5-13-2011

The Role of the SUPRMAM1 Locus in Responses to Ionizing Radiation and Susceptibility to Mammary Tumors

Nicholas B. Griner
University of Massachusetts Amherst, ngriner@mcb.umass.edu

Recommended Citation

Griner, Nicholas B., "The Role of the SUPRMAM1 Locus in Responses to Ionizing Radiation and Susceptibility to Mammary Tumors" (2011). *Open Access Dissertations*. 392.
https://scholarworks.umass.edu/open_access_dissertations/392

THE ROLE OF THE *SUPRMAM1* LOCUS IN RESPONSES TO IONIZING RADIATION AND SUSCEPTIBILITY TO MAMMARY TUMORS

A Dissertation Presented

By

NICHOLAS B. GRINER

Submitted to the Graduate School of the
University of Massachusetts Amherst in partial fulfillment
of the requirements for the degree of

DOCTOR OF PHILOSOPHY

May 2011

Program in Molecular and Cellular Biology

THE ROLE OF THE *SUPRMAM1* LOCUS IN RESPONSES TO IONIZING RADIATION AND SUSCEPTIBILITY TO MAMMARY TUMORS

A Dissertation Presented

By

NICHOLAS B. GRINER

Approved as to style and content by:

____
D. Joseph Jerry, Chair

____
Sallie Smith Schneider, Member

____
Steven J. Sandler, Member

____
Alan Schneyer, Member

____
Barbara A. Osborne, Director
Program in Molecular and Cellular Biology

DEDICATION

To my parents: Mark and Suzanne Griner

ACKNOWLEDGMENTS

I wish to acknowledge and thank first my advisor D. Joseph Jerry. He has been instrumental in my graduate training and has taught me much in the scientific process. In addition, Joe has been incredibly supportive of my work and in guiding me through the Ph.D process. I also would like to thank all of the current and past members of the Jerry lab. This includes Ellen Dickinson, Luwei Tao, Haoheng Yan, Mary Hagen, Amy Roberts, Karen Dunphy, Erick Perez, Cindy Kane, Trevor Baptiste, Shannon Compton and Linda Hill. Jeff Kane's technical skills were incredibly helpful in much of this research. Many thanks to Brooke Bentley and Sharon Marconi for their histology work. A special thanks to Kelly Gauger and other members of the Smith-Schneider lab including Matthew Carter for insightful and entertaining conversations. I would also like to thank my committee members, Alan Schneyer, Steve Sandler and Sallie Smith-Schneider for their helpful comments and suggestions in my research. Special thanks to Sallie for sharing her lab space with me. Thanks to all of the members of the PVLSI including members of the mouse facility who were instrumental for many of these studies. Finally, a special thanks to Lesley Mathews for her advise and overall support throughout my graduate school experience.

ABSTRACT

THE ROLE OF THE SUPRMAM1 LOCUS IN RESPONSES TO IONIZING RADIATION AND SUSCEPTIBILITY TO MAMMARY TUMORS

MAY 2011

NICHOLAS B. GRINER, B.S., UNIVERSITY OF WASHINGTON

Ph.D., UNIVERSITY OF MASSACHUSETTTS, AMHERST

Directed by: Professor D. Joseph Jerry

Loss of p53 function can lead to a variety of cancers, including breast cancer. Mice heterozygous for the p53 gene (designated *Trp53*$^{+/-}$) develop spontaneous mammary tumors, but this depends on the strain background and has been linked to a locus on chromosome 7 (designated *SuprMam1*). Mammary tumors are common in BALB/c-*Trp53*$^{+/-}$females, but are rare in C57BL/6-*Trp53*$^{+/-}$ mice. Prevalence of genomic instability appears to contribute to the phenotype as loss of heterozygosity (LOH) is significantly more common among tumors arising in BALB/c-*Trp53*$^{+/-}$ mice compared to C57BL/6J-*Trp53*$^{+/-}$ mice. This increased LOH in BALB/c-*Trp53*$^{+/-}$ tumors was shown to be due to recombination events. The BALB/c strain has been shown to have a deficiency in non-homologous end joining (NHEJ) of DNA double strand breaks (dsb), however, this does not account for the increase of LOH events in tumors. Our hypothesis was that BALB/c-*Trp53*$^{+/-}$ mice are more susceptible to mammary tumors due to impaired Homologous Recombination Repair (HRR) leading to LOH. Using the COMET assay, we demonstrate that dsbs persist longer in BALB/c-*Trp53*$^{+/-}$ mouse embryonic fibroblasts (MEFs) compared to C57BL/6J-*Trp53*$^{+/-}$ MEFs. Similarly, co-localization of H2AX and the homologous recombination protein RAD51 remain at dsbs longer in BALB/c-*Trp53*$^{+/-}$ MEFs compared to C57BL/6-*Trp53*$^{+/-}$ MEFs. *Palb2*, a gene that lies within the *SuprMam1* interval and has been shown to contribute to heritable breast cancer, was chosen as an initial candidate gene. No coding SNPs or expression differences of *Palb2* were found in the mammary glands between the two strains. Additional fine mapping and use of a filtering criteria in the *SuprMam1* region yielded an additional 34 candidate genes. We demonstrate no significant differences in any of these genes in whole mammary glands and primary mammary epithelial cells between the two strains. Finally, using a congenic mouse strain, we demonstrate the lack of irradiation (IR) sensitivity alleles within the *SuprMam1* region. These results suggest a possible defect in HRR in the BALB/c strain that is unlikely related to *Palb2*. The gene or genes respsonsible for increased mammary tumor incidence in the BALB/c-*Trp53*$^{+/-}$ remain to be identified.

TABLE OF CONTENTS

Page

APPENDICES

LIST OF TABLES

LIST OF FIGURES

Figure **Page**

CHAPTER 1

INTRODUCTION TO BREAST CANCER RISK ALLELES AND THEIR ROLE IN DNA DOUBLE-STRAND BREAK REPAIR

Breast cancer is one of the leading causes of cancer death in women behind only lung cancer (Jemal et al., 2009). Despite decreases in breast cancer related deaths, this disease still leads to the death of over 40,000 women a year. Advances in treatment and early detection continue to lead to better prognoses. However, the incidence rate has continued at a steady rate, accounting for 23% of total cancer cases. Identification of risk factors on the molecular level would provide new and valuable insights towards the treatment of this devastating disease.

Most of the understanding of the mechanisms of susceptibility to breast cancer comes from the identification of hereditary risk alleles. *BRCA1* and *BRCA2* are two genes identified in the mid-1990's by positional cloning (Miki et al., 1994; Wooster et al., 1994). Individuals that are *BRCA1* or *BRCA2* carriers inherit one defective copy of the gene. Inheriting a defective copy of either gene is rather rare, a population carrier frequency of <0.1% (Peto et al., 1999b). Although these high penetrance susceptibility alleles impart a 10-20 fold risk in breast cancer incidence, there are other non-genetic modifiers of risk that can increase or decrease the relative risk for *BRCA1/2* carriers. These include age of menarche (Kotsopoulos et al., 2005), pregnancy (McLaughlin et al., 2007), breastfeeding (Jernstrom et al., 2004) and oral contraceptives (Narod et al., 2002) among others. Individuals that carry disease causing *BRCA1* or *BRCA2* alleles commonly have mutations that lead to inactivation of the encoded proteins mostly due to truncations. Families with a history of breast cancer are now genetically screened for mutations in *BRCA1/2* due to the risk these alleles impart.

P53 has a role in many cell pathways including apoptosis, cell cycle control and DNA repair (Vogelstein et al., 2000). Its role in suppressing tumors is critical and has been termed the "Guardian of the Genome". P53 appears to be critical in determining whether a cell initiates apoptosis or DNA repair following genomic damage. Studies have identified a large number of *TP53* mutations in breast cancer establishing its role in breast cancer development (Gasco et al., 2003; Soussi et al., 2006). Many of these mutations are within the DNA binding domain which is critical for its function in DNA double-strand break repair (Dudenhoffer et al., 1999). This role in dsb repair appears to be separate from other transcription-dependent roles of p53 (Gatz and Wiesmuller, 2006). Individuals who inherit germline mutations of *TP*53 develop Li-Fraumeni syndrome characterized by increased rates of many cancers including brain tumors, soft tissue sarcomas, leukemia and breast cancer. Nearly 100% of Li-Fraumeni women will develop some kind of cancer (Chompret et al., 2000). In addition, many of the *TP*53 mutations identified in Li-Fraumeni patients are localized in the DNA binding region of the protein (Petitjean et al., 2007). The role of p53 in HRR appears to be in repressing it (Akyuz et al., 2002d; Wiesmuller et al., 1996). Specifically, studies have shown that p53 represses hyper-recombination in response to replication fork stalling, thus acting as fidelity control (Janz and Wiesmuller, 2002). These studies highlight the significance of p53 and its role in dsb repair within the breast.

Together, *BRCA1, BRCA2* and *TP53* make up approximately 16% of hereditable risk for breast cancer (Peto et al., 1999a). The discovery of other high penetrance alleles over the years has proven fruitless. This leaves approximately 80% of hereditary risk to unknown genes. Some groups have suggested a polygenic model where multiple common genes impart a small risk and together may account for the remaining 80% familial risk (Ponder, 2001b). Accordingly, multiple low penetrance alleles that have been identified including *CHEK2, PALB2, BRIP1, NBN, RAD50* and *ATM* (Nevanlinna and Bartek, 2006; Erkko et al., 2008; Rahman et al., 2007b; Seal et al., 2006; Swift et al., 1991; Heikkinen et al., 2006). Individuals who inherit a defective copy of any of these genes have a two to fourfold risk for breast cancer compared to a 10-20 fold with *BRCA1/2*. While these alleles are more frequent in the population than the high penetrance *BRCA1* and *BRCA2* risk alleles, they are still relatively uncommon (~0.6%). Interestingly, all of these genes are involved in dsb repair. Bi-allelic loss of *PALB2* and *BRIP1* causes Fanconi Anemia similar to bi-allelic loss of *BRCA2* (Xia et al., 2007a). In addition, bi-allelic loss of *ATM* and *NBS1* lead to the genomic instability-like diseases ataxia-telangectasia and Nijmigen breakage syndrome, respectively. Thus, breast cancer susceptibility is the phenotype in mono-allelic genotypes with these low penetrance alleles and more severe diseases in bi-allelic genetic backgrounds.

Genome-wide association studies have identified additional low penetrance modifiers (Easton et al., 2007b; Ahmed et al., 2009; Cox et al., 2007; Hunter et al., 2007). Initial studies identified *CASP8, TFGB1* and *TNF* as potential risk alleles. Additional studies identified an additional six loci including *FGFR2 ,TOX3, MAP3K1* and *LSP1* (Easton et al., 2007a). Interestingly enough, two of the SNPs used to identify regions of the genome linked to breast cancer susceptibility are localized within non-coding regions. How these SNPs may be affecting breast cancer risk is unknown. Despite the recent identification of these low penetrance alleles, estimates still put the percentage of unknown hereditary breast cancer risk alleles at 70% (Szpirer and Szpirer, 2007) **(Figure 1.1)**. Much work is still to be done to identify additional candidate risk alleles and their respective roles in hopes for development of novel treatments towards breast caner.

The DNA repair pathway is highly linked to breast cancer susceptibility. This is primarily due to all breast cancer hereditary risk alleles being involved in DNA repair. In fact, they are all involved in one subset of DNA repair, double-strand break repair. This makes sense as cells from breast tumors show increased chromosomal breaks after irradiation suggesting these cells are deficient in DNA repair (Parshad and Sanford, 2001). Normal DNA replication can also lead to dsbs if the polymerase complex runs into bulky lesions during processing (Arnaudeau et al., 2001). The two primary methods to resolve this break are nonhomologous end joining (NHEJ) and homologous recombinational repair (HRR) **(Figure 1.2)**. The choice of pathway is largely determined by the cell cycle stage when the damage is encountered (Rothkamm et al., 2003). If the double strand break occurs during the G1/G0 phase, NHEJ will be the preferred method. HRR is the method of choice during S-phase when sister chromatids are present to act as a template. NHEJ is traditionally thought to be a non-conservative repair pathway as some genetic material is lost during the process. HRR is considered a conservative repair as a sister chromatid or homologous chromosome is used as a template resulting in no loss of DNA sequence. There are many proteins involved in the correct sequence of events for each pathway. A group of proteins termed the MRN complex consisting of MRE11, RAD50 and NBS1 are the first to recognize the double strand break (Valerie and Povirk, 2003a). In addition, immediately following DNA damage, ATM phosphorylates the histone H2A which acts as a scaffold for the accumulation of DNA repair proteins. H2AX thus acts a marker for the DNA damage response that can be measured in cells. The MRN complex binds to the ends of the broken DNA and proceeds to perform end processing and act as a scaffold. Next, RAD51 is loaded onto the DNA forming nucleoprotein filaments. RAD51 with cofactors acts as a recombinase and initiates the strand invasion into the complimentery homologous chromosome or sister chromatid (Hartlerode and Scully, 2009). After branch migration and repair synthesis has occurred, RAD51C and XRCC3 resolve the holiday junction and ligate the ends together. Another form of HRR can occur that requires RAD52 instead of RAD51. This non-conservative pathway directly anneals the ssDNA overhangs at the break site leading to degradation of the overhangs and loss of genetic material (Ahmad et al., 2008).

The other major DSB repair pathway is NHEJ. This process first involves the binding of KU70/80 to the ends of the broken DNA (Burma et al., 2006). DNA protein kinase (DNA-PK$_{cs}$) then forms a complex with KU70/80 and the catalytic sub-unit is activated. XRCC4 and DNA Ligase IV (LIG4) are then recruited and the break is directly annealed. Mammalian cells have been shown to primarily employ the NHEJ pathway to repair double strand breaks (Shrivastav et al., 2008). There appears to be both an error-prone and error-free NHEJ pathway that relies on how “clean” the double strand break is (Zhang and Powell, 2005). Error-free NHEJ appears to be regulated at least partly by BRCA1 and its ability to suppress the more error-prone pathway (Zhuang et al., 2006). BRCA1 also appears to direct the cell towards the HRR pathway over the error-prone microhomology directed NHEJ (Baldeyron et al., 2002).

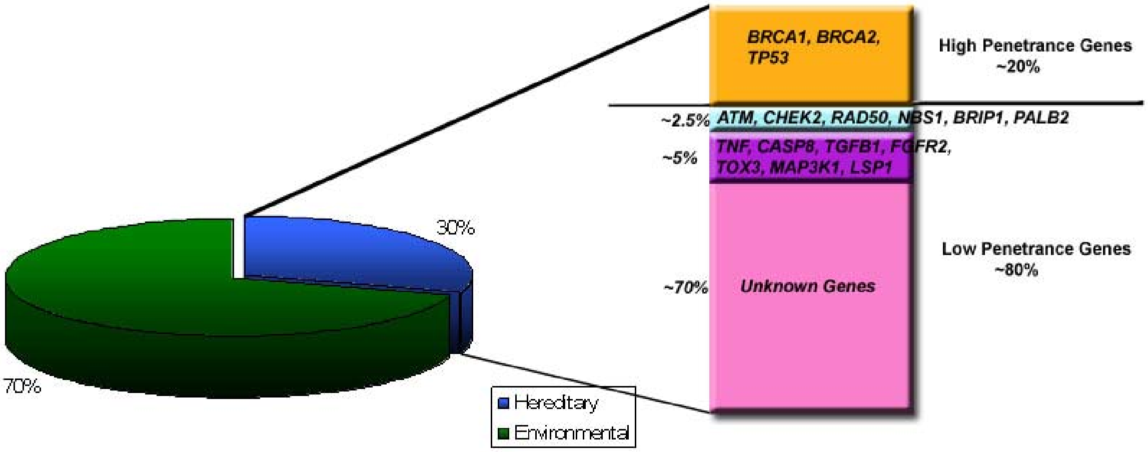
Loss of *TP*53 is the most commonly mutated gene observed in tumors (Hollstein et al., 1994). Attempts to create mouse models of Li-Fraumeni disease have proven difficult due to genetic strain differences (Backlund et al., 2001a). C57BL/6 mice heterozygous for *p*53 have extremely low rates of mammary tumors. In contrast, BALB/c mice heterozygous for *p*53 develop mammary tumors at frequencies similar to Li-Fraumeni individuals (Kuperwasser et al., 2000c). Previous work in our lab performing genetic linkage mapping studies identified a region on chromosome 7, termed *SuprMam1*, that showed significant linkage to the mammary tumor phenotype (Blackburn et al., 2007e) **(Figure 1.3)**. *Dmbt1* was identified as a candidate due to expression differences observed between the strains. Protein expression for DMBT1 was also shown to be significantly reduced in breast tissue from women with breast cancer compared with cancer-free controls. However, the *Dmbt1* gene is located at the boundary of the *SuprMam1* region suggesting other genes within the interval may explain strain differences in mammary tumor incidence. A separate quantitative trait loci (QTL) was also mapped proximal to *SuprMam1* and is believed to contain dominant modifier(s) to mammary tumor latency (Koch et al., 2007). The gene or genes responsible for mammary tumor latency differences between these two strains is still unknown.

The goal of this dissertation was to use the BALB/c *Trp53*$^{+/-}$ mouse strain as a model for breast cancer to answer the following questions.

- Is the BALB/c-*Trp53*$^{+/-}$ strain defective in DNA dsb repair?
- Are there DNA repair genes within the *SuprMam1* interval that could explain increased mammary tumor latency in the BALB/c *Trp53*$^{+/-}$ strain?

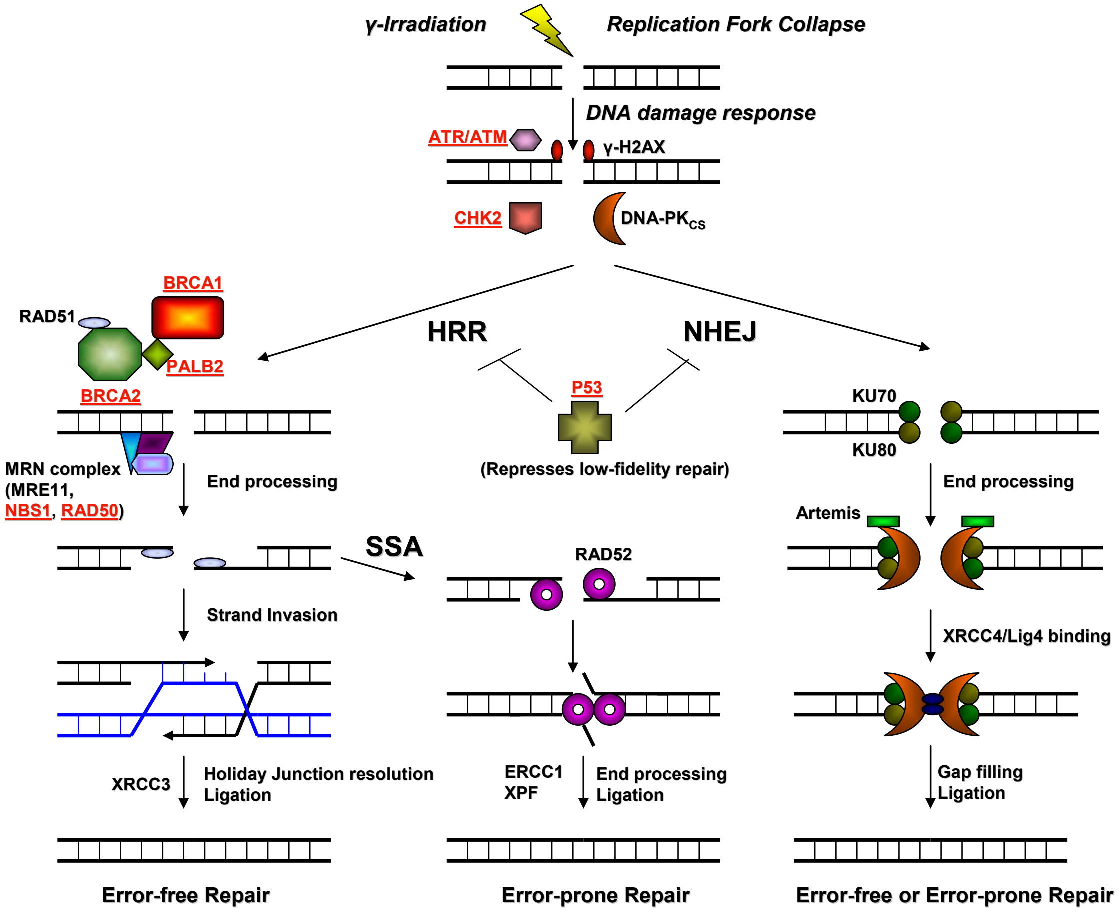
- Are there significant SNP differences within the *SuprMam1* region of the BALB/c *Trp53*$^{+/-}$ strain?
- Are there corresponding expression differences in the BALB/c *Trp53*$^{+/-}$ strain?
- Are there alleles within the *SuprMam1* region that contribute to the increased IR sensitivity in the BALB/c *Trp53*$^{+/-}$ strain?

The following dissertation describes the strategies and ultimately the answers to these questions and the implications in breast cancer risk.



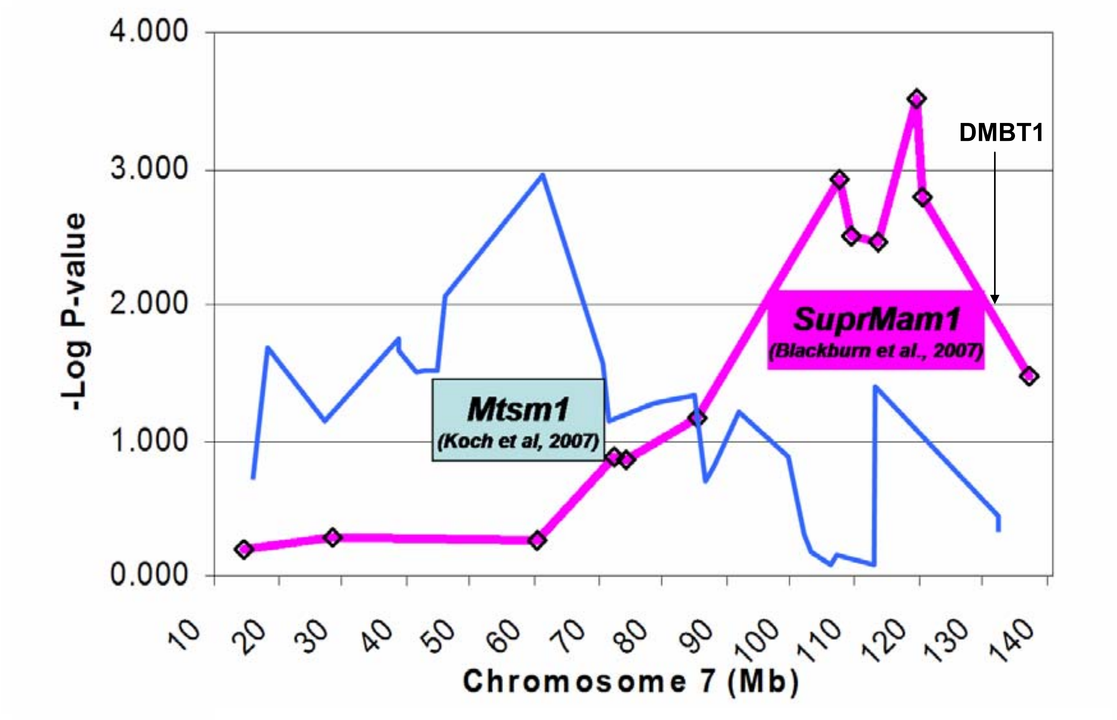
Adapted from Szpirer C et al.

Figure 1.1 Diagram describing the known genes involved in hereditary risk for breast cancer and the percentage of risk they impart.



(Jerry et al., 2010)

Figure 1.2 Overview of the DNA double-strand break pathways in mammalian cells.



Adapted from Blackburn A et al, 2007 and Kock et al, 2007 .

Figure 1.3 Published linkage maps of mammary tumor susceptibility in the BALB/c *Trp53*$^{+/-}$ strain. *Mtsm1* describes a linked region containing dominant modifiers while *SuprMam1* contains recessive modifiers to mammary tumor susceptibility.

CHAPTER 2

DIFFERENCES IN DNA REPAIR BETWEEN THE MOUSE STRAINS C57BL/6 AND BALB/C ON A TRP53$^{+/-}$ GENETIC BACKGROUND

Introduction

Loss of heterozygosity (LOH) is a critical step in the pathway towards tumorigenesis (Donahue et al., 2006). LOH for p53 is a very common event in breast cancer (Johnson et al., 2002). Studies have demonstrated that tumors from BALB/cMed-*Trp53*$^{+/-}$ mice have increased LOH compared to tumors from C57BL/6-*Trp53*$^{+/-}$ mice (Blackburn et al., 2004c) and the increase LOH is inherited as an autosomal dominant trait in the F1 progeny. Analysis of mammary tumors from F1 and N2 backcross mice demonstrated that LOH occurred via a recombination pathway. These data suggest that the increased LOH in BALB/c tumors may be a genetic defect in double strand break repair.

Non-homologous end-joining (NHEJ) and homologous recombination repair (HRR) are the major pathways used to repair DNA double-strand breaks. Although NHEJ is considered a non-conservative repair pathway as genetic material is loss during this process, it is believed to be the more prominent dsb repair pathway in mammalian species (Lieber et al., 2003). In contrast, the HRR pathway uses sister chromatids or homologous chromosomes as templates to fill in dsbs. This results in the loss of no genetic material and is the preferred pathway in stem cells (Francis and Richardson, 2007). Interestingly, most breast cancer risk alleles have prominent roles in the HRR pathway **(summarized in Figure 1.2)** implicating the importance of this pathway in genetic stability.

In addition to the observed increased LOH in BALB/c tumors, other lines of evidence suggest differences in DNA double-strand break repair may be responsible for mammary tumor susceptibility in BALB/c-*Trp53*+/- mice. The BALB/c strain is known to have a defect in NHEJ due to a polymorphism in *Prkdc*, the gene that encodes DNA-PK_{cs}. Defects in NHEJ will likely increase the rates of HRR, possibly leading to inappropriate recombination and LOH. To test these hypotheses, we implemented multiple methods in hopes to establish clear differences in DNA dsb repair between these two strains. We first used a novel DNA double-strand break repair assay that distinguishes HRR from NHEJ. We also used immunofluorescence as a technique to analyze the amount of proper localization of DNA repair proteins following DNA damage. A cell viability assay was implemented to test the sensitivity of MEFs from both strains to DNA damage inducing drugs. Finally, we used the Comet assay that measures unrepaired DNA following DNA damage.

Methods

Cell Culture Media:

MEFs were grown in alpha MEM media (Fisher Scientific) with 10% FBS, AB/AM (Gibco), 2mM glutamine, 15 µg/ml gentamycin (Gibco) and 8 µg/ml tylocin (Gibco). Uterine rinse for MEF isolation consisted of PBS, AB/AM, 1.25% Fungizone (Gibco), 15 µg/ml gentamycin (Gibco) and 8 µg/ml tylocin (Gibco). Collagenase mixture contained 0.2% collagenase (Gibco) desolved in alpha MEM, AB/AM, 1.25% Fungizone, 15 µg/ml gentamycin (Gibco) and 8 µg/ml tylocin (Gibco).

P53 LOH genotyping:

Early passage MEFs from both strains were grown in standard growth medium. At approximately 90% confluency, the cells were passed at a 1:2 ratio. DNA was isolated from each plate at every passage by a standard protocol. P53 amplification was performed using PCR and the following primers, 5'-TATACTCAGAGCCGGCCT-3', 5'-ACAGCGTGGTGGTACCTTAT-3', 5'-CTATCAGGACATAGCGTTGG-3'. Completed PCR reactions were then run out on a 1% agarose gel and stained with ethidium bromide. The amount of each amplified amplicon was measured using a standard phosporimager and the accompanying software.

Isolation of mouse embryonic fibroblasts (MEFs):

Female pregnant mice (day 14 of pregnancy) were sacrificed and their uterus were removed. Each individual embryo was removed from a uterine chamber and the head was removed using a sterile razor blade. Any reddish mesenchymal internal tissue was scraped out of the embryo before being minced up with scissors. This tissue was then mixed with 0.2% collagenase (Gibco) in alpha MEM media with antibiotics but without serum. This was incubated for 30 minutes at 37^{o}C. Cells were pelleted by centrifugation at 1500 RPM for 5 minutes. Each batch of cells was washed with alpha MEM and pelleted again. Each separate fetus was then plated on a T-75 plate. At least 6 plates worth of cells were combined to create a batch of homogenous mouse embryonic fibroblasts for each strain and genotype.

Double-strand break repair assay:

Rates of NHEJ and HRR were determined by transfection of different combinations of plasmids depending on which pathway was being assessed. Briefly, 8 x 10^{5} cells were mixed with a combination of a meganuclease expression vector (pCMV-I-SceI) and either EJ-EGFP or HR-EGFP/3′EGFP constructs, corresponding to NHEJ and HRR, respectively. Control samples contained a mixture of pCMV-I-SceI and wtEGFP plasmid. Transfection was performed by AMAXA (Lonza) nucleofection procedure A23. Tweny four hours following transfection, the percentage of GFP positive cells was determined by flow cytometry. 50,000 cells were counted per sample. The percentage of repair was calculated by the percentage of GFP positive cells divided by the transfection efficiency. Three transfection replicates were performed for each experiment and averaged. Statistical analysis was performed by student t-test.

Immunofluorescence:

MEFs were seeded 500,000 cells/60 mm dish containing coverslips. Plates were irradiated with 2.5 Gy for the appropriate time points. Next, 500 μl of 3.7% formaldehyde was added for 7 minutes to fix cells. Formaldehyde was removed followed by washing cells 2 times with PBS. 500 μl of .05% TritonX in PBS was added to the cells for 7 minutes on ice. TritonX was removed and cells were washed once with PBS. Using tweezers, coverslips were removed from well, dipped in PBS/.05% Tween and then placed coverslips on an upside down top of a 24-well plate with the cells facing up. 25 μl of primary antibodies (RAD51 1:100 and γH2AX 1:1000) diluted in PBS with 5% goat serum was added to the coverslip, covered and incubated at 37 degrees for 1 hour. Coverslips were then placed back into 24 well plate and washed with PBS 3 times, 5 minutes each. Secondary antibodies were then diluted in PBS (1:1000 for Alexafluors 488 and 594) with 5% goat serum and 25 μl was added to each coverslip and incubated for 40 minutes at 37 degrees. Coverslips were placed back into 24 well plate and wash 3 times, 5 minutes each. DAPI was diluted in PBS (1:5000) and incubated with coverslips in 500 µl for 5 minutes. Coverslips were washed 2 more times with PBS and mounted on microscope slides with about 7 µl of Mowiol with 2.5% Dabco. Slides were then placed in the dark overnight and were washed the next day to remove salts off coverslips. Slides were analyzed by immunofluoresence microscope at 60X magnification. The number of cells were counted by DAPI staining and the percentage of H2AX and RAD51 positive cells was determined ("positive" indicates two or more foci per cell).

MTS assays (MMC and Camptothecin treatment):

MEFs were seeded in 96-well plates so that the control groups for each genotype produced similar proliferation rates (previously determined). 2500 cells/well for B6 *Trp53*$^{+/+}$, 1850 cells/well for B6 *Trp53*$^{+/-}$, 5000 cells/well for Balb/c *Trp53*$^{+/+}$ and 3250 cells/well for Balb/c *Trp53*$^{+/-}$ were seeded into a 96-well plate with 100 µl of α-MEM media with serum. The next day, media was replaced with media containing concentrations of either MMC or Camptothecin and cells were incubated for three days at 37 degrees. At the end of the third day, 20 µl of MTS reagent (Promega CellTiter 96) was dispensed into each well and plates were incubated for two and a half hours at 37 degrees. Plates were then read on a plate reader at 490 nm wavelength and data points (triplicate) from each dose was plotted relative to control.

Comet Assay:

MEFs for each genotype were seeded into 60 mm plates at a density of 100,000 cells. Six hours later, plates were irradiated with 5 Gy and incubated for ~15 hours at 37 degrees. Cells were then trypsinized, spun down and resuspended in 10 µl PBS. 75 µl of low melting agarose was mixed with each cell suspension and pipetted onto pre-coated microscope slides (slides were processed by first removing the oil surface by methanol flame followed by dipping half the slide into 1% agarose and dried overnight). A coverslip was applied and the slides were placed in 4 degrees to allow agarose to harden. Another 80 µl of low melt agarose was applied to each slide and coverslip placed on top. Following this, coverslips were removed and slides were placed in coplin jars with enough lysis buffer to cover the slides. Jars were placed at 4 degrees for 2 hours to allow lysis of cells. Slides were then placed into gel electrophoresis boxes with enough buffer to cover slides and incubated for 20 minutes at room temperature to allow DNA to unwind. Electrophoresis for 30 min. was performed at 24 volts and 300 milliamperes (volume of buffer was adjusted to achieve 300 mAmps). Slides were removed from boxes and neutralization buffer was added (~ 1 mL) for 5 minutes. This was repeated two more times and then slides were washed briefly with dH_2O. Slides were stained with DAPI for 5 min., washed again with dH_2O and coverslips were put into place. Pictures of slides were taken at 40X magnification on a fluorescent microscope. Comets were analyzed by KOMET software to determine the olive tail moment for ~75 images for each genotype and treatment.

Results

Shorter latency for p53 LOH in BALB/c-Trp53$^{+/-}$ MEFs

Increased loss of heterozygosity for p53 was observed in tumors from BALB/c *Trp53*$^{+/-}$ mice compared to their C57BL/6-*Trp53*$^{+/-}$ counterparts (Blackburn et al., 2004b). We were interested whether a similar increased LOH for *Trp53* occurred in cultured cells. Using BALB/c-*Trp53*$^{+/-}$ and C57BL/6-*Trp53*$^{+/-}$ MEFs, we determined the p53 genotype after each population doubling using PCR. LOH for the remaining p53 allele was designated for any batch of cells that showed greater than 50% signal loss of the WT p53 allele. Our results show a significantly increased amount of p53 LOH in the BALB/c strain compared to the C57BL/6 strains, agreeing with previous mammary tumor data (p=.018) **(Figure 2.1)**.

DNA double-strand break repair assay that distinguishes HRR from NHEJ

In order to address whether there are differences in DNA double-strand break repair between MEFs from BALB/c-*Trp53*$^{+/-}$ and C57BL/6-*Trp53*$^{+/-}$ mice, we utilized a plasmid dsb repair assay previously described (Akyuz et al., 2002c). This assay had the advantage of having quick turnaround in the amount of data it provided. Despite much effort and time, we were unable to attain consistent results using the assay (**Figure 2.2)**.

We also plotted the transfection rates for each experiment with the corresponding HR and NHEJ rates using C57BL/6-*Trp53*$^{+/-}$ MEFs **(Figure 2.3)**. The plotted regression lines demonstrate a relationship of HR and NHEJ rates with increased transfection rates.

BALB/c MEFs show an overall decrease in RAD51 accumulation at dsbs following irradiation

Localization of DNA repair proteins is an essential step in DNA double-strand break repair. The timely delivery of repair proteins to the site as well as their clearance dictates how fast the repair is completed. Much work has been done to understand the steps at which different proteins accumulate at the DNA double-strand break (Berkovich et al., 2007; Bekker-Jensen et al., 2006). Using fluorescent antibodies, the accumulation of these proteins at DNA double-strand breaks was quantified following DNA damage in MEFs from BALB/cMed-*Trp53+/-* and C57BL/6-*Trp53+/-* mice. We observed a robust time responsive curve following irradiation in both strains **(Figure 2.4)**. However, no significant differences in the percentage of cells with two or more γ-H2AX foci were observed between the strains. We chose to look at the accumulation of RAD51 to regions of DNA damage by measuring the percentage of cells that had co-localization of γ-H2AX and RAD51 in the nucleus. While no clear differences were observed at any given time point, BALB/cMed-*Trp53+/-* MEFs had an overall significant decrease in co-localization of γ-H2AX and RAD51 ($p<.05$). By 24 hours, the percentage of co-localization is back to base-line for both strains.

The BALB/c strain does not show cell growth sensitivity to DNA damage inducing agents

The ability of cells to halt the cell cycle to repair damaged DNA before replication is crucial in preventing genomic instability. Cells that have defects in DNA repair proteins can become sensitive to various DNA damaging agents. A common method to diagnose a patient with Fanconi Anemia is to test the sensitivity of their cells to Mitomycin C (MMC) (Sasaki and Tonomura, 1973). We tested the sensitivity of MEFs from both strains to survive in increasing concentrations of drugs causing DNA dsbs. Our results clearly show dose responsive sensitivities to both camptothecin and MMC **(Figure 2.5)**. However, no differences in sensitivity to either drug were observed between the strains. In addition, no sensitivity due to p53 haploinsufficiency was observed between the strains.

DNA-PKcs is not responsible for the increased DNA damage in BALB/c-Trp53+/- MEFs

The comet assay is a general DNA damage assay that has been utilized in many applications (Singh et al., 1988b). Previous studies have shown that the BALB/c strain is sensitive to irradiation (Ponnaiya et al., 1997c; Ullrich et al., 1996b; Yu et al., 2001a). To demonstrate this in MEFs, we induced DNA damage by various methods and analyzed the amount of damage for numerous timepoints. To confirm the validity of the comet assay in our hands, we first irradiated MEFs from both strains on a p53+/- background and analyzed the amount of damage after 5 minutes. This time point was chosen so as to look at overall DNA damage before any DNA repair occurs. Our results show little difference in DNA damage between the two strains using 5 Gy of irradiation **(Figure 2.6)**. Only at 20 Gy do we see significant DNA damage differences with BALB/c MEFs showing clear radiation sensitivity.

We next inquired if there was a difference in DNA repair between the two strains. We performed a time course experiment where we irradiated MEFs from both strains and fixed at various time points. Our results show an overall increase in post-IR DNA damage in BALB/c-*Trp53*$^{+/-}$ MEFs (ANOVA $p<.05$) **(Figure 2.7)**. NHEJ repair is completed rapidly within 1-2 h whereas homologous recombination repair can take up to 24 hours. We chose a time point of 15 hours to properly measure the amount of unrepaired damage that persists after completion of NHEJ repair and may reflect differences in HRR efficiency. Our results demonstrate a robust increase in IR-induced damage after 15 hours that was significantly higher in BALB/c MEFs compared to C57BL/6 MEFs **(Figure 2.8)**. Similar results were observed in wildtype MEFs where there was also a significant difference in damaged DNA in the control groups between the strains.

Camptothecin is a topoisomerase I inhibitor that causes DNA stress and eventually double-strand breaks. We tested the ability of this drug to induce DNA damage by adding it to the media of the cells for 15 hours before fixation. We see similar results as when we induce DNA damage using irradiation with BALB/c MEFs showing significantly more DNA damage than C57BL/6 MEFs after 15 hours **(Figure 2.9)**. Interestingly, this effect was not seen using p53 wildtype cells despite the control group showing significant differences.

While our choice of a timepoint of 15 hours most likely rules out the NHEJ pathway to explain DNA damage differences between the strains, we decided to address DNA-PK$_{cs}$ function directly. We accomplished this by adding a specific inhibitor to DNA-PK$_{cs}$ function, Vanillin, to the media during the 15 hour incubation post-irradiation. Our results show that we see similar differences in damaged DNA between the p53$^{+/-}$ MEFs suggesting this difference is not due to DNA-PK$_{cs}$ function **(Figure 2.10)**. Wildtype MEFs demonstrated no significant differences in the amount of DNA damage suggesting DNA-PK$_{cs}$ function may explain differences in DNA damage on a wildtype background.

The neutral comet assay is a variation that has been suggested to specifically select for DNA damage solely due to DNA double-strand breaks (Olive and Banath, 1993). We employed this method for various doses of irradiation and fixed and counted cells after 15 hours. This variation appeared much less robust compared to the alkaline version as we only started to see an effect at 40 Gy of IR **(Figure 2.11)**. We also measured tail length as an alternative method to quantify our results which has been reported when using this assay. We see a similar trend as with olive tail moment with BALB/c MEFs showing significantly more damage at 40 Gy IR.

Discussion

Proper repair of damaged DNA is essential for the prevention of mutagenesis and tumorigenesis. Defects in proteins involved in these repair pathways can increase the risk of cancer incidence. Mutations in members of the DNA double-strand break repair pathway are strongly linked to familial breast cancer risk (Ralhan et al., 2006). In addition, it now appears that some of these proteins, such as BRCA1, have duel roles in both HR and NHEJ (Zhong et al., 2002). Due to the importance of these pathways, much work has been done to identify new genes (Xia et al., 2006d) for which mutations may increase an individual's risk for breast cancer (Tischkowitz et al., 2007).

Our mouse model of the BALB/c strain on a *Trp53*$^{+/-}$ background has allowed us to identify potential new risk alleles in breast cancer (Blackburn et al., 2003a). The larger amount of p53 LOH observed in the BALB/c strain suggests defects in HRR which are likely related to this strain's increased susceptibility to mammary tumors. The goal for this study was to show clear differences in DNA repair between the two strains that could explain a difference in mammary tumor latency.

Mouse embryonic fibroblasts (MEFs) were the model we used to address these questions. These types of cells are easily isolated from the respective strains and are very simple to grow. Because they are primary cells, they have a finite lifespan before senescing. Before that, these cells tend to lose their remaining p53 allele within a few passages. We followed MEFs from both strains for up to 10 passages and measured the amount of p53 signal was present by PCR after each passage. We were interested in how soon MEFs from each strain lose their remaining p53 allele as well as relate this data to the amount of LOH seen in tumors from both strains of mice (Blackburn et al., 2004a). Our results suggest that the BALB/c strain loses its p53 allele much sooner than the C57BL/6 strain, agreeing with observations in tumors from the strains **(Figure 2.1)**. Overall, MEFs from both strains lose their remaining p53 allele within a few passages leading to an increased growth advantage. This is most likely due to selection pressure, however, the BALB/c MEFs have also been shown to be sensitive to DNA damage from 20% oxygen growing conditions (Parrinello et al., 2003b). Due to the similar differences in LOH for p53 in both MEFs and tumors from the two strains, we conclude that MEFs are an appropriate model to test hypotheses concerning DNA double-strand break repair differences.

GFP reactivation assays were used to distinguish differences in the amount of HRR and NHEJ between the strains (Akyuz et al., 2002b). This repair assay has the advantage of distinguishing between the two main pathways of DNA double-strand break repair by simply measuring GFP signal as an output in a very short waiting period. Unfortunately, we were unable to make firm conclusions using this assay. Results day to day were rarely consistent despite using the same batch of cells and procedures. Transfection rates between different cell batches and genotypes were measured by GFP signal. Transfection efficiency does not appear to be affected by MEF genotype or strain origin. Percentage of GFP positive cells from proper DNA double-strand break repair ranged between 0.1% and 5% after correcting for transfection efficiency. The transfection efficiencies also had a wide range of between 15% and 35%, leading to baseline corrections that led to a large amount of statistical error. Increases in transfection efficiency also seemed to correlate with increase repair **(Figure 2.3)**. With such a low percentage of positive cells, it is possible the amount of background noise could mask any significant differences in signals. Using gates in the FACS software helped control for any background noise from dead cells, however, the possibility of other background noise cannot be dismissed. The determining factor for the cell to use one DNA double-strand break repair pathway from another is largely dependent on which stage of the cell cycle it is in (Valerie and Povirk, 2003b). Synchronizing each cell line might have aided in decreasing the amount of variation seen in each assay by favoring one repair pathway from another. We performed our assays using baseline conditions, eg. no DNA damage. It is possible that a more robust increase in repair might have been observed if we had irradiated the cells prior to transfection with the repair constructs. The downside to this is of course decreased transfection efficiency and most likely cell viability due to both the irradiation and transfection stresses to the cell.

The difficulties using the DNA repair construct assays led us to more defined and broader assays to measure DNA repair. One of these assays is monitoring the accumulation of DNA repair proteins to sites of DNA damage by immunofluorescence. The advantages of this method include being able to visualize the specific repair protein and subsequently, certain step of DNA repair. Accumulation of a repair protein to the nucleus does not necessarily implicate DNA repair. However, the use of co-localization using different fluorescent anti-bodies to a repair protein and a marker for DNA damage allows greater specificity. The most common marker for a DNA dsb is phosphorylation of the histone H2AX (Furuta et al., 2003). Co-localization of any repair protein with γ-

H2AX in the nucleus is thus a measure of proper accumulation and proper DNA dsb repair.

We chose to measure the amount of co-localization of RAD51 to γ-H2AX following DNA damage in the form of irradiation. RAD51 is the recombinase responsible for strand invasion during HRR. Cells without RAD51 have been shown to have large amounts of genetic instability due to deficiencies in HRR (Deans et al., 2003). In addition, studies have shown that mutations in H2AX lead to deficiencies in HRR due to improper accumulation of repair proteins like RAD51 and BRCA2 (Celeste et al., 2002; Xie et al., 2004). We first counted the percentage of cells containing two or more γ-H2AX foci following irradiation. We also counted the percentage of cells that had two or more foci containing co-localization of RAD51 and γ-H2AX. Our results show a clear time-responsive curve of H2AX activation after 5 Gy of irradiation **(Figure 2.4)**. This suggests damage is being detected and then eventually repaired. No difference in γ-H2AX foci was detected between the strains. The antibody used detects only phosphorylated H2AX distinguishing inactive histone H2AX from the active version. However, because co-localization was not possible for γ-H2AX quantification, it is feasible any signal observed could be independent of DNA breaks. This could be due to non-specific antibody binding that could also explain the high basal signal (~50%) observed in both strains. The threshold used for quantification can also explain the high basal signal observed. In addition, the basal signal observed could also be explained by the amount of oxygen damage primary MEFs encounter in 20% oxygen incubators (Parrinello et al., 2003a). Co-localization of RAD51 with γ-H2AX showed a less robust curve following IR but enough of a curve to imply DNA repair. ANOVA demonstrated a significant effect of strain on co-localization of γ-H2AX and RAD51. The BALB/c strain showed significantly decreased co-localization following IR suggesting either repair was being accomplished more quickly or that there was a defect in the accumulation of RAD51 to DNA double-strand breaks. In addition, it is possible that the BALB/c strain was implementing a different pathway other than HRR in repair. However, the BALB/c strain is previously known to be defective in the NHEJ pathway making this possibility unlikely (Yu et al., 2001b). A defect in the accumulation of a repair protein suggests a possible defect in proper repair due to either an aberration in the protein itself or in the overall signaling process.

Cells that are defective in DNA repair are sensitive to DNA damaging drugs. This can be exploited in tumors defective in BRCA1 or BRCA2 by treating with a DNA damage inducing drug that can increase genomic instability in tumor cells while minimizing damage in repair efficient cells (McCabe et al., 2006). Sensitivity to DNA damaging drugs is an effective test to determine if cells isolated from a patient are defective in a repair pathway. Individuals suspected of having Fanconi Anemia will have isolated cells tested for their sensitivity to Mitomycin C (MMC) by viability. We were interested if BALB/c MEFs were sensitive to DNA damaging drugs, possibly implicating defects in DNA repair. We performed dose response curves using two common chemotherapeutics, MMC and Camptothecin. Mitomycin C (MMC) is an anti-biotic that inhibits DNA synthesis by covalently cross-linking complementary strands of DNA (Yun et al., 2005). This stalls DNA replication by preventing the separation of the complementary strand. Camptothecin is another DNA damaging agent that exerts its effect by indirectly causing DNA double-strand breaks. This agent is an inhibitor of the

DNA unwinding enzyme topoisomerase. Inhibition of topoisomerase can lead to physical stress of the DNA during replication resulting in DNA double-strand breaks.

We observed dose response curves from all strains using both drugs **(Figure 2.5)**. No differences in drug sensitivity were observed between both strains. Interestingly, neither strain with a p53 WT genotype demonstrated any sensitivity differences between each other as well as between MEFs with a p53$^{+/-}$ genotype. These results were surprising due to our previous experiments establishing the BALB/c strain as having a defect in RAD51 localization following IR. Any defect in DNA repair should makes cells sensitive to DNA damaging agents. It is possible that the DNA repair defect may be so minor that it may not effect a cell's sensitivity to a DNA damaging drug but can still cause genomic instability over time. This is true for many carcinogens causing mutations that can increase risk for tumorigenesis. However, the drugs used in this study cause replication fork dsbs by either cross-linking the DNA (MMC) or increasing DNA tension (Camptothecin inhibiting topoisomerase) during DNA replication. The fact that we see a robust viability curve suggests the drugs are working properly. It was also very interesting that the dose of p53 in the cell does not appear to effect drug sensitivity. This was somewhat unexpected as p53 appears to be haploinsufficient as a tumor suppressor and in carcinogen-induced LOH (Venkatachalam et al., 2001).

Damaged DNA that is not repaired efficiently or in a timely matter have the potential to become mutations when the genome is replicated during mitosis. The proper repair of damaged DNA is essential for the growth and continued proliferation of a cell. Single Cell Gel Electrophoresis (Comet Assay) is a relatively simple and sensitive assay to measure DNA damage at the single cell level (Singh et al., 1988a). This assay allows the user to detect the amount of unrepaired DNA damage over time by the way the DNA migrates through an agarose matrix. Damaged DNA will run slower as breaks in the DNA lead to some unraveling and overall slower migration. This slower migration of damaged DNA forms a “comet tail” behind the migrating nucleus which can then be measured and quantified.

