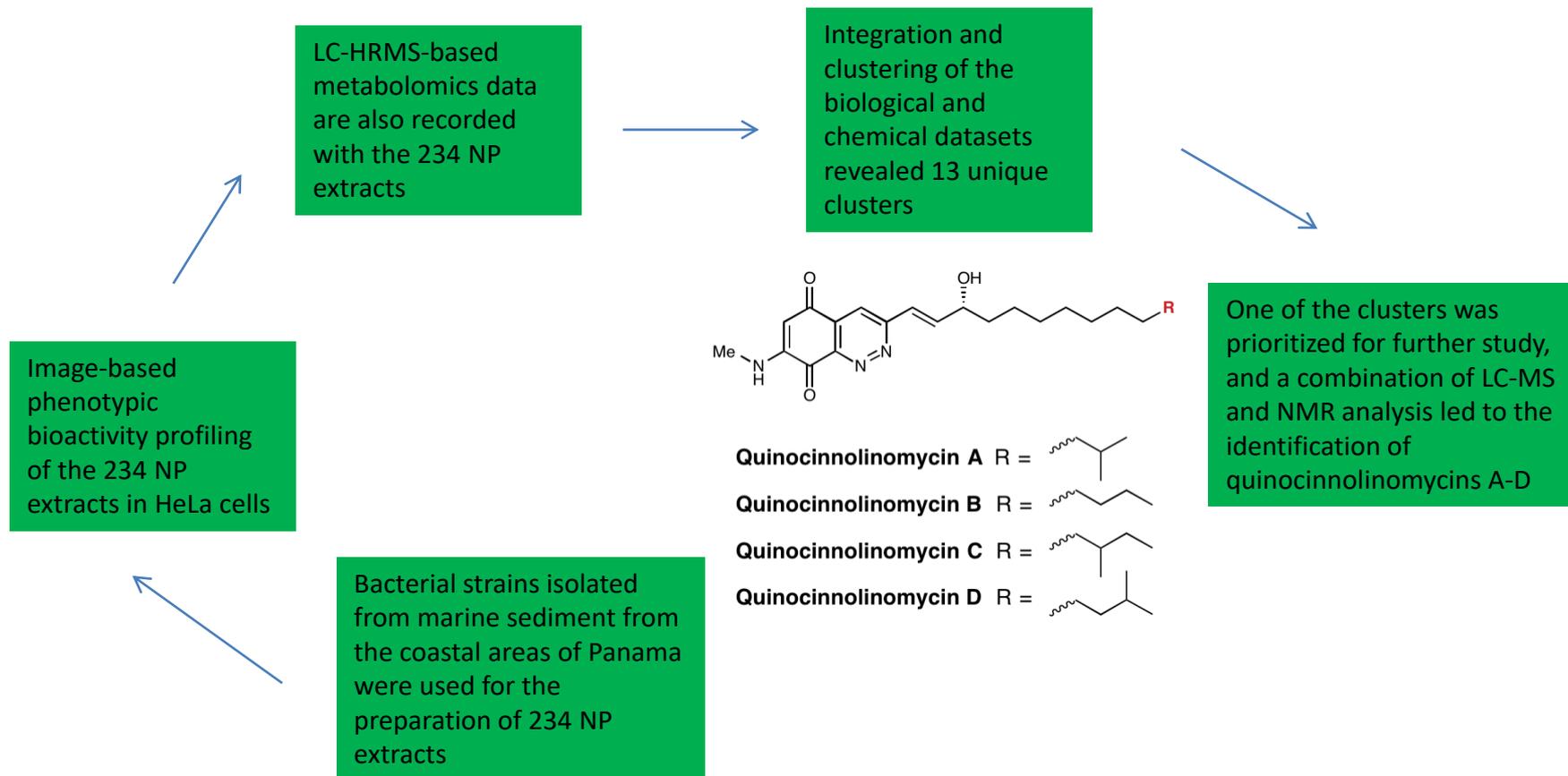
