28.0	12.4
	GGG	17.3	19.2	5.1	28.5	22.8
	GGU	11.2	11.8	34.9	9.6	18.6
VAL	GUA	5.9	5.1	10.0	4.4	15.5
	GUC	16.3	18.4	14.9	14.8	6.2
	GUG	30.9	32.9	9.5	12.9	23.8
	GUU	10.4	9.9	26.6	11.6	16.6
LYS	AAA	22.2	21.6	37.7	4.5	37.2
	AAG	34.9	37.1	35.2	17.4	13.5
ASN	AAC	22.6	22.4	25.8	14.2	10.3
	AAU	16.6	12.5	31.4	6.7	24.8
GLN	CAA	11.1	9.7	29.8	171.8	22.8
	CAG	33.6	34.4	10.4	79.4	17.6
HIS	CAC	14.2	14.0	8.2	8.2	6.2
	CAU	9.3	7.5	12.3	7.1	13.4
GLU	GAA	26.8	24.4	48.9	7.8	36.2
	GAG	41.4	45.4	16.9	19.7	21.7
ASP	GAC	29.0	31.5	22.3	13.0	18.6
	GAU	21.7	19.2	37.0	4.0	33.1

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Amino acids	Codons	Human	Cow	Yeast	Wheat	BPVL1/ L2
TYR	UAC	18.8	20.3	16.5	24.5	17.6
	UAU	12.5	10.5	16.5	12.5	18.6
CYS	UGC	14.5	13.9	3.7	14.8	5.2
	UGU	9.9	9.4	7.6	4.9	5.2
PHE	UUC	22.6	25.5	20.0	14.1	7.2
	UUU	15.8	17.0	23.2	15.0	23.8
ILE	AUA	5.8	5.2	12.8	5.4	22.7
	AUC	24.3	25.8	18.4	19.7	8.2
	AUU	14.9	13.1	31.1	10.7	20.7

TABLE 2

tRNA population changes as KC starts to differentiate.

tRNA	Arg ^{GCA}	Ala ^{GCA}	His ^{CAC}	Leu ^{CTT}	Leu ^{CTA}	Lys ^{AAG}	Lys ^{AAA}	Met ^{INI}	Pro ^{CCI}
Supra	+	+++	+	+++	+++	++	+	+	+
Basal	+++	+	++	+	+	+	+	++	+++
tRNA	Val ^{GTA}	Val ^{GTT}	His ^{CAC}	Asn ^{AAC}	Thr ^{ACA}	Met ^{ETG}	Gly ^{GGA}		
Supra	++	+	++	+	+	+	+		
Basal	+	+	+	+++	+	++	+		

SEQUENCE LISTING

<110> The University of Queensland

<120> NUCLEIC ACID SEQUENCE AND METHOD FOR SELECTIVELY
EXPRESSING A PROTEIN IN A TARGET CELL OR TISSUE

<130> 5508-53 JHW

<140> PCT/AU98/00530

<141> 1998-07-09

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<151> 1997-09-11

<160> 34

<170> PatentIn Ver. 2.0

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<211> 1488

<212> DNA

<213> Bovine papillomavirus type 1

<220>

<221> CDS

<222> (1)..(1488)

<220>

<223> L1 open reading frame (wild-type)

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Met Ala Leu Trp Gln Gln Gly Gln Lys Leu Tyr Leu Pro Pro Thr Pro	
1 5 10 15	
gta agc aag gtg ctt tgc agt gaa acc tat gtg caa aga aaa agc att	96
Val Ser Lys Val Leu Cys Ser Glu Thr Tyr Val Gln Arg Lys Ser Ile	
20 25 30	
ttt tat cat gca gaa acg gag cgc ctg cta act ata gga cat cca tat	144
Phe Tyr His Ala Glu Thr Glu Arg Leu Leu Thr Ile Gly His Pro Tyr	
35 40 45	
tac cca gtg tct atc ggg gcc aaa act gtt cct aag gtc tct gca aat	192
Tyr Pro Val Ser Ile Gly Ala Lys Thr Val Pro Lys Val Ser Ala Asn	
50 55 60	
cag tat agg gta ttt aaa ata caa cta cct gat ccc aat caa ttt gca	240
Gln Tyr Arg Val Phe Lys Ile Gln Leu Pro Asp Pro Asn Gln Phe Ala	
65 70 75 80	
cta cct gac agg act gtt cac aac cca agt aaa gag cgg ctg gtg tgg	288

Leu	Pro	Asp	Arg	Thr	Val	His	Asn	Pro	Ser	Lys	Glu	Arg	Leu	Val	Trp	
				85					90					95		
cca	gtc	ata	ggg	gtg	cag	gtg	tcc	aga	ggg	cag	cct	ctt	gga	ggg	act	336
Pro	Val	Ile	Gly	Val	Gln	Val	Ser	Arg	Gly	Gln	Pro	Leu	Gly	Gly	Thr	
			100					105					110			
gta	act	ggg	cac	ccc	act	ttt	aat	gct	ttg	ctt	gat	gca	gaa	aat	gtg	384
Val	Thr	Gly	His	Pro	Thr	Phe	Asn	Ala	Leu	Leu	Asp	Ala	Glu	Asn	Val	
		115					120					125				
aat	aga	aaa	gtc	acc	acc	caa	aca	aca	gat	gac	agg	aaa	caa	aca	ggc	432
Asn	Arg	Lys	Val	Thr	Thr	Gln	Thr	Thr	Asp	Asp	Arg	Lys	Gln	Thr	Gly	
	130					135					140					
cta	gat	gct	aag	caa	caa	cag	att	ctg	ttg	cta	ggc	tgt	acc	cct	gct	480
Leu	Asp	Ala	Lys	Gln	Gln	Gln	Ile	Leu	Leu	Leu	Gly	Cys	Thr	Pro	Ala	
145					150					155					160	
gaa	ggg	gaa	tat	tgg	aca	aca	gcc	cgt	cca	tgt	gtt	act	gat	cgt	cta	528
Glu	Gly	Glu	Tyr	Trp	Thr	Thr	Ala	Arg	Pro	Cys	Val	Thr	Asp	Arg	Leu	
				165				170						175		
gaa	aat	ggc	gcc	tgc	cct	cct	ctt	gaa	tta	aaa	aac	aag	cac	ata	gaa	576
Glu	Asn	Gly	Ala	Cys	Pro	Pro	Leu	Glu	Leu	Lys	Asn	Lys	His	Ile	Glu	
			180					185					190			
gat	ggg	gat	atg	atg	gaa	att	ggg	ttt	ggg	gca	gcc	aac	ttc	aaa	gaa	624
Asp	Gly	Asp	Met	Met	Glu	Ile	Gly	Phe	Gly	Ala	Ala	Asn	Phe	Lys	Glu	
		195					200					205				
att	aat	gca	agt	aaa	tca	gat	cta	cct	ctt	gac	att	caa	aat	gag	atc	672
Ile	Asn	Ala	Ser	Lys	Ser	Asp	Leu	Pro	Leu	Asp	Ile	Gln	Asn	Glu	Ile	
	210					215					220					
tgc	ttg	tac	cca	gac	tac	ctc	aaa	atg	gct	gag	gac	gct	gct	ggg	aat	720
Cys	Leu	Tyr	Pro	Asp	Tyr	Leu	Lys	Met	Ala	Glu	Asp	Ala	Ala	Gly	Asn	
225					230					235				240		
agc	atg	ttc	ttt	ttt	gca	agg	aaa	gaa	cag	gtg	tat	gtt	aga	cac	atc	768
Ser	Met	Phe	Phe	Phe	Ala	Arg	Lys	Glu	Gln	Val	Tyr	Val	Arg	His	Ile	
				245					250					255		
tgg	acc	aga	ggg	ggc	tcg	gag	aaa	gaa	gcc	cct	acc	aca	gat	ttt	tat	816
Trp	Thr	Arg	Gly	Gly	Ser	Glu	Lys	Glu	Ala	Pro	Thr	Thr	Asp	Phe	Tyr	
			260					265					270			
tta	aag	aat	aat	aaa	ggg	gat	gcc	acc	ctt	aaa	ata	ccc	agt	gtg	cat	864
Leu	Lys	Asn	Asn	Lys	Gly	Asp	Ala	Thr	Leu	Lys	Ile	Pro	Ser	Val	His	
		275					280					285				
ttt	ggg	agt	ccc	agt	ggc	tca	cta	gtc	tca	act	gat	aat	caa	att	ttt	912
Phe	Gly	Ser	Pro	Ser	Gly	Ser	Leu	Val	Ser	Thr	Asp	Asn	Gln	Ile	Phe	
	290					295					300					
aat	cgg	ccc	tac	tgg	cta	ttc	cgt	gcc	cag	ggc	atg	aac	aat	gga	att	960
Asn	Arg	Pro	Tyr	Trp	Leu	Phe	Arg	Ala	Gln	Gly	Met	Asn	Asn	Gly	Ile	

305	310	315	320	
gca tgg aat aat tta ttg ttt tta aca gtg ggg gac aat aca cgt ggt				1008
Ala Trp Asn Asn Leu Leu Phe Leu Thr Val Gly Asp Asn Thr Arg Gly				
	325	330	335	
act aat ctt acc ata agt gta gcc tca gat gga acc cca cta aca gag				1056
Thr Asn Leu Thr Ile Ser Val Ala Ser Asp Gly Thr Pro Leu Thr Glu				
	340	345	350	
tat gat agc tca aaa ttc aat gta tac cat aga cat atg gaa gaa tat				1104
Tyr Asp Ser Ser Lys Phe Asn Val Tyr His Arg His Met Glu Glu Tyr				
	355	360	365	
aag cta gcc ttt ata tta gag cta tgc tct gtg gaa atc aca gct caa				1152
Lys Leu Ala Phe Ile Leu Glu Leu Cys Ser Val Glu Ile Thr Ala Gln				
	370	375	380	
act gtg tca cat ctg caa gga ctt atg ccc tct gtg ctt gaa aat tgg				1200
Thr Val Ser His Leu Gln Gly Leu Met Pro Ser Val Leu Glu Asn Trp				
	385	390	395	400
gaa ata ggt gtg cag cct cct acc tca tcg ata tta gag gac acc tat				1248
Glu Ile Gly Val Gln Pro Pro Thr Ser Ser Ile Leu Glu Asp Thr Tyr				
	405	410	415	
cgc tat ata gag tct cct gca act aaa tgt gca agc aat gta att cct				1296
Arg Tyr Ile Glu Ser Pro Ala Thr Lys Cys Ala Ser Asn Val Ile Pro				
	420	425	430	
gca aaa gaa gac cct tat gca ggg ttt aag ttt tgg aac ata gat ctt				1344
Ala Lys Glu Asp Pro Tyr Ala Gly Phe Lys Phe Trp Asn Ile Asp Leu				
	435	440	445	
aaa gaa aag ctt tct ttg gac tta gat caa ttt ccc ttg gga aga aga				1392
Lys Glu Lys Leu Ser Leu Asp Leu Asp Gln Phe Pro Leu Gly Arg Arg				
	450	455	460	
ttt tta gca cag caa ggg gca gga tgt tca act gtg aga aaa cga aga				1440
Phe Leu Ala Gln Gln Gly Ala Gly Cys Ser Thr Val Arg Lys Arg Arg				
	465	470	475	480
att agc caa aaa act tcc agt aag cct gca aaa aaa aaa aaa aaa taa				1488
Ile Ser Gln Lys Thr Ser Ser Lys Pro Ala Lys Lys Lys Lys Lys				
	485	490	495	

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<211> 495

<212> PRT

<213> Bovine papillomavirus type 1

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Val Ser Lys Val Leu Cys Ser Glu Thr Tyr Val Gln Arg Lys Ser Ile

20					25					30						
Phe	Tyr	His	Ala	Glu	Thr	Glu	Arg	Leu	Leu	Thr	Ile	Gly	His	Pro	Tyr	
35					40					45						
Tyr	Pro	Val	Ser	Ile	Gly	Ala	Lys	Thr	Val	Pro	Lys	Val	Ser	Ala	Asn	
50					55					60						
Gln	Tyr	Arg	Val	Phe	Lys	Ile	Gln	Leu	Pro	Asp	Pro	Asn	Gln	Phe	Ala	
65					70					75					80	
Leu	Pro	Asp	Arg	Thr	Val	His	Asn	Pro	Ser	Lys	Glu	Arg	Leu	Val	Trp	
85					90					95						
Pro	Val	Ile	Gly	Val	Gln	Val	Ser	Arg	Gly	Gln	Pro	Leu	Gly	Gly	Thr	
100					105					110						
Val	Thr	Gly	His	Pro	Thr	Phe	Asn	Ala	Leu	Leu	Asp	Ala	Glu	Asn	Val	
115					120					125						
Asn	Arg	Lys	Val	Thr	Thr	Gln	Thr	Thr	Asp	Asp	Arg	Lys	Gln	Thr	Gly	
130					135					140						
Leu	Asp	Ala	Lys	Gln	Gln	Gln	Ile	Leu	Leu	Leu	Gly	Cys	Thr	Pro	Ala	
145					150					155					160	
Glu	Gly	Glu	Tyr	Trp	Thr	Thr	Ala	Arg	Pro	Cys	Val	Thr	Asp	Arg	Leu	
165					170					175						
Glu	Asn	Gly	Ala	Cys	Pro	Pro	Leu	Glu	Leu	Lys	Asn	Lys	His	Ile	Glu	
180					185					190						
Asp	Gly	Asp	Met	Met	Glu	Ile	Gly	Phe	Gly	Ala	Ala	Asn	Phe	Lys	Glu	
195					200					205						
Ile	Asn	Ala	Ser	Lys	Ser	Asp	Leu	Pro	Leu	Asp	Ile	Gln	Asn	Glu	Ile	
210					215					220						
Cys	Leu	Tyr	Pro	Asp	Tyr	Leu	Lys	Met	Ala	Glu	Asp	Ala	Ala	Gly	Asn	
225					230					235					240	
Ser	Met	Phe	Phe	Phe	Ala	Arg	Lys	Glu	Gln	Val	Tyr	Val	Arg	His	Ile	
245					250					255						
Trp	Thr	Arg	Gly	Gly	Ser	Glu	Lys	Glu	Ala	Pro	Thr	Thr	Asp	Phe	Tyr	
260					265					270						
Leu	Lys	Asn	Asn	Lys	Gly	Asp	Ala	Thr	Leu	Lys	Ile	Pro	Ser	Val	His	
275					280					285						
Phe	Gly	Ser	Pro	Ser	Gly	Ser	Leu	Val	Ser	Thr	Asp	Asn	Gln	Ile	Phe	
290					295					300						
Asn	Arg	Pro	Tyr	Trp	Leu	Phe	Arg	Ala	Gln	Gly	Met	Asn	Asn	Gly	Ile	
305					310					315					320	
Ala	Trp	Asn	Asn	Leu	Leu	Phe	Leu	Thr	Val	Gly	Asp	Asn	Thr	Arg	Gly	

325					330					335						
Thr	Asn	Leu	Thr	Ile	Ser	Val	Ala	Ser	Asp	Gly	Thr	Pro	Leu	Thr	Glu	
340					345					350						
Tyr	Asp	Ser	Ser	Lys	Phe	Asn	Val	Tyr	His	Arg	His	Met	Glu	Glu	Tyr	
355					360					365						
Lys	Leu	Ala	Phe	Ile	Leu	Glu	Leu	Cys	Ser	Val	Glu	Ile	Thr	Ala	Gln	
370					375					380						
Thr	Val	Ser	His	Leu	Gln	Gly	Leu	Met	Pro	Ser	Val	Leu	Glu	Asn	Trp	
385					390					395					400	
Glu	Ile	Gly	Val	Gln	Pro	Pro	Thr	Ser	Ser	Ile	Leu	Glu	Asp	Thr	Tyr	
405					410					415						
Arg	Tyr	Ile	Glu	Ser	Pro	Ala	Thr	Lys	Cys	Ala	Ser	Asn	Val	Ile	Pro	
420					425					430						
Ala	Lys	Glu	Asp	Pro	Tyr	Ala	Gly	Phe	Lys	Phe	Trp	Asn	Ile	Asp	Leu	
435					440					445						
Lys	Glu	Lys	Leu	Ser	Leu	Asp	Leu	Asp	Gln	Phe	Pro	Leu	Gly	Arg	Arg	
450					455					460						
Phe	Leu	Ala	Gln	Gln	Gly	Ala	Gly	Cys	Ser	Thr	Val	Arg	Lys	Arg	Arg	
465					470					475					480	
Ile	Ser	Gln	Lys	Thr	Ser	Ser	Lys	Pro	Ala	Lys	Lys	Lys	Lys	Lys		
485					490					495						

