MGF 100 Figure Legend

MGF 100 ortholog group

Approximate size of genes with this ortholog

| MGF 100-2L 426 bp | MGF 100-3L 441 bp |

Ortholog columns and gene size:

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

MGF 100-1R ortholog present in OURT_88_3 strain

MGF 100-1R ortholog missing in these strains

| Strain	MGF 100-1R 375 bp	MGF 100-2L 426 bp
Benin_97_1		2L - 146
L60		2L - 152
E75		2L - 151
BA71V		2L - 143
OURT_88_3	1R - 014	2L - 146
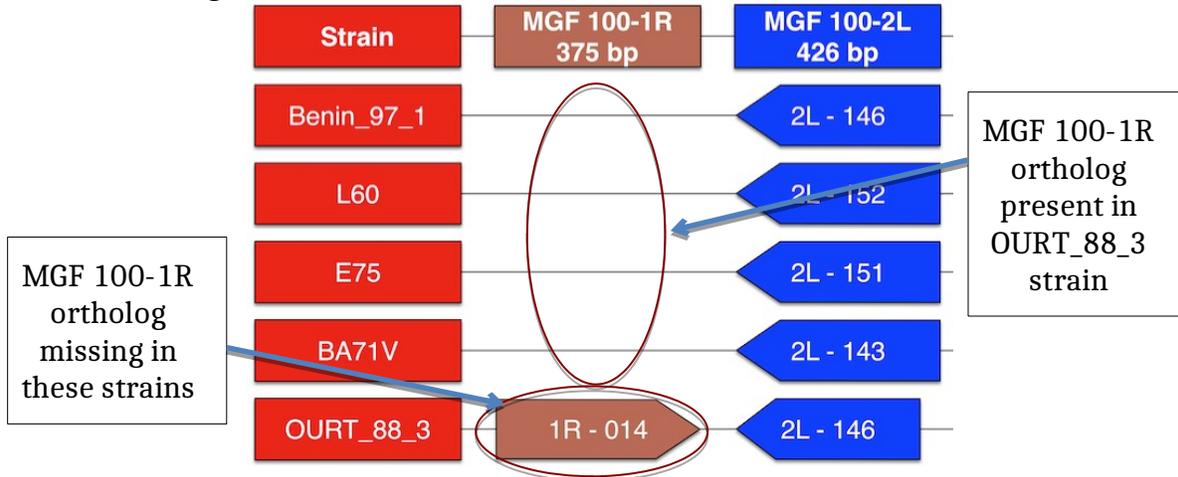
Genes:

The above figure indicates MGF 100-1R ortholog is missing in strains Benin_97_1, L60, E75, and BA71V but is present in strain OURT_88_3.

Gene: Mkuzi_1979 – 018
Assigned Ortholog: MGF 100 – 1R

Gene: GEO_2007|1 – 157
Assigned Ortholog: MGF 100 – 1R
The assigned ortholog (1R) is contrary to the orthologs aligned (2L)

