PROMOTERS FOR ENHANCING EXPRESSION IN POXVIRUSES

FIELD OF THE INVENTION

[001] The present invention relates to one or more novel promoters of protein expression in poxviruses, especially avipoxviruses such as fowlpoxvirus and canarypoxvirus. The invention further relates to polynucleotides comprising said promoter, in particular, polynucleotides comprising said promoter and a nucleic acid to be expressed; vectors comprising the same; host cells comprising the above constructs; and compositions comprising any of the above. Additionally the invention relates to one or more novel polypeptides operably linked to the one or more promoters. More particularly, the one or more novel polypeptides are related to the Brachury protein.

BACKGROUND OF THE INVENTION

[002] Recombinant poxviruses have been used as vaccines for infectious organisms and, more recently, for tumors. Mastrangelo et al. J Clin Invest. 2000;105(8):1031–1034. Two of these poxvirus groups, avipoxvirus and orthopoxvirus, have been shown to be effective at battling tumors and have been involved with potential cancer treatments. *Id.*

[003] One exemplary avipoxvirus species, fowlpox, has been shown to be a safe vehicle for human administrations as fowlpox virus enters mammalian cells and expresses proteins, but replicates abortively. Skinner et al. Expert Rev Vaccines. 2005 Feb;4(1):63-76. Additionally, the use of fowlpox virus as a vehicle for expression is being evaluated in numerous clinical trials of vaccines against cancer, malaria, tuberculosis, AIDS, and EBOLA. *Id.*

[004] Recombinant poxviruses, such as fowlpox, has been used to express a wide range of inserted genes, including several infectious disease and tumor associated genes such as p97,

HER-2/neu, p53 and ETA (Paoletti, et al., 1993). One exemplary tumor antigen that is recently being studied is Brachyury (also known as "T").

[005] Brachyury was identified in mice as a dominant short tail mutant that is also a recessive lethal; homozygous T/T embryos die in mid-gestation due to a failure of posterior mesoderm formation (Chesley, J. Exp. Zool., 70: 429-459, 1935). The murine Brachyury gene has been cloned (Herrmann et al., Nature (Lond.), 343: 617-622, 1990), as well as the homologs in other species, such as humans. The expression of the human homologue of the mouse Brachyury was detected by RT-PCR in the notochord remnant, the nucleus pulposus, of human abortuses at 14-15 weeks gestation (Edwards et al., Genome Res., 6: 226-233, 1996).

[006] Brachyury has generally proved to be a valuable marker for recognition of mesodermal differentiation (Herrmann et al., Trends Genet., 10: 280-286, 1994). For example, apart from expression in embryos themselves, Brachyury has been reported to be activated during the differentiation of certain murine EC and ES cell lines differentiating along mesodermal lineages in vitro (see, for example, Bain et al., Biochem. Biophys. Res. Commun., 223: 691-694, 1996). In humans, Brachyury has been shown to be expressed in teratocarcinomas (Gokhele et al., Cell Growth and Differentiation 11:157-62, 2000), chordomas (Vujovic et al., J. Pathol. 2: 157-65, 2006) and hemagioblastomas (Glasker et al., Cancer Res. 66: 4167-4172, 2006).

[007] More recently, it has been described that poxviruses expressing Brachyury can be effective as an active immunotherapeutic against tumors. (*See,* WO 2014/043535).

[008] There is clearly a substantial unmet medical need for improving infectious disease and cancer treatments, including active immunotherapies and vaccines. Based on the above, a

need in the art exists for improving expression of antigens, like Brachyury, used in active immunotherapies. The present invention fulfills this need.

BRIEF SUMMARY OF THE INVENTION

[009] The present invention provides one or more promoters, nucleic acids, expression cassettes, recombinant peptides, and recombinant poxviruses associated with enhancements in expression of coding sequences and antigens incorporated as part of poxviruses

[010] In one aspect of the invention, there is an expression cassette comprising:

a. a promoter comprising a nucleic sequence having at least 70% identity to any one of SEQ ID NOs: 1-10, and 77; and
b. a coding sequence operably linked to the promoter;

wherein expression of the coding sequence is controlled by the promoter.

[011] In further aspects of the present invention, the expression cassette can be incorporated as part of a vector such as a virus or plasmid, for enhanced expression of the coding sequence therein. Preferably, the expression cassette is part of a poxvirus, such as but not limited to, orthopoxvirus and avipoxvirus. More preferably, the expression cassette is an avipoxvirus such as fowlpoxvirus. In still further aspects, the expression cassette is not an expression cassette that naturally occurs in the genome of a poxvirus.

[012] In additional aspects, there are one or more promoters comprising or consisting of a) a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-10, b) a subsequence of any one of SEQ ID NOs: 1-10, and 77, or c) a derivative sequence of any one of SEQ ID NOs: 1-10, and 77, wherein the derivative has one or more substitutions, deletions, and/or insertions, and wherein the derivative sequence is active as a poxvirus promoter and/or active in a poxvirus infected cell.

[013] In still additional aspects, the present invention includes one or more nucleic acid sequences encoding one or more novel Brachyury proteins selected from the group consisting of: SEQ ID NOs: 18-19, 22-23, 26-27, 30-31, 34-35, 38-39, 42-43, 46-47, 50-51, 54-55, 58-59, 62-63, 66-67, 70, and 71. In yet further aspects, the present invention includes one more novel nucleic acid sequences selected from the group consisting of: 16-17, 20-21, 24-25, 28-29, 32-33, 36-37, 40-41, 44-45, 48-49, 52-53, 56-57, 60-61, 64-65, 68, and 69.

[014] In still further aspects, the present invention includes an expression cassette comprising:

a. a promoter comprising a nucleic acid sequence having at least 70% identity to any one of SEQ ID NOs: 1-10, and 77; and
b. a coding sequence operably linked to the promoter, wherein the coding sequences includes either i) a nucleic acid encoding a Brachyury protein selected from the group consisting of: SEQ ID NOs: 11, 13, 18-19, 22-23, 26-27, 30-31, 34-35, 38-39, 42-43, 46-47, 50-51, 54-55, 58-59, 62-63, 66-67, 70, and 71 or ii) comprises or consists of a nucleic acid having at least 70% identity to any one of the nucleic acids selected from the group consisting of: SEQ ID NOs12, 14-17, 20-21, 24-25, 28-29, 32-33, 36-37, 40-41, 44-45, 48-49, 52-53, 56-57, 60-61, 64-65, 68, and 69;

wherein expression of the coding sequence is controlled by the promoter.

[015] Additional objects and advantages of the invention will be set forth in part in the description which follows, and in part will be obvious from the description or may be learned by practice of the invention. The objects and advantages of the invention will be realized and attained by means of the elements and combinations particularly pointed out in the appended claims.

[016] It is to be understood that both the foregoing general description and the following detailed description are exemplary and explanatory only and are not restrictive of the invention, as claimed.

BRIEF DESCRIPTION OF THE DRAWINGS

[017] Figure 1 illustrates expression of the Brachyury protein in human dendritic cells (DCs) infected with the non-recombinant virus FPV-WT, or recombinant viruses FPV-mBN343A, FPV-mBN344A, or FPV-mBN345A . A western blot analysis was performed using rabbit monoclonal anti-Brachyury antibody as detailed in Example 1.

[018] Figure 2 illustrates expression of the Brachyury protein in human dendritic cells (DCs) infected with non-recombinant viruses MVA-WT or FPV-WT or recombinant viruses MVA-Brachyury-TRICOM, FPV-mBN249B, FPV-mBN281A clone 32, FPV-mBN281A clone 35, FPV-mBN343A, FPV-mBN344A, FPV-mBN345A, FPV-mBN354A, or FPV-mBN355A. A western blot analysis was performed using rabbit monoclonal anti-Brachyury antibody as detailed in Example 2.

[019] Figure 3 depicts the relative expression of Brachyury protein compared to GAPDH from western blot analysis of human dendritic cells (DCs) infected with non-recombinant viruses MVA-WT or FPV-WT or recombinant viruses MVA-Brachyury-TRICOM, FPV-mBN249B, FPV-mBN281A clone 32, FPV-mBN281A clone 35, FPV-mBN343A, FPV-mBN344A, FPV-mBN345A, FPV-mBN354A, or FPV-mBN355A, as detailed in Example 2.

[020] Figure 4 illustrates expression of Brachyury and TRICOM proteins in CMMT cells (a rhesus macaque mammary tumor cell line) infected with the recombinant viruses MVA-Brachyury-TRICOM, FPV-mBN249B, FPV-mBN343A, or FPV-mBN345A assessed by flow

cytometry using fluorescently labeled antibodies specific for each protein, as described in Example 3.

[021] Figure 5 depicts median expression levels of Brachyury protein in CMMT cells (a rhesus macaque mammary tumor cell line) infected with the recombinant viruses MVA-Brachyury-TRICOM, FPV-mBN249B, FPV-mBN343A, or FPV-mBN345A assessed by flow cytometry, as described in Example 3.

[022] Figure 6 depicts expression of Brachyury and TRICOM proteins in CMMT cells (a rhesus macaque mammary tumor cell line) infected with a recombinant virus FPV-mBN345B assessed by flow cytometry, as described in Example 4.

DETAILED DESCRIPTION OF THE INVENTION

[023] The invention is based on the surprising determination that the promoter sequences as set out in SEQ ID NOs:1-10, and 77 enhance expression of the tumor antigen Brachyury. Shown in Figures 1-6 and described in more detail herein, expression of Brachyury antigen is enhanced when using promoters of present invention. Expression is further enhanced when the promoters and Brachyury antigen are used as part of a recombinant poxvirus.

[024] In at least one aspect, the various embodiments of the present disclosure were created as a result of insufficient expression levels of Brachyury protein using known Vaccinia promoters, such as PrS and Vaccinia virus 40k (VV-40K). In trying to enhance Brachyury expression levels, the present inventors analyzed various vaccinia promoters and associated proteins (e.g., VV-40k, I3, etc.) and any possible homologues in FPV. The inventors realized that some FPV homologous sequences were previously discovered. *See, e.g.*, Zantinge, J Gen Virol. 1996 Apr;77 (Pt 4):603-14 and Gene FPV 088 at NCBI Reference Sequence: NP_039051.1, Afonso,C.L et al., J. Virol. 74 (8), 3815-3831 (2000).

[025] In an initial attempt to enhance Brachyury expression, a possible promoter region of Gene FPV 088 at NCBI Reference Sequence: NP_039051.1 was constructed with Brachyury by the inventors and tested yielding undesired results (*see, e.g.,* Figures 1 and 2 at mBN344A) promoter. The inventors created a subsequent promoter with an addition of nucleotides from the ORF of Gene FPV 088, which similarly yielded undesired results. (*see, e.g.,* Figures 1 and 2 at mBN354A). Further constructs were created by the present inventors with yet additional nucleotides from the ORF of Gene FPV 088, which, as described and illustrated herein, enhance expression of the tumor antigen Brachyury.

[026] Thus, in various embodiments, the present invention is directed to one or more nucleic acid sequences, one or more promoters comprising the nucleic acids sequences, one or more expression cassettes comprising the nucleic acids, one or more peptides and/or peptide sequences for enhancing/expression of coding sequences and/or nucleic acids in expression vectors such as, but not limited to, plasmids, recombinant virus and so forth. In further embodiments, the present invention is directed to one or more recombinant poxviruses comprising one or more of the nucleic acid sequences, promoters, expression cassettes, and/or peptides and/or peptide sequences described herein.

[027] Additionally, in various embodiments of the invention, there are one or more nucleic acids sequences encoding brachyury polypeptides. In one embodiment, the one or more nucleic acids encoding a brachyury polypeptide are selected from the group consisting of: SEQ ID NOs: 11, 13, 18-19, 22-23, 26-27, 30-31, 34-35, 38-39, 42-43, 46-47, 50-51, 54-55, 58-59, 62-63, 66-67, 70, and 71. The nucleotide sequences encoding the brachyury polypeptides according to the present invention are selected from the group consisting of: SEQ ID NOs: 12,

14-17, 20-21, 24-25, 28-29, 32-33, 36-37, 40-41, 44-45, 48-49, 52-53, 56-57, 60-61, 64-65, 68, and 69.

Definitions

[028] It must be noted that, as used herein, the singular forms "a", "an", and "the", include plural references unless the context clearly indicates otherwise. Thus, for example, reference to "an epitope" includes one or more of epitopes and reference to "the method" includes reference to equivalent steps and methods known to those of ordinary skill in the art that could be modified or substituted for the methods described herein.

[029] Unless otherwise indicated, the term "at least" preceding a series of elements is to be understood to refer to every element in the series. Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the present invention.

[030] Throughout this specification and the claims which follow, unless the context requires otherwise, the word "comprise", and variations such as "comprises" and "comprising", will be understood to imply the inclusion of a stated integer or step or group of integers or steps but not the exclusion of any other integer or step or group of integer or step. When used herein the term "comprising" can be substituted with the term "containing" or "including" or sometimes when used herein with the term "having". Any of the aforementioned terms (comprising, containing, including, having), though less preferred, whenever used herein in the context of an aspect or embodiment of the present invention can be substituted with the term "consisting of. When used herein "consisting of excludes any element, step, or ingredient not specified in the

claim element. When used herein, "consisting essentially of" does not exclude materials or steps that do not materially affect the basic and novel characteristics of the claim.

[031] As used herein, the conjunctive term "and/or" between multiple recited elements is understood as encompassing both individual and combined options. For instance, where two elements are conjoined by "and/or", a first option refers to the applicability of the first element without the second. A second option refers to the applicability of the second element without the first. A third option refers to the applicability of the first and second elements together. Any one of these options is understood to fall within the meaning, and therefore satisfy the requirement of the term "and/or" as used herein. Concurrent applicability of more than one of the options is also understood to fall within the meaning, and therefore satisfy the requirement of the term "and/or."

[032] As used herein, the term “promoter” denotes a regulatory region of nucleic acid, usually DNA, located upstream of the sequence of a nucleic acid to be expressed, which contains specific DNA sequence elements, that are recognized and bound e.g. by protein transcription factors and polymerases responsible for synthesizing the RNA from the coding region of the gene being promoted. As promoters are typically immediately adjacent to the gene in question, positions in the promoter are designated relative to the transcriptional start site, where transcription of DNA begins for a particular gene (i.e., positions upstream are negative numbers counting back from -1, for example -100 is a position 100 base pairs upstream). Thus, the promoter sequence may comprise nucleotides until position −1. However, nucleotides from position +1 are not part of the promoter, i.e. in this regard it has to be noted that the translation initiation codon (ATG or AUG) is not part of the promoter. Thus, SEQ ID NOs: 1-10, and 77 are polynucleotides comprising promoters of the invention.

[033] As used herein, the term "enhancing" or "enhanced" when used with respect to expression levels of a coding sequence, nucleic acid, protein, and/or antigen, refers to an increase in expression of a coding sequence, nucleic acid, protein, and/or antigen when associated with and/or as part of one or more of the promoters, expression cassettes, nucleic acids, proteins, and/or vectors of the present invention relative to expression levels of a coding sequence, nucleic acids, protein, and/or antigen when associated with and/or as part of one or more of the promoters know in the art, such as PrS or VV-40k.

[034] As used herein, a nucleotide sequence having "essentially the same expression characteristics" as the nucleotide sequence set out in SEQ ID NO s: 1-10, and 77 will exhibit at least 70%, preferably at least 80%, even more preferably at least 90% of the promoter activity of SEQ ID NO s: 1-10, and 77, as measured by amount of recombinant protein produced. Whether or not a promoter sequence in question has "essentially the same expression characteristics" as any of SEQ ID NO s: 1-10, and 77 may be readily determined by one of ordinary skill in the art using the methods set forth in Examples 1-4 of the present application. The promoters according to the present invention are preferably active as poxvirus promoters, preferably avipoxvirus or active as promoters in poxvirus infected cells, preferably avipoxvirus infected cells. The avipoxvirus is preferably Fowlpox virus. "Active as pox virus promoter" means that the promoter is able to direct the expression of a gene to which it is operably linked in a pox virus after infection of cells with said virus. The cells are preferably cells that allow late and/or early and/or early/late expression of the poxvirus. "A promoter active in poxvirus infected cells" includes also the situation in which the promoter is not part of a poxvirus genome, e.g. part of a plasmid or linear polynucleotide or a non-poxvirus viral genome; in such a situation the promoter according to the present invention is active if the cell comprising the promoter also comprises a

poxvirus genome, e.g. if the cell is infected with a poxvirus. Under these circumstances the viral RNA polymerase recognizes the promoter according to the present invention and the expression of the gene/coding sequence that is linked to the promoter is activated.

[035] As used herein, the term "derived from the nucleic acid set out in SEQ ID NOs: 1-10, and 77" means that the nucleotide sequence of SEQ ID NOs: 1-10, and 77 is taken as a basis for effecting the nucleotide modifications specified, for example, at least one nucleotide addition, deletion, substitution and/or inversion. The term "derived" includes the possibility, for example, of actually modifying the physical sequence corresponding to SEQ ID NOs: 1-10, and 77 by known methods, for example, error-prone PCR. The term "derived" additionally includes the possibility of performing modifications on the sequence of SEQ ID NOs: 1-10, and 77 in silico, and then synthesizing the thus determined sequence as a physical nucleic acid. For example, the term "derived" encompasses the possibility of using any known computer program for the analysis of nucleic acid sequences with regard to, for example, hybridization stability and the possibility of any secondary nucleic acid structure in modifying the starting sequence of SEQ ID NOs: 1-10, and 77. Preferably, not more than 10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 nucleotides have been added, deleted, substituted and/or inverted from the nucleic acids of SEQ ID NOs: 1-10, and 77. Furthermore, addition, insertion or deletion of at least one nucleotide should not result to a start codon of the nucleic acid to be expressed.

[036] As used herein, the terms "expressed", "express", "expression" and the like denote the transcription alone as well as both the transcription and translation of a sequence of interest. Thus, in referring to expression of a nucleic acid present in the form of DNA, the product resulting from this expression may be either RNA (resulting from transcription alone of the sequence to be expressed) or a polypeptide sequence (resulting from both transcription and

translation of the sequence to be expressed). The term “expression” thus also includes the possibility that both RNA and polypeptide product result from said expression and remain together in the same shared milieu. For example, this is the case when the mRNA persists following its translation into polypeptide product.

[037] As used herein, the term “expression cassette” is defined as a part of a vector or recombinant virus typically used for cloning and/or transformation. An expression cassette is typically comprised of a) one or more coding sequences (e.g., , open reading frame (ORF), genes, nucleic acids encoding a protein and/or antigen), and b) sequences controlling expression the one or more coding sequences. Additionally, an expression cassette may comprise a 3’ untranslated region that in eukaryotes usually contain a polyadenylation site.

[038] The term "recombinant" means a polynucleotide or polypeptide of semi-synthetic, or synthetic origin which either does not occur in nature or is linked to another polynucleotide in an arrangement not found in nature.

[039] One aspect of the invention includes promoters with nucleic acids having at least 70%, preferably 75%, 80%, 85%, 90% or 95% identity with SEQ ID NOs: 1-10, and 77 and having essentially the same expression characteristics as SEQ ID NOs: 1-10, and 77.

[040] "Percent (%) sequence homology or identity" with respect to nucleic acid sequences described herein is defined as the percentage of nucleotides in a candidate sequence that are identical with the nucleotides in the reference sequence (i.e., the nucleic acid sequence from which it is derived), after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Alignment for purposes of determining percent nucleotide sequence identity or homology can be achieved in various ways that are within the

skill in the art, for example, using publically available computer software such as BLAST, ALIGN, or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximum alignment over the full length of the sequences being compared.

[041] For example, an appropriate alignment for nucleic acid sequences is provided by the local homology algorithm of Smith and Waterman, (1981), Advances in Applied Mathematics 2:482- 489. This algorithm can be applied to amino acid sequences by using the scoring matrix developed by Dayhoff, Atlas of Protein Sequences and Structure, M. O. Dayhoff ed., 5 suppl. 3:353-358, National Biomedical Research Foundation, Washington, D.C., USA, and normalized by Gribskov (1986), Nucl. Acids Res. 14(6):6745-6763. An exemplary implementation of this algorithm to determine percent identity of a sequence is provided by the Genetics Computer Group (Madison, Wis.) in the "BestFit" utility application. The default parameters for this method are described in the Wisconsin Sequence Analysis Package Program Manual, Version 8 (1995) (available from Genetics Computer Group, Madison, Wis.). A preferred method of establishing percent identity in the context of the present invention is to use the MPSRCH package of programs copyrighted by the University of Edinburgh, developed by John F. Collins and Shane S. Sturrok, and distributed by IntelliGenetics, Inc. (Mountain View, Calif). From this suite of packages the Smith-Waterman algorithm can be employed where default parameters are used for the scoring table (for example, gap open penalty of 12, gap extension penalty of one, and a gap of six). From the data generated the "Match" value reflects "sequence identity." Other suitable programs for calculating the percent identity or similarity between sequences are generally known in the art, for example, another alignment program is BLAST, used with default parameters. For example, BLASTN and BLASTP can be used using

the following default parameters: genetic code=standard; filter=none; strand=both; cutoff=60; expect=10; Matrix=BLOSUM62; Descriptions=50 sequences; sort by=HIGH SCORE; Databases=non- redundant, GenBank+EMBL+DDBJ+PDB+ GenBank CDS translations+Swiss protein+Spupdate+PIR. Details of these programs can be found at the following internet address: http:// http://blast.ncbi.nlm.nih.gov/.

Promoters and Nucleic Acid Sequences

[042] In one embodiment, the present disclosure includes a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-10, and 77.

[043] In another embodiment, the present disclosure includes a nucleic acid sequence having at least 70% identity with a nucleic acid selected from the group consisting of SEQ ID NOs: 1-10, and 77 and having essentially the same expression characteristics as a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-10, and 77. In further embodiments, there is a nucleic acid sequence having at least 75%, 80%, 85%, 90%, or 95% identity with a nucleic acid selected from the group consisting of SEQ ID NOs: 1-10, and 77 and having essentially the same expression characteristics as a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-10, and 77.

[044] In yet additional embodiment, there is a nucleic acid having a nucleotide sequence derived from the nucleic acid set out in SEQ ID NOs: 1-10, and 77, comprising at least one nucleotide addition, deletion, substitution and/or inversion as compared to the nucleotide sequence of SEQ ID NOs: 1-10, and 77 and having essentially the same expression characteristics as the nucleic acid of SEQ ID NOs: 1-10, and 77.

[045] In still an additional embodiment, there is a nucleic acid having a nucleotide sequence capable of hybridizing to a nucleic acid sequence selected from the group consisting of

SEQ ID NOs: 1-10, and 77, and having essentially the same expression characteristics as a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-10, and 77.

[046] In one aspect of the invention, there is a promoter for enhancing the expression of a coding and/or gene sequence, the promoter selected from the group consisting of:

a) a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-10, and 77 or a subsequence thereof;

b) a nucleic acid having a nucleotide sequence derived from the nucleic acid set out in (a), comprising at least one nucleotide addition, deletion, substitution and/or inversion as compared to the nucleotide sequence of (a) and having essentially the same expression characteristics as the nucleic acid of (a);

c) a nucleic acid sequence having at least 70% identity with the nucleic acid of (a) and having essentially the same expression characteristics as the nucleic acid of (a); and

d) a nucleic acid capable of hybridizing to a nucleic acid sequence of (a), (b) or (c) and having essentially the same expression characteristics as the nucleic acid of (a).

e) a nucleic acid sequence comprising SEQ ID NOs:3, 4, 5, 6, 7, 8, or 9, wherein the nucleic acid sequence includes up to 245 nucleotides.

[047] A further aspect of the invention relates to a nucleic acid capable of hybridizing to a nucleic acid sequence of (a), (b) or (c) and having essentially the same expression characteristics as the nucleic acid of (a). The term "capable of hybridizing" means hybridization in conditions in which any portion of the nucleic acid of (a), (b) or (c) is able to hybridize to another DNA sequence to allow detection and isolation of any DNA sequence having essentially the same expression characteristics as the nucleic acid of (a). The hybridization is carried out in stringent conditions; the more stringent the conditions, the more likely partially complementary

sequences are to be forced apart, i.e. higher stringency lowers the probability of hybridization. In practice, the term "stringent conditions" means hybridization conditions with high temperature (e.g. 65° C.) and/or low salt concentration (e.g. 0.1×SSC). Increasing the temperature and/or decreasing the salt concentration increases the stringency. Under stringent conditions hybridization will occur only if there is at least 70% or preferably at least 75, 80, 85, 90 or 95% identity between the sequences. Hybridization can be carried out as set out in Ausubel et al. (2002) Short Protocols in Molecular Biology Vol. 1 5th ed. Canada.

[048] Preferably, the promoter and/or nucleic acid of the invention has a length of up to and including 245 or 242 nucleotides. Also, the promoter and/or nucleic acid of the invention has a length of up to and including 232 or 215 nucleotides. More preferably, the promoter of the invention has a length of up to and including 212, 200, or a length of up to and including 195 nucleotides, or a length of up to and including 183, or a length of up to and including 170 or 167 nucleotides. In one embodiment, the nucleic acid of (b), (c) or (d), as set out above, comprises about 50-250 nucleotides, about 60-220 nucleotides, about 70-200 nucleotides, about 80-190 nucleotides, or about 90-180 nucleotides.

[049] Alternatively it is within the scope of the present invention to use a derivative of these promoters, which may be a subsequence of the sequences as defined in anyone of SEQ ID NOs: 1-10, and 77. The term "subsequence of the sequences according to anyone of SEQ ID NOs: 1-10, and 77" refers to shorter fragments of anyone of SEQ ID NO: 1 to 10, and 77 that are still active as a promoter, in particular as promoter in an orthopoxvirus, such as FPV, or in an orthopoxvirus, such as FPV, infected cells.

[050] In various embodiments, exemplary subsequences of SEQ ID NO:9 are selected from SEQ ID NOs:2-8. In one aspect, SEQ ID NOs: 4 or 5 are preferred subsequence of SEQ ID

NO: 9. In other aspects, subsequences of SEQ ID NO: 8 include SEQ ID NOs: 2-7, subsequences of SEQ ID NO:7 include SEQ ID NO:s 2-6, subsequences of SEQ ID NO:6 includes SEQ ID NOs: 2-5, subsequences of SEQ ID NO:5 include SEQ ID NOs: 2-4 subsequences of SEQ ID NO:6 includes SEQ ID NOs: 2-5, subsequences of SEQ ID NO:5 include SEQ ID NOs: 2-4, subsequences of SEQ ID NO: 4 includes SEQ ID NOs: 2-3, and subsequences of SEQ ID NO: 3 includes SEQ ID NO: 2.

[051] The derivative of the promoter comprising or consisting of a nucleotide sequence of anyone of SEQ ID NOs: 1-10, and 77 or subsequences thereof, can also be a sequence that has one or more nucleotide substitutions, deletions and/or insertions with respect to any one of the sequences of SEQ ID NOs: 1-10, and 77. The derivatives according to the present invention are still active as a promoter, in particular as orthopoxvirus and/or avipoxvirus promoter in an orthopoxvirus and/or avipoxvirus virus infected cells, more preferably as an avipoxvirus promoter in avipoxvirus infected cells. In the derivatives according to the present invention deletions, substitutions and insertions may be combined in one sequence.

[052] Preferably the derivative has a homology of at least 40%, more preferably of at least 60%, even more preferably of at least 80%, most preferably of at least 90% when compared to anyone of the sequence of SEQ ID NOs: 1-10, and 77 or subsequences thereof, as described herein.

Brachyury proteins

[053] In several aspects of the present invention, the inventors' determined that as a result of synthesizing the various promoters described herein, the inventors' created one or more recombinant Brachyury proteins. In particular, the one or more recombinant Brachyury proteins are fusion proteins resulting from the combination of one or more of the promoters of the

invention and the Brachyury protein. It is contemplated that one or more of the recombinant Brachyury proteins can be useful as a part of a vaccine, pharmaceutical or other therapeutic composition.

[054] Thus, in various aspects, the invention includes one or more synthetic and novel recombinant Brachyury proteins and/or synthetic and novel nucleic acids encoding recombinant Brachyury proteins.

[055] In one embodiment, there are one or more nucleic acids sequences having at least 70% identity to a nucleic acid encoding a Brachyury protein, wherein the Brachyury protein is selected from the group consisting of: SEQ ID NOs: 18-19, 22-23, 26-27, 30-31, 34-35, 38-39, 42-43, 46-47, 50-51, 54-55, 58-59, 62-63, 66-67, 70, and 71. In additional embodiments, there are one or more nucleic acids having at least 75%, 80%, 85%, 90%, or 95% identity to a nucleic acid encoding a Brachyury protein, wherein the Brachyury protein is selected from the group consisting of: SEQ ID NOs: 18-19, 22-23, 26-27, 30-31, 34-35, 38-39, 42-43, 46-47, 50-51, 54-55, 58-59, 62-63, 66-67, 70, and 71.

[056] In various other embodiments of the invention, there are one or more Brachyury proteins selected from the group consisting of: SEQ ID NOs: 18-19, 22-23, 26-27, 30-31, 34-35, 38-39, 42-43, 46-47, 50-51, 54-55, 58-59, 62-63, 66-67, 70, and 71. In further embodiments, there are one or more Brachyury proteins having at least 70% identity with a peptide selected from the group consisting of: SEQ ID NOs: 18-19, 22-23, 26-27, 30-31, 34-35, 38-39, 42-43, 46-47, 50-51, 54-55, 58-59, 62-63, 66-67, 70, and 71. In still further embodiments, there is a peptide having at least 75%, 80%, 85%, 90%, or 95% identity with a peptide selected from the group consisting of SEQ ID NOs: 18-19, 22-23, 26-27, 30-31, 34-35, 38-39, 42-43, 46-47, 50-51, 54-55, 58-59, 62-63, 66-67, 70, and 71.

[057] In another embodiment, there are one or more nucleic acids sequences encoding a Brachyury protein, the nucleic acid sequence selected from the group consisting of: SEQ ID NOs: 16-17, 20-21, 24-25, 28-29, 32-33, 36-37, 40-41, 44-45, 48-49, 52-53, 56-57, 60-61, 64-65, 68, and 69.

[058] In other embodiments, there are one or more nucleic acid sequences having at least 70% identity with a nucleic acid selected from the group consisting of SEQ ID NOs: 16-17, 20-21, 24-25, 28-29, 32-33, 36-37, 40-41, 44-45, 48-49, 52-53, 56-57, 60-61, 64-65, 68, and 69 and having essentially the same expression characteristics as a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 16-17, 20-21, 24-25, 28-29, 32-33, 36-37, 40-41, 44-45, 48-49, 52-53, 56-57, 60-61, 64-65, 68, and 69. In further embodiments, there is a nucleic acid sequence having at least 75%, 80%, 85%, 90%, or 95% identity with a nucleic acid selected from the group consisting of SEQ ID NOs: 16-17, 20-21, 24-25, 28-29, 32-33, 36-37, 40-41, 44-45, 48-49, 52-53, 56-57, 60-61, 64-65, 68, and 69 and having essentially the same expression characteristics as a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 16-17, 20-21, 24-25, 28-29, 32-33, 36-37, 40-41, 44-45, 48-49, 52-53, 56-57, 60-61, 64-65, 68, and 69.

[059] In a preferred embodiment, there are one or more nucleic acid sequences selected from the group consisting of SEQ ID NOs: 16-17, 20-21, 24-25, 28-29, 32-33, 36-37, 40-41, 44-45, 48-49, 52-53, 56-57, 60-61, 64-65, 68, and 69.

Expression Cassettes

[060] According to a further embodiment, the present invention refers to an expression cassette comprising one or more of the promoters and/or Brachyury recombinant proteins and/or nucleic acids according to the present invention.

[061] In one embodiment, there is an expression cassette comprising a promoter having at least 70% identity with a nucleic acid selected from the group consisting of SEQ ID NOs: 1-10 and a nucleic acid encoding a Brachyury peptide selected from the group consisting of: SEQ ID NOs: 11, 13, 18-19, 22-23, 26-27, 30-31, 34-35, 38-39, 42-43, 46-47, 50-51, 54-55, 58-59, 62-63, 66-67, 70, and 71. In an another embodiment, there is an expression cassette comprising a promoter selected from the group consisting of SEQ ID NOs: 1-10, and 77 and/or a nucleic acid encoding a Brachyury peptide, wherein the nucleic acid is selected from the group consisting of: SEQ ID NOs: 12, 14-17, 20-21, 24-25, 28-29, 32-33, 36-37, 40-41, 44-45, 48-49, 52-53, 56-57, 60-61, 64-65, 68, and 69.

[062] In a preferred embodiment, there is an expression cassette comprising a nucleic acid sequence at least 70% homologous to a nucleic acid sequence selected from the group consisting of: SEQ ID NOs: 72-76. In further embodiments, there is an expression cassette comprising a nucleic acid sequence having at least 75%, 80%, 85%, 90%, or 95% identity with a nucleic acid selected from the group consisting of SEQ ID NOs:72-76.

[063] In a more preferred embodiment, there is an expression cassette comprising SEQ ID NO: 72.

[064] In a more preferred embodiment, there is an expression cassette comprising SEQ ID NO: 73.

[065] In a more preferred embodiment, there is an expression cassette comprising SEQ ID NO: 74.

Recombinant Poxviruses

[066] According to a further embodiment the nucleic acids, promoters, recombinant proteins, and/or expression cassettes according to the present invention may be part of a vector.

