MOVIE - Supplementary Materials

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1 Supplementary Methods

1.1 Data Pre-processing

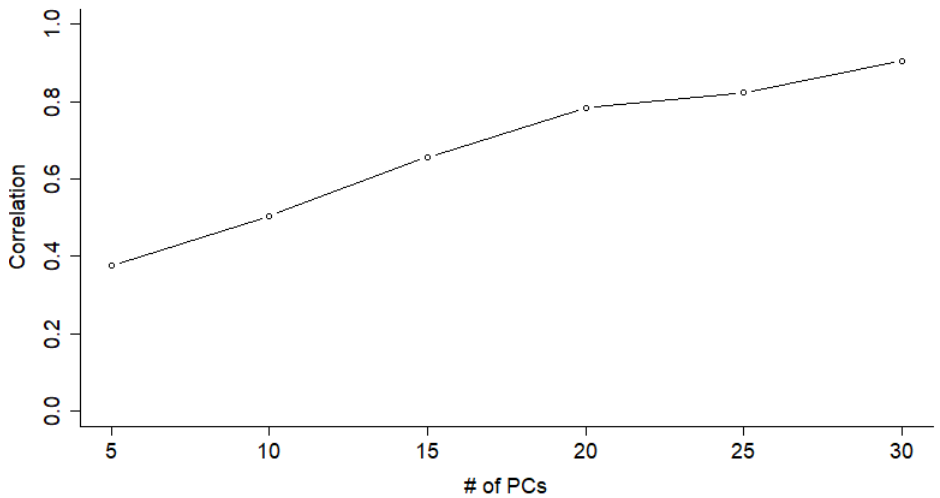
Data from The Cancer Genome Atlas (TCGA) [3] was collected for 558 breast cancer samples using Copy Number Variation (CNV), RNA expression, and micro RNA expression. CNV was summarized for 216 genes; RNA expression was measured for 12,434 genes; and miRNA expression was measured for 305 genes. Examination of the scree plot for each data type resulted in selecting AJIVE initial signal values of 25, 25, and 50 components for CNV, RNA, and miRNA, respectively.

RNA expression, DNase, and protein expression were collected for Yoruban lymphoblastoid cell lines from Li, et al (2016). To avoid dealing with issues of missing data, only samples that had all three data types observed were used in the analysis (n=55). Two samples were identified as outliers in the DNase data by examing the first two principal components; these were subsequently removed from the analysis. DNase was measured for 699,906 genes; RNA expression was measured for 13,967 genes; and protein was measured expression for 4,375 genes. The protein expression data had a high number of missing values, and thus, only genes that were observed for all samples were included in the analysis (2,435). To accommodate the large differences in dimensionality of the data types, the DNase dataset was reduced to the top 5000 most variable genes, as recommended by MOFA [20]. For consistency across methods, the reduced DNase dataset was used for all analyses. Examination of the scree plot for each data type resulted in the selection of AJIVE initial signal values of 3, 3, and 2 components for DNase, RNA, and protein expression, respectively.

2 Supplementary Figures

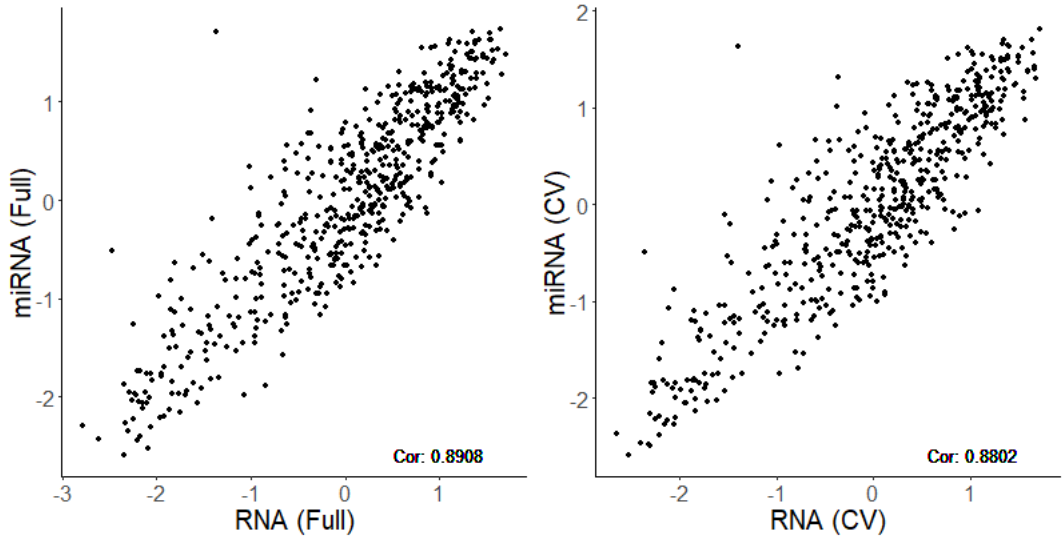
2.1 Motivation

Supplementary Figure 1: CCA on PCs of null Gaussian data returns correlations as high as 0.9, for datasets of sizes that are typical genomics (e.g. 100 samples, 5000 genes).

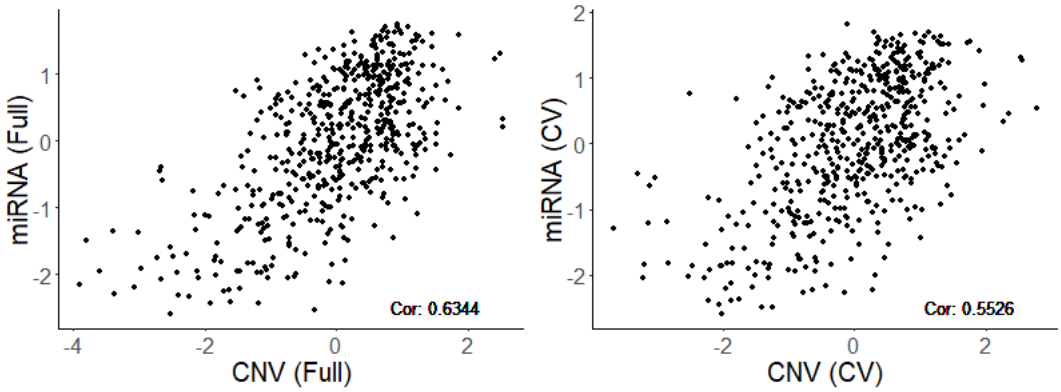


2.2 Large Sample Size - TCGA Data

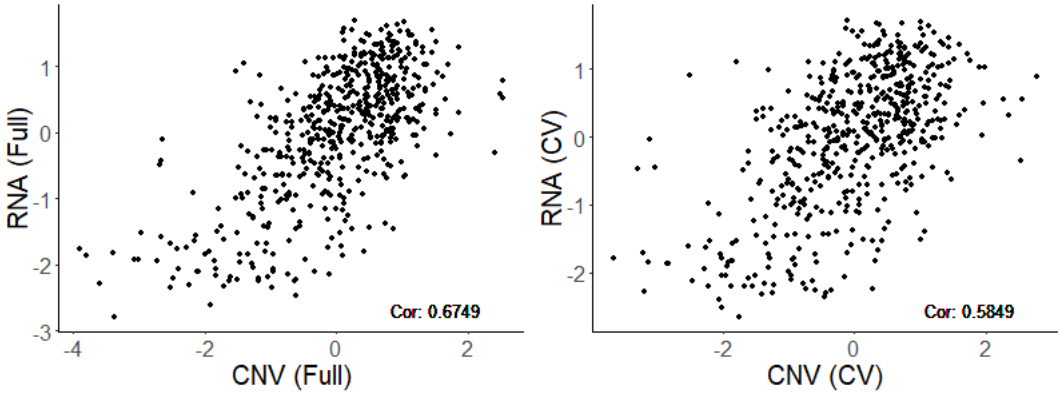
Supplementary Figure 2: Sparse mCCA with experimental data: Side-by-side contribution plots for gene expression versus miRNA using Sparse mCCA.



Supplementary Figure 3: Sparse mCCA with experimental data: Side-by-side contribution plots for CNV versus miRNA using Sparse mCCA.



Supplementary Figure 4: Sparse mCCA with experimental data: Side-by-side contribution plots for CNV versus gene expression using Sparse mCCA.



