

# Supplementary Materials:

Table S1: Bovine alleles used for T –cells epitope prediction.

S.NO	MHC1	MHCII
01	BoLA-T2C	BoLA-DRB3*0101
02	BoLA-HD6	BoLA-DRB3*0401
03	BoLA-D18.4	BoLA-DRB3*0501
04	BoLA-T2a	BoLA-DRB3*0801
05	BoLA-T2b	BoLA-DRB3*1103
06	BoLA-JSP.1	BoLA-DRB3*1902

Table S2: Designed vaccine constructs with allergenicity, antigenicity and solubility analysis.

Vaccine construct	Adjuvant	Construct	Allergenicity	Antigenpro	Vaxijen	Solubility Protein-sol	Dock TLR2	Dock TLR4
LSDV-V1	Beta defensin adjuvant	EAAAKLALLFLVLSAGSGFT QGVRNHVTCRINRGFCVPIR CPGRTRQIGTCFGPRIKCCRS WEAAAKAKFVAAWTLKAA AGGGSEGVYLCSTITDTRCN PGPGPKKALIIKEVKRKYLA AYNVLDYDRSKGGGSHEYG AEALERAGGGGSYGLVKKK NNIWVDVNSGPGPKKNVS IRHLKVISLAAYAFMLVSTIG GGSEYGAEALERAGGGGS YTTQQYCNVSPFINDNGPGP GKKKTDLSSLKRRIQAAAYDK KGCIVEFHEYGAEALERAGA KFVAAWTLKAAAGGGS	Non allergen- Allertop	0.792602	0.5682	0.663	-884.2	-963.8
LSDV - V2	Beta defensin adjuvant	EAAAKLALLFLVLSAGSGFT QGVRNHVTCRINRGFCVPIR CPGRTRQIGTCFGPRIKCCRS WEAAAKAKFVAAWTLKAA AGGGSNSVIGTNYELLCINT KPGPGKKLIIKEVKRKYLSA AYNSTIALGKNGGGSEHYG AEALERAGGGGSLSNIKKSS KGDINACYGPGPKKVSIIIC VKRLYNAAYNVSCNYVSYG GGSEYGAEALERAGGGGS KGCIVEFGSQEKVCVTGPGP GKKDLSLLKRRIQKVAAYDF WIKFISIHEYGAEALERAGAK FVAAWTLKAAAGGGS	Non allergen- Allertop	0.732347	0.5099	0.636	-796.4	-1157.4

LSDV - V3	Beta defensin adjuvant	EAAAKLALLFLVLSAGSGFT QGVRNHVTCRINRGFCVPIR CPGRTRQIGTCFGPRIKCCRS WEAAAKAKFVAAWTLKAA AGGGSSITTDTRCNPKNLAL KGP <del>PG</del> PKKIALIIEVKRKYA AYTVNFLNSTIGGG <del>SH</del> EYGA EALERAGGGGSSCNYSYIIC VKRLYN <del>GP</del> <del>PG</del> <del>PK</del> KSIRHLKV ISLTYAAYNYVSYIICVGGGS HEYGAEALERAGGGGSKGCI VEFGSQEKVCVT <del>GP</del> <del>PG</del> <del>PK</del> KV FIKRQDVNTVLAA <del>Y</del> NTDDF WIKFHEYGAEALERAGAKFV AAWTLKAAAGGGGS	Non allergen- Allertop	0.779016	0.5364	0.625	-858.1	-1026.2
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Table S3: Refine models of vaccine construct LSDV-V2 predicted by GalaxyRefine server

Model	GDT-HA	RMSD	MolProbity	Clash score	Poor rotamers	Rama favored
Initial	1.0000	0.000	1.846	5.4	0.0	89.7
MODEL 1	0.9872	0.290	2.097	12.4	0.9	91.8
MODEL 2	0.9906	0.264	2.157	15.3	0.9	92.5
MODEL 3	0.9881	0.279	2.176	15.1	0.5	91.8
MODEL 4	0.9855	0.298	2.192	14.8	0.5	91.1
MODEL 5	0.9847	0.307	2.224	17.5	0.0	92.1

Table S4: DNA and RNA sequences of the peptide vaccine constructs.

Vaccine construct	Adjuvant	Construct	DNA Sequences	RNA Sequences
LSDV-V1	Beta defensin adjuvant	EAAAKLALLFLVLSAGSGFTQ GVRNHVTCRINRGFCVPIRCP GRTRQIGTCFGPRIKCCRSWE AAAKAKFVAAWTLKAAAGG GSEGVYLCSTITDTRCN <del>PG</del> <del>PG</del> <del>PK</del> KALIIKEVKRKYLAAYNV LDYDRSKGGG <del>SH</del> EYGAEALE RAGGGGSYGLVKKKNNIWV DVNS <del>GP</del> <del>PG</del> <del>PK</del> KNVSIRHLKVI SLAAYAIFMLVSTIGGG <del>SH</del> EY GAEALERAGGGGSYTTQQYC NVSPFINDN <del>GP</del> <del>PG</del> <del>PK</del> KTDLS LLKRRIQAA <del>Y</del> DKKGCIVEFHE	GAAGCTGCTGCTAAACT GGCTCTGCTGTTCTGGT TCTGTCTGCTGGTTCTGG TTTCACCCAGGGTGTTT GTAACCACGTTACCTGC CGTATCAACCGTGTTT CTGCGTTCGATCCGTT GCCCCGGGTCGTACCCGT CAGATCGGTACCTGCTT CGGTCCGCGTATCAAAT GCTGCCGTTCTTGGGAA GCTGCTGCTAAAGCTAA ATTCGTTGCTGCTTGAC	GAAGCUGCUGCUAAACU GGCUCUGCUGUCCUGG UUCUGUCUGCUGGUUCU GGUUUCACCCAGGGUGU UCGUAACCACGUUACCU GCCGUAUCAACCGUGGU UUCUGCGUCCGAUCCG UUGCCCCGGGUCGUACCC GUCAGAUCCGUACCUGC UUCGGUCCGCGUAUCAA AUGCUGCCGUUCUUGGG AAGCUGCUGCUAAAGCU AAAUUCGUUGCUGCUUG

