

10 20 30 40 50 60 70 80 90 100 110 120
>NTP1_chrXII ATGGGGG-TTCCTATCTGGGCTGGTTGTTTCTGGTGTGGGTGTGAGTTTGATCCTCCCTTAGGAGGCTGTGCCGACGAGCCAGCGACACTTCGCGGAGTGAGCGCCGAGACGAAAA
>NTP2_chrXIIG.....A.....G.....
>NTP3_chrXIIG..T.....
>XM_003886392.1
>AB525222.1G.....
>AB010444.1G.....
>Clone 1
>Clone 2
>Clone 3

130 140 150 160 170 180 190 200 210 220 230 240
>NTP1_chrXII ACATATTTCTGCCGGTAAAGCACGCCCTGCAGGACCTCCGCGATGCGGAACGTCGCTGTCAATGATGCTGGCAAGCAATTGTTGTGATCGATGGAGGCAGTAGTGCCGACGCCGAGCAATGT
>NTP2_chrXII
>NTP3_chrXII
>XM_003886392.1
>AB525222.1
>AB010444.1G.....
>Clone 1
>Clone 2
>Clone 3

250 260 270 280 290 300 310 320 330 340 350 360
>NTP1_chrXII ATTTCTGCCGAAAGACCCGGTCAATGCCACGTGGAGGCCGACACATTGACCCCGACAGTATTCGACTCCTCGGCGGGTAAGCGCTTCGCAGGACTTCGTGGAGTTTAGAAAGCTGGCT
>NTP2_chrXII
>NTP3_chrXII
>XM_003886392.1
>AB525222.1
>AB010444.1
>Clone 1
>Clone 2
>Clone 3

370 380 390 400 410 420 430 440 450 460 470 480
>NTP1_chrXII AGACGCGTACGCTGGAGAGGACTGGGAGTCGAGGTCCTGTTGATTCCAAGCGTCTCTCCAGCACGTTCCCTGAGATGGAAGACAGTGCAAGGGGCCATCGCAGCTCTTGGAGGACGACGC
>NTP2_chrXII
>NTP3_chrXII
>XM_003886392.1
>AB525222.1
>AB010444.1
>Clone 1
>Clone 2
>Clone 3

490 500 510 520 530 540 550 560 570 580 590 600
>NTP1_chrXII AGTTTCGCATCTTGGACGAGAACTCACTGAGGAACAAAAGGTTTCAGGTTCAAGCGATGGGCGTTCCAGTCTGTGCTGAGCAGCGGCAGGAGTTCGTGATTTCCACGACTGGTACCGCGA
>NTP2_chrXII
>NTP3_chrXII
>XM_003886392.1
>AB525222.1
>AB010444.1
>Clone 1
>Clone 2
>Clone 3

610 620 630 640 650 660 670 680 690 700 710 720
>NTP1_chrXII AGCCCTCTTTGTCATTCTTCGCTTTCATCAATCACCCGAAGCCTGGCCACGGGTACAAATTCCTTACCACACCCCGAATGGACCCGACCGATCACGGGCGCTGAGGAAGGTCTGTACGC
>NTP2_chrXII
>NTP3_chrXII
>XM_003886392.1
>AB525222.1
>AB010444.1
>Clone 1
>Clone 2
>Clone 3

730 740 750 760 770 780 790 800 810 820 830 840
>NTP1_chrXII ATTTCTCGCGCTCAACCATCTTTCGGGGCGGTTAGGCGAAGACCCAGCTAGGTGTTACGTTGATGAATACGGGATGAAGCAGTGCCGCAATGACCTTGTGGCGTGGTTGAAGTGGGCGG
>NTP2_chrXII
>NTP3_chrXII
>XM_003886392.1
>AB525222.1
>AB010444.1
>Clone 1
>Clone 2
>Clone 3

850 860 870 880 890 900 910 920 930 940 950 960
>NTP1_chrXII TGCTTCTACCCAAATCGTTTTTCCACTACAGGACGGCAGTGCCTGCCCTCGTCCATCCGTGCCGTTAACCTGCAGCACGAACGCTTTCTCCCATCGCGTTTTCCGAGTGCCGACGTCAT
>NTP2_chrXII
>NTP3_chrXII
>XM_003886392.1
>AB525222.1
>AB010444.1
>Clone 1
>Clone 2
>Clone 3

970 980 990 1000 1010 1020 1030 1040 1050 1060 1070 1080
>NTP1_chrXII ATCGGTTTCTTTTATGCAGCTGGGTGTGGCCAGTTCCTCCGGACTGTTTTTCAAGGAGCTGTGCAGTAACGCCGAATTCGGCATCAGGGGATTTGCTATAATCCCTGTATTTTCAGAGG
>NTP2_chrXII
>NTP3_chrXII
>XM_003886392.1
>AB525222.1
>AB010444.1
>Clone 1
>Clone 2
>Clone 3

