Supporting Information:

RNA-binding proteomics reveals MATR3 interacting with lncRNA SNHG1 to enhance neuroblastoma progression

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Figure S1. The mass spectrum of candidate proteins.

Table S1. The list of identified proteins interacting with SNHG1 in SK-N-BE(2)C cells. Protein identification was performed by MaxQuant Version 1.5.2.8.

Table S2. The list of identified proteins interacting with SNHG1 in SK-N-DZ cells. Protein identification was performed by MaxQuant Version 1.5.2.8.

Table S3. The list of identified proteins interacting with SNHG1 in SK-N-AS cells. Protein identification was performed by MaxQuant Version 1.5.2.8.

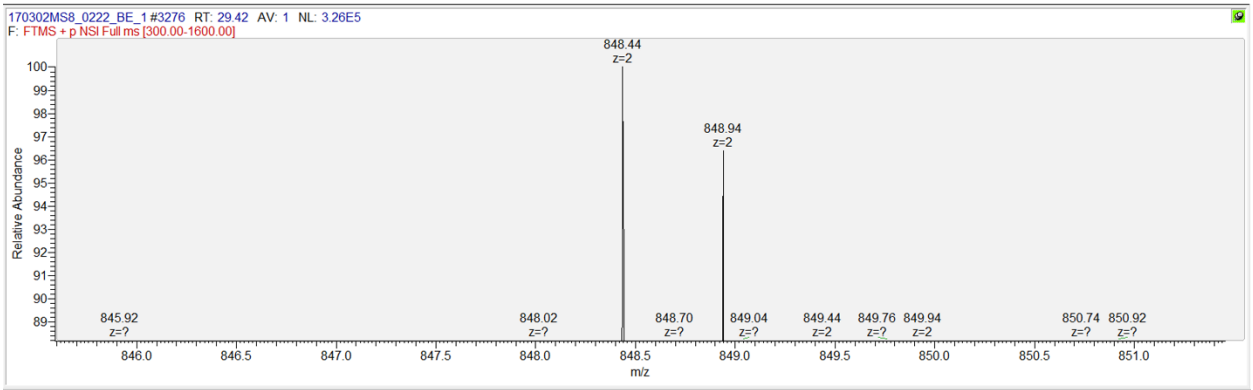
Table S4. GSEA report for SNHG1 positive correlated genes.

Table S5. GSEA report for MATR3 positive correlated genes.

a

Evidence ID: 5238 YBX1

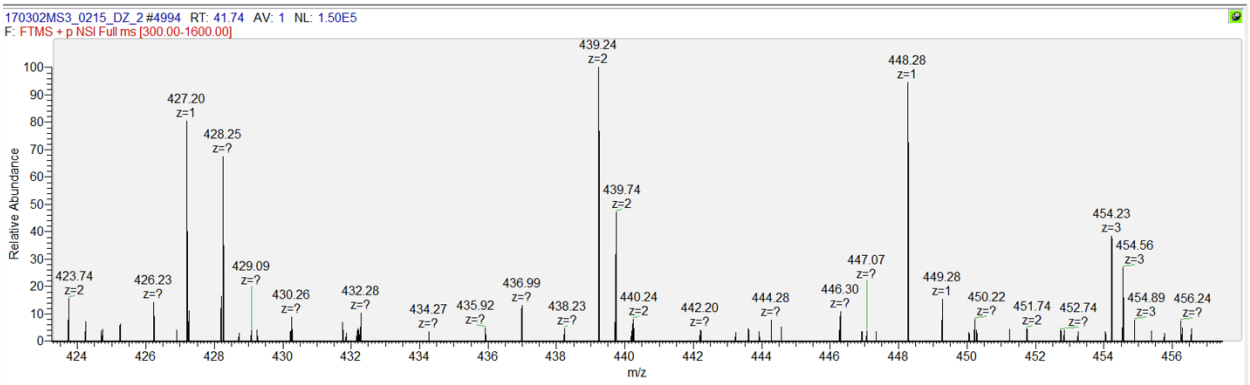
Retention time: 29.395; m/z: 848.44; Charge: 2; Coverage: 46.6%



b

Evidence ID: 1154 MATR3

Retention time: 41.728; m/z: 439.24; Charge: 2; Coverage: 45.3%



c

Evidence ID: 2800 DDX5

Retention time: 49.505; m/z: 525.77; Charge: 2; Coverage: 42.5%

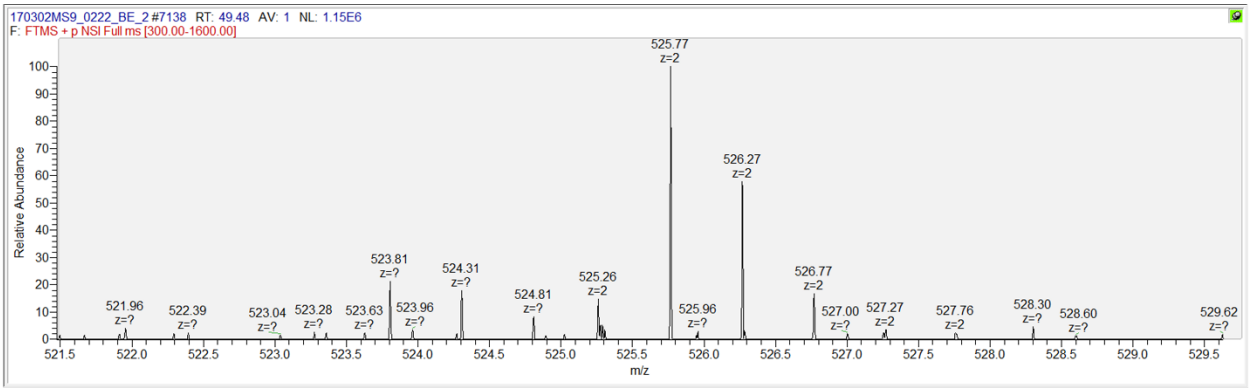


Figure S1. The mass spectrum of candidate proteins. The MS/MS spectrum of YBX1 **(A)**, MATR3 **(B)** and DDX5 **(C).** The retention time, m/z and charge of YBX1, MATR3 and DDX5 were obtained from proteomics data.