Strain	MGF 100-1R 375 bp	MGF 100-2L 426 bp
Mkuzi_1979	1R - 018	2L - 163
GEO_2007l1	1R - 015	1R - 157
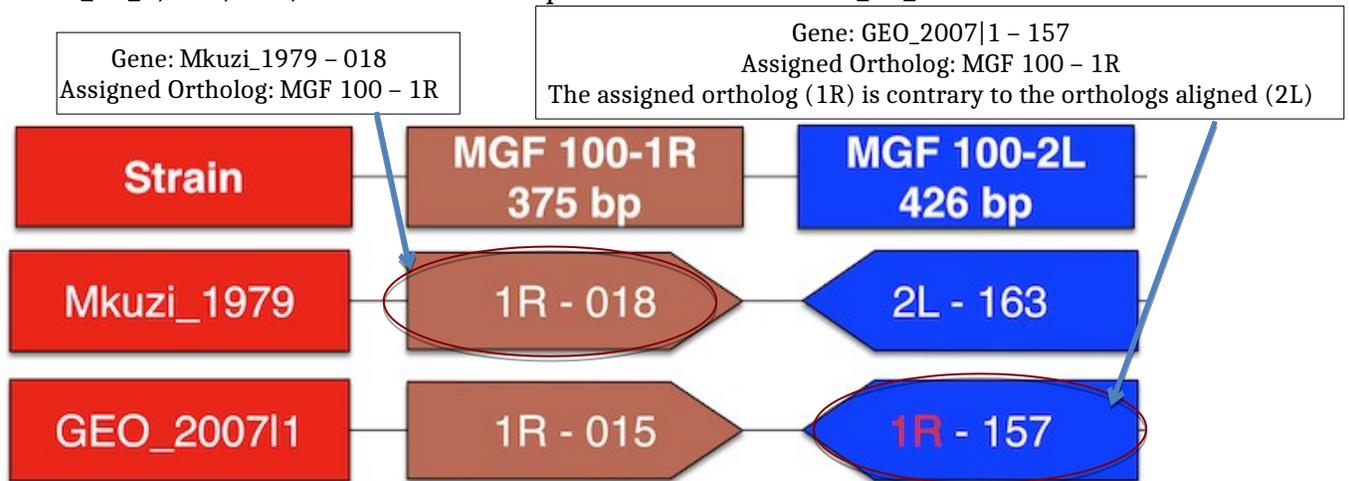
Gene labels:

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 100 Figure Legend

ORF for this gene is located on the forward strand

ORF for this gene is located on the reverse strand

5'/Amino Terminus

3'/Carboxy Terminus

5'/Amino Terminus
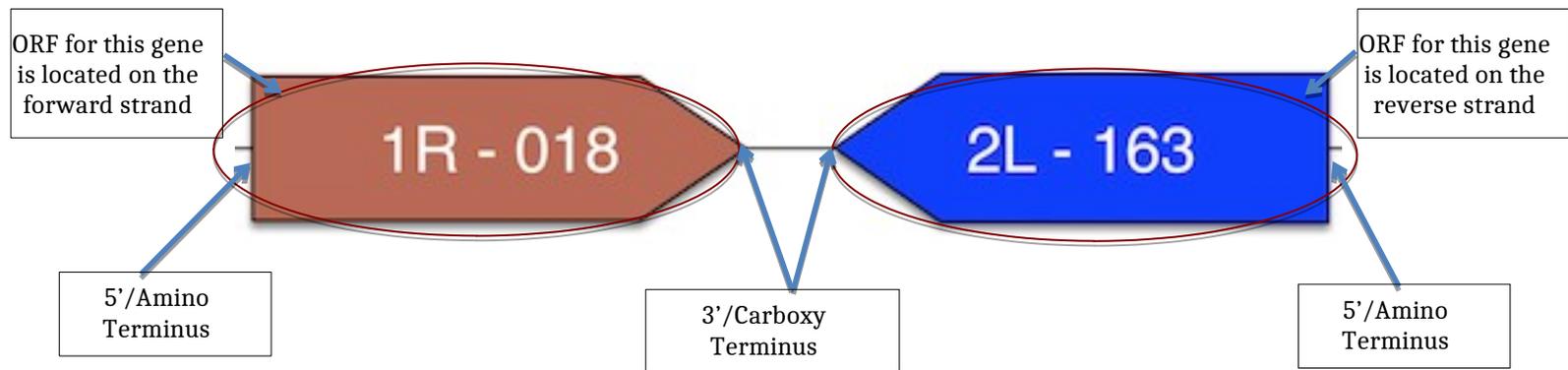
Gene Orientation:

MGF 100 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.