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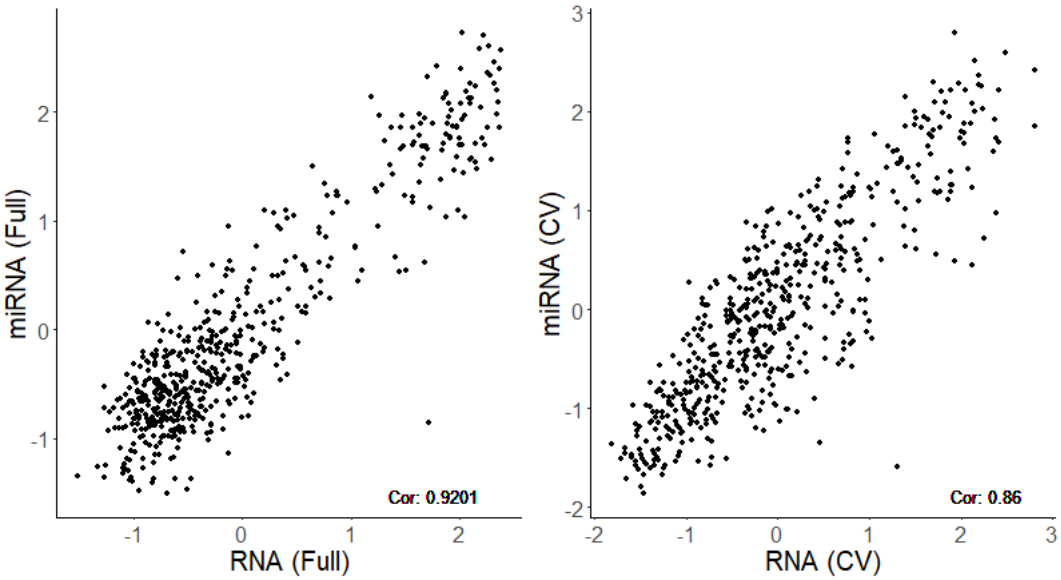
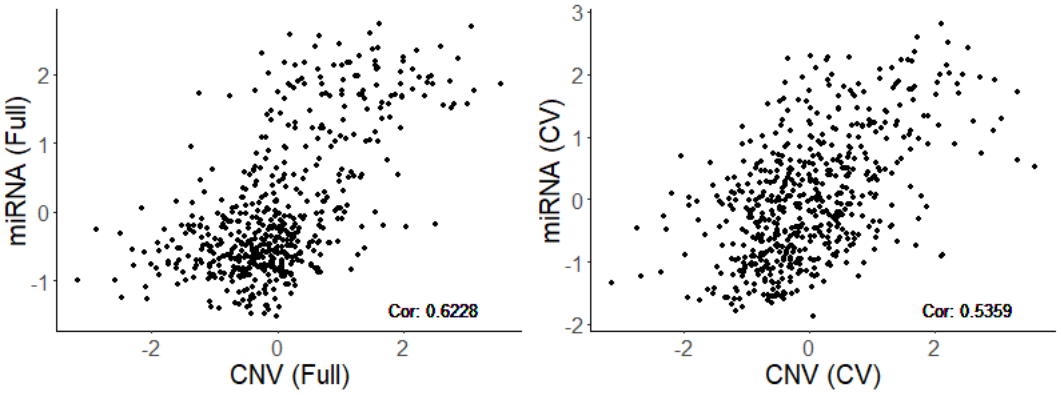
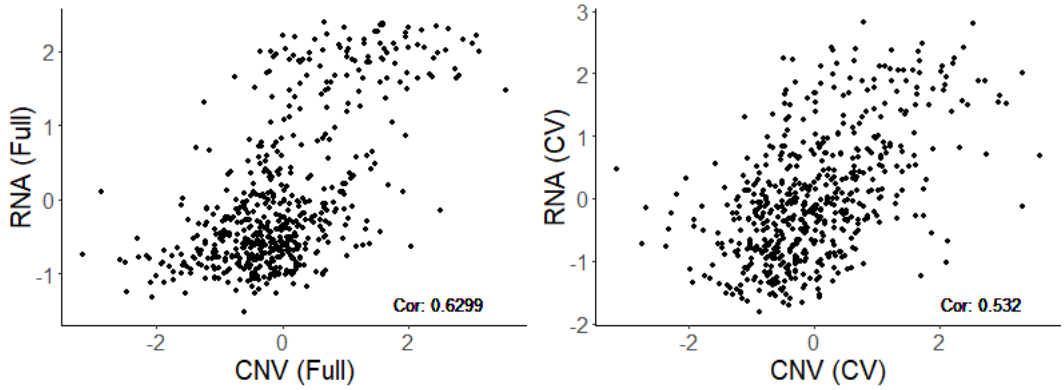
Supplementary Figure 5: MOFA with experimental data: Side-by-side contribution plots for gene expression versus miRNA using MOFA.



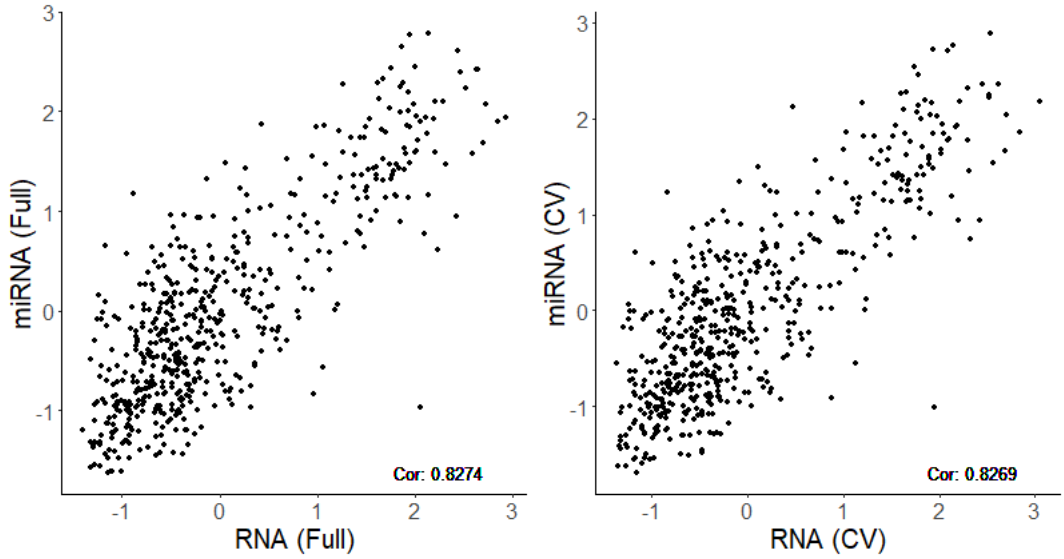
Supplementary Figure 6: MOFA with experimental data: Side-by-side contribution plots for CNV versus miRNA in experimental data using MOFA.



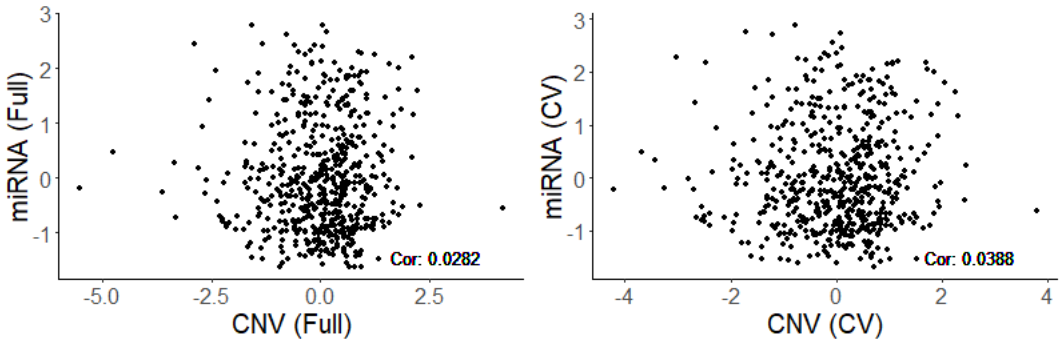
Supplementary Figure 7: MOFA with experimental data: Side-by-side contribution plots for CNV versus gene expression using MOFA.



