

```

DIP      : CTCTCTCTCTC-----AAATAAATAAATAA-----: 208
PVKW010131 : TCCTCTCTC-----AAATAAATAAATAA-----: 225
PVKW010029 : CCCTCTCTCTG-----TCGCTAATAAATAAATAA-----GGCTGGGCATGGTGACGCTCACCTT-----: 260
PVKW010005 : CTCTCTG-----AAATAAATAAATAA-----GAAGCTCATTGGAAACCTTTTGGAA-----: 262
PVKW010011 : CTCTCTCTCTC-----TCTCTCTGAAATAAATAA-----CAGCAGGTGTATGCTCTACAAATTCA-----: 256
PVKW010022 : CTCTC-----AAATAAATAAATAA-----CTTTTAAACAAGATCTCAGCACTTGGCAGGCAGAG-----: 257
PVKW010034 : CTCTCTCTCTC-----TAATAAATAAATAAATAA-----: 240
PVKW010007 : CTCTCTCTCTC-----AAATAAATAAATAA-----CCTCTGCACGTGAGTCT-----: 261
PVKW010021 : -----ACATAAATAAATAAATAAATAA-----: 257
PVKW010016 : -----AAATAAATAAATAAATAAATAA-----CGCTACATAAATAACGTGTGAT-----: 263
PVKW010072 : -----AAATAAATAAATAAATAAATAA-----CCTTTCCTCA-----: 228
PVKW010029 : ---TCTCT-----AATAAATAGATGAATAAATAA-----GCTTTTAGGCCAGGGAGAGAGACTGAATG-----: 263
PVKW010003 : -----AAATTAAATAAATAAATAAATAA-----CCTTACTGTATGTGACTGAGTGTGAATCTTGACAAGCATGGTATCTA-----: 262
PVKW010052 : -----AAATAAACAATAATTTCCAAAAATAAATAA-----CACATAGCATGGTATCTAGGTGTGTAAGACCGAGTTCAAATCATGACTCT-----: 260
PVKW010503 : -----AGATAAAGATTAAATAAATAAATAA-----: 205
PVKW010044 : TCTCTGCTTGA-----AAATAAATAAATAAATAA-----GAACCTAACACAGACAGGAAC-----: 261
PVKW010069 : CTC-----AAATTAAATAAATAAATAAATAA-----: 221
PVKW010063 : TGCTTGC-----AAATAAATAAATAAATAA-----CTACCTTGAGATTCCATCTCACTCTCTGTCAGATT-----: 260
PVKW010011 : -----AATAAATAAATAAATAA-----GAAAGGAGCTGGGCATA-----: 259
PVKW010057 : TTCTGTCTCTC-----AATAAAGTAAATAAATAAATAA-----GGCCAGGCATGGTGGCATACCC-----: 257
PVKW010014 : TT-----AGTAATAAATAAATAA-----CAGCCCTTCTGAGCCAGGCATGGTGGCACATGCCTTTAAT-----: 261
PVKW010021 : TTCTCTCA-----AATAAATAAATAAATAA-----: 259
PVKW010000 : CCCTCTCTGTCTTTAATAAGTAAACAATAAATAA-----CATGAAATCTTAAATAAATAAATAA-----GAATCTGTTTAAG-----: 258
PVKW010040 : CTCTCTCTCTC-----AAATTAAATAAATAAATAAATAA-----ATATTAAATAAATAAATAA-----GAATATATAAAGA-----: 266
PVKW010219 : TTCTCTCTCTC-----AAATAAATAAATAAATAA-----ATCAATAAATAAATAAATAA-----: 269
PVKW010304 : CTCTCTCTCTC-----TCAAAATTAAATAAATAAATAA-----: 254
PVKW010062 : CTGTCTGTCACTC-----TAATAAATAAATAA-----TAAGAAATTTAAATAAATAA-----GGGCTCTGGGGAA-----: 268
PVKW010003 : CTCTCTCTCTC-----AAATAAATAAATAAATAA-----GAAATGC-----: 269
PVKW010034 : CT-----TTCTC-----TAATAAATAAATAA-----ATCTTAAATAAATAAATAA-----CTATGGCTGGGGAGGCCATAAGACCTAGCCAGG-----: 267
PVKW010991 : CTGTGCGTCTC-----AAACAATAAATAAATAA-----GAATGTAAGAGCCAAAGGAAGGGTAGGACT-----: 222
PVKW010041 : CTGTTGCTCTC-----AAACAATAAATAAATAA-----GAATGTAAGAGCCAAAGGAAGGGTAGGACT-----: 267
