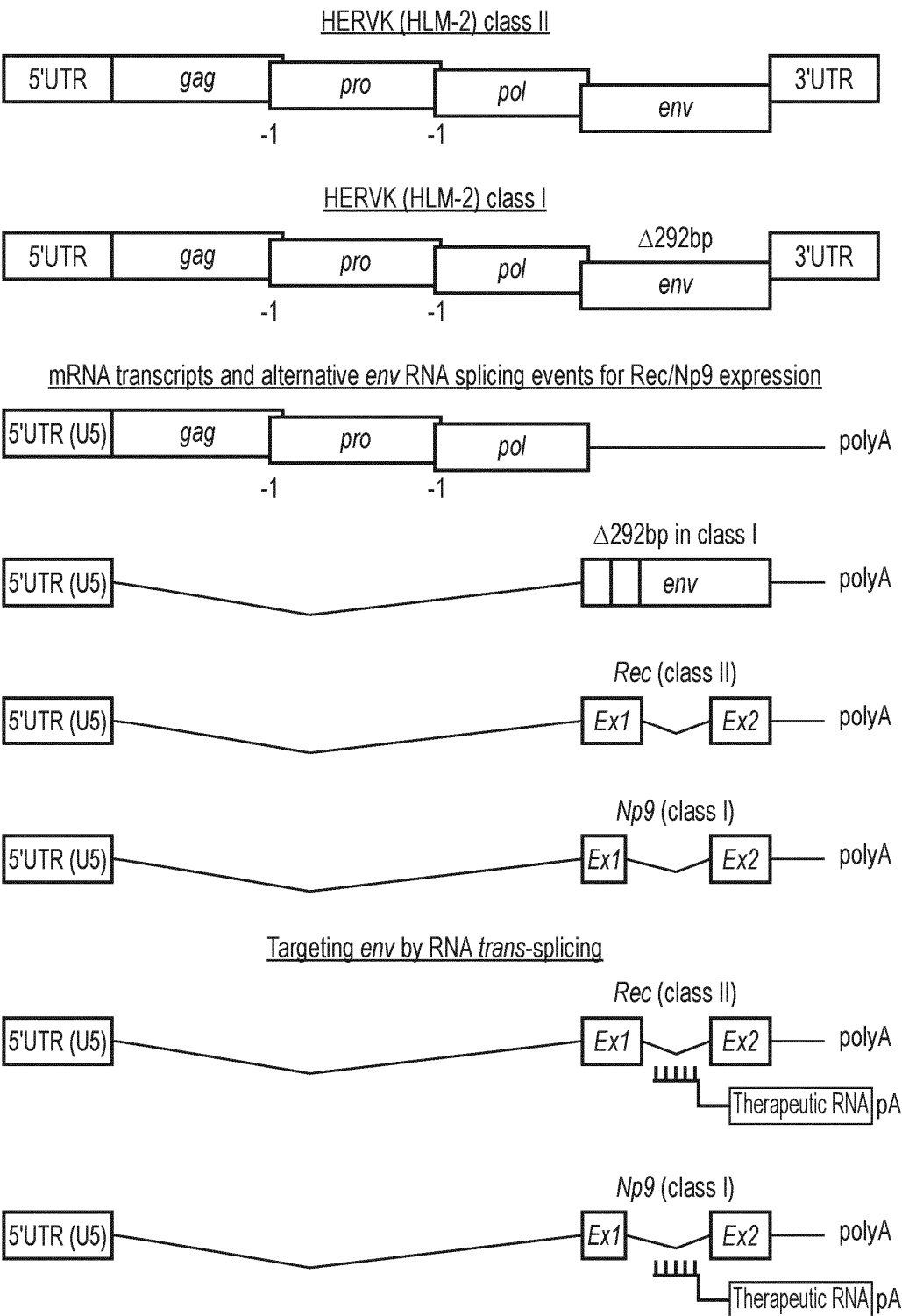




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A. Target sequence:

TGGATAATCCTATAGAAGTATATGTTAATGATAGCGAATGGGTA

B. Sequence alignment against Homo sapiens isolate HML-2_22q11.21 endogenous virus HERV-K, Sequence ID: JN675087.1

Score	Expect	Identities	Gaps	Strand
82.4 bits(44)	7e-13	44/44(100%)	0/44(0%)	Plus/Plus

Query 1 TGGATAATCCTATAGAAGTATATGTTAATGATAGCGAATGGGTA 44
 |||||
 Sbjct 6513 TGGATAATCCTATAGAAGTATATGTTAATGATAGCGAATGGGTA 6556

C.**Reverse complementarity of target sequence:**

TACCCATTCGCTATCATTAAACATATACTTCTATAGGATTATCCA

Binding domain sequence targeting Np9:

TACTCATTTCGCTATCATTTCATATACTTCTCTGGGATTATCCA (DNA) (44nts)

UACUCAUUCGCUAUCAUUUUCAUAUACUUCUGUGGGAUUAUCCA (RNA)

C to U (wobble)

Two AA to UU mismatch

AUA to GUG wobble (A to G)

D. Sequence alignment against Homo sapiens isolate HML-2_22q11.21 endogenous virus HERV-K, Sequence ID: JN675087.1

Score	Expect	Identities	Gaps	Strand
58.1 bits(63)	2e-05	39/44(89%)	0/44(0%)	Plus/Minus

Query 1 TACTCATTTCGCTATCATTTCATATACTTCTGTGGGATTATCCA 44
 ||| |||||
 Sbjct 6556 TACCCATTCGCTATCATTAAACATATACTTCTATAGGATTATCCA 6513

FIG. 2

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A. RNA structures of BD (RNA fold)

MFE

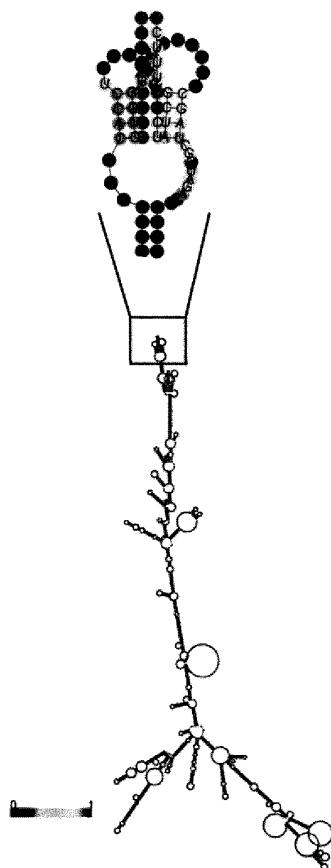


centroid



B. RNA folds in BD in backbone plasmid

Centroid fold (pVAX)



MFE (pVAX)

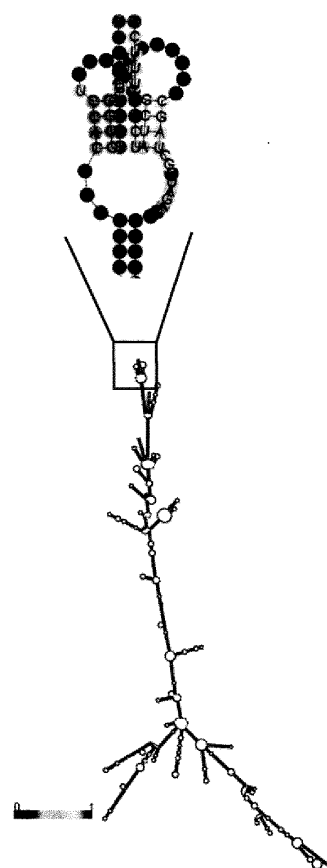


FIG. 3

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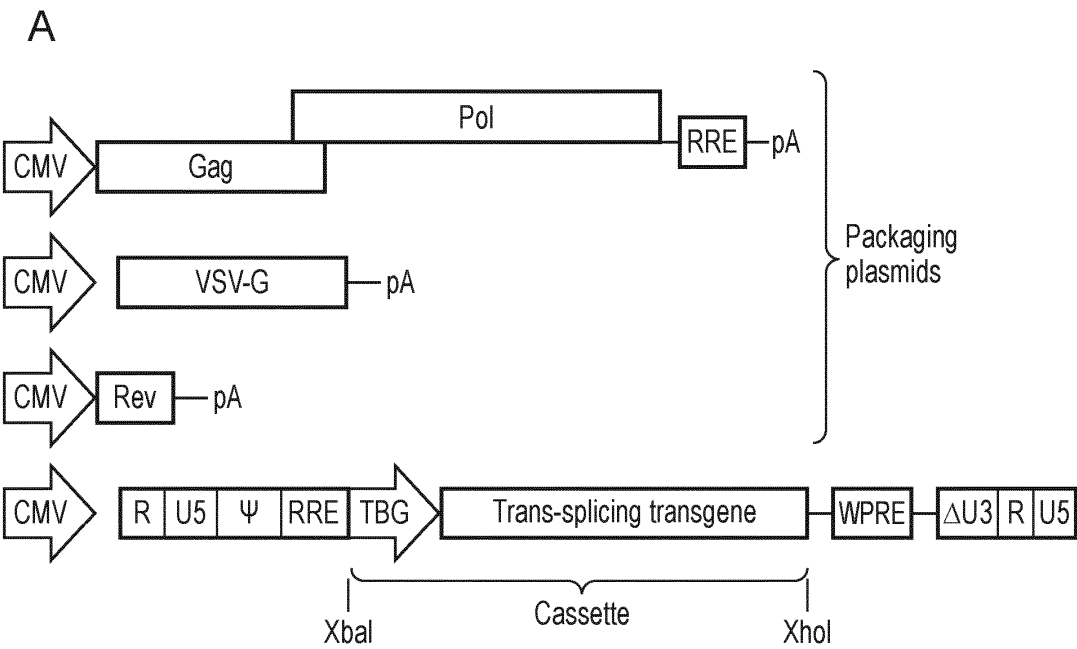


