

ANEXOS

ANEXO I – ALINEAMIENTO DE SECUENCIAS DE LA FAMILIA AIF

hAIF	-----MFRCGGLAAGALKQKLVPLVRTVCVRSRQRNRLPGNLFQRWHVPLELQMTRO	
hAMID	-----	
hAIFL	MGGCFSKPKPVELKIEVVLPEKERGKEELSASGKGSPRAYQNGTARHFHTEERLSTPHP	
hAIF	MASSGASGGKIDNSVLVLIVGLSTVGAGAYAYKTMKEDEKRYNER-----	
hAMID	-----	
hAIFL	YPSQDCVEAAVCHVKDLENGQMRREVELGWGKVLVVDNGEFHALGHKCPHYGAPLVKGV	
hAIF	-----ISGLGLTPEQKQKKAALSASEGEEVPQDKAPSHVPF----LLTGGGTAA	
hAMID	-----MGSQVSVESGALHV-----VIVGGGFGG	
hAIFL	LSRGRVRCPWGACFNISTGDLEDFPGLDSLHKFQVKIEKVKVVRASKQALQLQRRTKV	
	:* :. :* : :	
hAIF	FAAARSIRARDPGARVLIVSEDPPELPMRPPISKELWFSDDPNVTKTLRFKQWNGKERSI	
hAMID	IAAASQLQALN-----VPFMLVDMKDSFHHN-----VAALRASVETGFAKKT	
hAIFL	MAKCISPSAGYSSSTNVLIVGAGAAGLCAETLRQEGFSDRIVLCTLDRHLPYDRPKLSK	
	:* . . * : . . . *	
hAIF	YFPPSFYVSAQDLPHIENGAVVLTGKKVVQLDVRDNMVKLNDGSQITYEKCLIAITGGT	
hAMID	FIS---YSVTFKDN-----FRQGLVVGIDLNQMVLLQGGEALPFSHLILATGST	
hAIFL	SLDTQPEQLALRPKEFFRAYGIEVLTEAQVTVDVRTKKVVKDGFKLEYSKLLAPGSS	
	:. : : : ** : : : * : : * : : : : *	
hAIF	PRLSAIDRAGAEVKSRTTLFRKIGDFRSLEKISREVKSITIIIGGGFLGSELACALGRKA	
hAMID	G-----PFPGKFNEVSSQAAIQAYEDMVRQVQRSRFIVVVGGSAGVEMAAEIKTEY	
hAIFL	PK----TLSCKGKEVENVFTIRTPEDANRVVRLARG-RNVVVVGAGFLGMEVAAYLTEKA	
	:. . : : : : : * * * * . :	
hAIF	RALGTEVIQLFPEKGNMGKILPEYLSNWTMEKVRREGVKVMPNAIVQSVGV-----SGK	
hAMID	PEK--EVTLIHSQVALADKELLPSVRQEVKEILLRKGVLQLLSERVSNLLELPLNEYREY	
hAIFL	HSVS----VVELEETPFRRFLGERVGRALMKMFENNRVKFYMQTEVSELRGQE----GKL	
	: : : * : . : . : * : . * . :	
hAIF	LLIKLKDGKRVETDHIVAAGLEPNVELAKTGGLEIDSDFGGFRVNAELQAR--SNIWVA	
hAMID	IKVQTDKGTEVATNLVILCTGIKINSSAYRKAFESRLASSGALRVNEHLQVEGHSNYYAI	
hAIFL	KEVVLKSSKVVVRADVVCVVGIGAVPATGFLRQSGIGLDS-RGFIPVNKMMQTN-VPGVFAA	
	: . . . * : : : * : . : : * : * : * . . . :	
hAIF	GDAACFYDIKLGRRRVEHHDHAVVSGRLAGENMTGAAPYWHOSMFHSDLGPDVGYEAIG	
hAMID	GDCADVRTPKMAYLAGLHANTAVAN-----TVNSVKQR	
hAIFL	GDAVTFPLAWRNNRKVNIPHWMHAHQG-----RVAAQNML	
	** . . . : . :	
hAIF	LVDSSLPTVGVFAKATAQDNPKSATEQSGTGIRSESESEASEITIPPSTPAVPQAPVQ	
hAMID	PLQAYKPGALTFLLSMGRND--GVGQISGFYVGRMLVRLTKSRDLFVSTSWKTMRSQSP-	
hAIFL	AQEAEASTVPYLTAMFGKSLRYAGYGEFDDVIIQGDLEELKFVAFYTKGDEVIASVM	
	: : . . : : . . . *	
hAIF	GEDYGKGVIFYLRDKVVVGIVLWNIFNRMPIARKIIKDGEQHEDLNEVAKLFNIHED	
hAMID	-----	
hAIFL	NYDP-----IVSKVAEVLASGRAIRKREVELFVLHSTGDMSWLTGKGS-	

—	MLS
—	uniónFAD
—	uniónNADH
—	Apoptótico

ANEXO II – ANÁLISIS BLAST DE LA SECUENCIA DE AIFL HUMANO

BLAST® » blastp suite » RID-MJ8UCDDW013

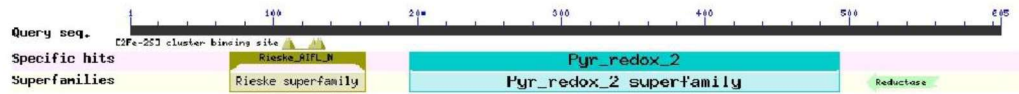
BLAST Results

Job title: Protein Sequence (605 letters)

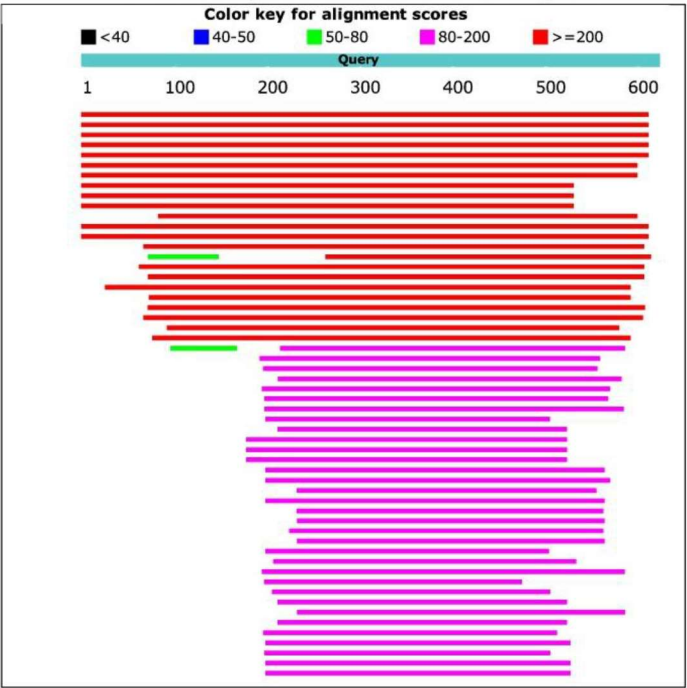
RID	MJ8UCDDW013 (Expires on 06-21 21:29 pm)	Database Name	SMARTBLAST/landmark
Query ID	Icl Query_314072	Description	Landmark database for SmartBLAST
Description	None	Program	BLASTP 2.6.1+
Molecule type	amino acid		
Query Length	605		

Graphic Summary

Putative conserved domains have been detected, click on the image below for detailed results.



Distribution of the top 100 Blast Hits on 100 subject sequences



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
apoptosis-inducing factor 3 isoform 1 [Homo sapiens]	1247	1247	100%	0.0	100%	NP_653305.1
apoptosis-inducing factor 3 isoform 2 [Homo sapiens]	1226	1226	100%	0.0	99%	NP_001018070.1
apoptosis-inducing factor 3 isoform 3 [Homo sapiens]	1220	1220	100%	0.0	98%	NP_001139760.1
apoptosis-inducing factor 3 isoform 1 [Mus musculus]	1207	1207	100%	0.0	96%	NP_001277999.1
apoptosis-inducing factor 3 isoform 2 [Mus musculus]	1187	1187	100%	0.0	95%	NP_780387.2
PREDICTED: apoptosis-inducing factor 3 isoform X1 [Mus musculus]	1182	1182	98%	0.0	96%	XP_006522653.1
PREDICTED: apoptosis-inducing factor 3 isoform X3 [Mus musculus]	1146	1146	98%	0.0	94%	XP_006522656.1
PREDICTED: apoptosis-inducing factor 3 isoform X5 [Mus musculus]	1050	1050	86%	0.0	96%	XP_006522658.1
PREDICTED: apoptosis-inducing factor 3 isoform X6 [Mus musculus]	1049	1049	86%	0.0	96%	XP_017172624.1
PREDICTED: apoptosis-inducing factor 3 isoform X4 [Mus musculus]	1046	1046	86%	0.0	96%	XP_006522657.1
PREDICTED: apoptosis-inducing factor 3 isoform X7 [Mus musculus]	1019	1019	84%	0.0	96%	XP_017172625.1
apoptosis-inducing factor 3 [Danio rerio]	848	848	100%	0.0	66%	NP_001121885.1
PREDICTED: apoptosis-inducing factor 3 isoform X2 [Danio rerio]	842	842	100%	0.0	66%	XP_009299502.1
PREDICTED: uncharacterized protein LOC791218 isoform X1 [Danio rerio]	521	521	88%	1e-179	47%	XP_005157647.1
PREDICTED: apoptosis-inducing factor 3 isoform X3 [Danio rerio]	499	499	57%	1e-173	68%	XP_009299503.1
PREDICTED: apoptosis-inducing factor 3-like [Danio rerio]	483	483	88%	2e-164	43%	XP_001920911.2
uncharacterized protein LOC791218 [Danio rerio]	372	372	87%	3e-122	39%	NP_001074169.1
CG4199, isoform D [Drosophila melanogaster]	374	374	92%	4e-121	37%	NP_569976.1
CG4199, isoform A [Drosophila melanogaster]	372	372	84%	7e-121	38%	NP_726790.1
uncharacterized protein Dmel_CG10700 [Drosophila melanogaster]	363	363	87%	7e-118	37%	NP_609942.1
Uncharacterized protein CELE_F20D6.11 [Caenorhabditis elegans]	316	316	87%	2e-99	33%	NP_505112.1
flavoprotein [Schizosaccharomyces pombe 972h-]	295	295	79%	1e-90	36%	XP_001713117.2
ferrodoxin reductase-like protein [Plasmodium falciparum 3D7]	295	295	84%	2e-90	31%	XP_001349105.1
ferredoxin reductase [Streptomyces coelicolor A3(2)]	194	194	60%	2e-54	32%	NP_631178.1
reductase [Mycobacterium tuberculosis H37Rv]	184	184	59%	9e-51	33%	NP_216385.1
ferredoxin reductase [Mycobacterium tuberculosis H37Rv]	176	176	58%	4e-48	32%	NP_215202.1
reductase [Streptomyces coelicolor A3(2)]	172	172	60%	1e-46	30%	NP_626711.1
FAD-dependent oxidoreductase [Sulfolobus acidocaldarius]	160	160	61%	3e-42	28%	WP_011279075.1
oxidoreductase [Streptomyces coelicolor A3(2)]	160	160	60%	5e-42	31%	NP_626364.1
phenylpropionate dioxygenase, ferredoxin reductase subunit [Escherichia coli str. K-12 substr. MG1655]	145	145	63%	7e-37	28%	NP_417037.1
NADH oxidase [Thermotoga maritima MSB8]	131	131	50%	1e-31	31%	NP_228205.1
monodehydroascorbate reductase 6 [Arabidopsis thaliana]	128	128	50%	9e-31	27%	NP_849840.1
monodehydroascorbate reductase 6 [Arabidopsis thaliana]	127	127	56%	4e-30	26%	NP_564818.1
monodehydroascorbate reductase 6 [Arabidopsis thaliana]	127	127	56%	4e-30	26%	NP_849841.1
monodehydroascorbate reductase 6 [Arabidopsis thaliana]	127	127	56%	7e-30	26%	NP_849839.1
PREDICTED: monodehydroascorbate reductase [Glycine max]	125	125	59%	2e-29	26%	XP_003557022.1
uncharacterized protein LOC100787700 [Glycine max]	122	122	60%	5e-29	26%	NP_001276311.1
PREDICTED: probable monodehydroascorbate reductase, cytoplasmic isoform 2 [Glycine max]	123	123	52%	9e-29	29%	XP_006599107.1
PREDICTED: uncharacterized protein LOC100787700 isoform X1 [Glycine max]	122	122	59%	2e-28	26%	XP_003535365.1

ANEXO III – ALINEAMIENTO CON CLUSTAL_w DE VARIAS DE LAS SECUENCIAS OBTENIDAS TRAS EL ANÁLISIS BLAST DE AIFL HUMANO

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MmAIFL -----MGGCFSPKPKVELKIEVVLPKEKRGKEEL
HsAIFL -----MGGCFSPKPKVELKIEVVLPKEKRGKEEL
BtAIFL -----MGGCFSPKPKVELKIEVVLPKEKRGKEEL
DrAIFL -----MGGCLSKPKPVEVKVELTLDDKEKEVDLM
CeAIFL -----MALANWLTPVEPCDND--
DmAIFL -----MGSVNCKEYKTTGSTPKKEKSTGGA
MtAIFL -----
SpAIFL -----MLLRFFINQPRFIQFTFLRNKKDRILGLQ
PFAIFL MRRNLLSLNGKISTIIKSDKLKTRGISSYNILKNNINVSLEKKNKRRFFSSSLKGHQKIG
SaAIFL -----

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MmAIFL SASGKGSPPR-GYQNGTARHFHAEERLPTQPYPSPQDCVEATVCHVKDLENGQMREVEL
HsAIFL SASGKGSPPR-AYQNGTARHFHTEERLSTPHYPSPQDCVEAAVCHVKDLENGQMREVEL
BtAIFL STGSRGSPR-AYQNGAARHFHADERLPTAHPYPGAQDCVEAAVCHVKDLENGQMREVEL
DrAIFL SPNGKASPFSECRPNGLGHCSDEDSM-TLRPQRKNRDYIEASVCHIKDLENGQMREVDL
CeAIFL -----DSPAVEEILGRIEDVPPGTTKMFV
DmAIFL VGSYQSKCS-----NQSPSTTMSTEESPSEYTSAPVDCRVDTLKENEMKQVDF
MtAIFL -----
SpAIFL LGKQPFRRMS-----SSSGLKQQGLAQKKFQLEFDPSSVSKNGTKTEAKVV
PFAIFL GVLNSYDIFLIISLLAVPTILNNKFGKMSNSIANCSNVEKVFLIKSNELQDGEMKEIKV
SaAIFL -----

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MmAIFL GWG--KVLLVKDNGEFHALGHKCPHYGAPLVKGVLS-RGRVRCPPWHGACFNISTGDLEDF
HsAIFL GWG--KVLLVKDNGEFHALGHKCPHYGAPLVKGVLS-RGRVRCPPWHGACFNISTGDLEDF
BtAIFL GWG--KVLLVKDNGEFHALGHKCPHYGAPLVKGVLS-RGRVRCPPWHGACFNISTGDLEDF
DrAIFL GAG--RALLIKEHEGFFAMGHKCPHYGAPLVKGVLS-KGHVRCPPWHGACFNISTGDIEDF
CeAIFL RDR--KVLVINDEGRIYAINGLCSHYNFLENGTYA-KGRIRCPHAGACFNVRSGDIEDY
DmAIFL DEDT-RVLLVKQNDRLAVGAKCTHYGAPLQTGALG-LGRVRCPPWHGACFNLENGDIEDF
MtAIFL -----MNAHVTSR
SpAIFL GTEF-GVLLVRARNTYFATAGKCSHYGAPLAKGVVTSBGHIVCPWHGACFNAATGDVEDT
PFAIFL HEEDTVLLVRVNNKYCLGPKCPHYSAPLKSGVLT-NEYITCPWHDAKFDIKTGECING
SaAIFL -----MKYEIIYYVIDILDVSSK

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MmAIFL PGLDSLHKFQVKIEKE-KVTIRASKQA-----LQLQRRTKVMAKCISPSAGHSST
HsAIFL PGLDSLHKFQVKIEKE-KVYVRASKQA-----LQLQRRTKVMAKCISPSAGYSST
BtAIFL PGLDSLHKFQVKIEKE-KVYIRASKQA-----LQLQRRTKVMAKCISPSAGYSGST
DrAIFL PGLDSLPTFQVRVEKE-KVIIRANKQA-----LQTQRRSKVMSKCSAVINSSTGFS
CeAIFL PGFDSLHSYVTVNDG-NLIKTTEKK-----LGSDDRIRHLPKMKQCNQND-----R
DmAIFL PGLDSLPCYRVEVGNEGQVMLRAKRS-----LVNNKRLKNMVRKPPDDQ-----R
MtAIFL EGVN-----EFDDG-----
SpAIFL PAIAALRTFPVTEEGDGLWIEVEDKNDNGASVLQPEGCWNRKATEVYNKGSVETVETAP
PFAIFL PSFDDIPKYEVVIEGNEVYALLPKKLEIFE-----KKRICECKGSGCEK-----K
SaAIFL LTSK-----

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MmAIFL NVLIVGAGAAGLVCAETLRQEGFSDRIVLCTLDRLHPYDRAKLSKSLDAQP-----EQL
HsAIFL NVLIVGAGAAGLVCAETLRQEGFSDRIVLCTLDRLHPYDRPKLSKSLDTQP-----EQL
BtAIFL NVLIVGAGAAGLVCAETLRQEGFSDRIVLCTLDRLHPYDRPKLSKSLDAQP-----EQL
DrAIFL HVLIIIGSGPAGLVCAETLRQEGFTDRIVICTTDKHLPYDRPKLSKSLLEST-----EQL
CeAIFL PVVIIGGGVATATFIEHSRLNGLITPILVISEESLPPYDRVLLSKKPAATG-----EDI
DmAIFL VFIVVGGGPGSAGAVETIRQEGFTGRILFVCRELYLPYDRVKISKAMNLEI-----EQL
MtAIFL -IVIVGGGLAAARTAEQLRRAGYSRLTIVSDEVHLPYDRPPLSKEVLRSE-----VDD
SpAIFL HVCIIIGGGKASVAAEYLREKNFKGKITIFTREDEVPYDRPKLSKSLLDHI-----SKL
PFAIFL NILIVGGGAATLGALETFLKLGYNGLIICSKDAYKPYDRPTLSKNVSNCCNCDLEYEEI
SaAIFL -YVIIGSGIAGYHALKEMLNIDPKANITLVTSDDLPPYDRPPLSKEYMRSER----DRDS

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MmAIFL ALRPK-EFFRAYGIEMLTEAQVVTVDVRNKKVFKDGF--KLEYSKLLLAPGSSPKLTLC
HsAIFL ALRPK-EFFRAYGIEVLTEAQVVTVDVRTKKVFKDGF--KLEYSKLLLAPGSSPKLTSC
BtAIFL ALRPK-EFFRAYGIEVLTEAQVVTVDVRNKKAVFKDGF--KLEYSKLLLAPGSSPKLTSC
DrAIFL QLRSS-DFFQMHDIIEVLLEKEVVSVDVKTHTVTFRDGF--KMEYRKLIATGSRPKPLSY
CeAIFL RLRKDDAFYEERNVKFLKTSVIAVNHKSREVSLSNGE--TVVYSKLIATGGNVRLQV
DmAIFL RFRDE-EFYKEYDIELWQGVAAEKLDTAQKELHCSNGY--VVKYDKIYLATGCSAFRPPPI
MtAIFL VALKPREFYDEKDIALRLGSAVSLDTGEQVTTLADGT--VLGYDELVIATGLVPRRIPS
SpAIFL ALRSK-EYYDDLDSFHFNTDVTIKDLAEKKIYCGSDEKPTESYTKLILATGGEPNKLPI
PFAIFL KLKED-SYYNKSNIIYKNNVVEKVDTENKKAHLNNGE--IINFDKILITTGISPSPSPM
SaAIFL LFFEKPEFYQRDNLKVMLNTTVERLNVKEKFLTLSTGQ--TLNFDKLLITTGKPKRLGI

