

Supplementary Materials

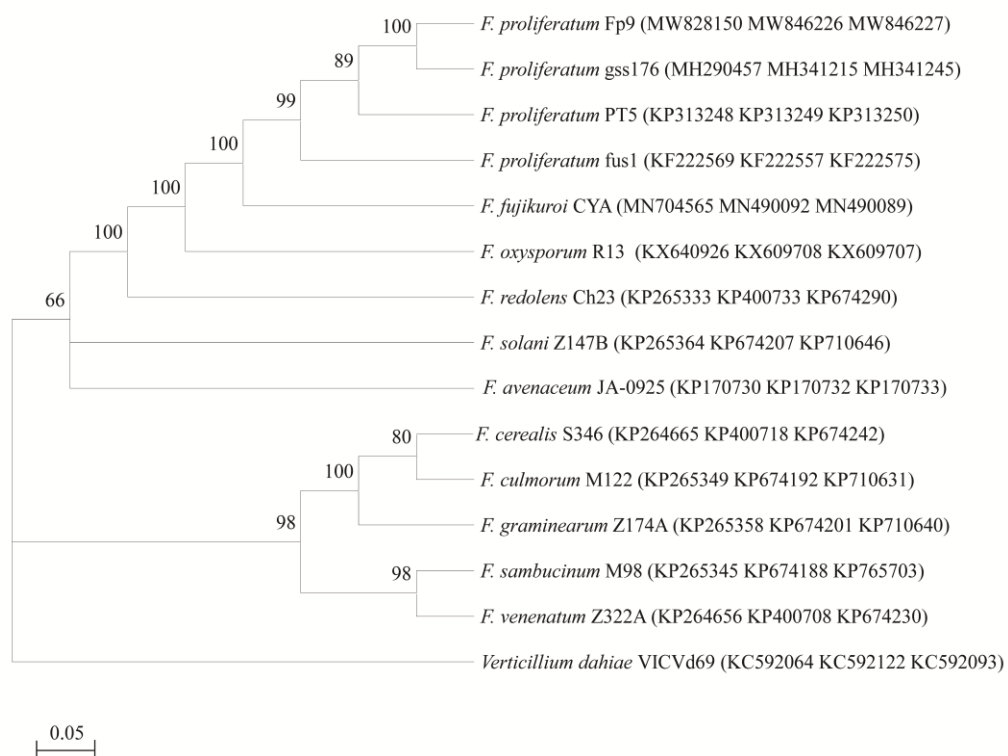


Figure S1. Neighbor-joining tree inferred from the concatenated nucleotide sequences of *ITS*, *TEF1 α* and β -*TUB* of the strains of *F. proliferatum* and other *Fusarium* species.

Note: *Verticillium dahliae* was used as an outgroup. The GenBank accession numbers from left to right in parentheses were the sequences of *ITS*, *TEF* and β -*TUB* genes, respectively. Numbers near branches were bootstrap values based on 1,000 replicates.

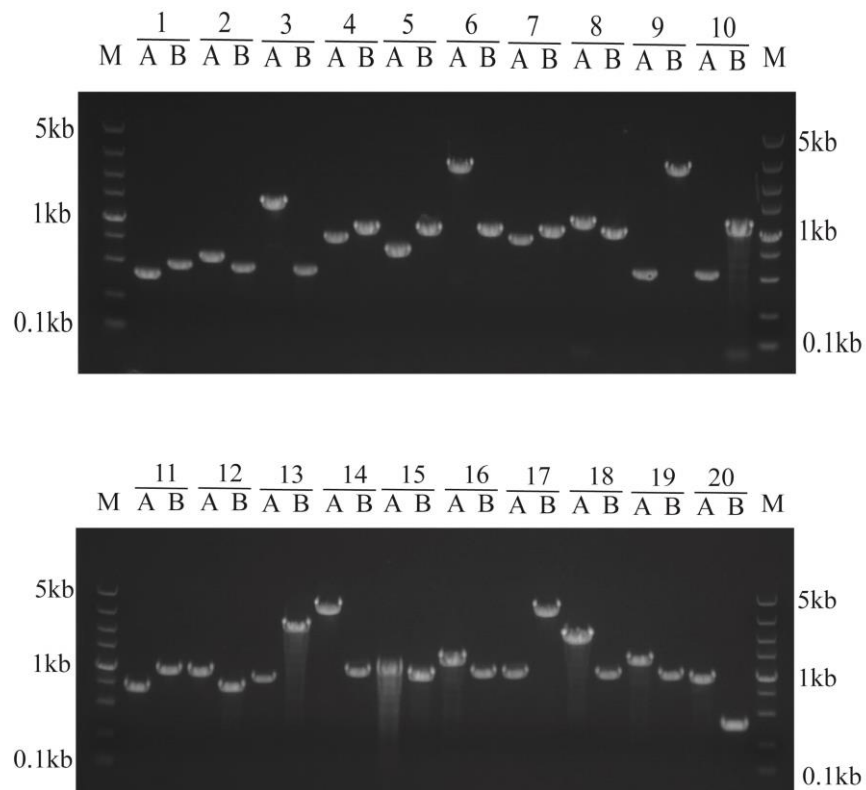


Figure S2. Gel electrophoresis images of PCR validation of structural variants (SVs) between *F. proliferatum* and *F. fujikuroi*

Note: PCR reactions used DNA from the *F. proliferatum* (A) and *F. fujikuroi* (B). Gel electrophoresis images of PCR products corresponding to the SVs in Table S3. Numbers above the small horizontal line represented SV ID. PCR validations of SV1 to SV10 was in top and SV11 to SV20 was in bottom, respectively.

Table S1 Specific regions in the subtelomeres present in *E. proliferatum* but absent in *E. fujikuroi*

Scaffold	Left/Right arms	Locus boundary	Fragments (bp)
Scaffold I	Left	35777: 42225	6448
Scaffold I	Right	6080517: 6114445	33928
Scaffold II	Left	126954: 138359	11405
Scaffold II	Right	4594735: 4601872	7137
Scaffold II	Right	4729844: 4744065	14221
Scaffold IV	Left	14338: 70572	56234
Scaffold IV	Right	4454458: 4479090	24632
Scaffold VII	Right	2897101: 2974289	77188
Scaffold IX	Right	2876122: 2929835	53713
Scaffold IX	Right	2973049: 3023339	50290
Scaffold X	Left	26521: 36495	9974
Scaffold X	Right	79679: 91925	12246
Scaffold XI	Left	10360: 18871	8511
Scaffold XI	Right	339337: 364692	25355
Scaffold XII	Left	12623: 47357	34734
Scaffold XII	Right	619632: 674151	54519

Table S2 GO enrichment analysis of genes present in the genome of *F. proliferatum* and absent in that of *F. fujikuroi*

Type	GO ID	Function	No. of genes present in <i>F. proliferatum</i>	No. of genes present in <i>F. fujikuroi</i>
Biological Process	GO:0005975	carbohydrate metabolic process	1	5
	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	1	0
	GO:0006200	ATP catabolic process	1	0
	GO:0006313	transposition, DNA-mediated	0	1
	GO:0006351	transcription, DNA-dependent	2	4
	GO:0006357	regulation of transcription from RNA polymerase II promoter	3	0
	GO:0006412	translation	1	0
	GO:0006418	tRNA aminoacylation for protein translation	1	0
	GO:0006457	protein folding	1	0
	GO:0006508	proteolysis	2	0
	GO:0006520	cellular amino acid metabolic process	0	1
	GO:0006629	lipid metabolic process	0	3
	GO:0006807	nitrogen compound metabolic process	2	0
	GO:0006950	response to stress	0	1
	GO:0007155	cell adhesion	0	1
	GO:0008152	metabolic process	0	5
	GO:0008643	carbohydrate transport	1	0
	GO:0009058	biosynthetic process	0	1
	GO:0009081	branched chain family amino acid metabolic process	1	0
	GO:0009098	leucine biosynthetic process	1	0
	GO:0009116	nucleoside metabolic process	1	3
	GO:0009409	response to cold	1	0
	GO:0009637	response to blue light	2	0
	GO:0009765	photosynthesis, light harvesting	1	0

	GO:0010114	response to red light	2	0
	GO:0010218	response to far red light	1	0
	GO:0015074	DNA integration	0	6
	GO:0016042	lipid catabolic process	0	2
	GO:0016310	phosphorylation	1	0
	GO:0018298	protein-chromophore linkage	1	0
	GO:0019253	reductive pentose-phosphate cycle	1	0
	GO:0031221	arabinan metabolic process	0	1
	GO:0044237	cellular metabolic process	1	0
	GO:0044249	cellular biosynthetic process	1	0
	GO:0045454	cell redox homeostasis	0	2
	GO:0046148	pigment biosynthetic process	1	0
	GO:0046373	L-arabinose metabolic process	0	1
	GO:0055085	transmembrane transport	3	8
	GO:0055114	oxidation-reduction process	7	0
	GO:0070941	eisosome assembly	0	11
Cellular Component	GO:0071704	organic substance metabolic process	1	0
	GO:0000124	SAGA complex	1	0
	GO:0005618	cell wall	1	0
	GO:0005623	cell	0	2
	GO:0005634	nucleus	1	9
	GO:0005737	cytoplasm	1	0
	GO:0005739	mitochondrion	1	0
	GO:0005832	chaperonin-containing T-complex	1	0
	GO:0009522	photosystem I	1	0
	GO:0009523	photosystem II	1	0
	GO:0009535	chloroplast thylakoid membrane	2	0
	GO:0009573	chloroplast ribulose biphosphate carboxylase complex	1	0

	GO:0009941	chloroplast envelope	1	0
	GO:0010287	plastoglobule	1	0
	GO:0016020	membrane	1	0
	GO:0016021	integral to membrane	3	57
	GO:0022626	cytosolic ribosome	1	0
	GO:0031977	thylakoid lumen	1	0
	GO:0032126	eisosome	0	11
	GO:0048046	apoplast	3	0
Molecular Function	GO:0000166	nucleotide binding	4	0
	GO:0000287	magnesium ion binding	1	0
	GO:0000981	sequence-specific DNA binding RNA polymerase II transcription factor activity	3	8
	GO:0003676	nucleic acid binding	0	13
	GO:0003677	DNA binding	1	6
	GO:0003700	DNA-binding transcription factor activity	0	2
	GO:0003824	catalytic activity	0	5
	GO:0003862	3-isopropylmalate dehydrogenase activity	1	0
	GO:0003924	GTPase activity	0	1
	GO:0003979	UDP-glucose 6-dehydrogenase activity	1	0
	GO:0003995	acyl-CoA dehydrogenase activity	2	0
	GO:0004040	amidase activity	0	1
	GO:0004084	branched-chain-amino-acid transaminase activity	1	0
	GO:0004177	aminopeptidase activity	1	0
	GO:0004252	serine-type endopeptidase activity	1	2
	GO:0004386	helicase activity	0	1
	GO:0004402	histone acetyltransferase activity	0	1
	GO:0004497	monooxygenase activity	3	1
	GO:0004553	hydrolase activity, hydrolyzing O-glycosyl compounds	1	5

GO:0004672	protein kinase activity	0	5
GO:0004806	triglyceride lipase activity	0	1
GO:0004812	aminoacyl-tRNA ligase activity	1	0
GO:0005506	iron ion binding	1	1
GO:0005507	copper ion binding	1	0
GO:0005524	ATP binding	2	7
GO:0005525	GTP binding	0	2
GO:0008061	chitin binding	0	2
GO:0008081	phosphoric diester hydrolase activity	0	2
GO:0008171	O-methyltransferase activity	0	1
GO:0008233	peptidase activity	1	0
GO:0008236	serine-type peptidase activity	0	1
GO:0008237	metallopeptidase activity	1	2
GO:0008239	dipeptidyl-peptidase activity	1	0
GO:0008270	zinc ion binding	1	9
GO:0008408	3'-5' exonuclease activity	0	1
GO:0008483	transaminase activity	1	1
GO:0009055	electron transfer activity	0	1
GO:0009853	photorespiration	1	0
GO:0010218	response to far red light	1	0
GO:0010484	H3 histone acetyltransferase activity	1	0
GO:0016168	chlorophyll binding	1	0
GO:0016301	kinase activity	2	0
GO:0016407	acetyltransferase activity	0	1
GO:0016491	oxidoreductase activity	4	7
GO:0016614	oxidoreductase activity, acting on CH-OH group of donors	0	2
GO:0016616	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	0	1

GO:0016620	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	0	1
GO:0016702	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	0	1
GO:0016705	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	1	1
GO:0016747	transferase activity, transferring acyl groups other than amino-acyl groups	0	1
GO:0016758	transferase activity, transferring hexosyl groups	1	0
GO:0016772	transferase activity, transferring phosphorus-containing groups	1	0
GO:0016787	hydrolase activity	1	7
GO:0016798	hydrolase activity, acting on glycosyl bonds	1	0
GO:0016810	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds	1	1
GO:0016829	lyase activity	1	1
GO:0016836	hydro-lyase activity	0	1
GO:0016853	isomerase activity	0	2
GO:0016984	ribulose-bisphosphate carboxylase activity	1	0
GO:0020037	heme binding	1	1
GO:0022857	transmembrane transporter activity	0	1
GO:0022891	substrate-specific transmembrane transporter activity	1	0
GO:0030151	molybdenum ion binding	0	1
GO:0030170	pyridoxal phosphate binding	0	2
GO:0030246	carbohydrate binding	0	1
GO:0042626	ATPase activity, coupled to transmembrane movement of substances	1	0
GO:0043169	cation binding	1	0
GO:0043531	ADP binding	0	2
GO:0046556	alpha-L-arabinofuranosidase activity	0	1
GO:0046872	metal ion binding	4	3

GO:0046873	metal ion transmembrane transporter activity	0	1
GO:0050660	flavin adenine dinucleotide binding	1	2
GO:0050662	coenzyme binding	1	0
GO:0051082	unfolded protein binding	1	0
GO:0051213	dioxygenase activity	0	1
GO:0051287	NAD binding	2	0
GO:0051537	2 iron, 2 sulfur cluster binding	0	1
GO:0051920	peroxiredoxin activity	0	1
GO:0052664	nitroalkane oxidase activity	1	0
GO:0070011	peptidase activity, acting on L-amino acid peptides	1	0
GO:0071949	FAD binding	1	2
GO:0071704	organic substance metabolic process	1	0

Table S3 Summary of PCR validations of structural variants (SVs) between *F. proliferatum* and *F. fujikuroi*

SV ID	SV class	SV size (bp)	A (bp)	B (bp)	Forward Primer (5'-3')	Reverse Primer (5'-3')
1	Deletion	80	418	495	AGGGGACAAGAGGTAAG	TCAGGCTATCTGTGCAG
2	Insertion	101	610	509	TAACCTCTCCTATCTCT	ACGCTCCCTTGAACAAC
3	Insertion	892	1386	494	ACTCAGTCTGTCCGTTG	GGTCCTGTTTTCTCTA
4	Deletion	162	840	1005	CGGATAGTCGTCTTCAT	AACTGATTGAGAGCCC
5	Deletion	280	728	1008	ATGACAACCATGAATCA	AACAAGAAGACCCTGTG
6	Insertion	1476	2443	968	ATTTATGTGATGCCGCC	ATCGACAACATCATGCTTGA
7	Deletion	145	843	993	GCCTCGGGATATGGAGG	TCGAGAACAGGGATGAGG
8	Insertion	146	1107	959	GTCTCCTCTTTCCTCAC	GAACCAACAGAACCTTT
9	Deletion	1968	573	2541	AGGTCGGTGTGCGGTATC	GCTTGTGTGCGGGTGTC
10	Deletion	579	591	1170	GCTGCCCATCATAAGTG	TCACCCCAATCTCGGT
11	Deletion	295	709	998	CTCTAATAGTGATGCGAGGTG	AGCGTTTTGTTTGGGTC
12	Insertion	206	973	767	TGCCCAGTGATAACGA	AGATGGAAAGAACATGATG
13	Deletion	1383	848	2231	ATGTCTTCAAATGTAACGAGA	TGTGAGCCAGCGGGTTA
14	Insertion	2008	2915	908	CCTCGGTTCTGCTGTCT	TGTTTGCTGTGAAGTCT
15	Insertion	153	1103	950	ACGGCGTTGGATATATA	TACCAATGGTTCTCAAT
16	Insertion	290	1261	982	ATGACTCTCGTGTTAAG	TTCCATTTATTCTTTGAA
17	Deletion	1850	985	2828	GTTTCGTCGCCAAAGCT	AACCATGAGGCTTCAGC
18	Insertion	1067	2017	950	GCGTGTTGACCCATTTT	CGCAACTTGATTAGCC
19	Insertion	409	1407	998	AGTATCTGAACCAATGC	AGAAGGAAGTAGTCGTG
20	Insertion	743	1105	362	AAAGCAGTGGCGAACAT	CAGCAAAACGAAAACGA

Note: A indicated PCR size (bp) in *F. proliferatum* strain Fp9; B indicated PCR size (bp) in *F. fujikuroi* strain IMI 58289.

