Identification of miRNA-mediated drought responsive multi-tiered regulatory network in drought tolerant rice, Nagina 22

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Supplementary Information



Supplementary Fig. S1. Field set up for implicating drought stress on rice cultivars. (a) Three feet deep pits were lined with polyethene were prepared to regulate water supply and avoid the water leakage from outside. (b) N22 and PB1 plants growing in the specially designed fields. (c) Picture showing the measurment of soil moisture content in the fields.



Supplementary Fig. S2. qRT-PCR analysis of Rubisco small sub-unit (*RBCS*) in flag leaf and *OsbZIP23* in flag leaf and spikelet of N22 and PB1 under drought stress at heading stage. Four biological replicate were performed and the standard error is represented as error bar on the top of the bar.



Supplementary Fig. S3. Flag leaf and spikelet preferential miRNAs in N22 and PB1. (a) Hierarchical clustering of log₂ transformed expression levels (TPM) of flag leaf and spikelet enriched miRNAs (having 10 fold higher expression in one tissue w.r.t to the other) in N22 and PB1. The clustering was performed using the Euclidean distance algorithm with average linkage. (b) qRT-PCR analysis of spikelets enriched miRNAs in spikelets relative to the expression in flag leaf of N22 and PB1, respectively. The expression represents the data of 3 biological replicates with three technical repeats. The error bar represents the standard error. FL- flag leaf; SP- spikelet; C- control; DT- drought.



b



Supplementary Fig. S4. Drought regulated miRNAs in flag leaf and spikelet. Hierarchical clustering of log_2 transformed expression levels (TPM) of drought responsive miRNAs in flag leaf (a) and spikelet (b) of N22 and PB1. miRNAs with ≥ 2 fold up/down regulation in flag leaf of spikelet dought samples w.r.t. respective control in N22 and PB1. The clustering was performed using the Euclidean distance algorithm with average linkage.

Biological Process

Adaxial/abaxial axis specification		2
adaxial/abaxial pattern specification		2
Adventitious root development		3
Anatomical structure development		38
ATP synthesis coupled proton transport		3
Auxin metabolic process		3
Auxin polar transport		4
auxin-activated signaling pathway		9
Biological_process		299
Biosynthetic process		118
Catabolic process		43
Cellular amino acid metabolic process		18
Cellular carbohydrate metabolic process		3
Cellular component assembly		19
Cellular nitrogen compound metabolic process		85
Chiorophyli metabolic process		3
Connamic acid biosynthetic process		2
Defense regnance to heatarium		10
Detense response to bacterium		10
Electron transport choin		2
ambrua davalorment		5
embryo development	_	13
ambryo development ending in seed dormancy		4
Endervalachtic closucce in ITS1 to concrete SSU me		4
Endonucleolytic cleavage in 1151 to separate SSU-rma		
transport		2
SSU man from		2
SSU-mainom		2
Gana gilanging by mima		2
Gene silencing by mirna		5
Generation of measureer metabolites and energy		3
Generation of precursor metabolites and energy		10
glycolytic process		0
Innote immuno nonnon	_	2
Inflate Infindule Tesponse		2
L asf mamba ann asia	_	2
Lear morphogenesis		2
Meansmalequier complex assembly		2
Malata matabalia process		2
Mariatem initiation		5
modulation by virus of host morphology or physiology		2
Mrna transport		2
Photorespiration		2
Phyllome development		2
Polarity specification of adayial/abayial axis		4
Posttranscriptional gene silencing		3
Primary cell wall biogenesis		2
Primary shoot apical meristem specification		4
Proteasome core complex assembly	_	4
Protein complex assembly		12
Protein folding		12
Proteolysis involved in cellular protein catabolic		
process		5
Proton transport		4
Purine nucleotide transport		2
Pyridoxine biosynthetic process		2
Radial pattern formation		2
Regulation of cell cycle process		3
Regulation of lipid metabolic process		2
Regulation of photomorphogenesis		2
response to auxin		12
Response to cadmium ion		35
Response to cold		18
Response to far red light		7
Response to fructose		4
response to hormone		4
Response to light stimulus		10
Response to misfolded protein		5
Response to salt stress		18
Response to stress		58
Response to sucrose		0
Ribosomai small subunit biogenesis		2
sheet system development		4
Small malagula metabolia process		51
Spermidine biosynthetic process		2
Sphingolinid biosynthetic process		2
Stomatal lineage progression		2
Stomatar Inteage progression		5
symptosis, encompassing mutualism through parasitism		21
Transcription, DNA-templated		27
Translation		2/ 5
Tricarboxylic acid evela		5
Ubiquitin-dependent protein catabalia process		11
Virus induced gene silencing		5
Vitamin B6 biosynthetic process		2

Cellular Component

Apopiasi	22
Cell	237
Cell wall	26
Cellular_component	262
Chloroplast	69
Chloroplast envelope	25
Chloroplast stroma	29
Cytoplasm	168
Cytoskeleton	10
Cytosol	60
Cytosolic ribosome	17
Cytosolic small ribosomal subunit	8
Eukaryotic translation elongation factor 1 complex	2
External encapsulating structure	21
Extracellular region	21
Golgi apparatus	19
Intracellular	223
Membrane	75
Mitochondrial proton-transporting ATP synthase	
complex, catalytic core F(1)	2
Mitochondrial respiratory chain complex I	7
Mitochondrion	38
Nucleolus	19
Nucleus	99
Organelle	198
Phragmoplast	5
Plasma membrane	69
Plasmodesma	21
Plastid	69
Proteasome complex	6
Proteasome core complex	5
Proteasome core complex, alpha-subunit complex	3
Protein complex	39
Ribonucleoprotein complex	13
Ribosome	25
Stromule	6
Vacuole	33

Molecular Function

2 iron, 2 sulfur cluster binding		5
Ammonia-lyase activity		2
ATP:ADP antiporter activity		2
Copper ion binding		14
Endopeptidase activity		5
Endoribonuclease activity		4
Hydrogen-translocating pyrophosphatase activity		2
Inositol phosphoceramide synthase activity		2
Iron-sulfur cluster binding		6
Lipid binding		11
L-malate dehydrogenase activity		3
Malate dehydrogenase activity		3
Mirna hinding		3
initia officing		1. Contract (1. Co
Molecular_function		344
Molecular_function Oxidoreductase activity, acting on the CH-OH group of	_	344
Molecular_function Oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor		344 6
Molecular_function Oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor Phenylalanine ammonia-lyase activity		344 6 2
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Ministry function Oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor Phenylalanine ammonia-lyase activity Phospholipid binding Protein domain specific binding RNA binding Sirna binding		344 6 2 5 2 27 3
Minite Johang Molecular function Oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor Phenylalanine ammonia-lyase activity Phospholipid binding Protein domain specific binding RNA binding Sirna binding Structural constituent of ribosome		344 6 2 5 2 27 3 20
Minimo Management Molecular function Oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor Phenylalanine ammonia-lyase activity Phospholipid binding Protein domain specific binding RNA binding Sirna binding Siructural constituent of ribosome Structural molecule activity		344 6 2 5 2 27 3 20 25
Ministry Control of the control of t		344 6 2 5 2 2 27 3 20 25 5 5
Minimo Management Molecular function Oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor Phenylalanine ammonia-lyase activity Phospholipid binding Protein domain specific binding RNA binding Structural constituent of ribosome Structural molecule activity Threonine-type endopeptidase activity Transcription factor binding		344 6 2 2 27 3 20 25 5 3

P-value 0.01

Supplementary Fig. S5. Gene Ontology enrichment analysis of genes targeted by miRNAs showing drought mediated downregulation in N22 flag leaf. The different GO terms with an enrichment pvalue of ≤ 0.01 belonging to biological process, molecular function and cellular component were shown with the number of genes and heat map representing the p-value.

Biological Process

Cellular response to UV-B	2
Cysteine biosynthetic process	3
Multicellular organismal development	3
Removal of superoxide radicals	3
Response to copper ion	2
Response to iron ion	2
Response to ozone	2
Response to salt stress	8
Stomatal lineage progression	2
Superoxide metabolic process	3
Ubiquitin-dependent protein catabolic process	4
Vegetative phase change	2
Virus induced gene silencing	2

Cellular Component

Cell	46
Chloroplast	14
Chloroplast envelope	7
Cytoplasm	32
Cytosol	12
Cytosolic large ribosomal subunit	3
Cytosolic ribosome	6
Intracellular	41
Membrane	20
Mitochondrial inner membrane	3
Nucleolus	6
Organelle	35
Plastid	19
Ribonucleoprotein complex	5
Ribosome	8

Molecular Function

Copper ion binding	14
Superoxide dismutase activity	3
Electron carrier activity	9
Antioxidant activity	2
Protein homodimerization activity	3
Phosphoprotein phosphatase activity	3
Structural constituent of ribosome	5

P-value 0.01

Supplementary Fig. S6. Gene Ontology enrichment analysis of genes targeted by miRNAs showing drought mediated up-regulation in N22 flag leaf. The different GO terms with an enrichment pvalue of ≤ 0.01 belonging to biological process, molecular function and cellular component were shown with the number of genes and heat map representing the p-value.

a

Biological Process

Adaxial/abaxial axis specification	2
adaxial/abaxial pattern specification	2
Biosynthetic process	35
Chlorophyll metabolic process	2
Determination of bilateral symmetry	4
Embryonic pattern specification	2
Integument development	2
Lignin biosynthetic process	2
Malate metabolic process	2
Meristem initiation	4
Polarity specification of adaxial/abaxial axis	4
Primary shoot apical meristem specification	2
Proteolysis involved in cellular protein catabolic	
process	2
Radial pattern formation	2
regulation of transcription, DNA-templated	14
transcription, DNA-templated	13
Translation	8
Xylem and phloem pattern formation	2

Cellular Component

Cell	62
Cellular_component	73
Chloroplast	17
Cytoplasm	39
Cytosol	20
Intracellular	54
Membrane	24
Nucleolus	7
Nucleus	30
Organelle	52
Plasma membrane	25
Plasmodesma	11
Plastid	18
Proteasome core complex	2
Ribonucleoprotein complex	7
Ribosome	7
Vacuolar membrane	7
Vacuole	10

Molecular Function

Copper ion binding	9
Electron carrier activity	8
Endopeptidase activity	2
Hydrolase activity, acting on acid anhydrides, in	
phosphorus-containing anhydrides	8
Lipid binding	5
Structural constituent of ribosome	7
Structural molecule activity	7
Threonine-type endopeptidase activity	2

Supplementary Fig. S7. Gene Ontology enrichment analysis of genes targeted by miRNAs showing drought mediated (a) down and (b) up-regulation in PB1 flag leaf. The different GO terms with an enrichment pvalue of ≤ 0.01 belonging to biological process, molecular function and cellular component were shown with the number of genes and heat map representing the p-value.

Biological Process

Aging	4
Anatomical structure development	10
Biosynthetic process	18
Leaf senescence	2
Methionine biosynthetic process	2
regulation of transcription, DNA-templated	13
Response to cold	4
Response to salt stress	6
transcription, DNA-templated	7
Water transport	2

Cellular Component

Cell	34
Chloroplast envelope	6
Intracellular	31
Mitochondrial respiratory chain complex I	2
Mitochondrion	8
Organelle	27
Plastid	12

Molecular Function

2 iron, 2 sulfur cluster binding	2
DNA binding	14
Transporter activity	5

P-value C		0.C	0.01						

Biological Process

а

Biosynthetic process	25
Catabolic process	18
Cellular amino acid biosynthetic process	3
Cellular amino acid metabolic process	7
Cellular nitrogen compound metabolic process	23
endonucleolytic cleavage in ITS1 to separate SSU-rRNA	
from 5.8S rRNA and LSU-rRNA from tricistronic rRNA	
transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	2
Endonucleolytic cleavage to generate mature 3'-end of SSU-	
rrna from (SSU-rrna, 5.8S rrna, LSU-rrna)	2
Nitrogen compound metabolic process	3
N-terminal protein myristoylation	2
Pentose-phosphate shunt	4
Peptidyl-proline modification	2
Photorespiration	3
Response to cadmium ion	7
Ribosomal small subunit biogenesis	2
Small molecule metabolic process	20
sulfur compound metabolic process	5
Translation	8
Translational elongation	4
Ubiquitin-dependent protein catabolic process	5
	•

Cellular Component

Cell	57
Cellular_component	63
Chloroplast	18
Chloroplast envelope	7
Chloroplast thylakoid membrane	5
Cytoplasm	41
Cytoplasmic vesicle	2
Cytosol	17
Intracellular	52
Membrane	22
Organelle	44
Plasma membrane	18
Plastid	21
Protein complex	13
Thylakoid	6

Molecular Function

Coenzyme binding	3
Copper ion binding	6
FK506 binding	2
Hydrolase activity, acting on carbon-nitrogen (but not	
peptide) bonds	3
Isomerase activity	5
Ligase activity	6
Racemase and epimerase activity, acting on carbohydrates	
and derivatives	2
Structural molecule activity	6
Translation elongation factor activity	2

Supplementary Fig. S8. Gene Ontology enrichment analysis of genes targeted by miRNAs showing drought mediated (a) down and (b) up-regulation in N22 spikelet. The different GO terms with an enrichment pvalue of ≤ 0.01 belonging to biological process, molecular function and cellular component were shown with the number of genes and heat map representing the p-value.

Biological Process

Biosynthetic process	9
Transcription, DNA-templated	5
Stomatal lineage progression	2

Cellular Component

Cytosol	5
Intracellular	13

Molecular Function

Transcription factor binding	2
DNA binding	7
Protein dimerization activity	3
ATP binding	7
Helicase activity	3



Biological Process

Anthocyanin-containing compound metabolic process	2
ATP biosynthetic process	2
Biosynthetic process	35
Catabolic process	17
Cellular amino acid metabolic process	9
Cysteine biosynthetic process	3
Defense response to bacterium	5
Endonucleolytic cleavage in ITS1 to separate SSU-rrna from	
5.8S rrna and LSU-rrna from tricistronic rrna transcript	2
Endonucleolytic cleavage to generate mature 3'-end of SSU-	
rrna from (SSU-rrna, 5.8S rrna, LSU-rrna)	2
Regulation of ARF gtpase activity	2
Ribosomal small subunit biogenesis	2
Salicylic acid biosynthetic process	2
Small molecule metabolic process	22
Translation	11
Translational elongation	5
Ubiquitin-dependent protein catabolic process	6

Cellular Component

Cell	63
Cellular_component	71
Chloroplast	24
Chloroplast envelope	9
Cytoplasm	43
Cytosol	18
Cytosolic ribosome	6
Cytosolic small ribosomal subunit	3
Intracellular	56
Organelle	48
Plastid	25
Ribonucleoprotein complex	6
Ribosome	8

Molecular Function

Acid-amino acid ligase activity	4
ARF gtpase activator activity	2
Copper ion binding	10
Electron carrier activity	9
Ligase activity	8
Phosphotransferase activity, alcohol group as acceptor	3
Structural constituent of ribosome	8
Structural molecule activity	8



Biological Process

ATP synthesis coupled proton transport	2
auxin-activated signaling pathway	3
Biosynthetic process	25
Calcium-mediated signaling	2
Cellular component assembly	6
Cellular protein metabolic process	2
Cellular response to nitrate	2
Cellular response to phosphate starvation	3
Iron ion homeostasis	2
Lateral root development	2
Lateral root formation	2
Macromolecular complex assembly	6
Pollen maturation	2
Protein complex assembly	5
Protein folding	4
Protein targeting to chloroplast	2
Regulation of photomorphogenesis	2
Response to cadmium ion	10
Response to molecule of bacterial origin	2
Response to salt stress	7
Stamen development	2

Cellular Component

Apoplast	7
Cell	54
Cell wall	8
Cellular_component	60
Chloroplast stroma	7
Cytoplasm	39
Cytosol	17
Extracellular region	7
Intracellular	49
Membrane	20
Mitochondrial respiratory chain complex I	3
Mitochondrion	11
Nucleolus	6
Nucleus	19
Organelle	43
Plasma membrane	22
Plasmodesma	8
Protein complex	12
SCF ubiquitin ligase complex	2
Vacuolar membrane	6
Vacuole	8

Molecular Function

Auxin binding	2
Inositol hexakisphosphate binding	2
Transcription factor binding	2

Supplementary Fig. S9. Gene Ontology enrichment analysis of genes targeted by miRNAs showing drought mediated (a) down and (b) up-regulation in PB1 spikelet. The different GO terms with an enrichment pvalue of ≤ 0.01 belonging to biological process, molecular function and cellular component were shown with the number of genes and heat map representing the p-value.



Supplementary Fig. S10. Multiple sequence alignment of MIR-precursor sequences from N22, PB1, Vandana and IR64. (a) MIR1871 precursor; (b) MIR159f; (c) MIR2878; (d) MIR528; (e) MIR408; (f) MIR398b and (g) MIR397a. Dots (.) represents the identical sequence bases and SNPs are shown in red letters.

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	122 181 181	Martin Arage Anticenting and Arage A	MYCCONSENSUSA	T AGCTTTATGTGCA	4.CATACTTTGSAIA		 ABRELATERD1 √CACGEGTTAATT 	11CTATACTTC	CURECORECRAYCI	CONSENSUSAT	ATCAATAACTTCT	GCTGCATTGCTGC	1,120 AGCCCATTTACAA	CURECORECR LINO ATTAGTGTACCAGTC	ATGCCTATAGTA
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	ACCTATERD1	MYCCC	NSENSUSAT	CURECORECR		WYCATRD22	
IR64 PB1 N22 Vandana	GTGCTCGGATTGGCTGCCCGTACGTTGTCCCCTTC	akcagagaakggatgactgactgacgaggaagaakaagaag	CAGACACGGGCCATTTCTGTGAGGTGTAA	TACTGAACTTTG <mark>BTAQ</mark> AGACTTCAGGATTTT	ITTTTTCGAGTCTTGTTTTACTTCTCTGTGTGTGTGT	IGT GO DA A TE CGT CT GT TT GT CC GA A TT CT (BARETCARAGETTAGAGTTTOGAATTTCGGGAGCCGAT 231 231 231 231 231
IR64	АТСАТСТСАААСТӨТСАТАӨАССӨӨССӨӨСӨАААА	ABRELATERDI ABRELATERDI .AAT ABCARATCAABCAATACAAGGATGC	ACGTATERDI ACGTATERDI CURECORER CURECORER 1871ACGTCACGGCAAGGTCTATT	твовововтет севая тет тастая гтотатт	ICAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	асталанотавасятаттстатотавата.	MYSCORE MYSCORE MYSCOREALGTATCTTATTTGATCGTAAGCTGTTATAT 498
PB1 N22					<mark></mark>	<mark>чс</mark>	502 547.4
Vandana IR64 PB1	TTTAGACGAATGAAGTGGTTGTTTTGTCCCGCA	ICA CGGATACAGCTTCCACAGGGGGGCACGGAGAGGACAC	CGCTTTTACCATCAGACTTGGTCTCTGCTGGG	104AGCTTATGTCAGCCAAAATCAGATATTCTC	21141C49111A1111111111110100	ATTTAAGGGCCTGTTCACTTTGATGACATTT	100 1040011100140411110011401140114011749 104001140141411100144444444444447
N22 Vandana							749
PB1	GGCTACATTTAATTTGCTGTCAAAATTTGATAACTA	TGTAAGAAATCCTGCCAAAAATTTGGCAACTATATCAA	AATTTTGGCAATACCAAAATTTTGGTAATGTTT	TTTTGTCATCAAAGTGAACAGGCCATAAAT	IAGAAGCCATAAGGTAGAAAAAAACCCAGGTTTTTTTC-	AGATTCTCGAAAGTTTACAACCAATTAGTTATI	FTCTCGGGAATTTTTAAGCTACTCAAACAGACCCTCGGTGCC 999
N22 Vandana			G	ТТ.	A		1003
			MYBCORE MYCATRD22				
IR64	GTAAGTGCAAACCTGCTCTGGCTCAATCGCATAGAG(30ACGCGCTGCGCACAGCCCGATGCTTTTCTATAGTTC A	сатавтесас <mark>савтта</mark> с <mark>сасатв</mark> васвватав	0AT0AT000A0A0TTTTCT0TAT0CTCACA	<pre>fitattgaatcttactaaacccacttttataatgcatgaca</pre>	3CATTGACTTTTGAACATATATTATCTTAATT1	FITAAAAATGAATTAATTATTATTGITTGITGTGAGT 1250 1749
N22			GTAC.			c	1254
vanuana	LORECORECR			ICURECORECR	CURECORECR	ICURECORECR	
IR64 PB1 N22 Vandana	TTTTTATGAA <mark>GTAC</mark> TTGAACATGATTTATATT	TTATGGATTTGGTAAAAATTTTGTAATAAGAGGAAGGA AG	TGGTATTTAAAAACGAGAGTATTTAACA	TTTTAATGT <mark>STAG</mark> TATCATTG6CGACAATTT	TTTTTCAAAATTGGGGGAGTA <mark>GTAG</mark> TTCACATATTGGCATGG	ISTACATCAGACGATACTAGTAGGATAGATAGATAGATAGAT	5TC6FC6C6TTCAACTTGTTGGA6ATCTGATGC6ATATAA 1501 1500 1505 1505
	ACGTATERD1 MYCATRD22	0	URECORECR		MYB2CONSENSUSAT	IMYB2CONSENSUSAT	I MYBCORE
IR64 PB1	ATCGATCCTACGTOACATGACAGACTGGACCCTTGTC	SAAATTATGGATTGGATGATTAATCACTGATAGGTA <mark>G</mark>	TACTAGCAACTCAATCACACAAGCGAAGT	GAGAAGAAAGGAACCTCTTCCTGCATTAG	L <mark>MADDE</mark> CGACGGGGTCACTGAAAGTGAAGCCTGTGGGGGCAC	ACGACCACCTCCTDAACGGATCTGTGGCTT/	ACCCGTCGCCTTAGAGCGTTTGCTCCAACGCTTCTGCA6 1751
N22 Vandana							0¢/1 25/1
i	CURECORECR CURECORECR	CURECORECR	ICURECORECR MYCCONSENSUSAT	ECORECR	83		
PB1	I AGAAGAGI ACAAGCGAAAGGCGA I GI GA	4 A 1 GCAAGGC GAA <mark>G AC</mark> AAGGGGGGCCCC AAVGA	010000000818101801801801900	1.4.1.4.0.4.4.9.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4	AI A I GCCAGCCI I CACCAA I GGA I GCA I CAGCAGCAGCACA 	30AAAATTT 061111 06651 A661 A661 61 1 A 10	3 AGG CIGG GGCIGIAGCAGCAGC 1995
N22 Vandana							1995

d.

		ABRELATERD1	.MVRCOPE	ILTRECOREATCOR15	ACCTATERNI	
Vandana PB1 IR64		200011110200001111116110202010111021102041110210110201102	TODOGITEAACCTGTCATTGTCG	csadecerecocon coa acon occon acce	354/05/07 05/05/05/05/05/05/05/05/05/05/05/07/07/02/05/07/07/02/05/05/07/07/02/05/05/07/07/02/05/05/07/07/02/05/05/05/07/05/05/05/05/05/05/05/05/05/05/05/05/05/	251
N22	2	Γ	1000			254
Vandana		00000000000110011111011111111111111111	NUBCORE COCTOOCCAGETTCCTOGTAAATGOOC	TGAAT 066600AT 00TT 600A000CT06760A1		505
IR64 N22					508	508 508
	ICBHY ACGTATERD1 ACGTATERD1	INVCONSENSISAT			INVCCONSENSISAT	
Vandana PB1		TTTAOCTAOCGAACTTTTTTTTTTTTT <mark>DATOTG</mark> ATATGCTTTAAGAACTTTAAGCAAAAATCAAACTCTACCGATGAAAGCGACGCGAA	VAGTGOGAAGGAGGAAGAAGGAGGCAAG	A GOGGA GGA A OCCAAT A A OGT OCGAT A T CAO	CATCTCTGCDATCTETGAAGAGCTCGAGGAGATAGAGGTAGGAGGGTCAGG 759	759
IR64 N22	2				267 267	762 761
		JOUREOBECK	IMYCATERD1	IACGTATERD1		
Vandana	a TGGAGAAGCAGGACCCACTGACCACTATTTTTATCTTCTTGTTTGATTGA	CCCACATATTTTGETTTTATATTTTTAGTTTTCAATGCTTTTATATTTTTTTGGGGGGATT <mark>GTAC</mark> TGTC <mark>ACGET</mark> AGGCATC	CATGTCAATGC <mark>CATGTGGGGGGGGAATA</mark> T	CTAGTTATAAGGAGTC <mark>ACGT</mark> AGACGCTCATG	AGATAAAACCGGGGGATAATACTTCCGGGGGGGGCCTTGTTTGCACTATTTTTTA 1013	1013
IR64	4				101	1016
N22	2				101	1015
Vandana	A CONTROLOGICATION OF A DATA TO THE TO THE TO THE A DATA	CONTRACTOR AND	MYCCONSENSUSAT	01101010000000000000000000000000000000	A TACCARDAN AND A TACCARD TO TACTART A TACTARD AND A TACCARD	201
PB1		6. 6. 10 10 10 10 10 10 10 10 10 10 10 10 10			1270	1270
IR64 N22	2				1265	1269 1268
		MYBIAT CU	RECORECR			
Vandana PB1	a AAAAGAAACTAAACAATTAAAAATTATTATGACTATCATTAAACTATCATAAAAAGAACT 1	COGAAATTAACTTAAAATAGGTTTCAAAATTTTTTTTTTT	ACTTCTACTTAAGGAGAGAATAATAA	GTAGGACTAACAACCACAAACTGGTAAAOCGG	STAGCTACTTCAGACTCTCAGCATTTTAGCATTTTAAGATCOCATCCAGACT 1520 1510	1520
IR64 N22	4 0				151	1515
		CURECORECR MATCORE CUREORECORECR CURECORECR CORECR CORECR CURECORECR CORECR	MYCCONSEN	USAT ICURECORECR	СПИЕСОИЕСЯ	
Vandana PB4	a CCATCGAATTTACAATATTCTCTTAAAATAGCTCAAAATTCCSTAGAAATTCGTCTCGAT	GAGA T <mark>OT AO</mark> GACA TET C <mark>OT OT TO</mark> CT GCO <mark>GT AODT AOT</mark> AOT AOT AA AOOGOOT GAGCAGOOCOGOT CGAA GAAGGAAGA	NGTGTTTCAGCTCOCCCACCATTTGC1	OCTODETETECA <mark>CTAC</mark> OCATETTOGAGAG	324GTTISTACTACCATCCTT602ACAGGTCA02AT03TGTACT02A6CTTT 1774	1774
IR64 N22	- 4 0				92/1 1921	1776
	I CURECORECR	CURECORECR				
Vandana PB1 IR64	a controccontanactiontoontococovanttoococociatoadanterdanacta 4	GIACTACT <mark>GIAC</mark> TACAGTCCAATGGTTCAAGGCAAAQACATTCCGGTGGGGTGG	21TGAOGATGATGGCGTTGGCCTAACC	05ATTT0CAGT0CATCA0GTAAG000AAAA00	ATGGTTAGATAGAGAAG 1996 1992 1992	
N22	2				1998	

	SCORT CONCEALC
1	A GROGET TTOCT CARGE OGG
ACGTATERD1	CARCARGEATTICARSOCTOCISCARCARGARAA
	TOPOPOP

			ACGTATERD1		ACGTATERDI
N22 PB1 IR64 Vandana	TOGT DESAIGT CAT DEALESANDETT DEALEODRESANDERANDT POPULAR SOCIESANDERANDER	DOBOCIONALTI TRACIMICOCOCIONO DO TRACIONACIÓN COCIÁNT CIMICOCO DO COCIÓNICON A A	Water T COCA GSOCIET T CCT CA GST CAST CASCAST T COCCANTC	MAGNATTGGTGT 024ACTT 02020202020217 0200	20234/65/401 02020/67 And 53307 02/4A 0202050504/60591 020-665 11 231 231
N22 PB1 IR64	06911100AGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	דפספטאטנטטר פרר רפסטפטנטון פרי רטפטטסטר פרי רטפטטסטר פרי ראטטער איז דפיז איז איז איז דפטטער דפר דער דפר דער דע א	TT RECT T CCCREMENT ON CONCREMENT OF CONTROL	GGT AN GOM GAN GANGAGGAA GAGGAAGAGGGGGC A A A	ATTT GGT CACCET GT GT AM AM T GT GGGT CCCCT CT PARCH (SGT CA 502 302 302 303 303 303 303 303 303 303 303 303
Vandana	, MOBIAT	Α	MYCCONSENSUSAT	Α	
N22 PB1 IR64	GOROMANATACTAANTTAGTGGATGGAGTGTCOCGTGGGAAAA <mark>TAACCA</mark> CATTTACATAG	GBOCTGT TTAGTT OSCRAMAGAWATTTT TTGST GCOCOTOSATGTT ANOCGATGTT	341 6341 I TT 0654 CA <mark>RMAN]</mark> SAAAAA CTAATT CATAACT	CGCCTGAAAACT GCAAGACGAAT CTTTTAAGCTTAATT, G G	WACTER ATTACTATACTERACACTTA-TAACTAAT 72 73 A. 73
Vandana N22 N22	CATAGGTAATTAGGCTCAAAAAATTCGTCGCACGATTTCCATAGAAATTATGGCAATTAG	MICATEROL MICATEROL GTTTTGTTTTATCATARATEROL	MYBIAT DGAGGAAAAAATTAGAAACT <mark>AAAACA</mark> GGCCACATTGTCTTCC	MYELAN	ACANTER CETCA-ACAMANTTTACATTTTCATGGAA 1002
IR64 Vandana	L	c. c.		Å	T
	CURECORECR	CURECORECR	CURECORECR	TALAN	CURECORECK
PB1 PB1 IR64 Vandana	GGSAGGSAGGSATATATATATGTT GGTTATATGGGG <mark>GIA</mark> GTT <mark>GIA</mark> GTTAGATO	asadan adam adam adam adam adam adam adam	NT CACAG <mark>IA</mark> NT ACT OF CLOCENTIAL ACAT THORIGET AACH	TTTCAGTGFCCAAATTCTTTTAACCAAGTTAAAAAA	ai a lacangi ti a taawaa <mark>gi a</mark> dke aacaa ti ti taacacaa ka 1353 1265 1255
N22 PB1 IR64 Vandana	ANONIATTATOATTATATTAATGAMOTAATTTIGITGIOGIMAATGITGITATTITT	TTANTTT AGTT AAACCTAAAAAAATTGAATAGAAAAAATAAAAACGGCTTATAATATATAT	NAMAGNATATATAATAACAAGNCIACATTITTATGIA	CURCORECK	Contrant Control Theorem Contrant 1981 Contrant Control Control Control 1986 Control Control Control 1986 Control Control C
	TLEW	, CURECORECR , CURECORECR	CURECORECR	CURECORECR	ACCTATERD1 CURECORECR CURECORECR ACCTATERD1 CURECORECR]
N22 PB1 IR64 Vandana	ATCTTGCTANTCTGCAMTINGCQAGATCCCAGATTGCTGCTGTTGCC	ICAN <mark>EMICATINE CONCUTATTIATIC CONCUTECCANCTTICS (ATTACIA) ACIA.</mark> Canada Catalogo C Catalogo Catalogo Cata	3/GGT 6/GGC/GG/A/GGC/A/T <mark>GT M</mark> /CT 6/GGGC/GGGC/GGGC/GG	AGTARAGCI GIACTOTI GOCTI COOSCAAAGCCAATG	1.14 <mark>81.14031.14</mark> 011.04 <mark>8031.16</mark> 11.0004.00041.0640.0440 1757 1757
N22 PB1 IR64	CUMERCINECK CAMANGETAJDEA COSCAT COAT COT COT COT COET COMES CAMANGETAJDEA COSCAT COAT COAT COT COT COT COET COMES	ABRILATISOL MATALOGISA OSOSTITI OSOTI OSOTI AT TO OSOCIA OSOCIA OSOCIA OSOTI CONTINATO COSTI OL MATALOGISA OSOCIATI OSOTI OSOCIA OSOCIA OSOCIA OSOCIA OSOCIA OSOCIATISOL	INTCAROLARGETTAATTAG2000G64G4TTTTTGaarderise	MT 200004400441009410090410011AT0920 A	1TC02C16000C01TG3464C464C464TG34AC02C646 3885 2000
Vandana					6667

f.



Supplementary Fig. S11. Sequence alignment of DTA-miRNA promoter sequences in N22, Vandana, PB1 and IR64. Sequence alignment of 2kb upstream region of (a) MIR1871, (b) MIR159f 2kb, (c) MIR2878, (d) MIR528, (e) MIR408, (f) MIR398b, (g) MIR397a in four cultivars namely N22, Vandana, PB1 and IR64. Dots (.) represents the identical sequence, dashes (-) represents gaps and the cis-acting elements associated with stress were highlighted.