PVKW010002 : CTGTTGCTCCC-----AATAAATAAATAAATAA-----GAAGAAGAAATACAATGGCCAAT-----: 269
PVKW010380 : -----GTGCAATAAATAAATAA-----: 217
PVKW010064 : -----AATAAATAAATAA-----CAAAATCTAAATAAATAA-----GGGCCAGGCATGGTGGCTCATGACTTCAATCCCAGCACTGGGGAGG-----: 269
PVKW010043 : -----TCTC-----AAACAATAAATAA-----GAGTTCAAGGGCAACCTGGCCAAGAGCTGTCTCAAAACAAAACCAAA-----: 267
PVKW010036 : TTCCCTCTCTC-----AAATAAATAAATAA-----GAGCCAGGTGTGGTGGTGCAT-----: 263
PVKW010102 : CTCTCTCTCTC-----AATAAATAAAGTTAAATAATAA-----CCTTGGGATAAACCTAACAGACACTGA-----: 258
PVKW010009 : -----AAATAAATAAATAA-----AAGAATTAAATAAATAA-----GCTCTTGCTTCTTACATTGAGTTTCTGTGTGTACCATTCTATGGCAGA-A-----: 261
PVKW010061 : CTCTTTCTCTC-----AATAAATAAAGTTAAATAAATAA-----GCTTCTGCATGGCCAAGCAACAATCATGAGAGTGAAGAGACACTC-----: 262
PVKW010543 : -----AAATAAGTTAACAATGTTAAATAAATAA-----GAGGGCTGGAGAGATGGCTTAGCTTAGCAGTTAAGGCATTGCTTACAAA-----: 260
PVKW010024 : -----CTCCCTC-----AATAAATAAATAA-----GAGGGCTGGAGAGATGAGGGCTGGAGAGATGGCTTAGTGGT-----: 260
PVKW010038 : -----CTAACAAATAAATAAATAA-----ATAGAAATTTTAAATAAATAA-----GGAGAGAGGGGAGCTGGAGAGATGGCTTAGCAGTTAA-----: 255
PVKW010031 : -----AAATAAATAAATAA-----TATTAAATAAATAA-----GGAGGTAGAGGTGAGCAGAGCAAGAAGTTTCTTTTCTTTTGG-----: 258
PVKW010000 : -----AAATAAATAA-----TATTAAATAAATAA-----GAAAGAAAGAAAGTCACAATCAGACAGTGAAGAACACATAGGAAGCTG-----: 262
PVKW010011 : -----AAATAAATAAATAA-----TCCAAAAATAAATAA-----GAAAAATTTGACTATTTCATTAACATGCAATGGACATCATTTCTTA-----: 261
PVKW010093 : -----AACAAATAAATAAATAA-----ATATCAAAAAATAAATAA-----GCGAGATGGTTAAG-----: 257
PVKW010020 : -----AATAAATAAATAA-----TAGAATATTAAATAAATAA-----: 264
PVKW010006 : CTTTCTCTCTC-----AAATAAATAAATAA-----CAAG-----: 272
PVKW010118 : -----AAATAAATAAATAA-----CACCTGAGACTACATAGTGAATTCCAGGTACAGCCAGGTACGCCAGGGCTAGAGCGAAACCTTAC-----: 258
PVKW010159 : -----AATAAATAAATAA-----GAATTCTTAGATAAATGGGTTCTCGGGCCTCACTGGTGAAGCAGGTTGCAGGTGTGCCTGT-----: 252
PVKW010074 : CTCTGTTGTTT-----TCAATAAATAA-----CGGGCTGGAGAGATGGCTTAGCAATTAGCATTTGCCT-----: 263
PVKW010055 : -----AATAAATAAATAA-----TAAATTACCTAAATAAATAA-----GGTTCAGCACTCAGGAGGCAGAGCTGTAGGAGGATCACTGTGAGTTC-----: 261
PVKW010009 : -----ATAAATACC-----AATAAATAAATAA-----GGAAGGAAGGAAGAAATAGGGGAAGGGCAAGGAAATAAAATGCTCTGTTG-----: 263
PVKW010011 : -----AATACATAAATAA-----AATAAATAAATAA-----GGAAGGAGTGGGCTATGAGATAACTCAGTTTGTAAAGTGCCGTGATTGTGA-----: 266

```

Terminator statistics:		
	Number of Copies	Percentage
T>4	1	1.8%
T4, TVTTT	4	7.5%
TTT, TVTT	18	34.0%
TT, T	30	56.6%
Total	53	

Figure S20. Tail sequences of Dip_a copies with poly(A)_{>20}. PAS, AATAAA; terminators: TTTT, TVTTT, and T>4 ; rudimentary terminators: TTT, TVTT, and TT.