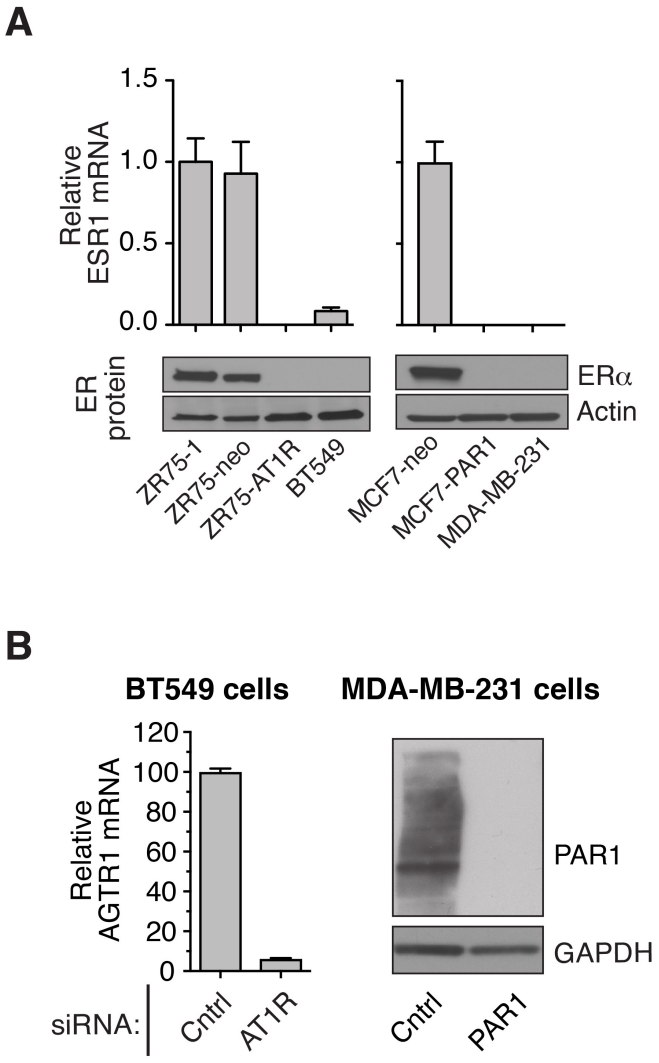
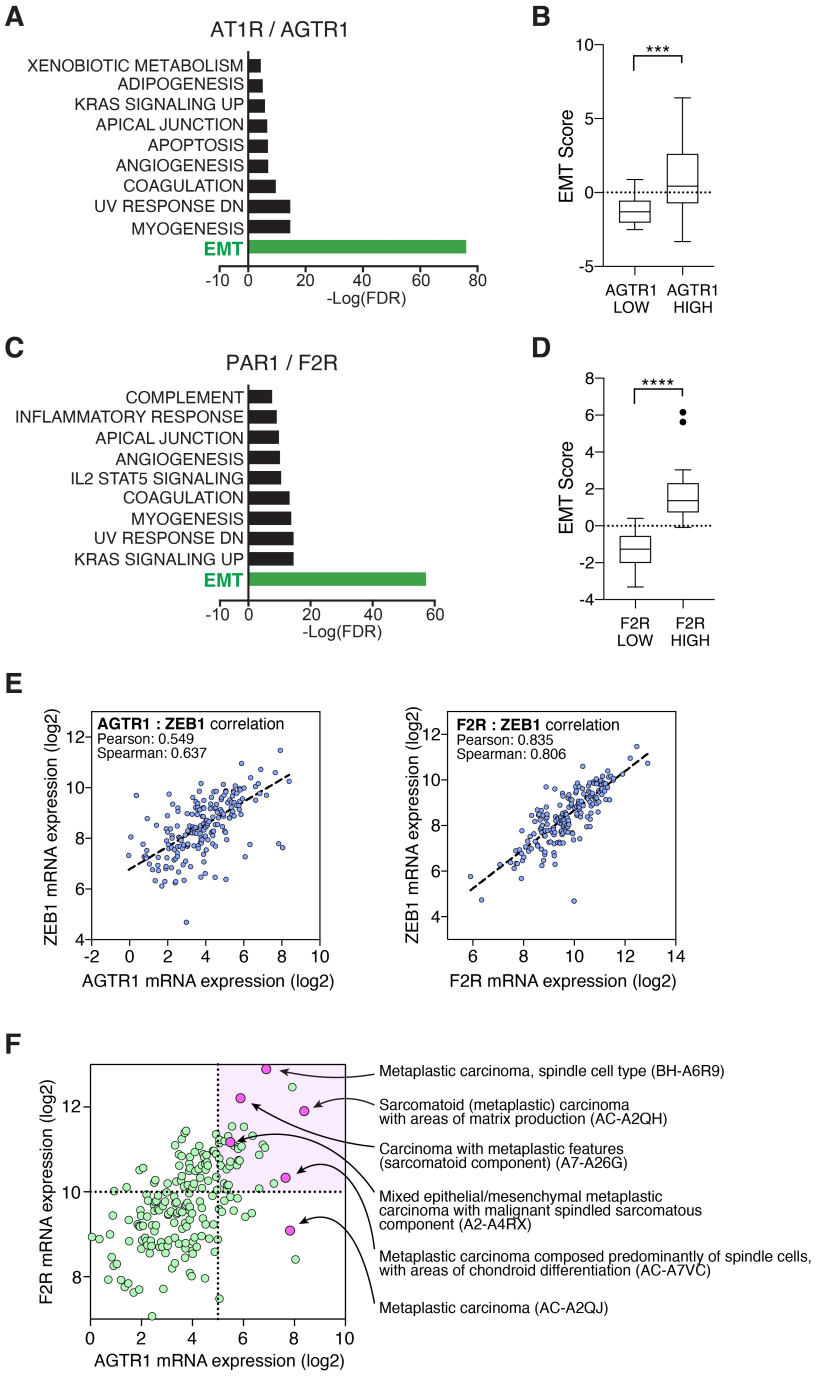
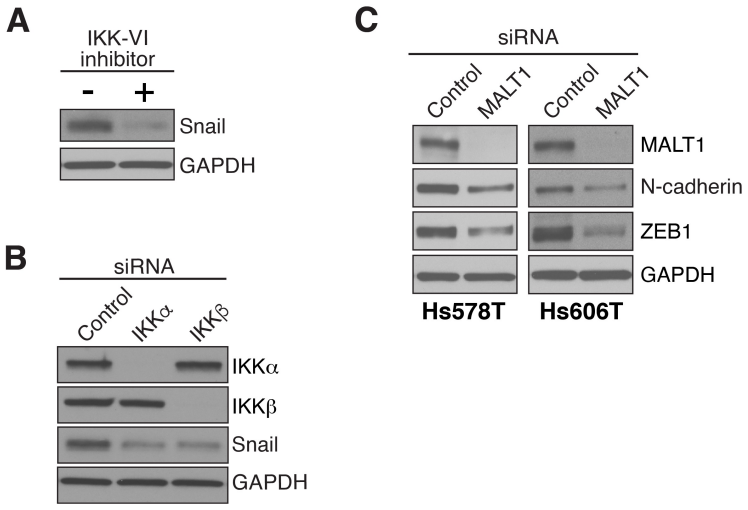