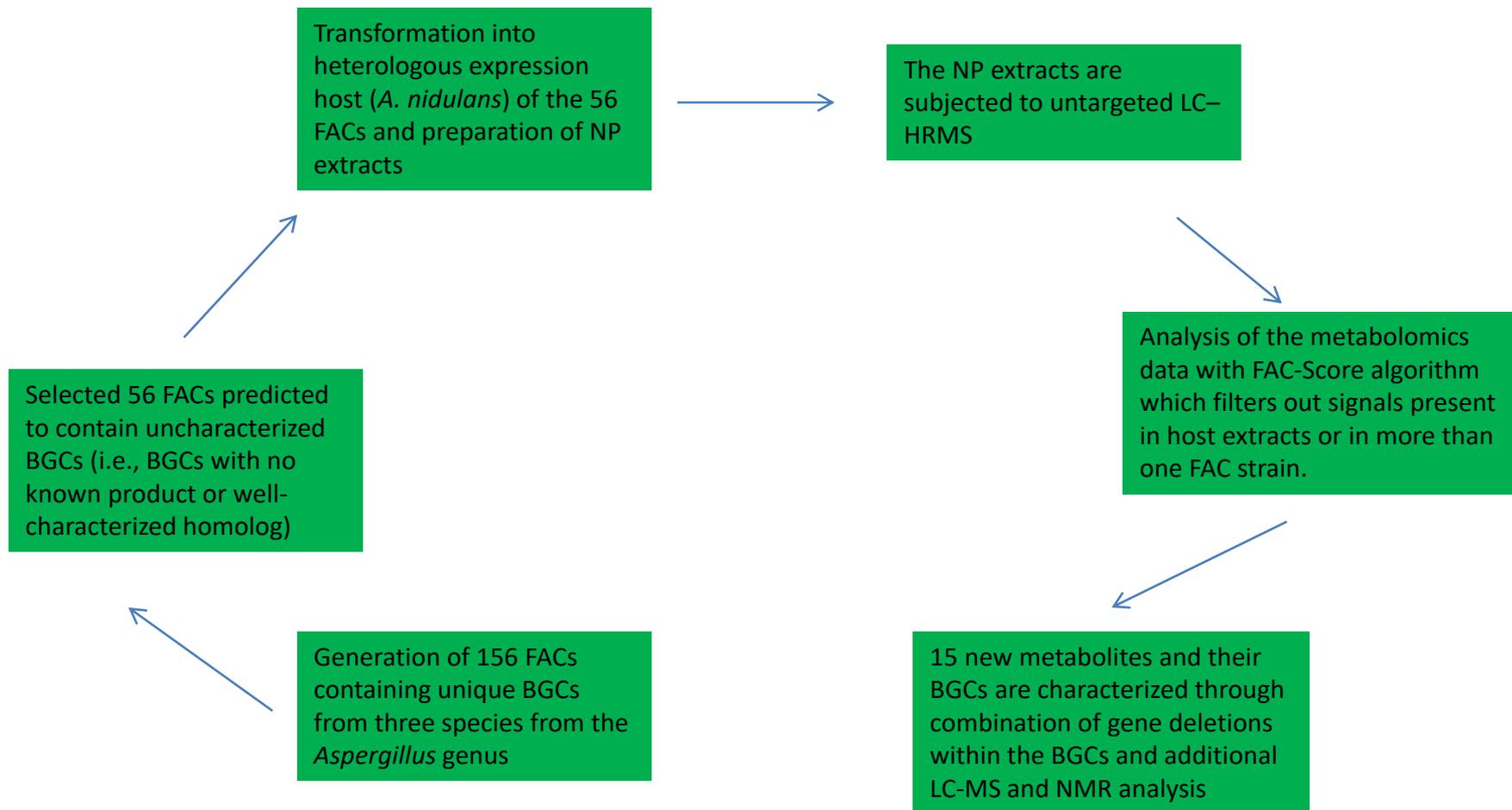