Table S4 Comparison of genes encoding for membrane transporters in *F. proliferatum* with that in other fungi

Superfamilies	TC No.	Subclass description	FP	FG	MO	BC	SS	NC	AN
Channels/Pores	1.A	α -Type channels	69	76	64	64	118	52	52
	1.B	β -Barrel porins	1	1	2	0	2	1	0
	1.C	Pore-forming toxins(proteins and peptides)	6	4	5	7	12	6	4
	1.F	Vesicle Fusion Pores	5	8	6	3	7	4	6
	1.H	Paracellular channels	5	5	3	3	6	3	3
	1.I	Membrane-bounded Channels	10	8	5	3	7	5	4
	1.P	Non-Envelop Virus Penetration Complex: A complex of host cell proteins that allow non-envelop virus to penetrate the endoplasmic reticular membrane.	2	3	2	1	2	3	3
	1.Q	Fungal Septal Pores	1	1	1	0	1	1	1
Electrochemical potential-driven transporters	2.A	Porters (uniporters, symporters, antiporters)	905	772	501	517	879	341	636
	2.A.1	The Major Facilitator Superfamily (MFS)	567	421	271	299	451	157	390
	2.A.2	The Glycoside-Pentoside-Hexuronide (GPH):Cation Symporter Family	2	2	4	4	6	2	2
	2.A.3	The Amino Acid-Polyamine-Organocation (APC) Superfamily	74	71	32	45	80	18	57
	2.A.4	The Cation Diffusion Facilitator (CDF) Family	9	7	8	6	13	9	6
	2.A.5	The Zinc (Zn^{2+})-Iron (Fe^{2+}) Permease (ZIP) Family	10	9	8	8	14	8	7
	2.A.6	The Resistance-Nodulation-Cell Division (RND) Superfamily	3	3	3	3	6	3	2
	2.A.7	The Drug/Metabolite Transporter (DMT) Superfamily	24	29	23	16	41	21	20
	2.A.9	The Membrane Protein Insertase (YidC/Alb3/Oxa1) Family	2	1	1	1	4	1	2
	2.A.16	The Tellurite-resistance/Dicarboxylate Transporter (TDT) Family	8	12	5	5	6	3	4
	2.A.17	The Proton-dependent Oligopeptide Transporter (POT) Family	6	5	4	3	9	2	4
	2.A.18	The Amino Acid/Auxin Permease (AAP) Family	26	32	12	12	22	6	14
	2.A.19	The Ca^{2+} :Cation Antiporter (CaCA) Family	8	10	7	10	19	10	6
	2.A.20	The Inorganic Phosphate Transporter (PiT) Family	4	4	3	1	2	0	4
	2.A.21	The Solute:Sodium Symporter (SSS) Family	5	3	3	2	2	3	4
	2.A.22	The Neurotransmitter:Sodium Symporter (NSS) Family	2	3	3	0	0	0	1
	2.A.23	The Dicarboxylate/Amino Acid:Cation (Na^+ or H^+) Symporter (DAACS) Family	1	1	1	0	0	0	1

2.A.25	The Alanine or Glycine:Cation Symporter (AGCS) Family	0	0	1	0	1	0	0
2.A.28	The Bile Acid:Na ⁺ Symporter (BASS) Family	1	1	1	0	0	0	1
2.A.29	The Mitochondrial Carrier (MC) Family	17	16	13	14	23	16	17
2.A.30	The Cation-Chloride Cotransporter (CCC) Family	1	1	1	1	2	1	1
2.A.31	The Anion Exchanger (AE) Family	3	4	1	2	2	2	2
2.A.36	The Monovalent Cation:Proton Antiporter-1 (CPA1) Family	4	5	4	5	8	3	6
2.A.37	The Monovalent Cation:Proton Antiporter-2 (CPA2) Family	2	1	3	2	4	2	2
2.A.38	The K ⁺ Transporter (Trk) Family	5	6	5	3	5	2	3
2.A.39	The Nucleobase:Cation Symporter-1 (NCS1) Family	13	9	7	8	17	3	11
2.A.40	The Nucleobase:Cation Symporter-2 (NCS2) Family	5	4	3	3	8	4	3
2.A.41	The Concentrative Nucleoside Transporter (CNT) Family	1	1	1	0	0	1	1
2.A.43	The Lysosomal Cystine Transporter (LCT) Family	6	6	7	5	12	7	5
2.A.47	The Divalent Anion:Na ⁺ Symporter (DASS) Family	1	2	1	1	2	1	1
2.A.49	The Chloride Carrier/Channel (ClC) Family	4	5	3	3	7	4	3
2.A.50	The Glycerol Uptake (GUP) Family	1	1	1	1	2	2	1
2.A.51	The Chromate Ion Transporter (CHR) Family	1	2	1	0	0	1	2
2.A.52	The Ni ²⁺ -Co ²⁺ Transporter (NiCoT) Family	1	2	2	1	2	1	1
2.A.53	The Sulfate Permease (SulP) Family	7	8	8	4	10	4	4
2.A.54	The Mitochondrial Tricarboxylate Carrier (MTC) Family	1	1	1	1	2	1	1
2.A.55	The Metal Ion (Mn ²⁺ -iron) Transporter (Nramp) Family	2	1	0	1	4	2	1
2.A.57	The Equilibrative Nucleoside Transporter (ENT) Family	3	4	2	2	4	1	2
2.A.59	The Arsenical Resistance-3 (ACR3) Family	2	1	1	1	2	1	1
2.A.66	The Multidrug/Oligosaccharidyl-lipid/Polysaccharide (MOP) Flippase Superfamily	6	8	4	3	7	5	5
2.A.67	The Oligopeptide Transporter (OPT) Family	13	13	12	12	23	11	6
2.A.69	The Auxin Efflux Carrier (AEC) Family	1	2	2	3	6	2	2
2.A.72	The K ⁺ Uptake Permease (KUP) Family	1	1	1	1	2	0	0
2.A.77	The Cadmium Resistance (CadD) Family	1	1	1	0	0	0	0

	2.A.79	The Threonine/Serine Exporter (ThrE) Family	2	2	1	1	2	1	3
	2.A.82	The Organic Solute Transporter (OST) Family	2	2	2	3	4	2	2
	2.A.85	The Aromatic Acid Exporter (ArAE) Family	6	7	2	5	8	2	4
	2.A.89	The Vacuolar Iron Transporter (VIT) Family	2	2	1	1	2	1	2
	2.A.90	The Vitamin A Receptor/Transporter (STRA6) Family	1	1	1	1	2	1	1
	2.A.92	The Choline Transporter-like (CTL) Family	1	1	1	0	1		1
	2.A.94	The Phosphate Permease (Pho1) Family	2	2	3	2	4	3	2
	2.A.96	The YaaH (YaaH) Family	11	7	2	3	4	1	6
	2.A.97	The Mitochondrial Inner Membrane K ⁺ /H ⁺ and Ca ²⁺ /H ⁺ Exchanger (LetM1) Family	0	0	1	1	2	1	1
	2.A.100	The Ferroportin (Fpn) Family	1	2	1	1	2	1	1
	2.A.105	The Mitochondrial Pyruvate Carrier (MPC) Family	1	1	3	1	2	2	1
	2.A.106	The Ca ²⁺ -H ⁺ Antiporter-2 (CaCA2) Family	1	2	1	1	2	1	1
	2.A.108	The Iron/Lead Transporter (ILT) Family	9	9	4	3	6	2	
	2.A.121	The Sulfate Transporter (CysZ) Family	2	3	3	1	4	2	2
	2.A.122	The LrgB/CidB Holin-like Glycolate/Glycerate Transporter (LrgB/CidB/GGT) Family	2	2	0	0	2	0	0
	2.A.126	The Fatty Acid Exporter (FAX) Family	1	2	0	1	2	1	2
	2.A.127	The Enterobacterial Cardiolipin Transporter (CLT) Family	7	8	0	0	0	0	1
Primary active transporters	3.A	P-P-bond-hydrolysis-driven transporters	127	147	111	105	187	75	99
	3.A.1	The ATP-binding Cassette (ABC) Superfamily	59	65	42	47	79	27	45
	3.A.2	The H ⁺ - or Na ⁺ -translocating F-type, V-type and A-type ATPase (F-ATPase) Superfamily	7	12	8	6	14	3	6
	3.A.3	The P-type ATPase (P-ATPase) Superfamily	30	32	24	20	33	19	21
	3.A.4	The Arsenite-Antimonite (ArsAB) Efflux Family	1	1	1	0	2	0	0
	3.A.5	The General Secretory Pathway (Sec) Family	8	7	8	6	14	5	7
	3.A.8	The Mitochondrial Protein Translocase (MPT) Family	5	5	5	8	12	1	6
	3.A.9	The Chloroplast Envelope Protein Translocase (CEPT or Tic-Toc) Family	0	3	3	1	0	0	0
	3.A.16	The Endoplasmic Reticular Retrotranslocon (ER-RT) Fam	6	8	8	4	10	6	5

	3.A.19	The TMS Recognition/Insertion Complex (TRC) Family	1	1	0	1	1		1
	3.A.20	The Peroxisomal Protein Importer (PPI) Family	2	4	2	4	6	5	2
	3.A.25	The Symbiont-specific ERAD-like Machinery (SELMA) Family	1	0	1	0	1	1	1
	3.A.27	The C-terminal Tail-Anchored Membrane Protein Biogenesis/ Insertion Complex-2 (TAMP-B2) Family	4	4	6	4	8	4	3
	3.A.28	The AAA-ATPase, Bcs1 (Bcs1) Family	2	3	2	3	5	2	2
	3.A.29	The Mitochondrial Inner Membrane i-AAA Protease Complex (MIMP) Family	1	2	1	1	2	2	0
	3.B	Decarboxylation-driven transporters	0	0	0	0	0	0	1
	3.D	Oxidoreduction-driven transporters	10	27	10	8	34	9	11
	3.E	Light absorption-driven transporters	5	4	1	2	4	1	1
	4.C	Acyl CoA ligase-coupled transporters	11	8	3	3	3	4	4
	4.D	Polysaccharide Synthase/Exporters	27	31	14	21	44	14	14
	4.E	Vacuolar Polyphosphate Polymerase-catalyzed Group Translocators	2	4	2	2	4	2	1
	4.F	Choline/EthanolaminePhosphotransferase 1 (CEPT1)	3	4	4	3	6	4	3
Transmembrane electron carriers	5.B	Transmembrane one-electron transfer carriers	26	34	20	19	31	15	15
Accessory electron carriers	8.A	Auxiliary transport proteins	29	38	26	24	56	28	25
	8.B	Ribosomally synthesized protein/peptide toxins that target channels and carriers	0	1	1	0	0	0	0
Incompletely characterized transporters	9.A	Recognized transporters of unknown biochemical mechanism	74	70	29	42	58	27	46
	9.B	Putative uncharacterized transport proteins	84	103	87	65	164	75	81
Total			1402	1349	897	892	1625	670	1010

Note: Organisms, FP, *Fusarium proliferatum*; FG, *Fusarium graminearum*; MO, *Magnaporthe oryzae*; BC, *Botrytis cinerea*; SS, *Sclerotinia sclerotiorum*; NC, *Neurospora crassa*; AN, *Aspergillus nidulans*.

Table S5 Characterization of carbohydrate-active enzymes (CAZymes) of *F. proliferatum* and other fungi

Species	Glycoside Hydrolase Family (GHs)																										
	1	2	3	5	6	7	8	9	10	11	12	13	15	16	17	18	20	23	24	25	26	27	28	29	30	31	
FP	5	10	25	19	1	3	0	0	5	3	4	9	4	24	6	18	4	0	1	0	0	4	12	3	3	8	
FG	3	10	21	14	1	2	0	0	5	3	4	8	3	24	6	19	3	0	0	0	0	2	6	1	0	8	
FF	4	9	24	18	1	3	0	0	3	3	4	10	3	24	6	17	4	0	1	0	0	3	8	2	2	8	
LM	3	7	13	15	3	3	0	0	3	2	3	7	3	18	8	11	2	0	1	0	0	4	7	1	2	8	
MO	2	8	18	13	3	6	0	0	6	5	3	11	2	18	7	17	3	0	1	0	0	4	4	4	1	6	
BC	3	2	16	16	1	2	0	0	2	3	5	11	5	21	6	11	1	0	0	0	2	4	19	0	0	4	
SS	3	2	13	14	1	3	0	0	2	3	5	10	4	20	6	14	1	0	0	1	1	4	17	0	0	6	
AN	3	10	20	15	2	3	0	0	3	2	1	14	2	13	5	9	2	0	1	3	3	3	9	0	0	10	
NC	1	5	9	7	3	5	0	0	4	2	1	10	2	14	4	12	1	0	0	1	1	0	2	0	2	5	
UB	0	2	4	10	0	0	1	1	2	1	0	5	1	14	2	2	2	1	0	1	1	1	1	0	2	3	
MP	0	1	2	10	0	0	0	1	1	1	0	4	1	16	2	3	2	1	0	0	2	3	1	0	2	3	

Species	Glycoside Hydrolase Family (GHs)																									
	32	33	35	36	37	38	39	42	43	45	47	49	51	53	54	55	62	63	64	65	67	71	72	74	75	76
FP	7	1	3	4	2	1	3	0	27	1	10	2	2	1	1	2	1	1	2	1	2	3	4	1	3	9
FG	5	1	3	3	2	1	2	0	18	1	10	0	2	1	1	0	2	1	2	0	1	0	3	1	1	8
FF	6	1	2	4	2	1	5	0	27	1	10	1	2	1	2	0	1	1	2	1	2	2	3	0	2	9
LM	2	4	4	2	2	1	1	0	12	2	8	0	3	1	0	0	1	3	1	1	1	1	6	0	0	7
MO	5	0	0	2	2	2	2	0	19	1	9	0	3	1	1	0	4	2	2	0	1	1	5	1	1	8
BC	1	0	4	2	1	1	1	0	5	2	8	0	4	2	1	0	1	1	2	2	0	11	6	0	0	11
SS	1	0	4	2	1	1	0	0	5	2	8	0	2	2	1	0	0	1	2	3	0	10	6	0	0	11
AN	2	0	4	4	1	1	1	0	18	1	7	0	2	1	1	6	2	1	0	1	1	5	5	2	2	7
NC	0	0	2	1	2	1	0	0	7	1	8	0	1	1	1	0	0	1	2	0	1	6	5	1	1	10
UB	3	0	1	1	2	1	0	1	3	4	3	0	3	0	1	0	1	1	0	0	0	0	1	0	0	0

