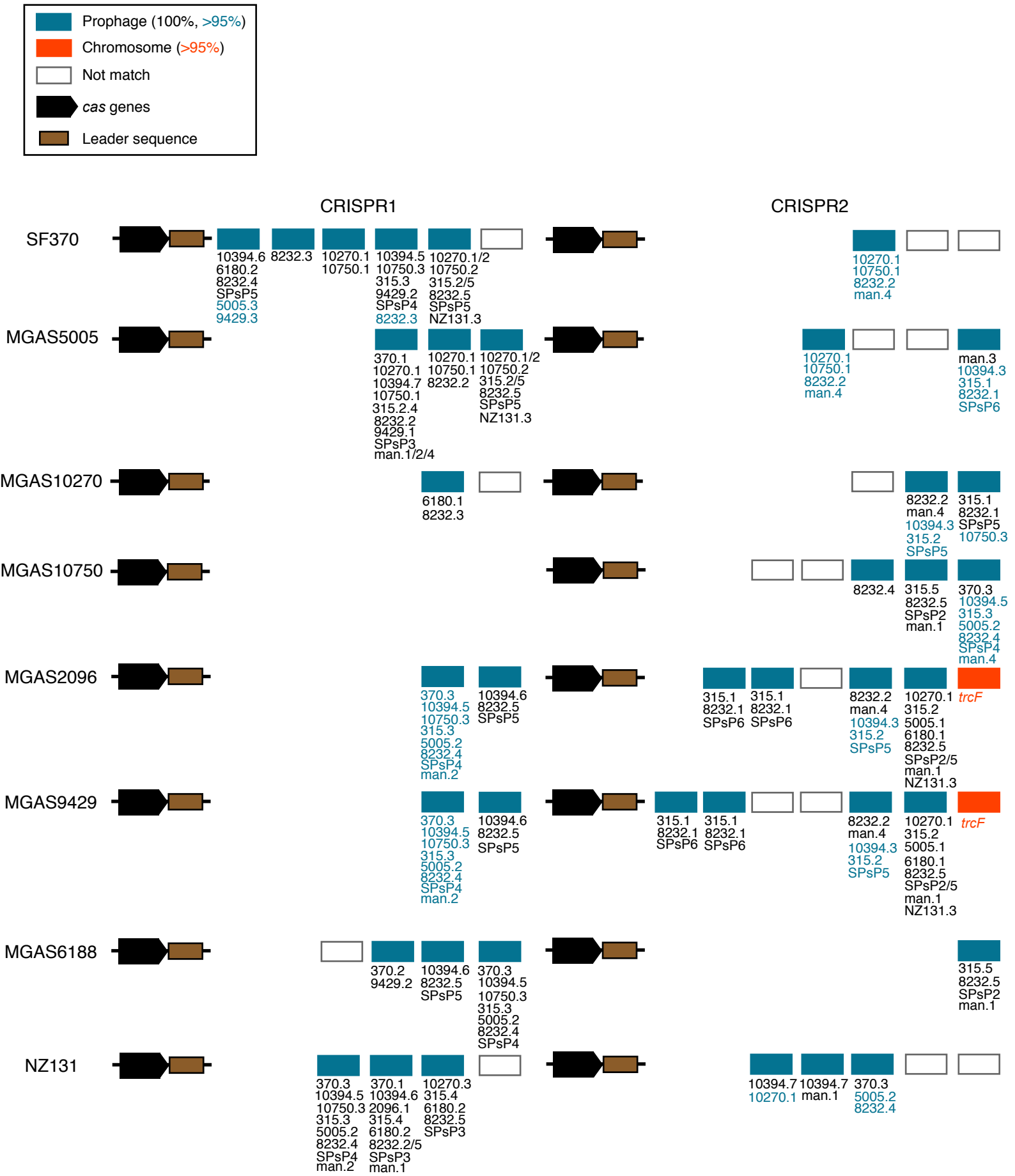
Prophage (100%, >95%)
Chromosome (>95%)
Not match
cas genes
Leader sequence
CRISPR1
CRISPR2
SF370
10394.6 6180.2 8232.4 SPsP5 5005.3 9429.3
8232.3
10270.1 10750.1
10394.5 10750.3 315.3 9429.2 SPsP4 8232.3
10270.1/2 10750.2 315.2/5 8232.5 SPsP5 NZ131.3
10270.1 10750.1 8232.2 man.4
MGAS5005
370.1 10270.1 10394.7 10750.1 315.2.4 8232.2 9429.1 SPsP3 man.1/2/4
10270.1 10750.1 8232.2
10270.1/2 10750.2 315.2/5 8232.5 SPsP5 NZ131.3
10270.1 10750.1 8232.2 man.4
man.3 10394.3 315.1 8232.1 SPsP6
MGAS10270
6180.1 8232.3
8232.2 man.4 10394.3 315.2 SPsP5
315.1 8232.1 SPsP5 10750.3
MGAS10750
8232.4
315.5 8232.5 SPsP2 man.1
370.3 10394.5 315.3 5005.2 8232.4 SPsP4 man.4
MGAS2096
370.3 10394.5 10750.3 315.3 5005.2 8232.4 SPsP4 man.2
10394.6 8232.5 SPsP5
315.1 8232.1 SPsP6
315.1 8232.1 SPsP6
8232.2 man.4 10394.3 315.2 SPsP5
10270.1 315.2 5005.1 6180.1 8232.5 SPsP2/5 man.1 NZ131.3
trcF
MGAS9429
370.3 10394.5 10750.3 315.3 5005.2 8232.4 SPsP4 man.2
10394.6 8232.5 SPsP5
315.1 8232.1 SPsP6
315.1 8232.1 SPsP6
8232.2 man.4 10394.3 315.2 SPsP5
10270.1 315.2 5005.1 6180.1 8232.5 SPsP2/5 man.1 NZ131.3
trcF
MGAS6188
370.2 9429.2
10394.6 8232.5 SPsP5
370.3 10394.5 10750.3 315.3 5005.2 8232.4 SPsP4
315.5 8232.5 SPsP2 man.1
NZ131
370.3 10394.5 10750.3 315.3 5005.2 8232.4 SPsP4 man.2
370.1 10394.6 2096.1 315.4 6180.2 8232.2/5 SPsP3 man.1
10270.3 315.4 6180.2 8232.5 SPsP3
10394.7 10270.1
10394.7 man.1
370.3 5005.2 8232.4