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ORIGINAL ARTICLE

METTL7A as a New Candidate Biomarker in Gastric Cancer by Genomics and Data-Independent Acquisition Proteomic Analysis

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SUMMARY

Background: **Early diagnosis and intervention are essential for improving the prognosis and survival of gastric cancer (GC) patients. However, specific biomarkers for early GC diagnosis are still unavailable.**
Methods: **Data-independent acquisition (DIA) proteomics was employed to identify differentially expressed proteins (DEPs) between GC and adjacent non-tumor tissues. Functional and pathway enrichment analyses were conducted, with subsequent genomic-level validation. Methyltransferase-like 7A (METTL7A) expression in GC versus adjacent tissues was confirmed via tissue microarray analysis. Correlations between METTL7A expression, clinical characteristics, and immune infiltration were also explored. Additionally, co-expressed genes related to METTL7A were analyzed, and gene set variation analysis (GSVA) was performed.**
Results: **DIA proteomics identified 84 DEPs, mainly involved in protein binding and enriched in complement and coagulation pathways. Eight DEPs overlapped with results from the gene expression omnibus (GEO) dataset. METTL7A expression was significantly lower in GC tissues compared to adjacent tissues, confirmed at the genomic level. The cancer genome atlas (TCGA) analysis revealed an area under the receiver operating characteristic (ROC) curve (AUC) of 0.81, with METTL7A expression inversely correlated with age (p = 7.307e-05). Tissue microarray analysis further confirmed reduced METTL7A expression in GC tissues (p = 0.000). METTL7A expression was positively correlated with activated B cells and negatively correlated with activated CD4 T cells.**
Conclusions: **METTL7A is a promising biomarker for early GC diagnosis.**
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Supplementary Data

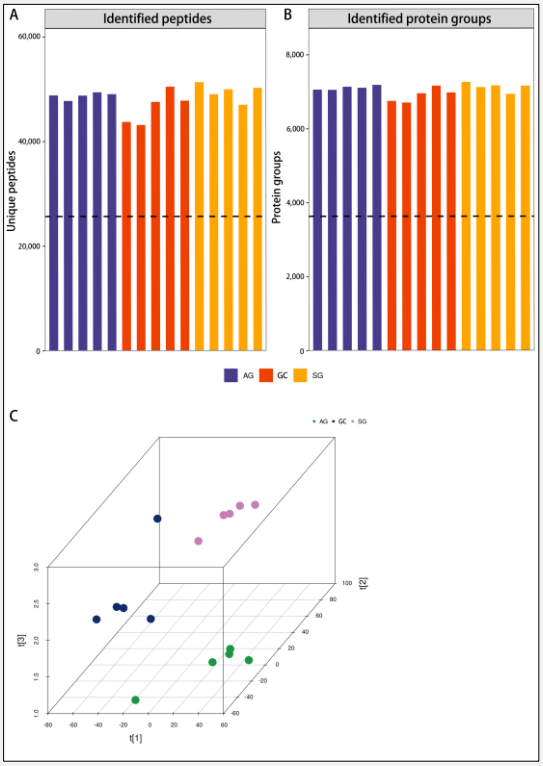

Figure S1. DIA proteomics identification, quantitative analysis, and PCA principal component analysis.

A) The total number of identified peptide segments. B) The total number of identified proteins. C) 3D PCA analysis of all samples. AG - chronic atrophic gastritis, GC - gastric cancer, SG - chronic superficial gastritis, t[1] - principal component 1, t[2] - principal component 2, t[3] - principal component 3.

