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Transcriptional Activation by Islet1 Isoforms

A Thesis submitted in partial satisfaction of the requirements for the degree

Master of Arts

in Psychology

by

Amanda Grace Kautzman

Thesis Committee:
Professor Benjamin Reese, Chair
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Professor Tod Kippin

June 2014

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Benjamin Reese, Committee Chan	May 2014	

Transcriptional Activation by Islet1 Isoforms

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by

Amanda Grace Kautzman

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This thesis is dedicated to my late grandmother, Doris Kautzman, who was and ever will be the driving force behind my desire to keep learning.

ABSTRACT

Transcriptional Activation by Islet1 Isoforms

by

Amanda Grace Kautzman

The present study examined the role of alternative splicing as a mechanism to create neuronal diversity within the developing retina. The *Isl1* gene has two alternatively spliced isoforms, α and β , that are present in the developing retina. The Isl1 β isoform lacks a critical portion of a protein-binding domain with which Isl1 binds to Lhx3 in a known transcriptional complex (Isl1:Lhx3:Ldb1). Developmental analysis of *Isl1* expression reveals the *Isl1* α isoform is expressed at higher levels than Isl1 β throughout development and persisting into adulthood. *Isl1* isoforms are present in distinct subsets of retinal ganglion cells, with Isl1 β -expressing cells being restricted to cells with soma sizes under 175 μ m². A luciferase assay demonstrates the Isl1 β isoform is functionally distinct from Isl1 α and is not capable of activating the Isl1:Lhx3:Ldb1 complex as Isl1 α is. These results suggest that Isl1 β containing-complexes may have unique gene targets from Isl1 α and implicate the alternative splicing of *Isl1* as a mechanism contributing to neuronal differentiation during retinal development.

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Introduction

The complexity of the central nervous system can be accredited to a combination of cell intrinsic factors as well as environmental cues during development that influence cell genesis, fate determination, migration, arborization, in addition to others. The different influences on these events provide the developing nervous system with the potential for great diversity. Many of these developmental mechanisms have been studied extensively in the visual system, making it an ideal system to study how complexity in the nervous system arises. There are five neuronal cell classes in the retina that contain numerous subtypes, each of which exhibit unique morphologies, connectivity, positions, and gene expression profiles. This paper will explore differentiation within specific neuronal populations of the developing retina by the transcription factor Islet1 (Isl1).

Alternative RNA splicing plays an essential role in diversifying gene regulation and function. RNA splicing is the process by which internal sequences are removed from precursor-mRNA (pre-mRNA) while being processed into mature mRNA, as a complex of proteins called a spliceosome remove the intron and join the flanking exons (Query & Konarska, 2013). This mechanism can generate multiple unique mRNAs through a process known as alternative splicing, leading to the translation of different protein sequences (Nester, Hyman, & Malenka, 2008). This explains how 150,000 different mRNAs are coded for by only about 30,000 genes in the human genome (Elliot & Ladomery, 2011), which could in turn greatly increase the complexity of the nervous system (Wan et al., 2011).

Isl1 is an alternatively spliced LIM-homeodomain (LIM-HD) transcription factor that plays many roles in development. LIM-HD transcription factors represent a highly conserved subset of homeobox-containing proteins (Hobert & Westphal, 2000). They are capable of binding to other LIM-HD proteins as well as other proteins, transcription factor families, and kinases (Bach 2000). The diversity of binding partners allows for participation in a wide range of developmental events. For example, LIM-HD proteins can form complexes with POU-HD transcription factors to repress gene transcription, while forming complexes with RLIM factors leading to transcriptional activation. They also interact with the Lbd (Lim domain-binding protein 1) co-factor family, which greatly increases their ability to affect gene transcription. Lbd proteins intrinsically dimerize and allow LIM-HD proteins to interact with specific regulatory proteins like Otx2 or Isl1 (Hobert & Westphal, 2000). In addition, Ldb proteins can form either homodimers or heterodimers to further diversify the combination of complexes that can assemble.

The LIM-HD transcription factor, Isl1, has been studied in many tissues including cardiac and skeletal muscle, pancreas, kidney, brain, and spinal cord. It has been shown to bind and regulate insulin promoters and has been implicated as a key component of motor neuron specification (Ando, Shioda, Handa, & Kataoka, 2003). Isl1 has been shown to play a role in the differentiation of bipolar cells, cholinergic amacrine cells, and retinal ganglion cells (RGCs) in the developing retina: when Isl1 is conditionally knocked out of the embryonic retina, these cell types are born, but later are not detectable and therefore either died or switched fates (Elshatory et al.,

2007a). This implicates *Isl1* as a gene that could be important for cells to maintain a differentiated state.

Recently, two alternatively spliced isoforms of Isl1, the canonical alpha form (α) and alternative beta (β) form, were described in pancreatic cell lines (Ando et al., 2003). The Isl1 β isoform is missing 23 amino acids in the C-terminus that corresponds to the protein-binding domain LBD (Lhx3-binding domain). Figure 1A shows the two isoforms of Isl1 and highlights the missing amino acids in the Isl1 β isoform. The two isoforms are of interest because Isl1 forms a well characterized transcriptional ternary complex with two other proteins, Lhx3 and Ldb1 (Isl1:Lhx3:Ldb1) (Figure 1B). Therefore, the absence of this Lhx3-binding domain in Isl1 β suggests there may be functional differences between the two isoforms of Isl1, such as their ability to form transcriptional complexes and activate gene targets.

Both isoforms of *Isl1* are expressed in the developing mouse retina and persist into adulthood (Whitney, 2013). Reverse transcriptase PCR with a primer pair capable of amplifying both *Isl1* transcripts showed that *Isl1* α and *Isl1* β are expressed in the mouse retina at E12.5, E14.5, P1 and adulthood (Figure 2A). Quantitative RT-PCR also showed that *Isl1* α is also more abundant than *Isl1* β and this difference becomes more pronounced as development proceeds (Figure 2B; Whitney, 2013). Both isoforms are also present in other central nervous system tissue such as the brain and spinal cord. Western blots using an antibody recognizing both isoforms, Isl1-Pan, confirmed that both of these proteins are expressed in the retina (Figure 3A).

Isl1 isoform immunostaining from adult retinal tissue reveals a population of retinal ganglion cells that only express the Isl1β isoform (Whitney, 2013). An Isl1 antibody w as produced and its specificity was confirmed in Western blots of HEK293T cells that were transfected with overexpression plasmids designed to express Isl1α, Isl1β, and Lhx3 proteins (Figure 3B). Since no Isl1β-specific antibody exists, Isl1β cells are recognized as Isl1-Pan-positive and Isl1α-negative cells. Figure 4A shows a subset of RGCs that are Isl1-Pan-positive as well as Isl1α-negative RGCs, indicating they are a population of RGCs that only express Isl1β (blue). These cells were also ChAT-negative and therefore were verified as RGCs and not displaced cholinergic amacrine cells. These Isl1β RGCs make up 25.7% of all Isl1-Pan-positive cells within the GCL (Whitney, 2013).

Isl1β is not equally distributed across all RGC subtypes as they are restricted to certain ranges of soma size, in dicating that they might be indicative of particular cell types. At least 22 morphologically distinct RGC cell types have been described (Volgyi et al., 2009) and they range from a soma size of roughly 60μm² to 600μm². (Coombs et al., 2009) The soma sizes of Isl1-Pan-positive cells within the GCL were found to be in the range from about 50μm² to 300μm² but Isl1β RGCs, however, are restricted to the range of RGCs under 175μm² (Figure 4B). These cells are likely from multiple subsets of RGCs since they were found to be randomly spaced from one another while single populations of RGCs exhibit non-random spacing (Whitney, 2013). This data suggests that the presence of different isoforms of Isl1 may play an important role in the differentiation of specific RGC subtypes.

Given the expression profile of Isl1 isoforms and the previous discovery of an Isl1 β -only popul ation of R GCs in the a dult r etina, we have hypothesize that each Isl1 isoform has a specific role in the development or differentiation of these RGCs. In addition, we speculate that Isl1 β is not capable of forming the same Isl1:Lhx3:Ldb1 complex as Isl1 α due to its missing functional domain. This paper seeks to evaluate the functional role of Isl1 alternative splicing in the developing retina.