The term “vector ” refers to any vectors known to the person skilled in the art. A vector can be a plasmid vector such as pBR322 or a vector of the pUC series. More preferably the vector is a recombinant virus. In the context of the present invention the term “virus” or “recombinant virus” refers to an infectious virus comprising a viral genome. In this case the nucleic acids, promoters, recombinant proteins, and/or expression cassettes of the present invention are part of the viral genome of the respective recombinant virus. The recombinant viral genome is packaged and the obtained recombinant viruses can be used for the infection of cells and cell lines, in particular for the infection of living animals including humans. Typical recombinant viruses that may be used according to the present invention are adenoviral vectors, retroviral vectors or vectors on the basis of the adeno associated virus 2 (AAV2). Most preferred are poxviral vectors.

[067] In several embodiments, the nucleic acids, promoters, polypeptides, and expression cassettes according to the present invention are preferably active as poxviral promoters or active as promoters in poxvirus infected cells. The poxvirus is preferably an avipoxvirus or an orthopoxvirus. More preferably, the poxvirus is an avipoxvirus.

[068] The term "avipoxvirus" refers to any avipoxvirus, such as Fowlpoxvirus, Canarypoxvirus, Uncopoxvirus, Mynahpoxvirus, Pigeonpoxvirus, Psittacinepoxvirus, Quailpoxvirus, Peacockpoxvirus, Penguinpoxvirus, Sparrowpoxvirus, Starlingpoxvirus and Turkeypoxvirus. Preferred avipoxviruses are Canarypoxvirus and Fowlpoxvirus.

[069] An example of a canarypox virus is strain Rentschler. A plaque purified Canarypox strain termed ALVAC (U.S. Pat. No. 5,766,598) was deposited under the terms of the Budapest treaty with the American Type Culture Collection (ATCC), accession number VR-

2547. Another Canarypox strain is the commercial canarypox vaccine strain designated LF2 CEP 524 24 10 75, available from Institute Merieux, Inc.

[070] Examples of a Fowlpox virus are strains FP-1, FP-5, TROVAC (U.S. Pat. No. 5,766,598), and POXVAC-TC (U.S. Patent 7,410,644). FP-1 is a Duvette strain modified to be used as a vaccine in one-day old chickens. The strain is a commercial fowlpox virus vaccine strain designated O DCEP 25/CEP67/2309 October 1980 and is available from Institute Merieux, Inc. FP-5 is a commercial fowlpox virus vaccine strain of chicken embryo origin available from American Scientific Laboratories (Division of Schering Corp.) Madison, Wis., United States Veterinary License No. 165, serial No. 30321.

[071] In certain embodiments, the recombinant FPV comprises a nucleic acid sequence selected from the group consisting of: SEQ ID NOs: 1-10, and 77. In various additional embodiments, the recombinant FPV comprises an expression cassette comprising a nucleic acid sequence selected from SEQ ID NOs: 72-76. In a more preferred embodiment, the recombinant FPV comprises an expression cassette comprising a nucleic acid sequence selected from SEQ ID NOs: 72, 73, and 74.

[072] In other embodiments, the recombinant FPV comprises a nucleic acid encoding a brachyury antigen selected from the group consisting of: SEQ ID NOs: 11, 13, 18-19, 22-23, 26-27, 30-31, 34-35, 38-39, 42-43, 46-47, 50-51, 54-55, 58-59, 62-63, 66-67, 70, and 71. In further embodiments, the recombinant FPV comprises a Brachyury peptide selected from the group consisting of: SEQ ID NOs: 11, 13, 18-19, 22-23, 26-27, 30-31, 34-35, 38-39, 42-43, 46-47, 50-51, 54-55, 58-59, 62-63, 66-67, 70, and 71. In further embodiments, the recombinant FPV comprises a nucleic acid selected from the group consisting of: SEQ ID NOs: 12, 14-17, 20-21, 24-25, 28-29, 32-33, 36-37, 40-41, 44-45, 48-49, 52-53, 56-57, 60-61, 64-65, 68, and 69.

In more preferred embodiments, , the recombinant FPV comprises a Brachyury peptide selected from the group consisting of: SEQ ID NOs: 18-19, 22-23, 26-27, 30-31, 34-35, 38-39, 42-43, 46-47, 50-51, 54-55, 58-59, 62-63, 66-67, 70, and 71 and/or a nucleic acid selected from the group consisting of: SEQ ID NOs: 16-17, 20-21, 24-25, 28-29, 32-33, 36-37, 40-41, 44-45, 48-49, 52-53, 56-57, 60-61, 64-65, 68, and 69.

[073] In the various other embodiments of the present disclosure, the recombinant poxvirus is an orthopoxvirus such as, but not limited to, a vaccinia virus, a Modified Vaccinia Virus Ankara (MVA), or MVA-BN.

[074] Examples of vaccinia virus strains are the strains Temple of Heaven, Copenhagen, Paris, Budapest, Dairen, Gam, MRIVP, Per, Tashkent, TBK, Tom, Bern, Patwadangar, BIEM, B-15, Lister, EM-63, New York City Board of Health, Elstree, Ikeda and WR. A preferred vaccinia virus (VV) strain is the Wyeth (DRYVAX) strain (U.S. Patent 7,410,644). Another preferred VV strain is MVA (Sutter, G. et al. [1994], Vaccine 12: 1032-40). Another preferred VV strain is MVA-BN.

[075] Examples of MVA virus strains that are useful in the practice of the present invention and that have been deposited in compliance with the requirements of the Budapest Treaty are strains MVA 572, deposited at the European Collection of Animal Cell Cultures (ECACC), Vaccine Research and Production Laboratory, Public Health Laboratory Service, Centre for Applied Microbiology and Research, Porton Down, Salisbury, Wiltshire SP4 0JG, United Kingdom, with the deposition number ECACC 94012707 on January 27, 1994, and MVA 575, deposited under ECACC 00120707 on December 7, 2000. MVA-BN, deposited on Aug. 30, 2000 at the European Collection of Cell Cultures (ECACC) under number V00083008, and its derivatives, are additional exemplary strains.

[076] Although MVA-BN is preferred for its higher safety (less replication competent), all MVAs are suitable for this invention. According to an embodiment of the present invention, the MVA strain is MVA-BN and its derivatives. A definition of MVA-BN and its derivatives is given in PCT/EP01/13628 which is incorporated by reference herein.

[077] In one embodiment, the invention encompasses recombinant orthopoxviruses, preferably a vaccinia virus (VV), a Wyeth strain, ACAM 1000, ACAM 2000, MVA, or MVA-BN for cancer therapy. Recombinant orthopoxviruses are generated by insertion of heterologous sequences into an orthopoxvirus.

~~[078]~~ In certain embodiments, the MVA is MVA-BN, deposited on Aug. 30, 2000, at the European Collection of Cell Cultures (ECACC) under number V00083008, and described in International PCT publication WO2002042480 (see also e.g. U.S. Pat. Nos. 6,761,893 and 6,913,752), which are incorporated by reference herein.

[079] In certain embodiments, a recombinant MVA is a derivative of MVA-BN. Such "derivatives" include viruses exhibiting essentially the same replication characteristics as the deposited strain (ECACC No. V00083008), but exhibiting differences in one or more parts of its genome. Viruses having the same "replication characteristics" as the deposited virus are viruses that replicate with similar amplification ratios as the deposited strain in CEF cells and the cell lines, HeLa, HaCat and 143B; and that show similar replication. characteristics *in vivo*, as determined, for example, in the AGR129 transgenic mouse model.

[080] In certain embodiments, the recombinant orthopoxvirus comprises a nucleic acid selected from the group consisting of: SEQ ID NOs: 1-10, and 77. In various additional embodiments, the recombinant orthopoxvirus comprises an expression cassette comprising a nucleic acid sequence selected from SEQ ID NOs: 72-76. In a more preferred embodiment, the

recombinant orthopoxvirus comprises an expression cassette comprising a nucleic acid sequence selected from SEQ ID NOs: 72, 73, and 74.

[081] In other embodiments, the recombinant orthopoxvirus comprises a nucleic acid encoding a brachyury antigen selected from the group consisting of: SEQ ID NOs: 11, 13, 18-19, 22-23, 26-27, 30-31, 34-35, 38-39, 42-43, 46-47, 50-51, 54-55, 58-59, 62-63, 66-67, 70, and 71. In further embodiments, the recombinant orthopoxvirus comprises a nucleic acid selected from the group consisting of: SEQ ID NOs: 12, 14-17, 20-21, 24-25, 28-29, 32-33, 36-37, 40-41, 44-45, 48-49, 52-53, 56-57, 60-61, 64-65, 68, and 69. In more preferred embodiments, the recombinant orthopoxvirus comprises a Brachyury peptide selected from the group consisting of: SEQ ID NOs: 18-19, 22-23, 26-27, 30-31, 34-35, 38-39, 42-43, 46-47, 50-51, 54-55, 58-59, 62-63, 66-67, 70, and 71 and/or a nucleic acid selected from the group consisting of: SEQ ID NOs: 16-17, 20-21, 24-25, 28-29, 32-33, 36-37, 40-41, 44-45, 48-49, 52-53, 56-57, 60-61, 64-65, 68, and 69.

[082] Methods are known to the person skilled in the art how the expression cassette or the promoter according to the present invention can be inserted into a viral genome, in particular into the genome of a poxvirus, most preferably into the genome of an orthopoxvirus and/or FPV. For example, the expression cassette or the promoter or derivative thereof according to the present invention may be inserted into the genome of a poxvirus by homologous recombination. To this end a nucleic acid is transfected into a permissive cell line such as CEF or BHK cells, wherein the nucleic acid comprises the expression cassette or the promoter or derivative thereof according to the present invention flanked by nucleotide stretches that are homologous to the region of the poxviral genome in which the expression cassette or the promoter or derivative thereof according to the present invention is to be inserted. The cells are infected by the poxvirus

and in the infected cells homologous recombination occurs between the nucleic acid and the viral genome. Alternatively, it is also possible to first infect the cells with a poxvirus and then to transfect the nucleic acid into the infected cells. Again recombination occurs in the cells. The recombinant poxvirus is then selected by methods known in the prior art. The construction of recombinant poxvirus is not restricted to this particular method. Instead, any suitable method known to the person skilled in the art may be used to this end.

[083] The expression cassette or the promoter according to the present invention may be introduced into any suitable part of the virus or viral vector, in particular into a viral, genome. In case of an orthopoxvirus and an avipoxvirus, the insertion may be made into non-essential parts of the viral genome or into an intergenic region of the viral genome. The term "intergenic region" refers preferably to those parts of the viral genome located between two adjacent genes that do not comprise coding sequences. If the virus is an orthopoxvirus and an avipoxvirus the insertion may also be made into a deletion site of the viral genome. The term "deletion site" refers to those parts of the viral genome that are deleted with respect to the genome of a naturally occurring orthopoxvirus or avipoxvirus. However, the insertion sites are not restricted to these preferred insertion sites in the orthopoxvirus and an avipoxvirus genome, since it is within the scope of the present invention that the expression cassette may be inserted anywhere in the viral genome as long as it is possible to obtain recombinants that can be amplified and propagated in at least one cell culture system, such as Chicken Embryo Fibroblasts (CEF cells).

[084] The promoter according to the present invention may be used to express a gene that is already part of the vector, e.g. the genome of an orthopoxvirus and/or an avipoxvirus. Such a gene may be a gene that is naturally part of the viral genome or a foreign gene that has already been inserted into the vector. In these cases the promoter according to the present

invention is inserted upstream of the gene in the vector, the expression of which is to be controlled by the promoter.

Vaccines and/or Compositions

[085] According to a further embodiment the invention concerns the vector according to the present invention as vaccine or medicament. In more general term the invention relates to a vaccine or pharmaceutical composition comprising an expression cassette, a DNA or a vector according to the present invention. Methods are known to the person skilled in the art how the vaccine or pharmaceutical composition can be administered to the animal or human body. In case of DNA and recombinant plasmid vectors the DNA and the vector can simply be administered by injection. If the vaccine or composition is a recombinant virus such as an orthopoxvirus or an avipoxvirus , in particular a recombinant MVA or recombinant FPV, it may also be administered to the animal or human body according to the knowledge of the person skilled in the art, e.g. by intra venous, intra muscular, intra nasal, intra dermal or subcutaneous administration. Further details on the amount of virus administered are given below.

[086] The pharmaceutical composition or the vaccine may generally include one or more pharmaceutical acceptable and/or approved carriers, additives, antibiotics, preservatives, adjuvants, diluents and/or stabilizers in addition to the promoter, expression cassette or vector according to the present invention. Such auxiliary substances can be water, saline, glycerol, ethanol, wetting or emulsifying agents, pH buffering substances, or the like. Suitable carriers are typically large, slowly metabolized molecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, lipid aggregates, or the like.

[087] For the preparation of pharmaceutical compositions or vaccines, the DNA, expression cassette or vector according to the present invention, in particular a recombinant

orthopoxvirus or avipoxvirus such as recombinant MVA or recombinant FPV is converted into a physiologically acceptable form. For MVA and FPV, this can be done based on the experience in the preparation of poxvirus vaccines used for vaccination against smallpox (as described by Stickl, H. et al. [1974] Dtsch. med. Wschr. 99, 2386-2392). For example, the purified virus is stored at −80° C. with a titre of 5×10^8 TCID50/ml formulated in about 10 mM Tris, 140 mM NaCl pH 7.4. For the preparation of vaccine shots, e.g., 10^1-10^9 particles of the recombinant virus according to the present invention are lyophilized in phosphate-buffered saline (PBS) in the presence of 2% peptone and 1% human albumin in an ampoule, preferably a glass ampoule. Alternatively, the vaccine shots can be produced by stepwise freeze-drying of the virus in a formulation. This formulation can contain additional additives such as mannitol, dextran, sugar, glycine, lactose or polyvinylpyrrolidone or other additives such as antioxidants or inert gas, stabilizers or recombinant proteins (e.g. human serum albumin) suitable for in vivo administration. A typical virus containing formulation suitable for freeze-drying comprises 10 mM Tris-buffer, 140 mM NaCl, 18.9 g/l Dextran (MW 36000-40000), 45 g/l Sucrose, 0.108 g/l L-glutamic acid mono potassium salt monohydrate pH 7.4. The glass ampoule is then sealed and can be stored between 4° C. and room temperature for several months. However, as long as no need exists the ampoule is stored preferably at temperatures below −20° C.

[088] For vaccination or therapy the lyophilisate or the freeze-dried product can be dissolved in 0.1 to 0.5 ml of an aqueous solution, preferably water, physiological saline or Tris buffer, and administered either systemically or locally, i.e. by parenteral, intramuscular or any other path of administration know to the skilled practitioner. The mode of administration, the dose and the number of administrations can be optimized by those skilled in the art in a known manner.

[089] In one or more embodiments, the invention further concerns a method for introducing a coding sequence into a target cell, such as human cell for therapeutic purposes, comprising the introduction of the nucleic acids, promoters, recombinant proteins, and/or expression cassettes according to the present invention into the target cell. Exemplary human target cells can include antigen presenting cells (APCs) such as dendritic cells, macrophages and other non APC'S such as fibroblasts, tumor cells, and so forth.

[090] The invention further relates to a method for producing a peptide, protein and/or virus comprising the infection of a host cell with a recombinant virus according to the present invention, followed by the cultivation of the infected host cell under suitable conditions, and further followed by the isolation and/or enrichment of the peptide and/or protein and/or viruses produced by said host cell. If it is intended to produce, i.e. amplify the virus according to the present invention the cell has to be a cell in which the virus is able to replicate. For poxviruses, in particular MVA, suitable cells are CEF (chicken embryonic fibroblast) or BHK (baby hamster kidney) cells. For avipoxviruses, such as fowlpoxvirus, suitable cells include CEF or CED (chicken embryonic dermal) cells. If it is intended to produce a peptide/protein encoded by the recombinant virus according to the present invention the cell may be any cell that can be infected by the recombinant virus vector and that allows the expression of the virus encoded proteins/peptides.

[091] The invention further relates to a method for producing a peptide, protein and/or virus comprising the transfection of a cell with the expression cassette, a nucleic acid, promoter, recombinant protein, and/or expression cassette DNA according to the present invention, followed by the infection of the cell with a poxvirus. The infected host cell is cultivated under suitable conditions. A further step comprises the isolation and/or enrichment of the peptide

and/or protein and/or viruses produced by said host cell. The step of infecting the cells with a poxvirus may be made before or after the step of transfection of the cells.

[092] The invention further relates to cells comprising a nucleic acid, promoter, recombinant protein, and/or expression cassette according to the present invention. In particular the invention relates to cells infected with the recombinant virus according to the present invention.

Examples

[093] The following examples further illustrate the present invention. It will be understood by a person of skill in the art that the provided examples in no way may be interpreted as limiting the applicability of the technology.

Example 1: Expression of Brachyury in Human DCs infected with recombinant fowlpox viruses

[094] To identify expression of Brachyury protein, human dendritic cells (DC) were infected with a positive control virus, recombinant MVA comprising Brachyury and TRICOM, at a multiplicity of infection (MOI) of 2.5. Human DCs were also infected with a negative control non-recombinant fowlpox (FPV-WT) or recombinant fowlpox virus strains comprising of a Brachyury expression cassette and TRICOM in accordance with the present disclosure. Each FPV strain, (listed in more detail in Table 1) including FPV-WT, FPV-mBN343A, FPV-mBN344A, and FPV-mBN345A were used to infect DCs with an MOI of 20. FPVBrachyury expression was detected via western blot analysis performed with a rabbit monoclonal anti-Brachyury antibody. The housekeeping protein glyceraldehyde 3-phoshate dehyrdrogenase (GAPDH) was also detected via western blot analysis as a loading control.

Table 1. Recombinant fowlpox virus strains comprising a Brachyury expression cassette and TRICOM

Recombinant FPV strain	Expression Cassette
FPV-mBN343A	SEQ ID NO: 74
FPV-mBN344A	SEQ ID NO: 75
FPV-mBN345A	SEQ ID NO: 72
FPV-mBN354A	SEQ ID NO: 76
FPV-mBN355A	SEQ ID NO: 73

[095] Results are shown in Figure 1. Expression of Brachyury was detected with the FPV-mBN343A and FPVmBN345 recombinant FPVs, but was not detected using the FPV-mBN344A recombinant FPV. Brachyury expression was also detected with MVA-Brachyury-TRICOM. Similar loading of samples was demonstrated by GAPDH expression.

Example 2: Expression of Brachyury in Human DCs infected with recombinant fowlpox viruses

[096] Expression-levels of Brachyury protein were also compared between additional recombinant FPV strains expressing Brachyury with different promoters. Human dendritic cells (DC) were infected with an MOI of 5 of the positive control recombinant MVA comprising Brachyury and TRICOM, and the negative control non-recombinant strain MVA-WT. Human DCs were also infected with a recombinant FPVs comprising of a Brachyury expression cassette and TRICOM in accordance with the present disclosure (e.g, FPV-mBN343A, FPV-mBN344A, FPV-mBN345A, FPV-mBN354A, FPV-mBN355A, See Table 1). Human DCs were additionally infected with a recombinant Fowlpoxvirus (FPV) comprising a Brachyury expression cassette having either a Vaccinia Virus (VV)-40k promoter or a PrS promoter. The non-recombinant FPV-WT strain served as a negative control. All of the FPVs were used at an MOI of 40. Brachyury expression was detected via western blot analysis performed with a rabbit monoclonal anti-Brachyury antibody. GAPDH was also detected as a loading control.

[097] Results are shown in Figure 2. Expression of Brachyury was detected with the FPV-mBN343A and FPV-mBN345A recombinant FPVs, but was not detected using the FPV-mBN344A and FPV-mBN354A recombinant FPV. More particularly, expression of Brachyury was detected at lower levels for the recombinant FPVs having the VV-40k or PrS promoters driving Brachyury (i.e., FVP-mBN281A, FVP-mBN249B). No Brachyury expression was detected in the negative controls (uninfected DCs, MVA-WT, or FPV-WT). Similar loading of samples was demonstrated by GAPDH expression.

[098] The Brachyury expression levels from the Western blot shown in Example 2 were normalized relative to expression of the housekeeping gene GAPDH, which is expected to be expressed at equivalent levels between cells. The intensity of each Brachyury and GAPDH band was measured and a ratio was calculated between the intensity of the Brachyury and GAPDH bands within the same sample.

[099] Results are shown in Figure 3. Among the FPV constructs, the highest expression of Brachyury relative to GAPDH was detected in DCs infected with FPV-mBN355A. Moderate relative Brachyury expression was detected in DCs infected with FPV-mBN343A or FPV-mBN345A. The lowest relative Brachyury expression was detected from the recombinant FPVs having the VV-40k or PrS promoters driving Brachyury (i.e., FVP-mBN281A, FVP-mBN249B). Highest relative expression of Brachyury was observed from infection with the positive control virus MVA-Brachyury-TRICOM; no Brachyury expression was detected in the negative control samples. Therefore, among the recombinant FPV strains, superior expression of Brachyury was induced by vectors driving Brachyury expression from the FPV-mBN355, FPV-mBN345, or FPV-mBN344 promoters.

Example 3: Expression of Brachyury and TRICOM in CMMT cells infected with recombinant fowlpox viruses

[0100] Expression of the Brachyury and TRICOM proteins was also assessed by flow cytometry using fluorescently labeled antibodies specific for each protein. CMMT cells (a rhesus macaque mammary tumor cell line) were infected with the positive control recombinant MVA comprising Brachyury and TRICOM, or with a recombinant FPVs comprising of a Brachyury expression cassette and TRICOM in accordance with the present disclosure (e.g, FPV-mBN343A, FPV-mBN345A), or with the recombinant FPV having the PrS promoter driving Brachyury (FVP-mBN249B). Cells were infected with an MOI below 1, so that a mixture of uninfected and infected cells were analyzed. Uninfected CMMT cells served as a negative control.

[0101] FACS samples were acquired on the BD LSRII or Fortessa and analyzed using BD FACSDIVA software (BD Bioscience, San Jose, CA) or FlowJo (TreeStar Inc., Ashland, OR).

[0102] Results are shown in Figure 4. Histograms of the signals detected for Brachyury and the three TRICOM proteins (CD80, CD54, and CD58) were plotted, and gates were drawn where positive signal was detected (black lines). Among the FPV constructs, the highest expression of Brachyury (shown by the biggest shift in signal along the x-axis) was detected in CMMT cells infected with FPV-mBN343A or FPV-mBN345A. The lowest Brachyury expression was detected from the recombinant FPV with the PrS promoter driving Brachyury (i.e., FVP-mBN281A, FVP-mBN249B). Similar expression levels of the TRICOM proteins were detected among the FPV constructs. Expression of Brachyury and the TRICOM proteins were also observed from infection with the positive control virus MVA-Brachyury-TRICOM.

[0103] To quantify the expression level of Brachyury in infected cells the median fluorescence intensity (MFI) was calculated for the Brachyury-positive cells gated in Figure 4.

[0104] Results are shown in Figure 5. Among the FPV constructs, the highest Brachyury MFI was detected in CMMT cells infected with FPV-mBN343A or FPV-mBN345A. The lowest Brachyury MFI was detected from the recombinant FPV with the PrS promoter driving Brachyury (FVP-mBN249B). The highest Brachyury MFI of all tested constructs was in cells infected with the positive control virus MVA-Brachyury-TRICOM. Therefore, the median expression level of Brachyury in infected CMMT cells was higher from vectors driving Brachyury expression from the FPV-mBN345 or FPV-mBN344 promoters than from the PrS promoter.

Example 4: Expression of Brachyury from FPV-mBN345B

[0105] The drug selection cassette used to initially generate the recombinant FPV-mBN345A strain was removed to generate a recombinant vector suitable for clinical development. This was accomplished by passaging the virus on chicken embryonic fibroblast (CEF) cells without drug selection, plaque purifying individual clones, and identifying clones lacking the selection cassette by PCR and DNA sequencing. This resulted in generation of FPV-mBN345B which comprises of a Brachyury expression cassette driven by the I3+15aa promoter and TRICOM, but does not contain the drug selection cassette.

[0106] Expression of Brachyury and the TRICOM proteins from FPV-mBN345B was confirmed in CMMT cells by infecting them with FPV-BN345B at an MOI of 0.625 to infect a subset of cells, or of 40 to infect all cells.

[0107] Results are shown in Figure 6. Histograms of the signals detected for Brachyury and the three TRICOM proteins (CD80, CD54, and CD58) were plotted with a red lines for

samples infected with an MOI of 0.625 and blue lines for samples infected with an MOI of 40. Uninfected cells served as a negative control (black lines). At the MOI of 0.625, expression of Brachyury and the three TRICOM proteins was detected as a peak shifted to the right of the taller peak from uninfected cells. At the MOI of 40, expression of Brachyury and TRICOM was detected in all cells as a peak shifted to the right of the uninfected cells.

[0108] Other embodiments of the invention will be apparent to those skilled in the art from consideration of the specification and practice of the invention disclosed herein. It is intended that the specification and examples be considered as exemplary only, with a true scope and spirit of the invention being indicated by the following claims.

SEQUENCE LISTING

<110> BAVARIAN NORDIC A/S

<120> PROMOTERS FOR ENHANCING EXPRESSION IN POXVIRUSES

<130> BNIT0010PCT

<140> 62/199681
<141> 2015-07-31

<160> 77

<170> PatentIn version 3.5

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gggaaaaatc tttacaaaat tagtatagaa gctatagata tatcaaaagg tagacaacaa 120

ataatcagaa cctaattttt ttatcaaaaa attaaaatat aaataaa 167

<210> 2
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<212> DNA
<213> Artificial Sequence

<220>
<223> Promoter Sequence with nucleotides 5' of Gene FPV 088 + atc sequence

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<223> Promoter Sequence with nucleotides 5' of Gene FPV 088 plus addition of 16 nucleotides of FPV 088

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gggaaaaatc tttacaaaat tagtatagaa gctatagata tatcaaaagg tagacaacaa 120

ataatcagaa cctaattttt ttatcaaaaa attaaaatat aaataaaatg aaaaataact 180

tgt 183

<210> 4
<211> 194
<212> DNA
<213> Artificial Sequence

<220>
<223> Promoter Sequence with region from Gene FPV 088 plus addition of 27 nucleotides

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ataatcagaa cctaattttt ttatcaaaaa attaaaatat aaataaaatg aaaaataact 180

tgtatgaaga aaaa 194

<210> 5
<211> 200
<212> DNA
<213> Artificial Sequence

<220>
<223> Promoter Sequence with region from Gene FPV 088 plus addition of 33 nucleotides

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tgtatgaaga aaaaatgaac 200

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<211> 212
<212> DNA

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<220>
<223> Promoter Sequence with region from Gene FPV 088 plus addition of 45 nucleotides

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gggaaaaatc tttacaaaat tagtatagaa gctatagata tatcaaaagg tagacaacaa 120

ataatcagaa cctaattttt ttatcaaaaa attaaaatat aaataaaatg aaaaataact 180

tgtatgaaga aaaaatgaac atgagtaaga aa 212

<210> 7
<211> 232
<212> DNA
<213> Artificial Sequence

<220>
<223> Promoter Sequence with region from Gene FPV 088 plus addition of 65 nucleotides

<400> 7
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ataatcagaa cctaattttt ttatcaaaaa attaaaatat aaataaaatg aaaaataact 180

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<211> 245
<212> DNA
<213> Artificial Sequence

<220>
<223> Promoter Sequence with region from Gene FPV 088 plus addition of 78 nucleotides

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gggaaaaatc tttacaaaat tagtatagaa gctatagata tatcaaaagg tagacaacaa 120

ataatcagaa cctaattttt ttatcaaaaa attaaaatat aaataaaatg aaaaataact 180

tgtatgaaga aaaaatgaac atgagtaaga aacaagtaaa aactcaaagt aaatgtaata 240

atatc 245

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<211> 119
<212> DNA
<213> Artificial Sequence

<220>
<223> Promoter Sequence with nucleotides 5' of the Gene FPV L2R

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taattaaaat tgaaaaaaaa atatcattat aaaacgtaaa cgaacaaaaa acattaatt 119

<210> 11
<211> 435
<212> PRT
<213> Artificial Sequence

<220>
<223> Brachyury protein Isoform 1 from GenBank Accession No. O15178.1

<400> 11

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Val Asp His Leu Leu Ser Ala Val Glu Asn Glu Leu Gln Ala Gly Ser
20 25 30

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        35                  40                  45

Ser Glu Leu Trp Leu Arg Phe Lys Glu Leu Thr Asn Glu Met Ile Val
    50                  55                  60

Thr Lys Asn Gly Arg Arg Met Phe Pro Val Leu Lys Val Asn Val Ser
65                  70                  75                  80

Gly Leu Asp Pro Asn Ala Met Tyr Ser Phe Leu Leu Asp Phe Val Ala
                85                  90                  95

Ala Asp Asn His Arg Trp Lys Tyr Val Asn Gly Glu Trp Val Pro Gly
            100                 105                 110

Gly Lys Pro Glu Pro Gln Ala Pro Ser Cys Val Tyr Ile His Pro Asp
        115                 120                 125

Ser Pro Asn Phe Gly Ala His Trp Met Lys Ala Pro Val Ser Phe Ser
    130                 135                 140

Lys Val Lys Leu Thr Asn Lys Leu Asn Gly Gly Gly Gln Ile Met Leu
145                 150                 155                 160

Asn Ser Leu His Lys Tyr Glu Pro Arg Ile His Ile Val Arg Val Gly
                165                 170                 175

Gly Pro Gln Arg Met Ile Thr Ser His Cys Phe Pro Glu Thr Gln Phe
            180                 185                 190

Ile Ala Val Thr Ala Tyr Gln Asn Glu Glu Ile Thr Ala Leu Lys Ile
        195                 200                 205

Lys Tyr Asn Pro Phe Ala Lys Ala Phe Leu Asp Ala Lys Glu Arg Ser
    210                 215                 220

Asp His Lys Glu Met Met Glu Glu Pro Gly Asp Ser Gln Gln Pro Gly
225                 230                 235                 240

Tyr Ser Gln Trp Gly Trp Leu Leu Pro Gly Thr Ser Thr Leu Cys Pro
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245 250 255

Pro Ala Asn Pro His Pro Gln Phe Gly Gly Ala Leu Ser Leu Pro Ser
260 265 270

Thr His Ser Cys Asp Arg Tyr Pro Thr Leu Arg Ser His Arg Ser Ser
275 280 285

Pro Tyr Pro Ser Pro Tyr Ala His Arg Asn Asn Ser Pro Thr Tyr Ser
290 295 300

Asp Asn Ser Pro Ala Cys Leu Ser Met Leu Gln Ser His Asp Asn Trp
305 310 315 320

Ser Ser Leu Gly Met Pro Ala His Pro Ser Met Leu Pro Val Ser His
325 330 335

Asn Ala Ser Pro Pro Thr Ser Ser Ser Gln Tyr Pro Ser Leu Trp Ser
340 345 350

Val Ser Asn Gly Ala Val Thr Pro Gly Ser Gln Ala Ala Ala Val Ser
355 360 365

Asn Gly Leu Gly Ala Gln Phe Phe Arg Gly Ser Pro Ala His Tyr Thr
370 375 380

Pro Leu Thr His Pro Val Ser Ala Pro Ser Ser Ser Gly Ser Pro Leu
385 390 395 400

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Ala Ala Ala Gln Gly Arg Leu Ile Ala Ser Trp Thr Pro Val Ser Pro
420 425 430

Pro Ser Met
435

<210> 12
<211> 1308
<212> DNA

<213> Artificial Sequence

<220>
<223> Coding sequence for Brachyury protein Isoform 1 GenBank Accession No. O15178.1

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gaactgcgcg tgggcctgga ggagagcgag ctgtggctgc gcttcaagga gctcaccaat 180

gagatgatcg tgaccaagaa cggcaggagg atgtttccgg tgctgaaggt gaacgtgtct 240

ggcctggacc ccaacgccat gtactccttc ctgctggact tcgtggcggc ggacaaccac 300

cgctggaagt acgtgaacgg ggaatgggtg ccgggggggca agccggagcc gcaggcgccc 360

agctgcgtct acatccaccc cgactcgccc aacttcgggg cccactggat gaaggctccc 420

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aactccttgc ataagtatga gcctcgaatc cacatagtga gagttggggg tccacagcgc 540

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gaggagatca cagctcttaa aattaagtac aatccatttg caaaagcttt ccttgatgca 660

aaggaaagaa gtgatcacaa agagatgatg gaggaacccg gagacagcca gcaacctggg 720

tactcccaat gggggtggct tcttcctgga accagcaccc tgtgtccacc tgcaaatcct 780

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cctaccagct ccagtcagta ccccagcctg tggtctgtga gcaacggcgc cgtcaccccg 1080

ggctcccagg cagcagccgt gtccaacggg ctgggggccc agttcttccg gggctccccc 1140

gcgcactaca cacccctcac ccatccggtc tcggcgccct cttcctcggg atccccactg 1200

tacgaagggg cggccgcggc cacagacatc gtggacagcc agtacgacgc cgcagcccaa 1260

ggccgcctca tagcctcatg gacacctgtg tcgccacctt ccatgtga 1308

<210> 13
<211> 435

<212> PRT
<213> Artificial Sequence

<220>
<223> Brachyury protein Isoform 1 (L254V)

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Val Asp His Leu Leu Ser Ala Val Glu Asn Glu Leu Gln Ala Gly Ser
20 25 30