<210> 3
 <211> 1488
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1) .. (1488)

<220>
 <223> Description of Artificial Sequence: Bovine
 papillomavirus type 1 L1 open reading frame
 (humanized)

<220>
 <223> Wild-type codons replaced with synonymous codons
 used at relatively high frequency by human genes

<400> 3																
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Met	Ala	Leu	Trp	Gln	Gln	Gly	Gln	Lys	Leu	Tyr	Leu	Pro	Pro	Thr	Pro	
1				5				10						15		
gtg agc aag gtg ctt tgc agt gaa acc tat gtg caa aga aaa agc att																96

Val	Ser	Lys	Val	Leu	Cys	Ser	Glu	Thr	Tyr	Val	Gln	Arg	Lys	Ser	Ile	
			20					25					30			
ttt	tat	cat	gca	gaa	acg	gag	cgc	ctg	ctg	acc	atc	gga	cac	ccc	tat	144
Phe	Tyr	His	Ala	Glu	Thr	Glu	Arg	Leu	Leu	Thr	Ile	Gly	His	Pro	Tyr	
		35					40					45				
tac	ccc	gtg	tcc	atc	ggg	gcc	aag	act	gtg	cct	aag	gtg	tcc	gcc	aat	192
Tyr	Pro	Val	Ser	Ile	Gly	Ala	Lys	Thr	Val	Pro	Lys	Val	Ser	Ala	Asn	
	50					55					60					
cag	tat	agg	gtg	ttc	aaa	atc	caa	ctg	cct	gat	ccc	aat	caa	ttt	gca	240
Gln	Tyr	Arg	Val	Phe	Lys	Ile	Gln	Leu	Pro	Asp	Pro	Asn	Gln	Phe	Ala	
65					70				75						80	
ctg	cct	gac	agg	acc	gtg	cac	aac	ccc	agc	aaa	gag	cgg	ctg	gtg	tgg	288
Leu	Pro	Asp	Arg	Thr	Val	His	Asn	Pro	Ser	Lys	Glu	Arg	Leu	Val	Trp	
				85					90					95		
cca	gtg	atc	ggc	gtg	cag	gtg	tcc	aga	ggc	cag	cct	ctg	ggc	ggc	acc	336
Pro	Val	Ile	Gly	Val	Gln	Val	Ser	Arg	Gly	Gln	Pro	Leu	Gly	Gly	Thr	
			100					105					110			
gtg	act	ggg	cac	ccc	act	ttt	aat	gct	ttg	ctt	gat	gca	gaa	aat	gtg	384
Val	Thr	Gly	His	Pro	Thr	Phe	Asn	Ala	Leu	Leu	Asp	Ala	Glu	Asn	Val	
		115					120					125				
aat	aga	aaa	gtc	acc	acc	cag	acc	acc	gac	gac	agg	aaa	cag	aca	ggc	432
Asn	Arg	Lys	Val	Thr	Thr	Gln	Thr	Thr	Asp	Asp	Arg	Lys	Gln	Thr	Gly	
	130					135					140					
ctg	gat	gcc	aag	cag	cag	cag	atc	ctg	ctg	ctg	ggc	tgt	acc	cct	gct	480
Leu	Asp	Ala	Lys	Gln	Gln	Gln	Ile	Leu	Leu	Leu	Gly	Cys	Thr	Pro	Ala	
145					150				155						160	
gaa	ggg	gaa	tat	tgg	aca	aca	gcc	cgt	cca	tgt	gtg	acc	gac	cgt	cta	528
Glu	Gly	Glu	Tyr	Trp	Thr	Thr	Ala	Arg	Pro	Cys	Val	Thr	Asp	Arg	Leu	
				165					170					175		
gaa	aac	ggc	gcc	tgc	cct	cct	ctg	gag	ctg	aaa	aac	aag	cac	atc	gaa	576
Glu	Asn	Gly	Ala	Cys	Pro	Pro	Leu	Glu	Leu	Lys	Asn	Lys	His	Ile	Glu	
			180					185					190			
gat	ggg	gat	atg	atg	gaa	att	ggg	ttt	ggt	gca	gcc	aac	ttc	aaa	gaa	624
Asp	Gly	Asp	Met	Met	Glu	Ile	Gly	Phe	Gly	Ala	Ala	Asn	Phe	Lys	Glu	
		195					200					205				
att	aat	gca	agt	aaa	tca	gat	cta	cct	ctg	gac	atc	caa	aat	gag	atc	672
Ile	Asn	Ala	Ser	Lys	Ser	Asp	Leu	Pro	Leu	Asp	Ile	Gln	Asn	Glu	Ile	
	210					215					220					
tgc	ctg	tac	ccc	gac	tac	ctg	aaa	atg	gct	gag	gac	gcc	gcc	ggc	aac	720
Cys	Leu	Tyr	Pro	Asp	Tyr	Leu	Lys	Met	Ala	Glu	Asp	Ala	Ala	Gly	Asn	
225					230				235						240	
agc	atg	ttc	ttc	ttc	gcc	agg	aag	gag	cag	gtg	tac	gtg	aga	cac	atc	768
Ser	Met	Phe	Phe	Phe	Ala	Arg	Lys	Glu	Gln	Val	Tyr	Val	Arg	His	Ile	

245										250					255					
tgg	acc	aga	ggc	ggc	tcc	gag	aaa	gaa	gcc	cct	acc	aca	gat	ttt	tat	816				
Trp	Thr	Arg	Gly	Gly	Ser	Glu	Lys	Glu	Ala	Pro	Thr	Thr	Asp	Phe	Tyr					
			260					265					270							
ttg	aag	aac	aac	aag	ggc	gac	gcc	acc	ctg	aag	atc	ccc	agc	gtg	cac	864				
Leu	Lys	Asn	Asn	Lys	Gly	Asp	Ala	Thr	Leu	Lys	Ile	Pro	Ser	Val	His					
		275					280					285								
ttc	ggc	agc	ccc	agc	ggc	tca	cta	gtg	tcc	acc	gac	aac	cag	atc	ttc	912				
Phe	Gly	Ser	Pro	Ser	Gly	Ser	Leu	Val	Ser	Thr	Asp	Asn	Gln	Ile	Phe					
	290					295					300									
aac	cgg	ccc	tac	tgg	ctg	ttc	cgc	gcc	cag	ggc	atg	aac	aat	gga	att	960				
Asn	Arg	Pro	Tyr	Trp	Leu	Phe	Arg	Ala	Gln	Gly	Met	Asn	Asn	Gly	Ile					
305					310					315				320						
gcc	tgg	aac	aac	ctg	ctg	ttc	ctg	acc	gtg	ggc	gac	aac	aca	cgt	ggc	1008				
Ala	Trp	Asn	Asn	Leu	Leu	Phe	Leu	Thr	Val	Gly	Asp	Asn	Thr	Arg	Gly					
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acc	aac	ctg	acc	atc	agc	gtg	gcc	tcc	gat	gga	acc	cca	ctg	acc	gag	1056				
Thr	Asn	Leu	Thr	Ile	Ser	Val	Ala	Ser	Asp	Gly	Thr	Pro	Leu	Thr	Glu					
			340					345					350							
tat	gat	agc	tcg	aaa	ttc	aac	gtg	tac	cac	aga	cac	atg	gag	gag	tat	1104				
Tyr	Asp	Ser	Ser	Lys	Phe	Asn	Val	Tyr	His	Arg	His	Met	Glu	Glu	Tyr					
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Lys	Leu	Ala	Phe	Ile	Leu	Glu	Leu	Cys	Ser	Val	Glu	Ile	Thr	Ala	Gln					
	370					375					380									
acc	gtg	tcc	cat	ctg	caa	gga	ctg	atg	ccc	tcc	gtg	ctg	gag	aat	tgg	1200				
Thr	Val	Ser	His	Leu	Gln	Gly	Leu	Met	Pro	Ser	Val	Leu	Glu	Asn	Trp					
385					390					395				400						
gag	atc	ggc	gtg	cag	ccc	ccc	acc	tca	tcg	atc	ttg	gag	gac	acc	tac	1248				
Glu	Ile	Gly	Val	Gln	Pro	Pro	Thr	Ser	Ser	Ile	Leu	Glu	Asp	Thr	Tyr					
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cgc	tac	atc	gag	tcc	ccc	gcc	acc	aag	tgt	gcc	agc	aac	gtg	att	cct	1296				
Arg	Tyr	Ile	Glu	Ser	Pro	Ala	Thr	Lys	Cys	Ala	Ser	Asn	Val	Ile	Pro					
			420					425					430							
gca	aaa	gaa	gac	cct	tat	gca	ggg	ttt	aag	ttc	tgg	aac	atc	gac	ctg	1344				
Ala	Lys	Glu	Asp	Pro	Tyr	Ala	Gly	Phe	Lys	Phe	Trp	Asn	Ile	Asp	Leu					
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Lys	Glu	Lys	Leu	Ser	Leu	Asp	Leu	Asp	Gln	Phe	Pro	Leu	Gly	Arg	Arg					
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Phe	Leu	Ala	Gln	Gln	Gly	Ala	Gly	Cys	Ser	Thr	Val	Arg	Lys	Arg	Arg					

465		470		475		480	
atc agc cag aag acc tcc agc aag ccc gcc aag aag aag aaa aag taa							1488
Ile Ser Gln Lys Thr Ser Ser Lys Pro Ala Lys Lys Lys Lys Lys							
		485		490		495	

<210> 4
 <211> 495
 <212> PRT
 <213> Artificial Sequence

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 Phe Tyr His Ala Glu Thr Glu Arg Leu Leu Thr Ile Gly His Pro Tyr
 35 40 45
 Tyr Pro Val Ser Ile Gly Ala Lys Thr Val Pro Lys Val Ser Ala Asn
 50 55 60
 Gln Tyr Arg Val Phe Lys Ile Gln Leu Pro Asp Pro Asn Gln Phe Ala
 65 70 75 80
 Leu Pro Asp Arg Thr Val His Asn Pro Ser Lys Glu Arg Leu Val Trp
 85 90 95
 Pro Val Ile Gly Val Gln Val Ser Arg Gly Gln Pro Leu Gly Gly Thr
 100 105 110
 Val Thr Gly His Pro Thr Phe Asn Ala Leu Leu Asp Ala Glu Asn Val
 115 120 125
 Asn Arg Lys Val Thr Thr Gln Thr Thr Asp Asp Arg Lys Gln Thr Gly
 130 135 140
 Leu Asp Ala Lys Gln Gln Gln Ile Leu Leu Leu Gly Cys Thr Pro Ala
 145 150 155 160
 Glu Gly Glu Tyr Trp Thr Thr Ala Arg Pro Cys Val Thr Asp Arg Leu
 165 170 175
 Glu Asn Gly Ala Cys Pro Pro Leu Glu Leu Lys Asn Lys His Ile Glu
 180 185 190
 Asp Gly Asp Met Met Glu Ile Gly Phe Gly Ala Ala Asn Phe Lys Glu
 195 200 205
 Ile Asn Ala Ser Lys Ser Asp Leu Pro Leu Asp Ile Gln Asn Glu Ile
 210 215 220
 Cys Leu Tyr Pro Asp Tyr Leu Lys Met Ala Glu Asp Ala Ala Gly Asn
 225 230 235 240

Ser	Met	Phe	Phe	Phe	Ala	Arg	Lys	Glu	Gln	Val	Tyr	Val	Arg	His	Ile
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Trp	Thr	Arg	Gly	Gly	Ser	Glu	Lys	Glu	Ala	Pro	Thr	Thr	Asp	Phe	Tyr
			260					265					270		
Leu	Lys	Asn	Asn	Lys	Gly	Asp	Ala	Thr	Leu	Lys	Ile	Pro	Ser	Val	His
		275					280					285			
Phe	Gly	Ser	Pro	Ser	Gly	Ser	Leu	Val	Ser	Thr	Asp	Asn	Gln	Ile	Phe
	290					295					300				
Asn	Arg	Pro	Tyr	Trp	Leu	Phe	Arg	Ala	Gln	Gly	Met	Asn	Asn	Gly	Ile
305					310					315					320
Ala	Trp	Asn	Asn	Leu	Leu	Phe	Leu	Thr	Val	Gly	Asp	Asn	Thr	Arg	Gly
				325					330					335	
Thr	Asn	Leu	Thr	Ile	Ser	Val	Ala	Ser	Asp	Gly	Thr	Pro	Leu	Thr	Glu
			340					345					350		
Tyr	Asp	Ser	Ser	Lys	Phe	Asn	Val	Tyr	His	Arg	His	Met	Glu	Glu	Tyr
		355					360					365			
Lys	Leu	Ala	Phe	Ile	Leu	Glu	Leu	Cys	Ser	Val	Glu	Ile	Thr	Ala	Gln
	370					375					380				
Thr	Val	Ser	His	Leu	Gln	Gly	Leu	Met	Pro	Ser	Val	Leu	Glu	Asn	Trp
385					390					395					400
Glu	Ile	Gly	Val	Gln	Pro	Pro	Thr	Ser	Ser	Ile	Leu	Glu	Asp	Thr	Tyr
				405					410					415	
Arg	Tyr	Ile	Glu	Ser	Pro	Ala	Thr	Lys	Cys	Ala	Ser	Asn	Val	Ile	Pro
			420					425					430		
Ala	Lys	Glu	Asp	Pro	Tyr	Ala	Gly	Phe	Lys	Phe	Trp	Asn	Ile	Asp	Leu
		435					440					445			
Lys	Glu	Lys	Leu	Ser	Leu	Asp	Leu	Asp	Gln	Phe	Pro	Leu	Gly	Arg	Arg
	450					455					460				
Phe	Leu	Ala	Gln	Gln	Gly	Ala	Gly	Cys	Ser	Thr	Val	Arg	Lys	Arg	Arg
465					470					475					480
Ile	Ser	Gln	Lys	Thr	Ser	Ser	Lys	Pro	Ala	Lys	Lys	Lys	Lys	Lys	
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<210> 5
<211> 1410
<212> DNA
<213> Bovine papillomavirus type 1

<220>
<221> CDS
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<222> (1)..(1410)

<220>

<223> L2 open reading frame (wild-type)

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Arg Thr Cys Lys Gln Ala Gly Thr Cys Pro Pro Asp Val Ile Arg Lys	
20 25 30	
gta gaa gga gat act ata gca gat aaa att ttg aaa ttt ggg ggt ctt	144
Val Glu Gly Asp Thr Ile Ala Asp Lys Ile Leu Lys Phe Gly Gly Leu	
35 40 45	
gca atc tac tta gga ggg cta gga ata gga aca tgg tct act gga agg	192
Ala Ile Tyr Leu Gly Gly Leu Gly Ile Gly Thr Trp Ser Thr Gly Arg	
50 55 60	
gtg gcc gca ggt gga tca cca agg tac aca cca ctc cga aca gca ggg	240
Val Ala Ala Gly Gly Ser Pro Arg Tyr Thr Pro Leu Arg Thr Ala Gly	
65 70 75 80	
tcc aca tca tcg ctt gca tca ata gga tcc aga gct gta aca gca ggg	288
Ser Thr Ser Ser Leu Ala Ser Ile Gly Ser Arg Ala Val Thr Ala Gly	
85 90 95	
acc cgc ccc agt ata ggt gcg ggc att cct tta gac acc ctt gaa act	336
Thr Arg Pro Ser Ile Gly Ala Gly Ile Pro Leu Asp Thr Leu Glu Thr	
100 105 110	
ctt ggg gcc ttg cgt cca ggg gtg tat gag gac act gtg cta cca gag	384
Leu Gly Ala Leu Arg Pro Gly Val Tyr Glu Asp Thr Val Leu Pro Glu	
115 120 125	
gcc cct gca ata gtc act cct gat gct gtt cct gca gat tca ggg ctt	432
Ala Pro Ala Ile Val Thr Pro Asp Ala Val Pro Ala Asp Ser Gly Leu	
130 135 140	
gat gcc ctg tcc ata ggt aca gac tcg tcc acg gag acc ctc att act	480
Asp Ala Leu Ser Ile Gly Thr Asp Ser Ser Thr Glu Thr Leu Ile Thr	
145 150 155 160	
ctg cta gag cct gag ggt ccc gag gac ata gcg gtt ctt gag ctg caa	528
Leu Leu Glu Pro Glu Gly Pro Glu Asp Ile Ala Val Leu Glu Leu Gln	
165 170 175	
ccc ctg gac cgt cca act tgg caa gta agc aat gct gtt cat cag tcc	576
Pro Leu Asp Arg Pro Thr Trp Gln Val Ser Asn Ala Val His Gln Ser	
180 185 190	
tct gca tac cac gcc cct ctg cag ctg caa tcg tcc att gca gaa aca	624
Ser Ala Tyr His Ala Pro Leu Gln Leu Gln Ser Ser Ile Ala Glu Thr	

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Ser	Gly	Leu	Glu	Asn	Ile	Phe	Val	Gly	Gly	Ser	Gly	Leu	Gly	Asp	Thr	
210						215					220					
gga	gga	gaa	aac	att	gaa	ctg	aca	tac	ttc	ggg	tcc	cca	cga	aca	agc	720
Gly	Gly	Glu	Asn	Ile	Glu	Leu	Thr	Tyr	Phe	Gly	Ser	Pro	Arg	Thr	Ser	
225					230					235					240	
acg	ccc	cgc	agt	att	gcc	tct	aaa	tca	cgt	ggc	att	tta	aac	tgg	ttc	768
Thr	Pro	Arg	Ser	Ile	Ala	Ser	Lys	Ser	Arg	Gly	Ile	Leu	Asn	Trp	Phe	
				245					250					255		
agt	aaa	cgg	tac	tac	aca	cag	gtg	ccc	acg	gaa	gat	cct	gaa	gtg	ttt	816
Ser	Lys	Arg	Tyr	Tyr	Thr	Gln	Val	Pro	Thr	Glu	Asp	Pro	Glu	Val	Phe	
			260				265					270				
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Ser	Ser	Gln	Thr	Phe	Ala	Asn	Pro	Leu	Tyr	Glu	Ala	Glu	Pro	Ala	Val	
		275					280					285				
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Leu	Lys	Gly	Pro	Ser	Gly	Arg	Val	Gly	Leu	Ser	Gln	Val	Tyr	Lys	Pro	
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Asp	Thr	Leu	Thr	Thr	Arg	Ser	Gly	Thr	Glu	Val	Gly	Pro	Gln	Leu	His	
305					310					315					320	
gtc	agg	tac	tca	ttg	agt	act	ata	cat	gaa	gat	gta	gaa	gca	atc	ccc	1008
Val	Arg	Tyr	Ser	Leu	Ser	Thr	Ile	His	Glu	Asp	Val	Glu	Ala	Ile	Pro	
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tac	aca	gtt	gat	gaa	aat	aca	cag	gga	ctt	gca	ttc	gta	ccc	ttg	cat	1056
Tyr	Thr	Val	Asp	Glu	Asn	Thr	Gln	Gly	Leu	Ala	Phe	Val	Pro	Leu	His	
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gaa	gag	caa	gca	ggt	ttt	gag	gag	ata	gaa	tta	gat	gat	ttt	agt	gag	1104
Glu	Glu	Gln	Ala	Gly	Phe	Glu	Glu	Ile	Glu	Leu	Asp	Asp	Phe	Ser	Glu	
		355					360					365				
aca	cat	aga	ctg	cta	cct	cag	aac	acc	tct	tct	aca	cct	gtt	ggt	agt	1152
Thr	His	Arg	Leu	Leu	Pro	Gln	Asn	Thr	Ser	Ser	Thr	Pro	Val	Gly	Ser	
	370					375					380					
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Gly	Val	Arg	Arg	Ser	Leu	Ile	Pro	Thr	Arg	Glu	Phe	Ser	Ala	Thr	Arg	
385					390					395					400	
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Pro	Thr	Gly	Val	Val	Thr	Tyr	Gly	Ser	Pro	Asp	Thr	Tyr	Ser	Ala	Ser	
				405					410					415		
cca	gtt	act	gac	cct	gat	tct	acc	tct	cct	agt	cta	gtt	atc	gat	gac	1296
Pro	Val	Thr	Asp	Pro	Asp	Ser	Thr	Ser	Pro	Ser	Leu	Val	Ile	Asp	Asp	

420						425						430						
act	act	act	aca	cca	atc	att	ata	att	gat	ggg	cac	aca	gtt	gat	ttg	1344		
Thr	Thr	Thr	Thr	Pro	Ile	Ile	Ile	Ile	Asp	Gly	His	Thr	Val	Asp	Leu			
			435					440				445						
tac	agc	agt	aac	tac	acc	ttg	cat	ccc	tcc	ttg	ttg	agg	aaa	cga	aaa	1392		
Tyr	Ser	Ser	Asn	Tyr	Thr	Leu	His	Pro	Ser	Leu	Leu	Arg	Lys	Arg	Lys			
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Lys	Arg	Lys	His	Ala														
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			20					25					30					
Val	Glu	Gly	Asp	Thr	Ile	Ala	Asp	Lys	Ile	Leu	Lys	Phe	Gly	Gly	Leu			
		35					40					45						
Ala	Ile	Tyr	Leu	Gly	Gly	Leu	Gly	Ile	Gly	Thr	Trp	Ser	Thr	Gly	Arg			
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Val	Ala	Ala	Gly	Gly	Ser	Pro	Arg	Tyr	Thr	Pro	Leu	Arg	Thr	Ala	Gly			
65					70					75					80			
Ser	Thr	Ser	Ser	Leu	Ala	Ser	Ile	Gly	Ser	Arg	Ala	Val	Thr	Ala	Gly			
				85					90					95				
Thr	Arg	Pro	Ser	Ile	Gly	Ala	Gly	Ile	Pro	Leu	Asp	Thr	Leu	Glu	Thr			
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Leu	Gly	Ala	Leu	Arg	Pro	Gly	Val	Tyr	Glu	Asp	Thr	Val	Leu	Pro	Glu			
		115					120					125						
Ala	Pro	Ala	Ile	Val	Thr	Pro	Asp	Ala	Val	Pro	Ala	Asp	Ser	Gly	Leu			
	130						135				140							
Asp	Ala	Leu	Ser	Ile	Gly	Thr	Asp	Ser	Ser	Thr	Glu	Thr	Leu	Ile	Thr			
145					150					155				160				
Leu	Leu	Glu	Pro	Glu	Gly	Pro	Glu	Asp	Ile	Ala	Val	Leu	Glu	Leu	Gln			
				165				170					175					
Pro	Leu	Asp	Arg	Pro	Thr	Trp	Gln	Val	Ser	Asn	Ala	Val	His	Gln	Ser			
			180				185						190					

Ser Ala Tyr His Ala Pro Leu Gln Leu Gln Ser Ser Ile Ala Glu Thr
 195 200 205
 Ser Gly Leu Glu Asn Ile Phe Val Gly Gly Ser Gly Leu Gly Asp Thr
 210 215 220
 Gly Gly Glu Asn Ile Glu Leu Thr Tyr Phe Gly Ser Pro Arg Thr Ser
 225 230 235 240
 Thr Pro Arg Ser Ile Ala Ser Lys Ser Arg Gly Ile Leu Asn Trp Phe
 245 250 255
 Ser Lys Arg Tyr Tyr Thr Gln Val Pro Thr Glu Asp Pro Glu Val Phe
 260 265 270
 Ser Ser Gln Thr Phe Ala Asn Pro Leu Tyr Glu Ala Glu Pro Ala Val
 275 280 285
 Leu Lys Gly Pro Ser Gly Arg Val Gly Leu Ser Gln Val Tyr Lys Pro
 290 295 300
 Asp Thr Leu Thr Thr Arg Ser Gly Thr Glu Val Gly Pro Gln Leu His
 305 310 315 320
 Val Arg Tyr Ser Leu Ser Thr Ile His Glu Asp Val Glu Ala Ile Pro
 325 330 335
 Tyr Thr Val Asp Glu Asn Thr Gln Gly Leu Ala Phe Val Pro Leu His
 340 345 350
 Glu Glu Gln Ala Gly Phe Glu Glu Ile Glu Leu Asp Asp Phe Ser Glu
 355 360 365
 Thr His Arg Leu Leu Pro Gln Asn Thr Ser Ser Thr Pro Val Gly Ser
 370 375 380
 Gly Val Arg Arg Ser Leu Ile Pro Thr Arg Glu Phe Ser Ala Thr Arg
 385 390 395 400
 Pro Thr Gly Val Val Thr Tyr Gly Ser Pro Asp Thr Tyr Ser Ala Ser
 405 410 415
 Pro Val Thr Asp Pro Asp Ser Thr Ser Pro Ser Leu Val Ile Asp Asp
 420 425 430
 Thr Thr Thr Thr Pro Ile Ile Ile Ile Asp Gly His Thr Val Asp Leu
 435 440 445
 Tyr Ser Ser Asn Tyr Thr Leu His Pro Ser Leu Leu Arg Lys Arg Lys
 450 455 460
 Lys Arg Lys His Ala
 465

<211> 1410
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(1410)

<220>
 <223> Description of Artificial Sequence: Bovine
 papillomavirus type 1 L2 open reading frame
 (humanized)

<220>
 <223> Wild-type codons replaced with synonymous codons
 used at relatively high frequency by human genes

<400> 7

atg agc gcc cgc aag aga gtg aag cgc gcc agc gcc tac gac ctg tac	48
Met Ser Ala Arg Lys Arg Val Lys Arg Ala Ser Ala Tyr Asp Leu Tyr	
1 5 10 15	
agg acc tgc aag cag gcc ggc aca tgt cca cca gat gtg atc cga aag	96
Arg Thr Cys Lys Gln Ala Gly Thr Cys Pro Pro Asp Val Ile Arg Lys	
20 25 30	
gtg gag ggc gac acc atc gcc gac aag atc ctg aag ttc ggc ggc ctg	144
Val Glu Gly Asp Thr Ile Ala Asp Lys Ile Leu Lys Phe Gly Gly Leu	
35 40 45	
gcc atc tac ctg ggc ggc ctg ggc atc gga aca tgg tct acc ggc agg	192
Ala Ile Tyr Leu Gly Gly Leu Gly Ile Gly Thr Trp Ser Thr Gly Arg	
50 55 60	
gtg gcc gcc ggc ggc tca cca agg tac acc cca ctg cgc acc gcc ggc	240
Val Ala Ala Gly Gly Ser Pro Arg Tyr Thr Pro Leu Arg Thr Ala Gly	
65 70 75 80	
tcc acc tcc tcc ctg gcc tcc atc gga tcc aga gcc gtg acc gcc ggg	288
Ser Thr Ser Ser Leu Ala Ser Ile Gly Ser Arg Ala Val Thr Ala Gly	
85 90 95	
acc cgc ccc tcc atc ggc gcg ggc atc cct ctg gac acc ctg gaa act	336
Thr Arg Pro Ser Ile Gly Ala Gly Ile Pro Leu Asp Thr Leu Glu Thr	
100 105 110	
ctt ggg gcc ctg cgc cct ggc gtg tac gag gac acc gtg ctg ccc gaa	384
Leu Gly Ala Leu Arg Pro Gly Val Tyr Glu Asp Thr Val Leu Pro Glu	
115 120 125	
gcc cct gcc atc gtg acc cct gac gcc gtg cct gca gac tcc ggc ctg	432
Ala Pro Ala Ile Val Thr Pro Asp Ala Val Pro Ala Asp Ser Gly Leu	
130 135 140	
gac gcc ctg tcc atc ggc aca gac tcc tcc acc gag acc ctg atc acc	480
Asp Ala Leu Ser Ile Gly Thr Asp Ser Ser Thr Glu Thr Leu Ile Thr	

145		150		155		160	
ctg ctg gag cct gag ggc ccc gaa gac ata gcc gtg ctg gaa ctc cag	528						
Leu Leu Glu Pro Glu Gly Pro Glu Asp Ile Ala Val Leu Glu Leu Gln							
		165		170		175	
ccc ctg gac cgc cca acc tgg cag gtg agc aat gct gtg cac cag tcc	576						
Pro Leu Asp Arg Pro Thr Trp Gln Val Ser Asn Ala Val His Gln Ser							
		180		185		190	
tct gcc tac cac gcc cct ctc cag ctg caa tcc tcc atc gcc gag aca	624						
Ser Ala Tyr His Ala Pro Leu Gln Leu Gln Ser Ser Ile Ala Glu Thr							
		195		200		205	
tct ggt tta gaa aat att ttt gta gga ggc tcg ggt tta ggg gat acc	672						
Ser Gly Leu Glu Asn Ile Phe Val Gly Gly Ser Gly Leu Gly Asp Thr							
		210		215		220	
ggc ggc gag aac atc gag ctg acc tac ttc gcc tcc ccc cgc acc agc	720						
Gly Gly Glu Asn Ile Glu Leu Thr Tyr Phe Gly Ser Pro Arg Thr Ser							
		225		230		235	
acc ccc cgc tcc atc gcc tcc aag tcc cgc gcc atc ctg aac tgg ttc	768						
Thr Pro Arg Ser Ile Ala Ser Lys Ser Arg Gly Ile Leu Asn Trp Phe							
		245		250		255	
agc aag cgg tac tac acc cag gtg ccc acc gaa gat ccc gaa gtg ttc	816						
Ser Lys Arg Tyr Tyr Thr Gln Val Pro Thr Glu Asp Pro Glu Val Phe							
		260		265		270	
tcc tcc cag acc ttc gcc aac ccc ctg tac gag gcc gag ccc gcc gtg	864						
Ser Ser Gln Thr Phe Ala Asn Pro Leu Tyr Glu Ala Glu Pro Ala Val							
		275		280		285	
ctg aag ggc cct agc ggc cgc gtg ggc ctg tcc cag gtg tac aag cct	912						
Leu Lys Gly Pro Ser Gly Arg Val Gly Leu Ser Gln Val Tyr Lys Pro							
		290		295		300	
gat acc ctg acc aca cgt agc ggc aca gag gtg ggc ccc cag ctg cat	960						
Asp Thr Leu Thr Thr Arg Ser Gly Thr Glu Val Gly Pro Gln Leu His							
		305		310		315	
gtg agg tac tcc ctg tcc acc atc cat gag gat gtg gag gct atc ccc	1008						
Val Arg Tyr Ser Leu Ser Thr Ile His Glu Asp Val Glu Ala Ile Pro							
		325		330		335	
tac acc gtg gat gag aac acc cag ggc ctg gcc ttc gtg ccc ctg cat	1056						
Tyr Thr Val Asp Glu Asn Thr Gln Gly Leu Ala Phe Val Pro Leu His							
		340		345		350	
gag gag cag gcc ggc ttc gag gag atc gag ctc gac gat ttc agc gag	1104						
Glu Glu Gln Ala Gly Phe Glu Glu Ile Glu Leu Asp Asp Phe Ser Glu							
		355		360		365	
acc cat cgc ctg ctg ccc cag aac acc tcc tcc acc ccc gtg ggc agc	1152						
Thr His Arg Leu Leu Pro Gln Asn Thr Ser Ser Thr Pro Val Gly Ser							

370	375	380	
ggc gtg cgc aga agc ctg atc cct acc cga gag ttc agc gcc acc cgg			1200
Gly Val Arg Arg Ser Leu Ile Pro Thr Arg Glu Phe Ser Ala Thr Arg			
385	390	395	400
cct acc ggc gtg gtg acc tac ggc tcc ccc gac acc tac tcc gct agc			1248
Pro Thr Gly Val Val Thr Tyr Gly Ser Pro Asp Thr Tyr Ser Ala Ser			
	405	410	415
ccc gtg acc gac cct gat tct acc tct cct agc ctg gtg atc gac gac			1296
Pro Val Thr Asp Pro Asp Ser Thr Ser Pro Ser Leu Val Ile Asp Asp			
	420	425	430
acc acc acc acc ccc atc atc atc atc gac ggc cac aca gtg gat ctg			1344
Thr Thr Thr Thr Pro Ile Ile Ile Ile Asp Gly His Thr Val Asp Leu			
	435	440	445
tac agc agc aac tac acc ctg cat ccc tcc ctg ctg agg aag cgc aag			1392
Tyr Ser Ser Asn Tyr Thr Leu His Pro Ser Leu Leu Arg Lys Arg Lys			
	450	455	460
aag cgc aag cat gcc taa			1410
Lys Arg Lys His Ala			
465	470		