Methods

Isl1α, Isl1β, Lhx3 Overexpression Plasmids

Gateway cloning (Invitrogen) was used to make $Isl1\alpha$ and $Isl1\beta$ overexpressing plasmids. The open reading frame (ORF) of $Isl1\alpha$ was amplified from adult mouse retinal cDNA using primers with attB adapter sequences. This product was gel-purified and inserted into a donor vector (pDONR221, Invitrogen) to create an empty vector using BP Clonase to mediate the BP recombination reaction. O ne Shot S tbl3 c hemically c ompetent E . c oli (Invitrogen) w ere transformed w ith this reaction, and k anamycin resistant clones were selected for overnight culture in LB broth. A QIAprep Spin Miniprep kit (Qiagen) was used to extract plasmid DNA from the bacteria, and the successful recombination of the $Isl1\alpha$ ORF into the donor vector was confirmed by restriction digest and sequencing. The $Isl1\alpha$ -containing entry vector was then recombined w ith a destination vector, using LR C lonase, and transformed into E . c oli for plasmid a mplification and purification, as described above. The destination vector, p Lenti C MV/TO G FP-Zeo D est (Campeau et al.,

2009; Addgene plasmid #17431), will express the gene of interest and GFP using two different c onstitutive C MV pr omoters. O nce t he s equence of t he ORF i n t he destination vector was validated, the plasmid was replicated and purified from E. coli using an EndoFree Plasmid Maxi kit (Qiagen). The Isl1β ORF was generated using deletion PCR, to remove the 69 nucleotides from Isl1α that are not present in Isl1β (Whitney, 2013). Once isolated, the Isl1β ORF was also cloned into the same destination vector described above, and large amounts were purified.

HEK293T Transfection and Luciferase Assay

HEK293T c ells w ere t ransiently transfected w ith c ombinations of experimental plasmids designed to express Is11α, Is11β, Lhx3, or GFP (control plasmid with n o gene of interest inserted). C ells were also co-transfected with a luciferase reporter that has been previously shown to be specifically activated by the Is11:Lhx3:Ldb1 complex (Hx:RE) as well as CMV-β-Galactosidase (β-Gal) (Lee et al., 2008). T he cells maintained in a media of high glucose (4.5g/L) DMEM plus 10% Fetal Bovine Serum, with penicillin (100 U/mL) and streptomycin (100 µg/mL), in a T 75 tissue culture flask. M edia was changed every two days and cells were passaged once per week or when cells reached 75% confluency. Cells were counted and plated in 12 well tissue culture plates at 150,000 cells per well and media was changed 24 hours later. 48 hours post-plating, cells were transiently transfected with the transfection reagent TurboFect (Thermo Scientific). 250ng of Hx:RE reporter plasmid, 20ng of β-Gal, and 400ng of experimental plasmids were transfected into

each well, and the transfectant was removed 1 6 hours later. Cell lysates were collected 24 hours from the start of transfection.

Cell lysates were assayed for luciferase (Promega) and β -Gal activity on a Perkin-Elmer p late r eader, and 3 w ells of the same c ondition were assayed and averaged to serve as internal experimental replicates. Luciferase units were corrected by subtraction of untransfected well units, and then were normalized using β -Gal. Each bar represents mean fold induction with respect to the β -Gal control and error bars represent SEM. Results are representative of three independent experiments. A one-way AN OVA and Tukey's post-hoc test were used to determine significance. Asterisks indicate a significant difference with a p-value <0.05.

Protein Collection

For luciferase assays, HEK293T cells were lysed in 100ul per well of cold 1X Passive Lysis Buffer (Promega). Cells were lifted from plate with cell scraper, vortexed, and centrifuged at 12,000g for two minutes at 4°C. Protein lysates were stored at -80°C.

Results

Transcriptional Activation of Isl1 Isoforms

Since t he t wo i soforms of Isl1 w ere f ound t o be e xpressed i n di fferent populations of R GCs, f unctional di fferences between t hese t wo pr oteins w ere assessed using a transcriptional activation assay. A luciferase assay was used to test

directly if the two Isl1 is oforms function distinctly in their ability to regulate gene expression. HEK293T cells were transfected with either the Isl1 α or Isl1 β isoform, as well as Lhx3, to allow the Isl1 complex to form (HEK293T endogenously express Ldb1). In a ddition, cells were co-transfected with a H examer R esponse E lement (Hx:RE) luciferase reporter that has been shown to be activated specifically by the formation of this complex (Lee et al., 2003). The Hx:RE plasmid was previously shown to have a DNA sequence specific to the Isl1:Lhx3:Ldb1 complex that is not recognized by either Isl1 or Lhx3 alone (Lee et al., 2008).