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MmAIFL	KGKDVENVFTIRTPEDANRVLRL-----LARGNNAVVGAGFLGMEVAAYL TEKAHSVSVVE
HsAIFL	KGKEVENVFTIRTPEDANRVVR-----LARGNNAVVGAGFLGMEVAAYL TEKAHSVSVVE
BtAIFL	KGKDVENVFTIRTPEDANRVRL-----LARGNNAVVGAGFLGMEVAAYL TEKAHSVSVVE
DrAIFL	KGKDVGNVFLHRTPEDANSIVT-----LASKNAVIIGTSFIMGELAVVLKD--HNVSVIG
CeAIFL	PGSDLKNICYLRKVEEANIISN-----LHPGKHVVCVGSSFIGMEVASALAEKAASVTVIS
DmAIFL	PGVNLENVRTVRELADTKAILAS-----ITPESRVVCLGSSFIAL EAAAGLVSKVQSVTVVVG
MtAIFL	LP-DLDGIRVLRSFDESMALRKH-----ASAARHAVVGAGFIGCEVAASLRGLGVDVVLVE
SpAIFL	PGLDSKNVYLLRSADASKLAVTTEAGDKNNVIIGSSFIGLELAVVLKD--HNVSVIG
PfAIFL	KNMNLDNLFTHLNSDNIKIGEY-----AKEGSKCVIIGSSFIACELSSALKKKNNVNTLIS
SaAIFL	HGENLNGVHYLRTLSDADSIKED-----LKHGKPKVIVGAGFIGVEAASLRSLGFEPVVE
	: .: :: : : . *: :*. :. * : *
MmAIFL	LEETPFRFLGERVGRALMKMFENNRVKFYMQTEVSELR-----AQE-GKLQEVLVKS
HsAIFL	LEETPFRFLGERVGRALMKMFENNRVKFYMQTEVSELR-----GQE-GKLKEVLVKS
BtAIFL	VEETPFRFLGERVGHGLTMKMFENNRVKFYMQTEVSELR-----AQE-GKLKEVLVKS
DrAIFL	IEAVPFRKALGEVGTALMKLFESNRVKFYMLNEVWEMR-----GHN-GQLKEVLVKS
CeAIFL	NTPEPLP-VFGSDIGKGIRLKFEEKGVKFELAAVVALR-----GNDQGEVSKVILEN
DmAIFL	RENVPLKAAFGAETGQRVLQLFEDKNVVMRMESGIAEIV-----GNEDGKVSEVVLVD
MtAIFL	PQPAPLASVLGEQIGQLVTRLHRDEGVDVRTGVTVAEVR-----GKG--HVDVAVLTD
SpAIFL	MESIPFEKVGSGTALMKLKEVGTALFYDLSNIKEVKT-----SSNDSSKAEHVILKD
PfAIFL	KDDVPFYGSGFEKIGNIVLNILKEKNIKFYPSMHPTEYIIDKRFFSRKSGNIHGVRLNN
SaAIFL	VKPFIIWSTFVDEKVSSEMRKYFENKGVTFLLNEGKFEF-----GSQRVNSVITSG
	. . : . : : . : : : . : :
MmAIFL	SKVLRADVCVLGIGAVPATGFLRQSGIGLDSRGFIPVNKMMQTN-VPGVFAAGDAVTFPL
HsAIFL	SKVVRADVCVVGIGAVPATGFLRQSGIGLDSRGFIPVNKMMQTN-VPGVFAAGDAVTFPL
BtAIFL	SKVVRADVCVVGIGAVPATGFLRQSGIGLDSRGFIPVNKMMQTN-IDGVFAAGDAVTFPL
DrAIFL	GKVLRADVCVIGSSPATFLKQSGVHLDNSKGFIPVNKTMQTN-IPGVFAGGDVTFPL
CeAIFL	GKELDVDLLVCGIGVTPATKFLGSGIGKLDNRGFI EVDKFRTN- ISYIFAMGDVVTAPL
DmAIFL	DTRLPCDLLLIGTSGSKLNTQFLAKSGVKVNNRNGSVVDVDFLESN-VPDVVYVGGDIANAHI
MtAIFL	GTELPADLVVVGISTPATEWIGLESGVEVDNG--VICDKAGRTS-APNVVALGDVASWRD
SpAIFL	GQSIPADVVILAAGVKPNRLRYLG-NAVSLKEDGGVKVDEHCRVLGAEDVYAVGDIAHAPF
PfAIFL	GEVINCDYVIEALGCCIPNSDFLDEKYKNVNN--FIEVDKHFKVKNSDNMYAAGDVCTFPY
SaAIFL	GKKIESSMVLVAVGISPNVEIAN----ELQVNNGILVDEHLKAK--EDIYVAGDVANILD
	. : . : . * :: : . . :.: **
MmAIFL	AWRN----NRKVNIPHWQMAHAQGRVAAQNMLAQEAIE---NTVPYLWTAMFGKS-LRY
HsAIFL	AWRN----NRKVNIPHWQMAHAQGRVAAQNMLAQEAEM---STVPYLWTAMFGKS-LRY
BtAIFL	AWRN----NRKVNIPHWQMAHAQGRVAAQNMLAQEAIE---STVPFLWTAMFGKS-LRY
DrAIFL	GLRS----NKKVNIPHWQMAHVHGRALALGIMGKASDI---KTVPYFWTAMFGKS-IRY
CeAIFL	PLWD----IDSINIQHFTQAAHQHQLGYTIVGKPPQG---PIVPYFWTLFFFAFLKF
DmAIFL	HGLA----HDRVNIHGYQLAQYHGRVAAINMCGGVKKL---EAVPFFFTLIFGKG-IRY
MtAIFL	PMG----HQARVEHNSNVADQARVVVPAMLGDVPTG---VVVPYFWSQDYDK-IQC
SpAIFL	AGLPSSGEKSHTRIEHWDVAGNLGRVAADHILFGNKAGYTTKSFTPYFWSAQGKQLRYCG
PfAIFL	FLTD----EMVNICHWNVAIQQGRIAAHNMLRDDKKE---FNFIPFFNTNIFGKN-FRY
SaAIFL	PVSG----KRRRIEHWNNAYYTGQLAARNMMGQNESY---NFLSTVWSIDIFDLH-IES
	: : *. . : : : . . :
MmAIFL	AGYGEGFDDVVIQGDLEELKFVAFYT-KSDEVIIVASMNYDPIVSKVAEVLASGRAIRK-
HsAIFL	AGYGEGFDDVVIQGDLEELKFVAFYT-KGDEVIIVASMNYDPIVSKVAEVLASGRAIRK-
BtAIFL	AGYGEGFDDVVIQGDLEELKFVAFYT-KGDEVLSVASMNYDPIVSKVAEVLASGRITRK-
DrAIFL	AGYGDGFDDVVVIQGDLEELKFVAFYT-KSEEVVAVASMNYDPIVSRVAEVEFGSGKTIRK-
CeAIFL	SGCNQGSSTKEYTNGDPTGTGTFIRYFL-KKDKVVAVAAAGGPSSVASQFAEIFKKGTEVTL-
DmAIFL	AGHG-SYKDVIIDGSMEDFKFVAFYINEADTVTAVASGRDPIVAQFAELISQKCLGR-
MtAIFL	LGEPHATDVHHLVED-DGRKL LAYYE-RDGLVLGVVGGGMAGVKVMFAGKIAAGAPIAE-
SpAIFL	NNAAEFGDDVVVIQGSLSDYKFACFFT-KGEKVVGVCSIMKDPVVSQCARLF IKDAMPSKS
PfAIFL	SGVYKNYDKIIEYEGDLLKHNFJGYFV-KNDKVASIITLG--NNKMASLNECMANKNVKPVY
SaAIFL	GGETTGYDDVVMRGNFDDKSLNVIYV-KGGLVIGYVAFNRDMSELEAINKLQDKVDIKS
	. : . : . : : : . : . : :
MmAIFL	-----REVELFMLHSKTGDMSWL TGKGS-----
HsAIFL	-----REVELFVLHSKTGDMSWL TGKGS-----
BtAIFL	-----REVE-----TGDMSWL TGKGS-----
DrAIFL	-----RDVE-----TGDMSWL TVKGSQ-----
CeAIFL	-----KDLK-----NSSDHTWGHLLL-----
DmAIFL	-----GQIEDP-----ATREDWTKKLGQPLPQVR-----
MtAIFL	-----VLDQTQA-----
SpAIFL	QLKEN-----FDVLSIPL-----
PfAIFL	-----ELEGG-----LKNSDSMIASLKI-----
SaAIFL	-----KVDKLK-----DESFDIRKLSS-----

ANEXO IV – LISTA DE MEDIOS Y TAMPONES EMPLEADOS

CULTIVO CELULAR

Bacterias

- *Medio LB*: 10g/L peptona, 5 g/L extracto de levadura, 5 g/L NaCl
- *Medio LB-agar*: 20 g/L agar, 10g/L triptona, 5 g/L extracto de levadura, 10 g/L NaCl. Ajustar pH a 7,5 con NaOH

Células humanas

- *Medio DMEM* (Dulbecco's Modified Eagle Medium, *PAN-Biotech*) *completo*: 4,5 g/L glucosa, rojo de fenol, 3,7 g/L NaHCO₃. Añadidos posteriormente: 10% FBS (suero fetal bovino), 1% penicilina/streptomicina, 1% glutamina
- *Medio Gibco OptiMem* (*Thermo Fisher Scientific*): modificación del medio *Eagle's Minimum Essential Media* (MEM), tamponado con HEPES y NaHCO₃ y suplementado con hipoxantina, timidina, piruvato sódico, L-glutamina, elementos traza y factores de crecimiento

ELECTROFORESIS HORIZONTAL

- *Tampón de carga 6x*: 0,02% azul de bromofenol, 30% glicerol, 10 mM Tris pH 8, 1 mM EDTA
- *Tampón TBE 1x*: 0,5M Tris pH 8, 0,5M ácido bórico, 10 mM EDTA
- *Gel de agarosa 1% o 2%*: 1% o 2% de agarosa en tampón TBE 1x (1g o 2g de agarosa/100mL de tampón TBE)

ELECTROFORESIS VERTICAL

- *Tampón de carga 2x SLB*: 0,05% azul de bromofenol, 25% β-mercaptoetanol, 4% SDS, 20% glicerol, 0,1M Tris-HCl pH 6,8
- *Tampón separador 1x*: 0,25 M Tris pH 8, 1,9 M glicina, 35 mM SDS. Sin ajustar, pH 8,3
- *Geles de acrilamida*:

Compuesto	Gel concentrador (4% poliacrilamida)	Gel separador (10% poliacrilamida)
Agua	2,8 mL	1,28 mL
Acrilamida/Bisacrilamida	1 mL	3,6 mL
Tris-HCl 1M pH 6.8	625 µL	-
Tris-HCl 1M pH 8.8	-	3 mL
10% SDS	50 µL	80 µL
10% APS	25 µL	40 µL
TEMED	5 µL	5 µL

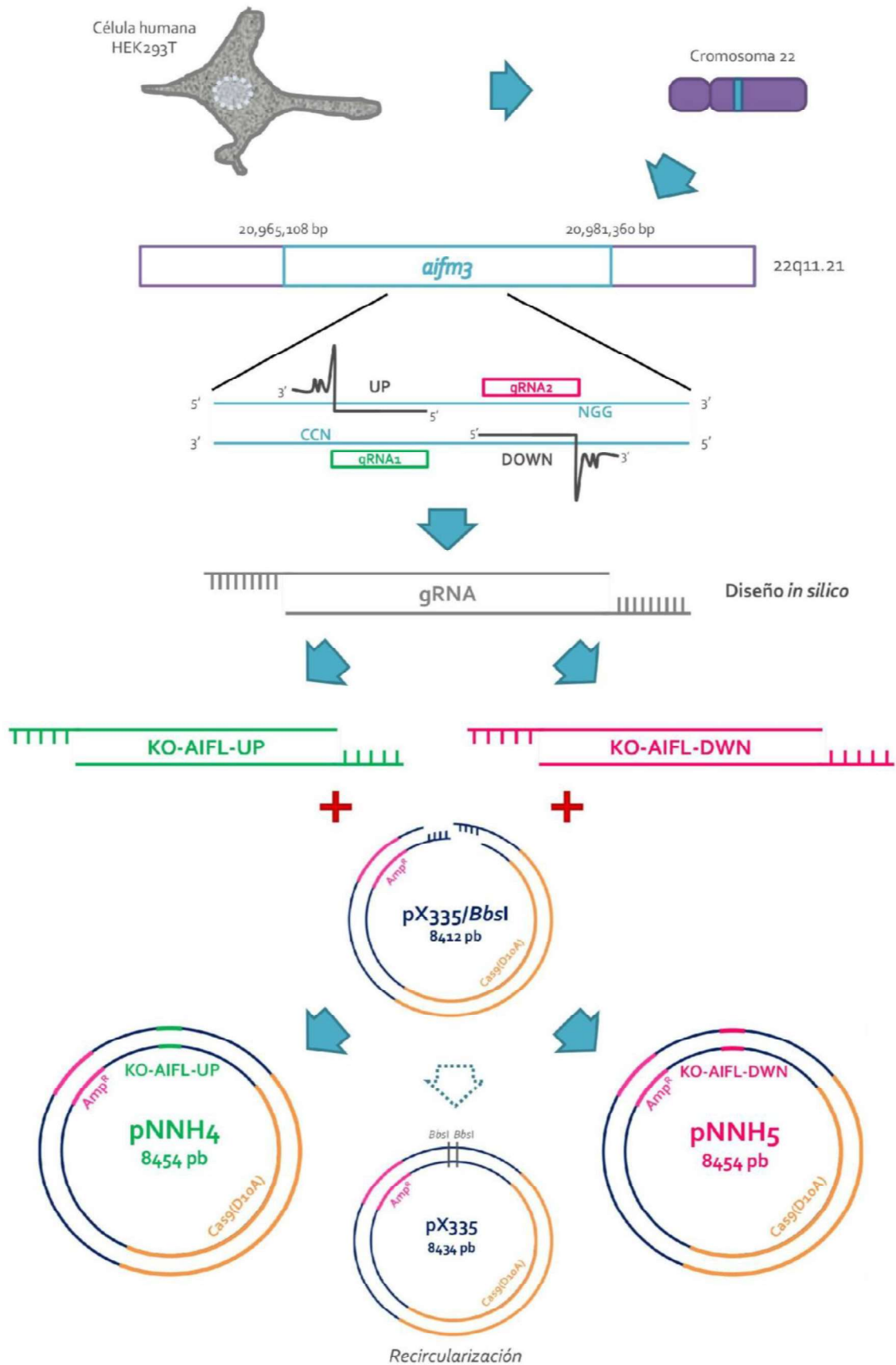
TINCIÓN CON COOMASSIE

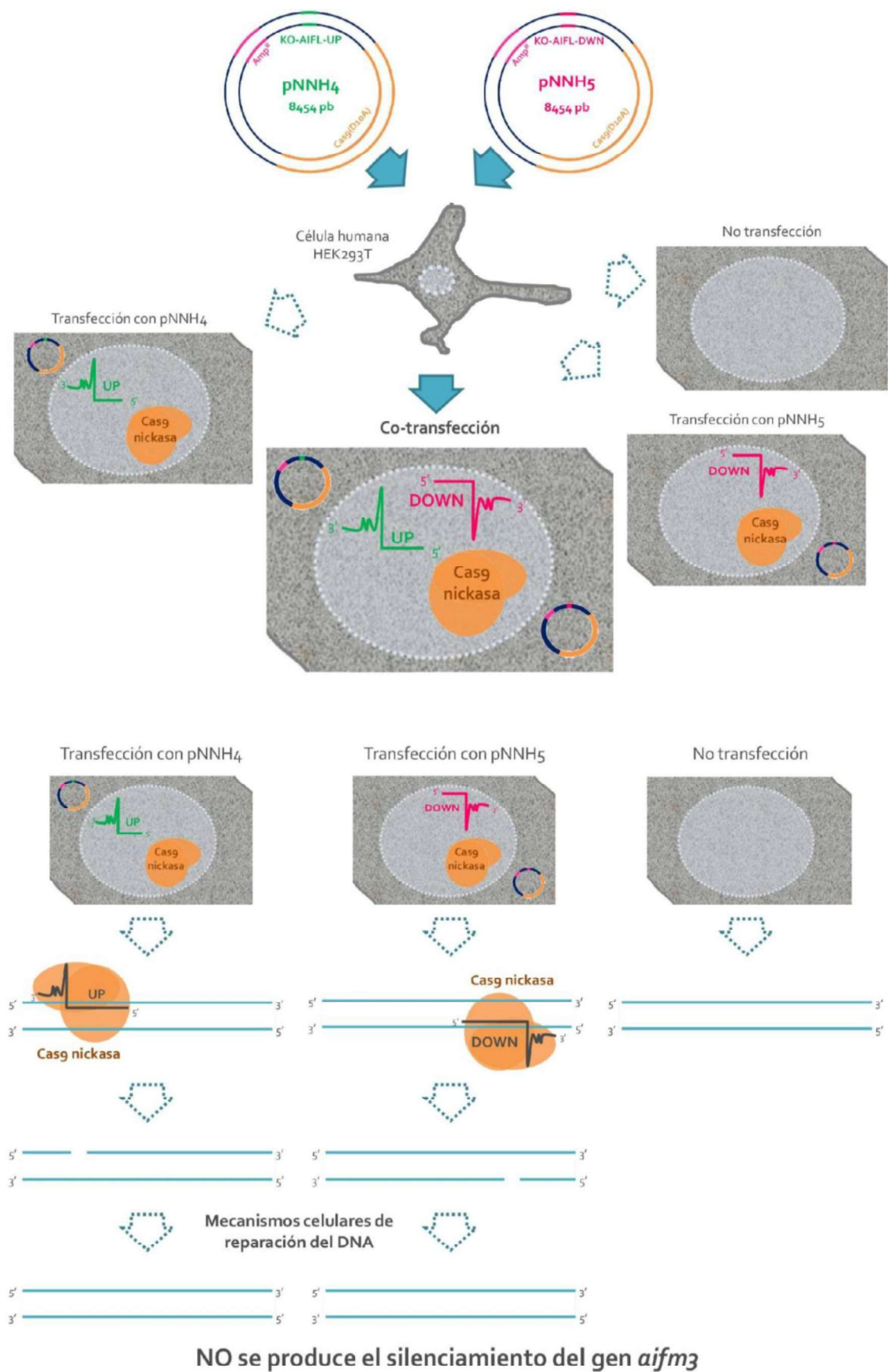
- *Solución colorante*: 0,5 g/L azul Coomassie, 45% metanol, 6% ácido acético (CH₃COOH)
- *Solución decolorante*: 25% metanol, 10% CH₃COOH, 2% glicerol

ELECTROTRANSFERENCIA

- *Tampón de transferencia 1x*: 25 mM Tris pH 8, 0,2M glicina, 20% metanol

ANEXO V –SILENCIAMIENTO DEL GEN *aifm3* MEDIANTE CRISPR/Cas9





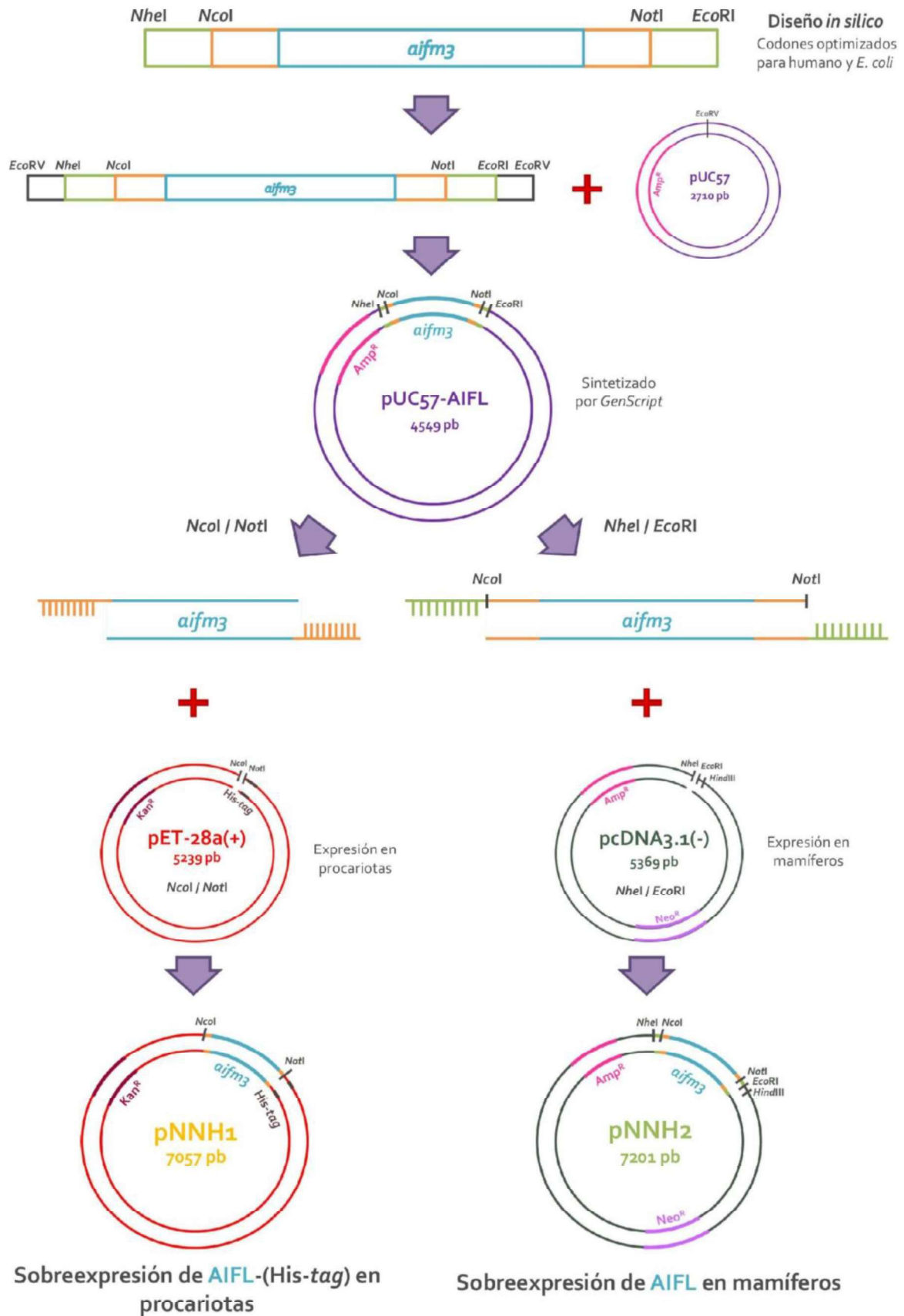


ANEXO VI – ALINEAMIENTO DE LAS SECUENCIAS DE pNNH4.1, pNNH4.2, pNNH5.4 Y pNNH5.5 CON SUS INSERTOS (KO-AIFL-UP Y KO-AIFL-DWN)