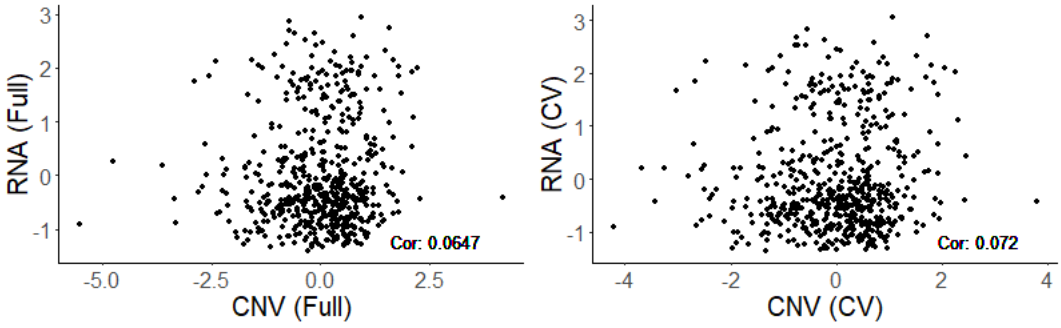
Supplementary Figure 8: AJIVE with experimental data: Side-by-side contribution plots for gene expression versus miRNA using AJIVE.



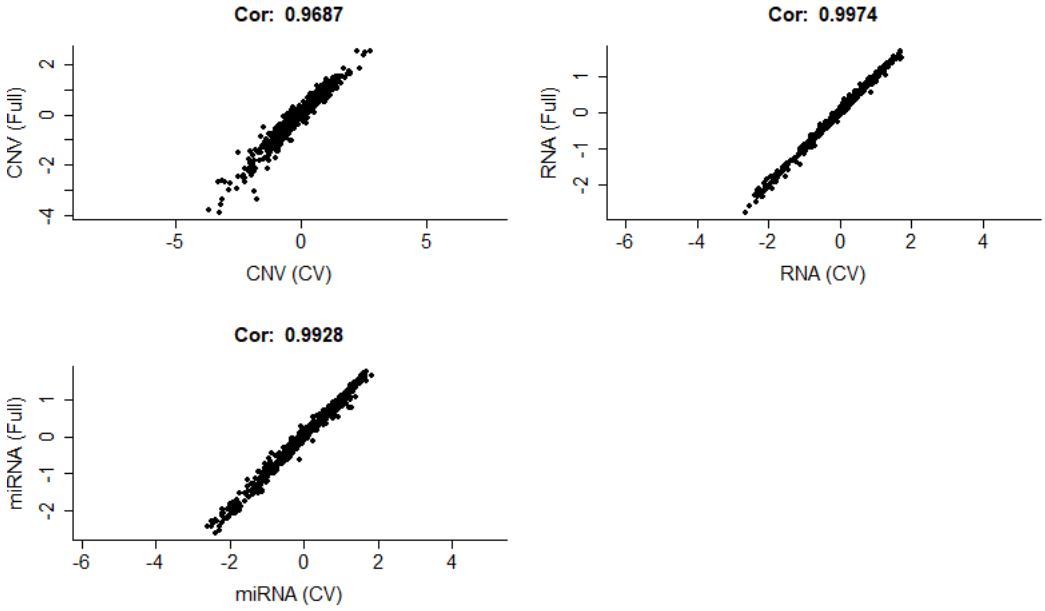
Supplementary Figure 9: AJIVE with experimental data: Side-by-side contribution plots for CNV versus micro RNA using AJIVE.



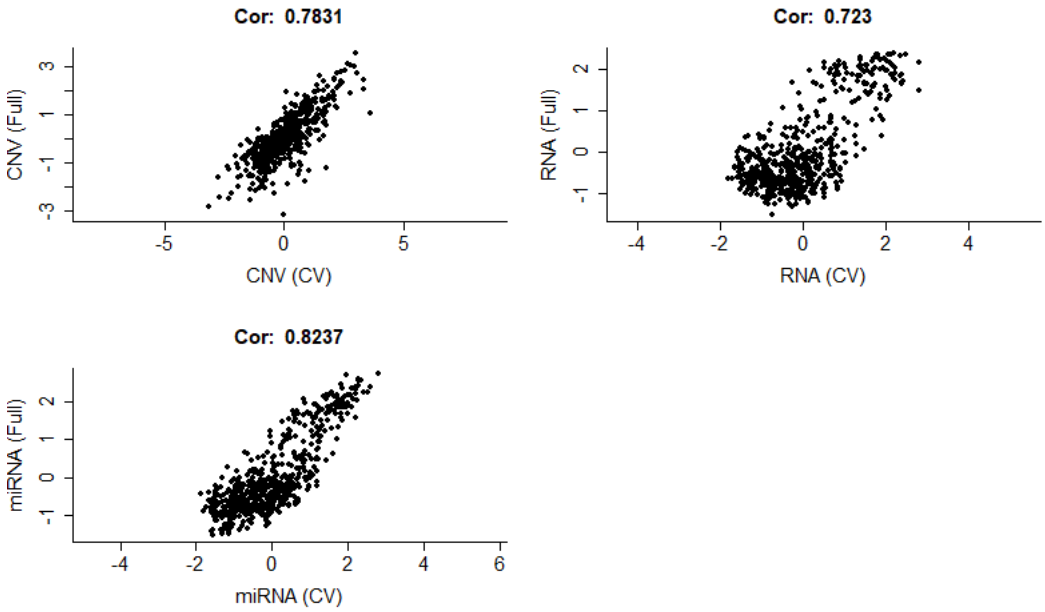
Supplementary Figure 10: AJIVE with experimental data: Side-by-side contribution plots for CNV versus gene expression using AJIVE.



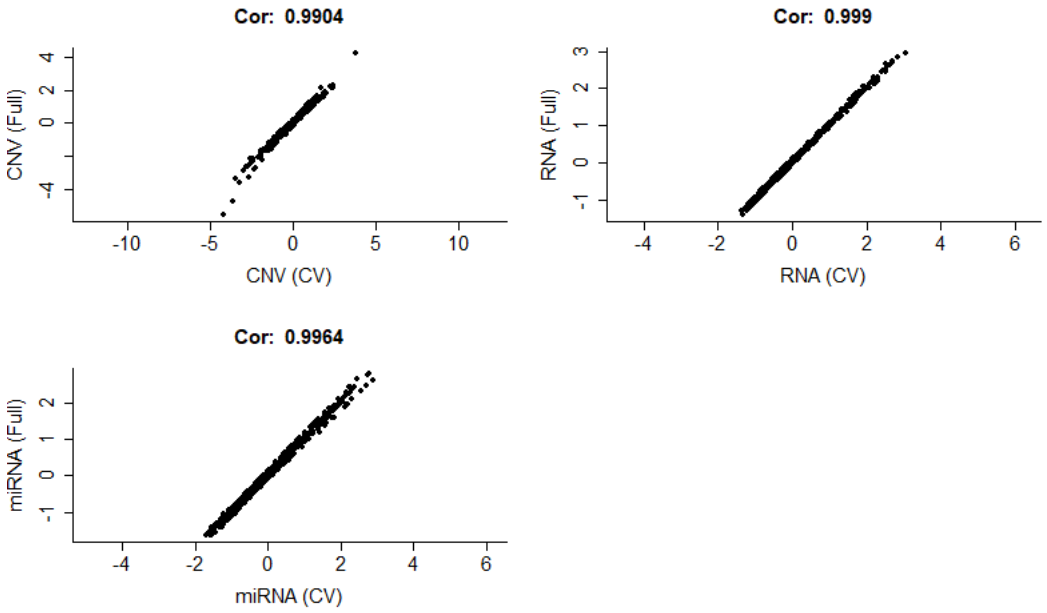
Supplementary Figure 11: Sparse mCCA with experimental data: Comparison plots for CNV, gene expression, and miRNA using Sparse mCCA.



