Figure S1. Expression of 17 N7-methylguanosine RNA methylation regulators in tumor and normal tissue samples from the Gene Expression Profiling Interactive Analysis 2 database (black represents normal tissue, while red represents tumor tissue). *P<0.05. TPM, transcripts per million. num(T), number of tumor tissue samples; num(T), number of normal tissue samples.
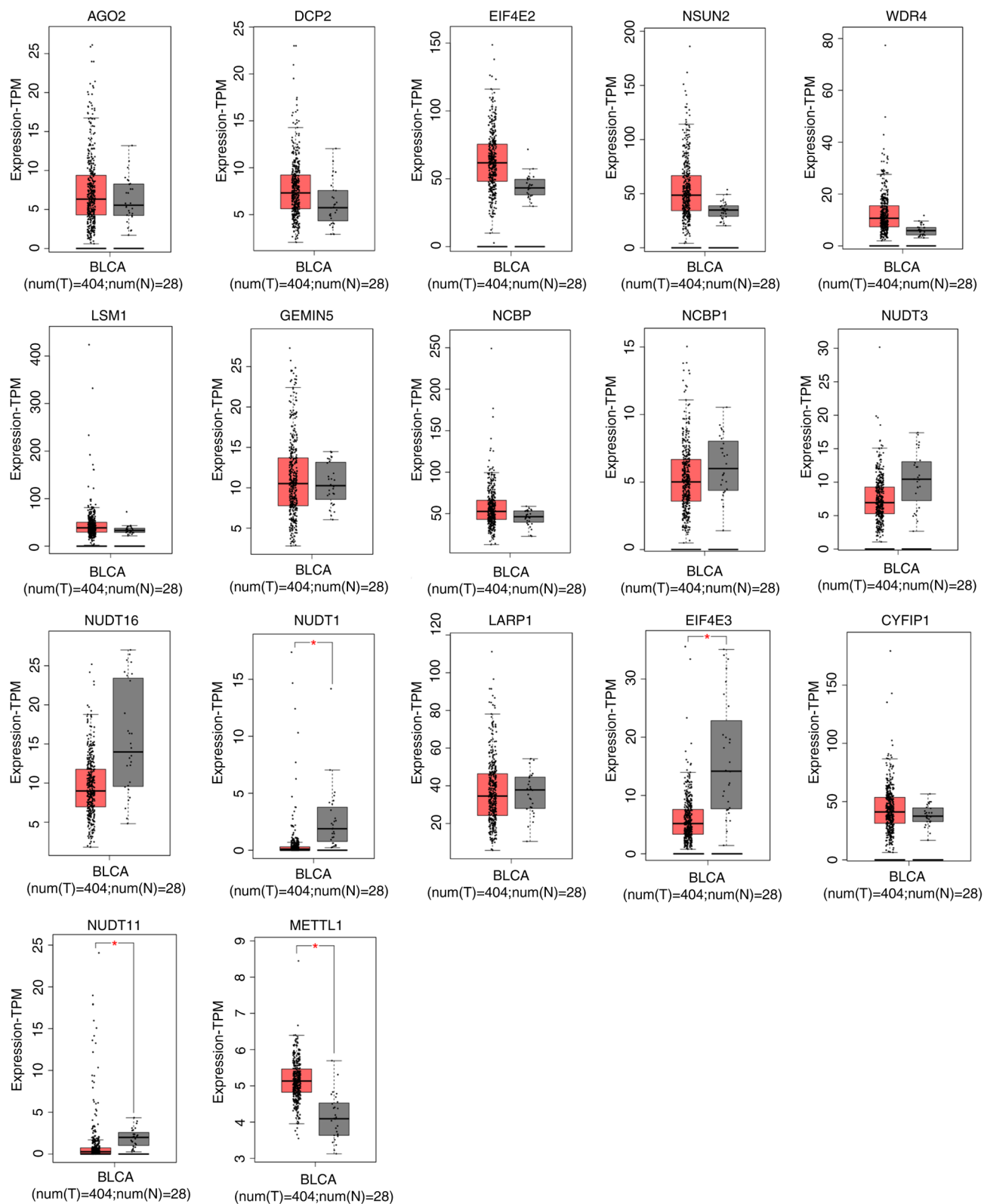
Figure S2. Protein-protein interaction network. (A) Network 1: Minimum required interaction score: 0.4; line color indicates the type of interaction. (B) Network 2: The circle represents the target genes, while the edges describe the association. The size and color intensity of the circle is proportional to the clustering coefficient.
