

# Discover, Connect, Contribute: Engagement Pathways within the Atlas of Variant Effects Alliance

AVE is a hub for the functional genomics community

Lara A Muffley<sup>1,2</sup>, Lea M Starita<sup>1,2</sup>, Alan F Rubin<sup>3,4</sup>,  
Atlas of Variant Effects Alliance Research Group, Douglas M Fowler<sup>1,2</sup>

<sup>1</sup> Department of Genome Sciences, University of Washington, Seattle, WA  
<sup>2</sup> Brotman Baty Institute for Precision Medicine, Seattle, WA  
<sup>3</sup> Bioinformatics Division, The Walter and Eliza Hall Institute of Medical Research, Parkville, VIC, Australia  
<sup>4</sup> Department of Medical Biology, University of Melbourne, Parkville, VIC, Australia

**Acknowledgments:**  
This work was supported by the National Institutes of Health (NIH) Centers of Excellence in Genomic Science (CEGS) Grant RM1HG010461  
Graphics Sayeh Gorjifard, Noun Project, Uta Mackensen

**Keywords:**  
Atlas of Variant Effects, Community Outreach, Cross-Consortium Collaboration, International Coordination



The Atlas of Variant Effects (AVE) Alliance is a global community of over 800 members across 57 countries, dedicated to accelerating discoveries in functional genomics with direct applications in precision medicine. At its core are Multiplexed Assays of Variant Effect (MAVEs), which enable high-throughput measurement of thousands of genetic variants in a single experiment.

The Alliance fosters a collaborative and inclusive community committed to the open exchange of MAVE data, protocols, and methodologies. Outputs from Alliance activities include shared resources that accelerate progress in variant interpretation.

Through our community of practice, we have now amassed over 7 million variant effect measurements. These measurements span over 700 distinct human genes as well as genes in model organisms, all publicly available through MaveDB, our open-source database built to enable FAIR (Findable, Accessible, Interoperable, and Reusable) data sharing and reuse.

Through dedicated workstreams and collaborations, AVE has produced a rich community-driven body of work which include over a dozen peer-reviewed publications that advance MAVE tools, set standards, inform experimental design, and clinical interpretation of the data.

Here we outline specific pathways for participation in this growing international effort to map and apply variant effects at scale.



## Participation in the Alliance is open to all, and members are actively encouraged to engage through a variety of pathways:

