

Supplementary Material

1 Supplementary Figures and Tables

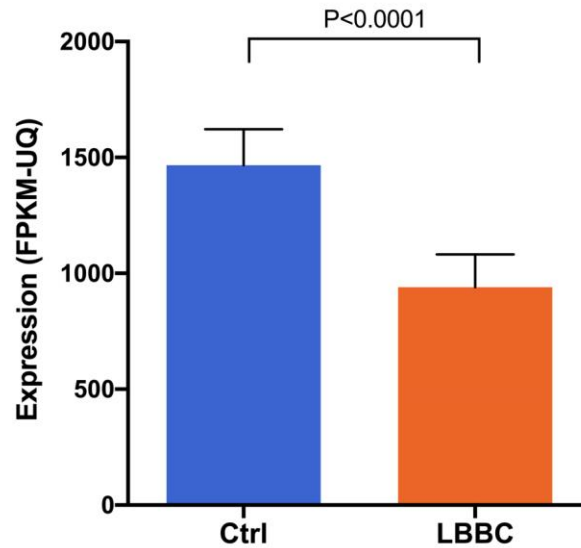
1.1 Supplementary Tables

Supplementary Table 1. List of primers used for the methylation analysis of *WNT1* by ddPCR.

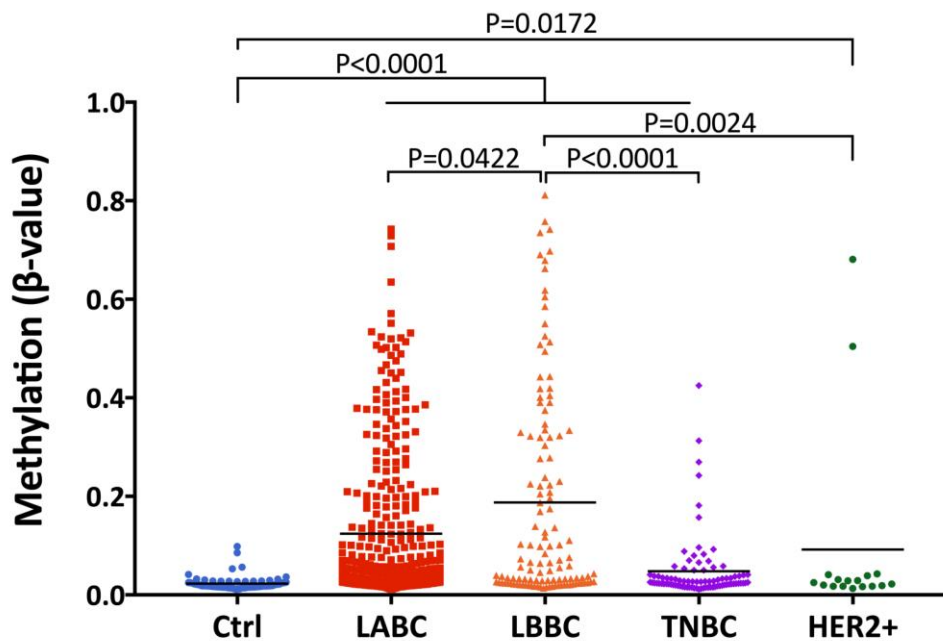
Assay	Primers/Probe	5'-Sequence-3'
<i>WNT1</i> -M	Forward	GAGGGGTAGTTTTTTTT
	Reverse	TCTAACTTTAACAACCCTAAA
	Probe (FAM)	GATCGCGAGTTATGTTGT
<i>WNT1</i> -U	Forward	GAGGGGTAGTTTTTTTT
	Reverse	TCTAACTTTAACAACCCTAAA
	Probe (HEX)	GGATTGTGAGTTATGTTGTT

Supplementary Table 2. Clinical characteristics of metastatic patients with luminal B breast cancer included in the study.

Characteristics	Patients (n=9)	
	No.	%
Age (years)		
<65	3	33
65-75	3	33
>75	3	33
Immunohistochemistry		
PR+	8	89
ER+	9	100
HER2+	2	22
Ki-67 \geq 20%	9	100
Histology		
Ductal	9	100
Stage		
IV	9	100
Metastatic sites		
1	4	44
2	2	22
3	3	33
Metastatic location		
Visceral	6	66
Bone	4	44



Supplementary Figure 2. Expression of *WNT1* in primary luminal B breast tumors. Gene expression levels of *WNT1* available in primary tumors of luminal B breast cancer patients (n=122) and nontumor controls (n=67) obtained by RNA-seq from TCGA. Expression levels are represented as the mean \pm SEM.



Supplementary Figure 3. Methylation status of *WNT1* in primary tumors of breast cancer subtypes (LABC, n=358; LBBC, n=122; TNBC, n=87; HER2+, n=17) and nontumor controls (n=79) from TCGA. Methylation data have been obtained from EPIC array analysis considering all TNM stages together (stages I-IV). Ctrl, control; P, p-value. LABC, luminal A breast cancer; LBBC, Luminal B breast cancer; TNBC, triple negative breast cancer; HER2+, HER2-positive.