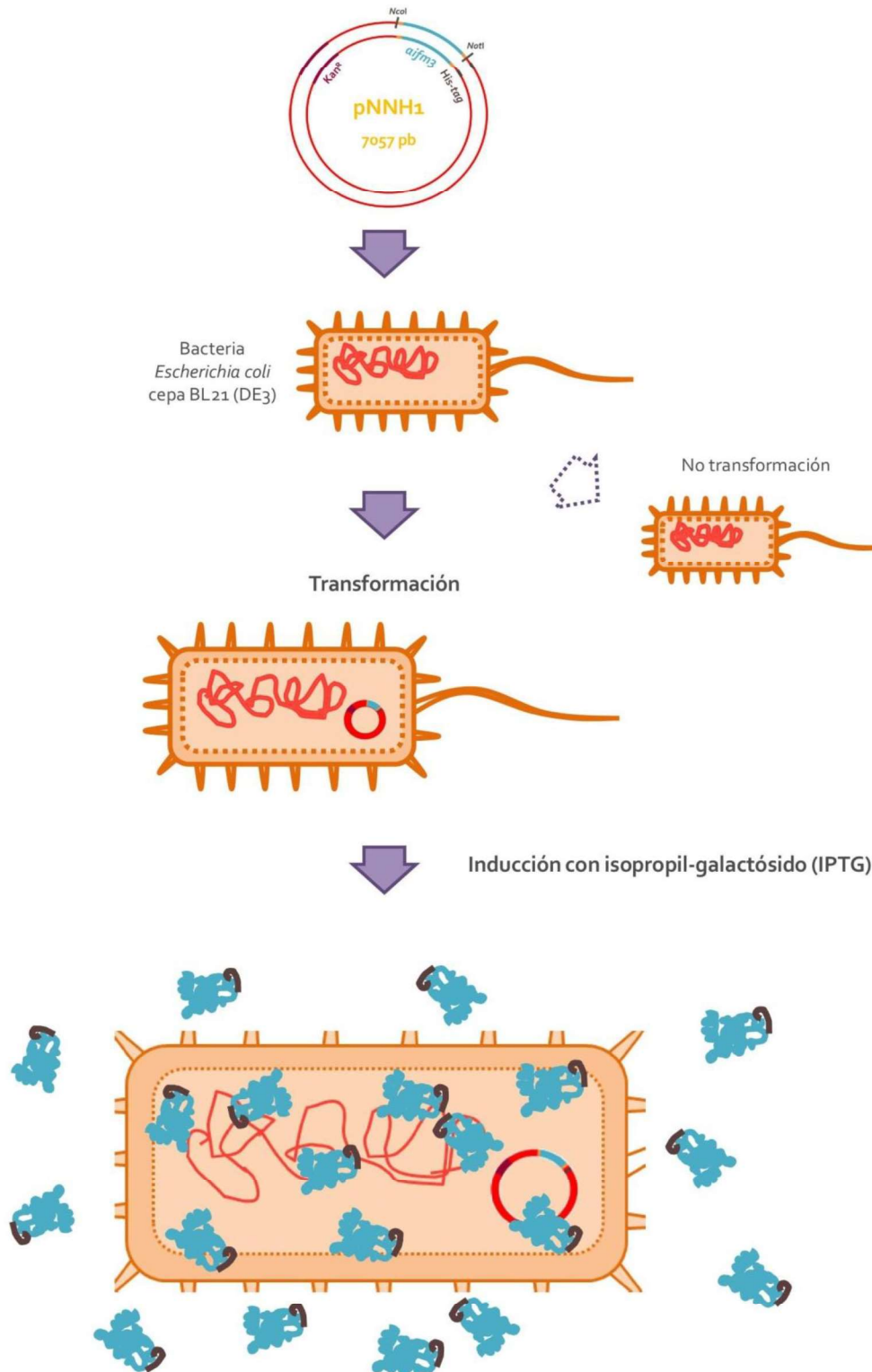
pNNH4.2 pNNH4.1 KO-AIFL-UP	NNNNNNAANNNNNNNNNTNTTGGCTTTATATATCTTGTGGAAGGACGAAACACCGCTGAG ---NNNNNNNNNNNATTTCTTGGCTTTATATATCTTGTGGAAGGACGAAACACCGCTGAG -----CACCCTGAG *****
pNNH4.2 pNNH4.1 KO-AIFL-UP	GATGGCCGGCAGGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT GATGGCCGGCAGGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTAT GATGGCCGGCAGGC----- *****
pNNH4.2 pNNH4.1 KO-AIFL-UP	CAACTTGAAAAAGTGGCACCAGTCGGTGCTTTTTTGTGTTTAGAGCTAGAAATAGCAAGT CAACTTGAAAAAGTGGCACCAGTCGGTGCTTTTTTGTGTTTAGAGCTAGAAATAGCAAGT -----
pNNH4.2 pNNH4.1 KO-AIFL-UP	TAAAATAAGGCTAGTCCGTTTTTAGCGCGTGCGCCAATTCTGCAGACAAATGGCTCTAGA TAAAATAAGGCTAGTCCGTTTTTAGCGCGTGCGCCAATTCTGCAGACAAATGGCTCTAGA -----
pNNH4.2 pNNH4.1 KO-AIFL-UP	GGTACCCGTTACATAAATTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCCG GGTACCCGTTACATAAATTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCCG -----
pNNH4.2 pNNH4.1 KO-AIFL-UP	CCCATTGACGTCAATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTA CCCATTGACGTCAATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTA -----
pNNH4.2 pNNH4.1 KO-AIFL-UP	TTTACGGTAAACTGCCCCTTGGCAGTACATCAAGTGATCATATGCCAAGTACGCCCCC TTTACGGTAAACTGCCCCTTGGCAGTACATCAAGTGATCATATGCCAAGTACGCCCCC -----
pNNH4.2 pNNH4.1 KO-AIFL-UP	TATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTGTGCCCAGTACATGACCTTATG TATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTGTGCCCAGTACATGACCTTATG -----
pNNH4.2 pNNH4.1 KO-AIFL-UP	GGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTCGAGGT GGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTCGAGGT -----
pNNH4.2 pNNH4.1 KO-AIFL-UP	GAGCCCCACGTTCTGCTTCACTCTCCCCATCTCCCCCCCCCTCCCCACCCCCAATTTTGT GAGCCCCACGTTCTGCTTCACTCTCCCCATCTCCCCCCCCCTCCCCACCCCCAATTTTGT -----
pNNH4.2 pNNH4.1 KO-AIFL-UP	TTTATTTATTTTTTAATTATTTTGTGCAGCGATGGGGGCGGGGGGGGGGGGGGGGTN TTTATTTATTTTTTAATTATTTTGTGCAGCGATGGGGGCGGGGGGGGGGGGGGGG----- -----

pNNH5.4 pNNH5.5 KO-AIFL-DWN	NNNNNNNNNNNNNTTCTTGCTTTATATATCTTGTGGAAGGACGAAA-CACGGCTTCT --NNNNNNNNNNNATTTCTTGCTTTATATATCTTGTGGAAGGACGAAACACCGGCTTCT -----CACCGGCTTCT *****
pNNH5.4 pNNH5.5 KO-AIFL-DWN	CCAAACCCAAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAGGCTAGTCCGTTATC CCAAACCCAAACCGTTTTAGAGCTAGAAATAGCAAGTTAAAAATAAGGCTAGTCCGTTATC CCAAACCCAAACC----- *****
pNNH5.4 pNNH5.5 KO-AIFL-DWN	AAC TTGAAAAAGTGGCACCAGT CGGTGCTTTTTTTGTTT TAGAGCTAGAAATAGCAAGTT AAC TTGAAAAAGTGGCACCAGT CGGTGCTTTTTTTGTTT TAGAGCTAGAAATAGCAAGTT -----
pNNH5.4 pNNH5.5 KO-AIFL-DWN	AAAATAAGGCTAGTCCGTTTTTAGCGCGTGCGCCAATTCTGCAGACAAATGGCTCTAGAG AAAATAAGGCTAGTCCGTTTTTAGCGCGTGCGCCAATTCTGCAGACAAATGGCTCTAGAG -----
pNNH5.4 pNNH5.5 KO-AIFL-DWN	GTACCGTTACATAACTTACGGTAAATGGCCCGCTGGCTGACCGCCCAACGACCCCCGC GTACCGTTACATAACTTACGGTAAATGGCCCGCTGGCTGACCGCCCAACGACCCCCGC -----
pNNH5.4 pNNH5.5 KO-AIFL-DWN	CCATTGACGTCAATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTAT CCATTGACGTCAATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTAT -----
pNNH5.4 pNNH5.5 KO-AIFL-DWN	TTACGGTAACTGCCCACTTGCCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCT TTACGGTAACTGCCCACTTGCCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCT -----
pNNH5.4 pNNH5.5 KO-AIFL-DWN	ATTGACGTCAATGACGGTAAATGGCCCGCTGGCATTGTGCCAGTACATGACCTTATGG ATTGACGTCAATGACGGTAAATGGCCCGCTGGCATTGTGCCAGTACATGACCTTATGG -----
pNNH5.4 pNNH5.5 KO-AIFL-DWN	GAC TTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTCGAGGTG GAC TTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTCGAGGTG -----
pNNH5.4 pNNH5.5 KO-AIFL-DWN	AGCCCCACGTTCTGCTTCACTCTCCCCATCTCCCCCCCCTCCCCACCCCAATTTTGTAT AGCCCCACGTTCTGCTTCACTCTCCCCATCTCCCCCCCCTCCCCACCCCAATTTTGTAT -----
pNNH5.4 pNNH5.5 KO-AIFL-DWN	TTATTTATTTTAAATTATTTTGTGCAGCGATGGGGGCGGGGGGGGGGGGGGGGGGGGGGG TTATTTATTTTAAATTATTTTGTGCAGCGATGGGGGCGGGGGGGGGGGGGGGGGGGGGGG -----
pNNH5.4 pNNH5.5 KO-AIFL-DWN	GAGTN --- GAGTNNGN -----

ANEXO VII –SOBREEXPRESIÓN DEL GEN *aifm3*

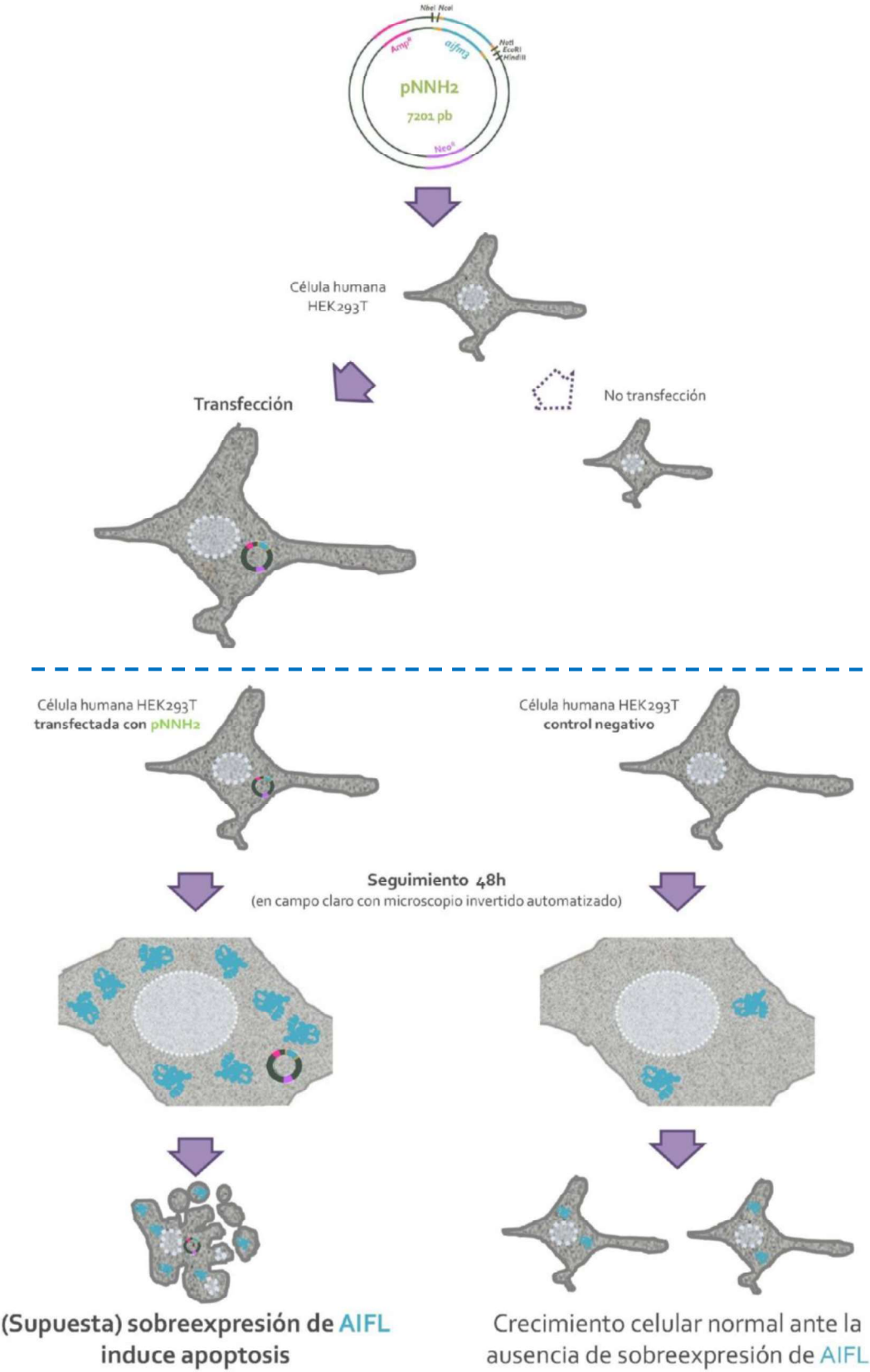


Sobreexpresión de AIFL-(His-tag) en procariotas

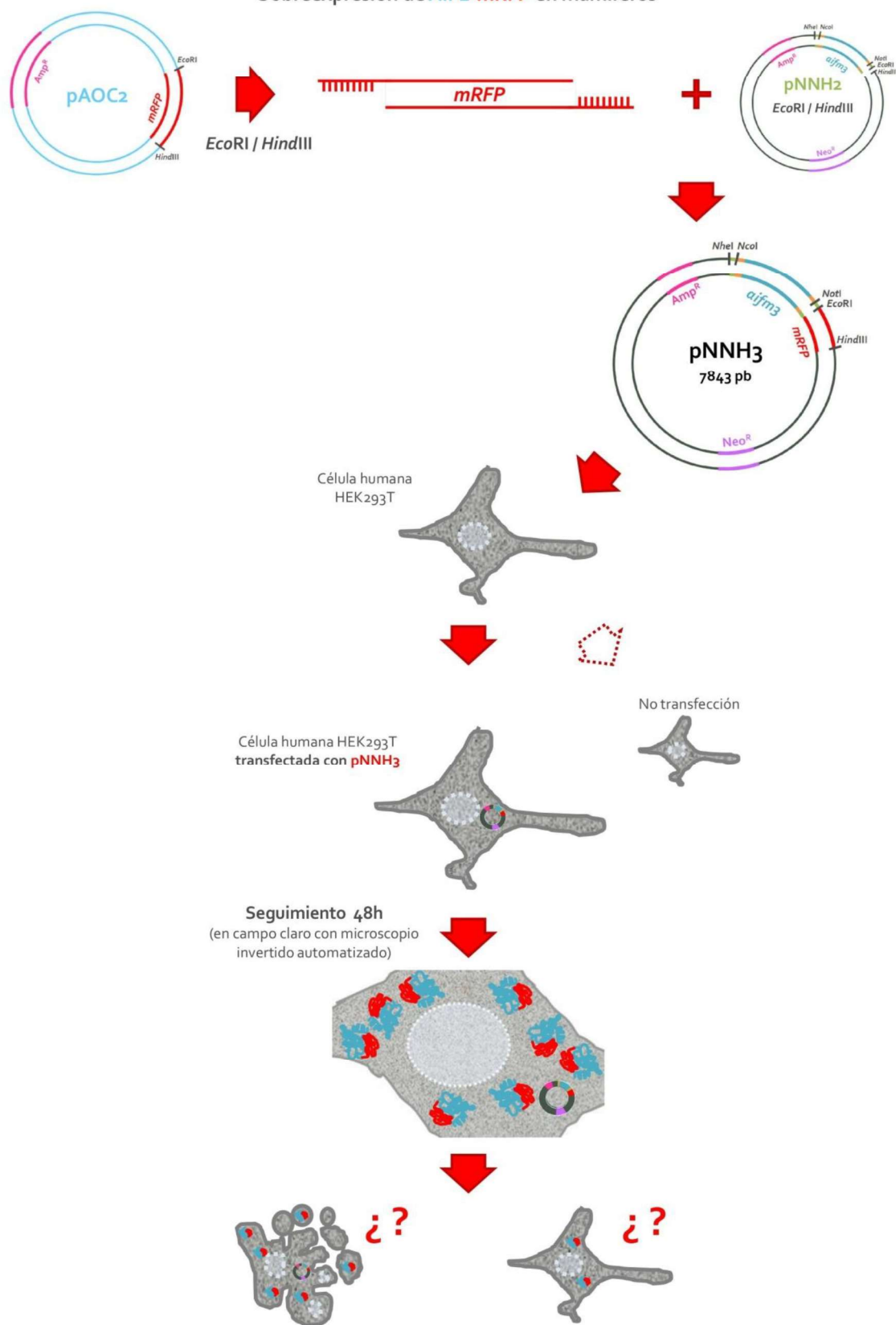


Sobreexpresión de AIFL-(His-tag) en *E. coli*

Sobreexpresión de AIFL en mamíferos



Sobreexpresión de AIFL-mRFP en mamíferos



Comprobación de la sobreexpresión de AIFL-mRFP y observación de sus efectos

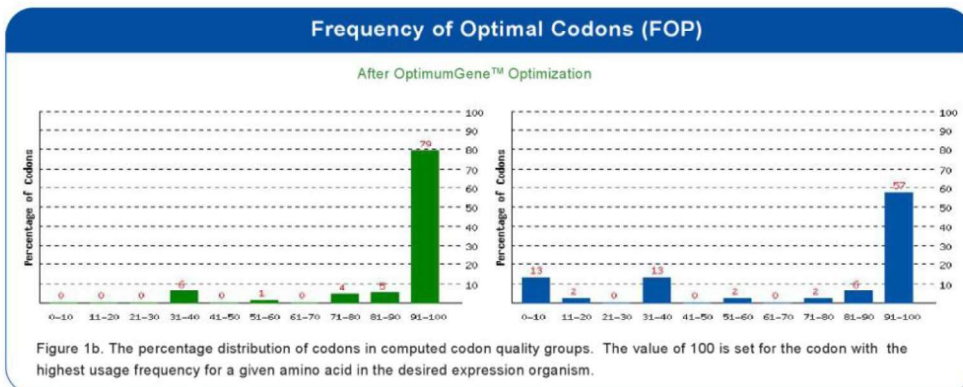
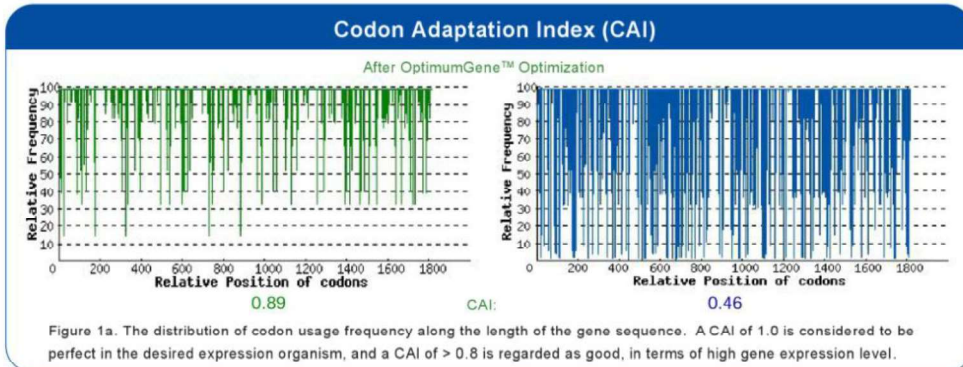
ANEXO VIII – INFORME DE LA OPTIMIZACIÓN DEL GEN *aifm3*



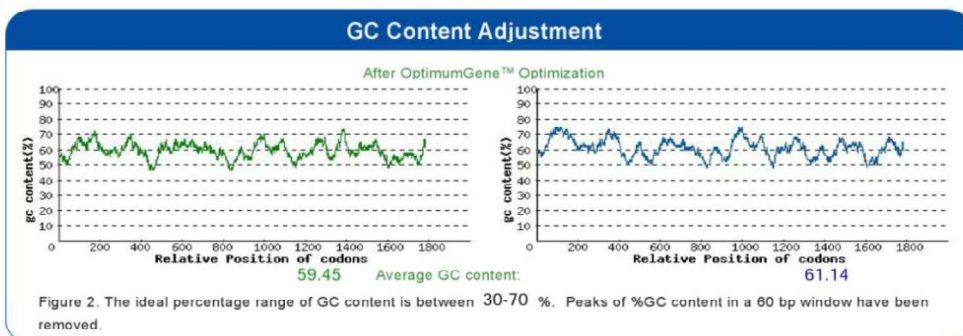
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Results *E. coli*

1. Codon usage bias adjustment



2. GC Content Adjustment

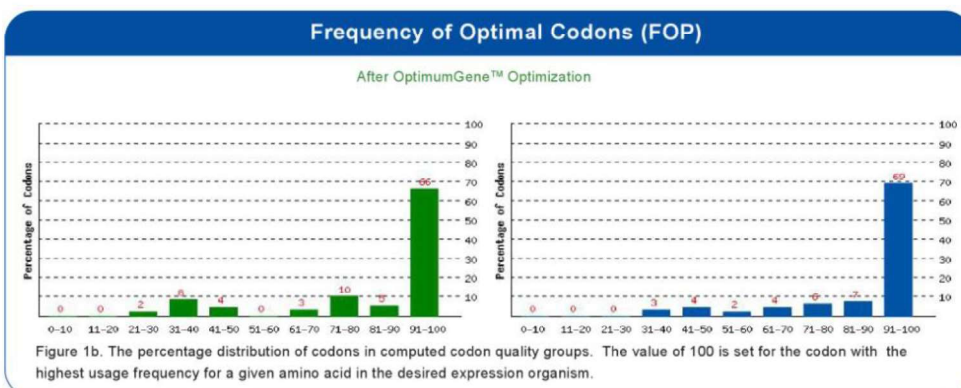
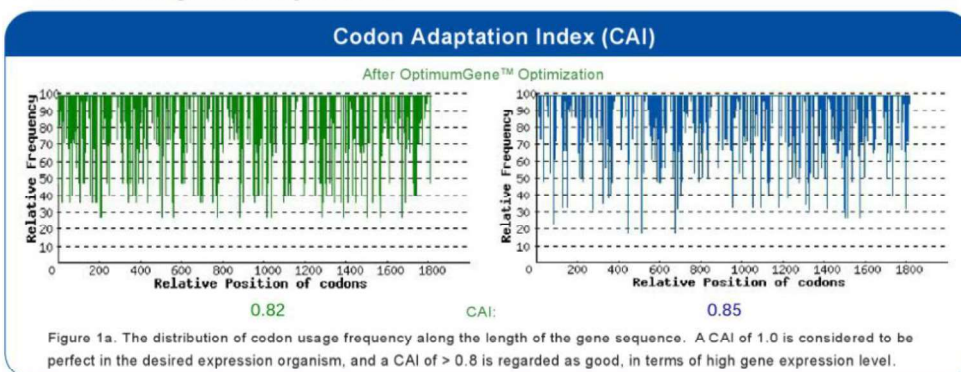


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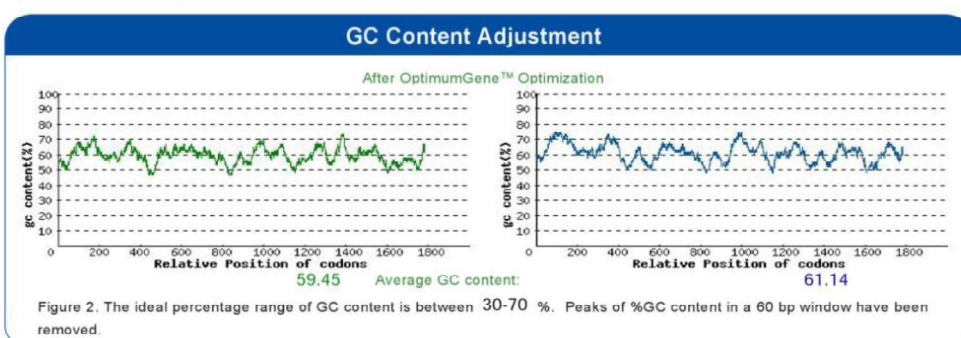
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Results *Human*

1. Codon usage bias adjustment



2. GC Content Adjustment



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3. Restriction Enzymes and CIS-Acting Elements

Restriction Enzymes	Optimized	Original
* Green: filtered sites; Blue: checked sites (not filtered); Red: kept sites.		
NheI(GCTAGC)	1(1)	1(1)
NcoI(CCATGG)	1(7)	1(7)
EcoRI(GAATTC)	1(1834)	1(1834)
NotI(GCGGCCGC)	1(1824)	1(1824)
Polymerase slippage site 1	0	0
Polymerase slippage site 2	0	0
Frameshift element	0	0
ARE	0	0
Ribosome binding site	0	6(85,652,1113,1216,1231,1516)
CIS-Acting Elements	Optimized	Original
E.coli_RBS(AGGAGG)	0	6
PolyT(TTTTTT)	0	0
PolyA(AAAAAA)	0	0
Chi_sites(GCTGGTGG)	0	0
T7Cis(ATCTGTT)	0	0
SD_like(GGRGGT)	0	5
Splice(GGTAAG)	0	0
Splice(GGTGAT)	0	2
PolyA(AATAAA)	0	0
PolyA(ATTAAA)	0	0
Destabilizing(ATTTA)	0	0
Antiviral Motifs	Optimized	Original
	0	5

