

SIPA1 Regulates LINC01615 to Promote Metastasis in Triple-Negative Breast Cancer

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Sample	Total Raw Reads (M)	Total Clean Reads (M)	Total Clean Bases (Gb)	Clean Reads Q30 (%)	Clean Reads Ratio (%)
MDA-MB-231_1	119.94	113.48	11.35	92.83	94.62
MDA-MB-231_2	119.94	113.12	11.31	93.28	94.32
MDA-MB-231/sh-SIPA1_1	119.94	113.71	11.37	93.36	94.81
MDA-MB-231/sh-SIPA1_2	119.94	114.03	11.4	93.77	95.08

Figure S1. High-throughput sequencing data output and post-QC results.

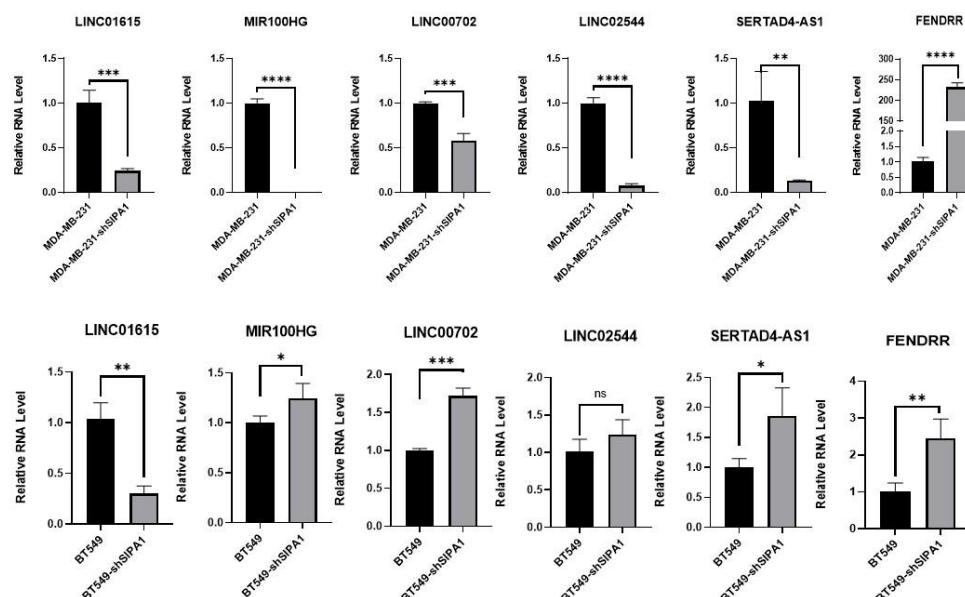


Figure S2. The expression of LINC01615 was decreased after knockdown of SIPA1. Real-time RT-PCR was used to detect the relative expression of MIR100HG, LINC00702, LINC01615, LINC02544, SERTAD4-AS1 and FENDRR in BT549 and BT549/sh-SIPA1 and MDA-MB-231 and MDA-MB-231/sh-SIPA1 cells. Data represent the means \pm SD. **P < 0.01.

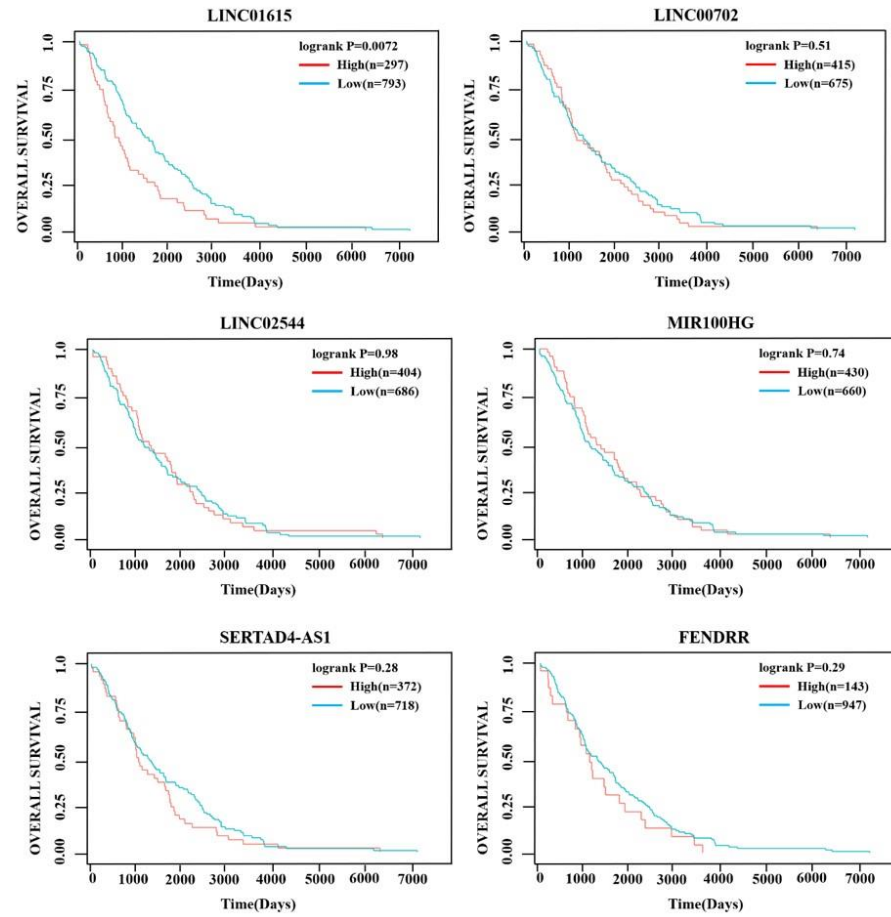


Figure S3. The expression level of LINC01615 was negatively correlated with the prognosis of breast cancer. Survival analysis of MIR100HG, LINC00702, LINC01615, LINC02544, SERTAD4-AS1 and FENDRR in breast cancer patients.

