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| S2 Table. Associations between previously identified SNPs and DFS of breast cancer by tumor subtypes in the discovery set |
| SNPa | Loci | Gene | Allelesb | SEBCS | Previous GWAS |
| MAF | Subtype | HRc | (95% CI) | *P*trend | Genotyping | MAF | Outcome | HR | (95% CI) | *P*trend | Ref. |
| rs10509373 | 10q22 | *C10orf11* | T | C | 0.03  | Overall | 1.78  | (0.86-3.69) | 0.12  | imputed | 0.02  | RFS | 4.53  | (2.62-7.83) | 6.3×10-8 | ([1](#_ENREF_1)) |
| HR+ HER2- | 3.53  | (0.82-15.32) | 0.09  |
| HR+ HER2+ | 0.50  | (0.12-2.14) | 0.35  |
| HR- HER2+ | 0.71  | (0.09-5.75) | 0.75  |
| HR- HER2- | 0.78  | (0.22-2.76) | 0.70  |
| rs421379 | 5q14 | *ARRDC3* | C | T | 0.03  | Overall | 0.91  | (0.51-1.64) | 0.76  | typed | 0.05  | BCSS | 1.61  | (1.33-1.96) | 9.5×10-7 | ([2](#_ENREF_2)) |
| HR+ HER2- | 0.95  | (0.39-2.30) | 0.90  |
| HR+ HER2+ | 1.66  | (0.58-4.74) | 0.34  |
| HR- HER2+ | 1.19  | (0.17-8.09) | 0.86  |
| HR- HER2- | 0.24  | (0.03-1.77) | 0.16  |
| rs3784099 | 14q24 | *RAD51L1* | G | A | 0.15  | Overall | 1.27  | (0.96-1.67) | 0.09  | imputed | 0.13  | DFSOS | 1.431.49 | (1.25-1.64)(1.28-1.72) | 2.8×10-71.2×10-7 | ([3](#_ENREF_3)) |
| HR+ HER2- | 1.51  | (0.94-2.44) | 0.09  |
| HR+ HER2+ | **3.77**  | **(1.12-12.74)** | **0.03**  |
| HR- HER2+ | 0.92  | (0.48-1.79) | 0.81  |
| HR- HER2- | 1.14  | (0.71-1.84) | 0.59  |
| rs1387389 | 1q23 | *PBX1* | A | G | 0.49  | Overall | 1.15  | (0.95-1.38) | 0.15  | imputed | 0.36  | BCSS | 1.28  | (1.16-1.43) | 3.8×10-6 | ([2](#_ENREF_2)) |
| HR+ HER2- | 1.26  | (0.94-1.71) | 0.13  |
| HR+ HER2+ | 1.03  | (0.57-1.88) | 0.92  |
| HR- HER2+ | **1.73**  | **(1.05-2.85)** | **0.03**  |
| HR- HER2- | 0.96  | (0.67-1.38) | 0.83  |
| rs3884558 | 15q22 | *RORα* | A | G | 0.31  | Overall | 1.04  | (0.86-1.27) | 0.69  | typed | 0.07  | BCSS | 1.46  | (1.24-1.72) | 3.9×10-6 | ([2](#_ENREF_2)) |
| HR+ HER2- | 0.96  | (0.70-1.32) | 0.81  |
| HR+ HER2+ | 1.15  | (0.66-2.03) | 0.62  |
| HR- HER2+ | 0.89  | (0.51-1.53) | 0.66  |
| HR- HER2- | 1.09  | (0.73-1.64) | 0.66  |
| rs2774307 | 1p13 | *SYT6* | G | A | 0.08  | Overall | 0.96  | (0.69-1.32) | 0.78  | typed | 0.26  | BCSS | 1.30  | (1.16-1.47) | 7.9×10-6 | ([2](#_ENREF_2)) |
| HR+ HER2- | 0.63  | (0.33-1.22) | 0.17  |
| HR+ HER2+ | 1.09  | (0.42-2.85) | 0.87  |
| HR- HER2+ | 1.13  | (0.48-2.69) | 0.78  |
| HR- HER2- | 1.60  | (0.92-2.77) | 0.10  |
| rs3785982 | 17p13 | *NTN1* | C | T | 0.19  | Overall | 1.03  | (0.82-1.28) | 0.82  | typed | 0.12  | BCSS | 1.40  | (1.21-1.62) | 7.9×10-6 | ([2](#_ENREF_2)) |
| HR+ HER2- | 1.12  | (0.77-1.62) | 0.55  |
| HR+ HER2+ | 1.24  | (0.69-2.24) | 0.47  |
| HR- HER2+ | 0.54  | (0.28-1.04) | 0.06  |
| HR- HER2- | 0.88  | (0.55-1.39) | 0.57  |
| rs4778137 | 15q13 | *OCA2* | C | G | 0.22  | Overall | 0.95  | (0.74-1.22) | 0.69  | imputed | 0.30  | OSOS, ER+OS, ER- | 0.930.990.82 | (0.87-0.98)(0.91-1.10)(0.73-0.92) | 0.010.755.0×10-4 | ([4](#_ENREF_4)) |
| HR+ HER2- | 1.42  | (0.98-2.06) | 0.07  |
| HR+ HER2+ | 0.63  | (0.26-1.51) | 0.63  |
| HR- HER2+ | 1.40  | (0.76-2.56) | 0.28  |
| HR- HER2- | **0.45**  | **(0.25-0.84)** | **0.01**  |
| rs9934948 | 16q22 | *ZFHX3* | T | C | 0.38  | Overall | 0.90  | (0.73-1.11) | 0.30  | imputed | 0.46  | DFSOS | 1.191.29 | (1.08-1.31)(1.16-1.44) | 7.3×10-45.8×10-4 | ([3](#_ENREF_3)) |
| HR+ HER2- | 0.87  | (0.61-1.23) | 0.42  |
| HR+ HER2+ | 2.00  | (0.91-4.41) | 0.09  |
| HR- HER2+ | **0.54**  | **(0.32-0.90)** | **0.02**  |
| HR- HER2- | 1.08  | (0.73-1.60) | 0.70  |
| Abbreviations: SNP, single-nucleotide polymorphism; DFS, disease-free survival; SEBCS, Seoul breast cancer study; GWAS, genome-wide association study; MAF, minor allele frequency; HR, hazard ratio; CI, confidence interval; Ref. reference; HR, hormone receptor; HER2, human epidermal growth factor receptor 2; RFS, recurrence-free survival; BCSS, breast cancer-specific survival; OS, overall survival. |
| aSNP identified by previous GWAS on survival. |
| bMajor and minor alleles. |
| cCox proportional hazard model adjusted for age, recruiting center, and TNM stage. |

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