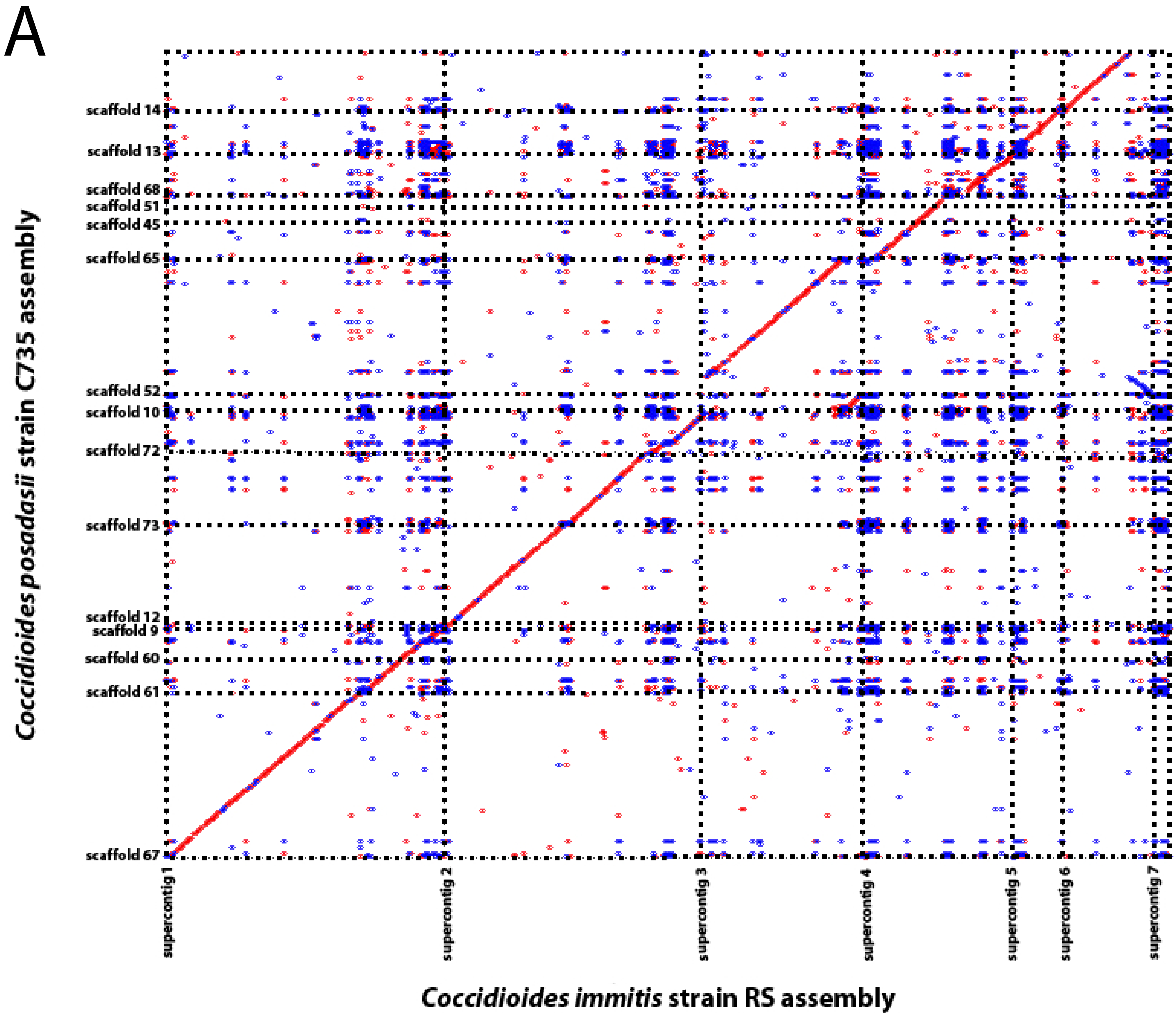
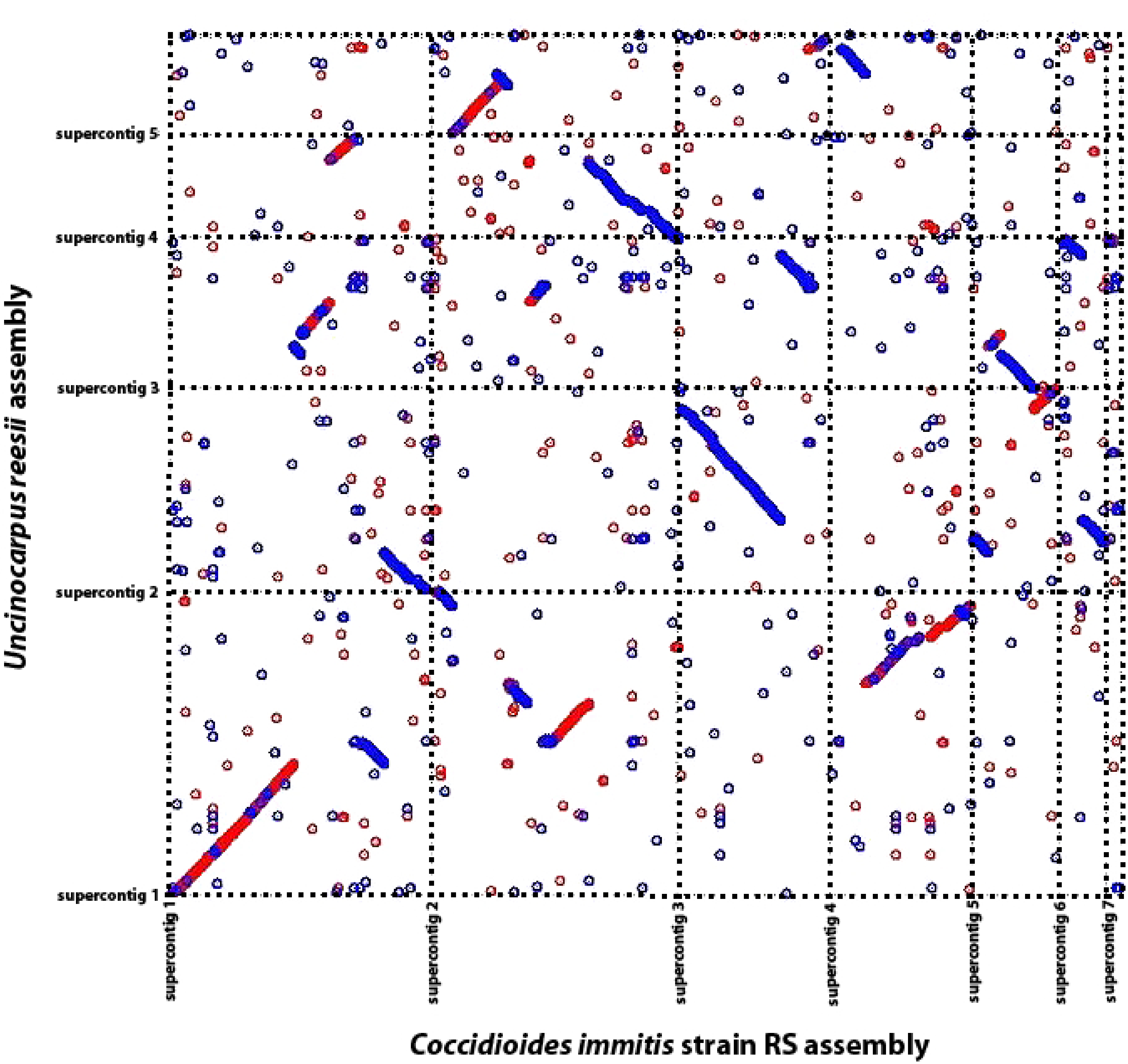
Figure SI2: Whole genome syntenic alignments

Dotplots generated via the MUMMER software package illustrate homologous regions between two genome sequenes. Dotted lines that intersect the axes represent contig boudaries. A) A NUCMER generated dot plot between the *C. immitis* (x-axis) and *C. posadasii* (y-axis) genomes. Only those C. posadasii contigs linked via the optical map were used in this analysis. B) A PROMER generated dot plot between the *C. immitis* (x-axis) and *U. reesii* (y-axis).


A
Coccidioides posadasii strain C735 assembly
scaffold 14
scaffold 13
scaffold 68
scaffold 51
scaffold 45
scaffold 65
scaffold 52
scaffold 10
scaffold 72
scaffold 73
scaffold 12
scaffold 9
scaffold 60
scaffold 61
scaffold 67
supercontig 1
supercontig 2
supercontig 3
supercontig 4
supercontig 5
supercontig 6
supercontig 7
Coccidioides immitis strain RS assembly


B
supercontig 5
supercontig 4
supercontig 3
supercontig 2
supercontig 1
Uncinocarpus reesii assembly
supercontig 1
supercontig 2
supercontig 3
supercontig 4
supercontig 5
supercontig 6
supercontig 7
Coccidioides immitis strain RS assembly