Figure 2A



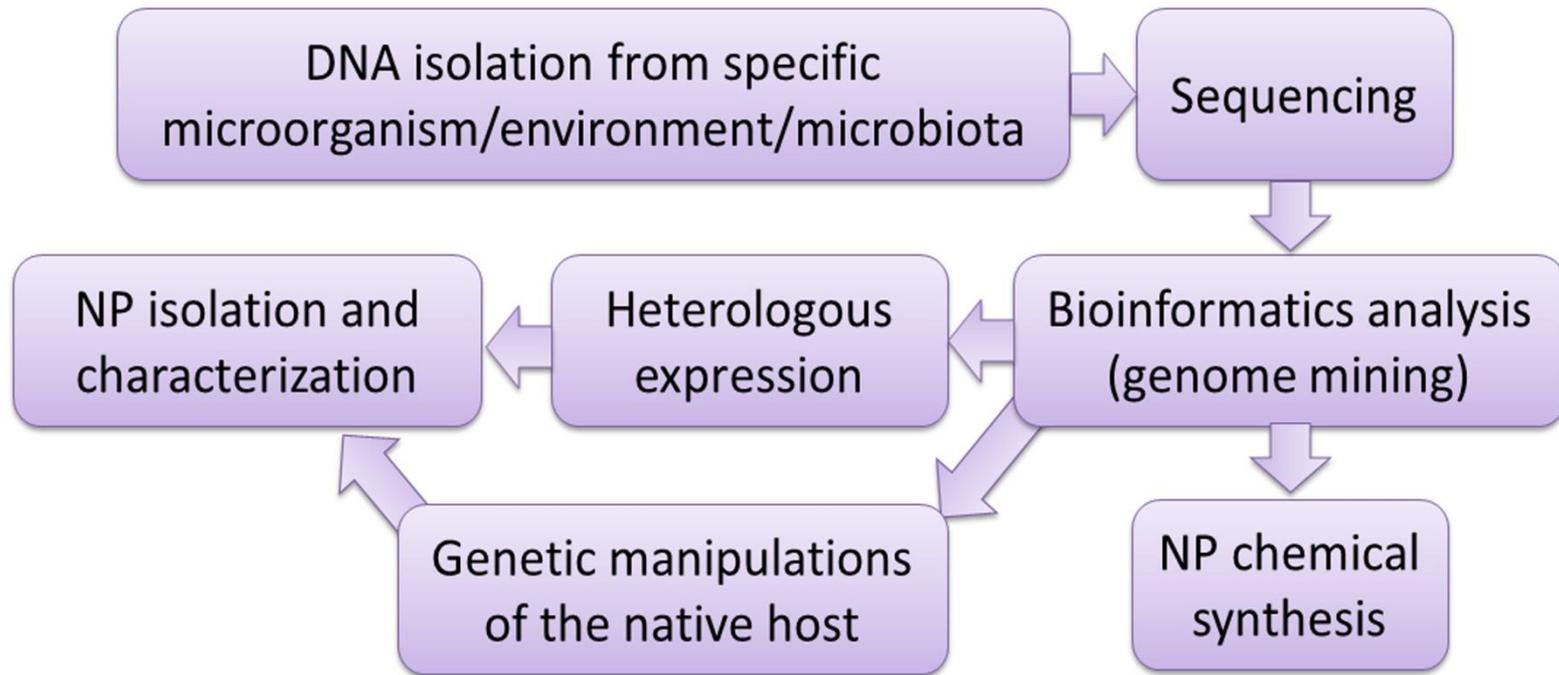
Kurita, K. L., Glassey, E. & Linington, R. G. Integration of high-content screening and untargeted metabolomics for comprehensive functional annotation of natural product libraries. *Proc. Natl. Acad. Sci. U. S. A.* 112, 11999–2004 (2015).

Figure 2B



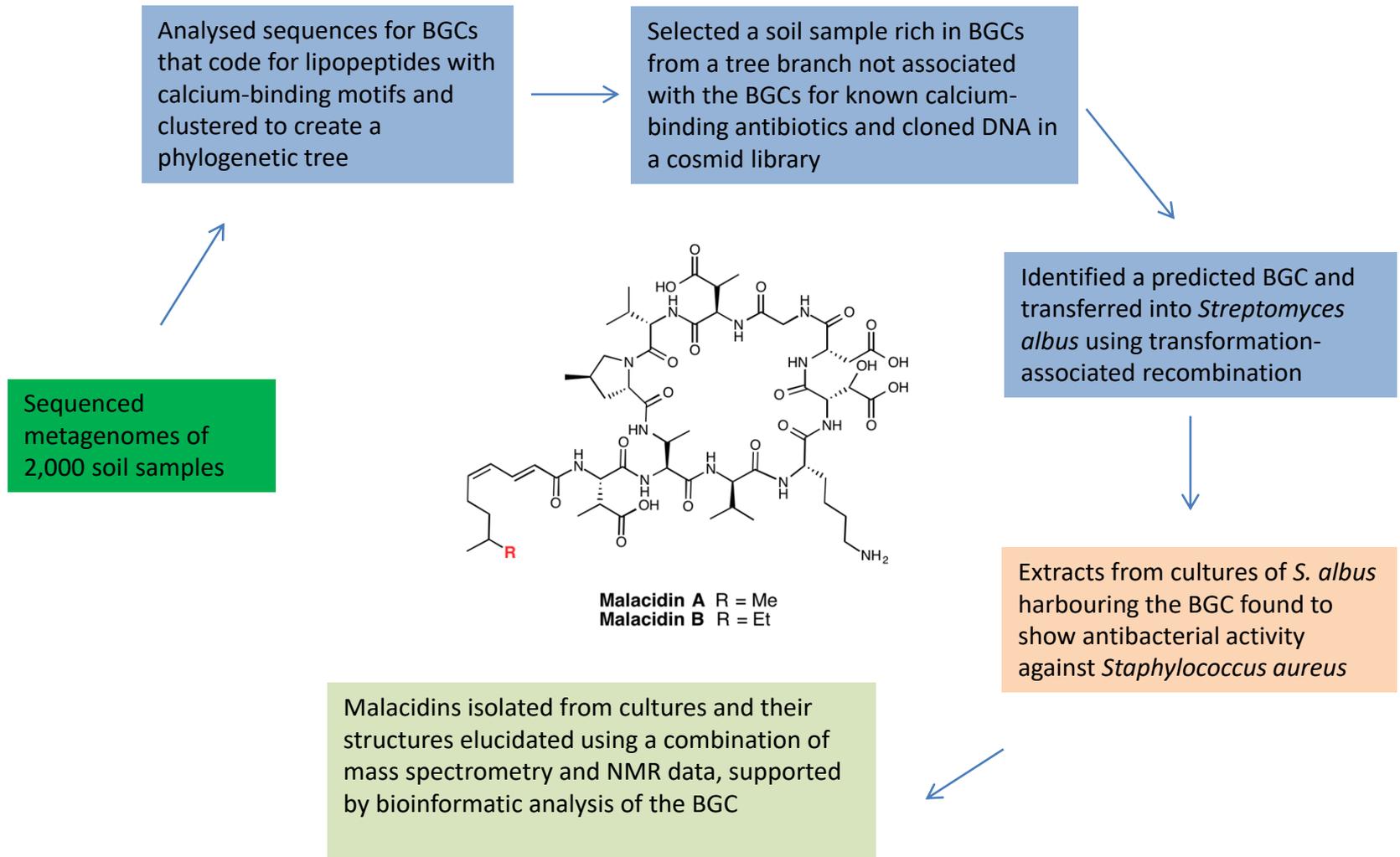
Clevenger, K. D. et al. A scalable platform to identify fungal secondary metabolites and their gene clusters. *Nat. Chem. Biol.* 13, 895–901 (2017).

