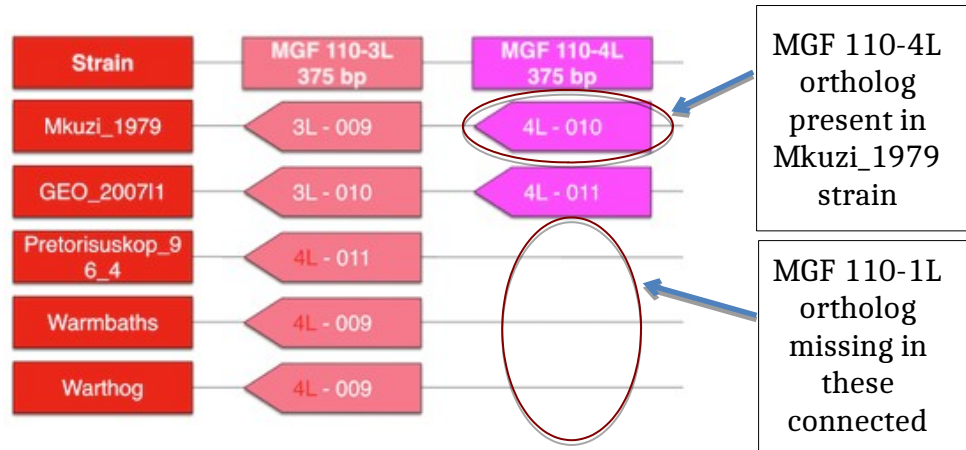


MGF Compilation Figure Legend



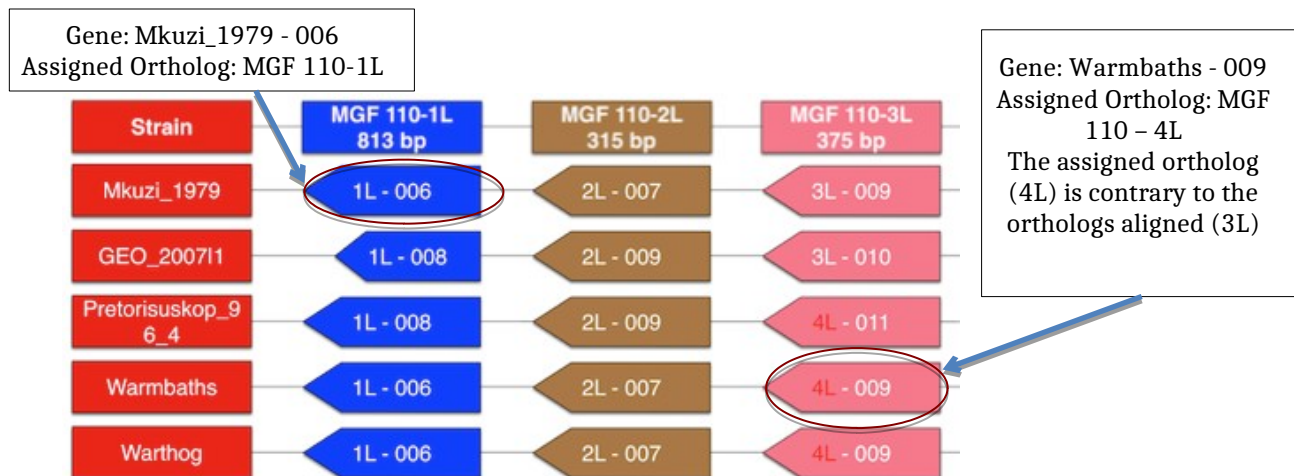
Ortholog columns and gene size

All genes of same width as the heading are approximately the length of the reference length stated.