Supplementary Fig. S12. OsSPL9 promoter analysis (a) Cis-regulatory elements in the 2kb upstream promoter of OsSPL9. (b) RT-PCR of OsSPL9 in response to copper starvation in N22 seedlings. Data represents the mean value of three biological replicates and three technical repeats.

b



Supplementary Fig. S13. qRT-PCR of copper ATPases in N22 and PB1 flag leaf in response to drought. Three biological replicates were analyzed with three technical repeats. Error bars represent the standard error.

a COPT1



1100	20 40 1 1	60 1	80 1	100 	120
N22 ANDANA	CTACCTTCCTCTTTTGTGTTGCTGACCCAAAATTGCTCCTCTGCATGCA	GAGTTCATGTTGCTGAAT	TCCTCATGCCACTGTATT	GTCCATTTTTTGCTGGTA	AAAAGCACTGAACT 120
PB1			.т		
IR64			. т		
	140 160	180 CURE	200	220	240
N22	ACTGACTGGATTGGCAATTCCATGAATGATGATTAGCTCTACCGAAACAGTAT	IGCTACCCTGAAAGTACT	GTCTTACTGCCTCTATAA	STTTGCTTTGCTCCATCO	SATTTGACGCTCTAT 240
ANDANA					
PB1					
IR64					
	ACGTATERD1 280	300	320	MYCCONSENSUSAT	360
N22	GGGTTATCCTTCACGTTCTCCCATCTTCTTCCTGCTGCACCATGGGCCACCG	SCCAGTGGTAAATTCTCT	GCGACGCAAAACAGAGAG	CATATOCAGCAAACATT	CAAAAGGTTACTGG 360
ANDANA					
PB1	C		. A		
IR64	C		. A		
	CURE 380 MYBCORE	420	440 10	JRE 460	CURE
N22			CGTCACCACTTTTAGTAG		
ANDANA					452
PB1	ΤC				
IR64	ΤC.				
		MYCCONSENS	JSAT MYCCONSENSUSAT		
	MYBCO	RE	MYCCONSENSUSAT	500	
N22			TTCCACATGICGAAGAAC		
NDANA			ITCCACATO I GGAAGAACA		
PB1					600
IR64					600
	ALL CLIDE	MYCCONSENSUSAT	122.9		N-2221
NIGO					
NZ2	- TIGGA TOAGAATA TA TOAAACUGGACTU I <u>BTAB</u> AATACTATACAATACTCC	ATTOTA			691
PB1	. A				
IR64	. A				
					c
	740 760 I I	780 MYCC		820 CUF	840 I
N22	A A CONCENTRATE OF A CONCENTE OF A CONCENTE OF A CONCENTE	JIIIIIATGCACCCAAC	TOAACAAAAGTTAATCAA	IIIGAUGACATAATT <u>GTA</u>	R11
PB1					
IR64					
	MYCCONSENSUSAT	50/1001			
	860 I	900 MYCCO	ISENSUSAT 920	940 I	960 I
N22	TGAACACTTCGCGGAGGGGGCAATTATAATTGGTCAGTTGTGTGTG	CTTAAAATCTGGCCACTT	GTAAATTCTACAATTTCG	TCTTGACAGTGGAAGCCT	CCGAAGGAAACCTT 959
PB1					
IR64					
	CURE		ICURE		
00000	980 1.000	1,020 I	1,040	1,060 I	1,080 I
N22	III GUGCCCATGCCGTAUGATGGATTTTCCTCGTTGACATTCTGCGCCCAACG	JUACAGCATGGCATGTCG	I I GT CCATAAACGTACAC	AUAAAAAAAAGCACCAAA	IIGGCITCAAGATA 1079
					1051
PB1					
PB1 IR64					
PB1 IR64					
PB1 IR64	1,100 1,120	1,140 MYBCORE	1,160 ^{CURE}	1,180	CURE 1,200
PB1 IR64 N22	1,100 1,120 AGGTCGTGGAAGCGTGCTACGGGGGGGGGGGTGATTTGTCTGGTGGAATCTAAGGCC1	1,140 MYBCORE		1,180 I ATAGGATGATTAGAGCAA	CURE 1200 GTACAATAGCAGGC 1199
PB1 IR64 N22 ANDANA PB1	1.100 1.120 Aggtcgtggaagggatgattttgtctgggaatctaaggcc1	1,140 MYBCORE TCCATCAATGATCTGTTA	1,160 CURE CCAGAATACCTGCCGTAG	1,100 NTAGGATGATTAGAGCAA	CURE 1,200 GTACAATAGCAGGC 1199 170 170 170 170
PB1 IR64 N22 NDANA PB1 IR64	I,100 I,100 AGGTCGTGGAAGCGTGCTACGGGGGGATGATTTGTCTGGTGGAATCTAAGGCC1	1,40 MYBCORE TCCATCAATGATCTGTTA A.	1,160 CURE	1,100 NTAGGATGATTAGAGCAA 	CURE 1.200 GTAGAATAGCAGGC 1199
PB1 IR64 N22 ANDANA PB1 IR64	L100 L120 Aggtcgtggaaggatgattattgtctggaatctaaggc	1,40 MYBCORE TCCATCAATGATCTGTTA A A	1,100 CURE	1,000 A TAGGA TGA TTAGAGCAA C	CURE 1200 GTACAATAGCAGGC 1199
PB1 IR64 N22 ANDANA PB1 IR64	1,100 1,120 Aggtcgtggaagggatgattatttgttggaatcaaggga	1.140 MYBCORE TCCATCAATGATCTGTTA A.A. Y 200 MYC	T, 100 CURE	1,100 NTAGGATGATTAGAGCAA 	CURE 1,200 GTACATAGCAGGC 1199 TTACATAGCAGGC 1199 TTACATAGCAGGC 1199 TT 1200 MYCCONSENSUSAT
PB1 IR64 N22 ANDANA PB1 IR64	1,10 AGGTCGTGGAAGCGTGCTACGGGGGATGATTTGTCTGGTGGAATCTAAGGCCT 1,200 1,200 1,200 1,200 1,200	1,140 MYBCORI TCCATCATGATGTGTTA A.	1,160 CURE	1,00 XTAGGATGATTAGAGCA/ 	CURE 1200 GTACAATAGCAGGC 1199 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
PB1 IR64 N22 ANDANA PB1 IR64 N22 ANDANA	1,100 1,100 АGGTCGTGGAAGCGTGCTACGGGGGGATGATTTGTCTGGTGGAATCTAAGGCC1 1,200 1,200 ТАТААGCTAACTATAATATTTCAAAGATATAAGAAAAGGAGAAAAGG	I,140 MYBCORI ICCATCAATGATCIGITA A. A. MYC CAGCGGGCTACAGATCIG	1,160 CURE CCAGAATACCTGCCGTAG	1,500 ATAGGATGATTAGGAA 	1051 1060 CURE 1200 GTACAATAGCAGGC 1199
PB1 IR64 N22 NDANA PB1 IR64 N22 NDANA PB1	1,100 1,100 AGGTCGTGGAAGCGTGCTACGGGGGGGGGGGATGATTTGTCTGGTGGAATCTAAGGCCT 1,200 1,220 1,200 TATAAGCTAACTATAAATATATTCAAAGATATAAAGAAAAGAGAGAG	I, HO MYBCORE ICCATCAATGATGTGTTA A.A.A.A.A.A.A.A.A.A.A.A.A.A.A.A.A.A.	I, 160 CURE CCAGAATACCTGCCETAG CONSENSUSAT, 10 TAGCCAGCTGCAGTACAGG A. C. G. C. G.	1,160 ATAGGATGATTAGAGCAA 	CURE 1200 GENECATACAGGC 1199 GETACAATACAGGC 1199 CTACAATACAGGC 1199 CTACAATACAGGC 1199 CTATAACAGGC 1199 CTGTATAACAGGC 1319 CGC 1265 CTGTATAACAGGC 1319 CGC 13
PB1 IR64 N22 ANDANA PB1 IR64 N22 ANDANA PB1 IR64	1,100 1,120 AGGTCGTGGAAGCGTGCTACGGGGGTGATTTGTCTGGGAATCTAAGGCC1 1,200 1,200 1,240 TATAAGCTAACTATAAATATATTTCAAAGATATAAAGAAAAGAGAGAAAAAG A.	т,но МУВСОRI ТССАТСААТGАТСТСТТА А.А.А. 1,250 МУС САВССБОСТАСАGАТСТС САВССБОСТАСАGАТСТС Т.	TAGCCAGCTGCAGTAGA	1,100 ATAGGATGATTÅGAGGAA 	CURE 1,200 GTACAATAGCAGGC 1199 GTACAATAGCAGGC 1199 GTACAATAGCAGGC 1199 J.C. T. 1200 MYCCONSENSUSAT J.S. G. 1285 G. 1285 J.S. 1320 J.S. 1320
PB1 IR64 N22 ANDANA PB1 IR64 N22 ANDANA PB1 IR64	1,100 1,120 АGGTCGTGGAAGCGTGCTACGGGGGGATGATTTGTCTGGTGGAATCTAAGGCCT 1,200 1,200 ТАТААGCTAACTATAATATATTCAAAGATATAAAGAAAAAGAGAGAAAAGG 	I,140 MYBCORI ICCATCAATGATGTGTTA A.A. I.200 MYC CAGCGGGCTACAGATCTG CAGCGGGCTACAGATCTG T. T.	s, 160 CURE CCAGAATACCTGCCGTAG CONSENSUSAT CURE 1,200 TAGCCAGTAGAGTAGAGT A. C. G. C. G. C. G.	1,500 ATAGGATGATTAGAGGA C	CURE 1,200 GTACAATAGCAGGC 1199 GTACAATAGCAGGC 1199 GTACAATAGCAGGC 1199 J. T. 1200 MYCCONSENSUSAT 1320 MYCCONSENSUSAT 1320 MYCCONSENSUSAT
PB1 IR64 N22 ANDANA PB1 IR64 N22 ANDANA PB1 IR64	L100 L.100 AGGTCGTGGAAGCGTGCTACGGGGGGATGATTTGTCTGGTGGAATCTAAGGCC1 L200 L200 TATAAGCTAACTATAATATTTTCAAAGATATAAGAAAAGAGAGAAAAGG 	т. на МУВСОВ I ССАТСААТСАТЕТЕТТА 	1,160 CURE CCAGAATACTGCCGTAG CONSENSUSAT CURE TAGCAGCTGCASTAGAG A.C.G. 	1,60 1,50 1,50 3CTCCAAGATGTAATGTC C C C C C C C C C C C C C	CURE 1200 ETACAATAGCAGGC 1199 ETACAATAGCAGGC 1199 T. 1200
PB1 IR64 N22 ANDANA PB1 IR64 N22 ANDANA PB1 IR64 N22 ANDANA	1,100 1,100 AGGTCGTGGAAGCGTGCTACGGGGGGGGGGGGGGGATGATTTGTCTGGTGGAATCTAAGGCCT 1,200 1,200 1,200 TATAAGCTAACTATAATTATTTCCAAGGATATAAGAAAAAGGAGAAAAAG	т.но МУВСОРС ТССАТСААТСАТСТСТТА А	TAGO CAGATACTACAGA CONSENSUSAT TAGO CAGATACAGA A. C. G. C. G. C. G. C. G. C. G. C. G. C. G. C. G.	1,100 1745GATGATTAGAGCAA 1,00 30CTCCAAGATGTAATGTC 	CURE 1200 GTACAATAGCAGGC 1199 GTACAATAGCAGGC 1199 GTACAATAGCAGGC 1199 GTACAATAGCAGGC 1199 GTATAACAGGTGG 1319 GG 1285 GTGTATAACAGGTGG 1319 GG 1285 1320 MYCCONSENSUSAT 1320 MYCCONSENSUSAT 1320 MYCCONSENSUSAT 1320 1
PB1 IR64 N22 ANDANA PB1 IR64 N22 ANDANA PB1 IR64 N22 ANDANA PB1	1,100 1,120 AGGTCGTGGAAGCGTGCTACGGGGGATGATTTGTCTGGTGGAATCTAAGGCCT 1,200 TATAAGCTAACTATAAATATATTTCAAAGATATAAAGAAAAGAGAGAG	1,10 MYBCORI ICCATCAATGATGTTAT A.A.A. 1,20 MYC CAGCGGGCTACAGATCTG A.A.T. T. 1,300 ITGGCTATAGATGATTTA G	1,160 CURE CCAGAATACCTGCCGTAG CONSENSUSAT TAGCCAGTAGAGTAGAGTAGAG AC.G. C.G. GAGATAGTAGTGGGCTGC 	1,100 ATAGGATGATTÅGAGGAA 	CURE 1,200 GTACAATAGCAGGC 1199 GTACAATAGCAGGC 1199 GTACAATAGCAGGC 1199 GTACAATAGCAGGC 1199 GTACAATAGCAGGC 1199 JUNCCONSENSUSAT 1320 MYCCONSENSUSAT 1320 MYCCONSENSUSAT 1320 MYCCONSENSUSAT 1320
PB1 IR64 IR64 N22 ANDANA PB1 IR64 N22 ANDANA PB1 IR64 N22 IR64 IR64	1,100 1,100 AGGTCGTGGAAGCGTGCTACGGGGGGGATGATTTGTCTGGTGGAATCTAAGGCC1 1,200 1,240 TATAAGCTAACTATAATATATTTCAAAGAAAAGAAAAAGAGAGAAAAAG G. C. C. G. C. T. G. C. G. G. C. G. G. G. G. G. I.300 I.300 GACCAAGTATTAATAGTAAGAAACTATTGTATGAATTAGCAATTATAT A. A.	1,10 MYBCORI TCCATCAATGATGTGTTA 	1,100 CURE CCAGAATACCTGCCGTAC CONSENSUSAT ICURE TAGCCAGTACAGTACAGT A. C. G. C. G. 1,400 GAGATACTAGTGGGCTGC. C. T.	1,00 1,00 1,00 3CTCCAAGATGTAATGTC 3CTCCAAGATGTAATGTC C 1,00	CURE 1,200 GTACAATAGCAGGC 1199 GTACAATAGCAGGC 1199 GTACAATAGCAGGC 1199 3
PB1 IR64 N22 ANDANA PB1 IR64 N22 N22 N22 N22 N22 N22 N22 N22 N22 N2	1,100 1,100 AGGTCGTGGAAGCGTGCTACGGGGGGGGGGGGGGGGGGG	т.но МУВСОРИ ГССАТСААТСАТЕТЕТТА 	т.,160 СURE ССАGAATACCTGCCETAG, CONSENSUSAT ICURE TAGCCAGCTGCASTACAGG A.C.G. C.G. 1400 GAGATAGTAGTGGGCTGC, C.T.	1,160 XTAGGATGATTAGAGCAA 	CURE 1200 ET REA A TACCAGGC 1199 ET REA A TACCAGGC 1199 TT T 1200 MYCCONSENSUSAT 1320 MYCCONSENSUSAT 1320 MYCCONSENSUSAT 1320 MYCCONSENSUSAT 1320 1320 MYCCONSENSUSAT 1440 1440
PB1 IR64 N222 INDANA PB1 IR64 N22 NDANA PB1 IR64 N22 NDANA PB1 IR64	1,100 1,100 AGGTCGTGGAAGCGTGCTACGGGGGGGGGGGGGGGGGGG	1,40 MYBCOR TCCATCAATGATGTGTTA A.A.A. 1,300 MYC CAGCGGGGTACAGATCTG CAGCGGGGTACAGATCTG T.T. T. 1,300 TTGGCTATAGATGATTTA G	I,100 CCAGAATACCTGCCGTAG CONSENSUSAT TAGCCAGCTGCAGTAGAG A. C. G. C. G. I.400 GAGATAGTAGTGGGCTGC. C. T.	1,100 TTAGGATGATTAGAGCAA TAGGATGATTAGAGCAA C SCTCCAAGATGTAGTC C C C C C C C C C C C C C	CURE 1200 GTACAATAGCAGGC 1199 GTACAATAGCAGGC 1199 GTACAATAGCAGGC 1199 GTACAATAGCAGGC 1199 GTGTATAACAGGTGG 1319 G. 1285 G. 1285 1320 MYCCONSENSUSAT 1320 MYCCONSENSUSAT 1320 MYCCONSENSUSAT 1320 1320 1320 1320 1320 1320 1320 1320
PB1 IR64 N222 INDANA PB1 IR64 N22 IR64 N22 IR64 N22 IR64	1,100 1,100 AGGTCGTGGAAGCGTGCTACGGGGGGGATGATTGTCGGGGAATCTAAGGCCT 1200 1,200 TATAAGCTAACTATAATATATTTCAAAGATATAAAGAAAAAGAAGAAAAAGAAGAAAAAGAGAGAAAAAG	1,10 MYBCORI ICCATCAATGATGTTAA A.A. 1,20 MYC CAGCGGGCTACAGATCTG CAGCGGGCTACAGATCTG T.T. 1,300 ITGGCTATAGATGATTTA G	1,160 CURE CCAGAATACCTGCCGTAG CONSENSUSAT TAGCCAGTCAGTAGAG CAGTAGCAGTCAGTAGAG C. G. C. G. C. G. GAGATAGTAGTGGGCTGC/ C. T. C. T.	1,160 ATAGGATGATTÅGAGGAA 	CURE 1,200 GTACAATAGCAGGC 1199 GTACAATAGCAGGC 1199 GTACAATAGCAGGC 1199 J. T 1200 MYCCONSENSUSAT 1320 MYCCONSENSUSAT 1320 MYCCONSENSUSAT 1320 ATTCCTTCATTCAR 1439 ATTCCTTCATTCAR 1439 1440
PB1 IR64 N222 ANDANA PB1 IR64 N22 ANDANA PB1 IR64 N22 ANDANA PB1 IR64 N222 ANDANA	1,100 1,100 AGGTCGTGGAAGCGTGCTACGGGGGGATGATTTGTCTGGTGGAATCTAAGGCC1 1,200 1,240 TATAAGCTAACTATAATATTATTTCAAAGATATAAGAAAAAGAGAGAAAAGG G. C. G. C. C. G. G. C. G. G. GACCAAGTATTAATAGTATAGCAACTATTGTATGAATTAGCATATTATAT A. A NYCCONSENSUSAT 1,460 IA40 1,440 ITGATCCATCCATAGAGCATGATATATTATCCATCTCAAGAGGGAAAAAGGGC	т. на МУВСОВ ГССАТСААТСАТСТТТА 	1,100 CURE CCAGAATACCTGCCGTAC CONSENSUSAT CURE 1,200 TAGCCAGTACAGTACAGT C. G. C. G. 1,400 GAGATACTAGTGGGCTGC. C. T. C. T. 1,500 ATCAAGTCCAAGCCCGAT	1,60 XTAGGATGATTAGAGCAA 	CURE 1200 ETECATAGCAGGC 1199 ETECATAGCAGGC 1199 ETECATAGCAGGC 1199 T. 1200
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PB1 IR64 N222 NNDANA PB1 IR64 N222 NNDANA PB1 IR64 N222 NNDANA PB1 IR64 N222 NNDANA PB1 IR64 IR64 N222 INDANA PB1 IR64 IR64 IR64 IR64 IR64 IR64 IR64 IR64	1,100 1,130 AGGTCGTGGAAGCGTGCTACGGGGGGGGGGGGGGGGGGG	1,40 MYBCOR TCCATCAATGATGTTAA A.A.A. 1,300 MYC CAGCGGGGTACAGATCTG CAGCGGGGTACAGATCTG T.T. 1,300 TTGGCTATAGATGATTTA G 1,000 CAGTAAGCTGTAAGCCCA	I,100 CONSENSUSAT TAGCCAGCTGCCGTAG TAGCCAGCTGCAGTAGAG A. C. G. C. G. C. G. C. G. C. T. C. T. C. T. T. C. T. T. C. T. T. C. T.	1,160 XTAGGATGATTAGAGCAA C C C C C C C C C C C C C	CURE 1,200 GTACAATAGCAGGC 1199 GTACAATAGCAGGC 1199 GTACAATAGCAGGC 1199 GTACAATAGCAGGC 1199 GTACATACATACAGCTGC 1199 GTGATCACASS MYCCONSENSUSAT 1320 MYCCONSENSUSAT 1405 TICCTTCATTCAAT 1439 TICCTTCATTCAAT 1439 1440 1560 TGATCTCACTTTT 1559 1529 1529 1529
PB1 IR64 N22 NNDANA PB1 IR64 N222 NNDANA PB1 IR64 N222 NNDANA PB1 IR64	1,100 1,100 AGGTCGTGGAAGCGTGCTACGGGGGGGATGATTTGTCTGGTGGAATCTAAGGCC1 1200 1240 TATAAGCTAACTATAATATTATTTCAAAGATATAAAGAAAAGAAGAAGAAAAGGAGAAAAGG C.G. C. Jaja0 1200 GACCAAGTATTAATAGTATAGTAAGCAACTATTGTATGAATTAGCTATTATAT A. A. MYCCONSENSUSAT 1400 TEBATCCATCCATAAGACCATGATTATTATTATCCATCTCAAGAGGGAAAATGGCC	1,100 М/ВСОRU ICCATCAATGATETETEA 	I,160 CURE CCAGAATACCTGCCGTAG CONSENSUSAT TAGCCAGTCAGTAGAGT AC.G. C.G. C.G. C.G. C.T. C.T. C.T. ILSO ATCAAGTCCAAGCCCAGT T. T.	1.50 XTAGGATGATTAGAGCAA 	CURE 1.200 CURE 1.200 GTACAATAGCAGGC 1199 GTACAATAGCAGGC 1199 GTACAATAGCAGGC 1199 GTACATAGCAGGC 1199 GT T 1200 MYCCONSENSUSAT 1320 MYCCONSENSUSAT 1320 MYCCONSENSUSAT 1320 TATCCTTCATTCAR 1439 T440 T440 TGATCCCACTTTT 1559 1525 1529 1560
PB1 IR64 N22 INDANA PB1 IR64 N22 IR64 N22 IR64 N22 IR64 N22 IR64 N22 IR64	I.100 I.100 AGGTCGTGGAAGCGTGCTACGGGGGGATGATTTGTCTGGTGGAATCTAAGGCC1 I.200 I.200 TATAAGCTAACTATAATATTATTTCAAAGATATAAGAAAAGAGAGAAAAGGGGAGAAAAGG G	т.но МУВСОРИ ГССАТСААТСАТСТЕТЕТТА 	I, 160 CCAGAATACCTGCCTAG CONSENSUSAT_ TAGCCAGCTGCASTACAG A. C. G. C. G. C. G. C. G. ATCAAGTCCAGCTGCA ATCAAGTCCAGCCCGAT T. T.	1,160 XTAGGATGATTAGAGCAA 	CURE 1200 GET REA AT A CCA GG C 1199 GET REA AT A CCA GG C 1199 T T 1200 T 1200
PB1 IR64 N22 NNDANA PB1 IR64 N22 NDDANA PB1 IR64 N22 NDDANA PB1 IR64	1,100 1,100 AGGTCGTGGAAGCGTGCTACGGGGGGGGGGGGGGGGGGG	Lino MYBCORE ICCATCAATGATGTGTTA A. A. Lino MYC CAGCGGGGTACAGATCTG T. T. T. Lino Lino CAGTAAGCTGTAAGCCCA C. C.	I,100 CCURE CCAGAATACCTGCCCTAG CONSENSUSAT TAGCCAGCTGCAGTAGAG A. C. G. C. G. C. G. C. G. I.400 GAGATAGTAGTGGGCTGC. C. T. I.500 ATCAAGTCCAAGCCCGAT T. T. I.440 MYCCONSE	1,100 TTAGGATGATTAGAGCAA CONSTRUCTION SCTCCAAGATGTAATGTC CONSTRUCTION CCATTGACCTTGCTCT TA A CCONSTRUCTION CCATGTTGGCCCTAATT MYSCORE 1540 SATGTGTTGGCCCTAATT MYSCORE 1540 15	CURE 1200 GTACAATAGCAGGC 1199 GTACAATAGCAGGC 1199 CTACAATAGCAGGC 1199 CTACAATAGCAGGC 119 CONSENSUSAT CONSENSUSAT CONSENSUSAT 1320 MYCCONSENSUSAT 1320 MYCCONSENSUSAT 1320 MYCCONSENSUSAT 1320 CONSENSUSAT 1320 1320 CONSENSUSAT 1320 1320 1320 CONSENSUSAT 1320 1320 1320 1320 1320 1320 1320 1320
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PB1 IR64 N222 ANDANA PB1 IR64 N222 ANDANA PB1 IR64 N222 ANDANA PB1 IR64 N222 ANDANA PB1 IR64 IR64 IR64 IR64 IR64 IR64	1,100 1,100 AGGTCGTGGAAGCGTGCTACGGGGGGGGGGGGGGGGATTTGTCTGCGGGGAATCTAAGGCCI 1200 1200 TATAAGCTAACTATAATATATTTCAAAGATATAAGAAAAGAGAGAAAAGG G. C. G. C. C. G. T. GACCAAGTATTAATAGTATGGTATGGATTGGATTGGATT	I, 10 MYBCORE ICCATCAATGATGTGTTA A.A.A. I.200 MYC CAGCGGGGTACAGATCTG 	I,100 CURE CCAGAATACCTGCCCTAG CONSENSUSAT TAGCCAGCTGCASTAGAG A. C. G. C. G. C. G. C. G. C. T. C. G. T. C. T. T. T. T. T. T. T. T. T. T. T. T. T. T	1,100 TTAGGATGATTAGAGCAA 	CURE 1200 GTACAATACACAGGC 1199 GTACAATACCACGC 1199 GTACAATACCACGC 1199 GTACAATACCACGC 1199 GTACACACGC 1199 GTATAACACGC 1199 GTATAACACGC 1199 GTATAACACGC 1199 GTATAACACGC 1199 GTATAACACGC 1199 GTATAACACGC 1199 GTATAACACGC 1199 1320 MYCCONSENSUSAT 1320 MYCCONSENSUSAT 1320
PB1 IR64 N222 NDANA PB1 IR64 N222 NDANA PB1 IR64 N222 NDANA PB1 IR64 N222 NDANA PB1 IR64	1,100 1,100 AGGTCGTGGAAGCGTGCTACGGGGGGGGGGGGATGATTGTCTGGTGGAATCTAAGGCCT 1,200 1,200 TATAAGCTAACTATAATATATTTCAAAGAATAAAGAAGAAGAGAAAAGGGGAGAAAAGG C.G. C. C.G. C. 1,200 1,200 TATAAGCTAACTATAATATATTTCAAAGAATAAAGAAGAAGAGAAAAAGAGAGAAAAGG C.G. C. C.G. C. C.G. C. 1,200 1,200 GACCAAGTATTAATAGTAGTAAGCAACTATTGTATGAATTAGCATTATATT A. A. A. A. A. A. A. G. 1,200 1,200 GACCAAGTATTAATAGTAGTAAGCAACTATTGTATGAATTAGCATTATATTATGCATTGGAATTAGCAAGAGAGAAAATGGC MYCCONSENSUSAT 1,400 LI200 1,400 CTTTCATCTCATAAGGCCACTGATGATTATTATCCATCTCAAGAGAGAAAATGGCC LI200 1,400 LI200 1,400 LI200 1,400 LI200 1,400	1,40 MYBCORI TCCATCAATGATGTGTTA A. A. A. 1,200 MYC CAGCGGGGTACAGATCTG A. T. T. 1,200 1,200 CAGTAAGCTGTAAGCCCA 1,200 CAGTAAGCTGTAAGCCCA C. 1,200 C. C. C. C. 1,200 C. C. C. C. C. C. C. C. C. C.	I,100 CONSENSUSAT TAGCCAGCTGCCGTAGA CONSENSUSAT TAGCCAGCTGCAGTAGAG A. C. G. C. G. C. G. C. G. C. G. C. G. C. T. C. T. T. C. T. T. T. T. T. T. T. T. T. T. T. T. T. T	1,100 XTAGGATGATTAGAGCAA C C C C C C C C C C C C C	CURE 1200 GTACAATAGCAGGC 1199 GTACAATAGCAGGC 1199 GTACAATAGCAGGC 1199 GTACAATAGCAGGC 1199 GTACATAGCAGGC 1199 GTGATCATAGCAGGC 1319 G. 1285 1320 MYCCONSENSUSAT 1320 MYCCONSENSUSAT 1320 MYCCONSENSUSAT 1440 1440 1440 1440 1560 1529 1529 1529 1529 1529 1529 1529 1529
PB1 IR64 N222 INDANA PB1 IR64 N22 INDANA PB1 IR64 N222 INDANA PB1 IR64 N222 INDANA PB1 IR64 N222 INDANA	1,100 1,100 AGGTCGTGGAAGCGTGCTACGGGGGGATGATTTGTCTGGTGGAATCTAAGGCCT 1200 1240 TATAAGCTAACTATAAATATTATTTCAAAGAATAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG	т. на МУВСОВ ГССАТСААТСАТСАТСТТТА 	I,160 CURE CCAGAATACCTGCCGTAG CONSENSUSAT TAGCCAGTCAGTAGAGT AC.C.G. C.G. C.G. C.G. C.G. C.T. C.T. T.C.T. I,500 ATCAAGTCCAAGCCCGAT T. T. T. T. T. T. T. T. T. T. T. T. T.	1.60 1.50 3.50	1051 1060 1060 CURE 1200 ETACATACAGGC 199 ETACATACAGGC 199 T. 1200
PB1 IR64 N222 INDANA PB1 IR64 N22 INDANA PB1 IR64 N22 INDANA PB1 IR64 N22 INDANA PB1 IR64 N22 INDANA PB1 IR64 N22 INDANA PB1 IR64 N22 INDANA PB1 IR64 N22 INDANA PB1 IR64 N22 INDANA PB1 IR64 N22 INDANA PB1 IR64 N22 INDANA PB1 IR64 N22 INDANA PB1 IR64 N22 INDANA PB1 IR64 PB1	I.100 I.100 AGGTCGTGGAAGCGTGCTACGGGGGGATGATTTGTCTGGTGGAATCTAAGGCCT I.200 I.200 TATAAGCTAACTATAATTATATTCAAAGAAAAGAAGAGAAAAGAGAGAAAAGG GC.T.O.C.T.O.CA. C.G.C.T.GC.GG. I.200 I.200 GACCAAGTATTAATAGTATAGTAAGAAAAGAGAGAAAAGGAGAAAAGG GACCAAGTATTAATAGTAAGTAAGAAAAGAGAGAAAAGGAGAAAAGG I.200 I.200 GACCAAGTATTAATAGTAAGTAAGAAAAGAGAAAAGAGAGAAAAAGGAGAAAAAGG I.200 I.200	т.но МУВСОРИ ГССАТСААТСАТСТЕТЕТТА 	I, 160 CCAGAATACCTGCCTAG CONSENSUSAT_0 TAGCCAGCTGCAGTAGAG A. C. G. C. G. C. G. C. G. C. T. C. G. ATCAAGTCCAGCCGAT T. T. T. T. T. T. T. T. T. T. T. T. T.	1,50 XTAGGATGATTAGAGCAA 	CURE 1200 GET REALT ACCAGG 1199 GET AT AACAGG TEG 1319 GET ACCONSENSUSAT 1320 MYCCONSENSUSAT 1320 MYCCONSENSUSAT 1440 1440 1440 1440 1440 1525 1525 1529 1529 1529 1529 1529 1529 1520 1529 1520 152
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PB1 IR64 N222 ANDANA PB1 IR64 N222 ANDANA PB1 IR64 N222 ANDANA PB1 IR64 N222 ANDANA PB1 IR64 N222 ANDANA PB1 IR64	1,100 1,100 AGGTCGTGGAAGCGTGCTACGGGGGGGATGATTTGTCTGGTGGAATCTAAGGCCT 1200 1240 TATAAGCTAACTATAAATATATTTCAAAGATATAAAGAAAAAGAAGAAGAAAAAG C. C. C	1,100 М/ВСОRU ICCATCAATGATGTTA A.A.A. .A.A. .A.A. A.	I,100 CURE CCAGAATACCTGCCTAG CONSENSUSAT TAGCCAGCTGCAGTAGAG A. C. G. C. G. C. G. C. G. C. T. C. T. C. T. T. C. T. T. T. C. G. T. T. C. G. T. T. T. T. T. T. T. T. T. T. T. T. T.	1.50 XTAGGATGATTAGAGCAA 	CURE 1200 GTACAATAGCAGGC 1199 GTACAATAGCAGGC 1199 GTACAATAGCAGGC 1199 GTACAATAGCAGGC 1199 GTACATACATAGCAGGC 1199 GTGATCATAACAGGTG 1319 GTGATCACAST AUXCONSENSUSAT 1225 I320 MYCCONSENSUSAT 1429 I320 MYCCONSENSUSAT 1405 I320
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	20	40	60 MYC	CONSESSAN	100	120
N22	ATTTTCTTAGGCTATCTTTAGATCCAGGGTGAAAAT	TTTTGCCCTGTCACATCGG	ATATACTGACACACAT	TTGAAGTATTAAACATAGTO	TAATAACAAAACAAACTACAG	AATCTGCC 120
VANDANA						120
PB1						
IR64						
		MYBCORE				
	140 I	160 I	180 I	200 I	220 I	240 I
N22	TGTAAAATACAAGACGAATTTATTAAGCCTAATTAA	TCCGTTATTAGTAAATGTT	TACTGTAGCATCACAT	TATCAAATCATGGCATAATT	TAAACTCAAAAGATTCATCTCG	CAATTTAC 240
VANDANA		C				
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11(04						
	10/00010501/047	MYCCONSES	USAT NYCOONCECUCAT			
	MYCCONSESUSAT 260	280	300	320	340	360
N22	ATGCAAACTGTGCAATTGATTTTTTCGTCCACATTT	AATGCTCCATACATGTGTT	CAAACATTTGATGTGA	TGTTTTTCGCCAAATTTTT	GGAATCTAAAGACACCCTATA	ттааатст 360
VANDANA	G	C				
PB1		C				
IR64	T					
	MYBCORE 380	400 I	420 1	440	460 1	480 I
N22	AAACTGTTATAATCTGAATCTACTATGACCCAATGG	STTATTTTTTTTTTTTTTTTT	TCTTGATTAGCATGGG	AATTTCTATTTTTCTTGTCC	CATTTTCACTTTTTTCTATCTT	TCTTGTCC 480
VANDANA						
PB1						
11104	500	520	540	560	580	600
N22	GTTTCCAAGTTATTTTTGTCCGTTTACTCTTTGCTT	TTTTGTCCGTTTCCAAGTT	TTTTTTGTCCGTTTCA	GCTCTTAGGTTTTTATTTT	TGTCCGTTTCCAAGTATTTTT	TTGTCCGA 600
VANDANA	T					600
PB1	T					600
IR64	T					600
		CUPE		ACGTATERD		CGTATERD1
	620 I	640 CORE	660 I	680 ADRELATERI	700	I I
N22	TTCGAATTTTTTTTTGTCCGTTTCTAAGTTTGTGTG	SCTTTGCAAAGTACTCCTCC	TTCTATTTTTCTTTT	TTCTTTCGATTAACGTGGGA	ATTTTCTAGGCCGTGAGAGCGA	ACGTGGAG 720
VANDANA PB1						
PB1						
11(04						
	740	760	CURE	800	820 MYCCONSE	SUSAT 840
LICO.	/40 	CATTICCTCCTCCTCCTC	TCACTACTOACCOTA			
VANDANA	GCITCITITICIATIACITIATAGATATAATAGATA	GATTIGCIGCICCIGAGAG	TCAGTACTGACGCTAA	AAATTATCGTTGTTTTTATT	ACCATTCGACAGCACAGATGA	10010AC0 840
PR1						
IR64						
	MYCCONSESUSAT 860	880	900	920	940	960
N22	ATGGCAACAGATGAACGATCGATCCCCTTCACTTC	GTCTGTGCTGGTATGCTGA	TTCTGCTCATGGAGGA	CAGGATGCAGTCATCAGCTT	I I GGCTAGTGGAAACATGAGGCG	I TGTCCGAG 960
VANDANA						
PB1						
IR64						
	IN/2001/0501/047	N/0001/0501/017				
	980	1,000	1,020	1,040	1,060	1,080
N22	AGAAAAGCATCAATTGCCACTACATTATCTGTCGCC	ATTTGCCGATACAGTCGTG	TGCGTTTCTCAGTCTC	GAAACGACACCTAGGACTTT	TAGGACAGAAACAAAAGGGCA	AACGGCGC 1080
VANDANA						1080
PB1						1080
IR64						1080
			MYCCONSESUSAT			
	1,100	1,120	MYCCONSESUSAT	1.160 I	1,180 I	1,200 I
N22	1.00 I CTCCGTTTTTTCTTGGCTCACTCAATCACCTCGCTT	1,120 I ACCTCGCCATTCTGTCATG	MYCCONSESUSAT	1.160 I TAGCACACACTAATCTCTCT	1,180 I TTTGAGCAAGTTTAATACTATA	1,200 I TCCAACTA 1200
N22 VANDANA	1.100 CTCCGTTTTTTCTTGGCTCACTCAATCACCTCGCTT	1,120 I ACCTCGCCATTCTGTCATG	MYCCONSESUSAT	1,160 I TAGCACACACTAATCTCTCT	1,180 I I TTGAGCAAGTTTAATACTATA C	1,200 TCCAACTA 1200
N22 VANDANA PB1	1.100 CTCCGTTTTTTCTTGGCTCACTCAATCACCTCGCTT	1.120 TACCTCGCCATTCTGTCATG	MYCCONSESUSAT	1.160 TAGCACACACTAATCTCTCT	1.180 ITTGAGCAAGTTTAATACTATA 	1,200 I TCCAACTA 1200
N22 VANDANA PB1 IR64	1.100 CTCCGTTTTTTTTTGGCTCACTCAATCACCTCGCTT	1.120 I ACCTCGCCATTCTGTCATG	MYCCONSESUSAT	1.160 TAGCACACACTAATCTCTCT	1,190 ITTGAGCAAGTTTAATACTATA CTT	1,200 I TCCAACTA 1200
N22 VANDANA PB1 IR64	1,100 CTCCGTTTTTTCTTGGCTCACTCAATCACCTCGCTT	1.120 I ACCTCGCCATTCTGTCATG A	MYCCONSESUSAT	1,160 TAGCACACACATATCTCTCT	1,180 ITTGAGCAAGTTTAATACTATA 	1.200 I TCCAACTA 1200
N22 VANDANA PB1 IR64	1.100 CTCCGTTTTTTCTTGGCTCACTCAATCACCTCGCTT	1,20 ACCTCGCCATTCTGTCATG A	MYCCONSESUSAT 1.140 GCATTTGCCAAAACAG	1.160 TAGCACACACTAATCTCTCT 1.280 AC	1.100 ITTGAGCAAGTTTAATACTATA CT CT CT. CURE 1,200	1,200 I TCCAACTA 1200
N22 VANDANA PB1 IR64 N22	1,100 CTCCGTTTTTTCTTGGCTCACTCAATCACCTCGCTT 1200 TTAGCTTCAAATCACCTCATCTAATAGCCA	1,120 CACCTOGCCATTCTGTCATG 	MYCCONSESUSAT	1.10 TAGCACACACTAATCTCTCT 1.200 1.200 TAATAATAGCTGGTCTTAG	1,100 ITTGAGCAAGTTTAATACTATA' 	1,200 I TCCAACTA 1200
N22 VANDANA PB1 IR64 N22 VANDANA	1,10 CTCCGTTTTTTCTTGGCTCACTCAATCACCTCGCTT 	1.130 ACCTGGCATTCTGTCATG . A	MYCCONSESUSAT 1,140 GCATTTGGCAAAACAG 1,280 ATAAACATATACTAAC	1.160 TAGCACCACTAATCTCTCT 1.260 TAATAATAGCTGGTCTTAGE	1.100 ITTGAGCAAGTTAATACTATA 	1,200 I TCCAACTA 1200
N22 VANDANA PB1 IR64 N22 VANDANA PB1	1.100 CTCCGTTTTTTCTTGGCTCACTCAATCACCTCGCTT 	1,120 ACCTCGCCATTCTGTCATG A	MYCCONSESUSAT 1.140 GCATTTGCCAAAACAG 1.200 ATAAACATATACTAAC	LIGO TAGGACACACTAATCTCTCT 1.200 TAATAATAGCTGGTCTTAGG	1.100 ITTGAGCAAGTTTAATACTATA 	1,200 TCCAACTA 1200
N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64	LINO CTCCGTTTTTTTTTTGGCTCACTCAATCACCTCGCTT 1.200 TTAGCTTCAAATCATCTATAGTCAATTTAATAGCCA	1.130 - ACCTGGCATTCTGTCATG - A - A - A - 1.240 I.240 I.240 I.240	MYCCONSESUSAT 1:10 GGATTTGGCAAAACAG 1:200 ATAAACATATACTAAC	1.160 TAGCACACACTAATCTCTC1 1.200 ACC TAATAATAGCTGGTCTTAC	1,100 ITTGAGCAAGTTTAATACTATA 	1,200 1 TCCAACTA 1200 1200 1,320 TGAAGTCC 1320 1,320 TGAAGTCC 1320 1320 1320 1320
N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64	1,100 CTCCGTTTTTTCTTGGCTCACTCAATCACCTCGCTT	1.130 - ACCTGGCATTCTGTCATG - A - A - A - A - 1240 - 1 - 1240 - 1 - 1240 - 1 - 1240 - 1 - 1240 - 1 - 1240 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1	MYCCONSESUSAT 1.100 GCATTTEGCAAAACAG 1.200 1.200 ATAAACATATACTAAC	1.160 TAGCACACCTAATCTCTCT 1.260 TAATAATAGCTGGTCTTAG	1,100 ITTGAGCAAGTTAATACTATA 	1.200 TCCAACTA 1200 1200 1200 1200 1200 1200 1200 1200
N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64	1,10 CTCCGTTTTTTCTTGGCTCACTCAATCACCTCGCTT 1,20 TTAGCTTCAAATCATCTATAGTCAATTTAATAGCCA CURE MYBCORE 1,30 MYBCORE	1120 ACCTCGCCATTCTGTCATG A A A 1240 INTTCATATAATAGTTACCT 1360	MYCCONSESUSAT 1,100 GCATTTEGCAAAACAG 1,200 ATAAACATATACTAAC 1,300	1.160 TAGCACACACTAATCTCTCT 1.280 ACC TAATAATAGCTGGCTCTTACC 1.400 MYB1AT	1,100 ITTGAGCAAGTTTAATACTATA 	1.200 TCCAACTA 1200
N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22	LINO CTCCGTTTTTTCTTGGCTCACTCAATCACCTCGCTT 1.200 TTAGCTTCAAATCATCTATAGTCAATTTAATAGCCA CURE MYBCORE 1.340 MYBCORE GTACTGCAGTTATCTACCAATCGTTATCTCCTTAA	1.120 - ACCTGGCATTCTGTCATG - A - A - 1240 1.240 INTCATATAATAGTTACCT - 1,500 - 1,500	MYCCONSESUSAT 1.100 GGATTTIGCCAAAACAG 1.200 ATAAACATATACTAAC 1.300 TATAGTCCGATAACCT	1.140 TAGCACACACTAATCTCTCT 1.200 ACC TAATAATAGCTGGCTCTTAG 1.400 MYBIAT ACTCTTATCACTAAGCACAC	1,100 ITTGAGCAAGTTTAATACTATA 	1,200 TCCAACTA 1200