MP	2	0	1	1	1	1	0	1	5	2	4	1	1	0	1	0	0	1	0	0	0	0	1	0	0	0
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Species	Glycoside Hydrolase Family (GHs)																										
	78	79	81	85	88	89	92	93	94	95	105	114	115	125	127	128	131	132	133	134	135	141	142	145	146	No classified	Total
FP	12	1	3	0	3	0	0	3	0	1	3	3	2	3	1	3	1	3	1	0	0	0	0	0	0	0	308
FG	7	1	1	0	1	0	0	2	0	2	3	2	2	3	1	4	1	2	1	0	0	0	1	1	1	4	252
FF	9	2	3	0	3	0	0	4	0	2	4	2	2	3	2	4	1	2	1	1	0	0	1	1	1	6	299
LM	1	1	2	1	1	0	6	2	0	1	3	2	2	3	0	4	2	1	1	1	0	1	0	0	1	4	227
MO	3	2	2	0	1	0	6	1	1	1	4	1	3	6	0	5	6	2	2	0	0	0	0	1	2	2	265
BC	8	2	1	0	1	0	5	1	0	2	1	1	1	3	1	1	1	2	1	0	2	0	0	1	0	0	235
SS	4	2	1	0	0	1	5	1	0	1	1	1	1	3	0	3	2	2	1	0	3	0	0	0	0	9	233
AN	8	1	2	0	2	0	5	2	0	3	3	2	1	1	1	2	1	2	2	4	3	0	0	0	0	4	257
NC	0	2	1	0	0	0	2	2	1	0	1	1	1	3	0	2	3	2	1	0	0	0	2	1	0	2	170
UB	0	1	0	1	0	0	3	1	0	0	1	0	1	0	0	5	0	0	1	0	1	0	0	0	0	3	101
MP	0	1	0	1	0	0	2	1	0	0	1	0	1	1	0	5	0	0	1	0	0	0	0	0	0	5	98

Species	Glycosyltransferase Family (GTs)																	
	1	2	3	4	5	8	15	17	20	21	22	24	25	30	31	32	33	34
FP	18	1	1	0	0	7	5	2	3	1	4	1	0	1	7	5	1	3
FG	16	20	1	0	0	6	4	2	3	1	4	1	0	0	5	5	1	2
FF	13	23	1	0	0	7	5	2	3	1	4	1	0	0	6	6	1	3
LM	6	16	1	0	0	9	3	0	3	1	4	1	2	0	7	5	1	7
MO	13	11	1	0	1	2	4	1	3	1	4	1	6	0	4	10	1	2
BC	13	13	1	0	1	7	4	2	3	1	4	1	2	0	6	6	0	1
SS	10	17	1	0	1	6	4	2	3	1	4	1	3	0	6	4	1	2

AN	9	12	1	7	2	4	3	0	3	1	4	1	4	0	5	7	1	3
NC	6	11	1	0	2	2	5	1	3	1	3	1	1	0	3	4	1	2
UB	5	15	1	0	0	2	1	1	3	1	4	1	0	0	3	2	1	0
MP	5	13	1	0	0	2	2	0	3	1	3	1	0	0	3	2	1	0

Species	Glycosyltransferase Family (GTs)																		
	35	39	41	48	50	55	57	58	59	61	62	64	66	69	71	76	90	No classified	Total
FP	1	3	1	1	1	0	2	1	1	0	3	2	1	3	3	1	5	0	89
FG	1	3	1	1	1	0	2	1	1	0	3	2	1	2	4	1	6	4	105
FF	1	3	1	1	1	0	2	1	1	0	3	2	1	3	3	1	6	2	108
LM	1	3	1	1	1	0	2	1	1	0	3	0	1	2	2	1	4	2	92
MO	1	3	1	1	1	1	2	1	1	3	3	0	1	4	4	1	6	2	101
BC	1	3	1	2	1	0	2	1	0	0	3	0	1	3	5	2	3	6	99
SS	1	3	1	1	1	0	2	1	1	0	3	0	1	2	2	1	3	4	93
AN	1	3	1	1	1	0	2	1	1	0	3	0	1	3	2	0	2	2	91
NC	1	3	1	1	1	1	2	1	1	0	3	0	1	2	1	1	3	4	74
UB	0	3	1	1	1	0	2	1	1	0	0	0	1	2	2	1	1	0	57
MP	0	3	1	1	1	1	2	1	0	0	0	0	1	1	2	1	2	3	57

Species	Polysaccharide Lyase Family (PLs)										
	1	3	4	9	11	14	20	26	27	No classified	Total
FP	11	7	3	2	0	0	0	0	0	0	23
FG	9	7	3	1	0	0	1	1	0	0	22
FF	11	7	2	2	0	0	0	1	0	0	23

LM	9	6	4	1	0	0	0	1	0	0	21
MO	2	1	1	0	0	0	1	1	0	0	6
BC	6	2	0	0	0	0	0	0	0	0	8
SS	4	0	0	0	0	0	0	0	0	0	4
AN	8	5	4	1	1	0	2	1	1	0	23
NC	1	1	1	0	0	0	1	0	0	0	4
UB	1	0	0	0	0	1	0	0	0	1	3
MP	1	0	0	0	0	1	0	0	0	1	3

Species	Carbohydrate Esterase Family (CEs)											Total
	1	2	3	4	5	8	9	12	15	16	No classified	
FP	7	1	9	8	11	4	1	3	0	5	0	49
FG	4	1	5	7	13	6	1	3	0	5	0	45
FF	3	1	7	9	11	7	1	3	0	5	0	47
LM	3	1	2	7	8	3	2	3	2	2	0	33
MO	10	1	6	9	17	1	1	3	1	2	0	51
BC	2	0	1	4	11	5	2	3	0	6	1	35
SS	2	0	1	4	8	5	2	3	1	6	1	33
AN	1	0	5	6	4	3	1	2	0	3	4	29
NC	6	0	3	3	3	1	1	1	1	1	1	21
UB	1	0	0	5	2	1	1	0	0	0	0	10
MP	0	0	0	7	1	1	1	0	0	0	0	10

Species	Auxiliary Activity Family (AAs)													
	1	2	3	4	5	6	7	8	9	10	11	12	13	Total
FP	14	3	29	0	5	2	5	7	14	0	4	3	0	86
FG	14	1	20	0	5	1	4	4	13	0	4	2	1	69
FF	12	0	24	0	4	2	4	3	13	0	4	1	1	68
LM	2	0	4	0	2	0	1	3	20	0	3	3	1	39
MO	15	3	22	0	4	1	3	7	24	0	7	5	1	92
BC	1	0	6	0	3	1	1	3	9	0	2	0	1	27
SS	8	0	23	0	5	1	1	2	9	0	2	1	1	53
AN	2	0	16	0	0	0	0	2	9	0	2	0	2	33
NC	8	0	2	0	1	0	0	2	14	0	4	3	1	35
UB	5	0	7	0	2	1	2	0	0	1	0	0	0	18
MP	5	0	8	0	3	1	2	0	0	1	0	0	0	20

Species	Carbohydrate-Binding Module Family (CBMs)																					
	1	2	5	6	13	14	18	20	21	24	32	35	38	42	43	48	50	52	63	66	No classified	Total
FP	14	1	2	1	12	0	11	5	1	1	3	4	1	1	1	3	2	0	4	0	0	67
FG	13	0	0	1	2	0	34	2	2	0	3	3	0	1	1	3	19	0	3	0	0	87
FF	12	0	0	1	1	0	22	2	2	2	3	3	1	2	1	3	21	0	3	0	0	79
LM	5	0	0	0	0	0	30	3	1	0	1	4	0	0	2	2	5	0	1	0	1	55
MO	28	0	0	2	0	0	53	3	1	0	0	3	0	2	2	3	14	1	1	1	0	114
BC	17	0	0	0	1	0	17	3	1	17	2	3	0	1	1	3	1	0	1	0	0	68
SS	24	0	0	0	1	0	28	3	1	17	2	2	0	1	1	3	10	0	1	0	0	94
AN	7	0	0	1	0	1	17	4	1	2	0	3	0	1	1	1	4	0	1	0	0	44
NC	19	0	0	0	2	0	3	2	1	8	1	0	1	0	1	1	2	1	0	0	0	42

UB	0	0	0	0	0	0	1	0	1	0	0	1	0	0	1	2	0	0	0	0	0	6
MP	0	0	0	0	0	0	1	0	1	0	0	1	0	0	1	2	0	0	0	0	0	6

Note: The enzyme classes were predicted by the CAZyme database (<http://www.cazy.org/>). Organisms, FP, *Fusarium proliferatum*; FG, *Fusarium graminearum*; FF, *Fusarium fujikuroi*; LM, *Leptosphaeria maculans*; MO, *Magnaporthe oryzae*; BC, *Botrytis cinerea*; SS, *Sclerotinia sclerotiorum*; AN, *Aspergillus nidulans*; NC, *Neurospora crassa*; UB, *Ustilago bromivora*; MP, *Melanopsichium pennsylvanicum*.

Table S6 The protein-encoding genes and genomes of species used in this study

Species	Genome size (Mb)	No. of genes	NCBI accessions	BioProject	BioSample
<i>Aspergillus nidulans</i>	30.05	10,045	AACD000000000	PRJNA130	SAMN02953587
<i>Aspergillus niger</i>	34.85	10,947	ACJE000000000	PRJNA15785	SAMN02953752
<i>Botrytis cinerea</i>	42.63	13,703	AAID000000000	PRJNA15632	SAMN02953628
<i>Fusarium circinatum</i>	43.95	15,022	AYJV000000000	PRJNA41113	SAMN02371877
<i>Fusarium fujikuroi</i>	43.83	14,810	HF679023 to HF679034	PRJNA322155	SAMEA3724789
<i>Fusarium graminearum</i>	36.45	13,826	AACM000000000	PRJNA13839	SAMN02953593
<i>Fusarium oxysporum</i>	61.38	17,458	AAXH000000000	PRJNA18813	SAMN02953675
<i>Fusarium solani</i>	45.81	15,702	NGZQ000000000	PRJNA368786	SAMN06272960
<i>Fusarium verticillioides</i>	41.84	14,180	AAIM000000000	PRJNA15553	SAMN02953630
<i>Leptosphaeria maculans</i>	45.12	12,469	UNSE010000000	PRJEB24468	SAMEA104483101
<i>Magnaporthe oryzae</i>	40.97	13,184	AACU000000000	PRJNA13840	SAMN02953596
<i>Melanopsichium pennsylvanicum</i>	19.15	6,280	HG529494 to HG529928	PRJEB4565	SAMEA2178376
<i>Neurospora crassa</i>	39.23	9,841	AABX000000000	PRJNA13841	SAMN02953583
<i>Rhizoctonia solani</i> AG-I IA	36.93	10,593	AFRT000000000	PRJNA51401	SAMN02981347
<i>Saccharomyces cerevisiae</i>	38.1	5,645	AMQD000000000	PRJNA174690	SAMN02769632
<i>Sclerotinia sclerotiorum</i>	38.45	14,714	AAGT000000000	PRJNA15530	SAMN02953621
<i>Ustilaginoidea virens</i>	38.96	8,426	PGGP000000000	PRJNA414696	SAMN07807409
<i>Ustilago bromivora</i>	20.77	7,408	FMVU000000000	PRJEB7751	SAMEA4497028

Additional File S1. Sanger sequencing results of structural variants (SVs) based on PCR validation for *F. proliferatum* and *F. fujikuroi*

This Additional file 1 contained Sanger sequencing results of structural variants (SVs) based on PCR validation for *F. proliferatum* and *F. fujikuroi*. Results were presented in FASTA format where the read ID corresponded to SV ID in table S3. **A** indicated sequences in *F. proliferatum* strain Fp9. **B** indicated sequences in *F. fujikuroi* strain IMI 58289. The terminal regions in light gray background are primer sequences.

>1-A

AGGGGACAAGAGGTAAGGCGCCGCGCTGACAGCTTCTTGGTCCCTTCAGGGTGACGATGATATCAAAAATCGAGAATAGAGGTTGTCTACGTAGGCTATCCCTGCTTC
GCCTCCCCTGTCAAGCTGGCTACCAGCCCCTGACGGTGCTCCATACCCAGCGACTTCCCCAAAGGATGGGCCCCGCTCGGTGCTCCGCTCATCGTCCGAGCCGGCCCC
GTGTTGAGACGCTCTGGTGGTTGTGAGGTGGTTCCTTCTTGCGGGGAAAACCTACCCAATTAACAAAATTTGAAGCCGGGGAACTTAATGGGGCCATCTCAGTATGGTAT
CAAGGTTGAAGTAGTAACAAGTGGTTCATAATTGAAATTGAGCATGCCAAGATCAATCCAAAGGTCTCGCGATCT**CTGCACAGATAGCCTGA**

> 1-B

AGGGGACAAGAGGTAAGGCGCTGCGCTGACAGCTTCTTGGTCCCTTCAGGGTGATGATATCAAAAATCGAGAATAGAGGTTGTCTACGTAGGCTATCCCTGCTTCGCC
TCCCCTGTCAAGCTGGCTACCAGCCCCTGACGGTGCTCCATCGCCAGCGACTTCCCCAAAGGATGGGCCCCGCTCGGTGCTCCGCTCATCGTCCGAGCCGGCCCGGTG
TTGAGACGCTCTGGTGGTTGTGAGGTGGTTTCTAAAGGTCCGAGCCACAAAACCCCCTCAATCTGAATGCAATGAGGACCTGTCTTTGTTCCATGAAGCGGTTTGCGTT
TCCTTCTTGCGGGGAAAACCTACCCAATTAACACAATTTGAAGCCGGGGAACTTAATGGGGCCATCGCAGTATGGTATAAAGGTTGAAATTGTCAACAAGTGGTTCATA
GTTGAAATTGAGCATGCCAAGATCAATCCAAAGTCTCACGATCT**CTGCACAGATAGCCTGA**

> 2-A

TAACCTCTCCTATCTCTCAGCCGCGATGCGGAGACACCTCACCCCATTCCTGATCTGGAAAGACTTCCAATATTGGGCGTAACTGGATCTGGTCTCGCAGATTCAACA
TGTTATACTATATATCTGCCGAGATCAGGCTTCCTTTGGAGTGACAGCATGATCTGGCAGCAGAGTCGACCTGATCAGATATCTAACTCCGTGAAAGACCATGTTGACGA
AAACGGAGAACATTGGTCTGTTGAGGGTTCTCGCCGTGTGTTTTCCAGGACAGTTTTCTGGCACGACATCCGTGGGAAGTTCAGAAATATCCCCGCCCTAAGCATACA
GCACAATGGAATAAACGGGTTCTCTCGGGCGATACTGTCCGCCTATATGACCCTATGACTAGCCAATATCTTTGCGCAATACCTGGTGAGCGAGTAGTCAGTGAAGCGG
GTTATTTCCGCACGAAAAGTAGCACTGAGCAGGACCTTGATAGAATTCGAATAGGGTAAGCATATACAACCTGTTAACAGGATTCGTGCTGACGTACTATCCAAGAAGTG
TCTTAAATACTGGCTCTGCGAGCTGTGACTGGAAAGTGATTATGAT**GTTGTTCAAGGGAGCGT**

> 2-B

TAACCTCTCCTATCTCTCAGCCGCGATGCGGAGACACCTCACCCCATTCCTGATCTGGAAAGACTTCCAATATTAGGCGTAACTGGATCTGGTCTCGCAGATTCAACA
TGTTATACTATATATCTGCCGAGATCAGGCTTCCTTTGGAGTGACAGCATGATCTGGCAGCAGAGTCGACCTGATCAGGTATCTAACTCCGTGAAAGACCATGTTGACGA
AAACGGAGAACATTGGTCTGTTGAGGGTTCTCTCGGGCGATACTGTCCGCCTATATGACCCTATGGCTAGCCAATATCTTTGCGCAATACCTGGTGAGCGAGTCGTCAGT
GAAGCGGGTTATTTCCGGCACGAAAAGTAGCACTGAGCAGGACCTTGACAGAATTCTGAATAGGGTAAGCATATACAACCTGTTAACAGGATTCGTGCTGACGTACTATCC
AAGAACTGTCTTAAATACTGGCTCTGCGAGCTGTGACTGGAAAGTGTATTATGAT**GTTGTTCAAGGGAGCGT**