		YGAEALERAGAKFVAAWTLK AAAGGGS	CCTGAAAGCTGCTGCTG GTGGTGGTTCTGAAGGT GTTTACCTGTGCTCTATC ACCACCGACACCCGTTG CAACCCGGGTCCGGGTC CGGGTAAAAAAGCTCTG ATCATCAAAGAAGTTAA ACGTAAATACCTGGCTG CTTACAACGTTCTGGAC TACGACCGTTCTAAAGG TGGTGGTTCTCACGAAT ACGGTGCTGAAGCTCTG GAACGTGCTGGTGGTGG TGGTTCTTACGGTCTGGT TAAAAAACAAC ATCTGGGTGACGTTAA CTCTGGTCCGGGTCCGG GTAAAAAACGTTTCT ATCCGTCACCTGAAAGT TATCTCTCTGGCTGCTTA CGCTATCTTCATGCTGGT TTCTACCATCGGTGGTG GTTCTCACGAATACGGT GCTGAAGCTCTGGAACG TGCTGGTGGTGGTGGTT CTTACACCACCCAGCAG TACTGCAACGTTTCTCC GTTCATCAACGACAACG GTCCGGGTCCGGGTAAA AAAAAAACCGACCTGTC TCTGCTGAAACGTCGTA TCCAGGCTGCTTACGAC AAAAAAGGTTGCATCGT TGAATTCCACGAATACG GTGCTGAAGCTCTGGAA CGTGCTGGTGCTAAATT CGTTGCTGCTTGGACCC TGAAAGCTGCTGCTGGT GGTGGTTCT	GACCCUGAAAGCUGCUG CUGGUGGUGGUUCUGA AGGUGUUUACCUGUGCU CUAUCACCACCGACACC CGUUGCAACCCGGGUCC GGGUCCGGGUAAAAAA GCUCUGAUCAUCAAAGA AGUUAACGUAAAUAC CUGGCUGCUUACAACGU UCUGGACUACGACCGUU CUAAGGUGGUGGUUC UCACGAUACGGUGCUG AAGCUCUGGAACGUGCU GGUGGUGGUGGUUCUU ACGGUCUGGUUAAAAA AAAAAACAACUCUGG GUUGACGUUACUCUGG UCCGGGUCCGGGUAAAA AAAACGUUUCUACCGU CACCUGAAAGUUUUCUC UCUGGCUGCUUACGCUA UCUUCAUGCUGGUUCU ACCAUCGGUGGUGGUUC UCACGAUACGGUGCUG AAGCUCUGGAACGUGCU GGUGGUGGUGGUUCUU ACACCACCCAGCAGUAC UGCAACGUUUCUCCGUU CAUCAACGACAACGGUC CGGGUCCGGGUAAAAAA AAAACCGACCUGUCUCU GCUGAAACGUCGUAUCC AGGCUGCUUACGACAAA AAAGGUUGCAUCGUUG AAUUCCACGAUACGGU GCUGAAGCUCUGGAACG UGCUGGUGCUAAAUUCG UUGCUGCUUGGACCCUG AAAGCUGCUGCUGGUGG UGGUUCU
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LSDV - V2	Beta defensin adjuvan t	EAAAKLALLFLVLSAGSGFTQ GVRNHVTCRINRGFCVPIRCP GRTRQIGTCFGPRIKCCRSWE AAAKAKFVAAWTLKAAAGG GSNSVIGTNYELLCINTKPGP PGKKLIIKEVKRKYLSAAYNST IALGKNGGGSHEYGAALER AGGGGSLSNIKKSSKGDINAC YGPGPKKVSYIICVKRLYN AYNVSCNYVSYGGGSHEYGA EALERAGGGGSKGCIVEFGSQ EKVCVTGPGPKKDLSLLKRR IQKVAAAYDFWIKFISIHEYGAE ALERAGAKFVAAWTLKAAA GGGS	GAAGCTGCTGCTAAACT GGCTCTGCTGTTCTCTGGT TCTGTCTGCTGGTTCTGG TTTCACCCAGGGTGTTT GTAACCACGTTACCTGC CGTATCAACCGTGGTTT CTGCGTTCCGATCCGTT GCCCCGGGTCGTACCCGT CAGATCGGTACCTGCTT CGGTCCGCGTATCAAAT GCTGCCGTTCTTGGGAA GCTGCTGCTAAAGCTAA ATTGCTTGCTGCTTGGAC CCTGAAAGCTGCTGCTG GTGGTGGTTCTAACTCT GTTATCGGTACCAACTA CGAACTGCTGTGCATCA ACACCAAAGGTCCGGGT CCGGGTAAAAAACTGAT CATCAAAGAAGTTAAAC GTAAATACCTGTCTGCT GCTTACAACCTTACCAT CGCTCTGGGTAAAAACG GTGGTGGTTCTCACGAA TACGGTGCTGAAGCTCT GGAACGTGCTGGTGGTG GTGGTTCTCTGTCTAACA TCAAAAAATCTTCTAAA GGTGACATCAACGCTTG CTACGGTCCGGGTCCGG GTAAAAAAGTTTCTTAC ATCATCTGCGTTAAACG TCTGTACAACGCTGCTT ACAACGTTTCTTGCAAC TACGTTTCTTACGGTGGT GGTTCTCACGAATACGG TGCTGAAGCTCTGGAAC GTGCTGGTGGTGGTGGT TCTAAAGTTGCATCGT TGAATTCGGTTCTCAGG AAAAAGTTTGCGTTACC GGTCCGGGTCCGGGTAA AAAAGACCTGTCTCTGC TGAAACGTCGTATCCAG AAAGTTGCTGCTTACGA CTTCTGGATCAAATTCA TCTCTATCCACGAATAC GGTGCTGAAGCTCTGGA ACGTGCTGGTGCTAAAT	GAAGCUGCUGCUAAACU GGCUCUGCUGUCCUGG