FIG. 4

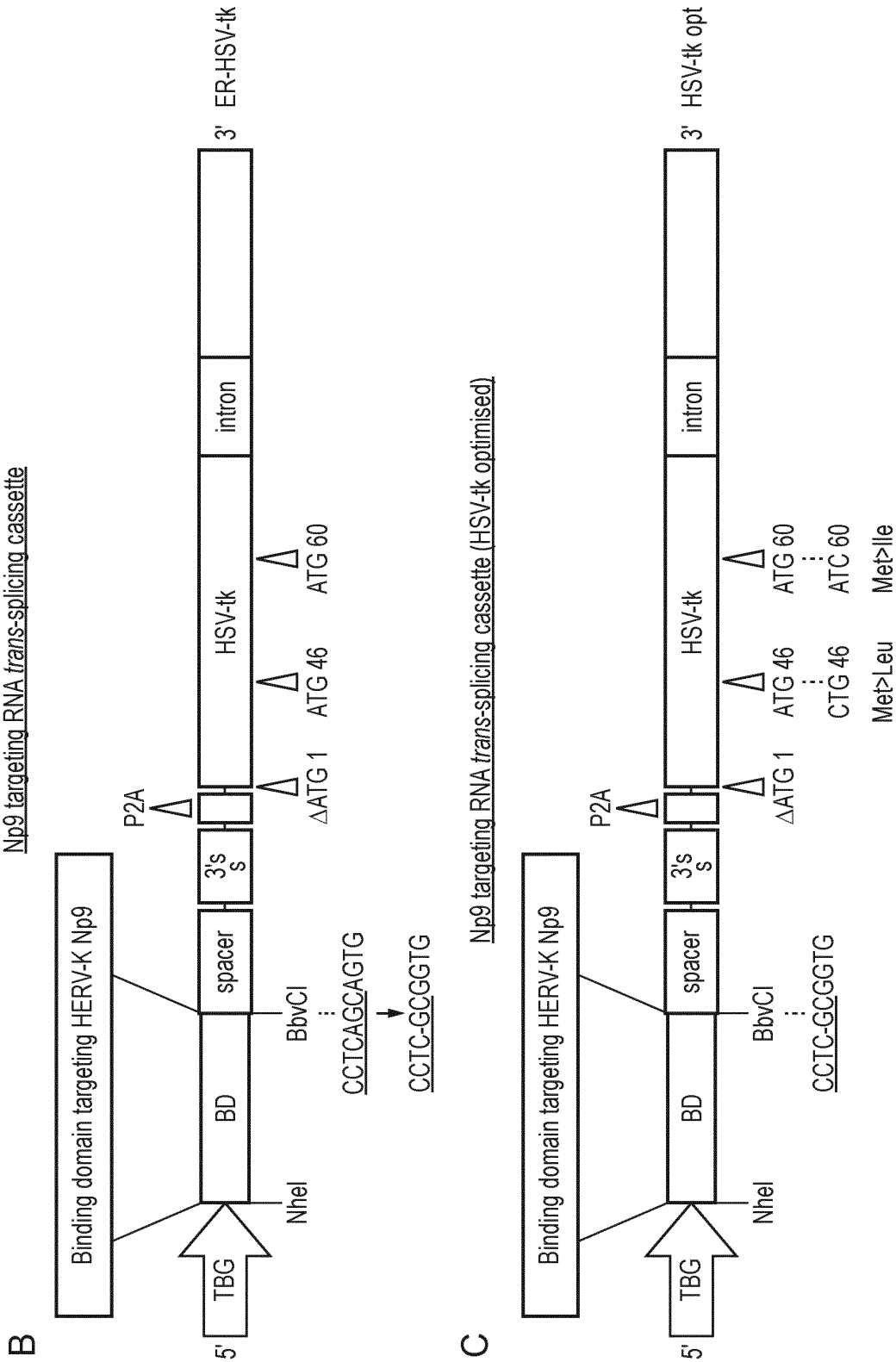


FIG. 4

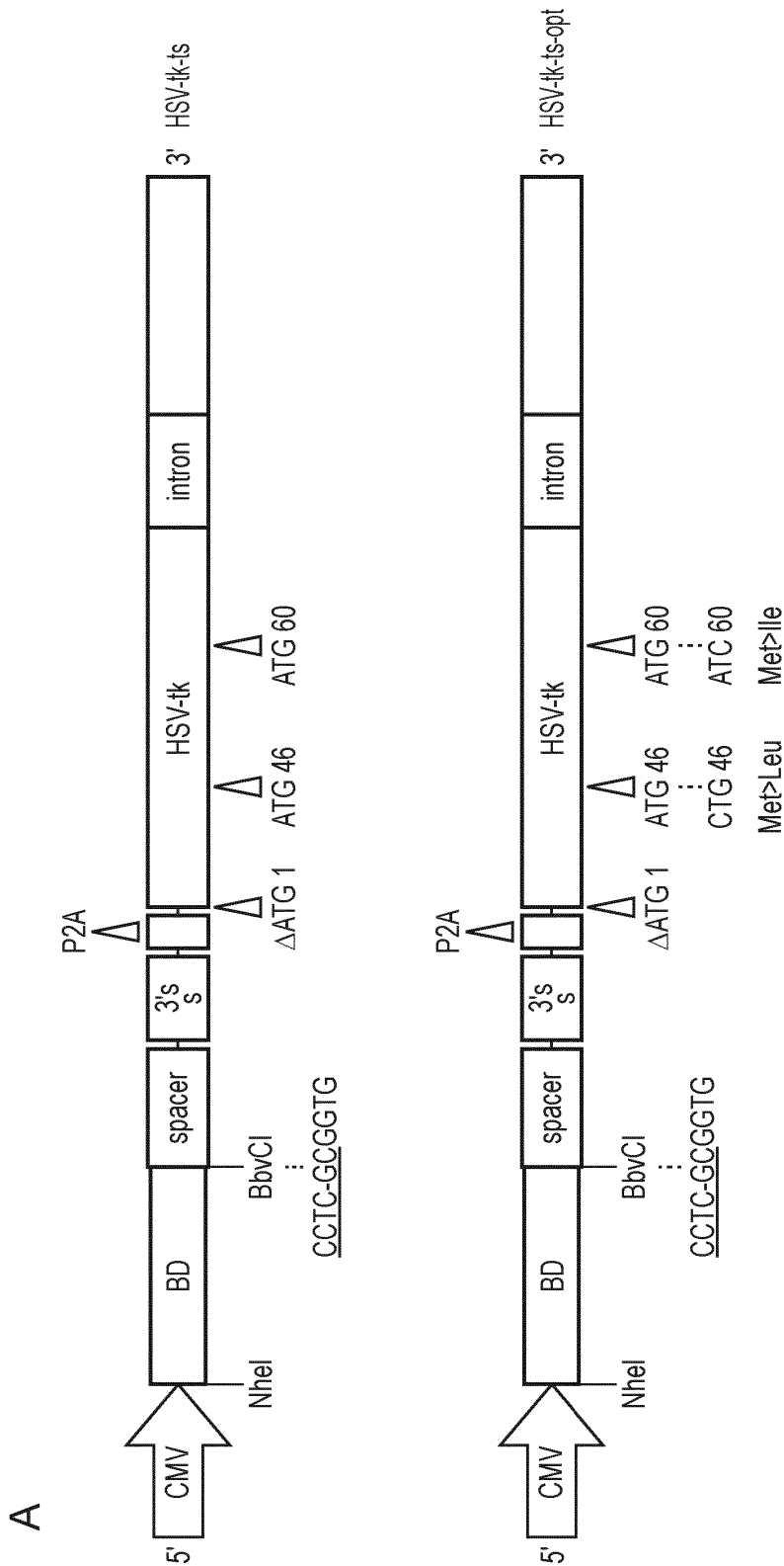