N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA	1,100 CTCCGTTTTTTCTTGGCTCACTCACTCACTCGCTT 1,200 TTAGCTTCAAATCATCATCTATAGTCAATTTAATAGCCA CURE MYBCORE 1,300 MYBCORE GTAGTCGCAGTTATCTACCAATCTGTGTTATCTCCTTAA A	1.130 - ACCTGGCCATTCTGTCATG - A - A - A - A - 1240 - 1 - 1 - 1240 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1	MYCCONSESUSAT 1.100 GCATTIGCCAAAACAG 1.200 1.200 1.300 1.300 1.300 1.300 1.300 1.4TAGTCCGATAACCT G	1.160 TAGCACACCTAATCTCTCT 1.260 TAATAATAGCTGGTCTTAG 1.400 MYB1AT ACTCTTATCACTAAGCACAC	1,100 ITTGAGCAAGTTAATACTATA 	1.200 TCCAACTA 1200 1200 1200 1200 1200 1200 1200 1200
N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1	1,10 CTCCGTTTTTTCTTGGCTCACTCACTCACTCGCTT 120 TTAGCTTCAAATCATCTATAGTCAATTTAATAGCCA CURE MYBCORE 1,340 MYBCORE GTAGTGCAGTTATCTACAATCTGTTATCTCCTTAA A	1.120 ACCTCGCCATTCTGTCATG .A. .A. 1.200 1 1.200 1.200 1.200 .GGC. .GGC. 	MYCCONSESUSAT 1,100 GCATTTGCCAAAACAG 1,200 ATAAACATATACTAAC 1,200 1,200 TATAGTCCGATAACCT G. G.	1.160 TAGCACACACTAATCTCTCT 1.280 TAATAATAGCTGGTCTTAGC ACTCTTATCACTAACCACAC	1.100 ITTGAGCAAGTTAATACTATA 	1,200 TCCAACTA 1200 1200 1200 1,320 TGAAGTCC 1320 1,320 TGAAGTCC 1320 1320 1320 1320 1320 1320 1320 1320
N22 VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA PB1 IR64	LINO CTCCGTTTTTTCTTGGCTCACTCAATCACCTCGCTT 1.200 TTAGCTTCAAATCATCTATAGTCAATTTAATAGCCA CURE IMYBCORE 1,340 MYBCORE GTACTGCAGTTATCTACCAATCTGTTATCTCCTTAA A.A.A.A.	1.120 ACCTGGCATTCTGTCATG .A. .A. .1340 1.340 .ATTCATATAATAGTTACCT 	МУССОNSESUSAT 1,100 GCATTTEGCAAAACAG 1,200 АТАААСАТАТАСТААС 1,300 ТАТАĞTCCGATAACCT G. .G.	1.140 TAGCACACACTAATCTCTCT 1.200 ACC TAATAATAGCTGGTCTTAC 1.400 MYBIAT ACTCTTATCACTAAGGACAC	1,100 ITTGAGCAAGTTTAATACTATA 	1,200 TCCAACTA 1200 1200 1200 1320 TGAAGTCC 1320 1320 1320 1320 GTTCCAAA 1440
N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64	LING CTCCGTTTTTTCTTGGCTCACTCACTCACTCGCTT 1220 TTAGCTTCAAATCATCTTTAGTCAATTTAATAGCCA CURE MYBOORE 1340 MYBOORE GTACTCCAGTTATCTACAAATCGTGTTATCTCCTTAA A.A.A.A.A.A.A.A.A.A.A.A.A.A.A.A.A.A	1.120 	MYCCONSESUSAT 1.100 GGATTTEGCAAAACAG 1.200 1.200 1.300 1.300 1.300 1.300 1.300 1.300 0	1.160 TAGCACACCTAATCTCTCT 1.260 TAATAATAGCTGGTCTTACC 1.400 MYBIAT ACTCTTATCACTAAGCGCAC	1,100 ITTGAGCAAGTTAATACTATA 	1.200 TCCAACTA 1200 1200 1200 1200 1200 1200 1200 1200
N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64	1,10 CTCCGTTTTTTCTTGGCTCACTCAATCACCTCGCTT 1,20 TTAGCTTCAAATCATCTATAGTCAATTTAATAGCCA CURE MYBCORE 1,340 MYBCORE GTACTGCAGTTATCTACAATCTGTTATCTCCTTAA A A A 1,460 ACGTATERD1	1.120 ACCTCGCCATTCTGTCATG .A. .A. 1.200 1 AATTCATATAATAGTTACCT 1.300 1.300 	MYCCONSESUSAT 1,140 1,240 1,240 1,240 1,240 1,240 1,240 1,240 1,240 1,240 1,240 1,240 1,240 1,240 1,240 1,40	1.160 TAGCACACCTAATCTCTCT 1,280 TAATAATAGCTGGTCTTAGC ACTCTTATACCTAACCACAC	1,100 ITTGAGCAAGTTTAATACTATA 	1,200 TCCAACTA 1200 1200 1200 1320 TGAAGTCC 1320 TGAAGTCC 1320 1320 TGAAGTCC 1320 1320 TGAAGTCC 1320 1320 1320 1320 1320 1320 1320 1320
N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA	LINO CTCCGTTTTTTCTTGGCTCACTCAATCACCTCGCTT 1.20 TTAGCTTCAAATCATCTATAGTCAATTTAATAGCCA CURE MYBCORE 1.340 MYBCORE GTAGTGCAGTTATCTACAATCTGTTATCTCCTTAA A	1.120 -ACCTGGCATTCTGTCATG -A. -A. -1.240 1.240 1.240 -1	МУССОЛЯЕЗUSAT 1.100 GATTIGCCAAAACAG 1.200 АТАААСАТАТАСТААС 1.300 ТАТАСТССGATAACCT 6	1.160 TAGCACACACTAATCTCTC1 1.200 TAATAATAGCTGGTCTTAG ACTCTTATCACTAAGGACAC 1.200 1.200 1.200 1.200 1.200	1,100 ITTGAGCAAGTTTAATACTATA 	1,200 TCCAACTA 1200 1200 1200 1200 1320 TGAAGTCC 1320 1320 TGAAGTCC 1320 1320 1320 1320 1320 1320 1320 1320
N22 VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1	LINO CTCCGTTTTTTCTTGGCTCACTCAATCACCTCGCTT 1200 TTAGCTTCAAATCATCATCATTATAGCCA CURE MYBOORE 1,300 MYBOORE GTACTCCAGTTATCTACAAATCTGTTATCTCCTTAA A.A.A.A.A.A.A.A.A.A.A.A.A.A.A.A.A.A	1.120 ACCTGGCATTCTGTCATG A	MYCCONSESUSAT 1.100 GATTIEGCAAAACAG 1.200 ATAAACATATACTAAC 1.300 TATAGTCCGATAACCT .G	1.160 TAGCACACACTAATCTCTC1 1.260 1.260 TAATAATAGCTGGTCTTAGC 1.400 MYBIAT ACTCTTATCACTAAGCACAC 1.500 TCGCACGGCATCAATAGTCC	1,100 ITTGAGCAAGTTAATACTATA 	1.200 TCCAACTA 1200
N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA RE1 IR64	1,10 CTCCGTTTTTTCTTGGCTCACTCACTCACTCACTCGCTT 1,220 TTAGCTTCAAATCATCTATAGTCAATTTAATAGCCA CURE IMVBCORE 1,340 IMVBCORE GTACTGCAGTTATCTACAATCTGTTATCTCCTTAA A A A C CURE IMVBCORE 1,340 IMVBCORE GTACTGCAGTTATCTACAATCTGTTATCTCCTTAA A A A A A A A A A A A A A A	1.120 ACCTOGCCATTCTGTCATG A .A .A .A .A .A 	MYCCONSESUSAT 1.100 1.200 1	1.160 TAGCACACCTAATCTCTCT 1,280 TAATAATACCTGGTCTTAC 1,400 MYBIAT ACTCTTATCACTAAGGACAC 1,500 TCGCACGGCATGAATAGTCC	1,00 ITTGAGCAAGTTTAATACTATA 	1,200 TCCAACTA 1200 1200 1200 1320 TGAAGTCC 1320 TGAAGTCC 1320 1320 GTTCCAAA 1440 1440 1500 GTTCCAAA 1440 1440 1500 AAATAAAT 1560 C. 1560 C. 1560
N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64	LINO CTCCGTTTTTTCTTGGCTCACTCACTCACTCACTCGCTT 120 TTAGCTTCAAATCATCTATAGTCAATTTAATAGCCA CURE IMYBCORE 1340 MYBCORE GTAGTGCAGTTATCTACAATCTGTTATCTCCTTAA A	1.130 ACCTGGCATTCTGTCATG .A. .A. .A. .A. .1340 1.340 	МУССОЛЯЕЗUSAT 1.100 1.200 АТАААСААТАТАСТААС 1.200 АТАААСАТАТАСТААССА 1.200 ТАТАСТСССАТААССТ 6	1.160 TAGCACACACTAATCTCT 1.200 TAATAATAGCTGGTCTTAG ACTCTTATCACTAACGACAC 1.200 1.200 TCGCACGGCATCAATAGTCC	1,100 ITTGAGCAAGTTTAATACTATA 	1.200 TCCAACTA 1200 1200 1200 TGAAGTCC 1320 TGAAGTCC 1320 1320 GTTCCAAA 1440 1440 1440 1440 AAATAAAT 1560 C. 1560
N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64	LINO CTCCGTTTTTTCTTGGCTCACTCAATCACCTCGCTT 1200 TTAGCTTCAAATCATCATCATAGTCAATTTAATAGCCA CURE MYBOORE 1300 MYBOORE GTAGTCGGAGTTATCTACAAATCTGTTATCTCCTTAA A.A.A.A.A.A.A.A.A.A.A.A.A.A.A.A.A.A	1.120 ACCTGGCATTCTGTCATG A	MYCCONSESUSAT 1.100 GATTIGCCAAAACAG 1.200 ATAAACATATACTAAC 1.300 TATAGTCCGATAACCT G	1.160 TAGCACACACTAATCTCT 1.260 TAATAATAGCTGGTCTTAG 1.260 MYBIAT ACTCTTATCACTAAGGACAC	1,100 ITTGAGCAAGTTAATACTATA' 	1,200 TCCAACTA 1200 1200 1200 1,320 TCAAGTCC 1320 1320 1320 1320 1320 1320 1320 1320
N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64	LING CICCGTITITICTIGGCTCACTCACTCACTCACTCGCTT 1,200 TTAGGTTCAAATCATCTATAGTCAATTTAATAGCCA CURE MYBCORE 1,340 MYBCORE GTAGTGCAGTTATCTACAAATCITGTTATCTCCTTAA A. A. A. A. A. A. A. A. A.	1.120 *ACCTGGCCATTCTGTCATG . A	MYCCONSESUSAT 1,100 GCATTTEGCAAAACAG 1,200 ATAAACATATACTAAC 1,300 TATGTCCGATAACCT G	1.160 TAGCACACACTAATCTCTCT 1.260 TAATAATAGCTGGTCTTAC 1.460 MYB1AT ACTCTTATCACTAATAGCGACAC 1.500 TCGCACGGCATCAATAGTCC	1,00 ITTGAGCAAGTTTAATACTATA 	1200 TCCAACTA 1200 1200 1200 1320 TGAAGTCC 1320 1320 TGAAGTCC 1320 1320 GTTCCAAA 1440 1440 1500 CAAATAAAT 1560 CC 1560 CC 1560 1560 1860
N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64	LINO CTCCGTTTTTTCTTGGCTCACTCACTCACTCACTCACTCA	1.120 ACCTOGCATTCTGTCATG .A. .A. 1.240 1.240 1.240 1.240 1.240 1.240 	МУССОЛЯЕSUSAT 1.100 1.200 АТААСААТТТІĞССААААСАĞ 1.200 ТАТАĞТССĞАТААССА С	1.140 TAGCACACACTAATCTCTC1 1.200 ACC TAATAATAGCTGGTCTTAE ACTCTTATCACTAAGEACAC 1.200 MVBIAT ACTCTTATCACTAAGEACAC 1.200 CCCACGGCATCAATAGTCC AAAATATTTGACATCGTTGA	1,100 ITTGAGCAAGTTTAATACTATA 	1.200 TCCAACTA 1200 1200 1200 TGAAGTCC 1320 TGAAGTCC 1320 1.320 TGAAGTCC 1320 1.320 TGAAGTCC 1320 1.320 TGAAGTCC 1320 1.440 GTTCCAAA 1440 1.440 AAATAAT 1560 C. 1560 C. 1560 STTCGGCT 1680
N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64	LINO CTCCGTTTTTTCTTGGCTCACTCAATCACCTCGCTT 1.200 TTAGCTTCAAATCATCTATGTCAATTAATAGCCA CURE MYBOORE 1.300 MYBOORE GTAGTCGAGTTATCTACAAATCTGTGTTATCTCCTTAA A. A. A. A. A. A. A. A. A. A. A. A. A	1.120 ACCTOGCCATTCTGTCATG . A	MYCCONSESUSAT 1.100 GATTTEGCAAAACAG 1.200 1.300 TATAGTCCGATAACCT G	1.160 TAGCACACACTAATCTCTC1 1.260 TAGTATAATAGCTGGTCTTAG 1.260 MYBIAT ACTCTTATCACTAAGGACAC TCGCACGGCATCAATAGTCC 1.460 AAAATATTTGACATCGTTGA	1,100 ITTGAGCAAGTTTAATACTATA' 	1.200 TCCAACTA 1200 1200 1200 1320 TGAAGTCC 1322 1320 TGAAGTCC 1322 1320 1320 1320 1320 1320 1320 1320
N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64	LINO CICCGTITITICITIGGCICACICACICACICACICGCII 1200 TIAGGTICAAATCATCATCIATAGICAATITAATAGCCA CURE MYBCORE 1340 MYBCORE GIACIGCAGITAICTACACAATOIGITAICICCITAA A	1.130 ACCTOGCCATTCTGTCATG A .A .A .A .A .240 .4 .4 .4 .4 .4 .4 .4 .4 .4 .4	MYCCONSESUSAT 1.10 1.20 1.20 1.20 1.20 1.30 1.30 1.30 1.30 1.30 1.50 CCTCGCTTTTCACGGC 1.50 CCTCGCTTTTCACGGC 1.50 1.50 CCTCGCTTTTCACGGC	1.160 TAGCACACACTAATCTCTCT 1.260 TAATAATAGCTGGTCTTAG 1.260 MYB1AT ACTCTTATCACTAATAGCGACAC 1.50 TCGCACGGCATCAATAGTCC 1.60 AAAATATTTGACATCGTTGA	1,00 ITTGAGCAAGTTTAATACTATA' 	1.200 TCCAACTA 1200 1200 1200 TGAAGTCC 1320 TGAAGTCC 1320 TGAAGTCC 1320 1320 TGAAGTCC 1320 1320 TGAAGTCC 1320 1320 TGAAGTCC 1320 1320 TGAAGTCC 1320 TGAAGTCC
N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64	LINO CTCCGTTTTTTCTTGGCTCACTCACTCACTCACTCACTCA	1.120 ACCTOGCATTCTGTCATG .A. .A. 1.240 1.240 1.240 1.240 1.240 	МУССОЛЯЕЗUSAT 1.100 1.200 1.200 1.200 1.200 1.200 ТАТАСТССВАТААССТ 6	1,160 TAGCACACACTAATCTCTC1 1,200 TAATAATAGCTGGTCTTACC TAATAATAGCTGGTCTTACC 1,200 MWBIAT ACTCTTATCACTAATCGTCA 1,200 1,200 TCGCACGGCATCAATAGTCC AAAATATTTGACATCGTTGA	1,100 ITTGAGCAAGTTTAATACTATA' 	1.200 TCCAACTA 1200 1200 1200 TGAAGTCC 1320 TGAAGTCC 1320 1.320 TGAAGTCC 1320 1.320 TGAAGTCC 1320 1.320 TGAAGTCC 1320 1.440 GTTCCAAA 1440 1.440 AAATAAT 1560 C. 1560 C. 1560 GTTCGGCT 1680 GTTCGGCT 1680 GTTCGGCT 1680
N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64	LINO CICCGTTITTTCTTGGGTCACTCAATCACCTCGCTT 1200 TTAGGTTGAAATCATCATCTATGGTGAATTTAATAGCCA CURE MYBOORE 1300 MYBOORE GTAGTGGAGTTATCTACAAAATCTGGTTATGTCCCTTAA A. A. A. A. A. A. A. A. A. A. A. A. A	1.120 ACCTOGCCATTCTGTCATG A	MYCCONSESUSAT 1.100 GATTTEGCAAAACAG 1.200 ATAAACATATACTAAC 1.300 TATAGTCCGATAACCT G	1.160 TAGCACACACTAATCTCTC1 1.260 1.260 TAATAATAGCTGGTCTTAGC 1.260 1.260 1.260 1.260 TCGCACCGGCATCAATAGTCC 1.260 1.260 TCGCACCGCATCAATAGTCC	1,100 ITTGAGCAAGTTTAATACTATA' 	1,200 TCCAACTA 1200 1200 1200 1320 TGAAGTCC 1322 1320 TGAAGTCC 1322 1320 1320 TGAAGTCC 1322 1320 1320 1320 1320 1320 1320 1320
N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA	1,10 CICCGTTITTTCTTGGCTCACTCACTCACTCACTCACTCACTCACTCA	1.120 ACCTCGCCATTCTGTCATG A	MYCCONSESUSAT 1,100 GCATTTEGCAAAACAG 1,200 ATAAACATATACTAAC 1,300 TATAGTCCGATAACCT 6	1,400 TAGCACACACTAATCTCTC1 1,200 TAATAATAGCTGGTCTTAGG TAATAATAGCTGGTCTTAGG 1,400 MYBIAT ACTCTTATCACTAAGGACACG 1,500 TCGCACGGCATCAATAGTCC 1,500 1,500 TCGCACGGCATCAATAGTCC 1,500 1	1,190 ITTGAGCAAGTTTAATACTATAT 	1.200 TCCAACTA 1200 1200 1200 TGAAGTCC 1320 TGAAGTCC 1320 1320 TGAAGTCC 1320 1320 TGAAGTCC 1320 1320 TGAAGTCC 1320 1320 TGAAGTCC 1320 1320 TGAAGTCC 1320 TGAAGTCC 1320 TGA
N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA	LINO CICCGTTTTTTCTTGGGTCACTCACTCACTCACTCACTCACT	1.120 ACCTOGCATTCTGTCATG A A 1.240 1.440	МУССОЛЯЕЗUSAT 1.100 1.200 1.200 1.200 1.200 1.200 ТАТАСТСССАТААССА 0	1,140 TAGCACACACTAATCTCTCT 1,200 TAATAATAGCTGGTCTTACC AATAATAATAGCTGGTCTTACC 1,200 TCGCACGGCATCAATAGTCC AAAATATTTGACATCGTTGA 1,200 TCGCACGGCATCAATAGTCC AAAATATTTGACATCGTTGA	1,100 ITTGAGCAAGTTTAATACTATA 	1.200 TCCAACTA 1200 1200 1200 TGAAGTCC 1320 TGAAGTCC 1322 1320 TGAAGTCC 1322 1320 TGAAGTCC 1322 1320 TGAAGTCC 1322 1320 TGAAGTAAA 1440 1440 TAATAAT 1560 TAGTCGCC 1560 TGGCC 1560 TGGCC 1680 TGGCC 1680 TGCGCC 1680 TGCCCC 1680 TGCCCC 1680 TGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
N22 VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64	LINO CICCGTTITTTCTTGGGTCACTCAATCAACCICGCTT 1200 TTAGGTTGAAATGATCATCTATGGTGAATTTAATAGGCA CURE MYBOORE 1300 MYBOORE GTAGTGGAGTTATCTACAAATGTGTTATCTCCCTTAA A A A A A A A A A A A A A	1.120 ACCTOGCCATTCTGTCATG A	MYCCONSESUSAT 1.100 GATTTEGCAAAACAG 1.200 ATAAACATATACTAAC 1.300 TATAGTCCGATAACCT G	1.160 TAGCACACACTAATCTCTC1 1.260 1.260 TAATAATAGCTGGTCTTAGC 1.260 1.260 1.260 TCGCACCGGATCAATAGTCC 1.260 TCGCACCGGATCAATAGTCC 1.260 1.260 TCGCACCGGATCAATAGTCC 1.260 1.260 TCGCACCGGATCAATAGTCC 1.260 1.260 TCGCACCGGATCAATAGTCC	1,100 ITTGAGCAAGGTTAATACTATA' 	1.200 TCCAACTA 1200 1200 1200 1320 TGAAGTCC 1322 1320 TGAAGTCC 1322 1320 TGAAGTCC 1322 1320 TGAAGTCC 1322 1320 TGCAAGTCC 1320 TGCAAGTCC 1320
N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA	1,10 CTCCGTTTTTTCTTGGCTCACTCACTCACTCACTCACTCA	1.120 ACCTCGCCATTCTGTCATG A	MYCCONSESUSAT 1,100 GCATTTEGCAAAACAG 1,200 ATAAACATATACTAAC 1,200 TATAGTCCGATAACCT 6	1,460 TAGCACACACTAATCTCTCT 1,260 TAATAATAGCTGGTCTTAGC ACCTTATCACTAAGGTGGTCTTAGC 1,460 1,460 1,500 TCGCACGGCATCAATAGTCC 1,500 TCGCACGGCATCAATAGTCC 1,500 TCGCACGGCATCAATAGTCC 1,500 TCGCACGGCATCAATAGTCC 1,500 TCGCACGGCATCAATAGTCC 1,500 TCGCACGCCTCAATAGTCC 1,500 1,500 TCGCACGCCTCAATAGTCC 1,500 1,500 TCGCACGCCTCAATAGTCC 1,500 1,500 1,500 TCGCACGCCTCAATAGTCC 1,500 1,700 1,7	1,100 ITTGAGCAAGTTTAATACTATAT 	1.200 TCCAACTA 1200 1200 1200 1.320 TGAAGTCC 1320 TGAAGTCC 1320
N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64	LINO CICCGTTITITICITIGGCICACICACICACICACICGCIT 1200 TIAGCITICAAAATCAACCACICACITAATAGCCA CURE MYBCORE 1300 MYBCORE SIACIGGAGITAICIACAAATCIGITAICICCITAA A	1.120 ACCTOGCATTCTGTCATG A A 1.240	MYCCONSESUSAT 1.100 1.200 1.200 1.200 1.200 1.200 1.200 1.200 CCTCGCTTTTCACGGC 1.500 CCTCGCTTTTCACGGC 1.500 CCTCGCTTTTCACGGC 1.500 CCTCGCTTCCCTCCATCCC 1.500 CCTCGCTTCCCCTCCATCCC	1,140 TAGCACACACTAATCTCTCT 1,200 TAATAATAGCTGGTCTTACC 1,200 TAATAATAGCTGGTCTTACC 1,200 1,200 TCGCACGGCATCAATAGTCC AAAATATTTGACATCGTTGA 1,200 TCGCACGGCATCAATAGTCC 1,200 TCGCACGGCATCAATAGTCC 1,200 TCGCACGGCATCAATAGTCC 1,200 1	1,100 ITTGAGCAAGTTTAATACTATAT 	1,200 TCCAACTA 1200 1200 1300 TGAAGTCC 1320 TGAAGTCC 1320 1320 TGAAGTCC 1320 1320 TGAAGTCC 1320 1320 TGAAGTCC 1320 1320 TGAAGTAA 1440 TA40 TA40 TA40 TA40 TA40 TA40 TA40 T
N22 VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64	LINO CICCGTTITTTCTTGGGTCACTCACTCACTCACTCACTCACT 1.200 TTAGGTTCAAATCATCATCTATAGTCAATTTAATAGCCA CURE MYBOORE 1.300 MYBOORE GTAGTCGAGTTATCTACAAATCTGTTATCTCCTTAA A. A. A. A. A. A. A. A. A.	1.50 ACCTOGCCATTCTGTCATG A	MYCCONSESUSAT 1.100 GATTIEGCAAAACAG 1.200 ATAAACATATACTAAC G. G. G. G. G. 1.200 1.200 1.200 CTCGCTTTTCACGGC 1.200 CTCGCTTTTCACGGC 1.200 CTCGCTCCATCCC 1.200 1.200 CTCGCTCCATCCC 1.200 1.200 CTCGCTCCATCCC 1.200	1,40 TAGCACACACTAATCTCT 1,200 1,200 1,200 1,200 TAATAATAGCTGGTCTTAC 1,400 MYBIAT ACTCTTATCACTAAGGGCAC 1,400 1,400 1,400 AAAATATTTGACATCGTTGA 1,400 1	1,100 ITTGAGCAAGTTTAATACTATA 	1,200 TCCAACTA 1200 1200 1,300 TGAAGTCC 1320 1,320 TGAAGTCC 1320 1,320 GTTCCAAC 1320 GTTCCAAC 1320 GTTCCAAC 1440 1,550 1,550 1
N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA	1,100 СТСССТТТТТТСТТБССТСАСТСАСТСАСТСАСТСАСТСА	1,120 ACCTCGCCATTCTGTCATG A .A .A .A .A .A .A .A .A .A	МУССОNSESUSAT 1,100 GCATTTEGCCAAAACAG 1,200 ATAAACATATACTAAC 1,200 TATAGTCCGATAACCT 6	1,460 TAGCACACACTAATCTCTCT 1,260 TAATAATAGCTGGTCTTAGC ACCTTATCACTAAGGACAC 1,460 M/WB1AT ACTCTTATCACTAAGGACAC 1,460 1,500 TCGCACGGCATCAATAGTCC 1,500 TCGCACGGCATCAATAGTCC 1,500 TCGCACGGCATCAATAGTCC 1,500 TCGCACGGCATCAATAGTCC 1,500 TCGCACGGCATCAATAGTCC 1,500 TCGCACGGCATCAATAGTCC 1,500 TCGCACGGCATCAATAGTCC 1,500 1,500 TCGCACGGCATCAATAGTCC 1,500 1,500 TCGCACGGCATCAATAGTCC 1,500 1,500 TCGCACGGCATCAATAGTCC 1,500 1,500 TCGCACGGCATCAATAGTCC 1,500 1,500 TCGCACGGCATCAATAGTCC 1,500 1,500 TCGCACGGCATCAATAGTCC 1,500 1,500 TCGCACGGCATCAATAGTCC 1,500 TCGCACGGCATCAATAGTCC 1,500 TCGCACGGCATCAATAGTCC 1,500 TCGCACGGCATCAATAGTCC 1,500 TCGCACGGCATCAATAGTCC 1,500 TCGCACGGCATCAATAGTCC 1,500 TCGCACGGCATCAATAGTCC 1,500 TCGCACGGCATCAATAGTCC 1,500 TCGCACGGCATCAATAGTCC 1,500 TCGCACGGCATCCAATAGTCC 1,500 TCGCACGGCATCCAATAGTCC 1,500 TCGCACGGCATCCAATAGTCC 1,500 TCGCACGGCATCCAATAGTCC 1,500 TCGCACGGCATCCATCGTTGA 1,500 TCGCACGGCATCCATCGTTGA 1,500 TCGCACGGCATCCATCGTTGA 1,500 TCGCACGGCATCCATCGTTGA 1,500 TCGCACGGCATCCATCGTTGA 1,500 TCGCACGGCATCCATCGTTGA 1,500 TCGCACGGCATCCATCGTTGA 1,500 TCGCACGGCATCCATCGTTGA 1,500 TCGCACGGCATCCATCGTTGA 1,500 TCGCACGGCATCCATCGTTGA 1,500 TCGCACGGCATCCATCGTTGA 1,500 TCGCACGGCATCCATCGTTGA 1,500 TCGCACGGCATCCATCGTTGA 1,500 TCGCACGGCATCCATCGTTGA 1,500 TCGCACGGCATCGTGA 1,500 TCGCACGGCATCGTGA 1,500 TCGCACGGCATCGTGA 1,500 TCGCACGGCATCGTGA 1,500 TCGCACGCACGCATCGTGA 1,500 TCGCACGGCATCGTGA 1,500 TCGCACGGCATCGTG	1,100 ITTGAGCAAGTTTAATACTATAT 	1,200 TCCAACTA 1200 1200 1,320 TGAAGTCC 1320 TGAAGTCC 1320 1320 TGAAGTCC 1320 TGAAGTCC 1320 TGAAGTCC 1320 TGAAGTCC 1320 TGAAGTCC 1320 TGACGAC 1560 T 1560 T 1560 T 1560 T 1680 T
N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA	LIND CTCCGTTTTTTCTTGGCTCACTCACTCACTCACTCGCTT 1.200 TTAGCTTGAAATGATCATCTATGTGAATTTAATAGCCA CURE MYBCORE 1.300 MYBCORE GTAGTGCAGTTATCTACAATCTGTTATCTCCTTAA A	1.130 ACCTOGCCATTCTGTCATG A A 1.340 1.34	МYCCONSESUSAT 1,100 1,200	1,140 TAGCACACACTAATCTCTCT 1,200 1,200 TAATAATAGCTGGTCTTAC 1,200 1,200 TAATAATAGCTGGTCTTAC 1,200 1,200 TCGCACGGCATGAATAGTCC 1,200 1,200 TCGCACGGCATGAATAGTCC 1,200 1,200 TCGCACGGCATGAATAGTCC 1,200 1,200 TCGCACGGCATGAATAGTCC 1,200 1,200 TCGCACGGCATGAATAGTCC 1,200 1,200 TCGCACGGCATGAATAGTCC 1,200 1,200 TCGCACGGCATGAATAGTCC 1,200 1,200 TCGCACGGCATGAATAGTCC 1,200 1,200 TCGCACGGCATGAATAGTCC 1,200	1,100 ITTGAGCAAGTTTAATACTATA 	1,200 TCCAACTA 1200 1200 1320 TGAAGTCC 1320 TGAAGTCC 1320 1320 GTTCCAAA 1440 GTTCCAAA 1440
N22 VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA	LIND CICCGTTTTTTCTTGGGTCACTCACTCACTCACTCGCTT 1.200 TTAGGTTGAAATGATCATCTATGGTGAATTTAATAGGCA CURE MYBOORE 1.300 MYBOORE GTAGTGCGAGTTATCTACACAATGTGTTATCTCCCTTAA A	1.120 ACCTOGCCATTCTGTCATG A	MYCCONSESUSAT 1.00 GATTIEGCAAAACAG 1.200 ATAAACATATACTAAC 1.200 TATAGTCCGATAACCT G. G. 	1,40 TAGCACACACTAATCTCTT 1,200 1,200 TAATAATAGCTGGTCTTAG 1,200 1,200 MYBIAT ACTCTTATCCCTAAGGACAC TCGCACGGCATCAATAGTCC 1,200 AAAATATTTGACATCGTTGA 1,200 TCGCACGGCATCAATAGTCC 1,200 TCGCACGGCACGGCATCAATAGTCC 1,200 TCGCACGGCACGGCATCAATAGTCC 1,200 TCGCACGGCACGGCATCAATAGTCC 1,200 TCGCACGGCACGGCATCAATAGTCC 1,200 TCGCACGGCACGGCATCAATAGTCC 1,200 TCGCACGGCACGGCATCAATAGTCC 1,200 TCGCACGGCACGGCATCAATAGTCC 1,200 TCGCACGGCACGGCATCAATAGTCC 1,200 TCGCACGGCACGGCATCAATAGTCC 1,200 TCGCACGGCACGCACGCACGCACGCACGCACGCACGCACG	1,90 ITTGAGCAAGTTTAATACTATA' 	1,200 TCCAACTA 1200
N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA	LIMO CICCGTTITITICTIGGCICACICACICACICACICGCTI LIZIO TAGGTICAAAATGATCATCTATAGICAATCACCICGCTI CURE MYBCORE 1.340 MYBCORE GIACIGGAGITATCACAATCIGITATCTCCTTAA A.A.A.A.A.A. I.A.O.A.CITATCIGITATCTCCTTAA CCGGGCTITICCTIGTICTATCACAGGICITITIGAE .T. 	1,120 ACCTCGCCATTCTGTCATG A A A A A A A A	МYCCONSESUSAT 1,500 1,500 1,500 ТАТАФТССДАТААСАД ТАТАФТССДАТААССТ С. 	1,460 TAGCACACACTAATCTCTCT 1,200 TAATAATAGCTGGTCTTAGC ACCTTATCAC MAGGACAC 1,400 MYBIAT ACTCTTATCAC MAGGACAC 1,400 1,400 1,400 AAGGACAGGCATCAATAGTCC 1,400 1,4	1,100 ITTGAGCAAGTTTAATACTATA 	1.200 TCCAACTA 1200 1200 1200 TGAAGTCC 1320 TGAAGTCC 1320 1320 TGAAGTCC 1320 1320 TGAAGTCC 1320 1320 TGAAGTCC 1320 1320 TGAAGTCC 1320 TGAAGTCC 1320 TGAAGTCC 1320 TGAAGTCC 1320 TGAAGTCC 1560 TGCC 1560 TGGC 1660 TGGC 1
N22 VANDANA PB1 IR64 PB1 IR64 PB1 PB1 IR64 PB1 PB1 PB1 PB1 PB1 PB1 PB1 PB1 PB1 PB1	LIND CTCCGTTTTTTCTTGGCTCACTCACTCACTCACTCGCTT 1.200 TTAGGCTGAAATGATGATGATGATGATTTAATAGGCA CURE MYBCORE LIND MYBCORE GTAGTGCAGTTATCTACAAATGTGTTATCTCCTTAA A A A A A A A A A A A A	1.130 ACCTOGCCATTCTGTCATG A A 1.240 1.2	МYCCONSESUSAT 1,100 1,200 АТАААСААТАТАСТААС 1,200 1,200 ТАТААТСССАТААССА 1,300 ССТСОСТТАТАСТАССА 1,500 ССТСОСТТСАТСССА 1,500 ССТСОСТТСАТСССА 1,500 ССТСОСТТСАТСССА 1,500 ССТСОСТССАТССС 1,500 ССТСОСТССАТССС 1,500 ССТСОСТССАТССС 1,500 ССТСОСТССАТСССА 1,500 ССТСОСТССАТССС 1,500 ССТСОСТССАТССС 1,500 ССТСОСТССАТССА 1,500 ССТСОСТССАТССА 1,500 ССТСОСТССАТССА 1,500 ССТСОСТССАТССА 1,500 ССТСОСТССАТСССА 1,500 ССТСОСТССАТССС 1,500 ССТСОСТССАТСССА 1,500 ССТСОСТССАТСССА 1,500 ССТСОСТССАТСССА 1,500 ССТСОСТССАТСССА 1,500 ССТСОСТССАТСССА 1,500 ССТСОСТССАТСССА 1,500 ССТСОСТССАТССА 1,500 ССТСОСТССАТССА 1,500 ССТСОСТССАТССА 1,500 ССТСОСТССАТССА 1,500 ССТСОСТССАТССА 1,500 ССТСОСТССАТССА 1,500 ССТСОСТССАТССА 1,500 ССТСОСТССАТССА 1,500 ССТСОСТССАТССА 1,500 ССТСОСТССАТССА 1,500 ССТСОСТССАТССА 1,500 ССТСОСТССАТССА 1,500 ССТСОСТССАТССА 1,500 ССТСОСТССАТССА 1,500 ССТСОСТССАТССА 1,500 ССТСОСТССАТССА 1,500 ССТСОСТССАТССА 1,500 ССТСОСТССАТССА 1,500 ССТСОСТССАТССА 1,500 ССТСОСТССАТССА 1,500 ССТСОСТСАТССА 1,500 ССТСОСТСАТССА 1,500 ССТСОСТССАТССА 1,500 ССТСОСТССАТССА 1,500 ССТСОСТССАТССА 1,500 ССТСОСТССАТССА 1,500 ССТСОСТССАТССА 1,500 ССТСОСТССАТССАСССА 1,500 ССССОСТСАТСАСССА 1,500 ССССОСТСАТСАСССА 1,500 ССССОСТССАТССА 1,500 ССССОСТССАТССАСССА 1,500 ССССОССАССАССАССАССАССАССАССАССАССАССАСС	1,140 TAGCACACACTAATCTCTCT 1,200 TAATAATAGCTGGTCTTAC 1,200 TAATAATAGCTGGTCTTAC 1,200 1,200 1,200 1,200 TGGCACGGCATGAATAGTCC 1,200 1,200 TGGCACGGCATGAATAGTCC 1,200 1,200 1,200 TGGCACGGCATGAATAGTCC 1,200	1,100 ITTGAGCAAGTTTAATACTATA 	1,200 TCCAACTA 1200 1,200 1,320 TGAAGTCC 1320 1,320 TGAAGTCC 1320 1,320 1,440 GTTCCAAA 1440 1,440 1,440 1,440 1,440 1,440 1,560 GTTCGGC 1580 C. 1560 C. 1560 GTTCGGC 1680 C. 1560 GTTCGGC 1680 1,600 GTTCGGC 1680 1,600 1,700
N22 VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64	LIND CICCGTTITTTCTTGGGTCACTCACTCACTCACTCGCTT 1.200 TTAGCTTCAAATCATCATCATCATCACCCCGCT CURE MYBOORE 1.300 MYBOORE GTAGTCGAGTTATCTACAAATCTGTTATCTCCCTTAA A A A A A A A A A A A A	1.120 ACCTOGCCATTCTGTCATG A	MYCCONSESUSAT 1.00 GATTIEGCAAAACAG 1.200 ATAAACATATACTAAC 1.200 TATAGTCCGATAACCT G	1,40 TAGCACACACTAATCTCTT 1,200 1,200 TAATAATAGCTGGTCTTAG 1,200 MYBIAT ACTCTTATCACTAAGGACAC TCGCACCGGCATCAATAGTCC 1,200 TCGCACCGGCATCAATAGTCC 1,200 TCGCACCGCATCAATAGTCC 1,200 TCGCACCGCATCAATAGTCC 1,200 TCGCACCGCATCAATAGTCC 1,200 TCGCACCGCATCAATAGTCC 1,200 TCGCACCGCATCAATAGTCC 1,200 TCGCACCGCATCAATAGTCC 1,200 TCGCACCGCATCAATAGTCC 1,200 TCGCACCGCATCAATAGTCC 1,200 TCGCACCGCATCAATAGTCC 1,200 TCGCACCGCATCAATAGTCC 1,200 TCGCACCGCATCAATAGTCC 1,200 TCGCACCGCATCAATAGTCC 1,200 TCGCACCGCATCAATAGTCC 1,200 TCGCACCGCATCAATAGTCC 1,200 TCGCACCGCATCAATAGTCC 1,200 TCGCACCGCATCAATCACCGCACCAC	1,90 ITTGAGCAAGTTTAATACTATA' 	1,200 TCCAACTA 1200 1200 1,300 TGAAGTCC 1320 1,300 TGAAGTCC 1320 1,300 TGAAGTCC 1320 1,300 GTTCCAAA 1440 1,440 1,440 1,440 1,440 1,440 1,500 GTTCGCC 1560 GTTCGCC 1680 GTTCGCC 1680 1,500 GTTCGCC 1680 1,500 GTTCGCC 1680 1,500 GTTCGCC 1680 1,500
N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA	LIND CTCCGTTTTTTCTTGGCTCACTCACTCACTCACTCACTCA	1,120 ACCTCGCCATTCTGTCATG A A A 1,340 1,340 1,340 1,340 1,340 1,340 1,350 1,450	МYCCONSESUSAT 1,500 GATTIGCCAAAACAG 1,500 ТАТААТССБАТААССА С. 	1,400 TAGCACACACTAATCTCTCT 1,200 TAATAATAGCTGGCTCTTACC 1,200 TAATAATAGCTGGCTCTTACC 1,400 M/WBIAT ACTCTTATCACTAAGCGACAC 1,400 1,200 1,200 M/WBIAT ACTCTTATCACTAAGCGACAC 1,200 1,2	1,100 ITTGAGCAAGTTTAATACTATAT 	1,200 TCCAACTA 1200 1200 1,320 TGAAGTCC 1320 TGAAGTCC 1320 1,320 TGAAGTCC 1320 1,320 GTTCCAAA 1440
N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA	LIND CICCGTTITITICTIGGCICACICACICACICGCTI 1200 TTAGCTIGAAATGATCATCTATGIGAATTAATAGCCA CURE MYBCORE 1300 MYBCORE GIAGIGCAGITAICTACAATCIGITAICICCITAA A A A A A A A A A A A A	1.130 ACCTOGCCATTCTGTCATG A A 1.240 1.2	МYCCONSESUSAT 1,500 1,500 1,500 1,500 1,500 ССТСССТТСАТССС ССТСССТТСАТССС 1,500 ССТСССТТСАТССС 1,500 ССТСССТТСАТССС 1,500 ССТСССТССАТССС 1,500 ССТСССТССАТССС 1,500 ССТСССТССАТССС 1,500 ССТСССТССАТССС 1,500 ССТСССТССАТССС 1,500 ССТСССТССАТССС 1,500 ССТССССТССАТССС 1,500 ССТССССТССАТССС 1,500 ССТССССТССАТСССС 1,500 ССТССССТССАТСССС 1,500 ССТССССТССАТССС 1,500 ССТССССТССАТССС 1,500 ССТССССТССАТССС 1,500 ССТССССТССАТССС 1,500 ССТССССТССАТСССС 1,500 ССТССССТССАТССС 1,500 ССТССССТССАТССС 1,500 ССТССССТССАТССС 1,500 ССТССССТССАТССС 1,500 ССТССССТССАТССС 1,500 ССТССССТССАТССС 1,500 ССТССССТССАТССС 1,500 ССТССССТССАТССС 1,500 ССТССССТССАТССС 1,500 ССТССССТССАТСССС 1,500 ССТССССТССАТСССС СССССССССССССССССССС	1,140 TAGCACACACTAATCTCTCT 1,200 TACT TAATAATAGCTGGTCTTAC 1,200 TAATAATAGCTGGTCTTAC 1,200 1,200 TGGCACGGCATGAATAGTCC 1,200 TGGCACGGCATGAATAGTCC 1,200 TGGCACGGCATGAATAGTCC 1,200 TGGCACGGCATGAATAGTCC 1,200 TGGCACGGCATGAATAGTCC 1,200 TGGCACGGCATGAATAGTCC 1,200 1,200 TGGCACGGCATGAATAGTCC 1,200 1,200 TGGCACGGCATGAATAGTCC 1,200 1,200 TGGCACGGCATGAATAGTCC 1,200 1,200 TGGCACGGCATGAATAGTCC 1,200 1,200 TGGCACGGCATGAATAGTCC 1,200 1,200 TGGCACGGCATGAATAGTCC 1,200 1,200 TGGCACGGCATGAATAGTCC 1,200 1,200 TGGCACGGCATGAATAGTCC 1,200 1,200 TGGCACGGCATGAATAGTCC 1,200 1,200 TGGCACGGCATGAATAGTCC 1,200 1,200 TGGCACGGCATGAATAGTCC 1,200 1,200 TGGCACGGCATGAATAGTCC 1,200 TGGCACGGC 1,200 TGGCACGGC 1,200 TGGCACGGC 1,200 TGGCACGGC 1,200 TGGCACGGC 1,200 TGGCACGGC 1,200 TGGCACGGC 1,200 TGGCACGC 1,200	1,100 ITTGAGCAAGTTTAATACTATA 	1,200 TCCAACTA 1200 1200 1320 TGAAGTCC 1320 TGAAGTCC 1320 1,320 TGAAGTCC 1320 1,440 GTTCCAAA 1440