UUCUGUCUGCUGGUUCU GGUUUCACCCAGGGUGU UCGUAACCACGUUACCU GCCGUAUCAACCGUGGU UUCUGCGUCCGAUCCG UUGCCCCGGGUCGUACCC GUCAGAUCCGUACCUGC UUCGGUCCGCGUAUCAA AUGCUGCCGUUCUUGGG AAGCUGCUGCUAAAGCU AAAUUCGUUGCUGCUUG GACCCUGAAAGCUGCUG CUGGUGGUGGUUCUAAAC UCUGUUAUCGGUACCAA CUACGAACUGCUGUGCA UCAACACCAAAGGUCCG GGUCCGGUAAAAAACU GAUCAUCAAGAAGUU AAACGUAAAUACCUGUC UGCUGCUUACAACUCUA CCAUCGCUCUGGGUAAA AACGGUGGUGGUUCUCA CGAAUACGGUGCUGAAG CUCUGGAACGUGCUGGU GGUGGUGGUUCUCUGUC UAACAUCAAAAAAUCU UCUAAAAGGUGACAUCA ACGCUUGCUCACGGUCCG GGUCCGGUAAAAAAG UUUCUUACAUCUACUGC GUUAAAACGUCUGUACA ACGCUGCUUACAACGUU UCUUGCAACUACGUUUC UUACGGUGGUGGUUCUC ACGAAUACGGUGCUGAA GCUCUGGAACGUGCUGG UGGUGGUGGUUCUAAA GGUUGCAUCGUUGAAU UCGGUUCUCAGGAAAAA GUUUGCGUUAACGGUCC GGGUCCGGGUAAAAAA GACCUGUCUCUGCUGAA ACGUCGUAUCCAGAAAG UUGCUGCUUACGACUUC UGGAUCAAAUUCUUCUC UAUCCACGAAUACGGUG CUGAAGCUCUGGAACGU
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			TCGTTGCTGCTTGGACC CTGAAAGCTGCTGCTGG TGGTGGTTCT	GCUGGUGCUAAAUUCGU UGCUGCUUGGACCCUGA AAGCUGCUGCUGGUGGU GGUUCU
LSDV - V3	Beta defensin adjuvan t	<a href="#">EAAAK</a> LALLFLVLSAGSGFTQ GVRNHVTCRINRGFCVPIRCP GRTRQIGTCFGPRIKCCRSWE <a href="#">AAAKAKFVA</a> AWTLKAAAGG GSSITTDTRCNPKNLALKGPG PGKKIALIIEVKRKYAAYTV NFLNSTIGGGSHEYGAELER AGGGGSSCNYVSYIICVKRLY NPGPGKKSIRHLKVISLTYA AYNYVSYIICVGGGSHEYGAE ALERAGGGGSKGCIVEFGSQE KVCVTGPGPGKKVFIKRQDV NTVLAAYNTDDFWIKFHEYG AEALERAGAKFVAAWTLKA AAGGGS	GAAGCTGCTGCTAAACT GGCTCTGCTGTTCTTGGT TCTGTCTGCTGGTTCTGG TTTACCCAGGGTGTTT GTAACCACGTTACCTGC CGTATCAACCGTGTTT CTGCGTTCGATCCGT GCCCCGGTCTACCCGT CAGATCGGTACCTGCTT CGGTCCGCGTATCAAAT GCTGCCGTTCTTGGGAA GCTGCTGCTAAAGCTAA ATTGCTTGCTGCTTGGAC CCTGAAAGCTGCTGCTG GTGGTGGTTCTTCTATCA CCACCGACACCCGTTGC AACCCGAAAAACCTGG CTCTGAAAGGTCCGGGT CCGGGTAAAAAAATCG CTCTGATCATCAAAGAA GTAAACGTAAATACGC TGCTTACACCGTTAACTT CCTGAACTCTACCATCG GTGGTGGTTCTCACGAA TACGGTGCTGAAGCTCT GGAACGTGCTGGTGGTG GTGGTTCTTCTTGCAACT ACGTTTCTTACATCATCT GCGTTAAACGTCTGTAC AACGGTCCGGGTCCGGG TAAAAAATCTATCCGTC ACCTGAAAGTTATCTCT CTGACCTACGCTGCTTA CAACTACGTTTCTTACAT CATCTGCGTTGGTGGTG GTTCTCACGAATACGGT GCTGAAAGCTCTGGAACG TGCTGGTGGTGGTGGTT	GAAGCUGCUGCUAAACU GGCUCUGCUGUCCUGG UUCUGUCUGCUGGUUCU GGUUUCACCCAGGGUGU UCGUAACCACGUUACCU GCCGUAUCAACCGUGGU UUCUGCGUCCGAUCCG UUGCCCGGGUCGUACCC GUCAGAUCCGUACCUGC UUCGGUCCGCGUAUCAA AUGCUGCCGUUCUUGGG AAGCUGCUGCUAAAGCU AAAUUCGUUGCUGCUUG GACCCUGAAAGCUGCUG CUGGUGGUGGUUCUUCU AUCACCACCGACACCCG UUGCAACCCGAAAAACC UGGCUCUGAAAGGUCCG GGUCCGGGUAAAAAAA UCGCUCUGAUCAUCAA GAAGUUAACGUAAAU ACGCUGCUUACACCGUU AACUCCUGAACUCUAC CAUCGGUGGUGGUUCUC ACGAAUACGGUGCUGAA GCUCUGGAACGUGCUGG UGGUGGUGGUUCUUCU UGCAACUACGUUUCUUA CAUCAUCUGCGUAAAC GUCUGUACAACGGUCCG GGUCCGGGUAAAAAUC UAUCCGUCACCUGAAAG UUAUCUCUCUGACCUAC GCUGCUUACAACUACGU UUCUUAUCAUCUGCG UUGGUGGUGGUUCUCAC GAUACGGUGCUGAAGC UCUGGAACGUGCUGGUG

