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14. ABSTRACT The prolactin receptor (PRLr) is a cytokine receptor that binds prolactin (PRL) via its extracellular domain and consequently signals through the Jak2/Stat5 pathway. The canonical function of PRLr in this pathway is to serve as a membrane bound intermediary between PRL and downstream secondary messengers. However, recent data from our lab has revealed that PRLr localizes to the nucleus of breast cancer cells tissue. Preliminary experiments also demonstrated that PRL initiates nuclear localization of PRLr and the interaction between nuclear PRLr and the transcription factor, Stat5a. We therefore hypothesized that PRLr functions as a Stat5a co-activator. Investigation of this hypothesis via ChIP revealed that PRLr binds to the Stat5 responsive CISH promoter and reporter assays demonstrated that PRLr promoter engagement results in CISH activation. As these results pointed to a role for the PRLr in transactivation, we utilized the Gal4 assay, to determine that residues 404-448 of PRLr intracellular domain were necessary and sufficient for transactivation. Consequentially, mutation of two conserved residues Y406, and D411 disrupted transactivation, demonstrating the necessity of these residues for PRLr specific gene activation. In addition, immunoprecipitation analysis led us to reveal a novel finding; that the PRLr transactivation domain is necessary for recruitment of the chromatin modifying protein, HMGN2. Subsequent studies demonstrated that HMGN2 is also recruited to the Stat5a-driven CISH promoter in a PRL dependant manner. In addition, overexpression of HMGN2 enhances Stat5a driven CISH expression, while stable knockdown of HMGN2 impairs this expression. HMGN2 knockdown also prevents binding of the PRLr to the CISH promoter suggesting that HMGN2 is required to PRLr promoter binding. Since HMGN2 possesses no sequence specificity, our findings suggest that nuclear PRLr may serve as the adaptor molecule that tethers HMGN2 to Stat5a, resulting in full transcriptional activity of Stat5a. Ongoing research will seek to determine the mechanism of HMGN2 recruitment, as well as the phenotypic effects of transactivation-deficient PRLr.						
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Table of Contents

	<u>Page</u>
Part I - Introduction.....	4
Part II – Proposed Aims.....	4
Part III – Statement of Work	4
Part IV- Results	6
Part V – Key Research Accomplishments.....	9
Part VI – Reportable Outcomes.....	10
Part VII – Summary	10
Part VIII -Appendices.....	10

Part I - Introduction

The prolactin receptor (PRLr) is a cytokine receptor that binds prolactin (PRL) via its extracellular domain and consequently signals through the Jak2/Stat5 pathway. The canonical function of PRLr in this pathway is to serve as a membrane bound intermediary between PRL and downstream secondary messengers. However, recent data from our lab has revealed that PRLr localizes to the nucleus of breast cancer cells tissue. Preliminary experiments also demonstrated that PRL initiates nuclear localization of PRLr and the interaction between nuclear PRLr and the transcription factor, Stat5a. We therefore hypothesized that PRLr functions as a Stat5a co-activator. Investigation of this hypothesis via ChIP revealed that PRLr binds to the Stat5 responsive CISH promoter and reporter assays demonstrated that PRLr promoter engagement results in CISH activation. As these results pointed to a role for the PRLr in transactivation, we utilized the Gal4 assay, to determine that residues 404-448 of PRLr intracellular domain were necessary and sufficient for transactivation. Consequentially, mutation of two conserved residues Y406, and D411 disrupted transactivation, demonstrating the necessity of these residues for PRLr specific gene activation. In addition, immunoprecipitation analysis led us to reveal a novel finding; that the PRLr transactivation domain is necessary for recruitment of the chromatin modifying protein, HMGN2. Subsequent studies demonstrated that HMGN2 is also recruited to the Stat5a-driven CISH promoter in a PRL dependant manner. In addition, overexpression of HMGN2 enhances Stat5a driven CISH expression, while stable knockdown of HMGN2 impairs this expression. HMGN2 knockdown also prevents binding of the PRLr to the CISH promoter suggesting that HMGN2 is required to PRLr promoter binding. Since HMGN2 possesses no sequence specificity, our findings suggest that nuclear PRLr may serve as the adaptor molecule that tethers HMGN2 to Stat5a, resulting in full transcriptional activity of Stat5a. Ongoing research will seek to determine the mechanism of HMGN2 recruitment, as well as the phenotypic effects of transactivation-deficient PRLr.

Part II – Proposed Aims

Three specific aims were proposed in this pre-doctoral award.

Specific Aims

- (1) Evaluate the function of the PRLr as a potential transcription factor and/or Stat5a co-activator.
- (2) Determine the molecular mechanism of PRLr nuclear localization.
- (3) Analyze the role of nuclear PRLr in the pathogenesis of human breast carcinoma.

Part III - Statement of Work

The tasks to achieve the specific aims above are covered in the statement of work as outlined below. Items that had to be completed in the first year of the proposal are **indicated in bold**.

Specific Aim 1. Evaluate the function of the PRLr as a potential transcription factor and/or Stat5a co-activator (Months 1-20):

Experiment 1.1 – What domains of PRLr are necessary and sufficient for transactivation?

- a. **Months 1-4: Construct Gal4-PRLr truncation mutants to elucidate the transactivation domain of PRLr**
- b. **Months 4-7: Perform luciferase experiments with constructs in 293, MCF7 and T47D cells**
- c. **Months 7-12 Fine map the transactivation domain of the PRLr.**

Some of the above data were reported in the 2009 Summary of Work. More detailed work has since been performed and the results of this are reported.

Experiment 1.2 - Does PRLr bind DNA in a Stat5a independent manner

- a. Months 6-7: Acquire biotinylated probes for EMSA
- b. Months 7-8: Perform EMSA studies using nuclear extracts
- c. Months : 8-10: Perform *in vitro* transcription/translation of PRLr and Stat5a
- d. Months 10-20: Perform EMSA studies on using *in vitro* transcribed/translated proteins

We have identified that the nuclear protein HMG2 binds to both the PRLr transactivation domain, and Stat5a. We therefore performed experiments that ask the question: What is the role of HMG2 in Stat5a driven gene expression?

Specific Aim 2. Determine the molecular mechanism of PRLr nuclear localization (Months 1-24):

Experiment 2.1 - Does PRLr sequence KPKK facilitate PRLr and Stat5a nuclear localization through a "classic" nuclear import pathway?

- a. Months 1-4: Construct muPRLr (KPKK mutation) construct
- b. Months 4-8: Perform transfections of wt and mutant PRLr constructs in CHO cells
- c. Months 4-8: Perform western blots on cytoplasmic and nuclear extracts of CHO transfectants

We have performed these experiments which were reported last year, but have since seen that mutation of the PRLr NLS has no effect of its nuclear localization. However, we have also identified two specific residues that are necessary for PRLr transactivation function. Therefore, we are utilizing a PRLr transactivation deficient construct to ask the question: What are the mechanistic and functional effects of mutation of the PRLr transactivation domain?

Experiment 2.2 - Is Jak2 tyrosine kinase necessary for initiating PRLr nuclear localization?

- a. Month 8: Acquire Jak2 inhibitor (AG-490) and Jak2 siRNA
- b. Months 9-10: Perform drug treatment and on T47D cells
- c. Months 9-10: Perform western blot analysis on T47D nuclear and cytoplasmic lysates
-Probe for PRLr, controls
- d. Months 10-12: Optimize si-RNA knockdown of Jak2
- e. Months 12-14: Perform western blot analysis of T47D cells with Jak2 knockdown
-Probe for PRLr, controls

We have chosen to hold off on these experiments so that we can explore other aims more rigorously.

Experiment 2.3 - Is nuclear PRLr derived from the cell surface?

- a. Months 14-16: Optimize biotinylation conditions
- b. Months 16-24: Perform biotinylation experiments in nuclear/cytoplasmic lysates.

These results were reported in the 2009 Summary of work, but since we have performed a more thorough timecourse of this experiment. The results of this study are shown in this report.

Specific Aim 3. Analyze the role of nuclear PRLr in the pathogenesis of human breast carcinoma (Months 12-36):

Experiment 3.1 – Does nuclear targeted PRLr have the ability to induce neoplastic abnormalities in vitro?

- a. Months 12-16: Create lentiviral constructs
- b. Months 16-20: Create stable cell lines
- c. Months 20-24: Perform 3-D matrigel assay
- d. Months 22-24: Perform proliferation assay
- e. Months 24-28: Perform Growth on soft agar assay

We have identified the PRLr transactivation domain and HMG2, the protein that is recruited to the PRLr transactivation domain, and is involved in chromatin regulation. We have therefore generated the following cells lines to study functional effects:

1. HMG2 knockdown
2. PRLr knockdown
3. wt PRLr overexpression
4. transactivation-deficient PRLr overexpression (PRLr Y406FD411A)

As the PRLr knockdown shRNA targets the 3'UTR, we are also in the process of making rescue cell lines:

1. PRLr knockdown, wt PRLr overexpression
2. PRLr knockdown, Y406FD411A overexpression

Experiments 3.2 – Does a nuclear targeted PRLr have the ability to induce in vivo tumor formation?

- a. Months 24-28: Inject nude mice with stable cell lines (created in experiemnet#1 above)
- b. Months 28-36: Analyze tumor formation and metastasis in live mice and at experimental endpoints
- c. Months 28-26: Analyze histology of tumors, analyze markers such as Cyclin D1 by RT-PCR and western blot

Part IV - Results

Specific Aim 1. Evaluate the function of the PRLr as a potential transcription factor and/or Stat5a co-activator:

Identification of a PRLr transactivation domain.

Preliminary experiments have demonstrated that a portion of the PRLr intracellular domain, when fused to a Gal4 DNA binding domain, is able to strongly transactivate a reporter that contains 5 Gal4 binding sites upstream DNA encoding luciferase. This data suggests that PRLr ICD possesses a transactivation domain. Thus, the goal of this experiment is to determine which domain within the PRLr intracellular domain and which residues are responsible for PRLr transactivation function.

Over the part year we have identified the PRLr transactivation domain within residues 404-448. When aligned across mammalian species, we identified 4 highly conserved residues which were mutated to determine importance within the PRLr transactivation domain (Figure 1A). While mutation of Y406 or D411 alone decreased Gal4 transactivation, combining these mutations completely abrogated transactivation function (Figure 1B, 1C).

These data led us to ask the question; what might the PRLr be recruiting to chromatin to enable transcriptional activation? To answer this question, we revisited previous yeast two hybrid data in which the goal of the experiment was to identify proteins that bound specifically to the PRLr intracellular domain.