Glu Lys Gly Asp Pro Thr Glu Arg Glu Leu Arg Val Gly Leu Glu Glu
35 40 45

Ser Glu Leu Trp Leu Arg Phe Lys Glu Leu Thr Asn Glu Met Ile Val
50 55 60

Thr Lys Asn Gly Arg Arg Met Phe Pro Val Leu Lys Val Asn Val Ser
65 70 75 80

Gly Leu Asp Pro Asn Ala Met Tyr Ser Phe Leu Leu Asp Phe Val Ala
85 90 95

Ala Asp Asn His Arg Trp Lys Tyr Val Asn Gly Glu Trp Val Pro Gly
100 105 110

Gly Lys Pro Glu Pro Gln Ala Pro Ser Cys Val Tyr Ile His Pro Asp
115 120 125

Ser Pro Asn Phe Gly Ala His Trp Met Lys Ala Pro Val Ser Phe Ser
130 135 140

Lys Val Lys Leu Thr Asn Lys Leu Asn Gly Gly Gly Gln Ile Met Leu
145 150 155 160

Asn Ser Leu His Lys Tyr Glu Pro Arg Ile His Ile Val Arg Val Gly
165 170 175

Gly Pro Gln Arg Met Ile Thr Ser His Cys Phe Pro Glu Thr Gln Phe
180 185 190

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Ile Ala Val Thr Ala Tyr Gln Asn Glu Glu Ile Thr Ala Leu Lys Ile
        195                 200                 205

Lys Tyr Asn Pro Phe Ala Lys Ala Phe Leu Asp Ala Lys Glu Arg Ser
    210                 215                 220

Asp His Lys Glu Met Met Glu Glu Pro Gly Asp Ser Gln Gln Pro Gly
225                 230                 235                 240

Tyr Ser Gln Trp Gly Trp Leu Leu Pro Gly Thr Ser Thr Val Cys Pro
                245                 250                 255

Pro Ala Asn Pro His Pro Gln Phe Gly Gly Ala Leu Ser Leu Pro Ser
            260                 265                 270

Thr His Ser Cys Asp Arg Tyr Pro Thr Leu Arg Ser His Arg Ser Ser
        275                 280                 285

Pro Tyr Pro Ser Pro Tyr Ala His Arg Asn Asn Ser Pro Thr Tyr Ser
    290                 295                 300

Asp Asn Ser Pro Ala Cys Leu Ser Met Leu Gln Ser His Asp Asn Trp
305                 310                 315                 320

Ser Ser Leu Gly Met Pro Ala His Pro Ser Met Leu Pro Val Ser His
                325                 330                 335

Asn Ala Ser Pro Pro Thr Ser Ser Ser Gln Tyr Pro Ser Leu Trp Ser
            340                 345                 350

Val Ser Asn Gly Ala Val Thr Pro Gly Ser Gln Ala Ala Ala Val Ser
        355                 360                 365

Asn Gly Leu Gly Ala Gln Phe Phe Arg Gly Ser Pro Ala His Tyr Thr
    370                 375                 380

Pro Leu Thr His Pro Val Ser Ala Pro Ser Ser Ser Gly Ser Pro Leu
385                 390                 395                 400
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Tyr Glu Gly Ala Ala Ala Ala Thr Asp Ile Val Asp Ser Gln Tyr Asp
405 410 415

Ala Ala Ala Gln Gly Arg Leu Ile Ala Ser Trp Thr Pro Val Ser Pro
420 425 430

Pro Ser Met
435

<210> 14
<211> 1308
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence encoding Brachyury protein Isoform 1 with L254V

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ctgagcgccg tggagaatga gctgcaggcg ggcagcgaga agggcgaccc cacagagcgc 120

gaactgcgcg tgggcctgga ggagagcgag ctgtggctgc gcttcaagga gctcaccaat 180

gagatgatcg tgaccaagaa cggcaggagg atgtttccgg tgctgaaggt gaacgtgtct 240

ggcctggacc ccaacgccat gtactccttc ctgctggact tcgtggcggc ggacaaccac 300

cgctggaagt acgtgaacgg ggaatgggtg ccgggggggca agccggagcc gcaggcgccc 360

agctgcgtct acatccaccc cgactcgccc aacttcgggg cccactggat gaaggctccc 420

gtctccttca gcaaagtcaa gctcaccaac aagctcaacg gaggggggca gatcatgctg 480

aactccttgc ataagtatga gcctcgaatc cacatagtga gagttggggg tccacagcgc 540

atgatcacca gccactgctt ccctgagacc cagttcatag cggtgactgc ttatcagaac 600

gaggagatca cagctcttaa aattaagtac aatccatttg caaaggcttt ccttgatgca 660

aaggaaagaa gtgatcacaa agagatgatg gaggaacccg gagacagcca gcaacctggg 720

tactcccaat gggggtggct tcttcctgga accagcaccg tttgtccacc tgcaaatcct 780

catcctcagt ttggaggtgc cctctccctc ccctccacgc acagctgtga caggtaccca 840

accctgagga gccaccggtc ctcaccctac cccagcccct atgctcatcg gaacaattct 900

ccaacctatt ctgacaactc acctgcatgt ttatccatgc tgcaatccca tgacaattgg 960

tccagccttg gaatgcctgc ccatcccagc atgctccccg tgagccacaa tgccagccca 1020

cctaccagct ccagtcagta ccccagcctg tggtctgtga gcaacggcgc cgtcaccccg 1080

ggctcccagg cagcagccgt gtccaacggg ctgggggccc agttcttccg gggctccccc 1140

gcgcactaca cacccctcac ccatccggtc tcggcgccct cttcctcggg atccccactg 1200

tacgaagggg cggccgcggc cacagacatc gtggacagcc agtacgacgc cgcagcccaa 1260

ggccgcctca tagcctcatg gacacctgtg tcgccacctt ccatgtga 1308

<210> 15
<211> 1305
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence encoding Brachyury protein Isoform 1 with L254V without 5' atg sequence

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agcgccgtgg agaatgagct gcaggcgggc agcgagaagg gcgaccccac agagcgcgaa 120

ctgcgcgtgg gcctggagga gagcgagctg tggctgcgct tcaaggagct caccaatgag 180

atgatcgtga ccaagaacgg caggaggatg tttccggtgc tgaaggtgaa cgtgtctggc 240

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tgcgtctaca tccaccccga ctcgcccaac ttcggggccc actggatgaa ggctcccgtc 420

tccttcagca aagtcaagct caccaacaag ctcaacggag ggggccagat catgctgaac 480

tccttgcata agtatgagcc tcgaatccac atagtgagag ttgggggtcc acagcgcatg 540

atcaccagcc actgcttccc tgagacccag ttcatagcgg tgactgctta tcagaacgag 600

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gaaagaagtg atcacaaaga gatgatggag gaacccggag acagccagca acctgggtac 720

tcccaatggg ggtggcttct tcctggaacc agcaccgttt gtccacctgc aaatcctcat 780

cctcagtttg gaggtgccct ctccctcccc tccacgcaca gctgtgacag gtacccaacc 840

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acctattctg acaactcacc tgcatgttta tccatgctgc aatcccatga caattggtcc 960

agccttggaa tgcctgccca tcccagcatg ctccccgtga gccacaatgc cagcccacct 1020

accagctcca gtcagtaccc cagcctgtgg tctgtgagca acggcgccgt caccccgggc 1080

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<210> 16
<211> 1323
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence encoding fusion protein comprising Brachyury (L254V) Protein plus addition of 15 nucleotides from Gene FPV 088

<400> 16
atgaaaaata acttgatgag ctcccctggc accgagagcg cgggaaagag cctgcagtac 60

cgagtggacc acctgctgag cgccgtggag aatgagctgc aggcgggcag cgagaagggc 120

gaccccacag agcgcgaact gcgcgtgggc ctggaggaga gcgagctgtg gctgcgcttc 180

aaggagctca ccaatgagat gatcgtgacc aagaacggca ggaggatgtt tccggtgctg 240

aaggtgaacg tgtctggcct ggaccccaac gccatgtact ccttcctgct ggacttcgtg 300

gcggcggaca accaccgctg gaagtacgtg aacggggaat gggtgccggg gggcaagccg 360

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gctttccttg atgcaaagga aagaagtgat cacaaagaga tgatggagga acccggagac 720

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ccacctgcaa atcctcatcc tcagtttgga ggtgccctct ccctcccctc cacgcacagc 840

tgtgacaggt acccaaccct gaggagccac cggtcctcac cctaccccag cccctatgct 900

catcggaaca attctccaac ctattctgac aactcacctg catgtttatc catgctgcaa 960

tcccatgaca attggtccag ccttggaatg cctgcccatc ccagcatgct ccccgtgagc 1020

cacaatgcca gcccacctac cagctccagt cagtacccca gcctgtggtc tgtgagcaac 1080

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gacgccgcag cccaaggccg cctcatagcc tcatggacac ctgtgtcgcc accttccatg 1320

tga 1323

<210> 17
<211> 1320
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence encoding fusion protein comprising Brachyury (L254V) Protein plus addition of 15 nucleotides from Gene FPV 088 without Brachyury protein atg start codon

<400> 17
atgaaaaata acttgagctc ccctggcacc gagagcgcgg gaaagagcct gcagtaccga 60

gtggaccacc tgctgagcgc cgtggagaat gagctgcagg cgggcagcga gaagggcgac 120

cccacagagc gcgaactgcg cgtgggcctg gaggagagcg agctgtggct gcgcttcaag 180

gagctcacca atgagatgat cgtgaccaag aacggcagga ggatgtttcc ggtgctgaag 240

gtgaacgtgt ctggcctgga ccccaacgcc atgtactcct tcctgctgga cttcgtggcg 300

gcggacaacc accgctggaa gtacgtgaac ggggaatggg tgccgggggg caagccggag 360

ccgcaggcgc ccagctgcgt ctacatccac cccgactcgc ccaacttcgg ggcccactgg 420

atgaaggctc ccgtctcctt cagcaaagtc aagctcacca acaagctcaa cggagggggc 480

cagatcatgc tgaactcctt gcataagtat gagcctcgaa tccacatagt gagagttggg 540

ggtccacagc gcatgatcac cagccactgc ttccctgaga cccagttcat agcggtgact 600

gcttatcaga acgaggagat cacagctctt aaaattaagt acaatccatt tgcaaaggct 660

ttccttgatg caaaggaaag aagtgatcac aaagagatga tggaggaacc cggagacagc 720

cagcaacctg ggtactccca atgggggtgg cttcttcctg gaaccagcac cgtttgtcca 780

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gccgcagccc aaggccgcct catagcctca tggacacctg tgtcgccacc ttccatgtga 1320

<210> 18
<211> 440
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion protein comprising Brachyury (L254V) Protein encoded by SEQ ID NO:16

<400> 18

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1 5 10 15

Ser Leu Gln Tyr Arg Val Asp His Leu Leu Ser Ala Val Glu Asn Glu
20 25 30

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

Val Gly Leu Glu Glu Ser Glu Leu Trp Leu Arg Phe Lys Glu Leu Thr
50 55 60

Asn Glu Met Ile Val Thr Lys Asn Gly Arg Arg Met Phe Pro Val Leu
65 70 75 80

Lys Val Asn Val Ser Gly Leu Asp Pro Asn Ala Met Tyr Ser Phe Leu
85 90 95

Leu Asp Phe Val Ala Ala Asp Asn His Arg Trp Lys Tyr Val Asn Gly

```
            100                 105                 110

Glu Trp Val Pro Gly Gly Lys Pro Glu Pro Gln Ala Pro Ser Cys Val
        115                 120                 125

Tyr Ile His Pro Asp Ser Pro Asn Phe Gly Ala His Trp Met Lys Ala
    130                 135                 140

Pro Val Ser Phe Ser Lys Val Lys Leu Thr Asn Lys Leu Asn Gly Gly
145                 150                 155                 160

Gly Gln Ile Met Leu Asn Ser Leu His Lys Tyr Glu Pro Arg Ile His
                165                 170                 175

Ile Val Arg Val Gly Gly Pro Gln Arg Met Ile Thr Ser His Cys Phe
            180                 185                 190

Pro Glu Thr Gln Phe Ile Ala Val Thr Ala Tyr Gln Asn Glu Glu Ile
        195                 200                 205

Thr Ala Leu Lys Ile Lys Tyr Asn Pro Phe Ala Lys Ala Phe Leu Asp
    210                 215                 220

Ala Lys Glu Arg Ser Asp His Lys Glu Met Met Glu Glu Pro Gly Asp
225                 230                 235                 240

Ser Gln Gln Pro Gly Tyr Ser Gln Trp Gly Trp Leu Leu Pro Gly Thr
                245                 250                 255

Ser Thr Val Cys Pro Pro Ala Asn Pro His Pro Gln Phe Gly Gly Ala
            260                 265                 270

Leu Ser Leu Pro Ser Thr His Ser Cys Asp Arg Tyr Pro Thr Leu Arg
        275                 280                 285

Ser His Arg Ser Ser Pro Tyr Pro Ser Pro Tyr Ala His Arg Asn Asn
    290                 295                 300

Ser Pro Thr Tyr Ser Asp Asn Ser Pro Ala Cys Leu Ser Met Leu Gln
305                 310                 315                 320
```

```
Ser His Asp Asn Trp Ser Ser Leu Gly Met Pro Ala His Pro Ser Met
                325                 330                 335


Leu Pro Val Ser His Asn Ala Ser Pro Pro Thr Ser Ser Ser Gln Tyr
            340                 345                 350


Pro Ser Leu Trp Ser Val Ser Asn Gly Ala Val Thr Pro Gly Ser Gln
        355                 360                 365


Ala Ala Ala Val Ser Asn Gly Leu Gly Ala Gln Phe Phe Arg Gly Ser
    370                 375                 380


Pro Ala His Tyr Thr Pro Leu Thr His Pro Val Ser Ala Pro Ser Ser
385                 390                 395                 400


Ser Gly Ser Pro Leu Tyr Glu Gly Ala Ala Ala Ala Thr Asp Ile Val
                405                 410                 415


Asp Ser Gln Tyr Asp Ala Ala Ala Gln Gly Arg Leu Ile Ala Ser Trp
            420                 425                 430


Thr Pro Val Ser Pro Pro Ser Met
        435                 440


<210>  19
<211>  439
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Fusion protein comprising Brachyury (L254V) Protein encoded by
       SEQ ID NO:17 plus addition of 15 nucleotides from Gene FPV 088
       without Brachyury atg start codon.

<400>  19

Met Lys Asn Asn Leu Ser Ser Pro Gly Thr Glu Ser Ala Gly Lys Ser
1               5                   10                  15


Leu Gln Tyr Arg Val Asp His Leu Leu Ser Ala Val Glu Asn Glu Leu
            20                  25                  30


Gln Ala Gly Ser Glu Lys Gly Asp Pro Thr Glu Arg Glu Leu Arg Val
```

```
        35                  40                  45

Gly Leu Glu Glu Ser Glu Leu Trp Leu Arg Phe Lys Glu Leu Thr Asn
    50                  55                  60

Glu Met Ile Val Thr Lys Asn Gly Arg Arg Met Phe Pro Val Leu Lys
65                  70                  75                  80

Val Asn Val Ser Gly Leu Asp Pro Asn Ala Met Tyr Ser Phe Leu Leu
                85                  90                  95

Asp Phe Val Ala Ala Asp Asn His Arg Trp Lys Tyr Val Asn Gly Glu
            100                 105                 110

Trp Val Pro Gly Gly Lys Pro Glu Pro Gln Ala Pro Ser Cys Val Tyr
        115                 120                 125

Ile His Pro Asp Ser Pro Asn Phe Gly Ala His Trp Met Lys Ala Pro
    130                 135                 140

Val Ser Phe Ser Lys Val Lys Leu Thr Asn Lys Leu Asn Gly Gly Gly
145                 150                 155                 160

Gln Ile Met Leu Asn Ser Leu His Lys Tyr Glu Pro Arg Ile His Ile
                165                 170                 175

Val Arg Val Gly Gly Pro Gln Arg Met Ile Thr Ser His Cys Phe Pro
            180                 185                 190

Glu Thr Gln Phe Ile Ala Val Thr Ala Tyr Gln Asn Glu Glu Ile Thr
        195                 200                 205

Ala Leu Lys Ile Lys Tyr Asn Pro Phe Ala Lys Ala Phe Leu Asp Ala
    210                 215                 220

Lys Glu Arg Ser Asp His Lys Glu Met Met Glu Glu Pro Gly Asp Ser
225                 230                 235                 240

Gln Gln Pro Gly Tyr Ser Gln Trp Gly Trp Leu Leu Pro Gly Thr Ser
                245                 250                 255
```

```
Thr Val Cys Pro Pro Ala Asn Pro His Pro Gln Phe Gly Gly Ala Leu
            260                 265                 270

Ser Leu Pro Ser Thr His Ser Cys Asp Arg Tyr Pro Thr Leu Arg Ser
        275                 280                 285

His Arg Ser Ser Pro Tyr Pro Ser Pro Tyr Ala His Arg Asn Asn Ser
    290                 295                 300

Pro Thr Tyr Ser Asp Asn Ser Pro Ala Cys Leu Ser Met Leu Gln Ser
305                 310                 315                 320

His Asp Asn Trp Ser Ser Leu Gly Met Pro Ala His Pro Ser Met Leu
                325                 330                 335

Pro Val Ser His Asn Ala Ser Pro Pro Thr Ser Ser Ser Gln Tyr Pro
            340                 345                 350

Ser Leu Trp Ser Val Ser Asn Gly Ala Val Thr Pro Gly Ser Gln Ala
        355                 360                 365

Ala Ala Val Ser Asn Gly Leu Gly Ala Gln Phe Phe Arg Gly Ser Pro
    370                 375                 380

Ala His Tyr Thr Pro Leu Thr His Pro Val Ser Ala Pro Ser Ser Ser
385                 390                 395                 400

Gly Ser Pro Leu Tyr Glu Gly Ala Ala Ala Ala Thr Asp Ile Val Asp
                405                 410                 415

Ser Gln Tyr Asp Ala Ala Ala Gln Gly Arg Leu Ile Ala Ser Trp Thr
            420                 425                 430

Pro Val Ser Pro Pro Ser Met
        435
```

<210> 20
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence encoding fusion protein comprising Brachyury (L254V) Protein plus addition of 45 nucleotides from Gene FPV 088

<400> 20
atgaaaaata acttgtatga agaaaaaatg aacatgagta agaaaatgag ctcccctggc 60

accgagagcg cgggaaagag cctgcagtac cgagtggacc acctgctgag cgccgtggag 120

aatgagctgc aggcgggcag cgagaagggc gaccccacag agcgcgaact gcgcgtgggc 180

ctggaggaga gcgagctgtg gctgcgcttc aaggagctca ccaatgagat gatcgtgacc 240

aagaacggca ggaggatgtt tccggtgctg aaggtgaacg tgtctggcct ggaccccaac 300

gccatgtact ccttcctgct ggacttcgtg gcggcggaca accaccgctg gaagtacgtg 360

aacggggaat gggtgccggg gggcaagccg gagccgcagg cgcccagctg cgtctacatc 420

caccccgact cgcccaactt cggggcccac tggatgaagg ctcccgtctc cttcagcaaa 480

gtcaagctca ccaacaagct caacggaggg ggccagatca tgctgaactc cttgcataag 540

tatgagcctc gaatccacat agtgagagtt gggggtccac agcgcatgat caccagccac 600

tgcttccctg agacccagtt catagcggtg actgcttatc agaacgagga gatcacagct 660

cttaaaatta agtacaatcc atttgcaaag gctttccttg atgcaaagga aagaagtgat 720

cacaaagaga tgatggagga acccggagac agccagcaac ctgggtactc ccaatggggg 780

tggcttcttc ctggaaccag caccgtttgt ccacctgcaa atcctcatcc tcagtttgga 840

ggtgccctct ccctcccctc cacgcacagc tgtgacaggt acccaaccct gaggagccac 900

cggtcctcac cctaccccag cccctatgct catcggaaca attctccaac ctattctgac 960

aactcacctg catgtttatc catgctgcaa tcccatgaca attggtccag ccttggaatg 1020

cctgcccatc ccagcatgct ccccgtgagc cacaatgcca gcccacctac cagctccagt 1080

cagtacccca gcctgtggtc tgtgagcaac ggcgccgtca ccccgggctc ccaggcagca 1140

gccgtgtcca acgggctggg ggcccagttc ttccggggct cccccgcgca ctacacaccc 1200

ctcacccatc cggtctcggc gccctcttcc tcgggatccc cactgtacga aggggcggcc 1260

gcggccacag acatcgtgga cagccagtac gacgccgcag cccaaggccg cctcatagcc 1320

tcatggacac ctgtgtcgcc accttccatg tga 1353

<210> 21
<211> 1350

<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence encoding fusion protein comprising Brachyury (L254V) Protein plus addition of 45 nucleotides from Gene FPV 088 without Brachyury atg

<400> 21
atgaaaaata acttgtatga agaaaaaatg aacatgagta agaaaagctc ccctggcacc 60

gagagcgcgg gaaagagcct gcagtaccga gtggaccacc tgctgagcgc cgtggagaat 120

gagctgcagg cgggcagcga gaagggcgac cccacagagc gcgaactgcg cgtgggcctg 180

gaggagagcg agctgtggct gcgcttcaag gagctcacca atgagatgat cgtgaccaag 240

aacggcagga ggatgtttcc ggtgctgaag gtgaacgtgt ctggcctgga ccccaacgcc 300

atgtactcct tcctgctgga cttcgtggcg gcggacaacc accgctggaa gtacgtgaac 360

ggggaatggg tgccgggggg caagccggag ccgcaggcgc ccagctgcgt ctacatccac 420

cccgactcgc ccaacttcgg ggcccactgg atgaaggctc ccgtctcctt cagcaaagtc 480

aagctcacca acaagctcaa cggaggggcc cagatcatgc tgaactcctt gcataagtat 540

gagcctcgaa tccacatagt gagagttggg ggtccacagc gcatgatcac cagccactgc 600

ttccctgaga cccagttcat agcggtgact gcttatcaga acgaggagat cacagctctt 660

aaaattaagt acaatccatt tgcaaaggct ttccttgatg caaaggaaag aagtgatcac 720

aaagagatga tggaggaacc cggagacagc cagcaacctg ggtactccca atgggggtgg 780

cttcttcctg gaaccagcac cgtttgtcca cctgcaaatc ctcatcctca gtttggaggt 840

gccctctccc tcccctccac gcacagctgt gacaggtacc caaccctgag gagccaccgg 900

tcctcaccct accccagccc ctatgctcat cggaacaatt ctccaaccta ttctgacaac 960

tcacctgcat gtttatccat gctgcaatcc catgacaatt ggtccagcct tggaatgcct 1020

gcccatccca gcatgctccc cgtgagccac aatgccagcc cacctaccag ctccagtcag 1080

taccccagcc tgtggtctgt gagcaacggc gccgtcaccc cgggctccca ggcagcagcc 1140

gtgtccaacg ggctgggggc ccagttcttc cggggctccc ccgcgcacta cacacccctc 1200

acccatccgg tctcggcgcc ctcttcctcg ggatccccac tgtacgaagg ggcggccgcg 1260

gccacagaca tcgtggacag ccagtacgac gccgcagccc aaggccgcct catagcctca 1320

tggacacctg tgtcgccacc ttccatgtga 1350

<210> 22
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion protein comprising Brachyury (L254V) Protein encoded by SEQ ID NO:20

<400> 22

Met Lys Asn Asn Leu Tyr Glu Glu Lys Met Asn Met Ser Lys Lys Met
1 5 10 15

Ser Ser Pro Gly Thr Glu Ser Ala Gly Lys Ser Leu Gln Tyr Arg Val
20 25 30

Asp His Leu Leu Ser Ala Val Glu Asn Glu Leu Gln Ala Gly Ser Glu
35 40 45

Lys Gly Asp Pro Thr Glu Arg Glu Leu Arg Val Gly Leu Glu Glu Ser
50 55 60

Glu Leu Trp Leu Arg Phe Lys Glu Leu Thr Asn Glu Met Ile Val Thr
65 70 75 80

Lys Asn Gly Arg Arg Met Phe Pro Val Leu Lys Val Asn Val Ser Gly
85 90 95

Leu Asp Pro Asn Ala Met Tyr Ser Phe Leu Leu Asp Phe Val Ala Ala
100 105 110

Asp Asn His Arg Trp Lys Tyr Val Asn Gly Glu Trp Val Pro Gly Gly
115 120 125

Lys Pro Glu Pro Gln Ala Pro Ser Cys Val Tyr Ile His Pro Asp Ser
130 135 140

Pro Asn Phe Gly Ala His Trp Met Lys Ala Pro Val Ser Phe Ser Lys
145 150 155 160

Val Lys Leu Thr Asn Lys Leu Asn Gly Gly Gly Gln Ile Met Leu Asn

```
                165                 170                 175

Ser Leu His Lys Tyr Glu Pro Arg Ile His Ile Val Arg Val Gly Gly
            180                 185                 190

Pro Gln Arg Met Ile Thr Ser His Cys Phe Pro Glu Thr Gln Phe Ile
        195                 200                 205

Ala Val Thr Ala Tyr Gln Asn Glu Glu Ile Thr Ala Leu Lys Ile Lys
    210                 215                 220

Tyr Asn Pro Phe Ala Lys Ala Phe Leu Asp Ala Lys Glu Arg Ser Asp
225                 230                 235                 240

His Lys Glu Met Met Glu Glu Pro Gly Asp Ser Gln Gln Pro Gly Tyr
                245                 250                 255

Ser Gln Trp Gly Trp Leu Leu Pro Gly Thr Ser Thr Val Cys Pro Pro
            260                 265                 270

Ala Asn Pro His Pro Gln Phe Gly Gly Ala Leu Ser Leu Pro Ser Thr
        275                 280                 285

His Ser Cys Asp Arg Tyr Pro Thr Leu Arg Ser His Arg Ser Ser Pro
    290                 295                 300

Tyr Pro Ser Pro Tyr Ala His Arg Asn Asn Ser Pro Thr Tyr Ser Asp
305                 310                 315                 320

Asn Ser Pro Ala Cys Leu Ser Met Leu Gln Ser His Asp Asn Trp Ser
                325                 330                 335

Ser Leu Gly Met Pro Ala His Pro Ser Met Leu Pro Val Ser His Asn
            340                 345                 350

Ala Ser Pro Pro Thr Ser Ser Ser Gln Tyr Pro Ser Leu Trp Ser Val
        355                 360                 365

Ser Asn Gly Ala Val Thr Pro Gly Ser Gln Ala Ala Ala Val Ser Asn
    370                 375                 380
```

```
Gly Leu Gly Ala Gln Phe Phe Arg Gly Ser Pro Ala His Tyr Thr Pro
385                 390                 395                 400

Leu Thr His Pro Val Ser Ala Pro Ser Ser Ser Gly Ser Pro Leu Tyr
                405                 410                 415

Glu Gly Ala Ala Ala Ala Thr Asp Ile Val Asp Ser Gln Tyr Asp Ala
            420                 425                 430

Ala Ala Gln Gly Arg Leu Ile Ala Ser Trp Thr Pro Val Ser Pro Pro
        435                 440                 445

Ser Met
    450
```

<210> 23
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion protein comprising Brachyury (L254V) Protein encoded by SEQ ID NO:21

<400> 23

```
Met Lys Asn Asn Leu Tyr Glu Glu Lys Met Asn Met Ser Lys Lys Ser
1               5                   10                  15

Ser Pro Gly Thr Glu Ser Ala Gly Lys Ser Leu Gln Tyr Arg Val Asp
            20                  25                  30

His Leu Leu Ser Ala Val Glu Asn Glu Leu Gln Ala Gly Ser Glu Lys
        35                  40                  45

Gly Asp Pro Thr Glu Arg Glu Leu Arg Val Gly Leu Glu Glu Ser Glu
    50                  55                  60

Leu Trp Leu Arg Phe Lys Glu Leu Thr Asn Glu Met Ile Val Thr Lys
65                  70                  75                  80

Asn Gly Arg Arg Met Phe Pro Val Leu Lys Val Asn Val Ser Gly Leu
                85                  90                  95
```

```
Asp Pro Asn Ala Met Tyr Ser Phe Leu Leu Asp Phe Val Ala Ala Asp
            100                 105                 110

Asn His Arg Trp Lys Tyr Val Asn Gly Glu Trp Val Pro Gly Gly Lys
        115                 120                 125

Pro Glu Pro Gln Ala Pro Ser Cys Val Tyr Ile His Pro Asp Ser Pro
    130                 135                 140

Asn Phe Gly Ala His Trp Met Lys Ala Pro Val Ser Phe Ser Lys Val
145                 150                 155                 160

Lys Leu Thr Asn Lys Leu Asn Gly Gly Gly Gln Ile Met Leu Asn Ser
                165                 170                 175

Leu His Lys Tyr Glu Pro Arg Ile His Ile Val Arg Val Gly Gly Pro
            180                 185                 190

Gln Arg Met Ile Thr Ser His Cys Phe Pro Glu Thr Gln Phe Ile Ala
        195                 200                 205

Val Thr Ala Tyr Gln Asn Glu Glu Ile Thr Ala Leu Lys Ile Lys Tyr
    210                 215                 220

Asn Pro Phe Ala Lys Ala Phe Leu Asp Ala Lys Glu Arg Ser Asp His
225                 230                 235                 240

Lys Glu Met Met Glu Glu Pro Gly Asp Ser Gln Gln Pro Gly Tyr Ser
                245                 250                 255

Gln Trp Gly Trp Leu Leu Pro Gly Thr Ser Thr Val Cys Pro Pro Ala
            260                 265                 270

Asn Pro His Pro Gln Phe Gly Gly Ala Leu Ser Leu Pro Ser Thr His
        275                 280                 285

Ser Cys Asp Arg Tyr Pro Thr Leu Arg Ser His Arg Ser Ser Pro Tyr
    290                 295                 300
```

```
Pro Ser Pro Tyr Ala His Arg Asn Asn Ser Pro Thr Tyr Ser Asp Asn
305                 310                 315                 320

Ser Pro Ala Cys Leu Ser Met Leu Gln Ser His Asp Asn Trp Ser Ser
                325                 330                 335

Leu Gly Met Pro Ala His Pro Ser Met Leu Pro Val Ser His Asn Ala
            340                 345                 350

Ser Pro Pro Thr Ser Ser Ser Gln Tyr Pro Ser Leu Trp Ser Val Ser
        355                 360                 365

Asn Gly Ala Val Thr Pro Gly Ser Gln Ala Ala Ala Val Ser Asn Gly
    370                 375                 380

Leu Gly Ala Gln Phe Phe Arg Gly Ser Pro Ala His Tyr Thr Pro Leu
385                 390                 395                 400

Thr His Pro Val Ser Ala Pro Ser Ser Ser Gly Ser Pro Leu Tyr Glu
                405                 410                 415

Gly Ala Ala Ala Ala Thr Asp Ile Val Asp Ser Gln Tyr Asp Ala Ala
            420                 425                 430

Ala Gln Gly Arg Leu Ile Ala Ser Trp Thr Pro Val Ser Pro Pro Ser
        435                 440                 445

Met
```

<210> 24
<211> 1326
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence encoding fusion protein comprising Brachyury (L254V) Protein plus addition of 18 nucleotides from Gene FPV 088

<400> 24
atgaacatga gtaagaaaat gagctcccct ggcaccgaga gcgcgggaaa gagcctgcag 60

taccgagtgg accacctgct gagcgccgtg gagaatgagc tgcaggcggg cagcgagaag 120

ggcgacccca cagagcgcga actgcgcgtg ggcctggagg agagcgagct gtggctgcgc 180

ttcaaggagc tcaccaatga gatgatcgtg accaagaacg gcaggaggat gtttccggtg 240

ctgaaggtga acgtgtctgg cctggacccc aacgccatgt actccttcct gctggacttc 300

gtggcggcgg acaaccaccg ctggaagtac gtgaacgggg aatgggtgcc gggggcaag 360

ccggagccgc aggcgcccag ctgcgtctac atccaccccg actcgcccaa cttcggggcc 420

cactggatga aggctcccgt ctccttcagc aaagtcaagc tcaccaacaa gctcaacgga 480

gggggccaga tcatgctgaa ctccttgcat aagtatgagc ctcgaatcca catagtgaga 540

gttgggggtc cacagcgcat gatcaccagc cactgcttcc ctgagaccca gttcatagcg 600

gtgactgctt atcagaacga ggagatcaca gctcttaaaa ttaagtacaa tccatttgca 660

aaggctttcc ttgatgcaaa ggaaagaagt gatcacaaag agatgatgga ggaacccgga 720

gacagccagc aacctgggta ctcccaatgg gggtggcttc ttcctggaac cagcaccgtt 780

tgtccacctg caaatcctca tcctcagttt ggaggtgccc tctccctccc ctccacgcac 840

agctgtgaca ggtacccaac cctgaggagc caccggtcct caccctaccc cagcccctat 900

gctcatcgga acaattctcc aacctattct gacaactcac ctgcatgttt atccatgctg 960

caatcccatg acaattggtc cagccttgga atgcctgccc atcccagcat gctccccgtg 1020

agccacaatg ccagcccacc taccagctcc agtcagtacc ccagcctgtg gtctgtgagc 1080

aacggcgccg tcaccccggg ctcccaggca gcagccgtgt ccaacgggct gggggcccag 1140

ttcttccggg gctcccccgc gcactacaca cccctcaccc atccggtctc ggcgccctct 1200

tcctcgggat ccccactgta cgaaggggcg gccgcggcca cagacatcgt ggacagccag 1260

tacgacgccg cagcccaagg ccgcctcata gcctcatgga cacctgtgtc gccaccttcc 1320

atgtga 1326

<210> 25
<211> 1323
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence encoding fusion protein comprising Brachyury (L254V) Protein plus addition of 18 nucleotides from Gene FPV 088 without Brachyury atg

