

Appendix

Figures

Figure A1 Sequence analysis of the eluted and purified PCR amplified band at 475 bp.	2
Figure A2 Sequence analysis of plasmid (sample 2) from the pENTR/D-Topo reaction.	4
Figure A3 Sequence analysis of the plasmid (sample 1) from the LR clonase reaction.	6
Figure A4 Sequence analysis of Line LinA2(b) from the <i>Agrobacterium</i> -mediated transformation.	7
Figure A5 Sequence analysis of Line LinA4(a) from the <i>Agrobacterium</i> -mediated transformation.	8
Figure A6 Serial Dilution Series Chromatogram of Aldrin (n=3).	9

Tables

Table A1 Area Comparison between T = 1.40 minutes (Acetonitrile) and 14.37 minutes (Aldrin)	9
---	---

	1				50
F_LinA_PCR				NNNNNNNN	NNTCAGGACC
CACC_LinA	CACCATGAGT	GATCTAGACA	GA	CTTGCAAG	CCGGGCCGCG ATTCAGGACC
Consensusnnnnnnnn	anTCAGGACC
	51				100
F_LinA_PCR	TCTACTCTGA	C-AGCTCATT	GGCCGTAGAC	AAGCGCCAAG	AGGGCCGTCT
CACC_LinA	TCTACTCTGA	CCAGCTCATT	GGC-GTAGAC	AAGCGCCAAG	AGGGCCGTCT
Consensus	TCTACTCTGA	C.AGCTCATT	GGC.GTAGAC	AAGCGCCAAG	AGGGCCGTCT
	101				150
F_LinA_PCR	CGCTTCTATT	TGGTGGGATG	ATGCAGAGTG	GACCATTGAG	GGAATCGGCA
CACC_LinA	CGCTTCTATT	TGGTGGGATG	ATGCAGAGTG	GACCATTGAG	GGAATCGGCA
Consensus	CGCTTCTATT	TGGTGGGATG	ATGCAGAGTG	GACCATTGAG	GGAATCGGCA
	151				200
F_LinA_PCR	CCTACAAGGG	CCCGGAAGGC	GCCCTCGATT	TGGCCAATAA	CGTACTCTGG
CACC_LinA	CCTACAAGGG	CCCGGAAGGC	GCCCTCGATT	TGGCCAATAA	CGTACTCTGG
Consensus	CCTACAAGGG	CCCGGAAGGC	GCCCTCGATT	TGGCCAATAA	CGTACTCTGG
	201				250
F_LinA_PCR	CCAATGTTC	ACGAATGTAT	TCATTATGGA	ACCAATCTGC	GCTTGGAATT
CACC_LinA	CCAATGTATC	ACGAAACTAT	TCATTATGGA	ACCAATCTGC	GCTTGGAATT
Consensus	CCAATGTaTC	ACGAAacTAT	TCATTATGGA	ACCAATCTGC	GCTTGGAATT
	251				300
F_LinA_PCR	TGTGAGCGCG	GACAAGGTAA	ATGGTATTGG	CGACGTCCTT	CTCCTTGAA
CACC_LinA	TGTGAGCGCG	GACAAGGTAA	ATGGTATTGG	CGACGTCCTT	CTCCTTGAA
Consensus	TGTGAGCGCG	GACAAGGTAA	ATGGTATTGG	CGACGTCCTT	CTCCTTGAA
	301				350
F_LinA_PCR	ATCTCGTCGA	AGGTAATCAG	TCGATTCTTA	TCGCTGCGGT	CTTCACGGAT
CACC_LinA	ATCTCGTCGA	AGGTAATCAG	TCGATTCTTA	TCGCTGCGGT	CTTCACGGAT
Consensus	ATCTCGTCGA	AGGTAATCAG	TCGATTCTTA	TCGCTGCGGT	CTTCACGGAT
	351				400
F_LinA_PCR	GAGTATGAGC	GCCGTGACGG	GGTGTGGAAG	TTCTCTAANC	GCAACGCATG
CACC_LinA	GAGTATGAGC	GCCGTGACGG	GGTGTGGAAG	TTCTCTAAGC	GCAACGTATG
Consensus	GAGTATGAGC	GCCGTGACGG	GGTGTGGAAG	TTCTCTAAnC	GCAACGcATG
	401				450
F_LinA_PCR	CACGAACTAT	TTCACCCCGC	TGGCCGGCAT	TCATTTGCA	CCGCCCGGCA
CACC_LinA	CACGAACTAT	TTCACCCCGC	TGGCCGGCAT	TCATTTGCA	CCGCCCGGCA
Consensus	CACGAACTAT	TTCACCCCGC	TGGCCGGCAT	TCATTTGCA	CCGCCCGGCA
	451		479		
F_LinA_PCR	TTCATTTGCG	ACCGTCCGGC	GCATAANAN		
CACC_LinA	TTCATTTGCG	ACCGTCCGGC	GCATAA		
Consensus	TTCATTTGCG	ACCGTCCGGC	GCATAA...		

Figure A1 Sequence analysis of the eluted and purified PCR amplified band at 475 bp.

F_LinA_PCR represents the results of DNA sequencing using the For_linA primer.
CACC_LinA represents the theoretical sequence predicted using the For_linA and Rev_linA primers.
Red text indicates high consensus, Blue text indicates low consensus. Black is neutral.

(created using Multalin-Multiple sequence alignment with hierarchical clustering)
(<http://multalin.toulouse.inra.fr/multalin/>)

	651				700
F_LinA_DT2					NNN
DTOPO_LinA	TGTACAAAAA	AGCAGGCTCC	GCGGCCGCC	CCTTCACCAT	GAGTGATCTA
Consensusnna
	701				750
F_LinA_DT2	NNNANNNTTG	CAAGCCGGGC	CGCGATTCAG	GACCTCTACT	CTGAC-AGCT
DTOPO_LinA	GACAGACTTG	CAAGCCGGGC	CGCGATTCAG	GACCTCTACT	CTGACCAGCT
Consensus	nanAnanTTG	CAAGCCGGGC	CGCGATTCAG	GACCTCTACT	CTGAC.AGCT
	751				800
F_LinA_DT2	CATTGGCCGT	AGACAAGCGC	CAAGAGGGCC	GTCTCGCTTC	TATTTGGTGG
DTOPO_LinA	CATTGGC-GT	AGACAAGCGC	CAAGAGGGCC	GTCTCGCTTC	TATTTGGTGG
Consensus	CATTGGC.GT	AGACAAGCGC	CAAGAGGGCC	GTCTCGCTTC	TATTTGGTGG
	801				850
F_LinA_DT2	GATGATGCAG	AGTGGACCAT	TGAGGGAATC	GGCACCTACA	AGGGCCCGBA
DTOPO_LinA	GATGATGCAG	AGTGGACCAT	TGAGGGAATC	GGCACCTACA	AGGGCCCGBA
Consensus	GATGATGCAG	AGTGGACCAT	TGAGGGAATC	GGCACCTACA	AGGGCCCGBA
	851				900
F_LinA_DT2	AGGCGCCCTC	GATTTGGCCA	ATAACGTACT	CTGGCCAATG	TTTCACGAA
DTOPO_LinA	AGGCGCCCTC	GATTTGGCCA	ATAACGTACT	CTGGCCAATG	TATCACGAAA
Consensus	AGGCGCCCTC	GATTTGGCCA	ATAACGTACT	CTGGCCAATG	TaTCACGAAa
	901				950
F_LinA_DT2	GTATTCATTA	TGGAACCAAT	CTGCGCTTGG	AATTTGTGAG	CGCGGACAAG
DTOPO_LinA	CTATTCATTA	TGGAACCAAT	CTGCGCTTGG	AATTTGTGAG	CGCGGACAAG
Consensus	cTATTCATTA	TGGAACCAAT	CTGCGCTTGG	AATTTGTGAG	CGCGGACAAG
	951				1000
F_LinA_DT2	GTAAATGGTA	TTGGCGACGT	CCTTCTCCTT	GGAAATCTCG	TCGAAGGTAA
DTOPO_LinA	GTAAATGGTA	TTGGCGACGT	CCTTCTCCTT	GGAAATCTCG	TCGAAGGTAA
Consensus	GTAAATGGTA	TTGGCGACGT	CCTTCTCCTT	GGAAATCTCG	TCGAAGGTAA
	1001				1050
F_LinA_DT2	TCAGTCGATT	CTTATCGCTG	CGGTCTTCAC	GGATGAGTAT	GAGCGCCGTG
DTOPO_LinA	TCAGTCGATT	CTTATCGCTG	CGGTCTTCAC	GGATGAGTAT	GAGCGCCGTG
Consensus	TCAGTCGATT	CTTATCGCTG	CGGTCTTCAC	GGATGAGTAT	GAGCGCCGTG
	1051				1100
F_LinA_DT2	ACGGGGTGTG	GAAGTTCTCT	AANCGCAACG	CATGCACGAA	CTATTTACC
DTOPO_LinA	ACGGGGTGTG	GAAGTTCTCT	AAGCGCAACG	TATGCACGAA	CTATTTACC
Consensus	ACGGGGTGTG	GAAGTTCTCT	AAnCGCAACG	cATGCACGAA	CTATTTACC
	1101				1150
F_LinA_DT2	CCGCTGGCCG	GCATTCATTT	CGCACCGCC	GGCATTTCATT	TCGCACCGTC
DTOPO_LinA	CCGCTGGCCG	GCATTCATTT	CGCACCGCC	GGCATTTCATT	TCGCACCGTC
Consensus	CCGCTGGCCG	GCATTCATTT	CGCACCGCC	GGCATTTCATT	TCGCACCGTC
	1151				1200
F_LinA_DT2	CGGCGCATAA	AAGGGTGGGC	GCGCCGACCC	AGCTTTCTTG	TACAAAGTTG
DTOPO_LinA	CGGCGCATAA	AAGGGTGGGC	GCGCCGACCC	AGCTTTCTTG	TACAAAGTTG
Consensus	CGGCGCATAA	AAGGGTGGGC	GCGCCGACCC	AGCTTTCTTG	TACAAAGTTG
	1201				1250
F_LinA_DT2	GCATTATAAG	AAAGCATTGC	TTATCAATTT	GTTGCAACGA	ACAGGTCACT
DTOPO_LinA	GCATTATAAG	AAAGCATTGC	TTATCAATTT	GTTGCAACGA	ACAGGTCACT
Consensus	GCATTATAAG	AAAGCATTGC	TTATCAATTT	GTTGCAACGA	ACAGGTCACT