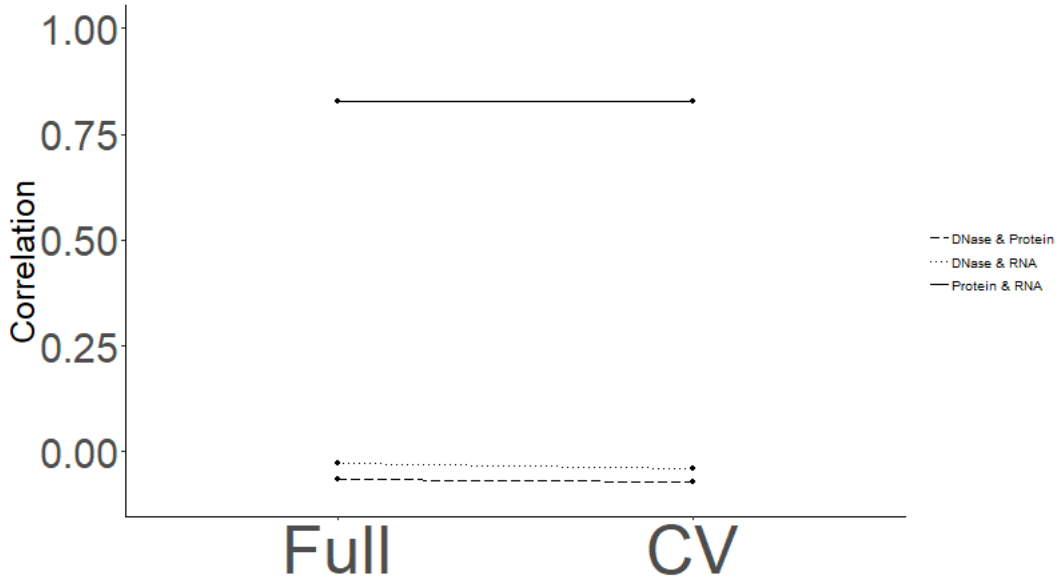
Supplementary Figure 12: MOFA with experimental data: Comparison plots for CNV, gene expression, and miRNA using MOFA.



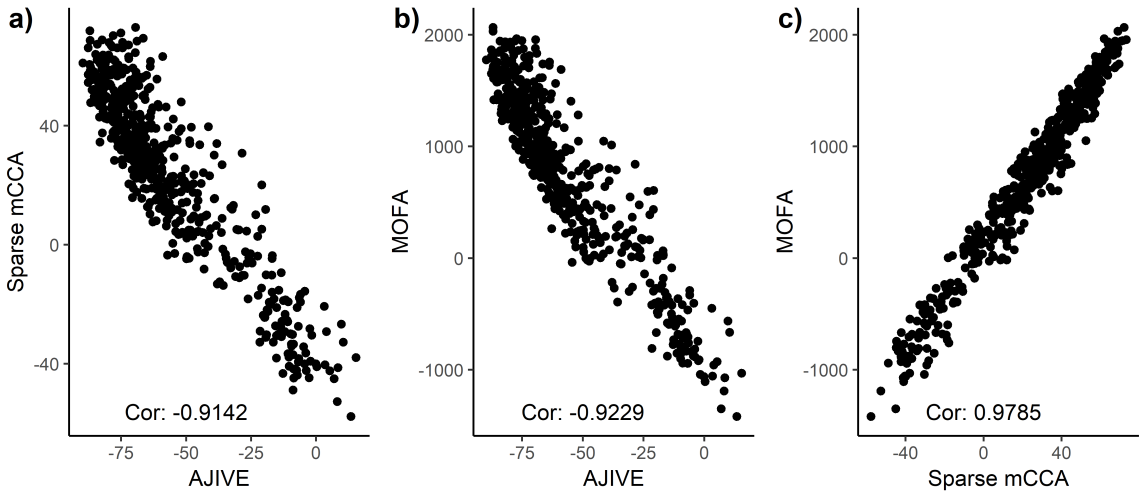
Supplementary Figure 13: AJIVE with experimental data: Comparison plots for CNV, gene expression, and miRNA using AJIVE.



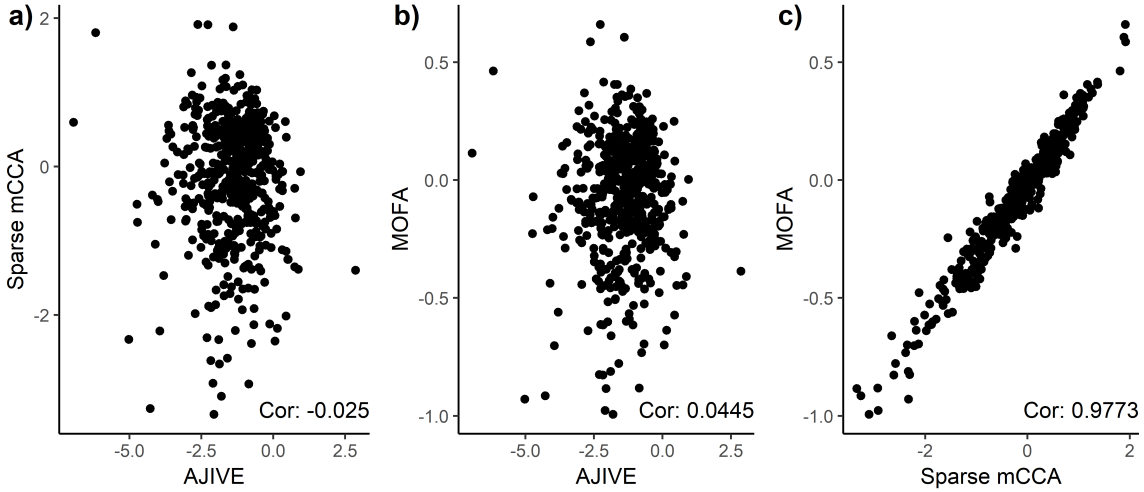
Supplementary Figure 14: Contribution correlations for AJIVE for each pair of data sets in an analysis with increased ranks for CNV.



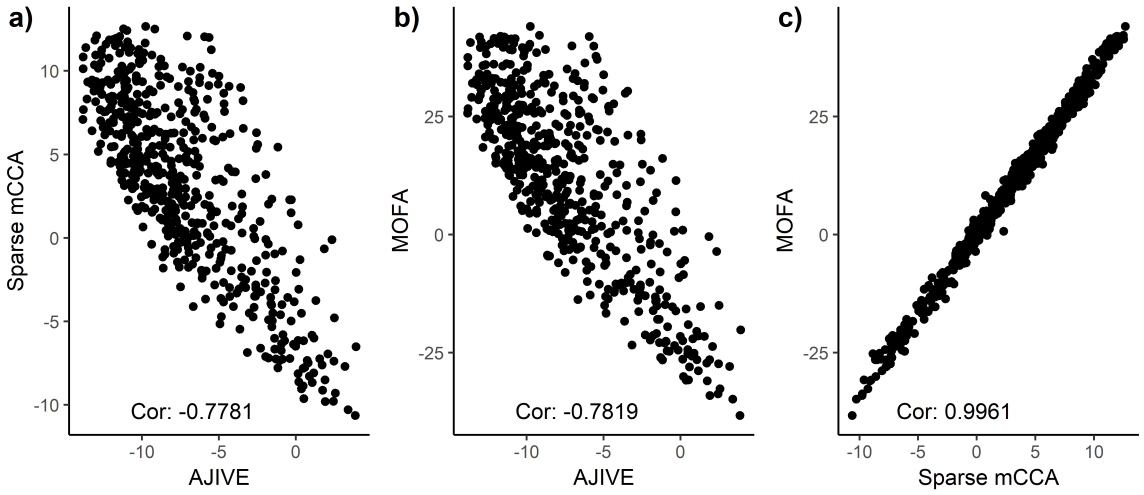
Supplementary Figure 15: Pairwise plots of RNA contributions for **a)** Sparse mCCA vs. AJIVE, **b)** MOFA vs. AJIVE, and **c)** MOFA vs. Sparse mCCA



