Research Article

Genetic interactions between INPP4B and RAD50 is prognostic of breast cancer survival

Xiao Chen1, Rutaganda Theobard1, Jianying Zhang2 and Xiaofeng Dai3,4

1School of Biotechnology, Jiangnan University, Wuxi, China; 2Henan Institute of Medical and Pharmaceutical Sciences and Henan Key Laboratory of Tumor Epidemiology, Zhengzhou University, Zhengzhou 450001, China; 3Hospital of Xi’an Jiaotong University, Xi’an, 710061, China; 4Wuxi School of Medicine, Jiangnan University, Wuxi, China

Correspondence: Xiaofeng Dai (1281423490@qq.com)

RAD50 is commonly depleted in basal-like breast cancer with concomitant absence of INPP4B and several tumor suppressors such as BRCA1 and TP53. Our previous study revealed that INPP4B and RAD50 interact and such an interaction is associated with breast cancer survival at the transcriptional, translational and genomic levels. In the present study, we explored single nucleotide polymorphisms (SNPs) of these two genes that have synergistic effects on breast cancer survival to decipher mechanisms driving their interactions at the genetic level. The Cox’s proportional hazards model was used to test whether SNPs of these two genes are interactively associated with breast cancer survival, following expression quantitative trait loci (eQTL) analysis and functional investigations. Our study revealed two disease-associating blocks, each encompassing five and two non-linkage disequilibrium linked SNPs of INPP4B and RAD50, respectively. Concomitant presence of any rare homozygote from each disease-associating block is synergistically prognostic of poor breast cancer survival. Such synergy is mediated via bypassing pathways controlling cell proliferation and DNA damage repair, which are represented by INPP4B and RAD50. Our study provided genetic evidence of interactions between INPP4B and RAD50, and deepened our understandings on the orchestrated genetic machinery governing tumor progression.

Introduction

As the second leading cause of deaths worldwide, great attention has been paid in order to reveal the underlying factors that drive the genesis of cancer [1]. Evidences showed that various factors are linked with growth and development of different types of cancer which include mutation [2], radiation [3], inflammatory bowel disease [4], viral [5,6] and bacterial infection [4,7]. Breast cancer is the leading cause of death among women with the annual mortality rate being estimated over 570000 worldwide [8,9]. Most breast cancers are sporadic cancers caused by accumulation of acquired yet uncorrected genetic alterations in somatic genes, while other cases are associated with inherited genetic changes in disease predisposing genes [10]. As one of the most common types of genetic variations in human genome, single nucleotide polymorphisms (SNPs) in genes involved in DNA damage repair, metabolism, carcinogen metabolism, cell-cycle control, apoptosis and immunity are likely to be associated with genetic susceptibility to various cancer types including breast cancer [11,12]. So far, common SNPs can account for 18% of breast cancer familial risk among women [13].

SNPs can be located in either coding or non-coding regions. SNPs located in the coding regions are assumed to be able to affect protein production and functionalities, and thus more likely to cause phenotypic changes [14]. SNPs located in the non-coding region are less toxic and more easily to be inherited. However, recent advances suggest that SNPs in the non-coding regions may also play a functional role including, e.g. RNA splicing, genome imprinting, long non-coding RNAs binding etc [11].
Figure 1. Schematic diagram of the analytic flow in the present study
The purple oval and blue rhombi represent the SNPs in TCGA and analytical methods, respectively. Rectangle represents obtained results at each stage of analysis, where green represents ‘genes’, yellow represents ‘SNPs’, bronze represents ‘block’. Abbreviation: TCGA, The Cancer Genome Atlas.

RAD50 is crucial to maintain genomic integrity and prevent tumorigenesis [15]. It is a key protein involved in DNA double-strand breaks repair and frequently deleted in basal-like breast tumors [16]. RAD50 is a breast cancer susceptibility gene associated with genomic instability [17]. Loss of RAD50 often co-occurs with deletion of one or more tumor suppressor genes BRCA1, TP53, PTEN, RB1 and INPP4B [18]. INPP4B is involved in the control of cell proliferation, cell metabolism and apoptosis [19]. INPP4B resides in the PI3K/Pten/mTOR pathway which is a complex network that controls cell proliferation and survival and is deregulated in over 70% of breast cancers [20]. Moreover, INPP4B deficiency affects BRCA1, ATM and ATR protein stability, which may lead to the deficit of DNA repair machinery and, ultimately, uncontrolled cancer growth [21].

We have previously demonstrated that INPP4B and RAD50 collectively affect breast cancer survival at the transcriptional and translational levels [22]. To further identify the synergies between INPP4B and RAD50 on clinical consequences at the genetic level, we are motivated to identify the relevant disease-associating SNPs that affect the expression of each gene and are collectively prognostic of the clinical outcome of breast cancer patients.

Materials and methods
The workflow of the methods is presented in Figure 1.

Datasets
We retrieved 184485 SNPs of INPP4B and 19974 SNPs of RAD50 from the dbSNP NCBI database [23]. Among these SNPs, 269 SNPs of INPP4B and 15 SNPs of RAD50 were mapped to the Affymetrix SNP6.0 Array which was used in The Cancer Genome Atlas (TCGA). Information of the 284 SNPs covering 501 samples was retrieved from TCGA (http://cancergenome.nih.gov) and used for the downstream analysis. The gene expression data were retrieved from TCGA biportal (http://www.cbioportal.org/), which contained 20440 genes and 1102 samples.

The GSE24450 dataset containing gene expression and clinical information of 183 breast tumors from the Helsinki University Central Hospital was retrieved from GEO with 10-year follow up information included in this dataset [24,25].
TCGA cohort and GEO cohort were merged followed by log2 transformation and batch correction using the ‘ComBat’ function in ‘sva’ package (version 3.30.1) in R [26]. These merged data were used in expression Quantitative Trait Loci (eQTL) analysis and pair-wise expression survival analysis.

**Pair-wise SNP survival analysis**
We conducted breast cancer overall survival (OS) analysis on interactions between SNPs of INPP4B and RAD50 using the Cox’s proportional hazard model. The recessive model was used in the pair-wise SNP association analysis, where the heterozygote was combined with the common homozygote assuming that the disease-associating phenotype is caused by the concomitant presence of both rare alleles in both interacting SNPs. The 10-year breast cancer OS survival analysis utilizing the ‘survival’ package (version 2.44.1.1) [27]. An SNP pair was considered interactive if the P-value of the Cox repression model was <0.05, the P-value of the interaction term was <0.05, and the number of iterations showing the model convergence rate was <10.

**Block-wise SNP survival analysis**
Haplotype block refers to the inheritance of a cluster of SNPs [28]. LDlink (https://analysistools.nci.nih.gov/LDlink/) was used to calculate pair-wise linkage disequilibrium (LD) among SNPs associated with the same gene. SNPs with r² greater than 0.8 were considered linked to the same haplotype. Non-LD linked SNPs were considered independent. We randomly selected one SNP among its LD-linked peers, and grouped independent SNPs of INPP4B and RAD50 into distinct disease-associating blocks, respectively.

Block-wise survival analysis was performed between the disease-associating blocks of INPP4B and RAD50, respectively, assuming that the presence of the rare allele of any SNP within the block contributes equally to the synergistic clinical association. PredictSNP2 [29], a unified platform for predicting SNP effect, was employed to analyze the functionalities of non-LD linked SNPs. SNP2TFBS tool was used to check whether an SNP affects transcription factor binding site affinity [30].

**eQTL analysis**
To identify genes whose expressions are significantly affected by the identified SNPs in each disease-associating block or the disease-associating block as a whole, we conducted the eQTL analysis. In single SNP eQTL analysis, gene expression was modeled against the allele status of an SNP using logistic regression. SNPs with a P-value of the linear model <0.01 were considered eQTLs of a gene. SNPs significantly affecting patient OS and expression of the gene it resides in were defined as disease-associating SNPs. In block-wise eQTL analysis, the allele statuses were combined and binarized such that concomitant presence of all rare alleles in a disease-associating block was considered as ‘1’ and block alleles containing any common allele was considered as ‘0’. Top genes filtered using P<0.01 and the coefficient β > 0.3 from the linear regression were selected as being significantly affected by the disease-associating block at the transcriptional level.

**Pair-wise expression survival analysis**
We conducted breast cancer OS analysis on interactions between the expressions of a gene identified in the eQTL analysis to identify the quantitative association of a gene and its eQTLs using the Cox’s proportional hazard model. Gene expression of a gene was binarized by its median level, and the 10-year breast cancer OS survival analysis was conducted using the ‘survival’ package [27]. A gene pair was considered interactive if the P-values of the Cox repression model and the interaction term were both 0.05.

In addition, the expression of one gene was stratified by that of another to assess the influence of one gene on another or the interactions between two genes at the transcriptional level. ANOVA test was used to assess the statistical significance with P<0.05 being the threshold.

**Functional analysis**
In order to investigate the functional consequences introduced by SNPs, pathway enrichment analysis was performed using genes affected by SNPs with statistical significance. Gene Ontology (GO) term, KEGG pathway and Reactome pathway were enriched using the web interface ‘Metascape’ [31]. Genes identified from the enriched pathways were collected for gene regulatory network construction using GeneMANIA (http://www.genemania.org) [32]. GeneMANIA uses the label propagation algorithm to predict gene–gene interactions at 7 levels (co-expression, co-localization,
Results and discussion
SNPs of INPP4B and RAD50 synergistically affect breast cancer survival

Multivariate Cox regression model was constructed to perform pair-wise interaction analysis using SNPs of INPP4B and RAD50 on breast cancer OS. The results revealed nine SNPs, five from INPP4B (rs1219269, rs17016021, rs2636683, rs336298, rs9996933) and four from RAD50 (rs3798134, rs3798135, rs2040704, rs2706347), having significant association with patient clinical outcome (Table 1).

Concomitant presence of rare homozygotes of SNPs from disease-associating blocks is associated with poor breast cancer OS

The four identified SNPs of RAD50 are linked to two haplotypes, i.e., the $r^2$ between rs2706347 and rs2040704 is 0.911, and that between rs3798135 and rs3798134 is 0.999 (Figure 2A). All SNPs of INPP4B are non-LD linked (Figure 2B).

Two disease-associating blocks were constructed where one SNP was randomly selected if multiple SNPs resided in one haplotype. That is, the INPP4B block includes rs336298, rs9996933, rs1219269, rs2636683, rs17016021, and the RAD50 block contains rs3798134 and rs2040704. The results of the block-wise OS analysis using recessive model indicated that concomitant presence of the rare homozygote of any SNPs from each disease-associating block is associated with significantly reduced breast cancer OS (Figure 2E). The presence of all common homozygotes in either INPP4B or RAD50 is sufficient to rescue patient clinical outcome.

On the other hand, either of the two disease-associating blocks drives significant differences on patient OS (Figure 2C,D), suggesting that it is the interaction between the two disease-associating blocks that differentiate breast cancer clinical outcome but not either one of the two blocks.

We performed the eQTL analysis followed by the pair-wise expression survival analysis, which revealed that concomitant presence of the rare allele in the disease-associating block of INPP4B was positively associated with low BCKDHB expression that is risky ($P=0.023$, HR = 0.81, Figure 3), and that of RAD50 was positively associated with RMND5A and PWP2 high expression which were risky ($RMND5A: P=0.0005$, $HR = 1.39$; $PWP2: P=0.029$, HR = 1.23, Figure 3). In addition, RMND5A or PWP2 overexpression was associated with breast cancer clinical outcome under BCKDHB low-expression, which were both risky ($RMND5A$ and $BCKDHB$: $P=0.0025$, $HR = 1.48$; $PWP2$ and $BCKDHB$: $P=0.03$, HR = 1.32, Figure 4), and such a prognostic value diminishes under BCKDHB high expression. Therefore, the joint prognostic value of the two disease-associating blocks was in agreement with those from the pair-wise joint expression between BCKDHB and RMND5A, BCKDHB and PWP2. Further, BCKDHB interacts with INPP4B, where low BCKDHB under low INPP4B expression was risky ($P=0.03$, HR = 0.75, Figure 3), high RMND5A or PWP2 was risky under high RAD50 expression ($RMND5A: P=0.001$, HR = 1.54; $PWP2: P=0.015$, HR = 1.37, Figure 3). On the other hand, low INPP4B and high RAD50 expression are risky ($P=0.00296$, HR = 3.15, Figure 4), and high INPP4B and low RAD50 convey unfavorable clinical outcome ($P=0.03$, HR = 1.6, Figure 4).

Table 1 SNPs significantly affecting breast cancer OS

| Gene  | SNP          | Position          | Alleles | MAF  | Consequence       |
|-------|--------------|-------------------|---------|------|-------------------|
| RAD50 | rs3798134    | chr5:132629487    | G>A     | 0.2564 | Intron variant    |
|       | rs3798135    | chr5:132629417    | C>T     | 0.2566 | Intron variant    |
|       | rs2040704    | chr5:132637485    | A>G     | 0.3297 | Intron variant    |
|       | rs2706347    | chr5:132569425    | G>T     | 0.3095 | Intron variant    |
| INPP4B| rs1219269    | chr4:142174118    | A>T     | 0.2726 | Intron variant    |
|       | rs17016021   | chr4:142373233    | A>T     | 0.0260 | Intron variant    |
|       | rs2636683    | chr4:142176930    | C>T     | 0.3758 | Intron variant    |
|       | rs336298     | chr4:142094199    | T>C     | 0.4002 | Intron variant    |
|       | rs9996933    | chr4:142087174    | T>C     | 0.2676 | Intron variant    |

*MAF* represents minor allele frequency.
Figure 2. Interactions between SNPs in INPP4B and RAD50

Heatmaps showing LD associations among SNPs of (A) RAD50 and (B) INPP4B. OS analysis of (C) interactions of disease-associating block of RAD50, (D) disease-associating block of INPP4B, and (E) disease-associating blocks of INPP4B and RAD50. In subgraph (E), green curve represents concomitant presence of the rare homozygote of SNPs in both disease-associating blocks of INPP4B and RAD50; pink curve represents concomitant presence of the common homozygote of SNPs in both disease-associating blocks of INPP4B and RAD50; purple curve and bronze curve each represents the presence of the rare homozygote of SNPs in the disease-associating blocks of INPP4B and RAD50, respectively. The x-axis indicates the follow-up time, and the vertical axis shows the cumulative OS of breast cancer patients.
Figure 3. Associations between each disease-associating block and the corresponding gene

(A) Correlation between RMND5A gene expression and allele status of the RAD50 disease-associating block. The prognostic value of RMND5A on breast cancer OS (B) alone, (C) under low RAD50 gene expression, (D) under high RAD50 gene expression. (E) Correlation between PWP2 gene expression and allele status of the RAD50 disease-associating block. The prognostic value of PWP2 on breast cancer OS (F) alone, (G) under low RAD50 gene expression, (H) under high RAD50 gene expression. (I) Correlation between BCKDHB gene expression and allele status of the INPP4B disease-associating block. The prognostic value of BCKDHB on breast cancer OS (J) alone, (K) under low INPP4B gene expression, (L) under high INPP4B gene expression.
Figure 4. Pair-wise gene interactions
(A) The prognostic value of INPP4B gene expression on breast cancer OS under high and low RAD50 expression. (B) The prognostic value of RAD50 gene expression on breast cancer OS under high and low INPP4B expression. (C) The prognostic value of PWP2 gene expression on breast cancer OS under high and low BCKDHB expression. (D) The prognostic value of RMND5A gene expression on breast cancer OS under high and low BCKDHB expression.
Gene function analysis of non-LD linked SNPs

We obtained 89 genes from the eQTL analysis, whose expression were significantly affected by the allele status of identified non-LD linked SNPs. GO and KEGG gene enrichment analysis showed that these genes were significantly enriched in ‘PI3K/AKT activation process’ (Figure 5A).

The regulatory network involving INPP4B and RAD50 showed that BCKDHB and INPP4B, as well as RMND5A and RAD50 have direct genetic interactions, PWP2 and RAD50 have indirect genetic interactions via ALDH1L1 and NAA40 (Figure 5B).

Discussion

Through pair-wise and block-wise interactive OS analyses on SNPs of INPP4B and RAD50, we identified two disease-associating blocks, each containing five SNPs (INPP4B) and two SNPs (RAD50), respectively, which synergistically affect breast cancer clinical outcome. Specifically, concomitant presence of the rare homozygotes of all SNPs within each block is associated with decreased breast cancer OS, while neither one of these blocks differentiates breast cancer clinical outcome with statistical significance. Both RAD50 and INPP4B are crucial to maintain genomic integrity and prevent tumorigenesis [7,12,13], and co-deletion of both genes commonly co-occurs in many types of cancers including breast cancer [10]. Our results further consolidate our understandings on cells and carcinogenesis, i.e. cells are robust systems having multiple ways to suppress tumorigenesis, and carcinogenesis is likely to occur when all tumor suppressive systems are dysfunctional.

The two disease-associating SNP blocks were each associated with the expression of genes that interacted with INPP4B and RAD50, respectively, with consistent directions regarding their prognostic values. For instance, concomitant presence of rare alleles in the disease-associating block of INPP4B was positively associated low BCKDHB expression, and the rare status of the RAD50 disease-associating block was positively correlated with high RMND5A or PWP2 expression. Importantly, concomitant presence of rare statuses of INPP4B and RAD50 was risky, which was consistent with joint low BCKDHB and high RMND5A or PWP2 expression (risky). This makes it possible to associate interactions at the genetic level with interactions at the gene expression level regarding clinical outcomes. Meanwhile, BCKDHB interacted with INPP4B, RMND5A and PWP2 each interacted with RAD50, and INPP4B interacted with RAD50 regarding clinical associations, and these clinical associations shared consistent directions. That is, low BCKDHB and low INPP4B is risky, high RMND5A and high RAD50 is risky, low BCKDHB and high RMND5A is risky, low INPP4B and high RAD50, where the clinical association of each of these genes is transferable among these pair-wise joint clinical associations. Provided the strong correlation between the INPP4B disease-associating block and BCKDHB, and RAD50 disease-associating block and RMND5A, it is highly likely that BCKDHB and RMND5A reflected and/or mediated interactions between INPP4B and RAD50 at the gene expression level which also applies for pair BCKDHB and PWP2. Indeed, we found from GeneMania that BCKDHB had genetic interactions with INPP4B and RAD50, respectively, which were previously reported by [32], and RMND5A and PWP2 had known genetic interactions with RAD50, which were in agreement with what we observed in the present study and supported our findings. Interestingly, BCKDHB was also genetically associated with TGFβ1 that plays critical roles in TGFβ signaling and responsible for cancer stemness; and PWP2 genetically interacted with RAD50 via ALDH1L1 that is associated with neural stem cells in vivo [33], suggesting a trilateral connection among uncontrolled cell proliferation (as represented by INPP4B and PI3K/Pten pathway), DNA damage repair (as represented here by RAD50), and cancer stemness (as featured by TGFβ-mediated signaling and ALDH1L1).

Among the three genes mediating interactions between INPP4B and RAD50, only RMND5A has known evidence which is a tumor vasculature-associated gene with transmembrane or secreted protein products identified through expression profiling of ovarian cancer vascular cells [34]. BCKDHB encodes the E1 β subunit of branched-chain keto acid dehydrogenase and is a multienzyme complex associated with the inner membrane of mitochondria [35]. PWP2 is involved in humoral immunity [36]. Their relevance with cancer initiation and progression is worthy to be investigated. INPP4B and RAD50 were also genetically connected via TRIM47 and TRIM65, and TRIM family proteins are known players in innate immunity, and have recognized roles in carcinogenesis [37]. These together suggest the involvement of immune response, metabolism and angiogenesis in mediating synergies between INPP4B and RAD50.

We further identified disease-associating SNPs in both disease-associating blocks. That is, both rs2040740 residing in the intron of RAD50 and rs17016021 from the intron of INPP4B are deleterious; and the rare allele of rs2040740 is significantly associated with reduced RAD50 expression. The minor allele frequency (MAF) of the RAD50 disease-associating SNP (rs2040704) is the highest among all SNPs in the RAD50 disease-associating block, which is ~0.33 (Table 1), suggesting its prevalence. Actually all SNPs in the RAD50 disease-associating block have a
Figure 5. Pathway enrichment and network construction using genes quantitatively associated with INPP4B and RAD50 disease-associating blocks
(A) GO and KEGG enrichment analysis. (B) Network constructed using GeneMania where only genetic interactions were preserved.
relatively high prevalence (i.e. ranging from 0.25 to 0.33, Table 1), indicating that the pathway represented by RAD50 is more likely to be dysfunctional. However, the MAF of the INPP4B disease-associating SNP (rs17016021) is rather rare, i.e. 0.026 (Table 1), suggesting that dysfunction of the pathway represented by INPP4B is less likely to occur whose mutation functions as a pivotal switch toward enhanced cancer cell proliferation potential.

Importantly, PCR assays testing the polymorphisms of both SNPs in clinical materials that are associated with differential clinical outcomes are necessary before translating our discovery into clinics, and this would be our next endeavor to make.

As aforementioned, we hypothesize that synergies created from the identified disease-associating blocks of INPP4B and RAD50 are related to cell progression and mutation accumulation that ultimately affect patient clinical outcome from our eQTL and pathway enrichment analyses. Such synergies may also involve altered immune response and cancer stemness. However, the exact underlying mechanism still awaits to be explored and experimentally validated.

**Conclusion**

We identified two disease-associating blocks of INPP4B and RAD50, each containing five and two SNPs, respectively. Concomitant presence of any rare homozygote from each of the two disease-associating blocks is associated with decreased breast cancer survival, through disenabling breast cancer cell proliferation and DNA repair signaling pathways as represented by INPP4B and RAD50. Our study provides genetic evidence on the prognostic synergies between INPP4B and RAD50 on breast cancer outcome and deepens our understandings toward cancer progression that ultimately facilitates cancer precision medicine.

**Author Contribution**

X.C. conducted the computational analysis and R.T. helped in this process. X.D. designed and supervised the present study. X.C. and X.D. prepared the manuscript. X.D. and J.Z. co-funded this work.

**Competing Interests**

The authors declare that there are no competing interests associated with the manuscript.

**Funding**

This work was supported by the National Natural Science Foundation of China [grant number 81972789]; the National Science and Technology Major Project [grant number 2018ZX10022005-004-002]; the Six Talent Peaks Project in Jiangsu Province [grant number SWYY-128]; and the Technology Development Funding of Wuxi [grant number WX18IVJN017]. These funding sources have no role in the study design, data collection and analysis, decision to publish, or preparation of the manuscript.

**Ethical Approval**

This article does not contain any studies with human participants or animals performed by any of the authors.

**Abbreviations**

eQTL, expression Quantitative Trait Loci; GEO, Gene Expression Omnibus; GO, Gene Ontology; HR, Hazard Ratio; KEGG, Kyoto Encyclopedia of Genes and Genomes; LD, linkage disequilibrium; MAF, minor allele frequency; OS, overall survival; SNP, single nucleotide polymorphism; TCGA, The Cancer Genome Atlas.

**References**

1. Blackadar, C.B. (2016) Historical review of the causes of cancer. *World J. Clin. Oncol.* 7, 54–86, [https://doi.org/10.5306/wjco.v7i1.54](https://doi.org/10.5306/wjco.v7i1.54)
2. Duffy, M.J., Synnott, N.C. and Crown, J. (2018) Mutant p53 in breast cancer: potential as a therapeutic target and biomarker. *Breast Cancer Res. Treat.* 170, 213–219, [https://doi.org/10.1007/s10549-018-4753-7](https://doi.org/10.1007/s10549-018-4753-7)
3. Hall, J. and Angele, S. (1999) Radiation, DNA damage and cancer. *Mol. Med. Today* 5, 157–164, [https://doi.org/10.1016/S1357-4310(99)01435-5](https://doi.org/10.1016/S1357-4310(99)01435-5)
4. Khan, S. (2015) Potential role of *Escherichia coli* DNA mismatch repair proteins in colon cancer. *Crit. Rev. Oncol. Hematol.* 96, 475–482, [https://doi.org/10.1016/j.critrevonc.2015.05.002](https://doi.org/10.1016/j.critrevonc.2015.05.002)
5. Khan, S., Zakariah, M., Roffo, C. et al. (2017) Prediction of mycoplasma hominis proteins targeting in mitochondria and cytoplasm of host cells and their implication in prostate cancer etiology. *Oncotarget* 8, 30830–30843
6. Alshamsan, A., Khan, S., Imran, A. et al. (2017) Prediction of *Chlamydia pneumoniae* protein localization in host mitochondria and cytoplasm and possible involvements in lung cancer etiology: a computational approach. *Saud. Pharm. J.* 25, 1151–1157, [https://doi.org/10.1016/j.jsps.2017.05.007](https://doi.org/10.1016/j.jsps.2017.05.007)
7. Khan, S., Imran, A., Malik, A. et al. (2019) Bacterial imbalance and gut pathologies: association and contribution of E. coli in inflammatory bowel disease. *Crit. Rev. Clin. Lab. Sci.* 56, 1–17
8 DeSantis, C.E., Ma, J., Gaudet, M.M. et al. (2019) Breast cancer statistics, 2019. CA Cancer J. Clin. 69, 438–451, https://doi.org/10.3322/caac.21583
9 Sun, Y.S., Zhao, Z., Yang, Z.N. et al. (2017) Risk factors and prevention of breast cancer. Int. J. Biol. Sci. 13, 1387–1397, https://doi.org/10.7150/ijbs.21635
10 Mahdi, K.M., Nassir, M.R. and Nasiri, K. (2013) Hereditary genes and SNPs associated with breast cancer. Asian Pac. J. Cancer Prev. 14, 3403–3409, https://doi.org/10.7314/APJCP.2013.14.3.3403
11 Deng, N., Zhou, H., Fan, H. et al. (2017) Single nucleotide polymorphisms and cancer susceptibility. Oncotarget 8, 110635–110649, https://doi.org/10.18632/oncotarget.22372
12 Nelson, M.R., Marnellos, G., Kammerer, S. et al. (2004) Large-scale validation of single nucleotide polymorphisms in gene regions. Genome Res. 14, 1664–1668, https://doi.org/10.1101/gr.2421604
13 Llyijuist, J., Ruddy, K.J., Vachon, C.M. et al. (2018) Common genetic variation and breast cancer risk-past, present, and future. Cancer Epidemiol. Biomark. Prev. 27, 380–394
14 Vage, J. and Lingaas, F. (2008) Single nucleotide polymorphisms (SNPs) in coding regions of canine dopamine- and serotonin-related genes. BMC Genet. 9, 10, https://doi.org/10.1186/1471-2156-9-10
15 Scott, S.P. and Pandita, T.K. (2006) The cellular control of DNA double-strand breaks. J. Cell. Biochem. 99, 1463–1475, https://doi.org/10.1002/jcb.20167
16 Johansson, H.K., Jonsson, G., Johannesdottir, G. et al. (2006) Chromosome 5 imbalance mapping in breast tumors from BRCA1 and BRCA2 mutation carriers and sporadic breast cancer patients. Int. J. Cancer 119, 1052–1060, https://doi.org/10.1002/ijc.21934
17 Heikkinen, K., Rapakko, K., Karpipinen, S.M. et al. (2006) RAD50 and NBST are breast cancer susceptibility genes associated with genomic instability. Carcinogenesis 27, 1593–1599, https://doi.org/10.1093/carcin/bgi360
18 Wei, L., Chao, H.H., Shabalin, A.A. et al. (2012) Basal-like breast cancer DNA copy number losses identify genes involved in genomic instability, response to therapy, and patient survival. Breast Cancer Res. Treat. 133, 865–880, https://doi.org/10.1007/s10549-011-1846-y
19 Miller, T.W., Rexer, B.N., Garrett, J.T. et al. (2011) Mutations in the phosphatidylinositol 3-kinase pathway role in tumor progression and therapeutic implications in breast cancer. Breast Cancer Res. Treat. 123, 224, https://doi.org/10.1186/bc3039
20 Lopez-Knowles, E., O’Toole, S.A., McNiel, C.M. et al. (2010) PI3K pathway activation in breast cancer is associated with the basal-like phenotype and cancer-specific mortality. Int. J. Cancer 126, 1121–1131, https://doi.org/10.1002/ijc.24831
21 Zhu, K., Liu, Q., Zhou, Y. et al. (2015) Oncogenes and tumor suppressor genes: comparative genomics and network perspectives. BMC Genomics 16, S8, https://doi.org/10.1186/1471-2164-16-S7-S8
22 Dai, X., Fagerholm, R., Khan, S. et al. (2015) INPP4B and RAD50 have an interactive effect on survival after breast cancer. Breast Cancer Res. Treat. 149, 363–371, https://doi.org/10.1007/s10549-014-3241-y
23 Sherry, S.T., Ward, M.H., Kholodov, M. et al. (2001) dbSNP: the NCBI database of genetic variation. Nucleic Acids Res. 29, 308–311, https://doi.org/10.1093/nar/29.1.308
24 Heikkinen, T., Greco, D., Pettitari, L.M. et al. (2011) Variants on the promoter region of PTEN affect breast cancer progression and patient survival. Breast Cancer Res. 13, R130, https://doi.org/10.1186/bcr2076
25 Muranen, T.A., Greco, D., Fagerholm, R. et al. (2011) Breast tumors from CHEK2 1100delC-mutation carriers: genomic landscape and clinical implications. Breast Cancer Res. 13, R90, https://doi.org/10.1186/bcr2015
26 Leek, J.T., Johnson, W.E., Parker, H.S. et al. (2012) The sva package for removing batch effects and other unwanted variation in high-throughput experiments. Bioinformatics 28, 862–863, https://doi.org/10.1093/bioinformatics/bts034
27 Therneau, T.M. and Grambsch, P.M. (2000) Modeling Survival Data: Extending the Cox Model, Springer-Verlag, New York, ISBN: 0-387-98784-3
28 Khan, S., Fagerholm, R., Kadaliyil, L. et al. (2018) Meta-analysis of three genome-wide association studies identifies two loci that predict survival and treatment outcome in breast cancer. Oncotarget 9, 4249–4257, https://doi.org/10.18632/oncotarget.22747
29 Bendj, J., Musti, M., Šťurcak, J. et al. (2016) PredictSNP2: a unified platform for accurately evaluating SNP effects by exploiting the different characteristics of variants in distinct genomic regions. PLoS Comput. Biol. 12, e1004962, https://doi.org/10.1101/pbc.1004962
30 Kumar, S., Ambrosini, G. and Bucher, P. (2017) SNP2TFBS - a database of regulatory SNPs affecting predicted transcription factor binding site affinity. Nucleic Acids Res. 45, D139–D144, https://doi.org/10.1093/nar/gkw1064
31 Zhou, Y., Zhou, B., Pache, L. et al. (2019) Metascape provides a biologist-oriented resource for the analysis of systems-level datasets. Nat. Commun. 10, 1523, https://doi.org/10.1038/s41467-019-09234-6
32 Warde-Farley, D., Donaldson, S.L., Comes, O. et al. (2010) The GeneMANIA prediction server: biological network integration for gene prioritization and predicting gene function. Nucleic Acids Res. 38, W214–W220
33 Foo, L.C. and Dougherty, J.D. (2013) Aldhi1L1 is expressed by postnatal neural stem cells in vivo. Glia 61, 1533–1541, https://doi.org/10.1002/glia.22539
34 Dahiya, N., Sherman-Baust, C.A., Wang, T.L. et al. (2008) MicroRNA expression and identification of putative miRNA targets in ovarian cancer. PLoS ONE 3, e2436, https://doi.org/10.1371/journal.pone.0002436
35 Nobukuni, Y., Mitsubuchi, H., Endo, F. et al. (1990) Maple syrup urine disease. Complete primary structure of the E1 beta subunit of human branched chain alpha-ketoacid dehydrogenase complex deduced from the nucleotide sequence and a gene analysis of patients with this disease. J. Clin. Invest. 86, 242–247, https://doi.org/10.1172/JCI114690
36 Yamakawa, K., Gao, D.Q. and Korenberg, J.R. (1996) A periodic tryptophan protein 2 gene homologue (PWP2H) in the candidate region of progressive myoclonus epilepsy on 21q22.3. Cytogenet. Cell Genet. 74, 140–145, https://doi.org/10.1159/000134402
37 Hatakayama, S. (2017) TRIM family proteins: roles in autophagy, immunity, and carcinogenesis. Trends Biochem. Sci. 42, 297–311, https://doi.org/10.1016/j.tibs.2017.01.002