	1251				1300
F_LinA_DT2	ATCAGTCAA	ATAAAATCAT	TATTTGCCAT	CCAGCTGATA	TCCCCTATAG
DTOPO_LinA	ATCAGTCAA	ATAAAATCAT	TATTTGCCAT	CCAGCTGATA	TCCCCTATAG
Consensus	ATCAGTCAA	ATAAAATCAT	TATTTGCCAT	CCAGCTGATA	TCCCCTATAG
	1301				1350
F_LinA_DT2	TGAGTCGTAT	TACATGGTCA	TAGCTGTTTC	CTGGCAGCTC	TGGCCCCTGT
DTOPO_LinA	TGAGTCGTAT	TACATGGTCA	TAGCTGTTTC	CTGGCAGCTC	TGGCCCCTGT
Consensus	TGAGTCGTAT	TACATGGTCA	TAGCTGTTTC	CTGGCAGCTC	TGGCCCCTGT
	1351				1400
F_LinA_DT2	CTCAAAATCT	CTGATGTTAC	ATTGCACAAG	ATAAAAATAT	ATCATCATGA
DTOPO_LinA	CTCAAAATCT	CTGATGTTAC	ATTGCACAAG	ATAAAAATAT	ATCATCATGA
Consensus	CTCAAAATCT	CTGATGTTAC	ATTGCACAAG	ATAAAAATAT	ATCATCATGA
	1401				1450
F_LinA_DT2	ACAATAAAAC	TGTCTGCTTA	CATAAACAGT	AATACAAGGG	GTGTTATGAG
DTOPO_LinA	ACAATAAAAC	TGTCTGCTTA	CATAAACAGT	AATACAAGGG	GTGTTATGAG
Consensus	ACAATAAAAC	TGTCTGCTTA	CATAAACAGT	AATACAAGGG	GTGTTATGAG
	1451				1500
F_LinA_DT2	CCATATTCAA	CGGGAAACGT	CGAGGCCGCG	ATTAAATTCC	AACATGGATG
DTOPO_LinA	CCATATTCAA	CGGGAAACGT	CGAGGCCGCG	ATTAAATTCC	AACATGGATG
Consensus	CCATATTCAA	CGGGAAACGT	CGAGGCCGCG	ATTAAATTCC	AACATGGATG
	1501				1550
F_LinA_DT2	CTGATTTATA	TGGGTATAAA	TGGGCTCGCG	ATAATGTCGG	GCAATCAGGT
DTOPO_LinA	CTGATTTATA	TGGGTATAAA	TGGGCTCGCG	ATAATGTCGG	GCAATCAGGT
Consensus	CTGATTTATA	TGGGTATAAA	TGGGCTCGCG	ATAATGTCGG	GCAATCAGGT
	1551				1600
F_LinA_DT2	GCGACAATCT	ATCGCTTGTA	TGGGAAGCCC	GATGCGCCAG	AGTTGTTTCT
DTOPO_LinA	GCGACAATCT	ATCGCTTGTA	TGGGAAGCCC	GATGCGCCAG	AGTTGTTTCT
Consensus	GCGACAATCT	ATCGCTTGTA	TGGGAAGCCC	GATGCGCCAG	AGTTGTTTCT
	1601				1650
F_LinA_DT2	GAAACATGGC	AAAGGTAGCG	TTGCCA-TGA	TGTTACAGAT	GAGATGGTCA
DTOPO_LinA	GAAACATGGC	AAAGGTAGCG	TTGCCAATGA	TGTTACAGAT	GAGATGGTCA
Consensus	GAAACATGGC	AAAGGTAGCG	TTGCCA.TGA	TGTTACAGAT	GAGATGGTCA
	1651				1700
F_LinA_DT2	GACTAAACTG	GCTGACGGAA	TTNANNCNNN	NNNNNNNNNN	NNNNN
DTOPO_LinA	GACTAAACTG	GCTGACGGAA	TTTATGCCTC	TTCCGACCAT	CAAGCATTTT
Consensus	GACTAAACTG	GCTGACGGAA	TTnAnnCnnn	nnnnnannan	naann.....

