

Supplementary Data

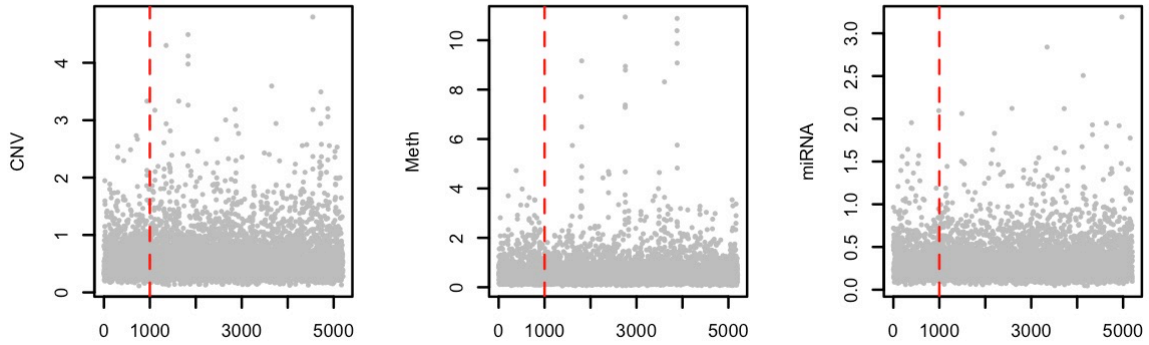


Figure S1.1. Trace plots of variance parameters associated to CNV, Methylation and miRNA, derived from the models presented in Case Study 3.

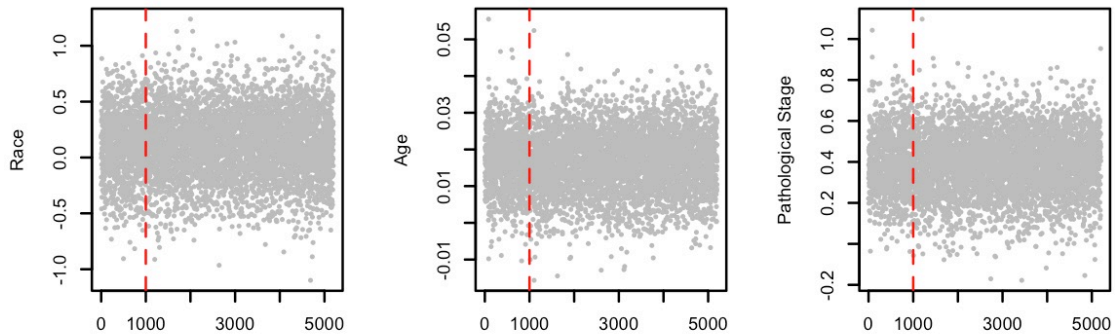


Figure S1.2. Trace plot of fixed effects obtained from the samples collected when fitting a model for clinical covariates and CNV (COV+CNV), case study III.

Table S1.1. Dispersion Separability Criterion (DSC) due to batch computed with the R package MBatch (“MBatch” by Weinstein's group).

Omic	Dispersion Separability Criterion*
CNV	0.224
Methylation	0.234
miRNA	0.343
Gene Expression	0.272

*The authors of ‘MBatch’ suggest problematic threshold is a DSC of 0.5.

Table S1.2. Cross-validation AUC (average over 100 cross validations) and SD of the AUC for models with different inputs and priors.

Model	AUC in CV	
	Average	SD
GE (Gaussian Prior)	0.658	0.011
GE (Bayes B)	0.653	0.012
COV (Fixed Effect)	0.703	0.007
COV (Fixed Effect)+GE (Gaussian Prior)	0.721	0.008
COV (Fixed Effect)+GE (Bayes B)	0.717	0.008

Table S1.3. Estimated posterior mean and the estimated Monte Carlo standard error of mean for selected parameters (all obtained from models in case study 3, the fixed effects parameter correspond to the model using covariates plus CNV).

Parameter being Estimated:	Posterior Mean	MC SE
Variance associated to CNV	0.637	0.011
Variance associated to Methylation	0.652	0.025
Variance associated to miRNA	0.338	0.004
Race (African American versus White)	0.114	0.005
Age effect	0.017	0.0001
Pathological Stage	0.387	0.002

Table S1.4. Cross-validation AUC (average over 100 cross validations) and SD of the AUC for models with layer-specific prior and layer-specific regularization parameters (first row) versus models (rows 2 and 3) where all predictors were assigned the same prior and same regularization parameters (either Gaussian, row 2 or Bayes B, row 3).

Model	AUC in CV	
	Average	SD
COV (Fixed)+GE (Gaussian)+METH (Gaussian)	0.754	0.004
COV+GE+METH (All with the same Gaussian Prior)	0.561	0.025
COV+GE+METH (All with the same prior: Bayes B)	0.637	0.022

GE: gene expression, COV: clinical covariates, METH=METHYLATION.

Table S1.5: P-values results from Likelihood Ratio Test of extending the clinical model (short model) with GE-derived and methylation-derived PCs (1 to 5 successively) to model breast cancer alive status with a logit link.

Short model (H ₀)	Long model (H _A)	p-Value -PC derived from GE	p-Value -PC derived from Methylation
COV	COV +PC1	0.740	0.453
COV	COV +PC1+PC2	0.070	0.123
COV	COV +PC1+PC2+PC3	0.056	0.241
COV	COV +PC1+PC2+PC3+PC4	0.072	0.089
COV	COV +PC1+PC2+PC3+PC4+PC5	0.091	0.152