> 3-A

ACTCAGTCTGTCCGTTGACGGTAACTGGGGGATCTGTTGCAACCCGAACCTCTTATTTCGCATGGGTTACTGAAAAATCCTTGCGGATACGAATATTCCGAGGATCAGGT
GTCTGAAGGCCGTGAGAGTCGTTTGGTGAAGGGCTTCCCTCATCTTGTTTCTGGTAAGTTGTCCTAGGGCTCGAGACCGCTTTGTTCTGTAGTGGCGAAGGCTTTGAGTG
CGGCTTGCGGAGACTATTGAACGTGAGGTGCGAAGATTGGCTCCATCAACTTTAACGGGGAAACGCCTGGCACGGATTGGCTTTGAAGAGTGCTGGCGCGTTTCGAA
CTGTTGATTTGAACCCTGCGGAATCGGTAGCTCAGACCGGCTGGCAGTAGATGTGGCCTCCTGTTTCAAAAATTGCTTTATCTGAGCCGTGACAGCCATATCAGTGCTTC
CGTTGTCCCGTGCAGTGTGGAAGCATCTTCAAGGTAAGTGTGCTTCGACAATACGACTCAGCATCAGAGTCAACGGGTTGCCGTGATCTTGAGGGCGAGGAGTGCAG
TCATCTCGGAGATGCATAATGGCAGATGCTGAATCTTATTCTTTTGGATTCCCAGGACCTTGAGAGACGCCATCTTTGCTATGTCATCTGGGAGGCATTCAATCTTGTTTCT
ACTTAGATCGAGGATCTCGAGACGACTTAACTCCAAGAGCTGCCTTGTAGTTAGCCTTCAGCGGCATGCATATCACGGCTTGAGGGAATATGTACCACAGGAGGAAAA
GTGTGGATGCAATTGCTCCGGATGTTAAGGTAGCGCAAGGAAGTAAATAGAGACAGATGTGGCGGGATGTTTGAAAGATGGTTGTGAGATAAAGCTAGCCTATTGGTG
AGCTAGGTTAGCAGTTGGATATAAGCCTGAATTATGGAAGTACAGACCGCTCAACGTTCCGATTGAGGTTATCGAGAGTATTAGCGGATGAGTCTGAGAGACCACTGTG
GCTAAGGTCGATGGTGACGCCTTGGTCAACAAATAGCCCAGACATGGCCATCACTACTATTCAATACTCCCGTCGACAGTCGCTTCAAGCCTTCTTGTAGCTGCGCCGG
ATCGGGAGATAACCACTATGGTGGGTGATGAAGATGTCTGGCCGCTGTAAGTTTAAAGATTAATGCTCTGTTCCCTGGTGTCTAAGTGAAGATATTATTCTTTAATGGAGGTG
ACACTAGATCTGGTGGGGCTGTGGTGTGATGTTGTAAATTGACAGATTCCGGTCGTGGCAGGGCGGGGACATTCATTGGAAACGCGGAGTCACATGTTGGCTTAGGTAA
GATGCTTTTCGTAGGCCAACATCATAATCATAACTTATTCCGCATTTCCCTCATCAATCA**TAGAGGAAAACAGGACC**

> 3-B

ACTCAGTCTGTCCGTTGACGGTAACTGGGGGATCTGTTGCAACCCGAATCTTATTTCGCATGGGTTACTGAAAAGTCCTTGCGGATACGAATAGTCCGAGTATCAGGT
GTCTGAAGGCCGTGAGAGTTGTTTGGTGAAGGGCTTCCCTCATCTTGTTCTCTGGTAAGTTGTCCTAGGGCTCGAGACCGCTTTGTTCTGTAGTGGCGAAGCCTTTGAGTG

CGGCTTGGGCATCACTATTGAACGTGTAAGTTTAAAGATTAATGCTCTGTTCTGGCGTCTGAGTGAAGATATTATTCTTTAATGGAGTTGACAGTAGATCTGGTGGGGCT
GTGGTGTTGATGTTGTAAATCGACAGATTCGGTCGTGGCAGGGCGAGGACACTCATTGGAAACGCGGAGTCACATGTTGGCTTAGGTAAGGTGCTTTCGTAGGCCAAC
ATCAAACTCATAACTTATCCGCATTCCTCATCAATCA**TAGAGGAAAACAGGACC**

>4-A

CGGATAGTCGTCTTCATGGGAGTAGATTGAACCGATGTTGTTTCCCGTCGATCACTGGGAGGGTTAAATGCCAGTTTTGATGGGCAAGATGCTCTTCTTTGGGGTATGCT
TGGATAGGCAGGGCTTCCAGTCAATTTGCCAACTTGTCCCATGAGCTTTGAGGAATGAATCTCTTCTTGATTGAAGTTCTGAGAAGATACTCAGCATGAGAAGGTGTTG
TGGGCGTCGTATCAGCCTCGCGACGACGTCCTACCAAGGTTTGTGGCGTCCTATTATTGAGTGTTGTTGGGGATACGACTTCAGTGGCTTTCGCTTTGCCAACCTCTTCCT
CTTCGTCGCTAGATTCATCCACGGAGGCAGTGACACAGCCTCCGTGGTTTTTCAGTTACAGCTAGGCTGCTGGTGACATCGGCTGTCGCAGTCACACCCATGTCCTCATCT
TCTGACCCTGTGGCTGATTGACATTCGCTGACCGAATCAGATGGCGTGGTGTCAATCATCGAAGAAGGTGGCAGTCAGAAATCTCGAATCCACGAAACTCCTTGCTTG
AGATAGATGACAGAGGACTTGTACAGCGATTGGTCAATTTCCATTGCTGATTGAGACTCTCGTAGGCTGCGCCCCCTCCTCTACTGGTGTGCTGGCCATATCATCGTTG
GGCGACGACAGGCCAGACCAAGTGTCTCGTCTCTGGATATGGACACATCTTGGTCTGATGCAGTCTCAACAGCTTGATTGAGCGTTGGCCGCATTTTAAACAGAAA
CTGTCATCTTCTTGGGTCTCAAAAGCGGAGCGAGGATTCTGACAACTTCATCTT**GGGCTCTCAAATCAGTT**

>4-B

CGGATAGTCGTCTTCATGGGAGTAGATTGAACCGATGTTGTTTCCCGTCGATCACTGGGAGAGTTAAATGCCAGTTTCGATGGGCAAGATGCTCTTCTTTGGGGTATGCT
TTGATAGGCAGGGCTTCCAGTCAATTTGCCAACTTTCCCATGAGCTTTGAGGAATGAATCTCTTCTTGATTGAAGTTCTGAGAAGATACTCAGCATGAGAAGGTGTTG
TGGATTTTGATGGCGTCGTATCAGCCTCGCGACGACGTCCTGCTAAGGTTTGTGGCGTCCTATTATTGAGTGTTGTTGGGGATACGACTTCAGTGGCTTTCGCTTTGCTGG
TGACATCCGTTGTCCCAACCATATCTTCATCTTCTGACTCTGTGGCCGATTGGCATTGCTGGGCATTTCTTCAGTGACGAGCACTATTGCGTCTTCCGCTGACACTTGAC
TAGGACAACTTGTGAGTTCTGAAGCAGATGGCGTGGTGTCAATCATCGAAGAAGCACTGGCGCTATCTGGTCGGATGTGATCGGAGGCAGTGACAATGCTCTCGTGAT
TTTCAGTTACAGCCAGGCTGCTGGCGACATCGGCTGTCACAGTCACACCCATGTCCTCATCTTCTGACCCTGTGGCTGATTGACATTGCTGATCGAATCAGATGGCGTG
GTGTCAATCATCGAAGAAGGTGGCTGTCAGAAATCTCGAATCCACGAAACTCCTTGCTTGAGATAGATGACAGAGGACTTGTCAACGATTTGATCAATTTCCATTG
CTGAGTCTCGTAGGCTGCGCCCCCTCCTCTACTGGTGTGCTGGCCATATCATCGTTGGGCGATGACAGGCCAGACCAAGTGTCTCGTCTCTAGATATGGACATATCTTGG
TCTGATGCAGTCTTAACAGCTTGATTGAGCTTTGGCCGCATTTTAAACAGAAACTGTCATCTTCTTGGGTCTCAAAAGCTGGGCGAGAATTCCTGAAAACCTTCATCTT**G**
GGCTCTCAAATCAGTT

> 5-A

ATGACAACCATGAATCAGGAGTTAGTGAGCCTTGTGCCGCCAGTACTGGTTGAGCTCCATAGCTTCATAGCTCCACTAGCCAAGCAGTCAGATAGTAGCCAGATAACC
GCTGAACCATGCCAGACCGCACAGACGATGTGTTTCAGTTCTGAGACTACACCCTGATGTGTGCAATCGCCTGCAAACATGTCACTTTCACATAAGTAACTCGATTGGA
TCGATACGTACGAACTTTGGTTCCGGCTGCATATTATTGCAAGGTGCTATGCCCCGGGAATCTGGGAATAGATCTGACTTATTATAGTGGTATTTTGTACATTAGAATCAACT
CAACGTGTCTGAGATTGAGGTTGAGATTGAGGCGAATTTTCTGGGCCTCATCTACGAATACCTGACCGGCCTTACTATAACAAGGCACGCCGATCTAGGTGCGGGGGTAG
CACATGGCATCGCGGATAACACAAGGCACAGATGACCGAATATCGACCGGCTTGTGTTGTGCATAACATCTTCCGGAAGTACCAAGCTTTTCTCAGCAGACCAGCGCCG
AGAAAAGCTTGGTCCAGACGGGCATATCGGTCAGCAAAGCGCCGGGAAATGGCTCACTCAGTCGTTGGTCACTGAACATATAGTGCGCTTACCGAACCGACCAAGCC
TTGAGGGCATATGCTCTATAGTCATGCTCATGCCTGGCATAGCTGAGAGCATTGCGCG**CACAGGGTCTTCTTGTT**

> 5-B

ATGACAACCATGAATCAGGAGTTAGTGAGCCTTGTGCCGTCCAGTACTGGTTGAGCTCCATAGCTTCATAGCTCCACTAGCCAAGCAGTCAGATAGTAGCCAGATAACC
GCTGAACCATGCCAGACCGCACAGACGATGTGTTTCAGTTCTGAGACTAAACCCTGATGTGTGCAATCGCCTGCAAACATGTCACTTTCACATAAGTAACTCGATTGGA
TCGATACGTACGAACTTTGGTTCCGGCTGCATATTATTGCAAGGTGCTATGCCCCGGGAATCTGGGAATAGATCTGGCTTATTATAGTGGTATTTTGTACATTACGGAGGTC
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ATAACCTTTCCCCTAAAGTCTACTATAATTATAATTATAGCGCTTACTTTACTATCAATAAGAGACCTCTTGACCTTCTGGGTATCGATAGGGGCATTCCCTGCTAGCTTCA
TTTGGCTAATAGGGGGTCAGGATAAACTTTTGGCAGGGACCTCCGTAGAATCAACTCAACGTGTTTGAGATTGAGGTTGAGATTGCGCGAATTTTCTGGGCCTCATCTA
CGAATACCTGACCGGCCTTACTACAACAAGGCACGCCGATCTAGGTGCGGGGGTAGCACATGGCATCGCGGATAACACAAGGCACAGATGACCGAATATCGACCGGC
TTGTTTGTGCATAACATCTTCCGGAAGTACCAAGCTTTTCTCAGCAGACCAGCGCCGAGGAAAGCTTGGTCCAGACGGGCATATCGGTCAGCAAAGCGCCGGGAAATG
GCTCACTCAGTCGTTGGTCACTGAACATATAGTGCGCTTACTGAACCAACCAAGCTTTGAGGGCATATGCTCTATAGTCATGCTCATGCCTGGCATAGCTGAGAGCATT
GGCG**CACAGGGTCTTCTTGTT**

> 6-A

ATTATGTGATGCCGCCGGCATCTGCATGGCGCAGGCGTGGGACCAGTTCAAATACCGCGGCGACGGCGGTAAATCATCAACCTGCTGGTGCTGATCAACTTCCGAGC
AAGAGAATGGGTGCTCATCAACACTTTTATCGACATTGTAGCCATATAATGCTTGCAAATAGAGAGCAATTGCCCTGCAGTCACAGGGTATCACATTGAAGGGGAAAG
AAGCAGGGGTTGTGTTAAAATCCATCATCTGCCTTAAGCAATACGAAGAGGAGTGAAGGCTTACAAAACCTGCCGGAACCTCGCTCTTAGCGCGGCAACG
CACTGTCTGTTCCCTGTCATCCTAAATGGATCTCTGCTTTGGCGTGACATGGCAGCTGGGTTGCTGCTGATCGTTTGATCCCGATGAGATGAGCAATCGGCCGAGTCGAG

CTCACAGACATTTGCCCCTGACACTTGTGGGGAGCGGAAAACATCAAGCAGAGCAGAGCCTGAGAAGATCTAGGTAGAGCTCACGCCCTCTACCCCTGTAAACGAAC
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TGTGGCCCATGACGGACGGAAAGAGACGTCAGTTGTTATAAAGAAGCAATGCAGCGGCACATGGAAAAGCAAGTTTTAACAAGTTCCTCAGCATAACTAGTCGCCGAG
TCCCTTGACAGTGAGGCATATCAAAATGAGGGGGTTTTGGGCGGCACAACTATCATCAGAACTGGGGTATTCAACTACCAATTTGCACGACGATCAATTGATCGAGAATC
TTGGCCCAAGGCTCGACCTGCTCACTGCTTTTTGTATATTGTTGCCTGAACAGGCCTTGCTCCCAGGTGTCAATTCGAATCCCCACACAATACTGATATAAGCAGGGTTG
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TCTTCACATCCCCTGAATAACAGTCGGTATATGGTCAACCATATTGGTGCCTGGATGCCTCTATATTGACTATATTGAGCGTAAATTATTCTCTGCGAACTAGGGATTTCCT
TGTCTATCAGTTCTCCTTGTTTACATATACCCAGGCCTATGCGGAACCGCAATATTAAATTCGCTAAACAAATTGTTGGAGCTGCCTTCGTCCTGACTAGGAAATGGA
AACGAATCGGTGAGCTCTCCCTTGATTCCCTCATGATCCCTCACTGCCTTATCCTTCGTGCGCTTCCCAAGGGTGTTGGTTGATCAGGTGTGAGAGACTTGTGTCTTCTCAA
CTGACGCGTGGTGACCTGAAT**CAAGCATGAGTTGTGAT**

> 6-B

ATTATGTGATGCCGCCGGCATCTGCATGGCGCAGGCGTGGGACCAGTTCAAATACCGCGGCGACGGCGGTAAATCATCAACCTGCTGGTGCTGATCAACTTCCGAGC
AAGAGAATGGGTGCTCATCAACACTTTTATCGACATTGTAGCCATATAATGCTTGCAAATAGAGAGCAATTGCCCTGCAGTCACAGGGTATCACATTGAAAGGGAAAGG
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CTCACAGACATTTGCCCCTGACACTTGTGGGGAGCCCATACTCTGCGTTACATCGTAGGGGGGCTAAGCGGCTCGGAGTTAGCCTTTGCCATGGTAGCTATACCGCTGC

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TTCGCTAAATCAAATTGTTGGAGCTGCCTTCGTCTGACTAGGAAATGGAAACGAATCGGTGAGCTCTCCCTTGATTCTCATGATCCCTCACTGCCTTATCCTTCGTGCG
CTTCCCAAGGGTGTGGTTAATCAGGTGTGAGAGACTTGTGTCTTCTCAACTGACCGCGTGGTTACCTGAA**TCAAGCATGAGTTGTCGAT**

>7-A

GCCTCGGGATATGGAGGTCTCTATGCCGAGCGGGGCTTCGTTTCGTGGGTGAGGCCTTGGCCAACTCTTGGTGAGACTATCGTCAATGTCGTCACTTTTGCCAACTCGT
GCAATGCCTACATTCCGATACAGGAGAAAGAGGCAGCTTGTGCGATTGTCTAGTCACGAGATCCGATTCAATGCTTTTCTTGACGACTATTCTTTGAATCAACTAAACCCA
TGCGCCTCAAGCCAACATTGGTCCAGAATATGCCAACATACCTATCGATCGATGTCTTTAGACCAACAACCTCCTCAATTTTGCCAAGCCTTACAATTGTCCCCTGCTTTAC
CCAGTGACATACAGAATCGAGACCCTTGCAGGGATATTCTGACGGGCAGTTATCTCAACACCAACTAGAGTCAAAAAGTCCTCCTATACCTTCCCGATTGGGATGTCCA
GCTATTGACACGATGAAGGACTTTAGGCGCGGTCTGAGGTGACTCTCGAAAGAGCGATCGATTGGTAGTACGAGCTATGATATTCTGTAATCAAGATAACAAGACGGTT
ATGTGAGGATATCCCTGGGATCTAGTTAAAGACCTCGGATTATTATTGGTCACGGTTCCTGACCAAAGGCTTGGTGGTGAATCAGATATCTCTCGCAGATGTGGCCATG
GTGCAATTGAAAGTCTGAAACTAGATTCTAGATTCAGTGCTAATCAATACCAATACCAGAACCTAATGATTTTCTCATCTGTCCGACACCGAGGATTTCATAAACCCGTC
GGCCTCCAAATCTCTAAAGCTCCGACACCAGCAACGCCACAACGCACAAGCCACCCG**CCTCATCCCTGTTCTCGA**