			CTAAAGGTTGCATCGTT GAATTCGGTTCTCAGGA AAAAGTTTTCGTTACCG GTCCGGGTCCGGGTAAA AAAGTTTTTCATCAAACG TCAGGACGTTAACACCG TTCTGGCTGCTTACAAC ACCGACGACTTCTGGAT CAAATTCCACGAATACG GTGCTGAAGCTCTGGAA CGTGCTGGTGCTAAATT CGTTGCTGCTTGGACCC TGAAAGCTGCTGCTGGT GGTGGTTCT	GUGGUGGUUCUAAAGG UUGCAUCGUUGAAUUCG GUUCUCAGGAAAAAGU UUGCGUUACCGGUCCGG GUCCGGGUAAAAAGU UUUCAUCAAACGUCAGG ACGUUAAACACCGUUCUG GCUGCUUACAACACCGA CGACUUCUGGAUCAAU UCCACGAUACGGUGCU GAAGCUCUGGAACGUGC UGGUGCUAAAUUCGUU GCUGCUUGGACCCUGAA AGCUGCUGCUGGUGGUG GUUCU
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Table S5: Different residues of vaccine construct and TLR4 involved in hydrogen bonding.

NO.	NAME	NO.	CHAIN	NAME	NO.	CHAIN
1.	GLN 39	A <-->	GLY 16	B		
2.	ASP 84	A <-->	ARG 46	B		
3.	ASP 84	A <-->	ARG 46	B		
4.	SER 86	A <-->	ARG 46	B		
5.	ARG 87	A <-->	ASN 190	B		
6.	LYS 130	A <-->	GLN 47	B		
7.	GLU 135	A <-->	TRP 62	B		
8.	GLU 135	A <-->	ARG 44	B		
9.	GLU 135	A <-->	ARG 44	B		
10.	GLU 154	A <-->	ARG 40	B		
11.	ASP 181	A <-->	ARG 40	B		
12.	ASP 181	A <-->	ARG 40	B		
13.	ASP 181	A <-->	GLY 43	B		
14.	ARG 234	A <-->	CYS 36	B		
15.	ARG 257	A <-->	PRO 38	B		
16.	ARG 257	A <-->	ILE 39	B		
17.	LYS 264	A <-->	ARG 33	B		
18.	LYS 264	A <-->	GLY 34	B		
19.	ARG 382	A <-->	GLY 133	B		
20.	ARG 382	A <-->	TYR 138	B		

21. ASP 617 A <--> ARG 115 B

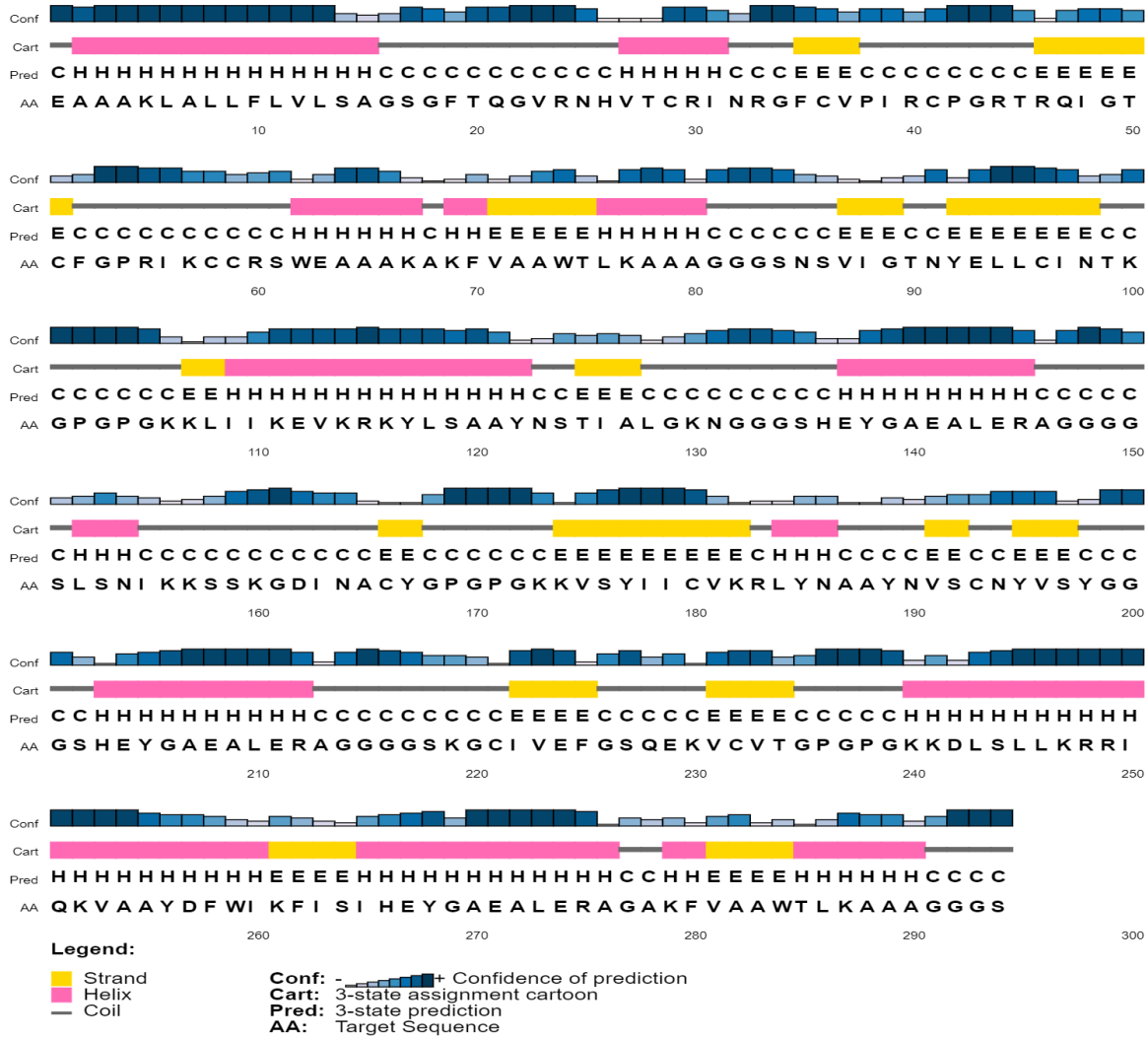


Figure S1a: Secondary structure prediction of LSDV-V1 by PSIPRED server.

