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The SNP rs6500843 in 16p13.3 is associated with survival specifically among chemotherapy-treated breast cancer patients

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INTRODUCTION

Breast cancer is the most common type of malignancy and one of the leading causes of death among women worldwide. Susceptibility to the disease is heavily influenced by inherited factors, with roughly 50% of familial breast cancer risk attributable to genetic variation [1, 2]. Genetic variation also contributes to the phenotypic spectrum of the disease, with both high-penetrance and common variants associating with various histopathological features, most notably estrogen receptor status [3].

The impact of genetic variation on breast cancer prognosis is less well understood. The prognosis and...
indicated treatment for breast cancer is influenced by tumor
grade, stage, HER2 expression, and hormone receptor
status [4, 5], and it is plausible that genetic variants
associated with these features would be of prognostic
and predictive interest. Additionally, genetic variation
may contribute to breast cancer survival independently of
these markers, potentially by affecting the efficacy of the
treatment. For example, prognostic and predictive SNPs
have been reported in the *TP53* gene and its regulatory
network, as well as in genes involved in oxidative stress
[6-10]. Such findings have emerged primarily from
candidate gene based approaches, as more comprehensive
GWS-based survival analyses tend to be problematic due
to issues of statistical power: very large sample sizes are
required to reach GWS significance. The collaborative
iCOGS genotyping project [2] now enables this type of
a study, with over 30,000 genotyped breast cancer cases
eligible for survival analysis, of which 17828 cases have
adjuvant treatment information available, although it can
still be challenging to detect modest effect sizes in smaller
subgroups, such as genetic effects that modulate survival
after a specific type of adjuvant treatment.

We have utilized a two-stage study design to search
for genetic variants associated with survival after adjuvant
chemotherapy in breast cancer. First, we conducted an
initial pilot GWS in an event-enriched set of 805 Finnish
breast cancer cases. We then sought to validate our
findings in an independent validation material consisting
of three separate studies: iCOGS [2], POSH [11], and
SUCCESS-A (dbGaP Study Accession: phs000547.v1.p1).
SNPs associated with survival after treatment were further
characterized using eQTL analysis in two large gene
expression data sets and subsequent *in silico* analyses.

**RESULTS**

**rs6500843 and rs11155012 are associated with
survival after adjuvant chemotherapy**

Initially, a genome-wide study (Stage I: HEBCS-
GWS; n = 805) was conducted to discover candidate SNPs
that may be associated with breast cancer survival, with
an emphasis on treatment-based subgroups. This initial
stage of the analysis was carried out using three different
endpoints in parallel: five-year BDDM (breast cancer
death or distant metastasis), 10-year breast cancer specific
survival, and 10-year overall survival, using a codominant
genetic model (test for heterogeneity between genotypes).
We used fairly lenient statistical criteria to select candidate
SNPs at this stage: a SNP would be selected for validation
if it fulfilled any of the following criteria: 1) main effect p
< 10⁻³ and p < 0.01 among chemotherapy-treated cases, 2)
p < 10⁻⁴ among chemotherapy-treated cases, or 3) p < 10⁻³
among chemotherapy-treated cases and a homozygote-
associated hazard ratio > 3.0. In total, we identified 45
putative hits from this Stage I pilot that were represented
by 39 nominal and tagging SNPs on the iCOGS chip
(Supplementary Table 1).

The candidate SNPs from Stage I were then
analyzed in Stage II, comprising of the iCOGS, POSH
and SUCCESS-A data sets. All Stage II survival analyses
were restricted to cases who had received adjuvant
chemotherapy. The analyses were run under the additive
genetic model with left-truncated follow-up times,
adjusted for patient age at diagnosis, and (in the case of
iCOGS) stratified by study. Ten-year overall survival
(death from any cause) was used as the end-point in these
analyses for reasons of data availability and consistency.
Three of the SNPs were statistically significant at this
stage (Benjamini-Hochberg-adjusted p < 0.05): rs6500843
(any chemotherapy; HR 1.16, 95% C.I. 1.08 - 1.26, p =
0.0001, \(p_{\text{adjusted}} = 0.0091\)); rs4502225 (any chemotherapy;
HR 0.78, 95% C.I. 0.67 - 0.90, p = 0.0007, \(p_{\text{adjusted}} =
0.0263\)); and rs11155012 (anthracycline therapy; HR 1.21,
95% C.I. 1.08 - 1.35, p = 0.0010, \(p_{\text{adjusted}} = 0.0270\))(Table
1). Of these, the calculated hazard ratio for rs4502225 was
in the opposite direction than in Stage I, and therefore this
SNP cannot be considered a validated hit.

Finally, we performed a meta-analysis of both the
Stage I and Stage II data sets, resulting in very slight
improvement in the precision of the per-allele HR
estimates for the remaining two SNPs: HR 1.18 (95% C.I.
1.10 – 1.27; p = 6.96 \times 10⁻⁵) for rs6500843 in the
chemotherapy-treated group, and HR 1.23 (95% C.I. 1.11 –
1.37; p = 8.41 \times 10⁻⁵) for rs11155012 in the anthracycline-
treated group. See Figure 1 for forest plots displaying
hazard ratios from Stage I and Stage II data sets, as well
as from individual participant studies within the iCOGS
data set. We detected nominally significant heterogeneity
(p = 0.048) among the data sets in the rs6500843 analysis,
indicating some disagreement between data sets; the
SNP-associated increased hazard was not seen in the
SUCCESS-A data set. No heterogeneity was observed
in the case of rs11155012 (p = 0.415). Neither rs6500843 nor
rs11155012 were associated with tumor histopathological
characteristics (Supplementary Table 2), nor were the
survival analyses described above adjusted for patient
or tumor characteristics except age at diagnosis. More
detailed phenotypes were taken into account in the
subsequent interaction analyses (see below).

