Global Expressions Landscape of NAC Transcription Factor Family and Their Responses to Abiotic Stresses in *Citrullus lanatus*

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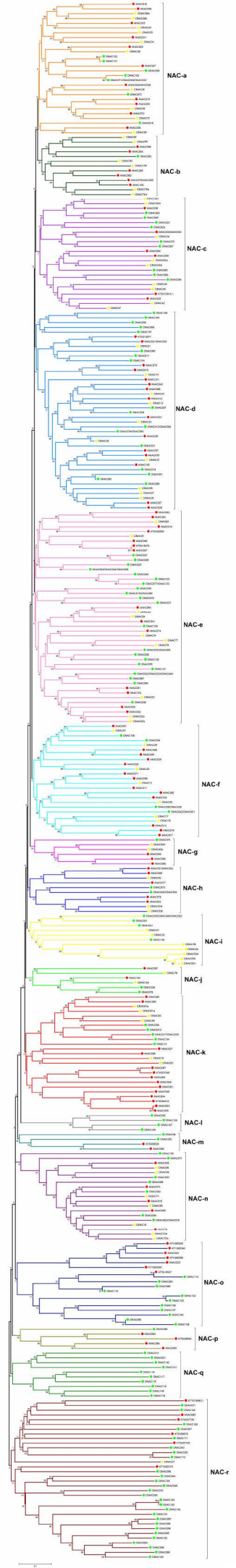
[*] Corresponding author: Zhongyuan Hu