One protein of interest that was identified from this experiment was the nucleosome binding protein HMG2. The HMG2 family of proteins is known to modulate the chromatin structure in vertebrates. These proteins bind with higher affinity to nucleosomes than to double stranded DNA and their binding to nucleosomes also alters the posttranslational modification of nucleosomal histones at several distinct sites. The binding of these proteins to nucleosomes therefore results in transcriptional stimulation or inhibition. HMG2 possesses no DNA sequence specificity since it binds generically to nucleosomes. It is therefore hypothesized that the targeting of HMG2 proteins to DNA is mediated by an adapter protein that confers DNA sequence specificity.

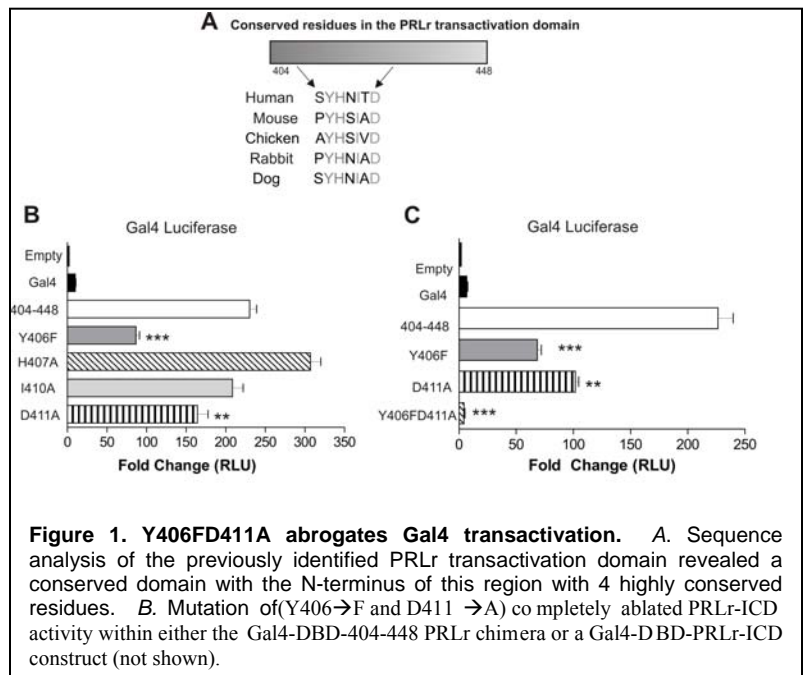


Figure 1. Y406FD411A abrogates Gal4 transactivation. A. Sequence analysis of the previously identified PRLr transactivation domain revealed a conserved domain with the N-terminus of this region with 4 highly conserved residues. B. Mutation of (Y406→F and D411→A) co completely ablated PRLr-ICD activity within either the Gal4-DBD-404-448 PRLr chimera or a Gal4-DBD-PRLr-ICD construct (not shown).

The PRLr transactivation domain, but not the transactivation mutant binds to HMGN2

We first sought to confirm that HMGN2 the yeast-two hybrid findings – that HMGN2 binds to the PRLr intracellular domain. To do this we utilized the heterologous Gal4 system, since within this system the PRLr is specifically targeted to chromatin. As the role of a transactivation domain is to activation transcription by interacting with other co-factors/transcriptional regulators, we hypothesized that if PRLr and HMGN2 do indeed bind, the PRLr transactivation domain would be the site of their interaction. Since Y406 and D411A are critical for PRLr transactivation function, we also reasoned that the TAD mutation (Y406F411A) would not have the ability to bind HMGN2.

As expected, HMGN2 strongly bound to the PRLr transactivation domain (404-448), but not the mutated TAD (Y406DD411A) or a region just outside of the PRLr TAD (485-517), (Figure 2A).

Endogenous PRLr and Stat5a bind to HMGN2 in T47D breast cancer cells

When we examined endogenous binding of the PRLr and HMGN2 in T47D breast cancer cells by co-immunoprecipitation analysis, we again confirmed binding. In addition, analysis also revealed that Stat5a binds to HMGN2, supporting the notion that the PRLr functions a Stat5a-coactivator, and recruits HMGN2 to the transcriptional complex.

Chromatin immunoprecipitation of HMGN2 and PRLr to the CISH promoter

To determine if HMGN2 is bound to the PRLr/Stat5a chromatin complex on the CISH promoter, we performed

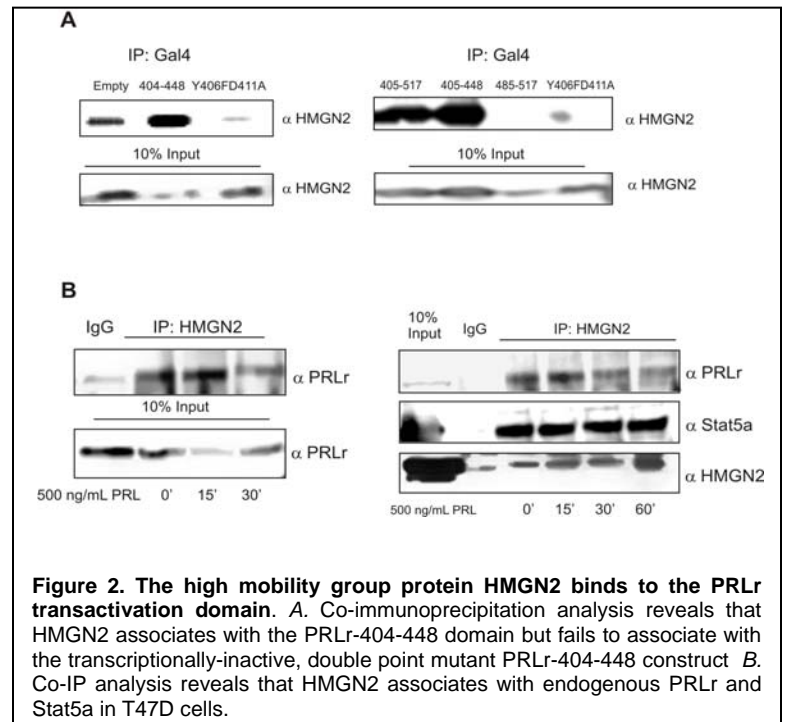


Figure 2. The high mobility group protein HMGN2 binds to the PRLr transactivation domain. A. Co-immunoprecipitation analysis reveals that HMGN2 associates with the PRLr-404-448 domain but fails to associate with the transcriptionally-inactive, double point mutant PRLr-404-448 construct B. Co-IP analysis reveals that HMGN2 associates with endogenous PRLr and Stat5a in T47D cells.

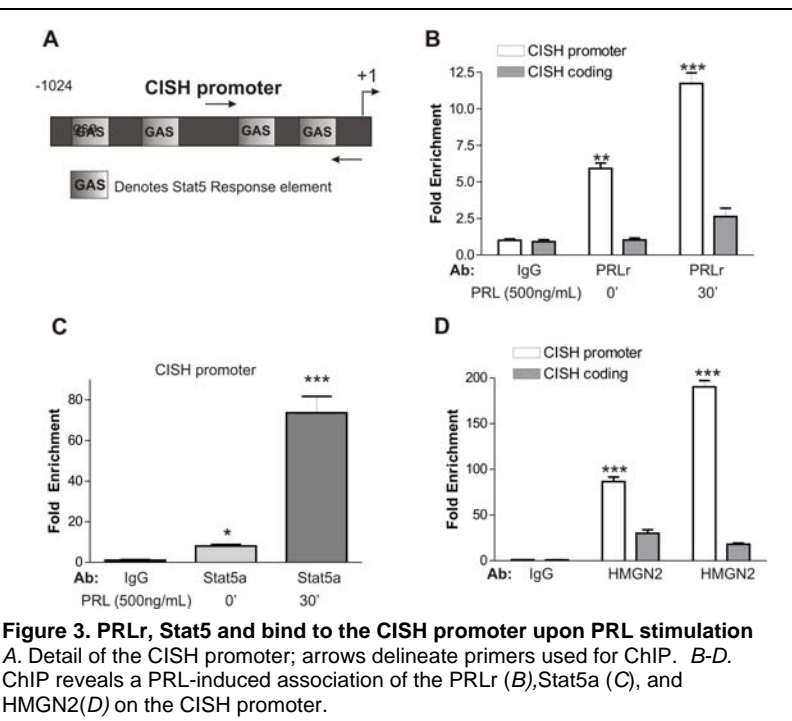
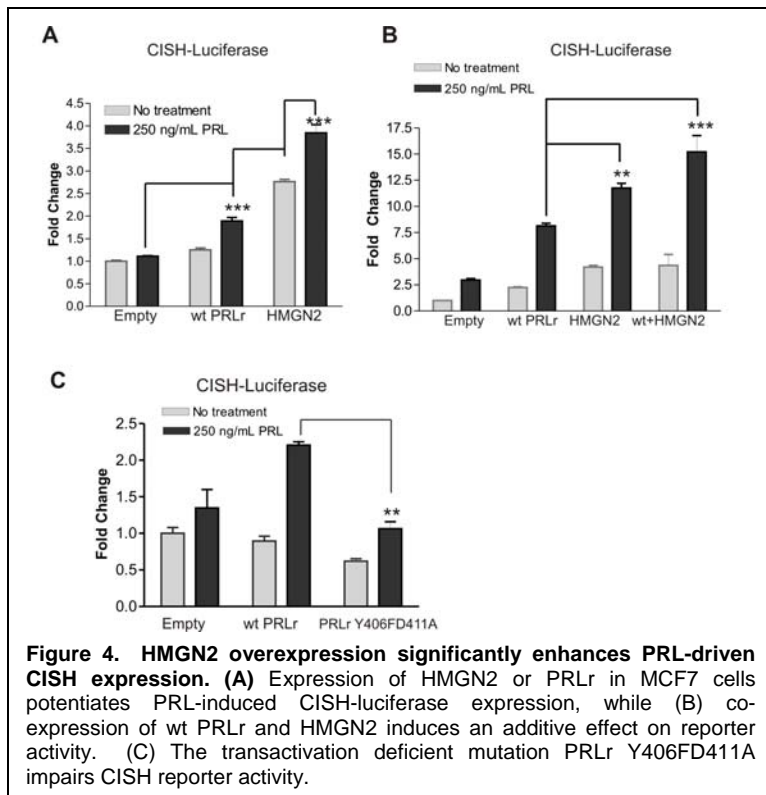


Figure 3. PRLr, Stat5a and bind to the CISH promoter upon PRL stimulation A. Detail of the CISH promoter; arrows delineate primers used for ChIP. B-D. ChIP reveals a PRL-induced association of the PRLr (B), Stat5a (C), and HMGN2 (D) on the CISH promoter.

chromatin immunoprecipitation analysis using primers that overlap a Stat5a consensus sequence (Figure 3A). As previous data has demonstrated, PRLr binds strongly to the CISH promoter upon PRL stimulation (Figure 3B). Similarly, we observed HMGN2 recruitment to the CISH promoter in a PRL-driven manner (Figure 3D). As a negative control in this assay primers that overlapped the CISH coding region were used. As shown in Figure 3, PRLr, Stat5a and HMGN2 bind specifically to the CISH promoter, while binding to the CISH coding region is negligible.

