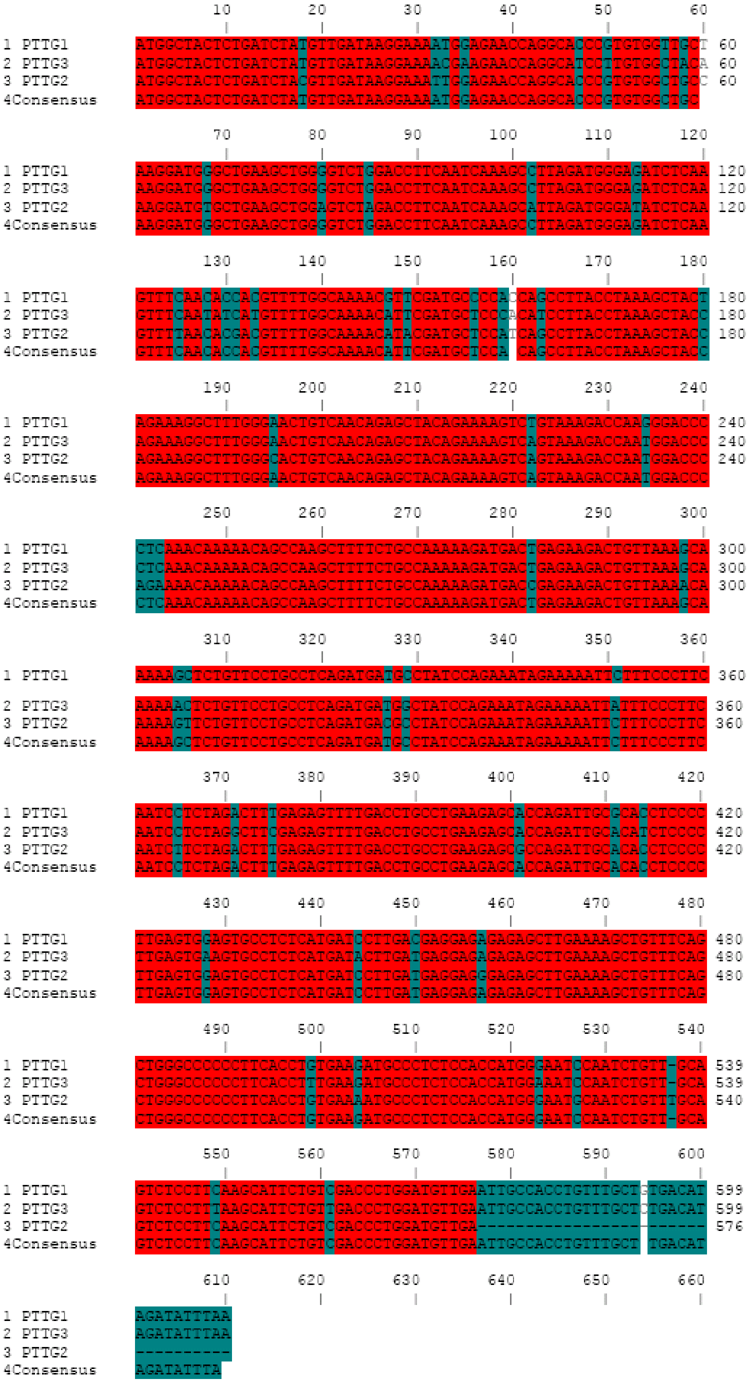

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                  10        20        30        40        50        60
                   |         |         |         |         |         |
1 PTTG1      ATGGCTACTCTGATCTATGTTGATAAGGAAAATGGAGAACCAGGCACCCGTGTGGTTGCT 60
2 PTTG3      ATGGCTACTCTGATCTATGTTGATAAGGAAAACGAAGAACCAGGCATCCTTGTGGCTACA 60
3 PTTG2      ATGGCTACTCTGATCTACGTTGATAAGGAAATTGGAGAACCAGGCACCCGTGTGGCTGCC 60
4Consensus   ATGGCTACTCTGATCTATGTTGATAAGGAAAATGGAGAACCAGGCACCCGTGTGGCTGC

                  70        80        90       100       110       120
                   |         |         |         |         |         |
1 PTTG1      AAGGATGGGCTGAAGCTGGGGTCTGGACCTTCAATCAAAGCCTTAGATGGGAGATCTCAA 120
2 PTTG3      AAGGATGGGCTGAAGCTGGGGTCTGGACCTTCAATCAAAGCCTTAGATGGGAGATCTCAA 120
3 PTTG2      AAGGATGTGCTGAAGCTGGAGTCTAGACCTTCAATCAAAGCATTAGATGGGATATCTCAA 120
4Consensus   AAGGATGGGCTGAAGCTGGGGTCTGGACCTTCAATCAAAGCCTTAGATGGGAGATCTCAA

                 130       140       150       160       170       180
                   |         |         |         |         |         |
1 PTTG1      GTTTCAACACCACGTTTTGGCAAAACGTTCGATGCCCCACCAGCCTTACCTAAAGCTACT 180
2 PTTG3      GTTTCAATATCATGTTTTGGCAAAACATTCGATGCTCCCACATCCTTACCTAAAGCTACC 180
3 PTTG2      GTTTTAACACGACGTTTTGGCAAAACATACGATGCTCCATCAGCCTTACCTAAAGCTACC 180
4Consensus   GTTTCAACACCACGTTTTGGCAAAACATTCGATGCTCCA CAGCCTTACCTAAAGCTACC

                 190       200       210       220       230       240
                   |         |         |         |         |         |
1 PTTG1      AGAAAGGCTTTGGGAACTGTCAACAGAGCTACAGAAAAGTCTGTAAAGACCAAGGGACCC 240
2 PTTG3      AGAAAGGCTTTGGGAACTGTCAACAGAGCTACAGAAAAGTCAGTAAAGACCAATGGACCC 240
3 PTTG2      AGAAAGGCTTTGGGCACTGTCAACAGAGCTACAGAAAAGTCAGTAAAGACCAATGGACCC 240
4Consensus   AGAAAGGCTTTGGGAACTGTCAACAGAGCTACAGAAAAGTCAGTAAAGACCAATGGACCC

                 250       260       270       280       290       300
                   |         |         |         |         |         |
1 PTTG1      CTCAAACAAAAACAGCCAAGCTTTTCTGCCAAAAAGATGACTGAGAAGACTGTTAAAGCA 300
2 PTTG3      CTCAAACAAAAACAGCCAAGCTTTTCTGCCAAAAAGATGACTGAGAAGACTGTTAAAGCA 300
3 PTTG2      AGAAAACAAAAACAGCCAAGCTTTTCTGCCAAAAAGATGACCGAGAAGACTGTTAAAACA 300
4Consensus   CTCAAACAAAAACAGCCAAGCTTTTCTGCCAAAAAGATGACTGAGAAGACTGTTAAAGCA

                 310       320       330       340       350       360
                   |         |         |         |         |         |
1 PTTG1      AAAAGCTCTGTTCCTGCCTCAGATGATGCCTATCCAGAAATAGAAAAATTCTTTCCCTTC 360

2 PTTG3      AAAAACTCTGTTCCTGCCTCAGATGATGGCTATCCAGAAATAGAAAAATTATTTCCCTTC 360
3 PTTG2      AAAAGTTCTGTTCCTGCCTCAGATGACGCCTATCCAGAAATAGAAAAATTCTTTCCCTTC 360
4Consensus   AAAAGCTCTGTTCCTGCCTCAGATGATGCCTATCCAGAAATAGAAAAATTCTTTCCCTTC

                 370       380       390       400       410       420
                   |         |         |         |         |         |
1 PTTG1      AATCCTCTAGACTTTGAGAGTTTTGACCTGCCTGAAGAGCACCAGATTGCGCACCTCCCC 420
2 PTTG3      AATCCTCTAGGCTTCGAGAGTTTTGACCTGCCTGAAGAGCACCAGATTGCACATCTCCCC 420
3 PTTG2      AATCTTCTAGACTTTGAGAGTTTTGACCTGCCTGAAGAGCGCCAGATTGCACACCTCCCC 420
4Consensus   AATCCTCTAGACTTTGAGAGTTTTGACCTGCCTGAAGAGCACCAGATTGCACACCTCCCC

                 430       440       450       460       470       480
                   |         |         |         |         |         |
1 PTTG1      TTGAGTGGAGTGCCTCTCATGATCCTTGACGAGGAGAGAGAGCTTGAAAAGCTGTTTCAG 480
2 PTTG3      TTGAGTGAAGTGCCTCTCATGATACTTGATGAGGAGAGAGAGCTTGAAAAGCTGTTTCAG 480
3 PTTG2      TTGAGTGGAGTGCCTCTCATGATCCTTGATGAGGAGGGAGAGCTTGAAAAGCTGTTTCAG 480
4Consensus   TTGAGTGGAGTGCCTCTCATGATCCTTGATGAGGAGAGAGAGCTTGAAAAGCTGTTTCAG

                 490       500       510       520       530       540
                   |         |         |         |         |         |
1 PTTG1      CTGGGCCCCCCTTCACCTGTGAAGATGCCCTCTCCACCATGGGAATCCAATCTGTT-GCA 539
2 PTTG3      CTGGGCCCCCCTTCACCTTTGAAGATGCCCTCTCCACCATGGAAATCCAATCTGTT-GCA 539
3 PTTG2      CTGGGCCCCCCTTCACCTGTGAAAATGCCCTCTCCACCATGGGAATGCAATCTGTTTGCA 540
4Consensus   CTGGGCCCCCCTTCACCTGTGAAGATGCCCTCTCCACCATGGGAATCCAATCTGTT-GCA

                 550       560       570       580       590       600
                   |         |         |         |         |         |
1 PTTG1      GTCTCCTTCAAGCATTCTGTCGACCCTGGATGTTGAATTGCCACCTGTTTGCTGTGACAT 599
2 PTTG3      GTCTCCTTTAAGCATTCTGTTGACCCTGGATGTTGAATTGCCACCTGTTTGCTCTGACAT 599
3 PTTG2      GTCTCCTTCAAGCATTCTGTCGACCCTGGATGTTGA------------------------ 576
4Consensus   GTCTCCTTCAAGCATTCTGTCGACCCTGGATGTTGAATTGCCACCTGTTTGCT TGACAT

                 610       620       630       640       650       660
                   |         |         |         |         |         |
1 PTTG1      AGATATTTAA
2 PTTG3      AGATATTTAA
3 PTTG2      ----------
4Consensus   AGATATTTA
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