Figure 3A



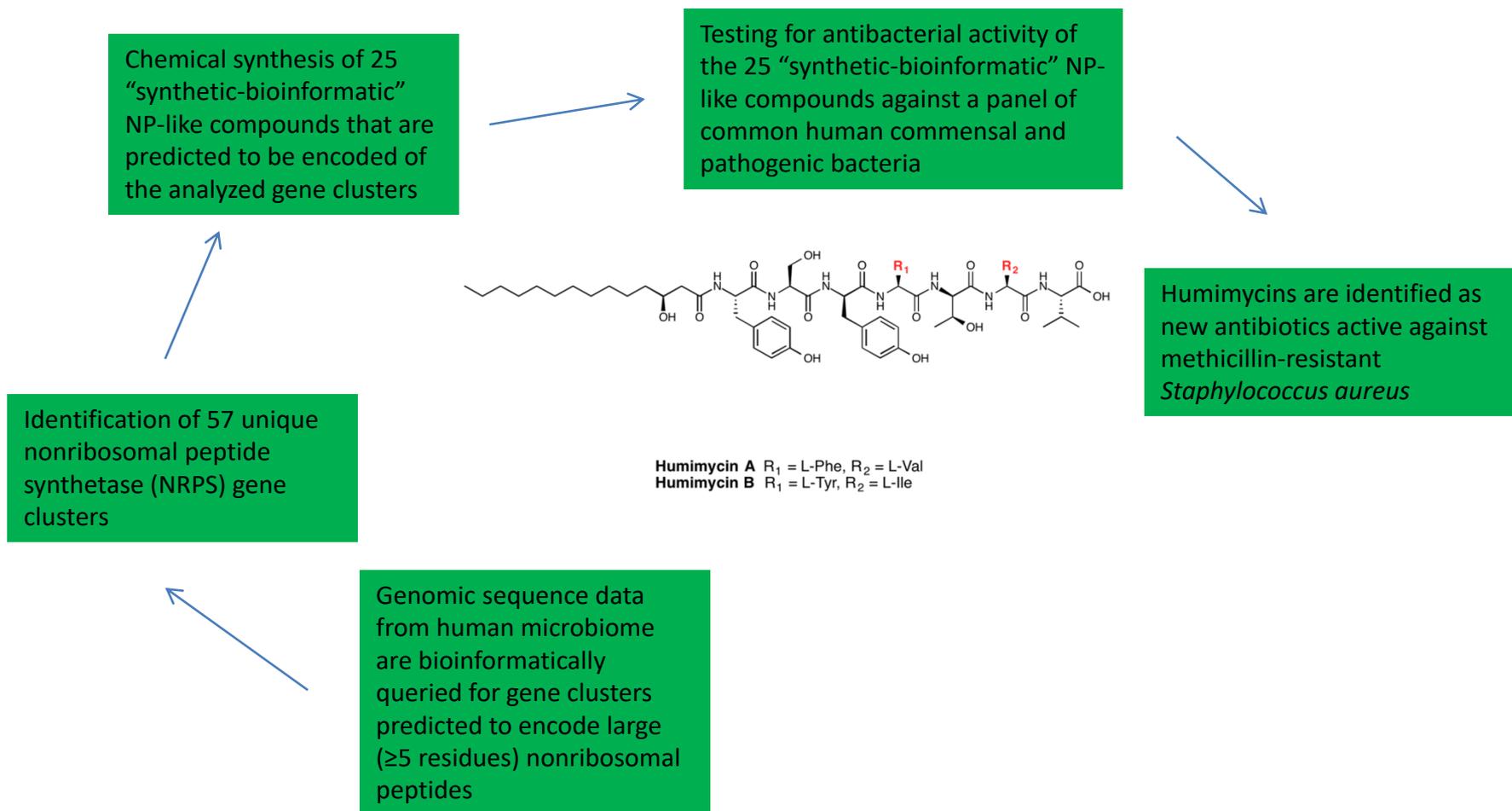
General scheme

Figure 3B



Hover, B. M. et al. Culture-independent discovery of the malacidins as calcium-dependent antibiotics with activity against multidrug-resistant Gram-positive pathogens. Nat. Microbiol. 3, 415–422 (2018).