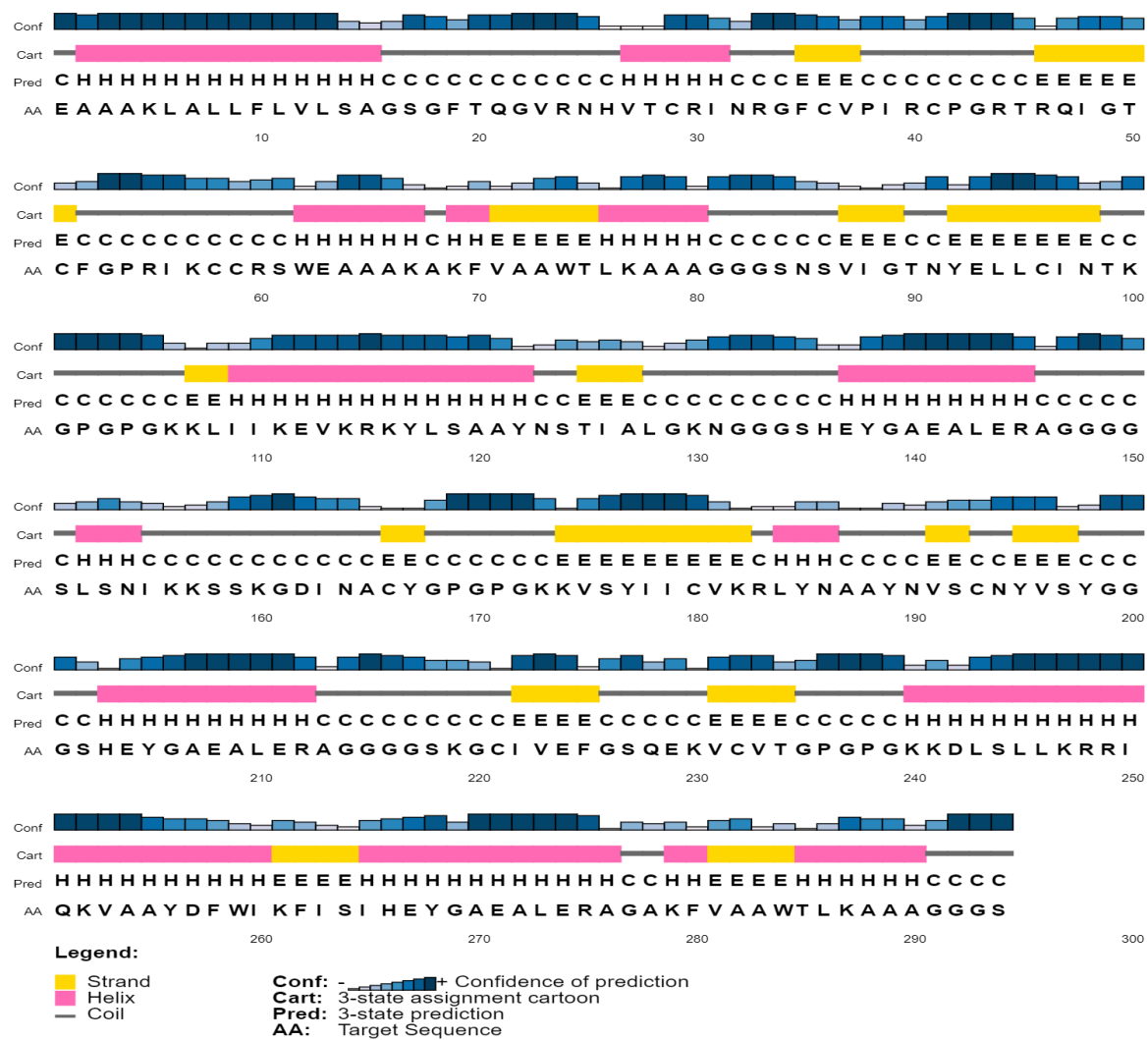


Figure S1b: Secondary structure prediction of LSDV-V2 by PSIPRED server.

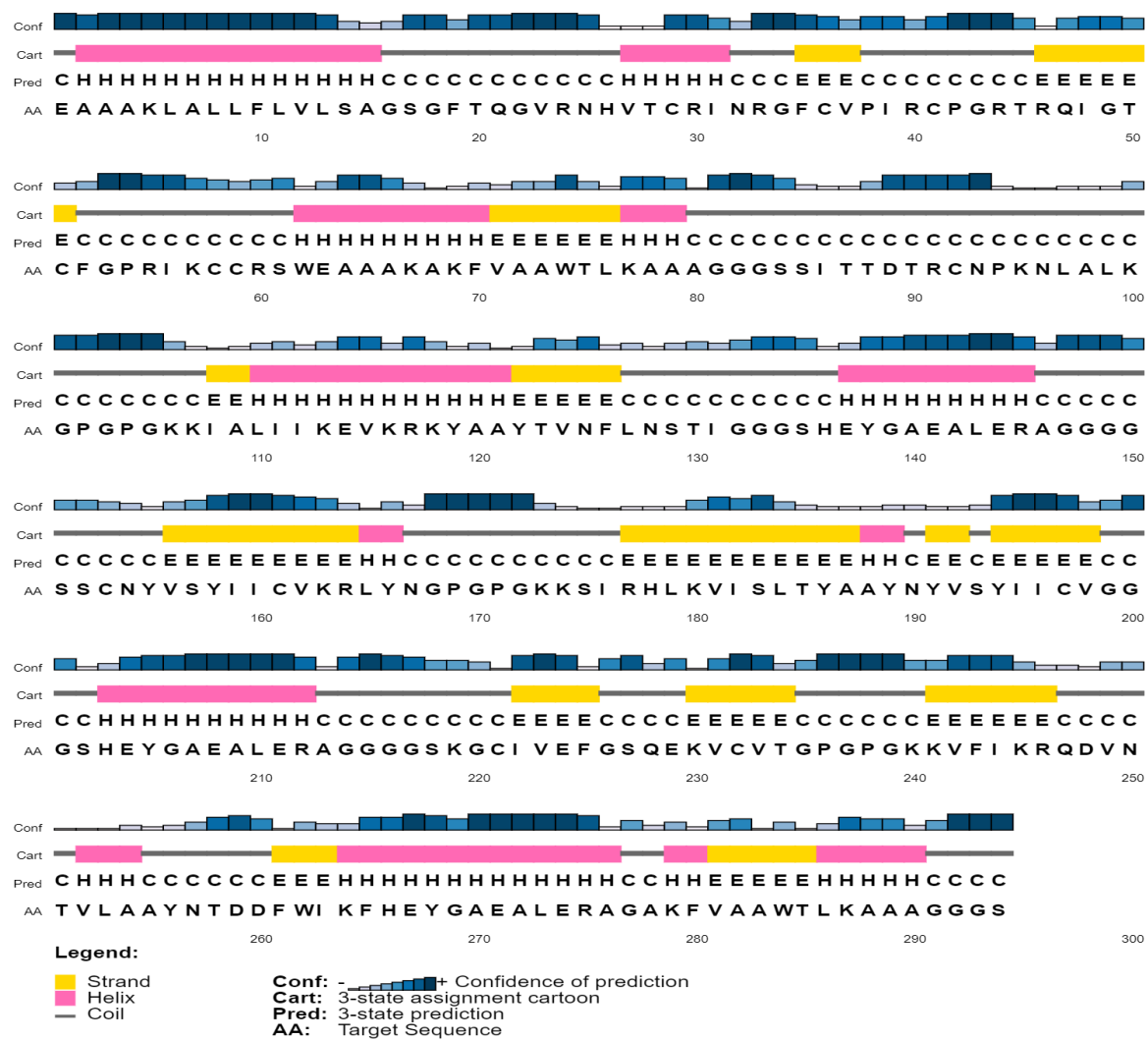


Figure S1c: Secondary structure prediction of LSDV-V3 by PSIPRED server.

