CCT01

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2355F_Cmax_pum_KaP    TCAACACCTCGAACAGAAGGTTCTCGTCCAGATTTGTGAAGCCAGTTTCTTCGGATTGCTCTCCCTCTTCCTCCTCCACCTCCACCTCCTCCTCCTCTTGTTTGACTAACTTCCAAGTGAAAATTTTCAAAAACCCAT
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2554F_Ptri_tri_Bar    TCAACACCTCGAACAGAAGGTCCTCGTCCAGACTTGTGAAGCCAGTTTCTTCGGATTGCTCTCTCTCTTCCTCCTCCACCTCC---TCCTCC---TCTTGTTTGACTAACTTCCAAGTGAGAATTTTCAAAAACTCAT
2554R_Ptri_tri_Bar    TCAACACCTCGAACAGAAGGTCCTCGTCCAGACTTGTGAAGCCAGTTTCTTCGGATTGCTCTCTCTCTTCCTCCTCCACCTCC---TCCTCC---TCTTGTTTGACTAACTTCCAAGTGAGAATTTTCAAAAACTCAT
300F_Cret_man_Par     TCAACACCTCGAACAGAAGGTTCTCGTCCAGATTTGTGAAGCCAGTTTCTTCGGATTGCTCTCCCTCTTCCTCCTCCACCTCC---TCCTCC---TCTTGTTTGACTAACTTCCAAGTGAAAATTTTCAAAAACTCAC
300R_Cret_man_Par     TCAACACCTCGAACAGAAGGTTCTCGTCCAGATTTGTGAAGCCAGTTTCTTCGGATTGCTCTCCCTCTTCCTCCTCCACCTCC---TCCTCC---TCTTGTTTGACTAACTTCCAAGTGAAAATTTTCAAAAACTCAC
3055F_Cmed_citr_Be    TCAACACCTCGAACAGAAGGTTCTCGTCCAGATTTGTGAAGCCAGTTTCTTCGGATTGCTCTCCCTCTTCCTCCTCCACCTCC---TCCTCCTCCTCTTGTTTGACTAACTTCCAAGTGGAAATTTTCAAAAACTCAT
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3066F_Cmax_pum_Sou    TCAACACCTCGAACAGAAGGTTCTCGTCCAGATTTGTGAAGCCAGTTTCTTCGGATTGCTCTCCCTCTTCCTCCTCCACCTCCACCTCCTCCTCCTCTTGTTTGACTAACTTCCAAGTGAAAATTTTCAAAAACTCAT
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3780F_Chal_cithyb_U   TCAACACCTCGAACAGAAGGTTCTCGTCCAGATTTGTGAAGCCAGTTTCTTCGGATTGCCCTCCCTCTTCCTCCTCCATCTCC---TCC------TCTTGTTTGACTAACTTCCAAGTGAAAAATTTCAAAAACTCAT
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cAGG9

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4008F_Ptri_tri_Seed   AATGCTGAAGATAATCCGCGAAATGAGTATCCAGATGAGATTTCTGATGAGCAAGAGGAGGAGGAGGAGGAGGAAGAAGAAGAAGAA---GAGGTAGATGAAGATGGAGTGGAGAGCAAGGCA
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138F_Cmed_cit_Ind     AATGCTGAAGATAATCCGCGAAATGAGTATCCAGATGAGATTTCGGATGAGCAAGAGGAGGAG---------GAAGAAGAA---------GAGGTAGATGAA-ATGGAGTGGAGAGCAAGGCA
138R_Cmed_cit_Ind     AATGCTGAAGATAATCCGCGAAATGAGTATCCAGATGAGATTTCGGATGAGCAAGAGGAGGAG---------GAAGAAGAA---------GAGGTAGATGAA-ATGGAGTGGAGAGCAAGGCA
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644F_Cmax_pum_Phi      GCCTTCTTGATTTAACCGGACAAAGAATGGTGAATATATCTTACTAGTAGTGTGTTTCTCTGTGTGTGTGTGTGTGTGTGTGTGT------AATCTTTGGAGAACTCTCTCATTGATTAAGACCCATTTTATCTAC
644R_Cmax_pum_Phi      GCCTTCTTGATTTAACCGGACAAAGAATGGTGAATATATCTTACTAGTAGTGTGTTTCTCTGTGTGTGTGTGTGTGTGTGTGTGT------AATCTTTGGAGAACTCTCTCATTGATTAAGACCCATTTTATCTAC
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p123_Coun_1    GCTCTGCTTTCCATTTCTCAGTTCTCACACACCACACACGCTGACCGCCAGAGAGAGATCTGGTAATTGTTCCACCAAACAATAAGCTCCACAAACACAAAACACACCCGCA--CTCTCTCTCTCTCTCTCTCTCTCTCT----
p123_Coun_2    GCTCTGCTTTCCATTTCTCAGTTCTCACACACCACACACGCTGACCGCCAGAGAGAGATCTGGTAATTGTTCCACCAAACAATAAGCTCCACAAACACAAAACACACCCGCA--CTCTCTCTCTCTCTCTCTCTCTCTCT----
p186_Coun_1    GCTCTGCTTTCCATTTCTCAGTTCTCACACACCACACACGCTGACCGCCAGAGAGAGATCTGGTAATTGTTCCACCAAACAATAAGCTCCACAAACACAAAACACACCCGCA--CTCTCTCTCTCTCTCTCT--------------
p186_Coun_2    GCTCTGCTTTCCATTTCTCAGTTCTCACACACCACACACGCTGACCGCCAGAGAGAGATCTGGTAATTGTTCCACCAAACAATAAGCTCCACAAACACAAAACACACCCGCA—CTCTCTCTCTCTCTCTCTCTCTCTCTC--
p188_Coun_1    GCTCTGCTTTCCATTTCTCAGTTCTCACACACCACACACGCTGACCGCCAGAGAGAGATCTGGTAATTGTTCCACCAAACAATAAGCTCCACAAACACAAAACACACCCGCA--CTCTCTCTCTCTCTCT--------------
p188_Coun_2    GCTCTGCTTTCCATTTCTCAGTTCTCACACACCACACACGCTGACCGCCAGAGAGAGATCTGGTAATTGTTCCACCAAACAATAAGCTCCACAAACACAAAACACACCCGCA--CTCTCTCTCT----------
