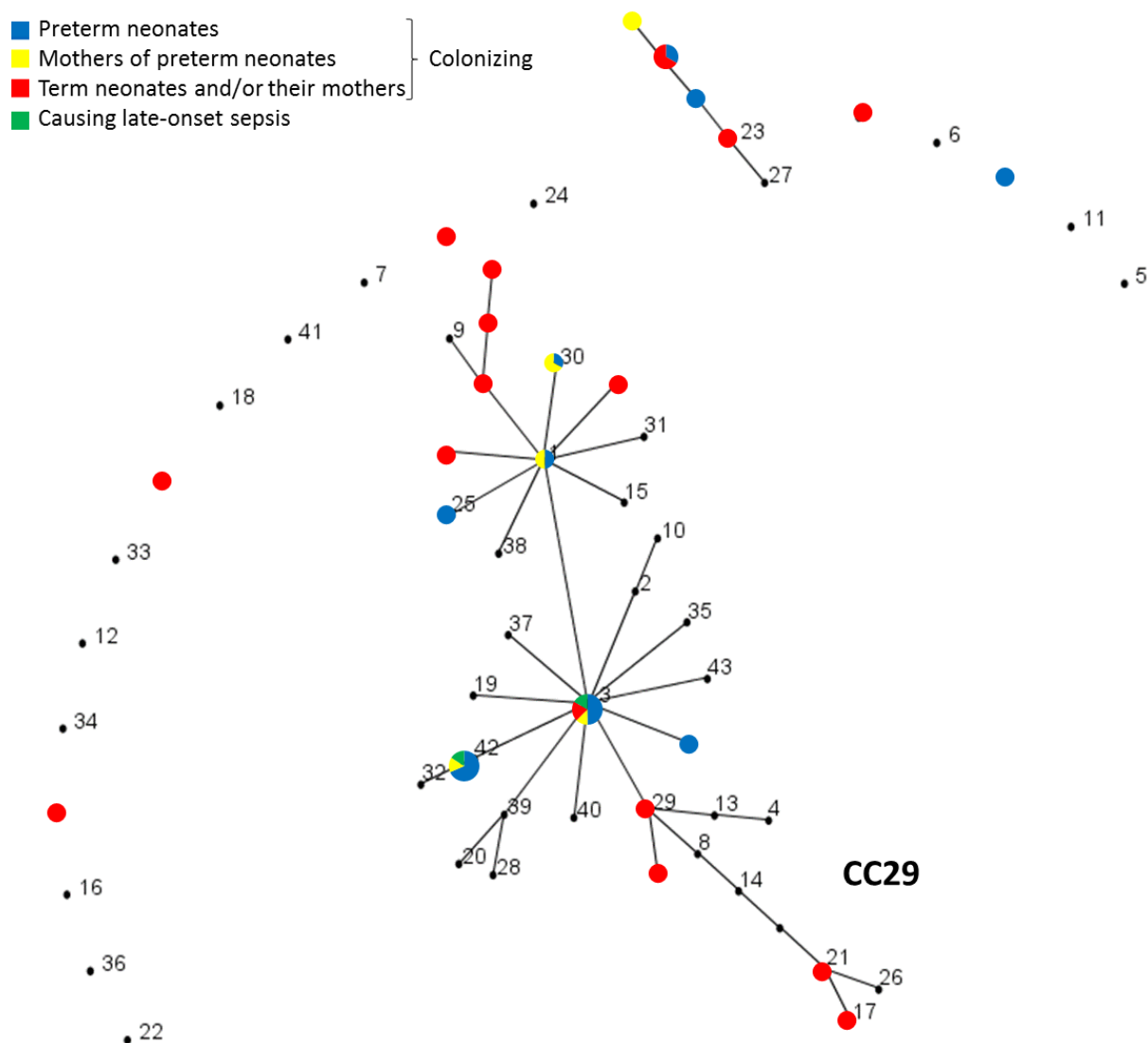


#### Supplemental Digital Content 4. eBURST analysis of *S. haemolyticus* multilocus sequence

types.



The analysis included all sequence types (STs) in the multilocus sequence typing (MLST) database (as of August 29, 2017) and new STs detected in our study. STs are represented by nodes and the number of ST is indicated. STs without numbers are new types detected in this study and submitted to the database. Links connect STs differing only in one locus. STs colonizing preterm neonates are indicated in blue, mothers of preterm neonates in yellow, term neonates or their mothers in red and STs causing late-onset sepsis in preterm neonates in green. The number of isolates from each group is proportional to the area of the node colored

accordingly. STs not detected in our study, but present in the MLST database are indicated in black. The largest group of STs is clonal complex 29, as indicated by CC29.