

Supplementary Table S1. Association analysis between germline genetic polymorphisms of *STIM1* and TNM stage in progesterone receptor (PR) positive breast cancer patients

| dbSNV ID | Genotype | Late stage ^a N (%) | Early stage ^b N (%) | Genotype model | |
|-----------|----------|----------------------------------|-----------------------------------|----------------------------|-------------------------------|
| | | | | OR (95% C.I.) ^c | <i>p</i> value |
| rs2304891 | G/G | 8 (32.0) | 17 (14.7) | 10.51 (2.02~54.74) | 3.47×10^{-3**} |
| | A/G | 15 (60.0) | 55 (47.4) | 6.02 (1.31~27.75) | |
| | A/A | 2 (8.0) | 44 (37.9) | Reference | |
| rs3750996 | G/G | 0 (0) | 7 (5.9) | 0 | 8.53×10^{-3*} |
| | A/G | 3 (12.0) | 41 (34.7) | 0.23 (0.07~0.82) | |
| | A/A | 22 (88.0) | 70 (59.3) | Reference | |
| rs1561876 | G/G | 0 (0) | 10 (8.9) | 0 | 0.1038 |
| | A/G | 14 (58.3) | 51 (45.5) | 1.40 (0.57~3.44) | |
| | A/A | 10 (41.7) | 51 (45.5) | Reference | |
| rs3750994 | G/G | 1 (4.3) | 5 (4.2) | 1.02 (0.11~9.79) | 0.9826 |
| | T/G | 9 (39.1) | 44 (37.3) | 1.09 (0.43~2.78) | |
| | T/T | 13 (56.5) | 69 (58.5) | Reference | |

The *p* value was adjusted for age. **p* value <0.05 and ***p* value <0.005 are shown in bold. ^aLate stage included stage III. ^bEarly stage included stages I and II. ^cOdds ratio (OR) and 95% confidence intervals (C.I.).

Supplementary Table S2. Association analysis between germline genetic polymorphisms of *STIM1* and TNM stage in human epidermal growth factor receptor 2 (HER2) positive breast cancer patients

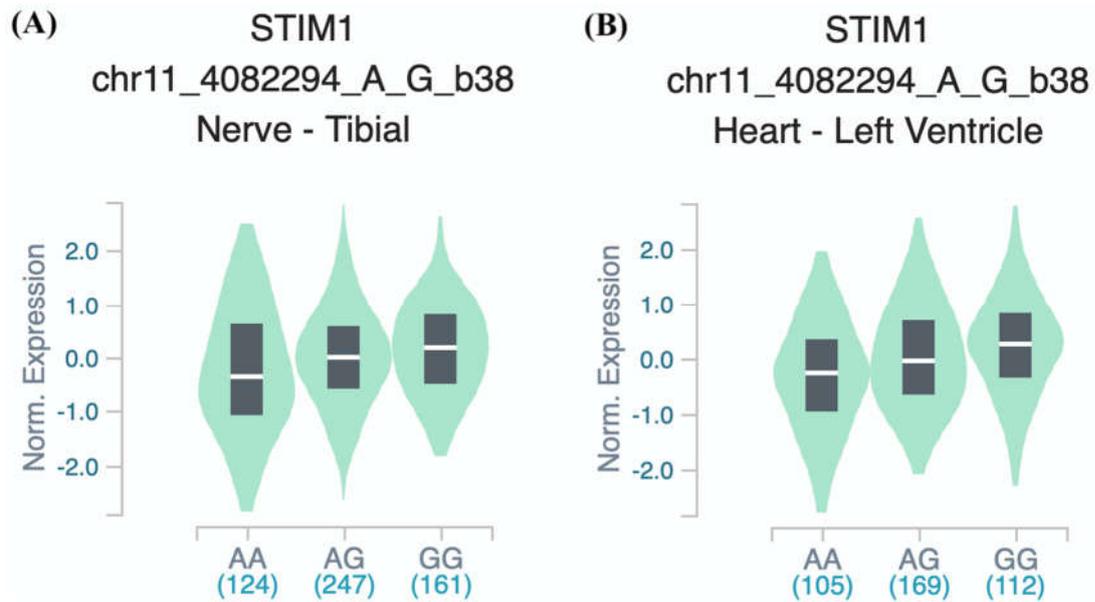
| dbSNV ID | Genotype | Late stage ^a N (%) | Early stage ^b N (%) | Genotype model | |
|-----------|----------|----------------------------------|-----------------------------------|----------------------------|----------------|
| | | | | OR (95% C.I.) ^c | <i>p</i> value |
| rs2304891 | G/G | 10 (34.5) | 18 (16.4) | 4.11 (1.21~13.92) | 0.0618 |
| | A/G | 14 (48.3) | 56 (50.9) | 1.85 (0.61~5.59) | |
| | A/A | 5 (17.2) | 36 (32.7) | Reference | |
| rs3750996 | G/G | 0 (0) | 6 (5.4) | 0 | 0.0315* |
| | A/G | 5 (16.7) | 36 (32.4) | 0.38 (0.13~1.07) | |
| | A/A | 25 (83.3) | 69 (62.2) | Reference | |
| rs1561876 | G/G | 1 (3.8) | 6 (5.6) | 0.87 (0.09~8.29) | 0.8979 |
| | A/G | 13 (50.0) | 47 (43.9) | 1.21 (0.50~2.92) | |
| | A/A | 12 (46.2) | 54 (50.5) | Reference | |
| rs3750994 | G/G | 2 (7.1) | 2 (1.8) | 5.17 (0.61~43.91) | 0.3360 |
| | T/G | 9 (32.1) | 37 (33.9) | 0.97 (0.39~2.41) | |
| | T/T | 17 (60.7) | 70 (64.2) | Reference | |

The *p* value was adjusted for age. **p* value <0.05 are shown in bold. ^aLate stage included stage III. ^bEarly stage included stages I and II. ^cOdds ratio (OR) and 95% confidence intervals (C.I.).

Supplementary Table S3. Expression quantitative trait locus (eQTL) analysis of *STIM1* SNPs

| Gene | dbSNP | alt allele | Tissue | p-value | NES ^a |
|--------------|-----------|------------|----------------------|-----------------------|------------------|
| <i>STIM1</i> | rs2304891 | G | Nerve-Tibial | 2.70×10 ⁻⁹ | 0.17 |
| <i>STIM1</i> | rs2304891 | G | Heart-Left Ventricle | 2.10×10 ⁻⁸ | 0.22 |

^aNES: Normalized effect size



Supplementary Figure S1. *STIM1* gene expression among different genotypes of rs2304891 in (A) nerve-tibial tissue and (B) heart-left ventricle tissue.