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N22	TCTCCCTCTACATGTTTATCTATC	GTTTTGTTAGTATTG	GTTGTATTGCTCTCAC	TAAGCCTAGATGCTCGCTA	GATATAATGTATTTTTG	CTTACTTGTACTCCCCTCCGTA	CGTTCAAAT 720	1
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VANDANA PB1 IR64			GIGGAAACIGIGAACC	ACTGAACCACCACCATAGA	CGATAGCGTTTGTAGCT		107 	9 6 6
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VANDANA PB1 IR64 N22 VANDANA	1.100 CCTCCGTAACCGCGAGATTCCAAC	GTTTTCAACGAAGGC		ACTGAACCACCACCATAGA GTATERD]140 GTCAAAATTAAAAGTTTGA	CGATAGCGTTTGTAGCT 1,160 AGAAATTAGAATGATGT AC.	1.180 GACAGAAAAGTTAGAAGTTTGT	1,200 GTGT AGA 119 	7 9 6 6 5 7
VANDANA PB1 IR64 N22 VANDANA PB1	1,100 CCTCCGTAACCGCGAGATTCCAAG	GTTTTCAACGAAGGC	1,120 ACCESTING 1,120 ACCESTING CTGTATTTATTTCCAC 	ACTGAACCACCACCATAGA GTATERDI ₁₄₀ GTCAAAATTAAAAGTTTGA	CGATAGCGTTTGTAGCT 1,160 AGAAATTAGAATGATG ACA.A.	1.100 GACAGAAAAGTTAGAAGTTIGT	1,200 1,200 1,200 1,200 1,200 1,200 1,200 1,200 1,200 1,200 1,200 1,200 GTGT AGA 119 	7 9 6 6 5 7 6
VANDANA PB1 IR64 N22 VANDANA PB1 IR64	1,10 CCTCCGTAACCGCGAGATTCCAAC	GTTTTCAACGAAGGC	1,120 ACC 10 1 GAACC	ACTGAACCACCACATAGA GTATERDhao GTCAAAATTAAAAGTTTGA	1,160 AGAAATAGAATGATGT A	1:00 GACAGAAAAGTTAGAAGTTIGT	GTGT AGA 119 	7 9 6 6 5 7 6 4
VANDANA PB1 IR64 N22 VANDANA PB1 IR64	1.100 CCTCCGTAACCGCGAGATTCCAAG	STTTTCAACGAAGGC	1,120 AAAC	ACTGAACCACCACATAGA GTATERDItan GTAAAATTAAAAGTTTGA	1,160 AGAAATAGATGATGAT A	1.50 GACAGAAAGTTAGAAGTTTGT	GTGT AGA 119 	7 9 6 6 15 17 6 4
VANDANA PB1 IR64 VANDANA PB1 IR64	CCTCCGTAACCGCGAGATTCCAAC	STTTTCAACGAAGG	1,120 AAC	ACTGAACCACCACCATAGA GTATERDH40 GTCAAAATTAAAAGTTTGA 1,200	CGATAGCGTT GTAGCT 1,150 AGAAATTAGAATGATGT ACA.A. A.A.	1.180 GACAGAAAGTTAGAAGTTTGT 	1.200 1.200 GTGT AGA 119 	7 9 6 6 15 17 16 4
VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22	1,100 CCTCCGTAACCGCGAGATTCCAAC	STTTTCAACGAAGGC	1.120 AAC 1.120 AC GT 1.20	ACTGAACCACCACCATAGA GTATERDito GTCAAAAATTAAAAGTTTGA 1,700 AATAGGGCCAAAGCGAGAA	CGATAGCGTTTGTAGCT 1,160 AGAAATTAGAATGATGATG 	1.180 GACAGAAAAGTTAGAAGTTTGT A. A. MYCCONSENSUSAT ;CURE 100 110 110 110 110 110 110 110 110 11	GTGT AG 119 	7 9 6 6 15 17 16 14 1
VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA	1.100 CCTCCGTAACCGCGAGATTCCAAG 1.20 AAAGTTCGATATGACGAAAAAGTT 	STTTTCAACGAAGGC	1.120 AAC 1.120 AC 1.121 AC 1.120 AC 	ACTGAACCACCACCATAGA GTATERDI _{NO} GTCAAAATTAAAAGTTTGA 1,200 AATAGGGCCAAAGCGAGAA	1,160 AGAAATTAGAATGATGAT A	1.100 GACAGAAAAGTTAGAAGTTTGT AA	GTGT AGA 119 	7 9 6 6 15 17 16 14 1 3
VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 PB1 PB1 PB1 PB1 PB1 PB1 PB1 PB1 PB1	1.100 CCTCCGTAACCGCGAGATTCCAAG AAAGTTCGATATGACGAAAAAGT G. A.	STTTTCAACGAAGGC	1,120 AAC CIGTATTTATTTCCAG 	ACTGAACCACCACCATAGA GTATERDhao GTCAAAATTAAAAGTTTGA 1,200 AATAGGGCCAAAGCGAGAA	1,160 AGAAATTAGAATGATGT .AAA. AA.A. AGCTTCCTTCCAAATCC .G	1.100 GACAGAAAAGTTAGAAGTTTGT A MYCCONSENSUSAT ICURE 1000 TGGCTGTGTCCATATGTA TGTA	GTGT AGA 119 	7 9 6 6 5 7 16 4 1 3 6 4
VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64	1,100 CCTCCGTAACCGCGGGATTCCAAG AAAGTTCGATATGACGAAAAGTT 	STTTTCAACGAAGGC	1,120 AAAC (STAAACC) CTGTATTTATTTCC G	ACTGAACCACCACCATAGA GTATERDH40 GTCAAAATTAAAAGTTTGA 1,200 AATAGGGCCAAAGCGAGAA	CGATAGCGTTTGTAGCT 1,150 AGAAATTAGAATGATGT ACA.A. AA.A.A. 1,280 AGCTTCCTTCCAAATCC G.	1.100 GACAGAAAAGTTAGAAGTTTGT A. A. MYCCONSENSUSAT (CURE 1000 TGGCTGTGTGCATATGTA 	GTGT AG 119 	7966 1576 4 1364
VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA PB1 IR64	1.00 CCTCCGTAACCGCGGGATTCCAAC AAAGTTCGATATGACGAAAAAGTT 	STTTTCAACGAAGGC	1,120 AAAC IS ISAACC CTGTATTTATTTCCAG 	ACTGAACCACCACCATAGA GTATERDHo GTCAAAATTAAAAGTTTGA 1,200 AATTAGGGCAAAGCGAGAA 1,200 AATTTATTTTAAAGTAAT	1,150 AGAAATAGAATGATGA 	1.180 GACAGAAAAGTTAGAAGTTTGTU A. MYCCONSENSUSAT (CURE 1000 TGGCTGTGCGCATAGTA TGTA 	CURE 1.20 CURE 1.20 CURE 1.20 CORE 1.10 CURE 1.20 CORE 1.20	7966 15764 1364 0
VANDANA PB1 IR64 N22 VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA	1,100 CCTCCGTAACCGCGAGATTCCAAC AAAGTTCGATATGACGAAAAGTT G. A. G. A. G. A. CCTTCGTCTCAGTAAGTTAATTTT	STTTTCAACGAAGGC FAAAAGTTTAAAGAA	1,120 AA IGTATTATTTCCAR 1,200	ACTGAACCACCACCATAGA GTATERDHao GTCAAAAATTAAAAGTTTGA 1,000 AATAGGGGCAAAGCGAGAA 1,000 AATTTATTTTAAAGTAAT	CGATAGCGTTTGTAGCT 1,100 AGAAATTAGAATGATGT AAA. 1,200 AGCTTCCTTCCAAATCC .G 1,400 AATTGTATCAAAATTGA	1.180 GACAGAAAAGTTAGAAGTTTGT A.A.A. MYCCONSENSUSAT (CURE 100 TGCTGTGTGCCATATGTA TGTA 1400 TGAAAGTAGAAATAATTATAT	GTGT AGA 119 	7966 15764 1364 00
VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1	1.100 CCTCCGTAACCGCGAGATTCCAAG AAAGTTCGATATGACGAAAAAGT G. A. G. A. G. A. CCTTCGTCTCAGTAAGTTAATTTI	5TTTTCAACGAAGGC FAAAAGTTTAAAGAA TTTATT-TTTTTTCT 	1,120 AAA CGTGATTTATTTCCAG 	AGTGAACGACCACCATAGA GTATERDI _{N0} GTCAAAATTAAAAGTTTGA 1,200 AATAGGGCCAAAGCGAGAA 1,200 AATTATTTATAAAGTAAT	CGATAGCGTTTGTAGCT 1,160 AGAAATTAGAATGATGT .A	1:00 GACAGAAAAGTTAGAAGTTTGT A MYCCONSENSUSAT ;CURE 100 TGGCTGTGTCCATATGTA TGTA 100 TGAAAGTAGAAAATAATTATT G	GTGT - AGA 119 GTGT - AGA 119 GTGT - AGA 119 	7966 15764 1364 000
VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 IR64	1.100 CCTCCGTAACCGCGGGGATTCCAAC AAAGTTCGATATGACGAAAAAGT 	5TTTTCAACGAAGGC 1AAAAGTTTAAAGAA 1TTATT-TTTTTCT 	1,120 AAAC GIGAAAC CTGTATTTATTTCCAG 	GTATERDI ₁₄₀ GTATERDI ₁₄₀ GTCAAAATTAAAAGTTTGA 1,200 AATTAGGGCCAAAGCGAGAA 1,200 AATTAGTTTTTTAAAGTAAT	CGATAGCGTTTGTAGCT 1,160 AGAAATTAGAATGATGT ACA.A. AA.A.A. 1,260 AGCTTCCTTCCAAATCC G. 1,460 AATTGTATCAAAATTGA	1.100 GACAGAAAAGTTAGAAGTTTGT A.A. MYCCONSENSUSAT ICURE 100 TGGCTGTGTGCGATATGTA TGTA TGTA TGTA TGTA	CURE 1.30 CURE 1.30	79966 1576 14 1364 0001
VANDANA PB1 IR64 N22 VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA PB1 IR64	1.100 CCTCCGTAACCGCGGGATTCCAAC AAAGTTCGATATGACGAAAAAGTT 	5TTTTCAACGAAGGC FAAAAGTTTAAAGAA TTTATT-TTTTTTC1 	1,120 AAAC IGIGAACC CTGTATTTATTTCCAC 	ACTGAACCACCACCATAGA GTATERDHe0 GTCAAAATTAAAAGTTTGA 1,200 AATAGGGCCAAAGCGAGAA 1,200 AATTTATTTTTAAAGTAAT	CGATAGCGTTTGTAGCT 1,160 AGAAATTAGAATGATGT ACA.A. AA.A. AGCTTCCTTCCAAATCC G. G. G. 	1.180 GACAGAAAAGTTAGAAGTTTGTU A. A. MYCCONSENSUSAT (CURE 100 TGGCTGTGTGCGATATGTA TGTA TGTA 140 TGAAAGTAGAAAATAATTATAT G. G. S. WECORE 1560	CURE 1320 GTGT AGA 119 	7996 1577 164 1364 000 1
VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64	1,100 CCTCCGTAACCGCGAGATTCCAAC AAAGTTCGATATGACGAAAAAGTT G.A.A G.A. G.A. CCTTCGTCTCAGTAAGTTAATTTT 1,400 ATAAATGAGAAAATGATGACTACTTCA	3TTTTCAACGAAGGC 7AAAAGTTTAAAGAA 1TTATT-TTTTTC1 	1,120 CTGTATTTATTTCCA 	ACTGAACCACCACCATAGA GTATERDHuo GTCAAAATTAAAAGTTTGA 1,200 AATAGGGGCCAAAGCGAGAA 1,200 AATTTATTTTTTTAAAGTAAT 1,200 TTATTGATAATATGTGAAA	1,160 AGAAATTAGAATGATGT AAA. AA. AA. AA. AA. AA. AA. AA. AA. AA. AA. AA. AA. AA. AA. AA. GG. AAG. AAAAAAAA	1:00 GACAGAAAAAAATTAGAAGTTTGT A.A. MYCCONSENSUSAT ;CURE 1000 TGGCTGTGTCCATAGTA TGAAGTGGTCCATAGTA TGAAGTAGAAAAAATAATTATAT G.G. G. YBCORE 1540 CGTTAAAAAAATTAAATTAAATTAG	GTGT AGA 119 	79 6 15 17 16 14 1 3 16 4 0 0 0 1 0
VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA	1.100 CCTCCGTAACCGCGAGATTCCAAG AAAGTTCGATATGACGAAAAAGTT G. A. G. A. G. A. CCTTCGTCTCAGTAAGTTAATTTI	5TTTTCAACGAAGGC FAAAAGTTTAAAGAA TTTATT-TTTTTTCT T.A.T. ACATTGATAAAGCAA	1,120 ACC GIGAACC TIGTATTTATTTCCAG 1,200 ACC G T 1,200 ACC G T	ACTGAACCACCACCATAGA GTATERDH40 GTCAAAATTAAAAGTTTGA AATAGGGCCAAAGCGAGAA 1.300 AATTTATTTTTAAAGTAAT 1.000 TTATTGATAATATGGAAA 	CGATAGCGTTTGTAGCT 1,160 AGAAATTAGAATGATGT .ACA.A.A. .1,260 AGCTTCCTTCCAAATCC 	1:00 GACAGAAAAGTTAGAAGTTTGT A.A. MYCCONSENSUSAT ICURE 100 TGGCTGTGTCCATATGTA 	CURE, 530 CURE, 530	79665765764 138640001 06
VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64	1.100 CCTCCGTAACCGCGGGGATTCCAAC AAAGTTCGATATGACGAAAAAGTT 	5TTTTCAACGAAGGC TAAAAGTTTAAAGAA TTTATT-TTTTTTCT 	1,100 AAAC GIGAAAC CTGTATTTATTTCCAC CTGTATTTATTTCCAC C	ACTGAACCACCACCATAGA GTATERDH40 GTCAAAATTAAAAGTTTGA 1,260 AATTAGGGCCAAAGCGAGAA 1,260 AATTTATTTATTTTAAAGTAAT 1,200 TTATTGATAATATGTGAAA G	CGATAGCGTTTGTAGCT AGAAATTAGAATGATGT ACA.A. AGCTTCCTTCCAAATCC G. AGCTTCCTTCCAAATCGA AGCTTCCTTCCAAATTGA G. G. G. G. 	1.100 GACAGAAAAGTTAGAAGTTTGT A.A. MYCCONSENSUSAT CURE 100 TGGCTGTGTGCGATATGTA TGTA TGTA TGTAAGTAGAAAATAATTATAT G.G. G. G. WBCORE 1540 EGTTAAAAAAAATTAAATTAG	CURE 1.30 GTGT - AGA 119 GTGT - AGA 119 GTGT - A 119 CURE 1.30 ETAGTAGT 131 CURE 1.30 TGGAAATAG 143 A 140 AACAGGATA 155 GG G 154 A 152 A 152 CG G 154 CG C 157 CG C 1	7966 057664 1364 00001 060
VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64	1,100 CCTCCGTAACCGCGGGATTCCAAG AAAGTTCGATATGACGAAAAAGTT 	БТТТТСААСБААББС ГААААБТТТАААБАА ГТТАТТ - ТТТТТСТ Т А Т. ХСАТТБАТАААБСАА А.	1,120 CTGTATTTATTTCCAG 	ACTGAACCACCACCATAGA GTATERDHe0 GTCAAAATTAAAAGTTTGA AATAGGCCAAAGCGAGAA 1.200 AATTATTATTTTTTAAAGTAAT 1.200 TTATTGATAATATGTGAAA	CGATAGCGTTTGTAGCT 1,160 AGAAATTAGAATGATGT ACAA. AA.A. AGCTTCCTTCCAAATCC G AATTGTATCAAAATTGA 1,550 M GAAGATACTACTTCCT G	1.180 GACAGAAAAGTTAGAAGTTTGTI 	CURE 1300 GTGT AGA 119 	7966 957764 13664 0001 0601
VANDANA PB1 IR64 N22 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64	1,100 CCTCCGTAACCGCGAGATTCCAAC AAAGTTCGATATGACGAAAAAGTT G. A. G. A. G. A. CCTTCGTCTCAGTAGTTAATTTT	STTTTCAACGAAGGC TAAAAGTTTAAAGAA TTTATT-TTTTTTC1 	1,120 AAA IIGTATTTATTTCCAE 1200	ACTGAACCACCACCATAGA GTATERDHio GTCAAAATTAAAAGTTTGA 1,200 AATAGGGGCCAAAGCGAGAA 1,200 AATTTATTTTTTAAAGTAAT 1,200 TTATTGATAATATGTGAAA G	CGATAGCGTTTGTAGCT 1,160 AGAAATTAGAATGATGT AA. AA. 1,260 AGCTTCCTTCCAAATCC G 4G. 1,400 AATTGTATCAAAATTGA 1,400 AATTGTATCAAAATTGA 1,500 M GAAGATACTACTTCCT	1:00 GACAGAAAAGTTAGAAGTTTGT A.A. MYCCONSENSUSAT ;CURE 100 TGGCTGTGTCCATATGTA 	GTGT AGA 119 	796 957 164 1364 000 11 060 1
VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64	1,100 CCTCCGTAACCGCGGGGATTCCAAC 1200 AAAGTTCGATATGACGAAAAGTT G. A. G. A. G. A. G. A. 1,200 CCTTCGTCTCAGTAGTTAATTTI 1,400 ATAAATGAGAAATAGTTGCATTGA	5TTTTCAACGAAGGC TAAAAGTTTAAAGAA TTTATT-TTTTTTCI 	1,120 ACC GIGAACC CIGTATTTATTTCCAG 1,20 ACC G T 1,20 AC	ACTGAACCACCACCATAGA GTATERD/140 GTCAAAATTAAAAGTTTGA 1,200 AATTAGGGCCAAAGCGAGAA 1,200 AATTTATTTTTTAAAGTAAT 1,200 TTATTGATAATATGTGAAA G	CGATAGCGTTTGTAGCT AGAAATTAGAATGATGT AA.A.A. AGCTTCCTTCCAAATCC AGCTTCCTTCCAAATCC G. G. G. G. G. G. G. G. G. 	1.100 GACAGAAAAGTTAGAAGTTTGT A.A. MYCCONSENSUSATICURE 100 TGGCTGTGTCCATATGTA	CURE 1,500 GTGT AGA 119 GTGT AGA 119 GTGT AGA 119 CURE 1,500 CURE 1,500 TGGAAATAG 143 	796 9576 4 1384 000011 0601
VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA PB1 IR64	1.100 CCTCCGTAACCGCGGGGATTCCAAC 1.20 AAAGTTCGATATGACGAAAAAGTT 	STTTTCAACGAAGGC IAAAAGTTTAAAGAA ITTATT-TTTTTCT 	1,120 ACC GIGAACC GIGAACC CIGTATTTATTICCAG 	ACTGAACCACCACCACATAGA GTATERDH40 GTCAAAATTAAAAGTTTGA 1,260 AATTAGGGCCAAAGCGAGAA AATTAATTTATTTAAAGTAAT 1,200 TTATTGATAATATGTGAAA G. 1,000 1	CGATAGCGTTTGTAGCT 1,150 AGAAATTAGAATGATGT AC AA.A. AGCTTCCTTCCAAATCC G. 	1.100 GACAGAAAAGTTAGAAGTTGTI A	CURE 1.30 GTGT - AGA 119 GTGT - AGA 119 GTGT - AGA 119 CURE 1.30 ETAGTACT 131 CURE 1.30 TGGAAATAG 143 A. 140 A. 143 A. 144 A. 143 A. 144 A. 143 A. 144 A. 143 A. 144 A. 155 GTACAGGATA 155 A. 155 A. 155 A. 155 A. 156 A. 1	7966 95764 1364 0001 0601 55
VANDANA PB1 IR64 N22 VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64	1,100 CCTCCGTAACCGCGGGATTCCAAG 1,200 AAAGTTCGATATGACGAAAAAGT 	БТТТТСААСGAAGGC ГААААGTTТАААGAA ГТТАТТ - ТТТТТСТ 	1,120 ACC GIGAAAC GIGAAAC GIGAAAC GIGAAAC GIGAAAC GIGAAAC GIGAAAC GIGAAAC GIGAAAC A A A A A A A A A A A A A A A A A	ACTGAACCACCACCATAGA GTATERDH40 GTCAAAATTAAAAGTTTGA AATAGGGCCAAAGCGAGAA AATTTATTTTTTTAAAGTAAT 1,000 TTATTGATAATATGTGAAA G	CGATAGCGTTTGTAGCT 1,160 AGAAATTAGAATGATGT ACAA. AAA. AGCTTCCTTCCAAATCC GAAGATATGTATCAAAATTGA 1,200 AATTGTATCAAAATTGA 1,400 GAAGATACTACTTCCT GT. 1,640 GCACACCACAACAA GGG.G.G.	1.100 GACAGAAAAGTTAGAAGTTTGTI 	CURE 1300 GTGT - AGA 119 	7966 95764 1364 000011 06001 556
VANDANA PB1 IR64 N22 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA PB1 IR64	1,100 CCTCCGTAACCGCGAGATTCCAAC AAAGTTCGATATGACGAAAAAGTT G. A. G. A. G. A. G. A. CCTTCGTCTCAGTAGTAATTTT 1,400 ATAAATGAGAAATAGTTGCATTGA 1,400 ATAAATGAGAAATAGTTGCATTGA CGACACATTCTAGTAGAATAGTTGCATTGA AAATA A. T. T. AATA	STTTTCAACGAAGGC IAAAAGTTTAAAGAA ITTATT-TTTTTTC1 	1,120 AAAC GIGAAAC GIGAAAC GIGAAAC GIGAAAC GIGAAAC GIGAAAC GIGAAAC GIGAAAC A A A A A A A A A A A A A A A A A	ACTGAACCACCACCATAGA GTATERDH60 GTCAAAATTAAAAGTTTGA 1,200 AATAGGGCAAAGCGAGAA 1,200 1,200 TTATTGATAATATGTGAAA G	CGATAGCGTTTGTAGCT 1,160 AGAAATTAGAATGATGT ACAA. AA	1.00 GACAGAAAAAGTTAGAAGTTTGT A.A. MYCCONSENSUSAT ICURE IP00 TGGCTGTGTGCATATGTA TGGTGTGTGCATATGTA TGAAAGTAGAAAATAATTAT G.G. G.G. YBCORE 1.540 CGTTAAAAAAAAATTAAATCTAG A.A.A.A.AAAAAATTAAATCTAG G.G. G.G. 1.60 CACCAGGAACGGGGATTAGAAG	GTGT AGA 119 	7966 95764 13864 00001 5561
VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64	1.100 ССТСССТААСССССАВАТТССААС 1200 АААGTTCGATATGACGAAAAAGTT G	STTTTCAACGAAGGC TAAAAGTTTAAAGAA TTTATT-TTTTTTC1 	1,120 ACC GIGAAAC GIGAAAC	ACTGAACCACCACCACCATAGA	CGATAGCGTTTGTAGCT 1,160 AGAAATTAGAATGATGT .ACA.A. .AA.A. 1,260 AGCTTCCTTCCAAATCC GA.A. 1,260 AATTGTATCAAAATTGA AATTGTATCAAAATTGA G	1.100 GACAGAAAAGTTAGAAGTTTGT A.A. MYCCONSENSUSAT (CURE 100 TGGCTGTGTCCATATGTA 	CURE, 530 GTGT AGA 119 	7966 95764 1364 00001 15561
VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64	1,100 CCTCCGTAACCGCGGGGATTCCAAC 1,20 AAAGTTCGATATGACGAAAAAGTT G. A. G. A. G. A. CCTTCGTCTCAGTAAGTTAATTTT 1,400 ATAAATGAGAAAATAGTTGCATTCA TGACACATTCTAGTAGAAT A. T. T. TATGAAA A. T. T. TATGAAA	STTTTCAACGAAGGC TAAAAGTTTAAAGAA TTTATT - TTTTTTCT 	1,100 AAAC GIGAAAC GIGAAAC GIGAAAC GIGAAAC GIGAAAC GIGAAAC GIGAAAC GIGAAAC A A A A A A A A A A A A A A A A A	ACTGAACCACCACCATAGA	CGATAGCGTTTGTAGCT 1,150 AGAAATTAGAATGATGT AC AA.A. AGCTTCCTTCCAAATCC G. 	1.100 GACAGGAAAAGTTAGAAGTTTGT A. A. MYCCONSENSUSAT ICURE 100 TGGCTGTGTGCGATATCTA. TGTA TGTA TGTA G. G. G. G. G. G. G. G. G. G. G. G. G.	CURE 1.30 GTGT - AGA 119 GTGT - AGA 119 GTGT - AGA 119 CURE 1.30 ETAGTACT 131 CURE 1.30 ETAGTACT 131 CGAAATAG 143 A. 143 A. 143 A. 144 A. 143 A. 144 A. 155 GGAACAGGATA 155 G. G 154 G. G 154 CTGACAGGATA 155 G. A. 152 CTGACAGGATA 155 G. A. 152 CTGACAGGATA 155 G. A. 152 CTGACAGGATA 155 C. 156 C. 166 C. 16	7966 157664 13864 800011 8060011 55661
VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64	1,10 CCTCCGTAACCGCGAGATTCCAAC 1,200 AAAGTTCGATATGACGAAAAAGTT G. A. G. A. G. A. CCTTCGTCTCAGTAGTAATTTT 1,400 ATAAATGAGAAATAGTTGCATTGA TGACACATTCTAGTAGAATAGTTAGTTGA A.T.T. AAAT A.T.T. TATG A.T.T.	STTTTTCAACGAAGGC TAAAAGTTTAAAGAA TTTATT - TTTTTTCT 	1,50 ACC CTGTATTATTTCCA G. T 1,20 AAAAGTTAGAATCTA A. A. 1,20 AATTATTCCAAAATA 1,20 AATTATTCCAAAATA 1,20 AATTATTCCAAAATA 1,40 AAGTATTTATTCCAAAATA 1,40 AAGTATTTATTCCAAAATA 1,40 AAGTATTTATTCCAAAATA 1,40 AAGTATTTATTCCAAAATA A. A. A. A. A. A. A. A. A. A	ACTGAACCACCACCATAGA	CGATAGCGTTTGTAGCT 1,160 AGAAATTAGAATGATGT AC. AA	1.100 GACAGAAAAGTTAGAAGTTTGTI A. A. MYCCONSENSUSAT [CURE 1000 TGGCTGTGTGCGATATGTATGTA 	GTGT - AGA 119 	796 5764 1364 00001 0601 5561 5
VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA	1,100 CCTCCGTAACCGCGAGATTCCAAC 1,200 AAAGTTCGATATGACGAAAAAGTT G. A. G. A. G. A. CCTTCGTCTCAGTAGTTAATTTT 1,400 ATAAATGAGAAATAGTTGCATTGA TGACACATTCTAGTAGAATAGTTGCATTGA AAAT A. T. T. AATGA	STTTTTCAACGAAGGC STTTTTCAACGAAGGC TAAAAGTTTAAAGAA TTTATT-TTTTTTCT T. A. T. ACATTGATAAAGCAA ATGAACAAAGATATC	1,120 ACC GIGAAAC GIGAAAC GIGAAAC GIGAAAC GIGAAAC GIGAAAC GIGAAAC GIGAAAC AC A A A A A A A A A A A A A A A A	ACTGAACCACCACCATAGA	CGATAGCGTTTGTAGCT AGAAATTAGAATGATGT ACA. AA.A.A. AGCTTCCTTCCAAATGC AGCTTCCTTCCAAATCC GGG. 1,000 AATTGTATCAAAATTGA AATTGTATCAAAATTGA AATTGTATCAAAATTGA GCACACCACACACA GGGG. GGGG. GGGG. GGCACGACGCGATGGGG GCCACGACGCGATGGGG	1,100 GACAGAAAAGTTAGAAGTTTGT A.A. MYCCONSENSUSAT (CURE 1000 TGGCTGTGTCCATATGTA 	GTGT - AGA 119 	796 5764 1364 00001 06001 5561 55
VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64	1,100 ССТСССБТААСССССВАВАТТССААС 1200 АААGTTCGATATGACGAAAAAGTT G	STTTTTCAACGAAGGC STTTTTCAACGAAGGC IAAAAGTTTAAAGAA ITTATT-TTTTTTCT T. A. T. ACATTGATAAAGCAA ATGAACAAAGATATC C. IGCTGCGGTAGGAAG	1,120 AAAC GIGAAAC CIGTATTTATTICCAG CIGTATTTATTICCAG A. A. A	ACTGAACCACCACCATAGA	CGATAGCGTTTGTAGCT AGAAATTAGAATGAATGAATGAATGAATGAATGAATGAA	1.100 GACAGGAAAAGTTAGAAGTTTGT A. A. MYCCONSENSUSAT (CURE 100 TGGCTGTGTCCATATGTA 	GTGT AGA 119 GTGT AGA 119 	7966 957964 1364 000011 0060011 5561 556
VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA PB1 IR64	1.00 ССТСССТААСССССАВАТТССААС АААСТТССАТАТСАССАААААСТТССААС С	STTTTTCAACGAAGGC STTTTTCAACGAAGGC TAAAAGTTTAAAGAA TTTATT-TTTTTTCT T.A.T.T ACATTGATAAAGCAA A ATGAACAAAGATATC C TGCTGCGGTAGCAAC	1,100 ACC CTGTATTTATTTCCAG CTGTATTTATTTCCAG 1,200 AAAAGTTAGAATCTA A A 1,200 AAAAGTTAGAATCTA A 1,200 AAAAGTTAGAAATCTA A 1,200 AAAAGTTAGAAATCTA A 1,200 AAAAGTTAGAAATCA A 1,200 AAAAGTTAGAAATCA A 1,200 AAAAGTTAGAAATCA A 1,200 AAAAGTTAGAAATCA A A 1,200 AAAAGTTAGAAATCA A A 1,200 AAAAGTTAGAAATCA A A 1,200 AAAAGTTAGAAATCA A A 1,200 AAAAGTTAGAAATCA A A 1,200 AAAAGTTAGAAATCA A A 1,200 AAAAGTTAGAAATCA A A 1,200 AAAAGTTAGAAATCA A A A 1,200 AAAAGTTAGAAATCA A A A A A A A A A A A A A	ACTGAACCACCACCATAGA	CGATAGCGTTTGTAGCT AGAAATTAGAATGATGT AC AA.A.A. AGCTTCCTTCCAAATCC G. G. AATTGTATCAAAATTGA GAAGATACTACTTCCTG GCACACCACACACA GGG.G.G. GGG.G.G. TAG.G.G. GCACGCGATGGGG GCCACGACGCGATGGGG	1.100 GACAGAAAAGTTAGAAGTTTGT A. A. MYCCONSENSUSAT CURE 100 TGGCTGTGTGCGATATCTA. TGTA TGGAAGTAGAAAATAATTATAT G. G. G. WBCORE 150 GGTTAAAAAAAATAATTAAATCTAG. A. A. 	GT A - 119 A - 119 	7966 5764 1364 00001 5561 5561 5561
VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64	1,10 CCTCCGTAACCGCGAGATTCCAAC 1,200 AAAGTTCGATATGACGAGAAAAGT G. A. G. A. G. A. CCTCGTCTCAGTAGTAATTTT 1,400 ATAAATGAGAAATAGTTGCATTGA TGACACATTCTAGTAGAAT A. T. T. ATG A. T. T. T. TATG A. T. T	STTTTTCAACGAAGGC	1,50 AAAC GIGAAAC GIGAAAC GIGAAAC GIGAAAC GIGAAAC GIGAAAC GIGAAAC GIGAAAC GIGAAAC A A A A A A A A A A A A A A A A A	ACTGAACCACCACCATAGA GTATERDH40 GTCAAAATTAAAAGTTTGA 1,200 AATAGGGCCAAAGCGAGAA 1,200 TTATTGATAATATGTGAAA G G G G G G G G G G G G G G G G G 	CGATAGCGTTTGTAGCT 1,160 AGAAATTAGAATGATGT AC. AAA. AA. AA. AA. AAA. AA. A	1.60 GACAGAAAAAGTTAGAAGTTTGT A.A. MYCCONSENSUSAT .CURE IP00 TGGCTGTGTCCATAGTA TGAAGTAGTAGTA TGAAGTAGAAAATAATTAT G.G. G. YBCORE 1540 CGTTAAAAAAAAATTAAATCTAG CACCAGCAACGGGGATTAGAAG 1.60 CACCAGCAACGGGGATTAGAAG MITCCCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT	GTGT - AGA 119 	7966 5764 1364 00001 0601 5561 5561
VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64	1,100 CCTCCGTAACCGCGAGATTCCAAC 1,200 AAAGTTCGATATGACGAAAAAGTT G. A. G. A. G. A. CCTTCGTCTCAGTAGTTAATTTT ATAAATGAGAAATAGTTGCATTGA TGACACATTCTAGTAGAATAGTTGCATTGA CTGTCTATCTGGAATCCTAGCTGT 1,200 1,400 1,	STTTTTCAACGAAGGC	1,120 ACC GIGAAAC GIGAAAAAAC GIGAAAC GIGAAAAC GIGAAAC GIGAAAC GIGAAAAAAC GIGAAAAAAAC GIGAAAAAAAAAC GIGAAAAAAAAAA	ACTGAACCACCACCATAGA	CGATAGCGTTTGTAGCT AGAAATTAGAATGATGT A	1,100 GACAGAAAAGTTAGAAGTTTGT A. A. MYCCONSENSUSAT (CURE 1000 TGGCTGTGTGCATATGTA 1000 TGGAAGTAGAAAATAATTATAT G. G. G. G. G. 1500 CACCAGCAACGGGGATTAGAAG 1360 CACCAGCAACGGGGATTAGAAG M 1270 1270 1	Gr A GG T A 119 CURE 130 GT GT - AGA 119 , A 119 , A 119 CURE 130 GT GT A 119 CURE 130 GT GAAATAG 113 , A 119 , A 11	7966 5764 1364 00001 5561 5561
VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA	1,100 ССТСССБТААСССССАВАТТССААС 1200 АААДТТССАТАТСАСССАВАТТССААС С	STTTTTCAACGAAGGC	1,120 AAAC GIGAAAC GIGAAAC GIGAAAC GIGAAAC GIGAAAC GIGAAAC GIGAAAC GIGAAAC AC A A A A A A A A A A A A A A A A	ACTGAACCACCACCATAGA	CGATAGCGITTGTAGCT 1,160 AGAAATTAGAATGATGT .ACA. AGCTTCCTTCCAAATCC G. 	1.100 GACAGGAAAAGTTAGAAGTTTGT A.A. MYCCONSENSUSATICURE III0 TGGCTGTGTGCATATGTA 	GTGTAGA 119 GTGTAGA 119 GTGTAGA 119 GTGTAGA 119 CURE,1,300 GTGTA-119 CURE,1,300 GTGAAATAG 13 	7966 57664 1364 00001 06001 55561 5561 55
VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64	1.00 CCTCCGTAACCGCGAGATTCCAAC 1.20 AAAGTTCGATATGACGAAAAAGTT G. A. G. A. G. A. CCTTCGTCTCAGTAAGTTAATTTT 1.40 ATAAATGAGAAAATAGTTGCATTGA TGACACATTCTAGTAGAAT A. T. T. TATG A. T. T. TATG A. T. T. TATG A. T. T. TATG A. T. T. TATG 1.100 TGTGTCTATCTGGAATCCTAGCTGT 1.400 1	STTITTCAACGAAGGC	1,100 AAAC GIGAAAC GIGAAAC GIGAAAC GIGAAAC GIGAAAC GIGAAAC GIGAAAC GIGAAAC A A A A A A A A A A A A A A A A A	ACTGAACCACCACCATAGA	CGATAGCGTTTGTAGCT AGAAATTAGAATGATGT AC AA.A.A. AGCTTCCTTCCAAATCC G AGCTTCCTTCCAAATCC G AGCTTCCTTCCAAATCGA G G G 	1.100 GACAGAAAAGT TAGAAGTT TGT A. A. MYCCONSENSUSAT ICURE 100 TGGCTGTGTGCCATATCTA. TGTA 1400 TGAAAGTAGAAAATAATTATAT G. G. G. 1500 TGAAAGTAGAAAAATAATTAAATCTAG. ACGTATCAGGGGGATTAGAAG 1700 TGCCCATCCATCCTCCCCCCTCT ACGTATCERD1 1500 TGATCCCATTAACGTTTCACCCC	GT AG 119 A 119 	7966 5764 1364 00001 0601 5561 5561 556
VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64	1,100 CCTCCGTAACCGCGAGATTCCAAC 1,200 AAAGTTCGATATGACGAGAAAAGTT G. A. G. A. G. A. CCTTCGTCTCAGTAGTAATTTT 1,400 ATAAATGAGAAATAGTTGCATTGA TGACACATTCTAGTAGAATAGTT A. T. T. AATG A. T. T. TATG A. T. T. AATG	STTTTTCAACGAAGGC	1,120 AAAC GIAAACC 1,120 ACC IGTATTTATTCCAE 1,200 AAAAGTAGAATCTA A.A.A.A.A.A.A.A.A.A.A.A.A.A.A.A.A.A.A	ACTGAACCACCACCATAGA	CGATAGCGTTTGTAGCT 1,160 AGAAATTAGAATGATGT AC. AA AA. AA. AA. AA. AA.	1,00 GACAGAAAAGT TAGAAGT T GTA A.A. MYCCONSENSUSAT ,CURE IP00 TGGCTGTGTGCATAGTA TGGAAGTAGAGAAATAATTAT G.G. G.G. ISCONSENSUSAT ,CURE IP00 TGAAGTAGAAAATAATTAT G.G. G.G. ISCONSENSUSAT ,CURE ISCONSENSUSAT ,CURE	GTGT AGA 119 	7966 5764 1364 00001 0601 5561 5561 5561
VANDANA PB1 IR64 N22 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64	1,100 CCTCCGTAACCGCGAGATTCCAAC 1,200 AAAGTTCGATATGACGAAAAAGTTCCAAC G. A. G. A. G. A. CCTTCGTCTCAGTAGTTAATTTT ATAAATGAGAAATAGTTGCATTGA TGACACATTCTAGTAGAATAGTTGCATTGA CTGTCTATCTGGAATCCTAGCTGT 1,200 TTTTCGCTTCAGGTTCAGTCCAGTG 1,200 1,400	STTTTTCAACGAAGGC	1,120 ACC GIGAAAC GIGAAAAAAAC GIGAAAAAAAAC GIGAAAAAAAC GIGAAAAAAAAAA	ACTGAACCACCACCATAGA	CGATAGCGTTTGTAGCT 1,160 AGAAATTAGAATGATGT .ACA. AGCTTCCTTCCAAATGC A. AGCTTCCTTCCAAATCC A. AGCTTCCTTCCAAATCC 	1,100 GACAGAAAAGTTAGAAGTTTGT A. A. MYCCONSENSUSAT (CURE 1000 TGGCTGTGTGCATATGTA 1000 TGGAAGTAGAAAATAATTATAT G. G. G. G. G. 1500 CACCAGCAACGGGGATTAGAAG 1360 CACCAGCAACGGGGATTAGAAG 1360 CACCATCCATCCTCCCCTCT ACGTATERDI 1300 TGATCCCATTAACGTTTCACCC	Grand Carl Carl Carl Carl Carl Carl Carl Carl	796 95764 1364 00001 06001 55561 5561 5561
VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64	1,100 ССТСССБТААСССССАВАТТССААС 1,200 АААGTTCGATATGACGAAAAAGTT G G G 	STTTTTCAACGAAGGC	1,120 AAAC GIGAAAC GIGAAAC GIGAAAC GIGAAAC GIGAAAC GIGAAAC GIGAAAC GIGAAAC GA AAAAG TAGAAAC TAGAAAC TAGAAAC TAGAAAC TAGAAAAAAC TAGAAAAAAC TAGAAAAAAC TAGAAAAAAC TAGAAAAAAC TAGAAAAAAAC TAGAAAAAAC TAGAAAAAAAC TAGAAAAAAAC TAGAAAAAAAC TAGAAAAAAAC TAGAAAAAAAC TAGAAAAAAAC TAGAAAAAAAAAA	ACTGAACCACCACCATAGA	CGATAGCGITTGTAGCT 1,160 AGAAATTAGAATGATGT .ACA.A. AGCTTCCTTCCAAATCC GA.A. AGCTTCCTTCCAAATCC GA.A. GA.A. GA.A. 1,200 AATTGTATCAAAATCGA GGACACCAAAATTGA GGGG. GGGACACCACACACACA GGGG. 1,600 GCCACGACGCGATGGGG GGATGCGGATGCGCG GGCACGCGGATCCCCC 	1.100 GACAGGAAAAGTTAGAAGTTTGT A. A. MYCCONSENSUSATICURE 100 TGGCTGTGTCCATATGTA 	GTGGAAATAG GTGT AGA 119 	7966 57764 13764 00001 06001 55561 5561 5561