<400> 25

atgaacatga gtaagaaaag ctcccctggc accgagagcg cgggaaagag cctgcagtac 60

cgagtggacc acctgctgag cgccgtggag aatgagctgc aggcgggcag cgagaagggc 120

gaccccacag agcgcgaact gcgcgtgggc ctggaggaga gcgagctgtg gctgcgcttc 180

aaggagctca ccaatgagat gatcgtgacc aagaacggca ggaggatgtt tccggtgctg 240

aaggtgaacg tgtctggcct ggaccccaac gccatgtact ccttcctgct ggacttcgtg 300

gcggcggaca accaccgctg gaagtacgtg aacggggaat gggtgccggg gggcaagccg 360

gagccgcagg cgcccagctg cgtctacatc caccccgact cgcccaactt cggggcccac 420

tggatgaagg ctcccgtctc cttcagcaaa gtcaagctca ccaacaagct caacggaggg 480

ggccagatca tgctgaactc cttgcataag tatgagcctc gaatccacat agtgagagtt 540

gggggtccac agcgcatgat caccagccac tgcttccctg agacccagtt catagcggtg 600

actgcttatc agaacgagga gatcacagct cttaaaatta agtacaatcc atttgcaaag 660

gctttccttg atgcaaagga aagaagtgat cacaaagaga tgatggagga acccggagac 720

agccagcaac ctgggtactc ccaatggggg tggcttcttc ctggaaccag caccgtttgt 780

ccacctgcaa atcctcatcc tcagtttgga ggtgccctct ccctcccctc cacgcacagc 840

tgtgacaggt acccaaccct gaggagccac cggtcctcac cctaccccag cccctatgct 900

catcggaaca attctccaac ctattctgac aactcacctg catgtttatc catgctgcaa 960

tcccatgaca attggtccag ccttggaatg cctgcccatc ccagcatgct ccccgtgagc 1020

cacaatgcca gcccacctac cagctccagt cagtacccca gcctgtggtc tgtgagcaac 1080

ggcgccgtca ccccgggctc ccaggcagca gccgtgtcca acgggctggg ggcccagttc 1140

ttccggggct cccccgcgca ctacacaccc ctcacccatc cggtctcggc gccctcttcc 1200

tcgggatccc cactgtacga aggggcggcc gcggccacag acatcgtgga cagccagtac 1260

gacgccgcag cccaaggccg cctcatagcc tcatggacac ctgtgtcgcc accttccatg 1320

tga 1323

<210> 26
<211> 441
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion protein comprising Brachyury (L254V) Protein encoded by

SEQ ID NO:24

<400> 26

```
Met Asn Met Ser Lys Lys Met Ser Ser Pro Gly Thr Glu Ser Ala Gly
1               5                  10                  15

Lys Ser Leu Gln Tyr Arg Val Asp His Leu Leu Ser Ala Val Glu Asn
            20                  25                  30

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

Arg Val Gly Leu Glu Glu Ser Glu Leu Trp Leu Arg Phe Lys Glu Leu
    50                  55                  60

Thr Asn Glu Met Ile Val Thr Lys Asn Gly Arg Arg Met Phe Pro Val
65                  70                  75                  80

Leu Lys Val Asn Val Ser Gly Leu Asp Pro Asn Ala Met Tyr Ser Phe
                85                  90                  95

Leu Leu Asp Phe Val Ala Ala Asp Asn His Arg Trp Lys Tyr Val Asn
            100                 105                 110

Gly Glu Trp Val Pro Gly Gly Lys Pro Glu Pro Gln Ala Pro Ser Cys
        115                 120                 125

Val Tyr Ile His Pro Asp Ser Pro Asn Phe Gly Ala His Trp Met Lys
    130                 135                 140

Ala Pro Val Ser Phe Ser Lys Val Lys Leu Thr Asn Lys Leu Asn Gly
145                 150                 155                 160

Gly Gly Gln Ile Met Leu Asn Ser Leu His Lys Tyr Glu Pro Arg Ile
                165                 170                 175

His Ile Val Arg Val Gly Gly Pro Gln Arg Met Ile Thr Ser His Cys
            180                 185                 190

Phe Pro Glu Thr Gln Phe Ile Ala Val Thr Ala Tyr Gln Asn Glu Glu
        195                 200                 205
```

```
Ile Thr Ala Leu Lys Ile Lys Tyr Asn Pro Phe Ala Lys Ala Phe Leu
    210                 215                 220

Asp Ala Lys Glu Arg Ser Asp His Lys Glu Met Met Glu Glu Pro Gly
225                 230                 235                 240

Asp Ser Gln Gln Pro Gly Tyr Ser Gln Trp Gly Trp Leu Leu Pro Gly
                245                 250                 255

Thr Ser Thr Val Cys Pro Pro Ala Asn Pro His Pro Gln Phe Gly Gly
            260                 265                 270

Ala Leu Ser Leu Pro Ser Thr His Ser Cys Asp Arg Tyr Pro Thr Leu
        275                 280                 285

Arg Ser His Arg Ser Ser Pro Tyr Pro Ser Pro Tyr Ala His Arg Asn
    290                 295                 300

Asn Ser Pro Thr Tyr Ser Asp Asn Ser Pro Ala Cys Leu Ser Met Leu
305                 310                 315                 320

Gln Ser His Asp Asn Trp Ser Ser Leu Gly Met Pro Ala His Pro Ser
                325                 330                 335

Met Leu Pro Val Ser His Asn Ala Ser Pro Pro Thr Ser Ser Ser Gln
            340                 345                 350

Tyr Pro Ser Leu Trp Ser Val Ser Asn Gly Ala Val Thr Pro Gly Ser
        355                 360                 365

Gln Ala Ala Ala Val Ser Asn Gly Leu Gly Ala Gln Phe Phe Arg Gly
    370                 375                 380

Ser Pro Ala His Tyr Thr Pro Leu Thr His Pro Val Ser Ala Pro Ser
385                 390                 395                 400

Ser Ser Gly Ser Pro Leu Tyr Glu Gly Ala Ala Ala Ala Thr Asp Ile
                405                 410                 415
```

```
Val Asp Ser Gln Tyr Asp Ala Ala Ala Gln Gly Arg Leu Ile Ala Ser
            420                 425                 430


Trp Thr Pro Val Ser Pro Pro Ser Met
        435                 440


<210>  27
<211>  440
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Fusion protein comprising Brachyury (L254V) Protein encoded by
       SEQ ID NO:25

<400>  27

Met Asn Met Ser Lys Lys Ser Ser Pro Gly Thr Glu Ser Ala Gly Lys
1               5                   10                  15


Ser Leu Gln Tyr Arg Val Asp His Leu Leu Ser Ala Val Glu Asn Glu
            20                  25                  30


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


Val Gly Leu Glu Glu Ser Glu Leu Trp Leu Arg Phe Lys Glu Leu Thr
    50                  55                  60


Asn Glu Met Ile Val Thr Lys Asn Gly Arg Arg Met Phe Pro Val Leu
65                  70                  75                  80


Lys Val Asn Val Ser Gly Leu Asp Pro Asn Ala Met Tyr Ser Phe Leu
                85                  90                  95


Leu Asp Phe Val Ala Ala Asp Asn His Arg Trp Lys Tyr Val Asn Gly
            100                 105                 110


Glu Trp Val Pro Gly Gly Lys Pro Glu Pro Gln Ala Pro Ser Cys Val
        115                 120                 125


Tyr Ile His Pro Asp Ser Pro Asn Phe Gly Ala His Trp Met Lys Ala
    130                 135                 140
```

```
Pro Val Ser Phe Ser Lys Val Lys Leu Thr Asn Lys Leu Asn Gly Gly
145                 150                 155                 160

Gly Gln Ile Met Leu Asn Ser Leu His Lys Tyr Glu Pro Arg Ile His
                165                 170                 175

Ile Val Arg Val Gly Gly Pro Gln Arg Met Ile Thr Ser His Cys Phe
            180                 185                 190

Pro Glu Thr Gln Phe Ile Ala Val Thr Ala Tyr Gln Asn Glu Glu Ile
        195                 200                 205

Thr Ala Leu Lys Ile Lys Tyr Asn Pro Phe Ala Lys Ala Phe Leu Asp
    210                 215                 220

Ala Lys Glu Arg Ser Asp His Lys Glu Met Met Glu Glu Pro Gly Asp
225                 230                 235                 240

Ser Gln Gln Pro Gly Tyr Ser Gln Trp Gly Trp Leu Leu Pro Gly Thr
                245                 250                 255

Ser Thr Val Cys Pro Pro Ala Asn Pro His Pro Gln Phe Gly Gly Ala
            260                 265                 270

Leu Ser Leu Pro Ser Thr His Ser Cys Asp Arg Tyr Pro Thr Leu Arg
        275                 280                 285

Ser His Arg Ser Ser Pro Tyr Pro Ser Pro Tyr Ala His Arg Asn Asn
    290                 295                 300

Ser Pro Thr Tyr Ser Asp Asn Ser Pro Ala Cys Leu Ser Met Leu Gln
305                 310                 315                 320

Ser His Asp Asn Trp Ser Ser Leu Gly Met Pro Ala His Pro Ser Met
                325                 330                 335

Leu Pro Val Ser His Asn Ala Ser Pro Pro Thr Ser Ser Ser Gln Tyr
            340                 345                 350

Pro Ser Leu Trp Ser Val Ser Asn Gly Ala Val Thr Pro Gly Ser Gln
```

355 360 365

Ala Ala Ala Val Ser Asn Gly Leu Gly Ala Gln Phe Phe Arg Gly Ser
370 375 380

Pro Ala His Tyr Thr Pro Leu Thr His Pro Val Ser Ala Pro Ser Ser
385 390 395 400

Ser Gly Ser Pro Leu Tyr Glu Gly Ala Ala Ala Ala Thr Asp Ile Val
405 410 415

Asp Ser Gln Tyr Asp Ala Ala Ala Gln Gly Arg Leu Ile Ala Ser Trp
420 425 430

Thr Pro Val Ser Pro Pro Ser Met
435 440

<210> 28
<211> 1320
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence encoding Fusion protein comprising Brachyury (L254V) Protein plus addition of 12 nucleotides from Gene FPV 088

<400> 28
atgagtaaga aaatgagctc ccctggcacc gagagcgcgg gaaagagcct gcagtaccga 60

gtggaccacc tgctgagcgc cgtggagaat gagctgcagg cgggcagcga gaagggcgac 120

cccacagagc gcgaactgcg cgtgggcctg gaggagagcg agctgtggct gcgcttcaag 180

gagctcacca atgagatgat cgtgaccaag aacggcagga ggatgtttcc ggtgctgaag 240

gtgaacgtgt ctggcctgga ccccaacgcc atgtactcct tcctgctgga cttcgtggcg 300

gcggacaacc accgctggaa gtacgtgaac ggggaatggg tgccgggggg caagccggag 360

ccgcaggcgc ccagctgcgt ctacatccac cccgactcgc ccaacttcgg ggcccactgg 420

atgaaggctc ccgtctcctt cagcaaagtc aagctcacca acaagctcaa cggaggggc 480

cagatcatgc tgaactcctt gcataagtat gagcctcgaa tccacatagt gagagttggg 540

ggtccacagc gcatgatcac cagccactgc ttccctgaga cccagttcat agcggtgact 600

gcttatcaga acgaggagat cacagctctt aaaattaagt acaatccatt tgcaaaggct 660

ttccttgatg caaaggaaag aagtgatcac aaagagatga tggaggaacc cggagacagc 720

cagcaacctg ggtactccca atgggggtgg cttcttcctg gaaccagcac cgtttgtcca 780

cctgcaaatc ctcatcctca gtttggaggt gccctctccc tcccctccac gcacagctgt 840

gacaggtacc caaccctgag gagccaccgg tcctcaccct accccagccc ctatgctcat 900

cggaacaatt ctccaaccta ttctgacaac tcacctgcat gtttatccat gctgcaatcc 960

catgacaatt ggtccagcct tggaatgcct gcccatccca gcatgctccc cgtgagccac 1020

aatgccagcc cacctaccag ctccagtcag taccccagcc tgtggtctgt gagcaacggc 1080

gccgtcaccc cgggctccca ggcagcagcc gtgtccaacg ggctgggggc ccagttcttc 1140

cggggctccc ccgcgcacta cacacccctc acccatccgg tctcggcgcc ctcttcctcg 1200

ggatccccac tgtacgaagg ggcggccgcg gccacagaca tcgtggacag ccagtacgac 1260

gccgcagccc aaggccgcct catagcctca tggacacctg tgtcgccacc ttccatgtga 1320

<210> 29
<211> 1317
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence encoding Fusion protein comprising Brachyury (L254V) Protein plus addition of 12 nucleotides from Gene FPV 088 without Brachyury atg start codon

<400> 29
atgagtaaga aaagctcccc tggcaccgag agcgcgggaa agagcctgca gtaccgagtg 60

gaccacctgc tgagcgccgt ggagaatgag ctgcaggcgg gcagcgagaa gggcgacccc 120

acagagcgcg aactgcgcgt gggcctggag gagagcgagc tgtggctgcg cttcaaggag 180

ctcaccaatg agatgatcgt gaccaagaac ggcaggagga tgtttccggt gctgaaggtg 240

aacgtgtctg gcctggaccc caacgccatg tactccttcc tgctggactt cgtggcggcg 300

gacaaccacc gctggaagta cgtgaacggg gaatgggtgc cgggggggcaa gccggagccg 360

caggcgccca gctgcgtcta catccacccc gactcgccca acttcggggc ccactggatg 420

aaggctcccg tctccttcag caaagtcaag ctcaccaaca agctcaacgg agggggccag 480

atcatgctga actccttgca taagtatgag cctcgaatcc acatagtgag agttgggggt 540

ccacagcgca tgatcaccag ccactgcttc cctgagaccc agttcatagc ggtgactgct 600

tatcagaacg aggagatcac agctcttaaa attaagtaca atccatttgc aaaggctttc 660

cttgatgcaa aggaaagaag tgatcacaaa gagatgatgg aggaacccgg agacagccag 720

caacctgggt actcccaatg ggggtggctt cttcctggaa ccagcaccgt ttgtccacct 780

gcaaatcctc atcctcagtt tggaggtgcc ctctccctcc cctccacgca cagctgtgac 840

aggtacccaa ccctgaggag ccaccggtcc tcaccctacc ccagccccta tgctcatcgg 900

aacaattctc caacctattc tgacaactca cctgcatgtt tatccatgct gcaatcccat 960

gacaattggt ccagccttgg aatgcctgcc catcccagca tgctccccgt gagccacaat 1020

gccagcccac ctaccagctc cagtcagtac cccagcctgt ggtctgtgag caacggcgcc 1080

gtcaccccgg gctcccaggc agcagccgtg tccaacgggc tgggggccca gttcttccgg 1140

ggctcccccg cgcactacac acccctcacc catccggtct cggcgccctc ttcctcggga 1200

tccccactgt acgaaggggc ggccgcggcc acagacatcg tggacagcca gtacgacgcc 1260

gcagcccaag gccgcctcat agcctcatgg acacctgtgt cgccaccttc catgtga 1317

<210> 30
<211> 439
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion protein comprising Brachyury (L254V) Protein encoded by SEQ ID NO:28

<400> 30

Met Ser Lys Lys Met Ser Ser Pro Gly Thr Glu Ser Ala Gly Lys Ser
1 5 10 15

Leu Gln Tyr Arg Val Asp His Leu Leu Ser Ala Val Glu Asn Glu Leu
20 25 30

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

Gly Leu Glu Glu Ser Glu Leu Trp Leu Arg Phe Lys Glu Leu Thr Asn
50 55 60

Glu Met Ile Val Thr Lys Asn Gly Arg Arg Met Phe Pro Val Leu Lys

```
65                  70                  75                  80

Val Asn Val Ser Gly Leu Asp Pro Asn Ala Met Tyr Ser Phe Leu Leu
                85                  90                  95

Asp Phe Val Ala Ala Asp Asn His Arg Trp Lys Tyr Val Asn Gly Glu
            100                 105                 110

Trp Val Pro Gly Gly Lys Pro Glu Pro Gln Ala Pro Ser Cys Val Tyr
        115                 120                 125

Ile His Pro Asp Ser Pro Asn Phe Gly Ala His Trp Met Lys Ala Pro
    130                 135                 140

Val Ser Phe Ser Lys Val Lys Leu Thr Asn Lys Leu Asn Gly Gly Gly
145                 150                 155                 160

Gln Ile Met Leu Asn Ser Leu His Lys Tyr Glu Pro Arg Ile His Ile
                165                 170                 175

Val Arg Val Gly Gly Pro Gln Arg Met Ile Thr Ser His Cys Phe Pro
            180                 185                 190

Glu Thr Gln Phe Ile Ala Val Thr Ala Tyr Gln Asn Glu Glu Ile Thr
        195                 200                 205

Ala Leu Lys Ile Lys Tyr Asn Pro Phe Ala Lys Ala Phe Leu Asp Ala
    210                 215                 220

Lys Glu Arg Ser Asp His Lys Glu Met Met Glu Glu Pro Gly Asp Ser
225                 230                 235                 240

Gln Gln Pro Gly Tyr Ser Gln Trp Gly Trp Leu Leu Pro Gly Thr Ser
                245                 250                 255

Thr Val Cys Pro Pro Ala Asn Pro His Pro Gln Phe Gly Gly Ala Leu
            260                 265                 270

Ser Leu Pro Ser Thr His Ser Cys Asp Arg Tyr Pro Thr Leu Arg Ser
        275                 280                 285
```

```
His Arg Ser Ser Pro Tyr Pro Ser Pro Tyr Ala His Arg Asn Asn Ser
    290                 295                 300

Pro Thr Tyr Ser Asp Asn Ser Pro Ala Cys Leu Ser Met Leu Gln Ser
305                 310                 315                 320

His Asp Asn Trp Ser Ser Leu Gly Met Pro Ala His Pro Ser Met Leu
                325                 330                 335

Pro Val Ser His Asn Ala Ser Pro Pro Thr Ser Ser Ser Gln Tyr Pro
            340                 345                 350

Ser Leu Trp Ser Val Ser Asn Gly Ala Val Thr Pro Gly Ser Gln Ala
        355                 360                 365

Ala Ala Val Ser Asn Gly Leu Gly Ala Gln Phe Phe Arg Gly Ser Pro
    370                 375                 380

Ala His Tyr Thr Pro Leu Thr His Pro Val Ser Ala Pro Ser Ser Ser
385                 390                 395                 400

Gly Ser Pro Leu Tyr Glu Gly Ala Ala Ala Ala Thr Asp Ile Val Asp
                405                 410                 415

Ser Gln Tyr Asp Ala Ala Ala Gln Gly Arg Leu Ile Ala Ser Trp Thr
            420                 425                 430

Pro Val Ser Pro Pro Ser Met
        435
```

<210> 31
<211> 438
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion protein comprising Brachyury (L254V) Protein encoded by SEQ ID NO:29

<400> 31

```
Met Ser Lys Lys Ser Ser Pro Gly Thr Glu Ser Ala Gly Lys Ser Leu
1               5                   10                  15
```

```
Gln Tyr Arg Val Asp His Leu Leu Ser Ala Val Glu Asn Glu Leu Gln
            20                  25                  30

Ala Gly Ser Glu Lys Gly Asp Pro Thr Glu Arg Glu Leu Arg Val Gly
        35                  40                  45

Leu Glu Glu Ser Glu Leu Trp Leu Arg Phe Lys Glu Leu Thr Asn Glu
    50                  55                  60

Met Ile Val Thr Lys Asn Gly Arg Arg Met Phe Pro Val Leu Lys Val
65                  70                  75                  80

Asn Val Ser Gly Leu Asp Pro Asn Ala Met Tyr Ser Phe Leu Leu Asp
                85                  90                  95

Phe Val Ala Ala Asp Asn His Arg Trp Lys Tyr Val Asn Gly Glu Trp
            100                 105                 110

Val Pro Gly Gly Lys Pro Glu Pro Gln Ala Pro Ser Cys Val Tyr Ile
        115                 120                 125

His Pro Asp Ser Pro Asn Phe Gly Ala His Trp Met Lys Ala Pro Val
    130                 135                 140

Ser Phe Ser Lys Val Lys Leu Thr Asn Lys Leu Asn Gly Gly Gly Gln
145                 150                 155                 160

Ile Met Leu Asn Ser Leu His Lys Tyr Glu Pro Arg Ile His Ile Val
                165                 170                 175

Arg Val Gly Gly Pro Gln Arg Met Ile Thr Ser His Cys Phe Pro Glu
            180                 185                 190

Thr Gln Phe Ile Ala Val Thr Ala Tyr Gln Asn Glu Glu Ile Thr Ala
        195                 200                 205

Leu Lys Ile Lys Tyr Asn Pro Phe Ala Lys Ala Phe Leu Asp Ala Lys
    210                 215                 220
```

```
Glu Arg Ser Asp His Lys Glu Met Met Glu Glu Pro Gly Asp Ser Gln
225                 230                 235                 240

Gln Pro Gly Tyr Ser Gln Trp Gly Trp Leu Leu Pro Gly Thr Ser Thr
                245                 250                 255

Val Cys Pro Pro Ala Asn Pro His Pro Gln Phe Gly Gly Ala Leu Ser
            260                 265                 270

Leu Pro Ser Thr His Ser Cys Asp Arg Tyr Pro Thr Leu Arg Ser His
        275                 280                 285

Arg Ser Ser Pro Tyr Pro Ser Pro Tyr Ala His Arg Asn Asn Ser Pro
    290                 295                 300

Thr Tyr Ser Asp Asn Ser Pro Ala Cys Leu Ser Met Leu Gln Ser His
305                 310                 315                 320

Asp Asn Trp Ser Ser Leu Gly Met Pro Ala His Pro Ser Met Leu Pro
                325                 330                 335

Val Ser His Asn Ala Ser Pro Pro Thr Ser Ser Ser Gln Tyr Pro Ser
            340                 345                 350

Leu Trp Ser Val Ser Asn Gly Ala Val Thr Pro Gly Ser Gln Ala Ala
        355                 360                 365

Ala Val Ser Asn Gly Leu Gly Ala Gln Phe Phe Arg Gly Ser Pro Ala
    370                 375                 380

His Tyr Thr Pro Leu Thr His Pro Val Ser Ala Pro Ser Ser Ser Gly
385                 390                 395                 400

Ser Pro Leu Tyr Glu Gly Ala Ala Ala Ala Thr Asp Ile Val Asp Ser
                405                 410                 415

Gln Tyr Asp Ala Ala Ala Gln Gly Arg Leu Ile Ala Ser Trp Thr Pro
            420                 425                 430

Val Ser Pro Pro Ser Met
        435
```

<210> 32
<211> 1386
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence encoding Fusion protein comprising Brachyury (L254V) Protein plus addition of 75 nucleotides from Gene FPV 088 and an atc

<400> 32
atgaaaaata acttgtatga agaaaaaatg aacatgagta agaaacaagt aaaaactcaa 60

agtaaatgta ataatatcat gagctcccct ggcaccgaga gcgcgggaaa gagcctgcag 120

taccgagtgg accacctgct gagcgccgtg gagaatgagc tgcaggcggg cagcgagaag 180

ggcgacccca cagagcgcga actgcgcgtg ggcctggagg agagcgagct gtggctgcgc 240

ttcaaggagc tcaccaatga gatgatcgtg accaagaacg gcaggaggat gtttccggtg 300

ctgaaggtga acgtgtctgg cctggacccc aacgccatgt actccttcct gctggacttc 360

gtggcggcgg acaaccaccg ctggaagtac gtgaacgggg aatgggtgcc gggggcaag 420

ccggagccgc aggcgcccag ctgcgtctac atccaccccg actcgcccaa cttcggggcc 480

cactggatga aggctcccgt ctccttcagc aaagtcaagc tcaccaacaa gctcaacgga 540

gggggccaga tcatgctgaa ctccttgcat aagtatgagc ctcgaatcca catagtgaga 600

gttgggggtc cacagcgcat gatcaccagc cactgcttcc ctgagaccca gttcatagcg 660

gtgactgctt atcagaacga ggagatcaca gctcttaaaa ttaagtacaa tccatttgca 720

aaggctttcc ttgatgcaaa ggaaagaagt gatcacaaag agatgatgga ggaacccgga 780

gacagccagc aacctgggta ctcccaatgg gggtggcttc ttcctggaac cagcaccgtt 840

tgtccacctg caaatcctca tcctcagttt ggaggtgccc tctccctccc ctccacgcac 900

agctgtgaca ggtacccaac cctgaggagc caccggtcct caccctaccc cagcccctat 960

gctcatcgga acaattctcc aacctattct gacaactcac ctgcatgttt atccatgctg 1020

caatcccatg acaattggtc cagccttgga atgcctgccc atcccagcat gctccccgtg 1080

agccacaatg ccagcccacc taccagctcc agtcagtacc ccagcctgtg gtctgtgagc 1140

aacggcgccg tcaccccggg ctcccaggca gcagccgtgt ccaacgggct gggggcccag 1200

ttcttccggg gctcccccgc gcactacaca cccctcaccc atccggtctc ggcgccctct 1260

tcctcgggat ccccactgta cgaaggggcg gccgcggcca cagacatcgt ggacagccag 1320

tacgacgccg cagcccaagg ccgcctcata gcctcatgga cacctgtgtc gccaccttcc 1380

atgtga 1386

<210> 33
<211> 1383
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence encoding Fusion protein comprising Brachyury (L254V) Protein plus addition of 75 nucleotides from Gene FPV 088 and an atc, without Brachyury atg start codon

<400> 33
atgaaaaata acttgtatga agaaaaaatg aacatgagta agaaacaagt aaaaactcaa 60

agtaaatgta ataatatcag ctcccctggc accgagagcg cgggaaagag cctgcagtac 120

cgagtggacc acctgctgag cgccgtggag aatgagctgc aggcgggcag cgagaagggc 180

gaccccacag agcgcgaact gcgcgtgggc ctggaggaga gcgagctgtg gctgcgcttc 240

aaggagctca ccaatgagat gatcgtgacc aagaacggca ggaggatgtt tccggtgctg 300

aaggtgaacg tgtctggcct ggaccccaac gccatgtact ccttcctgct ggacttcgtg 360

gcggcggaca accaccgctg gaagtacgtg aacggggaat gggtgccggg gggcaagccg 420

gagccgcagg cgcccagctg cgtctacatc caccccgact cgcccaactt cggggcccac 480

tggatgaagg ctcccgtctc cttcagcaaa gtcaagctca ccaacaagct caacggaggg 540

ggccagatca tgctgaactc cttgcataag tatgagcctc gaatccacat agtgagagtt 600

gggggtccac agcgcatgat caccagccac tgcttccctg agacccagtt catagcggtg 660

actgcttatc agaacgagga gatcacagct cttaaaatta agtacaatcc atttgcaaag 720

gctttccttg atgcaaagga aagaagtgat cacaaagaga tgatggagga acccggagac 780

agccagcaac ctgggtactc ccaatggggg tggcttcttc ctggaaccag caccgtttgt 840

ccacctgcaa atcctcatcc tcagtttgga ggtgccctct ccctcccctc cacgcacagc 900

tgtgacaggt acccaaccct gaggagccac cggtcctcac cctaccccag cccctatgct 960

catcggaaca attctccaac ctattctgac aactcacctg catgtttatc catgctgcaa 1020

tcccatgaca attggtccag ccttggaatg cctgcccatc ccagcatgct ccccgtgagc 1080

cacaatgcca gcccacctac cagctccagt cagtacccca gcctgtggtc tgtgagcaac 1140

ggcgccgtca ccccgggctc ccaggcagca gccgtgtcca acgggctggg ggcccagttc 1200

ttccggggct cccccgcgca ctacacaccc ctcacccatc cggtctcggc gccctcttcc 1260

tcgggatccc cactgtacga aggggcggcc gcggccacag acatcgtgga cagccagtac 1320

gacgccgcag cccaaggccg cctcatagcc tcatggacac ctgtgtcgcc accttccatg 1380

tga 1383

<210> 34
<211> 461
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion protein comprising Brachyury (L254V) Protein encoded by SEQ ID NO: 32

<400> 34

Met Lys Asn Asn Leu Tyr Glu Glu Lys Met Asn Met Ser Lys Lys Gln
1 5 10 15

Val Lys Thr Gln Ser Lys Cys Asn Asn Ile Met Ser Ser Pro Gly Thr
20 25 30

Glu Ser Ala Gly Lys Ser Leu Gln Tyr Arg Val Asp His Leu Leu Ser
35 40 45

Ala Val Glu Asn Glu Leu Gln Ala Gly Ser Glu Lys Gly Asp Pro Thr
50 55 60

Glu Arg Glu Leu Arg Val Gly Leu Glu Glu Ser Glu Leu Trp Leu Arg
65 70 75 80

Phe Lys Glu Leu Thr Asn Glu Met Ile Val Thr Lys Asn Gly Arg Arg
85 90 95

Met Phe Pro Val Leu Lys Val Asn Val Ser Gly Leu Asp Pro Asn Ala
100 105 110

Met Tyr Ser Phe Leu Leu Asp Phe Val Ala Ala Asp Asn His Arg Trp

```
        115                 120                 125

Lys Tyr Val Asn Gly Glu Trp Val Pro Gly Gly Lys Pro Glu Pro Gln
    130                 135                 140

Ala Pro Ser Cys Val Tyr Ile His Pro Asp Ser Pro Asn Phe Gly Ala
145                 150                 155                 160

His Trp Met Lys Ala Pro Val Ser Phe Ser Lys Val Lys Leu Thr Asn
                165                 170                 175

Lys Leu Asn Gly Gly Gly Gln Ile Met Leu Asn Ser Leu His Lys Tyr
            180                 185                 190

Glu Pro Arg Ile His Ile Val Arg Val Gly Gly Pro Gln Arg Met Ile
        195                 200                 205

Thr Ser His Cys Phe Pro Glu Thr Gln Phe Ile Ala Val Thr Ala Tyr
    210                 215                 220

Gln Asn Glu Glu Ile Thr Ala Leu Lys Ile Lys Tyr Asn Pro Phe Ala
225                 230                 235                 240

Lys Ala Phe Leu Asp Ala Lys Glu Arg Ser Asp His Lys Glu Met Met
                245                 250                 255

Glu Glu Pro Gly Asp Ser Gln Gln Pro Gly Tyr Ser Gln Trp Gly Trp
            260                 265                 270

Leu Leu Pro Gly Thr Ser Thr Val Cys Pro Pro Ala Asn Pro His Pro
        275                 280                 285

Gln Phe Gly Gly Ala Leu Ser Leu Pro Ser Thr His Ser Cys Asp Arg
    290                 295                 300

Tyr Pro Thr Leu Arg Ser His Arg Ser Ser Pro Tyr Pro Ser Pro Tyr
305                 310                 315                 320

Ala His Arg Asn Asn Ser Pro Thr Tyr Ser Asp Asn Ser Pro Ala Cys
                325                 330                 335
```

```
Leu Ser Met Leu Gln Ser His Asp Asn Trp Ser Ser Leu Gly Met Pro
            340                 345                 350

Ala His Pro Ser Met Leu Pro Val Ser His Asn Ala Ser Pro Pro Thr
        355                 360                 365

Ser Ser Ser Gln Tyr Pro Ser Leu Trp Ser Val Ser Asn Gly Ala Val
    370                 375                 380

Thr Pro Gly Ser Gln Ala Ala Ala Val Ser Asn Gly Leu Gly Ala Gln
385                 390                 395                 400

Phe Phe Arg Gly Ser Pro Ala His Tyr Thr Pro Leu Thr His Pro Val
                405                 410                 415

Ser Ala Pro Ser Ser Ser Gly Ser Pro Leu Tyr Glu Gly Ala Ala Ala
            420                 425                 430

Ala Thr Asp Ile Val Asp Ser Gln Tyr Asp Ala Ala Ala Gln Gly Arg
        435                 440                 445

Leu Ile Ala Ser Trp Thr Pro Val Ser Pro Pro Ser Met
    450                 455                 460
```

<210> 35
<211> 460
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion protein comprising Brachyury (L254V) Protein encoded by SEQ ID NO: 33