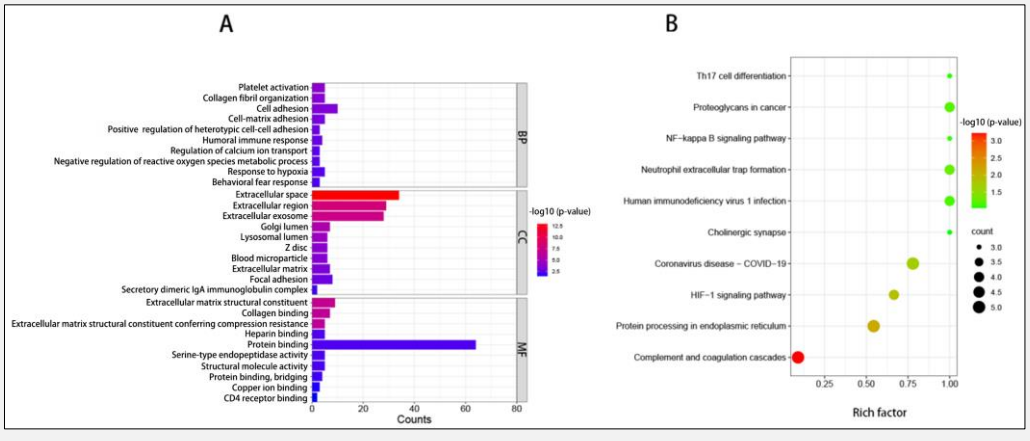

Figure S2. Functional and pathway enrichment analyses of DEPs.

A) The top 10 functional enrichment in BP, CC, and MF analysis of DEPs, respectively. B) The KEGG analysis of DEPs. BP - biological process, CC - cellular component, MF - molecular function.

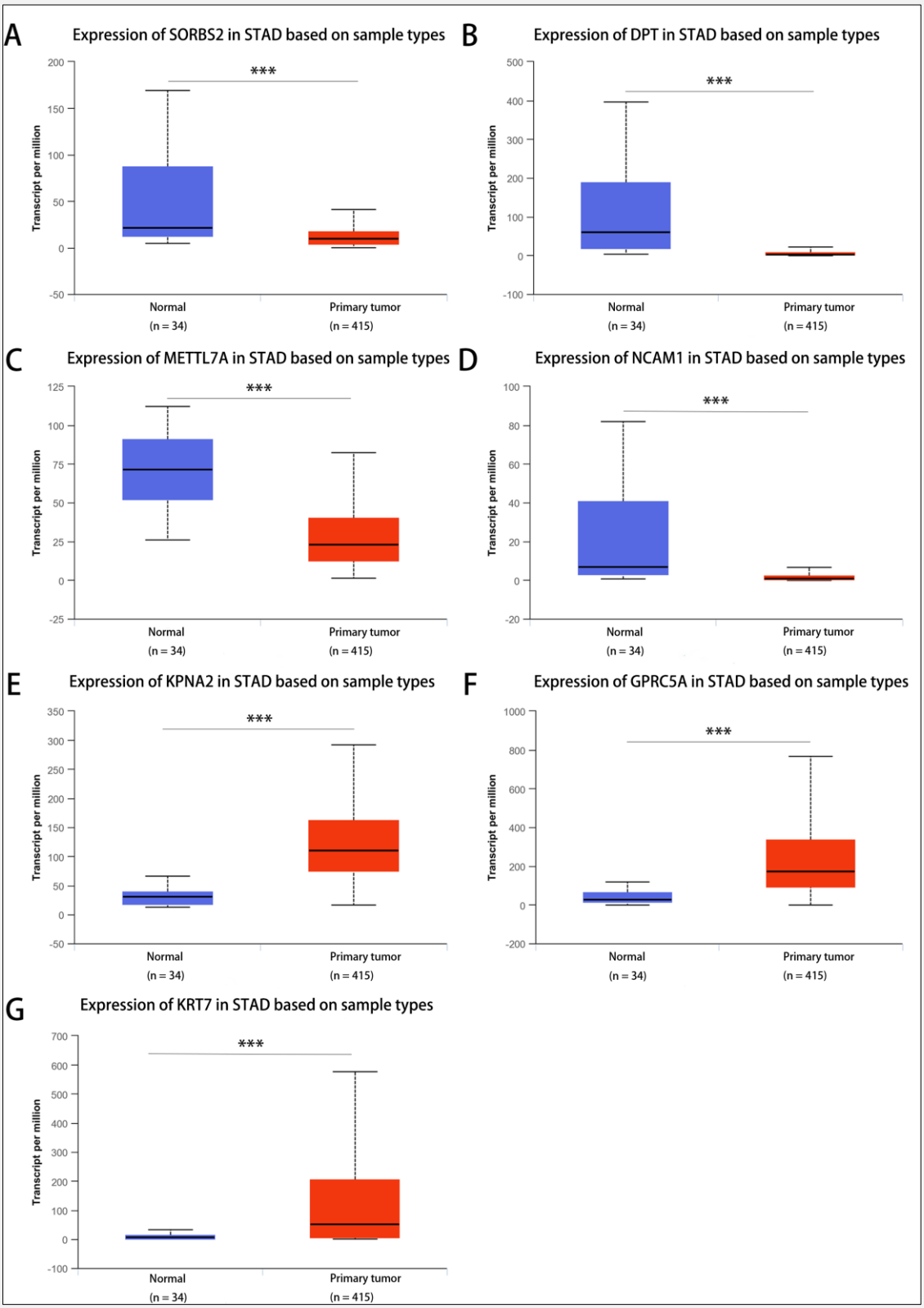

Figure S3. The expression of DEGs in the STAD dataset of the TCGA database in UALCAN.