We then asked the question, does this binding result in enhanced transcriptional activation of CISH? Overexpression of HMGN2 in MCF7 cells significantly enhanced both basal and PRL-induced CISH-reporter activity. In addition, overexpression of PRLr and HMGN2 together produced an additive effect on CISH-reporter activity (Figure 4A-B).



As demonstrated by co-immunoprecipitation analysis, HMGN2 cannot bind to the Gal4-PRLr transactivation domain mutant. We therefore postulated that introducing this mutation into full length PRLr would prevent PRL-induced CISH transcriptional activity. As expected this mutation significantly decreased CISH reporter activity over wt PRLr levels (Figure 4C). These results suggest that the PRLr transactivation domain, and HMGN2 play a crucial role in the activation of PRL-induced gene expression.

Specific Aim 2 – Determine the molecular mechanism of PRLr nuclear localization. *It has been demonstrated that the PRLr binds to the CISH promoter upon PRL stimulation. Therefore, we hypothesize that nuclear PRLr is derived from the cell surface, and does not exist as an independent pool of non-membrane targeted protein. Given that PRL binds PRLr on the cell surface, it is also conceivable that PRL may also be an initiating*

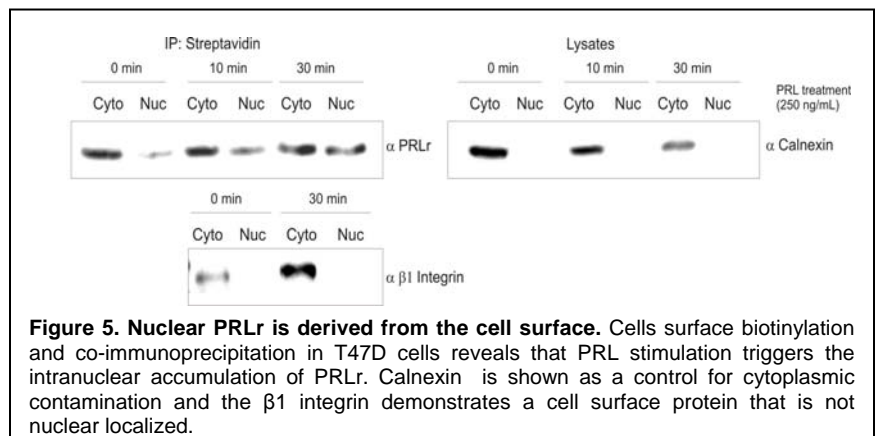
factor in PRLr nuclear trafficking. This set of experiments will therefore serve a dual purpose: 1) to demonstrate that PRLr is shuttled from the cell membrane to the nucleus and 2) to determine how PRL stimulation may initiate or regulate this event.

Cell Surface PRLr localizes to the nucleus upon PRL stimulation

In the 2009 summary we demonstrated by biotinylation of cell surface proteins that nuclear PRLr is indeed derived from the cell surface, and this nuclear localization is initiated by PRL. Since that time, we have performed a more thorough timecourse as shown in Figure 5.

Specific Aim 3 – Analyze the role of nuclear PRLr in the pathogenesis of human breast carcinoma.

It has been demonstrated in preliminary studies that PRLr is present within the nucleus of malignant mammary epithelial cells as well as ductal and invasive ductal carcinomas. In addition, enhanced PRLr nuclear localization can potentiate Stat5a-mediated gene transcription. As such, the identification that nuclear PRLr can enhance the actions of Stat5a may serve to mediate the larger function of proliferation, survival and progression of breast cancer. This aim will test the central hypothesis that nuclear PRLr contributes to the progression of human breast cancer.



Creation of T47D stable knockdown cell pools, shHMGN2 and shPRLr

We have determined that HMGN2 is recruited to the CISH promoter by the PRLr. Based on this data, we postulated that HMGN2 knockdown would produce a similar phenotype to PRLr knockdown.

We obtained an shRNA targeting HMGN2 from origene, and designed an shRNA targeting the 3'UTR of PRLr. Knockdown results are shown in Figure 6 (A,B and C).

When these cell lines were analyzed for their ability to activate CISH mRNA expression, knockdown of HMGN2 and PRLr both significantly decreased CISH mRNA levels.

To determine if PRLr was being recruited to the CISH promoter, a CHIP was performed utilizing the generated stable knockdown cell pools shown in Figure 6. Unexpectedly, knockdown of HMGN2 prevented PRLr recruitment to the CISH promoter. We therefore postulate that HMGN2 might be required to stabilize PRLr binding on the CISH promoter. Similarly, PRLr may be required to HMGN2 recruitment and binding to the CISH promoter.

Therefore, future CHIP studies will determine if PRL is necessary for HMGN2 docking to the CISH promoter. We also plan on determining what marks of transcriptional activation are impaired in shHMGN2 cells.

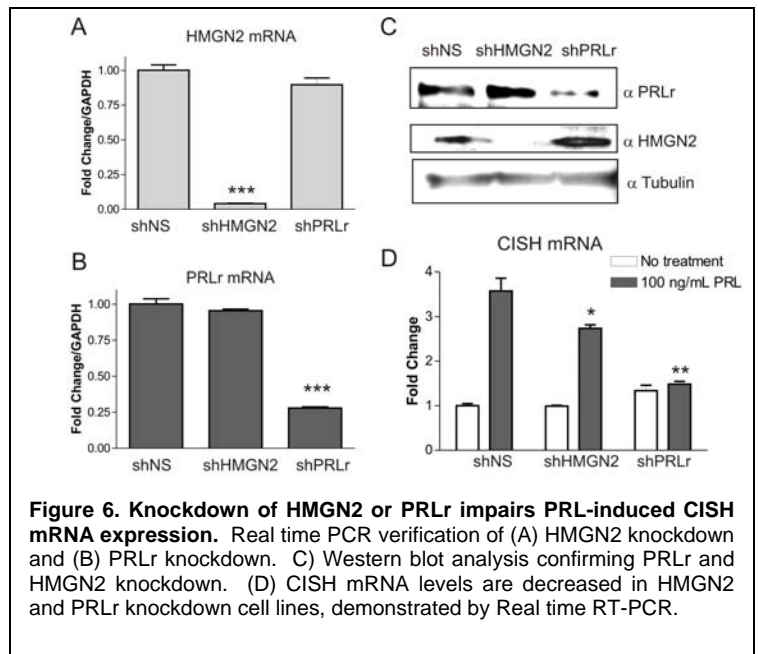


Figure 6. Knockdown of HMGN2 or PRLr impairs PRL-induced CISH mRNA expression. Real time PCR verification of (A) HMGN2 knockdown and (B) PRLr knockdown. (C) Western blot analysis confirming PRLr and HMGN2 knockdown. (D) CISH mRNA levels are decreased in HMGN2 and PRLr knockdown cell lines, demonstrated by Real time RT-PCR.

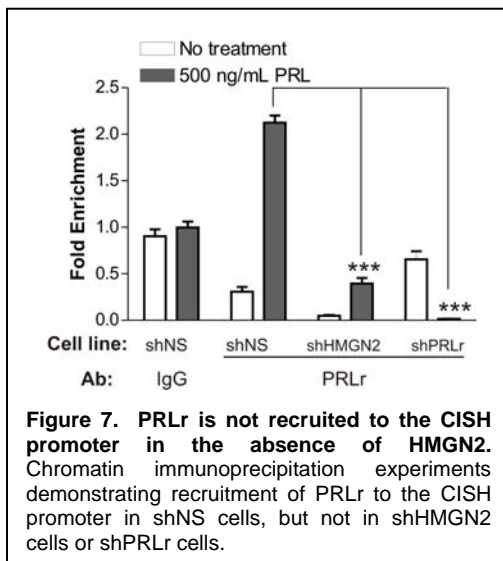


Figure 7. PRLr is not recruited to the CISH promoter in the absence of HMGN2. Chromatin immunoprecipitation experiments demonstrating recruitment of PRLr to the CISH promoter in shNS cells, but not in shHMGN2 cells or shPRLr cells.

Creation of stable overexpression cell pools

We have generated stable PRLr knockdown cell pool that targets the PRLr 3'UTR. Utilizing stable cell pools, we plan on performing rescue experiments by re-introduce either wt PRLr or transactivation deficient Y406FD411APRLr into shPRLr cells. Figure 8 shows epitope tagged PRLr expression for both wt and mutant PRLr. Future experiments will utilize these cell lines to examine both the mechanism of functional consequences of transactivation deficient PRLr.

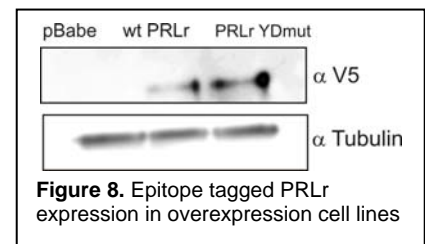


Figure 8. Epitope tagged PRLr expression in overexpression cell lines

Translational implications of Nuclear PRLr

Data from our lab has demonstrated that one of the critical residues in PRLr transactivation, Y406, is phosphorylated. A phospho-specific antibody was therefore developed against Y406 to determine where this phosphorylation might occur, and how this phosphorylation might be related to breast cancer progression. A breast cancer and normal adjacent tissue was stained via immunohistochemistry using the phosphospecific PRLr Y406 antibody. In this study total PY406 staining increased in malignant tissue, and a majority of this staining was localized to the nucleus (Figure 9). This data suggests that phosphorylation of Y406 may be crucial for PRLr transactivation, and may initiate or contribute to a tumorigenic phenotype.

Part V - Key Research Accomplishments

- Identification of critical residues in the PRLr transactivation domain
- Verification that HMGN2 binds to the PRLr and is recruited to the CISH promoter upon PRL stimulation
- Cloning of several retroviral constructs, and development of expertise in retroviral transduction

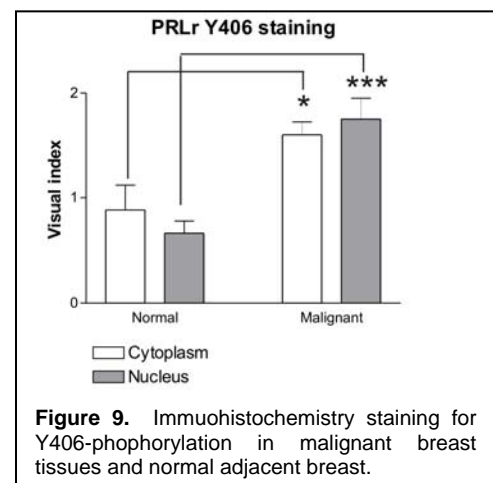


Figure 9. Immunohistochemistry staining for Y406-phosphorylation in malignant breast tissues and normal adjacent breast.

