minimum, experimental studies of multiple BDCPs together will be necessary to test the *in silico* predictions that they bind to each other. With more BDCP functional data emerging, possible targets for therapy, including modification of autophagy, can be evaluated for the increasing number of BDCP-related human diseases.

ACKNOWLEDGEMENTS

We thank Dr. Murat Sincam for his skillful assistance with identifying genetic variants in human BDCPs. We thank the NIH Undiagnosed Diseases program for providing access to their exome sequencing database. We thank two reviewers for their helpful corrections and suggestions. This research was supported by the Intramural Research Programs of the National Institutes of Health, NHGRI and NLM.

SUPPORTING INFORMATION

Additional Supporting Information may be found in the online version of this article.

Figure S1: Phylogenetic tree of human BDCPs in diagonal format. This tree was created by comparing the BEACH domain regions from each BDCP, as annotated in Entrez**.** WRD81 is the most divergent followed by NSMAF. LRBA and NBEA, NBEAL1 and NBEAL2, and LYST, WDFY3 and WDFY4 are most like each other. The scale bar represents a degree of divergence 0.1, as is typically shown for phylogenetic trees.

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Figure S1: