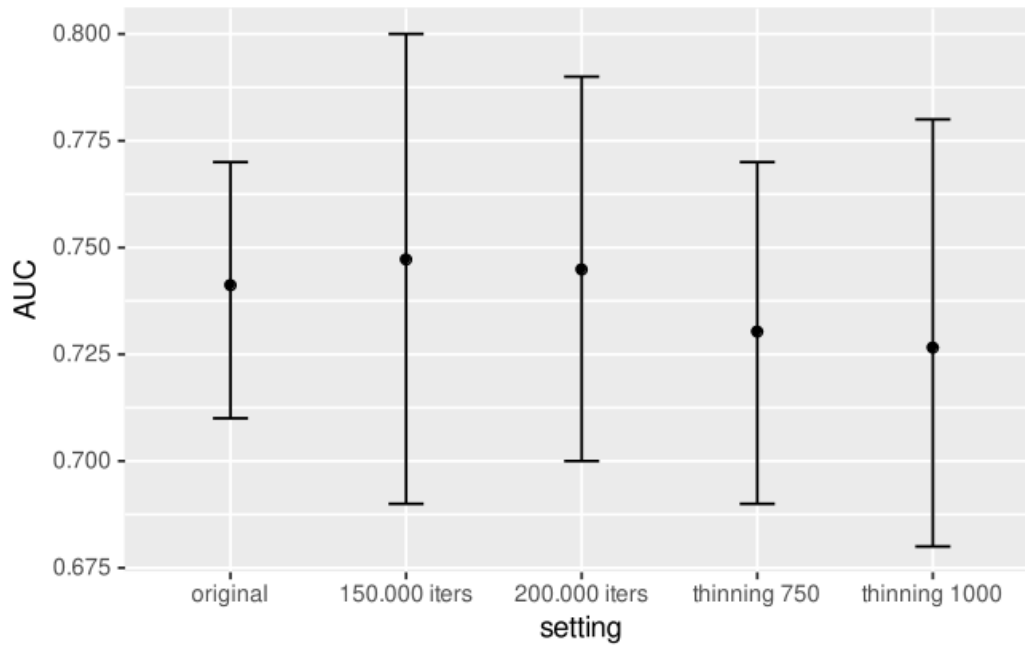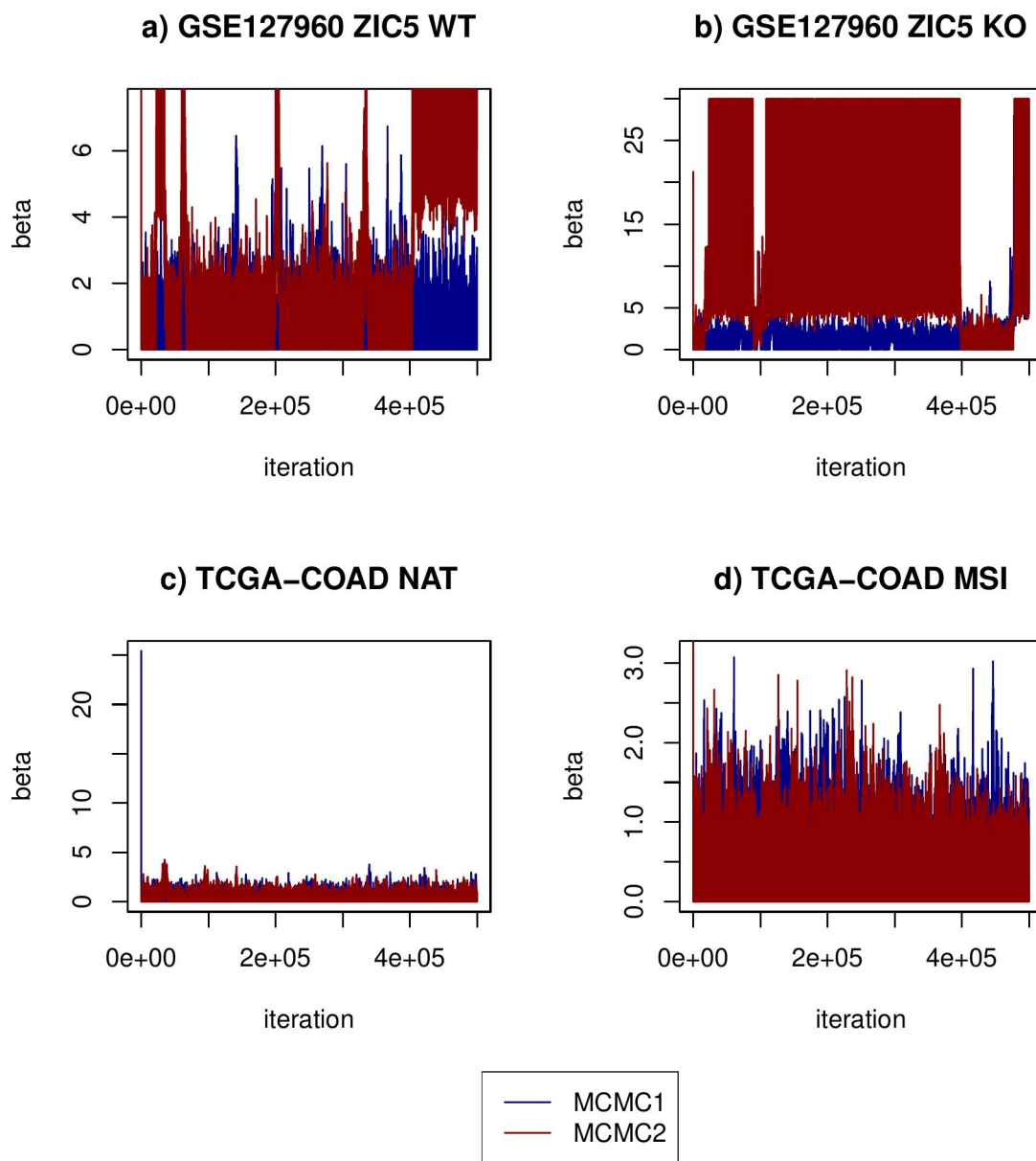Supplementary Figure 1: Different IntOMICS hyperparameters setting in DREAM4 *in silico* dataset and the resulting ROC with 95% confidence intervals.
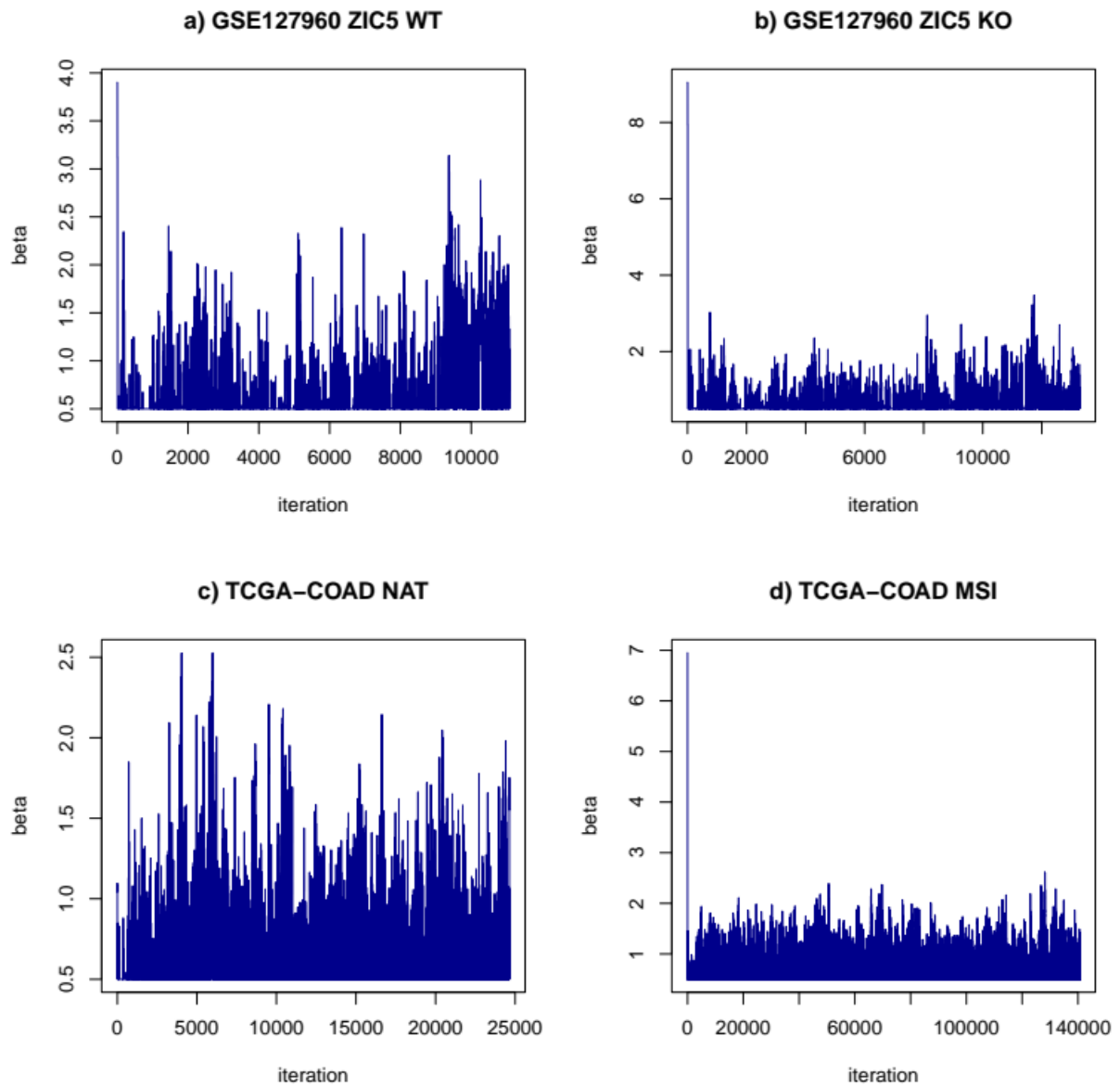
Supplementary Figure 2: Different IntOMICS hyperparameters setting in DREAM4 *in