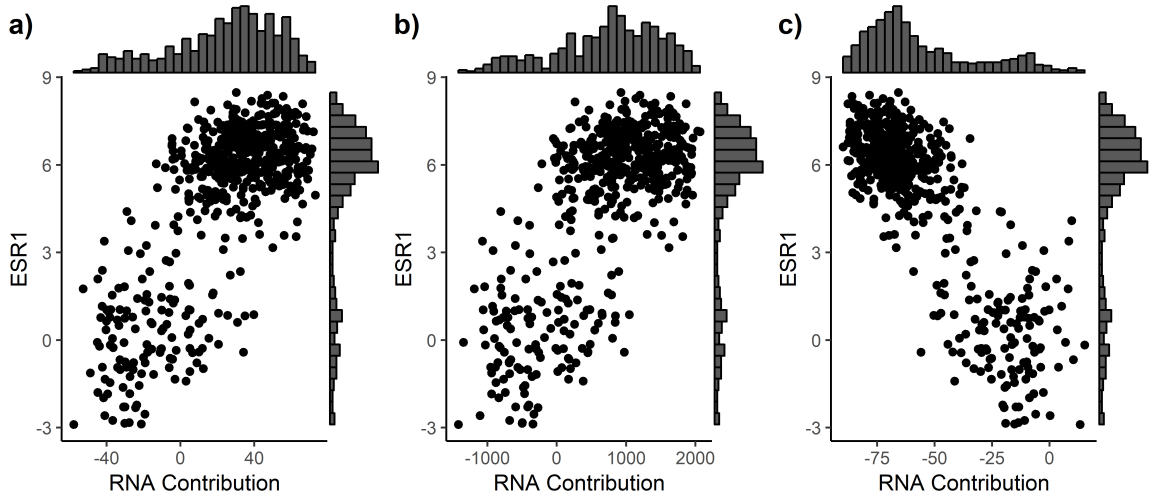
Supplementary Figure 16: Pairwise plots of CNV contributions for **a)** Sparse mCCA vs. AJIVE, **b)** MOFA vs. AJIVE, and **c)** MOFA vs. Sparse mCCA



Supplementary Figure 17: Pairwise plots of miRNA contributions for **a)** Sparse mCCA vs. AJIVE, **b)** MOFA vs. AJIVE, and **c)** MOFA vs. Sparse mCCA

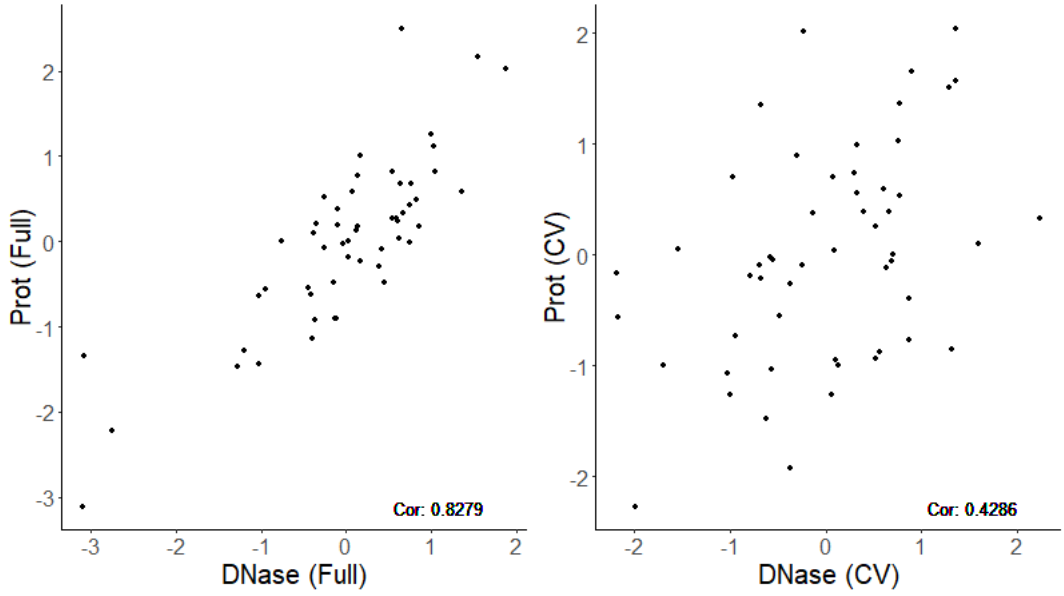


Supplementary Figure 18: Plot of expression of ESR1 gene against the RNA contribution for **a)** Sparse mCCA, **b)** MOFA, and **c)** AJIVE.

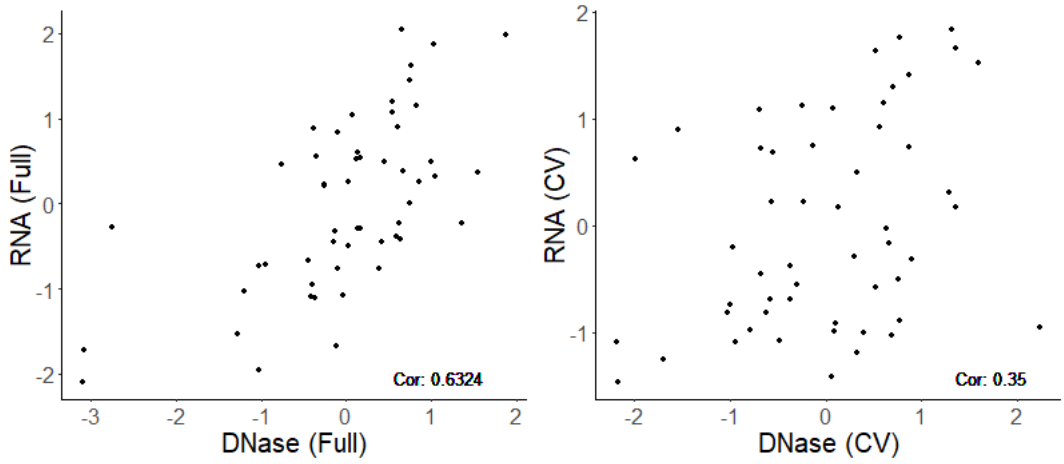


2.3 Small Sample Size - Li et al, 2016

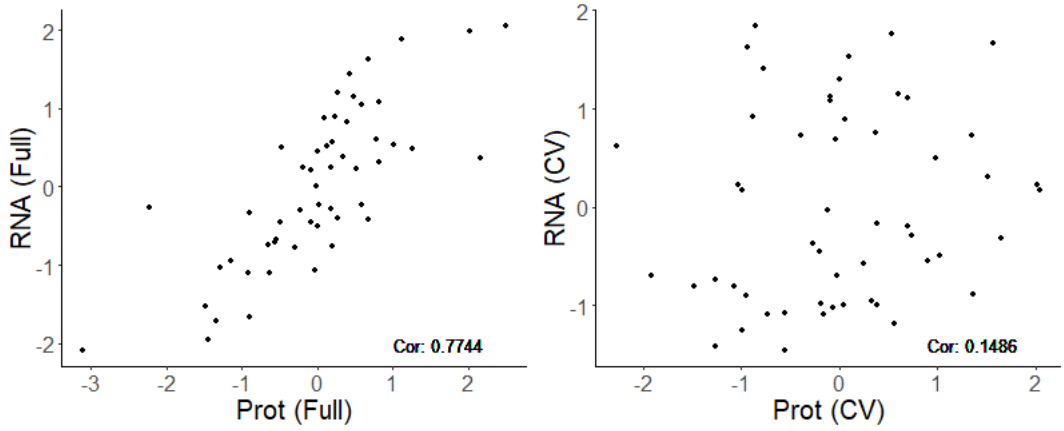
Supplementary Figure 19: MCCA with small-sample dataset: Contribution plots for DNase and Protein expression using MCCA.



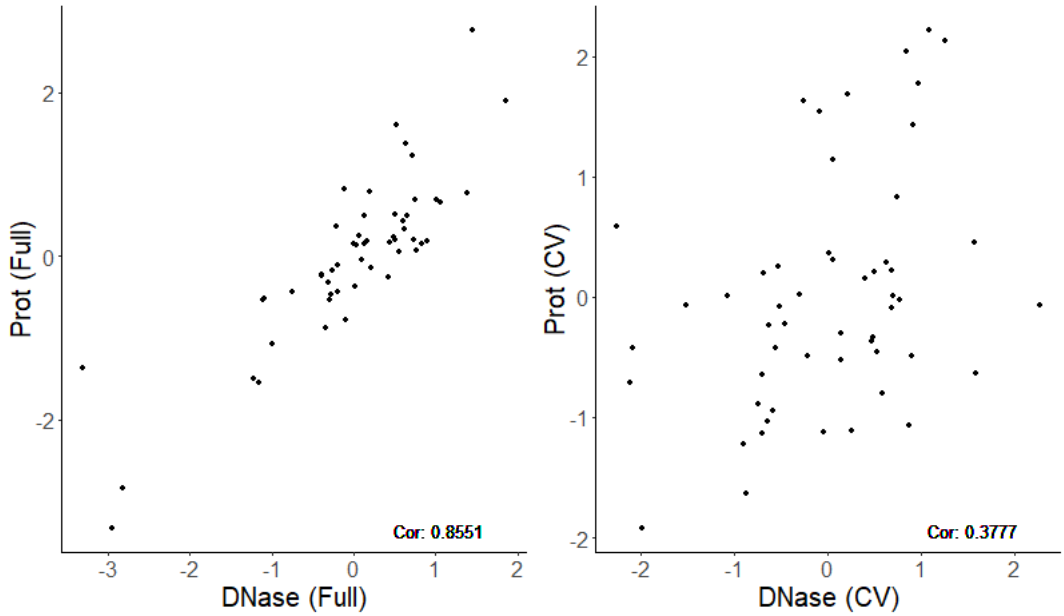
Supplementary Figure 20: MCCA with small-sample dataset: Contribution plots for DNase and gene expression using MCCA.



