Table **S1**: Summary statistics for taxonomic composition of subgraphs uniting at least two genome assemblies.

Category	Count	Percentage
$\geq 50\%$ coverage; $\geq 95\%$ identity	154	84.62%
$\geq 50\%$ coverage; $\prec 95\%$ identity	25	13.74%
$\prec 50\%$ coverage; $\prec 50\%$ identity	3	1.65%