Figure A2 Sequence analysis of plasmid (sample 2) from the pENTR/D-Topo reaction.

F_LinA_DT2 represents the results of DNA sequencing using the For_linA primer.

D-Topo_LinA represents the theoretical construct sequence.

Red text indicates high consensus, Blue text indicates low consensus. Black is neutral.

(created using Multalin-Multiple sequence alignment with hierarchical clustering)
[\(http://multalin.toulouse.inra.fr/multalin/\)](http://multalin.toulouse.inra.fr/multalin/)

	51				100
F LinA CT1		NNNNNNNANN	GGCCGCGATT	CAGGACCTCT	ACTCTGACA-
Ctapi_LinA	CTAGACAGAC	TTGCAAGCCG	GGCCGCGATT	CAGGACCTCT	ACTCTGACAA
Consensus	nnnnaaannn	GGCCGCGATT	CAGGACCTCT	ACTCTGACA.
	101				150
F LinA CT1	GCTCATTGGC	CGTAGACAAG	CGCCAAGAGG	GCCGTCTCGC	TTCTATTTGG
Ctapi_LinA	GCTCATTG-C	CGTAGACAAG	CGCCAAGAGG	GCCGTCTCGC	TTCTATTTGG
Consensus	GCTCATTG.C	CGTAGACAAG	CGCCAAGAGG	GCCGTCTCGC	TTCTATTTGG
	151				200
F LinA CT1	TGGGATGATG	CAGAGTGGAC	CATTGAGGGA	ATCGGCACCT	ACAAGGGCCC
Ctapi_LinA	TGGGATGATG	CAGAGTGGAC	CATTGAGGGA	ATCGGCACCT	ACAAGGGCCC
Consensus	TGGGATGATG	CAGAGTGGAC	CATTGAGGGA	ATCGGCACCT	ACAAGGGCCC
	201				250
F LinA CT1	GGAAGGCGCC	CTCGATTTGG	CCAATAACGT	ACTCTGGCCA	ATGTTTCACG
Ctapi_LinA	GGAAGGCGCC	CTCGATTTGG	CCAATAACGT	ACTCTGGCCA	ATGTTTCACG
Consensus	GGAAGGCGCC	CTCGATTTGG	CCAATAACGT	ACTCTGGCCA	ATGTTTCACG
	251				300
F LinA CT1	AATGTATTCA	TTATGGAACC	AATCTGCGCT	TGGAATTTGT	GAGCGCGGAC
Ctapi_LinA	AATGTATTCA	TTATGGAACC	AATCTGCGCT	TGGAATTTGT	GAGCGCGGAC
Consensus	AATGTATTCA	TTATGGAACC	AATCTGCGCT	TGGAATTTGT	GAGCGCGGAC
	301				350
F LinA CT1	AAGGTAAATG	GTATTGGCGA	CGTCCTTCTC	CTTGAAATC	TCGTGGAAGG
Ctapi_LinA	AAGGTAAATG	GTATTGGCGA	CGTCCTTCTC	CTTGAAATC	TCGTGGAAGG
Consensus	AAGGTAAATG	GTATTGGCGA	CGTCCTTCTC	CTTGAAATC	TCGTGGAAGG
	351				400
F LinA CT1	TAATCAGTCG	ATTCTTATCG	CTGCGGTCTT	CACGGATGAG	TATGAGCGCC
Ctapi_LinA	TAATCAGTCG	ATTCTTATCG	CTGCGGTCTT	CACGGATGAG	TATGAGCGCC
Consensus	TAATCAGTCG	ATTCTTATCG	CTGCGGTCTT	CACGGATGAG	TATGAGCGCC
	401				450
F LinA CT1	GTGACGGGGT	GTGGAAGTTC	TCTAANCGCA	ACGCATGCAC	GAACTATTTT
Ctapi_LinA	GTGACGGGGT	GTGGAAGTTC	TCTAAGCGCA	ACGCATGCAC	GAACTATTTT
Consensus	GTGACGGGGT	GTGGAAGTTC	TCTAANCGCA	ACGCATGCAC	GAACTATTTT
	451				500
F LinA CT1	ACCCCGCTGG	CCGGCATTCA	TTTCGCACCG	CCCGGCATTC	ATTTTCGCACC
Ctapi_LinA	ACCCCGCTGG	CCGGCATTCA	TTTCGCACCG	CCCGGCATTC	ATTTTCGCACC
Consensus	ACCCCGCTGG	CCGGCATTCA	TTTCGCACCG	CCCGGCATTC	ATTTTCGCACC
	501				550
F LinA CT1	GTCCGGCGCA	TAATCTTGTG	AAATTGTTAT	CCGCAAGGGT	GGGCGCGCCG
Ctapi_LinA	GTCCGGCGCA	TAATCTTGTG	AAATTGTTAT	CCGCAAGGGT	GGGCGCGCCG
Consensus	GTCCGGCGCA	TAATCTTGTG	AAATTGTTAT	CCGCAAGGGT	GGGCGCGCCG
	551				600
F LinA CT1	ACCCAGCTTT	CTTGTACAAA	GTGGTGACTA	GTGGAGGGTA	AATTTCTAGT
Ctapi_LinA	ACCCAGCTTT	CTTGTACAAA	GTGGTGACTA	GTGGAGGGTA	AATTTCTAGT
Consensus	ACCCAGCTTT	CTTGTACAAA	GTGGTGACTA	GTGGAGGGTA	AATTTCTAGT


```

601                                     650
F_LinA_CT1 TTTTCTCCTT CATTTCCTTG GTTAGGACCC TTTTCTCTTT TTATTTTTTT -
Ctapi_LinA TTTTCTCCTT CATTTCCTTG GTTAGGACCC TTTTCTCTTT TTATTTTTTT
Consensus TTTTCTCCTT CATTTCCTTG GTTAGGACCC TTTTCTCTTT TTATTTTTTT.

651                                     700
F_LinA_CT1 GAGCTTTGAT CTTTCTTTAA ACTGATCTAT TTTTAAATTG ATTGGTTATG
Ctapi_LinA GAGCTTTGAT CTTTCTTTAA ACTGATCTAT TTTTAAATTG ATTGGTTATG
Consensus GAGCTTTGAT CTTTCTTTAA ACTGATCTAT TTTTAAATTG ATTGGTTATG

701                                     750
F_LinA_CT1 GTGTAAATAT TACATAGCTT TAACTGATAA TCTGATTACT TTATTTTCGTG
Ctapi_LinA GTGTAAATAT TACATAGCTT TAACTGATAA TCTGATTACT TTATTTTCGTG
Consensus GTGTAAATAT TACATAGCTT TAACTGATAA TCTGATTACT TTATTTTCGTG

751                                     800
F_LinA_CT1 TGTCTATGAT GATGATGATA GTTACAGAAC CGCTTCTAGT GGAAGTACCT
Ctapi_LinA TGTCTATGAT GATGATGATA GTTACAGAAC CGCTTCTAGT GGAAGTACCT
Consensus TGTCTATGAT GATGATGATA GTTACAGAAC CGCTTCTAGT GGAAGTACCT

801                                     850
F_LinA_CT1 CCATGGAGAG CAGCAGATGG AAGAGCAACT TCATCGCAGT GAGCGCCGCA
Ctapi_LinA CCATGGAGAG CAGCAGATGG AAGAGCAACT TCATCGCAGT GAGCGCCGCA
Consensus CCATGGAGAG CAGCAGATGG AAGAGCAACT TCATCGCAGT GAGCGCCGCA

851                                     900
F_LinA_CT1 AACCGCTTCA AGAAGATCAG CTCCAGCGGC GCACTGGACT ACGACATCCC
Ctapi_LinA AACCGCTTCA AGAAGATCAG CTCCAGCGGC GCACTGGACT ACGACATCCC
Consensus AACCGCTTCA AGAAGATCAG CTCCAGCGGC GCACTGGACT ACGACATCCC

901                                     950
F_LinA_CT1 AACCACTGCC AGCGAGAACC TGTACTTCCA GGGCGAGCTG AAGACCGCAG
Ctapi_LinA AACCACTGCC AGCGAGAACC TGTACTTCCA GGGCGAGCTG AAGACCGCAG
Consensus AACCACTGCC AGCGAGAACC TGTACTTCCA GGGCGAGCTG AAGACCGCAG

951                                     1000
F_LinA_CT1 NA--NNCNNN NNNNNNNNNN NNNNN
Ctapi_LinA CTCTGGCACA GCACGACGAG GTGGTCGACA ACAAGTTCAA CAAGGAACAG
Consensus na..nnCana nnannannan nnnnn.....

```

Figure A3 Sequence analysis of the plasmid (sample 1) from the LR clonase reaction.

F_LinA_CT1 represents the results of DNA sequencing using the For_linA primer.

Ctapi_LinA represents the theoretical construct sequence.

Red text indicates high consensus, Blue text indicates low consensus. Black is neutral.

(created using Multalin- Multiple sequence alignment with hierarchical clustering)
(<http://multalin.toulouse.inra.fr/multalin/>)

	1					50
LinA2			NNNNNNN	NNNNNNNNNC	AGGACCTCTA	
LinA	ATGAGTGATC	TAGACAGACT	TGC	AAGCCGG	GCCGCGATTC	AGGACCTCTA
Consensusaannnnn	nnnnnnannC	AGGACCTCTA	
	51					100
LinA2	CTCTGAC-AG	CTCATTGGCG	TAGACAAGCG	CCAAGAGGGC	CGTCTCGCTT	
LinA	CTCTGACCAG	CTCATTGGCG	TAGACAAGCG	CCAAGAGGGC	CGTCTCGCTT	
Consensus	CTCTGAC.AG	CTCATTGGCG	TAGACAAGCG	CCAAGAGGGC	CGTCTCGCTT	
	101					150
LinA2	CTATTTGGTG	GGATGATGCA	GAGTGGACCA	TTGAGGGAAT	CGGCACCTAC	
LinA	CTATTTGGTG	GGATGATGCA	GAGTGGACCA	TTGAGGGAAT	CGGCACCTAC	
Consensus	CTATTTGGTG	GGATGATGCA	GAGTGGACCA	TTGAGGGAAT	CGGCACCTAC	
	151					200
LinA2	AAGGGCCCGG	AAGGCGCCCT	CGATTTGGCC	AATAACGTAC	TCTGGCCAAT	
LinA	AAGGGCCCGG	AAGGCGCCCT	CGATTTGGCC	AATAACGTAC	TCTGGCCAAT	
Consensus	AAGGGCCCGG	AAGGCGCCCT	CGATTTGGCC	AATAACGTAC	TCTGGCCAAT	
	201					250
LinA2	GTATCACGAA	TCTATTCATT	ATGGAACCAA	TCTGCGCTTG	GAATTTGTGA	
LinA	GTATCACGAA	ACTATTCATT	ATGGAACCAA	TCTGCGCTTG	GAATTTGTGA	
Consensus	GTATCACGAA	aCTATTCATT	ATGGAACCAA	TCTGCGCTTG	GAATTTGTGA	
	251					300
LinA2	GCGCGGACCA	GGTAAATGGT	ATTGGCGACG	TCCTTCTCCT	TGAAATCTC	
LinA	GCGCGGACAA	GGTAAATGGT	ATTGGCGACG	TCCTTCTCCT	TGAAATCTC	
Consensus	GCGCGGACaA	GGTAAATGGT	ATTGGCGACG	TCCTTCTCCT	TGAAATCTC	
	301					350
LinA2	GTCGAAGGTA	ATCAGTCGAT	TCTTATCGCT	GCGGTCTTCA	CGGATGAGTA	
LinA	GTCGAAGGTA	ATCAGTCGAT	TCTTATCGCT	GCGGTCTTCA	CGGATGAGTA	
Consensus	GTCGAAGGTA	ATCAGTCGAT	TCTTATCGCT	GCGGTCTTCA	CGGATGAGTA	
	351					400
LinA2	TGAGCGCCGT	GACGGGGTGT	GGAAGTTCTC	TAAGCGCAAC	GTATGCACGA	
LinA	TGAGCGCCGT	GACGGGGTGT	GGAAGTTCTC	TAAGCGCAAC	GTATGCACGA	
Consensus	TGAGCGCCGT	GACGGGGTGT	GGAAGTTCTC	TAAGCGCAAC	GTATGCACGA	
	401					450
LinA2	ACTATTTAC	CCCCTGGCC	GGCATTTCATT	TCGCACCGCC	CGGGATTTCAT	
LinA	ACTATTTAC	CCCCTGGCC	GGCATTTCATT	TCGCACCGCC	CGGCATTTCAT	
Consensus	ACTATTTAC	CCCCTGGCC	GGCATTTCATT	TCGCACCGCC	CGGcATTTCAT	
	451		471			
LinA2	TTCGCACCGT	CCGGCGCATA	A			
LinA	TTCGCACCGT	CCGGCGCATA	A			
Consensus	TTCGCACCGT	CCGGCGCATA	A			

Figure A4 Sequence analysis of Line LinA2(b) from the *Agrobacterium*-mediated transformation.

