

p Babe Puro hSNA, ER, NoTag

580 590 600 610 620 630 640 650 660 670 680

TATCCAGGCTCACTCTCTCTCTAGGGGCGGGCGGATCCATGCGGCGCTCTTTCTCTGTCAGGAAGCCCTCCGACCCCAATCGGAAGCCCTAACTACAGCGAGCTGGC

SNA-ER-NoTag.191AS (1>782) <- TATCCAGGCTCACTCTCTCTCTAGGGGCGGGCGGATCCATGCGGCGCTCTTTCTCTGTCAGGAAGCCCTCCGACCCCAATCGGAAGCCCTAACTACAGCGAGCTGGC

nSNA1L ORF (1>795) -> [ATGCGGCGCTCTTTCTCTGTCAGGAAGCCCTCCGACCCCAATCGGAAGCCCTAACTACAGCGAGCTGGC]

BamHI

690 700 710 720 730 740 750 760 770 780 790

GGACTCTAATCCAGAGTTTACCTTCCAGCAGGCCCTACGACAGGCCCACTGCTGGCAGCCATCCCACTCCGGAGATCCCAACCCCAAGCCCTCGCTGCCAATGCT

SNA-ER-NoTag.191AS (1>782) <- GGACTCTAATCCAGAGTTTACCTTCCAGCAGGCCCTACGACAGGCCCACTGCTGGCAGCCATCCCACTCCGGAGATCCCAACCCCAAGCCCTCGCTGCCAATGCT

nSNA1L ORF (1>795) -> GGACTCTAATCCAGAGTTTACCTTCCAGCAGGCCCTACGACAGGCCCACTGCTGGCAGCCATCCCACTCCGGAGATCCCAACCCCAAGCCCTCGCTGCCAATGCT

SNA-ER-NoTag.146S (1>575) -> CACTGCTGGCAGCCATCCCACTCCGGAGATCCCAACCCCAAGCCCTCGCTGCCAATGCT

800 810 820 830 840 850 860 870 880 890 900

CATCTGGGACTCTGTCTGGCGCCCAAGCCAGCCCAATGTCCTGGGCTCCCTTCCTGGCTCCAGGAGAGTCCAGGGTGGCAGAGCTGAOCTCCCTGTTCAGATCAGGA

nSNA1L ORF (1>795) -> CATCTGGGACTCTGTCTGGCGCCCAAGCCAGCCCAATGTCCTGGGCTCCCTTCCTGGCTCCAGGAGAGTCCAGGGTGGCAGAGCTGAOCTCCCTGTTCAGATCAGGA

SNA-ER-NoTag.146S (1>575) -> CATCTGGGACTCTGTCTGGCGCCCAAGCCAGCCCAATGTCCTGGGCTCCCTTCCTGGCTCCAGGAGAGTCCAGGGTGGCAGAGCTGAOCTCCCTGTTCAGATCAGGA

910 920 930 940 950 960 970 980 990 1000 1010

CAGTGGGAAAGGCTCCAGCCCAAGCCCAAGCCCAATGTCCTGGGCTCCCTTCCTGGCTCCAGGAGAGTCCAGGGTGGCAGAGCTGAOCTCCCTGTTCAGATCAGGA

nSNA1L ORF (1>795) -> CAGTGGGAAAGGCTCCAGCCCAAGCCCAAGCCCAATGTCCTGGGCTCCCTTCCTGGCTCCAGGAGAGTCCAGGGTGGCAGAGCTGAOCTCCCTGTTCAGATCAGGA

SNA-ER-NoTag.146S (1>575) -> CAGTGGGAAAGGCTCCAGCCCAAGCCCAAGCCCAATGTCCTGGGCTCCCTTCCTGGCTCCAGGAGAGTCCAGGGTGGCAGAGCTGAOCTCCCTGTTCAGATCAGGA

SNA-ER-NoTag.337S (1>787) -> TCCAGCCCAAGCCCAAGCCCAATGTCCTGGGCTCCCTTCCTGGCTCCAGGAGAGTCCAGGGTGGCAGAGCTGAOCTCCCTGTTCAGATCAGGA

1020 1030 1040 1050 1060 1070 1080 1090 1100 1110

CTTGGGCAAGTGGCCCAAGCAGCTGGCCAGCTCTCTGAGGCCAAGGATCTCCAGGCTCCGAAAGGCCCTTCAACTGCAAAATACGCAACAAGGAATACCTCAGCCTGGG

nSNA1L ORF (1>795) -> CTTGGGCAAGTGGCCCAAGCAGCTGGCCAGCTCTCTGAGGCCAAGGATCTCCAGGCTCCGAAAGGCCCTTCAACTGCAAAATACGCAACAAGGAATACCTCAGCCTGGG

SNA-ER-NoTag.146S (1>575) -> CTTGGGCAAGTGGCCCAAGCAGCTGGCCAGCTCTCTGAGGCCAAGGATCTCCAGGCTCCGAAAGGCCCTTCAACTGCAAAATACGCAACAAGGAATACCTCAGCCTGGG