<210> 8
 <211> 469
 <212> PRT
 <213> Artificial Sequence

<400> 8
 Met Ser Ala Arg Lys Arg Val Lys Arg Ala Ser Ala Tyr Asp Leu Tyr
 1 5 10 15
 Arg Thr Cys Lys Gln Ala Gly Thr Cys Pro Pro Asp Val Ile Arg Lys
 20 25 30
 Val Glu Gly Asp Thr Ile Ala Asp Lys Ile Leu Lys Phe Gly Gly Leu
 35 40 45
 Ala Ile Tyr Leu Gly Gly Leu Gly Ile Gly Thr Trp Ser Thr Gly Arg
 50 55 60
 Val Ala Ala Gly Gly Ser Pro Arg Tyr Thr Pro Leu Arg Thr Ala Gly
 65 70 75 80
 Ser Thr Ser Ser Leu Ala Ser Ile Gly Ser Arg Ala Val Thr Ala Gly
 85 90 95
 Thr Arg Pro Ser Ile Gly Ala Gly Ile Pro Leu Asp Thr Leu Glu Thr
 100 105 110
 Leu Gly Ala Leu Arg Pro Gly Val Tyr Glu Asp Thr Val Leu Pro Glu
 115 120 125

Ala	Pro	Ala	Ile	Val	Thr	Pro	Asp	Ala	Val	Pro	Ala	Asp	Ser	Gly	Leu	130	135	140	
Asp	Ala	Leu	Ser	Ile	Gly	Thr	Asp	Ser	Ser	Thr	Glu	Thr	Leu	Ile	Thr	145	150	155	160
Leu	Leu	Glu	Pro	Glu	Gly	Pro	Glu	Asp	Ile	Ala	Val	Leu	Glu	Leu	Gln	165	170	175	
Pro	Leu	Asp	Arg	Pro	Thr	Trp	Gln	Val	Ser	Asn	Ala	Val	His	Gln	Ser	180	185	190	
Ser	Ala	Tyr	His	Ala	Pro	Leu	Gln	Leu	Gln	Ser	Ser	Ile	Ala	Glu	Thr	195	200	205	
Ser	Gly	Leu	Glu	Asn	Ile	Phe	Val	Gly	Gly	Ser	Gly	Leu	Gly	Asp	Thr	210	215	220	
Gly	Gly	Glu	Asn	Ile	Glu	Leu	Thr	Tyr	Phe	Gly	Ser	Pro	Arg	Thr	Ser	225	230	235	240
Thr	Pro	Arg	Ser	Ile	Ala	Ser	Lys	Ser	Arg	Gly	Ile	Leu	Asn	Trp	Phe	245	250	255	
Ser	Lys	Arg	Tyr	Tyr	Thr	Gln	Val	Pro	Thr	Glu	Asp	Pro	Glu	Val	Phe	260	265	270	
Ser	Ser	Gln	Thr	Phe	Ala	Asn	Pro	Leu	Tyr	Glu	Ala	Glu	Pro	Ala	Val	275	280	285	
Leu	Lys	Gly	Pro	Ser	Gly	Arg	Val	Gly	Leu	Ser	Gln	Val	Tyr	Lys	Pro	290	295	300	
Asp	Thr	Leu	Thr	Thr	Arg	Ser	Gly	Thr	Glu	Val	Gly	Pro	Gln	Leu	His	305	310	315	320
Val	Arg	Tyr	Ser	Leu	Ser	Thr	Ile	His	Glu	Asp	Val	Glu	Ala	Ile	Pro	325	330	335	
Tyr	Thr	Val	Asp	Glu	Asn	Thr	Gln	Gly	Leu	Ala	Phe	Val	Pro	Leu	His	340	345	350	
Glu	Glu	Gln	Ala	Gly	Phe	Glu	Glu	Ile	Glu	Leu	Asp	Asp	Phe	Ser	Glu	355	360	365	
Thr	His	Arg	Leu	Leu	Pro	Gln	Asn	Thr	Ser	Ser	Thr	Pro	Val	Gly	Ser	370	375	380	
Gly	Val	Arg	Arg	Ser	Leu	Ile	Pro	Thr	Arg	Glu	Phe	Ser	Ala	Thr	Arg	385	390	395	400
Pro	Thr	Gly	Val	Val	Thr	Tyr	Gly	Ser	Pro	Asp	Thr	Tyr	Ser	Ala	Ser	405	410	415	
Pro	Val	Thr	Asp	Pro	Asp	Ser	Thr	Ser	Pro	Ser	Leu	Val	Ile	Asp	Asp	420	425	430	

Thr Thr Thr Thr Pro Ile Ile Ile Ile Asp Gly His Thr Val Asp Leu
 435 440 445

Tyr Ser Ser Asn Tyr Thr Leu His Pro Ser Leu Leu Arg Lys Arg Lys
 450 455 460

Lys Arg Lys His Ala
 465

<210> 9

<211> 717

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Aequorea
 victoria gfp gene (humanized)

<220>

<221> CDS

<222> (1)..(717)

<400> 9

atg agc aag ggc gag gaa ctg ttc act ggc gtg gtc cca att ctc gtg 48
 Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

gaa ctg gat ggc gat gtg aat ggg cac aaa ttt tct gtc agc gga gag 96
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

ggt gaa ggt gat gcc aca tac gga aag ctc acc ctg aaa ttc atc tgc 144
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

acc act gga aag ctc cct gtg cca tgg cca aca ctg gtc act acc ttc 192
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

tct tat ggc gtg cag tgc ttt tcc aga tac cca gac cat atg aag cag 240
 Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
 65 70 75 80

cat gac ttt ttc aag agc gcc atg ccc gag ggc tat gtg cag gag aga 288
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

acc atc ttt ttc aaa gat gac ggg aac tac aag acc cgc gct gaa gtc 336
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

aag ttc gaa ggt gac acc ctg gtg aat aga atc gag ctg aag ggc att 384
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

gac ttt aag gag gat gga aac att ctc ggc cac aag ctg gaa tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	
tat aac tcc cac aat gtg tac atc atg gcc gac aag caa aag aat ggc	480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
145 150 155 160	
atc aag gtc aac ttc aag atc aga cac aac att gag gat gga tcc gtg	528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val	
165 170 175	
cag ctg gcc gac cat tat caa cag aac act cca atc ggc gac ggc cct	576
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro	
180 185 190	
gtg ctc ctc cca gac aac cat tac ctg tcc acc cag tct gcc ctg tct	624
Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser	
195 200 205	
aaa gat ccc aac gaa aag aga gac cac atg gtc ctg ctg gag ttt gtg	672
Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val	
210 215 220	
acc gct gct ggg atc aca cat ggc atg gac gag ctg tac aag tga	717
Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys	
225 230 235	

<210> 10
 <211> 238
 <212> PRT
 <213> Artificial Sequence

<400> 10	
Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
1 5 10 15	
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	
Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln	
65 70 75 80	
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	

115					120					125					
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn
130						135					140				
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly
145					150					155					160
Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val
				165					170					175	
Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro
			180					185					190		
Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser
			195				200					205			
Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val
	210					215					220				
Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	Leu	Tyr	Lys		
225						230					235				

<210> 11
 <211> 717
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(717)

<220>
 <223> Description of Artificial Sequence: Synthetic gfp
 gene (Papillomavirusized)

<220>
 <223> Codons of humanized gfp gene replaced with
 synonymous codons used at relatively high
 frequency by papillomavirus genes

<400> 11																
atg	agt	aaa	ggg	gaa	gaa	cta	ttt	aca	ggg	gtg	gtg	cct	ata	cta	gtg	48
Met	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	
1				5					10					15		
gaa	cta	gat	ggg	gat	gtg	aat	ggg	cac	aaa	ttt	tct	gtc	agt	ggg	gaa	96
Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	
			20					25					30			
ggg	gaa	ggg	gat	gca	aca	tat	ggg	aaa	cta	aca	cta	aaa	ttt	ata	tgc	144
Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	
			35				40					45				
aca	aca	ggg	aaa	cta	cct	gtg	cca	tgg	cct	aca	cta	gtg	aca	aca	ttt	192
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe	

50	55	60	
agt tat ggg gtg caa tgc ttt agt aga tat cct gat cat atg aaa caa			240
Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln			
65	70	75	80
cat gat ttt ttt aaa agt gca atg ccc gag ggg tat gtg caa gaa aga			288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg			
	85	90	95
aca ata ttt ttt aaa gat gat ggg aat tat aaa aca aga gca gaa gtc			336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val			
	100	105	110
aaa ttt gaa ggg gat aca cta gtg aat aga ata gag ctc aaa ggg ata			384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile			
	115	120	125
gat ttt aaa gaa gat ggg aat ata cta ggg cat aaa cta gaa tat aat			432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn			
	130	135	140
tat aat agt cat aat gtg tat ata atg gca gat aaa caa aaa aat ggg			480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly			
145	150	155	160
ata aaa gtg aat ttt aaa ata ata aga cat ata gaa gat gga tcc gtg			528
Ile Lys Val Asn Phe Lys Ile Ile Arg His Ile Glu Asp Gly Ser Val			
	165	170	175
caa cta gca gat cat tat caa caa aat aca cct ata ggg gat ggg cct			576
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro			
	180	185	190
gtg cta cta cct gat aac cat tat cta agt aca caa agt gca cta agt			624
Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser			
	195	200	205
aaa gat cct aat gaa aaa aga gat cat atg gtg cta ctc gag ttt gtg			672
Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val			
	210	215	220
aca gca gca ggg ata aca cat ggg atg gat gaa cta tat aaa tga			717
Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys			
225	230	235	

<210> 12

<211> 238

<212> PRT

<213> Artificial Sequence

<400> 12

Met	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val
1				5					10					15	

Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

20							25					30				
Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	
		35					40					45				
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe	
	50					55					60					
Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	
65					70				75						80	
His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	
				85					90					95		
Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	
			100				105						110			
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	
		115				120						125				
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	
	130					135					140					
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	
145				150						155					160	
Ile	Lys	Val	Asn	Phe	Lys	Ile	Ile	Arg	His	Ile	Glu	Asp	Gly	Ser	Val	
			165					170						175		
Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	
		180						185					190			
Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser	
		195				200					205					
Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val	
	210					215					220					
Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	Leu	Tyr	Lys			
225					230					235						

<210> 13
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Oligonucleotide specific for Ala(GCA)

<400> 13
 taaggactgt aagactt

<210> 14
 <211> 17

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide specific for Arg(CGA)

<400> 14
cgagccagcc aggagtc

17

<210> 15
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide specific for Asn(AAC)

<400> 15
ctagattggc aggaatt

17

<210> 16
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide specific for Asp(GAC)

<400> 16
taagatatat agattat

17

<210> 17
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide specific for Cys(TGC)

<400> 17
aagtcttagt agagatt

17

<210> 18
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:

Oligonucleotide specific for Glu(GAA)

<400> 18

tatttctaca cagcatt

17

<210> 19

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide specific for Gln(CAA)

<400> 19

ctaggacaat aggaatt

17

<210> 20

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide specific for Gly(GGA)

<400> 20

tactctcttc tgggttt

17

<210> 21

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide specific for His(CAC)

<400> 21

tgccgtgact cggattc

17

<210> 22

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide specific for Ile(ATC)

<400> 22

tagaaataag agggctt

17

<210> 23
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide specific for Leu(CTA)

<400> 23
tactttttatt tggattt

17

<210> 24
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide specific for Leu(CTT)

<400> 24
tattagggag aggattt

17

<210> 25
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide specific for Lys(AAA)

<400> 25
tcactatgga gatttta

17

<210> 26
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide specific for Lys(AAG)

<400> 26
cgcccaacgt ggggctc

17

<210> 27
<211> 17
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide specific for Met (elong)

<400> 27

tagtacggga aggattt

17

<210> 28

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide specific for Phe(TTC)

<400> 28

tgtttatggg atacaat

17

<210> 29

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide specific for Pro(CCA)

<400> 29

tcaagaagaa ggagcta

17

<210> 30

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide specific for Pro(CCI)

<400> 30

gggctcgtcc gggattt

17

<210> 31

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide specific for Ser(AGC)

<400> 31
ataagaaagg aagatcg

17

<210> 32
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide specific for Thr(ACA)

<400> 32
tgtcttgaga agagaag

17

<210> 33
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide specific for Tyr(TAC)

<400> 33
tggtaaaaag aggattt

17

<210> 34
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide specific for Val(GTA)

<400> 34
tcagagtgtt cattggt

17

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WHAT IS CLAIMED IS:

1. A method of constructing a synthetic polynucleotide that encodes a polypeptide, the method comprising:
 - selecting a first codon of a parent polynucleotide for
5 replacement with a synonymous codon, wherein the synonymous codon is selected on the basis that it exhibits a higher translational efficiency in a first cell of a mammal than in a second cell of the mammal; and
 - replacing the first codon with the synonymous
10 codon to construct the synthetic polynucleotide.
2. The method of claim 1, wherein the first codon and the synonymous codon are selected by:
 - comparing translational efficiencies of individual
codons in the first cell relative to the second cell; and
 - 15 - selecting the first codon and the synonymous codon based on the comparison.
3. The method of claim 2, wherein the translational efficiency of an individual codon is compared by measuring the abundance of an iso-tRNA corresponding to the
20 individual codon in the first cell relative to the second cell.
4. The method of claim 3, wherein the synonymous codon corresponds to an iso-tRNA which is in higher abundance in the first cell relative to the second cell.
- 25 5. The method of claim 3, wherein selecting the first codon and the synonymous codon comprises:
 - measuring abundance of different iso-tRNAs in the first cell relative to the second cell; and
 - selecting the first codon and the synonymous codon
30 based on the measurement, wherein the synonymous codon

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corresponds to an iso-tRNA which is in higher abundance in the first cell than in the second cell.

6. The method of claim 3, wherein the synonymous codon corresponds to an iso-tRNA that is present in the first cell
5 at a level which is at least 110% of the level of the iso-tRNA that is present in the second cell.
7. The method of claim 1, wherein the synonymous codon is selected from the group consisting of (1) a codon used at relatively high frequency by genes of the first cell, (2) a
10 codon used at relatively high frequency by genes of the mammal, (3) a codon used at relatively low frequency by genes of the second cell, and (4) a codon used at relatively low frequency by genes of an organism other than the mammal.
- 15 8. The method of claim 1, wherein the first codon and the synonymous codon are selected such that the polypeptide is expressed from the synthetic polynucleotide in the first cell at a level which is at least 110% of the level at which the polypeptide is expressed from the parent
20 polynucleotide in the first cell.
9. The method of claim 1, wherein the second cell is a precursor cell of the first cell.
10. The method of claim 1, wherein the second cell is a cell derived from the first cell.
- 25 11. The method of claim 1, wherein the polypeptide is not substantially expressible in the second cell.
12. The method of claim 1, wherein the first cell is of the same type as the second cell, but is at a different stage of differentiation.
- 30 13. The method of claim 1, wherein the first cell is of the

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same type as the second cell, but is at a different stage of the cell cycle.

14. A method of selectively expressing a polypeptide in a first cell of a mammal, the method comprising:

- 5 - selecting a first codon of a parent polynucleotide encoding the polypeptide for replacement with a synonymous codon, wherein the synonymous codon is selected on the basis that it exhibits a higher translational efficiency in the first cell than in a second cell of the mammal;
- 10 - replacing the first codon with the synonymous codon to construct a synthetic polynucleotide; and
- introducing the synthetic polynucleotide into a cell selected from the group consisting of the first cell and a precursor of the first cell, the synthetic polynucleotide
- 15 being operably linked to a regulatory polynucleotide, whereby the polypeptide is selectively expressed in the first cell.

15. The method of claim 14, wherein the synonymous codon has a higher translational efficiency in the

20 first cell than in the second cell.

16. A method of expressing a polypeptide from a first polynucleotide in a mammalian cell, the method comprising:

- 25 - selecting an iso-tRNA on the basis that it is normally in lower abundance in the cell than other isotRNAs and corresponds to a codon of the first polynucleotide;
- introducing into the cell a second polynucleotide that encodes the selected iso-tRNA and that is operably linked to a regulatory polynucleotide; and
- 30 - expressing the second polynucleotide in the cell, whereby the polypeptide is expressed in the cell.

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17. A method of expressing a polypeptide from a first polynucleotide in a mammalian cell, the method comprising

- selecting an iso-tRNA on the basis that it is normally in lower abundance in the cell than other isotRNAs
- 5 and corresponds to a codon of the first polynucleotide;
- introducing into a precursor of the cell a second polynucleotide that encodes the selected iso-tRNA and that is operably linked to a regulatory polynucleotide, wherein the precursor is exposed to conditions sufficient to
- 10 produce the cell; and

expressing the second polynucleotide in the cell, whereby the polypeptide is expressed in the cell.

18. A method of producing a virus particle in a cycling animal cell, wherein the virus particle comprises a

15 polypeptide necessary for assembly of the virus particle, and wherein the polypeptide is expressed in the cell from a parent polynucleotide, but not at a level sufficient to permit virus assembly therein, the method comprising:

- 20 - providing a comparison of translational efficiencies of individual codons in the cell;
- selecting from the comparison a first codon of the parent polynucleotide for replacement with a synonymous codon, wherein the synonymous codon is selected on the
- 25 basis that it exhibits a higher translational efficiency in the cell than the first codon; and
- replacing the first codon with the synonymous codon to construct a synthetic polynucleotide having enhanced translational kinetics compared to the parent
- 30 polynucleotide, such that the polypeptide is expressible from the synthetic polynucleotide in the cell at a level sufficient to permit virus assembly therein; and

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- introducing into the cell the synthetic polynucleotide operably linked to a regulatory polynucleotide,

whereby the polypeptide is expressed and the virus
5 particle is produced in the cell.

19. The method of claim 18, wherein the synonymous codon has a higher translational efficiency in the cell than the first codon.

20. A method of producing a virus particle in a cycling
10 cell, wherein the virus particle comprises at least one polypeptide necessary for assembly of the virus particle, wherein the polypeptide is expressed in the cell from a first polynucleotide, but not at a level sufficient to permit virus assembly therein, the method comprising:

15 - providing a comparison of translational efficiencies of individual codons in the cell;

- selecting from the comparison a first codon of the first polynucleotide that exhibits a lower translational efficiency in the cell than a synonymous
20 codon;

- introducing into the cell a second polynucleotide encoding an iso-tRNA specific for the first codon; and
- expressing the second polynucleotide in the cell,
whereby the virus particle is produced in the cycling
25 cell.

21. A method of producing a virus particle in a cycling eukaryotic cell, wherein the virus particle comprises a polypeptide necessary for assembly of the virus particle, and wherein the polypeptide is expressed in the
30 cell from a parent polynucleotide, but not at a level sufficient to permit virus assembly therein, the method comprising:

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- providing a comparison of translational efficiencies of individual codons in the cell;

- selecting from the comparison a first codon of the parent polynucleotide for replacement with a synonymous
5 codon, wherein the synonymous codon is selected on the basis that it exhibits a higher translational efficiency in the cell than the first codon; and

- replacing the first codon with the synonymous codon to construct a synthetic polynucleotide having
10 increased translational kinetics compared to the parent polynucleotide, such that the polypeptide is expressible from the synthetic polynucleotide in the cell at a level sufficient to permit virus assembly therein;

- introducing into a precursor of the cell the
15 synthetic polynucleotide operably linked to a regulatory polynucleotide; and

- exposing the precursor to conditions sufficient to produce the cell, wherein the cell comprises the polypeptide necessary for assembly of the virus
20 particle,

whereby the polypeptide is expressed and the virus particle is produced in the cell.

22. A method of constructing a synthetic polynucleotide that encodes a polypeptide, the method comprising:

25 - selecting a first codon of a parent polynucleotide for replacement with a synonymous codon, wherein the synonymous codon is selected on the basis that it exhibits a lower translational efficiency in a first cell of a mammal than in a second cell of the mammal; and

30 - replacing the first codon with the synonymous codon to construct the synthetic polynucleotide.

23. The method of claim 22, wherein the first codon and the

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synonymous codon are selected by:

- comparing translational efficiencies of individual codons in the first cell relative to the second cell; and
 - selecting the first codon and the synonymous codon
- 5 based on the comparison.

24. The method of claim 23, wherein the translational efficiency of an individual codon is compared by measuring the abundance of an iso-tRNA corresponding to the individual codon in the first cell relative to the second

10 cell.

25. The method of claim 24, wherein the synonymous codon corresponds to an iso-tRNA which is in lower abundance in the first cell relative to the second cell.

15 26. The method of claim 23, wherein selecting the first codon and the synonymous codon comprises:

- measuring abundance of different iso-tRNAs in the first cell relative to the second cell; and
 - selecting the first codon and the synonymous codon
- 20 based on the measurement, wherein the synonymous codon corresponds to an iso-tRNA which is in lower abundance in the first cell than in the second cell.

27. A method of constructing a synthetic polynucleotide that encodes a polypeptide, the method comprising:

- 25 - providing a comparison of translational efficiencies of individual codons in a cell of a mammal;
 - selecting from the comparison a first codon of the parent polynucleotide for replacement with a synonymous
- 30 codon, wherein the synonymous codon is selected on the basis that it exhibits a higher translational efficiency

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in the cell than the first codon; and

- replacing the first codon with the synonymous codon to construct the synthetic polynucleotide.

28. The method of claim 27, wherein the synonymous codon
5 corresponds to an iso-tRNA which is in higher abundance in the cell relative to the iso-tRNA corresponding to the first codon.

29. The method of claim 27, wherein the first codon and the
synonymous codon are selected such that the polypeptide
10 is expressed from the synthetic polynucleotide in the cell at a level which is at least 110%, of the level at which the polypeptide is expressed from the parent polynucleotide in the cell.

30. The method of claim 27, wherein the comparison is
15 provided by comparing translational efficiencies of individual codons in the cell.

31. The method of claim 27, wherein the translational efficiencies are compared by measuring abundance of different iso-tRNAs in the cell.

20 32. A method of constructing a synthetic polynucleotide encoding a polypeptide, the method comprising:

- providing a comparison of translational efficiencies of individual codons in a cell of a mammal;

25 - selecting from the comparison a first codon of the parent polynucleotide for replacement with a synonymous codon, wherein the synonymous codon is selected on the basis that it exhibits a lower translational efficiency in the cell than the first codon; and

30 - replacing the first codon with the synonymous codon to construct the synthetic polynucleotide.

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33. The method of claim 31, wherein the synonymous codon corresponds to an iso-tRNA which is in lower abundance in the cell relative to the iso-tRNA corresponding to the first codon.

5 34. The method of claim 31, wherein the comparison is provided by comparing translational efficiencies of individual codons in the cell.

35. The method of claim 34, wherein the translational efficiencies are compared by measuring abundance of
10 different iso-tRNAs in the cell.

Figure 1A

	C	C		G	G		C	G	C	T	C					
1	ATG	GCG	TTG	TGG	CAA	CAA	GGC	CAG	AAG	CTG	TAT	CTC	CCT	CCA	ACC	CCT
	M	A	L	W	Q	Q	G	Q	K	L	Y	L	P	P	T	P
	G															
49	GTA	AGC	AAG	GTG	CTT	TGC	AGT	GAA	ACC	TAT	GTG	CAA	AGA	AAA	AGC	ATT
	V	S	K	V	L	C	S	E	T	Y	V	Q	R	K	S	I
	G															
97	TTT	TAT	CAT	GCA	GAA	ACG	GAG	CGC	CTG	CTA	ACT	ATA	GGA	CAT	CCA	TAT
	F	Y	H	A	E	T	E	R	L	L	T	I	G	H	P	Y
	G															
145	TAC	CCA	GTG	TCT	ATC	GGG	GCC	AAA	ACT	GTT	<u>CCT</u>	<u>AAG</u>	GTC	TCT	GCA	AAT
	Y	P	V	S	I	G	A	K	T	V	P	K	V	S	A	N
	(Saul)															
193	CAG	TAT	AGG	GTA	TTT	AAA	ATA	CAA	CTA	CCT	GAT	CCC	AAT	CAA	TTT	GCA
	Q	Y	R	V	F	K	I	Q	L	P	D	P	N	Q	F	A
	G															
241	CTA	CCT	GAC	AGG	ACT	GTT	CAC	AAC	CCA	AGT	AAA	GAG	CGG	CTG	GTG	<u>TGG</u>
	L	P	D	R	T	V	H	N	P	S	K	E	R	L	V	W
	(Ball)															
289	<u>CCA</u>	GTC	ATA	GGT	GTG	CAG	GTG	TCC	AGA	GGG	CAG	CCT	CTT	GGA	GGT	ACT
	P	V	I	G	V	Q	V	S	R	G	Q	P	L	G	G	T
	G															

Figure 1A cont'd

337	GTA	ACT	GGG	CAC	CCC	ACT	TTT	AAT	GCT	TTG	CTT	GAT	GCA	GAA	AAT	GTG	
	V	T	G	H	P	T	F	N	A	L	L	D	A	E	N	V	
								G	C	C	C					G	
385	AAT	AGA	AAA	GTC	ACC	ACC	CAA	ACA	ACA	GAT	GAC	AGG	AAA	CAA	ACA	GGC	(StuI)
	N	R	K	V	T	T	Q	T	T	D	D	R	K	Q	T	G	
			G		G			C		C	G						
433	CTA	GAT	GCT	AAG	CAA	CAG	ATT	CTG	TTG	CTA	GGC	TGT	ACC	CCT	GCT		
	L	D	A	K	Q	Q	I	L	L	L	G	C	T	P	A		
											G	C	C				
481	GAA	GGG	GAA	TAT	TGG	ACA	ACA	GCC	CGT	CCA	TGT	GTT	ACT	GAT	CGT	CTA	(XbaI)
	E	G	E	Y	W	T	A	R	P	C	V	T	D	R	L		
			C					G	G	C	G					C	
529	GAA	AAT	GGC	GCC	TGC	CCT	CCT	CTT	GAA	TTA	AAA	AAC	AAG	CAC	ATA	GAA	
	E	N	G	A	C	P	P	L	E	L	K	N	K	H	I	E	
577	GAT	GGG	GAT	ATG	ATG	GAA	ATT	GGG	TTT	GGT	GCA	GCC	AAC	TTC	AAA	GAA	
	D	G	D	M	M	E	I	G	F	G	A	A	N	F	K	E	

Figure 1A cont'd

625	ATT AAT GCA AGT AAA TCA GAT CTA CCT CTT GAC ATT CAA AAT GAG ATC	G	C
	I N A S K S D L P L D I Q N E I		
	C	C	C
673	TGC TTG TAC CCA GAC TAC CTC AAA ATG GCT GAG GAC GCT <u>GCT</u> GGT AAT		(NaeI)
	C L Y P D Y L K M A E D A A G N		
	C	C	G
721	AGC ATG TTC TTT TTT GCA AGG AAA GAA CAG GTG TAT GTT AGA CAC ATC		
	S M F F F A R K E Q V Y V R H I		
	C		
769	TGG ACC AGA GGG GGC TCG GAG AAA GAA GCC CCT ACC ACA GAT TTT TAT		
	W T R G G S E K E A P T T D F Y		
	G	C	C
817	TTA AAG AAT AAT AAA GGG GAT GCC ACC CTT AAA ATA CCC AGT GTG CAT		
	L K N N K G D A T L K I P S V H		
	C	C	C
865	TTT GGT AGT CCC AGT GGC TCA <u>CTA</u> GTC TCA ACT GAT AAT CAA ATT TTT		(SpeI)
	F G S P S G S L V S T D N Q I F		
	C	G	C
913	AAT CGG CCC TAC TGG CTA TTC CGT GCC CAG GGC ATG AAC AAT GGA ATT		
	N R P Y W L F R A Q G M N N G I		

Figure 1A cont'd

[illegible]

Figure 1A cont'd

1297	GCA	AAA	GAA	GAC	CCT	TAT	GCA	GGG	TTT	AAG	TTT	TGG	AAC	ATA	GAT	CTT	C	C	C	G
	A	K	E	D	P	Y	A	G	F	K	F	W	N	I	D	L				
	G	G		G		C		C	G	G	C			C						
1345	AAA	GAA	AAG	CTT	TCT	TTG	GAC	TTA	GAT	CAA	TTT	<u>CCC TTG</u>	GGA	AGA	AGA	AGA	(StyI)			
	K	E	K	L	S	L	D	L	D	Q	F	P	L	G	R	R				
	C	G	C		G		C	C		C	C				C	G				
1393	TTT	TTA	GCA	CAG	CAA	GGG	GCA	GGA	TGT	TCA	ACT	GTG	AGA	AAA	CGA	AGA				
	F	L	A	Q	Q	G	A	G	C	S	T	V	R	K	R	R				
	C		G	G	C		C		C	C	G	G			G					
1441	ATT	AGC	CAA	AAA	ACT	TCC	AGT	AAG	CCT	GCA	AAA	AAA	AAA	AAA	AAA	TAA				
	I	S	Q	K	T	S	S	K	P	A	K	K	K	K	K	-				

Figure 1B

	C	C	C	G	G	C	C	C								
1	ATG	AGT	GCA	CGA	AAA	AGA	GTA	AAA	CGT	GCC	AGT	GCC	TAT	GAC	CTG	TAC
	M	S	A	R	K	R	V	K	R	A	S	A	Y	D	L	Y
	C				G	C										C
49	AGG	ACC	TGC	AAG	CAA	GCG	GGC	ACA	TGT	CCA	CCA	GAT	GTG	ATA	CGA	AAG
	R	T	C	K	Q	A	G	T	C	P	P	D	V	I	R	K
	G	G	C	C	C	C	C	C	G	C	C	G	C	C	C	G
97	GTA	GAA	GGA	GAT	ACT	ATA	GCA	GAT	AAA	ATT	TTG	AAA	TTT	GGG	GGT	CTT
	V	E	G	D	T	I	A	D	K	I	L	K	F	G	G	L
	C			C	G	C	C	C	C							C
145	GCA	ATC	TAC	TTA	GGA	GGG	CTA	GGA	ATA	GGA	ACA	TGG	TCT	ACT	GGA	AGG
	A	I	Y	L	G	G	L	G	I	G	T	W	S	T	G	R
	G	C	C	C	C					C		G	C	C	C	C
193	GTG	GCC	GCA	GGT	GGA	TCA	CCA	AGG	TAC	ACA	CCA	CTC	CGA	ACA	GCA	GGG
	V	A	A	G	G	S	P	R	Y	T	P	L	R	T	A	G
	C	C	C	C	G	C	C	C				C	G	C	C	
241	TCC	ACA	TCA	TCG	CTT	GCA	TCA	ATA	GGA	TCC	AGA	GCT	GTA	ACA	GCA	GGG
	S	T	S	S	L	A	S	I	G	S	R	A	V	T	A	G

Figure 1B cont'd

289	TCC C C G	ACC CGC CCC AGT ATA GGT GCG GGC ATT CCT TTA GAC ACC CTT GAA ACT
	C C C T C	T R P S I G A G I P L D T L E T
337	CTT GGG GCC TTG CGT CCA GGG GTG TAT GAG GAC ACT GTG CTA CCA GAG	L G A L R P G V Y E D T V L P E
	C C G C C C C	
385	GCC CCT GCA ATA GTC ACT CCT GAT GCT GTT CCT GCA GAT TCA GGG CTT	A P A I V T P D A V P A D S G L
	C C C C C C C	
433	GAT GCC CTG TCC ATA GGT ACA GAC TCG TCC ACG GAG ACC CTC ATT ACT	D A L S I G T D S S T E T L I T
	G C C C A C G A C	
481	CTG CTA GAG CCT GAG GGT CCC GAG GAC ATA GCG GTT CTT GAG CTG CAA	L L E P E G P E D I A V L E L Q
	C C C G G G C	
529	CCC CTG GAC CGT CCA ACT TGG CAA GTA AGC AAT GCT GTT CAT CAG TCC	P L D R P T W Q V S N A V H Q S
	C C C C C C C	
577	TCT GCA TAC CAC GCC CCT CTG CAG CTG CAA TCG TCC ATT GCA GAA ACA	S A Y H A P L Q Q L Q S S I A E T

Figure 1B cont'd

625	TCT	GGT	TTA	GAA	AAT	ATT	TTT	GTA	GGA	GGC	TCG	GGT	TTA	GGG	GAT	ACA	(AvaI)
	S	G	L	E	N	I	F	V	G	G	S	G	L	G	D	T	
	C	C	G		C	G		C		C		C	C	C	C	C	
673	GGA	GGA	GAA	AAC	ATT	GAA	CTG	ACA	TAC	TTC	GGG	TCC	CCA	CGA	ACA	AGC	
	G	G	E	N	I	E	L	T	Y	F	G	S	P	R	T	S	
	C		TCC	C		C	G	C	C	C		C	C	G			
721	ACG	CCC	CGC	AGT	ATT	GCC	TCT	AAA	TCA	CGT	GGC	ATT	TTA	AAC	TGG	TTC	
	T	P	R	S	I	A	S	K	S	R	G	I	L	N	W	F	
	C	G			C			C		C			C			C	
769	AGT	AAA	CGG	TAC	TAC	ACA	CAG	GTG	CCC	ACG	GAA	GAT	CCT	GAA	GTG	TTT	(BamI)
	S	K	R	Y	Y	T	Q	V	P	T	E	D	P	E	V	F	
	C		G	C	C	C		C		C	G	C	G	C	C		
817	TCA	TCC	CAA	ACA	TTT	GCA	AAC	CCA	CTG	TAT	GAA	GCA	GAA	CCA	GCT	GTG	
	S	S	Q	T	F	A	N	P	L	Y	E	A	E	P	A	V	
	G		C		C	C	C	G	C	G	TCC		G	C	G		
865	CTT	AAG	GGA	CCT	AGT	GGA	CGT	GTT	GGA	CTC	AGT	CAG	GTT	TAT	AAA	CCT	
	L	K	G	P	S	G	R	V	G	L	S	Q	V	Y	K	P	
	C	G	C					C			C		C		G		
913	GAT	ACA	CTT	ACA	ACA	CGT	AGC	GGG	ACA	GAG	GTG	GGA	CCA	CAG	CTA	CAT	(BsaAI)
	D	T	L	T	T	R	S	G	T	E	V	G	P	Q	L	H	

Figure 1B cont'd

	G	C	C	TCC	C	C	G	G	T							
961	GTC	AGG	TAC	TCA	TTG	AGT	ACT	ATA	CAT	GAA	GAT	GTA	GAA	GCA	ATC	CCC
	V	R	Y	S	L	S	T	I	H	E	D	V	E	A	I	P
		C	G		G	C	C	C	C	G	C		G		C	
1009	TAC	ACA	GTT	GAT	GAA	AAT	ACA	CAG	GGA	CTT	GCA	TTC	GTA	CCC	TTG	CAT
	Y	T	V	D	E	N	T	Q	G	L	A	F	V	P	L	H
		G		G	C	C	C		C	G	C	C		C		
1057	GAA	GAG	CAA	GCA	GGT	TTT	GAG	GAG	ATA	<u>GAA</u>	TTA	GAT	GAT	TTT	AGT	GAG
	E	E	Q	A	G	F	E	E	I	E	L	D	D	F	S	E
		C	C	C		G	C			C	C	C	C	G	C	C
1105	ACA	CAT	AGA	CTG	CTA	CCT	CAG	AAC	ACC	TCT	TCT	ACA	CCT	GTT	GGT	AGT
	T	H	R	L	L	P	Q	N	T	S	S	T	P	V	G	S
		C	G	C			G	C	T	C		G	C	C	C	
1153	GGT	GTA	CGA	AGA	AGC	CTC	ATT	CCA	ACT	CGA	GAA	TTT	AGT	GCA	ACA	CGG
	G	V	R	R	S	L	I	P	T	Q	E	F	S	A	T	R
			C	C	G		C		C	C		C		C		
1201	CCT	ACA	GGT	GTT	GTA	ACC	TAT	GGC	TCA	CCT	GAC	ACT	TAC	TCT	<u>GCT</u>	AGC
	P	T	G	V	V	T	Y	G	S	P	D	T	Y	S	A	S
		C	G	C							C	G	G		C	
1249	CCA	GTT	ACT	GAC	CCT	GAT	TCT	ACC	TCT	CCT	AGT	CTA	GTT	ATC	GAT	GAC
	P	V	T	D	P	D	S	T	S	P	S	L	V	I	D	D

Figure 1B cont'd

[illegible]

Figure 1C

	T	A	G	A	A	T	A	G	T	A	A					
1	ATG	AGC	AAG	GGC	GAG	GAA	CTG	TTC	ACT	GGC	GTG	GTC	CCA	ATT	CTC	GTG
	M	S	K	G	E	E	L	F	T	G	V	V	P	I	L	V
	A			G										T	G	A
49	GAA	CTG	GAT	GGC	GAT	GTG	AAT	GGG	CAC	AAA	TTT	TCT	GTC	AGC	GGA	GAG
	E	L	D	G	D	V	N	G	H	K	F	S	V	S	G	E
	G		G		A		T	G	A	A	A	A		T	A	
97	GGT	GAA	GGT	GAT	GCC	ACA	TAC	GGA	AAG	CTC	ACC	CTG	AAA	TTC	ATC	TGC
	G	E	G	D	A	T	Y	G	K	L	T	L	K	F	I	C
	A	A	G	A	A					T		A	G	A	A	T
145	ACC	ACT	GGA	AAG	CTC	CCT	GTG	CCA	TGG	CCA	ACA	CTG	GTC	ACT	ACC	TTC
	T	T	G	K	L	P	V	P	W	P	T	L	V	T	T	F
	AG		G		A			AGT		T	T	T			A	A
193	TCT	TAT	GGC	GTG	CAG	TGC	TTT	TCC	AGA	TAC	CCA	GAC	CAT	ATG	AAG	CAG
	S	Y	G	V	Q	C	F	S	R	Y	P	D	H	M	K	Q
	T			T	A	T	A				G			A	A	
241	CAT	GAC	TTT	TTC	AAG	AGC	GCC	ATG	CCC	GAG	GGC	TAT	GTG	CAG	GAG	AGA
	H	D	F	F	K	S	A	M	P	E	G	Y	V	Q	E	R
	A	A		T			T		T	T	A	A	A	A		G
289	ACC	ATC	TTT	TTC	AAA	GAT	GAC	GGG	AAC	TAC	AAG	ACC	CGC	GCT	GAA	GTC
	T	I	F	F	K	D	D	G	N	Y	K	T	R	A	E	V

Figure 1C cont'd

	A	T	G	T	A	A	A	A	C	A	G	A					
337	AAG	TTC	GAA	GGT	GAC	ACC	CTG	GTG	AAT	AGA	ATC	<u>GAG</u>	CTG	AAG	GGC	ATT	(SacI)
	K	F	E	G	D	T	L	V	N	R	I	E	L	K	G	I	
	T		A	A		G	T	A	A	G	T	A	A		T	T	
385	GAC	TTT	AAG	GAG	GAT	GGA	AAC	ATT	CTC	GGC	CAC	AAG	CTG	GAA	TAC	AAC	
	D	F	K	E	D	G	N	I	L	G	H	K	L	E	Y	N	
	T	AGT	T				T	A		A	T	A		A		G	
433	TAT	AAC	TCC	CAC	AAT	GTG	TAC	ATC	ATG	GCC	GAC	AAG	CAA	AAG	AAT	GGC	
	Y	N	S	H	N	V	Y	I	M	A	D	K	Q	K	N	G	
	A	A	G	T	T	A	A	T	AGA	CAT	A	A					
481	ATC	AAG	GTC	AAC	TTC	AAG	ATC	AGA	CAC	AAC	ATT	GAG	GAT	<u>GGA</u>	<u>TCC</u>	GTG	BamHI)
	I	K	V	N	F	K	I	R	H	N	I	E	D	G	S	V	
	A	A	A	T				A	T	A	T	A	G	T	G		
529	CAG	CTG	GCC	GAC	CAT	TAT	CAA	CAG	AAC	ACT	CCA	ATC	GGC	GAC	GGC	CCT	
	Q	L	A	D	H	Y	Q	Q	N	T	P	I	G	D	G	P	
	A	A	A	T	T			T	A	AGT	A	A	AGT	A	A	AG	
577	GTG	CTC	CTC	CCA	GAC	AAC	CAT	TAC	CTG	TCC	ACC	CAG	TCT	GCC	CTG	TCT	
	V	L	L	P	D	N	H	Y	L	S	T	Q	S	A	L	S	
		T	T		A			T	T		G	A	C				
625	AAA	GAT	CCC	AAC	GAA	AAG	AGA	GAC	CAC	ATG	GTC	CTG	<u>CTG</u>	<u>GAG</u>	TTT	GTG	(XhoI)
	K	D	P	N	E	K	R	D	H	M	V	L	L	E	F	V	

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Figure 1C cont'd

A	A	A	A	A	T	A	A	T	A						
673	ACC	GCT	GCT	GGG	ATC	ACA	CAT	GGC	ATG	GAC	GAG	CTG	TAC	AAG	TGA
	T	A	A	G	I	T	H	G	M	D	E	L	Y	K	-

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Wt BPV1L1 HB BPV1 L1

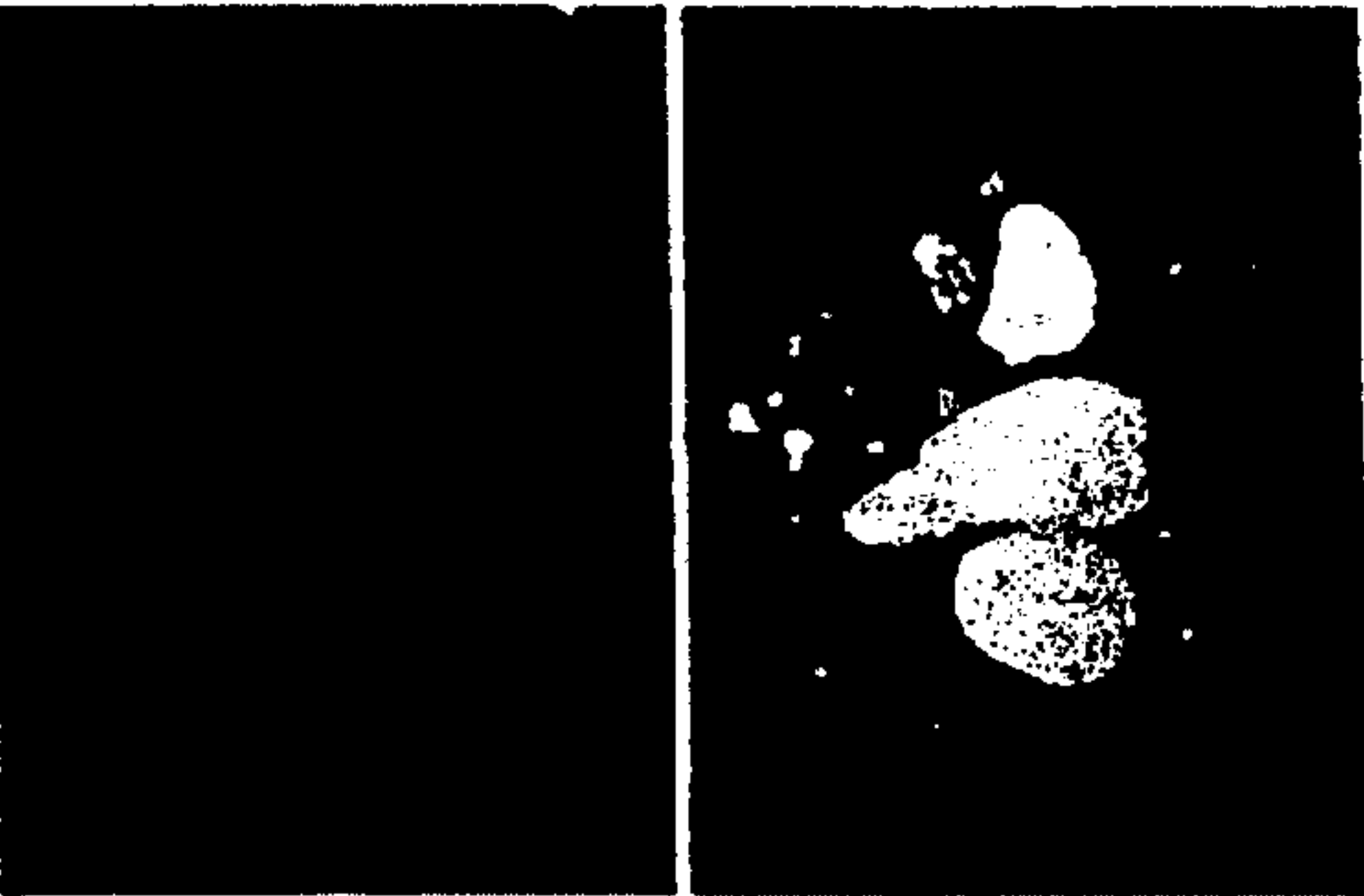


FIG. 2A

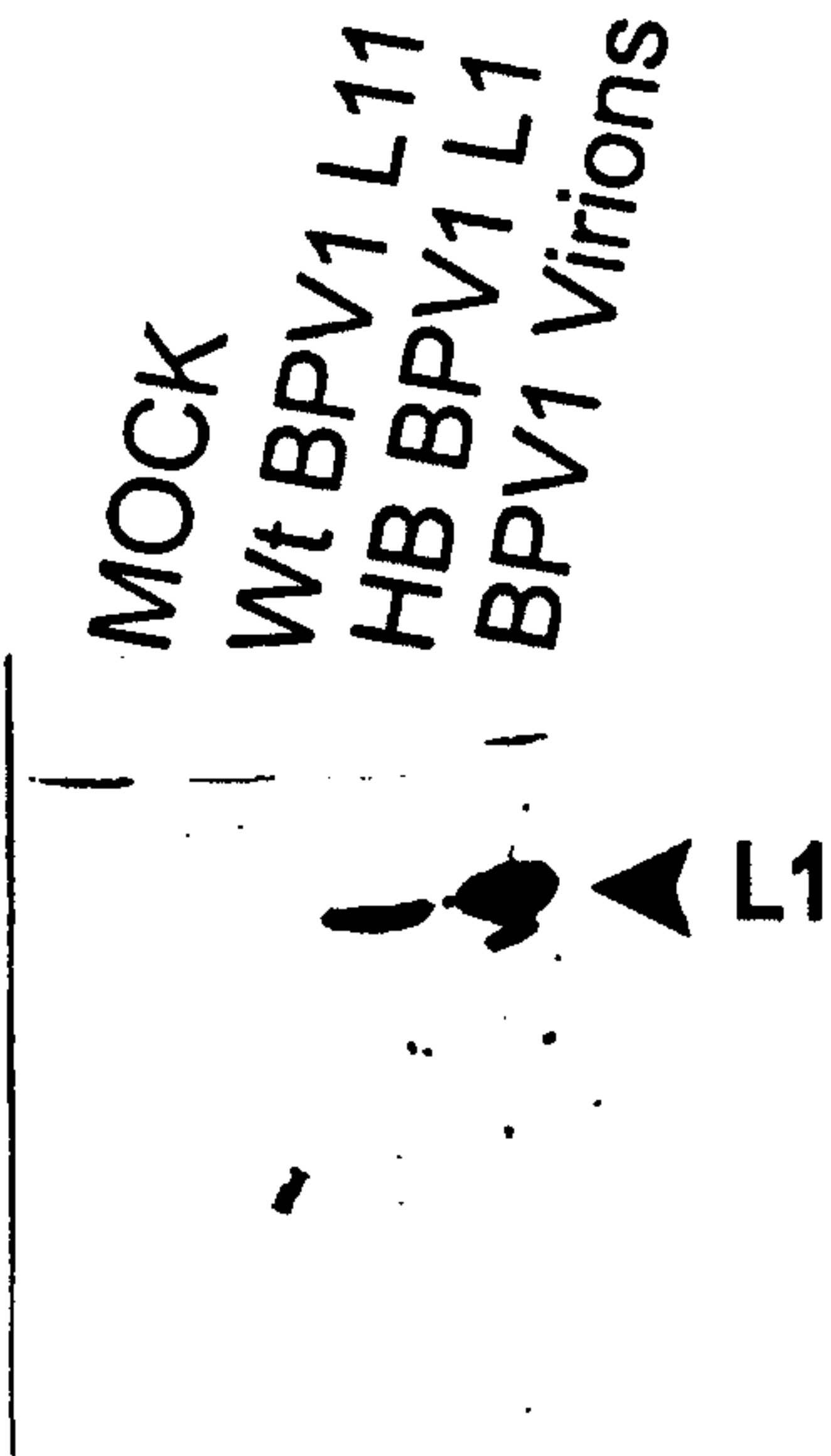


FIG. 2B

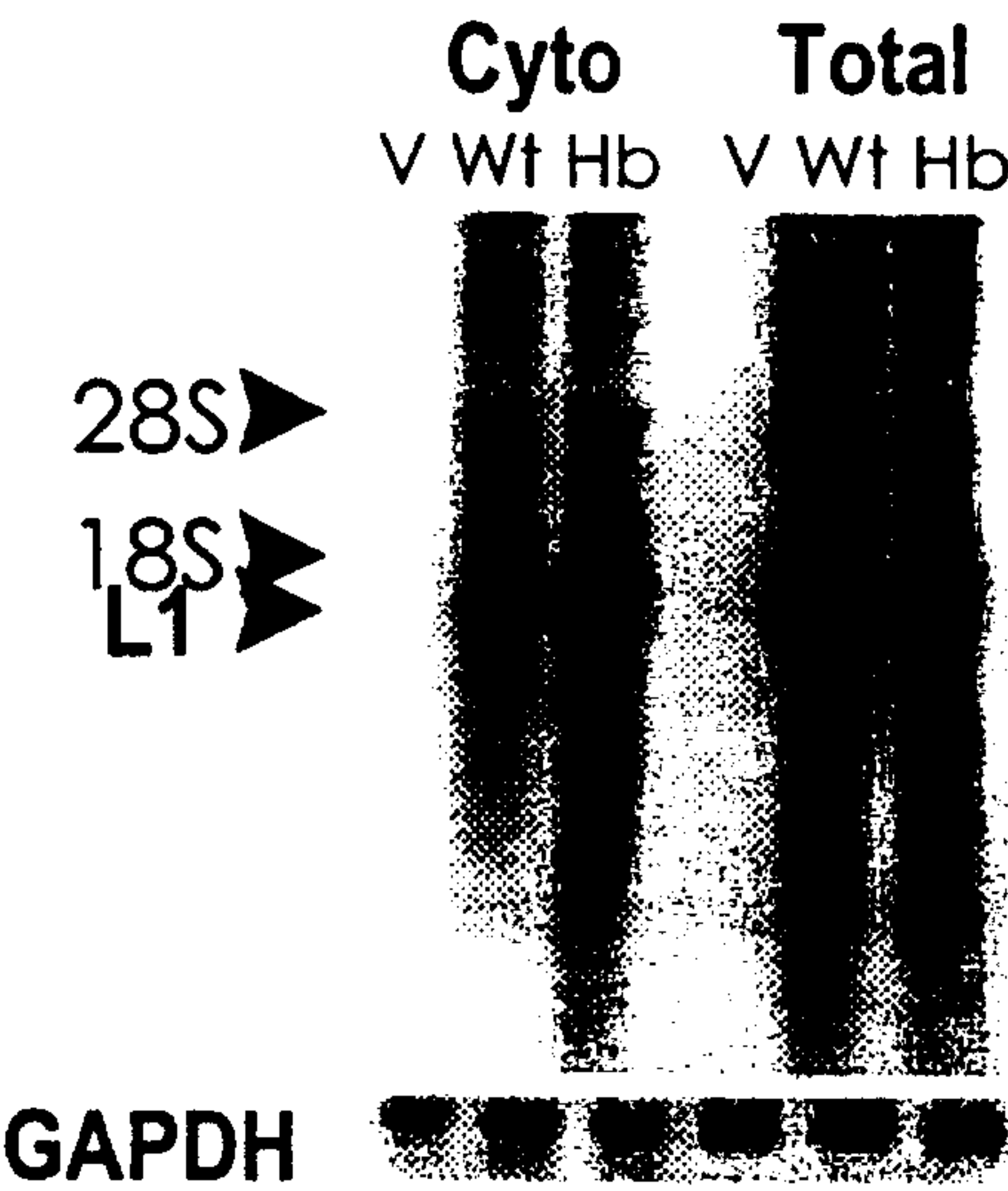


FIG. 2C

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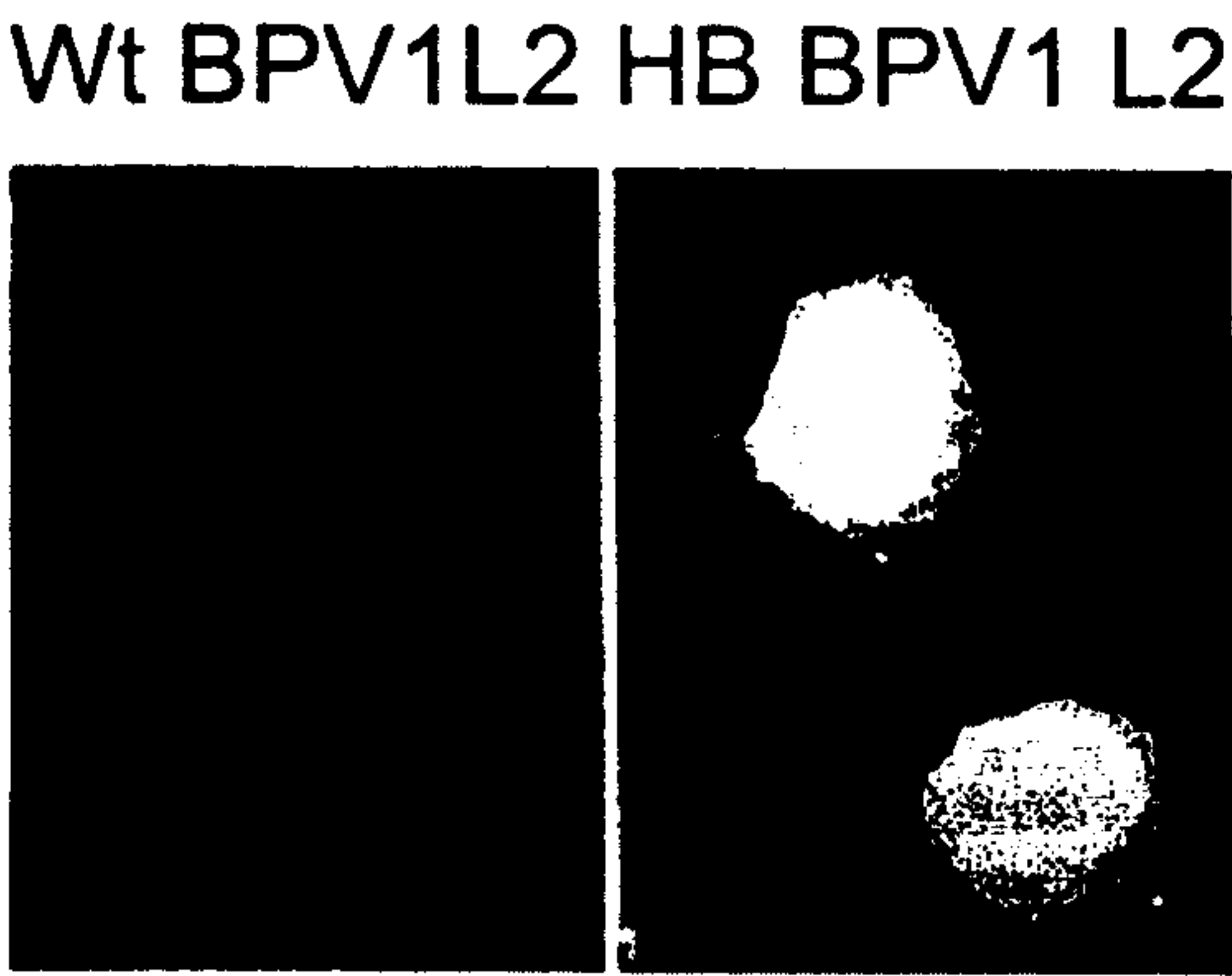