***** - p < 0.001.**

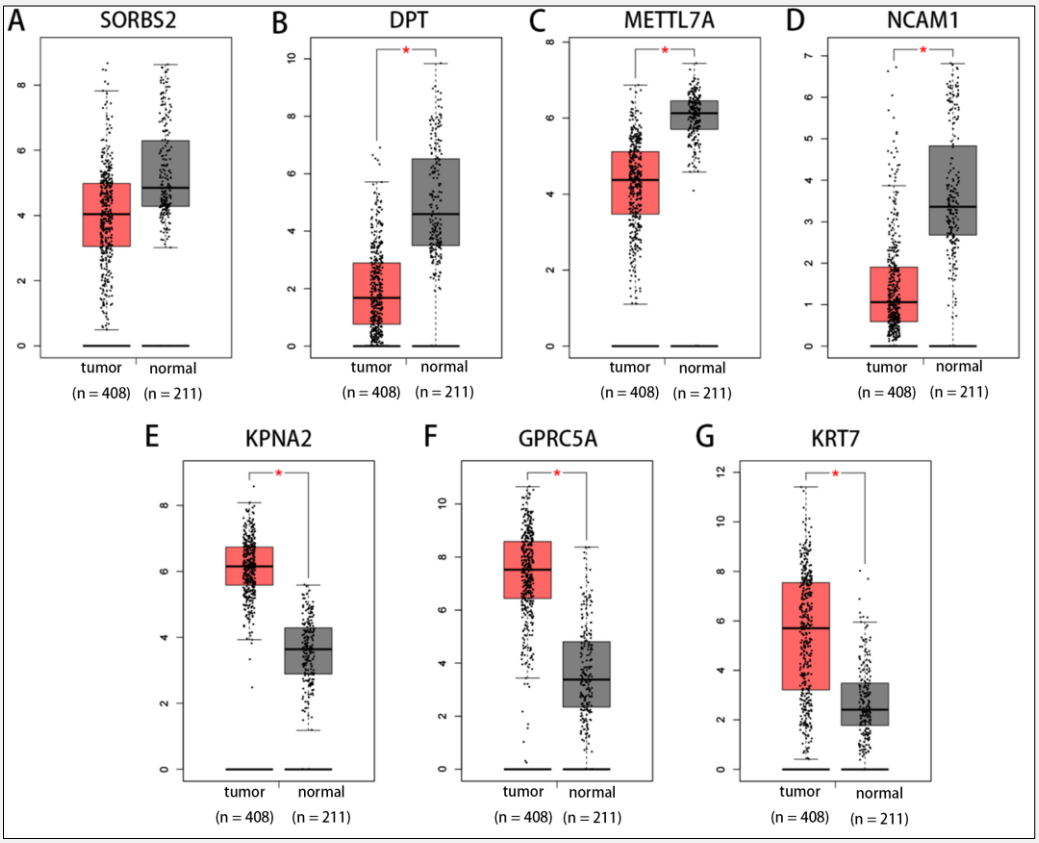

Figure S4. The expression of DEGS in the STAD dataset of the GEPIA database.

*** - p < 0.05.**

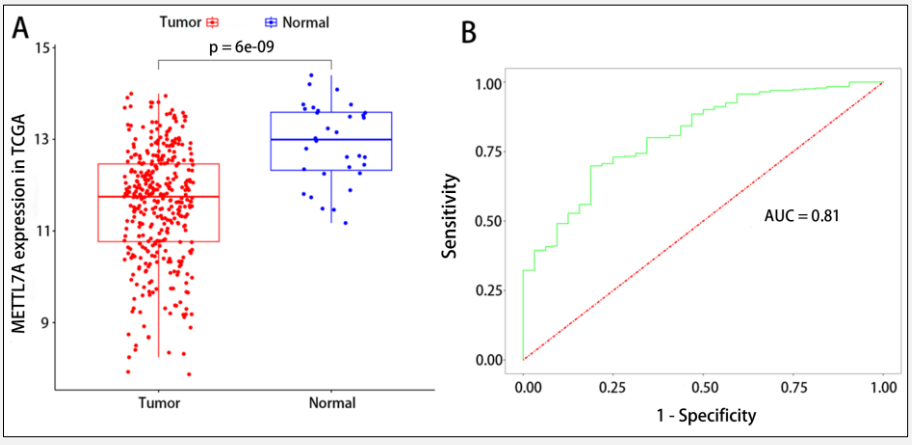

Figure S5. METTL7A mRNA levels in GC tissue compared to normal tissue.

A) The mRNA expression level of METTL7A was significantly lower in GC tissues compared to normal tissues. B) The ROC curve of METTL7A expression in GC and control.

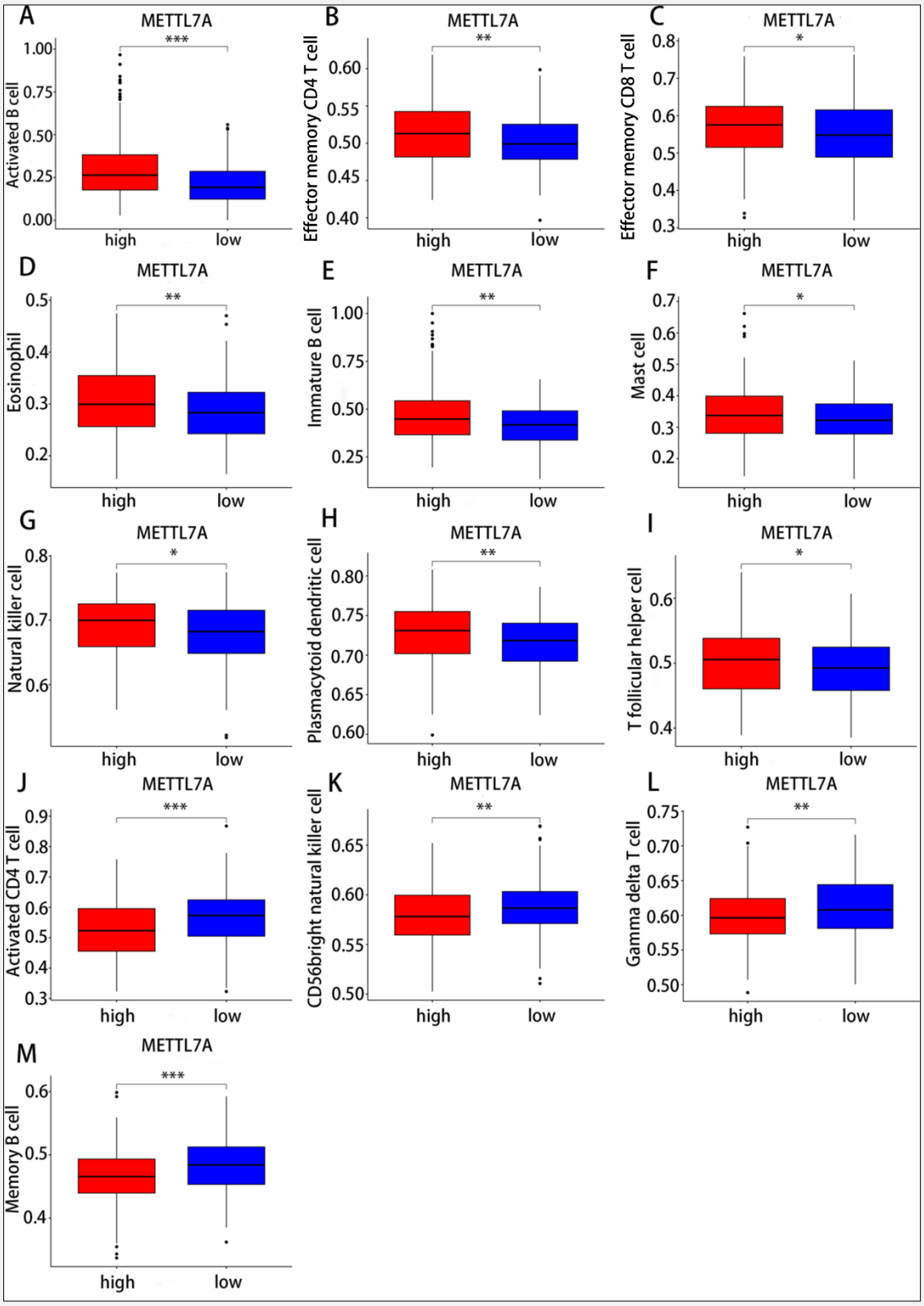

Figure S6. The enrichment level of immune cells in the METTL7A high-expression group and low-expression group.

