

Supplementary data 2

Full sequence information of Smo mutants plasmids are provided below.

Smo D473H:

CAGAGCTCTCTGGCTAACTAGAGAACCCACTGCTTACTGGCTTATCGAAATTAATACGA
CTCACTATAGGGAGACCCAAGCTGGCTAGCGTTTAACTTAAGCTTGGTACCGAGCTC
GGATCCGCCACCATGGCCGCTGCCC GCCAGCGCGGGGGCCGGAGCTCCCGCTCCTG
GGGCTGCTGCTGCTGCTGCTGCTGGGGGACCCGGGCGGGGGGCGGCCTCGAGCGGG
AACGCGACCGGGCCTGGGCCTCGGAGCGCGGGCGGGAGCGCGAGGAGGAGCGCGGC
GGTACTGGCCCTCCGCCGCCGCTGAGCCACTGCGGCCGGGCTGCCCCCTGCGAGCC
GCTGCGCTACAACGTGTGCCTGGGCTCGGTGCTGCCCTACGGGGCCACCTCCACTG
CTGGCCGGAGACTCGGACTCCCAGGAGGAAGCGCACGGCAAGCTCGTGCTCTGGTCG
GGCCTCCGGAATGCCCCCGCTGCTGGGCAGTGATCCAGCCCCTGCTGTGTGCCGTAT
ACATGCCCAAGTGTGAGAATGACCGGGTGGAGCTGCCAGCCGTACCCTCTGCCAGGC
CACCCGAGGCCCTGTGCCATCGTGGAGAGGGAGCGGGGCTGGCCTGACTTCCTGCG
CTGCACTCCTGACCGCTTCCCTGAAGGCTGCACGAATGAGGTGCAGAACATCAAGTTC
AACAGTTCAGGCCAGTGCGAAGTGCCCTTGGTTCCGACAGACAACCCCAAGAGCTGG
TACGAGGACGTGGAGGGCTGCGGCATCCAGTGCCAGAACCCGCTCTTCACAGAGGCT
GAGCACCAGGACATGCACAGCTACATCGCGGCCTTCGGGGCCGTCACGGGCCTCTGCA
CGCTCTTCACCCTGGCCACATTCGTGGCTGACTGGCGGAACTCGAATCGCTACCCTGCT
GTTATTCTCTTCTACGTCAATGCGTGCTTCTTTGTGGGCAGCATTGGCTGGCTGGCCCA
GTTTCATGGATGGTGCCCGCCGAGAGATCGTCTGCCGTGCAGATGGCACCATGAGGCTT
GGGGAGCCCACCTCCAATGAGACTCTGTCCCTGCGTCATCATCTTGTGCATCGTGTACTA
CGCCCTGATGGCTGGTGTGGTTTGGTTTGTGGTCTCACCTATGCCTGGCACACTTCCT
TCAAAGCCCTGGGCACCACCTACCAGCCTCTCTCGGGCAAGACCTCCTACTTCCACCT
GCTCACCTGGTCACTCCCCTTTGTCCCTACTGTGGCAATCCTTGCTGTGGCGCAGGTGG
ATGGGGACTCTGTGAGTGGCATTGTTTTGTGGGCTACAAGA ACTACCGATAACCGTGCG
GGCTTCGTGCTGGCCCCAATCGGCCTGGTGCTCATCGTGGGAGGCTACTTCCTCATCCG
AGGAGTCATGACTCTGTTCTCCATCAAGAGCAACCACCCCGGGCTGCTGAGTGAGAA
GGCTGCCAGCAAGATCAACGAGACCATGCTGCGCCTGGGCATTTTTGGCTTCCTGGCC
TTTGGCTTTGTGCTCATTACCTTCAGCTGCCACTTCTACCCTTCTTCAACCAGGCTGA
GTGGGAGCGCAGCTTCCGGGACTATGTGCTATGTCAGGCCAATGTGACCATCGGGCTG
CCCACCAAGCAGCCCATCCCTGACTGTGAGATCAAGAATCGCCCAGCCTTCTGGTGG
AGAAGATCAACCTGTTTGCCATGTTTGGAACTGGCATCGCCATGAGCACCTGGGTCTG
GACCAAGGCCACGCTGCTCATCTGGAGGCGTACCTGGTGCAGGTTGACTGGGCAGAG
TGACGATGAGCCAAAGCGGATCAAGAAGAGCAAGATGATTGCCAAGGCCTTCTCTAA
GCGGCACGAGCTCCTGCAGAACCCAGGCCAGGAGCTGTCCTTCAGCATGCACACTGT
GTCCACGACGGGCCCCTGGCGGGCTTGGCCTTTGACCTCAATGAGCCCTCAGCTGAT
GTCTCCTCTGCCTGGGCCAGCATGTCACCAAGATGGTGGCTCGGAGAGGAGCCATAC
TGCCCCAGGATATTTCTGTACCCCTGTGGCAACTCCAGTGCCCCAGAGGAACAAGC
CAACCTGTGGCTGGTTGAGGCAGAGATCTCCCAGAGCTGCAGAAGCGCCTGGGCCG
GAAGAAGAAGAGGAGGAAGAGGAAGAAGGAGGTGTGCCCGCTGGCGCCGCCCCCTG
AGTTTACCCCCCTGCCCTGCCCCAGTACCATTCTCGACTGCCTCAGCTGCCCCGG
CAGAAATGCCTGGTGGCTGCAGGTGCCTGGGGAGCTGGGGACTCTTGCCGACAGGGA

GCGTGGACCCTGGTCTCCAACCCATTCTGCCAGAGCCCAGTCCCCCTCAGGATCCAT
TTCTGCCAGTGCACCGGCCCGTGGCATGGGCTCATGGCCGCCGACAGGGCCTGGG
GCCTATTACTIONCCGCACCAACCTGATGGACACAGAACTCATGGATGCAGACTCGGAC
TTCTGACTCGAGTCT

Smo W535L:

TGCGATGGTGAATAGCAGAGCTCGTTTAGTGACCGTCAGAATTTTGTAAATACGACTCA
CTATAGGGCGGCCGGAATTCGTCGACTGGATCCGGTACCGAGGAGATCTGCCGCCGC
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GCTGCTGCTGCTGCTGCTGGGGGACCCGGGCCGGGGGGCGGCCTCGAGCGGGAACGC
GACCGGGCCTGGGCCTCGGAGCGCGGGCGGGAGCGCGAGGAGGAGCGCGGCGGTGA
CTGGCCCTCCGCCGCCGCTGAGCCACTGCGGCCGGGCTGCCCCCTGCGAGCCGCTGC
GCTACAACGTGTGCCTGGGCTCGGTGCTGCCCTACGGGGCCACCTCCACACTGCTGGC
CGGAGACTCGGACTCCAGGAGGAAGCGCACGGCAAGCTCGTGCTCTGGTCCGGCCT
CCGAATGCCCCCGCTGCTGGGCAGTGATCCAGCCCCTGCTGTGTGCCGTATACATGC
CCAAGTGTGAGAATGACCGGGTGGAGCTGCCAGCCGTACCCTCTGCCAGGCCACCC
GAGGCCCTGTGCCATCGTGGAGAGGGAGCGGGGCTGGCCTGACTTCCTGCGCTGCA
CTCCTGACCCTCCCTGAAGGCTGCACGAATGAGGTGCAGAACATCAAGTTCAACAG
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GGACGTGGAGGGCTGCGGCATCCAGTGCCAGAACCCGCTCTTCACAGAGGCTGAGCA
CCAGGACATGCACAGCTACATCGCGGCCTTCGGGGCCGTACGGGCCTCTGCACGCTC
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TCTCTTCTACGTCAATGCGTGCTTCTTTGTGGGCAGCATTGGCTGGCTGGCCCAGTTCA
TGGATGGTGCCCGCCGAGAGATCGTCTGCCGTGCAGATGGCACCATGAGGCTTGGGGA
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GATGGCTGGTGTGGTTTTGGTTTTGTGGTCCCTACCTATGCCTGGCACACTTCCTTCAAAG
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CGTGCTGGCCCCAATCGGCCTGGTGTCTCATCGTGGGAGGCTACTTCCTCATCCGAGGA
GTCATGACTCTGTTCTCCATCAAGAGCAACCACCCGGGCTGCTGAGTGAGAAGGCTG
CCAGCAAGATCAACGAGACCATGCTGCGCCTGGGCATTTTTGGCTTCCTGGCCTTTGG
CTTTGTGCTCATTACCTCAGCTGCCACTTCTACGACTTCTTCAACCAGGCTGAGTGGG
AGCGCAGCTTCCGGGACTATGTGCTATGTCAGGCCAATGTGACCATCGGGCTGCCAC
CAAGCAGCCCATCCCTGACTGTGAGATCAAGAATCGCCCAGCCTTCTGGTGGAGAAG
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GGCCACGCTGCTCATCTGGAGGCGTACCTGGTGCAGGTTGACTGGGCAGAGTGACGAT
GAGCCAAAGCGGATCAAGAAGAGCAAGATGATTGCCAAGGCCTTCTCTAAGCGGCAC
GAGCTCCTGCAGAACCAGGCCAGGAGCTGTCCTTCAGCATGCACACTGTGTCCCACG
ACGGGCCCCGTGGCGGGCTTGGCCTTTGACCTCAATGAGCCCTCAGCTGATGTCTCCTC
TGCCTGGGCCCAGCATGTCACCAAGATGGTGGCTCGGAGAGGAGCCATACTGCCCCAG
GATATTTCTGTCACCCCTGTGGCAACTCCAGTGCCCCAGAGGAACAAGCCAACCTGT
GGCTGGTTGAGGCAGAGATCTCCCCAGAGCTGCAGAAGCGCCTGGGCCGGAAGAAGA
AGAGGAGGAAGAGGAAGAAGGAGGTGTGCCCGCTGGCGCCGCCCTGAGCTTCAC

CCCCCTGCCCTGCCCCAGTACCATTCTCGACTGCCTCAGCTGCCCCGGCAGAAAT
GCCTGGTGGCTGCAGGTGCCTGGGGAGCTGGGGACTCTTGCCGACAGGGAGCGTGGA
CCCTGGTCTCCAACCCATTCTGCCAGAGCCCAGTCCCCCTCAGGATCCATTTCTGCC
AGTGACCCGGCCCCCGTGGCATGGGCTCATGGCCGCGACAGGGCCTGGGGCCTATTC
ACTCCCGCACCAACCTGATGGACACAGAACTCATGGATGCAGACTCGGACTTCACGCG
TACGCGGCCGCTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATC
CTGGATTACAAGGATGACGACGATAAGGTTTAAACGGCCGGCCGCGGTTCATAGCTGTT
TCCTGAACAGATCCCGGGTGGCATCCCTGTGACCCCTCCCAGTGCCTCTCTGGCCCT
GGAAGTTGCCACTCCAGTGCCACCAGCCTGTCCTAATAAATAGTCAACGT

Smo H231R:

CTAGAGAACCCACTGCTTACTGGCTTATCGAAATTAATACGACTCACTATAGGGAGACC
CAAGCTGGCTAGCGTTTAACTTAAGCTTGGTACCGAGCTCGGATCCGCCACCATGGC
CGCTGCCCGCCAGCGCGGGGGCCGGAGCTCCCGCTCCTGGGGCTGCTGCTGCTGCT
GCTGCTGGGGACCCGGGCCGGGGGGCGCCTCGAGCGGGAACGCGACCGGGCCTG
GGCCTCGGAGCGCGGGGCGGAGCGCGAGGAGGAGCGCGGCGGTGACTGGCCCTCCG
CCGCCGCTGAGCCACTGCGGCCGGGCTGCCCCCTGCGAGCCGCTGCGCTACAACGTGT
GCCTGGGCTCGGTGCTGCCCTACGGGGCCACCTCCACACTGCTGGCCGGAGACTCGG
ACTCCCAGGAGGAAGCGCACGGCAAGCTCGTGCTCTGGTCGGGCCTCCGGAATGCCC
CCCGCTGCTGGGCAGTGATCCAGCCCCTGCTGTGTGCCGTATACATGCCCAAGTGTGA
GAATGACCGGGTGGAGCTGCCAGCCGTACCCTCTGCCAGGCCACCCGAGGCCCTGT
GCCATCGTGGAGAGGGAGCGGGGCTGGCCTGACTTCCTGCGCTGCACTCCTGACCGCT
TCCCTGAAGGCTGCACGAATGAGGTGCAGAACATCAAGTTCAACAGTTCAGGCCAGT
GCGAAGTGCCCTTGGTTCGGACAGACAACCCCAAGAGCTGGTACGAGGACGTGGAGG
GCTGCGGCATCCAGTGCCAGAACCCGCTCTTCACAGAGGCTGAGCACCAGGACATGC
GCAGCTACATCGCGGCCTTCGGGGCCGTCACGGGCCTCTGCACGCTCTTCACCCTGGC
CACATTCGTGGCTGACTGGCGGAACCTCGAATCGCTACCCTGCTGTTATTCTTTCTACG
TCAATGCGTGCTTCTTTGTGGGCAGCATTGGCTGGCTGGCCCAGTTCATGGATGGTGCC
CGCCGAGAGATCGTCTGCCGTGCAGATGGCACCATGAGGCTTGGGGAGCCCACCTCCA
ATGAGACTCTGTCCTGCGTCATCATCTTTGTTCATCGTGTACTACGCCCTGATGGCTGGTG
TGGTTTGGTTTGTGGTCTCACCTATGCCTGGCACACTTCCTTCAAAGCCCTGGGCACC
ACCTACCAGCCTCTCTCGGGCAAGACCTCCTACTTCCACCTGCTCACCTGGTCACTCCC
CTTTGTCTCACTGTGGCAATCCTTGTGTGGCGCAGGTGGATGGGGACTCTGTGAGT
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AATCGGCCTGGTGCTCATCGTGGGAGGCTACTTCCTCATCCGAGGAGTCATGACTCTGT
TCTCCATCAAGAGCAACCACCCCGGGCTGCTGAGTGAGAAGGCTGCCAGCAAGATCA
ACGAGACCATGCTGCGCCTGGGCATTTTTGGCTTCTGGCCTTTGGCTTTGTGCTCATT
ACCTTACAGCTGCCACTTCTACGACTTCTTCAACCAGGCTGAGTGGGAGCGCAGCTTCC
GGACTATGTGCTATGTCAGGCCAATGTGACCATCGGGCTGCCACCAAGCAGCCCAT
CCCTGACTGTGAGATCAAGAATCGCCGAGCCTTCTGGTGGAGAAGATCAACCTGTTT
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TCATCTGGAGGCGTACCTGGTGCAGGTTGACTGGGCAGAGTGACGATGAGCCAAAGC
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GAACCCAGGCCAGGAGCTGTCCTTCAGCATGCACACTGTGTCCCACGACGGGCCCGT

