**Data for: (Epi)genomic adaptation driven by fine geographical scale environmental heterogeneity after recent biological invasions**

**Appendix S2 Table S1**: Gene annotation of EMSs. A total of 1,544 genes annotated from environment-associated methylation sites.

EMS: environment-associated methylation site; EMG: environment-associated methylation gene; E-value: the number of alignments expected by chance with the calculated score or better. The expect value is the default sorting metric; for significant alignments the E-value should be very close to zero; Similarity[%]: the percent identity for a set of aligned segments to the same subject sequence; Coverage[%]: the percent of the query length that is included in the aligned segments.

**Appendix S2 Table S2**: Gene annotation of EGSs. A total of 607 genes annotated from environment-associated SNPs.

EGS: environment-associated genetic site; EGG: environment-associated genetic gene; E-value: the number of alignments expected by chance with the calculated score or better. The expect value is the default sorting metric; for significant alignments the E-value should be very close to zero; Similarity[%]: the percent identity for a set of aligned segments to the same subject sequence; Coverage[%]: the percent of the query length that is included in the aligned segments.

**Appendix S2 Table S3**: GO enrichment of EMSs. GO enrichment analysis with candidate environment-associated methylation sites.

GO Class: three types of terms in the gene ontology, including Molecular function, Cellular component, and Biological process; GO Name: the name of the significant GO term; GO ID: the ID of the significant GO term; p-value: the probability of each GO term; Enrichment Score: the degree of over-representation of a GO at the extremes of the ranked list. Gene Count: the number of genes involved in the significant GO term; Gene List: the genes involved in over-representation of a significant GO term.

**Appendix S2 Table S4**: GO enrichment of EGSs. GO enrichment analysis with candidate environment-associated SNPs.

GO Class: three types of terms in the gene ontology, including Molecular function, Cellular component, and Biological process; GO Name: the name of the significant GO term; GO ID: the ID of the significant GO term; p-value: the probability of each GO term; Enrichment Score: the degree of over-representation of a GO at the extremes of the ranked list. Gene Count: the number of genes involved in the significant GO term; Gene List: the genes involved in over-representation of a significant GO term.