Size: ~426 bp

Size: ~441 bp

Size: less than 426 bp. Amino terminus truncation

Size: less than 441 bp. Carboxy terminus truncation
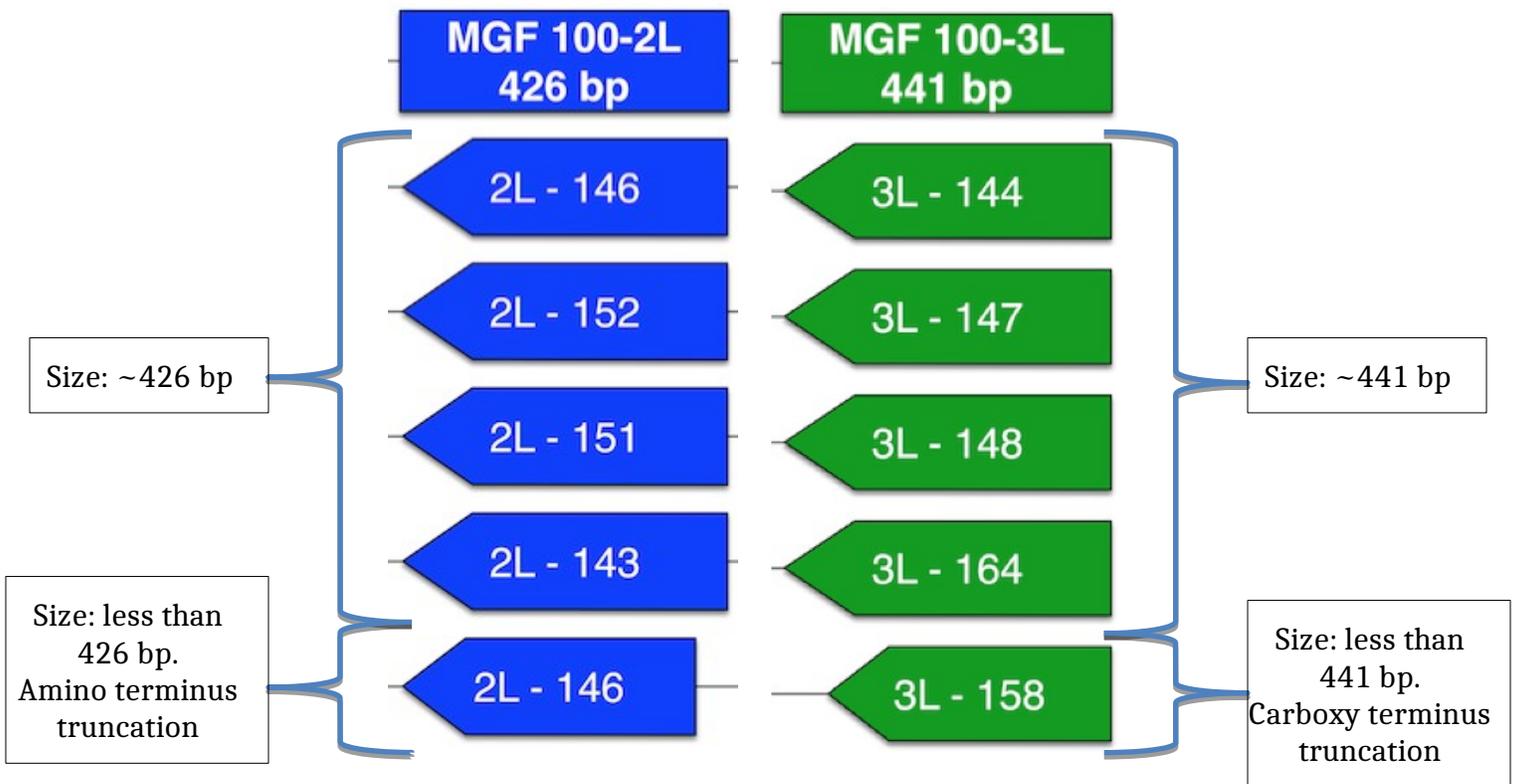
Relative gene size and truncations:

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.