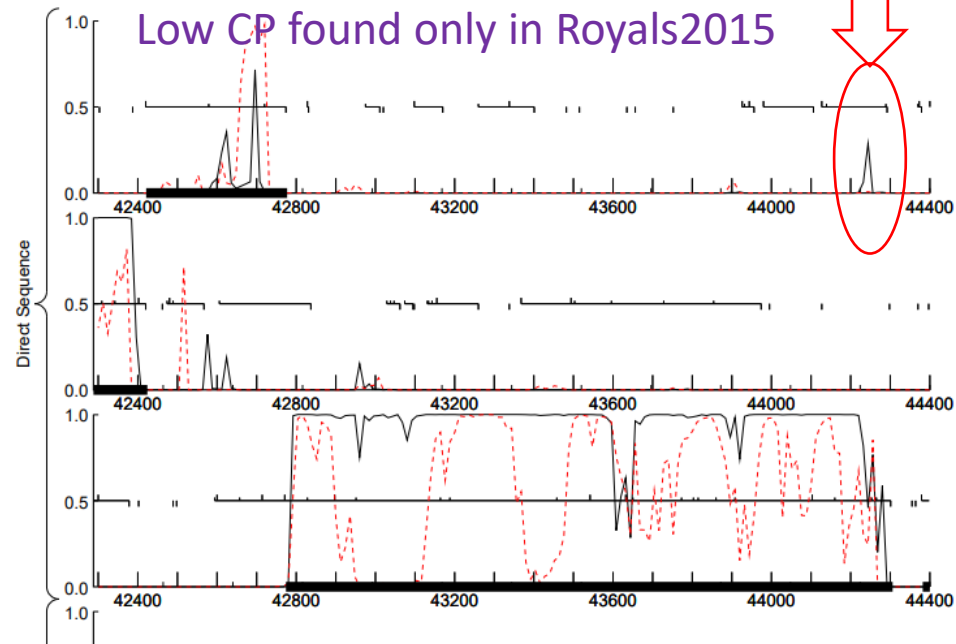complete sequence, 57356 bp including 10-base 3' overhang (CGGAAGGCGC), Cluster F1, Order 4, Window 96, Step 12, 22/29

GeneMark.hmm prediction

complete sequence, 57356 bp including 10-base 3' overhang (CGGAAGGCGC), Cluster F1, Order 2, Window 96, Step 12, 22/29

Low CP found only in Royals2015

Direct Sequence

Sequences producing significant alignments:

	Score (bits)	E Value
Zilizebeth_64, function unknown, 27	57	2e-08
Royals2015_70, function unknown, 27	57	2e-08
HUHilltop_56, function unknown, 27	57	2e-08
Malithi_54, function unknown, 262	39	0.003
Camster_55, function unknown, 262	39	0.003
Techage_59, function unknown, 262	28	5.7

>Zilizebeth_64, function unknown, 27
        Length = 27

 Score = 56.6 bits (135), Expect = 2e-08
 Identities = 27/27 (100%), Positives = 27/27 (100%)

Query: 1 MTDFLGATIRIVAQIGFPTVNPIEVMR 27
          MTDFLGATIRIVAQIGFPTVNPIEVMR
Sbjct: 1 MTDFLGATIRIVAQIGFPTVNPIEVMR 27

< Previous Gene   Next Gene >

Details for gene Royals2015_70

Phage	Royals2015 · Cluster F · 57356 bp
Gene	Royals2015_70
Pham (click for Pham view →)	108105
Starterator	Pham 108105 report
Genome Position	44299 to 44382 (Forward)
Length	84 base pairs / 27 amino acids
Amino Acid Sequence	Click to View
Notes	

Members (3) of Pham 108105

HUHilltop_56	Royals2015_70
Zilizebeth_64	

Insert this gene?