<400> 35

```
Met Lys Asn Asn Leu Tyr Glu Glu Lys Met Asn Met Ser Lys Lys Gln
1               5                   10                  15

Val Lys Thr Gln Ser Lys Cys Asn Asn Ile Ser Ser Pro Gly Thr Glu
            20                  25                  30

Ser Ala Gly Lys Ser Leu Gln Tyr Arg Val Asp His Leu Leu Ser Ala
        35                  40                  45
```

```
Val Glu Asn Glu Leu Gln Ala Gly Ser Glu Lys Gly Asp Pro Thr Glu
    50                  55                  60

Arg Glu Leu Arg Val Gly Leu Glu Glu Ser Glu Leu Trp Leu Arg Phe
65                  70                  75                  80

Lys Glu Leu Thr Asn Glu Met Ile Val Thr Lys Asn Gly Arg Arg Met
                85                  90                  95

Phe Pro Val Leu Lys Val Asn Val Ser Gly Leu Asp Pro Asn Ala Met
            100                 105                 110

Tyr Ser Phe Leu Leu Asp Phe Val Ala Ala Asp Asn His Arg Trp Lys
        115                 120                 125

Tyr Val Asn Gly Glu Trp Val Pro Gly Gly Lys Pro Glu Pro Gln Ala
    130                 135                 140

Pro Ser Cys Val Tyr Ile His Pro Asp Ser Pro Asn Phe Gly Ala His
145                 150                 155                 160

Trp Met Lys Ala Pro Val Ser Phe Ser Lys Val Lys Leu Thr Asn Lys
                165                 170                 175

Leu Asn Gly Gly Gly Gln Ile Met Leu Asn Ser Leu His Lys Tyr Glu
            180                 185                 190

Pro Arg Ile His Ile Val Arg Val Gly Gly Pro Gln Arg Met Ile Thr
        195                 200                 205

Ser His Cys Phe Pro Glu Thr Gln Phe Ile Ala Val Thr Ala Tyr Gln
    210                 215                 220

Asn Glu Glu Ile Thr Ala Leu Lys Ile Lys Tyr Asn Pro Phe Ala Lys
225                 230                 235                 240

Ala Phe Leu Asp Ala Lys Glu Arg Ser Asp His Lys Glu Met Met Glu
                245                 250                 255
```

```
Glu Pro Gly Asp Ser Gln Gln Pro Gly Tyr Ser Gln Trp Gly Trp Leu
            260                 265                 270

Leu Pro Gly Thr Ser Thr Val Cys Pro Pro Ala Asn Pro His Pro Gln
        275                 280                 285

Phe Gly Gly Ala Leu Ser Leu Pro Ser Thr His Ser Cys Asp Arg Tyr
    290                 295                 300

Pro Thr Leu Arg Ser His Arg Ser Ser Pro Tyr Pro Ser Pro Tyr Ala
305                 310                 315                 320

His Arg Asn Asn Ser Pro Thr Tyr Ser Asp Asn Ser Pro Ala Cys Leu
                325                 330                 335

Ser Met Leu Gln Ser His Asp Asn Trp Ser Ser Leu Gly Met Pro Ala
            340                 345                 350

His Pro Ser Met Leu Pro Val Ser His Asn Ala Ser Pro Pro Thr Ser
        355                 360                 365

Ser Ser Gln Tyr Pro Ser Leu Trp Ser Val Ser Asn Gly Ala Val Thr
    370                 375                 380

Pro Gly Ser Gln Ala Ala Ala Val Ser Asn Gly Leu Gly Ala Gln Phe
385                 390                 395                 400

Phe Arg Gly Ser Pro Ala His Tyr Thr Pro Leu Thr His Pro Val Ser
                405                 410                 415

Ala Pro Ser Ser Ser Gly Ser Pro Leu Tyr Glu Gly Ala Ala Ala Ala
            420                 425                 430

Thr Asp Ile Val Asp Ser Gln Tyr Asp Ala Ala Ala Gln Gly Arg Leu
        435                 440                 445

Ile Ala Ser Trp Thr Pro Val Ser Pro Pro Ser Met
    450                 455                 460

<210>  36
<211>  1359
```

<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence encoding Fusion protein comprising Brachyury (L254V) Protein plus addition of 48 nucleotides from Gene FPV 088 and an atc

<400> 36
atgaacatga gtaagaaaca agtaaaaact caaagtaaat gtaataatat catgagctcc 60

cctggcaccg agagcgcggg aaagagcctg cagtaccgag tggaccacct gctgagcgcc 120

gtggagaatg agctgcaggc gggcagcgag aagggcgacc ccacagagcg cgaactgcgc 180

gtgggcctgg aggagagcga gctgtggctg cgcttcaagg agctcaccaa tgagatgatc 240

gtgaccaaga acggcaggag gatgtttccg gtgctgaagg tgaacgtgtc tggcctggac 300

cccaacgcca tgtactcctt cctgctggac ttcgtggcgg cggacaacca ccgctggaag 360

tacgtgaacg gggaatgggt gccgggggcc aagccggagc cgcaggcgcc cagctgcgtc 420

tacatccacc ccgactcgcc caacttcggg gcccactgga tgaaggctcc cgtctccttc 480

agcaaagtca agctcaccaa caagctcaac ggaggggccc agatcatgct gaactccttg 540

cataagtatg agcctcgaat ccacatagtg agagttgggg gtccacagcg catgatcacc 600

agccactgct tccctgagac ccagttcata gcggtgactg cttatcagaa cgaggagatc 660

acagctctta aaattaagta caatccattt gcaaaggctt tccttgatgc aaaggaaaga 720

agtgatcaca aagagatgat ggaggaaccc ggagacagcc agcaacctgg gtactcccaa 780

tgggggtggc ttcttcctgg aaccagcacc gtttgtccac ctgcaaatcc tcatcctcag 840

tttggaggtg ccctctccct cccctccacg cacagctgtg acaggtaccc aaccctgagg 900

agccaccggt cctcacccta ccccagcccc tatgctcatc ggaacaattc tccaacctat 960

tctgacaact cacctgcatg tttatccatg ctgcaatccc atgacaattg gtccagcctt 1020

ggaatgcctg cccatcccag catgctcccc gtgagccaca atgccagccc acctaccagc 1080

tccagtcagt accccagcct gtggtctgtg agcaacggcg ccgtcacccc gggctcccag 1140

gcagcagccg tgtccaacgg gctgggggcc cagttcttcc ggggctcccc cgcgcactac 1200

acacccctca cccatccggt ctcggcgccc tcttcctcgg gatccccact gtacgaaggg 1260

gcggccgcgg ccacagacat cgtggacagc cagtacgacg ccgcagccca aggccgcctc 1320

atagcctcat ggacacctgt gtcgccacct tccatgtga 1359

<210> 37
<211> 1356
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence encoding Fusion protein comprising Brachyury (L254V) Protein plus addition of 48 nucleotides from Gene FPV 088 and an atc, without Brachyury atg start codon

<400> 37
atgaacatga gtaagaaaca agtaaaaact caaagtaaat gtaataatat cagctcccct 60

ggcaccgaga gcgcgggaaa gagcctgcag taccgagtgg accacctgct gagcgccgtg 120

gagaatgagc tgcaggcggg cagcgagaag ggcgacccca cagagcgcga actgcgcgtg 180

ggcctggagg agagcgagct gtggctgcgc ttcaaggagc tcaccaatga gatgatcgtg 240

accaagaacg gcaggaggat gtttccggtg ctgaaggtga acgtgtctgg cctggacccc 300

aacgccatgt actccttcct gctggacttc gtggcggcgg acaaccaccg ctggaagtac 360

gtgaacgggg aatgggtgcc ggggggcaag ccggagccgc aggcgcccag ctgcgtctac 420

atccaccccg actcgcccaa cttcggggcc cactggatga aggctcccgt ctccttcagc 480

aaagtcaagc tcaccaacaa gctcaacgga gggggccaga tcatgctgaa ctccttgcat 540

aagtatgagc ctcgaatcca catagtgaga gttgggggtc cacagcgcat gatcaccagc 600

cactgcttcc ctgagaccca gttcatagcg gtgactgctt atcagaacga ggagatcaca 660

gctcttaaaa ttaagtacaa tccatttgca aaggctttcc ttgatgcaaa ggaaagaagt 720

gatcacaaag agatgatgga ggaacccgga gacagccagc aacctgggta ctcccaatgg 780

gggtggcttc ttcctggaac cagcaccgtt tgtccacctg caaatcctca tcctcagttt 840

ggaggtgccc tctccctccc ctccacgcac agctgtgaca ggtacccaac cctgaggagc 900

caccggtcct caccctaccc cagcccctat gctcatcgga acaattctcc aacctattct 960

gacaactcac ctgcatgttt atccatgctg caatcccatg acaattggtc cagccttgga 1020

atgcctgccc atcccagcat gctccccgtg agccacaatg ccagcccacc taccagctcc 1080

agtcagtacc ccagcctgtg gtctgtgagc aacggcgccg tcaccccggg ctcccaggca 1140

gcagccgtgt ccaacgggct gggggcccag ttcttccggg gctcccccgc gcactacaca 1200

cccctcaccc atccggtctc ggcgccctct tcctcgggat ccccactgta cgaaggggcg 1260

gccgcggcca cagacatcgt ggacagccag tacgacgccg cagcccaagg ccgcctcata 1320

gcctcatgga cacctgtgtc gccaccttcc atgtga 1356

<210> 38
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion protein comprising Brachyury (L254V) Protein encoded by SEQ ID NO:36

<400> 38

Met Asn Met Ser Lys Lys Gln Val Lys Thr Gln Ser Lys Cys Asn Asn
1 5 10 15

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

Arg Val Asp His Leu Leu Ser Ala Val Glu Asn Glu Leu Gln Ala Gly
35 40 45

Ser Glu Lys Gly Asp Pro Thr Glu Arg Glu Leu Arg Val Gly Leu Glu
50 55 60

Glu Ser Glu Leu Trp Leu Arg Phe Lys Glu Leu Thr Asn Glu Met Ile
65 70 75 80

Val Thr Lys Asn Gly Arg Arg Met Phe Pro Val Leu Lys Val Asn Val
85 90 95

Ser Gly Leu Asp Pro Asn Ala Met Tyr Ser Phe Leu Leu Asp Phe Val
100 105 110

Ala Ala Asp Asn His Arg Trp Lys Tyr Val Asn Gly Glu Trp Val Pro
115 120 125

Gly Gly Lys Pro Glu Pro Gln Ala Pro Ser Cys Val Tyr Ile His Pro
130 135 140

Asp Ser Pro Asn Phe Gly Ala His Trp Met Lys Ala Pro Val Ser Phe

```
145                 150                 155                 160

Ser Lys Val Lys Leu Thr Asn Lys Leu Asn Gly Gly Gly Gln Ile Met
                165                 170                 175

Leu Asn Ser Leu His Lys Tyr Glu Pro Arg Ile His Ile Val Arg Val
            180                 185                 190

Gly Gly Pro Gln Arg Met Ile Thr Ser His Cys Phe Pro Glu Thr Gln
        195                 200                 205

Phe Ile Ala Val Thr Ala Tyr Gln Asn Glu Glu Ile Thr Ala Leu Lys
    210                 215                 220

Ile Lys Tyr Asn Pro Phe Ala Lys Ala Phe Leu Asp Ala Lys Glu Arg
225                 230                 235                 240

Ser Asp His Lys Glu Met Met Glu Glu Pro Gly Asp Ser Gln Gln Pro
                245                 250                 255

Gly Tyr Ser Gln Trp Gly Trp Leu Leu Pro Gly Thr Ser Thr Val Cys
            260                 265                 270

Pro Pro Ala Asn Pro His Pro Gln Phe Gly Gly Ala Leu Ser Leu Pro
        275                 280                 285

Ser Thr His Ser Cys Asp Arg Tyr Pro Thr Leu Arg Ser His Arg Ser
    290                 295                 300

Ser Pro Tyr Pro Ser Pro Tyr Ala His Arg Asn Asn Ser Pro Thr Tyr
305                 310                 315                 320

Ser Asp Asn Ser Pro Ala Cys Leu Ser Met Leu Gln Ser His Asp Asn
                325                 330                 335

Trp Ser Ser Leu Gly Met Pro Ala His Pro Ser Met Leu Pro Val Ser
            340                 345                 350

His Asn Ala Ser Pro Pro Thr Ser Ser Ser Gln Tyr Pro Ser Leu Trp
        355                 360                 365
```

Ser Val Ser Asn Gly Ala Val Thr Pro Gly Ser Gln Ala Ala Ala Val
370 375 380

Ser Asn Gly Leu Gly Ala Gln Phe Phe Arg Gly Ser Pro Ala His Tyr
385 390 395 400

Thr Pro Leu Thr His Pro Val Ser Ala Pro Ser Ser Ser Gly Ser Pro
405 410 415

Leu Tyr Glu Gly Ala Ala Ala Ala Thr Asp Ile Val Asp Ser Gln Tyr
420 425 430

Asp Ala Ala Ala Gln Gly Arg Leu Ile Ala Ser Trp Thr Pro Val Ser
435 440 445

Pro Pro Ser Met
450

<210> 39
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion protein comprising Brachyury (L254V) Protein encoded by SEQ ID NO:37

<400> 39

Met Asn Met Ser Lys Lys Gln Val Lys Thr Gln Ser Lys Cys Asn Asn
1 5 10 15

Ile Ser Ser Pro Gly Thr Glu Ser Ala Gly Lys Ser Leu Gln Tyr Arg
20 25 30

Val Asp His Leu Leu Ser Ala Val Glu Asn Glu Leu Gln Ala Gly Ser
35 40 45

Glu Lys Gly Asp Pro Thr Glu Arg Glu Leu Arg Val Gly Leu Glu Glu
50 55 60

Ser Glu Leu Trp Leu Arg Phe Lys Glu Leu Thr Asn Glu Met Ile Val
65 70 75 80

```
Thr Lys Asn Gly Arg Arg Met Phe Pro Val Leu Lys Val Asn Val Ser
                85                  90                  95

Gly Leu Asp Pro Asn Ala Met Tyr Ser Phe Leu Leu Asp Phe Val Ala
            100                 105                 110

Ala Asp Asn His Arg Trp Lys Tyr Val Asn Gly Glu Trp Val Pro Gly
        115                 120                 125

Gly Lys Pro Glu Pro Gln Ala Pro Ser Cys Val Tyr Ile His Pro Asp
    130                 135                 140

Ser Pro Asn Phe Gly Ala His Trp Met Lys Ala Pro Val Ser Phe Ser
145                 150                 155                 160

Lys Val Lys Leu Thr Asn Lys Leu Asn Gly Gly Gly Gln Ile Met Leu
                165                 170                 175

Asn Ser Leu His Lys Tyr Glu Pro Arg Ile His Ile Val Arg Val Gly
            180                 185                 190

Gly Pro Gln Arg Met Ile Thr Ser His Cys Phe Pro Glu Thr Gln Phe
        195                 200                 205

Ile Ala Val Thr Ala Tyr Gln Asn Glu Glu Ile Thr Ala Leu Lys Ile
    210                 215                 220

Lys Tyr Asn Pro Phe Ala Lys Ala Phe Leu Asp Ala Lys Glu Arg Ser
225                 230                 235                 240

Asp His Lys Glu Met Met Glu Glu Pro Gly Asp Ser Gln Gln Pro Gly
                245                 250                 255

Tyr Ser Gln Trp Gly Trp Leu Leu Pro Gly Thr Ser Thr Val Cys Pro
            260                 265                 270

Pro Ala Asn Pro His Pro Gln Phe Gly Gly Ala Leu Ser Leu Pro Ser
        275                 280                 285
```

```
Thr His Ser Cys Asp Arg Tyr Pro Thr Leu Arg Ser His Arg Ser Ser
    290                 295                 300

Pro Tyr Pro Ser Pro Tyr Ala His Arg Asn Asn Ser Pro Thr Tyr Ser
305                 310                 315                 320

Asp Asn Ser Pro Ala Cys Leu Ser Met Leu Gln Ser His Asp Asn Trp
                325                 330                 335

Ser Ser Leu Gly Met Pro Ala His Pro Ser Met Leu Pro Val Ser His
            340                 345                 350

Asn Ala Ser Pro Pro Thr Ser Ser Ser Gln Tyr Pro Ser Leu Trp Ser
        355                 360                 365

Val Ser Asn Gly Ala Val Thr Pro Gly Ser Gln Ala Ala Ala Val Ser
    370                 375                 380

Asn Gly Leu Gly Ala Gln Phe Phe Arg Gly Ser Pro Ala His Tyr Thr
385                 390                 395                 400

Pro Leu Thr His Pro Val Ser Ala Pro Ser Ser Ser Gly Ser Pro Leu
                405                 410                 415

Tyr Glu Gly Ala Ala Ala Ala Thr Asp Ile Val Asp Ser Gln Tyr Asp
            420                 425                 430

Ala Ala Ala Gln Gly Arg Leu Ile Ala Ser Trp Thr Pro Val Ser Pro
        435                 440                 445

Pro Ser Met
    450
```

<210> 40
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence encoding Fusion protein comprising Brachyury (L254V) Protein plus addition of 42 nucleotides from Gene FPV 088 and an atc

<400> 40
atgagtaaga aacaagtaaa aactcaaagt aaatgtaata atatcatgag ctcccctggc 60

accgagagcg cgggaaagag cctgcagtac cgagtggacc acctgctgag cgccgtggag 120

aatgagctgc aggcgggcag cgagaagggc gaccccacag agcgcgaact gcgcgtgggc 180

ctggaggaga gcgagctgtg gctgcgcttc aaggagctca ccaatgagat gatcgtgacc 240

aagaacggca ggaggatgtt tccggtgctg aaggtgaacg tgtctggcct ggaccccaac 300

gccatgtact ccttcctgct ggacttcgtg gcggcggaca accaccgctg gaagtacgtg 360

aacggggaat gggtgccggg gggcaagccg gagccgcagg cgcccagctg cgtctacatc 420

caccccgact cgcccaactt cggggcccac tggatgaagg ctcccgtctc cttcagcaaa 480

gtcaagctca ccaacaagct caacggaggg ggccagatca tgctgaactc cttgcataag 540

tatgagcctc gaatccacat agtgagagtt gggggtccac agcgcatgat caccagccac 600

tgcttccctg agacccagtt catagcggtg actgcttatc agaacgagga gatcacagct 660

cttaaaatta agtacaatcc atttgcaaag gctttccttg atgcaaagga aagaagtgat 720

cacaaagaga tgatggagga acccggagac agccagcaac ctgggtactc ccaatggggg 780

tggcttcttc ctggaaccag caccgtttgt ccacctgcaa atcctcatcc tcagtttgga 840

ggtgccctct ccctcccctc cacgcacagc tgtgacaggt acccaaccct gaggagccac 900

cggtcctcac cctaccccag cccctatgct catcggaaca attctccaac ctattctgac 960

aactcacctg catgtttatc catgctgcaa tcccatgaca attggtccag ccttggaatg 1020

cctgcccatc ccagcatgct ccccgtgagc cacaatgcca gcccacctac cagctccagt 1080

cagtacccca gcctgtggtc tgtgagcaac ggcgccgtca ccccgggctc ccaggcagca 1140

gccgtgtcca acgggctggg ggcccagttc ttccggggct cccccgcgca ctacacaccc 1200

ctcacccatc cggtctcggc gccctcttcc tcgggatccc cactgtacga aggggcggcc 1260

gcggccacag acatcgtgga cagccagtac gacgccgcag cccaaggccg cctcatagcc 1320

tcatggacac ctgtgtcgcc accttccatg tga 1353

<210> 41
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>

<223> Coding sequence encoding Fusion protein comprising Brachyury (L254V) Protein plus addition of 42 nucleotides from Gene FPV 088 and an atc, without Brachyury atg start codon

<400> 41

atgagtaaga aacaagtaaa aactcaaagt aaatgtaata atatcagctc ccctggcacc 60

gagagcgcgg gaaagagcct gcagtaccga gtggaccacc tgctgagcgc cgtggagaat 120

gagctgcagg cgggcagcga gaagggcgac cccacagagc gcgaactgcg cgtgggcctg 180

gaggagagcg agctgtggct gcgcttcaag gagctcacca atgagatgat cgtgaccaag 240

aacggcagga ggatgtttcc ggtgctgaag gtgaacgtgt ctggcctgga ccccaacgcc 300

atgtactcct tcctgctgga cttcgtggcg gcggacaacc accgctggaa gtacgtgaac 360

ggggaatggg tgccgggggg caagccggag ccgcaggcgc ccagctgcgt ctacatccac 420

cccgactcgc ccaacttcgg ggcccactgg atgaaggctc ccgtctcctt cagcaaagtc 480

aagctcacca acaagctcaa cggaggggc cagatcatgc tgaactcctt gcataagtat 540

gagcctcgaa tccacatagt gagagttggg ggtccacagc gcatgatcac cagccactgc 600

ttccctgaga cccagttcat agcggtgact gcttatcaga acgaggagat cacagctctt 660

aaaattaagt acaatccatt tgcaaaggct ttccttgatg caaaggaaag aagtgatcac 720

aaagagatga tggaggaacc cggagacagc cagcaacctg ggtactccca atgggggtgg 780

cttcttcctg gaaccagcac cgtttgtcca cctgcaaatc ctcatcctca gtttggaggt 840

gccctctccc tcccctccac gcacagctgt gacaggtacc caaccctgag gagccaccgg 900

tcctcaccct accccagccc ctatgctcat cggaacaatt ctccaaccta ttctgacaac 960

tcacctgcat gtttatccat gctgcaatcc catgacaatt ggtccagcct tggaatgcct 1020

gcccatccca gcatgctccc cgtgagccac aatgccagcc cacctaccag ctccagtcag 1080

taccccagcc tgtggtctgt gagcaacggc gccgtcaccc cgggctccca ggcagcagcc 1140

gtgtccaacg ggctgggggc ccagttcttc cggggctccc ccgcgcacta cacacccctc 1200

acccatccgg tctcggcgcc ctcttcctcg ggatccccac tgtacgaagg ggcggccgcg 1260

gccacagaca tcgtggacag ccagtacgac gccgcagccc aaggccgcct catagcctca 1320

tggacacctg tgtcgccacc ttccatgtga 1350

<210> 42
<211> 450

<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion protein comprising Brachyury (L254V) Protein encoded by SEQ ID NO:40

<400> 42

Met Ser Lys Lys Gln Val Lys Thr Gln Ser Lys Cys Asn Asn Ile Met
1 5 10 15

Ser Ser Pro Gly Thr Glu Ser Ala Gly Lys Ser Leu Gln Tyr Arg Val
20 25 30

Asp His Leu Leu Ser Ala Val Glu Asn Glu Leu Gln Ala Gly Ser Glu
35 40 45

Lys Gly Asp Pro Thr Glu Arg Glu Leu Arg Val Gly Leu Glu Glu Ser
50 55 60

Glu Leu Trp Leu Arg Phe Lys Glu Leu Thr Asn Glu Met Ile Val Thr
65 70 75 80

Lys Asn Gly Arg Arg Met Phe Pro Val Leu Lys Val Asn Val Ser Gly
85 90 95

Leu Asp Pro Asn Ala Met Tyr Ser Phe Leu Leu Asp Phe Val Ala Ala
100 105 110

Asp Asn His Arg Trp Lys Tyr Val Asn Gly Glu Trp Val Pro Gly Gly
115 120 125

Lys Pro Glu Pro Gln Ala Pro Ser Cys Val Tyr Ile His Pro Asp Ser
130 135 140

Pro Asn Phe Gly Ala His Trp Met Lys Ala Pro Val Ser Phe Ser Lys
145 150 155 160

Val Lys Leu Thr Asn Lys Leu Asn Gly Gly Gly Gln Ile Met Leu Asn
165 170 175

Ser Leu His Lys Tyr Glu Pro Arg Ile His Ile Val Arg Val Gly Gly

```
            180                 185                 190

Pro Gln Arg Met Ile Thr Ser His Cys Phe Pro Glu Thr Gln Phe Ile
        195                 200                 205

Ala Val Thr Ala Tyr Gln Asn Glu Glu Ile Thr Ala Leu Lys Ile Lys
    210                 215                 220

Tyr Asn Pro Phe Ala Lys Ala Phe Leu Asp Ala Lys Glu Arg Ser Asp
225                 230                 235                 240

His Lys Glu Met Met Glu Glu Pro Gly Asp Ser Gln Gln Pro Gly Tyr
                245                 250                 255

Ser Gln Trp Gly Trp Leu Leu Pro Gly Thr Ser Thr Val Cys Pro Pro
            260                 265                 270

Ala Asn Pro His Pro Gln Phe Gly Gly Ala Leu Ser Leu Pro Ser Thr
        275                 280                 285

His Ser Cys Asp Arg Tyr Pro Thr Leu Arg Ser His Arg Ser Ser Pro
    290                 295                 300

Tyr Pro Ser Pro Tyr Ala His Arg Asn Asn Ser Pro Thr Tyr Ser Asp
305                 310                 315                 320

Asn Ser Pro Ala Cys Leu Ser Met Leu Gln Ser His Asp Asn Trp Ser
                325                 330                 335

Ser Leu Gly Met Pro Ala His Pro Ser Met Leu Pro Val Ser His Asn
            340                 345                 350

Ala Ser Pro Pro Thr Ser Ser Ser Gln Tyr Pro Ser Leu Trp Ser Val
        355                 360                 365

Ser Asn Gly Ala Val Thr Pro Gly Ser Gln Ala Ala Ala Val Ser Asn
    370                 375                 380

Gly Leu Gly Ala Gln Phe Phe Arg Gly Ser Pro Ala His Tyr Thr Pro
385                 390                 395                 400
```

```
Leu Thr His Pro Val Ser Ala Pro Ser Ser Ser Gly Ser Pro Leu Tyr
                405                 410                 415


Glu Gly Ala Ala Ala Ala Thr Asp Ile Val Asp Ser Gln Tyr Asp Ala
            420                 425                 430


Ala Ala Gln Gly Arg Leu Ile Ala Ser Trp Thr Pro Val Ser Pro Pro
        435                 440                 445


Ser Met
    450
```

<210> 43
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion protein comprising Brachyury (L254V) Protein encoded by SEQ ID NO:41

<400> 43

```
Met Ser Lys Lys Gln Val Lys Thr Gln Ser Lys Cys Asn Asn Ile Ser
1               5                   10                  15


Ser Pro Gly Thr Glu Ser Ala Gly Lys Ser Leu Gln Tyr Arg Val Asp
            20                  25                  30


His Leu Leu Ser Ala Val Glu Asn Glu Leu Gln Ala Gly Ser Glu Lys
        35                  40                  45


Gly Asp Pro Thr Glu Arg Glu Leu Arg Val Gly Leu Glu Glu Ser Glu
    50                  55                  60


Leu Trp Leu Arg Phe Lys Glu Leu Thr Asn Glu Met Ile Val Thr Lys
65                  70                  75                  80


Asn Gly Arg Arg Met Phe Pro Val Leu Lys Val Asn Val Ser Gly Leu
                85                  90                  95


Asp Pro Asn Ala Met Tyr Ser Phe Leu Leu Asp Phe Val Ala Ala Asp
            100                 105                 110
```

```
Asn His Arg Trp Lys Tyr Val Asn Gly Glu Trp Val Pro Gly Gly Lys
        115                 120                 125

Pro Glu Pro Gln Ala Pro Ser Cys Val Tyr Ile His Pro Asp Ser Pro
    130                 135                 140

Asn Phe Gly Ala His Trp Met Lys Ala Pro Val Ser Phe Ser Lys Val
145                 150                 155                 160

Lys Leu Thr Asn Lys Leu Asn Gly Gly Gly Gln Ile Met Leu Asn Ser
                165                 170                 175

Leu His Lys Tyr Glu Pro Arg Ile His Ile Val Arg Val Gly Gly Pro
            180                 185                 190

Gln Arg Met Ile Thr Ser His Cys Phe Pro Glu Thr Gln Phe Ile Ala
        195                 200                 205

Val Thr Ala Tyr Gln Asn Glu Glu Ile Thr Ala Leu Lys Ile Lys Tyr
    210                 215                 220

Asn Pro Phe Ala Lys Ala Phe Leu Asp Ala Lys Glu Arg Ser Asp His
225                 230                 235                 240

Lys Glu Met Met Glu Glu Pro Gly Asp Ser Gln Gln Pro Gly Tyr Ser
                245                 250                 255

Gln Trp Gly Trp Leu Leu Pro Gly Thr Ser Thr Val Cys Pro Pro Ala
            260                 265                 270

Asn Pro His Pro Gln Phe Gly Gly Ala Leu Ser Leu Pro Ser Thr His
        275                 280                 285

Ser Cys Asp Arg Tyr Pro Thr Leu Arg Ser His Arg Ser Ser Pro Tyr
    290                 295                 300

Pro Ser Pro Tyr Ala His Arg Asn Asn Ser Pro Thr Tyr Ser Asp Asn
305                 310                 315                 320
```

```
Ser Pro Ala Cys Leu Ser Met Leu Gln Ser His Asp Asn Trp Ser Ser
                325                 330                 335

Leu Gly Met Pro Ala His Pro Ser Met Leu Pro Val Ser His Asn Ala
            340                 345                 350

Ser Pro Pro Thr Ser Ser Ser Gln Tyr Pro Ser Leu Trp Ser Val Ser
        355                 360                 365

Asn Gly Ala Val Thr Pro Gly Ser Gln Ala Ala Ala Val Ser Asn Gly
    370                 375                 380

Leu Gly Ala Gln Phe Phe Arg Gly Ser Pro Ala His Tyr Thr Pro Leu
385                 390                 395                 400

Thr His Pro Val Ser Ala Pro Ser Ser Ser Gly Ser Pro Leu Tyr Glu
                405                 410                 415

Gly Ala Ala Ala Ala Thr Asp Ile Val Asp Ser Gln Tyr Asp Ala Ala
            420                 425                 430

Ala Gln Gly Arg Leu Ile Ala Ser Trp Thr Pro Val Ser Pro Pro Ser
        435                 440                 445

Met
```

<210> 44
<211> 1323
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence encoding fusion protein comprising Brachyury protein Isoform 1 plus addition of 15 nucleotides from Gene FPV 088

<400> 44
atgaaaaata acttgatgag ctcccctggc accgagagcg cgggaaagag cctgcagtac 60

cgagtggacc acctgctgag cgccgtggag aatgagctgc aggcgggcag cgagaagggc 120

gaccccacag agcgcgaact gcgcgtgggc ctggaggaga gcgagctgtg gctgcgcttc 180

aaggagctca ccaatgagat gatcgtgacc aagaacggca ggaggatgtt tccggtgctg 240

aaggtgaacg tgtctggcct ggaccccaac gccatgtact ccttcctgct ggacttcgtg 300

gcggcggaca accaccgctg gaagtacgtg aacggggaat gggtgccggg gggcaagccg 360

gagccgcagg cgcccagctg cgtctacatc caccccgact cgcccaactt cggggcccac 420

tggatgaagg ctcccgtctc cttcagcaaa gtcaagctca ccaacaagct caacggaggg 480

ggccagatca tgctgaactc cttgcataag tatgagcctc gaatccacat agtgagagtt 540

gggggtccac agcgcatgat caccagccac tgcttccctg agacccagtt catagcggtg 600

actgcttatc agaacgagga gatcacagct cttaaaatta agtacaatcc atttgcaaaa 660

gctttccttg atgcaaagga aagaagtgat cacaaagaga tgatggagga acccggagac 720

agccagcaac ctgggtactc ccaatggggg tggcttcttc ctggaaccag caccgtttgt 780

ccacctgcaa atcctcatcc tcagtttgga ggtgccctct ccctcccctc cacgcacagc 840

tgtgacaggt acccaaccct gaggagccac cggtcctcac cctaccccag cccctatgct 900

catcggaaca attctccaac ctattctgac aactcacctg catgtttatc catgctgcaa 960

tcccatgaca attggtccag ccttggaatg cctgcccatc ccagcatgct ccccgtgagc 1020

cacaatgcca gcccacctac cagctccagt cagtacccca gcctgtggtc tgtgagcaac 1080

ggcgccgtca ccccgggctc ccaggcagca gccgtgtcca acgggctggg ggcccagttc 1140

ttccggggct cccccgcgca ctacacaccc ctcacccatc cggtctcggc gccctcttcc 1200

tcgggatccc cactgtacga aggggcggcc gcggccacag acatcgtgga cagccagtac 1260

gacgccgcag cccaaggccg cctcatagcc tcatggacac ctgtgtcgcc accttccatg 1320

tga 1323

<210> 45
<211> 1320
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence encoding fusion protein comprising Brachyury protein Isoform 1 plus addition of 15 nucleotides from Gene FPV 088 without Brachyury protein atg start codon

<400> 45
atgaaaaata acttgagctc ccctggcacc gagagcgcgg gaaagagcct gcagtaccga 60

gtggaccacc tgctgagcgc cgtggagaat gagctgcagg cgggcagcga gaagggcgac 120

cccacagagc gcgaactgcg cgtgggcctg gaggagagcg agctgtggct gcgcttcaag 180

gagctcacca atgagatgat cgtgaccaag aacggcagga ggatgtttcc ggtgctgaag 240

gtgaacgtgt ctggcctgga ccccaacgcc atgtactcct tcctgctgga cttcgtggcg 300

gcggacaacc accgctggaa gtacgtgaac ggggaatggg tgccgggggg caagccggag 360

ccgcaggcgc ccagctgcgt ctacatccac cccgactcgc ccaacttcgg ggcccactgg 420

atgaaggctc ccgtctcctt cagcaaagtc aagctcacca acaagctcaa cggaggggc 480

cagatcatgc tgaactcctt gcataagtat gagcctcgaa tccacatagt gagagttggg 540

ggtccacagc gcatgatcac cagccactgc ttccctgaga cccagttcat agcggtgact 600

gcttatcaga acgaggagat cacagctctt aaaattaagt acaatccatt tgcaaaagct 660

ttccttgatg caaaggaaag aagtgatcac aaagagatga tggaggaacc cggagacagc 720

cagcaacctg ggtactccca atgggggtgg cttcttcctg gaaccagcac cgtttgtcca 780

cctgcaaatc ctcatcctca gtttggaggt gccctctccc tcccctccac gcacagctgt 840

gacaggtacc caaccctgag gagccaccgg tcctcaccct accccagccc ctatgctcat 900

cggaacaatt ctccaaccta ttctgacaac tcacctgcat gtttatccat gctgcaatcc 960

catgacaatt ggtccagcct tggaatgcct gcccatccca gcatgctccc cgtgagccac 1020

aatgccagcc cacctaccag ctccagtcag taccccagcc tgtggtctgt gagcaacggc 1080

gccgtcaccc cgggctccca ggcagcagcc gtgtccaacg ggctgggggc ccagttcttc 1140

cggggctccc ccgcgcacta cacacccctc acccatccgg tctcggcgcc ctcttcctcg 1200

ggatccccac tgtacgaagg ggcggccgcg gccacagaca tcgtggacag ccagtacgac 1260

gccgcagccc aaggccgcct catagcctca tggacacctg tgtcgccacc ttccatgtga 1320

<210> 46
<211> 440
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion protein comprising Brachyury protein Isoform 1 encoded by SEQ ID NO:44