The activation of luciferase by the Isl1 α :Lhx3:Ldb1 complex was found to be 5 f old greater than the Isl1 β :Lhx3:Ldb1 c omplex (Figure 5) a nd t his luciferase activation in Lhx3+Isl1 α overexpressing cells was significantly d ifferent f rom Lhx3+Isl1 β and all other conditions (p-value = 0.035), w hile activation of Lhx3+Isl1 β was i ndistinguishable f rom Lhx3 a lone. T hese da ta de monstrate a functional difference between the two isoforms of Isl1, and furthermore suggest that the β isoform might not be capable of forming a complex with Lhx3 and Ldb1.

Discussion

This paper identified that through a Iternative splicing, the *Isl1* gene creates two functionally distinct isoforms. This luciferase a ssay is the first demonstration that Isl1 isoforms have different transcriptional activation abilities and therefore, are likely contributing to the differentiation of RGC subtypes. This finding allows for a deeper understanding of how the retina forms and provides first direct evidence for

the importance of having two isoforms of Isl1, as Isl1 α was shown to a ctivate the Isl1:Lhx3:Ldb1 complex significantly more robustly than Isl1 β . The data also show that the Isl1 β isoform does not further enhance activation binding of Lhx3 and Ldb1. It remains unknown how Isl1 β is functioning in specific RGC subtypes. Perhaps it is forming a unique complex with other LIM-HD transcription factors and binds to a unique promoter sequence distinct from the Isl1:Lhx3:Ldb1 complex.

The d ata p resented i n t his pa per e nhances what w as know n a bout t he developmental expression profile and protein localization of Isl1 α and Isl1 β in the retina (Whitney, 2013). It was previously shown that Isl1 β is present in a subset of RGCs, but the mechanism by which Isl1 β is contributing to the differentiation of these cells remains unclear (Whitney, 2013). We can now confidently presume that the Isl1 isoforms are contributing to RGC differentiation given their ability to regulate gene t ranscription t hrough different m echanisms. These results suggest that alternative splicing of Isl1 creates different is oforms which differ in their ability to alter gene t ranscription, and that this difference may contribute to retinal differentiation.

The current findings allow for expansion of the combinational code of LIM-HD transcription factors. It was previously known that a complex of Isl1, Lhx3, and Ldb1 p roteins c ause cells be come m otorneurons, w hile w ith Lhx3 and Ldb1 complexes, w ithout Isl1, be come V 2 i nterneurons (Bhati et a l., 200 0). These complexes were shown to bind to different transcriptional promoter sequences and provided the first demonstration that Isl1 plays a role in fate determination in the

periphery. Given that Isl1 isoforms also function distinctly in the developing retina, this f urther e xpands t he pot ential num ber of LIM-HD complexes t hat Isl1 c an complex w ith, a nd o ffers in sight in to the extent of cell type d iversity w ithin the developing nervous system.

Until this study, Isl1 isoforms had only been identified in the earlier described pancreatic cell lines (Bhati et al, 2000). Isl1 alternative splicing is conserved between mice and rat species, but is not conserved be tween rodents and humans. This is surprising given 100% homology of their protein sequences, but it remains unclear if there are splice variants in humans that exhibit similar functions. In the retina, Isl1 has also been shown to interact with other transcription factors and form complexes independent of Isl1:Lhx3:Ld1b. F or e xample, Isl1 bi nds t o a P OU dom ain transcription f actors l ike P ou4f2 a nd B rn3b, a nd t hey c o-regulate t arget g enes i n developing R GCs (Pan et al., 2008 & Li et al., 2014). Isl1 also participates in protein-protein i nteractions i n ot her c ellular t issues. F or i nstance, Isl1 pr omotes insulin-gene t ranscription by direct binding to the basic he lix-loop-helix (bHLH) transcription factor, BETA2 (Peng et al, 2005). In addition, Isl1 binds to the estrogen receptor in the rat arcuate nucleus and implicates Isl1 as a player in controlling brain function via interaction with steroid hormones (Gay et al., 2000). Lastly, Isl1 has been documented to influence gene transcription by binding with multiple factors to form "enhancer c omplexes" that bind to specific intronic sequences within other genes. Isl1 complexes with two transcription factors, TBX20 and GATA4, and this

binding t o t he *FGF10* gene c auses r egulation o f d ownstream t argets af fecting development of cardiac outflow muscles in humans (Golzio et al., 2012).