Supplemental Figures and Tables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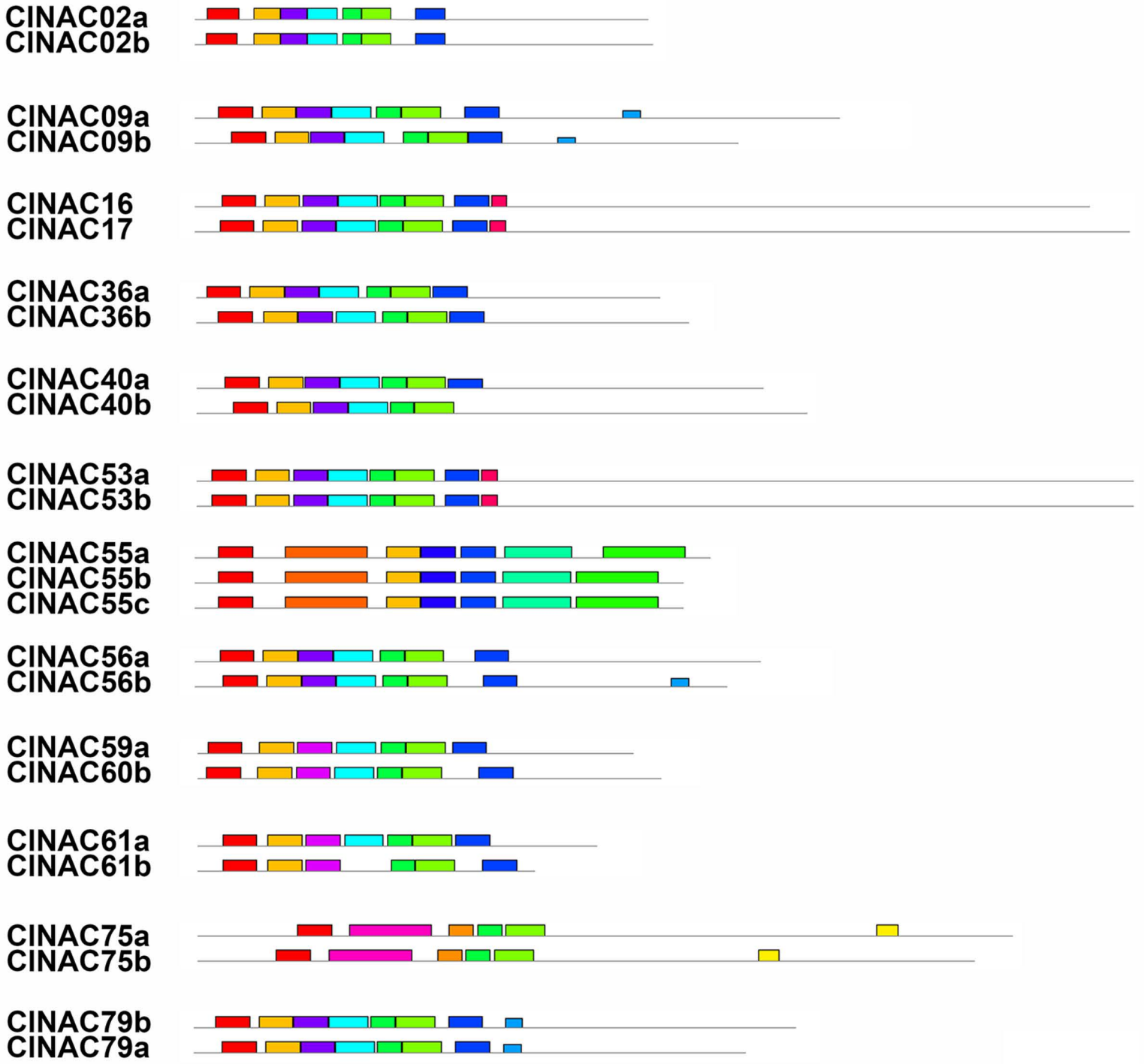
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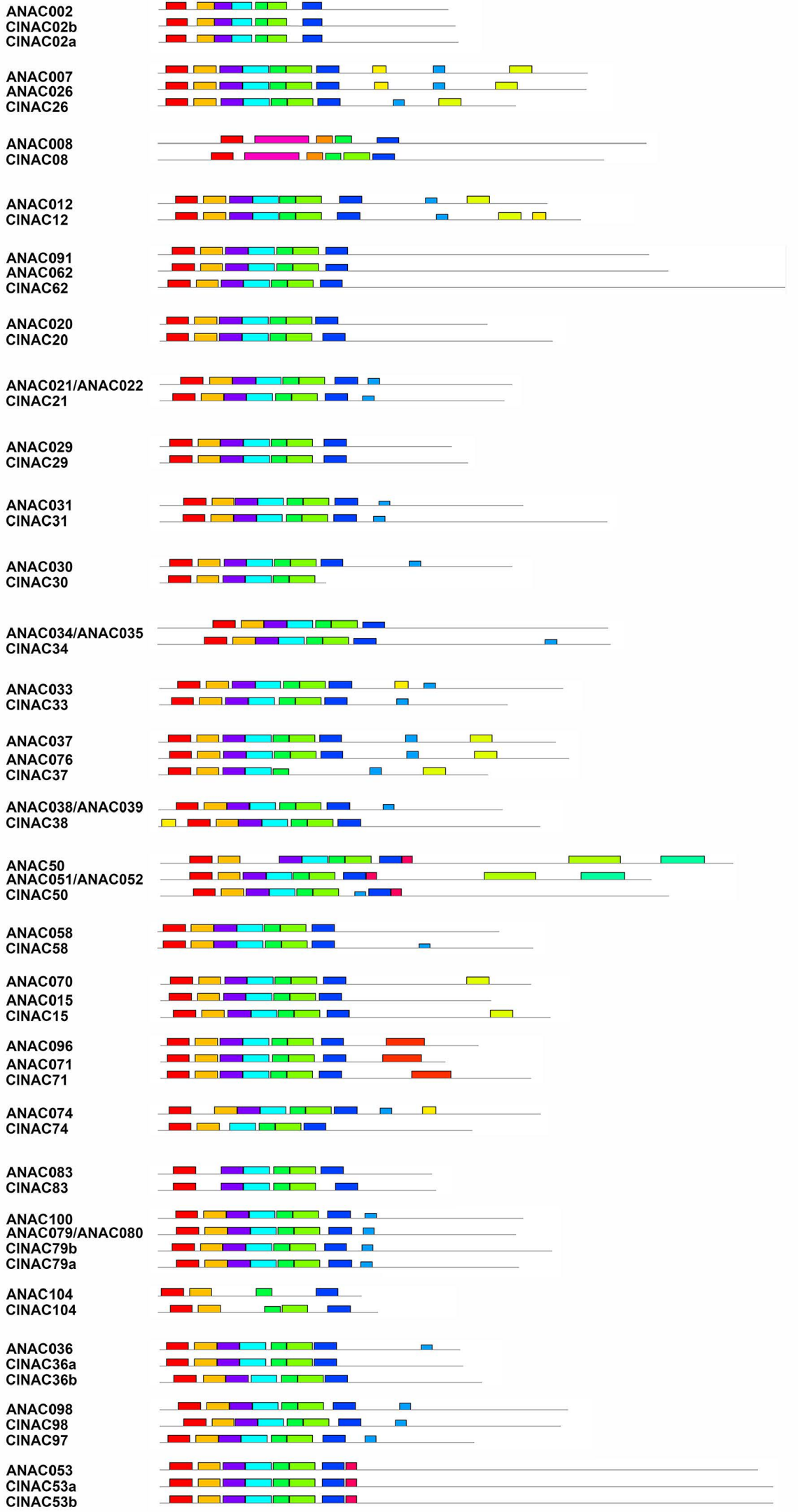
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ANAC020
CINAC20
ANAC021/ANAC022
CINAC21
ANAC029
CINAC29
ANAC031
CINAC31
ANAC030
CINAC30
ANAC034/ANAC035
CINAC34
ANAC033
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CINAC15
ANAC096
ANAC071
CINAC71
ANAC074
CINAC74
ANAC083
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ANAC100
ANAC079/ANAC080
CINAC79b
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ANAC104
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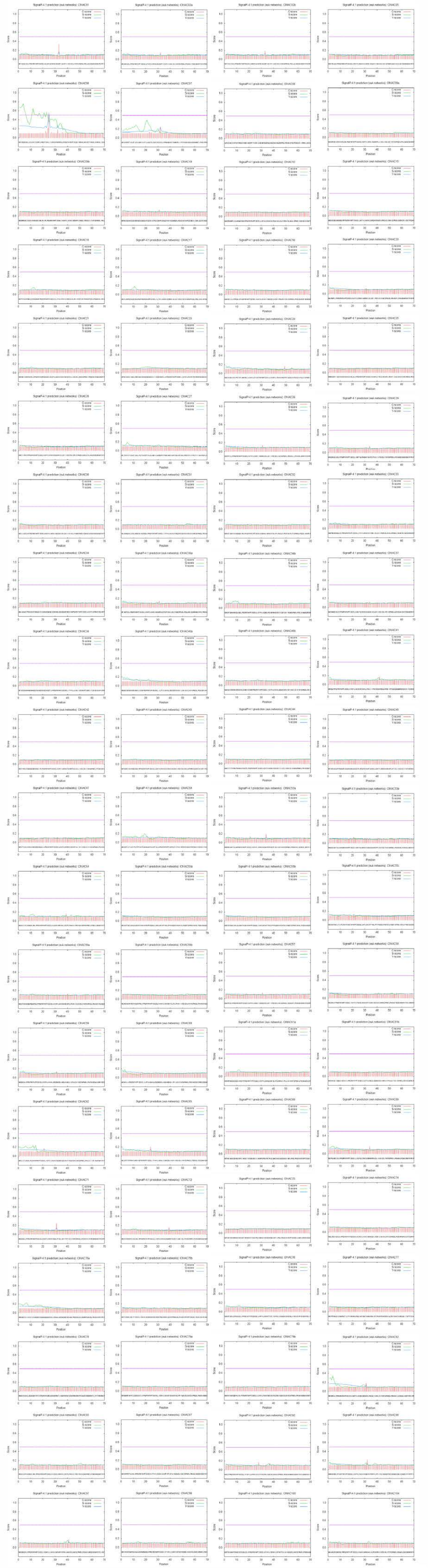

