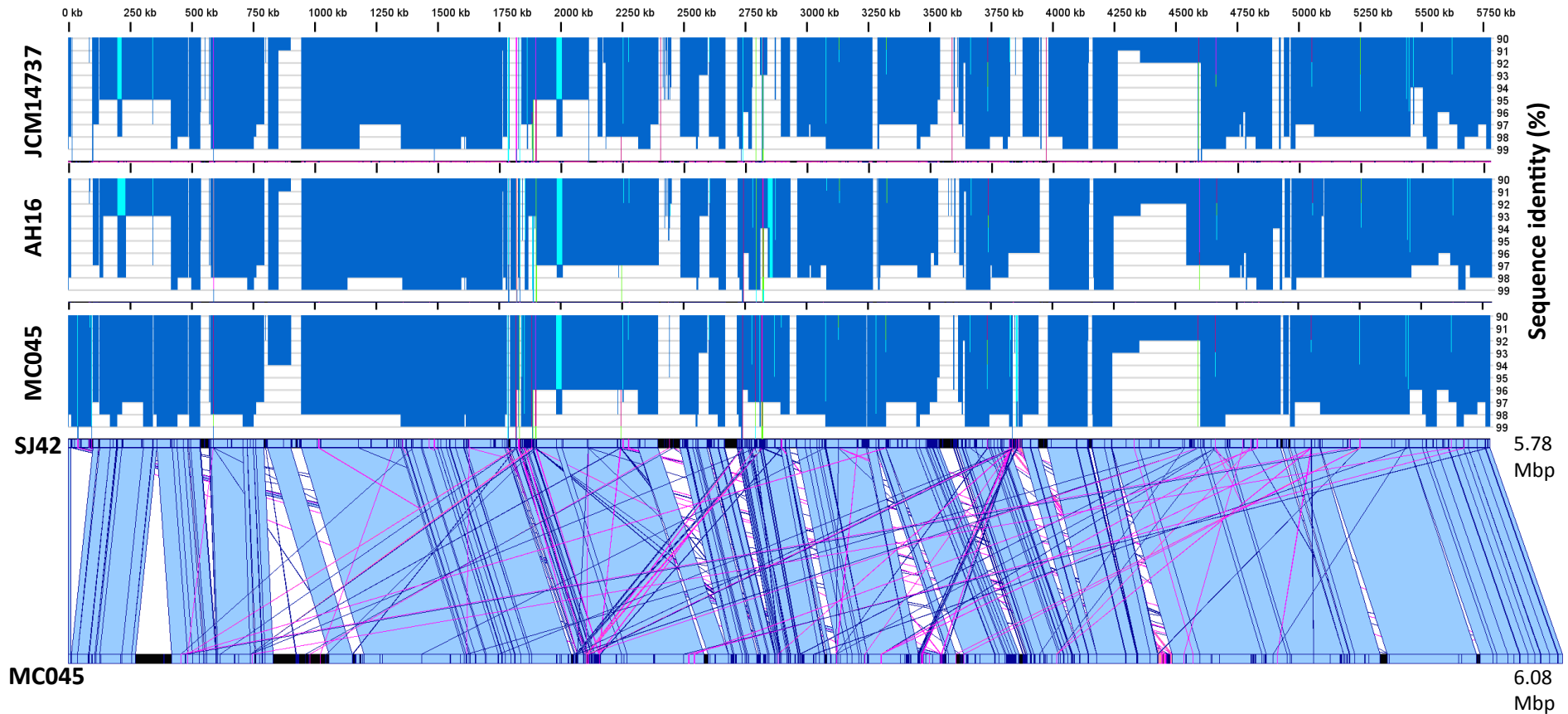


Synteny between SJ42 and complete *M. chimaera* genomes



Legend

Frequency Repeated

- 1X
- 2X
- 3X
- 4X
- 5X
- 6X
- 7X
- 8X and over

Collinear Blocks

- Direct
- Inverted

Other

- Mismatch threshold

Mismatch threshold 10
Minimum Block Length=50
Scale=1:2500
Wed Feb 15 13:45:59 PST 2017
XMatchView v0.2 :: rwarren@bcgsc.ca

SJ42 canu + LINKS + ragout	Genome Coverage (%)	Sequence Identity (%)
JCM14737	90.41	95.03
AH16	92.77	94.95
MC045	93.45	95.42