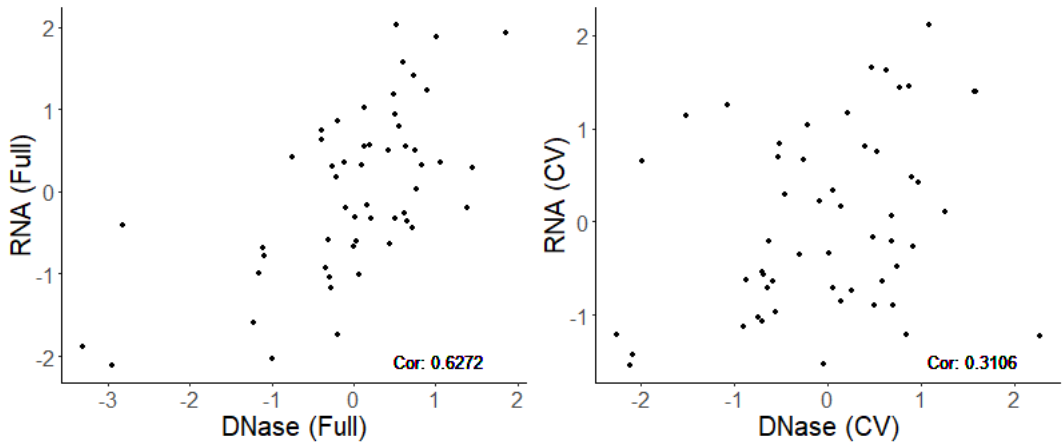
Supplementary Figure 21: MCCA with small-sample dataset: Contribution plots for protein expression and gene expression using MCCA.



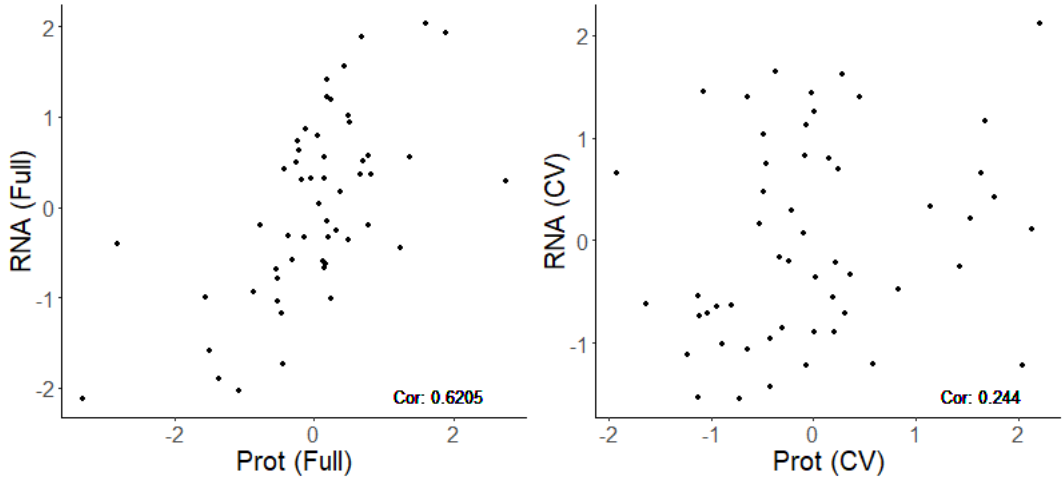
Supplementary Figure 22: MOFA with small-sample dataset: Contribution plots for DNase and protein expression using MOFA.



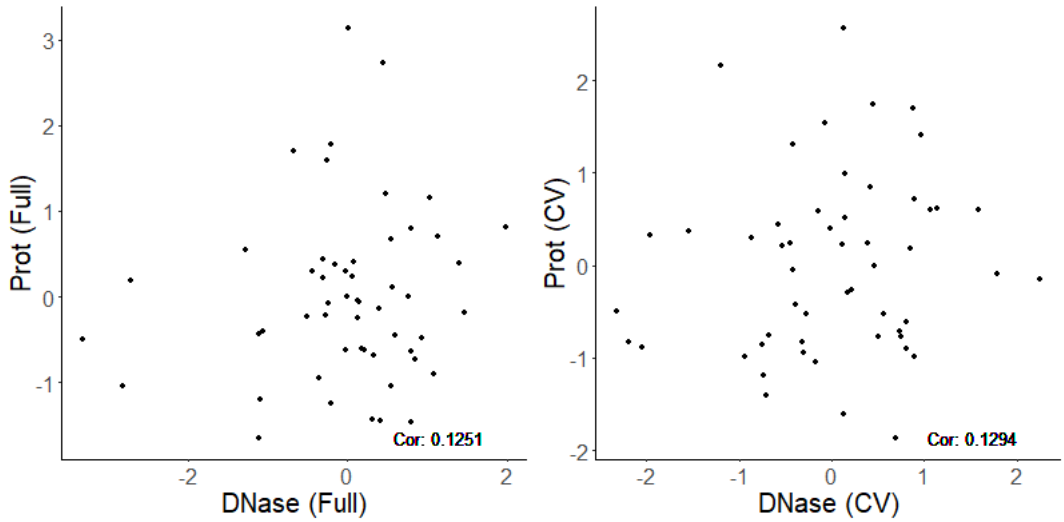
Supplementary Figure 23: MOFA with small-sample dataset: Contribution plots for DNase and gene expression using MOFA.



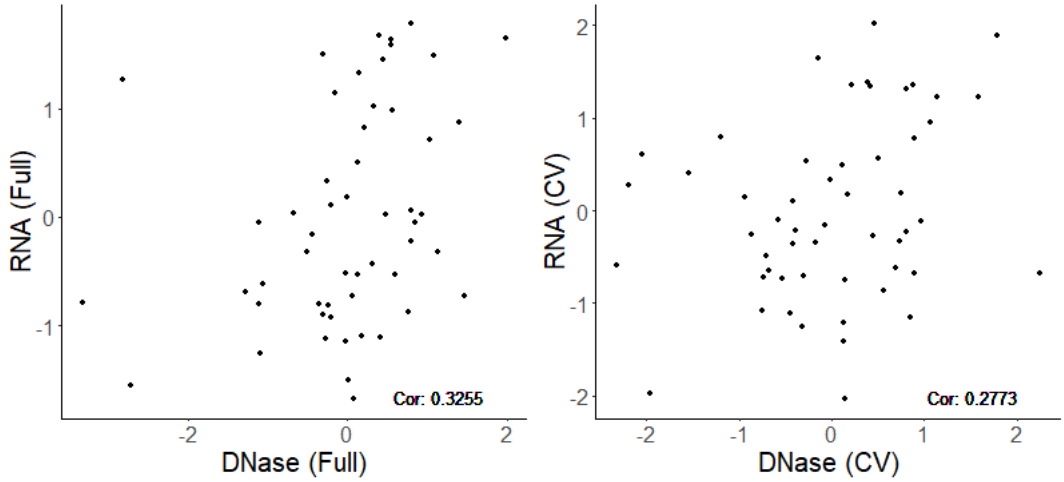
Supplementary Figure 24: MOFA with small-sample dataset: Contribution plots for protein expression and gene expression using MOFA.