The idea of alternative splicing as a mechanism for directly creating neuronal diversity through differentiation is a relatively new idea. The retinoid-related orphan receptor (Rorb) was described to have two isoforms that are expressed at different time points in development and directly affect neuronal differentiation (Liu et al., 2013). Pax6, a critical transcription factor to eye development, has an alternatively spliced isoform that is necessary for proper development of retina architecture (Azuma et al., 2005). Alternatively spliced isoforms can also be expressed during varied developmental windows implicating isoform-specific physiological roles. For example, the two PAC1-R isoforms, Hip and Hop1, have varied expression patterns throughout postnatal retinal development and are likely playing distinct in structive roles (Denes et al., 2014).

Isl1 is not the only LIM-HD transcription factor with known alternative isoforms; Lhx9 and Lhx7 have a lso be endocumented, but their effect on retinal development still remains to be explored (Failli et al, 2000). Since LIM-HD proteins are able to interact with one another though binding of their hom eodomains, it is unclear if any of these other transcription factor family members may be interacting with Isl1. Given the findings of this paper, it would be prudent to explore the role of Isl1 isoforms in forming complexes with other documented binding partners in the retina.

While a functional difference was shown between the two isoforms of Isl1, further studies are needed to assess the consequence of this *in vivo*. One way this could be accomplished is by creating conditional-knockout mice that are genetically engineered to lack both of the Isl1 isoforms in the retina by utilization of Cre-Lox technology. Cells from these same animals can be electroporated to re-introduce one of the isoforms and explore the functional consequence of just having one specific Isl1 isoform. One caveat to this experiment is that mice lacking Isl1 specifically in the retina have previously been shown to have the birth of all cell types followed by subsequent de ath or switching of f ate (Elshatory et al., 2007b), therefore electroporation experiments would need to occur *in utero* before these events occur. Given that Isl1 β is endogenously expressed in much lower quantities than Isl1 α , retinas from Isl1 β -only rescue retinas may provide striking *in vivo* insight into the function of *Isl1* alternative splicing.

This pa per pr ovides t he f irst e vidence t hat Isl1 i soforms ha ve di ffering activational abilities and therefore suggests a possible role for the alternative splicing of *Isl1* in the differentiation of RGCs, c ontributing to ne uronal diversity. Further studies are needed to elucidate the mechanism by which each is oform is helping to specify the cell fate of their cells they are present in.

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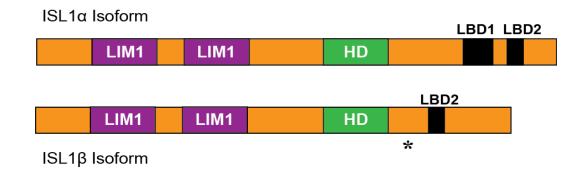
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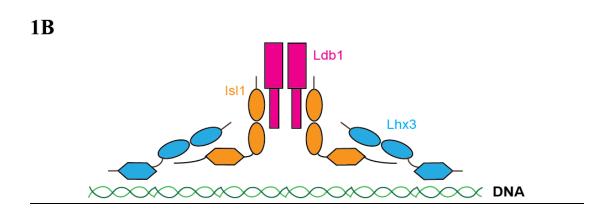
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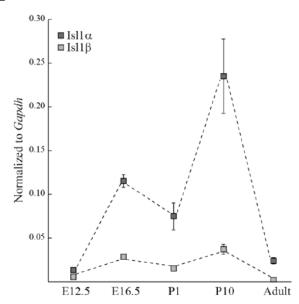


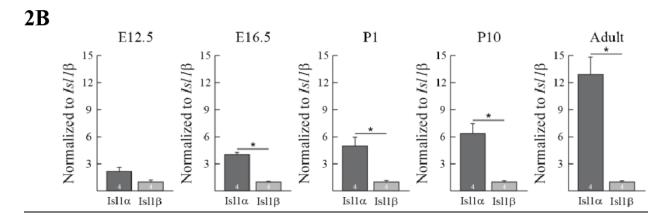


Structure of Isl1 isoforms and Isl1 transcriptional complex. (**A**). Isl1 β is missing 23 amino acids that correspond to one of the Lhx3-binding domains (Ldb1) with which Isl1 binds to Lhx3. A sterisk denotes region of missing amino acids in Isl1 β , relative to Isl1 α (**B**). Hexameric transcriptional complex formed with Ldb1 dimer (pink), Isl1 (orange), and Lhx3 (blue). Figure adapted from Matthews et al., 2006.