GGCGGGCTTGGCCTTTGACCTCAATGAGCCCTCAGCTGATGTCTCCTCTGCCTGGGCC
CAGCATGTCACCAAGATGGTGGCTCGGAGAGGAGCCATACTGCCCCAGGATATTTCTG
TCACCCCTGTGGCAACTCCAGTGCCCCCAGAGGAACAAGCCAACCTGTGGCTGGTTG
AGGCAGAGATCTCCCAGAGCTGCAGAAGCGCCTGGGCCGGAAGAAGAAGAGGAGG
AAGAGGAAGAAGGAGGTGTGCCCGCTGGCGCCGCCCTGAGCTTCACCCCCCTGCC
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CTGCAGGTGCCTGGGGAGCTGGGGACTCTTGCCGACAGGGAGCGTGGACCCTGGTCT
CCAACCCATTCTGCCAGAGCCCAGTCCCCCTCAGGATCCATTTCTGCCAGTGCACC
GGCCCCGTGGCATGGGCTCATGGCCGCCGACAGGGCCTGGGGCCTATTCCTCCCGC
ACCAACCTGATGGACACAGAACTCATGGATGCAGACTCGGACTTCGAACAAAACTC
ATCTCAGAAGAGGATCTGGACTACAAGGATGACGATGACAAGGATTACAAAGACGAC
GATGATAAGGACTATAAGGATGATGACGACAAATAATCTAGAGGGCCCGTTTAAACCCG
CTGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTT

Smo W281C:

CTAGAGAACCCACTGCTTACTGGCTTATCGAAATTAATACGACTCACTATAGGGAGACC
CAAGCTGGCTAGCGTTTAAACTTAAGCTTGGTACCGAGCTCGGATCCGCCACCATGGC
CGCTGCCCCGCCAGCGCGGGGGCCGGAGCTCCCGCTCCTGGGGCTGCTGCTGCTGCT
GCTGCTGGGGGACCCGGGCCGGGGGGCGGCCTCGAGCGGGAACGCGACCCGGGCCTG
GGCCTCGGAGCGCGGGCGGGAGCGCGAGGAGGAGCGCGGCGGTGACTGGCCCTCCG
CCGCCGCTGAGCCACTGCGGCCGGGCTGCCCCCTGCGAGCCGCTGCGCTACAACGTGT
GCCTGGGCTCGGTGCTGCCCTACGGGGCCACCTCCACACTGCTGGCCGGAGACTCGG
ACTCCCAGGAGGAAGCGCACGGCAAGCTCGTGCTCTGGTCGGGCCTCCGGAATGCC
CCCGCTGCTGGGCAGTGATCCAGCCCCTGCTGTGTGCCGTATACATGCCCAAGTGTGA
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GCCATCGTGGAGAGGGAGCGGGGCTGGCCTGACTTCCTGCGCTGCACTCCTGACCGCT
TCCCTGAAGGCTGCACGAATGAGGTGCAGAACATCAAGTTCAACAGTTCAGGCCAGT
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ACAGCTACATCGCGGCCTTCGGGGCCGTCACGGGCCTCTGCACGCTCTTACCCTGGC
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TCAATGCGTGCTTCTTTGTGGGCAGCATTGGCTGCCTGGCCCAGTTCATGGATGGTGCC
CGCCGAGAGATCGTCTGCCGTGCAGATGGCACCATGAGGCTTGGGGAGCCCACCTCCA
ATGAGACTCTGTCTGCGTCATCATCTTTGTGCATCGTGTACTACGCCCTGATGGCTGGTG
TGTTTTGGTTTGTGGTCCCTCACCTATGCCTGGCACACTTCCTTCAAAGCCCTGGGCACC
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GCCATGTTTGGAACTGGCATCGCCATGAGCACCTGGGTCTGGACCAAGGCCACGCTGC
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Smo L412F:

CTAGAGAACCCACTGCTTACTGGCTTATCGAAATTAATACGACTCACTATAGGGAGACC
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ACTCCCAGGAGGAAGCGCACGGCAAGCTCGTGCTCTGGTCGGGCCTCCGGAATGCC
CCCGCTGCTGGGCAGTGATCCAGCCCCTGCTGTGTGCCGTATACATGCCCAAGTGTGA
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GCCATCGTGGAGAGGGAGCGGGGCTGGCCTGACTTCCTGCGCTGCACTCCTGACCGCT
TCCCTGAAGGCTGCACGAATGAGGTGCAGAACATCAAGTTCAACAGTTCAGGCCAGT
GCGAAGTGCCCTTGGTTCGGACAGACAACCCCAAGAGCTGGTACGAGGACGTGGAGG
GCTGCGGCATCCAGTGCCAGAACCCGCTCTTCACAGAGGCTGAGCACCAGGACATGC
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CGCCGAGAGATCGTCTGCCGTGCAGATGGCACCATGAGGCTTGGGGAGCCCACCTCCA
ATGAGACTCTGTCTGCGTCATCATCTTTGTTCATCGTGTACTACGCCCTGATGGCTGGTG
TGGTTTGGTTTGTGGTCCTCACCTATGCCTGGCACACTTCCTTCAAAGCCCTGGGCACC
ACCTACCAGCCTCTCTCGGGCAAGACCTCCTACTTCCACCTGCTCACCTGGTCACTCCC
CTTTGTCTCACTGTGGCAATCCTTGCTGTGGCGCAGGTGGATGGGGACTCTGTGAGT
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AATCGGCCTGGTGTTCATCGTGGGAGGCTACTTCTCATCCGAGGAGTCATGACTCTGT
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ACGAGACCATGCTGCGCCTGGGCATTTTTGGCTTCTGGCCTTTGGCTTTGTGCTCATT
ACCTTCAGCTGCCACTTCTACGACTTCTTCAACCAGGCTGAGTGGGAGCGCAGCTTCC
GGGACTATGTGCTATGTCAGGCCAATGTGACCATCGGGCTGCCACCAAGCAGCCAT
CCCTGACTGTGAGATCAAGAATCGCCGAGCCTTCTGGTGGAGAAGATCAACCTGTTT
GCCATGTTTGGAAGTGGCATCGCCATGAGCACCTGGGTCTGGACCAAGGCCACGCTGC
TCATCTGGAGGCGTACCTGGTGCAGGTTGACTGGGCAGAGTGACGATGAGCCAAAGC
GGATCAAGAAGAGCAAGATGATTGCCAAGGCCTTCTCTAAGCGGCACGAGCTCCTGCA
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GGCGGGCTTGGCCTTTGACCTCAATGAGCCCTCAGCTGATGTCTCCTCTGCCTGGGCC
CAGCATGTCACCAAGATGGTGGCTCGGAGAGGAGCCATACTGCCCCAGGATATTTCTG
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AGGCAGAGATCTCCCAGAGCTGCAGAAGCGCCTGGGCCGGAAGAAGAAGAGGAGG
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CCTGCCCCAGTACCATTCTCGACTGCCTCAGCTGCCCCGGCAGAAATGCCTGGTGG
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GGCCCCCGTGGCATGGGCTCATGGCCGCCGACAGGGCCTGGGGCCTATTCACTCCCGC
ACCAACCTGATGGACACAGAACTCATGGATGCAGACTCGGACTTCGAACAAAACTC
ATCTCAGAAGAGGATCTGGACTACAAGGATGACGATGACAAGGATTACAAAGACGAC
GATGATAAGGACTATAAGGATGATGACGACAAATAATCTAGAGGGGCCGTTTAAACCCG
CTGATCAGCCTCGACTGTGC

Smo F460L:

CTAGAGAACCCACTGCTTACTGGCTTATCGAAATTAATACGACTCACTATAGGGAGACC
CAAGCTGGCTAGCGTTTAAACTTAAGCTTGGTACCGAGCTCGGATCCGCCACCATGGC
CGCTGCCCCGCCAGCGCGGGGGCCGGAGCTCCCGCTCCTGGGGCTGCTGCTGCTGCT
GCTGCTGGGGGACCCGGGCCGGGGGGCGGCCTCGAGCGGGAACGCGACCGGGCCTG
GGCCTCGGAGCGCGGGCGGGAGCGCGAGGAGGAGCGCGGCGGTGACTGGCCCTCCG
CCGCCGCTGAGCCACTGCGGCCGGGCTGCCCCCTGCGAGCCGCTGCGCTACAACGTGT
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CCCGCTGCTGGGCAGTGATCCAGCCCCTGCTGTGTGCCGTATACATGCCCAAGTGTGA
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GCCATCGTGGAGAGGGAGCGGGGCTGGCCTGACTTCTGCGCTGCACTCCTGACCGCT
TCCCTGAAGGCTGCACGAATGAGGTGCAGAACATCAAGTTCAACAGTTCAGGCCAGT
GCGAAGTGCCCTTGGTTCGGACAGACAACCCCAAGAGCTGGTACGAGGACGTGGAGG
GCTGCGGCATCCAGTGCCAGAACCCGCTCTTCACAGAGGCTGAGCACCAGGACATGC
ACAGCTACATCGCGCCTTCGGGGCCGTCACGGGCCTCTGCACGCTCTTACCCTGGC
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TCAATGCGTGCTTCTTTGTGGGCAGCATTGGCTGGCTGGCCCAGTTCATGGATGGTGCC
CGCCGAGAGATCGTCTGCCGTGCAGATGCCACCATGAGGCTTGGGGAGCCCACCTCCA
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TGGTTTGGTTTGTGGTCCACCTATGCCCTGGCACACTTCCTTCAAAGCCCTGGGCACC
ACCTACCAGCCTCTCTCGGGCAAGACCTCCTACTTCCACCTGCTCACCTGGTCACTCCC

CTTTGTCCTCACTGTGGCAATCCTTGCTGTGGCGCAGGTGGATGGGGACTCTGTGAGT
GGCATTGTGTTTGTGGGCTACAAGAACTACCGATAACCGTGCGGGCTTCGTGCTGGCCCC
AATCGGCCCTGGTGCTCATCGTGGGAGGCTACTTCCTCATCCGAGGAGTCATGACTCTGT
TCTCCATCAAGAGCAACCACCCCGGGCTGCTGAGTGAGAAGGCTGCCAGCAAGATCA
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ACCTTCAGCTGCCACTTCTACGACTTCTTCAACCAGGCTGAGTGGGAGCGCAGCTTCC
GGGACTATGTGCTATGTCAGGCCAATGTGACCATCGGGCTGCCACCAAGCAGCCCAT
CCCTGACTGTGAGATCAAGAATCGCCGAGCCTTCTGGTGGAGAAGATCAACCTGTTT
GCCATGTTTGAACTGGCATCGCCATGAGCACCTGGGTCTGGACCAAGGCCACGCTGC
TCATCTGGAGGCGTACCTGGTGCAGGTTGACTGGGCAGAGTGACGATGAGCCAAAGC
GGATCAAGAAGAGCAAGATGATTGCCAAGGCCTTCTCTAAGCGGCACGAGCTCCTGCA
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CAGCATGTCACCAAGATGGTGGCTCGGAGAGGAGCCATACTGCCCCAGGATATTTCTG
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CCTGCCCCCAGTACCATTCTCGACTGCCTCAGCTGCCCCGGCAGAAATGCCTGGTGG
CTGCAGGTGCCTGGGGAGCTGGGGACTCTTGCCGACAGGGAGCGTGGACCCTGGTCT
CCAACCCATTCTGCCAGAGCCCAGTCCCCCTCAGGATCCATTTCTGCCAGTGCACC
GGCCCCCGTGGCATGGGCTCATGGCCGCCGACAGGGCCTGGGGCCTATTCCTCCCGC
ACCAACCTGATGGACACAGAACTCATGGATGCAGACTCGGACTTCGAACAAAACTC
ATCTCAGAAGAGGATCTGGACTACAAGGATGACGATGACAAGGATTACAAAGACGAC
GATGATAAGGACTATAAGGATGATGACGACAAATAATCTAGAGGGCCCGTTTAAACCCG
CTGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTT

DNA sequencing results are provided below.

Smo D473H:

		1	50
pSB1296-1	(1)	CAGAGCTCTCTGGCTAACTAGAGAACCCACTGCTTACTGGCTTATCGAAA	
NM_005631.4 CDS	(1)	-----	
		51	100
pSB1296-1	(51)	TTAATACGACTCACTATAGGGAGACCCAAGCTGGCTAGCGTTTAACTTA	
NM_005631.4 CDS	(1)	-----	
		101	150
pSB1296-1	(101)	AGCTTGGTACCGAGCTCGGATCCGCCACCATGGCCGCTGCCCGCCAGCG	
NM_005631.4 CDS	(1)	-----ATGGCCGCTGCCCGCCAGCG	
		151	200
pSB1296-1	(151)	CGGGGGCCGGAGCTCCCGCTCCTGGGGCTGCTGCTGCTGCTGCTGGG	
NM_005631.4 CDS	(22)	CGGGGGCCGGAGCTCCCGCTCCTGGGGCTGCTGCTGCTGCTGCTGGG	
		201	250
pSB1296-1	(201)	GGACCCGGGCCGGGGGGCGGCCTCGAGCGGGAACGCGACCGGGCCTGGGC	
NM_005631.4 CDS	(72)	GGACCCGGGCCGGGGGGCGGCCTCGAGCGGGAACGCGACCGGGCCTGGGC	
		251	300
pSB1296-1	(251)	CTCGGAGCGCGGGCGGGAGCGGAGGAGGAGCGCGGCGGTGACTGGCCCT	
NM_005631.4 CDS	(122)	CTCGGAGCGCGGGCGGGAGCGGAGGAGGAGCGCGGCGGTGACTGGCCCT	
		301	350
pSB1296-1	(301)	CCGCCGCCGCTGAGCCACTGCGGCCGGGCTGCCCCCTGCGAGCCGCTGCG	
NM_005631.4 CDS	(172)	CCGCCGCCGCTGAGCCACTGCGGCCGGGCTGCCCCCTGCGAGCCGCTGCG	
		351	400
pSB1296-1	(351)	CTACAACGTGTGCCTGGGCTCGGTGCTGCCCTACGGGGCCACCTCCACAC	
NM_005631.4 CDS	(222)	CTACAACGTGTGCCTGGGCTCGGTGCTGCCCTACGGGGCCACCTCCACAC	
		401	450
pSB1296-1	(401)	TGCTGGCCGGAGACTCGGACTCCCAGGAGGAAGCGCACGGCAAGCTCGTG	
NM_005631.4 CDS	(272)	TGCTGGCCGGAGACTCGGACTCCCAGGAGGAAGCGCACGGCAAGCTCGTG	
		451	500
pSB1296-1	(451)	CTCTGGTTCGGGCCTCCGGAATGCCCCCGCTGCTGGGCAGTGATCCAGCC	
NM_005631.4 CDS	(322)	CTCTGGTTCGGGCCTCCGGAATGCCCCCGCTGCTGGGCAGTGATCCAGCC	
		501	550
pSB1296-1	(501)	CCTGCTGTGTGCCGTATACATGCCCAAGTGTGAGAAATGACCGGGTGGAGC	
NM_005631.4 CDS	(372)	CCTGCTGTGTGCCGTATACATGCCCAAGTGTGAGAAATGACCGGGTGGAGC	
		551	600
pSB1296-1	(551)	TGCCCAGCCGTACCCTCTGCCAGGCCACCCGAGGCCCTGTGCCATCGTG	
NM_005631.4 CDS	(422)	TGCCCAGCCGTACCCTCTGCCAGGCCACCCGAGGCCCTGTGCCATCGTG	
		601	650
pSB1296-1	(601)	GAGAGGGAGCGGGGCTGGCCTGACTTCCTGCGCTGCACCTCCTGACCGCTT	