- Providing key insight into the role of the PRLr as a transcriptional coactivator
- Providing evidence for the mechanism of PRLr nuclear localization
- Development of presentation skills through numerous departmental and cancer center wide talks
- Development of collaboration skills by learning techniques perfected by adjacent laboratories
- Development of mentor skills by assisting in colleagues paper revisions and by teaching new techniques

Part VI - Reportable Outcomes

Publications:

Fang F, Zheng J, Galbaugh T, **Fiorillo A**, Hjort E, Zeng X, Clevenger C. J Mol Endocrinol. 2010 Mar 17. Cyclophilin B as a co-regulator of prolactin-induced gene expression and function in breast cancer cells.

Conference Abstracts:

- **AACR Annual Meeting (2009) Denver, CO. Alyson A. Fiorillo, Samantha L. Gadd, Feng Fang and Charles V. Clevenger.** "Nuclear PRLr functions as a transcriptional activator.
- **Northwestern University CGSA Fall Poster Session (2008) Alyson A. Fiorillo, Samantha L. Gadd, Feng Fang and Charles V. Clevenger.** "Nuclear PRLr functions as a transcriptional activator.
- **Endocrine Society Annual Meeting (2008) San Francisco, CA (Invited Poster Competition) Alyson A. Fiorillo, Samantha L. Gadd, Feng Fang and Charles V. Clevenger.** "The Role of Nuclear Prolactin Receptor as a Transcriptional Activator."
- **Northwestern University, Lewis Landsberg Research Day Annual Symposium (2008) Chicago, IL Alyson A. Fiorillo, Samantha L. Gadd, Feng Fang and Charles V. Clevenger.** "The Role of Nuclear Prolactin Receptor as a Transcriptional Activator."
- **Gordon Research Conferences, Prolactin and Growth Hormone (2008) Ventura Beach, CA Alyson A. Fiorillo, Samantha L. Gadd, Feng Fang and Charles V. Clevenger.** "The Role of Nuclear Prolactin Receptor as a Transcriptional Activator."

Part VII - Conclusions

The central goal of this proposal was to determine the role of the PRLr in the nucleus. Over the past year the experiments performed have provided significant evidence that this role is to function as a transcriptional co-activator. We have also identified that HMGN2, a nucleosome binding protein, interacts with the PRLr, and is recruited to the PRLr-Stat5a chromatin complex on the CISH promoter. Since there is little data describing how HMGN proteins alter transcription or what proteins confer their promoter specificity, the study of how PRLr might tether HMGN2 to the CISH promoter is highly relevant to understanding its cellular function and mechanism of action. We have also demonstrated that transactivation deficient PRLr, Y406FD411A cannot activate Gal4 transcription, bind to HMGN2 or promote the full activation of the Stat5a-driven CISH reporter. As knockdown of HMGN2 yields a similar effect to that of PRLr Y406FD411A, our data suggests that both transactivation-competent PRLr and HMGN2 may be required for the full transcriptional activity of Stat5a. In addition, immunohistochemistry data implicates that phosphorylation of the Y406, a critical residue in PRLr transactivation, is amplified in the nucleus of malignant breast tissue. This data therefore implies that a functional PRLr transactivation domain may be a hallmark of a tumorigenic phenotype. Our proposed work and work to date encompassing a transcriptional, mechanistic and functional analysis of nuclear PRLr, is integral in defining the role of this potential transcriptional regulator in the initiation and progression of breast cancer.

Part VIII – Appendices

1 **Cyclophilin B as a Co-regulator of Prolactin-induced Gene Expression**
2 **and Function in Breast Cancer Cells**

3
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13
14
15 **Running title:** CypB in PRL signaling

16 **Keywords:** prolactin; gene profiling; CypB; breast cancer

17 Abstract

18 The effects of prolactin (PRL) during the pathogenesis of breast cancer are mediated in
19 part though Stat5 activity enhanced by its interaction with its transcriptional inducer, the prolyl
20 isomerase cyclophilin B (CypB). We have demonstrated that knockdown of CypB decreases cell
21 growth, proliferation, and migration, and CypB expression is associated with malignant
22 progression of breast cancer. In this study, we examined the effect of CypB knockdown on PRL
23 signaling in breast cancer cells. CypB knockdown with two independent siRNA was shown to
24 impair PRL-induced reporter expression in breast cancer cell line. cDNA microarray analysis
25 was performed on these cells to assess the effect of CypB reduction, and revealed a significant
26 decrease PRL-induced endogenous gene expression in two breast cancer cell lines. Parallel
27 functional assays revealed corresponding alterations of both anchorage-independent cell growth
28 and cell motility of breast cancer cells. Our results demonstrate that CypB expression levels
29 significantly modulate PRL-induced function in breast cancer cells ultimately resulting in
30 enhanced levels of PRL-responsive gene expression, cell growth and migration. Given the
31 increasingly appreciated role of PRL in the pathogenesis of breast cancer, the actions of CypB
32 detailed here are of biological significance.

33 **Introduction**

34 An increasing body of literature supports a significant role for the hormone prolactin
35 (PRL) in the pathogenesis of human breast cancer. Epidemiologic analysis has revealed that PRL
36 concentration is associated with an increased risk for breast cancer (Eliassen, et al. 2007;
37 Hankinson, et al. 1999; Tworoger, et al. 2007) particularly in post-menopausal women. These
38 clinical observations are further substantiated by the PRL transgenic mouse model, which
39 develops both ER+ and ER- mammary tumors after 12-18 months (Rose-Hellekant, et al. 2003;
40 Wennbo, et al. 1997; Wennbo and Tornell 2000). Several lines of evidence have also indicated
41 that PRL acts as both an endocrine and autocrine/ paracrine progression factor for mammary
42 carcinoma *in vitro* and *in vivo* in rodents and humans (Clevenger, et al. 1995; Das and
43 Vonderhaar 1997).

44 The effects of PRL are mediated by the interaction to its receptor (PRLr) (Clevenger, et
45 al. 2003). Binding of PRL activates the pre-dimerized PRLr (Gadd and Clevenger 2006) and
46 results in the activation of PRLr-associated signaling cascades such as Jak2/Stat5, Fyn/Src,
47 Shc/Grb2, Sos/Raf/MAPK, and Tec/Nek3/Vav/Rac (Clevenger et al. 2003), resulting in the
48 transactivation of PRL-responsive genes, that include cyclin D1, CISH, and β -casein (Brockman
49 and Schuler 2005; Fang, et al. 2008; Guyette, et al. 1979; Pezet, et al. 1999; Utama, et al. 2006).
50 The summation of these signaling events results in the terminal maturation of normal mammary
51 tissues (Maus, et al. 1999; Miller, et al. 2007) and contributes to the PRL induced growth (18-
52 20), and motility (Maus et al. 1999; Miller et al. 2007) of malignant breast cells and tissues.

53 Previous research in our laboratory had demonstrated that some of the actions of PRL are
54 directly mediated by the localization and function of this ligand within the nucleus (Clevenger, et
55 al. 1991; Rycyzyn, et al. 2000). Yeast two-hybrid screening was used to identify binding partners

56 involved in this process (Rycyzyn and Clevenger 2002; Rycyzyn et al. 2000) and identified that
57 the cis-trans peptidyl prolyl isomerase, cyclophilin B (CypB), was a binding partner required for
58 the nuclear translocation of PRL (Rycyzyn et al. 2000). Within the nucleus, the PRL-CypB
59 complex was found to function as an inducer for the latent transcription factor Stat5, through its
60 induction of the release of the Stat5 inhibitor, PIAS3 (Rycyzyn and Clevenger 2002). CypB has
61 also been demonstrated to be associated with malignant progression and regulation of genes
62 implicated in the pathogenesis of breast cancer (Fang, et al. 2009a).

63 The cyclophilins are members of a larger class of PPIase proteins widely expressed
64 throughout the body, known as the immunophilins that are targets for the immunosuppressive
65 agents FK506, cyclosporine A (CsA), and rapamycin (Fischer, et al. 1998; Kofron, et al. 1991).
66 Although classically thought to assist in protein folding, immunophilins also serve as signaling
67 switches via prolyl isomerization (Hunter 1998), regulating the activity of cell surface receptors
68 TGF β (Huse, et al. 1999), tyrosine kinases (Brazin, et al. 2002; Zheng, et al. 2008), and
69 transcription factors such as c-Myb (Levenson and Ness 1998) and IRF4 (Mamane, et al. 2000).
70 In addition to its actions within the nucleus as a transcriptional inducer, CypB as a secreted
71 protein is also thought to serve as a ligand for the CD147 receptor, thereby regulating the
72 motility of cells expressing this receptor (Melchior, et al. 2008; Pakula, et al. 2007; Yang, et al.
73 2006; Yurchenko, et al. 2001). Indeed, a recent study revealed that CypB present in the
74 conditioned medium of the breast carcinoma cell line MDA-MB231 promoted chemotaxis of
75 bone marrow-derived mesenchymal stromal cells (MSCs) (Lin, et al. 2008). However, despite
76 these insights into CypB action, the function of CypB during PRL-induced gene expression and
77 action in breast cancer cells has remained undocumented.

78 In this study for the first time, the effects of altering CypB levels in breast cancer cells
79 during PRL stimulation were examined at the level of gene expression profiling, anchorage
80 independent growth, and cell migration. These studies demonstrate that expression levels of
81 CypB significantly augmented PRL-induced action in breast cancer cells ultimately resulting in
82 enhanced levels of growth and migration of breast cancer cells.

83

84 **Materials and methods**

85 **Cell lines, vectors and reagents**

86 The human breast cancer cell lines (T47D and MCF7) from American Type Culture
87 Collection (ATCC, Manassas, VA) were maintained in DMEM (Hyclone) supplemented with
88 10% fetal bovine serum (FBS), 50 µg/ml penicillin, and 50 µg/ml streptomycin in a humidified
89 atmosphere of 5% CO₂ at 37°C. The si-CypB cells (T47D siRNA CypB knockdown stable cells)
90 and si-Luc cells (siRNA control cells for non-genomic target) were described before (Fang et al.
91 2009a). Vectors used in this study are: firefly luciferase reporter pGL4-CISH (Fang et al. 2008),
92 pGL4-LHRE (Fang, et al. 2009b), renilla luciferase reporter pGL4.73 (Promega), pGL410-SV40
93 (Fang et al. 2009a), pcDNA3.1 (Invitrogen, Casbad, CA), and pcDNA3.1-CypB (Rycyzyn et al.
94 2000). Human recombinant prolactin was a gift from Dr Tony Kossiakoff (University of
95 Chicago). Antibodies used in this study are: anti-CypB (Invitrogen, 37-0600) and α-tubulin
96 (Zymed, 32-2500).