silico* dataset and the resulting AUC with 83% confidence intervals.
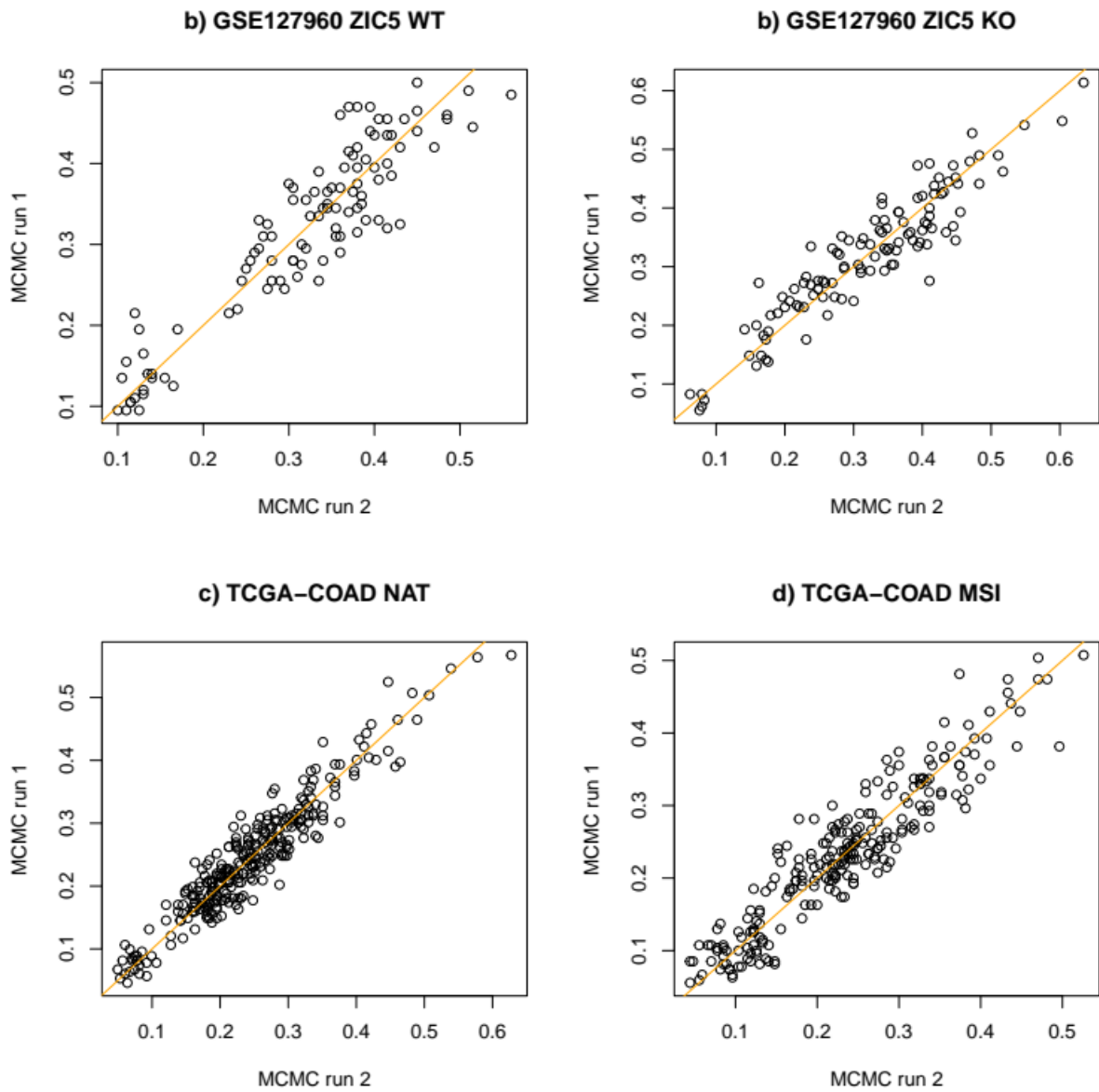
Supplementary Figure 3: Trace plot of β values using the W&H algorithm.
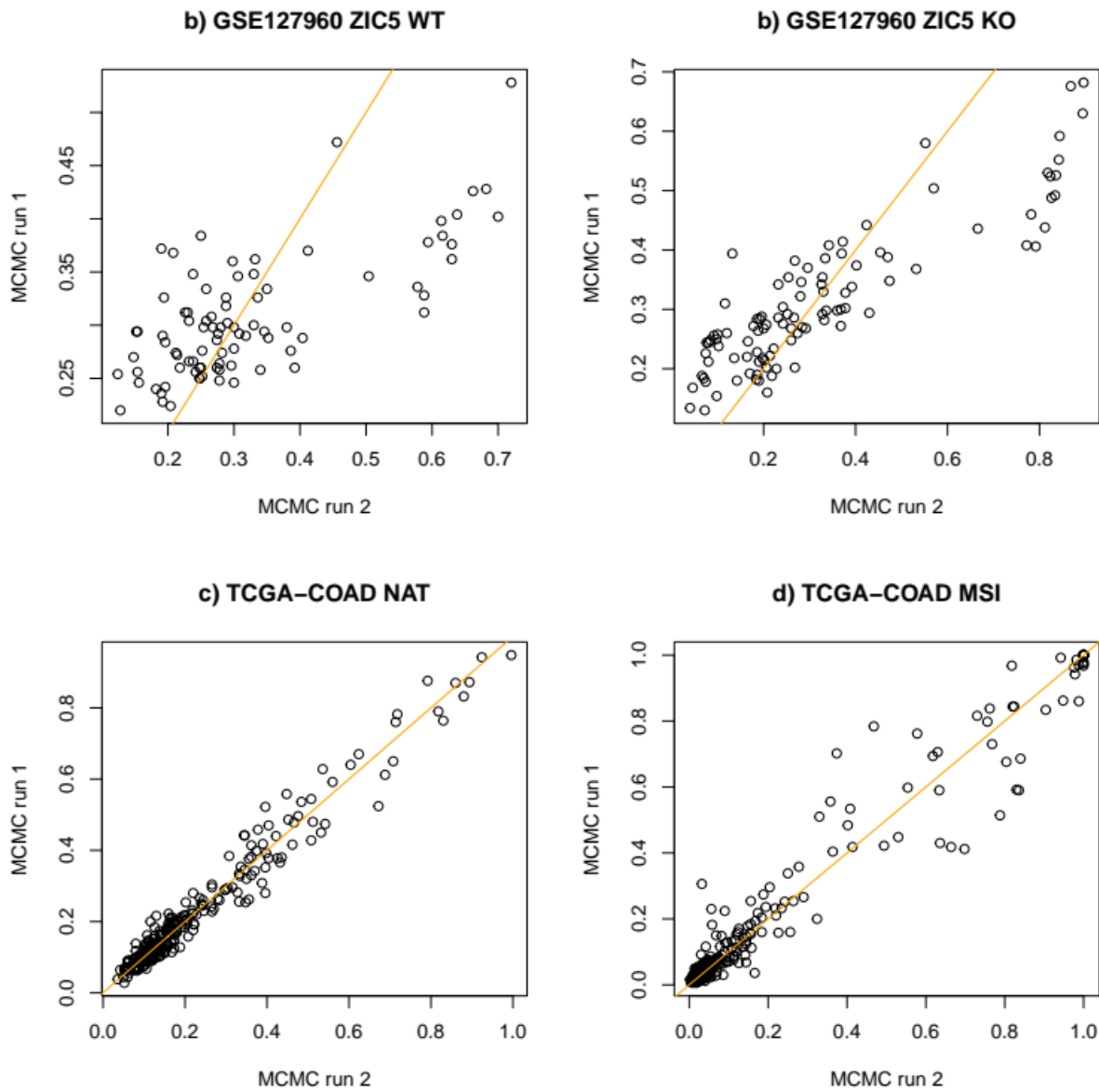
Supplementary Figure 4: Consistency in the marginal posterior probabilities of the edges using the W&H algorithm.

Supplementary Figure 5: Trace plot of β values using the IntOMICS algorithm.

Supplementary Figure 6: Consistency in the marginal posterior probabilities of the edges using the IntOMICS algorithm.
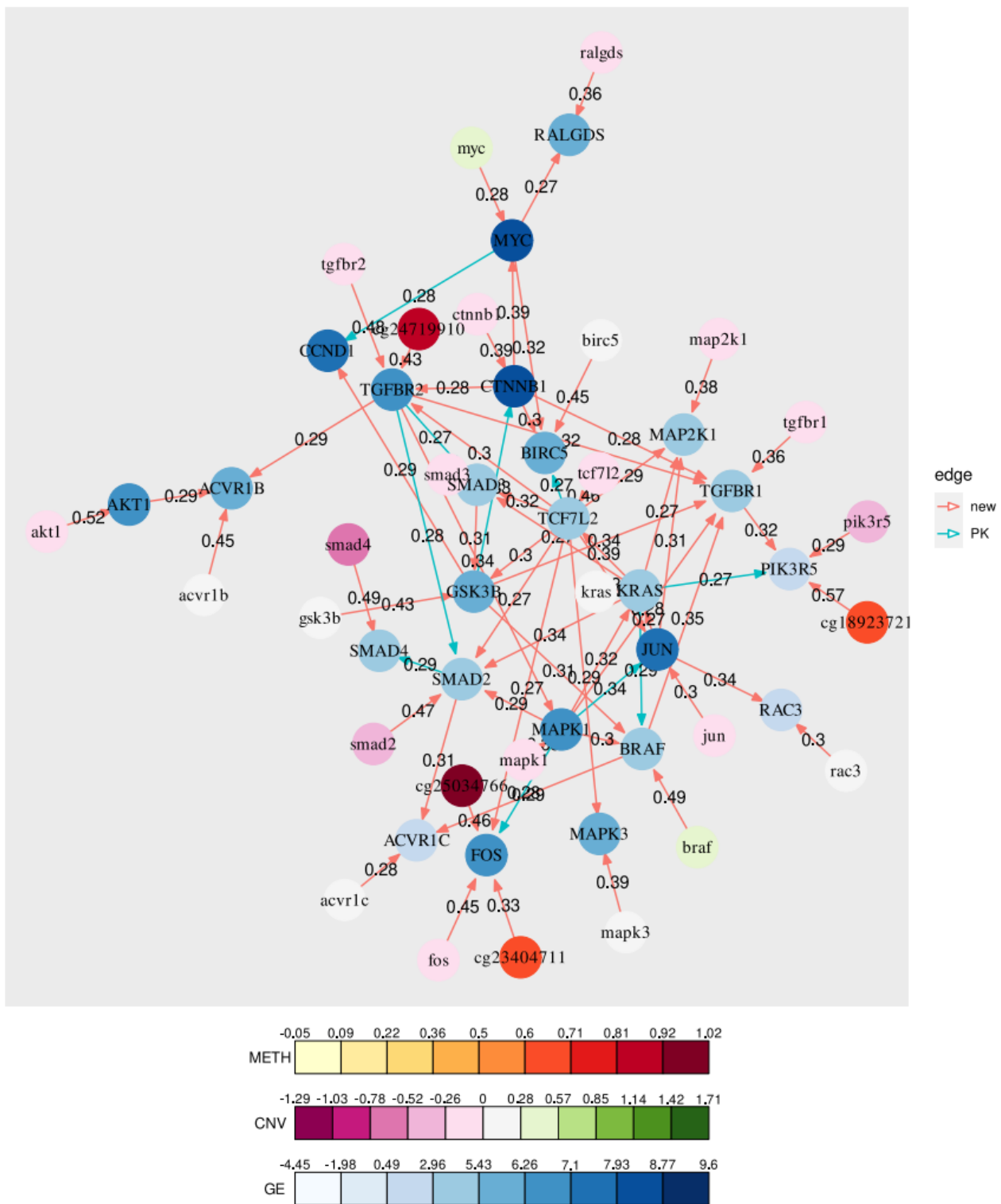
Supplementary Figure 7: CNVs specific for MSS colon cancer investigation and the resulting regulatory network inferred by IntOMICS algorithm using TCGA-COAD MSS stageII/III samples.