A - I) Immune cells positively-correlated with METTL7A expression. J - M) Immune cells negatively-correlated with METTL7A expression. * - p < 0.05, ** - p < 0.01, * - p < 0.001.**

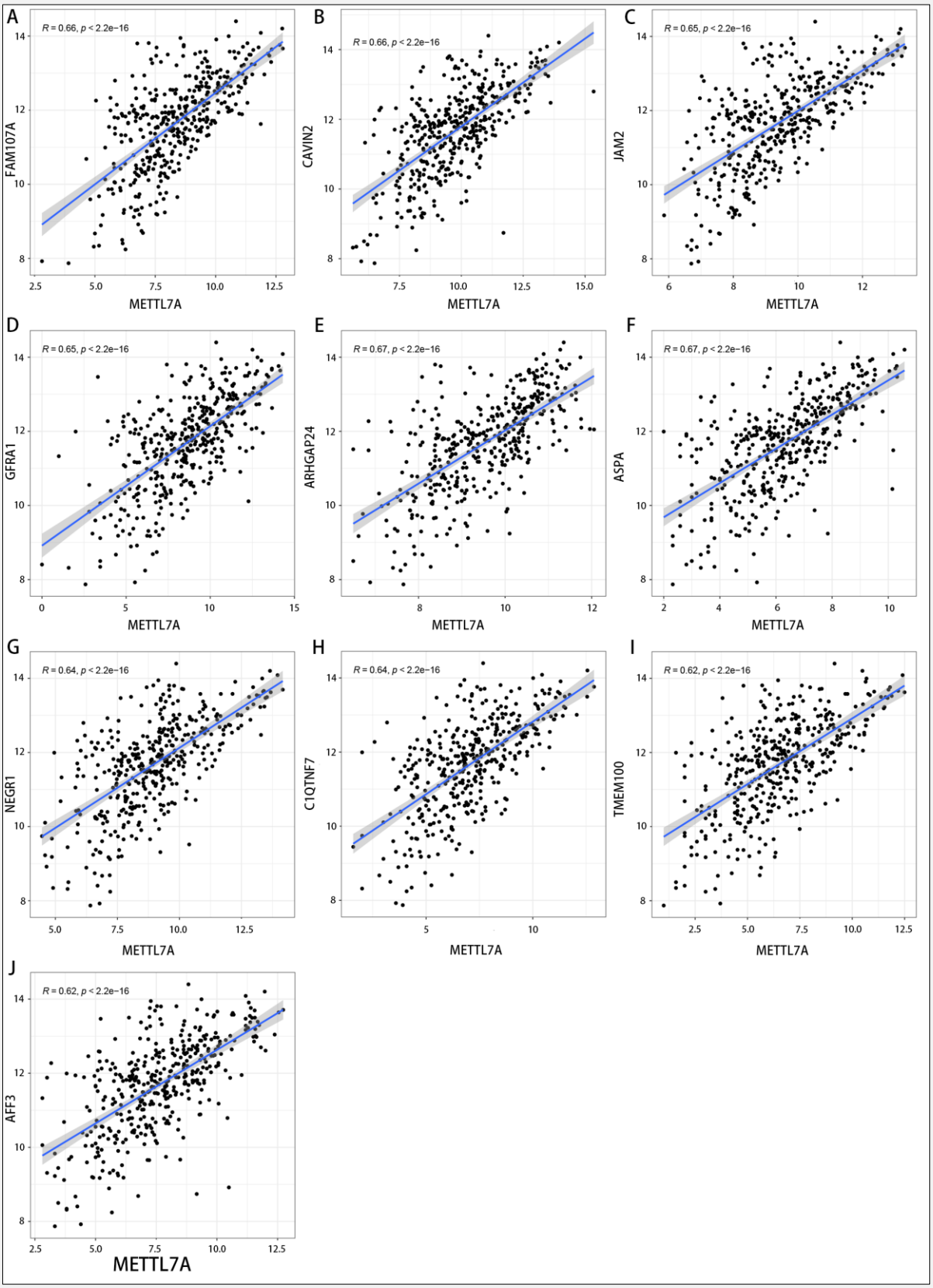

Figure S7. The top 10 co-expressed genes positively-correlated with the expression level of METTL7A.