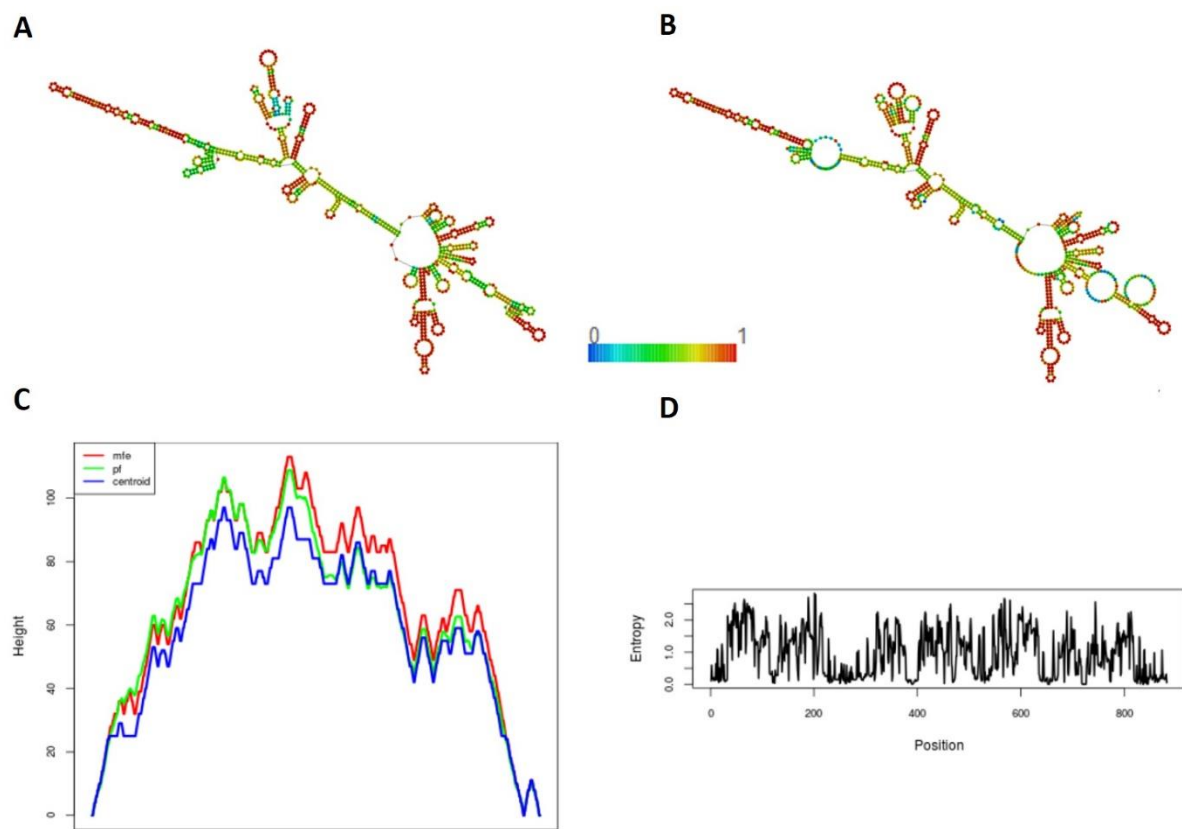


Figure S2a: Secondary Structure prediction of the prioritized LSDV-V1 mRNA construct. (A) Model presentation of minimum free energy of the LSDV-V1 mRNA structure (B) The proposed model of the minimum free energy (MFE) of secondary centroid LSDV-V1 mRNA structure (C) The mountain plot representation of the MFE structure, the thermodynamic ensemble of RNA structures, and the centroid structure. (D) The positional entropy plot for each position.

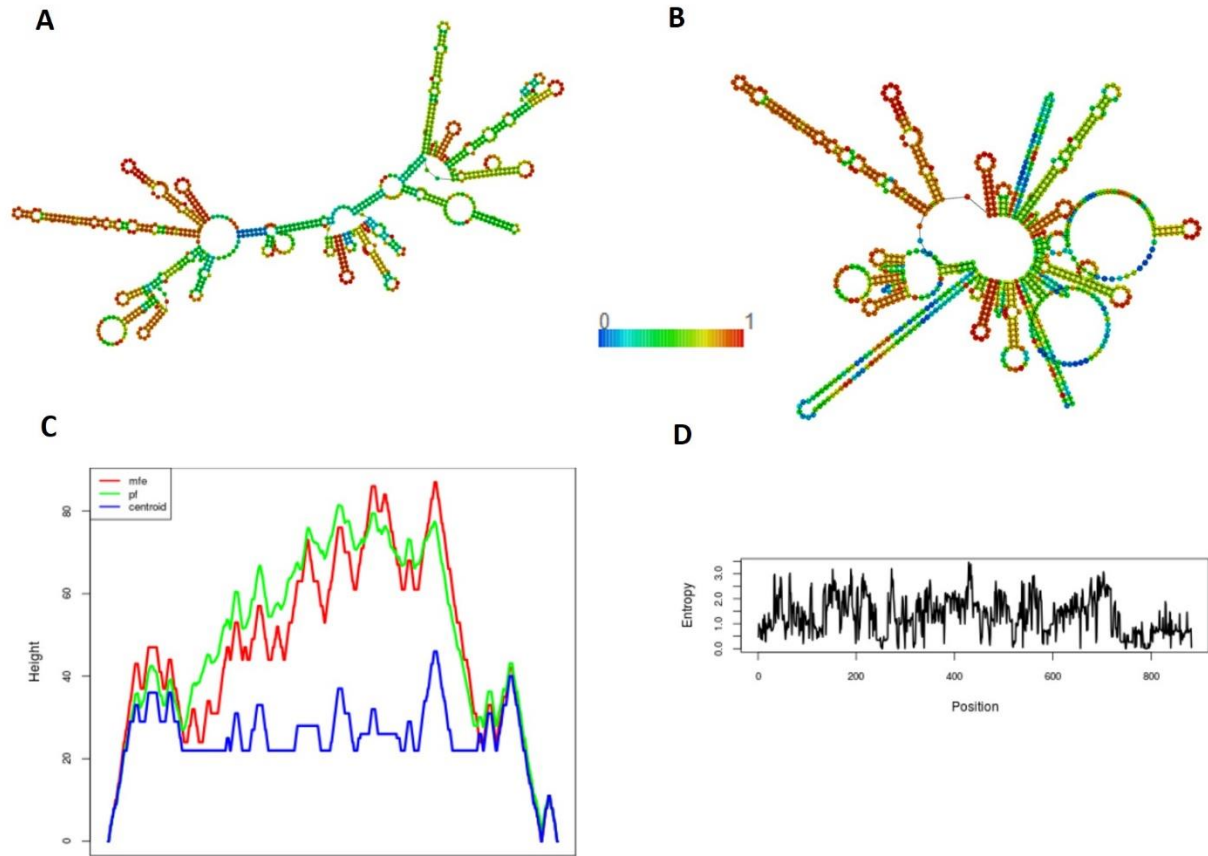


Figure S2b: Secondary Structure prediction of the prioritized LSDV-V3 mRNA construct. (A) Model presentation of minimum free energy of the LSDV-V3 mRNA structure (B) The proposed model of the minimum free energy of secondary centroid LSDV-V3 mRNA structure (C) The mountain plot representation of the MFE structure, the thermodynamic ensemble of mRNA structure, and the centroid structure. (D) The positional entropy plot for each position.