d COPT4

e COPT5	е	COPT5
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	20	40	CURE	80	100	120	140ACGTATERD1	160
N22	GCCATTCCGCAGTCGTATCGCACGCGAATAAAGG	AGGCTGCATCGGTGTGGG	AGAAAGTACTCATGCATG	GCACCGAAAGGTATCGTGCI	TTCGTAAAAAGTAACAGCGA	AGTTTAGGGATGCGAAACCC	GAATAGCAACAACGTATTCATTCTACA	AGCA 160
VANDANA								160
PB1								160
IR64								160
					ACGTATERD1	ACGTATERD1		
					ABRELATERD1			
A122								1 200
VANDANA	A	GARGICIGETETACTOGE			CIGIGCICOCACGIGCICCI	SOCADIACOTOXACCOATCO		320
PB1	A							320
IR64	AA							320
	MYCGONSENSUSAT DREC	LTRECOREATCOR15	ACGTATERD \$80	400	420	ICURE	450	480
N22	GCGGCGGAGTGGAGGGCAACTGGTCCTGCGTCTC	CACCGACTGGTCCGATGA	CGTCCTCTATCGAGCGCT	GGAAGTCGAAGTCGCTGAT	GTCGAAGTGCAAGGTGGAAG	CCCACACGTACTCCGATGAT	GTCCCGGCATGGTCCAGTGGTGGACCC	GAC 480
VANDANA						C		480
PB1						C		480
IR64						C		480
			LTRECORE	ATCOR15				
	CURE		DRECRTCOR	EAT		0.005		
	ACGIATERD1 500	520 I	540 MYOC	UNSENSUSAT 500	580 I	600 CURE	620	640 I
VANDANA	TCGACGTACCGGCTGCCTGTGACGAAGTCCCCGGC	CATCCTACTAGAATTGCGC	CAGAGTGCGAGGCCGACGC	AGTTGCCTGAGACGCTGAC	CTTGCAACCTGGGAGAAGTG	GGCGGTCTGTGTCGTACCAA	ACTEGECGAAACCTATACATCEACAAC	LAGA 640
PB1						C		640
IR64						C		640
	660 I	680	700 CURE	720	740	760 1	780 I	800 1
N22	CCCTTGTAAGCTAACACATAAATTGCATGTAAAT	TGATTGTCGATATAATGT	TGTTTTTTAGTACCTGT	GGGGGGGCACAATAGGAGGG	ATACTCGTGGAAGGCGGGGT	GGTGAACGGTGCACGAAATC	CTGAAGCAATCGGATCAATCGGTTCAC	TAT 800
PB1								800
IR64						C.		800
			la la	ACGTATERD1			ACGTATERD1	
	600	840	890	MYCGONSENSUSAT	900	920	CBEHV MYCCONSENS	USATO
N22	ATGTGTGGGGCATGTAAAAATAAACCTTAAATAT	ACTTACCTCCGTGGGGGAG	GGGGGAGTTAGCCTAGGA	CGTGTGCAGCTGGACGAG	ACCAGTCGGTCGGGGTGGCC	вствтветвствсетствсе	TGAGCAACGTCGACAGGACGACAGGTG	3ACG 960
VANDANA								960
PB1								960
11104								
		ACGTATERD1						
	600 1	ACGTATERD1 1000 MYCCON	SENSUSAT 1,020	1,040 1	1,000 I	1,080 AC	2GTATERD1 1,100	1,120 I
N22	90 CTCGGAGAACCGAGCGCACCGAGTCCAGTATCCC	ACGTATERD1 1000 MYCCON II GCGTGCACGTCGTCAGGTC	SENSUSAT 1.020 CURE	1,040 I CAATCCCCTTGGTGTTACA/	1000 TAAATTCTAACAGATCTATC	1.000 AC	GTATERDI 1,100 I GTTTCCTGGGCCATGGTATAGTTAAAAA	1.120 I ATA 1120
N22 VANDANA PB1	500 CTCGGAGAACCGAGCGCACCGAGTCCAGTATCCC		SENSUSAT 1.000 CURE CTCATCTACAAGTAGTGC G	1,040 I CAATCCCCTTGGTGTTACAA A. A.	1000 I TAAATTCTAACAGATCTATC	1,080 CTAATCGGCCCGTAACGGAC	IGTATERD1 1,100 I IGTTTCCTGGGCCATGGTATAGTTAAAA G G	1.120 I FATA 1120 1120 1120
N22 VANDANA PB1 IR64	MO CTCGGAGAACCGAGCGCACCGAGTCCAGTATCCC	ACGTATERD1 100 MYCCON 3CGTGCACGTCGTCAGGTC	SENSUSAT 1,000 CURE ICTCATCTACAAGTACTGC .G	1,040 I CAATCCCCTTGGTGTTACAA 	1000 ITAAATTCTAACAGATCTATC	1.000 AC	IGTATERDI 1.100 IGTITICCTGGGCCATGGTATAGTTAAAA G. G. G. G. G.	1,120 I FATA 1120 1120 1120 1120
N22 VANDANA PB1 IR64	т Стобалалосалосалосалосалосалосалосалосалосал	ACGTATERD1 100 MYCCON SCGTGCACGTCGTCAGGTC	SENSUSAT 1,000 CURE SCTCATCTACAAGTACTGC GG	1.040 AATCCCCTTGGTGTTACA/ A A A	1980 ITAAATTCTAACAGATCTATC	1.000 JAC CTAATCGGCCCGTAACGGAG	SGTATERD1 1,100 SGT_TTCCTGGGCCATGGTATAGTTAAAA G	1.120 ГАТА 1120
N22 VANDANA PB1 IR64	NO CTCGGAGAACCGAGCGCACCGAGTCCAGTATCCC	ACGTATERD1 poo MYCCON SCGTGCACGTCGTCAGGTC	SENSUSAT 1,200 CURE CCCATCTACAAGTAGTGC G. G. 	1,000 FAATCCCCTTGGTGTTACAA AA.	1000 TAAATTCTAACAGATCTATC	TAATCGGCCCGTAACGGAG	GTATERDI 1:10 GETTCCTGGGCCATGGTATAGTTAAAA G	1.120 I FATA 1120
N22 VANDANA PB1 IR64 N22	MARCONSTRUCTION CONSTRUCTION CONSTRUCTURA CO		SENSUSAT 100 CURE SCTCATCTACAA GTACTGC G. G. G. 	1,000 IAATCCCCTTGGTGTTACA/ A. A. A. A. A. A. A.	1000 TAAATTCTAACAGATCTATC CURE 1220 ATGTAATGGTABTCAACAAC	1,000 PAC	STATERDI 1100 GETT TCC TGGGCCA TGGT AT AG T AAAAA G. G. G. CGTATERDI See ACCTATERDI LCAGA TC TKGGT AT AC T AA T C T AAA	1.120 I FATA 1120
N22 VANDANA PB1 IR64 N22 VANDANA	CTCGGAGAACCGAGCGCACCGAGTCCAGTATCCC MYBCGRE TGTTTGTTGGACATATETGTTMACCGAAATAACTA		SENSUSAT 1,200 CURE SCTCATCTAGAAGTAGTGG G. G. G. ,100 1,100 1,100 1,100 1,100 1,100 1,100 1,100 1,100 1,100 1,100 1,100 1,100 1,100 1,100 1,000	1,540 AATCCCCTTGGTGTTACA/ A. A. A. A. A. A. A. A. A. A.	1960 ITAAATTCTAACAGATCTATC CURE 2001 ATGTAATGETABTCAACAAC	TAATCGGCCCGTAACGGAG	GTATERDI LUN LETTICCIGGCCCATGGTATAGTTAAAA G G COTATERDI UN PACOTATERDI CAGATCTREDE AGTTAGGTATATCTAA	1,120 TATA 1120
N22 VANDANA PB1 IR64 N22 VANDANA PB1		ACGTATERDI Tom MYCCON SIGGTGCARGETCOT CAGGTE SIGGTCATTCTTCATGTAA	SENSURAT 1,000 CURE actcatctacagtagtagt 	Lan Lan Lan Lan Lan Lan Lan Lan	1000 ITAAATTCTAACAGATCTATC CURE_200 ATGTAATGTAATCAACAAC	1.000 AG CTAATCGGCCCGTAACGGR TAATCGGCCCGTAACGGR ATTTAAAACTACAAAGACTA	COTATERDI UN BETTICCTGGGCATGGTATAGTTAAAN G. G. G. G. G. G. G. G. G. G. G. G. G.	1.120 TATA 1120 1120 1120 1120 1.280 1280 1280 1280
N22 VANDANA PB1 IR84 N22 VANDANA PB1 IR84	иларие стовалассалассалассалатасса млярове тотттоттовалататототтиласалаталасти	INCOTATERDI Too INTCON SCOTOCARGETCOTOAGGTE SCOTOCARGETCOTOAGGTE SCOTOCARGETCOTOAGGTE NO	SENSUSAT 1,000 CURE GCTCATCTACAAETACTGC G. G. G. 1.300 1.300 ATAAATGCCCAAAATGTAA	1.90 CAATCCCCTTGGTGTTACAA A A A A L200 ATATCTTGTTATGTATGCT	1966 ITAAATTCTAACAGATCTATC CURE 1275 IATGTAATGGTAATCAACAAC	тар да Сталтседессаталсеой талтседессаталсеой талта 130 аттталалстасаладаста	СТАТЕВОТ 1,100 КОПТИССТОВОВСАТОСТАТАСТТАЛАЛА С С С С С С С С С С С С С С С С С	1.120 I TATA 1120 1120 1120 1120 1.280 1280 1280 1280
N22 VANDANA PB1 IR64 VANDANA PB1 IR64	mp ctcggagaaccgagcggagcggggtcagtatccg mmggre tgtttgttggagatatattg	LAGGATERDI Too MYCCON SCGTCCACGGTCGTCACAGGTE L.100 GATCATTCTTCATGTAA	SENSUSAT 1.000 CURE GCTCATCTACAAETAETGC .G	130 2AATCCCCTTGGTGTTACAA A A A 1200 1ATCTTGTTATGTATGCTA		TIME PAGE CTAATCOGGCCGTAACGORE Use ATTTAAAACTACAAAGACTA	SGTATERDI 1,00 BERTTOCT GOGOCA TGGTATAGTAAAA 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0.	1,120 TATA 1120
N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64		LSS LSS LSS LSS LSS LSS LSS LSS	SENSURAT 1,200 CURE GCTCATCTACAA ETAGTOG .G. .G. .TABATGCCCAAAATGTAA 1,360 1,260 11CAAACAAAGTTTAAAA	L00 2AATCCCCTTGGTGTTACAA A A A A TATCTTGTTATGTATGCT/ L300 L300 L300 L300 L300 L300 L300 L30		торо рАС СТААТССВСССССТААССОВЕ 1366 АТТТААЛАСТАСАААЗАСТА 1,000 1000 АТСААТАТТАССТААААТСА	СТАТЕВОТ ЦВ ВЕТТ ССТОВОССАТО СТАТАЛТАЛАТ С. С. С. С. С. С. С. С. С. С.	1.120 TATA 1120
N22 VANDANA PB1 IR84 VANDANA PB1 IR84 N22 VANDANA			SENSUSAT 1.000 CURE 1 CTATCTACAAETAETGC 0 0 0 0 1.00 1.00 1.30 1.30 1.30 1.30	146 3AATCCCCTTGGTGTTACAA A A A A A A A A A A A A A A A A A		торо рабо стаатсодоссобтаасооро заев атттааластасаалабаста горо атбаататтасстоалаатса	цар ВЕТТССТОСОССАТОСТАТАСТАЛА ВЕТТССТОСОССАТОСТАТАСТАЛА С. С. С. С. С. С. С. С. С. С.	1.10 TATA 1120
N22 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 PB1	TCCGGAGAACCGAGGGGAGGGAGCGAGTCCAGTATCCG protocord totttottggacatatettgaccgaatacta coccagttctaccgtagtageactaaaaccctag	LGG LGG LGG LGG LGG LGG LGG LGG LGG LGG	SENSUSAT 1000 CURE ECTCATC AGARETAG TGC G G 	Lan Lan Lan Lan Lan Lan Lan Lan Lan Lan		торо рас сталтосососсоталсооре 1.200 аттталалстаслаладаста 1.000 атолататтасстолалатса	одатево! ца вет тосторосса годата от талала о состатево! ца ростатево! состатево!	1.30 TATA 1120
N22 VANDANA P81 IR64 VANDANA P81 IR64 VANDANA P81 IR64	илароре тотототоралассанассоната. милароре тотототоралата. ссилен асослатототаласана. ссилен асослатототаласана.	Incontreme in Arccon Luco Costocatore in Arccon Luco Costocatore in Arcon Costocatore in Arcon Luco Costocatore in Arcon Luco Costocatore Costocat	СИВЕНИЛАТ (100) СССАТСТАСААВТАЕТОС О. О. О. О. О. О. О. О. О. О.	1400 24ATCCCCTTGGGGTTACAA A A A A A A A A A A A A A A A A A		тара рабо сталтовоссосталовой тара аттталалостасалалдаста тора атбалтаттассталалатся	адателен 1990 ВЕТТССТОСОССАТОСТАТАОТТААЛ О	1,120 TATA 1120
N22 VANDANA PB1 IR84 VANDANA PB1 IR84 VANDANA PB1 IR84		LOG LAND LAND LAND LAND LAND LAND LAND LAND	SENSURAT 100 CURE GTCATCH CAADGTAGT OC 0 0 0 100 100 100 100 100 100	Lan Lan Lan Lan Lan Lan Lan Lan Lan Lan		тор рас сталтовоссоталовория цае аттталалотасталадаета атодататтасстолалатса	одателен (ув вет тостовоссладата от тала о. 	1,120 TATA 1120
N22 VANDANA PB1 IR84 VANDANA PB1 IR84 N22 VANDANA PB1 IR84			SENSURAT 1200 CURE ICTCATCTACATACTACTOR 0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.	1460 24ATCCCCTTGGGTTACAA A A A A A A A A A A A A A A A A A	LTANATTCTANCAGATCTATC	тара рабо сталтсовоссоталсовая аттталаластасаладаста аттолататтасствалалатся стора атолататтасствалалатся стора с сто стора стора стора стора стора с стор с с с с с с с с с с с с	СТАТЕВОТ ЦВ ВЕТТ ТСС ТО СОССАТО СТАТАТАТАЛАЛ С С С С С С С С С С С С С	1.120 TATA 1120
N22 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA	MYSGRE TEGERGARACEGAGEGEACEGAGTCCAGTATECC MYSGRE TETTTETTEGACATATETETAACEAAATAACTA CURRE: ACGCAGTTCTACAGTABTAGAACCTAG TTETCTTETCECECCCCTGTCTTTTTTTTCTC	LOGOTATERS THE CONTRACTOR LOGOTAGACOTACACTACT LOGOTAGACOT	SENSURAT 100 CURE GTCATCA CAADEMETICO 0. 0. 0. 100 100 100 100 100 1	Lan Toccott og Titan A. A. A. A. A. A. A. A. A. A. A. A. A. A		тор рас сталтовоссосталово акталаловоста акталаловоста аталалататастаралалова акталалататастаралалов ославовоссосласовоос	адалевот ца вертностоорсалорана та та Алала о о о о о сарана с жеветносторована та соба сарана с жеветносторована та соба стана собана с жеветносторована та собана собана с жеветносторована та собана собана с карана собана собана собана собана с карана собана собана собана собана собана собана собана с собана собана собана собана собана собана собана с собана собана собана собана собана собана собана с собана собана собана собана собана собана собана собана собана собана собана собана собана собана собана собана собана собана со	1.300 TATA 1120
N22 VANDANA PB1 IR84 VANDANA PB1 IR84 VANDANA PB1 IR84 N22 VANDANA PB1		ILCOTATERDI ILCOTO COTOCARGOLICO I EXPOSIT ILCO ILCOTO ILC	SENSURAT 1000 CURE ICTCATCTACAGATAGTOC G. G. G. G. G. G. G. G. G. G.	LAN CATCCCCTTGGTGTTACAA A A A A A A A A A A A A A A A A A		тора рас Стаатсовоссобтаасообео цае атттаалаастасааладаста тора атораататтаастараалатса с	СТАТЕВОТ 1,100 ВЕТТОСТОВОССАТОСТАТАСТАА. 	1.120 TATA 1120
N22 VANDANA PB1 IR84 VANDANA PB1 IR84 VANDANA PB1 IR84 VANDANA PB1 IR84	тоттоттостосссоотоститититотос	LOGOTATERS THE DECONSTRUCTION LOGOTACATEGET CO LEAGUETE LOGO LOGOTACATECET TEATURA LOGOTAC LOGO LOGOTAC LO	SENSURAT 1000 CURE GICACTCA CAADEMETIG 0. 0. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1	Lint Cocct Tog Tot Tog An A A A A A A A A A A A A A A A A A A		тор рас сталтососссоталособе аттталалостаслановаета аттталалостаслановаета атолататтасстолалатса соб ослововоссодоглавовосс	адалевот 1,00 Верттост обоссла болтата от талала 0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.	1.120 TATA 1120
N22 VANDANA P81 IR64 VANDANA P81 IR64 VANDANA P81 IR64		NCOTATERDI NCOCARGUECO I EXPOSIT INFO INFO INFO INFO INFO INFO INFO INFO	SENSURAT 100 CURE GTCATCTACAGATAGTOC G	Lan Lan Lan Lan Lan Lan Lan Lan Lan Lan		торо рас сталтосососсоталосооне гзе атоталалоста атолататтасстолалоста всладаевсе состолалотся scale Litecoreatoconts	СКАТЕВСІ (198 ВЕТТОСТОВОССАТОСТАТАТАТАЛАЛ С	1.520 TATA 1120
N22 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64	стовалалассалассалассаласталаста тотттоттоалалтатететияловалатласта сосолоттотасалтатететияловалатласта почто сосососто состатититити стол сосососто сосососто состатититити стол сососососососососососо состатититити стол сосососососососососо сососососо сосососо сососо сососо типиста праваласта почто сосососо сососо		SENSURAT 100 CURE GICACTCA CAADEMETIG 0. 0. 0. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1	чен СААТССССТТОСТОТТАСАЛ А. А. А. А. А. А. А. А. А. А.		тор рас сталтососссоталособе атталалостасаладаста тор талаластасаладаста тор талаластасаладаста с	адалевот ца вет то стоороса та от та ала а от то стоороса та от та ала а от то стоороса та от та ала а от то стоите во стоитево са от стоитевот а от та вебела та стоита са от стоитевот а стоите во стоитево са от стоитевот а стоите во стоитево са от стоитевот а стоитево стоитево са от стоите во стоитево стоитево са от стоитево стоитево стоитево са от стоите во стоитево стоитево са от стоитево стоитево стоитево са от стоите во стоитево стоитево са от стоитево сто	1.120 TATA 1120
N22 VANDANA PB1 IR84 VADDANA PB1 IR84 VANDANA PB1 IR86 VANDANA PB1 IR86 N222 VANDANA		HOUNTERD HOCON COTCARDED OF EASTER SATO SATO SATO SATO SATO SATO SATO SATO	ВЕНВИЛАТ 100 (URE BTCATCH CAADATABETGO 0	чер катосссттобаттасал А. А. А. А. А. А. А. А. А. А.		тово рабо сталтовороссоталоворае аттталалостаславана аттталалостаславана атодалтаттасствалалтса всаядаевосбаславевое Lirrecoreatochis Lirrecoreatochis 1990 атттиттероватосни	адалевот ца вет тос тоодосла до та та та ла ла о о о о о о о о о о о о о о о о о о о	L100 L100 L120 L120 L120 L120 L280 L280 L280 L280 L280 L280 L280 L280 L120 L140 L140 L140 L160 L170 L170 L177
N22 VANDANA PB19 IR84 VANDANA PB19 IR84 VANDANA PB19 IR84 VANDANA PB19 IR84 VANDANA PB19 IR84	тотттоттоского соссосование и интернетории и интер		SENSURAT 100 CURE GICACTCA CAADEMET GO 0. 0. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1	че САТССССТТОСТОТАСАЛ А. А. А. А. А. А. А. А. А. А.		тор рас сталтососссоталособе аттталалостасаладаста атолататтасстасаладаста атолататтасстасаладаста с	адалевот 1,100 ВЕСТТССТОСОССАТОСТАТАСТАААА О	1.500 1.500 1.200 1.440 1.500 1.
N22 VANDANA PB19 IR84 VANDANA PB19 IR84 VANDANA PB19 IR84 VANDANA PB19 IR84 VANDANA PB19 IR84 IR84 IR84 IR84 IR84	ре стовалалоссаладосалоссалататосо миссине тотттоттовалотателения лосослаттстволоссалаталота сообрание	LOGOTATERS THE CONTRACT LOGOTAGASSICS TEASSITE LOGOTAGASSICS TEASSITE LOGOTAGASSICS ACTION LOGOTAGASSICS ACTION LOGOTAGASICS ACTION LOGOTAGASICS ACTION LOGOTAGASSICS ACTION LOGOTAGASSICS ACTION LOGOTAGASSICS ACTION LOGOTAGASSICS ACTION LOGOTAGASICS ACTION LOGOTAGASICS ACTION LOGOTAGASICS ACTION LOGOTAGASICS ACTION LOGOTAGASSICS ACTION LOGOTAGASICS ACTION LO	SENSURAT 1000 CURE GICCATCA CAADEMETICO 0. 0. 0. 1001 100 1001 1	тер КАТССССТТОСТОТТАСАЛ А. А. А. А. А. А. А. А. А. А.	талаттсталсадатстатс соне датотал обетается салосалс алтотал обетается салосалс алтадосала талторато исталодадовоствое соста обе совосавое от статт ттота обе	тово рабо сталтовосссоталовойна изе аттталалосталаловоста атодалтаттасствалалтса вслабавоссогалавовост Lifecoreatochis Lifecoreatochis изе атттитиссоналаста	адалевот цар вертностоорссладаталаталалал о о о о о о о о о о о о о о о	L30 L30 L40 L40 L40 L40 L40 L40 L40 L4
N22 VANDANA PB1 IIR84 VANDANA PB1 IIR84 N22 VANDANA PB1 IIR84 N22 VANDANA PB1 IIR84	стоваядлассаяссалосаяттаса татттатадаата <mark>ртати</mark> асалаталасти сище лоослатистасаята <mark>ртати</mark> асалалаласти лоослатистасая та ртати асалалаласти тотститасата аласта 		SENSURAT top: CURE GC CATCA CAADEMET GC G. G. G. G. G. G. G. G. G. G. G. G. G.	- Seo CATCCCCTTGCTTGCTTACA A A A A A A A A A A A A A A A A A		тар Ас таласарсскаталосожи таласарскаталосо	адателен 1,100 ВЕТТССТОСОССАТОСТАТАОТАААА ОСОСТАТЕЛО САСОАТСТАТОТ СОСТАТЕЛО СОСТАТОТА СОСТАТ	1,550 TATA 1120 1120 1120 120 120 120
N22 VANDANA PB1 IIR84 VANDANA PB1 IIR84 VANDANA N22 VANDANA IIR84 N22 VANDANA PB1 IIR84 VANDANA PB1 IIR84	ре стовалалоссалассалассаласта тотттоттовалоста технолого силяс- лосслоттоттовалоста технолого тоттоттовалоста технолого тоттоттовалоссото соттоттитититотол с. с.	LAND LAND LAND LAND LAND LAND LAND LAND	SENSURAT 100 CURE GICACTCA CAADEMET GO 0. 0. 0. 100 100 100 100 100 1	чен КАТССССТТОСТСТТАСАЛ А. А. А. А. А. А. А. А. А. А.	۲۹۹۵ TAAATTCTAACAGATCTATC CUME Lan ATGTAATOERARTCAACAAC AATAGTCACATATATGATCT Lan Lan Lan Lan Lan Lan Lan Lan	тор рас сталтососссоталособе изм аттталалостаслалодаста атолататтасстолалодаста сосососалособесос Lirecoreanocons сосососенныцият мтссокенныцият П	адалевот ца вертностооросалорана такала о о о о о о о о о о о о о о о	1,500 TA TA 1120 1120 1120 1120 120 1200 1280 1280 1280 1280 1280 1280 1280 1400
N22 VANDANA PB15 IR64 VANDANA PB15 IR64 VANDANA PB15 IR64 VANDANA PB15 IR64 VANDANA N22 VANDANA	стовалалоссалассолассолосологолатассо имасряе таттатасала татететели солаталассала соласолатасто солаталассала татететететелесососососолосолаталассала татететететететелесосососолосолатассала татетететететететелесосососолосолатас татететететететететелесосососолосолата татететететететететелесосососолосолата татететететететететелесосососолососолососолосо татетететететететететететететететете со с с	MCGTATERDI LICOTO ARGETE COLERGETE LICOTO ARGETE COLERGETE LICOTO LICOTO ARGETE COLERGETE LICOTO LICOTO LICOTO ARGETE COLERGETE LICOTO LICOTO ARGETE COLERGETE LICOTO LICOTO ARGETE COLERGETE LICOTO LICOTO ARGETE COLERGETE LICOTO ARGETE COLERGETE ARGETE LICOTO ARGETE COLERGETE LICOTO ARGETE COLERGETE LICOTO ARGETE COLERGETE LICOTO ARGETE COLERGETE LICOTO ARGETE COLERGETE LICOTO ARGETE COLERGETE LICOTO ARGETE ARGETE ARGETE ARGETE LICOTO ARGETE ARGETE ARGETE ARGETE ARGETE LICOTO ARGETE ARGETE ARGETE ARGETE ARGETE LICOTO ARGETE ARGETE ARGETE ARGETE ARGETE ARGETE LICOTO ARGETE ARGETE ARGETE ARGETE ARGETE ARGETE ARGETE ARGETE LICOTO ARGETE AR	ВЕНВИЛАТ 100 (URE ICTCATCTACAADTAGTOC CO. 0. 1.00	Lan Lan Lan Lan Lan Lan Lan Lan Lan Lan		тата совете совете со совете совете со совете	адалевон 1,00 ВЕТТССТОСОССАТОСТАТАОТАААА ОССОЛОВИТОСТОСТОСТАТВОН ОССОЛОВИТОСТОВО ОССОЛОВИТОСТОВО САСАТСТКОВТАСТТВОИТАТАТСТАА ОССОЛОВИТОСТОВОСТТВОИТАТАТСТАА ОССОЛОВИТОСТОВОСТТВОИТАТАТСТАА ОССОЛОВИТОСТОВОСТТВОИТАТАТСТАА ОССОЛОВИТОСТОВОСТТВОИТАТАТСТАА ОССОЛОВИТОСТОВОСТТВОИТАТАТСТАА ОССОЛОВИТОСТОВОСТТВОИТАТАТСТАА ОССОЛОВИТОСТОВОСТТВОИТАТАТСТАА ОССОЛОВИТОСТОВОСТОВОССТТВОИТАТАТСТАА ОССОЛОВИТОСТОВОСТОВОССТТВОИТАТАТСТАА ОССОЛОВИТОСТОВОСТОВОССТТВОИТАТАТСТАА ОССОЛОВИТОСТОВОСТОВОССТТВОИТАТАСТОВА ОССОЛОВИТОСТОВОСТОВОССТТВОИТАТАСТОВА ОССОЛОВИТОСТОВОСТОВОСССОВОСТТВОИТАТАТОТТАА ОССОЛОВИТОСТОВОСТОВОСТОВОСССОВОСТАТИОНОВОССОВОСТАТИОНОВОСТОВОСТОВОСТОВОСТОВОСТОВОСТОВОСТОВО	L30 FATA 1120
N22 VANDAMA PB3 IR54 N22 VANDAMA PB3 IR56 VANDAMA VANDAMA PB3 IR56 VANDAMA PB3 IR56 VANDAMA PB3 IR56 VANDAMA PB3 IR56 VANDAMA PB3 IR56 VANDAMA PB3 IR56 VANDAMA VANDAMA VANDAMA PB3 IR56 VANDAMA PB3 IR56 VANDAMA PB3 IR56 VANDAMA PB3 IR56 VANDAMA PB3 IR56 VANDAMA PB3 IR56 VANDAMA PB3 IR56 VANDAMA PB3 IR56 VANDAMA PB3 IR56 VANDAMA PB3 IR56 VANDAMA PB3 IR56 VANDAMA PB3 IR56 VANDAMA PB3 IR56 VANDAMA PB3 IR56 VANDAMA PB3 IR56 VANDAMA PB3 IR56 VANDAMA PB3 IR56 VANDAMA PB3 IR56 VANDA VAN	тоттоттостосссоотоссилоссилоссилости сторалалассалассалассаласти тоттоттостостосссилоссилоссилоссилос соссаласти стораласти соссаласти стораласти тототтостостосссоотоссититититотоси тотостостосссоотоссититититотоси тотостостосссоотоссилоссилоссилос тотостостососсоотоссилоссилоссилос тотостостососсоотоссилоссилосоно соссаласти со	Land Land Land Land Land Land Land Land	SENSURAT 100 CURE GICACTOLAADEMETGO 0	чен КАТССССТТОСТСТТАСАЛ А. А. А. А. А. А. А. А. А. А.		торон рас таката состата соорен атта ала состата соорен атта ала состата соорен атта ала состата соорен состата соорен соорен соорен тороне соорен соорен соорен тороне соорен соорен соорен тороне соорен соорен соорен тороне соорен соорен соорен соорен тороне соорен сооре	ЗДАТЕВОІ 1,100 ВЕВТІ ССІ ГОСОССА ГОСІАТА ОТ ТАЛАЛА О. 	1.00 TATA 1120 TATA 1120 11
N22 VANDAMA PB3 IR54 N22 VANDAMA PB3 IR54 VANDAMA N22 VANDAMA PB3 IR54 VANDAMA PB3 IR54 VANDAMA PB3 IR54 IR54 IR54 IR54 IR54 IR54 IR54 IR54		HEGGTATERDI LINCOLO LINCOLO LEAGUTE LINCOLO LI	СКВ 2004 СССС ССС ССС ССС ССС ССС ССС ССС ССС С			тово рабо сталтовоссосталоводаета аттталалосталоваета атталалосталоваета атодалататтасстоалалтса всалаловатастасстоалалтса цинесовелсония сосославения тосославсе сосоставения сосославсе сосоставения не	GTATERDI (198 ВЕТТОСТОСОССАТОСТАТАСТАЛААТ О	1327 TATA 1220 TATA 1220 1280 1280 1280 1280 1280 1280 1280
N22 VANDAMA PB1 IR54 N22 VANDAMA PB1 IR54 VANDAMA PB1 IR54 VANDAMA PB1 IR54 VANDAMA PB1 IR54 VANDAMA PB1 IR54	тоттотторадата состаета со состаета со	LODATERS THE DECOMPOSITION LODATE CALCENCE OF LARGENE LODATE CALCENCE OF LARGENE L	SENSURAT 100 CURE GICACTOLAADEMETGO G. G. G. G. G. G. G. G. G. G.	чен КАТССССТТОТТАТТАСА А. А. А. А. А. А. А. А. А. А		торо рас сталтососссоталособе атталалостасаладаста атталалостасаладаста сово атодататтасстасаладаста сово	адалевот 1,100 ВЕВТТССТОСОССАТОСТАТАСТАЛАА С	1437 17474 1743 1750 1750 1750 1750 1750 1750 1750 1750
N22 VARDAMA PB3 IR84 VARDAMA PB3 IR84 N22 VARDAMA PB3 IR84 VARDAMA PB3 IR84 VARDAMA PB3 IR84 VARDAMA PB3 IR84 VARDAMA PB3 IR84 VARDAMA			СКВИЛАТ (др.) СИКЕ БГСАТСЯ СААВТАКТ ОС 0. 0. 0. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1	Lan Control transmission A A A A A A A A A A A A A A A A A A A		тово рас сталтовосссоталовойна аттталалосталоводста аттталалосталоводста атодалататтасствалалоса сове соверсовалоснія соверсовалосновання соверсовалоснія соверсовалосни соверсовалосно	адалевот ца вестностводосладаталаталала о о о о о о о о о о о о о о о о о о о	1027 TATA 1220 1230 1
N22 VANDAMA PB1 IR84 VADDAMA PB1 IR84 VANDAMA PB1 IR84 VANDAMA PB1 IR84 VANDAMA PB1 IR84 VANDAMA PB1 IR84 VANDAMA	СтСОВАКААСССААСССААСССААСТААТАССА тотттоттоалсатателетия соссаатателетия соссаатателетия соссаатателетия соссаатателетия тоттотстостосссоотототтититителе соссаатателетия тите тите тите соссаатателетия соссаателетия	LODIATES The Andrew And	SENSURAT 100 CURE GICACTCA CAADEMETICO 0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.	че катоссоттостатаса АА. АА. ча ча татостоттататаста катасасастаоттаата катасасастаоттаата соо сттттскаестосоесеессее соо соо соо соо соо со		торо рас сталтососссоталособе атталаластасаладаста атолататтасстасаладаста атолататтасстоладаста с	ЗДАТЕЛЕНІ 1,190 ВЕПТТІСТІ GOGCCA TGGTATA TAAAAA 	1439 1474 1430 1530 1530 1530 1530 1530 1530 1530 15