We first investigated if there were any IR sensitivity differences between the two strains before DNA repair occurred. Our results showed no significant differences in the amount of DNA damage after 5 minutes of 5 Gy of IR **(Figure 2.6)**. However, using 20 Gy IR clearly shows that BALB/c MEFs acquire more damage than the C57BL/6 strain. Because these cells were fixed and processed only 5 minutes following IR, any damage observed is most likely not due to DNA repair differences. This increased initial damage in the BALB/c strain could be explained by the effect of IR on Reactive Oxidative Species (ROS). It is well established that IR will increase the amount of ROS due to the high energy waves disrupting members of the electron transport chain yielding increased free radicals (Halliwell and Gutteridge, 1984a). These free radicals are particularly damaging to DNA in addition to proteins and other cellular components. Cells that already have aberrations in the electron transport chain could be predisposed to increased IR-induced DNA damage due to the increased amount of ROS (ykin-Burns et al., 2010).

In order to assess the DNA repair difference, we performed a time course experiment after 5 Gy of IR. We saw significantly more damage in the BALB/c strain (ANOVA $p<.05$) compared to the C57BL/6 strain **(Figure 2.7)**. This may reflect differences in NHEJ as this pathway occurs almost immediately following DNA damage compared to HRR which usually finishes within 24 hours. We next chose a time point of

15 hours post-IR to determine if we could detect any differences in HRR between the strains. Our results clearly show BALB/c MEFs having significantly more damage after 15 hours post-IR compared to C57BL/6 MEFs **(Figure 2.8)**. This data suggests the BALB/c strain has a defect in HRR because of the increased DNA damage. Because we picked 5 Gy of IR, it is unlikely the BALB/c strain has more initial damage that needs to be repaired due to similar amounts of damage in both strains after 5 minutes **(Figure 2.6)**. In addition, choosing a 15 hour time point all but eliminates NHEJ as an explanation due to this pathway being completed within 2 hours post-IR. It is still possible that any leftover damage not repaired by NHEJ in the BALB/c strain might have carried over to the 15h timepoint.

We were interested if this increased damage observed in the BALB/c strain was exclusive to IR or was similar with other DNA damaging agents. We chose to incubate MEFs from both strains with the topoisomerase inhibitor Camptothecin for 15 hours. Our results show significantly more damage in the BALB/c strain similar to our IR results **(Figure 2.9)**. Thus, the BALB/c strain appears to be sensitive to DNA damaging agents.

The BALB/c strain is well known to be sensitive to IR due to a mutation in the NHEJ pathway component DNA-PK$_{cs}$. We decided to address whether this defect in DNA-PK$_{cs}$ function could explain the increased damage we observed in the BALB/c strain. This was accomplished by incubating the MEFs in growth media supplemented with Vanillin. Vanillin has been demonstrated to be a specific inhibitor of DNA-PK$_{cs}$ (Durant and Karran, 2003). Thus, if this protein is responsible for the increased DNA damage in the BALB/c strain, incubation with Vanillin should bring levels of damage in the C57BL/6 strains similar to the BALB/c strain. Our results suggest that DNA-PK$_{cs}$ is not completely responsible for the increased damage post-IR observed in the BALB/c strain as inhibiting this protein does not affect the amount of damage observed at the 15 hour timepoint **(Figure 2.10)**. In contrast, wildtype p53 MEFs from both strains did not show any significant differences in damage after treatment with Vanillin. This was surprising and not easily explained. Obviously, p53 is having an effect and perhaps DNA-PK$_{cs}$ function is inhibited in a p53$^{+/-}$ background. This is not completely unforseen as both of these proteins have been known to interact (Woo et al., 1998). While we assume Vanillin is effecting DNA-PK$_{cs}$ function, we could not demonstrate this directly. Inhibiting DNA-PK$_{cs}$ function by siRNA treatment in the C57BL/6 strain would be an appropriate alternative experiment to test this hypothesis.

The neutral comet assay is a variation of the comet assay that supposedly selects for only dsbs. It involves running the agarose embedded cells in a neutral pH solution instead of an alkaline solution. The other difference is the comets are usually quantified by measuring the tail length instead of the olive tail moment in the alkaline assay. Our results suggest this assay is not as robust as the alkaline assay and we only see significant differences in damage at 40 Gy IR **(Figure 2.11)**. The olive tail moment quantification was also not very encouraging.

Overall, we have demonstrated differences in DNA repair between the strains using multiple methods. We clearly show that the BALB/c strain has a defect in DNA repair due to the increased damage present over time. In addition, this increased damage does not appear to be specific to IR as similar differences in DNA damage were observed between the strains following Camptothecin treatment. This increased damage in the

BALB/c strain does not appear to be due to a well known defect in the NHEJ component DNA-PK$_{cs}$. Immunofluorescence was used to ascertain at which step of repair is perturbed by showing that the BALB/c strain has a defect in the localization of RAD51 at dsbs following IR.

Figure 2.1 Differences in loss of heterozygosity in *Trp53*$^{+/-}$ MEFs from BALB/c and C57BL/6J mice. Regression analysis demonstrated that slopes of the lines were significantly different (F-test, p=.018)

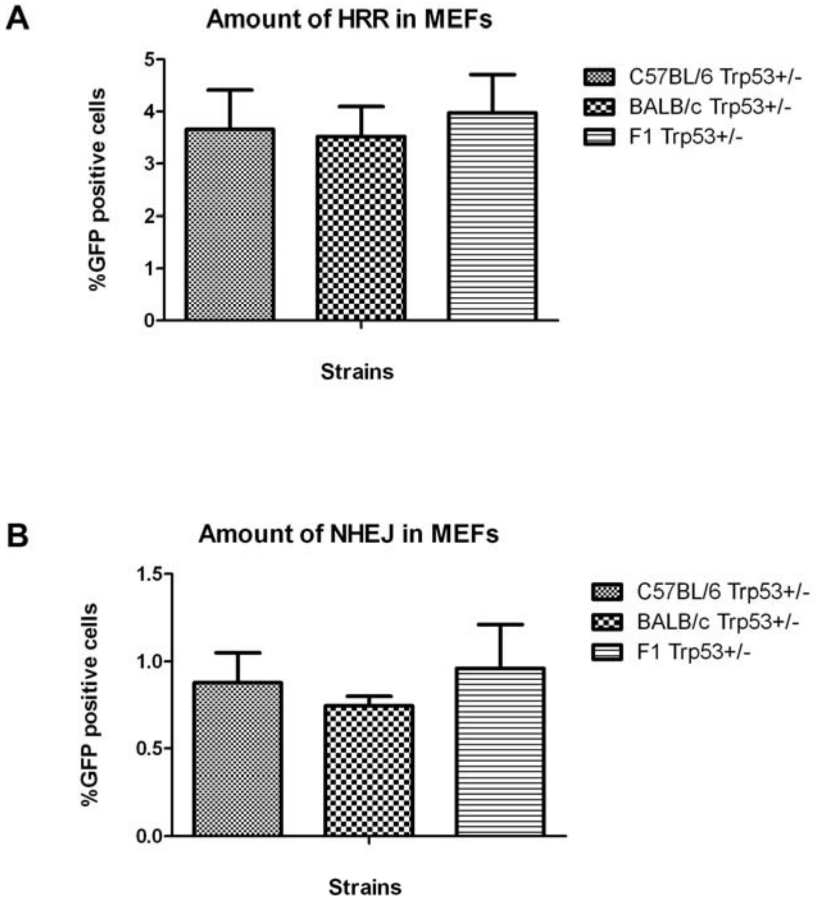


Figure 2.2 DNA double-strand break repair assay. **(A)** Amount of relative HRR in MEFs of different strains. **(B)** Same as above, except measuring amount of NHEJ in MEFs using an alternative construct. Percentage of GFP positive cells, indicative of proper repair, were counted by FACS analysis and made relative to transfection efficiency. Data plotted as 3 independent experiments with an n=3 for each experiment.

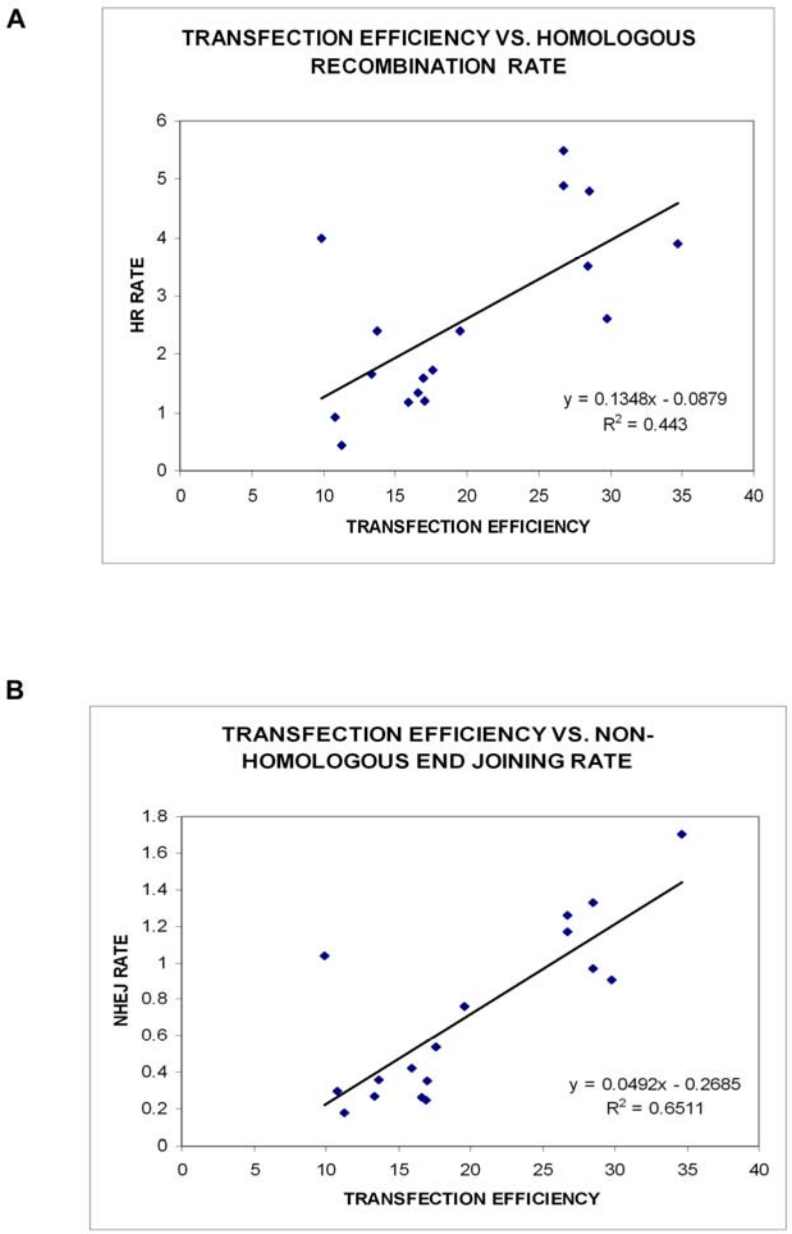


Figure 2.3 Effect of transfection rate on the amount of repair using the Repair assay **(A)** Individual experiments were plotted based on the calculated HR rate and the accompanying transfection efficiency using C57BL/6-*Trp53*$^{+/-}$ MEFs **(B)** Same as above, except NHEJ rates are plotted with the accompanying transfection efficiency

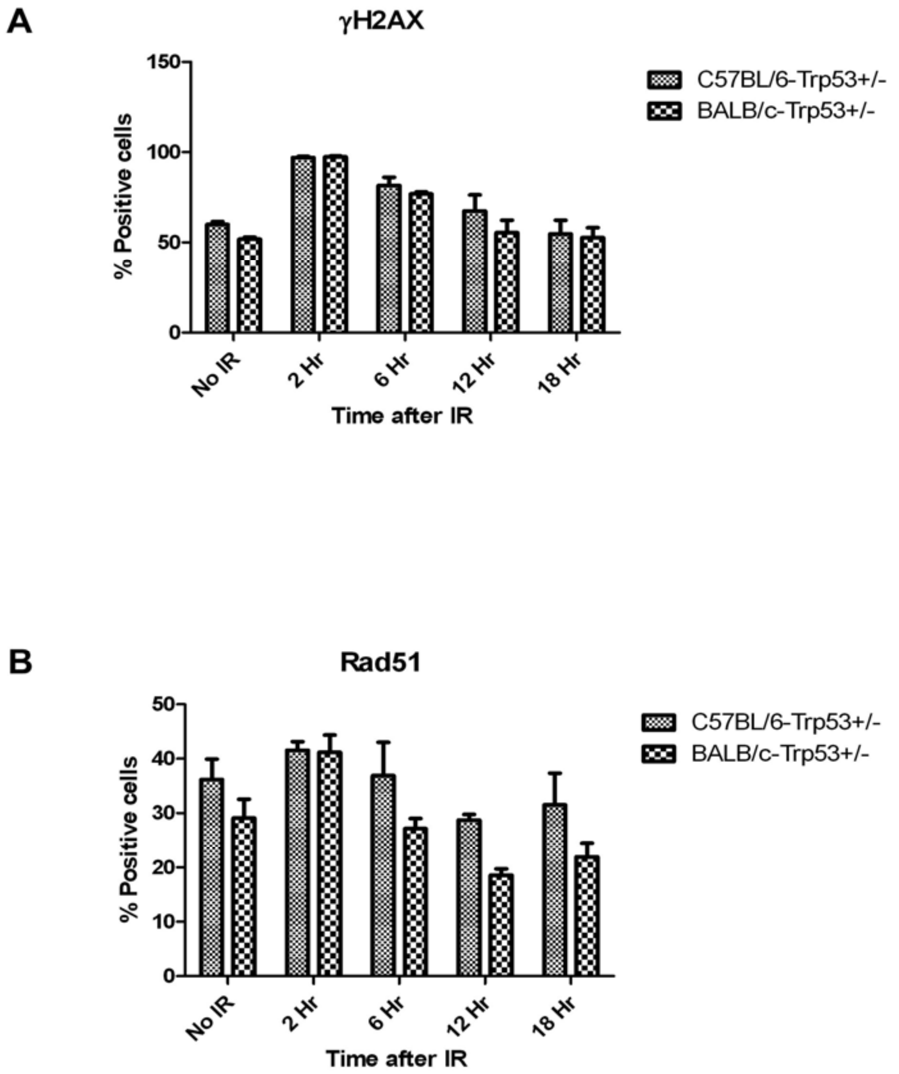


Figure 2.4 Immunofluorescence of DNA repair proteins **(A)** The percentage of positive cells for γ-H2AX immunofluorescence were quantified following 2.5 Gy IR. Values are expressed as the mean percentage of cells that have two or more foci ± standard error. Each bar represents at least three independent experiments. **(B)** The percentage of positive cells with co-localization of RAD51 with γ-H2AX. Values are expressed as the mean percentage of cells that have two or more foci ± standard error. Each bar represents at least three independent experiments. ANOVA *$p<.05$

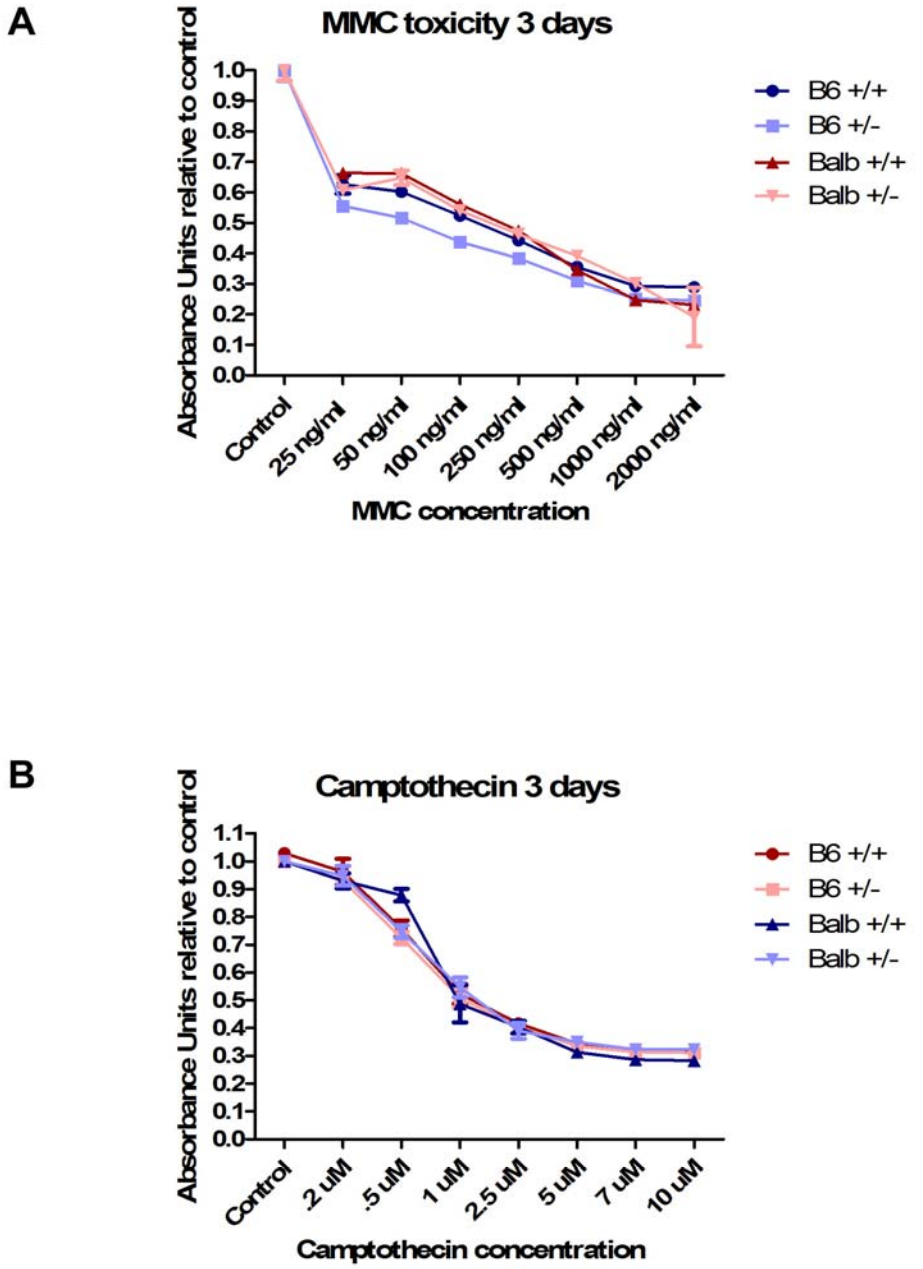


Figure 2.5 MTS assays measuring cell proliferation **(A)** Camptothecin was added at the appropriate dose and cells were incubated for three days. MTS reagent was added to each well and quantified. Data points are plotted as mean absorbance units ± standard error in triplicate. **(B)** Same procedure as above, except MMC was added to each well for the appropriate dose. Data points are plotted as mean absorbance units ± standard error in triplicate.

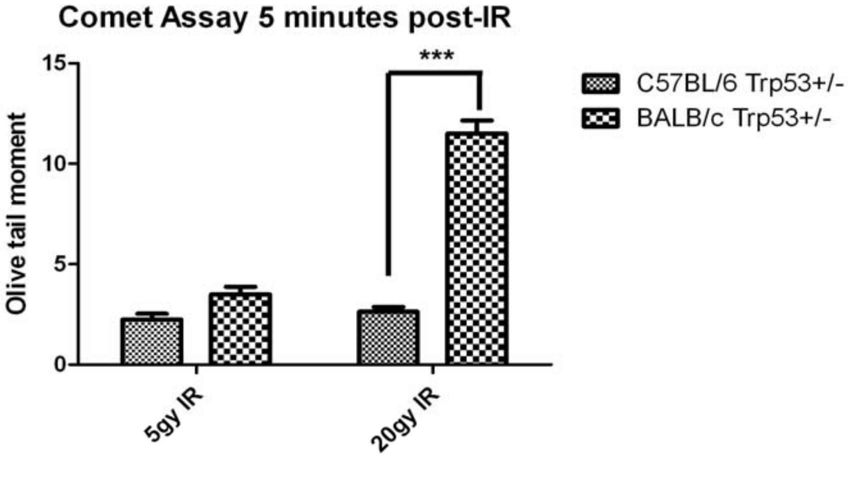


Figure 2.6 Initial IR-induced DNA damage before DNA repair. Each bar represents at least three independent experiments. Students t-test used, ***p<.001

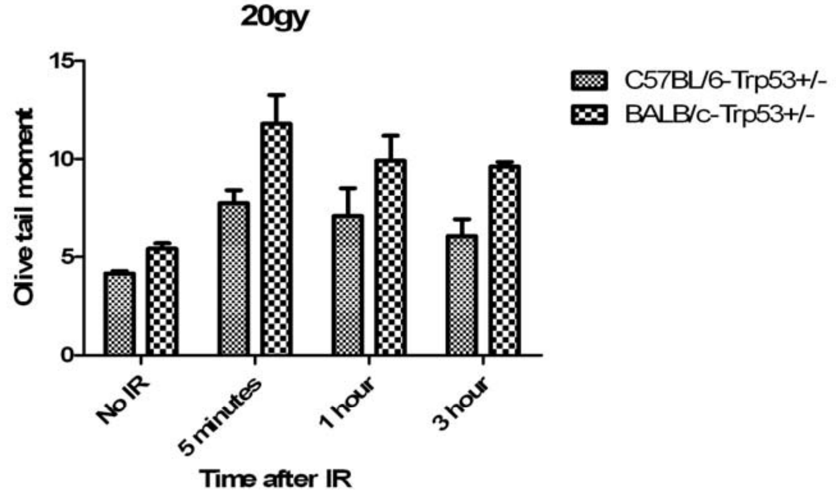


Figure 2.7 Timecourse comet assay after 20 Gy of IR. Each bar represents at least three independent experiments. ANOVA used, p<.05 significance was found.

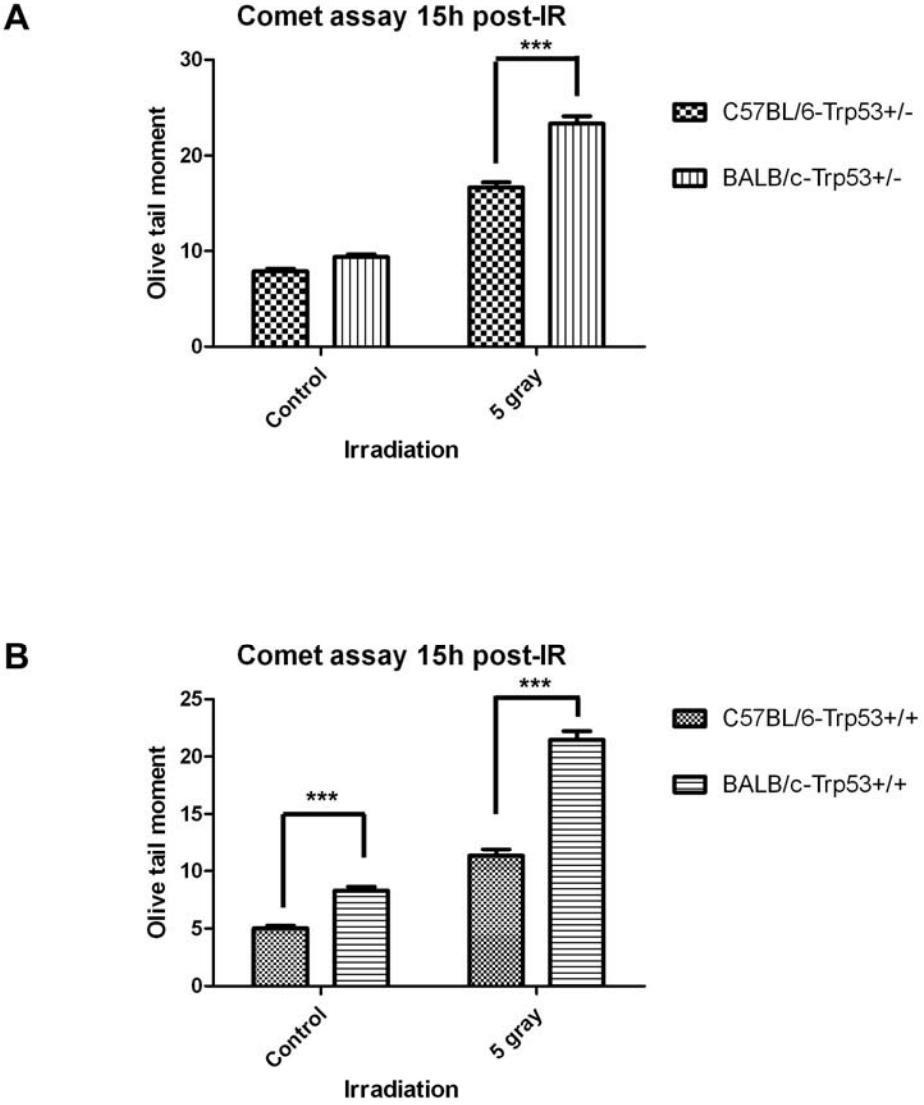


Figure 2.8 Amount of residual DNA damage 15 hours post-IR **(A)** MEFs on a p53$^{+/-}$ background were quantified. Each bar represents at least three independent experiments. Students T-test used, ***p<.001 significance was found. **(B)** MEFs on a p53$^{+/+}$ background were quantified. Each bar represents at least three independent experiments. Students T-test used, ***p<.001 significance was found.

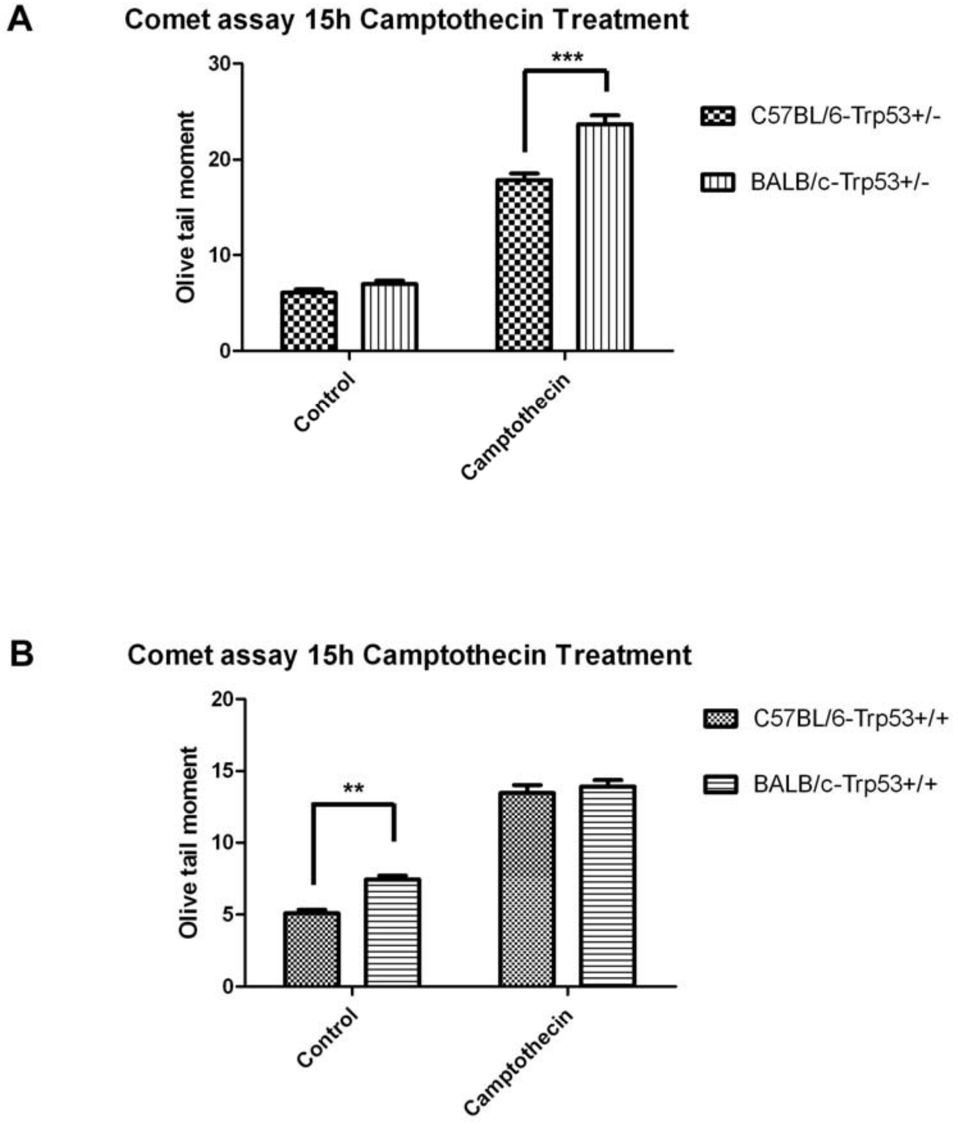
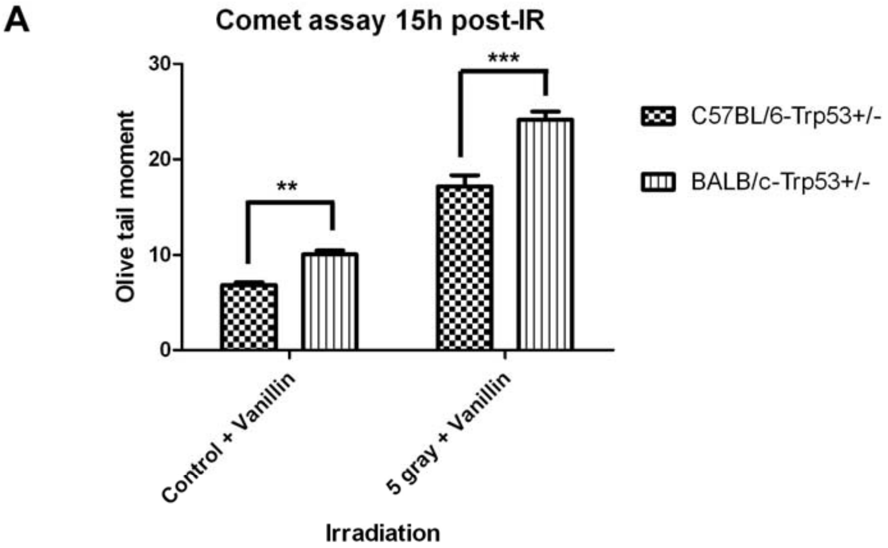


Figure 2.9 Amount of residual DNA damage in MEFs after 15 hours incubation with Camptothecin 5μM **(A)** MEFs on a p53$^{+/-}$ background were quantified. Each bar represents at least three independent experiments. Students T-test used, ***p<.001 significance was found in the treated group. **(B)** MEFs on a p53$^{+/+}$ background were quantified. Each bar represents at least three independent experiments. Students T-test used, **p<.01 significance was found in the control group.



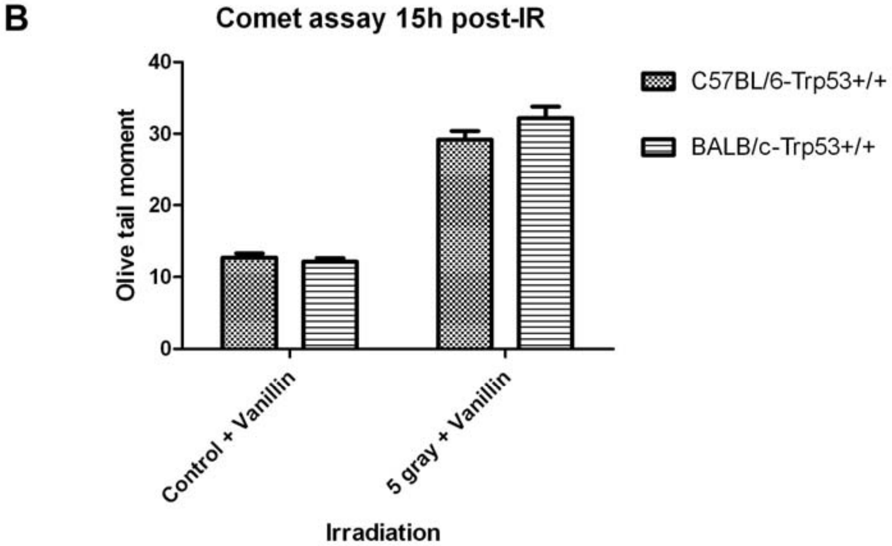


Figure 2.10 Effect of DNA-PK$_{cs}$ inhibitor on IR-induced dsb repair **(A)** MEFs on a p53$^{+/-}$ background were quantified. Each bar represents at least three independent experiments. Students T-test used, **p<.01 significance was found in the control group and ***p<.001 in the treated group. **(B)** MEFs on a p53$^{+/+}$ background were quantified. Each bar represents at least three independent experiments. Students T-test used, no significance.

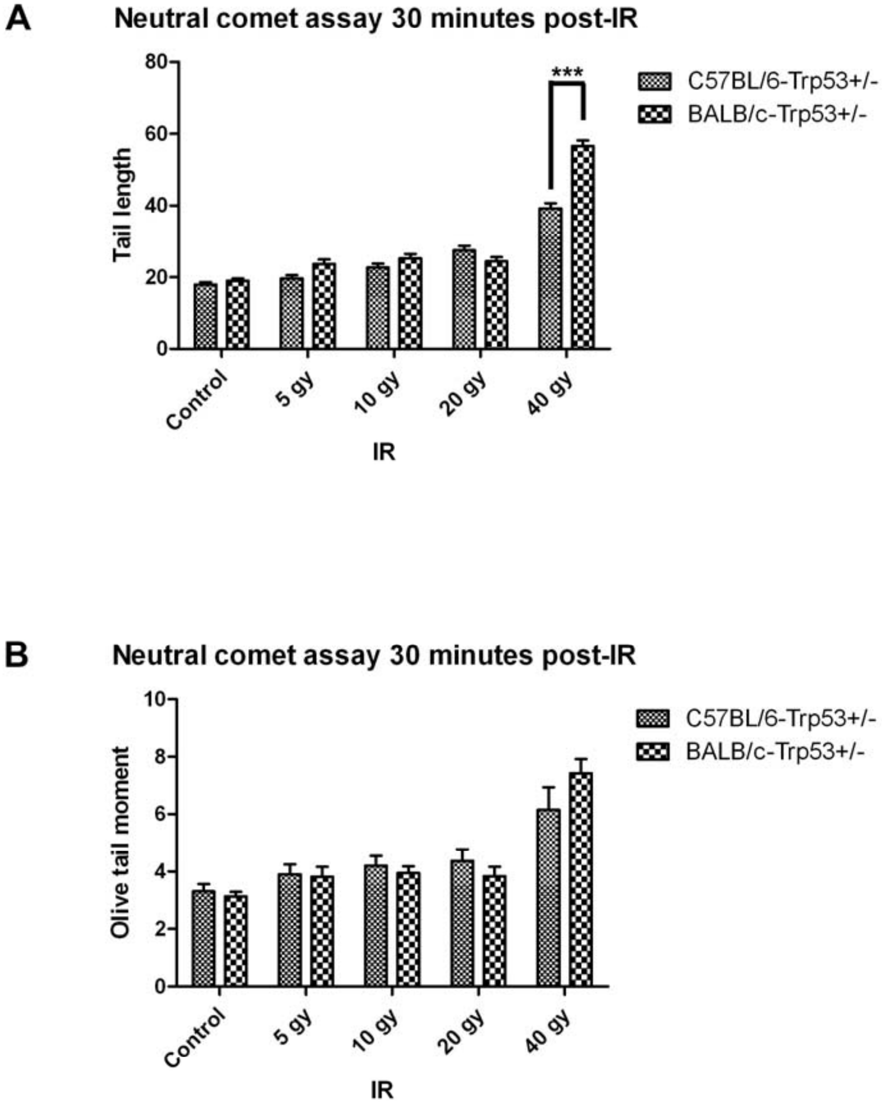


Figure 2.11 Dose response curve for Neutral Comet Assay **(A)** MEFs on a p53$^{+/-}$ background were quantified by tail length. Each bar represents at least three independent experiments. Students T-test used, ***p<.001 significance was found in the "40Gy" group **(B)** MEFs on a p53$^{+/-}$ background were quantified by olive tail moment. Each bar represents at least three independent experiments. Students T-test used, no significance.

CHAPTER 3

ANALYZING THE ROLE OF PALB2 IN MAMMARY TUMOR SUSCEPTIBILITY IN THE BALB/C TRP53$^{+/-}$ STRAIN

Introduction

Inheriting mutations in the most commonly known breast cancer risk alleles, *BRCA1* and *BRCA2*, leads to a 80% and 60% risk of acquiring the disease in an individual's lifetime (Narod, 2002). While BRCA1 appears to have many functions in the cell, BRCA2 appears to be primarily involved in the DNA double-strand break repair pathway (Abaji et al., 2005). This suggests the DNA double-strand break repair pathway as being an essential component of the cell to prevent genomic instability and thus tumorigenesis. BRCA2 has been shown to work as a complex with a number of other proteins to perform dsb repair. One member was identified bound to a complex of BRCA2 and a number of other proteins previously identified (Xia et al., 2006c). This particular member was subsequently named Partner and localizer of BRCA2 (PALB2). It was demonstrated that PALB2 is necessary for BRCA2 to localize to DNA double-strand breaks and that when PALB2 is knocked down by siRNA, HRR function is diminished. PALB2 appears to bind to D-loop DNA and help stimulate strand invasion through RAD51 (Buisson et al., 2010). Complete loss of PALB2 was shown to result in a new subtype (N) of Fanconi Anemia (FA) in an individual (Xia et al., 2007b). Cells from this patient showed sensitivity to DNA cross-linkers such as MMC that is a hallmark of FA cells.

PALB2 is an 1,186 amino acid protein that has an N-terminal coiled-coil region and C-terminal WD-repeats (Xia et al., 2006b). The C-terminal region was later identified as where the extreme N-terminal region of BRCA2 binds to (Oliver et al., 2009). PALB2 has been shown by multiple studies that to bind both BRCA1 and BRCA2 in a complex by way of its N-terminal domain binding BRCA1 and its C-terminal domain binding BRCA2 (Zhang et al., 2009b; Zhang et al., 2009a; Sy et al., 2009). Mutations in this region abrogate the binding of PALB2 to BRCA2 and lead to diminished HRR function. Interestingly, there were 3 mutations in the N-terminal region of *BRCA2* from breast cancer patients that disrupted PALB2 to binding highlighting the significance of this gene. Recent work has identified a number of mutations and truncations in *PALB2* in breast cancer families. An initial study identified 10 familial breast cancer patients that had monoallelic truncating *PALB2* mutations (Rahman et al., 2007a). These mutations conferred a 2.3-fold increased risk of breast cancer. A frameshift mutation, 1592delT, was seen at a higher frequency in Finnish breast cancer patients compared to the control population (Erkko et al., 2007). Numerous other studies have identified other mutations of *PALB2* in breast cancer patients (Tischkowitz and Xia, 2010). All of these studies demonstrate the importance of PALB2 in complex with BRCA1 and BRCA2 in performing HRR. Individuals with mutations in any one of these genes can have an increased risk of genomic instability and breast cancer.

The *Palb2* gene in the mouse is located at 129.25 Mb on chromosome 7 (ensemble v.60). This location is almost directly under the prominent second peak in the mapped *SuprMam1* region. With its clear role in DNA double-strand break repair and being a breast cancer risk allele, this gene was chosen as an obvious candidate to explain spontaneous mammary tumor differences between C57BL/6 and BALB/c mice on a $p53^{+/-}$ background. In addition, our work demonstrating decreased RAD51 localization to

DNA double-strand breaks in the BALB/c strain implicates PALB2 by its association to RAD51 in a complex with BRCA1 and BRCA2 **(Figure 1.2)**. To explore this, we sought to examine expression differences of this gene in the mammary gland of both strains. In addition, we also attempted to identify sequence differences in the form of SNPs between the two strains. This was accomplished in two ways. First, we searched for SNPs using an online database. Next, we sequenced the entire coding region of *Palb2* between the two strains of mice. Finally, we generated an expression vector of *Palb2*, with and without a GFP and IRES section.

Methods

QPCR expression of Palb2:

The fourth mammary gland was removed from mice 8-10 weeks of age and stored at -80^{o}C. Total RNA was isolated using Trizol solution according to protocol. Isolated RNA was reverse transcribed using Stratagene AffinityScript cDNA kit and analyzed for gene expression using Stratagene Brilliant II SYBR Green kit. Three animals were used for each strain and normalized to Actin expression. Primers for *Palb2* expression were 5'-GACCTGCTGGAAAGGCCACCAC-3' for the forward primer and 5'-CAGTTTTTCCGAGCAGGACTTCAAT-3' for the reverse primer. Actin primers were 5'-CTAAGGCCAACCGTGAAAAG-3' for the forward primer and 5'-ACCAGAGGCATACAGGGACA-3' for the reverse primer. Fold change was established by dividing mean BALB/c expression to mean C57BL/6 expression. Statistical significance was determined by using Student's T-test.

Generation of primary mammary epithelial cells:

Primary mammary epithelial cells were dissociated from isolate mammary glands using the protocol associated with the product EpiCult-B medium (Stemcell Technologies). Briefly, the fourth mammary gland was removed from mice 8-10 weeks of age and minced using a razor blade. The minced tissue was then incubated with a digestion medium containing collagenase type 3 (Worthington), hyaluronidase (Sigma), FBS (Gibco) and antibiotics for 1-3 hours. The tissue was then spun down by centrifugation and washed multiple times with Hanks buffered solution (Gibco) containing 2% FBS. After being pelleted, the tissue mixture was then resuspended in trypsin-EDTA for 1-2 min., followed by a wash of Hanks buffered solution with FBS. Following centrifugation, the pellet was resuspended in 5mg/ml of Dispase (Gibco) for 1 minute before being washed by Hanks buffered solution and pelleted by centrifugation. The pellet was resuspended in Complete Epicult-B Medium supplemented with 10 ng/mL mouse Epidermal Growth Factor (mEGF) (Sigma), 10 ng/mL recombinant human Fibroblast Growth Factor (rh bFGF) (Stemcell Technologies), 5% FBS (Gibco), 4 µg/mL Heparin (Stemcell Technologies), 1X Pen/Strep (Gibco) and Gentamycin (Gibco) and plated in a 6-well plate. Two days later, medium with floating cells and debris was removed and any plated cells were incubated with EpiCult-B medium without FBS. Cells continued to grow in this media until wells were 70% confluent at which point RNA was isolated.

SNP identification:

The database located at http://www.genenetwork.org/webqtl/snpBrowser.py was used to identify any SNP differences in *Palb2* between the C57BL/6 and BALB/c strains.

Palb2 mRNA sequencing:

RNA was isolated from the fourth inguinal mammary gland of BALB/c and C57BL/6 mice using Trizol. Reverse transcription was performed by Stratagene's cDNA synthesis kit (Stratagene). Because the coding region of *Palb2* is 3747 bp, we decided to amplify this region in two sections. The first section was amplified using the forward primer 5'-AACCTGTGTGGCTCGGCAGGAACATAGT-3' and the reverse primer 5'-CCAGTGTGGAGGTGCGGGCTGATT-3'. The second section was amplified by using the primers 5'- TGCAGAATACTATGTTAGAACAACCCGTCGTAT-3' and 5'-GTCACAAGCAGGGCGATCTGCAGTTTC-3'. After each subsequent PCR, the amplified product was subcloned into a blunt end pCR-Blunt-II-TOPO vector (Invitrogen) and transformed into *E.coli* GC-10 competent bacteria. After confirmation for colonies with the appropriate vector insertion, the plasmids were sent out for sequencing. *Palb2* was sequenced using two primers that bound to the TOPO vector (T7 and M13R) and flanked the coding region. In addition, an internal primer was used (5'-CTTCATCCATAGTGCTTTTC-3') to sequence toward the 3' end. Analysis of the sequencing data was performed by using Vector NTI (Invitrogen) software.

Construction of a Palb2 expression vector:

RNA was isolated from the fourth inguinal mammary gland of BALB/c and C57BL/6 mice using Trizol. Reverse transcription was performed by Stratagene's cDNA synthesis kit (Stratagene). *Palb2* coding sequence was amplified using two primers (5'-AACCTGTGTGGCTCGGCAGGAACATAGT-3' and 5'-TCACTGGTTATGTACAGCTGTAATAGCAAATGTGC-3') before being cloned into a TOPO vector and transformed into TOP10 cells. After confirmation of appropriate insertion by restriction enzyme cutting and DNA sequencing, the *Palb2* insert was cut out using the endonucleases SpeI and NotI. The SpeI end of the *Palb2* insertion was then blunt ended by T4 polymerase (Roche) and ligated into the EcoRV and NotI sites of the pIRES-hrGFP II construct. The GFP-IRES (4262-5920 bp) portion of the pIRES-GFP-*Palb2* plasmid was removed by cutting the construct with XbaI and NotI. The cut sites for the construct minus the GFP-IRES portion (Stratagene) was then filled in for blunt-end ligation by T4 polymaerase (New England BioLabs). Gel purification was then performed and the construct minus the GFP-IRES portion was ligated together and transformed into GC10 cells. Restriction enzyme cutting and DNA sequencing was used to screen for positive clones that contained the pIRES-ΔGFP-ΔIRES-*Palb* construct.

Results

No difference in Palb2 expression observed in the mammary gland between both strains

Sequencing of genomes of different mouse strains has produced a wealth of data available in the public domain. Using a SNP database developed by members at the University of Tennessee, we examined SNPs within the promoter and transcribed region of *Palb2*. One polymorphic intronic SNP for *Palb2* was identified **(Figure 3.2)**. This SNP was located in intron 7 of *Palb2* which is unlikely to affect the protein’s function but could alter levels of mRNA. No differing SNPs were identified in the promoter region of *Palb2* between the strains.

Palb2 expression was measured by RT-QPCR in the mammary glands of both BALB/c and C57BL/6J strains **(Figure 3.1)**. No difference in expression was observed for *Palb2* between the strains using RNA isolated from whole mammary glands. Because *Palb2* is involved in the DNA double-strand break repair pathway, stimulation of the

DNA damage response may increase the expression of this gene. Thus, RNA was isolated from mammary glands from both strains 6h following 5 Gy of IR. No difference in *Palb2* expression was seen in mammary glands from both strains post DNA damage stimulation. Epithelial cells make up approximately 30% of the mass of the mammary gland. Thus, any signals from these cells may be masked by signals from the surrounding stroma and adipose tissue. Primary mammary epithelial cells were isolated from mammary glands of both strains. At approximately 70% confluency, RNA was isolated. No difference in *Palb2* was seen in primary mammary epithelial cells from these strains.

No sequence differences in Palb2 mRNA was observed between the strains

Despite the amount of information available in the public domain, not all of this data is complete. Sequence variations can sometimes be difficult to detect in large-scale sequencing projects due to the overwhelming amount of data and inherent error that accompanies these studies. Insertions and deletions are especially under-represented. With this in mind, the entire protein coding region of the *Palb2* mRNA was cloned and sequenced for both strains. We used primers for sequencing that overlapped allowing redundant sequencing for any given nucleotide and demonstrated that the sequences were identical for both strains **(Figure 3.3)**.

Creating an expression vector for *Palb2*

Little work has been done identifying the function and expression of *Palb2* in mice compared to humans (Xia et al., 2006a). To help in the production of these experiments, we proceeded to clone *Palb2* into an expression vector under the control of a CMV promoter **(Figure 3.4)**. The construct also has an IRES site and GFP signal. Another construct was made exactly the same but minus the IRES and GFP for use in Dr. Lisa Wiesmüller's DNA repair assays **(Figure 3.5)** (Akyuz et al., 2002a). Transfection of the vector into MEFs increased the reactivation of GFP-reporters in C57BL/6J MEFs (personal communication, L. Wiesmüller).

Discussion

The amount of familial breast cancer cases due to inherited mutations in genes involved in DNA repair highlights this pathway as critical in the prevention of breast tumorigenesis. Much work has been done over the years to identify new potential breast cancer risk alleles since the most common high penetrant alleles only make up of approximately 20% familial risk (Ponder, 2001a).

Palb2 was chosen as a viable candidate to explain spontaneous mammary tumors in the BALB/c strand for a number reasons. First, the gene for *Palb2* in mouse was localized directly under the second prominent peak in the *SuprMam1* interval. Second, *Palb2* is considered a low penetrance modifier due to confering a 2.3 fold risk for breast cancer which is precisely the relative risk associated with the *SuprMam1* region in the BALB/c strain.

We were interested to determine if there were any SNP differences for *Palb2* between the strains. Using a public domain database, we identified one SNP between the two strains. Unfortunately, this SNP is localized in the intron of the gene where it is most likely not affecting the protein. This intron is unlikely to affect splicing as it is localized too far away from the exon-intron borders. In addition, the database takes into account SNPs that are possible splice site variants.

To verify the results from the database, we proceeded to sequence the coding region of *Palb2* using RNA isolated from mammary glands of both strains. Using a strategy of overlapping sequencing results, we did not identify any sequence differences between the strains.

We also looked at expression of this gene in whole mammary gland, irradiated mammary gland and primary mammary epithelial cells. We did not observe a significant difference in expression of this gene between the strains in any of the three sources. This includes primary mammary epithelial cells which were used in case any signal was masked by stromal or adipose cells in the whole mammary gland. Because *Palb2* is active in the DNA damage response, we supposed that irradiating the mammary gland might boost the expression of this gene. Though unlikely, it is possible that there are differences in *Palb2* expression between the strains that are too subtle to be detected by QPCR alone.

These results suggest there are no differences in *Palb2* expression or protein function between the strains. However, this does not fully rule out *Palb2* as a candidate gene. We had thought about assaying PALB2 function by observing BRCA2 localization to DNA double-strand breaks following DNA damage (Xia et al., 2006e). However, antibodies for mouse BRCA2 are very unreliable and immunofluorescence for BRCA2 requires very robust antibodies. It is also possible an element within the *SuprMam1* region may be affecting Palb2 function post-translationally. In fact, using simple protein modeling software (**Figure 3.6**), we identified Polo-like Kinase 1 (*Plk1*) as a potential binding partner of *Palb2*. *Plk1*, like *Palb2*, is localized within the *SuprMam1* region, where it could be modifying PALB2 function post-translationally. Therefore, further assays of PALB2 activity are needed.

Searching for additional DNA repair genes within the *SuprMam1* interval resulted in no other candidates besides *Palb2*. This suggests genes in other pathways besides DNA repair may be responsible for increased tumor latency in the BALB/c strain. It is possible there are genes within this interval with undefined roles in DNA repair yet to be identified. Since *Palb2* was one of these genes prior to the 2006 study, this remains a reasonable possibility.

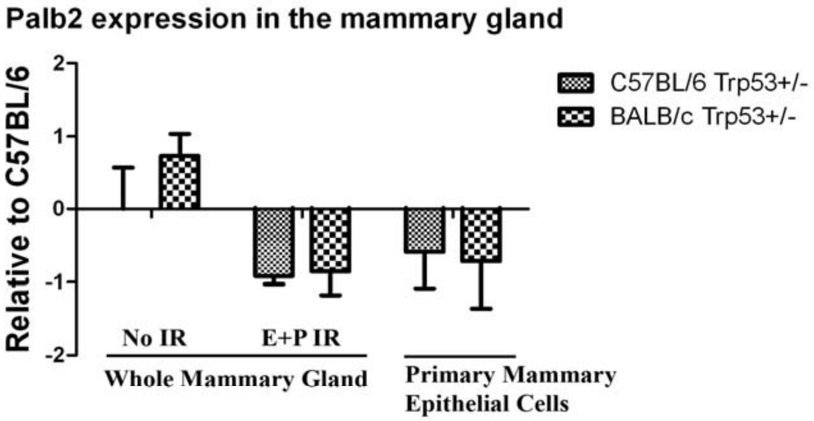


Figure 3.1 *Palb2* expression from whole mammary gland RNA is shown relative to C57BL/6 expression and normalized to Actin expression. Expression of *Palb2* is also shown for mammary glands 6 hours post-IR 5 Gy. Finally, expression of *Palb2* was ascertained from primary epithelial cells from both strains of mice. No significant expression differences were observed.

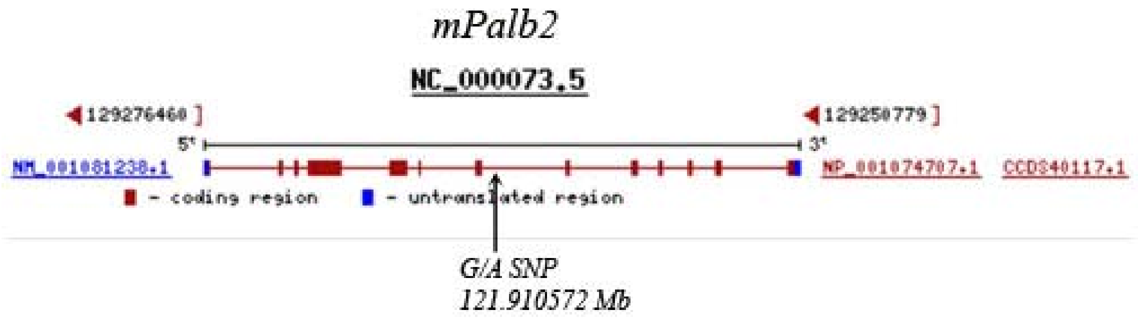
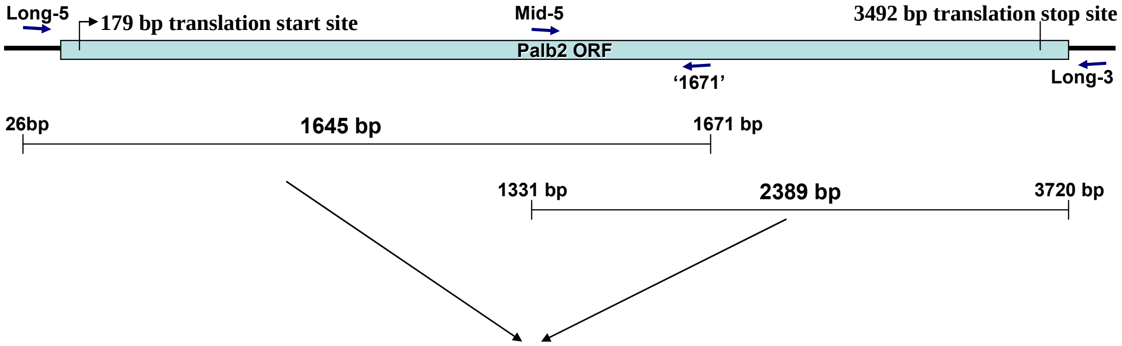


Figure 3.2 Diagram of the mouse *Palb2* gene showing the location of the one SNP identified that differs between the strains (G=C57BL/6, A=BALB/c). No SNP differences were observed between the strains in the *Palb2* promoter region.



PCR pieces cloned into pCR TOPO plasmids and sent for sequencing

Cloning Primers

Long-5:

5' AACCTGTGTGGCTCGGCAGGAACATAGT 3'

Mid5:

5' TGCAGAATACTATGTTAGAACAACCCGTCGTAT 3'

'1671':

5' CCAGTGTGGAGGTGCGGGCTGATT 3'

Long-3:

5' TCACTGGTTATGTACAGCTGTAATAGCAAATGTCG3'

Sequencing Primers

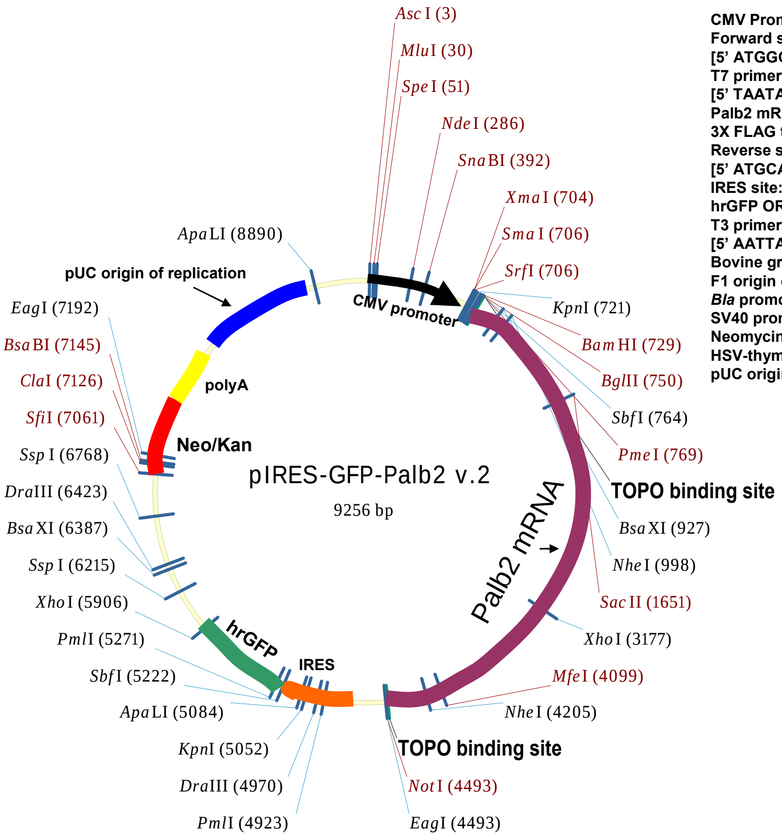
M-13:

5' TAATACGACTCACTATAGGG3'

T7:

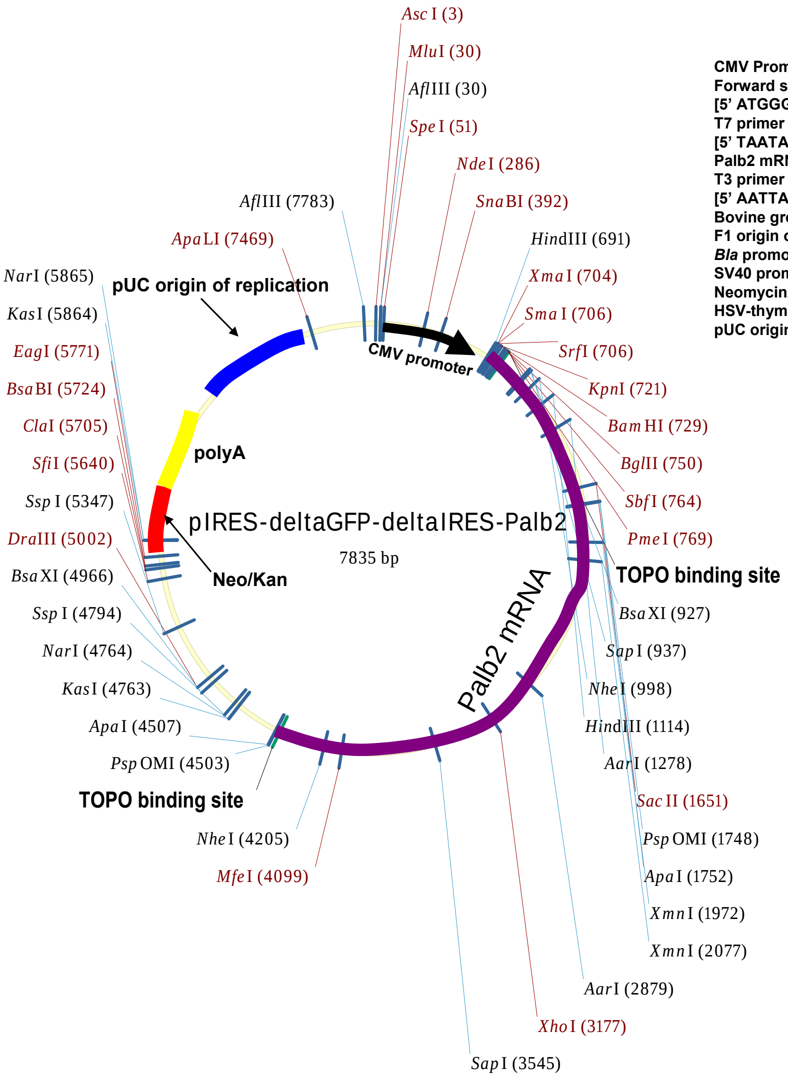
5' CAGGAAACAGCTATGAC 3'

Figure 3.3 Sequencing strategy for *Palb2* coding region. Due to the length of the mRNA, two separate sections were amplified using RNA isolated from the mammary glands of both strains. The above cloning primers were used in an RT-PCR reaction and the subsequent amplicons were subcloned into a pCR TOPO vector. Sequencing was done using the above primers and Vector NTI software was used to visualize the sequencing results.



CMV Promoter: 1-665 bp
Forward sequencing primer binding site
[5' ATGGGCGGTAGGCGTGTA 3'] : 576-593
T7 primer binding site
[5' TAATACGACTCACTATAGGG 3'] : 665-684
Palb2 mRNA: 785-4478
3X FLAG tag: 4519-4590
Reverse sequencing primer binding site
[5' ATGCAGTCGTCGAGGAATTG 3'] : 4597- 4616
IRES site: 4626-5200
hrGFP ORF: 5204-5920
T3 primer binding site
[5' AATTAACCCTCACTAAAGGG 3'] : 5953-5972
Bovine growth hormone (BGH) polyA signal: 5974-6204
F1 origin of ss-DNA replication: 6221-6505
***Bla* promoter:** 6541-6665
SV40 promoter: 6685-7002
Neomycin/kanamycin resistance ORF: 7037-7486
HSV-thymidine kinase (TK) polyA signal: 7487-7936
pUC origin of replication: 8074-8741

Figure 3.4 Plasmid map of pIRES-GFP-Palb2, an expression vector for *Palb2*.



CMV Promoter: 1-665 bp
Forward sequencing primer binding site
[5' ATGGGCGGTAGGCGTGTA 3'] : 576-593
T7 primer binding site
[5' TAATACGACTCACTATAGGG 3'] : 665-684
Palb2 mRNA: 785-4478
T3 primer binding site
[5' AATTAACCCTCACTAAAGGG 3'] : 4532-4551
Bovine growth hormone (BGH) polyA signal: 4553-4783
F1 origin of ss-DNA replication: 4800-5084
***Bla* promoter:** 5121-5245
SV40 promoter: 5265-5582
Neomycin/kanamycin resistance ORF: 5617-6066
HSV-thymidine kinase (TK) polyA signal: 6067-6516
pUC origin of replication: 6654-7321

Figure 3.5 Plasmid map for pIRES-deltaGPP-deltaIRES-Palb2, an expression vector for *Palb2*. The region of the plasmid containing the IRES and hrGFP features were removed and the resulting linear plasmid was re-ligated.

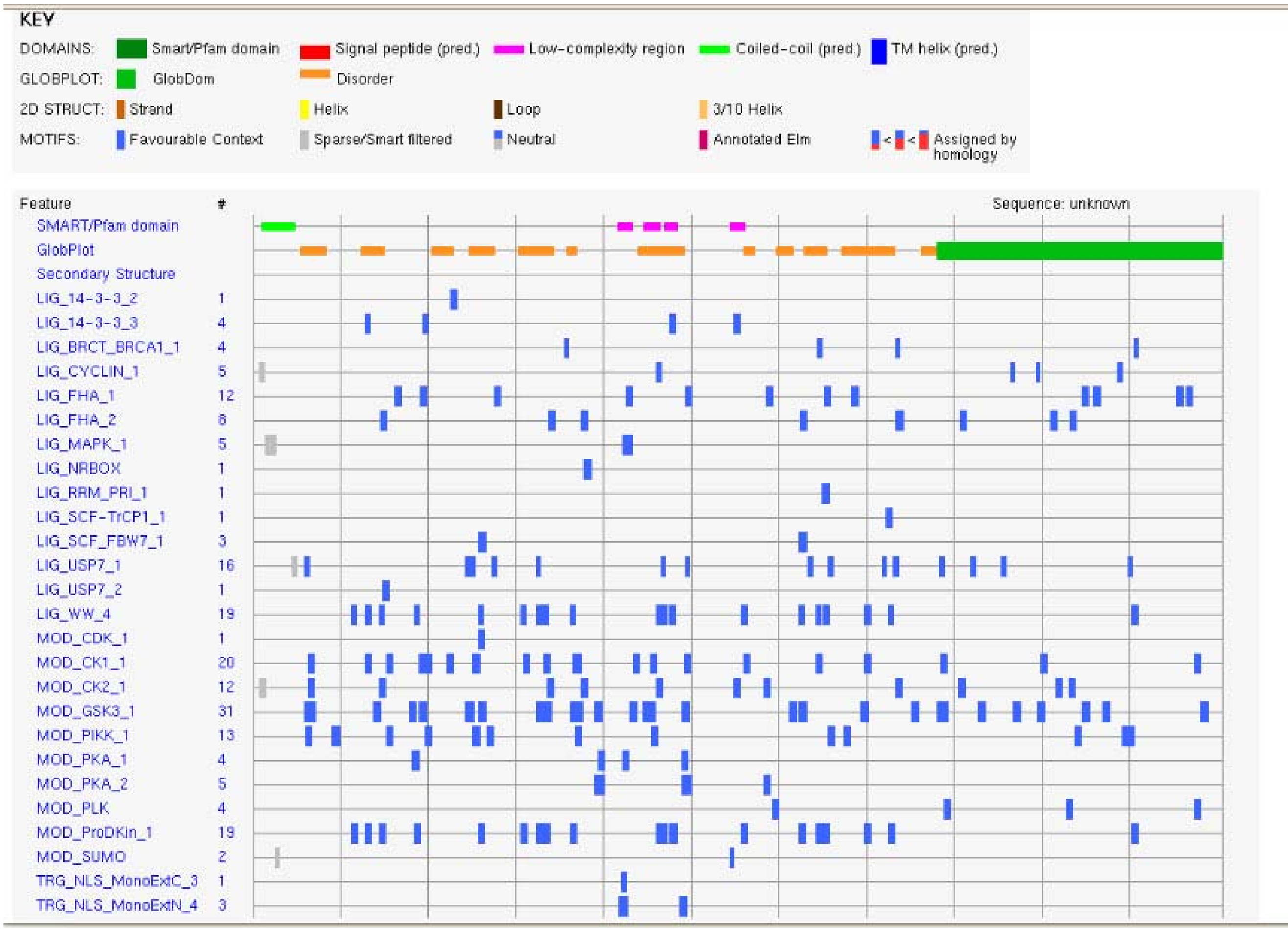


Figure 3.6 Mouse PALB2 protein modeling using PVS protein modeling software (http://imed.med.ucm.es/PVS/). “LIG” designates proteins that theoretically bind to PALB2 while “MOD” designates proteins that modify PALB2. Polo-like kinase 1 (PLK) is fifth from the bottom.

CHAPTER 4

IDENTFICATION OF GENES WITHIN THE *SUPRMAM1* INTERVAL THAT CONTRIBUTE TO INCREASED MAMMARY SUSCEPTIBILITY IN THE BALB/C STRAIN

Introduction

The search for high penetrance genetic modifiers for breast cancer using linkage approaches has been successful and has led to the identification of *BRCA1*, *BRCA2* and *TP53* which make up 20% of the familial breast cancer risk (Antoniou and Easton, 2006). However, this leaves genes contributing to 80% of familial risk of breast cancer unaccounted for.

Genome wide association studies have been relatively successful in identifying low penetrance modifiers to breast cancer. However, the disadvantages of requiring thousands of patients and controls makes these studies difficult to reproduce. The use of inbred mice provides the necessary tools to identify low penetrance alleles. Specifically, the BALB/c strain has proven to be useful to due its propensity for mammary tumors (Heston and Vlahakis, 1971). On a p53$^{+/-}$ background, this increased mammary tumor frequency becomes even more apparent. BALB/cMed *Trp53+/-* have spontaneous mammary tumor incidence rates between 42% and 65% (Kuperwasser et al., 2000b; Blackburn et al., 2003b). In contrast, the C57BL/6 develops mammary tumors less than 1% of the time (Donehower et al., 1992; Jacks et al., 1994). These two strains are useful models in identifying potential new low penetrance modifiers to breast cancer.

Previous work from our lab identified a region on chromosome 7 that linked to decreased mammary tumor latency in the BALB/c *Trp53*$^{+/-}$ strain (Blackburn et al., 2007d). Based on microarray data and the mapping data, *Dmbt1* was chosen as a suitable candidate. However, higher resolution mapping is needed to refine the localization of candidates.

In order to identify new candidates to explain the observed genetic linkage, we analyzed new markers within the *SuprMam1* region with the intention to provide better mapping resolution. We also employed a strategy to narrow down the list of candidates by selecting for genes that have coding SNP differences between the strains. Finally, we looked at gene expression by QPCR of our list of candidates between the strains.

Methods

Real-time RT-PCR:

The fourth mammary gland was removed from mice 8-10 weeks of age and placed at -80°C. Total RNA was isolated using Trizol solution according to protocol. Isolated RNA was reverse transcribed using Stratagene cDNA kit and analyzed for gene expression using Stratagene Brilliant-II-SYBR Green kit. Three animals were used for each strain and normalized to Actin expression. Fold change was established by dividing mean BALB/c expression to mean C57BL/6 expression. Statistical significance was determined by using Student's T-test.

Defining the SuprMam1 region:

An additional 8 SNPs were selected based on the ability of the SNP to disrupt a restriction enzyme cut site **(Table 4.1b)**. Flanking primers to the SNP were used to generate an amplicon by PCR which was then cut with the appropriate restriction enzyme

(Table 4.1a). The genotype for each marker in an animal was determined by the size of the cut or uncut amplicon by electrophoresis. LOD scores were determined by Chi-squared tests for each marker.

Selection of Candidate Genes:

The total list of genes within the SuprMAM1 interval was generated by using the Ensembl database (http://www.ensembl.org/index.html) version 59. Using the Jackson Labs SNP database (http://phenome.jax.org/), the total list of genes within the SuprMam1 interval was filtered down to only include non-synonymous SNPs that were contained within exons, untranslated regions as well as potential splice sites. SNP density maps were also generated using the Jackson Labs SNP database. Genes that showed significant differences in expression (p<.05) between the respective strains by microarray(Blackburn et al., 2007c) were also included.

Results

Narrowing of the SuprMam1 interval

There are 199 genes within the 15 Mb of the defined *SuprMam1* region from 120-135 Mb. In order to narrow down the list of candidate genes, eight more SNP markers were chosen within this region to achieve greater resolution. Use of these markers led to the narrowing of the interval from 100 Mb-135 Mb to 120-135 Mb total. Two distinct peaks correspond to the SNP marker *Plekha7* and the markers *Jmjd5, Il21r* and *Rabep*, respectively. Analysis for genes within the *SuprMam1* interval that had SNP differences between the susceptible BALB/c strain and three resistant to mammary tumors strains (C57BL/6, DBA/2J and 129SvJ) identified two distinct quantitative trait loci (QTLs) termed *SM1a* and *SM1b*. These QTLs were localized directly under the peaks identified within the *SuprMam1* region.

Candidate genes within the SuprMam1 interval

A criterion was used to narrow the total genes within the *SuprMam1* region. Using this filtering revealed a total of 34 genes that grouped into two apparent haplotype blocks, one that spanned from 122.6 Mb to 127.35 Mb and the other from 132.6 Mb to 134.5 Mb **(Table 4.2)**. Primers were designed for 32 of these genes using the Roche primer design database. Only 17 primer sets were able to demonstrate clear expression of the respective genes in the mammary gland. Eleven of the remaining primers that did not work were used to amplify MEF RNA to confirm that these genes were not expressed in the mammary gland **(Table 4.3)**. QPCR was used to examine expression differences within the mammary glands of the respective strains. No significant expression differences were observed in 17 of the candidate genes tested **(Figure 4.2)**. Similarly, no expression differences were observed in mammary glands that had been irradiated *in vivo* from the two strains **(Figure 4.3)**. Expression of stromal and adipose tissue can mask signals from the epithelium. We observe a significant increase in IL21r in the BALB/c strain in primary mammary epithelial cells **(Figure 4.4)**. When we compared C57BL/6 expression with BALB.B6-*SuprMam1* mammary epithelial cell expression, we observed significant differences in three genes, *Tmem159*, *Il21r* and *Itgal* **(Figure 4.5)**. *Tmem159* was significantly decreased in the congenic strain while *Il21r* and *Itgal* were found to be significantly increased in expression.

Discussion

In this study, we have attempted to utilize our model for spontaneous mammary tumor incidence to identify potential new low penetrance modifiers. The initial map for *SuprMam1* published by our group spanned approximately 30Mb on chromosome 7 and contained approximately 200 genes. It contained two subtle peaks that may correspond to more than one gene in our interval. Using eight additional markers within the *SuprMam1* interval, we were able to achieve greater resolution. The peaks revealing more prominent peaks with more defined boundaries. The result suggests that at least 2 genes within the *SuprMam1* region contribute to the mammary tumor phenotypes in the *Trp53*+/- mice.

Attempting to analyze 199 genes was a daunting task, so a filtering strategy was devised to narrow this list down. Utilizing the criteria in Figure 4.1, we filtered the initial 199 genes to 27 total which grouped into two distinct haplotype blocks, *SM1a* and *SM1b*. Grouping these two haplotype blocks on our map placed them almost directly under the two prominent peaks of *SuprMam1*. In addition, we included another 7 genes based on significant expression differences from a microarray comparing gene expression signatures between our two strains (Blackburn et al., 2007b).

A SNP database was used to identify regions of SNP density differences between different strains of mice. The DBA and 129/Sv strains are resistant to mammary tumors similar to the C57BL/6 mice (Backlund et al., 2001b; Ghebranious and Donehower, 1998). Thus, we searched for SNP density differences in the *SuprMam1* region between the susceptible strain BALB/c and the three common resistant strains. We then proceeded to determine where the two haplotype blocks *SM1a* and *SM1b* corresponded to the SNP densities. Interestingly, both blocks were localized to regions of high SNP difference densities. In particular, *SM1b* was localized to a previously identified haploblock, *IL4PPQ*. This region was identified in a genetic linkage study for lupus and corresponds to the gene *Il4r* in addition to a few other genes (Shiroiwa et al., 2007). The *Il4r* pathway has been shown to contribute to apoptosis resistance in epithelial cancer cells (Todaro et al., 2008). We did not detect any expression differences in the *Il4r* between the strains but did detect non-synonymous SNP differences **(Table 2, as a candidate gene)**. There are clear immune response differences between these two strains as the BALB/c strain has a T helper cell type 2 (T_H2) response to immune system stimulation while the C57BL/6 strains is more T_H1(Liu et al., 2002). This is evident in the BALB/c strains susceptibility to intracellular parasite infection, resistance to autoimmune disease and overall increased cancer incidence compared to the C57BL/6 strain. How relevant the *IL4PPQ* and/or *Il4r* is to mammary susceptibility is unknown, but it is tempting to speculate that a common gene may explain increased susceptibilities to both phenotypes.

We proceeded to examine gene expression of our candidate genes in RNA isolated from whole mammary glands. Unfortunately, no significant expression differences were detected. Similarly, no expression differences were detected in RNA isolated from mammary glands following irradiation. Because the mammary epithelium only makes up 30% of total tissue within the breast, any signals from the stroma or adipose cells could mask epithelial signals. Using RNA from primary mammary epithelial cells, our QPCR results show a significant increase in the *Il21r* in the BALB/c strain. Analyzing expression of genes from the congenic strain allows us to eliminate genes being activated by promoter elements contained outside the *SuprMam1* region. Our QPCR results from BALB.B6-*SuprMam1* mammary epithelial cells show significant increases in expression of *Il21r* and *Itgal* in contrast to a decreased *Tmem159* expression. The increased *Il21r* expression present in both the BALB/c and BALB.B6-*SuprMam1* strains suggest that despite this gene being contained within the *SuprMam1* region, its expression is being controlled by an element outside the interval. The increased expression of *Itgal* and decreased expression of *Tmem159* in the congenic strain is a little more difficult to explain. No expression differences were observed in BALB/c cells with these two genes suggesting a possible disruption of signaling with BALB/c elements outside the interval and C57BL/6 elements within the interval. Normalizing to *Actin* was necessary for this data as this gene was found to be differentially expressed between the congenic and C57BL/6 strains. While care is taken to be certain the same amounts of input RNA are added for cDNA synthesis, it is possible there were user or technical errors in this case.

The lack of significant gene expression differences between the two strains was disappointing. It is possible that our method of narrowing the list of candidates was too stringent and excluded other candidates. We were also unable to confirm any of the seven genes identified in the microarray by QPCR. While we were able to identify a list of candidates with a non-synomymous SNP difference between the strains, we did not have the resources or tools to test the functionality of these SNPs on protein function. There is a third possibility in which non-coding regions within *SuprMam1* encode miRNAs. This is not beyond the realm of possibilities as many of the SNPs identified in genome wide association studies were located in non-coding regions (Easton et al., 2007c). It is also possible that there is a gene exerting its effect on mammary latency through a host effect. This was apparent in a study by Veillet et al where they identified a gene whose differential expression in the thymus was exerting its effect on mammary carcinogenesis (Veillet et al., 2011). Future studies will need to be done to follow up these possibilities.

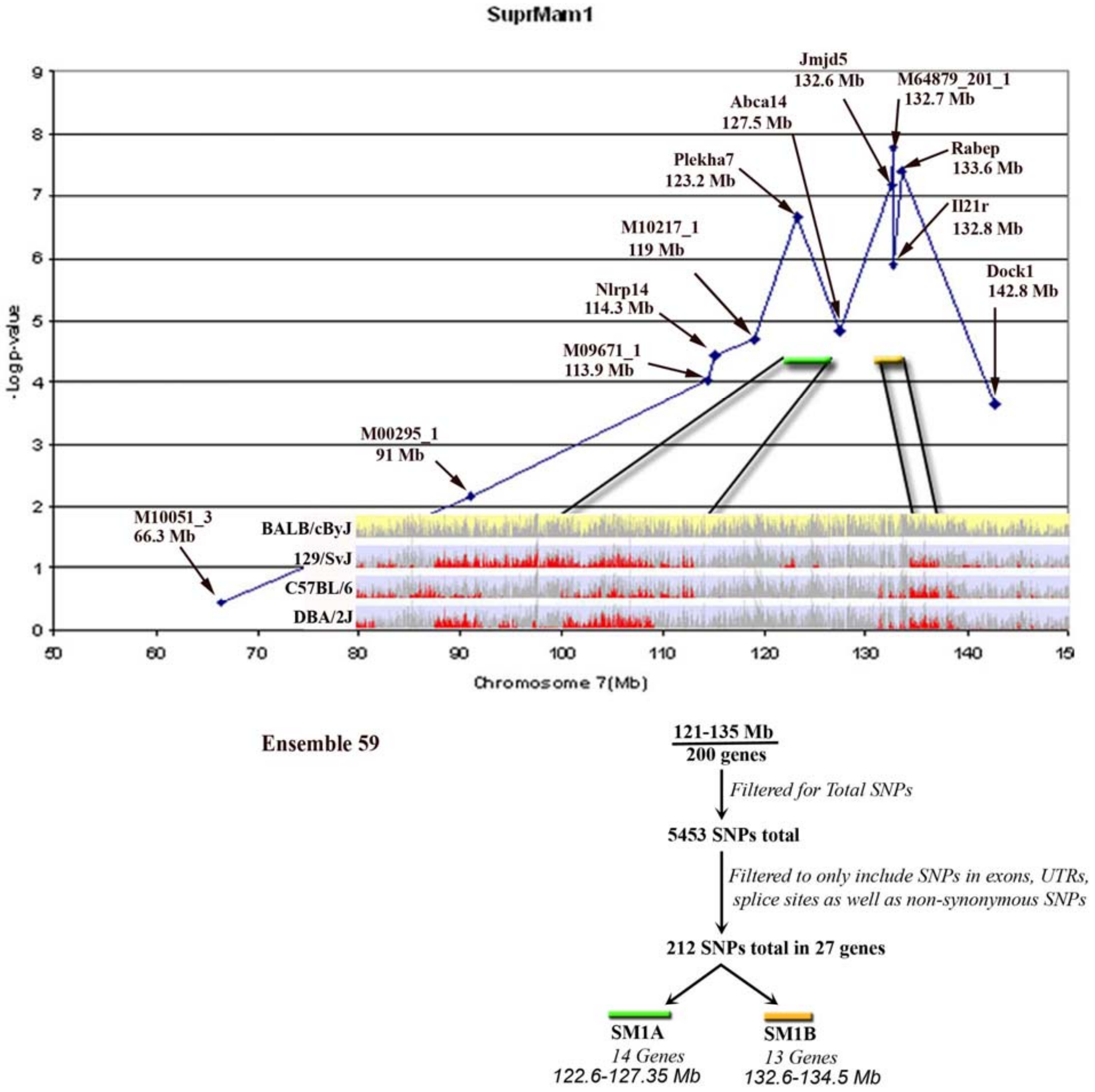


Figure 4.1 Revised *SuprMam1* interval with 8 additional markers. Flow chart describes the candidate gene filtering process. Candidates grouped into two distinctive haploblocks that mapped directly under the prominent peaks. Below the mapped haploblocks are the SNP densities for (Top to bottom): BALB/c (yellow background), C57BL/6, DBA and 129Sv strains.

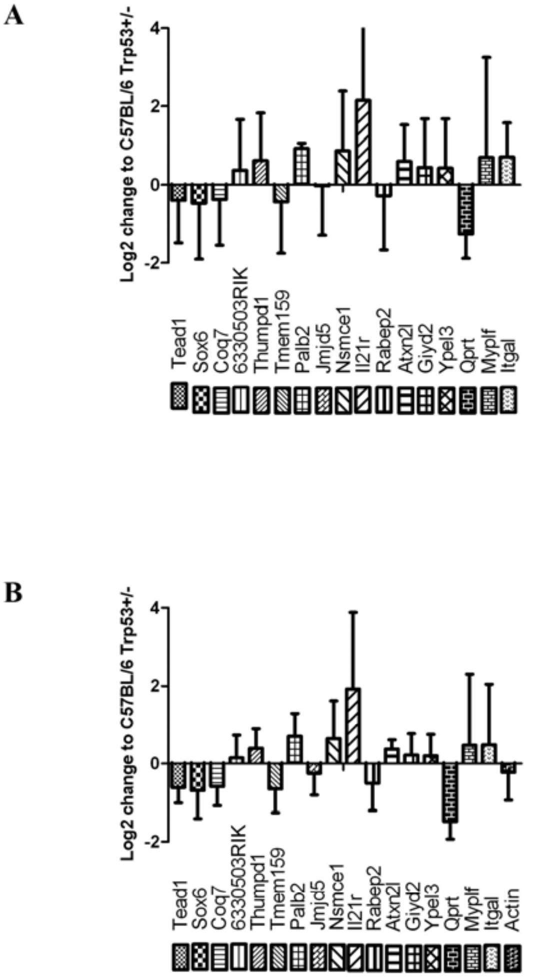


Figure 4.2 Candidate gene expression from whole mammary glands. **(A)** Expression of BALB/c *Trp53*$^{+/-}$ mammary glands Log2 change to C57BL/6 *Trp53*$^{+/-}$ mammary glands. Mammary glands were IR at 5 Gy and harvested 6 hours later. At least three mice were used per group, error bars represent standard error. No significant differences observed by ANOVA. **(B)** Same as above, but not normalized to Actin.

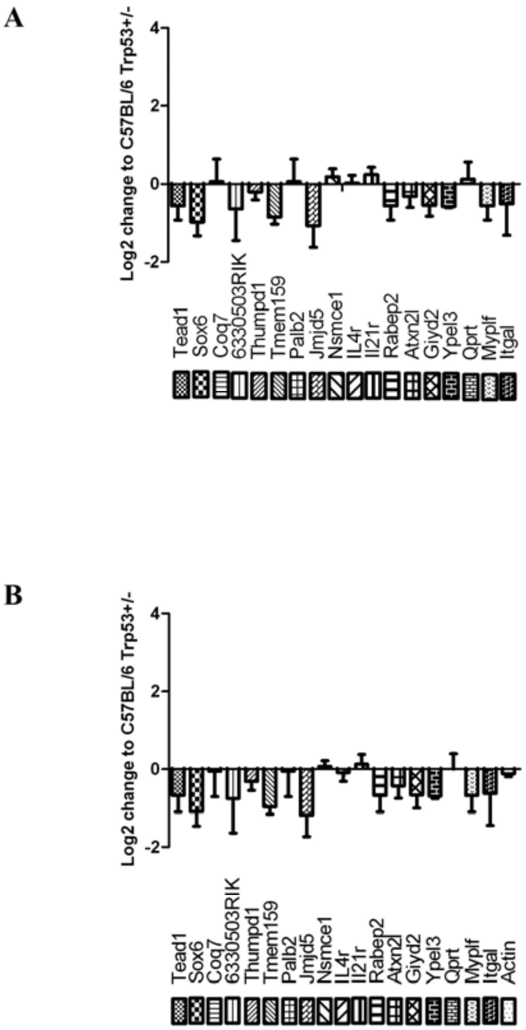


Figure 4.3 Candidate gene expression from IR mammary glands **(A)** Expression of BALB/c *Trp53*$^{+/-}$ IR mammary glands Log2 change to C57BL/6 *Trp53*$^{+/-}$ IR mammary glands. At least three mice were used per group, error bars represent standard error. No significance by ANOVA. **(B)** Same as above, but not normalized to Actin.

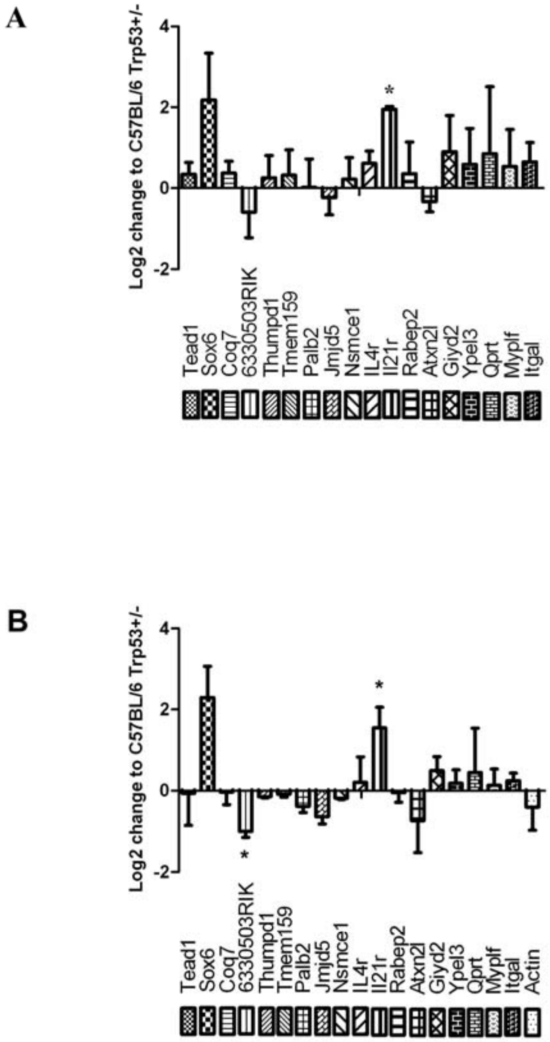


Figure 4.4 Candidate gene expression from BALB/c *Trp53*$^{+/-}$ primary mammary epithelial cells. **(A)** Expression of BALB/c *Trp53*$^{+/-}$ epithelial cells Log2 change to C57BL/6 *Trp53*$^{+/-}$ epithelial cells. At least three mice were used per group, error bars represent standard error. Significance by ANOVA, *p<.05. **(B)** Same as above, but not normalized for Actin

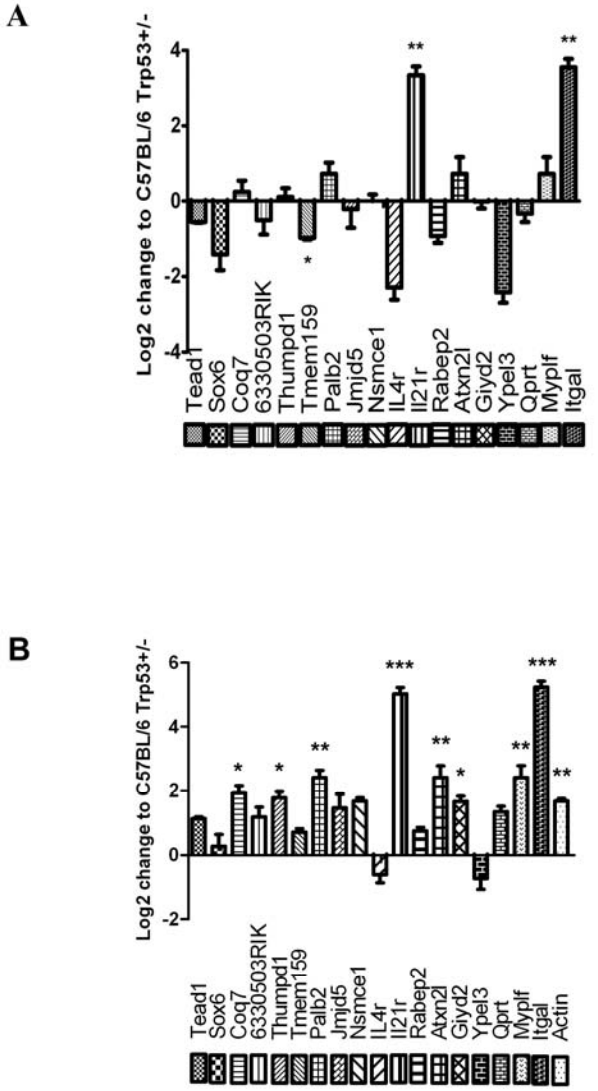


Figure 4.5 Candidate gene expression from BALB.B6-*SuprMam1 Trp53*$^{+/-}$ primary mammary epithelial cells. **(A)** Expression of BALB.B6-*SuprMam1 Trp53*$^{+/-}$ epithelial cells Log2 change to C57BL/6 *Trp53*$^{+/-}$ epithelial cells. At least three mice were used per group, error bars represent standard error. Significance by ANOVA, *p<.05, **p<.01. **(B)** Same as above, but not normalized for β-actin. Significance by ANOVA, *p<.05, **p<.01, ***p<.001

A

Gene	forward	reverse
Plekha7	GTCATTTACACCTTGTTAGTCTGTGTC	CCTTTCAGCCTCTCTTCTGTGGTA
Tmc5	GCCCTCTCAGGCTTATCCTCCA	GGGACAGCCCTGTTTGAGTTCC
Abca14	CACGTTGATGTGGCAACTTGGAC	TCACCTGAAGTGGCAAGCGTTC
Jmjd5	CCACTAACGCAGATTCCTGACAC	CCTGGGGACACTCACTGG
Rabep2	GGTAGGTACTATCCCTGCCAGCA	GTTGAACTCACCTGCTTGGCAC
Dock1	CAGGGGCAAGGAGAAGAAGGAA	GCAGGTGGCTGATGGTTCTGAG

B

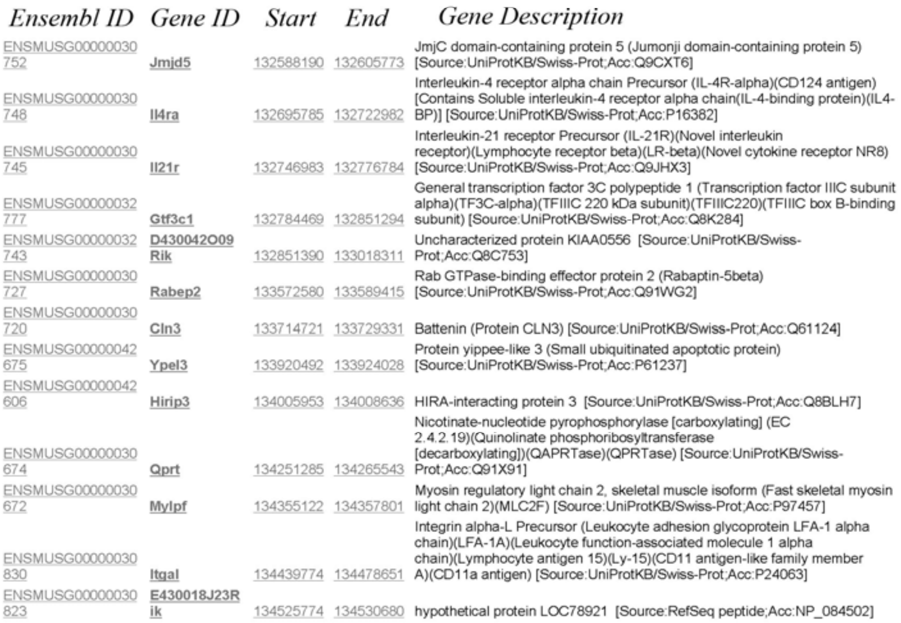
Gene	Mb	b6/balb	Enzyme	Cuts	Bk6 Amplicon	Balb/c Amplicon
Plekha7	115.966915	A/G	BsaxI	Balb/C	374bp	202bp 172bp
Tmc5	118.443806	A/G	MboI	Balb/C	466bp	268bp 178bp
Abca14	120.042328	C/T	HhaI	C57/BK6	97bp 72bp	169bp
Jmjd5	125.246382	C/T	BsrI	C57/BK6	203bp 65bp 58bp	261bp 65bp
Rabep2	126.231357	G/A	BsrbI	C57/BK6	97bp 67bp	164bp
Dock1	134.627560	G/C	PvuII	C57/BK6	296bp 209bp	505bp

Table 4.1 Primers and SNPs used for *SuprMam1* genotyping. **(A)** Primers used to amplify amplicon containing the SNP in the appropriate gene. **(B)** Table showing the SNP associated gene, its location and the SNP for each strain. In addition, the enzyme next to each SNP indicates the restriction enzyme cut site used to genotype each N2 mouse at that particular genomic location.

SuprMam1a

Ensembl ID	*Gene ID*	*Start*	*End*	*Gene Description*
ENSMUSG00000051910	**Sox6**	122614858	123174561	Transcription factor SOX-6 (SOX-LZ) [Source:UniProtKB/Swiss-Prot;Acc:P40645]
ENSMUSG00000008683	**Rps15a**	125252578	125259674	40S ribosomal protein S15a [Source:UniProtKB/Swiss-Prot;Acc:P62245]
ENSMUSG00000030652	**Coq7**	125653324	125676798	Ubiquinone biosynthesis protein COQ7 homolog (Coenzyme Q biosynthesis protein 7 homolog)(Timing protein clk-1 homolog) [Source:UniProtKB/Swiss-Prot;Acc:P97478]
ENSMUSG00000073859	**Itpripl2**	125629325	125629678	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q3TNW6]
ENSMUSG00000042246	**Tmc7**	125679358	125728200	Transmembrane channel-like protein 7 [Source:UniProtKB/Swiss-Prot;Acc:Q8C428]
ENSMUSG00000030650	**Tmc5**	125740811	125818600	Transmembrane channel-like protein 5 [Source:UniProtKB/Swiss-Prot;Acc:Q32NZ6]
ENSMUSG00000033904	**6330503K22Rik**	125856066	125880538	Centrosomal protein of 110 kDa (Cep110) [Source:UniProtKB/Swiss-Prot;Acc:Q7TSH4]
ENSMUSG00000030954	**Gp2**	126586058	126602786	Pancreatic secretory granule membrane major glycoprotein GP2 Precursor (Pancreatic zymogen granule membrane protein GP-2) [Source:UniProtKB/Swiss-Prot;Acc:Q9D733]
ENSMUSG00000033533	**Acsm1**	126761327	126806028	Acyl-coenzyme A synthetase ACSM1, mitochondrial Precursor (EC 6.2.1.2)(Acyl-CoA synthetase medium-chain family member 1)(Middle-chain acyl-CoA synthetase 1)(Butyryl coenzyme A synthetase 1)(Butyrate--CoA ligase 1)(Lipoate-activating enzyme) [Source:UniProtKB/Swiss-Prot;Acc:Q91VA0]
ENSMUSG00000030929	**Exod1**	126912193	126937516	Exonuclease domain-containing protein 1 (EC 3.1.-.-) [Source:UniProtKB/Swiss-Prot;Acc:Q5BKS4]
ENSMUSG00000052273	**Dnahc3**	127069493	127095671	Dynein heavy chain 3, axonemal (Axonemal beta dynein heavy chain 3)(Ciliary dynein heavy chain 3) [Source:UniProtKB/Swiss-Prot;Acc:Q8BW94]
ENSMUSG00000030917	**Tmem159**	127245889	127264506	Promethin (Transmembrane protein 159) [Source:UniProtKB/Swiss-Prot;Acc:Q922Z1]
ENSMUSG00000030911	**Zp2**	127275875	127288804	Zona pellucida sperm-binding protein 2 Precursor (Zona pellucida glycoprotein ZP2)(Zona pellucida protein A) [Contains Processed zona pellucida sperm-binding protein 2] [Source:UniProtKB/Swiss-Prot;Acc:P20239]
ENSMUSG00000062017	**Abca14**	127347475	127468866	ATP-binding cassette, sub-family A (ABC1), member 14 [Source:RefSeq peptide;Acc:NP_080734]

SuprMam1b



Ensembl ID	*Gene ID*	*Start*	*End*	*Gene Description*
ENSMUSG00000030752	**Jmjd5**	132588190	132605773	JmjC domain-containing protein 5 (Jumonji domain-containing protein 5) [Source:UniProtKB/Swiss-Prot;Acc:Q9CXT6]
ENSMUSG00000030748	**Il4ra**	132695785	132722982	Interleukin-4 receptor alpha chain Precursor (IL-4R-alpha)(CD124 antigen) [Contains Soluble interleukin-4 receptor alpha chain(IL-4-binding protein)(IL4-BP)] [Source:UniProtKB/Swiss-Prot;Acc:P16382]
ENSMUSG00000030745	**Il21r**	132746983	132776784	Interleukin-21 receptor Precursor (IL-21R)(Novel interleukin receptor)(Lymphocyte receptor beta)(LR-beta)(Novel cytokine receptor NR8) [Source:UniProtKB/Swiss-Prot;Acc:Q9JHX3]
ENSMUSG00000032777	**Gtf3c1**	132784469	132851294	General transcription factor 3C polypeptide 1 (Transcription factor IIIC subunit alpha)(TF3C-alpha)(TFIIIC 220 kDa subunit)(TFIIIC220)(TFIIIC box B-binding subunit) [Source:UniProtKB/Swiss-Prot;Acc:Q8K284]
ENSMUSG00000032743	**D430042O09Rik**	132851390	133018311	Uncharacterized protein KIAA0556 [Source:UniProtKB/Swiss-Prot;Acc:Q8C753]
ENSMUSG00000030727	**Rabep2**	133572580	133589415	Rab GTPase-binding effector protein 2 (Rabaptin-5beta) [Source:UniProtKB/Swiss-Prot;Acc:Q91WG2]
ENSMUSG00000030720	**Cln3**	133714721	133729331	Battenin (Protein CLN3) [Source:UniProtKB/Swiss-Prot;Acc:Q61124]
ENSMUSG00000042675	**Ypel3**	133920492	133924028	Protein yippee-like 3 (Small ubiquitinated apoptotic protein) [Source:UniProtKB/Swiss-Prot;Acc:P61237]
ENSMUSG00000042606	**Hirip3**	134005953	134008636	HIRA-interacting protein 3 [Source:UniProtKB/Swiss-Prot;Acc:Q8BLH7]
ENSMUSG00000030674	**Qprt**	134251285	134265543	Nicotinate-nucleotide pyrophosphorylase [carboxylating] (EC 2.4.2.19)(Quinolinate phosphoribosyltransferase [decarboxylating])(QAPRTase)(QPRTase) [Source:UniProtKB/Swiss-Prot;Acc:Q91X91]
ENSMUSG00000030672	**Mylpf**	134355122	134357801	Myosin regulatory light chain 2, skeletal muscle isoform (Fast skeletal myosin light chain 2)(MLC2F) [Source:UniProtKB/Swiss-Prot;Acc:P97457]
ENSMUSG00000030830	**Itgal**	134439774	134478651	Integrin alpha-L Precursor (Leukocyte adhesion glycoprotein LFA-1 alpha chain)(LFA-1A)(Leukocyte function-associated molecule 1 alpha chain)(Lymphocyte antigen 15)(Ly-15)(CD11 antigen-like family member A)(CD11a antigen) [Source:UniProtKB/Swiss-Prot;Acc:P24063]
ENSMUSG00000030823	**E430018J23Rik**	134525774	134530680	hypothetical protein LOC78921 [Source:RefSeq peptide;Acc:NP_084502]

Table 4.2 List of candidate genes within the *SuprMam1* interval that fit the filtering criteria. Each gene has at least one non-synonymous SNP that differs between the C57BL/6 and BALB/c strains.

Primer set name	+RT sample QPCR Ct	-RT sample QPCR Ct
Smg1	28.43	No Ct
Tmc5	37.29	No Ct
Gp2	No Ct	No Ct
Acsm1	37.53	No Ct
Dnahc1	36.61	No Ct
Zp2	38.52	No Ct
Abca14	No Ct	No Ct
Il4r	26.16	35.15
Gtf3c1	25.83	No Ct
Cln3	36.44	No Ct
Hirip3	26.84	35.95

Table 4.3 List of candidate genes that did not amplify in the mammary gland. We examined expression of C57BL/6 *Trp53*$^{+/-}$ MEF RNA using the above primer sets. The Ct values generated by the QPCR Stratagene MxPro software are shown using cDNA reactions with Reverse Transcriptase or no Reverse Transcriptase controls.

CHAPTER 5

THE ROLE OF THE SUPRMAM1 REGION IN THE IRRADIATION RESPONSE OF THE MAMMARY GLANDS

Introduction

The DNA double-strand break repair pathway is fundamental in the prevention of breast cancer. Mutations in genes involved in DNA double-strand break repair lead to an increased risk for breast cancer confirming the importance of this pathway in the breast. Double-strand breaks are considered the most lethal DNA damage due to the complete shearing of the genomic DNA and the lack of template DNA to repair the gap. The two most common causes of DNA double-strand breaks are stalling of replication polymerases at sites of damage and exposure to ionizing radiation. IR can cause DNA double-strand breaks by direct energy transfer or by increasing ROS within the cell. Numerous studies have demonstrated the effect of IR on breast cancer risk. Cells that are defective in any of the DNA double-strand break repair pathways are sensitive to IR, highlighting the its link to breast cancer risk.

Identifying genes involved in IR sensitivity have largely been performed in the BALB/c mouse strain (Weil et al., 1996; Ponnaiya et al., 1997b; Okayasu et al., 2000a). Mori et al. was the first group to use genetic linkage analyses to identify Resistance to Apoptosis alleles in thymocytes from BALB/c mice (Mori et al., 1995b). *Rapop1* was located in the proximal region of chromosome 16 and was later identified as the gene *Prkdc*, which encodes the NHEJ component DNA-PK$_{cs}$ (Okayasu et al., 2000b). The BALB/c mouse strain has two polymorphisms in DNA-PK$_{cs}$ that appear to affect protein expression and end-joining function (Yu et al., 2001c). In addition, *Rapop1* and *Tp53* appeared to be linked in glucocortocoid induced apoptosis in thymocytes (Mori et al., 1999). Other IR-sensitive loci were identified in genetic linkage studies including *Rapop2* and *Rapop3* (Mori et al., 1995a). *Rapop2* was mapped to chromosome 9 with DNA damage response gene *Atm* identified as a viable candidate. Chromosome 3 contains *Rapop3* with a possible candidate being *Mcl-1*, a gene belonging in the *Bcl-2* apoptosis family.

The BALB/c strain, in addition to IR sensitivity, is prone to IR-induced mammary tumors (Butel et al., 1981; Ethier and Ullrich, 1982). Mammary epithelial cells from BALB/c mice have been shown to be susceptible to IR-induced neoplastic transformation (Ullrich et al., 1996a). In addition, these cells showed more IR-induced genomic instability(Ponnaiya et al., 1997a). Finally, mice with the $Prkdc^{BALB/BALB}$ genotype had more IR-induced genomic instability in mammary cells than mice with a $Prkdc^{BALB/C57BL}$ (Yu et al., 2001d).

While this evidence suggests that a defect in DNA-PK_{cs} might explain IR-induced mammary tumorigenesis in the BALB/c strain, it does not address the role of spontaneous mammary tumors in $p53^{+/-}$ mice. Mice on a 129/SvJ strain background have the same polymorphism in DNA-PK_{cs} as BALB/c, however, they are not prone to spontaneous mammary tumors (Mori et al., 2001; Kuperwasser et al., 2000a). In addition, none of the *Rapop* genes are contained within the *SuprMam1* interval, including *Prkdc*. Many of the studies identifying IR susceptibility alleles were performed in thymocytes. Because IR sensitivity can vary by tissue type, the response in the mammary gland is unclear.

Using apoptosis of mammary epithelial cells as a marker, we measured the IR response between four strains of mice. We first tested the IR sensitive and IR resistance strains, BALB/c and C57BL/6, respectively. We next looked at the first generational (F1) cross responses to IR to determine if the IR sensitivity in the BALB/c strain was dominant or recessive. Finally, we generated a congenic strain which consisted of C57BL/6 *SuprMam1* alleles on a BALB/c strain background. This allowed us to test if there are alleles within the *SuprMam1* region that conferred a resistance to apoptosis and IR sensitivity.

Methods

Mouse surgery and hormonal treatment::

Medical grade silastic tubing was cut to a length of 1.2 cm and filled with 50 μg Beta estradiol (Sigma) and 20 mg of progesterone (Sigma). Both ends were sealed with clear silicone. Mice at 9 weeks of age were ovariectomized and allowed one week for any endogenous hormones reach baseline levels. Capsules were implanted subcutaneously on the dorsal side of the mouse, ½ inch distal to the neck. On the fourth day after implantation, mice were subjected to 5 Gy ionizing irradiation from a ^{137}Cs source. Six hours later, the mouse was sacrificed and the fourth mammary glands were harvested. One mammary gland was fixed in 10% neutral-buffered formalin and the other was flash frozen in liquid nitrogen.

Apoptosis assay:

Sections of paraffin embedded mammary glands were subjected to TUNEL assay using ApopTag Plus Peroxidase In Situ Apoptosis Kit (Chemicon International). 1200 epithelial cells were counted per slide.

Generation of BALB.B6-SuprMam1 mice:

BALB.B6-*SuprMam1* mice were generated by backcrossing mice with C57BL/6 *SuprMam1* alleles on a BALB/c genetic background at least 7 generations **(Figure 5.1)**. Primers for the SNP markers used to define the *SuprMam1* region include *Plekha7* and *Dock1* which flank the SuprMam1 region. Internal primers to SNPs within the *SuprMam1* region were also used for genotyping.

Results

The SuprMam1 region does not contain any alleles that affect IR sensitivity

Hormones have a clear effect on the IR response within the mammary gland of mice (Becker et al., 2005). To control for this, we ovariectomized the mice and allowed seven days for any endogenous hormones to clear before re-introducing hormones by capsule implantation **(Figure 5.2)**. Our results clearly show that the BALB/c strain had significantly more apoptosis than the C57BL/6 strain regardless of p53 genotype **(Figure 5.3)**. The F1 mice had slightly lower levels of apoptosis than the BALB/c strain, although not significant. The BALB.B6-*SuprMam1* congenic strain had similar levels to the F1 and was not significantly different than the BALB/c strain. Apoptosis levels of wildtype mice had similar trends to p53 heterozygous mice.

Discussion

The IR sensitivity of the BALB/c strain is well documented. However, the IR sensitivity of the whole mammary gland and the genes involved is less clear. We examined whether there were IR sensitivity differences in the mammary gland of different strains of mice. The purpose was to help establish the idea that there are alleles within the *SuprMam1* interval that contribute to IR sensitivity and mammary tumor latency.

Our results confirm earlier studies showing that the BALB/c strain is sensitive to IR-induced apoptosis while the C57BL/6 strain is resistant. The status of p53 does not appear to have a dramatic effect as there were significant differences in IR-induced apoptosis between the strains of both genotypes. The amount of apoptosis in the BALB/c $p53^{+/+}$ mammary gland was surprisingly slightly lower than in the BALB/c-$p53^{+/-}$ gland, although not significant. This was in contrast to a study showing diminished apoptosis in $p53^{+/-}$ mice. We did not test IR sensitivity in p53 null mice due to the necessity of p53 in mammary gland apoptosis. The F1 mice were also tested for their IR sensitivity and showed a slight decrease in apoptosis compared to the BALB/c strain without being significant. Because multiple genes are involved in IR-sensitivity in the BALB/c strain (*Rapops1-3*), it is much more difficult to interpret this data. IR-sensitivity appears to be a dominant trait since the F1 apoptosis levels were not significantly different than the BALB/c.

Finally, we generated a congenic strain as described in **Figure 1**. The apoptosis levels from the BALB.B6-*SuprMam1* strain were not significantly different from the BALB/c suggesting there are no significant alleles that contribute to IR sensitivity within the *SuprMam1* region. This was not totally unexpected since previous studies did not detect any obvious IR sensitivity alleles within this region (Blackburn et al., 2007a). Almost all breast cancer risk alleles play a prominent role in the DNA damage and DNA dsb repair response. Cells defective in these pathways are sensitive to IR. Our data suggests that the gene or genes responsible for decreased spontaneous mammary tumor latency in the BALB/c strain is not likely involved in the aforementioned pathways. More importantly, this data eliminates *Palb2* as a likely candidate due to its location within the SuprMam1 interval as well as the observation that cells defective in *Palb2* are sensitive to DNA damaging drugs (Zhang et al., 2009c). This experiment measured the amount of apoptosis as an indicator of proper DNA double-strand break repair in the mammary gland. Thus, it is possible any difference observed between the strains is due to a gene involved in the apoptosis pathway. It is also possible that any effect from a gene within the *SuprMam1* interval is being masked from other genes within the genome of the BALB.B6-*SuprMam1* congenic strain. This is not unfeasible as multiple genes are involved in the DNA damage response in addition to the apparent IR-sensitivity dominance in the BALB/c strain.

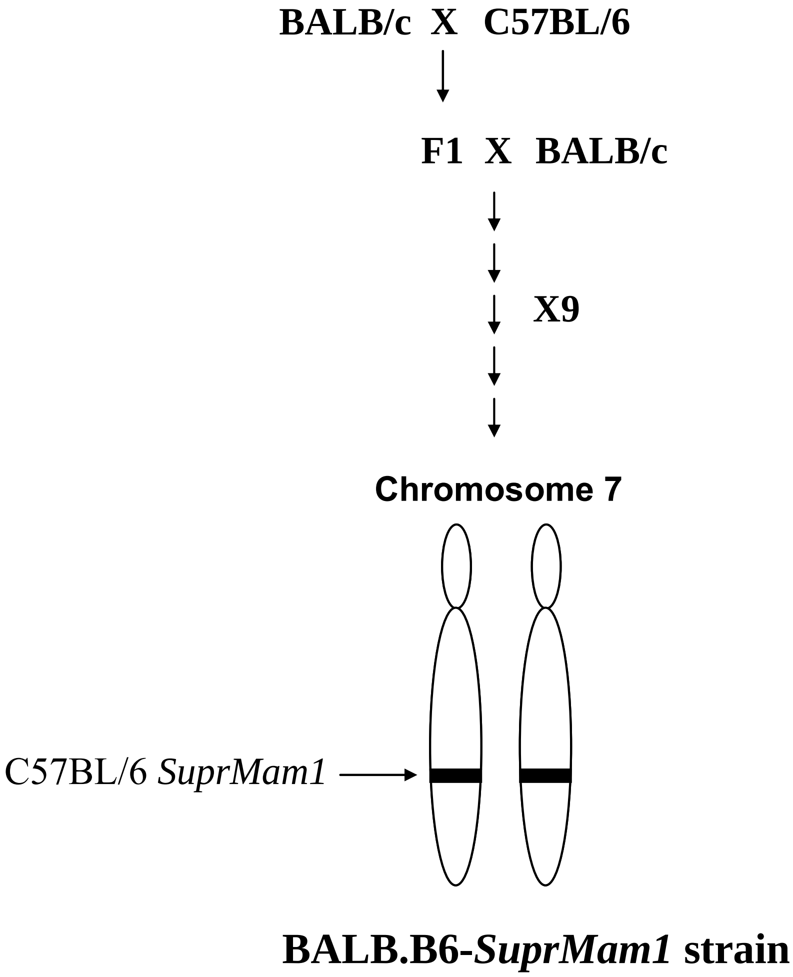


Figure 5.1 Flow chart describing the strategy in creating the congenic strain. The F1 mice were backcrossed at least 9 times, keeping the C57BL/6 *SuprMam1* region intact. After ten generations, the background genetic identity would be 98.5% BALB/c (Silver, 1995).

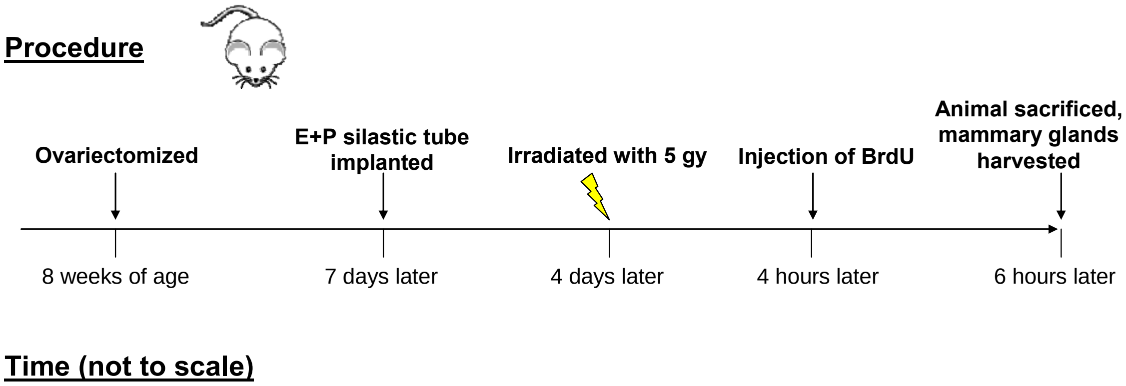


Figure 5.2 Timeline protocol for harvesting mammary glands to perform TUNEL apoptosis assays.

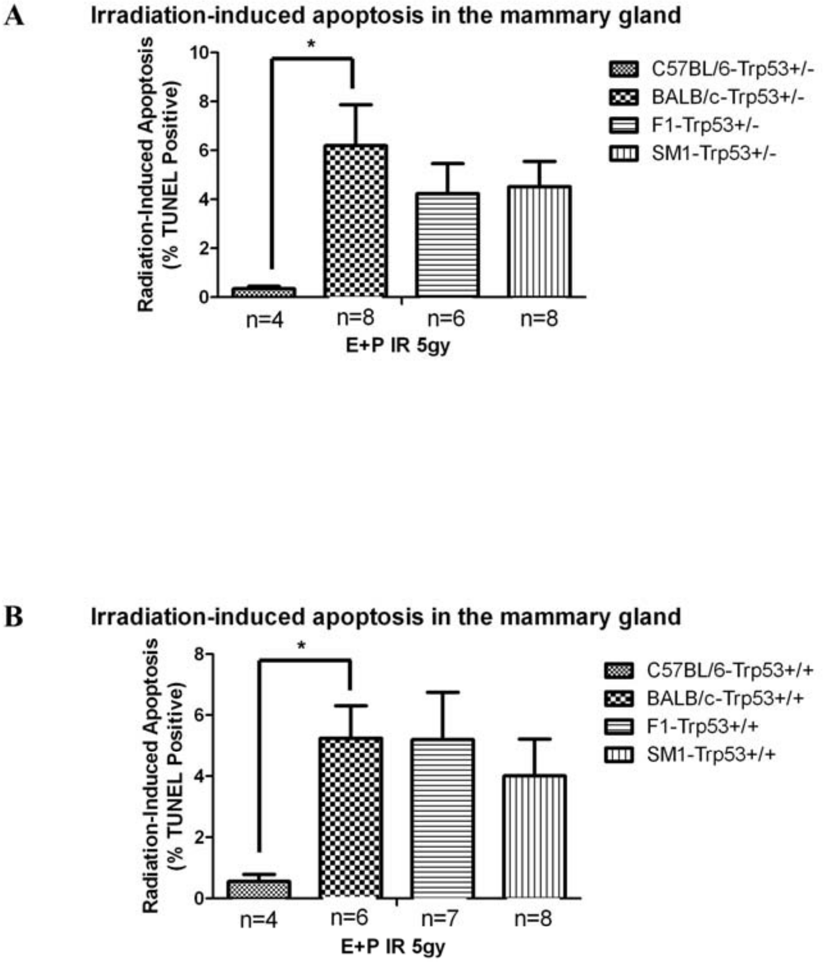


Figure 5.3 Irradiation induced apoptosis in the mammary gland. At least 1200 epithelial cells were counted per mammary gland. The percentage of positive cells (brown) are graphed with the number of mice at the bottom of each bar. **(A)** TUNEL positive cells in mammary glands from mice on a $p53^{+/-}$ background. Students t-test, significance *p<.05. **(B)** TUNEL positive cells in mammary glands from mice on a $p53^{+/+}$ background. Students t-test, significance *p<.05

CHAPTER 6

SUMMARY

These studies have attempted to identify the genes and pathways responsible for the increased mammary tumor susceptibility in the BALB/c-*Trp53*$^{+/-}$ mouse strain. Identification of these genes and pathways could lead to further insights into breast cancer detection and treatment. In addition, this model provides the means to identify new low penetrance modifiers to breast cancer susceptibility.

We first tried to establish differences in DNA repair between our spontaneous mammary tumor susceptible strain, BALB/c-*Trp53*$^{+/-}$, and our resistant strain, C57BL/6-*Trp53*$^{+/-}$. Using a novel DNA double-strand break repair assay developed by the Wiesmüller lab, we were unable to establish clear differences in DNA repair. This was due to inconsistent results from experiment to experiment. We next employed an immunofluorescence assay that allows the observation of proper localization of DNA repair proteins following DNA damage. We observed a significantly decreased localization of RAD51 in the BALB/c MEFs following irradiation. This indicates a possible signaling defect in the BALB/c strain that occurs after the initial DNA damage response as no difference in H2AX signaling was observed. Cells that are defective in DNA repair are sensitive to DNA damaging agents. Specifically, cells defective in any Fanconi Anemia component, (eg. *BRCA2, BRIP1, PALB2*) show heightened sensitivity to MMC and Camptothecin (Patel, 2007). Our results suggest no defects in any of these components as sensitivity to these drugs were not significantly different between the strains.

Finally, we employed the comet assay, a more robust and generalized assay that established clear differences in DNA repair between the strains. First, we observed clear differences in initial damage before repair has begun in the BALB/c strain. Second, BALB/c-*Trp53*$^{+/-}$ MEFs demonstrated significantly more damage over time following irradiation. Third, we observe significantly more DNA damage in the BALB/c strain 15 hours post-irradiation, the window when HRR is the predominant repair pathway. We see similar increases in damage after Camptothecin treatment in BALB/c MEFs as well. Finally, treatment with Vanillin, a specific inhibitor for NHEJ component DNA-PK$_{cs}$, did not change the significant amounts of damage observed between the strains. This suggests the increased irradiation-induced damage observed in the BALB/c strain is not due to its inherent defect in DNA-PK$_{cs}$.

The BALB/c strain has a clear defect in the NHEJ pathway due to a SNP in DNA-PK$_{cs}$. However, our results suggest that this strain may also have other defects independent of the NHEJ pathway. First, we chose a timepoint of 15 hours to measure the amount of irradiation-inducing damage which is much later than the one or two hour window that NHEJ occurs post DNA damage. Second, we specifically inhibited DNA-PK$_{cs}$ and show that there is still increased damage in the BALB/c strain suggesting this protein is not a factor at this timepoint. We also observed an increase in damage immediately following irradiation suggesting the BALB/c strain may be sensitive to the actual damage due to increased ROS (Halliwell and Gutteridge, 1984b). Our immunofluorescence data suggests a defect in HRR signaling as RAD51 localization was decreased in the BALB/c strain. What signaling pathways may be responsible for this is unknown, however, the ATM DNA damage response pathway is a viable target (Bartkova et al., 2005).

The *SuprMam1* linkage mapping provided us powerful tools to identify genes responsible for mammary tumor susceptibility in the BALB/c strain. Searching for genes involved in DNA repair and breast cancer susceptibility identified *Palb2* as a candidate gene localized in this region. Subsequent gene expression analysis demonstrated no difference between the strains. In addition, no coding SNPs were identified between the strains effectively eliminating this gene as a candidate.

Further narrowing of the interval with additional markers as well as a filtering criteria produced a list of 34 candidate genes. Gene expression analyses were performed and identified *Il21r* as a gene significantly more highly expressed in the BALB/c strain. Unfortunately, this same gene was significantly overexpressed in the BALB.B6-*SuprMam1* congenic strain suggesting the activation of this gene lies outside the *SuprMam1* region eliminating it as a candidate. The inability to identify any candidate genes with significantly different gene expression between the strains was disappointing. However, the possibility remains that any of the coding SNPs in the candidate genes may effect the function of the corresponding protein and possibly increase mammary tumor susceptibility. This was the case in genes involved in double-strand break repair whose SNPs were linked to breast cancer (Goode et al., 2002). It remains to be seen if this is the case or perhaps another gene outside of our list of candidates but contained within the *SuprMam1* interval is a better candidate.

Finally, we were interested in determining if there were any irradiation sensitivity alleles within the *SuprMam1* region. To test this, we measured irradiation-induced apoptosis in the mammary gland of various strains including C57BL/6, BALB/c, F1 and BALB.B6-*SuprMam1*. Our results recapitulate previous work showing the BALB/c strain being sensitive to irradiation. We also concluded that there does not appear to be any irradiation sensitivity alleles within the *SuprMam1* region as no differences in apoptosis were observed between the BALB/c strain and the BALB.B6-*SuprMam1* strain.

We have established a defect in RAD51 localization to DNA double-strand breaks following DNA damage suggesting an error in this pathway. This defect in addition to the defect in NHEJ present in the BALB/c strain may predispose to increase mammary tumor susceptibility. It appears likely that either our filtering criteria was too stringent or that the function of one of our candidate genes is diminished by a coding SNP. In addition, the possibility exists for other non-coding elements within the *SuprMam1* region may be affecting mammary tumor susceptibility in the BALB/c strain. Future work will need to be done to address these hypotheses.

CHAPTER 7

PROTOCOLS

Double-strand break DNA repair Assay

List of equipment:

AMAXA Nucleoporator
FACS tubes
Alpha MEM media (Gibco) + 10%FBS + additions (glutamine, BME, antibiotics)
PBS + 0.2% EDTA
Plasmids: J04-38 wt-EGFP control plasmid
J04-39 NHEJ construct plasmid
J04-40 HR-3' construct plasmid

Prepare Cells

a. Friday before:
    i. Thaw 2 vials of passage 0-3 MEF cells of each desired cell line into 2 T-75 flasks using 10ml/ flask Alpha mem medium with all additions
    ii. Let grow over the weekend
b. Monday before experiment
    i. Trypsinize cells and count
    ii. Seed 3 x 10^6 into 4 T-75 flasks with 10 ml/ flask DMEM/F12 medium + all additions
    iii. Freeze left over cells if necessary
c. Thursday (the day of the experiment)
    i. Trypsinize cells (2 ml trypsin, when cells come up add 2 ml D/F medium + 10% FBS
    ii. Count cells
    iii. Spin in a 50 ml conical; remove supernatant
    iv. Dilute with PBS so that cells number 8 x 10^5 / ml
    v. Add 3 ml / 15 ml conical for a triplicate electroporation (e.g. for testing HR in triplicate)
    vi. Generally 4 tubes / cell line:
        A. 5 ml in 15 ml conical for 2 control and 3 NHEJ electroporations
        B. 3ml in 15 ml conical for 3 HR electroporations
        C. 3ml in 15 ml conical for 3 GFP electroporations
        D. 3 ml in 14 ml conical for extra cells in case of mistake
    vii. Spin tubes 5 min 200 x g, aspirate supernatant and put pellet on ice

Electroporation

d. Remove one 15 ml conical from ice and remove any excess PBS from pellet with P200 set at 100
e. Resuspend pellet in 310 ul room temperature AMAXA solution (pipette up and down gently – no bubbles)
f. Remove caps from 3 cuvettes and place caps upside down in front of the cuvettes.
g. In the cap, place 5.1 ul of the plasmid mixture.
h. Remove 100 ul of cells from the resuspended solution and mix with plasmid in the cap; place suspension of cells + plasmid into cuvette.
i. Using same pipette tip, mix the remaining cells, 100 ul at a time with the plasmid in the cap and place in cuvette; cap all cuvettes
j. Electroporate with program A23 in Nucleoporator
k. Remove the 6 well plate and the 60 ml dish from the incubator
l. Remove caps from cuvettes and add 0.5 ml D/F medium + additions to each cuvette
m. Using transfer pipette transfer cells electroporated with plasmid from 1 cuvette to 1 well of 6 well plate. Rinse cuvette with medium taken by transfer pipette from a different part of the well.

FACS Set-up

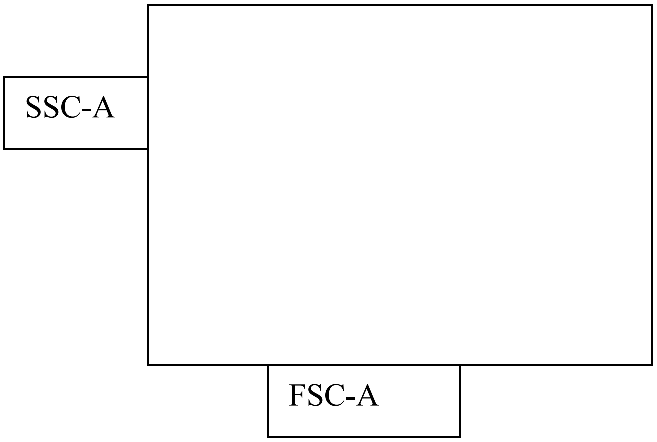
-Open up 2 dot plots on the global worksheet (right screen) and one histogram

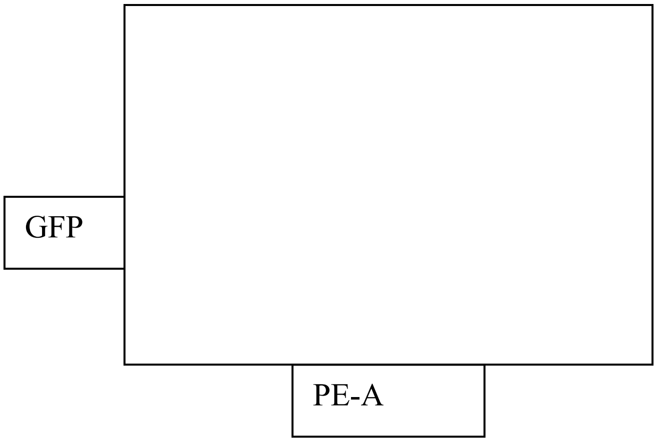
-Click the Parameters tab under Instrument Settings in the Browser Window

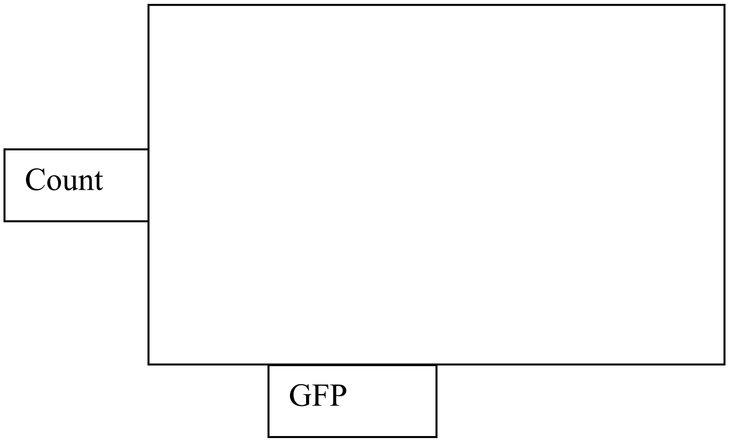
-Change FITC to GFP and delete everything except: FSC, SSC, GFP, PE

-GFP: LA
PE: LA
All others have area

-Switch windows accordingly:







-Change Voltage in Instrument Window: FSC: 340
SSC: 285
GFP: 430
PE: 401
-Record 50,000 events: Experiment Layout, acquisitions to 50,000

Comet Assay

Solutions:

Lysing Solution: Ingredients per 1000 mL: 2.5 M NaCl 146.1 gm
100 mM EDTA 37.2 gm
10 mM Trizma base 1.2 gm

Add ingredients to about 700 mL dH2O and begin stirring the mixture. Add ~8 gm NaOH and allow the mixture to dissolve (about 20 min). Adjust the pH to 10.0 using concentrated HCl or NaOH. q.s. to 890 mL with dH2O (the Triton X-100 and DMSO will increase the volume to the correct amount), store at room temperature.

Final lysing solution: add fresh 1% Triton X-100 and 10% DMSO, and then refrigerate for at least 30 minutes prior to slide addition.

NOTE**:** The purpose of the DMSO in the lysing solution is to scavenge radicals generated by the iron released from hemoglobin when blood or animal tissues are used. It is not needed for other situations or where the slides will be kept in lysing for a brief time only.

Electrophoresis Buffer (300 mM NaOH / 1 mM EDTA):
Prepare from stock solutions:
1. 10 N NaOH (200 g/500 mL dH2O)
2. 200 mM EDTA (14.89 g/200 mL dH2O, pH 10)

Store both at room temperature. We prepare the NaOH and EDTA stock solutions every ~2
weeks.

For 1X Buffer (made fresh before each electrophoresis run): per liter, add 30 mL NaOH and
5.0 mL EDTA, q.s. to 1000 mL, mix well. The total volume depends on the gel box capacity.
Prior to use, measure the pH of the buffer to ensure >13.

Neutralization Buffer: 0.4 M Tris - 48.5 gm added to ~800 mL dH2O, adjust pH to 7.5 with
concentrated (>10 M) HCl: q.s. to 1000 mL with dH2O, store at room temperature.

Staining Solution: DAPI at a concentration of 0.1 µg/mL in PBS. Stock is 500 µg/mL, do a 1:5000 dilution.

Procedure: I typically add 100,000 cells per 60 mm plate and process the next day. Depending on your cell type, you may have to adjust.

1. The day before running the assay, prepare slides by dipping in methanol and flaming them to remove oil layer on slide. Next, dip slides into beaker with 1% normal agarose (recommended 50 mL of agarose diluted in water in 250 mL beaker). You may have to flame the slides further for agarose to coat slides properly. Wipe off bottom and place in dust free area to cool overnight.

2. The day of the assay, trypsinize cells off plates, neutralize trypsin with media plus serum and spin down cells. Remove media leaving pellet.

3. Resuspend cells in 10 µl PBS. Add 75 µl of 0.5% low melting agarose (made with PBS) to tube and pipet up and down to mix. Pipet mixture on pre-coated slides and carefully place coverslip on top. Place slides in 4 degree for 5 min.

4. Take out slides from fridge and carefully remove coverslips. Pipet another 80 µl of 0.5% low melting agarose on top of slides and place coverslips back on. Place slides back in 4 degrees for 5 more minutes.

5. Remove slides from fridge and remove coverslip carefully. Place slides vertically in coplin jars with ~25 mL of lysis buffer or enough to cover

6. Remove slides from coplin jars and place in electrophoresis box with just enough buffer to cover slides. Make sure the agarose part of the slide faces or is closer to the cathode (red or positive end). Let the slides sit in the box with buffer for 20 minutes to allow DNA to unwind.

7. Electrophorese the slides at 24 volts and 300 mAmps. Adjust buffer volume to achieve 300 mAmps while keeping 24 volts constant. Run slides for 30 minutes.

8. Remove slides from electrophoresis box and add ~750 µl of neutralization solution to slides. Allow slides to sit for 5 min. at RT. Repeat procedure 2 more times. After last incubation, wash slides gently with dH2O (by pipetting or squirt bottle).

9. Add ~750 µl of DAPI to slide and incubate 5 min. at RT. Wash off excess DAPI with dH2O and place coverslip on top of slide. Place slides in dark or analyze.

MEF Immunofluorescence

Materials:

- Cell culture plates
- MEF media
- PBS
- Formaldehyde
- Triton X-100 0.5%
- Tweezers
- Round microscope coverslips
- 12-well plate
- Goat Serum 5%
- Primary and Secondary anti-bodies
- Mounting solution (recipe in protocol)
- DAPI stain (0.1 µg/mL in PBS)

1. Irradiate plates using the gamma irradiator
2. Incubate 37 degrees for appropriate timepoint.
3. Remove media and wash cells once with PBS.
4. Add 500 µl of 3.7% formaldehyde for 7 minutes to fix cells.
5. Remove formaldehyde and wash cells 2 times with PBS.
6. Add 500 µl of .5% TritonX in PBS to the cells for 7 minutes on ice.
7. Remove TritonX and wash cells once with PBS.

8. Using tweezers, carefully remove coverslips from wells and dip in PBS/.05% Tween before placing coverslip on an upside down top of a 24-well plate with the cells facing up.
9. Add 25 µl of primary antibody diluted in PBS with 5% goat serum to coverslip.
10. Cover and either incubate 37 degrees for 1 hour or 4 degrees overnight.
11. Place coverslips back into 24 well plate and wash coverslips 3 times, 5 minutes each.
12. Dilute secondary antibody in PBS with 5% goat serum and add 25 µl to each coverslip on upside down top of a 24 well plate as described in step 9.
13. Incubate 30-45 minutes at 37 degrees.
14. Place coverslips back into 24 well plate and wash coverslips 3 times, 5 minutes each.
15. Dilute DAPI in PBS and incubate coverslips in 250 µl for 5 minutes.
16. Wash coverslips 2 times with PBS.
17. Mounting solution composes of 3 parts Mowial(Calbiochem) and 1 part DABCO (Sigma).
18. Place a drop of mounting solution on glass slide, then carefully place coverslip with cells facing down onto slide.
19. Cover slides (protect from light) and let sit overnight.
20. Next day, wash salt off slides with deionized water and wait 1 hour to dry.
21. Capture pictures of cells using a fluorescence microscope.

Mounting Agent Recipe

1. Put 6 grams glycerol in 150 ml glass beacker and add a small stir bar
2. Add 2.4 g Mowiol (Calbiochem); stir to mix
3. While stirring, add 6 ml distilled water and leave for 2 hours at room temperature
4. Add 12 ml 0.2M Tris (pH 8.5)
5. Incubate the tube in hot water (50-60°C) for 10 minutes to dissolve the Mowiol. This can be repeated over several hours if necessary.
6. Centrifuge at 5000 g for 15 minutes to remove any undissolved solids. Store 1 ml aliquots in eppendorf tubes at -20 °C.
7. Warm tubes to room temperature for use. Opened tubes can be stored at 4 °C for approximately 1 month.

Mouse Ovariectomy

Equipment:

Hair clippers
Surgical scissors
Surgical forceps
Serrifin clamps
Ethicon sutures 6-0 gauge

Wound stapler
9mm stainless steel wound clips
1 mL 26G syringes (Becton Dickinson)
70% ethanol
Avertin (.02g/mL)

Procedure:

1. Shave the back of the mouse.
2. Make a single mid-line incision along the back.
3. Lay the mouse on its side and locate one ovary. The ovary is beneath a deposit of white fat that is quite apparent in contrast to the surrounding dark red organs. Make an incision through the peritonium and pull the ovary out using the sharp jewlers forceps (#6). Note that the kidney can be easily damage because it is attached to the ovary by loose tissues.
4. Use the Serrifin clamp to hold the ovary. Place a ligature at the base of the ovary, but try to remain above the Fallopian tubes.
5. Remove the ovary, then close the peritoneum with one or two stitches.
6. Repeat the procedure on the contralateral side.
7. Close the skin with 2-9 mm wound clips.

MEF isolation

Materials:

Uterine Rinse:
125 ml Phospate Buffered Solution
2 ml AB/AM (100U/ml penicillin, 100 µg/ml streptomycin, .25 µg/ml amphotericin final) (Gibco 100X)
1 ml Fungizone
0.5 ml Tylosin tartarate (Gibco) (8 µg/ml final concentration)
30 µl Gentamycin (Gibco) (15 µg/ml final concentration)

Collagenase solution:
0.1 g Collagenase (Gibco)
50 ml Alpha MEM media (Fisher Scientific)
10 µl Gentamycin
0.25 ml AB/AM
0.25 Fungizone
0.25 Tylosin

Medium:
500 ml Alpha MEM
50 ml Fetal Bovine Serum (FBS)
5 ml AB/AM

1.4 ml Beta mercapto ethanol (Gibco 1000X)
5 ml Glutamine (Gibco 100X) (2mM final concentration)
150 µl Gentamycin
.5 ml Tylosin

Procedure:
1. Mate animals, check for plugs to confirm mating
2. Sacrifice pregnant mouse 14 days after plug confirmation
3. Collect uterus of p14 mouse in 100mm dish of uterine rinse solution
4. Transfer uterus to clean 100mm dish of sterile uterine rinse
5. Using forceps, gently tear the uterine walls so that fetus pops out
6. Remove head of fetus and any internal organs that appear a crimson red
7. Transfer bodies to a clean 100mm dish
8. When done with all fetuses, place each individual in a clean 60mm dish with uterine rinse.
9. Transfer all material to tissue culture hood. Aspirate rinse and mince each fetus separately with scissors.
10. Add 2 ml of 0.2% collagenase (Worthington Collagenase type 3, 0.1 g in 50 ml Alpha MEM media without serum but with appropriate antiobiotics.
11. Transfer minced fetuses each to a 15 ml conical tube and incubate 30 minutes at 37°C. Every 10 minutes, gently invert tubes. Do not overdigest.
12. Pellet cells by centrifugation at 1200xG for 5 minutes
13. Wash pellet with Alpha MEM media no serum
14. Resuspend pellet and plate on a T-75 plate with Alpha MEM complete media.

Hormone filled silastic tubing capsules and Implantation

Reagents:

Medical grade silastic tubing (Dow Corning, 508-009)
Clear silicone
Beta Estradiol 50 µg/tube (Sigma, E2758-1G)
Progesterone 20 mg/tube (Sigma, P0130-25G)
Wound Clips
Hair clippers
Scissors, forceps
Avertin (

II. Preparation
   A. Silastic tubing (can be autoclaved if sterility is an issue)
      1) Cut silastic tubing the length of 1.2 to 1.5 cm

2) Seal one end of the tubing with clear silicone. Squeeze silicone on end of tubing and scrape off any extra, being sure the end is completely sealed. Allow to dry 2 to 3 hours.

B. Prepare steroid stock

1) Master mix – prepare enough master mix for double the amount of samples you have (ex. for 4 mice make enough MM for 8)
2) Weigh out hormones on the small balance, see dosage column above. (ex. if I had 4 mice I and wanted to treat them with Progestrone I would multiply 8(because we double the amount of samples) by 400ug. This would be .003g.
3) If treating with a combination of hormones, weigh the hormones individually. Then stir them together well in a small beaker with a spatula
4) Cut the end of a 5ml pipette to use for a funnel and insert it into the open end of the capsule.
5) Weigh the capsule prior to filling and pack with 20-30mg of hormone master mix. As the master mix is being added use the wooden end of a swab to pack the hormones in.
6) Seal opposite end if the tubing. Let silicone set 2 to 3 hours.
7) After 2 to 3hrs incubate capsule at 37C overnight in PBS, the next day implant.

C. Implantation

1) Keep capsules in PBS until implantation.
2) Prepare the area by shaving the dorsal region of the mouse. Make an incision through the skin over the shoulders. Implant subcutaneously. Close with a wound clip.

RT and QPCR reactions

Total RNA was isolated using Trizol solution according to protocol. Isolated RNA was reverse transcribed using Stratagene cDNA kit and analyzed for gene expression using Stratagene Syber Green kit.

<u>cDNA protocol</u>:

<u>1X</u>
10 ul Master Mix
1.5 ul Random Hexamer primers
1.5 ul oligo dT
3 ul dH2O
<u>3 ul of RNA (1ug total)</u>

Mix random hexamer primers, olido dT and RNA together and incubate at 65 degrees for 7 minutes. Then add master mix and 1 ul Reverse transcriptase in RT samples. Incubate at 50 degrees for 45 minutes then 85 degrees for 10 minutes.

This cDNA is then diluted 1:5 and 1 ul is used for each sample in a QPCR reaction.

QPCR reaction:

1X
10 ul Master Mix
8 ul dH20
.2 ul F primer (50 pm/ul)
.2 ul R primer (50 pm/ul)
1 ul cDNA reaction

Basic reaction conditions, primer Tm is 58 degrees for 45 seconds and then extension at 72 degrees for 45 seconds.

SM1 genotyping protocols

PCR mix

1 reaction	
dH2O	21.8 µl
Thermopol buffer (Roche)	2.7 µl
dNTP mix (Roche)	1.09 µl
Primer set (F and R)(50 pm/ µl each)	0.45 µl
	26.04 µl

Enzyme Mix

1 reaction	
dH2O	4 µl
Thermopol buffer (Roche)	0.5 µl
Taq polymerase (Roche)	0.5 µl
	5 µl

1. Add 1ul of DNA aprox .08-2ug/ul to 26ul of MM, add
2. Add 5ul of EM for each RX

Thermocycler conditions:
95C 8min
95C 30 Sec
57C 45 sec
72C 1min

Go to 2 35X
72C 10 min
4C forever

Restriction Enzyme digestion:

<u>1 reaction</u>	
dH2O	12 µl
Restriction enzyme buffer (NEB)	3 µl
Restriction enzyme	1.5 U
BSA (if needed)	0.3 µl

1. Add 15ul of digest mix to 15ul of the PCR product and incubate at 37C for 3hr.
2. 2. Make a 2% TBE gel with ethidium bromide and run the digested amplicon at 150 volts. Take a picture of the gel and analyze bands.

Apoptosis Assay

TdT-FragEL^{TM} DNA Fragmentation Dectection Kit (TUNEL) (Calbiochem QIA33)

Cut 4mm mammary gland sections and put on slide warmer the night before TUNEL assay. Maximum number of slides one can effectively use is 12-14. During assay do not ever let tissue dry out. Store in 1X PBS when necessary.

1. Prior to beginning assay do the following:
    a. Prewarm incubator and water bath to 37^{o}C
    b. Defrost on ice
        i. Proteinase K
        ii. 5X TdT equilibration buffer
        iii. TdT labeling reaction mix
    c. Prepare 10mM Tris, pH 8.0
        i. 100µl of 1M Tris, pH 8.0 in 9900µl MQH2O
    d. Prepare 1X TBS
2. Deparaffin and rehydrate tissue (prepare ProK during rehydration steps)
    a. 3 X 5 minutes in Xylene
    b. 2 X 5 minutes in 100% EtOH
    c. 1 X 3 minutes in 95% EtOH
    d. 1 X 3 minute in 70% EtOH
    e. 1 X 5 minute in PBS
3. Permeabilization of specimen
    a. Prepare 20µg/mL 1:100 Pro K in 10mM Tris, pH 8.0
    b. Example: 14 + 1 specimens = 15µl of Pro K and 1485µl of 10mM Tris, pH 8.0

- c. Do slides one at a time. Start the timer at 12 minutes after the very first slide. When complete note the time remaining on the timer and calculate average time in seconds for draining Pro K from slides so all slides have equal exposure time.
- d. Drain TBS from slide and wipe around tissue
- e. Add 100µl of 10µg/ml Proteinase K
- f. Incubate 12 minutes (Prepare PBS/H_2O_2)
- g. When complete, put slides in fresh dH2O 2X for 2 minutes each.

4. Inactivation of endogenous peroxidases
    - a. Make PBS/H_2O_2 of 180ml PBS plus 20ml of 30% H_2O_2
    - b. Drain PBS from slide
    - c. Put slides in slide jar with PBS/H_2O_2
    - d. Incubate 5 minutes at RT – DO NOT OVER INCUBATE (Prepare TdT buffer)
    - e. Transfer slides back to PBS 2X for 5 minutes each.
5. Equilibration
    - a. Tap off excess liquid, wipe around tissue
    - b. Add 75µl of TdT equilibration buffer
    - c. Incubate 10 minutes (prepare labeling reaction mix after 10 minutes)
6. Labeling
    - a. Prepare microfuge tube with 77 µl reaction buffer (6 tubes for 12 samples)
    - b. Work with two slides each time
    - c. Tap off excess liquid, wipe around tissue
    - d. Add 33 µl of TdT enzyme to microfuge tube.
    - e. Add 50 µl of diluted TdT enzyme to tissue, seal top cover with parafilm
    - f. Add hot sponges to humidity chamber
    - g. Incubate 1 hours at 37°C
7. Termination of Labeling
    - a. Prepare ~100 mL of working strength stop/wash buffer- 3mL stop/wash + 102 H2O
    - b. Put stop/wash buffer in coplin jar, add slides
    - c. Incubate agitating for 15 seconds
    - d. Incubate 10 minutes at room temperature
8. anti-digoxigen conjugate
    - a. Wash specimen 3X in PBS one minute each
    - b. Tap off excess liquid and wipe around the tissue
    - c. Apply room temperature anti-digoxigen to tissue ~65 µl

   d. Cover slides with square piece of parafilm
   e. Incubate at room temperature in humidity chamber with sponges for 30 minutes

9. Develop color in peroxidase substrate
   a. Wash slides in 4 changes of PBS at room temperature, 2 minutes each
   b. Add 147 µl of DAB dilution buffer plus 3 µl DAB substrate (enough for 2 slides)
   c. Tap off liquide and wipe around tissue
   d. Cover tissue with 75 µl of peroxidase substrate
   e. Stain for 5 minutes
10. Counterstain
   a. Wash specimen 3X in dH2O one minute each
   b. Incubate slides in dH2O for 5 minutes at room temperature
   c. Counterstain with hematoxylin for 20 seconds
   d. Rinse in hot water
   e. Incubate in glacial acetic acid for 20 seconds
   f. Incubate in ammonia water for 15 seconds
   g. Dehydrate in classic 95%, 100%, xylene run through, 3 minutes each.
   h. Mount specimen with permount and coverslip, allow slides to dry overnight

Solutions for cell culture

2X Freeze media
40 ml desired media (DMEM:F12 with 10% FBS)
10 ml DMSO (5ml glass vials of Dimethyl Sulphoxide)
Store at -20^{o}C in 10 ml aliquots

DMEM:F12 Media
1 bottle of DMEM:F12 powered media
1.2g $NaHCO_3$ sodium bicarbonate
2.38g of HEPES
Bring volume up to ~ 800 ml with MQ H2O
Adjust pH to 7.6
Filter sterilize into 2 – 500ml bottles
Store at 4^{o}C

Add to DMEM:F12 media before use (500ml bottle)

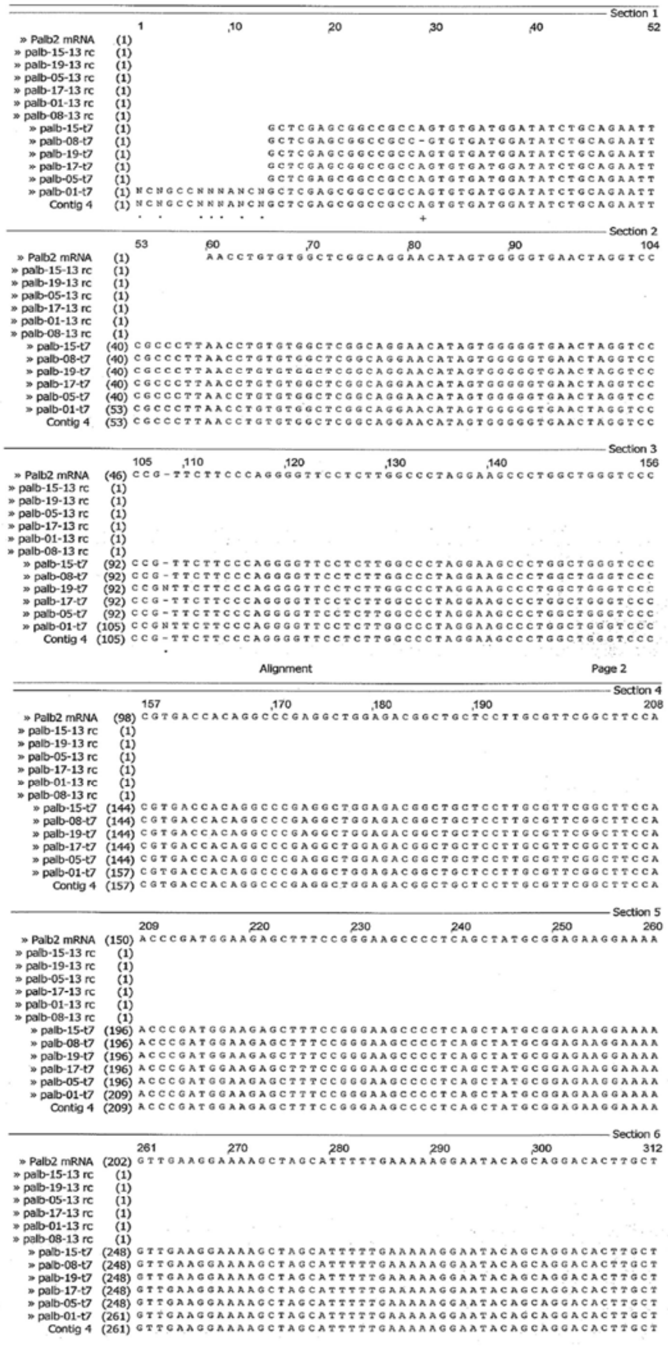
10% heat treated (30 minutes at 55^{o}C) FBS	50ml
L-glutamine	5ml
Bins (bovine insulin)	500µl
Gentamycin	150µl
AB/AM	5ml

Mouse tail DNA isolation

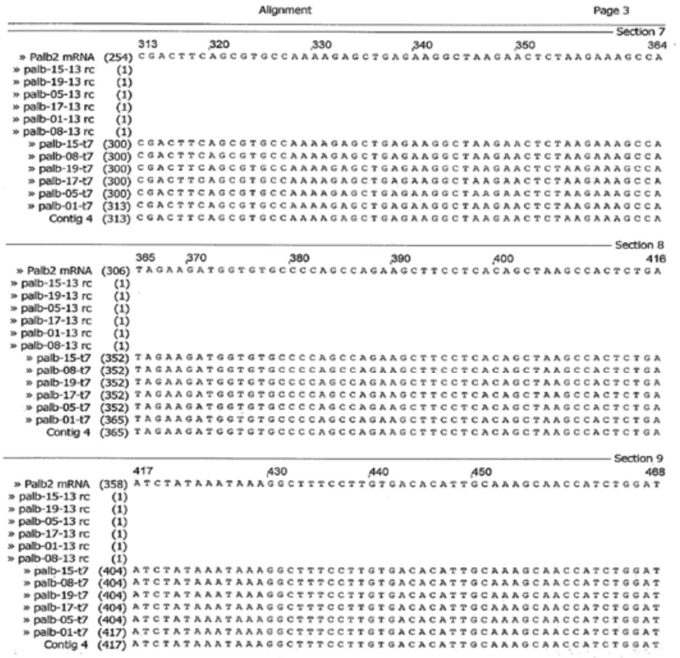
1. 0.5-1 cm mouse tail to be genotyped in 1.5 ml Eppendorf tube
2. Add 0.5 ml TENS buffer to tube (100 mM Tris-HCl pH 8.5; 5 mM EDTA; 0.2% SDS; 200 mM NaCl)
3. Add 5 µl of stock 10 mg/ml proteinase K (100X) to 100 µg/ml final
4. Vortex and incubate overnight at $55C^o$ in water bath or hybe-oven
5. Next day, vortex and centrifuge 13K RPM at room temperature for 5 minutes. Transfer supernatant to a new tube.
6. Add 0.5 ml isopropanon; invert and shake tubes until DNA precipatates
7. 3 options:
   a. Centrifuge 5 min. 13K RPM
   b. Pick DNA precipitate with pipette tip and transfer to clean tube
   c. Hold the DNA precipitate on side of tube and decant supernatant
8. Wash DNA precipitate with 70% ethanol, centrifuge for 5 minutes at 13K RPM
9. Remove liquide and dry tubes upside down for 5 minutes and vacuum dry for 5 minutes or air dry an additional 30 minutes.
10. Add 50 to 100 µl TE (Tris-EDTA) and solubilize for 2 hours to overnight at 37-65C. Vortex.

APPENDIX A

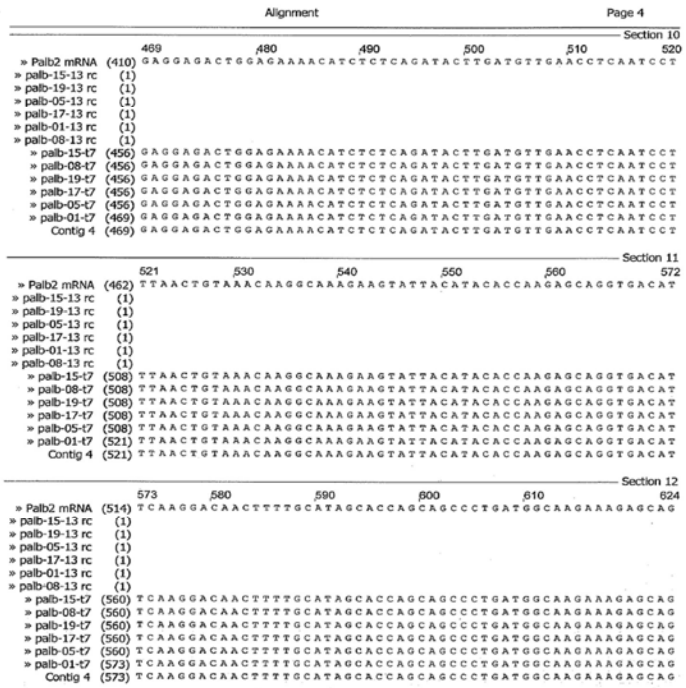
PALB2 SEQUENCING RESULTS



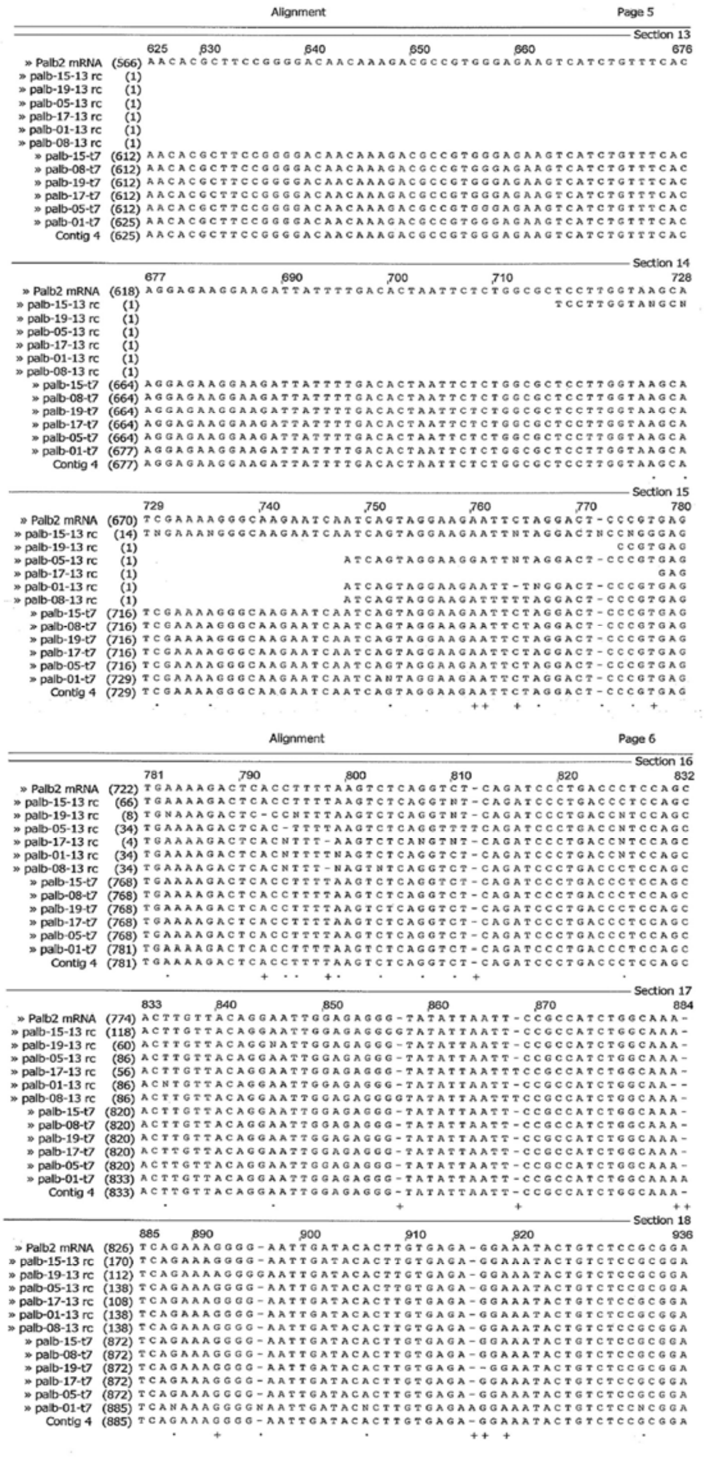
```
---------------------------------------------------------------- Section 1
                      1       ,10       ,20       ,30       ,40         52
   » Palb2 mRNA   (1)
» palb-15-13 rc   (1)
» palb-19-13 rc   (1)
» palb-05-13 rc   (1)
» palb-17-13 rc   (1)
» palb-01-13 rc   (1)
» palb-08-13 rc   (1)
   » palb-15-t7   (1)              GCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATT
   » palb-08-t7   (1)              GCTCGAGCGGCCGCC-GTGTGATGGATATCTGCAGAATT
   » palb-19-t7   (1)              GCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATT
   » palb-17-t7   (1)              GCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATT
   » palb-05-t7   (1)              GCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATT
   » palb-01-t7   (1) NCNGCCNNNANCNGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATT
       Contig 4   (1) NCNGCCNNNANCNGCTCGAGCGGCCGCCAGTGTGATGGATATCTGCAGAATT
                      . .   ... . .               +
---------------------------------------------------------------- Section 2
                      53    ,60       ,70       ,80       ,90          104
   » Palb2 mRNA   (1)        AACCTGTGTGGCTCGGCAGGAACATAGTGGGGGTGAACTAGGTCC
» palb-15-13 rc   (1)
» palb-19-13 rc   (1)
» palb-05-13 rc   (1)
» palb-17-13 rc   (1)
» palb-01-13 rc   (1)
» palb-08-13 rc   (1)
   » palb-15-t7  (40) CGCCCTTAACCTGTGTGGCTCGGCAGGAACATAGTGGGGGTGAACTAGGTCC
   » palb-08-t7  (40) CGCCCTTAACCTGTGTGGCTCGGCAGGAACATAGTGGGGGTGAACTAGGTCC
   » palb-19-t7  (40) CGCCCTTAACCTGTGTGGCTCGGCAGGAACATAGTGGGGGTGAACTAGGTCC
   » palb-17-t7  (40) CGCCCTTAACCTGTGTGGCTCGGCAGGAACATAGTGGGGGTGAACTAGGTCC
   » palb-05-t7  (40) CGCCCTTAACCTGTGTGGCTCGGCAGGAACATAGTGGGGGTGAACTAGGTCC
   » palb-01-t7  (53) CGCCCTTAACCTGTGTGGCTCGGCAGGAACATAGTGGGGGTGAACTAGGTCC
       Contig 4  (53) CGCCCTTAACCTGTGTGGCTCGGCAGGAACATAGTGGGGGTGAACTAGGTCC
---------------------------------------------------------------- Section 3
                      105 ,110      ,120      ,130      ,140           156
   » Palb2 mRNA  (46) CCG-TTCTTCCCAGGGGTTCCTCTTGGCCCTAGGAAGCCCTGGCTGGGTCCC
» palb-15-13 rc   (1)
» palb-19-13 rc   (1)
» palb-05-13 rc   (1)
» palb-17-13 rc   (1)
» palb-01-13 rc   (1)
» palb-08-13 rc   (1)
   » palb-15-t7  (92) CCG-TTCTTCCCAGGGGTTCCTCTTGGCCCTAGGAAGCCCTGGCTGGGTCCC
   » palb-08-t7  (92) CCG-TTCTTCCCAGGGGTTCCTCTTGGCCCTAGGAAGCCCTGGCTGGGTCCC
   » palb-19-t7  (92) CCGNTTCTTCCCAGGGGTTCCTCTTGGCCCTAGGAAGCCCTGGCTGGGTCCC
   » palb-17-t7  (92) CCG-TTCTTCCCAGGGGTTCCTCTTGGCCCTAGGAAGCCCTGGCTGGGTCCC
   » palb-05-t7  (92) CCG-TTCTTCCCAGGGGTTCCTCTTGGCCCTAGGAAGCCCTGGCTGGGTCCC
   » palb-01-t7 (105) CCGNTTCTTCCCAGGGGTTCCTCTTGGCCCTAGGAAGCCCTGGCTGGGTCCC
       Contig 4 (105) CCG-TTCTTCCCAGGGGTTCCTCTTGGCCCTAGGAAGCCCTGGCTGGGTCCC
                         .

                              Alignment                          Page 2
---------------------------------------------------------------- Section 4
                      157         ,170      ,180      ,190             208
   » Palb2 mRNA  (98) CGTGACCACAGGCCCGAGGCTGGAGACGGCTGCTCCTTGCGTTCGGCTTCCA
» palb-15-13 rc   (1)
» palb-19-13 rc   (1)
» palb-05-13 rc   (1)
» palb-17-13 rc   (1)
» palb-01-13 rc   (1)
» palb-08-13 rc   (1)
   » palb-15-t7 (144) CGTGACCACAGGCCCGAGGCTGGAGACGGCTGCTCCTTGCGTTCGGCTTCCA
   » palb-08-t7 (144) CGTGACCACAGGCCCGAGGCTGGAGACGGCTGCTCCTTGCGTTCGGCTTCCA
   » palb-19-t7 (144) CGTGACCACAGGCCCGAGGCTGGAGACGGCTGCTCCTTGCGTTCGGCTTCCA
   » palb-17-t7 (144) CGTGACCACAGGCCCGAGGCTGGAGACGGCTGCTCCTTGCGTTCGGCTTCCA
   » palb-05-t7 (144) CGTGACCACAGGCCCGAGGCTGGAGACGGCTGCTCCTTGCGTTCGGCTTCCA
   » palb-01-t7 (157) CGTGACCACAGGCCCGAGGCTGGAGACGGCTGCTCCTTGCGTTCGGCTTCCA
       Contig 4 (157) CGTGACCACAGGCCCGAGGCTGGAGACGGCTGCTCCTTGCGTTCGGCTTCCA
---------------------------------------------------------------- Section 5
                      209       ,220      ,230      ,240      ,250     260
   » Palb2 mRNA (150) ACCCGATGGAAGAGCTTTCCGGGAAGCCCCTCAGCTATGCGGAGAAGGAAAA
» palb-15-13 rc   (1)
» palb-19-13 rc   (1)
» palb-05-13 rc   (1)
» palb-17-13 rc   (1)
» palb-01-13 rc   (1)
» palb-08-13 rc   (1)
   » palb-15-t7 (196) ACCCGATGGAAGAGCTTTCCGGGAAGCCCCTCAGCTATGCGGAGAAGGAAAA
   » palb-08-t7 (196) ACCCGATGGAAGAGCTTTCCGGGAAGCCCCTCAGCTATGCGGAGAAGGAAAA
   » palb-19-t7 (196) ACCCGATGGAAGAGCTTTCCGGGAAGCCCCTCAGCTATGCGGAGAAGGAAAA
   » palb-17-t7 (196) ACCCGATGGAAGAGCTTTCCGGGAAGCCCCTCAGCTATGCGGAGAAGGAAAA
   » palb-05-t7 (196) ACCCGATGGAAGAGCTTTCCGGGAAGCCCCTCAGCTATGCGGAGAAGGAAAA
   » palb-01-t7 (209) ACCCGATGGAAGAGCTTTCCGGGAAGCCCCTCAGCTATGCGGAGAAGGAAAA
       Contig 4 (209) ACCCGATGGAAGAGCTTTCCGGGAAGCCCCTCAGCTATGCGGAGAAGGAAAA
---------------------------------------------------------------- Section 6
                      261     ,270      ,280      ,290      ,300       312
   » Palb2 mRNA (202) GTTGAAGGAAAAGCTAGCATTTTTGAAAAAGGAATACAGCAGGACACTTGCT
» palb-15-13 rc   (1)
» palb-19-13 rc   (1)
» palb-05-13 rc   (1)
» palb-17-13 rc   (1)
» palb-01-13 rc   (1)
» palb-08-13 rc   (1)
   » palb-15-t7 (248) GTTGAAGGAAAAGCTAGCATTTTTGAAAAAGGAATACAGCAGGACACTTGCT
   » palb-08-t7 (248) GTTGAAGGAAAAGCTAGCATTTTTGAAAAAGGAATACAGCAGGACACTTGCT
   » palb-19-t7 (248) GTTGAAGGAAAAGCTAGCATTTTTGAAAAAGGAATACAGCAGGACACTTGCT
   » palb-17-t7 (248) GTTGAAGGAAAAGCTAGCATTTTTGAAAAAGGAATACAGCAGGACACTTGCT
   » palb-05-t7 (248) GTTGAAGGAAAAGCTAGCATTTTTGAAAAAGGAATACAGCAGGACACTTGCT
   » palb-01-t7 (261) GTTGAAGGAAAAGCTAGCATTTTTGAAAAAGGAATACAGCAGGACACTTGCT
       Contig 4 (261) GTTGAAGGAAAAGCTAGCATTTTTGAAAAAGGAATACAGCAGGACACTTGCT
```



```
                  Alignment                                              Page 3
------------------------------------------------------------------ Section 7
                    313    320       330       340       350            364
 » Palb2 mRNA  (254) CGACTTCAGCGTGCCAAAAGAGCTGAGAAGGCTAAGAACTCTAAGAAAGCCA
» palb-15-13 rc  (1)
» palb-19-13 rc  (1)
» palb-05-13 rc  (1)
» palb-17-13 rc  (1)
» palb-01-13 rc  (1)
» palb-08-13 rc  (1)
   » palb-15-t7 (300) CGACTTCAGCGTGCCAAAAGAGCTGAGAAGGCTAAGAACTCTAAGAAAGCCA
   » palb-08-t7 (300) CGACTTCAGCGTGCCAAAAGAGCTGAGAAGGCTAAGAACTCTAAGAAAGCCA
   » palb-19-t7 (300) CGACTTCAGCGTGCCAAAAGAGCTGAGAAGGCTAAGAACTCTAAGAAAGCCA
   » palb-17-t7 (300) CGACTTCAGCGTGCCAAAAGAGCTGAGAAGGCTAAGAACTCTAAGAAAGCCA
   » palb-05-t7 (300) CGACTTCAGCGTGCCAAAAGAGCTGAGAAGGCTAAGAACTCTAAGAAAGCCA
   » palb-01-t7 (313) CGACTTCAGCGTGCCAAAAGAGCTGAGAAGGCTAAGAACTCTAAGAAAGCCA
       Contig 4 (313) CGACTTCAGCGTGCCAAAAGAGCTGAGAAGGCTAAGAACTCTAAGAAAGCCA

------------------------------------------------------------------ Section 8
                    365  370         380       390       400            416
 » Palb2 mRNA  (306) TAGAAGATGGTGTGCCCCAGCCAGAAGCTTCCTCACAGCTAAGCCACTCTGA
» palb-15-13 rc  (1)
» palb-19-13 rc  (1)
» palb-05-13 rc  (1)
» palb-17-13 rc  (1)
» palb-01-13 rc  (1)
» palb-08-13 rc  (1)
   » palb-15-t7 (352) TAGAAGATGGTGTGCCCCAGCCAGAAGCTTCCTCACAGCTAAGCCACTCTGA
   » palb-08-t7 (352) TAGAAGATGGTGTGCCCCAGCCAGAAGCTTCCTCACAGCTAAGCCACTCTGA
   » palb-19-t7 (352) TAGAAGATGGTGTGCCCCAGCCAGAAGCTTCCTCACAGCTAAGCCACTCTGA
   » palb-17-t7 (352) TAGAAGATGGTGTGCCCCAGCCAGAAGCTTCCTCACAGCTAAGCCACTCTGA
   » palb-05-t7 (352) TAGAAGATGGTGTGCCCCAGCCAGAAGCTTCCTCACAGCTAAGCCACTCTGA
   » palb-01-t7 (365) TAGAAGATGGTGTGCCCCAGCCAGAAGCTTCCTCACAGCTAAGCCACTCTGA
       Contig 4 (365) TAGAAGATGGTGTGCCCCAGCCAGAAGCTTCCTCACAGCTAAGCCACTCTGA

------------------------------------------------------------------ Section 9
                    417           430       440       450               468
 » Palb2 mRNA  (358) ATCTATAAATAAAGGCTTTCCTTGTGACACATTGCAAAGCAACCATCTGGAT
» palb-15-13 rc  (1)
» palb-19-13 rc  (1)
» palb-05-13 rc  (1)
» palb-17-13 rc  (1)
» palb-01-13 rc  (1)
» palb-08-13 rc  (1)
   » palb-15-t7 (404) ATCTATAAATAAAGGCTTTCCTTGTGACACATTGCAAAGCAACCATCTGGAT
   » palb-08-t7 (404) ATCTATAAATAAAGGCTTTCCTTGTGACACATTGCAAAGCAACCATCTGGAT
   » palb-19-t7 (404) ATCTATAAATAAAGGCTTTCCTTGTGACACATTGCAAAGCAACCATCTGGAT
   » palb-17-t7 (404) ATCTATAAATAAAGGCTTTCCTTGTGACACATTGCAAAGCAACCATCTGGAT
   » palb-05-t7 (404) ATCTATAAATAAAGGCTTTCCTTGTGACACATTGCAAAGCAACCATCTGGAT
   » palb-01-t7 (417) ATCTATAAATAAAGGCTTTCCTTGTGACACATTGCAAAGCAACCATCTGGAT
       Contig 4 (417) ATCTATAAATAAAGGCTTTCCTTGTGACACATTGCAAAGCAACCATCTGGAT
```

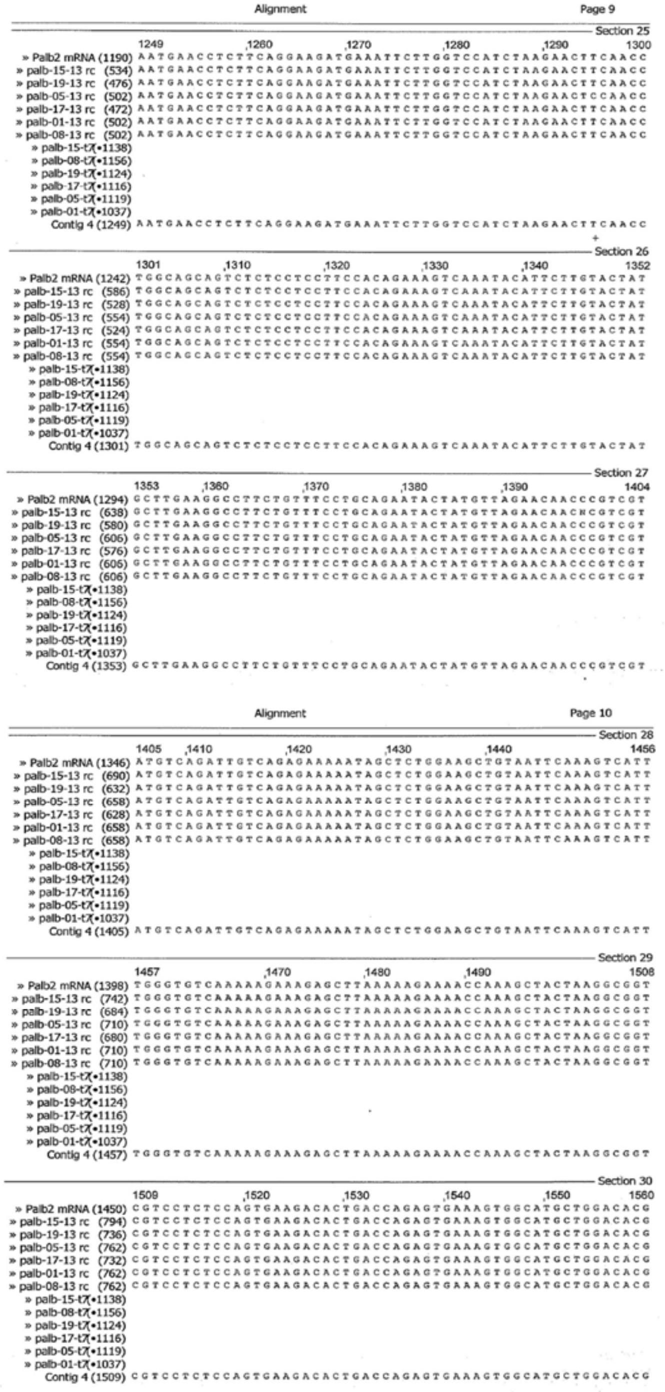


```
                  Alignment                                              Page 4
------------------------------------------------------------------ Section 10
                    469        480       490       500       510        520
 » Palb2 mRNA  (410) GAGGAGACTGGAGAAAACATCTCTCAGATACTTGATGTTGAACCTCAATCCT
» palb-15-13 rc  (1)
» palb-19-13 rc  (1)
» palb-05-13 rc  (1)
» palb-17-13 rc  (1)
» palb-01-13 rc  (1)
» palb-08-13 rc  (1)
   » palb-15-t7 (456) GAGGAGACTGGAGAAAACATCTCTCAGATACTTGATGTTGAACCTCAATCCT
   » palb-08-t7 (456) GAGGAGACTGGAGAAAACATCTCTCAGATACTTGATGTTGAACCTCAATCCT
   » palb-19-t7 (456) GAGGAGACTGGAGAAAACATCTCTCAGATACTTGATGTTGAACCTCAATCCT
   » palb-17-t7 (456) GAGGAGACTGGAGAAAACATCTCTCAGATACTTGATGTTGAACCTCAATCCT
   » palb-05-t7 (456) GAGGAGACTGGAGAAAACATCTCTCAGATACTTGATGTTGAACCTCAATCCT
   » palb-01-t7 (469) GAGGAGACTGGAGAAAACATCTCTCAGATACTTGATGTTGAACCTCAATCCT
       Contig 4 (469) GAGGAGACTGGAGAAAACATCTCTCAGATACTTGATGTTGAACCTCAATCCT

------------------------------------------------------------------ Section 11
                    521       530       540       550       560         572
 » Palb2 mRNA  (462) TTAACTGTAAACAAGGCAAAGAAGTATTACATACACCAAGAGCAGGTGACAT
» palb-15-13 rc  (1)
» palb-19-13 rc  (1)
» palb-05-13 rc  (1)
» palb-17-13 rc  (1)
» palb-01-13 rc  (1)
» palb-08-13 rc  (1)
   » palb-15-t7 (508) TTAACTGTAAACAAGGCAAAGAAGTATTACATACACCAAGAGCAGGTGACAT
   » palb-08-t7 (508) TTAACTGTAAACAAGGCAAAGAAGTATTACATACACCAAGAGCAGGTGACAT
   » palb-19-t7 (508) TTAACTGTAAACAAGGCAAAGAAGTATTACATACACCAAGAGCAGGTGACAT
   » palb-17-t7 (508) TTAACTGTAAACAAGGCAAAGAAGTATTACATACACCAAGAGCAGGTGACAT
   » palb-05-t7 (508) TTAACTGTAAACAAGGCAAAGAAGTATTACATACACCAAGAGCAGGTGACAT
   » palb-01-t7 (521) TTAACTGTAAACAAGGCAAAGAAGTATTACATACACCAAGAGCAGGTGACAT
       Contig 4 (521) TTAACTGTAAACAAGGCAAAGAAGTATTACATACACCAAGAGCAGGTGACAT

------------------------------------------------------------------ Section 12
                    573    580        590       600       610           624
 » Palb2 mRNA  (514) TCAAGGACAACTTTTGCATAGCACCAGCAGCCCTGATGGCAAGAAAGAGCAG
» palb-15-13 rc  (1)
» palb-19-13 rc  (1)
» palb-05-13 rc  (1)
» palb-17-13 rc  (1)
» palb-01-13 rc  (1)
» palb-08-13 rc  (1)
   » palb-15-t7 (560) TCAAGGACAACTTTTGCATAGCACCAGCAGCCCTGATGGCAAGAAAGAGCAG
   » palb-08-t7 (560) TCAAGGACAACTTTTGCATAGCACCAGCAGCCCTGATGGCAAGAAAGAGCAG
   » palb-19-t7 (560) TCAAGGACAACTTTTGCATAGCACCAGCAGCCCTGATGGCAAGAAAGAGCAG
   » palb-17-t7 (560) TCAAGGACAACTTTTGCATAGCACCAGCAGCCCTGATGGCAAGAAAGAGCAG
   » palb-05-t7 (560) TCAAGGACAACTTTTGCATAGCACCAGCAGCCCTGATGGCAAGAAAGAGCAG
   » palb-01-t7 (573) TCAAGGACAACTTTTGCATAGCACCAGCAGCCCTGATGGCAAGAAAGAGCAG
       Contig 4 (573) TCAAGGACAACTTTTGCATAGCACCAGCAGCCCTGATGGCAAGAAAGAGCAG
```

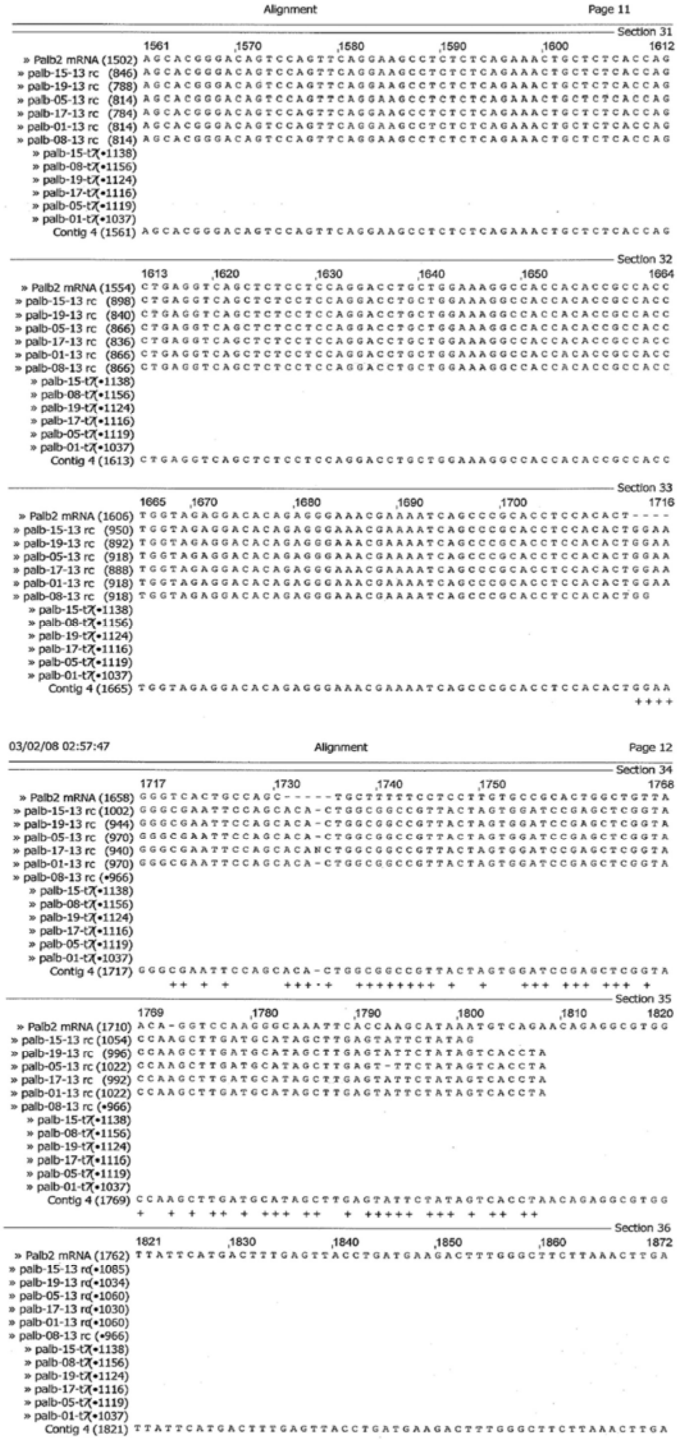


```
                                    Alignment                      Page 5
                                                               Section 13
                       625  630       640       650       660          676
   » Palb2 mRNA (566) AACACGCTTCCGGGGACAACAAAGACGCCGTGGGAGAAGTCATCTGTTTCAC
» palb-15-13 rc   (1)
» palb-19-13 rc   (1)
» palb-05-13 rc   (1)
» palb-17-13 rc   (1)
» palb-01-13 rc   (1)
» palb-08-13 rc   (1)
   » palb-15-t7 (612) AACACGCTTCCGGGGACAACAAAGACGCCGTGGGAGAAGTCATCTGTTTCAC
   » palb-08-t7 (612) AACACGCTTCCGGGGACAACAAAGACGCCGTGGGAGAAGTCATCTGTTTCAC
   » palb-19-t7 (612) AACACGCTTCCGGGGACAACAAAGACGCCGTGGGAGAAGTCATCTGTTTCAC
   » palb-17-t7 (612) AACACGCTTCCGGGGACAACAAAGACGCCGTGGGAGAAGTCATCTGTTTCAC
   » palb-05-t7 (612) AACACGCTTCCGGGGACAACAAAGACGCCGTGGGAGAAGTCATCTGTTTCAC
   » palb-01-t7 (625) AACACGCTTCCGGGGACAACAAAGACGCCGTGGGAGAAGTCATCTGTTTCAC
       Contig 4 (625) AACACGCTTCCGGGGACAACAAAGACGCCGTGGGAGAAGTCATCTGTTTCAC

                                                               Section 14
                       677          690       700       710             728
   » Palb2 mRNA (618) AGGAGAAGGAAGATTATTTTGACACTAATTCTCTGGCGCTCCTTGGTAAGCA
» palb-15-13 rc   (1)                                        TCCTTGGTANGCN
» palb-19-13 rc   (1)
» palb-05-13 rc   (1)
» palb-17-13 rc   (1)
» palb-01-13 rc   (1)
» palb-08-13 rc   (1)
   » palb-15-t7 (664) AGGAGAAGGAAGATTATTTTGACACTAATTCTCTGGCGCTCCTTGGTAAGCA
   » palb-08-t7 (664) AGGAGAAGGAAGATTATTTTGACACTAATTCTCTGGCGCTCCTTGGTAAGCA
   » palb-19-t7 (664) AGGAGAAGGAAGATTATTTTGACACTAATTCTCTGGCGCTCCTTGGTAAGCA
   » palb-17-t7 (664) AGGAGAAGGAAGATTATTTTGACACTAATTCTCTGGCGCTCCTTGGTAAGCA
   » palb-05-t7 (664) AGGAGAAGGAAGATTATTTTGACACTAATTCTCTGGCGCTCCTTGGTAAGCA
   » palb-01-t7 (677) AGGAGAAGGAAGATTATTTTGACACTAATTCTCTGGCGCTCCTTGGTAAGCA
       Contig 4 (677) AGGAGAAGGAAGATTATTTTGACACTAATTCTCTGGCGCTCCTTGGTAAGCA
                                                                  .  .
                                                               Section 15
                       729        740       750       760       770     780
   » Palb2 mRNA (670) TCGAAAAGGGCAAGAATCAATCAGTAGGAAGAATTCTAGGACT-CCCGTGAG
» palb-15-13 rc  (14) TNGAAANGGGCAAGAATCAATCAGTAGGAAGAATTNTAGGACTNCCNGGGAG
» palb-19-13 rc   (1)                                              CCGTGAG
» palb-05-13 rc   (1)                    ATCAGTAGGAAGGATTNTAGGACT-CCCGTGAG
» palb-17-13 rc   (1)                                                  GAG
» palb-01-13 rc   (1)                    ATCAGTAGGAAGAATT-TNGGACT-CCCGTGAG
» palb-08-13 rc   (1)                    ATCAGTAGGAAGATTTTTAGGACT-CCCGTGAG
   » palb-15-t7 (716) TCGAAAAGGGCAAGAATCAATCAGTAGGAAGAATTCTAGGACT-CCCGTGAG
   » palb-08-t7 (716) TCGAAAAGGGCAAGAATCAATCAGTAGGAAGAATTCTAGGACT-CCCGTGAG
   » palb-19-t7 (716) TCGAAAAGGGCAAGAATCAATCAGTAGGAAGAATTCTAGGACT-CCCGTGAG
   » palb-17-t7 (716) TCGAAAAGGGCAAGAATCAATCAGTAGGAAGAATTCTAGGACT-CCCGTGAG
   » palb-05-t7 (716) TCGAAAAGGGCAAGAATCAATCAGTAGGAAGAATTCTAGGACT-CCCGTGAG
   » palb-01-t7 (729) TCGAAAAGGGCAAGAATCAATCANTAGGAAGAATTCTAGGACT-CCCGTGAG
       Contig 4 (729) TCGAAAAGGGCAAGAATCAATCAGTAGGAAGAATTCTAGGACT-CCCGTGAG
                       .    .                .       ++  + .     .  . +

                                    Alignment                      Page 6
                                                               Section 16
                       781      790       800       810       820       832
   » Palb2 mRNA (722) TGAAAAGACTCACCTTTTAAGTCTCAGGTCT-CAGATCCCTGACCCTCCAGC
» palb-15-13 rc  (66) TGAAAAGACTCACCTTTTAAGTCTCAGGTNT-CAGATCCCTGACCCTCCAGC
» palb-19-13 rc   (8) TGNAAAGACTC-CCNTTTAAGTCTCAGGTNT-CAGATCCCTGACCNTCCAGC
» palb-05-13 rc  (34) TGAAAAGACTCAC-TTTTAAGTCTCAGGTTTTCAGATCCCTGACCNTCCAGC
» palb-17-13 rc   (4) TGAAAAGACTCACNTTT-AAGTCTCANGTNT-CAGATCCCTGACCNTCCAGC
» palb-01-13 rc  (34) TGAAAAGACTCACNTTTTNAGTCTCAGGTCT-CAGATCCCTGACCNTCCAGC
» palb-08-13 rc  (34) TGAAAAGACTCACNTTT-NAGTNTCAGGTCT-CAGATCCCTGACCCTCCAGC
   » palb-15-t7 (768) TGAAAAGACTCACCTTTTAAGTCTCAGGTCT-CAGATCCCTGACCCTCCAGC
   » palb-08-t7 (768) TGAAAAGACTCACCTTTTAAGTCTCAGGTCT-CAGATCCCTGACCCTCCAGC
   » palb-19-t7 (768) TGAAAAGACTCACCTTTTAAGTCTCAGGTCT-CAGATCCCTGACCCTCCAGC
   » palb-17-t7 (768) TGAAAAGACTCACCTTTTAAGTCTCAGGTCT-CAGATCCCTGACCCTCCAGC
   » palb-05-t7 (768) TGAAAAGACTCACCTTTTAAGTCTCAGGTCT-CAGATCCCTGACCCTCCAGC
   » palb-01-t7 (781) TGAAAAGACTCACCTTTTAAGTCTCAGGTCT-CAGATCCCTGACCCTCCAGC
       Contig 4 (781) TGAAAAGACTCACCTTTTAAGTCTCAGGTCT-CAGATCCCTGACCCTCCAGC
                        .        + ..  +.   .   .  . +             .
                                                               Section 17
                       833    840       850       860       870         884
   » Palb2 mRNA (774) ACTTGTTACAGGAATTGGAGAGGG-TATATTAATT-CCGCCATCTGGCAAA-
» palb-15-13 rc (118) ACTTGTTACAGGAATTGGAGAGGGGTATATTAATT-CCGCCATCTGGCAAA-
» palb-19-13 rc  (60) ACTTGTTACAGGNATTGGAGAGGG-TATATTAATT-CCGCCATCTGGCAAA-
» palb-05-13 rc  (86) ACTTGTTACAGGAATTGGAGAGGG-TATATTAATT-CCGCCATCTGGCAAA-
» palb-17-13 rc  (56) ACTTGTTACAGGAATTGGAGAGGG-TATATTAATTTCCGCCATCTGGCAAA-
» palb-01-13 rc  (86) ACNTGTTACAGGAATTGGAGAGGG-TATATTAATT-CCGCCATCTGGCAA--
» palb-08-13 rc  (86) ACTTGTTACAGGAATTGGAGAGGGGTATATTAATTTCCGCCATCTGGCAAA-
   » palb-15-t7 (820) ACTTGTTACAGGAATTGGAGAGGG-TATATTAATT-CCGCCATCTGGCAAA-
   » palb-08-t7 (820) ACTTGTTACAGGAATTGGAGAGGG-TATATTAATT-CCGCCATCTGGCAAA-
   » palb-19-t7 (820) ACTTGTTACAGGAATTGGAGAGGG-TATATTAATT-CCGCCATCTGGCAAA-
   » palb-17-t7 (820) ACTTGTTACAGGAATTGGAGAGGG-TATATTAATT-CCGCCATCTGGCAAA-
   » palb-05-t7 (820) ACTTGTTACAGGAATTGGAGAGGG-TATATTAATT-CCGCCATCTGGCAAA-
   » palb-01-t7 (833) ACTTGTTACAGGAATTGGAGAGGG-TATATTAATT-CCGCCATCTGGCAAAA
       Contig 4 (833) ACTTGTTACAGGAATTGGAGAGGG-TATATTAATT-CCGCCATCTGGCAAA-
                        .         .           +          +              ++
                                                               Section 18
                       885  890       900       910       920           936
   » Palb2 mRNA (826) TCAGAAAGGGG-AATTGATACACTTGTGAGA-GGAAATACTGTCTCCGCGGA
» palb-15-13 rc (170) TCAGAAAGGGG-AATTGATACACTTGTGAGA-GGAAATACTGTCTCCGCGGA
» palb-19-13 rc (112) TCAGAAAAGGGGAATTGATACACTTGTGAGA-GGAAATACTGTCTCCGCGGA
» palb-05-13 rc (138) TCAGAAAGGGG-AATTGATACACTTGTGAGA-GGAAATACTGTCTCCGCGGA
» palb-17-13 rc (108) TCAGAAAGGGG-AATTGATACACTTGTGAGA-GGAAATACTGTCTCCGCGGA
» palb-01-13 rc (138) TCAGAAAGGGG-AATTGATACACTTGTGAGA-GGAAATACTGTCTCCGCGGA
» palb-08-13 rc (138) TCAGAAAGGGG-AATTGATACACTTGTGAGA-GGAAATACTGTCTCCGCGGA
   » palb-15-t7 (872) TCAGAAAGGGG-AATTGATACACTTGTGAGA-GGAAATACTGTCTCCGCGGA
   » palb-08-t7 (872) TCAGAAAGGGG-AATTGATACACTTGTGAGA-GGAAATACTGTCTCCGCGGA
   » palb-19-t7 (872) TCAGAAAGGGG-AATTGATACACTTGTGAGA--GGAATACTGTCTCCGCGGA
   » palb-17-t7 (872) TCAGAAAGGGG-AATTGATACACTTGTGAGA-GGAAATACTGTCTCCGCGGA
   » palb-05-t7 (872) TCAGAAAGGGG-AATTGATACACTTGTGAGA-GGAAATACTGTCTCCGCGGA
   » palb-01-t7 (885) TCANAAAGGGGNAATTGATACNCTTGTGAGAAGGAAATACTGTCTCCNCGGA
       Contig 4 (885) TCAGAAAGGGG-AATTGATACACTTGTGAGA-GGAAATACTGTCTCCGCGGA
                         .   +   .         .         ++ +            .
```

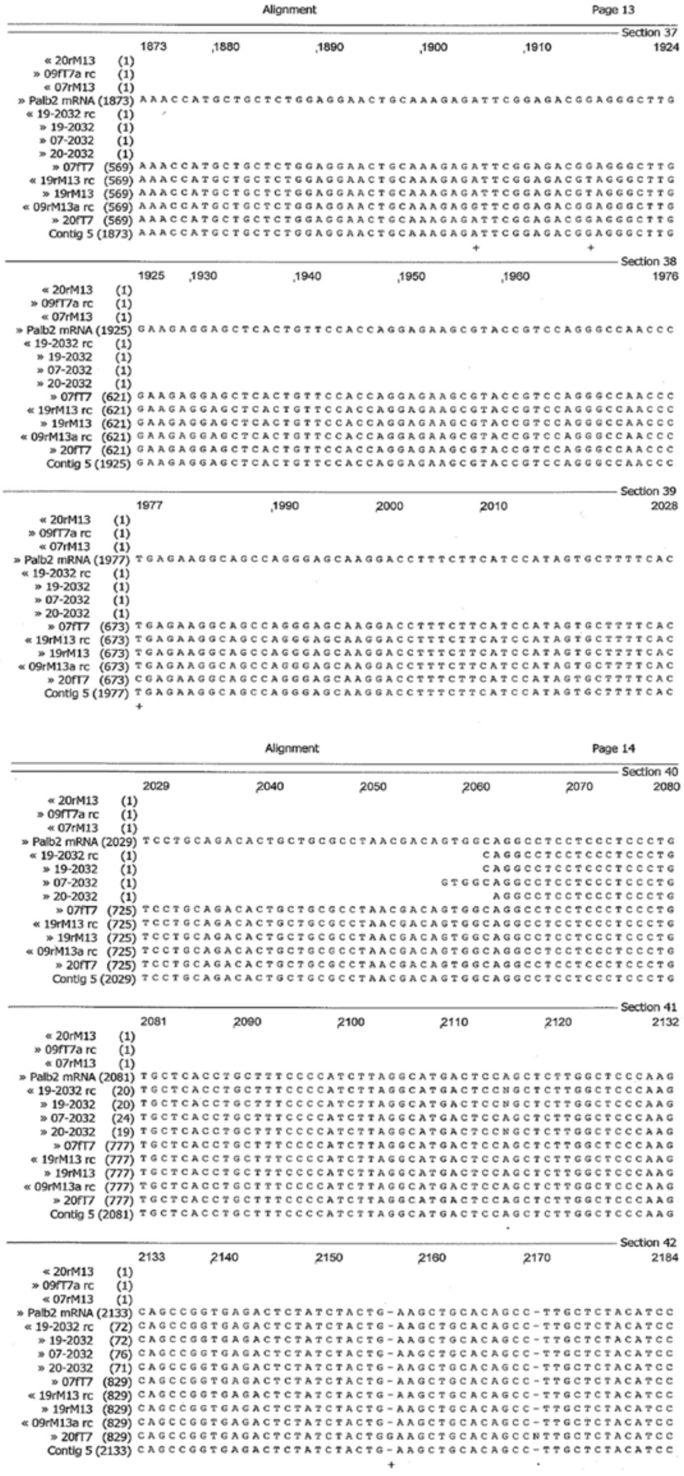
```
                                  Alignment                        Page 7
==========================================================================
----------------------------------------------------------------- Section 19
                      937          ,950      ,960      ,970            988
  » Palb2 mRNA  (878) GGCTGCAGTTCCTT-CATGTACTGCGTCAAACAGCAATCACAGTCAGCACCT
» palb-15-13 rc (222) GGCTGCAGTTCCTT-CATGTACTGCGTCAAACAGCAATCACAGTCAGCACCT
» palb-19-13 rc (164) GGCTGCAGTTCCTT-CATGTACTGCGTCAAACAGCAATCACAGTCAGCACCT
» palb-05-13 rc (190) GGCTGCAGTTCCTT-CATGTACTGCGTCAAACAGCAATCACAGTCAGCACCT
» palb-17-13 rc (160) GGCTGCAGTTCCTT-CATGTACTGCGTCAAACAGCAATCACAGTCAGCACCT
» palb-01-13 rc (190) GGCTGCAGTTCCTT-CATGTACTGCGTCAAACAGCAATCACAGTCAGCACCT
» palb-08-13 rc (190) GGCTGCAGTTCCTT-CATGTACTGCGTCAAACAGCAATCACAGTCAGCACCT
   » palb-15-t7 (924) NGCTGCAGTTCCTT-CATGTACTGCGTCAAACAGCAATCACAGTCAGCACCT
   » palb-08-t7 (924) GGCTGCAGTTCCTT-CATGTACTGCGTCAAACAGCAATCACAGTCAGCACCT
   » palb-19-t7 (924) NGCTGCAGTTTCCTTCATGTACTGCGTCAAACAGCAATCACAGTCAGCACCT
   » palb-17-t7 (924) GGCTGCAGTTCCTT-CATGTACTGCGTCAAACAGCAATCACAGTCAGCACCT
   » palb-05-t7 (924) NGCTGCAGTTCCTT-CATGTACTGCGTCAAACAGCAATCACAGTCAGCACCT
   » palb-01-t7 (937) NGCTGCANTTCCTTTCATGTACTGCGTNAAACANCA-TCACAGTCANCACCT
       Contig 4 (937) GGCTGCAGTTCCTT-CATGTACTGCGTCAAACAGCAATCACAGTCAGCACCT
                      .      .  + + +            .     .  +         .
----------------------------------------------------------------- Section 20
                      989        ,1000     ,1010     ,1020     ,1030  1040
  » Palb2 mRNA  (930) TGAGCATACACCTCCTAAAAGTGGCTGCAAAATTACTACTCAGGGCCCGGCT
» palb-15-13 rc (274) TGAGCATACACCTCCTAAAAGTGGCTGCAAAATTACTACTCAGGGCCCGGCT
» palb-19-13 rc (216) TGAGCATACACCTCCTAAAAGTGGCTGCAAAATTACTACTCAGGGCCCGGCT
» palb-05-13 rc (242) TGAGCATACACCTCCTAAAAGTGGCTGCAAAATTACTACTCAGGGCCCGGCT
» palb-17-13 rc (212) TGAGCATACACCTCCTAAAAGTGGCTGCAAAATTACTACTCAGGGCCCGGCT
» palb-01-13 rc (242) TGAGCATACACCTCCTAAAAGTGGCTGCAAAATTACTACTCAGGGCCCGGCT
» palb-08-13 rc (242) TGAGCATACACCTCCTAAAAGTGGCTGCAAAATTACTACTCAGGGCCCGGCT
   » palb-15-t7 (976) TGAGCATACACCTCCTAAANGTGGCTGCAAAATTACTACTCAGGGCCCGGCT
   » palb-08-t7 (976) TGAGCATACACCTCNTAAA-GTGGCTGCAAAATTACTACTCAGGGCCCGGCT
   » palb-19-t7 (976) TGAGCATACACCTCCTAAAAGTGGCTGCAAANTTACTACTCAGGGCCCGGCT
   » palb-17-t7 (976) TGAGCATACACCTCCTAAAAGTGGCTGCAAAATTACTACTCAGGGCCCGGCT
   » palb-05-t7 (976) TGAGCATACACCTCCTAAAAGTGGCTGCAAAATTACTACTCAGGGCCCGGCT
   » palb-01-t7 (989) TGANCATACACCTCCTAAAA-TGGCTGCAAAATTACTACTCAGGGCCCGG
       Contig 4 (989) TGAGCATACACCTCCTAAAAGTGGCTGCAAAATTACTACTCAGGGCCCGGCT
                         .          .    ++          .
----------------------------------------------------------------- Section 21
                      1041     ,1050     ,1060     ,1070     ,1080    1092
  » Palb2 mRNA  (982) TCATCCACAAACCTGGTGGCACAAGACCAAAAAATGACTATATTTA-CAGTA
» palb-15-13 rc (326) TCATCCACAAACCTGGTGGCACAAGACCAAAAAATGACTATATTTA-CAGTA
» palb-19-13 rc (268) TCATCCACAAACCTGGTGGCACAAGACCAAAAAATGACTATATTTA-CAGTA
» palb-05-13 rc (294) TCATCCACAAACCTGGTGGCACAAGACCAAAAAATGACTATATTTA-CAGTA
» palb-17-13 rc (264) TCATCCACAAACCTGGTGGCACAAGACCAAAAAATGACTATATTTA-CAGTA
» palb-01-13 rc (294) TCATCCACAAACCTGGTGGCACAAGACCAAAAAATGACTATATTTA-CAGTA
» palb-08-13 rc (294) TCATCCACAAACCTGGTGGCACAAGACCAAAAAATGACTATATTTA-CAGTA
  » palb-15-t7 (1028) TCATCCACAAACCTGGTGGCACAAGACCAAAAAATGACTNTNTTTN-CGGTA
  » palb-08-t7 (1028) TCATCCACAAACCTGGTGGCNCAAGACCAAAAAATGACTATNTTTNNCGNTA
  » palb-19-t7 (1028) TCATCCACAAACCTGGTGGCACAAGANCCAAAAATGACTATNTTTN-CGGTA
  » palb-17-t7 (1028) TCATCCCCAAACCTGGTGGCNCAAGACCAAAAAATGACTATNTTTA-CGGTA
  » palb-05-t7 (1028) TCATCCACAAACCTGGTGGCACAAGACCAAAAAATGACTATNTTTA-CAGTA
  » palb-01-t7(•1037)
      Contig 4 (1041) TCATCCACAAACCTGGTGGCACAAGACCAAAAAATGACTATATTTA-CAGTA
                            +             .     . +          . .   .. +.

                                  Alignment                        Page 8
==========================================================================
----------------------------------------------------------------- Section 22
                      1093   ,1100     ,1110     ,1120     ,1130      1144
  » Palb2 mRNA (1034) AACTCAGTAGTATATAAAGCTGTGCGTGCCCATGGTCAGCTGCCAGGAAGTC
» palb-15-13 rc (378) AACTCAGTAGTATATAAAGCTGTGCGTGCCCATGGTCAGCTGCCAGGAAGTC
» palb-19-13 rc (320) AACTCAGTAGTATATAAAGCTGTGCGTGCCCATGGTCAGCTGCCAGGAAGTC
» palb-05-13 rc (346) AACTCAGTAGTATATAAAGCTGTGCGTGCCCATGGTCAGCTGCCAGGAAGTC
» palb-17-13 rc (316) AACTCAGTAGTATATAAAGCTGTGCGTGCCCATGGTCAGCTGCCAGGAAGTC
» palb-01-13 rc (346) AACTCAGTAGTATATAAAGCTGTGCGTGCCCATGGTCAGCTGCCAGGAAGTC
» palb-08-13 rc (346) AACTCAGTAGTATATAAAGCTGTGCGTGCCCATGGTCAGCTGCCAGGAAGTC
  » palb-15-t7 (1080) ANCTCNGTAGTAT-TAAAGCTGTGCGTGCCCATGGTCAGCTGCCAG-AANTC
  » palb-08-t7 (1080) AACTCAGTA-TATTTTAAGCTGTGCGTGCCCATGGTCANCTGCCAG-AANTC
  » palb-19-t7 (1080) A-CTCNGTAGTATATAANGCTGTGCGTGCCCATGGTCANCTGCCAG
  » palb-17-t7 (1080) A-CTCAGTAGTATTTAANGCTGTGCGTGCCCNTGGTCA
  » palb-05-t7 (1080) AACTCAGTANTATNNAAAGCTGTGCGTGCCCATGGTCAGCT
  » palb-01-t7(•1037)
      Contig 4 (1093) AACTCAGTAGTATATAAAGCTGTGCGTGCCCATGGTCAGCTGCCAGGAAGTC
                       +   .   .   ..+ .             .      .       +  .
----------------------------------------------------------------- Section 23
                      1145 ,1150     ,1160     ,1170     ,1180        1196
  » Palb2 mRNA (1086) CCAATTCTTGTTCTGTAAATGATCTCACGCATAGTAACTTGCCAGCAAATAG
» palb-15-13 rc (430) CCAATTCTTGTTCTGTAAATGATCTCACGCATAGTAACTTGCCAGCAAATAG
» palb-19-13 rc (372) CCAATTCTTGTTCTGTAAATGATCTCACGCATAGTAACTTGCCAGCAAATAG
» palb-05-13 rc (398) CCAATTCTTGTTCTGTAAATGATCTCACGCATAGTAACTTGCCAGCAAATAG
» palb-17-13 rc (368) CCAATTCTTGTTCTGTAAATGATCTCACGCATAGTAACTTGCCAGCAAATAG
» palb-01-13 rc (398) CCAATTCTTGTTCTGTAAATGATCTCACGCATAGTAACTTGCCAGCAAATAG
» palb-08-13 rc (398) CCAATTCTTGTTCTGTAAATGATCTCACGCATAGTAACTTGCCAGCAAATAG
  » palb-15-t7 (1132) CCAATTCT
  » palb-08-t7 (1132) CCAATTNTTGTTTTGTAANTGATCTC
  » palb-19-t7(•1124)
  » palb-17-t7(•1116)
  » palb-05-t7(•1119)
  » palb-01-t7(•1037)
      Contig 4 (1145) CCAATTCTTGTTCTGTAAATGATCTCACGCATAGTAACTTGCCAGCAAATAG
                            .     +     .
----------------------------------------------------------------- Section 24
                      1197         ,1210     ,1220     ,1230          1248
  » Palb2 mRNA (1138) TACCCCAAACTCTAAATCTTTAAAATCTCCCAGTAACACTGTTGATGAGAGA
» palb-15-13 rc (482) TACCCCAAACTCTAAATCTTTAAAATCTCCCAGTAACACTGTTGATGAGAGA
» palb-19-13 rc (424) TACCCCAAACTCTAAATCTTTAAAATCTCCCAGTAACACTGTTGATGAGAGA
» palb-05-13 rc (450) TACCCCAAACTCTAAATCTTTAAAATCTCCCAGTAACACTGTTGATGAGAGA
» palb-17-13 rc (420) TACCCCAAACTCTAAATCTTTAAAATCTCCCAGTAACACTGTTGATGAGAGA
» palb-01-13 rc (450) TACCCCAAACTCTAAATCTTTAAAATCTCCCAGTAACACTGTTGATGAGAGA
» palb-08-13 rc (450) TACCCCAAACTCTAAATCTTTAAAATCTCCCAGTAACACTGTTGATGAGAGA
  » palb-15-t7(•1138)
  » palb-08-t7(•1156)
  » palb-19-t7(•1124)
  » palb-17-t7(•1116)
  » palb-05-t7(•1119)
  » palb-01-t7(•1037)
      Contig 4 (1197) TACCCCAAACTCTAAATCTTTAAAATCTCCCAGTAACACTGTTGATGAGAGA
```



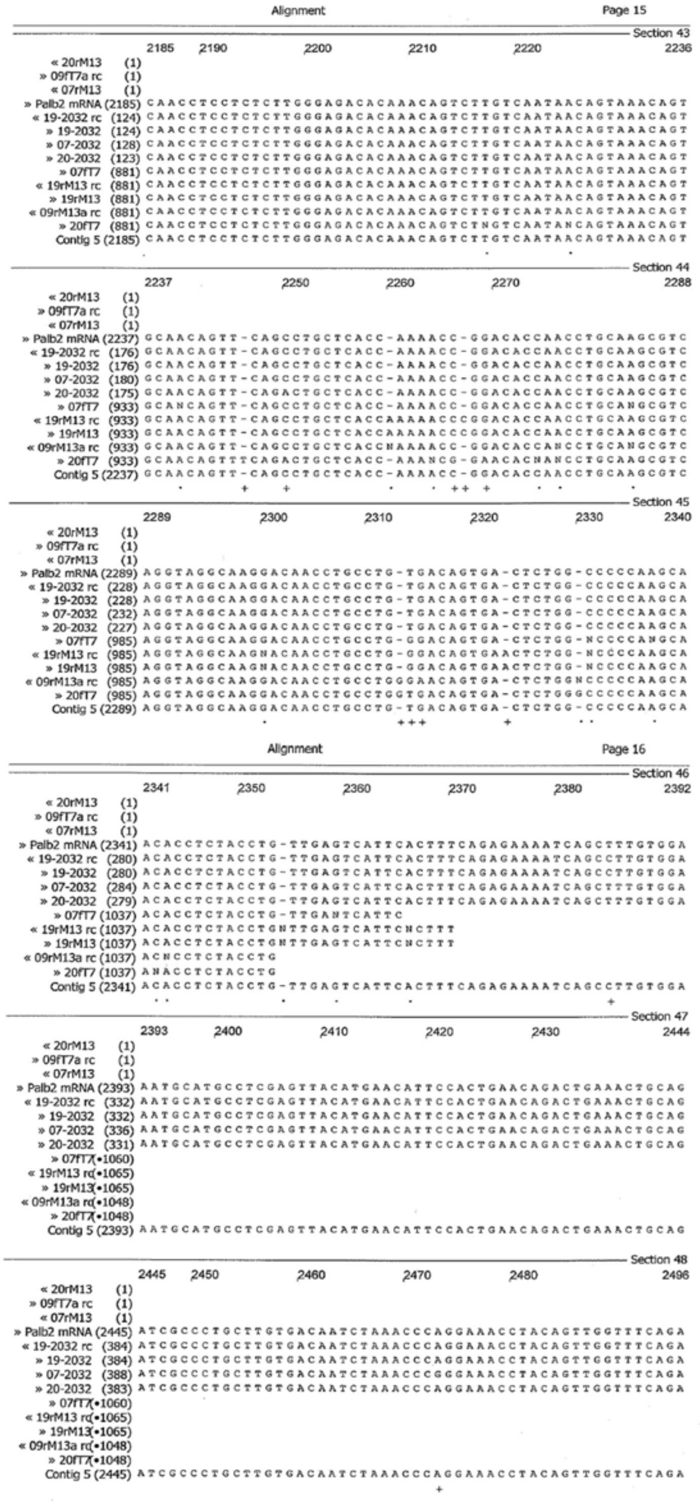
```
                         Alignment                                          Page 9
==================================================================================
---------------------------------------------------------------------- Section 25
                     1249       ,1260      ,1270      ,1280      ,1290       1300
 » Palb2 mRNA (1190) AATGAACCTCTTCAGGAAGATGAAATTCTTGGTCCATCTAAGAACTTCAACC
» palb-15-13 rc (534) AATGAACCTCTTCAGGAAGATGAAATTCTTGGTCCATCTAAGAACTTCAACC
» palb-19-13 rc (476) AATGAACCTCTTCAGGAAGATGAAATTCTTGGTCCATCTAAGAACTTCAACC
» palb-05-13 rc (502) AATGAACCTCTTCAGGAAGATGAAATTCTTGGTCCATCTAAGAACTCCAACC
» palb-17-13 rc (472) AATGAACCTCTTCAGGAAGATGAAATTCTTGGTCCATCTAAGAACTTCAACC
» palb-01-13 rc (502) AATGAACCTCTTCAGGAAGATGAAATTCTTGGTCCATCTAAGAACTTCAACC
» palb-08-13 rc (502) AATGAACCTCTTCAGGAAGATGAAATTCTTGGTCCATCTAAGAACTTCAACC
   » palb-15-t7(•1138)
   » palb-08-t7(•1156)
   » palb-19-t7(•1124)
   » palb-17-t7(•1116)
   » palb-05-t7(•1119)
   » palb-01-t7(•1037)
     Contig 4 (1249) AATGAACCTCTTCAGGAAGATGAAATTCTTGGTCCATCTAAGAACTTCAACC
                                                                    +
---------------------------------------------------------------------- Section 26
                     1301      ,1310      ,1320      ,1330      ,1340       1352
 » Palb2 mRNA (1242) TGGCAGCAGTCTCTCCTCCTTCCACAGAAAGTCAAATACATTCTTGTACTAT
» palb-15-13 rc (586) TGGCAGCAGTCTCTCCTCCTTCCACAGAAAGTCAAATACATTCTTGTACTAT
» palb-19-13 rc (528) TGGCAGCAGTCTCTCCTCCTTCCACAGAAAGTCAAATACATTCTTGTACTAT
» palb-05-13 rc (554) TGGCAGCAGTCTCTCCTCCTTCCACAGAAAGTCAAATACATTCTTGTACTAT
» palb-17-13 rc (524) TGGCAGCAGTCTCTCCTCCTTCCACAGAAAGTCAAATACATTCTTGTACTAT
» palb-01-13 rc (554) TGGCAGCAGTCTCTCCTCCTTCCACAGAAAGTCAAATACATTCTTGTACTAT
» palb-08-13 rc (554) TGGCAGCAGTCTCTCCTCCTTCCACAGAAAGTCAAATACATTCTTGTACTAT
   » palb-15-t7(•1138)
   » palb-08-t7(•1156)
   » palb-19-t7(•1124)
   » palb-17-t7(•1116)
   » palb-05-t7(•1119)
   » palb-01-t7(•1037)
     Contig 4 (1301) TGGCAGCAGTCTCTCCTCCTTCCACAGAAAGTCAAATACATTCTTGTACTAT

---------------------------------------------------------------------- Section 27
                     1353   ,1360      ,1370      ,1380      ,1390          1404
 » Palb2 mRNA (1294) GCTTGAAGGCCTTCTGTTTCCTGCAGAATACTATGTTAGAACAACCCGTCGT
» palb-15-13 rc (638) GCTTGAAGGCCTTCTGTTTCCTGCAGAATACTATGTTAGAACAACNCGTCGT
» palb-19-13 rc (580) GCTTGAAGGCCTTCTGTTTCCTGCAGAATACTATGTTAGAACAACCCGTCGT
» palb-05-13 rc (606) GCTTGAAGGCCTTCTGTTTCCTGCAGAATACTATGTTAGAACAACCCGTCGT
» palb-17-13 rc (576) GCTTGAAGGCCTTCTGTTTCCTGCAGAATACTATGTTAGAACAACCCGTCGT
» palb-01-13 rc (606) GCTTGAAGGCCTTCTGTTTCCTGCAGAATACTATGTTAGAACAACCCGTCGT
» palb-08-13 rc (606) GCTTGAAGGCCTTCTGTTTCCTGCAGAATACTATGTTAGAACAACCCGTCGT
   » palb-15-t7(•1138)
   » palb-08-t7(•1156)
   » palb-19-t7(•1124)
   » palb-17-t7(•1116)
   » palb-05-t7(•1119)
   » palb-01-t7(•1037)
     Contig 4 (1353) GCTTGAAGGCCTTCTGTTTCCTGCAGAATACTATGTTAGAACAACCCGTCGT


                         Alignment                                          Page 10
==================================================================================
---------------------------------------------------------------------- Section 28
                     1405 ,1410      ,1420      ,1430      ,1440            1456
 » Palb2 mRNA (1346) ATGTCAGATTGTCAGAGAAAAATAGCTCTGGAAGCTGTAATTCAAAGTCATT
» palb-15-13 rc (690) ATGTCAGATTGTCAGAGAAAAATAGCTCTGGAAGCTGTAATTCAAAGTCATT
» palb-19-13 rc (632) ATGTCAGATTGTCAGAGAAAAATAGCTCTGGAAGCTGTAATTCAAAGTCATT
» palb-05-13 rc (658) ATGTCAGATTGTCAGAGAAAAATAGCTCTGGAAGCTGTAATTCAAAGTCATT
» palb-17-13 rc (628) ATGTCAGATTGTCAGAGAAAAATAGCTCTGGAAGCTGTAATTCAAAGTCATT
» palb-01-13 rc (658) ATGTCAGATTGTCAGAGAAAAATAGCTCTGGAAGCTGTAATTCAAAGTCATT
» palb-08-13 rc (658) ATGTCAGATTGTCAGAGAAAAATAGCTCTGGAAGCTGTAATTCAAAGTCATT
   » palb-15-t7(•1138)
   » palb-08-t7(•1156)
   » palb-19-t7(•1124)
   » palb-17-t7(•1116)
   » palb-05-t7(•1119)
   » palb-01-t7(•1037)
     Contig 4 (1405) ATGTCAGATTGTCAGAGAAAAATAGCTCTGGAAGCTGTAATTCAAAGTCATT

---------------------------------------------------------------------- Section 29
                     1457         ,1470      ,1480      ,1490               1508
 » Palb2 mRNA (1398) TGGGTGTCAAAAAGAAAGAGCTTAAAAAGAAAACCAAAGCTACTAAGGCGGT
» palb-15-13 rc (742) TGGGTGTCAAAAAGAAAGAGCTTAAAAAGAAAACCAAAGCTACTAAGGCGGT
» palb-19-13 rc (684) TGGGTGTCAAAAAGAAAGAGCTTAAAAAGAAAACCAAAGCTACTAAGGCGGT
» palb-05-13 rc (710) TGGGTGTCAAAAAGAAAGAGCTTAAAAAGAAAACCAAAGCTACTAAGGCGGT
» palb-17-13 rc (680) TGGGTGTCAAAAAGAAAGAGCTTAAAAAGAAAACCAAAGCTACTAAGGCGGT
» palb-01-13 rc (710) TGGGTGTCAAAAAGAAAGAGCTTAAAAAGAAAACCAAAGCTACTAAGGCGGT
» palb-08-13 rc (710) TGGGTGTCAAAAAGAAAGAGCTTAAAAAGAAAACCAAAGCTACTAAGGCGGT
   » palb-15-t7(•1138)
   » palb-08-t7(•1156)
   » palb-19-t7(•1124)
   » palb-17-t7(•1116)
   » palb-05-t7(•1119)
   » palb-01-t7(•1037)
     Contig 4 (1457) TGGGTGTCAAAAAGAAAGAGCTTAAAAAGAAAACCAAAGCTACTAAGGCGGT

---------------------------------------------------------------------- Section 30
                     1509       ,1520      ,1530      ,1540      ,1550       1560
 » Palb2 mRNA (1450) CGTCCTCTCCAGTGAAGACACTGACCAGAGTGAAAGTGGCATGCTGGACACG
» palb-15-13 rc (794) CGTCCTCTCCAGTGAAGACACTGACCAGAGTGAAAGTGGCATGCTGGACACG
» palb-19-13 rc (736) CGTCCTCTCCAGTGAAGACACTGACCAGAGTGAAAGTGGCATGCTGGACACG
» palb-05-13 rc (762) CGTCCTCTCCAGTGAAGACACTGACCAGAGTGAAAGTGGCATGCTGGACACG
» palb-17-13 rc (732) CGTCCTCTCCAGTGAAGACACTGACCAGAGTGAAAGTGGCATGCTGGACACG
» palb-01-13 rc (762) CGTCCTCTCCAGTGAAGACACTGACCAGAGTGAAAGTGGCATGCTGGACACG
» palb-08-13 rc (762) CGTCCTCTCCAGTGAAGACACTGACCAGAGTGAAAGTGGCATGCTGGACACG
   » palb-15-t7(•1138)
   » palb-08-t7(•1156)
   » palb-19-t7(•1124)
   » palb-17-t7(•1116)
   » palb-05-t7(•1119)
   » palb-01-t7(•1037)
     Contig 4 (1509) CGTCCTCTCCAGTGAAGACACTGACCAGAGTGAAAGTGGCATGCTGGACACG
```



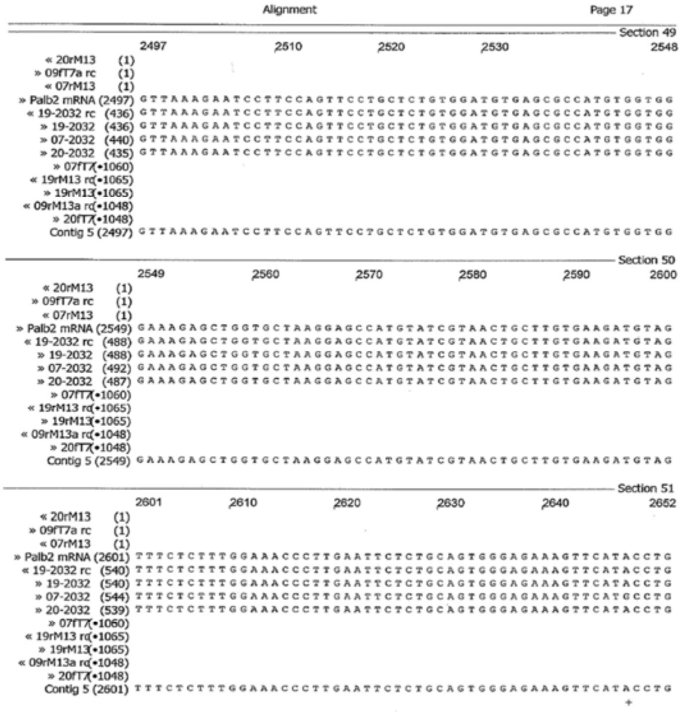
```
                                Alignment                                   Page 11
------------------------------------------------------------------------ Section 31
                     1561     ,1570     ,1580     ,1590     ,1600     ,1612
  » Palb2 mRNA (1502) AGCACGGGACAGTCCAGTTCAGGAAGCCTCTCTCAGAAACTGCTCTCACCAG
  » palb-15-13 rc (846) AGCACGGGACAGTCCAGTTCAGGAAGCCTCTCTCAGAAACTGCTCTCACCAG
  » palb-19-13 rc (788) AGCACGGGACAGTCCAGTTCAGGAAGCCTCTCTCAGAAACTGCTCTCACCAG
  » palb-05-13 rc (814) AGCACGGGACAGTCCAGTTCAGGAAGCCTCTCTCAGAAACTGCTCTCACCAG
  » palb-17-13 rc (784) AGCACGGGACAGTCCAGTTCAGGAAGCCTCTCTCAGAAACTGCTCTCACCAG
  » palb-01-13 rc (814) AGCACGGGACAGTCCAGTTCAGGAAGCCTCTCTCAGAAACTGCTCTCACCAG
  » palb-08-13 rc (814) AGCACGGGACAGTCCAGTTCAGGAAGCCTCTCTCAGAAACTGCTCTCACCAG
    » palb-15-t7(•1138)
    » palb-08-t7(•1156)
    » palb-19-t7(•1124)
    » palb-17-t7(•1116)
    » palb-05-t7(•1119)
    » palb-01-t7(•1037)
       Contig 4 (1561) AGCACGGGACAGTCCAGTTCAGGAAGCCTCTCTCAGAAACTGCTCTCACCAG
------------------------------------------------------------------------ Section 32
                     1613  ,1620     ,1630     ,1640     ,1650          1664
  » Palb2 mRNA (1554) CTGAGGTCAGCTCTCCTCCAGGACCTGCTGGAAAGGCCACCACACCGCCACC
  » palb-15-13 rc (898) CTGAGGTCAGCTCTCCTCCAGGACCTGCTGGAAAGGCCACCACACCGCCACC
  » palb-19-13 rc (840) CTGAGGTCAGCTCTCCTCCAGGACCTGCTGGAAAGGCCACCACACCGCCACC
  » palb-05-13 rc (866) CTGAGGTCAGCTCTCCTCCAGGACCTGCTGGAAAGGCCACCACACCGCCACC
  » palb-17-13 rc (836) CTGAGGTCAGCTCTCCTCCAGGACCTGCTGGAAAGGCCACCACACCGCCACC
  » palb-01-13 rc (866) CTGAGGTCAGCTCTCCTCCAGGACCTGCTGGAAAGGCCACCACACCGCCACC
  » palb-08-13 rc (866) CTGAGGTCAGCTCTCCTCCAGGACCTGCTGGAAAGGCCACCACACCGCCACC
    » palb-15-t7(•1138)
    » palb-08-t7(•1156)
    » palb-19-t7(•1124)
    » palb-17-t7(•1116)
    » palb-05-t7(•1119)
    » palb-01-t7(•1037)
       Contig 4 (1613) CTGAGGTCAGCTCTCCTCCAGGACCTGCTGGAAAGGCCACCACACCGCCACC
------------------------------------------------------------------------ Section 33
                     1665 ,1670     ,1680     ,1690     ,1700          1716
  » Palb2 mRNA (1606) TGGTAGAGGACACAGAGGGAAACGAAAATCAGCCCGCACCTCCACACT----
  » palb-15-13 rc (950) TGGTAGAGGACACAGAGGGAAACGAAAATCAGCCCGCACCTCCACACTGGAA
  » palb-19-13 rc (892) TGGTAGAGGACACAGAGGGAAACGAAAATCAGCCCGCACCTCCACACTGGAA
  » palb-05-13 rc (918) TGGTAGAGGACACAGAGGGAAACGAAAATCAGCCCGCACCTCCACACTGGAA
  » palb-17-13 rc (888) TGGTAGAGGACACAGAGGGAAACGAAAATCAGCCCGCACCTCCACACTGGAA
  » palb-01-13 rc (918) TGGTAGAGGACACAGAGGGAAACGAAAATCAGCCCGCACCTCCACACTGGAA
  » palb-08-13 rc (918) TGGTAGAGGACACAGAGGGAAACGAAAATCAGCCCGCACCTCCACACTGG
    » palb-15-t7(•1138)
    » palb-08-t7(•1156)
    » palb-19-t7(•1124)
    » palb-17-t7(•1116)
    » palb-05-t7(•1119)
    » palb-01-t7(•1037)
       Contig 4 (1665) TGGTAGAGGACACAGAGGGAAACGAAAATCAGCCCGCACCTCCACACTGGAA
                                                                       ++++

03/02/08 02:57:47               Alignment                                   Page 12
------------------------------------------------------------------------ Section 34
                     1717         ,1730     ,1740     ,1750             1768
  » Palb2 mRNA (1658) GGGTCACTGCCAGC-----TGCTTTTTCCTCCTTGTGCCGCACTGGCTGTTA
 » palb-15-13 rc (1002) GGGCGAATTCCAGCACA-CTGGCGGCCGTTACTAGTGGATCCGAGCTCGGTA
  » palb-19-13 rc (944) GGGCGAATTCCAGCACA-CTGGCGGCCGTTACTAGTGGATCCGAGCTCGGTA
  » palb-05-13 rc (970) GGGCGAATTCCAGCACA-CTGGCGGCCGTTACTAGTGGATCCGAGCTCGGTA
  » palb-17-13 rc (940) GGGCGAATTCCAGCACANCTGGCGGCCGTTACTAGTGGATCCGAGCTCGGTA
  » palb-01-13 rc (970) GGGCGAATTCCAGCACA-CTGGCGGCCGTTACTAGTGGATCCGAGCTCGGTA
 » palb-08-13 rc (•966)
    » palb-15-t7(•1138)
    » palb-08-t7(•1156)
    » palb-19-t7(•1124)
    » palb-17-t7(•1116)
    » palb-05-t7(•1119)
    » palb-01-t7(•1037)
       Contig 4 (1717) GGGCGAATTCCAGCACA-CTGGCGGCCGTTACTAGTGGATCCGAGCTCGGTA
                          ++ + +     +++·+  ++++++++ +  +   +++ +++ +++ +
------------------------------------------------------------------------ Section 35
                     1769       ,1780     ,1790     ,1800     ,1810     1820
  » Palb2 mRNA (1710) ACA-GGTCCAAGGGCAAATTCACCAAGCATAAATGTCAGAACAGAGGCGTGG
 » palb-15-13 rc (1054) CCAAGCTTGATGCATAGCTTGAGTATTCTATAG
  » palb-19-13 rc (996) CCAAGCTTGATGCATAGCTTGAGTATTCTATAGTCACCTA
 » palb-05-13 rc (1022) CCAAGCTTGATGCATAGCTTGAGT-TTCTATAGTCACCTA
  » palb-17-13 rc (992) CCAAGCTTGATGCATAGCTTGAGTATTCTATAGTCACCTA
 » palb-01-13 rc (1022) CCAAGCTTGATGCATAGCTTGAGTATTCTATAGTCACCTA
 » palb-08-13 rc (•966)
    » palb-15-t7(•1138)
    » palb-08-t7(•1156)
    » palb-19-t7(•1124)
    » palb-17-t7(•1116)
    » palb-05-t7(•1119)
    » palb-01-t7(•1037)
       Contig 4 (1769) CCAAGCTTGATGCATAGCTTGAGTATTCTATAGTCACCTAACAGAGGCGTGG
                       +  + + ++ + +++ ++  + +++++ +++ + ++ ++
------------------------------------------------------------------------ Section 36
                     1821     ,1830     ,1840     ,1850     ,1860         1872
  » Palb2 mRNA (1762) TTATTCATGACTTTGAGTTACCTGATGAAGACTTTGGGCTTCTTAAACTTGA
 » palb-15-13 rc(•1085)
 » palb-19-13 rc(•1034)
 » palb-05-13 rc(•1060)
 » palb-17-13 rc(•1030)
 » palb-01-13 rc(•1060)
 » palb-08-13 rc (•966)
    » palb-15-t7(•1138)
    » palb-08-t7(•1156)
    » palb-19-t7(•1124)
    » palb-17-t7(•1116)
    » palb-05-t7(•1119)
    » palb-01-t7(•1037)
       Contig 4 (1821) TTATTCATGACTTTGAGTTACCTGATGAAGACTTTGGGCTTCTTAAACTTGA
```



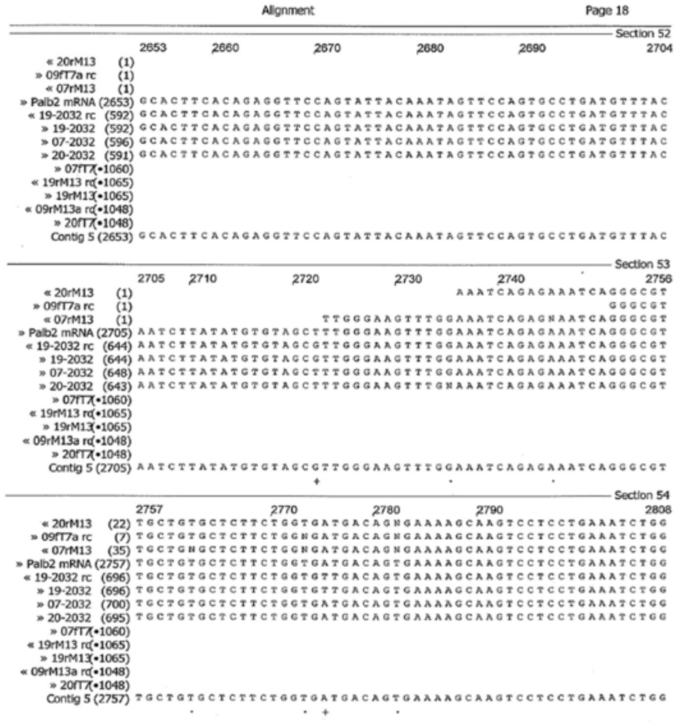
```
                         Alignment                                     Page 13
======================================================================= Section 37
                    1873     ,1880      ,1890      ,1900      ,1910         1924
      « 20rM13    (1)
   » 09fT7a rc    (1)
      « 07rM13    (1)
» Palb2 mRNA (1873) AAACCATGCTGCTCTGGAGGAACTGCAAAGAGATTCGGAGACGGAGGGCTTG
   « 19-2032 rc   (1)
     » 19-2032    (1)
     » 07-2032    (1)
     » 20-2032    (1)
       » 07fT7  (569) AAACCATGCTGCTCTGGAGGAACTGCAAAGAGATTCGGAGACGGAGGGCTTG
   « 19rM13 rc  (569) AAACCATGCTGCTCTGGAGGAACTGCAAAGAGATTCGGAGACGTAGGGCTTG
      » 19rM13  (569) AAACCATGCTGCTCTGGAGGAACTGCAAAGAGATTCGGAGACGTAGGGCTTG
 « 09rM13a rc   (569) AAACCATGCTGCTCTGGAGGAACTGCAAAGAGGTTCGGAGACGGAGGGCTTG
       » 20fT7  (569) AAACCATGCTGCTCTGGAGGAACTGCAAAGAGATTCGGAGACGGAGGGCTTG
  Contig 5 (1873) AAACCATGCTGCTCTGGAGGAACTGCAAAGAGATTCGGAGACGGAGGGCTTG
                                                  +          +
----------------------------------------------------------------------- Section 38
                    1925  ,1930         ,1940      ,1950      ,1960         1976
      « 20rM13    (1)
   » 09fT7a rc    (1)
      « 07rM13    (1)
» Palb2 mRNA (1925) GAAGAGGAGCTCACTGTTCCACCAGGAGAAGCGTACCGTCCAGGGCCAACCC
   « 19-2032 rc   (1)
     » 19-2032    (1)
     » 07-2032    (1)
     » 20-2032    (1)
       » 07fT7  (621) GAAGAGGAGCTCACTGTTCCACCAGGAGAAGCGTACCGTCCAGGGCCAACCC
   « 19rM13 rc  (621) GAAGAGGAGCTCACTGTTCCACCAGGAGAAGCGTACCGTCCAGGGCCAACCC
      » 19rM13  (621) GAAGAGGAGCTCACTGTTCCACCAGGAGAAGCGTACCGTCCAGGGCCAACCC
 « 09rM13a rc   (621) GAAGAGGAGCTCACTGTTCCACCAGGAGAAGCGTACCGTCCAGGGCCAACCC
       » 20fT7  (621) GAAGAGGAGCTCACTGTTCCACCAGGAGAAGCGTACCGTCCAGGGCCAACCC
  Contig 5 (1925) GAAGAGGAGCTCACTGTTCCACCAGGAGAAGCGTACCGTCCAGGGCCAACCC

----------------------------------------------------------------------- Section 39
                    1977             ,1990       2000       2010            2028
      « 20rM13    (1)
   » 09fT7a rc    (1)
      « 07rM13    (1)
» Palb2 mRNA (1977) TGAGAAGGCAGCCAGGGAGCAAGGACCTTTCTTCATCCATAGTGCTTTTCAC
   « 19-2032 rc   (1)
     » 19-2032    (1)
     » 07-2032    (1)
     » 20-2032    (1)
       » 07fT7  (673) TGAGAAGGCAGCCAGGGAGCAAGGACCTTTCTTCATCCATAGTGCTTTTCAC
   « 19rM13 rc  (673) TGAGAAGGCAGCCAGGGAGCAAGGACCTTTCTTCATCCATAGTGCTTTTCAC
      » 19rM13  (673) TGAGAAGGCAGCCAGGGAGCAAGGACCTTTCTTCATCCATAGTGCTTTTCAC
 « 09rM13a rc   (673) TGAGAAGGCAGCCAGGGAGCAAGGACCTTTCTTCATCCATAGTGCTTTTCAC
       » 20fT7  (673) CGAGAAGGCAGCCAGGGAGCAAGGACCTTTCTTCATCCATAGTGCTTTTCAC
  Contig 5 (1977) TGAGAAGGCAGCCAGGGAGCAAGGACCTTTCTTCATCCATAGTGCTTTTCAC
                  +

                         Alignment                                     Page 14
======================================================================= Section 40
                    2029            2040       2050       2060       2070   2080
      « 20rM13    (1)
   » 09fT7a rc    (1)
      « 07rM13    (1)
» Palb2 mRNA (2029) TCCTGCAGACACTGCTGCGCCTAACGACAGTGGCAGGCCTCCTCCCTCCCTG
   « 19-2032 rc   (1)                                  CAGGCCTCCTCCCTCCCTG
     » 19-2032    (1)                                  CAGGCCTCCTCCCTCCCTG
     » 07-2032    (1)                              GTGGCAGGCCTCCTCCCTCCCTG
     » 20-2032    (1)                                   AGGCCTCCTCCCTCCCTG
       » 07fT7  (725) TCCTGCAGACACTGCTGCGCCTAACGACAGTGGCAGGCCTCCTCCCTCCCTG
   « 19rM13 rc  (725) TCCTGCAGACACTGCTGCGCCTAACGACAGTGGCAGGCCTCCTCCCTCCCTG
      » 19rM13  (725) TCCTGCAGACACTGCTGCGCCTAACGACAGTGGCAGGCCTCCTCCCTCCCTG
 « 09rM13a rc   (725) TCCTGCAGACACTGCTGCGCCTAACGACAGTGGCAGGCCTCCTCCCTCCCTG
       » 20fT7  (725) TCCTGCAGACACTGCTGCGCCTAACGACAGTGGCAGGCCTCCTCCCTCCCTG
  Contig 5 (2029) TCCTGCAGACACTGCTGCGCCTAACGACAGTGGCAGGCCTCCTCCCTCCCTG

----------------------------------------------------------------------- Section 41
                    2081         2090       2100       2110       2120      2132
      « 20rM13    (1)
   » 09fT7a rc    (1)
      « 07rM13    (1)
» Palb2 mRNA (2081) TGCTCACCTGCTTTCCCCATCTTAGGCATGACTCCAGCTCTTGGCTCCCAAG
   « 19-2032 rc  (20) TGCTCACCTGCTTTCCCCATCTTAGGCATGACTCCNGCTCTTGGCTCCCAAG
     » 19-2032   (20) TGCTCACCTGCTTTCCCCATCTTAGGCATGACTCCNGCTCTTGGCTCCCAAG
     » 07-2032   (24) TGCTCACCTGCTTTCCCCATCTTAGGCATGACTCCAGCTCTTGGCTCCCAAG
     » 20-2032   (19) TGCTCACCTGCTTTCCCCATCTTAGGCATGACTCCNGCTCTTGGCTCCCAAG
       » 07fT7  (777) TGCTCACCTGCTTTCCCCATCTTAGGCATGACTCCAGCTCTTGGCTCCCAAG
   « 19rM13 rc  (777) TGCTCACCTGCTTTCCCCATCTTAGGCATGACTCCAGCTCTTGGCTCCCAAG
      » 19rM13  (777) TGCTCACCTGCTTTCCCCATCTTAGGCATGACTCCAGCTCTTGGCTCCCAAG
 « 09rM13a rc   (777) TGCTCACCTGCTTTCCCCATCTTAGGCATGACTCCAGCTCTTGGCTCCCAAG
       » 20fT7  (777) TGCTCACCTGCTTTCCCCATCTTAGGCATGACTCCAGCTCTTGGCTCCCAAG
  Contig 5 (2081) TGCTCACCTGCTTTCCCCATCTTAGGCATGACTCCAGCTCTTGGCTCCCAAG
                                                     .
----------------------------------------------------------------------- Section 42
                    2133  2140         2150       2160       2170           2184
      « 20rM13    (1)
   » 09fT7a rc    (1)
      « 07rM13    (1)
» Palb2 mRNA (2133) CAGCCGGTGAGACTCTATCTACTG-AAGCTGCACAGCC-TTGCTCTACATCC
   « 19-2032 rc  (72) CAGCCGGTGAGACTCTATCTACTG-AAGCTGCACAGCC-TTGCTCTACATCC
     » 19-2032   (72) CAGCCGGTGAGACTCTATCTACTG-AAGCTGCACAGCC-TTGCTCTACATCC
     » 07-2032   (76) CAGCCGGTGAGACTCTATCTACTG-AAGCTGCACAGCC-TTGCTCTACATCC
     » 20-2032   (71) CAGCCGGTGAGACTCTATCTACTG-AAGCTGCACAGCC-TTGCTCTACATCC
       » 07fT7  (829) CAGCCGGTGAGACTCTATCTACTG-AAGCTGCACAGCC-TTGCTCTACATCC
   « 19rM13 rc  (829) CAGCCGGTGAGACTCTATCTACTG-AAGCTGCACAGCC-TTGCTCTACATCC
      » 19rM13  (829) CAGCCGGTGAGACTCTATCTACTG-AAGCTGCACAGCC-TTGCTCTACATCC
 « 09rM13a rc   (829) CAGCCGGTGAGACTCTATCTACTG-AAGCTGCACAGCC-TTGCTCTACATCC
       » 20fT7  (829) CAGCCGGTGAGACTCTATCTACTGGAAGCTGCACAGCCNTTGCTCTACATCC
  Contig 5 (2133) CAGCCGGTGAGACTCTATCTACTG-AAGCTGCACAGCC-TTGCTCTACATCC
                                          +             .
```



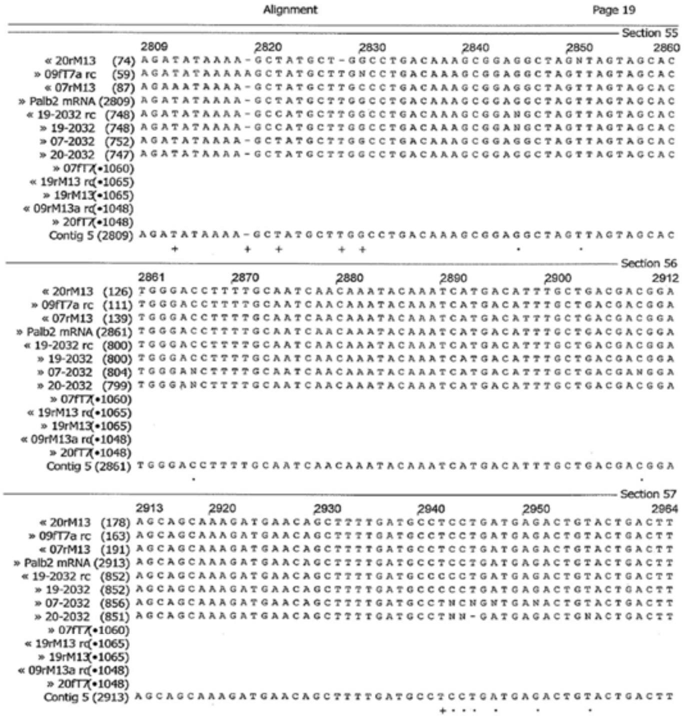
```
                              Alignment                                   Page 15
======================================================================================
---------------------------------------------------------------------------- Section 43
                     2185 2190      2200      2210      2220               2236
      « 20rM13    (1)
    » 09fT7a rc   (1)
      « 07rM13    (1)
» Palb2 mRNA (2185) CAACCTCCTCTCTTGGGAGACACAAACAGTCTTGTCAATAACAGTAAACAGT
  « 19-2032 rc  (124) CAACCTCCTCTCTTGGGAGACACAAACAGTCTTGTCAATAACAGTAAACAGT
     » 19-2032  (124) CAACCTCCTCTCTTGGGAGACACAAACAGTCTTGTCAATAACAGTAAACAGT
     » 07-2032  (128) CAACCTCCTCTCTTGGGAGACACAAACAGTCTTGTCAATAACAGTAAACAGT
     » 20-2032  (123) CAACCTCCTCTCTTGGGAGACACAAACAGTCTTGTCAATAACAGTAAACAGT
       » 07fT7  (881) CAACCTCCTCTCTTGGGAGACACAAACAGTCTTGTCAATAACAGTAAACAGT
   « 19rM13 rc  (881) CAACCTCCTCTCTTGGGAGACACAAACAGTCTTGTCAATAACAGTAAACAGT
      » 19rM13  (881) CAACCTCCTCTCTTGGGAGACACAAACAGTCTTGTCAATAACAGTAAACAGT
  « 09rM13a rc  (881) CAACCTCCTCTCTTGGGAGACACAAACAGTCTTGTCAATAACAGTAAACAGT
       » 20fT7  (881) CAACCTCCTCTCTTGGGAGACACAAACAGTCTNGTCAATANCAGTAAACAGT
    Contig 5 (2185) CAACCTCCTCTCTTGGGAGACACAAACAGTCTTGTCAATAACAGTAAACAGT
                    .                                 .       .
---------------------------------------------------------------------------- Section 44
                     2237         2250      2260      2270               2288
      « 20rM13    (1)
    » 09fT7a rc   (1)
      « 07rM13    (1)
» Palb2 mRNA (2237) GCAACAGTT-CAGCCTGCTCACC-AAAACC-GGACACCAACCTGCAAGCGTC
  « 19-2032 rc  (176) GCAACAGTT-CAGCCTGCTCACC-AAAACC-GGACACCAACCTGCAAGCGTC
     » 19-2032  (176) GCAACAGTT-CAGCCTGCTCACC-AAAACC-GGACACCAACCTGCAAGCGTC
     » 07-2032  (180) GCAACAGTT-CAGCCTGCTCACC-AAAACC-GGACACCAACCTGCAAGCGTC
     » 20-2032  (175) GCAACAGTT-CAGACTGCTCACC-AAAACC-GGACACCAACCTGCAAGCGTC
       » 07fT7  (933) GCANCAGTT-CAGCCTGCTCACC-AAAACC-GGACACCAACCTGCANGCGTC
   « 19rM13 rc  (933) GCAACAGTT-CAGCCTGCTCACCAAAAACCCGGACACCAACCTGCAAGCGTC
      » 19rM13  (933) GCAACAGTT-CAGCCTGCTCACCAAAAACCCGGACACCAACCTGCAAGCGTC
  « 09rM13a rc  (933) GCAACAGTT-CAGCCTGCTCACCNAAAACC-GGACACCANCCTGCANGCGTC
       » 20fT7  (933) GCAACAGTTTCAGACTGCTCACC-AAANCG-GAACACNANCCTGCAAGCGTC
    Contig 5 (2237) GCAACAGTT-CAGCCTGCTCACC-AAAACC-GGACACCAACCTGCAAGCGTC
                       .     +   +         .   . ++ +     . .      .
---------------------------------------------------------------------------- Section 45
                     2289        2300      2310      2320      2330      2340
      « 20rM13    (1)
    » 09fT7a rc   (1)
      « 07rM13    (1)
» Palb2 mRNA (2289) AGGTAGGCAAGGACAACCTGCCTG-TGACAGTGA-CTCTGG-CCCCCAAGCA
  « 19-2032 rc  (228) AGGTAGGCAAGGACAACCTGCCTG-TGACAGTGA-CTCTGG-CCCCCAAGCA
     » 19-2032  (228) AGGTAGGCAAGGACAACCTGCCTG-TGACAGTGA-CTCTGG-CCCCCAAGCA
     » 07-2032  (232) AGGTAGGCAAGGACAACCTGCCTG-TGACAGTGA-CTCTGG-CCCCCAAGCA
     » 20-2032  (227) AGGTAGGCAAGGACAACCTGCCTG-TGACAGTGA-CTCTGG-CCCCCAAGCA
       » 07fT7  (985) AGGTAGGCAAGGACAACCTGCCTG-GGACAGTGA-CTCTGG-NCCCCANGCA
   « 19rM13 rc  (985) AGGTAGGCAAGNACAACCTGCCTG-GGACAGTGAACTCTGG-NCCCCAAGCA
      » 19rM13  (985) AGGTAGGCAAGNACAACCTGCCTG-GGACAGTGAACTCTGG-NCCCCAAGCA
  « 09rM13a rc  (985) AGGTAGGCAAGGACAACCTGCCTGGGAACAGTGA-CTCTGGNCCCCCAAGCA
       » 20fT7  (985) AGGTAGGCAAGGACAACCTGCCTGGTGACAGTGA-CTCTGGGCCCCCAAGCA
    Contig 5 (2289) AGGTAGGCAAGGACAACCTGCCTG-TGACAGTGA-CTCTGG-CCCCCAAGCA
                             .           +++       +       . .     .

                              Alignment                                   Page 16
======================================================================================
---------------------------------------------------------------------------- Section 46
                     2341        2350      2360      2370      2380      2392
      « 20rM13    (1)
    » 09fT7a rc   (1)
      « 07rM13    (1)
» Palb2 mRNA (2341) ACACCTCTACCTG-TTGAGTCATTCACTTTCAGAGAAAATCAGCTTTGTGGA
  « 19-2032 rc  (280) ACACCTCTACCTG-TTGAGTCATTCACTTTCAGAGAAAATCAGCCTTGTGGA
     » 19-2032  (280) ACACCTCTACCTG-TTGAGTCATTCACTTTCAGAGAAAATCAGCCTTGTGGA
     » 07-2032  (284) ACACCTCTACCTG-TTGAGTCATTCACTTTCAGAGAAAATCAGCTTTGTGGA
     » 20-2032  (279) ACACCTCTACCTG-TTGAGTCATTCACTTTCAGAGAAAATCAGCTTTGTGGA
       » 07fT7 (1037) ACACCTCTACCTG-TTGANTCATTC
   « 19rM13 rc (1037) ACACCTCTACCTGNTTGAGTCATTCNCTTT
      » 19rM13 (1037) ACACCTCTACCTGNTTGAGTCATTCNCTTT
  « 09rM13a rc (1037) ACNCCTCTACCTG
       » 20fT7 (1037) ANACCTCTACCTG
    Contig 5 (2341) ACACCTCTACCTG-TTGAGTCATTCACTTTCAGAGAAAATCAGCCTTGTGGA
                     ..          .    .      .                    +
---------------------------------------------------------------------------- Section 47
                     2393  2400      2410      2420      2430              2444
      « 20rM13    (1)
    » 09fT7a rc   (1)
      « 07rM13    (1)
» Palb2 mRNA (2393) AATGCATGCCTCGAGTTACATGAACATTCCACTGAACAGACTGAAACTGCAG
  « 19-2032 rc  (332) AATGCATGCCTCGAGTTACATGAACATTCCACTGAACAGACTGAAACTGCAG
     » 19-2032  (332) AATGCATGCCTCGAGTTACATGAACATTCCACTGAACAGACTGAAACTGCAG
     » 07-2032  (336) AATGCATGCCTCGAGTTACATGAACATTCCACTGAACAGACTGAAACTGCAG
     » 20-2032  (331) AATGCATGCCTCGAGTTACATGAACATTCCACTGAACAGACTGAAACTGCAG
       » 07fT7(•1060)
   « 19rM13 rc(•1065)
      » 19rM13(•1065)
  « 09rM13a rc(•1048)
       » 20fT7(•1048)
    Contig 5 (2393) AATGCATGCCTCGAGTTACATGAACATTCCACTGAACAGACTGAAACTGCAG
---------------------------------------------------------------------------- Section 48
                     2445 2450       2460      2470      2480              2496
      « 20rM13    (1)
    » 09fT7a rc   (1)
      « 07rM13    (1)
» Palb2 mRNA (2445) ATCGCCCTGCTTGTGACAATCTAAACCCAGGAAACCTACAGTTGGTTTCAGA
  « 19-2032 rc  (384) ATCGCCCTGCTTGTGACAATCTAAACCCAGGAAACCTACAGTTGGTTTCAGA
     » 19-2032  (384) ATCGCCCTGCTTGTGACAATCTAAACCCAGGAAACCTACAGTTGGTTTCAGA
     » 07-2032  (388) ATCGCCCTGCTTGTGACAATCTAAACCCGGGAAACCTACAGTTGGTTTCAGA
     » 20-2032  (383) ATCGCCCTGCTTGTGACAATCTAAACCCAGGAAACCTACAGTTGGTTTCAGA
       » 07fT7(•1060)
   « 19rM13 rc(•1065)
      » 19rM13(•1065)
  « 09rM13a rc(•1048)
       » 20fT7(•1048)
    Contig 5 (2445) ATCGCCCTGCTTGTGACAATCTAAACCCAGGAAACCTACAGTTGGTTTCAGA
                                               +
```



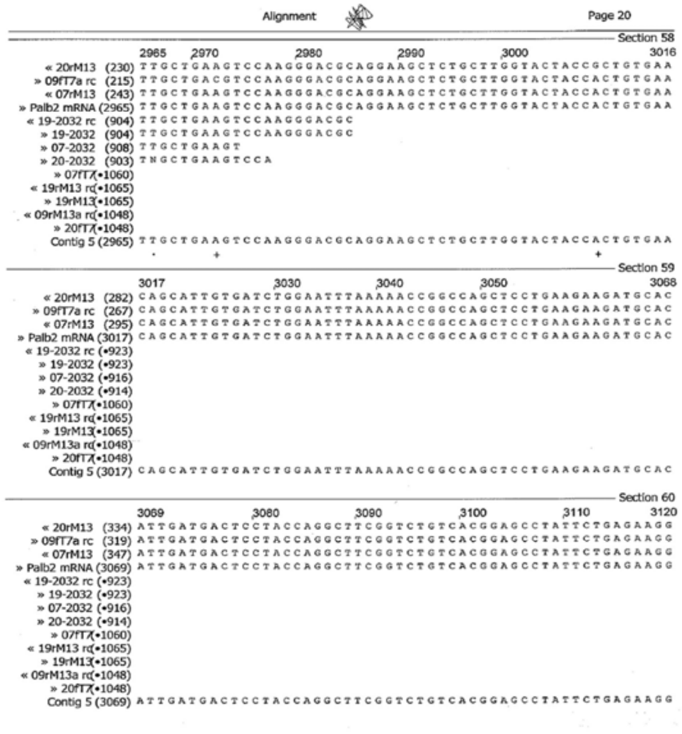
```
                    Alignment                                   Page 17
==========================================================================
------------------------------------------------------------- Section 49
                    2497         2510      2520      2530              2548
        « 20rM13    (1)
      » 09fT7a rc   (1)
        « 07rM13    (1)
» Palb2 mRNA (2497) GTTAAAGAATCCTTCCAGTTCCTGCTCTGTGGATGTGAGCGCCATGTGGTGG
  « 19-2032 rc (436) GTTAAAGAATCCTTCCAGTTCCTGCTCTGTGGATGTGAGCGCCATGTGGTGG
     » 19-2032 (436) GTTAAAGAATCCTTCCAGTTCCTGCTCTGTGGATGTGAGCGCCATGTGGTGG
     » 07-2032 (440) GTTAAAGAATCCTTCCAGTTCCTGCTCTGTGGATGTGAGCGCCATGTGGTGG
     » 20-2032 (435) GTTAAAGAATCCTTCCAGTTCCTGCTCTGTGGATGTGAGCGCCATGTGGTGG
   » 07fT7(•1060)
« 19rM13 rc(•1065)
   » 19rM13(•1065)
« 09rM13a rc(•1048)
   » 20fT7(•1048)
   Contig 5 (2497) GTTAAAGAATCCTTCCAGTTCCTGCTCTGTGGATGTGAGCGCCATGTGGTGG

------------------------------------------------------------- Section 50
                    2549       2560      2570      2580      2590      2600
        « 20rM13    (1)
      » 09fT7a rc   (1)
        « 07rM13    (1)
» Palb2 mRNA (2549) GAAAGAGCTGGTGCTAAGGAGCCATGTATCGTAACTGCTTGTGAAGATGTAG
  « 19-2032 rc (488) GAAAGAGCTGGTGCTAAGGAGCCATGTATCGTAACTGCTTGTGAAGATGTAG
     » 19-2032 (488) GAAAGAGCTGGTGCTAAGGAGCCATGTATCGTAACTGCTTGTGAAGATGTAG
     » 07-2032 (492) GAAAGAGCTGGTGCTAAGGAGCCATGTATCGTAACTGCTTGTGAAGATGTAG
     » 20-2032 (487) GAAAGAGCTGGTGCTAAGGAGCCATGTATCGTAACTGCTTGTGAAGATGTAG
   » 07fT7(•1060)
« 19rM13 rc(•1065)
   » 19rM13(•1065)
« 09rM13a rc(•1048)
   » 20fT7(•1048)
   Contig 5 (2549) GAAAGAGCTGGTGCTAAGGAGCCATGTATCGTAACTGCTTGTGAAGATGTAG

------------------------------------------------------------- Section 51
                    2601     2610      2620      2630      2640        2652
        « 20rM13    (1)
      » 09fT7a rc   (1)
        « 07rM13    (1)
» Palb2 mRNA (2601) TTTCTCTTTGGAAACCCTTGAATTCTCTGCAGTGGGAGAAAGTTCATACCTG
  « 19-2032 rc (540) TTTCTCTTTGGAAACCCTTGAATTCTCTGCAGTGGGAGAAAGTTCATACCTG
     » 19-2032 (540) TTTCTCTTTGGAAACCCTTGAATTCTCTGCAGTGGGAGAAAGTTCATACCTG
     » 07-2032 (544) TTTCTCTTTGGAAACCCTTGAATTCTCTGCAGTGGGAGAAAGTTCATGCCTG
     » 20-2032 (539) TTTCTCTTTGGAAACCCTTGAATTCTCTGCAGTGGGAGAAAGTTCATACCTG
   » 07fT7(•1060)
« 19rM13 rc(•1065)
   » 19rM13(•1065)
« 09rM13a rc(•1048)
   » 20fT7(•1048)
   Contig 5 (2601) TTTCTCTTTGGAAACCCTTGAATTCTCTGCAGTGGGAGAAAGTTCATACCTG
                                                                  +
```



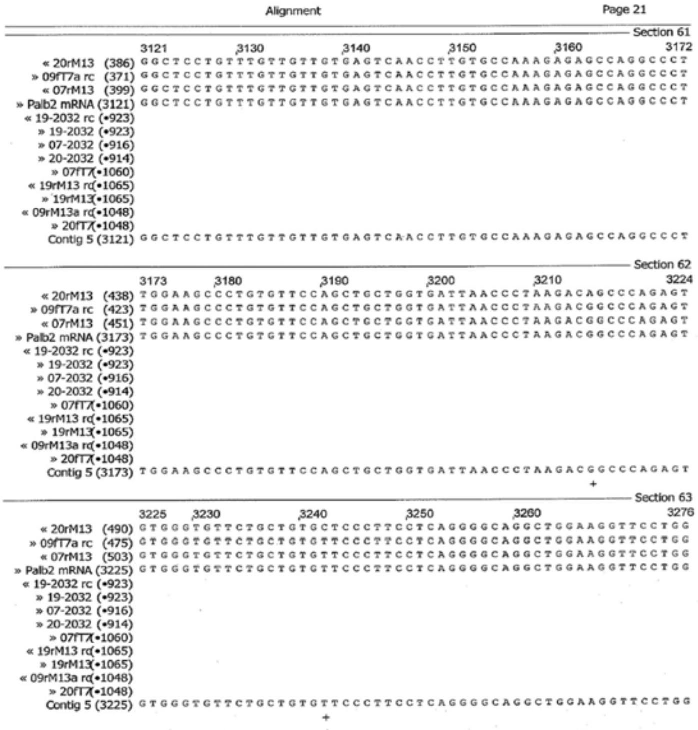
```
                    Alignment                                   Page 18
==========================================================================
------------------------------------------------------------- Section 52
                    2653   2660       2670      2680      2690         2704
        « 20rM13    (1)
      » 09fT7a rc   (1)
        « 07rM13    (1)
» Palb2 mRNA (2653) GCACTTCACAGAGGTTCCAGTATTACAAATAGTTCCAGTGCCTGATGTTTAC
  « 19-2032 rc (592) GCACTTCACAGAGGTTCCAGTATTACAAATAGTTCCAGTGCCTGATGTTTAC
     » 19-2032 (592) GCACTTCACAGAGGTTCCAGTATTACAAATAGTTCCAGTGCCTGATGTTTAC
     » 07-2032 (596) GCACTTCACAGAGGTTCCAGTATTACAAATAGTTCCAGTGCCTGATGTTTAC
     » 20-2032 (591) GCACTTCACAGAGGTTCCAGTATTACAAATAGTTCCAGTGCCTGATGTTTAC
   » 07fT7(•1060)
« 19rM13 rc(•1065)
   » 19rM13(•1065)
« 09rM13a rc(•1048)
   » 20fT7(•1048)
   Contig 5 (2653) GCACTTCACAGAGGTTCCAGTATTACAAATAGTTCCAGTGCCTGATGTTTAC

------------------------------------------------------------- Section 53
                    2705 2710      2720      2730      2740            2756
        « 20rM13    (1)                                AAATCAGAGAAATCAGGGCGT
      » 09fT7a rc   (1)                                               GGGCGT
        « 07rM13    (1)                   TTGGGAAGTTTGGAAATCAGAGNAATCAGGGCGT
» Palb2 mRNA (2705) AATCTTATATGTGTAGCTTTGGGAAGTTTGGAAATCAGAGAAATCAGGGCGT
  « 19-2032 rc (644) AATCTTATATGTGTAGCGTTGGGAAGTTTGGAAATCAGAGAAATCAGGGCGT
     » 19-2032 (644) AATCTTATATGTGTAGCGTTGGGAAGTTTGGAAATCAGAGAAATCAGGGCGT
     » 07-2032 (648) AATCTTATATGTGTAGCTTTGGGAAGTTTGGAAATCAGAGAAATCAGGGCGT
     » 20-2032 (643) AATCTTATATGTGTAGCTTTGGGAAGTTTGNAAATCAGAGAAATCAGGGCGT
   » 07fT7(•1060)
« 19rM13 rc(•1065)
   » 19rM13(•1065)
« 09rM13a rc(•1048)
   » 20fT7(•1048)
   Contig 5 (2705) AATCTTATATGTGTAGCGTTGGGAAGTTTGGAAATCAGAGAAATCAGGGCGT
                                    +            .         .

------------------------------------------------------------- Section 54
                    2757         2770      2780      2790              2808
        « 20rM13   (22) TGCTGTGCTCTTCTGGTGATGACAGNGAAAAGCAAGTCCTCCTGAAATCTGG
      » 09fT7a rc   (7) TGCTGTGCTCTTCTGGNGATGACAGNGAAAAGCAAGTCCTCCTGAAATCTGG
        « 07rM13   (35) TGCTGNGCTCTTCTGGNGATGACAGNGAAAAGCAAGTCCTCCTGAAATCTGG
» Palb2 mRNA (2757) TGCTGTGCTCTTCTGGTGATGACAGTGAAAAGCAAGTCCTCCTGAAATCTGG
  « 19-2032 rc (696) TGCTGTGCTCTTCTGGTGTTGACAGTGAAAAGCAAGTCCTCCTGAAATCTGG
     » 19-2032 (696) TGCTGTGCTCTTCTGGTGTTGACAGTGAAAAGCAAGTCCTCCTGAAATCTGG
     » 07-2032 (700) TGCTGTGCTCTTCTGGTGATGACAGTGAAAAGCAAGTCCTCCTGAAATCTGG
     » 20-2032 (695) TGCTGTGCTCTTCTGGTGATGACAGTGAAAAGCAAGTCCTCCTGAAATCTGG
   » 07fT7(•1060)
« 19rM13 rc(•1065)
   » 19rM13(•1065)
« 09rM13a rc(•1048)
   » 20fT7(•1048)
   Contig 5 (2757) TGCTGTGCTCTTCTGGTGATGACAGTGAAAAGCAAGTCCTCCTGAAATCTGG
                        .          . +      .
```



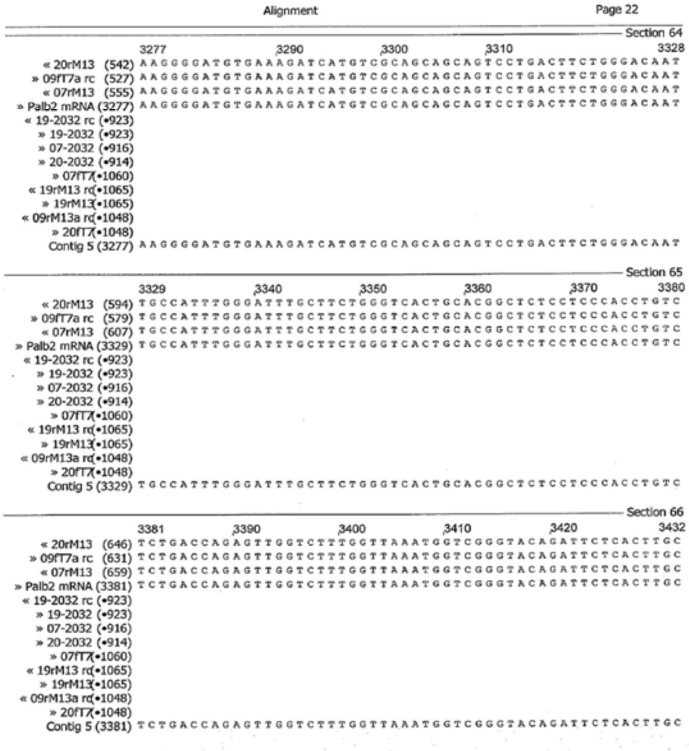
```
                       Alignment                                Page 19
============================================================================
------------------------------------------------------------- Section 55
                      2809       2820      2830      2840      2850   2860
        « 20rM13 (74) AGATATAAAA-GCTATGCT-GGCCTGACAAAGCGGAGGCTAGNTAGTAGCAC
     » 09fT7a rc (59) AGATATAAAAAGCTATGCTTGNCCTGACAAAGCGGAGGCTAGTTAGTAGCAC
        « 07rM13 (87) AGAAATAAAA-GCTATGCTTGCCCTGACAAAGCGGAGGCTAGTTAGTAGCAC
  » Palb2 mRNA (2809) AGATATAAAA-GCTATGCTTGGCCTGACAAAGCGGAGGCTAGTTAGTAGCAC
   « 19-2032 rc (748) AGATATAAAA-GCCATGCTTGGCCTGACAAAGCGGANGCTAGTTAGTAGCAC
      » 19-2032 (748) AGATATAAAA-GCCATGCTTGGCCTGACAAAGCGGANGCTAGTTAGTAGCAC
      » 07-2032 (752) AGATATAAAA-GCTATGCTTGGCCTGACAAAGCGGAGGCTAGTTAGTAGCAC
      » 20-2032 (747) AGATATAAAA-GCTATGCTTGGCCTGACAAAGCGGAGGCTAGTTAGTAGCAC
       » 07fT7(•1060)
   « 19rM13 rc(•1065)
      » 19rM13(•1065)
  « 09rM13a rc(•1048)
       » 20fT7(•1048)
      Contig 5 (2809) AGATATAAAA-GCTATGCTTGGCCTGACAAAGCGGAGGCTAGTTAGTAGCAC
                         +      +  +     + +              .     .
------------------------------------------------------------- Section 56
                      2861     2870      2880      2890      2900     2912
       « 20rM13 (126) TGGGACCTTTTGCAATCAACAAATACAAATCATGACATTTGCTGACGACGGA
    » 09fT7a rc (111) TGGGACCTTTTGCAATCAACAAATACAAATCATGACATTTGCTGACGACGGA
       « 07rM13 (139) TGGGACCTTTTGCAATCAACAAATACAAATCATGACATTTGCTGACGACGGA
  » Palb2 mRNA (2861) TGGGACCTTTTGCAATCAACAAATACAAATCATGACATTTGCTGACGACGGA
   « 19-2032 rc (800) TGGGACCTTTTGCAATCAACAAATACAAATCATGACATTTGCTGACGACGGA
      » 19-2032 (800) TGGGACCTTTTGCAATCAACAAATACAAATCATGACATTTGCTGACGACGGA
      » 07-2032 (804) TGGGANCTTTTGCAATCAACAAATACAAATCATGACATTTGCTGACGANGGA
      » 20-2032 (799) TGGGANCTTTTGCAATCAACAAATACAAATCATGACATTTGCTGACGACGGA
       » 07fT7(•1060)
   « 19rM13 rc(•1065)
      » 19rM13(•1065)
  « 09rM13a rc(•1048)
       » 20fT7(•1048)
      Contig 5 (2861) TGGGACCTTTTGCAATCAACAAATACAAATCATGACATTTGCTGACGACGGA
                           .                                          .
------------------------------------------------------------- Section 57
                      2913   2920      2930      2940      2950       2964
       « 20rM13 (178) AGCAGCAAAGATGAACAGCTTTTGATGCCTCCTGATGAGACTGTACTGACTT
    » 09fT7a rc (163) AGCAGCAAAGATGAACAGCTTTTGATGCCTCCTGATGAGACTGTACTGACTT
       « 07rM13 (191) AGCAGCAAAGATGAACAGCTTTTGATGCCTCCTGATGAGACTGTACTGACTT
  » Palb2 mRNA (2913) AGCAGCAAAGATGAACAGCTTTTGATGCCTCCTGATGAGACTGTACTGACTT
   « 19-2032 rc (852) AGCAGCAAAGATGAACAGCTTTTGATGCCCCCTGATGAGACTGTACTGACTT
      » 19-2032 (852) AGCAGCAAAGATGAACAGCTTTTGATGCCCCCTGATGAGACTGTACTGACTT
      » 07-2032 (856) AGCAGCAAAGATGAACAGCTTTTGATGCCTNCNGNTGANACTGTACTGACTT
      » 20-2032 (851) AGCAGCAAAGATGAACAGCTTTTGATGCCTNN-GATGAGACTGNACTGACTT
       » 07fT7(•1060)
   « 19rM13 rc(•1065)
      » 19rM13(•1065)
  « 09rM13a rc(•1048)
       » 20fT7(•1048)
      Contig 5 (2913) AGCAGCAAAGATGAACAGCTTTTGATGCCTCCTGATGAGACTGTACTGACTT
                                                   +... .   .    .
```



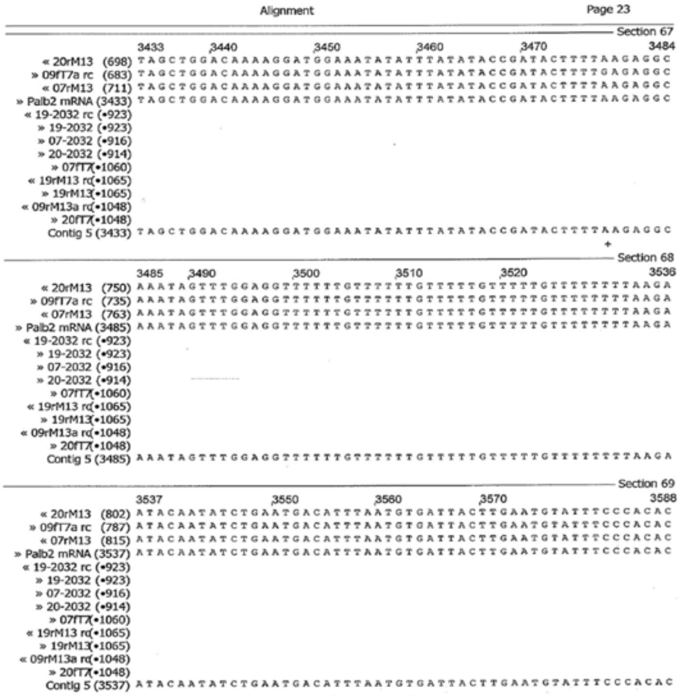
```
                       Alignment                                Page 20
============================================================================
------------------------------------------------------------- Section 58
                      2965 2970      2980      2990      3000         3016
       « 20rM13 (230) TTGCTGAAGTCCAAGGGACGCAGGAAGCTCTGCTTGGTACTACCGCTGTGAA
    » 09fT7a rc (215) TTGCTGACGTCCAAGGGACGCAGGAAGCTCTGCTTGGTACTACCACTGTGAA
       « 07rM13 (243) TTGCTGAAGTCCAAGGGACGCAGGAAGCTCTGCTTGGTACTACCACTGTGAA
  » Palb2 mRNA (2965) TTGCTGAAGTCCAAGGGACGCAGGAAGCTCTGCTTGGTACTACCACTGTGAA
   « 19-2032 rc (904) TTGCTGAAGTCCAAGGGACGC
      » 19-2032 (904) TTGCTGAAGTCCAAGGGACGC
      » 07-2032 (908) TTGCTGAAGT
      » 20-2032 (903) TNGCTGAAGTCCA
       » 07fT7(•1060)
   « 19rM13 rc(•1065)
      » 19rM13(•1065)
  « 09rM13a rc(•1048)
       » 20fT7(•1048)
      Contig 5 (2965) TTGCTGAAGTCCAAGGGACGCAGGAAGCTCTGCTTGGTACTACCACTGTGAA
                       .     +                                    +
------------------------------------------------------------- Section 59
                      3017         3030      3040      3050           3068
       « 20rM13 (282) CAGCATTGTGATCTGGAATTTAAAAACCGGCCAGCTCCTGAAGAAGATGCAC
    » 09fT7a rc (267) CAGCATTGTGATCTGGAATTTAAAAACCGGCCAGCTCCTGAAGAAGATGCAC
       « 07rM13 (295) CAGCATTGTGATCTGGAATTTAAAAACCGGCCAGCTCCTGAAGAAGATGCAC
  » Palb2 mRNA (3017) CAGCATTGTGATCTGGAATTTAAAAACCGGCCAGCTCCTGAAGAAGATGCAC
   « 19-2032 rc (•923)
      » 19-2032 (•923)
      » 07-2032 (•916)
      » 20-2032 (•914)
       » 07fT7(•1060)
   « 19rM13 rc(•1065)
      » 19rM13(•1065)
  « 09rM13a rc(•1048)
       » 20fT7(•1048)
      Contig 5 (3017) CAGCATTGTGATCTGGAATTTAAAAACCGGCCAGCTCCTGAAGAAGATGCAC
------------------------------------------------------------- Section 60
                      3069       3080      3090      3100      3110   3120
       « 20rM13 (334) ATTGATGACTCCTACCAGGCTTCGGTCTGTCACGGAGCCTATTCTGAGAAGG
    » 09fT7a rc (319) ATTGATGACTCCTACCAGGCTTCGGTCTGTCACGGAGCCTATTCTGAGAAGG
       « 07rM13 (347) ATTGATGACTCCTACCAGGCTTCGGTCTGTCACGGAGCCTATTCTGAGAAGG
  » Palb2 mRNA (3069) ATTGATGACTCCTACCAGGCTTCGGTCTGTCACGGAGCCTATTCTGAGAAGG
   « 19-2032 rc (•923)
      » 19-2032 (•923)
      » 07-2032 (•916)
      » 20-2032 (•914)
       » 07fT7(•1060)
   « 19rM13 rc(•1065)
      » 19rM13(•1065)
  « 09rM13a rc(•1048)
       » 20fT7(•1048)
      Contig 5 (3069) ATTGATGACTCCTACCAGGCTTCGGTCTGTCACGGAGCCTATTCTGAGAAGG
```



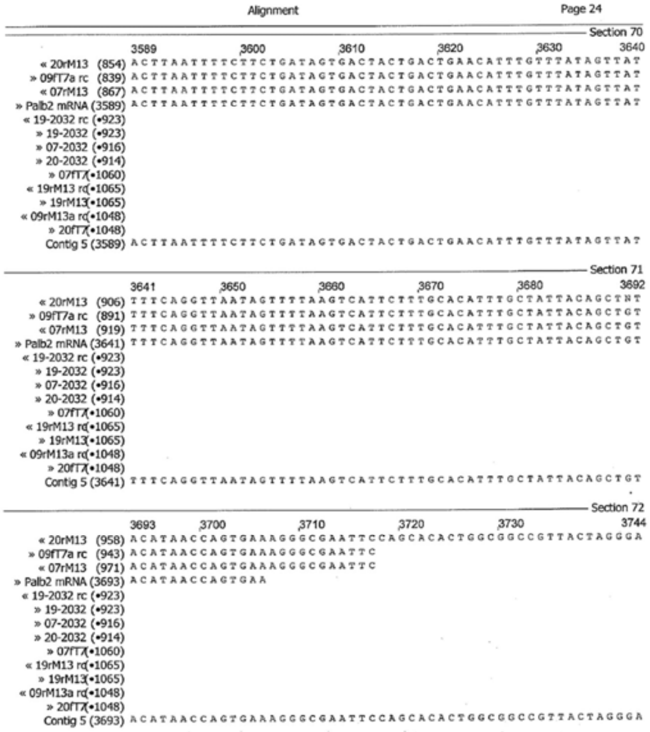
```
                    Alignment                                  Page 21
=============================================================================
--------------------------------------------------------------- Section 61
                      3121      3130      3140      3150      3160       3172
      « 20rM13  (386) GGCTCCTGTTTGTTGTTGTGAGTCAACCTTGTGCCAAAGAGAGCCAGGCCCT
    » 09fT7a rc  (371) GGCTCCTGTTTGTTGTTGTGAGTCAACCTTGTGCCAAAGAGAGCCAGGCCCT
      « 07rM13  (399) GGCTCCTGTTTGTTGTTGTGAGTCAACCTTGTGCCAAAGAGAGCCAGGCCCT
 » Palb2 mRNA (3121) GGCTCCTGTTTGTTGTTGTGAGTCAACCTTGTGCCAAAGAGAGCCAGGCCCT
 « 19-2032 rc (•923)
    » 19-2032 (•923)
    » 07-2032 (•916)
    » 20-2032 (•914)
     » 07fT7(•1060)
 « 19rM13 rc(•1065)
    » 19rM13(•1065)
« 09rM13a rc(•1048)
     » 20fT7(•1048)
   Contig 5 (3121) GGCTCCTGTTTGTTGTTGTGAGTCAACCTTGTGCCAAAGAGAGCCAGGCCCT

--------------------------------------------------------------- Section 62
                      3173   3180       3190      3200      3210       3224
      « 20rM13  (438) TGGAAGCCCTGTGTTCCAGCTGCTGGTGATTAACCCTAAGACAGCCCAGAGT
    » 09fT7a rc  (423) TGGAAGCCCTGTGTTCCAGCTGCTGGTGATTAACCCTAAGACGGCCCAGAGT
      « 07rM13  (451) TGGAAGCCCTGTGTTCCAGCTGCTGGTGATTAACCCTAAGACGGCCCAGAGT
 » Palb2 mRNA (3173) TGGAAGCCCTGTGTTCCAGCTGCTGGTGATTAACCCTAAGACGGCCCAGAGT
 « 19-2032 rc (•923)
    » 19-2032 (•923)
    » 07-2032 (•916)
    » 20-2032 (•914)
     » 07fT7(•1060)
 « 19rM13 rc(•1065)
    » 19rM13(•1065)
« 09rM13a rc(•1048)
     » 20fT7(•1048)
   Contig 5 (3173) TGGAAGCCCTGTGTTCCAGCTGCTGGTGATTAACCCTAAGACGGCCCAGAGT
                                                              +
--------------------------------------------------------------- Section 63
                      3225 3230       3240      3250      3260       3276
      « 20rM13  (490) GTGGGTGTTCTGCTGTGCTCCCTTCCTCAGGGGCAGGCTGGAAGGTTCCTGG
    » 09fT7a rc  (475) GTGGGTGTTCTGCTGTGTTCCCTTCCTCAGGGGCAGGCTGGAAGGTTCCTGG
      « 07rM13  (503) GTGGGTGTTCTGCTGTGTTCCCTTCCTCAGGGGCAGGCTGGAAGGTTCCTGG
 » Palb2 mRNA (3225) GTGGGTGTTCTGCTGTGTTCCCTTCCTCAGGGGCAGGCTGGAAGGTTCCTGG
 « 19-2032 rc (•923)
    » 19-2032 (•923)
    » 07-2032 (•916)
    » 20-2032 (•914)
     » 07fT7(•1060)
 « 19rM13 rc(•1065)
    » 19rM13(•1065)
« 09rM13a rc(•1048)
     » 20fT7(•1048)
   Contig 5 (3225) GTGGGTGTTCTGCTGTGTTCCCTTCCTCAGGGGCAGGCTGGAAGGTTCCTGG
                                    +
```



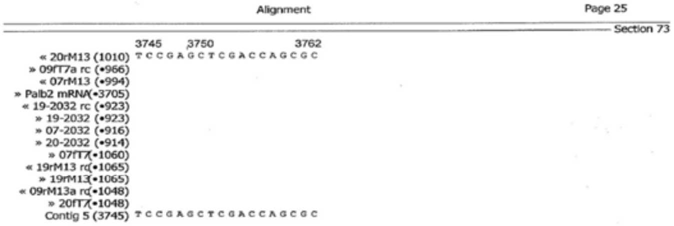
```
                    Alignment                                  Page 22
=============================================================================
--------------------------------------------------------------- Section 64
                      3277          3290      3300      3310           3328
      « 20rM13  (542) AAGGGGATGTGAAAGATCATGTCGCAGCAGCAGTCCTGACTTCTGGGACAAT
    » 09fT7a rc  (527) AAGGGGATGTGAAAGATCATGTCGCAGCAGCAGTCCTGACTTCTGGGACAAT
      « 07rM13  (555) AAGGGGATGTGAAAGATCATGTCGCAGCAGCAGTCCTGACTTCTGGGACAAT
 » Palb2 mRNA (3277) AAGGGGATGTGAAAGATCATGTCGCAGCAGCAGTCCTGACTTCTGGGACAAT
 « 19-2032 rc (•923)
    » 19-2032 (•923)
    » 07-2032 (•916)
    » 20-2032 (•914)
     » 07fT7(•1060)
 « 19rM13 rc(•1065)
    » 19rM13(•1065)
« 09rM13a rc(•1048)
     » 20fT7(•1048)
   Contig 5 (3277) AAGGGGATGTGAAAGATCATGTCGCAGCAGCAGTCCTGACTTCTGGGACAAT

--------------------------------------------------------------- Section 65
                      3329      3340      3350      3360      3370       3380
      « 20rM13  (594) TGCCATTTGGGATTTGCTTCTGGGTCACTGCACGGCTCTCCTCCCACCTGTC
    » 09fT7a rc  (579) TGCCATTTGGGATTTGCTTCTGGGTCACTGCACGGCTCTCCTCCCACCTGTC
      « 07rM13  (607) TGCCATTTGGGATTTGCTTCTGGGTCACTGCACGGCTCTCCTCCCACCTGTC
 » Palb2 mRNA (3329) TGCCATTTGGGATTTGCTTCTGGGTCACTGCACGGCTCTCCTCCCACCTGTC
 « 19-2032 rc (•923)
    » 19-2032 (•923)
    » 07-2032 (•916)
    » 20-2032 (•914)
     » 07fT7(•1060)
 « 19rM13 rc(•1065)
    » 19rM13(•1065)
« 09rM13a rc(•1048)
     » 20fT7(•1048)
   Contig 5 (3329) TGCCATTTGGGATTTGCTTCTGGGTCACTGCACGGCTCTCCTCCCACCTGTC

--------------------------------------------------------------- Section 66
                      3381      3390      3400      3410      3420       3432
      « 20rM13  (646) TCTGACCAGAGTTGGTCTTTGGTTAAATGGTCGGGTACAGATTCTCACTTGC
    » 09fT7a rc  (631) TCTGACCAGAGTTGGTCTTTGGTTAAATGGTCGGGTACAGATTCTCACTTGC
      « 07rM13  (659) TCTGACCAGAGTTGGTCTTTGGTTAAATGGTCGGGTACAGATTCTCACTTGC
 » Palb2 mRNA (3381) TCTGACCAGAGTTGGTCTTTGGTTAAATGGTCGGGTACAGATTCTCACTTGC
 « 19-2032 rc (•923)
    » 19-2032 (•923)
    » 07-2032 (•916)
    » 20-2032 (•914)
     » 07fT7(•1060)
 « 19rM13 rc(•1065)
    » 19rM13(•1065)
« 09rM13a rc(•1048)
     » 20fT7(•1048)
   Contig 5 (3381) TCTGACCAGAGTTGGTCTTTGGTTAAATGGTCGGGTACAGATTCTCACTTGC
```



```
                         Alignment                                      Page 23
                                                                     Section 67
                    3433      3440      3450      3460      3470              3484
   « 20rM13   (698) TAGCTGGACAAAAGGATGGAAATATATTTATATACCGATACTTTTAAGAGGC
   » 09fT7a rc (683) TAGCTGGACAAAAGGATGGAAATATATTTATATACCGATACTTTTGAGAGGC
   « 07rM13   (711) TAGCTGGACAAAAGGATGGAAATATATTTATATACCGATACTTTTAAGAGGC
» Palb2 mRNA (3433) TAGCTGGACAAAAGGATGGAAATATATTTATATACCGATACTTTTAAGAGGC
 « 19-2032 rc (•923)
    » 19-2032 (•923)
    » 07-2032 (•916)
    » 20-2032 (•914)
     » 07fT7(•1060)
 « 19rM13 rc(•1065)
    » 19rM13(•1065)
« 09rM13a rc(•1048)
     » 20fT7(•1048)
   Contig 5 (3433) TAGCTGGACAAAAGGATGGAAATATATTTATATACCGATACTTTTAAGAGGC
                                                                +
                                                                     Section 68
                    3485 3490      3500      3510      3520              3536
   « 20rM13   (750) AAATAGTTTGGAGGTTTTTTGTTTTTTGTTTTTGTTTTTGTTTTTTTTAAGA
   » 09fT7a rc (735) AAATAGTTTGGAGGTTTTTTGTTTTTTGTTTTTGTTTTTGTTTTTTTTAAGA
   « 07rM13   (763) AAATAGTTTGGAGGTTTTTTGTTTTTTGTTTTTGTTTTTGTTTTTTTTAAGA
» Palb2 mRNA (3485) AAATAGTTTGGAGGTTTTTTGTTTTTTGTTTTTGTTTTTGTTTTTTTTAAGA
 « 19-2032 rc (•923)
    » 19-2032 (•923)
    » 07-2032 (•916)
    » 20-2032 (•914)
     » 07fT7(•1060)
 « 19rM13 rc(•1065)
    » 19rM13(•1065)
« 09rM13a rc(•1048)
     » 20fT7(•1048)
   Contig 5 (3485) AAATAGTTTGGAGGTTTTTTGTTTTTTGTTTTTGTTTTTGTTTTTTTTAAGA
                                                                     Section 69
                    3537        3550      3560      3570              3588
   « 20rM13   (802) ATACAATATCTGAATGACATTTAATGTGATTACTTGAATGTATTTCCCACAC
   » 09fT7a rc (787) ATACAATATCTGAATGACATTTAATGTGATTACTTGAATGTATTTCCCACAC
   « 07rM13   (815) ATACAATATCTGAATGACATTTAATGTGATTACTTGAATGTATTTCCCACAC
» Palb2 mRNA (3537) ATACAATATCTGAATGACATTTAATGTGATTACTTGAATGTATTTCCCACAC
 « 19-2032 rc (•923)
    » 19-2032 (•923)
    » 07-2032 (•916)
    » 20-2032 (•914)
     » 07fT7(•1060)
 « 19rM13 rc(•1065)
    » 19rM13(•1065)
« 09rM13a rc(•1048)
     » 20fT7(•1048)
   Contig 5 (3537) ATACAATATCTGAATGACATTTAATGTGATTACTTGAATGTATTTCCCACAC
```



```
                         Alignment                                      Page 24
                                                                     Section 70
                    3589       3600      3610      3620      3630      3640
   « 20rM13   (854) ACTTAATTTTCTTCTGATAGTGACTACTGACTGAACATTTGTTTATAGTTAT
   » 09fT7a rc (839) ACTTAATTTTCTTCTGATAGTGACTACTGACTGAACATTTGTTTATAGTTAT
   « 07rM13   (867) ACTTAATTTTCTTCTGATAGTGACTACTGACTGAACATTTGTTTATAGTTAT
» Palb2 mRNA (3589) ACTTAATTTTCTTCTGATAGTGACTACTGACTGAACATTTGTTTATAGTTAT
 « 19-2032 rc (•923)
    » 19-2032 (•923)
    » 07-2032 (•916)
    » 20-2032 (•914)
     » 07fT7(•1060)
 « 19rM13 rc(•1065)
    » 19rM13(•1065)
« 09rM13a rc(•1048)
     » 20fT7(•1048)
   Contig 5 (3589) ACTTAATTTTCTTCTGATAGTGACTACTGACTGAACATTTGTTTATAGTTAT
                                                                     Section 71
                    3641     3650      3660      3670      3680        3692
   « 20rM13   (906) TTTCAGGTTAATAGTTTTAAGTCATTCTTTGCACATTTGCTATTACAGCTNT
   » 09fT7a rc (891) TTTCAGGTTAATAGTTTTAAGTCATTCTTTGCACATTTGCTATTACAGCTGT
   « 07rM13   (919) TTTCAGGTTAATAGTTTTAAGTCATTCTTTGCACATTTGCTATTACAGCTGT
» Palb2 mRNA (3641) TTTCAGGTTAATAGTTTTAAGTCATTCTTTGCACATTTGCTATTACAGCTGT
 « 19-2032 rc (•923)
    » 19-2032 (•923)
    » 07-2032 (•916)
    » 20-2032 (•914)
     » 07fT7(•1060)
 « 19rM13 rc(•1065)
    » 19rM13(•1065)
« 09rM13a rc(•1048)
     » 20fT7(•1048)
   Contig 5 (3641) TTTCAGGTTAATAGTTTTAAGTCATTCTTTGCACATTTGCTATTACAGCTGT
                                                                     Section 72
                    3693   3700      3710      3720      3730          3744
   « 20rM13   (958) ACATAACCAGTGAAAGGGCGAATTCCAGCACACTGGCGGCCGTTACTAGGGA
   » 09fT7a rc (943) ACATAACCAGTGAAAGGGCGAATTC
   « 07rM13   (971) ACATAACCAGTGAAAGGGCGAATTC
» Palb2 mRNA (3693) ACATAACCAGTGAA
 « 19-2032 rc (•923)
    » 19-2032 (•923)
    » 07-2032 (•916)
    » 20-2032 (•914)
     » 07fT7(•1060)
 « 19rM13 rc(•1065)
    » 19rM13(•1065)
« 09rM13a rc(•1048)
     » 20fT7(•1048)
   Contig 5 (3693) ACATAACCAGTGAAAGGGCGAATTCCAGCACACTGGCGGCCGTTACTAGGGA
```

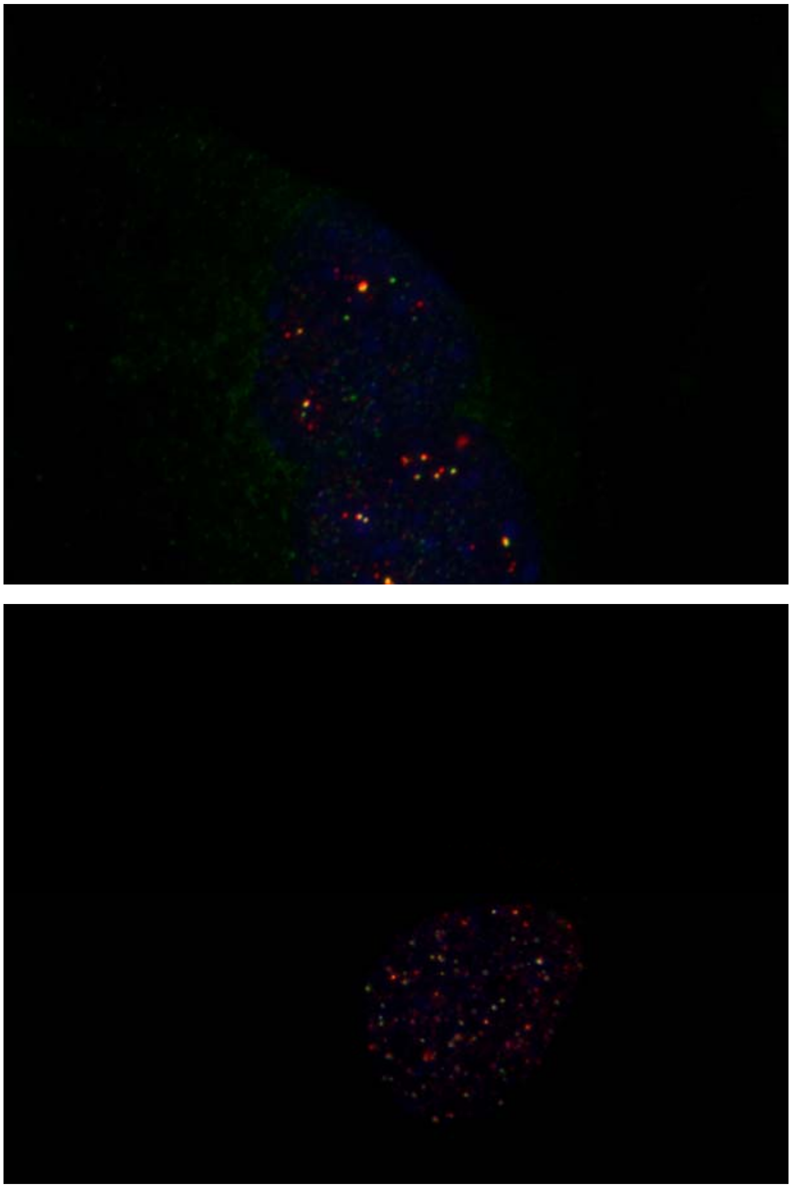


```
                              Alignment                                  Page 25
================================================================================
                                                                      Section 73
                    3745    3750              3762
   « 20rM13 (1010)  T C C G A G C T C G A C C A G C G C
  » 09fT7a rc (•966)
    « 07rM13 (•994)
» Palb2 mRNA(•3705)
 « 19-2032 rc (•923)
   » 19-2032 (•923)
   » 07-2032 (•916)
   » 20-2032 (•914)
     » 07fT7(•1060)
  « 19rM13 rc(•1065)
    » 19rM13(•1065)
 « 09rM13a rc(•1048)
     » 20fT7(•1048)
   Contig 5 (3745)  T C C G A G C T C G A C C A G C G C
```

Appendix A notes: Alignment of *Palb2* sequencing. “Palb2 mRNA” is the established coding sequence of *Palb2*. First two numbers of each sequence correspond to the following: C57BL/6-*Trp53*$^{+/-}$ samples include 15, 17 and 19 while BALB/c- *Trp53*$^{+/-}$ samples include 1, 5 and 8. Second group of numbers/letters indicate sequencing primer used (sequence for primers in methods). “rc” stands for reverse compliment. “Contig 4” indicates the consensus sequence. Dots below the consensus sequence indicate different bases among the alignment while a “+” sign indicates a space or miscall.

APPENDIX B

IMMUNOFLUORESCENCE IMAGES



Appendix B notes: Examples of immunofluorescence images. Co-localization of RAD51 and γ-H2AX with DAPI nuclear stain. Images consist of 3 images overlayed at the following wavelengths: 488 nm (RAD51), 594 nm (γ-H2AX) and 350 nm (DAPI).

REFERENCES

Abaji,C., Cousineau,I., and Belmaaza,A. (2005). BRCA2 regulates homologous recombination in response to DNA damage: implications for genome stability and carcinogenesis. Cancer Res. *65*, 4117-4125.

Ahmad,A., Robinson,A.R., Duensing,A., van,D.E., Beverloo,H.B., Weisberg,D.B., Hasty,P., Hoeijmakers,J.H., and Niedernhofer,L.J. (2008). ERCC1-XPF endonuclease facilitates DNA double-strand break repair. Mol. Cell Biol. *28*, 5082-5092.

Ahmed,S., Thomas,G., Ghoussaini,M., Healey,C.S., Humphreys,M.K., Platte,R., Morrison,J., Maranian,M., Pooley,K.A., Luben,R., Eccles,D., Evans,D.G., Fletcher,O., Johnson,N., dos,S.S., I, Peto,J., Stratton,M.R., Rahman,N., Jacobs,K., Prentice,R., Anderson,G.L., Rajkovic,A., Curb,J.D., Ziegler,R.G., Berg,C.D., Buys,S.S., McCarty,C.A., Feigelson,H.S., Calle,E.E., Thun,M.J., Diver,W.R., Bojesen,S., Nordestgaard,B.G., Flyger,H., Dork,T., Schurmann,P., Hillemanns,P., Karstens,J.H., Bogdanova,N.V., Antonenkova,N.N., Zalutsky,I.V., Bermisheva,M., Fedorova,S., Khusnutdinova,E., Kang,D., Yoo,K.Y., Noh,D.Y., Ahn,S.H., Devilee,P., van Asperen,C.J., Tollenaar,R.A., Seynaeve,C., Garcia-Closas,M., Lissowska,J., Brinton,L., Peplonska,B., Nevanlinna,H., Heikkinen,T., Aittomaki,K., Blomqvist,C., Hopper,J.L., Southey,M.C., Smith,L., Spurdle,A.B., Schmidt,M.K., Broeks,A., van Hien,R.R., Cornelissen,S., Milne,R.L., Ribas,G., Gonzalez-Neira,A., Benitez,J., Schmutzler,R.K., Burwinkel,B., Bartram,C.R., Meindl,A., Brauch,H., Justenhoven,C., Hamann,U., Chang-Claude,J., Hein,R., Wang-Gohrke,S., Lindblom,A., Margolin,S., Mannermaa,A., Kosma,V.M., Kataja,V., Olson,J.E., Wang,X., Fredericksen,Z., Giles,G.G., Severi,G., Baglietto,L., English,D.R., Hankinson,S.E., Cox,D.G., Kraft,P., Vatten,L.J., Hveem,K., Kumle,M., Sigurdson,A., Doody,M., Bhatti,P., Alexander,B.H., Hooning,M.J., van den Ouweland,A.M., Oldenburg,R.A., Schutte,M., Hall,P., Czene,K., Liu,J., Li,Y., Cox,A., Elliott,G., Brock,I., Reed,M.W., Shen,C.Y., Yu,J.C., Hsu,G.C., Chen,S.T., nton-Culver,H., Ziogas,A., Andrulis,I.L., Knight,J.A., Beesley,J., Goode,E.L., Couch,F., Chenevix-Trench,G., Hoover,R.N., Ponder,B.A., Hunter,D.J., Pharoah,P.D., Dunning,A.M., Chanock,S.J., and Easton,D.F. (2009). Newly discovered breast cancer susceptibility loci on 3p24 and 17q23.2. Nat. Genet. *41*, 585-590.

Akyuz,N., Boehden,G.S., Susse,S., Rimek,A., Preuss,U., Scheidtmann,K.H., and Wiesmuller,L. (2002c). DNA substrate dependence of p53-mediated regulation of double-strand break repair. Mol. Cell Biol. *22*, 6306-6317.

Akyuz,N., Boehden,G.S., Susse,S., Rimek,A., Preuss,U., Scheidtmann,K.H., and Wiesmuller,L. (2002a). DNA substrate dependence of p53-mediated regulation of double-strand break repair. Mol. Cell Biol. *22*, 6306-6317.

Akyuz,N., Boehden,G.S., Susse,S., Rimek,A., Preuss,U., Scheidtmann,K.H., and Wiesmuller,L. (2002b). DNA substrate dependence of p53-mediated regulation of double-strand break repair. Mol. Cell Biol. *22*, 6306-6317.

Akyuz,N., Boehden,G.S., Susse,S., Rimek,A., Preuss,U., Scheidtmann,K.H., and Wiesmuller,L. (2002d). DNA substrate dependence of p53-mediated regulation of double-strand break repair. Mol. Cell Biol. *22*, 6306-6317.

Antoniou,A.C. and Easton,D.F. (2006). Models of genetic susceptibility to breast cancer. Oncogene *25*, 5898-5905.

Arnaudeau,C., Lundin,C., and Helleday,T. (2001). DNA double-strand breaks associated with replication forks are predominantly repaired by homologous recombination involving an exchange mechanism in mammalian cells. J. Mol. Biol. *307*, 1235-1245.

Backlund,M.G., Trasti,S.L., Backlund,D.C., Cressman,V.L., Godfrey,V., and Koller,B.H. (2001a). Impact of ionizing radiation and genetic background on mammary tumorigenesis in p53-deficient mice. Cancer Res. *61*, 6577-6582.

Backlund,M.G., Trasti,S.L., Backlund,D.C., Cressman,V.L., Godfrey,V., and Koller,B.H. (2001b). Impact of ionizing radiation and genetic background on mammary tumorigenesis in p53-deficient mice. Cancer Res. *61*, 6577-6582.

Baldeyron,C., Jacquemin,E., Smith,J., Jacquemont,C., De,O., I, Gad,S., Feunteun,J., Stoppa-Lyonnet,D., and Papadopoulo,D. (2002). A single mutated BRCA1 allele leads to impaired fidelity of double strand break end-joining. Oncogene *21*, 1401-1410.

Bartkova,J., Horejsi,Z., Koed,K., Kramer,A., Tort,F., Zieger,K., Guldberg,P., Sehested,M., Nesland,J.M., Lukas,C., Orntoft,T., Lukas,J., and Bartek,J. (2005). DNA damage response as a candidate anti-cancer barrier in early human tumorigenesis. Nature *434*, 864-870.

Becker,K.A., Lu,S., Dickinson,E.S., Dunphy,K.A., Mathews,L., Schneider,S.S., and Jerry,D.J. (2005). Estrogen and progesterone regulate radiation-induced p53 activity in mammary epithelium through TGF-beta-dependent pathways. Oncogene *24*, 6345-6353.

Bekker-Jensen,S., Lukas,C., Kitagawa,R., Melander,F., Kastan,M.B., Bartek,J., and Lukas,J. (2006). Spatial organization of the mammalian genome surveillance machinery in response to DNA strand breaks. J. Cell Biol. *173*, 195-206.

Berkovich,E., Monnat,R.J., Jr., and Kastan,M.B. (2007). Roles of ATM and NBS1 in chromatin structure modulation and DNA double-strand break repair. Nat. Cell Biol. *9*, 683-690.

Blackburn,A.C., Brown,J.S., Naber,S.P., Otis,C.N., Wood,J.T., and Jerry,D.J. (2003a). BALB/c alleles for Prkdc and Cdkn2a interact to modify tumor susceptibility in Trp53+/- mice. Cancer Res. *63*, 2364-2368.

Blackburn,A.C., Brown,J.S., Naber,S.P., Otis,C.N., Wood,J.T., and Jerry,D.J. (2003b). BALB/c alleles for Prkdc and Cdkn2a interact to modify tumor susceptibility in Trp53+/- mice. Cancer Res. *63*, 2364-2368.

Blackburn,A.C., Hill,L.Z., Roberts,A.L., Wang,J., Aud,D., Jung,J., Nikolcheva,T., Allard,J., Peltz,G., Otis,C.N., Cao,Q.J., Ricketts,R.S., Naber,S.P., Mollenhauer,J., Poustka,A., Malamud,D., and Jerry,D.J. (2007a). Genetic mapping in mice identifies DMBT1 as a candidate modifier of mammary tumors and breast cancer risk. Am. J. Pathol. *170*, 2030-2041.

Blackburn,A.C., Hill,L.Z., Roberts,A.L., Wang,J., Aud,D., Jung,J., Nikolcheva,T., Allard,J., Peltz,G., Otis,C.N., Cao,Q.J., Ricketts,R.S., Naber,S.P., Mollenhauer,J., Poustka,A., Malamud,D., and Jerry,D.J. (2007b). Genetic mapping in mice identifies DMBT1 as a candidate modifier of mammary tumors and breast cancer risk. Am. J. Pathol. *170*, 2030-2041.

Blackburn,A.C., Hill,L.Z., Roberts,A.L., Wang,J., Aud,D., Jung,J., Nikolcheva,T., Allard,J., Peltz,G., Otis,C.N., Cao,Q.J., Ricketts,R.S., Naber,S.P., Mollenhauer,J., Poustka,A., Malamud,D., and Jerry,D.J. (2007c). Genetic mapping in mice identifies DMBT1 as a candidate modifier of mammary tumors and breast cancer risk. Am. J. Pathol. *170*, 2030-2041.

Blackburn,A.C., Hill,L.Z., Roberts,A.L., Wang,J., Aud,D., Jung,J., Nikolcheva,T., Allard,J., Peltz,G., Otis,C.N., Cao,Q.J., Ricketts,R.S., Naber,S.P., Mollenhauer,J., Poustka,A., Malamud,D., and Jerry,D.J. (2007d). Genetic mapping in mice identifies DMBT1 as a candidate modifier of mammary tumors and breast cancer risk. Am. J. Pathol. *170*, 2030-2041.

Blackburn,A.C., Hill,L.Z., Roberts,A.L., Wang,J., Aud,D., Jung,J., Nikolcheva,T., Allard,J., Peltz,G., Otis,C.N., Cao,Q.J., Ricketts,R.S., Naber,S.P., Mollenhauer,J., Poustka,A., Malamud,D., and Jerry,D.J. (2007e). Genetic mapping in mice identifies DMBT1 as a candidate modifier of mammary tumors and breast cancer risk. Am. J. Pathol. *170*, 2030-2041.

Blackburn,A.C., McLary,S.C., Naeem,R., Luszcz,J., Stockton,D.W., Donehower,L.A., Mohammed,M., Mailhes,J.B., Soferr,T., Naber,S.P., Otis,C.N., and Jerry,D.J. (2004b). Loss of heterozygosity occurs via mitotic recombination in Trp53+/- mice and associates with mammary tumor susceptibility of the BALB/c strain. Cancer Res. *64*, 5140-5147.

Blackburn,A.C., McLary,S.C., Naeem,R., Luszcz,J., Stockton,D.W., Donehower,L.A., Mohammed,M., Mailhes,J.B., Soferr,T., Naber,S.P., Otis,C.N., and Jerry,D.J. (2004a). Loss of heterozygosity occurs via mitotic recombination in Trp53+/- mice and associates with mammary tumor susceptibility of the BALB/c strain. Cancer Res. *64*, 5140-5147.

Blackburn,A.C., McLary,S.C., Naeem,R., Luszcz,J., Stockton,D.W., Donehower,L.A., Mohammed,M., Mailhes,J.B., Soferr,T., Naber,S.P., Otis,C.N., and Jerry,D.J. (2004c). Loss of heterozygosity occurs via mitotic recombination in Trp53+/- mice and associates with mammary tumor susceptibility of the BALB/c strain. Cancer Res. *64*, 5140-5147.

Buisson,R., on-Cote,A.M., Coulombe,Y., Launay,H., Cai,H., Stasiak,A.Z., Stasiak,A., Xia,B., and Masson,J.Y. (2010). Cooperation of breast cancer proteins PALB2 and piccolo BRCA2 in stimulating homologous recombination. Nat. Struct. Mol. Biol. *17*, 1247-1254.

Burma,S., Chen,B.P., and Chen,D.J. (2006). Role of non-homologous end joining (NHEJ) in maintaining genomic integrity. DNA Repair (Amst) *5*, 1042-1048.

Butel,J.S., Dusing-Swartz,S., Socher,S.H., and Medina,D. (1981). Partial expression of endogenous mouse mammary tumor virus in mammary tumors induced in BALB/c mice by chemical, hormonal, and physical agents. J. Virol. *38*, 571-580.

Celeste,A., Petersen,S., Romanienko,P.J., Fernandez-Capetillo,O., Chen,H.T., Sedelnikova,O.A., Reina-San-Martin,B., Coppola,V., Meffre,E., Difilippantonio,M.J., Redon,C., Pilch,D.R., Olaru,A., Eckhaus,M., Camerini-Otero,R.D., Tessarollo,L., Livak,F., Manova,K., Bonner,W.M., Nussenzweig,M.C., and Nussenzweig,A. (2002). Genomic instability in mice lacking histone H2AX. Science *296*, 922-927.

Chompret,A., Brugieres,L., Ronsin,M., Gardes,M., ssarps-Freichey,F., Abel,A., Hua,D., Ligot,L., Dondon,M.G., Bressac-De,P.B., Frebourg,T., Lemerle,J., Bonaiti-Pellie,C., and Feunteun,J. (2000). P53 germline mutations in childhood cancers and cancer risk for carrier individuals. Br. J. Cancer *82*, 1932-1937.

Cox,A., Dunning,A.M., Garcia-Closas,M., Balasubramanian,S., Reed,M.W., Pooley,K.A., Scollen,S., Baynes,C., Ponder,B.A., Chanock,S., Lissowska,J., Brinton,L., Peplonska,B., Southey,M.C., Hopper,J.L., McCredie,M.R., Giles,G.G., Fletcher,O., Johnson,N., dos,S.S., I, Gibson,L., Bojesen,S.E., Nordestgaard,B.G., Axelsson,C.K., Torres,D., Hamann,U., Justenhoven,C., Brauch,H., Chang-Claude,J., Kropp,S., Risch,A., Wang-Gohrke,S., Schurmann,P., Bogdanova,N., Dork,T., Fagerholm,R., Aaltonen,K., Blomqvist,C., Nevanlinna,H., Seal,S., Renwick,A., Stratton,M.R., Rahman,N., Sangrajrang,S., Hughes,D., Odefrey,F., Brennan,P., Spurdle,A.B., Chenevix-Trench,G., Beesley,J., Mannermaa,A., Hartikainen,J., Kataja,V., Kosma,V.M., Couch,F.J., Olson,J.E., Goode,E.L., Broeks,A., Schmidt,M.K., Hogervorst,F.B., Van't Veer,L.J., Kang,D., Yoo,K.Y., Noh,D.Y., Ahn,S.H., Wedren,S., Hall,P., Low,Y.L., Liu,J., Milne,R.L., Ribas,G., Gonzalez-Neira,A., Benitez,J., Sigurdson,A.J., Stredrick,D.L., Alexander,B.H., Struewing,J.P., Pharoah,P.D., and Easton,D.F. (2007). A common coding variant in CASP8 is associated with breast cancer risk. Nat. Genet. *39*, 352-358.

Deans,B., Griffin,C.S., O'Regan,P., Jasin,M., and Thacker,J. (2003). Homologous recombination deficiency leads to profound genetic instability in cells derived from Xrcc2-knockout mice. Cancer Res. *63*, 8181-8187.

Donahue,S.L., Lin,Q., Cao,S., and Ruley,H.E. (2006). Carcinogens induce genome-wide loss of heterozygosity in normal stem cells without persistent chromosomal instability. Proc. Natl. Acad. Sci. U. S. A *103*, 11642-11646.

Donehower,L.A., Harvey,M., Slagle,B.L., McArthur,M.J., Montgomery,C.A., Jr., Butel,J.S., and Bradley,A. (1992). Mice deficient for p53 are developmentally normal but susceptible to spontaneous tumours. Nature *356*, 215-221.

Dudenhoffer,C., Kurth,M., Janus,F., Deppert,W., and Wiesmuller,L. (1999). Dissociation of the recombination control and the sequence-specific transactivation function of P53. Oncogene *18*, 5773-5784.

Durant,S. and Karran,P. (2003). Vanillins--a novel family of DNA-PK inhibitors. Nucleic Acids Res. *31*, 5501-5512.

Easton,D.F., Pooley,K.A., Dunning,A.M., Pharoah,P.D., Thompson,D., Ballinger,D.G., Struewing,J.P., Morrison,J., Field,H., Luben,R., Wareham,N., Ahmed,S., Healey,C.S., Bowman,R., Meyer,K.B., Haiman,C.A., Kolonel,L.K., Henderson,B.E., Le,M.L., Brennan,P., Sangrajrang,S., Gaborieau,V., Odefrey,F., Shen,C.Y., Wu,P.E., Wang,H.C., Eccles,D., Evans,D.G., Peto,J., Fletcher,O., Johnson,N., Seal,S., Stratton,M.R., Rahman,N., Chenevix-Trench,G., Bojesen,S.E., Nordestgaard,B.G., Axelsson,C.K., Garcia-Closas,M., Brinton,L., Chanock,S., Lissowska,J., Peplonska,B., Nevanlinna,H., Fagerholm,R., Eerola,H., Kang,D., Yoo,K.Y., Noh,D.Y., Ahn,S.H., Hunter,D.J., Hankinson,S.E., Cox,D.G., Hall,P., Wedren,S., Liu,J., Low,Y.L., Bogdanova,N., Schurmann,P., Dork,T., Tollenaar,R.A., Jacobi,C.E., Devilee,P., Klijn,J.G., Sigurdson,A.J., Doody,M.M., Alexander,B.H., Zhang,J., Cox,A., Brock,I.W., MacPherson,G., Reed,M.W., Couch,F.J., Goode,E.L., Olson,J.E., Meijers-Heijboer,H., van den,O.A., Uitterlinden,A., Rivadeneira,F., Milne,R.L., Ribas,G., Gonzalez-Neira,A., Benitez,J., Hopper,J.L., McCredie,M., Southey,M., Giles,G.G., Schroen,C., Justenhoven,C., Brauch,H., Hamann,U., Ko,Y.D., Spurdle,A.B., Beesley,J., Chen,X., Mannermaa,A., Kosma,V.M., Kataja,V., Hartikainen,J., Day,N.E., Cox,D.R., and Ponder,B.A. (2007a). Genome-wide association study identifies novel breast cancer susceptibility loci. Nature *447*, 1087-1093.

Easton,D.F., Pooley,K.A., Dunning,A.M., Pharoah,P.D., Thompson,D., Ballinger,D.G., Struewing,J.P., Morrison,J., Field,H., Luben,R., Wareham,N., Ahmed,S., Healey,C.S., Bowman,R., Meyer,K.B., Haiman,C.A., Kolonel,L.K., Henderson,B.E., Le,M.L., Brennan,P., Sangrajrang,S., Gaborieau,V., Odefrey,F., Shen,C.Y., Wu,P.E., Wang,H.C., Eccles,D., Evans,D.G., Peto,J., Fletcher,O., Johnson,N., Seal,S., Stratton,M.R., Rahman,N., Chenevix-Trench,G., Bojesen,S.E., Nordestgaard,B.G., Axelsson,C.K., Garcia-Closas,M., Brinton,L., Chanock,S., Lissowska,J., Peplonska,B., Nevanlinna,H., Fagerholm,R., Eerola,H., Kang,D., Yoo,K.Y., Noh,D.Y., Ahn,S.H., Hunter,D.J., Hankinson,S.E., Cox,D.G., Hall,P., Wedren,S., Liu,J., Low,Y.L., Bogdanova,N., Schurmann,P., Dork,T., Tollenaar,R.A., Jacobi,C.E., Devilee,P., Klijn,J.G., Sigurdson,A.J., Doody,M.M., Alexander,B.H., Zhang,J., Cox,A., Brock,I.W., MacPherson,G., Reed,M.W., Couch,F.J., Goode,E.L., Olson,J.E., Meijers-Heijboer,H., van den,O.A., Uitterlinden,A., Rivadeneira,F., Milne,R.L., Ribas,G., Gonzalez-Neira,A., Benitez,J., Hopper,J.L., McCredie,M., Southey,M., Giles,G.G., Schroen,C., Justenhoven,C., Brauch,H., Hamann,U., Ko,Y.D., Spurdle,A.B., Beesley,J., Chen,X., Mannermaa,A., Kosma,V.M., Kataja,V., Hartikainen,J., Day,N.E., Cox,D.R., and Ponder,B.A. (2007b). Genome-wide association study identifies novel breast cancer susceptibility loci. Nature *447*, 1087-1093.

Easton,D.F., Pooley,K.A., Dunning,A.M., Pharoah,P.D., Thompson,D., Ballinger,D.G., Struewing,J.P., Morrison,J., Field,H., Luben,R., Wareham,N., Ahmed,S., Healey,C.S., Bowman,R., Meyer,K.B., Haiman,C.A., Kolonel,L.K., Henderson,B.E., Le,M.L., Brennan,P., Sangrajrang,S., Gaborieau,V., Odefrey,F., Shen,C.Y., Wu,P.E., Wang,H.C., Eccles,D., Evans,D.G., Peto,J., Fletcher,O., Johnson,N., Seal,S., Stratton,M.R., Rahman,N., Chenevix-Trench,G., Bojesen,S.E., Nordestgaard,B.G., Axelsson,C.K., Garcia-Closas,M., Brinton,L., Chanock,S., Lissowska,J., Peplonska,B., Nevanlinna,H., Fagerholm,R., Eerola,H., Kang,D., Yoo,K.Y., Noh,D.Y., Ahn,S.H., Hunter,D.J., Hankinson,S.E., Cox,D.G., Hall,P., Wedren,S., Liu,J., Low,Y.L., Bogdanova,N., Schurmann,P., Dork,T., Tollenaar,R.A., Jacobi,C.E., Devilee,P., Klijn,J.G., Sigurdson,A.J., Doody,M.M., Alexander,B.H., Zhang,J., Cox,A., Brock,I.W., MacPherson,G., Reed,M.W., Couch,F.J., Goode,E.L., Olson,J.E., Meijers-Heijboer,H., van den,O.A., Uitterlinden,A., Rivadeneira,F., Milne,R.L., Ribas,G., Gonzalez-Neira,A., Benitez,J., Hopper,J.L., McCredie,M., Southey,M., Giles,G.G., Schroen,C., Justenhoven,C., Brauch,H., Hamann,U., Ko,Y.D., Spurdle,A.B., Beesley,J., Chen,X., Mannermaa,A., Kosma,V.M., Kataja,V., Hartikainen,J., Day,N.E., Cox,D.R., and Ponder,B.A. (2007c). Genome-wide association study identifies novel breast cancer susceptibility loci. Nature *447*, 1087-1093.

Erkko,H., Dowty,J.G., Nikkila,J., Syrjakoski,K., Mannermaa,A., Pylkas,K., Southey,M.C., Holli,K., Kallioniemi,A., Jukkola-Vuorinen,A., Kataja,V., Kosma,V.M., Xia,B., Livingston,D.M., Winqvist,R., and Hopper,J.L. (2008). Penetrance analysis of the PALB2 c.1592delT founder mutation. Clin. Cancer Res. *14*, 4667-4671.

Erkko,H., Xia,B., Nikkila,J., Schleutker,J., Syrjakoski,K., Mannermaa,A., Kallioniemi,A., Pylkas,K., Karppinen,S.M., Rapakko,K., Miron,A., Sheng,Q., Li,G., Mattila,H., Bell,D.W., Haber,D.A., Grip,M., Reiman,M., Jukkola-Vuorinen,A., Mustonen,A., Kere,J., Aaltonen,L.A., Kosma,V.M., Kataja,V., Soini,Y., Drapkin,R.I., Livingston,D.M., and Winqvist,R. (2007). A recurrent mutation in PALB2 in Finnish cancer families. Nature *446*, 316-319.

Ethier,S.P. and Ullrich,R.L. (1982). Detection of ductal dysplasia in mammary outgrowths derived from carcinogen-treated virgin female BALB/c mice. Cancer Res. *42*, 1753-1760.

Francis,R. and Richardson,C. (2007). Multipotent hematopoietic cells susceptible to alternative double-strand break repair pathways that promote genome rearrangements. Genes Dev. *21*, 1064-1074.

Furuta,T., Takemura,H., Liao,Z.Y., Aune,G.J., Redon,C., Sedelnikova,O.A., Pilch,D.R., Rogakou,E.P., Celeste,A., Chen,H.T., Nussenzweig,A., Aladjem,M.I., Bonner,W.M., and Pommier,Y. (2003). Phosphorylation of histone H2AX and activation of Mre11, Rad50, and Nbs1 in response to replication-dependent DNA double-strand breaks induced by mammalian DNA topoisomerase I cleavage complexes. J. Biol. Chem. *278*, 20303-20312.

Gasco,M., Yulug,I.G., and Crook,T. (2003). TP53 mutations in familial breast cancer: functional aspects. Hum. Mutat. *21*, 301-306.

Gatz,S.A. and Wiesmuller,L. (2006). p53 in recombination and repair. Cell Death Differ. *13*, 1003-1016.

Ghebranious,N. and Donehower,L.A. (1998). Mouse models in tumor suppression. Oncogene *17*, 3385-3400.

Goode,E.L., Ulrich,C.M., and Potter,J.D. (2002). Polymorphisms in DNA repair genes and associations with cancer risk. Cancer Epidemiol. Biomarkers Prev. *11*, 1513-1530.

Halliwell,B. and Gutteridge,J.M. (1984a). Oxygen toxicity, oxygen radicals, transition metals and disease. Biochem. J. *219*, 1-14.

Halliwell,B. and Gutteridge,J.M. (1984b). Oxygen toxicity, oxygen radicals, transition metals and disease. Biochem. J. *219*, 1-14.

Hartlerode,A.J. and Scully,R. (2009). Mechanisms of double-strand break repair in somatic mammalian cells. Biochem. J. *423*, 157-168.

Heikkinen,K., Rapakko,K., Karppinen,S.M., Erkko,H., Knuutila,S., Lundan,T., Mannermaa,A., Borresen-Dale,A.L., Borg,A., Barkardottir,R.B., Petrini,J., and Winqvist,R. (2006). RAD50 and NBS1 are breast cancer susceptibility genes associated with genomic instability. Carcinogenesis *27*, 1593-1599.

Heston,W.E. and Vlahakis,G. (1971). Mammary tumors, plaques, and hyperplastic alveolar nodules in various combinations of mouse inbred strains and the different lines of the mammary tumor virus. Int. J. Cancer *7*, 141-148.

Hollstein,M., Rice,K., Greenblatt,M.S., Soussi,T., Fuchs,R., Sorlie,T., Hovig,E., Smith-Sorensen,B., Montesano,R., and Harris,C.C. (1994). Database of p53 gene somatic mutations in human tumors and cell lines. Nucleic Acids Res. *22*, 3551-3555.

Hunter,D.J., Kraft,P., Jacobs,K.B., Cox,D.G., Yeager,M., Hankinson,S.E., Wacholder,S., Wang,Z., Welch,R., Hutchinson,A., Wang,J., Yu,K., Chatterjee,N., Orr,N., Willett,W.C., Colditz,G.A., Ziegler,R.G., Berg,C.D., Buys,S.S., McCarty,C.A., Feigelson,H.S., Calle,E.E., Thun,M.J., Hayes,R.B., Tucker,M., Gerhard,D.S., Fraumeni,J.F., Jr., Hoover,R.N., Thomas,G., and Chanock,S.J. (2007). A genome-wide association study identifies alleles in FGFR2 associated with risk of sporadic postmenopausal breast cancer. Nat. Genet. *39*, 870-874.

Jacks,T., Remington,L., Williams,B.O., Schmitt,E.M., Halachmi,S., Bronson,R.T., and Weinberg,R.A. (1994). Tumor spectrum analysis in p53-mutant mice. Curr. Biol. *4*, 1-7.

Janz,C. and Wiesmuller,L. (2002). Wild-type p53 inhibits replication-associated homologous recombination. Oncogene *21*, 5929-5933.

Jemal,A., Siegel,R., Ward,E., Hao,Y., Xu,J., and Thun,M.J. (2009). Cancer statistics, 2009. CA Cancer J. Clin. *59*, 225-249.

Jernstrom,H., Lubinski,J., Lynch,H.T., Ghadirian,P., Neuhausen,S., Isaacs,C., Weber,B.L., Horsman,D., Rosen,B., Foulkes,W.D., Friedman,E., Gershoni-Baruch,R., Ainsworth,P., Daly,M., Garber,J., Olsson,H., Sun,P., and Narod,S.A. (2004). Breast-feeding and the risk of breast cancer in BRCA1 and BRCA2 mutation carriers. J. Natl. Cancer Inst. *96*, 1094-1098.

Jerry, D. J., Griner N.B., and Tao L. Tumor Suppressor Pathways and Cellular Origins of Breast Cancer: New Complexities and New Hopes. Nano LIFE , 1-16. 6-13-2010.
Ref Type: Generic

Johnson,S.M., Shaw,J.A., and Walker,R.A. (2002). Sporadic breast cancer in young women: prevalence of loss of heterozygosity at p53, BRCA1 and BRCA2. Int. J. Cancer *98*, 205-209.

Koch,J.G., Gu,X., Han,Y., El-Naggar,A.K., Olson,M.V., Medina,D., Jerry,D.J., Blackburn,A.C., Peltz,G., Amos,C.I., and Lozano,G. (2007). Mammary tumor modifiers in BALB/cJ mice heterozygous for p53. Mamm. Genome *18*, 300-309.

Kotsopoulos,J., Lubinski,J., Lynch,H.T., Neuhausen,S.L., Ghadirian,P., Isaacs,C., Weber,B., Kim-Sing,C., Foulkes,W.D., Gershoni-Baruch,R., Ainsworth,P., Friedman,E., Daly,M., Garber,J.E., Karlan,B., Olopade,O.I., Tung,N., Saal,H.M., Eisen,A., Osborne,M., Olsson,H., Gilchrist,D., Sun,P., and Narod,S.A. (2005). Age at menarche and the risk of breast cancer in BRCA1 and BRCA2 mutation carriers. Cancer Causes Control *16*, 667-674.

Kuperwasser,C., Hurlbut,G.D., Kittrell,F.S., Dickinson,E.S., Laucirica,R., Medina,D., Naber,S.P., and Jerry,D.J. (2000c). Development of spontaneous mammary tumors in BALB/c p53 heterozygous mice. A model for Li-Fraumeni syndrome. Am. J. Pathol. *157*, 2151-2159.

Kuperwasser,C., Hurlbut,G.D., Kittrell,F.S., Dickinson,E.S., Laucirica,R., Medina,D., Naber,S.P., and Jerry,D.J. (2000b). Development of spontaneous mammary tumors in BALB/c p53 heterozygous mice. A model for Li-Fraumeni syndrome. Am. J. Pathol. *157*, 2151-2159.

Kuperwasser,C., Hurlbut,G.D., Kittrell,F.S., Dickinson,E.S., Laucirica,R., Medina,D., Naber,S.P., and Jerry,D.J. (2000a). Development of spontaneous mammary tumors in BALB/c p53 heterozygous mice. A model for Li-Fraumeni syndrome. Am. J. Pathol. *157*, 2151-2159.

Lieber,M.R., Ma,Y., Pannicke,U., and Schwarz,K. (2003). Mechanism and regulation of human non-homologous DNA end-joining. Nat. Rev. Mol. Cell Biol. *4*, 712-720.

Liu,T., Matsuguchi,T., Tsuboi,N., Yajima,T., and Yoshikai,Y. (2002). Differences in expression of toll-like receptors and their reactivities in dendritic cells in BALB/c and C57BL/6 mice. Infect. Immun. *70*, 6638-6645.

McCabe,N., Turner,N.C., Lord,C.J., Kluzek,K., Bialkowska,A., Swift,S., Giavara,S., O'connor,M.J., Tutt,A.N., Zdzienicka,M.Z., Smith,G.C., and Ashworth,A. (2006). Deficiency in the Repair of DNA Damage by Homologous Recombination and Sensitivity to Poly(ADP-Ribose) Polymerase Inhibition. Cancer Res. *66*, 8109-8115.

McLaughlin,J.R., Risch,H.A., Lubinski,J., Moller,P., Ghadirian,P., Lynch,H., Karlan,B., Fishman,D., Rosen,B., Neuhausen,S.L., Offit,K., Kauff,N., Domchek,S., Tung,N., Friedman,E., Foulkes,W., Sun,P., and Narod,S.A. (2007). Reproductive risk factors for ovarian cancer in carriers of BRCA1 or BRCA2 mutations: a case-control study. Lancet Oncol. *8*, 26-34.

Miki,Y., Swensen,J., Shattuck-Eidens,D., Futreal,P.A., Harshman,K., Tavtigian,S., Liu,Q., Cochran,C., Bennett,L.M., Ding,W., and . (1994). A strong candidate for the breast and ovarian cancer susceptibility gene BRCA1. Science *266*, 66-71.

Mori,N., Matsumoto,Y., Okumoto,M., Suzuki,N., and Yamate,J. (2001). Variations in Prkdc encoding the catalytic subunit of DNA-dependent protein kinase (DNA-PKcs) and susceptibility to radiation-induced apoptosis and lymphomagenesis. Oncogene *20*, 3609-3619.

Mori,N., Okumoto,M., Hart,A.A., and Demant,P. (1995a). Apoptosis susceptibility genes on mouse chromosome 9 (Rapop2) and chromosome 3 (Rapop3). Genomics *30*, 553-557.

Mori,N., Okumoto,M., Hart,A.A., and Demant,P. (1995b). Apoptosis susceptibility genes on mouse chromosome 9 (Rapop2) and chromosome 3 (Rapop3). Genomics *30*, 553-557.

Mori,N., Yamate,J., Stassen,A.P., Oka,S., Okumoto,M., Tsubura,A., Akamatsu,T., Sakuma,S., and Demant,P. (1999). Modulations of glucocorticoid-induced apoptosis linked to the p53 deletion and to the apoptosis susceptibility gene Rapop1 (Radiation-induced apoptosis 1). Oncogene *18*, 4282-4285.

Narod,S.A. (2002). Modifiers of risk of hereditary breast and ovarian cancer. Nat. Rev. Cancer *2*, 113-123.

Narod,S.A., Dube,M.P., Klijn,J., Lubinski,J., Lynch,H.T., Ghadirian,P., Provencher,D., Heimdal,K., Moller,P., Robson,M., Offit,K., Isaacs,C., Weber,B., Friedman,E., Gershoni-Baruch,R., Rennert,G., Pasini,B., Wagner,T., Daly,M., Garber,J.E., Neuhausen,S.L., Ainsworth,P., Olsson,H., Evans,G., Osborne,M., Couch,F., Foulkes,W.D., Warner,E., Kim-Sing,C., Olopade,O., Tung,N., Saal,H.M., Weitzel,J., Merajver,S., Gauthier-Villars,M., Jernstrom,H., Sun,P., and Brunet,J.S. (2002). Oral contraceptives and the risk of breast cancer in BRCA1 and BRCA2 mutation carriers. J. Natl. Cancer Inst. *94*, 1773-1779.

Nevanlinna,H. and Bartek,J. (2006). The CHEK2 gene and inherited breast cancer susceptibility. Oncogene *25*, 5912-5919.

Okayasu,R., Suetomi,K., Yu,Y., Silver,A., Bedford,J.S., Cox,R., and Ullrich,R.L. (2000a). A deficiency in DNA repair and DNA-PKcs expression in the radiosensitive BALB/c mouse. Cancer Res. *60*, 4342-4345.

Okayasu,R., Suetomi,K., Yu,Y., Silver,A., Bedford,J.S., Cox,R., and Ullrich,R.L. (2000b). A deficiency in DNA repair and DNA-PKcs expression in the radiosensitive BALB/c mouse. Cancer Res. *60*, 4342-4345.

Olive,P.L. and Banath,J.P. (1993). Induction and rejoining of radiation-induced DNA single-strand breaks: "tail moment" as a function of position in the cell cycle. Mutat. Res. *294*, 275-283.

Oliver,A.W., Swift,S., Lord,C.J., Ashworth,A., and Pearl,L.H. (2009). Structural basis for recruitment of BRCA2 by PALB2. EMBO Rep. *10*, 990-996.

Parrinello,S., Samper,E., Krtolica,A., Goldstein,J., Melov,S., and Campisi,J. (2003a). Oxygen sensitivity severely limits the replicative lifespan of murine fibroblasts. Nat. Cell Biol. *5*, 741-747.

Parrinello,S., Samper,E., Krtolica,A., Goldstein,J., Melov,S., and Campisi,J. (2003b). Oxygen sensitivity severely limits the replicative lifespan of murine fibroblasts. Nat. Cell Biol. *5*, 741-747.

Parshad,R. and Sanford,K.K. (2001). Radiation-induced chromatid breaks and deficient DNA repair in cancer predisposition. Crit Rev. Oncol. Hematol. *37*, 87-96.

Patel,K.J. (2007). Fanconi anemia and breast cancer susceptibility. Nat. Genet. *39*, 142-143.

Petitjean,A., Mathe,E., Kato,S., Ishioka,C., Tavtigian,S.V., Hainaut,P., and Olivier,M. (2007). Impact of mutant p53 functional properties on TP53 mutation patterns and tumor phenotype: lessons from recent developments in the IARC TP53 database. Hum. Mutat. *28*, 622-629.

Peto,J., Collins,N., Barfoot,R., Seal,S., Warren,W., Rahman,N., Easton,D.F., Evans,C., Deacon,J., and Stratton,M.R. (1999a). Prevalence of BRCA1 and BRCA2 gene mutations in patients with early-onset breast cancer. J. Natl. Cancer Inst. *91*, 943-949.

Peto,J., Collins,N., Barfoot,R., Seal,S., Warren,W., Rahman,N., Easton,D.F., Evans,C., Deacon,J., and Stratton,M.R. (1999b). Prevalence of BRCA1 and BRCA2 gene mutations in patients with early-onset breast cancer. J. Natl. Cancer Inst. *91*, 943-949.

Ponder,B.A. (2001a). Cancer genetics. Nature *411*, 336-341.

Ponder,B.A. (2001b). Cancer genetics. Nature *411*, 336-341.

Ponnaiya,B., Cornforth,M.N., and Ullrich,R.L. (1997b). Radiation-induced chromosomal instability in BALB/c and C57BL/6 mice: the difference is as clear as black and white. Radiat. Res. *147*, 121-125.

Ponnaiya,B., Cornforth,M.N., and Ullrich,R.L. (1997a). Radiation-induced chromosomal instability in BALB/c and C57BL/6 mice: the difference is as clear as black and white. Radiat. Res. *147*, 121-125.

Ponnaiya,B., Cornforth,M.N., and Ullrich,R.L. (1997c). Radiation-induced chromosomal instability in BALB/c and C57BL/6 mice: the difference is as clear as black and white. Radiat. Res. *147*, 121-125.

Rahman,N., Seal,S., Thompson,D., Kelly,P., Renwick,A., Elliott,A., Reid,S., Spanova,K., Barfoot,R., Chagtai,T., Jayatilake,H., McGuffog,L., Hanks,S., Evans,D.G., Eccles,D., Easton,D.F., and Stratton,M.R. (2007a). PALB2, which encodes a BRCA2-interacting protein, is a breast cancer susceptibility gene. Nat. Genet. *39*, 165-167.

Rahman,N., Seal,S., Thompson,D., Kelly,P., Renwick,A., Elliott,A., Reid,S., Spanova,K., Barfoot,R., Chagtai,T., Jayatilake,H., McGuffog,L., Hanks,S., Evans,D.G., Eccles,D., Easton,D.F., and Stratton,M.R. (2007b). PALB2, which encodes a BRCA2-interacting protein, is a breast cancer susceptibility gene. Nat. Genet. *39*, 165-167.

Ralhan,R., Kaur,J., Kreienberg,R., and Wiesmuller,L. (2006). Links between DNA double strand break repair and breast cancer: Accumulating evidence from both familial and nonfamilial cases. Cancer Lett.

Rothkamm,K., Kruger,I., Thompson,L.H., and Lobrich,M. (2003). Pathways of DNA double-strand break repair during the mammalian cell cycle. Mol. Cell Biol. *23*, 5706-5715.

Sasaki,M.S. and Tonomura,A. (1973). A high susceptibility of Fanconi's anemia to chromosome breakage by DNA cross-linking agents. Cancer Res. *33*, 1829-1836.

Seal,S., Thompson,D., Renwick,A., Elliott,A., Kelly,P., Barfoot,R., Chagtai,T., Jayatilake,H., Ahmed,M., Spanova,K., North,B., McGuffog,L., Evans,D.G., Eccles,D., Easton,D.F., Stratton,M.R., and Rahman,N. (2006). Truncating mutations in the Fanconi anemia J gene BRIP1 are low-penetrance breast cancer susceptibility alleles. Nat. Genet. *38*, 1239-1241.

Shiroiwa,W., Tsukamoto,K., Ohtsuji,M., Lin,Q., Ida,A., Kodera,S., Ohtsuji,N., Nakamura,K., Tsurui,H., Kinoshita,K., Nishimura,H., Shirai,T., and Hirose,S. (2007). IL-4Ralpha polymorphism in regulation of IL-4 synthesis by T cells: implication in susceptibility to a subset of murine lupus. Int. Immunol. *19*, 175-183.

Shrivastav,M., De Haro,L.P., and Nickoloff,J.A. (2008). Regulation of DNA double-strand break repair pathway choice. Cell Res. *18*, 134-147.

Silver, LM. Mouse Genetics. 1995. Oxford University Press.
Ref Type: Generic

Singh,N.P., McCoy,M.T., Tice,R.R., and Schneider,E.L. (1988a). A simple technique for quantitation of low levels of DNA damage in individual cells. Exp. Cell Res. *175*, 184-191.

Singh,N.P., McCoy,M.T., Tice,R.R., and Schneider,E.L. (1988b). A simple technique for quantitation of low levels of DNA damage in individual cells. Exp. Cell Res. *175*, 184-191.

Soussi,T., Asselain,B., Hamroun,D., Kato,S., Ishioka,C., Claustres,M., and Beroud,C. (2006). Meta-analysis of the p53 mutation database for mutant p53 biological activity reveals a methodologic bias in mutation detection. Clin. Cancer Res. *12*, 62-69.

Swift,M., Morrell,D., Massey,R.B., and Chase,C.L. (1991). Incidence of cancer in 161 families affected by ataxia-telangiectasia. N. Engl. J. Med. *325*, 1831-1836.

Sy,S.M., Huen,M.S., and Chen,J. (2009). PALB2 is an integral component of the BRCA complex required for homologous recombination repair. Proc. Natl. Acad. Sci. U. S. A *106*, 7155-7160.

Szpirer,C. and Szpirer,J. (2007). Mammary cancer susceptibility: human genes and rodent models. Mamm. Genome *18*, 817-831.

Tischkowitz,M. and Xia,B. (2010). PALB2/FANCN: recombining cancer and Fanconi anemia. Cancer Res. *70*, 7353-7359.

Tischkowitz,M., Xia,B., Sabbaghian,N., Reis-Filho,J.S., Hamel,N., Li,G., van Beers,E.H., Li,L., Khalil,T., Quenneville,L.A., Omeroglu,A., Poll,A., Lepage,P., Wong,N., Nederlof,P.M., Ashworth,A., Tonin,P.N., Narod,S.A., Livingston,D.M., and Foulkes,W.D. (2007). Analysis of PALB2/FANCN-associated breast cancer families. Proc. Natl. Acad. Sci. U. S. A *104*, 6788-6793.

Todaro,M., Lombardo,Y., Francipane,M.G., Alea,M.P., Cammareri,P., Iovino,F., Di Stefano,A.B., Di,B.C., Agrusa,A., Condorelli,G., Walczak,H., and Stassi,G. (2008). Apoptosis resistance in epithelial tumors is mediated by tumor-cell-derived interleukin-4. Cell Death. Differ. *15*, 762-772.

Ullrich,R.L., Bowles,N.D., Satterfield,L.C., and Davis,C.M. (1996b). Strain-dependent susceptibility to radiation-induced mammary cancer is a result of differences in epithelial cell sensitivity to transformation. Radiat. Res. *146*, 353-355.

Ullrich,R.L., Bowles,N.D., Satterfield,L.C., and Davis,C.M. (1996a). Strain-dependent susceptibility to radiation-induced mammary cancer is a result of differences in epithelial cell sensitivity to transformation. Radiat. Res. *146*, 353-355.

Valerie,K. and Povirk,L.F. (2003a). Regulation and mechanisms of mammalian double-strand break repair. Oncogene *22*, 5792-5812.

Valerie,K. and Povirk,L.F. (2003b). Regulation and mechanisms of mammalian double-strand break repair. Oncogene *22*, 5792-5812.

Veillet,A.L., Haag,J.D., Remfert,J.L., Meilahn,A.L., Samuelson,D.J., and Gould,M.N. (2011). Mcs5c: a mammary carcinoma susceptibility locus located in a gene desert that associates with tenascin C expression. Cancer Prev. Res. (Phila) *4*, 97-106.

Venkatachalam,S., Tyner,S.D., Pickering,C.R., Boley,S., Recio,L., French,J.E., and Donehower,L.A. (2001). Is p53 haploinsufficient for tumor suppression? Implications for the p53+/- mouse model in carcinogenicity testing. Toxicol. Pathol. *29 Suppl*, 147-154.

Vogelstein,B., Lane,D., and Levine,A.J. (2000). Surfing the p53 network. Nature *408*, 307-310.

Weil,M.M., Amos,C.I., Mason,K.A., and Stephens,L.C. (1996). Genetic basis of strain variation in levels of radiation-induced apoptosis of thymocytes. Radiat. Res. *146*, 646-651.

Wiesmuller,L., Cammenga,J., and Deppert,W.W. (1996). In vivo assay of p53 function in homologous recombination between simian virus 40 chromosomes. J. Virol. *70*, 737-744.

Woo,R.A., McLure,K.G., Lees-Miller,S.P., Rancourt,D.E., and Lee,P.W. (1998). DNA-dependent protein kinase acts upstream of p53 in response to DNA damage. Nature *394*, 700-704.

Wooster,R., Neuhausen,S.L., Mangion,J., Quirk,Y., Ford,D., Collins,N., Nguyen,K., Seal,S., Tran,T., Averill,D., and . (1994). Localization of a breast cancer susceptibility gene, BRCA2, to chromosome 13q12-13. Science *265*, 2088-2090.

Xia,B., Dorsman,J.C., Ameziane,N., de,V.Y., Rooimans,M.A., Sheng,Q., Pals,G., Errami,A., Gluckman,E., Llera,J., Wang,W., Livingston,D.M., Joenje,H., and de Winter,J.P. (2007b). Fanconi anemia is associated with a defect in the BRCA2 partner PALB2. Nat. Genet. *39*, 159-161.

Xia,B., Dorsman,J.C., Ameziane,N., de,V.Y., Rooimans,M.A., Sheng,Q., Pals,G., Errami,A., Gluckman,E., Llera,J., Wang,W., Livingston,D.M., Joenje,H., and de Winter,J.P. (2007a). Fanconi anemia is associated with a defect in the BRCA2 partner PALB2. Nat. Genet. *39*, 159-161.

Xia,B., Sheng,Q., Nakanishi,K., Ohashi,A., Wu,J., Christ,N., Liu,X., Jasin,M., Couch,F.J., and Livingston,D.M. (2006a). Control of BRCA2 cellular and clinical functions by a nuclear partner, PALB2. Mol. Cell *22*, 719-729.

Xia,B., Sheng,Q., Nakanishi,K., Ohashi,A., Wu,J., Christ,N., Liu,X., Jasin,M., Couch,F.J., and Livingston,D.M. (2006b). Control of BRCA2 cellular and clinical functions by a nuclear partner, PALB2. Mol. Cell *22*, 719-729.

Xia,B., Sheng,Q., Nakanishi,K., Ohashi,A., Wu,J., Christ,N., Liu,X., Jasin,M., Couch,F.J., and Livingston,D.M. (2006c). Control of BRCA2 cellular and clinical functions by a nuclear partner, PALB2. Mol. Cell *22*, 719-729.

Xia,B., Sheng,Q., Nakanishi,K., Ohashi,A., Wu,J., Christ,N., Liu,X., Jasin,M., Couch,F.J., and Livingston,D.M. (2006d). Control of BRCA2 cellular and clinical functions by a nuclear partner, PALB2. Mol. Cell *22*, 719-729.

Xia,B., Sheng,Q., Nakanishi,K., Ohashi,A., Wu,J., Christ,N., Liu,X., Jasin,M., Couch,F.J., and Livingston,D.M. (2006e). Control of BRCA2 cellular and clinical functions by a nuclear partner, PALB2. Mol. Cell *22*, 719-729.

Xie,A., Puget,N., Shim,I., Odate,S., Jarzyna,I., Bassing,C.H., Alt,F.W., and Scully,R. (2004). Control of sister chromatid recombination by histone H2AX. Mol. Cell *16*, 1017-1025.

ykin-Burns,N., Slane,B.G., Liu,A.T., Owens,K.M., O'Malley,M.S., Smith,B.J., Domann,F.E., and Spitz,D.R. (2010). Sensitivity to Low-Dose/Low-LET Ionizing Radiation in Mammalian Cells Harboring Mutations in Succinate Dehydrogenase Subunit C is Governed by Mitochondria-Derived Reactive Oxygen Species. Radiat. Res.

Yu,Y., Okayasu,R., Weil,M.M., Silver,A., McCarthy,M., Zabriskie,R., Long,S., Cox,R., and Ullrich,R.L. (2001c). Elevated breast cancer risk in irradiated BALB/c mice associates with unique functional polymorphism of the Prkdc (DNA-dependent protein kinase catalytic subunit) gene. Cancer Res. *61*, 1820-1824.

Yu,Y., Okayasu,R., Weil,M.M., Silver,A., McCarthy,M., Zabriskie,R., Long,S., Cox,R., and Ullrich,R.L. (2001b). Elevated breast cancer risk in irradiated BALB/c mice associates with unique functional polymorphism of the Prkdc (DNA-dependent protein kinase catalytic subunit) gene. Cancer Res. *61*, 1820-1824.

Yu,Y., Okayasu,R., Weil,M.M., Silver,A., McCarthy,M., Zabriskie,R., Long,S., Cox,R., and Ullrich,R.L. (2001d). Elevated breast cancer risk in irradiated BALB/c mice associates with unique functional polymorphism of the Prkdc (DNA-dependent protein kinase catalytic subunit) gene. Cancer Res. *61*, 1820-1824.

Yu,Y., Okayasu,R., Weil,M.M., Silver,A., McCarthy,M., Zabriskie,R., Long,S., Cox,R., and Ullrich,R.L. (2001a). Elevated breast cancer risk in irradiated BALB/c mice associates with unique functional polymorphism of the Prkdc (DNA-dependent protein kinase catalytic subunit) gene. Cancer Res. *61*, 1820-1824.

Yun,J., Zhong,Q., Kwak,J.Y., and Lee,W.H. (2005). Hypersensitivity of Brca1-deficient MEF to the DNA interstrand crosslinking agent mitomycin C is associated with defect in homologous recombination repair and aberrant S-phase arrest. Oncogene *24*, 4009-4016.

Zhang,F., Fan,Q., Ren,K., and Andreassen,P.R. (2009a). PALB2 functionally connects the breast cancer susceptibility proteins BRCA1 and BRCA2. Mol. Cancer Res. *7*, 1110-1118.

Zhang,F., Fan,Q., Ren,K., and Andreassen,P.R. (2009b). PALB2 functionally connects the breast cancer susceptibility proteins BRCA1 and BRCA2. Mol. Cancer Res. *7*, 1110-1118.

Zhang,F., Ma,J., Wu,J., Ye,L., Cai,H., Xia,B., and Yu,X. (2009c). PALB2 links BRCA1 and BRCA2 in the DNA-damage response. Curr. Biol. *19*, 524-529.

Zhang,J. and Powell,S.N. (2005). The role of the BRCA1 tumor suppressor in DNA double-strand break repair. Mol. Cancer Res. *3*, 531-539.

Zhong,Q., Chen,C.F., Chen,P.L., and Lee,W.H. (2002). BRCA1 facilitates microhomology-mediated end joining of DNA double strand breaks. J. Biol. Chem. *277*, 28641-28647.

Zhuang,J., Zhang,J., Willers,H., Wang,H., Chung,J.H., van,G., Hallahan,D.E., Powell,S.N., and Xia,F. (2006). Checkpoint kinase 2-mediated phosphorylation of BRCA1 regulates the fidelity of nonhomologous end-joining. Cancer Res. *66*, 1401-1408.