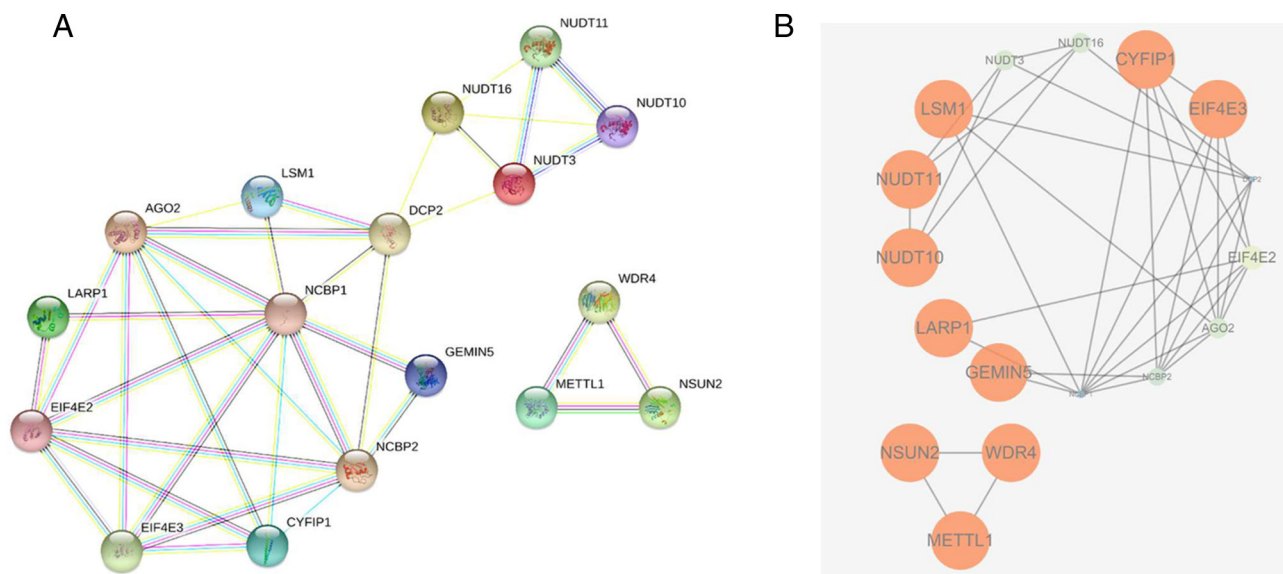
Figure S3. Effect of knockdown or overexpression of four genes on the immune microenvironment and prognosis. Effect of knockdown or overexpression of (A) Nudix hydrolase 11; (B) Gem nuclear organelle-associated protein 5; (C) Cytoplasmic FMR1 interacting protein 1; and (D) Eukaryotic translation initiation factor 3 subunit D. (E) Survival curves showing the effect of expression on survival, where the blue line represents low levels and red line represents high levels.
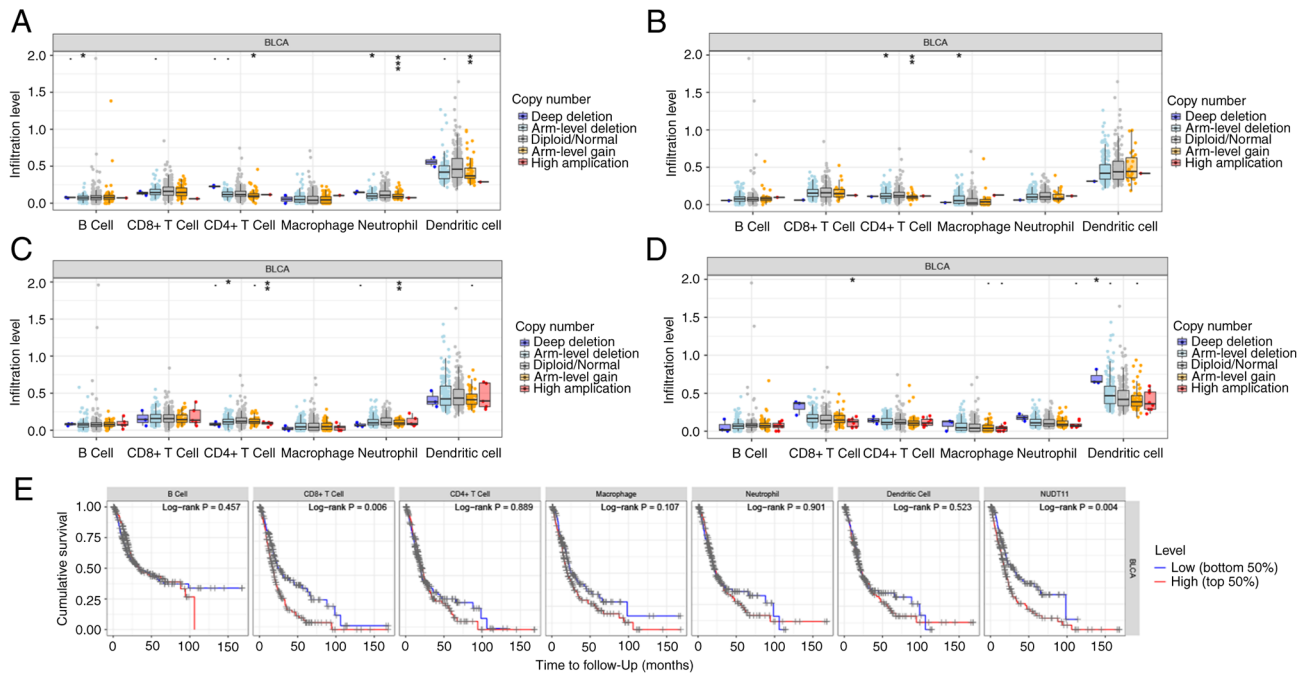
Figure S4. Protein expression of three of the prognostic genes according to the Human Protein Atlas database. N, normal samples; T, tumor samples.