

Table S2. Multivariate analysis of pN, pT, 4 BC360 signatures and 22 DEGs

Factor	<i>p</i> -value	HR	95%CI	
			lower	higher
pN	0.007	2.742	1.325	5.675
pT	0.69	-	-	-
PGR	0.20	-	-	-
ROR	0.54	-	-	-
Claudin-low	0.53	-	-	-
Mammary stemness	0.36	-	-	-
<i>LRP2</i>	<0.001	0.728	0.615	0.862
<i>SFRP1</i>	0.39	-	-	-
<i>CDC14A</i>	0.17	-	-	-
<i>OGN</i>	0.96	-	-	-
<i>ABCA8</i>	0.93	-	-	-
<i>IGF1</i>	0.58	-	-	-
<i>BCAS1</i>	0.13	-	-	-
<i>IBSP</i>	0.025	1.437	1.047	1.972
<i>WNT11</i>	0.21	-	-	-
<i>IRX1</i>	0.57	-	-	-
<i>ERBB4</i>	0.80	-	-	-
<i>SOX10</i>	0.40	-	-	-
<i>MIA</i>	0.14	-	-	-
<i>PGR</i>	0.20	-	-	-
<i>HOXA5</i>	0.80	-	-	-
<i>STC1</i>	0.13	-	-	-
<i>THBS4</i>	0.65	-	-	-
<i>PTGER3</i>	0.24	-	-	-
<i>SCUBE2</i>	0.037	0.82	0.681	0.988
<i>SFRP4</i>	0.97	-	-	-
<i>HSPA2</i>	0.62	-	-	-
<i>ZBTB16</i>	0.80	-	-	-

DEG: differentially expressed genes, HR: hazard ratio, CI confidence interval

Forward stepwise regression (likelihood ratio) was used. This method selected the most significant independent prognostic factors to be included into the final equation and calculated the HR of the selected factors.