FIG. 3A

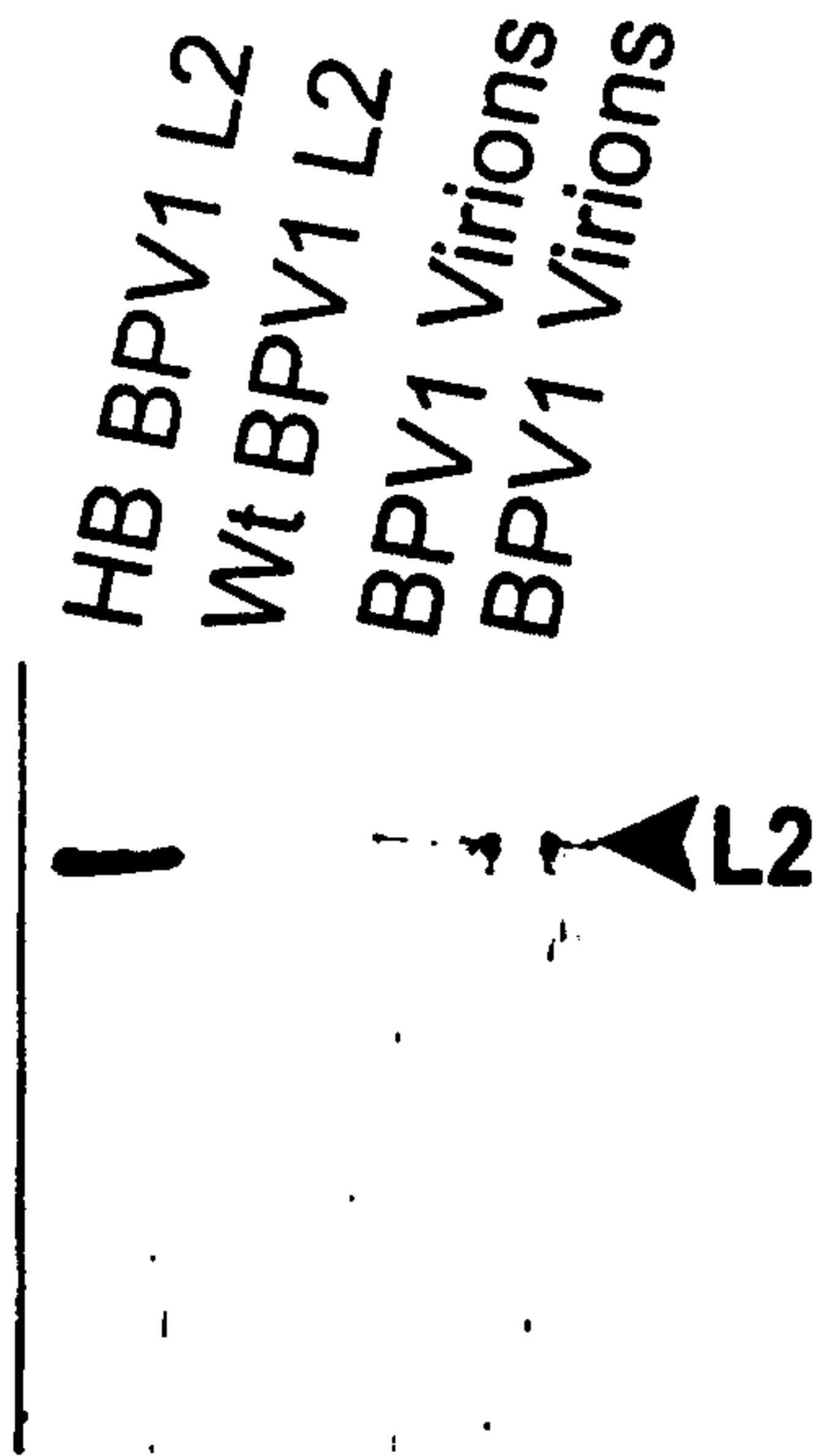


FIG. 3B

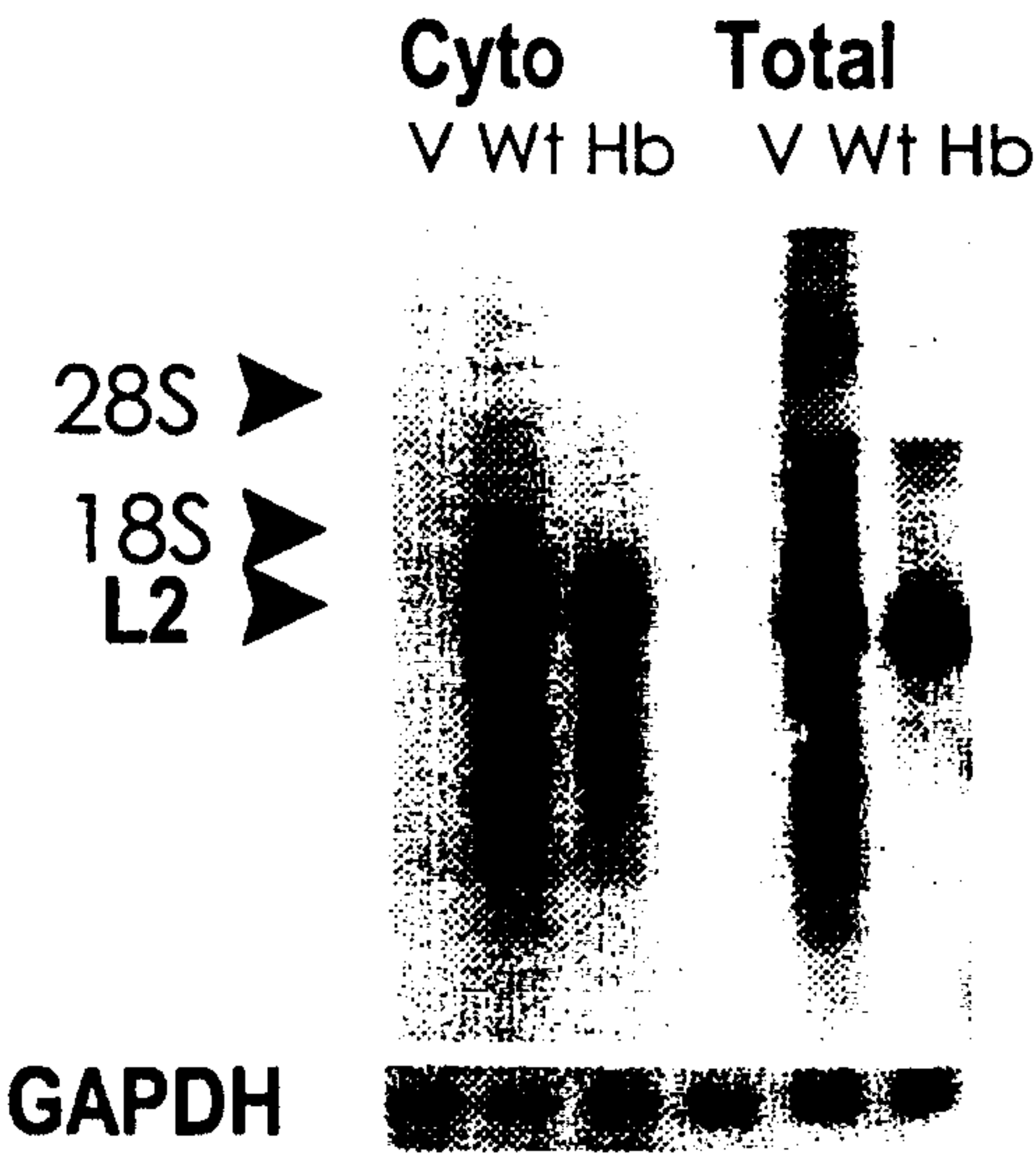


FIG. 3C

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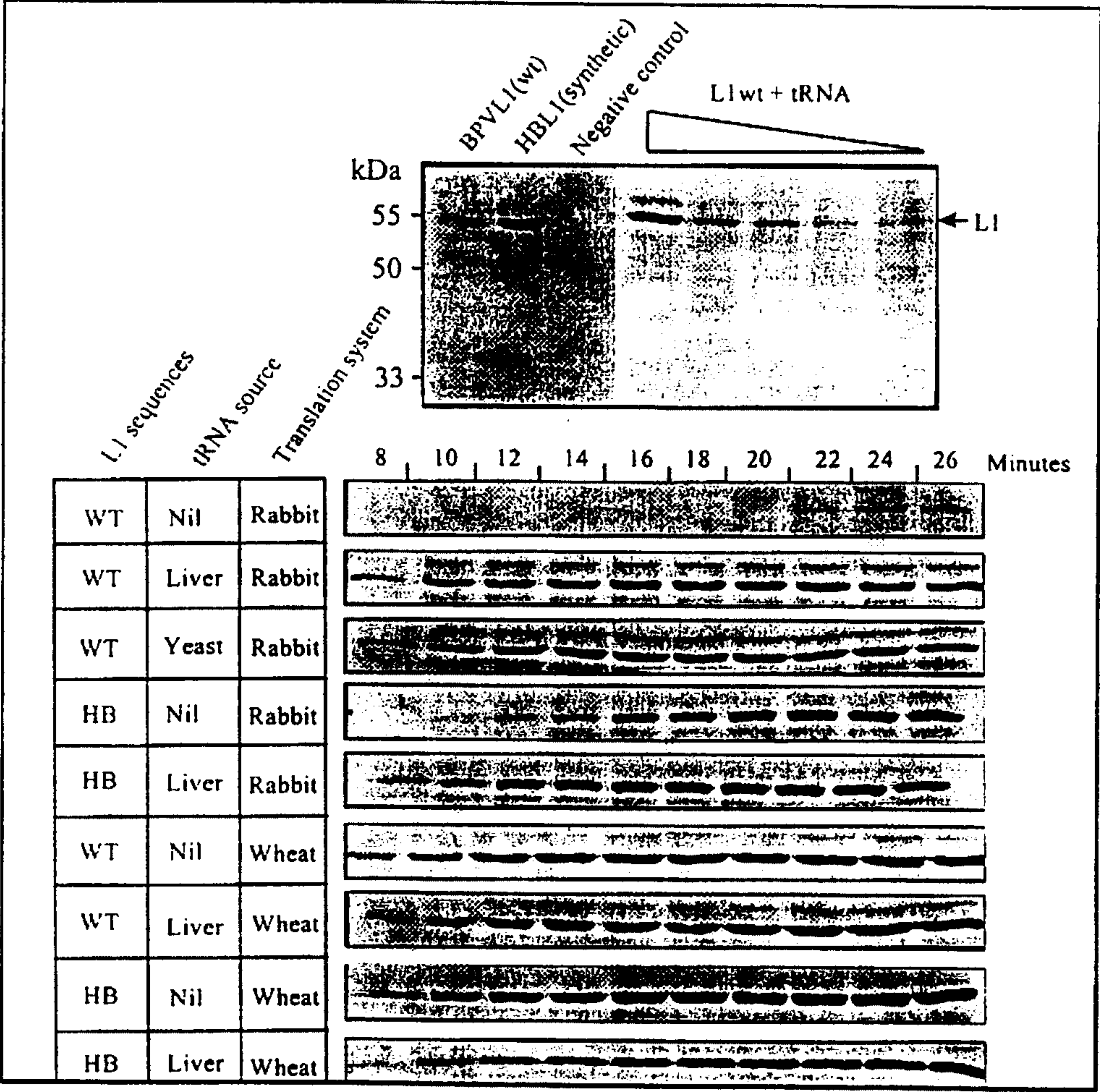
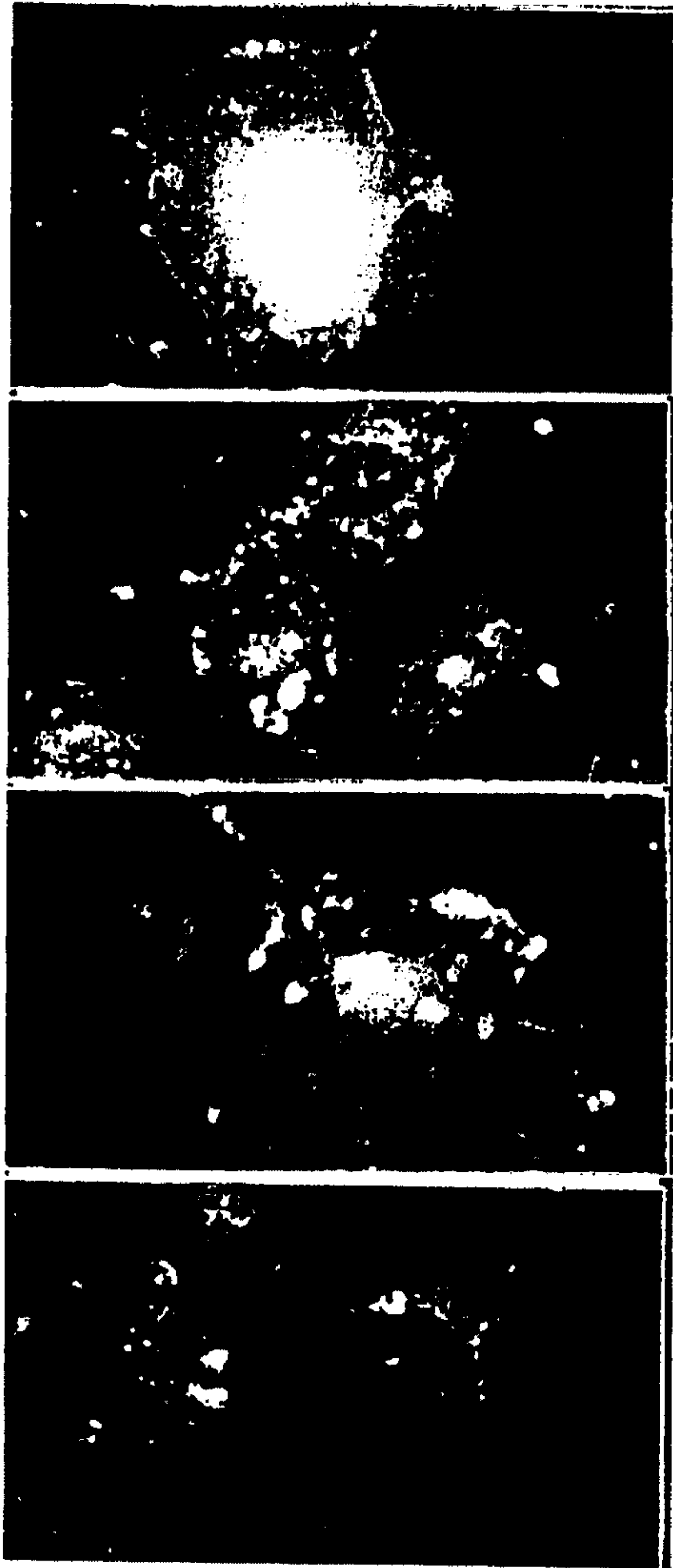


FIG. 4

pCICR1	E6	E7	E1	E2	L2(HB)	SV40
pCICR2	E6	E7	E1	E2	L2(wt)	SV40
pCICR3	E6	E7	E1	E2	L2(HB)	

FIG. 5A



Mock pCICR3 pCICR2 pCICR1

FIG. 5B

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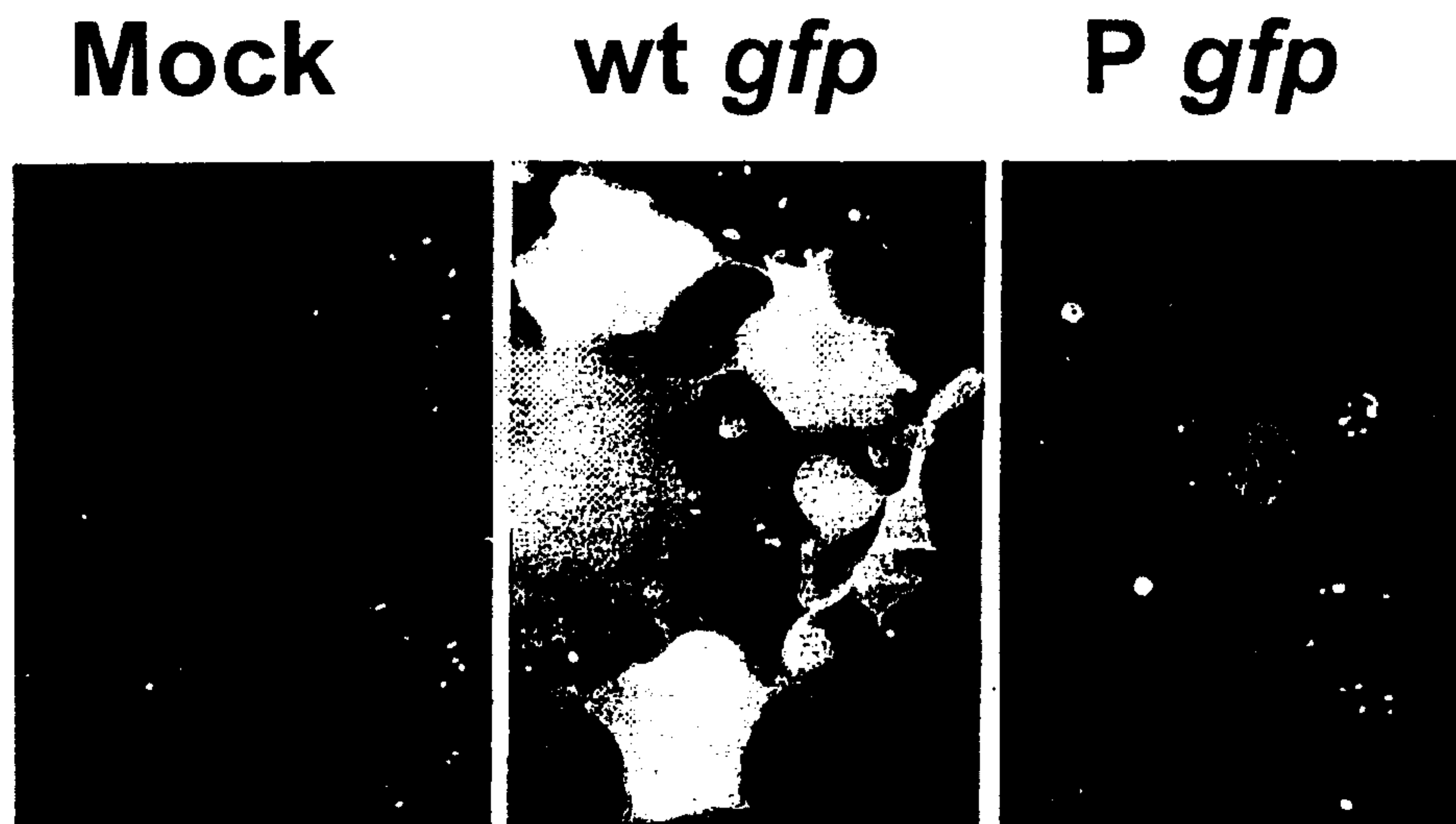


FIG. 6A

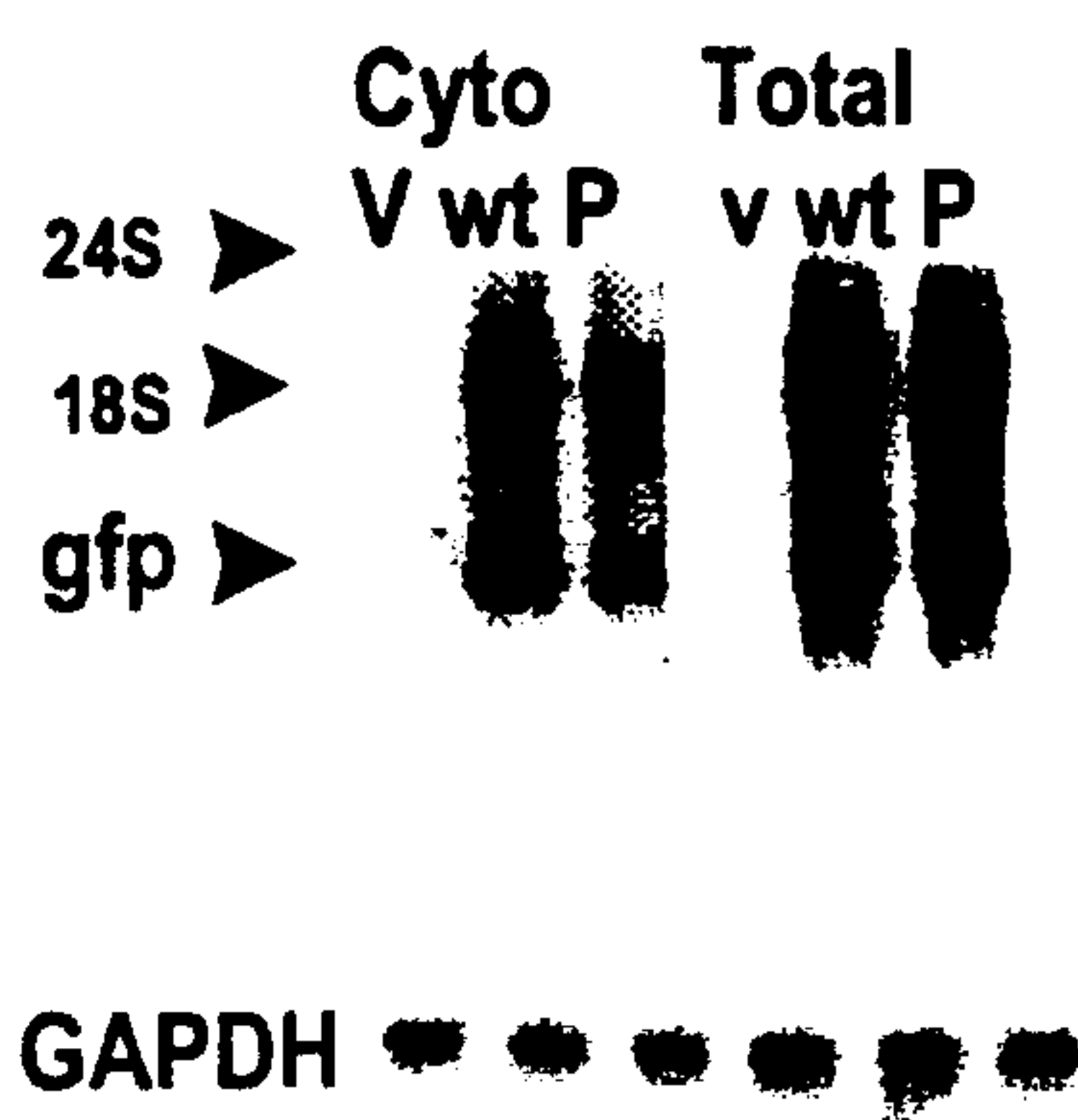


FIG. 6B

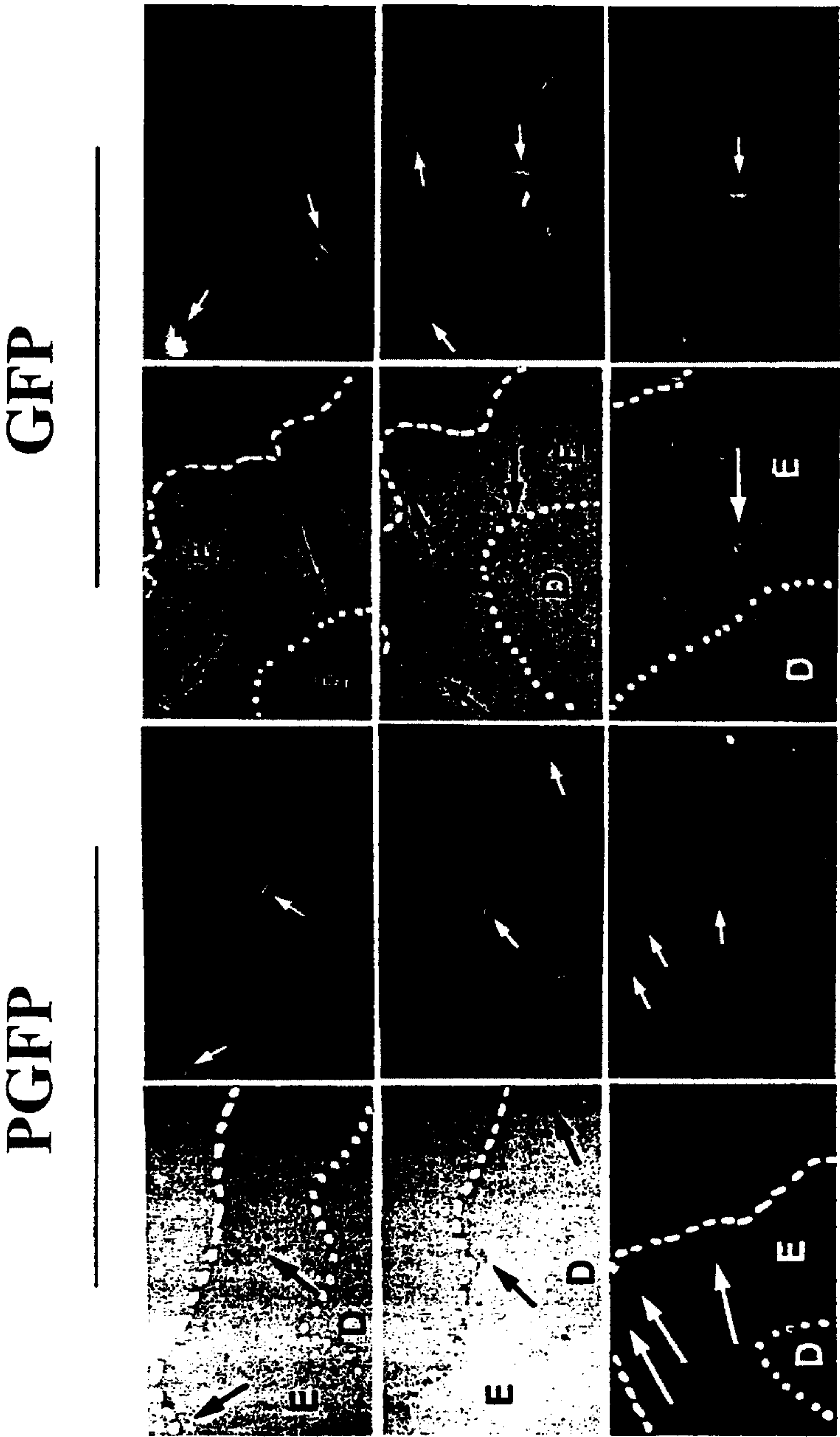


FIG. 7