Supplemental data 2 (a) tobacco sRNA and NLR target alignments

DysRNA\_arrange\_TPM 02390238\_21 AAATGTTCTTCGAGTATCTTC

target id: NTK326\_mRNA\_79633\_cds

74 5'-GAGGTGAAGATACTCGAAGGACATTTACAGA-3' 104 cleavage site: 89

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3'-CTTCTATGAGCTTCTTGTAAA-5'

DysRNA\_arrange\_TPM 02367577\_21 AAATGTACTTCGAGTATCTTC

target id: NTK326\_mRNA\_79633\_cds

74 5'-GAGGTGAAGATACTCGAAGGACATTTACAGA-3' 104 cleavage site: 89

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3'-CTTCTATGAGCTTCATGTAAA-5'

DysRNA\_arrange\_TPM 02390667\_21 AAATGTTCTTCGATTATCTTC

target id: NTK326\_mRNA\_79633\_cds

74 5'-GAGGTGAAGATACTCGAAGGACATTTACAGA-3' 104 cleavage site: 89

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3'-CTTCTATTAGCTTCTTGTAAA-5'

DysRNA\_arrange\_TPM 22153796\_21 GAATGTTCTTCGAGTATCTTC

target id: NTK326\_mRNA\_79633\_cds

74 5'-GAGGTGAAGATACTCGAAGGACATTTACAGA-3' 104 cleavage site: 89

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3'-CTTCTATGAGCTTCTTGTAAG-5'

DysRNA\_arrange\_TPM 02392110\_21 AAATGTTTTTCGAGTATCTTC

target id: NTK326\_mRNA\_79633\_cds

74 5'-GAGGTGAAGATACTCGAAGGACATTTACAGA-3' 104 cleavage site: 89

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3'-CTTCTATGAGCTTTTTGTAAA-5'

DysRNA\_arrange\_TPM 02374763\_21 AAATGTGCTTCGAGTATCTTC

target id: NTK326\_mRNA\_79633\_cds

74 5'-GAGGTGAAGATACTCGAAGGACATTTACAGA-3' 104 cleavage site: 89

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3'-CTTCTATGAGCTTCGTGTAAA-5'

DysRNA\_arrange\_TPM 06471153\_20 AATGTTCTTCGAGTATCTTC

target id: NTK326\_mRNA\_79633\_cds

74 5'-GAGGTGAAGATACTCGAAGGACATTTACAG-3' 103 cleavage site: 88

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3'-CTTCTATGAGCTTCTTGTAA-5'

DysRNA\_arrange\_TPM 34632662\_21 TAATTTGGACGAGATTCGGTC

target id: NTTN90\_mRNA\_35268\_cds

521 5'-TTGTTGACCGAATCTCGTCCAAATTATGCAA-3' 551 cleavage site: 536

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3'-CTGGCTTAGAGCAGGTTTAAT-5'

DysRNA\_arrange\_TPM 43206041\_21 TTTGAGATTGGCCGCTGCAGT

target id: NTTN90\_mRNA\_35268\_cds

449 5'-CTTTAACTGCAGCGGCCAATCTCAAAGGCTG-3' 479 cleavage site: 464

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3'-TGACGTCGCCGGTTAGAGTTT-5'

DysRNA\_arrange\_TPM 34633256\_21 TAATTTGGACGAGATTTGGTC

target id: NTTN90\_mRNA\_35268\_cds

521 5'-TTGTTGACCGAATCTCGTCCAAATTATGCAA-3' 551 cleavage site: 536

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3'-CTGGTTTAGAGCAGGTTTAAT-5'

DysRNA\_arrange\_TPM 40864778\_21 TTATGGATTCAAATGTAGCTG

target id: NTTN90\_mRNA\_35268\_cds

1785 5'-ATTGCCATCTACATTTGAACCCA-AAATGCT-3' 1814 cleavage site: 1799

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3'-GTCGATGTAAACTTAGGTATT-5'

DysRNA\_arrange\_TPM 34632839\_21 TAATTTGGACGAGATTTGATC

target id: NTTN90\_mRNA\_35268\_cds

521 5'-TTGTTGACCGAATCTCGTCCAAATTATGCAA-3' 551 cleavage site: 536

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3'-CTAGTTTAGAGCAGGTTTAAT-5'

DysRNA\_arrange\_TPM 19766731\_21 ATTATGGATTCAAATGTAGCT

target id: NTTN90\_mRNA\_35268\_cds

1786 5'-TTGCCATCTACATTTGAACCCAAAATGCTTG-3' 1816 cleavage site: 1801

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3'-TCGATGTAAACTTAGGTATTA-5'

DysRNA\_arrange\_TPM 35198903\_22 TACAGGTGACTTGTAAATGTTT

target id: NTTN90\_mRNA\_35268\_cds

87 5'-TCGGAAAACATTTACGAGTCACCTGTACGAAA-3' 118 cleavage site: 103

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3'-TTTGTAAATGTTCAGTGGACAT-5'

DysRNA\_arrange\_TPM 41151740\_21 TTGAGATTGGCCGCTGCAGTT

target id: NTTN90\_mRNA\_35268\_cds

448 5'-GCTTTAACTGCAGCGGCCAATCTCAAAGGCT-3' 478 cleavage site: 463

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3'-TTGACGTCGCCGGTTAGAGTT-5'

DysRNA\_arrange\_TPM 34632315\_22 TAATTTGGACGAGATTCGGTCA

target id: NTTN90\_mRNA\_35268\_cds

520 5'-ATTGTTGACCGAATCTCGTCCAAATTATGCAA-3' 551 cleavage site: 536

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3'-ACTGGCTTAGAGCAGGTTTAAT-5'

DysRNA\_arrange\_TPM 43963689\_22 TTTTAGCCAGAGTTGTTTTCCC

target id: NTK326\_mRNA\_99997\_cds

680 5'-GCATAGGGAAAACAACTCTGGC-AAAAGCTAT-3' 710 cleavage site: 695

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3'-CCCTTTTGTTGAGACCGATTTT-5'

DysRNA\_arrange\_TPM 42993390\_21 TTTAGCCAGAGTTGTTTTCCC

target id: NTK326\_mRNA\_99997\_cds

680 5'-GCATAGGGAAAACAACTCTGGC-AAAAGCTA-3' 709 cleavage site: 694

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3'-CCCTTTTGTTGAGACCGATTT-5'

DysRNA\_arrange\_TPM 43964061\_21 TTTTAGCCAGAGTTGTTTTCC

target id: NTK326\_mRNA\_99997\_cds

681 5'-CATAGGGAAAACAACTCTGGC-AAAAGCTAT-3' 710 cleavage site: 695

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3'-CCTTTTGTTGAGACCGATTTT-5'

DysRNA\_arrange\_TPM 40391668\_20 TTAATATTTCAGCTCGAACT

target id: NTTN90\_mRNA\_46474\_cds

1342 5'-CATGAAG-TT-A-CTGAAATATTAAATGCA-3' 1368 cleavage site: 1353

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3'-TCAAGCTCGACTTTATAATT-5'

DysRNA\_arrange\_TPM 39183736\_22 TCCACTGAGATTCAGCCCTTTG

target id: NTTN90\_mRNA\_56562\_cds

2608 5'-TCTTTGAAAGAGTTGGATCTCAGTAGAAATAA-3' 2639 cleavage site: 2624

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3'-GTTTCCCGACTTAGAGTCACCT-5'

DysRNA\_arrange\_TPM 39184277\_21 TCCACTGAGATTCAGCCCTTT

target id: NTTN90\_mRNA\_56562\_cds

2609 5'-CTTTGAAAGAGTTGGATCTCAGTAGAAATAA-3' 2639 cleavage site: 2624

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3'-TTTCCCGACTTAGAGTCACCT-5'

DysRNA\_arrange\_TPM 34632662\_21 TAATTTGGACGAGATTCGGTC

target id: NTK326\_mRNA\_39598\_cds

518 5'-TTGTTGATCAAATCTCGTCCAAATTATGCAA-3' 548 cleavage site: 533

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3'-CTGGCTTAGAGCAGGTTTAAT-5'

DysRNA\_arrange\_TPM 43206041\_21 TTTGAGATTGGCCGCTGCAGT

target id: NTK326\_mRNA\_39598\_cds

446 5'-CTTTAACTGCAGCGGCCAATCTCAAAGGTTG-3' 476 cleavage site: 461

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3'-TGACGTCGCCGGTTAGAGTTT-5'

DysRNA\_arrange\_TPM 34633256\_21 TAATTTGGACGAGATTTGGTC

target id: NTK326\_mRNA\_39598\_cds

518 5'-TTGTTGATCAAATCTCGTCCAAATTATGCAA-3' 548 cleavage site: 533

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3'-CTGGTTTAGAGCAGGTTTAAT-5'

DysRNA\_arrange\_TPM 34632839\_21 TAATTTGGACGAGATTTGATC

target id: NTK326\_mRNA\_39598\_cds

518 5'-TTGTTGATCAAATCTCGTCCAAATTATGCAA-3' 548 cleavage site: 533

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3'-CTAGTTTAGAGCAGGTTTAAT-5'

DysRNA\_arrange\_TPM 35198903\_22 TACAGGTGACTTGTAAATGTTT

target id: NTK326\_mRNA\_39598\_cds

84 5'-TCGGAAAACATTTACGAGTCACCTGTACGAAA-3' 115 cleavage site: 100

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3'-TTTGTAAATGTTCAGTGGACAT-5'

DysRNA\_arrange\_TPM 41151740\_21 TTGAGATTGGCCGCTGCAGTT

target id: NTK326\_mRNA\_39598\_cds

445 5'-GCTTTAACTGCAGCGGCCAATCTCAAAGGTT-3' 475 cleavage site: 460

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3'-TTGACGTCGCCGGTTAGAGTT-5'

DysRNA\_arrange\_TPM 34632315\_22 TAATTTGGACGAGATTCGGTCA

target id: NTK326\_mRNA\_39598\_cds

517 5'-ATTGTTGATCAAATCTCGTCCAAATTATGCAA-3' 548 cleavage site: 533

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3'-ACTGGCTTAGAGCAGGTTTAAT-5'

DysRNA\_arrange\_TPM 34632662\_21 TAATTTGGACGAGATTCGGTC

target id: NTBX\_mRNA\_29733\_cds

518 5'-TTGTTGATCAAATCTCGTCCAAATTATGCAA-3' 548 cleavage site: 533

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3'-CTGGCTTAGAGCAGGTTTAAT-5'

DysRNA\_arrange\_TPM 43206041\_21 TTTGAGATTGGCCGCTGCAGT

target id: NTBX\_mRNA\_29733\_cds

446 5'-CTTTAACTGCAGCGGCCAATCTCAAAGGTTG-3' 476 cleavage site: 461

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3'-TGACGTCGCCGGTTAGAGTTT-5'

DysRNA\_arrange\_TPM 34633256\_21 TAATTTGGACGAGATTTGGTC

target id: NTBX\_mRNA\_29733\_cds

518 5'-TTGTTGATCAAATCTCGTCCAAATTATGCAA-3' 548 cleavage site: 533

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3'-CTGGTTTAGAGCAGGTTTAAT-5'

DysRNA\_arrange\_TPM 34632839\_21 TAATTTGGACGAGATTTGATC

target id: NTBX\_mRNA\_29733\_cds

518 5'-TTGTTGATCAAATCTCGTCCAAATTATGCAA-3' 548 cleavage site: 533

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3'-CTAGTTTAGAGCAGGTTTAAT-5'

DysRNA\_arrange\_TPM 35198903\_22 TACAGGTGACTTGTAAATGTTT

target id: NTBX\_mRNA\_29733\_cds

84 5'-TCGGAAAACATTTACGAGTCACCTGTACGAAA-3' 115 cleavage site: 100

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3'-TTTGTAAATGTTCAGTGGACAT-5'

DysRNA\_arrange\_TPM 41151740\_21 TTGAGATTGGCCGCTGCAGTT

target id: NTBX\_mRNA\_29733\_cds

445 5'-GCTTTAACTGCAGCGGCCAATCTCAAAGGTT-3' 475 cleavage site: 460

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3'-TTGACGTCGCCGGTTAGAGTT-5'

DysRNA\_arrange\_TPM 34632315\_22 TAATTTGGACGAGATTCGGTCA

target id: NTBX\_mRNA\_29733\_cds

517 5'-ATTGTTGATCAAATCTCGTCCAAATTATGCAA-3' 548 cleavage site: 533

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3'-ACTGGCTTAGAGCAGGTTTAAT-5'

DysRNA\_arrange\_TPM 27046016\_20 GTGAAATTCTTGGATCGTCT

target id: NTTN90\_mRNA\_51079\_cds

1834 5'-GAGAGTGAT-ATCCAAGAATTTCGATTGAA-3' 1862 cleavage site: 1847

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3'-TCTGCTAGGTTCTTAAAGTG-5'

DysRNA\_arrange\_TPM 43963689\_22 TTTTAGCCAGAGTTGTTTTCCC

target id: NTTN90\_mRNA\_42249\_cds

680 5'-GCATAGGGAAAACAACTCTGGC-AAAAGCTAT-3' 710 cleavage site: 695

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3'-CCCTTTTGTTGAGACCGATTTT-5'

DysRNA\_arrange\_TPM 44325453\_23 TTTTTGATCCTTCGATGTCGGCT

target id: NTTN90\_mRNA\_42249\_cds

196 5'-GAGAAAG-C-A-ATTGAAGGATCAAGAATTTCC-3' 225 cleavage site: 210

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3'-TCGGCTGTAGCTTCCTAGTTTTT-5'

DysRNA\_arrange\_TPM 20072557\_21 ATTGGTCAAGGAAGTTTTTCT

target id: NTTN90\_mRNA\_42249\_cds

796 5'-CTACAAGAGAAACTTCTTCGACAAATTCTCA-3' 826 cleavage site: 811

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3'-TCTTTTTGAAGGAACTGGTTA-5'

DysRNA\_arrange\_TPM 44061720\_22 TTTTGATCCTTCGATGTCGGCT

target id: NTTN90\_mRNA\_42249\_cds

196 5'-GAGAAAG-C-A-ATTGAAGGATCAAGAATTTC-3' 224 cleavage site: 209

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3'-TCGGCTGTAGCTTCCTAGTTTT-5'

DysRNA\_arrange\_TPM 41297271\_20 TTGATCCTTCGATGTCGGCT

target id: NTTN90\_mRNA\_42249\_cds

196 5'-GAGAAAG-C-A-ATTGAAGGATCAAGAATT-3' 222 cleavage site: 207

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3'-TCGGCTGTAGCTTCCTAGTT-5'

DysRNA\_arrange\_TPM 42993390\_21 TTTAGCCAGAGTTGTTTTCCC

target id: NTTN90\_mRNA\_42249\_cds

680 5'-GCATAGGGAAAACAACTCTGGC-AAAAGCTA-3' 709 cleavage site: 694

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3'-CCCTTTTGTTGAGACCGATTT-5'

DysRNA\_arrange\_TPM 43964061\_21 TTTTAGCCAGAGTTGTTTTCC

target id: NTTN90\_mRNA\_42249\_cds

681 5'-CATAGGGAAAACAACTCTGGC-AAAAGCTAT-3' 710 cleavage site: 695

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3'-CCTTTTGTTGAGACCGATTTT-5'

DysRNA\_arrange\_TPM 40391668\_20 TTAATATTTCAGCTCGAACT

target id: NTTN90\_mRNA\_42249\_cds

1369 5'-CATGAAG-TT-A-CTGAAATATTAAATGCA-3' 1395 cleavage site: 1380

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3'-TCAAGCTCGACTTTATAATT-5'

DysRNA\_arrange\_TPM 32487580\_22 CCTTTCGTGCTCAAGTTCTCTC

target id: NTTN90\_mRNA\_42249\_cds

1641 5'-AAAGGGAGTGAACTTGAGCACCAAAGCATTTG-3' 1672 cleavage site: 1657

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3'-CTCTCTTGAACTCGTGCTTTCC-5'

DysRNA\_arrange\_TPM 40586237\_20 TTAGCTGTATCAGAACACCT

target id: NTBX\_mRNA\_13089\_cds

3814 5'-TTGATGGGGGTTCCTGATACAGATGACGATC-3' 3844 cleavage site: 3829

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3'-TCCACAA-GACTATGTCGATT-5'

DysRNA\_arrange\_TPM 43963689\_22 TTTTAGCCAGAGTTGTTTTCCC

target id: NTTN90\_mRNA\_89783\_cds

680 5'-GCATAGGGAAAACAACTCTGGC-AAAAGCTAT-3' 710 cleavage site: 695

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3'-CCCTTTTGTTGAGACCGATTTT-5'

DysRNA\_arrange\_TPM 42993390\_21 TTTAGCCAGAGTTGTTTTCCC

target id: NTTN90\_mRNA\_89783\_cds

680 5'-GCATAGGGAAAACAACTCTGGC-AAAAGCTA-3' 709 cleavage site: 694

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3'-CCCTTTTGTTGAGACCGATTT-5'

DysRNA\_arrange\_TPM 43964061\_21 TTTTAGCCAGAGTTGTTTTCC

target id: NTTN90\_mRNA\_89783\_cds

681 5'-CATAGGGAAAACAACTCTGGC-AAAAGCTAT-3' 710 cleavage site: 695

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3'-CCTTTTGTTGAGACCGATTTT-5'

DysRNA\_arrange\_TPM 36082679\_22 TATTGTGGTGTCGGATCCTCCT

target id: NTBX\_mRNA\_99245\_cds

3425 5'-GCATAAGGAGGACCCGATATAACAATAGTGAA-3' 3456 cleavage site: 3441

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3'-TCCTCCTAGGCTGTGGTGTTAT-5'

DysRNA\_arrange\_TPM 35978105\_20 TATCTGATATGTGGGCCATC

target id: NTTN90\_mRNA\_90522\_cds

3445 5'-GTCTTTAT-GCCTTCATATCAGATGGCGGC-3' 3473 cleavage site: 3458

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3'-CTACCGGGTGTATAGTCTAT-5'

DysRNA\_arrange\_TPM 03780453\_24 AAGCGAGGCAATGAAACAGTAACT

target id: NTTN90\_mRNA\_90522\_cds

3261 5'-TGATCAGATTAATGTTTCATTGCCTTGTTGGGGTA-3' 3295 cleavage site: 3280

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3'-TC-AATGACAAAGTAACGGAGCGAA-5'

DysRNA\_arrange\_TPM 29446078\_21 CACTAGAAGATGCTGCAGCGC

target id: NTTN90\_mRNA\_90522\_cds

3352 5'-GACCAGTCCT-CAGCATCTACTAGTGACGCA-3' 3381 cleavage site: 3366

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3'-CGCGACGTCGTAGAAGATCAC-5'

DysRNA\_arrange\_TPM 40586237\_20 TTAGCTGTATCAGAACACCT

target id: NTTN90\_mRNA\_13879\_cds

3814 5'-TTGATGGGGGTTCCTGATACAGATGACGATC-3' 3844 cleavage site: 3829

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3'-TCCACAA-GACTATGTCGATT-5'

DysRNA\_arrange\_TPM 40498063\_21 TTAGATACTGAAACAACAGGT

target id: NTK326\_mRNA\_109102\_cds

2200 5'-CCATCATCTATT-TTTCAGTATC-AAACTCA-3' 2228 cleavage site: 2213

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3'-TGGACAACAAAGTCATAGATT-5'

DysRNA\_arrange\_TPM 43963689\_22 TTTTAGCCAGAGTTGTTTTCCC

target id: NTBX\_mRNA\_99861\_cds

680 5'-GCATAGGGAAAACAACTCTGGC-AAAAGCTAT-3' 710 cleavage site: 695

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3'-CCCTTTTGTTGAGACCGATTTT-5'

DysRNA\_arrange\_TPM 42993390\_21 TTTAGCCAGAGTTGTTTTCCC

target id: NTBX\_mRNA\_99861\_cds

680 5'-GCATAGGGAAAACAACTCTGGC-AAAAGCTA-3' 709 cleavage site: 694

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3'-CCCTTTTGTTGAGACCGATTT-5'

DysRNA\_arrange\_TPM 43964061\_21 TTTTAGCCAGAGTTGTTTTCC

target id: NTBX\_mRNA\_99861\_cds

681 5'-CATAGGGAAAACAACTCTGGC-AAAAGCTAT-3' 710 cleavage site: 695

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3'-CCTTTTGTTGAGACCGATTTT-5'

DysRNA\_arrange\_TPM 43963689\_22 TTTTAGCCAGAGTTGTTTTCCC

target id: NTBX\_mRNA\_95736\_cds

671 5'-GCATAGGGAAAACAACTCTGGC-AAAAGCTAT-3' 701 cleavage site: 686

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3'-CCCTTTTGTTGAGACCGATTTT-5'

DysRNA\_arrange\_TPM 42993390\_21 TTTAGCCAGAGTTGTTTTCCC

target id: NTBX\_mRNA\_95736\_cds

671 5'-GCATAGGGAAAACAACTCTGGC-AAAAGCTA-3' 700 cleavage site: 685

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3'-CCCTTTTGTTGAGACCGATTT-5'

DysRNA\_arrange\_TPM 43964061\_21 TTTTAGCCAGAGTTGTTTTCC

target id: NTBX\_mRNA\_95736\_cds

672 5'-CATAGGGAAAACAACTCTGGC-AAAAGCTAT-3' 701 cleavage site: 686

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3'-CCTTTTGTTGAGACCGATTTT-5'

DysRNA\_arrange\_TPM 40391668\_20 TTAATATTTCAGCTCGAACT

target id: NTBX\_mRNA\_95736\_cds

1360 5'-CATGAAG-TT-A-CTGAAATATTAAATGCA-3' 1386 cleavage site: 1371

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3'-TCAAGCTCGACTTTATAATT-5'

DysRNA\_arrange\_TPM 34632662\_21 TAATTTGGACGAGATTCGGTC

target id: NTBX\_mRNA\_42672\_cds

521 5'-TTGTTGACCGAATCTCGTCCAAATTATGCAA-3' 551 cleavage site: 536

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3'-CTGGCTTAGAGCAGGTTTAAT-5'

DysRNA\_arrange\_TPM 43206041\_21 TTTGAGATTGGCCGCTGCAGT

target id: NTBX\_mRNA\_42672\_cds

449 5'-CTTTAACTGCAGCGGCCAATCTCAAAGGCTG-3' 479 cleavage site: 464

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3'-TGACGTCGCCGGTTAGAGTTT-5'

DysRNA\_arrange\_TPM 34633256\_21 TAATTTGGACGAGATTTGGTC

target id: NTBX\_mRNA\_42672\_cds

521 5'-TTGTTGACCGAATCTCGTCCAAATTATGCAA-3' 551 cleavage site: 536

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3'-CTGGTTTAGAGCAGGTTTAAT-5'

DysRNA\_arrange\_TPM 35716976\_20 TATATCGAGTCCTGTTAATT

target id: NTBX\_mRNA\_42672\_cds

3319 5'-ACTTGGATAAGGAGGACCCGATATAACAAT-3' 3348 cleavage site: 3333

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3'-TTAATTGTCCTGAGCTATAT-5'

DysRNA\_arrange\_TPM 34632839\_21 TAATTTGGACGAGATTTGATC

target id: NTBX\_mRNA\_42672\_cds

521 5'-TTGTTGACCGAATCTCGTCCAAATTATGCAA-3' 551 cleavage site: 536

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3'-CTAGTTTAGAGCAGGTTTAAT-5'

DysRNA\_arrange\_TPM 35198903\_22 TACAGGTGACTTGTAAATGTTT

target id: NTBX\_mRNA\_42672\_cds

87 5'-TCGGAAAACATTTACGAGTCACCTGTACGAAA-3' 118 cleavage site: 103

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3'-TTTGTAAATGTTCAGTGGACAT-5'

DysRNA\_arrange\_TPM 41151740\_21 TTGAGATTGGCCGCTGCAGTT

target id: NTBX\_mRNA\_42672\_cds

448 5'-GCTTTAACTGCAGCGGCCAATCTCAAAGGCT-3' 478 cleavage site: 463

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3'-TTGACGTCGCCGGTTAGAGTT-5'

DysRNA\_arrange\_TPM 34632315\_22 TAATTTGGACGAGATTCGGTCA

target id: NTBX\_mRNA\_42672\_cds

520 5'-ATTGTTGACCGAATCTCGTCCAAATTATGCAA-3' 551 cleavage site: 536

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3'-ACTGGCTTAGAGCAGGTTTAAT-5'

DysRNA\_arrange\_TPM 34632662\_21 TAATTTGGACGAGATTCGGTC

target id: NTTN90\_mRNA\_68293\_cds

518 5'-TTGTTGATCAAATCTCGTCCAAATTATGCAA-3' 548 cleavage site: 533

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3'-CTGGCTTAGAGCAGGTTTAAT-5'

DysRNA\_arrange\_TPM 43206041\_21 TTTGAGATTGGCCGCTGCAGT

target id: NTTN90\_mRNA\_68293\_cds

446 5'-CTTTAACTGCAGCGGCCAATCTCAAAGGTTG-3' 476 cleavage site: 461

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3'-TGACGTCGCCGGTTAGAGTTT-5'

DysRNA\_arrange\_TPM 34633256\_21 TAATTTGGACGAGATTTGGTC

target id: NTTN90\_mRNA\_68293\_cds

518 5'-TTGTTGATCAAATCTCGTCCAAATTATGCAA-3' 548 cleavage site: 533

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3'-CTGGTTTAGAGCAGGTTTAAT-5'

DysRNA\_arrange\_TPM 34632839\_21 TAATTTGGACGAGATTTGATC

target id: NTTN90\_mRNA\_68293\_cds

518 5'-TTGTTGATCAAATCTCGTCCAAATTATGCAA-3' 548 cleavage site: 533

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3'-CTAGTTTAGAGCAGGTTTAAT-5'

DysRNA\_arrange\_TPM 35198903\_22 TACAGGTGACTTGTAAATGTTT

target id: NTTN90\_mRNA\_68293\_cds

84 5'-TCGGAAAACATTTACGAGTCACCTGTACGAAA-3' 115 cleavage site: 100

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3'-TTTGTAAATGTTCAGTGGACAT-5'

DysRNA\_arrange\_TPM 41151740\_21 TTGAGATTGGCCGCTGCAGTT

target id: NTTN90\_mRNA\_68293\_cds

445 5'-GCTTTAACTGCAGCGGCCAATCTCAAAGGTT-3' 475 cleavage site: 460

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3'-TTGACGTCGCCGGTTAGAGTT-5'

DysRNA\_arrange\_TPM 34632315\_22 TAATTTGGACGAGATTCGGTCA

target id: NTTN90\_mRNA\_68293\_cds

517 5'-ATTGTTGATCAAATCTCGTCCAAATTATGCAA-3' 548 cleavage site: 533

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3'-ACTGGCTTAGAGCAGGTTTAAT-5'

DysRNA\_arrange\_TPM 43963689\_22 TTTTAGCCAGAGTTGTTTTCCC

target id: NTBX\_mRNA\_49496\_cds

680 5'-GCATAGGGAAAACAACTCTGGC-AAAAGCTAT-3' 710 cleavage site: 695

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3'-CCCTTTTGTTGAGACCGATTTT-5'

DysRNA\_arrange\_TPM 42993390\_21 TTTAGCCAGAGTTGTTTTCCC

target id: NTBX\_mRNA\_49496\_cds

680 5'-GCATAGGGAAAACAACTCTGGC-AAAAGCTA-3' 709 cleavage site: 694

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3'-CCCTTTTGTTGAGACCGATTT-5'

DysRNA\_arrange\_TPM 43964061\_21 TTTTAGCCAGAGTTGTTTTCC

target id: NTBX\_mRNA\_49496\_cds

681 5'-CATAGGGAAAACAACTCTGGC-AAAAGCTAT-3' 710 cleavage site: 695

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3'-CCTTTTGTTGAGACCGATTTT-5'

DysRNA\_arrange\_TPM 27046016\_20 GTGAAATTCTTGGATCGTCT

target id: NTBX\_mRNA\_49496\_cds

1897 5'-GAGAGTGAT-ATCCAAGAATTTCGATTGAA-3' 1925 cleavage site: 1910

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3'-TCTGCTAGGTTCTTAAAGTG-5'

DysRNA\_arrange\_TPM 33334126\_21 CTCCGCCCTTCTGTTTTTCTC

target id: NTTN90\_mRNA\_98067\_cds

376 5'-GTAGTGA-GAAAACAGAA-GG-GGAGTTATC-3' 403 cleavage site: 388

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3'-CTCTTTTTGTCTTCCCGCCTC-5'

DysRNA\_arrange\_TPM 30920174\_21 CGCCCTTCTGTTTTTCTCGCT

target id: NTTN90\_mRNA\_98067\_cds

373 5'-TCAGTAGTGA-GAAAACAGAAGGGGAGTTAT-3' 402 cleavage site: 387

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3'-TCGCTCTTTTTGTCTTCCCGC-5'

DysRNA\_arrange\_TPM 34174695\_22 TAAGAACTTGCATGATGGCACC

target id: NTK326\_mRNA\_90605\_cds

1355 5'-AAAAAGGTGCCATCATGCAAGTTCTTAAGAGT-3' 1386 cleavage site: 1371

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3'-CCACGGTAGTACGTTCAAGAAT-5'

DysRNA\_arrange\_TPM 36089404\_21 TATTGTTGATCACCCTTTCCT

target id: NTK326\_mRNA\_90605\_cds

1557 5'-TTTTGAAGAAATGATGATCAACAATACGGGT-3' 1587 cleavage site: 1572

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3'-TCCTTTCCCACTAGTTGTTAT-5'

DysRNA\_arrange\_TPM 34632662\_21 TAATTTGGACGAGATTCGGTC

target id: NTTN90\_mRNA\_35271\_cds

521 5'-TTGTTGACCGAATCTCGTCCAAATTATGCAA-3' 551 cleavage site: 536

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3'-CTGGCTTAGAGCAGGTTTAAT-5'

DysRNA\_arrange\_TPM 43206041\_21 TTTGAGATTGGCCGCTGCAGT

target id: NTTN90\_mRNA\_35271\_cds

449 5'-CTTTAACTGCAGCGGCCAATCTCAAAGGCTG-3' 479 cleavage site: 464

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3'-TGACGTCGCCGGTTAGAGTTT-5'

DysRNA\_arrange\_TPM 34633256\_21 TAATTTGGACGAGATTTGGTC

target id: NTTN90\_mRNA\_35271\_cds

521 5'-TTGTTGACCGAATCTCGTCCAAATTATGCAA-3' 551 cleavage site: 536

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3'-CTGGTTTAGAGCAGGTTTAAT-5'

DysRNA\_arrange\_TPM 34632839\_21 TAATTTGGACGAGATTTGATC

target id: NTTN90\_mRNA\_35271\_cds

521 5'-TTGTTGACCGAATCTCGTCCAAATTATGCAA-3' 551 cleavage site: 536

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3'-CTAGTTTAGAGCAGGTTTAAT-5'

DysRNA\_arrange\_TPM 35198903\_22 TACAGGTGACTTGTAAATGTTT

target id: NTTN90\_mRNA\_35271\_cds

87 5'-TCGGAAAACATTTACGAGTCACCTGTACGAAA-3' 118 cleavage site: 103

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3'-TTTGTAAATGTTCAGTGGACAT-5'

DysRNA\_arrange\_TPM 41151740\_21 TTGAGATTGGCCGCTGCAGTT

target id: NTTN90\_mRNA\_35271\_cds

448 5'-GCTTTAACTGCAGCGGCCAATCTCAAAGGCT-3' 478 cleavage site: 463

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3'-TTGACGTCGCCGGTTAGAGTT-5'

DysRNA\_arrange\_TPM 34632315\_22 TAATTTGGACGAGATTCGGTCA

target id: NTTN90\_mRNA\_35271\_cds

520 5'-ATTGTTGACCGAATCTCGTCCAAATTATGCAA-3' 551 cleavage site: 536

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3'-ACTGGCTTAGAGCAGGTTTAAT-5'

DysRNA\_arrange\_TPM 43963689\_22 TTTTAGCCAGAGTTGTTTTCCC

target id: NTTN90\_mRNA\_42253\_cds

680 5'-GCATAGGGAAAACAACTCTGGC-AAAAGCTAT-3' 710 cleavage site: 695

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3'-CCCTTTTGTTGAGACCGATTTT-5'

DysRNA\_arrange\_TPM 20072557\_21 ATTGGTCAAGGAAGTTTTTCT

target id: NTTN90\_mRNA\_42253\_cds

796 5'-CTACAAGAGAAACTTCTTCGACAAATTCTCA-3' 826 cleavage site: 811

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3'-TCTTTTTGAAGGAACTGGTTA-5'

DysRNA\_arrange\_TPM 42993390\_21 TTTAGCCAGAGTTGTTTTCCC

target id: NTTN90\_mRNA\_42253\_cds

680 5'-GCATAGGGAAAACAACTCTGGC-AAAAGCTA-3' 709 cleavage site: 694

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3'-CCCTTTTGTTGAGACCGATTT-5'

DysRNA\_arrange\_TPM 43964061\_21 TTTTAGCCAGAGTTGTTTTCC

target id: NTTN90\_mRNA\_42253\_cds

681 5'-CATAGGGAAAACAACTCTGGC-AAAAGCTAT-3' 710 cleavage site: 695

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3'-CCTTTTGTTGAGACCGATTTT-5'

DysRNA\_arrange\_TPM 32487580\_22 CCTTTCGTGCTCAAGTTCTCTC

target id: NTTN90\_mRNA\_42253\_cds

1641 5'-AAAGGGAGTGAACTTGAGCACCAAAGCATTTG-3' 1672 cleavage site: 1657

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3'-CTCTCTTGAACTCGTGCTTTCC-5'

DysRNA\_arrange\_TPM 40391668\_20 TTAATATTTCAGCTCGAACT

target id: NTTN90\_mRNA\_42253\_cds

1369 5'-CATGAAG-TT-A-CTGAAATATTAAATGCA-3' 1395 cleavage site: 1380

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3'-TCAAGCTCGACTTTATAATT-5'

DysRNA\_arrange\_TPM 43963689\_22 TTTTAGCCAGAGTTGTTTTCCC

target id: NTTN90\_mRNA\_86966\_cds

671 5'-GCATAGGGAAAACAACTCTGGC-AAAAGCTAT-3' 701 cleavage site: 686

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3'-CCCTTTTGTTGAGACCGATTTT-5'

DysRNA\_arrange\_TPM 42993390\_21 TTTAGCCAGAGTTGTTTTCCC

target id: NTTN90\_mRNA\_86966\_cds

671 5'-GCATAGGGAAAACAACTCTGGC-AAAAGCTA-3' 700 cleavage site: 685

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3'-CCCTTTTGTTGAGACCGATTT-5'

DysRNA\_arrange\_TPM 43964061\_21 TTTTAGCCAGAGTTGTTTTCC

target id: NTTN90\_mRNA\_86966\_cds

672 5'-CATAGGGAAAACAACTCTGGC-AAAAGCTAT-3' 701 cleavage site: 686

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3'-CCTTTTGTTGAGACCGATTTT-5'

DysRNA\_arrange\_TPM 40391668\_20 TTAATATTTCAGCTCGAACT

target id: NTTN90\_mRNA\_86966\_cds

1360 5'-CATGAAG-TT-A-CTGAAATATTAAATGCA-3' 1386 cleavage site: 1371

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3'-TCAAGCTCGACTTTATAATT-5'

DysRNA\_arrange\_TPM 36654165\_22 TGACTGCACATTGAGACTCTTC

target id: NTTN90\_mRNA\_69999\_cds

200 5'-CTATCGAAGAGTCTCAATGTGCAGTCATCATT-3' 231 cleavage site: 216

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3'-CTTCTCAGAGTTACACGTCAGT-5'

DysRNA\_arrange\_TPM 36564529\_22 TGACAGCACATTGAGACTCTTC

target id: NTTN90\_mRNA\_69999\_cds

200 5'-CTATCGAAGAGTCTCAATGTGCAGTCATCATT-3' 231 cleavage site: 216

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3'-CTTCTCAGAGTTACACGACAGT-5'

DysRNA\_arrange\_TPM 43206041\_21 TTTGAGATTGGCCGCTGCAGT

target id: NTTN90\_mRNA\_69999\_cds

446 5'-CTTTAACTGCAGCGGCCAATCTCAAAGGCTG-3' 476 cleavage site: 461

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3'-TGACGTCGCCGGTTAGAGTTT-5'

DysRNA\_arrange\_TPM 35198903\_22 TACAGGTGACTTGTAAATGTTT

target id: NTTN90\_mRNA\_69999\_cds

84 5'-TCGGAAAACATTTACGAGTCACCTGTACGAAA-3' 115 cleavage site: 100

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3'-TTTGTAAATGTTCAGTGGACAT-5'

DysRNA\_arrange\_TPM 41151740\_21 TTGAGATTGGCCGCTGCAGTT

target id: NTTN90\_mRNA\_69999\_cds

445 5'-GCTTTAACTGCAGCGGCCAATCTCAAAGGCT-3' 475 cleavage site: 460

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3'-TTGACGTCGCCGGTTAGAGTT-5'

DysRNA\_arrange\_TPM 34632662\_21 TAATTTGGACGAGATTCGGTC

target id: NTK326\_mRNA\_39595\_cds

518 5'-TTGTTGATCAAATCTCGTCCAAATTATGCAA-3' 548 cleavage site: 533

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3'-CTGGCTTAGAGCAGGTTTAAT-5'

DysRNA\_arrange\_TPM 43206041\_21 TTTGAGATTGGCCGCTGCAGT

target id: NTK326\_mRNA\_39595\_cds

446 5'-CTTTAACTGCAGCGGCCAATCTCAAAGGTTG-3' 476 cleavage site: 461

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3'-TGACGTCGCCGGTTAGAGTTT-5'

DysRNA\_arrange\_TPM 34633256\_21 TAATTTGGACGAGATTTGGTC

target id: NTK326\_mRNA\_39595\_cds

518 5'-TTGTTGATCAAATCTCGTCCAAATTATGCAA-3' 548 cleavage site: 533

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3'-CTGGTTTAGAGCAGGTTTAAT-5'

DysRNA\_arrange\_TPM 34632839\_21 TAATTTGGACGAGATTTGATC

target id: NTK326\_mRNA\_39595\_cds

518 5'-TTGTTGATCAAATCTCGTCCAAATTATGCAA-3' 548 cleavage site: 533

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3'-CTAGTTTAGAGCAGGTTTAAT-5'

DysRNA\_arrange\_TPM 35198903\_22 TACAGGTGACTTGTAAATGTTT

target id: NTK326\_mRNA\_39595\_cds

84 5'-TCGGAAAACATTTACGAGTCACCTGTACGAAA-3' 115 cleavage site: 100

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3'-TTTGTAAATGTTCAGTGGACAT-5'

DysRNA\_arrange\_TPM 41151740\_21 TTGAGATTGGCCGCTGCAGTT

target id: NTK326\_mRNA\_39595\_cds

445 5'-GCTTTAACTGCAGCGGCCAATCTCAAAGGTT-3' 475 cleavage site: 460

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3'-TTGACGTCGCCGGTTAGAGTT-5'

DysRNA\_arrange\_TPM 34632315\_22 TAATTTGGACGAGATTCGGTCA

target id: NTK326\_mRNA\_39595\_cds

517 5'-ATTGTTGATCAAATCTCGTCCAAATTATGCAA-3' 548 cleavage site: 533

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3'-ACTGGCTTAGAGCAGGTTTAAT-5'

DysRNA\_arrange\_TPM 40498063\_21 TTAGATACTGAAACAACAGGT

target id: NTBX\_mRNA\_108279\_cds

2200 5'-CCATCATCTATT-TTTCAGTATC-AAACTCA-3' 2228 cleavage site: 2213

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3'-TGGACAACAAAGTCATAGATT-5'

DysRNA\_arrange\_TPM 34632662\_21 TAATTTGGACGAGATTCGGTC

target id: NTK326\_mRNA\_43111\_cds

521 5'-TTGTTGACCGAATCTCGTCCAAATTATGCAA-3' 551 cleavage site: 536

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3'-CTGGCTTAGAGCAGGTTTAAT-5'

DysRNA\_arrange\_TPM 43206041\_21 TTTGAGATTGGCCGCTGCAGT

target id: NTK326\_mRNA\_43111\_cds

449 5'-CTTTAACTGCAGCGGCCAATCTCAAAGGCTG-3' 479 cleavage site: 464

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3'-TGACGTCGCCGGTTAGAGTTT-5'

DysRNA\_arrange\_TPM 34633256\_21 TAATTTGGACGAGATTTGGTC

target id: NTK326\_mRNA\_43111\_cds

521 5'-TTGTTGACCGAATCTCGTCCAAATTATGCAA-3' 551 cleavage site: 536

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3'-CTGGTTTAGAGCAGGTTTAAT-5'

DysRNA\_arrange\_TPM 35716976\_20 TATATCGAGTCCTGTTAATT

target id: NTK326\_mRNA\_43111\_cds

3319 5'-ACTTGGATAAGGAGGACCCGATATAACAAT-3' 3348 cleavage site: 3333

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3'-TTAATTGTCCTGAGCTATAT-5'

DysRNA\_arrange\_TPM 34632839\_21 TAATTTGGACGAGATTTGATC

target id: NTK326\_mRNA\_43111\_cds

521 5'-TTGTTGACCGAATCTCGTCCAAATTATGCAA-3' 551 cleavage site: 536

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3'-CTAGTTTAGAGCAGGTTTAAT-5'

DysRNA\_arrange\_TPM 35198903\_22 TACAGGTGACTTGTAAATGTTT

target id: NTK326\_mRNA\_43111\_cds

87 5'-TCGGAAAACATTTACGAGTCACCTGTACGAAA-3' 118 cleavage site: 103

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3'-TTTGTAAATGTTCAGTGGACAT-5'

DysRNA\_arrange\_TPM 41151740\_21 TTGAGATTGGCCGCTGCAGTT

target id: NTK326\_mRNA\_43111\_cds

448 5'-GCTTTAACTGCAGCGGCCAATCTCAAAGGCT-3' 478 cleavage site: 463

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3'-TTGACGTCGCCGGTTAGAGTT-5'

DysRNA\_arrange\_TPM 34632315\_22 TAATTTGGACGAGATTCGGTCA

target id: NTK326\_mRNA\_43111\_cds

520 5'-ATTGTTGACCGAATCTCGTCCAAATTATGCAA-3' 551 cleavage site: 536

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3'-ACTGGCTTAGAGCAGGTTTAAT-5'

DysRNA\_arrange\_TPM 39288440\_22 TCCGGGAAATGAAAATAGCTGC

target id: NTTN90\_mRNA\_90508\_cds

3000 5'-TATACACAGC-ATTTTCA-TTCCTGGAGGCAA-3' 3029 cleavage site: 3014

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3'-CGTCGATAAAAGTAAAGGGCCT-5'

DysRNA\_arrange\_TPM 43963689\_22 TTTTAGCCAGAGTTGTTTTCCC

target id: NTTN90\_mRNA\_72762\_cds

680 5'-GCATAGGGAAAACAACTCTGGC-AAAAGCTAT-3' 710 cleavage site: 695

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3'-CCCTTTTGTTGAGACCGATTTT-5'

DysRNA\_arrange\_TPM 42993390\_21 TTTAGCCAGAGTTGTTTTCCC

target id: NTTN90\_mRNA\_72762\_cds

680 5'-GCATAGGGAAAACAACTCTGGC-AAAAGCTA-3' 709 cleavage site: 694

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3'-CCCTTTTGTTGAGACCGATTT-5'

DysRNA\_arrange\_TPM 43964061\_21 TTTTAGCCAGAGTTGTTTTCC

target id: NTTN90\_mRNA\_72762\_cds

681 5'-CATAGGGAAAACAACTCTGGC-AAAAGCTAT-3' 710 cleavage site: 695

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3'-CCTTTTGTTGAGACCGATTTT-5'

DysRNA\_arrange\_TPM 40391668\_20 TTAATATTTCAGCTCGAACT

target id: NTTN90\_mRNA\_72762\_cds

1369 5'-CATGAAG-TT-A-CTGAAATATTAAATGCA-3' 1395 cleavage site: 1380

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3'-TCAAGCTCGACTTTATAATT-5'

DysRNA\_arrange\_TPM 43963689\_22 TTTTAGCCAGAGTTGTTTTCCC

target id: NTBX\_mRNA\_95914\_cds

671 5'-GCATAGGGAAAACAACTCTGGC-AAAAGCTAT-3' 701 cleavage site: 686

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3'-CCCTTTTGTTGAGACCGATTTT-5'

DysRNA\_arrange\_TPM 42993390\_21 TTTAGCCAGAGTTGTTTTCCC

target id: NTBX\_mRNA\_95914\_cds

671 5'-GCATAGGGAAAACAACTCTGGC-AAAAGCTA-3' 700 cleavage site: 685

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3'-CCCTTTTGTTGAGACCGATTT-5'

DysRNA\_arrange\_TPM 43964061\_21 TTTTAGCCAGAGTTGTTTTCC

target id: NTBX\_mRNA\_95914\_cds

672 5'-CATAGGGAAAACAACTCTGGC-AAAAGCTAT-3' 701 cleavage site: 686

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3'-CCTTTTGTTGAGACCGATTTT-5'

DysRNA\_arrange\_TPM 40391668\_20 TTAATATTTCAGCTCGAACT

target id: NTBX\_mRNA\_95914\_cds

1360 5'-CATGAAG-TT-A-CTGAAATATTAAATGCA-3' 1386 cleavage site: 1371

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3'-TCAAGCTCGACTTTATAATT-5'

DysRNA\_arrange\_TPM 43499236\_21 TTTGTCATGATAAATAAAGTC

target id: NTTN90\_mRNA\_42140\_cds

950 5'-CCAAGGACTTTATTTATCATGACAAATTGTT-3' 980 cleavage site: 965

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3'-CTGAAATAAATAGTACTGTTT-5'

DysRNA\_arrange\_TPM 43498503\_21 TTTGTCATGATGAATAAAGTC

target id: NTTN90\_mRNA\_42140\_cds

950 5'-CCAAGGACTTTATTTATCATGACAAATTGTT-3' 980 cleavage site: 965

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3'-CTGAAATAAGTAGTACTGTTT-5'

DysRNA\_arrange\_TPM 39918426\_21 TCTCGTTGAAATCTAGCTACC

target id: NTTN90\_mRNA\_42140\_cds

2548 5'-AGCTTGGT-GATCGTTTTCAACGAGAGAGGT-3' 2577 cleavage site: 2562

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3'-CCATCGATCTAAAGTTGCTCT-5'

DysRNA\_arrange\_TPM 41905826\_21 TTGTCTCACGTCATTCCATGC

target id: NTBX\_mRNA\_24678\_cds

611 5'-GTAAAGCATGGGATGACGTGAGACTATGCTT-3' 641 cleavage site: 626

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3'-CGTACCTTACTGCACTCTGTT-5'

DysRNA\_arrange\_TPM 37756134\_21 TGTCTCACGTCATTCCATGCA

target id: NTBX\_mRNA\_24678\_cds

610 5'-AGTAAAGCATGGGATGACGTGAGACTATGCT-3' 640 cleavage site: 625

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3'-ACGTACCTTACTGCACTCTGT-5'

DysRNA\_arrange\_TPM 38706727\_21 TCGACTCCCATTGTTTTGACT

target id: NTBX\_mRNA\_24678\_cds

641 5'-TTCCAAGTGAAAACAATGGGAGTCGAATACT-3' 671 cleavage site: 656

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3'-TCAGTTTTGTTACCCTCAGCT-5'

DysRNA\_arrange\_TPM 30234614\_21 CGACTCCCATTGTTTTGACTT

target id: NTBX\_mRNA\_24678\_cds

640 5'-TTTCCAAGTGAAAACAATGGGAGTCGAATAC-3' 670 cleavage site: 655

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3'-TTCAGTTTTGTTACCCTCAGC-5'

DysRNA\_arrange\_TPM 32948576\_20 CTGGGAAGTCCTCGTGTTGC

target id: NTTN90\_mRNA\_102492\_cds

3412 5'-CGGCTACAACATGTGGACTTCTCAGGTGTC-3' 3441 cleavage site: 3426

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3'-CGTTGTGCTCCTGAAGGGTC-5'

DysRNA\_arrange\_TPM 38030093\_21 TCAACATCATCAGACATATGG

target id: NTTN90\_mRNA\_124334\_cds

2241 5'-TTTGCCTATATGTCTGAAGAGGTTGACTTTA-3' 2271 cleavage site: 2256

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3'-GGTATACAGACTACTACAACT-5'

DysRNA\_arrange\_TPM 32948576\_20 CTGGGAAGTCCTCGTGTTGC

target id: NTTN90\_mRNA\_102488\_cds

3412 5'-CGGCTACAACATGTGGACTTCTCAGGTGTC-3' 3441 cleavage site: 3426

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3'-CGTTGTGCTCCTGAAGGGTC-5'

DysRNA\_arrange\_TPM 41911182\_21 TTGTCTTTCCGATACCTCCCA

target id: NTK326\_mRNA\_115279\_cds

621 5'-TGGAATGGCAGGTGTTGGCAAGACAACACTT-3' 651 cleavage site: 636

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3'-ACCCTCCATAGCCTTTCTGTT-5'

DysRNA\_arrange\_TPM 22042883\_24 GAACTGTAGAGTTTGATCCTGGCT

target id: NTTN90\_mRNA\_46764\_cds

66 5'-AAGGGAG-CA-GATCAAACTCTGTAGTTACTTTT-3' 97 cleavage site: 82

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3'-TCGGTCCTAGTTTGAGATGTCAAG-5'

DysRNA\_arrange\_TPM 22043376\_20 GAACTGTAGAGTTTGATCCT

target id: NTTN90\_mRNA\_46764\_cds

68 5'-GGGAGCAGATCAAACTCTGTAGTTACTTTT-3' 97 cleavage site: 82

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3'-TCCTAGTTTGAGATGTCAAG-5'

DysRNA\_arrange\_TPM 22746892\_21 GAGGTAGTGACAATAAATAAC

target id: NTBX\_mRNA\_91223\_cds

2744 5'-TACGTCTTATTGATTGTCACTCTCTTACCTC-3' 2774 cleavage site: 2759

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3'-CAATAAATAACAGTGATGGAG-5'

DysRNA\_arrange\_TPM 02841428\_21 AAGAACTTTGAAGAGAGAGTT

target id: NTBX\_mRNA\_91223\_cds

3577 5'-CGCCTAAC-CTCACTTCAAAG-TCTACGGAT-3' 3605 cleavage site: 3590

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3'-TTGAGAGAGAAGTTTCAAGAA-5'

DysRNA\_arrange\_TPM 02842108\_20 AAGAACTTTGAAGAGAGAGT

target id: NTBX\_mRNA\_91223\_cds

3578 5'-GCCTAAC-CTCACTTCAAAG-TCTACGGAT-3' 3605 cleavage site: 3590

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3'-TGAGAGAGAAGTTTCAAGAA-5'

DysRNA\_arrange\_TPM 10032960\_20 AGGTAGTGACAATAAATAAC

target id: NTBX\_mRNA\_91223\_cds

2744 5'-TACGTCTTATTGATTGTCACTCTCTTACCT-3' 2773 cleavage site: 2758

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3'-CAATAAATAACAGTGATGGA-5'

DysRNA\_arrange\_TPM 41905826\_21 TTGTCTCACGTCATTCCATGC

target id: NTBX\_mRNA\_24683\_cds

797 5'-GTAAAGCATGGGATGATGTGAGACAATGCTT-3' 827 cleavage site: 812

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3'-CGTACCTTACTGCACTCTGTT-5'

DysRNA\_arrange\_TPM 37756134\_21 TGTCTCACGTCATTCCATGCA

target id: NTBX\_mRNA\_24683\_cds

796 5'-AGTAAAGCATGGGATGATGTGAGACAATGCT-3' 826 cleavage site: 811

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3'-ACGTACCTTACTGCACTCTGT-5'

DysRNA\_arrange\_TPM 32948576\_20 CTGGGAAGTCCTCGTGTTGC

target id: NTTN90\_mRNA\_102491\_cds

3412 5'-CGGCTACAACATGTGGACTTCTCAGGTGTC-3' 3441 cleavage site: 3426

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3'-CGTTGTGCTCCTGAAGGGTC-5'

DysRNA\_arrange\_TPM 31384081\_21 CCACGATCCACTGAGATTCAG

target id: NTBX\_mRNA\_132524\_cds

1643 5'-GAGTTCTGAATCTGAGTGGAAC-TGGTATTA-3' 1672 cleavage site: 1657

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3'-GACTTAGAGTCACCTAGCACC-5'

DysRNA\_arrange\_TPM 31383804\_22 CCACGATCCACTGAGATTCAGC

target id: NTBX\_mRNA\_132524\_cds

1642 5'-AGAGTTCTGAATCTGAGTGGAAC-TGGTATTA-3' 1672 cleavage site: 1657

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3'-CGACTTAGAGTCACCTAGCACC-5'

DysRNA\_arrange\_TPM 32948576\_20 CTGGGAAGTCCTCGTGTTGC

target id: NTK326\_mRNA\_117088\_cds

3412 5'-CGGCTACAACATGTGGACTTCTCAGGTGTC-3' 3441 cleavage site: 3426

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3'-CGTTGTGCTCCTGAAGGGTC-5'

DysRNA\_arrange\_TPM 40742547\_22 TTACCTGAACCTGGCATACCAA

target id: NTBX\_mRNA\_20748\_cds

1863 5'-GATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-AACCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40741736\_21 TTACCTGAACCTGGCATACCA

target id: NTBX\_mRNA\_20748\_cds

1864 5'-ATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-ACCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40740236\_21 TTACCTGAACCTGGCATACCT

target id: NTBX\_mRNA\_20748\_cds

1864 5'-ATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-TCCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40741593\_20 TTACCTGAACCTGGCATACC

target id: NTBX\_mRNA\_20748\_cds

1865 5'-TCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-CCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40742348\_23 TTACCTGAACCTGGCATACCAAA

target id: NTBX\_mRNA\_20748\_cds

1862 5'-CGATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-AAACCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40740693\_23 TTACCTGAACCTGGCATACCAAT

target id: NTBX\_mRNA\_20748\_cds

1862 5'-CGATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-TAACCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 35450798\_21 TACCTGAACCTGGCATACCAA

target id: NTBX\_mRNA\_20748\_cds

1863 5'-GATCACTGGTATGCCGGGTTCGGGTAAAACT-3' 1893 cleavage site: 1878

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3'-AACCATACGGTCCAAGTCCAT-5'

DysRNA\_arrange\_TPM 40740134\_22 TTACCTGAACCTGGCATACCAT

target id: NTBX\_mRNA\_20748\_cds

1863 5'-GATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-TACCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40741540\_22 TTACCTGAACCTGGCATACCTT

target id: NTBX\_mRNA\_20748\_cds

1863 5'-GATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-TTCCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40742481\_23 TTACCTGAACCTGGCATACCATT

target id: NTBX\_mRNA\_20748\_cds

1862 5'-CGATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-TTACCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40741489\_20 TTACCTGAACCTGGCATACT

target id: NTBX\_mRNA\_20748\_cds

1865 5'-TCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-TCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40742536\_21 TTACCTGAACCTGGCATACCG

target id: NTBX\_mRNA\_20748\_cds

1864 5'-ATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-GCCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40742033\_21 TTACCTGAACCTGGCATACCC

target id: NTBX\_mRNA\_20748\_cds

1864 5'-ATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-CCCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40739408\_23 TTACCTGAACCTGGCATACCAAG

target id: NTBX\_mRNA\_20748\_cds

1862 5'-CGATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-GAACCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 43050316\_22 TTTACCTGAACCTGGCATACCA

target id: NTBX\_mRNA\_20748\_cds

1864 5'-ATCACTGGTATGCCGGGTTCGGGTAAAACTAC-3' 1895 cleavage site: 1880

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3'-ACCATACGGTCCAAGTCCATTT-5'

DysRNA\_arrange\_TPM 40741174\_22 TTACCTGAACCTGGCATACCAG

target id: NTBX\_mRNA\_20748\_cds

1863 5'-GATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-GACCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 43050143\_24 TTTACCTGAACCTGGCATACCAAC

target id: NTBX\_mRNA\_20748\_cds

1862 5'-CGATCACTGGTATGCCGGGTTCGGGTAAAACTAC-3' 1895 cleavage site: 1880

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3'-CAACCATACGGTCCAAGTCCATTT-5'

DysRNA\_arrange\_TPM 13424659\_24 ACGTGCCCAGAGATCTTTATAGAA

target id: NTBX\_mRNA\_20748\_cds

1529 5'-AAGAATTGTATAAAGATCTCTGGGCACGTACTTT-3' 1562 cleavage site: 1547

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3'-AAGATATTTCTAGAGACCCGTGCA-5'

DysRNA\_arrange\_TPM 35450403\_20 TACCTGAACCTGGCATACCA

target id: NTBX\_mRNA\_20748\_cds

1864 5'-ATCACTGGTATGCCGGGTTCGGGTAAAACT-3' 1893 cleavage site: 1878

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3'-ACCATACGGTCCAAGTCCAT-5'

DysRNA\_arrange\_TPM 40739753\_22 TTACCTGAACCTGGCATACCTA

target id: NTBX\_mRNA\_20748\_cds

1863 5'-GATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-ATCCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40742347\_21 TTACCTGAACCTGGCATACTT

target id: NTBX\_mRNA\_20748\_cds

1864 5'-ATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-TTCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 13424647\_24 ACGTGCCCAGAGATCTTTATACAA

target id: NTBX\_mRNA\_20748\_cds

1529 5'-AAGAATTGTATAAAGATCTCTGGGCACGTACTTT-3' 1562 cleavage site: 1547

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3'-AACATATTTCTAGAGACCCGTGCA-5'

DysRNA\_arrange\_TPM 40739960\_22 TTACCTGAGCCTGGCATACCAA

target id: NTBX\_mRNA\_20748\_cds

1863 5'-GATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-AACCATACGGTCCGAGTCCATT-5'

DysRNA\_arrange\_TPM 40741291\_23 TTACCTGAACCTGGCATACCATC

target id: NTBX\_mRNA\_20748\_cds

1862 5'-CGATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-CTACCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40741578\_22 TTACCTGAACCAGGCATACCAA

target id: NTBX\_mRNA\_20748\_cds

1863 5'-GATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-AACCATACGGACCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40739574\_21 TTACCTGAACCTGGCATACTA

target id: NTBX\_mRNA\_20748\_cds

1864 5'-ATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-ATCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40665598\_22 TTACATGAACCTGGCATACCAA

target id: NTBX\_mRNA\_20748\_cds

1863 5'-GATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-AACCATACGGTCCAAGTACATT-5'

DysRNA\_arrange\_TPM 43050825\_21 TTTACCTGAACCTGGCATACC

target id: NTBX\_mRNA\_20748\_cds

1865 5'-TCACTGGTATGCCGGGTTCGGGTAAAACTAC-3' 1895 cleavage site: 1880

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3'-CCATACGGTCCAAGTCCATTT-5'