4. Remove Repeat Sequences

After Optimization

Max Direct Repeat: Size:14 Distance:1194 Frequency:2
 Max Inverted Repeat: None
 Max Dyad Repeat: None

Before Optimization

Max Direct Repeat: Size:11 Distance:526 Frequency:2
 Max Inverted Repeat: None
 Max Dyad Repeat: Size: 13 Tm: 46.8 Start Positions: 1107, 433

5. Optimized Sequence (Optimized Sequence Length:1839, GC%:59.45)

GCTAGCCCATGGGC

GGTTGTTTCTCCAAGCCGAAGCCAGTGGAACTGAAGATTGAGGTGGTGTGCTGCCGAAAAGAACGTGGTAAAGAG
 GAACTGAGCGCAAGCGCAAGGGTAGCCCGCGCGCTACCAGGGTAATGGTACCGCTCGCCACTTCCACACCGAG
 GAACGTCTGAGCACCACCCGACCCATATCCGAGCCCGCAGGACTGCGTGAGGCGGCGGTGTGCCACGTGAAAGAT
 CTGGAAAACGGTCAGATGCGTGAGGTGGAAGTGGGCTGGGGCAAGGTGCTGCTGGTAAAGATAACGGCGAGTTT
 CACGCTCTGGGTACAAGTGGCCACACTATGGTGGCCGCTGGTGAAGGTGCTGAGCCGTGGCCGCGTGCCT
 TGCCCGTGGCATTGGTCTTGAATCATCAGCACCCTGACCTGGAGGATTTCCCGGGCTGGACAGCTGCAC
 AAGTTTCAGGTGAAAATTGAGAAGGAAAAAGTGTACGTGCTGCCAGCAAGCGCGCTGCAGCTGCAGCGTCGC
 ACCAAAGTGATGGCCAAATGCATCAGCCCGAGCGCGGGCTATAGCAGCAGCACCACGTGCTGATTGTGGTGCC
 GGTGCTGCTGGTCTGGTGTGCGCTGAAACCTGCGCCAGGAAGGCTTCAGCGACCGTATCGTGTGTCACCTG
 GACCGTCACCTGCCGTACGATCGTCCGAAAGCTGAGCAAAAGCCTGGATACCGCCAGAGCAGCTGGCCCTGCGC
 CCGAAAGAGTTCTTCCGTGCGTATGGTATTGAGGTGCTGACCGAAGCTCAGGTGGTACCGTGGACGTGCGCACC
 AAGAAAGTGGTGTCAAGGATGGCTTTAACTGGAGTATAGCAAACTGCTGCTGGCGCCAGGTAGCAGCCGAAA
 ACCCTGAGCTCAAGGGCAAGAGGTGGAACCGTGTTCACCATCCGTACCCCGGAAGATGTAACCGTGTGGTG
 CGTCTGGCCCGCGGTGTAACGTGGTGGTGGTGGGCGCGGGTTTCTGGGCATGGAAGTGGCGGCTTACCTGACC
 GAAAAGGCTCACAGCGTGAGCGTGGTGGAGCTGGAGGAAACCCGTTCCGTCGCTTTCTGGCGAGCGTGTGGGT
 CGTGCCCTGATGAAGATGTTGAAAACAACCGCTGAAGTTCTACATGCAGACCGAGGTGAGCGAACTGCGTGGT
 CAGGAAGGCAAGCTGAAAGAGGTGGTGTGAAGAGCAGCAAGTGGTGGTGGCGACGTGCGTGGTGGGTATT
 GGTGCGGTGCCGGCTACCGTTTCTGCGTCAAGCGGCGATCGGTCTGGATAGCCGTGGCTTTATTCGGTGAAC
 AAGATGATGCAGACCAACGTGCCGGCGTGTTCGCGGCCGGCGACGCTGTGACCTTTCCGCTGGCCTGGCGCAAC
 AACCGTAAAGTGAACATTCGCACTGGCAGATGGCCATGCTCAGGGTCTGTGGTGTCTCAGAACATGCTGGCG
 CAGGAAGCGAAATGAGCACCCTGCCGTACCTGTGGACCGCATGTTCCGCAAGAGCTGCGTTACGCGGGCTAT
 GGCGAGGGCTTTGACGATGTGATCATTAGGGTGACCTGGAGGAACTGAAGTTCTGGGCTTTTACACCAAGGC
 GACGAAGTGATCGCCGTGGCGAGCATGAACATGATCCGATTGTGAGCAAGTGGCTGAGGTGCTGGCCAGCGGT
 CGTGCCATCCGTAACGTGAAGTGAACGTGTTTGTGCTGATTCCAAGACCGGCGATATGCTCTGGTACCGGC
 AAGGGTAGC

GCGGCCCGGAGAATTG

6. DNA Alignment (Optimized Region)

Optimized	15	GGTTGTTTCTCCAAGCCGAAGCCAGTGGAACTGAAGATTGAGGTGGTGTGCTGCCGAAAAG
Original	15	GGCTGCTTCTCCAACCCAAACAGTGGAGCTCAAGATCGAGGTGGTGTGCTGCTGAGAAG
Optimized	75	GAACTGAGCGCAAGCGCAAGGGTAGCCCGCGCGCTACCAGGGT
Original	75	GAGCGAGGCAAGGAGGAGCTGTCGGCAGTGGGAAGGCGAGCCCGGGCTACCAGGGC
Optimized	135	AATGGTACCGCTCGCCACTTCCACACCGAGGAACGTCTGAGCACCCTGACCCATATCCG
Original	135	AATGGCACGGCCCGCACTTCCACACGAGGAGCGCTGTCCACCCCTACCCCTACCC

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Optimized	195	AGC CCG CAG GAC TGCGTGGAG GGCGCGGT GTGCCAC GTGAAAGATCTG AAAAC GGT CAG
Original	195	AGCCCTCAGGATTGCGTGGAGGCTGCTGTGCCACGTCAAGGACCTCGAGAATGGCCAG
Optimized	255	ATG CGTGAGGTG AACTGGGCTGG GGCA AGGTG CTGT CTGGT AAAGATAAC GGCGAGTTC
Original	255	ATGCGGGAAGTGAGCTGGGCTGGGGAAAGGTGTTGCTGGTGAAGGACAATGGGGAGTTC
Optimized	315	CAC GTCTGGGT CACAAG TGCC CACACTAT GGTGCCCCG CTGGTAAA GGTGTG CTG AGC
Original	315	CAGCCCTGGGCCATAAGTGTCCGCACTACGGCGCACCCCTGGTGAAGGCGTTCTGTCC
Optimized	375	CGT GGCCGCGT G CGT TG CCG TGG CATGGTGCT TGCTTTAACATCAGC ACCGGT GACCTG
Original	375	CGTGGTCGGGTGCGCTGCCCCTGGCACGGCGCCTGCTTCAACATCAGCACTGGGGACCTG
Optimized	435	GAG GATTTCC GGGCTGGAC AGCT GCACAAG TTT CAGGT AAA ATTGAGAAG GA AAAA
Original	435	GAGGACTTCCCTGGCCTGGACAGTCTACACAAGTTCCAGGTGAAGATTGAGAAGGAGAAG
Optimized	495	GTGTAC GTGCGT GCCAGCAAGCAG GGCGTG CAGCTGCAG CGTCG CA CCAA GTGATGGCC
Original	495	GTGTACGTCCGGGCCAGCAAGCAGGCCCTACAGCTGCAGCGAAGGACCAAGGTGATGGCC
Optimized	555	AAATGCATAG CCCCAGCGCGGGCTATAGC AGC AGCACCA AC GTG CTG ATTGTGGGT GCC
Original	555	AAGTGTATCTCTCCAAGTGCTGGGTACAGCAGTAGCACCAATGTGCTCATTGTGGGTGCA
Optimized	615	GGT GCTGCTGGT CTGGT TGCGCT GAAAC CTGCGC CAGGAAGGCTTC AGCGACCGT ATC
Original	615	GGTGCAGCTGGCCTGGTGTGTGCAGAGACACTGCGGCAGGAGGGCTTCTCCGACCGGATC
Optimized	675	GTGCTGTGC ACC CTGG AC CGT CAC CTGCC TAC GATCGTCCG AAG CTG AGC AAAAGC CTG
Original	675	GTCCGTGTGCACGCTAGACCGGCACCTTCCCTACGACCGTCCAAGCTCAGCAAGTCCCTG
Optimized	735	GATACC CAGCCAGAGCAGCTGGCCCT GCGCCG AAAGAGT TTCTTCCGTGCGTATGGTATT
Original	735	GACACACAGCCTGAGCAGCTGGCCCTGAGGCCCAAGGAGTTTTTCCGAGCCTATGGCATC
Optimized	795	GAGGTG CTG ACC GAA GCTCAGGT GTGACC GTGGACGT GCGACCA AG AAAGTGGT GTTC
Original	795	GAGGTGCTCACCAGGCTCAGGTGGTCACAGTGGACGTGAGAACTAAGAAGGTCGTGTTC
Optimized	855	AAGGATGGCT TTAA ACTGGAGTATAGC AA ACTGCTGCTG GGCC AG GTAGCAGCCG AAA
Original	855	AAGGATGGCTTCAAGCTGGAGTACAGCAAGCTGCTGCTGGCACCAAGGAGCAGCCCCAAG
Optimized	915	ACCCTGAGCTG CAAGGGCAAAGAGGT GGA AACGTGTT CACCATCCGTACCCG GAAAGAT
Original	915	ACTCTGAGCTGCAAGGGCAAAGAAGTGGAGAACGTGTTCACTATCCGGACGCCAGAGGAT

Optimized	975	GCTAACCGTGTGGTGGTCTGGCCCGCGGTCTAACGTGGTGGTGGTGGCGGGTTTT
Original	975	GCCAATCGCTGGTGAGGCTGGCCGAGGCCGCAACGTGGTCTGCTGGGAGCCGGCTTC
Optimized	1035	CTGGGCATGGAAGTGGCGGCTTACCTGACCGAAAGGCTCACAGCGTAGCGTGGTGGAG
Original	1035	CTGGGGATGGAGTGGCCGCTTACCTGACGGAGAAGGCCACTCTGTGTCTGTGGTGGAG
Optimized	1095	CTGGAGGAAACCCGTTCCGTCGGTTTTCTGGCGAGCGTGTGGTCTGTGCCCTGATGAAG
Original	1095	CTGGAGGAGACGCCCTTCAGGAGGTTCTGGGGGAGCGGTGGTCTGTGCCCTCATGAAG
Optimized	1155	ATGTTTCGAAAACAACCGCGTGAAGTTCTACATGCAGACCGAGGTGAGCGAACTGCGTGGT
Original	1155	ATGTTTGAGAACACCGGGTGAAGTTCTACATGCAGACGGAGGTGTCTGAGCTGCGGGGC
Optimized	1215	CAGGAAGGCAAGCTGAAAGAGGTGTGTGTAAGAGCAGCAAGGTGGTGGTGGCGGACGTG
Original	1215	CAGGAGGGAAAGCTGAAGGAGGTTGTGTGTAAGAGCAGCAAGGTGTGGCGGGCTGACGTC
Optimized	1275	TGCGTGGTGGGTATTGGTGGCGGTGCCGGTACCGGTTTCCTGCGTCAGAGCGGCATCGGT
Original	1275	TGCGTGGTGGGCATTGGTGCAGTGCCCGCCACAGGCTTCCTGAGGCAAAGCGGCATCGGT
Optimized	1335	CTGGATAGCCGTGGCTTTATTCGGTGAACAAGATGATGCAGACCAACGTGCCGGCGGTG
Original	1335	TTGGATTCCCGAGGCTTCATCCCTGTCAACAAGATGATGCAGACCAATGTCCAGGCGTG
Optimized	1395	TTCCGGGCGGCGACGCTGTGACCTTTCCGCTGGCCTGGCGCAACAACCGTAAAGTGAAC
Original	1395	TTTGACGTGGCGATGCTGTCACTTCCCCCTTGCTGGAGGAACAACCGCAAAGTGAAC
Optimized	1455	ATTCCGCACTGGCAGATGGCCATGCTCAGGGTCTGTGGTCTCAGAACATGCTGGCG
Original	1455	ATTCCACATTGGCAGATGGCTCATGCTCAGGGGCGCGTGGCAGCCAGAACATGTTGGCG
Optimized	1515	CAGGAAGCCGAAATGAGCACCGTGCCGTACCTGTGGACCGCCATGTTGGCAAGAGCCTG
Original	1515	CAGGAGGCGGAGATGAGCACTGTGCCCTACCTCTGGACCGCCATGTTTGGCAAGAGCCTG
Optimized	1575	CGTTACGCGGGCTATGGCGAGGGCTTTGACGATGTGATCATTAGGGTGACCTGGAGGAA
Original	1575	CGCTACGCGGGCTACGGAGAAGGCTTCGACGACGTATCATCCAGGGGGATCTGGAGGAG
Optimized	1635	CTGAAGTTCGTGGCTTTTACACCAAGGCGACGAAAGTATCGCCGTGGCGAGCATGAAC
Original	1635	CTGAAGTTTGTGGCTTTTACACTAAAGGCGACGAGGTATCGCCGTGGCCAGCATGAAC
Optimized	1695	TATGATCCGATTGTGAGCAAGTGGCTGAGGTGCTGGCCAGCGGTCTGCCATCCGTAAA
Original	1695	TACGATCCCATTTGTGTCGAAGTCCGCTGAGGTGCTGGCCTCAGGCCGTGCCATCCGGAAG
Optimized	1755	CGTGAAAGTGAACTGTTTGTGCTGATTCCAAAGACCGGCGATATGTCTGGCTGACCGGC

Original	1755	CGGGAGGTGGAGCTGTTTGTGCTGCACAGCAAGACTGGCGACATGTCCTGGCTTACGGGG
Optimized	1815	AAGGGTAGC
Original	1815	AAAGGATCC

Supplementary

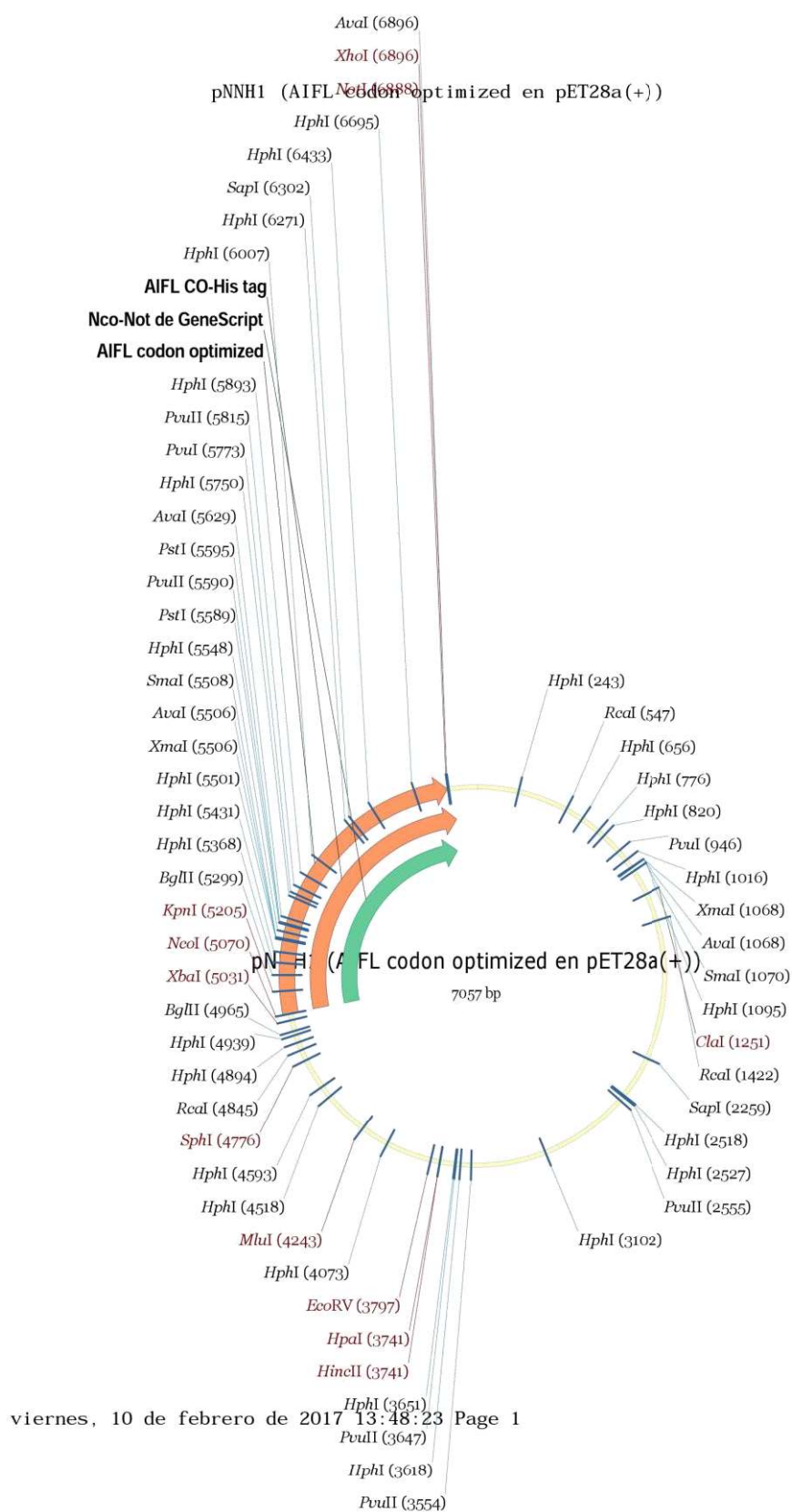
1. Protein Alignment (Optimized Region)

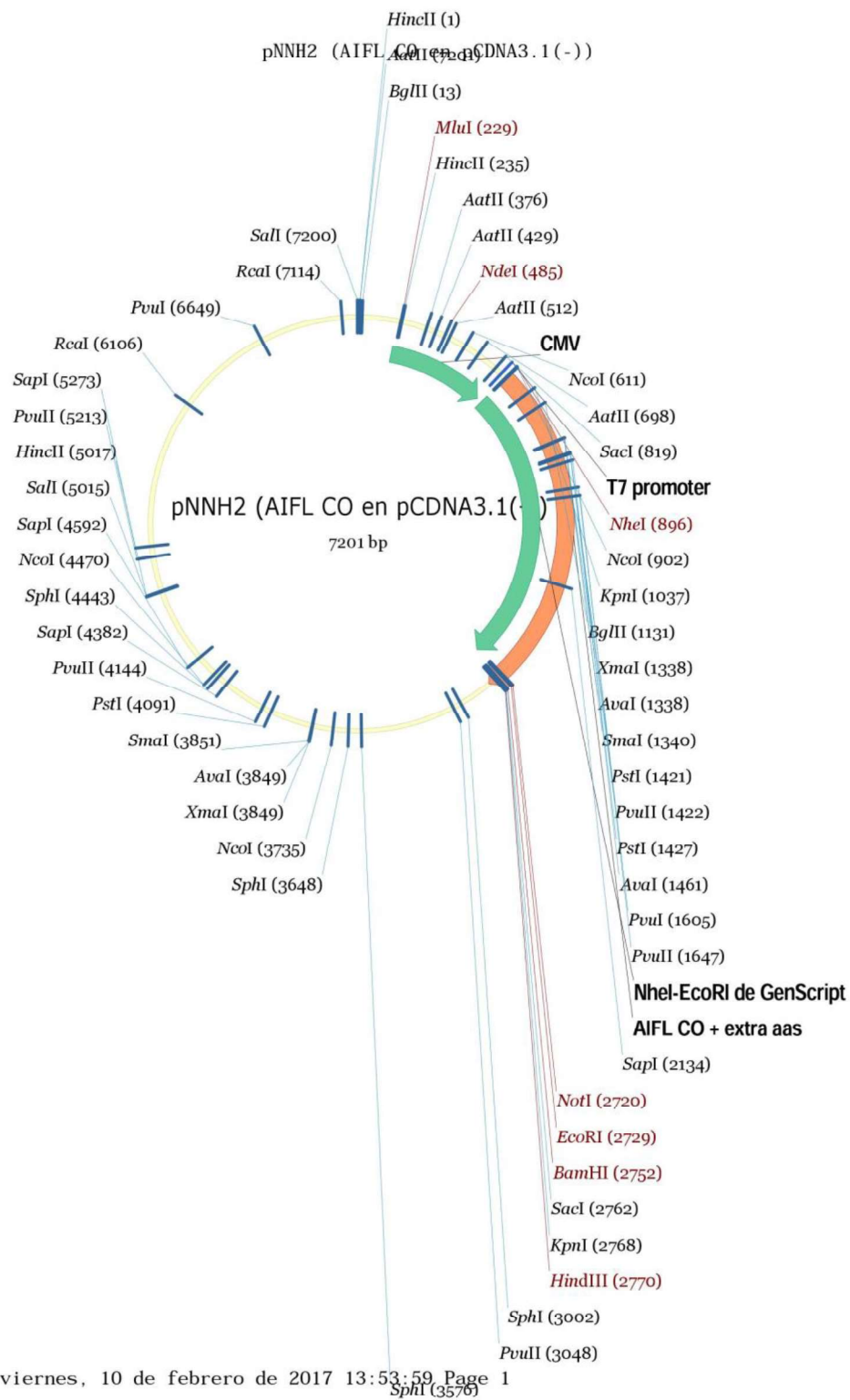
Optimized	1	GCFSKPKPVELKIEVVLPEKERGKEELSASGKGSPPRAYQNGTARHFHTEERLSTPHYP
Original	1	GCFSKPKPVELKIEVVLPEKERGKEELSASGKGSPPRAYQNGTARHFHTEERLSTPHYP
Optimized	61	SPQDCVEAAVCHVKDLENGQMREVELGWGKVLLVKDNGEFHALGHKCPHYGAPLVKGVLS
Original	61	SPQDCVEAAVCHVKDLENGQMREVELGWGKVLLVKDNGEFHALGHKCPHYGAPLVKGVLS
Optimized	121	RGRVRCPPWHGACFNISTGDLEDFPGLDSLHKFQVKIEKEKVYVRASKQALQLQRRTKVMA
Original	121	RGRVRCPPWHGACFNISTGDLEDFPGLDSLHKFQVKIEKEKVYVRASKQALQLQRRTKVMA
Optimized	181	KCISPSAGYSSSTNVLIVGAGAAGLVCAETLRQEGFSDRIVLCTLDRHLPYDRPKLSKSL
Original	181	KCISPSAGYSSSTNVLIVGAGAAGLVCAETLRQEGFSDRIVLCTLDRHLPYDRPKLSKSL
Optimized	241	DTQPEQLALRPKEFFRAYGIEVLTEAQVVTVDVRTKKVVKDGFKLEYSKLLAPGSSPK
Original	241	DTQPEQLALRPKEFFRAYGIEVLTEAQVVTVDVRTKKVVKDGFKLEYSKLLAPGSSPK
Optimized	301	TLCKGKEVENVFTIRTPEDANRVVRLARGRNVVVGAGFLGMEVAAYLTEKAHSVSVVE
Original	301	TLCKGKEVENVFTIRTPEDANRVVRLARGRNVVVGAGFLGMEVAAYLTEKAHSVSVVE
Optimized	361	LEETPFRRFLGERVGRALMKMFENNRVKFYMQTEVSELRGQEGKLEKVVLSKSKVVRADV
Original	361	LEETPFRRFLGERVGRALMKMFENNRVKFYMQTEVSELRGQEGKLEKVVLSKSKVVRADV
Optimized	421	CVVGIGAVPATGFLRQSGIGLDSRGFIPVNKMMQTNVPGVFAAGDAVTFPLAWRNNRKVN
Original	421	CVVGIGAVPATGFLRQSGIGLDSRGFIPVNKMMQTNVPGVFAAGDAVTFPLAWRNNRKVN
Optimized	481	IPHWQMAHAQGRVAAQNMLAQEAEMSTVPYLWTAMFGKSLRYAGYGEFDDVIIQGDLEE
Original	481	IPHWQMAHAQGRVAAQNMLAQEAEMSTVPYLWTAMFGKSLRYAGYGEFDDVIIQGDLEE
Optimized	541	LKFVAFYTKGDEVIAVASMNYDPIVSKVAEVLASGRAIRKREVELFVLHSGTGDMSWLTG
Original	541	LKFVAFYTKGDEVIAVASMNYDPIVSKVAEVLASGRAIRKREVELFVLHSGTGDMSWLTG
Optimized	601	KGS
Original	601	KGS