NM_005631.4 CDS	(472)	GAGAGGGAGCGGGGCTGGCCTGACTTCCTGCGCTGCACTCCTGACCGCTT	651	700
pSB1296-1	(651)	CCCTGAAGGCTGCACGAATGAGGTGCAGAACATCAAGTTCAACAGTTCAG		
NM_005631.4 CDS	(522)	CCCTGAAGGCTGCACGAATGAGGTGCAGAACATCAAGTTCAACAGTTCAG	701	750
pSB1296-1	(701)	GCCAGTGCGAAGTGCCCTTGGTTCCGGACAGACAACCCCAAGAGCTGGTAC		
NM_005631.4 CDS	(572)	GCCAGTGCGAAGTGCCCTTGGTTCCGGACAGACAACCCCAAGAGCTGGTAC	751	800
pSB1296-1	(751)	GAGGACGTGGAGGGCTGCGGCATCCAGTGCCAGAACCCGCTCTTCACAGA		
NM_005631.4 CDS	(622)	GAGGACGTGGAGGGCTGCGGCATCCAGTGCCAGAACCCGCTCTTCACAGA	801	850
pSB1296-1	(801)	GGCTGAGCACCAGGACATGCACAGCTACATCGCGGCCCTTCGGGGCCGTCA		
NM_005631.4 CDS	(672)	GGCTGAGCACCAGGACATGCACAGCTACATCGCGGCCCTTCGGGGCCGTCA	851	900
pSB1296-1	(851)	CGGGCCTCTGCACGCTCTTCACCCCTGGCCACATTCGTGGCTGACTGGCGG		
NM_005631.4 CDS	(722)	CGGGCCTCTGCACGCTCTTCACCCCTGGCCACATTCGTGGCTGACTGGCGG	901	950
pSB1296-1	(901)	AACTCGAATCGCTACCCTGCTGTTATTCTCTTCTACGTCAATGCGTGCTT		
NM_005631.4 CDS	(772)	AACTCGAATCGCTACCCTGCTGTTATTCTCTTCTACGTCAATGCGTGCTT	951	1000
pSB1296-1	(951)	CTTTGTGGGCAGCATTGGCTGGCTGGCCAGTTCATGGATGGTGCCCGCC		
NM_005631.4 CDS	(822)	CTTTGTGGGCAGCATTGGCTGGCTGGCCAGTTCATGGATGGTGCCCGCC	1001	1050
pSB1296-1	(1001)	GAGAGATCGTCTGCCGTGCAGATGGCACCATGAGGCTTGGGGAGCCCACC		
NM_005631.4 CDS	(872)	GAGAGATCGTCTGCCGTGCAGATGGCACCATGAGGCTTGGGGAGCCCACC	1051	1100
pSB1296-1	(1051)	TCCAATGAGACTCTGTCCCTGCGTCATCATCTTTGTCATCGTGTACTACGC		
NM_005631.4 CDS	(922)	TCCAATGAGACTCTGTCCCTGCGTCATCATCTTTGTCATCGTGTACTACGC	1101	1150
pSB1296-1	(1101)	CCTGATGGCTGGTGTGGTTTGGTTTGTGGTCCCTCACCTATGCCTGGCACA		
NM_005631.4 CDS	(972)	CCTGATGGCTGGTGTGGTTTGGTTTGTGGTCCCTCACCTATGCCTGGCACA	1151	1200
pSB1296-1	(1151)	CTTCCTTCAAAGCCCTGGGCACCACCTACCAGCCTCTCTCGGGCAAGACC		
NM_005631.4 CDS	(1022)	CTTCCTTCAAAGCCCTGGGCACCACCTACCAGCCTCTCTCGGGCAAGACC	1201	1250
pSB1296-1	(1201)	TCCTACTTCCACCTGCTCACCTGGTCACTCCCCTTTGTCCTCACTGTGGC		
NM_005631.4 CDS	(1072)	TCCTACTTCCACCTGCTCACCTGGTCACTCCCCTTTGTCCTCACTGTGGC	1251	1300
pSB1296-1	(1251)	AATCCTTGCTGTGGCGCAGGTGGATGGGGACTCTGTGAGTGGCATTGTGT		
NM_005631.4 CDS	(1122)	AATCCTTGCTGTGGCGCAGGTGGATGGGGACTCTGTGAGTGGCATTGTGT	1301	1350
pSB1296-1	(1301)	TTGTGGGCTACAAGAACTACCGATACCGTGCGGGCTTCGTGCTGGCCCCA		
NM_005631.4 CDS	(1172)	TTGTGGGCTACAAGAACTACCGATACCGTGCGGGCTTCGTGCTGGCCCCA	1351	1400

pSB1296-1	(1351)	ATCGGCCTGGTGCTCATCGTGGGAGGCTACTTCCTCATCCGAGGAGTCAT
NM_005631.4 CDS	(1222)	ATCGGCCTGGTGCTCATCGTGGGAGGCTACTTCCTCATCCGAGGAGTCAT
	1401	1450
pSB1296-1	(1401)	GACTCTGTTCTCCATCAAGAGCAACCACCCCGGGCTGCTGAGTGAGAAGG
NM_005631.4 CDS	(1272)	GACTCTGTTCTCCATCAAGAGCAACCACCCCGGGCTGCTGAGTGAGAAGG
	1451	1500
pSB1296-1	(1451)	CTGCCAGCAAGATCAACGAGACCATGCTGCGCCTGGGCATTTTTGGCTTC
NM_005631.4 CDS	(1322)	CTGCCAGCAAGATCAACGAGACCATGCTGCGCCTGGGCATTTTTGGCTTC
	1501	1550
pSB1296-1	(1501)	CTGGCCTTTGGCTTTGTGCTCATTACCTTCAGCTGCCACTTCTACCACTT
NM_005631.4 CDS	(1372)	CTGGCCTTTGGCTTTGTGCTCATTACCTTCAGCTGCCACTTCTACCACTT
	1551	1600
pSB1296-1	(1551)	CTTCAACCAGGCTGAGTGGGAGCGCAGCTTCCGGGACTATGTGCTATGTC
NM_005631.4 CDS	(1422)	CTTCAACCAGGCTGAGTGGGAGCGCAGCTTCCGGGACTATGTGCTATGTC
	1601	1650
pSB1296-1	(1601)	AGGCCAATGTGACCATCGGGCTGCCACCAAGCAGCCCATCCCTGACTGT
NM_005631.4 CDS	(1472)	AGGCCAATGTGACCATCGGGCTGCCACCAAGCAGCCCATCCCTGACTGT
	1651	1700
pSB1296-1	(1651)	GAGATCAAGAATCGCCCGAGCCTTCTGGTGGAGAAGATCAACCTGTTTGC
NM_005631.4 CDS	(1522)	GAGATCAAGAATCGCCCGAGCCTTCTGGTGGAGAAGATCAACCTGTTTGC
	1701	1750
pSB1296-1	(1701)	CATGTTTGGAACTGGCATCGCCATGAGCACCTGGGTCTGGACCAAGGCCA
NM_005631.4 CDS	(1572)	CATGTTTGGAACTGGCATCGCCATGAGCACCTGGGTCTGGACCAAGGCCA
	1751	1800
pSB1296-1	(1751)	CGCTGCTCATCTGGAGGCGTACCTGGTGCAGGTTGACTGGGCAGAGTGAC
NM_005631.4 CDS	(1622)	CGCTGCTCATCTGGAGGCGTACCTGGTGCAGGTTGACTGGGCAGAGTGAC
	1801	1850
pSB1296-1	(1801)	GATGAGCCAAAGCGGATCAAGAAGAGCAAGATGATTGCCAAGGCCTTCTC
NM_005631.4 CDS	(1672)	GATGAGCCAAAGCGGATCAAGAAGAGCAAGATGATTGCCAAGGCCTTCTC
	1851	1900
pSB1296-1	(1851)	TAAGCGGCACGAGCTCCTGCAGAACCCAGGCCAGGAGCTGTCCTTCAGCA
NM_005631.4 CDS	(1722)	TAAGCGGCACGAGCTCCTGCAGAACCCAGGCCAGGAGCTGTCCTTCAGCA
	1901	1950
pSB1296-1	(1901)	TGCACACTGTGTCCACGACGGGCCCGTGGCGGGCTTGGCCTTTGACCTC
NM_005631.4 CDS	(1772)	TGCACACTGTGTCCACGACGGGCCCGTGGCGGGCTTGGCCTTTGACCTC
	1951	2000
pSB1296-1	(1951)	AATGAGCCCTCAGCTGATGTCTCCTCTGCCTGGGCCCAGCATGTCACCAA
NM_005631.4 CDS	(1822)	AATGAGCCCTCAGCTGATGTCTCCTCTGCCTGGGCCCAGCATGTCACCAA
	2001	2050
pSB1296-1	(2001)	GATGGTGGCTCGGAGAGGAGCCATACTGCCCCAGGATATTTCTGTCACCC
NM_005631.4 CDS	(1872)	GATGGTGGCTCGGAGAGGAGCCATACTGCCCCAGGATATTTCTGTCACCC
	2051	2100
pSB1296-1	(2051)	CTGTGGCAACTCCAGTGCCCCCAGAGGAACAAGCCAACCTGTGGCTGGTT
NM_005631.4 CDS	(1922)	CTGTGGCAACTCCAGTGCCCCCAGAGGAACAAGCCAACCTGTGGCTGGTT

		2101		2150
pSB1296-1	(2101)	GAGGCAGAGATCTCCCCAGAGCTGCAGAAGCGCCTGGGCCGGAAGAAGAA		
NM_005631.4 CDS	(1972)	GAGGCAGAGATCTCCCCAGAGCTGCAGAAGCGCCTGGGCCGGAAGAAGAA		
		2151		2200
pSB1296-1	(2151)	GAGGAGGAAGAGGAAGAAGGAGGTGTGCCCGCTGGCGCCGCCCTGAGC		
NM_005631.4 CDS	(2022)	GAGGAGGAAGAGGAAGAAGGAGGTGTGCCCGCTGGCGCCGCCCTGAGC		
		2201		2250
pSB1296-1	(2201)	TTCACCCCCCTGCCCTGCCCCAGTACCATTCTCGACTGCCTCAGCTG		
NM_005631.4 CDS	(2072)	TTCACCCCCCTGCCCTGCCCCAGTACCATTCTCGACTGCCTCAGCTG		
		2251		2300
pSB1296-1	(2251)	CCCCGGCAGAAATGCCTGGTGGCTGCAGGTGCCTGGGGAGCTGGGGACTC		
NM_005631.4 CDS	(2122)	CCCCGGCAGAAATGCCTGGTGGCTGCAGGTGCCTGGGGAGCTGGGGACTC		
		2301		2350
pSB1296-1	(2301)	TTGCCGACAGGGAGCGTGGACCCTGGTCTCCAACCCATTCTGCCCAGAGC		
NM_005631.4 CDS	(2172)	TTGCCGACAGGGAGCGTGGACCCTGGTCTCCAACCCATTCTGCCCAGAGC		
		2351		2400
pSB1296-1	(2351)	CCAGTCCCCCTCAGGATCCATTTCTGCCAGTGCACCGGCCCCCGTGGCA		
NM_005631.4 CDS	(2222)	CCAGTCCCCCTCAGGATCCATTTCTGCCAGTGCACCGGCCCCCGTGGCA		
		2401		2450
pSB1296-1	(2401)	TGGGCTCATGGCCGCCGACAGGGCCTGGGGCCTATTCACCTCCCGCACCAA		
NM_005631.4 CDS	(2272)	TGGGCTCATGGCCGCCGACAGGGCCTGGGGCCTATTCACCTCCCGCACCAA		
		2451		2500
pSB1296-1	(2451)	CCTGATGGACACAGAACTCATGGATGCAGACTCGGACTTCTGACTCGAGT		
NM_005631.4 CDS	(2322)	CCTGATGGACACAGAACTCATGGATGCAGACTCGGACTTCTGACTCGAGT		
				2501
			pSB1296-1 (2501) CT	
			NM_005631.4 CDS (2365) --	

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		1		50
pSB936-4	(1)	TGCGATGGTGCAATAGCAGAGCTCGTTTAGTGACCGTCAGAAATTTGTAA		
NM_005631.4 CDS	(1)	-----		
		51		100
pSB936-4	(51)	TACGACTCACTATAGGGCGGCCGGGAATTCGTCGACTGGATCCGGTACCG		
NM_005631.4 CDS	(1)	-----		
		101		150
pSB936-4	(101)	AGGAGATCTGCCGCCGCGATCGCCATGGCCGCTGCCCGCCCAGCGCGGGG		
NM_005631.4 CDS	(1)	-----ATGGCCGCTGCCCGCCCAGCGCGGGG		
		151		200
pSB936-4	(151)	GCCGGAGCTCCCGCTCCTGGGGCTGCTGCTGCTGCTGCTGCTGGGGGACC		
NM_005631.4 CDS	(27)	GCCGGAGCTCCCGCTCCTGGGGCTGCTGCTGCTGCTGCTGCTGGGGGACC		
		201		250
pSB936-4	(201)	CGGGCCGGGGGGCGGCCTCGAGCGGGAACGCGACCGGGCCTGGGCCTCGG		
NM_005631.4 CDS	(77)	CGGGCCGGGGGGCGGCCTCGAGCGGGAACGCGACCGGGCCTGGGCCTCGG		
		251		300
pSB936-4	(251)	AGCGCGGGCGGGAGCGCGAGGAGCGCGGCGGTGACTGGCCCTCCGCC		
NM_005631.4 CDS	(127)	AGCGCGGGCGGGAGCGCGAGGAGCGCGGCGGTGACTGGCCCTCCGCC		
		301		350
pSB936-4	(301)	GCCGCTGAGCCACTGCGGCCGGGCTGCCCCCTGCGAGCCGCTGCGCTACA		
NM_005631.4 CDS	(177)	GCCGCTGAGCCACTGCGGCCGGGCTGCCCCCTGCGAGCCGCTGCGCTACA		
		351		400
pSB936-4	(351)	ACGTGTGCCTGGGCTCGGTGCTGCCCTACGGGGCCACCTCCACACTGCTG		
NM_005631.4 CDS	(227)	ACGTGTGCCTGGGCTCGGTGCTGCCCTACGGGGCCACCTCCACACTGCTG		
		401		450
pSB936-4	(401)	GCCGGAGACTCGGACTCCCAGGAGGAAGCGCACGGCAAGCTCGTGCTCTG		
NM_005631.4 CDS	(277)	GCCGGAGACTCGGACTCCCAGGAGGAAGCGCACGGCAAGCTCGTGCTCTG		
		451		500
pSB936-4	(451)	GTCGGGCCTCCGGAATGCCCCCGCTGCTGGGCAGTGATCCAGCCCCTGC		
NM_005631.4 CDS	(327)	GTCGGGCCTCCGGAATGCCCCCGCTGCTGGGCAGTGATCCAGCCCCTGC		
		501		550
pSB936-4	(501)	TGTGTGCCGTATACATGCCCAAGTGTGAGAATGACCGGGTGGAGCTGCC		
NM_005631.4 CDS	(377)	TGTGTGCCGTATACATGCCCAAGTGTGAGAATGACCGGGTGGAGCTGCC		
		551		600
pSB936-4	(551)	AGCCGTACCCTCTGCCAGGCCACCCGAGGCCCTGTGCCATCGTGGAGAG		
NM_005631.4 CDS	(427)	AGCCGTACCCTCTGCCAGGCCACCCGAGGCCCTGTGCCATCGTGGAGAG		
		601		650
pSB936-4	(601)	GGAGCGGGGCTGGCCTGACTTCCTGCGCTGCACTCCTGACCGCTTCCCTG		