DysRNA\_arrange\_TPM 40741435\_21 TTACCTGAACCTGACATACCA

target id: NTBX\_mRNA\_20748\_cds

1864 5'-ATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-ACCATACAGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40742312\_23 TTACCTGAACCTGGCATACCAAC

target id: NTBX\_mRNA\_20748\_cds

1862 5'-CGATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-CAACCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40739464\_22 TTACCTGAACCTGGCATACCAC

target id: NTBX\_mRNA\_20748\_cds

1863 5'-GATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-CACCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40740425\_22 TTACCTGAACCTGACATACCAA

target id: NTBX\_mRNA\_20748\_cds

1863 5'-GATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-AACCATACAGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 35450164\_20 TACCTGAACCTGGCATACCT

target id: NTBX\_mRNA\_20748\_cds

1864 5'-ATCACTGGTATGCCGGGTTCGGGTAAAACT-3' 1893 cleavage site: 1878

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3'-TCCATACGGTCCAAGTCCAT-5'

DysRNA\_arrange\_TPM 43050821\_23 TTTACCTGAACCTGGCATACCAA

target id: NTBX\_mRNA\_20748\_cds

1863 5'-GATCACTGGTATGCCGGGTTCGGGTAAAACTAC-3' 1895 cleavage site: 1880

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3'-AACCATACGGTCCAAGTCCATTT-5'

DysRNA\_arrange\_TPM 40741495\_22 TTACCTGAACCTGGCATACCTC

target id: NTBX\_mRNA\_20748\_cds

1863 5'-GATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-CTCCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 43983812\_21 TTTTACCTGAACCTGGCATAC

target id: NTBX\_mRNA\_20748\_cds

1866 5'-CACTGGTATGCCGGGTTCGGGTAAAACTACT-3' 1896 cleavage site: 1881

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3'-CATACGGTCCAAGTCCATTTT-5'

DysRNA\_arrange\_TPM 40739986\_22 TTACCTGAACCTAGCATACCAA

target id: NTBX\_mRNA\_20748\_cds

1863 5'-GATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-AACCATACGATCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40741138\_22 TTACCTGAACCTGGCATACTTT

target id: NTBX\_mRNA\_20748\_cds

1863 5'-GATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-TTTCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40739646\_22 TTACCTGAACCGGGCATACCAA

target id: NTBX\_mRNA\_20748\_cds

1863 5'-GATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-AACCATACGGGCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40740203\_21 TTACCTGAACCTGGCATACTC

target id: NTBX\_mRNA\_20748\_cds

1864 5'-ATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-CTCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40740924\_20 TTACCTGAACCTGGCATACA

target id: NTBX\_mRNA\_20748\_cds

1865 5'-TCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-ACATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40738063\_22 TTACCTAAACCTGGCATACCAA

target id: NTBX\_mRNA\_20748\_cds

1863 5'-GATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-AACCATACGGTCCAAATCCATT-5'

DysRNA\_arrange\_TPM 40745342\_22 TTACCTCAACCTGGCATACCAA

target id: NTBX\_mRNA\_20748\_cds

1863 5'-GATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-AACCATACGGTCCAACTCCATT-5'

DysRNA\_arrange\_TPM 40747677\_21 TTACCTTAACCTGGCATACCA

target id: NTBX\_mRNA\_20748\_cds

1864 5'-ATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-ACCATACGGTCCAATTCCATT-5'

DysRNA\_arrange\_TPM 40737853\_21 TTACCTAAACCTGGCATACCA

target id: NTBX\_mRNA\_20748\_cds

1864 5'-ATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-ACCATACGGTCCAAATCCATT-5'

DysRNA\_arrange\_TPM 26914223\_21 GTACCTGAACCTGGCATACCT

target id: NTBX\_mRNA\_20748\_cds

1864 5'-ATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-TCCATACGGTCCAAGTCCATG-5'

DysRNA\_arrange\_TPM 26914450\_20 GTACCTGAACCTGGCATACC

target id: NTBX\_mRNA\_20748\_cds

1865 5'-TCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-CCATACGGTCCAAGTCCATG-5'

DysRNA\_arrange\_TPM 26914545\_21 GTACCTGAACCTGGCATACCA

target id: NTBX\_mRNA\_20748\_cds

1864 5'-ATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-ACCATACGGTCCAAGTCCATG-5'

DysRNA\_arrange\_TPM 40741202\_22 TTACCTGAACCTGGCATACTAA

target id: NTBX\_mRNA\_20748\_cds

1863 5'-GATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-AATCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 16439463\_22 ATACCTGAACCTGGCATACCAA

target id: NTBX\_mRNA\_20748\_cds

1863 5'-GATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-AACCATACGGTCCAAGTCCATA-5'

DysRNA\_arrange\_TPM 35451289\_22 TACCTGAACCTGGCATACCAAA

target id: NTBX\_mRNA\_20748\_cds

1862 5'-CGATCACTGGTATGCCGGGTTCGGGTAAAACT-3' 1893 cleavage site: 1878

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3'-AAACCATACGGTCCAAGTCCAT-5'

DysRNA\_arrange\_TPM 40739499\_22 TTACCTGAACCTGTCATACCAA

target id: NTBX\_mRNA\_20748\_cds

1863 5'-GATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-AACCATACTGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 35450589\_22 TACCTGAACCTGGCATACCAAT

target id: NTBX\_mRNA\_20748\_cds

1862 5'-CGATCACTGGTATGCCGGGTTCGGGTAAAACT-3' 1893 cleavage site: 1878

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3'-TAACCATACGGTCCAAGTCCAT-5'

DysRNA\_arrange\_TPM 40717233\_22 TTACCGGAACCTGGCATACCAA

target id: NTBX\_mRNA\_20748\_cds

1863 5'-GATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-AACCATACGGTCCAAGGCCATT-5'

DysRNA\_arrange\_TPM 40747954\_22 TTACCTTAACCTGGCATACCAA

target id: NTBX\_mRNA\_20748\_cds

1863 5'-GATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-AACCATACGGTCCAATTCCATT-5'

DysRNA\_arrange\_TPM 26914581\_22 GTACCTGAACCTGGCATACCAA

target id: NTBX\_mRNA\_20748\_cds

1863 5'-GATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-AACCATACGGTCCAAGTCCATG-5'

DysRNA\_arrange\_TPM 40742285\_22 TTACCTGAACCTGGCATACTTC

target id: NTBX\_mRNA\_20748\_cds

1863 5'-GATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-CTTCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40727231\_22 TTACCCGAACCTGGCATACCAA

target id: NTBX\_mRNA\_20748\_cds

1863 5'-GATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-AACCATACGGTCCAAGCCCATT-5'

DysRNA\_arrange\_TPM 40741969\_22 TTACCTGAACCTTGCATACCAA

target id: NTBX\_mRNA\_20748\_cds

1863 5'-GATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-AACCATACGTTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40741702\_22 TTACCTGAACCCGGCATACCAA

target id: NTBX\_mRNA\_20748\_cds

1863 5'-GATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-AACCATACGGCCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40741040\_22 TTACCTGATCCTGGCATACCAA

target id: NTBX\_mRNA\_20748\_cds

1863 5'-GATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-AACCATACGGTCCTAGTCCATT-5'

DysRNA\_arrange\_TPM 40739525\_22 TTACCTGAATCTGGCATACCAA

target id: NTBX\_mRNA\_20748\_cds

1863 5'-GATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-AACCATACGGTCTAAGTCCATT-5'

DysRNA\_arrange\_TPM 40745543\_21 TTACCTCAACCTGGCATACCA

target id: NTBX\_mRNA\_20748\_cds

1864 5'-ATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-ACCATACGGTCCAACTCCATT-5'

DysRNA\_arrange\_TPM 40785222\_22 TTACTTGAACCTGGCATACCAA

target id: NTBX\_mRNA\_20748\_cds

1863 5'-GATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-AACCATACGGTCCAAGTTCATT-5'

DysRNA\_arrange\_TPM 40740904\_22 TTACCTGAACTTGGCATACCAA

target id: NTBX\_mRNA\_20748\_cds

1863 5'-GATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-AACCATACGGTTCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40741094\_23 TTACCTGAACCTGGCATACCACT

target id: NTBX\_mRNA\_20748\_cds

1862 5'-CGATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-TCACCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40932757\_22 TTATCTGAACCTGGCATACCAA

target id: NTBX\_mRNA\_20748\_cds

1863 5'-GATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-AACCATACGGTCCAAGTCTATT-5'

DysRNA\_arrange\_TPM 40740779\_22 TTACCTGAACCTGGCATACCCT

target id: NTBX\_mRNA\_20748\_cds

1863 5'-GATCACTGGTATGCCGGGTTCGGGTAAAACTA-3' 1894 cleavage site: 1879

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3'-TCCCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 31384081\_21 CCACGATCCACTGAGATTCAG

target id: NTBX\_mRNA\_132526\_cds

1436 5'-GAGTTCTGAATCTGAGTGGAAC-TGGTATTA-3' 1465 cleavage site: 1450

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3'-GACTTAGAGTCACCTAGCACC-5'

DysRNA\_arrange\_TPM 31383804\_22 CCACGATCCACTGAGATTCAGC

target id: NTBX\_mRNA\_132526\_cds

1435 5'-AGAGTTCTGAATCTGAGTGGAAC-TGGTATTA-3' 1465 cleavage site: 1450

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3'-CGACTTAGAGTCACCTAGCACC-5'

DysRNA\_arrange\_TPM 41911182\_21 TTGTCTTTCCGATACCTCCCA

target id: NTTN90\_mRNA\_103113\_cds

621 5'-TGGAATGGCAGGTGTTGGCAAGACAACACTT-3' 651 cleavage site: 636

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3'-ACCCTCCATAGCCTTTCTGTT-5'

DysRNA\_arrange\_TPM 37472283\_20 TGCTTGAAATTGTCGGGAGG

target id: NTBX\_mRNA\_97358\_cds

674 5'-ATGTCCCTCAAGTCAATTTCAAGCTAGCTC-3' 703 cleavage site: 688

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3'-GGAGGGCTGTTAAAGTTCGT-5'

DysRNA\_arrange\_TPM 26571156\_22 GCTTGAAATTGTCGGGAGGGAA

target id: NTBX\_mRNA\_97358\_cds

671 5'-TTGATGTCCCTCAAGTCAATTTCAAGCTAGCT-3' 702 cleavage site: 687

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3'-AAGGGAGGGCTGTTAAAGTTCG-5'

DysRNA\_arrange\_TPM 26571173\_21 GCTTGAAATTGTCGGGAGGGA

target id: NTBX\_mRNA\_97358\_cds

672 5'-TGATGTCCCTCAAGTCAATTTCAAGCTAGCT-3' 702 cleavage site: 687

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3'-AGGGAGGGCTGTTAAAGTTCG-5'

DysRNA\_arrange\_TPM 37472140\_21 TGCTTGAAATTGTCGGGAGGG

target id: NTBX\_mRNA\_97358\_cds

673 5'-GATGTCCCTCAAGTCAATTTCAAGCTAGCTC-3' 703 cleavage site: 688

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3'-GGGAGGGCTGTTAAAGTTCGT-5'

DysRNA\_arrange\_TPM 43499236\_21 TTTGTCATGATAAATAAAGTC

target id: NTBX\_mRNA\_97358\_cds

950 5'-CCAAGGACTTTATTTATCATGACAAATTGTT-3' 980 cleavage site: 965

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3'-CTGAAATAAATAGTACTGTTT-5'

DysRNA\_arrange\_TPM 41815455\_20 TTGTGAAATGACTTGAGAGG

target id: NTBX\_mRNA\_97358\_cds

672 5'-TGATGTCCCTCAAGTCAATTTCA-AGCTAGC-3' 701 cleavage site: 686

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3'-GGAGAGTTCAG-TAAAGTGTT-5'

DysRNA\_arrange\_TPM 37472075\_22 TGCTTGAAATTGTCGGGAGGGA

target id: NTBX\_mRNA\_97358\_cds

672 5'-TGATGTCCCTCAAGTCAATTTCAAGCTAGCTC-3' 703 cleavage site: 688

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3'-AGGGAGGGCTGTTAAAGTTCGT-5'

DysRNA\_arrange\_TPM 43498503\_21 TTTGTCATGATGAATAAAGTC

target id: NTBX\_mRNA\_97358\_cds

950 5'-CCAAGGACTTTATTTATCATGACAAATTGTT-3' 980 cleavage site: 965

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3'-CTGAAATAAGTAGTACTGTTT-5'

DysRNA\_arrange\_TPM 26571723\_20 GCTTGAAATTGTCGGGAGGG

target id: NTBX\_mRNA\_97358\_cds

673 5'-GATGTCCCTCAAGTCAATTTCAAGCTAGCT-3' 702 cleavage site: 687

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3'-GGGAGGGCTGTTAAAGTTCG-5'

DysRNA\_arrange\_TPM 22746892\_21 GAGGTAGTGACAATAAATAAC

target id: NTTN90\_mRNA\_98286\_cds

2846 5'-TACGTCTTATTGATTGTCACTCTCTTACCTC-3' 2876 cleavage site: 2861

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3'-CAATAAATAACAGTGATGGAG-5'

DysRNA\_arrange\_TPM 02841428\_21 AAGAACTTTGAAGAGAGAGTT

target id: NTTN90\_mRNA\_98286\_cds

3679 5'-CGCCTAAC-CTCACTTCAAAG-TCTACGGAT-3' 3707 cleavage site: 3692

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3'-TTGAGAGAGAAGTTTCAAGAA-5'

DysRNA\_arrange\_TPM 02842108\_20 AAGAACTTTGAAGAGAGAGT

target id: NTTN90\_mRNA\_98286\_cds

3680 5'-GCCTAAC-CTCACTTCAAAG-TCTACGGAT-3' 3707 cleavage site: 3692

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3'-TGAGAGAGAAGTTTCAAGAA-5'

DysRNA\_arrange\_TPM 10032960\_20 AGGTAGTGACAATAAATAAC

target id: NTTN90\_mRNA\_98286\_cds

2846 5'-TACGTCTTATTGATTGTCACTCTCTTACCT-3' 2875 cleavage site: 2860

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3'-CAATAAATAACAGTGATGGA-5'

DysRNA\_arrange\_TPM 38030093\_21 TCAACATCATCAGACATATGG

target id: NTK326\_mRNA\_108678\_cds

2223 5'-TTTGCCTGTATGTCTGAAGAGGTTGACTTTA-3' 2253 cleavage site: 2238

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3'-GGTATACAGACTACTACAACT-5'

DysRNA\_arrange\_TPM 37756134\_21 TGTCTCACGTCATTCCATGCA

target id: NTTN90\_mRNA\_15578\_cds

610 5'-AGTAAAGCATGGGATGACGTGAGACTATGCT-3' 640 cleavage site: 625

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3'-ACGTACCTTACTGCACTCTGT-5'

DysRNA\_arrange\_TPM 38706727\_21 TCGACTCCCATTGTTTTGACT

target id: NTTN90\_mRNA\_15578\_cds

641 5'-TTCCAAGTGAAAACAATGGGAGTCGAATACT-3' 671 cleavage site: 656

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3'-TCAGTTTTGTTACCCTCAGCT-5'

DysRNA\_arrange\_TPM 41905826\_21 TTGTCTCACGTCATTCCATGC

target id: NTTN90\_mRNA\_15578\_cds

611 5'-GTAAAGCATGGGATGACGTGAGACTATGCTT-3' 641 cleavage site: 626

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3'-CGTACCTTACTGCACTCTGTT-5'

DysRNA\_arrange\_TPM 30234614\_21 CGACTCCCATTGTTTTGACTT

target id: NTTN90\_mRNA\_15578\_cds

640 5'-TTTCCAAGTGAAAACAATGGGAGTCGAATAC-3' 670 cleavage site: 655

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3'-TTCAGTTTTGTTACCCTCAGC-5'

DysRNA\_arrange\_TPM 38030093\_21 TCAACATCATCAGACATATGG

target id: NTK326\_mRNA\_108677\_cds

2223 5'-TTTGCCTGTATGTCTGAAGAGGTTGACTTTA-3' 2253 cleavage site: 2238

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3'-GGTATACAGACTACTACAACT-5'

DysRNA\_arrange\_TPM 37756134\_21 TGTCTCACGTCATTCCATGCA

target id: NTTN90\_mRNA\_15580\_cds

796 5'-AGTAAAGCATGGGATGATGTGAGACAATGCT-3' 826 cleavage site: 811

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3'-ACGTACCTTACTGCACTCTGT-5'

DysRNA\_arrange\_TPM 41905826\_21 TTGTCTCACGTCATTCCATGC

target id: NTTN90\_mRNA\_15580\_cds

797 5'-GTAAAGCATGGGATGATGTGAGACAATGCTT-3' 827 cleavage site: 812

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3'-CGTACCTTACTGCACTCTGTT-5'

DysRNA\_arrange\_TPM 37756134\_21 TGTCTCACGTCATTCCATGCA

target id: NTBX\_mRNA\_24682\_cds

796 5'-AGTAAAGCATGGGATGATGTGAGACAATGCT-3' 826 cleavage site: 811

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3'-ACGTACCTTACTGCACTCTGT-5'

DysRNA\_arrange\_TPM 41905826\_21 TTGTCTCACGTCATTCCATGC

target id: NTBX\_mRNA\_24682\_cds

797 5'-GTAAAGCATGGGATGATGTGAGACAATGCTT-3' 827 cleavage site: 812

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3'-CGTACCTTACTGCACTCTGTT-5'

DysRNA\_arrange\_TPM 24549066\_21 GGGGATGTATCTCAAATGGTA

target id: NTTN90\_mRNA\_42816\_cds

1736 5'-AGCTATATCTTTTGAGATACATCGCTTTATCA-3' 1767 cleavage site: 1752

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3'-ATGGTAAACTCTATGTAG-GGG-5'

DysRNA\_arrange\_TPM 02221656\_22 AAATATAGATTTGGTTAAGGCT

target id: NTTN90\_mRNA\_98694\_cds

2123 5'-TTGAGAGCCTTCAACCAAATTCTG-ATTTGAGCA-3' 2155 cleavage site: 2140

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3'-TCGGAA-TTGGTTT-AGATATAAA-5'

DysRNA\_arrange\_TPM 43499236\_21 TTTGTCATGATAAATAAAGTC

target id: NTTN90\_mRNA\_42144\_cds

950 5'-CCAAGGACTTTATTTATCATGACAAATTGTT-3' 980 cleavage site: 965

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3'-CTGAAATAAATAGTACTGTTT-5'

DysRNA\_arrange\_TPM 43498503\_21 TTTGTCATGATGAATAAAGTC

target id: NTTN90\_mRNA\_42144\_cds

950 5'-CCAAGGACTTTATTTATCATGACAAATTGTT-3' 980 cleavage site: 965

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3'-CTGAAATAAGTAGTACTGTTT-5'

DysRNA\_arrange\_TPM 39918426\_21 TCTCGTTGAAATCTAGCTACC

target id: NTTN90\_mRNA\_42144\_cds

2548 5'-AGCTTGGT-GATCGTTTTCAACGAGAGAGGT-3' 2577 cleavage site: 2562

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3'-CCATCGATCTAAAGTTGCTCT-5'

DysRNA\_arrange\_TPM 22746892\_21 GAGGTAGTGACAATAAATAAC

target id: NTBX\_mRNA\_91224\_cds

2846 5'-TACGTCTTATTGATTGTCACTCTCTTACCTC-3' 2876 cleavage site: 2861

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3'-CAATAAATAACAGTGATGGAG-5'

DysRNA\_arrange\_TPM 02841428\_21 AAGAACTTTGAAGAGAGAGTT

target id: NTBX\_mRNA\_91224\_cds

3679 5'-CGCCTAAC-CTCACTTCAAAG-TCTACGGAT-3' 3707 cleavage site: 3692

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3'-TTGAGAGAGAAGTTTCAAGAA-5'

DysRNA\_arrange\_TPM 02842108\_20 AAGAACTTTGAAGAGAGAGT

target id: NTBX\_mRNA\_91224\_cds

3680 5'-GCCTAAC-CTCACTTCAAAG-TCTACGGAT-3' 3707 cleavage site: 3692

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3'-TGAGAGAGAAGTTTCAAGAA-5'

DysRNA\_arrange\_TPM 10032960\_20 AGGTAGTGACAATAAATAAC

target id: NTBX\_mRNA\_91224\_cds

2846 5'-TACGTCTTATTGATTGTCACTCTCTTACCT-3' 2875 cleavage site: 2860

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3'-CAATAAATAACAGTGATGGA-5'

DysRNA\_arrange\_TPM 22746892\_21 GAGGTAGTGACAATAAATAAC

target id: NTTN90\_mRNA\_98279\_cds

2591 5'-TACGTCTTATTGATTGTCACTCTCTTACCTC-3' 2621 cleavage site: 2606

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3'-CAATAAATAACAGTGATGGAG-5'

DysRNA\_arrange\_TPM 02841428\_21 AAGAACTTTGAAGAGAGAGTT

target id: NTTN90\_mRNA\_98279\_cds

3424 5'-CGCCTAAC-CTCACTTCAAAG-TCTACGGAT-3' 3452 cleavage site: 3437

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3'-TTGAGAGAGAAGTTTCAAGAA-5'

DysRNA\_arrange\_TPM 02842108\_20 AAGAACTTTGAAGAGAGAGT

target id: NTTN90\_mRNA\_98279\_cds

3425 5'-GCCTAAC-CTCACTTCAAAG-TCTACGGAT-3' 3452 cleavage site: 3437

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3'-TGAGAGAGAAGTTTCAAGAA-5'

DysRNA\_arrange\_TPM 10032960\_20 AGGTAGTGACAATAAATAAC

target id: NTTN90\_mRNA\_98279\_cds

2591 5'-TACGTCTTATTGATTGTCACTCTCTTACCT-3' 2620 cleavage site: 2605

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3'-CAATAAATAACAGTGATGGA-5'

DysRNA\_arrange\_TPM 37472283\_20 TGCTTGAAATTGTCGGGAGG

target id: NTK326\_mRNA\_97821\_cds

674 5'-ATGTCCCTCAAGTCAATTTCAAGCTAGCTC-3' 703 cleavage site: 688

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3'-GGAGGGCTGTTAAAGTTCGT-5'

DysRNA\_arrange\_TPM 26571156\_22 GCTTGAAATTGTCGGGAGGGAA

target id: NTK326\_mRNA\_97821\_cds

671 5'-TTGATGTCCCTCAAGTCAATTTCAAGCTAGCT-3' 702 cleavage site: 687

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3'-AAGGGAGGGCTGTTAAAGTTCG-5'

DysRNA\_arrange\_TPM 26571173\_21 GCTTGAAATTGTCGGGAGGGA

target id: NTK326\_mRNA\_97821\_cds

672 5'-TGATGTCCCTCAAGTCAATTTCAAGCTAGCT-3' 702 cleavage site: 687

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3'-AGGGAGGGCTGTTAAAGTTCG-5'

DysRNA\_arrange\_TPM 37472140\_21 TGCTTGAAATTGTCGGGAGGG

target id: NTK326\_mRNA\_97821\_cds

673 5'-GATGTCCCTCAAGTCAATTTCAAGCTAGCTC-3' 703 cleavage site: 688

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3'-GGGAGGGCTGTTAAAGTTCGT-5'

DysRNA\_arrange\_TPM 43499236\_21 TTTGTCATGATAAATAAAGTC

target id: NTK326\_mRNA\_97821\_cds

950 5'-CCAAGGACTTTATTTATCATGACAAATTGTT-3' 980 cleavage site: 965

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3'-CTGAAATAAATAGTACTGTTT-5'

DysRNA\_arrange\_TPM 41815455\_20 TTGTGAAATGACTTGAGAGG

target id: NTK326\_mRNA\_97821\_cds

672 5'-TGATGTCCCTCAAGTCAATTTCA-AGCTAGC-3' 701 cleavage site: 686

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3'-GGAGAGTTCAG-TAAAGTGTT-5'

DysRNA\_arrange\_TPM 37472075\_22 TGCTTGAAATTGTCGGGAGGGA

target id: NTK326\_mRNA\_97821\_cds

672 5'-TGATGTCCCTCAAGTCAATTTCAAGCTAGCTC-3' 703 cleavage site: 688

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3'-AGGGAGGGCTGTTAAAGTTCGT-5'

DysRNA\_arrange\_TPM 43498503\_21 TTTGTCATGATGAATAAAGTC

target id: NTK326\_mRNA\_97821\_cds

950 5'-CCAAGGACTTTATTTATCATGACAAATTGTT-3' 980 cleavage site: 965

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3'-CTGAAATAAGTAGTACTGTTT-5'

DysRNA\_arrange\_TPM 26571723\_20 GCTTGAAATTGTCGGGAGGG

target id: NTK326\_mRNA\_97821\_cds

673 5'-GATGTCCCTCAAGTCAATTTCAAGCTAGCT-3' 702 cleavage site: 687

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3'-GGGAGGGCTGTTAAAGTTCG-5'

DysRNA\_arrange\_TPM 43499236\_21 TTTGTCATGATAAATAAAGTC

target id: NTBX\_mRNA\_49338\_cds

917 5'-CCAAGGACTTTATTTATCATGACAAATTGTT-3' 947 cleavage site: 932

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3'-CTGAAATAAATAGTACTGTTT-5'

DysRNA\_arrange\_TPM 43498503\_21 TTTGTCATGATGAATAAAGTC

target id: NTBX\_mRNA\_49338\_cds

917 5'-CCAAGGACTTTATTTATCATGACAAATTGTT-3' 947 cleavage site: 932

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3'-CTGAAATAAGTAGTACTGTTT-5'

DysRNA\_arrange\_TPM 39918426\_21 TCTCGTTGAAATCTAGCTACC

target id: NTBX\_mRNA\_49338\_cds

2458 5'-AGCTTGGT-GATCGTTTTCAACGAGAGAGGT-3' 2487 cleavage site: 2472

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3'-CCATCGATCTAAAGTTGCTCT-5'

DysRNA\_arrange\_TPM 37472283\_20 TGCTTGAAATTGTCGGGAGG

target id: NTTN90\_mRNA\_15567\_cds

674 5'-ATGTCCCTCAAGTCAATTTCAAGCTAGCTC-3' 703 cleavage site: 688

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3'-GGAGGGCTGTTAAAGTTCGT-5'

DysRNA\_arrange\_TPM 26571156\_22 GCTTGAAATTGTCGGGAGGGAA

target id: NTTN90\_mRNA\_15567\_cds

671 5'-TTGATGTCCCTCAAGTCAATTTCAAGCTAGCT-3' 702 cleavage site: 687

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3'-AAGGGAGGGCTGTTAAAGTTCG-5'

DysRNA\_arrange\_TPM 26571173\_21 GCTTGAAATTGTCGGGAGGGA

target id: NTTN90\_mRNA\_15567\_cds

672 5'-TGATGTCCCTCAAGTCAATTTCAAGCTAGCT-3' 702 cleavage site: 687

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3'-AGGGAGGGCTGTTAAAGTTCG-5'

DysRNA\_arrange\_TPM 37472140\_21 TGCTTGAAATTGTCGGGAGGG

target id: NTTN90\_mRNA\_15567\_cds

673 5'-GATGTCCCTCAAGTCAATTTCAAGCTAGCTC-3' 703 cleavage site: 688

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3'-GGGAGGGCTGTTAAAGTTCGT-5'

DysRNA\_arrange\_TPM 43499236\_21 TTTGTCATGATAAATAAAGTC

target id: NTTN90\_mRNA\_15567\_cds

950 5'-CCAAGGACTTTATTTATCATGACAAATTGTT-3' 980 cleavage site: 965

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3'-CTGAAATAAATAGTACTGTTT-5'

DysRNA\_arrange\_TPM 41815455\_20 TTGTGAAATGACTTGAGAGG

target id: NTTN90\_mRNA\_15567\_cds

672 5'-TGATGTCCCTCAAGTCAATTTCA-AGCTAGC-3' 701 cleavage site: 686

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3'-GGAGAGTTCAG-TAAAGTGTT-5'

DysRNA\_arrange\_TPM 37472075\_22 TGCTTGAAATTGTCGGGAGGGA

target id: NTTN90\_mRNA\_15567\_cds

672 5'-TGATGTCCCTCAAGTCAATTTCAAGCTAGCTC-3' 703 cleavage site: 688

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3'-AGGGAGGGCTGTTAAAGTTCGT-5'

DysRNA\_arrange\_TPM 43498503\_21 TTTGTCATGATGAATAAAGTC

target id: NTTN90\_mRNA\_15567\_cds

950 5'-CCAAGGACTTTATTTATCATGACAAATTGTT-3' 980 cleavage site: 965

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3'-CTGAAATAAGTAGTACTGTTT-5'

DysRNA\_arrange\_TPM 26571723\_20 GCTTGAAATTGTCGGGAGGG

target id: NTTN90\_mRNA\_15567\_cds

673 5'-GATGTCCCTCAAGTCAATTTCAAGCTAGCT-3' 702 cleavage site: 687

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3'-GGGAGGGCTGTTAAAGTTCG-5'

DysRNA\_arrange\_TPM 41911182\_21 TTGTCTTTCCGATACCTCCCA

target id: NTTN90\_mRNA\_103115\_cds

732 5'-TGGAATGGCAGGTGTTGGCAAGACAACACTT-3' 762 cleavage site: 747

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3'-ACCCTCCATAGCCTTTCTGTT-5'

DysRNA\_arrange\_TPM 37756134\_21 TGTCTCACGTCATTCCATGCA

target id: NTTN90\_mRNA\_109401\_cds

769 5'-AGTGAAGCATGGGATGACGTGAGACTATGCT-3' 799 cleavage site: 784

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3'-ACGTACCTTACTGCACTCTGT-5'

DysRNA\_arrange\_TPM 41905826\_21 TTGTCTCACGTCATTCCATGC

target id: NTTN90\_mRNA\_109401\_cds

770 5'-GTGAAGCATGGGATGACGTGAGACTATGCTT-3' 800 cleavage site: 785

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3'-CGTACCTTACTGCACTCTGTT-5'

DysRNA\_arrange\_TPM 38030093\_21 TCAACATCATCAGACATATGG

target id: NTTN90\_mRNA\_98323\_cds

2223 5'-TTTGCCTGTATGTCTGAAGAGGTTGACTTTA-3' 2253 cleavage site: 2238

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3'-GGTATACAGACTACTACAACT-5'

DysRNA\_arrange\_TPM 40123240\_21 TCTTCTTTGTAGCCTTTCATA

target id: NTTN90\_mRNA\_64613\_cds

3467 5'-GAGTTTGTGATAGCCTATCAAAGAAGATGGAC-3' 3498 cleavage site: 3483

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3'-ATACTTTCCGAT-GTTTCTTCT-5'

DysRNA\_arrange\_TPM 41935941\_21 TTGTTGGTAGCTTGATGTATG

target id: NTTN90\_mRNA\_21859\_cds

2333 5'-TCGGACATATCAGTAAGCTACCAG-AACACCA-3' 2363 cleavage site: 2348

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3'-GTAT-GTAGTTCGATGGTTGTT-5'

DysRNA\_arrange\_TPM 38030093\_21 TCAACATCATCAGACATATGG

target id: NTK326\_mRNA\_140205\_cds

2223 5'-TTTGCCTATATGTCTGAAGAGGTTGACTTTA-3' 2253 cleavage site: 2238

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3'-GGTATACAGACTACTACAACT-5'

DysRNA\_arrange\_TPM 02221656\_22 AAATATAGATTTGGTTAAGGCT

target id: NTBX\_mRNA\_113576\_cds

2024 5'-TTGAGAGCCTTCAACCAAATTCTG-ATTTGAGCA-3' 2056 cleavage site: 2041

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3'-TCGGAA-TTGGTTT-AGATATAAA-5'

DysRNA\_arrange\_TPM 38030093\_21 TCAACATCATCAGACATATGG

target id: NTTN90\_mRNA\_98324\_cds

2223 5'-TTTGCCTGTATGTCTGAAGAGGTTGACTTTA-3' 2253 cleavage site: 2238

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3'-GGTATACAGACTACTACAACT-5'

DysRNA\_arrange\_TPM 43499236\_21 TTTGTCATGATAAATAAAGTC

target id: NTTN90\_mRNA\_42145\_cds

917 5'-CCAAGGACTTTATTTATCATGACAAATTGTT-3' 947 cleavage site: 932

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3'-CTGAAATAAATAGTACTGTTT-5'

DysRNA\_arrange\_TPM 43498503\_21 TTTGTCATGATGAATAAAGTC

target id: NTTN90\_mRNA\_42145\_cds

917 5'-CCAAGGACTTTATTTATCATGACAAATTGTT-3' 947 cleavage site: 932

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3'-CTGAAATAAGTAGTACTGTTT-5'

DysRNA\_arrange\_TPM 39918426\_21 TCTCGTTGAAATCTAGCTACC

target id: NTTN90\_mRNA\_42145\_cds

2515 5'-AGCTTGGT-GATCGTTTTCAACGAGAGAGGT-3' 2544 cleavage site: 2529

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3'-CCATCGATCTAAAGTTGCTCT-5'

DysRNA\_arrange\_TPM 32948576\_20 CTGGGAAGTCCTCGTGTTGC

target id: NTTN90\_mRNA\_102494\_cds

3082 5'-CGGCTACAACATGTGGACTTCTCAGGTGTC-3' 3111 cleavage site: 3096

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3'-CGTTGTGCTCCTGAAGGGTC-5'

DysRNA\_arrange\_TPM 41911182\_21 TTGTCTTTCCGATACCTCCCA

target id: NTK326\_mRNA\_115281\_cds

732 5'-TGGAATGGCAGGTGTTGGCAAGACAACACTT-3' 762 cleavage site: 747

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3'-ACCCTCCATAGCCTTTCTGTT-5'

DysRNA\_arrange\_TPM 22746892\_21 GAGGTAGTGACAATAAATAAC

target id: NTTN90\_mRNA\_98280\_cds

2693 5'-TACGTCTTATTGATTGTCACTCTCTTACCTC-3' 2723 cleavage site: 2708

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3'-CAATAAATAACAGTGATGGAG-5'

DysRNA\_arrange\_TPM 02841428\_21 AAGAACTTTGAAGAGAGAGTT

target id: NTTN90\_mRNA\_98280\_cds

3526 5'-CGCCTAAC-CTCACTTCAAAG-TCTACGGAT-3' 3554 cleavage site: 3539

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3'-TTGAGAGAGAAGTTTCAAGAA-5'

DysRNA\_arrange\_TPM 02842108\_20 AAGAACTTTGAAGAGAGAGT

target id: NTTN90\_mRNA\_98280\_cds

3527 5'-GCCTAAC-CTCACTTCAAAG-TCTACGGAT-3' 3554 cleavage site: 3539

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3'-TGAGAGAGAAGTTTCAAGAA-5'

DysRNA\_arrange\_TPM 10032960\_20 AGGTAGTGACAATAAATAAC

target id: NTTN90\_mRNA\_98280\_cds

2693 5'-TACGTCTTATTGATTGTCACTCTCTTACCT-3' 2722 cleavage site: 2707

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3'-CAATAAATAACAGTGATGGA-5'

DysRNA\_arrange\_TPM 22746892\_21 GAGGTAGTGACAATAAATAAC

target id: NTK326\_mRNA\_85299\_cds

2846 5'-TACGTCTTATTGATTGTCACTCTCTTACCTC-3' 2876 cleavage site: 2861

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3'-CAATAAATAACAGTGATGGAG-5'

DysRNA\_arrange\_TPM 02841428\_21 AAGAACTTTGAAGAGAGAGTT

target id: NTK326\_mRNA\_85299\_cds

3679 5'-CGCCTAAC-CTCACTTCAAAG-TCTACGGAT-3' 3707 cleavage site: 3692

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3'-TTGAGAGAGAAGTTTCAAGAA-5'

DysRNA\_arrange\_TPM 02842108\_20 AAGAACTTTGAAGAGAGAGT

target id: NTK326\_mRNA\_85299\_cds

3680 5'-GCCTAAC-CTCACTTCAAAG-TCTACGGAT-3' 3707 cleavage site: 3692

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3'-TGAGAGAGAAGTTTCAAGAA-5'

DysRNA\_arrange\_TPM 10032960\_20 AGGTAGTGACAATAAATAAC

target id: NTK326\_mRNA\_85299\_cds

2846 5'-TACGTCTTATTGATTGTCACTCTCTTACCT-3' 2875 cleavage site: 2860

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3'-CAATAAATAACAGTGATGGA-5'

DysRNA\_arrange\_TPM 38706727\_21 TCGACTCCCATTGTTTTGACT

target id: NTK326\_mRNA\_61519\_cds

818 5'-TTCCAAGTGAAAACAATGGGAGTCGAATACT-3' 848 cleavage site: 833

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3'-TCAGTTTTGTTACCCTCAGCT-5'

DysRNA\_arrange\_TPM 30234614\_21 CGACTCCCATTGTTTTGACTT

target id: NTK326\_mRNA\_61519\_cds

817 5'-TTTCCAAGTGAAAACAATGGGAGTCGAATAC-3' 847 cleavage site: 832

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3'-TTCAGTTTTGTTACCCTCAGC-5'

DysRNA\_arrange\_TPM 02767294\_21 AAGAAGATGATTATGGAGGGC

target id: NTK326\_mRNA\_72001\_cds

2319 5'-TCCAAGTGCTCCATCATCATCTTCTTCAGAT-3' 2349 cleavage site: 2334

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3'-CGGGAGGTATTAGTAGAAGAA-5'

DysRNA\_arrange\_TPM 02768834\_22 AAGAAGATGATTATGGAGGGCA

target id: NTK326\_mRNA\_72001\_cds

2318 5'-GTCCAAGTGCTCCATCATCATCTTCTTCAGAT-3' 2349 cleavage site: 2334

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3'-ACGGGAGGTATTAGTAGAAGAA-5'

DysRNA\_arrange\_TPM 32195924\_21 CCTAAGATTGTATGGACGTGG

target id: NTK326\_mRNA\_3237\_cds

766 5'-GAAACCCA-G-CCAGACATTCTTAGGGGATA-3' 794 cleavage site: 779

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3'-GGTGCAGGTATGTTAGAATCC-5'

DysRNA\_arrange\_TPM 15928038\_22 ATAGAATAATTATGAATGTGCT

target id: NTTN90\_mRNA\_117651\_cds

2280 5'-ATCATGTCGCATTCATAATTA-TCTATATCAT-3' 2310 cleavage site: 2295

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3'-TCGTGTAAGTATTAATAAGATA-5'

DysRNA\_arrange\_TPM 43514857\_22 TTTGTCTTTCCGATACCTCCCA

target id: NTTN90\_mRNA\_82332\_cds

516 5'-AGGGATGGGTGGCATCGGTAAGACAACTTTAG-3' 547 cleavage site: 532

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3'-ACCCTCCATAGCCTTTCTGTTT-5'

DysRNA\_arrange\_TPM 43514186\_22 TTTGTCTTTCCGATGCCTCCCA

target id: NTTN90\_mRNA\_82332\_cds

516 5'-AGGGATGGGTGGCATCGGTAAGACAACTTTAG-3' 547 cleavage site: 532

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3'-ACCCTCCGTAGCCTTTCTGTTT-5'

DysRNA\_arrange\_TPM 41911182\_21 TTGTCTTTCCGATACCTCCCA

target id: NTTN90\_mRNA\_82332\_cds

516 5'-AGGGATGGGTGGCATCGGTAAGACAACTTTA-3' 546 cleavage site: 531

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3'-ACCCTCCATAGCCTTTCTGTT-5'

DysRNA\_arrange\_TPM 43513291\_22 TTTGTCTTTCCGATGCCTCCCT

target id: NTTN90\_mRNA\_82332\_cds

516 5'-AGGGATGGGTGGCATCGGTAAGACAACTTTAG-3' 547 cleavage site: 532

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3'-TCCCTCCGTAGCCTTTCTGTTT-5'

DysRNA\_arrange\_TPM 20802129\_24 ATTTACACTTTGTAGGCCCGAGTA

target id: NTTN90\_mRNA\_37812\_cds

1513 5'-AAAACTACTTTGGCATACAAAGTGTATAGTGATAA-3' 1547 cleavage site: 1532

||||o ||| ||||||||||| |o|

3'-ATGAGCCCGGATGTTTCACAT-TTA-5'

DysRNA\_arrange\_TPM 21202783\_24 ATTTTACACTTTGTAGGCCCGAGT

target id: NTTN90\_mRNA\_37812\_cds

1514 5'-AAACTACTTTGGCATACAAAGTGTATAGTGATAA-3' 1547 cleavage site: 1532

|||o ||| ||||||||||| |o|

3'-TGAGCCCGGATGTTTCACATTTTA-5'

DysRNA\_arrange\_TPM 20608921\_24 ATTCTAGATCTTCTTTCACCAGTC

target id: NTTN90\_mRNA\_37812\_cds

1095 5'-AATTGGACTGGTGAAAGAAGATCTAGAATTCATA-3' 1128 cleavage site: 1113

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3'-CTGACCACTTTCTTCTAGATCTTA-5'

DysRNA\_arrange\_TPM 40506628\_21 TTAGATCTTCTTTCACCAGCT

target id: NTTN90\_mRNA\_37812\_cds

1094 5'-AAATTGGACTGGTGAAAGAAGATCTAGAATTC-3' 1125 cleavage site: 1110

o| ||||||||||||||||||o

3'-TC-GACCACTTTCTTCTAGATT-5'

DysRNA\_arrange\_TPM 43983812\_21 TTTTACCTGAACCTGGCATAC

target id: NTTN90\_mRNA\_63333\_cds

1878 5'-CACTGGCATGCCGGGTTCGGGTAAAACTACT-3' 1908 cleavage site: 1893

|||||o|||||o|||||||

3'-CATACGGTCCAAGTCCATTTT-5'

DysRNA\_arrange\_TPM 40741688\_22 TTACCTGAACCTGGCATGCCAA

target id: NTTN90\_mRNA\_63333\_cds

1875 5'-GATCACTGGCATGCCGGGTTCGGGTAAAACTA-3' 1906 cleavage site: 1891

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3'-AACCGTACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40727231\_22 TTACCCGAACCTGGCATACCAA

target id: NTTN90\_mRNA\_63333\_cds

1875 5'-GATCACTGGCATGCCGGGTTCGGGTAAAACTA-3' 1906 cleavage site: 1891

||| |||||o|||||||||||

3'-AACCATACGGTCCAAGCCCATT-5'

DysRNA\_arrange\_TPM 40741702\_22 TTACCTGAACCCGGCATACCAA

target id: NTTN90\_mRNA\_63333\_cds

1875 5'-GATCACTGGCATGCCGGGTTCGGGTAAAACTA-3' 1906 cleavage site: 1891

||| |||||||||||o|||||

3'-AACCATACGGCCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 07119696\_21 AATTGTCACTTGATTGTTGCA

target id: NTBX\_mRNA\_49494\_cds

1850 5'-AATGGTGCAGGAATCAAGTAACAGCTTCATCT-3' 1881 cleavage site: 1866

||||o |||||||| |||o ||

3'-ACGTTGTTAGTTCACTGTT-AA-5'

DysRNA\_arrange\_TPM 40391668\_20 TTAATATTTCAGCTCGAACT

target id: NTBX\_mRNA\_49494\_cds

448 5'-CATGAAG-TT-A-CTGAAATATTAAATGCA-3' 474 cleavage site: 459

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3'-TCAAGCTCGACTTTATAATT-5'

DysRNA\_arrange\_TPM 32487580\_22 CCTTTCGTGCTCAAGTTCTCTC

target id: NTBX\_mRNA\_49494\_cds

720 5'-AAAGGGAGTGAACTTGAGCACCAAAGCATTTG-3' 751 cleavage site: 736

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3'-CTCTCTTGAACTCGTGCTTTCC-5'

DysRNA\_arrange\_TPM 38561019\_24 TCGAAGAAGATGATGAATAGTAGT

target id: NTBX\_mRNA\_83517\_cds

1871 5'-CAAGTGCT-CTA-TCATCATCTTCTTCAGATCTGA-3' 1903 cleavage site: 1888

o|| ||| |||||||||||||| ||

3'-TGATGATAAGTAGTAGAAGAAG-CT-5'

DysRNA\_arrange\_TPM 02767294\_21 AAGAAGATGATTATGGAGGGC

target id: NTBX\_mRNA\_83517\_cds

1869 5'-TTCAAGTGCTCTATCATCATCTTCTTCAGAT-3' 1899 cleavage site: 1884

|o |||o|| |||||||||||

3'-CGGGAGGTATTAGTAGAAGAA-5'

DysRNA\_arrange\_TPM 24021801\_23 GGAGAAGATGATGAATAGTAATT

target id: NTBX\_mRNA\_83517\_cds

1867 5'-AGTTCAAGTGCTCTATCATCATCTTCTTCAGATC-3' 1900 cleavage site: 1885

|| |o|| | ||||||||||||o|

3'-TTAATGATA-AGTAGTAGAAGAGG-5'

DysRNA\_arrange\_TPM 02768834\_22 AAGAAGATGATTATGGAGGGCA

target id: NTBX\_mRNA\_83517\_cds

1868 5'-GTTCAAGTGCTCTATCATCATCTTCTTCAGAT-3' 1899 cleavage site: 1884

|o |||o|| |||||||||||

3'-ACGGGAGGTATTAGTAGAAGAA-5'

DysRNA\_arrange\_TPM 41343934\_21 TTGGAGAAGATGATGAATAGT

target id: NTBX\_mRNA\_83517\_cds

1873 5'-AGTGCTCTA-TCATCATCTTCTTCAGATCTG-3' 1902 cleavage site: 1887

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3'-TGATAAGTAGTAGAAGAGGTT-5'

DysRNA\_arrange\_TPM 24023543\_24 GGAGAAGATGATGAATAGTAATTG

target id: NTBX\_mRNA\_83517\_cds

1866 5'-AAGTTCAAGTGCTCTATCATCATCTTCTTCAGATC-3' 1900 cleavage site: 1885

||| |o|| | ||||||||||||o|

3'-GTTAATGATA-AGTAGTAGAAGAGG-5'

DysRNA\_arrange\_TPM 27959210\_20 GTTGTTTTGAGTTTGAGGCC

target id: NTBX\_mRNA\_122265\_cds

1250 5'-CTGATTGCATTAAACTCAAAA-AATTGCCA-3' 1278 cleavage site: 1263

|| |o|||||||||| ||o

3'-CCGGAGTTTGAGTTTTGTTG-5'

DysRNA\_arrange\_TPM 27959210\_20 GTTGTTTTGAGTTTGAGGCC

target id: NTK326\_mRNA\_95708\_cds

1394 5'-TTGATTGCATTAAACTCAAAA-AATTGCCA-3' 1422 cleavage site: 1407

|| |o|||||||||| ||o

3'-CCGGAGTTTGAGTTTTGTTG-5'

DysRNA\_arrange\_TPM 40969969\_23 TTATTGCTTGAGAATACACGTAG

target id: NTTN90\_mRNA\_16577\_cds

519 5'-ATGGGTTAC-TGT-TTCTCAAGCATATGATGCAA-3' 550 cleavage site: 535

o||| ||| |||||||||| ||o|

3'-GATGCACATAAGAGTTCGT-TATT-5'

DysRNA\_arrange\_TPM 36076634\_22 TATTGCTTGAGAATACACGTAG

target id: NTTN90\_mRNA\_16577\_cds

519 5'-ATGGGTTAC-TGT-TTCTCAAGCATATGATGCA-3' 549 cleavage site: 534

o||| ||| |||||||||| ||o

3'-GATGCACATAAGAGTTCGT-TAT-5'

DysRNA\_arrange\_TPM 38561019\_24 TCGAAGAAGATGATGAATAGTAGT

target id: NTTN90\_mRNA\_63309\_cds

2867 5'-CAAGTGCT-CTA-TCATCATCTTCTTCAGATCTGA-3' 2899 cleavage site: 2884

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3'-TGATGATAAGTAGTAGAAGAAG-CT-5'

DysRNA\_arrange\_TPM 02767294\_21 AAGAAGATGATTATGGAGGGC

target id: NTTN90\_mRNA\_63309\_cds

2865 5'-TTCAAGTGCTCTATCATCATCTTCTTCAGAT-3' 2895 cleavage site: 2880

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3'-CGGGAGGTATTAGTAGAAGAA-5'

DysRNA\_arrange\_TPM 24021801\_23 GGAGAAGATGATGAATAGTAATT

target id: NTTN90\_mRNA\_63309\_cds

2863 5'-AGTTCAAGTGCTCTATCATCATCTTCTTCAGATC-3' 2896 cleavage site: 2881

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3'-TTAATGATA-AGTAGTAGAAGAGG-5'

DysRNA\_arrange\_TPM 02768834\_22 AAGAAGATGATTATGGAGGGCA

target id: NTTN90\_mRNA\_63309\_cds

2864 5'-GTTCAAGTGCTCTATCATCATCTTCTTCAGAT-3' 2895 cleavage site: 2880

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3'-ACGGGAGGTATTAGTAGAAGAA-5'

DysRNA\_arrange\_TPM 41343934\_21 TTGGAGAAGATGATGAATAGT

target id: NTTN90\_mRNA\_63309\_cds

2869 5'-AGTGCTCTA-TCATCATCTTCTTCAGATCTG-3' 2898 cleavage site: 2883

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3'-TGATAAGTAGTAGAAGAGGTT-5'

DysRNA\_arrange\_TPM 24023543\_24 GGAGAAGATGATGAATAGTAATTG

target id: NTTN90\_mRNA\_63309\_cds

2862 5'-AAGTTCAAGTGCTCTATCATCATCTTCTTCAGATC-3' 2896 cleavage site: 2881

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3'-GTTAATGATA-AGTAGTAGAAGAGG-5'

DysRNA\_arrange\_TPM 43514857\_22 TTTGTCTTTCCGATACCTCCCA

target id: NTTN90\_mRNA\_82331\_cds

516 5'-AGGGATGGGTGGCATCGGTAAGACAACTTTAG-3' 547 cleavage site: 532

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3'-ACCCTCCATAGCCTTTCTGTTT-5'

DysRNA\_arrange\_TPM 43514186\_22 TTTGTCTTTCCGATGCCTCCCA

target id: NTTN90\_mRNA\_82331\_cds

516 5'-AGGGATGGGTGGCATCGGTAAGACAACTTTAG-3' 547 cleavage site: 532

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3'-ACCCTCCGTAGCCTTTCTGTTT-5'

DysRNA\_arrange\_TPM 41911182\_21 TTGTCTTTCCGATACCTCCCA

target id: NTTN90\_mRNA\_82331\_cds

516 5'-AGGGATGGGTGGCATCGGTAAGACAACTTTA-3' 546 cleavage site: 531

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3'-ACCCTCCATAGCCTTTCTGTT-5'

DysRNA\_arrange\_TPM 43513291\_22 TTTGTCTTTCCGATGCCTCCCT

target id: NTTN90\_mRNA\_82331\_cds

516 5'-AGGGATGGGTGGCATCGGTAAGACAACTTTAG-3' 547 cleavage site: 532

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3'-TCCCTCCGTAGCCTTTCTGTTT-5'

DysRNA\_arrange\_TPM 15928038\_22 ATAGAATAATTATGAATGTGCT

target id: NTBX\_mRNA\_124800\_cds

2178 5'-ATCATGTCGCATTCATAATTA-TCTATATCAT-3' 2208 cleavage site: 2193

|o|||||||||||| |||||

3'-TCGTGTAAGTATTAATAAGATA-5'

DysRNA\_arrange\_TPM 40742547\_22 TTACCTGAACCTGGCATACCAA

target id: NTTN90\_mRNA\_37813\_cds

1449 5'-GATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

||||| |||||||||o|||||

3'-AACCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40741736\_21 TTACCTGAACCTGGCATACCA

target id: NTTN90\_mRNA\_37813\_cds

1450 5'-ATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

||||| |||||||||o|||||

3'-ACCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40740236\_21 TTACCTGAACCTGGCATACCT

target id: NTTN90\_mRNA\_37813\_cds

1450 5'-ATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

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3'-TCCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40741593\_20 TTACCTGAACCTGGCATACC

target id: NTTN90\_mRNA\_37813\_cds

1451 5'-TCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

|||| |||||||||o|||||

3'-CCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40742348\_23 TTACCTGAACCTGGCATACCAAA

target id: NTTN90\_mRNA\_37813\_cds

1448 5'-CGATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

||||| |||||||||o|||||

3'-AAACCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40740693\_23 TTACCTGAACCTGGCATACCAAT

target id: NTTN90\_mRNA\_37813\_cds

1448 5'-CGATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

||||| |||||||||o|||||

3'-TAACCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 35450798\_21 TACCTGAACCTGGCATACCAA

target id: NTTN90\_mRNA\_37813\_cds

1449 5'-GATCACTGGTACGCCAGGTTCGGGTAAAACT-3' 1479 cleavage site: 1464

||||| |||||||||o||||

3'-AACCATACGGTCCAAGTCCAT-5'

DysRNA\_arrange\_TPM 40740134\_22 TTACCTGAACCTGGCATACCAT

target id: NTTN90\_mRNA\_37813\_cds

1449 5'-GATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

||||| |||||||||o|||||

3'-TACCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40741540\_22 TTACCTGAACCTGGCATACCTT

target id: NTTN90\_mRNA\_37813\_cds

1449 5'-GATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

|||| |||||||||o|||||

3'-TTCCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40742481\_23 TTACCTGAACCTGGCATACCATT

target id: NTTN90\_mRNA\_37813\_cds

1448 5'-CGATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

||||| |||||||||o|||||

3'-TTACCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40741489\_20 TTACCTGAACCTGGCATACT

target id: NTTN90\_mRNA\_37813\_cds

1451 5'-TCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

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3'-TCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40742536\_21 TTACCTGAACCTGGCATACCG

target id: NTTN90\_mRNA\_37813\_cds

1450 5'-ATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

o|||| |||||||||o|||||

3'-GCCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40742033\_21 TTACCTGAACCTGGCATACCC

target id: NTTN90\_mRNA\_37813\_cds

1450 5'-ATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

|||| |||||||||o|||||

3'-CCCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40739408\_23 TTACCTGAACCTGGCATACCAAG

target id: NTTN90\_mRNA\_37813\_cds

1448 5'-CGATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

||||| |||||||||o|||||

3'-GAACCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 43050316\_22 TTTACCTGAACCTGGCATACCA

target id: NTTN90\_mRNA\_37813\_cds

1450 5'-ATCACTGGTACGCCAGGTTCGGGTAAAACTAC-3' 1481 cleavage site: 1466

||||| |||||||||o||||||

3'-ACCATACGGTCCAAGTCCATTT-5'

DysRNA\_arrange\_TPM 40741174\_22 TTACCTGAACCTGGCATACCAG

target id: NTTN90\_mRNA\_37813\_cds

1449 5'-GATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

|||||| |||||||||o|||||

3'-GACCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 43050143\_24 TTTACCTGAACCTGGCATACCAAC

target id: NTTN90\_mRNA\_37813\_cds

1448 5'-CGATCACTGGTACGCCAGGTTCGGGTAAAACTAC-3' 1481 cleavage site: 1466

||||| |||||||||o||||||

3'-CAACCATACGGTCCAAGTCCATTT-5'

DysRNA\_arrange\_TPM 35450403\_20 TACCTGAACCTGGCATACCA

target id: NTTN90\_mRNA\_37813\_cds

1450 5'-ATCACTGGTACGCCAGGTTCGGGTAAAACT-3' 1479 cleavage site: 1464

||||| |||||||||o||||

3'-ACCATACGGTCCAAGTCCAT-5'

DysRNA\_arrange\_TPM 40739753\_22 TTACCTGAACCTGGCATACCTA

target id: NTTN90\_mRNA\_37813\_cds

1449 5'-GATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

|||| |||||||||o|||||

3'-ATCCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40742347\_21 TTACCTGAACCTGGCATACTT

target id: NTTN90\_mRNA\_37813\_cds

1450 5'-ATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

o||| |||||||||o|||||

3'-TTCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40741291\_23 TTACCTGAACCTGGCATACCATC

target id: NTTN90\_mRNA\_37813\_cds

1448 5'-CGATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

||||| |||||||||o|||||

3'-CTACCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40739574\_21 TTACCTGAACCTGGCATACTA

target id: NTTN90\_mRNA\_37813\_cds

1450 5'-ATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

|o||| |||||||||o|||||

3'-ATCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40742607\_22 TTACCTGAACCTGGTATACCAA

target id: NTTN90\_mRNA\_37813\_cds

1449 5'-GATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

||||| o||||||||o|||||

3'-AACCATATGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40665598\_22 TTACATGAACCTGGCATACCAA

target id: NTTN90\_mRNA\_37813\_cds

1449 5'-GATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

||||| |||||||||o ||||

3'-AACCATACGGTCCAAGTACATT-5'

DysRNA\_arrange\_TPM 43050825\_21 TTTACCTGAACCTGGCATACC

target id: NTTN90\_mRNA\_37813\_cds

1451 5'-TCACTGGTACGCCAGGTTCGGGTAAAACTAC-3' 1481 cleavage site: 1466

|||| |||||||||o||||||

3'-CCATACGGTCCAAGTCCATTT-5'

DysRNA\_arrange\_TPM 40741435\_21 TTACCTGAACCTGACATACCA

target id: NTTN90\_mRNA\_37813\_cds

1450 5'-ATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

||||| | |||||||o|||||

3'-ACCATACAGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40742312\_23 TTACCTGAACCTGGCATACCAAC

target id: NTTN90\_mRNA\_37813\_cds

1448 5'-CGATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

||||| |||||||||o|||||

3'-CAACCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40739464\_22 TTACCTGAACCTGGCATACCAC

target id: NTTN90\_mRNA\_37813\_cds

1449 5'-GATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

||||| |||||||||o|||||

3'-CACCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40740425\_22 TTACCTGAACCTGACATACCAA

target id: NTTN90\_mRNA\_37813\_cds

1449 5'-GATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

||||| | |||||||o|||||

3'-AACCATACAGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 35450164\_20 TACCTGAACCTGGCATACCT

target id: NTTN90\_mRNA\_37813\_cds

1450 5'-ATCACTGGTACGCCAGGTTCGGGTAAAACT-3' 1479 cleavage site: 1464

|||| |||||||||o||||

3'-TCCATACGGTCCAAGTCCAT-5'

DysRNA\_arrange\_TPM 43050821\_23 TTTACCTGAACCTGGCATACCAA

target id: NTTN90\_mRNA\_37813\_cds

1449 5'-GATCACTGGTACGCCAGGTTCGGGTAAAACTAC-3' 1481 cleavage site: 1466

||||| |||||||||o||||||

3'-AACCATACGGTCCAAGTCCATTT-5'

DysRNA\_arrange\_TPM 40740942\_22 TTACCTGAACCTGGCATAACAA

target id: NTTN90\_mRNA\_37813\_cds

1449 5'-GATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

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3'-AACAATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40741495\_22 TTACCTGAACCTGGCATACCTC

target id: NTTN90\_mRNA\_37813\_cds

1449 5'-GATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

|||| |||||||||o|||||

3'-CTCCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 43983812\_21 TTTTACCTGAACCTGGCATAC

target id: NTTN90\_mRNA\_37813\_cds

1452 5'-CACTGGTACGCCAGGTTCGGGTAAAACTACT-3' 1482 cleavage site: 1467

||| |||||||||o|||||||

3'-CATACGGTCCAAGTCCATTTT-5'