FIG. 5A Enlarged

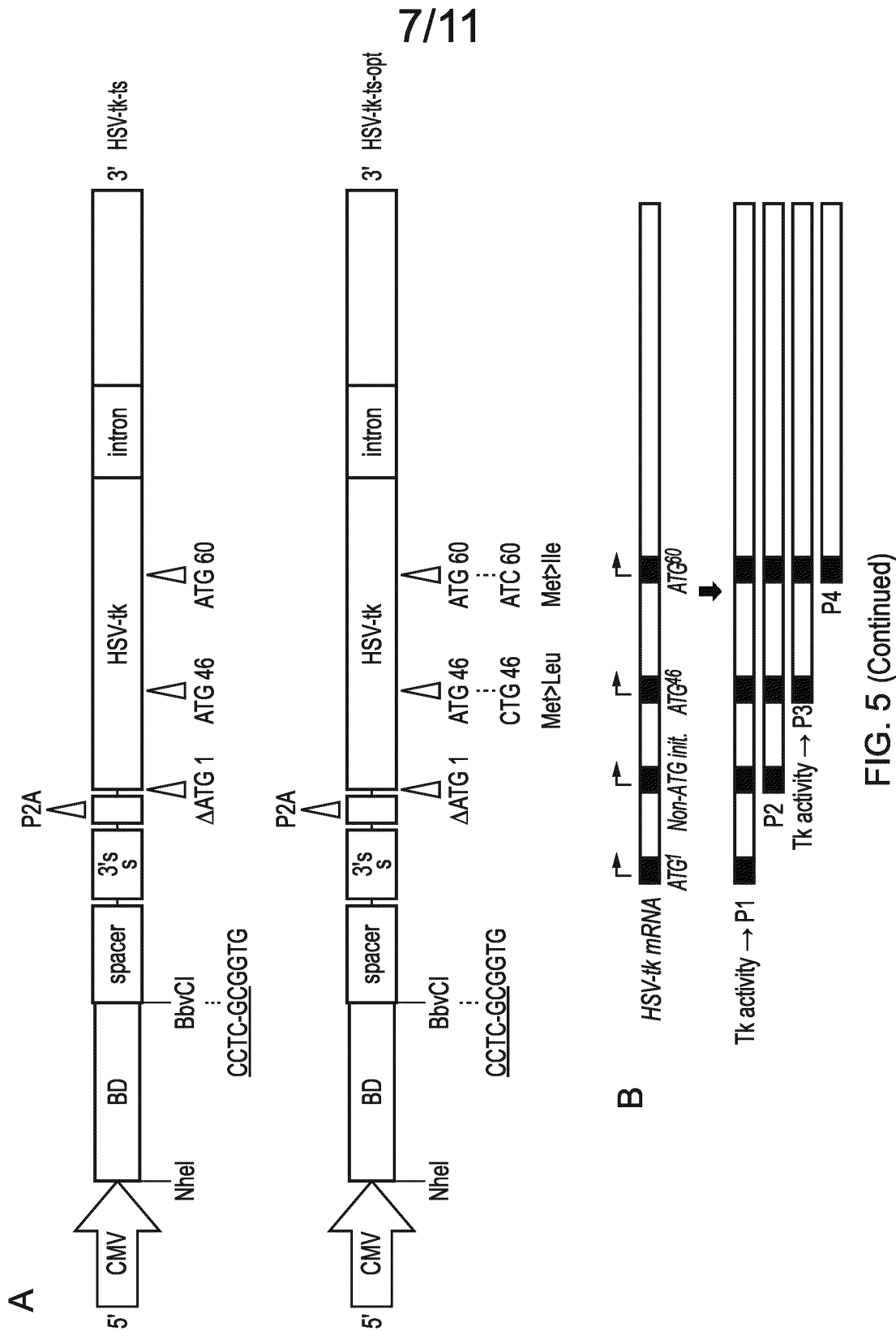
