

10 20 30 40 50 60 70 80 90 100
 PouSF1_mRNA_Ch7ATGGCGGGACACCTGGCTTCCGACTTTCGCCTTCTCGCCCCCGCGGGCGGTGGAAGCGATGGGC
 PouSF1_like_Ch5 TACCGGGGCCCTGGCTTGGGGGTGCCCTTCCTTCACCATCGTGGGACACCTGGCTTCCGACTTTGCCCTTTGNCCTCCCCAGGCCGGTGGAGGCGATGGGC
 PouSF1_like_Ch10GGCTGAACACCTGGCTTCCAAACCTGCCTTCTTTTTCCTTGCATGCAGTGCAGATGATGGGC
 Clustal Consensus ***** * * * * *

110 120 130 140 150 160 170 180 190 200
 PouSF1_mRNA_Ch7 CCGGAGGGCCGGAGCCGGGCTGGGTTGATCCTCGGACCTGGCTGAGCTTCCAAAGGGCCCTCCCGTGGTCAAGGATCGGGCC GGGGGTTGGGCCGGGG
 PouSF1_like_Ch5 CAGAAAGGCCAGAGCCAGGCTGGGTTGATCCTCTGACCTGGCTGTGCTTCCAAAGGGCCCTCCTGGTGGGTCAAGGATCTGGCG GGGGGCTGCTNNGGACG
 PouSF1_like_Ch10 TGGAGGGCCAGAGCCTGGCTGGGATGATCCTCAGCATGGGTCAGCTTCCAAAGGAACCCAAAGCAGTCAGGGATTAAGGCCAGGGGGATGGCTGGCC
 Clustal Consensus * * * * * * * * * * * * * * *

210 220 230 240 250 260 270 280 290 300
 PouSF1_mRNA_Ch7 CCGAGGTGTGGGGGCCCTCCCGCGTGGCC---CCGCCATAGACTTTCGCGGAGGGATGGCCCTACTCGCCACCTCAGGTCGGAGTGGGGCTGGTGCCCC
 PouSF1_like_Ch5 CAGAGGTGGGGAGGCTTCCTCTATGCC---CCGCCATAGACTTTCGCGGAGGGATGGCCCTACTGTGACCTCAGGTCAGAGAGGGGCCCTGGTGCCCC
 PouSF1_like_Ch10 CCAAGGTGTGAGGGCTTCCACA-ATCCCCACCACCATCTTATGGCTTCTGAAAGGGTATGGCCCTCTGCACACCTCAGGTCAGAGTGGGGCTTGTGCTC
 Clustal Consensus * * * * * * * * * * * * * * *

AF1 : 5'-CCGAGCCCTGTGCCGCC-3'

310 320 330 340 350 360 370 380 390 400
 PouSF1_mRNA_Ch7 AGGGCGCCCTGGAGACCCCTCAGCCGAGGGCCAGGCGGGGGCCGGGTGGAGAGCAACTCCGAGGGGGCCCTCCCCCGAGCCCTGTGCCGCCCCCGCTGG
 PouSF1_like_Ch5 AAGGGCGCCCTGGAGACCCCTCAGCCCTAGGGCCAGGCAGGAGTCCGGGTGGGGAGCAACTCCGAGGGGGCCCTCCCTGGAGCCCTATGCCACCCCGCTGG
 PouSF1_like_Ch10 AGCACAGCCTGGAGACTCCTCAGCA-TAAGCCAAATAGGAGCTTGGGTGGGGAGCAACTCCAAAGAGGCCACCCCC-ATCCCTGTGCCACC-TGCTGG
 Clustal Consensus * * * * * * * * * * * * * * *

AF2 : 5'-GCTGGAGCCGAAACCCGAGG-3'

410 420 430 440 450 460 470 480 490 500
 PouSF1_mRNA_Ch7 CCGCCGAAAGCTGGACAAAGGAAAGCTGGAGCCGAAAC---CCGAGGAGTCCAGGACATCAAAGCGCTTCAGAAAGATCTCGAACAAATTTGCCAAGCTC
 PouSF1_like_Ch5 CACTGCACAGCTGGACAAAGGAGAAACTAGAGCCGAAAC---CTGAGAAAGTCCAGGACATCAAAGCGCTTCAGAAAGACCCTTGAAACAAATTTGCCAAGCTT
 PouSF1_like_Ch10 TGCTGCAAGAGCTGGACAAAGGAAAGCTGGAAACCAACCTCCCAAGGAGTCCAGGACATAAAATCACCCTTTAGAAATGACATCAAACAAATCTGCCAAGCTC
 Clustal Consensus * * * * * * * * * * * * * * *

AR1 : 5'-CCCCAAAGTGAGCCCAACATCG-3'

510 520 530 540 550 560 570 580 590 600
 PouSF1_mRNA_Ch7 CTAAAGCAGAAGAGGATCACCCCTGGGATATACCCAGGCGATGTGGGGCTCACCTTTGGGGTTCTTTTGGGAAAGGTTTCAGCCAAAACGACCATCTGCC
 PouSF1_like_Ch5 CTAAAGCAGAAGAGGATCACCCCTGGGATATACCCAGGCGATGTGGGGCTCACCC---TGTTCCTTTTGGGAAAGGTTTCAGCCAAAATGACCATCTGCA
 PouSF1_like_Ch10 CTAAAGCAGAAGAGGATCACCCCTGATATATACCCAGGCTGATGTGGGGCTCAACTTGTGGGTTCTTTTGGGAACACATTCAGCCAAAATGACCATCCACC
 Clustal Consensus * * * * * * * * * * * * * * *

AR2 : 5'-CACCTCCCAAAGAGAACCCCCAAA-3'