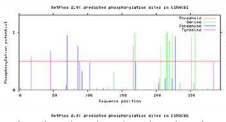
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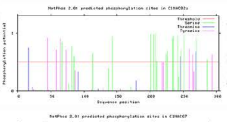
Serine
Tyrosine
Phosphorylation potential
Sequence position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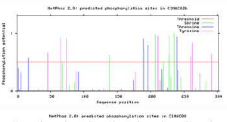
Tyrosine
Phosphorylation potential
Sequence position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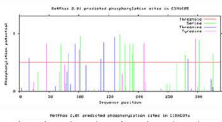
Serine
Tyrosine
Phosphorylation potential
Sequence position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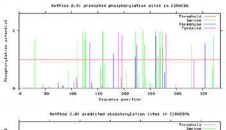
Serine
Tyrosine
Phosphorylation potential
Sequence position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Serine
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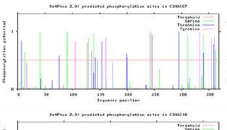
Phosphorylation potential
Sequence position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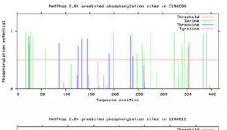
Serine
Tyrosine
Phosphorylation potential
Sequence position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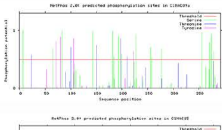
Phosphorylation potential
Sequence position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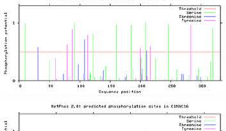
Phosphorylation potential
Sequence position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Phosphorylation potential
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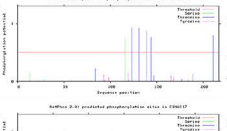
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Serine
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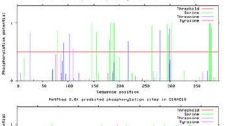
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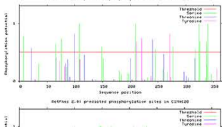
Phosphorylation potential
Sequence position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Serine
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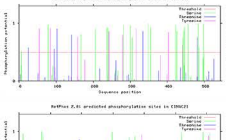
Phosphorylation potential
Sequence position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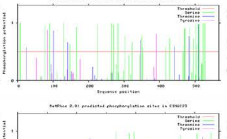
Sequence position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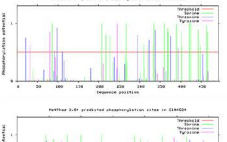
Sequence position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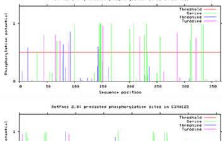
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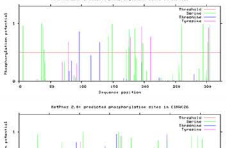
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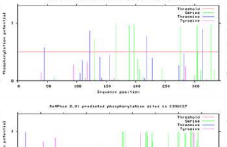
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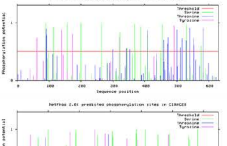
Serine
Tyrosine
Phosphorylation potential
Sequence position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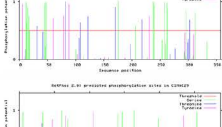
Phosphorylation potential
Sequence position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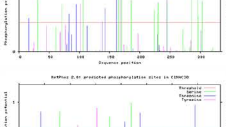
Sequence position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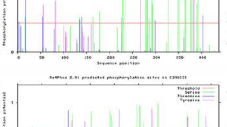
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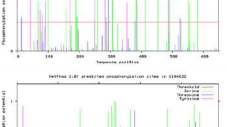
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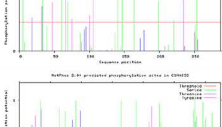
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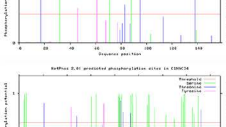
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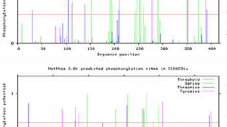
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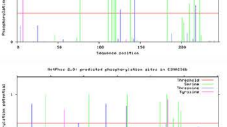
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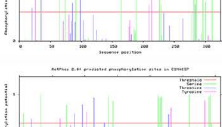
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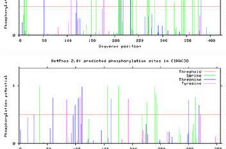
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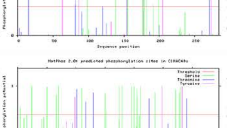
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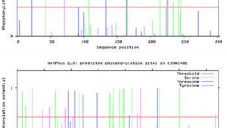
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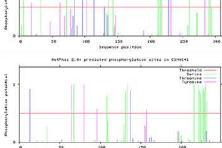
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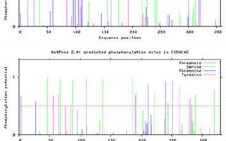
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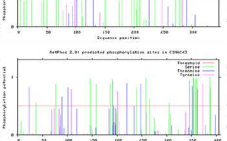
Sequence position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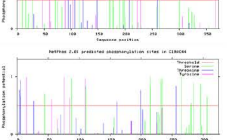
Sequence position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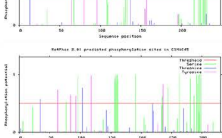
Phosphorylation potential
Sequence position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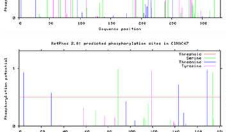
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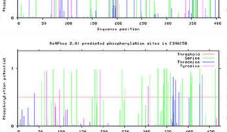
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Phosphorylation potential
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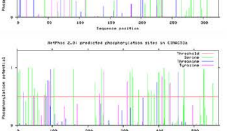
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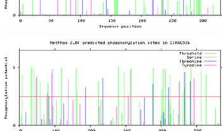
Phosphorylation potential
Sequence position