>7-B

GCCTCGGGATATGGAGGTCTCTATGCCGAGCGGGGCTTCGTTTCGTGGGTGAGGCCTTGGCCAACTCTTGGTGAGACTATCGTCAATGTCGTCACTTTTGCCAACTCGT
GCAATGCCTACATTCCGATACAGGAGAAAGAGGCAGCTCGTTCGATCGTCTAGTCACGAGATCCGATTCAATGCTGTTCTTGACGACTATTCTTTGAATCAACTAAACCC
ATACGCCTCAAGCCAACATTGGTCCAGAATATGCCAACATACCTATCGATCGATGTCTTTAGACCAACGACTCCTCAATTTTGCCAAGCCTTACAATTGTCCCCTGCTTTA
TCCAGTGACATACAAAATCGAAACCCTTGCAGGGATATTCTGACGGGCAGTCTAGGGGAGGAAAGAAAACCTCTGGACCTTGATCCTAGATGGCAAAAAGACTTAGGT
AAATTTGCATAAATTTAGGATATCTTTTGCTGGGTTTATTTTGACCCCTTATATCAAGGTCCAGTGTTTTCTTTCTCCCTGAGGGCAGTTATCTCAACACCAACTACTAAGA
GTCAAAAAGTCTTCTATACCTTCCCGATTGGGAAGTCCAAACATTGACACGATGAAGGACTTTAGGCGAGGTCTGAGGTGACTCTCGAAAGAGCGATTGATTGGTAGT
ACAAGCTATGATATTCTGTAATCAAGATAACAAGACGATTATGTGAGGATACCTATCCATGGGATCTACTTAAAGACCTCGGATTATTGGTCACGGTTCCTGACCAAAGG
CTTGATGGTGAATCAGATATCTCTCGCAGATGTGGCCATGGTACAATTGAAAGTCTGAAACGAGAATCTATATTAGTGCTAATCAATACCAATACCAAAACCTAATGA
TCTTCTCATCTGTCCGACACCGAGGAATTCAATAACTCGTCGGCCTCCAAATCTCTAAAGCTCCGAAACCAGCAACGCCACAGCGCACAAGCCACCCG**CCTCATCCCT**
GTTCTCGA

> 8-A

GTCTCCTCTTTCCTCACTTGAATCTTGCCGTCCCGTACCGTGCTGCTCATCTCCCTCTCATACTGTGACGAGCACTGACACCGCCAGAACAATATCCATTAAACACTGGC
CCAGAGGAGGACCTAAAAGACCGCCAACCATCAACTAACTCTATATCTCTGGCTGGTTTCAAGTGTAACCTCTCCGCAAAGGCAGGCGACTTGCGTTGAAAATGTTTGT
TTGTGCAATGCATATGCACATATATGCACATAGGCTGATGCAACTGATGCAACAGCAACACACTAACGTGGGTATGCCAGGGATACCCACGACTAATCTCCAGCCACG
CATTCTCTGTCCTTGACTGTCAGTGGCCAACTGTACGATGTGTATGCCAACTCGACAATCCAAATGCTTGATCCAGCATCTCTGGAATACGACCTGATGCATCCATGTTT
CAAGATTGGCTGCCAGTTGTAGGCAGCCTAGGGGAGGAAAGAAAACACAGGACCTTGGTCCTAAATGACAAAAAGACTTGGGGTAATATAGCCTAAGTTTAGGATGA
CTTTTGCTAAGTTTATTTTGACACCCTACAGTAAGGTTTCGCTGTTTTCTTGCCCCGGAGGGCAGCCCTTCAAATGCTGTGCACCACACCACTTTCTCTTGTCGGGAGCAT
CAACTGTCAGCGGCAATGGAATGCATACGTACGTACTCCAAATCCACGTTGTTAACCGCCAGCTAGGACTGGTTGTTTCAGTCGATTATTCCTCGGCTCACACAACCCAT
CCATGTTTCAGTTATGGATACTTGATCGTTTAATACAACCTTGAGGGTCGCATTGCCCGGACATGGGCTCCGGCAGAGTCATGTTGCCTACCATCCTTGACATTTACAAGT
CATGTCAACTCATCTCGGTACTTTATTTCGAAACTGCCTAGCTGTCAAAAACATCTGACATTTCGCAGGTAGCCACAATGCGCTGACCAACTGCATCACGGCATTTCGCTCC
ATCACGAAGTCTATCAGAACAAAGAAACCCAACTCCCTGGCCACGGCGCTGCGGGTACCATTTTGCTGCATTCCGGTCTCCTCCAGAAATTCACCGTGCGTAA**AAAGG**
TTCTGTTGGTTC

> 8-B

GTCTCCTCTTTCCTCACTTGAATCTTGCCGTCCCGTACCGTGCTGCTCATCTCCCTCTCATACTGTGACGAGCACTGACACCGCCAGAACAATATCCATTAAACACTGGC
CCAGAGGAGGACCTAAAAGACCGCCAACCATCAACTAACTCTATATCTCTGGCTGGTTTCAAGTATAACTCTTCCGCAAAGGCAGGCGACTTGCGTTGAAAATGTTTGT
TTGTGCAATGCATATGCACATATGCACATAGGCTGATGCAACTGATGCAACAGCAACACACTAACGTGGGTATGCCAGGGATACCCACGACTAATCTCCAGCCACGCA
TTCTCTGTCCTTGACTGTCAGTGGCCAACTGTACGATGTGCATGCCCAACTCGACAATCCAAATGCTTGGTCCAGCATATCTGGAATACGACCTGATGCATCTATGTTTCA
AGATTGGCTGCCAGTTGTAGGCAGCCCTTCAAATGCTGTGCACCACACCACTTTCTCTTGTCGGGAGCATCAACTGTCAGCGGCAATGGAATACATACGTACGTACTCC
AAATCCACGTTGTTAACCGCCAGCTAAGACTGGTTGTTTCAGTCGATTATTCCTCGGCTCACACAACCCATCCATGTTTCAGTTATGGATACTTGATCGTTTAATACAACCT
CGAGGGTCGCATTGCCCGGACATGGGCTCCGGCAGAGTCATGTTGCCTACCATCCTTGACATTTACAAGTCATGTCAACTCATCTCGGTACTTTATTTCGAAACTGCCTA
GCTGTCAAAAACATCAGACGTTTCGCAGGTAGCCACAATGCGCTGACCAACTGCATCACGGCATTTCGCTCCATCACGAAGTCTATCAGAACAAAGAAACCCAACTCCC
TGGCCACGGCGCTGCGGGTACCATTTTGCTGCATTCCGGTCTCCTCCAGAAATTCACCGTGCGTAA**AAAGGTTCTGTTGGTTC**

> 9-A

AGGTCGGTGTCGGTATCGTGCGCTCTGGTGTCGCCAAGGCCAAGGCCGATCACATCCTGATCTCTGGTCACGATGGTGGTACTGGTGCCTCTCGATGGACTGGTATCA
AGTATGCCGGTCTTCCTTGGGAGTTGGGTCTGGCTGAGACTCATCAGACTCTGGTTCTCAACGATCTTCGTGGTCGTGTCGTTGTCCAGACTGATGGTCAGCTCAAGACC
GGTCGTGATGTTGCACTGGCTTGTCTGCTAGGTGCTGAGGAATGGGGCTTTGCCACCGCTCCTCTCATCGCTATGGGCTGTGTCTTCATGAGAAAGTGCCACTTGAACAC
TTGCCCTGTTGGTATCGCTACGCAGGATCCTGAGCTTCGCAAGAAGTTCAGTGGAACTCCTGAGCACGTCATCAACTTCTTCTACTATGTTGCCAACGAGCTCCGGGGCTA
TCATGGCCCAGCTTGGTTTCCGAACCATCAACGAGATGGTTGGCCACGTCGAAGTCCTCAAGATGCGTGATGACCTTCGAACCCACAAGACAGCCAACATTGACCTGT
CTCTCCTCCT**GACACCCGCACACAAGC**

> 9-B

AGGTCGGTGTCGGTATCGTGCGCTCTGGTGTCGCCAAGGCCAAGGCCGATCACATCCTGATCTCTGGTCACGATGGTGGTACTGGTGCCTCTCGATGGACTGGTATCA
AGTACGCCGGTCTTCCTTGGGAGTTGGGTCTGGCTGAGACTCATCAGACTCTGGTTCTCAACGATCTTCGTGGCCGTGTCGTTGTCCAGACTGATGGTCAGCTCAAGAC
CGGTCGTGACGTTGCACTGGCTTGTCTGTTAGGTGCTGAGGAATGGGGCTTTGCCACCGCTCCTCTCATCGCTATGGGCTGTGTCTTTATGAGAAAGTGCCCTCGAAATTA
GCACTATGGTTAGGACATCCCAAGGACCTAAGCCTATCTCTGCTATCAACATTGGGGACACACTATATGATCCCAATGATAACCCTGTCCTATGTCTTGCCGTGGCTCCTG
TTCAACAAGGTCGTTTGAAGGAGATACGCTATAAAGAGTTCGATTCACGACGCAACGTGTCTTTCAAGTGACGCCTGATCACATATTGCCCCCTTCGAACCTATGGCAC
CAGGCCTTCGGTCAGCAAGATCAGTGTGACTTGGTTCACGTATTGTGATAGACACTCCCTTGATCGCCAGGCGGACAATCTTCGCTTTGAAGATTTGGTTGACACTATCT
ACAGAGACTTGATGGATAGTCATGAAGTTGAGATTCTTGACAAAGCCGCGGCCCATGGGTATATCGATACTATTCTAACACGACACTACCACCAAGGACAAGACGATC
GTTACTCGAACAAGATCGTTGAAGTTCTTCTCGATTGGCCAACCATGAACTTGAAAACAATCCAGACCTGGTTCGTGAGGCTATGCACGATGCTGTAGATCTGTACTTT
GAAAATCCTCCCAATCTCGTGACGATGCAGAGTACGATGATGATGCCCCTACCATCGATCTTGCCCTGACTTTGTGGCTCTTCGAGACGCTACCCTGGCAAGTACAA
CTGCTGGCAGTACTTATCGCCGCACACCTTCGTTGAATCAGCCAGACTCACAGTCATCTCGCCAATCTCAGCAAACCCAGCGGGACTCTCAACAGTCTGGAGGCATAC
CTCAAGGCTCTGGCGGTATATCTAGACAAGTATCGTTGAATACCCAAGCATCCAGCTCCTCGTTCTGTTGATTCTTCGGCCATAGCTCTATCTGAAGAGGCCATTCAACGA
TTCAATCGGGTAAAGACATCTATCAACCGTAAGCCTTGTCCATGTGGTGGTATTCGCAAGATCTATCGCCAGTTTGCCTCTGAAGAAACAAGCCCAGCTTGTTTCAGTCTCT
ACTACTCAGTCAACATGCTCATATGGTAGACCCATATGTTGTTTCGAGATGGAGATGAGATCAATGTTTCTGTCGAGACATTTGAGGGCTTCTGCAATAAAGAAGCTAAAC
GGATGCACCTCAAGCTGCATCGTGCTCCATTGACCTTTGTCCCGGCTCCTAGTGGACAAGATCAAGCAACAGATGAAGCTCTACCAATCGACCCATACTTCCTTGGTTTA
TGGCTTGGTGATGGTGGAGCTGAGGGTCTTTTATCTATGGCAGTGACCATGAGACTCGTGTGTTGGCTATCCAGCTATGTTGATCGTTTGAATAATGGCAGACCAGCTGGT
ACTAGGCCATTGAAACTTAGAGAGTATCGAACGCAGCAAGCTAGTGAAGTCTCTGCGTAACTCTAACTATAGGGCTAGAGTTGATGTCTTCCGTTGGGCCATTACTTCAG
AGTTACATGCACCTGGCCGGCCATGGAGTCCCATTGAGAAGGCTTACAAAACCTTGGGCTTCTCAACAACAAGAGCGCTGGTATCCCAGACTGCTACCTCCAGGCCA
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AGATCGTCGAAGATGCTAAGACTTTGGCTCTTAGCTGTGGCATTTCAGTGACAGGTGTTGACACGTGACACCTCTCAACCAGTGGAACAACAGGCATGGGCCAAGCG
TCCAGTACGTGATCTATCTAGGTAAAGGTTCAAACGAGTTCAGAACACCTGTTGATCCCACGCAAGAGAATGAACCCAGCAAAGACATTCTATACGCACGATGCAC
GACCTTTTACTGTCTCGGACGTGAGGATGGTCAGTACAGAGGAATCCAGGTTTCTGGAGGGCTATTCCAGCTCCAGAACCGCCTCGTTACTCACAATTGCCACCTGAA
CACTTGCCCTGTTGGTATCGCTACCCAGGATCCTGAGCTTCGCAAGAAGTTCACCGGAACTCCCGAGCACGTCAATTTCTTCTACTATGTTGCCAACGAGCTCCGG
GCTATCATGGCCCAGCTTGGTTTCCGAACCATCAACGAGATGGTTGGCCATGTCGAAGTCCTCAAGATGCGTGATGACCTTCGAACCCACAAGACAGCCAACATTGAC
CTGTCTCTCCTCCT**GACACCCGCACACAAGC**

> 10-A

GCTGCCCATCATAAGTGGAAAGTTATCACGATTTCTGCCAATTGCTAATGCATAGTAGGTCATAGGGGAGCTTCCATGAGAATACTATATCCTGTAGGAAGCGCAATGG
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CATCATGTTGGCGGGGTTGAGGGGTTATCTTTCAACTTTAGGGTAGCTAAATTGCACGGCTCACACCTCGCTGGGCGGCACTTTTGTATGAGGATGATTCTACAAGGTG
GAGAAGAGCCTTGTTACTAGGGATGGAGAGTCCCTGTCGTTGCCACACGGAGATTCTGGTCCGGCGATTTCATTGTGCGCTGATCTCCTTTCTGTATATCCTAAAGCACT
ACACGGAAGATATCGAGATGAAGCAAAATTGCCATTGCTTGTGCGCAAGGTGAGGCCATCGTGAAGTTCGGGGAAGATGTCACAAACGGACATTTTAAAGGATGAGC
CGCATTTATGGAACCCCGGCCCGGTG**ACCGAGATTGGGGTGA**

> 10-B

GCTGCCCATCATAAGTGGATGGTTATCACGATTTCTGCCAATTACTAATGCATGGTAGGTCATAGGCGAGCTTCCATGGGAATACTACATCCTGTAGGAAGCGCAATGG
CTTATTGCAATGTGTGCGAGTTCTGATTGCATTAGCATGGATGTTTTCTCTGCCCTTGTCCTTTCATTCATTCAATTTATAAGGATCATATTGGCTGTCATGACAAGACAGTTC
ATCATGTTGGCGGGGTTGAGGGGTTATCTATCAGCTTTAGGGTAGCTAAATTGCACGGCTCACACCTCGGTGGGCGGCACTTTTGTATGAGGGAGGATCTGATATCAAA
GATCCGTAATTACATTTCAATCTAGCTCCAGCCACAAAAAATCATCAAACCCCATTAAGTGCATCGTGTCTTATGACTTGAATGTGATGGAGTATGAGGTCTGGGCGCCC
CGATTGAGGACTATTGGATCATGAGAAGATATATCGAAAAGCGTTGCAGATAACGGCTGGTCTAACACTCCACCATTGGCAGCCTTGTCAGCTGATGTGATGATAGCA
GTAGAGCGAGGGTATGTATTTTCATCTACAACCTCCAGACTGAACAAATAGCCAGCGATCGTTAAGAAAGAAGGAAATAAAGCGACATGAATTGCTGGCAGCTACCAGC
CATAAGACTGGCACTGCATAATATGGTAGCTACCTAAGTAGGTAGTGATACTATTAGAGGTACATAACCAAATGACGTCTGCGGGCCTGGAAATGACGGTGTCTCT
GTTTCATCCACGCTTGCCCTTGTGTTGGACATAAAGCCAGGCGTACAAAGGACACATGACGGATCTATACAGTTGACTGATGTATGTCACGAAAAATATGTTGTCCAGGGC
ATGATCGACTTGGCATGATGATTCTACAAGGTGGAGAAGAGCCTTGTTACTAGGGATGGAGAGTCCCTGTCGTTGCCACAAAGGAGATTCTGGTCCGGCGAGTCATTGT
GCGCTGATCTCCTTTCTGTATATCCTAAAGCACTACACGGAAGATATCGAAATGAAGCAAAATTACCATTCGTTGTGCGCGAGGTGAGGCCATCGTGAAGTTCGGGGAA