NM_005631.4 CDS	(477)	GGAGCGGGGCTGGCCTGACTTCTCGCGCTGCACTCCTGACCGCTTCCCTG	651	700
pSB936-4	(651)	AAGGCTGCACGAATGAGGTGCAGAACATCAAGTTCAACAGTTCAGGCCAG		
NM_005631.4 CDS	(527)	AAGGCTGCACGAATGAGGTGCAGAACATCAAGTTCAACAGTTCAGGCCAG	701	750
pSB936-4	(701)	TGCGAAGTGCCTTGGTTTCGGACAGACAACCCCAAGAGCTGGTACGAGGA		
NM_005631.4 CDS	(577)	TGCGAAGTGCCTTGGTTTCGGACAGACAACCCCAAGAGCTGGTACGAGGA	751	800
pSB936-4	(751)	CGTGGAGGGCTGCGGCATCCAGTGCCAGAACCCGCTCTTCACAGAGGCTG		
NM_005631.4 CDS	(627)	CGTGGAGGGCTGCGGCATCCAGTGCCAGAACCCGCTCTTCACAGAGGCTG	801	850
pSB936-4	(801)	AGCACCAGGACATGCACAGCTACATCGCGGCCTTCGGGGCCGTACAGGGC		
NM_005631.4 CDS	(677)	AGCACCAGGACATGCACAGCTACATCGCGGCCTTCGGGGCCGTACAGGGC	851	900
pSB936-4	(851)	CTCTGCACGCTCTTCACCCTGGCCACATTCGTGGCTGACTGGCGGAACTC		
NM_005631.4 CDS	(727)	CTCTGCACGCTCTTCACCCTGGCCACATTCGTGGCTGACTGGCGGAACTC	901	950
pSB936-4	(901)	GAATCGCTACCCTGCTGTTATTCTCTTCTACGTCAATGCGTGCTTCTTTG		
NM_005631.4 CDS	(777)	GAATCGCTACCCTGCTGTTATTCTCTTCTACGTCAATGCGTGCTTCTTTG	951	1000
pSB936-4	(951)	TGGGCAGCATTGGCTGGCTGGCCCAGTTCATGGATGGTGCCCGCCGAGAG		
NM_005631.4 CDS	(827)	TGGGCAGCATTGGCTGGCTGGCCCAGTTCATGGATGGTGCCCGCCGAGAG	1001	1050
pSB936-4	(1001)	ATCGTCTGCCGTGCAGATGGCACCATGAGGCTTGGGGAGCCCACCTCCAA		
NM_005631.4 CDS	(877)	ATCGTCTGCCGTGCAGATGGCACCATGAGGCTTGGGGAGCCCACCTCCAA	1051	1100
pSB936-4	(1051)	TGAGACTCTGTCTCGTCATCATCTTTGTCATCGTGTACTACGCCCTGA		
NM_005631.4 CDS	(927)	TGAGACTCTGTCTCGTCATCATCTTTGTCATCGTGTACTACGCCCTGA	1101	1150
pSB936-4	(1101)	TGGCTGGTGTGGTTTGGTTTGTGGTCCCTCACCTATGCCTGGCACACTTCC		
NM_005631.4 CDS	(977)	TGGCTGGTGTGGTTTGGTTTGTGGTCCCTCACCTATGCCTGGCACACTTCC	1151	1200
pSB936-4	(1151)	TTCAAAGCCCTGGGCACCACCTACCAGCCTCTCTCGGGCAAGACCTCCTA		
NM_005631.4 CDS	(1027)	TTCAAAGCCCTGGGCACCACCTACCAGCCTCTCTCGGGCAAGACCTCCTA	1201	1250
pSB936-4	(1201)	CTTCCACCTGCTCACCTGGTCACTCCCCTTTGTCTCACTGTGGCAATCC		
NM_005631.4 CDS	(1077)	CTTCCACCTGCTCACCTGGTCACTCCCCTTTGTCTCACTGTGGCAATCC	1251	1300
pSB936-4	(1251)	TTGCTGTGGCGCAGGTGGATGGGGACTCTGTGAGTGGCATTGTTTTGTG		
NM_005631.4 CDS	(1127)	TTGCTGTGGCGCAGGTGGATGGGGACTCTGTGAGTGGCATTGTTTTGTG	1301	1350
pSB936-4	(1301)	GGCTACAAGAACTACCGATACCGTGCGGGCTTCGTGCTGGCCCCAATCGG		
NM_005631.4 CDS	(1177)	GGCTACAAGAACTACCGATACCGTGCGGGCTTCGTGCTGGCCCCAATCGG	1351	1400

pSB936-4	(1351)	CCTGGTGCTCATCGTGGGAGGCTACTTCCTCATCCGAGGAGTCATGACTC
NM_005631.4 CDS	(1227)	CCTGGTGCTCATCGTGGGAGGCTACTTCCTCATCCGAGGAGTCATGACTC
		1401 1450
pSB936-4	(1401)	TGTTCTCCATCAAGAGCAACCACCCCGGGCTGCTGAGTGAGAAGGCTGCC
NM_005631.4 CDS	(1277)	TGTTCTCCATCAAGAGCAACCACCCCGGGCTGCTGAGTGAGAAGGCTGCC
		1451 1500
pSB936-4	(1451)	AGCAAGATCAACGAGACCATGCTGCGCCTGGGCATTTTGGCTTCCTGGC
NM_005631.4 CDS	(1327)	AGCAAGATCAACGAGACCATGCTGCGCCTGGGCATTTTGGCTTCCTGGC
		1501 1550
pSB936-4	(1501)	CTTTGGCTTTGTGCTCATTACCTTCAGCTGCCACTTCTACGACTTCTTCA
NM_005631.4 CDS	(1377)	CTTTGGCTTTGTGCTCATTACCTTCAGCTGCCACTTCTACGACTTCTTCA
		1551 1600
pSB936-4	(1551)	ACCAGGCTGAGTGGGAGCGCAGCTTCCGGGACTATGTGCTATGTCAGGCC
NM_005631.4 CDS	(1427)	ACCAGGCTGAGTGGGAGCGCAGCTTCCGGGACTATGTGCTATGTCAGGCC
		1601 1650
pSB936-4	(1601)	AATGTGACCATCGGGCTGCCCACCAAGCAGCCCATCCCTGACTGTGAGAT
NM_005631.4 CDS	(1477)	AATGTGACCATCGGGCTGCCCACCAAGCAGCCCATCCCTGACTGTGAGAT
		1651 1700
pSB936-4	(1651)	CAAGAATCGCCCGAGCCTTCTGGTGGAGAAGATCAACCTGTTTGCCATGT
NM_005631.4 CDS	(1527)	CAAGAATCGCCCGAGCCTTCTGGTGGAGAAGATCAACCTGTTTGCCATGT
		1701 1750
pSB936-4	(1701)	TTGGAACTGGCATCGCCATGAGCACCTGGTCTGGACCAAGGCCACGCTG
NM_005631.4 CDS	(1577)	TTGGAACTGGCATCGCCATGAGCACCTGGTCTGGACCAAGGCCACGCTG
		1751 1800
pSB936-4	(1751)	CTCATCTGGAGGCGTACCTGGTGCAGGTTGACTGGGCAGAGTGACGATGA
NM_005631.4 CDS	(1627)	CTCATCTGGAGGCGTACCTGGTGCAGGTTGACTGGGCAGAGTGACGATGA
		1801 1850
pSB936-4	(1801)	GCCAAAGCGGATCAAGAAGAGCAAGATGATTGCCAAGGCCTTCTCTAAGC
NM_005631.4 CDS	(1677)	GCCAAAGCGGATCAAGAAGAGCAAGATGATTGCCAAGGCCTTCTCTAAGC
		1851 1900
pSB936-4	(1851)	GGCACGAGCTCCTGCAGAACCAGGCCAGGAGCTGTCCTTCAGCATGCAC
NM_005631.4 CDS	(1727)	GGCACGAGCTCCTGCAGAACCAGGCCAGGAGCTGTCCTTCAGCATGCAC
		1901 1950
pSB936-4	(1901)	ACTGTGTCCCACGACGGGCCCGTGGCGGGCTTGGCCTTTGACCTCAATGA
NM_005631.4 CDS	(1777)	ACTGTGTCCCACGACGGGCCCGTGGCGGGCTTGGCCTTTGACCTCAATGA
		1951 2000
pSB936-4	(1951)	GCCCTCAGCTGATGTCTCCTCTGCCTGGGCCAGCATGTCACCAAGATGG
NM_005631.4 CDS	(1827)	GCCCTCAGCTGATGTCTCCTCTGCCTGGGCCAGCATGTCACCAAGATGG
		2001 2050
pSB936-4	(2001)	TGGCTCGGAGAGGAGCCATACTGCCCCAGGATATTTCTGTCACCCCTGTG
NM_005631.4 CDS	(1877)	TGGCTCGGAGAGGAGCCATACTGCCCCAGGATATTTCTGTCACCCCTGTG
		2051 2100
pSB936-4	(2051)	GCAACTCCAGTGCCCCCAGAGGAACAAGCCAACCTGTGGCTGGTTGAGGC
NM_005631.4 CDS	(1927)	GCAACTCCAGTGCCCCCAGAGGAACAAGCCAACCTGTGGCTGGTTGAGGC

			2101		2150
pSB936-4	(2101)		AGAGATCTCCCCAGAGCTGCAGAAGCGCCTGGGCCGGAAGAAGAGAGGA		
NM_005631.4	CDS	(1977)	AGAGATCTCCCCAGAGCTGCAGAAGCGCCTGGGCCGGAAGAAGAGAGGA		
			2151		2200
pSB936-4	(2151)		GGAAGAGGAAGAAGGAGGTGTGCCCCGCTGGCGCCGCCCCCTGAGCTTCAC		
NM_005631.4	CDS	(2027)	GGAAGAGGAAGAAGGAGGTGTGCCCCGCTGGCGCCGCCCCCTGAGCTTCAC		
			2201		2250
pSB936-4	(2201)		CCCCCTGCCCTGCCCCAGTACCATTCCCTCGACTGCCTCAGCTGCCCCG		
NM_005631.4	CDS	(2077)	CCCCCTGCCCTGCCCCAGTACCATTCCCTCGACTGCCTCAGCTGCCCCG		
			2251		2300
pSB936-4	(2251)		GCAGAAATGCCTGGTGGCTGCAGGTGCCTGGGGAGCTGGGGACTCTTGCC		
NM_005631.4	CDS	(2127)	GCAGAAATGCCTGGTGGCTGCAGGTGCCTGGGGAGCTGGGGACTCTTGCC		
			2301		2350
pSB936-4	(2301)		GACAGGGAGCGTGGACCCTGGTCTCCAACCCATTCTGCCAGAGCCCAGT		
NM_005631.4	CDS	(2177)	GACAGGGAGCGTGGACCCTGGTCTCCAACCCATTCTGCCAGAGCCCAGT		
			2351		2400
pSB936-4	(2351)		CCCCCTCAGGATCCATTTCTGCCAGTGCACCGGCCCCCGTGGCATGGGC		
NM_005631.4	CDS	(2227)	CCCCCTCAGGATCCATTTCTGCCAGTGCACCGGCCCCCGTGGCATGGGC		
			2401		2450
pSB936-4	(2401)		TCATGGCCGCCGACAGGGCCTGGGGCCTATTCACTCCCGCACCAACCTGA		
NM_005631.4	CDS	(2277)	TCATGGCCGCCGACAGGGCCTGGGGCCTATTCACTCCCGCACCAACCTGA		
			2451		2500
pSB936-4	(2451)		TGGACACAGAACTCATGGATGCAGACTCGGACTTCACGCGTACGCGGCCG		
NM_005631.4	CDS	(2327)	TGGACACAGAACTCATGGATGCAGACTCGGACTTCACGCGTACGCGGCCG		
			2501		2550
pSB936-4	(2501)		CTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAATGATATCCT		
NM_005631.4	CDS	(2365)	-----		
			2551		2600
pSB936-4	(2551)		GGATTACAAGGATGACGACGATAAGGTTTAAACGGCCGCGCGGTCATA		
NM_005631.4	CDS	(2365)	-----		
			2601		2650
pSB936-4	(2601)		GCTGTTTCTGAAACAGATCCCGGGTGGCATCCCTGTGACCCCTCCCAGT		
NM_005631.4	CDS	(2365)	-----		
			2651		2700
pSB936-4	(2651)		GCCTCTCCTGGCCCTGGAAGTTGCCACTCCAGTGCCCACCAGCCTGTCCCT		
NM_005631.4	CDS	(2365)	-----		
				2701	2716
		pSB936-4	(2701)	AATAAATAGTCAACGT	
		NM_005631.4	CDS	(2365)	-----

Smo H231R:

		829		878
PSE2260	(829)	CTAGAGAACCCACTGCTTACTGGCTTATCGAAATTAATACGACTCACTAT		
			PSE2260 seq splicing	(1)
		CTAGAGAACCCACTGCTTACTGGCTTATCGAAATTAATACGACTCACTAT		
		879		928
PSE2260	(879)	AGGGAGACCCAAGCTGGCTAGCGTTTAAACTTAAGCTTGGTACCGAGCTC		
			PSE2260 seq splicing	(51)
		AGGGAGACCCAAGCTGGCTAGCGTTTAAACTTAAGCTTGGTACCGAGCTC		
		929		978
PSE2260	(929)	GGATCCGCCACG	ATGGCCGCTGCCCGCCAGCGCGGGGGCCGGAGCTCCC	
			PSE2260 seq splicing	(101)
		GGATCCGCCACG	ATGGCCGCTGCCCGCCAGCGCGGGGGCCGGAGCTCCC	
		979		1028
PSE2260	(979)	GCTCCTGGGGCTGCTGCTGCTGCTGCTGCTGGGGGACCCGGGCCGGGGG		
			PSE2260 seq splicing	(151)
		GCTCCTGGGGCTGCTGCTGCTGCTGCTGCTGGGGGACCCGGGCCGGGGG		
		1029		1078
PSE2260	(1029)	CGGCCTCGAGCGGGAACGCGACCGGGCCTGGGCCTCGGAGCGCGGGCGGG		
			PSE2260 seq splicing	(201)
		CGGCCTCGAGCGGGAACGCGACCGGGCCTGGGCCTCGGAGCGCGGGCGGG		
		1079		1128
PSE2260	(1079)	AGCGCGAGGAGGAGCGCGGGCGGTGACTGGCCCTCCGCCCGCGCTGAGCCA		
			PSE2260 seq splicing	(251)
		AGCGCGAGGAGGAGCGCGGGCGGTGACTGGCCCTCCGCCCGCGCTGAGCCA		
		1129		1178
PSE2260	(1129)	CTGCGGCCGGGCTGCCCCCTGCGAGCCGCTGCGCTACAACGTGTGCCTGG		
			PSE2260 seq splicing	(301)
		CTGCGGCCGGGCTGCCCCCTGCGAGCCGCTGCGCTACAACGTGTGCCTGG		
		1179		1228
PSE2260	(1179)	GCTCGGTGCTGCCCTACGGGGCCACCTCCACACTGCTGGCCGGAGACTCG		
			PSE2260 seq splicing	(351)
		GCTCGGTGCTGCCCTACGGGGCCACCTCCACACTGCTGGCCGGAGACTCG		
		1229		1278
PSE2260	(1229)	GACTCCCAGGAGGAAGCGCACGGCAAGCTCGTGCTCTGGTCGGGCCTCCG		
			PSE2260 seq splicing	(401)
		GACTCCCAGGAGGAAGCGCACGGCAAGCTCGTGCTCTGGTCGGGCCTCCG		
		1279		1328
PSE2260	(1279)	GAATGCCCCCGCTGCTGGGCAGTGATCCAGCCCCTGCTGTGTGCCGTAT		
			PSE2260 seq splicing	(451)
		GAATGCCCCCGCTGCTGGGCAGTGATCCAGCCCCTGCTGTGTGCCGTAT		
		1329		1378
PSE2260	(1329)	ACATGCCCAAGTGTGAGAATGACCGGGTGGAGCTGCCAGCCGTACCCTC		