NetPhos 2.0: predicted phosphorylation sites in C1H6C9R6
Threonine
Serine
Tyrosine
Phosphorylation potential
Sequence position

NetPhos 2.0: predicted phosphorylation sites in C1H6C9S1
Threonine
Serine
Tyrosine
Phosphorylation potential
Sequence position

NetPhos 2.0: predicted phosphorylation sites in C1H6C9S4
Threonine
Serine
Tyrosine
Phosphorylation potential
Sequence position

NetPhos 2.0: predicted phosphorylation sites in C1H6C9S7
Threonine
Serine
Tyrosine
Phosphorylation potential
Sequence position

NetPhos 2.0: predicted phosphorylation sites in C1H6C9S8
Threonine
Serine
Tyrosine
Phosphorylation potential
Sequence position

NetPhos 2.0: predicted phosphorylation sites in C1H6C9T0
Threonine
Serine
Tyrosine
Phosphorylation potential
Sequence position

NetPhos 2.0: predicted phosphorylation sites in C1H6C9T2
Threonine
Serine
Tyrosine
Phosphorylation potential
Sequence position

NetPhos 2.0: predicted phosphorylation sites in C1H6C9T3
Threonine
Serine
Tyrosine
Phosphorylation potential
Sequence position

NetPhos 2.0: predicted phosphorylation sites in C1H6C9T4
Threonine
Serine
Tyrosine
Phosphorylation potential
Sequence position

NetPhos 2.0: predicted phosphorylation sites in C1H6C9T6
Threonine
Serine
Tyrosine
Phosphorylation potential
Sequence position

NetPhos 2.0: predicted phosphorylation sites in C1H6C9T8
Threonine
Serine
Tyrosine
Phosphorylation potential
Sequence position

NetPhos 2.0: predicted phosphorylation sites in C1H6C9T9
Threonine
Serine
Tyrosine
Phosphorylation potential
Sequence position

NetPhos 2.0: predicted phosphorylation sites in C1H6C9U0
Threonine
Serine
Tyrosine
Phosphorylation potential
Sequence position

NetPhos 2.0: predicted phosphorylation sites in C1H6C9U3
Threonine
Serine
Tyrosine
Phosphorylation potential
Sequence position

NetPhos 2.0: predicted phosphorylation sites in C1H6C9U5
Threonine
Serine
Tyrosine
Phosphorylation potential
Sequence position

NetPhos 2.0: predicted phosphorylation sites in C1H6C9U6
Threonine
Serine
Tyrosine
Phosphorylation potential
Sequence position

NetPhos 2.0: predicted phosphorylation sites in C1H6C9U7
Threonine
Serine
Tyrosine
Phosphorylation potential
Sequence position

NetPhos 2.0: predicted phosphorylation sites in C1H6C9V0
Threonine
Serine
Tyrosine
Phosphorylation potential
Sequence position

NetPhos 2.0: predicted phosphorylation sites in C1H6C9V4
Threonine
Serine
Tyrosine
Phosphorylation potential
Sequence position

NetPhos 2.0: predicted phosphorylation sites in C1H6C9V9
Threonine
Serine
Tyrosine
Phosphorylation potential
Sequence position

NetPhos 2.0: predicted phosphorylation sites in C1H6C9W2
Threonine
Serine
Tyrosine
Phosphorylation potential
Sequence position

NetPhos 2.0: predicted phosphorylation sites in C1H6C9W5
Threonine
Serine
Tyrosine
Phosphorylation potential
Sequence position

NetPhos 2.0: predicted phosphorylation sites in C1H6C9W6
Threonine
Serine
Tyrosine
Phosphorylation potential
Sequence position