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	20	40	MYCCONSENSUSAT 6	0	80	100 120	3
N22	GGGAGAGCCTCTCACGGTTAGAATATTT	CTTTCACCTTGTTCA	CCCATTTGCCTGCTTAT	CCATGACTAGAGAAATTT	CCACATTGTATGAAAGATAG	CCTCTAATGAAGGCTGCCCTCT	120
VANDANA							120
PB1							120
IR64							120
	140	160	18	MYCCONSENSUSAT	200	220 MYCCONSENSUSAT 240	J
N22	CCTTATTGTAGGTCTTTGAGCTACACGA	TGATGGACACATTGA	CCTCACTGTCATCGGTC	CACACCTGGAGGCTGGCC	AGCGTCCCCAGTATACCGTG	CCACCAAATGTGTGGTTCGGTT	240
VANDANA							240
PB1							240
IR64							240
	260	MYCCONSENSUSAT 280	30	10	320	340MYCCONSENSUSAT 360	
N22	CTTTCCCTACCCTGGATGTTGAATCATT	CGCATCTGATGGCAG	CGTTCTTGTCAAGTCTC	GAAAGAGGGATCCTGAGC	TTCATTACTCCCTAGTTGGC	TGCACTTGTGCCCCTGGCTTCC	360
VANDANA							360
PB1							360
IR64							360
	380	400	42	D ICURE	440	460 480	
N22	ACTATCACCATTICCAAATCCCCAATT	TCATCATCTCAAATC	CATTOCTCCTAACCCAC	AACCOLLCOLCAACTAC	TATICCTICCACCAACTAA	TCATCTTTTCACCTCAACATAC	490
VANDANA	AGTATGAGGATTTCGAAATGGCCAATTT	IGATGATGTGAAATC	CATTOCTCCTAAGGCAG	AACCOTTECTEAAGTAC		TEATETTTEAGETEAACATAC	400
DR1							480
IR64							480
							100
	500	500			CURE	F00 000	
	500 I	520	54 	0	560 CORE	580 600	4
N22	TGTATTTTAGCAGCCTGTCTGGCAAGAT	TGCCTGACGGTATTG	GACGCCATTTTTAGTGT	GATTGCTTCGGGTTTGTG	TTCTTGTCTTGTACACTTAA	3AACACGCATGTCCTTGGTGAT	600
VANDANA							600
PB1							600
IR64							600
	CURE						
	620 I	640	66 I	0	680 I	700 720 I I	1
N22	AGTTGTAACACTCTCCTGTACGAAAAACA	GAATAAAACACTGGC	AATGTTGAGATGAAATT	TGCTTGTGCTAAGCCTTC	AAAAGTTGGAACTGGATAGT	GATGAAATATATATACTGTGAA	720
VANDANA							720
PB1							720
IR64							720
	MYCCONSENSUSAT 740	760	78	CBFHV	800	820 840)
N22	TTACCAAATGAATCATTGTCAATGAACA	ACCAAATTGAAGTCC	TCTGAAGTTAAGCTGAA	TTGCAATCTTTATCGACT	TCTATACGCAGTTTTAACTA	стссстсстасссалалаладай	840
VANDANA							840
PB1							840
IR64							840
	680	anaCUR	F	10	020	040 080	
	1	1		~	1	1	
N22	TCGATTCTCAGAAAAGTTTATTGTTTTT	AAGACGGAGGGTGTA	CIGAACAATTACAGGGA	CGAATTGACATTATTTTT	TITCTCCTTCCTTGCAGGAT	3GACTGAAAGATCTTGTGCCAA	. 960
VANDANA							960
PB1							960
IR64							960
	080	1.000		MYB1AT	1.040	ACGTATERDI	
1000	980	1,000 	1,0 	20	1,040 I	1,060	·
N22	AGACAAAAGCATCCTCATCAGATTTCTC	TGAAACAAGCAGTGG	AGTGGAGCAGCGGATGA	TTGCAAACCAATGCTTTG	CTCTCGTCGGGTTTTTGCCTG	CTCTAAGCGTTAGAGAGTGTAC	
							1080
VANDANA							1080
VANDANA PB1							1080 1080 1080
VANDANA PB1 IR64		· · · · · · · · · · · · · · · · · · ·					1080 1080 1080 1080
VANDANA PB1 IR64							1080 1080 1080 1080
VANDANA PB1 IR64	JACGTATERD1		E ICURE	NIDE	ACGTATERD1	Clips	1080 1080 1080 1080
VANDANA PB1 IR64	ACGTATERD1 CURE 1.00	CURE 1.120	E ICURE CGTATERD1 IG	QURE	1,160 ACGTATERD1	1,180 CURE 1.200	1080 1080 1080 1080
VANDANA PB1 IR64 N22	ACGTATERD1 CURE 1,00 G∎CTCTCCCTCTGTGTGTGCGCTTTTGGT	CURE 1,120 P	e _I CURE CGTATERDI II CGTTTAGTAGTAGCTAG	QURE TACTATCTGCTTGGACAC	1,100 ACGTATERD1 TGCACGT TGTTATTAGTTAT	1,160 CURE 1,200 2TGCACTGTACTTCTACTTCCT	1080 1080 1080 1080 1080
VANDANA PB1 IR64 N22 VANDANA	ACGTATERD1 CURE 1.00 GTCTCTCCCTCTGTGTGTGCGTTTTGGT	CURE LURE CURE LUP A GCAGTACAAATTGTA	E ICURE CGTATERD1 IL CGTTTAGTAGTAGCTAG	aure Stactatctgcttggacac	1,100 ACGTATERD1 1 1 1 1 1 5 CACGTTGTTATTAGTTAT	1.160 CURE 1.200 1 2TGCACTGTACTTCTACTTCCT	1080 1080 1080 1080 1080 1080 1200 1200
VANDANA PB1 IR64 N22 VANDANA PB1	ACGTATERD1 CURE 1,000 GT_CTCTCCCTCTGTGTGTGCGTTTTGGT	CURE 1.15 A	E ;CURE CGTATERD1 II CGTTTAGTAGTAGCTAG	JURE STAGTATCTGCTTGGACAC	1,100 ACGTATERD1 TGCAGGTTGTTATTAGTTAT	1,160 CURE 1.200 CTGCACTGTACTTCTACTTCCT	1080 1080 1080 1080 1080 1080 1200 1200
VANDANA PB1 IR64 N22 VANDANA PB1 IR64	JACGTATERD1 CURE 1,00 G∎CTCTCCCTCTGTGTGTGCGCTTTTGGT	CURE 1,20 Å GCAGTAGAAATTGTA	E ¡CURE CGTATERD1 11 CGTTTAGTAGTAGCTAG	LURE STAGTATCTGCTTGGACAC	1,100 ACGTATERD1 TGCAGGTTGTTATTAGTTAT	1.180 CURE 1.200 CTGCACTGTACTTCTACTTCCT	1080 1080 1080 1080 1080 1080 1200 1200
VANDANA PB1 IR64 N22 VANDANA PB1 IR64	ACGTATERD1 CURE 1.00 STCTCTCCCTCTGTGTGTGCGTTTTGGT	CURE LIAD A	E (CURE CGTATERDI () GGTTTAGTACTAGCTAG CURE	2JURE STAGTATCTGCTTGGACAC	1,100 ACGTATERD1 TCCACGTTGTTATTAGTTAT	1.180 CURE 1.200 TGGACTGTACTTCTACTTCCT	1080 1080 1080 1080 1080 1080 1200 1200
VANDANA PB1 IR64 N22 VANDANA PB1 IR64		CURE 1,120 P GCAGTACAAATTGTA 1240	E CURE CGTATERD1 II GGTTTAGTAGTAGCTAG CURE	JURE STACTATCTGCTTGGACAC 90 CURE	1, 160 ACGTATERD1 TGCACGTTGTTATTAGTTAT 1,200 ACGTATERD1	1.100 CURE 1.200 CTGCACT <mark>GTAC</mark> TTCTACTTCCT 1300 1.300	1080 1080 1080 1080 1080 1200 1200 1200
VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22	ACGTATERD1 CURE 1:00 GTCTCTCCCTCTGTGTGTGCGCTTTTGGT CURE CURE 1220 AACCCTGTTGATTAGCGTCAGGATCAGGC	CURE CURE CURE 1:40 / GCAGTAGAAATTGTA 1240 CATGCACGCTGGGGGG	E (CURE CGTATERDI IL CGTITAGTAGTAGCTAGCTAG CURE TCGCTCTTAGCTAAC	UPE TAGTATCTGCTTGGACAC 00 CURE ABCGTACCTTGACTTTCT	1,100 ACGTATERD1 TCCACGTTGTTATTAGTTAT1 1,200 ACGTATERD1 TCACGTTGTCACGAAGGAGA	1.180 CURE 1.200 CTGCACTGTACTTCTACTTCCT 1.200 1.200 TCCATCGAGTGGTATCAACCTA	1080 1080 1080 1080 1080 1200 1200 1200
VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA	ACGTATERD1 CURE 1,100 GTCTCTCCCTGTGTGTGCGTTTTGGT CURE MMBCORE 1220 AACCCTGTTGATTAGCGTACGGTCAGGC	CURE LIZO P IGCACTACAAATTGTA 1240 1240 1240	E CURE CGTATERDI II GGTITAGTAGTAGCTAG CURE TCGCTCTTAGCTAAGT	JURE 11 AGTATCTGCTTGGACAC 00 CURE 14 CCTACCTTGACTTTCT	1,100 ACGTATERD1 TGCAGGTTGTTATTAGTTAT 1,200 ACGTATERD1 TCAGGTTGTCAGCAAGGAGA	1,160 CURE 1,200 CTGCACTGTACTTCTACTTCCT 1,200 1,200 TGCATCGAGTGGTATCAACCTA	1080 1080 1080 1080 1080 1200 1200 1200
VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1	ACGTATERD1 CURE 1,00 GT_CT_CCCTCTGTGTGTGCGTTTTGGT GT_CT_CCCTCTGTGTGTGCGCTTTTGGT CURE 220 AACCCTGTTGATTAGCGTACGATCAGGC	CURE 1:20 P GCAGTACAAATTGTA GCAGTACAAATTGTA 1240 ATGCACGCTGGGGGGG	E CURE CGTATERD1 II CGTTTASTAGTAGCTAS CURE II TCGCTCTTAGCTAAAST	UVRE ITAGTATCTGCTTGGACAC 00 CURE IAGCGTACCTTGACTTTCT	1, 160 ACGTATERD1 TGCACGTTGTTATTAGTTAT 1, 194 CGTATERD1 TCACGTTGTCAGCAAGGAGA	1.100 CURE 1.200 CTGCACT <mark>GTAC</mark> TTCTACTTCCT 1.300 L300 ICCATCGAGTGGTATCAACCTA	1080 1080 1080 1080 1080 1200 1200 1200
VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64	ACGTATERD1 CURE 1,100 STCTCTCCCTCTGTGTGTGCGCTTTTGGT GTCTCTCCCTCTGTGTGTG	CURE 1,20 P GCAGTACAAATTGTA GCAGTACAAATTGTA 1240 ATGCACGCTGGGGCC	E CURE CGTATERDI I CGTITAGTAGTAGCTAG CURE TCGCTCTTAGCTAAAGT	LURE STAGTATCTGCTTGGACAC 60 CURE AGCGTACCTTGACTTTCT	1,160 ACGTATERD1 TGCAGGTTGTTATTAGTTAT 1,200 ACGTTGTCAGCAAGGAGA 1,200 ACGTTGTCAGCAAGGAGA	1.190 CURE 1.200 CTGCACTGTACTTCTACTTCCT 1.300 1.320 TGCATCGAGTGGTATCAACCTA	1080 1080 1080 1080 1200 1200 1200 1200
VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 IR64	ACGTATERD1 CURE 1,100 GT_CTCCCCTCTGTGTGCGTTTTGGT GT_CTCCCCTCTGTGTGGCGTTTTGGT CURE MMBCORE 1220 AACCCTGTTGATTAGCGTACGATCAGGC	CURE LID P IGCACTACAAATTGTA 1240 ATGCACGCTGGGGCC MYCCONSENSUSAT	E CURE COTATERDI IL COTTTABTACTAGCTA CURE TCGCTCTTAGCTAAA	URE STAGTATCTGCTTGGACAC 00 CURE TAGCGTAGCTTGACTTTCT	1,100 ACGTATERD1 TCCACGTTGTTATTAGTTAT ,200 ACGTTGTCACCAAGGAGA TCACGTTGTCACCAAGGAGA	1,160 CURE 1.200 CTGCACTGTACTTCTACTTCCT 1,200 1.200 TCCATCGAGTGGTATCAACCTA	1080 1080 1080 1080 1200 1200 1200 1200
VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64	ACGTATERD1 CURE 1.00 GTLTCTCCCTCTGTGTGTGCGTTTTGGT MYBCORE CURE 1.20 AACCCTGTTGATTAGCGTACGATCAGGC	CURE 1,120 P GCAGTACAAATTGTA 1,240 ATGCACGCTGGGGCC MYCCONSENSUSAT 1,340	E CURE CGTATERD1 II CGTITAGTAGTAGCTAG CURE II TCGCTCTTAGCTAAAGI	URE TAGTATCTGCTTGGACAC CURE TAGCGTAGCTTGACTTTCT MYCCONSENSUSAT	1,100 ACGTATERD1 TGCACGT TGTTATTAGTTAT 1,200 CGTATERD1 TCACGT TGTCAGCAAGGAGA 1,400 MYCCONSENSUS	1.100 (CURE 1.200 СТБСАСТ <mark>БТАС</mark> ТТСТАСТТССТ 1.300 1.230 ГССАТСБАБТОБТАТСААССТА ЧЙЩТО 1.400	1080 1080 1080 1080 1080 1080 1200 1200
VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64	ACGTATERD1 CURE 1.00 GTCTCTCCCTGTGTGTGCGTTTTGGT MYBCORE CURE 120 AACCGTGTTGATTAGCGTAGGATCAGGC 1300	CURE LIND A GCAGTACAAATTGTA ISAG ATGCACGCTGGGGGCG MYCCONSENSUSAT ISAGTGCTTGCTG	E CURE CGTATERDI I CGTITAGTAGTAGCTAG CURE TCGCTCTTAGCTAAAGT CTTCTAAAGAAGCAAGC	2URE BTAGTATCTGCTTGGACAC CURE ACCGTACCTTGACTTTCT MYCCONSENSUSAT ACCAAGTGACGATGTTT	1,160 ACGTATERD1 TGCAGGTTGTTATTAGTTAT 1,260 CGTATERD1 TCAGGTTGTCAGCAAGGAGA 1,400 MYCCONSENSUS TACCATATTTAGACATGCATT	1.190 CURE 1.200 CTGCACTGTACTTCTACTTCCT 1.300 1.320 TGCATCGAGTGGTATCAACCTA 4450 1.440 TCCCAGTATACGCTATTCTAC	1080 1080 1080 1080 1200 1200 1200 1200
VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA	ACGTATERD1 CURE 1.100 GT_CTCCCCTGTGTGTGCGTTTTGGT AGCCGTGTTGATTAGCGTACGATCAGGC AACCCTGTTGATTAGCGTACGATCAGGC 1.340	CURE LIZO GGAGTACAAATTGTA 1240 ATGCACGCTGGGGGG MYCCONSENSUSAT 1340 TCCATGTGCTTGCTG	E CURE CGTATERD1 U GGTTTABTAGTAGCTAG CURE TCGCTCTTAGCTAAAG TCGCTCTTAGCTAAAG 13 CTTCTAAAGAAGCAACT	URE TAGTATCTGCTTGGACAC CURE TAGCGTACCTTGACTTTCT MYCCONSENSUSAT TAGCAAGTGACGTATTAT	1,100 ACGTATERD1 TGCAGGTTGTTATTAGTTAT 129ACGTATERD1 TCAGGTTGTCAGCAAGGAGA 1,400 MYCCONSENSUE TAGATATTTAGAGATGCATT,	1,160 CURE 1,200 CTGCACTGTACTTCTACTTCCT 1,200 1,200 TCCATCGAGTGGTATCAACCTA 1450 1,440 TTCCCAGTATACGCTATTCTAC	1080 1080 1080 1080 1200 1200 1200 1200
VANDANA PB11 IR64 V22 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 VANDANA PB1	ACGTATERD1 CURE 1,00 GT_CT_CCCT_CT_GTGTGCGCGTTTTGGT ACCCT_GTTGATTAGCGTACGATCAGGC AACCCT_GTTGATTAGCGTACGATCAGGC 1300 CAAGAAAAGAAAAAAAAATGAACGAGAAA	CURE 1,120 GCA GTACAAA TT GTA 1240 A TGCA CGG TGGGGGG MYCCONSENSUSAT 1340 TCCA TGTGC TTGCTG	E CURE CGTATERD1 II CGTTTAGTAGTAGCTAG CURE TCGCTCTTAGCTAAAGT CTTCTAAAGAAGCAACT	URE TAGTATCTGCTTGGACAC CURE TAGCGTAGCTTGACTTTCT MYCCONSENSUSAT TAGCAAGTGACGATGTATT	1,100 ACGTATERD1 TGCAGGTTGTTATTAGTTAT 1,200 CGTATERD1 TCAGGTTGTCAGCAAGGAGA 1,400 MYCCONSENSUS TACATATTTAGAGATGCATT.	1.100 (CURE 1.200 СТБСАСТ <mark>ВТАС</mark> ТТСТАСТТССТ 1.300 1.230 ГССАТСБАБТБСБАТСААССТА ЧФЕ0 1.440 АТСССАБТАТАСОСТАТТСТАС	1080 1080 1080 1080 1080 1200 1200 1200
VANDANA PB11 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64	ACGTATERD1 CURE 1.00 STCTCTCCCTGTGTGTGCGTTTTGGT ACCCTGTGTTGATTAGCGTACGATCAGGC AACCCTGTTGATTAGCGTACGATCAGGC 1.300 CAAGAAAAGAAAAAAATGAACGAGGAAA	CURE LID P GCAGTACAAATTG A 1240 ATGCACGCTGOGGCG MYCCONSENSUSAT LIGATGTGCTTGCTG	E ICURE CGTATERD1 II CGTITTASTACTAGCTAG CURE TCGCTCTTAGCTAAAG CTTCTAAAGAAGCAACT	JURE 11 AGTATCTGCTTGGACAC 00 CURE 14 CCGTACCTTGACTTTCT 10 MYCCONSENSUSAT 14 GGAAGTGACGATGTATT	1,100 ACGTATERD1 TGCAGGTTGTTATTAGTTAT 1,200 ACGTTGTCATRD1 TCAGGTTGTCAGCAAGGAGA 1,400 MYCCONSENSUS TACATATTTAGAGATGCATT	1,160 CURE 1,200 CTGCACTGTACTTCTACTTCCT 1,300 1,320 TGCATCGAGTGGTATCAACCTA 45450 1,440 ATCCCAGTATACGCTATTCTAC	1080 1080 1080 1080 1200 1200 1200 1200
VANDANA PB11 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA PB1 IR64	ACGTATERD1 CURE 1.100 GT_CTCCCCTCTGTGTGCGTTTTGGT ACCCGTGTTGATTAGCGTACGATCAGGC AACCGTGTTGATTAGCGTACGATCAGGC 1340 CAAGAAAAGAAAAAAAATGAACGAGAAA	CURE 1:20 P GCAGIACAAATIGIA 1240 CATGCACGCTGGGGCG MYCCONSENSUSAT 1300 TCCATGTGCTTGCTG	E (CURE CGTATERD) U CGTTTABTAGTAGCTAG CURE TOGCTCTTAGCTAAAB TGCTCTAAAGAAGCAACT	JURE ITAGTATCTGCTTGGACAC CURE ACCGTACCTTGACTTTCT MYCCONSENSUSAT ACCAAGTGACGATGTATT	1,100 ACGTATERD1 TGCACGTTGTTATTAGTTAT 1,200ACGTATERD1 TCACGTTGTCAGCAAGGAGA 1,400 MYCCONSENSUS TACATATTTAGACATGCATT	1.140 CURE 1.200 CTGCACTGTACTTCTACTTCCT 1.300 1.200 TCCATCGAGTGGTATCAACCTA 'Mato 1.400 ATCCCAGTATACGCTATTCTAC	1080 1080 1080 1080 1080 1200 1200 1200
VANDANA PB11 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64	ACGTATERD1 CURE 1,00 GTCTCTCCCTTGTGTGTGCGTTTTGGT ACCCTTGTGTGTGTGCGCTTTTGGT AACCCTGGTGGTCACGTACGGATCAGGC 1340 CAAGAAAAGAAAAAAAAATGAACGAGAAA	CURE 1,120 P GCA GTACAAA TT GTA 1240 ATGCACGC TGGGGGC MYCCONSENSUSAT 1,300 TCCATGTGC TTGCTC 1,400	E CURE CGTATERD1 II CGTTTAGTAGTAGCTAG CURE II TCGCTCTTAGCTAAAG CTTCTAAAGAAGCAACT	URE TACTATCTGCTTGGACAC CURE TACCGTACCTTGACTTTCT MYCCONSENSUSAT TAGCAAGTGACGATGTATT	1,100 ACGTATERD1 TGCAGGT TGTTATTAGTTAT 1,200 CGTATERD1 TCAGGT TGTCAGCAAGGAGA 1,400 MYCCONSENSUS TACATATTTAGAGATGCATT. 1,500 CURE	1.100 (CURE 1.200 СТБСАСТ <mark>БТАС</mark> ТТСТАСТТССТ 1.300 1.200 ГССАТСБАБТОБТАТСААССТА 14450 1.400 1.500 1.400	1080 1080 1080 1080 1080 1200 1200 1200
VANDANA PB11 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA	АССТАТЕRD1 CURE 1,00 GTCTCCCTCTGTGTGCGTTTTGGT MYBCORE 1,20 ААСССТGTTGATTAGCGTACGATCAGGC 1,30 СААGAAAAGAAAAAAAAATGAACGAGAAAA 1,400 TTTAATTAAGTGCTCCATCAGGCAAAACA	CURE 1.20 / GCAETACAAATTETA 1.240 ATGCACGCTGGGGGG MYCCONSENSUSAT 1.340 TCCATGTGCTTGCTG TCCATGTGCTTGCTG 1.400	E ICURE COTATERDI II GET TT A BT AG T AG CT AG CURE T C G C T T A G T AG CT AG C T C T A A A G A A G C AA CT T A C A T T G C A A G A A C C BT	URE TAGTATCTGCTTGGACAC CURE ACCTACTTGACTTTCT MYCCONSENSUSAT ACCAAGTGACGATGTATT ACCAAGTGACGATACTAATT	1,100 ACGTATERD1 TGCAGGT TGTTATTAGTTAT 2,200 CGTATERD1 TGAGGT TGTCAGCAAGGAGA 1,000 MYCCONSENSUS TACATATTTAGTAGTAGCATTGCATT. 1,500 CURE AAAATTAGTAGTCATACCGT	1,160 CURE 1.200 CTGCACTGTACTTCTACTTCCT 1,200 1.200 TCCATCGAGTGGTATCAACCTA 1440 ATCCCAGTATACGCTATTCTAC 1,540 1.550 CCCAAAATATAAGTATTTTAA	1080 1080 1080 1080 1200 1200 1200 1200
VANDANA PB11 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA N22 VANDANA	ACGTATERD1 CURE 1.100 GTCTCTCCCTCTGTGTGTGCGTTTTGGT ACCCTGTTGATTAGCGTACGATCAGGC AACCCTGTTGATTAGCGTACGATCAGGC 1.200 AACCCTGTTGATTAGCGTACGATCAGGC 1.400 TTTAATTAAGTGCTCCATCAGCAAAACA	CURE 1:20 P GCA GTACAAA TT GTA 1240 ATGCACGC TGGGGGG ATGCACGC TGGGGGG TCCAT GTECTTGCTG 1480 IGGA TGCAACAAGCTT	E CURE CGTATERD1 II CGTTTABTACTAGCTAG CURE TCGCTCTTAGCTAAASI CTTCTAAAGAAGCAACT	JURE STAGTATCTGCTTGGACAC CURE COURE	1, 100 ACGTATERD1 TGCACGT TGTTATTAGTTAT 1,200 ACGTTGTTATCAGTTAT 1,200 ACGTTGTCAGCAAGGAGA 1,400 MYCCONSENSUS TACATATTTACACATGCATT 1,500 CURE AAAATTAGTAGTCATACCGT G	1.100 CURE 1.200 CTGCACTGTACTTCTACTTCCT 1.300 L.300 TCCATCGAGTGGTATCAACCTA 14%50 1.440 ATCCCAGTATACGCTATTCTAC 1.540 1.060 CCCAAAATATAAGTATTTTTAA C	1080 1080 1080 1080 1200 1200 1200 1200
VANDANA PB11 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64	ACGTATERD1 CURE 1.00 GTCTCTCCCTCTGTGTGTGCGTTTTGGT AACCGTGTTGATTAGCGTACGAGACAGGC AACCGTGTTGATTAGCGTACGAGGACAGGC CAAGAAAAGAA	CURE LID P GCAGTACAAATTGTA 1,240 ATGCACGCTGCGGCCC MYCCONSENSUSAT 1,200 TCCATGTGCTGCTG CGATGCAACAAGCTT 1,400	E ICURE GGTATERD1 IL COTTATACTAGCTAG CURE TCGCTCTTAGCTAACTAG CTTCTAAAGAAGCAACT	UPRE TAGTATCTGCTTGGACAC CURE TAGCGTAGCTTGACTTTCT MYCCONSENSUSAT TAGGAAGTGACGATGTATT LEE TAGGACACACATACTAATT	1,100 ACGTATERD1 TGCAGGT TGTTATTAGTTAT 1,200 CGTATERD1 TCAGGT TGTCAGCAAGGAGA 1,400 MYCCONSENSUS TACATATTTAGAGATGCATT. 1,500 CURE AAAATTAGTAGTCATACCGTI G. G.	1.100 CURE 1.200 СТ GCACT GTAC TT CT ACT T C C T 1.300 1.330 T CCAT CGAG T GG T AT C AA C C T A 14450 1.440 A T C C C A GT AT T A C C C C C C C C C C C C C C C C	1080 1080 1080 1080 1080 1200 1200 1200
VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA PB1 IR64	ACGTATERD1 CURE 1,100 GT_CTCCCCTCTGTGTGCGTTTTGGT MYBCORE 1220 AACCGTGTTGATTAGCGTACGATCAGGC 1,240 1,340 1,44	CURE LIZO GCA ET AC AAAT T GT A 1240 CAT GCA CGC T GGGGGG MYCCONSENSUSAT 1.300 T CCAT GT GC T T GC T G LATGCA CGC T GGGGT GCAACAAGC T T	E CURE CGTATERD1 II CGTTTABTAGTAGCTAG CURE TCGCTCTTAGCTAAAG CTTCTAAAGAAGCAACT TACATTGCAAGAACCG	URE TABETATCTGCTTGGACAC CURE TABEGT ACCTTGACTTTCT MYCCONSENSUSAT TAGEAAGTGACGATGTATT ACGACACACATACTAATT	1,100 ACGTATERD1 TGCAGGTTGTTATTAGTTAT 1200ACGTATERD1 TCAGGTTGTCAGCAAGGAGA 1,400 MYCCONSENSUS TACATATTTAGAGATGCATT, 1,500 CURE AAAATTAGTAGTCATACCGT G G G	1,160 CURE 1,200 CTGCACTGTACTTCTACTTCCT 1,200 1,200 1,200 1,200 1,200 TCCATCGAGTGGTATCAACCTA 1,200 1,200 YA500 1,440 1,200 TCCCATCGAGTGGTATCGACTATCTAC 1,200 1,200 TCCCAGTATACGCTATTCTAC 1,200 1,200 CCAAAATATAAGTATTTTTTAA C C CC C C C	1080 1080 1080 1080 1200 1200 1200 1200
VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64	ACGTATERD1 CURE 1,100 GT_CTCCCCTCTGTGTGTGCGTTTTGGT ACCCTGTTGATTACCGTACGATCAGGC AACCCTGTTGATTACCGTACGATCAGGC 1200 AACCCTGTTGATTACCGTACGATCAGGC 1340 CAAGAAAAGAAAAAAAATGAACGAGAAA 1,400 TTTAATTAAGTGCTCCATCAGCAAAACA	CURE 1:20 P GCA GTACAAATT GTA 1240 ATGCACGC TGGGGGG ATGCACGC TGGGGGG TCCAT GTECTTGCTG 1400 GGATGCAACAAGCTT	E CURE CGTATERD1 11 CGTTTABTACTAGCTAG CURE TCGCTCTTAGCTAAAS CTTCTAAAGAAGCAACT	JURE STAGTATCTGCTTGGACAC CURE COURE	1,100 ACGTATERD1 TGCACGTTGTTATTAGTTATT 1,200 ACGTTGTCAGCAAGGAGA 1,200 MYCCONSENSUS 1,400 MYCCONSENSUS 1,400 MYCCONSENSUS 1,400 CURE AAAATTAGTAGTCATACGTT 0,500 CURE AAAATTAGTAGTCATACCGT 0,500 G.	1.100 CURE 1.200 CTGCACTGTACTTCTACTTCCT 1.300 L.300 TCCATCGAGTGGTATCAACCTA 1440 1.400 ATCCCAGTATACGCTATTCTAC 1.540 1.540 ATCCCAAAATATACGCTATTCTAC C	1080 1080 1080 1080 1080 1200 1200 1200
VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64	ACGTATERD1 CURE 1,00 STCTCTCCCTCTGTGTGTGCGTTTTGGT ACCCTGTGTTGATTAGCGTACGATCAGGC AACCCTGTTGATTAGCGTACGATCAGGC CAAGAAAAGAA	CURE LID P GCAGTACAAATTG A 1240 ATGCACGCTGOGGCG MYCCONSENSUSAT LICEATGTGCTTGCTG CGATGCAACAAGCTT I,400 IGGATGCAACAAGCTT	E ICURE COTATERDI II COTITASTACTAGOTAG CURE TCGCTCTTAGCTAAGA CTTCTAAAGAAGCAACT	JURE 11 AGTATCTGCTTGGACAC 10 CURE 14 CCTTGACTTGACTTTCT 14 GCAAGTGACGATGTATT 14 GCAAGTGACGATGTATT	1,100 ACGTATERD1 TGCAGGTTGTTATTAGTTAT 1,200 ACGTATERD1 TCAGGTTGTCAGCAAGGAGA 1,400 MYCCONSENSUS TACATATTTAGAGATGCATT, 1,500 CURE AAAATTAGTAGTCATACCGT G. G. G.	1,160 CURE 1,200 CTGCACTGTACTTCTACTTCCT 1,300 1,320 1,300 1,320 1,320 TGCATCGAGTGGTATCAACCTA 1,540 1,540 1,540 1,540 1,540 1,540 1,540 1,540 1,540 1,540 1,540 CCAAAATATAAGTATTTTAA C. C. C C. C.	1080 1080 1080 1080 1080 1200 1200 1200
VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64	ACGTATERD1 CURE 1,100 ST_CTCCCCTCTGTGTGCGTTTTGGT ACCCTGTTGATTAGCGTACGATCAGGC 1,200 AACCCTGTTGATTAGCGTACGATCAGGC 1,340 1,460 TTTAATTAAGTGCTCCATCAGGCAAAACA 1,460 1,150	CURE LIZO GCA CIACAAATT CIA 1240 CATGCACGCTGGGGCC ATGCACGCTGGGGCC MYCCONSENSUSAT LIZO CATGTCTTGCTG CATGTCTTGCTG LIARO LI	E CURE CGTATERD1 U CGTTTABTAGTAGCTAG CURE TCGCTCTTAGCTAAGT CTTCTAAAGAAGCAACT TACATTGCAAGAACCG	URE TAGTATCTGCTTGGACAC CURE ACCGTACCTTGACTTTCT MYCCONSENSUSAT ACCAAGTGACGATGTATT ACCAAGTGACGATGTATT	1,100 ACGTATERD1 TGCAGGTTGTTATTAGTTAT 1.200ACGTTGTCAGCAAGGAGA 1.400 MYCCONSENSUS TACATATTTAGTAGTCATGCATT 1.400 CURE AAAATTAGTAGTCATACCGTU G.G. G. 1,400	1,140 [CURE 1,200 CTGCACTGTACTTCTACTTCCT 1,300 1,320 1,300 1,320 1,320 TCCATCGAGTGGTATCAACTA 1,320 1,320 TCCATCGAGTGGTATCAACCTA 1,320 1,320 TCCATCGAGTGGTATCAACCTA 1,320 1,440 TCCCAGTGTATCGCGTATTCTAC 1,320 1,440 TCCCAGTATACGCTATTCTAC 1,320 1,440 TCCCAGTATACGCTATTCTAC 1,320 1,440 TCCCAAAATATAAGTATTTTTAA C C C C C 1,440 1,540 1,540 1,540 1,540	1080 1080 1080 1080 1080 1200 1200 1200
VANDANA PB11 IR64 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB11 IR64 N22 VANDANA PB11 IR64 N22 VANDANA	ACGTATERD1 CURE 1,00 GTCTCTCCCTCTGTGTGTGCGTTTTGGT AACCCTGTTGATTAGCGTAGGATCAGGC 1340 CAAGAAAAGAAAAAAAAATGAACGAGAAA TTTAATTAAGTGCTCCATGAGCAAAACA	CURE 1.120 P GCAGTACAAATTGTA 1,240 ATGCACGCTGGGGCC MYCCONSENSUSAT 1,200 TCCATGTECTTGCTG GGATGCAACAAGCTT 1,400 IGGATGCAACAAGCTT 1,400 IGGATGCAACAAGCTT 1,400 IGGATGCAACAAGCTT	E ICURE CGTATERDI II CGTTTABTACTAGCTA CURE II TCGCTCTTAGCTAAASI CTTCTAAAGAAGCAACT TACAATTGCAAGAACCSI	UVRE TAGTATCTGCTTGGACAC CURE ACCGTACCTTGACTTTCT MYCCONSENSUSAT AGGAAGTGACGATGTATT JEE ACGACACACATACTAATT 20 TTTTAAATAAAAAGACTTG	1,100 ACGTATERD1 TGCACGT TGTTATTAGTTAT 1,200 CGTATERD1 TCACGT TGTCAGCAAGGAGA 1,400 MYCCONSENSUS TACATATTTACACATECATT 1,500 CURE AAAATTAGTAGTAGTAGCATCGTT G. G. 1,400 1,400 CURE AAAATTAGTAGTAGTTGTT.	1.100 CURE 1.200 CTGCACTGTACTTCTACTTCCT 1.300 1.320 1.300 1.320 1.320 TCCATCGAGTGGTATCAACCTA 1.400 1.400 ATCCCAGTATACGCTATTCTAC 1.400 1.400 1.540 1.400 1.500 2CCAAAATATAAGTATTTTAACTC C C	1080 1080 1080 1080 1080 1200 1200 1200
VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA	ACGTATERD1 CURE 1.00 STCTCTCCCTCTGTGTGCGTTTTGGT ACCCTGTGTTGATTAGCGTAGGATCAGGC 1.20 AACCCTGTTGATTAGCGTAGGATCAGGC 1.30 CAAGAAAAGAAAAAAAATGAACGAGAAA TTTAATTAAGTGCTCCATCAGGCAAAACA ATCCTGACACGGTCTTCGAGATGCTAAT	CURE 1.120 / GCAGTACAAATTGTA 1.240 ATGCACGCTGGGGGG MYCCONSENSUSAT 1.340 TCCATGTGCTTGCTG GGATGCAACAAGCTT 1.400 GGATGCAACAAGCTT 1.400 GGATGCAACAAGCTT 1.400 	E ICURE COTATERDI II CETTTAETACTACTAC CURE TCGCTCTTAGCTAACTAC CURE TCCCTCTAAAGAAGCAACCTA TACATTGCAAGAACCAS TACATTGCAAGAACCAS	UPRE TAGTATCTGCTTGGACAC CURE ACCOTACCTTGACTTTCT MYCCONSENSUSAT IAGCAAGTGACGATGTATT ARE AGCAAGTGACGATACTAATT 20 TTTTAAATAAAAAAGACTTG	1,160 ACGTATERDI TCCACGT TGTTATTAGTTAT 1.200 CGTATERDI TCACGTTGTCAGCAAGGAGA 1.400 MYCCONSENSUS TACATATTAGTAGTCATGCATT 1.500 CURE AAAATTAGTAGTCATACCGT G. G. 1,440 G. G. 1,440 C. C.	1,160 CURE 1,200 CTGCACTGTACTTCTACTTCCT 1,200 1,200 1,300 1,200 1,200 TCCATCGAGTGGTATCAACCTA 4,400 1,400 ATCCCAGGTATACGCTATTCTAC 1,400 1,400 1,540 1,540 1,540 CCCAAAATATAAGTATTTTAA C C CC C C 1,540 1,560 1,660 1,540 1,550 1,560 CAGAAATATAAGTATTTTAA C C	1080 1080 1080 1080 1080 1200 1200 1200 1200 1200 1320 1440 1440 1560
VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64	ACGTATERD1 CURE 1,100 GT_CTCCCTCTGTGTGTGCGTTTTGGT ACCCTGTGTGATTAGCGTACGATCAGGC AACCCTGTTGATTAGCGTACGATCAGGC 1,200 1,340 1,340 1,340 1,340 1,340 1,340 1,340 1,150 1,150 1	CURE I TO P GCAGTACAAATTGTA GCAGTACAAATTGTA 1240 CATGCACGCTGGGGCG MYCCONSENSUSAT 1300 TCGATGTGCTTGCTG GGATGCAACAAGCTT 1400 IGGATGCAACGAAGGTTATC C. C	E CURE CGTATERD1 U CGT TT A BT AG T AG CT A CURE T CGC TC T A GC T A A A T CT T C T A A GA AG C A A T A C A T T G C A A GA AG C A T A C A T T G C A A GA AG C A T A C A T T G C A A GA AG C A T T T T A A A A A A GT A A GT A A GT A A GT A T T T T T T T T T T T T T T T T T T	JURE ITAGTATCTGCTTGGACAC CURE ACCGTACCTTGACTTTCT MYCCONSENSUSAT ACCAAGTGACGATGTTTT ACCAAGTGACGATGTTTTT ACCAAGTGACGATGTTTTTTTTTTTTTTTTTTTTTTTTT	1,100 ACGTATERD1 TGCACGTTGTTATTAGTTAT 1,200 ACGTTGTTATTAGTTAT 1,200 ACGTTGTCAGCAAGGAGA 1,400 MYCCONSENSUS TACATATTAGTAGTAGCATGCATT 1,500 CURE AAAATTAGTAGTAGTAACGTI G.G.G. 1,440 C.C.	1.160 CURE 1.200 CTGCACTGTACTTCTACTTCCT 1.300 1.300 1.300 1.300 1.300 TCCATCGAGTGGTATCAACCTA 1.300 1.300 TCCATCGAGTGGTATCAACCTA 1.300 1.300 TCCATCGAGTGGTATCAACCTA 1.300 1.400 TCCCAGTATACGCTATTCTAC 1.500 1.600 CCAAAAATATAAGTATTTTAA C C CC C C 1.500 1.600 1.600 AATGATAAATCTAGTAACTTTA T T	1080 1080 1080 1080 1080 1200 1200 1200
VANDANA PB11 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 IR64	ACGTATERD1 CURE 1,00 STCTCTCCCTCTGTGTGTGCGTTTTGGT AACCCTGTTGATTACCGTACGATCAGGC AACCCTGTTGATTACCGTACGATCAGGC CAAGAAAAGAA	CURE LIND A GCAGTACAAATTGTA 1,240 ATGCACGCTGCGGCGG MYCCONSENSUSAT LCCATGTGCTGCTG LIND LCCATGTGCTTGCTG LIND LIND LINCACGAACAAGCTT LIND LINCACGAACGATCATC C. G. G. G.	E ICURE COTATERDI IL COTTERDI CAGOTAG CURE TCGCTCTTAGCTAGCTAG TCGCTCTTAGCTAAGAGCAACT TACATTGCAAGAAGCAACT TACATTGCAAGAACCC TACATTGCAAGAACCC TACATTGCAAGAACCC TACATTGCAAGAACCC	JURE STACTATCTGCTTGGACAC CURE ACCGTACCTTGACTTTCT MYCCONSENSUSAT AGGAAATGACGATGTATT JEE ACGACACACATACTAATT 20 ITTTAAATAAAAAGACTTG	1,100 ACGTATERD1 TGCAGGTTGTTATTAGTTAT 1,200 ACGTTGTCAGCAAGGAGA 1,400 MYCCONSENSUS 1,400 MYCCONSENSUS 1,400 CURE AAAATTAGTAGTCATACCGTI G G G 1,400 CURE AAAATTAGTAGTCATACCGTI G G G 1,400 C C C C	1,160 CURE 1,200 CTGCACTGTACTTCTACTTCCT 1,300 1,320 1,300 1,320 1,320 TGCATCGAGTGGTATCAACCTA 1,440 1,440 ATCCCAGTATACGCTATTCTAC 1,440 1,640 1,540 1,640 1,640 1,540 1,640 1,640 1,540 1,640 1,640 1,540 1,640 1,640 1,540 1,640 1,640 ATCCCAAGTATACGCTATTTTAACC C C C C C C C C ATGATAAATCTAGTAACTTAGTAACTTTA T T T T	1080 1080 1080 1080 1200 1200 1200 1200
VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA PB1 IR64	ACGTATERD1 CURE 1,00 GTCTCTCCTTGTGTGTGCGTTTTGGT MMBCORE 120 AACCCTGTTGATTAGCGTACGATCAGGC 1340 CAAGAAAAGAAAAAAAAATGAACGAGAAAACA 1400 TTTAATTAAGTGCTCCATCAGGAAAACA ATCCTGACACGGTCTTCGAGATGCTAAT	CURE 1.120 GCA CT AC AAAT T GT A 1240 AT GCA CGC T GGGGCC MYCCONSENSUSAT 1.380 AT GCA CGC T GGGGCC MYCCONSENSUSAT 1.380 ACCOTATERD 1.400 ACCOT	E CURE CGTATERDI II CGT TT A BT ACT A GCT A G CURE TCGCTCT T A GCT A GCT A G T A CA TT GC A A A GC A A C T A CA TT GC A A GA A A C T A CA TT GC A A GA A A C T A CA TT GC A A GA A A C T A CA TT GC A A GA A A C T A CA TT GC A A GA A A C T A CA TT GC A A GA A A C T T T T T T T T T T T T T T T T T T T	URE TAGTATCTGCTTGGACAC CURE ACCGTACCTGACTTTCT MYCCONSENSUSAT ACCAAGTGACGATGTATT ACCAAGTGACGATGTATT ACCAACTGACATACTAATT ACGACACACACATACTAATT 20 TTTTAAATAAAAAGACTTG 40	1,100 ACGTATERD1 TCCACGT TGTTATTAGTTAT 1,200 ACGTATERD1 TCACGT TGTCAGCAAGGAGA 1,400 MYCCONSENSUS TACATATTACACGT TGCATT 1,400 CURE AAAATTAGTAGTCATACGT G. G. 1,400 G. 1,400 CURE AAAATTAGTAGTCATACCGT G. G. 1,400 CURE AAAATTAGTAGTCATACCGT G. 1,400 CURE AAAATTAGTAGTCATACCGT	1,160 CURE 1,200 CTGCACTGTACTTCTACTTCCT 1,200 1,200 1,200 1,200 1,200 1,200 1,200 1,200 TCCATCGAGTGGTATCAACCTA 1,200 1,200 YARE0 1,400 1,200 TCCATCGAGTGGTATCAACCTA 1,200 1,200 CCCAAAATATAAGTATTTTTAA C. C. CC C. C. 1,800 1,600 1,600 NATGATAAATCTAGTAACTTAGTAACTTTA T. T. 1,700 1,800 1,800	1080 1080 1080 1080 1200 1200 1200 1200
VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA PB1 IR64	ACGTATERD1 CURE 1,00 GTCTCTCCCTCTGTGTGTGCGTTTTGGT MYBCORE L120 AACCETGTTGATTAGCGTACGATCAGGC 1,20 CAAGAAAAGAAAAAAAAAAATGAACGAGAAA 1,400 TTTAATTAAGTGCTCCATCAGGCAAAACA 1,500 TTTAATTAAGTGCTCCATCAGGATGCTAAT 1,00 ATCCTGACACGGTCTTCGAGATGCTAAT	CURE 1:20 P GCAGTACAAATTGTA GCAGTACAAATTGTA 1240 ATGCACGCTGGGGGG ATGCACGCTGGGGGGG ATGCACGCTGGGGGGG ATGCACGCTGGGGGGG ATGCAAGCTTGCTG GGATGCAACAAGCTT TAAGCAAGGTTATC G. G. G. J20 TCTATTAATAATCAA	E ICURE CGTATERDI II CGTTTABTACTAGCTAG CURE CCUR	JURE ITAGTATCTGCTTGGACAC CURE COURE	1,100 ACGTATERD1 1.100 ACGTATERD1 1.200 ACGTTGTTATTAGTTATT 1.200 ACGTTGTCAGCAAGGAGA 1.400 MYCCONSENSUS 1.400 MYCCONSENSUS 1.400 CURE AAAATTAGTAGTAGCATGCATT 1.500 CURE AAAATTAGTAGTAGTAGCATGCATT 	1.100 CURE 1.200 CTGCACTGTACTTCTACTTCCT 1.300 1.200 1.300 1.200 1.200 TCCATCGAGTGGTATCAACCTA 1.400 1.400 ATCCCAGTATACGCTATTCTAC C. C. 1.540 1.600 1.600 CCCAAAATATAAGTATTTTAA C. C. TATGATAAATCTAGTAACTTTA T. T. 1.540 1.600 1.600 TATGATAAATCTAGTAACTTTA T. T. T. T. T. 1.540 1.600 1.600 TATGATAAATCTAGTAACTTTA T. T. T. T. T. T. T. T. T. T. T. T. T. T.	1080 1080 1080 1080 1080 1200 1200 1200
VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA	АССТАТЕРО1 CURE 1,00 STCTCTCCCTCTGTGTGCGTTTTGGT MYBCORE CURE 1,20 AACCOTGTTGATTAGCGTACGATCAGGC AACCOTGTTGATTAGCGTAGGATCAGGA 1,300 1,300 1,300 1,300 1,300 TTTAATTAAGTGCTCCATCAGGATAGAACCA ATTTAACTGATCATCAGGATGCTAAT 1,500 ATTTTACTGATATTTTTTTTTTTTTTTTTTTTTTTTTTT	CURE 1.120 / GCAETACAAATTEL 1240 ATGCACGCTGGGGGG ATGCACGCTGGGGGG MYCCONSENSUSAT 1.340 TCCATGTGCTTGCTG GGATGCAACGAGGTT 1,400 GGATGCAACGAAGCTT 1,400 GGATGCAACGAAGCTT 1,400 GGATGCAACGAGGTTATC G. G. G. G. G. G. G. G. G. G. G. G. G.	е ;CURE CGTATERD1 ;; GGT IT A STACT AG CT AG CURE TGGCTCT TAGCT AG CT AG CURE TGGCTCT TAGCT AAGAACCAACT TACAATTGCAAAGAAGCAACT TACAATTGCAAAGAACCAT TATAAAAAGTAAGATAAT T	UPRE STAGTATCTGCTTGGACAC CURE ACCOTACCTTGACTTTCT MYCCONSENSUSAT ACCAAGTGACGATGTATT AGCAAGTGACGATACTAATT AGE AGCACACACATACTAATA AAAAAAAAGACTTG CTTTTAAATAAAAAAGACTTG 40 CTTGTGGCCATACTTAAAAA	1,160 ACGTATERD1 TGCAGGT TGTTATTAGTTAT 1.294CGTATERD1 TCAGGTTGTCAGCAAGGAGA 1.400 MYCCONSENSUS TACATATTAGTAGTCATGCATT. 1.500 CURE AAAATTAGTAGTCATACCGT G. G. 1,640 	1,160 CURE 1,200 CTGCACTGTAQTTCTACTTCT 1,200 1,200 1,300 1,200 1,200 TCCATCGAGTGGTATCAACCTA 1,200 1,200 MATCCCAGGTATCAACCTA 1,200 1,200 TCCATCGAGTGGTATCAACCTA 1,200 1,200 1,300 1,200 1,200 1,300 1,200 1,200 1,300 1,200 1,200 1,300 1,000 1,000 CCCAAAATATAAGTATTTTTAA C C CC C C C 1,800 1,800 1,800 1,800 ATGGTAAAATCTAGGTAACTTAGTAACTTA T T T 1,700 T T 1,000 1,000 3ATGGTTGAGAGAAAATCTCCCC G 1,000 1,000 1,000	1080 1080 1080 1080 1080 1200 1200 1200
VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64	ACGTATERD1 CURE 1,100 GTCTCTCCCTGTGTGTGCGTTTTGGT ACCCTGTTGATTAGCGTACGATCAGGC 1,200 AACCCTGTTGATTAGCGTACGATCAGGC 1,340 1,440 1,4	CURE 1.120 GCA GT AC AAAT T GT A 1240 CAT GC AC GC T GG GG CG CAT GC AC GC T GG GG CG CAT GC AC GC T GG GG CG CAT GC AC GG T T C GC G CG CAT GC AC CAA GC T T C CAT GT GC T GC T GC CG CG CAT GC AC CAA GC T T C C G. C.	E CURE CGTATERD1 11 CGTTTABTAGTAGCTAG CURE TCGCTCTTAGCTAAGT CTTCTAAAGAAGCAAGT TACAATTGCAAGAAGCAG TACAATTGCAAGAAGCAG T TATAAAAAGTAAGATA T T T T T T T T T	URE TAGTATCTGCTTGGACAC CURE ACCGTACCTTGACTTTCT MYCCONSENSUSAT ACCAAGTGACGATGTATT ACCAAGTGACGATGATGTATT ACCAAGTGACGATACTAATT ACGACACACACATACTAATT 20 TTTTAAATAAAAAGACTTG 40 TTGTCGCCTATACTTAAAA	1,100 ACGTATERD1 TGCACGTTGTTATTAGTTAT 1,200 ACGTTGTTATTAGTTAT 1,200 ACGTTGTCAGCAAGGAGA 1,400 MYCCONSENSUS TACATATTTACACATGCATG 1,400 CURE AAAATTAGTAGTCATACCGTU G.G.G.G.G.G.G.G.G.G.G.G.G.G.G.G.G.G.G.	1,140 CURE 1,200 CTGCACTGTACTTCTACTTCCT 1,200 1,200 1,200 1,200 1,200 TCCATCGAGTGGTATCAACCTA 1,200 1,200 TCCATCGAGTGGTATCAACCTA 1,200 1,200 TCCATCGAGTGGTATCAACCTA 1,200 1,200 TCCCAAAATATAAGTATTTTTAA C C CC C C 1,500 1,600 1,600 TATGATAAATCTAGTAACTTTA T T 1,500 1,600 1,600 TATGATAAATCTAGTAACTTAGTAACTTTA T T T,000 1,600 1,600 T,000 1,600 1,600 SATGGTTGAGGAGAAAATCTCCC G. G.	1080 1080 1080 1080 1080 1200 1200 1200
VANDANA PB11 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64	ACGTATERD1 CURE 1,00 STCTCTCCCTCTGTGTGTGCGTTTTGGT ACCCGTGTTGATTACCGTACGTACGGTCAGGC AACCCGTGTTGATTACCGTACGACGACGACAA CAAGAAAAGAA	CURE 1.120 / GCAGT ACAAAT TG A GCAGT ACAAAT TG A 1.240 ATGCACGCC TGGGGCG MYCCONSENSUSAT 1.200 TCATGCT CTGCTG 1.200 CGATGCAACAAGCTTACCAAGCTT	е ICURE CGTATERD1 II CGTITTASTACTAGCTAG CURE TCGCTCTTAGCTAACTAG CTTCTAAAGAAGCAACT TACATTGCAAGAACCAT TATAAAAAAGTAAGATAT T T T T T T T T T	JURE STAGTATCTGCTTGGACAC CURE ACCGTACCTTGACTTTCT MYCCONSENSUSAT AGBAAGTGACGATGTATT JEE AGGAAGACACATACTAATT 20 11TTAAATAAAAAAGACTTG 20 11TTAAATAAAAAAGACTTG 20 11TTAAATAAAAAAGACTTG	1,100 ACGTATERD1 120 ACGTATERD1 120 ACGTATERD1 120 ACGTTGTCAGCAAGGAGA 1.40 MYCCONSENSUS 1.40 MYCCONSENSUS 1.40 CURE AAAATTAGTAGTAGTAGCATGCATT 1.50 CURE AAAATTAGTAGTAGTAGCATGCATT G. G. G. G. C. 1.40 CURE AAAATTAGTAGTAGTTGTT, C. C. 1.700 CURE AAAATTAGTAGTAGTTGTT, C. 	1,160 CURE 1,200 CTGCACTGTACTTCTACTTCCT 1,300 1,320 1,300 1,320 1,320 TGCATCGAGTGGTATCAACCTA 1,440 1,440 ATCCCAGTATAGGCTATTCTAC 1,440 1,640 ATCCCAGTATAGGCTATTCTAC 1,540 1,540 1,540 1,640 1,640 ATCCCAGTATAGGCTATTTTTAA C C C C C C C C ATGATAAATCTAGTAACTTTA T T ATGATAAATCTAGGTAACTTTA T T J300 1,560 1,560 ATGATAAATCTAGTAACTTTAGTAACTTTA C C G G G 1,560	1080 1080 1080 1080 1080 1200 1200 1200
VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA	ACGTATERD1 CURE 1,00 GTCTCTCCTTGTGTGTGCGTTTTGGT MMBCORE 1,20 AACCCTGTTGATTAGCGTAGGATCAGGC 1,30 CAAGAAAAGAAAAAAAAATGAACGAGAAA 1,30 TTTAATTAAGTGCTCCATCAGGCAAAACA 1,00 TTTAATTAAGTGCTCCATCAGGCAAAACA 1,00 1,20	CURE LID / GCACTACAAATTETA 1240 1240 ATGCACGCTGGGGCG ATGCACGCTGGGGCG MYCCONSENSUSAT 1340 ICCATGTGCTTGCTG ICCATGTGCTTGCTG GGATGCAACGAAGCTT 140 IGGATGCAACGAAGCTT 140 IGGATGCAACGAAGCTT 140 IGGATGCAACGAAGCTT ICCATGTGCTGCTG ICCATGTGCTGCTG ICCATGTGCTGCTG ICCATGTGCTGCTG ICCATGTGCTGCTG ICCATGTGCTGCTG ICCATGTGCTGCTG ICCATGTGCTGCTG ICCATGTGCTGCTG ICCATGTGCTGCTG ICCATGTGCTGCTG ICCATGTGCTGCTG ICCATGTGCTGCTG ICCATGTGCTGCTG ICCATGTGCTGCTG ICCATGTGCTGCTG ICCATGTGCTG ICCATGTGCTGCTGCTG ICCATGTGCTGCTG ICCATGTGCTGCTG ICCATGTGCTGCTG ICCATGTGCTGCTGCTG ICCATGTGCTGCTGCTG ICCATGTGCTGCTGCTG ICCATGTGCTGCTGCTG ICCATGTGCTGCTGCTG ICCATGTGCTGCTGCTG ICCATGTGCTGCTGCTGCTG ICCATGTGCTGCTGCTGCTG ICCATGTGCTGCTGCTGCTG ICCATGTGCTGCTGCTGCTG ICCATGTGCTGCTGCTGCTGCTG ICCATGTGCTGCTGCTGCTGCTGCTG ICCATGTGCTGCTGCTGCTGCTGCTGC ICCATGTGCCTGCTGCTGCCTGCG ICCATGTGCCTGCCGCTGCGCGCGCGCGCGCGCGCGCGCGC	е , сике сотатекої і сотт т латаста ст ас сике то сотт т аста ста со сике то со	URE TAGTATCTGCTTGGACAC CURE ACCGTACCTTGACTTTCT MYCCONSENSUSAT ACCGAAGTGACGATGTATT ACGAAGTGACGATGTGATT ACGAACACACATACTAATT ACGACACACACATACTAATT ACGACACACACATACTAATT ACGACACACACATACTAAAA	1,100 ACGTATERD1 TCCACGT TGTTATTAGTTAT 1.20ACGTATERD1 TCACGTTGTCAGCAAGGAGA 1.400 MYCCONSENSUS TCCATATTACACGTTGCATT 1.000 CURE AAAATTAGTAGTCATACCGT G. G. G. 1.400 G. 1.400 G. 1.400 CURE AAAATTAGTAGTCATACCGT G. G. G. 1.400 CURE AAAATTAGTAGTCATACCGT G. G. 1.400 CURE AAAATTAGTAGTCATACCGT G. 1.400 CURE AAAATTAGTAGTCATACCGT G. 1.400 CURE AAAATTAGTAGTCATACCGT G. 1.400 CURE AAAATTAGTAGTCATACCGT G. 1.400 CURE AAAATTAGTAGTCATACCGT G. 1.400 CURE AAAATTAGTAGTCATACCGT G. 	1,160 CURE 1.200 CTGCACTGTACTTCTACTTCCT 1.200 1.200 1,200 1.200 1.200 1,200 1.200 1.200 TCCATCGAGTGGTATCAACCTA 1.200 1.200 1,200 1.200 1.200 TCCATCGAGTGGTATCAACCTA 1.200 1.200 1,200 1.200 1.200 CCCAAAATATAAGTATTTTTAA C C CC C C 1,800 1.600 1.600 1,800 1.000 1.000 1,800 1.000 1.000 1,800 1.000 1.000 1,800 1.000 1.000 1,800 1.000 1.000 1,800 1.000 1.000 1,800 1.000 1.000 1,800 1.000 1.000 1,800 1.000 1.000 1,900 1.000 1.000 1,900 1.000 1.000 1,900 1.000	1080 1080 1080 1080 1080 1200 1200 1200
VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA PB1 IR64	ACGTATERD1 CURE 1,00 GTCTCTCCCTGTGTGTGCGCTTTTGGT MYBCORE L120 AACCCTGTTGATTACCGTACGATCAGGC 1,00 1,00 11TAATTAAGTGCTCCATCAGGCAAAACA 1,00 11TAATTAAGTGCTCCATCAGCAAAACA ACCCTGACACGGTCTTCGAGATGCTAAT 1,00	CURE 1:20 GCA GT AC AAA TT GT A GCA GT AC AAA TT GT A 1240 CAT GC AC GC T GG GG GG CAT GC AC GC T GG GG GG GG T C CAT GT GC TT GC T G GG AT GC AA C AAGC T T T T AA C GA AG GT T AT C G G G. 1770 T C T AT T AA T AA T C AA	E (CURE CGTATERD) 11 CGTTTABTAGTAGCTAG CURE TOGCTCTTAGCTAAAG TGCTCTTAGCTAAAG TGCTCTTAGCTAAAG TGCTCTTAGCTAAAG TGCTCTTAGCAAGAAGCAACT TGCTTCTAAAGAAGCAAGCA TACAATTGCAAGAAGCAACT T T T T T T T T T T T T T T T T T	URE TAGTATCTGCTTGGACAC CURE ACCGTACCTTGACTTTCT MYCCONSENSUSAT ACCAAGTGACGATGTTTT ACCAAGTGACGATGTTTT ACCAAGTGACGATGTTTTT ACCAAGTGACGACACATACTAATT 20 TTTTAAATAAAAAAGACTTG 20 TTTTAAATAAAAAAGACTTG 20 TTTTGTCGCTATACTTAAAA	1,100 ACGTATERD1 1,200 ACGTATERD1 1,200 ACGTATERD1 1,200 ACGTTGTCAGCAAGGAGA 1,400 MVCCONSENSUS 1,400 CURE AAAATTAGTAGTAGCATGCATT 1,500 CURE AAAATTAGTAGTAGTAGCATGCATT G.G.G.G.G.G.G.G.G.G.G.G.G.G.G.G.G.G.G.	1.140 CURE 1.200 CTGCACTGTATETTCTACTTCCT 1.300 1.300 1.300 1.300 1.300 TCCATCGAGTGGTATCAACCTA 1.300 1.300 TCCATCGAGTGGTATCAACCTA 1.300 1.300 TCCATCGAGTGGTATCAACCTA 1.300 1.400 TCCCAGTATACGCTATTCTAC C C CCAAAAATATAAGTATTTAA C C CCAAAAATCTAGTAACTTTA C C T T T T Jafdo 1.400 1.400 1.400 AATGATAAATCTAGTAACTTTA C C C GO .600 .600 1.400 AATGATGAAAATCTAGTAAAATCTCCC G .600 .600 G	1080 1080 1080 1080 1080 1200 1200 1200
VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64	ACGTATERD1 CURE 1,00 STCTCTCCCTCTGTGTGTGCGTTTTGGT ACCCTGTTGATTAGCGTAGGATCAGGC AACCCTGTTGATTAGCGTAGGATCAGGA CAAGAAAAGAA	CURE 1.20 GCAGT ACAAAT TG TA 1.240 AT GCACGC TG GGGC G MYCCONSENSUSAT 1.300 TC CAT TG CT GC TG CGA TG CT GC TG CT G GGA TG CAACAAGC TT TT CCAT GT TG CT GC TG G GGA TG CAACAAGC TT TT TAACGAAGG TA TC G G C C C C C C C C C C C C C C C C C	е ;CURE CGTATERD1 ;; GGT IT TASTACTAGCTAG CURE TCGCTCTTAGCTAACGACTAG TCGCTCTTAGCAAAGAGCAACT TACATTGCAAAGAAGCAACT TACATTGCAAGAACCAG TACATTGCAAGAACCAG TACATTGCAAGAACCAG TACATTGCAAGAACCAG TACATTGCAAGAACCAG	JURE STAGTATCTGCTTGGACAC CURE ACCGTACCTTGACTTTCT MYCCONSENSUSAT AGGAAGTGACGATGTATT AGGAAGTGACGATGCTATT AGGAAGTGACGATACTAATT 20 TTTTAAATAAAAAAGACTTG 40 21 TTTGTCGCTATACTTAAAAA	1,100 ACGTATERD1 1.200 ACGTATERD1 1.200 MYCCONSENSUS 1.400 MYCCONSENSUS 1.400 MYCCONSENSUS 1.400 CURE AAAATTAGTAGTCATACCGT 1.500 CURE AAAATTAGTAGTCATACCGT G. G. G. 1,400 1,400 1,400 C. C. C. C. C. C. C. C. C. C.	1,160 CURE 1,200 CTGCACTGTACTTCTACTTCCT 1,300 1,320 1,300 1,320 1,320 TGCATCGAGTGGTATCAACCTA 1,400 1,400 ATCCCAGTATACGCTATTCTAC C C CCCAAAATATAAGTATTTTAA C C CC C C 1,540 1,560 1,560 ATCCCAAATATAAGTATTTTAA C C C C C T T T	1080 1080 1080 1080 1080 1200 1200 1200
VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA	АССТАТЕRD1 CURE 1,100 GTCTCTCCTTGTGTGGGTTTTGGT AACCCTGTTGATTAGCGTAGGATCAGGC 1,20 AACCCTGTTGATTAGCGTAGGATCAGGC 1,340 1,500 1,50	CURE LID / GCA CT AC AAAT T GT A 1240 ATGCACGC TGGGGCC ATGCACGC TGGGGCC MYCCONSENSUSAT 1.340 .GGATGCAACGACGT TA C .G. .G. .G. .G. .G. .G. .G. .G. .G. .G	E CURE CGTATERDI II COLTTABTACTAGCTAG CURE TCGCTCTTAGCTAGCTAG TACATTGCAAGAAGCAACT TACATTGCAAGAAGCAACT TACATTGCAAGAAGCAACT T. T. T. T. T. T. GATCAGGGGGCCTGGACT	UVRE TAGTATCTGCTTGGACAC CURE AGCGTACCTTGACTTTGT MYCCONSENSUSAT ACCAAGTGACGAGTGATGTATT ACCAAGTGACGATGATGTATT ACGACACACATACTAATT ACGACACACACATACTAATT ACGACACACATACTAATT ACGACACACACATACTAATT ACGACCACACACATACTTAAAA ACGACCACACACATACTTAAAA ACGACCACACACATACTTAAAA	1,100 ACGTATERD1 1.200 ACGTATERD1 1.200 CURE 1.400 MYCCONSENSUS 1.400 MYCCONSENSUS 1.400 CURE 1.400 CURE AAAATTAGTAGTCATACCGT G. G. G. G. 1.500 CURE AAAATTAGTAGTCATACCGT G. G. G. I.500 CURE AAAATTAGTAGTCATACCGT G. G. I.500 CURE AAAATTAGTAGTCATACCGT G. G. I.500 CURE AAAATTAGTAGTCATACCGT G. I.500 CURE AAAATTAGTAGTCATACCGTATGTCATACCGT I.500 CURE AAAATTAGTAGTCATACCGTATGTCATACCGT I.500 CURE AAAATTAGTAGTCATACCGTATGTCATACCGT I.500 CURE AAAATTAGTAGTCATACCGTATGTCATACCGT G. I.500 CURE AAAATTAGTAGTCATACCGTA G. I.500 CURE AAAATTAGTAGTCATACCGTAGCGTATGTCATACCGT I.500 CURE AAAATTAGTAGTCATACCGTATGTCATACCGTATGTCATACCGTAGTCGTATGTCATACCGTAGTCGTATGTCATACCGTAGTCGTATTAAACCGTAGTCGTATTAAACCGTAGTCGTATTAAACCGTAGTCGTATTAAACCGTAGTCGTATTAAACCGTAGTCGTAGTCGTATTAAACCGTAGTCGTAGTCGTAGTCGTAGTCGTAGTCGTAGTCGTAGTCGTATTAAACCGTAGTCGTAG	1,160 CURE 1,200 CTGCACTGTACTTCTACTTCCT 1,200 1,200 1,200 1,200 1,200 1,200 1,200 1,200 TCCATCGAGTGGTATCAACCTA 1,200 1,200 ATCCCAGTGTGTATCGACCTA 1,200 1,200 1,500 1,440 1,200 CCCAAAATATAAGTATTTTTAA C. C. CC C. C. 1,800 1,600 1,600 AATGATAAATCTAGTAACTTTA T. T. 1,800 1,600 1,600 AATGATGAAAATCTAGTAACTTAC T. T. 1,800 1,600 1,600 C. C. C. T.	1080 1080 1080 1080 1080 1200 1200 1200
VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA	ACGTATERD1 CURE 1,00 GTCTCTCCCTCTGTGTGTGCGTTTTGGT AACCCTGTTGATTATTACCGTAGGATCAGGC 1340 CAAGAAAAGAAAAAAAATGAACGAGAAA TTTAATTAAGTGCTCCATGAGCAAAACA ATCCTGACACGGTCTTCGAGATGCTAAT 1,00 ATCCTGACACGGTCTTCGAGATGCTAAT 1,00 ATCCTGACACGGTCTTCGAGATGCTAAT 1,00 ATTTTACTGATTATTTTTATTTTCTTTT A. A. A. A.	CURE 110 P GCAGTACAAATTGTA 1340 ATGCACGCTGGGGCC MYCCONSENSUSAT 1350 TCATGTACTACAAGCTTGCTG 1350 140 140 150 170 170 170 170 170 170 170 170 170 17	E ICURE GGTATERD1 IL CURE CURE TGGCTCTTAGTAGTAGCTAG CURE CURE CURE CURE CURE CURE CURE CURE	JURE TAGTATCTGCTTGGACAC CURE COURE COURE CONSENSUSAT CONSENSUS CONSENS CONSENSUS CONS	1,100 ACGTATERD1 1.200 ACGTATERD1 1.200 ACGTTGTTATTAGTTATT 1.200 ACGTTGTCAGCAAGGAGA 1.400 MYCCONSENSUS 1.400 MYCCONSENSUS 1.400 CURE AAAATTAGTAGTAGCATGCATT 1.200 CURE AAAATTAGTAGTAGTAGCATGCATT 1.200 CURE AAAATTAGTAGTAGTCATACGT C. C. C. 1.700 ATGCT-TATATTAGTAGTTGTTT, C. C. 1.700 ATGCT-TATATTTTGGGATG 1.400 LTRECORE 1.400 LTRECORE	1,100 [CURE 1,200 CTGCACTGTACTTCTACTTCCT 1,300 1,200 1,300 1,200 1,200 TCCATCGAGTGGTATCAACCTA 1,200 1,200 TCCATCGAGTGGTATCAACCTA 1,200 1,200 TCCATCGAGTGGTATCAACCTA 1,200 1,200 TCCCAGTATACGCTATTCTAC 1,200 1,200 TACCCAAAATATACGCTATTCTAC C C CAAAAATATAAGTATTTTA C C C C C T, T T T T, T T T T T, G G G G G G G T G G T T G G T T G <th>1080 1080 1080 1080 1080 1200 1200 1200</th>	1080 1080 1080 1080 1080 1200 1200 1200
VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64	АССТАТЕRD1 CURE 1,00 STCTCTCCCTCTGTGTGCGTTTTGGT ACCCTGTTGATTACCGTAGGATCAGGC AACCCTGTTGATTACCGTAGGATCAGGC 1,20 1,30 CAAGAAAAGAAAAAAAAATGAACGAGAAAACA 1,30 TTTAATTAAGTGCTCCATCAGGAAAACA ATCCTGACACGGTCTTCGAGATGCTAAT 1,500 ATTTTACTGATTATTTTTTTTTTTTTTTT A. A. A. A. A. A. A. A. A. A.	CURE 1.10 / GCAGTACAAATTGTA 1.240 ATGCACGCTGGGGGG MYCCONSENSUSAT 1.340 TCCATGTGCTTGCTG GGATGCAACAAGCTT 1.400 GGATGCAACAAGCTTATCA 1.400 TTAACGAAGGTTATCA G. G. G. G. G. G. G. G. G. G. G. G. G.	E ICURE COTATERDI II COTTATATACTACTAC CURE TCGCTCTTAGCAAAGAACCAACT TACATTGCAAAGAAGCAACT TACATTGCAAAGAACCAT TATAAAAAGTAAGAACCAT T.T.T.T.T. AATTAAAAAGTAAGAATTTTGAC	UPRE TAGTATCTGCTTGGACAC CURE ACCGTACCTTGACTTTCT MYCCONSENSUSAT ACCGAAGTGACCATGCTATT ACCGAAGTGACCATACTAATT ACCGAAGTGACCATACTAATT ACCGAAGTGACACATACTTAAAA ACCGAAGTGACACATACTTAAAA ACCGAAGTGACACATACTTAAAA ACCGATCGTCAGTGTGTG TG	1,100 ACGTATERD1 TCCAGGT TGTTATTAGTTAT 1,200 CGTATERD1 TCAGGT TGTCAGCAAGGAGA 1,400 MYCCONSENSUS 1,400 MYCCONSENSUS 1,400 CURE 1,400 CURE AAAATTAGTAGTCATACCGT 1,500 CURE AAAATTAGTAGTCATACCGT G 1,500 CURE AAAATTAGTAGTCATACCGT G 1,500 CURE AAAATTAGTAGTCATACCGT G 1,500 CURE AAAATTAGTAGTCATACCGT G 1,500 CURE AAAATTAGTAGTCATACGGT G 1,500 CURE 1,500 CURE AAAATTAGTAGTCATACGGT G 1,500 CURE 1,500 CURE AAAATTAGTAGTCATACGGT G 1,500 CURE AAAATTAGTAGTCATACGGT G LTRECORE 1,500 LTRECORE 1,500 LTRECORE	1,160 CURE 1,200 CTGCACTGTACTTCTACTTCCT 1,200 1,200 1,200 1,200 1,200 1,200 1,200 1,200 TCCATCGAGTGGTATCAACCTA 1,200 1,200 1,200 1,200 1,200 TCCATCGAGTGGTATCAACCTA 1,200 1,200 1,200 1,200 1,200 1,200 1,200 1,200 1,540 1,550 1,550 CCCAAAATATAAGTATTTTAA C C CC C C C C T T T T T T	1080 1080 1080 1080 1200 1200 1200 1200
VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA	ACGTATERD1 CURE 1,100 GTCTCTCCTTGTGTGTGCGTTTTGGT ACCCTGTTGATTAGCGTACGATCAGGC AACCGTGTTGATTAGCGTACGATCAGGC CAAGAAAAGAA	CURE LIZO GCA GT AC AAAT T GT A 1240 CAT GCA CGC T GG GG CG AT GCA CGC T GG GG CG AT GCA CGC T GG GG CG CAT GT GC T GC T G GG AT GCA AC AA GC T T T TAACCAACG T AT C G G G C T CT AT T AA AA CG GG T AA 140 SGT AA T AA AC GG GT AA	E CURE CGTATERDI U COLLE	JURE ITAGTATCTGCTTGGACAC CURE ACCGTACCTTGACTTTCT MYCCONSENSUSAT ACCAAGTGACGATGTATT ACCAAGTGACGATGATGTATT ACCAAGTGACGATACTAATT ACCAAGTGACGATACTAATT ACCAAGTGACGATACTAATT ACCAAGTGACGATACTAATT ACCAAGTGACGATACTTAAAA ACCAAGTGACGATACTTAAAA ACCAAGTGACGATACTTAAAA ACCAAGTGACGATACTTAAAA ACCAAGTGACGATACTTAAAA ACCAAGTGACGATACTTAAAA ACCAAGTGACGATACTTAAAAA ACCAAGTGACGATACTTAAAAAAGACTTG ACCAAGTGACGATACTTAAAAAAGACTTG ACCAAGTGACGATACTTAAAAAAGACTTG ACCAAGTGACGATACTTAAAAAAGACTTG ACCAAGTGACGATACTTAAAAAAAGACTTG ACCAAGTGACGATACTTAAAAAAGACTTG ACCAAGTGACGATACTTAAAAAAGACTTG	1,100 ACGTATERD1 1.200 CGTGTTGTTATTAGTTATT 1.200 CGTGTTGTCAGCAAGGAGA 1.400 MYCCONSENSUS 1.400 MYCCONSENSUS 1.400 MYCCONSENSUS 1.400 MYCCONSENSUS 1.400 MYCCONSENSUS 1.400 MYCCONSENSUS 1.400 GCURE AAAATTAGTAGTCATACCGTU G.G.G.G.G.G.G.G.G.G.G.G.G.G.G.G.G.G.G.	1,140 CURE 1,200 CTGCACTGTACTTCTACTTCCT 1,300 1,320 1,300 1,320 1,320 TCCATCGAGTGGTATCAACCTA 1,200 1,200 TCCATCGAGTGGTATCAACCTA 1,200 1,200 TCCATCGAGTGGTATCAACCTA 1,200 1,200 TCCCATCGAGTATCGCGCTATTCTAC 1,200 1,200 TCCCAAAATATAAGTATTTTTAA C C CC C C	1080 1080 1080 1080 1080 1080 1080 1080 1200 1560 1680 1680 1680 1690 1791 1791 1917 1911 1919 1918
VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64	ACGTATERD1 CURE 1,00 STCTCTCCCTCTGTGTGTGCGTTTTGGT AACCCTGTTGATTACCGTAGGATCAGGC AACCCTGTTGATTACCGTAGGATCAGGC CAAGAAAAGAA	CURE LID P GCAGTACAAATTG A GGAGTACAAAATTG A 1,240 ATGCACGCCGGGGGG MYCCONSENSUSAT LICEATGTGCTTGCTG LICEATGTGCTTGCTG GGATGCAACAAGCTT TTAACCAACGAGCTTATC G. G. G. C. C. C. C. C. C. C. C. C. C. C. C. C.	E ICURE COTATERDI II COURE COURE TCGCTCTTAGTAGTAGCTAG TCGCTCTTAGCTAAAGA TTCTAAAAAAGTAAGAACCA TACATTGCAAAGAACCA TATAAAAAAGTAAGAACCA TATAAAAAAGTAAGAAACCA GATCAAGGGGCCTGGAAT	JURE STACTATCTGCTTGGACAC CURE ACCGTACCTTGACTTTCT MYCCONSENSUSAT AGGAAACTGACGATGTATT AGGAAACTGACGATGTATT AGGAAACTGACGATGTATT AGGAAACTGACGATGTATT CO TTTTAAATAAAAAAGACTTG G CGATCGTCAG TGTGTG TG 	1,100 ACGTATERD1 1208 CGTATERD1 1208 CGTATERD1 1 TO ACGTITGTCAGCAAGGAGA 1.400 MYCCONSENSUS 1.400 MYCCONSENSUS 1.400 MYCCONSENSUS 1.400 CURE AAAATTAGTAETCATACCGT G G G 1.400 CURE AAAATTAGTAETCATACCGT G G G	1,160 CURE 1,200 CTGCACTGTACTTCTACTTCCT 1,300 1,320 1,300 1,320 1,320 TGCATCGAGTGGTATCAACCTA 1,440 1,440 ATCCCAGTATACGCTATTCTAC 1,440 1,440 ATCCCAGTATACGCTATTCTAC 0,000 1,000 ATCCCAGTATACGCTATTTTTAA 0,000 1,000 ATGATAAAATCTAGTAATTTTTAA 0,000 1,000 ATGATAAAATCTAGTAATTTTAA 0,000 1,000 ATGATAAAATCTAGTAATTTT 1,000 1,000 ATGATGATTGAGAGAAAAATCTCCCC 0,000 1,000 G 0,000 1,000 1,000 ATGGTTGAGAGAAAAATCTCCCC 0,000 1,000 1,000 G 0,000 1,000 1,000 1,000 C 0,000 1,000 1,000 1,000 1,000 G 0,000 1,000 1,000 1,000 1,000 1,000 1,000 1,000 1,000 1,000 1,000 1,000 1,000 1,000 1,000 1,000	1080 1080 1080 1080 1080 1200 1200 1200
VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA	ACCTATERD1 CURE 1,00 STCTCTCCCTCTGTGTGCGTTTTGGT ACCCTGTTGATTACCGTAGGATCAGGC AACCCTGTTGATTACCGTAGGATCAGGC 1,20 1,30 CAAGAAAAGAAAAAAAAATGAACGAGAAA 1,30 TTTAATTAAGTGCTCCATCAGGAAAACA 1,400 TTTAATTAAGTGCTCCATCAGGAAAACA ATCCTGACACGGTCTTCGAGATGCTAAT 1,500 ATCCTGACACGGTCTTCGAGATGCTAAT 1,500 TGATTGATGATCCAATGGCATCCGGGCC 1,500 TGATTGATGATCCAATGGCATCCGGGCC	CURE 1.10 / GCAGTACAAATTGTA 1240 ATGCACGCTGGGGGG ATGCACGCTGGGGGG MYCCONSENSUSAT 1.340 .CGATGTACTTGCTG .GGATGCAACAAGCTT TCATGTACAAGAGGTTATCA .GGATGCAACGAGGTTATCA .G. .G. .G. .G. .G. .G. .G. .G. .G. .G	E ICURE COTATERDI II COTTATATACTACTAC CURE TCGCTCTTAGCAAAGCAACTA TACATTGCAAAGAAGCAACT TACATTGCAAAGAAGCAACT TATAAAAAGTAAGAACCAT TATAAAAAGTAAGAACT T. 	UVRE ITAGTATCTGCTTGGACAC CURE ACCGTACCTTGACTTTCT MYCCONSENSUSAT ACGAAGTGACGATGTATT AGGAAGTGACGATGATGTATT AGGAACACACATACTAATT AGGACACACACATACTAATT AGGACACACACATACTAATT AGGACCACACATACTTAAAA AGGACCACACATACTTAAAA AGGACCACACATACTTAAAA AGGACCACACATACTTAAAAA AGGACCACACATACTTAAAAA AGGACCACACATACTTAAAAA AGGACCACACATACTTAAAAA AGGACCACACATACTTAAAAA AGGACCACACATACTTAAAAAAGACTTG AGGACCACCACATACTTAAAAA AGGACCACACATACTTAAAAAAGACTTG AGGACCACCACATACTTAAAAAAGACTTG AGGACCACCACATACTTAAAAAAGACTTG AGGACCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	1,100 ACGTATERD1 TCCAGGT TGTTATTAGTTAT 1,200 ACGTATERD1 TCAGGT TGTCAGCAAGGAGA 1,400 MYCCONSENSUS 1,400 MYCCONSENSUS 1,400 CURE 1,400 CURE 1,40	1,160 CURE 1,200 CTGCACTGTACTTCTACTTCCT 1,200 1,200 1,200 1,200 1,200 1,200 1,200 1,200 TCCATCGAGTGGTATCAACCTA 1,200 1,200 1,200 1,200 1,200 TCCATCGAGTGGTATCAACCTA 1,200 1,200 1,200 1,200 1,200 1,200 1,200 1,200 1,200 1,200 1,200 CCCAAAATATAAGTATTTTAA C C CC	1080 1080 1080 1080 1080 1080 1200 1200
VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA	ACGTATERD1 CURE 1,00 GTCTCTCCCTCTGTGTGTGCGTTTTGGT MYBCORE L220 AACCCTGTTGATTATTAGCGTACGATCAGGC 1,20 AACCCTGTTGATTATTAGCGTAAGAAAAAAAAAAAAAGAAAAAAAGAAAAAAAA	CURE LID P GCAGTACAAATTGTA ISAO ATGCACGCTGGGGCC ISATGCACGCTGGGGCC ISATGCACGCTGGGGCC ISATGCACGCTGGGGCC ISATGCACGCTGCTG ISACCAACGATGCTT ISACCCAACGAGCTT ISACCAACGAGCTATCA G. G. G. ISACCAACGAGCGTAATCAA ISAO IGTAATAAACGCGTAA ISAO IGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	E CURE CGTATERD1 11 COLTTABTACTAGCTAG CURE TCGCTCTTAGCTAACTAG TACAATTGCAAGAAGCAACT TACAATTGCAAGAAGCAACT TATAAAAAGTAAGAACCA GATCAGGGGCCTGGACT AGTTGCTGCTGCA	URE TAGTATCTGCTTGGACAC CURE CURE CURE CONSENSUSAT COCONSENSUS COCONSENSUS	1,100 ACGTATERD1 1,200 ACGTATERD1 1,200 CGTATERD1 1 TC ACGT TGT CAGCAAGGAGA 1,400 MYCCONSENSUE 1,400 MYCCONSENSUE 1,400 MYCCONSENSUE 1,400 MYCCONSENSUE 1,400 G. 1,400 LTRECORE	1,140 [CURE 1,200 CTGCACT GTACTTCTACTTCCT 1,200 1,200 1,200 1,200 1,200 TCCATCGAGTGGTATCAACCTA 1,200 1,200 TCCATCGAGTGGTATCAACCTA 1,200 1,200 TCCATCGAGTGGTATCGACCTA 1,200 1,200 TCCCAGTATACGCTATTCTAC C C CCAAAAATATAAGTATTTTAA C C CCAAAAATCTAGTAACTTTA T T AATGATAAATCTAGTAAACTTTA T T 1,200 1,200 1,200 AATGATGATGAGAGAAAATCTCCC G G GATGGTTGAGGAGAAAATCTCCC G G GCAACGTCCCCCCCCCCCCCCCCCC G 1,200	1080 1080 1080 1080 1080 1200 1200 1200
VANDANA PB11 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA	ACGTATERD1 CURE 1,00 STCTCCCCTCTGTGTGTGCGTTTTGGT ACCCGTGTTGATTAGCGTAGGATCAGGC AACCCGTGTTGATTAGCGTAGGATCAGGC CAAGAAAAGAA	CURE 1.20 GCAGT ACAAAT TG A GGAGT ACAAAT TG A 1.240 ATGCACGCC TGOGGCG MYCCONSENSUSAT 1.300 TC CATGT GC TG CTG CGA TGCACGAGGT TG CTG 1.400 GGATGCAACAAGCT T TTAACCGAGGT TA TC G. G. G. G. G. G. G. G. G. G. G. G. G.	е ICURE CGTATERD1 II CGTITTASTACTAGCTAG CURE TCGCTCTTAGCTAACTAG TCGCTCTTAGCTAACAGCAACT TACATTGCAAAGAACCAACT TACATTGCAAAGAACCAACT TATAAAAAGTAAGAACTA TATAAAAAGTAAGAACTA TATAAAAAGTAAGAACTA TATAAAAAGTAAGAACTA TATAAAAAAGTAGAAGAACTA TACATTGCAAGAAGCCAACTA GATCAGGGGCCTGGAACT	JURE ITAGEATATCTGCTTGGACAC CURE ACCGTACCTTGACTTTCT MYCCONSENSUSAT AGGAAGTGACGATGTATT AGGAAGTGACGATGATGTATT AGGAAGTGACGATACTAATT CONTACTAAAAAAAAGACTTG CGATCGTCGCCAGCAGCAGCGGG CGCTCGCCGCGCGCGCGGGGGGGGGGGGGGGGG	1,100 ACGTATERD1 1.200 CGTATERD1 1.200 MYCCONSENSUS 1.400 CURE AAAATTAGTAGTAGCATACCGT G	1,160 CURE 1,200 CTGCACTGTACTTCTACTTCCT 1,300 1,320 1,300 1,320 1,320 TGCATCGAGTGGTATCAACCTA 1,400 1,400 ATCCCAGGTATACGCTATTCTAC 1,400 1,400 1,540 1,540 1,540 1,540 1,550 1,550 CCCAAAATATAAGTATTTTAA C C C C C 1,540 1,550 1,550 CATGGTAAAATCTAGTAACTTTA C C C C C C C C 1,550 1,550 1,550 C C C C C C C C C	1080 1080 1080 1080 1080 1080 1200 1200