DysRNA\_arrange\_TPM 40741138\_22 TTACCTGAACCTGGCATACTTT

target id: NTTN90\_mRNA\_37813\_cds

1449 5'-GATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

o||| |||||||||o|||||

3'-TTTCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40740203\_21 TTACCTGAACCTGGCATACTC

target id: NTTN90\_mRNA\_37813\_cds

1450 5'-ATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

o||| |||||||||o|||||

3'-CTCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40740924\_20 TTACCTGAACCTGGCATACA

target id: NTTN90\_mRNA\_37813\_cds

1451 5'-TCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

||| |||||||||o|||||

3'-ACATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40742510\_22 TTACCTGAACCTGGCATTCCAA

target id: NTTN90\_mRNA\_37813\_cds

1449 5'-GATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

||| | |||||||||o|||||

3'-AACCTTACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40740451\_21 TTACCTGAACCTGGCATATCA

target id: NTTN90\_mRNA\_37813\_cds

1450 5'-ATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

||o|| |||||||||o|||||

3'-ACTATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40738063\_22 TTACCTAAACCTGGCATACCAA

target id: NTTN90\_mRNA\_37813\_cds

1449 5'-GATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

||||| |||||||| o|||||

3'-AACCATACGGTCCAAATCCATT-5'

DysRNA\_arrange\_TPM 34428539\_21 TAACCTGAACCTGGCATACCA

target id: NTTN90\_mRNA\_37813\_cds

1450 5'-ATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

||||| |||||||||o|||

3'-ACCATACGGTCCAAGTCCAAT-5'

DysRNA\_arrange\_TPM 40745342\_22 TTACCTCAACCTGGCATACCAA

target id: NTTN90\_mRNA\_37813\_cds

1449 5'-GATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

||||| |||||||| o|||||

3'-AACCATACGGTCCAACTCCATT-5'

DysRNA\_arrange\_TPM 40747677\_21 TTACCTTAACCTGGCATACCA

target id: NTTN90\_mRNA\_37813\_cds

1450 5'-ATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

||||| |||||||| o|||||

3'-ACCATACGGTCCAATTCCATT-5'

DysRNA\_arrange\_TPM 40737853\_21 TTACCTAAACCTGGCATACCA

target id: NTTN90\_mRNA\_37813\_cds

1450 5'-ATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

||||| |||||||| o|||||

3'-ACCATACGGTCCAAATCCATT-5'

DysRNA\_arrange\_TPM 40739905\_22 TTACCTGAACCTGGCATATCAA

target id: NTTN90\_mRNA\_37813\_cds

1449 5'-GATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

||o|| |||||||||o|||||

3'-AACTATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40740398\_22 TTACCTGAACCTGGCATAGCAA

target id: NTTN90\_mRNA\_37813\_cds

1449 5'-GATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

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3'-AACGATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 26914223\_21 GTACCTGAACCTGGCATACCT

target id: NTTN90\_mRNA\_37813\_cds

1450 5'-ATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

|||| |||||||||o||||

3'-TCCATACGGTCCAAGTCCATG-5'

DysRNA\_arrange\_TPM 26914450\_20 GTACCTGAACCTGGCATACC

target id: NTTN90\_mRNA\_37813\_cds

1451 5'-TCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

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3'-CCATACGGTCCAAGTCCATG-5'

DysRNA\_arrange\_TPM 40741207\_20 TTACCTGAACCTGGCATTTC

target id: NTTN90\_mRNA\_37813\_cds

1451 5'-TCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

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3'-CTTTACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 26914545\_21 GTACCTGAACCTGGCATACCA

target id: NTTN90\_mRNA\_37813\_cds

1450 5'-ATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

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3'-ACCATACGGTCCAAGTCCATG-5'

DysRNA\_arrange\_TPM 40741304\_22 TTACCTGAACCTGGCATCCCAA

target id: NTTN90\_mRNA\_37813\_cds

1449 5'-GATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

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3'-AACCCTACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40741202\_22 TTACCTGAACCTGGCATACTAA

target id: NTTN90\_mRNA\_37813\_cds

1449 5'-GATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

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3'-AATCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 16439463\_22 ATACCTGAACCTGGCATACCAA

target id: NTTN90\_mRNA\_37813\_cds

1449 5'-GATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

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3'-AACCATACGGTCCAAGTCCATA-5'

DysRNA\_arrange\_TPM 35451289\_22 TACCTGAACCTGGCATACCAAA

target id: NTTN90\_mRNA\_37813\_cds

1448 5'-CGATCACTGGTACGCCAGGTTCGGGTAAAACT-3' 1479 cleavage site: 1464

||||| |||||||||o||||

3'-AAACCATACGGTCCAAGTCCAT-5'

DysRNA\_arrange\_TPM 40741342\_22 TTACCTGAACCTGGCACACCAA

target id: NTTN90\_mRNA\_37813\_cds

1449 5'-GATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

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3'-AACCACACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40739499\_22 TTACCTGAACCTGTCATACCAA

target id: NTTN90\_mRNA\_37813\_cds

1449 5'-GATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

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3'-AACCATACTGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 35450589\_22 TACCTGAACCTGGCATACCAAT

target id: NTTN90\_mRNA\_37813\_cds

1448 5'-CGATCACTGGTACGCCAGGTTCGGGTAAAACT-3' 1479 cleavage site: 1464

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3'-TAACCATACGGTCCAAGTCCAT-5'

DysRNA\_arrange\_TPM 40741351\_22 TTACCTGAACCTGGCGTACCAA

target id: NTTN90\_mRNA\_37813\_cds

1449 5'-GATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

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3'-AACCATGCGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40717233\_22 TTACCGGAACCTGGCATACCAA

target id: NTTN90\_mRNA\_37813\_cds

1449 5'-GATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

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3'-AACCATACGGTCCAAGGCCATT-5'

DysRNA\_arrange\_TPM 40747954\_22 TTACCTTAACCTGGCATACCAA

target id: NTTN90\_mRNA\_37813\_cds

1449 5'-GATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

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3'-AACCATACGGTCCAATTCCATT-5'

DysRNA\_arrange\_TPM 36635486\_21 TGACCTGAACCTGGCATACCA

target id: NTTN90\_mRNA\_37813\_cds

1450 5'-ATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

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3'-ACCATACGGTCCAAGTCCAGT-5'

DysRNA\_arrange\_TPM 40741331\_21 TTACCTGAACCTGGCATCCCT

target id: NTTN90\_mRNA\_37813\_cds

1450 5'-ATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

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3'-TCCCTACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 26914581\_22 GTACCTGAACCTGGCATACCAA

target id: NTTN90\_mRNA\_37813\_cds

1449 5'-GATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

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3'-AACCATACGGTCCAAGTCCATG-5'

DysRNA\_arrange\_TPM 40742285\_22 TTACCTGAACCTGGCATACTTC

target id: NTTN90\_mRNA\_37813\_cds

1449 5'-GATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

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3'-CTTCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40741688\_22 TTACCTGAACCTGGCATGCCAA

target id: NTTN90\_mRNA\_37813\_cds

1449 5'-GATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

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3'-AACCGTACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40727231\_22 TTACCCGAACCTGGCATACCAA

target id: NTTN90\_mRNA\_37813\_cds

1449 5'-GATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

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3'-AACCATACGGTCCAAGCCCATT-5'

DysRNA\_arrange\_TPM 40745543\_21 TTACCTCAACCTGGCATACCA

target id: NTTN90\_mRNA\_37813\_cds

1450 5'-ATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

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3'-ACCATACGGTCCAACTCCATT-5'

DysRNA\_arrange\_TPM 40785222\_22 TTACTTGAACCTGGCATACCAA

target id: NTTN90\_mRNA\_37813\_cds

1449 5'-GATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

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3'-AACCATACGGTCCAAGTTCATT-5'

DysRNA\_arrange\_TPM 40741094\_23 TTACCTGAACCTGGCATACCACT

target id: NTTN90\_mRNA\_37813\_cds

1448 5'-CGATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

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3'-TCACCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40739650\_22 TTACCTGAACCTGGCTTACCAA

target id: NTTN90\_mRNA\_37813\_cds

1449 5'-GATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

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3'-AACCATTCGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40932757\_22 TTATCTGAACCTGGCATACCAA

target id: NTTN90\_mRNA\_37813\_cds

1449 5'-GATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

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3'-AACCATACGGTCCAAGTCTATT-5'

DysRNA\_arrange\_TPM 40740779\_22 TTACCTGAACCTGGCATACCCT

target id: NTTN90\_mRNA\_37813\_cds

1449 5'-GATCACTGGTACGCCAGGTTCGGGTAAAACTA-3' 1480 cleavage site: 1465

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3'-TCCCATACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 27959210\_20 GTTGTTTTGAGTTTGAGGCC

target id: NTTN90\_mRNA\_81051\_cds

1349 5'-TTGATTGCATTAAACTCAAAA-AATTGCCA-3' 1377 cleavage site: 1362

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3'-CCGGAGTTTGAGTTTTGTTG-5'

DysRNA\_arrange\_TPM 43983812\_21 TTTTACCTGAACCTGGCATAC

target id: NTTN90\_mRNA\_63335\_cds

1926 5'-CACTGGCATGCCGGGTTCGGGTAAAACTACT-3' 1956 cleavage site: 1941

|||||o|||||o|||||||

3'-CATACGGTCCAAGTCCATTTT-5'

DysRNA\_arrange\_TPM 40741688\_22 TTACCTGAACCTGGCATGCCAA

target id: NTTN90\_mRNA\_63335\_cds

1923 5'-GATCACTGGCATGCCGGGTTCGGGTAAAACTA-3' 1954 cleavage site: 1939

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3'-AACCGTACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40727231\_22 TTACCCGAACCTGGCATACCAA

target id: NTTN90\_mRNA\_63335\_cds

1923 5'-GATCACTGGCATGCCGGGTTCGGGTAAAACTA-3' 1954 cleavage site: 1939

||| |||||o|||||||||||

3'-AACCATACGGTCCAAGCCCATT-5'

DysRNA\_arrange\_TPM 40741702\_22 TTACCTGAACCCGGCATACCAA

target id: NTTN90\_mRNA\_63335\_cds

1923 5'-GATCACTGGCATGCCGGGTTCGGGTAAAACTA-3' 1954 cleavage site: 1939

||| |||||||||||o|||||

3'-AACCATACGGCCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 37959495\_22 TCAAATCCAATAGTAGGTACCA

target id: NTTN90\_mRNA\_59866\_cds

2370 5'-ATTGTTGGAATCT-TTATCGGATTTGAGATTG-3' 2400 cleavage site: 2385

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3'-ACCATGGATGATAACCTAAACT-5'

DysRNA\_arrange\_TPM 37959584\_22 TCAAATCCGATAAGGGGCTCCA

target id: NTTN90\_mRNA\_59866\_cds

2370 5'-ATTGTTGGA-ATCTTTATCGGATTTGAGATTG-3' 2400 cleavage site: 2385

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3'-ACCTCGGGGAATAGCCTAAACT-5'

DysRNA\_arrange\_TPM 28460746\_21 CAAATCCGATAAGGGGCTCCA

target id: NTTN90\_mRNA\_59866\_cds

2370 5'-ATTGTTGGA-ATCTTTATCGGATTTGAGATT-3' 2399 cleavage site: 2384

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3'-ACCTCGGGGAATAGCCTAAAC-5'

DysRNA\_arrange\_TPM 02453693\_20 AAATCCGATAAGGGGCTCCA

target id: NTTN90\_mRNA\_59866\_cds

2370 5'-ATTGTTGGA-ATCTTTATCGGATTTGAGAT-3' 2398 cleavage site: 2383

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3'-ACCTCGGGGAATAGCCTAAA-5'

DysRNA\_arrange\_TPM 43983812\_21 TTTTACCTGAACCTGGCATAC

target id: NTK326\_mRNA\_53814\_cds

1380 5'-CACTGGCATGCCGGGTTCGGGTAAAACTACT-3' 1410 cleavage site: 1395

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3'-CATACGGTCCAAGTCCATTTT-5'

DysRNA\_arrange\_TPM 40741688\_22 TTACCTGAACCTGGCATGCCAA

target id: NTK326\_mRNA\_53814\_cds

1377 5'-GATCACTGGCATGCCGGGTTCGGGTAAAACTA-3' 1408 cleavage site: 1393

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3'-AACCGTACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40727231\_22 TTACCCGAACCTGGCATACCAA

target id: NTK326\_mRNA\_53814\_cds

1377 5'-GATCACTGGCATGCCGGGTTCGGGTAAAACTA-3' 1408 cleavage site: 1393

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3'-AACCATACGGTCCAAGCCCATT-5'

DysRNA\_arrange\_TPM 40741702\_22 TTACCTGAACCCGGCATACCAA

target id: NTK326\_mRNA\_53814\_cds

1377 5'-GATCACTGGCATGCCGGGTTCGGGTAAAACTA-3' 1408 cleavage site: 1393

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3'-AACCATACGGCCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 20608921\_24 ATTCTAGATCTTCTTTCACCAGTC

target id: NTTN90\_mRNA\_37809\_cds

1122 5'-AATTGGACTGGTGAAAGAAGATCTAGAATTCATA-3' 1155 cleavage site: 1140

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3'-CTGACCACTTTCTTCTAGATCTTA-5'

DysRNA\_arrange\_TPM 40506628\_21 TTAGATCTTCTTTCACCAGCT

target id: NTTN90\_mRNA\_37809\_cds

1121 5'-AAATTGGACTGGTGAAAGAAGATCTAGAATTC-3' 1152 cleavage site: 1137

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3'-TC-GACCACTTTCTTCTAGATT-5'

DysRNA\_arrange\_TPM 27959210\_20 GTTGTTTTGAGTTTGAGGCC

target id: NTBX\_mRNA\_122255\_cds

1247 5'-TTAATTGCATTAAACTCAAAA-AATTGCCA-3' 1275 cleavage site: 1260

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3'-CCGGAGTTTGAGTTTTGTTG-5'

DysRNA\_arrange\_TPM 27959210\_20 GTTGTTTTGAGTTTGAGGCC

target id: NTK326\_mRNA\_121252\_cds

1097 5'-TTAATTGCATTAAACTCAAAA-AATTGCCA-3' 1125 cleavage site: 1110

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3'-CCGGAGTTTGAGTTTTGTTG-5'

DysRNA\_arrange\_TPM 27959210\_20 GTTGTTTTGAGTTTGAGGCC

target id: NTTN90\_mRNA\_134534\_cds

1413 5'-TTAATTGCATTAAACTCAAAA-AATTGCCA-3' 1441 cleavage site: 1426

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3'-CCGGAGTTTGAGTTTTGTTG-5'

DysRNA\_arrange\_TPM 43319357\_21 TTTGGATTGAAGGGAGCTCTA

target id: NTTN90\_mRNA\_87634\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGAGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 41411013\_20 TTGGATTGAAGGGAGCTCTA

target id: NTTN90\_mRNA\_87634\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGT-3' 140 cleavage site: 125

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3'-ATCTCGAGGGAAGTTAGGTT-5'

DysRNA\_arrange\_TPM 43319585\_22 TTTGGATTGAAGGGAGCTCTAT

target id: NTTN90\_mRNA\_87634\_cds

111 5'-TTCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-TATCTCGAGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43316465\_21 TTTGGATTGAAGGGAGCTCTG

target id: NTTN90\_mRNA\_87634\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-GTCTCGAGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43316124\_21 TTTGGATTGAAGGGGGCTCTA

target id: NTTN90\_mRNA\_87634\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGGGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43315582\_22 TTTGGATTGAAGGGAGCTCTAC

target id: NTTN90\_mRNA\_87634\_cds

111 5'-TTCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-CATCTCGAGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43321659\_21 TTTGGATTGAAGGAAGCTCTA

target id: NTTN90\_mRNA\_87634\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGAAGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43317025\_21 TTTGGATTGAAGGTAGCTCTA

target id: NTTN90\_mRNA\_87634\_cds

112 5'-TCTGGTACAGTT-TCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGATGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43320131\_21 TTTGGATTGAAGTGAGCTCTA

target id: NTTN90\_mRNA\_87634\_cds

112 5'-TCTGGTACAGTTT-CTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGAGTGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43320956\_21 TTTGGATTGAAGGGAGCTGTA

target id: NTTN90\_mRNA\_87634\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATGTCGAGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43317682\_21 TTTGGATTGAAGGGAGCTATA

target id: NTTN90\_mRNA\_87634\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATATCGAGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 20002187\_21 ATTGGATTGAAGGGAGCTCTA

target id: NTTN90\_mRNA\_87634\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGAGGGAAGTTAGGTTA-5'

DysRNA\_arrange\_TPM 43317086\_21 TTTGGATTGAAGGGCGCTCTA

target id: NTTN90\_mRNA\_87634\_cds

112 5'-TCTGGTACAGT-TTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGCGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 33578164\_21 CTTGGATTGAAGGGAGCTCTA

target id: NTTN90\_mRNA\_87634\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGAGGGAAGTTAGGTTC-5'

DysRNA\_arrange\_TPM 43316328\_21 TTTGGATTGAAGGGAGCTTTA

target id: NTTN90\_mRNA\_87634\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATTTCGAGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43315028\_21 TTTGGATTGAAGGGTGCTCTA

target id: NTTN90\_mRNA\_87634\_cds

112 5'-TCTGGTACAGT-TTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGTGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 42289602\_21 TTCGGATTGAAGGGAGCTCTA

target id: NTTN90\_mRNA\_87634\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCC-AAGCTGT-3' 140 cleavage site: 125

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3'-ATCTCGAGGGAAGTTAGGCTT-5'

DysRNA\_arrange\_TPM 43317643\_23 TTTGGATTGAAGGGAGCTCTACT

target id: NTTN90\_mRNA\_87634\_cds

110 5'-TTTCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-TCATCTCGAGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43317291\_21 TTTGGATTGAAGAGAGCTCTA

target id: NTTN90\_mRNA\_87634\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGAGAGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43317729\_20 TTTGGATTGAAGGAGCTCTA

target id: NTTN90\_mRNA\_87634\_cds

112 5'-TCTGGTACAGTTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGAGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43316738\_21 TTTGGATTGAAGGGAACTCTA

target id: NTTN90\_mRNA\_87634\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCAAGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 40528105\_21 TTAGGATTGAAGGGAGCTCTA

target id: NTTN90\_mRNA\_87634\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCC-AAGCTGT-3' 140 cleavage site: 125

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3'-ATCTCGAGGGAAGTTAGGATT-5'

DysRNA\_arrange\_TPM 27871038\_21 GTTGGATTGAAGGGAGCTCTA

target id: NTTN90\_mRNA\_87634\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGAGGGAAGTTAGGTTG-5'

DysRNA\_arrange\_TPM 43321070\_21 TTTGGATTGAAGCGAGCTCTA

target id: NTTN90\_mRNA\_87634\_cds

112 5'-TCTGGTACAGTTT-CTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGAGCGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43983812\_21 TTTTACCTGAACCTGGCATAC

target id: NTBX\_mRNA\_72663\_cds

1488 5'-CACTGGCATGCCGGGTTCGGGTAAAACTACT-3' 1518 cleavage site: 1503

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3'-CATACGGTCCAAGTCCATTTT-5'

DysRNA\_arrange\_TPM 40741688\_22 TTACCTGAACCTGGCATGCCAA

target id: NTBX\_mRNA\_72663\_cds

1485 5'-GATCACTGGCATGCCGGGTTCGGGTAAAACTA-3' 1516 cleavage site: 1501

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3'-AACCGTACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40727231\_22 TTACCCGAACCTGGCATACCAA

target id: NTBX\_mRNA\_72663\_cds

1485 5'-GATCACTGGCATGCCGGGTTCGGGTAAAACTA-3' 1516 cleavage site: 1501

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3'-AACCATACGGTCCAAGCCCATT-5'

DysRNA\_arrange\_TPM 40741702\_22 TTACCTGAACCCGGCATACCAA

target id: NTBX\_mRNA\_72663\_cds

1485 5'-GATCACTGGCATGCCGGGTTCGGGTAAAACTA-3' 1516 cleavage site: 1501

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3'-AACCATACGGCCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 43983812\_21 TTTTACCTGAACCTGGCATAC

target id: NTK326\_mRNA\_53821\_cds

1167 5'-CACTGGCATGCCGGGTTCGGGTAAAACTACT-3' 1197 cleavage site: 1182

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3'-CATACGGTCCAAGTCCATTTT-5'

DysRNA\_arrange\_TPM 40741688\_22 TTACCTGAACCTGGCATGCCAA

target id: NTK326\_mRNA\_53821\_cds

1164 5'-GATCACTGGCATGCCGGGTTCGGGTAAAACTA-3' 1195 cleavage site: 1180

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3'-AACCGTACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40727231\_22 TTACCCGAACCTGGCATACCAA

target id: NTK326\_mRNA\_53821\_cds

1164 5'-GATCACTGGCATGCCGGGTTCGGGTAAAACTA-3' 1195 cleavage site: 1180

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3'-AACCATACGGTCCAAGCCCATT-5'

DysRNA\_arrange\_TPM 40741702\_22 TTACCTGAACCCGGCATACCAA

target id: NTK326\_mRNA\_53821\_cds

1164 5'-GATCACTGGCATGCCGGGTTCGGGTAAAACTA-3' 1195 cleavage site: 1180

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3'-AACCATACGGCCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 43983812\_21 TTTTACCTGAACCTGGCATAC

target id: NTBX\_mRNA\_20754\_cds

1884 5'-CACTGGCATGCCGGGTTCGGGTAAAACTACT-3' 1914 cleavage site: 1899

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3'-CATACGGTCCAAGTCCATTTT-5'

DysRNA\_arrange\_TPM 40741688\_22 TTACCTGAACCTGGCATGCCAA

target id: NTBX\_mRNA\_20754\_cds

1881 5'-GATCACTGGCATGCCGGGTTCGGGTAAAACTA-3' 1912 cleavage site: 1897

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3'-AACCGTACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40727231\_22 TTACCCGAACCTGGCATACCAA

target id: NTBX\_mRNA\_20754\_cds

1881 5'-GATCACTGGCATGCCGGGTTCGGGTAAAACTA-3' 1912 cleavage site: 1897

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3'-AACCATACGGTCCAAGCCCATT-5'

DysRNA\_arrange\_TPM 40741702\_22 TTACCTGAACCCGGCATACCAA

target id: NTBX\_mRNA\_20754\_cds

1881 5'-GATCACTGGCATGCCGGGTTCGGGTAAAACTA-3' 1912 cleavage site: 1897

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3'-AACCATACGGCCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 02767294\_21 AAGAAGATGATTATGGAGGGC

target id: NTK326\_mRNA\_72003\_cds

3471 5'-TCCAAGTGCTCCATCATCATCTTCTTCAGAT-3' 3501 cleavage site: 3486

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3'-CGGGAGGTATTAGTAGAAGAA-5'

DysRNA\_arrange\_TPM 02768834\_22 AAGAAGATGATTATGGAGGGCA

target id: NTK326\_mRNA\_72003\_cds

3470 5'-GTCCAAGTGCTCCATCATCATCTTCTTCAGAT-3' 3501 cleavage site: 3486

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3'-ACGGGAGGTATTAGTAGAAGAA-5'

DysRNA\_arrange\_TPM 40391668\_20 TTAATATTTCAGCTCGAACT

target id: NTTN90\_mRNA\_46479\_cds

715 5'-TGTGAAG-TT-A-CTGAAATATTAAATGCA-3' 741 cleavage site: 726

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3'-TCAAGCTCGACTTTATAATT-5'

DysRNA\_arrange\_TPM 20608921\_24 ATTCTAGATCTTCTTTCACCAGTC

target id: NTTN90\_mRNA\_37810\_cds

1095 5'-AATTGGACTGGTGAAAGAAGATCTAGAATTCATA-3' 1128 cleavage site: 1113

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3'-CTGACCACTTTCTTCTAGATCTTA-5'

DysRNA\_arrange\_TPM 40506628\_21 TTAGATCTTCTTTCACCAGCT

target id: NTTN90\_mRNA\_37810\_cds

1094 5'-AAATTGGACTGGTGAAAGAAGATCTAGAATTC-3' 1125 cleavage site: 1110

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3'-TC-GACCACTTTCTTCTAGATT-5'

DysRNA\_arrange\_TPM 27046016\_20 GTGAAATTCTTGGATCGTCT

target id: NTTN90\_mRNA\_42243\_cds

1522 5'-GAGAGTGAT-ATCCAAGAATTTCGATTGAA-3' 1550 cleavage site: 1535

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3'-TCTGCTAGGTTCTTAAAGTG-5'

DysRNA\_arrange\_TPM 28228704\_20 GTTTCCCGGAACACCCCCCA

target id: NTBX\_mRNA\_69716\_cds

457 5'-GGAGGTGGAGGGTGTTTAGGGAAAGCTGTG-3' 486 cleavage site: 471

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3'-ACCCCCCACAAGGCCCTTTG-5'

DysRNA\_arrange\_TPM 42440292\_21 TTCCACAGCTTTCTTTAACTG

target id: NTBX\_mRNA\_69716\_cds

464 5'-GAGGGTGTTTAGGGAAAGCTGT-GAAAAGAA-3' 493 cleavage site: 478

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3'-GTCAATTTCTTTCGACACCTT-5'

DysRNA\_arrange\_TPM 42441010\_21 TTCCACAGCTTTCTTGAAATG

target id: NTBX\_mRNA\_69716\_cds

464 5'-GAGGGTGTTTAGGGAAAGCTGT-GAAAAGAA-3' 493 cleavage site: 478

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3'-GTAAAGTTCTTTCGACACCTT-5'

DysRNA\_arrange\_TPM 19415850\_21 ATCTCCTCTACTGGCTCTCCT

target id: NTTN90\_mRNA\_54536\_cds

1587 5'-TGATAAGGAGA--CAGTAGAAGAGAGAAAGA-3' 1615 cleavage site: 1600

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3'-TCCTCTCGGTCATCTCCTCTA-5'

DysRNA\_arrange\_TPM 02940567\_21 AAGAGAGTTGGGAATTATTGC

target id: NTTN90\_mRNA\_54536\_cds

1442 5'-CAATGGCAATCTTCTTTCAACTCTCTTCACAA-3' 1473 cleavage site: 1458

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3'-CGTTATTA-AGGGTTGAGAGAA-5'

DysRNA\_arrange\_TPM 43499236\_21 TTTGTCATGATAAATAAAGTC

target id: NTBX\_mRNA\_97357\_cds

5 5'-CCAAGGACTTTATTTATCATGACAAATTGTT-3' 35 cleavage site: 20

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3'-CTGAAATAAATAGTACTGTTT-5'

DysRNA\_arrange\_TPM 43498503\_21 TTTGTCATGATGAATAAAGTC

target id: NTBX\_mRNA\_97357\_cds

5 5'-CCAAGGACTTTATTTATCATGACAAATTGTT-3' 35 cleavage site: 20

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3'-CTGAAATAAGTAGTACTGTTT-5'

DysRNA\_arrange\_TPM 07119696\_21 AATTGTCACTTGATTGTTGCA

target id: NTBX\_mRNA\_49495\_cds

1832 5'-AATGGTGCAGGAATCAAGTAACAGCTTCATCT-3' 1863 cleavage site: 1848

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3'-ACGTTGTTAGTTCACTGTT-AA-5'

DysRNA\_arrange\_TPM 27046016\_20 GTGAAATTCTTGGATCGTCT

target id: NTBX\_mRNA\_49495\_cds

898 5'-GAGAGTGAT-ATCCAAGAATTTCGATTGAA-3' 926 cleavage site: 911

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3'-TCTGCTAGGTTCTTAAAGTG-5'

DysRNA\_arrange\_TPM 15928038\_22 ATAGAATAATTATGAATGTGCT

target id: NTBX\_mRNA\_124795\_cds

2307 5'-ATCATGTCGCATTCATAATTA-TCTATATCAT-3' 2337 cleavage site: 2322

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3'-TCGTGTAAGTATTAATAAGATA-5'

DysRNA\_arrange\_TPM 02767294\_21 AAGAAGATGATTATGGAGGGC

target id: NTTN90\_mRNA\_63311\_cds

2931 5'-TTCAAGTGCTCTATCATCATCTTCTTCAGAT-3' 2961 cleavage site: 2946

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3'-CGGGAGGTATTAGTAGAAGAA-5'

DysRNA\_arrange\_TPM 38561019\_24 TCGAAGAAGATGATGAATAGTAGT

target id: NTTN90\_mRNA\_63311\_cds

2933 5'-CAAGTGCT-CTA-TCATCATCTTCTTCAGATCTGA-3' 2965 cleavage site: 2950

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3'-TGATGATAAGTAGTAGAAGAAG-CT-5'

DysRNA\_arrange\_TPM 24021801\_23 GGAGAAGATGATGAATAGTAATT

target id: NTTN90\_mRNA\_63311\_cds

2929 5'-AGTTCAAGTGCTCTATCATCATCTTCTTCAGATC-3' 2962 cleavage site: 2947

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3'-TTAATGATA-AGTAGTAGAAGAGG-5'

DysRNA\_arrange\_TPM 41343934\_21 TTGGAGAAGATGATGAATAGT

target id: NTTN90\_mRNA\_63311\_cds

2935 5'-AGTGCTCTA-TCATCATCTTCTTCAGATCTG-3' 2964 cleavage site: 2949

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3'-TGATAAGTAGTAGAAGAGGTT-5'

DysRNA\_arrange\_TPM 24023543\_24 GGAGAAGATGATGAATAGTAATTG

target id: NTTN90\_mRNA\_63311\_cds

2928 5'-AAGTTCAAGTGCTCTATCATCATCTTCTTCAGATC-3' 2962 cleavage site: 2947

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3'-GTTAATGATA-AGTAGTAGAAGAGG-5'

DysRNA\_arrange\_TPM 02768834\_22 AAGAAGATGATTATGGAGGGCA

target id: NTTN90\_mRNA\_63311\_cds

2930 5'-GTTCAAGTGCTCTATCATCATCTTCTTCAGAT-3' 2961 cleavage site: 2946

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3'-ACGGGAGGTATTAGTAGAAGAA-5'

DysRNA\_arrange\_TPM 27959210\_20 GTTGTTTTGAGTTTGAGGCC

target id: NTK326\_mRNA\_121253\_cds

1247 5'-TTAATTGCATTAAACTCAAAA-AATTGCCA-3' 1275 cleavage site: 1260

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3'-CCGGAGTTTGAGTTTTGTTG-5'

DysRNA\_arrange\_TPM 08965277\_24 AGATTTAGGCAAATGGAAAGAACT

target id: NTBX\_mRNA\_125078\_cds

1928 5'-AATTGAGTTCATTTCATTTGCC-AAATCCTCCAA-3' 1960 cleavage site: 1945

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3'-TCAAGAAAGGTAAACGGATTTAGA-5'

DysRNA\_arrange\_TPM 43880920\_20 TTTCTCTTTTTATTTATCGT

target id: NTBX\_mRNA\_125078\_cds

2599 5'-ATTCAAC-ATGAACAAAAAGAGAACCTCGG-3' 2627 cleavage site: 2612

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3'-TGCTATTTATTTTTCTCTTT-5'

DysRNA\_arrange\_TPM 08965277\_24 AGATTTAGGCAAATGGAAAGAACT

target id: NTK326\_mRNA\_123992\_cds

1868 5'-AATTGAGTTCATTTCATTTGCC-AAATCCTCCAA-3' 1900 cleavage site: 1885

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3'-TCAAGAAAGGTAAACGGATTTAGA-5'

DysRNA\_arrange\_TPM 43880920\_20 TTTCTCTTTTTATTTATCGT

target id: NTK326\_mRNA\_123992\_cds

2539 5'-ATTCAAC-ATGAACAAAAAGAGAACCTCGG-3' 2567 cleavage site: 2552

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3'-TGCTATTTATTTTTCTCTTT-5'

DysRNA\_arrange\_TPM 27959210\_20 GTTGTTTTGAGTTTGAGGCC

target id: NTBX\_mRNA\_91409\_cds

1100 5'-TTGATTGCATTAAACTCAAAA-AATTGCCA-3' 1128 cleavage site: 1113

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3'-CCGGAGTTTGAGTTTTGTTG-5'

DysRNA\_arrange\_TPM 08965277\_24 AGATTTAGGCAAATGGAAAGAACT

target id: NTK326\_mRNA\_123993\_cds

1868 5'-AATTGAGTTCATTTCATTTGCC-AAATCCTCCAA-3' 1900 cleavage site: 1885

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3'-TCAAGAAAGGTAAACGGATTTAGA-5'

DysRNA\_arrange\_TPM 43983812\_21 TTTTACCTGAACCTGGCATAC

target id: NTBX\_mRNA\_20755\_cds

1932 5'-CACTGGCATGCCGGGTTCGGGTAAAACTACT-3' 1962 cleavage site: 1947

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3'-CATACGGTCCAAGTCCATTTT-5'

DysRNA\_arrange\_TPM 40741688\_22 TTACCTGAACCTGGCATGCCAA

target id: NTBX\_mRNA\_20755\_cds

1929 5'-GATCACTGGCATGCCGGGTTCGGGTAAAACTA-3' 1960 cleavage site: 1945

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3'-AACCGTACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40727231\_22 TTACCCGAACCTGGCATACCAA

target id: NTBX\_mRNA\_20755\_cds

1929 5'-GATCACTGGCATGCCGGGTTCGGGTAAAACTA-3' 1960 cleavage site: 1945

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3'-AACCATACGGTCCAAGCCCATT-5'

DysRNA\_arrange\_TPM 40741702\_22 TTACCTGAACCCGGCATACCAA

target id: NTBX\_mRNA\_20755\_cds

1929 5'-GATCACTGGCATGCCGGGTTCGGGTAAAACTA-3' 1960 cleavage site: 1945

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3'-AACCATACGGCCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 27046016\_20 GTGAAATTCTTGGATCGTCT

target id: NTTN90\_mRNA\_42242\_cds

1522 5'-GAGAGTGAT-ATCCAAGAATTTCGATTGAA-3' 1550 cleavage site: 1535

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3'-TCTGCTAGGTTCTTAAAGTG-5'

DysRNA\_arrange\_TPM 15928038\_22 ATAGAATAATTATGAATGTGCT

target id: NTTN90\_mRNA\_117647\_cds

2307 5'-ATCATGTCGCATTCATAATTA-TCTATATCAT-3' 2337 cleavage site: 2322

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3'-TCGTGTAAGTATTAATAAGATA-5'

DysRNA\_arrange\_TPM 28228704\_20 GTTTCCCGGAACACCCCCCA

target id: NTK326\_mRNA\_69163\_cds

457 5'-GGAGGTGGAGGGTGTTTAGGGAAAGCTGTG-3' 486 cleavage site: 471

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3'-ACCCCCCACAAGGCCCTTTG-5'

DysRNA\_arrange\_TPM 42440292\_21 TTCCACAGCTTTCTTTAACTG

target id: NTK326\_mRNA\_69163\_cds

464 5'-GAGGGTGTTTAGGGAAAGCTGT-GAAAAGAA-3' 493 cleavage site: 478

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3'-GTCAATTTCTTTCGACACCTT-5'

DysRNA\_arrange\_TPM 42441010\_21 TTCCACAGCTTTCTTGAAATG

target id: NTK326\_mRNA\_69163\_cds

464 5'-GAGGGTGTTTAGGGAAAGCTGT-GAAAAGAA-3' 493 cleavage site: 478

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3'-GTAAAGTTCTTTCGACACCTT-5'

DysRNA\_arrange\_TPM 02767294\_21 AAGAAGATGATTATGGAGGGC

target id: NTTN90\_mRNA\_6839\_cds

2430 5'-TTCAAGTGCTCCATCATCATCTTCTTCAGAT-3' 2460 cleavage site: 2445

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3'-CGGGAGGTATTAGTAGAAGAA-5'

DysRNA\_arrange\_TPM 02768834\_22 AAGAAGATGATTATGGAGGGCA

target id: NTTN90\_mRNA\_6839\_cds

2429 5'-GTTCAAGTGCTCCATCATCATCTTCTTCAGAT-3' 2460 cleavage site: 2445

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3'-ACGGGAGGTATTAGTAGAAGAA-5'

DysRNA\_arrange\_TPM 43983812\_21 TTTTACCTGAACCTGGCATAC

target id: NTTN90\_mRNA\_63334\_cds

1488 5'-CACTGGCATGCCGGGTTCGGGTAAAACTACT-3' 1518 cleavage site: 1503

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3'-CATACGGTCCAAGTCCATTTT-5'

DysRNA\_arrange\_TPM 40741688\_22 TTACCTGAACCTGGCATGCCAA

target id: NTTN90\_mRNA\_63334\_cds

1485 5'-GATCACTGGCATGCCGGGTTCGGGTAAAACTA-3' 1516 cleavage site: 1501

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3'-AACCGTACGGTCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 40727231\_22 TTACCCGAACCTGGCATACCAA

target id: NTTN90\_mRNA\_63334\_cds

1485 5'-GATCACTGGCATGCCGGGTTCGGGTAAAACTA-3' 1516 cleavage site: 1501

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3'-AACCATACGGTCCAAGCCCATT-5'

DysRNA\_arrange\_TPM 40741702\_22 TTACCTGAACCCGGCATACCAA

target id: NTTN90\_mRNA\_63334\_cds

1485 5'-GATCACTGGCATGCCGGGTTCGGGTAAAACTA-3' 1516 cleavage site: 1501

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3'-AACCATACGGCCCAAGTCCATT-5'

DysRNA\_arrange\_TPM 28228704\_20 GTTTCCCGGAACACCCCCCA

target id: NTTN90\_mRNA\_60680\_cds

457 5'-GGAGGTGGAGGGTGTTTAGGGAAAGCTGTG-3' 486 cleavage site: 471

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3'-ACCCCCCACAAGGCCCTTTG-5'

DysRNA\_arrange\_TPM 42440292\_21 TTCCACAGCTTTCTTTAACTG

target id: NTTN90\_mRNA\_60680\_cds

464 5'-GAGGGTGTTTAGGGAAAGCTGT-GAAAAGAA-3' 493 cleavage site: 478

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3'-GTCAATTTCTTTCGACACCTT-5'

DysRNA\_arrange\_TPM 42441010\_21 TTCCACAGCTTTCTTGAAATG

target id: NTTN90\_mRNA\_60680\_cds

464 5'-GAGGGTGTTTAGGGAAAGCTGT-GAAAAGAA-3' 493 cleavage site: 478

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3'-GTAAAGTTCTTTCGACACCTT-5'

DysRNA\_arrange\_TPM 19415850\_21 ATCTCCTCTACTGGCTCTCCT

target id: NTTN90\_mRNA\_54533\_cds

639 5'-TGATAAGGAGA--CAGTAGAAGAGAGAAAGA-3' 667 cleavage site: 652

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3'-TCCTCTCGGTCATCTCCTCTA-5'

DysRNA\_arrange\_TPM 02940567\_21 AAGAGAGTTGGGAATTATTGC

target id: NTTN90\_mRNA\_54533\_cds

494 5'-CAATGGCAATCTTCTTTCAACTCTCTTCACAA-3' 525 cleavage site: 510

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3'-CGTTATTA-AGGGTTGAGAGAA-5'

DysRNA\_arrange\_TPM 02767294\_21 AAGAAGATGATTATGGAGGGC

target id: NTBX\_mRNA\_81028\_cds

1659 5'-TTCAAGTGCTCCATCATCATCTTCTTCAGAT-3' 1689 cleavage site: 1674

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3'-CGGGAGGTATTAGTAGAAGAA-5'

DysRNA\_arrange\_TPM 02768834\_22 AAGAAGATGATTATGGAGGGCA

target id: NTBX\_mRNA\_81028\_cds

1658 5'-GTTCAAGTGCTCCATCATCATCTTCTTCAGAT-3' 1689 cleavage site: 1674

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3'-ACGGGAGGTATTAGTAGAAGAA-5'

DysRNA\_arrange\_TPM 08965277\_24 AGATTTAGGCAAATGGAAAGAACT

target id: NTTN90\_mRNA\_109400\_cds

1868 5'-AATTGAGTTCATTTCATTTGCC-AAATCCTCCAA-3' 1900 cleavage site: 1885

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3'-TCAAGAAAGGTAAACGGATTTAGA-5'

DysRNA\_arrange\_TPM 43880920\_20 TTTCTCTTTTTATTTATCGT

target id: NTTN90\_mRNA\_109400\_cds

2539 5'-ATTCAAC-ATGAACAAAAAGAGAACCTCGG-3' 2567 cleavage site: 2552

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3'-TGCTATTTATTTTTCTCTTT-5'

DysRNA\_arrange\_TPM 43319357\_21 TTTGGATTGAAGGGAGCTCTA

target id: NTK326\_mRNA\_95709\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGAGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 41411013\_20 TTGGATTGAAGGGAGCTCTA

target id: NTK326\_mRNA\_95709\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGT-3' 140 cleavage site: 125

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3'-ATCTCGAGGGAAGTTAGGTT-5'

DysRNA\_arrange\_TPM 43319585\_22 TTTGGATTGAAGGGAGCTCTAT

target id: NTK326\_mRNA\_95709\_cds

111 5'-TTCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-TATCTCGAGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43316465\_21 TTTGGATTGAAGGGAGCTCTG

target id: NTK326\_mRNA\_95709\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-GTCTCGAGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43316124\_21 TTTGGATTGAAGGGGGCTCTA

target id: NTK326\_mRNA\_95709\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGGGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43315582\_22 TTTGGATTGAAGGGAGCTCTAC

target id: NTK326\_mRNA\_95709\_cds

111 5'-TTCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-CATCTCGAGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43321659\_21 TTTGGATTGAAGGAAGCTCTA

target id: NTK326\_mRNA\_95709\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGAAGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43317025\_21 TTTGGATTGAAGGTAGCTCTA

target id: NTK326\_mRNA\_95709\_cds

112 5'-TCTGGTACAGTT-TCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGATGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43320131\_21 TTTGGATTGAAGTGAGCTCTA

target id: NTK326\_mRNA\_95709\_cds

112 5'-TCTGGTACAGTTT-CTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGAGTGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43320956\_21 TTTGGATTGAAGGGAGCTGTA

target id: NTK326\_mRNA\_95709\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATGTCGAGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43317682\_21 TTTGGATTGAAGGGAGCTATA

target id: NTK326\_mRNA\_95709\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATATCGAGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 20002187\_21 ATTGGATTGAAGGGAGCTCTA

target id: NTK326\_mRNA\_95709\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGAGGGAAGTTAGGTTA-5'

DysRNA\_arrange\_TPM 43317086\_21 TTTGGATTGAAGGGCGCTCTA

target id: NTK326\_mRNA\_95709\_cds

112 5'-TCTGGTACAGT-TTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGCGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 33578164\_21 CTTGGATTGAAGGGAGCTCTA

target id: NTK326\_mRNA\_95709\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGAGGGAAGTTAGGTTC-5'

DysRNA\_arrange\_TPM 43316328\_21 TTTGGATTGAAGGGAGCTTTA

target id: NTK326\_mRNA\_95709\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATTTCGAGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43315028\_21 TTTGGATTGAAGGGTGCTCTA

target id: NTK326\_mRNA\_95709\_cds

112 5'-TCTGGTACAGT-TTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGTGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 42289602\_21 TTCGGATTGAAGGGAGCTCTA

target id: NTK326\_mRNA\_95709\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCC-AAGCTGT-3' 140 cleavage site: 125

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3'-ATCTCGAGGGAAGTTAGGCTT-5'

DysRNA\_arrange\_TPM 43317643\_23 TTTGGATTGAAGGGAGCTCTACT

target id: NTK326\_mRNA\_95709\_cds

110 5'-TTTCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-TCATCTCGAGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43317291\_21 TTTGGATTGAAGAGAGCTCTA

target id: NTK326\_mRNA\_95709\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGAGAGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43317729\_20 TTTGGATTGAAGGAGCTCTA

target id: NTK326\_mRNA\_95709\_cds

112 5'-TCTGGTACAGTTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGAGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43316738\_21 TTTGGATTGAAGGGAACTCTA

target id: NTK326\_mRNA\_95709\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCAAGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 40528105\_21 TTAGGATTGAAGGGAGCTCTA

target id: NTK326\_mRNA\_95709\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCC-AAGCTGT-3' 140 cleavage site: 125

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3'-ATCTCGAGGGAAGTTAGGATT-5'

DysRNA\_arrange\_TPM 27871038\_21 GTTGGATTGAAGGGAGCTCTA

target id: NTK326\_mRNA\_95709\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGAGGGAAGTTAGGTTG-5'

DysRNA\_arrange\_TPM 43321070\_21 TTTGGATTGAAGCGAGCTCTA

target id: NTK326\_mRNA\_95709\_cds

112 5'-TCTGGTACAGTTT-CTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGAGCGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 27959210\_20 GTTGTTTTGAGTTTGAGGCC

target id: NTK326\_mRNA\_95709\_cds

1916 5'-TTGATTGCATTAAACTCAAAA-AATTGCCA-3' 1944 cleavage site: 1929

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3'-CCGGAGTTTGAGTTTTGTTG-5'

DysRNA\_arrange\_TPM 02767294\_21 AAGAAGATGATTATGGAGGGC

target id: NTTN90\_mRNA\_63305\_cds

3012 5'-TTCAAGTGCTCTATCATCATCTTCTTCAGAT-3' 3042 cleavage site: 3027

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3'-CGGGAGGTATTAGTAGAAGAA-5'

DysRNA\_arrange\_TPM 38561019\_24 TCGAAGAAGATGATGAATAGTAGT

target id: NTTN90\_mRNA\_63305\_cds

3014 5'-CAAGTGCT-CTA-TCATCATCTTCTTCAGATCTGA-3' 3046 cleavage site: 3031

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3'-TGATGATAAGTAGTAGAAGAAG-CT-5'

DysRNA\_arrange\_TPM 24021801\_23 GGAGAAGATGATGAATAGTAATT

target id: NTTN90\_mRNA\_63305\_cds

3010 5'-AGTTCAAGTGCTCTATCATCATCTTCTTCAGATC-3' 3043 cleavage site: 3028

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3'-TTAATGATA-AGTAGTAGAAGAGG-5'

DysRNA\_arrange\_TPM 41343934\_21 TTGGAGAAGATGATGAATAGT

target id: NTTN90\_mRNA\_63305\_cds

3016 5'-AGTGCTCTA-TCATCATCTTCTTCAGATCTG-3' 3045 cleavage site: 3030

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3'-TGATAAGTAGTAGAAGAGGTT-5'

DysRNA\_arrange\_TPM 24023543\_24 GGAGAAGATGATGAATAGTAATTG

target id: NTTN90\_mRNA\_63305\_cds

3009 5'-AAGTTCAAGTGCTCTATCATCATCTTCTTCAGATC-3' 3043 cleavage site: 3028

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3'-GTTAATGATA-AGTAGTAGAAGAGG-5'

DysRNA\_arrange\_TPM 02768834\_22 AAGAAGATGATTATGGAGGGCA

target id: NTTN90\_mRNA\_63305\_cds

3011 5'-GTTCAAGTGCTCTATCATCATCTTCTTCAGAT-3' 3042 cleavage site: 3027

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3'-ACGGGAGGTATTAGTAGAAGAA-5'

DysRNA\_arrange\_TPM 02767294\_21 AAGAAGATGATTATGGAGGGC

target id: NTTN90\_mRNA\_63326\_cds

2841 5'-TTCAAGTGCTCCATCATCATCTTCTTCAGAT-3' 2871 cleavage site: 2856

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3'-CGGGAGGTATTAGTAGAAGAA-5'

DysRNA\_arrange\_TPM 31162881\_20 CGTTGCTGCGATGATTCATG

target id: NTTN90\_mRNA\_63326\_cds

3513 5'-TGAACTA-GAAATCATCGCAGTAACTTTTCA-3' 3542 cleavage site: 3527

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3'-GTAC-TTAGTAGCGTCGTTGC-5'

DysRNA\_arrange\_TPM 27913008\_20 GTTGCTGCGATGATTCATGA

target id: NTTN90\_mRNA\_63326\_cds

3512 5'-ATGAACTA-GAAATCATCGCAGTAACTTTTC-3' 3541 cleavage site: 3526

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3'-AGTAC-TTAGTAGCGTCGTTG-5'

DysRNA\_arrange\_TPM 02768834\_22 AAGAAGATGATTATGGAGGGCA

target id: NTTN90\_mRNA\_63326\_cds

2840 5'-GTTCAAGTGCTCCATCATCATCTTCTTCAGAT-3' 2871 cleavage site: 2856

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3'-ACGGGAGGTATTAGTAGAAGAA-5'

DysRNA\_arrange\_TPM 15928038\_22 ATAGAATAATTATGAATGTGCT

target id: NTTN90\_mRNA\_117652\_cds

2178 5'-ATCATGTCGCATTCATAATTA-TCTATATCAT-3' 2208 cleavage site: 2193

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3'-TCGTGTAAGTATTAATAAGATA-5'

DysRNA\_arrange\_TPM 43319357\_21 TTTGGATTGAAGGGAGCTCTA

target id: NTBX\_mRNA\_122258\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGAGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 41411013\_20 TTGGATTGAAGGGAGCTCTA

target id: NTBX\_mRNA\_122258\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGT-3' 140 cleavage site: 125

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3'-ATCTCGAGGGAAGTTAGGTT-5'

DysRNA\_arrange\_TPM 43319585\_22 TTTGGATTGAAGGGAGCTCTAT

target id: NTBX\_mRNA\_122258\_cds

111 5'-TTCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-TATCTCGAGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43316465\_21 TTTGGATTGAAGGGAGCTCTG

target id: NTBX\_mRNA\_122258\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-GTCTCGAGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43316124\_21 TTTGGATTGAAGGGGGCTCTA

target id: NTBX\_mRNA\_122258\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGGGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43315582\_22 TTTGGATTGAAGGGAGCTCTAC

target id: NTBX\_mRNA\_122258\_cds

111 5'-TTCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-CATCTCGAGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43321659\_21 TTTGGATTGAAGGAAGCTCTA

target id: NTBX\_mRNA\_122258\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGAAGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43317025\_21 TTTGGATTGAAGGTAGCTCTA

target id: NTBX\_mRNA\_122258\_cds

112 5'-TCTGGTACAGTT-TCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGATGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43320131\_21 TTTGGATTGAAGTGAGCTCTA

target id: NTBX\_mRNA\_122258\_cds

112 5'-TCTGGTACAGTTT-CTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGAGTGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43320956\_21 TTTGGATTGAAGGGAGCTGTA

target id: NTBX\_mRNA\_122258\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATGTCGAGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43317682\_21 TTTGGATTGAAGGGAGCTATA

target id: NTBX\_mRNA\_122258\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATATCGAGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 20002187\_21 ATTGGATTGAAGGGAGCTCTA

target id: NTBX\_mRNA\_122258\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGAGGGAAGTTAGGTTA-5'

DysRNA\_arrange\_TPM 43317086\_21 TTTGGATTGAAGGGCGCTCTA

target id: NTBX\_mRNA\_122258\_cds

112 5'-TCTGGTACAGT-TTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGCGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 33578164\_21 CTTGGATTGAAGGGAGCTCTA

target id: NTBX\_mRNA\_122258\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGAGGGAAGTTAGGTTC-5'

DysRNA\_arrange\_TPM 43316328\_21 TTTGGATTGAAGGGAGCTTTA

target id: NTBX\_mRNA\_122258\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATTTCGAGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43315028\_21 TTTGGATTGAAGGGTGCTCTA

target id: NTBX\_mRNA\_122258\_cds

112 5'-TCTGGTACAGT-TTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGTGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 42289602\_21 TTCGGATTGAAGGGAGCTCTA

target id: NTBX\_mRNA\_122258\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCC-AAGCTGT-3' 140 cleavage site: 125

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3'-ATCTCGAGGGAAGTTAGGCTT-5'

DysRNA\_arrange\_TPM 43317643\_23 TTTGGATTGAAGGGAGCTCTACT

target id: NTBX\_mRNA\_122258\_cds

110 5'-TTTCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-TCATCTCGAGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43317291\_21 TTTGGATTGAAGAGAGCTCTA

target id: NTBX\_mRNA\_122258\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGAGAGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43317729\_20 TTTGGATTGAAGGAGCTCTA

target id: NTBX\_mRNA\_122258\_cds

112 5'-TCTGGTACAGTTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGAGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43316738\_21 TTTGGATTGAAGGGAACTCTA

target id: NTBX\_mRNA\_122258\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCAAGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 40528105\_21 TTAGGATTGAAGGGAGCTCTA

target id: NTBX\_mRNA\_122258\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCC-AAGCTGT-3' 140 cleavage site: 125

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3'-ATCTCGAGGGAAGTTAGGATT-5'

DysRNA\_arrange\_TPM 27871038\_21 GTTGGATTGAAGGGAGCTCTA

target id: NTBX\_mRNA\_122258\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGAGGGAAGTTAGGTTG-5'

DysRNA\_arrange\_TPM 43321070\_21 TTTGGATTGAAGCGAGCTCTA

target id: NTBX\_mRNA\_122258\_cds

112 5'-TCTGGTACAGTTT-CTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGAGCGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 27046016\_20 GTGAAATTCTTGGATCGTCT

target id: NTTN90\_mRNA\_42244\_cds

1183 5'-GAGAGTGAT-ATCCAAGAATTTCGATTGAA-3' 1211 cleavage site: 1196

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3'-TCTGCTAGGTTCTTAAAGTG-5'

DysRNA\_arrange\_TPM 15928038\_22 ATAGAATAATTATGAATGTGCT

target id: NTBX\_mRNA\_124794\_cds

2532 5'-ATCATGTCGCATTCATAATTA-TCTATATCAT-3' 2562 cleavage site: 2547

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3'-TCGTGTAAGTATTAATAAGATA-5'

DysRNA\_arrange\_TPM 02767294\_21 AAGAAGATGATTATGGAGGGC

target id: NTK326\_mRNA\_72004\_cds

3177 5'-TCCAAGTGCTCCATCATCATCTTCTTCAGAT-3' 3207 cleavage site: 3192

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3'-CGGGAGGTATTAGTAGAAGAA-5'

DysRNA\_arrange\_TPM 02768834\_22 AAGAAGATGATTATGGAGGGCA

target id: NTK326\_mRNA\_72004\_cds

3176 5'-GTCCAAGTGCTCCATCATCATCTTCTTCAGAT-3' 3207 cleavage site: 3192

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3'-ACGGGAGGTATTAGTAGAAGAA-5'

DysRNA\_arrange\_TPM 02767294\_21 AAGAAGATGATTATGGAGGGC

target id: NTK326\_mRNA\_72002\_cds

2529 5'-TCCAAGTGCTCCATCATCATCTTCTTCAGAT-3' 2559 cleavage site: 2544

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3'-CGGGAGGTATTAGTAGAAGAA-5'

DysRNA\_arrange\_TPM 02768834\_22 AAGAAGATGATTATGGAGGGCA

target id: NTK326\_mRNA\_72002\_cds

2528 5'-GTCCAAGTGCTCCATCATCATCTTCTTCAGAT-3' 2559 cleavage site: 2544

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3'-ACGGGAGGTATTAGTAGAAGAA-5'

DysRNA\_arrange\_TPM 43963689\_22 TTTTAGCCAGAGTTGTTTTCCC

target id: NTK326\_mRNA\_99998\_cds

26 5'-GCATAGGGAAAACAACTCTGGC-AAAAGCTAT-3' 56 cleavage site: 41

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3'-CCCTTTTGTTGAGACCGATTTT-5'

DysRNA\_arrange\_TPM 42993390\_21 TTTAGCCAGAGTTGTTTTCCC

target id: NTK326\_mRNA\_99998\_cds

26 5'-GCATAGGGAAAACAACTCTGGC-AAAAGCTA-3' 55 cleavage site: 40

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3'-CCCTTTTGTTGAGACCGATTT-5'

DysRNA\_arrange\_TPM 43964061\_21 TTTTAGCCAGAGTTGTTTTCC

target id: NTK326\_mRNA\_99998\_cds

27 5'-CATAGGGAAAACAACTCTGGC-AAAAGCTAT-3' 56 cleavage site: 41

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3'-CCTTTTGTTGAGACCGATTTT-5'

DysRNA\_arrange\_TPM 43499236\_21 TTTGTCATGATAAATAAAGTC

target id: NTK326\_mRNA\_49586\_cds

5 5'-CCAAGGACTTTATTTATCATGACAAATTGTT-3' 35 cleavage site: 20

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3'-CTGAAATAAATAGTACTGTTT-5'

DysRNA\_arrange\_TPM 43498503\_21 TTTGTCATGATGAATAAAGTC

target id: NTK326\_mRNA\_49586\_cds

5 5'-CCAAGGACTTTATTTATCATGACAAATTGTT-3' 35 cleavage site: 20

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3'-CTGAAATAAGTAGTACTGTTT-5'

DysRNA\_arrange\_TPM 39918426\_21 TCTCGTTGAAATCTAGCTACC

target id: NTK326\_mRNA\_49586\_cds

1546 5'-AGCTTGGT-GATCGTTTTCAACGAGAGAGGT-3' 1575 cleavage site: 1560

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3'-CCATCGATCTAAAGTTGCTCT-5'

DysRNA\_arrange\_TPM 43963689\_22 TTTTAGCCAGAGTTGTTTTCCC

target id: NTTN90\_mRNA\_54399\_cds

152 5'-GCATAGGAAAAACAACTCTGGC-AAAAGCTAT-3' 182 cleavage site: 167

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3'-CCCTTTTGTTGAGACCGATTTT-5'

DysRNA\_arrange\_TPM 40391668\_20 TTAATATTTCAGCTCGAACT

target id: NTTN90\_mRNA\_54399\_cds

841 5'-CGTGTAG-TT-A-CTGAAATATTAAATGCA-3' 867 cleavage site: 852

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3'-TCAAGCTCGACTTTATAATT-5'

DysRNA\_arrange\_TPM 42993390\_21 TTTAGCCAGAGTTGTTTTCCC

target id: NTTN90\_mRNA\_54399\_cds

152 5'-GCATAGGAAAAACAACTCTGGC-AAAAGCTA-3' 181 cleavage site: 166

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3'-CCCTTTTGTTGAGACCGATTT-5'

DysRNA\_arrange\_TPM 43964061\_21 TTTTAGCCAGAGTTGTTTTCC

target id: NTTN90\_mRNA\_54399\_cds

152 5'-GCATAGGAAAAACAACTCTGGC-AAAAGCTAT-3' 182 cleavage site: 167

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3'-CC-TTTTGTTGAGACCGATTTT-5'

DysRNA\_arrange\_TPM 43319357\_21 TTTGGATTGAAGGGAGCTCTA

target id: NTTN90\_mRNA\_106750\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGAGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 41411013\_20 TTGGATTGAAGGGAGCTCTA

target id: NTTN90\_mRNA\_106750\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGT-3' 140 cleavage site: 125

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3'-ATCTCGAGGGAAGTTAGGTT-5'