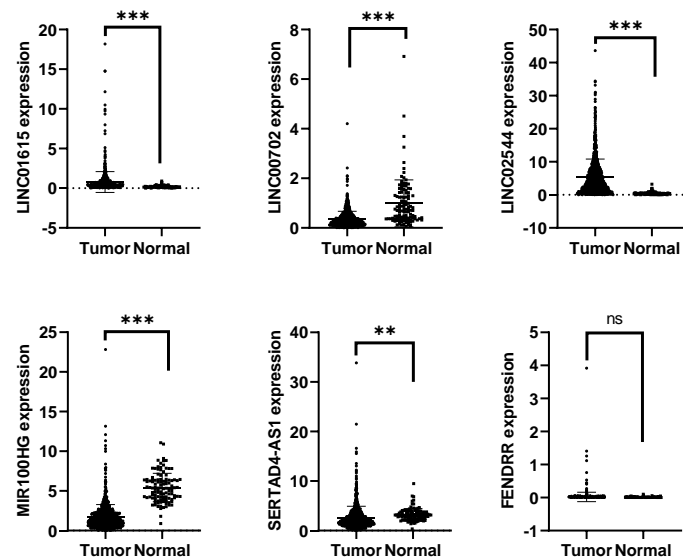


Figure S4. LINC01615 expression is elevated in breast cancer tissues. Differences in the expression levels of MIR100HG, LINC00702, LINC01615, LINC02544, SERTAD4-AS1 and FENDRR in breast tumor tissues and normal breast tissues.

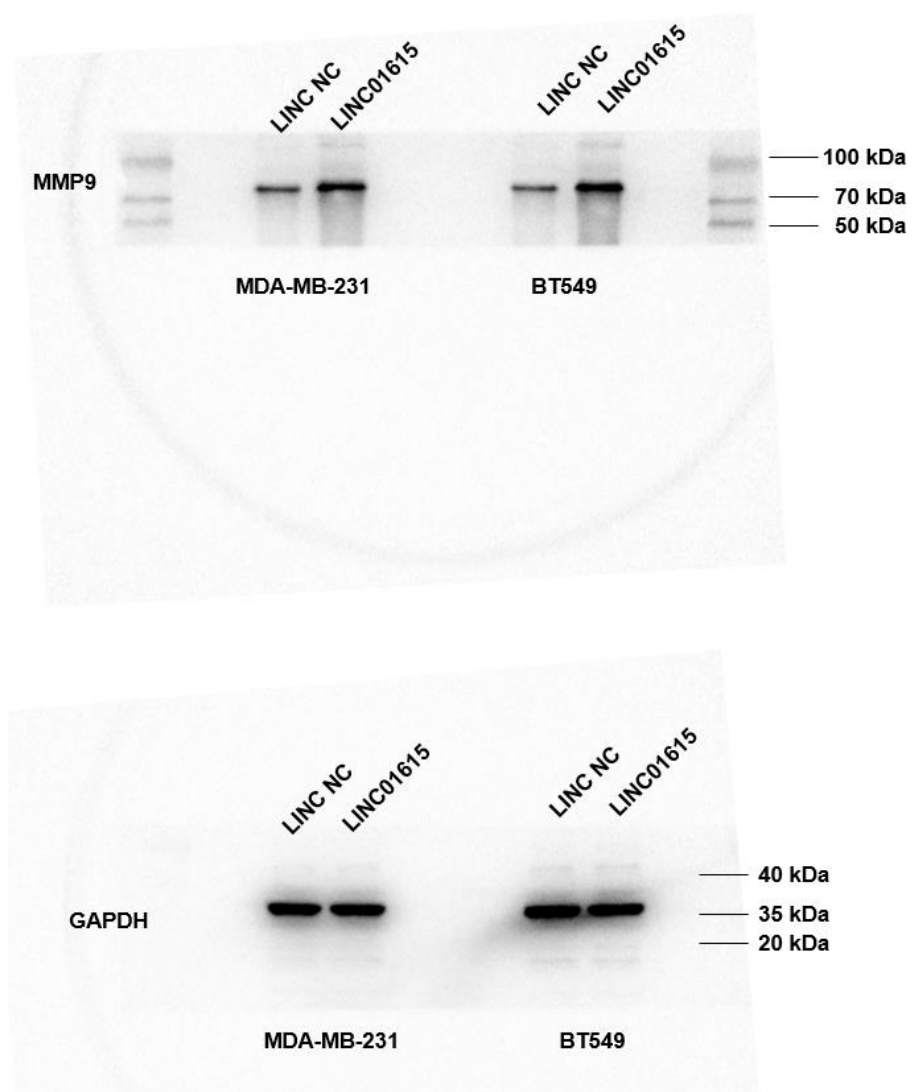


Figure S5. Original Western Blot.