97 **Knockdown of CypB**

98 For these studies two separate knockdown approaches were utilized for cross-validation
99 purposes to exclude off target effects. The first approach used the lentiviral si-CypB sequence

100 (this siRNA sequence is against the 3'-end region of the CypB coding sequence) (Robida, et al.
101 2007). The si-CypB cells (T47D siRNA CypB knockdown stable cells) and si-Luc cells (siRNA
102 control cells for non-genomic target) (Fang et al. 2009a) were previously used before. For
103 independent validation of the effects of siRNA knockdown of CypB, a second approach used a
104 different siRNA (si-CypB-T, against the central region of the CypB coding sequence, Cat#: D-
105 001136-01-05, Dharmacon, Lafayette, CO) that was transiently transfected in T47D and MCF7
106 cells in parallel with si-control RNA (Cat# D-001210-01 from Dharmacon) using RNAiMAX
107 (Invitrogen). After 48 hours, cells were harvested for RNA isolation.

108 **Luciferase assay, Western blot, microarray and data analysis, RT-PCR and real-time PCR,**
109 **soft agar growth and cell motility assay (also in the supplemental methods)**

110 Dual luciferase assay was conducted according to Fang (Fang et al. 2008), and details are
111 described in the figure legends. Microarray was conducted on Illumina Human Ref-6 Version 2
112 Expression Chip (Illumina, San Diego, CA). T47D si-CypB cells were cultured in the growth
113 medium for three days followed by 24 hours arrest prior to PRL treatment (100 ng/ml) for 2
114 hours. RNA isolation for microarray analysis was conducted as described in Fang et al (Fang et
115 al. 2009a) and supplemental methods. Primers for real-time PCR are listed in the table in the
116 supplemental methods. Microarray data were deposited in Gene Expression Omnibus database
117 with accession number GSE15505 (GEO, <http://www.ncbi.nlm.nih.gov/geo/>). Soft agar growth
118 and cell motility assay were conducted according to Zheng et al (Zheng et al. 2008). The details
119 of methods are in the supplemental methods.

120 **Statistical analysis**

121 All experiments described here were performed at least three times. Statistical analysis
122 was performed on GraphPad Prism 4 (GraphPad Software, La Jolla, CA), and specified in the

123 figure legends. The results are shown as the means with error bars depicting +/- Standard Error
124 Mean (SEM). * denotes $p < 0.05$, ** denotes $p < 0.01$ and *** denotes $p < 0.001$. $p < 0.05$ is
125 considered as statistically significant.

126

127 **Results**

128 **The genes regulated by PRL contribute to essential cell functions**

129 In addition to its well-recognized regulation of genes associated with milk production and
130 lactation (Clevenger, et al. 2008), PRL has been shown to induce expression of many genes
131 involved in cell proliferation and survival including BCL2 (Beck, et al. 2002), CEBP β (Nanbu-
132 Wakao, et al. 2000), CISH (Pezet et al. 1999; Utama et al. 2006), c-Myc (Dominguez-Caceres, et
133 al. 2004), and cyclin D1 (Brockman, et al. 2002). To systematically query the effects of PRL on
134 global gene expression in human breast cancer cells, the estrogen receptor positive (ER+) T47D
135 breast cancer cell line was used for microarray analysis with or without PRL treatment. Two
136 hours of PRL stimulation (100 ng/ml) was selected as the optimal time course length, given the
137 preliminary data from our lab that had shown maximal RNA expression from the PRL-
138 responsive CISH, c-Myc and cyclin D1 gene loci at that time (Fang et al. 2009b). RNA isolated
139 from these cells was subject to cDNA synthesis, labeling, and hybridization to the Illumina
140 human cDNA chip. In order to reduce false positives, probes with measurement value below the
141 background level (detection p-value < 0.01) in all hybridizations were filtered out. 17901 probes
142 were kept for subsequent statistical analysis. To establish a physiologically relevant cut-point for
143 analysis of PRL-induced gene expression, the RNA levels of the PRL-induced c-Myc gene
144 (Dominguez-Caceres et al. 2004) was assessed. While microarray analysis demonstrated a 1.4-
145 fold induction of c-Myc expression, real-time PCR revealed that c-Myc was induced 2.4-fold

146 following PRL treatment. Similar phenomenon was also observed for BCL3, CEBP β , CISH, and
147 cyclin D1 (see Fig 5). In addition, as documented by the manufacturer, the Illumina cDNA array
148 is sensitive to detect as little as 1.3-fold change in either direction (up or down). Given this, the
149 criterion to filter the microarray data was set to 1.3-fold (up or down regulation) for subsequent
150 analysis.

151 To simultaneously indicate the size biological effects (log₂ fold change as X-axis) and
152 the statistical significance (-log₁₀ p-value as Y-axis) at global level, a volcano plot was used to
153 compare the difference of gene expression between two groups (Fig 1A). As seen in volcano
154 map, the red dots represent the selected differentially expressed genes significantly regulated by
155 PRL treatment (p<0.05, FDR<0.05, fold change \geq 1.3 up or down). Two-dimensional hierarchical
156 clustering was applied to these filtered probes to generate a global overview of gene expression
157 map in the form of a heat map. Heat map analysis showed a remarkable difference in gene
158 expression pattern between PRL treatment and non-PRL treatment groups. It also indicated, in a
159 global view, highly consistent results among the triplicates in each group (Fig 1B). Of 28
160 significantly differentially expressed genes, 19 genes were up-regulated and 9 genes were down-
161 regulated. Many genes listed therein have not been reported upon before as PRL-responsive
162 genes in breast cancer, including BCL3 and BCL6 (Fig 1B). Subsequent real-time PCR analysis
163 confirmed the PRL-regulated mRNA upregulation of BCL3 expression and downregulation
164 BCL6 expression (Fig 1C and 1D). BCL3 plays an important role in cell proliferation (Na, et al.
165 1999), and sequence analysis using TFsearch program revealed 10 Stat binding sites within the
166 10 kb region including promoter/enhancer upstream of transcriptional start point, as well as
167 within the exons, introns and the 3' untranslated region. BCL6 is a zinc finger transcription
168 factor and found to be expressed in the breast cancer cells (Logarajah, et al. 2003), and

169 overexpression of Stat5 has been found to repress BCL6 expression (Scheeren, et al. 2005;
170 Walker, et al. 2007). Interestingly, the regulation of menin expression via PRL regulation of
171 BCL6 regulates pancreatic β -cell growth in pregnant mice; loss of this process may contribute to
172 gestational diabetes mellitus (Karnik, et al. 2007).

173 Ingenuity Pathway Analysis (IPA) has been widely used for analysis of gene expression,
174 proteomics and metabolic data to elucidate tumor progression, biomarker discovery and drug
175 discovery (Ganter and Giroux 2008). To assess the global effects of PRL on gene expression,
176 IPA was used to systematically visualize the relationships of genes regulated by PRL. The
177 transcripts from microarray results were filtered and 28 transcripts were input into the IPA Base
178 (see Material and methods). IPA was used to overlay the PRL-regulated genes onto the global
179 networks developed from the information contained in the Ingenuity Pathways Knowledge Base.
180 The genes regulated by PRL were categorized into different biological functions, with the
181 “cancer” biological function shown as the most significant category (Fig 1E). When the 28
182 transcripts were mapped into the IPA Base, the most significant modulated interaction
183 network was associated with those genes implicated in the pathogenesis of “cancer,
184 hematological disease and cell cycle” (Fig 1F). This interaction network revealed that many of
185 these PRL-regulated genes interact with each other, and in doing so may enhance PRL-induced
186 tumorigenesis. Network analysis of these cancer associated genes reveals a central role for many
187 gene products involved in PRL-signaling, such as CISH, MAPK, CEBP β , ERK and c-Myc.

188 **Ectopic expression of CypB enhanced Stat5-responsive reporter expression**

189 PRL action is mediated in the cells through distinct signaling pathways including the
190 Jak2/Stat5 signaling pathway. In this pathway, the intranuclear PRL/CypB complex acts as a
191 Stat5 transcriptional inducer to regulate gene expression (Rycyzyn and Clevenger 2002;

192 Rycyzyn et al. 2000). To characterize the role of CypB during PRL-induced expression of Stat5-
193 responsive genes in breast cancer cells, reporter assay was used to test the effect of CypB ectopic
194 expression on such promoters in T47D cells. This cell line was selected for our initial screening
195 studies given its regulatory robust expression of both the PRLr and CypB (data not shown). For
196 these studies, the pGL4-CISH luciferase reporter was used for PRL-induced reporter assay (Fang
197 et al. 2008); this expression construct contained the 1kb CISH promoter region fused upstream of
198 firefly luciferase reporter gene. These results showed that ectopic expression of CypB itself had
199 no effect on luciferase expression of the pGL4-CISH reporter in the absence of PRL (Fig 2A). In
200 the presence of PRL, CypB enhanced PRL-induced luciferase expression of pGL4-CISH reporter
201 (Fig 2A). As a parallel control experiment, we also co-transfected pGL4-CISH with the
202 pcDNA3.1-CypB-PPIase construct (a CypB mutant construct lacking activity of peptidyl-prolyl
203 cis/trans isomerase (PPIase or PPI)) in T47D cells. Results showed that compared to non-PRL
204 treatment, PRL-induced luciferase fold change is 22.5 ± 3.3 and 22.0 ± 3.0 respectively in
205 pcDNA3.1 and pcDNA3.1-CypB-PPIase transfectants, suggesting that the CypB-mediated
206 enhancement of PRL-induced luciferase expression was dependent upon PPI activity. These
207 results confirmed the effects of CypB on PRL-induced gene expression (Rycyzyn and Clevenger
208 2002) in T47D breast cancer cells.