DysRNA\_arrange\_TPM 43319585\_22 TTTGGATTGAAGGGAGCTCTAT

target id: NTTN90\_mRNA\_106750\_cds

111 5'-TTCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-TATCTCGAGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43316465\_21 TTTGGATTGAAGGGAGCTCTG

target id: NTTN90\_mRNA\_106750\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-GTCTCGAGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43316124\_21 TTTGGATTGAAGGGGGCTCTA

target id: NTTN90\_mRNA\_106750\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGGGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43315582\_22 TTTGGATTGAAGGGAGCTCTAC

target id: NTTN90\_mRNA\_106750\_cds

111 5'-TTCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-CATCTCGAGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43321659\_21 TTTGGATTGAAGGAAGCTCTA

target id: NTTN90\_mRNA\_106750\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGAAGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43317025\_21 TTTGGATTGAAGGTAGCTCTA

target id: NTTN90\_mRNA\_106750\_cds

112 5'-TCTGGTACAGTT-TCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGATGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43320131\_21 TTTGGATTGAAGTGAGCTCTA

target id: NTTN90\_mRNA\_106750\_cds

112 5'-TCTGGTACAGTTT-CTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGAGTGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43320956\_21 TTTGGATTGAAGGGAGCTGTA

target id: NTTN90\_mRNA\_106750\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATGTCGAGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43317682\_21 TTTGGATTGAAGGGAGCTATA

target id: NTTN90\_mRNA\_106750\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATATCGAGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 20002187\_21 ATTGGATTGAAGGGAGCTCTA

target id: NTTN90\_mRNA\_106750\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGAGGGAAGTTAGGTTA-5'

DysRNA\_arrange\_TPM 43317086\_21 TTTGGATTGAAGGGCGCTCTA

target id: NTTN90\_mRNA\_106750\_cds

112 5'-TCTGGTACAGT-TTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGCGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 33578164\_21 CTTGGATTGAAGGGAGCTCTA

target id: NTTN90\_mRNA\_106750\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGAGGGAAGTTAGGTTC-5'

DysRNA\_arrange\_TPM 43316328\_21 TTTGGATTGAAGGGAGCTTTA

target id: NTTN90\_mRNA\_106750\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATTTCGAGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43315028\_21 TTTGGATTGAAGGGTGCTCTA

target id: NTTN90\_mRNA\_106750\_cds

112 5'-TCTGGTACAGT-TTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGTGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 42289602\_21 TTCGGATTGAAGGGAGCTCTA

target id: NTTN90\_mRNA\_106750\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCC-AAGCTGT-3' 140 cleavage site: 125

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3'-ATCTCGAGGGAAGTTAGGCTT-5'

DysRNA\_arrange\_TPM 43317643\_23 TTTGGATTGAAGGGAGCTCTACT

target id: NTTN90\_mRNA\_106750\_cds

110 5'-TTTCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-TCATCTCGAGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43317291\_21 TTTGGATTGAAGAGAGCTCTA

target id: NTTN90\_mRNA\_106750\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGAGAGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43317729\_20 TTTGGATTGAAGGAGCTCTA

target id: NTTN90\_mRNA\_106750\_cds

112 5'-TCTGGTACAGTTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGAGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 43316738\_21 TTTGGATTGAAGGGAACTCTA

target id: NTTN90\_mRNA\_106750\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCAAGGGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 40528105\_21 TTAGGATTGAAGGGAGCTCTA

target id: NTTN90\_mRNA\_106750\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCC-AAGCTGT-3' 140 cleavage site: 125

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3'-ATCTCGAGGGAAGTTAGGATT-5'

DysRNA\_arrange\_TPM 27871038\_21 GTTGGATTGAAGGGAGCTCTA

target id: NTTN90\_mRNA\_106750\_cds

112 5'-TCTGGTACAG-TTTCTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGAGGGAAGTTAGGTTG-5'

DysRNA\_arrange\_TPM 43321070\_21 TTTGGATTGAAGCGAGCTCTA

target id: NTTN90\_mRNA\_106750\_cds

112 5'-TCTGGTACAGTTT-CTTCAATCCAAGCTGTA-3' 141 cleavage site: 126

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3'-ATCTCGAGCGAAGTTAGGTTT-5'

DysRNA\_arrange\_TPM 27959210\_20 GTTGTTTTGAGTTTGAGGCC

target id: NTTN90\_mRNA\_106747\_cds

1247 5'-TTAATTGCATTAAACTCAAAA-AATTGCCA-3' 1275 cleavage site: 1260

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3'-CCGGAGTTTGAGTTTTGTTG-5'

DysRNA\_arrange\_TPM 02767294\_21 AAGAAGATGATTATGGAGGGC

target id: NTTN90\_mRNA\_63328\_cds

3567 5'-TTCAAGTGCTCCATCATCATCTTCTTCAGAT-3' 3597 cleavage site: 3582

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3'-CGGGAGGTATTAGTAGAAGAA-5'

DysRNA\_arrange\_TPM 31162881\_20 CGTTGCTGCGATGATTCATG

target id: NTTN90\_mRNA\_63328\_cds

4239 5'-TGAACTA-GAAATCATCGCAGTAACTTTTCA-3' 4268 cleavage site: 4253

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3'-GTAC-TTAGTAGCGTCGTTGC-5'

DysRNA\_arrange\_TPM 27913008\_20 GTTGCTGCGATGATTCATGA

target id: NTTN90\_mRNA\_63328\_cds

4238 5'-ATGAACTA-GAAATCATCGCAGTAACTTTTC-3' 4267 cleavage site: 4252

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3'-AGTAC-TTAGTAGCGTCGTTG-5'

DysRNA\_arrange\_TPM 02768834\_22 AAGAAGATGATTATGGAGGGCA

target id: NTTN90\_mRNA\_63328\_cds

3566 5'-GTTCAAGTGCTCCATCATCATCTTCTTCAGAT-3' 3597 cleavage site: 3582

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3'-ACGGGAGGTATTAGTAGAAGAA-5'

DysRNA\_arrange\_TPM 27959210\_20 GTTGTTTTGAGTTTGAGGCC

target id: NTTN90\_mRNA\_106745\_cds

1097 5'-TTAATTGCATTAAACTCAAAA-AATTGCCA-3' 1125 cleavage site: 1110

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3'-CCGGAGTTTGAGTTTTGTTG-5'

Supplemental data 2 (b) tomato sRNA and NLR target alignment

D51\_TPM.filter 26469771\_21 TTTCCAATTCCACCCATTCCC

target id: Solyc01g008800.1.1

675 5'-GATCTGGGGCATGGGGGGAATTGGTAAGACGAC-3' 707 cleavage site: 692

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3'-CCCT-TACCCACCTTAACC-TTT-5'

D51\_TPM.filter 15303725\_21 GTTGCTGGCTTCACTGTGTGA

target id: Solyc01g008800.1.1

3879 5'-CTCCGTCAC-CAATGAAGCCAGTTGCTCCTC-3' 3908 cleavage site: 3893

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3'-AGTGTGTCACTTCGGTCGTTG-5'

D51\_TPM.filter 24955707\_21 TTGCCATGTTTCTCAAACACG

target id: Solyc01g008800.1.1

3950 5'-TAGCCCGTCTCTTCAGAAACATTGCAACTCTT-3' 3981 cleavage site: 3966

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3'-GCACA-AACTCTTTGTACCGTT-5'

D51\_TPM.filter 26469519\_22 TTTCCAATTCCACCCATTCCCA

target id: Solyc01g008800.1.1

674 5'-GGATCTGGGGCATGGGGGGAATTGGTAAGACGAC-3' 707 cleavage site: 692

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3'-ACCCT-TACCCACCTTAACC-TTT-5'

D51\_TPM.filter 20736031\_21 TATTTCTGGAAAGATTCTTCT

target id: Solyc11g011090.1.1

7171 5'-AGTTTAGAA-AA-TTTTCCAGAAATCACCGG-3' 7199 cleavage site: 7184

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3'-TCTTCTTAGAAAGGTCTTTAT-5'

D51\_TPM.filter 26295007\_21 TTTGTCGTCTAAAAACTAGAG

target id: Solyc11g011090.1.1

6400 5'-GATTGCTCTAG--TTTAGA-GA-AAATTCCG-3' 6426 cleavage site: 6411

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3'-GAGATCAAAAATCTGCTGTTT-5'

D51\_TPM.filter 25755064\_21 TTTAAATGACGTGGAAACTCT

target id: Solyc11g011080.1.1

2935 5'-CTGCCAGAATTTCCACGGCAATTAGACACAA-3' 2965 cleavage site: 2950

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3'-TCTCAAAGGTGCAGTAAATTT-5'

D51\_TPM.filter 25490144\_21 TTCCATGATCTTCTGAGCTTC

target id: Solyc11g011080.1.1

482 5'-TGAATGAA-CTAGTGAAGATCATGGAATGCAA-3' 512 cleavage site: 497

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3'-CTTCGAGT-CTTCTAGTACCTT-5'

D51\_TPM.filter 16350356\_22 CATCTGTTCTACTTTCATTGGT

target id: Solyc11g011080.1.1

120 5'-TGGGAATGAATTGAAGATAGAACAGATGAATCT-3' 152 cleavage site: 137

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3'-TGGTT-ACTTTCATCTTGTCTAC-5'

D51\_TPM.filter 25585965\_21 TTCTACTTCCATTACCAAACC

target id: Solyc11g011350.1.1

1089 5'-TGGTTGGTTTGGTAATGGCAGCAGAATTGTT-3' 1119 cleavage site: 1104

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3'-CCAAACCATTACCTTCATCTT-5'

D51\_TPM.filter 25585868\_22 TTCTACTTCCATTACCAAACCA

target id: Solyc11g011350.1.1

1088 5'-TTGGTTGGTTTGGTAATGGCAGCAGAATTGTT-3' 1119 cleavage site: 1104

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3'-ACCAAACCATTACCTTCATCTT-5'

D51\_TPM.filter 23336413\_21 TCTACTTCCATTACCAAACCA

target id: Solyc11g011350.1.1

1088 5'-TTGGTTGGTTTGGTAATGGCAGCAGAATTGT-3' 1118 cleavage site: 1103

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3'-ACCAAACCATTACCTTCATCT-5'

D51\_TPM.filter 25585907\_21 TTCTACTTCCATTACCAAACT

target id: Solyc11g011350.1.1

1089 5'-TGGTTGGTTTGGTAATGGCAGCAGAATTGTT-3' 1119 cleavage site: 1104

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3'-TCAAACCATTACCTTCATCTT-5'

D51\_TPM.filter 23721561\_22 TCTTTCCTACTCCTCCCATACC

target id: Solyc05g006630.2.1

679 5'-TGTACGGAATGGGAGGAGTGGGCAAGACCACT-3' 710 cleavage site: 695

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3'-CCATACCCTCCTCATCCTTTCT-5'

D51\_TPM.filter 23721573\_22 TCTTTCCTACTCCTCCCATACT

target id: Solyc05g006630.2.1

679 5'-TGTACGGAATGGGAGGAGTGGGCAAGACCACT-3' 710 cleavage site: 695

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3'-TCATACCCTCCTCATCCTTTCT-5'

D51\_TPM.filter 03891831\_24 AGAAAGACTGTTTCTGATAGACGG

target id: Solyc05g006630.2.1

4173 5'-GCGGATGGTCTATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-GGCAGATAGTCTTTGTCAGAAAGA-5'

D51\_TPM.filter 04105884\_24 AGAGAGGTTGTTTCTGATAGACGT

target id: Solyc05g006630.2.1

4172 5'-TGCGGATGGTCTATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-TG-CAGATAGTCTTTGTTGGAGAGA-5'

D51\_TPM.filter 23720788\_20 TCTTTCCTACTCCTCCCATA

target id: Solyc05g006630.2.1

681 5'-TACGGAATGGGAGGAGTGGGCAAGACCACT-3' 710 cleavage site: 695

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3'-ATACCCTCCTCATCCTTTCT-5'

D51\_TPM.filter 08114450\_24 ATAGAGTGGTTGTTTCTGAAAGAC

target id: Solyc05g006630.2.1

4175 5'-GGATGGTCTATCAGAAACAATCTCTCTACCTTCT-3' 4208 cleavage site: 4193

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3'-CAGAAAGTCTTTGTTGGTGAGATA-5'

D51\_TPM.filter 04118657\_24 AGAGACGTTGTTTCTGATAGAACG

target id: Solyc05g006630.2.1

4173 5'-GCGGATGGTCTATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-GCAAGATAGTCTTTGTTGCAGAGA-5'

D51\_TPM.filter 04102043\_23 AGAGAGATTGTTTCTGATAGACC

target id: Solyc05g006630.2.1

4174 5'-CGGATGGTCTATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-CCAGATAGTCTTTGTTAGAGAGA-5'

D51\_TPM.filter 04105614\_24 AGAGAGGTTGTTTCTGATAGACGC

target id: Solyc05g006630.2.1

4173 5'-GCGGATGGTCTATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-CGCAGATAGTCTTTGTTGGAGAGA-5'

D51\_TPM.filter 04150134\_24 AGAGATTGTTTCTAGAGTAGAACA

target id: Solyc05g006630.2.1

4173 5'-GCGGATGGTCTA-TC-AGAAACAATCTCTCTACC-3' 4204 cleavage site: 4189

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3'-ACAAGATGAGATCTTTGTTAGAGA-5'

D51\_TPM.filter 03895766\_24 AGAAAGGATTGTTTCTGATAGACC

target id: Solyc05g006630.2.1

4174 5'-CGGATGGTCTATCAGAAACAA-TCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-CCAGATAGTCTTTGTTAGGAAAGA-5'

D51\_TPM.filter 04194430\_24 AGAGGTTGTTTCTGATAGACGTTC

target id: Solyc05g006630.2.1

4170 5'-AATGCGGATGGTCTATCAGAAACAATCTCTCTACC-3' 4204 cleavage site: 4189

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3'-CTTG-CAGATAGTCTTTGTTGGAGA-5'

D51\_TPM.filter 04119374\_24 AGAGACGTTGTTTCTGATAGAACA

target id: Solyc05g006630.2.1

4173 5'-GCGGATGGTCTATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-ACAAGATAGTCTTTGTTGCAGAGA-5'

D51\_TPM.filter 03891018\_24 AGAAAGACTGTTTCTGATAGACGA

target id: Solyc05g006630.2.1

4173 5'-GCGGATGGTCTATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-AGCAGATAGTCTTTGTCAGAAAGA-5'

D51\_TPM.filter 04128258\_24 AGAGACTGTTTCCGATAGACGTTC

target id: Solyc05g006630.2.1

4170 5'-AATGCGGATGGTCTATCAGAAACAATCTCTCTACC-3' 4204 cleavage site: 4189

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3'-CTTG-CAGATAGCCTTTGTCAGAGA-5'

D51\_TPM.filter 14624692\_22 GTATTTTGAGCATGTAGACATG

target id: Solyc05g006630.2.1

3404 5'-TTTGGTATGTTTACATGCTGCAAACTGCTCCGC-3' 3436 cleavage site: 3421

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3'-GTACAGATGTACGA-GTTTTATG-5'

D51\_TPM.filter 04100338\_24 AGAGAGACTGTTTCCGAAAGACCT

target id: Solyc05g006630.2.1

4173 5'-GCGGATGGTCTATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-TCCAGAAAGCCTTTGTCAGAGAGA-5'

D51\_TPM.filter 19690207\_24 TAGAAAGATTGTTTCCGATAAGAC

target id: Solyc05g006630.2.1

4175 5'-GGATGGTC-TATCAGAAACAATCTCTCTACCTTC-3' 4207 cleavage site: 4192

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3'-CAGAATAGCCTTTGTTAGAAAGAT-5'

D51\_TPM.filter 03893284\_24 AGAAAGACTGTTTCTGATAGACGT

target id: Solyc05g006630.2.1

4172 5'-TGCGGATGGTCTATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-TG-CAGATAGTCTTTGTCAGAAAGA-5'

D51\_TPM.filter 03895968\_24 AGAAAGGATTGTTTCTGATAGACT

target id: Solyc05g006630.2.1

4174 5'-CGGATGGTCTATCAGAAACAA-TCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-TCAGATAGTCTTTGTTAGGAAAGA-5'

D51\_TPM.filter 03894391\_24 AGAAAGATTGTTTCCGATAAGACC

target id: Solyc05g006630.2.1

4174 5'-CGGATGGTC-TATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-CCAGAATAGCCTTTGTTAGAAAGA-5'

D51\_TPM.filter 23721641\_22 TCTTTCCTACTCCTCCCATGCC

target id: Solyc05g006630.2.1

679 5'-TGTACGGAATGGGAGGAGTGGGCAAGACCACT-3' 710 cleavage site: 695

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3'-CCGTACCCTCCTCATCCTTTCT-5'

D51\_TPM.filter 12134699\_24 GAGAGATTGTTTCTGAAAGACTAT

target id: Solyc05g006630.2.1

4172 5'-TGCGGATGGTCTATCAGAAACAATCTCTCTACCT-3' 4205 cleavage site: 4190

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3'-TATCAGAAAGTCTTTGTTAGAGAG-5'

D51\_TPM.filter 12134986\_24 GAGAGATTGTTTCTGATAGACTTC

target id: Solyc05g006630.2.1

4171 5'-ATGCGGATGGTCTATCAGAAACAATCTCTCTACCT-3' 4205 cleavage site: 4190

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3'-CT-TCAGATAGTCTTTGTTAGAGAG-5'

D51\_TPM.filter 04101898\_24 AGAGAGATTGTTTCTGATAGACCC

target id: Solyc05g006630.2.1

4173 5'-GCGGATGGTCTATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-CCCAGATAGTCTTTGTTAGAGAGA-5'

D51\_TPM.filter 04415961\_24 AGACTGTTTCTGATAGACCTCGGC

target id: Solyc05g006630.2.1

4168 5'-TAAATGCGGATGGTCTATCAGAAACAATCTCTCTA-3' 4202 cleavage site: 4187

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3'-CGGCT-CCAGATAGTCTTTGTCAGA-5'

D51\_TPM.filter 23720544\_22 TCTTTCCTGCTCCTCCCATACC

target id: Solyc05g006630.2.1

679 5'-TGTACGGAATGGGAGGAGTGGGCAAGACCACT-3' 710 cleavage site: 695

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3'-CCATACCCTCCTCGTCCTTTCT-5'

D51\_TPM.filter 23720488\_22 TCTTTCCTACTCCTCCCGTACC

target id: Solyc05g006630.2.1

679 5'-TGTACGGAATGGGAGGAGTGGGCAAGACCACT-3' 710 cleavage site: 695

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3'-CCATGCCCTCCTCATCCTTTCT-5'

D51\_TPM.filter 12143148\_24 GAGAGGTTGTTTCTGATAGACGTT

target id: Solyc05g006630.2.1

4171 5'-ATGCGGATGGTCTATCAGAAACAATCTCTCTACCT-3' 4205 cleavage site: 4190

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3'-TTG-CAGATAGTCTTTGTTGGAGAG-5'

D51\_TPM.filter 03902786\_24 AGAAAGTTTGTTTCTGATAGACGT

target id: Solyc05g006630.2.1

4172 5'-TGCGGATGGTCTATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-TG-CAGATAGTCTTTGTTTGAAAGA-5'

D51\_TPM.filter 23720639\_22 TCTTTCCTACTCCTCCCATATC

target id: Solyc05g006630.2.1

679 5'-TGTACGGAATGGGAGGAGTGGGCAAGACCACT-3' 710 cleavage site: 695

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3'-CTATACCCTCCTCATCCTTTCT-5'

D51\_TPM.filter 23720411\_22 TCTTTCCCACTCCTCCCATACC

target id: Solyc05g006630.2.1

679 5'-TGTACGGAATGGGAGGAGTGGGCAAGACCACT-3' 710 cleavage site: 695

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3'-CCATACCCTCCTCACCCTTTCT-5'

D51\_TPM.filter 12134806\_24 GAGAGATTGTTTCTGATAGACCAT

target id: Solyc05g006630.2.1

4172 5'-TGCGGATGGTCTATCAGAAACAATCTCTCTACCT-3' 4205 cleavage site: 4190

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3'-TACCAGATAGTCTTTGTTAGAGAG-5'

D51\_TPM.filter 23721096\_21 TCTTTCCTACTCCTCCCATAC

target id: Solyc05g006630.2.1

680 5'-GTACGGAATGGGAGGAGTGGGCAAGACCACT-3' 710 cleavage site: 695

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3'-CATACCCTCCTCATCCTTTCT-5'

D51\_TPM.filter 04551713\_24 AGATGTTGTTTCTGATAGACCCGT

target id: Solyc05g006630.2.1

4172 5'-TGCGGAT-GGTCTATCAGAAACAATCTCTCTACC-3' 4204 cleavage site: 4189

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3'-TGCCCAGATAGTCTTTGTTGTAGA-5'

D51\_TPM.filter 11762965\_24 GAAAGACTGTTTCTGAAAGACTAT

target id: Solyc05g006630.2.1

4172 5'-TGCGGATGGTCTATCAGAAACAATCTCTCTACCT-3' 4205 cleavage site: 4190

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3'-TATCAGAAAGTCTTTGTCAGAAAG-5'

D51\_TPM.filter 04150041\_24 AGAGATTGTTTCTGATAGACCATC

target id: Solyc05g006630.2.1

4171 5'-ATGCGGATGGTCTATCAGAAACAATCTCTCTACC-3' 4204 cleavage site: 4189

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3'-CTACCAGATAGTCTTTGTTAGAGA-5'

D51\_TPM.filter 13022104\_24 GGAGAGGTTGTTTCTGATAGACGT

target id: Solyc05g006630.2.1

4172 5'-TGCGGATGGTCTATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-TG-CAGATAGTCTTTGTTGGAGAGG-5'

D51\_TPM.filter 04550849\_24 AGATGTTGTTTCTGATAGACCCTC

target id: Solyc05g006630.2.1

4171 5'-ATGCGGATGGTCTATCAGAAACAATCTCTCTACC-3' 4204 cleavage site: 4189

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3'-CTCCCAGATAGTCTTTGTTGTAGA-5'

D51\_TPM.filter 23583218\_22 TCTCTCCTACTCCTCCCATACC

target id: Solyc05g006630.2.1

679 5'-TGTACGGAATGGGAGGAGTGGGCA-AGACCACT-3' 710 cleavage site: 695

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3'-CCATACCCTCCTCATCC-TCTCT-5'

D51\_TPM.filter 01550132\_23 AAGACTGTTTCTGAAAGACTATC

target id: Solyc05g006630.2.1

4171 5'-ATGCGGATGGTCTATCAGAAACAATCTCTCTAC-3' 4203 cleavage site: 4188

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3'-CTATCAGAAAGTCTTTGTCAGAA-5'

D51\_TPM.filter 03895569\_24 AGAAAGATTGTTTCCGATAAGACT

target id: Solyc05g006630.2.1

4174 5'-CGGATGGTC-TATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-TCAGAATAGCCTTTGTTAGAAAGA-5'

D51\_TPM.filter 23681971\_22 TCTTCCCTACTCCTCCCATACC

target id: Solyc05g006630.2.1

679 5'-TGTACGGAATGGGAGGAGTGGGCAAGACCACT-3' 710 cleavage site: 695

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3'-CCATACCCTCCTCATCCCTTCT-5'

D51\_TPM.filter 03892961\_24 AGAAAGACTGTTTTTGATAGACCT

target id: Solyc05g006630.2.1

4173 5'-GCGGATGGTCTATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-TCCAGATAGTTTTTGTCAGAAAGA-5'

D51\_TPM.filter 04150597\_24 AGAGATTGATTCTGATAGATTAAG

target id: Solyc05g006630.2.1

4171 5'-ATGCGGATGGTCTATCAGAAACAATCTCTCTACC-3' 4204 cleavage site: 4189

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3'-GAATTAGATAGTCTTAGTTAGAGA-5'

D51\_TPM.filter 04128232\_23 AGAGACTGTTTCCGATAGACGTT

target id: Solyc05g006630.2.1

4171 5'-ATGCGGATGGTCTATCAGAAACAATCTCTCTACC-3' 4204 cleavage site: 4189

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3'-TTG-CAGATAGCCTTTGTCAGAGA-5'

D51\_TPM.filter 04099040\_24 AGAGAGACTGTTTTCGATAGATCC

target id: Solyc05g006630.2.1

4173 5'-GCGGATGGTCTATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-CCTAGATAGCTTTTGTCAGAGAGA-5'

D51\_TPM.filter 04102608\_23 AGAGAGATTGTTTCTGATAGATC

target id: Solyc05g006630.2.1

4174 5'-CGGATGGTCTATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-CTAGATAGTCTTTGTTAGAGAGA-5'

D51\_TPM.filter 04127744\_24 AGAGACTGTTTCTGATAAACCTTT

target id: Solyc05g006630.2.1

4170 5'-AATGCGGATGGTCTATCAGAAACAATCTCTCTACC-3' 4204 cleavage site: 4189

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3'-TTT-CCAAATAGTCTTTGTCAGAGA-5'

D51\_TPM.filter 04148791\_24 AGAGATTGTTTCTGATAGACTTCA

target id: Solyc05g006630.2.1

4170 5'-AATGCGGATGGTCTATCAGAAACAATCTCTCTACC-3' 4204 cleavage site: 4189

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3'-ACT-TCAGATAGTCTTTGTTAGAGA-5'

D51\_TPM.filter 04101122\_24 AGAGAGATTGTTTCTGATAGACCA

target id: Solyc05g006630.2.1

4173 5'-GCGGATGGTCTATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-ACCAGATAGTCTTTGTTAGAGAGA-5'

D51\_TPM.filter 04194591\_23 AGAGGTTGTTTCTGATAGACGTT

target id: Solyc05g006630.2.1

4171 5'-ATGCGGATGGTCTATCAGAAACAATCTCTCTACC-3' 4204 cleavage site: 4189

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3'-TTG-CAGATAGTCTTTGTTGGAGA-5'

D51\_TPM.filter 03895727\_23 AGAAAGATTGTTTCTGATAGACT

target id: Solyc05g006630.2.1

4174 5'-CGGATGGTCTATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-TCAGATAGTCTTTGTTAGAAAGA-5'

D51\_TPM.filter 14438775\_24 GTAGAGAGATTGTTTCTGATAGAT

target id: Solyc05g006630.2.1

4175 5'-GGATGGTCTATCAGAAACAATCTCTCTACCTTCT-3' 4208 cleavage site: 4193

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3'-TAGATAGTCTTTGTTAGAGAGATG-5'

D51\_TPM.filter 04100957\_24 AGAGAGACTGTTTCCAATAGACCC

target id: Solyc05g006630.2.1

4173 5'-GCGGATGGTCTATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-CCCAGATAACCTTTGTCAGAGAGA-5'

D51\_TPM.filter 04149726\_24 AGAGATTGTTTCTGATAGACCCTC

target id: Solyc05g006630.2.1

4171 5'-ATGCGGATGGTCTATCAGAAACAATCTCTCTACC-3' 4204 cleavage site: 4189

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3'-CTCCCAGATAGTCTTTGTTAGAGA-5'

D51\_TPM.filter 03894700\_24 AGAAAGATTGTTTCTGATAGACTC

target id: Solyc05g006630.2.1

4173 5'-GCGGATGGTCTATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-CTCAGATAGTCTTTGTTAGAAAGA-5'

D51\_TPM.filter 04101801\_24 AGAGAGATTGTTTCTGATAGATTC

target id: Solyc05g006630.2.1

4173 5'-GCGGATGGTCTATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-CTTAGATAGTCTTTGTTAGAGAGA-5'

D51\_TPM.filter 04902030\_24 AGGATTGTTTCTGATAGACCTTCA

target id: Solyc05g006630.2.1

4169 5'-AAATGCGGATGGTCTATCAGAAACAATCTCTCTAC-3' 4203 cleavage site: 4188

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3'-ACTT-CCAGATAGTCTTTGTTAGGA-5'

D51\_TPM.filter 04105464\_24 AGAGAGGTTGTTTCTGAACAGACA

target id: Solyc05g006630.2.1

4174 5'-CGGATGGTCT-ATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-ACAGACAAGTCTTTGTTGGAGAGA-5'

D51\_TPM.filter 01728719\_24 AAGGATTGTTTCTGATAGATTATC

target id: Solyc05g006630.2.1

4171 5'-ATGCGGATGGTCTATCAGAAACAATCTCTCTACC-3' 4204 cleavage site: 4189

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3'-CTATTAGATAGTCTTTGTTAGGAA-5'

D51\_TPM.filter 12100626\_24 GAGAAAGATTGTTTCTGATAGACT

target id: Solyc05g006630.2.1

4174 5'-CGGATGGTCTATCAGAAACAATCTCTCTACCTTC-3' 4207 cleavage site: 4192

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3'-TCAGATAGTCTTTGTTAGAAAGAG-5'

D51\_TPM.filter 23720275\_22 TCTTTCCCACTCCTCCCATACT

target id: Solyc05g006630.2.1

679 5'-TGTACGGAATGGGAGGAGTGGGCAAGACCACT-3' 710 cleavage site: 695

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3'-TCATACCCTCCTCACCCTTTCT-5'

D51\_TPM.filter 23720810\_22 TCTTTCCTACTCCTCCCGTACT

target id: Solyc05g006630.2.1

679 5'-TGTACGGAATGGGAGGAGTGGGCAAGACCACT-3' 710 cleavage site: 695

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3'-TCATGCCCTCCTCATCCTTTCT-5'

D51\_TPM.filter 04099907\_23 AGAGAGACTGTTTCCGATAAACT

target id: Solyc05g006630.2.1

4174 5'-CGGATGGTCTATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-TCAAATAGCCTTTGTCAGAGAGA-5'

D51\_TPM.filter 12131357\_24 GAGAGACTGTTTCTGAAAGACTTT

target id: Solyc05g006630.2.1

4171 5'-ATGCGGATGGTCTATCAGAAACAATCTCTCTACCT-3' 4205 cleavage site: 4190

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3'-TT-TCAGAAAGTCTTTGTCAGAGAG-5'

D51\_TPM.filter 04101483\_23 AGAGAGATTGTTTCTGAAAGACT

target id: Solyc05g006630.2.1

4174 5'-CGGATGGTCTATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-TCAGAAAGTCTTTGTTAGAGAGA-5'

D51\_TPM.filter 12134584\_24 GAGAGATTGTTTCTGATAGACCCT

target id: Solyc05g006630.2.1

4172 5'-TGCGGATGGTCTATCAGAAACAATCTCTCTACCT-3' 4205 cleavage site: 4190

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3'-TCCCAGATAGTCTTTGTTAGAGAG-5'

D51\_TPM.filter 03892022\_23 AGAAAGACTGTTTCTGAAAGACT

target id: Solyc05g006630.2.1

4174 5'-CGGATGGTCTATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-TCAGAAAGTCTTTGTCAGAAAGA-5'

D51\_TPM.filter 13550532\_24 GGTGAGGTTGTTTCTGATAGACGT

target id: Solyc05g006630.2.1

4172 5'-TGCGGATGGTCTATCAGAAACAATCTC-TCTACCT-3' 4205 cleavage site: 4190

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3'-TG-CAGATAGTCTTTGTTGGAGTGG-5'

D51\_TPM.filter 03894949\_24 AGAAAGATTGTTTCTGATAGAACC

target id: Solyc05g006630.2.1

4174 5'-CGGATGG-TCTATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-CCAAGATAGTCTTTGTTAGAAAGA-5'

D51\_TPM.filter 03891198\_24 AGAAAGACTGTTTTCGATAGACCA

target id: Solyc05g006630.2.1

4173 5'-GCGGATGGTCTATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-ACCAGATAGCTTTTGTCAGAAAGA-5'

D51\_TPM.filter 04150186\_24 AGAGATTGTTTCTGATAGACCATT

target id: Solyc05g006630.2.1

4171 5'-ATGCGGATGGTCTATCAGAAACAATCTCTCTACC-3' 4204 cleavage site: 4189

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3'-TTACCAGATAGTCTTTGTTAGAGA-5'

D51\_TPM.filter 12134589\_24 GAGAGATTGTTTCTGATAGATTCT

target id: Solyc05g006630.2.1

4172 5'-TGCGGATGGTCTATCAGAAACAATCTCTCTACCT-3' 4205 cleavage site: 4190

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3'-TCTTAGATAGTCTTTGTTAGAGAG-5'

D51\_TPM.filter 12286999\_21 GAGGTTGTTTCTGATAGACGT

target id: Solyc05g006630.2.1

4172 5'-TGCGGATGGTCTATCAGAAACAATCTCTCTAC-3' 4203 cleavage site: 4188

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3'-TG-CAGATAGTCTTTGTTGGAG-5'

D51\_TPM.filter 04419739\_23 AGACTGTTTCTGATAGATCCTCA

target id: Solyc05g006630.2.1

4170 5'-AATGCGGATGGTCTATCAGAAACAATCTCTCTA-3' 4202 cleavage site: 4187

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3'-ACTCCTAGATAGTCTTTGTCAGA-5'

D51\_TPM.filter 04099698\_24 AGAGAGACTGTTTCTGATAAACCT

target id: Solyc05g006630.2.1

4173 5'-GCGGATGGTCTATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-TCCAAATAGTCTTTGTCAGAGAGA-5'

D51\_TPM.filter 03892421\_24 AGAAAGACTGTTTCTGACAGACCT

target id: Solyc05g006630.2.1

4173 5'-GCGGATGGTCTATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-TCCAGACAGTCTTTGTCAGAAAGA-5'

D51\_TPM.filter 01547968\_24 AAGACTGTTTTTGATAGACCTTCC

target id: Solyc05g006630.2.1

4170 5'-AATGCGGATGGTCTATCAGAAACAATCTCTCTAC-3' 4203 cleavage site: 4188

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3'-CCTTCCAGATAGTTTTTGTCAGAA-5'

D51\_TPM.filter 13033486\_24 GGAGATTGTTTCTGATAGACCATC

target id: Solyc05g006630.2.1

4171 5'-ATGCGGATGGTCTATCAGAAACAATCTCTCTACC-3' 4204 cleavage site: 4189

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3'-CTACCAGATAGTCTTTGTTAGAGG-5'

D51\_TPM.filter 04101414\_23 AGAGAGATTGTTTCTGATAGACA

target id: Solyc05g006630.2.1

4174 5'-CGGATGGTCTATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-ACAGATAGTCTTTGTTAGAGAGA-5'

D51\_TPM.filter 04344329\_24 AGACGTTGTTTCTGACAGACTATT

target id: Solyc05g006630.2.1

4171 5'-ATGCGGATGGTCTATCAGAAACAATCTCTCTACC-3' 4204 cleavage site: 4189

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3'-TTATCAGACAGTCTTTGTTGCAGA-5'

D51\_TPM.filter 04105355\_24 AGAGAGGTTGTTTCTGATAGACGA

target id: Solyc05g006630.2.1

4173 5'-GCGGATGGTCTATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-AGCAGATAGTCTTTGTTGGAGAGA-5'

D51\_TPM.filter 04102163\_24 AGAGAGATTGTTTCTGATAGACCT

target id: Solyc05g006630.2.1

4173 5'-GCGGATGGTCTATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-TCCAGATAGTCTTTGTTAGAGAGA-5'

D51\_TPM.filter 19722314\_24 TAGAGAGATTGTTTCTGATAGACC

target id: Solyc05g006630.2.1

4174 5'-CGGATGGTCTATCAGAAACAATCTCTCTACCTTC-3' 4207 cleavage site: 4192

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3'-CCAGATAGTCTTTGTTAGAGAGAT-5'

D51\_TPM.filter 01550992\_24 AAGACTGTTTTTGATAGACCTTCT

target id: Solyc05g006630.2.1

4170 5'-AATGCGGATGGTCTATCAGAAACAATCTCTCTAC-3' 4203 cleavage site: 4188

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3'-TCTTCCAGATAGTTTTTGTCAGAA-5'

D51\_TPM.filter 04100262\_24 AGAGAGACTGTTTCCGATAGACCC

target id: Solyc05g006630.2.1

4173 5'-GCGGATGGTCTATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-CCCAGATAGCCTTTGTCAGAGAGA-5'

D51\_TPM.filter 04415284\_24 AGACTGTTTTTGATAGACCTTCCA

target id: Solyc05g006630.2.1

4167 5'-ATAAATGCGGATGGTCTATCAGAAACAATCTCTCTA-3' 4202 cleavage site: 4187

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3'-AC-CTT-CCAGATAGTTTTTGTCAGA-5'

D51\_TPM.filter 04415020\_24 AGACTGTTTCTGATAGACCTCGGT

target id: Solyc05g006630.2.1

4168 5'-TAAATGCGGATGGTCTATCAGAAACAATCTCTCTA-3' 4202 cleavage site: 4187

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3'-TGGCT-CCAGATAGTCTTTGTCAGA-5'

D51\_TPM.filter 04716074\_24 AGGAGATTGTTTCTGAAAGACATT

target id: Solyc05g006630.2.1

4171 5'-ATGCGGATGGTCTATCAGAAACAATCTCTCTACCT-3' 4205 cleavage site: 4190

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3'-TTA-CAGAAAGTCTTTGTTAGAGGA-5'

D51\_TPM.filter 23682147\_22 TCTTCCCTACTCCTCCCATACT

target id: Solyc05g006630.2.1

679 5'-TGTACGGAATGGGAGGAGTGGGCAAGACCACT-3' 710 cleavage site: 695

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3'-TCATACCCTCCTCATCCCTTCT-5'

D51\_TPM.filter 04149350\_24 AGAGATTGTTTCTGATAGACCCTT

target id: Solyc05g006630.2.1

4171 5'-ATGCGGATGGTCTATCAGAAACAATCTCTCTACC-3' 4204 cleavage site: 4189

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3'-TTCCCAGATAGTCTTTGTTAGAGA-5'

D51\_TPM.filter 04099751\_23 AGAGAGACTGTTTCTGAAAGATT

target id: Solyc05g006630.2.1

4174 5'-CGGATGGTCTATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-TTAGAAAGTCTTTGTCAGAGAGA-5'

D51\_TPM.filter 04194100\_24 AGAGGTTGTTTCTGATAGATCATC

target id: Solyc05g006630.2.1

4171 5'-ATGCGGATGGTCTATCAGAAACAATCTCTCTACC-3' 4204 cleavage site: 4189

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3'-CTACTAGATAGTCTTTGTTGGAGA-5'

D51\_TPM.filter 04101818\_23 AGAGAGATTGTTTCTGATAGACT

target id: Solyc05g006630.2.1

4174 5'-CGGATGGTCTATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-TCAGATAGTCTTTGTTAGAGAGA-5'

D51\_TPM.filter 04082495\_24 AGAGAAACTGTTACTGATAGATCA

target id: Solyc05g006630.2.1

4173 5'-GCGGATGGTCTATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-ACTAGATAGTCATTGTCAAAGAGA-5'

D51\_TPM.filter 04148894\_24 AGAGATTGTTTCGGAAAGGCCATC

target id: Solyc05g006630.2.1

4171 5'-ATGCGGATGGTCTATCAGAAACAATCTCTCTACC-3' 4204 cleavage site: 4189

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3'-CTACCGGAAAGGCTTTGTTAGAGA-5'

D51\_TPM.filter 04105307\_23 AGAGAGGTTGTTTCTGATAGACA

target id: Solyc05g006630.2.1

4174 5'-CGGATGGTCTATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-ACAGATAGTCTTTGTTGGAGAGA-5'

D51\_TPM.filter 04101813\_22 AGAGAGATTGTTTCTGATAGAC

target id: Solyc05g006630.2.1

4175 5'-GGATGGTCTATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-CAGATAGTCTTTGTTAGAGAGA-5'

D51\_TPM.filter 23720471\_22 TCTTTCCTACTCCTCCCATGCT

target id: Solyc05g006630.2.1

679 5'-TGTACGGAATGGGAGGAGTGGGCAAGACCACT-3' 710 cleavage site: 695

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3'-TCGTACCCTCCTCATCCTTTCT-5'

D51\_TPM.filter 01449341\_24 AAGAGATTGTTTTTGATAGACCCT

target id: Solyc05g006630.2.1

4172 5'-TGCGGATGGTCTATCAGAAACAATCTCTCTACCT-3' 4205 cleavage site: 4190

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3'-TCCCAGATAGTTTTTGTTAGAGAA-5'

D51\_TPM.filter 04127623\_24 AGAGACTGTTTCTGATAGACCCTC

target id: Solyc05g006630.2.1

4171 5'-ATGCGGATGGTCTATCAGAAACAATCTCTCTACC-3' 4204 cleavage site: 4189

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3'-CTCCCAGATAGTCTTTGTCAGAGA-5'

D51\_TPM.filter 14438774\_24 GTAGAGAGATTGTTTCTGATAGAC

target id: Solyc05g006630.2.1

4175 5'-GGATGGTCTATCAGAAACAATCTCTCTACCTTCT-3' 4208 cleavage site: 4193

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3'-CAGATAGTCTTTGTTAGAGAGATG-5'

D51\_TPM.filter 23734664\_22 TCTTTTCTACTCCTCCCATACC

target id: Solyc05g006630.2.1

679 5'-TGTACGGAATGGGAGGAGTGGGCAAGACCACT-3' 710 cleavage site: 695

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3'-CCATACCCTCCTCATCTTTTCT-5'

D51\_TPM.filter 23721242\_22 TCTTTCCTACTCCTCCTATACC

target id: Solyc05g006630.2.1

679 5'-TGTACGGAATGGGAGGAGTGGGCAAGACCACT-3' 710 cleavage site: 695

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3'-CCATATCCTCCTCATCCTTTCT-5'

D51\_TPM.filter 23481048\_22 TCTGTCCTACTCCTCCCATACC

target id: Solyc05g006630.2.1

679 5'-TGTACGGAATGGGAGGAGTGGGCA-AGACCACT-3' 710 cleavage site: 695

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3'-CCATACCCTCCTCATCC-TGTCT-5'

D51\_TPM.filter 14438772\_24 GTAGAGAGGTTGTTTCTGATAGAC

target id: Solyc05g006630.2.1

4175 5'-GGATGGTCTATCAGAAACAATCTCTCTACCTTCT-3' 4208 cleavage site: 4193

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3'-CAGATAGTCTTTGTTGGAGAGATG-5'

D51\_TPM.filter 04140284\_23 AGAGATGTTGTTTCTGTTAGACA

target id: Solyc05g006630.2.1

4174 5'-CGGATGGTCTATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-ACAGATTGTCTTTGTTGTAGAGA-5'

D51\_TPM.filter 04099295\_24 AGAGAGACTGTTTTCGATAGACCT

target id: Solyc05g006630.2.1

4173 5'-GCGGATGGTCTATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-TCCAGATAGCTTTTGTCAGAGAGA-5'

D51\_TPM.filter 04723617\_24 AGGAGGTTGTTTCTGATAGATCTT

target id: Solyc05g006630.2.1

4171 5'-ATGCGGATGGTCTATCAGAAACAATCTCTCTACCT-3' 4205 cleavage site: 4190

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3'-TT-CTAGATAGTCTTTGTTGGAGGA-5'

D51\_TPM.filter 00661060\_24 AAAGATTGTTTCTGATAGACTCTC

target id: Solyc05g006630.2.1

4171 5'-ATGCGGATGGTCTATCAGAAACAATCTCTCTACC-3' 4204 cleavage site: 4189

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3'-CTCTCAGATAGTCTTTGTTAGAAA-5'

D51\_TPM.filter 08115503\_24 ATAGAGTGGTTGTTTCTGAAAGAT

target id: Solyc05g006630.2.1

4175 5'-GGATGGTCTATCAGAAACAATCTCTCTACCTTCT-3' 4208 cleavage site: 4193

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3'-TAGAAAGTCTTTGTTGGTGAGATA-5'

D51\_TPM.filter 23721541\_23 TCTTTCCTACTCCTCCCATACCT

target id: Solyc05g006630.2.1

678 5'-TTGTACGGAATGGGAGGAGTGGGCAAGACCACT-3' 710 cleavage site: 695

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3'-TCCATACCCTCCTCATCCTTTCT-5'

D51\_TPM.filter 04104922\_24 AGAGAGGTTGTTTCTGATAGACAT

target id: Solyc05g006630.2.1

4172 5'-TGCGGATGGTCTATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-TA-CAGATAGTCTTTGTTGGAGAGA-5'

D51\_TPM.filter 23720962\_23 TCTTTCCTACTCCTCCCATACCA

target id: Solyc05g006630.2.1

678 5'-TTGTACGGAATGGGAGGAGTGGGCAAGACCACT-3' 710 cleavage site: 695

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3'-ACCATACCCTCCTCATCCTTTCT-5'

D51\_TPM.filter 04105339\_24 AGAGAGGTTGTTTCTGATAGACCT

target id: Solyc05g006630.2.1

4173 5'-GCGGATGGTCTATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-TCCAGATAGTCTTTGTTGGAGAGA-5'

D51\_TPM.filter 04148858\_24 AGAGATTGTTTCTGATAAGATGTC

target id: Solyc05g006630.2.1

4171 5'-ATGCGGATGGTC-TATCAGAAACAATCTCTCTACC-3' 4204 cleavage site: 4189

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3'-CTG-TAGAATAGTCTTTGTTAGAGA-5'

D51\_TPM.filter 01448641\_24 AAGAGATTGTTTCTCAGAGACTAT

target id: Solyc05g006630.2.1

4172 5'-TGCGGATGGTCTATCAGAAACAATCTCTCTACCT-3' 4205 cleavage site: 4190

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3'-TATCAGAGACTCTTTGTTAGAGAA-5'

D51\_TPM.filter 23721693\_22 TCTTTCCTACTCCTCTCATACC

target id: Solyc05g006630.2.1

679 5'-TGTACGGAATGGGAGGAGTGGGCAAGACCACT-3' 710 cleavage site: 695

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3'-CCATACTCTCCTCATCCTTTCT-5'

D51\_TPM.filter 19690230\_23 TAGAAAGACTGTTTTTGATAGAC

target id: Solyc05g006630.2.1

4175 5'-GGATGGTCTATCAGAAACAATCTCTCTACCTTC-3' 4207 cleavage site: 4192

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3'-CAGATAGTTTTTGTCAGAAAGAT-5'

D51\_TPM.filter 04149702\_24 AGAGATTGTTTCTGATAGATCTTT

target id: Solyc05g006630.2.1

4170 5'-AATGCGGATGGTCTATCAGAAACAATCTCTCTACC-3' 4204 cleavage site: 4189

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3'-TTT-CTAGATAGTCTTTGTTAGAGA-5'

D51\_TPM.filter 03895761\_24 AGAAAGGATTGTTTCTGATAGACA

target id: Solyc05g006630.2.1

4174 5'-CGGATGGTCTATCAGAAACAA-TCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-ACAGATAGTCTTTGTTAGGAAAGA-5'

D51\_TPM.filter 01547094\_23 AAGACTGTTTTTGATAGACCTTC

target id: Solyc05g006630.2.1

4170 5'-AATGCGGATGGTCTATCAGAAACAATCTCTCTAC-3' 4203 cleavage site: 4188

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3'-CTT-CCAGATAGTTTTTGTCAGAA-5'

D51\_TPM.filter 04102331\_24 AGAGAGATTGTTTCTGATAGACTT

target id: Solyc05g006630.2.1

4173 5'-GCGGATGGTCTATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-TTCAGATAGTCTTTGTTAGAGAGA-5'

D51\_TPM.filter 04100183\_23 AGAGAGACTGTTTTTGATAGATC

target id: Solyc05g006630.2.1

4174 5'-CGGATGGTCTATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-CTAGATAGTTTTTGTCAGAGAGA-5'

D51\_TPM.filter 01731232\_24 AAGGATTGTTTCTGATAGACCTTC

target id: Solyc05g006630.2.1

4170 5'-AATGCGGATGGTCTATCAGAAACAATCTCTCTACC-3' 4204 cleavage site: 4189

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3'-CTT-CCAGATAGTCTTTGTTAGGAA-5'

D51\_TPM.filter 04100848\_23 AGAGAGACTGTTTTCGATAGATC

target id: Solyc05g006630.2.1

4174 5'-CGGATGGTCTATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-CTAGATAGCTTTTGTCAGAGAGA-5'

D51\_TPM.filter 12131742\_24 GAGAGACTGTTTCTGATAGACCCT

target id: Solyc05g006630.2.1

4172 5'-TGCGGATGGTCTATCAGAAACAATCTCTCTACCT-3' 4205 cleavage site: 4190

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3'-TCCCAGATAGTCTTTGTCAGAGAG-5'

D51\_TPM.filter 04102083\_23 AGAGAGATTGTTTCTGATAGATT

target id: Solyc05g006630.2.1

4174 5'-CGGATGGTCTATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-TTAGATAGTCTTTGTTAGAGAGA-5'

D51\_TPM.filter 04105706\_23 AGAGAGGTTGTTTCTGATAGATC

target id: Solyc05g006630.2.1

4174 5'-CGGATGGTCTATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-CTAGATAGTCTTTGTTGGAGAGA-5'

D51\_TPM.filter 04105654\_24 AGAGAGGTTGTTTCTGATAGACGG

target id: Solyc05g006630.2.1

4173 5'-GCGGATGGTCTATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-GGCAGATAGTCTTTGTTGGAGAGA-5'

D51\_TPM.filter 12134681\_24 GAGAGATTGTTTCTGATAGACTTT

target id: Solyc05g006630.2.1

4171 5'-ATGCGGATGGTCTATCAGAAACAATCTCTCTACCT-3' 4205 cleavage site: 4190

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3'-TT-TCAGATAGTCTTTGTTAGAGAG-5'

D51\_TPM.filter 15467463\_24 GTTTCTGATAGACCCTCGACCATT

target id: Solyc05g006630.2.1

4165 5'-TTATAAATGCG--GATGGTCTATCAGAAACAATCT-3' 4197 cleavage site: 4182

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3'-TTAC-CAGCTCCCAGATAGTCTTTG-5'

D51\_TPM.filter 03892387\_24 AGAAAGACTGTTTCTGACAGACCC

target id: Solyc05g006630.2.1

4173 5'-GCGGATGGTCTATCAGAAACAATCTCTCTACCTT-3' 4206 cleavage site: 4191

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3'-CCCAGACAGTCTTTGTCAGAAAGA-5'

D51\_TPM.filter 23721661\_22 TCTTTCCTATTCCTCCCATACC

target id: Solyc05g006630.2.1

679 5'-TGTACGGAATGGGAGGAGTGGGCAAGACCACT-3' 710 cleavage site: 695

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3'-CCATACCCTCCTTATCCTTTCT-5'

D51\_TPM.filter 13676454\_20 GGTTGTTCGATGATGTTGTT

target id: Solyc09g007710.2.1

3325 5'-TATTTCACAACATCATCGGCAC-ACCTTTCC-3' 3354 cleavage site: 3339

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3'-TTGTTGTAGTAGCT-TGTTGG-5'

D51\_TPM.filter 01442869\_24 AAGAGACTTCTTGAAAAACTAAGA

target id: Solyc05g006620.2.1

4415 5'-AACTTTCTTAGTTTTGTTAAGGAGATTTTTTGTGCT-3' 4450 cleavage site: 4435

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3'-AGAATCAAAA-AGTTCTTC-AGAGAA-5'

D51\_TPM.filter 23811530\_20 TTAAATGATCTCTTGAATAG

target id: Solyc05g006620.2.1

4458 5'-ACCTTTTCTTCAAGAGA-T-TTTAAACCTC-3' 4485 cleavage site: 4470

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3'-GATAAGTTCTCTAGTAAATT-5'

D51\_TPM.filter 08131702\_21 ATAGACTGTTCATATTCAATA

target id: Solyc05g006620.2.1

4489 5'-ACCGCGGTTGAATATGAAC-GTCGTGTGTTTG-3' 4519 cleavage site: 4504

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3'-ATAACTTATACTTGTCAG-ATA-5'

D51\_TPM.filter 21609381\_23 TGGTGGAATGATTGAGATCTCTT

target id: Solyc05g007850.1.1

2875 5'-TTTCTAA-ATATCTC-ATCATTCCAACATAACA-3' 2905 cleavage site: 2890

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3'-TTCTCTAGAGTTAGTAAGGTGGT-5'

D51\_TPM.filter 21889278\_21 TGTAGCAATAGATTCTTTGAT

target id: Solyc05g007850.1.1

238 5'-ATTTTCTCAAAGAA-TTA-TGCTACATCTAG-3' 266 cleavage site: 251

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3'-TAGTTTCTTAGATAACGATGT-5'

D51\_TPM.filter 00871983\_22 AAACGATATGAAGCTTTGATTA

target id: Solyc01g014840.2.1

2554 5'-CTTCGTGAGCTAAGCTTCTTATCGTTTTCTCG-3' 2585 cleavage site: 2570

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3'-ATTAGTTTCGAAGTATAGCAAA-5'

D51\_TPM.filter 25095444\_24 TTGTGTCTCCAATTCTGTAATGGG

target id: Solyc01g014840.2.1

3906 5'-AGTATCCCA--AC--AATTGGAGACACAATGCAC-3' 3935 cleavage site: 3920

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3'-GGGTAATGTCTTAACCTCTGTGTT-5'

D51\_TPM.filter 07886306\_21 ATAAGCAACAATCTCTGTTCA

target id: Solyc01g102850.1.1

2998 5'-AAAAGTGAACAGAGATTGTTGACATTGTATGTG-3' 3030 cleavage site: 3015

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3'-ACTTGTCTCTAACAAC-G-AATA-5'

D51\_TPM.filter 19421447\_22 TAAGCAACAATCTCTGTTCATA

target id: Solyc01g102850.1.1

2996 5'-ACAAAAGTGAACAGAGATTGTTGACATTGTATGT-3' 3029 cleavage site: 3014

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3'-ATACTTGTCTCTAACAAC-G-AAT-5'

D51\_TPM.filter 26816211\_21 TTTTGTTGGTGAACCTTTTTG

target id: Solyc01g102850.1.1

2976 5'-GGTTCCAAGCTGGTTCAGCAACAAAAGTGAA-3' 3006 cleavage site: 2991

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3'-GTTTTTCCAAGTGGTTGTTTT-5'

D51\_TPM.filter 07886425\_20 ATAAGCAACAATCTCTGTTC

target id: Solyc01g102850.1.1

2999 5'-AAAGTGAACAGAGATTGTTGACATTGTATGTG-3' 3030 cleavage site: 3015

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3'-CTTGTCTCTAACAAC-G-AATA-5'

D51\_TPM.filter 19421557\_21 TAAGCAACAATCTCTGTTCAT

target id: Solyc01g102850.1.1

2997 5'-CAAAAGTGAACAGAGATTGTTGACATTGTATGT-3' 3029 cleavage site: 3014

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3'-TACTTGTCTCTAACAAC-G-AAT-5'

D51\_TPM.filter 01861783\_23 AAGCAACAATCTCTGTTCATATT

target id: Solyc01g102850.1.1

2994 5'-CAACAAAAGTGAACAGAGATTGTTGACATTGTATG-3' 3028 cleavage site: 3013

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3'-TTATACTTGTCTCTAACAAC-G-AA-5'

D51\_TPM.filter 07886270\_21 ATAAGCAACAATCTCTGTTCG

target id: Solyc01g102850.1.1

2998 5'-AAAAGTGAACAGAGATTGTTGACATTGTATGTG-3' 3030 cleavage site: 3015

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3'-GCTTGTCTCTAACAAC-G-AATA-5'

D51\_TPM.filter 07886623\_21 ATAAGCAACAATCTCTGTTCT

target id: Solyc01g102850.1.1

2998 5'-AAAAGTGAACAGAGATTGTTGACATTGTATGTG-3' 3030 cleavage site: 3015

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3'-TCTTGTCTCTAACAAC-G-AATA-5'

D51\_TPM.filter 19421763\_22 TAAGCAACAATCTCTGTTCATG

target id: Solyc01g102850.1.1

2996 5'-ACAAAAGTGAACAGAGATTGTTGACATTGTATGT-3' 3029 cleavage site: 3014

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3'-GTACTTGTCTCTAACAAC-G-AAT-5'

D51\_TPM.filter 20923589\_22 TGAGAACTTTGAAGGCCGAAGA

target id: Solyc04g007490.2.1

2613 5'-TTTCATCTTTGGCAACTTCAAATTTCTCAGGGTG-3' 2646 cleavage site: 2631

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3'-AGAAGCCG--GAAGTTTCAAGAGT-5'

D51\_TPM.filter 22378270\_23 TCAGACTGTCTTTTATTAATATA

target id: Solyc04g007490.2.1

1655 5'-TCACTGATATTAGTAAAAGA-GGTGCTGATATAT-3' 1687 cleavage site: 1672

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3'-ATATAATTATTTTCTGTCA-GACT-5'

D51\_TPM.filter 20923365\_21 TGAGAACTTTGAAGGCCGAAG

target id: Solyc04g007490.2.1

2614 5'-TTCATCTTTGGCAACTTCAAATTTCTCAGGGTG-3' 2646 cleavage site: 2631

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3'-GAAGCCG--GAAGTTTCAAGAGT-5'

D51\_TPM.filter 20922957\_20 TGAGAACTTTGAAGGCCGAA

target id: Solyc04g007490.2.1

2615 5'-TCATCTTTGGCAACTTCAAATTTCTCAGGGTG-3' 2646 cleavage site: 2631

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3'-AAGCCG--GAAGTTTCAAGAGT-5'

D51\_TPM.filter 12117058\_21 GAGAACTTTGAAGGCCGAAGA

target id: Solyc04g007490.2.1

2613 5'-TTTCATCTTTGGCAACTTCAAATTTCTCAGGGT-3' 2645 cleavage site: 2630

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3'-AGAAGCCG--GAAGTTTCAAGAG-5'

D51\_TPM.filter 12116877\_20 GAGAACTTTGAAGGCCGAAG

target id: Solyc04g007490.2.1

2614 5'-TTCATCTTTGGCAACTTCAAATTTCTCAGGGT-3' 2645 cleavage site: 2630

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3'-GAAGCCG--GAAGTTTCAAGAG-5'

D51\_TPM.filter 26409180\_21 TTTCGAGTCCTGAAATCCATC

target id: Solyc04g007490.2.1

3416 5'-TCCCTGATGGTTTTCAGGAC-CTAAATTGTT-3' 3445 cleavage site: 3430

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3'-CTACCTAAAGTCCTGAGCTTT-5'

D51\_TPM.filter 07221053\_24 ACTAATGCTGACTATATCTGAATT

target id: Solyc04g007490.2.1

2829 5'-GAGTAAGTTGAGATAT-GTTAGCATTAGTGATGG-3' 2861 cleavage site: 2846

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3'-TTAAGTCTATATCAGTCGTAATCA-5'

D51\_TPM.filter 25569464\_21 TTCTAACCTTGTATCGCTTGT

target id: Solyc05g054010.2.1

2997 5'-GTTAAATGAG-GATTTAAGGTTAGAAAATTT-3' 3026 cleavage site: 3011

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3'-TGTTCGCTATGTTCCAATCTT-5'

D51\_TPM.filter 03712288\_24 AATTCTACGTCTAGCTCTGATACT

target id: Solyc05g054010.2.1

3688 5'-GGAGAAG-A-CA-AGCTTGACGTAGAATTCTACG-3' 3718 cleavage site: 3703

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3'-TCATAGTCTCGATCTGCATCTTAA-5'