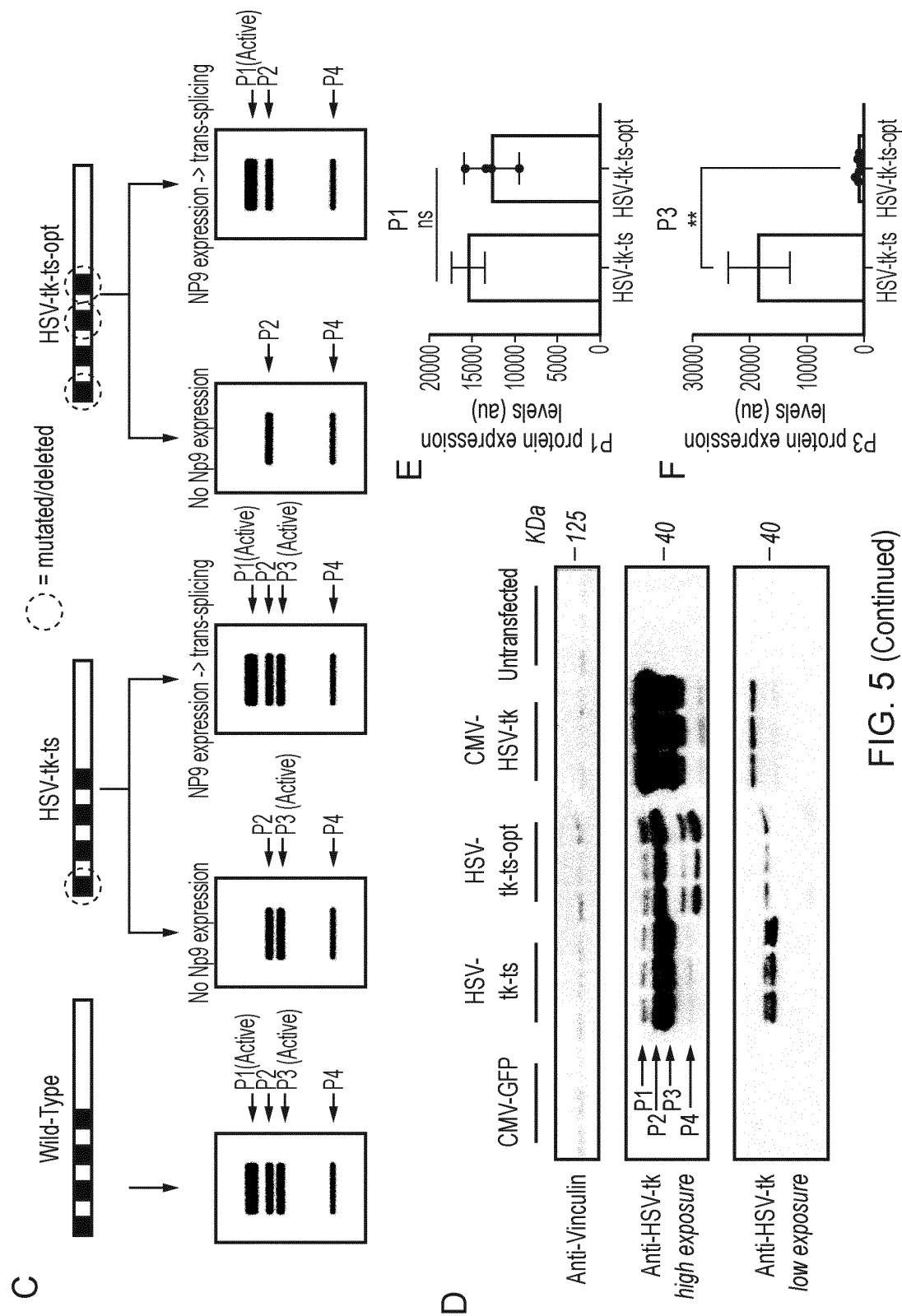