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1090 1100 1110 1120 1130 1140 1150 1160 1170 1180 1190 1200
>NTP1_chrXII CTTCCGACAGGCGTTTCGCGGGCGATGTCGAGATCCTTCCAGACGGAAACCATAGTTGTGGATGAAGATGTGCGAAAGAACAAGCTGAAGCCGGTGGCGACATCTTGCTCAGCGAACAA
>NTP2_chrXII .....A.....
>NTP3_chrXII .....
>XM_003886392.1 .....
>AB525222.1 .....A.....
>AB010444.1 .....
>Clone 1 .....A.....
>Clone 2 .....A.....
>Clone 3 .....A.....
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1210 1220 1230 1240 1250 1260 1270 1280 1290 1300 1310 1320
>NTP1_chrXII TCCGGAATTAGTTTCAAGGCAATGAATGAAATGCAATGTCGCGAAAACAAGATTGATCCGACGAAATCACTCGCGGAGCGGCTGAGGATCGACGACTGCTTCCAGATTGTAGGAACTGG
>NTP2_chrXII .....T.....T.....
>NTP3_chrXII .....
>XM_003886392.1 .....
>AB525222.1 .....T.....T.....
>AB010444.1 .....
>Clone 1 .....T.....T.....
>Clone 2 .....T.....T.....
>Clone 3 .....T.....T.....
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1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430 1440
>NTP1_chrXII TGATTTGACACATGCCAAGCCCAGGTAGAAGAACTTCTCGTCAGTCCCAGGTTTCCACTTCCAGCGAACATTGAGGCAGCGTCGTCAGGCTTCGAATCTGTTGGTCAGGTTTTCAGT
>NTP2_chrXII .....
>NTP3_chrXII .....
>XM_003886392.1 .....
>AB525222.1 .....
>AB010444.1 .....
>Clone 1 .....
>Clone 2 .....
>Clone 3 .....
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1450 1460 1470 1480 1490 1500 1510 1520 1530 1540 1550 1560
>NTP1_chrXII CGCGTCTACGGCGTCGCCGATGGTCATTACAGGAGGAGCGATGTATGCGAGCATCAGCACAAATGCAAGGTTTCGGACTTCTCCGAAAGACTTCCAGGGTGATCTAGAACAACGTGATAGC
>NTP2_chrXII .....C.....C.....C.....
>NTP3_chrXII .....C.....C.....C.....
>XM_003886392.1 .....
>AB525222.1 .....C.....C.....C.....
>AB010444.1 .....C.....C.....C.....
>Clone 1 .....C.....C.....C.....
>Clone 2 .....C.....C.....C.....
>Clone 3 .....C.....C.....C.....
```

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1570 1580 1590 1600 1610 1620 1630 1640 1650 1660 1670 1680
>NTP1_chrXII TGCATCACGTACATACTGTTCTCTCCAGTAGTTAACAGTGGAGATGGCCTTGTCATTCAGTTGCCAAACGCGGAACAAAAGCTGACTAGTATGAACTACGACTTATGCAAGACGATCGC
>NTP2_chrXII .....A.....G.....G.....
>NTP3_chrXII .....A.....G.....G.....
>XM_003886392.1 .....
>AB525222.1 .....A.....G.....G.....
>AB010444.1 .....A.....G.....G.....
>Clone 1 .....A.....G.....G.....
>Clone 2 .....A.....G.....G.....
>Clone 3 .....A.....G.....G.....
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      1690      1700      1710      1720      1730      1740      1750      1760      1770      1780      1790      1800
>NTP1_chrXII  GCTGACGTTTTCGCTGCTTCAGCACATGGAGGCAGGCGAGCATAAACCGTCATCCATTTCCCTGGCAAAAAACCGTTGTGGGACCAGATGGAAAACCACGTGCTGATCTTGGGTGGCATGT
>NTP2_chrXII  .....
>NTP3_chrXII  .....A.....G.....
>XM_003886392.1 .....
>AB525222.1 .....C.....
>AB010444.1 .....A.....G.....
>Clone 1 .....A.....G.....
>Clone 2 .....C.....
>Clone 3 .....C.....

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      1810      1820      1830      1840      1850      1860      1870      1880
>NTP1_chrXII  TGGGGCAATTCCTTCATCGTGTCCCTTCACGGAAGAATGGGGACGTACAGCTTATGAGACGGGATTTACCTACAACATGTGA
>NTP2_chrXII  .....
>NTP3_chrXII  .....
>XM_003886392.1 .....A.....
>AB525222.1 .....
>AB010444.1 .....
>Clone 1 .....
>Clone 2 .....
>Clone 3 .....

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Primer	Sequence
Fw-T7	TAATACGACTCACTATAGGG
Fw-1	GAGCTCATGGCCGACGAGCCAGCGACACTT
Fw-int-1	CGTCGTCAGGCTTCGAATCTGTT
Fw-int-2	GATTTCCACGACTGGTACCG
Rv-SP6	ATTTAGGTGACACTATAG
Rv-1	GGCCTTAATTAATCACATGTTGTAGGTAAATCCCG
Rv-int-1	TTCTTCTACCTGGGCTTGGC
Rv-int-2	ACGCTTGAATCAACAGACCT