D51\_TPM.filter 12426895\_23 GACACTTTTAGAATTTTGAGATT

target id: Solyc05g054010.2.1

3383 5'-TCCAGAATCTC-AAATCTCTAAAATTGTCTTGTC-3' 3415 cleavage site: 3400

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3'-TTAGAGTTTTA-AGATTTTCACAG-5'

D51\_TPM.filter 08974426\_24 ATGAATTTTGAATAATTGAAGTGT

target id: Solyc05g054010.2.1

2433 5'-TTTCGATGATTCTATT-TTCAAAATTCATGATCT-3' 2465 cleavage site: 2450

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3'-TGTGAAGTTAATAAGTTTTAAGTA-5'

D51\_TPM.filter 05470250\_24 AGCTGAGATCTCTTCATTCTTAAG

target id: Solyc06g008450.2.1

1424 5'-TCAAACTTATCAAAGAAGAGATCTCTGCTTTAGA-3' 1457 cleavage site: 1442

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3'-GAATTCTTACTTCTCTAGAGTCGA-5'

D51\_TPM.filter 22274495\_20 TCAAGAGTTTGTAGACGAGG

target id: Solyc04g007060.2.1

2026 5'-AATCTTCTTCTCTACAAACTCTTTCTATGG-3' 2055 cleavage site: 2040

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3'-GGAGCAGATGTTTGAGAACT-5'

D51\_TPM.filter 22922690\_24 TCGTGATCTAATGACATTTGTTCT

target id: Solyc04g007060.2.1

861 5'-GTGTGGGAAGCAAATGTCATT-GATCACGTAAAGA-3' 894 cleavage site: 879

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3'-TC-TTGTTTACAGTAATCTAGTGCT-5'

D51\_TPM.filter 01724746\_22 AAGGATCTGACATGCATCTGTC

target id: Solyc04g007060.2.1

1650 5'-CCATCTGCAGA-ACATGTCAGATCTTTCTATT-3' 1680 cleavage site: 1665

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3'-CTGTCTACGTACAGTCTAGGAA-5'

D51\_TPM.filter 00227355\_22 AAAAGACACAACTTTCTGGATA

target id: Solyc04g007060.2.1

2952 5'-GTATGTACTCCCTGGAGTTGTGTCTTTTTCGAG-3' 2984 cleavage site: 2969

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3'-AT-AGGTCTTTCAACACAGAAAA-5'

D51\_TPM.filter 05604292\_24 AGTAGCTACTCCATTTATTTTAGT

target id: Solyc04g007060.2.1

2933 5'-AATACGCT-AAATAAATGGAGTATG-TACTCCCTG-3' 2965 cleavage site: 2950

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3'-TGATTTTATTTACCTCAT-CGATGA-5'

D51\_TPM.filter 11722156\_21 GAAAAGAACTTTGAAGAGAGA

target id: Solyc04g007060.2.1

1769 5'-TGTTGAATCTC-TCAAATTTCTTTTCTCCAA-3' 1798 cleavage site: 1783

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3'-AGAGAGAAGTTTCAAGAAAAG-5'

D51\_TPM.filter 04746779\_21 AGGACAACTACAGAAAGTGGA

target id: Solyc04g007060.2.1

1104 5'-GGAGTACCACTTATTGTAGTTGTCATTGCAGG-3' 1135 cleavage site: 1120

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3'-AGGTGAAAGACATCAACAG-GA-5'

D51\_TPM.filter 11721523\_20 GAAAAGAACTTTGAAGAGAG

target id: Solyc04g007060.2.1

1770 5'-GTTGAATCTC-TCAAATTTCTTTTCTCCAA-3' 1798 cleavage site: 1783

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3'-GAGAGAAGTTTCAAGAAAAG-5'

D51\_TPM.filter 23251003\_21 TCCTTGACATTGTTGTATGAT

target id: Solyc04g011990.1.1

1004 5'-AGGAAATAGTAGAAAAATGTCAAGGACTACC-3' 1034 cleavage site: 1019

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3'-TAGTATGTTGTTACAGTTCCT-5'

D51\_TPM.filter 26744759\_22 TTTTGATGTGGGTGTAGTTATT

target id: Solyc11g071420.1.1

2256 5'-ACTTGAGGAGCTACGCCCACA-TAAAAACATA-3' 2286 cleavage site: 2271

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3'-TTATTGATGTGGGTGTAGTTTT-5'

D51\_TPM.filter 10671292\_21 ATTATTTTCCTCAAACAAGGA

target id: Solyc12g044180.1.1

1214 5'-TTTGTTCTTTATTTGAGGAAGATAGTGACAT-3' 1244 cleavage site: 1229

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3'-AGGAACAAACTCCTTTTATTA-5'

D51\_TPM.filter 25866430\_21 TTTAGCAAGAGTTGTTTTACC

target id: Solyc05g005330.2.1

1748 5'-GATTGGGTAAGACAACTCTCGCTAACAAGCT-3' 1778 cleavage site: 1763

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3'-CCATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 26653861\_22 TTTTAGCAAGAGTTGTTTTACC

target id: Solyc05g005330.2.1

1748 5'-GATTGGGTAAGACAACTCTCGCTAACAAGCTAT-3' 1780 cleavage site: 1765

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3'-CCATTTTGTTGAGAACGATT-TT-5'

D51\_TPM.filter 22272625\_21 TCAAGAATTTGTAGACGAGGT

target id: Solyc05g005330.2.1

3481 5'-CATTTCCCTCACCT-CAAATTCTTGAAACTG-3' 3510 cleavage site: 3495

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3'-TGGAGCAGATGTTTAAGAACT-5'

D51\_TPM.filter 25866155\_21 TTTAGCAAGAGTTGTTTTACT

target id: Solyc05g005330.2.1

1748 5'-GATTGGGTAAGACAACTCTCGCTAACAAGCT-3' 1778 cleavage site: 1763

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3'-TCATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 26654022\_22 TTTTAGCAAGAGTTGTTTTACT

target id: Solyc05g005330.2.1

1748 5'-GATTGGGTAAGACAACTCTCGCTAACAAGCTAT-3' 1780 cleavage site: 1765

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3'-TCATTTTGTTGAGAACGATT-TT-5'

D51\_TPM.filter 22272871\_20 TCAAGAATTTGTAGACGAGG

target id: Solyc05g005330.2.1

3482 5'-ATTTCCCTCACCT-CAAATTCTTGAAACTG-3' 3510 cleavage site: 3495

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3'-GGAGCAGATGTTTAAGAACT-5'

D51\_TPM.filter 24840868\_21 TTGGCATCATAGAAGCATGGC

target id: Solyc05g005330.2.1

2014 5'-CTAATGCCATGCTTCTATGATGCCAATAATG-3' 2044 cleavage site: 2029

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3'-CGGTACGAAGATACTACGGTT-5'

D51\_TPM.filter 22272968\_21 TCAAGAATTTGTAGACGAGGC

target id: Solyc05g005330.2.1

3481 5'-CATTTCCCTCACCT-CAAATTCTTGAAACTG-3' 3510 cleavage site: 3495

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3'-CGGAGCAGATGTTTAAGAACT-5'

D51\_TPM.filter 22850645\_20 TCGGTCTGCATGCTCCATGT

target id: Solyc05g005330.2.1

3177 5'-TTCTTGTGTGGAGGATGCAGACAGGATCTT-3' 3206 cleavage site: 3191

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3'-TGTACCTCGTACGTCTGGCT-5'

D51\_TPM.filter 26653812\_23 TTTTAGCAAGAGTTGTTTTACCT

target id: Solyc05g005330.2.1

1747 5'-GGATTGGGTAAGACAACTCTCGCTAACAAGCTAT-3' 1780 cleavage site: 1765

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3'-TCCATTTTGTTGAGAACGATT-TT-5'

D51\_TPM.filter 23394319\_21 TCTGACTTAGCCTGGATATGT

target id: Solyc05g005330.2.1

2326 5'-GGTCCACATATCCAGGCTAAGTCAGAGGATA-3' 2356 cleavage site: 2341

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3'-TGTATAGGTCCGATTCAGTCT-5'

D51\_TPM.filter 19300725\_24 TAAACTTTAAATCTTGCATCCACT

target id: Solyc05g005330.2.1

2880 5'-GTTCCTGTGGGTGCTAGATTTAGAATTTACTGTA-3' 2913 cleavage site: 2898

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3'-TCACCTACGTTCTAAATTTCAAAT-5'

D51\_TPM.filter 18737068\_21 CTCTTCTGCAACTTTGACTGC

target id: Solyc05g005330.2.1

2951 5'-ATGTTGCTGTTAAAGTTGCTGAAGATTCTTC-3' 2981 cleavage site: 2966

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3'-CGTCAGTTTCAACGTCTTCTC-5'

D51\_TPM.filter 23600566\_21 TCTTAACACTCCGAAGAATGG

target id: Solyc05g005330.2.1

1863 5'-ACTAACCATTCTTCGGAGTGTTAAGAAGGAT-3' 1893 cleavage site: 1878

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3'-GGTAAGAAGCCTCACAATTCT-5'

D51\_TPM.filter 22273044\_21 TCAAGAATTTGTAGACGAGGA

target id: Solyc05g005330.2.1

3481 5'-CATTTCCCTCACCT-CAAATTCTTGAAACTG-3' 3510 cleavage site: 3495

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3'-AGGAGCAGATGTTTAAGAACT-5'

D51\_TPM.filter 24841039\_21 TTGGCATCATAGAAGCATGGT

target id: Solyc05g005330.2.1

2014 5'-CTAATGCCATGCTTCTATGATGCCAATAATG-3' 2044 cleavage site: 2029

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3'-TGGTACGAAGATACTACGGTT-5'

D51\_TPM.filter 26654357\_22 TTTTAGCAAGAGTTGTTTTACA

target id: Solyc05g005330.2.1

1748 5'-GATTGGGTAAGACAACTCTCGCTAACAAGCTAT-3' 1780 cleavage site: 1765

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3'-ACATTTTGTTGAGAACGATT-TT-5'

D51\_TPM.filter 18062356\_21 CTAATTCATTCTCTGGTAGTT

target id: Solyc05g005330.2.1

1905 5'-TGATAAACTACCAGAGAATGAATTAGCAGAT-3' 1935 cleavage site: 1920

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3'-TTGATGGTCTCTTACTTAATC-5'

D51\_TPM.filter 25866253\_21 TTTAGCAAGAGTTGTTTTACA

target id: Solyc05g005330.2.1

1748 5'-GATTGGGTAAGACAACTCTCGCTAACAAGCT-3' 1778 cleavage site: 1763

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3'-ACATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 25866391\_22 TTTAGCAAGAGTTGTTTTACCT

target id: Solyc05g005330.2.1

1747 5'-GGATTGGGTAAGACAACTCTCGCTAACAAGCT-3' 1778 cleavage site: 1763

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3'-TCCATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 21236840\_20 TGATTGTTGCAACTTTGATT

target id: Solyc05g005330.2.1

3070 5'-AAGATGGTC-AAGTTGCAACATTTGCATGT-3' 3098 cleavage site: 3083

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3'-TTAGTTTCAACGTTGTTAGT-5'

D51\_TPM.filter 25866557\_21 TTTAGCAAGAGTTGTTTTACG

target id: Solyc05g005330.2.1

1748 5'-GATTGGGTAAGACAACTCTCGCTAACAAGCT-3' 1778 cleavage site: 1763

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3'-GCATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 25866736\_20 TTTAGCAAGAGTTGTTTTAC

target id: Solyc05g005330.2.1

1749 5'-ATTGGGTAAGACAACTCTCGCTAACAAGCT-3' 1778 cleavage site: 1763

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3'-CATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 26654347\_23 TTTTAGCAAGAGTTGTTTTACCA

target id: Solyc05g005330.2.1

1747 5'-GGATTGGGTAAGACAACTCTCGCTAACAAGCTAT-3' 1780 cleavage site: 1765

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3'-ACCATTTTGTTGAGAACGATT-TT-5'

D51\_TPM.filter 25866163\_22 TTTAGCAAGAGTTGTTTTACCC

target id: Solyc05g005330.2.1

1747 5'-GGATTGGGTAAGACAACTCTCGCTAACAAGCT-3' 1778 cleavage site: 1763

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3'-CCCATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 26654102\_21 TTTTAGCAAGAGTTGTTTTAC

target id: Solyc05g005330.2.1

1749 5'-ATTGGGTAAGACAACTCTCGCTAACAAGCTAT-3' 1780 cleavage site: 1765

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3'-CATTTTGTTGAGAACGATT-TT-5'

D51\_TPM.filter 22273205\_20 TCAAGAATTTGTAGACGAGA

target id: Solyc05g005330.2.1

3482 5'-ATTTCCCTCACCT-CAAATTCTTGAAACTG-3' 3510 cleavage site: 3495

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3'-AGAGCAGATGTTTAAGAACT-5'

D51\_TPM.filter 26653916\_22 TTTTAGCAAGAGTTGTTTTACG

target id: Solyc05g005330.2.1

1748 5'-GATTGGGTAAGACAACTCTCGCTAACAAGCTAT-3' 1780 cleavage site: 1765

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3'-GCATTTTGTTGAGAACGATT-TT-5'

D51\_TPM.filter 25866348\_22 TTTAGCAAGAGTTGTTTTACCA

target id: Solyc05g005330.2.1

1747 5'-GGATTGGGTAAGACAACTCTCGCTAACAAGCT-3' 1778 cleavage site: 1763

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3'-ACCATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 22272516\_21 TCAAGAATTTGTAGACGAGGG

target id: Solyc05g005330.2.1

3481 5'-CATTTCCCTCACCT-CAAATTCTTGAAACTG-3' 3510 cleavage site: 3495

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3'-GGGAGCAGATGTTTAAGAACT-5'

D51\_TPM.filter 10284897\_22 ATCTCTGTATGATGTTCTTGTC

target id: Solyc05g005330.2.1

2479 5'-GGTTTGGTAAGAAC-TCATACAGAGAAGCTTT-3' 2509 cleavage site: 2494

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3'-CTGTTCTTGTAGTATGTCTCTA-5'

D51\_TPM.filter 26653934\_23 TTTTAGCAAGAGTTGTTTTACCC

target id: Solyc05g005330.2.1

1747 5'-GGATTGGGTAAGACAACTCTCGCTAACAAGCTAT-3' 1780 cleavage site: 1765

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3'-CCCATTTTGTTGAGAACGATT-TT-5'

D51\_TPM.filter 25425552\_21 TTCGGTAAAACTCCTTTGAGA

target id: Solyc05g005330.2.1

3793 5'-ATCAGTTTTTAAGGAGTTTTATC-AGCTGAA-3' 3822 cleavage site: 3807

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3'-AGAGTTTCCTCAAAATGGCTT-5'

D51\_TPM.filter 24280214\_20 TTATAGTTTGTTTGATGGTA

target id: Solyc06g062440.2.1

1879 5'-CCCTATTCCATCAAACAAGCTACAAAATCT-3' 1908 cleavage site: 1893

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3'-ATGGTAGTTTGTTTGATATT-5'

D51\_TPM.filter 24280482\_22 TTATAGTTTGTTTGATGGTATC

target id: Solyc06g062440.2.1

1877 5'-TTCCCTATTCCATCAAACAAGCTACAAAATCT-3' 1908 cleavage site: 1893

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3'-CTATGGTAGTTTGTTTGATATT-5'

D51\_TPM.filter 11609576\_21 ATTTTGTAGATTTGTAGCTTC

target id: Solyc06g062440.2.1

1889 5'-TCAAACAAGCTACAAAATCTACAGGAACTCTC-3' 1920 cleavage site: 1905

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3'-CTTCGATG-TTTAGATGTTTTA-5'

D51\_TPM.filter 14630656\_21 GTGAAAGAGACATAACTTTGG

target id: Solyc06g062440.2.1

2605 5'-TCATTCTGCAAGTTAAGTCTCTTTTATGTTCC-3' 2636 cleavage site: 2621

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3'-GGT-TTCAATACAGAGAAAGTG-5'

D51\_TPM.filter 26793551\_21 TTTTGTAGATTTGTAGCTTCA

target id: Solyc06g062440.2.1

1888 5'-ATCAAACAAGCTACAAAATCTACAGGAACTCT-3' 1919 cleavage site: 1904

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3'-ACTTCGATG-TTTAGATGTTTT-5'

D51\_TPM.filter 20334398\_20 TATAGTTTGTTTGATGGTAT

target id: Solyc06g062440.2.1

1878 5'-TCCCTATTCCATCAAACAAGCTACAAAATC-3' 1907 cleavage site: 1892

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3'-TATGGTAGTTTGTTTGATAT-5'

D51\_TPM.filter 22272625\_21 TCAAGAATTTGTAGACGAGGT

target id: Solyc05g012740.1.1

3331 5'-CAGTTCCCTCACCT-CAAATTCTTGAAACTG-3' 3360 cleavage site: 3345

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3'-TGGAGCAGATGTTTAAGAACT-5'

D51\_TPM.filter 22272871\_20 TCAAGAATTTGTAGACGAGG

target id: Solyc05g012740.1.1

3332 5'-AGTTCCCTCACCT-CAAATTCTTGAAACTG-3' 3360 cleavage site: 3345

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3'-GGAGCAGATGTTTAAGAACT-5'

D51\_TPM.filter 22272968\_21 TCAAGAATTTGTAGACGAGGC

target id: Solyc05g012740.1.1

3331 5'-CAGTTCCCTCACCT-CAAATTCTTGAAACTG-3' 3360 cleavage site: 3345

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3'-CGGAGCAGATGTTTAAGAACT-5'

D51\_TPM.filter 22273044\_21 TCAAGAATTTGTAGACGAGGA

target id: Solyc05g012740.1.1

3331 5'-CAGTTCCCTCACCT-CAAATTCTTGAAACTG-3' 3360 cleavage site: 3345

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3'-AGGAGCAGATGTTTAAGAACT-5'

D51\_TPM.filter 22273205\_20 TCAAGAATTTGTAGACGAGA

target id: Solyc05g012740.1.1

3332 5'-AGTTCCCTCACCT-CAAATTCTTGAAACTG-3' 3360 cleavage site: 3345

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3'-AGAGCAGATGTTTAAGAACT-5'

D51\_TPM.filter 22272516\_21 TCAAGAATTTGTAGACGAGGG

target id: Solyc05g012740.1.1

3331 5'-CAGTTCCCTCACCT-CAAATTCTTGAAACTG-3' 3360 cleavage site: 3345

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3'-GGGAGCAGATGTTTAAGAACT-5'

D51\_TPM.filter 23646402\_22 TCTTGCCTACACCGCCCATGCC

target id: Solyc02g036270.2.1

509 5'-TTTGTGGTATGGGTGGTGTAGGTAAGACGACA-3' 540 cleavage site: 525

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3'-CCGTACCCGCCACATCCGTTCT-5'

D51\_TPM.filter 23646461\_22 TCTTGCCTACACCGCCCATGCT

target id: Solyc02g036270.2.1

509 5'-TTTGTGGTATGGGTGGTGTAGGTAAGACGACA-3' 540 cleavage site: 525

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3'-TCGTACCCGCCACATCCGTTCT-5'

D51\_TPM.filter 23646169\_22 TCTTGCCTACACCGCCCATGCA

target id: Solyc02g036270.2.1

509 5'-TTTGTGGTATGGGTGGTGTAGGTAAGACGACA-3' 540 cleavage site: 525

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3'-ACGTACCCGCCACATCCGTTCT-5'

D51\_TPM.filter 16288140\_21 CATGTGATTGTATTGTTCGTA

target id: Solyc02g036270.2.1

1484 5'-CCTCTTACGAGCCATACAGTCACATGTCAAT-3' 1514 cleavage site: 1499

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3'-ATGCTTGTTATGTTAGTGTAC-5'

D51\_TPM.filter 25283883\_21 TTCACAAACATCTCGGAGTCG

target id: Solyc02g036270.2.1

836 5'-CAACGCGACTCCGAGATGTTTGTGAAACAAT-3' 866 cleavage site: 851

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3'-GCTGAGGCTCTACAAACACTT-5'

D51\_TPM.filter 22451103\_21 TCACAAACATCTCGGAGTCGC

target id: Solyc02g036270.2.1

835 5'-ACAACGCGACTCCGAGATGTTTGTGAAACAA-3' 865 cleavage site: 850

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3'-CGCTGAGGCTCTACAAACACT-5'

D51\_TPM.filter 16288287\_20 CATGTGATTGTATTGTTCGT

target id: Solyc02g036270.2.1

1485 5'-CTCTTACGAGCCATACAGTCACATGTCAAT-3' 1514 cleavage site: 1499

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3'-TGCTTGTTATGTTAGTGTAC-5'

D51\_TPM.filter 22146615\_21 TGTTGATTTTTGTGTGTAGTT

target id: Solyc02g036270.2.1

1074 5'-CCTTAAACAAT-TACAAAAATCCACACCAAA-3' 1103 cleavage site: 1088

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3'-TTGATGTGTGTTTTTAGTTGT-5'

D51\_TPM.filter 25906981\_21 TTTACGCTTTAGCGCTCCTGC

target id: Solyc02g036270.2.1

1025 5'-CAGTTGCAGGAGCGCTAAAGCGTAAAAGCAA-3' 1055 cleavage site: 1040

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3'-CGTCCTCGCGATTTCGCATTT-5'

D51\_TPM.filter 24188044\_21 TTACGCTTTAGCGCTCCTGCA

target id: Solyc02g036270.2.1

1024 5'-ACAGTTGCAGGAGCGCTAAAGCGTAAAAGCA-3' 1054 cleavage site: 1039

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3'-ACGTCCTCGCGATTTCGCATT-5'

D51\_TPM.filter 22451027\_21 TCACAAACATCTCGGAGTCGT

target id: Solyc02g036270.2.1

835 5'-ACAACGCGACTCCGAGATGTTTGTGAAACAA-3' 865 cleavage site: 850

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3'-TGCTGAGGCTCTACAAACACT-5'

D51\_TPM.filter 26994070\_21 TTTTTGTAATTGTTTAAGGGC

target id: Solyc02g036270.2.1

1067 5'-AGGATGCCCTTAAACAATTACAAAAATCCAC-3' 1097 cleavage site: 1082

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3'-CGGGAATTTGTTAATGTTTTT-5'

D51\_TPM.filter 26791466\_20 TTTTGTAATTGTTTAAGGGC

target id: Solyc02g036270.2.1

1067 5'-AGGATGCCCTTAAACAATTACAAAAATCCA-3' 1096 cleavage site: 1081

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3'-CGGGAATTTGTTAATGTTTT-5'

D51\_TPM.filter 23218350\_22 TCCTGCCTACACCGCCCATGCC

target id: Solyc02g036270.2.1

509 5'-TTTGTGGTATGGGTGGTGTAGGTAAGACGACA-3' 540 cleavage site: 525

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3'-CCGTACCCGCCACATCCGTCCT-5'

D51\_TPM.filter 16017999\_21 CACAAACATCTCGGAGTCGCG

target id: Solyc02g036270.2.1

834 5'-GACAACGCGACTCCGAGATGTTTGTGAAACA-3' 864 cleavage site: 849

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3'-GCGCTGAGGCTCTACAAACAC-5'

D51\_TPM.filter 09830638\_21 ATCATCCTGTAATTTGAACGG

target id: Solyc02g036270.2.1

1592 5'-AAGAGCCGTTCAAATTACAGGATGATTTTTT-3' 1622 cleavage site: 1607

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3'-GGCAAGTTTAATGTCCTACTA-5'

D51\_TPM.filter 21451263\_22 TGGGATATTTTTTGGTGTGGAT

target id: Solyc02g036270.2.1

1087 5'-CAAAAATCCACACCAAAAAATATCCCAGGAGT-3' 1118 cleavage site: 1103

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3'-TAGGTGTGGTTTTTTATAGGGT-5'

D51\_TPM.filter 23646688\_21 TCTTGCCTACACCGCCCATGC

target id: Solyc02g036270.2.1

510 5'-TTGTGGTATGGGTGGTGTAGGTAAGACGACA-3' 540 cleavage site: 525

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3'-CGTACCCGCCACATCCGTTCT-5'

D51\_TPM.filter 26668496\_21 TTTTACGCTTTAGCGCTCCTG

target id: Solyc02g036270.2.1

1026 5'-AGTTGCAGGAGCGCTAAAGCGTAAAAGCAAG-3' 1056 cleavage site: 1041

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3'-GTCCTCGCGATTTCGCATTTT-5'

D51\_TPM.filter 23646640\_22 TCTTGCCTACACCGCCCATGTC

target id: Solyc02g036270.2.1

509 5'-TTTGTGGTATGGGTGGTGTAGGTAAGACGACA-3' 540 cleavage site: 525

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3'-CTGTACCCGCCACATCCGTTCT-5'

D51\_TPM.filter 23646467\_20 TCTTGCCTACACCGCCCATG

target id: Solyc02g036270.2.1

511 5'-TGTGGTATGGGTGGTGTAGGTAAGACGACA-3' 540 cleavage site: 525

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3'-GTACCCGCCACATCCGTTCT-5'

D51\_TPM.filter 22578698\_21 TCATCCTGTAATTTGAACGGC

target id: Solyc02g036270.2.1

1591 5'-GAAGAGCCGTTCAAATTACAGGATGATTTTT-3' 1621 cleavage site: 1606

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3'-CGGCAAGTTTAATGTCCTACT-5'

D51\_TPM.filter 25284143\_21 TTCACAAACATCTCGGAGTCA

target id: Solyc02g036270.2.1

836 5'-CAACGCGACTCCGAGATGTTTGTGAAACAAT-3' 866 cleavage site: 851

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3'-ACTGAGGCTCTACAAACACTT-5'

D51\_TPM.filter 21450901\_21 TGGGATATTTTTTGGTGTGGA

target id: Solyc02g036270.2.1

1088 5'-AAAAATCCACACCAAAAAATATCCCAGGAGT-3' 1118 cleavage site: 1103

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3'-AGGTGTGGTTTTTTATAGGGT-5'

D51\_TPM.filter 23540290\_22 TCTCGCCTACACCGCCCATGCC

target id: Solyc02g036270.2.1

509 5'-TTTGTGGTATGGGTGGTGTAGGTAAGACGACA-3' 540 cleavage site: 525

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3'-CCGTACCCGCCACATCCGCTCT-5'

D51\_TPM.filter 26791535\_21 TTTTGTAATTGTTTAAGGGCA

target id: Solyc02g036270.2.1

1066 5'-GAGGATGCCCTTAAACAATTACAAAAATCCA-3' 1096 cleavage site: 1081

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3'-ACGGGAATTTGTTAATGTTTT-5'

D51\_TPM.filter 25907065\_21 TTTACGCTTTAGCGCTCCTGT

target id: Solyc02g036270.2.1

1025 5'-CAGTTGCAGGAGCGCTAAAGCGTAAAAGCAA-3' 1055 cleavage site: 1040

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3'-TGTCCTCGCGATTTCGCATTT-5'

D51\_TPM.filter 23646606\_22 TCTTGCCTACACCGCCCATGAC

target id: Solyc02g036270.2.1

509 5'-TTTGTGGTATGGGTGGTGTAGGTAAGACGACA-3' 540 cleavage site: 525

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3'-CAGTACCCGCCACATCCGTTCT-5'

D51\_TPM.filter 23646244\_22 TCTTGCCTACACCGCCCACGCC

target id: Solyc02g036270.2.1

509 5'-TTTGTGGTATGGGTGGTGTAGGTAAGACGACA-3' 540 cleavage site: 525

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3'-CCGCACCCGCCACATCCGTTCT-5'

D51\_TPM.filter 21182359\_21 TGATGGTTGTGATTGCTACAA

target id: Solyc02g036270.2.1

793 5'-CCTAGTTGTAGCAATCACAACCATCAGTGCA-3' 823 cleavage site: 808

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3'-AACATCGTTAGTGTTGGTAGT-5'

D51\_TPM.filter 16810111\_23 CGGATTTCTGTAATTATTTTAAG

target id: Solyc02g036270.2.1

1070 5'-ATGCCCTT-AAACAATTACAAAAATCCACACCA-3' 1101 cleavage site: 1086

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3'-GAATTTTATTAATGTCTTTAGGC-5'

D51\_TPM.filter 16288438\_20 CATGTGATTGTATTGTTCGG

target id: Solyc02g036270.2.1

1485 5'-CTCTTACGAGCCATACAGTCACATGTCAAT-3' 1514 cleavage site: 1499

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3'-GGCTTGTTATGTTAGTGTAC-5'

D51\_TPM.filter 06515870\_20 ACATCTATAGTAGAATCTCT

target id: Solyc02g036270.2.1

1793 5'-TTATTAGAGATTCTACTATAGATGTGCTTC-3' 1822 cleavage site: 1807

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3'-TCTCTAAGATGATATCTACA-5'

D51\_TPM.filter 26668585\_21 TTTTACGCTTTAGCGCTCCTA

target id: Solyc02g036270.2.1

1026 5'-AGTTGCAGGAGCGCTAAAGCGTAAAAGCAAG-3' 1056 cleavage site: 1041

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3'-ATCCTCGCGATTTCGCATTTT-5'

D51\_TPM.filter 16288141\_20 CATGTGATTGTATTGTTCGC

target id: Solyc02g036270.2.1

1485 5'-CTCTTACGAGCCATACAGTCACATGTCAAT-3' 1514 cleavage site: 1499

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3'-CGCTTGTTATGTTAGTGTAC-5'

D51\_TPM.filter 16288446\_21 CATGTGATTGTATTGTTCGTG

target id: Solyc02g036270.2.1

1484 5'-CCTCTTACGAGCCATACAGTCACATGTCAAT-3' 1514 cleavage site: 1499

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3'-GTGCTTGTTATGTTAGTGTAC-5'

D51\_TPM.filter 23646300\_22 TCTTGCCTACACCGCCCGTGCC

target id: Solyc02g036270.2.1

509 5'-TTTGTGGTATGGGTGGTGTAGGTAAGACGACA-3' 540 cleavage site: 525

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3'-CCGTGCCCGCCACATCCGTTCT-5'

D51\_TPM.filter 16287866\_21 CATGTGACTGTATGGCTCGTA

target id: Solyc02g036270.2.1

1484 5'-CCTCTTACGAGCCATACAGTCACATGTCAAT-3' 1514 cleavage site: 1499

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3'-ATGCTCGGTATGTCAGTGTAC-5'

D51\_TPM.filter 23219160\_21 TCCTGTAATTTGAACGGCTCT

target id: Solyc02g036270.2.1

1588 5'-TTAGAAGAGCCGTTCAAATTACAGGATGATT-3' 1618 cleavage site: 1603

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3'-TCTCGGCAAGTTTAATGTCCT-5'

D51\_TPM.filter 26994308\_21 TTTTTGTAATTGTTTAAGGGT

target id: Solyc02g036270.2.1

1067 5'-AGGATGCCCTTAAACAATTACAAAAATCCAC-3' 1097 cleavage site: 1082

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3'-TGGGAATTTGTTAATGTTTTT-5'

D51\_TPM.filter 06104606\_21 ACAAACATGTCGGAAACGCGT

target id: Solyc02g036270.2.1

833 5'-TGACAACGCGACTCCGAGATGTTTGTGAAAC-3' 863 cleavage site: 848

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3'-TGCGCAAAGGCTGTACAAACA-5'

D51\_TPM.filter 23646419\_22 TCTTGCCTACACCGCCCATGCG

target id: Solyc02g036270.2.1

509 5'-TTTGTGGTATGGGTGGTGTAGGTAAGACGACA-3' 540 cleavage site: 525

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3'-GCGTACCCGCCACATCCGTTCT-5'

D51\_TPM.filter 26238477\_21 TTTGTAATTGTTTAAGGGCAT

target id: Solyc02g036270.2.1

1065 5'-GGAGGATGCCCTTAAACAATTACAAAAATCC-3' 1095 cleavage site: 1080

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3'-TACGGGAATTTGTTAATGTTT-5'

D51\_TPM.filter 17943644\_22 CCTTGCCTACACCGCCCATGCT

target id: Solyc02g036270.2.1

509 5'-TTTGTGGTATGGGTGGTGTAGGTAAGACGACA-3' 540 cleavage site: 525

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3'-TCGTACCCGCCACATCCGTTCC-5'

D51\_TPM.filter 17943647\_22 CCTTGCCTACACCGCCCATGCC

target id: Solyc02g036270.2.1

509 5'-TTTGTGGTATGGGTGGTGTAGGTAAGACGACA-3' 540 cleavage site: 525

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3'-CCGTACCCGCCACATCCGTTCC-5'

D51\_TPM.filter 16018140\_21 CACAAACATCTCGGAGTCGCA

target id: Solyc02g036270.2.1

834 5'-GACAACGCGACTCCGAGATGTTTGTGAAACA-3' 864 cleavage site: 849

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3'-ACGCTGAGGCTCTACAAACAC-5'

D51\_TPM.filter 23646712\_23 TCTTGCCTACACCGCCCATGCCA

target id: Solyc02g036270.2.1

508 5'-ATTTGTGGTATGGGTGGTGTAGGTAAGACGACA-3' 540 cleavage site: 525

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3'-ACCGTACCCGCCACATCCGTTCT-5'

D51\_TPM.filter 06515505\_21 ACATCTATAGTAGAATCTCTA

target id: Solyc02g036270.2.1

1792 5'-ATTATTAGAGATTCTACTATAGATGTGCTTC-3' 1822 cleavage site: 1807

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3'-ATCTCTAAGATGATATCTACA-5'

D51\_TPM.filter 21109233\_21 TGACTGTATGGCTCGTAAGAG

target id: Solyc02g036270.2.1

1480 5'-AGAACCTCTTACGAGCCATACAGTCACATGT-3' 1510 cleavage site: 1495

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3'-GAGAATGCTCGGTATGTCAGT-5'

D51\_TPM.filter 24188068\_20 TTACGCTTTAGCGCTCCTGC

target id: Solyc02g036270.2.1

1025 5'-CAGTTGCAGGAGCGCTAAAGCGTAAAAGCA-3' 1054 cleavage site: 1039

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3'-CGTCCTCGCGATTTCGCATT-5'

D51\_TPM.filter 22578697\_21 TCATCCTGTAATTTGAACGGT

target id: Solyc02g036270.2.1

1591 5'-GAAGAGCCGTTCAAATTACAGGATGATTTTT-3' 1621 cleavage site: 1606

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3'-TGGCAAGTTTAATGTCCTACT-5'

D51\_TPM.filter 23646515\_22 TCTTGCCTACACCGCCCATCCT

target id: Solyc02g036270.2.1

509 5'-TTTGTGGTATGGGTGGTGTAGGTAAGACGACA-3' 540 cleavage site: 525

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3'-TCCTACCCGCCACATCCGTTCT-5'

D51\_TPM.filter 06187027\_21 ACAACGATCTTTTCTGAATAG

target id: Solyc05g008070.2.1

949 5'-AAAAGCTATTCAGAAAAGATCGTTGTCCTCC-3' 979 cleavage site: 964

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3'-GATAAGTCTTTTCTAGCAACA-5'

D51\_TPM.filter 22612814\_21 TCATTTCTTGATTGTTGACTC

target id: Solyc05g008070.2.1

674 5'-TAGTGGAGTCAACAATCAAGAAATGAGCAAT-3' 704 cleavage site: 689

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3'-CTCAGTTGTTAGTTCTTTACT-5'

D51\_TPM.filter 06675206\_21 ACGATCTTTTCTGAATAGCTT

target id: Solyc05g008070.2.1

946 5'-CCAAAAAGCTATTCAGAAAAGATCGTTGTCC-3' 976 cleavage site: 961

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3'-TTCGATAAGTCTTTTCTAGCA-5'

D51\_TPM.filter 25866430\_21 TTTAGCAAGAGTTGTTTTACC

target id: Solyc05g008070.2.1

538 5'-GTATAGGTAAGACAACTCTTGCTAGAAAAGT-3' 568 cleavage site: 553

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3'-CCATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 26653861\_22 TTTTAGCAAGAGTTGTTTTACC

target id: Solyc05g008070.2.1

538 5'-GTATAGGTAAGACAACTCTTGCTAGAAAAGTT-3' 569 cleavage site: 554

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3'-CCATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 06186295\_21 ACAACGATCTTTTCTGAATAA

target id: Solyc05g008070.2.1

949 5'-AAAAGCTATTCAGAAAAGATCGTTGTCCTCC-3' 979 cleavage site: 964

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3'-AATAAGTCTTTTCTAGCAACA-5'

D51\_TPM.filter 21792301\_21 TGCCTTAATGAACTGCTCAGC

target id: Solyc05g008070.2.1

1264 5'-GGATAGCTGAGCAGTTCATTAAGGCAACAAG-3' 1294 cleavage site: 1279

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3'-CGACTCGTCAAGTAATTCCGT-5'

D51\_TPM.filter 21054313\_21 TGACGATTAGAAATCTCCTAC

target id: Solyc05g008070.2.1

737 5'-CAAGGGTAGGAGATTTCTAATCGTCATAGAT-3' 767 cleavage site: 752

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3'-CATCCTCTAAAGATTAGCAGT-5'

D51\_TPM.filter 25866155\_21 TTTAGCAAGAGTTGTTTTACT

target id: Solyc05g008070.2.1

538 5'-GTATAGGTAAGACAACTCTTGCTAGAAAAGT-3' 568 cleavage site: 553

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3'-TCATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 22612900\_21 TCATTTCTTGATTGTTGACTT

target id: Solyc05g008070.2.1

674 5'-TAGTGGAGTCAACAATCAAGAAATGAGCAAT-3' 704 cleavage site: 689

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3'-TTCAGTTGTTAGTTCTTTACT-5'

D51\_TPM.filter 26654022\_22 TTTTAGCAAGAGTTGTTTTACT

target id: Solyc05g008070.2.1

538 5'-GTATAGGTAAGACAACTCTTGCTAGAAAAGTT-3' 569 cleavage site: 554

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3'-TCATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 06673952\_21 ACGATCTTTTCTGAATAGCTC

target id: Solyc05g008070.2.1

946 5'-CCAAAAAGCTATTCAGAAAAGATCGTTGTCC-3' 976 cleavage site: 961

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3'-CTCGATAAGTCTTTTCTAGCA-5'

D51\_TPM.filter 24963827\_22 TTGCCTTAATGAACTGCTCAGC

target id: Solyc05g008070.2.1

1264 5'-GGATAGCTGAGCAGTTCATTAAGGCAACAAGC-3' 1295 cleavage site: 1280

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3'-CGACTCGTCAAGTAATTCCGTT-5'

D51\_TPM.filter 06673767\_20 ACGATCTTTTCTGAATAGCT

target id: Solyc05g008070.2.1

947 5'-CAAAAAGCTATTCAGAAAAGATCGTTGTCC-3' 976 cleavage site: 961

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3'-TCGATAAGTCTTTTCTAGCA-5'

D51\_TPM.filter 06673453\_22 ACGATCTTTTCTGAATAGCTTT

target id: Solyc05g008070.2.1

945 5'-ACCAAAAAGCTATTCAGAAAAGATCGTTGTCC-3' 976 cleavage site: 961

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3'-TTTCGATAAGTCTTTTCTAGCA-5'

D51\_TPM.filter 16681326\_21 CGATCTTTTCTGAATAGCTTT

target id: Solyc05g008070.2.1

945 5'-ACCAAAAAGCTATTCAGAAAAGATCGTTGTC-3' 975 cleavage site: 960

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3'-TTTCGATAAGTCTTTTCTAGC-5'

D51\_TPM.filter 04747075\_21 AGGACAACGATCTTTTCTGAA

target id: Solyc05g008070.2.1

952 5'-AGCTATTCAGAAAAGATCGTTGTCCTCCACA-3' 982 cleavage site: 967

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3'-AAGTCTTTTCTAGCAACAGGA-5'

D51\_TPM.filter 22612566\_21 TCATTTCTTGATTGTTGACTA

target id: Solyc05g008070.2.1

674 5'-TAGTGGAGTCAACAATCAAGAAATGAGCAAT-3' 704 cleavage site: 689

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3'-ATCAGTTGTTAGTTCTTTACT-5'

D51\_TPM.filter 26653812\_23 TTTTAGCAAGAGTTGTTTTACCT

target id: Solyc05g008070.2.1

537 5'-GGTATAGGTAAGACAACTCTTGCTAGAAAAGTT-3' 569 cleavage site: 554

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3'-TCCATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 06674117\_21 ACGATCTTTTCTGAATAGCTA

target id: Solyc05g008070.2.1

946 5'-CCAAAAAGCTATTCAGAAAAGATCGTTGTCC-3' 976 cleavage site: 961

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3'-ATCGATAAGTCTTTTCTAGCA-5'

D51\_TPM.filter 15702558\_21 CAACGATCTTTTCTGAATAGC

target id: Solyc05g008070.2.1

948 5'-AAAAAGCTATTCAGAAAAGATCGTTGTCCTC-3' 978 cleavage site: 963

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3'-CGATAAGTCTTTTCTAGCAAC-5'

D51\_TPM.filter 06299020\_21 ACAGCGATCTTTTCTGAATAG

target id: Solyc05g008070.2.1

949 5'-AAAAGCTATTCAGAAAAGATCGTTGTCCTCC-3' 979 cleavage site: 964

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3'-GATAAGTCTTTTCTAGCGACA-5'

D51\_TPM.filter 06674680\_21 ACGATCTTTTCTGAATAGCGT

target id: Solyc05g008070.2.1

946 5'-CCAAAAAGCTATTCAGAAAAGATCGTTGTCC-3' 976 cleavage site: 961

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3'-TGCGATAAGTCTTTTCTAGCA-5'

D51\_TPM.filter 19348773\_21 TAAGAAGATCATGAATTTTGC

target id: Solyc05g008070.2.1

1394 5'-AACTTGCAAAATTCATGATCTTCTTAGGCAG-3' 1424 cleavage site: 1409

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3'-CGTTTTAAGTACTAGAAGAAT-5'

D51\_TPM.filter 04746133\_24 AGGACAACGATCTTTTCTGAATAG

target id: Solyc05g008070.2.1

949 5'-AAAAGCTATTCAGAAAAGATCGTTGTCCTCCACA-3' 982 cleavage site: 967

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3'-GATAAGTCTTTTCTAGCAACAGGA-5'

D51\_TPM.filter 06186245\_21 ACAACGATCTTCTCTGAATAG

target id: Solyc05g008070.2.1

949 5'-AAAAGCTATTCAGAAAAGATCGTTGTCCTCC-3' 979 cleavage site: 964

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3'-GATAAGTCTCTTCTAGCAACA-5'

D51\_TPM.filter 06186470\_21 ACAACGATCTTTTCTGAGTAG

target id: Solyc05g008070.2.1

949 5'-AAAAGCTATTCAGAAAAGATCGTTGTCCTCC-3' 979 cleavage site: 964

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3'-GATGAGTCTTTTCTAGCAACA-5'

D51\_TPM.filter 26654357\_22 TTTTAGCAAGAGTTGTTTTACA

target id: Solyc05g008070.2.1

538 5'-GTATAGGTAAGACAACTCTTGCTAGAAAAGTT-3' 569 cleavage site: 554

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3'-ACATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 21792344\_21 TGCCTTAATGAACTGCTCAGT

target id: Solyc05g008070.2.1

1264 5'-GGATAGCTGAGCAGTTCATTAAGGCAACAAG-3' 1294 cleavage site: 1279

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3'-TGACTCGTCAAGTAATTCCGT-5'

D51\_TPM.filter 06186540\_20 ACAACGATCTTTTCTGAATA

target id: Solyc05g008070.2.1

950 5'-AAAGCTATTCAGAAAAGATCGTTGTCCTCC-3' 979 cleavage site: 964

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3'-ATAAGTCTTTTCTAGCAACA-5'

D51\_TPM.filter 25866253\_21 TTTAGCAAGAGTTGTTTTACA

target id: Solyc05g008070.2.1

538 5'-GTATAGGTAAGACAACTCTTGCTAGAAAAGT-3' 568 cleavage site: 553

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3'-ACATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 06623130\_21 ACGACGATCTTTTCTGAATAG

target id: Solyc05g008070.2.1

949 5'-AAAAGCTATTCAGAAAAGATCGTTGTCCTCC-3' 979 cleavage site: 964

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3'-GATAAGTCTTTTCTAGCAGCA-5'

D51\_TPM.filter 25866391\_22 TTTAGCAAGAGTTGTTTTACCT

target id: Solyc05g008070.2.1

537 5'-GGTATAGGTAAGACAACTCTTGCTAGAAAAGT-3' 568 cleavage site: 553

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3'-TCCATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 18929669\_21 CTTGTTGCCTTAATGAACTGC

target id: Solyc05g008070.2.1

1269 5'-GCTGAGCAGTTCATTAAGGCAACAAGCGATA-3' 1299 cleavage site: 1284

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3'-CGTCAAGTAATTCCGTTGTTC-5'

D51\_TPM.filter 19521143\_21 TAACCATCAATTCATCATTGT

target id: Solyc05g008070.2.1

695 5'-AATGAGCAATGATGAATTGATGGTTATTGTG-3' 725 cleavage site: 710

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3'-TGTTACTACTTAACTACCAAT-5'

D51\_TPM.filter 22612283\_20 TCATTTCTTGATTGTTGACT

target id: Solyc05g008070.2.1

675 5'-AGTGGAGTCAACAATCAAGAAATGAGCAAT-3' 704 cleavage site: 689

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3'-TCAGTTGTTAGTTCTTTACT-5'

D51\_TPM.filter 23985396\_21 TTAGAAAAGACACCTCGCGAG

target id: Solyc05g008070.2.1

893 5'-TCCTCCTCGCGAGGTGTCTTTTCTAAGTTTT-3' 923 cleavage site: 908

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3'-GAGCGCTCCACAGAAAAGATT-5'

D51\_TPM.filter 26653543\_24 TTTTAGCAAGAGTTGTTTTACTTT

target id: Solyc05g008070.2.1

536 5'-CGGTATAGGTAAGACAACTCTTGCTAGAAAAGTT-3' 569 cleavage site: 554

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3'-TTTCATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 25866686\_23 TTTAGCAAGAGTTGTTTTACTTT

target id: Solyc05g008070.2.1

536 5'-CGGTATAGGTAAGACAACTCTTGCTAGAAAAGT-3' 568 cleavage site: 553

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3'-TTTCATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 24963894\_22 TTGCCTTAATGAACTGCTCAGT

target id: Solyc05g008070.2.1

1264 5'-GGATAGCTGAGCAGTTCATTAAGGCAACAAGC-3' 1295 cleavage site: 1280

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3'-TGACTCGTCAAGTAATTCCGTT-5'

D51\_TPM.filter 06186440\_22 ACAACGATCTTTTCTGAATAGC

target id: Solyc05g008070.2.1

948 5'-AAAAAGCTATTCAGAAAAGATCGTTGTCCTCC-3' 979 cleavage site: 964

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3'-CGATAAGTCTTTTCTAGCAACA-5'

D51\_TPM.filter 08383950\_24 ATACGTCGACGTTTCTATCTTGCT

target id: Solyc05g008070.2.1

1057 5'-TTCTTAGCAAGAT--AGACG-TGACGTATGATAA-3' 1087 cleavage site: 1072

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3'-TCGTTCTATCTTTGCAGCTGCATA-5'

D51\_TPM.filter 26362070\_21 TTTCAGGTACTAGATAAGATC

target id: Solyc05g008070.2.1

1616 5'-TGGTAGATCTTATCTAGTACCTGAAATGAAC-3' 1646 cleavage site: 1631

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3'-CTAGAATAGATCATGGACTTT-5'

D51\_TPM.filter 23651578\_21 TCTTGTGAGTAAGTAGAAACA

target id: Solyc05g008070.2.1

1476 5'-GATCTTGTTTCTACTTACTCACAAGACATAA-3' 1506 cleavage site: 1491

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3'-ACAAAGATGAATGAGTGTTCT-5'

D51\_TPM.filter 09051143\_20 ATGACGATTAGAAATCTCCT

target id: Solyc05g008070.2.1

739 5'-AGGGTAGGAGATTTCTAATCGTCATAGATG-3' 768 cleavage site: 753

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3'-TCCTCTAAAGATTAGCAGTA-5'

D51\_TPM.filter 06186423\_21 ACAACGATCTTTTCTGGATAG

target id: Solyc05g008070.2.1

949 5'-AAAAGCTATTCAGAAAAGATCGTTGTCCTCC-3' 979 cleavage site: 964

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3'-GATAGGTCTTTTCTAGCAACA-5'

D51\_TPM.filter 06673968\_21 ACGATCTTTTCTGAATAGCTG

target id: Solyc05g008070.2.1

946 5'-CCAAAAAGCTATTCAGAAAAGATCGTTGTCC-3' 976 cleavage site: 961

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3'-GTCGATAAGTCTTTTCTAGCA-5'

D51\_TPM.filter 21054411\_21 TGACGATTAGAAATCTCCTAT

target id: Solyc05g008070.2.1

737 5'-CAAGGGTAGGAGATTTCTAATCGTCATAGAT-3' 767 cleavage site: 752

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3'-TATCCTCTAAAGATTAGCAGT-5'

D51\_TPM.filter 22144770\_22 TGTTGATCTTCCATACATTGAA

target id: Solyc05g008070.2.1

1908 5'-AATCCTTTTA-GTATTGGAGATCAACAAACTC-3' 1938 cleavage site: 1923

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3'-AAGTTACATACCTTCTAGTTGT-5'

D51\_TPM.filter 06674072\_21 ACGATCTTTTCTGAATAGCCT

target id: Solyc05g008070.2.1

946 5'-CCAAAAAGCTATTCAGAAAAGATCGTTGTCC-3' 976 cleavage site: 961

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3'-TCCGATAAGTCTTTTCTAGCA-5'

D51\_TPM.filter 19521300\_21 TAACCATCAATTCATCATTGC

target id: Solyc05g008070.2.1

695 5'-AATGAGCAATGATGAATTGATGGTTATTGTG-3' 725 cleavage site: 710

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3'-CGTTACTACTTAACTACCAAT-5'

D51\_TPM.filter 11529788\_21 ATTTCTTGATTGTTGACTCCA

target id: Solyc05g008070.2.1

672 5'-ATTAGTGGAGTCAACAATCAAGAAATGAGCA-3' 702 cleavage site: 687

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3'-ACCTCAGTTGTTAGTTCTTTA-5'

D51\_TPM.filter 15702362\_22 CAACGATCTTTTCTGAATAGCT

target id: Solyc05g008070.2.1

947 5'-CAAAAAGCTATTCAGAAAAGATCGTTGTCCTC-3' 978 cleavage site: 963

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3'-TCGATAAGTCTTTTCTAGCAAC-5'

D51\_TPM.filter 12402716\_24 GACAACGATCTTTTCTGAATAGCT

target id: Solyc05g008070.2.1

947 5'-CAAAAAGCTATTCAGAAAAGATCGTTGTCCTCCA-3' 980 cleavage site: 965

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3'-TCGATAAGTCTTTTCTAGCAACAG-5'

D51\_TPM.filter 06186298\_21 ACAACGATCTTTTCTGAATAT

target id: Solyc05g008070.2.1

949 5'-AAAAGCTATTCAGAAAAGATCGTTGTCCTCC-3' 979 cleavage site: 964

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3'-TATAAGTCTTTTCTAGCAACA-5'

D51\_TPM.filter 22047720\_21 TGTGTCTATTTGTTCAACTTC

target id: Solyc05g008070.2.1

1879 5'-ATGTTGATA-TTGAACAAATGGATATGCCTAA-3' 1909 cleavage site: 1894

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3'-CT-TCAACTTGTTTATCTGTGT-5'

D51\_TPM.filter 06186518\_24 ACAACGATCTTTTCTGAATAGCTT

target id: Solyc05g008070.2.1

946 5'-CCAAAAAGCTATTCAGAAAAGATCGTTGTCCTCC-3' 979 cleavage site: 964

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3'-TTCGATAAGTCTTTTCTAGCAACA-5'

D51\_TPM.filter 06187126\_23 ACAACGATCTTTTCTGAATAGCT

target id: Solyc05g008070.2.1

947 5'-CAAAAAGCTATTCAGAAAAGATCGTTGTCCTCC-3' 979 cleavage site: 964

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3'-TCGATAAGTCTTTTCTAGCAACA-5'

D51\_TPM.filter 23400199\_21 TCTGATGCTGTTATACTTAGC

target id: Solyc05g008070.2.1

2106 5'-GAAAAGCTAAGTATAACAGCATCAGATGACA-3' 2136 cleavage site: 2121

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3'-CGATTCATATTGTCGTAGTCT-5'

D51\_TPM.filter 22191575\_21 TGTTTGAGACGAGTGGTTAGT

target id: Solyc05g008070.2.1

837 5'-ATTATACTAACCACTCGTCTCAAACATGTTG-3' 867 cleavage site: 852

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3'-TGATTGGTGAGCAGAGTTTGT-5'

D51\_TPM.filter 24451788\_21 TTATTTCTTGATTGTTGACTC

target id: Solyc05g008070.2.1

674 5'-TAGTGGAGTCAACAATCAAGAAATGAGCAAT-3' 704 cleavage site: 689

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3'-CTCAGTTGTTAGTTCTTTATT-5'

D51\_TPM.filter 06186408\_21 ACAACGATCTTTTCTAAATAG

target id: Solyc05g008070.2.1

949 5'-AAAAGCTATTCAGAAAAGATCGTTGTCCTCC-3' 979 cleavage site: 964

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3'-GATAAATCTTTTCTAGCAACA-5'

D51\_TPM.filter 14996699\_20 GTGTCTATTTGTTCAACTTT

target id: Solyc05g008070.2.1

1879 5'-ATGTTGATA-TTGAACAAATGGATATGCCTA-3' 1908 cleavage site: 1893

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3'-TT-TCAACTTGTTTATCTGTG-5'

D51\_TPM.filter 25269398\_21 TTCAGGTACTAGATAAGATCT

target id: Solyc05g008070.2.1

1615 5'-GTGGTAGATCTTATCTAGTACCTGAAATGAA-3' 1645 cleavage site: 1630

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3'-TCTAGAATAGATCATGGACTT-5'

D51\_TPM.filter 12219929\_21 GAGGACAACGATCTTTTCTGA

target id: Solyc05g008070.2.1

953 5'-GCTATTCAGAAAAGATCGTTGTCCTCCACAA-3' 983 cleavage site: 968

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3'-AGTCTTTTCTAGCAACAGGAG-5'

D51\_TPM.filter 22307430\_21 TCAACGATCTTTTCTGAATAG

target id: Solyc05g008070.2.1

949 5'-AAAAGCTATTCAGAAAAGATCGTTGTCCTCC-3' 979 cleavage site: 964

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3'-GATAAGTCTTTTCTAGCAACT-5'

D51\_TPM.filter 25866557\_21 TTTAGCAAGAGTTGTTTTACG

target id: Solyc05g008070.2.1

538 5'-GTATAGGTAAGACAACTCTTGCTAGAAAAGT-3' 568 cleavage site: 553

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3'-GCATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 18573702\_22 CTCATTTCTTGATTGTTGACTC

target id: Solyc05g008070.2.1

674 5'-TAGTGGAGTCAACAATCAAGAAATGAGCAATG-3' 705 cleavage site: 690

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3'-CTCAGTTGTTAGTTCTTTACTC-5'

D51\_TPM.filter 26654347\_23 TTTTAGCAAGAGTTGTTTTACCA

target id: Solyc05g008070.2.1

537 5'-GGTATAGGTAAGACAACTCTTGCTAGAAAAGTT-3' 569 cleavage site: 554

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3'-ACCATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 22047067\_21 TGTGTCTATTTGTTCAATTTT

target id: Solyc05g008070.2.1

1879 5'-ATGTTGATATTGAACAAATGGATATGCCTAA-3' 1909 cleavage site: 1894

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3'-TTTTAACTTGTTTATCTGTGT-5'

D51\_TPM.filter 25866163\_22 TTTAGCAAGAGTTGTTTTACCC

target id: Solyc05g008070.2.1

537 5'-GGTATAGGTAAGACAACTCTTGCTAGAAAAGT-3' 568 cleavage site: 553

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3'-CCCATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 19059194\_22 CTTTAGCAAGAGTTGTTTTACC

target id: Solyc05g008070.2.1

538 5'-GTATAGGTAAGACAACTCTTGCTAGAAAAGTT-3' 569 cleavage site: 554

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3'-CCATTTTGTTGAGAACGATTTC-5'

D51\_TPM.filter 26654102\_21 TTTTAGCAAGAGTTGTTTTAC

target id: Solyc05g008070.2.1

539 5'-TATAGGTAAGACAACTCTTGCTAGAAAAGTT-3' 569 cleavage site: 554

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3'-CATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 22047447\_21 TGTGTCTATTTGTTCAACTGT

target id: Solyc05g008070.2.1

1880 5'-TGTTGATA-TTGAACAAATGGATATGCCTAA-3' 1909 cleavage site: 1894

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3'-TGTCAACTTGTTTATCTGTGT-5'

D51\_TPM.filter 25374791\_21 TTCGATACACGAATCTCCATA

target id: Solyc05g008070.2.1

1224 5'-GAAGATATGGAGATTCGTGTATCGAAGATGA-3' 1254 cleavage site: 1239

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3'-ATACCTCTAAGCACATAGCTT-5'

D51\_TPM.filter 25866348\_22 TTTAGCAAGAGTTGTTTTACCA

target id: Solyc05g008070.2.1

537 5'-GGTATAGGTAAGACAACTCTTGCTAGAAAAGT-3' 568 cleavage site: 553

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3'-ACCATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 17260698\_21 CGTGTCTATTTGTTCAACTTT

target id: Solyc05g008070.2.1

1879 5'-ATGTTGATA-TTGAACAAATGGATATGCCTAA-3' 1909 cleavage site: 1894

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3'-TT-TCAACTTGTTTATCTGTGC-5'

D51\_TPM.filter 21054734\_21 TGACGATTAGAAATCTCCTAA

target id: Solyc05g008070.2.1

737 5'-CAAGGGTAGGAGATTTCTAATCGTCATAGAT-3' 767 cleavage site: 752

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3'-AATCCTCTAAAGATTAGCAGT-5'

D51\_TPM.filter 24978863\_24 TTGCTCATTTCTTGATTGTTGACT

target id: Solyc05g008070.2.1

675 5'-AGTGGAGTCAACAATCAAGAAATGAGCAATGATG-3' 708 cleavage site: 693

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3'-TCAGTTGTTAGTTCTTTACTCGTT-5'

D51\_TPM.filter 16681520\_21 CGATCTTTTCTGAATAGCTTC

target id: Solyc05g008070.2.1

945 5'-ACCAAAAAGCTATTCAGAAAAGATCGTTGTC-3' 975 cleavage site: 960

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3'-CTTCGATAAGTCTTTTCTAGC-5'

D51\_TPM.filter 19348359\_21 TAAGAAGATCATGAATTTTGT

target id: Solyc05g008070.2.1

1394 5'-AACTTGCAAAATTCATGATCTTCTTAGGCAG-3' 1424 cleavage site: 1409

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3'-TGTTTTAAGTACTAGAAGAAT-5'