PSE2260 seq splicing (501)

ACATGCCCAAGTGTGAGAATGACCGGGTGGAGCTGCCAGCCGTACCCTC
1379 1428

PSE2260 (1379) TGCCAGGCCACCCGAGGCCCTGTGCCATCGTGGAGAGGGAGCGGGGCTG
PSE2260 seq splicing (551)

TGCCAGGCCACCCGAGGCCCTGTGCCATCGTGGAGAGGGAGCGGGGCTG
1429 1478

PSE2260 (1429) GCCTGACTTCCTGCGCTGCACTCCTGACCGCTTCCCTGAAGGCTGCACGA
PSE2260 seq splicing (601)

GCCTGACTTCCTGCGCTGCACTCCTGACCGCTTCCCTGAAGGCTGCACGA
1479 1528

PSE2260 (1479) ATGAGGTGCAGAACATCAAGTTCAACAGTTCAGGCCAGTGCGAAGTGCCC
PSE2260 seq splicing (651)

ATGAGGTGCAGAACATCAAGTTCAACAGTTCAGGCCAGTGCGAAGTGCCC
1529 1578

PSE2260 (1529) TTGGTTCGGACAGACAACCCCAAGAGCTGGTACGAGGACGTGGAGGGCTG
PSE2260 seq splicing (701)

TTGGTTCGGACAGACAACCCCAAGAGCTGGTACGAGGACGTGGAGGGCTG
1579 1628

PSE2260 (1579) CGGCATCCAGTGCCAGAACCCGCTCTTCACAGAGGCTGAGCACCAGGACA
PSE2260 seq splicing (751)

CGGCATCCAGTGCCAGAACCCGCTCTTCACAGAGGCTGAGCACCAGGACA
1629 1678

PSE2260 (1629) TGCGCAGCTACATCGCGGCCTTCGGGGCCGTACGGGCCTCTGCACGCTC
PSE2260 seq splicing (801)

TGCGCAGCTACATCGCGGCCTTCGGGGCCGTACGGGCCTCTGCACGCTC
1679 1728

PSE2260 (1679) TTCACCCTGGCCACATTCGTGGCTGACTGGCGGAACTCGAATCGCTACCC
PSE2260 seq splicing (851)

TTCACCCTGGCCACATTCGTGGCTGACTGGCGGAACTCGAATCGCTACCC
1729 1778

PSE2260 (1729) TGCTGTTATTCTTCTTCTACGTCAATGCGTGCTTCTTTGTGGGCAGCATTG
PSE2260 seq splicing (901)

TGCTGTTATTCTTCTTCTACGTCAATGCGTGCTTCTTTGTGGGCAGCATTG
1779 1828

PSE2260 (1779) GCTGGCTGGCCCAGTTCATGGATGGTGCCCGCCGAGAGATCGTCTGCCGT
PSE2260 seq splicing (951)

GCTGGCTGGCCCAGTTCATGGATGGTGCCCGCCGAGAGATCGTCTGCCGT
1829 1878

PSE2260 (1829) GCAGATGGCACCATGAGGCTTGGGGAGCCACCTCCAATGAGACTCTGTC
PSE2260 seq splicing (1001)

GCAGATGGCACCATGAGGCTTGGGGAGCCACCTCCAATGAGACTCTGTC
1879 1928

PSE2260 (1879) CTGCGTCATCATCTTTGTCATCGTGTACTACGCCCTGATGGCTGGTGTGG

PSE2260 seq splicing (1051)
CTGCGTCATCATCTTTGTCATCGTGTACTACGCCCTGATGGCTGGTGTGG
1929 1978
PSE2260 (1929) FTTGGTTTGTGGTCCCTCACCTATGCCTGGCACACTTCCTTCAAAGCCCTG
PSE2260 seq splicing (1101)
FTTGGTTTGTGGTCCCTCACCTATGCCTGGCACACTTCCTTCAAAGCCCTG
1979 2028
PSE2260 (1979) GGCACCACCTACCAGCCTCTCTCGGGCAAGACCTCCTACTTCCACCTGCT
PSE2260 seq splicing (1151)
GGCACCACCTACCAGCCTCTCTCGGGCAAGACCTCCTACTTCCACCTGCT
2029 2078
PSE2260 (2029) CACCTGGTCACTCCCCTTTGTCCTCACTGTGGCAATCCTTGCTGTGGCGC
PSE2260 seq splicing (1201)
CACCTGGTCACTCCCCTTTGTCCTCACTGTGGCAATCCTTGCTGTGGCGC
2079 2128
PSE2260 (2079) AGGTGGATGGGGACTCTGTGAGTGGGATTGTTTGTGGGCTACAAGAAC
PSE2260 seq splicing (1251)
AGGTGGATGGGGACTCTGTGAGTGGGATTGTTTGTGGGCTACAAGAAC
2129 2178
PSE2260 (2129) TACCGATACCGTGCGGGCTTCGTGCTGGCCCAATCGGCCTGGTGCTCAT
PSE2260 seq splicing (1301)
TACCGATACCGTGCGGGCTTCGTGCTGGCCCAATCGGCCTGGTGCTCAT
2179 2228
PSE2260 (2179) CGTGGGAGGCTACTTCCTCATCCGAGGAGTCATGACTCTGTTCTCCATCA
PSE2260 seq splicing (1351)
CGTGGGAGGCTACTTCCTCATCCGAGGAGTCATGACTCTGTTCTCCATCA
2229 2278
PSE2260 (2229) AGAGCAACCACCCCGGGCTGCTGAGTGAGAAGGCTGCCAGCAAGATCAAC
PSE2260 seq splicing (1401)
AGAGCAACCACCCCGGGCTGCTGAGTGAGAAGGCTGCCAGCAAGATCAAC
2279 2328
PSE2260 (2279) GAGACCATGCTGCGCCTGGGCATTTTTGGCTTCCTGGCCTTTGGCTTTGT
PSE2260 seq splicing (1451)
GAGACCATGCTGCGCCTGGGCATTTTTGGCTTCCTGGCCTTTGGCTTTGT
2329 2378
PSE2260 (2329) GCTCATTACCTTCAGCTGCCACTTCTACGACTTCTTCAACCAGGCTGAGT
PSE2260 seq splicing (1501)
GCTCATTACCTTCAGCTGCCACTTCTACGACTTCTTCAACCAGGCTGAGT
2379 2428
PSE2260 (2379) GGGAGCGCAGCTTCCGGGACTATGTGCTATGTCAGGCCAATGTGACCATC
PSE2260 seq splicing (1551)
GGGAGCGCAGCTTCCGGGACTATGTGCTATGTCAGGCCAATGTGACCATC
2429 2478
PSE2260 (2429) GGGCTGCCACCAAGCAGCCATCCCTGACTGTGAGATCAAGAATCGCCC

PSE2260 seq splicing (1601)
GGGCTGCCACCAAGCAGCCATCCCTGACTGTGAGATCAAGAATCGCCC
2479 2528
PSE2260 (2479) GAGCCTTCTGGTGGAGAAGATCAACCTGTTTGCCATGTTTGGAAGTGGCA
PSE2260 seq splicing (1651)
GAGCCTTCTGGTGGAGAAGATCAACCTGTTTGCCATGTTTGGAAGTGGCA
2529 2578
PSE2260 (2529) TCGCCATGAGCACCTGGGTCTGGACCAAGGCCACGCTGCTCATCTGGAGG
PSE2260 seq splicing (1701)
TCGCCATGAGCACCTGGGTCTGGACCAAGGCCACGCTGCTCATCTGGAGG
2579 2628
PSE2260 (2579) CGTACCTGGTGCAGGTTGACTGGGCAGAGTGACGATGAGCCAAAGCGGAT
PSE2260 seq splicing (1751)
CGTACCTGGTGCAGGTTGACTGGGCAGAGTGACGATGAGCCAAAGCGGAT
2629 2678
PSE2260 (2629) CAAGAAGAGCAAGATGATTGCCAAGGCCTTCTCTAAGCGGCACGAGCTCC
PSE2260 seq splicing (1801)
CAAGAAGAGCAAGATGATTGCCAAGGCCTTCTCTAAGCGGCACGAGCTCC
2679 2728
PSE2260 (2679) TGCAGAACCAGGCCAGGAGCTGTCC TTCAGCATGCACACTGTGTCCCAC
PSE2260 seq splicing (1851)
TGCAGAACCAGGCCAGGAGCTGTCC TTCAGCATGCACACTGTGTCCCAC
2729 2778
PSE2260 (2729) GACGGGCCCGTGGCGGGCTTGGCCTTTGACCTCAATGAGCCCTCAGCTGA
PSE2260 seq splicing (1901)
GACGGGCCCGTGGCGGGCTTGGCCTTTGACCTCAATGAGCCCTCAGCTGA
2779 2828
PSE2260 (2779) TGTCTCCTCTGCCTGGGCCAGCATGTCACCAAGATGGTGGCTCGGAGAG
PSE2260 seq splicing (1951)
TGTCTCCTCTGCCTGGGCCAGCATGTCACCAAGATGGTGGCTCGGAGAG
2829 2878
PSE2260 (2829) GAGCCATACTGCCCCAGGATATTTCTGTCACCCCTGTGGCAACTCCAGTG
PSE2260 seq splicing (2001)
GAGCCATACTGCCCCAGGATATTTCTGTCACCCCTGTGGCAACTCCAGTG
2879 2928
PSE2260 (2879) CCCCCAGAGGAACAAGCCAACCTGTGGCTGGTTGAGGCAGAGATCTCCCC
PSE2260 seq splicing (2051)
CCCCCAGAGGAACAAGCCAACCTGTGGCTGGTTGAGGCAGAGATCTCCCC
2929 2978
PSE2260 (2929) AGAGCTGCAGAAGCGCCTGGGCCGGAAGAAGAAGAGGAGGAAGAGGAAGA
PSE2260 seq splicing (2101)
AGAGCTGCAGAAGCGCCTGGGCCGGAAGAAGAAGAGGAGGAAGAGGAAGA
2979 3028
PSE2260 (2979) AGGAGGTGTGCCGCTGGCGCCGCCCTGAGCTTACCCCCCTGCCCT

PSE2260 seq splicing (2151)

AGGAGGTGTGCCCGCTGGCGCCGCCCCCTGAGCTTCACCCCCCTGCCCT
3029 3078

PSE2260 (3029) GCCCCAGTACCATTCTCGACTGCCTCAGCTGCCCGGCAGAAATGCCT
PSE2260 seq splicing (2201)

GCCCCAGTACCATTCTCGACTGCCTCAGCTGCCCGGCAGAAATGCCT
3079 3128

PSE2260 (3079) GGTGGCTGCAGGTGCCTGGGGAGCTGGGGACTCTTGCCGACAGGGAGCGT
PSE2260 seq splicing (2251)

GGTGGCTGCAGGTGCCTGGGGAGCTGGGGACTCTTGCCGACAGGGAGCGT
3129 3178

PSE2260 (3129) GGACCCTGGTCTCCAACCCATTCTGCCAGAGCCCAGTCCCCCTCAGGAT
PSE2260 seq splicing (2301)

GGACCCTGGTCTCCAACCCATTCTGCCAGAGCCCAGTCCCCCTCAGGAT
3179 3228

PSE2260 (3179) CCATTTCTGCCAGTGCACCGGCCCGCGTGGCATGGGCTCATGGCCGCC
PSE2260 seq splicing (2351)

CCATTTCTGCCAGTGCACCGGCCCGCGTGGCATGGGCTCATGGCCGCC
3229 3278

PSE2260 (3229) ACAGGGCCTGGGGCCTATTCACTCCCGCACCAACCTGATGGACACAGAAC
PSE2260 seq splicing (2401)

ACAGGGCCTGGGGCCTATTCACTCCCGCACCAACCTGATGGACACAGAAC
3279 3328

PSE2260 (3279) TCATGGATGCAGACTCGGACTTCGAACAAAACTCATCTCAGAAGAGGAT
PSE2260 seq splicing (2451)

TCATGGATGCAGACTCGGACTTCGAACAAAACTCATCTCAGAAGAGGAT
3329 3378

PSE2260 (3329) CTGGACTACAAGGATGACGATGACAAGGATTACAAAGACGACGATGATAA
PSE2260 seq splicing (2501)

CTGGACTACAAGGATGACGATGACAAGGATTACAAAGACGACGATGATAA
3379 3428

PSE2260 (3379) GGACTATAAGGATGATGACGACAAATAATCTAGAGGGCCCGTTTAAACCC
PSE2260 seq splicing (2551)

GGACTATAAGGATGATGACGACAAATAATCTAGAGGGCCCGTTTAAACCC
3429 3475

PSE2260 (3429) GCTGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTT
PSE2260 seq splicing (2601)

GCTGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTT

Smo W281C:

		829		878
PSE2261	(829)	CTAGAGAACCCACTGCTTACTGGCTTATCGAAATTAATACGACTCACTAT		
			PSE2261 seq splicing	(1)
		CTAGAGAACCCACTGCTTACTGGCTTATCGAAATTAATACGACTCACTAT		
		879		928
PSE2261	(879)	AGGGAGACCCAAGCTGGCTAGCGTTTAAACTTAAGCTTGGTACCGAGCTC		
			PSE2261 seq splicing	(51)
		AGGGAGACCCAAGCTGGCTAGCGTTTAAACTTAAGCTTGGTACCGAGCTC		
		929		978
PSE2261	(929)	GGATCCGCCACG	ATGGCCGCTGCCCGCCAGCGCGGGGGCCGGAGCTCCC	
			PSE2261 seq splicing	(101)
		GGATCCGCCACG	ATGGCCGCTGCCCGCCAGCGCGGGGGCCGGAGCTCCC	
		979		1028
PSE2261	(979)	GCTCCTGGGGCTGCTGCTGCTGCTGCTGCTGGGGGACCCGGGCCGGGGG		
			PSE2261 seq splicing	(151)
		GCTCCTGGGGCTGCTGCTGCTGCTGCTGCTGGGGGACCCGGGCCGGGGG		
		1029		1078
PSE2261	(1029)	CGGCCTCGAGCGGGAACGCGACCGGGCCTGGGCCTCGGAGCGCGGGCGGG		
			PSE2261 seq splicing	(201)
		CGGCCTCGAGCGGGAACGCGACCGGGCCTGGGCCTCGGAGCGCGGGCGGG		
		1079		1128
PSE2261	(1079)	AGCGCGAGGAGGAGCGCGGGCGGTGACTGGCCCTCCGCCGCCGCTGAGCCA		
			PSE2261 seq splicing	(251)
		AGCGCGAGGAGGAGCGCGGGCGGTGACTGGCCCTCCGCCGCCGCTGAGCCA		
		1129		1178
PSE2261	(1129)	CTGCGGCCGGGCTGCCCCCTGCGAGCCGCTGCGCTACAACGTGTGCCTGG		
			PSE2261 seq splicing	(301)
		CTGCGGCCGGGCTGCCCCCTGCGAGCCGCTGCGCTACAACGTGTGCCTGG		
		1179		1228
PSE2261	(1179)	GCTCGGTGCTGCCCTACGGGGCCACCTCCACACTGCTGGCCGGAGACTCG		
			PSE2261 seq splicing	(351)
		GCTCGGTGCTGCCCTACGGGGCCACCTCCACACTGCTGGCCGGAGACTCG		
		1229		1278
PSE2261	(1229)	GACTCCCAGGAGGAAGCGCACGGCAAGCTCGTGCTCTGGTCGGGCCTCCG		
			PSE2261 seq splicing	(401)
		GACTCCCAGGAGGAAGCGCACGGCAAGCTCGTGCTCTGGTCGGGCCTCCG		
		1279		1328
PSE2261	(1279)	GAATGCCCCCGCTGCTGGGCAGTGATCCAGCCCCTGCTGTGTGCCGTAT		
			PSE2261 seq splicing	(451)
		GAATGCCCCCGCTGCTGGGCAGTGATCCAGCCCCTGCTGTGTGCCGTAT		
		1329		1378
PSE2261	(1329)	ACATGCCCAAGTGTGAGAATGACCGGGTGGAGCTGCCAGCCGTACCCTC		

PSE2261 seq splicing (501)

ACATGCCCAAGTGTGAGAATGACCGGGTGGAGCTGCCAGCCGTACCCTC
1379 1428

PSE2261 (1379) TGCCAGGCCACCCGAGGCCCTGTGCCATCGTGGAGAGGGAGCGGGGCTG
PSE2261 seq splicing (551)

TGCCAGGCCACCCGAGGCCCTGTGCCATCGTGGAGAGGGAGCGGGGCTG
1429 1478

PSE2261 (1429) GCCTGACTTCCTGCGCTGCACTCCTGACCGCTTCCCTGAAGGCTGCACGA
PSE2261 seq splicing (601)

GCCTGACTTCCTGCGCTGCACTCCTGACCGCTTCCCTGAAGGCTGCACGA
1479 1528

PSE2261 (1479) ATGAGGTGCAGAACATCAAGTTCAACAGTTCAGGCCAGTGCGAAGTGCCC
PSE2261 seq splicing (651)

ATGAGGTGCAGAACATCAAGTTCAACAGTTCAGGCCAGTGCGAAGTGCCC
1529 1578

PSE2261 (1529) TTGGTTCGGACAGACAACCCCAAGAGCTGGTACGAGGACGTGGAGGGCTG
PSE2261 seq splicing (701)

TTGGTTCGGACAGACAACCCCAAGAGCTGGTACGAGGACGTGGAGGGCTG
1579 1628

PSE2261 (1579) CGGCATCCAGTGCCAGAACCCGCTCTTCACAGAGGCTGAGCACCAGGACA
PSE2261 seq splicing (751)

CGGCATCCAGTGCCAGAACCCGCTCTTCACAGAGGCTGAGCACCAGGACA
1629 1678

PSE2261 (1629) TGCACAGCTACATCGCGGCCTTCGGGGCCGTACGGGCCTCTGCACGCTC
PSE2261 seq splicing (801)

TGCACAGCTACATCGCGGCCTTCGGGGCCGTACGGGCCTCTGCACGCTC
1679 1728

PSE2261 (1679) TTCACCCTGGCCACATTCGTGGCTGACTGGCGGAACTCGAATCGCTACCC
PSE2261 seq splicing (851)

TTCACCCTGGCCACATTCGTGGCTGACTGGCGGAACTCGAATCGCTACCC
1729 1778

PSE2261 (1729) TGCTGTTATTCTCTTCTACGTCAATGCGTGCTTCTTTGTGGGCAGCATTG
PSE2261 seq splicing (901)

TGCTGTTATTCTCTTCTACGTCAATGCGTGCTTCTTTGTGGGCAGCATTG
1779 1828

PSE2261 (1779) GCTGCTGGCCAGTTCATGGATGGTGCCCGCCGAGAGATCGTCTGCCGT
PSE2261 seq splicing (951)

GCTGCTGGCCAGTTCATGGATGGTGCCCGCCGAGAGATCGTCTGCCGT
1829 1878

PSE2261 (1829) GCAGATGGCACCATGAGGCTTGGGGAGCCACCTCCAATGAGACTCTGTC
PSE2261 seq splicing (1001)

GCAGATGGCACCATGAGGCTTGGGGAGCCACCTCCAATGAGACTCTGTC
1879 1928

PSE2261 (1879) CTGCGTCATCATCTTTGTATCGTGTACTACGCCCTGATGGCTGGTGTGG

PSE2261 seq splicing (1051)

CTGCGTCATCATCTTTGTCATCGTGTACTACGCCCTGATGGCTGGTGTGG
1929 1978

PSE2261 (1929) FTTGGTTTGTGGTCCCTCACCTATGCCTGGCACACTTCCTTCAAAGCCCTG
PSE2261 seq splicing (1101)

FTTGGTTTGTGGTCCCTCACCTATGCCTGGCACACTTCCTTCAAAGCCCTG
1979 2028

PSE2261 (1979) GGCACCACCTACCAGCCTCTCTCGGGCAAGACCTCCTACTTCCACCTGCT
PSE2261 seq splicing (1151)

GGCACCACCTACCAGCCTCTCTCGGGCAAGACCTCCTACTTCCACCTGCT
2029 2078

PSE2261 (2029) CACCTGGTCACTCCCCTTTGTCCTCACTGTGGCAATCCTTGCTGTGGCGC
PSE2261 seq splicing (1201)

CACCTGGTCACTCCCCTTTGTCCTCACTGTGGCAATCCTTGCTGTGGCGC
2079 2128

PSE2261 (2079) AGGTGGATGGGGACTCTGTGAGTGGGATTGTTTGTGGGCTACAAGAAC
PSE2261 seq splicing (1251)

AGGTGGATGGGGACTCTGTGAGTGGGATTGTTTGTGGGCTACAAGAAC
2129 2178

PSE2261 (2129) TACCGATACCGTGCGGGCTTCGTGCTGGCCCAATCGGCCTGGTGCTCAT
PSE2261 seq splicing (1301)

TACCGATACCGTGCGGGCTTCGTGCTGGCCCAATCGGCCTGGTGCTCAT
2179 2228

PSE2261 (2179) CGTGGGAGGCTACTTCCTCATCCGAGGAGTCATGACTCTGTTCTCCATCA
PSE2261 seq splicing (1351)

CGTGGGAGGCTACTTCCTCATCCGAGGAGTCATGACTCTGTTCTCCATCA
2229 2278

PSE2261 (2229) AGAGCAACCACCCCGGGCTGCTGAGTGAGAAGGCTGCCAGCAAGATCAAC
PSE2261 seq splicing (1401)

AGAGCAACCACCCCGGGCTGCTGAGTGAGAAGGCTGCCAGCAAGATCAAC
2279 2328

PSE2261 (2279) GAGACCATGCTGCGCCTGGGCATTTTTGGCTTCCTGGCCTTTGGCTTTGT
PSE2261 seq splicing (1451)

GAGACCATGCTGCGCCTGGGCATTTTTGGCTTCCTGGCCTTTGGCTTTGT
2329 2378

PSE2261 (2329) GCTCATTACCTTCAGCTGCCACTTCTACGACTTCTTCAACCAGGCTGAGT
PSE2261 seq splicing (1501)

GCTCATTACCTTCAGCTGCCACTTCTACGACTTCTTCAACCAGGCTGAGT
2379 2428

PSE2261 (2379) GGGAGCGCAGCTTCCGGGACTATGTGCTATGTCAGGCCAATGTGACCATC
PSE2261 seq splicing (1551)

GGGAGCGCAGCTTCCGGGACTATGTGCTATGTCAGGCCAATGTGACCATC
2429 2478

PSE2261 (2429) GGGCTGCCACCAAGCAGCCATCCCTGACTGTGAGATCAAGAATCGCCC

PSE2261 seq splicing (1601)

GGGCTGCCACCAAGCAGCCATCCCTGACTGTGAGATCAAGAATCGCCC
2479 2528

PSE2261 (2479) GAGCCTTCTGGTGGAGAAGATCAACCTGTTTGCCATGTTTGGAAGTGGCA
PSE2261 seq splicing (1651)

GAGCCTTCTGGTGGAGAAGATCAACCTGTTTGCCATGTTTGGAAGTGGCA
2529 2578

PSE2261 (2529) TCGCCATGAGCACCTGGGTCTGGACCAAGGCCACGCTGCTCATCTGGAGG
PSE2261 seq splicing (1701)

TCGCCATGAGCACCTGGGTCTGGACCAAGGCCACGCTGCTCATCTGGAGG
2579 2628

PSE2261 (2579) CGTACCTGGTGCAGGTTGACTGGGCAGAGTGACGATGAGCCAAAGCGGAT
PSE2261 seq splicing (1751)

CGTACCTGGTGCAGGTTGACTGGGCAGAGTGACGATGAGCCAAAGCGGAT
2629 2678

PSE2261 (2629) CAAGAAGAGCAAGATGATTGCCAAGGCCTTCTCTAAGCGGCACGAGCTCC
PSE2261 seq splicing (1801)

CAAGAAGAGCAAGATGATTGCCAAGGCCTTCTCTAAGCGGCACGAGCTCC
2679 2728

PSE2261 (2679) TGCAGAACCAGGCCAGGAGCTGTCC TTCAGCATGCACACTGTGTCCCAC
PSE2261 seq splicing (1851)

TGCAGAACCAGGCCAGGAGCTGTCC TTCAGCATGCACACTGTGTCCCAC
2729 2778

PSE2261 (2729) GACGGGCCCGTGGCGGGCTTGGCCTTTGACCTCAATGAGCCCTCAGCTGA
PSE2261 seq splicing (1901)

GACGGGCCCGTGGCGGGCTTGGCCTTTGACCTCAATGAGCCCTCAGCTGA
2779 2828

PSE2261 (2779) TGTCTCCTCTGCCTGGGCCAGCATGTCACCAAGATGGTGGCTCGGAGAG
PSE2261 seq splicing (1951)

TGTCTCCTCTGCCTGGGCCAGCATGTCACCAAGATGGTGGCTCGGAGAG
2829 2878

PSE2261 (2829) GAGCCATACTGCCCCAGGATATTTCTGTCACCCCTGTGGCAACTCCAGTG
PSE2261 seq splicing (2001)

GAGCCATACTGCCCCAGGATATTTCTGTCACCCCTGTGGCAACTCCAGTG
2879 2928

PSE2261 (2879) CCCCCAGAGGAACAAGCCAACCTGTGGCTGGTTGAGGCAGAGATCTCCCC
PSE2261 seq splicing (2051)

CCCCCAGAGGAACAAGCCAACCTGTGGCTGGTTGAGGCAGAGATCTCCCC
2929 2978

PSE2261 (2929) AGAGCTGCAGAAGCGCCTGGGCCGGAAGAAGAAGAGGAGGAAGAGGAAGA
PSE2261 seq splicing (2101)

AGAGCTGCAGAAGCGCCTGGGCCGGAAGAAGAAGAGGAGGAAGAGGAAGA
2979 3028

PSE2261 (2979) AGGAGGTGTGCCGCTGGCGCCGCCCTGAGCTTCACCCCTGCCCCT

PSE2261 seq splicing (2151)

AGGAGGTGTGCCCGCTGGCGCCGCCCCCTGAGCTTCACCCCCCTGCCCT
3029 3078

PSE2261 (3029) GCCCCCAGTACCATTCTCGACTGCCTCAGCTGCCCCGGCAGAAATGCCT
PSE2261 seq splicing (2201)

GCCCCAGTACCATTCTCGACTGCCTCAGCTGCCCCGGCAGAAATGCCT
3079 3128

PSE2261 (3079) GGTGGCTGCAGGTGCCTGGGGAGCTGGGGACTCTTGCCGACAGGGAGCGT
PSE2261 seq splicing (2251)

GGTGGCTGCAGGTGCCTGGGGAGCTGGGGACTCTTGCCGACAGGGAGCGT
3129 3178

PSE2261 (3129) GGACCCTGGTCTCCAACCCATTCTGCCAGAGCCCAGTCCCCCTCAGGAT
PSE2261 seq splicing (2301)

GGACCCTGGTCTCCAACCCATTCTGCCAGAGCCCAGTCCCCCTCAGGAT
3179 3228

PSE2261 (3179) CCATTTCTGCCAGTGCACCGGCCCGTGGCATGGGCTCATGGCCGCC
PSE2261 seq splicing (2351)

CCATTTCTGCCAGTGCACCGGCCCGTGGCATGGGCTCATGGCCGCC
3229 3278

PSE2261 (3229) ACAGGGCCTGGGGCCTATTCACTCCCGCACCAACCTGATGGACACAGAAC
PSE2261 seq splicing (2401)

ACAGGGCCTGGGGCCTATTCACTCCCGCACCAACCTGATGGACACAGAAC
3279 3328

PSE2261 (3279) TCATGGATGCAGACTCGGACTTCGAACAAAACCTCATCTCAGAAGAGGAT
PSE2261 seq splicing (2451)

TCATGGATGCAGACTCGGACTTCGAACAAAACCTCATCTCAGAAGAGGAT
3329 3378

PSE2261 (3329) CTGGACTACAAGGATGACGATGACAAGGATTACAAAGACGACGATGATAA
PSE2261 seq splicing (2501)

CTGGACTACAAGGATGACGATGACAAGGATTACAAAGACGACGATGATAA
3379 3428

PSE2261 (3379) GGACTATAAGGATGATGACGACAAATAATCTAGAGGGCCCGTTTAAACCC
PSE2261 seq splicing (2551)

GGACTATAAGGATGATGACGACAAATAATCTAGAGGGCCCGTTTAAACCC
3429 3475

PSE2261 (3429) GCTGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTT
PSE2261 seq splicing (2601)

GCTGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTT

Smo L412F:

829 878
PSE2262 (829) CTAGAGAACCCACTGCTTACTGGCTTATCGAAATTAATACGACTCACTAT
PSE2262 seq splicing (1)
CTAGAGAACCCACTGCTTACTGGCTTATCGAAATTAATACGACTCACTAT

