

PA01 GCGGCACTGAATCGCCTCGCGCCGGA<<Insertion1>>ACGAGCAGCCTGGCGCGCAGAAACGAAA

C3719 GCGGCACTAAGCCCGCCACGGCCACC<<Insertion1>>CAGGGCGGTGCGGATCGCAGAAACGAAA

PA14
PACS2 GCGGCACTGAGCCCGCCACGGCCACC<<Insertion1>>CAGGGCGGTGCGGATCGCAGAAACGAAA

GCGGCACTGAGCCCGCCACGGCCACC<<Insertion1>>CAGGGCGGTGCGGATCGCAGAAACGAAA

AAAGGGCCCGAAGGCCCTTTTCTTTCGACCCAGGCCGAAACCTGGATCATGTTTGGAGCGGGAAACG

PA2192 GGACAAACCTTTTCCGCGTATCTCCTTGATTCAACAAAG<<DiTIsland>>TCCCAGGGCTAAAC

CCTGTTGAATCAAGAATCTATAGACTTTGGTGGACGTCTATAGATGAAGAAATTGGAGCGGGAGACGAG

TCATGCACTAGAGCGCTAAG<<PAGI_2>>TTCCGTGGCTTTGGCTGGAATGAAAAAAGGGGCCGAAG

CCCCTAATTTCAATGACTTACAGACGTCAGTGGAAAGTCTGTAGATCAAACTTGGAGCGGGAAACGAG