209 **Knockdown of CypB impaired the expression of Stat5-responsive reporters**

210 To complement the overexpression-based studies, the effects of CypB knockdown on the
211 PRL/Stat5 signaling pathway were assessed in T47D transfected stably with si-RNA against a
212 control (luciferase; termed si-Luc) or CypB (termed si-CypB) (Fang et al. 2009a). Results from
213 real-time PCR and microarray confirmed a significant knockdown of CypB (Fig 2B). A second
214 different sequence directed against CypB (termed as si-CypB-T, and control as si-control-T) was

215 transiently transfected into T47D and MCF7 cells to validate that the effects noted in siCypB
216 stable transfectant were not due to off-target action (Fang et al. 2009a). The effect of transient
217 transfection of this siRNA also resulted in significantly reduced CypB levels (Fig 2C). This
218 second si-RNA was also used later in gene profile validation studies (see Fig 3). Two PRL-
219 induced, Stat5 responsive promoter reporter constructs, termed pGL4-LHRE (a synthetic
220 construct containing six Stat5 responsive elements) and pGL4-CISH were then introduced into
221 the stable T47D si-CypB cells to evaluate the effects of CypB knockdown on PRL signaling.
222 Results (Fig 2D) showed that, compared to wild type cells, the luciferase expression of pGL4-
223 CISH in si-CypB cells had little change in the absence of PRL. In the presence of PRL, the
224 luciferase expression of pGL4-CISH in si-CypB cells decreased significantly compared to wild
225 type cells. Similar results were observed for pGL4-LHRE (Fig 2E). These findings revealed that
226 CypB knockdown decreased PRL-induced expression luciferase in si-CypB cells, further
227 demonstrating the potentiating effects of CypB on PRL-mediated gene expression.

228 **Knockdown of CypB impaired the PRLr and PRL-inducible endogenous gene expression**

229 To determine the effects of CypB knockdown on PRL-regulated gene expression,
230 microarray analysis was conducted using si-CypB cells treated with or without PRL. To
231 characterize the effect of CypB on PRL signaling in this analysis, “prolactin” was used as the
232 key word in the “Gene Ontology (GO)” program to search for PRL-related genes significantly
233 regulated by CypB knockdown. Results revealed that the expression of the prolactin receptor
234 (PRLr), S100A6, and PIP (the prolactin-inducible protein) were significantly altered in si-CypB
235 cells compared to si-Luc cells (Fig 3A), a finding further confirmed by both real-time PCR and
236 Western blot analysis for PRLr gene (Fig 3B and 3C).

237 Microarray analysis and subsequent validation studies suggested that the panel of the
238 PRL-induced genes was regulated differently by PRL in si-Luc and si-CypB cells. Real-time
239 PCR confirmed that CEBP β , c-Myc, and cyclin D1 mRNA expression were significantly
240 decreased in si-CypB stable cells compared to that of si-Luc stable cells, while little effect on
241 BCL3 and CISH was observed (Fig 4A-E). Real-time PCR results also showed that the PRL-
242 repressed BCL6 mRNA expression was also significantly decreased in si-CypB cells compared
243 to that of si-Luc cells (Fig 4F). The effect of transient transfection of a second differing siRNA
244 (used in Fig. 2E, termed as si-CypB-T, and control as si-control-T)) into both T47D and MCF7
245 cells was also tested in the context of PRL to further rule out off target effects. The PRL-induced
246 CEBP β and cyclin D1 mRNA expression were significantly decreased in cells with CypB
247 knockdown (Fig 4G-L). While si-CypB-T cells resulted in a decrease in c-Myc and BCL6 levels,
248 these results did not achieve statistical significance compared to results from the siCypB stable
249 T47D cells. This may be due to cell line variance (high PRLr level in T47D and modest PRLr in
250 MCF7) and difference in knockdown efficiency (stable vs transient). Taken together, these
251 findings indicate that reductions in CypB levels significantly impacted on PRL-induced gene
252 expression at both global and locus-specific levels.

253 **CypB knockdown impaired the PRL-induced colony growth on the soft agar**

254 Given that CypB knockdown significantly modulated the expression of the PRL-
255 regulated CEBP β , c-Myc, cyclin D1 and BCL6 genes in T47D cells, the effect of CypB
256 knockdown on PRL-induced anchorage-dependent cell growth was tested using soft agar assay.
257 These analysis revealed colony number (counted by single colonies) and size (determined by the
258 colony area) of si-Luc cells were increased in the presence of PRL. Colony number and size of

259 si-CypB cells was significantly attenuated, showing that CypB is involved in the anchorage-
260 independent cell growth (Fig 5A-F).

261 **CypB knockdown impaired the PRL-induced cell motility**

262 PRL has also been shown to stimulate T47D cell motility (Maus et al. 1999; Miller et al.
263 2007). To investigate if CypB knockdown affected PRL-induced cell motility, Boyden chamber
264 cell migration assay was conducted using PRL as a chemoattractant. These data revealed that
265 PRL stimulated si-Luc cell motility, as previously described (Miller et al. 2007). The PRL-
266 induced motility of the si-CypB cells were significantly decreased, revealing a contribution of
267 CypB to PRL-mediated cell motility (Fig 6). In our previous publication (Fang et al. 2009a), we
268 have shown that knockdown of CypB impaired the FBS-inducible and estradiol-inducible cell
269 migration, suggesting the impairment of cell motility in si-CypB cells is due to global effects on
270 gene expression involved in motility regulation. It is also noted that CypB knockdown decreased
271 migration and colony formation even without PRL. This input may be due to the inhibition of the
272 actions of autocrine PRL produced by these cells. In the presence of PRL, CypB knockdown
273 impaired PRL-induced migration and colony formation (Fig 5 and 6).

274

275 **Discussion**

276 Given the increasingly appreciated role of PRL in the pathogenesis of breast cancer,
277 surprisingly little is known in regards to it regulation of gene expression in such cells. In this
278 context, this study sought to examine the effects of both PRL stimulation and CypB knockdown
279 on PRL-induced gene expression by validated gene profiling and relate these observations to
280 PRL-induced growth and motility. CypB has been shown previously to play an important role in

281 cell survival (Kim, et al. 2008), cancer progression, cell proliferation and cell growth (Fang et al.
282 2009a). Our results indicate that absence of CypB significantly impair the patterns of gene
283 expression induced by PRL in breast cancer cells.

284 Gene profiling analysis performed here and elsewhere (Fang et al. 2009a) showed that
285 CypB knockdown regulated PRL-related genes included: 1), the PRLr. It is important to note that
286 given widely varying effects of CypB knockdown on PRL-induced genes (see Fig 3), we believe
287 that the effects of CypB extend beyond that of a mere reduction in PRLr levels, 2) the prolactin-
288 inducible protein mRNA (PIP or GCPD15); this protein was noted to be increased two-fold in si-
289 CypB cells. PIP was first cloned from T47D cells and was induced by five days treatment of
290 PRL and/or growth hormone (Murphy, et al. 1987). Higher mRNA levels of PIP has a high
291 correlation with the expression of estrogen receptor alpha (ER α), progesterone receptor (PR) and
292 low-grade tumours (Clark, et al. 1999), 3) mRNA for the prolactin regulatory element binding
293 protein (PREB, also known as SEC12 or MGC3467); this mRNA was up-regulated by PRL only
294 in si-CypB cells (not in si-Luc cells). PREB acts as a transcriptional activator on PRL promoter
295 region to regulate PRL expression (Fliss, et al. 1999), 4) S100A6 mRNA; this is a S100 calcium
296 binding protein, also known as prolactin receptor-associated protein, and is down-regulated in si-
297 CypB cells (Fang et al. 2009a). S100A6 has been observed in prolactin receptor
298 immunoprecipitates (Murphy, et al. 1988). S100A6 is up-regulated in breast cancer cells and
299 tissues (Maelandsmo, et al. 1997) and knockdown of this gene appears to decrease both cell
300 proliferation and motility (Breen and Tang 2003), 5) the c-Myb proto-oncogene mRNA; this
301 oncogene was downregulated in PRL-stimulated si-CypB cells ($p < 0.05$). c-Myb is associated
302 with cell differentiation and proliferation (Weston 1999). c-Myb protein level is increased in *in*
303 *situ* and invasive breast cancers (McHale, et al. 2008). The c-Myb mRNA levels were regulated

304 by cyclophilin isomerase activity (Levenson and Ness 1998). c-Myb is a Stat5a co-activator
305 during PRL/Stat5a-driven gene expression (Fang et al. 2009b), and 6) the CEBP β transcription
306 factor; the level of its mRNA was also downregulated in si-CypB cells. CEBP β is bZIP
307 transcription factor acting as a Stat5 co-activator and is also a Stat5-regulated gene (Nanbu-
308 Wakao et al. 2000). The PRLr promoter has CEBP β binding sites and overexpression of CEBP β
309 upregulates PRLr expression (Hu, et al. 1998). This suggests CypB has a profound impact on
310 PRL-related gene expression.

311 Our previous work using a matched, progressive-based breast tissue microarray (TMA)
312 (Fang et al. 2009a) showed that CypB levels were increased in malignant breast epithelium,
313 suggesting that the up-regulation of CypB in breast cancer could significantly modulate the
314 biology of this disease. Si-RNA-mediated knockdown of CypB was found by gene profiling to
315 significantly regulate genes related cell proliferation, motility and receptors (Fang et al. 2009a).
316 Since CypB mediates PRL-responsive gene expression with profound effects, we hypothesized
317 that CypB is multi-faceted, serving as: 1) an activator of receptor expression (i.e. PRLr), 2) a
318 chaperone for ligand (i.e. PRL), and 3) an inducer for the transcriptional factor (i.e. Stat5)
319 (Rycyzyn and Clevenger 2002), all of which may collectively contribute to the regulation of the
320 PRL-responsive genes. Given the significant effect of CypB knockdown on the PRL-induced
321 anchorage-independent cell growth and cell motility, these results would suggest that the
322 molecular actions of CypB within the cell during PRL-induced signaling impacts significantly on
323 the biology of breast cancer cells.

324 The precise role of Stat5 in the pathogenesis of breast cancer remains to be fully clarified.
325 While data from mouse models of mammary cancer clearly indicate that loss of Stat5 function
326 results a significant delay in the pathogenesis of malignancy at this site (Ren, et al. 2002), data

327 from human tissues has shown that phosphorylated/nuclear Stat5 is associated with a favorable
328 histopathology (Sultan, et al. 2005). Although CypB could influence Stat5 function both through
329 its indirect actions at the cell surface, or by its direct interaction with Stat5, it is interesting to
330 note that many of the gene transcripts influenced by reduction in CypB expression in this
331 manuscript demonstrate multiple Stat5-binding sites within their proximal promoter regions. As
332 such, these findings would suggest that inhibitors that target both PRL-induced signals and CypB
333 may have a synergistic potential at the level of Stat5 function in the treatment of breast cancer.