p236_Coun_1    GCTCTGCTTTCCATTTCTCAGTTCTCACCCACCACACACGCTGACCGCCAGAGAGAGATCTGGTAATTGTTCCACCAAACAATAAGCTCCACAAACACAAAACACACCCGCA--CTCTCTCTCTCTCTCTCTCTCT----------
p236_Coun_2    GCTCTGCTTTCCATTTCTCAGTTCTCACCCACCACACACGCTGACCGCCAGAGAGAGATCTGGTAATTGTTCCACCAAACAATAAGCTCCACAAACACAAAACACACCCGCA--CTCTCTCTCTCTCTCTCTCTCT--------
p269_Coun_1    GCTCTGCTTTCCATTTCTCAGTTCTCACACACCACACACGCTGACCGCCAGAGAGAGATCTGGTAATTGTTCCACCAAACAATAAGCTCCACAAACACAAAACACACCCGCA--CTCTCTCTCTCTCTCTCTCT----------
p269_Coun_2    GCTCTGCTTTCCATTTCTCAGTTCTCACACACCACACACGCTGACCGCCAGAGAGAGATCTGGTAATTGTTCCACCAAACAATAAGCTCCACAAACACAAAACACACCCGCA--CTCTCTCTCTCTCTCTCTCTCT--------
p277_Coun_1    GCTCTGCTTTCCATTTCTCAGTTCTCACACACCACACACGCTGACCGCCAGAGAGAGATCTGGTAATTGTTCCACCAAACAATAAGCTCCACAAACACAAAACACACCCGCA--CTCTCTCTCTCTCTCT--------------
p277_Coun_2    GCTCTGCTTTCCATTTCTCAGTTCTCACACACCACACACGCTGACCGCCAGAGAGAGATCTGGTAATTGTTCCACCAAACAATAAGCTCCACAAACACAAAACACACCCGCA--CTCTCTCTCTCTCTCTCTCTCT----------
p305_Coun_1    GCTCTGCTTTCCATTTCTCAGTTCTCACACACCACACACGCTGACCGCCAGAGAGAGATCTGGTAATTGTTCCACCAAACAATAAGCTCCACAAACACAAAACACACCCGCA--CTCTCTCTCTCTCTCT--------------
p305_Coun_2    GCTCTGCTTTCCATTTCTCAGTTCTCACACACCACACACGCTGACCGCCAGAGAGAGATCTGGTAATTGTTCCACCAAACAATAAGCTCCACAAACACAAAACACACCCGCA--CTCTCTCTCTCTCTCT--------------
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p441_Coun_1    GCTCTGCTTTCCATTTCTCAGTTCTCACACACCACACACGCTGACCGCCAGAGAGAGATCTGGTAATTGTTCCACCAAACAATAAGCTCCACAAACACAAAACACACCCGCA--CTCTCTCTCTCTCTCT--------------
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F1038_Para_1   GCTCTGCTTTCCATTTCTCAGTTCTCACACACCACACACGCTGACCGCCAGAGAGAGATCTGGTAATTGTTCCACCAAACAATAAGCTCCACAAACACAAAACACACCCGCA--CTCTCTCTCTCTCTCT--------------
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F852_Para_1    GCTCTGCTTTCCATTTCTCAGTTCTCACACACCACACACGCTGACCGCCAGAGAGAGATCTGGTAATTGTTCCACCAAACAATAAGCTCCACAAACACAAAACACACCCGCA--CTCTCTCTCTCTCTCTCTCTCT--------
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F885_Para_1    GCTCTGCTTTCCATTTCTCAGTTCTCACACACCACACACGCTGACCGCCAGAGAGAGATCTGGTAATTGTTCCACCAAACAATAAGCTCCACAAACACAAAACACACCCGCA--CTCTCTCTCTCTCTCTCT--------------
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F946_Para_1    GCTCTGCTTTCCATTTCTCAGTTCTCACACACCACACACGCTGACCGCCAGAGAGAGATCTGGTAATTGTTCCACCAAACAATAAGCTCCACAAACACAAAACACACCCGCA--CTCTCTCTCTCTCTCTCTCTCTCTCT----
F946_Para_2    GCTCTGCTTTCCATTTCTCAGTTCTCACACACCACACACGCTGACCGCCAGAGAGAGATCTGGTAATTGTTCCACCAAACAATAAGCTCCACAAACACAAAACACACCCGCA--CTCTCTCTCTCTCTCTCT--------------
F960_Para_1    GCTCTGCTTTCCATTTCTCAGTTCTCACACACCACACACGCTGACCGCCAGAGAGAGATCTGGTAATTGTTCCACCAAACAATAAGCTCCACAAACACAAAACACACCCGCA--CTCTCTCTCTCTCTCTCT--------------
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T366_Para_1    GCTCTGCTTTCCATTTCTCAGTTCTCACACACCACACACGCTGACCGCCAGAGAGAGATCTGGTAATTGTTCCACCAAACAATAAGCTCCACAAACACAAAACACACCCGCA--CTCTCTCTCTCTCTCTCTCTCTCTCTCT
T366_Para_2    GCTCTGCTTTCCATTTCTCAGTTCTCACACACCACACACGCTGACCGCCAGAGAGAGATCTGGTAATTGTTCCACCAAACAATAAGCTCCACAAACACAAAACACACCCGCA--CTCTCTCTCTCTCTCTCT--------------
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S274_Ouest_1   GCTCTGCTTTCCATTTCTCAGTTCTCACACACCACACACGCTGACCGCCAGAGAGAGATCTGGTAATTGTTCCACCAAACAATAAGCTCCACAAACACAAAACACACCCGCA--CTCTCTCTCTCTCTCTCT------------
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p186_Coun_2    ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTG
p188_Coun_1    ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGA----------TTG
p188_Coun_2    ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCAAACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGA----------TTG
p216_Coun_1    ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGA----------TTG
p216_Coun_2    ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA--TTG
p236_Coun_1    ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAATTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCACTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGAGA----------TTG
p236_Coun_2    ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAATTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCACTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGAGA----------TTG
p277_Coun_1    ACAC-GTAACCTCCTCCTTCCAT-ACTCCTCTAATTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCACTGTGTGTGCTTATATGT--GAGAGAGAGAGA----------TTG
p277_Coun_2    ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAATTCT-CCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCACTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGAGAGAGAGAGAGA----------TTG
p305_Coun_1    ACACGGTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGA----------TTG
p305_Coun_2    ACACGGTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGAGAGAGAGA----------TTG
p337_Coun_1    ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGA----------TTG
p337_Coun_2    ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA--TTG
p340_Coun_1    ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGA----------TTG
p340_Coun_2    ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA------TTG
p345_Coun_1    ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAATTCT-CCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGA----------TTG
p345_Coun_2    ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAATTCT-CCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCACTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGAGAGAGAGA----------TTG
p346_Coun_1    ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGAGA----------TTG
p346_Coun_2    ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGA----------TTG
p349_Coun_1    ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGA----------TTG
p349_Coun_2    ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGAGA----------TTG
p390_Coun_1    ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA--------TTG
p390_Coun_2    ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGAGAGAGAGAGAGA----------TTG
p470_Coun_1    ACAC-GTAACCTCCTCCTTCCAT-ACTCCTCTAATTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCACTGTGTGTGCTTATATGT--GAGAGAGAGAGA----------TTG
p470_Coun_2    ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGAGAGA----------TTG
p495_Coun_1    ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGTGTGAGAGAGAGAGAGAGAGAGA----------TTG
p575_Coun_1    ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGA----------TTG
p575_Coun_2    ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGA----------TTG
F810_Para_1    ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGAGA----------TTG
F810_Para_2    ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGA----------TTG
F885_Para_1    ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGAGA----------TTG
F885_Para_2    ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCAAACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGAGA----------TT?