LinA4 represents the results of DNA sequencing using the For_linA primer.

LinA represents the known sequence.

Red text indicates high consensus, Blue text indicates low consensus. Black is neutral.

(created using Multalin- Multiple sequence alignment with hierarchical clustering)
(<http://multalin.toulouse.inra.fr/multalin/>)

	1				50
LinA4			NNNNNNN	NNNNNNNNNN	NNNNNCTCTA
LinA	ATGAGTGATC	TAGACAGACT	TGC	AAGCCGG	GCCGCGATTC
Consensusa	nnnnnn	nnnnnannn
	51				100
LinA4	CTCTGAC-AG	CTCATTGGCG	TAGACAAGCG	CCAAGCAGGG	CCGTCTCGCT
LinA	CTCTGACCAG	CTCATTGGCG	TAGACAAGCG	CCAAG-AGGG	CCGTCTCGCT
Consensus	CTCTGAC.AG	CTCATTGGCG	TAGACAAGCG	CCAAG.AGGG	CCGTCTCGCT
	101				150
LinA4	TCTATTTGGT	GGGATGATGC	ACAGTGGACC	ATTGAGGGAA	TCGGCACCTA
LinA	TCTATTTGGT	GGGATGATGC	AGAGTGGACC	ATTGAGGGAA	TCGGCACCTA
Consensus	TCTATTTGGT	GGGATGATGC	A	cAGTGGACC	ATTGAGGGAA
	151				200
LinA4	CAAGGGCCCG	GAAGGCGCC	TCGATTTGGC	CAATAACGTA	CTCTGGCCAA
LinA	CAAGGGCCCG	GAAGGCGCC	TCGATTTGGC	CAATAACGTA	CTCTGGCCAA
Consensus	CAAGGGCCCG	GAAGGCGCC	TCGATTTGGC	CAATAACGTA	CTCTGGCCAA
	201				250
LinA4	TGTATCACGA	ATCTATTCAT	TATGGAACCA	ATCTGCGCTT	GGAATTTGTG
LinA	TGTATCACGA	A	ACTATTCAT	TATGGAACCA	ATCTGCGCTT
Consensus	TGTATCACGA	A	aCTATTCAT	TATGGAACCA	ATCTGCGCTT
	251				300
LinA4	AGTCGGACA	AGGTAAATGG	TATTGGCGAC	CTCCTTCTCC	TTGGAAATCT
LinA	AGC	GCGGACA	AGGTAAATGG	TATTGGCGAC	GTCCTTCTCC
Consensus	AGC	gCGGACA	AGGTAAATGG	TATTGGCGAC	cTCCTTCTCC
	301				350
LinA4	CGTCGAAGGT	AATCAGTCGA	TTCTTATCGC	TGCGCTCTTC	ACGGATGAGT
LinA	CGTCGAAGGT	AATCAGTCGA	TTCTTATCGC	TGCGG	TCTTC
Consensus	CGTCGAAGGT	AATCAGTCGA	TTCTTATCGC	TGCG	cTCTTC
	351				400
LinA4	ATGATCGCCG	TGACGGGGTG	TGGAAGTTCT	CTAAGCGCAA	CTGATGCACG
LinA	ATGAG	CGCCG	TGACGGGGTG	TGGAAGTTCT	CTAAGCGCAA
Consensus	ATGAG	gCGCCG	TGACGGGGTG	TGGAAGTTCT	CTAAGCGCAA
	401				450
LinA4	AACTATTTCA	GCCCGCTGGC	CGGCATTCAT	TTCGCACCGC	C--GCATTCA
LinA	AACTATTTCA	C	CCCGCTGGC	CGGCATTCAT	TTCGCACCGC
Consensus	AACTATTTCA	c	CCCGCTGGC	CGGCATTCAT	TTCGCACCGC
	451				500
LinA4	TTTCGCACCG	TCCGGCGATA	ACACAGCGTA	CTCCTGGATT	CTTAGCGCGA
LinA	TTTCGCACCG	TCCGGCGCAT	AA		
Consensus	TTTCGCACCG	TCCGGCG	aaa	Aa.....

Figure A5 Sequence analysis of Line LinA4(a) from the *Agrobacterium*-mediated transformation.