879 928
PSE2262 (879) AGGGAGACCCAAGCTGGCTAGCGTTTAAACTTAAGCTTGGTACCGAGCTC
PSE2262 seq splicing (51)
AGGGAGACCCAAGCTGGCTAGCGTTTAAACTTAAGCTTGGTACCGAGCTC

929 978
PSE2262 (929) SGATCCGCCACCATGGCCGCTGCCCGCCAGCGCGGGGGCCGGAGCTCCC
PSE2262 seq splicing (101)
SGATCCGCCACCATGGCCGCTGCCCGCCAGCGCGGGGGCCGGAGCTCCC

979 1028
PSE2262 (979) GCTCCTGGGGCTGCTGCTGCTGCTGCTGCTGGGGGACCCGGGCCGGGGG
PSE2262 seq splicing (151)
GCTCCTGGGGCTGCTGCTGCTGCTGCTGCTGGGGGACCCGGGCCGGGGG

1029 1078
PSE2262 (1029) CGGCCTCGAGCGGGAACGCGACCGGGCCTGGGCCTCGGAGCGCGGGCGGG
PSE2262 seq splicing (201)
CGGCCTCGAGCGGGAACGCGACCGGGCCTGGGCCTCGGAGCGCGGGCGGG

1079 1128
PSE2262 (1079) AGCGCGAGGAGGAGCGCGGGCGGTGACTGGCCCTCCGCCCGCGCTGAGCCA
PSE2262 seq splicing (251)
AGCGCGAGGAGGAGCGCGGGCGGTGACTGGCCCTCCGCCCGCGCTGAGCCA

1129 1178
PSE2262 (1129) CTGCGGCCGGGCTGCCCCCTGCGAGCCGCTGCGCTACAACGTGTGCCTGG
PSE2262 seq splicing (301)
CTGCGGCCGGGCTGCCCCCTGCGAGCCGCTGCGCTACAACGTGTGCCTGG

1179 1228
PSE2262 (1179) GCTCGGTGCTGCCCTACGGGGCCACCTCCACACTGCTGGCCGGAGACTCG
PSE2262 seq splicing (351)
GCTCGGTGCTGCCCTACGGGGCCACCTCCACACTGCTGGCCGGAGACTCG

1229 1278
PSE2262 (1229) GACTCCCAGGAGGAAGCGCACGGCAAGCTCGTGCTCTGGTCGGGCCTCCG
PSE2262 seq splicing (401)
GACTCCCAGGAGGAAGCGCACGGCAAGCTCGTGCTCTGGTCGGGCCTCCG

1279 1328
PSE2262 (1279) GAATGCCCCCGCTGCTGGGCAGTGATCCAGCCCCTGCTGTGTGCCGTAT
PSE2262 seq splicing (451)
GAATGCCCCCGCTGCTGGGCAGTGATCCAGCCCCTGCTGTGTGCCGTAT

1329 1378
PSE2262 (1329) ACATGCCCAAGTGTGAGAATGACCGGGTGGAGCTGCCAGCCGTACCCTC

PSE2262 seq splicing (501)

ACATGCCCAAGTGTGAGAATGACCGGGTGGAGCTGCCAGCCGTACCCTC
1379 1428

PSE2262 (1379) TGCCAGGCCACCCGAGGCCCTGTGCCATCGTGGAGAGGGAGCGGGGCTG
PSE2262 seq splicing (551)

TGCCAGGCCACCCGAGGCCCTGTGCCATCGTGGAGAGGGAGCGGGGCTG
1429 1478

PSE2262 (1429) GCCTGACTTCCTGCGCTGCACTCCTGACCGCTTCCCTGAAGGCTGCACGA
PSE2262 seq splicing (601)

GCCTGACTTCCTGCGCTGCACTCCTGACCGCTTCCCTGAAGGCTGCACGA
1479 1528

PSE2262 (1479) ATGAGGTGCAGAACATCAAGTTCAACAGTTCAGGCCAGTGCGAAGTGCCC
PSE2262 seq splicing (651)

ATGAGGTGCAGAACATCAAGTTCAACAGTTCAGGCCAGTGCGAAGTGCCC
1529 1578

PSE2262 (1529) TTGGTTCGGACAGACAACCCCAAGAGCTGGTACGAGGACGTGGAGGGCTG
PSE2262 seq splicing (701)

TTGGTTCGGACAGACAACCCCAAGAGCTGGTACGAGGACGTGGAGGGCTG
1579 1628

PSE2262 (1579) CGGCATCCAGTGCCAGAACCCGCTCTTCACAGAGGCTGAGCACCAGGACA
PSE2262 seq splicing (751)

CGGCATCCAGTGCCAGAACCCGCTCTTCACAGAGGCTGAGCACCAGGACA
1629 1678

PSE2262 (1629) TGCACAGCTACATCGCGGCCTTCGGGGCCGTACGGGCCTCTGCACGCTC
PSE2262 seq splicing (801)

TGCACAGCTACATCGCGGCCTTCGGGGCCGTACGGGCCTCTGCACGCTC
1679 1728

PSE2262 (1679) TTCACCCTGGCCACATTCGTGGCTGACTGGCGGAACTCGAATCGCTACCC
PSE2262 seq splicing (851)

TTCACCCTGGCCACATTCGTGGCTGACTGGCGGAACTCGAATCGCTACCC
1729 1778

PSE2262 (1729) TGCTGTTATTCTTCTTCTACGTCAATGCGTGCTTCTTTGTGGGCAGCATTG
PSE2262 seq splicing (901)

TGCTGTTATTCTTCTTCTACGTCAATGCGTGCTTCTTTGTGGGCAGCATTG
1779 1828

PSE2262 (1779) GCTGGCTGGCCCAGTTCATGGATGGTGCCCGCCGAGAGATCGTCTGCCGT
PSE2262 seq splicing (951)

GCTGGCTGGCCCAGTTCATGGATGGTGCCCGCCGAGAGATCGTCTGCCGT
1829 1878

PSE2262 (1829) GCAGATGGCACCATGAGGCTTGGGGAGCCACCTCCAATGAGACTCTGTC
PSE2262 seq splicing (1001)

GCAGATGGCACCATGAGGCTTGGGGAGCCACCTCCAATGAGACTCTGTC
1879 1928

PSE2262 (1879) CTGCGTCATCATCTTTGTCATCGTGTACTACGCCCTGATGGCTGGTGTGG

PSE2262 seq splicing (1051)

CTGCGTCATCATCTTTGTCATCGTGTACTACGCCCTGATGGCTGGTGTGG
1929 1978

PSE2262 (1929) FTTGGTTTGTGGTCCTCACCTATGCCTGGCACACTTCCTTCAAAGCCCTG
PSE2262 seq splicing (1101)

FTTGGTTTGTGGTCCTCACCTATGCCTGGCACACTTCCTTCAAAGCCCTG
1979 2028

PSE2262 (1979) GGCACCACCTACCAGCCTCTCTCGGGCAAGACCTCCTACTTCCACCTGCT
PSE2262 seq splicing (1151)

GGCACCACCTACCAGCCTCTCTCGGGCAAGACCTCCTACTTCCACCTGCT
2029 2078

PSE2262 (2029) CACCTGGTCACTCCCCTTTGTCCTCACTGTGGCAATCCTTGCTGTGGCGC
PSE2262 seq splicing (1201)

CACCTGGTCACTCCCCTTTGTCCTCACTGTGGCAATCCTTGCTGTGGCGC
2079 2128

PSE2262 (2079) AGGTGGATGGGGACTCTGTGAGTGGGATTGTTTGTGGGCTACAAGAAC
PSE2262 seq splicing (1251)

AGGTGGATGGGGACTCTGTGAGTGGGATTGTTTGTGGGCTACAAGAAC
2129 2178

PSE2262 (2129) TACCGATACCGTGC GGGCTTCGTGCTGGCCCAATCGGCCTGGTGTTTCAT
PSE2262 seq splicing (1301)

TACCGATACCGTGC GGGCTTCGTGCTGGCCCAATCGGCCTGGTGTTTCAT
2179 2228

PSE2262 (2179) CGTGGGAGGCTACTTCCTCATCCGAGGAGTCATGACTCTGTTCTCCATCA
PSE2262 seq splicing (1351)

CGTGGGAGGCTACTTCCTCATCCGAGGAGTCATGACTCTGTTCTCCATCA
2229 2278

PSE2262 (2229) AGAGCAACCACCCCGGGCTGCTGAGTGAGAAGGCTGCCAGCAAGATCAAC
PSE2262 seq splicing (1401)

AGAGCAACCACCCCGGGCTGCTGAGTGAGAAGGCTGCCAGCAAGATCAAC
2279 2328

PSE2262 (2279) GAGACCATGCTGCGCCTGGGCATTTTTGGCTTCCTGGCCTTTGGCTTTGT
PSE2262 seq splicing (1451)

GAGACCATGCTGCGCCTGGGCATTTTTGGCTTCCTGGCCTTTGGCTTTGT
2329 2378

PSE2262 (2329) GCTCATTACCTTCAGCTGCCACTTCTACGACTTCTTCAACCAGGCTGAGT
PSE2262 seq splicing (1501)

GCTCATTACCTTCAGCTGCCACTTCTACGACTTCTTCAACCAGGCTGAGT
2379 2428

PSE2262 (2379) GGGAGCGCAGCTTCCGGGACTATGTGCTATGTCAGGCCAATGTGACCATC
PSE2262 seq splicing (1551)

GGGAGCGCAGCTTCCGGGACTATGTGCTATGTCAGGCCAATGTGACCATC
2429 2478

PSE2262 (2429) GGGCTGCCACCAAGCAGCCATCCCTGACTGTGAGATCAAGAATCGCCC

PSE2262 seq splicing (1601)

GGGCTGCCACCAAGCAGCCCATCCCTGACTGTGAGATCAAGAATCGCCC
2479 2528

PSE2262 (2479) GAGCCTTCTGGTGGAGAAGATCAACCTGTTTGCCATGTTTGGAAGTGGCA
PSE2262 seq splicing (1651)

GAGCCTTCTGGTGGAGAAGATCAACCTGTTTGCCATGTTTGGAAGTGGCA
2529 2578

PSE2262 (2529) TCGCCATGAGCACCTGGGTCTGGACCAAGGCCACGCTGCTCATCTGGAGG
PSE2262 seq splicing (1701)

TCGCCATGAGCACCTGGGTCTGGACCAAGGCCACGCTGCTCATCTGGAGG
2579 2628

PSE2262 (2579) CGTACCTGGTGCAGGTTGACTGGGCAGAGTGACGATGAGCCAAAGCGGAT
PSE2262 seq splicing (1751)

CGTACCTGGTGCAGGTTGACTGGGCAGAGTGACGATGAGCCAAAGCGGAT
2629 2678

PSE2262 (2629) CAAGAAGAGCAAGATGATTGCCAAGGCCTTCTCTAAGCGGCACGAGCTCC
PSE2262 seq splicing (1801)

CAAGAAGAGCAAGATGATTGCCAAGGCCTTCTCTAAGCGGCACGAGCTCC
2679 2728

PSE2262 (2679) TGCAGAACCAGGCCAGGAGCTGTCC TTCAGCATGCACACTGTGTCCCAC
PSE2262 seq splicing (1851)

TGCAGAACCAGGCCAGGAGCTGTCC TTCAGCATGCACACTGTGTCCCAC
2729 2778

PSE2262 (2729) GACGGGCCCGTGGCGGGCTTGGCCTTTGACCTCAATGAGCCCTCAGCTGA
PSE2262 seq splicing (1901)

GACGGGCCCGTGGCGGGCTTGGCCTTTGACCTCAATGAGCCCTCAGCTGA
2779 2828

PSE2262 (2779) TGTCTCCTCTGCCTGGGCCAGCATGTCACCAAGATGGTGGCTCGGAGAG
PSE2262 seq splicing (1951)

TGTCTCCTCTGCCTGGGCCAGCATGTCACCAAGATGGTGGCTCGGAGAG
2829 2878

PSE2262 (2829) GAGCCATACTGCCCCAGGATATTTCTGTCACCCCTGTGGCAACTCCAGTG
PSE2262 seq splicing (2001)

GAGCCATACTGCCCCAGGATATTTCTGTCACCCCTGTGGCAACTCCAGTG
2879 2928

PSE2262 (2879) CCCCCAGAGGAACAAGCCAACCTGTGGCTGGTTGAGGCAGAGATCTCCCC
PSE2262 seq splicing (2051)

CCCCCAGAGGAACAAGCCAACCTGTGGCTGGTTGAGGCAGAGATCTCCCC
2929 2978

PSE2262 (2929) AGAGCTGCAGAAGCGCCTGGGCCGGAAGAAGAAGAGGAGGAAGAGGAAGA
PSE2262 seq splicing (2101)

AGAGCTGCAGAAGCGCCTGGGCCGGAAGAAGAAGAGGAGGAAGAGGAAGA
2979 3028

PSE2262 (2979) AGGAGGTGTGCCGCTGGCGCCGCCCCCTGAGCTTCACCCCCCTGCCCT

PSE2262 seq splicing (2151)

AGGAGGTGTGCCCGCTGGCGCCGCCCCCTGAGCTTCACCCCCCTGCCCT
3029 3078

PSE2262 (3029) GCCCCCAGTACCATTCCCTCGACTGCCTCAGCTGCCCCGGCAGAAATGCCT
PSE2262 seq splicing (2201)

GCCCCAGTACCATTCCCTCGACTGCCTCAGCTGCCCCGGCAGAAATGCCT
3079 3128

PSE2262 (3079) GGTGGCTGCAGGTGCCTGGGGAGCTGGGGACTCTTGCCGACAGGGAGCGT
PSE2262 seq splicing (2251)

GGTGGCTGCAGGTGCCTGGGGAGCTGGGGACTCTTGCCGACAGGGAGCGT
3129 3178

PSE2262 (3129) GGACCCTGGTCTCCAACCCATTCTGCCAGAGCCCAGTCCCCCTCAGGAT
PSE2262 seq splicing (2301)

GGACCCTGGTCTCCAACCCATTCTGCCAGAGCCCAGTCCCCCTCAGGAT
3179 3228

PSE2262 (3179) CCATTTCTGCCAGTGCACCGGCCCCCGTGGCATGGGCTCATGGCCGCC
PSE2262 seq splicing (2351)

CCATTTCTGCCAGTGCACCGGCCCCCGTGGCATGGGCTCATGGCCGCC
3229 3278

PSE2262 (3229) ACAGGGCCTGGGGCCTATTCACTCCCGCACCAACCTGATGGACACAGAAC
PSE2262 seq splicing (2401)

ACAGGGCCTGGGGCCTATTCACTCCCGCACCAACCTGATGGACACAGAAC
3279 3328

PSE2262 (3279) TCATGGATGCAGACTCGGACTTCGAACAAAACTCATCTCAGAAGAGGAT
PSE2262 seq splicing (2451)

TCATGGATGCAGACTCGGACTTCGAACAAAACTCATCTCAGAAGAGGAT
3329 3378

PSE2262 (3329) CTGGACTACAAGGATGACGATGACAAGGATTACAAAGACGACGATGATAA
PSE2262 seq splicing (2501)

