Invertebrate methylomes provide insight into mechanisms of environmental tolerance and reveal methodological biases

Shelly A. Trigg*1, Yaamini R. Venkataraman*1, Mackenzie R. Gavery², Steven B. Roberts1, Debashish Bhattacharya3, Alan Downey-Wall4, Jose M. Eirin-Lopez5, Kevin M. Johnson6, Katie E/ Lotterhos4, Jonathan B. Puritz7 and Hollie M. Putnam7+

- ¹ University of Washington, School of Aquatic and Fishery Sciences 1122 NE Boat St. Seattle, WA, 98195, USA
- NOAA Northwest Fisheries Science Center Montlake 2725 Montlake Blvd E, Seattle, WA, 98112, USA
- ³ Department of Biochemistry and Microbiology, Rutgers University, New Brunswick, NJ 08901 USA
- ⁴ Department of Marine and Environmental Sciences, Northeastern University, 430 Nahant Road, Nahant, MA 01908
- ⁵ Florida International University, Environmental Epigenetics Laboratory, Institute of Environment 3000 NE 151 St. North Miami, FL, 33181, USA
- ⁶Department of Biological Sciences, University of Rhode Island, Kingston, RI 02881, USA

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[†]corresponding author: hputnam@uri.edu

^{*} equal contribution

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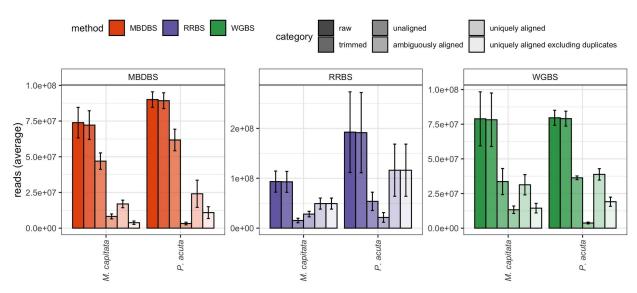


Figure SF1. Summary of sequencing depth and alignments for all libraries. Bars show average number of reads for each method and species and error bars show standard deviation.

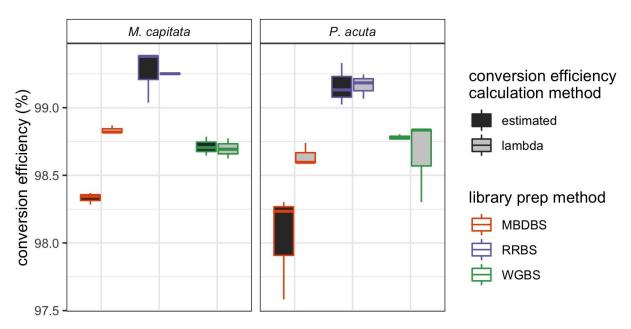


Figure SF2. Bisulfite conversion efficiency assessment. Bisulfite conversion efficiency calculated from lambda alignments or estimated from non-CpG methylation from coral alignments for *M. capitata* libraries and *P. acuta* libraries.

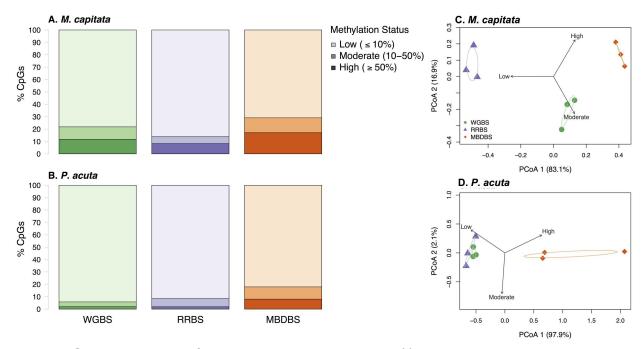


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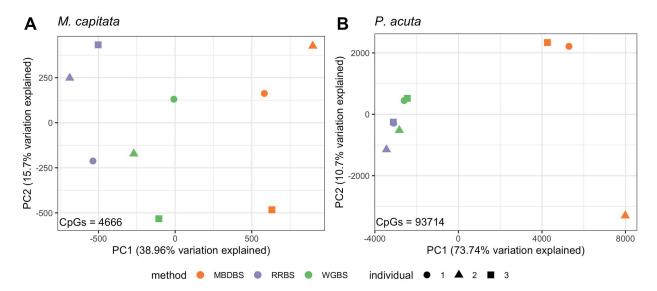


Figure SF4. PCA of CpG methylation for loci covered at 5x read depth in all samples for (**A**) *M. capitata* and (**B**) *P. acuta*.

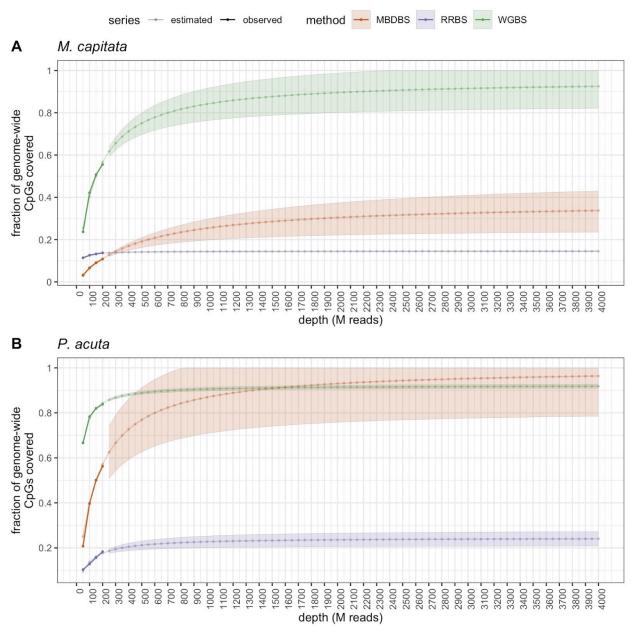


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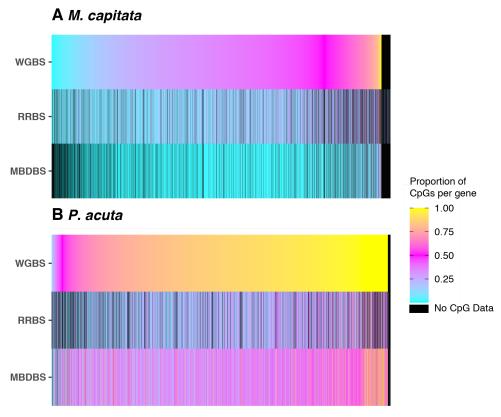


Figure SF6. Mean proportion (n=3 samples per method) of CpGs per gene that have at least 5x coverage in all of the one-to-one orthologous genes, as identified by OrthoFinder (Putnam et al., 2020) for **A**) *M. capitata* and **B**) *P. acuta*.