T308_Para_1    ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGA----------TTG
T308_Para_2    ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGA----------TTG
T348_Para_1    ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGAGA----------TTG
T348_Para_2    ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGA----------TTG
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T352_Para_1    ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA----------TTG
T352_Para_2    ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGA----------TTG
T354_Para_1    ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA------TTG
T354_Para_2    ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA------TTG
T358_Para_1    ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGA----------TTG
T358_Para_2    ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGA----------TTG
T386_Para_1    ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAATTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGAGAGAGAGAGA----------TTG
T386_Para_2    ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGAGAGA----------TTG
C731_Ouest_1   ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAATTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCACTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGAGAGA----------TTG
C731_Ouest_2   ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAATTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCACTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGAGAGA----------TTG
C733_Ouest_1   ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGAGAGA----------TTG
C733_Ouest_2   ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAATTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCACTGTGTGTGCTTATATGT--GAGAGAGAGAGA----------TTG
C735_Ouest_1   ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGAGA----------TTG
C735_Ouest_2   ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGAGA----------TTG
C737_Ouest_1   ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA--TTG
C737_Ouest_2   ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGA----------TTG
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C758_Ouest_1   ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGA----------TTG
C758_Ouest_2   ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGA----------TTG
C784_Ouest_1   ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGAGA----------TTG
C784_Ouest_2   ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGA----------TTG
C793_Ouest_1   ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGAGA----------TTG
C793_Ouest_2   ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGA----------TTG
C913_Ouest_1   ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAATTCT-CCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCACTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGAGAGAGA----------TTG
C913_Ouest_2   ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAATTCT-CCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCACTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGA----------TTG
C916_Ouest_1   ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAATTCT-CCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCACTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGAGAGAGA----------TTG
C916_Ouest_2   ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAATTCT-CCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCACTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGAGAGAGA----------TTG
C921_Ouest_1   ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAATTCT-CCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCACTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGAGAGAGA----------TTG
S252_Ouest_1   ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAATTCT-CCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCACTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGA----------TTG
S252_Ouest_2   ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAATTCT-CCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCACTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGA----------TTG
S256_Ouest_1   ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAATTCT-CCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCACTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGA----------TTG
S256_Ouest_2   ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAATTCT-CCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCACTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGA----------TTG
S258_Ouest_1   ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAATTCT-CCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCACTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGAGAGAGA----------TTG
S258_Ouest_2   ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAATTCT-CCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCACTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGA----------TTG
S260_Ouest_1   ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAATTCT-CCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCACTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGA----------TTG
S260_Ouest_2   ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAATTCT-CCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCACTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGA----------TTG
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S263_Ouest_1   ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAATTCT-CCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCACTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGA----------TTG
S263_Ouest_2   ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAATTCT-CCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCACTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGA----------TTG
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S264_Ouest_2   ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAATTCT-CCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCACTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGA----------TTG
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S270_Ouest_2   ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAATTCT-CCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCACTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGA----------TTG
S274_Ouest_1   ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCGCTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGAGAGAGA----------TTG
S274_Ouest_2   ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAATTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCACTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGAGAGAGAGA----------TTG
S295_Ouest_1   ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAACTCTTCCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCACTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGAGA----------TTG
OUT192_Bre_1   ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAATTCT-CCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCACTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGA----------TTG
OUT192_Bre_2   ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAATTCT-CCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCACTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGAGAGAGA----------TTG
OUT194_Bre_1   ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAATTCT-CCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCACTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGA----------TTG
OUT194_Bre_2   ACAC-GTAACCTCCTCCTTCCATTACCCCCTCTAATTCT-CCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCACTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGAGAGAGA----------TTG
OUT198_Bre_1   ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAATTCT-CCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCACTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGA----------TTG
OUT198_Bre_2   ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAATTCT-CCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCACTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGAGAGAGA----------TTG
OUT204_Bre_1   ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAATTCT-CCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCACTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGA----------TTG
OUT204_Bre_2   ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAATTCT-CCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCACTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGAGAGAGA----------TTG
OUT213_Bre_1   ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAATTCT-CCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCACTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGAGAGAGA----------TTG
OUT213_Bre_2   ACAC-GTAACCTCCTCCTTCCATTACTCCTCTAATTCT-CCCCCACACCTCACTGCACTTAAAATGCGCAGTTGCGCACTCACTGTGTGTGCTTATATGT--GAGAGAGAGAGAGAGAGAGAGA----------TTG
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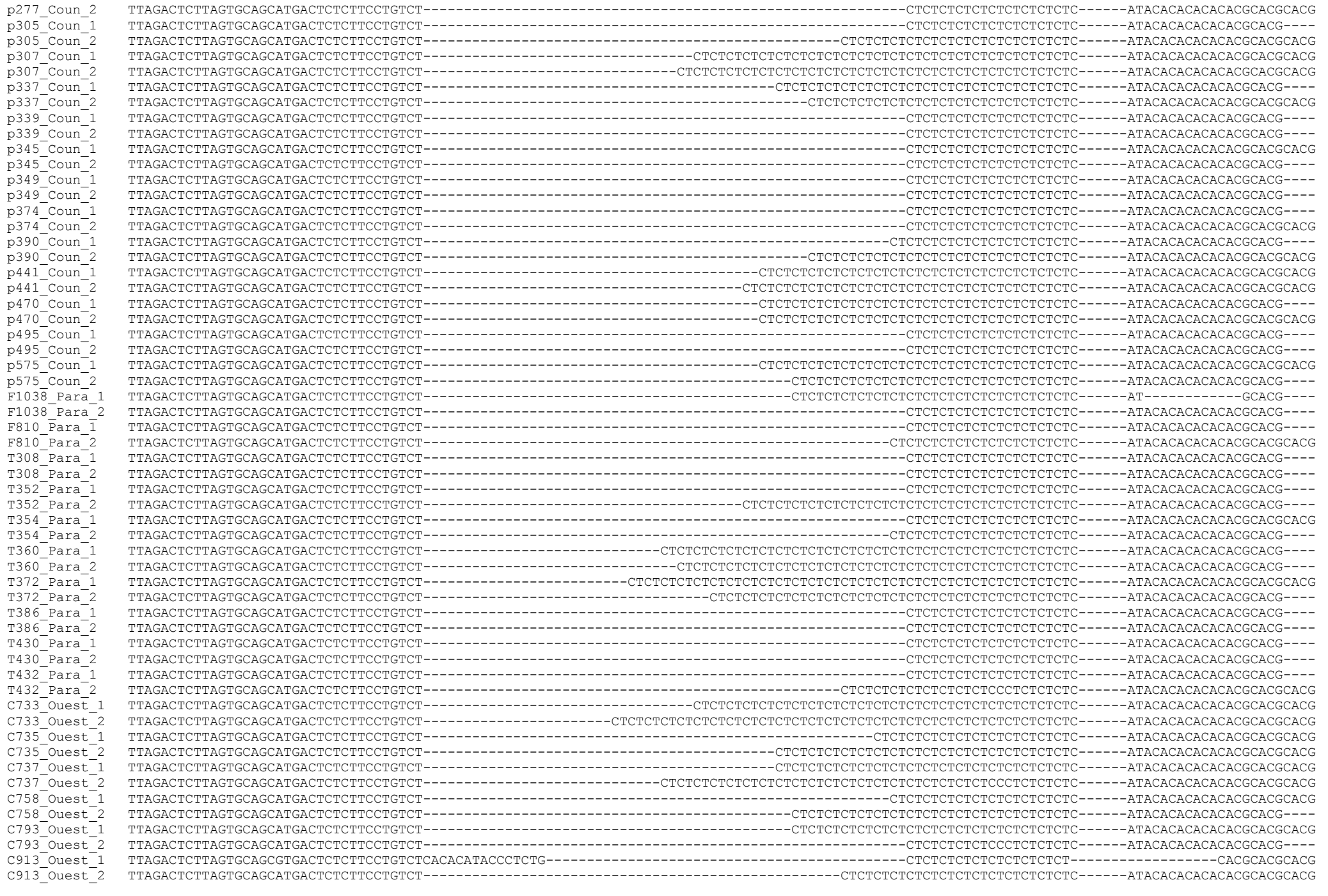
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