NetPhos 2.0: predicted phosphorylation sites in C1H6C9W7
Threonine
Serine
Tyrosine
Phosphorylation potential
Sequence position

NetPhos 2.0: predicted phosphorylation sites in C1H6C9W8
Threonine
Serine
Tyrosine
Phosphorylation potential
Sequence position

NetPhos 2.0: predicted phosphorylation sites in C1H6C9X1
Threonine
Serine
Tyrosine
Phosphorylation potential
Sequence position

NetPhos 2.0: predicted phosphorylation sites in C1H6C9X2
Threonine
Serine
Tyrosine
Phosphorylation potential
Sequence position

NetPhos 2.0: predicted phosphorylation sites in C1H6C9X3
Threonine
Serine
Tyrosine
Phosphorylation potential
Sequence position

NetPhos 2.0: predicted phosphorylation sites in C1H6C9X4
Threonine
Serine
Tyrosine
Phosphorylation potential
Sequence position

NetPhos 2.0: predicted phosphorylation sites in C1H6C9X5
Threonine
Serine
Tyrosine
Phosphorylation potential
Sequence position

NetPhos 2.0: predicted phosphorylation sites in C1H6C9X6
Threonine
Serine
Tyrosine
Phosphorylation potential
Sequence position

NetPhos 2.0: predicted phosphorylation sites in C1H6C9X8
Threonine
Serine
Tyrosine
Phosphorylation potential
Sequence position

NetPhos 2.0: predicted phosphorylation sites in C1H6C9Y1
Threonine
Serine
Tyrosine
Phosphorylation potential
Sequence position

Table S1. Sequence logos for the conserved motifs of watermelon NAC domain proteins.

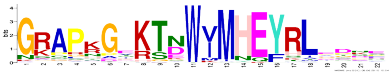
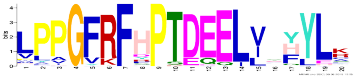
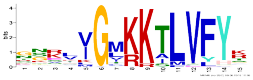
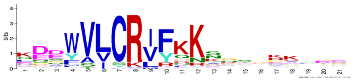
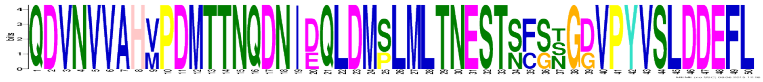
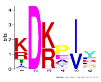
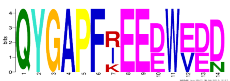
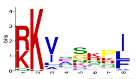
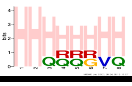
Motif	E-value	Sites	Width	Logo
Motif 1	4.2e-906	80	22	
Motif 2	1.9e-1031	77	20	
Motif 3	7.1e-876	60	21	
Motif 4	3.3e-619	65	21	
Motif 5	2.5e-482	74	15	
Motif 6	3.2e-403	62	15	
Motif 7	7.4e-368	71	21	
Motif 8	7.90E-110	7	34	
Motif 9	2.40E-82	4	50	
Motif 10	2.40E-49	3	50	
Motif 11	6.10E-49	7	21	
Motif 12	1.00E-43	3	50	
Motif 13	6.90E-42	4	29	
Motif 14	2.20E-38	7	15	
Motif 15	1.90E-26	5	15	
Motif 16	2.20E-24	47	6	
Motif 17	1.10E-20	7	16	
Motif 18	2.90E-20	5	14	
Motif 19	2.20E-13	47	8	
Motif 20	1.80E-08	5	8	

Table S3. Number of different cis-elements presented in the promoter regions of the CINAC genes.

Gene name	MBS	LTR	ABRE	TCA-element	HSE	ERE	ARE	TGACG-motif	CGTCA-motif
CINAC01	1		1		1	1		1	1
CINAC02a	1		4		1		1	4	4
CINAC02b	1		7	1	2	1	3	1	1
CINAC05	1		2	2	1	1			
CINAC06	1						2		
CINAC07	1		2	2	1	1			
CINAC08					1		3	1	1
CINAC09a			1	1	1	2			
CINAC09b					1				
CINAC10				1			1	1	1
CINAC12				3		1	1		
CINAC15			3		1		2	1	1
CINAC16		1				2		1	1
CINAC17	1					1	2		
CINAC18		1				1			
CINAC20				4	1		3	3	3
CINAC21	1		1	2				1	1
CINAC23			1		1		1		
CINAC24					1	1	1	2	2
CINAC25			1	2		3	3		
CINAC26	1				2	1	5		
CINAC27	1		2				3		
CINAC28		1		3					
CINAC29				2	3	1	2		
CINAC30	1	1	1	1	1		2		
CINAC31		1	1	2			2		
CINAC32			1	1		2		1	1
CINAC33				1	1		1		
CINAC34				4	1			1	1
CINAC36a	2	1			1	2	1		
CINAC36b	1			1		1	1		
CINAC37	2		2		1		1	1	
CINAC38		1			1	1	1		
CINAC40a			1				1	1	1
CINAC40b	2		2		1		1	1	1
CINAC41	1			1			1	2	2
CINAC42				1	2		2		
CINAC43		1		5			1	1	1
CINAC44		1		1	2			1	1
CINAC45				1	1		2		
CINAC47	2		1		1	1		1	1
CINAC50	1					1	1		
CINAC53a			2					2	2
CINAC53b			1				2	4	4
CINAC54					2				
CINAC55a							1		
CINAC55b		1		1	2		1	1	1
CINAC55c		1	1	1		1	1	2	2
CINAC56a			3		1	1		2	
CINAC56b	3		1		2			1	1
CINAC57				1					
CINAC58				1	1				
CINAC59					1		2		
CINAC60				1			1		
CINAC61a	1			1			1	1	
CINAC61b				1	1				
CINAC62				4	1		3	3	3
CINAC63				1			2	1	1
CINAC68		1		1	1		1	1	
CINAC69			8				2	2	
CINAC71					2	1	1		
CINAC72			3		1		3	2	2
CINAC73	1			1	2		3		
CINAC74	1		1	1			1	2	2
CINAC75a	1		2	3	1		1		
CINAC75b	1			1			3		
CINAC76		1	5	1	4			1	1
CINAC77	1	2		1		1	1		
CINAC78					2	1			
CINAC79a	1		2	1				1	1
CINAC79b				2	1		1	1	1
CINAC82	3			2					
CINAC83				1				1	1
CINAC87		1		1	1	2			
CINAC92	1			1	2		2	2	
CINAC96	2		1	1				3	3
CINAC97			1	1	2				
CINAC98					1		1	1	1
CINAC100					2			1	1
CINAC104				2			1	2	2