FIG. 5 (Continued)



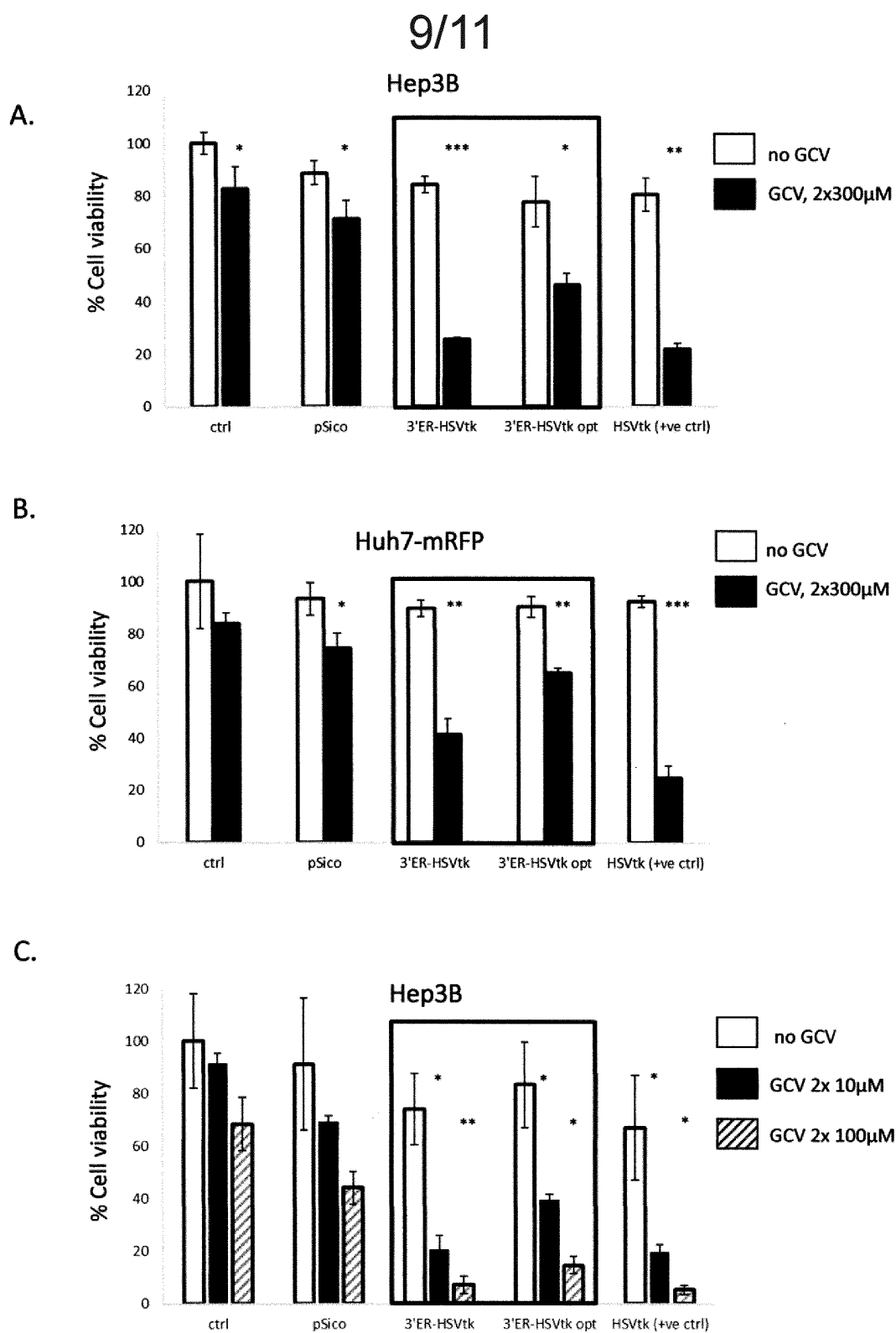


FIG. 6

SUBSTITUTE SHEET (RULE 26)

A HEK 293T

MOI 1

% Viability

Legend: -GCV (hatched), +GCV (diagonal)

Condition	-GCV (% Viability)	+GCV (% Viability)
LvCM-GFP	~100	~100
LvHSV-k-ts	~100	~100
LvCMV-HSV-k	~100	~100
LvHSV-k-ts-opt	~100	~100
Untreated	~100	~100

B HEK 293T

MOI 2

% Viability

Condition	-GCV (% Viability)	+GCV (% Viability)
LvCM-GFP	~100	~100
LvHSV-k-ts	~100	~100
LvCMV-HSV-k	~100	~100
LvHSV-k-ts-opt	~100	~100
Untreated	~100	~100

C Panc-1

% Viability

Condition	-GCV (% Viability)	+GCV (% Viability)
LvCM-GFP	~100	~100
LvHSV-k-ts	~100	~100
LvCMV-HSV-k	~100	~100
LvHSV-k-ts-opt	~100	~100
Untreated	~100	~100

D Panc-1

% Viability

Condition	-GCV (% Viability)	+GCV (% Viability)
LvCM-GFP	~100	~100
LvHSV-k-ts	~100	~100
LvCMV-HSV-k	~100	~100
LvHSV-k-ts-opt	~100	~100
Untreated	~100	~100

FIG. 7

