

Whole genome sequencing for investigations of meningococcal outbreaks in the United States: a retrospective analysis

**Melissa J. Whaley^{1†}, Sandeep J. Joseph^{1†}, Adam C. Retchless¹, Cecilia B. Kretz¹, Amy Blain¹,
Fang Hu¹, How-Yi Chang¹, Sarah A. Meyer¹, Jessica R. MacNeil¹, Timothy D. Read², and Xin
Wang^{1*}**

¹Meningitis and Vaccine Preventable Diseases Branch, Centers for Disease Control and Prevention,
Atlanta, Georgia, USA. ²Division of Infectious Diseases, Department of Medicine, Emory University
School of Medicine, Atlanta, Georgia, USA.

Supplementary Table 3. Pairwise weighted Robinson-Foulds tree distance estimates between the phylogenetic trees reconstructed using the WGS analysis methods for NmB and NmC isolates used in this study. Phylogenetic trees inferred from SNIPPY, Parsnp and Roary were corrected for homologous recombination using ClonalFrameML.

NmB Phylogenetic trees				
	SNIPPY	Parsnp	Roary	cgMLST
Parsnp	0.1481			
Roary	0.1415	0.00294		
cgMLST	5.5085	4.4961	4.4963	
kSNP	4.1821	4.1695	4.1695	0.6192
NmC Phylogenetic trees				
	SNIPPY	Parsnp	Roary	cgMLST
Parsnp	0.0026			
Roary	0.0020	0.0009		
cgMLST	2.0464	2.0450	2.0454	
kSNP	2.0933	2.0919	2.0924	0.3624