Having trouble deciding on current Genes 42 and 43 in Phage MrMiyagi. These two apparently have overlapping ORFs. No CP seen in GeneMark-smeg & TB, but strong coding potential for both in GeneMarkS. Start for gp 43 (45 in pharmerator) called by GL & in Cuke & Fowlmouth; staterator; SSC: 35734; Z= 1.676, F= -6.512; spacer distance 16; with 6 bp overlap; we were selecting the start at 35716, Z= 2.487, F= -5.050, 26 bp overlap with gene 42 (44 in phamerator); with a shorter spacer distance of 5, but realize this gene 43 ORF is continuous from 35449 bp (Z= 2.018, F= -5.536; the next start is with a better RBS at 35572 bp with Z= 2.673, F= -3.504). The short gene 43 (45 in phamerator) apparently currently has only 3 members in the pham 32826; compared to 44 which has 61 members (pharm 40615). Start for gene 42 (44 in phamerator) is inside CP plateau, hence not covering all CP, but it’s the 1st one; see CP figure attached.

Since there is no break/stop codon in the ORF for gene 43(45 in phamerator) and there’s strong RBS scores for the 1st and 3rd starts which are overlapping gene 42 (44 in phamerator) is there no chance that this is the same gene? Should I delete 42 (44 in phamerator) and take the start at 35572 bp with Z= 2.673, F= -3.504, or should I just overlook this, keep gene 42 (44 in phamerator) and take the start called by GL at 35734; z= 1.676, F= -6.512 and in Cuke & Fowlmouth 6bp overlap, or the one I am considering with a better RBS score at 35716, Z= 2.487, F= -5.050, 26 bp overlap? Please advise.