**rs6500843 interacts with adjuvant chemotherapy
in multivariate survival analysis**

Next, we investigated whether the observed survival
effects are specific to the chemotherapy-treated subgroup,
and whether these effects occur independently of standard
prognostic factors. To this end, we tested for interaction
between treatment and the rs6500843 and rs11155012
SNP genotypes in multivariate Cox proportional hazards
models adjusted for ER, grade, tumor size, and nodal metastasis. This analysis was only performed in the iCOGS data set, as it contains both treated and non-treated cases in abundant numbers, enabling robust interaction testing. A likelihood-ratio test comparing models with interaction terms with models with only independent covariates indicated an interactive effect between rs6500843 and adjuvant chemotherapy ($p_{\text{interaction}} = 0.0009$, N = 9680 [1176 events]; Table 2), consistent with the finding that the SNP was associated with survival in the “any chemotherapy” subset in univariate analysis. See Figure 2 for a visualization of rs6500843-associated survival within the chemotherapy-treated and untreated subgroups in the iCOGS data set. Consistent with the additive model employed in the survival analyses, the genotype-specific hazard ratios for rs6500843 in the chemotherapy-treated group increase in an allele dose dependent manner (HR$^{\text{AG}}$ = 1.22 (95% C.I. 1.00 - 1.49); HR$^{\text{GG}}$ = 1.47 (95% C.I. 1.20 - 1.80). In contrast, no heterogeneity between genotypes can be observed in the untreated group. The conclusion of the interaction analysis did not change when radiotherapy, surgery, and adjuvant endocrine therapy were added as additional covariates in the model ($p_{\text{interaction}} = 0.0035$, N = 8943 [1110 events]). Despite its association with survival in the anthracycline-treated and any chemotherapy treated subsets, no evidence of interaction was observed for the rs11155012 SNP (Supplementary Table 3), suggesting that its possible association with survival is not entirely treatment-specific.

eQTL analysis of SNPs in the survival-associated loci

To determine if rs6500483 or rs11155012, or other SNPs in the surrounding LD regions ($r^2 > 0.1$), associate with gene expression in breast cancer, two publicly available data sets (containing both genotype and gene expression data) were used for expression quantitative loci (eQTL) analysis: TCGA [12], and METABRIC [13]. We classified eQTLs as $\text{cis}$ if they occurred within ±1 Mb from any SNP in the LD region; any eQTLs outside these regions were classified as $\text{trans}$. The SNP rs6500843 is located in chromosome 16, in an intron of the $RBFOX1$ gene, which is the

---

**Table 1: Survival statistics for the three SNPs associated with 10-year overall survival in the Stage II analysis.**

<table>
<thead>
<tr>
<th>Subgroup</th>
<th>rs6500843</th>
<th>rs4502225</th>
<th>rs11155012</th>
</tr>
</thead>
<tbody>
<tr>
<td>Chromosome</td>
<td>16</td>
<td>16</td>
<td>6</td>
</tr>
<tr>
<td>Position</td>
<td>6 870 855</td>
<td>78 424 831</td>
<td>139 151 784</td>
</tr>
<tr>
<td>Genes in LD region</td>
<td>$RBFOX1$</td>
<td>$WWOX$</td>
<td>$ECT2L$, $CCDC28A$</td>
</tr>
<tr>
<td>Subgroup</td>
<td>Chemotherapy+</td>
<td>Chemotherapy+</td>
<td>Anthracycline+</td>
</tr>
<tr>
<td>Model</td>
<td>additive</td>
<td>additive</td>
<td>additive</td>
</tr>
<tr>
<td>Stage I (HEBCS-GWS)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>p-value</td>
<td>0.0081</td>
<td>0.0045</td>
<td>0.0073</td>
</tr>
<tr>
<td>HR</td>
<td>1.36</td>
<td>1.55</td>
<td>1.50</td>
</tr>
<tr>
<td>95% C.I.</td>
<td>1.08-1.70</td>
<td>1.14-2.09</td>
<td>1.12-2.02</td>
</tr>
<tr>
<td>Stage II (iCOGS, POSH, SUCCESS-A)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>p-value</td>
<td>0.0001</td>
<td>0.0007</td>
<td>0.0010</td>
</tr>
<tr>
<td>(Adjusted)*</td>
<td>0.0091</td>
<td>0.0263</td>
<td>0.0270</td>
</tr>
<tr>
<td>HR</td>
<td>1.16</td>
<td>0.78</td>
<td>1.21</td>
</tr>
<tr>
<td>95% C.I.</td>
<td>1.08-1.26</td>
<td>0.67-0.90</td>
<td>1.08-1.35</td>
</tr>
<tr>
<td>Meta-analysis (Stage I, Stage II)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>p-value</td>
<td>$6.96 \times 10^{-6}$</td>
<td>0.0594</td>
<td>$8.41 \times 10^{-5}$</td>
</tr>
<tr>
<td>HR</td>
<td>1.18</td>
<td>0.88</td>
<td>1.23</td>
</tr>
<tr>
<td>95% C.I.</td>
<td>1.10-1.27</td>
<td>0.77-1.01</td>
<td>1.11-1.37</td>
</tr>
<tr>
<td>* Benjamini-Hochberg correction for multiple testing</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
only gene in the immediate LD region surrounding the SNP. The expanded cis-eQTL region (±1 Mb) surrounding the SNP also contains the RNA coding genes MIR8065, LINC01570, and LOC102723308, as well as the uncharacterized gene LOC440337. No cis-eQTLs were observed in the rs6500843 locus. When we examined trans-eQTLs, the expression levels of six genes were associated with genotypes in the rs6500843 locus; MCM3, CENPM, PKMYT1, AURKA, KIFC1, TK1 (Bonferroni-corrected for all genes on the array; p < 0.05). In an enrichment analysis for Gene Ontology biological processes, using an arbitrary raw eQTL p-value threshold of p < 10⁻⁵ to select an expanded candidate gene list, GO terms involved in cell cycle control, mitosis and DNA replication emerged as highly significant for the trans-eQTLs (34 probes representing 28 genes) in the rs6500843 locus (Table 3). Note that rs6500843 itself was not present in the data set, nor were any SNPs in complete LD with it. The vast majority of eQTLs in this region are associated with the SNPs rs6500842 (r² 0.54, D’ 0.87 with rs6500843) and rs7205424 (r² 0.26, D’ 0.53), suggesting a biologically significant role for the haplotype(s) tagged by these two SNPs.

The LD region around rs11155012 contains two genes: CCDC28A and ECT2L. In total, 34 genes are located in the expanded cis-eQTL region around this locus. One nominally significant cis-eQTL was observed in this region, and occurred as a positive correlation between the rare allele of rs9321678 (r² 0.147, D’ = 1 with rs11155012) and the neighboring CCDC28A gene (t = 2.003, p = 0.0454). In the trans-eQTL analysis, the rs11155012 locus was associated with the expression of the genes CHRFAM7A, CRYBB2, RASGRP4, MOCS1, SOX21, and UPK3B. No statistically significant GO term enrichment was detected for the rs11155012 locus.

The complete trans-eQTL results for both loci are presented in detail in Supplementary Table 4.

**Figure 1:** Forest plots depicting study-wise hazard ratios for the statistically significant SNPs detected in Stage II. a) Hazard ratios for rs6500843 among cases treated with any adjuvant chemotherapy (additive model); b) Hazard ratios for rs11155012 among anthracycline-treated cases (additive model).
Expression based survival analysis of the genes associated with the rs6500483 and rs11155012 loci

Next, we utilized the Kaplan-Meier Plotter database [14] to investigate whether any of the genes surrounding our statistically significant SNPs are associated with breast cancer survival (10 year relapse-free survival) at the gene expression level. Regions of interest were defined as regions containing SNPs with $r^2 > 0.2$ to the nominal SNP. The region for rs11155012 contained two genes (ECT2L, CCDC28A), and the region for rs6500483 contained one (RBFOX1/A2BP1). These candidate genes were analyzed in the “any adjuvant chemotherapy” category, as information on specific types of chemotherapy was not available in the database. Among these cases ($N = 425$), high expression of the gene CCDC28A was associated with better prognosis ($p = 0.00012, HR 0.5, 95\% \text{ C.I. } 0.35 - 0.72$) (Supplementary Figure 1). It was also associated with prognosis in the full data set, irrespective of treatment ($N = 3455$, $p = 0$, HR 0.56, 95\% C.I. 0.49 - 0.63). This is consistent with the results of the cis-eQTL analysis: the rare allele of rs9321678 was associated with increased CCDC28A expression, which in turn is associated with better prognosis. The rare alleles of rs11155012 and rs9321678 segregate in different haplotypes (negative correlation), as can be deduced from the LD information ($r^2 = 0.147, D' = 1, \text{ MAFs are roughly equal [0.20 and 0.18, respectively]}$). Consequently, the rare allele of rs11155012 would be expected to associate with worse prognosis, which is indeed the case in our SNP survival analysis.

Of the trans-eQTL genes associated with the rs11155012 locus, the genes CHRF AM7A, CRYBB2, MOCS1 and SOX21 were associated with survival among all cases in the KM-Plotter analysis, whereas only one (SOX21) was associated with survival among chemotherapy-treated cases (Supplementary Table 5). Significant heterogeneity ($p = 0.0044; 0.0239$ after BH-adjustment for multiple testing) was observed for SOX21: high SOX21 associated with better prognosis among untreated cases (HR 0.82, 95\% C.I. 0.69 – 0.98), but the effect was reversed among

### Model without interaction

<table>
<thead>
<tr>
<th>Gene / Variable</th>
<th>HR</th>
<th>95% C.I.</th>
<th>p</th>
</tr>
</thead>
<tbody>
<tr>
<td>rs6500483</td>
<td>1.05</td>
<td>0.97 - 1.14</td>
<td>0.240</td>
</tr>
<tr>
<td>Chemotherapy</td>
<td>1.16</td>
<td>0.99 - 1.35</td>
<td>0.066</td>
</tr>
<tr>
<td>Age</td>
<td>1.04</td>
<td>1.04 - 1.05</td>
<td>$&lt; 10^{-16}$</td>
</tr>
<tr>
<td>Grade</td>
<td>1.40</td>
<td>1.27 - 1.54</td>
<td>$8.5 \times 10^{-12}$</td>
</tr>
<tr>
<td>ER</td>
<td>0.75</td>
<td>0.64 - 0.86</td>
<td>$8.1 \times 10^{-5}$</td>
</tr>
<tr>
<td>T</td>
<td>1.53</td>
<td>1.39 - 1.69</td>
<td>$&lt; 10^{-16}$</td>
</tr>
<tr>
<td>N</td>
<td>2.03</td>
<td>1.78 - 2.31</td>
<td>$&lt; 10^{-16}$</td>
</tr>
</tbody>
</table>

$Likelihood \text{ ratio test=640 on 10 df, } p=0 \ n= 9680, \text{ number of events= 1176}$

### Model with an interaction term (rs6500483:Chemotherapy)

<table>
<thead>
<tr>
<th>Gene / Variable</th>
<th>HR</th>
<th>95% C.I.</th>
<th>p</th>
</tr>
</thead>
<tbody>
<tr>
<td>rs6500483</td>
<td>0.93</td>
<td>0.84 - 1.04</td>
<td>0.210</td>
</tr>
<tr>
<td>Chemotherapy</td>
<td>0.60</td>
<td>0.40 - 0.92</td>
<td>0.018</td>
</tr>
<tr>
<td>Age</td>
<td>1.04</td>
<td>1.04 - 1.05</td>
<td>$&lt; 10^{-16}$</td>
</tr>
<tr>
<td>Grade</td>
<td>1.40</td>
<td>1.27 - 1.54</td>
<td>$6.4 \times 10^{-12}$</td>
</tr>
<tr>
<td>ER</td>
<td>0.74</td>
<td>0.64 - 0.86</td>
<td>$7.3 \times 10^{-5}$</td>
</tr>
<tr>
<td>T</td>
<td>1.53</td>
<td>1.39 - 1.69</td>
<td>$&lt; 10^{-16}$</td>
</tr>
<tr>
<td>N</td>
<td>2.03</td>
<td>1.78 - 2.32</td>
<td>$&lt; 10^{-16}$</td>
</tr>
<tr>
<td>rs6500483:Chemotherapy</td>
<td>1.33</td>
<td>1.12 - 1.58</td>
<td>$9.6 \times 10^{-4}$</td>
</tr>
</tbody>
</table>

$Likelihood \text{ ratio test=651 on 11 df, } p=0 \ n= 9680, \text{ number of events= 1176}$

$Likelihood \text{ ratio test between models: chisq=10.98, df=1, } p = 0.000921$
Expression of the RBFOX1 gene at the rs6500483 locus did not associate with survival in the KM-plotter database, either among chemotherapy-treated cases or among all cases. In contrast, all six trans-eQTL genes associated with the rs6500843 locus (MCM3, CENPM, PKMYT1, AURKA, KIFC1, TK1) were associated with survival when analyzing all cases irrespective of treatment, as well as among cases who specifically had not received systemic chemotherapy. All other genes but AURKA associated also with survival among cases treated with adjuvant chemotherapy (Supplementary Table 5) which would suggest a treatment-independent effect for most of these genes. However, a test of heterogeneity between the treated and non-treated groups indicated a statistically significant difference in AURKA-associated survival between treated and non-treated cases (heterogeneity...
Table 4: Description of the data sets used in this study.

<table>
<thead>
<tr>
<th></th>
<th>HEBCS GWS</th>
<th>POSH GWS</th>
<th>SUCCESS-A</th>
<th>iCOGS</th>
</tr>
</thead>
<tbody>
<tr>
<td>No. of cases</td>
<td>805</td>
<td>536</td>
<td>3596</td>
<td>17828</td>
</tr>
<tr>
<td>Vital status</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Alive</td>
<td>466 (58%)</td>
<td>300 (56%)</td>
<td>3389 (94%)</td>
<td>15630 (88%)</td>
</tr>
<tr>
<td>Deceased: all-cause</td>
<td>339 (42%)</td>
<td>236 (44%)</td>
<td>207 (6%)</td>
<td>2198 (12%)</td>
</tr>
<tr>
<td>Follow-up mean ±SD (years)</td>
<td>10.6 ± 6.6</td>
<td>4.1 ± 2.0</td>
<td>3.9 ± 1.7</td>
<td>7.3 ± 4.0</td>
</tr>
<tr>
<td>ER</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Negative</td>
<td>230 (29%)</td>
<td>370 (69%)</td>
<td>1106 (31%)</td>
<td>3002 (17%)</td>
</tr>
<tr>
<td>Positive</td>
<td>513 (64%)</td>
<td>165 (31%)</td>
<td>2458 (68%)</td>
<td>11753 (66%)</td>
</tr>
<tr>
<td>Missing data</td>
<td>62 (8%)</td>
<td>1 (0.2%)</td>
<td>32 (1%)</td>
<td>3073 (17%)</td>
</tr>
<tr>
<td>Grade</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>144 (18%)</td>
<td>13 (2%)</td>
<td>165 (5%)</td>
<td>2911 (16%)</td>
</tr>
<tr>
<td>2</td>
<td>312 (39%)</td>
<td>84 (16%)</td>
<td>1698 (47%)</td>
<td>6354 (36%)</td>
</tr>
<tr>
<td>3</td>
<td>280 (35%)</td>
<td>422 (79%)</td>
<td>1698 (47%)</td>
<td>4414 (25%)</td>
</tr>
<tr>
<td>Missing data</td>
<td>69 (9%)</td>
<td>17 (3%)</td>
<td>35 (1%)</td>
<td>4149 (23%)</td>
</tr>
<tr>
<td>T / tumor size category a</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>390 (48%)</td>
<td>232 (43%)</td>
<td>1464 (41%)</td>
<td>9338 (52%)</td>
</tr>
<tr>
<td>2</td>
<td>304 (38%)</td>
<td>236 (44%)</td>
<td>1856 (52%)</td>
<td>4615 (26%)</td>
</tr>
<tr>
<td>3</td>
<td>50 (6%)</td>
<td>49 (9%)</td>
<td>192 (5%)</td>
<td>635 (4%)</td>
</tr>
<tr>
<td>4</td>
<td>47 (6%)</td>
<td>12 (2%)</td>
<td>50 (1%)</td>
<td>n/a</td>
</tr>
<tr>
<td>Missing data</td>
<td>14 (2%)</td>
<td>7 (1%)</td>
<td>34 (1%)</td>
<td>3240 (18%)</td>
</tr>
<tr>
<td>N (nodal metastasis)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Negative</td>
<td>338 (42%)</td>
<td>248 (46%)</td>
<td>1248 (35%)</td>
<td>8976 (50%)</td>
</tr>
<tr>
<td>Positive</td>
<td>446 (55%)</td>
<td>262 (49%)</td>
<td>2311 (64%)</td>
<td>5471 (31%)</td>
</tr>
<tr>
<td>Missing data</td>
<td>21 (3%)</td>
<td>26 (5%)</td>
<td>37 (1%)</td>
<td>3381 (19%)</td>
</tr>
<tr>
<td>M (distant metastasis)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Negative</td>
<td>740 (92%)</td>
<td>481 (90%)</td>
<td>3487 (97%)</td>
<td>2834 (16%)</td>
</tr>
<tr>
<td>Positive</td>
<td>57 (7%)</td>
<td>50 (9%)</td>
<td>4 (0.1%)</td>
<td>267 (1.5%)</td>
</tr>
<tr>
<td>Missing data</td>
<td>8 (1%)</td>
<td>5 (1%)</td>
<td>105 (2.9%)</td>
<td>14727 (83%)</td>
</tr>
<tr>
<td>Adjuvant chemotherapy treatment</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>No adjuvant chemotherapy</td>
<td>445 (55%)</td>
<td>18 (3.4%)</td>
<td>0 (0%)</td>
<td>11108 (62%)</td>
</tr>
<tr>
<td>Anthracycline+Taxane</td>
<td>14 (2%)</td>
<td>129 (24%)</td>
<td>3596 (100%)</td>
<td>733 (4%)</td>
</tr>
<tr>
<td>Anthracycline</td>
<td>191 (24%)</td>
<td>375 (70%)</td>
<td>-</td>
<td>2277 (13%)</td>
</tr>
<tr>
<td>Taxane</td>
<td>2 (0.2%)</td>
<td>8 (1.5%)</td>
<td>-</td>
<td>135 (0.8%)</td>
</tr>
<tr>
<td>Methotrexate</td>
<td>153 (19%)</td>
<td>4 (0.7%)</td>
<td>-</td>
<td>1022 (6%)</td>
</tr>
<tr>
<td>Missing data</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>2528 (14%)</td>
</tr>
<tr>
<td>Adjuvant Endocrine treatment</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Treated</td>
<td>282 (35%)</td>
<td>183 (34%)</td>
<td>2458 (68%)</td>
<td>11340 (64%)</td>
</tr>
<tr>
<td>Not treated</td>
<td>520 (65%)</td>
<td>344 (64%)</td>
<td>1138 (32%)</td>
<td>5670 (32%)</td>
</tr>
<tr>
<td>Missing data</td>
<td>3 (0.4%)</td>
<td>9 (1.7%)</td>
<td>-</td>
<td>818 (5%)</td>
</tr>
</tbody>
</table>

a T was acquired from TNM staging for HEBCS, POSH, SUCCESS-A, and derived from tumor diameter in iCOGS (1: ≤2cm, 2: >2cm and ≤5cm, 3: >5cm); T4 (inflammatory carcinoma) is therefore undefined for iCOGS.
p=0.021 after BH-adjustment for multiple testing): while high AURKA expression associated with poor survival in untreated cases, no such effect was seen in chemotherapy-treated cases.

Next, we investigated the possible connection between the rs6500843 locus and the trans-eQTL genes. Rs6500843 is located in an intron of RBFOX1, a tissue-specific splicing regulator, for which target genes have been previously published [15]. Given that the genetic neighborhood around rs6500843 contains no other protein coding genes, and little is known about the three RNA coding genes in the region, we operated here under the hypothesis that the SNP is functionally associated with the RBFOX1 gene. As splice variants of gene products may give rise to different signals in microarray experiments, we cross-referenced the published list of RBFOX1 targets against our expanded list of putative trans-eQTL genes (raw p < 10^{-5} in the eQTL analysis) that also fall within the enriched GO:0007049 (cell cycle) Gene Ontology group (Table 3), and came up with one gene: the transcription factor FOXM1. Genome-wide target genes for FOXM1 have also been previously published [16]; comparison of the statistically significant sites (combined genomic binding and coexpression) with our trans-eQTL list yielded four genes regulated by FOXM1: EXO1, MCM6, UHRF1, and KPNA2. These connections between the genomic locus and the eQTL genes have been schematically summarized in Figure 3.

The rs11155012 locus contains a genomic regulatory region

Finally, we investigated the possibility that the prognostic SNPs identified in this study are in linkage disequilibrium with other, functionally significant variants in their genomic vicinity. All SNPs in linkage disequilibrium (r^2 > 0.2) with rs6500843 and rs11155012 were analyzed using HaploReg, a database of genomic regulatory elements [17]. Rs11155012 is in high LD with a number of SNPs affecting a genomic enhancer.

Figure 2: Kaplan-Meier curves illustrating cumulative 10-year overall survival among cases of the pooled iCOGS data set categorized by rs6500843 genotype. The HRs indicate genotype-specific hazard ratios relative to the reference genotype (AA). Censoring marks have been omitted to make the curves clearer. The data set has been subgrouped according to treatment: a) patients treated with any adjuvant chemotherapy, b) patients who did not receive adjuvant chemotherapy.
site (Supplementary Table 6) active in human mammary epithelial cells (HMEC). The site has been experimentally shown to bind the proteins FOXA1 and FOXA2, and a Foxa binding motif is predicted to be altered by rs6570291, a SNP in near-complete LD with rs11155012 ($r^2 = 0.99$).

Equally strong evidence of an active regulatory site was not observed for the rs6500843 locus. The SNP itself is predicted to alter 33 transcription factor binding motifs, mostly homeobox-containing tissue-specific transcription factors, but no supporting experimental evidence is present in the HaploReg data.

**DISCUSSION**

We have utilized three independent data sets to evaluate the significance of putative prognostic/predictive SNPs from an initial GWS pilot investigating survival after adjuvant chemotherapy in breast cancer. This analysis was carried out as a meta-analysis between iCOGS studies and two additional data sets (SUCCESS-A, POSH). Two loci emerged as statistically significant in the two-stage analysis: rs6500843 among cases treated with any chemotherapy, and rs11155012 among cases treated with anthracyclines. Of these, rs6500843 was found to interact with adjuvant chemotherapy in a subsequent multivariate interaction analysis, reinforcing the notion that its association with survival may have a predictive basis: carriers of the rs6500843 G-allele appear to have somewhat worse survival than other chemotherapy-treated cases.

The only gene in the LD region surrounding rs6500843 is RBFOX1 (A2BP1), which encodes a highly conserved RNA-binding protein involved in the control of tissue-specific mRNA splicing [18]. It has been identified as a common target of LOH and copy number variation in other types of malignancies [19-21], and a SNP in the gene (not in LD with rs6500843) has been reported to associate with survival in non-small-cell lung cancer [22], but little is known about its role in breast cancer. While the rs6500843 SNP is predicted to alter a homeobox transcription factor binding site targeted by 33 transcription factors, we did not find further experimentally verified evidence of a genetically modulated regulatory region in this locus, nor was RBFOX1 gene expression itself associated with breast cancer survival. However, a trans-eQTL analysis of the

![Diagram](https://example.com/diagram.png)

**Figure 3:** Schematic summary of the putative evidence connecting the rs6500843 SNP to the trans-eQTL SNPs associated with this locus. The eQTL genes marked in bold are associated with the rs6500843 locus at a statistically significant level after conservative Bonferroni correction; the remaining genes listed here are associated with SNP genotype at $p < 10^{-5}$, and also belong to the Gene Ontology group GO:0007049 (cell cycle) which was most strongly enriched in the DAVID analysis. RBFOX1 and FOXM1 target gene identification is based on previously published data [13, 14].
SNPs in the rs6500843 region identified six statistically significant genes, all of which were associated with survival in breast cancer in the Kaplan-Meier Plotter analysis (and five in the chemotherapy-only subgroup). Notably, the Aurora-A kinase (AURKA) associated with differential survival when comparing chemotherapy-treated and non-treated cases. High AURKA expression appeared to associate with poor survival in untreated cases, whereas no such effect was seen in chemotherapy-treated cases, which suggests a favorable response to the chemotherapy regimens administered to these cases. AURKA has been previously suggested to be a master regulator of cellular radio- and chemoresistance, proliferation, cell cycle progression and anchorage-independent growth [23].

In order to detect enriched Gene Ontology biological processes among the eQTL genes, we relaxed the criteria of statistical significance and analyzed a slightly larger list of candidate genes (n = 28). This set of candidates was strongly enriched for genes involved in cell cycle control (GO: 0007049; cell cycle): 15 out of 28 genes fell within this category, an 11-fold enrichment compared to a random selection of genes. The set of genes includes EXO1, knockdown of which has been reported to desensitize H196 lung cancer cells to paclitaxel treatment [24]; KIFC1, reported to modulate docetaxel sensitivity [25]; the breast cancer susceptibility gene CHEK2 [26, 27]; the Bloom syndrome gene BLM [28]; and the Survivin gene BIRC5, reported to associate with chemoresistance and radioresistance in breast cancer [29]. It is intriguing to see this group of cell cycle control and chemoresistance-associated genes emerge in eQTL with a SNP associated with survival after chemotherapy, especially as there is a plausible connection between the rs6500843 locus and this set of trans-eQTL genes (Figure 3). Rs6500843 is located in an intron of RBFOX1, a tissue-specific splicing regulator that targets the proto-oncogene FOXM1, a transcription factor involved in cell cycle control. In our analyses, FOXM1 itself emerged as a putative trans-eQTL gene associated with the rs6500843 locus, and it has been reported to regulate four other genes on that list: EXO1, MCM6, UHRF1, and KPNA2. Of these, EXO1 is of particular interest, as the FOXM1-EXO1 regulatory connection has been previously reported to modulate chemoresistance in ovarian carcinoma cells [30]. An important caveat to this analysis is that the SNP rs6500843 itself was not present in the eQTL data set, and the eQTL results are based on SNPs in incomplete linkage disequilibrium with it. The functional significance of rs6500843 itself, and the putative transcription factor binding site it resides in, therefore remains unclear.

The other SNP emerging as statistically significant in the validation analysis, rs11155012, is located in a LD region that contains two genes, CCDC28A and ECT2L, the biological functions of which are poorly understood. Our analysis of publicly available gene expression data [12] indicates that CCDC28A transcript abundance is associated with relapse-free survival in breast cancer, which suggests that rs11155012 may be linked to a prognostically significant functional variant in this gene. Indeed, rs11155012 is in LD with a number of SNPs affecting a genomic enhancer site active in human mammary epithelial cells. The site has been experimentally shown to bind the proteins FOXA1 and FOXA2, and a Foxa binding motif is predicted to be altered by rs6570291, a SNP in near-complete LD with rs11155012 (r² = 0.99). FOXA1 (Hnf-3-alpha) is a key transcription factor involved in mechanisms known to be critical in breast carcinogenesis: estrogen receptor -mediated signaling, and cell cycle control in conjunction with BRCA1 [31, 32]. Furthermore, a modest cis-eQTL effect was observed between rs9321678 (r² = 0.147, D' = 1 with rs11155012) and the CCDC28A gene. We also detected a trans-eQTL between rs9495127 (r² = 0.129, D' = 1) and the transcription factor SOX21, a gene whose expression associates with increasing hazard among chemotherapy-treated cases despite being protective in untreated cases. While causality cannot be established without experimental work, these findings provide supporting evidence for an association between genetic variation in this regulatory site and breast cancer survival. The predictive value of this genetic locus remains questionable, however, as we did not observe an interaction between rs11155012 and treatment in the clinical data.

The hazard ratios for rs6500483 show some heterogeneity between the data sets used in this study: SUCCESS-A appears to disagree with the other data sets. Rs6500483 is represented in SUCCESS-A by rs4786939, but these two SNPs are in nearly complete linkage disequilibrium (r² 0.967, D' 1.0), indicating that the use of a tagging SNP is an unlikely source of heterogeneity here. Heterogeneity between follow-up times and treatment regimens would be a more likely reason: the cases in SUCCESS-A have all received taxane-based therapy, a regimen poorly represented in the other data sets. Unfortunately, the specific chemotherapy agents involved in the genetic association cannot be resolved using our currently available data. Additionally, in light of our use of GWAS as a starting point, it must be noted that our findings do not reach genome-wide significance. However, the purpose of the initial Stage I GWAS was to define a candidate SNP set that would most likely capture any true survival-associated SNPs, the statistical significance of which would then be evaluated in the substantially more powerful Stage II analysis. We do not anticipate very large effect sizes in SNP-based survival analyses, and therefore utilized a stepwise study design to alleviate the problem of multiple testing and resultant loss of statistical power. Only 39 SNPs were analyzed in Stage II, two of which meet our criteria of statistical significance. Both findings are supported by additional lines of evidence from gene expression- and regulome-based analyses. Nevertheless, these results must be viewed as exploratory
In conclusion, we have conducted a two-stage genetic association study to detect SNPs associated with survival after chemotherapy. One SNP, rs6500843, was found to interact specifically with adjuvant chemotherapy, independently of standard prognostic markers, whereas rs11155012 may associate with survival in general. eQTL analysis of the rs6500843 locus identified a group of genes known to associate with cancer progression, chemoresistance, and survival. We propose that these genes may be connected to the rs6500843 locus via a RBFOX1-FOXM1-mediated regulatory pathway. If confirmed, these findings may aid in the development of better predictive markers and improved individualized cancer therapy.

MATERIALS AND METHODS

Study design

Initially, a genome-wide study (Stage I: HEBCS-GWS) was conducted to discover candidate SNPs that may be associated with breast cancer survival, with an emphasis on treatment-based subgroups. This candidate SNP set was then analyzed in three validation datasets (Stage II: iCOGS, SUCCESS-A, POSH). SNPs emerging as statistically significant within Stage II were further examined in an eQTL analysis of two breast cancer data sets (TCGA, METABRIC), supported by in silico genomic feature analysis. The data sets used in this study are described below, and summarized in Table 4. Informed consent has been obtained from all patients included in this study.

Discovery GWS (Stage I: HEBCS-GWS)

Genotype information was obtained from a study series consisting of 805 Finnish breast cancer cases (HEBCS-GWS). All cases were female, ascertained for their first primary invasive breast cancer. Of these, 423 cases originated from a prospective patient series of consecutive unselected, incident breast cancer patients treated in the Helsinki University Hospital Department of Oncology in years 1997–1998 and 2000 [33, 34]. The series also includes 140 cases recruited between 2001 and 2004, and 242 additional familial cases [7, 35]. To increase the statistical power of survival analyses, the GWS series was specifically enriched for cases with reduced survival (distant metastasis or death at the time of the initiation of the study in 2008): in total, the series includes 312 breast cancer specific events, and 339 any-cause mortality events at the time of analysis. The cancer diagnoses were confirmed through the Finnish Cancer Registry and hospital records. Information on the date and cause of death was obtained from the Finnish Cancer Registry, a central database of diagnostic and death information on all cancer patients in Finland.

The HEBCS-GWS series (“Stage I”) was genotyped using the Illumina 550K platform as previously described [36]. The preliminary survival analysis was carried out using three different endpoints in parallel: five-year BDDM (breast cancer death or distant metastasis), 10-year breast cancer specific survival, and 10-year overall survival, using a codominant genetic model (test for heterogeneity between genotypes). Since survival after chemotherapy was the main focus of this study, it would have been ideal to entirely restrict the initial Stage I analysis only to chemotherapy-treated cases (comprising 45% of the data set; Table 4), given sufficient statistical power. To determine the feasibility of this approach, the R package ‘survSNP’ was employed to estimate the statistical power of our survival analysis [37]. Using a significance threshold of p < 10^{-4} and a hypothetical SNP with a minor allele frequency of 0.25 as the ad hoc target for discovery, we had 80% power to detect a per-allele HR of 1.6 in the whole sample set, but only 32% power if the analysis was restricted to chemotherapy-treated cases only. Analysis of specific chemotherapy regimens would have decreased the statistical power further. Based on this, we concluded that a treatment-based subgroup analysis alone would be unacceptably underpowered. Therefore, to be eligible for subsequent validation, SNPs had to meet one of these three more inclusive criteria: 1) main effect p < 10^{-4} and p < 0.01 among chemotherapy-treated cases, 2) p < 10^{-4} among chemotherapy-treated cases, or 3) p < 10^{-3} among chemotherapy-treated cases and a homozygote-associated hazard ratio > 3.0. These SNPs (n = 45) were then selected as candidates for Stage II validation and genotyping as part of the iCOGS project [2].

Validation studies (Stage II: iCOGS, POSH, SUCCESS-A)

The candidate SNPs from Stage I were analyzed in three additional data sets: iCOGS, POSH, SUCCESS-A (described in detail below).

iCOGS

SNPs identified as putatively significant in Stage I HEBCS GWAS analysis of chemotherapy-treated cases were included on a custom Illumina Infinium array (iCOGS) for large scale genotyping of a data set of 50927 individuals from 52 Breast Cancer Association Consortium (BCAC) member studies, 41 of which were of predominantly European ancestry, 9 of Asian, and 2 of African-American ancestry. Genotyping and quality control was carried out as previously described [2].

Studies represented on the iCOGS chip were
included in survival analysis here if sufficient follow-up data was available, with a minimum requirement of at least 10 survival events (deaths from any cause) per study. Additionally, we included only studies with cases from predominantly European ancestry, and from which adjuvant chemotherapy information was available. At the individual level, we included only female cases ascertained for their first primary, invasive tumor. After these filtering steps, the data set consisted of 17828 eligible cases (2198 any-cause deaths; 12%), of which 6720 cases were treated with any adjuvant chemotherapy. Of these, 3010 cases were known to have been treated with anthracycline-based chemotherapy. While data on taxane (n = 868) and methotrexate-based (n = 1022) adjuvant treatment was also available, these treatments were not analyzed as separate subgroups due to the small sample sizes and poor comparability with the other data sets (Table 4). For 2528 cases, the specific type of chemotherapy regimen was unknown. The cases included here come from 16 separate BCAC studies, which have been described in Supplementary Table 7.