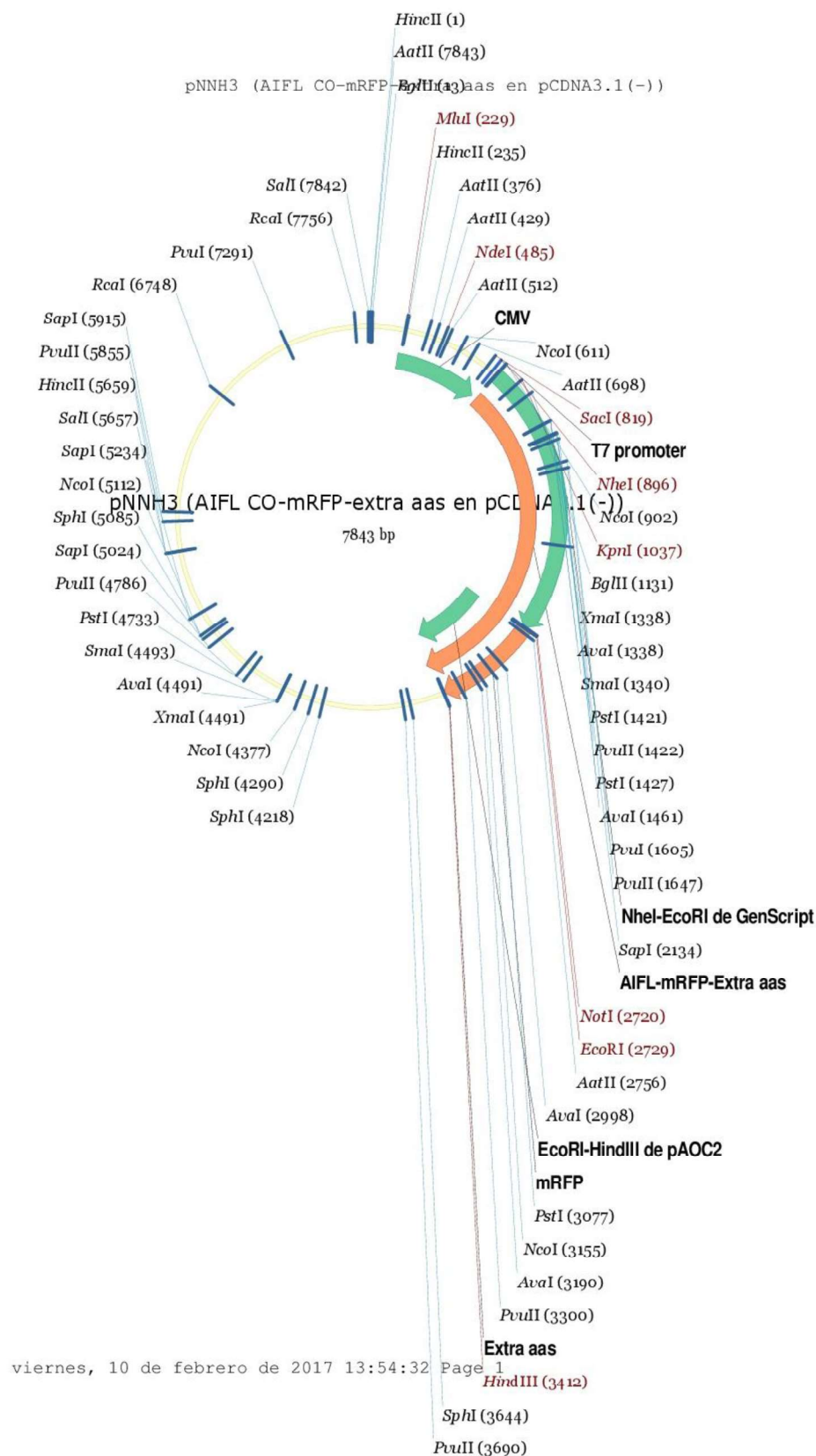
ANEXO IX – TABLA DE VECTORES EMPLEADOS

Nombre	Origen	Vector de origen	Marcador de resistencia bacteriana	Inserto/s	Digestión enzimática	Descripción
pET28a(+)	Sintético	pBR322	Kanamicina	-	-	Expresión en procariontes
pcDNA3.1(-)	Sintético	pcDNA	Ampicilina	-	-	Expresión en eucariotas
pX335	Sintético	pUC	Ampicilina	Cas9D10A gRNA scaffold	-	Expresión en mamíferos
pUC57-AIFL	Sintético + clonaje	pUC57	Ampicilina	AIFL	EcoRV	Clonaje del gen <i>aifm3</i>
pAOC2	Clonaje	pCMVMyc	Ampicilina	mRFP-TM VAMP ₂	EcoRI-HindIII	Clonaje del gen marcador <i>mRFP</i>
pNNH1	Clonaje	pET28a(+)	Kanamicina	AIFL	NcoI-NotI	Sobreexpresión del AIFL en procariontes
pNNH2	Clonaje	pcDNA3.1(-)	Ampicilina	AIFL	NheI-EcoRI	Sobreexpresión del AIFL en eucariotas
pNNH3	Clonaje	pNNH2	Ampicilina	mRFP	EcoRI-HindIII	Sobreexpresión del AIFL-mRFP en eucariotas
pNNH4	Clonaje	pX335	Ampicilina	KO-AIFL-UP	BbsI	Expresión de la nickasa y el gRNA1
pNNH5	Clonaje	pX335	Ampicilina	KO-AIFL-DWN	BbsI	Expresión de la nickasa y el gRNA2

ANEXO X – MAPAS GENERADOS CON EL PROGRAMA VECTOR NTI DE LOS PLÁSMIDOS pNNH₁, pNNH₂ Y pNNH₃







ANEXO XI – ALINEAMIENTO DE LAS SECUENCIAS DE LAS MUESTRAS DE pNNH₁ Y pNNH₂ CON SUS SECUENCIAS TEÓRICAS

pNNH ₁ .3P	-----
pNNH ₁	TGGCGAATGGGACGCGCCCTGTAGCGGCGCATTAAAGCGGGCGGGTGTGGTGGTTACGCG
pNNH ₁ .1P	-----
pNNH ₁ .5P	-----
pNNH ₁ .3P	-----
pNNH ₁	CAGCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTCGCTTCTTCCCTTC
pNNH ₁ .1P	-----
pNNH ₁ .5P	-----
pNNH ₁ .3P	-----
pNNH ₁	CTTCTCGCCACGTTGCGCGGCTTCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGG
pNNH ₁ .1P	-----
pNNH ₁ .5P	-----
pNNH ₁ .3P	-----
pNNH ₁	GTTCCGATTTAGTGCTTTACGGCACCTCGACCCAAAAAACTTGATTAGGGTGATGGTTC
pNNH ₁ .1P	-----
pNNH ₁ .5P	-----
pNNH ₁ .3P	-----
pNNH ₁	ACGTAGTGGGCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTT
pNNH ₁ .1P	-----
pNNH ₁ .5P	-----
pNNH ₁ .3P	-----
pNNH ₁	CTTTAATAGTGGACTCTTGTTCCAACTGGAACAACACTCAACCCTATCTCGGTCTATTC
pNNH ₁ .1P	-----
pNNH ₁ .5P	-----
pNNH ₁ .3P	-----
pNNH ₁	TTTTGATTATAAGGGATTTTGCCGATTTGCGCTATTGGTTAAAAAATGAGCTGATTTA
pNNH ₁ .1P	-----
pNNH ₁ .5P	-----
pNNH ₁ .3P	-----
pNNH ₁	ACAAAAATTTAACGCGAATTTTAACAAATATTAACGTTTACAATTCAGGTGGCACTTT
pNNH ₁ .1P	-----
pNNH ₁ .5P	-----
pNNH ₁ .3P	-----
pNNH ₁	TCGGGGAAATGTGCGCGGAACCCCTATTTGTTATTTTCTAAATACATTCAAATATGTA
pNNH ₁ .1P	-----
pNNH ₁ .5P	-----
pNNH ₁ .3P	-----
pNNH ₁	TCCGCTCATGAATTAATCTTAGAAAACTCATCGAGCATCAATGAACTGCAATTTAT
pNNH ₁ .1P	-----
pNNH ₁ .5P	-----
pNNH ₁ .3P	-----
pNNH ₁	TCATATCAGGATTATCAATACCATATTTTGAAGGAGCCGTTCTGTAATGAAGGAGAAA
pNNH ₁ .1P	-----
pNNH ₁ .5P	-----
pNNH ₁ .3P	-----
pNNH ₁	ACTCACCGAGGCAGTTCCATAGGATGGCAAGATCCTGGTATCGGTCTGCGATTCCGACTC
pNNH ₁ .1P	-----
pNNH ₁ .5P	-----

pNNH1 . 3P	-----
pNNH1	GTCCAACATCAATACAACCTATTAATTTCCCTCGTCAAAAATAAGGTTATCAAGTGAGA
pNNH1 . 1P	-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	AATCACCATGAGTGACGACTGAATCCGGTGAGAATGGCAAAAGTTTATGCATTCTTTCC
pNNH1 . 1P	-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	AGACTTGTTCAACAGGCCAGCCATTACGCTCGTCATCAAAATCACTCGCATCAACCAAAC
pNNH1 . 1P	-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	CGTTATTCATTCGTGATTGCGCCTGAGCGAGACGAAATACGCGATCGCTGTTAAAAGGAC
pNNH1 . 1P	-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	AATTACAAACAGGAATCGAATGCAACCGGCGCAGGAACACTGCCAGCGCATCAACAATAT
pNNH1 . 1P	-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	TTTCACCTGAATCAGGATATTCCTTAATACCTGGAATGCTGTTTTCCCGGGATCGCAG
pNNH1 . 1P	-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	TGGTGAGTAACCATGCATCATCAGGAGTACGGATAAAATGCTTGATGGTCGGAAGAGGCA
pNNH1 . 1P	-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	TAAATCCGTCAGCCAGTTTAGTCTGACCATCTCATCTGTAACATCATTGGCAACGCTAC
pNNH1 . 1P	-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	CTTTGCCATGTTTCAGAAACAACTCTGGCGCATCGGGCTTCCCATACAATCGATAGATTG
pNNH1 . 1P	-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	TCGCACCTGATTGCCCCGACATTATCGCGAGCCCATTTATACCCATATAAATCAGCATCCA
pNNH1 . 1P	-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	TGTTGGAATTTAATCGCGGCCTAGAGCAAGACGTTTCCCGTTGAATATGGCTCATAACAC
pNNH1 . 1P	-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	CCCTTGATTACTGTTTATGTAAGCAGACAGTTTTATTGTTTCATGACCAAAATCCCTTAA
pNNH1 . 1P	-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	CGTGAGTTTTCGTTCCTGAGCGTCAGACCCCGTAGAAAAAGATCAAAGGATCTTCTTGA
pNNH1 . 1P	-----
pNNH1 . 5P	-----

pNNH1.3P	-----
pNNH1	GATCCTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAACACCGCTACCAGCG
pNNH1.1P	-----
pNNH1.5P	-----
pNNH1.3P	-----
pNNH1	GTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTCCGAAGGTAACGGCTTCAGC
pNNH1.1P	-----
pNNH1.5P	-----
pNNH1.3P	-----
pNNH1	AGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAG
pNNH1.1P	-----
pNNH1.5P	-----
pNNH1.3P	-----
pNNH1	AACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAAGTGGCTGCTGCC
pNNH1.1P	-----
pNNH1.5P	-----
pNNH1.3P	-----
pNNH1	AGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCG
pNNH1.1P	-----
pNNH1.5P	-----
pNNH1.3P	-----
pNNH1	CAGCGGTCGGGCTGAACGGGGGTTCTGTGCACACAGCCAGCTTGGAGCGAACGACCTAC
pNNH1.1P	-----
pNNH1.5P	-----
pNNH1.3P	-----
pNNH1	ACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGA
pNNH1.1P	-----
pNNH1.5P	-----
pNNH1.3P	-----
pNNH1	AAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTT
pNNH1.1P	-----
pNNH1.5P	-----
pNNH1.3P	-----
pNNH1	CCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTGCGGGTTTCGCCACCTCTGACTTGAG
pNNH1.1P	-----
pNNH1.5P	-----
pNNH1.3P	-----
pNNH1	CGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCG
pNNH1.1P	-----
pNNH1.5P	-----
pNNH1.3P	-----
pNNH1	GCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTCTGCGTTA
pNNH1.1P	-----
pNNH1.5P	-----
pNNH1.3P	-----
pNNH1	TCCCTGATTCTGTGGATAACCGTATTACCGCCTTTGAGTGAGCTGATACCGCTCGCCGC
pNNH1.1P	-----
pNNH1.5P	-----
pNNH1.3P	-----
pNNH1	AGCCGAACGACCGAGCGCAGCGAGTCAGTGAGCGAGGAAGCGGAAGAGCGCCTGATGCGG
pNNH1.1P	-----
pNNH1.5P	-----

pNNH1 . 3P	-----
pNNH1	TATTTTCTCCTTACGCATCTGTGCGGTATTTACACCGCATATATGGTGCACTCTCAGTA
pNNH1 . 1P	-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	CAATCTGCTCTGATGCCGCATAGTTAAGCCAGTATACACTCCGCTATCGCTACGTGACTG
pNNH1 . 1P	-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	GGTCATGGCTGCGCCCCGACACCCGCCAACACCCGCTGACGCGCCCTGACGGGCTTGTCT
pNNH1 . 1P	-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	GCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGCTGCATGTGTCAGAG
pNNH1 . 1P	-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	GTTTTACCGTCATCACCGAAACGCGGAGGCAGCTGCGGTAAAGCTCATCAGCGTGGTC
pNNH1 . 1P	-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	GTGAAGCGATTACAGATGTCTGCCTGTTTCATCCGCGTCCAGCTCGTTGAGTTTCTCCAG
pNNH1 . 1P	-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	AAGCGTTAATGTCTGGCTTCTGATAAAGCGGGCCATGTTAAGGGCGGTTTTTCCTGTTT
pNNH1 . 1P	-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	GGTCACTGATGCCTCCGTGTAAGGGGGATTCTGTTTCATGGGGTAATGATACCGATGAA
pNNH1 . 1P	-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	ACGAGAGAGGATGCTCACGATACGGGTTACTGATGATGAACATGCCCGGTTACTGGAACG
pNNH1 . 1P	-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	TTGTGAGGGTAAACAAC TGGCGGTATGGATGCGGCGGGACCAGAGAAAAATCACTCAGGG
pNNH1 . 1P	-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	TCAATGCCAGCGCTTCGTTAATACAGATGTAGGTGTTCCACAGGGTAGCCAGCAGCATCC
pNNH1 . 1P	-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	TGCGATGCAGATCCGGAACATAATGGTGCAGGGCGCTGACTTCCGCGTTTCCAGACTTTA
pNNH1 . 1P	-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	CGAAACACGGAAACCGAAGACCATTTCATGTTGTTGCTCAGGTCGCAGACGTTTTGCAGCA
pNNH1 . 1P	-----
pNNH1 . 5P	-----

pNNH1.3P	-----
pNNH1	GCAGTCGCTTCACGTTTCGCTCGCGTATCGGTGATTTCATTCTGCTAACCAAGGCAACC
pNNH1.1P	-----
pNNH1.5P	-----
pNNH1.3P	-----
pNNH1	CCGCCAGCCTAGCCGGGTCTCAACGACAGGAGCACGATCATGCGCACCCGTGGGGCCGC
pNNH1.1P	-----
pNNH1.5P	-----
pNNH1.3P	-----
pNNH1	CATGCCGGCGATAATGGCCTGCTTCTCGCCGAAACGTTTGGTGGCGGGACCAAGTGACGAA
pNNH1.1P	-----
pNNH1.5P	-----
pNNH1.3P	-----
pNNH1	GGCTTGAGCGAGGGCGTGAAGATTCCGAATACCGCAAGCGACAGGCCGATCATCGTCGC
pNNH1.1P	-----
pNNH1.5P	-----
pNNH1.3P	-----
pNNH1	GCTCCAGCGAAAGCGGTCTCGCCGAAAATGACCCAGAGCGCTGCCGGCACCTGTCCTAC
pNNH1.1P	-----
pNNH1.5P	-----
pNNH1.3P	-----
pNNH1	GAGTTGCATGATAAAGAAGACAGTCATAAGTGCGGCGACGATAGTCATGCCCCGCGCCA
pNNH1.1P	-----
pNNH1.5P	-----
pNNH1.3P	-----
pNNH1	CCGGAAGGAGCTGACTGGGTTGAAGGCTCTCAAGGGCATCGGTGAGATCCCGGTGCCTA
pNNH1.1P	-----
pNNH1.5P	-----
pNNH1.3P	-----
pNNH1	ATGAGTGAGCTAAGTTACATTAATTGCGTTGCGCTCACTGCCCGCTTTCAGTCGGGAAA
pNNH1.1P	-----
pNNH1.5P	-----
pNNH1.3P	-----
pNNH1	CCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCCTAT
pNNH1.1P	-----
pNNH1.5P	-----
pNNH1.3P	-----
pNNH1	TGGGCGCCAGGGTGGTTTTCTTTTACCAGTGAGACGGGCAACAGCTGATTGCCCTTCA
pNNH1.1P	-----
pNNH1.5P	-----
pNNH1.3P	-----
pNNH1	CCGCCTGGCCCTGAGAGAGTTGCAGCAAGCGGTCCACGCTGGTTTGCCCAGCAGGCGAA
pNNH1.1P	-----
pNNH1.5P	-----
pNNH1.3P	-----
pNNH1	AATCCTGTTTGATGGTGGTTAACGGCGGGATATAACATGAGCTGTCTTCGGTATCGTCGT
pNNH1.1P	-----
pNNH1.5P	-----
pNNH1.3P	-----
pNNH1	ATCCCACTACCGAGATATCCGCACCAACGCGCAGCCCGGACTCGGTAATGGCGCGCATTG
pNNH1.1P	-----
pNNH1.5P	-----
pNNH1.3P	-----
pNNH1	CGCCAGCGCCATCTGATCGTTGGCAACCAAGCATCGCAGTGGGAACGATGCCCTCATTCA
pNNH1.1P	-----
pNNH1.5P	-----

pNNH1 . 3P	-----
pNNH1	GCATTTGCATGGTTTGTGAAAACCGGACATGGCACTCCAGTCGCCTTCCCGTTCCGCTA
pNNH1 . 1P	-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	TCGGCTGAATTTGATTGCGAGTGAGATATTTATGCCAGCCAGCCAGACGCAGACGCGCCG
pNNH1 . 1P	-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	AGACAGAACTTAATGGGCCCGCTAACAGCGCGATTTGCTGGTGACCCAATGCGACCAGAT
pNNH1 . 1P	-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	GCTCCACGCCAGTCGCGTACCGTCTTCATGGGAGAAAATAATACTGTTGATGGGTGTCT
pNNH1 . 1P	-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	GGTCAGAGACATCAAGAAATAACGCCGGAACATTAGTGCAGGCAGCTTCCACAGCAATGG
pNNH1 . 1P	-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	CATCCTGGTCATCCAGCGGATAGTTAATGATCAGCCCACTGACGCGTTGCGCGAGAAGAT
pNNH1 . 1P	-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	TGTGCACCGCCGCTTACAGGCTTCGACGCCGCTTCGTTCTACCATCGACACCACCACGC
pNNH1 . 1P	-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	TGGCACCCAGTTGATCGGCGCGAGATTTAATCGCCGCGACAATTTGCGACGGCGCGTGCA
pNNH1 . 1P	-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	GGGCCAGACTGGAGGTGGCAACGCCAATCAGCAACGACTGTTTGCCCGCCAGTTGTTGTG
pNNH1 . 1P	-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	CCACGCGGTTGGGAATGTAATTCAGCTCCGCCATCGCCGCTTCCACTTTTTCCCGCGTTT
pNNH1 . 1P	-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	TCGCAGAAACGTGGCTGGCCTGGTTCACCACGCGGAAACGGTCTGATAAGAGACACCGG
pNNH1 . 1P	-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	CATACTCTGCGACATCGTATAACGTTACTGGTTTCACATTCACCACCCTGAATTGACTCT
pNNH1 . 1P	-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	CTTCCGGGCGCTATCATGCCATACCGCGAAAGGTTTGCGCCATTTCGATGGTGTCGGGA
pNNH1 . 1P	-----
pNNH1 . 5P	-----