<400> 46

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

```
1               5                   10                  15

Ser Leu Gln Tyr Arg Val Asp His Leu Leu Ser Ala Val Glu Asn Glu
            20                  25                  30

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

Val Gly Leu Glu Glu Ser Glu Leu Trp Leu Arg Phe Lys Glu Leu Thr
    50                  55                  60

Asn Glu Met Ile Val Thr Lys Asn Gly Arg Arg Met Phe Pro Val Leu
65                  70                  75                  80

Lys Val Asn Val Ser Gly Leu Asp Pro Asn Ala Met Tyr Ser Phe Leu
                85                  90                  95

Leu Asp Phe Val Ala Ala Asp Asn His Arg Trp Lys Tyr Val Asn Gly
            100                 105                 110

Glu Trp Val Pro Gly Gly Lys Pro Glu Pro Gln Ala Pro Ser Cys Val
        115                 120                 125

Tyr Ile His Pro Asp Ser Pro Asn Phe Gly Ala His Trp Met Lys Ala
    130                 135                 140

Pro Val Ser Phe Ser Lys Val Lys Leu Thr Asn Lys Leu Asn Gly Gly
145                 150                 155                 160

Gly Gln Ile Met Leu Asn Ser Leu His Lys Tyr Glu Pro Arg Ile His
                165                 170                 175

Ile Val Arg Val Gly Gly Pro Gln Arg Met Ile Thr Ser His Cys Phe
            180                 185                 190

Pro Glu Thr Gln Phe Ile Ala Val Thr Ala Tyr Gln Asn Glu Glu Ile
        195                 200                 205

Thr Ala Leu Lys Ile Lys Tyr Asn Pro Phe Ala Lys Ala Phe Leu Asp
    210                 215                 220
```

```
Ala Lys Glu Arg Ser Asp His Lys Glu Met Met Glu Glu Pro Gly Asp
225                 230                 235                 240

Ser Gln Gln Pro Gly Tyr Ser Gln Trp Gly Trp Leu Leu Pro Gly Thr
                245                 250                 255

Ser Thr Leu Cys Pro Pro Ala Asn Pro His Pro Gln Phe Gly Gly Ala
            260                 265                 270

Leu Ser Leu Pro Ser Thr His Ser Cys Asp Arg Tyr Pro Thr Leu Arg
        275                 280                 285

Ser His Arg Ser Ser Pro Tyr Pro Ser Pro Tyr Ala His Arg Asn Asn
    290                 295                 300

Ser Pro Thr Tyr Ser Asp Asn Ser Pro Ala Cys Leu Ser Met Leu Gln
305                 310                 315                 320

Ser His Asp Asn Trp Ser Ser Leu Gly Met Pro Ala His Pro Ser Met
                325                 330                 335

Leu Pro Val Ser His Asn Ala Ser Pro Pro Thr Ser Ser Ser Gln Tyr
            340                 345                 350

Pro Ser Leu Trp Ser Val Ser Asn Gly Ala Val Thr Pro Gly Ser Gln
        355                 360                 365

Ala Ala Ala Val Ser Asn Gly Leu Gly Ala Gln Phe Phe Arg Gly Ser
    370                 375                 380

Pro Ala His Tyr Thr Pro Leu Thr His Pro Val Ser Ala Pro Ser Ser
385                 390                 395                 400

Ser Gly Ser Pro Leu Tyr Glu Gly Ala Ala Ala Ala Thr Asp Ile Val
                405                 410                 415

Asp Ser Gln Tyr Asp Ala Ala Ala Gln Gly Arg Leu Ile Ala Ser Trp
            420                 425                 430

Thr Pro Val Ser Pro Pro Ser Met
```

435 440

<210> 47
<211> 439
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion protein comprising Brachyury protein Isoform 1 encoded by SEQ ID NO:45

<400> 47

Met Lys Asn Asn Leu Ser Ser Pro Gly Thr Glu Ser Ala Gly Lys Ser
1 5 10 15

Leu Gln Tyr Arg Val Asp His Leu Leu Ser Ala Val Glu Asn Glu Leu
20 25 30

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

Gly Leu Glu Glu Ser Glu Leu Trp Leu Arg Phe Lys Glu Leu Thr Asn
50 55 60

Glu Met Ile Val Thr Lys Asn Gly Arg Arg Met Phe Pro Val Leu Lys
65 70 75 80

Val Asn Val Ser Gly Leu Asp Pro Asn Ala Met Tyr Ser Phe Leu Leu
85 90 95

Asp Phe Val Ala Ala Asp Asn His Arg Trp Lys Tyr Val Asn Gly Glu
100 105 110

Trp Val Pro Gly Gly Lys Pro Glu Pro Gln Ala Pro Ser Cys Val Tyr
115 120 125

Ile His Pro Asp Ser Pro Asn Phe Gly Ala His Trp Met Lys Ala Pro
130 135 140

Val Ser Phe Ser Lys Val Lys Leu Thr Asn Lys Leu Asn Gly Gly Gly
145 150 155 160

```
Gln Ile Met Leu Asn Ser Leu His Lys Tyr Glu Pro Arg Ile His Ile
                165                 170                 175

Val Arg Val Gly Gly Pro Gln Arg Met Ile Thr Ser His Cys Phe Pro
            180                 185                 190

Glu Thr Gln Phe Ile Ala Val Thr Ala Tyr Gln Asn Glu Glu Ile Thr
        195                 200                 205

Ala Leu Lys Ile Lys Tyr Asn Pro Phe Ala Lys Ala Phe Leu Asp Ala
    210                 215                 220

Lys Glu Arg Ser Asp His Lys Glu Met Met Glu Glu Pro Gly Asp Ser
225                 230                 235                 240

Gln Gln Pro Gly Tyr Ser Gln Trp Gly Trp Leu Leu Pro Gly Thr Ser
                245                 250                 255

Thr Leu Cys Pro Pro Ala Asn Pro His Pro Gln Phe Gly Gly Ala Leu
            260                 265                 270

Ser Leu Pro Ser Thr His Ser Cys Asp Arg Tyr Pro Thr Leu Arg Ser
        275                 280                 285

His Arg Ser Ser Pro Tyr Pro Ser Pro Tyr Ala His Arg Asn Asn Ser
    290                 295                 300

Pro Thr Tyr Ser Asp Asn Ser Pro Ala Cys Leu Ser Met Leu Gln Ser
305                 310                 315                 320

His Asp Asn Trp Ser Ser Leu Gly Met Pro Ala His Pro Ser Met Leu
                325                 330                 335

Pro Val Ser His Asn Ala Ser Pro Pro Thr Ser Ser Ser Gln Tyr Pro
            340                 345                 350

Ser Leu Trp Ser Val Ser Asn Gly Ala Val Thr Pro Gly Ser Gln Ala
        355                 360                 365

Ala Ala Val Ser Asn Gly Leu Gly Ala Gln Phe Phe Arg Gly Ser Pro
    370                 375                 380
```

Ala His Tyr Thr Pro Leu Thr His Pro Val Ser Ala Pro Ser Ser Ser
385 390 395 400

Gly Ser Pro Leu Tyr Glu Gly Ala Ala Ala Ala Thr Asp Ile Val Asp
405 410 415

Ser Gln Tyr Asp Ala Ala Ala Gln Gly Arg Leu Ile Ala Ser Trp Thr
420 425 430

Pro Val Ser Pro Pro Ser Met
435

<210> 48
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence encoding fusion protein comprising Brachyury protein Isoform 1 plus addition of 45 nucleotides from Gene FPV 088

<400> 48
atgaaaaata acttgtatga agaaaaaatg aacatgagta agaaaatgag ctcccctggc 60

accgagagcg cgggaaagag cctgcagtac cgagtggacc acctgctgag cgccgtggag 120

aatgagctgc aggcgggcag cgagaagggc gaccccacag agcgcgaact gcgcgtgggc 180

ctggaggaga gcgagctgtg gctgcgcttc aaggagctca ccaatgagat gatcgtgacc 240

aagaacggca ggaggatgtt tccggtgctg aaggtgaacg tgtctggcct ggaccccaac 300

gccatgtact ccttcctgct ggacttcgtg gcggcggaca accaccgctg gaagtacgtg 360

aacggggaat gggtgccggg gggcaagccg gagccgcagg cgcccagctg cgtctacatc 420

caccccgact cgcccaactt cggggcccac tggatgaagg ctcccgtctc cttcagcaaa 480

gtcaagctca ccaacaagct caacggaggg ggccagatca tgctgaactc cttgcataag 540

tatgagcctc gaatccacat agtgagagtt gggggtccac agcgcatgat caccagccac 600

tgcttccctg agacccagtt catagcggtg actgcttatc agaacgagga gatcacagct 660

cttaaaatta agtacaatcc atttgcaaag gctttccttg atgcaaagga aagaagtgat 720

cacaaagaga tgatggagga acccggagac agccagcaac ctgggtactc ccaatggggg 780

tggcttcttc ctggaaccag caccgtttgt ccacctgcaa atcctcatcc tcagtttgga 840

ggtgccctct ccctcccctc cacgcacagc tgtgacaggt acccaaccct gaggagccac 900

cggtcctcac cctaccccag cccctatgct catcggaaca attctccaac ctattctgac 960

aactcacctg catgtttatc catgctgcaa tcccatgaca attggtccag ccttggaatg 1020

cctgcccatc ccagcatgct ccccgtgagc cacaatgcca gcccacctac cagctccagt 1080

cagtacccca gcctgtggtc tgtgagcaac ggcgccgtca ccccgggctc ccaggcagca 1140

gccgtgtcca acgggctggg ggcccagttc ttccggggct cccccgcgca ctacacaccc 1200

ctcacccatc cggtctcggc gccctcttcc tcgggatccc cactgtacga aggggcggcc 1260

gcggccacag acatcgtgga cagccagtac gacgccgcag cccaaggccg cctcatagcc 1320

tcatggacac ctgtgtcgcc accttccatg tga 1353

<210> 49
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence encoding fusion protein comprising Brachyury protein Isoform 1 plus addition of 45 nucleotides from Gene FPV 088 without Brachyury atg

<400> 49
atgaaaaata acttgtatga agaaaaaatg aacatgagta agaaaagctc ccctggcacc 60

gagagcgcgg gaaagagcct gcagtaccga gtggaccacc tgctgagcgc cgtggagaat 120

gagctgcagg cgggcagcga gaagggcgac cccacagagc gcgaactgcg cgtgggcctg 180

gaggagagcg agctgtggct gcgcttcaag gagctcacca atgagatgat cgtgaccaag 240

aacggcagga ggatgtttcc ggtgctgaag gtgaacgtgt ctggcctgga ccccaacgcc 300

atgtactcct tcctgctgga cttcgtggcg gcggacaacc accgctggaa gtacgtgaac 360

ggggaatggg tgccgggggg caagccggag ccgcaggcgc ccagctgcgt ctacatccac 420

cccgactcgc ccaacttcgg ggcccactgg atgaaggctc ccgtctcctt cagcaaagtc 480

aagctcacca acaagctcaa cggaggggcc cagatcatgc tgaactcctt gcataagtat 540

gagcctcgaa tccacatagt gagagttggg ggtccacagc gcatgatcac cagccactgc 600

ttccctgaga cccagttcat agcggtgact gcttatcaga acgaggagat cacagctctt 660

aaaattaagt acaatccatt tgcaaaagct ttccttgatg caaaggaaag aagtgatcac 720

aaagagatga tggaggaacc cggagacagc cagcaacctg ggtactccca atgggggtgg 780

cttcttcctg gaaccagcac cgtttgtcca cctgcaaatc ctcatcctca gtttggaggt 840

gccctctccc tcccctccac gcacagctgt gacaggtacc caaccctgag gagccaccgg 900

tcctcaccct accccagccc ctatgctcat cggaacaatt ctccaaccta ttctgacaac 960

tcacctgcat gtttatccat gctgcaatcc catgacaatt ggtccagcct tggaatgcct 1020

gcccatccca gcatgctccc cgtgagccac aatgccagcc cacctaccag ctccagtcag 1080

taccccagcc tgtggtctgt gagcaacggc gccgtcaccc cgggctccca ggcagcagcc 1140

gtgtccaacg ggctgggggc ccagttcttc cggggctccc ccgcgcacta cacacccctc 1200

acccatccgg tctcggcgcc ctcttcctcg ggatccccac tgtacgaagg ggcggccgcg 1260

gccacagaca tcgtggacag ccagtacgac gccgcagccc aaggccgcct catagcctca 1320

tggacacctg tgtcgccacc ttccatgtga 1350

<210> 50
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion protein comprising Brachyury protein Isoform 1 encoded by SEQ ID NO:48

<400> 50

Met Lys Asn Asn Leu Tyr Glu Glu Lys Met Asn Met Ser Lys Lys Met
1 5 10 15

Ser Ser Pro Gly Thr Glu Ser Ala Gly Lys Ser Leu Gln Tyr Arg Val
20 25 30

Asp His Leu Leu Ser Ala Val Glu Asn Glu Leu Gln Ala Gly Ser Glu
35 40 45

Lys Gly Asp Pro Thr Glu Arg Glu Leu Arg Val Gly Leu Glu Glu Ser
50 55 60

Glu Leu Trp Leu Arg Phe Lys Glu Leu Thr Asn Glu Met Ile Val Thr

```
65                  70                  75                  80

Lys Asn Gly Arg Arg Met Phe Pro Val Leu Lys Val Asn Val Ser Gly
                85                  90                  95

Leu Asp Pro Asn Ala Met Tyr Ser Phe Leu Leu Asp Phe Val Ala Ala
            100                 105                 110

Asp Asn His Arg Trp Lys Tyr Val Asn Gly Glu Trp Val Pro Gly Gly
        115                 120                 125

Lys Pro Glu Pro Gln Ala Pro Ser Cys Val Tyr Ile His Pro Asp Ser
    130                 135                 140

Pro Asn Phe Gly Ala His Trp Met Lys Ala Pro Val Ser Phe Ser Lys
145                 150                 155                 160

Val Lys Leu Thr Asn Lys Leu Asn Gly Gly Gly Gln Ile Met Leu Asn
                165                 170                 175

Ser Leu His Lys Tyr Glu Pro Arg Ile His Ile Val Arg Val Gly Gly
            180                 185                 190

Pro Gln Arg Met Ile Thr Ser His Cys Phe Pro Glu Thr Gln Phe Ile
        195                 200                 205

Ala Val Thr Ala Tyr Gln Asn Glu Glu Ile Thr Ala Leu Lys Ile Lys
    210                 215                 220

Tyr Asn Pro Phe Ala Lys Ala Phe Leu Asp Ala Lys Glu Arg Ser Asp
225                 230                 235                 240

His Lys Glu Met Met Glu Glu Pro Gly Asp Ser Gln Gln Pro Gly Tyr
                245                 250                 255

Ser Gln Trp Gly Trp Leu Leu Pro Gly Thr Ser Thr Leu Cys Pro Pro
            260                 265                 270

Ala Asn Pro His Pro Gln Phe Gly Gly Ala Leu Ser Leu Pro Ser Thr
        275                 280                 285
```

```
His Ser Cys Asp Arg Tyr Pro Thr Leu Arg Ser His Arg Ser Ser Pro
    290                 295                 300

Tyr Pro Ser Pro Tyr Ala His Arg Asn Asn Ser Pro Thr Tyr Ser Asp
305                 310                 315                 320

Asn Ser Pro Ala Cys Leu Ser Met Leu Gln Ser His Asp Asn Trp Ser
                325                 330                 335

Ser Leu Gly Met Pro Ala His Pro Ser Met Leu Pro Val Ser His Asn
            340                 345                 350

Ala Ser Pro Pro Thr Ser Ser Ser Gln Tyr Pro Ser Leu Trp Ser Val
        355                 360                 365

Ser Asn Gly Ala Val Thr Pro Gly Ser Gln Ala Ala Ala Val Ser Asn
    370                 375                 380

Gly Leu Gly Ala Gln Phe Phe Arg Gly Ser Pro Ala His Tyr Thr Pro
385                 390                 395                 400

Leu Thr His Pro Val Ser Ala Pro Ser Ser Ser Gly Ser Pro Leu Tyr
                405                 410                 415

Glu Gly Ala Ala Ala Ala Thr Asp Ile Val Asp Ser Gln Tyr Asp Ala
            420                 425                 430

Ala Ala Gln Gly Arg Leu Ile Ala Ser Trp Thr Pro Val Ser Pro Pro
        435                 440                 445

Ser Met
    450
```

<210> 51
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion protein comprising Brachyury protein Isoform 1 encoded by SEQ ID NO:49

<400> 51

Met Lys Asn Asn Leu Tyr Glu Glu Lys Met Asn Met Ser Lys Lys Ser
1 5 10 15

Ser Pro Gly Thr Glu Ser Ala Gly Lys Ser Leu Gln Tyr Arg Val Asp
20 25 30

His Leu Leu Ser Ala Val Glu Asn Glu Leu Gln Ala Gly Ser Glu Lys
35 40 45

Gly Asp Pro Thr Glu Arg Glu Leu Arg Val Gly Leu Glu Glu Ser Glu
50 55 60

Leu Trp Leu Arg Phe Lys Glu Leu Thr Asn Glu Met Ile Val Thr Lys
65 70 75 80

Asn Gly Arg Arg Met Phe Pro Val Leu Lys Val Asn Val Ser Gly Leu
85 90 95

Asp Pro Asn Ala Met Tyr Ser Phe Leu Leu Asp Phe Val Ala Ala Asp
100 105 110

Asn His Arg Trp Lys Tyr Val Asn Gly Glu Trp Val Pro Gly Gly Lys
115 120 125

Pro Glu Pro Gln Ala Pro Ser Cys Val Tyr Ile His Pro Asp Ser Pro
130 135 140

Asn Phe Gly Ala His Trp Met Lys Ala Pro Val Ser Phe Ser Lys Val
145 150 155 160

Lys Leu Thr Asn Lys Leu Asn Gly Gly Gly Gln Ile Met Leu Asn Ser
165 170 175

Leu His Lys Tyr Glu Pro Arg Ile His Ile Val Arg Val Gly Gly Pro
180 185 190

Gln Arg Met Ile Thr Ser His Cys Phe Pro Glu Thr Gln Phe Ile Ala
195 200 205

```
Val Thr Ala Tyr Gln Asn Glu Glu Ile Thr Ala Leu Lys Ile Lys Tyr
    210                 215                 220

Asn Pro Phe Ala Lys Ala Phe Leu Asp Ala Lys Glu Arg Ser Asp His
225                 230                 235                 240

Lys Glu Met Met Glu Glu Pro Gly Asp Ser Gln Gln Pro Gly Tyr Ser
                245                 250                 255

Gln Trp Gly Trp Leu Leu Pro Gly Thr Ser Thr Leu Cys Pro Pro Ala
            260                 265                 270

Asn Pro His Pro Gln Phe Gly Gly Ala Leu Ser Leu Pro Ser Thr His
        275                 280                 285

Ser Cys Asp Arg Tyr Pro Thr Leu Arg Ser His Arg Ser Ser Pro Tyr
    290                 295                 300

Pro Ser Pro Tyr Ala His Arg Asn Asn Ser Pro Thr Tyr Ser Asp Asn
305                 310                 315                 320

Ser Pro Ala Cys Leu Ser Met Leu Gln Ser His Asp Asn Trp Ser Ser
                325                 330                 335

Leu Gly Met Pro Ala His Pro Ser Met Leu Pro Val Ser His Asn Ala
            340                 345                 350

Ser Pro Pro Thr Ser Ser Ser Gln Tyr Pro Ser Leu Trp Ser Val Ser
        355                 360                 365

Asn Gly Ala Val Thr Pro Gly Ser Gln Ala Ala Ala Val Ser Asn Gly
    370                 375                 380

Leu Gly Ala Gln Phe Phe Arg Gly Ser Pro Ala His Tyr Thr Pro Leu
385                 390                 395                 400

Thr His Pro Val Ser Ala Pro Ser Ser Ser Gly Ser Pro Leu Tyr Glu
                405                 410                 415

Gly Ala Ala Ala Ala Thr Asp Ile Val Asp Ser Gln Tyr Asp Ala Ala
            420                 425                 430
```

Ala Gln Gly Arg Leu Ile Ala Ser Trp Thr Pro Val Ser Pro Pro Ser
435 440 445

Met

<210> 52
<211> 1326
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence encoding fusion protein comprising Brachyury protein Isoform 1 plus addition of 18 nucleotides from Gene FPV 088

<400> 52
atgaacatga gtaagaaaat gagctcccct ggcaccgaga gcgcgggaaa gagcctgcag 60

taccgagtgg accacctgct gagcgccgtg gagaatgagc tgcaggcggg cagcgagaag 120

ggcgacccca cagagcgcga actgcgcgtg ggcctggagg agagcgagct gtggctgcgc 180

ttcaaggagc tcaccaatga gatgatcgtg accaagaacg gcaggaggat gtttccggtg 240

ctgaaggtga acgtgtctgg cctggacccc aacgccatgt actccttcct gctggacttc 300

gtggcggcgg acaaccaccg ctggaagtac gtgaacgggg aatgggtgcc gggggcaag 360

ccggagccgc aggcgcccag ctgcgtctac atccaccccg actcgcccaa cttcggggcc 420

cactggatga aggctcccgt ctccttcagc aaagtcaagc tcaccaacaa gctcaacgga 480

gggggccaga tcatgctgaa ctccttgcat aagtatgagc ctcgaatcca catagtgaga 540

gttgggggtc cacagcgcat gatcaccagc cactgcttcc ctgagaccca gttcatagcg 600

gtgactgctt atcagaacga ggagatcaca gctcttaaaa ttaagtacaa tccatttgca 660

aaggctttcc ttgatgcaaa ggaaagaagt gatcacaaag agatgatgga ggaacccgga 720

gacagccagc aacctgggta ctcccaatgg gggtggcttc ttcctggaac cagcaccgtt 780

tgtccacctg caaatcctca tcctcagttt ggaggtgccc tctccctccc ctccacgcac 840

agctgtgaca ggtacccaac cctgaggagc caccggtcct caccctaccc cagcccctat 900

gctcatcgga acaattctcc aacctattct gacaactcac ctgcatgttt atccatgctg 960

caatcccatg acaattggtc cagccttgga atgcctgccc atcccagcat gctccccgtg 1020

agccacaatg ccagcccacc taccagctcc agtcagtacc ccagcctgtg gtctgtgagc 1080

aacggcgccg tcaccccggg ctcccaggca gcagccgtgt ccaacgggct gggggcccag 1140

ttcttccggg gctcccccgc gcactacaca cccctcaccc atccggtctc ggcgccctct 1200

tcctcgggat ccccactgta cgaaggggcg gccgcggcca cagacatcgt ggacagccag 1260

tacgacgccg cagcccaagg ccgcctcata gcctcatgga cacctgtgtc gccaccttcc 1320

atgtga 1326

<210> 53
<211> 1323
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence encoding fusion protein comprising Brachyury protein Isoform 1 plus addition of 18 nucleotides from Gene FPV 088 without brachyury atg

<400> 53
atgaacatga gtaagaaaag ctcccctggc accgagagcg cgggaaagag cctgcagtac 60

cgagtggacc acctgctgag cgccgtggag aatgagctgc aggcgggcag cgagaagggc 120

gaccccacag agcgcgaact gcgcgtgggc ctggaggaga gcgagctgtg gctgcgcttc 180

aaggagctca ccaatgagat gatcgtgacc aagaacggca ggaggatgtt tccggtgctg 240

aaggtgaacg tgtctggcct ggaccccaac gccatgtact ccttcctgct ggacttcgtg 300

gcggcggaca accaccgctg gaagtacgtg aacggggaat gggtgccggg gggcaagccg 360

gagccgcagg cgcccagctg cgtctacatc caccccgact cgcccaactt cggggcccac 420

tggatgaagg ctcccgtctc cttcagcaaa gtcaagctca ccaacaagct caacggaggg 480

ggccagatca tgctgaactc cttgcataag tatgagcctc gaatccacat agtgagagtt 540

gggggtccac agcgcatgat caccagccac tgcttccctg agacccagtt catagcggtg 600

actgcttatc agaacgagga gatcacagct cttaaaatta agtacaatcc atttgcaaaa 660

gctttccttg atgcaaagga aagaagtgat cacaaagaga tgatggagga acccggagac 720

agccagcaac ctgggtactc ccaatggggg tggcttcttc ctggaaccag caccgtttgt 780

ccacctgcaa atcctcatcc tcagtttgga ggtgccctct ccctcccctc cacgcacagc 840

tgtgacaggt acccaaccct gaggagccac cggtcctcac cctaccccag cccctatgct 900

catcggaaca attctccaac ctattctgac aactcacctg catgtttatc catgctgcaa 960

tcccatgaca attggtccag ccttggaatg cctgcccatc ccagcatgct ccccgtgagc 1020

cacaatgcca gcccacctac cagctccagt cagtacccca gcctgtggtc tgtgagcaac 1080

ggcgccgtca ccccgggctc ccaggcagca gccgtgtcca acgggctggg ggcccagttc 1140

ttccggggct cccccgcgca ctacacaccc ctcacccatc cggtctcggc gccctcttcc 1200

tcgggatccc cactgtacga aggggcggcc gcggccacag acatcgtgga cagccagtac 1260

gacgccgcag cccaaggccg cctcatagcc tcatggacac ctgtgtcgcc accttccatg 1320

tga 1323

<210> 54
<211> 441
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion protein comprising Brachyury protein Isoform 1 encoded by SEQ ID NO:52

<400> 54

Met Asn Met Ser Lys Lys Met Ser Ser Pro Gly Thr Glu Ser Ala Gly
1 5 10 15

Lys Ser Leu Gln Tyr Arg Val Asp His Leu Leu Ser Ala Val Glu Asn
20 25 30

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

Arg Val Gly Leu Glu Glu Ser Glu Leu Trp Leu Arg Phe Lys Glu Leu
50 55 60

Thr Asn Glu Met Ile Val Thr Lys Asn Gly Arg Arg Met Phe Pro Val
65 70 75 80

Leu Lys Val Asn Val Ser Gly Leu Asp Pro Asn Ala Met Tyr Ser Phe
85 90 95

Leu Leu Asp Phe Val Ala Ala Asp Asn His Arg Trp Lys Tyr Val Asn

```
            100                 105                 110

Gly Glu Trp Val Pro Gly Gly Lys Pro Glu Pro Gln Ala Pro Ser Cys
        115                 120                 125

Val Tyr Ile His Pro Asp Ser Pro Asn Phe Gly Ala His Trp Met Lys
    130                 135                 140

Ala Pro Val Ser Phe Ser Lys Val Lys Leu Thr Asn Lys Leu Asn Gly
145                 150                 155                 160

Gly Gly Gln Ile Met Leu Asn Ser Leu His Lys Tyr Glu Pro Arg Ile
                165                 170                 175

His Ile Val Arg Val Gly Gly Pro Gln Arg Met Ile Thr Ser His Cys
            180                 185                 190

Phe Pro Glu Thr Gln Phe Ile Ala Val Thr Ala Tyr Gln Asn Glu Glu
        195                 200                 205

Ile Thr Ala Leu Lys Ile Lys Tyr Asn Pro Phe Ala Lys Ala Phe Leu
    210                 215                 220

Asp Ala Lys Glu Arg Ser Asp His Lys Glu Met Met Glu Glu Pro Gly
225                 230                 235                 240

Asp Ser Gln Gln Pro Gly Tyr Ser Gln Trp Gly Trp Leu Leu Pro Gly
                245                 250                 255

Thr Ser Thr Leu Cys Pro Pro Ala Asn Pro His Pro Gln Phe Gly Gly
            260                 265                 270

Ala Leu Ser Leu Pro Ser Thr His Ser Cys Asp Arg Tyr Pro Thr Leu
        275                 280                 285

Arg Ser His Arg Ser Ser Pro Tyr Pro Ser Pro Tyr Ala His Arg Asn
    290                 295                 300

Asn Ser Pro Thr Tyr Ser Asp Asn Ser Pro Ala Cys Leu Ser Met Leu
305                 310                 315                 320
```

Gln Ser His Asp Asn Trp Ser Ser Leu Gly Met Pro Ala His Pro Ser
325 330 335

Met Leu Pro Val Ser His Asn Ala Ser Pro Pro Thr Ser Ser Ser Gln
340 345 350

Tyr Pro Ser Leu Trp Ser Val Ser Asn Gly Ala Val Thr Pro Gly Ser
355 360 365

Gln Ala Ala Ala Val Ser Asn Gly Leu Gly Ala Gln Phe Phe Arg Gly
370 375 380

Ser Pro Ala His Tyr Thr Pro Leu Thr His Pro Val Ser Ala Pro Ser
385 390 395 400

Ser Ser Gly Ser Pro Leu Tyr Glu Gly Ala Ala Ala Ala Thr Asp Ile
405 410 415

Val Asp Ser Gln Tyr Asp Ala Ala Ala Gln Gly Arg Leu Ile Ala Ser
420 425 430

Trp Thr Pro Val Ser Pro Pro Ser Met
435 440

<210> 55
<211> 440
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion protein comprising Brachyury protein Isoform 1 encoded by SEQ ID NO:53

<400> 55

Met Asn Met Ser Lys Lys Ser Ser Pro Gly Thr Glu Ser Ala Gly Lys
1 5 10 15

Ser Leu Gln Tyr Arg Val Asp His Leu Leu Ser Ala Val Glu Asn Glu
20 25 30

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

```
Val Gly Leu Glu Glu Ser Glu Leu Trp Leu Arg Phe Lys Glu Leu Thr
    50                  55                  60

Asn Glu Met Ile Val Thr Lys Asn Gly Arg Arg Met Phe Pro Val Leu
65                  70                  75                  80

Lys Val Asn Val Ser Gly Leu Asp Pro Asn Ala Met Tyr Ser Phe Leu
                85                  90                  95

Leu Asp Phe Val Ala Ala Asp Asn His Arg Trp Lys Tyr Val Asn Gly
            100                 105                 110

Glu Trp Val Pro Gly Gly Lys Pro Glu Pro Gln Ala Pro Ser Cys Val
        115                 120                 125

Tyr Ile His Pro Asp Ser Pro Asn Phe Gly Ala His Trp Met Lys Ala
    130                 135                 140

Pro Val Ser Phe Ser Lys Val Lys Leu Thr Asn Lys Leu Asn Gly Gly
145                 150                 155                 160

Gly Gln Ile Met Leu Asn Ser Leu His Lys Tyr Glu Pro Arg Ile His
                165                 170                 175

Ile Val Arg Val Gly Gly Pro Gln Arg Met Ile Thr Ser His Cys Phe
            180                 185                 190

Pro Glu Thr Gln Phe Ile Ala Val Thr Ala Tyr Gln Asn Glu Glu Ile
        195                 200                 205

Thr Ala Leu Lys Ile Lys Tyr Asn Pro Phe Ala Lys Ala Phe Leu Asp
    210                 215                 220

Ala Lys Glu Arg Ser Asp His Lys Glu Met Met Glu Glu Pro Gly Asp
225                 230                 235                 240

Ser Gln Gln Pro Gly Tyr Ser Gln Trp Gly Trp Leu Leu Pro Gly Thr
                245                 250                 255
```

```
Ser Thr Leu Cys Pro Pro Ala Asn Pro His Pro Gln Phe Gly Gly Ala
            260                 265                 270

Leu Ser Leu Pro Ser Thr His Ser Cys Asp Arg Tyr Pro Thr Leu Arg
        275                 280                 285

Ser His Arg Ser Ser Pro Tyr Pro Ser Pro Tyr Ala His Arg Asn Asn
    290                 295                 300

Ser Pro Thr Tyr Ser Asp Asn Ser Pro Ala Cys Leu Ser Met Leu Gln
305                 310                 315                 320

Ser His Asp Asn Trp Ser Ser Leu Gly Met Pro Ala His Pro Ser Met
                325                 330                 335

Leu Pro Val Ser His Asn Ala Ser Pro Pro Thr Ser Ser Ser Gln Tyr
            340                 345                 350

Pro Ser Leu Trp Ser Val Ser Asn Gly Ala Val Thr Pro Gly Ser Gln
        355                 360                 365

Ala Ala Ala Val Ser Asn Gly Leu Gly Ala Gln Phe Phe Arg Gly Ser
    370                 375                 380

Pro Ala His Tyr Thr Pro Leu Thr His Pro Val Ser Ala Pro Ser Ser
385                 390                 395                 400

Ser Gly Ser Pro Leu Tyr Glu Gly Ala Ala Ala Ala Thr Asp Ile Val
                405                 410                 415

Asp Ser Gln Tyr Asp Ala Ala Ala Gln Gly Arg Leu Ile Ala Ser Trp
            420                 425                 430

Thr Pro Val Ser Pro Pro Ser Met
        435                 440
```

<210> 56
<211> 1320
<212> DNA
<213> Artificial Sequence

<220>

<223> Coding sequence encoding Fusion protein comprising Brachyury protein Isoform 1 plus addition of 12 nucleotides from Gene FPV 088

<400> 56
atgagtaaga aaatgagctc ccctggcacc gagagcgcgg gaaagagcct gcagtaccga 60

gtggaccacc tgctgagcgc cgtggagaat gagctgcagg cgggcagcga gaagggcgac 120

cccacagagc gcgaactgcg cgtgggcctg gaggagagcg agctgtggct gcgcttcaag 180

gagctcacca atgagatgat cgtgaccaag aacggcagga ggatgtttcc ggtgctgaag 240

gtgaacgtgt ctggcctgga ccccaacgcc atgtactcct tcctgctgga cttcgtggcg 300

gcggacaacc accgctggaa gtacgtgaac ggggaatggg tgccgggggg caagccggag 360

ccgcaggcgc ccagctgcgt ctacatccac cccgactcgc ccaacttcgg ggcccactgg 420

atgaaggctc ccgtctcctt cagcaaagtc aagctcacca acaagctcaa cggagggggc 480

cagatcatgc tgaactcctt gcataagtat gagcctcgaa tccacatagt gagagttggg 540

ggtccacagc gcatgatcac cagccactgc ttccctgaga cccagttcat agcggtgact 600

gcttatcaga acgaggagat cacagctctt aaaattaagt acaatccatt tgcaaaagct 660

ttccttgatg caaaggaaag aagtgatcac aaagagatga tggaggaacc cggagacagc 720

cagcaacctg ggtactccca atgggggtgg cttcttcctg gaaccagcac cgtttgtcca 780

cctgcaaatc ctcatcctca gtttggaggt gccctctccc tcccctccac gcacagctgt 840

gacaggtacc caaccctgag gagccaccgg tcctcaccct accccagccc ctatgctcat 900

cggaacaatt ctccaaccta ttctgacaac tcacctgcat gtttatccat gctgcaatcc 960

catgacaatt ggtccagcct tggaatgcct gcccatccca gcatgctccc cgtgagccac 1020

aatgccagcc cacctaccag ctccagtcag taccccagcc tgtggtctgt gagcaacggc 1080

gccgtcaccc cgggctccca ggcagcagcc gtgtccaacg ggctgggggc ccagttcttc 1140

cggggctccc ccgcgcacta cacacccctc acccatccgg tctcggcgcc ctcttcctcg 1200

ggatccccac tgtacgaagg ggcggccgcg gccacagaca tcgtggacag ccagtacgac 1260

gccgcagccc aaggccgcct catagcctca tggacacctg tgtcgccacc ttccatgtga 1320

<210> 57
<211> 1317
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence encoding Fusion protein comprising Brachyury protein Isoform 1 plus addition of 12 nucleotides from Gene FPV 088 without Brachyury atg start codon

<400> 57
atgagtaaga aaagctcccc tggcaccgag agcgcgggaa agagcctgca gtaccgagtg 60

gaccacctgc tgagcgccgt ggagaatgag ctgcaggcgg gcagcgagaa gggcgacccc 120

acagagcgcg aactgcgcgt gggcctggag gagagcgagc tgtggctgcg cttcaaggag 180

ctcaccaatg agatgatcgt gaccaagaac ggcaggagga tgtttccggt gctgaaggtg 240

aacgtgtctg gcctggaccc caacgccatg tactccttcc tgctggactt cgtggcggcg 300

gacaaccacc gctggaagta cgtgaacggg gaatgggtgc cgggggcaa gccggagccg 360

caggcgccca gctgcgtcta catccacccc gactcgccca acttcggggc ccactggatg 420

aaggctcccg tctccttcag caaagtcaag ctcaccaaca agctcaacgg agggggccag 480

atcatgctga actccttgca taagtatgag cctcgaatcc acatagtgag agttgggggt 540

ccacagcgca tgatcaccag ccactgcttc cctgagaccc agttcatagc ggtgactgct 600

tatcagaacg aggagatcac agctcttaaa attaagtaca atccatttgc aaaagctttc 660

cttgatgcaa aggaaagaag tgatcacaaa gagatgatgg aggaacccgg agacagccag 720

caacctgggt actcccaatg ggggtggctt cttcctggaa ccagcaccgt ttgtccacct 780

gcaaatcctc atcctcagtt tggaggtgcc ctctccctcc cctccacgca cagctgtgac 840

aggtacccaa ccctgaggag ccaccggtcc tcaccctacc ccagccccta tgctcatcgg 900

aacaattctc caacctattc tgacaactca cctgcatgtt tatccatgct gcaatcccat 960

gacaattggt ccagccttgg aatgcctgcc catcccagca tgctccccgt gagccacaat 1020

gccagcccac ctaccagctc cagtcagtac cccagcctgt ggtctgtgag caacggcgcc 1080

gtcaccccgg gctcccaggc agcagccgtg tccaacgggc tgggggccca gttcttccgg 1140

ggctcccccg cgcactacac acccctcacc catccggtct cggcgccctc ttcctcggga 1200

tccccactgt acgaaggggc ggccgcggcc acagacatcg tggacagcca gtacgacgcc 1260

gcagcccaag gccgcctcat agcctcatgg acacctgtgt cgccaccttc catgtga 1317

<210> 58
<211> 439

<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion protein comprising Brachyury protein Isoform 1 encoded by SEQ ID NO: 56

<400> 58

Met Ser Lys Lys Met Ser Ser Pro Gly Thr Glu Ser Ala Gly Lys Ser
1 5 10 15

Leu Gln Tyr Arg Val Asp His Leu Leu Ser Ala Val Glu Asn Glu Leu
20 25 30

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

Gly Leu Glu Glu Ser Glu Leu Trp Leu Arg Phe Lys Glu Leu Thr Asn
50 55 60

Glu Met Ile Val Thr Lys Asn Gly Arg Arg Met Phe Pro Val Leu Lys
65 70 75 80

Val Asn Val Ser Gly Leu Asp Pro Asn Ala Met Tyr Ser Phe Leu Leu
85 90 95

Asp Phe Val Ala Ala Asp Asn His Arg Trp Lys Tyr Val Asn Gly Glu
100 105 110

Trp Val Pro Gly Gly Lys Pro Glu Pro Gln Ala Pro Ser Cys Val Tyr
115 120 125

Ile His Pro Asp Ser Pro Asn Phe Gly Ala His Trp Met Lys Ala Pro
130 135 140

Val Ser Phe Ser Lys Val Lys Leu Thr Asn Lys Leu Asn Gly Gly Gly
145 150 155 160

Gln Ile Met Leu Asn Ser Leu His Lys Tyr Glu Pro Arg Ile His Ile
165 170 175

Val Arg Val Gly Gly Pro Gln Arg Met Ile Thr Ser His Cys Phe Pro

```
            180                 185                 190

Glu Thr Gln Phe Ile Ala Val Thr Ala Tyr Gln Asn Glu Glu Ile Thr
        195                 200                 205

Ala Leu Lys Ile Lys Tyr Asn Pro Phe Ala Lys Ala Phe Leu Asp Ala
    210                 215                 220

Lys Glu Arg Ser Asp His Lys Glu Met Met Glu Glu Pro Gly Asp Ser
225                 230                 235                 240

Gln Gln Pro Gly Tyr Ser Gln Trp Gly Trp Leu Leu Pro Gly Thr Ser
                245                 250                 255

Thr Leu Cys Pro Pro Ala Asn Pro His Pro Gln Phe Gly Gly Ala Leu
            260                 265                 270

Ser Leu Pro Ser Thr His Ser Cys Asp Arg Tyr Pro Thr Leu Arg Ser
        275                 280                 285

His Arg Ser Ser Pro Tyr Pro Ser Pro Tyr Ala His Arg Asn Asn Ser
    290                 295                 300

Pro Thr Tyr Ser Asp Asn Ser Pro Ala Cys Leu Ser Met Leu Gln Ser
305                 310                 315                 320

His Asp Asn Trp Ser Ser Leu Gly Met Pro Ala His Pro Ser Met Leu
                325                 330                 335

Pro Val Ser His Asn Ala Ser Pro Pro Thr Ser Ser Ser Gln Tyr Pro
            340                 345                 350

Ser Leu Trp Ser Val Ser Asn Gly Ala Val Thr Pro Gly Ser Gln Ala
        355                 360                 365

Ala Ala Val Ser Asn Gly Leu Gly Ala Gln Phe Phe Arg Gly Ser Pro
    370                 375                 380

Ala His Tyr Thr Pro Leu Thr His Pro Val Ser Ala Pro Ser Ser Ser
385                 390                 395                 400
```

Gly Ser Pro Leu Tyr Glu Gly Ala Ala Ala Ala Thr Asp Ile Val Asp
405 410 415

Ser Gln Tyr Asp Ala Ala Ala Gln Gly Arg Leu Ile Ala Ser Trp Thr
420 425 430

Pro Val Ser Pro Pro Ser Met
435

<210> 59
<211> 438
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion protein comprising Brachyury protein Isoform 1 encoded by SEQ ID NO:57

<400> 59

Met Ser Lys Lys Ser Ser Pro Gly Thr Glu Ser Ala Gly Lys Ser Leu
1 5 10 15

Gln Tyr Arg Val Asp His Leu Leu Ser Ala Val Glu Asn Glu Leu Gln
20 25 30

Ala Gly Ser Glu Lys Gly Asp Pro Thr Glu Arg Glu Leu Arg Val Gly
35 40 45

Leu Glu Glu Ser Glu Leu Trp Leu Arg Phe Lys Glu Leu Thr Asn Glu
50 55 60

Met Ile Val Thr Lys Asn Gly Arg Arg Met Phe Pro Val Leu Lys Val
65 70 75 80

Asn Val Ser Gly Leu Asp Pro Asn Ala Met Tyr Ser Phe Leu Leu Asp
85 90 95

Phe Val Ala Ala Asp Asn His Arg Trp Lys Tyr Val Asn Gly Glu Trp
100 105 110

Val Pro Gly Gly Lys Pro Glu Pro Gln Ala Pro Ser Cys Val Tyr Ile
115 120 125

```
His Pro Asp Ser Pro Asn Phe Gly Ala His Trp Met Lys Ala Pro Val
    130                 135                 140

Ser Phe Ser Lys Val Lys Leu Thr Asn Lys Leu Asn Gly Gly Gly Gln
145                 150                 155                 160

Ile Met Leu Asn Ser Leu His Lys Tyr Glu Pro Arg Ile His Ile Val
                165                 170                 175

Arg Val Gly Gly Pro Gln Arg Met Ile Thr Ser His Cys Phe Pro Glu
            180                 185                 190

Thr Gln Phe Ile Ala Val Thr Ala Tyr Gln Asn Glu Glu Ile Thr Ala
        195                 200                 205

Leu Lys Ile Lys Tyr Asn Pro Phe Ala Lys Ala Phe Leu Asp Ala Lys
    210                 215                 220

Glu Arg Ser Asp His Lys Glu Met Met Glu Glu Pro Gly Asp Ser Gln
225                 230                 235                 240

Gln Pro Gly Tyr Ser Gln Trp Gly Trp Leu Leu Pro Gly Thr Ser Thr
                245                 250                 255

Leu Cys Pro Pro Ala Asn Pro His Pro Gln Phe Gly Gly Ala Leu Ser
            260                 265                 270

Leu Pro Ser Thr His Ser Cys Asp Arg Tyr Pro Thr Leu Arg Ser His
        275                 280                 285

Arg Ser Ser Pro Tyr Pro Ser Pro Tyr Ala His Arg Asn Asn Ser Pro
    290                 295                 300

Thr Tyr Ser Asp Asn Ser Pro Ala Cys Leu Ser Met Leu Gln Ser His
305                 310                 315                 320

Asp Asn Trp Ser Ser Leu Gly Met Pro Ala His Pro Ser Met Leu Pro
                325                 330                 335
```

Val Ser His Asn Ala Ser Pro Pro Thr Ser Ser Ser Gln Tyr Pro Ser
340 345 350

Leu Trp Ser Val Ser Asn Gly Ala Val Thr Pro Gly Ser Gln Ala Ala
355 360 365

Ala Val Ser Asn Gly Leu Gly Ala Gln Phe Phe Arg Gly Ser Pro Ala
370 375 380

His Tyr Thr Pro Leu Thr His Pro Val Ser Ala Pro Ser Ser Ser Gly
385 390 395 400

Ser Pro Leu Tyr Glu Gly Ala Ala Ala Ala Thr Asp Ile Val Asp Ser
405 410 415

Gln Tyr Asp Ala Ala Ala Gln Gly Arg Leu Ile Ala Ser Trp Thr Pro
420 425 430

Val Ser Pro Pro Ser Met
435

<210> 60
<211> 1386
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence encoding Fusion protein comprising Brachyury protein Isoform 1 plus addition of 75 nucleotides from Gene FPV 088 and an atc

<400> 60
atgaaaaata acttgtatga agaaaaaatg aacatgagta agaaacaagt aaaaactcaa 60

agtaaatgta ataatatcat gagctcccct ggcaccgaga gcgcgggaaa gagcctgcag 120

taccgagtgg accacctgct gagcgccgtg gagaatgagc tgcaggcggg cagcgagaag 180

ggcgacccca cagagcgcga actgcgcgtg ggcctggagg agagcgagct gtggctgcgc 240

ttcaaggagc tcaccaatga gatgatcgtg accaagaacg gcaggaggat gtttccggtg 300

ctgaaggtga acgtgtctgg cctggacccc aacgccatgt actccttcct gctggacttc 360

gtggcggcgg acaaccaccg ctggaagtac gtgaacgggg aatgggtgcc gggggcaag 420

ccggagccgc aggcgcccag ctgcgtctac atccaccccg actcgcccaa cttcggggcc 480

cactggatga aggctcccgt ctccttcagc aaagtcaagc tcaccaacaa gctcaacgga 540

gggggccaga tcatgctgaa ctccttgcat aagtatgagc ctcgaatcca catagtgaga 600

gttgggggtc cacagcgcat gatcaccagc cactgcttcc ctgagaccca gttcatagcg 660

gtgactgctt atcagaacga ggagatcaca gctcttaaaa ttaagtacaa tccatttgca 720

aaagctttcc ttgatgcaaa ggaaagaagt gatcacaaag agatgatgga ggaacccgga 780

gacagccagc aacctgggta ctcccaatgg gggtggcttc ttcctggaac cagcaccgtt 840

tgtccacctg caaatcctca tcctcagttt ggaggtgccc tctccctccc ctccacgcac 900

agctgtgaca ggtacccaac cctgaggagc caccggtcct caccctaccc cagcccctat 960

gctcatcgga acaattctcc aacctattct gacaactcac ctgcatgttt atccatgctg 1020

caatcccatg acaattggtc cagccttgga atgcctgccc atcccagcat gctccccgtg 1080

agccacaatg ccagcccacc taccagctcc agtcagtacc ccagcctgtg gtctgtgagc 1140

aacggcgccg tcaccccggg ctcccaggca gcagccgtgt ccaacgggct gggggcccag 1200

ttcttccggg gctcccccgc gcactacaca cccctcaccc atccggtctc ggcgccctct 1260

tcctcgggat ccccactgta cgaaggggcg gccgcggcca cagacatcgt ggacagccag 1320

tacgacgccg cagcccaagg ccgcctcata gcctcatgga cacctgtgtc gccaccttcc 1380

atgtga 1386

<210> 61
<211> 1383
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence encoding Fusion protein comprising Brachyury protein Isoform 1 plus addition of 75 nucleotides from Gene FPV 088 and an atc, without Brachyury atg start codon

<400> 61
atgaaaaata acttgtatga agaaaaaatg aacatgagta agaaacaagt aaaaactcaa 60

agtaaatgta ataatatcag ctcccctggc accgagagcg cgggaaagag cctgcagtac 120

cgagtggacc acctgctgag cgccgtggag aatgagctgc aggcgggcag cgagaagggc 180

gaccccacag agcgcgaact gcgcgtgggc ctggaggaga gcgagctgtg gctgcgcttc 240

aaggagctca ccaatgagat gatcgtgacc aagaacggca ggaggatgtt tccggtgctg 300

aaggtgaacg tgtctggcct ggaccccaac gccatgtact ccttcctgct ggacttcgtg 360

gcggcggaca accaccgctg gaagtacgtg aacggggaat gggtgccggg gggcaagccg 420

gagccgcagg cgcccagctg cgtctacatc caccccgact cgcccaactt cggggcccac 480

tggatgaagg ctcccgtctc cttcagcaaa gtcaagctca ccaacaagct caacggaggg 540

ggccagatca tgctgaactc cttgcataag tatgagcctc gaatccacat agtgagagtt 600

gggggtccac agcgcatgat caccagccac tgcttccctg agacccagtt catagcggtg 660

actgcttatc agaacgagga gatcacagct cttaaaatta agtacaatcc atttgcaaaa 720

gctttccttg atgcaaagga aagaagtgat cacaaagaga tgatggagga acccggagac 780

agccagcaac ctgggtactc ccaatggggg tggcttcttc ctggaaccag caccgtttgt 840

ccacctgcaa atcctcatcc tcagtttgga ggtgccctct ccctcccctc cacgcacagc 900

tgtgacaggt acccaaccct gaggagccac cggtcctcac cctaccccag cccctatgct 960

catcggaaca attctccaac ctattctgac aactcacctg catgtttatc catgctgcaa 1020

tcccatgaca attggtccag ccttggaatg cctgcccatc ccagcatgct ccccgtgagc 1080

cacaatgcca gcccacctac cagctccagt cagtacccca gcctgtggtc tgtgagcaac 1140

ggcgccgtca ccccgggctc ccaggcagca gccgtgtcca acgggctggg ggcccagttc 1200

ttccggggct cccccgcgca ctacacaccc ctcacccatc cggtctcggc gccctcttcc 1260

tcgggatccc cactgtacga aggggcggcc gcggccacag acatcgtgga cagccagtac 1320

gacgccgcag cccaaggccg cctcatagcc tcatggacac ctgtgtcgcc accttccatg 1380

tga 1383

<210> 62
<211> 461
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion protein comprising Brachyury protein Isoform 1 encoded by SEQ ID NO:60

<400> 62

Met Lys Asn Asn Leu Tyr Glu Glu Lys Met Asn Met Ser Lys Lys Gln
1 5 10 15

```
Val Lys Thr Gln Ser Lys Cys Asn Asn Ile Met Ser Ser Pro Gly Thr
            20                  25                  30

Glu Ser Ala Gly Lys Ser Leu Gln Tyr Arg Val Asp His Leu Leu Ser
        35                  40                  45

Ala Val Glu Asn Glu Leu Gln Ala Gly Ser Glu Lys Gly Asp Pro Thr
    50                  55                  60

Glu Arg Glu Leu Arg Val Gly Leu Glu Glu Ser Glu Leu Trp Leu Arg
65                  70                  75                  80

Phe Lys Glu Leu Thr Asn Glu Met Ile Val Thr Lys Asn Gly Arg Arg
                85                  90                  95

Met Phe Pro Val Leu Lys Val Asn Val Ser Gly Leu Asp Pro Asn Ala
            100                 105                 110

Met Tyr Ser Phe Leu Leu Asp Phe Val Ala Ala Asp Asn His Arg Trp
        115                 120                 125

Lys Tyr Val Asn Gly Glu Trp Val Pro Gly Gly Lys Pro Glu Pro Gln
    130                 135                 140

Ala Pro Ser Cys Val Tyr Ile His Pro Asp Ser Pro Asn Phe Gly Ala
145                 150                 155                 160

His Trp Met Lys Ala Pro Val Ser Phe Ser Lys Val Lys Leu Thr Asn
                165                 170                 175

Lys Leu Asn Gly Gly Gly Gln Ile Met Leu Asn Ser Leu His Lys Tyr
            180                 185                 190

Glu Pro Arg Ile His Ile Val Arg Val Gly Gly Pro Gln Arg Met Ile
        195                 200                 205

Thr Ser His Cys Phe Pro Glu Thr Gln Phe Ile Ala Val Thr Ala Tyr
    210                 215                 220

Gln Asn Glu Glu Ile Thr Ala Leu Lys Ile Lys Tyr Asn Pro Phe Ala
```

```
225                 230                 235                 240

Lys Ala Phe Leu Asp Ala Lys Glu Arg Ser Asp His Lys Glu Met Met
                245                 250                 255

Glu Glu Pro Gly Asp Ser Gln Gln Pro Gly Tyr Ser Gln Trp Gly Trp
            260                 265                 270

Leu Leu Pro Gly Thr Ser Thr Leu Cys Pro Pro Ala Asn Pro His Pro
        275                 280                 285

Gln Phe Gly Gly Ala Leu Ser Leu Pro Ser Thr His Ser Cys Asp Arg
    290                 295                 300

Tyr Pro Thr Leu Arg Ser His Arg Ser Ser Pro Tyr Pro Ser Pro Tyr
305                 310                 315                 320

Ala His Arg Asn Asn Ser Pro Thr Tyr Ser Asp Asn Ser Pro Ala Cys
                325                 330                 335

Leu Ser Met Leu Gln Ser His Asp Asn Trp Ser Ser Leu Gly Met Pro
            340                 345                 350

Ala His Pro Ser Met Leu Pro Val Ser His Asn Ala Ser Pro Pro Thr
        355                 360                 365

Ser Ser Ser Gln Tyr Pro Ser Leu Trp Ser Val Ser Asn Gly Ala Val
    370                 375                 380

Thr Pro Gly Ser Gln Ala Ala Ala Val Ser Asn Gly Leu Gly Ala Gln
385                 390                 395                 400

Phe Phe Arg Gly Ser Pro Ala His Tyr Thr Pro Leu Thr His Pro Val
                405                 410                 415

Ser Ala Pro Ser Ser Ser Gly Ser Pro Leu Tyr Glu Gly Ala Ala Ala
            420                 425                 430

Ala Thr Asp Ile Val Asp Ser Gln Tyr Asp Ala Ala Ala Gln Gly Arg
        435                 440                 445
```

```
Leu Ile Ala Ser Trp Thr Pro Val Ser Pro Pro Ser Met
    450                 455                 460


<210>  63
<211>  460
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Fusion protein comprising Brachyury protein Isoform 1 encoded by
       SEQ ID NO:61

<400>  63

Met Lys Asn Asn Leu Tyr Glu Glu Lys Met Asn Met Ser Lys Lys Gln
1               5                   10                  15


Val Lys Thr Gln Ser Lys Cys Asn Asn Ile Ser Ser Pro Gly Thr Glu
            20                  25                  30


Ser Ala Gly Lys Ser Leu Gln Tyr Arg Val Asp His Leu Leu Ser Ala
        35                  40                  45


Val Glu Asn Glu Leu Gln Ala Gly Ser Glu Lys Gly Asp Pro Thr Glu
    50                  55                  60


Arg Glu Leu Arg Val Gly Leu Glu Glu Ser Glu Leu Trp Leu Arg Phe
65                  70                  75                  80


Lys Glu Leu Thr Asn Glu Met Ile Val Thr Lys Asn Gly Arg Arg Met
                85                  90                  95


Phe Pro Val Leu Lys Val Asn Val Ser Gly Leu Asp Pro Asn Ala Met
            100                 105                 110


Tyr Ser Phe Leu Leu Asp Phe Val Ala Ala Asp Asn His Arg Trp Lys
        115                 120                 125


Tyr Val Asn Gly Glu Trp Val Pro Gly Gly Lys Pro Glu Pro Gln Ala
    130                 135                 140


Pro Ser Cys Val Tyr Ile His Pro Asp Ser Pro Asn Phe Gly Ala His
145                 150                 155                 160
```

```
Trp Met Lys Ala Pro Val Ser Phe Ser Lys Val Lys Leu Thr Asn Lys
                165                 170                 175

Leu Asn Gly Gly Gly Gln Ile Met Leu Asn Ser Leu His Lys Tyr Glu
            180                 185                 190

Pro Arg Ile His Ile Val Arg Val Gly Gly Pro Gln Arg Met Ile Thr
        195                 200                 205

Ser His Cys Phe Pro Glu Thr Gln Phe Ile Ala Val Thr Ala Tyr Gln
    210                 215                 220

Asn Glu Glu Ile Thr Ala Leu Lys Ile Lys Tyr Asn Pro Phe Ala Lys
225                 230                 235                 240

Ala Phe Leu Asp Ala Lys Glu Arg Ser Asp His Lys Glu Met Met Glu
                245                 250                 255

Glu Pro Gly Asp Ser Gln Gln Pro Gly Tyr Ser Gln Trp Gly Trp Leu
            260                 265                 270

Leu Pro Gly Thr Ser Thr Leu Cys Pro Pro Ala Asn Pro His Pro Gln
        275                 280                 285

Phe Gly Gly Ala Leu Ser Leu Pro Ser Thr His Ser Cys Asp Arg Tyr
    290                 295                 300

Pro Thr Leu Arg Ser His Arg Ser Ser Pro Tyr Pro Ser Pro Tyr Ala
305                 310                 315                 320

His Arg Asn Asn Ser Pro Thr Tyr Ser Asp Asn Ser Pro Ala Cys Leu
                325                 330                 335

Ser Met Leu Gln Ser His Asp Asn Trp Ser Ser Leu Gly Met Pro Ala
            340                 345                 350

His Pro Ser Met Leu Pro Val Ser His Asn Ala Ser Pro Pro Thr Ser
        355                 360                 365
```

```
Ser Ser Gln Tyr Pro Ser Leu Trp Ser Val Ser Asn Gly Ala Val Thr
    370                 375                 380

Pro Gly Ser Gln Ala Ala Ala Val Ser Asn Gly Leu Gly Ala Gln Phe
385                 390                 395                 400

Phe Arg Gly Ser Pro Ala His Tyr Thr Pro Leu Thr His Pro Val Ser
                405                 410                 415

Ala Pro Ser Ser Ser Gly Ser Pro Leu Tyr Glu Gly Ala Ala Ala Ala
            420                 425                 430

Thr Asp Ile Val Asp Ser Gln Tyr Asp Ala Ala Ala Gln Gly Arg Leu
        435                 440                 445

Ile Ala Ser Trp Thr Pro Val Ser Pro Pro Ser Met
    450                 455                 460
```

<210> 64
<211> 1359
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence encoding Fusion protein comprising Brachyury protein Isoform 1 plus addition of 48 nucleotides from Gene FPV 088 and an atc

<400> 64

```
atgaacatga gtaagaaaca agtaaaaact caaagtaaat gtaataatat catgagctcc       60

cctggcaccg agagcgcggg aaagagcctg cagtaccgag tggaccacct gctgagcgcc      120

gtggagaatg agctgcaggc gggcagcgag aagggcgacc ccacagagcg cgaactgcgc      180

gtgggcctgg aggagagcga gctgtggctg cgcttcaagg agctcaccaa tgagatgatc      240

gtgaccaaga acggcaggag gatgtttccg gtgctgaagg tgaacgtgtc tggcctggac      300

cccaacgcca tgtactcctt cctgctggac ttcgtggcgg cggacaacca ccgctggaag      360

tacgtgaacg gggaatgggt gccgggggcc aagccggagc cgcaggcgcc cagctgcgtc      420

tacatccacc ccgactcgcc caacttcggg gcccactgga tgaaggctcc cgtctccttc      480

agcaaagtca agctcaccaa caagctcaac ggaggggccc agatcatgct gaactccttg      540

cataagtatg agcctcgaat ccacatagtg agagttgggg gtccacagcg catgatcacc      600
```

agccactgct tccctgagac ccagttcata gcggtgactg cttatcagaa cgaggagatc 660

acagctctta aaattaagta caatccattt gcaaaagctt tccttgatgc aaaggaaaga 720

agtgatcaca aagagatgat ggaggaaccc ggagacagcc agcaacctgg gtactcccaa 780

tgggggtggc ttcttcctgg aaccagcacc gtttgtccac ctgcaaatcc tcatcctcag 840

tttggaggtg ccctctccct cccctccacg cacagctgtg acaggtaccc aaccctgagg 900

agccaccggt cctcacccta ccccagcccc tatgctcatc ggaacaattc tccaacctat 960

tctgacaact cacctgcatg tttatccatg ctgcaatccc atgacaattg gtccagcctt 1020

ggaatgcctg cccatcccag catgctcccc gtgagccaca atgccagccc acctaccagc 1080

tccagtcagt accccagcct gtggtctgtg agcaacggcg ccgtcacccc gggctcccag 1140

gcagcagccg tgtccaacgg gctgggggcc cagttcttcc ggggctcccc cgcgcactac 1200

acacccctca cccatccggt ctcggcgccc tcttcctcgg gatccccact gtacgaaggg 1260

gcggccgcgg ccacagacat cgtggacagc cagtacgacg ccgcagccca aggccgcctc 1320

atagcctcat ggacacctgt gtcgccacct tccatgtga 1359

<210> 65
<211> 1356
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence encoding Fusion protein comprising Brachyury protein Isoform 1 plus addition of 48 nucleotides from Gene FPV 088 and an atc, without Brachyury atg start codon

<400> 65
atgaacatga gtaagaaaca agtaaaaact caaagtaaat gtaataatat cagctcccct 60

ggcaccgaga gcgcgggaaa gagcctgcag taccgagtgg accacctgct gagcgccgtg 120

gagaatgagc tgcaggcggg cagcgagaag ggcgacccca cagagcgcga actgcgcgtg 180

ggcctggagg agagcgagct gtggctgcgc ttcaaggagc tcaccaatga gatgatcgtg 240

accaagaacg gcaggaggat gtttccggtg ctgaaggtga acgtgtctgg cctggacccc 300

aacgccatgt actccttcct gctggacttc gtggcggcgg acaaccaccg ctggaagtac 360

gtgaacgggg aatgggtgcc ggggggcaag ccggagccgc aggcgcccag ctgcgtctac 420

atccaccccg actcgcccaa cttcggggcc cactggatga aggctcccgt ctccttcagc 480

aaagtcaagc tcaccaacaa gctcaacgga gggggccaga tcatgctgaa ctccttgcat 540

aagtatgagc ctcgaatcca catagtgaga gttgggggtc cacagcgcat gatcaccagc 600

cactgcttcc ctgagaccca gttcatagcg gtgactgctt atcagaacga ggagatcaca 660

gctcttaaaa ttaagtacaa tccatttgca aaagctttcc ttgatgcaaa ggaaagaagt 720

gatcacaaag agatgatgga ggaacccgga gacagccagc aacctgggta ctcccaatgg 780

gggtggcttc ttcctggaac cagcaccgtt tgtccacctg caaatcctca tcctcagttt 840

ggaggtgccc tctccctccc ctccacgcac agctgtgaca ggtacccaac cctgaggagc 900

caccggtcct caccctaccc cagcccctat gctcatcgga acaattctcc aacctattct 960

gacaactcac ctgcatgttt atccatgctg caatcccatg acaattggtc cagccttgga 1020

atgcctgccc atcccagcat gctccccgtg agccacaatg ccagcccacc taccagctcc 1080

agtcagtacc ccagcctgtg gtctgtgagc aacggcgccg tcaccccggg ctcccaggca 1140

gcagccgtgt ccaacgggct gggggcccag ttcttccggg gctcccccgc gcactacaca 1200

cccctcaccc atccggtctc ggcgccctct tcctcgggat ccccactgta cgaaggggcg 1260

gccgcggcca cagacatcgt ggacagccag tacgacgccg cagcccaagg ccgcctcata 1320

gcctcatgga cacctgtgtc gccaccttcc atgtga 1356

<210> 66
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion protein comprising Brachyury protein Isoform 1 encoded by SEQ ID NO:64

<400> 66

Met Asn Met Ser Lys Lys Gln Val Lys Thr Gln Ser Lys Cys Asn Asn
1 5 10 15

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

Arg Val Asp His Leu Leu Ser Ala Val Glu Asn Glu Leu Gln Ala Gly
35 40 45

```
Ser Glu Lys Gly Asp Pro Thr Glu Arg Glu Leu Arg Val Gly Leu Glu
    50                  55                  60

Glu Ser Glu Leu Trp Leu Arg Phe Lys Glu Leu Thr Asn Glu Met Ile
65                  70                  75                  80

Val Thr Lys Asn Gly Arg Arg Met Phe Pro Val Leu Lys Val Asn Val
                85                  90                  95

Ser Gly Leu Asp Pro Asn Ala Met Tyr Ser Phe Leu Leu Asp Phe Val
            100                 105                 110

Ala Ala Asp Asn His Arg Trp Lys Tyr Val Asn Gly Glu Trp Val Pro
        115                 120                 125

Gly Gly Lys Pro Glu Pro Gln Ala Pro Ser Cys Val Tyr Ile His Pro
    130                 135                 140

Asp Ser Pro Asn Phe Gly Ala His Trp Met Lys Ala Pro Val Ser Phe
145                 150                 155                 160

Ser Lys Val Lys Leu Thr Asn Lys Leu Asn Gly Gly Gly Gln Ile Met
                165                 170                 175

Leu Asn Ser Leu His Lys Tyr Glu Pro Arg Ile His Ile Val Arg Val
            180                 185                 190

Gly Gly Pro Gln Arg Met Ile Thr Ser His Cys Phe Pro Glu Thr Gln
        195                 200                 205

Phe Ile Ala Val Thr Ala Tyr Gln Asn Glu Glu Ile Thr Ala Leu Lys
    210                 215                 220

Ile Lys Tyr Asn Pro Phe Ala Lys Ala Phe Leu Asp Ala Lys Glu Arg
225                 230                 235                 240

Ser Asp His Lys Glu Met Met Glu Glu Pro Gly Asp Ser Gln Gln Pro
                245                 250                 255

Gly Tyr Ser Gln Trp Gly Trp Leu Leu Pro Gly Thr Ser Thr Leu Cys
```

```
            260                 265                 270

Pro Pro Ala Asn Pro His Pro Gln Phe Gly Gly Ala Leu Ser Leu Pro
        275                 280                 285

Ser Thr His Ser Cys Asp Arg Tyr Pro Thr Leu Arg Ser His Arg Ser
    290                 295                 300

Ser Pro Tyr Pro Ser Pro Tyr Ala His Arg Asn Asn Ser Pro Thr Tyr
305                 310                 315                 320

Ser Asp Asn Ser Pro Ala Cys Leu Ser Met Leu Gln Ser His Asp Asn
                325                 330                 335

Trp Ser Ser Leu Gly Met Pro Ala His Pro Ser Met Leu Pro Val Ser
            340                 345                 350

His Asn Ala Ser Pro Pro Thr Ser Ser Ser Gln Tyr Pro Ser Leu Trp
        355                 360                 365

Ser Val Ser Asn Gly Ala Val Thr Pro Gly Ser Gln Ala Ala Ala Val
    370                 375                 380

Ser Asn Gly Leu Gly Ala Gln Phe Phe Arg Gly Ser Pro Ala His Tyr
385                 390                 395                 400

Thr Pro Leu Thr His Pro Val Ser Ala Pro Ser Ser Ser Gly Ser Pro
                405                 410                 415

Leu Tyr Glu Gly Ala Ala Ala Ala Thr Asp Ile Val Asp Ser Gln Tyr
            420                 425                 430

Asp Ala Ala Ala Gln Gly Arg Leu Ile Ala Ser Trp Thr Pro Val Ser
        435                 440                 445

Pro Pro Ser Met
    450


<210>  67
<211>  451
<212>  PRT
```