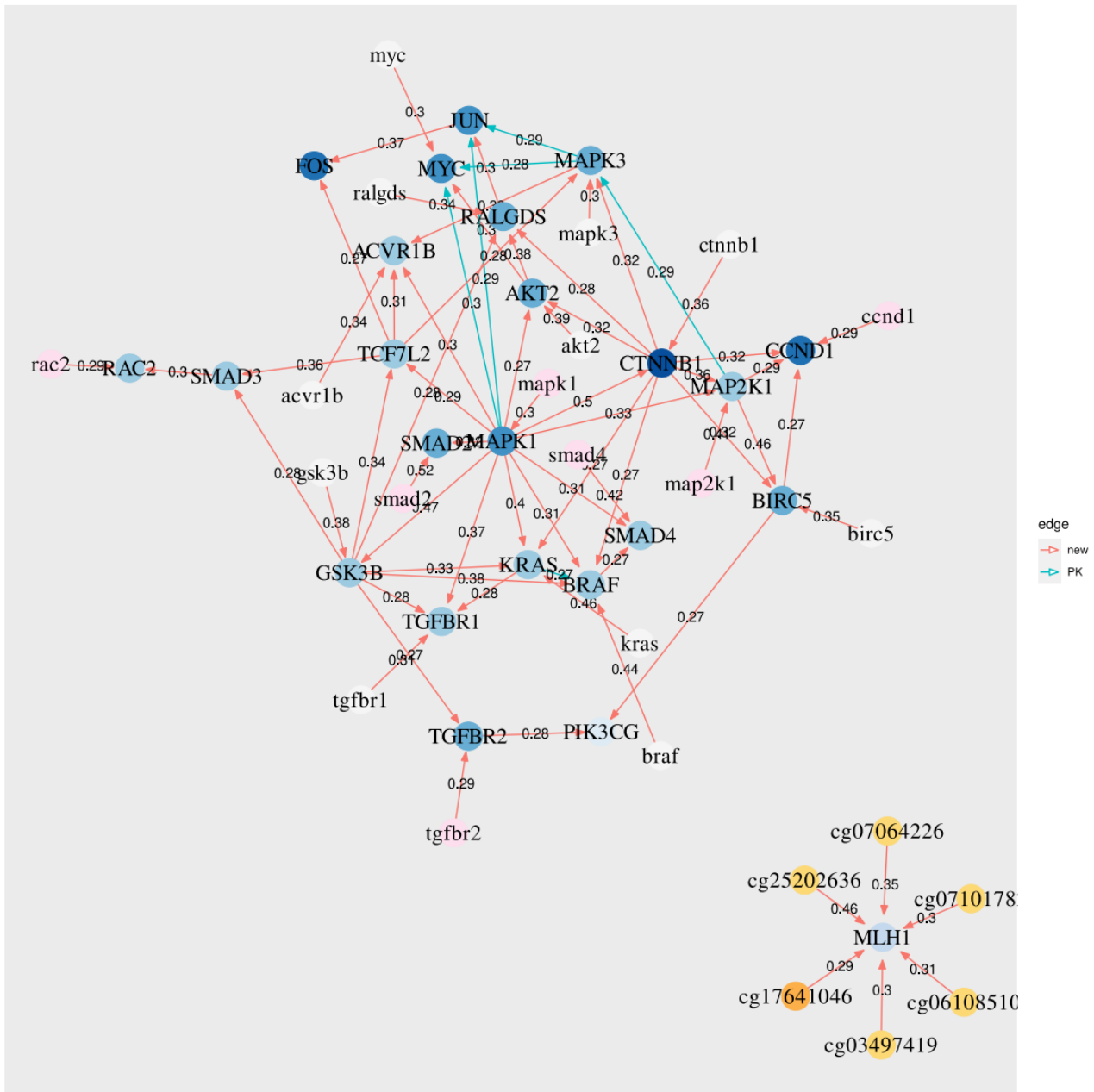
Supplementary Figure 8: DNA methylation specific for MSI colon cancer investigation and the resulting regulatory network inferred by IntOMICS algorithm using TCGA-COAD MSI samples.