### POSH GWS

The POSH GWS consisted of 536 individuals (236 any-cause deaths; 44%) selected from a consecutively ascertained cohort of early onset cases (diagnosed with invasive breast cancer at the age of 40 or earlier) from the United Kingdom. These cases were enrolled into the *Prospective study of Outcomes in Sporadic versus Hereditary breast cancer* (POSH) between 2000 and 2008, as previously described [38]. The POSH GWS material was enriched for cases with poor prognosis by including cases with triple-negative breast cancer (n=401), and cases with particularly short duration of breast cancer survival (<2 years, n=48); additional cases with relatively long survival were then included for contrast (>4 years, n=125) [39]. These cases were genotyped on the Illumina 600-Quad SNP array; genotyping and quality control was performed as previously described [39]. 518 cases (97%) in this data set were treated with adjuvant chemotherapy.

### SUCCESS-A

SUCCESS-A is a randomized Phase III study of response to treatment of early primary breast cancer with adjuvant therapy after surgical resection. The cases are all treated with anthracycline- and taxane-based adjuvant chemotherapy, and randomized for Gemcitabine treatment. The sample set consisted of 3596 cases (207 any-cause deaths; 6%) that were recruited between 2005 and 2007 from 250 study sites across Germany. Genotyping was carried out using the Illumina Human OmniExpress-FFPE BeadChip platform. The SUCCESS-A data as well as detailed descriptions of the materials and methodology can be acquired from the NCBI database of Genotypes and Phenotypes (dbGaP Study Accession: phs000547.v1.p) [40].

### Statistical analysis

In stage II, unless otherwise noted, 10-year overall survival (death from any cause) was used as the end point in all survival analyses, as all-cause mortality data was the most widely available in the iCOGS data set. This also allowed us to avoid the potential biases that can arise from clinical follow-up data in multicenter studies [41].

All survival analyses were run under the additive genetic model, follow-up times left-truncated, and adjusted for patient age at diagnosis, and (in the case of iCOGS) stratified by study in order to minimize potential biases arising from differing case recruitment strategies and different populations of origin. The analyses were performed within the same subgroups (chemotherapy-treated cases and anthracycline-specific analysis) as in stage I.

To alleviate potential biases arising from population stratification, e.g. cryptic relatedness of cases, the analysis was also adjusted for three genetic principal components to correct for possible population substructure. The principal components were calculated from the genotypes of uncorrelated \( r^2 < 0.2 \) SNPs in the genome-wide data sets. Briefly, for the HEBCS-GWS, POSH and SUCCESS-A data sets, we pruned a subset of SNPs not in substantial LD with any other SNPs \( r^2 < 0.2 \) and ran a principal component analysis (PCA) using the ‘GenABEL’ package in R. The PCA analysis for iCOGS has been described previously [2]; as with the other three data sets, only three principal components were used in this study.

The selected SNPs from the HEBCS-GWS data set (Stage I) were also re-analyzed at this point using the same parameters as with the validation data. This means that Stage I results were here re-analyzed only under the additive model (which can be expected to capture both dominant and recessive signals), regardless of the original selection criteria, reducing the amount of multiple testing in the final meta-analysis stage. While the original SNP selection was based on more inclusive criteria, the purpose of this was to ensure that the final results are directly comparable across the stages of the study. Thus, allele calling and quality control for HEBCS-GWS was performed as previously described [39], and the survival analysis was performed as described above. Similar to the validation data sets, principal component analysis (PCA) was included for HEBCS-GWS as well at this stage.

Results of the Stage II (iCOGS, POSH, SUCCESS-A) survival analysis were meta-analyzed under a fixed-effects model using the ‘rmeta’ package in R, and the resulting meta-statistics were used to determine statistical significance. Benjamini-Hochberg correction was applied to account for multiple testing [42].
Evaluating the association between genotype and gene expression in breast cancer, two publicly available data sets (containing both genotype and gene expression data) were used for eQTL analysis: TCGA [12], and METABRIC [13]. The TCGA gene expression data is mRNA sequencing data from the Illumina HiSeq 2000 platform, whereas the METABRIC gene expression data was generated by the Illumina Human WG6 v3 platform. Tumor tissue genotyping had been carried out using the Affymetrix Genome Wide Human SNP array 6.0 for both data sets. Of the two validated SNPs, rs11155012 itself was represented on this SNP array, whereas rs6500843 was not. The latter was best represented by the linked SNPs rs4786121 and rs7190693 (r² > 0.1). Candidate genes in the regions surrounding the SNPs were analyzed in the Kaplan-Meier plotter (http://kmplot.com/analysis/), a gene expression and survival database currently consisting of 4142 breast cancer cases, of which 425 were known to have been treated with adjuvant chemotherapy [12]. These analyses were performed using 10-year relapse-free survival, as this was the only end point available for the majority of cases in the Kaplan-Meier plotter data set, and optimized break points for the binarization of gene expression levels. All SNPs in these regions were further analyzed for their impact on regulatory features using HaploReg, a database of genomic functional annotations [15].

Further in silico evaluation of SNPs and candidate genes

It is likely that the prognostic SNPs identified in this study are merely linkage disequilibrium proxies for other, functionally significant variants in their genomic vicinity. In an effort to identify the SNPs and genes with a direct functional impact on breast cancer survival, we utilized a number of public databases. For these analyses, regions of interest were defined as regions containing SNPs in linkage disequilibrium with the survival-associated SNPs at r² > 0.1. Candidate genes in the regions surrounding the prognostic SNPs, as well as statistically significant trans-eQTL genes associated with the survival-associated loci, were analyzed in the Kaplan-Meier plotter. Using the DAVID Functional Annotation Tool [44, 45], we performed a pathway-enrichment analysis on a set of candidate genes statistically significant in the eQTL analysis, we also ran a pathway-enrichment analysis on a set of candidate genes selected using a more lenient p-value threshold from the eQTL analysis (raw p < 10⁻³). The analysis was restricted to Gene Ontology Biological Processes and was performed using the DAVID Functional Annotation Tool [44, 45].

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