pNNH1 . 3P	-----
pNNH1	CCGTGGCATGGTGCTTGTCTTAAACATCAGCACCGGTGACCTGGAGGATTTCCTGGGCCTG
pNNH1 . 1P	CCGTGGCATGGTGCTTGTCTTAAACATCAGCACCGGTGACCTGGAGGATTTCCTGGGCCTG
pNNH1 . 5P	CTATGGCATGGCGCTTGTCTTAAATATCATCCCC-----
pNNH1 . 3P	-----
pNNH1	GACAGCCTGCACAAGTTTCAGGTGAAAATTGAGAAGGAAAAAGTGACGTGCGTGCCAGC
pNNH1 . 1P	GACAGCCTGCACAAGTTTCAGGTGAAAATTGAGAAGGAAAAAGTGACGTGCGTGCCAGC
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	AAGCAGGCGCTGCAGCTGCAGCGTCGCACCAAAGTGATGGCCAAATGCATCAGCCCGAGC
pNNH1 . 1P	AAGCAGGCGCTGCAGCTGCAGCGTCGCACCAAAGTGATGGCCAAATGCATCAGCCCGAGC
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	GCGGGCTATAGCAGCAGCACCAACGTGCTGATTGTGGGTGCCGGTGCTGCTGGTCTGGTG
pNNH1 . 1P	GCGGGCTATAGCAGCAGCACCAACGTGCTGATTGTGGGTGCCGGTGCTGCTGGTCTGGTG
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	TGCGCTGAAACCTGCGCCAGGAAGGCTTCAGCGACCGTATCGTGCTGTCACCCCTGGAC
pNNH1 . 1P	TGCGCTGAAACCTGCGCCAGGAAGGCTTCAGCGACCGTATCGTGCTGTCACCCCTGGAC
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	CGTCACCTGCCGTACGATCGTCCGAAGCTGAGCAAAAGCCTGGATACCCAGCCAGAGCAG
pNNH1 . 1P	CGTCACCTGCCGTACGATCGTCCGAAGCTGANCAAAAGCCTGGATACCCAGCCAGAGCAG
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	CTGGCCCTGCGCCGAAAGAGTTCTTCCGTGCGTATGGT-ATTGAGGTGCTGACCGAAGC
pNNH1 . 1P	CTGGCCCTGCGCCGAAAGAGTTCTTCCGTGCGTATGGGTATTGAGGTGCTGACCNAAAGC
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	TCAGGTGGTGACCGTGGACGTGCGCA-CCAAGA-AAGTGGT-GTTCAAGGATGGCTTTAA
pNNH1 . 1P	TCANGTGGTGACCGTGGGACGTGCGCACCAAGAAAGTGGTGTCAAGGGATGGCTTTAA
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	ACTGGAGTATAG-CAAAGTGTGCTGGCGCCAGGTAGCAGCCGAAACCTGAGCTGCA
pNNH1 . 1P	NCTGGAGTATNNCAAAAGTGTGCTGGCGCCAGNTANCAAGCCNAAAACCTGAGCTGC
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	AGGGCAAGAGGTGGAAAACGTGTTACCATCCGTACCCCGGAAG-ATGCTAACCGTGTG
pNNH1 . 1P	AAGGGCAANAGTGGAAAACGTGTTACCATCCGTACCCCGGAGGATGCTAACCGNGTG
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	GTGCGT-CTGGCCCGCGGTCTAACGTG-GTGGTGGTGG-GCGCGGGTTTTTC-TGGGCAT
pNNH1 . 1P	GTGGCGTCTGGNCNGCGNTCGTAANNNGTGGTGGTGGTGAGNCGCGGNTNTCTTGGGNNT
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	GGAAGTGGCGGCTTACCTGACCGAAAAGGCTCACAG--CGTGAGCGTGGTGGAGCTGGAG
pNNH1 . 1P	GGAANNNGNNCNTTACNGAACCGAANAGANNNNNNNCTNNNNCNTTGGNNNANCTGGNN
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	GAAACCCCGTTCCGTGCTTTCTGGGCGAGCGTGTGGGTGCTGCCCTGATGAA----GA
pNNH1 . 1P	NGAANCNCGNTTCGNNTTNTCNGAGGNNANNGCANNNGNGACTNNGNNNNNNNTGANN
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	TGTTTGAAACAACCGCGTGAAGTTCATATGCAGACCGAGGTGAGCGAACTGCGTGGTC
pNNH1 . 1P	GNTTCNNNNNNAACNNNNNNNGTTNNNNNTNNNNNNNNC-----
pNNH1 . 5P	-----

pNNH1 . 3P	-----
pNNH1	AGGAAGGCAAGCTGAAAGAGGTGGTGCTGAAGAGCAGCAAAGTGGTGCGTGCCGACGTGT
pNNH1 . 1P	-----NNNNNGNNNNTCGNCGTA-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	GCGTGGTGGGTATTGGTGCGGTGCCGGCTACCGGTTTCCTGCGTCAGAGCGGCATCGGTC
pNNH1 . 1P	-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	TGGATAGCCGTGGCTTTATTCCGGTGAACAAGATGATGCAGACCAACGTGCCGGGCGTGT
pNNH1 . 1P	-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	TCGCGGCCGGCGACGCTGTGACCTTTCGCTGGCCTGGCGCAACAACCGTAAAGTGAACA
pNNH1 . 1P	-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	TTCCGCACTGGCAGATGGCCCATGCTCAGGGTCGTGTGGCTGCTCAGAACATGCTGGCGC
pNNH1 . 1P	-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	AGGAAGCCGAAATGAGCACCGTGCCGTACCTGTGGACCGCCATGTTCCGGCAAGAGCCTGC
pNNH1 . 1P	-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	GTTACGCGGGCTATGGCGAGGGCTTTGACGATGTGATCATTAGGGTGACCTGGAGGAAC
pNNH1 . 1P	-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	TGAAGTTCGTGGCCTTTTACACCAAAGGCGACGAAGTGATCGCCGTGGCGAGCATGAACT
pNNH1 . 1P	-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	ATGATCCGATTGTGAGCAAAGTGGCTGAGGTGCTGGCCAGCGGTCTGTCATCCGTAAAC
pNNH1 . 1P	-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	GTGAAGTGGAAGTGTGCTGCTGCAATCCAAAGACCGCGATATGTCCTGGCTGACCGGCA
pNNH1 . 1P	-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	AGGGTAGCGCGGCCGCACTCGAGCACCACCACCACCACCTGAGATCCGGCTGCTAACA
pNNH1 . 1P	-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	AAGCCCGAAAGGAAGCTGAGTTGGCTGCTGCCACCGCTGAGCAATAACTAGCATAACCCC
pNNH1 . 1P	-----
pNNH1 . 5P	-----
pNNH1 . 3P	-----
pNNH1	TTGGGGCCTCTAAACGGGTCTTGAGGGGTTTTTGTCTGAAAGGAGGAACATATCCGGAT
pNNH1 . 1P	-----
pNNH1 . 5P	-----

pNNH1	TGGCGAATGGGACGCGCCCTGTAGCGGCGCATTAAAGCGGGCGGGTGTGGTGGTTACGCG
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	CAGCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTCGCTTTCTTCCCTTC
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	CTTCTCGCCACGTTGCGCGGCTTTCCCGTCAAGCTCTAAATCGGGGGCTCCCTTAGG
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	GTTCCGATTAGTGCTTTACGGCACCTCGACCCCAAAAACTTGATTAGGGTGATGGTTC
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	ACGTAGTGGGCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTT
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	CTTTAATAGTGGACTCTTGTTCCAACTGGAACAACACTCAACCCTATCTCGGTCTATTC
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	TTTTGATTATAAGGGATTTTGCCGATTTGCGCTATTGGTTAAAAATGAGCTGATTTA
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	ACAAAAATTTAACGCGAATTTTAACAAAATATTAACGTTTACAATTTAGGTGGCACTTT
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	TCGGGGAATGTGCGCGGAACCCCTATTTGTTATTTTCTAAATACATTCAAATATGTA
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	TCCGCTCATGAATTAATCTTAGAAAACTCATCGAGCATCAAATGAAACTGCAATTTAT
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	TCATATCAGGATTATCAATACCATATTTTGAAGCCGTTTCTGTAATGAAGGAGAAA
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	ACTCACCAGGCGAGTTCCATAGGATGGCAAGATCCTGGTATCGGTCTGCGATTCCGACTC
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	GTCCAACATCAATACAACCTATTAATTTCCCTCGTCAAAAATAAGGTTATCAAGTGAGA
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	AATCACCATGAGTGACGACTGAATCCGGTGAGAATGGCAAAAGTTTATGCATTTCTTTCC
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----

pNNH1	AGACTTGTTC AACAGGCCAGCCATTACGCTCGTCATCAAAATCACTCGCATCAACCAAAC
pNNH1 . 3T	-----
pNNH1 . 1T	-----
pNNH1 . 5T	-----
pNNH1	CGTTATTCATTCTGATTGCGCCTGAGCGAGACGAAATACGCGATCGCTGTTAAAAGGAC
pNNH1 . 3T	-----
pNNH1 . 1T	-----
pNNH1 . 5T	-----
pNNH1	AATTACAAACAGGAATCGAATGCAACCGGCGCAGGAACACTGCCAGCGCATCAACAATAT
pNNH1 . 3T	-----
pNNH1 . 1T	-----
pNNH1 . 5T	-----
pNNH1	TTTCACCTGAATCAGGATATTCTTCTAATACCTGGAATGCTGTTTTCCCGGGGATCGCAG
pNNH1 . 3T	-----
pNNH1 . 1T	-----
pNNH1 . 5T	-----
pNNH1	TGGTGAGTAACCATGCATCATCAGGAGTACGGATAAAATGCTTGATGGTCGGAAGAGGCA
pNNH1 . 3T	-----
pNNH1 . 1T	-----
pNNH1 . 5T	-----
pNNH1	TAAATTCGGTCAGCCAGTTTAGTCTGACCATCTCATCTGTAACATCATTGGCAACGCTAC
pNNH1 . 3T	-----
pNNH1 . 1T	-----
pNNH1 . 5T	-----
pNNH1	CTTTGCCATGTTTCAGAAACAACTCTGGCGCATCGGGCTTCCCATACAATCGATAGATTG
pNNH1 . 3T	-----
pNNH1 . 1T	-----
pNNH1 . 5T	-----
pNNH1	TCGCACCTGATTGCCCGACATTATCGCGAGCCATTTATACCCATATAAATCAGCATCCA
pNNH1 . 3T	-----
pNNH1 . 1T	-----
pNNH1 . 5T	-----
pNNH1	TGTTGGAATTTAATCGCGCCTAGAGCAAGACGTTTCCCGTTGAATATGGCTCATAACAC
pNNH1 . 3T	-----
pNNH1 . 1T	-----
pNNH1 . 5T	-----
pNNH1	CCCTGTATTACTGTTTATGTAAGCAGACAGTTTATTGTTTCATGACCAAAATCCCTTAA
pNNH1 . 3T	-----
pNNH1 . 1T	-----
pNNH1 . 5T	-----
pNNH1	CGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGA
pNNH1 . 3T	-----
pNNH1 . 1T	-----
pNNH1 . 5T	-----
pNNH1	GATCCTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAACCACCGCTACCAGCG
pNNH1 . 3T	-----
pNNH1 . 1T	-----
pNNH1 . 5T	-----
pNNH1	GTGGTTTGTGGCCGGATCAAGAGCTACCAACTCTTTTCCGAAGGTAAGTGGCTTCAGC
pNNH1 . 3T	-----
pNNH1 . 1T	-----
pNNH1 . 5T	-----
pNNH1	AGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAG
pNNH1 . 3T	-----
pNNH1 . 1T	-----
pNNH1 . 5T	-----

pNNH1	TCGCGCTCCAGCGAAAGCGGTCTCGCCGAAAATGACCCAGAGCGCTGCCGGCACCTGTC
pNNH1 . 3T	-----
pNNH1 . 1T	-----
pNNH1 . 5T	-----
pNNH1	CTACGAGTTGCATGATAAAGAAGACAGTCATAAGTGCGGGACGATAGTCATGCCCCGCG
pNNH1 . 3T	-----
pNNH1 . 1T	-----
pNNH1 . 5T	-----
pNNH1	CCCACCGGAAGGAGCTGACTGGGTTGAAGGCTCTCAAGGGCATCGGTCGAGATCCCGGTG
pNNH1 . 3T	-----
pNNH1 . 1T	-----
pNNH1 . 5T	-----
pNNH1	CCTAATGAGTGAGCTAACTTACATTAATTGCGTTGCGCTCACTGCCCGCTTCCAGTCGG
pNNH1 . 3T	-----
pNNH1 . 1T	-----
pNNH1 . 5T	-----
pNNH1	GAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGC
pNNH1 . 3T	-----
pNNH1 . 1T	-----
pNNH1 . 5T	-----
pNNH1	GTATTGGGCGCCAGGGTGGTTTTCTTTTACCAGTGAGACGGGCAACAGCTGATTGCCC
pNNH1 . 3T	-----
pNNH1 . 1T	-----
pNNH1 . 5T	-----
pNNH1	TTCACCGCTGGCCCTGAGAGAGTTGCAGCAAGCGGTCCACGCTGGTTGCCCCAGCAGG
pNNH1 . 3T	-----
pNNH1 . 1T	-----
pNNH1 . 5T	-----
pNNH1	CGAAAATCCTGTTTGATGGTGGTTAACGGCGGGATATAACATGAGCTGTCTTCGGTATCG
pNNH1 . 3T	-----
pNNH1 . 1T	-----
pNNH1 . 5T	-----
pNNH1	TCGTATCCCACTACCGAGATATCCGCACCAACGCGCAGCCCGACTCGGTAATGGCGCGC
pNNH1 . 3T	-----
pNNH1 . 1T	-----
pNNH1 . 5T	-----
pNNH1	ATTGCGCCAGCGCCATCTGATCGTTGGCAACCAGCATCGCAGTGGGAACGATGCCCTCA
pNNH1 . 3T	-----
pNNH1 . 1T	-----
pNNH1 . 5T	-----
pNNH1	TTCAGCATTTGCATGGTTTGTGAAAACCGGACATGGCACTCCAGTCGCCTTCCCGTTCC
pNNH1 . 3T	-----
pNNH1 . 1T	-----
pNNH1 . 5T	-----
pNNH1	GCTATCGGCTGAATTTGATTGCGAGTGAGATATTTATGCCAGCCAGCCAGACGACGCG
pNNH1 . 3T	-----
pNNH1 . 1T	-----
pNNH1 . 5T	-----
pNNH1	GCCGAGACAGAACTTAATGGGCCCGCTAACAGCGGATTTGCTGGTGACCCAATGCGACC
pNNH1 . 3T	-----
pNNH1 . 1T	-----
pNNH1 . 5T	-----
pNNH1	AGATGCTCCACGCCAGTCGCGTACCGTCTTCATGGGAGAAAATAATACTGTTGATGGGT
pNNH1 . 3T	-----
pNNH1 . 1T	-----
pNNH1 . 5T	-----

pNNH1	GTCTGGTCAGAGACATCAAGAAATAACGCCGGAACATTAGTGCAGGCAGCTTCCACAGCA
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	ATGGCATCCTGGTCATCCAGCGGATAGTTAATGATCAGCCCACTGACGCGTTGCGCGAGA
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	AGATTGTGCACCGCCGCTTTACAGGCTTCGACGCGCTTCGTTCTACCATCGACACCACC
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	ACGCTGGCACCCAGTTGATCGGCGCGAGATTTAATCGCCGCGACAATTTGCGACGGCGCG
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	TGCAGGGCCAGACTGGAGGTGGCAACGCCAATCAGCAACGACTGTTTGCCCGCCAGTTGT
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	TGTGCCACGCGGTTGGGAATGTAATTCAGCTCCGCCATCGCCGCTTCCACTTTTCCCGC
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	GTTTTCGCAGAAACGTGGCTGGCTGGTTCAACACGCGGGAAACGGTCTGATAAGAGACA
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	CCGGCATACTCTGCGACATCGTATAACGTTACTGGTTTCACATTACCACCCTGAATTGA
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	CTCTCTCCGGGCGCTATCATGCCATACCGCGAAAGGTTTTGCGCCATTTCGATGGTGTCC
pNNH1.3T	-----
pNNH1.1T	-----TTGCCGAACATGGCGGT----
pNNH1.5T	-----TTGCCGAACATGGCGGT----
pNNH1	GGGATCTCGACGCTCTCCCTTATGCGACTCCTGCATTAGGAAGCAGCCCAGTAGTAGGTT
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	GAGGCCGTTGAGCACCGCCGCGCAAGGAATGGTGATGCAAGGAGATGGCGCCCAACAG
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	TCCCCGGCCACGGGGCTGCCACCATACCCACGCCGAAACAAGCGCTCATGAGCCCGAA
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	GTGGCGAGCCCGATCTTCCCATCGGTGATGTCGGCGATATAGGCGCCAGCAACCGCACC
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	TGTGGCGCCGGTGATGCCGGCCACGATGCGTCCGGCGTAGAGGATCGAGATCTCGATCCC
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----

pNNH1	GCGAAATTAATACGACTCACTATAGGGGAATTGTGAGCGGATAACAATTCCCCTCTAGAA
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	ATAATTTTGTTTAACTTTAAGAAGGAGATATACCATGGGCGGTTGTTTCTCCAAGCCGAA
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	GCCAGTGGAACGAAGATTGAGGTGGTGCTGCCGGAAGGAACGTGGTAAAGAGGAACT
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	GAGCGCAAGCGCAAGGGTAGCCCGCGCGCTACCAGGGTAATGGTACCGCTCGCCACTT
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	CCACACCGAGGAACGTCTGAGCACCCCGCACCCATATCCGAGCCCGCAGGACTGCGTGGA
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	GGCGGCGGTGTGCCACGTGAAAGATCTGGAACCGGTGAGTGCCTGAGGTGGAAGTGGG
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	CTGGGGCAAGGTGCTGCTGGTGAAAGATAACGGCGAGTTCACGCTCTGGGTACAAAGTG
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	CCCACACTATGGTGCCCGCTGGTGAAAGGTGTGCTGAGCCGTGGCCGCTGCGTTGCCC
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	GTGGCATGGTGCTTGCTTTAACATCAGCACCGGTGACCTGGAGGATTTCCCGGGCTGGA
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	CAGCCTGCACAAGTTTCAGGTGAAAATTGAGAAGGAAAAAGTGTACGTGCGTGCCAGCAA
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	GCAGGCGCTGCAGCTGCAGCGTCGACCAAAGTGATGGCCAAATGCATCAGCCCGAGCGC
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	GGGCTATAGCAGCAGCACCAACGTGCTGATTGTGGGTGCCGGTGCTGCTGGTCTGGTGTG
pNNH1.3T	-----
pNNH1.1T	-----CCACAGGTACGGCACGGTGCTCATTTGCGCTTCTGCGCC---AGCATGTTCTG
pNNH1.5T	-----CCACAGGTACGGCACGGTGCTCATTTGCGCTTCTGCGCC---AGCATGTTCTG
pNNH1	CGCTGAAACCCTGCGCCAGGAAGGCTTCAGCGACCGTATCGTGCTGTGCACCCTGGACCG
pNNH1.3T	-----
pNNH1.1T	AGCAGCCACAC-----
pNNH1.5T	AGCAGCCACAC-----
pNNH1	TCACCTGCCGTACGATCGTCCGAAGCTGAGCAAAAGCCTGGATACCCAGCCAGAGCAGCT
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----

pNNH1	GGCCCTGCGCCCGAAAGAGTTCTTCCGTGCGTATGGTATTGAGGTGCTGACCGAAGCTCA
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	GGTGGTGACCGTGGACGTGCGCACCAAGAAAGTGGTGTTCAAGGATGGCTTTAAACTGGA
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	GTATAGCAAACGTGCTGCTGGCGCCAGGTAGCAGCCCCGAAACCTGAGCTGCAAGGGCAA
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	AGAGGTGGAACGTGTTCAACATCCGTACCCGGAAGATGCTAACCGTGTGGTGCCTCT
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	GGCCCGCGGTGTAACGTGGTGGTGGTGGGCGCGGGTTTTCTGGGCATGGAAGTGGCGGC
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	TTACCTGACCGAAAAGGCTCACAGCGTGAGCGTGGTGGAGCTGGAGGAAACCCGTTCCG
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	TCGCTTTCTGGGCGAGCGTGTGGTCTGTCCTGATGAAGATGTTGAAAACAACCGCGT
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	GAGTTCTACATGCAGACCGAGGTGAGCGAACTGCGTGGTCAGGAAGGCAAGCTGAAAGA
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	GGTGGTGCTGAAGAGCAGCAAAGTGGTGCCTGCCGACGTGTGCTGGTGGGTATTGGTGC
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	GGTGCCGGCTACCGGTTTCCTGCGTCAGAGCGGCATCGGTCTGGATAGCCGTGGCTTTAT
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	TCCGGTGAACAAGATGATGCAGACCAACGTGCCGGCGTGTTCGCGGCCGGCGACGCTGT
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	GACCTTTCGCTGGCCTGGCGCAACAACCGTAAAGTGAACATTCCGCACTGGCAGATGGC
pNNH1.3T	-----
pNNH1.1T	-----GACCTGAGCATGGGCCATCTGCCAGTGCG
pNNH1.5T	-----GACCTGAGCATGGGCCATCTGCCAGTGCG
pNNH1	CCATGCTCAGGGTCGTGTGGCTGCTCAGAACATGCTGGCGCAGGAAGCCGAAATGAGCAC
pNNH1.3T	-----
pNNH1.1T	GAATGTTCACTTTACGGTTG-----TTGCGCCAGGCCAGCGGAAAGGTCAC
pNNH1.5T	GAATGTTCACTTTACNGTTG-----TTGCGCCAGGCCACCGGAAAGGTCAC
pNNH1	CGTGCCGTACCTGTGGACCGCCATGTTCTGGCAAGAGCCTGCGTTACGCGGGCTATGGCGA
pNNH1.3T	-----
pNNH1.1T	AGC-----
pNNH1.5T	AGC-----

pNNH1	GGGCTTTGACGATGTGATCATTGAGGGTGACCTGGAGGAACTGAAGTTCGTGGCCTTTTA
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	CACCAAAGGCGACGAAAGTGATCGCCGTGGCGAGCATGAACTATGATCCGATTGTGAGCAA
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	AGTGGCTGAGGTGCTGGCCAGCGGTCGTGCCATCCGTAAACGTGAAGTGGAAGTGTGTTGT
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	GCTGCATTCCAAGACCGGCGATATGTCCTGGCTGACCGGCAAGGGTAGCGCGGCCGCACT
pNNH1.3T	-----
pNNH1.1T	-----GTCGCCGGCCG
pNNH1.5T	-----GTCGCCGGCCG
pNNH1	CGAGCACCACCACCACCACCTGAGATCCGGCTGCTAACAAAGCCCGAAAGGAAGCTGA
pNNH1.3T	-----
pNNH1.1T	CGAACCCCCCGGCACGT-----
pNNH1.5T	CGAACACNCCCGGCACGTT---GG-----
pNNH1	GTTGGCTGCTGCCACCGCTGAGCAATAACTAGCATAACCCCTTGGGGCCTCTAAACGGGT
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----
pNNH1	CTTGAGGGGTTTTTTGCTGAAAGGAGGAACTATATCCGGAT
pNNH1.3T	-----
pNNH1.1T	-----
pNNH1.5T	-----

pNNH2	GACGGATCGGGAGATCTCCCGATCCCCTATGGTGCACTCTCAGTACAATCTGCTCTGATG
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTTGGAGGTCGCTGAGTAGTGCG
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	CGAGCAAAATTTAAGCTACAACAAGGCAAGGCTTGACCGACAATTGCATGAAGAATCTGC
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	TTAGGGTTAGGCGTTTTGCGCTGCTTCGCGATGTACGGGCCAGATATACGCGTTGACATT
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	GATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATA
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	TGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCTGGCTGACCGCCAACGACC
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	CCCCGCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCC
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	ATTGACGTCAATGGGTGGAGTATTTACGGTAACTGCCCACTTGGCAGTACATCAAGTGT
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	ATCATATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCTGGCATT
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	ATGCCCAGTACATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCA
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	TCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTG
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	ACTCACGGGGATTTCGAAGTCTCCACCCATTGACGTCAATGGGAGTTTGTGTTTGGCACC
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	AAAATCAACGGGACTTTCCAAAATGTCGTAACAACTCCGCCCATTTGACGCAATGGGCG
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----