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	20	10	MYCCONSENSUSAT	MYCCONSENSUSAT	ACGTATERD1	
N22	GCCTCGGCGTCGATGCCATCTATTAGCAC	TAGCACTAGTATTTATAG	TATCCATCTGGTTTGGCGTTTC	CTTGCCACTTGCCCATGATTC	CCACTCCTACGTCCTCTTGCCAGTTGCCAC 1	120
VANDANA						120
IR64						120
	140	160	180	200	ACGTATERD1	
N22	AGCATGATGACCAATGCAGCAGCAGCACT	CGAGGAAGGAGAGCCGGAC	GGGGCAATGCGCCGGCGAGCGG	GCCGAAAAGGAGGGGGGAAGGT	AAGGTACGTAAGCGTTGGATAGTGGCGGTT 2	240
VANDANA						240
IR64						240
			MYCCONS	ENSUSAT	MYCCOMPENDING AT	
N22	200 I IIIGACCCAGACTCGITCCAAACATGACGC					360
VANDANA						360
PB1					G	360 260
1104	380 I	400	420 I	440	460 480	100
N22	GTCGATCACCAACCATGATTATCAGATTA	ATCTAGGATAAAGTGAAGTG	AGTATAACTTATCTGGTTAGT	TTTTTTTTTTGGAACTAACTC	ATCCAGGTTAAGTCATAAACTTGACACGAG 4	180
PB1			т	• • • • • • • • • • • • • • • • • • • •	G	179
IR64					G	179
	500	520 CURE	BFHV 540	560	580 600	
N22	TGCTCGTATTTATTGCTTATTAGTTTTTA	AGTGGTAGGCAGCGTACCCG	ICGACAGCGAGATACCAGTGG1	TACTTTGTCAATTTCAAGAT	ATGTCCGTCCAATCTTTTGGAGATGCTCAT	500
VANDANA PB1						300 500
IR64						599
N22	AGAGATATGGTGTGCGTATGTGTGTCAT		000 I STAGGGATGTGCGTGTGTGTG		700 720 I TAGGGATGTGCGTGTGT TTATAGAGATG 7	718
VANDANA						718
PB1	A		CTA.AG		G	718
1104						10
	CURE 740	CURE 780	780 I	800 I	820 840 I I	
N22 VANDANA	AGTGTACCCGTGTCATGAACGCGTGCGTT	TTGTACTATGTTTCTAAAAC	AAAATTATGGGATAAAATACT/	ATACCTACATGTTGCTTCCAC	CTATAAACTTTTCACTTATTCAAAGCATCA 8	338 838
PB1		G				338
IR64	A	G				338
	MYBCORE 880	880	900	920	940 950	
N22	TGTTTCATGCCATACGGTTGCAAATTACT	TAAATTAGGCAGCGGGAAGC	CACCTCTTAAGCTAGTCAGACO	BATCACCTCAACAGAGCCAGC	TCCTCTGCTTTTAGGGGCTGAAGGTAGAGG 9) 58
VANDANA PB1)58 958
IR64						958
		1000	1000 CURE CURE	1040	1000 CURE 1000	
M22	CGTAGGGTAAAATGATCCTGCTACTACAG	TAGGGACAGTAATTTGTAG	TAATTACTATAGGTACAGTAC	AAAACACAGTAAATACAGTG	TTCCCGAATATTGTTTATGATGTACCTAGT 1	1078
1422						
VANDANA						1078
VANDANA PB1 IR64						1078 1078 1078
VANDANA PB1 IR64				ACCTATERDI		1078 1078 1078
VANDANA PB1 IR64	1,500	1,120 MYCCONSE	NSUSAT 1,140	ACGTATERD1	1	1078 1078 1078
VANDANA PB1 IR64 N22	1,00 ATACTGTAGTGATCGATCTCATTCC	1.120 MYCCONSE	NSUSAT 1,140 I JAATATCCCAAAGTAATGGCA(JACGTATERD1 JCURE 1,000 IT GTAGGTCTCTCTGACTTCA	1,100 1,200 1,100 1,200 TTATGTGAAGTCAGTGGATCCCAATCCCTG	1078 1078 1078
VANDANA PB1 IR64 N22 VANDANA PB1	LING ATACTGTAGTGATCGATCTCATTCATTC	1,120 MYCCONSE	NSUSAT 1,140 JAATATCCCAAAGTAATGGCA(IACGTATERDI CURE 1,100 DIGTACGTCTCTCTGACTTCA	1,00 1,200 TTATGTGAAGTCAGTGGATCCCAATCCCTG 1	1078 1078 1078 1198 1198 1198
VANDANA PB1 IR64 N22 VANDANA PB1 IR64	1,00 ATACTGTAGTGATCGATCCGATCCGATCCG	1,20 MYCCONSE SCTGTAAATCGGA <mark>GAACTG</mark> AC	NSUSAT 1,140 SAATATCCCAAAGTAATGGCA(ACGTATERD1 CURE 1,00 DTSTREGTCTCTCTGACTTCA	1,00 120 TTATGTGAAGTCAGTGGATCCCAATCCCTG 1 1	1078 1078 1078 1198 1198 1198 1198
VANDANA PB1 IR64 N22 VANDANA PB1 IR64	LINO ATACTGTAGTGATCGATCGATTCATTCC LITRECOREATCOR15	1,30 MYCCONSE SCTGTAAATCGGA <mark>GAACTG</mark> AG	NSUSAT 1,160 SAATATCCCAAAGTAATGGCAG	ACGTATERD1 CURE 1,100 TGTACGTCTCTCTGACTTCA	1,100 1300 TTATGTGAAGTCAGTGGATCCCAATCCCTG 1 1 1 1 1 1	1078 1078 1078 1198 1198 1198
VANDANA PB1 IR64 VANDANA PB1 IR64	1.00 ATACTGTAGTGATCGATCTCATTCATTCC LITRECOREATCORIS (CBFHY 1.20	LIJO MYCCONSE SCTGTAAATCOGACAACTGA 1240	NSUSAT 1,140 GAATATCCCAAAGTAATGGCAG 1280	ACGTATERDI CURE 1,100 TOTAGGTCTCTCTGACTTCA	1.100 1.200 TTATGTGAAGTCAGTGGATCCCAATCCCTG 1.100 1.100 1.100 1.100 1.100	1078 1078 1078 1198 1198 1198 1198
VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA	1,00 ATACTGTAGTGATCGATCTCATTCATTCC ,LTRECOREATCOR15 CBPHV 1,200 CTCARGEGRETACCGCCGATATTTGAAAA	ILIO MYCCONSE SCTGTAAATCGGADAACTGA 1340 1340	NSUSAT 1.140 GAATATCCCAAGTAATGGCAG 1.200 AAACACTATTAATTGTTTAGAG	ACGTATERD1 COVER 1,400 DT BT A GOT CT CT CT GA CT TC A 1,200 TC CAACGAT AT CGT TAGGT CC	1.100 1.300 TTATGTGAAGTCAGTGGATCCCAATCCCTG 1 1 1.300 1.300 ATTACTTGAGTTATACATAATCAGA 1	1078 1078 1078 1198 1198 1198 1198
VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA PB1 PB1 IR64	LIOD ATACTGTAGTGATCGATCTCATTCATTCC LLTRECOREATCOR15 CEPHY 1,200 CTCA ACEGAR TACCGCCGATATTTGAAAA	1,20 MYCCONSE 3CTGTAAATCGGAEAACTEA 1,300 AAAAAATAGCTAGCCAATAAA G	NSUSAT 1.140 SAATATCCCAAAGTAATGGCAG 1.340 AAACACATTATTAGTTTAGAG G	LACOTATEDI CURE Late TSTARGETOTOTOTACTTCA 1200 STCAACGATATCGTTAGGTCC G T	1.100 1.200 TTATGTGAAGTCAGTGGATCCCCAATCCCTG 1 1 1 1.200 1.200 ATTACTTGAGTTATACATAACTATATAGGA	1078 1078 1078 1198 1198 1198 1198 1198 1318 1318 131
VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64	LING ATACTGTAGTGATCGATCTCATTGATTCC LITRECOREATCORIS CGPFNY 1220 CTCA RCEGARC TACCGCCGATATTTGAAAA	1,00 MYCCONSE 3CTOTAAATCCGAEAACTEA 1200 AAAAAATAGCTAGCAATAA 	NSUSAT 1.10 SAATATCCCAAAGTAATGGGA 1200 AAAACACTATTAATTGTTAGAC G. G.	40001ATERD1 CURRE 1,100 TISTARGECTCTCTGACTTCA 1200 CTCAACGATATCGTTAGCTCC 0. T. 	1,100 1,200 TTATGTGAAGTCAGTGGATCCCAATCCCTG 1 1 1 1,300 1,300 ATTACTTGAGTTATACATAACTATATAGGA 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1078 1078 1078 1198 1198 1198 1198 1198 1318 1318 131
VANDANA PB1 IR64 N22 VANDANA PB1 IR64 VANDANA PB1 IR64	LINO ATACTGTAGTGATCGATCGTTGATTCG LUTRECOREATCORIS (CBFNV 120 CTCAAGCGGARTACCGCCGATATTTGAAAA 1340	1,50 МУССОНSE SCTGTAAATCGGAEAACTEAA 1,500 Алалалатаgctagccaataa 	NSUSAT 1,160 3AATATCCCAAAGTAATGGGAG 1,200 AAAACACTATTAATTGTTAGAG G. 	LACGTATERDI CURE 1,100 TISTAGGICICOTGACTICA 1,200 CICAACGATATCGITAGGICC 	1.100 1.200 TTATGTGAAGTCAGTGGATCCCAATCCCTG 1 1.100 1.200 TTATGTGAAGTCAGTGGATCCCAATCCCTG 1 1.100 1.200 ATTACTGAGTTATAGATAACTATATAGGA 1 1.100 1.400	1078 1078 1078 1198 1198 1198 1198 1318 1318 1318 131
VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA	Ligo ATACTGTAGTGATCGATCTCATTCATTCC LTRECOREATCORIS COPINY 1220 CTCAAGCGGACTACCCCCGATATTTGAAA 1246 ATCAACATCGGATATACAGATAACTTGC1	1.10 МУССОЛЯВ ЗСТОТАЛАТСОДА ДААСТОА 1.20 1.20 ААААААТАСТАДССААТАА 	NSUSAT 1,140 GAATATCCCAAAGTAATGGCAG 1,200 AAAACACTATTAATTGTTTAGAG 	исссататело! ССИРЕ 1.190 ОТ ОТ АВОСТСТСТСТСАСТТСА 1.200 СТСААССАТАТССТТАССТСС СТСААССАТАТССТТАССТС 0. Т. 	1.100 1.300 ТТАТБТБААĞТСАĞТĞĞATCCCAATCCCTG 1.200 1.300 АТТАСТТĞАĞТТАТАСАТААСТАТАТАĞĞ АТТАСТТĞАĞТТАТАСАТААСТАТАТАĞĞ 1.200 1.400 сСССССТТТАААТСАААĞĞAAAAATCATAĞ	1078 1078 1078 1198 1198 1198 1198 1318 1318 1317 1317 1317
VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1	1,00 ATACTGTAGTGATCGATCTCATTCATTCC LITRECOREATCOR15 CEPHY 1,200 CTCARECERETACCGCCCGATATTTGAAAA 1,340 ATCAACATCGGATATACAGATAACTTGCT	1.300 MYCCONSE 3CTGTAAATCGGA BAACTBA 1.300 AAAAAATGGCTAGCCAATAA G G G G G G G G G G G G G G G G G	NSUSAT 1:10 SAATATCCCAAAGTAATGGCAG 1.200 AAACACTATTAATTGTTTAGAG G. CCONSENSUSAT:230 FARTEGGCTACTATCAAGTAGAA	ACGTATERD1 CUTE 1400 CT 14 ACG CT CT CT GT ACT CA 1,500 CT CT ACG CT CT CT GT ACG CT C CT CT ACG CT CT CT CT CT CT CT CT C	1.100 1.300 ТТАТБТБААБТСАОТОБАТСССААТСССТБ 1 1.300 1.300 АТТАСТТОАОТТАТАСАТААСТАТАТАБСА 3 ССССССТТТАААТСАААСБАААААТСАТАБ 3 ССССССТТТАААТСАААСБАААААТСАТАБ	1078 1078 1078 1198 1198 1198 1198 1318 1318 1318 131
VAIDANA PB1 IR64 VAIDANA PB1 IR64 VAIDANA PB1 IR64 VAIDANA PB1 IR64	1,00 ATACTGTAGTGATCGATCTCATTCATTCC LITRECOREATCOR15 CEPHY 1,20 CTCAACCGGACTACCGCCGATATTTGAAAA 1,30 ATCAACATCGGATATACAGATAACTTGCT	1.100 MYCCONSE 3CTGTAAATCGGA BAACTBA 1.400 AAAAAATAGCTAGCCAATAA G. G. G. HITGACATGAATTATTGA BA 1.400	NSUSAT 1.140 SAATATCCCAAAGTAATGGCAA 1.260 AAACACTATTAATTGTTTAGAA G G CONSENSUSAT 1.360 FATEGGCTACTATCAAGTAGAA	ACCTATED1 CURE two TETARCECTCTCTGACTTCA 1,200 TCAACGATATCGTTAGCTCC 	1,100 1.200 TTATGTGAAGTCAGTGGATCCCAATCCCTG 1 1,200 1.200 ATTACTTGAGTTATACGATACTATATAGGA 4,100 1,200 1.200 1,200 1.400 GCCCCCTTTAAATCAAAGGAAAAAATCATAG 1 1,200 1.400 5,100 1.200 1.400 5,100 1.200 1.400 5,100 1.20	1078 1078 1078 1198 1198 1198 1318 1318 1318 1317 1317 1317 1317 1438 1438 1437
VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA PB1 IR64	۱.00 ATACTGTAGTGATCGATCTCATTCATTCC ILTRECOREATCORIS CCPFNU CTCAACCGGATACCGCCGATATTTGAAAA 1.30 ATCAACATCGGATATACAGATAACTTGCI 1.40 AAATTCTAGAGGATTTTATCCGTATGGAAA	1,00 MYCCONSE 3CTGTAAATCCGGAEAACTEA 1200 AAAAAATAGCTAGCCAATAA 	NSUSAT 1.10 SAATATCCCAAAGTAATGGCAG AAAACACTATTAATTGTTTAGAG G. CCONSENSUSAT 1.300 LATGGGCTACTATCAAGTAGAA 1.000 TITGGAACGGAGAATTATTT	LOCIATERD1 CURRE 1,100 TBTACGTCTCTCTGACTTCA 1,200 CTCAACGATATCGTTAGCTCC CTCAACGATATCGTTAGCTCC 	1,100 1,200 TTATGTGAAGTCAGTGGATCCCAATCCCTG 1 1 1,200 1,200 ATTACTTGAGTTATACATAACTATATAGGA 1 1,000 1,200 ATTACTTGAGTTATACATAACTATATAGGA 1 1,000 1,200 GGCCCCTTTAAATGAAAGGAAAAATGATAG A. T. 1 1,200 A. 1,100 A. 1,10	1078 1078 1078 1198 1198 1198 1318 1318 1317 1317 1317 1438 1438 1438 1437 1437
VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA PB1	L.100 ATACTGTAGTGATCGATCTCATTCATTCC LTRECOREATCORIS COBINY 1200 CTCAABCCGACTACCCCCATATTTGAAA L200 ATCAACCATCGGATATACCAGATAACTTCCT 1400 AAATTCTAGAGGATTTTATCCTATGGAAA	цар МУССОЛЯВ ЗСТОТАЛАТСОСА САЛСТОЛ 1500 1500 АЛАЛАЛАТАСТАДССАЛТАЛ 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0. 0.	NSUSAT 1,140 SAATATCCCAAAGTAATGGCAG 1,200 AAACACTATTAATTGTTTAGAG G. CCONSENSUSAT,1,200 EXTEGGCCTACTATCAAGTAGAA 1,200 CTTTGAAACGGAGAATTATTT	АССТАТЕРО! ССИРЕ 1.190 ОТ СТАРОСТСТСТСТСАСТТСА 1.200 СТСААССАТАТССТТАССТСАСТТСА СССААССАТАТССТТАССТСА 0. Т. 1.0000 1.0000 1.0000 1.0000 1.0000 1.0000 1.000	LIMO 1300 TTATGTGAAGTCAGTGGATCCCAATCCCTG 1300 1300 ATTACTTGAGTTATACATAACTATATGGA ATTACTTGAGTTATACATAACTATATGGA LIMO 1400 CCCCCCTTTAAATCAAAGGAAAAATCATAG A. T LIMO 1400 CCCCCTTAAATCAAAGGAAAAATCATAG A	1078 1078 1078 1198 1198 1198 1198 1318 1318 1317 1317 1438 1438 1437 1437 1558 1558
VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA PB1 IR64	1.00 ATACTGTAGTGATCGATCTGATTCATTCC iLTRECOREATCOR15 CBPHV 1.200 CTCAAGEGGGETACCGCCGATATTTGAAAA 1.340 ATCAACATCGGATATACCGCGATATTTGAAA AAATTCTAGAGGATATTACCTATGGAAA	LIN MYCCONSE SCTGTAAATCGGA ZAACTGA 1.40 AAAAAATGGTAGCCAATAA 	NSUSAT 1:46 GAATATCCCAAAGTAATGGCA(1:200 AAACACTATTAATTGTTAGAA G. G. CCONSENSUSAT 1:300 TATGGGCTACTATCAAGTAGAA LIGA CTTTGAAACGGAGAATTATTT	ACGTATERD1 CC/RE 1,400 DTGTAGGTCTCTCTGACTTCA 1,300 DTGTAGGTCTCTCTGACTTCA CCCCTCTCTGTTAGCTCC 	1.00	1078 1078 1078 1078 1198 1198 1198 1198 1318 1318 1318 131
VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 N22 VANDANA PB1 IR64 N22 VANDANA PB1 IR64	1,00 ATACTGTAGTGATCGATCTCATTCATTCC LITRECOREATCOR15 CBPHV 1200 CTCARCEGARETACCGCCCGATATTTGAAAA 1340 ATCCAGACATCGGATATACCGGATAACTTGCT 1,000 AAATTCTAGAGGATATACGGATAGGTCTCACC	1.50 MYCCONSE 3C TO TAAATC GGA BAACTBA 1.50 AAAAAATAGC TAGCCAATAA 	NSUSAT 1,140 SAATATCCCAAAGTAATGGCAG 1,200 L200 AAACACTATTAATTGTTTAGA G. G. CONSENSUSAT L300 L300 CONSENSUSAT L300 L300 CONSENSUSAT L300 L300 L300 L300 L300 L300 L300 L30	ACGTATED1 CURE 1,100 TEL ACGCTCTCTGACTTCA 1,200 TECAACGATATCGTTAGCTCC 	1.100 1.300 ТТАТБТБААДТСАЭТЭДАТСССААТСССТС 1 1.300 1.300 АТТАСТТВАЭТТАТАСАТААСТАТАТАДДА 3.100 1.300 СССССТТТАААТСАААДДАААААТСАТАД 1 1.400 1.400 1.500 1.400 ТТСТАТДДААТСАААДДАААТСАТАД 1 1.500 1.500 ТТСТАТДДААТСААСТТАСТАДДДСААТТ 1.500 1.500 1.000 1.500 1.000 1.500 1.000 1.500	1078 1078 1078 1198 1198 1198 1198 1318 1318 1318 131
VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA PB1 IR64 VANDANA	1,00 ATACTGTAGTGATCGATCTCATTCATTCC LITRECOREATCOR15 CBPHV 1,200 CTCAAGCGGATATCCGCCGATATTTGAAAA 1,200 ATCAACATCGGATATACCGCCGATATTTGAAAA 1,200 ATCAACATCGGATATACCGCCGATATTTGAAAA 1,200 TTAGAGAAAAATAAGCATGAGGTCTCACC	1.30 MYCCONSE 3CTGTAAATCCGGA ВААСТВА 1.300 АЛАААЛАТАGCTAGCCAATAA 	NSUBAT 1.140 SAATATCCCAAAGTAATGGCAA 1.340 AAACACTATTAATTGTTTAGAA G G CONSENSUSAT 1.340 CONSENSUSAT 1.3	цасотитер) ССИЯЕ 1,400 ТБТ АВСПОТОТОТОВАСТТСА 1,200 СТСААССАТАТССТТАСОТСС ОТСААССАТАТССТТАСОТСС 	1,100 1300 TTATGTGAAGTCAGTGGATCCCAATCCCTG 1 1,200 1300 ATTACTTGAGTTATACATAACTATATAGGA 1 1,200 1300 1,200 1400 GGCCCCCTTTATACAAAGGAAAAATCATAG 1 1,200 1400 TTCTATGGAATATACCTTAGTAGGAGAAATCATAG 1,000 1400 1,000 1400	1078 1078 1078 1198 1198 1198 1198 1318 1318 1318 131
VANDANA PB1 IR84 VANDANA PB1 IR84 VANDANA PB1 IR86 VANDANA PB1 IR86 VANDANA PB1 IR86 VANDANA PB1 IR86 VANDANA PB1 IR86 VANDANA	۱.00 ATACTGTAGTGATCGATCTCATTCATTCC LTTRECOREATCORIS CEPFON 1320 CTCAACCGGATATCCGCCGATATTTGAAAA 1300 ATCAACATCGGATATACAGGATAACCTTCCT 1400 AAATTCTAGAGGAAAAATAAGCATGAGGTCTCACC T. T.		1200 1200	АССТАТЕРО ССИРЕ 1,100 ОТ БТАССТСТСТСТСАСТТСА 1,200 СТСААССАТАТССТТАССТТСА СССААССАТАТССТТАССТСС С	LIMO LIMO TTATGTGAAGTCAGTGGATCCCAATCCCAG TTATGTGAAGTCAGTGGATCCCAG LIMO LIMO TTATGTGAGTTATACATAACTATATAGGA LIMO LIMO LIMO LIMO LIMO LIMO LIMO LIMO	1078 1078 1078 1198 1198 1198 1198 1318 1318 1318 131
VANDANA, MARKANA MA	Ligo ATACTGTAGTGATCGATCTGATTCATTCC LITRECOREATCORIS CORNY 1220 CTCAAGCGGACTACCCCCGATATTTGAAA 1,340 ATCAACATCGGATATACAGATAACTTGCT 4,400 AAATTCTAGAGGATTTTATCCTATGGAAA 1,400 TTAGAGAAAAATAAGCATGAGGTCTCACC T T T	ь цар МУССОЛЯВ ЗСТОТАЛААТСОСА БАЛОТОЛА 1340 1340 АЛАЛАЛАТАОСТАОССААТАЛ С. 	NSUSAT 1:40 SAATATCCCAAAGTAATGGCAG 1:300 AAACACTATTAATGTTTTAGAG AAACACTATTAATGTGTTAGAG G. CCONSENSUSAT 1:300 IAAGGGCTACTATCAAGTATGTGT 1:300 CTTTGAAACGGGGAATTATTTT 1:000 TATGCTAATCAAACGATAGTT 1:000 TATGCTAATCAAACGATAGTT G. G. G. G.	иссотатело! ССИРЕ 1.190 ОТ ОТ ROOG CT	LIMO 1300 TTATGTGAAGTCAGTGGATCCCAATCCCTG 1300 1300 ATTACTTGAGTTATACATAACTATATGGA ATTACTTGAGTTATACATAACTATATGGA GCCCCCTTTAAATCAAAGGAAAAATCATAG AT 1400 1400 TTCTATGGAATATCAATGAGAAAATCATAG 4T 1500 1400 TTCTATGGAATATCAATAGGAAAATCATAG 1400 1000	1078 1078 1078 1198 1198 1198 1198 1318 1318 1318 131
VANDANA, MARKANA SANA SANA SANA SANA SANA SANA SANA	1,00 ATACTGTAGTGATCGATCTGATTCATTCC ,LTRECOREATCOR15 CBPHV 1,200 CTCARBEGGAETACCGCCGATATTTGAAAA 1,340 ATCAACATCGGATATACAGATAACTTGC1 AAATTCTAGAGGATATTACCTATGGAAA 1,00 TTAGAGAAAAATAAGCATGAGGTCTCACC T. 	LIN MYCCONSE 3CTGTAAATCGGA GAACTGA 1,500 AAAAAAATGCTAGCCAATAA 	NSUSAT 1,46 GAATATCCCAAAGTAATGGCAG 1,200 1,200 AAACACTATTAATTGTTTAGAG G. CONSENSUSAT 1,300 TATGGCTACTATCAAGTAGAJ 1,000 TATGGCTACTATCAAGCAGTAGTT 1,000 TATGCTAATCAAACGATAGTT G. G. 1,200	ACGTATERD1 CURE 1,400 CT TAGGT CT CT CT CT CA CT TC A 1,300 CT CT AGGT CT CT CT CT CA CT TC A CT CT AGGT CT CT CT CT CA CT CA CT CT CT CT CT CT CT CA CT CA 1,500 CT CT AGGT CT CT CT CT CA CT CA 1,500 CT CT AGGT CT CT CT TT CA CT CT 1,500 CT CT AGGT CT CC CT TT CA CT CC A CT CT CC CT TT CA CT CC A CT CT CC CT CT CA CT CC A CT CC CT CC CT CC CC CC CC CC CC CC CC	цю ізю ттатбтбаадтсадтбдатсссаатссста 1.300 ізо аттасттаасттатасатаастататаса аттасттаастта	1078 1078 1078 1198 1198 1198 1198 1198 1198 1198 1318 131
VANDANA, PB1 IR664 N222 VANDANA N22 VANDANA VANDAN	1,00 ATACTGTAGTGATCGATCTCATTCATTCC LITRECOREATCOR15 CEPHY 1,200 CTCARECERETACCGCCCGATATTTGAAAA ATCAACATCGGATATACCGCCGATATTTGAAAA AATTCTAGAGGATATACCGATAGCTTGCT LA00 AAATTCTAGAGGATATACGGATGAGGTCTCACC T. 	1.100 1.200 1.	ISUSAT LIM SAATATCCCAAAGTAATGGCAG LIG AAACACTATTAATTGTTTAGAG G. CONSENSUSAT LIG TATGGCTACTATTACAGTAGAA LIG CATTTGAAACGGAGAATTATTT G. G. G. G. LIG SATTTTGGTGTCATGATTATTC/	ACGTATERD1 CUTE 1400 CT 21 A GC CT CT CT GA CT TC A 1,200 CT 21 A GC CT CT CT GA CT TC A CT CT A GC CT CT CT GT GA CT AGC CC 	1.100 1.300 ТТАТБТБААĞТСАĞТĞĞАТСССААТСССТĞ 1 1.300 1.300 АТТАСТТӨАĞТТАТАСАТААСТАТАТАĞĞ 3 СССССТТТАААТСАААĞĞАААААТСАТТА 1.500 А.11.1 1.500 A.11.1 1.500 A.11.1 1.	1078 1078 1078 1198 1198 1198 1198 1198 1318 1318 131
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Supplementary Fig. S14. Comparative sequence alignment of upstream regulatory region of the seven rice copper transporters. Sequence alignment of 2kb upstream region of (a) COPT1, (b) COPT2, (c) COPT3, (d) COPT4, (e) COPT5, (f) COPT6, (g) COPT7 in four cultivars namely N22, Vandana, PB1 and IR64. Dots (.) represents the identical sequence, dashes (-) represents gaps and the cis-acting elements associated with stress were highlighted



Supplementary Fig. 15. Differential copper homeostasis does not modulate plastocyanin levels but affects ROS homeostasis. (a) Quantitative immunoblot showing the plastocyanin protein levels in N22 and PB1 flag leaf under control (C) and drought stress (S) conditions. Ponceau S staining was used to show the equal loading of samples. (b) Relative expression analysis of plastocyanin in N22 seedlings under copper starvation and in N22 and PB1 flag leaf under drought. Three biological with three technical replicates were analyzed.



Supplementary Fig. S16. miRNA-mediated regulation of the pathways involved in the acquisition of ROS detoxification of ROS through removal of superoxide ions and ascorbate glutathione cycle. All genes were searched for putative targeting miRNA in the PARE data and the miRNA in green are significantly upregulated in N22 flag leaf while downregulated in PB1 flag leaf. miRNA in red are low in abundance but downregulated in N22 flag leaf and upregulated in PB1 flag leaf.



Supplementary Fig. S17. Expression analysis of genes involved in ROS homeostasis. qRT-PCR analysis of genes involved in the maintenance of ROS homeostasis in the flag leaf of N22 and PB1 under drought. Data represents the analyzed value of at least three biological and technical replicate. Error bars represents the standard error.



Supplementary Fig. S18. Electron micrographs showing the completely open, partially open and closed stomata in PB1 flag leaf.