Supplementary

Table S1 Age and sex for all study participants

Serial number	Sex	Age
1	Female	47
2	Female	48
3	Female	62
4	Female	46
5	Female	53
6	Female	64
7	Female	59
8	Female	39
9	Female	70
10	Female	46
11	Female	46
12	Female	61
13	Female	78
14	Female	54
15	Female	38
16	Female	33
17	Female	57
18	Female	42
19	Female	52
22	Female	44
20	Female	49
21	Female	73
23	Female	56
24	Female	56
25	Female	48
26	Female	46
27	Female	51
28	Female	55
29	Female	36
30	Female	48
31	Female	60
32	Female	48
33	Female	60
34	Female	55
35	Female	61

Table S1 *(continued)*

Table S1 *(continued)*

Serial number	Sex	Age
36	Female	63
37	Female	63
38	Female	40
39	Female	43
40	Female	46
41	Female	65
42	Female	32
43	Female	44
44	Female	66
45	Female	56
46	Female	64
47	Female	59
48	Female	55
49	Female	48
50	Female	56
51	Female	32
52	Female	66
53	Female	46
54	Female	49
55	Female	47
56	Female	38
57	Female	46
58	Female	56
59	Female	44
60	Female	53
61	Female	44
62	Female	58
63	Female	51
64	Female	44
65	Female	64
66	Female	59
67	Female	46
68	Female	63
69	Female	69
70	Female	50

Table S1 *(continued)*

http://dx.doi.org/10.21037/gs-21-84

Table S1 *(continued)*

Serial number	Sex	Age
71	Female	61
72	Female	46
73	Female	41
74	Female	64
75	Female	55
76	Female	50
77	Female	61
78	Female	59
79	Female	50
80	Female	63
81	Female	40
82	Female	46
83	Female	52
84	Female	73
85	Female	63
86	Female	68
87	Female	64
88	Female	53
89	Female	61
90	Female	39
91	Female	61
92	Female	59
93	Female	53
94	Female	42
95	Female	45
96	Female	62

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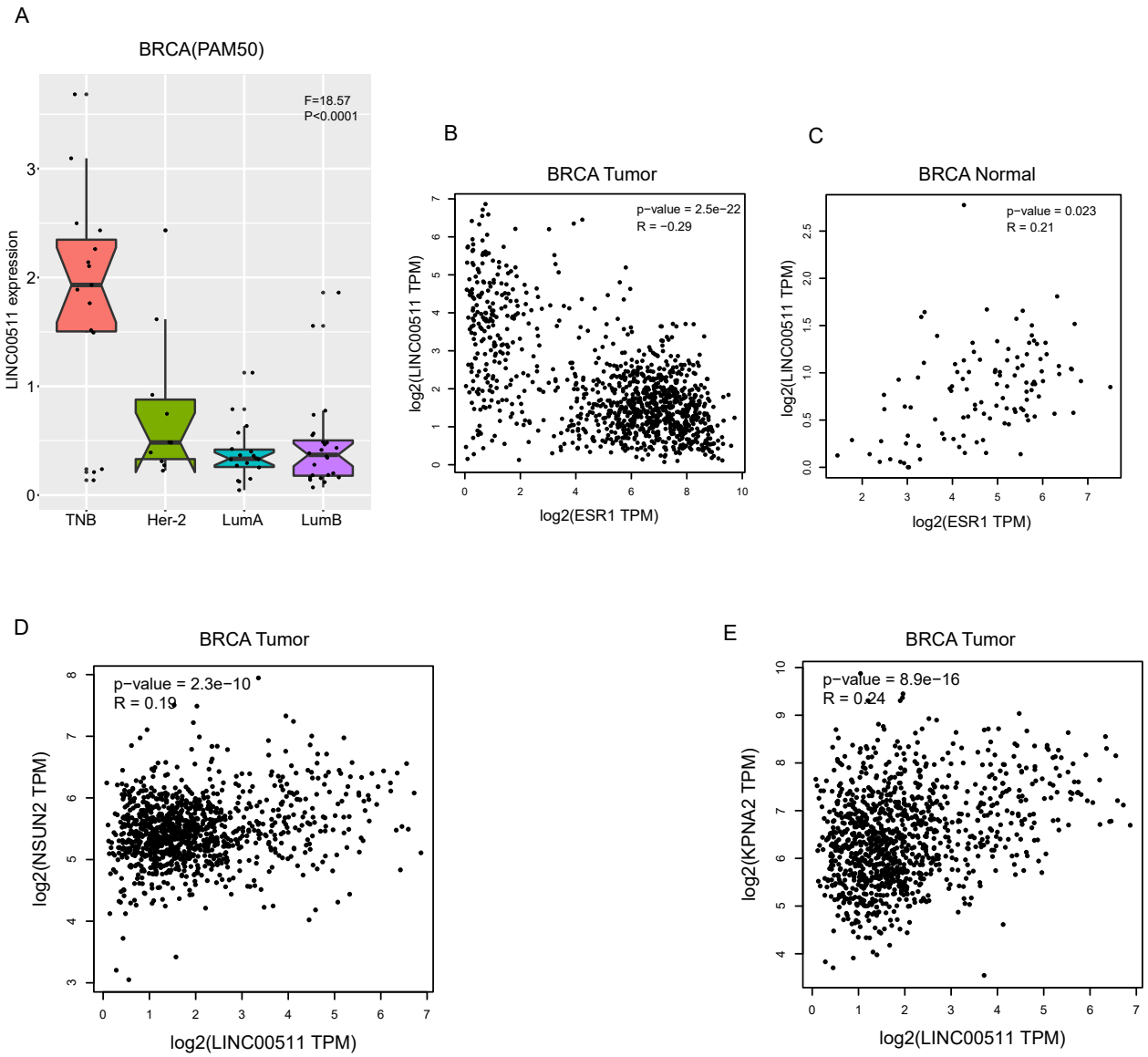

Figure S1 Analysis of the relationship between LINC00511 and molecular subtypes of breast cancer, estrogen receptor, NSUN2 and KPNA2. (A) LINC00511 was significantly correlated with the molecular typing of breast cancer in TCGA. (B) GEPIA database analysis showed that the expression of ER is negatively correlated with LINC00511 in breast cancer. (C) There is a positive correlation between the expression of estrogen receptor and LINC00511 in normal tissues adjacent to breast cancer in GEPIA. (D,E) The expression of LINC00511 was significantly correlated with NSUN2 and KPNA2 in GEPIA. P<0.05 means statistical significance. TCGA, the cancer genome atlas; ER, estrogen receptor; GEPIA, Gene Expression Profiling Interactive Analysis.

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