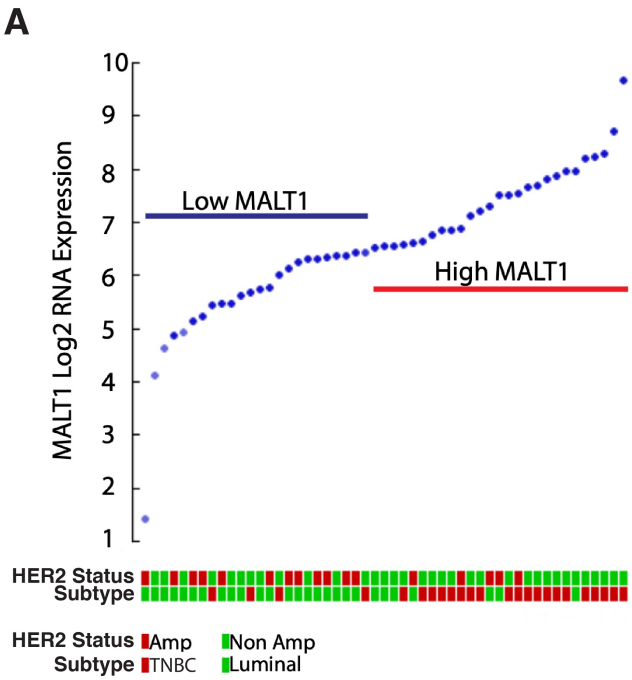
Supplementary Fig. S1. **AT1R and PAR1 overexpression and knockdown in breast cancer lines. A,** Effect of stable AT1R or PAR1 expression on ER expression at both the protein and mRNA level. **B,** The magnitude of AT1R knockdown in BT549 cells was assessed by quantitative RT-PCR due to the lack of commercially available specific antibodies to the AT1R protein. PAR1 knockdown efficacy was determined by western blotting. PAR1 protein appears as a smear in western blots due to multiple glycosylation-type modifications.