D51\_TPM.filter 10598242\_22 ATTATATTGTTCACTTATTGGT

target id: Solyc05g008070.2.1

613 5'-GGGTCACC-ATATCTGAACAATATAATAAGAG-3' 643 cleavage site: 628

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3'-TGGTTATTCACTTGTTATATTA-5'

D51\_TPM.filter 25866736\_20 TTTAGCAAGAGTTGTTTTAC

target id: Solyc05g008070.2.1

539 5'-TATAGGTAAGACAACTCTTGCTAGAAAAGT-3' 568 cleavage site: 553

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3'-CATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 25048327\_21 TTGTGAGTAAGTAGAAACAAG

target id: Solyc05g008070.2.1

1474 5'-GTGATCTTGTTTCTACTTACTCACAAGACAT-3' 1504 cleavage site: 1489

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3'-GAACAAAGATGAATGAGTGTT-5'

D51\_TPM.filter 12220148\_22 GAGGACAACGATCTTTTCTGAA

target id: Solyc05g008070.2.1

952 5'-AGCTATTCAGAAAAGATCGTTGTCCTCCACAA-3' 983 cleavage site: 968

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3'-AAGTCTTTTCTAGCAACAGGAG-5'

D51\_TPM.filter 03562038\_22 AATTATATTGTTCACTTATTGG

target id: Solyc05g008070.2.1

614 5'-GGTCACC-ATATCTGAACAATATAATAAGAGA-3' 644 cleavage site: 629

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3'-GGTTATTCACTTGTTATATTAA-5'

D51\_TPM.filter 24301904\_22 TTATATTGTTCAGATATGGTGA

target id: Solyc05g008070.2.1

611 5'-ATGGGTCACCATATCTGAACAATATAATAAGA-3' 642 cleavage site: 627

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3'-AGTGGTATAGACTTGTTATATT-5'

D51\_TPM.filter 24978911\_21 TTGCTCATTTCTTGATTGTTG

target id: Solyc05g008070.2.1

678 5'-GGAGTCAACAATCAAGAAATGAGCAATGATG-3' 708 cleavage site: 693

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3'-GTTGTTAGTTCTTTACTCGTT-5'

D51\_TPM.filter 20412523\_21 TATGACGATTAGAAATCTCCT

target id: Solyc05g008070.2.1

739 5'-AGGGTAGGAGATTTCTAATCGTCATAGATGA-3' 769 cleavage site: 754

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3'-TCCTCTAAAGATTAGCAGTAT-5'

D51\_TPM.filter 26653916\_22 TTTTAGCAAGAGTTGTTTTACG

target id: Solyc05g008070.2.1

538 5'-GTATAGGTAAGACAACTCTTGCTAGAAAAGTT-3' 569 cleavage site: 554

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3'-GCATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 26362371\_22 TTTCAGGTACTAGATAAGATCT

target id: Solyc05g008070.2.1

1615 5'-GTGGTAGATCTTATCTAGTACCTGAAATGAAC-3' 1646 cleavage site: 1631

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3'-TCTAGAATAGATCATGGACTTT-5'

D51\_TPM.filter 22612400\_21 TCATTTCTTGATTGTTGACGC

target id: Solyc05g008070.2.1

674 5'-TAGTGGAGTCAACAATCAAGAAATGAGCAAT-3' 704 cleavage site: 689

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3'-CGCAGTTGTTAGTTCTTTACT-5'

D51\_TPM.filter 06186628\_21 ACAACGATCTTTTCTGAATAC

target id: Solyc05g008070.2.1

949 5'-AAAAGCTATTCAGAAAAGATCGTTGTCCTCC-3' 979 cleavage site: 964

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3'-CATAAGTCTTTTCTAGCAACA-5'

D51\_TPM.filter 26653934\_23 TTTTAGCAAGAGTTGTTTTACCC

target id: Solyc05g008070.2.1

537 5'-GGTATAGGTAAGACAACTCTTGCTAGAAAAGTT-3' 569 cleavage site: 554

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3'-CCCATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 14979410\_22 GTGTGTCTATTTGTTCAACTTC

target id: Solyc05g008070.2.1

1879 5'-ATGTTGATA-TTGAACAAATGGATATGCCTAAT-3' 1910 cleavage site: 1895

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3'-CT-TCAACTTGTTTATCTGTGTG-5'

D51\_TPM.filter 25166580\_21 TTGTTGCCTTAATGAACTGCT

target id: Solyc05g008070.2.1

1268 5'-AGCTGAGCAGTTCATTAAGGCAACAAGCGAT-3' 1298 cleavage site: 1283

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3'-TCGTCAAGTAATTCCGTTGTT-5'

D51\_TPM.filter 05684092\_20 AGTGAACTGTAGTTGTGAAA

target id: Solyc04g009240.1.1

2351 5'-ACAGCTTCTGTCAACTACAGTTC-CTTCAAC-3' 2380 cleavage site: 2365

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3'-AAAGT-GTTGATGTCAAGTGA-5'

D51\_TPM.filter 10902796\_21 ATTGTGTTGTACTCTTGAGAG

target id: Solyc04g009240.1.1

655 5'-TGTGTTTCTCAAGAGTACAACACAATGGATC-3' 685 cleavage site: 670

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3'-GAGAGTTCTCATGTTGTGTTA-5'

D51\_TPM.filter 23617531\_22 TCTTATGAATTCTAGGTCTTCT

target id: Solyc05g053990.2.1

685 5'-GTGAAACAAGACCTCGAAATCATAAGATCGTT-3' 716 cleavage site: 701

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3'-TCTTCTGGATCTTAAGTATTCT-5'

D51\_TPM.filter 23617480\_21 TCTTATGAATTCTAGGTCTTC

target id: Solyc05g053990.2.1

686 5'-TGAAACAAGACCTCGAAATCATAAGATCGTT-3' 716 cleavage site: 701

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3'-CTTCTGGATCTTAAGTATTCT-5'

D51\_TPM.filter 23617435\_22 TCTTATGAATTCTAGGTCTTCA

target id: Solyc05g053990.2.1

685 5'-GTGAAACAAGACCTCGAAATCATAAGATCGTT-3' 716 cleavage site: 701

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3'-ACTTCTGGATCTTAAGTATTCT-5'

D51\_TPM.filter 23617345\_22 TCTTATGAATTCTAGGTCTTCC

target id: Solyc05g053990.2.1

685 5'-GTGAAACAAGACCTCGAAATCATAAGATCGTT-3' 716 cleavage site: 701

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3'-CCTTCTGGATCTTAAGTATTCT-5'

D51\_TPM.filter 23617392\_21 TCTTATGAATTCTAGGTCTTT

target id: Solyc05g053990.2.1

686 5'-TGAAACAAGACCTCGAAATCATAAGATCGTT-3' 716 cleavage site: 701

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3'-TTTCTGGATCTTAAGTATTCT-5'

D51\_TPM.filter 08974426\_24 ATGAATTTTGAATAATTGAAGTGT

target id: Solyc05g053990.2.1

1890 5'-TTTCGATGATTCTATT-TTCAAAATTCATGATCT-3' 1922 cleavage site: 1907

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3'-TGTGAAGTTAATAAGTTTTAAGTA-5'

D51\_TPM.filter 25776990\_20 TTTAAGTATGAGTTTGGACT

target id: Solyc11g006640.1.1

1346 5'-GCCTAAG-TGAAACTCATAC-TGAAAATGT-3' 1373 cleavage site: 1358

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3'-TCAGGTTTGAGTATGAATTT-5'

D51\_TPM.filter 20554586\_23 TATCCGATCAAAATTAAACTGTT

target id: Solyc11g006640.1.1

1259 5'-TTGATAGAAGTCTAATTTTGA-TGGATAGCTTA-3' 1290 cleavage site: 1275

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3'-TTGTCAAATTAAAACTAGCCTAT-5'

D51\_TPM.filter 20554474\_24 TATCCGATCAAAATTAAACTGTTT

target id: Solyc11g006640.1.1

1259 5'-TTGATAGA-AGTCTAATTTTGA-TGGATAGCTTA-3' 1290 cleavage site: 1275

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3'-TTTGTCAAATTAAAACTAGCCTAT-5'

D51\_TPM.filter 25374791\_21 TTCGATACACGAATCTCCATA

target id: Solyc11g006640.1.1

712 5'-GAACTAATGGAGA-TTGTGTATAGAGGTCTG-3' 741 cleavage site: 726

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3'-ATACCTCTAAGCACATAGCTT-5'

D51\_TPM.filter 24662617\_23 TTGATATAGGGACTTCATATTCT

target id: Solyc11g006640.1.1

2097 5'-AATCAAGAA-ATTAAGTCCTAATATCAAGAAAT-3' 2128 cleavage site: 2113

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3'-TCTTATACTTCAGGGATATAGTT-5'

D51\_TPM.filter 22162669\_21 TGTTGTCAGTAGATTTCTCGA

target id: Solyc11g006640.1.1

1703 5'-ATAAATTGAGAAATCTACAGACCATAATTCT-3' 1733 cleavage site: 1718

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3'-AGCTCTTTAGATGACTGTTGT-5'

D51\_TPM.filter 24330061\_20 TTATGGTCTTGGATATTTCT

target id: Solyc11g006640.1.1

1704 5'-TAAATTGAGAAATCTACAGACCATAATTCTT-3' 1734 cleavage site: 1719

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3'-TCTTTATAGGT-TCTGGTATT-5'

D51\_TPM.filter 20269440\_22 TACTTCTTCTATTGTATCTGGT

target id: Solyc04g005550.1.1

3411 5'-AGCCTGCCA-AT-CAATAGAAGAAGTGATCAC-3' 3440 cleavage site: 3425

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3'-TGGTCTATGTTATCTTCTTCAT-5'

D51\_TPM.filter 22129026\_21 TGTTACTTTGCACTGATGGTT

target id: Solyc04g005550.1.1

836 5'-ACCACAAACATCGGTGCAAAGTGACATTCAC-3' 866 cleavage site: 851

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3'-TTGGTAGTCACGTTTCATTGT-5'

D51\_TPM.filter 22987009\_21 TCCAGCTGCATACTGAGTAGT

target id: Solyc04g005550.1.1

3759 5'-CGATGGCTAC-CAATATGAAGCTGGAGATGT-3' 3788 cleavage site: 3773

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3'-TGATGAGTCATACGTCGACCT-5'

D51\_TPM.filter 22405750\_24 TCAGGGCACCTATCTAATCTAATT

target id: Solyc04g005550.1.1

3580 5'-AGAGTAGTATGGATTA-ATAGTTGCCCTGAAATGG-3' 3613 cleavage site: 3598

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3'-TTA-ATCTAATCTATCCACGGGACT-5'

D51\_TPM.filter 16707448\_21 CGGAAACGCGTTGTGAATGTC

target id: Solyc04g005550.1.1

853 5'-AAAGTGACATTCACAACGCGTTTCCGACATG-3' 883 cleavage site: 868

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3'-CTGTAAGTGTTGCGCAAAGGC-5'

D51\_TPM.filter 10554185\_21 ATTACCGACTTTCTGTCTGAA

target id: Solyc04g005550.1.1

950 5'-ACCTTTTCAGGCAGAAAGCCGGTAACTCAGT-3' 980 cleavage site: 965

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3'-AAGTCTGTCTTTCAGCCATTA-5'

D51\_TPM.filter 20738537\_22 TATTTCTTCTATTGTATCTGGT

target id: Solyc04g005550.1.1

3411 5'-AGCCTGCCA-AT-CAATAGAAGAAGTGATCAC-3' 3440 cleavage site: 3425

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3'-TGGTCTATGTTATCTTCTTTAT-5'

D51\_TPM.filter 02410133\_21 AACGCGTTGTGAATGTCACTT

target id: Solyc04g005550.1.1

849 5'-GTGCAAAGTGACATTCACAACGCGTTTCCGA-3' 879 cleavage site: 864

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3'-TTCACTGTAAGTGTTGCGCAA-5'

D51\_TPM.filter 03547390\_22 AATTACCGGCTTTCTGCCTGAA

target id: Solyc04g005550.1.1

950 5'-ACCTTTTCAGGCAGAAAGCCGGTAACTCAGTT-3' 981 cleavage site: 966

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3'-AAGTCCGTCTTTCGGCCATTAA-5'

D51\_TPM.filter 24207800\_21 TTACCGGCTTTCTGCCTGAAA

target id: Solyc04g005550.1.1

949 5'-AACCTTTTCAGGCAGAAAGCCGGTAACTCAG-3' 979 cleavage site: 964

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3'-AAAGTCCGTCTTTCGGCCATT-5'

D51\_TPM.filter 16707484\_21 CGGAAACGCGTTGTGAATGTT

target id: Solyc04g005550.1.1

853 5'-AAAGTGACATTCACAACGCGTTTCCGACATG-3' 883 cleavage site: 868

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3'-TTGTAAGTGTTGCGCAAAGGC-5'

D51\_TPM.filter 10554422\_21 ATTACCGGCTTTCTGCCTGAA

target id: Solyc04g005550.1.1

950 5'-ACCTTTTCAGGCAGAAAGCCGGTAACTCAGT-3' 980 cleavage site: 965

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3'-AAGTCCGTCTTTCGGCCATTA-5'

D51\_TPM.filter 17072469\_21 CGCGTTGTCAATGTTACTTTG

target id: Solyc04g005550.1.1

847 5'-CGGTGCAAAGTGACATTCACAACGCGTTTCC-3' 877 cleavage site: 862

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3'-GTTTCATTGTAACTGTTGCGC-5'

D51\_TPM.filter 24206278\_21 TTACCGACTTTCTGTCTGAAA

target id: Solyc04g005550.1.1

949 5'-AACCTTTTCAGGCAGAAAGCCGGTAACTCAG-3' 979 cleavage site: 964

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3'-AAAGTCTGTCTTTCAGCCATT-5'

D51\_TPM.filter 06217752\_21 ACAATGATCTTACTTCCTATA

target id: Solyc11g064770.1.1

682 5'-GGAGATTTGGGAAGTAAGATCATTGTAACTA-3' 712 cleavage site: 697

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3'-ATATCCTTCATTCTAGTAACA-5'

D51\_TPM.filter 10902796\_21 ATTGTGTTGTACTCTTGAGAG

target id: Solyc04g009150.1.1

655 5'-TGTGTTTCTCAAGAGTACAACACAATGGATC-3' 685 cleavage site: 670

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3'-GAGAGTTCTCATGTTGTGTTA-5'

D51\_TPM.filter 10823624\_21 ATTGGTGAAATATTCTAGAGT

target id: Solyc09g092310.1.1

2020 5'-GTTGAAC-CGAGATTATTTCACCGGTTGATC-3' 2049 cleavage site: 2034

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3'-TGAGATCTTATAAAGTGGTTA-5'

D51\_TPM.filter 24787600\_21 TTGGATCTTGGAATATTTCTC

target id: Solyc01g086810.2.1

1861 5'-AATGTGA-AAGTACTTCCAAGATCCATTGGAA-3' 1891 cleavage site: 1876

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3'-CTCTTTAT-AAGGTTCTAGGTT-5'

D51\_TPM.filter 03155661\_24 AATGGATCTTGTGAAACTTTCACC

target id: Solyc01g086810.2.1

1858 5'-ACCAATGTGAAAGTACTTC-CAAGATCCATTGGAAG-3' 1892 cleavage site: 1877

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3'-CCACTTTCA--AAGTGTTCTAGGTAA-5'

D51\_TPM.filter 25527754\_21 TTCCGTTCTTTTAGTCCTTTG

target id: Solyc01g086810.2.1

1398 5'-ATTTGTAAA--ACAAAAAGAACGGAGGACAG-3' 1426 cleavage site: 1411

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3'-GTTTCCTGATTTTCTTGCCTT-5'

D51\_TPM.filter 08974426\_24 ATGAATTTTGAATAATTGAAGTGT

target id: Solyc05g050430.1.1

2382 5'-TTTCGATGATTCTATT-TTCAAAATTCATGATCT-3' 2414 cleavage site: 2399

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3'-TGTGAAGTTAATAAGTTTTAAGTA-5'

D51\_TPM.filter 20685825\_20 TATTCCATGAGACTGTTTTT

target id: Solyc12g094660.1.1

2779 5'-AGGAAAAAAACAAGTCTCAGGGAATTGATCA-3' 2809 cleavage site: 2794

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3'-TTTTTG-TCAGAGTACCTTAT-5'

D51\_TPM.filter 20686125\_21 TATTCCATGAGACTGTTTTTG

target id: Solyc12g094660.1.1

2778 5'-GAGGAAAAAAACAAGTCTCAGGGAATTGATCA-3' 2809 cleavage site: 2794

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3'-GTTTTTG-TCAGAGTACCTTAT-5'

D51\_TPM.filter 25488995\_21 TTCCATGAGACTGTTTTTGTT

target id: Solyc12g094660.1.1

2776 5'-CTGAGGAAAAAAACAAGTCTCA-GGGAATTGA-3' 2806 cleavage site: 2791

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3'-TTGTTTTTG-TCAGAGTACCTT-5'

D51\_TPM.filter 25489540\_21 TTCCATGAGACTGTTTTTTTT

target id: Solyc12g094660.1.1

2776 5'-CTGAGGAAAAAAACAAGTCTCA-GGGAATTGA-3' 2806 cleavage site: 2791

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3'-TTTTTTTTG-TCAGAGTACCTT-5'

D51\_TPM.filter 20686002\_23 TATTCCATGAGACTGTTTTTTTT

target id: Solyc12g094660.1.1

2776 5'-CTGAGGAAAAAAACAAGTCTCAGGGAATTGATCA-3' 2809 cleavage site: 2794

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3'-TTTTTTTTG-TCAGAGTACCTTAT-5'

D51\_TPM.filter 20686090\_21 TATTCCATGAGACTGTTTTTT

target id: Solyc12g094660.1.1

2778 5'-GAGGAAAAAAACAAGTCTCAGGGAATTGATCA-3' 2809 cleavage site: 2794

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3'-TTTTTTG-TCAGAGTACCTTAT-5'

D51\_TPM.filter 20685962\_22 TATTCCATGAGACTGTTTTTTT

target id: Solyc12g094660.1.1

2777 5'-TGAGGAAAAAAACAAGTCTCAGGGAATTGATCA-3' 2809 cleavage site: 2794

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3'-TTTTTTTG-TCAGAGTACCTTAT-5'

D51\_TPM.filter 25490119\_20 TTCCATGAGACTGTTTTTTT

target id: Solyc12g094660.1.1

2777 5'-TGAGGAAAAAAACAAGTCTCA-GGGAATTGA-3' 2806 cleavage site: 2791

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3'-TTTTTTTG-TCAGAGTACCTT-5'

D51\_TPM.filter 25490165\_22 TTCCATGAGACTGTTTTTTTTT

target id: Solyc12g094660.1.1

2775 5'-ACTGAGGAAAAAAACAAGTCTCA-GGGAATTGA-3' 2806 cleavage site: 2791

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3'-TTTTTTTTTG-TCAGAGTACCTT-5'

D51\_TPM.filter 25489031\_22 TTCCATGAGACTGTTTTTGTTC

target id: Solyc12g094660.1.1

2775 5'-ACTGAGGAAAAAAACAAGTCTCA-GGGAATTGA-3' 2806 cleavage site: 2791

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3'-CTTGTTTTTG-TCAGAGTACCTT-5'

D51\_TPM.filter 20686722\_21 TATTCCATGAGACTGTTTTTC

target id: Solyc12g094660.1.1

2778 5'-GAGGAAAAAAACAAGTCTCAGGGAATTGATCA-3' 2809 cleavage site: 2794

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3'-CTTTTTG-TCAGAGTACCTTAT-5'

D51\_TPM.filter 20686987\_23 TATTCCATGAGACTGTTTTTTTC

target id: Solyc12g094660.1.1

2776 5'-CTGAGGAAAAAAACAAGTCTCAGGGAATTGATCA-3' 2809 cleavage site: 2794

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3'-CTTTTTTTG-TCAGAGTACCTTAT-5'

D51\_TPM.filter 25489643\_21 TTCCATGAGACTGTTTTTTTC

target id: Solyc12g094660.1.1

2776 5'-CTGAGGAAAAAAACAAGTCTCA-GGGAATTGA-3' 2806 cleavage site: 2791

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3'-CTTTTTTTG-TCAGAGTACCTT-5'

D51\_TPM.filter 20686860\_24 TATTCCATGAGACTGTTTTTTTTT

target id: Solyc12g094660.1.1

2775 5'-ACTGAGGAAAAAAACAAGTCTCAGGGAATTGATCA-3' 2809 cleavage site: 2794

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3'-TTTTTTTTTG-TCAGAGTACCTTAT-5'

D51\_TPM.filter 20685760\_21 TATTCCATGAGACTGTTTTTA

target id: Solyc12g094660.1.1

2778 5'-GAGGAAAAAAACAAGTCTCAGGGAATTGATCA-3' 2809 cleavage site: 2794

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3'-ATTTTTG-TCAGAGTACCTTAT-5'

D51\_TPM.filter 25489283\_23 TTCCATGAGACTGTTTTTTTTTT

target id: Solyc12g094660.1.1

2774 5'-TACTGAGGAAAAAAACAAGTCTCA-GGGAATTGA-3' 2806 cleavage site: 2791

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3'-TTTTTTTTTTG-TCAGAGTACCTT-5'

D51\_TPM.filter 25490151\_21 TTCCATGAGACTGTTTTTTCT

target id: Solyc12g094660.1.1

2775 5'-ACTGAGGAAAAAAACAAGTCTCA-GGGAATTGA-3' 2806 cleavage site: 2791

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3'-TC-TTTTTTG-TCAGAGTACCTT-5'

D51\_TPM.filter 25490326\_20 TTCCATGAGACTGTTTTTTC

target id: Solyc12g094660.1.1

2777 5'-TGAGGAAAAAAACAAGTCTCA-GGGAATTGA-3' 2806 cleavage site: 2791

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3'-CTTTTTTG-TCAGAGTACCTT-5'

D51\_TPM.filter 25490580\_21 TTCCATGAGACTGTTTTTGTC

target id: Solyc12g094660.1.1

2776 5'-CTGAGGAAAAAAACAAGTCTCA-GGGAATTGA-3' 2806 cleavage site: 2791

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3'-CTGTTTTTG-TCAGAGTACCTT-5'

D51\_TPM.filter 25490156\_22 TTCCATGAGACTGTTTTTTTTC

target id: Solyc12g094660.1.1

2775 5'-ACTGAGGAAAAAAACAAGTCTCA-GGGAATTGA-3' 2806 cleavage site: 2791

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3'-CTTTTTTTTG-TCAGAGTACCTT-5'

D51\_TPM.filter 20685809\_22 TATTCCATGAGACTGTTTTTTG

target id: Solyc12g094660.1.1

2777 5'-TGAGGAAAAAAACAAGTCTCAGGGAATTGATCA-3' 2809 cleavage site: 2794

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3'-GTTTTTTG-TCAGAGTACCTTAT-5'

D51\_TPM.filter 20686690\_22 TATTCCATGAGACTGTTTTTTC

target id: Solyc12g094660.1.1

2777 5'-TGAGGAAAAAAACAAGTCTCAGGGAATTGATCA-3' 2809 cleavage site: 2794

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3'-CTTTTTTG-TCAGAGTACCTTAT-5'

D51\_TPM.filter 03701049\_22 AATTCCATGAGACTGTTTTTGG

target id: Solyc12g094660.1.1

2777 5'-TGAGGAAAAAAACAAGTCTCAGGGAATTGATCA-3' 2809 cleavage site: 2794

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3'-GGTTTTTG-TCAGAGTACCTTAA-5'

D51\_TPM.filter 20685862\_24 TATTCCATGAGACTGTTTTTTTTC

target id: Solyc12g094660.1.1

2775 5'-ACTGAGGAAAAAAACAAGTCTCAGGGAATTGATCA-3' 2809 cleavage site: 2794

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3'-CTTTTTTTTG-TCAGAGTACCTTAT-5'

D51\_TPM.filter 20686721\_23 TATTCCATGAGACTGTTTTTGTC

target id: Solyc12g094660.1.1

2776 5'-CTGAGGAAAAAAACAAGTCTCAGGGAATTGATCA-3' 2809 cleavage site: 2794

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3'-CTGTTTTTG-TCAGAGTACCTTAT-5'

D51\_TPM.filter 26017789\_21 TTTGAAAATGGACCAACAATG

target id: Solyc10g085460.1.1

974 5'-ATGATCATTGTTTGTCCATTTTCAAACAAAG-3' 1004 cleavage site: 989

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3'-GTAACAACCAGGTAAAAGTTT-5'

D51\_TPM.filter 26323898\_21 TTTGTTTGAAAATGGACCAAC

target id: Solyc10g085460.1.1

978 5'-TCATTGTTTGTCCATTTTCAAACAAAGAGCA-3' 1008 cleavage site: 993

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3'-CAACCAGGTAAAAGTTTGTTT-5'

D51\_TPM.filter 20771087\_21 TGAAAATGGACCAACAATGAT

target id: Solyc10g085460.1.1

972 5'-AGATGATCATTGTTTGTCCATTTTCAAACAA-3' 1002 cleavage site: 987

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3'-TAGTAACAACCAGGTAAAAGT-5'

D51\_TPM.filter 00758108\_24 AAAGTATCGAACTGGAGTAAGATT

target id: Solyc10g085460.1.1

1523 5'-GTGAAAATCTTTCTCAAGTTCGATACTTTGGATG-3' 1556 cleavage site: 1541

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3'-TTAGAATGAGGTCAAGCTATGAAA-5'

D51\_TPM.filter 04526962\_21 AGATGGACTTGAGAAAGGGTT

target id: Solyc10g085460.1.1

1522 5'-GGTGAAAATCTTTCTCAAGTTCGATACTTTGGA-3' 1554 cleavage site: 1539

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3'-TTGGGAAAGAGTTCAGG-TA-GA-5'

D51\_TPM.filter 26324645\_21 TTTGTTTGAAAATGGACCAAT

target id: Solyc10g085460.1.1

978 5'-TCATTGTTTGTCCATTTTCAAACAAAGAGCA-3' 1008 cleavage site: 993

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3'-TAACCAGGTAAAAGTTTGTTT-5'

D51\_TPM.filter 24468620\_21 TTGAAAATGGACCAACAATGA

target id: Solyc10g085460.1.1

973 5'-GATGATCATTGTTTGTCCATTTTCAAACAAA-3' 1003 cleavage site: 988

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3'-AGTAACAACCAGGTAAAAGTT-5'

D51\_TPM.filter 02000669\_24 AAGTATCGAACTGGAGTAAGATTC

target id: Solyc10g085460.1.1

1522 5'-GGTGAAAATCTTTCTCAAGTTCGATACTTTGGAT-3' 1555 cleavage site: 1540

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3'-CTTAGAATGAGGTCAAGCTATGAA-5'

D51\_TPM.filter 01962304\_24 AAGTAACTGTTCAACGAAGCAATT

target id: Solyc10g085460.1.1

3475 5'-GGCAACCTTGCTTCTTTGGAACAGTTACTTATTTT-3' 3509 cleavage site: 3494

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3'-TTAACGAAGCAA-CTTGTCAATGAA-5'

D51\_TPM.filter 08685594\_24 ATATGTCATCTTTTGAATTTCAAG

target id: Solyc04g015210.2.1

2368 5'-CCACCCTTGAGA--TAAAAGAGGACATATGGAAA-3' 2399 cleavage site: 2384

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3'-GAACTTTAAGTTTTCTACTGTATA-5'

D51\_TPM.filter 18756713\_21 CTTAAGGATGTTAGTCTAGGC

target id: Solyc11g069620.1.1

1705 5'-ATACTGCCAAGACTGACATCCTTAAGGGCAT-3' 1735 cleavage site: 1720

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3'-CGGATCTGATTGTAGGAATTC-5'

D51\_TPM.filter 06217752\_21 ACAATGATCTTACTTCCTATA

target id: Solyc11g069620.1.1

922 5'-GGAGGTATGGGAAGTAAGATCATTGTAACTA-3' 952 cleavage site: 937

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3'-ATATCCTTCATTCTAGTAACA-5'

D51\_TPM.filter 24156334\_21 TTACAATGATCTTACTTCCTA

target id: Solyc11g069620.1.1

924 5'-AGGTATGGGAAGTAAGATCATTGTAACTACA-3' 954 cleavage site: 939

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3'-ATCCTTCATTCTAGTAACATT-5'

D51\_TPM.filter 23852157\_21 TTAAGGATGTTAGTCTAGGCA

target id: Solyc11g069620.1.1

1704 5'-CATACTGCCAAGACTGACATCCTTAAGGGCA-3' 1734 cleavage site: 1719

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3'-ACGGATCTGATTGTAGGAATT-5'

D51\_TPM.filter 23852925\_20 TTAAGGATGTTAGTCTAGGC

target id: Solyc11g069620.1.1

1705 5'-ATACTGCCAAGACTGACATCCTTAAGGGCA-3' 1734 cleavage site: 1719

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3'-CGGATCTGATTGTAGGAATT-5'

D51\_TPM.filter 18756878\_21 CTTAAGGATGTTAGTCTAGGT

target id: Solyc11g069620.1.1

1705 5'-ATACTGCCAAGACTGACATCCTTAAGGGCAT-3' 1735 cleavage site: 1720

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3'-TGGATCTGATTGTAGGAATTC-5'

D51\_TPM.filter 21734213\_21 TGCGGGAAGATCATTGTAGCT

target id: Solyc11g069620.1.1

1250 5'-TGTTGAGCTACAATGATCTTCCTGCACAATT-3' 1280 cleavage site: 1265

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3'-TCGATGTTACTAGAAGGGCGT-5'

D51\_TPM.filter 21688701\_21 TGCAGGAAGATCATTGTAGCT

target id: Solyc11g069620.1.1

1250 5'-TGTTGAGCTACAATGATCTTCCTGCACAATT-3' 1280 cleavage site: 1265

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3'-TCGATGTTACTAGAAGGACGT-5'

D51\_TPM.filter 20044818\_21 TACAATGATCTTACTTCCTAT

target id: Solyc11g069620.1.1

923 5'-GAGGTATGGGAAGTAAGATCATTGTAACTAC-3' 953 cleavage site: 938

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3'-TATCCTTCATTCTAGTAACAT-5'

D51\_TPM.filter 01607288\_21 AAGATCATTGTAGCTCAACAT

target id: Solyc11g069620.1.1

1244 5'-CATTGATGTTGAGCTACAATGATCTTCCTGC-3' 1274 cleavage site: 1259

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3'-TACAACTCGATGTTACTAGAA-5'

D51\_TPM.filter 01607370\_21 AAGATCATCGTAGCTCAACAT

target id: Solyc11g069620.1.1

1244 5'-CATTGATGTTGAGCTACAATGATCTTCCTGC-3' 1274 cleavage site: 1259

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3'-TACAACTCGATGCTACTAGAA-5'

D51\_TPM.filter 24156686\_22 TTACAATGATCTTACTTCCTAT

target id: Solyc11g069620.1.1

923 5'-GAGGTATGGGAAGTAAGATCATTGTAACTACA-3' 954 cleavage site: 939

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3'-TATCCTTCATTCTAGTAACATT-5'

D51\_TPM.filter 02685629\_24 AACTTATCGATTGATGTCAACTGC

target id: Solyc05g012910.2.1

3992 5'-GTGCTGCA-TTGACATCAGTCGATAAGCTGAAGC-3' 4024 cleavage site: 4009

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3'-CGTCAACTGTAGTTAGCTATTCAA-5'

D51\_TPM.filter 07559125\_24 ACTTATCGATTGATGTCAACTGCT

target id: Solyc05g012910.2.1

3991 5'-GGTGCTGCA-TTGACATCAGTCGATAAGCTGAAG-3' 4023 cleavage site: 4008

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3'-TCGTCAACTGTAGTTAGCTATTCA-5'

D51\_TPM.filter 23251003\_21 TCCTTGACATTGTTGTATGAT

target id: Solyc04g012010.2.1

1024 5'-AGGAAATAGTAGAAAAATGTCAAGGACTACC-3' 1054 cleavage site: 1039

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3'-TAGTATGTTGTTACAGTTCCT-5'

D51\_TPM.filter 10365346\_24 ATCTTTTTTGACTGTGTATAAATA

target id: Solyc07g005770.2.1

2571 5'-TAAGTTACTTGTACATAGTCAAAGAAGACATAAC-3' 2604 cleavage site: 2589

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3'-ATAAATATGTGTCAGTTTTTTCTA-5'

D51\_TPM.filter 09830638\_21 ATCATCCTGTAATTTGAACGG

target id: Solyc12g016220.1.1

1739 5'-AAGAGTCATTCAAGTTACAGGCTGATTTTTC-3' 1769 cleavage site: 1754

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3'-GGCAAGTTTAATGTCCTACTA-5'

D51\_TPM.filter 22578698\_21 TCATCCTGTAATTTGAACGGC

target id: Solyc12g016220.1.1

1738 5'-AAAGAGTCATTCAAGTTACAGGCTGATTTTT-3' 1768 cleavage site: 1753

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3'-CGGCAAGTTTAATGTCCTACT-5'

D51\_TPM.filter 23219160\_21 TCCTGTAATTTGAACGGCTCT

target id: Solyc12g016220.1.1

1735 5'-GTTAAAGAGTCATTCAAGTTACAGGCTGATT-3' 1765 cleavage site: 1750

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3'-TCTCGGCAAGTTTAATGTCCT-5'

D51\_TPM.filter 22578697\_21 TCATCCTGTAATTTGAACGGT

target id: Solyc12g016220.1.1

1738 5'-AAAGAGTCATTCAAGTTACAGGCTGATTTTT-3' 1768 cleavage site: 1753

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3'-TGGCAAGTTTAATGTCCTACT-5'

D51\_TPM.filter 20900898\_21 TGAATCCTTCGGCTATCCATA

target id: Solyc11g069020.1.1

1305 5'-AAGGTTATGGATTGCTGAAGGATTTATAAAG-3' 1335 cleavage site: 1320

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3'-ATACCTATCGGCTTCCTAAGT-5'

D51\_TPM.filter 25866430\_21 TTTAGCAAGAGTTGTTTTACC

target id: Solyc11g069020.1.1

566 5'-GTATAGGTAAAACCACTCTTGCTAAGAGAAT-3' 596 cleavage site: 581

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3'-CCATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 26653861\_22 TTTTAGCAAGAGTTGTTTTACC

target id: Solyc11g069020.1.1

566 5'-GTATAGGTAAAACCACTCTTGCTAAGAGAATT-3' 597 cleavage site: 582

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3'-CCATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 25866155\_21 TTTAGCAAGAGTTGTTTTACT

target id: Solyc11g069020.1.1

566 5'-GTATAGGTAAAACCACTCTTGCTAAGAGAAT-3' 596 cleavage site: 581

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3'-TCATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 26654022\_22 TTTTAGCAAGAGTTGTTTTACT

target id: Solyc11g069020.1.1

566 5'-GTATAGGTAAAACCACTCTTGCTAAGAGAATT-3' 597 cleavage site: 582

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3'-TCATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 20900987\_22 TGAATCCTTCGGCTATCCATAA

target id: Solyc11g069020.1.1

1304 5'-TAAGGTTATGGATTGCTGAAGGATTTATAAAG-3' 1335 cleavage site: 1320

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3'-AATACCTATCGGCTTCCTAAGT-5'

D51\_TPM.filter 20900999\_20 TGAATCCTTCGGCTATCCAT

target id: Solyc11g069020.1.1

1306 5'-AGGTTATGGATTGCTGAAGGATTTATAAAG-3' 1335 cleavage site: 1320

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3'-TACCTATCGGCTTCCTAAGT-5'

D51\_TPM.filter 26653812\_23 TTTTAGCAAGAGTTGTTTTACCT

target id: Solyc11g069020.1.1

565 5'-GGTATAGGTAAAACCACTCTTGCTAAGAGAATT-3' 597 cleavage site: 582

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3'-TCCATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 26654357\_22 TTTTAGCAAGAGTTGTTTTACA

target id: Solyc11g069020.1.1

566 5'-GTATAGGTAAAACCACTCTTGCTAAGAGAATT-3' 597 cleavage site: 582

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3'-ACATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 25866253\_21 TTTAGCAAGAGTTGTTTTACA

target id: Solyc11g069020.1.1

566 5'-GTATAGGTAAAACCACTCTTGCTAAGAGAAT-3' 596 cleavage site: 581

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3'-ACATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 25866391\_22 TTTAGCAAGAGTTGTTTTACCT

target id: Solyc11g069020.1.1

565 5'-GGTATAGGTAAAACCACTCTTGCTAAGAGAAT-3' 596 cleavage site: 581

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3'-TCCATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 20900927\_23 TGAATCCTTCGGCTATCCATAAT

target id: Solyc11g069020.1.1

1303 5'-ATAAGGTTATGGATTGCTGAAGGATTTATAAAG-3' 1335 cleavage site: 1320

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3'-TAATACCTATCGGCTTCCTAAGT-5'

D51\_TPM.filter 26653543\_24 TTTTAGCAAGAGTTGTTTTACTTT

target id: Solyc11g069020.1.1

564 5'-GGGTATAGGTAAAACCACTCTTGCTAAGAGAATT-3' 597 cleavage site: 582

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3'-TTTCATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 25866686\_23 TTTAGCAAGAGTTGTTTTACTTT

target id: Solyc11g069020.1.1

564 5'-GGGTATAGGTAAAACCACTCTTGCTAAGAGAAT-3' 596 cleavage site: 581

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3'-TTTCATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 20900852\_21 TGAATCCTTCGGCTATCCATT

target id: Solyc11g069020.1.1

1305 5'-AAGGTTATGGATTGCTGAAGGATTTATAAAG-3' 1335 cleavage site: 1320

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3'-TTACCTATCGGCTTCCTAAGT-5'

D51\_TPM.filter 20901206\_20 TGAATCCTTCGGCTATCCAC

target id: Solyc11g069020.1.1

1306 5'-AGGTTATGGATTGCTGAAGGATTTATAAAG-3' 1335 cleavage site: 1320

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3'-CACCTATCGGCTTCCTAAGT-5'

D51\_TPM.filter 25866557\_21 TTTAGCAAGAGTTGTTTTACG

target id: Solyc11g069020.1.1

566 5'-GTATAGGTAAAACCACTCTTGCTAAGAGAAT-3' 596 cleavage site: 581

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3'-GCATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 26654347\_23 TTTTAGCAAGAGTTGTTTTACCA

target id: Solyc11g069020.1.1

565 5'-GGTATAGGTAAAACCACTCTTGCTAAGAGAATT-3' 597 cleavage site: 582

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3'-ACCATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 25866163\_22 TTTAGCAAGAGTTGTTTTACCC

target id: Solyc11g069020.1.1

565 5'-GGTATAGGTAAAACCACTCTTGCTAAGAGAAT-3' 596 cleavage site: 581

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3'-CCCATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 19059194\_22 CTTTAGCAAGAGTTGTTTTACC

target id: Solyc11g069020.1.1

566 5'-GTATAGGTAAAACCACTCTTGCTAAGAGAATT-3' 597 cleavage site: 582

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3'-CCATTTTGTTGAGAACGATTTC-5'

D51\_TPM.filter 26654102\_21 TTTTAGCAAGAGTTGTTTTAC

target id: Solyc11g069020.1.1

567 5'-TATAGGTAAAACCACTCTTGCTAAGAGAATT-3' 597 cleavage site: 582

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3'-CATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 25866348\_22 TTTAGCAAGAGTTGTTTTACCA

target id: Solyc11g069020.1.1

565 5'-GGTATAGGTAAAACCACTCTTGCTAAGAGAAT-3' 596 cleavage site: 581

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3'-ACCATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 20900824\_21 TGAATCCTTCGGCTATCCATG

target id: Solyc11g069020.1.1

1305 5'-AAGGTTATGGATTGCTGAAGGATTTATAAAG-3' 1335 cleavage site: 1320

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3'-GTACCTATCGGCTTCCTAAGT-5'

D51\_TPM.filter 20901072\_21 TGAATCCTTCGGCTATCCACA

target id: Solyc11g069020.1.1

1305 5'-AAGGTTATGGATTGCTGAAGGATTTATAAAG-3' 1335 cleavage site: 1320

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3'-ACACCTATCGGCTTCCTAAGT-5'

D51\_TPM.filter 11370259\_24 ATTTGATCTTGTGAATATTCTATA

target id: Solyc11g069020.1.1

2588 5'-GACTCGCTAGAATGATTCAACAAGATCAAATTGACT-3' 2623 cleavage site: 2608

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3'-ATATCTTA-TAAG-TGTTCTAGTTTA-5'

D51\_TPM.filter 25866736\_20 TTTAGCAAGAGTTGTTTTAC

target id: Solyc11g069020.1.1

567 5'-TATAGGTAAAACCACTCTTGCTAAGAGAAT-3' 596 cleavage site: 581

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3'-CATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 26653916\_22 TTTTAGCAAGAGTTGTTTTACG

target id: Solyc11g069020.1.1

566 5'-GTATAGGTAAAACCACTCTTGCTAAGAGAATT-3' 597 cleavage site: 582

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3'-GCATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 02562802\_22 AACTAGATCTTGTGGAATCATA

target id: Solyc11g069020.1.1

2593 5'-GCTAGAATGATTCAACAAGATCAAATTGACTC-3' 2624 cleavage site: 2609

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3'-ATACTAAGGTGTTCTAGATCAA-5'

D51\_TPM.filter 26653934\_23 TTTTAGCAAGAGTTGTTTTACCC

target id: Solyc11g069020.1.1

565 5'-GGTATAGGTAAAACCACTCTTGCTAAGAGAATT-3' 597 cleavage site: 582

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3'-CCCATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 20900836\_21 TGAATCCTTCGGCTACCCATA

target id: Solyc11g069020.1.1

1305 5'-AAGGTTATGGATTGCTGAAGGATTTATAAAG-3' 1335 cleavage site: 1320

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3'-ATACCCATCGGCTTCCTAAGT-5'

D51\_TPM.filter 05291770\_22 AGCAACTAATTCATGATCTGGT

target id: Solyc02g084890.1.1

875 5'-TAACTACAAGA-AATGAGTTAGTTGCTCGCAA-3' 905 cleavage site: 890

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3'-TGGTCTAGTACTTAATCAACGA-5'

D51\_TPM.filter 05709005\_22 AGTGACTAACTCATGATCTGGT

target id: Solyc02g084890.1.1

875 5'-TAACTACAAGA-AATGAGTTAGTTGCTCGCAA-3' 905 cleavage site: 890

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3'-TGGTCTAGTACTCAATCAGTGA-5'

D51\_TPM.filter 05517686\_20 AGCTTGTCAATGACTGTACA

target id: Solyc04g009130.2.1

528 5'-GATGTTGTACAGACATT-GCTAGCTCAACT-3' 556 cleavage site: 541

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3'-ACATGTCAGTAACTGTTCGA-5'

D51\_TPM.filter 25866430\_21 TTTAGCAAGAGTTGTTTTACC

target id: Solyc10g008230.1.1

506 5'-GAATTGGCAAAACGACTCTTGCTAGAAAAGT-3' 536 cleavage site: 521

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3'-CCATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 26653861\_22 TTTTAGCAAGAGTTGTTTTACC

target id: Solyc10g008230.1.1

506 5'-GAATTGGCAAAACGACTCTTGCTAGAAAAGTT-3' 537 cleavage site: 522

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3'-CCATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 25866155\_21 TTTAGCAAGAGTTGTTTTACT

target id: Solyc10g008230.1.1

506 5'-GAATTGGCAAAACGACTCTTGCTAGAAAAGT-3' 536 cleavage site: 521

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3'-TCATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 26654022\_22 TTTTAGCAAGAGTTGTTTTACT

target id: Solyc10g008230.1.1

506 5'-GAATTGGCAAAACGACTCTTGCTAGAAAAGTT-3' 537 cleavage site: 522

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3'-TCATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 26653812\_23 TTTTAGCAAGAGTTGTTTTACCT

target id: Solyc10g008230.1.1

505 5'-GGAATTGGCAAAACGACTCTTGCTAGAAAAGTT-3' 537 cleavage site: 522

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3'-TCCATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 25866391\_22 TTTAGCAAGAGTTGTTTTACCT

target id: Solyc10g008230.1.1

505 5'-GGAATTGGCAAAACGACTCTTGCTAGAAAAGT-3' 536 cleavage site: 521

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3'-TCCATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 26654347\_23 TTTTAGCAAGAGTTGTTTTACCA

target id: Solyc10g008230.1.1

505 5'-GGAATTGGCAAAACGACTCTTGCTAGAAAAGTT-3' 537 cleavage site: 522

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3'-ACCATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 25866163\_22 TTTAGCAAGAGTTGTTTTACCC

target id: Solyc10g008230.1.1

505 5'-GGAATTGGCAAAACGACTCTTGCTAGAAAAGT-3' 536 cleavage site: 521

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3'-CCCATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 19059194\_22 CTTTAGCAAGAGTTGTTTTACC

target id: Solyc10g008230.1.1

506 5'-GAATTGGCAAAACGACTCTTGCTAGAAAAGTT-3' 537 cleavage site: 522

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3'-CCATTTTGTTGAGAACGATTTC-5'

D51\_TPM.filter 26654102\_21 TTTTAGCAAGAGTTGTTTTAC

target id: Solyc10g008230.1.1

507 5'-AATTGGCAAAACGACTCTTGCTAGAAAAGTT-3' 537 cleavage site: 522

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3'-CATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 25866348\_22 TTTAGCAAGAGTTGTTTTACCA

target id: Solyc10g008230.1.1

505 5'-GGAATTGGCAAAACGACTCTTGCTAGAAAAGT-3' 536 cleavage site: 521

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3'-ACCATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 25866736\_20 TTTAGCAAGAGTTGTTTTAC

target id: Solyc10g008230.1.1

507 5'-AATTGGCAAAACGACTCTTGCTAGAAAAGT-3' 536 cleavage site: 521

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3'-CATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 26653934\_23 TTTTAGCAAGAGTTGTTTTACCC

target id: Solyc10g008230.1.1

505 5'-GGAATTGGCAAAACGACTCTTGCTAGAAAAGTT-3' 537 cleavage site: 522

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3'-CCCATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 24998006\_21 TTGTAAGCGGCTTTAGCAAGA

target id: Solyc11g068360.1.1

643 5'-ACAACACTAGCTAAAGCGGTTTACAACGATG-3' 673 cleavage site: 658

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3'-AGAACGATTTCGGCGAATGTT-5'

D51\_TPM.filter 24997995\_21 TTGTAAGCGGCTTTAGCAAGT

target id: Solyc11g068360.1.1

643 5'-ACAACACTAGCTAAAGCGGTTTACAACGATG-3' 673 cleavage site: 658

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3'-TGAACGATTTCGGCGAATGTT-5'

D51\_TPM.filter 21859117\_20 TGTAAGCGGCTTTAGCAAGA

target id: Solyc11g068360.1.1

643 5'-ACAACACTAGCTAAAGCGGTTTACAACGAT-3' 672 cleavage site: 657

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3'-AGAACGATTTCGGCGAATGT-5'

D51\_TPM.filter 25984397\_22 TTTATCCCATATTTGTATTTTT

target id: Solyc11g068360.1.1

1121 5'-TTTTAAGAAGTG-AAATATGGGATCAGAAAAGT-3' 1152 cleavage site: 1137

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3'-TTTTTATGTTTATACCCTA-TTT-5'

D51\_TPM.filter 26699166\_22 TTTTATCCCATATTTGTATTTT

target id: Solyc11g068360.1.1

1122 5'-TTTAAGAAGTG-AAATATGGGATCAGAAAAGTT-3' 1153 cleavage site: 1138

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3'-TTTTATGTTTATACCCTA-TTTT-5'

D51\_TPM.filter 24997956\_21 TTGTAAGCGGCTTTAGCAAGG

target id: Solyc11g068360.1.1

643 5'-ACAACACTAGCTAAAGCGGTTTACAACGATG-3' 673 cleavage site: 658

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3'-GGAACGATTTCGGCGAATGTT-5'

D51\_TPM.filter 11510382\_24 ATTTCTATTTTCTACGTCACATGT

target id: Solyc11g068360.1.1

973 5'-AAACGACAT-TCAC-TAGAAAATAGGGATCATCC-3' 1004 cleavage site: 989

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3'-TGTACACTGCATCTTTTATCTTTA-5'

D51\_TPM.filter 21859136\_20 TGTAAGCGGCTTTAGCAAGG

target id: Solyc11g068360.1.1

643 5'-ACAACACTAGCTAAAGCGGTTTACAACGAT-3' 672 cleavage site: 657

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3'-GGAACGATTTCGGCGAATGT-5'

D51\_TPM.filter 21859201\_20 TGTAAGCGGCTTTAGCAAGT

target id: Solyc11g068360.1.1

643 5'-ACAACACTAGCTAAAGCGGTTTACAACGAT-3' 672 cleavage site: 657

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3'-TGAACGATTTCGGCGAATGT-5'

D51\_TPM.filter 21859116\_20 TGTAAGCGGCTTTAGCAAGC

target id: Solyc11g068360.1.1

643 5'-ACAACACTAGCTAAAGCGGTTTACAACGAT-3' 672 cleavage site: 657

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3'-CGAACGATTTCGGCGAATGT-5'

D51\_TPM.filter 03260061\_24 AATGTCTGGTATTTTTCATGAAGT

target id: Solyc01g090430.2.1

2961 5'-ATGTAACGTTCA--AGAAATATCAGACATTGTTTC-3' 2993 cleavage site: 2978

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3'-TG-AAGTACTTTTTATGGTCTGTAA-5'

D51\_TPM.filter 21584478\_21 TGGTAGAAATTGAAAGATGCT

target id: Solyc01g090430.2.1

1803 5'-CAAGGAGT-TCTTTCAA-TTGTATCATCTGA-3' 1831 cleavage site: 1816

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3'-TCGTAGAAAGTTAAAGATGGT-5'

D51\_TPM.filter 15129408\_22 GTCTGTAGATCAAAATTGCGAG

target id: Solyc01g090430.2.1

2697 5'-ATTCCCTCCTGATTCTGATGTACAGACAGCTT-3' 2728 cleavage site: 2713

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3'-GAGCGTTAAAACTAGATGTCTG-5'

D51\_TPM.filter 06660851\_24 ACGATGTCTGATATTACTTTGAAG

target id: Solyc01g090430.2.1

2963 5'-GTAACGTTC-AAGAAATATCAGACATTGTTTCTT-3' 2995 cleavage site: 2980

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3'-GAAGTTTCATTATAGTCTGTAGCA-5'

D51\_TPM.filter 08974426\_24 ATGAATTTTGAATAATTGAAGTGT

target id: Solyc05g054020.1.1

2463 5'-TTTCGATGATTCTATTA-TCAAAATTCATGATCT-3' 2495 cleavage site: 2480

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3'-TGTGAAGTTAATAAGTTTTAAGTA-5'

D51\_TPM.filter 05238206\_24 AGGTCTGTCAGAAACACTCTCTGT

target id: Solyc04g007070.2.1

1387 5'-AGGAGATAGCAGAGTTTTATTTGACAGACCTTCTCA-3' 1422 cleavage site: 1407

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3'-TGTC-TCTCACAA-AGACTGTCTGGA-5'

D51\_TPM.filter 02817047\_21 AATAATAGAATAGGACGTGTG

target id: Solyc04g007070.2.1

2840 5'-GTTTGCATCTTTCCTATTCTATTATCTTTGT-3' 2870 cleavage site: 2855

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3'-GTGTGCAGGATAAGATAATAA-5'

D51\_TPM.filter 15616407\_21 CAAGAGTTTGTAGACGAGGTG

target id: Solyc04g007070.2.1

2003 5'-TAAACCTTCTTGTCTACAAACTCTTTCTATG-3' 2033 cleavage site: 2018

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3'-GTGGAGCAGATGTTTGAGAAC-5'

D51\_TPM.filter 02817804\_20 AATAATAGAATAGGACGTGT

target id: Solyc04g007070.2.1

2841 5'-TTTGCATCTTTCCTATTCTATTATCTTTGT-3' 2870 cleavage site: 2855

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3'-TGTGCAGGATAAGATAATAA-5'

D51\_TPM.filter 22274775\_21 TCAAGAGTTTGTAGACGAGGT

target id: Solyc04g007070.2.1

2004 5'-AAACCTTCTTGTCTACAAACTCTTTCTATGG-3' 2034 cleavage site: 2019

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3'-TGGAGCAGATGTTTGAGAACT-5'

D51\_TPM.filter 08001492\_20 ATAATAGAATAGGACGTGTG

target id: Solyc04g007070.2.1

2840 5'-GTTTGCATCTTTCCTATTCTATTATCTTTG-3' 2869 cleavage site: 2854

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3'-GTGTGCAGGATAAGATAATA-5'

D51\_TPM.filter 20413660\_23 TATGACGTGTCTTTGATTTTATT

target id: Solyc04g007070.2.1

397 5'-TACATGATCAAATCAAAGACAT-TCGTAACAAC-3' 428 cleavage site: 413

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3'-TTATTTTAGTTTCTGTGCAGTAT-5'

D51\_TPM.filter 22274495\_20 TCAAGAGTTTGTAGACGAGG

target id: Solyc04g007070.2.1

2005 5'-AACCTTCTTGTCTACAAACTCTTTCTATGG-3' 2034 cleavage site: 2019

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3'-GGAGCAGATGTTTGAGAACT-5'

D51\_TPM.filter 05056565\_24 AGGCAAAAACAGAATTACAGAATA

target id: Solyc04g007070.2.1

2897 5'-TTTCCTATTCTGTAATCTTTGTATTTGCTTTGGTA-3' 2931 cleavage site: 2916

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3'-ATAAGACATTA-AGACAAAAACGGA-5'

D51\_TPM.filter 01724746\_22 AAGGATCTGACATGCATCTGTC

target id: Solyc04g007070.2.1

1629 5'-CCTTTTGCAGA-ACATGTCAGATCTTTCTATT-3' 1659 cleavage site: 1644

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3'-CTGTCTACGTACAGTCTAGGAA-5'

D51\_TPM.filter 11141430\_24 ATTCTGAACCTTTCAACCACTAAG

target id: Solyc04g007070.2.1

2403 5'-CAAGTCTT-GTGGATTGAAAGG-TCAGAATTAGAA-3' 2435 cleavage site: 2420

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3'-GAATCACC-AACTTTCCAAGTCTTA-5'

D51\_TPM.filter 23660461\_21 TCTTCAAACTTTGGACGTTCA

target id: Solyc04g007070.2.1

2325 5'-TCTCTTGAG-GTCCTAAAGTTTAAAGAAAATG-3' 2355 cleavage site: 2340

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3'-ACTTGCA-GGTTTCAAACTTCT-5'

D51\_TPM.filter 12256083\_24 GAGGCAAAAACAGAATTACAGAAT

target id: Solyc04g007070.2.1

2898 5'-TTCCTATTCTGTAATCTTTGTATTTGCTTTGGTAT-3' 2932 cleavage site: 2917

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3'-TAAGACATTA-AGACAAAAACGGAG-5'

D51\_TPM.filter 10823624\_21 ATTGGTGAAATATTCTAGAGT

target id: Solyc09g092280.1.1

2002 5'-GTTGAAC-CGAGATTATTTCACCGGTTGATC-3' 2031 cleavage site: 2016

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3'-TGAGATCTTATAAAGTGGTTA-5'

D51\_TPM.filter 25866430\_21 TTTAGCAAGAGTTGTTTTACC

target id: Solyc11g020100.1.1

530 5'-GTATCGGTAAGACAACTCTTGCCAAAAAAGT-3' 560 cleavage site: 545

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3'-CCATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 26653861\_22 TTTTAGCAAGAGTTGTTTTACC

target id: Solyc11g020100.1.1

530 5'-GTATCGGTAAGACAACTCTTGCCAAAAAAGTT-3' 561 cleavage site: 546

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3'-CCATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 25694497\_22 TTCTTGGCTAGAGTTGTATTGC

target id: Solyc11g020100.1.1

531 5'-TATCGGTAAGACAACTCTTGCCAA-AAAAGTT-3' 561 cleavage site: 546

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3'-CGTTATGTTGAGATCGGTTCTT-5'

D51\_TPM.filter 25866155\_21 TTTAGCAAGAGTTGTTTTACT

target id: Solyc11g020100.1.1

530 5'-GTATCGGTAAGACAACTCTTGCCAAAAAAGT-3' 560 cleavage site: 545

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3'-TCATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 26654022\_22 TTTTAGCAAGAGTTGTTTTACT

target id: Solyc11g020100.1.1

530 5'-GTATCGGTAAGACAACTCTTGCCAAAAAAGTT-3' 561 cleavage site: 546

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3'-TCATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 25694767\_22 TTCTTGGCTAGAGTTGTATTGT

target id: Solyc11g020100.1.1

531 5'-TATCGGTAAGACAACTCTTGCCAA-AAAAGTT-3' 561 cleavage site: 546

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3'-TGTTATGTTGAGATCGGTTCTT-5'

D51\_TPM.filter 02344324\_22 AACGATATGAATTTTGGCTAAC

target id: Solyc11g020100.1.1

1380 5'-GAGAAGTT-G-CAAAATTCATGATC-TTCTTCG-3' 1409 cleavage site: 1394

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3'-CAATCGGTTTTAAGTA-TAGCAA-5'

D51\_TPM.filter 20804880\_21 TGAAATCTTTAGAATATCTAG

target id: Solyc11g020100.1.1

603 5'-ATGGGTTA-CTATCTCTGAAGATTTCAACCAG-3' 633 cleavage site: 618

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3'-GATCTATA-AGATTTCTAAAGT-5'

D51\_TPM.filter 21647675\_21 TGGTTAATAGAATTCGGCTTT

target id: Solyc11g020100.1.1

813 5'-GAATAAAAGCCGAATTCTATTAACCACTCGT-3' 843 cleavage site: 828

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3'-TTTCGGCTTAAGATAATTGGT-5'

D51\_TPM.filter 26653812\_23 TTTTAGCAAGAGTTGTTTTACCT

target id: Solyc11g020100.1.1

529 5'-GGTATCGGTAAGACAACTCTTGCCAAAAAAGTT-3' 561 cleavage site: 546

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3'-TCCATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 19348773\_21 TAAGAAGATCATGAATTTTGC

target id: Solyc11g020100.1.1

1383 5'-AAGTTGCAAAATTCATGATCTTCTTCGCCAA-3' 1413 cleavage site: 1398

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3'-CGTTTTAAGTACTAGAAGAAT-5'

D51\_TPM.filter 26654357\_22 TTTTAGCAAGAGTTGTTTTACA

target id: Solyc11g020100.1.1

530 5'-GTATCGGTAAGACAACTCTTGCCAAAAAAGTT-3' 561 cleavage site: 546

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3'-ACATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 25694504\_20 TTCTTGGCTAGAGTTGTATT

target id: Solyc11g020100.1.1

533 5'-TCGGTAAGACAACTCTTGCCAA-AAAAGTT-3' 561 cleavage site: 546

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3'-TTATGTTGAGATCGGTTCTT-5'

