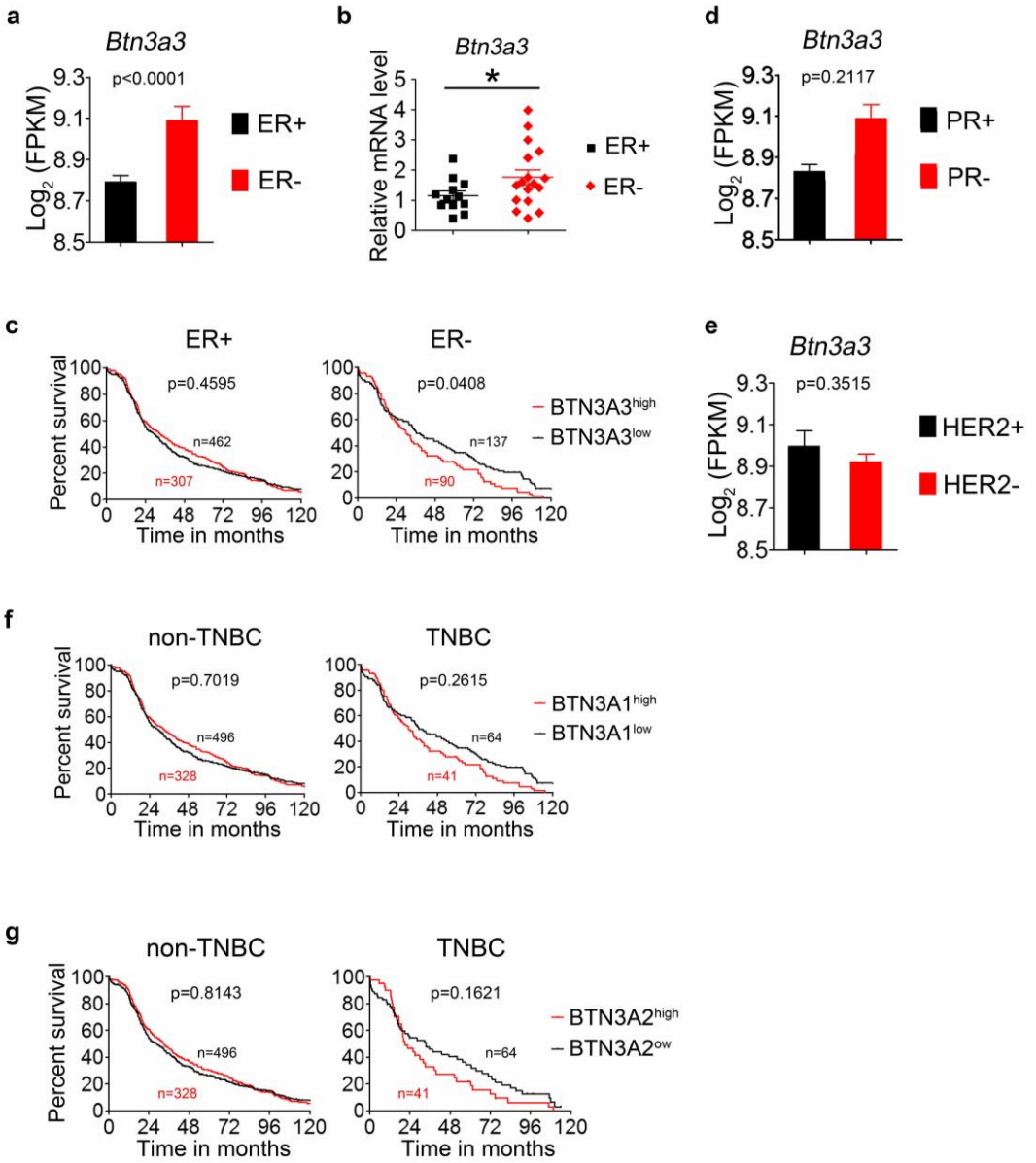
Supplementary information, Fig. S7



h

Database	Cd68		Csf1r		Il10	
	non-TNBC	TNBC	non-TNBC	TNBC	non-TNBC	TNBC
TCGA	0.072	0.54	0.14	0.53	0.14	0.33
GSE76275	0.28	0.37	0.59	0.44	0.23	0.35

Supplementary information, Fig. S7. Signatures of BTN3A3 and LSECtin abundance in the breast cancer

(a) *Btn3a3* mRNA expression in ER^+ and ER^- samples from the TCGA data set (ER^+ n = 769; ER^- n = 227).

(b) Real-time PCR analysis showing *Btn3a3* expression with cDNAs from ER^+ patients (n=12, black) and ER^- patients (n = 17, red) as templates.

(c) Kaplan-Meier survival curve of breast cancer patients from the TCGA data set (For ER^+ samples, $BTN3A3^{low}$: 60%, n = 462, $BTN3A3^{high}$: 40%, n = 307; for ER^- samples, $BTN3A3^{low}$: 60%, n = 137, $BTN3A3^{high}$: 40%, n = 90).

(d) *Btn3a3* mRNA expression in PR^+ and PR^- samples from the TCGA data set (PR^+ n = 667; PR^- n = 325).

(e) *Btn3a3* mRNA expression in $HER2^+$ and $HER2^-$ samples from the TCGA data set ($HER2^+$ n = 156; $HER2^-$ n = 537).

(f,g) Kaplan-Meier survival curve of breast cancer patients from the TCGA data set (For non-TNBC samples, $BTN3A1^{low}$/$BTN3A2^{low}$: 60%, n = 496, $BTN3A1^{high}$/$BTN3A2^{high}$: 40%, n = 328; for TNBC samples, $BTN3A1^{low}$/$BTN3A2^{low}$: 60%, n = 64, $BTN3A1^{high}$/$BTN3A2^{high}$: 40%, n = 41).

(h) Correlation between *Lsectin* expression and TAM-associated gene expression in human breast cancer samples from the TCGA data set (non-TNBC n = 824; TNBC n = 105), GSE76275 (non-TNBC n = 198; TNBC n = 65).

Data are presented as the mean ± SD. $*P < 0.05$, $**P < 0.01$, $***P < 0.001$ (unpaired Student's t test for a, b, d, e).