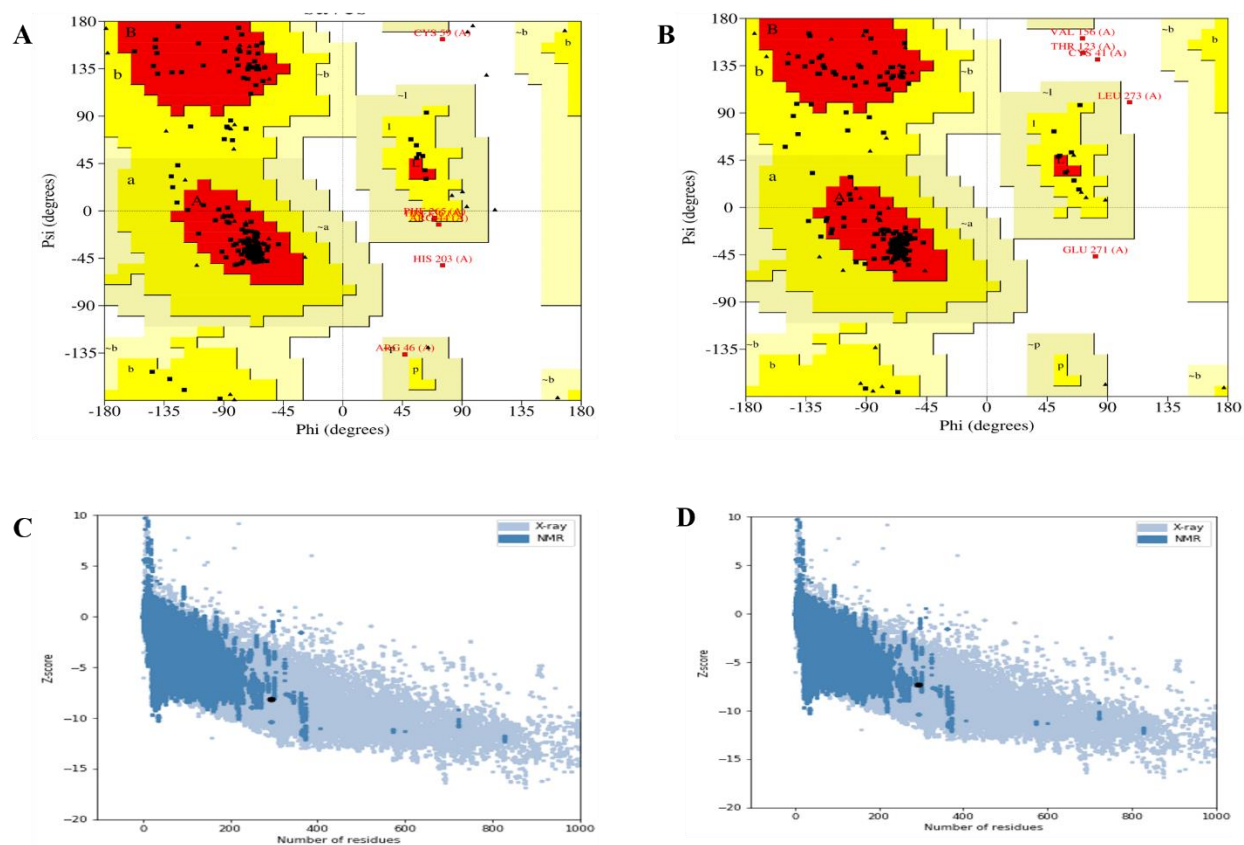


Figure S3: Three-dimensional structural validation of V1 and V3. (A) (B) Ramachandran plots showing 89.1% residues of V1 and 89.96% residues of V3 in the most favored regions of plots. (C) (D) structural validation by proSA web showing Z scores of -8.11 and -7.28 of V1 and V3 respectively.