Figure 2





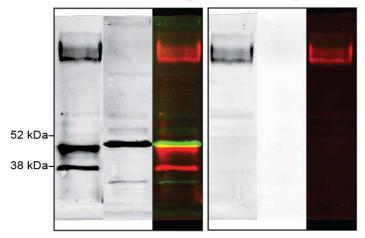


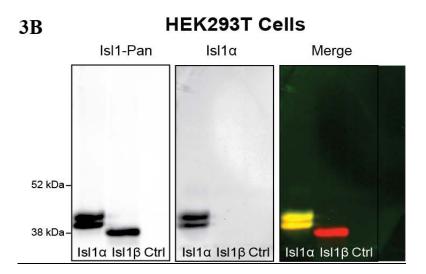
Developmental expression of Isl1 isoforms. (**A**). RT-PCR with Isl1 isoform-specific primers with values normalized to Gapdh, a housekeeping gene. (**B**). qPCR (real time RT-PCR) showing fold increase of Isl1 α expression over Isl1 β expression. A two-way mixed ANOVA and post-hoc t-test show Isl1 α expression is significantly higher than Isl β at E16.5, P1, P10, and adult (p-value <0.05). F igure taken from Whitney dissertation, 2013.

Figure 3



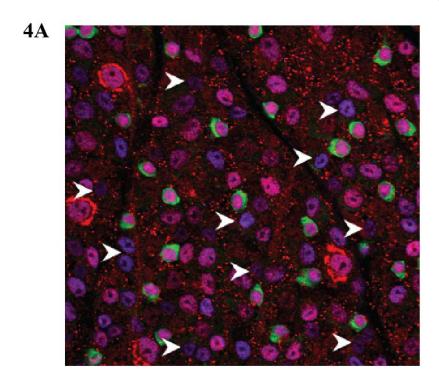
Isl1-Pan Isl1α Merge No Primary Control

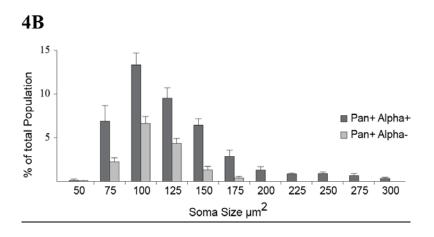




Immunoblotting of HEK293T cells and a dult retinal extracts for Isl1 with Isl1-Pan and Isl1 α antibodies. (A). Immunoblotting adult retinal lysates show overlap, though not complete, of the Isl1 α antibody band with the Isl1-Pan alpha antibody band. (B). HEK293T cells were used to specify Isl1-Pan and Isl1 α antibodies. Bands for Isl1 α (smaller kDa) and Isl1 β at 39 kDa and 36 kDa correspond to the predicted molecular weights, r espectively. The l arger band in the doublet r ecognized by the Isl1-Pan antibody corresponds to a phosphorylated version of the protein that is not recognized by the Isl1 α antibody. Figure taken from Whitney dissertation, 2013.

Figure 4

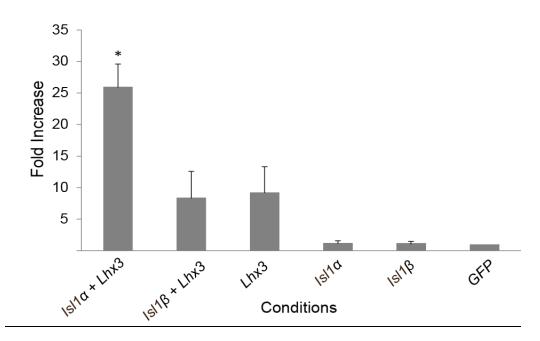




Soma size analysis of Isl1 β -positive cells. (**A**). Representative image showing Isl β -only cells in blue (white arrowheads). Isl1 α -positive cells are r ed, C hAT-positive cells are green, and Isl1-Pan -positive cells are blue. Isl1 β -only cells were identified as cells being Isl1-Pan-positive and Isl1- α -negative. (**B**). Soma size was measured from about 2000 cells in 8 fields in the ganglion cell layer of one retina. Isl1 β -only cells soma sizes range from about 50 μ m² to 175 μ m², compared to Isl1-Pan-positive soma sizes ranging from 50 μ m² to 300 μ m². F igure adapted f rom Whitney dissertation, 2013.

Figure 5





Transcriptional a ctivation of Isl1 i soforms a ssessed b yl uciferase assay. (A). Isl1 α +Lhx3 has ~20 fold increase over Isl1 β +Lhx3 in the ability to turn on transcription of the Hx:RE luciferase reporter. Isl1 α +Lhx3 is significantly different from all other conditions (asterisk denotes p-value <0.05). All results normalized to GFP.