

Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: List of selected feature names and their importances in each tissue

File Name: Supplementary Data 2

Description: List of credible sets where the number of variants became significantly smaller after updating the PIP using EMS as a functional prior in whole blood

File Name: Supplementary Data 3

Description: List of newly identified potentially causal/non-causal eQTLs

File Name: Supplementary Data 4

Description: List of candidate genes identified in co-localization analysis

File Name: Supplementary Data 5

Description: Abbreviation of the assay and the tissue names used in the study

File Name: Supplementary Data 6

Description: Details of grid search for hyperparameter tuning in the training of whole blood EMS

File Name: Supplementary Data 7

Description: List of tissue-specific putative causal eQTLs

File Name: Supplementary Data 8

Description: List of pairs of tissue-specific putative causal eQTLs on same genes

File Name: Supplementary Data 9

Description: Tissue-specific transcription factor (TF) related Basenji feature scores in the corresponding tissue-specific putative causal eQTLs identified by PIP_{EMS}