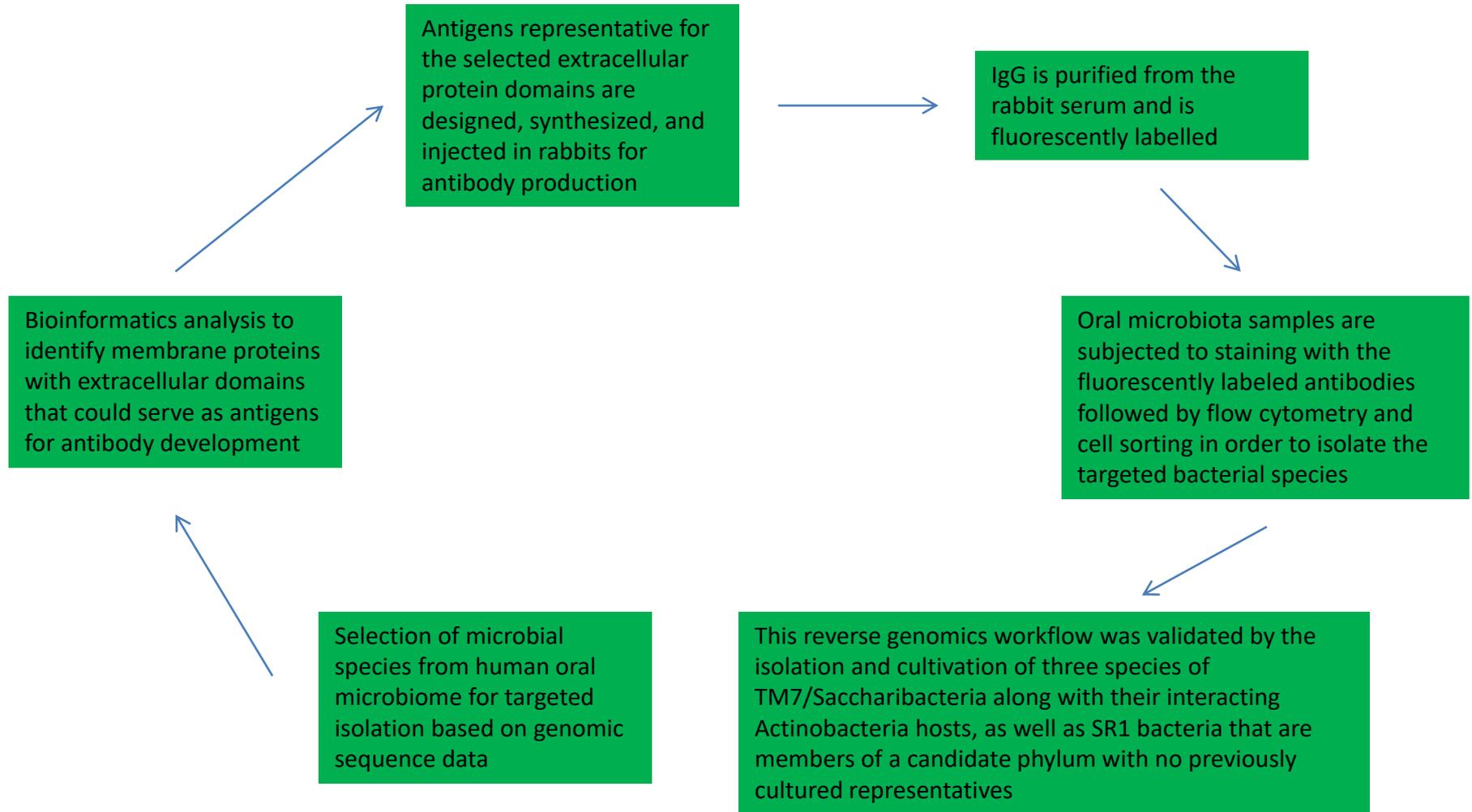
Figure 3C



Chu, J. et al. Discovery of MRSA active antibiotics using primary sequence from the human microbiome. Nat. Chem. Biol. 12, 1004–1006 (2016).



Figure 4B



Cross, K. L. et al. Targeted isolation and cultivation of uncultivated bacteria by reverse genomics. *Nat. Biotechnol.* (2019). doi:10.1038/s41587-019-0260-6