Table S4. Subcellular localization predictions for CINACs

Protein name	Nucl	Cyto	Mito	Chlo	Vacu	Extr	Golg	Cysk	Plas	Pero
CINAC01	5	5	2						2	
CINAC02	4	6		1						2
CINAC03	3									
CINAC04	3	2	4	3	1					
CINAC05	3	1		2						7
CINAC06	4	3								6
CINAC07	1	2	1	7		2				
CINAC08	4	6							2.5	
CINAC09	13									
CINAC10	8	4		1						
CINAC11	10	1							2	
CINAC12	9	2		1	1					
CINAC13	11	1			1					
CINAC14	8		1	2			2			
CINAC15	7	1		1	2					
CINAC16	4	2		5					2	
CINAC17	12			1						
CINAC18	14									
CINAC19	13									
CINAC20	3		1		1		1.5		6.5	
CINAC21	14									
CINAC22	12.5									
CINAC23		2	4	1		2		1		
CINAC24	13									
CINAC25	3	4						7		
CINAC26	9	2		1		1				
CINAC27	10	1		1		1				
CINAC28	11			2						
CINAC29	7	5						2		
CINAC30	12	1								
CINAC31	13									
CINAC32	6	3	2							2
CINAC33	9	1		1					1.5	
CINAC34	6	5	1	1						
CINAC35	7	4		1		1				
CINAC36	10	3								
CINAC37	7	4							2	
CINAC38	14									
CINAC39	8.5			2					1.5	
CINAC40	3	1		8					1	
CINAC41			2	5	3	1			1	
CINAC42	6	4	1	2						
CINAC43	7	5		1						
CINAC44	2	10		2						
CINAC45	13									
CINAC46	14									
CINAC47	3	3		3	1		2		1	
CINAC48	12		1							
CINAC49	12			1						
CINAC50	3	1	1	3		1		1	3	
CINAC51	11	1		1						
CINAC52	13									
CINAC53	13									
CINAC54	12		1							
CINAC55	13									
CINAC56	12								1	
CINAC57	9	2		2						
CINAC58		13								
CINAC59	1	11	1							
CINAC60		2		9						2
CINAC61	5	4	1		1				2	
CINAC62	14									
CINAC63	12		2							
CINAC64	4	1		8						
CINAC65	8	3	1	1						
CINAC66	12			2						
CINAC67	10	1	2							
CINAC68	7	4						2		
CINAC69	13									
CINAC70	5	4	2	2						
CINAC71	9			1	1	1			1	
CINAC72	9			2		2				
CINAC73	5	2		1		4				
CINAC74	13									
CINAC75	8	1	2	2						
CINAC76	6	3	1	1						2
CINAC77	11			1		1				
CINAC78	10	1		2						
CINAC79	6	1	4.5	1						
CINAC80	3	6	2	2						

Nucl: nucleus; **Cyto**:cytoplasm; **Mito**: mitochondria; **Chlo**: chloroplast; **Plas**: plasma membrane; **extr**: extracellular; **Pero**: peroxisome; **Vacu**: vacuole; **Cysk**: cytoskeleton； **Golg**： golgiosome.

Table S5. Phosphorylation site predictions in 80 CINACs.

