

## **Supplementary materials**

### **Supplementary Datasets.**

**Dataset S1.** Data of LC-MS/MS of immunoprecipitation 1 and 2.

**Dataset S2.** RNA sequence analysis of the gene expression profile of shLOXL2 silenced cells versus shSCR control cells.

**Dataset S3.** List of bibliographic references with experimental evidences of involvement in EMT of the EMT-related gene signature.

### **Supplementary figure legends.**

**Figure S1.** Silencing of LOXL2 in Hs578T and MDA-MB-231 cell lines. LOXL2 silencing using shRNAs (shLOXL2) and a scramble control (shSCR) sequence was confirmed by qPCR (left panel) and WB (right panel).

**Figure S2.** Distribution of RBP targets among EMT-related DEGs. Red or grey squares denoted the presence or absence of RBPs binding sites respectively

**Figure S3.** Distribution of RBP targets among no EMT-related DEGs. Red or grey squares denoted the presence or absence of RBPs binding sites respectively.

### **Supplementary table.**

**Table S1.** Number of genes targeted by the selected RBPs in EMT- and no EMT-related signatures.

**Table S2.** List of primers used for qPCR analyses.

**Table S1**

Table S1. Distribution of genes targeted by the indicated RBP in EMT-related and no EMT-related signatures. The p-value was obtained by analysing the enrichment of RBPs hits between both categories using the Fisher's exact test.

<b>RBP</b>	<b>EMT-related</b>	<b>no EMT-related</b>	<b>p-value</b>
<b>CSTF2T</b>	16	46	0.1775
<b>DDX3X</b>	0	0	na
<b>DDX54</b>	24	71	0.1213
<b>DGCR8</b>	18	72	0.8854
<b>DHX9</b>	47	176	0.4586
<b>ELAVL1</b>	42	77	4.1E-06
<b>FMR1</b>	75	258	0.0327
<b>FUS</b>	12	40	0.4659
<b>HNRNPA1</b>	85	180	0.137
<b>HNRNPC</b>	30	99	0.212
<b>HNRNPK</b>	8	26	0.5064
<b>IGF2BP1</b>	21	53	0.0419
<b>IGF2BP2</b>	31	104	0.2673
<b>IGF2BP3</b>	18	52	0.1514
<b>LIN28B</b>	13	35	0.1817
<b>METTL3</b>	0	0	na
<b>MOV10</b>	15	37	1.000
<b>RBFOX</b>	39	134	0.2143
<b>SRSF1</b>	32	95	0.0175
<b>TAF15</b>	68	224	0.0248
<b>TARDBP</b>	30	127	1.000
<b>U2AF2</b>	59	192	0.0381
<b>WTAP</b>	0	0	na
<b>YTHDC1</b>	3	8	0.4528

**Table S2**

Table S2: list of primers used for qPCR analysis.

Gene	Forward primer (5'→3')	Reverse primer (5'→3')
<b><i>AKR1C2</i></b>	CAGAGGTTCTCTAAAAGTAAAGC	TGTGCAGAATCAATATGGTG
<b><i>CCL2</i></b>	AGACTAACCCAGAAACATCC	ATTGATTGCATCCTGGCTG
<b><i>CLDN1</i></b>	TTGGCATGAAGTGTATGAAG	ACCTGCAAGAAGAAATATCG
<b><i>CXCL3</i></b>	CCTCAAGAACATCCAAAGTG	CCCCTTGTTTCAGTATCTTTTC
<b><i>DUSP6</i></b>	TTCTACCTGGAAGATGAAGC	CAATGTCATGGCATCGTTC
<b><i>ENPP2</i></b>	ATAAAACAGTACGTGGAAGG	CTACCCATTTTGATTGCGTC
<b><i>GAPDH</i></b>	CTTCACCACCATGGAGGAGGC	GGCATGGACTGTGGTCATGAG
<b><i>HEY2</i></b>	GGATTATAGAGAAAGGCGTC	GTTTTTCAAAGCAGTTGGC
<b><i>ID1</i></b>	ACTAAGTCACCAGAGACTTTAG	AAATCTGAGAAGCACCAAAC
<b><i>SLC2A3</i></b>	GGATAACTATAATGGGATGAGC	CCACAATAAACCAGGGAATG
<b><i>SOD2</i></b>	ATCATACCCTAATGATCCCAG	AGGACCTTATAGGGTTTTTCAG
<b><i>TULP3</i></b>	AGGTCCTAGGAAAATGTCTG	AAGTTGAGGACATAGGACTG