D51\_TPM.filter 25866253\_21 TTTAGCAAGAGTTGTTTTACA

target id: Solyc11g020100.1.1

530 5'-GTATCGGTAAGACAACTCTTGCCAAAAAAGT-3' 560 cleavage site: 545

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3'-ACATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 25866391\_22 TTTAGCAAGAGTTGTTTTACCT

target id: Solyc11g020100.1.1

529 5'-GGTATCGGTAAGACAACTCTTGCCAAAAAAGT-3' 560 cleavage site: 545

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3'-TCCATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 26653543\_24 TTTTAGCAAGAGTTGTTTTACTTT

target id: Solyc11g020100.1.1

528 5'-CGGTATCGGTAAGACAACTCTTGCCAAAAAAGTT-3' 561 cleavage site: 546

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3'-TTTCATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 20006612\_21 TAGTTAATAGAATTCGGCTTT

target id: Solyc11g020100.1.1

813 5'-GAATAAAAGCCGAATTCTATTAACCACTCGT-3' 843 cleavage site: 828

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3'-TTTCGGCTTAAGATAATTGAT-5'

D51\_TPM.filter 25866686\_23 TTTAGCAAGAGTTGTTTTACTTT

target id: Solyc11g020100.1.1

528 5'-CGGTATCGGTAAGACAACTCTTGCCAAAAAAGT-3' 560 cleavage site: 545

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3'-TTTCATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 15582627\_21 CAAATAGAGAAAACAGAACGT

target id: Solyc11g020100.1.1

1176 5'-TTTGAGCG-CTTGTTTTCTCTATGTTGGAGGT-3' 1206 cleavage site: 1191

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3'-TGCAAGACAAAAGAGATA-AAC-5'

D51\_TPM.filter 24483281\_22 TTGAAATCTTTAGAATATCTAG

target id: Solyc11g020100.1.1

603 5'-ATGGGTTA-CTATCTCTGAAGATTTCAACCAGA-3' 634 cleavage site: 619

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3'-GATCTATA-AGATTTCTAAAGTT-5'

D51\_TPM.filter 05613524\_21 AGTAGTTAATAGAATTCGGCT

target id: Solyc11g020100.1.1

815 5'-ATAAAAGCCGAATTCTATTAACCACTCGTCT-3' 845 cleavage site: 830

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3'-TCGGCTTAAGATAATTGATGA-5'

D51\_TPM.filter 05767456\_21 AGTGGTTAATAGAATTCGGCT

target id: Solyc11g020100.1.1

815 5'-ATAAAAGCCGAATTCTATTAACCACTCGTCT-3' 845 cleavage site: 830

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3'-TCGGCTTAAGATAATTGGTGA-5'

D51\_TPM.filter 05613335\_21 AGTAGTTAATAGAATTCGGCC

target id: Solyc11g020100.1.1

815 5'-ATAAAAGCCGAATTCTATTAACCACTCGTCT-3' 845 cleavage site: 830

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3'-CCGGCTTAAGATAATTGATGA-5'

D51\_TPM.filter 25866557\_21 TTTAGCAAGAGTTGTTTTACG

target id: Solyc11g020100.1.1

530 5'-GTATCGGTAAGACAACTCTTGCCAAAAAAGT-3' 560 cleavage site: 545

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3'-GCATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 26654347\_23 TTTTAGCAAGAGTTGTTTTACCA

target id: Solyc11g020100.1.1

529 5'-GGTATCGGTAAGACAACTCTTGCCAAAAAAGTT-3' 561 cleavage site: 546

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3'-ACCATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 25866163\_22 TTTAGCAAGAGTTGTTTTACCC

target id: Solyc11g020100.1.1

529 5'-GGTATCGGTAAGACAACTCTTGCCAAAAAAGT-3' 560 cleavage site: 545

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3'-CCCATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 19059194\_22 CTTTAGCAAGAGTTGTTTTACC

target id: Solyc11g020100.1.1

530 5'-GTATCGGTAAGACAACTCTTGCCAAAAAAGTT-3' 561 cleavage site: 546

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3'-CCATTTTGTTGAGAACGATTTC-5'

D51\_TPM.filter 26654102\_21 TTTTAGCAAGAGTTGTTTTAC

target id: Solyc11g020100.1.1

531 5'-TATCGGTAAGACAACTCTTGCCAAAAAAGTT-3' 561 cleavage site: 546

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3'-CATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 25866348\_22 TTTAGCAAGAGTTGTTTTACCA

target id: Solyc11g020100.1.1

529 5'-GGTATCGGTAAGACAACTCTTGCCAAAAAAGT-3' 560 cleavage site: 545

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3'-ACCATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 25039268\_21 TTGTATTCTTCAGAGATAGTG

target id: Solyc11g020100.1.1

604 5'-TGGGTTACTATCTCTGAAGATTTCAACCAGA-3' 634 cleavage site: 619

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3'-GTGATAGAGACTTCTTATGTT-5'

D51\_TPM.filter 19348359\_21 TAAGAAGATCATGAATTTTGT

target id: Solyc11g020100.1.1

1383 5'-AAGTTGCAAAATTCATGATCTTCTTCGCCAA-3' 1413 cleavage site: 1398

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3'-TGTTTTAAGTACTAGAAGAAT-5'

D51\_TPM.filter 25866736\_20 TTTAGCAAGAGTTGTTTTAC

target id: Solyc11g020100.1.1

32 5'-ATACATTAGAACAACTCTT-C-AAACCTAA-3' 59 cleavage site: 44

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3'-CATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 26653916\_22 TTTTAGCAAGAGTTGTTTTACG

target id: Solyc11g020100.1.1

530 5'-GTATCGGTAAGACAACTCTTGCCAAAAAAGTT-3' 561 cleavage site: 546

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3'-GCATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 12335067\_21 GAGTAGTTAATAGAATTCGGC

target id: Solyc11g020100.1.1

816 5'-TAAAAGCCGAATTCTATTAACCACTCGTCTC-3' 846 cleavage site: 831

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3'-CGGCTTAAGATAATTGATGAG-5'

D51\_TPM.filter 26653934\_23 TTTTAGCAAGAGTTGTTTTACCC

target id: Solyc11g020100.1.1

529 5'-GGTATCGGTAAGACAACTCTTGCCAAAAAAGTT-3' 561 cleavage site: 546

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3'-CCCATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 24396922\_22 TTATTAACAAGATCGTCCTGGA

target id: Solyc05g013280.2.1

4161 5'-AGGTTTCTTGGACGATCTTATTGGTAGGAATC-3' 4192 cleavage site: 4177

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3'-AGGTCCTGCTAGAACAATTATT-5'

D51\_TPM.filter 21044149\_21 TGACATCAGGGAGAGAAAGTA

target id: Solyc05g013280.2.1

2739 5'-TTACACACTATATCTCTCTGATGTCAAGCAA-3' 2769 cleavage site: 2754

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3'-ATGAAAGAGAGGGACTACAGT-5'

D51\_TPM.filter 24606163\_21 TTGACATCAGGGAGAGAAAGT

target id: Solyc05g013280.2.1

2740 5'-TACACACTATATCTCTCTGATGTCAAGCAAT-3' 2770 cleavage site: 2755

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3'-TGAAAGAGAGGGACTACAGTT-5'

D51\_TPM.filter 23721561\_22 TCTTTCCTACTCCTCCCATACC

target id: Solyc04g005540.2.1

633 5'-TATGTGGTATGGGTGGAGTTGGTAAGACAACA-3' 664 cleavage site: 649

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3'-CCATACCCTCCTCATCCTTTCT-5'

D51\_TPM.filter 26575701\_21 TTTCTCTTGTAGCTTGACTAG

target id: Solyc04g005540.2.1

170 5'-TATTTCTA--CTA-CTACAAGAGAAACATGA-3' 197 cleavage site: 182

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3'-GATCAGTTCGATGTTCTCTTT-5'

D51\_TPM.filter 23721573\_22 TCTTTCCTACTCCTCCCATACT

target id: Solyc04g005540.2.1

633 5'-TATGTGGTATGGGTGGAGTTGGTAAGACAACA-3' 664 cleavage site: 649

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3'-TCATACCCTCCTCATCCTTTCT-5'

D51\_TPM.filter 23720559\_22 TCTTTCCTACTCCTCCCATACA

target id: Solyc04g005540.2.1

633 5'-TATGTGGTATGGGTGGAGTTGGTAAGACAACA-3' 664 cleavage site: 649

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3'-ACATACCCTCCTCATCCTTTCT-5'

D51\_TPM.filter 18113632\_20 CTAGTGTCGTCTTACCTACT

target id: Solyc04g005540.2.1

644 5'-GGTGGAGTTGGTAAGACAACACTGACTGAG-3' 673 cleavage site: 658

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3'-TCATCCATTCTGCTGTGATC-5'

D51\_TPM.filter 07624441\_21 ACTTCCATGATCTTCTGAGCT

target id: Solyc04g005540.2.1

992 5'-ATGGGAGCTCAGAAGATCATGGAAGTTGGAA-3' 1022 cleavage site: 1007

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3'-TCGAGTCTTCTAGTACCTTCA-5'

D51\_TPM.filter 26469238\_21 TTTCCAATTCCACCCATTCCT

target id: Solyc04g005540.2.1

632 5'-ATATGTGGTATGGGTGGAGTTGGTAAGACAAC-3' 663 cleavage site: 648

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3'-TCCTTACCCACCTTAACC-TTT-5'

D51\_TPM.filter 04919682\_24 AGGATTTTAGTAAGTGAGATGAGT

target id: Solyc04g005540.2.1

2800 5'-CAACAACTC-TATCACTGACTCAAATCCTCTTTT-3' 2832 cleavage site: 2817

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3'-TGAGTAGAGTGAATGATTTTAGGA-5'

D51\_TPM.filter 25489903\_21 TTCCATGATCTTCTGAGCTCC

target id: Solyc04g005540.2.1

990 5'-CAATGGGAGCTCAGAAGATCATGGAAGTTGG-3' 1020 cleavage site: 1005

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3'-CCTCGAGTCTTCTAGTACCTT-5'

D51\_TPM.filter 18113699\_21 CTAGTGTCGTCTTACCTACTT

target id: Solyc04g005540.2.1

643 5'-GGGTGGAGTTGGTAAGACAACACTGACTGAG-3' 673 cleavage site: 658

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3'-TTCATCCATTCTGCTGTGATC-5'

D51\_TPM.filter 23720745\_22 TCTTTCCTACTCCCCCCATACC

target id: Solyc04g005540.2.1

633 5'-TATGTGGTATGGGTGGAGTTGGTAAGACAACA-3' 664 cleavage site: 649

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3'-CCATACCCCCCTCATCCTTTCT-5'

D51\_TPM.filter 09169183\_24 ATGATTTGAGTCGGTAGATAGAGT

target id: Solyc04g005540.2.1

2800 5'-CAACAACTCTATC-ACTGACTCAAATCCTCTTTT-3' 2832 cleavage site: 2817

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3'-TGAGATAGATGGCTGAGTTTAGTA-5'

D51\_TPM.filter 07629883\_21 ACTTCTATGATCTTTCGAGCC

target id: Solyc04g005540.2.1

992 5'-ATGGGAGCTCAGAAGATCATGGAAGTTGGAA-3' 1022 cleavage site: 1007

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3'-CCGAGCTTTCTAGTATCTTCA-5'

D51\_TPM.filter 19000618\_21 CTTCCATGATCTTCTGAGCTT

target id: Solyc04g005540.2.1

991 5'-AATGGGAGCTCAGAAGATCATGGAAGTTGGA-3' 1021 cleavage site: 1006

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3'-TTCGAGTCTTCTAGTACCTTC-5'

D51\_TPM.filter 15676271\_20 CAAGTGTTGTCTTACCTACT

target id: Solyc04g005540.2.1

644 5'-GGTGGAGTTGGTAAGACAACACTGACTGAG-3' 673 cleavage site: 658

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3'-TCATCCATTCTGTTGTGAAC-5'

D51\_TPM.filter 19000730\_21 CTTCCATGATCTTCTGAGCTC

target id: Solyc04g005540.2.1

991 5'-AATGGGAGCTCAGAAGATCATGGAAGTTGGA-3' 1021 cleavage site: 1006

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3'-CTCGAGTCTTCTAGTACCTTC-5'

D51\_TPM.filter 19439255\_21 TAAGTAATTCTTCAGGACAGA

target id: Solyc04g005540.2.1

1351 5'-TAATATCTGTCCTGAAGAATTACTTAGATAT-3' 1381 cleavage site: 1366

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3'-AGACAGGACTTCTTAATGAAT-5'

D51\_TPM.filter 18113819\_21 CTAGTGTCGTCTTACCTACTC

target id: Solyc04g005540.2.1

643 5'-GGGTGGAGTTGGTAAGACAACACTGACTGAG-3' 673 cleavage site: 658

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3'-CTCATCCATTCTGCTGTGATC-5'

D51\_TPM.filter 23636187\_21 TCTTGGAGCTCTCTTGAAGTT

target id: Solyc04g005540.2.1

2378 5'-GATTCAAC--CGGAGAGGGCTCCAAGAACGTG-3' 2407 cleavage site: 2392

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3'-TTGAAG-TTCTCTCGAGGTTCT-5'

D51\_TPM.filter 15546764\_21 CAAAGCAAAAATAGGTACCTG

target id: Solyc04g005540.2.1

1304 5'-GAAGCTAAGTACCTCTTTTTGCTTTGTTCCT-3' 1334 cleavage site: 1319

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3'-GTCCATGGATAAAAACGAAAC-5'

D51\_TPM.filter 07629765\_21 ACTTCTATGATCTTTCGAGCT

target id: Solyc04g005540.2.1

992 5'-ATGGGAGCTCAGAAGATCATGGAAGTTGGAA-3' 1022 cleavage site: 1007

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3'-TCGAGCTTTCTAGTATCTTCA-5'

D51\_TPM.filter 22129026\_21 TGTTACTTTGCACTGATGGTT

target id: Solyc04g005540.2.1

933 5'-ACCACAAACATCGGTGCAAAGTGACATTCAC-3' 963 cleavage site: 948

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3'-TTGGTAGTCACGTTTCATTGT-5'

D51\_TPM.filter 25490266\_21 TTCCATGATCTTCTGAGCTCT

target id: Solyc04g005540.2.1

990 5'-CAATGGGAGCTCAGAAGATCATGGAAGTTGG-3' 1020 cleavage site: 1005

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3'-TCTCGAGTCTTCTAGTACCTT-5'

D51\_TPM.filter 23721078\_22 TCTTTCCTACTCCTCCCATACG

target id: Solyc04g005540.2.1

633 5'-TATGTGGTATGGGTGGAGTTGGTAAGACAACA-3' 664 cleavage site: 649

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3'-GCATACCCTCCTCATCCTTTCT-5'

D51\_TPM.filter 25675546\_21 TTCTCTTCTGTGAATAATTCT

target id: Solyc04g005540.2.1

3050 5'-ATGGAAGAAGTGATCACAGAAGAGGAACAAC-3' 3080 cleavage site: 3065

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3'-TCTTAATAAGTGTCTTCTCTT-5'

D51\_TPM.filter 23720411\_22 TCTTTCCCACTCCTCCCATACC

target id: Solyc04g005540.2.1

633 5'-TATGTGGTATGGGTGGAGTTGGTAAGACAACA-3' 664 cleavage site: 649

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3'-CCATACCCTCCTCACCCTTTCT-5'

D51\_TPM.filter 02707603\_21 AACTTCTATGATCTTTCGAGC

target id: Solyc04g005540.2.1

993 5'-TGGGAGCTCAGAAGATCATGGAAGTTGGAAC-3' 1023 cleavage site: 1008

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3'-CGAGCTTTCTAGTATCTTCAA-5'

D51\_TPM.filter 07624113\_21 ACTTCCATGATCTTCTGAGCC

target id: Solyc04g005540.2.1

992 5'-ATGGGAGCTCAGAAGATCATGGAAGTTGGAA-3' 1022 cleavage site: 1007

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3'-CCGAGTCTTCTAGTACCTTCA-5'

D51\_TPM.filter 23721096\_21 TCTTTCCTACTCCTCCCATAC

target id: Solyc04g005540.2.1

634 5'-ATGTGGTATGGGTGGAGTTGGTAAGACAACA-3' 664 cleavage site: 649

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3'-CATACCCTCCTCATCCTTTCT-5'

D51\_TPM.filter 23721277\_22 TCTTTCCTACTCCCCCCATACT

target id: Solyc04g005540.2.1

633 5'-TATGTGGTATGGGTGGAGTTGGTAAGACAACA-3' 664 cleavage site: 649

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3'-TCATACCCCCCTCATCCTTTCT-5'

D51\_TPM.filter 26469771\_21 TTTCCAATTCCACCCATTCCC

target id: Solyc04g005540.2.1

632 5'-ATATGTGGTATGGGTGGAGTTGGTAAGACAAC-3' 663 cleavage site: 648

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3'-CCCTTACCCACCTTAACC-TTT-5'

D51\_TPM.filter 15676224\_20 CAAGTGTTGTCTTACCTACC

target id: Solyc04g005540.2.1

644 5'-GGTGGAGTTGGTAAGACAACACTGACTGAG-3' 673 cleavage site: 658

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3'-CCATCCATTCTGTTGTGAAC-5'

D51\_TPM.filter 26121034\_21 TTTGATTCCTGGAAAGATGTG

target id: Solyc04g005540.2.1

1389 5'-GGCTTCACATCTTTCCAGGAATCAAAAATTT-3' 1419 cleavage site: 1404

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3'-GTGTAGAAAGGTCCTTAGTTT-5'

D51\_TPM.filter 23002816\_21 TCCATGATCTTCTGAGCTCCC

target id: Solyc04g005540.2.1

989 5'-GCAATGGGAGCTCAGAAGATCATGGAAGTTG-3' 1019 cleavage site: 1004

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3'-CCCTCGAGTCTTCTAGTACCT-5'

D51\_TPM.filter 19273735\_21 TAAACAACCTTTCTTTTTTCG

target id: Solyc04g005540.2.1

685 5'-AATGGCGAAAAAAGAAAGGTTGTTTAAAGAT-3' 715 cleavage site: 700

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3'-GCTTTTTTCTTTCCAACAAAT-5'

D51\_TPM.filter 19000757\_20 CTTCCATGATCTTCTGAGCT

target id: Solyc04g005540.2.1

992 5'-ATGGGAGCTCAGAAGATCATGGAAGTTGGA-3' 1021 cleavage site: 1006

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3'-TCGAGTCTTCTAGTACCTTC-5'

D51\_TPM.filter 19674942\_22 TAATTCTTCTTCTGTATTCATT

target id: Solyc04g005540.2.1

4392 5'-ACGGTAATGAAT-CTGAAGAAGATTTAAGTGA-3' 4422 cleavage site: 4407

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3'-TTACTTATGTCTTCTTCTTAAT-5'

D51\_TPM.filter 23720544\_22 TCTTTCCTGCTCCTCCCATACC

target id: Solyc04g005540.2.1

633 5'-TATGTGGTATGGGTGGAGTTGGTAAGACAACA-3' 664 cleavage site: 649

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3'-CCATACCCTCCTCGTCCTTTCT-5'

D51\_TPM.filter 23681971\_22 TCTTCCCTACTCCTCCCATACC

target id: Solyc04g005540.2.1

633 5'-TATGTGGTATGGGTGGAGTTGGTAAGACAACA-3' 664 cleavage site: 649

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3'-CCATACCCTCCTCATCCCTTCT-5'

D51\_TPM.filter 07624096\_21 ACTTCCATGATCTTCTGAGCA

target id: Solyc04g005540.2.1

992 5'-ATGGGAGCTCAGAAGATCATGGAAGTTGGAA-3' 1022 cleavage site: 1007

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3'-ACGAGTCTTCTAGTACCTTCA-5'

D51\_TPM.filter 15546744\_22 CAAAGCAAAAATAGGTACCTGG

target id: Solyc04g005540.2.1

1303 5'-TGAAGCTAAGTACCTCTTTTTGCTTTGTTCCT-3' 1334 cleavage site: 1319

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3'-GGTCCATGGATAAAAACGAAAC-5'

D51\_TPM.filter 26575101\_21 TTTCTCTTGTAGCTTGGCTAG

target id: Solyc04g005540.2.1

170 5'-TATTTCTA-CT-A-CTACAAGAGAAACATGA-3' 197 cleavage site: 182

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3'-GATCGGTTCGATGTTCTCTTT-5'

D51\_TPM.filter 26469466\_21 TTTCCAATTCCACCCATTCCA

target id: Solyc04g005540.2.1

632 5'-ATATGTGGTATGGGTGGAGTTGGTAAGACAAC-3' 663 cleavage site: 648

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3'-ACCTTACCCACCTTAACC-TTT-5'

D51\_TPM.filter 24417457\_21 TTATTGGGGAACTTGTCACTT

target id: Solyc04g005540.2.1

2638 5'-ACGTGAAGTAATCAAGTTCCCCAATTTATATG-3' 2669 cleavage site: 2654

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3'-TTCACT-GTTCAAGGGGTTATT-5'

D51\_TPM.filter 23219160\_21 TCCTGTAATTTGAACGGCTCT

target id: Solyc04g005540.2.1

1724 5'-GAAGAAGAACCAATCAAATTACAGGATGATT-3' 1754 cleavage site: 1739

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3'-TCTCGGCAAGTTTAATGTCCT-5'

D51\_TPM.filter 02706291\_22 AACTTCCATGATCTTCTGAGCT

target id: Solyc04g005540.2.1

992 5'-ATGGGAGCTCAGAAGATCATGGAAGTTGGAAC-3' 1023 cleavage site: 1008

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3'-TCGAGTCTTCTAGTACCTTCAA-5'

D51\_TPM.filter 25490144\_21 TTCCATGATCTTCTGAGCTTC

target id: Solyc04g005540.2.1

990 5'-CAATGGGAGCTCAGAAGATCATGGAAGTTGG-3' 1020 cleavage site: 1005

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3'-CTTCGAGTCTTCTAGTACCTT-5'

D51\_TPM.filter 23721541\_23 TCTTTCCTACTCCTCCCATACCT

target id: Solyc04g005540.2.1

632 5'-ATATGTGGTATGGGTGGAGTTGGTAAGACAACA-3' 664 cleavage site: 649

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3'-TCCATACCCTCCTCATCCTTTCT-5'

D51\_TPM.filter 15676276\_20 CAAGTGTTGTCTTACCTACA

target id: Solyc04g005540.2.1

644 5'-GGTGGAGTTGGTAAGACAACACTGACTGAG-3' 673 cleavage site: 658

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3'-ACATCCATTCTGTTGTGAAC-5'

D51\_TPM.filter 20374407\_21 TATATCAAGTAGAGAAGGATC

target id: Solyc04g005540.2.1

1077 5'-TCGACGATCCTTCTCTACTTGATATAGCAAA-3' 1107 cleavage site: 1092

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3'-CTAGGAAGAGATGAACTATAT-5'

D51\_TPM.filter 15675722\_20 CAAGTGTTGTCTTACCTACG

target id: Solyc04g005540.2.1

644 5'-GGTGGAGTTGGTAAGACAACACTGACTGAG-3' 673 cleavage site: 658

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3'-GCATCCATTCTGTTGTGAAC-5'

D51\_TPM.filter 23720962\_23 TCTTTCCTACTCCTCCCATACCA

target id: Solyc04g005540.2.1

632 5'-ATATGTGGTATGGGTGGAGTTGGTAAGACAACA-3' 664 cleavage site: 649

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3'-ACCATACCCTCCTCATCCTTTCT-5'

D51\_TPM.filter 12762967\_21 GATGCTGGAAAAGGTAGACTG

target id: Solyc04g005540.2.1

1811 5'-TACACCAGTCTACCTTTTCCAGCATCCATTC-3' 1841 cleavage site: 1826

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3'-GTCAGATGGAAAAGGTCGTAG-5'

D51\_TPM.filter 23720275\_22 TCTTTCCCACTCCTCCCATACT

target id: Solyc04g005540.2.1

633 5'-TATGTGGTATGGGTGGAGTTGGTAAGACAACA-3' 664 cleavage site: 649

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3'-TCATACCCTCCTCACCCTTTCT-5'

D51\_TPM.filter 06097574\_21 ACAAAGCAAAAATAGGTACCT

target id: Solyc04g005540.2.1

1305 5'-AAGCTAAGTACCTCTTTTTGCTTTGTTCCTT-3' 1335 cleavage site: 1320

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3'-TCCATGGATAAAAACGAAACA-5'

D51\_TPM.filter 23721121\_22 TCTTTCCTACTCCACCCATACC

target id: Solyc04g005540.2.1

633 5'-TATGTGGTATGGGTGGAGTTGGTAAGACAACA-3' 664 cleavage site: 649

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3'-CCATACCCACCTCATCCTTTCT-5'

D51\_TPM.filter 24601758\_21 TTGACACAATTTTTTTCTGAA

target id: Solyc04g005540.2.1

1484 5'-CAAGGTTCAGAAAAAAATTGTGTCAAGATGC-3' 1514 cleavage site: 1499

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3'-AAGTCTTTTTTTAACACAGTT-5'

D51\_TPM.filter 02157709\_21 AACAAAGCAAAAATAGGTACC

target id: Solyc04g005540.2.1

1306 5'-AGCTAAGTACCTCTTTTTGCTTTGTTCCTTG-3' 1336 cleavage site: 1321

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3'-CCATGGATAAAAACGAAACAA-5'

D51\_TPM.filter 27044364\_21 TTTTTTAGTGCTCCTGCAACT

target id: Solyc04g005540.2.1

1148 5'-ATTACAGTTGCAGGAGCACTAAAAAAGCATA-3' 1178 cleavage site: 1163

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3'-TCAACGTCCTCGTGATTTTTT-5'

D51\_TPM.filter 04678105\_21 AGGAACAAAGCAAAAATAGGT

target id: Solyc04g005540.2.1

1309 5'-TAAGTACCTCTTTTTGCTTTGTTCCTTGTTT-3' 1339 cleavage site: 1324

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3'-TGGATAAAAACGAAACAAGGA-5'

D51\_TPM.filter 06097443\_21 ACAAAGCAAAAATAGGTACCC

target id: Solyc04g005540.2.1

1305 5'-AAGCTAAGTACCTCTTTTTGCTTTGTTCCTT-3' 1335 cleavage site: 1320

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3'-CCCATGGATAAAAACGAAACA-5'

D51\_TPM.filter 26469519\_22 TTTCCAATTCCACCCATTCCCA

target id: Solyc04g005540.2.1

630 5'-GGATATGTGGTATGGGTGGAGTTGGTAAGACAAC-3' 663 cleavage site: 648

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3'-AC-CCTTACCCACCTTAACC-TTT-5'

D51\_TPM.filter 23721073\_22 TCTTTCCTACTCTTCCCATACC

target id: Solyc04g005540.2.1

633 5'-TATGTGGTATGGGTGGAGTTGGTAAGACAACA-3' 664 cleavage site: 649

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3'-CCATACCCTTCTCATCCTTTCT-5'

D51\_TPM.filter 23682147\_22 TCTTCCCTACTCCTCCCATACT

target id: Solyc04g005540.2.1

633 5'-TATGTGGTATGGGTGGAGTTGGTAAGACAACA-3' 664 cleavage site: 649

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3'-TCATACCCTCCTCATCCCTTCT-5'

D51\_TPM.filter 15676233\_21 CAAGTGTTGTCTTACCTACTA

target id: Solyc04g005540.2.1

643 5'-GGGTGGAGTTGGTAAGACAACACTGACTGAG-3' 673 cleavage site: 658

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3'-ATCATCCATTCTGTTGTGAAC-5'

D51\_TPM.filter 15676078\_21 CAAGTGTTGTCTTACCTACTT

target id: Solyc04g005540.2.1

643 5'-GGGTGGAGTTGGTAAGACAACACTGACTGAG-3' 673 cleavage site: 658

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3'-TTCATCCATTCTGTTGTGAAC-5'

D51\_TPM.filter 02706558\_21 AACTTCCATGATCTTCTGAGC

target id: Solyc04g005540.2.1

993 5'-TGGGAGCTCAGAAGATCATGGAAGTTGGAAC-3' 1023 cleavage site: 1008

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3'-CGAGTCTTCTAGTACCTTCAA-5'

D51\_TPM.filter 23721661\_22 TCTTTCCTATTCCTCCCATACC

target id: Solyc04g005540.2.1

633 5'-TATGTGGTATGGGTGGAGTTGGTAAGACAACA-3' 664 cleavage site: 649

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3'-CCATACCCTCCTTATCCTTTCT-5'

D51\_TPM.filter 25866430\_21 TTTAGCAAGAGTTGTTTTACC

target id: Solyc10g008240.2.1

506 5'-GGATTGGCAAAACGACTCTTGCTAGAAAAGT-3' 536 cleavage site: 521

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3'-CCATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 26653861\_22 TTTTAGCAAGAGTTGTTTTACC

target id: Solyc10g008240.2.1

506 5'-GGATTGGCAAAACGACTCTTGCTAGAAAAGTT-3' 537 cleavage site: 522

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3'-CCATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 25866155\_21 TTTAGCAAGAGTTGTTTTACT

target id: Solyc10g008240.2.1

506 5'-GGATTGGCAAAACGACTCTTGCTAGAAAAGT-3' 536 cleavage site: 521

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3'-TCATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 26654022\_22 TTTTAGCAAGAGTTGTTTTACT

target id: Solyc10g008240.2.1

506 5'-GGATTGGCAAAACGACTCTTGCTAGAAAAGTT-3' 537 cleavage site: 522

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3'-TCATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 26653812\_23 TTTTAGCAAGAGTTGTTTTACCT

target id: Solyc10g008240.2.1

505 5'-GGGATTGGCAAAACGACTCTTGCTAGAAAAGTT-3' 537 cleavage site: 522

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3'-TCCATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 25866391\_22 TTTAGCAAGAGTTGTTTTACCT

target id: Solyc10g008240.2.1

505 5'-GGGATTGGCAAAACGACTCTTGCTAGAAAAGT-3' 536 cleavage site: 521

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3'-TCCATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 26654347\_23 TTTTAGCAAGAGTTGTTTTACCA

target id: Solyc10g008240.2.1

505 5'-GGGATTGGCAAAACGACTCTTGCTAGAAAAGTT-3' 537 cleavage site: 522

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3'-ACCATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 25866163\_22 TTTAGCAAGAGTTGTTTTACCC

target id: Solyc10g008240.2.1

505 5'-GGGATTGGCAAAACGACTCTTGCTAGAAAAGT-3' 536 cleavage site: 521

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3'-CCCATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 19059194\_22 CTTTAGCAAGAGTTGTTTTACC

target id: Solyc10g008240.2.1

506 5'-GGATTGGCAAAACGACTCTTGCTAGAAAAGTT-3' 537 cleavage site: 522

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3'-CCATTTTGTTGAGAACGATTTC-5'

D51\_TPM.filter 26654102\_21 TTTTAGCAAGAGTTGTTTTAC

target id: Solyc10g008240.2.1

507 5'-GATTGGCAAAACGACTCTTGCTAGAAAAGTT-3' 537 cleavage site: 522

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3'-CATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 25866348\_22 TTTAGCAAGAGTTGTTTTACCA

target id: Solyc10g008240.2.1

505 5'-GGGATTGGCAAAACGACTCTTGCTAGAAAAGT-3' 536 cleavage site: 521

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3'-ACCATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 25866736\_20 TTTAGCAAGAGTTGTTTTAC

target id: Solyc10g008240.2.1

507 5'-GATTGGCAAAACGACTCTTGCTAGAAAAGT-3' 536 cleavage site: 521

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3'-CATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 26653934\_23 TTTTAGCAAGAGTTGTTTTACCC

target id: Solyc10g008240.2.1

505 5'-GGGATTGGCAAAACGACTCTTGCTAGAAAAGTT-3' 537 cleavage site: 522

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3'-CCCATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 06513050\_24 ACATCCTTCTATCTTAAACTCTGT

target id: Solyc12g044200.1.1

1714 5'-AACCTCCGAAGTTTATGGATAGAAGGATGTTCATC-3' 1748 cleavage site: 1733

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3'-TGTCTCAAAT-TCTATCTTCCTACA-5'

D51\_TPM.filter 12762967\_21 GATGCTGGAAAAGGTAGACTG

target id: Solyc12g044200.1.1

1579 5'-GGCTCCA-TTTGTCGTTTTCCAGCATCCATTC-3' 1609 cleavage site: 1594

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3'-GTCAGATGG-AAAAGGTCGTAG-5'

D51\_TPM.filter 22430539\_21 TCAGTACTCCAAAGATCATCT

target id: Solyc07g053010.1.1

787 5'-GTTTTGGATGATGTATGGAGTATTGATGATG-3' 817 cleavage site: 802

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3'-TCTACTAGAAACCTCATGACT-5'

D51\_TPM.filter 22430596\_21 TCAGTACTCCAAAGATCATCC

target id: Solyc07g053010.1.1

787 5'-GTTTTGGATGATGTATGGAGTATTGATGATG-3' 817 cleavage site: 802

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3'-CCTACTAGAAACCTCATGACT-5'

D51\_TPM.filter 09403596\_22 ATGCCTGAGAGTCTTGACATTC

target id: Solyc07g053010.1.1

1670 5'-TGGCTGAA-ATCAAGACTCTCAGG-GTCTTGG-3' 1699 cleavage site: 1684

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3'-CTTACAGTTCTGAGAGTCCGTA-5'

D51\_TPM.filter 23202424\_21 TCCTACTACTTCTGGTTCTGG

target id: Solyc07g049700.1.1

989 5'-GTCCTCCACAACTAGAAGTAATAGGGAAGCA-3' 1019 cleavage site: 1004

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3'-GGTCTTGGTCTTCATCATCCT-5'

D51\_TPM.filter 23202273\_22 TCCTACTACTTCTGGTTCTGGG

target id: Solyc07g049700.1.1

988 5'-TGTCCTCCACAACTAGAAGTAATAGGGAAGCA-3' 1019 cleavage site: 1004

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3'-GGGTCTTGGTCTTCATCATCCT-5'

D51\_TPM.filter 23202482\_22 TCCTACTACTTCTGGTTCTGGC

target id: Solyc07g049700.1.1

988 5'-TGTCCTCCACAACTAGAAGTAATAGGGAAGCA-3' 1019 cleavage site: 1004

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3'-CGGTCTTGGTCTTCATCATCCT-5'

D51\_TPM.filter 23202385\_23 TCCTACTACTTCTGGTTCTGGGG

target id: Solyc07g049700.1.1

987 5'-TTGTCCTCCACAACTAGAAGTAATAGGGAAGCA-3' 1019 cleavage site: 1004

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3'-GGGGTCTTGGTCTTCATCATCCT-5'

D51\_TPM.filter 23202354\_21 TCCTACTACTTCTGGTTCTGA

target id: Solyc07g049700.1.1

989 5'-GTCCTCCACAACTAGAAGTAATAGGGAAGCA-3' 1019 cleavage site: 1004

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3'-AGTCTTGGTCTTCATCATCCT-5'

D51\_TPM.filter 25908487\_21 TTTACGTGTCGTCACAATGAT

target id: Solyc08g007630.1.1

935 5'-GTAAGATCATTGTGACGACACGTAAAGAGAG-3' 965 cleavage site: 950

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3'-TAGTAACACTGCTGTGCATTT-5'

D51\_TPM.filter 11530073\_21 ATTTCTTGAAGTAACCCTTTC

target id: Solyc08g007630.1.1

742 5'-ATAACGAAAGGGTTACTTCAAGAAATTGGCT-3' 772 cleavage site: 757

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3'-CTTTCCCAATGAAGTTCTTTA-5'

D51\_TPM.filter 23249027\_21 TCCTTACGTGTAGTTACAATG

target id: Solyc08g007630.1.1

937 5'-AAGATCATTGTGACGACACGTAAAGAGAGTG-3' 967 cleavage site: 952

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3'-GTAACATTGATGTGCATTCCT-5'

D51\_TPM.filter 24194266\_21 TTACGTGTCGTCACAATGATC

target id: Solyc08g007630.1.1

934 5'-AGTAAGATCATTGTGACGACACGTAAAGAGA-3' 964 cleavage site: 949

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3'-CTAGTAACACTGCTGTGCATT-5'

D51\_TPM.filter 20141108\_20 TACGTGTAGTTACAATGATT

target id: Solyc08g007630.1.1

934 5'-AGTAAGATCATTGTGACGACACGTAAAGAG-3' 963 cleavage site: 948

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3'-TTAGTAACATTGATGTGCAT-5'

D51\_TPM.filter 24193966\_21 TTACGTGTAGTTACAATGATT

target id: Solyc08g007630.1.1

934 5'-AGTAAGATCATTGTGACGACACGTAAAGAGA-3' 964 cleavage site: 949

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3'-TTAGTAACATTGATGTGCATT-5'

D51\_TPM.filter 23501236\_21 TCTCAAGTCATCCCACTCATT

target id: Solyc08g007630.1.1

881 5'-ACTACAATGAGTGGGATGACTTGAGAAATAT-3' 911 cleavage site: 896

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3'-TTACTCACCCTACTGAACTCT-5'

D51\_TPM.filter 25523143\_21 TTCCGTGTAGTTACAATGATT

target id: Solyc08g007630.1.1

934 5'-AGTAAGATCATTGTGACGACACGTAAAGAGA-3' 964 cleavage site: 949

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3'-TTAGTAACATTGATGTGCCTT-5'

D51\_TPM.filter 20140807\_21 TACGTGTAGTTACAATGATCT

target id: Solyc08g007630.1.1

933 5'-AAGTAAGATCATTGTGACGACACGTAAAGAG-3' 963 cleavage site: 948

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3'-TCTAGTAACATTGATGTGCAT-5'

D51\_TPM.filter 06217752\_21 ACAATGATCTTACTTCCTATA

target id: Solyc08g007630.1.1

922 5'-GGAGATATAGGAAGTAAGATCATTGTGACGA-3' 952 cleavage site: 937

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3'-ATATCCTTCATTCTAGTAACA-5'

D51\_TPM.filter 03821356\_21 AATTTCTTGAAGTAACCCTTT

target id: Solyc08g007630.1.1

743 5'-TAACGAAAGGGTTACTTCAAGAAATTGGCTC-3' 773 cleavage site: 758

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3'-TTTCCCAATGAAGTTCTTTAA-5'

D51\_TPM.filter 25908337\_21 TTTACGTGTCGTCACAATGAC

target id: Solyc08g007630.1.1

935 5'-GTAAGATCATTGTGACGACACGTAAAGAGAG-3' 965 cleavage site: 950

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3'-CAGTAACACTGCTGTGCATTT-5'

D51\_TPM.filter 24193570\_21 TTACGTGTAGTTACAATGATC

target id: Solyc08g007630.1.1

934 5'-AGTAAGATCATTGTGACGACACGTAAAGAGA-3' 964 cleavage site: 949

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3'-CTAGTAACATTGATGTGCATT-5'

D51\_TPM.filter 16180747\_22 CACTTTCTGTAGTTGTCCTTCT

target id: Solyc08g007630.1.1

867 5'-CGTGTGGAATGACAACTACA-ATGAGTGGGATG-3' 898 cleavage site: 883

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3'-TCTTCCTGTTGATGTCT-TTCAC-5'

D51\_TPM.filter 17440615\_22 CCACTTTCTGTAGTTGTCCTTC

target id: Solyc08g007630.1.1

868 5'-GTGTGGAATGACAACTACA-ATGAGTGGGATGA-3' 899 cleavage site: 884

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3'-CTTCCTGTTGATGTCT-TTCACC-5'

D51\_TPM.filter 21734213\_21 TGCGGGAAGATCATTGTAGCT

target id: Solyc08g007630.1.1

1250 5'-TGTTGAGCTACAATGATCTTCCCGCACATTT-3' 1280 cleavage site: 1265

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3'-TCGATGTTACTAGAAGGGCGT-5'

D51\_TPM.filter 25523171\_21 TTCCGTGTAGTTACAATGATC

target id: Solyc08g007630.1.1

934 5'-AGTAAGATCATTGTGACGACACGTAAAGAGA-3' 964 cleavage site: 949

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3'-CTAGTAACATTGATGTGCCTT-5'

D51\_TPM.filter 24194001\_21 TTACGTGTAGTTACGATGATT

target id: Solyc08g007630.1.1

934 5'-AGTAAGATCATTGTGACGACACGTAAAGAGA-3' 964 cleavage site: 949

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3'-TTAGTAGCATTGATGTGCATT-5'

D51\_TPM.filter 24193897\_21 TTACGTGTCGTCACAATGATT

target id: Solyc08g007630.1.1

934 5'-AGTAAGATCATTGTGACGACACGTAAAGAGA-3' 964 cleavage site: 949

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3'-TTAGTAACACTGCTGTGCATT-5'

D51\_TPM.filter 26210487\_21 TTTGCAGCGTAAAATACCAGC

target id: Solyc08g007630.1.1

1145 5'-CGCTCGCTGGCATGTTACGCTCCAAATCAGA-3' 1175 cleavage site: 1160

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3'-CGACCATAAAATGCGACGTTT-5'

D51\_TPM.filter 24194358\_22 TTACGTGTAGTTACAATGATCT

target id: Solyc08g007630.1.1

933 5'-AAGTAAGATCATTGTGACGACACGTAAAGAGA-3' 964 cleavage site: 949

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3'-TCTAGTAACATTGATGTGCATT-5'

D51\_TPM.filter 21688701\_21 TGCAGGAAGATCATTGTAGCT

target id: Solyc08g007630.1.1

1250 5'-TGTTGAGCTACAATGATCTTCCCGCACATTT-3' 1280 cleavage site: 1265

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3'-TCGATGTTACTAGAAGGACGT-5'

D51\_TPM.filter 20140474\_20 TACGTGTAGTTACAATGATG

target id: Solyc08g007630.1.1

934 5'-AGTAAGATCATTGTGACGACACGTAAAGAG-3' 963 cleavage site: 948

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3'-GTAGTAACATTGATGTGCAT-5'

D51\_TPM.filter 09531475\_21 ATGTGCGGGAAGATCATTGTA

target id: Solyc08g007630.1.1

1253 5'-TGAGCTACAATGATCTTCCCGCACATTTAAA-3' 1283 cleavage site: 1268

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3'-ATGTTACTAGAAGGGCGTGTA-5'

D51\_TPM.filter 24189463\_21 TTACGTATTGTTACAATGATT

target id: Solyc08g007630.1.1

934 5'-AGTAAGATCATTGTGACGACACGTAAAGAGA-3' 964 cleavage site: 949

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3'-TTAGTAACATTGTTATGCATT-5'

D51\_TPM.filter 25648313\_21 TTCTCAAGTCATCCCACTCAT

target id: Solyc08g007630.1.1

882 5'-CTACAATGAGTGGGATGACTTGAGAAATATT-3' 912 cleavage site: 897

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3'-TACTCACCCTACTGAACTCTT-5'

D51\_TPM.filter 24193976\_21 TTACGTGTAGTTACAATGATG

target id: Solyc08g007630.1.1

934 5'-AGTAAGATCATTGTGACGACACGTAAAGAGA-3' 964 cleavage site: 949

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3'-GTAGTAACATTGATGTGCATT-5'

D51\_TPM.filter 20140227\_20 TACGTGTAGTTACAATGATA

target id: Solyc08g007630.1.1

934 5'-AGTAAGATCATTGTGACGACACGTAAAGAG-3' 963 cleavage site: 948

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3'-ATAGTAACATTGATGTGCAT-5'

D51\_TPM.filter 20141079\_21 TACGTGTAGTTACAATGATCC

target id: Solyc08g007630.1.1

933 5'-AAGTAAGATCATTGTGACGACACGTAAAGAG-3' 963 cleavage site: 948

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3'-CCTAGTAACATTGATGTGCAT-5'

D51\_TPM.filter 18799966\_21 CTTACGTGTCGTCACAATGAT

target id: Solyc08g007630.1.1

935 5'-GTAAGATCATTGTGACGACACGTAAAGAGAG-3' 965 cleavage site: 950

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3'-TAGTAACACTGCTGTGCATTC-5'

D51\_TPM.filter 25909349\_21 TTTACGTGTCGTCACAATGAA

target id: Solyc08g007630.1.1

935 5'-GTAAGATCATTGTGACGACACGTAAAGAGAG-3' 965 cleavage site: 950

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3'-AAGTAACACTGCTGTGCATTT-5'

D51\_TPM.filter 24193674\_21 TTACGTGTAGTTACGATGATC

target id: Solyc08g007630.1.1

934 5'-AGTAAGATCATTGTGACGACACGTAAAGAGA-3' 964 cleavage site: 949

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3'-CTAGTAGCATTGATGTGCATT-5'

D51\_TPM.filter 26219011\_21 TTTGCGTGTCGTCACAATGAT

target id: Solyc08g007630.1.1

935 5'-GTAAGATCATTGTGACGACACGTAAAGAGAG-3' 965 cleavage site: 950

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3'-TAGTAACACTGCTGTGCGTTT-5'

D51\_TPM.filter 20132125\_20 TACGTATTGTTACAATGATT

target id: Solyc08g007630.1.1

934 5'-AGTAAGATCATTGTGACGACACGTAAAGAG-3' 963 cleavage site: 948

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3'-TTAGTAACATTGTTATGCAT-5'

D51\_TPM.filter 23561099\_21 TCTCCTTACGTGTAGTTACAA

target id: Solyc08g007630.1.1

939 5'-GATCATTGTGACGACACGTAAAGAGAGTGTT-3' 969 cleavage site: 954

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3'-AACATTGATGTGCATTCCTCT-5'

D51\_TPM.filter 25909254\_21 TTTACGTGTCGTCACAATGAG

target id: Solyc08g007630.1.1

935 5'-GTAAGATCATTGTGACGACACGTAAAGAGAG-3' 965 cleavage site: 950

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3'-GAGTAACACTGCTGTGCATTT-5'

D51\_TPM.filter 25908113\_21 TTTACGTGTCGTCACAATGGT

target id: Solyc08g007630.1.1

935 5'-GTAAGATCATTGTGACGACACGTAAAGAGAG-3' 965 cleavage site: 950

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3'-TGGTAACACTGCTGTGCATTT-5'

D51\_TPM.filter 03821873\_21 AATTTCTTGAAGTAACCCTTC

target id: Solyc08g007630.1.1

743 5'-TAACGAAAGGGTTACTTCAAGAAATTGGCTC-3' 773 cleavage site: 758

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3'-CTTCCCAATGAAGTTCTTTAA-5'

D51\_TPM.filter 23249093\_21 TCCTTACGTGTAGTTACAATA

target id: Solyc08g007630.1.1

937 5'-AAGATCATTGTGACGACACGTAAAGAGAGTG-3' 967 cleavage site: 952

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3'-ATAACATTGATGTGCATTCCT-5'

D51\_TPM.filter 11530192\_21 ATTTCTTGAAGTAACCCTTTT

target id: Solyc08g007630.1.1

742 5'-ATAACGAAAGGGTTACTTCAAGAAATTGGCT-3' 772 cleavage site: 757

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3'-TTTTCCCAATGAAGTTCTTTA-5'

D51\_TPM.filter 23248970\_22 TCCTTACGTGTAGTTACAATGA

target id: Solyc08g007630.1.1

936 5'-TAAGATCATTGTGACGACACGTAAAGAGAGTG-3' 967 cleavage site: 952

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3'-AGTAACATTGATGTGCATTCCT-5'

D51\_TPM.filter 20140343\_20 TACGTGTAGTTACGATGATT

target id: Solyc08g007630.1.1

934 5'-AGTAAGATCATTGTGACGACACGTAAAGAG-3' 963 cleavage site: 948

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3'-TTAGTAGCATTGATGTGCAT-5'

D51\_TPM.filter 23501427\_21 TCTCAAGTCATCCCACTCATC

target id: Solyc08g007630.1.1

881 5'-ACTACAATGAGTGGGATGACTTGAGAAATAT-3' 911 cleavage site: 896

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3'-CTACTCACCCTACTGAACTCT-5'

D51\_TPM.filter 20140844\_20 TACGTGTAGTTACAATGATC

target id: Solyc08g007630.1.1

934 5'-AGTAAGATCATTGTGACGACACGTAAAGAG-3' 963 cleavage site: 948

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3'-CTAGTAACATTGATGTGCAT-5'

D51\_TPM.filter 24321395\_21 TTATGGAACACCCTCTTGGTT

target id: Solyc08g007630.1.1

1708 5'-CCTCTAAGCAAGAGGGTGTTGCATAACATAC-3' 1738 cleavage site: 1723

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3'-TTGGTTCTCCCACAAGGTATT-5'

D51\_TPM.filter 24193509\_21 TTACGTGTAGTTACAATGATA

target id: Solyc08g007630.1.1

934 5'-AGTAAGATCATTGTGACGACACGTAAAGAGA-3' 964 cleavage site: 949

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3'-ATAGTAACATTGATGTGCATT-5'

D51\_TPM.filter 01607326\_22 AAGATCATGTGGAACACTTGTG

target id: Solyc02g027080.1.1

1334 5'-AAGCTGACAAGTG-TTTACAAGATCTTATCAA-3' 1364 cleavage site: 1349

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3'-GTGTTCACAAGGTGTACTAGAA-5'

D51\_TPM.filter 11357638\_22 ATTTGACGGATACTGCCATGCT

target id: Solyc09g064610.2.1

1115 5'-CATCAAGCA--GCAATATCCGTCAAGTACAAG-3' 1144 cleavage site: 1129

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3'-TCGTACCGTCATAGGCAGTTTA-5'

D51\_TPM.filter 06339668\_24 ACACAGTCTTGAATGAATAGCTCA

target id: Solyc09g064610.2.1

2216 5'-CTCATGGAGTTATTCATTCAGGATTGTGAGATGC-3' 2249 cleavage site: 2234

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3'-ACTCGATAAGTAAGTTCTGACACA-5'

D51\_TPM.filter 20716693\_22 TATTTGACGGATACTGCCATGC

target id: Solyc09g064610.2.1

1116 5'-ATCAAGCA--GCAATATCCGTCAAGTACAAGT-3' 1145 cleavage site: 1130

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3'-CGTACCGTCATAGGCAGTTTAT-5'

D51\_TPM.filter 20717144\_22 TATTTGACGGATACTGCCATGT

target id: Solyc09g064610.2.1

1116 5'-ATCAAGCA--GCAATATCCGTCAAGTACAAGT-3' 1145 cleavage site: 1130

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3'-TGTACCGTCATAGGCAGTTTAT-5'

D51\_TPM.filter 10920819\_22 ATTGTCTTGAATATGAATTACA

target id: Solyc09g064610.2.1

1729 5'-GGGTCTGTAGATTATATTGAAGACAATGTTCA-3' 1760 cleavage site: 1745

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3'-ACATTAAGTATAAGTTCTGTTA-5'

D51\_TPM.filter 14258948\_21 GCTCAGCGAGGACGGAAACCT

target id: Solyc09g064610.2.1

1766 5'-GTAGAAGGTTTCCATCCTTGC-GATGCCTTGT-3' 1796 cleavage site: 1781

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3'-TCCAAAGGCAGGAGCGACT-CG-5'

D51\_TPM.filter 08107654\_22 ATAGAGACGATATTTTTGATAG

target id: Solyc09g064610.2.1

1620 5'-TTCAGTT-TTGAAAAATGTTGTCTCTATTGATG-3' 1651 cleavage site: 1636

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3'-GATAG-TTTTTATAGCAGAGATA-5'

D51\_TPM.filter 24692840\_21 TTGATCTGTGAATGTCTTTGC

target id: Solyc09g064610.2.1

1935 5'-TTGAGGCAAAGACAGATCACAGATGCAACGACT-3' 1967 cleavage site: 1952

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3'-CGTTTCTG-TAAGTGTCTA-GTT-5'

D51\_TPM.filter 25668830\_22 TTCTCTGAGGACATAGATTCTC

target id: Solyc10g047320.1.1

158 5'-TCAACGAGAA-CGAAGTCCTCAGAGAACTTGT-3' 188 cleavage site: 173

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3'-CTCTTAGATACAGGAGTCTCTT-5'

D51\_TPM.filter 11201972\_22 ATTCTTTCGTATAGCTCTTGTC

target id: Solyc10g047320.1.1

325 5'-GGTGAGATCAA-AGCTATACGAAACAAAGTCAG-3' 356 cleavage site: 341

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3'-CT-GTTCTCGATATGCTTTCTTA-5'

D51\_TPM.filter 25187438\_21 TTGTTTATGTTTGATTGCTTT

target id: Solyc10g047320.1.1

2582 5'-CCAAAAAAGACAATCAAAC-TCAACAAGGGAC-3' 2612 cleavage site: 2597

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3'-TTTC-GTTAGTTTGTATTTGTT-5'

D51\_TPM.filter 01818007\_24 AAGGTATTCTAGTCATTTTGGATT

target id: Solyc10g047320.1.1

2123 5'-TAAAAAATGTGAAGAGGCTAGAATACCTTGAAAA-3' 2156 cleavage site: 2141

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3'-TTAGGTTTTACTGATCTTATGGAA-5'

D51\_TPM.filter 21221178\_20 TGATTAACAGGGACAGTCGA

target id: Solyc10g047320.1.1

1934 5'-CTAAGTTGCCTGTCCCTGTTGCTCCAAAAA-3' 1963 cleavage site: 1948

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3'-AGCTGACAGGGACAATTAGT-5'

D51\_TPM.filter 25668411\_22 TTCTCTGAGGACATAGATTCTA

target id: Solyc10g047320.1.1

158 5'-TCAACGAGAA-CGAAGTCCTCAGAGAACTTGT-3' 188 cleavage site: 173

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3'-ATCTTAGATACAGGAGTCTCTT-5'

D51\_TPM.filter 25668817\_22 TTCTCTGAGGACATAGATTCTT

target id: Solyc10g047320.1.1

158 5'-TCAACGAGAA-CGAAGTCCTCAGAGAACTTGT-3' 188 cleavage site: 173

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3'-TTCTTAGATACAGGAGTCTCTT-5'

D51\_TPM.filter 26469194\_22 TTTCCAATTCCACCCATTCCTA

target id: Solyc01g087200.2.1

510 5'-AATTACAGGTATGGGTGGGATTGGCAAAACGAC-3' 542 cleavage site: 527

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3'-ATCCTTACCCACCTTAACC-TTT-5'

D51\_TPM.filter 26653861\_22 TTTTAGCAAGAGTTGTTTTACC

target id: Solyc01g087200.2.1

527 5'-GGATTGGCAAAACGACTCTCGCTAAAAAAGCT-3' 558 cleavage site: 543

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3'-CCATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 26654022\_22 TTTTAGCAAGAGTTGTTTTACT

target id: Solyc01g087200.2.1

527 5'-GGATTGGCAAAACGACTCTCGCTAAAAAAGCT-3' 558 cleavage site: 543

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3'-TCATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 26469238\_21 TTTCCAATTCCACCCATTCCT

target id: Solyc01g087200.2.1

511 5'-ATTACAGGTATGGGTGGGATTGGCAAAACGAC-3' 542 cleavage site: 527

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3'-TCCTTACCCACCTTAACC-TTT-5'

D51\_TPM.filter 22430539\_21 TCAGTACTCCAAAGATCATCT

target id: Solyc01g087200.2.1

757 5'-GTCATTGATGATATTTGGAGTACTAAAGTTT-3' 787 cleavage site: 772

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3'-TCTACTAGAAACCTCATGACT-5'

D51\_TPM.filter 26653812\_23 TTTTAGCAAGAGTTGTTTTACCT

target id: Solyc01g087200.2.1

526 5'-GGGATTGGCAAAACGACTCTCGCTAAAAAAGCT-3' 558 cleavage site: 543

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3'-TCCATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 26469771\_21 TTTCCAATTCCACCCATTCCC

target id: Solyc01g087200.2.1

511 5'-ATTACAGGTATGGGTGGGATTGGCAAAACGAC-3' 542 cleavage site: 527

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3'-CCCTTACCCACCTTAACC-TTT-5'

D51\_TPM.filter 26469737\_22 TTTCCAATTCCACCCATTCCTG

target id: Solyc01g087200.2.1

510 5'-AATTACAGGTATGGGTGGGATTGGCAAAACGAC-3' 542 cleavage site: 527

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3'-GTCCTTACCCACCTTAACC-TTT-5'

D51\_TPM.filter 14693136\_21 GTGACAATAACAATAGGGATT

target id: Solyc01g087200.2.1

2672 5'-TGCTAAGTTTC--TTGTTATTGTTACTTTAA-3' 2700 cleavage site: 2685

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3'-TTAGGGATAACAATAACAGTG-5'

D51\_TPM.filter 26469466\_21 TTTCCAATTCCACCCATTCCA

target id: Solyc01g087200.2.1

511 5'-ATTACAGGTATGGGTGGGATTGGCAAAACGAC-3' 542 cleavage site: 527

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3'-ACCTTACCCACCTTAACC-TTT-5'

D51\_TPM.filter 15973909\_21 CAGTACTCCAAAGATCATCTA

target id: Solyc01g087200.2.1

756 5'-TGTCATTGATGATATTTGGAGTACTAAAGTT-3' 786 cleavage site: 771

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3'-ATCTACTAGAAACCTCATGAC-5'

D51\_TPM.filter 26654347\_23 TTTTAGCAAGAGTTGTTTTACCA

target id: Solyc01g087200.2.1

526 5'-GGGATTGGCAAAACGACTCTCGCTAAAAAAGCT-3' 558 cleavage site: 543

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3'-ACCATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 26654102\_21 TTTTAGCAAGAGTTGTTTTAC

target id: Solyc01g087200.2.1

528 5'-GATTGGCAAAACGACTCTCGCTAAAAAAGCT-3' 558 cleavage site: 543

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3'-CATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 22430596\_21 TCAGTACTCCAAAGATCATCC

target id: Solyc01g087200.2.1

757 5'-GTCATTGATGATATTTGGAGTACTAAAGTTT-3' 787 cleavage site: 772

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3'-CCTACTAGAAACCTCATGACT-5'

D51\_TPM.filter 26653934\_23 TTTTAGCAAGAGTTGTTTTACCC

target id: Solyc01g087200.2.1

526 5'-GGGATTGGCAAAACGACTCTCGCTAAAAAAGCT-3' 558 cleavage site: 543

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3'-CCCATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 25866430\_21 TTTAGCAAGAGTTGTTTTACC

target id: Solyc11g006520.1.1

521 5'-GTATCGGTAAGACAACTCTTGCCAAAAAAGT-3' 551 cleavage site: 536

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3'-CCATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 26653861\_22 TTTTAGCAAGAGTTGTTTTACC

target id: Solyc11g006520.1.1

521 5'-GTATCGGTAAGACAACTCTTGCCAAAAAAGTT-3' 552 cleavage site: 537

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3'-CCATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 25694497\_22 TTCTTGGCTAGAGTTGTATTGC

target id: Solyc11g006520.1.1

522 5'-TATCGGTAAGACAACTCTTGCCAA-AAAAGTT-3' 552 cleavage site: 537

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3'-CGTTATGTTGAGATCGGTTCTT-5'