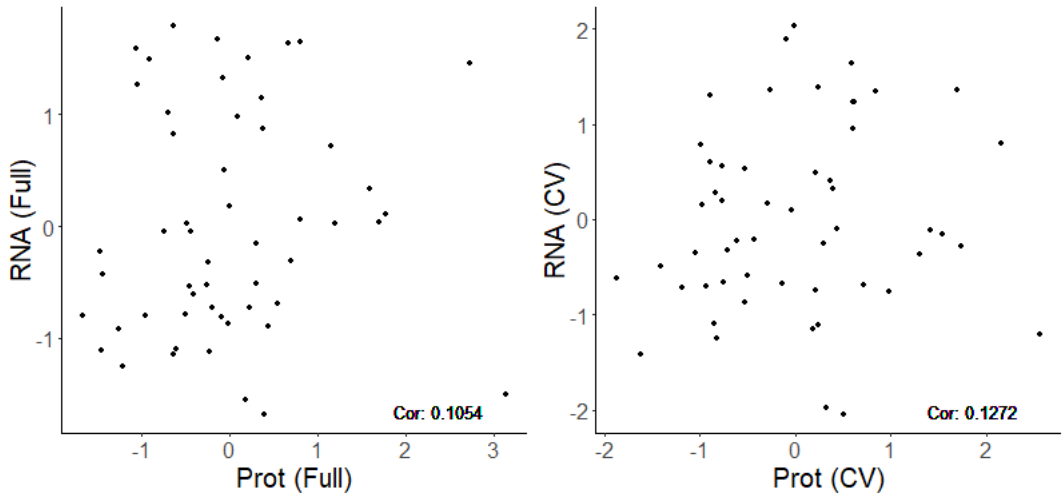
Supplementary Figure 25: AJIVE with small-sample dataset: Contribution plots for DNase and protein expression using AJIVE.



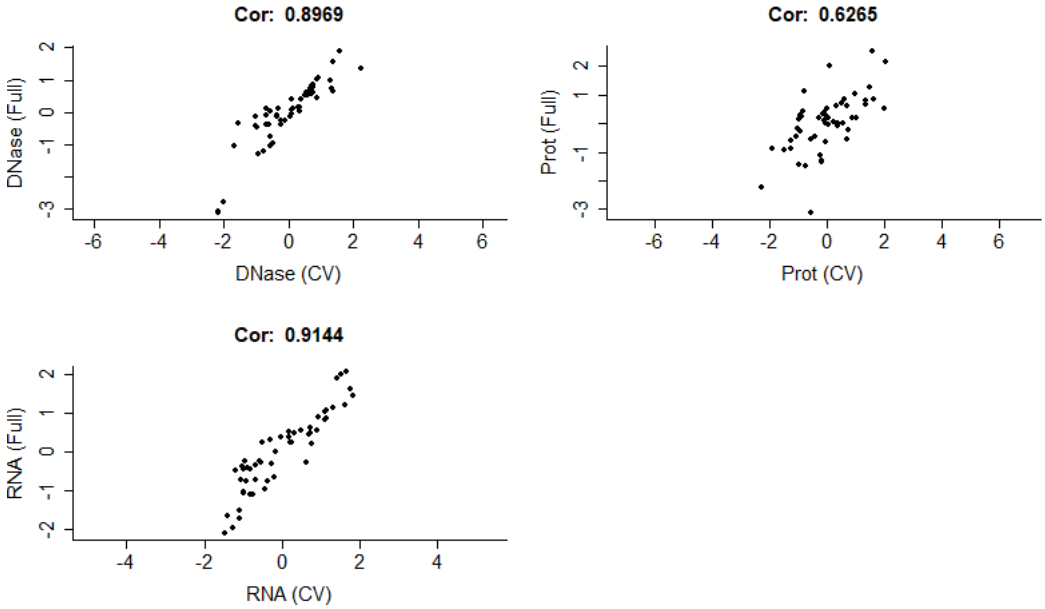
Supplementary Figure 26: AJIVE with small-sample dataset: Contribution plots for DNase and gene expression using AJIVE.



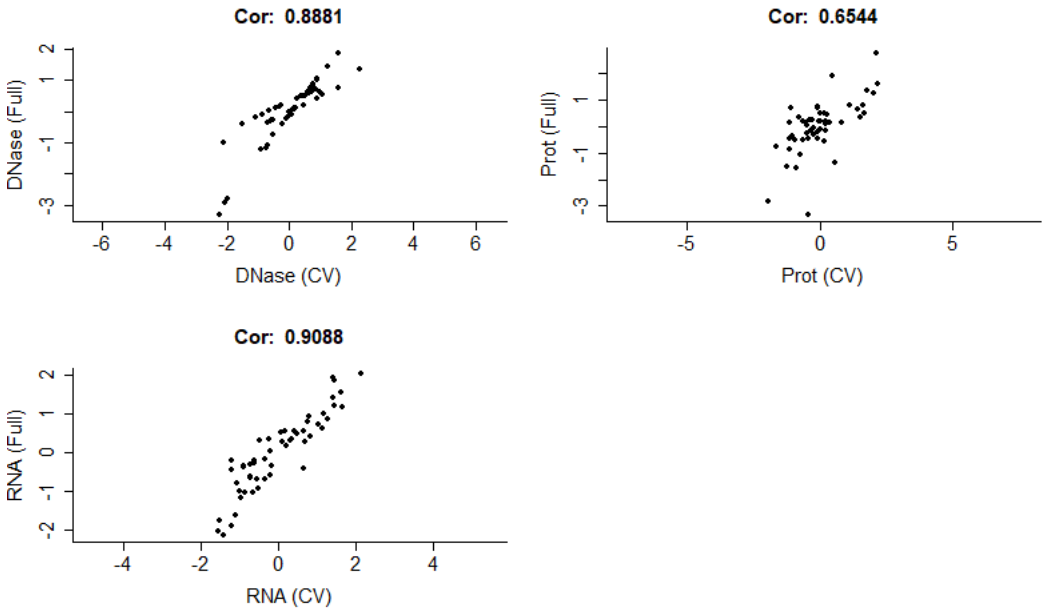
Supplementary Figure 27: AJIVE with small-sample dataset: Contribution plots for protein expression and gene expression using AJIVE.



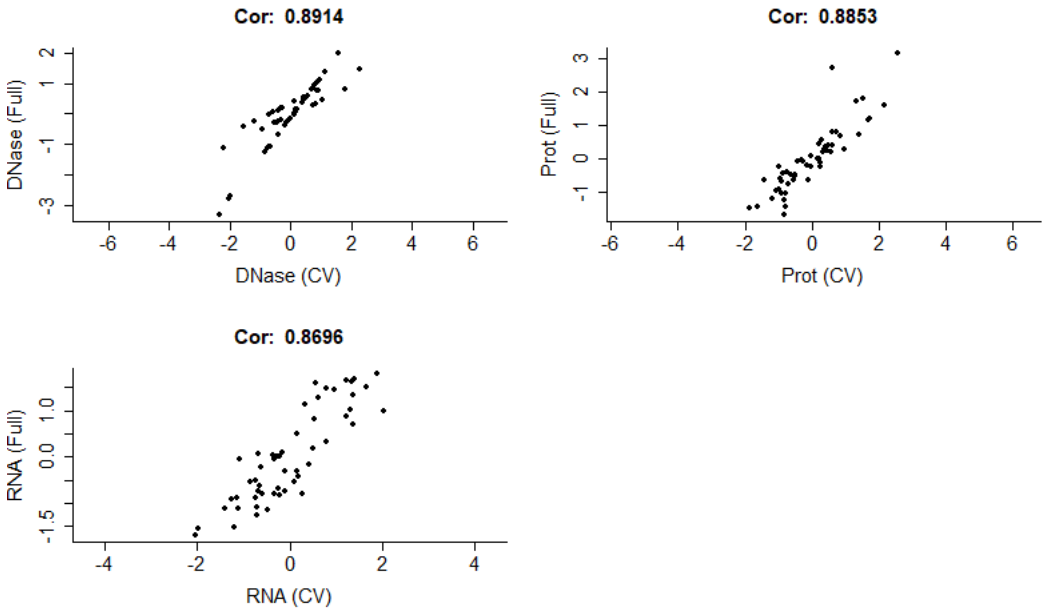
Supplementary Figure 28: MCCA with small-sample dataset: Comparison plots for DNase, protein expression, and gene expression using AJIVE.