GATGTCACAAACGGACATTTTCAAGGATGAGCCGCAATTATGGAACCCCGGCCCGGTG**ACCGAGATTGGGGTGA**

> 11-A

CTCTAATAGTGATGCGAGGTGGAGGAGGTCACACGGCTGGCCAACTGACACATGCAGATCTACGTAGCCTGTCTCGCAACTGCTTGGCTCTATCACCAGACATGTACC
AACTTTGTTGCCTCACTTACTGAAGGTAAGTAACTTACCCTGCGGCCTTGTTGTATTGTAGGACTTGCTGGTTTCACGATTAATAAGCTACAACGGGACTTGGAACGAC
CAAACACTTTGGCCGCTATGACCGCCTTTTGAGCTGATGTTTCTTGGTCTTATTGGCGTGCTCTCTATAAACACATCATCTTGAAGCGGCTTGTGCTTTATGTACCACCTAG
TAAAGA AACTTACGTTTCACGATCAACTAACTAATGTAGTTGCAGTATCTAACTGCGGCTCCCAACAGATGCTACTAGCTGCATCGGGGTGTCTTAGATCCAACACAAAC
ACCATCCTCAGGTT CAGCTTACTAGTAAATTCGTAGTGCGATTTCATTGACTATCTTCTGTACGCTGACCATCTAGCCCAGCAACCCAGCAACCCAGCATCTCTAGCCTC
GTCAATTTAGTCATT CAGTCGTACGAGCAATCTCCGCAAACAAGCGGCTCCTCCCTTCCCCAAGTTCCTACCTATAATTAACGGCATAACGAATGAATGAACACCATCA
TTGCTTCTTCCACAGACATTATTGCGCCCGC**GACCCAAACAAAACGCT**

> 11-B

CTCTAATAGTGATGCGAGGTGGAGGAGGTCACACGGCTGGCCAAACGGGCACATGCAGATCTACGTAGCCTGTCTCGCAACTGCTTGGCTCTATCACCAGACATGTAC
CAACTTTGTTGCCTCACTTACTAGGTA AACTTACCCTGCGGCCTTGTTGTATTGTAGGACTTGCTGGTTTCACGATTAATAAGCTACAACGGGACTTGGAACGACCAAAC
ACTTTGGCCGCTATGACCGCCTTTTGAGCTGATGTTTCTTGGTCTTATTGGCGTGCTCTCTATAAACACATCATCTTGAAGCGGCTTGTGCTTTGTGTACCACCTAGTACGG
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GTATCTGTGGCTGGTAAGCTTCTTCAGCCACAGTTTTCTCGGGCAAGAACTTTTCGCGGCTACCTCCGTACAGAACTCACGTTTCACGATCAACTAACTAATGTAGTTGC
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TTCATTGACTATCTTCTGTGCGCTGACCATCTAGCCCAGCAATCCAGCAACCCAGCATCTCTAGCCTCGTCAATTTAGTCATTCAGTCGTACGAGCAATCTCCGCAAACA
AGCGGCTCCTCCCTTCCCCCAAGTTCCTAACTATAATTAACGGCATAACGAATGAATGAACACCATGATTGCTTCCTCCACGGACATTATTGCGCCCGC**GACCCAAAC**
AAAACGCT

> 12-A

TGCCCAGTGATAACGACTAAGTAACGGTACTTGTGATGTGGGTGGGGAGACAGTGCGGGCTCGTGGCGCATACTAGTAGATAGCTACTTATGAAACAGCGATATGCCA
GGCATGTTCTCCATTTGGTGTAACAGTACTAATGCTGGAACGATGACGCTCTTCTTGTGCACTGTATATCTGTGGTCGCGAGAGCGGTGAAGCTCCTTTCTATAAGTA

TCGGTACATCAGCCCCGCGTTACCTACATCTGAGCACGCAGCACGGAACACTACTAACTTTACGGTCATGAGTACAAGGCGGGGTTTAGATCACCCAAATAAGCTTAC
AGCCGACCTCCCAAAAGAAATTCCAGCACCGTAAAGAGGATTGCAGGCAGATGGAAGAGGAAAGGGGGCTGGCTGGGGCTCCTGATAGACGTTAGGTATCCTCCGG
CCCATGTTCTTAAATGTACCTCGTAGTACTTACTTTGTTCAGCTTGACCATGTTTCAACATGAAGGAAAGTCTTTCGATGCCTCTTATGATATCCTGTGCCGACGTGGATAG
TTGAAGACCCTTTACTAAGCTCTGGGCTCATAGACCTGTCGACTTTTATGGATCTGCATTATTCGTGAAACAAATAATCATGGAACAATACCCTGGACCATTATTCCCTG
CCGACCTTGAAAGTGATGCCGCAACGATCATCCAGCCACCGCCTCAGTACAACACGGCAGCCGGGCCAAGCAAAACCTGACCTTGTTAATTATTACAATGCTTTACGT
GTTTGCATTATCTGTAGCTTTTGAATAATATCAGAACTGGAGCCCTAGATTAAAAGTATCGTGTATCAACCGGGAATGGTTAGTAACCTTAGTAGTTACCTGAATATCAAC
TACCTACCTACTGCCTAGGTACTGTAGCTTGACACCTCACCTCACCATACCTGGCAGCTGACTTTCAAGACTGACCTT**CATCATGTTCTTTCCATCT**

> 12-B

TGCCCAGTGATAACGACTAAGTAACGGTACTTGTGATGTGGGTGGGGAGACAGTGCGGGCTCGTGGCGCATACTAGTAGATAGCTACTTATGAAACAGCGATATGCCA
GGCATGTTCTCCATTTGGTGTAGCAGTACTAATGCTGGAACGATGACGCTCTTCTTGTTCACACTGTATATCTGTGGTCGCGAGAGCGGTGAAGCTCCTTTCTATGAGTA
TCAGTACATCAGCCCCGCGTTACCTACATCTGAGCACGCAGCACGGAACACTACTAACTTTACGGTCATGAAGGAAAGTCTTTCGATGCCTCTTATGATATACTGTGCC
GACGTGGATAGTTGAAGACCTTTTACTAAGCTCTGGGCTCATAGACCTGTCGACTTTTATGGATCTGCATTATGCGTGAAACAAAGAATCATGGAACAATACCCTGGAC
CATTTATTCCCTGTGACCTTGAAAGTGATGGCGCAACGATCATCCAGCCACCGCCTCAGTACAACACGGCAGCCGGGCCAAGCAAAACCTGACCTTGTTAATTATTAC
AATGCTTTATGTGTTTGCCTTATCTGTAGCTTTTGAATAATATCAAACTGGAGCCCTAGATTAAAAGTATCGTGTATCAACCGGGAATGGTTAGTACCTGTAGTAGTTAC
CTGAATATCAACTACCTACTACCTAGGTAGGTACTGTAGCTTGACACCTCACCTCACCATACCCAGCAGCTGACTTTCAAGACTGACCTT**CATCATGTTCTTTCCATCT**

> 13-A

ATGTCTTCAAATGTAACGAGAAGCTTGAAAACGATCCAAAGAAGCAAAAGGGAAATCGTATCAAGTTTACAAAGGCGCAATATGAGTATATATCCACCCATTACATG
CTTGGCGGAGTGCTCCTTACAACCCAGAGATATAATGATACAGGGAAGCTAATTGGAGGAGAACTATAAACATAGTGATGTGGGAAATGCTGAAACAAACGCTAGT
TTTCCGAGCAATGTTGCGATGCCCGTGCTTCTAAGACCAAGATTGGGGCAGGGATGGCAGCTCCTAGCAGACGGTTTTCTGTTTAAAGTGAGCTCCTCTCGGTGATGATT
GCAACGAATGCCGAACTGCCGCTTATTATTACCTAATTCGGGGGGAGTTGCAACGAAATATCTCCGAAGCTGATGTGATTCCCTTTATGGTATCTTGATAGAATGGTA
TTGGTGGGGAATTGTCCACTTCAACAGACCCTGGGCATGCCATTTTACATTTTGACAATCTGGATCATTATATCACAATATGTCGCAAGAGCCAATGTTAGTTGCCAGGG
TGCGAAAATTGGTTTCCGTTCAATATTTCTTTGTTTAGTTTCATCTTCTCCGTCAGATGCCAGATTGCAACAACCTTTATCCCGAAACGATAGTGGTCGTGATAAAGTCC
TGAGCCTAGCAAAGACTTCCCAGAGTAATCCAGAGACAGAAAATAACCACGAGAGTAATACCGTTTGACGAAGCTCTTGATCCCAAGTTGGATCCCCTACTACTCTGT
CCTTCAGCACGCCCATCGCCATTCCCTTGGCCATCATGTTCAATTCGAAAATTGTAGTCATCAGTG**TAACCCGCTGGCTCACA**

> 13-B

ATGTCTTCAAATGTAACGAGAAGCTTGAAAACGATCCAAAGAAGCAAAAGGGAAATCGTATTAAGTTTACAAAGGCGCAATATGAGTATATATCCACCCATTACATGC
TTGGCGGAGTGCTCCTTACAACCCCAGAGATATAATGATACAGGGAAGCTAATTGGAGGAGAACTATAAACATAGTGATGTGGGAAATGCTGAAACAAACGCTAGTT
TTCCGAGCAATGTTGCGATGCCCCTGCTTCTAAGACCAAGATTGGGGCAGGGATGGCAGCTCCTAGCAGACGGTTTTCTGTTTAAAGTGAGCTCCTCTCGGTGATGATTTG
CAACGAATGCCGAAACTGCCGCCTTATTATTACCTAGTTCGGGGGGAGTTGCAACGAAATATCTCCGAAGCTGATTTGATTTCCCTTTATGGTATCTTAATACAGTGCATA
GACAAAAGTTCCAATATATCCCGATTATACTCTAACTACCTCGATTACACCCTACTATTTCACTCTGCAATTAAGTGGCAATATTTATTTAATTATAATAATATATATATAAA
TCTATAGAGAATTAAGGAGATTCTAGCTATATAGCTTAATACTTAATATAGTAGCTATTTATATAATAATACTTATTTAATTAGTTAGGTATTGATTTTATTACGTTTTAAC
TATATTATCTTTAATTTTAGTTTATAAATTCTCTATAGCTATAATTAGCTAGCTAATTGCCCTAATAGACTTTAGATAAGTAGTAATTTTAGGATATATTTTATATATCCTTTCT
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TAAAGTATAAATTTATATTATTTTCTTATTAATAAGCTAGTAATAAATTATCTTTAGTAATACCTTTAGCTATACCTAATTTATAATATCTCTATATAAAATAAAAGGGTTAT
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GTAGAATGGTATTGGTGGGGAATTGTCCACTTCAACAGACCCTGGGCATGCCATTTTACATTCTAACAATCCGGATCATTATATCACAATATGTCGCAAGAGCTAATGTTA
GTTGCCAGGGTGCGAAAATTGGTTTCCGTTCAATATTTCCCTTTGTTTAGTTCATCCTCCTCAGTCAGATGCCAGATTGCAACAACCTTATCCCGAAACGATAGTGGTCGT
GATAAAGTCCTGAGCCTAGCAAAGACTTCCCAGAGTAATCCAGAGACAGAAAATAACCACGATAGTAATCCCGTTTGCCGAAGCTCTTGATCCCAAGTTGGATCCCT
ACTACTCTGTCTTCAGCACGCCCATCGCCATTCCCTTGGCCATCATGTTCAATTGCGAAAATTGTAGTCATCAGTG**TAACCCGCTGGCTCACA**

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CCTCGGTTCTGCTGTCTATTCAAGCTTGGGCCCCGGCCCCAATTCTCACTTTCTATGCTGCCTTAACCTTCAGCGTCCAAGCCCAGAATACCAGCAGAGTGACTACGC
TATAATGGCGTACCCGGGACGATCCTCTTCCCATCCGGCCTGCTGGTTCTTGACACACTGCAATGCAGAGTATACCAGCAGTTCTGGGCTTGAGTACATTTCACTCGATA

TTCACAGGTGGCTATTGATGTTGTGGGTATAAGCCTACTGTGCATCAGCTACAATGTTTACATCTAAAACAAC TAGAAGGACTAAGGAAAGGTCGTTTCACCTGTGACA
ATTCTTGATCCAAGGGTCCAGTTAGCTGAGTACTTCACTCCTGGTACTCATGGTCCGACGTCGGCTTCAGCATAGCCTTTCGTCAAGTGCTGACATCGTTGGCTGAACGA
GCTGCCTCCACTGTGCAGTCATGTTTCGCGCAATTTATGTCTCAAACAAACAAAGATCTGCAGATGATGAGACGTGAATCTACTCCTCCTACAGTCACAGTTGTGACATA
CCGTCAGCTTCTGATAGTACACCCTTTGCCAAAGAACAATGCCTACGGTCTGTTGATAGTCCCTCCACGTTTATTCATACCACACGGGATGACGAAGACTACACTCCCC
TCCAATCCAAGCGGTTTGAGCAAGTCTTTCAGCTCGGTAAACGGAATGCCCTAACTTGCTCAACGGCACATCTGGGTTTTTCGGATCGAAGGACTGGGCCTGTAAGCCA
CCAAGCAAACAACCTCGAGGCTTTTTGAATATGTCTCAAAGTCAAGTAATGTTCTTCAAACCTCTGTATGCTCCTTCTTTTTGCTCTTGAGGCGGTTTGATCCTATCACCTC
TAGCCAAGTTGGAAAGCTTATGTCAAGCCGCGTCTTCTCATCATTGACCTGGGTATAAGCCATGATCATAAATGAGATGGGGCATGAGCCAGTGGGCTTCTGAATGCA
GATTAAGGCTTCTCAATCAATTGGACAAGGTTGTTCTTTCGAATACCTGTTCTGAAATAACCTTCATATCTTCATATGCGGAGGTAAATTTGCTGGTACTTGTGACTGGCC
ATGAAACGTAGGTCTCTGGAAGCCCTTTTAATTACAGGTATTTTATGCAGCCTCTGTGGTCTAGTCGGTATCAATGAGTGCTGTGCACTACTTCAAGCACACACATCCA
TATCGGATCGTGCGGCCACTGGGGCCTGGGTATCAAAAGCTGCAAAAGCAGCTGGCTAGTGCCAAGCTCACTGCGCCATTCTGCAAATCACAGCATCCAGAGAGTG
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TCCTCGTCGAATCAAAATTACTCTGTGATGTTTTATCACAAGACCAGTATGTGCTTAGACTCCCCTTGTGTCCCAATACAGCGATGGATTTAAATTGAGGGGCTCCAAG
AATGATATGAGCTCTAATAAAGCAGGGGTATCCGAAAGGCAGATAGGCTACTTCATCTTTTACCCCTATGTCAGAAGACTCGACAGTTCCCACCCTACGTGAAACACGA
TTGCACAAAAGCTTGAGAGGTGTCATCCAACCTTTGAGAATTCCTGGCAAAAGAAGCAGCTGTGGGTGCGAATGGCCCAGAACAAATGATTGCTACACGAAGGCACCTT
TCAGATTTTCGAGGATCTGGGGCACGCCTTTCTCGCGGACAGTAGGGTCTTCTCGTTTCCATTTGTGGTGAACCTTCTCTAGAAGGTAACCCCTGACGTACTACATGTTCA
CTGGACTAAAGTTCACGGTGCCAGCCAGTTGTTTGTCTTACTCTTACAGACCTCAAATCCAAACATCTGTCTTCAAGATTGCTGATATGCTGCTGTTGGAATGAGTGCAA
CGCGGCTTCAAGCAACACACTTAACATGGTCCAGATGAGTCTAAGGGGCCCAGGCTTTGCAACACTTTTTTACGGCACGGGGCATCGGCTTCACCCAGTTCGATTTTCC
ATGCAACCGGATTGTGGAGGCTGGGGGCCTTGTGCACCTATGTTGTATGGTGGGTTTTACCTATAAACCATCGTTGGTTCTGGGAGGGCTCATTACATTGGGTGGCAC
ATAACCTTCTATGGACTCCTTTCTGTAAAGAGGTCAATGACAAAGTACCTTATCAAGTCACAGTTACGTTTCGGTAATATAGCGGATTTCAAGCGGTCTTCCCCCTGGGGCT
TTCGGACCTCACATGGCGCAGTGAACCTTTTCATCAGACACTGTTCTTGCTGGGATGTTACGCTGCCTCACCACACTTTACTCACAAACTGTTATCTCGACTTCACAGCCG
CAAGCTCGTAGATCGTCCGTAGTAGTATCCTTTTCGAGGTAAGGGTGACATCACTTCAAGCAACTCCACAATATCAAAGAAAGAAGTGATTGTGTCCAGGAACATCTTA
CTGTTGCCAGGACCTTTCTGGCCCTATCGGTTACCGCAGTTTAATCACGGGAGATTTAGTCTTAGAGAATACCAAGCGATGTCAGGACGTTATATATGGTACCAGTCTCAT
GTATAGTTCAATGGGTTGTCATGATGAGGGGGTCTTCGTGGCGTTACCCCCGTGGGTATGAGAGTTTCGGGTTTCCGTTTGTGGCCAAGACCATCATGACAACCTATTCTGA
CAGTAACAGCGCAACCAACCTATTTGTGTATTCGACAGAAGACTTCAGACTTCACAGCAAACA