SNA-ER-NoTag.337S (1>787) -> CTTGGGCAAGTGGCCCAAGCAGCTGGCCAGCTCTCTGAGGCCAAGGATCTCCAGGCTCCGAAAGGCCCTTCAACTGCAAAATACGCAACAAGGAATACCTCAGCCTGGG

1120 1130 1140 1150 1160 1170 1180 1190 1200 1210 1220

TGCCCTCAAGATGCACATCCGAAAGCCACAGCTGCGCTGGCTGCGGAACTCGGGGAAGGCCCTTCTCTAGGCGCTGGCTGCTACAAGGCCAATGTCCGACCCACAC

nSNA1L ORF (1>795) -> TGCCCTCAAGATGCACATCCGAAAGCCACAGCTGCGCTGGCTGCGGAACTCGGGGAAGGCCCTTCTCTAGGCGCTGGCTGCTACAAGGCCAATGTCCGACCCACAC

SNA-ER-NoTag.146S (1>575) -> TGCCCTCAAGATGCACATCCGAAAGCCACAGCTGCGCTGGCTGCGGAACTCGGGGAAGGCCCTTCTCTAGGCGCTGGCTGCTACAAGGCCAATGTCCGACCCACAC

SNA-ER-NoTag.337S (1>787) -> TGCCCTCAAGATGCACATCCGAAAGCCACAGCTGCGCTGGCTGCGGAACTCGGGGAAGGCCCTTCTCTAGGCGCTGGCTGCTACAAGGCCAATGTCCGACCCACAC

SNA-ER-NoTag.506S (1>785) -> CACGCTGCCCTGGCTGCTGCGGAACTCGGGGAAGGCCCTTCTCTAGGCGCTGGCTGCTACAAGGCCAATGTCCGACCCACAC

1230 1240 1250 1260 1270 1280 1290 1300 1310 1320 1330

TGGCGAGAAGCCCTTCTCTGTTCCCACTGACAGCGTGGCTTTCGCTGAGCCCTCCAACTCGGGGCCAACCCTCCAGACCCACTCAGATGTCAAGAAGTACCAGTGGC

nSNA1L ORF (1>795) -> TGGCGAGAAGCCCTTCTCTGTTCCCACTGACAGCGTGGCTTTCGCTGAGCCCTCCAACTCGGGGCCAACCCTCCAGACCCACTCAGATGTCAAGAAGTACCAGTGGC

SNA-ER-NoTag.146S (1>575) -> TGGCGAGAAGCCCTTCTCTGTTCCCACTGACAGCGTGGCTTTCGCTGAGCCCTCCAACTCGGGGCCAACCCTCCAGACCCACTCAGATGTCAAGAAGTACCAGTGGC

SNA-ER-NoTag.337S (1>787) -> TGGCGAGAAGCCCTTCTCTGTTCCCACTGACAGCGTGGCTTTCGCTGAGCCCTCCAACTCGGGGCCAACCCTCCAGACCCACTCAGATGTCAAGAAGTACCAGTGGC

SNA-ER-NoTag.506S (1>785) -> TGGCGAGAAGCCCTTCTCTGTTCCCACTGACAGCGTGGCTTTCGCTGAGCCCTCCAACTCGGGGCCAACCCTCCAGACCCACTCAGATGTCAAGAAGTACCAGTGGC

1340 1350 1360 1370 1380 1390 1400 1410 1420 1430 1440

AGGCGTGTGCTGGACCTTCTCCGAAATGTCCCTGCTCCACAAGCACCAAGAGTCCGGCTGCTCAGGATGTCCCGC-GAATTCGCTAATTCATATGGTGTCTTCAGGA

nSNA1L ORF (1>795) -> AGGCGTGTGCTGGACCTTCTCCGAAATGTCCCTGCTCCACAAGCACCAAGAGTCCGGCTGCTCAGGATGTCCCGC-GAATTCGCTAATTCATATGGTGTCTTCAGGA

SNA-ER-NoTag.337S (1>787) -> AGGCGTGTGCTGGACCTTCTCCGAAATGTCCCTGCTCCACAAGCACCAAGAGTCCGGCTGCTCAGGATGTCCCGC-GAATTCGCTAATTCATATGGTGTCTTCAGGA

SNA-ER-NoTag.506S (1>785) -> AGGCGTGTGCTGGACCTTCTCCGAAATGTCCCTGCTCCACAAGCACCAAGAGTCCGGCTGCTCAGGATGTCCCGC-GAATTCGCTAATTCATATGGTGTCTTCAGGA

EcoRI

ER hormone binding domain in frame

1450 1460 1470 1480 1490 1500

GACATGAGGCTGCCAACCCTTGGCCCAAGCCCTCTGTGATTAAGCACACTAAGAAG

SNA-ER-NoTag.337S (1>787) -> GACATGAGGCTGCCAACCCTTGGCCCAAGCCCTCTGTGATTAAGCACACTAAGAAG

SNA-ER-NoTag.506S (1>785) -> GACATGAGGCTGCCAACCCTTGGCCCAAGCCCTCTGTGATTAAGCACACTAAGAAG