LinA4 represents the results of DNA sequencing using the For_linA primer.

LinA represents the known sequence.

Red text indicates high consensus, Blue text indicates low consensus. Black is neutral.

(created using Multalin- Multiple sequence alignment with hierarchical clustering)

(<http://multalin.toulouse.inra.fr/multalin/>)

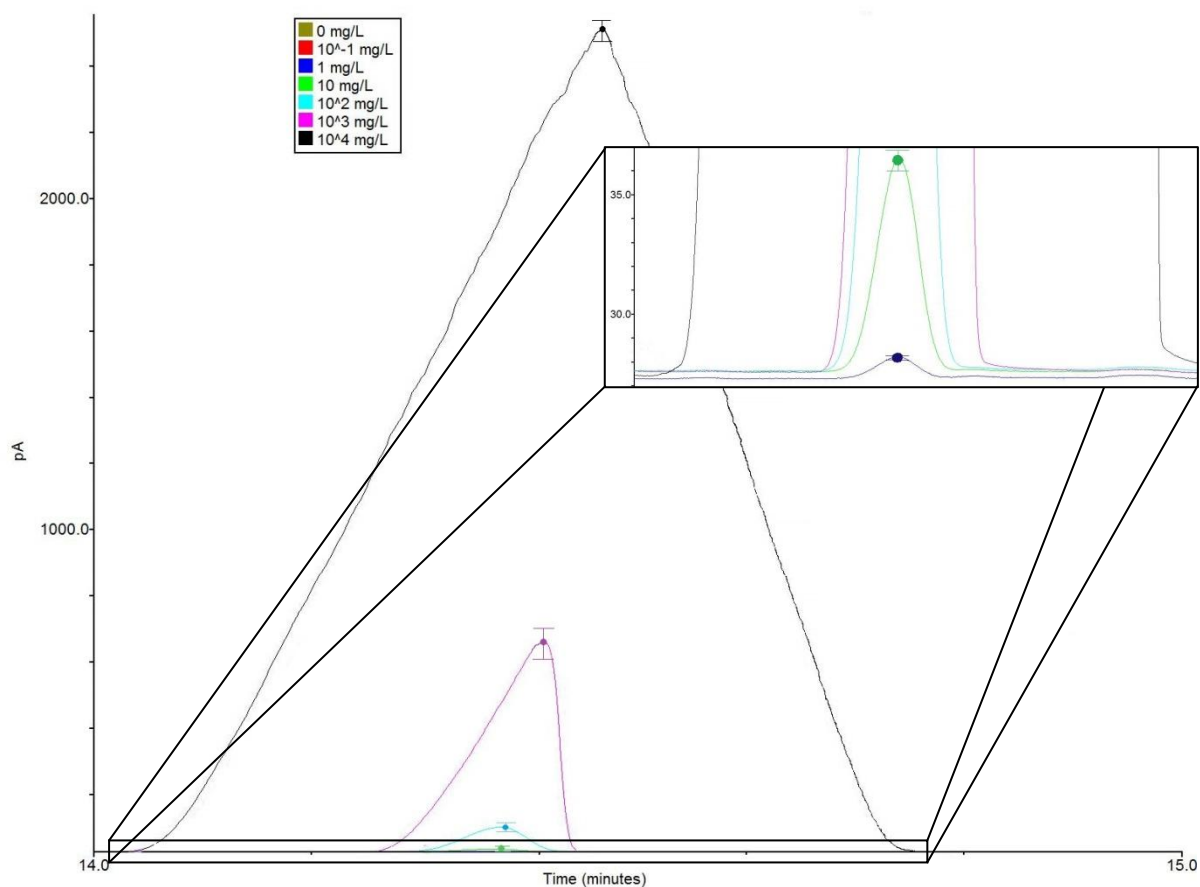


Figure A6 Serial Dilution Series Chromatogram of Aldrin (n=3).
Error bars represent standard deviation

Table A1 Area Comparison between T = 1.40 minutes (Acetonitrile) and 14.37 minutes (Aldrin)

Aldrin Concentration (mg/L)	Area under Peak at T = 1.40 minutes	Area under Peak at T = 14.37 minutes
0	2744037.50 ± 32204.50	0
10 ⁻¹	2744037.50 ± 30859.35	0
1	2717477.25 ± 29207.43	3.71 ± 1.25
10	2718963.50 ± 38634.73	35.03 ± 2.63
10 ²	2721763.00 ± 30328.46	301.60 ± 15.52
10 ³	2742638.00 ± 24224.45	2993.41 ± 92.83
10 ⁴	2754109.50 ± 37026.60	31225.25 ± 834.23