334

335 **Declaration of interest**

336 The authors have nothing to disclose.

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492

493 **Figure legends**

494 Fig. 1. Microarray analysis demonstrates the effects of PRL on global gene expression. A.
495 Volcano map demonstrates the relationship between the observed fold change in gene expression
496 and the P-value significance of such changes in PRL-treated cells. The dotted lines represent the
497 p-value and fold-change cut-offs. The red dots represent the selected genes filtered by criteria
498 (fold change ≥ 1.3 up or down, $p < 0.05$, $FDR < 0.05$). B. Heat map analysis reveals a global view
499 of genes up- and down-regulated in PRL-treated cells. C and D. Real-time PCR validates
500 microarray results for BCL3 (C) and BCL6 (D). Statistical analysis was performed using Student
501 t test. E. The biological functional categories were obtained from the Molecular and Cellular
502 Function in the IPA database. F. The top interaction networks generated using IPA analysis
503 included genes associated with “cancer, hematological disease and cell cycle”. The color
504 indicates genes up-regulation (red), down-regulation (green) and complexes (gray).

505

506 Fig. 2. The effects of CypB overexpression and CypB knockdown on a Stat5-responsive reporter.
507 A. Luciferase assay using pGL4-CISH reporter. Cells were transfected with pGL4-CISH
508 reporter, the renilla luciferase control (pGL4.73) and pcDNA3.1-CypB expression vector.
509 Transfectants were cultured in the minimal defined medium for 24 hours followed by 24 hours of
510 PRL stimulation prior to luminescence assay. B and C. CypB knockdown in T47D cells
511 confirmed by real-time PCR and microarray (B), and transient transfection (C). D and E.
512 Luciferase assay using pGL4-CISH (D) and pGL4-LHRE (E). T47D parental cells (wt) or si-
513 CypB cells were co-transfected with 100 ng of pGL4-CISH (D) or pGL4-LHRE (E), along with
514 2 ng of renilla luciferase control (pGL4.73) and 400 ng of pcDNA3.1-CypB expression vector,
515 and maintained in the FBS-containing growth medium overnight. Transfectants were then

516 starved in the FBS-free minimal defined medium for 24 hours followed by 24 hours of PRL
517 (10ng/ml for pGL4-CISH and 100ng/ml for pGL4-LHRE) stimulation prior to luminescence
518 assay. Statistical analysis was performed using two-way ANOVA.

519

520 Fig. 3. The characterization of PRL-related genes affected by CypB knockdown. A. Heatmap
521 showed downregulation of PRLr, S100A6 and PIP in si-CypB cells compared to si-Luc control
522 cells. B and C. Real-time PCR (B) and Western blot (C) confirmed the PRLr downregulation in
523 si-CypB cells. Statistical analysis was performed using Student t test.

524

525 Fig. 4. Real-time PCR validated the impairment of PRL-induced gene expression by CypB
526 knockdown. A-F in T47D si-CypB stable cells. G-H in MCF7 cells with transient transfect of si-
527 CypB-T. The y-axis label “Fold change” is defined in the materials and methods section.
528 Statistical analysis was performed using Student t test.

529

530 Fig. 5. CypB knockdown results in the decreased PRL-induced soft agar growth and cell
531 motility. Cells were grown on soft agar for two weeks, and the pictures were taken under phase
532 contrast microscopy. A, si-Luc without PRL treatment. B, si-Luc with PRL treatment (200
533 ng/ml). C, si-CypB without PRL treatment. D, si-CypB with PRL treatment (200 ng/ml). E,
534 colony number on the soft agar. F, the total colony area on the soft agar.

535

536 Fig. 6. CypB knockdown results in the decreased PRL-induced cell motility. Cell motility was
537 assayed using Boyden chamber migration assay. The inserts were coated with collagen I

538 overnight. T47D cells were arrested in the FBS-free medium and placed in the inserts. Cells were
539 cultured for 20 hours and the migrated cells were counted under microscope. Statistical analysis
540 was performed using two-way ANOVA.

A

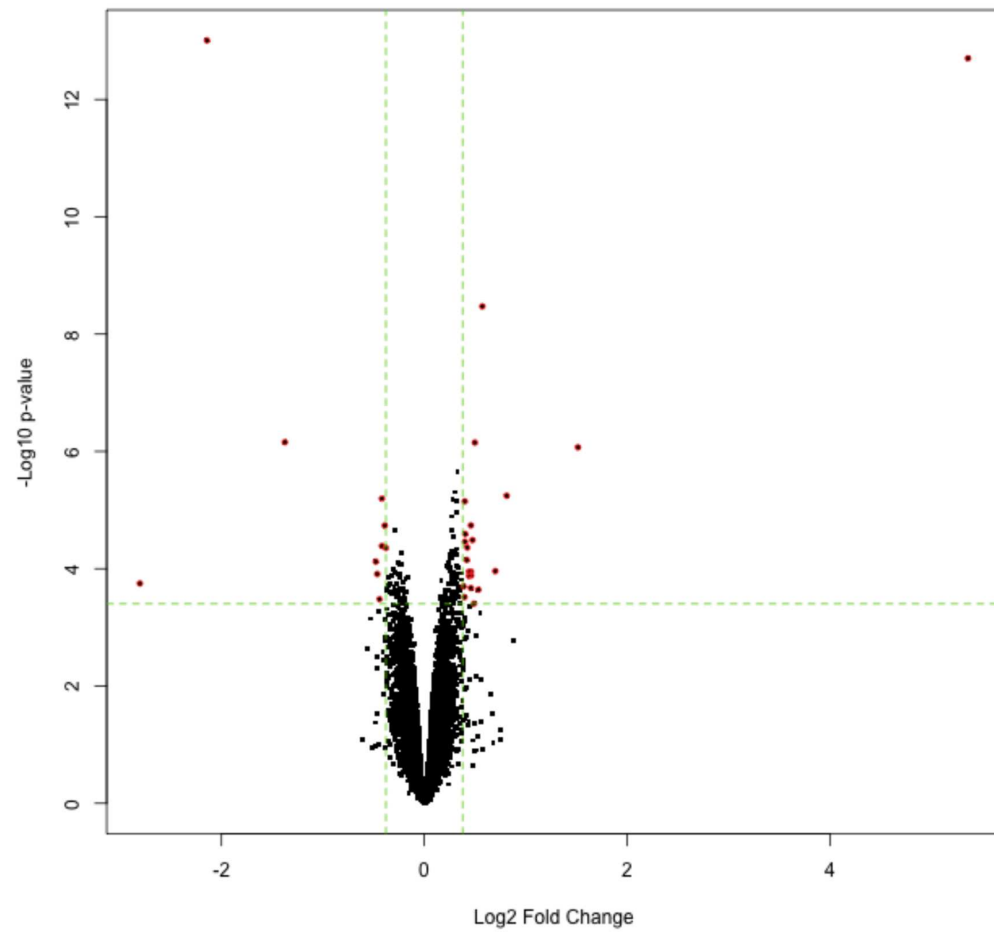


Fig1

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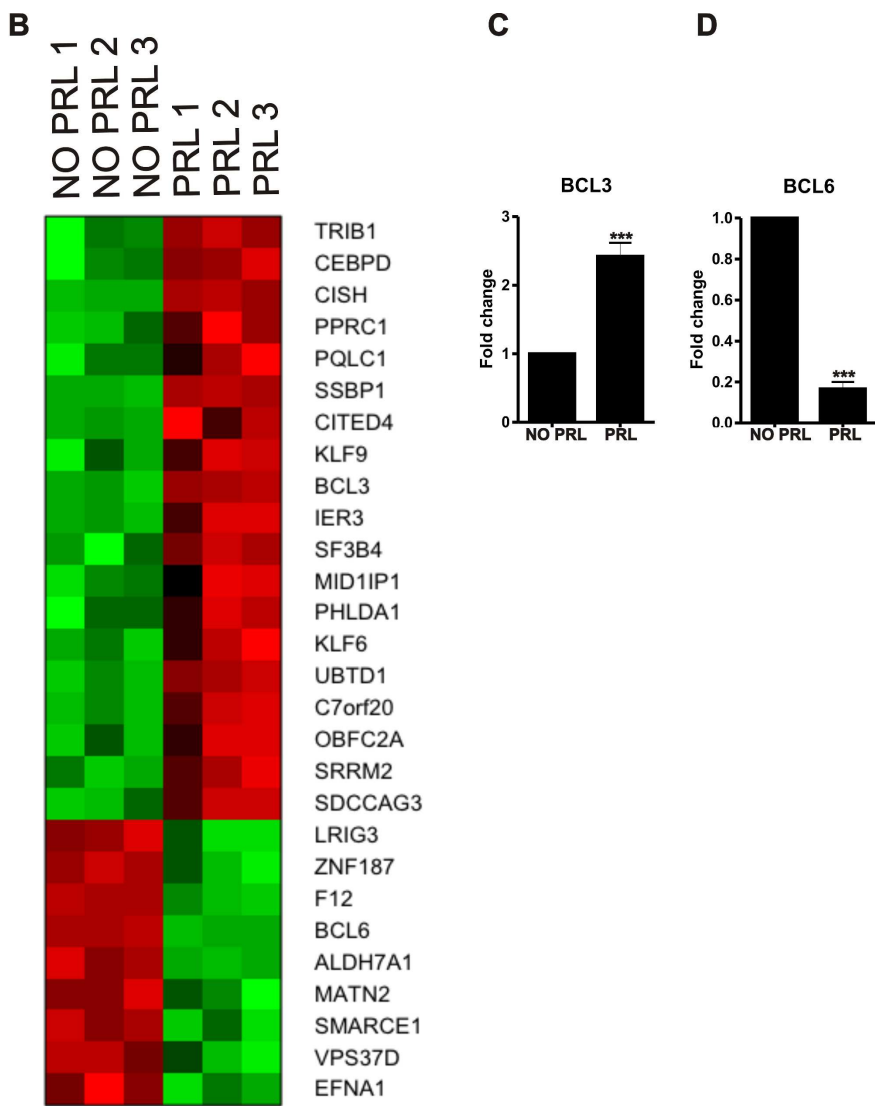