pNNH2	GTAGGCGTGACGGTGGGAGGTCTATATAAGCAGAGCTCTCTGGCTAACTAGAGAACCCA
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	CTGCTTACTGGCTTATCGAAATTAATACGACTCACTATAGGGAGACCCAAGCTGGCTAGC
pNNH2 . 2P	-----NNNNNNNNNNNN
pNNH2 . 1P	-----NNNNNNNNNNNN
pNNH2 . 3P	-----NNNNNNNNNNNN
pNNH2	CCATGGGCGGTTGTTTCTCCAAGCCGAAGCCAGTGGAAGTGAAGATTGAGGTGGTGCTGC
pNNH2 . 2P	NCATGGGCGGTTGTTTCTCCAAGCCGAAGCCAGTGGAAGTGAAGATTGAGGTGGTGCTGC
pNNH2 . 1P	NNNNTGGGCGGTTGTTTCTCAGCCGAAGCCAGTGGAAGTGAAGATTGAGGTGGTGCTGC
pNNH2 . 3P	NNNNTGGGCGGTTGTTTCTCAGCCGAAGCCAGTGGAAGTGAAGATTGAGGTGGTGCTGC
	* * * * *
pNNH2	CGGAAAAGGAACGTGGTAAAGAGGAAGTGAAGCAGCGCAAGGGTAGCCCGCGCGCCT
pNNH2 . 2P	CGGAAAAGGAACGTGGTAAAGAGGAAGTGAAGCAGCGCAAGGGTAGCCCGCGCGCCT
pNNH2 . 1P	CGGAAAAGGAACGTGGTAAAGAGGAAGTGAAGCAGCGCAAGGGTAGCCCGCGCGCCT
pNNH2 . 3P	CGGAAAAGGAACGTGGTAAAGAGGAAGTGAAGCAGCGCAAGGGTAGCCCGCGCGCCT

pNNH2	ACCAGGGTAATGGTACCGCTCGCCACTTCCACACCGAGGAACGTCTGAGCACCCCGCACCC
pNNH2 . 2P	ACCAGGGTAATGGTACCGCTCGCCACTTCCACACCGAGGAACGTCTGAGCACCCCGCACCC
pNNH2 . 1P	ACCAGGGTAATGGTACCGCTCGCCACTTCCACACCGAGGAACGTCTGAGCACCCCGCACCC
pNNH2 . 3P	ACCAGGGTAATGGTACCGCTCGCCACTTCCACACCGAGGAACGTCTGAGCACCCCGCACCC

pNNH2	CATATCCGAGCCCGCAGGACTGCGTGGAGGCGCGGTGTGCCACGTGAAAGATCTGGAAA
pNNH2 . 2P	CATATCCGAGCCCGCAGGACTGCGTGGAGGCGCGGTGTGCCACGTGAAAGATCTGGAAA
pNNH2 . 1P	CATATCCGAGCCCGCAGGACTGCGTGGAGGCGCGGTGTGCCACGTGAAAGATCTGGAAA
pNNH2 . 3P	CATATCCGAGCCCGCAGGACTGCGTGGAGGCGCGGTGTGCCACGTGAAAGATCTGGAAA

pNNH2	ACGGTCAGATGCGTGAGGTGGAAGTGGGCTGGGGCAAGGTGCTGCTGGTGAAAGATAACG
pNNH2 . 2P	ACGGTCAGATGCGTGAGGTGGAAGTGGGCTGGGGCAAGGTGCTGCTGGTGAAAGATAACG
pNNH2 . 1P	ACGGTCAGATGCGTGAGGTGGAAGTGGGCTGGGGCAAGGTGCTGCTGGTGAAAGATAACG
pNNH2 . 3P	ACGGTCAGATGCGTGAGGTGGAAGTGGGCTGGGGCAAGGTGCTGCTGGTGAAAGATAACG

pNNH2	GCGAGTTCACGCTCTGGGTCACAAGTGCCCACTATGGTGCCCGCTGGTGAAAGGTG
pNNH2 . 2P	GCGAGTTCACGCTCTGGGTCACAAGTGCCCACTATGGTGCCCGCTGGTGAAAGGTG
pNNH2 . 1P	GCGAGTTCACGCTCTGGGTCACAAGTGCCCACTATGGTGCCCGCTGGTGAAAGGTG
pNNH2 . 3P	GCGAGTTCACGCTCTGGGTCACAAGTGCCCACTATGGTGCCCGCTGGTGAAAGGTG

pNNH2	TGCTGAGCCGTGGCCGCGTGCCTGCCCCTGGCATGGTGCTTGAACATCAGCACCG
pNNH2 . 2P	TGCTGAGCCGTGGCCGCGTGCCTGCCCCTGGCATGGTGCTTGAACATCAGCACCG
pNNH2 . 1P	TGCTGAGCCGTGGCCGCGTGCCTGCCCCTGGCATGGTGCTTGAACATCAGCACCG
pNNH2 . 3P	TGCTGAGCCGTGGCCGCGTGCCTGCCCCTGGCATGGTGCTTGAACATCAGCACCG

pNNH2	GTGACCTGGAGGATTTCCCGGGCTGGACAGCCTGCACAAGTTTCAGGTGAAAATTGAGA
pNNH2 . 2P	GTGACCTGGAGGATTTCCCGGGCTGGACAGCCTGCACAAGTTTCAGGTGAAAATTGAGA
pNNH2 . 1P	GTGACCTGGAGGATTTCCCGGGCTGGACAGCCTGCACAAGTTTCAGGTGAAAATTGAGA
pNNH2 . 3P	GTGACCTGGAGGATTTCCCGGGCTGGACAGCCTGCACAAGTTTCAGGTGAAAATTGAGA

pNNH2	AGGAAAAAGTGACGTGCGTGCCAGCAAGCAGGCGCTGCAGCTGCAGCGTCGCACCAAAG
pNNH2 . 2P	AGGAAAAAGTGACGTGCGTGCCAGCAAGCAGGCGCTGCAGCTGCAGCGTCGCACCAAAG
pNNH2 . 1P	AGGAAAAAGTGACGTGCGTGCCAGCAAGCAGGCGCTGCAGCTGCAGCGTCGCACCAAAG
pNNH2 . 3P	AGGAAAAAGTGACGTGCGTGCCAGCAAGCAGGCGCTGCAGCTGCAGCGTCGCACCAAAG

pNNH2	TGATGGCCAAATGCATCAGCCCGAGCGCGGGCTATAGCAGCAGCACCAACGTGCTGATTG
pNNH2 . 2P	TGATGGCCAAATGCATCAGCCCGAGCGCGGGCTATAGCAGCAGCACCAACGTGCTGATTG
pNNH2 . 1P	TGATGGCCAAATGCATCAGCCCGAGCGCGGGCTATAGCAGCAGCACCAACGTGCTGATTG
pNNH2 . 3P	TGATGGCCAAATGCATCAGCCCGAGCGCGGGCTATAGCAGCAGCACCAACGTGCTGATTG

pNNH2	TGGGTGCCGGTGCTGCTGGTCTGGTGTGCGCTGAAACCTGCGCCAGGAAGGCTTCAGCG
pNNH2 . 2P	TGGGTGCCGGTGCTGCTGGTCTGGTGTGCGCTGAAACCTGCGCCAGGAAGGCTTCAGCG
pNNH2 . 1P	TGGGTGCCGGTGCTGCTGGTCTGGTGTGCGCTGAAACCTGCGCCAGGAAGGCTTCAGCG
pNNH2 . 3P	TGGGTGCCGGTGCTGCTGGTCTGGTGTGCGCTGAAACCTGCGCCAGGAAGGCTTCAGCG

pNNH2	ACCGTATCGTGCTGTGCACCTGGACCGTCACCTGCCGTACGATCGTCCGAAGCTGAGCA
pNNH2 . 2P	ACCGTATCGTGCTGTGCACCTGGACCGTCACCTGCCGTACGATCGTCCGAAGCTGAGCA
pNNH2 . 1P	ACCGTATCGTGCTGTGCACCTGGACCGTCACCTGCCGTACGATCGTCCGAAGCTGAGCA
pNNH2 . 3P	ACCGTATCGTGCTGTGCACCTGGACCGTCACCTGCCGTACGATCGTCCGAAGCTGAGCA

pNNH2 AAAGCCTGGATACCCAGCCAGAGCAGCTGGCCCTGCGCCCGAAAGAGTTCTTCCGTGCGT
pNNH2 . 2P AAAGCCTGGATACCCAGCCAGAGCAGCTGGCCCTGCGCCCGAAAGAGTTCTTCCGTGCGT
pNNH2 . 1P AAAGCCTGGATACCCAGCCAGAGCAGCTGGCCCTGCGCCCGAAAGAGTTCTTCCGTGCGT
pNNH2 . 3P AAAGCCTGGATACCCAGCCAGAGCAGCTGGCCCTGCGCCCGAAAGAGTTCTTCCGTGCGT

pNNH2 ATGGTATTGAGGTGCTGACCGAAGCTCAGGTGGTGACCGTGGACGTGCGCACCAAGAAAG
pNNH2 . 2P ATGGTATTGAGGTGCTGACCGAAGCTCN-GTGGTGACCGTGGACGTGCGCACCAAGAAAG
pNNH2 . 1P ATGGTATTGAGGTGCTGACCGAAGCTCANGTGGTGACCGTGGACGTGCGCACCAAGAAAG
pNNH2 . 3P ATGGTATTGAGGTGCTGACCGAAGCTCANGTGGTGACCGTGGACGTGCGCACCAAGAAAG

pNNH2 TGGTGTTCAAGGATGGCTTTAACTGGAGTATAGCAAAGTCTGCTGGCGCCAGGTAGCA
pNNH2 . 2P TGGTGTTCAAGGATGGCTTTAACTGGAGTATAGCAAAGTCTGCTGGCGCCAGGTAGCA
pNNH2 . 1P TGGTGTTCAAGGATGGCTTTAACTGGAGTATAGCAAAGTCTGCTGGCGCCAGGTAGCA
pNNH2 . 3P TGGTGTTCAAGGATGGCTTTAACTGGAGTATAGCAAAGTCTGCTGGCGCCAGGTAGCA

pNNH2 GCCCGAAAACCTGAGCTGCAAG-GGCAAGAGGTGGAAAACGTGTTACCATCCGTACC
pNNH2 . 2P GCCCGAAAACCTGAGCTGCAAG-GGCAAGAGGTGGAAAACGTGTTACCATCCGTACC
pNNH2 . 1P GCCCGAAAACCTGAGCTGCAAG-GGCAAGAGGTGGAAAACGTGTTACCATCCGTACC
pNNH2 . 3P GCCCGAAAACCTGAGCTGCAAGGGCAAGAGGTGGAAAACGTGTTACCATCCGTACC

pNNH2 CCGGAAGATGCTAACCGTGTGGTGCCTGCGCCCGCGTCTAACGTGGTGGTGGGCG
pNNH2 . 2P CCGGGANATGCTAACCGTGTGGTGCCTGCGCCCGCGTCTAACGTGNGG-TGGTGGGCG
pNNH2 . 1P CCGGAAGATGCTAACCGTGTGGTGCCTGCGCCCGCGN-CGTAACTGGTGGTGGTGGGCG
pNNH2 . 3P CCGGAAGATGCTAACCGTGTGGTGCCTGCGCCCGCGTCTAACGTGGTGGTGGTGGGCG
**** * *****

pNNH2 GCGGGTTTTCTGGGCATGGAAGTGCGGCTTACCTGACCGAAAAGGCTCACAGCTGAGC
pNNH2 . 2P GCGGTTTTCTGGGC-AT-GGAANTGCGGCTTACCTGACCGAAAAGCTCACANNNNGAGC
pNNH2 . 1P GCGGTTTTCTGGGC-AT-GGAAGTGCGGCTTACCTGACCGAANNNNNACAGNNNGAGC
pNNH2 . 3P GCGGTTTTCTGGGC-AT-GGAAGTGCGGCTTACCTGACCGAANNNTACAGCNNNA-NC

pNNH2 GTGGTGGAGCTGGAGGAAACCCGTTCCGTCGCTTTCTGGGCGAGCGTGTGGTCTGCC
pNNH2 . 2P GTGGTGGAGCTGGAGAAACCCGTTCCGTCNCTT-TNNGGNCNNNGCNGTNNNNNNNN
pNNH2 . 1P NTGNNNGNCTGNNAAC--CCGNTTCCGTCGCTT-CTGGNCGANNNGNNNGCCCT
pNNH2 . 3P GTGNNNN--CTGAGNAC--CCCGT--NNTCGCTTT-CTGGGCGANNNNNGGNNNGCCN
** **

pNNH2 CTGATGAAGATGTTGAAAACAACCGCTGAAGTTCTACATGCAGACCGAGGTGAGCGAA
pNNH2 . 2P CCNATGANANGTTGAAACNCNCN--NNNN-TNCTANNNGNNNNNNNGANNNNCTG
pNNH2 . 1P G--ANNAANANGTTCAAACAACNGCNCNNAG-TTNANNNNCCNNNCANNNNNNNNNN
pNNH2 . 3P G--ANNANA-TGTTCAAACNNNNNNNNNT-T-CTACNTNNNNNNNGNTGANCNNNA
**** **

pNNH2 CTGCGTGGTCAGGAAGGCAAGCTGAAAGAGGTGGTGTGAAGAGCAGCAAAGTGGTGCCT
pNNH2 . 2P CNNNNNGGA---AGGNNAAGCNCNAAANNAGGNGNGNNGNCCN--NANANNNNNTN--
pNNH2 . 1P NNNNNCAGG---ANNNNNNNNTAAAA--NNNNNGTNNCNT--AAAAANNNNN---
pNNH2 . 3P CTGNNNNNN---NNNNNNNAANCNNNA--NNNNNGGNNCTN--NNANNNNN-----

pNNH2 GCCGACGTGTCGTGGTGGGTATTGGTGCGGTGCCGGCTACCGGTTTCTGCGTCAGAGC
pNNH2 . 2P -----
pNNH2 . 1P -----
pNNH2 . 3P -----

pNNH2 GGCATCGGTCTGGATAGCCGTGGCTTTATTCGGTGAACAAGATGATGCAGACCAACGTG
pNNH2 . 2P -----
pNNH2 . 1P -----
pNNH2 . 3P -----

pNNH2 CCGGGCGTGTTCGCGCCGGCGACGCTGTGACCTTCCGCTGGCCTGGCGCAACAACCGT
pNNH2 . 2P -----
pNNH2 . 1P -----
pNNH2 . 3P -----

pNNH2 AAAGTGAACATTCCGCACTGGCAGATGGCCCATGCTCAGGGTCGTGTGGCTGCTCAGAAC
pNNH2 . 2P -----
pNNH2 . 1P -----
pNNH2 . 3P -----

pNNH2 ATGCTGGCGCAGGAAGCCGAAATGAGCACCGTCCGTACCTGTGGACCGCCATGTTCCGGC
pNNH2 . 2P -----
pNNH2 . 1P -----
pNNH2 . 3P -----

pNNH2	ATGCTGGCGCAGGAAGCCGAAATGAGCACCGTGCCGTACCTGTGGACCGCCATGTTTCGGC
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	AAGAGCCTGCGTTACGCGGGCTATGGCGAGGGCTTTGACGATGTGATCATTAGGGTGAC
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	CTGGAGGAACTGAAGTTCGTGGCCTTTTACACCAAAGGCGACGAAGTGATCGCCGTGGCG
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	AGCATGAACATGATCCGATTGTGAGCAAAGTGGCTGAGGTGCTGGCCAGCGGTCGTGCC
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	ATCCGTAAACGTGAAGTGGAAGTGTGCTGCTGCTTCAAGACCGGCGATATGTCCTGG
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	CTGACCGGCAAGGGTAGCGCGGCCGCGAGAATTCCACCACACTGGACTAGTGGATCCGAG
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	CTCGGTACCAAGCTTAAGTTTAAACCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGCCA
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	GCCATCTGTTGTTTGCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCAC
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	TGCTCTTTCCTAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTAT
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	TCTGGGGGTGGGGTGGGGCAGGACAGCAAGGGGAGGATTGGGAAGACAATAGCAGGCA
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	TGCTGGGGATGCGGTGGGCTCTATGGCTTCTGAGGCGGAAAGAACCAGCTGGGGCTCTAG
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	GGGGTATCCCCACGCGCCCTGTAGCGGCGCATTAAAGCGGCGGGTGTGGTGGTTACGCG
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	CAGCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTCTTCCCTTC
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	CTTCTCGCCACGTTGCGCGGCTTTCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGG
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----

pNNH2	GTTCCGATTTAGTGCTTTACGGCACCTCGACCCCAAAAACTTGATTAGGGTGATGGTTC
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	ACGTAGTGGGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTT
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	CTTTAATAGTGGACTCTTGTTCCAACTGGAACAACACTCAACCCCTATCTCGGTCTATTC
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	TTTTGATTATAAGGGATTTTGCCGATTCGGCCTATTGGTTAAAAAATGAGCTGATTTA
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	ACAAAAATTTAACGCGAATTAATTCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCC
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	CCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGG
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	TGTGGAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAG
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	TCAGCAACCATAGTCCCGCCCTAACTCCGCCCATCCCGCCCTAACTCCGCCAGTTCC
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	GCCCATTTCTCGCCCCATGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCC
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	TCTGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGAGGCCTAGGCTTTTGC
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	AAAAAGCTCCCGGGAGCTTGTATATCCATTTTCGGATCTGATCAAGAGACAGGATGAGGA
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	TCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAG
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	AGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTTC
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	CGGCTGTACGCGAGGGCGCCCGGTTCTTTTGTCAAGACCGACCTGTCCGGTGCCCTG
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----

pNNH2	AATGAACTGCAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGC
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	GCAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTG
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	CCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCT
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	GATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCG
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	AAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGAT
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	CTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAAGTTCGCCAGGCTCAAGGCGCGC
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	ATGCCCGACGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATG
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	GTGGAAAAATGGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGC
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	TATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGCGAATGGGCT
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	GACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTAT
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	CGCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGTTTCGAAATGACCGACCAAGCGA
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	CGCCCAACCTGCCATCACGAGATTTGATTCCACCGCCGCTTCTATGAAAGGTTGGGCT
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	TCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGG
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	AGTTCTTCGCCACCCCAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATA
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----

pNNH2	GCATCACAAATTTACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCA
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	AACATCAATGTATCTTATCATGTCTGTATACCGTCGACCTCTAGCTAGAGCTTGGCGT
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	AATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCACACAACA
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	TACGAGCCGGAAGCATAAAGTGTAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACAT
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	TAATTGCGTTGCGCTCACTGCCCGCTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATT
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	AATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCCTATTGGGCGCTCTCCGCTTCCT
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	CGCTCACTGACTCGCTGCGCTCGGTCGTTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAA
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	AGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAA
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	AAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGCTGGCGTTTTTCCATAGGC
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	TCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGA
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	CAGGACTATAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTT
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	CGACCTGCGGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTT
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	CTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGTTGCTCCAAGCTGGGCT
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	GTGTGCACGAACCCCCGTTTCAGCCGACCGCTGCGCCTTATCCGGTAACATATCGTCTTG
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----

pNNH2	AGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTA
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	GCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCT
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	ACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAA
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	GAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTTTTTTTGGTTGCA
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	AGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGG
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	GGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAA
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	AAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTA
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	TATATGAGTAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAG
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	CGATCTGTCTATTTCTGTTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGA
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	TACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTCAC
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	CGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTC
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	CTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGAAGCTAGAGTAAGTA
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	GTTCCGCAGTTAATAGTTTGCACAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTAC
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	GCTCGTCGTTTGGTATGGCTTCATTACGCTCCGGTTCCCAACGATCAAGGCGAGTTACAT
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----

pNNH2	GATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAA
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	GTAAGTTGGCCGAGTGTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTG
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	TCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAG
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	AATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAATACGGGATAATACCGCGC
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	CACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAACCTCT
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	CAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACGTAT
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	CTTCAGCATCTTTTACTTTTACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATG
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	CCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTTTCCTTTTTC
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	AATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTA
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	TTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCGAAAAGTGCCACCTGACG
pNNH2 . 2P	-----
pNNH2 . 1P	-----
pNNH2 . 3P	-----
pNNH2	TC
pNNH2 . 2P	--
pNNH2 . 1P	--
pNNH2 . 3P	--

ANEXO XII - SECUENCIAS

>**NP_004199.1** apoptosis-inducing factor 1, mitochondrial isoform AIF precursor [Homo sapiens]

MFRCCGLAAGALKQKLVPLVRTVCVRSRQNRNLPGNLFQRWHVPLELQMTQMASSGASGGKIDNSVLVLIVGLSTVGAGAY
AYKTMKEDEKRYNERISGLGLTPEQKQKKAALSASEGEEVPQDKAPSHVPFLLIGGGTAFAAARSIRARDPGARVLIVSEDP
ELPYMRPPLSKELWFSDDPNVTKTLRFKQWNGKERSIYFQPPSFYVSAQDLPHIENGAVVLTGKKVVQLDVRDNMVKLNDGS
QITYEKCLIATGGTPRSLSAIDRAGAEVKSRTTLFRKIGDFRSLEKISREVKSITIIGGGFLGSELACALGRKARALGTEVIQ
LFPEKGNMGKILPEYLSNWTMEKVRREGVKVMPNAIVQSVGVSSGKLLIKLDGRKVETDHIVAAGLEPNVELAKTGGLDID
SDFGGFRVNAELQARSNIWVAGDAACFYDIKLGRRRVEHHDHAVVSGRLAGENMTGAAKPYWHQSMFWSDLGPDVGYEAGLV
DSSLPTVGVFAKATAQDNPKSATEQSGTGIRSESETESEASEITIPPSTPAVPQAPVQGEDYGKGVIFYLRDKVVVGIVLWNI
FNRMPIARKIIKDGEQHEDLNEVAKLFNIHED

>**NP_001185625.1** apoptosis-inducing factor 2 [Homo sapiens]

MGSQVSVESGALHVIVGGGFGGIAAASQLQALNVPFMLVDMKDSFHHNVAALRASVETGFAKKTIFISYSVTFKDNFRQGLVV
GIDLKNQMVLLQGGEALPFSHLILATGSTGPFPGKFNEVSSQQAIIQAYEDMVRQVQSRFRIVVVGGSAGVEMAAEIKTEYP
EKEVTLIHSQVALADKELLPSVRQEVKEILLRKGVQLLSERVSNEELPLNEYREYIKVQTDKGTEVATNLVILCTGIKINS
SAYRKAFESRLASSGALRVNEHLQVEGHSNVYAIGDCADVTPKMAYLAGLHANIAVANIVNSVKQRPLQAYKPGALTFLLSM
GRNDGVGQISGFYVGRMLVRLTKSRDLFVSTSWKTMRSPP

>**NP_653305.1** apoptosis-inducing factor 3 isoform 1 [Homo sapiens]