<213> Artificial Sequence

<220>
<223> Fusion protein comprising Brachyury protein Isoform 1 encoded by SEQ ID NO:65

<400> 67

```
Met Asn Met Ser Lys Lys Gln Val Lys Thr Gln Ser Lys Cys Asn Asn
1               5                   10                  15


Ile Ser Ser Pro Gly Thr Glu Ser Ala Gly Lys Ser Leu Gln Tyr Arg
            20                  25                  30


Val Asp His Leu Leu Ser Ala Val Glu Asn Glu Leu Gln Ala Gly Ser
        35                  40                  45


Glu Lys Gly Asp Pro Thr Glu Arg Glu Leu Arg Val Gly Leu Glu Glu
    50                  55                  60


Ser Glu Leu Trp Leu Arg Phe Lys Glu Leu Thr Asn Glu Met Ile Val
65                  70                  75                  80


Thr Lys Asn Gly Arg Arg Met Phe Pro Val Leu Lys Val Asn Val Ser
                85                  90                  95


Gly Leu Asp Pro Asn Ala Met Tyr Ser Phe Leu Leu Asp Phe Val Ala
            100                 105                 110


Ala Asp Asn His Arg Trp Lys Tyr Val Asn Gly Glu Trp Val Pro Gly
        115                 120                 125


Gly Lys Pro Glu Pro Gln Ala Pro Ser Cys Val Tyr Ile His Pro Asp
    130                 135                 140


Ser Pro Asn Phe Gly Ala His Trp Met Lys Ala Pro Val Ser Phe Ser
145                 150                 155                 160


Lys Val Lys Leu Thr Asn Lys Leu Asn Gly Gly Gly Gln Ile Met Leu
                165                 170                 175


Asn Ser Leu His Lys Tyr Glu Pro Arg Ile His Ile Val Arg Val Gly
            180                 185                 190
```

```
Gly Pro Gln Arg Met Ile Thr Ser His Cys Phe Pro Glu Thr Gln Phe
        195                 200                 205

Ile Ala Val Thr Ala Tyr Gln Asn Glu Glu Ile Thr Ala Leu Lys Ile
    210                 215                 220

Lys Tyr Asn Pro Phe Ala Lys Ala Phe Leu Asp Ala Lys Glu Arg Ser
225                 230                 235                 240

Asp His Lys Glu Met Met Glu Glu Pro Gly Asp Ser Gln Gln Pro Gly
                245                 250                 255

Tyr Ser Gln Trp Gly Trp Leu Leu Pro Gly Thr Ser Thr Leu Cys Pro
            260                 265                 270

Pro Ala Asn Pro His Pro Gln Phe Gly Gly Ala Leu Ser Leu Pro Ser
        275                 280                 285

Thr His Ser Cys Asp Arg Tyr Pro Thr Leu Arg Ser His Arg Ser Ser
    290                 295                 300

Pro Tyr Pro Ser Pro Tyr Ala His Arg Asn Asn Ser Pro Thr Tyr Ser
305                 310                 315                 320

Asp Asn Ser Pro Ala Cys Leu Ser Met Leu Gln Ser His Asp Asn Trp
                325                 330                 335

Ser Ser Leu Gly Met Pro Ala His Pro Ser Met Leu Pro Val Ser His
            340                 345                 350

Asn Ala Ser Pro Pro Thr Ser Ser Ser Gln Tyr Pro Ser Leu Trp Ser
        355                 360                 365

Val Ser Asn Gly Ala Val Thr Pro Gly Ser Gln Ala Ala Ala Val Ser
    370                 375                 380

Asn Gly Leu Gly Ala Gln Phe Phe Arg Gly Ser Pro Ala His Tyr Thr
385                 390                 395                 400
```

Pro Leu Thr His Pro Val Ser Ala Pro Ser Ser Ser Gly Ser Pro Leu
405 410 415

Tyr Glu Gly Ala Ala Ala Ala Thr Asp Ile Val Asp Ser Gln Tyr Asp
420 425 430

Ala Ala Ala Gln Gly Arg Leu Ile Ala Ser Trp Thr Pro Val Ser Pro
435 440 445

Pro Ser Met
450

<210> 68
<211> 1353
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence encoding Fusion protein comprising Brachyury protein Isoform 1 plus addition of 42 nucleotides from Gene FPV 088 and an atc

<400> 68
atgagtaaga aacaagtaaa aactcaaagt aaatgtaata atatcatgag ctcccctggc 60

accgagagcg cgggaaagag cctgcagtac cgagtggacc acctgctgag cgccgtggag 120

aatgagctgc aggcgggcag cgagaagggc gaccccacag agcgcgaact gcgcgtgggc 180

ctggaggaga gcgagctgtg gctgcgcttc aaggagctca ccaatgagat gatcgtgacc 240

aagaacggca ggaggatgtt tccggtgctg aaggtgaacg tgtctggcct ggaccccaac 300

gccatgtact ccttcctgct ggacttcgtg gcggcggaca accaccgctg gaagtacgtg 360

aacggggaat gggtgccggg gggcaagccg gagccgcagg cgcccagctg cgtctacatc 420

caccccgact cgcccaactt cggggcccac tggatgaagg ctcccgtctc cttcagcaaa 480

gtcaagctca ccaacaagct caacggaggg ggccagatca tgctgaactc cttgcataag 540

tatgagcctc gaatccacat agtgagagtt gggggtccac agcgcatgat caccagccac 600

tgcttccctg agacccagtt catagcggtg actgcttatc agaacgagga gatcacagct 660

cttaaaatta agtacaatcc atttgcaaaa gctttccttg atgcaaagga aagaagtgat 720

cacaaagaga tgatggagga acccggagac agccagcaac ctgggtactc ccaatggggg 780

tggcttcttc ctggaaccag caccgtttgt ccacctgcaa atcctcatcc tcagtttgga 840

ggtgccctct ccctcccctc cacgcacagc tgtgacaggt acccaaccct gaggagccac 900

cggtcctcac cctaccccag cccctatgct catcggaaca attctccaac ctattctgac 960

aactcacctg catgtttatc catgctgcaa tcccatgaca attggtccag ccttggaatg 1020

cctgcccatc ccagcatgct ccccgtgagc cacaatgcca gcccacctac cagctccagt 1080

cagtacccca gcctgtggtc tgtgagcaac ggcgccgtca ccccgggctc ccaggcagca 1140

gccgtgtcca acgggctggg ggcccagttc ttccggggct cccccgcgca ctacacaccc 1200

ctcacccatc cggtctcggc gccctcttcc tcgggatccc cactgtacga aggggcggcc 1260

gcggccacag acatcgtgga cagccagtac gacgccgcag cccaaggccg cctcatagcc 1320

tcatggacac ctgtgtcgcc accttccatg tga 1353

<210> 69
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> Coding sequence encoding Fusion protein comprising Brachyury protein Isoform 1 plus addition of 42 nucleotides from Gene FPV 088 and an atc, without Brachyury atg start codon

<400> 69
atgagtaaga aacaagtaaa aactcaaagt aaatgtaata atatcagctc ccctggcacc 60

gagagcgcgg gaaagagcct gcagtaccga gtggaccacc tgctgagcgc cgtggagaat 120

gagctgcagg cgggcagcga gaagggcgac cccacagagc gcgaactgcg cgtgggcctg 180

gaggagagcg agctgtggct gcgcttcaag gagctcacca atgagatgat cgtgaccaag 240

aacggcagga ggatgtttcc ggtgctgaag gtgaacgtgt ctggcctgga ccccaacgcc 300

atgtactcct tcctgctgga cttcgtggcg gcggacaacc accgctggaa gtacgtgaac 360

ggggaatggg tgccgggggg caagccggag ccgcaggcgc ccagctgcgt ctacatccac 420

cccgactcgc ccaacttcgg ggcccactgg atgaaggctc ccgtctcctt cagcaaagtc 480

aagctcacca acaagctcaa cggaggggcc cagatcatgc tgaactcctt gcataagtat 540

gagcctcgaa tccacatagt gagagttggg ggtccacagc gcatgatcac cagccactgc 600

ttccctgaga cccagttcat agcggtgact gcttatcaga acgaggagat cacagctctt 660

aaaattaagt acaatccatt tgcaaaagct ttccttgatg caaaggaaag aagtgatcac 720

aaagagatga tggaggaacc cggagacagc cagcaacctg ggtactccca atgggggtgg 780

cttcttcctg gaaccagcac cgtttgtcca cctgcaaatc ctcatcctca gtttggaggt 840

gccctctccc tcccctccac gcacagctgt gacaggtacc caaccctgag gagccaccgg 900

tcctcaccct accccagccc ctatgctcat cggaacaatt ctccaaccta ttctgacaac 960

tcacctgcat gtttatccat gctgcaatcc catgacaatt ggtccagcct tggaatgcct 1020

gcccatccca gcatgctccc cgtgagccac aatgccagcc cacctaccag ctccagtcag 1080

taccccagcc tgtggtctgt gagcaacggc gccgtcaccc cgggctccca ggcagcagcc 1140

gtgtccaacg ggctgggggc ccagttcttc cggggctccc ccgcgcacta cacacccctc 1200

acccatccgg tctcggcgcc ctcttcctcg ggatccccac tgtacgaagg ggcggccgcg 1260

gccacagaca tcgtggacag ccagtacgac gccgcagccc aaggccgcct catagcctca 1320

tggacacctg tgtcgccacc ttccatgtga 1350

<210> 70
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion protein comprising Brachyury protein Isoform 1 encoded by SEQ ID NO:68

<400> 70

Met Ser Lys Lys Gln Val Lys Thr Gln Ser Lys Cys Asn Asn Ile Met
1 5 10 15

Ser Ser Pro Gly Thr Glu Ser Ala Gly Lys Ser Leu Gln Tyr Arg Val
20 25 30

Asp His Leu Leu Ser Ala Val Glu Asn Glu Leu Gln Ala Gly Ser Glu
35 40 45

Lys Gly Asp Pro Thr Glu Arg Glu Leu Arg Val Gly Leu Glu Glu Ser
50 55 60

Glu Leu Trp Leu Arg Phe Lys Glu Leu Thr Asn Glu Met Ile Val Thr
65 70 75 80

```
Lys Asn Gly Arg Arg Met Phe Pro Val Leu Lys Val Asn Val Ser Gly
                85                  90                  95

Leu Asp Pro Asn Ala Met Tyr Ser Phe Leu Leu Asp Phe Val Ala Ala
            100                 105                 110

Asp Asn His Arg Trp Lys Tyr Val Asn Gly Glu Trp Val Pro Gly Gly
        115                 120                 125

Lys Pro Glu Pro Gln Ala Pro Ser Cys Val Tyr Ile His Pro Asp Ser
    130                 135                 140

Pro Asn Phe Gly Ala His Trp Met Lys Ala Pro Val Ser Phe Ser Lys
145                 150                 155                 160

Val Lys Leu Thr Asn Lys Leu Asn Gly Gly Gly Gln Ile Met Leu Asn
                165                 170                 175

Ser Leu His Lys Tyr Glu Pro Arg Ile His Ile Val Arg Val Gly Gly
            180                 185                 190

Pro Gln Arg Met Ile Thr Ser His Cys Phe Pro Glu Thr Gln Phe Ile
        195                 200                 205

Ala Val Thr Ala Tyr Gln Asn Glu Glu Ile Thr Ala Leu Lys Ile Lys
    210                 215                 220

Tyr Asn Pro Phe Ala Lys Ala Phe Leu Asp Ala Lys Glu Arg Ser Asp
225                 230                 235                 240

His Lys Glu Met Met Glu Glu Pro Gly Asp Ser Gln Gln Pro Gly Tyr
                245                 250                 255

Ser Gln Trp Gly Trp Leu Leu Pro Gly Thr Ser Thr Leu Cys Pro Pro
            260                 265                 270

Ala Asn Pro His Pro Gln Phe Gly Gly Ala Leu Ser Leu Pro Ser Thr
        275                 280                 285

His Ser Cys Asp Arg Tyr Pro Thr Leu Arg Ser His Arg Ser Ser Pro
```

```
    290                 295                 300

Tyr Pro Ser Pro Tyr Ala His Arg Asn Asn Ser Pro Thr Tyr Ser Asp
305                 310                 315                 320

Asn Ser Pro Ala Cys Leu Ser Met Leu Gln Ser His Asp Asn Trp Ser
                325                 330                 335

Ser Leu Gly Met Pro Ala His Pro Ser Met Leu Pro Val Ser His Asn
            340                 345                 350

Ala Ser Pro Pro Thr Ser Ser Ser Gln Tyr Pro Ser Leu Trp Ser Val
        355                 360                 365

Ser Asn Gly Ala Val Thr Pro Gly Ser Gln Ala Ala Ala Val Ser Asn
    370                 375                 380

Gly Leu Gly Ala Gln Phe Phe Arg Gly Ser Pro Ala His Tyr Thr Pro
385                 390                 395                 400

Leu Thr His Pro Val Ser Ala Pro Ser Ser Ser Gly Ser Pro Leu Tyr
                405                 410                 415

Glu Gly Ala Ala Ala Ala Thr Asp Ile Val Asp Ser Gln Tyr Asp Ala
            420                 425                 430

Ala Ala Gln Gly Arg Leu Ile Ala Ser Trp Thr Pro Val Ser Pro Pro
        435                 440                 445

Ser Met
    450
```

<210> 71
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Fusion protein comprising Brachyury protein Isoform 1 encoded by SEQ ID NO:69

<400> 71

```
Met Ser Lys Lys Gln Val Lys Thr Gln Ser Lys Cys Asn Asn Ile Ser
1               5                   10                  15

Ser Pro Gly Thr Glu Ser Ala Gly Lys Ser Leu Gln Tyr Arg Val Asp
            20                  25                  30

His Leu Leu Ser Ala Val Glu Asn Glu Leu Gln Ala Gly Ser Glu Lys
        35                  40                  45

Gly Asp Pro Thr Glu Arg Glu Leu Arg Val Gly Leu Glu Glu Ser Glu
    50                  55                  60

Leu Trp Leu Arg Phe Lys Glu Leu Thr Asn Glu Met Ile Val Thr Lys
65                  70                  75                  80

Asn Gly Arg Arg Met Phe Pro Val Leu Lys Val Asn Val Ser Gly Leu
                85                  90                  95

Asp Pro Asn Ala Met Tyr Ser Phe Leu Leu Asp Phe Val Ala Ala Asp
            100                 105                 110

Asn His Arg Trp Lys Tyr Val Asn Gly Glu Trp Val Pro Gly Gly Lys
        115                 120                 125

Pro Glu Pro Gln Ala Pro Ser Cys Val Tyr Ile His Pro Asp Ser Pro
    130                 135                 140

Asn Phe Gly Ala His Trp Met Lys Ala Pro Val Ser Phe Ser Lys Val
145                 150                 155                 160

Lys Leu Thr Asn Lys Leu Asn Gly Gly Gly Gln Ile Met Leu Asn Ser
                165                 170                 175

Leu His Lys Tyr Glu Pro Arg Ile His Ile Val Arg Val Gly Gly Pro
            180                 185                 190

Gln Arg Met Ile Thr Ser His Cys Phe Pro Glu Thr Gln Phe Ile Ala
        195                 200                 205

Val Thr Ala Tyr Gln Asn Glu Glu Ile Thr Ala Leu Lys Ile Lys Tyr
    210                 215                 220
```

```
Asn Pro Phe Ala Lys Ala Phe Leu Asp Ala Lys Glu Arg Ser Asp His
225                 230                 235                 240

Lys Glu Met Met Glu Glu Pro Gly Asp Ser Gln Gln Pro Gly Tyr Ser
                245                 250                 255

Gln Trp Gly Trp Leu Leu Pro Gly Thr Ser Thr Leu Cys Pro Pro Ala
            260                 265                 270

Asn Pro His Pro Gln Phe Gly Gly Ala Leu Ser Leu Pro Ser Thr His
        275                 280                 285

Ser Cys Asp Arg Tyr Pro Thr Leu Arg Ser His Arg Ser Ser Pro Tyr
    290                 295                 300

Pro Ser Pro Tyr Ala His Arg Asn Asn Ser Pro Thr Tyr Ser Asp Asn
305                 310                 315                 320

Ser Pro Ala Cys Leu Ser Met Leu Gln Ser His Asp Asn Trp Ser Ser
                325                 330                 335

Leu Gly Met Pro Ala His Pro Ser Met Leu Pro Val Ser His Asn Ala
            340                 345                 350

Ser Pro Pro Thr Ser Ser Ser Gln Tyr Pro Ser Leu Trp Ser Val Ser
        355                 360                 365

Asn Gly Ala Val Thr Pro Gly Ser Gln Ala Ala Ala Val Ser Asn Gly
    370                 375                 380

Leu Gly Ala Gln Phe Phe Arg Gly Ser Pro Ala His Tyr Thr Pro Leu
385                 390                 395                 400

Thr His Pro Val Ser Ala Pro Ser Ser Ser Gly Ser Pro Leu Tyr Glu
                405                 410                 415

Gly Ala Ala Ala Ala Thr Asp Ile Val Asp Ser Gln Tyr Asp Ala Ala
            420                 425                 430
```

Ala Gln Gly Arg Leu Ile Ala Ser Trp Thr Pro Val Ser Pro Pro Ser
435 440 445

Met

<210> 72
<211> 1516
<212> DNA
<213> Artificial Sequence

<220>
<223> Expression Cassette found in mBN345 - Promoter + cDNA encoding
Fusion protein comprising Brachyury (L254V) Protein

<400> 72
atccgtacag gtttgtttct gaaattcact ttgtaagata cataattaac aaattcaggg 60

ggaaaaatct ttacaaaatt agtatagaag ctatagatat atcaaaaggt agacaacaaa 120

taatcagaac ctaatttttt tatcaaaaaa ttaaaatata aataaaatga aaaataactt 180

gtatgaagaa aaaatgaaca tgagtaagaa aagctcccct ggcaccgaga gcgcgggaaa 240

gagcctgcag taccgagtgg accacctgct gagcgccgtg gagaatgagc tgcaggcggg 300

cagcgagaag ggcgacccca cagagcgcga actgcgcgtg ggcctggagg agagcgagct 360

gtggctgcgc ttcaaggagc tcaccaatga gatgatcgtg accaagaacg gcaggaggat 420

gtttccggtg ctgaaggtga acgtgtctgg cctggacccc aacgccatgt actccttcct 480

gctggacttc gtggcggcgg acaaccaccg ctggaagtac gtgaacgggg aatgggtgcc 540

gggggggcaag ccggagccgc aggcgcccag ctgcgtctac atccaccccg actcgcccaa 600

cttcggggcc cactggatga aggctcccgt ctccttcagc aaagtcaagc tcaccaacaa 660

gctcaacgga gggggccaga tcatgctgaa ctccttgcat aagtatgagc ctcgaatcca 720

catagtgaga gttgggggtc cacagcgcat gatcaccagc cactgcttcc ctgagaccca 780

gttcatagcg gtgactgctt atcagaacga ggagatcaca gctcttaaaa ttaagtacaa 840

tccatttgca aaggctttcc ttgatgcaaa ggaaagaagt gatcacaaag agatgatgga 900

ggaacccgga gacagccagc aacctgggta ctcccaatgg gggtggcttc ttcctggaac 960

cagcaccgtt tgtccacctg caaatcctca tcctcagttt ggaggtgccc tctccctccc 1020

ctccacgcac agctgtgaca ggtacccaac cctgaggagc caccggtcct caccctaccc 1080

cagcccctat gctcatcgga acaattctcc aacctattct gacaactcac ctgcatgttt 1140

atccatgctg caatcccatg acaattggtc cagccttgga atgcctgccc atcccagcat 1200

gctccccgtg agccacaatg ccagcccacc taccagctcc agtcagtacc ccagcctgtg 1260

gtctgtgagc aacggcgccg tcaccccggg ctcccaggca gcagccgtgt ccaacgggct 1320

gggggcccag ttcttccggg gctcccccgc gcactacaca cccctcaccc atccggtctc 1380

ggcgccctct tcctcgggat ccccactgta cgaaggggcg gccgcggcca cagacatcgt 1440

ggacagccag tacgacgccg cagcccaagg ccgcctcata gcctcatgga cacctgtgtc 1500

gccaccttcc atgtga 1516

<210> 73
<211> 1552
<212> DNA
<213> Artificial Sequence

<220>
<223> Expression Cassette found in mBN355 - Promoter + cDNA encoding
Fusion protein comprising Brachyury (L254V) Protein

<400> 73
atccgtacag gtttgtttct gaaattcact ttgtaagata cataattaac aaattcaggg 60

ggaaaaatct ttacaaaatt agtatagaag ctatagatat atcaaaaggt agacaacaaa 120

taatcagaac ctaatttttt tatcaaaaaa ttaaaatata aataaaatga aaaataactt 180

gtatgaagaa aaaatgaaca tgagtaagaa acaagtaaaa actcaaagta aatgtaataa 240

tatcatgagc tcccctggca ccgagagcgc gggaaagagc ctgcagtacc gagtggacca 300

cctgctgagc gccgtggaga atgagctgca ggcgggcagc gagaagggcg accccacaga 360

gcgcgaactg cgcgtgggcc tggaggagag cgagctgtgg ctgcgcttca aggagctcac 420

caatgagatg atcgtgacca agaacggcag gaggatgttt ccggtgctga aggtgaacgt 480

gtctggcctg gaccccaacg ccatgtactc cttcctgctg gacttcgtgg cggcggacaa 540

ccaccgctgg aagtacgtga acggggaatg ggtgccgggg ggcaagccgg agccgcaggc 600

gcccagctgc gtctacatcc accccgactc gcccaacttc ggggcccact ggatgaaggc 660

tcccgtctcc ttcagcaaag tcaagctcac caacaagctc aacggagggg gccagatcat 720

gctgaactcc ttgcataagt atgagcctcg aatccacata gtgagagttg ggggtccaca 780

gcgcatgatc accagccact gcttccctga gacccagttc atagcggtga ctgcttatca 840

gaacgaggag atcacagctc ttaaaattaa gtacaatcca tttgcaaagg ctttccttga 900

tgcaaaggaa agaagtgatc acaaagagat gatggaggaa cccggagaca gccagcaacc 960

tgggtactcc caatgggggt ggcttcttcc tggaaccagc accgtttgtc cacctgcaaa 1020

tcctcatcct cagtttggag gtgccctctc cctcccctcc acgcacagct gtgacaggta 1080

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ttctccaacc tattctgaca actcacctgc atgtttatcc atgctgcaat cccatgacaa 1200

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cccacctacc agctccagtc agtaccccag cctgtggtct gtgagcaacg gcgccgtcac 1320

cccgggctcc caggcagcag ccgtgtccaa cgggctgggg gcccagttct tccggggctc 1380

ccccgcgcac tacacacccc tcacccatcc ggtctcggcg ccctcttcct cgggatcccc 1440

actgtacgaa ggggcggccg cggccacaga catcgtggac agccagtacg acgccgcagc 1500

ccaaggccgc ctcatagcct catggacacc tgtgtcgcca ccttccatgt ga 1552

<210> 74
<211> 1464
<212> DNA
<213> Artificial Sequence

<220>
<223> Expression Cassette found in mBN343 - Promoter + cDNA encoding
Fusion protein comprising Brachyury (L254V) Protein

<400> 74
taatgtatag aactaattta taataaacat agtaaatatg ggtaacttct taatagccat 60

aattaaaatt gaaaaaaaaa tatcattata aaacgtaaac gaacaaaaaa cattaattga 120

tccccccccc gtctcccccc tccagattga gcaatcatga gctcccctgg caccgagagc 180

gcgggaaaga gcctgcagta ccgagtggac cacctgctga gcgccgtgga gaatgagctg 240

caggcgggca gcgagaaggg cgaccccaca gagcgcgaac tgcgcgtggg cctggaggag 300

agcgagctgt ggctgcgctt caaggagctc accaatgaga tgatcgtgac caagaacggc 360

aggaggatgt ttccggtgct gaaggtgaac gtgtctggcc tggaccccaa cgccatgtac 420

tccttcctgc tggacttcgt ggcggcggac aaccaccgct ggaagtacgt gaacggggaa 480

tgggtgccgg ggggcaagcc ggagccgcag gcgcccagct gcgtctacat ccaccccgac 540

tcgcccaact tcggggccca ctggatgaag gctcccgtct ccttcagcaa agtcaagctc 600

accaacaagc tcaacggagg gggccagatc atgctgaact ccttgcataa gtatgagcct 660

cgaatccaca tagtgagagt tgggggtcca cagcgcatga tcaccagcca ctgcttccct 720

gagacccagt tcatagcggt gactgcttat cagaacgagg agatcacagc tcttaaaatt 780

aagtacaatc catttgcaaa ggctttcctt gatgcaaagg aaagaagtga tcacaaagag 840

atgatggagg aacccggaga cagccagcaa cctgggtact cccaatgggg gtggcttctt 900

cctggaacca gcaccgtttg tccacctgca aatcctcatc ctcagtttgg aggtgccctc 960

tccctcccct ccacgcacag ctgtgacagg tacccaaccc tgaggagcca ccggtcctca 1020

ccctacccca gcccctatgc tcatcggaac aattctccaa cctattctga caactcacct 1080

gcatgtttat ccatgctgca atcccatgac aattggtcca gccttggaat gcctgcccat 1140

cccagcatgc tccccgtgag ccacaatgcc agcccaccta ccagctccag tcagtacccc 1200

agcctgtggt ctgtgagcaa cggcgccgtc accccgggct cccaggcagc agccgtgtcc 1260

aacgggctgg gggcccagtt cttccggggc tcccccgcgc actacacacc cctcacccat 1320

ccggtctcgg cgccctcttc ctcgggatcc ccactgtacg aaggggcggc cgcggccaca 1380

gacatcgtgg acagccagta cgacgccgca gcccaaggcc gcctcatagc ctcatggaca 1440

cctgtgtcgc caccttccat gtga 1464

<210> 75
<211> 1478
<212> DNA
<213> Artificial Sequence

<220>
<223> Expression Cassette found in mBN344 - Promoter + cDNA encoding
Fusion protein comprising Brachyury (L254V) Protein

<400> 75
tatccgtaca ggtttgtttc tgaaattcac tttgtaagat acataattaa caaattcagg 60

gggaaaaatc tttacaaaat tagtatagaa gctatagata tatcaaaagg tagacaacaa 120

ataatcagaa cctaattttt ttatcaaaaa attaaaatat aaataaaatc atgagctccc 180

ctggcaccga gagcgcggga aagagcctgc agtaccgagt ggaccacctg ctgagcgccg 240

tggagaatga gctgcaggcg ggcagcgaga agggcgaccc cacagagcgc gaactgcgcg 300

tgggcctgga ggagagcgag ctgtggctgc gcttcaagga gctcaccaat gagatgatcg 360

tgaccaagaa cggcaggagg atgtttccgg tgctgaaggt gaacgtgtct ggcctggacc 420

ccaacgccat gtactccttc ctgctggact tcgtggcggc ggacaaccac cgctggaagt 480

acgtgaacgg ggaatgggtg ccgggggggca agccggagcc gcaggcgccc agctgcgtct 540

acatccaccc cgactcgccc aacttcgggg cccactggat gaaggctccc gtctccttca 600

gcaaagtcaa gctcaccaac aagctcaacg gaggggggca gatcatgctg aactccttgc 660

ataagtatga gcctcgaatc cacatagtga gagttggggg tccacagcgc atgatcacca 720

gccactgctt ccctgagacc cagttcatag cggtgactgc ttatcagaac gaggagatca 780

cagctcttaa aattaagtac aatccatttg caaaggcttt ccttgatgca aaggaaagaa 840

gtgatcacaa agagatgatg gaggaacccg gagacagcca gcaacctggg tactcccaat 900

gggggtggct tcttcctgga accagcaccg tttgtccacc tgcaaatcct catcctcagt 960

ttggaggtgc cctctccctc ccctccacgc acagctgtga caggtaccca accctgagga 1020

gccaccggtc ctcaccctac cccagcccct atgctcatcg gaacaattct ccaacctatt 1080

ctgacaactc acctgcatgt ttatccatgc tgcaatccca tgacaattgg tccagccttg 1140

gaatgcctgc ccatcccagc atgctccccg tgagccacaa tgccagccca cctaccagct 1200

ccagtcagta ccccagcctg tggtctgtga gcaacggcgc cgtcaccccg ggctcccagg 1260

cagcagccgt gtccaacggg ctgggggccc agttcttccg gggctccccc gcgcactaca 1320

cacccctcac ccatccggtc tcggcgccct cttcctcggg atccccactg tacgaagggg 1380

cggccgcggc cacagacatc gtggacagcc agtacgacgc cgcagcccaa ggccgcctca 1440

tagcctcatg gacacctgtg tcgccacctt ccatgtga 1478

<210> 76
<211> 1486
<212> DNA
<213> Artificial Sequence

<220>
<223> Expression Cassette found in mBN354 - Promoter + cDNA encoding
Fusion protein comprising Brachyury (L254V) Protein

<400> 76
atccgtacag gtttgtttct gaaattcact ttgtaagata cataattaac aaattcaggg 60

ggaaaaatct ttacaaaatt agtatagaag ctatagatat atcaaaaggt agacaacaaa 120

taatcagaac ctaatttttt tatcaaaaaa ttaaaatata aataaaatga aaaataactt 180

gagctcccct ggcaccgaga gcgcgggaaa gagcctgcag taccgagtgg accacctgct 240

gagcgccgtg gagaatgagc tgcaggcggg cagcgagaag ggcgacccca cagagcgcga 300

actgcgcgtg ggcctggagg agagcgagct gtggctgcgc ttcaaggagc tcaccaatga 360

gatgatcgtg accaagaacg gcaggaggat gtttccggtg ctgaaggtga acgtgtctgg 420

cctggacccc aacgccatgt actccttcct gctggacttc gtggcggcgg acaaccaccg 480

ctggaagtac gtgaacgggg aatgggtgcc ggggggcaag ccggagccgc aggcgcccag 540

ctgcgtctac atccaccccg actcgcccaa cttcggggcc cactggatga aggctcccgt 600

ctccttcagc aaagtcaagc tcaccaacaa gctcaacgga gggggccaga tcatgctgaa 660

ctccttgcat aagtatgagc ctcgaatcca catagtgaga gttgggggtc cacagcgcat 720

gatcaccagc cactgcttcc ctgagaccca gttcatagcg gtgactgctt atcagaacga 780

ggagatcaca gctcttaaaa ttaagtacaa tccatttgca aaggctttcc ttgatgcaaa 840

ggaaagaagt gatcacaaag agatgatgga ggaacccgga gacagccagc aacctgggta 900

ctcccaatgg gggtggcttc ttcctggaac cagcaccgtt tgtccacctg caaatcctca 960

tcctcagttt ggaggtgccc tctccctccc ctccacgcac agctgtgaca ggtacccaac 1020

cctgaggagc caccggtcct caccctaccc cagcccctat gctcatcgga acaattctcc 1080

aacctattct gacaactcac ctgcatgttt atccatgctg caatcccatg acaattggtc 1140

cagccttgga atgcctgccc atcccagcat gctccccgtg agccacaatg ccagcccacc 1200

taccagctcc agtcagtacc ccagcctgtg gtctgtgagc aacggcgccg tcaccccggg 1260

ctcccaggca gcagccgtgt ccaacgggct gggggcccag ttcttccggg gctcccccgc 1320

gcactacaca cccctcaccc atccggtctc ggcgccctct tcctcgggat ccccactgta 1380

cgaaggggcg gccgcggcca cagacatcgt ggacagccag tacgacgccg cagcccaagg 1440

ccgcctcata gcctcatgga cacctgtgtc gccaccttcc atgtga 1486

<210> 77
<211> 182
<212> DNA
<213> Artificial Sequence

<220>
<223> Promoter Sequence with nucleotides 5' of Gene FPV 088 + 15

nucleotides

<400> 77
tatccgtaca ggtttgtttc tgaaattcac tttgtaagat acataattaa caaattcagg 60

gggaaaaatc tttacaaaat tagtatagaa gctatagata tatcaaaagg tagacaacaa 120

ataatcagaa cctaattttt ttatcaaaaa attaaaatat aaataaaatg aaaaataact 180

tg 182

CLAIMS

We claim:

1. An expression cassette comprising a nucleic acid sequence having at least 90% identity with the nucleic acid sequence set forth in SEQ ID NO:72 or SEQ ID NO:73.

2. A poxviral vector comprising the expression cassette of claim 1.

3. The poxviral vector of claim 2, wherein the poxvirus is a fowlpox virus.

4. The poxviral vector of claim 2, wherein the poxvirus is a modified vaccinia virus Ankara that is MVA-BN.