Protein name	Ser	Thr	Tyr
CINAC01	8	4	3
CINAC02	6	4	7
CINAC03	18	3	8
CINAC04	10	9	9
CINAC05	11	7	4
CINAC06	14	7	2
CINAC07	17	6	5
CINAC08	16	9	2
CINAC09	16	5	4
CINAC10	9	3	6
CINAC11	1	5	0
CINAC12	16	6	1
CINAC13	22	6	8
CINAC14	29	7	2
CINAC15	21	9	3
CINAC16	30	6	6
CINAC17	19	4	8
CINAC18	15	2	5
CINAC19	16	7	5
CINAC20	22	6	9
CINAC21	23	8	4
CINAC22	10	2	6
CINAC23	3	4	2
CINAC24	16	17	5
CINAC25	7	4	0
CINAC26	14	6	4
CINAC27	14	4	4
CINAC28	27	6	2
CINAC29	8	6	5
CINAC30	8	4	2
CINAC31	12	6	4
CINAC32	9	7	4
CINAC33	15	6	6
CINAC34	20	5	3
CINAC35	11	4	8
CINAC36	12	7	5
CINAC37	20	2	5
CINAC38	2	4	1
CINAC39	20	8	4
CINAC40	26	7	4
CINAC41	30	6	8
CINAC42	9	2	6
CINAC43	10	3	4
CINAC44	8	2	4
CINAC45	15	4	5
CINAC46	14	3	5
CINAC47	27	9	7
CINAC48	10	3	1
CINAC49	13	5	3
CINAC50	19	11	3
CINAC51	13	3	3
CINAC52	17	8	5
CINAC53	10	1	3
CINAC54	20	1	6
CINAC55	12	3	1
CINAC56	7	5	2
CINAC57	10	2	2
CINAC58	3	4	2
CINAC59	3	3	2
CINAC60	7	3	2
CINAC61	16	6	0
CINAC62	19	5	1
CINAC63	15	2	2
CINAC64	12	3	1
CINAC65	13	2	4
CINAC66	16	2	2
CINAC67	8	4	5
CINAC68	8	5	4
CINAC69	15	9	3
CINAC70	8	6	2
CINAC71	8	2	5
CINAC72	17	4	3
CINAC73	12	6	6
CINAC74	16	6	6
CINAC75	11	5	4
CINAC76	7	8	1
CINAC77	14	7	2
CINAC78	15	3	3
CINAC79	9	6	7
CINAC80	7	1	1

Table S6. Primer sequences of CINAC genes for RT-PCR and qRT-PCR analyses.