CTGGACTACAAGGATGACGATGACAAGGATTACAAAGACGACGATGATAA
3379 3428

PSE2262 (3379) SGACTATAAGGATGATGACGACAAATAATCTAGAGGGCCCGTTTAAACCC
PSE2262 seq splicing (2551)

SGACTATAAGGATGATGACGACAAATAATCTAGAGGGCCCGTTTAAACCC
3429 3449

PSE2262 (3429) GCTGATCAGCCTCGACTGTGC
PSE2262 seq splicing (2601) GCTGATCAGCCTCGACTGTGC

Smo F460L:

829 878
PSE2263 (829) CTAGAGAACCCACTGCTTACTGGCTTATCGAAATTAATACGACTCACTAT
PSE2263 seq splicing (1)
CTAGAGAACCCACTGCTTACTGGCTTATCGAAATTAATACGACTCACTAT

879 928
PSE2263 (879) AGGGAGACCCAAGCTGGCTAGCGTTTAAACTTAAGCTTGGTACCGAGCTC
PSE2263 seq splicing (51)
AGGGAGACCCAAGCTGGCTAGCGTTTAAACTTAAGCTTGGTACCGAGCTC

929 978
PSE2263 (929) SGATCCGCCACCATGGCCGCTGCCCGCCAGCGCGGGGGCCGGAGCTCCC
PSE2263 seq splicing (101)
SGATCCGCCACCATGGCCGCTGCCCGCCAGCGCGGGGGCCGGAGCTCCC

979 1028
PSE2263 (979) GCTCCTGGGGCTGCTGCTGCTGCTGCTGCTGGGGGACCCGGGCCGGGGG
PSE2263 seq splicing (151)
GCTCCTGGGGCTGCTGCTGCTGCTGCTGCTGGGGGACCCGGGCCGGGGG

1029 1078
PSE2263 (1029) CGGCCTCGAGCGGGAACGCGACCGGGCCTGGGCCTCGGAGCGCGGGCGGG
PSE2263 seq splicing (201)
CGGCCTCGAGCGGGAACGCGACCGGGCCTGGGCCTCGGAGCGCGGGCGGG

1079 1128
PSE2263 (1079) AGCGCGAGGAGGAGCGCGGGCGGTGACTGGCCCTCCGCCCGCGCTGAGCCA
PSE2263 seq splicing (251)
AGCGCGAGGAGGAGCGCGGGCGGTGACTGGCCCTCCGCCCGCGCTGAGCCA

1129 1178
PSE2263 (1129) CTGCGGCCGGGCTGCCCCCTGCGAGCCGCTGCGCTACAACGTGTGCCTGG
PSE2263 seq splicing (301)
CTGCGGCCGGGCTGCCCCCTGCGAGCCGCTGCGCTACAACGTGTGCCTGG

1179 1228
PSE2263 (1179) GCTCGGTGCTGCCCTACGGGGCCACCTCCACACTGCTGGCCGGAGACTCG
PSE2263 seq splicing (351)
GCTCGGTGCTGCCCTACGGGGCCACCTCCACACTGCTGGCCGGAGACTCG

1229 1278
PSE2263 (1229) GACTCCCAGGAGGAAGCGCACGGCAAGCTCGTGCTCTGGTCGGGCCTCCG
PSE2263 seq splicing (401)
GACTCCCAGGAGGAAGCGCACGGCAAGCTCGTGCTCTGGTCGGGCCTCCG

1279 1328
PSE2263 (1279) GAATGCCCCCGCTGCTGGGCAGTGATCCAGCCCCTGCTGTGTGCCGTAT
PSE2263 seq splicing (451)
GAATGCCCCCGCTGCTGGGCAGTGATCCAGCCCCTGCTGTGTGCCGTAT

1329 1378
PSE2263 (1329) ACATGCCCAAGTGTGAGAATGACCGGGTGGAGCTGCCAGCCGTACCCTC

PSE2263 seq splicing (501)

ACATGCCCAAGTGTGAGAATGACCGGGTGGAGCTGCCAGCCGTACCCTC
1379 1428

PSE2263 (1379) TGCCAGGCCACCCGAGGCCCTGTGCCATCGTGGAGAGGGAGCGGGGCTG
PSE2263 seq splicing (551)

TGCCAGGCCACCCGAGGCCCTGTGCCATCGTGGAGAGGGAGCGGGGCTG
1429 1478

PSE2263 (1429) GCCTGACTTCCTGCGCTGCACTCCTGACCGCTTCCCTGAAGGCTGCACGA
PSE2263 seq splicing (601)

GCCTGACTTCCTGCGCTGCACTCCTGACCGCTTCCCTGAAGGCTGCACGA
1479 1528

PSE2263 (1479) ATGAGGTGCAGAACATCAAGTTCAACAGTTCAGGCCAGTGCGAAGTGCCC
PSE2263 seq splicing (651)

ATGAGGTGCAGAACATCAAGTTCAACAGTTCAGGCCAGTGCGAAGTGCCC
1529 1578

PSE2263 (1529) TTGGTTCGGACAGACAACCCCAAGAGCTGGTACGAGGACGTGGAGGGCTG
PSE2263 seq splicing (701)

TTGGTTCGGACAGACAACCCCAAGAGCTGGTACGAGGACGTGGAGGGCTG
1579 1628

PSE2263 (1579) CGGCATCCAGTGCCAGAACCCGCTCTTCACAGAGGCTGAGCACCAGGACA
PSE2263 seq splicing (751)

CGGCATCCAGTGCCAGAACCCGCTCTTCACAGAGGCTGAGCACCAGGACA
1629 1678

PSE2263 (1629) TGCACAGCTACATCGCGGCCTTCGGGGCCGTACGGGCCTCTGCACGCTC
PSE2263 seq splicing (801)

TGCACAGCTACATCGCGGCCTTCGGGGCCGTACGGGCCTCTGCACGCTC
1679 1728

PSE2263 (1679) TTCACCCCTGGCCACATTCGTGGCTGACTGGCGGAACTCGAATCGCTACCC
PSE2263 seq splicing (851)

TTCACCCCTGGCCACATTCGTGGCTGACTGGCGGAACTCGAATCGCTACCC
1729 1778

PSE2263 (1729) TGCTGTTATTCTCTTCTACGTCAATGCGTGCTTCTTTGTGGGCAGCATTG
PSE2263 seq splicing (901)

TGCTGTTATTCTCTTCTACGTCAATGCGTGCTTCTTTGTGGGCAGCATTG
1779 1828

PSE2263 (1779) GCTGGCTGGCCCAGTTCATGGATGGTGCCCGCCGAGAGATCGTCTGCCGT
PSE2263 seq splicing (951)

GCTGGCTGGCCCAGTTCATGGATGGTGCCCGCCGAGAGATCGTCTGCCGT
1829 1878

PSE2263 (1829) GCAGATGGCACCATGAGGCTTGGGGAGCCCACCTCCAATGAGACTCTGTG
PSE2263 seq splicing (1001)

GCAGATGGCACCATGAGGCTTGGGGAGCCCACCTCCAATGAGACTCTGTG
1879 1928

PSE2263 (1879) CTGCGTCATCATCTTTGTCATCGTGTACTACGCCCTGATGGCTGGTGTGG

PSE2263 seq splicing (1051)

CTGCGTCATCATCTTTGTCATCGTGTACTACGCCCTGATGGCTGGTGTGG
1929 1978

PSE2263 (1929) FTTGGTTTGTGGTCCCTCACCTATGCCTGGCACACTTCCTTCAAAGCCCTG
PSE2263 seq splicing (1101)

FTTGGTTTGTGGTCCCTCACCTATGCCTGGCACACTTCCTTCAAAGCCCTG
1979 2028

PSE2263 (1979) GGCACCACCTACCAGCCTCTCTCGGGCAAGACCTCCTACTTCCACCTGCT
PSE2263 seq splicing (1151)

GGCACCACCTACCAGCCTCTCTCGGGCAAGACCTCCTACTTCCACCTGCT
2029 2078

PSE2263 (2029) CACCTGGTCACTCCCCTTTGTCCTCACTGTGGCAATCCTTGCTGTGGCGC
PSE2263 seq splicing (1201)

CACCTGGTCACTCCCCTTTGTCCTCACTGTGGCAATCCTTGCTGTGGCGC
2079 2128

PSE2263 (2079) AGGTGGATGGGGACTCTGTGAGTGGGATTGTTTGTGGGCTACAAGAAC
PSE2263 seq splicing (1251)

AGGTGGATGGGGACTCTGTGAGTGGGATTGTTTGTGGGCTACAAGAAC
2129 2178

PSE2263 (2129) TACCGATACCGTGCGGGCTTCGTGCTGGCCCAATCGGCCTGGTGCTCAT
PSE2263 seq splicing (1301)

TACCGATACCGTGCGGGCTTCGTGCTGGCCCAATCGGCCTGGTGCTCAT
2179 2228

PSE2263 (2179) CGTGGGAGGCTACTTCCTCATCCGAGGAGTCATGACTCTGTTCTCCATCA
PSE2263 seq splicing (1351)

CGTGGGAGGCTACTTCCTCATCCGAGGAGTCATGACTCTGTTCTCCATCA
2229 2278

PSE2263 (2229) AGAGCAACCACCCCGGGCTGCTGAGTGAGAAGGCTGCCAGCAAGATCAAC
PSE2263 seq splicing (1401)

AGAGCAACCACCCCGGGCTGCTGAGTGAGAAGGCTGCCAGCAAGATCAAC
2279 2328

PSE2263 (2279) GAGACCATGCTGCGCCTGGGCATTTTTGGCTTCCTGGCCTTGGGCTTTGT
PSE2263 seq splicing (1451)

GAGACCATGCTGCGCCTGGGCATTTTTGGCTTCCTGGCCTTGGGCTTTGT
2329 2378

PSE2263 (2329) GCTCATTACCTTCAGCTGCCACTTCTACGACTTCTTCAACCAGGCTGAGT
PSE2263 seq splicing (1501)

GCTCATTACCTTCAGCTGCCACTTCTACGACTTCTTCAACCAGGCTGAGT
2379 2428

PSE2263 (2379) GGGAGCGCAGCTTCCGGGACTATGTGCTATGTCAGGCCAATGTGACCATC
PSE2263 seq splicing (1551)

GGGAGCGCAGCTTCCGGGACTATGTGCTATGTCAGGCCAATGTGACCATC
2429 2478

PSE2263 (2429) GGGCTGCCACCAAGCAGCCATCCCTGACTGTGAGATCAAGAATCGCCC

PSE2263 seq splicing (1601)

PSE2263 (2479) GGGCTGCCACCAAGCAGCCCATCCCTGACTGTGAGATCAAGAATCGCCC
2479 2528

PSE2263 seq splicing (1651)

PSE2263 (2529) GAGCCTTCTGGTGGAGAAGATCAACCTGTTTGCCATGTTTGGAAGTGGCA
2529 2578

PSE2263 seq splicing (1701)

PSE2263 (2579) TCGCCATGAGCACCTGGGTCTGGACCAAGGCCACGCTGCTCATCTGGAGG
2579 2628

PSE2263 seq splicing (1751)

PSE2263 (2629) CGTACCTGGTGCAGGTTGACTGGGCAGAGTGACGATGAGCCAAAGCGGAT
2629 2678

PSE2263 seq splicing (1801)

PSE2263 (2679) CAAGAAGAGCAAGATGATTGCCAAGGCCTTCTCTAAGCGGCACGAGCTCC
2679 2728

PSE2263 seq splicing (1851)

PSE2263 (2729) TGCAGAACCCAGGCCAGGAGCTGTCC TTCAGCATGCACACTGTGTCCCAC
2729 2778

PSE2263 seq splicing (1901)

PSE2263 (2779) GACGGGCCCCGTGGCGGGCTTGGCCTTTGACCTCAATGAGCCCTCAGCTGA
2779 2828

PSE2263 seq splicing (1951)

PSE2263 (2829) TGTCTCCTCTGCCTGGGCCAGCATGTCACCAAGATGGTGGCTCGGAGAG
2829 2878

PSE2263 seq splicing (2001)

PSE2263 (2879) GAGCCATACTGCCCCAGGATATTTCTGTCACCCCTGTGGCAACTCCAGTG
2879 2928

PSE2263 seq splicing (2051)

PSE2263 (2929) CCCCCAGAGGAACAAGCCAACCTGTGGCTGGTTGAGGCAGAGATCTCCCC
2929 2978

PSE2263 seq splicing (2101)

PSE2263 (2979) AGAGCTGCAGAAGCGCCTGGGCCGGAAGAAGAAGAGGAGGAAGAGGAAGA
2979 3028

PSE2263 (2979) AGGAGGTGTGCCCGCTGGCGCCGCCCCCTGAGCTTCACCCCCCTGCCCT

PSE2263 seq splicing (2151)

AGGAGGTGTGCCCGCTGGCGCCGCCCCCTGAGCTTCACCCCCCTGCCCT
3029 3078

PSE2263 (3029) GCCCCAGTACCATTCTCGACTGCCTCAGCTGCCCGGCAGAAATGCCT
PSE2263 seq splicing (2201)

GCCCCAGTACCATTCTCGACTGCCTCAGCTGCCCGGCAGAAATGCCT
3079 3128

PSE2263 (3079) GGTGGCTGCAGGTGCCTGGGGAGCTGGGGACTCTTGCCGACAGGGAGCGT
PSE2263 seq splicing (2251)

GGTGGCTGCAGGTGCCTGGGGAGCTGGGGACTCTTGCCGACAGGGAGCGT
3129 3178

PSE2263 (3129) GGACCCTGGTCTCCAACCCATTCTGCCAGAGCCCAGTCCCCCTCAGGAT
PSE2263 seq splicing (2301)

GGACCCTGGTCTCCAACCCATTCTGCCAGAGCCCAGTCCCCCTCAGGAT
3179 3228

PSE2263 (3179) CCATTTCTGCCAGTGCACCGGCCCGTGGCATGGGCTCATGGCCGCC
PSE2263 seq splicing (2351)

CCATTTCTGCCAGTGCACCGGCCCGTGGCATGGGCTCATGGCCGCC
3229 3278

PSE2263 (3229) ACAGGGCCTGGGGCCTATTCACTCCCGCACCAACCTGATGGACACAGAAC
PSE2263 seq splicing (2401)

ACAGGGCCTGGGGCCTATTCACTCCCGCACCAACCTGATGGACACAGAAC
3279 3328

PSE2263 (3279) TCATGGATGCAGACTCGGACTTCGAACAAAACATCTCAGAAGAGGAT
PSE2263 seq splicing (2451)

TCATGGATGCAGACTCGGACTTCGAACAAAACATCTCAGAAGAGGAT
3329 3378

PSE2263 (3329) CTGGACTACAAGGATGACGATGACAAGGATTACAAAGACGACGATGATAA
PSE2263 seq splicing (2501)

CTGGACTACAAGGATGACGATGACAAGGATTACAAAGACGACGATGATAA
3379 3428

PSE2263 (3379) GGACTATAAGGATGATGACGACAAATAATCTAGAGGGCCCGTTTAAACCC
PSE2263 seq splicing (2551)

GGACTATAAGGATGATGACGACAAATAATCTAGAGGGCCCGTTTAAACCC
3429 3475

PSE2263 (3429) GCTGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTT
PSE2263 seq splicing (2601)

GCTGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTT