Impact of germline and somatic cell cycle checkpoint kinase mutations on breast cancer presentation and prognosis.

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Abstract

Cell cycle checkpoint kinases activated by DNA repair pathways, ATM/Chk2 and ATR/Chk1 are important tumor suppressors. Germline mutations in these genes associate with increased cancer incidence. Specifically, *ATM* and *CHEK2* germline variants associate with increased incidence of estrogen receptor (ER)+ breast cancer with poor patient outcome. More recent investigations identified somatic inactivation of ATM/Chk2 as causal to endocrine therapy resistance in ER+ breast cancer patients. However, the relative contributions of germline and somatic inactivation of these cell cycle checkpoint kinases to ER+/HER2- and ER-/PR-/HER2- or triple negative breast cancer (TNBC) incidence and tumor characteristics has not yet been systematically assessed. Here, we comprehensively compare associations of *ATM/CHEK2* and *ATR/CHEK1* germline and somatic mutations with age, tumor stage and PR status at diagnosis, and metastatic potential using a meta-dataset compiled from six independent primary and metastatic patient datasets. We observe significantly higher frequency of *ATM* (29.6%) and *CHEK2* (9.5%) mutations in metastatic ER+/HER2- breast cancers relative to TNBC (~11% and 5% respectively) ($p=0.03$). *CHEK2* mutations associate with higher PR positivity, higher tumor stage and younger age at diagnosis for metastatic ER+/HER2- breast cancer patients. These associations are primarily driven by germline, rather than somatic *CHEK2* mutations. However, both germline and somatic mutations in *CHEK2* that are deleterious (nonsense, frameshift or splice site) associate with more rapid disease progression on early rounds of endocrine therapy when compared to tumors with wildtype *CHEK2* or with missense mutations in *CHEK2*. These results provide the first systematic analysis of the contribution of germline and somatic cell cycle checkpoint kinase mutations to tumor characteristics affecting patient prognosis and treatment response. Results of this study suggest potential for streamlined testing for status of these checkpoint kinases as prognostic and/or predictive biomarkers for ER+/HER2- breast cancer patients.

Background

ATM/Chk2 and ATR/Chk1 are cell cycle checkpoints activated by DNA damage as well as many other stressors. Although in reality the pathways are extremely complex, a simplified representation is that ATM/Chk2 and ATR/Chk1 inhibit the cell cycle at G1/S and G2/M phases, respectively, to allow the cell time to repair damaged DNA before proceeding with the cell cycle[1]. In cases where prolonged cell cycle arrest is not sufficient to facilitate DNA repair, these checkpoint kinases trigger cell death through both p53-dependent and p53-independent mechanisms[1].

Breast cancer is one of the most commonly diagnosed cancer types in the USA and globally. Estrogen receptor (ER) status of breast cancer dichotomizes diagnoses as ER+ and ER-. ER positivity predicts response to endocrine therapies that inhibit ER signaling and are highly effective initially. However, eventually ~40% of ER^+ breast cancer patients become resistant to endocrine therapy[1–3]. Discovering predictive biomarkers for endocrine therapy resistance is a significant clinical need. ER^-, and specifically tumors negative for ER, progesterone receptor (PR) and receptor tyrosine kinase growth factor HER2 (also known as triple negative breast cancer or TNBC) are the more aggressive subtype of breast cancer and have poor patient outcome[4]. Understanding fundamental factors that account for the evolution of ER+ and TNBC can refine current diagnoses and provide new therapeutic avenues to explore.

We recently uncovered a role for somatic inactivation of ATM/Chk2 signaling through loss of upstream DNA repair pathways in $ER^+/HER2^-$ breast cancer cells and patient tumors[14]. A role for germline variants in *ATM/CHEK2* in ER^+ breast cancer initiation and outcomes has been substantiated by large and multiple independent epidemiological studies[2–11]. Mutations in *CHEK2* and *ATM* associate specifically with increased incidence of ER^+ breast cancer. ER^+ breast cancer patients with *CHEK2* mutations have worse survival outcomes[3,6,12]. Two recent studies independently demonstrated significant association between levels of nuclear pATM and response to endocrine therapy in ER^+ patient tumors[7,13]. However, while germline *ATM/CHEK2* variants have been extensively studied in epidemiological study, there are few studies investigating the role of somatic inactivation of these genes on breast cancer incidence or prognosis. The few studies that have been published have conflicting or inconclusive results[15,16].

Similarly, previous studies of the association of *ATR/CHEK1* mutations, either germline or somatic with breast cancer incidence or prognosis are also inconclusive. Germline mutations in *ATR*, for instance, are observed in familial breast cancer, but whether they contribute substantially to tumor incidence or any specific tumor subtypes remains uncertain[17,18]. However, there appears to be a role for *ATR/CHEK1* somatic dysregulation in triple negative breast cancers (TNBCs)[19–21].

Overall, these cell cycle checkpoint kinases are important guardians of the genome, and well-established tumor suppressors. Understanding their relative contribution to different breast cancer subtypes and prognostic/predictive features is critical for identifying their potential as prognostic/predictive biomarkers as well as therapeutic targets. Here, we undertake a systematic evaluation of the relative contribution of germline and somatic

mutations in all four cell cycle checkpoint kinase genes to $ER^+/HER2^-$ and TNBC incidence and tumor characteristics, as described below.

Materials and Methods

Datasets

MSKCC, Cancer Cell 2019 [3], is composed of clinical and mutational data (*ESR1,TP53,ATM,ATR,CHEK2* and *CHEK1* mutations) collected from 1756 patients with hormone receptor positive (i.e. ER and/or PR+) HR+/HER2- (n=1365),HR-/HER2+(n=58), TNBC (n=168) and HR+/HER2+(n=165) primary and metastatic breast cancers. The data is published in 2019.

TCGA, Nature 2012 [5], was downloaded from cBioPortal[6] for clinical and mutational (ESR1,TP53,ATM,ATR,CHEK2 and CHEK1 mutations) analysis in December 2019.The data set is composed of clinical and mutational data collected from 825 patients with HR+/HER2- (n=486),HR-/HER2+(n=31), TNBC (n=123) and HR+/HER2+(n=79) and undetermined (n=106) primary breast cancers.

METABRIC Nature 2012 [7] *& Nat Commun 2016* [8], is downloaded from cBioPortal for clinical and mutational (ESR1,TP53,ATR and CHEK2) analysis in December 2019.The data set is composed of clinical and mutational data collected from 2509 patients with HR+/HER2- (n=1398),HR-/HER2+(n=139), TNBC (n=320) and HR+/HER2+(n=79108) and undetermined (n=544) primary breast cancers.

Broad, Nature 2012 [9], was downloaded from cBioPortal for clinical and mutational (ESR1,TP53,ATM,ATR,CHEK2 and CHEK1 mutations) analysis in March 2020.The data set is composed of clinical and mutational data collected from 825 patients with HR+/HER2- (n=37),HR-/HER2+(n=6), TNBC (n=320) and HR+/HER2+(n=108) and undetermined (n=544) primary breast cancers.

MBCP, Provisional, February 2020 [10], was downloaded from cBioPortal for clinical and mutational (*ESR1,TP53,ATM,ATR,CHEK2* and *CHEK1* mutations) analysis in March 2020.The data set is composed of clinical and mutational data collected from 825 patients with HR+/HER2- (n=50),HR-/HER2+(n=8), TNBC (n=8) and HR+/HER2+(n=21) and undetermined (n=93) metastatic breast cancers.

British Columbia, Nature 2012 [11], was downloaded from cBioPortal for clinical and mutational (*ESR1,TP53,ATM,ATR,CHEK2* and *CHEK1* mutations) analysis in March 2020.The data set is composed of clinical and mutational data collected from 825 patients with HR+/HER2- (n=9), TNBC (n=90) and undetermined (n=8) primary breast cancers.

Mutational analysis

For mutation analysis, *ATM, CHEK2, ATR* and *CHEK1* mutations were studied and *TP53* and *ESR1* mutations were used as controls. All non-synonymous mutations were included irrespective of category (i.e. missense, nonsense, frameshift, etc) or predicted pathogenicity. Mutational data were compared in three main categories: Receptor status (ER^+ vs TN), Sample site (primary, PRI vs metastatic, MET) and Mutation Type (Germline vs Somatic). Mutational frequency was calculated based on total number of mutations

identified in a category and the total patient size of the same category. Samples without any of the indicated mutations are labeled as wildtype (WT).

Tumor characteristics

PR status, tumor stage and age of diagnosis of the patients were used as categorical variables to determine patient sample characteristics with respect to mutational data. Fisher's exact test determined p-values by comparing different categories such as $ER^+/HER2^-$ vs TN or Germline vs Somatic for PR status and tumor stage while Two-tailed Wilcoxon rank sum tests were used for continuous age differences.

Survival and Disease Progression analysis

For univariate analyses, all tumors with associated survival data, is obtained from MSKCC data set. Outcome measures used were progression-free survival and progression on endocrine treatment. Only samples with survival metadata were included in the analysis.

Statistical analysis

Missing data were imputed with "NA" from mutation and survival data analysis. Samples classifying for more than one category were treated as separate set for statistical comparisons. Two-tailed Wilcoxon rank sum tests were used for age comparisons and Pearson's Chi Square test (or Fisher's Exact test) was used for comparing categorical data. Log rank test calculated p-values for survival analyses and Cox regression determined proportional hazards.

Results

***ATM/CHEK2* mutations are more frequent in ER+ breast cancer while TNBC is predisposed to *ATR* mutations**

Because mutations in cell cycle checkpoint kinase genes are relatively rare in breast cancer, we created a meta-dataset using six independent datasets to ensure sufficient sample size of ER^+ primary, ER^+ metastatic and TNBC (**Figure 1**). Using this meta-dataset, we first analyzed the incidence of mutations (germline or somatic) in each of the four cell cycle checkpoint kinases, *ATM, CHEK2, ATR, CHEK1*), in ER^+ vs TNBC samples. We included mutations in *ESR1* and *TP53* as positive controls (known drivers) for ER^+ and TNBC respectively. As expected, we found a statistically significant increase in frequency of *ESR1* mutations in ER^+ breast cancer and of *TP53* mutations in TNBC samples (**Figure 2A-B**). Overall, we observed comparable frequency of mutations in the cell cycle kinase genes between ER^+ and TNBC (**Figure 2A-B**).

However, when we considered mutational frequency of each cell cycle checkpoint kinase gene, we observed a statistically significant enrichment for *ATM* and *CHEK2* ($p=0.02$) mutations in ER^+ breast cancer samples but no enrichment for either *ATR* or *CHEK1* mutations (**Figure 2C-D**). Incidence of mutations in *CHEK1* was extremely rare in either ER^+ or TNBC. Of note, while mutations in any of these checkpoint kinases co-

occurred with mutations in *TP53* in TNBC, this was almost never the case in ER+ breast cancer (**Figure 2C-D**), likely due to the significantly higher incidence of *TP53* mutations in TNBC. These data suggest a fundamental dichotomy in the roles and importance of ATM/Chk2 and ATR/Chk1 pathways to ER+ and TNBC.

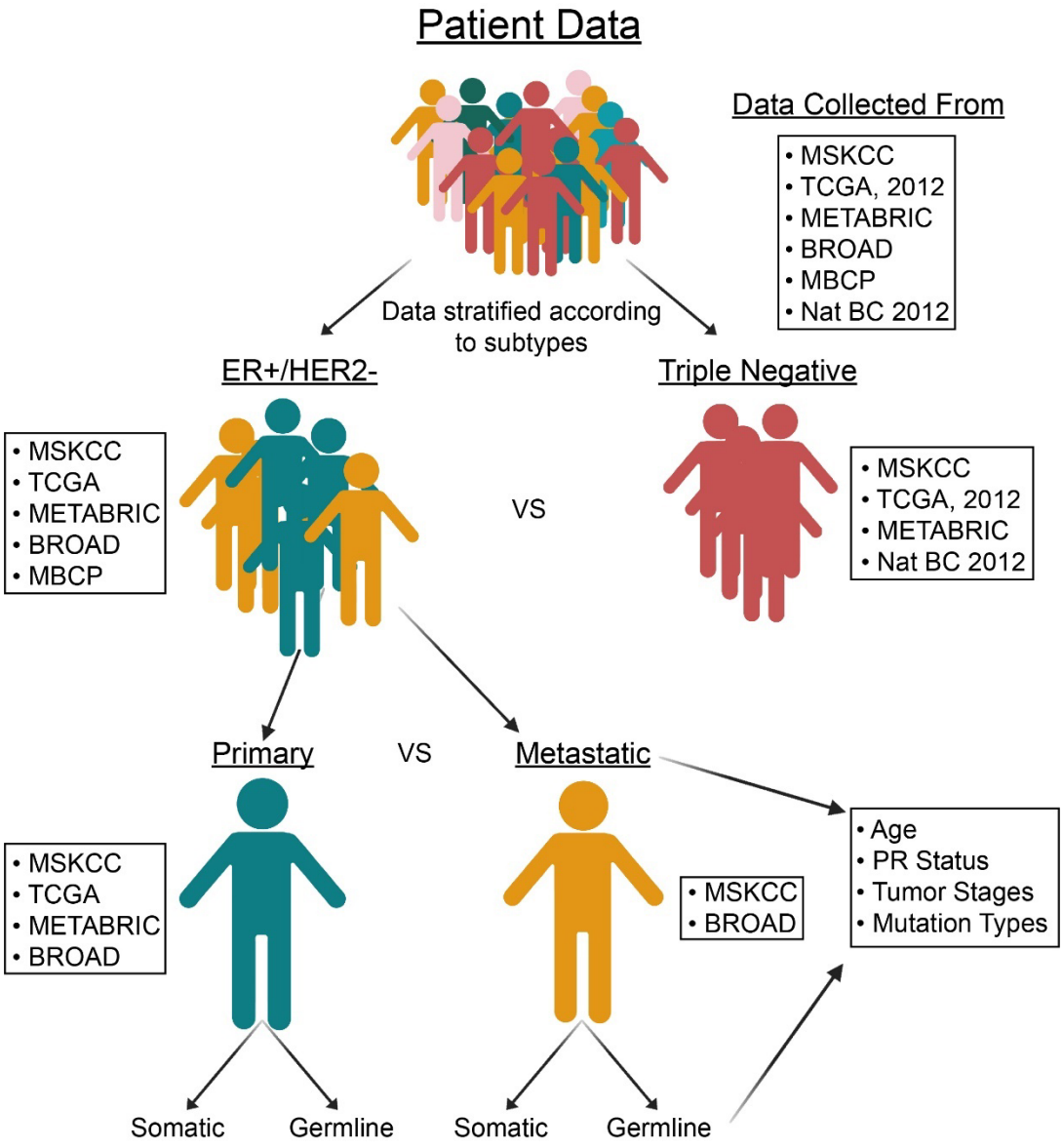

Figure 1: Outline of study. Data collected from: MSKCC, Cancer Cell 2019, TCGA Nature 2012, METABRIC, Nature 2012 & Nat Commun 2016, Broad, Nature 2012, MBCP, Provisional, February 2020, and British Columbia, Nature 2012. Patient data stratified and analyzed based on molecular subtype of disease, sample type, and occurrence of mutations (Germline Vs. Somatic). Data was further analyzed in the context of age of patient, PR status, tumor stage and mutation type.

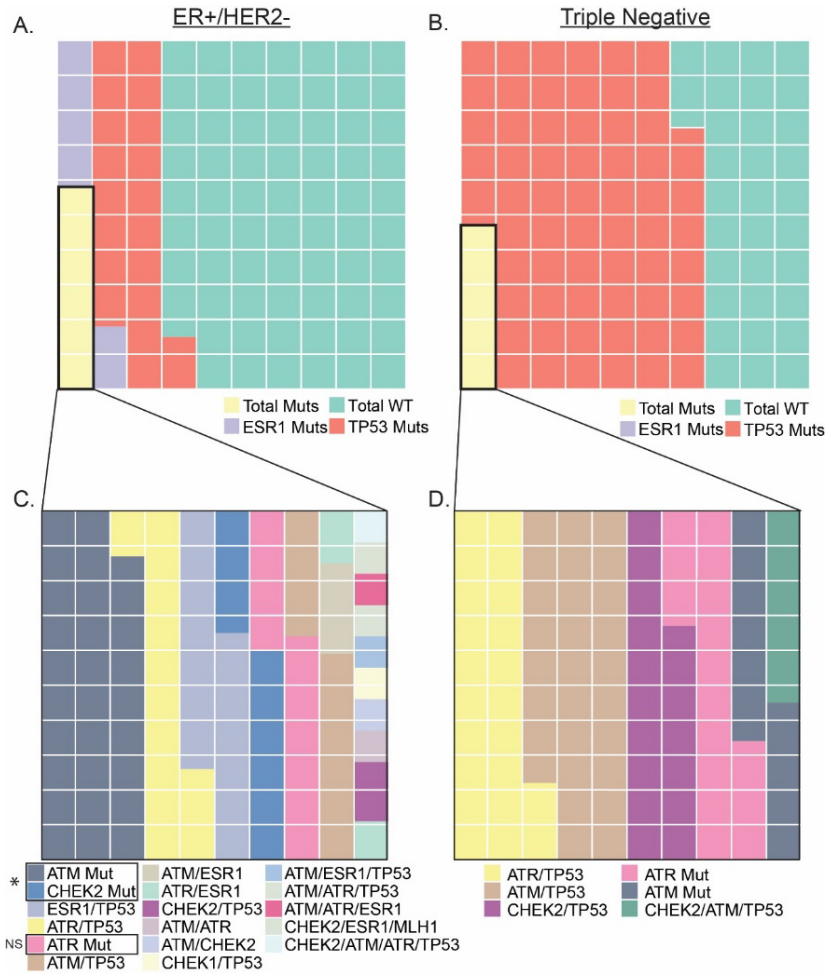

Figure 2. Mutational frequency of cell cycle checkpoint kinase genes based on breast cancer subtype. (A-B) Waffle chart charts showing *ESR1, TP53*, and cell cycle checkpoint kinase mutational frequencies in ER$^+$/HER2$^-$ vs TNBC and (C-D) frequency distribution of cell cycle checkpoint kinase mutations in ER$^+$/HER2$^-$ vs TNBC. Each square represents 1% of overall mutations in specified genes totaling 100% of our genes of interest. Fisher's Exact test determined p-values. $p<0.05$*, ns = not significant, WT, wildtype, Mut, mutant.

We next tested whether frequency of mutations in any cell cycle checkpoint kinase gene (except *CHEK1*, which is rarely mutated in ER$^+$ breast cancer and was therefore, excluded from subsequent analyses) was enriched in metastatic ER$^+$ breast cancer. We found significant increases in mutational frequency of *ATR* and *CHEK2* in metastatic ER$^+$ breast cancer relative to either primary ER$^+$ or TNBC (**Figure 3A-E, Figure S3**). Incidence pattern of mutations in these genes was highly comparable to that of *ESR1* mutations, a known driver of metastatic ER$^+$ breast cancer[22–25] (**Figure 3A**), and dissimilar to *TP53*, which is more frequently mutated in TNBC than either primary or metastatic ER$^+$ breast cancer (**Figure 3B**). We also assessed the landscape of mutations in *ATM* and *CHEK2*, the

two cell cycle checkpoint kinase genes most frequently mutated in ER+ breast cancer, between primary and metastatic samples. The overall mutational profile was comparable between primary tumors and metastases for both genes, with roughly 30% of mutations being deleterious (frameshift or nonsense) and the majority being missense (**Figure 3F-G**). Furthermore, we observed no detectable differences in mutation clusters in any specific protein domains. Overall, these data suggest a role for *CHEK2* mutation in metastatic ER+ breast cancer.

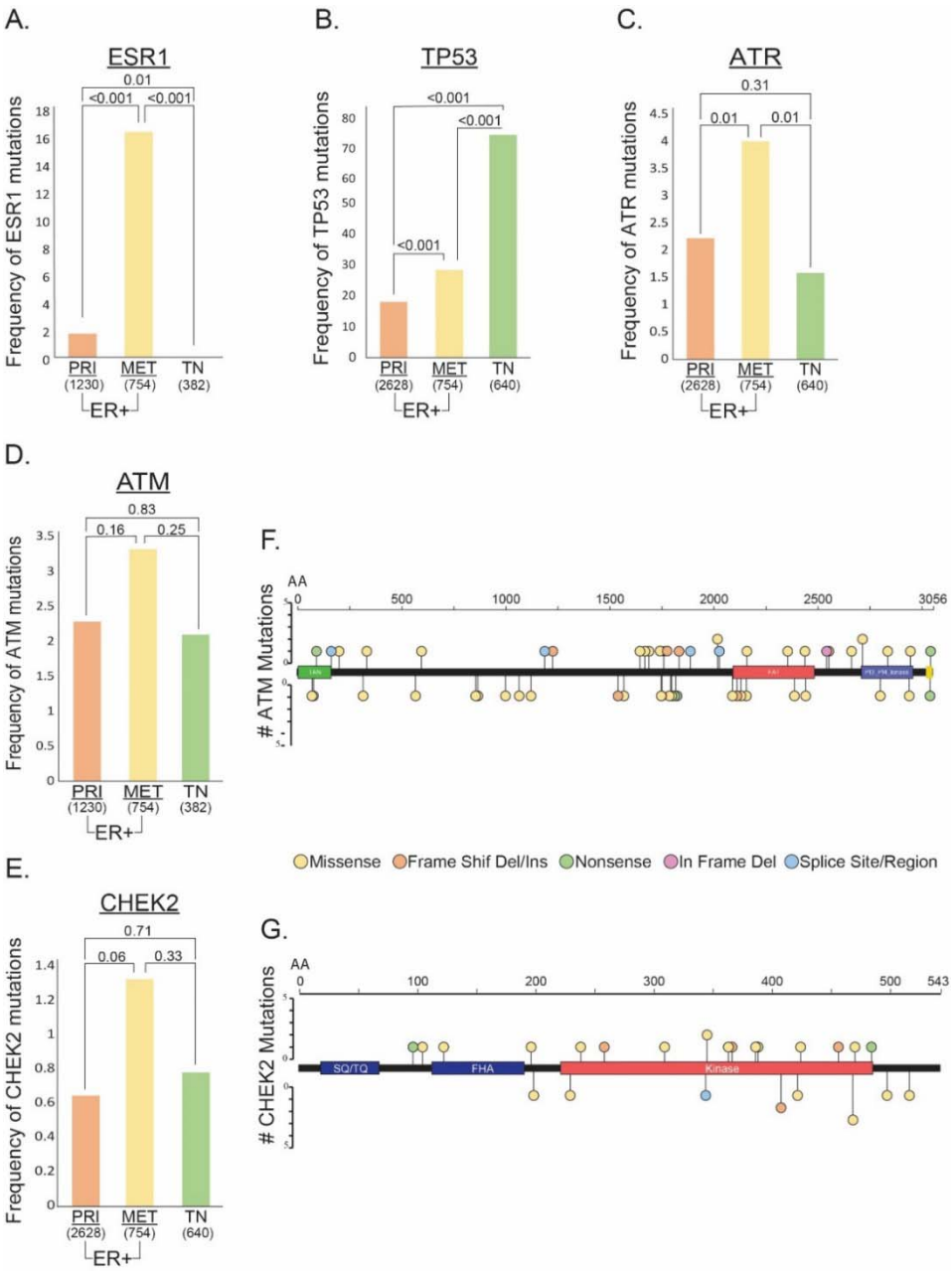

Figure 3. Mutational frequency of cell cycle checkpoint kinase genes based on tumor type (primary or metastatic). (A – E) Bar graphs representing frequency of *ESR1, TP53, ATR, ATM*, and *CHEK2* mutations in ER$^+$/HER2$^-$ primary versus metastatic and in TNBC. TNBC column is composed of both primary and metastatic samples. (F-G) Lolliplots of *ATM* and *CHEK2* mutations categorized by amino acid location and mutation type. Mutations found in primary samples are represented below the gene domain depiction while mutations in metastatic samples are represented above it.

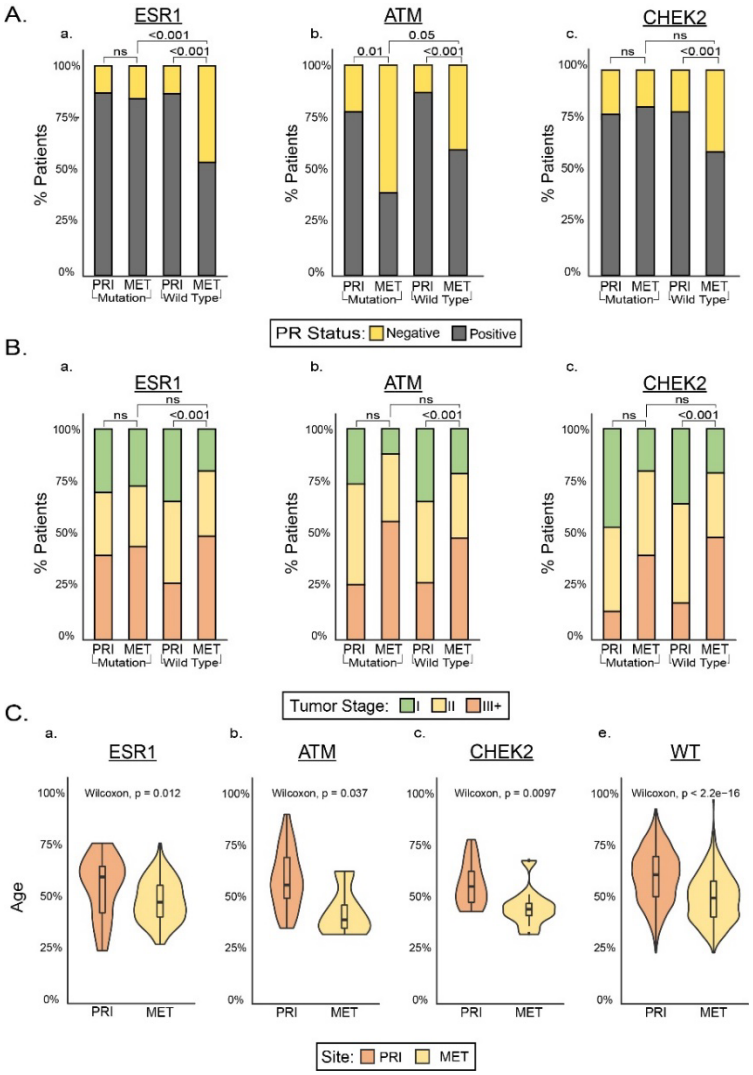

Figure 4. Comparison of primary versus metastatic samples based on PR status, tumor stage, and age at diagnosis in ER$^+$/HER2- disease. (A&B) Stacked columns graphs representing PR status (A) and tumor stage (B) at diagnosis of primary vs metastatic ER$^+$ breast cancer patients with mutations in any of the specific genes. Frequencies are compared for statistical significance to wildtype tumors lacking mutations in any of these genes, using Fisher's Exact test. (C) Violin plots representing age at diagnosis of primary vs metastatic ER$^+$ breast cancer patients whose tumors either had mutations in *ATM*, *CHEK2* or *ESR1* or were WT.

***CHEK2* mutations associate with higher PR positivity and younger age at diagnosis in metastatic ER$^+$ breast cancer.** We next tested whether *ATM* or *CHEK2* mutations associated with known prognostic factors in either primary or metastatic ER$^+$ breast cancer

samples. We found that *CHEK2* mutations had an association pattern that was comparable to that of *ESR1* mutations for all tumor characteristics assessed. Mutations in *CHEK2*, like mutations in *ESR1*, associated with significantly higher PR positivity in metastatic ER+ breast cancer (**Figure 4A**), supporting a role for these genes in regulating oncogenic ER signaling. We also observed no differences in tumor stage at diagnosis in primary or metastatic ER+ tumors with mutations in any of the genes analyzed, although wildtype tumors presented with significantly higher stage at diagnosis if the cancer was metastatic (**Figure 4B**). Also, *CHEK2*, but not *ATM*, mutations associate with a significantly younger age at diagnosis of metastatic ER+ breast cancer patients (**Figure 4C**), similar to *ESR1*. These differences were confirmed within MSKCC, the largest dataset in our meta-dataset that had both primary and metastatic samples (**Figure S3**).

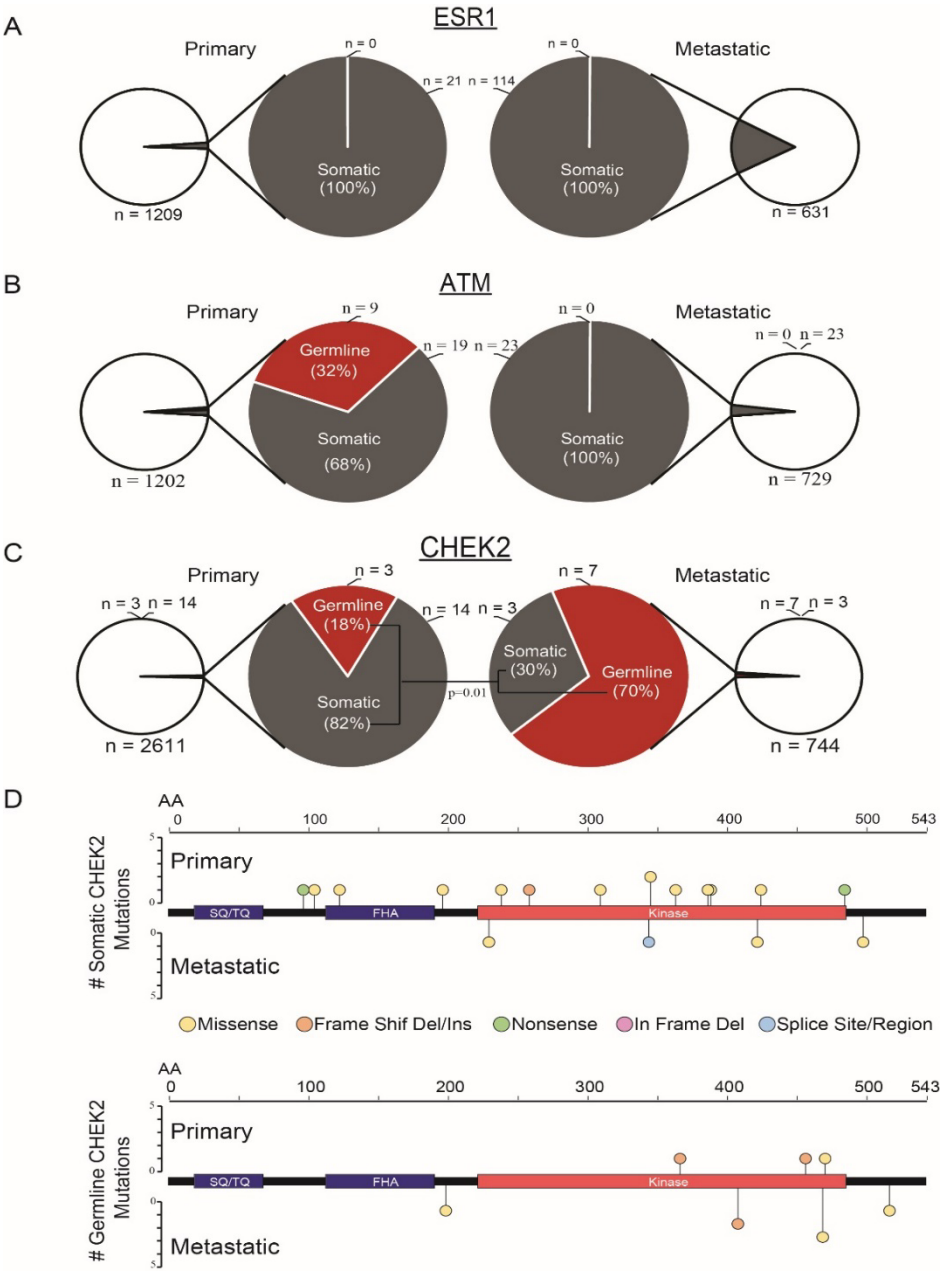

Figure 5. Percentage of germline vs somatic mutations in *ATM* and *CHEK2*. (A-C) Pie charts representing proportion of mutations in each specific gene, *ESR1* (A), *ATM* (B) and *CHEK2* (C) in ER+ primary and metastatic samples, with an expanded pie of the proportion of germline vs somatic mutations for each gene. (D) Lolliplots of CHEK2 germline and somatic mutations in primary vs metastatic ER+ breast cancer samples. Fisher's Exact test determined p-values.

This younger age at diagnosis could be primarily driven by germline, rather than somatic *CHEK2* mutations. Therefore, we parsed our meta-dataset to separate out germline and somatic mutations to assess their individual associations with these known tumor characteristics. As expected, we observed no germline *ESR1* mutations (**Figure 5A**). Interestingly, we found germline *ATM* mutations only in primary ER+ breast cancer samples (**Figure 5B**), while we found enrichment for germline *CHEK2* mutations in metastatic ER+ breast cancer (**Figure 5C**, p=0.01). We compared the landscape of germline *CHEK2* mutations to somatic ones and found a similar number of missense vs deleterious (nonsense, frameshift or splice site) mutations in both groups (**Figure 5D**). However, we found increased incidence of deemed pathogenic mutations in the germline vs somatic called variants, likely due to differences in call filtering (**Figure 5D**). These data suggest that *CHEK2* germline mutations are more likely to induce metastatic ER+ breast cancer at a younger age, while germline mutations in *ATM* associate with more benign primary ER+ breast cancer incidence.

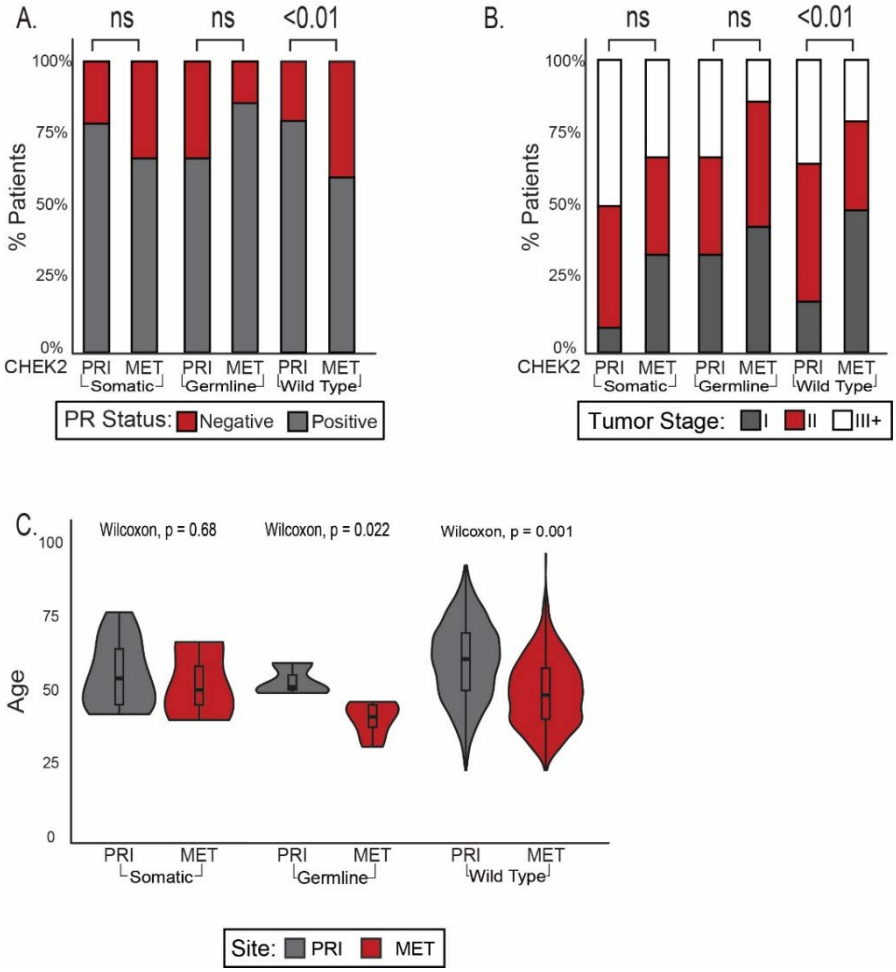

Figure 6. Association of germline vs somatic mutations in *CHEK2* with known prognostic tumor characteristics. Stacked columns graphs representing PR status (A) and tumor stage (B) at diagnosis of primary vs metastatic ER+ breast cancer patients with germline vs somatic mutations in *CHEK2*. Frequencies are compared for statistical significance to wildtype tumors lacking mutations in any of these genes, using Fisher's Exact test. (C) Violin plots representing age at diagnosis of primary vs metastatic ER+ breast cancer patients whose tumors either had germline or somatic mutations in *CHEK2* or were WT.

CHEK2 germline mutations drive associations with higher PR positivity and younger age at diagnosis in metastatic ER+ breast cancer

To identify individual contributions of germline and somatic *CHEK2* mutations to the various tumor characteristics analyzed, we assessed whether missense and deleterious somatic mutations in *CHEK2* compared to germline mutations in terms of PR positivity, tumor stage and age at diagnosis in primary and metastatic ER+ breast cancer. We found that metastatic samples with either germline or somatic mutations in *CHEK2* did not increase PR negativity, unlike *CHEK2* wildtype metastatic samples (**Figure 6A**).

Similarly, both germline and somatic mutations in *CHEK2* associated with high tumor stage irrespective of metastatic status, unlike wildtype tumors, which had lower tumor stage at diagnosis in primary samples relative to metastatic ones (**Figure 6B**). Finally, we found that the younger age at diagnosis for metastatic ER+ breast cancer patients was driven by germline, rather than somatic, mutations in *CHEK2* (**Figure 6C**). These differences remain statistically significant in a within-dataset comparison of MSKCC patient data (**Figure S4**).

Deleterious mutations in CHEK2 associate with early endocrine treatment resistance

We next tested whether mutations in *CHEK2* associate with worse overall survival in the MSKCC dataset. We did not have sufficient numbers of mutated tumors in the primary setting, so we restricted our analysis to metastatic ER+ breast cancer patients. While we found no significant association between mutations in *CHEK2* and disease-free or overall survival (**Figure S5**), we found significant association with deleterious *CHEK2* mutations and worse progression-free survival on endocrine treatment in metastatic ER+ breast cancer patients (**Figure 7A**). Specifically, we found a splice site mutation in *CHEK2* as associating significantly with progression on endocrine treatment (**Figure 7A**). No *ATR* mutation associated with progression free survival. This pattern was repeated when progression-free survival on first endocrine treatment was considered, with a trend towards decrease in time to progression for patients whose cancer harbored a deleterious *CHEK2* mutation, although sample sizes were low (**Figure 7B**).

To analyze this further, we assessed the number of patients whose cancer harbored either deleterious *ATM* or *CHEK2* mutations, missense *ATM* or *CHEK2* mutations or was wildtype for *ATM* and *CHEK2* and who progressed within one year of starting their first endocrine treatment. We included patients whose cancer had a mutation in either *ATR* or *CHEK1* as well to serve as controls in the analysis. We found that mutations in *CHEK2/ATM* associated with more rapid progression beginning with the very first endocrine treatment offered (**Figure 7C**), while mutations in *ATR/CHEK1* associated with

more gradual progression, similar to wildtype tumors. Further analysis identified that on average patients whose cancer was *ATM* or *CHEK2* mutant (irrespective of missense or deleterious) progressed within 6 months of each subsequent endocrine treatment as well, a significantly shorter time to progression than observed in *ATR/CHEK1* mutant or wildtype patients (**Figure 7D**). Overall, these data provide further evidence of a unique and robust association between ATM/Chk2 inactivation, whether germline or somatic, and endocrine therapy response.

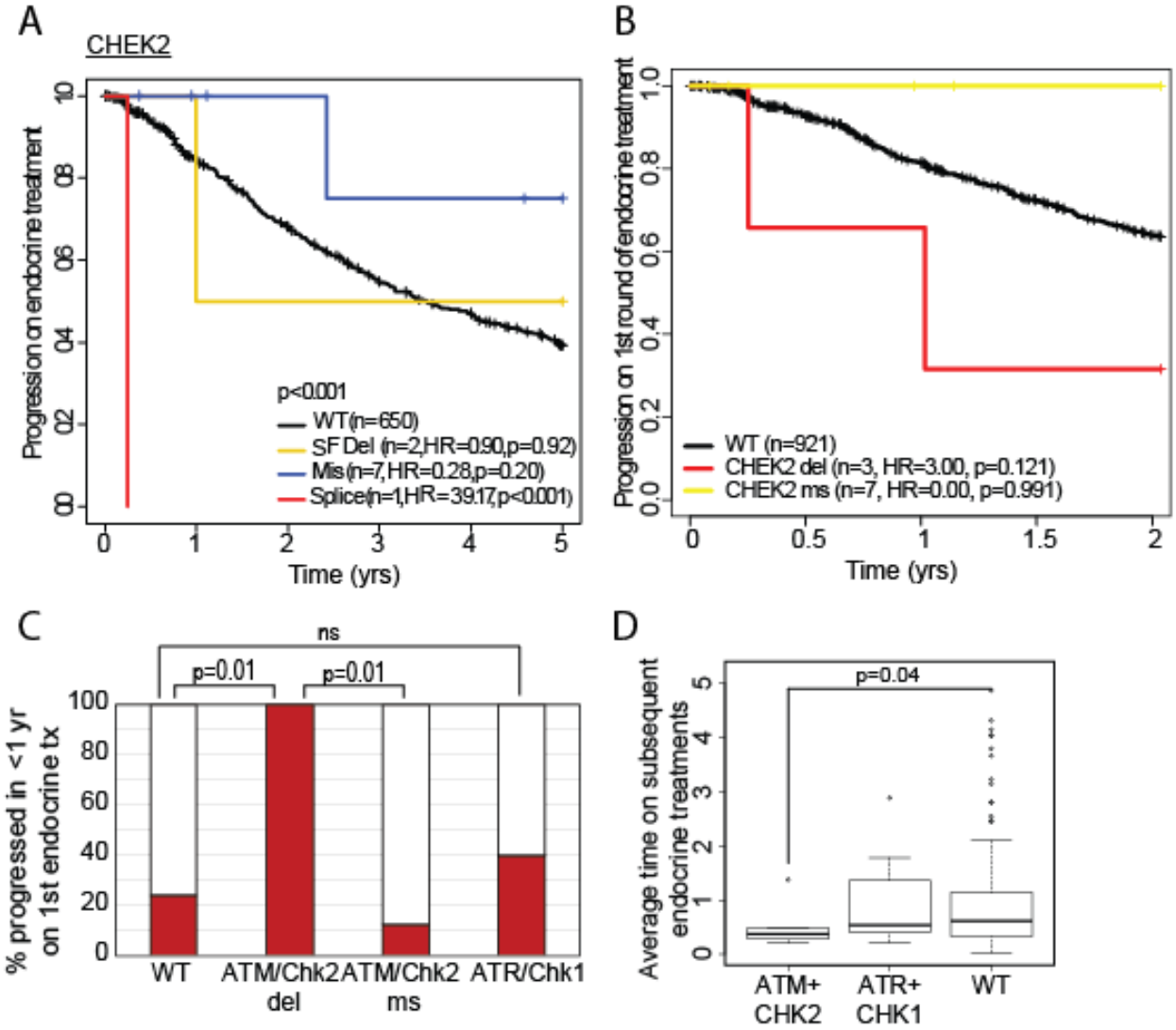

Figure 7. Association of cell cycle checkpoint kinase gene mutations with patient outcome. (A-B) Kaplan-Meier survival curves of progression-free survival on any endocrine treatment (A) and first endocrine treatment (B) of metastatic ER+ breast cancer patients with deleterious or missense mutations in *CHEK2*. Log rank test determined p-values. Associated data in Figure S6. (C) Column graph depicting proportion of metastatic ER+ breast cancer patients who progressed within 1 year of beginning their first endocrine treatment categorized based on the presence of any mutations in ATM/CHEK2 or ATR/CHEK1 as specified in X-axis labels. Pearson's Chi-Squared test determined p-value. (D) Box plot demonstrating average time before progression on every subsequent endocrine

treatment in each specified group of metastatic ER+ breast cancer patients. Two-tailed Student's T-test determined p-values.

Discussion

A role for cell cycle checkpoint kinases as tumor suppressors in many cancers, including breast is well-established[1]. Moreover, a distinction between ATM/CHK2 and ATR/CHK1 signaling in terms of cell cycle regulation has been well documented[26–28]. Generally, ATM/Chk2 appears integral to single strand break repair and G1/S cell cycle regulation[14,27,29], while ATR/Chk1 is activated by double strand break repair pathways and regulates G2/M[19,21]. Our systematic analysis of these two cell cycle signaling nodes across ER^+ and TNBC identifies a dichotomy where ATM/Chk2 associates with ER^+ breast cancer but ATR/Chk1 does not. These data suggest a division in terms of DNA repair between these two cancer types, which is reflected in the differential impact of these two cell cycle signaling nodes in ER^+ vs TNBC. A fundamental recharacterization of all breast cancer based on cell cycle signaling nodes, and DNA repair proficiencies might prove therapeutically important, as these cell cycle signaling nodes can translate to specific CDK dependencies, which can induce sensitivity to specific CDK inhibitors[30].

Germline variants in *ATM* and *CHEK2* are known to predispose women to ER^+ breast cancer. We further demonstrate that germline variants in these genes associate with younger age at diagnosis of metastatic ER^+ breast cancer, and higher tumor stage at diagnosis even in terms of primary ER^+ breast cancer, both poor prognosticators. Interestingly, we find that *CHEK2* variants associate with increased PR positivity in the metastatic ER^+ breast cancer setting. This is a curious finding, since PR positivity generally associates with better outcome. These data suggest more complex mechanistic underpinnings between Chk2 and ER signaling that require experimental investigation.

The role of somatic inactivation of *ATM* and *CHEK2* in ER^+ breast cancer outcome has remained conflicted, with few reported publications. We recently identified a role for lack of activation of ATM/Chk2 in endocrine therapy resistance, induced by somatic loss of DNA repair proteins[14,31]. Results described here suggest that somatic mutations in *CHEK2* may also play a role in defining tumor characteristics of primary ER^+ breast cancer. A specific and causal role for such mutations in treatment response remains to be tested. Importantly, both ATM and CHEK2 mutations, whether somatic or germline associate significantly with increased progression on endocrine treatments, suggesting strongly that treatment strategies for these patients should be reconsidered.

Overall, the systematic study of ATM and ATR signaling node mutation described here is the first to parse germline and somatic events in the context of primary and metastatic ER^+ breast cancer, as well as TNBC. The results of this study suggest a broader role for ATM/Chk2 in ER^+ breast cancer, and perhaps, a similarly important role for ATR in TNBC. There is potential for the development of prognostic and predictive biomarkers based on the status of these cell cycle checkpoint kinases, as well as avenues for development of CDK inhibitors or cell cycle checkpoint activators that can be matched to each tumor's cell cycle dependencies.

References

1. Smith, J., Tho, L. M., Xu, N. & Gillespie, D. A. The ATM-Chk2 and ATR-Chk1 pathways in DNA damage signaling and cancer. *Adv. Cancer Res.* **108**, 73–112 (2010).
2. Weischer, M. *et al.* CHEK2*1100delC heterozygosity in women with breast cancer associated with early death, breast cancer-specific death, and increased risk of a second breast cancer. *J. Clin. Oncol.* **30**, 4308–4316 (2012).
3. de Bock, G. H. *et al.* Association between the CHEK2*1100delC germ line mutation and estrogen receptor status. *Int. J. Gynecol. Cancer* **16 Suppl 2**, 552–555 (2006).
4. Nevanlinna, H. & Bartek, J. The *CHEK2* gene and inherited breast cancer susceptibility. *Oncogene* **25**, 5912–5919 (2006).
5. Southey, M. C. *et al.* PALB2, CHEK2 and ATM rare variants and cancer risk: data from COGS. *J Med Genet* **53**, 800–811 (2016).
6. Decker, B. *et al.* Rare, protein-truncating variants in ATM, CHEK2 and PALB2, but not XRCC2, are associated with increased breast cancer risks. *J. Med. Genet.* (2017) doi:10.1136/jmedgenet-2017-104588.
7. Feng, X. *et al.* Low Ki67/high ATM protein expression in malignant tumors predicts favorable prognosis in a retrospective study of early stage hormone receptor positive breast cancer. *Oncotarget* **7**, 85798–85812 (2016).
8. Abdel-Fatah, T. M. A. *et al.* Clinicopathological Significance of ATM-Chk2 Expression in Sporadic Breast Cancers: a Comprehensive Analysis in Large Cohorts. *Neoplasia* **16**, 982–991 (2014).
9. Cybulski, C. *et al.* Estrogen receptor status in CHEK2-positive breast cancers: implications for chemoprevention. *Clinical Genetics* **75**, 72–78 (2009).
10. Mohelnikova-Duchonova, B. *et al.* CHEK2 gene alterations in the forkhead-associated domain, 1100delC and del5395 do not modify the risk of sporadic pancreatic cancer. *Cancer Epidemiology* **34**, 656–658 (2010).
11. Vahteristo, P. *et al.* A CHEK2 Genetic Variant Contributing to a Substantial Fraction of Familial Breast Cancer. *Am J Hum Genet* **71**, 432–438 (2002).
12. Schmidt, M. K. *et al.* Age- and Tumor Subtype-Specific Breast Cancer Risk Estimates for CHEK2*1100delC Carriers. *J Clin Oncol* **34**, 2750–2760 (2016).
13. Di Benedetto, A. *et al.* Prognostic relevance of DNA damage and repair biomarkers in elderly patients with hormone-receptor-positive breast cancer treated with neoadjuvant hormone therapy: evidence from the real-world setting. *Ther Adv Med Oncol* **11**, 1758835919853192 (2019).
14. Haricharan, S. *et al.* Loss of MutL Disrupts Chk2-dependent Cell Cycle Control Through CDK4/6 to Promote Intrinsic Endocrine Therapy Resistance in Primary Breast Cancer. *Cancer Discov* (2017) doi:10.1158/2159-8290.CD-16-1179.
15. Xie, Y. *et al.* Mutation screening of 10 cancer susceptibility genes in unselected breast cancer patients. *Clin Genet* **93**, 41–51 (2018).
16. Staalesen, V. *et al.* Alternative splicing and mutation status of CHEK2 in stage III breast cancer. *Oncogene* **23**, 8535–8544 (2004).
17. Lin, W.-Y. *et al.* Associations of ATR and CHEK1 single nucleotide polymorphisms with breast cancer. *PLoS One* **8**, e68578 (2013).
18. Heikkinen, K., Mansikka, V., Karppinen, S.-M., Rapakko, K. & Winqvist, R. Mutation analysis of the ATR gene in breast and ovarian cancer families. *Breast Cancer Res* **7**, R495-501 (2005).

19. Abdel-Fatah, T. M. A. *et al.* Untangling the ATR-CHEK1 network for prognostication, prediction and therapeutic target validation in breast cancer. *Mol Oncol* **9**, 569–585 (2015).
20. Encinas, G. *et al.* Somatic mutations in early onset luminal breast cancer. *Oncotarget* **9**, 22460–22479 (2018).
21. Tu, X. *et al.* ATR Inhibition Is a Promising Radiosensitizing Strategy for Triple-Negative Breast Cancer. *Mol Cancer Ther* **17**, 2462–2472 (2018).
22. Dustin, D., Gu, G. & Fuqua, S. A. W. ESR1 mutations in breast cancer. *Cancer* **125**, 3714–3728 (2019).
23. Li, S. *et al.* Endocrine-Therapy-Resistant ESR1 Variants Revealed by Genomic Characterization of Breast-Cancer-Derived Xenografts. *Cell Rep* **4**, (2013).
24. Lei, J. T. *et al.* Functional Annotation of ESR1 Gene Fusions in Estrogen Receptor-Positive Breast Cancer. *Cell Rep* **24**, 1434-1444.e7 (2018).
25. Jeselsohn, R., Buchwalter, G., De Angelis, C., Brown, M. & Schiff, R. ESR1 mutations—a mechanism for acquired endocrine resistance in breast cancer. *Nat Rev Clin Oncol* **12**, 573–583 (2015).
26. Yan, T. *et al.* CHK1 and CHK2 are differentially involved in mismatch repair–mediated 6-thioguanine-induced cell cycle checkpoint responses. *Mol Cancer Ther* **3**, 1147–1157 (2004).
27. Lavin, M. F. & Kozlov, S. ATM Activation and DNA Damage Response. *Cell Cycle* **6**, 931–942 (2007).
28. Pedram, A., Razandi, M., Evinger, A. J., Lee, E. & Levin, E. R. Estrogen Inhibits ATR Signaling to Cell Cycle Checkpoints and DNA Repair. *Molecular Biology of the Cell* **20**, 3374–3389 (2009).
29. Adamowicz, M. Breaking up with ATM. *J Immunol Sci* **2**, 26–31 (2018).
30. Anurag, M., Haricharan, S. & Ellis, M. J. CDK4/6 Inhibitor Biomarker Research: Are We Barking Up the Wrong Tree? *Clin. Cancer Res.* **26**, 3–5 (2020).
31. Anurag, M. *et al.* Comprehensive Profiling of DNA Repair Defects in Breast Cancer Identifies a Novel Class of Endocrine Therapy Resistance Drivers. *Clin. Cancer Res.* **24**, 4887–4899 (2018).