

Maize Transposable Elements *Ac/Ds* as Insertion Mutagenesis Tools in *Candida albicans*

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Supplemental Data

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ATG GGG CCA AAA AAG AAG AGA AAG GTG GCC ATG GCT ATT GTT CAT GAA CCA CAA CCA CAA CCA CCA CAA CCA CAA CCA CAA CCA CAG < 90
M G P K K K R K V A M A I V H E P Q P Q P Q P Q P E P Q P Q
CCA CAA CCT GAA CCA GAA GAA GAA GCA CCA CAG AAG AGA GCA AAG AAG TGC ACA TCA GAT GTA TGG CAG CAT TTC ACC AAG AAG GAA ATT < 180
P Q P E P E E A P Q K R A K K C T S D V W Q H F T K K E I
GAA GTG GAG GTC GAT GGA AAG AAA TAC GTT CAG GTA TGG GGA CAT TGC AAC TTT CCT AAT TGC AAG GCT AAG TAT AGA GCT GAG GGT CAT < 270
E V E V D G K K Y V V Q V W G H C N F P N C K A K Y R A E G H
CAT GGA ACA TCT GGA TTT CGA AAT CAC TTG AGA ACA TCA CAT AGT TTA GTT AAA GGT CAG TTG TGT TTA AAA AGT GAA AAG GAT CAT GGA < 360
H G T S G F R N H L R T S H S L V K G Q L C L K S E K D H G
AAA GAC ATA AAT TTG ATT GAG CCT TAT AAG TAC GAT GAA GTG GTT TCT TTA AAG AAG TTA CAT TTG GCA ATA ATC ATG CAT GAA TAT CCT < 450
K D I N L I E P Y K Y V V T S L K K L H L A I I M H E Y P
TTT AAT ATT GTA GAA CAT GCT TAC TTT GTT GAG TTT AAG TCT TTG AGA CCT CAC TTT CCA ATA AAG TCA CGT GTC ACT GCT AGA AAA < 540
F N I V E H A Y F V E F V K S L R P H F P I K S R V T A R K
TAT ATC ATG GAT TTG TAT TTG GAA GAA AAA GAA AAG TTG TAT GGA AAA TTA AAA GAT GTT CAG TCT AGA TTC AGT ACA ACT ATG GAT ATG < 630
Y I M D L Y L E E K E K L Y G K L K D V Q S R F S T T M D M
TGG ACA TCT TGT CAA AAT AAG TCA TAC ATG TGT GTC ACC ATC CAT TGG ATT GAT GAT GAT TGG TGT TTG CAA AAA AGA ATT GTT GGA TTT < 720
W T S C Q N K S Y M C V T I H W I D D D W C L Q K R I V G F
TTT CAT GTT GCA GGG AGA CAC ACT GGA CAA AGA TTA TCA CAA ACC TTC ACT GCA ATC ATG GTT AAG TGG AAC ATT GAG AAA AAA TTG TTT < 810
K H I N A G R I E P Y K Y V V T S L K K L H L A I I M V K W N I E K K L F
GCC TTG TCT TTG GAT AAT GCT AGT GCA AAT GAA GTA GCT GTC GAT ATA ATT GAG GAT TTG CAG GAC ACT GAT TCA AAT TTA GTT TGT < 900
A L S L D N A S A N E V A V H D I I E D L Q D T D S N L V C
GAT GGT GCT TTC TTT CAT GTG AGA TGT GCT TGT CAC ATA TTG AAC TTG GTT GCA AAG GAT GGA TTG GCT GTA ATT GCA GGA ACA ATT GAG < 990
D G A F F H V R C A C H I L N L V A K D G L A V I A C T I E
AAA ATC AAA GCT ATT GTT TTA GCT GTA AAA TCT TCT CCT TTG CAG TGG GAA GAA TTA ATG AAG TGT GCT AGT GAA TGT GAC TTG GAT AAA < 1080
K I K A I V L A V K S S P L Q W E E L M K C A S E C D L D K
TCT AAA GGG ATC TCA TAT GCT GTC TCA ACT AGA TGG AAT TCA ACC TAT TTG ATG TTG AGA GAT GCC TTA TAT TAT AAG CCT GCA TTA ATA < 1170
S K G I S Y A O V S T R W N S T Y L M L R D A L Y Y K W K V
AGA TTA AAA ACA AGT GAT CCT AGA AGA TAC GAT GCA ATT TGT CCT AAA GCC GAG GAG TGG AAG ATG GCA TTA ACT TTA TTT AAG TGT TTG < 1260
R L K T S D P R R Y D A I C P K A E E W K M A L T L F K C L
AAG AAG TTT TTT GAT TTG ACT GAA TTG TTA TCT GGT ACT CAA TAT TCA ACT GCA AAT TTA TTT TAC AAA GGT TTC TGT GAG ATA AAG GAT < 1350
K K F F D L T E L L S G T Q Y S T A N L F Y K G F C E I K D
TTG ATT GCC CAA TGG TGT GTT CAT GAA AAA TTT GTC ATT AGA AGA ATG GCC GTT GCA ATG AGT GAA AAG TTT GAG AAA TAT TGG AAA GTG < 1440
L I A Q W C V H E K F V I R R M A V A M S E K F E K A M S A P K V
TCT AAT ATT GCA TTA GCT GTA GCA TGC TTC TTA GAC CCT AGA TAC AAG AAA ATA TTG ATT GAG TTC TAT ATG AAA AAA TTT CAT GGT GAT < 1530
S N I A L A V A C F L D P R Y K K I L I E F Y M K K F H G D
TCA TAC AAA GTT CAT GTA GAT GAC TTT GTT AGA GTC ATT AGA AAA TTG TAT CAA TTC TAT TCT AGT TGT AGT CCT TCA GCT CCA AAG ACA < 1620
S Y K V R V I R K L Y Q F Y S S C S P S A P K V
AAG ACA ACT ACT AAT GAT AGT ATG GAT GAT ACC TTG ATG GAA AAT GAA GAT GAT GAA TTT CAA AAC TAT TTG CAT GAG TTG AAG GAT TAT < 1710
K T T T N D S M D D T L M E N E D D E F Q N Y L H E L K D Y
GAT CAA GTA GAG TCA AAT GAA TTG GAT AAA TAT ATG TCT GAA CCA TTA TTG AAG CAT AGT GGT CAG TTT GAT ATT TTA TCA TGG TGG AGA < 1800
D Q V E S N E L D K Y M S E P L L K H S G Q F D I L S W W R
GGA AGA GTT GCA GAA TAT CCT ATT TTG ACC CAA ATT GCA AGA GAT GTG TTA GCA ATA CAA GTG TCA ACT GTT GCT TCT GAG TCT GCT TTC < 1890
G R V A E Y P I L T Q I A R D V L A I Q V S T V A S E S A F
AGT GCT GGT GGT CGT GTT GTT GAT CCT TAC AGA AAT CGT TTA GGT TCA GAG ATT GTT GAA GCT TTG ATA TGC ACA AAA GAT TGG GTA GCA < 1980
S A G G R V V D P Y R N R L G S E I V E A L I C T K D W V A
GCA TCT AGA AAA GGT GCT ACA TAT TTT CCA ACA ATG ATT GGT GAT TTG GAG GTG TTA GAC TCT GTT ATT GCT GCT GCA ACA AAT CAT GAG < 2070
A S R K G A T Y F P T M I G D L E V L D S V I A A A T N H E
AAT CAT ATG GAT GAA GAC GCA ATA GAA TTT TCT AAG AAT AAT GAA GAT GTA GCA AGT GGA TCA TCT CCA TGA < 2148
N H M D E D A I E F S K N N E D V A S G S S P *

