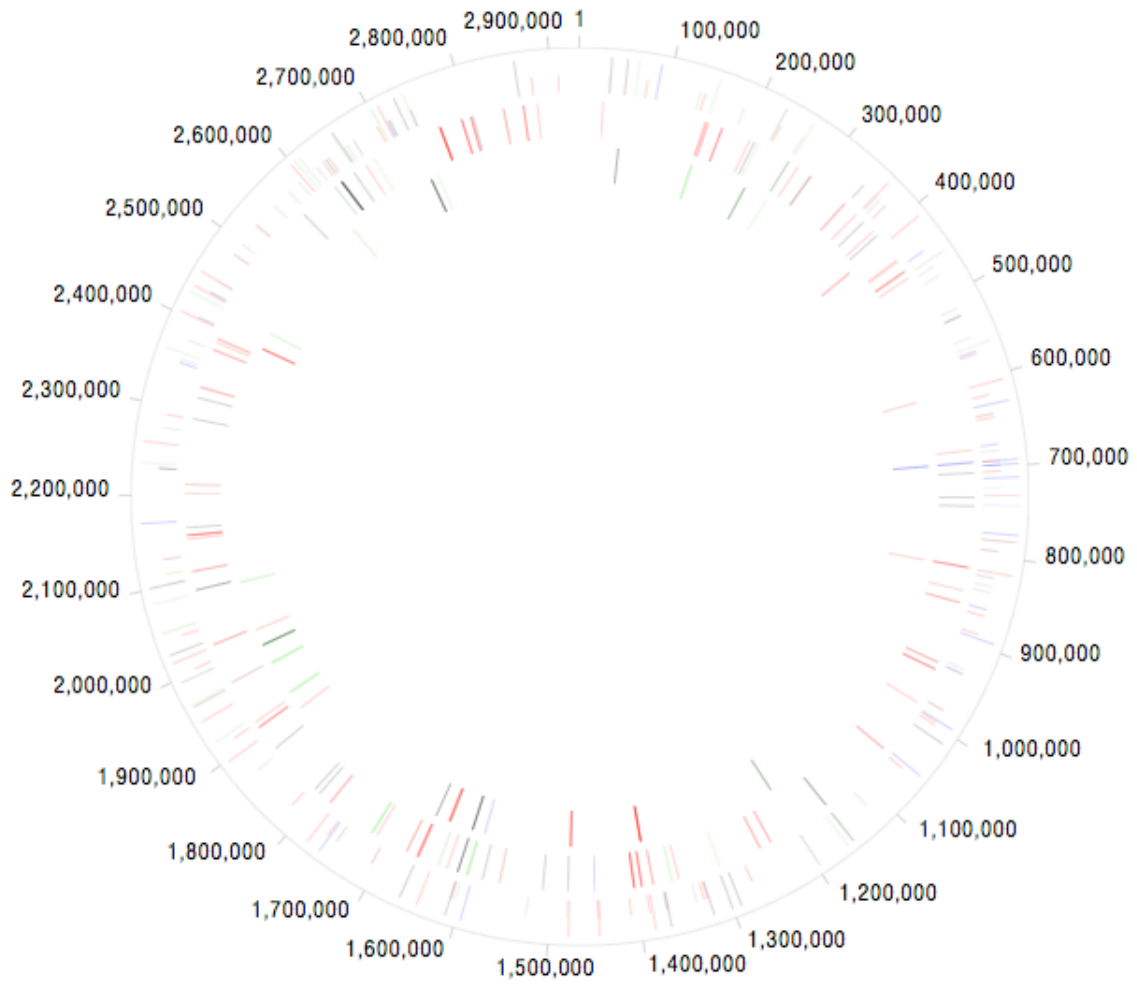


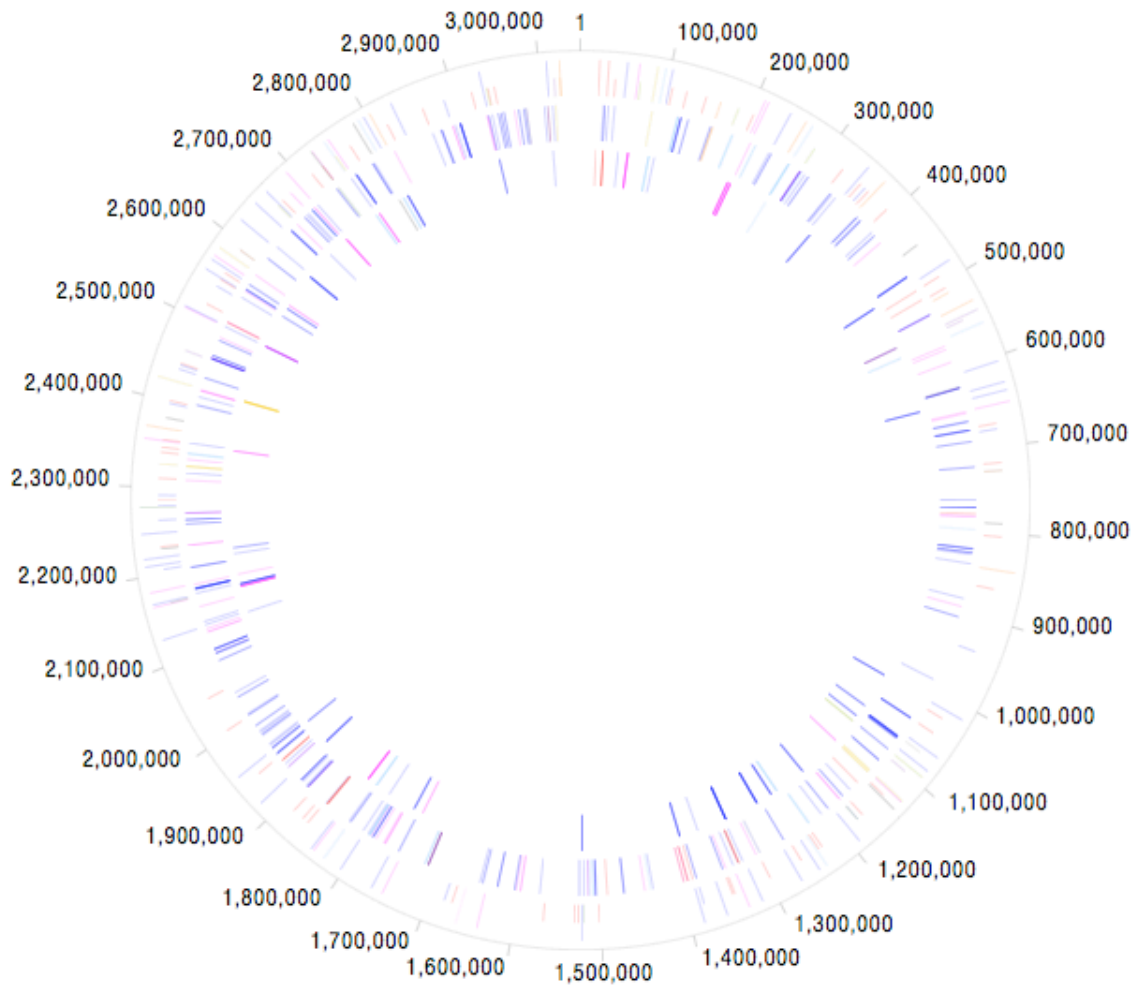
1 A



2

3

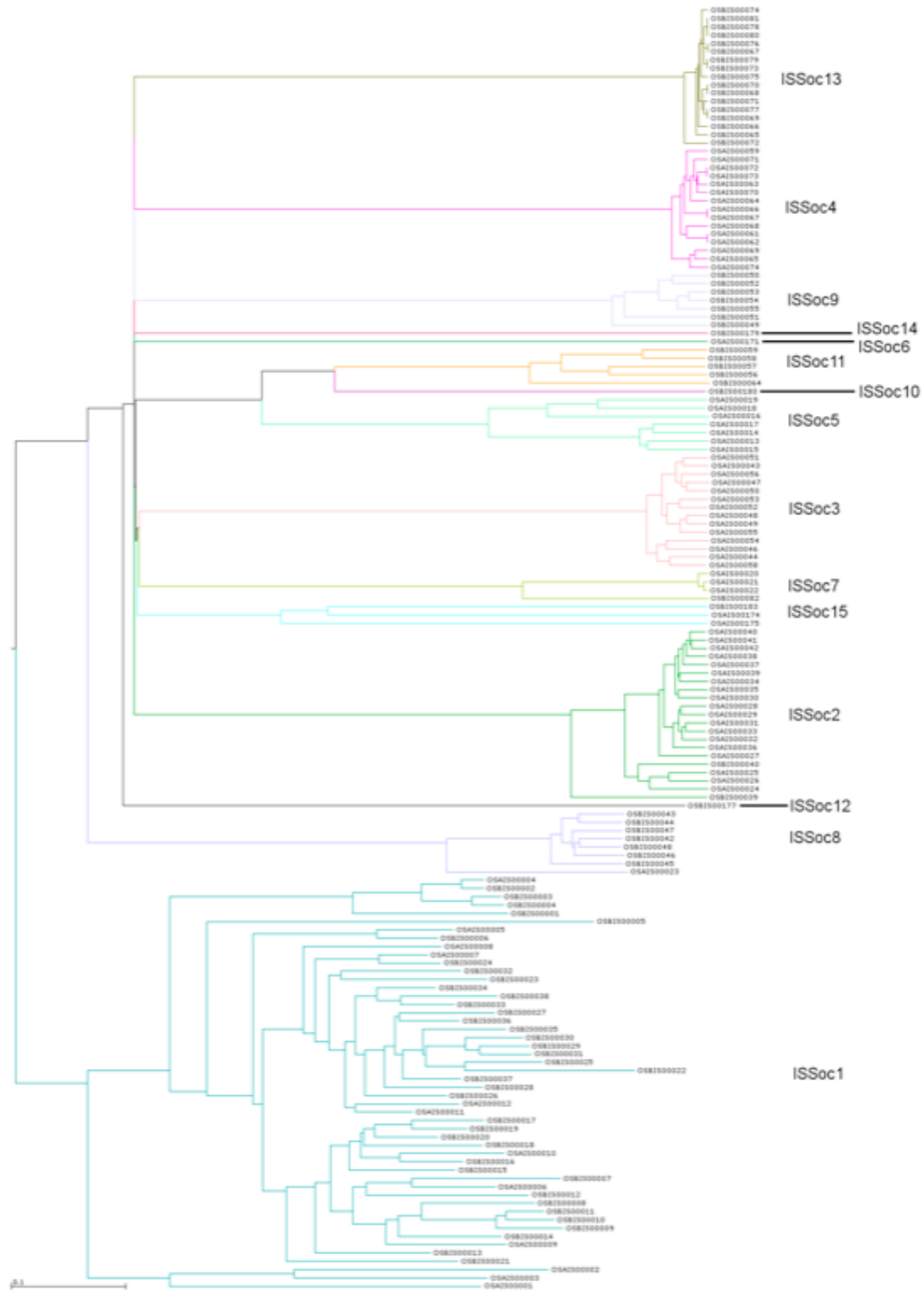
1 **B**



2

3 **Figure S1.** Genomic regions impacted by IS activity. **A** *Syn* OS-A; **B** *Syn* OS-B'. First  
4 ring (outermost): locations of ISs on the genome; *long bars*, full-length copies; *short*  
5 *bars*, truncated and fragmentary copies. Second ring: locations of IS insertion identified  
6 from metagenome read analysis. Third ring: locations of ISs absent from at least one  
7 metagenome read. ISSoc subfamilies are color coded: *blue* – ISSoc1, *red* – ISSoc2, *light*  
8 *green* – ISSoc3, *black* – ISSoc4, *brown* – ISSoc5, *gray* – ISSoc6, *dark green* – ISSoc7,  
9 *cyan* – ISSoc8, *orange* – ISSoc9, *violet* – ISSoc10, *gold* – ISSoc11, *blue-green* –  
10 ISSoc12, *magenta* – ISSoc13, *pink* – ISSoc14, *olive* – ISSoc15.

11



1

2 **Figure S2.** Phylogenetic tree defining ISSoc families. Neighbor-joining tree of full-  
 3 length ISSoc sequences from *Syn OS-A* and *Syn OS-B'*. Families are denoted by colored

- 1 branches and names to the right. See Materials and Methods for details of distance
- 2 calculation.