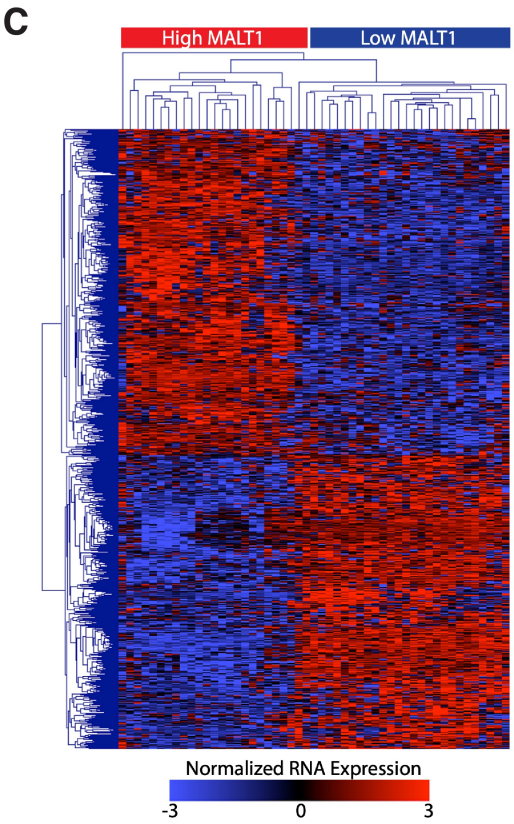


Supplementary Fig. S2. ***AGTR1* and *F2R* gene expression are strongly associated with EMT in TNBC. A,** Pathways associated with *AGTR1* expression in TNBCs within the TCGA cohort, ranked by false discovery rate (FDR). **B,** EMT scores, calculated by the method of Mak et al (reference 24 in main text) for the same set of high/low *AGTR1* expressing cases evaluated in panel A. ***, P < 0.001; Mann-Whitney U test. **C** and **D,** Pathways and EMT scores associated with *F2R* expression in the same TNBC cases from the TCGA. ****, P <0.001; Mann-Whitney U test. **E,** Associations between either *AGTR1* or *F2R* and *ZEB1* within TNBC cases included in the TCGA. **F,** Relationship between *AGTR1* and *F2R* expression in TNBC cases included in the TCGA. Highlighted in pink are the six cases within the TCGA breast dataset that were diagnosed as metaplastic carcinoma with spindle cell/sarcomatoid differentiation. Metaplastic carcinomas showing only squamous differentiation are not highlighted. The upper right quadrant (light pink) illustrates cases with combined high *AGTR1* and *F2R* expression.



Supplementary Fig. S3. **Role of CBM-dependent NF-κB signaling in mediating EMT**. **A**, Effect of pharmacologic NF-κB inhibition using the IKKβ inhibitor, IKK-VI (5 μM; 2 days), on Snail expression in BT549 cells. **B**, Effect of siRNA-mediated IKKα or IKKβ knockdown on Snail expression in BT549 cells. **C**, Effect of siRNA-mediated knockdown of MALT1 on N-cadherin and ZEB1 expression in Hs578T and Hs606T cells.





B

HER2 Status

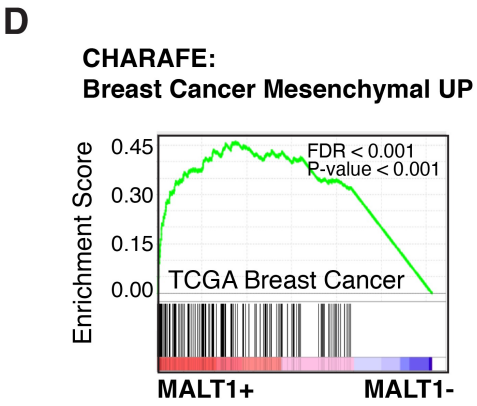
	Amplified	Non Amplified
Low MALT1	12	13
High MALT1	5	21

p=0.04

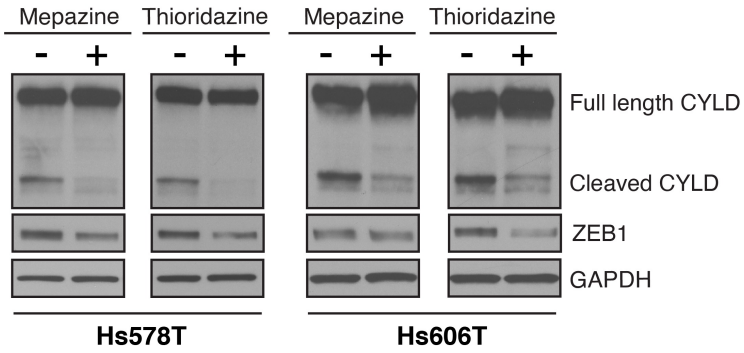
Subtype

	TNBC	Luminal
Low MALT1	4	22
High MALT1	18	7

p=0.0001



Supplementary Fig. S4. MALT1 levels are associated with the TNBC subtype and EMT signature in breast cancer. A and **B**, Breast cancer cell lines from the Hoeflich dataset, dichotomized for MALT1 gene expression, with their corresponding HER2 and molecular subtype status. **C**, Heatmap to display differentially expressed genes between high and low MALT1 expressing cell lines. Specific genes are listed in tabular form in Supplementary Table 1/2 (minimum fold change 2.0, Wilcoxon rank-sum test with adjusted *P* value using Benjamin and Hochberg correction). **D**, GSEA demonstrating an association between MALT1 expression and the Charafe mesenchymal UP signature in TCGA breast cancer cases.



Supplementary Fig. S5. **Pharmacologic MALT1 inhibition reduces ZEB1 expression in multiple AT1R+ breast cancer lines.** Hs578T and Hs606T cells were treated with or without mepazine (10 μM) or thioridazine (5 μM) for 2 days prior to harvesting and immunoblot analysis.