Gene symbol	Primer	
	F	R
CINAC01	AGAATGCACACCGACTCCTC	TTGGGTTGACTTTGGACCTC
CINAC02a	AAGGGCGTAATCGAGAAACA	GAAACTGCCCTTTCGTTCAG
CINAC02b	CAATACCGCGATTACACACG	TTCCAATTCCTTCCATTTCG
CINAC05	AAATGCCACTCCACAGGAAG	GTTCCTCGTACCAACACGGT
CINAC06	GAATCCTCCGATTCCACCTC	TGCAAATGACTGAGGCAGAC
CINAC07	CTTTGCAAGCATGAGGTTGA	CATAGGTGCACGACAAGACG
CINAC08	TTGATCCTGCAAACATCGAA	CCGAAATCAAGCTGGCTAAG
CINAC09a	TGGATGATGCATGAATTTCG	TCTTTGAGCTGTGGAGTTGG
CINAC09b	CGTGGACAGGAGAGAAGGAG	TGGGACGATCAGTTCCAGTA
CINAC10	CAAAGATTCATCCACTCATCCA	TGTCGGATTTCACCATCTTTC
CINAC12	GACGAAAGAGCCATGGAAGA	CTCATGCCCATATCCCAATC
CINAC15	ATGTTGGATCGGCTCGTTAC	TCACTGATGACGACCCATGT
CINAC16	AATGATGGAGGTGGTTCTGC	GATGCAGGAGTGGTCGGTAT
CINAC17	ACTCCTTATCCCTGGGTGCT	GCTGCTGCTCGGAATTAGAC
CINAC18	CAACTGGGAGGAGCTCTTTG	CCAGCTTAAACCCGTATCCA
CINAC20	TTCACATTGATTGCCCTTCA	CGAGCTCTAATGGCGGATAG
CINAC21	AGTACGCGACTGGGCTTAGA	ACGAGCTGATTGGCCTTATG
CINAC23	GCCTCGAAAGCTTCATCATC	ATAGTTCGTGTCGGTCGCTT
CINAC24	GCCTGAGATGAAGCAGGGTA	CGCCCATAACACATCATCAG
CINAC25	CCACCGACGAGGAATTAGTG	GTCCCATGGATCGAACTTGT
CINAC26	GAGCTCGATTCTCCAACCAC	AGTGCAACTCGAGCTCTTGC
CINAC27	ATTAACCAGGACAGGGCACA	CTTGATGCACCACCTCCTTC
CINAC28	TTTGATGTGGAAAGCTCGTG	TTCCATGCAATTCTTGTGGA
CINAC29	GGCTTCAGATTTCACCCAAC	TTATGGAAACAGGACATGGCT
CINAC30	AAATTTGGTTACGAGGAGCAAA	ACTGCCTTATCCCTCCCTGT
CINAC31	GAGACCGGAAATACCCAACA	GGGATCCATTTGAAGCACTG
CINAC32	TAAGCCAAGGGATCAACCAG	TGAGTTGGGAGTTGTTGCAG
CINAC33	CGCAGCTGTTTAGTCCAGAG	CCGCAACTTAACCTCCAGAT
CINAC34	GCTTCCATCCCACTGAAGAA	AAGCTCCCAAGGGTCATAGC
CINAC36a	AAGAGGCTGCAGTTTGATCC	CTCTCCAATCCTTGCCAATC
CINAC36b	GGCGAAGAATGGTGAGAGAG	CTTTCCAGTACCCAATTCCG
CINAC37	AGCAAGAGATGGAACAAGCTG	TCTTCATTGCACTCGGACAC
CINAC38	TTGGAATGAAGAAGACGTTGG	CACCCATTCGTCCTTAGCTG
CINAC40a	AAGGCGGCTTCGAGTAAAGT	AATTTGCTCCAGCGAATGAG
CINAC40b	TGCTTCGGATCCTTTACCAC	GCAGAACCTTGGTTCGGTAG
CINAC41	CTGCCTTGCCTGCTTCTATC	CCTGCGCCTGTAGGAATATC
CINAC42	CGTCTCCCTCCTCCTAATCC	TCTGCTTCTTGGGCAAAGTT
CINAC43	AAGTACCCGACTGGAACTCG	CAAGCGTCTTTCTCATTCCA
CINAC44	TCATTGCATTGGCCTAAAGA	GGCGAAGTGAGAAGTGGAAC
CINAC45	ACAGTGTGAGGCCAAACAGA	GCCTTTACCAGCAGATCCAC
CINAC47	AAAGTGAGCAATGTGGGAGA	TGTCAATGCCTGTTGCTTTC
CINAC50	GACCTCCAAATGGACATCGT	CCGTCTGCAATCTCTTCTCC
CINAC53a	CGCAGATGGTGATAATGCAG	CAGTGTGTTTGCTGGCAGAT
CINAC53b	AAACAATCGTCCATGGCTTC	CTGGCACGTTTCAAGAATGA
CINAC54	GGCTCAAGAACTGATTGGGT	CCGTCATTAAAGGTGGAAGG
CINAC55a	CGTCAAATTTAGGCCTACCG	GCTCGGTTCCACCATAAAGA
CINAC55b	CGTCAAATTTAGGCCTACCG	GCTCGGTTCCACCATAAAGA
CINAC55c	TGCCATTGAACCATTACGTG	GCTCGGTTCCACCATAAAGA
CINAC56a	ATGGAGAGCACCGACTCGT	GAACCACGAGCTCTTCATCG
CINAC56b	CTTCCAGCTAAGGCGAGCTA	TTCCAGTCGCCTTCCAATAC
CINAC57	GATGGCAGCTTCATCTTCTTG	GCTGATGAATTGGAAGCACA
CINAC58	CGATGGGAGAGAAAGAATGG	GACCAGTGCCAAAGATTTCC
CINAC59	GCGTGCAAGAGAGATGAAGA	CCAGTTGCTTTCCAATAGCC
CINAC60	CTCAGTTCGCTGCTGGAAG	GAGCGATTGAGGTTGGGTTA
CINAC61a	AACCAAATGGAAGATGAACGA	AAAGCATCCGGAAATCACAT
CINAC61b	GAGCCGTTCAATCTCTCCAG	CCTTCCAATACCCAGATCCA
CINAC62	ATGCAGAGTCCAGGAGCAGT	AAGGATTGAAGGTGGCAGTG
CINAC63	GAACCAACAAAGTGATCGCA	TCTGGGTGAAGGTGATACTCG
CINAC68	ATCCTGTGGCCATCAGATTC	ATTTCACTCCAGCTGGCAAC
CINAC69	GACGATTTCTTCGCGTATCC	GTTCCGGCACTGAGTAGAGC
CINAC71	TCGTCTCAGACCAATTTCCTG	CGTGCTATACCGAGACATGG
CINAC72	GCAACCACTGAGGAACACG	GGAGTTGGAGAAACTTTGCG
CINAC73	AGCCAGAGAAGACAAACTGGA	TGGAGTGAGTTCCCACATTG
CINAC74	ACTTCGAGCGTGTTCCATCT	TTGTAGTCACAAGGCATCGC
CINAC75a	AATTGGTCGGAGAGAAGCCT	TCTCCCGTCGACTCAAATTC
CINAC75b	CTCCTCTCCACCATTCCTCA	AAGCAGACCTCCCTCCTAGC
CINAC76	AGGGAGAACAGAGGACGGAT	CTCCTCTTCATCCCAAGCAC
CINAC77	TCACACTTTCCGTTTGATGC	CAGCCCATTTGAGTCGTTG
CINAC78	TGGCAAAGCTAAATGGGAAG	TCCAGTTGCTTTCCAATATCC
CINAC79a	GCCATTGAAGGATTCCTCTTC	ATCCATGGTGTTGGAGAAGC
CINAC79b	ATCGCCATGGATTCTCAAAG	TTGGCGGTGAATACATTGAA
CINAC82	TTTGGAAGATGCAGCTCAGA	TCAACCTCCTCCAGACCATC
CINAC83	TTTCTTCAGCACGAGAGAAGC	TCTTCAACCCAACCACTTGA
CINAC87	GGAAGCAACACTTCCATCGT	TTATCGACGTAGTCCCACCAG
CINAC92	AGAGCAACAGTCGCTTCTCAG	GTTGTTGACATCGGTGGTGA
CINAC96	AGTTGGATGGAGTCGGAGTG	TGCTGCTTCCAATGCTACAG
CINAC97	AACCGGGTTGAGAACGAAC	TTGGAGCTCTGCCTTTGTAGA
CINAC98	AGAGGAAGAGCACCCAAAGG	CCCTTGAAATCACCCACTCA
CINAC100	TGGAAGACGCAGAATGAGTG	CGATGGCAGTGAAATTGGTA
CINAC104	CGCCTCTTCTTCTTCCTCCT	TCATCCAAACACGACAGCTC