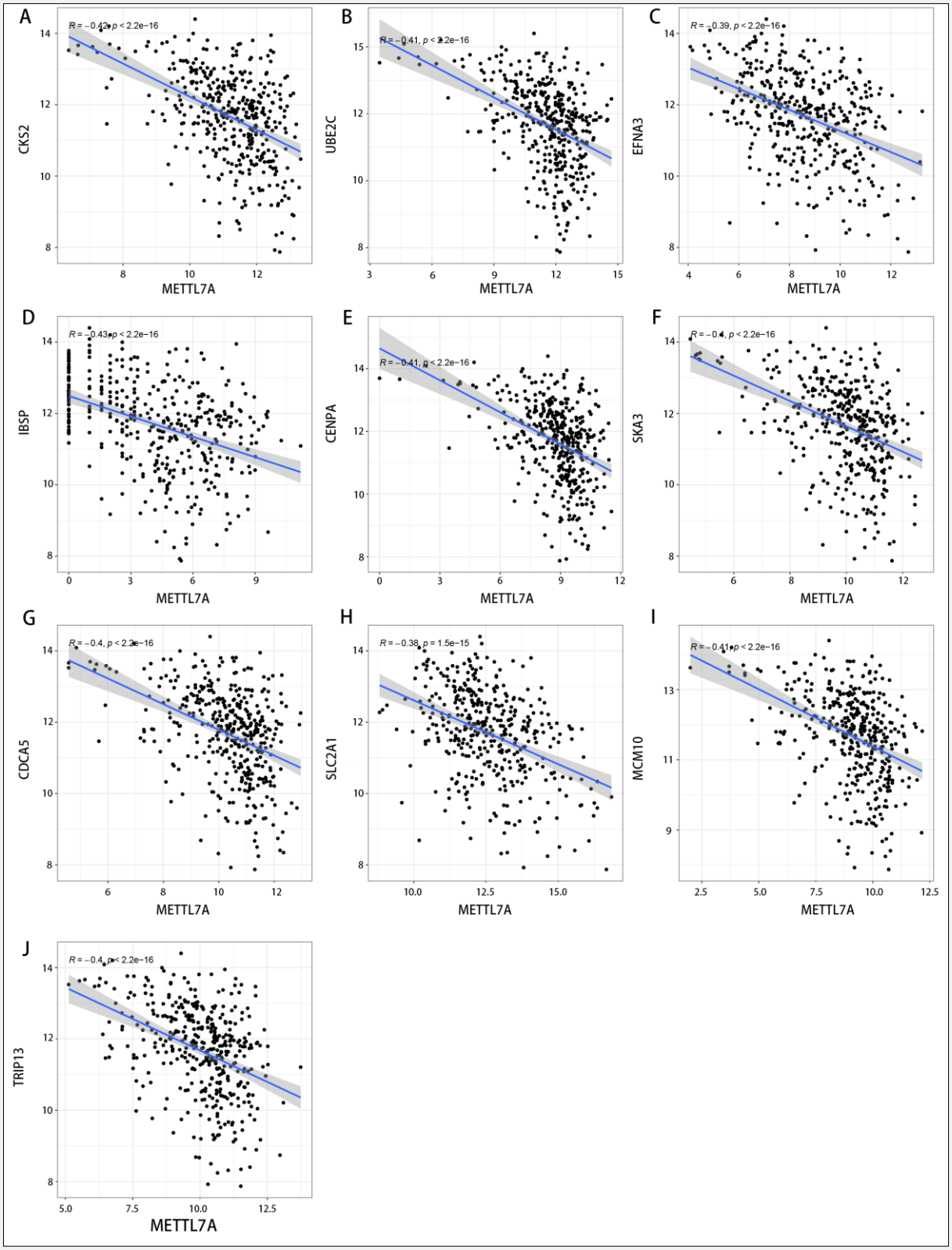

Figure S8. The top 10 co-expressed genes negatively-correlated with the expression level of METTL7A.