MGGCFSPKPKVELKIEVVLPEKERGKEELSASGKGS PRAYQNGTARHFHTEERLSTPHYPSPQDCVEAAVCHVKDLENGQM
REVELGKWKVLLVKDNGEFHALGHKCPHYGAPLVKGVLSRGRVRC PWHGACFNISTGDLEDFPGLDSLHKFQVKIEKEKVYVR
ASKQALQLQRRTKVMAKCISPSAGYSSTNV LIVGAGAAGLVCAETLRQEGFSDRIVLCTLDRHLPYDRPKLSKSLDTQPEQL
ALRPKEFFRAYGIEVLTEAQVTVDVRTKKVVF KDGFKLEYSKLL LAPGSSPKTLSCKGKEVENVFTIRTPEDANRVVRLARG
RNVVVVGAGFLGMEVAAYLTEKAHSVSVVELEETPFRFLGERVGRALMKMFENNRVKFYMQTEVSELRGQEGKLKEVVLKSS
KVVRAADV CVVGIGAVPATGFLRQSGIGLDSRGFIPVNKMMQTNVPGVFAAGDAVTFPLAWRNRKVNIPHWQMAHAQGRVAAQ
NMLAQEAEMSTVPYLWTAMFGKSLRYAGYGEGFDDV I IQGDLEELKFVAFYTKGDEVIAVASMNYDPIVSKVAEVLASGRAIR
KREVELFVLHSKTGDMSWLTGKGS

>**NM_144704.2** Homo sapiens apoptosis inducing factor, mitochondria associated 3 (AIFM3), transcript variant 1, mRNA

CGCCCCGCGCGCCTCCCCGCCCCCGCGCCCGCGGCCCAAGCGGTTCCTCAGCCCAGGCCCGCGCCGAGCCCAGGTCTCT
AGAGCAGCTCCAGCAGGATGGCGGCTCCAGCGTCTCTAAGGCCTGCAGGGGTCCAGCCCATGGGGGCGCCCTAGGCTCTCC
GACAGCTCCCCATCTGTGCTCCTGCCTGCCGCGCATCCTCAGGCCACTCGCCATGGGCGGCTGCTTCTCCAAACCCAAACCAG
TGGAGCTCAAGATCGAGGTGGTGTGCTGAGAGGAGCGAGGCAAGGAGGAGCTGTCCGCCAGTGGGAAGGGCAGCCCCCGG
GCCTACCAGGGCAATGGCACGGCCCGCCACTTCCACACGGAGGAGCGCTGTCCACCCCTCACCCCTACCCCTACCCCTCAGGGA
TTGCGTGGAGGCTGCTGTCTGCCACGTCAAGGACCTCGAGAATGGCCAGATGCGGGAAGTGGAGCTGGGCTGGGGGAAGGTGT
TGCTGGTGAAGGACAATGGGGAGTTCACGCCCTGGGCCATAAGTGTCCGCACTACGGCGCACCCCTGGTGAAAGGCGTTCTG
TCCCGTGGTGGGTGCGCTGCCCTGGCACGGCGCTGCTTCAACATCAGCACTGGGGACCTGGAGGACTTCCCTGGCCTGGA
CAGTCTACACAAGTTCAGGTGAAGATTGAGAAGGAGAAGGTGTACGTCCGGGCCAGCAAGCAGGCCCTACAGCTGCAGCGAA
GGACCAAGGTGATGGCCAAGTGTATCTCTCCAAGTGTGGGTACAGCAGTAGCACCAATGTGCTCATTGTGGGTGCAGGTGCA
GCTGGCCTGGTGTGTGCAGAGACACTGCGGCAGGAGGGCTTCTCCGACCGGATCGTCTGTGCACGCTAGACGGGCACCTTCC
CTACGACCGTCCCAAGCTCAGCAAGTCCCTGGACACACAGCCTGAGCAGCTGGCCCTGAGGCCCAAGGAGTTTTTCCGAGCCT
ATGGCATCGAGGTGCTCACCAGGCTCAGGTGGTCAAGTGGACGTGAGAACTAAGAAGGTCTGTGTTCAAGGATGGCTTCAAG
CTGGAGTACAGCAAGCTGCTGCTGGCACCCAGGAGCAGCCCCAAGACTCTGAGCTGCAAAGGCAAAGAAGTGGAGAACGTGTT
CACTATCCGGACGCCAGAGGATGCCAATCGCGTGGTGGAGCTGGCCCGAGGCCGCAACGTGGTCTGCTGTTGGGAGCCGGCTTCC
TGGGGATGGAGGTGGCCGCTTACCTGACGGAGAAGGCCACTCTGTGTCTGTGGTGGAGCTGGAGGAGACGCCCTTACAGGAGG
TTCCTGGGGGAGCGCTGGGTCTGTCCTCATGAAGATGTTTGAGAACAAACCGGGTGAAGTTCTACATGCAGACGGAGGTGTC
TGAGCTGCGGGGCCAGGAGGGAAGCTGAAGGAGGTGTGCTGAAGAGCAGCAAGGTCTGCGGGCTGACGTCTGCGTGGTGG
GCATTGGTGCAGTGCCCGCCACAGGCTTCCCTGAGGCAAAGCGGCATCGGTTTGGATTCCCGAGGCTTCACTCCCTGTCAACAAG
ATGATGCAGACCAATGTCCCAGGCGTGTGTCAGCTGGCGATGCTGTACCTTCCCCCTTGCCTGGAGGAACAACCGCAAAGT
GAACATTCCACATTGGCAGATGGCTCATGCTCAGGGGCGCGTGGCAGCCAGAACATGTTGGCGCAGGAGGCGGAGATGAGCA
CTGTGCCCTACCTCTGGACCGCCATGTTTGGCAAGAGCCTGCGCTACGCGGGCTACGGAGAAGGCTTCGACGACGTCATCATC
CAGGGGGATCTGGAGGAGCTGAAGTTTGTGGCTTTTACACTAAAGGCGACGAGGTGATCGCCGTGGCCAGCATGAACACGA
TCCCATTTGTGTCCAAGGTCTGCTGAGGTGCTGGCCTCAGGCCGTGCCATCCGGAAGCGGGAGGTGGAGCTGTTTGTGCTGCACA
GCAAGACTGGCGACATGTCTGGCTTACGGGGAAAGGATCCTGAGCTCATATGCAGTAGACTTGGGCAGGCAAAGGGGGCACC
AAGGGCACAGGCCAAGCCTTGGGGGAGGTGCCAATCTCCAGTCCCAGGATCCCCCAGGGCAGAACCTGAGCCCTCCAGTGC
TTGCCCTCAGCCACCTGGCTCCCTCTGGGAGGCTCTGCTGGATCCAGAAGATGCTCAACCTCAAGGCCTCTGCTGCCAC

TGACAGCTGGCACTGGAGGCAGGACAAGCCCTGCCTCTTCTCCCTCTATTGGGACTGGTCCCCTGAAGAACCCTGCAACATGT
TAGACATTACCGTAAATTAACGACAAATTTGCAGATCAAAAAAAAAA

Secuencia NheI-NcoI-AIFM3-NotI-EcoRI para clonaje en *E. coli* y *Homo sapiens*

GCTAGCC**CCATGG**CGCGCTGCTTCTCCAAACCCAAACCACTGGAGCTCAAGATCGAGGTGGTGTGCTGCCTGAGAAGGAGCGAGGC
AAGGAGGAGCTGTTCGCCAGTGGGAAGGGCAGCCCCGGGCTACCAGGGCAATGGCACGGCCCCGCACTTCCACACGGAGGA
GCGCTGTCCACCCCTCACCCCTACCCAGCCCTCAGGATTGCGTGGAGGCTGCTGTCTGCCACGTCAAGGACCTCGAGAATG
GCCAGATGCGGGAAGTGGAGCTGGGCTGGGGGAAGGTGTTGCTGGTGAAGGACAATGGGGAGTTCACGCCCTGGGCCATAAG
TGTCGCACTACGGCGCACCCCTGGTGAAAGGCGTTCTGTCCCGTGGTGGGTGCGCTGCCCCCTGGCACGGCGCCTGCTTCAA
CATCAGCACTGGGGACCTGGAGGACTTCCCTGGCCTGGACAGTCTACACAAGTTCAGGTGAAGATTGAGAAGGAGAAGGTGT
ACGTCCGGGCCAGCAAGCAGGCCCTACAGCTGCAGCGAAGGACCAAGGTGATGGCCAAGTGTATCTCTCCAAGTGTGGGTAC
AGCAGTAGCACCAATGTGCTCATTTGGGTGCAGGTGCAGCTGGCCTGGTGTGTGCAGAGACACTGCGGCAGGAGGGCTTCTC
CGACCGGATCGTCTGTGCACGCTAGACCGGCACCTTCCCTACGACCGTCCCAAGCTCAGCAAGTCCCTGGACACACAGCCTG
AGCAGCTGGCCCTGAGGCCCAAGGAGTTTTTCCGAGCCTATGGCATCGAGGTGCTCACCGAGGCTCAGGTGGTTCAGTGGAC
GTGAGAACTAAGAAGTTCGTGTTCAAGGATGGCTTCAAGCTGGAGTACAGCAAGCTGCTGCTGGCACCAGGGAGCAGCCCCAA
GACTCTGAGCTGCAAAGGCAAAGAAGTGGAGAACGTGTTCACTATCCGACGCCAGAGGATGCCAATCGCGTGGTGGAGCTGG
CCCGAGGCCGCAACGTGGTCTGCTGGGAGCCGGCTTCTGGGATGGAGGTGGCCGCTTACCTGACGGAGAAGGCCCACTCT
GTGCTGTGGTGGAGCTGGAGGAGACGCCCTTCAAGAGGTTCCTGGGGAGCGCGTGGTCTGCTGCTCATGAAGATGTTTGA
GAACAACCGGTGAAGTCTACATGCAGACGGAGGTGCTGAGCTGCGGGGCCAGGAGGAAAGCTGAAGGAGGTTGTGCTGA
AGAGCAGCAAGGTCTGCGGGCTGACGTCTGCGTGGTGGGCTTGGTGCAGTGGCCGCCACAGGCTTCTGAGGCAAAGCGGC
ATCGGTTTGGATTCCCGAGGCTTATCCCTGTCAACAAGATGATGCAGCAATGTCCAGGCGTGTTCGAGCTGGCGATGC
TGTACCTTCCCCCTTGCCTGGAGGAACAACCGCAAAGTGAACATTCACATTGGCAGATGGCTCATGCTCAGGGGCGCGTGG
CAGCCAGAACATGTTGGCGCAGGAGCGGAGATGAGCACTGTGCCCTACCTCTGGACGCCATGTTTGGCAAGAGCCTGCGC
TACGCGGGCTACGGAGAAGGCTTCGACGACGTATCATCCAGGGGATCTGGAGGAGCTGAAGTTTTGTGGCTTTTTACACTAA
AGGCGACGAGGTGATCGCCGTGGCCAGCATGAACACGATCCATTGTGTCCAAGTTCGCTGAGGTGCTGGCCTCAGGCCGTG
CCATCCGGAAGCGGGAGGTGGAGCTGTTTGTGCTGCACAGCAAGACTGGCGACATGTCTGGCTTACGGGGAAAGGATCC**GCG**
GCCGCGAGAATTC

>NP_001277999.1 apoptosis-inducing factor 3 isoform 1 [Mus musculus]

MGGCFSKPKPVELKIEVVLPEKERGKEELSASGKSPRGYQNGTARHFHAEERLPTPQYPSPQDCVEATVCHVKDLENGQM
REVELGWGKVLVLDNGEFHALGHKCPHYGAPLVKGVLSRGRVRCPWHGACFNISTGDLEDFPGLDSLHKFQVKIEKEKVTIR
ASKQALQLQRRTKVMAKICSPSAGHSSSTNVLIVGAGAAGLVCAETLRQEGFSDRIVLCTLDRLHPYDRAKLSKSLDAQPEQL
ALRPKEFFRAYGIEMLTEAQVVTVDVRNKKVVKDGFKLEYSKLLAPGSSPKTLTCKGKDVENVFTIRTPEDANRVLRLARG
RNAVVVGAGFLGMEVAAYLTEKAHSVSVVELEETPFRRFLGERVGRALMKMFENNRVKFYMQTEVSELRAQEGKLQEVVLKSS
KVLRADVCVLGIGAVPATGFLRQSGIGLDSRGFIPVNMMQTNVPGVFAAGDAVTFPLAWRNNRKNVNI PHWQMAHAQGRVAAQ
NMLAQEAEINTVPYLWTAMFGKSLRYAGYGEGFDDVIIQGDLEELKFVAFYTKSDEVIASVMNYDPIVSKVAEVLASGRAIR
KREVELFMLHSTGMSWLTGKGS

>NP_569976.1 CG4199, isoform D [Drosophila melanogaster]

MGSVNCKEYKTTGSTPKKEKSTGGAVGSYQSKCSNQSPSTTMSTEESPSEYTSAPVDCRVTDLKENEMKVDFDTRVL
LVKQNDRLAVGAKCTHYGAPLQTGALGLGRVRCPWHGACFNLENGDIEDFPGLDSLPCYRVEVGNQVMLRAKRSDLVNNK
RLKNMVRKPDQRFIVVGGGPGSAGAVETIRQEGFTGRILFVCREDYLPYDRVKISKAMNLEIEQLRFRDEEFYKEYDIEL
WQGVAAEKLDTAQKELHCSNGYVVKYDKIYLATGCSAFRPPIPGVNLNVRTVRELADTKAILASITPESRVVCLGSSFIALE
AAAGLVSKVQSVTVVGVRENVPKAAFGAEIGQRLQLFEDNKVMMRMESGIAEIVGNEDGKVSEVVLVDTRLPCDLLILGTG
SKLNTQFLAKSGVKVNRNGSVDVDFLESNPVYVGGDIANAHIHGLAHDVRNIGHYQLAQYHGRVAAINMCGGVKKLEAVP
FFFTLIFGKIRYAGHGSYKDVIIIDGSMEDFKFVAYFINEADTVTAVASCRDPIVAQFAELISQKCLGRGQIEDPATREDW
TKKLGQPLQVR

>NP_001039746.2 apoptosis-inducing factor 3 [Bos taurus]

MGGCFSKPKPVELKIEVVLPEKDRGKEELSTGSRGSPRAYQNGAARHFHADERLPTAHYPGAQDCVEAAVCHVKDLENGQM
REVELGWGKVLVLDNGELHALGHKCPHYGAPLVKGVLSRGRVRCPWHGACFNVSTGDLEDFPGLDSLHKFQVKIEKEKVYIR
ASKQALQLQRRTKVMATCISPSAGYSGSTNVLIVGAGAAGLVCAETLRQEGFSDRIVLCTLDRLHPYDRPKLSKSLDAQPEQL
ALRPKEFFRAHGIIEVLTEAQVVTVDVRNKKAVFKDGFKLEYSKLLAPGSSPKTLSCGKDVENVFTIRTPEDANRVLRLARG
RNAVVVGAGFLGMEVAAYLTEKAHSVSVVEVEETPFRRFLGERVGHITLMKMFENNRVKFYMQTEVSELRAQEGKLKEVVLKSS
KVVRADEVVVGIGAVPATGFLRQSGISLDSRGFIPVNMMQTNIPGVFAAGDAVTFPLAWRNNRKNVNI PHWQMAHAQGRVAAQ
NMLAQEAEISTVPFLWTAMFGKSLRYAGYGEGFDDVIIQGDLELKFVAFYTKGDEVISVSMNYDPIVSKVAEVLASGRTIR
KREVEVGMSWLTGKGS

>NP_001121885.1 apoptosis-inducing factor 3 [Danio rerio]

MGGCLSKPKPVEVKVELTLLDKEKEVDLMSPNGKASPFSECRPNGLGHCSDSDSMTLRPQRKNRDYIEASVCHIKDLENGQM
REVDLGAGRALLIKEHGEFFAMGHKCPHYGAPLVKGVLSKGVRCPWHGACFNIAATGDIEDFPGLDSLPTFQVRVEKEKVIIR

ANKQALQTQRRSKVMSKCSAVINSSTGFSHVLIIGSGPAGLVCAETLRQEGFTDRIVICTTDKHLPHYDRPKLSKSLESTAEQL
QLRSSDFFQMHDIENVLLEKEVSVSVKTHVTFRDGFKMEYRKLFIATGSRPKPLSYKGKDVGNVFHLRTPEDANSIVTLASS
KNAVIIGTSFIGMEVAAAALTDKAHSVSVIGIEAVPFRKALGEKV GKALMKLFESNRVKFYMLNEVWEMRGHNGQLKEVVLKSG
KVLRADVCVIGIGSSPATAFLKQSGVHIDSKGFIPVNMKTQTNIDGVFAGGDVVTFFPLGLRSNKKVNI PHWQMAHVHGRLLAL
GIMGKASDIKTPVYFWTAMFGKSIRYAGYGDGFDDVVIQGDLDLELKFVAFYTKSEEVVAVASMNYDPIVSRVAEVFGSGKTIR
KRDVETGDMSWLIVKGSQ

>NP_505112.1 Uncharacterized protein CELE_F20D6.11 [Caenorhabditis elegans]
MALANWLTPEPECDNDSPAVEEILGRIEDVPPGTGKMFVDRKVLVINDEGRIYAINGLCSHYNFSLNGTYAKGRIRCP
LHGACFNVRSGDIEDYPGFDLSHSYVTVNDGNLIKTTEKKLGSDRRIRHLPMKQCNDRPVVIIGGGVATATFIEHSRLNG
LITPILVISEESLPPYDRVLLSKKPAATGEDIRLRKDDAFYEERNVFKLLKTSVIAVNHSREVLSNGETVVYSKLIATGG
NVRKLQVPGSDLKNICYLRKVEEANIISNLHPGKHVVCVGSSFIGMEVASALAEKAASVTVISNTPEPLPVFGSDIGKIRLK
FEEKGVKFEAANVALRGNDQGEVSKVILENGKELDVLVCGIGVTPATKFLEGGSGIKLDNRGFIIEVDEKFRNTISYIFAM
GDVVTAPLPLWDIDSINIQHFQTAQAHGQHLGYTIVGKPPGPVPIVFWTLFFFAFGLKFGSGCNQGSTKEYTNGDPETGTFFIR
YFLKKDKVVAAGGPSSVASQFAEIFKKGIEVTLKDLKNSSDHTWGHLLL

>XP_001713117.2 flavoprotein [Schizosaccharomyces pombe 972h-]
MLLRFFINQPRFIQFTFLRNKKDRILGLQLGKQPPFRMSSSSGLKQQGLAQKKKFQLEFDPSSSVSKNGTKTEAKVVGTEFGVLL
VRARNTYFATAGKCSHYGAPLAKGVVTS DGHIVCPWHGACFNAATGDVEDTPAIAALRTFPVTEEGDGLWIEVEDKNDNGAS
VLQPEGCWRNKATEVYNKGSVETEVTAPHVCIIGGGKGASVAAEYLREKNFKGKITIFTREDEVYPDRPKLSKSLLDHISKLA
LRSKEYYDDLDISFHNFDVTKIDLAEEKIYCGSDEKPTESYTKLILATGGEPNKLPIPLGDSKNVYLLRSIADASKLAAVTT
EAGDKKNIVIIGSSFIGLELAVVLKDHNVSVIGMESIPFEKVMGKEVGTALKALHEQNGIAFYLENSIKEVKTSSNDSSKAH
IVLKDQGSIPADVILAAGVKPNRLYLGNVSLKDGGVKVDHECRVLGAEDVYAVGDIHAPFAGLPSSGEKSHTRIEHWDV
AGNLGRVAADHILFGNKAGYTTKSTPYFWSAQGKQLRYCGNNAEGFDDVVIQGSLSYKFAFFTKGEKVGVCSIMKDPV
VSQCARLFIKDAMPSKSQLKENFDVLSIPL

>XP_001349105.1 ferredoxin reductase-like protein [Plasmodium falciparum 3D7]
MRRNLLSLNGKISTIIKSDKLKTRGISSYNILKNNINVSLEKKNRFFSSSLKGHQKIGGGVLNSYDIFLIISLLAVPTILN
NKF GKMSNSIANCSNVEKVFLIKSNELQDGEMKEIKVHEEKDVTLLVRVNNKYCLGPKCPHYSAPLKSGLTNEYITCPWHD
AKFDIKTGECINGPSFDDIPKYEVEVIEGNEVYALLPKKLEIFEKKRICECKGSCEKKNILIVGGGAATLGALETFLKLGYNGK
LIICSKDAYKPYDRPTLSKNVSNCCNDELYEEIKLKEDSYNKSNIYKNNVYVEKVDTENKKAHLNNGEIIINFDKILITG
ISPSPPMKNMNLDNLFTLHNLSDNIKIGEYAKEGSKCVIIGSSFIACELSSALKKKNVNVTLSKDDVPFYGSFGEKIGNIV
LNLILKKNIKFYPSMHPTEYIIDKRFFSRKSGNIIHGVRLLNNGEVINCXYVIEALGCIPNSDFLDEKYKNVNNFIEVDKHKFV
KNSDNMYAAGDVCTFPYFLTDEMVNICHWNVAIQQGRIAAHNMLRDDKKEFNFI PFFNTNIFGKNFRYSGYVKNYDKIIYEGD
LLKHNFIFYGVKNDKVASIITLGNKMASLNECMAKNKVPKVYELEGGGLKNSDSMIASLKI

>NP_215202.1 ferredoxin reductase [Mycobacterium tuberculosis H37Rv]
MNAHVTSREGVNEFDGDGIVIVGGGLAAARTAEQLRRAGYSGRLTIVSDEVHLPYDRPPLSKEVLRSEVDDVALKPREFYDEKD
IALRLGSAAVSLDTGEQTVTLADGTVLGYDELVIATGLVPRRIPSLPDLGIRVLSFDESMA LRKHA SAARHAVVVGAGFIG
CEVAASLRGLGVDVVLVEPQPAPLASVLGEQIGQLVTRLHRDEGV DVRTGVTVAEVRGKGHVDAVVLTDGTELPADLVVVGIG
STPATEWLEGSGVEVDNGVICDKAGRTSAPNVWALGDVASWRDPMGHQARVEHWSNVADQARVVVPAMLGTDVPTGVVVYPYFW
SDQYDVKIQCLGEPHATDVVHLVEDDGRKFLAYYERDGVLVGVVGGGMAGKVMKVRGKIAAGAPIAEVLDQTQA

>WP_011279075.1 FAD-dependent oxidoreductase [Sulfolobus acidocaldarius]
MKYEIIYYVIDILDVSSKLT SKYVIIGSGIAGYHALKEMLNIDPKANITLVTS DSSLPYDRPPLSKEYMRSEDRDLSLFFEKP
EFYQRDNLKVMLNTTVERLNVKEKFLTLSTGQTLNFDKLLITTGKPRKLGIHGENLNGVHYLRTLSDADSIKEDLKHGKKPV
IVGAGFIGVEVAASLRSLGFEPVIEVKPFIWSTFVDEKVS EMVRKYFENKGVTFLLNEGKKEFEQSQRVNSVITSGGKKIES
SMVLVAVGISPNVEIANELQVNNGILVDEHLKAKEDIYVAGDVANILDVPVSGKRRRIEHWNNAYYTGQLAARNMMQNESYNF
LSTVWSDIFDLHIESGGETTGYDDYVMRGNFDDKSLNVIYVKGGLVIGYVAFNRDMSELEAINKLIQDKVDIKSKVDKLDKDES
FDIRKLSS