Genes:

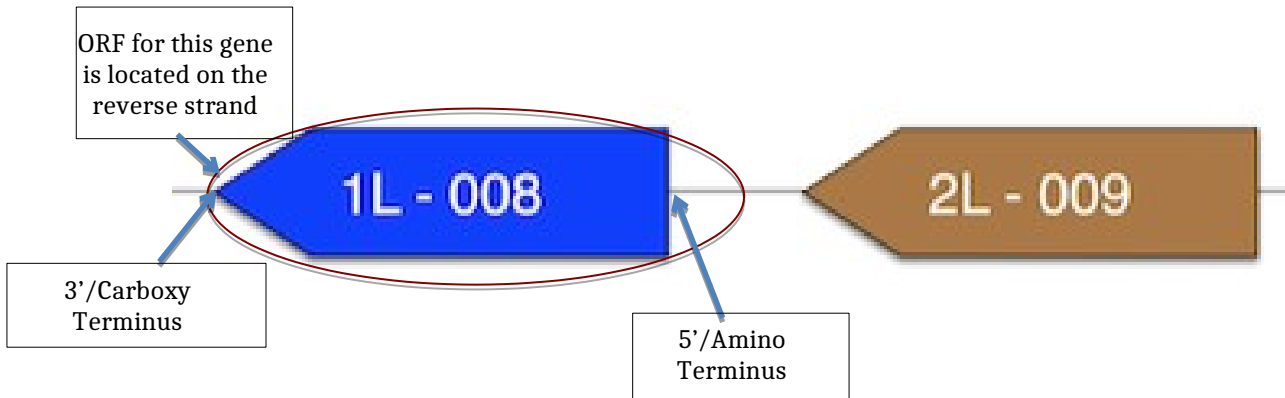
The above figure indicates MGF 110-4L ortholog is missing in strains Pretorisuskop_96_4, Warmbaths, and Warthog, but present in Mkuzi_1979 and GEO_2007|1.



Gene labels:

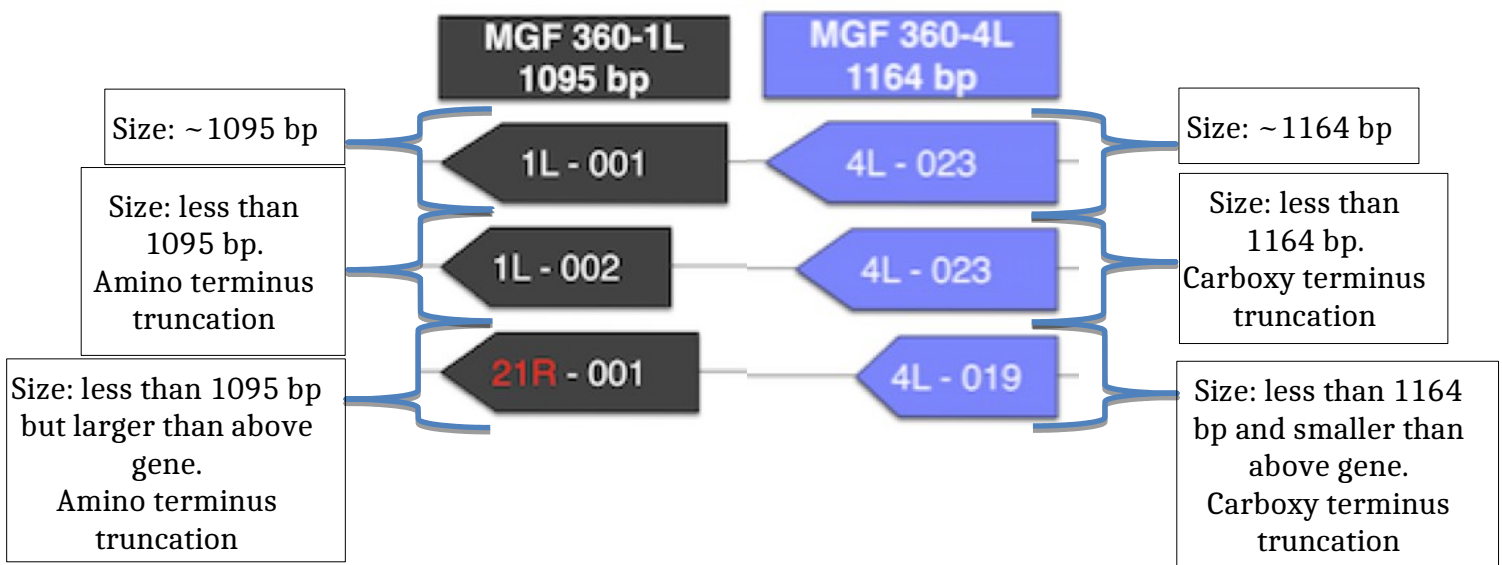
The annotation of each gene is in two parts: first, the ortholog group originally assigned during initial annotation, followed by the corresponding gene number of the connected strain. If the currently assigned ortholog group is labelled in red, this indicates that the currently assigned ortholog is contrary to orthologs it aligns to within this diagram.

MGF Compilation Figure Legend



Gene Orientation:

The ASFV MGF series has “R” orthologs that are transcribed on the forward strand (5' → 3') and “L” orthologs that are transcribed on the reverse strand (3' ← 5'). “R” gene boxes are pointed to the right and “L” gene boxes are pointed to the left.



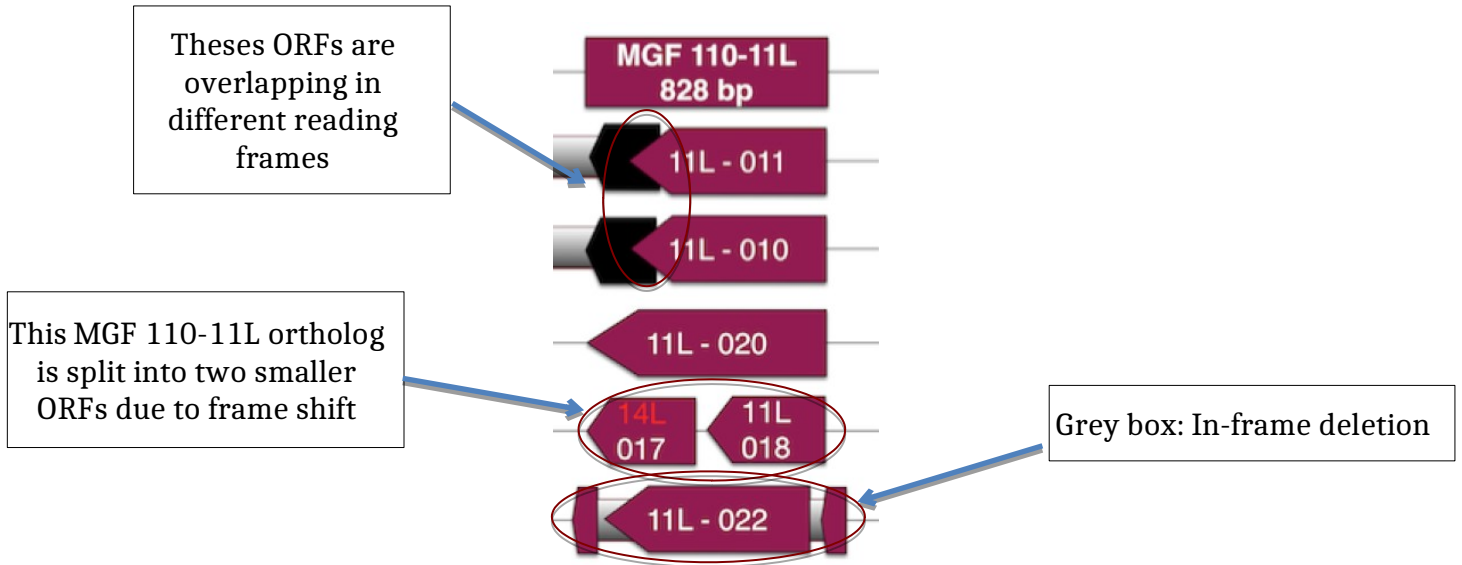
Relative gene size and truncations:

A smaller or larger gene box indicates the size difference of the gene relative to other genes of the same ortholog

A 5'/amino terminus that is not aligned with the amino terminus of the full-length genes indicates an amino terminus truncation of this gene.

A 3'/carboxy terminus that is not aligned with the carboxy terminus of the full-length genes indicates a carboxy terminus truncation of this gene.

MGF Compilation Figure Legend

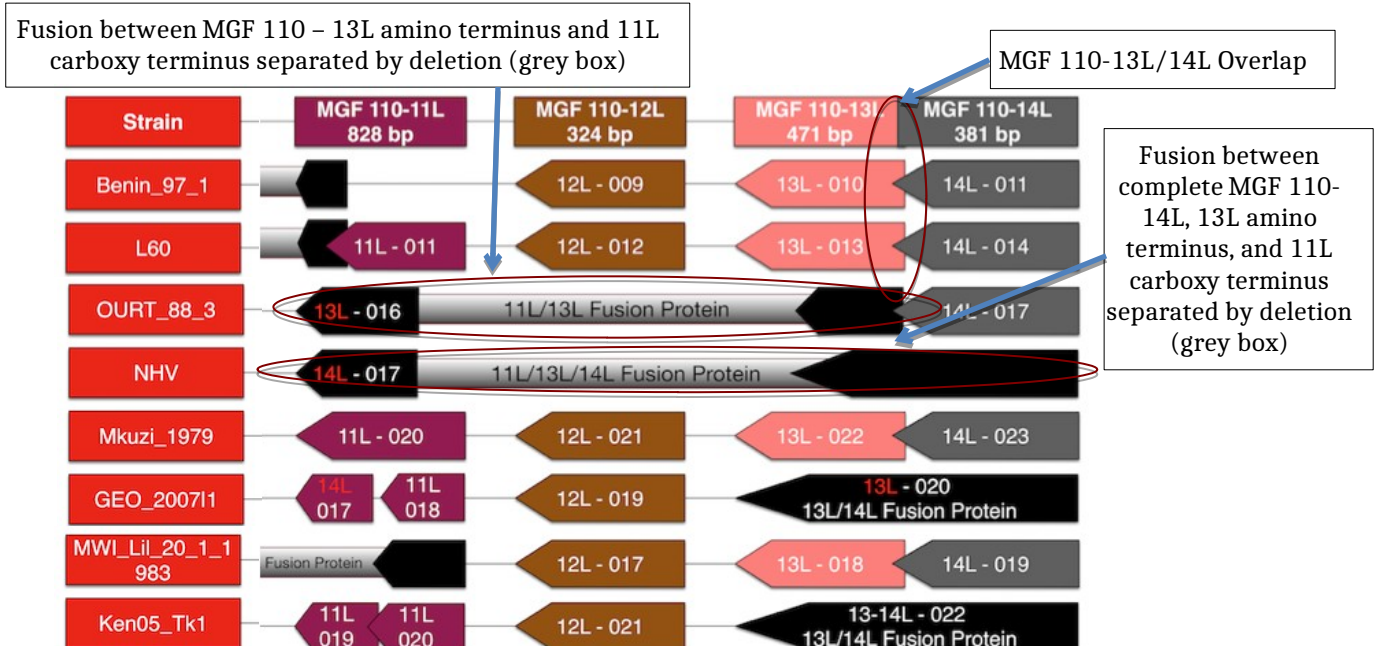


Special Note Gene Features:

The 5' end of the ORF for the top two 11L genes overlaps with the 3' end of the ORF for L60-011 in different reading frames.

The fragmentation of an ortholog into two smaller ORFs is represented by two smaller gene boxes underneath a single heading.

For the bottom most 11L ortholog showed in the above diagram is showed to have several large in-frame deletions in the gene when compared to the aligned genomes.



MGF Fusion:

Genes encoded by an open reading frame that aligns across multiple ortholog loci due to genomic deletions are labelled in the above diagram as "fusion" genes and are represented by black gene boxes. The size and alignment of the black gene

MGF Compilation Figure Legend

boxes to a given ortholog group is representative of how much of the ortholog is fused and which region.

The fused ortholog groups are labelled along the deletion box connecting the fragments.

The absence of a deletion box in a gene fusion indicates that the deletion that connects the two ORFs is only a few base pairs that would be too small to resolve on this diagram.