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CCCTCGGTTCTGCTGTCTATTCAAGCTTGGGCCCCCGGCCCAATTCTCACTTTCTATGCTGCCTTAACCTTCAGCGTCCAAGCCCAGAATACCAGCAGAGTGACTACGC
 TATAATGGCGTACCCGGGACGAGCCTCTTCCCATCCGGCCTGCTGGTTCTTGACACACTGCAATGCAGAGTATACCAGCAGTTCTGGGCTTGAGTACATTTCACTCGATA
 TTCACAGGTGGCTATTGATGTTGTGGGTATAAGCCTGCTGTGCATCAGCTACAATGTTTACATCTAAACAACCTAGAAGGACTAAGGAAAGGTCGTTTCACCTGTGACA
 ATTCTTGATCCAAGGGTCCAGTTGGCTGAGTACTTCACTCCTGGTTATCATGGTCCGACGTCGGCTTCAGCATAGCCTTTCGTCAAGTGCCGACATCGTTGGCTGAACGA
 GCTGCCTCCACTGTGCAGTCATGTTAAGCTGCCTCACCACACTTTACTCACAACTGTTATCTCGACTTCACAGCCGCAAGCTCGTAGATCGTCCGTAGTAGTATCCTTTT
 CGAGGTAAGGGTGACATCACTTCAAGTAATTCCACAATATCAAAGAAAGAAGTGATTGTGTCCAGGAACATCTTACTGTTGCCAGGACCTTTCTGGCCCTATCGGTTAC
 CCCAGTTCAATTACGGGAGATTCAGTCTTAGAGAATACCAAGCGATGTCAGGACGTTATATATGGTACCAGCTCATGCATAGTTCAATGGGTTGTATGATGAGGGGGTC
 TTTGTGGCGTTACCCCCGTGGCTATGAGAGTTTCGGGTTTCCGTTTGTGGCCAAGACCATCATGACAACTATTCGACAGTAACAGCGCAACCAACCTATTTGTGTATTC
 GACAGAAGACTTC**AGACTTCACAGCAAACA**

> 15-A

ACGGCGTTGGATATATAGATACCAATCTGATTTTATGCGCCTCTCACCTCCCCCTTTTCTCTCAGTGTCTATGGGCGTTGGAGAAAGGGGAGAGAGAAGAGGTAGGCC
AATTTCTTTCGGCATGTACACATGATTTAATGCAGCGTTATGATTTTGCTTTTGGTTGGGTGCTTTGCCGGTGGGCGATGGGATACGCGGGAATCTAAGGAACCAGAGTTT
AAGATAAAAATTTCAAATAGTTTCGCATCGATTCTGTGTTTAGTGAAGTGAAACGTGTTTGTGTTCTGGTGAATGTGTTAAAATGGACTGTAATATGATCATCTCGGCA
GTCACTCTAACACGGTGCGGTGAGAGTGATTCTGGGAGCCTTTGAGGCTGGTTCACCAGCTTATCGTTCAACTTGGTCGTGTAACATAATCGGTTCCATAGCAAATAGTTCG
GCATGATTACCATGAATTCTTACACTCTCTATGCCCAAGGACTCTCTATGCCCAAGGACTCTCTATACCCAAGGACTCTCTATGCCCAAGGACTCTCTATGCCCAAGGAC
TCTCTATGCCCAAGGACTCTCTATACCTAAGGACTCTCTATGCCTAAGGACTCTCTATACCTAAGGACTCTCTATGCCCAAGGACTCTCTATGCCCAACTTCTGGTCATTAT
CAGGAAGATGATATCAGATGCCGAGCCATATTTGCGATACAAGCTGCATGTAATTTACCTCGAGAGACACGAGTGTAACAAAGTAAGACATGAAAAGCGCCGAGCCA
GGGGCGCATCGAGATGTGATTTGGGATGGTATCTCTACTGATCCAGATCTCGGCCTCCGCAGCACCAGATTGTGTTTTACCGCCCCGTATTTCCTTGTGATTTCCAACAA
GAGACAGTCTACAAAACCAGCAAAACCATGAACGATTACATTTACCACACTGGGAGATGACTACGTCAAGGTTCCGGTCTATCCGGGGCAGCATAGCCAGTTTTGGTA
GCCTCCATCTTCTTTACCACGTCCATGCCGTGCAGCACCCTGCCAAAGACGACATGCTTGTTATCGAGGAAAGGTGTGGGAACAGTTGTGATGAAGA**ATTGAGAACCA**
TTGGTA

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ACGGCGTTGGATATATAGATACCAATCTGATTTTATGCGCCTCTCACCTCCCCCTTTTCTCTCAGTGTCTATGGGCGTTGGAGAAAGGGGGGAGAGAAGAGGTAGGCC

AATTTCTTTCCGGCATGTGCACATGATTTAATGCAGCGTTATGATTTTGCTTTTGGTTGGGTGCTTTGCCGGTGGGCGATGGGATACGCGGGAATCTAAGGAACCAGAGTTT
GAGATAAAAATTCCAAAATAGTTCGCATCGATTTCTGTGTTTGTAGTGAAGTGAACGTGTTTGTGTTCTGGTGAATGTGTTAAAGTGGACTGTAATATGATCATCTCGGCA
GTCATCTAACACGGTGCGGTGAGAGTGATTCTGGGAGCCTTTGAGGCTGGTTCACCAGCTTATCGTTCAACTTGGTCGTGTAACATAATCGGTTTCATGGCAAATAGTTTCG
GCATGATTACCATGAATTCTTACACTCTCTATGCCTAAGGACTCTCTATGCCCAGCTTCTGGTCATTATCAAGAAGATGATATCAGATGCCGAGCCATATTTGCGACACTA
GCTGCATGTAATTTACCTCGAGAGACACGAGTGTAACAAAAGTAAGACATGAAAAGCGCCGAGCCAGGGGCGCATCGAGATGTGTATTTGGGATGGTATCTCTACTGAT
CCAGATCTCGGCCTCCGCAGCACCAGATCGTGTTTTACCGCCCCGTATCTCCTTGTGGTTTCCAACAAGAGACAGTCTACAAAACCAGCAAAACCATGAACGATTACAT
TTCACCACACTGGGAGATGACTACGTCAAGGTTCCGTCTATCCGGGGCAGCATAGCCAGTTTTGGTAGCCTCCATCTTCTTTACCACGTCCATGCCGTGACGACCTTGC
CAAAGACGACATGCTTGTTATCGAGGAAAGGTGTGGGAACGGTTGTGATGAAGAATTGAGAACCATTGGTA

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ATGACTCTCGTGTTAAGATAGTCTGGATCGTAGAACTCCTGTGGTGGTAGACTAGCTGTCGCGACTGGAGCAGGCGTGGTGTTCGGCTCTGTTTTGGTATGACCGAGT
TCTTCTTGCCCGTCCCCTTCTGACTCGCCCCTGGAGGCATGACCGCGGGTGTGTGAGAGTATAAATGAGCGTGGTATGCGCTTGATTGGGGGTTTAGTTGCGCGTG
GTCTATCAGATAAGATCGAAGGTTGAGTGGAAGATTTTGATGATTATTGCGACAAGGGAACAATAACAGACTGTAACGACACGGCTCTAAAGCACGCGATCCTATTAA
AGTGCCTCACGGTACAGGTTGGGCGTCGGTACGTACCTGCCCCTTGATGTTCTCAGCTGAGGGGAAACAGATGCCCCGGATGAGACCCTTGCACTTGAAGAGCAGGCA
CGGAATATGTTTAATTCCGTTCCCTTTCAAGAGCAATCAGAAGCGAACAATTGAATGCCATCATCTTCAATCGTGAAGTCTCTGGTATCAGTACAAGTCACTGTCGCTAAC
GACTTTTCTCCGGATCCTTAGATTCAATTCTGGCTGCAAAGCCCTATTCGTGACGCTGCAACTCATTGACACTTACATAGGATGGCGACTCTCTTTGTAGTCAAACAGT
TATGAAAAACCATAATTGATACGAGAGCCGAGCTACGGCAATCCGACTTCATATACATAATCTTCAAGGAAGCCCGTTGATTGGTTTATCCAAAGTCAGCAGCGAAAG
GCAGTATCACTAACTTCAAATTAAGGAACTTGACTTGAAATCAAGGTGTCAAAATTAATAATCTATAGGCATAAAGTTATACGGACTTTACCCAAGTCATAGGATAAA
AGTTCTACACATGCAAATACTCCCTACCAAGACTCGGGCCTCAAAGCCACCAAGTGTTTCGGGAGGGTTAATAAACCAAGTCAACTGCATTTTTGCCAGCAATTTACTT
TGACGACCAAGATCGCGTTATTTGTCTGGACTAGATCAATCATGCACAAAACGTGTAATGACTCGCAGTGCAACCTTTCTATAGGTGCAATGGAGTTGCACGTTCTTTG
ATAGTTCTTCTTACTCGCGGCAAACCAGAAGAAAGCCCTCAACTTCATTCAAAACTTGGTCTTTGGGAAACAAATTGACAGTGCTTTTGTCACTGTCGATAAACACCAA
CACTGGAGGCATCAGCATCACCCATTAACAAATCATTGATGTTCAAAGAATAAATGGAA

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ATGACTCTCGTGTTAAGATAGTCTGGATCGTAGAACTCCTGTGGTGGTAGACTAGCTGTCGCGACTGGAGCAGGCGTGGTGTTCGGCTCTGTTTTGGTATGACCGAGT
TCTTCTTGCCCGTCCCCTTCTGACTCGCCCCTGGAGGCATGACCGCGGGTGTGTGAGGGTATAAATGAGCGTGGTATGCGCTTGATTGGGGGTTTAGTTGCGCGTG

GTCTATCAGATAAGATCGAAGGTTGAGTGGAAGATTTTGATGATTATTGCGACAAGGGAACAATAACAGGCTGTAACGACACGGCTCTAAAGCACGCGATCCTATTAA
AGTGCGTCACGGTACAGGTTGGGCGTCGGTACGTACCTGCCCCTTGATGTTACAGCTGAGGGGAAACAGATGCCCCGGATGAGACCTTGCACCTGAAGAGCAGGC
ACGGAATATGTTAATTCCGTTCTTTCAAGAGCGATCAGAAGCGAACAATTGAATGCCATCATCTTAACTTAACTTGAAATCAAGGTGTCAAATTCACCTAATCTATAG
GCATAAAGTTATACTGACTTTACCCAAGTCTTTTGTTCATCCATAGAATAAAAGTCCTACACATACAAATACTTCTACCAAGACTCAGGCCTCAAAGCCACCAAGTGTT
TCGGGGGTTTGATAAACCAAGTCAACTGCATTTTGGCCAGCAATTTACTTTGACGACCAAGATCGCGTTATTTGTCTTGGACTAGATCAATCATGCACAAAACGTGTAAT
GACTCGCAGTGCAACCTTTCTATAGGTGCAATGGAGTTGCACGTTTCGTCGATAGTTCTTCTTACTCGCGGCAAACCAGAAGAAAGCCTTCAACTTCATTCAAACTTGG
TCTTTGGGAAACAAATCAACAGTGCTTTTGTCACTGTGCATAAACACCAACACTGGAAGCATCAGCATCACCCATTAACAAATCATTCATGTTCAAAAGAATAAATGGA
A

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GTTTCGTCGCCAAAGCTGGAAGAGTCTCGACGAGAAGAACGATCCATCGCGGATACGGAATGATGAGATAATTTGCTGAATGCACGATGAAGGGCACAATCGCATTC
ACGAGGCCTGAGAGTGAGTGGTCAGTTGAGGCTTCATGTGAAGACATCCGATGAAGCAGTCAAAATTACCGAGAATCGCAAAACCGAGGTACGTTTGCATCGTAACA
CTCAACCTCGAGCTCTTCTGAGCATCCATATTGAACTCCATCACCTCAAATCCTCCATGAAAGAGTCAGATTAAAAAAGGAAGTGAATCAAGAAAAGAGGCTTTTCA
ACAAAGAACAAATCAACCAATACTTTACGCAGCCTCAAGTCAATAAATGCAATGTAAGCTTATTTATTTAACCTCTGCTCTGGCCGAATACGGTTTACGGAGCCCAA
ACACCGCGCGGATAAATACGAGAGGCCATGACTCTAATAGACTACCTTCCTTACCTTAATAGGAATTATAGAGCATCTTGTTACGAATCAATTCATCACCAGCGTAAAT
GACGTACAGAGATTGGATGGAAGAGGAAGCTGATGTAGAACCTCTTGTGGGCCACGTGGGGCTGTTTTCAAGGGCACGATGTCGAGTGATTGGCTGTAGCGTATTGA
TTCAACGCTAAAGATCTGCGGTGAATAGTGGGTTCATGATGGATTACAGAGGCTAGAGTCATGATAGATAAACTACATAGTACAATCTCATGAGGAGATGAAGGACA
AGATGATGATCATGGATCACAAGGGTCTCTTAGTATTCATATCTACTCAAGATGATTGTAGCACTCCTATCAACATGATCAAGGCGATCTGCAATGACCTCGTCTTCAAT
ATCACATCGCTCGTCTCCATGATGAGAAGAGCTCCAAATGCTGACCCTGAAGATGCATCGTTTCCATCTGCCAGTCAGCTCGACCTGTTCTAGCTCAGCTGAAGCCA
TCATGGTT

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GTTTCGTCGCCAAAGCTGGAAGAGTCTCGATGAGAAGAACGATCCATCGCGGATACGGAATGATGAGATAGTTTGTGAGTGCACGATGAAGGGCACAATCGCATTC
ACGAGGCCTGAGAGTGAGTGGTCAGTCGAGGCTTCATGTGAAGACATCCGATGAGGTAGTAAAAATTACCGAGAATCGCAAAATCCGAGGTACGTTAGCATCGTAACA
CTCAAGCTCGAGCTCTTCTGAGCATCCATGGTAACTCCATCACCTCAAATCCTCCATGAAAGAGTCAGACTAAAAAAGGAAGTGAATCAAGAAAAGAGGCTTTTC
AACAAAGAACAAATCAACCAATACTTTACGCAGCCTGAAGTCAATAAATGCAATGTAAGCTTATTTATTTAACCTCTGCTCTGGCCGAATACGGTTTACGGAGCCCAA