Fig1

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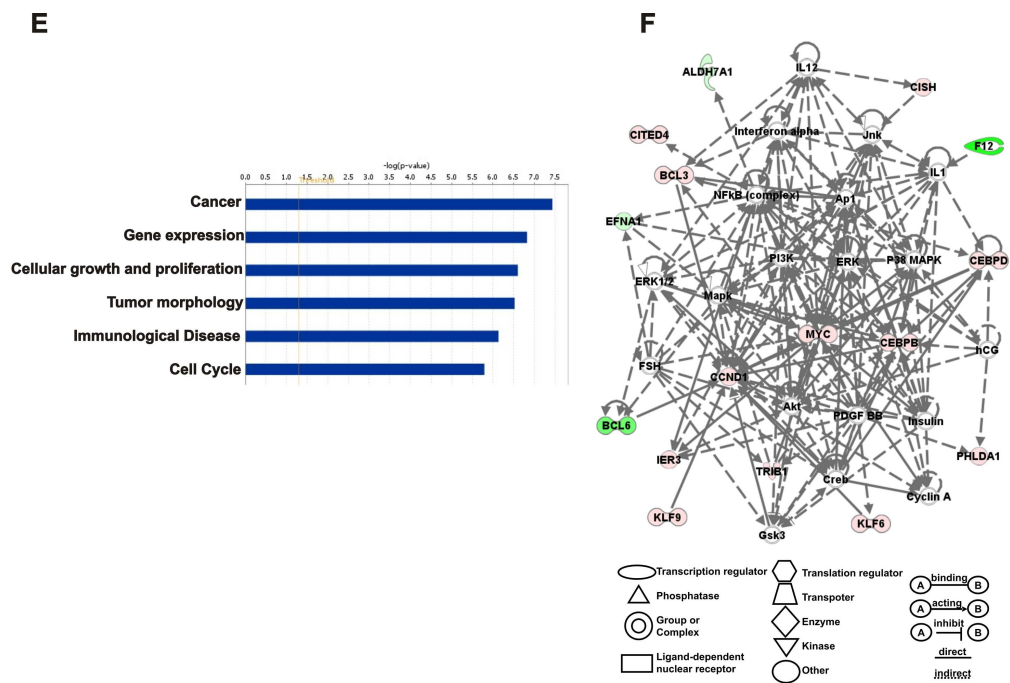


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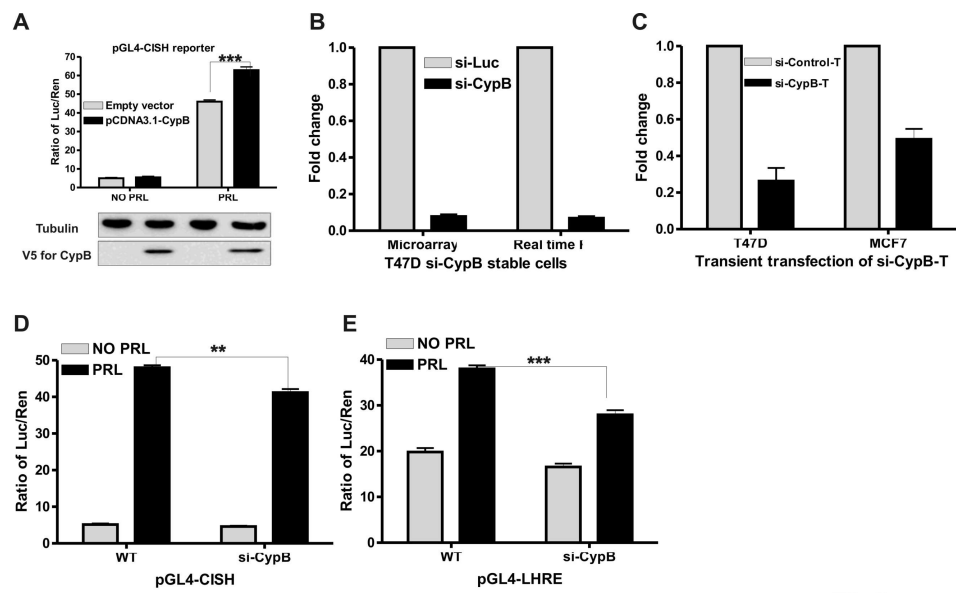


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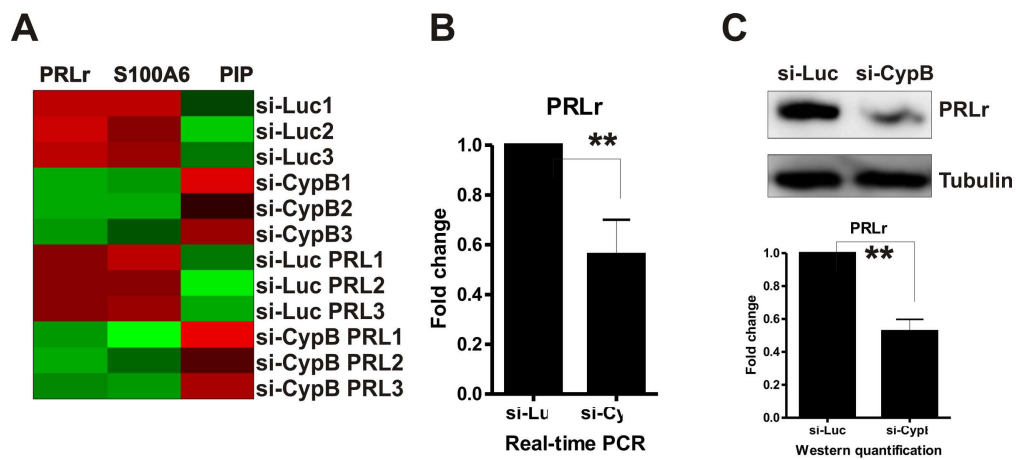


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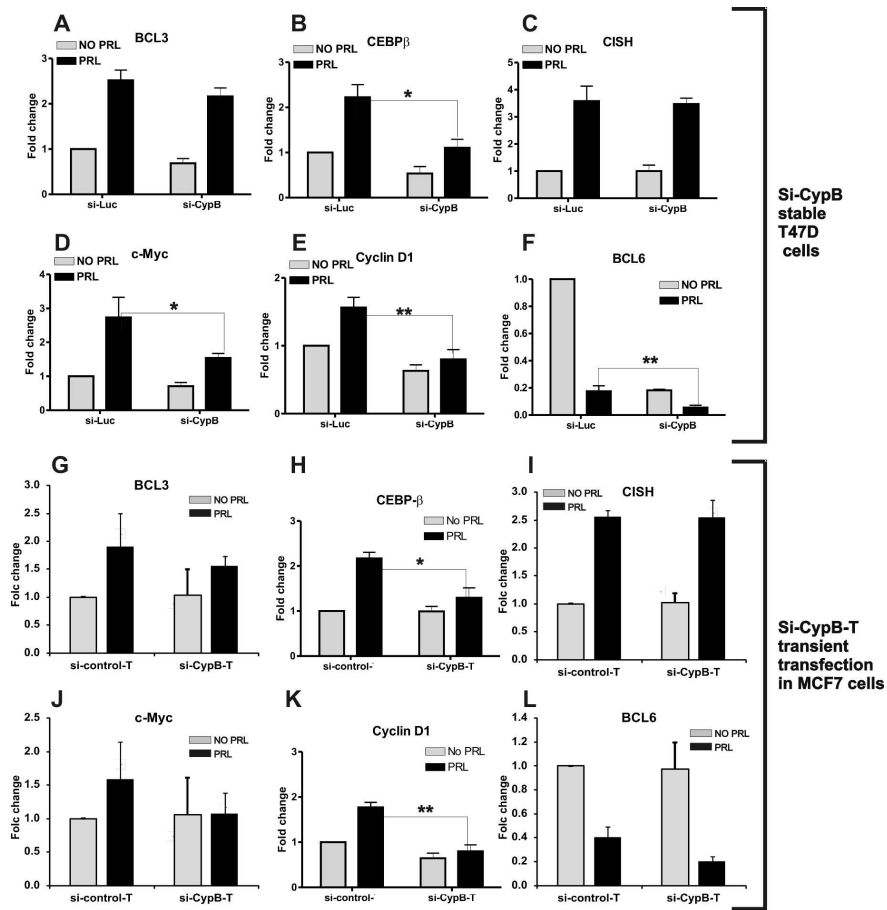
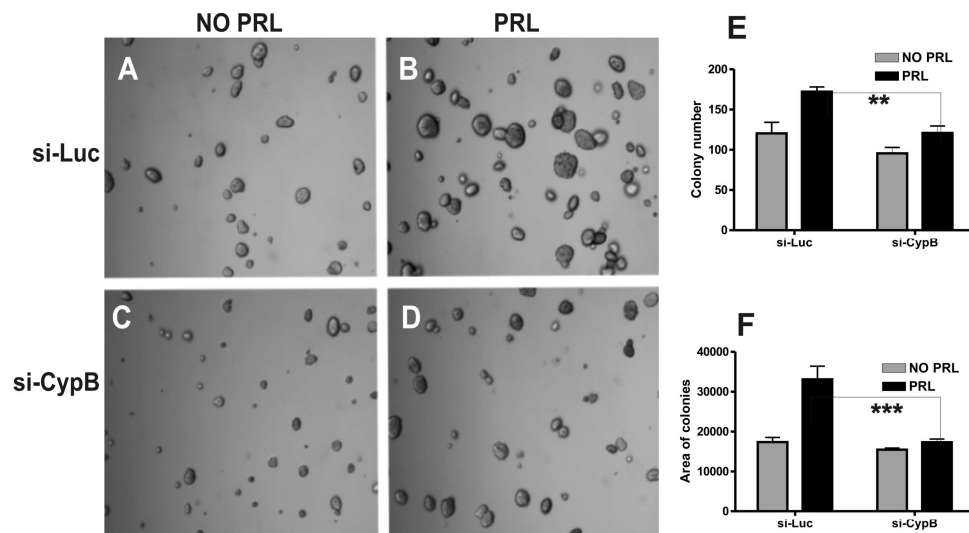


Fig4

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**Fig5**

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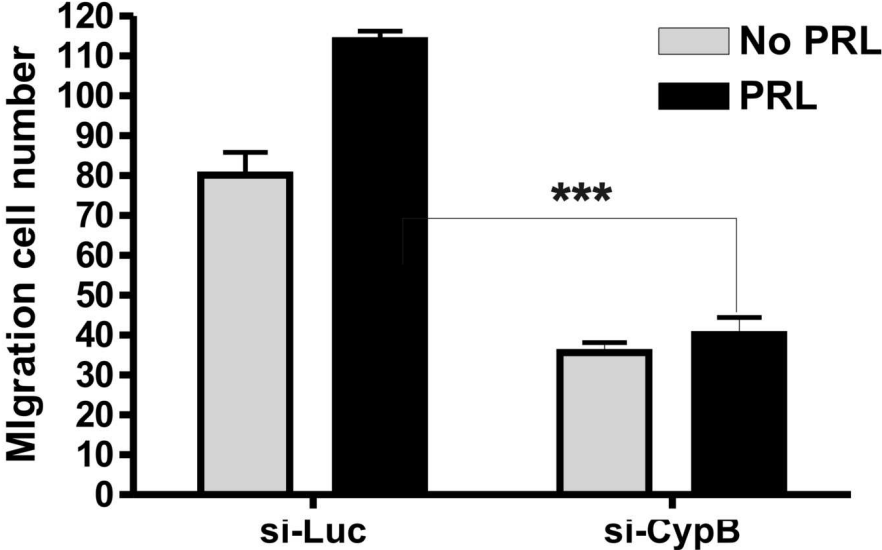


Fig6

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