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Supplemental Figure S1: Sequence of the *ActPase4xCa* coding region. The *ActPase4xCa* open reading frame is based on the *ActPase4x* sequence (Lazarow et al., 2012). It lacks the N-terminal 102 amino acids of the original *ActPase*, carries four amino acid substitutions (brown letters) and is N-terminally extended by the SV40 nuclear localization sequence (green box). Codons highlighted in blue were modified in the original SV40 NLS and *ActPase4x* sequence to optimize codon usage for protein expression in *C. albicans*. Two CTG leucine codons in the original sequence were exchanged by TTG (yellow boxes). The highlighted *BsrGI* and *SphI* restriction sites are lacking in the original sequence.

Supplemental Table S1. Primer sequences

Primers for cloning of *Ds-NAT1* and *AcTPase_{4x}Ca*

Primer	Sequence
oTEFmut-F	GCGGGTCGACACTGGATGGCGG
oTEFmut-R	CCAAGTCGACGACATGGAGGCCCA
oKM34	CTTGTATCGTTGAGGCAGGGATGAAAG
oKM35	CACTACACATAATGGATAGCAAAAC
oMAL2-F	CCGCGGTGACCTTTTTGTCTAGTACCATC
oMAL2-R	GCGGTTCGAATGTAGTTGATTATTAGTT
oADHT-F	GCGGGCTAGCTCTTGGACACCAGTAAAT
oADHT-R	CCGCGGTCACCCAAGTGTATAAGATAGTA
oKM222	GTAGCCAAACCCATCAAAGCTCTACC
oKM223	GACATGGAGGCCAGAATACCC

Primers for identification of footprints

Primer	Sequence
R2 (oCaADE2-up)	CCGCATCAACATCAACATG
F2 (oCaADE2-low)	GCTGAATCCACGACAAATAACG
F1 (oKM214)	GTTTTTGGAGTATTGTGATGGTAT
R1 (oKM215)	CCAAACTTTTCCCAATGTGTAAC

Primers for FPNI-PCR

round	Forward primer	Reverse primer
1st	CCGTTCGTTTTCGTTACCGGTATATC	CGCAGGTGACATAGATGC
2nd	CCGTCCC GCAAGTTAAATATG	GACATAGATGCTTAGCGCTGAGG
3rd	GTATTTTACCGACCGTTACCGACC	CGCAGGTGACATAGATGCTTAGCGCTGAGGNNNNNNNNN
TSD1	TCCCTAAAT TCTCTGTGCCCC	TGGTGGTTGCTGGAGTTGTT
TSD2	TTCCAGTGGTGCGAGGTAAA	TGACGGATAGCGGAACCAA
TSD3	TGGATCCCCGTCATTCTCTCT	GGTCAGCTATGGGCAAACCT

Supplemental Table S2: Reinsertion sites of three *Ds-NAT1* transposition events

Transposant no.	Chromosome	Reinsertion site	ORF annotation
1	3	orf19.5992 (position 1118783)	(orf19.5992) Zn(II)2Cys6 transcription factor; regulator of white-opaque switching; required for maintenance of opaque state; Hap43-induced
2	3	between orf19.319 and orf19.320 (position 679408)	
3	5	orf19.6679 (position 813686)	uncharacterized; (orf19.6679) Ortholog(s) have cytosol, nucleus localization