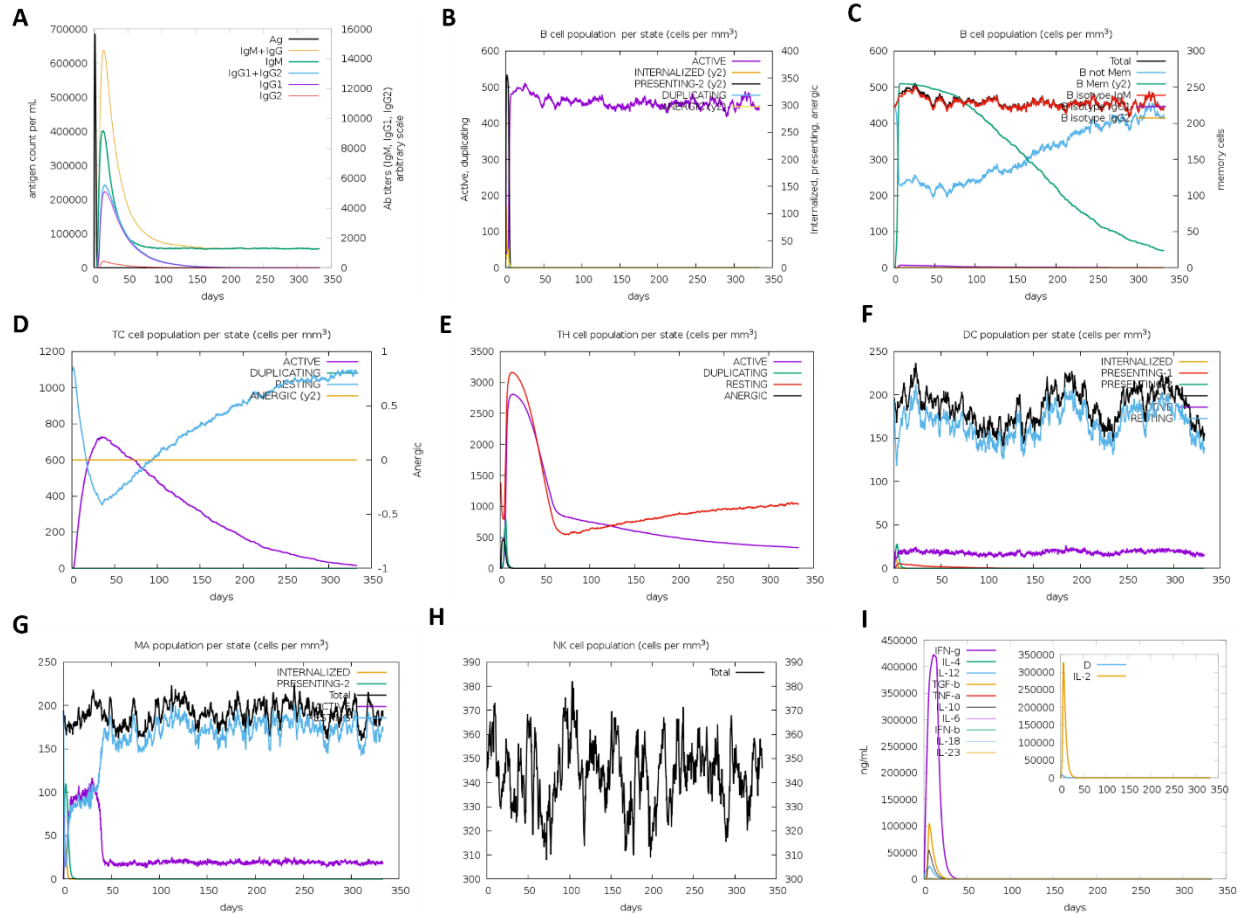


Figure S4: *In silico* immune simulation of LSDV-V2 chimeric peptide predicted by C-ImmSim Server. (A, B) Elevated level of immunoglobulin antibodies as well as B – cell populations while a decrease in antigen levels upon vaccine injections. (C) Significant increase in B- cell populations after repeated exposure to antigen. (D, E) The increase in the population of T -cytotoxic and T –helper cells upon repeated exposure. (F, G, H) The population increase of dendritic cells, macrophages, and natural killer cells during the immunization period. (I) increased concentration of cytokine and interleukin levels after repeated antigen exposure. Inset plot shows danger signal together with leukocyte growth factor IL-2.

## Section S1

### mRNA Vaccine Construct

5' m7GCap– 5' UTR–Kozak sequence–Signal peptide (tPA)–EAAAK-Adjuvant-peptide vaccine sequence-MITD sequence- Stop codon- 3' UTR-Poly (A) tail.

#### 5'm7G Cap

#### 5'UTR

NCA-7d (Derived from NCA-7)

GGCAAAAUAUCAAUCAAUCAUCAACAACAUAACAUAUCAAUCAAACACAUCAUCAAGACACCA  
CCGCCGCCGCAUGGCG

#### Kozak Sequence

GCCGCC(A/G)(C/A)CAUGGCG

GCCGCCGCCAUGGCG

#### Signal Peptide

>sp|Q28198|TPA\_BOVIN                      Tissue-type                      plasminogen                      activator                      OS=Bos                      taurus  
ATGATGAGCGCCATGAAGACCGAGTTCCTGTGCGTGCTGCTGCTGTCGCGCGCCGTGTTACACGACCCAGC  
CAGGAGACCTACAGGAGGCTGAGGAGGGGCGCCAGGAGCTACAAGGTGACCTGCAGGGACGGCAAGACCC  
AGATGACCTACAGGCAGCACGACAGCTGGCTGAGGCCCCCTGCTGAGGGGCAACCAGGTGGAGCACTGCTGG  
TGCGACGGCGGCAGGGCCAGTGCCACAGCGTGCCCGTGAGGAGCTGCAGCGAGCCCTGGTGCTTCAACGG  
CGGCACCTGCAGGCAGGCCCTGTACAGCAGCGACTTCGTGTGCCAGTGCCCCGAGGGCTTCATGGGCAAGC  
TGTGCGAGATCGACGCCACCGCCACCTGCTACAAGGACCAGGGCGTGCCCTACAGGGGCACCTGGAGCACC  
GCCGAGAGCGGCGCCGAGTGCGCCAAGTGAACAGCAGCGGCCTGGCCATGAAGCCCTACAGCGGCAGGA  
GGCCCAACGCCATCAGGCTGGGCCTGGGCAACCACAAGTACTGCAGGAACCCCGACAGGACAGCAAGCC  
CTGGTGCTACGTGTTCAAGGCCGGCAAGTACATCAGCGAGTTCTGCAGCACCCCGCCTGCGCCAAGGTGGC  
CGAGGAGGACGGCGACTGCTACACCGGCAACGGCCTGGCCTACAGGGGCACCAGGAGCCACACCAAGAGC  
GGCGCCAGCTGCCTGCCCTGGAACAGCGTGTTCTTGACCAGCAAGATCTACACCGCCTGGAAGAGCAACGC  
CCCCGCCCTGGGCCTGGGCAAGCACAACCACTGCAGGAACCCCGACGGCGACGCCAGCCCTGGTGCCACG  
TGTGGAAGGACAGGCAGCTGACCTGGGAGTACTGCGACGTGCCCCAGTGCGTGACCTGCGGCCTGAGGCAG  
TACAAGAGGCCCCAGTTCAGGATCAAGGGCGGCCTGTTGCGCCGACATCACCAGCCACCCCTGGCAGGCCGC  
CATCTTCGTGAAGAACAGGAGGAGCCCCGGCGAGAGGTTCTGTGCGGCGGCATCCTGATCAGCAGCTGCT  
GGGTGCTGAGCGCCGCCACTGCTTCCAGGAGAGGTACCCCCCCCACCACCTGAAGGTGTTCTGGGCAGG  
ACCTACAGGCTGGTGCCCGGCGAGGAGGAGCAGACCTTCGAGGTGGAGAAGTACATCATCCACAAGGAGTT  
CGACGACGACACCTACGACAACGACATCGCCCTGCTGCACCTGAAGAGCGACAGCCTGACCTGCGCCAGGG  
AGAGCGCCAGCGTGAGGACCATCTGCCTGCCCCAGCGCAGCCTGCAGCTGCCCCGACTGGACCGAGTGCGAG  
CTGAGCGGCTACGGCAAGCACGAGAGCAGCAGCCCCCTTCTTCAGCGAGAGGCTGAAGGAGGCCACGTGA  
GGCTGTACCCAGCAGCAGGTGCACCAGCCAGCACCTGTTCAACAGGACCGTGACCAACAACATGCTGTGC  
GCCGGCGACACCAGGAGCGGCGGGCGACCACCAACCTGCACGACGCCTGCCAGGGCGACAGCGGCGGCC  
CCCTGGTGTCATGAAGGACAACCATGACCCTGGTGGGCATCATCAGCTGGGGCCTGGGCTGCGGCAGG  
AAGGACGTGCCCGCGTGTACACCAAGGTGACCAACTACCTGGACTGGATCAGGGACAACACCAGGCCC

