

PFC	Dist to 3' gene	Length	Sequence
TniDA _{AD1b}	5,394	297	ATTCATCAGAAGTGCTCGCCGCTCGTTGTTAAAATGCTCGCTGA CGTCGCTCCAATGATCATTATTGTAACAGGTTTATCAGCAAAT AAATAGGAGAGGGCTGTCACCTTGATGATGGAGGCGCCTTCGG TCAGACGAATAATATCCAGGAGGAGAGGAGAGGAGGAGT GAGAGATGCTCGTCCCTGGGTTGATCTCTCCGTCTGCTCCACAT TGCTCTTGGGTTTGGCCTCTTGGGTGAAATTGACAGTCTGATTA ATAAAAATGAGCGCTGCAACATTTCCCTTTCATTTA
TniDA _{AD4}	111	75	TACTTTGCATATCACGTGACGCTGTATTAACAAATCAACAATTA CCTACCCTCGATTCTTCAGGAGTTGCTAAAA
TniDA _{DE7}	3,451	52	ATTAATTCTCCTAAATAAGACAATTATACTGTTTTTAAAAA GAAGAAGA
TniDA _{DE10cd}	2,186	28	GGGGCGCCAAAGCAAAGTTAAGGTCAAG
TniDA _{DE9abe}	241	155	TAATGACCGATATTGATGTATGGTAATTTCTTGGCCGGATCACA TGACGCGATCACCTCCAGAATCGATCCGGTTGTGCTGCAGGTC TGCCCACGACTCCGATTTGTTTCCCTCCCTGCCTGAGCTTTCCC ACACGCTTGC GCGGCTACAGATGG
TniDA _{EF11ab}	2,387	28	TGTTTAGCAAACCTTGAACCGTCTAGAC
TniDA _{EF19ac}	214	177	GTCGCTGTGACCACGTCTGTATCCGCAGTGC GCGGACGCAGA CGTGGGAGGGGAGAGAAAAGGCTGCGTCTCAAGGCCATTTTC AAATCTCATTGGTGGGCTTGTTCATGTGGTCGGGAGACATTCCG ACTGATCCGTAGATTGTTTTTCCCAGATATGTCGGCGTACAAAG GACA
TniDA _{FG21abc}	646	51	TTTTATTGACAGCACGTATAATCACACGCACCTAATAAACATT TATTGAT
TniDA _{FG22}	437	32	TTTACACCATATCATTACAGCATTTTACGAGG
TniDA _{FG23bcd}	137	122	GTAATATGACCACGTGATCTATGCAACCAATCCCTGTAGATG CAGGCCACCAGAAAAGGAAATACTATGATTGTTTCATAGAGGGA AGCTTCCCATAACAGCGCGACCCTTATTATATGAGT
TniDA _{GL32}	3,309	24	GGATTGGCCAGGATTAATGAATGA
TniDA _{GL35bc}	5,149	111	AATTTACAACCTTAGTAATAAACCTTTTTTATGTGCCTCCATCGC CTGTCAATTGGATGCCACTGGTCATGTGTGAGAGGGAAACGTCT TCATGGCTTTTCTCTGATTTCCC
TniDA _{GL37abcd}	2,995	136	TATTGAGTAAGTGCAAGTTTGC GGATTATTTATGGTCTTTTCGG GTGTTGTGAGTGGCTGTGAGGAAACACGTGACACCATTAAGT TTGTTTTATGACCCGGGAGTTGACAAGGCAAAAATATAATTCTC ATTGT
TniDA _{GL46b}	1,941	18	AAGGTGAAAGACAGGTCA
TniDA _{GL38}	575	184	TTATTGATTCCCAGAGGCGGCTGCTGCCACCAATAGGCTCCC GAGACAGTTTTTGGTGAAGGGGGGCAGCAGATGAAGTGATGAG ATTCGTGTAACCTTTGGATGACCCCTCCTTGACAAAGACAGTCT TCATCAATTGTCCCCAGTCATTCTCGCTGCTTTTATGTGATGG GGGCTTTTGT
TniDA _{GL40ab}	4,229	72	GAACAAAGACAGTATTTCACTGCGGCCTGACAAGCAGCTGCGA AAGTATTTACAGCCTTGCTGCAATGCGGC
