

Unsupervised machine learning organization of the functional dark proteome of gram-negative "superbugs": six protein clusters amenable for distinct scientific applications

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SUPPORTING INFORMATION

FIGURE S1

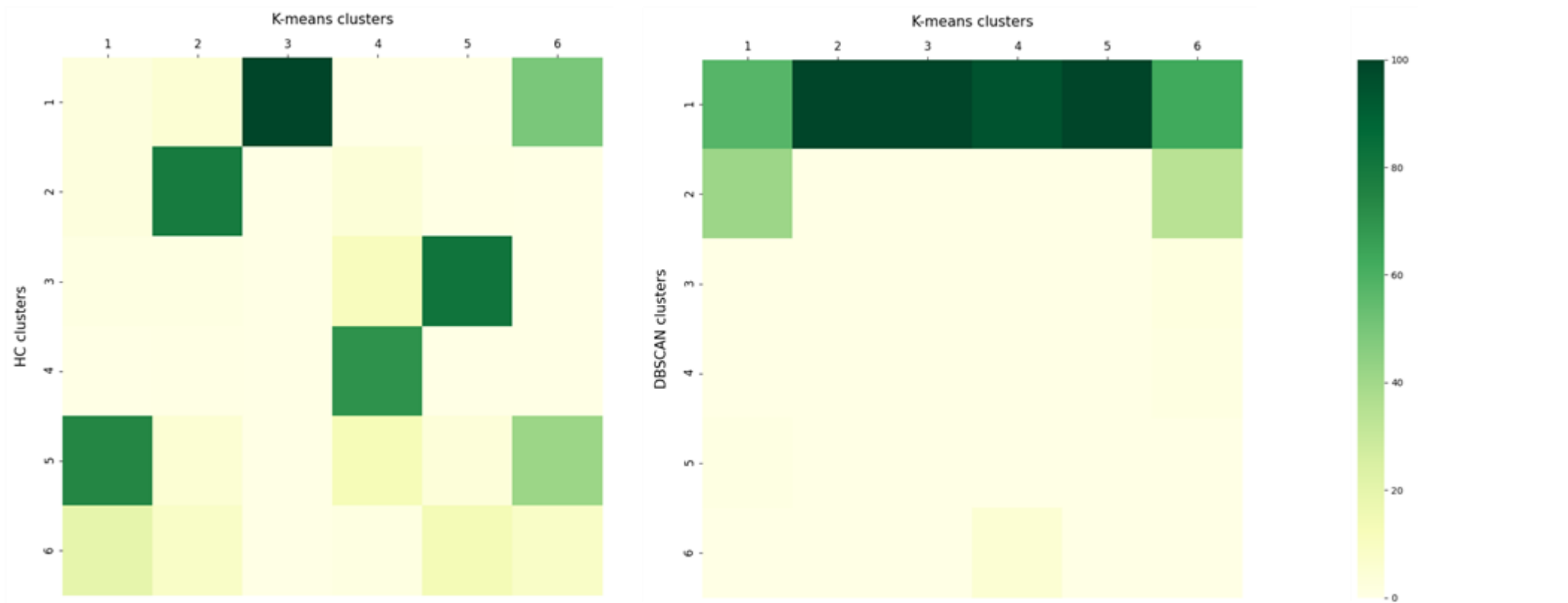


Figure S1. Cluster correspondence between *k-means* and other clustering methods. Percent protein coverage of *k-means* clusters by clusters generated by HC and DBSCAN methods (arbitrary cluster numbering) is color-ranked as indicated in the colorbar.