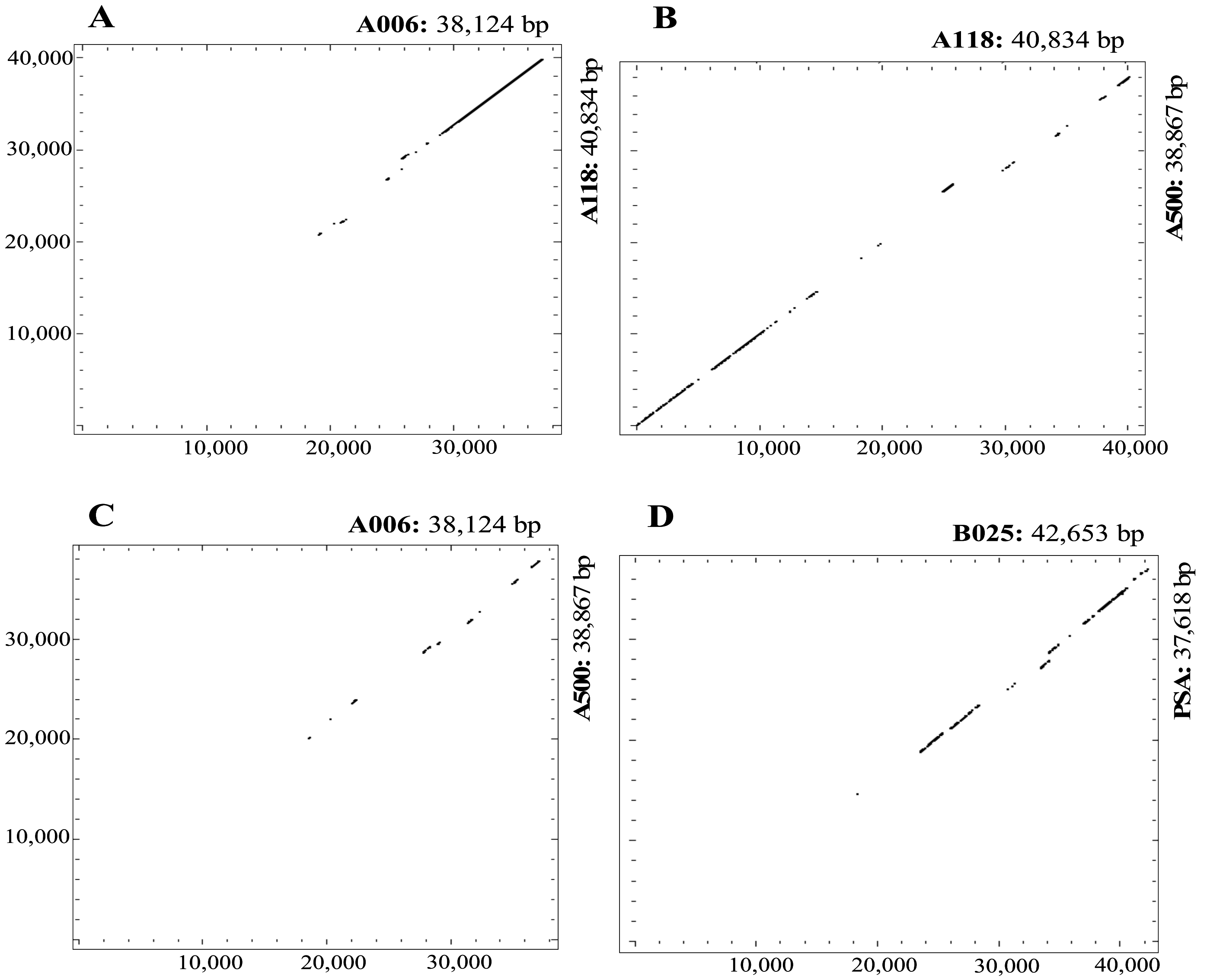

Supplementary Figure. Dot plot alignment of Listeria phages nucleotide sequences generated with the Husar sequence analysis suite. Word size was 20 and window size 25. A. A006 (38.1 kb) compared to A118 (40.8 kb). B. A118 (40.8 kb) compared to A500 (38.9 kb). C. A006 (38.1 kb) compared to A500 (38.9 kb). D. B025 (42.7 kb) compared to PSA (37.6 kb). Numbers indicated on the x- and y-axis correspond to base pair positions in the genomes of the respective phages.