TniDA _{GL48abcd}	930	76	GTCTATATATACCCTGTAGAACCGAATTTGTGTGATCAAGTCAC AGTCACAGATTCGATTCTAGGGGAGTATATGG
TniDA _{GL49b}	63	60	ATTGGCCGATCTGGTCACATGGTTCGCTAACTTTATTCAGTTGA CACCAAGTAGGAGGGC

TniDA _{LM} 52	10,660	305	TGTTTTAACTTATTTGTACAATAAAGCTTGAAATATTCTTAGC CTAAATATTATTCCCAACAGCAAGACCTTCCTGCGTCAAACCTC TTCCGAGTGCCCTAATAAAATCTTTGCTGACATCTATCTAAACAG TGTACATTTTCAGAGGGTCTTTTGTGCCATTTGAAAATTAATG AAAGATCGTTTCTTCTGTCATGGCATTAAATAATTGATGGTCTT TTTTGGTCAGAAATAATCAAAGCCAGATTATTTAGGACAAAAAT TGTGTATTTTTATATGATTACTTTCATTATTTATTTGTT
TniDA _{LM} 53	10,159	347	ATATTTCTTGTTGATACCGTCATTGTCCTGAAACAAAAAGCA CAGAATCTCTCGCAGTCCAAGGAGGTCTCTTTCTGAAGTCTTC ACCATGCCGAGCCTGAAAAGGTATTTACAGCCGAAGTCCGACAG AACAGCGGAGGCAGGTTTCATCCAGGGGACACGTTTCAGCCGCA AGGAGCTGACCCAGCACCCATGACCCGCTGGACGAGCGGCA TTTTCTCTCCAGGCGCTTTTGTCTTTTCAGTTTGGACCCCTTTTC CACTAAGAAAAAAGCCAAAGCATTGAAACAAAAA CCTACGCGGAAACCTCGTTACAGTGTGCTTTTCGTTATTTATA
TniDA _{LM} 55	9,047	56	AGACAAAGTGATGCTATTTTCACCATGCTGCCAGAAATGATCT GCACATATGCTGA
TniDA _{LM} 58 _{abcd}	8,782	423	TGACCTACATGTCTGAACAGCCATAAATGGGAAGCAAAGGCGC TGCCATTTCAATGACACTGCACCCGGTGCAGGAATACGGCGT CGTTCGCTCTCCATCCGGCCATATTTGATTTCCAGCTGTGTTCGC AGAAGCTGTGCGGCCAGACAGCCCCCAAAGATACATGA GAGCGCGCTGTCTGCATTCAGAGATATAAATACTGAGACTATAC CACTCCGCTCTTATTCTGGACCACGTGATTGTCTAAATAATA ATGCAGCACGTCCCCCTAGAAACACCGCGTCGTCATTAATCGC AAGGACTCTATCAGACTTGAAAAGTGAAGAGATCCCCAAGAA AATAATATCCGATAGCAGGCGCAGGCGTACCCGCGATTTGGCA ACACATCCGAACCGATGGATGCTTGGGTAGGTAAA
TniDA _{LM} 60	5,798	29	CAAACCTACCGTAACAGCGCGTAGGCGAA GTTCAATTAACCTTCGGCTTAACGCAAAATGACCCGGGGGTCAC
TniDA _{LM} 61 _{acd}	5,434	70	TAAAAAAGCTTATGACTGCTAAATATT
TniDA _{LM} 66	5,421	24	CGGCTTAACGCAAAATGACCCGGG TAAATCACTCTCGGTAATCCTAAAAGGGTGAAGGCTGTTGG GGGCCGGGCGAAAAGTGTAAATCTTTCATTTTATTGCCCTCCT
TniDA _{LM} 67 _{bc}	7,791	96	GAACATATG
TniDA _{LM} 69 _{bc}	7,004	41	TCACGTGAACAAATATCTTATAACGCTGCGCCATTATTTGT
TniDA _{LM} 70 _{ab}	6,797	225	TTTATTGGTAGCTGAACGCGAGTCTTCCATTCTTTCCGGGAATA CTGTCTCCGTTGGTTTATGGAAATGTCTGAAAAACAGCAAGAT CAGGTTTAGGACAGCACTGTCTGCAGACAAAGGGTGAAGGATT TATCCCCGTGCACTGCGTTTAAGGGAGCTGAGGCTGAGGAGGG AGAGGGCGCTCTCATGACAAATTGATGCCAGGTAAGAACTGC AACCTTTAA