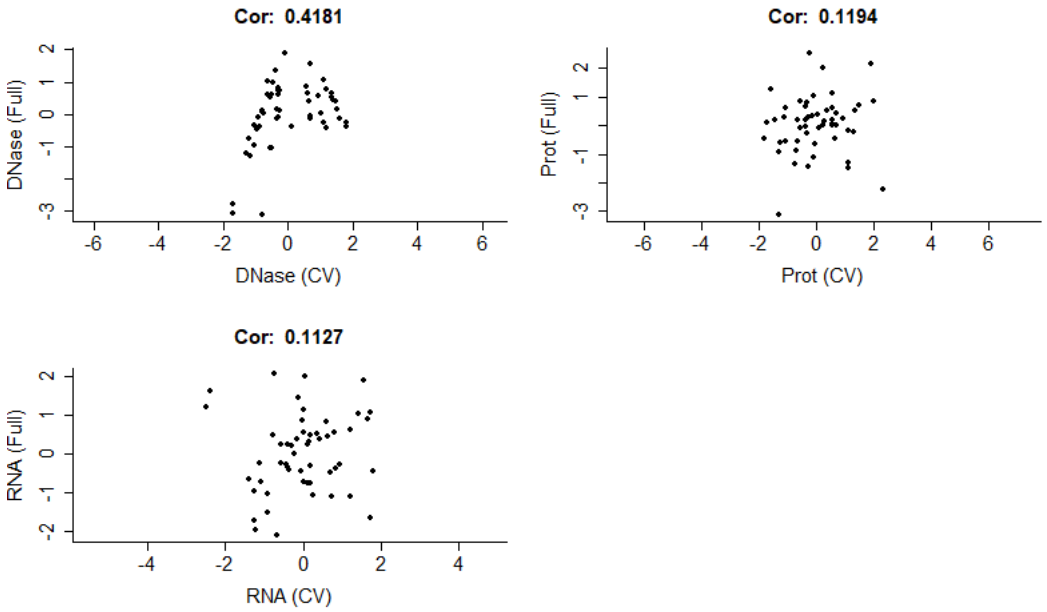
Supplementary Figure 29: MOFA with small-sample dataset: Comparison plots for DNase, protein expression, and gene expression using AJIVE.



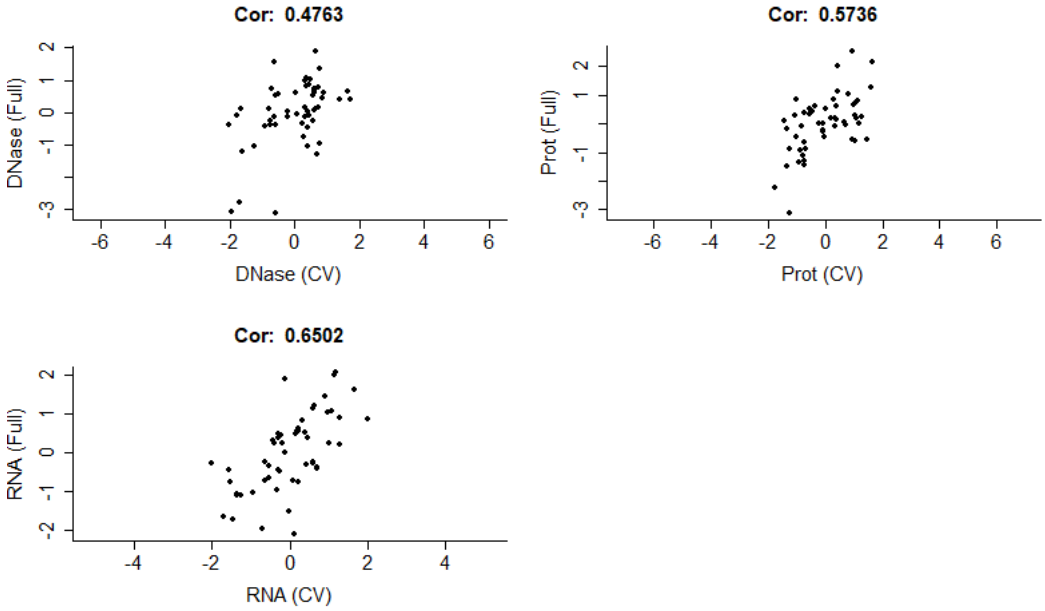
Supplementary Figure 30: AJIVE with small-sample dataset: Comparison plots for DNase, protein expression, and gene expression using AJIVE.



Supplementary Figure 31: Comparison plots of contributions from Sparse mCCA for the 3 fold analysis.

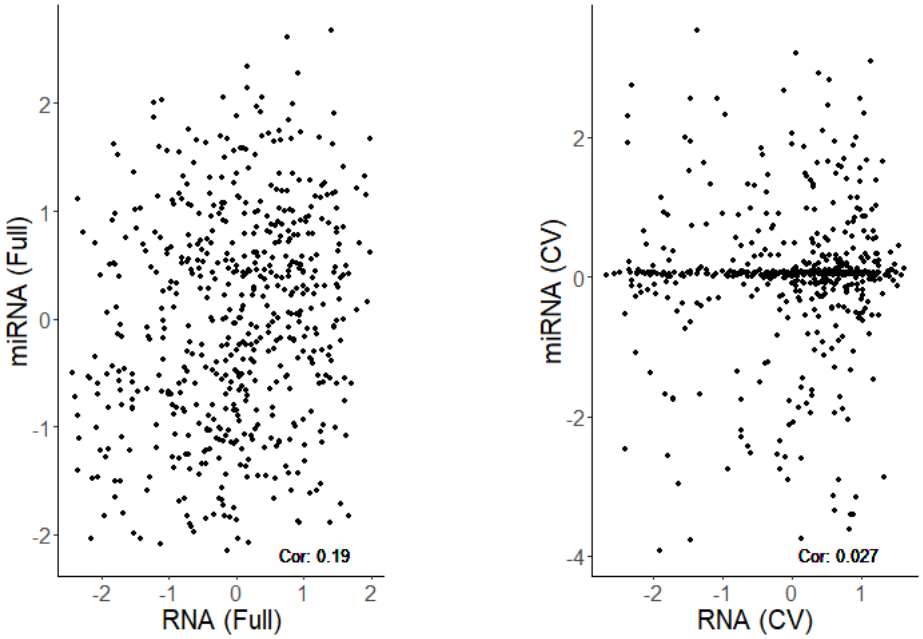


Supplementary Figure 32: Comparison plots of contributions from Sparse mCCA for the 10 fold analysis.

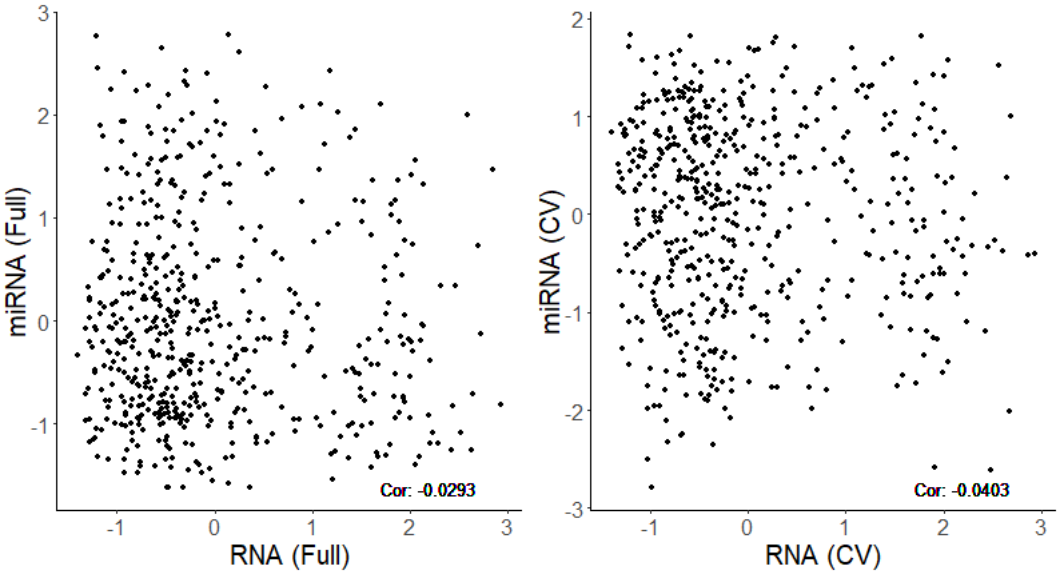


2.4 Permuted Null Data

Supplementary Figure 33: MOFA with null data: Side-by-side contribution plots for miRNA versus gene expression using MOFA.



Supplementary Figure 34: AJIVE with null data: Side-by-side contribution plots for miRNA versus gene expression using AJIVE.



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