AACACCGCGCGGATAAATACGAGAGGCCATGACTCTAAAAGAATACCTTCCTTACCTTGATAGGAATTAACGTCCCCTACCTAAAGACCGGCCACCCCTACAGACTGG
CCACCTCATTCTTAACCCAGCCACCTAATTTATATATACTTTAAACAGTTATAACTCTATTAATTTAATTCTAATTAATTTTAAACTAATACTAATTAATTTAGAATGCCTTCT
TTTACTAAAAAAGATATAAGCGTTGCACTTTAGATAGTTATAAATAGTATATCAGTAAATAAAGTAGCTAAAGCTTATAGTATTAACCGTTCTATACTTTAAGGTTAGATTA
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TAAGATATTTAAAGGTAAGAAAATTAACCTTTAATTAATATTATAGAGTTTCTTTTAACTAATAAAGGCATTCTTTATACTCTTTATAATACTAGCAATACACTTAATTAAGT
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AAAAATAACCCTAACTTTTTATTCTTAATAGCTATAGAAGTTATATTATAGAAGATTTCTCTAAAAATATTATAATAATAATATATATCTATTATTTCTTTCTATTTATATTTT
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GGGCTGTTTTCAAGGGCACGATGCCAAGTGATTGGCTGTAGCGTATTGTTTCAACGCTAAAGATCAGCGGTGAATAGTGGGTTCATGATGGATTACAGAGGCTAGAGTC
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ATCAACATGATCAAGGCGATCTGCAATGACCTCGTCTTCAATATCACATCGCTCGTCCTCCATGATGAGAAGAGCTCCAAATGCTCACCTGAAGATGCATCGTTTCCAT
CTGCCCAGTCAGCTCGACCTGTTCTAGCTCAGCTGAAGCCATCATGGTT

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GCGTGTTGACCCATTCTGCCAACACCCCTCCTCAAATCAGTACTGTCTGACTTGGTAGCACAATGTGACATCTAAAAGCACTAGTTATGTGTAATTACATGCACACTGT
ATCACAATATCACATATCGGTCGTGGGATTAGGGTGCGAGGGGCGTTGACTAGATTGAAGCTGAACGATGTTTTGAGAAACAGTGGCATTAAATATGGCTGAATGTGACC

AACTACAATGCCCTATGGTAATTTCAAGTTCTCCACCTGGGTCGACCTTATTATTTTAATATTAGTTATATAATATTATATAATAAACCGGCACTATATAAAAAGGAGAAAAA
GACTTAATGTATTTACTGAAGAATATAGTTAAAAGATAGCATAAAAATTAAATTTTAAAAATCAAAAGGCTTCAGAAATGCAAGAAAAAGTGATTTTATAAACTTACTG
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TTTTTCCAAGTAAACGTGAGCCCCCTTACCTCAATCGTTTGAAACATGCCAGGGTTTTGCTTTTTTCCACCTGAAGGCGTCATGGCCGAGTTTGATCAAAACATTACAGA
CCAGACCTACTGTAACATATAAAACATAGCACATTCCTGTTATCCAAGAATGGAGTTGGGAATCATAAATATCTGGTCCGATCTATTTCCCTGTATATCAATAATCGCCTTCTC
AAACATGTCTATCACTATCGACAGAAATCTCTTAACAGCATGCCCCAACGAGAATATTTCCGCCGAGAGCATTTCGACTCCCTCTCGACGTAGTCGAGTACTTATGCTCAC
AATCTAAGAACAGTACGGGACACACCCAGAGGCAGAGACTTGGAACCCCTGCGCCAGTTGGTCAGTAATTTGTCCCAAAATATCCCACCAAATTTACAGGCATAGGTC
TCGGGGGCTTTCTCCTTTGTGCAACACCCGTCTCACTGTCAGTCTCGAGCTCCAAGGAGTAGGAGTTTTGCTGCTGCTGCAAATATGTAAGGAAAGCCGCTGATCAC
CGGCCAAACTTGCTAACCGTCGACAGTGGTGCCTATCTGGGACTCGGCAGTGTGATGCTTATCCTTGGAGGGATTGGCGAGTGGGTTCTGGGTAAGTTAGCTGAACTCA
TATGATCTACCGACACTCACATATCAGGAAACACGTTTTCTTCTGTAGTATTCTGCCTTTTTGGCGGCTACTGGTTGACTTTAGGAATAACGATCATTCTTGATCTGGTGC
ATATGGCATTTACTCAACTACCGAATCAGCTGTAGATGTGCTTGATAATCCTCAGTTCTACGCTACGTTTTCTTTCATCCTCGTTGCTATGACGATACTCTGCGCCCTTCTTA
CAGTTGCAAGTATTCGAACCAATATCGTTTGTTCTTTATGTTCTGTTCTCCTCACTACTTACTGTAAGATTCTTATGCCTTGCTCCTCATTGTAACGACTGACAGGGGTCT
TTTTATAGTTGGCTGTCTTGCTGGTTCGTTTTTACATTCATGGAAAAACCTTCAAGTGCTCTTTTATTACAAAAGGTGGGTGCTGGGTTTCTTTTTGCAGCGACGATACTG
GGTTGGTACATGTGGTTTGCTCTTATACTCTTATCCGTCAACTTCCCGATTTCTCTACCTGTGGGTGAGCTTTCGTCAATCGTTCCCGGCCGGAACAACCAGGCAGAAATG
AAAAACACGAAAGATGCTTAAGCTCTTTACTCGGGCAGTTATTCGGCTGTATAAAACCAGAGTTGAAAGTAGGCGGGTACGATTGTTTAGCTCGATGGTTTCAAAAGCT
CAGTAGTGGATAAGTTCCAGTGCATCGTGTAGCTGGAACAATTTCTATTGTATCTTTGTAAATATTCTGGTTATTTAGACGAAAGCAAGAGATTTAATGTAATCTTCAATAT
CCCTCCAGTGGCTAAATCAAGTTGCG

> 18-B

CGGTGTTGACCCATTTCTGCCAACACCCTCCTCAAATCAGTGCTGTCTGACTTCGTAGCACAATGTGACATCTAAAAGCACTAGTAATGTGTAATTACATGCACACTGT
ATCACAATATCACATATCGGTCGTGGGATTAGGGTGCGAGGGGCGTTGACTAGATTGAAGCTGAACGATGTTTTGAGAAACAGTGGCATTAAATATGGCTGAATGTGACC
AACTACAATGCCCTATGGTAATTTCAAGTTCTCCACCTGGGTCGACCTTATTATTTTAATATTAGTTATATAATATTATATAATAAACCGGCACTATATAAAAAGGAGAAAAA
GACTTAATGTATTTACTGAAGAATATAGTTAAAAGATAGCACAAAAATTAAATTTTAAAAATCAAAAGGCTTCAGAAATGCAAGAAAAAGTGATTTTAATAAACTTACT
GTAGGGCCTGGTAAGCCTCGATCCTCGACTAACAGGGGTCTTTTTATAGTTGGCTGTCTTGCTGGTTCGTTTTTACATTCATGGAAAAACCTTCAAGTGCTCTTTTATTAC
AAAAGGTGGGTGCTGGGTTTCTTTTTGCAGCGACGATACTGGGTGGTACATGTGGTTTGCTCTTATACTCTTATCCGTCAACTTCCCGAGTTCTCTACCTGTGGGTGAGC
TTTCGTCAGTCGTTCCCGGCCGGAACAACCAGGCAGAAATGAAAAACACGAAAGATGCTTAAGCTCTTTACTCGGGCAGTTATTCGGCTGTATAAATCCAGAGTTGAA

AGTAGGCGGGTACGATTGTTTAGCTCGATGGTTTCAAAAGCTCAGTAGTGGATAAGTTCCAGTGCATCGTGTAGCTGGAACAATTTCTATTGTATCTTTGTAAATATTCTG
GTTATTTAGACGAAAGCAAGAGATGTAATGTAACCTTCAATATCCCTCCAGTGGCTAAATCAAGTTGCG

> 19-A

AGTATCTGAACCAATGCCACTTGTGGAGTGTTATAGACAATGGGCTTGGACAAGTTCAAAACATAGGTTCAACAGACCATTCTCAGGTACAAGGCCTTTTCCTTCCTGG
GCGTCTTTGGTGTCTTCAAGCCCATCCTGAGTTTGATCCAGCAGTTATGGGACAGGTGCTAGACCTGACTAGATCTGAATTGACAGATGAGGAATACCGAAAGGCAAA
GGCTCATAACCAACAAAAGCTTGACCAACAAGTCGCACTAGAAATCATTAGTTAATTTTATTCTAGAATAAGATATTTATAATATTTCCCTTTATATTATAGAATATATAGTTAT
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ATAATTATAAATAATAGGAAGATATAAAATTATCTATAATATTTTATAATATATTTCTCTCCTTTTAAATACTAGATAAAATATATTTTACTTTATTAGGCCGCTTTACAGCG
CTTCATATTTAAAGATAACAAATTGCAAATATATAAATACTTCTTTCCCTTCCCTCCACCAGGTCAGGGGTATTCTTTCAAGTATTACAAACATCTTGATTCTTAGAGGTA
CTTTACCGCCCCCTGGTAATATTTGTTAAGCCCAAAAGCAAGTAAAGGTTACGATTTCAGTCTATGCACATTATGCCCACACTGCCACATGCCACGTCATCACTTACGATGA
GAAGCTTACAATAGCTAGAAATGCCTTGAAGCCTTCAACGCTGAACGGGCTTCCTTTCCCAACTCTCAAGCCAGATATGGTATTGGAAGTAATATCCAACAGAACCCCC
TCACCTGACTTTAAAATAACCGGAATATAGTGGATGCCAATAGCATTGAGGAAGGAAACGCAATCATCGATGCCTATATGGGACAGGATCGAATCATGAAAGAAGTAA
CTAGGGATCAGAAATAAGAGGCTTACTGGGAAATACTCGCTGAGTTCCCAGTAAGTATGGCAAAGAACGATTTTATAAGTCCTTCTGGGTAAGCGGCTTTTCGGCATAAT
TGAAGAACATGTATTTCTCAACAACCTTTACAAGCGCTTAAGATTGACTTATTTAATTTAAGGCTGAATTACGCTATATAGTGCCGATATAGAGCCCGCTTTAGCTTCTCAA
ATAGGATATGTTATTATGACGACTTTTGCAAAAATAAATATATTTTAAAGAGTGCTTTGTAAATTTCTTGCCTAGGGAGTTTTGACATAGCGTGTCTGTAAGAATGACCAGCA
TCTAAACACAGCGTAAACAGAAATCCGATCAGTGGGCTTCGTAACAGTTTTGAAACTCAGCAGCTAGTTCCCTTCT

> 19-B

AGTATCTGAACCAATGCCACTTGTGGAGTGTTATAGACAATGGGCTTGGACAAGTTCAAAACATAGGTTCAACAGACCATTCTCAGGTACAAGGCCTTTTCCTTCCTGG
GCGTCTTTGGTGTCTTCAAGCCCATCCTGAGTTTGATCCAGCAGTTATGGGACAGGTGCTAGACCTGACTAGATCTGAATTGACAGATGAGGAATACCGAAAGGCAAG
GGCTCATAACCAACAAAAGCTTGACCAACAAGTCGCACTAGAAATCATTAGTTAATTTTATTCTAGAATAAGATGTTTATAATATTTCCCTTTATATCATAGAATATATAGTTA
TAACTATATAATATAGTAAATATATCATAAGAAAATAGTTTTAATTTATTATTATATTTTAAAGTAAAGTTAAATAATAACATACTTATACTTCTTTTCTTTTGAGTAAAT
ATAATTATAAATAATAGGAAGATATAAAGTTATCTATAATATTTTATAATATATTTCCGGAATATAGTGGATGCCAATAGCATTGAGGAAGGAAACGCAATCATCGATGCCT
ATATGGGACAGGATCGAATCATGAAAGAAGTAACTAGGGATCAGAAATAAGATGCTTACTGAGAAATACTCGCTGAGTTCACAGTAAGTATGGCAAAGAACGATTTTA
TAAGTCCTTCTGGGTAAGCGGTTTTTCGGCATAATTGAAGAATATGTATTTCTCAACAACCTTTACAAGCGCTTAAGATTGACTGATTTAATTTAAGGCTGAAATACGCTATA

TAGTGCCTATATAGAGCCCGCTTTAGCTTCTCAAATAGGATATGTTATTATGACGACTTTTGCAAAAATAAATATATTTTAAGAGTGCTTTGTAAATTTCTTGCCTAGGGAGT
TTTGACATAGCGTGCTGTGAAGAATGACCAGCATCTAAACACAGCGTAAACAGAATCCGATCAGTGGGCTTCGTAACAGTTTTGAAACTCAG**CACGACTAGTTCCTT**
CT

> 20-A

AAAGCAGTGGCGAACATCAACTTGACTACTTTCAAGTCGTCGGGACCGATGATGGTGGTATCTTGCAGAGAAATTCGCCCCGATCTATGTGCGAGACAGGATTGCAATG
GAGCCATATAACTTATCGACGTTGCTTCGAATCATTTCCATATCAAGGAAAGGATGTGAGATATTAATCTCTTCTTCGTAAACATTGCAAAGCCGCAGCGCCTCTGGTCTG
TCGATCAGCCAAATTGGATCGACAGGGGGCTCATTTCGATAGCGCAGTTTGTGGTGTAGGCGATGGCCGTCGGGTATTATTTCCAGCAGTCCATGCATCGCTATTATCGTT
GTGCGGTTGAGAGATACCTCGAGCAAGAAGGCTTGATTGTGCAAGGCTAATGTTGAACTTGTAGTGAGCAGTTGCAGGTGTATAGATGCTTGCTGCGCCGGCTTCGGAG
CTGCGGTTACTGTGCGACTGAGTAGGTATTTAGAATAGGGGGGGAGTTGAGGGATACGTTTAGATCAGTATTCATACTTTGTTGCATAGGCACATTGTCCTGACCTGGAAC
CTGTGCGAGGAGCTGAAGAATTTGTAAGAGGTTGCGGCGGTGACGGCGAAGGCGACGAAGCAAGATGCGTAAGGTCTGAGTTGTTGAGAATGGCTTCTTCGATGCTTGT
GTCAAAGGCAACTCTAGTAGATGAAGGATTTGTTGGGGCAGGCGGCTGGGCTGGTGATGACCGGATGTGATCTTCAATATCAGCCAACCTCTTGAGAATCACCTTGTG
TCATTTGTCTCACTATGGGGGTCAGTGACATTTTGTCTAAAGCTATACCCAAGAAGAAACAAGGCTTACAGAGTTGTCCCTCGGCGACGGGGCACATGTGGAGGAAAC
GTACCTGTTTGGTGTAAGTTGTTTTCAGAGCGCGACCATGGCGAGAATAACTTACAATCCTTACCGGCTTTAGCGCATTGGCTACATGGACGTTGCTGTTACATTTAGTT
TTGCGCTTCTTGCAATTCGTAACATGAGGTCACAAGAATGAGCTTCTAGACATCCAAGTGTCCAAGTAGCGAAGAGGTACCAGGCGAGATTTGTATATTGGCC**TCGTT**
TTCGTTTTGCTG

> 20-B

AAAGCAGTGGCGAACATCAACTTGACTACTTTCAAGTCGTCGGGACCGATGATGGTGGTATCTTGCAGAGAAATTCGCCCCGATCTATGTGCGAGACAGGATTGCAATG
GAGCCATATAACTTATCGACGTTGCTGCGAATCATTTCCATATCAAGGAAAGGATGTGAGATATTAATCTCTTCTTCGTAAACATTGCAAAGCCGCAGCGCCTCTGGTCT
GTCGATCAGCCAAATTGGATCGACAGGGGGCTCATTTCGATAGCGCAGTTTGTGGTGTAGGCGATGGCCGTCAGACATCCAAGTGTCCAAGTAGCGAAGAGGTACCAG
CGAGATTTGTATATTGGCC**TCGTTTTCGTTTTGCTG**