D51\_TPM.filter 25866155\_21 TTTAGCAAGAGTTGTTTTACT

target id: Solyc11g006520.1.1

521 5'-GTATCGGTAAGACAACTCTTGCCAAAAAAGT-3' 551 cleavage site: 536

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3'-TCATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 26654022\_22 TTTTAGCAAGAGTTGTTTTACT

target id: Solyc11g006520.1.1

521 5'-GTATCGGTAAGACAACTCTTGCCAAAAAAGTT-3' 552 cleavage site: 537

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3'-TCATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 25694767\_22 TTCTTGGCTAGAGTTGTATTGT

target id: Solyc11g006520.1.1

522 5'-TATCGGTAAGACAACTCTTGCCAA-AAAAGTT-3' 552 cleavage site: 537

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3'-TGTTATGTTGAGATCGGTTCTT-5'

D51\_TPM.filter 26653812\_23 TTTTAGCAAGAGTTGTTTTACCT

target id: Solyc11g006520.1.1

520 5'-GGTATCGGTAAGACAACTCTTGCCAAAAAAGTT-3' 552 cleavage site: 537

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3'-TCCATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 26654357\_22 TTTTAGCAAGAGTTGTTTTACA

target id: Solyc11g006520.1.1

521 5'-GTATCGGTAAGACAACTCTTGCCAAAAAAGTT-3' 552 cleavage site: 537

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3'-ACATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 25694504\_20 TTCTTGGCTAGAGTTGTATT

target id: Solyc11g006520.1.1

524 5'-TCGGTAAGACAACTCTTGCCAA-AAAAGTT-3' 552 cleavage site: 537

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3'-TTATGTTGAGATCGGTTCTT-5'

D51\_TPM.filter 25866253\_21 TTTAGCAAGAGTTGTTTTACA

target id: Solyc11g006520.1.1

521 5'-GTATCGGTAAGACAACTCTTGCCAAAAAAGT-3' 551 cleavage site: 536

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3'-ACATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 25866391\_22 TTTAGCAAGAGTTGTTTTACCT

target id: Solyc11g006520.1.1

520 5'-GGTATCGGTAAGACAACTCTTGCCAAAAAAGT-3' 551 cleavage site: 536

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3'-TCCATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 26653543\_24 TTTTAGCAAGAGTTGTTTTACTTT

target id: Solyc11g006520.1.1

519 5'-TGGTATCGGTAAGACAACTCTTGCCAAAAAAGTT-3' 552 cleavage site: 537

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3'-TTTCATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 25866686\_23 TTTAGCAAGAGTTGTTTTACTTT

target id: Solyc11g006520.1.1

519 5'-TGGTATCGGTAAGACAACTCTTGCCAAAAAAGT-3' 551 cleavage site: 536

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3'-TTTCATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 25866557\_21 TTTAGCAAGAGTTGTTTTACG

target id: Solyc11g006520.1.1

521 5'-GTATCGGTAAGACAACTCTTGCCAAAAAAGT-3' 551 cleavage site: 536

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3'-GCATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 26654347\_23 TTTTAGCAAGAGTTGTTTTACCA

target id: Solyc11g006520.1.1

520 5'-GGTATCGGTAAGACAACTCTTGCCAAAAAAGTT-3' 552 cleavage site: 537

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3'-ACCATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 06335281\_24 ACACAATTTGTAGAATTTCAACTT

target id: Solyc11g006520.1.1

2213 5'-TCCGCAAATTGAAATATCTACAAATTGTTTACATA-3' 2247 cleavage site: 2232

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3'-TTCAACTTTA-AGATGTTTAACACA-5'

D51\_TPM.filter 25866163\_22 TTTAGCAAGAGTTGTTTTACCC

target id: Solyc11g006520.1.1

520 5'-GGTATCGGTAAGACAACTCTTGCCAAAAAAGT-3' 551 cleavage site: 536

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3'-CCCATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 19059194\_22 CTTTAGCAAGAGTTGTTTTACC

target id: Solyc11g006520.1.1

521 5'-GTATCGGTAAGACAACTCTTGCCAAAAAAGTT-3' 552 cleavage site: 537

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3'-CCATTTTGTTGAGAACGATTTC-5'

D51\_TPM.filter 26654102\_21 TTTTAGCAAGAGTTGTTTTAC

target id: Solyc11g006520.1.1

522 5'-TATCGGTAAGACAACTCTTGCCAAAAAAGTT-3' 552 cleavage site: 537

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3'-CATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 25374791\_21 TTCGATACACGAATCTCCATA

target id: Solyc11g006520.1.1

691 5'-GAACTAATGGAGA-TTGTGTATAGAGGTCTG-3' 720 cleavage site: 705

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3'-ATACCTCTAAGCACATAGCTT-5'

D51\_TPM.filter 25866348\_22 TTTAGCAAGAGTTGTTTTACCA

target id: Solyc11g006520.1.1

520 5'-GGTATCGGTAAGACAACTCTTGCCAAAAAAGT-3' 551 cleavage site: 536

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3'-ACCATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 25039268\_21 TTGTATTCTTCAGAGATAGTG

target id: Solyc11g006520.1.1

595 5'-TGGGTCACTATCTCTGAAGAATACAATGAGA-3' 625 cleavage site: 610

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3'-GTGATAGAGACTTCTTATGTT-5'

D51\_TPM.filter 25866736\_20 TTTAGCAAGAGTTGTTTTAC

target id: Solyc11g006520.1.1

522 5'-TATCGGTAAGACAACTCTTGCCAAAAAAGT-3' 551 cleavage site: 536

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3'-CATTTTGTTGAGAACGATTT-5'

D51\_TPM.filter 06200968\_24 ACAACTCGTAGATATTTTAATTTG

target id: Solyc11g006520.1.1

2212 5'-TTCCGCAAATTGAAATATCTACAAATTGTTTACA-3' 2245 cleavage site: 2230

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3'-GTTTAATTTTATAGATGCTCAACA-5'

D51\_TPM.filter 26653916\_22 TTTTAGCAAGAGTTGTTTTACG

target id: Solyc11g006520.1.1

521 5'-GTATCGGTAAGACAACTCTTGCCAAAAAAGTT-3' 552 cleavage site: 537

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3'-GCATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 26653934\_23 TTTTAGCAAGAGTTGTTTTACCC

target id: Solyc11g006520.1.1

520 5'-GGTATCGGTAAGACAACTCTTGCCAAAAAAGTT-3' 552 cleavage site: 537

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3'-CCCATTTTGTTGAGAACGATTTT-5'

D51\_TPM.filter 16558487\_22 CGAGTCAACGGTGATCTTACGA

target id: Solyc12g005970.1.1

168 5'-TCAAGTTG-AAGA-TATTGTTGACTCGAAGCT-3' 197 cleavage site: 182

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3'-AGCATTCTAGTGGCAACTGAGC-5'

D51\_TPM.filter 05535911\_21 AGTAAAGATATTGTAGACTAT

target id: Solyc07g053020.1.1

2301 5'-GTTAAATGGACTACAATATCTTTGTATCGAA-3' 2331 cleavage site: 2316

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3'-TATCAGATGTTATAGAAATGA-5'

D51\_TPM.filter 01755447\_24 AAGGGCGATTGAATTATGTTAACT

target id: Solyc07g053020.1.1

1878 5'-AGAACAGCT-ACATAGATCAATCGCCCTTCTTCC-3' 1910 cleavage site: 1895

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3'-TCAATTGTATTAAGTTAGCGGGAA-5'

D51\_TPM.filter 21252343\_21 TGATTTCTGCCCAGTGCTCTG

target id: Solyc07g053020.1.1

2427 5'-TCTAGAAGAGACA-TGGGAAGAAATCACAAGT-3' 2457 cleavage site: 2442

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3'-GTCTC-GTGACCCGTCTTTAGT-5'

D51\_TPM.filter 21252993\_20 TGATTTCTGCCCAGTGCTCT

target id: Solyc07g053020.1.1

294 5'-TGGAAAGA-AGTT-GGCAGAAATCAACAGG-3' 321 cleavage site: 306

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3'-TCTCGTGACCCGTCTTTAGT-5'

D51\_TPM.filter 12943369\_20 GATTTCTGCCCAGTGCTCTG

target id: Solyc07g053020.1.1

2427 5'-TCTAGAAGAGACA-TGGGAAGAAATCACAAG-3' 2456 cleavage site: 2441

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3'-GTCTC-GTGACCCGTCTTTAG-5'

D51\_TPM.filter 09512444\_20 ATGTGATTTCTGCCCAGTGC

target id: Solyc07g053020.1.1

2432 5'-AAGAGACA-TGGGAAGAAATCACAAGTGCA-3' 2460 cleavage site: 2445

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3'-CGTGACCCGTCTTTAGTGTA-5'

D51\_TPM.filter 09512184\_23 ATGTGATTTCTGCCCAGTGCTCT

target id: Solyc07g053020.1.1

2428 5'-CTAGAAGAGACA-TGGGAAGAAATCACAAGTGCA-3' 2460 cleavage site: 2445

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3'-TCTC-GTGACCCGTCTTTAGTGTA-5'

D51\_TPM.filter 09513361\_21 ATGTGATTTCTGCCCAGTGCT

target id: Solyc07g053020.1.1

2430 5'-AGAAGAGACA-TGGGAAGAAATCACAAGTGCA-3' 2460 cleavage site: 2445

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3'-TC-GTGACCCGTCTTTAGTGTA-5'

D51\_TPM.filter 20703731\_21 TATTTAAGGATTTAGGAGATT

target id: Solyc07g053020.1.1

2284 5'-TGGATAG-CTCCTAAATTGTTAAATGGACTA-3' 2313 cleavage site: 2298

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3'-TTAGAGGATTTAGGAATTTAT-5'

D51\_TPM.filter 10902796\_21 ATTGTGTTGTACTCTTGAGAG

target id: Solyc04g009250.1.1

667 5'-TGTGTTTCTCAAGAGTACAACACAATGGATC-3' 697 cleavage site: 682

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3'-GAGAGTTCTCATGTTGTGTTA-5'

D51\_TPM.filter 13452591\_21 GGCCCATTAGCTCAGTTGGTT

target id: Solyc04g009250.1.1

1872 5'-CAGCGAAACAACTGAGCTAATAGATCTAAGA-3' 1902 cleavage site: 1887

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3'-TTGGTTGACTCGATTACCCGG-5'

D51\_TPM.filter 08160426\_22 ATAGATTTCTCTGTTCATACTG

target id: Solyc03g005660.2.1

268 5'-TGGAAGAGT-TGAACAGAGCAATCAATAAAGC-3' 298 cleavage site: 283

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3'-GTCATACTTGTCTCTTTAGATA-5'

D51\_TPM.filter 20318547\_22 TATAGATTTCTCTGTTCATACT

target id: Solyc03g005660.2.1

269 5'-GGAAGAGT-TGAACAGAGCAATCAATAAAGCT-3' 299 cleavage site: 284

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3'-TCATACTTGTCTCTTTAGATAT-5'

D51\_TPM.filter 08852194\_20 ATATTTGATTGTTCTGTTCA

target id: Solyc03g005660.2.1

272 5'-AGAGTTGAACAGAGCAATC-AATAAAGCTG-3' 300 cleavage site: 285

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3'-ACTTGTCTTGTTAGTTTATA-5'

D51\_TPM.filter 11188332\_22 ATTCTTGAAAGGAGAACTCAAA

target id: Solyc03g005660.2.1

1621 5'-TCAGCATTGA-TTCTTCTGTTCAAGAATTCATT-3' 1652 cleavage site: 1637

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3'-AAACTCAAGAGGA-AAGTTCTTA-5'

D51\_TPM.filter 20900898\_21 TGAATCCTTCGGCTATCCATA

target id: Solyc09g098130.1.1

2412 5'-AAGTTTATGGATTGCTGAAGGATTCGTGGAG-3' 2442 cleavage site: 2427

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3'-ATACCTATCGGCTTCCTAAGT-5'

D51\_TPM.filter 20900987\_22 TGAATCCTTCGGCTATCCATAA

target id: Solyc09g098130.1.1

2411 5'-TAAGTTTATGGATTGCTGAAGGATTCGTGGAG-3' 2442 cleavage site: 2427

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3'-AATACCTATCGGCTTCCTAAGT-5'

D51\_TPM.filter 20900999\_20 TGAATCCTTCGGCTATCCAT

target id: Solyc09g098130.1.1

2413 5'-AGTTTATGGATTGCTGAAGGATTCGTGGAG-3' 2442 cleavage site: 2427

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3'-TACCTATCGGCTTCCTAAGT-5'

D51\_TPM.filter 02315843\_21 AACGAACTTATTTAATTTGAC

target id: Solyc09g098130.1.1

3310 5'-TTGCCTTCAAATTTAAATAAGTTGGTACTTGA-3' 3341 cleavage site: 3326

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3'-CAGTTT-AATTTATTCAAGCAA-5'

D51\_TPM.filter 20900927\_23 TGAATCCTTCGGCTATCCATAAT

target id: Solyc09g098130.1.1

2410 5'-ATAAGTTTATGGATTGCTGAAGGATTCGTGGAG-3' 2442 cleavage site: 2427

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3'-TAATACCTATCGGCTTCCTAAGT-5'

D51\_TPM.filter 20900852\_21 TGAATCCTTCGGCTATCCATT

target id: Solyc09g098130.1.1

2412 5'-AAGTTTATGGATTGCTGAAGGATTCGTGGAG-3' 2442 cleavage site: 2427

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3'-TTACCTATCGGCTTCCTAAGT-5'

D51\_TPM.filter 20901206\_20 TGAATCCTTCGGCTATCCAC

target id: Solyc09g098130.1.1

2413 5'-AGTTTATGGATTGCTGAAGGATTCGTGGAG-3' 2442 cleavage site: 2427

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3'-CACCTATCGGCTTCCTAAGT-5'

D51\_TPM.filter 20900824\_21 TGAATCCTTCGGCTATCCATG

target id: Solyc09g098130.1.1

2412 5'-AAGTTTATGGATTGCTGAAGGATTCGTGGAG-3' 2442 cleavage site: 2427

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3'-GTACCTATCGGCTTCCTAAGT-5'

D51\_TPM.filter 20901072\_21 TGAATCCTTCGGCTATCCACA

target id: Solyc09g098130.1.1

2412 5'-AAGTTTATGGATTGCTGAAGGATTCGTGGAG-3' 2442 cleavage site: 2427

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3'-ACACCTATCGGCTTCCTAAGT-5'

D51\_TPM.filter 04438187\_24 AGACTTATTTGAATTTTGAAAGGC

target id: Solyc09g098130.1.1

3307 5'-CAGTTGCC-TTC-AAATTTAAATAAGTTGGTACT-3' 3338 cleavage site: 3323

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3'-CGGAAAGTTTTAAGTTTATTCAGA-5'

D51\_TPM.filter 20900836\_21 TGAATCCTTCGGCTACCCATA

target id: Solyc09g098130.1.1

2412 5'-AAGTTTATGGATTGCTGAAGGATTCGTGGAG-3' 2442 cleavage site: 2427

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3'-ATACCCATCGGCTTCCTAAGT-5'

D51\_TPM.filter 15696687\_21 CAACATGTTTGAGACGAGTGG

target id: Solyc03g078300.1.1

2405 5'-AACTGCCA-TC-TCTCAAACATCTTTCAGTC-3' 2433 cleavage site: 2418

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3'-GGTGAGCAGAGTTTGTACAAC-5'

D51\_TPM.filter 09170535\_24 ATGATTTGTAGACTATTACACAGT

target id: Solyc03g078300.1.1

1850 5'-TTTGTACTTTGT-ATAATCTACAAA-CATTGTTG-3' 1881 cleavage site: 1866

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3'-TGACACATTATCAGATGTTTAGTA-5'

D51\_TPM.filter 26501672\_22 TTTCCTATTCCACCCATGCCAA

target id: Solyc08g075630.2.1

531 5'-AATACTTGGTATGGG-GGGATTAGGAAAGACGA-3' 562 cleavage site: 547

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3'-AACCGTACCCACCTT-ATCCTTT-5'

D51\_TPM.filter 26502462\_20 TTTCCTATTCCACCCATGCC

target id: Solyc08g075630.2.1

533 5'-TACTTGGTATGGG-GGGATTAGGAAAGACGA-3' 562 cleavage site: 547

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3'-CCGTACCCACCTT-ATCCTTT-5'

D51\_TPM.filter 26501547\_21 TTTCCTATTCCACCCATGCCA

target id: Solyc08g075630.2.1

532 5'-ATACTTGGTATGGG-GGGATTAGGAAAGACGA-3' 562 cleavage site: 547

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3'-ACCGTACCCACCTT-ATCCTTT-5'

D51\_TPM.filter 26501688\_20 TTTCCTATTCCACCCATGCT

target id: Solyc08g075630.2.1

533 5'-TACTTGGTATGGG-GGGATTAGGAAAGACGA-3' 562 cleavage site: 547

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3'-TCGTACCCACCTT-ATCCTTT-5'

D51\_TPM.filter 19124997\_21 CTTTCCTACTCCTCCCATACC

target id: Solyc08g075630.2.1

533 5'-TACTTGGTATGGGGGGATTAGGAAAGACGAC-3' 563 cleavage site: 548

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3'-CCATACCCTCCTCATCCTTTC-5'

D51\_TPM.filter 26501726\_20 TTTCCTATTCCACCCATGCA

target id: Solyc08g075630.2.1

533 5'-TACTTGGTATGGG-GGGATTAGGAAAGACGA-3' 562 cleavage site: 547

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3'-ACGTACCCACCTT-ATCCTTT-5'

D51\_TPM.filter 10902796\_21 ATTGTGTTGTACTCTTGAGAG

target id: Solyc04g009260.1.1

670 5'-TGTGTTTCTCAAGAGTACAACACAATGGATC-3' 700 cleavage site: 685

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3'-GAGAGTTCTCATGTTGTGTTA-5'

D51\_TPM.filter 21290291\_21 TGGAATACCATCATCACCGTC

target id: Solyc04g009260.1.1

254 5'-AAGGTGATGATGATGAT-GAATTTCATAGTC-3' 283 cleavage site: 268

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3'-CTGCCACTACTACCATAAGGT-5'

D51\_TPM.filter 22690482\_24 TCGACTAAATTTGAATCACGCTTT

target id: Solyc05g012890.1.1

1704 5'-GTTTCAGAGCATGTATTCAAATTCAGTTGATTCGG-3' 1738 cleavage site: 1723

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3'-TTTCGCAC-TAAGTTTAAATCAGCT-5'

D51\_TPM.filter 05209942\_24 AGGTGTCTTTTTGTGAATCCAGAA

target id: Solyc09g018220.1.1

1616 5'-TACTTTTCT-GTTTCAC-AAAAGAC-CCTTCCAT-3' 1646 cleavage site: 1631

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3'-AAGACCTAAGTGTTTTTCTGTGGA-5'

D51\_TPM.filter 23501236\_21 TCTCAAGTCATCCCACTCATT

target id: Solyc11g071430.1.1

704 5'-ACTACAACGAGTGGGATGACTTGAGAAACAT-3' 734 cleavage site: 719

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3'-TTACTCACCCTACTGAACTCT-5'

D51\_TPM.filter 25171037\_22 TTGTTGTCCTATATCTTCTGGT

target id: Solyc11g071430.1.1

736 5'-TTTGTACAAGGAGATATAGGA-AGTAAGATCA-3' 766 cleavage site: 751

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3'-TGGTCTTCTATATCCTGTTGTT-5'

D51\_TPM.filter 21734213\_21 TGCGGGAAGATCATTGTAGCT

target id: Solyc11g071430.1.1

1073 5'-TGTTGAGCTACAATGATCTTCCCGCACATTT-3' 1103 cleavage site: 1088

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3'-TCGATGTTACTAGAAGGGCGT-5'

D51\_TPM.filter 21688701\_21 TGCAGGAAGATCATTGTAGCT

target id: Solyc11g071430.1.1

1073 5'-TGTTGAGCTACAATGATCTTCCCGCACATTT-3' 1103 cleavage site: 1088

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3'-TCGATGTTACTAGAAGGACGT-5'

D51\_TPM.filter 09531475\_21 ATGTGCGGGAAGATCATTGTA

target id: Solyc11g071430.1.1

1076 5'-TGAGCTACAATGATCTTCCCGCACATTTAAA-3' 1106 cleavage site: 1091

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3'-ATGTTACTAGAAGGGCGTGTA-5'

D51\_TPM.filter 25648313\_21 TTCTCAAGTCATCCCACTCAT

target id: Solyc11g071430.1.1

705 5'-CTACAACGAGTGGGATGACTTGAGAAACATT-3' 735 cleavage site: 720

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3'-TACTCACCCTACTGAACTCTT-5'

D51\_TPM.filter 24321395\_21 TTATGGAACACCCTCTTGGTT

target id: Solyc11g071430.1.1

1534 5'-CCTCTAAGCAAGAGGGTGTTGCATAACATAC-3' 1564 cleavage site: 1549

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3'-TTGGTTCTCCCACAAGGTATT-5'

D51\_TPM.filter 25483274\_21 TTCCACAGCTTTCTTGAACTT

target id: Solyc08g005440.2.1

2040 5'-GGTGCAAGTTCCGGGCAAGCTGTGGAAGATGA-3' 2071 cleavage site: 2056

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3'-TTCAA-GTTCTTTCGACACCTT-5'

D51\_TPM.filter 25483505\_21 TTCCACAGCTTTCTTGAACTG

target id: Solyc08g005440.2.1

2040 5'-GGTGCAAGTTCCGGGCAAGCTGTGGAAGATGA-3' 2071 cleavage site: 2056

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3'-GTCAA-GTTCTTTCGACACCTT-5'

D51\_TPM.filter 25484006\_20 TTCCACAGCTTTCTTGAACT

target id: Solyc08g005440.2.1

2041 5'-GTGCAAGTTCCGGGCAAGCTGTGGAAGATGA-3' 2071 cleavage site: 2056

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3'-TCAA-GTTCTTTCGACACCTT-5'

D51\_TPM.filter 25483500\_22 TTCCACAGCTTTCTTGAACTTC

target id: Solyc08g005440.2.1

2039 5'-GGGTGCAAGTTCCGGGCAAGCTGTGGAAGATGA-3' 2071 cleavage site: 2056

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3'-CTTCAA-GTTCTTTCGACACCTT-5'

D51\_TPM.filter 25484129\_21 TTCCACAGCTTTCTTGAACTC

target id: Solyc08g005440.2.1

2040 5'-GGTGCAAGTTCCGGGCAAGCTGTGGAAGATGA-3' 2071 cleavage site: 2056

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3'-CTCAA-GTTCTTTCGACACCTT-5'

D51\_TPM.filter 25482910\_22 TTCCACAGCTTTCTTGAACTTT

target id: Solyc08g005440.2.1

2039 5'-GGGTGCAAGTTCCGGGCAAGCTGTGGAAGATGA-3' 2071 cleavage site: 2056

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3'-TTTCAA-GTTCTTTCGACACCTT-5'

D51\_TPM.filter 25482556\_21 TTCCACAGCTTTCTTGAACTA

target id: Solyc08g005440.2.1

2040 5'-GGTGCAAGTTCCGGGCAAGCTGTGGAAGATGA-3' 2071 cleavage site: 2056

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3'-ATCAA-GTTCTTTCGACACCTT-5'

D51\_TPM.filter 25483836\_20 TTCCACAGCTTTCTTGAACC

target id: Solyc08g005440.2.1

2041 5'-GTGCAAGTTCCGGGCAAGCTGTGGAAGATGA-3' 2071 cleavage site: 2056

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3'-CCAA-GTTCTTTCGACACCTT-5'

D51\_TPM.filter 25483427\_21 TTCCACAGCTTTCTTGGACTT

target id: Solyc08g005440.2.1

2040 5'-GGTGCAAGTTCCGGGCAAGCTGTGGAAGATGA-3' 2071 cleavage site: 2056

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3'-TTC-AGGTTCTTTCGACACCTT-5'

D51\_TPM.filter 25484021\_21 TTCCACAGCTTTCTTGAGCTT

target id: Solyc08g005440.2.1

2040 5'-GGTGCAAGTTCCGGGCAAGCTGTGGAAGATGA-3' 2071 cleavage site: 2056

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3'-TTCGA-GTTCTTTCGACACCTT-5'

D51\_TPM.filter 25482540\_20 TTCCACAGCTTTCTTGAACA

target id: Solyc08g005440.2.1

2041 5'-GTGCAAGTTCCGGGCAAGCTGTGGAAGATGA-3' 2071 cleavage site: 2056

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3'-ACAA-GTTCTTTCGACACCTT-5'

D51\_TPM.filter 25482753\_21 TTCCACAGCTTCCTTGAACTT

target id: Solyc08g005440.2.1

2040 5'-GGTGCAAGTTCCGGGCAAGCTGTGGAAGATGA-3' 2071 cleavage site: 2056

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3'-TTCAA-GTTCCTTCGACACCTT-5'

D51\_TPM.filter 25483876\_20 TTCCACAGCTTTCTTGAACG

target id: Solyc08g005440.2.1

2041 5'-GTGCAAGTTCCGGGCAAGCTGTGGAAGATGA-3' 2071 cleavage site: 2056

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3'-GCAA-GTTCTTTCGACACCTT-5'

D51\_TPM.filter 25483020\_21 TTCCACAGCTTTCTTAAACTT

target id: Solyc08g005440.2.1

2040 5'-GGTGCAAGTTCCGGGCAAGCTGTGGAAGATGA-3' 2071 cleavage site: 2056

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3'-TTCAA-ATTCTTTCGACACCTT-5'

D51\_TPM.filter 25483307\_21 TTCCACAGCTTTCCTGAACTT

target id: Solyc08g005440.2.1

2040 5'-GGTGCAAGTTCCGGGCAAGCTGTGGAAGATGA-3' 2071 cleavage site: 2056

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3'-TTCAA-GTCCTTTCGACACCTT-5'

D51\_TPM.filter 25483253\_21 TTCCACAGCTTTCTCGAACTT

target id: Solyc08g005440.2.1

2040 5'-GGTGCAAGTTCCGGGCAAGCTGTGGAAGATGA-3' 2071 cleavage site: 2056

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3'-TTCAA-GCTCTTTCGACACCTT-5'

D51\_TPM.filter 25482974\_22 TTCCACAGCTTTCTTGAACTTA

target id: Solyc08g005440.2.1

2039 5'-GGGTGCAAGTTCCGGGCAAGCTGTGGAAGATGA-3' 2071 cleavage site: 2056

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3'-ATTCAA-GTTCTTTCGACACCTT-5'

D51\_TPM.filter 25483218\_21 TTCCACAGCTTTCCTGAACTG

target id: Solyc08g005440.2.1

2040 5'-GGTGCAAGTTCCGGGCAAGCTGTGGAAGATGA-3' 2071 cleavage site: 2056

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3'-GTCAA-GTCCTTTCGACACCTT-5'

D51\_TPM.filter 16602015\_21 CGACCTTGATCTTCTGAGAAG

target id: Solyc08g005440.2.1

2389 5'-AGCCACTTCCCAGAAGATCAGGATCCTATCC-3' 2419 cleavage site: 2404

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3'-GAAGAGTCTTCTAGTTCCAGC-5'

D51\_TPM.filter 16601847\_20 CGACCTTGATCTTCTGAGAA

target id: Solyc08g005440.2.1

2390 5'-GCCACTTCCCAGAAGATCAGGATCCTATCC-3' 2419 cleavage site: 2404

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3'-AAGAGTCTTCTAGTTCCAGC-5'

D51\_TPM.filter 25483933\_20 TTCCACAGCTTTCTTGGACT

target id: Solyc08g005440.2.1

2041 5'-GTGCAAGTTCCGGGCAAGCTGTGGAAGATGA-3' 2071 cleavage site: 2056

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3'-TC-AGGTTCTTTCGACACCTT-5'

D51\_TPM.filter 25483685\_22 TTCCACAGCTTTCTTGAACTGC

target id: Solyc08g005440.2.1

2038 5'-GGGGTGCAAGTTCCGGGCAAGCTGTGGAAGATGA-3' 2071 cleavage site: 2056

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3'-CG-TCAA-GTTCTTTCGACACCTT-5'

D51\_TPM.filter 25482533\_21 TTCCACAGCTTTCTTGAATTT

target id: Solyc08g005440.2.1

2040 5'-GGTGCAAGTTCCGGGCAAGCTGTGGAAGATGA-3' 2071 cleavage site: 2056

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3'-TTTAA-GTTCTTTCGACACCTT-5'

D51\_TPM.filter 26472044\_21 TTTCCACAGCTTTCTTGAACT

target id: Solyc08g005440.2.1

2041 5'-GTGCAAGTTCCGGGCAAGCTGTGGAAGATGAA-3' 2072 cleavage site: 2057

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3'-TCAA-GTTCTTTCGACACCTTT-5'

D51\_TPM.filter 25482725\_21 TTCCACAGCTTTCTTGGACTG

target id: Solyc08g005440.2.1

2040 5'-GGTGCAAGTTCCGGGCAAGCTGTGGAAGATGA-3' 2071 cleavage site: 2056

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3'-GTC-AGGTTCTTTCGACACCTT-5'

D51\_TPM.filter 25482628\_21 TTCCACAGCTTTCTTGGACTC

target id: Solyc08g005440.2.1

2040 5'-GGTGCAAGTTCCGGGCAAGCTGTGGAAGATGA-3' 2071 cleavage site: 2056

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3'-CTC-AGGTTCTTTCGACACCTT-5'

D51\_TPM.filter 25483704\_20 TTCCACAGCTTTCTTAAACT

target id: Solyc08g005440.2.1

2041 5'-GTGCAAGTTCCGGGCAAGCTGTGGAAGATGA-3' 2071 cleavage site: 2056

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3'-TCAA-ATTCTTTCGACACCTT-5'

D51\_TPM.filter 25483197\_20 TTCCACAGCTTTCTCGAACT

target id: Solyc08g005440.2.1

2041 5'-GTGCAAGTTCCGGGCAAGCTGTGGAAGATGA-3' 2071 cleavage site: 2056

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3'-TCAA-GCTCTTTCGACACCTT-5'

D51\_TPM.filter 25482922\_20 TTCCACAGCTTTCTTGAGCT

target id: Solyc08g005440.2.1

2041 5'-GTGCAAGTTCCGGGCAAGCTGTGGAAGATGA-3' 2071 cleavage site: 2056

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3'-TCGA-GTTCTTTCGACACCTT-5'

D51\_TPM.filter 25482587\_20 TTCCACAGCTTCCTTGAACT

target id: Solyc08g005440.2.1

2041 5'-GTGCAAGTTCCGGGCAAGCTGTGGAAGATGA-3' 2071 cleavage site: 2056

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3'-TCAA-GTTCCTTCGACACCTT-5'

D51\_TPM.filter 25482930\_21 TTCCACAGCTTCCTTGAACTG

target id: Solyc08g005440.2.1

2040 5'-GGTGCAAGTTCCGGGCAAGCTGTGGAAGATGA-3' 2071 cleavage site: 2056

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3'-GTCAA-GTTCCTTCGACACCTT-5'

D51\_TPM.filter 23617531\_22 TCTTATGAATTCTAGGTCTTCT

target id: Solyc05g054340.2.1

1108 5'-GTGAAAGAAGACCTGGAAATCATAAGATCGTT-3' 1139 cleavage site: 1124

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3'-TCTTCTGGATCTTAAGTATTCT-5'

D51\_TPM.filter 23617480\_21 TCTTATGAATTCTAGGTCTTC

target id: Solyc05g054340.2.1

1109 5'-TGAAAGAAGACCTGGAAATCATAAGATCGTT-3' 1139 cleavage site: 1124

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3'-CTTCTGGATCTTAAGTATTCT-5'

D51\_TPM.filter 25632153\_21 TTCTGTAATTCTGTTTTTTGC

target id: Solyc05g054340.2.1

3561 5'-AGCGAGTAAATAAACAGAATTGTA-AATAATA-3' 3591 cleavage site: 3576

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3'-CGTTT-TTTGTCTTAATGTCTT-5'

D51\_TPM.filter 23617435\_22 TCTTATGAATTCTAGGTCTTCA

target id: Solyc05g054340.2.1

1108 5'-GTGAAAGAAGACCTGGAAATCATAAGATCGTT-3' 1139 cleavage site: 1124

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3'-ACTTCTGGATCTTAAGTATTCT-5'

D51\_TPM.filter 15710389\_23 CAACGTGACTTATGATATATATA

target id: Solyc05g054340.2.1

1527 5'-CATAGTGTATA-ATCATAAGTCCATTGTTGATCAT-3' 1560 cleavage site: 1545

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3'-ATATATATAGTATTCA-GT-GCAAC-5'

D51\_TPM.filter 23617345\_22 TCTTATGAATTCTAGGTCTTCC

target id: Solyc05g054340.2.1

1108 5'-GTGAAAGAAGACCTGGAAATCATAAGATCGTT-3' 1139 cleavage site: 1124

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3'-CCTTCTGGATCTTAAGTATTCT-5'

D51\_TPM.filter 01038720\_22 AAATAATTGTCTGATCTCTGTC

target id: Solyc05g054340.2.1

3659 5'-TAGGCGATTGAAATCCGGACAATTATTTCTAGC-3' 3691 cleavage site: 3676

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3'-CTGTCTCTA-GTCTGTTAATAAA-5'

D51\_TPM.filter 23617392\_21 TCTTATGAATTCTAGGTCTTT

target id: Solyc05g054340.2.1

1109 5'-TGAAAGAAGACCTGGAAATCATAAGATCGTT-3' 1139 cleavage site: 1124

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3'-TTTCTGGATCTTAAGTATTCT-5'

D51\_TPM.filter 09001551\_20 ATGAGCAAATTCAGACTGTG

target id: Solyc02g090380.2.1

2626 5'-GAACATATCAATTTGAATTTGCTGCATAGATC-3' 2657 cleavage site: 2642

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3'-GT-GTCAGACTTAAACGA-GTA-5'

D51\_TPM.filter 05901770\_23 AGTCTGTTTCTCTCTGTGAAAAC

target id: Solyc02g090380.2.1

1412 5'-AAAAAGTTCTTTACAGCAGAGAAACA-ACTACATT-3' 1445 cleavage site: 1430

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3'-CAA-AAGTGTC-TCTCTTTGTCTGA-5'

D51\_TPM.filter 20407754\_21 TATGAGCAAATTCAGACTGTG

target id: Solyc02g090380.2.1

2626 5'-GAACATATCAATTTGAATTTGCTGCATAGATCA-3' 2658 cleavage site: 2643

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3'-GT-GTCAGACTTAAACGA-GTAT-5'

D51\_TPM.filter 12576523\_22 GACTCTCGGCAACGGATATCTC

target id: Solyc05g009760.1.1

1841 5'-TATCTGAGATATACT-TTGCAGGGAGTCATTGG-3' 1872 cleavage site: 1857

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3'-CTCTATA-GGCAACGGCTCTCAG-5'

D51\_TPM.filter 20994429\_21 TGAGTAAGTAGAAACAAGATC

target id: Solyc05g009760.1.1

1682 5'-TTGGAGATCATGTTTCTGATTACCCAAGCTC-3' 1712 cleavage site: 1697

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3'-CTAGAACAAAGATGAATGAGT-5'

D51\_TPM.filter 12577295\_23 GACTCTCGGCAACGGATATCTCA

target id: Solyc05g009760.1.1

1840 5'-TTATCTGAGATATACT-TTGCAGGGAGTCATTGG-3' 1872 cleavage site: 1857

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3'-ACTCTATA-GGCAACGGCTCTCAG-5'

D51\_TPM.filter 26760739\_21 TTTTGGACTATTAAACAAAGT

target id: Solyc05g009760.1.1

2016 5'-GGAGGCCTTTGTTT-ATATTCCAAGACTACG-3' 2045 cleavage site: 2030

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3'-TGAAACAAATTATCAGGTTTT-5'

D51\_TPM.filter 18732768\_20 CTCTTCAAACTTTGGACGTT

target id: Solyc05g009760.1.1

1985 5'-TAAAAAGTTGTCCCAAGCTTGAAGAGATCCC-3' 2015 cleavage site: 2000

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3'-TT-GCAGGTTTCAAACTTCTC-5'

D51\_TPM.filter 23014737\_21 TCCGAAAATTCTGACTCTGTC

target id: Solyc07g052790.1.1

2234 5'-TTTTTCCCAGAGTCAGAA-TTTCAGAGTTGT-3' 2263 cleavage site: 2248

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3'-CTGTCTCAGTCTTAAAAGCCT-5'

D51\_TPM.filter 19989762\_22 TAGTGTTTAAAATAGTATGTAG

target id: Solyc07g052790.1.1

2488 5'-TGCTTGTACATACCATTTGAAACATTGTGGAA-3' 2519 cleavage site: 2504

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3'-GATGTATGATAAAATTTGTGAT-5'

D51\_TPM.filter 18205016\_20 CTATCATTGTGAAGCAGAAT

target id: Solyc07g039410.2.1

917 5'-TTCAAATTC--CATCACAATGATAGATCTT-3' 944 cleavage site: 929

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3'-TAAGACGAAGTGTTACTATC-5'

D51\_TPM.filter 18205332\_22 CTATCATTGTGAAGCAGAATTC

target id: Solyc07g039410.2.1

915 5'-TTTTCAAATTC--CATCACAATGATAGATCTT-3' 944 cleavage site: 929

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3'-CTTAAGACGAAGTGTTACTATC-5'

D51\_TPM.filter 20527493\_21 TATCATTGTGAAGCAGAATTC

target id: Solyc07g039410.2.1

915 5'-TTTTCAAATTC--CATCACAATGATAGATCT-3' 943 cleavage site: 928

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3'-CTTAAGACGAAGTGTTACTAT-5'

D51\_TPM.filter 20527296\_20 TATCATTGTGAAGCAGAATT

target id: Solyc07g039410.2.1

916 5'-TTTCAAATTC--CATCACAATGATAGATCT-3' 943 cleavage site: 928

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3'-TTAAGACGAAGTGTTACTAT-5'

D51\_TPM.filter 25890832\_22 TTTAGTTTCTGTTCCATTTGTT

target id: Solyc01g088060.2.1

2609 5'-CTAGCTACAAATGGAAACA-AAGCTGAATACCT-3' 2640 cleavage site: 2625

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3'-TTGTTTACC-TTGTCTTTGATTT-5'

D51\_TPM.filter 01566387\_22 AAGACTTTGAATACTTTGCACA

target id: Solyc01g088060.2.1

2024 5'-GAGAGTGTCCAGAG-ATTCAAAGTCTTTCGAG-3' 2054 cleavage site: 2039

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3'-ACACGTTTCATAAGTTTCAGAA-5'

D51\_TPM.filter 25699572\_21 TTCTTGTCACTGATTCTGATG

target id: Solyc01g088060.2.1

2397 5'-TTCTCTACCAGAATCAGTGA-AA-AAGCTAA-3' 2425 cleavage site: 2410

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3'-GTAGTCTTAGTCACTGTTCTT-5'

D51\_TPM.filter 25874399\_24 TTTAGTAGCTAGTTCATTAAGACT

target id: Solyc01g088060.2.1

2594 5'-CAAGTAG-C-TGATGGACTAGCTAC-AAATGGAA-3' 2624 cleavage site: 2609

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3'-TCAGAATTACTTGATCGATGATTT-5'

D51\_TPM.filter 25393306\_24 TTCGATTTATTTCAAGACTTGAAT

target id: Solyc05g009740.1.1

1963 5'-CGAGAGTTCAAAGTCTTGAAAT-ATTTGAAACTAG-3' 1996 cleavage site: 1981

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3'-TAAG-TTCAGAACTTTATTTAGCTT-5'

D51\_TPM.filter 26472711\_24 TTTCCACGTGACATGTTTAAGAGT

target id: Solyc05g009740.1.1

260 5'-TTGATATTCTTAAACAAGTCAC-TGGTGAAAAACA-3' 293 cleavage site: 278

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3'-TGAGAATTTGTACAGTGCACC-TTT-5'

D51\_TPM.filter 03125976\_21 AATGATCTTGAACTCAACTCG

target id: Solyc11g069990.1.1

439 5'-TTTCTCGAGTTGAGGTCAAGATCATTATTCG-3' 469 cleavage site: 454

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3'-GCTCAACTCAAGTTCTAGTAA-5'

D51\_TPM.filter 03129505\_21 AATGATCTTGATCTCAACTCA

target id: Solyc11g069990.1.1

439 5'-TTTCTCGAGTTGAGGTCAAGATCATTATTCG-3' 469 cleavage site: 454

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3'-ACTCAACTCTAGTTCTAGTAA-5'

D51\_TPM.filter 03128094\_21 AATGATCTTGACCTCAACTCG

target id: Solyc11g069990.1.1

439 5'-TTTCTCGAGTTGAGGTCAAGATCATTATTCG-3' 469 cleavage site: 454

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3'-GCTCAACTCCAGTTCTAGTAA-5'

D51\_TPM.filter 03126219\_21 AATGATCTTGAACTCAACTCA

target id: Solyc11g069990.1.1

439 5'-TTTCTCGAGTTGAGGTCAAGATCATTATTCG-3' 469 cleavage site: 454

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3'-ACTCAACTCAAGTTCTAGTAA-5'

D51\_TPM.filter 19603416\_21 TAATGATCTTGAACTCAACTC

target id: Solyc11g069990.1.1

440 5'-TTCTCGAGTTGAGGTCAAGATCATTATTCGA-3' 470 cleavage site: 455

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3'-CTCAACTCAAGTTCTAGTAAT-5'

D51\_TPM.filter 21325976\_21 TGGAGTGTCTAAGTGAAAATT

target id: Solyc11g069990.1.1

1401 5'-GGTAGAATTGTCACTTAGGCACTGCAAGGAC-3' 1431 cleavage site: 1416

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3'-TTAAAAGTGAATCTGTGAGGT-5'

D51\_TPM.filter 24745631\_22 TTGGAGTGTCTAAGTGAAAATT

target id: Solyc11g069990.1.1

1401 5'-GGTAGAATTGTCACTTAGGCACTGCAAGGACT-3' 1432 cleavage site: 1417

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3'-TTAAAAGTGAATCTGTGAGGTT-5'

D51\_TPM.filter 19603252\_22 TAATGATCTTGAACTCAACTCG

target id: Solyc11g069990.1.1

439 5'-TTTCTCGAGTTGAGGTCAAGATCATTATTCGA-3' 470 cleavage site: 455

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3'-GCTCAACTCAAGTTCTAGTAAT-5'

D51\_TPM.filter 26210487\_21 TTTGCAGCGTAAAATACCAGC

target id: Solyc11g069990.1.1

167 5'-CTCTTGCTGGCATGTTACGCTCCAAATCAGA-3' 197 cleavage site: 182

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3'-CGACCATAAAATGCGACGTTT-5'

D51\_TPM.filter 19603637\_21 TAATGATCTTGATCTCAACTC

target id: Solyc11g069990.1.1

440 5'-TTCTCGAGTTGAGGTCAAGATCATTATTCGA-3' 470 cleavage site: 455

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3'-CTCAACTCTAGTTCTAGTAAT-5'

D51\_TPM.filter 03126376\_21 AATGATCTTGATCTCAACTCG

target id: Solyc11g069990.1.1

439 5'-TTTCTCGAGTTGAGGTCAAGATCATTATTCG-3' 469 cleavage site: 454

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3'-GCTCAACTCTAGTTCTAGTAA-5'

D51\_TPM.filter 24321395\_21 TTATGGAACACCCTCTTGGTT

target id: Solyc11g069990.1.1

730 5'-CCACTAAGCAAGAGGGTGTTGCATAACATAC-3' 760 cleavage site: 745

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3'-TTGGTTCTCCCACAAGGTATT-5'

D51\_TPM.filter 19604076\_21 TAATGATCTTGACCTCAACTC

target id: Solyc11g069990.1.1

440 5'-TTCTCGAGTTGAGGTCAAGATCATTATTCGA-3' 470 cleavage site: 455

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3'-CTCAACTCCAGTTCTAGTAAT-5'

D51\_TPM.filter 18070827\_21 CTAGAGAAACTTGGAATTCCC

target id: Solyc11g069660.1.1

778 5'-CTAGTGGGAG--CCAAGTTTCTTGTAGGTAGT-3' 807 cleavage site: 792

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3'-CCCTTAAGGTTCAAAGAG-ATC-5'

D51\_TPM.filter 18756713\_21 CTTAAGGATGTTAGTCTAGGC

target id: Solyc11g069660.1.1

466 5'-ATACTGCCAAGACTGACATCCTTAAGGGCAT-3' 496 cleavage site: 481

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3'-CGGATCTGATTGTAGGAATTC-5'

D51\_TPM.filter 18070593\_21 CTAGAGAAACTTGGAATTCCA

target id: Solyc11g069660.1.1

777 5'-GCTAGTGGGA-GCCAAGTTTCTTGTAGGTAGT-3' 807 cleavage site: 792

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3'-ACCTTAAGGTTCAAAGAG-ATC-5'

D51\_TPM.filter 23852925\_20 TTAAGGATGTTAGTCTAGGC

target id: Solyc11g069660.1.1

466 5'-ATACTGCCAAGACTGACATCCTTAAGGGCA-3' 495 cleavage site: 480

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3'-CGGATCTGATTGTAGGAATT-5'

D51\_TPM.filter 18756878\_21 CTTAAGGATGTTAGTCTAGGT

target id: Solyc11g069660.1.1

466 5'-ATACTGCCAAGACTGACATCCTTAAGGGCAT-3' 496 cleavage site: 481

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3'-TGGATCTGATTGTAGGAATTC-5'

D51\_TPM.filter 23852157\_21 TTAAGGATGTTAGTCTAGGCA

target id: Solyc11g069660.1.1

465 5'-CATACTGCCAAGACTGACATCCTTAAGGGCA-3' 495 cleavage site: 480

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3'-ACGGATCTGATTGTAGGAATT-5'

D51\_TPM.filter 25057979\_21 TTGTGATTGAAAAAGGAGATT

target id: Solyc11g069660.1.1

2013 5'-TTGGCAGTTGCCTTGTTCTATCACAAGACTT-3' 2043 cleavage site: 2028

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3'-TTAGAGGAAAAAGTTAGTGTT-5'

D51\_TPM.filter 24321395\_21 TTATGGAACACCCTCTTGGTT

target id: Solyc11g069660.1.1

439 5'-CATATAAGCAAGAGGGTGTTGCATAACATAC-3' 469 cleavage site: 454

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3'-TTGGTTCTCCCACAAGGTATT-5'

D51\_TPM.filter 18070482\_21 CTAGAGAAACTTGGAACTCCT

target id: Solyc11g069660.1.1

778 5'-CTAGTGGGAG--CCAAGTTTCTTGTAGGTAGT-3' 807 cleavage site: 792

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3'-TCCTCAAGGTTCAAAGAG-ATC-5'

D51\_TPM.filter 04338850\_24 AGACGTGTTAAACTATTATAGTAT

target id: Solyc08g013970.1.1

2042 5'-TTAACAT-TTGTGACAGTTTAACATGTCTGTTCA-3' 2074 cleavage site: 2059

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3'-TATGATATTATCAAATTGTGCAGA-5'

D51\_TPM.filter 06513050\_24 ACATCCTTCTATCTTAAACTCTGT

target id: Solyc12g044190.1.1

2869 5'-AACCTCCGAAGTTTACGGATAGAAGGATGTTCATC-3' 2903 cleavage site: 2888

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3'-TGTCTCAAAT-TCTATCTTCCTACA-5'

D51\_TPM.filter 22990149\_21 TCCACAAATCATCCCCTTCTA

target id: Solyc12g044190.1.1

573 5'-TACATTACAAGGGGATGATTTGTGGAGTCGT-3' 603 cleavage site: 588

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3'-ATCTTCCCCTACTAAACACCT-5'

D51\_TPM.filter 10671292\_21 ATTATTTTCCTCAAACAAGGA

target id: Solyc12g044190.1.1

1109 5'-TTTGTTCTTTGTTTGAGGAAGATAGTGACAT-3' 1139 cleavage site: 1124

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3'-AGGAACAAACTCCTTTTATTA-5'

D51\_TPM.filter 07624441\_21 ACTTCCATGATCTTCTGAGCT

target id: Solyc07g044800.2.1

454 5'-ATGAAAACTCAGAAGATCATGGAGGTTGGAA-3' 484 cleavage site: 469

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3'-TCGAGTCTTCTAGTACCTTCA-5'

D51\_TPM.filter 03461935\_24 AATCTCTATGATTCTTCTGAATTT

target id: Solyc07g044800.2.1

453 5'-AATGAAAACTCAGAA-GATCATGGAGGTTGGAAC-3' 485 cleavage site: 470

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3'-TTTAAGTCTTCTTAGTATCTCTAA-5'

D51\_TPM.filter 19000618\_21 CTTCCATGATCTTCTGAGCTT

target id: Solyc07g044800.2.1

453 5'-AATGAAAACTCAGAAGATCATGGAGGTTGGA-3' 483 cleavage site: 468

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3'-TTCGAGTCTTCTAGTACCTTC-5'

D51\_TPM.filter 19000757\_20 CTTCCATGATCTTCTGAGCT

target id: Solyc07g044800.2.1

454 5'-ATGAAAACTCAGAAGATCATGGAGGTTGGA-3' 483 cleavage site: 468

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3'-TCGAGTCTTCTAGTACCTTC-5'

D51\_TPM.filter 07624113\_21 ACTTCCATGATCTTCTGAGCC

target id: Solyc07g044800.2.1

454 5'-ATGAAAACTCAGAAGATCATGGAGGTTGGAA-3' 484 cleavage site: 469

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3'-CCGAGTCTTCTAGTACCTTCA-5'

D51\_TPM.filter 07624096\_21 ACTTCCATGATCTTCTGAGCA

target id: Solyc07g044800.2.1

454 5'-ATGAAAACTCAGAAGATCATGGAGGTTGGAA-3' 484 cleavage site: 469

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3'-ACGAGTCTTCTAGTACCTTCA-5'

D51\_TPM.filter 15741889\_21 CAACTTCCATGATCTTCTGAG

target id: Solyc07g044800.2.1

456 5'-GAAAACTCAGAAGATCATGGAGGTTGGAACC-3' 486 cleavage site: 471

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3'-GAGTCTTCTAGTACCTTCAAC-5'

D51\_TPM.filter 25490144\_21 TTCCATGATCTTCTGAGCTTC

target id: Solyc07g044800.2.1

452 5'-AAATGAAAACTCAGAAGATCATGGAGGTTGG-3' 482 cleavage site: 467

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3'-CTTCGAGTCTTCTAGTACCTT-5'

D51\_TPM.filter 02706291\_22 AACTTCCATGATCTTCTGAGCT

target id: Solyc07g044800.2.1

454 5'-ATGAAAACTCAGAAGATCATGGAGGTTGGAAC-3' 485 cleavage site: 470

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3'-TCGAGTCTTCTAGTACCTTCAA-5'

D51\_TPM.filter 02706558\_21 AACTTCCATGATCTTCTGAGC

target id: Solyc07g044800.2.1

455 5'-TGAAAACTCAGAAGATCATGGAGGTTGGAAC-3' 485 cleavage site: 470

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3'-CGAGTCTTCTAGTACCTTCAA-5'

D51\_TPM.filter 06187027\_21 ACAACGATCTTTTCTGAATAG

target id: Solyc10g051050.1.1

236 5'-AAAGACTATTCAAAAAAGATTTG-TGTCCTCC-3' 266 cleavage site: 251

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3'-GATAAGTCTTTTCT-AGCAACA-5'

D51\_TPM.filter 06186540\_20 ACAACGATCTTTTCTGAATA

target id: Solyc10g051050.1.1

237 5'-AAGACTATTCAAAAAAGATTTG-TGTCCTCC-3' 266 cleavage site: 251

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3'-ATAAGTCTTTTCT-AGCAACA-5'

D51\_TPM.filter 06299020\_21 ACAGCGATCTTTTCTGAATAG

target id: Solyc10g051050.1.1

236 5'-AAAGACTATTCAAAAAAGATTTG-TGTCCTCC-3' 266 cleavage site: 251

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3'-GATAAGTCTTTTCT-AGCGACA-5'

D51\_TPM.filter 25553387\_21 TTCCTCAGCTTTCTTGAACTT

target id: Solyc10g051050.1.1

368 5'-ATGACAA-TTGGAAGAAGGTTGAGGAAAATCT-3' 398 cleavage site: 383

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3'-TTCAA-GTTCTTTCGACTCCTT-5'

D51\_TPM.filter 18378363\_21 CTGGCATTGTTCGGAGACATG

target id: Solyc10g051050.1.1

411 5'-TGGTACG-GTATCCGAACGATGCCAATCAAT-3' 440 cleavage site: 425

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3'-GTACAGAGGCTTGTTACGGTC-5'

D51\_TPM.filter 21533248\_20 TGGCATTGTTCGGAGACATG

target id: Solyc10g051050.1.1

411 5'-TGGTACG-GTATCCGAACGATGCCAATCAA-3' 439 cleavage site: 424

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3'-GTACAGAGGCTTGTTACGGT-5'

D51\_TPM.filter 04908394\_23 AGGATTTAGGAGATTACTTTGTT

target id: Solyc04g079420.2.1

1449 5'-TTTCAGACAAA--AATCTCCTAAATCTAGTCAA-3' 1479 cleavage site: 1464

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3'-TTGTTTCATTAGAGGATTTAGGA-5'

D51\_TPM.filter 18429739\_20 CTGCCGAAGCTGTGGGATGC

target id: Solyc04g079420.2.1

2030 5'-GGTTTGT-TCCCACAGCTCTCGG-AGTTCAC-3' 2058 cleavage site: 2043

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3'-CGTAGGGTGTCGA-AGCCGTC-5'

D51\_TPM.filter 19556119\_22 TAACTTGTATGGATCTCTATCA

target id: Solyc04g079420.2.1

1487 5'-CGAGCTGG-AGACATGTATACAAGTTACTATG-3' 1517 cleavage site: 1502

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3'-ACTATCTCTAGGTATGTTCAAT-5'

D51\_TPM.filter 18429611\_20 CTGCCGAAGCTGTGGGATGA

target id: Solyc04g079420.2.1

2028 5'-CTGGTTTGTTCCCACAGCTCTCGG-AGTTCAC-3' 2058 cleavage site: 2043

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3'-AGT-AGGGTGTCGA-AGCCGTC-5'

D51\_TPM.filter 18429013\_21 CTGCCGAAGCTGTGGGATGCA

target id: Solyc04g079420.2.1

2029 5'-TGGTTTGT-TCCCACAGCTCTCGG-AGTTCAC-3' 2058 cleavage site: 2043

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3'-ACGTAGGGTGTCGA-AGCCGTC-5'

D51\_TPM.filter 12064522\_20 GAATCCCTCCTCGCCCACCA

target id: Solyc04g079420.2.1

488 5'-AGAAGTGGTGGAG-GAGGAGGGTGTTTAGGGG-3' 518 cleavage site: 503

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3'-ACCACC-CGCTCCTCCC-TAAG-5'

D51\_TPM.filter 18428999\_21 CTGCCGAAGCTGTGGGATGTA

target id: Solyc04g079420.2.1

2029 5'-TGGTTTGT-TCCCACAGCTCTCGG-AGTTCAC-3' 2058 cleavage site: 2043

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3'-ATGTAGGGTGTCGA-AGCCGTC-5'

D51\_TPM.filter 18429277\_22 CTGCCGAAGCTGTGGGATGTAA

target id: Solyc04g079420.2.1

2028 5'-CTGGTTTGT-TCCCACAGCTCTCGG-AGTTCAC-3' 2058 cleavage site: 2043

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3'-AATGTAGGGTGTCGA-AGCCGTC-5'

D51\_TPM.filter 06530231\_24 ACATTATCACTTGTGTGAACCTCC

target id: Solyc04g079420.2.1

355 5'-AGTAGCGAGGTTCATGCAAGTGACAATGCAAGCT-3' 388 cleavage site: 373

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3'-CCTCCAAGTGTGTTCACTATTACA-5'

D51\_TPM.filter 18429725\_20 CTGCCGAAGCTGTGGGATGT

target id: Solyc04g079420.2.1

2030 5'-GGTTTGT-TCCCACAGCTCTCGG-AGTTCAC-3' 2058 cleavage site: 2043

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3'-TGTAGGGTGTCGA-AGCCGTC-5'

D51\_TPM.filter 18429203\_20 CTGCCGAAGCTGTGGGACGT

target id: Solyc04g079420.2.1

2030 5'-GGTTTGT-TCCCACAGCTCTCGG-AGTTCAC-3' 2058 cleavage site: 2043

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3'-TGCAGGGTGTCGA-AGCCGTC-5'

D51\_TPM.filter 26206894\_21 TTTGCAAAACTGTGCTCAATT

target id: Solyc04g079420.2.1

547 5'-GAAATGGTTTGAGGATAGTTTTGTAAATTTAG-3' 578 cleavage site: 563

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3'-TT-AACTCGTGTCAAAACGTTT-5'

D51\_TPM.filter 18429386\_21 CTGCCGAAGCTGTGGGATACT

target id: Solyc04g079420.2.1

2029 5'-TGGTTTGT-TCCCACAGCTCTCGG-AGTTCAC-3' 2058 cleavage site: 2043

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3'-TCATAGGGTGTCGA-AGCCGTC-5'

D51\_TPM.filter 11630625\_22 ATTTTCGAACCAAAGTGATTCT

target id: Solyc04g079420.2.1

1890 5'-ACTTGAGAAGC-CTTTGGTTCGAGAAGATATC-3' 1920 cleavage site: 1905

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3'-TCTTAGTGAAACCAAGCTTTTA-5'

D51\_TPM.filter 04913432\_22 AGGATTTGTGGACTGGTAGATA

target id: Solyc04g079420.2.1

1927 5'-TCACTTATCTG--ACTCCACAAATCCTCTCAA-3' 1956 cleavage site: 1941

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3'-ATAGATGGTCAGGTGTTTAGGA-5'

D51\_TPM.filter 17487999\_20 CCGAAGCTGTGGGATGTAAA

target id: Solyc04g079420.2.1

2027 5'-CCTGGTTTGT-TCCCACAGCTCTCGGAGTTC-3' 2056 cleavage site: 2041

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3'-AAATGTAGGGTGTCGA-AGCC-5'

D51\_TPM.filter 18429391\_23 CTGCCGAAGCTGTGGGATGTAAA

target id: Solyc04g079420.2.1

2027 5'-CCTGGTTTGT-TCCCACAGCTCTCGG-AGTTCAC-3' 2058 cleavage site: 2043

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3'-AAATGTAGGGTGTCGA-AGCCGTC-5'

D51\_TPM.filter 07665318\_20 ACTTTGTGAAATGACTTGAG

target id: Solyc04g079420.2.1

2265 5'-AGTACCTTGA--CATTTCACAATGTGTTGG-3' 2292 cleavage site: 2277

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3'-GAGTTCAGTAAAGTGTTTCA-5'

D51\_TPM.filter 09799974\_23 ATCACTTGTGTGAACCTCCCATA

target id: Solyc04g079420.2.1

352 5'-AAGAGTA-GCGAGGTTCATGCAAGTGACAATGC-3' 383 cleavage site: 368

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3'-ATACCCTCCAAGTGTGTTCACTA-5'